		RPKM									Leaf PEG vs Leaf Mock			Leaf NaCl vs Leaf Mock			Stem PEG vs Stem Mock			Stem NaCl vs Stem Mock			Root PEG vs Root Mock			Root NaCl vs Root Mock										
Unigene ID	Unigene Lengt	Leaf Mock	Leaf PEG	Leaf NaCl	Stem Mock	Stem PEG	Stem NaCl	Root Mock	Root PEG	Root NaCl	log2 ratio	FDR	Change call	log2 ratio	FDR	Change call	log2 ratio	FDR	Change call	log2 ratio	FDR	Change call	log2 ratio	FDR	Change call	log2 ratio	FDR	Change call	Annotation	TIAR9 hit	Cotton EST hit	Transcripion factor fa	KO pathway	GO term	Transcript direction
Unigene10_All	4154	1.32	3.51	2.09	2.91	3.12	2.66	5.23	6.19	5.83	1.41E+00	1.28E-18	Up	6.60E-01	1.16E-03		9.71E-02	5.98E-01		-1.30E-01	5.02E-01		2.42E-01	1.50E-02		1.57E-01	1.36E-01		Unigene10_All//gi|124359633|gb|ABD32307.2|//0.00E+00//Nuclear factor related to kappa-B-binding protein , related [Medicago truncatula]	Unigene10_All//0.00E+00//AT3G45830| unknown protein	Unigene10_All//0.00E+00//ES821330				nr -
Unigene1000_All	2008	87.26	13.58	26.60	63.88	44.18	35.38	8.19	1.00	2.84	-2.68E+00	0.00E+00	Down	-1.71E+00	1.75E-280	Down	-5.32E-01	7.13E-38		-8.53E-01	9.16E-77		-3.04E+00	4.49E-67	Down	-1.53E+00	1.01E-29	Down	Unigene1000_All//gi|201969007|gb|AA867625.2|//1.00E-139//expressed protein [Arabidopsis thaliana]	Unigene1000_All//3.00E-141//AT1G29050| unknown protein	Unigene1000_All//0.00E+00//TC170634				nr -
Unigene100003_All	343	0.00	0.59	0.00	1.60	1.61	0.53	1.85	0.00	0.00	9.21E+00	1.38E-01		null	null		7.90E-03	9.83E-01		-1.60E+00	1.32E-01		-1.09E+01	1.24E-04	Down	-1.09E+01	7.13E-05	Down			Unigene100003_All//7.00E-15//C0112306				
Unigene100006_All	344	0.00	1.77	0.93	0.00	9.01	0.00	0.00	0.00	0.00	1.08E+01	1.17E-03		9.86E+00	4.54E-02		1.31E+01	1.41E-19	Up	null	null		null	null		null	null									
Unigene100007_All	345	0.00	0.59	0.15	0.00	1.80	0.00	0.00	0.12	0.23	9.20E+00	1.38E-01		7.27E+00	6.43E-01		1.08E+01	7.90E-04	Up	null	null		6.92E+00	6.41E-01		7.85E+00	4.07E-01									
Unigene10002_All	315	0.00	0.00	2.54	0.47	0.44	2.15	0.27	0.27	0.25	null	null		1.13E+01	1.72E-04	Up	-1.18E-01	9.12E-01		2.18E+00	3.15E-02		-1.62E-02	1.02E+00		-8.58E-02	9.75E-01		Unigene10002_All//gi|297817888|ref|XP_002876827.1|//3.00E-122//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297322265|gb|EFH53086.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene10002_All//2.00E-122//AT2G02750| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene100031_All	352	0.15	0.14	0.61	3.11	0.98	0.26	1.92	0.48	0.68	-4.64E-02	9.88E-01		2.03E+00	3.62E-01		-1.67E+00	9.38E-03		-3.60E+00	5.03E-05	Down	-2.02E+00	1.98E-02		-1.50E+00	5.44E-02		Unigene100031_All//gi|297598339|ref|NP_001045426.2|//6.00E-111//Os01g0953100 [Oryza sativa Japonica Group] >gi|255674080|db|BAF07340.2| Os01g0953100 [Oryza sativa Japonica Group]	Unigene100031_All//4.00E-13//AT5G45480| unknown protein					nr -
Unigene100049_All	362	0.58	1.68	0.88	1.65	5.23	6.99	0.00	0.35	0.33	1.54E+00	1.22E-01		6.10E-01	6.25E-01		1.66E+00	6.50E-04	Up	2.08E+00	2.87E-06	Up	8.44E+00	2.41E-01		8.37E+00	2.44E-01				Unigene100049_All//2.00E-117//EX165874				ESTscan +
Unigene10005_All	326	0.00	4.82	3.43	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.71E-09	Up	1.17E+01	3.44E-06	Up	null	null		null	null		null	null		null	null		Unigene10005_All//gi|226463414|gb|EEH59706.1|//5.00E-07//predicted protein [Micromonas pusilla CCMP1545]						nr -
Unigene100054_All	366	0.00	0.00	0.00	0.00	19.57	0.00	0.00	0.00	0.00	null	null		null	null		1.43E+01	4.05E-46	Up	null	null		null	null		null	null				Unigene100054_All//1.00E-176//TC177439				
Unigene100057_All	368	0.14	0.14	0.58	0.68	1.87	0.61	1.95	0.11	0.22	-4.64E-02	9.88E-01		2.03E+00	3.62E-01		1.47E+00	1.16E-01		-1.41E-01	9.29E-01		-4.10E+00	2.92E-04	Down	-3.17E+00	8.10E-04	Down			Unigene100057_All//5.00E-13//TC176573				ESTscan +
Unigene100060_All	369	1.84	0.00	1.15	0.27	2.05	0.61	0.46	0.45	0.54	-1.08E+01	4.10E-04	Down	-6.75E-01	4.41E-01		2.93E+00	4.37E-03		1.18E+00	5.50E-01		-1.65E-02	1.02E+00		2.36E-01	8.84E-01		Unigene100060_All//gi|8778340|gb|AAF79348.1|AC007887.7|//2.00E-111//F15O4.13 [Arabidopsis thaliana]						nr +
Unigene100062_All	370	0.28	0.27	0.00	0.27	2.98	0.98	0.00	0.00	0.00	-4.61E-02	9.91E-01		-8.14E+00	4.00E-01		3.47E+00	6.96E-05	Up	1.86E+00	2.20E-01		null	null		null	null		Unigene100062_All//gi|57282623|emb|CAE54309.1|//3.00E-66//peroxidase [Gossypium hirsutum]	Unigene100062_All//9.00E-37//AT4G29980| cationic peroxidase, putative	Unigene100062_All//0.00E+00//gi|21093393|gb|BQ405706.1|BQ405706		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene100069_All	375	0.84	0.00	0.00	0.13	1.19	2.29	0.68	0.33	0.00	-9.71E+00	3.67E-02		-9.71E+00	4.94E-02		3.17E+00	3.95E-02		4.11E+00	3.41E-04	Up	-1.02E+00	4.96E-01		-9.40E+00	3.06E-02								ESTscan -
Unigene100076_All	381	0.27	2.66	1.12	0.26	0.90	0.71	0.78	0.22	0.00	3.28E+00	3.79E-04	Up	2.03E+00	1.40E-01		1.79E+00	2.58E-01		1.44E+00	4.10E-01		-1.82E+00	2.11E-01		-9.60E+00	1.59E-02		Unigene100076_All//gi|75213194|sp|Q9SX85.1|SEC3A_ARATH//3.00E-32//RecName: Full=Exocyst complex component SEC3A >gi|5668806|gb|AAD46032.1|AC007519_17 Strong similarity to F16N3.17 from Arabidopsis thalian BAC gb|AC007519 [Arabidopsis thaliana]	Unigene100076_All//1.00E-33//AT1G47550| unknown protein	Unigene100076_All//0.00E+00//ES798551				nr +
Unigene100077_All	381	3.02	1.60	0.00	1.05	1.54	1.19	0.00	0.00	0.00	-9.21E-01	1.43E-01		-1.16E+01	2.60E-06	Down	5.55E-01	6.00E-01		1.81E-01	8.84E-01		null	null		null	null		Unigene100077_All//gi|3513745|gb|AAC33961.1|//2.00E-68//contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]	Unigene100077_All//1.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene100077_All//1.00E-25//gi|164240898|gb|ES823879.1|ES823879				nr +
Unigene100078_All	381	0.00	0.13	0.42	0.52	3.16	1.19	0.00	0.11	0.63	7.06E+00	6.24E-01		8.71E+00	2.40E-01		2.60E+00	3.41E-04	Up	1.18E+00	3.38E-01		6.78E+00	6.41E-01		9.29E+00	4.41E-02		Unigene100078_All//gi|297826769|ref|XP_002881267.1|//1.00E-40//TMS membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327106|gb|EFH57526.1| TMS membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene100078_All//2.00E-41//AT2G33205| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: TMS membrane protein/tumour differentially expressed protein (InterPro:IPR005016); BEST Arabidopsis thaliana protein match is: MEE55 (maternal effect embryo arrest 55) (TAIR:AT4G13345.1); Has 602 Blast hits to 593 proteins in 136 species: Archae - 0; Bacteria - 0; Metazoa - 380; Fungi - 90; Plants - 84; Viruses - 0; Other Eukaryotes - 48 (source: NCBI BLink).	Unigene100078_All//1.00E-72//TC144118				nr +
Unigene100081_All	383	1.23	1.06	0.56	0.13	1.98	1.06	0.00	0.00	0.00	-2.16E-01	8.17E-01		-1.14E+00	3.32E-01		3.93E+00	9.79E-04	Up	3.03E+00	6.04E-02		null	null		null	null		Unigene100081_All//sp|P16679|PHNL_ECOLI//6.00E-14//Phosphonates transport ATP-binding protein phnL OS=Escherichia coli (strain K12) GN=phnL PE=1 SV=1	Unigene100081_All//5.00E-05//AT5G61730| ATATH11: ATPase, coupled to transmembrane movement of substances / transporter					swissprot -
Unigene100083_All	384	0.00	0.26	0.00	0.00	2.24	0.00	0.00	0.00	0.00	8.04E+00	3.92E-01		null	null		1.11E+01	2.76E-05	Up	null	null		null	null		null	null		Unigene100083_All//gi|115438943|ref|NP_001043751.1|//2.00E-24//Os01g0655400 [Oryza sativa Japonica Group] >gi|55773937|dbj|BAD72325.1| eukaryotic translation initiation factor 3 subunit 10-like [Oryza sativa Japonica Group] >gi|113533282|dbj|BAF05665.1| Os01g0655400 [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr -
Unigene100086_All	385	1.90	0.00	2.49	2.20	3.49	1.29	0.77	0.43	0.83	-1.09E+01	2.11E-04	Down	3.88E-01	6.08E-01		6.65E-01	2.81E-01		-7.69E-01	3.34E-01		-8.24E-01	5.41E-01		1.07E-01	9.46E-01		Unigene100086_All//gi|30684737|ref|NP_196912.2|//1.00E-32//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|223635762|sp|Q9FM|2.2|PP380_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g14080	Unigene100086_All//6.00E-27//AT5G14080| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene100089_All	385	0.00	0.53	0.00	0.00	13.24	0.00	0.00	0.00	0.00	9.04E+00	1.38E-01		null	null		1.37E+01	1.36E-32	Up	null	null		null	null		null	null		Unigene100089_All//gi|116309014|emb|CAH66131.1|//4.00E-11//OS16G0413500L.5 [Oryza sativa (indica cultivar-group)]	Unigene100089_All//2.00E-06//AT3G09510| nucleic acid binding	Unigene100089_All//2.00E-163//TC177439				nr +
Unigene10009_All	669	0.00	1.51	0.24	0.07	0.62	0.20	0.76	0.94	2.14	1.06E+01	7.26E-06	Up	7.90E+00	2.40E-01		3.05E+00	5.68E-02		1.44E+00	6.41E-01		3.05E-01	7.04E-01		1.50E+00	2.97E-03				Unigene10009_All//8.00E-07//GE653373				
Unigene100108_All	395	0.40	0.51	0.40	0.13	2.18	0.00	0.11	0.42	0.00	3.69E-01	8.17E-01		2.52E-02	1.00E+00		4.11E+00	2.61E-04	Up	-6.98E+00	6.47E-01		1.98E+00	3.80E-01		-6.74E+00	6.21E-01									
Unigene10011_All	387	0.00	0.00	0.14	0.00	0.18	0.23	2.29	1.51	0.10	null	null		7.10E+00	6.43E-01		7.48E+00	6.18E-01		7.87E+00	4.84E-01		-6.02E-01	3.85E-01		-4.48E+00	1.24E-05	Down	Unigene10011_All//gi|255590973|ref|XP_002535407.1|//1.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223523200|gb|EEF26976.1| conserved hypothetical protein [Ricinus communis]	Unigene10011_All//2.00E-06//AT5G53840| F-box family protein (FBL13)					nr +
Unigene100114_All	399	0.52	0.13	1.07	0.12	1.90	0.23	0.32	0.31	0.20	-2.05E+00	3.34E-01		1.03E+00	3.97E-01		3.93E+00	9.79E-04	Up	8.59E-01	7.98E-01		-1.64E-02	1.02E+00		-6.71E-01	7.21E-01				Unigene100114_All//5.00E-07//ES811668				
Unigene100117_All	401	0.00	0.63	0.00	0.00	2.15	0.68	0.00	0.31	0.10	9.30E+00	7.89E-02		null	null		1.11E+01	2.76E-05	Up	9.40E+00	7.07E-02		8.29E+00	2.41E-01		6.63E+00	6.51E-01									
Unigene100122_All	406	0.00	1.00	0.92	0.00	17.13	0.00	0.00	0.00	0.00	9.96E+00	1.36E-02		9.84E+00	2.51E-02		1.41E+01	9.15E-45	Up	null	null		null	null		null	null									
Unigene100125_All	408	0.00	0.50	0.00	2.20	3.04	0.00	0.41	0.00	0.10	8.96E+00	1.38E-01		null	null		4.67E-01	4.92E-01		-1.11E+01	1.21E-05	Down	-8.70E+00	1.35E-01		-2.09E+00	3.14E-01		Unigene100125_All//gi|195621986|gb|ACG22823.1|//6.00E-24//BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor [Zea mays]	Unigene100125_All//3.00E-19//AT3G26700| protein kinase family protein	Unigene100125_All//0.00E+00//C0071070		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism		nr -
Unigene100132_All	420	1.00	0.60	0.76	0.47	3.85	0.11	0.30	0.20	0.00	-7.24E-01	5.26E-01		-3.90E-01	7.18E-01		3.02E+00	2.63E-06	Up	-2.14E+00	3.48E-01		-6.02E-01	7.68E-01		-8.24E+00	2.01E-01		Unigene100132_All//gi|295815790|gb|ADG36380.1|//4.00E-22//promoter-binding protein SPL9 [Vitis vinifera]		Unigene100132_All//1.00E-171//gi|78343657|gb|DT563931.1|DT563931				nr +
Unigene10014_All	680	0.15	0.00	0.16	0.15	0.41	0.00	3.05	0.68	1.46	-7.27E+00	3.78E-01		2.51E-02	1.00E+00		1.47E+00	4.20E-01		-7.19E+00	4.06E-01		-2.17E+00	1.96E-06	Down	-1.06E+00	6.48E-03		Unigene10014_All//gi|9739011|gb|AAF97863.1|//5.00E-68//outward-rectifying potassium channel KCO1 [Eucalyptus camaldulensis]	Unigene10014_All//7.00E-66//AT5G55630| ATKC01: calcium-activated potassium channel/ ion channel/ outward rectifier potassium channel	Unigene10014_All//1.00E-138//TC135368			GO:0005227//GO:0005249//GO:0006875//GO:0009845//GO:0010118//GO:0030001//GO:0031090//GO:0031224//GO:0046872//GO:0051259	nr -
Unigene100141_All	438	1.19	0.23	0.24	0.68	2.20	2.89	0.00	1.34	0.18	-2.37E+00	4.76E-02		-2.30E+00	6.77E-02		1.69E+00	2.52E-02		2.08E+00	1.96E-03		1.04E+01	2.82E-04	Up	7.51E+00	4.07E-01		Unigene100141_All//gi|225458882|ref|XP_002283431.1|//3.00E-09//PREDICTED: hypothetical protein [Vitis vinifera] >gi|302142175|emb|CBI19378.3| unnamed protein product [Vitis vinifera]		Unigene100141_All//0.00E+00//DW512687				nr -
Unigene100147_All	444	0.47	0.11	0.00	1.91	1.24	0.10	0.57	1.22	0.27	-2.05E+00	3.34E-01		-8.88E+00	1.47E-01		-6.20E-01	4.13E-01		-4.23E+00	2.18E-04	Down	1.10E+00	2.36E-01		-1.09E+00	4.29E-01				Unigene100147_All//5.00E-07//DW519735				
Unigene100149_All	446	0.00	0.00	0.00	0.00	3.01	0.51	0.00	0.00	0.00	null	null		null	null		1.16E+01	2.67E-08	Up	8.98E+00	1.19E-01		null	null		null	null		Unigene100149_All//gi|4001781|gb|AAC34980.1|//5.00E-62//cytochrome C oxidase subunit I [Ectocarpus sp.]	Unigene100149_All//6.00E-46//ATMG01360| cytochrome c oxidase subunit I	Unigene100149_All//2.00E-12//TC149581		ko00190|Oxidative phosphorylation		nr -
Unigene10015_All	336	0.00	7.84	2.69	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	5.45E-15	Up	1.14E+01	4.72E-05	Up	null	null		null	null		null	null		null	null		Unigene10015_All//gi|300175133|emb|CBK20444.2|//3.00E-07//Pyruvate Dehydrogenase E1 (subunit ?) [Blastocystis hominis]	Unigene10015_All//5.00E-05//AT5G50850| MAB1 (MACCI-BOU); catalytic/ pyruvate dehydrogenase (acetyl-transferring)			ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)//ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis		nr -
Unigene100150_All	446	0.00	0.00	0.00	0.00	3.78	0.91	0.00	0.00	0.00	null	null		null	null		1.19E+01	1.76E-10	Up	9.83E+00	1.37E-02		null	null		null	null		Unigene100150_All//gi|260766526|gb|ACX50285.1|//1.00E-32//cytochrome oxidase subunit I [Guillardia theta]	Unigene100150_All//4.00E-29//ATMG01360| cytochrome c oxidase subunit I			ko00190|Oxidative phosphorylation		nr -
Unigene10016_All	468	0.00	14.83	3.53	0.00	0.15	0.00	0.00	0.00	0.00	1.39E+01	1.15E-39	Up	1.18E+01	4.31E-09	Up	7.20E+00	6.18E-01		null	null		null	null		null	null									ESTscan -
Unigene100162_All	481	0.00	0.00	0.00	0.21	1.86	0.75	0.00	0.00	0.00	null	null		null	null		3.17E+00	8.78E-04	Up	1.86E+00	2.20E-01		null	null		null	null									
Unigene100163_All	483	0.11	0.00	0.33	1.24	1.07	0.00	0.88	0.00	0.00	-6.76E+00	6.24E-01		1.61E+00	5.12E-01		-2.11E-01	8.23E-01		-1.03E+01	7.71E-04	Down	-9.77E+00	3.26E-03		-9.77E+00	2.15E-03		Unigene100163_All//gi|54606737|dbj|BAD66760.1|//6.00E-06//orf120b [Beta vulgaris subsp. vulgaris] >gi|54606775|dbj|BAD66798.1| orf120b [Beta vulgaris subsp. vulgaris]		Unigene100163_All//8.00E-37//TC141826				nr +
Unigene100172_All	544	1.15	0.75	0.59	2.56	3.86	1.49	1.63	0.77	0.22	-6.31E-01	4.75E-01		-9.75E-01	3.16E-01		5.91E-01	2.02E-01		-7.79E-01	1.82E-01		-1.09E+00	1.07E-01		-2.89E+00	3.05E-04	Down	Unigene100172_All//gi|297799972|ref|XP_002867870.1|//3.00E-49//male sterility MS5 [Arabidopsis lyrata subsp. lyrata] >gi|297313706|gb|EFH44129.1| male sterility MS5 [Arabidopsis lyrata subsp. lyrata]	Unigene100172_All//6.00E-46//AT4G20900| MS5 (MALE-STERILE 5)					nr -

Unigene100173_All	559	0.00	0.73	0.00	0.00	3.08	0.73	0.00	0.00	0.00	9.50E+00	1.36E-02		null	null		1.16E+01	1.06E-10	Up	9.51E+00	1.37E-02		null	null		null	null		Unigene100173_All//gi|225703022|dbj|BAH30233.1//5.00E-46//cytochrome c oxidase subunit II [Haptoglossa sp. SZ03]	Unigene100173_All//5.00E-23//ATMG00160| cytochrome c oxidase subunit 2			ko00190|Oxidative phosphorylation		nr +
Unigene100175_All	591	0.09	0.51	0.00	0.00	2.56	0.00	0.00	0.00	0.00	2.54E+00	1.51E-01		-6.47E+00	6.37E-01		1.13E+01	2.18E-09	Up	null	null		null	null		null	null		Unigene100175_All//gi|297841083|ref|XP_002888423.1//8.00E-70//xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331264|gb|EFH64682.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene100175_All//5.00E-59//AT1G65550| xanthine/uracil permease family protein	Unigene100175_All//5.00E-11//TC129603				nr -
Unigene100176_All	602	1.30	0.00	0.18	5.05	2.00	0.23	0.70	0.07	0.13	-1.03E+01	1.09E-04	Down	-2.88E+00	6.35E-03		-1.33E+00	8.47E-05	Down	-4.49E+00	2.32E-15	Down	-3.34E+00	1.80E-02		-2.41E+00	3.94E-02		Unigene100176_All//gi|238909261|gb|ACR77749.1|//9.00E-77//12-oxophytodienoic acid 10,10-reductase [Astragalus sinicus]	Unigene100176_All//9.00E-75//AT1G76680| OPR1; 12-oxophytodienoate reductase	Unigene100176_All//5.00E-17//AI725636		ko00592|alpha-Linolenic acid metabolism		nr -
Unigene100180_All	665	0.00	0.00	0.00	0.00	2.74	0.54	0.00	0.00	0.00	null	null		null	null		1.14E+01	2.33E-11	Up	9.09E+00	2.38E-02		null	null		null	null		Unigene100180_All//gi|226347397|gb|ACO50109.1|//1.00E-76//elongation factor 1 alpha [Euglena longa]	Unigene100180_All//2.00E-62//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene100180_All//3.00E-12//TC143701				nr +
Unigene100181_All	784	0.00	0.00	0.00	0.00	2.99	0.69	0.00	0.00	0.00	null	null		null	null		1.15E+01	1.12E-14	Up	9.43E+00	2.46E-03		null	null		null	null		Unigene100181_All//gi|49147195|ref|XP_025788.1//2.00E-23//ATP synthase F0 subunit 6 [Pseudendoclonium akinetum] >gi|33439210|gb|AAQ18747.1| ATP synthase F0 subunit 6 [Pseudendoclonium akinetum]	Unigene100181_All//2.00E-08//ATMG00410| ATPase subunit 6			ko00190|Oxidative phosphorylation		nr -
Unigene100182_All	447	0.12	0.11	0.00	0.22	0.15	0.30	1.32	0.09	0.00	-4.51E-02	9.88E-01		-6.87E+00	6.37E-01		-5.33E-01	8.20E-01		4.43E-01	8.63E-01		-3.82E+00	1.79E-03		-1.04E+01	1.42E-04	Down				Unigene100182_All//8.00E-114//ES830419					
Unigene100186_All	292	4.30	3.82	10.76	7.68	4.84	8.35	3.33	1.57	2.32	-1.72E-01	7.55E-01		1.32E+00	4.53E-04	Up	-6.67E-01	1.08E-01		1.22E-01	7.81E-01		-1.08E+00	8.88E-02		-5.22E-01	3.89E-01		Unigene100186_All//gi|213990447|gb|ACJ60637.1|//2.00E-11//glutaredoxin S12 [Populus tremula x Populus tremuloides]	Unigene100186_All//6.00E-11//AT4G28730| glutaredoxin family protein	Unigene100186_All//2.00E-119//BG445794				nr +
Unigene100191_All	491	0.43	0.00	0.33	0.41	0.49	0.37	1.12	0.00	0.41	-8.74E+00	1.23E-01		-3.89E-01	8.08E-01		2.75E-01	8.96E-01		-1.42E-01	9.36E-01		-1.01E+01	4.62E-04	Down	-1.46E+00	9.77E-02		Unigene100191_All//gi|75146761|sp|Q84K11.1|PPP5_SOLLC//2.00E-55//RecName: Full=Serine/threonine-protein phosphatase 5; AltName: Full=LePP5 >gi|28141004|gb|AAO26213.1| type 5 protein serine/threonine phosphatase 62 kDa isoform [Solanum lycopersicum] >gi|28141085|gb|AAO26215.1| type 5 protein serine/threonine phosphatase 62 kDa isoform [Solanum lycopersicum]	Unigene100191_All//5.00E-47//AT2G42810| PP5,2 (PROTEIN PHOSPHATASE 5,2); phosphoprotein phosphatase/ protein binding / protein serine/threonine phosphatase	Unigene100191_All//2.00E-167//CO074097				nr +
Unigene100195_All	374	4.62	0.00	2.71	3.20	3.22	4.59	0.45	0.56	0.43	-1.22E+01	5.34E-10	Down	-7.71E-01	1.40E-01		1.17E-02	9.99E-01		5.22E-01	3.34E-01		3.05E-01	8.37E-01		-8.58E-02	9.67E-01					Unigene100195_All//3.00E-85//BF275481					
Unigene100196_All	376	3.48	3.77	3.26	1.06	2.56	2.52	1.01	4.45	1.17	1.17E-01	8.24E-01		-9.49E-02	8.72E-01		1.27E+00	8.43E-02		1.25E+00	9.60E-02		2.14E+00	3.22E-05	Up	2.04E-01	8.26E-01					Unigene100196_All//3.00E-131//TC172967					
Unigene100224_All	206	3.81	0.00	1.03	0.48	1.84	3.51	1.85	0.81	0.19	-1.19E-01	1.09E-04	Down	-1.88E+00	4.13E-02		1.93E+00	1.94E-01		2.86E+00	7.13E-03		-1.19E+00	3.10E-01		-3.26E+00	2.22E-02										
Unigene10024_All	305	0.00	1.00	1.75	0.00	0.11	0.00	0.55	3.01	3.40	9.96E+00	4.45E-02		1.08E+01	4.05E-03		6.82E+00	8.43E-01		null	null		2.44E+00	1.33E-03		2.61E+00	2.37E-04	Up									
Unigene10025_All	446	0.00	0.00	0.00	0.00	0.00	0.00	2.28	2.44	0.00	null	null		null	null		null	null		null	null		9.88E-02	8.71E-01		-1.12E+01	1.35E-07	Down	Unigene10025_All//gi|195606812|gb|ACG25236.1|//1.00E-66//60S ribosomal protein L3 [Zea mays] >gi|195619674|gb|ACG31667.1| 60S ribosomal protein L3 [Zea mays] >gi|195626206|gb|ACG34933.1| 60S ribosomal protein L3 [Zea mays] >gi|195641988|gb|ACG40462.1| 60S ribosomal protein L3 [Zea mays]	Unigene10025_All//3.00E-60//AT1G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	Unigene10025_All//6.00E-13//TC135599		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934	nr -
Unigene10028_All	568	0.00	0.00	0.00	0.44	0.55	0.32	2.90	1.47	0.35	null	null		null	null		3.15E-01	8.39E-01		-4.63E-01	7.45E-01		-9.80E-01	3.32E-02		-3.05E+00	1.31E-07	Down	Unigene10028_All//gi|324006679|gb|AAP80589.1|AP27702_1//1.00E-07//protease [Gossypium hirsutum]					GO:0003676//GO:0006259//GO:0008233	nr -
Unigene1003_All	1089	4.13	3.91	4.60	11.39	9.96	10.20	24.81	20.11	8.93	-8.02E-02	7.79E-01		1.54E-01	6.28E-01		-1.94E-01	2.78E-01		-1.59E-01	3.93E-01		-3.03E-01	1.36E-03		-1.47E+00	9.09E-46	Down	Unigene1003_All//gi|115441759|ref|NP_001045159.1|//2.00E-62//Os01g0911200 (Oryza sativa Japonica Group) >gi|113534690|dbj|BAF07073.1| Os01g0911200 (Oryza sativa Japonica Group)	Unigene1003_All//1.00E-54//AT4G21150| HAP6 (HAPLESS 6); dolichyl-diphosphooligosaccharide-protein glycotransferase	Unigene1003_All//0.00E+00//TC136242		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0005618//GO:0005789//GO:0006487//GO:0006950//GO:0031410	nr +
Unigene100305_All	321	2.12	4.42	6.30	2.48	4.51	3.80	1.05	4.82	4.10	1.06E+00	6.14E-02		1.57E+00	1.64E-03		8.60E-01	1.31E-01		6.14E-01	3.52E-01		2.19E+00	5.11E-05	Up	1.96E+00	5.04E-04	Up	Unigene100305_All//gi|30684602|ref|NP_850606.1|//2.00E-07//ATRBL14 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 14); zinc ion binding [Arabidopsis thaliana] >gi|75247670|sp|Q8RXW0.1|Y3761_ARATH RecName: Full=Uncharacterized protein At3g17611	Unigene100305_All//3.00E-12//AT3G17611| ATRBL14 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 14); zinc ion binding	Unigene100305_All//2.00E-116//gi|78346546|gb|DT566820.1|DT566820				nr -
Unigene10031_All	443	0.00	15.56	7.21	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	2.25E-39	Up	1.28E+01	1.15E-17	Up	null	null		null	null		null	null		null	null										
Unigene10032_All	274	13.75	4.99	9.33	16.00	23.50	19.78	96.60	86.79	79.97	-1.46E+00	1.16E-05	Down	-5.60E-01	9.29E-02		5.55E-01	1.45E-02		3.06E-01	2.81E-01		-1.54E-01	1.39E-01		-2.73E-01	3.59E-03					Unigene10032_All//2.00E-73//gi|48775848|gb|CO085214.1|CO085214					
Unigene100336_All	397	2.77	0.13	0.94	1.38	0.35	0.46	0.11	0.00	0.00	-4.44E+00	2.09E-05	Down	-1.56E+00	3.05E-02		-1.99E+00	5.13E-02		-1.60E+00	1.32E-01		-6.73E+00	6.68E-01		-6.73E+00	6.21E-01		Unigene100336_All//gi|50512303|gb|AAT77550.1|//1.00E-21//90C3 [Solanum pimpinellifolium]	Unigene100336_All//7.00E-07//AT3G53240| AtRLP45 (Receptor Like Protein 45); protein binding	Unigene100336_All//7.00E-09//gi|78354692|gb|DT574966.1|DT574966				nr +
Unigene10034_All	519	0.00	0.00	0.00	0.00	0.00	0.00	3.34	1.61	0.15	null	null		null	null		null	null		null	null		-1.05E+00	1.87E-02		-4.44E+00	1.94E-10	Down	Unigene10034_All//gi|19908695|gb|AM02970.1|AF421537_1/2.00E-86//beta-tubulin [Crypthecodinium cohnii]	Unigene10034_All//1.00E-70//AT1G75780| TUB1; GTP binding / GTPase/ structural molecule	Unigene10034_All//5.00E-32//TC141009		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene100353_All	206	0.00	4.18	0.00	0.00	0.67	0.66	0.62	0.81	0.58	1.20E+01	4.95E-05	Up	null	null		9.39E+00	3.21E-01		9.36E+00	3.14E-01		3.99E-01	8.15E-01		-8.57E-02	9.71E-01										
Unigene100355_All	246	2.98	8.86	8.66	3.44	2.66	19.09	386.71	542.50	1048.60	1.57E+00	6.61E-04	Up	1.54E+00	1.42E-03		-3.72E-01	6.06E-01		2.47E+00	1.25E-13	Up	4.88E-01	4.82E-34		1.44E+00	0.00E+00	Up	Unigene100355_All//gi|89258498|gb|ABD65462.1|//2.00E-26//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene100355_All//2.00E-16//AT2G47140| short-chain dehydrogenase/reductase (SDR) family protein	Unigene100355_All//2.00E-122//ES831528		ko00906|Carotenoid biosynthesis		nr +
Unigene10038_All	634	0.00	0.00	0.00	0.00	0.00	0.00	1.40	4.55	1.26	null	null		null	null		null	null		null	null		1.70E+00	1.80E-06	Up	-1.56E-01	7.94E-01		Unigene10038_All//gi|15227189|ref|NP_182322.1|//3.00E-59//RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase [Arabidopsis thaliana] >gi|75319082|sp|P92050.1|RKF3_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase RKF3; AltName: Full=Receptor-like kinase in flowers 3; Flags: Precursor >gi|1785621|emb|CAB06335.1| AtPK2324 [Arabidopsis thaliana] >gi|2463927|gb|AAC50045.1| receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi|14335116|gb|AAK59837.1| At2g48010/T9J23.16 [Arabidopsis thaliana] >gi|23308235|gb|AAN18087.1| At2g48010/T9J23.16 [Arabidopsis thaliana]	Unigene10038_All//6.00E-59//AT2G48010| RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase			ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism	GO:0004674//GO:0004713//GO:0004871//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene1004_All	2373	6.59	3.35	5.54	15.32	13.50	13.93	26.46	13.54	9.80	-9.76E-01	1.72E-11		-2.50E-01	1.08E-01		-1.83E-01	4.48E-02		-1.38E-01	1.74E-01		-9.66E-01	1.10E-52		-1.43E+00	9.45E-101	Down	Unigene1004_All//gi|297804040|ref|XP_002869904.1|//0.00E+00//ribophorin II family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315740|gb|EFH46163.1| ribophorin II family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1004_All//0.00E+00//AT4G21150| HAP6 (HAPLESS 6); dolichyl-diphosphooligosaccharide-protein glycotransferase	Unigene1004_All//0.00E+00//TC136242		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0005618//GO:0005789//GO:0006487//GO:0006950//GO:0031410	nr +
Unigene10040_All	235	2.67	11.00	4.31	2.54	0.73	0.77	0.36	0.36	0.17	2.04E+00	4.81E-06	Up	6.88E-01	3.42E-01		-1.80E+00	5.87E-02		-1.73E+00	9.04E-02		-1.65E-02	1.02E+00		-1.09E+00	6.79E-01										
Unigene10042_All	323	1.30	0.63	0.49	3.39	1.39	0.28	1.31	0.26	0.25	-1.05E+00	3.66E-01		-1.39E+00	2.80E-01		-1.29E+00	4.07E-02		-3.60E+00	5.02E-05	Down	-2.34E+00	5.47E-02		-2.41E+00	3.94E-02		Unigene10042_All//gi|147823314|emb|CAN77450.1|//2.00E-19//hypothetical protein [Vitis vinifera]		Unigene10042_All//3.00E-14//ES792704				nr -
Unigene10043_All	524	0.00	8.80	41.46	0.00	0.00	3.45	0.00	0.00	0.00	1.31E+01	2.84E-26	Up	1.53E+01	7.30E-123	Up	null	null		1.18E+01	8.92E-11	Up	null	null		null	null		Unigene10043_All//gi|270383724|dbj|BAI53120.1|//3.00E-83//ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [Eucalyptus globulus]	Unigene10043_All//1.00E-81//AT5G38430| ribulose bisphosphate carboxylase small chain 1B / RuBisCO small subunit 1B (RBCS-1B) (ATS1B)	Unigene10043_All//1.00E-23//gi|48752358|gb|CO082877.1|CO082877		ko00710|Carbon fixation in photosynthetic organisms//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005576//GO:0005840//GO:0006950//GO:0009526//GO:0009532//GO:0009534//GO:0009639//GO:0015977//GO:0016491//GO:0016831//GO:0043094//GO:0044436//GO:0046914	nr -
Unigene10044_All	400	0.00	20.77	12.11	0.00	0.00	0.00	0.00	0.00	0.00	1.43E+01	1.52E-47	Up	1.36E+01	6.11E-27	Up	null	null		null	null		null	null		null	null		Unigene10044_All//gi|89513312|gb|ABD74515.1|//1.00E-40//ribosomal protein [Pteris vittata]	Unigene10044_All//2.00E-39//AT1G36240| 60S ribosomal protein L30 (RPL30A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene100446_All	343	22.88	18.32	11.02	27.01	24.09	28.97	46.47	20.96	28.11	-3.21E-01	1.36E-01		-1.05E+00	1.56E-06	Down	-1.65E-01	4.51E-01		1.01E-01	6.43E-01		-1.15E+00	2.74E-18	Down	-7.25E-01	3.42E-09		Unigene100446_All//gi|164564736|dbj|BAF98218.1|//7.00E-29//CM02216.350.nc [Lotus japonicus]	Unigene100446_All//1.00E-08//AT4G39200| 40S ribosomal protein S25 (RPS25E)	Unigene100446_All//7.00E-86//BF276543		ko03010|Ribosome		nr -
Unigene10047_All	390	0.00	3.77	2.18	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.11E-08	Up	1.11E+01	9.04E-05	Up	null	null		null	null		null	null		null	null		Unigene10047_All//gi|224482651|gb|ACN50182.1|//5.00E-14//annexin [Annona cherimola]	Unigene10047_All//9.00E-10//AT1G68090| ANN5; calcium ion binding / calcium-dependent phospholipid binding					nr -
Unigene10048_All	592	0.00	4.02	1.71	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.50E-13	Up	1.07E+01	1.28E-05	Up	null	null		null	null		null	null		null	null		Unigene10048_All//gi|300120616|emb|CBK20170.2|//4.00E-23//unnamed protein product [Blastocystis hominis]						nr +
Unigene10049_All	212	7.16	0.96	1.76	4.46	4.39	5.75	0.20	0.20	0.00	-2.90E+00	2.07E-05	Down	-2.03E+00	1.23E-03		-2.57E-02	9.50E-01		3.66E-01	6.04E-01		-1.67E-02	1.01E+00		-7.64E+00	6.21E-01					Unigene10049_All//2.00E-10//ES837561					
Unigene1005_All	1493	17.24	6.99	18.94	4.77	7.80	7.77	1.61	1.23	0.80	-1.30E+00	7.72E-29	Down	1.36E-01	2.46E-01		7.08E-01	5.86E-06		7.04E-01	1.59E-05		-3.90E-01	3.15E-01		-1.01E+00	4.32E-03		Unigene1005_All//gi|75244391|sp|Q8S8.1|ANTR2_ARATH RecName: Full=Probable anion transporter 2, chloroplastic; AltName: Full=Phosphate transporter PHT4;4; Flags: Precursor >gi|32306495|gb|AAP78931.1| At4g00370 [Arabidopsis thaliana]	Unigene1005_All//7.00E-135//AT4G00370| ANTR2; inorganic phosphate transmembrane transporter/ organic anion transmembrane transporter	Unigene1005_All//0.00E+00//TC172647				nr -
Unigene10050_All	394	0.00	0.13	0.00	0.00	0.00	0.34	1.40	3.08	4.95	7.01E+00	6.24E-01		null	null		null	null		8.43E+00	3.14E-01		1.14E+00	4.07E-02		1.83E+00	3.51E-05	Up	Unigene10050_All//gi|224097212|ref|XP_002310878.1|//5.00E-19//1-aminocyclopropane-1-carboxylate [Populus trichocarpa] >gi|222853781|gb|EEF91328.1| 1-aminocyclopropane-1-carboxylate [Populus trichocarpa]	Unigene10050_All//7.00E-18//AT5G65800| ACS5 (ACC SYNTHASE 5); 1-aminocyclopropane-1-carboxylate synthase			ko00270|Cysteine and methionine metabolism	GO:0005515//GO:0006412//GO:0006555//GO:0009725//GO:0016846	nr +

Unigene100500_All	896	0.41	0.00	0.65	0.67	0.15	2.37	0.28	0.00	0.00	-8.68E+00	1.97E-02		6.77E-01	4.83E-01		-2.12E+00	3.06E-02		1.83E+00	1.26E-04	Up	-8.15E+00	4.07E-02		-8.15E+00	3.06E-02		Unigene100500_All//gi|5453379|gb|AD43561.1|AF155124_1//1.00E-125//bacterial-induced peroxidase precursor [Gossypium hirsutum]	Unigene100500_All//2.00E-83//AT5G05340| peroxidase, putative	Unigene100500_All//0.00E+00//NP385887		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209//GO:0031410	nr +
Unigene10051_All	479	0.55	4.23	2.11	0.62	0.93	0.66	0.35	0.44	1.33	2.95E+00	4.86E-07	Up	1.95E+00	1.37E-02		5.83E-01	6.26E-01		8.09E-02	9.50E-01		3.05E-01	8.37E-01		1.91E+00	2.60E-02								
Unigene100521_All	242	0.00	0.00	0.00	0.00	0.00	0.56	0.00	0.00	3.62	null	null		null	null		null	null		9.13E+00	3.14E-01		null	null		1.18E+01	2.05E-06	Up							
Unigene10053_All	497	0.00	0.00	0.43	0.00	0.62	1.54	0.00	0.25	1.52	null	null		8.74E+00	1.42E-01		9.28E+00	4.55E-02		1.06E+01	1.27E-04	Up	7.98E+00	2.41E-01		1.06E+01	1.39E-05	Up	Unigene10053_All//gi|66792688|gb|AAY56446.1|//5.00E-39//At1g63930 [Arabidopsis thaliana] >gi|115311479|gb|ABI93920.1| At1g63930 [Arabidopsis thaliana]	Unigene10053_All//9.00E-37//AT1G63930| unknown protein	Unigene10053_All//4.00E-113//TC174086				nr +
Unigene10057_All	358	32.30	27.60	34.21	25.60	27.51	40.75	17.83	13.66	3.23	-2.27E-01	2.05E-01		8.30E-02	6.36E-01		1.04E-01	6.29E-01		6.70E-01	2.90E-06		-3.85E-01	7.45E-02		-2.47E+00	5.41E-22	Down							
Unigene10058_All	372	9.14	1.50	2.29	4.55	2.68	1.58	0.00	0.00	0.00	-2.61E+00	3.46E-10	Down	-2.00E+00	3.48E-07	Down	-7.62E-01	1.18E-01		-1.53E+00	3.34E-03		null	null		null	null		Unigene10058_All//gi|73761705|gb|AB283352.1|//1.00E-21//myb transcription factor MYB30 [Gossypium hirsutum]		Unigene10058_All//1.00E-19//TC145072			GO:0009725//GO:0009987	nr +
Unigene10059_All	446	0.00	0.00	0.00	0.00	0.00	0.00	3.60	0.56	1.25	null	null		null	null		null	null		null	null		-2.68E+00	2.38E-06	Down	-1.53E+00	1.16E-03								ESTscan -
Unigene100616_All	511	3.38	0.59	2.40	2.05	1.95	0.44	0.66	0.16	2.11	-2.51E+00	2.66E-05	Down	-4.95E-01	3.58E-01		-6.70E-02	9.06E-01		-2.21E+00	3.25E-03		-2.02E+00	1.37E-01		1.67E+00	6.16E-03		Unigene100616_All//gi|115452803|ref|NP_001050002.1|//1.00E-14//Os03g0328900 [Oryza sativa Japonica Group] >gi|108707942|gb|ABF95737.1| Zinc finger C-x8-C-x5-C-x3-H type family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548473|dbj|BAF11916.1| Os03g0328900 [Oryza sativa Japonica Group]	Unigene100616_All//6.00E-14//AT3G51950| zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein		C3H		GO:0003676//GO:0046914	nr -
Unigene10062_All	329	0.16	0.31	0.00	2.73	0.84	1.51	7.07	40.40	7.63	9.54E-01	7.28E-01		-7.31E+00	6.36E-01		-1.70E+00	1.98E-02		-8.52E-01	2.63E-01		2.51E+00	2.22E-44	Up	1.10E-01	7.55E-01			Unigene10062_All//4.00E-07//TC158719				
Unigene10065_All	297	0.00	4.44	2.87	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.50E-07	Up	1.15E+01	9.04E-05	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene10066_All	248	0.00	0.00	3.01	0.60	1.39	1.27	1.02	0.67	0.16	null	null		1.16E+01	3.28E-04	Up	1.20E+00	4.26E-01		1.08E+00	4.76E-01		-6.02E-01	6.49E-01		-2.67E+00	1.15E-01								
Unigene10067_All	547	269.54	354.04	239.77	323.84	777.85	534.53	6.18	18.64	12.75	3.93E-01	4.11E-27		-1.69E-01	1.43E-04		1.26E+00	0.00E+00	Up	7.23E-01	3.30E-130		1.59E+00	3.53E-19	Up	1.04E+00	1.48E-07	Up	Unigene10067_All//gi|194466223|gb|ACF74342.1|//4.00E-34//gonadotropin beta chain [Arachis hypogaea]	Unigene10067_All//2.00E-21//AT5G14920| gibberellin-regulated family protein	Unigene10067_All//0.00E+00//TC163273				nr +
Unigene10068_All	577	0.00	28.01	7.38	0.00	0.00	0.00	0.00	0.00	0.00	1.48E+01	6.97E-93	Up	1.29E+01	1.22E-23	Up	null	null		null	null		null	null		null	null		Unigene10068_All//gi|116310923|emb|CAM67861.1|//1.00E-10//B0403H10-OS1GBa0105A11.13 [Oryza sativa (indica cultivar-group)]				ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr +
Unigene10069_All	323	0.00	0.00	0.00	0.00	0.00	0.00	10.08	11.78	0.37	null	null		null	null		null	null		null	null		2.24E-01	4.72E-01		-4.77E+00	6.52E-20	Down	Unigene10069_All//gi|297829770|ref|XP_002882767.1|//4.00E-52//actin-11 [Arabidopsis lyrata subsp. lyrata] >gi|297328607|gb|EFH59026.1| actin-11 [Arabidopsis lyrata subsp. lyrata]	Unigene10069_All//2.00E-53//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene10069_All//6.00E-40//TC153744		ko04145|Phagosome	GO:0007010//GO:0016020//GO:0032559//GO:0043231//GO:0043232	nr -
Unigene100697_All	211	0.00	0.96	0.00	0.47	0.49	1.50	0.40	3.96	0.00	9.91E+00	1.38E-01		null	null		5.22E-02	9.69E-01		1.67E+00	3.09E-01		3.31E+00	3.10E-04	Up	-8.65E+00	3.63E-01								
Unigene10070_All	624	0.08	0.00	0.00	0.08	0.11	0.22	0.14	0.00	1.79	-6.39E+00	6.24E-01		-6.39E+00	6.36E-01		4.68E-01	9.63E-01		1.44E+00	6.41E-01		-7.08E+00	4.09E-01		3.72E+00	4.35E-06	Up	Unigene10070_All//gi|124359981|gb|ABN07997.1|//7.00E-09//contains similarity to reverse trancriptase, related [Medicago truncatula]	Unigene10070_All//6.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative				GO:0005488	nr -
Unigene10071_All	379	0.28	6.82	4.36	0.39	0.36	2.74	3.79	8.71	98.49	4.63E+00	3.34E-12	Up	3.98E+00	5.16E-07	Up	-1.18E-01	9.12E-01		2.80E+00	8.13E-04	Up	1.20E+00	1.14E-04	Up	4.70E+00	8.30E-217	Up		Unigene10071_All//3.00E-159//DT461826					
Unigene100711_All	265	2.37	4.02	1.61	0.38	0.65	5.79	0.80	0.00	0.75	7.61E-01	2.48E-01		-5.60E-01	5.54E-01		7.89E-01	7.72E-01		3.95E+00	4.90E-07	Up	-9.64E+00	7.49E-02		-8.57E-02	9.62E-01		Unigene100711_All//gi|225451804|ref|XP_002281338.1|//2.00E-09//PREDICTED: brassinosteroid-6-oxidase [Vitis vinifera]	Unigene100711_All//7.00E-07//AT5G38970| BR6OX1 (BRASSINOSTEROID-6-OXIDASE 1); monooxygenase/ oxygen binding	Unigene100711_All//3.00E-103//TC166913		ko00905|Brassinosteroid biosynthesis	GO:0000226//GO:0005506//GO:0006091//GO:0009646//GO:0016129//GO:0016491//GO:0031224//GO:0032501//GO:0048878	nr +
Unigene10072_All	595	0.00	0.00	0.00	0.50	0.00	0.00	1.63	0.42	10.58	null	null		null	null		-8.97E+00	2.02E-02		-8.97E+00	4.01E-02		-1.96E+00	4.44E-03		2.69E+00	1.68E-23	Up		Unigene10072_All//0.00E+00//gi|109888809|gb|DW517778.1|DW517778					
Unigene10074_All	962	0.54	0.95	1.11	4.87	4.19	2.77	0.75	0.04	0.33	8.02E-01	2.71E-01		1.03E+00	1.43E-01		-2.17E-01	4.91E-01		-8.13E-01	3.07E-03		-4.11E+00	2.92E-04	Down	-1.17E+00	1.09E-01		Unigene10074_All//gi|39725413|emb|CAE09057.1|//2.00E-70//MYB transcription factor [Eucalyptus gunnii]	Unigene10074_All//4.00E-53//AT3G08500| MYB83 (myb domain protein 83); DNA binding / transcription factor	Unigene10074_All//1.00E-166//DW508945	MYB		GO:0001071//GO:0003676//GO:0006350//GO:0009832//GO:0010033//GO:0010468//GO:0043231	nr +
Unigene10075_All	585	0.00	9.79	5.46	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	1.13E-32	Up	1.24E+01	1.15E-17	Up	null	null		null	null		null	null		null	null		Unigene10075_All//gi|159483465|ref|XP_001699781.1|//2.00E-51//eukaryotic initiation factor [Chlamydomonas reinhardtii] >gi|158281723|gb|EDP07477.1| eukaryotic initiation factor [Chlamydomonas reinhardtii]	Unigene10075_All//1.00E-36//AT2G04520| eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative				GO:0006412//GO:0008135	nr +
Unigene100750_All	499	0.10	0.00	0.96	1.00	1.73	1.18	2.46	0.75	0.56	-6.71E+00	6.23E-01		3.19E+00	3.48E-02		7.89E-01	3.21E-01		2.37E-01	7.99E-01		-1.70E+00	3.32E-03		-2.14E+00	3.24E-04	Down	Unigene100750_All//gi|240254302|ref|NP_176378.4|//3.00E-60//galactolipase/ phospholipase [Arabidopsis thaliana]	Unigene100750_All//2.00E-61//AT1G61850| galactolipase/ phospholipase	Unigene100750_All//6.00E-10//EV498230			GO:0003824//GO:0005488//GO:0044238	nr -
Unigene10076_All	406	0.00	0.00	0.00	0.00	0.00	0.22	4.58	1.13	2.06	null	null		null	null		null	null		7.80E+00	4.84E-01		-2.02E+00	2.13E-05	Down	-1.15E+00	5.56E-03		Unigene10076_All//gi|224114738|ref|XP_002332312.1|//9.00E-08//predicted protein [Populus trichocarpa] >gi|222832311|gb|EEE70788.1| predicted protein [Populus trichocarpa]						nr -
Unigene10078_All	346	0.00	108.37	30.63	0.00	0.00	0.00	0.00	0.00	0.00	1.67E+01	2.24E-216	Up	1.49E+01	1.66E-59	Up	null	null		null	null		null	null		null	null		Unigene10078_All//gi|195620360|gb|ACG32010.1|//2.00E-39//60S ribosomal protein L27a-3 [Zea mays]	Unigene10078_All//26//AT1G23290| RPL27AB; structural constituent of ribosome	Unigene10078_All//3.00E-20//TC169611		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene100795_All	365	0.00	0.00	0.00	0.14	0.47	0.00	6.49	5.73	1.42	null	null		null	null		1.79E+00	5.22E-01		-7.09E+00	6.47E-01		-1.80E-01	6.34E-01		-2.19E+00	1.28E-07	Down	Unigene100795_All//gi|9294177|dbj|BAB02079.1|//9.00E-20//nodulin-like protein [Arabidopsis thaliana]	Unigene100795_All//4.00E-21//AT3G25190| nodulin, putative	Unigene100795_All//5.00E-62//gi|109868191|gb|DW497167.1|DW497167				nr -
Unigene10084_All	254	0.00	4.19	1.68	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.82E-06	Up	1.07E+01	1.39E-02		null	null		null	null		null	null		null	null		Unigene10084_All//gi|301111870|ref|XP_002905014.1|//6.00E-25//superoxide dismutase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262095344|gb|EEY53396.1| superoxide dismutase, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene10084_All//3.00E-19//AT3G10920| MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); metal ion binding / superoxide dismutase			ko04146|Peroxisome	GO:0003824//GO:0005488//GO:0044237	nr -
Unigene100844_All	296	53.38	23.28	17.63	74.89	57.47	77.82	80.99	27.82	35.80	-1.20E+00	7.32E-16	Down	-1.60E+00	3.29E-23	Down	-3.82E-01	4.81E-04		5.53E-02	6.72E-01		-1.54E+00	3.80E-42	Down	-1.18E+00	5.17E-29	Down	Unigene100844_All//gi|15231288|ref|NP_187967.1|//7.00E-26//60S ribosomal protein L7 (RPLTD) [Arabidopsis thaliana] >gi|42572417|ref|NP_974304.1| 60S ribosomal protein L7 (RPLTD) [Arabidopsis thaliana] >gi|42572419|ref|NP_974305.1| 60S ribosomal protein L7 (RPLTD) [Arabidopsis thaliana] >gi|38503370|sp|Q9LHP1.1|RL74_ARATH RecName: Full=60S ribosomal protein L7-4 >gi|11994560|dbj|BAB02600.1| 60S ribosomal protein L7 [Arabidopsis thaliana] >gi|14532552|gb|AAK64004.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] >gi|15810196|gb|AAL06999.1| AT3g13580/K20M4_2 [Arabidopsis thaliana] >gi|18655395|gb|AAL76153.1| AT3g13580/K20M4_2 [Arabidopsis thaliana]	Unigene100844_All//3.00E-27//AT3G13580| 60S ribosomal protein L7 (RPLTD)	Unigene100844_All//5.00E-74//EV497578		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0030312//GO:0031981	nr -
Unigene10085_All	234	65.07	19.70	29.58	99.20	79.61	118.51	62.70	16.61	42.90	-1.72E+00	6.70E-26	Down	-1.14E+00	1.52E-13	Down	-3.17E-01	3.63E-03		2.57E-01	1.58E-02		-1.92E+00	3.80E-35	Down	-5.47E-01	1.60E-05		Unigene10085_All//gi|76160947|gb|ABA40437.1|//3.00E-11//40S ribosomal protein S7-like protein [Solanum tuberosum] >gi|77999315|gb|ABB17004.1| ribosomal protein S7-like protein [Solanum tuberosum] >gi|82623373|gb|ABB87101.1| 40S ribosomal protein S7-like protein-like [Solanum tuberosum]	Unigene10085_All//2.00E-10//AT3G02560| 40S ribosomal protein S7 (RPS7B)	Unigene10085_All//1.00E-89//gi|13355512|gb|BG445860.1|BG445860		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene10088_All	459	0.00	0.00	0.00	0.33	0.68	0.79	1.47	1.73	3.99	null	null		null	null		1.05E+00	5.32E-01		1.27E+00	3.82E-01		2.31E-01	7.35E-01		1.44E+00	9.58E-04	Up							
Unigene10089_All	472	0.00	0.00	0.00	0.00	0.22	0.19	3.31	0.44	1.18	null	null		null	null		7.77E+00	4.59E-01		7.58E+00	4.84E-01		-2.90E+00	1.13E-06	Down	-1.49E+00	1.74E-03		Unigene10089_All//gi|15239653|ref|NP_200262.1|//1.00E-49//DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase [Arabidopsis thaliana] >gi|62900334|sp|Q9LSQ4.1|GH36_ARATH RecName: Full=Indole-3-acetic acid-amido synthetase GH3.6; AltName: Full=Auxin-responsive GH3-like protein 6; Short=AtGH3-6; AltName: Full=Protein DWARF IN LIGHT 1; Short=DFL-1 >gi|8885594|dbj|BAA97524.1| auxin-responsive-like protein [Arabidopsis thaliana] >gi|11041726|dbj|BAB17304.1| auxin-responsive GH3 homologue [Arabidopsis thaliana] >gi|59958336|gb|AAX12878.1| At5g54510 [Arabidopsis thaliana] >gi|209414530|gb|ACI46505.1| At5g54510 [Arabidopsis thaliana]	Unigene10089_All//7.00E-51//AT5G54510| DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase	Unigene10089_All//1.00E-07//DW501990			GO:0000902//GO:0009314//GO:0009536//GO:0009755//GO:0016881//GO:0048878	nr -
Unigene100896_All	313	0.33	0.97	0.68	3.18	0.44	0.87	0.54	0.00	0.25	1.54E+00	3.24E-01		1.03E+00	5.93E-01		-2.85E+00	2.37E-04	Down	-1.88E+00	1.18E-02		-9.08E+00	1.35E-01		-1.09E+00	5.54E-01								
Unigene100906_All	390	0.13	1.82	0.41	0.26	0.18	1.39	16.26	6.43	81.62	3.76E+00	2.36E-03		1.61E+00	5.12E-01		-5.33E-01	8.20E-01		2.44E+00	4.42E-02		-1.34E+00	1.23E-09	Down	2.33E+00	4.31E-98	Up	Unigene100906_All//gi|75297894|sp|Q84MB3.1|ACCH1_ARATH//4.00E-33//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene100906_All//2.00E-34//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene100906_All//1.00E-133//gi|109879784|gb|DW508754.1|DW508754		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0008152//GO:0016706//GO:0046914	nr -
Unigene100908_All	2421	0.04	0.46	0.24	0.06	0.16	14.31	0.00	0.00	0.00	3.41E+00	1.24E-04	Up	2.49E+00	3.76E-02		1.34E+00	3.40E-01		7.86E+00	2.13E-206	Up	null	null		null	null		Unigene100908_All//sp|Q16927|VIT1_AEDAE//3.00E-56//Vitellogenin-A1 OS=Aedes aegypti GN=VGA1 PE=1 SV=2						swissprot -

Unigene10091_All	904	0.00	8.02	2.71	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	2.04E-41	Up	1.14E+01	1.64E-13	Up	null	null		null	null		null	null		null	null		Unigene10091_All//gi|301107486|ref|XP_002902825.1|//7.00E-52//long-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4]>gi|262097943|gb|EEY55995.1| long-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4]	Unigene10091_All//5.00E-17//AT4G14070| AAE15 (acyl-activating enzyme 15); long-chain-fatty-acid-[acyl-carrier-protein] ligase			ko00940|Phenylpropanoid biosynthesis//ko04146|Peroxisome//ko00360|Phenylalanine metabolism//ko00071|Fatty acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene10092_All	391	0.13	56.50	24.11	0.00	0.00	0.00	0.00	0.00	0.00	8.72E+00	7.66E-125	Up	7.49E+00	6.51E-51	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene10093_All	346	0.30	0.00	0.00	1.87	2.99	0.52	0.00	1.57	0.23	-8.24E+00	3.78E-01		-8.24E+00	4.00E-01		6.74E-01	3.49E-01		-1.84E+00	6.01E-02		1.06E+01	5.37E-04	Up	7.85E+00	4.07E-01				Unigene10093_All//8.00E-172//TC147034				
Unigene10964_All	213	0.00	0.00	0.00	0.47	0.32	4.45	0.20	0.98	0.00	null	null		null	null		-5.33E-01	8.20E-01		3.25E+00	5.84E-04	Up	2.31E+00	2.40E-01		-7.63E+00	6.21E-01				Unigene10964_All//7.00E-20//DR457055				
Unigene10998_All	531	0.00	0.00	0.00	0.00	0.00	0.00	2.23	9.21	1.05	null	null		null	null		null	null		null	null		2.05E+00	3.31E-13	Up	-1.09E+00	4.38E-02									
Unigene1010_All	4361	4.57	2.21	3.50	3.03	3.00	2.59	12.27	9.90	5.23	-1.05E+00	3.47E-16	Down	-3.83E-01	3.03E-03		-1.26E-02	9.52E-01		-2.26E-01	1.90E-01		-3.10E-01	1.50E-06		-1.23E+00	2.47E-68	Down	Unigene1010_All//gi|224053809|ref|XP_002297990.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa]>gi|222845248|gb|EEE82795.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene1010_All//0.00E+00//AT3G13080| ATMRP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase	Unigene1010_All//3.00E-20//TC139924		ko02010|ABC transporters	GO:0006810//GO:0015405//GO:0017111//GO:0031224//GO:0032559	nr +
Unigene101002_All	382	0.00	0.00	0.00	0.52	0.09	0.12	1.77	0.11	0.52	null	null		null	null		-2.53E+00	2.34E-01		-2.14E+00	3.48E-01		-4.02E+00	5.36E-04	Down	-1.76E+00	2.80E-02		Unigene101002_All//gi|224097478|ref|XP_002310652.1|//9.00E-07//predicted protein [Populus trichocarpa]>gi|222850772|gb|EEE88319.1| predicted protein [Populus trichocarpa]	Unigene101002_All//2.00E-06//AT2G33840| tRNA synthetase class I (W and Y) family protein	Unigene101002_All//8.00E-126//gi|11204884|gb|BF273826.1|BF273826		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene10101_All	1285	0.00	0.00	0.00	0.00	0.00	0.00	4.71	11.84	1.58	null	null		null	null		null	null		null	null		1.33E+00	8.52E-22	Up	-1.57E+00	6.44E-12	Down								
Unigene101019_All	212	0.99	0.48	2.01	0.24	0.97	0.85	0.20	2.56	6.01	-1.05E+00	5.66E-01		1.03E+00	3.97E-01		2.05E+00	3.95E-01		1.88E+00	4.60E-01		3.68E+00	3.69E-03		4.91E+00	5.19E-08	Up			Unigene101019_All//4.00E-18//TC141091				
Unigene101039_All	270	0.39	0.38	0.20	0.92	1.79	2.01	0.16	0.93	9.74	-4.65E-02	9.91E-01		-9.75E-01	7.23E-01		9.53E-01	4.24E-01		1.12E+00	3.05E-01		2.57E+00	1.53E-01		5.96E+00	2.54E-17	Up			Unigene101039_All//2.00E-51//DT527515				
Unigene101047_All	207	2.27	1.22	7.97	6.26	3.99	0.65	0.61	0.00	0.00	-8.94E-01	3.89E-01		1.81E+00	1.76E-03		-6.48E-01	2.72E-01		-3.26E+00	1.98E-05	Down	-9.26E+00	2.37E-01		-9.26E+00	2.01E-01								
Unigene101050_All	625	0.00	0.00	0.00	0.32	0.11	0.72	1.76	0.00	0.45	null	null		null	null		-1.53E+00	4.17E-01		1.18E+00	3.38E-01		-1.08E+01	7.67E-08	Down	-1.98E+00	1.39E-03		Unigene101050_All//gi|119507465|dbj|BAF42040.1|//1.00E-90//pectin methylesterase 3 [Pyrus communis]	Unigene101050_All//6.00E-89//AT1G02810| pectinesterase family protein	Unigene101050_All//0.00E+00//TC138774		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0030234//GO:0071555	nr -
Unigene10106_All	383	0.96	0.26	0.83	1.30	1.17	0.59	2.21	0.11	0.31	-1.85E+00	1.87E-01		-1.97E-01	8.66E-01		-1.54E-01	8.50E-01		-1.14E+00	3.07E-01		-4.34E+00	4.56E-05	Down	-2.82E+00	5.38E-04	Down			Unigene10106_All//4.00E-07//ES837531				
Unigene10107_All	676	0.00	1.20	0.00	0.59	1.78	1.00	0.25	0.31	0.41	1.02E+01	9.39E-05	Up	null	null		1.60E+00	1.36E-02		7.66E-01	4.10E-01		3.05E-01	8.37E-01		7.21E-01	5.97E-01		Unigene10107_All//gi|297804010|ref|XP_002868889.1|//3.00E-63//At4g21420 [Arabidopsis lyrata subsp. lyrata]>gi|297315725|gb|EFH46148.1| At4g21420 [Arabidopsis lyrata subsp. lyrata]	Unigene10107_All//1.00E-08//AT5G42905| nucleic acid binding / ribonuclease H	Unigene10107_All//0.00E+00//gi|3326554|gb|AI055440.1|AI055440			GO:0005488//GO:0016891//GO:0043231	nr +
Unigene10109_All	924	0.00	12.94	4.21	0.05	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.36E-68	Up	1.20E+01	1.52E-21	Up	-5.75E+00	5.67E-01		-5.75E+00	6.47E-01		null	null		null	null		Unigene10109_All//gi|297800072|ref|XP_002867920.1|//1.00E-18//glycosyl hydrolase family 18 protein [Arabidopsis lyrata subsp. lyrata]>gi|297313756|gb|EFH44179.1| glycosyl hydrolase family 18 protein [Arabidopsis lyrata subsp. lyrata]	Unigene10109_All//3.00E-17//AT4G19810| glycosyl hydrolase family 18 protein				GO:0003824	nr -
Unigene101106_All	204	0.00	0.00	0.00	0.49	0.00	0.44	27.57	49.99	76.16	null	null		null	null		-8.93E+00	3.18E-01		-1.41E-01	9.54E-01		8.59E-01	1.02E-07		1.47E+00	3.29E-26	Up			Unigene101106_All//6.00E-42//gi|31407394|gb|CD486429.1|CD486429				
Unigene10111_All	570	0.00	10.93	4.11	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.38E-35	Up	1.20E+01	6.41E-13	Up	null	null		null	null		null	null		null	null		Unigene10111_All//gi|8954372|ref|NP_059361.1|//4.00E-34//NADH dehydrogenase subunit 4 [Cyanidioschyzon merolae]>gi|41157851|dbj|BAA36523.1| NADH-ubiquinone oxidoreductase chain 4 [Cyanidioschyzon merolae strain 10D]	Unigene10111_All//2.00E-14//ATMG00580| NADH dehydrogenase subunit 4			ko00190|Oxidative phosphorylation	GO:0016020//GO:0055114	nr -
Unigene10112_All	381	0.00	0.00	0.00	0.00	0.00	0.00	4.66	7.02	0.21	null	null		null	null		null	null		null	null		5.91E-01	8.97E-02		-4.48E+00	1.00E-10	Down								
Unigene10114_All	426	0.00	21.29	17.13	0.23	0.00	0.00	0.00	0.00	0.00	1.44E+01	6.32E-52	Up	1.41E+01	8.91E-41	Up	-7.87E+00	3.18E-01		-7.87E+00	4.06E-01		null	null		null	null		Unigene10114_All//gi|159483157|ref|XP_001699629.1|//4.00E-25//acidic ribosomal protein P1 [Chlamydomonas reinhardtii]>gi|266947|sp|P29763.1|RLA1_CHLREReCName: Full=60S acidic ribosomal protein P1>gi|18211|emb|CAA47042.1| ribosomal protein P1 [Chlamydomonas reinhardtii]>gi|158272734|gb|ED098531.1| acidic ribosomal protein P1 [Chlamydomonas reinhardtii]	Unigene10114_All//2.00E-14//AT5G24510| 60s acidic ribosomal protein P1, putative			ko03010|Ribosome	GO:0030529	nr +
Unigene10115_All	553	3.12	1.10	0.48	0.45	0.62	0.33	0.31	0.08	0.22	-1.51E+00	3.95E-03		-2.70E+00	2.40E-05	Down	4.67E-01	7.80E-01		-4.63E-01	7.45E-01		-2.02E+00	3.69E-01		-5.01E-01	7.47E-01									
Unigene101179_All	205	0.00	0.00	0.00	0.00	0.00	0.00	12.58	0.20	0.39	null	null		null	null		null	null		null	null		-5.95E+00	9.35E-17	Down	-5.02E+00	2.78E-16	Down	Unigene101179_All//gi|18558997|gb|AAL73112.1|//1.00E-10//bacterial-induced peroxidase [Gossypium hirsutum]	Unigene101179_All//8.00E-09//AT5G39580| peroxidase, putative	Unigene101179_All//4.00E-46//TC171015		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0016209//GO:0042743	nr -
Unigene10118_All	285	0.00	0.00	0.00	0.00	0.00	0.00	4.01	4.40	0.00	null	null		null	null		null	null		null	null		1.35E-01	8.03E-01		-1.20E+01	1.65E-08	Down	Unigene10118_All//gi|55168340|gb|AAV44205.1|//3.00E-10//unknow protein [Oryza sativa Japonica Group]						nr +
Unigene10119_All	409	0.00	0.00	0.00	0.00	0.00	0.00	1.86	4.29	0.00	null	null		null	null		null	null		null	null		1.21E+00	7.16E-03		-1.09E+01	8.89E-06	Down	Unigene10119_All//gi|297845688|ref|XP_002890725.1|//4.00E-28//60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata]>gi|297336567|gb|EFH66984.1| 60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata]	Unigene10119_All//3.00E-28//AT1G27400| 60S ribosomal protein L17 (RPL17A)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0003181	nr -
Unigene1012_All	811	1.68	3.31	1.90	5.96	6.28	6.18	8.81	17.99	15.77	9.81E-01	1.13E-02		1.83E-01	7.19E-01		7.69E-02	8.39E-01		5.31E-02	8.71E-01		1.03E+00	3.51E-14	Up	8.40E-01	2.07E-09		Unigene10012_All//gi|15230596|ref|NP_187250.1|//1.00E-06//leucine-rich repeat family protein [Arabidopsis thaliana]>gi|30102730|gb|AAP21283.1| At3g05990 [Arabidopsis thaliana]		Unigene10012_All//0.00E+00//gi|109888009|gb|DW516978.1|DW516978			GO:0005488//GO:0023060	nr +
Unigene10123_All	430	0.00	6.36	5.20	0.00	0.00	0.00	0.00	0.00	0.19	1.26E+01	1.44E-15	Up	1.23E+01	2.51E-12	Up	null	null		null	null		null	null		7.53E+00	4.07E-01		Unigene10123_All//gi|192910698|gb|ACF06452.1|//5.00E-42//60S ribosomal protein L35 [Elaeis guineensis]	Unigene10123_All//4.00E-31//AT2G39390| 60S ribosomal protein L35 (RPL35B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene10124_All	399	3.15	0.76	0.00	1.12	1.29	0.34	0.00	0.21	0.00	-2.05E+00	2.33E-03		-1.16E+01	7.11E-07	Down	2.04E-01	8.59E-01		-1.73E+00	1.61E-01		7.71E-00	4.04E-01		null	null									ESTscan -
Unigene101257_All	206	0.76	3.20	0.00	0.48	1.50	4.38	0.82	0.61	1.35	2.07E+00	3.93E-02		-9.57E+00	2.47E-01		1.61E+00	3.22E-01		3.18E+00	9.74E-04	Up	-4.32E-01	7.94E-01		7.22E-01	5.97E-01									
Unigene10126_All	379	0.00	4.41	6.04	0.00	0.18	0.00	0.00	0.00	0.00	1.21E+01	1.54E-09	Up	1.26E+01	1.27E-12	Up	7.51E+00	6.17E-01		null	null		null	null		null	null		Unigene10126_All//sp|Q95339|ATPK_PIG//6.00E-11//ATP synthase subunit f, mitochondrial OS=Sus scrofa GN=ATP5J2 PE=3 SV=4						swissprot +
Unigene10127_All	398	0.66	0.76	1.07	0.00	1.90	0.45	0.85	0.42	0.50	2.17E-01	8.65E-01		7.04E-01	5.54E-01		1.09E+01	1.17E-04	Up	8.83E+00	1.96E-01		-1.02E+00	4.00E-01		-7.64E-01	5.02E-01		Unigene10127_All//gi|186511604|ref|NP_192625.4|//9.00E-37//kinase [Arabidopsis thaliana]>gi|222423559|dbj|BAH19749.1| AT4G08850 [Arabidopsis thaliana]	Unigene10127_All//5.00E-38//AT4G08850| kinase	Unigene10127_All//7.00E-117//DR462992		ko03410|Base excision repair	GO:0004672//GO:0006464//GO:0016628//GO:0032559	nr -
Unigene101271_All	330	0.63	0.15	1.61	1.51	0.83	0.68	6.41	1.77	2.90	-2.05E+00	3.34E-01		1.35E+00	2.25E-01		-8.55E-01	4.07E-01		-1.14E+00	3.07E-01		-1.85E+00	1.76E-05	Down	-1.14E+00	3.04E-03		Unigene101271_All//gi|71535005|gb|AAZ32900.1|//2.00E-18//zinc finger Glo3-like protein [Medicago sativa]	Unigene101271_All//3.00E-19//AT4G17890| AGD8 (ARF-GAP DOMAIN 8); ARF GTPase activator/ DNA binding / zinc ion binding	Unigene101271_All//4.00E-81//TC132880		ko04144|Endocytosis	GO:0005083//GO:0032012//GO:0043231//GO:0046914	nr +
Unigene10129_All	356	0.00	1.85	2.69	1.12	0.10	0.00	0.59	0.12	0.00	1.09E+01	6.26E-04	Up	1.14E+01	2.46E-05	Up	-3.53E+00	2.10E-02		-1.01E+01	1.11E-02		-2.34E+00	2.38E-01		-9.21E+00	5.84E-02		Unigene10129_All//gi|223452526|gb|ACM89590.1|//6.00E-20//disease resistance protein [Glycine max]	Unigene10129_All//7.00E-10//AT1G58190| AtRLP9 (Receptor Like Protein 9); protein binding				GO:0005488//GO:0016301	nr +
Unigene10131_All	404	0.00	15.43	4.22	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	1.38E-35	Up	1.20E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene10131_All//gi|219125548|ref|XP_002183039.1|//1.00E-20//thioredoxin h [Phaeodactylum tricornutum CCAP 1055/1]>gi|217405314|gb|EEC45257.1| thioredoxin h [Phaeodactylum tricornutum CCAP 1055/1]	Unigene10131_All//2.00E-19//AT1G19730| ATTRX4; oxidoreductase, acting on sulfur group of donors, disulfide as acceptor				GO:0005488//GO:0005737//GO:0008152//GO:0009987	nr -
Unigene101317_All	718	0.00	0.00	0.00	0.14	0.00	0.19	1.12	0.06	0.11	null	null		null	null		-7.12E+00	3.18E-01		4.43E-01	8.63E-01		-4.26E+00	8.48E-05	Down	-3.33E+00	2.47E-04	Down	Unigene101317_All//gi|15241528|ref|NP_196427.1|//1.00E-88//L-asparaginase / L-asparagine amidohydrolase [Arabidopsis thaliana]>gi|25108880|sp|P50287.2|ASPG1_ARATH RecName: Full=Isoaspartyl peptidase/L-asparaginase 1; AltName: Full=L-asparagine amidohydrolase 1; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase 1 subunit alpha; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase 1 subunit beta; Flags: Precursor>gi|8346547|emb|CAB93711.1| asparaginase [Arabidopsis thaliana]>gi|14517440|gb|AAK62610.1| AT5g08100/T22D6_40 [Arabidopsis thaliana]>gi|20147331|gb|AAM10379.1| AT5g08100/T22D6_40 [Arabidopsis thaliana]	Unigene101317_All//8.00E-90//AT5G08100| L-asparaginase / L-asparagine amidohydrolase	Unigene101317_All//0.00E+00//gi|78347096|gb|DT567370.1|DT567370			GO:0008242//GO:0009057//GO:0016811	nr -
Unigene101318_All	212	0.25	0.00	0.00	0.24	0.81	4.26	0.00	0.20	0.00	-7.95E+00	6.23E-01		-7.95E+00	6.36E-01		1.79E+00	5.22E-01		4.18E+00	1.95E-04	Up	7.62E+00	6.41E-01		null	null									
Unigene101319_All	232	1.13	0.00	0.00	0.00	0.00	0.00	4.92	0.36	1.03	-1.01E+01	6.73E-02		-1.01E+01	8.61E-02		null	null		null	null		-3.77E+00	3.90E-06	Down	-2.26E+00	3.40E-04	Down	Unigene101319_All//gi|16416376|dbj|BAB21610.2|//6.00E-21//mangrin [Bruguiera sexangula]	Unigene101319_All//2.00E-15//AT3G25760| AOC1 (ALLENE OXIDE CYCLASE 1); allene-oxide cyclase	Unigene101319_All//7.00E-82//DW500651		ko00592|alpha-Linolenic acid metabolism	GO:0009536//GO:0009694//GO:0009975	nr +
Unigene10132_All	820	0.00	7.54	2.73	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.70E-35	Up	1.14E+01	2.51E-12	Up	null	null		null	null		null	null		null	null		Unigene10132_All//gi|115459616|ref|NP_001053408.1|//1.00E-103//Os04g0533000 [Oryza sativa Japonica Group]>gi|75327302|sp|Q7XMK8.1|RH6_ORYSJ RecName: Full=DEAD-box ATP-dependent RNA helicase 6>gi|32488627|emb|CAE04571.1| OSJNBb0039L24.10 [Oryza sativa (japonica cultivar-group)]>gi|113564979|dbj|BAF15322.1| Os04g0533000 [Oryza sativa Japonica Group]	Unigene10132_All//1.00E-103//AT4G00660| DEAD/DEAH box helicase, putative			ko03018|RNA degradation		nr +
Unigene10135_All	433	2.18	1.64	1.48	5.64	2.94	0.83	0.98	0.39	0.00	-4.09E-01	5.67E-01		-5.60E-01	4.39E-01		-9.38E-01	1.46E-02		-2.76E+00	2.09E-08	Down	-1.34E+00	2.25E-01		-9.93E+00	2.15E-03									

Unigene101358_All	379	0.00	0.67	0.00	0.13	0.00	1.91	45.96	79.84	261.32	9.38E+00	7.89E-02		null	null		-7.04E+00	5.67E-01		3.86E+00	1.75E-03		7.97E-01	7.87E-19		2.51E+00	0.00E+00	Up	Unigene101358_All//gi|224092400|ref|XP_002309592.1//4.00E-25/2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222855568|gb|EEE93115.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene101358_All//6.00E-18//AT1G52800| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene101358_All//3.00E-162//gi|31407058|gb|CD486093.1|CD486093			GO:0016491	nr -
Unigene101372_All	209	0.25	0.00	5.61	2.86	0.82	3.03	0.00	0.00	0.38	-7.97E+00	6.23E-01		4.49E+00	1.90E-05	Up	-1.80E+00	5.87E-02		8.10E-02	9.46E-01		null	null		8.57E+00	4.07E-01									
Unigene101390_All	266	0.00	0.00	0.00	0.37	0.26	6.45	0.00	0.79	0.00	null	null		null	null		-5.33E-01	8.20E-01		4.11E+00	5.03E-08	Up	9.62E+00	7.87E-02		null	null		Unigene101390_All//gi|224143857|ref|XP_002336087.1//4.00E-22//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222871834|gb|EEF08965.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene101390_All//5.00E-11//AT3G21090| ABC transporter family protein	Unigene101390_All//2.00E-70//C0132421			GO:0000166//GO:0017111	nr +
Unigene1014_All	456	0.11	0.22	0.93	1.42	1.96	1.09	1.95	1.56	4.81	9.54E-01	7.28E-01		3.03E+00	5.74E-02		4.67E-01	5.72E-01		-3.82E-01	6.78E-01		-3.21E-01	6.33E-01		1.30E+00	7.66E-04	Up	Unigene1014_All//gi|224085664|ref|XP_002307656.1|//1.00E-23//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222857105|gb|EEE94652.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene1014_All//1.00E-15//AT2G18760| CHR8 (chromatin remodeling 8); ATP binding / DNA binding / helicase/ nucleic acid binding			ko03420|Nucleotide excision repair	GO:0003676//GO:0003824//GO:0006259//GO:0010212	nr -
Unigene101404_All	205	0.00	20.27	0.26	0.49	0.84	1.54	0.00	0.00	0.00	1.43E+01	1.16E-23	Up	8.02E+00	6.43E-01		7.89E-01	7.72E-01		1.67E+00	3.09E-01		null	null		null	null		Unigene101404_All//gi|297812271|ref|XP_002874019.1|//3.00E-13//glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] >gi|297319856|gb|EFH50278.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	Unigene101404_All//2.00E-14//AT5G20870| glycosyl hydrolase family 17 protein	Unigene101404_All//2.00E-11//gi|78329547|gb|DT549821.1|DT549821				nr +
Unigene101141_All	663	0.00	10.93	5.78	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.04E-41	Up	1.25E+01	3.02E-21	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene101442_All	516	0.00	0.00	0.00	0.00	0.13	0.09	8.11	4.37	0.77	null	null		null	null		7.06E+00	6.17E-01		6.45E+00	7.05E-01		-8.91E-01	7.83E-04		-3.39E+00	4.51E-20	Down	Unigene101442_All//gi|254803073|gb|ACT82815.1|//8.00E-13//At1g29270 [Arabidopsis thaliana]	Unigene101442_All//4.00E-11//AT1G29270| unknown protein	Unigene101442_All//3.00E-89//gi|109881197|gb|DW510167.1|DW510167				nr +
Unigene101435_All	574	0.18	0.00	0.00	0.61	0.12	0.16	1.18	0.29	0.00	-7.51E+00	3.78E-01		-7.51E+00	4.00E-01		-2.34E+00	1.01E-01		-1.95E+00	1.96E-01		-2.02E+00	1.98E-02		-1.02E+01	3.57E-05	Down	Unigene101435_All//gi|260446978|emb|CBG76260.1|//1.00E-30//OO_Ba0005L10-00_Ba0081K17.11 [Oryza officinalis]	Unigene101435_All//5.00E-29//AT3G19850| phototropic-responsive NPH3 family protein				GO:0005488//GO:0009314//GO:0044464//GO:0060089	nr +
Unigene101444_All	449	0.00	20.65	7.47	0.00	0.00	0.00	0.00	0.00	0.00	1.43E+01	4.29E-53	Up	1.29E+01	1.47E-18	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene101445_All	410	0.00	0.00	0.00	10.57	4.79	3.41	0.00	0.00	0.00	null	null		null	null		-1.14E+00	2.80E-05	Down	-1.63E+00	9.03E-08	Down	null	null		null	null		Unigene101445_All//gi|104295001|gb|ABF72016.1|//9.00E-36//GDSL-motif lipase/hydrolase family protein [Musa acuminata]	Unigene101445_All//3.00E-26//AT5G45670| GDSL-motif lipase/hydrolase family protein	Unigene101445_All//6.00E-170//ES847780			GO:0016787//GO:0044238	nr -
Unigene101501_All	214	0.00	0.00	0.00	0.00	0.00	0.00	0.99	6.84	1.30	null	null		null	null		null	null		null	null		2.79E+00	4.85E-06	Up	4.00E-01	7.43E-01		Unigene101501_All//gi|225449847|ref|XP_002265001.1|//4.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene101501_All//5.00E-07//AT1G62600| flavin-containing monooxygenase family protein / FMO family protein				GO:0000166//GO:0004497	nr +
Unigene10151_All	283	0.00	1.79	0.00	0.00	0.73	0.32	0.45	0.74	3.24	1.08E+01	4.05E-03		null	null		9.51E+00	1.58E-01		8.32E+00	4.83E-01		7.20E-01	6.33E-01		2.85E+00	3.18E-04	Up				Unigene10151_All//2.00E-128//C0078325					
Unigene101522_All	572	0.18	0.18	0.09	5.66	3.25	1.66	0.96	0.44	0.14	-4.57E-02	9.91E-01		-9.74E-01	7.23E-01		-8.00E-01	1.40E-02		-1.77E+00	1.26E-06	Down	-1.13E+00	2.18E-01		-2.79E+00	7.97E-03		Unigene101522_All//gi|297821166|ref|XP_002878466.1|//9.00E-87//DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324304|gb|EFH54725.1| DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata]	Unigene101522_All//5.00E-88//AT4G20360| ATERDJ3B; heat shock protein binding / unfolded protein binding	Unigene101522_All//0.00E+00//D8456694		ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0016020//GO:0031410//GO:0044267//GO:0044432	nr -
Unigene101529_All	221	3.08	6.88	10.84	9.69	9.35	2.45	1.34	0.38	2.34	1.16E+00	3.43E-02		1.82E+00	9.66E-05	Up	-5.21E-02	9.02E-01		-1.98E+00	3.06E-05	Down	-1.82E+00	2.11E-01		8.07E-01	3.66E-01					Unigene101529_All//2.00E-69//DV849351				
Unigene101541_All	557	0.19	2.46	0.10	0.72	1.98	0.49	1.90	4.43	2.07	3.71E+00	7.18E-06	Up	-9.75E-01	7.23E-01		1.47E+00	3.09E-02		-5.57E-01	6.38E-01		1.22E+00	9.01E-04	Up	1.28E-01	8.11E-01									
Unigene101542_All	211	0.00	0.00	0.00	0.00	0.00	0.64	1.20	0.59	6.23	null	null		null	null		null	null		9.33E+00	3.13E-01		-1.02E+00	4.96E-01		2.37E+00	7.20E-05	Up	Unigene101542_All//gi|110738232|dbj|BAF01045.1|//1.00E-07//serine/threonine kinase - like protein [Arabidopsis thaliana]	Unigene101542_All//6.00E-09//AT4G21390| B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding				GO:0004672//GO:0005488//GO:0009987	nr +
Unigene101555_All	276	7.58	5.69	5.40	5.78	5.49	5.07	3.52	0.61	1.44	-4.14E-01	3.72E-01		-4.89E-01	3.03E-01		-7.32E-02	8.77E-01		-1.87E-01	7.18E-01		-2.54E+00	6.42E-04	Down	-1.29E+00	3.62E-02		Unigene101555_All//gi|226492900|ref|NP_001148774.1|//1.00E-08//mitochondrial ribosomal protein L43 [Zea mays] >gi|195622062|gb|ACG32861.1| mitochondrial ribosomal protein L43 [Zea mays]	Unigene101555_All//7.00E-10//AT3G39650| mitochondrial ribosomal protein L51/S25/C1-B8 family protein	Unigene101555_All//5.00E-83//TC165625			GO:0030529	nr -
Unigene101556_All	300	0.00	1.86	3.20	0.17	0.34	0.15	0.00	0.00	0.00	1.09E+01	2.19E-03		1.16E+01	2.46E-05	Up	1.05E+00	8.10E-01		-1.41E-01	9.58E-01		null	null		null	null		Unigene101556_All//gi|116056517|emb|CAL52806.1|//3.00E-10//Sel1-like repeat (SSS) [Ostreococcus tauri]	Unigene101556_All//2.00E-09//AT1G70590| F-box family protein			ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene101557_All	559	0.37	1.54	0.00	0.89	0.92	0.65	1.06	2.09	3.71	2.04E+00	1.59E-02		-8.55E+00	1.47E-01		5.23E-02	9.80E-01		-4.63E-01	6.59E-01		9.83E-01	8.30E-02		1.81E+00	2.23E-05	Up				Unigene101557_All//8.00E-19//TC146433				
Unigene1016_All	3371	3.21	5.05	3.60	3.50	7.80	5.55	22.75	39.28	35.54	6.53E-01	1.29E-06		1.65E-01	3.90E-01		1.16E+00	1.54E-28	Up	6.63E-01	1.05E-07		7.88E-01	4.09E-78		6.43E-01	4.77E-51		Unigene1016_All//gi|15239540|ref|NP_197963.1|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|5107831|gb|AAD40144.1|AF149413_25 contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana] >gi|224589685|gb|ACN59374.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene1016_All//0.00E+00//AT5G25930| leucine-rich repeat family protein / protein kinase family protein	Unigene1016_All//0.00E+00//TC138249			GO:0004674//GO:0006464//GO:0016491//GO:0031224//GO:0032559	nr +
Unigene101614_All	786	0.00	0.00	0.00	0.06	0.00	4.54	0.00	0.00	0.00	null	null		null	null		-5.99E+00	5.67E-01		6.16E+00	6.65E-20	Up	null	null		null	null		Unigene101614_All//gi|300268585|gb|EFJ52765.1|//2.00E-11//pathogenesis-related protein 1-like protein [Volvox carteri f. nagariensis]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene101662_All	305	0.00	0.00	0.17	2.94	2.15	0.15	0.83	0.00	0.26	null	null		7.45E+00	6.43E-01		-4.55E-01	5.58E-01		-4.31E+00	1.14E-04	Down	-9.70E+00	4.07E-02		-1.67E+00	2.57E-01					Unigene101662_All//8.00E-144//gi|78351568|gb|DT571842.1|DT571842					
Unigene101664_All	248	2.53	8.58	1.07	0.60	0.56	0.36	0.00	0.34	0.32	1.76E+00	2.38E-04	Up	-1.24E+00	2.13E-01		-1.18E-01	9.12E-01		-7.27E-01	7.17E-01		8.40E+00	4.04E-01		8.33E+00	4.07E-01									
Unigene101652_All	409	0.00	0.00	0.00	0.12	0.00	0.22	1.65	0.10	1.36	null	null		null	null		-6.93E+00	5.66E-01		8.58E-01	7.98E-01		-4.02E+00	5.36E-04	Down	-2.78E-01	6.89E-01		Unigene101652_All//gi|224053787|ref|XP_002297979.1|//2.00E-32//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222845237|gb|EEE82784.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene101652_All//1.00E-15//AT1G64380| AP2 domain-containing transcription factor, putative	Unigene101652_All//2.00E-46//TC154225	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0009743//GO:0010468//GO:0043231	nr -
Unigene101666_All	1138	0.00	0.00	0.00	0.00	0.00	0.04	10.18	0.29	2.35	null	null		null	null		null	null		5.31E+00	7.05E-01		-5.11E+00	8.05E-70	Down	-2.12E+00	1.00E-32	Down	Unigene101666_All//gi|297793821|ref|XP_002864795.1|//1.00E-125//aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310630|gb|EFH41054.1| aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene101666_All//3.00E-116//AT5G62420| aldo/keto reductase family protein			ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism	GO:0006970//GO:0016616	nr +
Unigene101666_All	258	1.42	1.18	0.62	1.74	1.74	1.40	0.98	4.70	0.46	-2.69E-01	8.01E-01		-1.20E+00	3.96E-01		-2.20E-03	9.69E-01		-3.11E-01	7.57E-01		2.26E+00	3.35E-04	Up	-1.09E+00	4.29E-01					Unigene101666_All//2.00E-64//CK640533					
Unigene101668_All	454	0.00	0.00	0.00	0.00	0.00	0.00	4.28	2.30	0.00	null	null		null	null		null	null		null	null		-8.96E-01	3.11E-02		-1.21E+01	2.41E-14	Down	Unigene101668_All//gi|240256452|ref|NP_200624.5|//3.00E-08//actin binding [Arabidopsis thaliana]					GO:0003824//GO:0008152	nr +
Unigene1017_All	941	5.78	4.95	3.73	6.83	4.14	2.30	6.52	0.84	1.14	-2.23E-01	3.97E-01		-6.31E-01	1.83E-02		-7.24E-01	8.18E-04		-1.57E+00	1.20E-10	Down	-2.95E+00	1.12E-24	Down	-2.51E+00	1.41E-21	Down	Unigene1017_All//gi|124359162|gb|AB005685.1|//4.00E-14//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene1017_All//3.00E-10//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene1017_All//7.00E-113//TC135736				nr -
Unigene10170_All	876	0.00	0.00	0.00	0.06	0.08	0.00	0.48	2.58	2.77	null	null		null	null		4.66E-01	9.62E-01		-5.83E+00	6.47E-01		2.42E+00	9.14E-08	Up	2.52E+00	6.53E-09	Up				Unigene10170_All//2.00E-23//DW234869					
Unigene101703_All	208	0.00	0.24	1.02	4.31	0.17	1.95	1.02	0.20	0.77	7.93E+00	6.24E-01		1.00E+01	1.42E-01		-4.70E+00	1.27E-05	Down	-1.14E+00	1.31E-01		-2.34E+00	2.37E-01		-4.08E-01	7.56E-01									
Unigene101708_All	211	9.67	0.72	2.27	1.89	1.80	0.64	0.00	0.00	0.00	-3.75E+00	1.18E-08	Down	-2.09E+00	8.44E-05	Down	-7.32E-02	9.26E-01		-1.56E+00	2.31E-01		null	null		null	null									
Unigene10172_All	201	11.97	15.63	14.84	111.03	105.02	102.46	45.44	31.81	20.81	3.84E-01	2.87E-01		3.09E-01	4.13E-01		-8.03E-02	5.79E-01		-1.16E-01	4.04E-01		-5.14E-01	2.51E-03		-1.13E+00	7.26E-11	Down	Unigene10172_All//gi|30725324|gb|AP237684.1|//3.00E-17//At3g01680 [Arabidopsis thaliana]	Unigene10172_All//1.00E-18//AT3G01680| unknown protein	Unigene10172_All//2.00E-88//ES843933				nr +
Unigene101722_All	247	0.21	0.41	0.00	1.41	0.00	1.65	1.88	13.37	5.00	9.54E-01	7.28E-01		-7.73E+00	6.36E-01		-1.05E+01	9.46E-03		2.21E-01	8.63E-01		2.83E+00	5.32E-13	Up	1.41E+00	9.74E-03		Unigene101722_All//gi|55818553|gb|AAV66071.1|//5.00E-08//acidic glucanase [Medicago sativa]			Unigene101722_All//2.00E-42//TC142668		GO:0016798	nr +
Unigene10174_All	397	0.00	3.57	2.28	0.00	0.09	0.00	0.00	0.00	0.00	1.18E+01	4.06E-08	Up	1.12E+01	4.72E-05	Up	6.44E+00	8.42E-01		null	null		null	null		null	null					Unigene10174_All//8.00E-18//FL577438					
Unigene10175_All	473	0.00	0.00	0.00	0.42	0.00	0.00	6.08	4.68	0.51	null	null		null	null		-8.72E+00	8.49E-02		-8.72E+00	1.34E-01		-3.76E-01	2.81E-01		-3.59E+00	1.22E-14	Down	Unigene10175_All//gi|297725019|ref|NP_001174873.1|//6.00E-19//Os06g0586150 (Oryza sativa Japonica Group) >gi|255677180|dbj|BAH93601.1| Os06g0586150 (Oryza sativa Japonica Group)	Unigene10175_All//3.00E-15//AT3G47580| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152	nr -
Unigene10177_All	277	0.00	0.00	0.00	0.00	0.00	0.00	2.75	0.00	1.15	null	null		null	null		null	null		null	null		-1.14E+01	1.68E-05	Down	-1.26E+00	7.70E-02		Unigene10177_All//gi|42568648|ref|NP_200715.2|//5.00E-23//glycosyl transferase family 1 protein [Arabidopsis thaliana]	Unigene10177_All//2.00E-24//AT5G59070| glycosyl transferase family 1 protein				GO:0008152//GO:0016740	nr -
Unigene10179_All	239	1.31	1.27	0.89	2.50	1.73	0.00	0.00	0.00	1.17	-4.63E-02	9.85E-01		-5.60E-01	6.64E-01		-5.33E-01	5.62E-01		-1.13E+01	7.71E-04	Down	null	null		1.02E+01	2.44E-02		Unigene10179_All//gi|77999307|gb|AB817000.1|//2.00E-13//ribosomal protein L23 family protein [Solanum tuberosum]	Unigene10179_All//5.00E-13//AT4G39880| ribosomal protein L23 family protein	Unigene10179_All//2.00E-26//TC146980			GO:0005198//GO:0005402//GO:0005488//GO:0006810//GO:0010467//GO:0012505//GO:0022613//GO:0030529//GO:0031224	nr -
Unigene1018_All	1337	50.79	20.31	31.34	68.11	35.75	16.08	10.44	4.47	2.21	-1.32E+00	9.37E-77	Down	-6.97E-01	6.92E-26		-9.30E-01	6.32E-72		-2.08E+00	1.17E-213	Down	-1.22E+00	1.04E-17	Down	-2.24E+00	3.98E-42	Down	Unigene1018_All//gi|297725701|ref|NP_001175214.1|//1.00E-11//Os07g0501200 (Oryza sativa Japonica Group) >gi|255677791|dbj|BAH93942.1| Os07g0501200 (Oryza sativa Japonica Group)	Unigene1018_All//3.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene1018_All//3.00E-91//TC135736				nr +
Unigene10181_All	827	0.00	9.44	4.25	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.26E-44	Up	1.21E+01	1.88E-19	Up	null	null		null	null		null	null		null	null		Unigene10181_All//gi|226502788|ref|NP_001148944.1|//1.00E-48//nascent polypeptide-associated complex alpha subunit-like protein [Zea mays] >gi|195623512|gb|ACG33586.1| nascent polypeptide-associated complex alpha subunit-like protein [Zea mays]	Unigene10181_All//1.00E-32//AT3G49470| NACA2 (NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX SUBUNIT ALPHA-LIKE PROTEIN 2)				GO:0006970	nr -
Unigene101816_All	208	0.25	0.00	1.28	1.20	0.33	1.30	0.00	2.61	0.38	-7.97E+00	6.23E-01		2.35E+00	2.40E-01		-1.85E+00	2.76E-01		1.22E-01	9.45E-01		1.14E+01	5.37E-04	Up	8.58E+00	4.07E-01									
Unigene101818_All	234	7.60	3.68	13.88	2.13	1.77	4.25	2.53	11.25	3.75	-1.05E+00	3.39E-02		8.69E-01	1.56E-02		-2.70E-01	8.02E-01		9.96E-01	1.72E-01		2.15E+00	6.92E-08	Up	5.66E-01	3.85E-01					Unigene101818_All//6.00E-42//TC156918					

Unigene10183_All	603	0.00	0.00	0.00	0.00	0.00	0.00	6.52	1.66	2.11	null	null		null	null		null	null		null	null		-1.97E+00	2.60E-10	Down	-1.62E+00	2.16E-08	Down	Unigene10183_All//gi|21322711|emb|CAD22154.1|//9.00E-53//pheropherin-dr1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome	GO:0044464	nr +
Unigene10185_All	666	0.00	0.00	0.00	0.00	0.00	0.27	2.73	6.02	2.51	null	null		null	null		null	null		8.08E+00	1.96E-01		1.14E+00	3.76E-05	Up	-1.20E-01	7.71E-01		Unigene10185_All//gi|224096718|ref|XP_002310710.1|//6.00E-88//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]>gi|222853613|gb|EEE91160.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene10185_All//9.00E-79//AT3G50210| 2-oxoacid-dependent oxidase, putative			ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016706//GO:0031669//GO:0032502//GO:0046914	nr -
Unigene10187_All	437	1.08	0.23	1.34	6.61	5.36	2.69	0.19	0.77	1.28	-2.22E+00	7.77E-02		3.15E-01	7.19E-01		-3.03E-01	4.44E-01		-1.30E+00	4.76E-04	Down	1.98E+00	1.45E-01		2.72E+00	9.39E-03		Unigene10187_All|gb|AN62348.1|AF506028_15//5.00E-31//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene10187_All//8.00E-22//AT5G63020| disease resistance protein (CC-NBS-LRR class), putative	Unigene10187_All//6.00E-136//DR461626		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016787	nr +
Unigene10188_All	459	0.00	12.58	9.28	0.00	0.00	0.00	0.18	0.00	0.00	1.36E+01	5.79E-33	Up	1.32E+01	1.22E-23	Up	null	null		null	null		-7.53E+00	4.09E-01		-7.53E+00	3.62E-01		Unigene10188_All//gi|15229631|ref|NP_190560.1|//1.00E-88//60S ribosomal protein L26 (RPL26A) [Arabidopsis thaliana]>gi|297816242|ref|XP_002876004.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]>gi|27735242|sp|P51414.2|RL261_ARATH RecName: Full=60S ribosomal protein L26-1>gi|6723436|emb|CAB66929.1| 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana]>gi|297321842|gb|EFH52263.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene10188_All//4.00E-41//AT3G49910| 60S ribosomal protein L26 (RPL26A)			ko03010|Ribosome	GO:0005198//GO:0006950//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene10191_All	445	0.00	0.00	0.00	0.00	0.00	0.00	1.43	8.27	4.48	null	null		null	null		null	null		null	null		2.54E+00	6.95E-13	Up	1.65E+00	1.08E-04	Up							
Unigene10192_All	672	0.16	15.31	7.69	0.00	0.00	0.00	0.00	0.00	6.62E+00	2.97E-55	Up	5.63E+00	1.12E-25	Up	null	null		null	null		null	null		null	null		Unigene10192_All//gi|585238|sp|Q08864.3|H11_VOLCA//6.00E-25//RecName: Full=Histone H1-I>gi|349585|gb|AAA74723.1| histone H1-I [Volvox carteri]>gi|300267026|gb|EFJ51211.1| histone H1 [Volvox carteri f. nagariensis]	Unigene10192_All//2.00E-65//AT3G18035| HON4; DNA binding					nr +
Unigene10193_All	642	2.12	0.55	1.00	10.32	8.69	7.18	7.05	4.56	1.92	-1.94E+00	2.18E-03		-1.09E+00	7.48E-02		-2.48E-01	3.12E-01		-5.24E-01	2.22E-02		-6.29E-01	1.31E-02		-1.87E+00	2.00E-11	Down	Unigene10193_All//gi|79499196|ref|NP_195518.2|//3.00E-21//transmembrane transporter [Arabidopsis thaliana]>gi|75128428|sp|Q6S287.1|NAT11_ARATH RecName: Full=Nucleobase-ascorbate transporter 11; Short=AtNAT11>gi|38350521|gb|AAR18373.1| nucleobase-ascorbate transporter 11 [Arabidopsis thaliana]	Unigene10193_All//6.00E-21//AT4G38050| transmembrane transporter				GO:0005215//GO:0006810//GO:0016020	nr +
Unigene101932_All	249	0.00	6.10	0.00	0.80	1.66	2.54	0.68	1.01	1.44	1.26E+01	1.10E-08	Up	null	null		1.05E+00	4.26E-01		1.67E+00	9.80E-02		5.68E-01	6.75E-01		1.08E+00	3.50E-01					Unigene101932_All//1.00E-58//gi|164243022|gb|ES823910.1|ES823910				
Unigene10196_All	312	1.17	12.83	4.27	5.43	3.31	2.46	2.03	1.88	2.04	3.45E+00	2.82E-15	Up	1.86E+00	4.86E-03		-7.13E-01	1.48E-01		-1.14E+00	2.50E-02		-1.16E-01	8.88E-01		7.30E-03	9.95E-01					Unigene10196_All//2.00E-11//TC153817				
Unigene101960_All	220	0.00	1.38	0.00	0.68	0.16	0.82	0.77	1.14	8.15	1.04E+01	4.45E-02		null	null		-2.12E+00	3.88E-01		2.74E-01	9.06E-01		5.68E-01	6.75E-01		3.41E+00	8.04E-09	Up	Unigene101960_All|gi|297806781|ref|XP_002871274.1|//3.00E-08//predicted protein [Arabidopsis lyrata subsp. lyrata]>gi|297317111|gb|EFH47533.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	Unigene101960_All//1.00E-09//AT5G07490| unknown protein					nr -
Unigene101985_All	271	0.97	1.68	0.59	0.74	1.27	1.50	10.61	8.79	1.47	8.02E-01	4.60E-01		-7.12E-01	6.22E-01		7.89E-01	5.96E-01		1.03E+00	4.29E-01		-2.71E-01	4.47E-01		-2.85E+00	5.76E-12	Down				Unigene101985_All//3.00E-69//TC172050				
Unigene10199_All	717	0.07	12.30	7.35	0.00	0.00	0.00	0.00	0.00	0.00	7.40E+00	1.54E-48	Up	6.65E+00	1.17E-27	Up	null	null		null	null		null	null		null	null		Unigene10199_All//gi|160895838|ref|YP_001561420.1|//2.00E-65//elongation factor Tu [Delftia acidovorans SPH-1]>gi|160361422|gb|ABX33035.1| translation elongation factor Tu [Delftia acidovorans SPH-1]	Unigene10199_All//3.00E-50//AT4G20360| ATRABE1B (ARABIDOPSIS RAB GTPASE HOMOLOG E1B); GTP binding / GTPase/ translation elongation factor	Unigene10199_All//6.00E-11//EX172631		ko04626|Plant-pathogen interaction	GO:0006412//GO:0008135//GO:0009536//GO:0016772//GO:0017111//GO:00325 61	nr +
Unigene102_All	1463	3.40	3.05	1.49	3.00	2.94	2.65	2.80	2.31	1.31	-1.57E-01	6.04E-01		-1.19E+00	3.56E-05	Down	-2.63E-02	9.35E-01		-1.75E-01	6.24E-01		-2.77E-01	3.52E-01		-1.10E+00	3.37E-05	Down	Unigene102_All//gi|297798410|ref|XP_002867089.1|//1.00E-150//transducin family protein [Arabidopsis lyrata subsp. lyrata]>gi|297312925|gb|EFH43348.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene102_All//4.00E-148//AT4G35140| transducin family protein / WD-40 repeat family protein	Unigene102_All//0.00E+00//gi|84164480|gb|DR453128.1|DR453128				nr +
Unigene1020_All	1402	8.84	20.38	16.75	22.28	42.42	51.90	51.39	96.86	22.42	1.20E+00	3.23E-28	Up	9.21E-01	9.14E-15		9.29E-01	3.79E-45		1.22E+00	1.31E-77	Up	9.14E-01	4.63E-103		-1.20E+00	1.37E-87	Down	Unigene1020_All//gi|79521554|ref|NP_197973.2|//3.00E-96//catalytic/ protein serine/threonine phosphatase [Arabidopsis thaliana]>gi|226739226|sp|Q9XGZ9.2|PC72_ARATH RecName: Full=Probable protein phosphatase 2C 72; Short=AtPP2C72	Unigene1020_All//2.00E-92//AT5G26010| catalytic/ protein serine/threonine phosphatase	Unigene1020_All//0.00E+00//TC156152			GO:0003824	nr -
Unigene10200_All	523	0.00	26.26	6.52	0.00	0.40	0.00	0.00	0.00	0.00	1.47E+01	7.80E-79	Up	1.27E+01	7.39E-19	Up	8.63E+00	1.58E-01		null	null		null	null		null	null		Unigene10200_All//gi|298711973|emb|CBJ32915.1|//6.00E-25//ribosomal protein L35 [Ectocarpus siliculosus]	Unigene10200_All//7.00E-24//AT1G74270| 60S ribosomal protein L35a (RPL35aC)			ko03010|Ribosome	GO:0043231	nr -
Unigene10201_All	1255	0.25	4.44	2.72	0.40	0.58	0.43	0.44	0.23	0.32	4.15E+00	3.21E-24	Up	3.44E+00	1.30E-12	Up	5.38E-01	5.64E-01		1.22E-01	9.21E-01		-9.10E-01	3.19E-01		-4.65E-01	5.97E-01		Unigene10201_All|gi|71905515|gb|AA252735.1|//7.00E-94//expressed protein [Arabidopsis thaliana]	Unigene10201_All//4.00E-90//AT4G12680| unknown protein	Unigene10201_All//0.00E+00//CO131664			GO:0003006//GO:0031410	nr +
Unigene10202_All	740	0.00	0.00	0.00	0.00	0.00	0.00	2.97	0.56	3.98	null	null		null	null		null	null		null	null		-2.40E+00	1.55E-07	Down	4.23E-01	1.93E-01		Unigene10202_All//gi|224077026|ref|XP_002305098.1|//2.00E-68//AP2/ERF domain-containing transcription factor [Populus trichocarpa]>gi|222848062|gb|EEE85609.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene10202_All//1.00E-26//AT4G18450| ethylene-responsive factor, putative	Unigene10202_All//1.00E-08//TC178583	AP2-EREBP		GO:0006350//GO:0010033//GO:0010468//GO:0043231	nr +
Unigene102075_All	420	61.41	49.95	55.28	5.81	8.77	6.77	3.22	1.69	0.76	-2.98E-01	6.26E-03		-1.52E-01	2.23E-01		5.94E-01	6.40E-02		2.21E-01	6.27E-01		-9.29E-01	7.36E-02		-2.09E+00	1.85E-04	Down	Unigene102075_All//gi|47155380|dbj|BAD18925.1|//2.00E-30//ferredoxin [Codonopsis lanceolata]	Unigene102075_All//2.00E-31//AT2G04700| ferredoxin thioredoxin reductase catalytic beta chain family protein	Unigene102075_All//4.00E-171//gi|109867808|gb|DW496784.1|DW496784			GO:0008152//GO:0009536//GO:0016731//GO:0043169//GO:0051536	nr +
Unigene10208_All	501	0.00	11.02	2.23	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.66E-31	Up	1.11E+01	3.44E-06	Up	null	null		null	null		null	null		null	null		Unigene10208_All//sp|P08285|H103_CHICK//4.00E-06//Histone H1.03 OS=Gallus gallus PE=3 SV=2						swissprot +
Unigene1021_All	3759	9.24	5.65	7.00	19.40	16.65	16.18	34.99	15.68	18.60	-7.11E-01	1.30E-14		-4.01E-01	1.98E-05		-2.20E-01	1.47E-04		-2.62E-01	1.27E-05		-1.16E+00	4.04E-147	Down	-9.12E-01	3.18E-102		Unigene1021_All//gi|15228737|ref|NP_191795.1|//0.00E+00//carbohydrate binding [Arabidopsis thaliana]	Unigene1021_All//0.00E+00//AT3G6236 0| carbohydrate binding	Unigene1021_All//0.00E+00//TC179301			GO:0005488//GO:0005618//GO:0008238//GO:0016020//GO:0031410//GO:0043231	nr +
Unigene10210_All	778	0.40	0.91	0.14	0.00	0.22	0.00	1.03	11.66	2.15	1.18E+00	1.75E-01		-1.56E+00	3.30E-01		7.79E+00	2.28E-01		null	null		3.50E+00	3.07E-42	Up	1.06E+00	1.67E-02		Unigene10210_All|gb|ACQ83519.1|//6.00E-20//CBL-interacting protein kinase 03 [Vitis vinifera]	Unigene10210_All//4.00E-15//AT4G30960| SIP3 (SOS3-INTERACTING PROTEIN 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene10210_All//6.00E-85//TC133167			GO:0006174//GO:0006464//GO:0006972//GO:0009926//GO:0023060//GO:0032501//GO:0032502//GO:0032559//GO:0046872	nr +
Unigene102112_All	480	1.42	0.00	0.33	4.36	1.43	0.56	0.35	0.00	0.50	-1.05E+01	4.10E-04	Down	-2.09E+00	4.38E-02		-1.60E+00	2.04E-04	Down	-2.95E+00	9.27E-08	Down	-8.46E+00	1.35E-01		4.99E-01	7.08E-01		Unigene102112_All//gi|115446245|ref|NP_001046902.1|//1.00E-14//Os02g0502500 [Oryza sativa Japonica Group]>gi|113536433|dbj|BAF08816.1| Os02g0502500 [Oryza sativa Japonica Group]	Unigene102112_All//6.00E-06//AT2G40980| LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein kinase-like (InterPro:IPR011009); Has 152 Blast hits to 139 proteins in 56 species: Archae - 0; Bacteria - 74; Metazoa - 0; Fungi - 0; Plants - 60; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink).					nr -
Unigene10213_All	796	0.00	1.02	0.13	0.06	0.04	0.11	0.85	3.10	30.03	9.99E+00	9.39E-05	Up	7.06E+00	4.03E-01		-5.32E-01	8.30E-01		8.59E-01	7.98E-01		1.87E+00	2.64E-06	Up	5.14E+00	8.58E-146	Up	Unigene10213_All//gi|224139556|ref|XP_002323167.1|//2.00E-09//ABC transporter family protein [Populus trichocarpa]>gi|222867797|gb|EEF04928.1| ABC transporter family protein [Populus trichocarpa]		Unigene10213_All//0.00E+00//DT463777				nr +
Unigene10215_All	575	0.00	0.00	0.00	0.00	0.00	0.00	2.43	1.89	0.35	null	null		null	null		null	null		null	null		-3.61E-01	5.05E-01		-2.81E+00	4.26E-06	Down	Unigene10215_All//gi|116222231|gb|ABJ80979.1|//8.00E-95//alpha tubulin [Porphyra yezoensis]	Unigene10215_All//1.00E-84//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene10215_All//5.00E-48//TC142299		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene10216_All	636	0.00	0.00	0.00	0.00	0.00	0.00	4.45	4.73	0.06	null	null		null	null		null	null		null	null		8.72E-02	8.00E-01		-6.15E+00	2.65E-19	Down	Unigene10216_All//gi|297844300|ref|XP_002890031.1|//2.00E-50//eukaryotic translation initiation factor 5A-1 [Arabidopsis lyrata subsp. lyrata]>gi|297338873|gb|EFH66290.1| eukaryotic translation initiation factor 5A-1 [Arabidopsis lyrata subsp. lyrata]	Unigene10216_All//1.00E-50//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor	Unigene10216_All//8.00E-07//EX164461			GO:0006448//GO:0006449//GO:0008135//GO:0010087//GO:0018205//GO:0043021	nr -
Unigene102186_All	206	0.51	1.48	0.00	2.42	0.00	2.63	0.41	0.41	0.00	1.54E+00	3.24E-01		-8.99E+00	4.00E-01		-1.12E+01	8.99E-04	Down	1.22E-01	9.21E-01		-1.66E-02	1.02E+00		-8.68E+00	3.62E-01					Unigene102186_All//2.00E-10//DW517741				
Unigene102197_All	486	0.11	0.00	0.00	0.31	0.43	2.23	0.52	0.00	2.38	-6.75E+00	6.23E-01		-6.75E+00	6.35E-01		4.67E-01	8.26E-01		2.86E+00	4.98E-04	Up	-9.03E+00	4.06E-02		2.19E+00	4.81E-04	Up	Unigene102197_All//gi|300507131|gb|ADK23941.1|//5.00E-43//KASIII [Gossypium hirsutum]	Unigene102197_All//4.00E-116//AT1G62640| KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III); 3-oxoacyl-[acyl-carrier-protein] synthase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene102197_All//4.00E-116//gi|48815960|gb|CO117273.1|CO117273		ko00061|Fatty acid biosynthesis	GO:0004312//GO:0006631	nr -
Unigene1022_All	3085	4.94	4.75	8.35	12.45	17.22	9.88	1.55	6.06	1.14	-5.62E-02	7.18E-01		7.59E-01	8.80E-12		4.68E-01	2.08E-12		-3.33E-01	8.28E-05		1.97E+00	5.24E-46	Up	-4.47E-01	6.33E-02		Unigene1022_All//gi|1321686|emb|CAA06376.1|//0.00E+00//light repressible receptor protein kinase [Arabidopsis thaliana]	Unigene1022_All//2.00E-178//AT4G29990| light repressible receptor protein kinase			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene10221_All	334	0.78	0.46	0.32	0.30	1.03	0.68	0.00	0.00	2.27	-7.83E-01	6.20E-01		-1.30E+00	4.37E-01		1.79E+00	2.58E-01		1.18E+00	5.50E-01		null	null		1.11E+01	1.39E-05	Up				Unigene10221_All//4.00E-07//TC142752				
Unigene10223_All	701	0.00	0.00	0.00	0.00	0.00	0.00	4.34	5.43	0.00	null	null		null	null		null	null		null	null		3.21E-01	2.87E-01		-1.21E+01	2.16E-22	Down	Unigene10223_All//gi|115445597|ref|NP_001046578.1|//6.00E-81//Os02g0287000 [Oryza sativa Japonica Group]>gi|113536109|dbj|BAF04892.1| Os02g0287000 [Oryza sativa Japonica Group]	Unigene10223_All//9.00E-80//AT4G34670| 40S ribosomal protein S3A (RPS3aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -

Unigene10226_All	711	0.00	71.91	36.10	0.00	0.00	0.00	0.00	0.00	0.00	1.61E+01	2.30E-295	Up	1.51E+01	2.51E-145	Up	null	null		null	null		null	null		null	null		Unigene10226_All//gi|57471708|gb|AW50985.1|/2.00E-61//ribosomal protein L18 [Triticum aestivum]	Unigene10226_All//2.00E-57//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene10227_All	473	0.77	0.32	0.00	1.90	1.89	1.81	2.68	0.35	3.54	-1.27E+00	3.36E-01		-9.60E+00	2.79E-02		-2.20E-03	9.78E-01		-6.34E-02	9.39E-01		-2.92E+00	1.46E-05	Down	4.00E-01	3.78E-01									
Unigene10229_All	254	2.88	0.00	0.42	2.55	1.90	3.56	0.33	0.49	0.16	-1.15E+01	2.11E-04	Down	-2.78E+00	1.05E-02		-4.26E-01	6.09E-01		4.80E-01	5.50E-01		5.69E-01	7.83E-01		-1.09E+00	6.78E-01									
Unigene102296_All	210	0.25	0.00	0.00	4.98	3.28	0.22	0.00	0.00	0.00	-7.96E+00	6.22E-01		-7.96E+00	6.35E-01		-6.03E-01	3.67E-01		-4.53E+00	1.60E-05	Down	null	null		null	null					Unigene102296_All//2.00E-29//gi|164354102|gb|ES849373.1|ES849373					
Unigene1023_All	1442	8.56	4.81	5.83	10.23	8.43	5.86	3.69	1.07	0.39	-8.31E-01	3.05E-07		-5.54E-01	9.15E-04		-2.79E-01	5.87E-02		-8.04E-01	1.66E-08		-1.78E+00	4.34E-12	Down	-3.26E+00	1.85E-24	Down	Unigene1023_All//gi|297791827|ref|XP_002863798.1|//2.00E-73//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297309633|gb|EFH40057.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene1023_All//2.00E-59//AT5G42340| binding / ubiquitin-protein ligase	Unigene1023_All//0.00E+00//TC179266			GO:0019787//GO:0032446//GO:0043234//GO:0044424	nr +
Unigene10230_All	691	0.00	53.82	27.36	0.00	0.00	0.00	0.00	0.00	0.00	1.57E+01	1.29E-214	Up	1.47E+01	8.83E-107	Up	null	null		null	null		null	null		null	null		Unigene10230_All//gi|297812211|ref|XP_002873989.1|//2.00E-69//ribosomal protein S8 [Arabidopsis lyrata subsp. lyrata] >gi|297319826|gb|EFH50248.1| ribosomal protein S8 [Arabidopsis lyrata subsp. lyrata]	Unigene10230_All//5.00E-62//AT5G20290| 40S ribosomal protein S8 (RPS8A)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0030312//GO:0031981	nr -
Unigene10232_All	521	1.41	0.97	0.00	2.87	3.04	0.35	0.89	0.16	0.00	-5.32E-01	5.13E-01		-1.05E+01	4.13E-04	Down	8.40E-02	8.96E-01		-3.05E+00	7.42E-06	Down	-2.48E+00	3.38E-02		-9.80E+00	1.10E-03					Unigene10232_All//3.00E-15//DR454672					
Unigene10234_All	314	0.17	2.58	0.00	1.90	1.75	1.73	1.48	0.93	1.14	3.95E+00	7.52E-04	Up	-7.38E+00	6.35E-01		-1.18E-01	8.76E-01		-1.41E-01	8.80E-01		-6.69E-01	5.09E-01		-3.75E-01	6.65E-01		Unigene10234_All//gi|17979268|gb|AAL49950.1|/3.00E-10//At1g22970/F19G10_8 [Arabidopsis thaliana] >gi|21700855|gb|AAM70551.1| At1g22970/F19G10_8 [Arabidopsis thaliana]	Unigene10234_All//1.00E-11//AT1G22970| unknown protein					nr -
Unigene102349_All	209	0.75	5.58	3.31	1.19	0.99	3.24	120.97	99.19	62.33	2.89E+00	2.98E-04	Up	2.14E+00	3.67E-02		-2.70E-01	8.23E-01		1.44E+00	1.28E-01		-2.86E-01	3.70E-03		-9.57E-01	5.16E-22					Unigene102349_All//6.00E-45//gi|109867479|gb|DR496455.1|DR496455					
Unigene10236_All	804	0.00	0.00	0.00	0.00	0.00	0.00	13.09	14.87	1.64	null	null		null	null		null	null		null	null		1.83E-01	2.62E-01		-3.00E+00	4.18E-44	Down	Unigene10236_All//gi|238014838|gb|ACR38454.1|//1.00E-14//unknown [Zea mays]		Unigene10236_All//9.00E-38//TC146753				nr -
Unigene10239_All	698	0.00	9.15	5.04	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.85E-36	Up	1.23E+01	1.88E-19	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene1024_All	2200	20.36	5.37	7.82	20.38	19.03	11.58	5.59	1.22	1.30	-1.92E+00	4.43E-87	Down	-1.38E+00	2.23E-52	Down	-9.85E-02	2.92E-01		-8.16E-01	3.22E-25		-2.20E+00	2.84E-35	Down	-2.10E+00	2.33E-34	Down	Unigene1024_All//gi|297791827|ref|XP_002863798.1|//0.00E+00//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297309633|gb|EFH40057.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene1024_All//0.00E+00//AT5G42340| binding / ubiquitin-protein ligase	Unigene1024_All//0.00E+00//TC179266	ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0019787//GO:0032446//GO:0043231//GO:0043234	nr +
Unigene10241_All	790	0.00	50.22	19.75	0.00	0.00	0.00	0.00	0.00	0.00	1.56E+01	5.33E-229	Up	1.43E+01	5.59E-88	Up	null	null		null	null		null	null		null	null		Unigene10241_All//sp|P92201|LCP8_DROME//5.00E-26//Larval cuticle protein 8 OS=Drosophila melanogaster GN=Lcp65Ag1 PE=1 SV=1						swissprot -
Unigene10242_All	517	0.00	12.84	6.90	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	6.43E-38	Up	1.28E+01	9.42E-20	Up	null	null		null	null		null	null		null	null		Unigene10242_All//sp|P56562|CUD5_SCHGR//2.00E-10//Endocuticle structural glycoprotein SgAbd-5 OS=Schistocerca gregaria PE=1 SV=1						swissprot -
Unigene10243_All	275	0.38	0.37	0.00	1.45	0.88	1.48	6.61	3.34	21.88	-4.62E-02	9.91E-01		-8.57E+00	4.00E-01		-7.25E-01	5.47E-01		2.86E-02	9.85E-01		-9.83E-01	2.32E-02		1.73E+00	2.90E-13	Up				Unigene10243_All//4.00E-25//gi|164363055|gb|ES820462.1|ES820462					
Unigene102458_All	289	7.06	4.38	2.21	13.79	9.65	9.38	32.19	33.70	26.47	-6.88E-01	1.27E-01		-1.68E+00	8.93E-04	Down	-5.15E-01	8.49E-02		-5.56E-01	7.28E-02		6.62E-02	7.27E-01		-2.82E-01	9.80E-02		Unigene102458_All//gi|45861745|gb|AAS78671.1|//1.00E-23//actin [Capsicum annuum]	Unigene102458_All//1.00E-23//AT5G59370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene102458_All//3.00E-84//TC171105	ko04145|Phagosome	GO:0032559//GO:0043232	nr +
Unigene10247_All	405	0.00	4.25	1.97	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	8.00E-10	Up	1.09E+01	1.72E-04	Up	null	null		null	null		null	null		null	null										
Unigene10248_All	675	0.00	23.50	10.33	0.00	0.00	0.00	0.00	0.00	0.00	1.45E+01	3.99E-91	Up	1.33E+01	5.73E-39	Up	null	null		null	null		null	null		null	null		Unigene10248_All//gi|24061807|gb|AAN39804.1|//5.00E-11//transferrin-like protein IDI-100 [Dunaliella salina]						nr -
Unigene10249_All	281	0.00	0.00	0.00	0.00	0.00	0.00	12.94	4.61	7.51	null	null		null	null		null	null		null	null		-1.49E+00	9.84E-07	Down	-7.84E-01	4.67E-03		Unigene10249_All//gi|117607067|gb|ABK42077.1|//9.00E-39//ubiquitin extension protein [Capsicum annuum]	Unigene10249_All//2.00E-21//AT3G62250| UBQ5 (ubiquitin 5); protein binding / structural constituent of ribosome	Unigene10249_All//3.00E-07//ES818268	ko03010|Ribosome	GO:0005198//GO:0005488//GO:0010467//GO:0015935//GO:0016567//GO:0019941	nr +
Unigene1025_All	2394	3.74	4.66	1.40	8.57	10.66	12.04	7.05	2.62	3.74	3.17E-01	7.13E-02		-1.42E+00	2.77E-11	Down	3.14E-01	2.65E-03		4.90E-01	5.93E-07		-1.43E+00	9.40E-27	Down	-9.12E-01	6.59E-14		Unigene1025_All//gi|297791827|ref|XP_002863798.1|//1.00E-166//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297309633|gb|EFH40057.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene1025_All//7.00E-154//AT5G42340| binding / ubiquitin-protein ligase	Unigene1025_All//0.00E+00//TC147579	ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene10250_All	619	0.00	9.25	3.79	0.00	0.06	0.00	0.00	0.00	0.00	1.32E+01	1.13E-32	Up	1.19E+01	6.41E-13	Up	5.80E+00	8.41E-01		null	null		null	null		null	null		Unigene10250_All//gi|261853464|gb|ACV00391.1|//9.00E-22//calmodulin [Polygonum sibiricum]	Unigene10250_All//5.00E-22//AT5G37780| CAM1 (CALMODULIN 1); calcium ion binding		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005488//GO:0019932	nr -
Unigene10251_All	456	0.00	0.11	0.23	0.22	0.00	0.59	1.76	1.74	64.30	6.80E+00	6.23E-01		7.87E+00	4.03E-01		-7.77E+00	3.18E-01		1.44E+00	4.10E-01		-1.66E-02	1.02E+00		5.19E+00	1.37E-179	Up	Unigene10251_All//gi|224061172|ref|XP_002300362.1|//5.00E-26//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222847620|gb|EEE85167.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene10251_All//7.00E-10//AT3G13100| ATMRP7; ATPase, coupled to transmembrane movement of substances	Unigene10251_All//6.00E-96//TC157562		GO:0009607//GO:0016020//GO:0017111	nr +
Unigene10510_All	318	14.64	35.37	7.87	23.03	21.77	19.32	12.76	17.35	7.14	1.27E+00	1.57E-12	Up	-8.96E-01	2.17E-03		-8.13E-02	7.69E-01		-2.54E-01	2.93E-01		4.43E-01	5.55E-02		-8.38E-01	1.34E-03					Unigene10510_All//1.00E-105//TC167368					
Unigene102517_All	339	2.47	0.15	0.47	0.29	0.81	0.27	2.37	2.10	1.65	-4.05E+00	4.66E-04	Down	-2.39E+00	1.14E-02		1.47E+00	4.20E-01		-1.41E-01	9.54E-01		-1.77E-01	7.93E-01		-5.26E-01	4.35E-01		Unigene102517_All//gi|226499554|ref|NP_001149976.1|//1.00E-10//SAM domain family protein [Zea mays] >gi|195635833|gb|ACG37285.1| SAM domain family protein [Zea mays]	Unigene102517_All//3.00E-10//AT1G70180| sterile alpha motif (SAM) domain-containing protein	Unigene102517_All//7.00E-95//TC167190			GO:0006464//GO:0016301//GO:0032559	nr -
Unigene10252_All	455	0.00	1.89	2.11	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	4.95E-05	Up	1.10E+01	2.46E-05	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene10254_All	574	0.00	2.38	3.25	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	7.80E-08	Up	1.17E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene10254_All//gi|116060285|emb|CAL55621.1|//1.00E-05//Myosin class II heavy chain (ISS) [Ostreococcus tauri]	Unigene10254_All//7.00E-05//AT5G41790| CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding					nr -
Unigene10563_All	403	0.26	6.16	0.26	0.00	0.17	0.90	0.00	0.00	0.00	4.57E+00	1.16E-11	Up	2.53E-02	1.00E+00		7.42E+00	6.17E-01		9.81E+00	2.38E-02		null	null		null	null		Unigene102563_All//gi|5031277|gb|AD38144.1|AF139497_1|/4.00E-26//homeobox leucine zipper protein [Prunus armeniaca]	Unigene102563_All//6.00E-25//AT2G46680| ATHB-7 (ARABIDOPSIS THALIANA HOMEOBOX 7); transcription activator/ transcription factor	Unigene102563_All//2.00E-142//ES813725	HB		GO:0001071//GO:0003677//GO:0006351//GO:0006970//GO:0009755//GO:0010468//GO:0010557//GO:0030528//GO:0043231	nr +
Unigene102572_All	210	0.00	3.14	1.01	2.61	1.48	3.87	1.01	1.00	0.38	1.16E+01	6.26E-04	Up	9.99E+00	1.42E-01		-8.22E-01	3.96E-01		5.69E-01	4.96E-01		-1.67E-02	1.02E+00		-1.41E+00	3.81E-01										
Unigene102582_All	298	0.00	0.51	0.00	0.00	0.00	0.91	0.43	6.87	2.94	8.99E+00	2.37E-01		null	null		null	null		9.83E+00	7.06E-02		4.01E+00	5.29E-11	Up	2.79E+00	5.37E-04	Up				Unigene102582_All//6.00E-46//DN799979					
Unigene102587_All	243	0.00	0.00	0.00	0.21	0.00	0.00	5.05	0.17	0.16	null	null		null	null		-7.68E+00	5.66E-01		-7.68E+00	6.47E-01		-4.87E+00	1.49E-07	Down	-4.94E+00	6.14E-08	Down	Unigene102587_All//gi|224140739|ref|XP_002323736.1|/3.00E-06//predicted protein [Populus trichocarpa] >gi|222866738|gb|EEF03869.1| predicted protein [Populus trichocarpa]		Unigene102587_All//5.00E-24//TC148715				nr +
Unigene102591_All	297	0.18	0.00	0.00	0.50	1.39	3.50	0.71	0.00	0.00	-7.46E+00	6.22E-01		-7.46E+00	6.35E-01		1.47E+00	2.80E-01		2.80E+00	8.13E-04	Up	-9.48E+00	7.48E-02		-9.48E+00	5.84E-02		Unigene102591_All//gi|15809986|gb|AAL06920.1|/2.00E-34//AT3g19540/T31J18_4 [Arabidopsis thaliana] >gi|22137022|gb|AAM91356.1| At3g19540/T31J18_4 [Arabidopsis thaliana]	Unigene102591_All//9.00E-36//AT3G19540| unknown protein	Unigene102591_All//9.00E-51//gi|78336860|gb|DT557134.1|DT557134			GO:0016020	nr -
Unigene10260_All	801	0.00	0.25	0.00	0.12	0.00	0.06	3.85	0.26	2.39	7.98E+00	1.38E-01		null	null		-6.96E+00	3.18E-01		-1.14E+00	6.79E-01		-3.88E+00	4.99E-16	Down	-6.91E-01	2.33E-02		Unigene10260_All//gi|224094005|ref|XP_002310060.1|//3.00E-45//cytochrome P450 [Populus trichocarpa] >gi|222852963|gb|EEE90510.1| cytochrome P450 [Populus trichocarpa]	Unigene10260_All//3.00E-29//AT3G26280| CYP71B4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene10260_All//4.00E-92//CO098968	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016709	nr +
Unigene10261_All	408	0.00	0.50	4.57	0.85	1.18	0.11	0.41	0.20	0.00	8.96E+00	1.38E-01		1.22E+01	2.89E-10	Up	4.67E-01	7.04E-01		-2.95E+00	8.31E-02		-1.02E+00	6.16E-01		-8.70E+00	1.09E-01					Unigene10261_All//1.00E-07//CA993990					
Unigene102612_All	200	0.00	0.00	0.00	0.00	0.00	0.00	1.90	9.82	6.97	null	null		null	null		null	null		null	null		2.37E+00	1.05E-06	Up	1.87E+00	4.97E-04	Up									
Unigene10262_All	338	0.00	5.55	2.52	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.11E-10	Up	1.13E+01	9.04E-05	Up	null	null		null	null		null	null		null	null		Unigene10262_All//gi|219112151|ref|XP_002177827.1|//1.00E-33//predicted protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|217410712|gb|EEC50641.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1]					GO:0003824	nr +
Unigene102629_All	363	0.00	0.00	0.00	0.00	0.09	0.25	0.23	0.00	2.63	null	null		null	null		6.57E+00	8.41E-01		7.96E+00	4.83E-01		-7.86E+00	4.08E-01		3.50E+00	4.29E-05	Up	Unigene102629_All//gi|75755957|gb|ABA27034.1|//1.00E-11//T066-1 [Taraxacum officinale]	Unigene102629_All//3.00E-10//AT1G17710| phosphatase	Unigene102629_All//2.00E-58//TC169946			GO:0016791	nr -
Unigene10263_All	622	0.00	9.04	4.71	0.00	0.11	0.00	0.00	0.00	0.00	1.31E+01	4.34E-32	Up	1.22E+01	3.52E-16	Up	6.79E+00	6.17E-01		null	null		null	null		null	null										
Unigene10266_All	712	0.00	45.47	14.51	0.00	0.19	0.00	0.00	0.00	0.00	1.55E+01	9.73E-187	Up	1.38E+01	5.38E-58	Up	7.60E+00	3.21E-01		null	null		null	null		null	null		Unigene10266_All//gi|38325811|gb|AAR17078.1|//3.00E-89//heat shock protein 70-1 [Nicotiana tabacum]	Unigene10266_All//2.00E-86//AT5G02500| HSC70-1 (HEAT SHOCK COGNATE PROTEIN 70-1); ATP binding	Unigene10266_All//2.00E-13//TC161167		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0004672//GO:0006464//GO:0032559//GO:0050896	nr +
Unigene102670_All	220	0.00	0.23	0.00	2.72	0.47	0.00	1.15	0.38	0.36	7.85E+00	6.23E-01		null	null		-2.53E+00	1.36E-02		-1.14E+01	7.71E-04	Down	-1.60E+00	3.11E-01		-1.67E+00	2.57E-01					Unigene102670_All//6.00E-45//ES832413					
Unigene10269_All	558	276.98	321.18	318.55	97.66	154.09	132.66	4.85	17.08	10.71	2.14E-01	1.90E-08		2.02E-01	3.02E-07		6.58E-01	3.26E-36		4.42E-01	4.51E-14		1.82E+00	1.79E-21	Up	1.14E+00	1.66E-07	Up	Unigene10269_All//gi|224058639|ref|XP_002299579.1|//9.00E-57//cytochrome P450 [Populus trichocarpa] >gi|222846837|gb|EEE84384.1| cytochrome P450 [Populus trichocarpa]	Unigene10269_All//2.00E-50//AT2G45550| CYP76C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene10269_All//0.00E+00//gi|48740564|gb|CO071083.1|CO071083		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr +
Unigene10271_All	347	0.00	6.57	3.53	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.64E-13	Up	1.18E+01	9.13E-07	Up	null	null		null	null		null	null		null	null										
Unigene10272_All	759	0.00	12.42	5.47	0.00	0.14	0.00	0.00	0.00	0.00	1.36E+01	5.67E-54	Up	1.24E+01	4.84E-23	Up	7.09E+00	4.59E-01		null	null		null	null		null	null		Unigene10272_All//sp|P27878|VIT1_CERCA//2.00E-119//Vitellogenin-1 OS=Ceratitis capitata GN=VG1-GAMMA PE=2 SV=1						swissprot -
Unigene102727_All	389	4.71	5.34	3.70	14.34	10.09	12.07	62.39	22.56	37.07	1.82E-01	6.73E-01		-3.49E-01	4.94E-01		-5.07E-01	3.80E-02		-2.48E-01	3.92E-01		-1.47E+00	1.07E-39	Down	-7.51E-01	2.64E-14		Unigene102727_All//gi|115473585|ref|NP_001060391.1|//1.00E-07//Os07g0636000 [Oryza sativa Japonica Group] >gi|113611927|dbj|BAF22305.1| Os07g0636000 [Oryza sativa Japonica Group]		Unigene102727_All//3.00E-23//TC179304			GO:0005488	nr +
Unigene102730_All	204	0.00	0.50	0.78	0.24	0.00	0.89	328.29	717.49	291.95	8.96E+00	3.91E-01		9.61E+00	2.40E-01		-7.93E+00	5.66E-01		1.86E+00	4.59E-01		1.13E+00	1.30E-156	Up	-1.69E-01	3.38E-03					Unigene102730_All//2.00E-57//CD485591					
Unigene10274_All	310	0.34	1.14	0.17	0.00	0.00	0.29	8.73	0.94	2.31	1.76E+00	2.18E-01		-9.75E-01	7.23E-01		null	null		8.19E+00	4.83E-01		-3.21E+00	3.86E-12	Down	-1.92E+00	2.33E-07	Down				Unigene10274_All//3.00E-146//ES846200					
Unigene102740_All	251	0.00	1.21	1.06	1.59	1.51	1.80	44.47	489.39	10.63	1.02E+01	4.45E-02		1.01E+01	8.04E-02		-7.32E-02	9.26E-01		1.81E-01	8.84E-01		3.46E+00	0.00E+00	Up	-2.06E+00	1.46E-30	Down	Unigene102740_All//gi|294992077|gb|ABG90381.2|//6.00E-21//glutathione S-transferase [Caragana korshinskii]	Unigene102740_All//2.00E-20//AT1G78380| ATGSTU19 (GLUTATHIONE S-TRANSFERASE TAU 19); glutathione binding / glutathione transferase	Unigene102740_All//2.00E-82//gi|31407290|gb|CD486325.1|CD486325		ko00480|Glutathione metabolism	GO:0009755//GO:0016765	nr -

Unigene10276_All	868	0.00	0.00	0.00	0.00	0.00	0.00	2.78	0.39	7.48	null	null		null	null		null	null		null	null		-2.85E+00	9.15E-10	Down	1.43E+00	4.61E-11	Up	Unigene10276_All//gi|5080804|gb|AAD39313.1|AC007258_2//5.00E-54//Hypothetical protein [Arabidopsis thaliana] >gi|15010642|gb|AAK73980.1| At1g59710/T30E16_31 [Arabidopsis thaliana] >gi|22137290|gb|AAM91490.1| At1g59710/T30E16_31 [Arabidopsis thaliana]	Unigene10276_All//2.00E-61//AT3G28630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf whorl, male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, W germinated pollen stage, 4 anthesis; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G59710.1); Has 121 Blast hits to 110 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 117; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene10277_All	217	0.00	0.00	0.00	0.00	0.00	0.00	0.39	0.00	3.49	null	null		null	null		null	null		null	null		-8.61E+00	4.08E-01		3.16E+00	6.83E-04	Up			Unigene10277_All//4.00E-15//TC171388				
Unigene10279_All	257	0.00	0.00	0.00	0.00	0.00	0.00	1.97	5.69	0.00	null	null		null	null		null	null		null	null		1.53E+00	2.96E-03		-1.09E+01	5.56E-04	Down							
Unigene102790_All	362	0.14	0.00	0.00	3.44	1.43	0.50	0.58	1.50	7.48	-7.17E+00	6.22E-01		-7.17E+00	6.35E-01		-1.27E+00	2.92E-02		-2.79E+00	1.35E-04	Down	1.36E+00	1.44E-01		3.68E+00	8.19E-14	Up	Unigene102790_All//gi|269996964|gb|ACZ57767.1|//5.00E-35//phospholipase A1 [Nicotiana attenuata]	Unigene102790_All//2.00E-24//AT4G16820| lipase class 3 family protein	Unigene102790_All//1.00E-115//gi|78333729|gb|DT554003.1|DT554003			GO:0004091//GO:0009536//GO:0044238	nr +
Unigene102794_All	255	0.00	0.00	0.00	0.59	0.54	0.00	0.99	0.66	5.16	null	null		null	null		-1.17E-01	9.12E-01		-9.19E+00	2.35E-01		-6.02E-01	6.49E-01		2.37E+00	7.20E-05	Up	Unigene102794_All//gi|7211984|gb|AF40455.1|AC004809_13//1.00E-11//Strong similarity to the SEN3-like tRNA-processing protein F24J7.13 from A. thaliana gi|2914700 on BAC gb|AC003974. EST gb|AA712969 comes from this gene [Arabidopsis thaliana]	Unigene102794_All//4.00E-13//AT1G04810| 26S proteasome regulatory subunit, putative	Unigene102794_All//3.00E-87//C0124331		ko03050|Proteasome	GO:0005838//GO:0009894//GO:0016020//GO:0019941//GO:0031410//GO:0043231	nr -
Unigene102797_All	210	0.00	0.00	0.00	0.71	0.66	4.30	55.77	41.99	115.72	null	null		null	null		-1.18E-01	9.12E-01		2.60E+00	3.43E-03		-4.09E-01	6.17E-03		1.05E+00	1.65E-24	Up	Unigene102797_All//gi|18766934|gb|AAL79181.1|//5.00E-13//beta-caryophyllene synthase QHS1 [Artemisia annua]	Unigene102797_All//1.00E-69//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene102797_All//6.00E-48//C0111120		ko00904|Diterpenoid biosynthesis//ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0046872	nr +
Unigene10281_All	794	0.00	0.00	0.00	0.00	0.00	0.00	7.35	63.43	0.25	null	null		null	null		null	null		null	null		3.11E+00	1.39E-208	Up	-4.87E+00	1.01E-35	Down			Unigene10281_All//6.00E-08//ES813936				
Unigene10282_All	577	0.00	22.22	7.57	0.00	0.00	0.00	0.00	0.00	0.00	1.44E+01	1.45E-73	Up	1.29E+01	3.09E-24	Up	null	null		null	null		null	null		null	null		Unigene10282_All//gi|219109896|ref|XP_002176701.1|//3.00E-55//nucleoside diphosphate kinase 1 [Phaeodactylum tricornutum CCAP 1055/1] >gi|217411236|gb|EEC51164.1| nucleoside diphosphate kinase 1 [Phaeodactylum tricornutum CCAP 1055/1]	Unigene10282_All//1.00E-51//AT4G09320| NDPK1; ATP binding / nucleoside diphosphate kinase			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism	GO:0007602//GO:0009206//GO:0009209//GO:0016776//GO:0023033//GO:0032559//GO:0042995//GO:0043169//GO:0044424	nr +
Unigene10283_All	674	0.00	4.66	6.95	0.00	0.00	0.07	0.13	0.00	0.12	1.22E+01	7.08E-18	Up	1.28E+01	4.86E-26	Up	null	null		6.07E+00	7.05E-01		-6.97E+00	4.08E-01		-8.65E-02	9.74E-01		Unigene10283_All//gi|40287526|gb|AAR83877.1|//4.00E-69//60S ribosomal protein L19 [Capsicum annuum]	Unigene10283_All//2.00E-50//AT4G02230| 60S ribosomal protein L19 (RPL19C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr +
Unigene102840_All	205	0.00	3.21	0.52	1.46	1.34	1.98	0.00	0.61	0.19	1.16E+01	6.26E-04	Up	9.02E+00	4.03E-01		-1.18E-01	9.01E-01		4.44E-01	7.01E-01		9.26E+00	2.41E-01		7.60E+00	6.50E-01								
Unigene102848_All	334	0.00	0.30	1.12	0.45	0.31	0.54	1.52	7.51	21.95	8.25E+00	3.91E-01		1.01E+01	2.51E-02		-5.33E-01	7.86E-01		2.74E-01	9.06E-01		2.31E+00	3.91E-08	Up	3.85E+00	1.15E-37	Up	Unigene102848_All//gi|264664459|sp|COLGJ1.1|Y1743_ARATH//3.00E-43//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g74360; Flags: Precursor >gi|224589485|gb|ACN59276.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene102848_All//1.00E-44//AT1G74360| leucine-rich repeat transmembrane protein kinase, putative	Unigene102848_All//1.00E-155//DT467067			GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016791//GO:0031224//GO:0031410//GO:0032559//GO:0043231	nr -
Unigene10286_All	650	0.00	0.08	0.00	0.31	0.05	0.14	0.46	1.99	1.72	6.29E+00	6.23E-01		null	null		-2.53E+00	2.34E-01		-1.14E+00	5.70E-01		2.13E+00	3.40E-04	Up	1.91E+00	1.87E-03		Unigene10286_All//gi|18416730|ref|NP_567744.1|//3.00E-21//UNE17 (UNFERTILIZED EMBRYO SAC 17); identical protein binding / serine-type endopeptidase [Arabidopsis thaliana] >gi|4539429|emb|CAB38962.1| subtilisin protease-like [Arabidopsis thaliana] >gi|7269485|emb|CAB79488.1| subtilisin protease-like [Arabidopsis thaliana]	Unigene10286_All//2.00E-22//AT4G26330| UNE17 (UNFERTILIZED EMBRYO SAC 17); identical protein binding / serine-type endopeptidase				GO:0004175//GO:0005515//GO:0009566//GO:0019538//GO:0042579//GO:0044192	nr -
Unigene10287_All	312	0.17	2.92	1.19	2.24	2.65	1.30	0.68	0.00	0.64	4.12E+00	2.34E-04	Up	2.83E+00	9.32E-02		2.45E-01	8.03E-01		-7.79E-01	3.93E-01		-9.40E+00	7.48E-02		-8.60E-02	9.61E-01								
Unigene10289_All	708	0.00	0.00	0.00	0.00	0.00	0.00	12.00	7.85	1.24	null	null		null	null		null	null		null	null		-6.12E-01	5.16E-04		-3.28E+00	7.60E-39	Down			Unigene10289_All//1.00E-11//TC165956				
Unigene10290_All	331	0.00	0.46	0.00	3.31	1.46	0.00	2.17	0.38	1.44	8.84E+00	2.37E-01		null	null		-1.18E+00	5.94E-02		-1.17E+01	7.26E-07	Down	-2.52E+00	4.69E-03		-5.88E-01	4.09E-01		Unigene10290_All//gi|224101869|ref|XP_002312452.1|//5.00E-11//predicted protein [Populus trichocarpa] >gi|222852272|gb|EEE89819.1| predicted protein [Populus trichocarpa]		Unigene10290_All//1.00E-10//DW225279			GO:0016798	nr -
Unigene10291_All	665	0.00	0.00	0.00	0.00	0.00	0.00	2.29	0.19	1.14	null	null		null	null		null	null		null	null		-3.60E+00	9.55E-08	Down	-1.01E+00	2.94E-02		Unigene10291_All//gi|225447256|ref|XP_002272957.1|//2.00E-26//PREDICTED: similar to Os04g0636200 [Vitis vinifera]						nr -
Unigene10293_All	415	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.91	0.29	null	null		null	null		null	null		null	null		-1.17E+00	9.29E-02		-2.82E+00	5.38E-04	Down	Unigene10293_All//gi|159473469|ref|XP_001694856.1|//1.00E-07//acidic ribosomal protein P2 [Chlamydomonas reinhardtii] >gi|158276235|gb|EDP02008.1| acidic ribosomal protein P2 [Chlamydomonas reinhardtii]	Unigene10293_All//7.00E-06//AT3G44590| 60S acidic ribosomal protein P2 (RPP2D)			ko03010|Ribosome	GO:0043229	nr +
Unigene10299_All	386	0.00	0.00	0.00	0.00	0.00	0.00	1.10	3.79	2.99	null	null		null	null		null	null		null	null		1.79E+00	7.25E-04	Up	1.45E+00	1.09E-02								
Unigene102998_All	284	0.00	0.00	0.38	0.18	0.12	2.86	66.25	74.17	60.88	null	null		8.55E+00	4.03E-01		-5.32E-01	8.29E-01		4.03E+00	5.91E-04	Up	1.63E-01	1.70E-01		-1.22E-01	3.39E-01		Unigene102998_All//gi|14582310|gb|AAK69146.1|//4.00E-51//proline-rich protein-2 [Gossypium hirsutum]		Unigene102998_All//3.00E-140//NP386003				nr -
Unigene10300_All	1671	0.00	0.00	0.00	0.00	0.00	0.00	8.35	12.18	0.19	null	null		null	null		null	null		null	null		5.45E-01	5.21E-07		-5.45E+00	1.23E-89	Down	Unigene10300_All//gi|299470262|emb|CBN79566.1|//1.00E-13//RecName: Full=Spherulin-4; Flags: Precursor [Ectocarpus siliculosus]						nr +
Unigene10301_All	896	0.00	5.09	2.50	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.54E-26	Up	1.13E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene10301_All//gi|301098633|ref|XP_002898409.1|//2.00E-06//lamin-like protein [Phytophthora infestans T30-4] >gi|262105180|gb|EEY63232.1| lamin-like protein [Phytophthora infestans T30-4]	Unigene10301_All//2.00E-05//AT2G32240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cadmium ion; LOCATED IN: plasma membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G05320.3); Has 221693 Blast hits to 95553 proteins in 2574 species: Archae - 2848; Bacteria - 44259; Metazoa - 97474; Fungi - 15490; Plants - 8386; Viruses - 1229; Other Eukaryotes - 52007 (source: NCBI BLink).			ko03440|Homologous recombination//ko03450|Non-homologous end-joining		nr +
Unigene10302_All	605	0.61	0.67	0.35	3.87	1.88	0.82	0.77	0.35	0.59	1.46E-01	8.98E-01		-7.82E-01	5.53E-01		-1.04E+00	8.02E-03		-2.24E+00	1.70E-06	Down	-1.15E+00	2.53E-01		-3.75E-01	6.65E-01		Unigene10302_All//gi|28950973|gb|AAO63110.1|//2.00E-89//At1g23340 [Arabidopsis thaliana]	Unigene10302_All//1.00E-88//AT1G10750| unknown protein	Unigene10302_All//4.00E-138//NP508247			GO:0044464	nr +
Unigene10303_All	322	0.33	1.57	3.14	0.00	0.00	0.00	0.00	0.00	0.00	2.28E+00	6.23E-02		3.27E+00	5.93E-04	Up	null	null		null	null		null	null		null	null		Unigene10303_All//gi|224138866|ref|XP_002322921.1|//4.00E-44//aldose reductase with ABC domain [Populus trichocarpa] >gi|222867551|gb|EEF04682.1| aldose reductase with ABC domain [Populus trichocarpa]	Unigene10303_All//2.00E-32//AT2G37770| aldo/keto reductase family protein	Unigene10303_All//2.00E-67//DR460967			ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism	GO:0004033//GO:0006970//GO:0008152	nr +
Unigene10305_All	842	0.00	0.00	0.00	0.12	0.12	0.59	0.60	2.53	4.64	null	null		null	null		5.27E-02	9.69E-01		2.32E+00	6.89E-02		2.07E+00	3.04E-06	Up	2.94E+00	3.32E-16	Up							
Unigene103070_All	375	0.14	0.00	0.00	0.00	0.09	0.00	1.35	0.00	0.00	-7.12E+00	6.22E-01		-7.12E+00	6.35E-01		6.52E+00	8.41E-01		null	null		-1.04E+01	8.91E-04	Down	-1.04E+01	5.56E-04	Down	Unigene103070_All//gi|18412056|ref|NP_565185.1|//9.00E-08//POLD3; DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|4836868|gb|AAD30571.1|AC007260_2 Hypothetical protein [Arabidopsis thaliana]		Unigene103070_All//1.00E-109//BG445037			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +
Unigene10309_All	376	0.00	0.00	0.00	0.27	0.00	0.00	281.57	54.91	230.87	null	null		null	null		-8.05E+00	3.18E-01		-8.05E+00	4.06E-01		-2.36E+00	0.00E+00	Down	-2.86E-01	6.87E-11		Unigene10309_All//gi|15224236|ref|NP_181844.1|//4.00E-07//proline-rich extensin-like family protein [Arabidopsis thaliana]		Unigene10309_All//0.00E+00//TC158176				nr +
Unigene1031_All	930	8.27	6.37	6.53	13.61	10.77	13.50	25.23	11.68	11.01	-3.76E-01	7.88E-02		-3.41E-01	1.38E-01		-3.37E-01	3.18E-02		-1.11E-02	9.42E-01		-1.11E+00	3.54E-25	Down	-1.20E+00	4.04E-29	Down	Unigene1031_All//gi|297842397|ref|XP_002889080.1|//1.00E-107//ribophorin I family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334921|gb|EFH65339.1| ribophorin I family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1031_All//3.00E-101//AT1G76400| ribophorin I family protein	Unigene1031_All//0.00E+00//gi|48813336|gb|CO114649.1|CO114649		ko01141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0006464//GO:0031224//GO:0031410//GO:0043231	nr -
Unigene10310_All	639	0.25	1.03	0.00	2.03	0.00	0.00	2.58	0.78	0.69	2.07E+00	3.93E-02		-7.94E+00	2.47E-01		-1.10E+01	1.34E-09	Down	-1.10E+01	4.24E-08	Down	-1.72E+00	4.45E-04	Down	-1.91E+00	8.63E-05	Down	Unigene10310_All//gi|16326137|dbj|BAB70512.1|//7.00E-64//Myb [Nicotiana tabacum]	Unigene10310_All//4.00E-55//AT5G11510| MYB3R-4 (myb domain protein 3R-4); DNA binding / transcription coactivator/ transcription factor	Unigene10310_All//8.00E-07//ES830113	MYB		GO:0006350//GO:0010468//GO:0043231	nr -
Unigene103112_All	231	0.45	0.00	0.00	3.88	1.04	0.39	0.18	0.00	0.00	-8.82E+00	3.78E-01		-8.82E+00	4.00E-01		-1.90E+00	1.06E-02		-3.31E+00	5.80E-04	Down	-7.52E+00	6.65E-01		-7.52E+00	6.19E-01				Unigene103112_All//2.00E-32//DW500061				
Unigene10315_All	483	0.00	0.00	0.00	0.00	0.00	0.00	4.55	4.59	0.25	null	null		null	null		null	null		null	null		1.09E-02	1.02E+00		-4.20E+00	1.16E-12	Down	Unigene10315_All//gi|192910854|gb|ACF06535.1|//2.00E-39//60S ribosomal protein L27 [Elaeis guineensis]	Unigene10315_All//1.00E-38//AT2G32220| 60S ribosomal protein L27 (RPL27A)	Unigene10315_All//1.00E-07//gi|78337699|gb|DT557973.1|DT557973		ko03010|Ribosome	GO:0030529	nr +
Unigene10316_All	264	0.00	0.00	3.03	0.00	0.78	1.88	0.00	0.48	2.72	null	null		1.16E+01	1.72E-04	Up	9.61E+00	1.58E-01		1.09E+01	4.38E-03		8.89E+00	2.41E-01		1.14E+01	2.63E-05	Up							

Unigene103176_All	631	0.50	1.20	0.42	2.13	1.31	1.65	0.87	1.59	5.24	1.28E+00	1.28E-01			-2.38E-01	8.50E-01		-7.03E-01	2.18E-01			-3.73E-01	5.53E-01		8.68E-01	1.64E-01		2.59E+00	3.51E-12	Up	Unigene103176_All//gi|297839709|ref|XP_002887736.1|//2.00E-45//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297333577|gb|EFH63995.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene103176_All//1.00E-46//AT1G78420| protein binding / zinc ion binding	Unigene103176_All//3.00E-163//TC172240			GO:0003824//GO:0043231//GO:0046914	nr -
Unigene10318_All	972	0.00	37.85	14.52	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	2.87E-212	Up	1.38E+01	1.69E-79	Up	null	null		null	null		null	null		null	null		null	null		Unigene10318_All//gi|226505998|ref|NP_001146929.1|//1.00E-115//60S ribosomal protein L7a [Zea mays] >gi|195605318|gb|ACG24489.1| 60S ribosomal protein L7a [Zea mays]	Unigene10318_All//1.00E-80//AT3G02870| 60S ribosomal protein L7A (RPL7AB)			ko03010|Ribosome	GO:0005198//GO:0009987//GO:0010467//GO:0030529//GO:0046872	nr +
Unigene10032_All	2509	11.49	9.21	11.08	21.96	22.37	24.08	33.64	19.42	12.85	-3.19E-01	1.73E-03		-5.26E-02	6.46E-01		2.68E-02	8.03E-01		1.33E-01	7.30E-02		-7.92E-01	1.33E-50		-1.39E+00	5.34E-129	Down	Unigene10032_All//0.00E+00//AT1G76400| ribophorin I family protein	Unigene10032_All//0.00E+00//TC167797		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0006464//GO:0031224//GO:0043231	nr +
Unigene10320_All	352	0.00	0.00	0.00	0.00	0.00	0.00	4.68	1.31	0.57	null	null		null	null		null	null		null	null		-1.84E+00	2.07E-04	Down	-3.05E+00	1.31E-07	Down	Unigene10320_All//gi|149392583|gb|ABR26094.1|//2.00E-10//retrotransposon protein [Oryza sativa Indica Group]		Unigene10320_All//8.00E-24//TC152783				nr +
Unigene10323_All	312	43.60	29.39	22.53	61.79	50.55	32.57	61.93	33.49	16.60	-5.69E-01	1.81E-04		-9.53E-01	2.84E-09		-2.90E-01	1.97E-02		-9.24E-01	1.13E-13		-8.87E-01	1.20E-14		-1.90E+00	6.17E-47	Down	Unigene10323_All//gi|416641|sp|P32294.1|AX22B_PHAAU//3.00E-09//RecName: Full=Auxin-induced protein 22B; AltName: Full=Indole-3-acetic acid-induced protein ARG4	Unigene10323_All//9.00E-10//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene10323_All//2.00E-141//CB066529				nr -
Unigene103235_All	610	8.66	7.64	6.55	8.17	5.42	2.96	0.97	0.82	0.39	-1.81E-01	5.19E-01		-4.04E-01	1.44E-01		-5.92E-01	2.11E-02		-1.46E+00	1.22E-07	Down	-2.39E-01	7.65E-01		-1.31E+00	1.15E-01		Unigene103235_All//gi|158427472|gb|ABR38331.1|//7.00E-87//chloroplast fructose-1,6-bisphosphatase II [Fragaria x ananassa] >gi|190151803|gb|ACE63522.1| chloroplast fructose-1,6-bisphosphatase [Fragaria x ananassa]	Unigene103235_All//2.00E-82//AT5G64380| fructose-1,6-bisphosphatase family protein	Unigene103235_All//0.00E+00//gi|48800926|gb|CO102240.1|CO102240		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway	GO:0005975//GO:0009536//GO:0019203	nr +
Unigene10324_All	320	15.21	6.33	14.48	12.61	8.82	3.25	0.00	0.00	0.00	-1.26E+00	7.65E-06	Down	-7.08E-02	8.06E-01		-5.15E-01	8.41E-02		-1.96E+00	3.44E-09	Down	null	null		null	null					Unigene10324_All//8.00E-30//gi|164302226|gb|ES807570.1|ES807570				
Unigene103249_All	281	0.00	0.00	1.14	0.18	0.25	2.89	0.00	0.00	0.00	null	null		1.02E+01	4.54E-02		4.67E-01	9.62E-01		4.03E+00	5.91E-04	Up	null	null		null	null					Unigene103249_All//2.00E-11//TC171826				
Unigene10326_All	341	0.00	3.86	1.25	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.50E-07	Up	1.03E+01	1.39E-02		null	null		null	null		null	null		null	null										ESTscan +
Unigene10328_All	321	0.00	0.00	0.00	0.31	0.64	0.14	441.51	118.88	71.98	null	null		null	null		1.05E+00	6.13E-01		-1.14E+00	6.79E-01		-1.89E+00	0.00E+00	Down	-2.62E+00	0.00E+00	Down										ESTscan +
Unigene10329_All	929	0.00	0.38	0.11	0.00	0.00	0.00	0.27	2.92	14.32	8.58E+00	2.47E-02		6.84E+00	4.03E-01		null	null		null	null		3.42E+00	8.23E-13	Up	5.71E+00	4.04E-85	Up	Unigene10329_All//gi|224054472|ref|XP_002298277.1|//5.00E-68//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|224149083|ref|XP_002336754.1| NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222836661|gb|EEE75054.1| NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222845535|gb|EEE83082.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene10329_All//6.00E-61//AT5G22380| anac090 (Arabidopsis NAC domain containing protein 90); transcription factor	Unigene10329_All//0.00E+00//TC166110	NAC		GO:0001071//GO:0009743//GO:0010468//GO:0032501	nr +
Unigene1033_All	686	12.13	17.21	19.56	20.33	15.16	42.20	50.79	109.18	86.47	5.05E-01	2.23E-03		6.90E-01	1.39E-05		-4.24E-01	2.99E-03		1.05E+00	9.65E-25	Up	1.10E+00	8.74E-78	Up	7.68E-01	9.20E-35		Unigene1033_All//gi|4263517|gb|AAD15343.1|//5.00E-58//similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana] >gi|51972158|gb|AAU15183.1| At4g02860 [Arabidopsis thaliana]	Unigene1033_All//3.00E-59//AT4G02860| catalytic	Unigene1033_All//0.00E+00//gi|164253821|gb|ES839366.1|ES839366			GO:0008152	nr -
Unigene10330_All	493	0.00	0.00	0.00	0.00	0.00	0.00	2.92	2.71	0.00	null	null		null	null		null	null		null	null		-1.04E-01	8.37E-01		-1.15E+01	1.19E-10	Down										ESTscan +
Unigene103316_All	377	0.00	0.00	0.00	1.45	0.00	0.00	0.00	0.00	0.00	null	null		null	null		-1.05E+01	4.01E-04	Down	-1.05E+01	1.52E-03		null	null		null	null		Unigene103316_All//gi|115452451|ref|NP_001049826.1|//1.00E-15//0s03g0295700 [Oryza sativa Japonica Group] >gi|108707640|gb|ABF95435.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548297|dbj|BAF11740.1| Os03g0295700 [Oryza sativa Japonica Group]	Unigene103316_All//3.00E-21//AT5G58510| unknown protein	Unigene103316_All//1.00E-121//TC142475			GO:0009536	nr -
Unigene10332_All	470	0.00	43.88	21.98	0.00	0.00	0.00	0.00	0.00	0.00	1.54E+01	1.15E-118	Up	1.44E+01	5.37E-58	Up	null	null		null	null		null	null		null	null		Unigene10332_All//gi|15229845|ref|NP_187143.1|//7.00E-41//40S ribosomal protein S24 (RPS24A) [Arabidopsis thaliana] >gi|11134742|sp|Q9SS17.1|RS241_ARATH RecName: Full=40S ribosomal protein S24-1 >gi|15215672|gb|AAK91381.1| AT3g04920/T9J14_13 [Arabidopsis thaliana] >gi|20334888|gb|AAM16200.1| AT3g04920/T9J14_13 [Arabidopsis thaliana]	Unigene10332_All//4.00E-34//AT3G04920| 40S ribosomal protein S24 (RPS24A)			ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0031981	nr -
Unigene103341_All	215	0.00	0.47	0.25	0.23	0.00	0.42	0.79	4.67	0.37	8.88E+00	3.91E-01		7.95E+00	6.42E-01		-7.86E+00	5.65E-01		8.59E-01	7.97E-01		2.57E+00	4.79E-04	Up	-1.09E+00	5.54E-01		Unigene103341_All//gi|51536426|gb|AAU05451.1|//1.00E-13//At5g19870 [Arabidopsis thaliana] >gi|51972068|gb|AAU15138.1| At5g19870 [Arabidopsis thaliana]	Unigene103341_All//4.00E-15//AT5G19870| unknown protein	Unigene103341_All//3.00E-56//CO129484			GO:0044464	nr +
Unigene10335_All	579	0.72	0.70	0.92	0.60	2.68	3.43	0.07	0.00	0.00	-4.62E-02	9.80E-01		3.47E-01	7.06E-01		2.15E+00	2.30E-04	Up	2.51E+00	3.78E-06	Up	-6.19E+00	6.65E-01		-6.19E+00	6.19E-01		Unigene10335_All//gi|297832296|ref|XP_002884030.1|//1.00E-34//tetracycline transporter [Arabidopsis lyrata subsp. lyrata] >gi|297329870|gb|EFH60289.1| tetracycline transporter [Arabidopsis lyrata subsp. lyrata]	Unigene10335_All//4.00E-32//AT2G16990| tetracycline transporter	Unigene10335_All//1.00E-66//TC151593			GO:0005215//GO:0006810//GO:0016020//GO:0031410//GO:0042221	nr +
Unigene103358_All	211	0.74	1.20	0.76	1.18	2.12	7.49	2.00	0.79	0.19	6.91E-01	6.27E-01		2.54E-02	1.00E+00		8.46E-01	5.14E-01		2.67E+00	2.71E-05	Up	-1.34E+00	2.25E-01		-3.41E+00	1.24E-02										
Unigene10338_All	545	0.00	0.00	0.00	0.46	1.01	0.00	0.39	0.84	2.19	null	null		null	null		1.15E+00	2.97E-01		-8.84E+00	7.36E-02		1.12E+00	2.74E-01		2.50E+00	1.03E-04	Up	Unigene10338_All//gi|66792688|gb|AA56446.1|//3.00E-46//At1g63930 [Arabidopsis thaliana] >gi|115311479|gb|AB193920.1| At1g63930 [Arabidopsis thaliana]	Unigene10338_All//2.00E-38//AT1G63930| unknown protein	Unigene10338_All//0.00E+00//TC174086			GO:0003824//GO:0008152//GO:0030554	nr -
Unigene103382_All	234	96.82	35.95	76.69	247.79	237.52	174.86	267.41	251.49	161.40	-1.43E+00	2.98E-29	Down	-3.36E-01	5.60E-03		-6.11E-02	4.84E-01		-5.03E-01	4.57E-14		-8.86E-02	2.00E-01		-7.29E-01	1.14E-33					Unigene103382_All//4.00E-80//gi|78347287|gb|DT567561.1|DT567561				
Unigene1034_All	616	1.53	2.96	1.30	0.16	1.90	3.23	1.51	7.67	11.32	9.54E-01	4.89E-02		-2.38E-01	7.23E-01		3.56E+00	2.92E-05	Up	4.32E+00	1.57E-09	Up	2.34E+00	5.50E-15	Up	2.91E+00	4.94E-28	Up	Unigene1034_All//gi|79461947|ref|NP_192195.2|//2.00E-27//catalytic [Arabidopsis thaliana]	Unigene1034_All//6.00E-29//AT4G02860| catalytic	Unigene1034_All//6.00E-140//gi|48778677|gb|CO088043.1|CO088043			GO:0008152	nr -
Unigene10343_All	513	0.00	0.00	0.00	0.00	0.00	0.00	5.69	0.65	2.95	null	null		null	null		null	null		null	null		-3.13E+00	9.74E-13	Down	-9.46E-01	2.81E-03		Unigene10343_All//gi|15236902|ref|NP_194418.1|//3.00E-33//stigma-specific Stig1 family protein [Arabidopsis thaliana] >gi|4455211|emb|CAB36534.1| STIG1 like protein [Arabidopsis thaliana] >gi|7269541|emb|CAB79543.1| STIG1 like protein [Arabidopsis thaliana]	Unigene10343_All//2.00E-34//AT4G26880| stigma-specific Stig1 family protein					nr +
Unigene103449_All	402	0.00	0.00	0.00	0.12	0.00	0.00	4.52	0.31	0.89	null	null		null	null		-6.95E+00	5.65E-01		-6.95E+00	6.46E-01		-3.86E+00	1.31E-09	Down	-2.34E+00	1.83E-06	Down										ESTscan -
Unigene10345_All	494	0.00	6.56	6.68	0.00	0.07	0.00	0.00	0.00	0.16	1.27E+01	1.88E-18	Up	1.27E+01	2.92E-18	Up	6.12E+00	8.41E-01		null	null		null	null		7.33E+00	4.06E-01		Unigene10345_All//gi|157093615|gb|ABV22462.1|//2.00E-63//ribosomal protein S23e [Oxyrrhis marina]	Unigene10345_All//8.00E-61//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene10345_All//8.00E-28//TC142994		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene103456_All	251	1.67	3.23	1.27	6.35	10.70	3.96	2.36	0.83	0.00	9.54E-01	2.27E-01		-3.90E-01	7.18E-01		7.53E-01	4.91E-02		-6.82E-01	2.07E-01		-1.50E+00	9.14E-02		-1.12E+01	1.42E-04	Down				Unigene103456_All//4.00E-80//TC163108				
Unigene10346_All	1122	0.00	16.62	0.09	0.09	0.06	0.48	0.00	0.30	4.54	1.40E+01	3.09E-107	Up	6.57E+00	4.03E-01		-5.32E-01	8.20E-01		2.44E+00	4.41E-02		8.22E+00	1.28E-02		1.22E+01	1.69E-36	Up	Unigene10346_All//gi|225436325|ref|XP_002267961.1|//2.00E-53//PREDICTED: similar to CBF-like transcription factor [Vitis vinifera] >gi|39578548|gb|AAR28676.1| CBF-like transcription factor [Vitis vinifera]	Unigene10346_All//8.00E-35//AT4G25490| CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene10346_All//0.00E+00//TC142390	AP2-EREBP			nr +
Unigene10347_All	1014	0.36	0.10	0.00	0.20	0.75	0.27	1.33	2.39	4.13	-1.85E+00	1.87E-01		-8.50E+00	2.79E-02		1.93E+00	3.36E-02		4.43E-01	7.64E-01		8.41E-01	2.12E-02		1.63E+00	8.52E-09	Up	Unigene10347_All//gi|264664473|sp|C0LGK4.1|Y2165_ARATH//6.00E-92//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At2g16250; Flags: Precursor >gi|224589511|gb|ACN59289.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene10347_All//8.00E-70//AT2G16250| leucine-rich repeat transmembrane protein kinase, putative	Unigene10347_All//4.00E-28//TC176578		ko04626|Plant-pathogen interaction	GO:0004672//GO:0005618//GO:0006464//GO:0007167//GO:0016020//GO:0032559	nr -
Unigene103479_All	364	0.58	0.14	0.15	0.96	0.19	2.85	0.12	0.34	1.97	-2.05E+00	3.34E-01		-1.97E+00	3.82E-01		-2.34E+00	1.01E-01		1.57E+00	2.92E-02		1.57E+00	5.46E-01		4.08E+00	2.41E-04	Up				Unigene103479_All//4.00E-10//TC158284				
Unigene10348_All	346	2.12	0.00	0.15	1.01	1.59	0.26	0.24	0.00	0.00	-1.10E+01	2.11E-04	Down	-3.78E+00	2.79E-03		6.60E-01	5.44E-01		-1.95E+00	1.96E-01		-7.93E+00	4.08E-01		-7.93E+00	3.62E-01		Unigene10348_All//gi|297839191|ref|XP_002887477.1|//2.00E-17//sugar transporter family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333318|gb|EFH63736.1| sugar transporter family protein [Arabidopsis lyrata subsp. lyrata]	Unigene10348_All//7.00E-18//AT1G73220| At0CT1 (Arabidopsis thaliana ORGANIC CATION/CARNITINE TRANSPORTER1); carbohydrate transmembrane transporter/ carnitine transporter/ transporter				GO:0006810//GO:0022891//GO:0031224//GO:0051183	nr -
Unigene103480_All	232	0.90	0.00	0.00	0.64	0.89	1.17	6.01	9.37	0.69	-9.82E+00	1.23E-01		-9.82E+00	1.47E-01		4.68E-01	8.26E-01		8.59E-01	6.32E-01		6.39E-01	1.05E-01		-3.13E+00	1.09E-06	Down				Unigene103480_All//2.00E-60//gi|109874097|gb|DW503072.1|DW503072				
Unigene10349_All	317	2.97	0.16	0.67	1.41	0.76	0.28	0.40	0.13	0.00	-4.22E+00	1.36E-04	Down	-2.14E+00	1.16E-02		-8.95E-01	4.13E-01		-2.31E+00	7.82E-02		-1.60E+00	5.36E-01		-8.64E+00	2.01E-01		Unigene10349_All//gi|15241158|ref|NP_197471.1|//5.00E-35//MATE efflux protein-related [Arabidopsis thaliana] >gi|67633808|gb|AAY78828.1| MATE efflux protein-related [Arabidopsis thaliana]	Unigene10349_All//2.00E-36//AT5G19700| MATE efflux protein-related	Unigene10349_All//2.00E-169//gi|78347917|gb|DT568191.1|DT568191			GO:0015291//GO:0015893//GO:0044464	nr -
Unigene1035_All	1492	0.18	1.87	0.43	0.40	0.78	1.15	1.16	6.42	8.41	3.41E+00	1.06E-10	Up	1.29E+00	1.87E-01		9.70E-01	1.37E-01		1.52E+00	3.74E-03		2.47E+00	1.99E-31	Up	2.86E+00	5.03E-49	Up	Unigene1035_All//gi|15218739|ref|NP_171820.1|//5.00E-23//phenazine biosynthesis PhzC/PhzF family protein [Arabidopsis thaliana] >gi|3850584|gb|AAC72124.1| ESTs gb|H37641 and gb|AA651422 come from this gene [Arabidopsis thaliana]	Unigene1035_All//6.00E-24//AT1G03210| phenazine biosynthesis PhzC/PhzF family protein	Unigene1035_All//2.00E-101//TC165972				nr -

Unigene103566_All	259	6.26	0.00	0.00	0.00	0.27	0.52	0.00	0.00	0.00	-1.26E+01	2.11E-09	Down	-1.26E+01	7.39E-09	Down	8.05E+00	6.17E-01		9.03E+00	3.13E-01		null	null		null	null		Unigene103566_All//gi|297813081|ref|XP_002874424.1//4.00E-06//hypothetical protein ARALYDRAFT_489647 [Arabidopsis lyrata subsp. lyrata] >gi|297320261|gb|EFH50683.1| hypothetical protein ARALYDRAFT_489647 [Arabidopsis lyrata subsp. lyrata]						nr +
Unigene10357_All	413	0.00	0.00	0.00	0.00	0.00	0.00	1.64	3.04	5.98	null	null		null	null		null	null		null	null		8.90E-01	1.02E-01		1.87E+00	1.66E-06	Up	Unigene10357_All//gi|224137294|ref|XP_002327090.1//1.00E-32//cytochrome P450 [Populus trichocarpa] >gi|222835405|gb|EEE73840.1| cytochrome P450 [Populus trichocarpa]	Unigene10357_All//6.00E-26//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene10357_All//3.00E-33//TC132245		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0016491	nr -
Unigene10358_All	631	0.17	2.25	0.00	0.71	1.75	3.44	0.87	2.25	1.01	3.76E+00	3.98E-06	Up	-7.37E+00	4.00E-01		1.30E+00	5.46E-02		2.27E+00	5.25E-06	Up	1.37E+00	7.78E-03		2.14E-01	7.73E-01		Unigene10358_All//gi|124359162|gb|ABN05683.1\//6.00E-08//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene10358_All//1.00E-20//ES811125			GO:0005488	nr -
Unigene103595_All	326	22.63	6.68	17.48	9.32	9.72	9.28	33.72	17.44	10.14	-1.76E+00	2.80E-13	Down	-3.73E-01	1.08E-01		6.01E-02	8.86E-01		-6.10E-03	9.82E-01		-9.52E-01	1.14E-09		-1.73E+00	5.91E-24	Down	Unigene103595_All//gi|297807807|ref|XP_002871787.1\//7.00E-12//cobalamin-independent methionine synthase [Arabidopsis lyrata subsp. lyrata] >gi|297317624|gb|EFH48046.1| cobalamin-independent methionine synthase [Arabidopsis lyrata subsp. lyrata]		Unigene103595_All//4.00E-47//EX163984		ko00270|Cysteine and methionine metabolism	GO:0000097//GO:0005576//GO:0006970//GO:0008172//GO:0009526//GO:0009532//GO:0010038//GO:0016020//GO:0042579//GO:0046914	nr -
Unigene1036_All	492	1.81	3.60	0.22	1.72	0.42	4.31	4.38	11.72	16.36	9.96E-01	4.45E-02		-3.06E+00	2.25E-03		-2.04E+00	9.05E-03		1.33E+00	3.50E-03		1.42E+00	1.45E-09	Up	1.90E+00	8.59E-20	Up	Unigene1036_All//gi|4263517|gb|AAD15343.1\//3.00E-30//similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana] >gi|51972158|gb|AAU15183.1| At4g02860 [Arabidopsis thaliana]	Unigene1036_All//2.00E-31//AT4G02860| catalytic	Unigene1036_All//0.00E+00//TC131623			GO:0008152	nr +
Unigene10361_All	601	0.52	0.51	2.66	0.00	0.57	0.98	0.00	0.00	0.00	-4.60E-02	9.85E-01		2.35E+00	2.09E-04	Up	9.16E+00	3.02E-02		9.93E+00	1.37E-03		null	null		null	null		Unigene10361_All//gi|194476845|ref|XP_002049024.1\//5.00E-14//DnaB helicase:RecA bacterial DNA recombination protein [Paulinella chromatophora] >gi|171191852|gb|ACB42814.1| DnaB helicase:RecA bacterial DNA recombination protein [Paulinella chromatophora]				ko03040|Spliceosome		nr -
Unigene103677_All	1075	0.00	0.00	0.00	0.14	0.13	0.08	0.71	0.00	0.04	null	null		null	null		-1.18E-01	9.12E-01		-7.27E-01	7.17E-01		-9.47E+00	1.68E-05	Down	-4.25E+00	8.66E-05	Down	Unigene103677_All//gi|600111|emb|CAA84378.1\//1.00E-117//cysteine proteinase [Vicia sativa]	Unigene103677_All//2.00E-127//AT5G50260| cysteine proteinase, putative	Unigene103677_All//0.00E+00//TC172692				nr +
Unigene103690_All	214	3.18	2.37	0.00	5.59	0.64	3.80	2.57	1.95	4.28	-4.25E-01	5.97E-01		-1.16E+01	7.65E-04	Down	-3.12E+00	1.54E-05	Down	-5.56E-01	3.87E-01		-3.95E-01	6.34E-01		7.37E-01	2.43E-01									
Unigene1037_All	1388	7.12	11.32	8.63	11.20	8.34	26.52	57.08	102.77	76.81	6.68E-01	2.17E-06		2.77E-01	1.25E-01		-4.26E-01	1.43E-03		1.24E+00	1.12E-40	Up	8.48E-01	2.18E-95		4.28E-01	3.17E-22		Unigene1037_All//gi|4263517|gb|AAD15343.1\//1.00E-89//similar to PHZF, catalyzing the hydroxylation of phenazine-1-carboxylic acid to 2-hydroxy-phenazine-1-carboxylic acid [Arabidopsis thaliana] >gi|51972158|gb|AAU15183.1| At4g02860 [Arabidopsis thaliana]	Unigene1037_All//6.00E-91//AT4G02860| catalytic	Unigene1037_All//0.00E+00//gi|164253821|gb|ES839366.1|ES839366			GO:0008152	nr +
Unigene10371_All	634	0.00	0.08	0.00	8.17	2.28	1.28	0.33	0.86	0.57	6.32E+00	6.23E-01		null	null		-1.84E+00	3.35E-12	Down	-2.67E+00	9.28E-17	Down	1.36E+00	1.44E-01		7.62E-01	5.00E-01		Unigene10371_All//gi|51536456|gb|AAU05466.1\//1.00E-12//At5g44660 [Arabidopsis thaliana] >gi|53828621|gb|AAU94420.1| At5g44660 [Arabidopsis thaliana] >gi|60543337|gb|AAX22266.1| At5g44650 [Arabidopsis thaliana]	Unigene10371_All//5.00E-21//AT4G20190| unknown protein	Unigene10371_All//6.00E-23//gi|73859175|gb|DT461914.1|DT461914				nr +
Unigene103722_All	213	2.21	3.33	1.75	17.07	12.29	2.12	0.40	0.20	0.00	5.91E-01	4.78E-01		-3.37E-01	7.34E-01		-4.75E-01	1.41E-01		-3.01E+00	2.09E-13	Down	-1.02E+00	7.27E-01		-8.63E+00	3.62E-01								
Unigene10374_All	418	2.50	0.00	0.38	9.53	5.52	1.84	1.52	0.00	1.24	-1.13E+01	3.80E-06	Down	-2.71E+00	1.65E-03		-7.89E-01	6.01E-03		-2.38E+00	1.98E-11	Down	-1.06E+01	1.24E-04	Down	-2.92E-01	6.84E-01								
Unigene10375_All	513	0.71	0.79	0.21	1.26	2.28	1.32	4.29	5.21	9.55	1.47E-01	8.98E-01		-1.78E+00	2.34E-01		8.54E-01	1.91E-01		6.51E-02	9.50E-01		2.83E-01	4.46E-01		1.16E+00	2.07E-06	Up	Unigene10375_All//gi|297827079|ref|XP_002881422.1\//8.00E-37//abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327261|gb|EFH57681.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene10375_All//5.00E-38//AT2G36020| HVA22J (HVA22-LIKE PROTEIN J)	Unigene10375_All//4.00E-119//ES833630			GO:0004871//GO:0044464	nr +
Unigene10376_All	767	0.96	0.26	0.56	3.83	1.66	1.88	0.72	0.60	0.57	-1.85E+00	4.08E-02		-7.82E-01	3.80E-01		-1.21E+00	4.51E-04	Down	-1.02E+00	4.81E-03		-2.58E-01	7.60E-01		-3.27E-01	6.72E-01		Unigene10376_All//gi|38346596|emb|CAE04660.2\//2.00E-06//OSJNBa0061G20.16 [Oryza sativa (japonica cultivar-group)]						nr +
Unigene103773_All	1190	0.00	0.38	0.98	0.21	0.58	10.82	227.00	95.67	504.91	8.58E+00	7.45E-03		9.94E+00	1.77E-06	Up	1.47E+00	1.16E-01		5.69E+00	4.11E-70	Up	-1.25E+00	0.00E+00	Down	1.15E+00	0.00E+00	Up	Unigene103773_All//gi|124365601|gb|AAK50778.4|AF361893_1\//1.00E-146//bacterial-induced lipoxygenase [Gossypium hirsutum]	Unigene103773_All//3.00E-127//AT3G22400| LOX5; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene103773_All//0.00E+00//gi|164244850|gb|ES799168.1|ES799168		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr +
Unigene1038_All	1132	7.30	5.86	8.42	7.57	19.89	10.73	1.12	0.78	1.06	-3.17E-01	1.30E-01		2.05E-01	3.34E-01		1.39E+00	1.56E-32	Up	5.04E-01	1.74E-03		-5.31E-01	3.43E-01		-8.58E-02	8.72E-01		Unigene1038_All//gi|269980442|gb|ACZ56416.1\//1.00E-134//ankyrin-like protein [Vitis vinifera]	Unigene1038_All//6.00E-120//AT3G01750| ankyrin repeat family protein	Unigene1038_All//0.00E+00//gi|78354540|gb|DT574814.1|DT574814				nr +
Unigene103802_All	367	0.00	0.55	2.47	5.84	4.41	3.08	1.15	2.16	0.76	9.11E+00	1.37E-01		1.13E+01	4.71E-05	Up	-4.04E-01	3.75E-01		-9.24E-01	3.62E-02		9.09E-01	2.11E-01		-6.00E-01	5.53E-01				Unigene103802_All//6.00E-77//gi|109890213|gb|DW519177.1|DW519177				
Unigene10382_All	346	6.65	2.20	2.15	0.43	0.60	0.39	0.00	0.00	0.00	-1.60E+00	3.45E-04	Down	-1.63E+00	5.02E-04	Down	4.67E-01	8.26E-01		-1.41E-01	9.44E-01		null	null		null	null				Unigene10382_All//1.00E-07//DT048782				
Unigene103835_All	298	0.00	0.00	2.14	0.00	0.00	3.33	0.00	0.00	0.00	null	null		1.11E+01	1.16E-03		null	null		1.17E+01	6.15E-06	Up	null	null		null	null		Unigene103835_All//gi|124359981|gb|ABN07907.1\//1.00E-08//contains similarity to reverse trancriptase, related [Medicago truncatula]		Unigene103835_All//3.00E-07//gi|78324173|gb|DT544447.1|DT544447				nr +
Unigene103839_All	227	2.77	0.00	0.00	0.44	0.00	0.60	0.37	1.10	0.18	-1.14E+01	7.92E-04	Down	-1.14E+01	1.41E-03		-8.78E+00	3.18E-01		4.44E-01	8.63E-01		1.57E+00	3.27E-01		-1.09E+00	6.78E-01									
Unigene10385_All	655	0.00	0.00	0.00	0.00	0.00	0.00	5.62	1.08	0.97	null	null		null	null		null	null		null	null		-2.37E+00	5.08E-12	Down	-2.53E+00	2.37E-13	Down								ESTscan -
Unigene103855_All	317	0.33	4.00	0.17	1.26	1.52	2.28	0.13	0.13	0.00	3.60E+00	2.27E-05	Up	-9.74E-01	7.23E-01		2.75E-01	8.20E-01		8.59E-01	3.42E-01		-1.74E-02	1.01E+00		-7.06E+00	6.19E-01		Unigene103855_All//gi|115476212|ref|NP_001061702.1\//1.00E-48//Os08g0384500 [Oryza sativa Japonica Group] >gi|113623671|dbj|BAF23616.1| Os08g0384500 [Oryza sativa Japonica Group]	Unigene103855_All//5.00E-47//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene103855_All//4.00E-59//TC147767		ko03040|Spliceosome//ko02010|ABC transporters	GO:0032559//GO:0042626//GO:0043231	nr +
Unigene10386_All	407	0.00	6.85	4.19	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	7.44E-16	Up	1.20E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene10386_All//sp|P17275|JUNB_HUMAN//6.00E-26//Transcription factor jun-B OS=Homo sapiens GN=JUNB PE=1 SV=1						swissprot +
Unigene10387_All	422	1.36	0.24	2.02	2.12	1.14	0.86	4.01	1.09	3.40	-2.51E+00	2.94E-02		5.66E-01	4.61E-01		-8.95E-01	2.14E-01		-1.31E+00	8.52E-02		-1.88E+00	1.33E-04	Down	-2.38E-01	5.94E-01		Unigene10387_All//gi|21901929|emb|CAC86383.1\//2.00E-11//carboxypeptidase type III [Theobroma cacao]	Unigene10387_All//2.00E-08//AT3G10410| scp149 (serine carboxypeptidase-like 49); serine-type carboxypeptidase	Unigene10387_All//2.00E-46//gi|11206118|gb|BF275048.1|BF275048		ko00940|Phenylpropanoid biosynthesis	GO:0004180//GO:0019538//GO:0043231	nr -
Unigene10388_All	417	0.00	4.01	0.51	2.51	3.80	3.79	0.00	1.10	0.00	1.20E+01	1.54E-09	Up	9.00E+00	1.42E-01		5.99E-01	2.87E-01		5.96E-01	2.89E-01		1.01E+01	1.94E-03		null	null		Unigene10388_All//gi|255562741|ref|XP_002522376.1\//8.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223538454|gb|EEF40060.1| conserved hypothetical protein [Ricinus communis]		Unigene10388_All//5.00E-16//TC168014				nr +
Unigene10390_All	676	0.31	0.00	0.00	0.81	1.02	0.00	2.13	0.19	0.77	-8.27E+00	1.23E-01		-8.27E+00	1.47E-01		3.30E-01	7.52E-01		-9.66E+00	1.52E-03		-3.52E+00	3.19E-07	Down	-1.47E+00	3.09E-03		Unigene10390_All//gi|15224831|ref|NP_181947.1\//3.00E-40//EDE1 (ENDOSPERM DEFECTIVE 1); microtubule binding [Arabidopsis thaliana] >gi|63003848|gb|AAY25453.1| At2g44190 [Arabidopsis thaliana]	Unigene10390_All//1.00E-40//AT2G44190| EDE1 (ENDOSPERM DEFECTIVE 1); microtubule binding	Unigene10390_All//0.00E+00//TC170349			GO:0003006//GO:0005874//GO:0007349//GO:0009791//GO:0009987//GO:0015631//GO:0043231	nr +
Unigene10391_All	528	0.00	125.91	50.33	0.00	0.13	0.00	0.00	0.00	0.00	1.69E+01	0.00E+00	Up	1.56E+01	1.70E-150	Up	7.03E+00	6.17E-01		null	null		null	null		null	null		Unigene10391_All//gi|223995201|ref|XP_002287284.1\//2.00E-16//RL14, ribosomal protein 14 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335] >gi|220976400|gb|EED94727.1| RL14, ribosomal protein 14 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335]	Unigene10391_All//6.00E-12//AT2G20450| 60S ribosomal protein L14 (RPL14A)			ko03010|Ribosome	GO:0044424	nr -
Unigene103930_All	395	0.00	3.98	0.13	0.13	0.26	0.11	4.07	3.39	4.24	1.20E+01	5.71E-09	Up	7.07E+00	6.42E-01		1.05E+00	8.10E-01		-1.42E-01	9.57E-01		-2.65E-01	6.15E-01		5.86E-02	9.12E-01		Unigene103930_All//gi|225436241|ref|XP_002275171.1\//8.00E-16//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene103930_All//6.00E-176//gi|84174516|gb|DR463164.1|DR463164			GO:0000166	nr +
Unigene10395_All	867	0.48	16.71	0.43	0.23	1.39	0.21	0.15	0.00	0.18	5.11E+00	1.26E-70	Up	-1.67E-01	8.79E-01		2.60E+00	3.41E-04	Up	-1.41E-01	9.36E-01		-7.19E+00	2.37E-01		3.29E-01	8.52E-01		Unigene10395_All//gi|224069539|ref|XP_002326368.1\//3.00E-27//SAUR family protein [Populus trichocarpa] >gi|222833561|gb|EEE72038.1| SAUR family protein [Populus trichocarpa]	Unigene10395_All//3.00E-20//AT3G09870| auxin-responsive family protein	Unigene10395_All//0.00E+00//TC150348				nr -
Unigene103975_All	362	0.00	0.00	0.00	0.00	0.10	0.00	3.97	1.04	0.11	null	null		null	null		6.57E+00	8.40E-01		null	null		-1.93E+00	3.78E-04	Down	-5.17E+00	2.09E-09	Down	Unigene103975_All//gi|18396925|ref|NP_566232.1\//1.00E-21//DNA-binding protein-related [Arabidopsis thaliana] >gi|29028876|gb|AAO64817.1| At3g04570 [Arabidopsis thaliana] >gi|119657382|tpd|FAA00290.1| TPA: AT-hook motif nuclear localized protein 19 [Arabidopsis thaliana]	Unigene103975_All//1.00E-07//AT3G04570| DNA-binding protein-related	Unigene103975_All//3.00E-57//DW502620				nr -
Unigene103977_All	503	0.10	1.01	2.12	0.59	0.89	0.99	0.00	0.00	0.08	3.28E+00	2.11E-02		4.35E+00	6.46E-05	Up	5.83E-01	6.26E-01		7.33E-01	5.16E-01		null	null		6.31E+00	6.49E-01		Unigene103977_All//gi|270342124|gb|ACZ74707.1\//2.00E-44//carbonic anhydrase [Phaseolus vulgaris]	Unigene103977_All//4.00E-44//AT5G14740| CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding	Unigene103977_All//4.00E-162//TC141146		ko00910|Nitrogen metabolism		nr -

Unigene10398_All	1740	0.00	0.00	0.00	0.06	0.00	0.00	1.26	1.56	5.84	null	null		null	null		-5.84E+00	3.18E-01			-5.84E+00	4.06E-01		3.05E-01	3.98E-01		2.21E+00	6.82E-30	Up	Unigene10398_All//gi|115485949|ref|NP_001068118.1|//1.00E-104//Os11g0569600 [Oryza sativa Japonica Group] >gi|113645340|dbj|BAF28481.1| Os11g0569600 [Oryza sativa Japonica Group]	Unigene10398_All//2.00E-92//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative	Unigene10398_All//4.00E-23//TC151383		ko04626|Plant-pathogen interaction		nr +
Unigene10399_All	542	0.00	0.00	0.00	0.00	0.00	0.00	4.91	6.40	0.00	null	null		null	null		null	null			null	null		3.81E-01	2.24E-01		-1.23E+01	1.34E-19	Down	Unigene10399_All//gi|195618110|gb|ACG30885.1|//2.00E-27//translationally-controlled tumor protein [Zea mays] >gi|195618316|gb|ACG30988.1| translationally-controlled tumor protein [Zea mays]	Unigene10399_All//7.00E-28//AT3G05540| INVOLVED IN: biological_process unknown; LOCATED IN: cytoplasm; CONTAINS InterPro DOMAIN/s: Translationally controlled tumour protein (InterPro:IPR018105), Translationally controlled tumour-associated TCTP (InterPro:IPR001983), Mss4/translationally controlled tumour-associated TCTP (InterPro:IPR011323), Translationally controlled tumour protein, conserved site (InterPro:IPR018103), Mss4-like (InterPro:IPR011057); BEST Arabidopsis thaliana protein match is: TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN) (TAIR:AT3G16640.1); Has 640 Blast hits to 640 proteins in 231 species: Archae - 0; Bacteria - 0; Metazoa - 343; Fungi - 110; Plants - 105; Viruses - 0; Other Eukaryotes - 82 (source: NCBI BLink).				GO:0000904//GO:0005488//GO:0005576//GO:0006952//GO:0009536//GO:0010038//GO:0016020//GO:0016049//GO:0048528//GO:0048878	nr +
Unigene103996_All	204	0.26	1.24	0.00	0.49	0.84	2.88	5.18	1.84	0.00	2.28E+00	2.34E-01		-8.00E+00	6.34E-01		7.89E-01	7.72E-01			2.56E+00	2.87E-02		-1.49E+00	1.64E-02		-1.23E+01	6.73E-08	Down	Unigene103996_All//gi|46396756|sp|P93194.2|RPK1_IPONI//1.00E-11//RecName: Full=Receptor-like protein kinase; Flags: Precursor >gi|14495542|gb|AAB36558.2| receptor-like protein kinase INRPK1 [Ipomoea nil]	Unigene103996_All//3.00E-11//AT1G73066| protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene103999_All	272	74.25	16.95	61.28	20.51	28.99	14.61	1.40	0.92	0.44	-2.13E+00	3.48E-45	Down	-2.77E-01	3.66E-02		4.99E-01	1.36E-02			-4.89E-01	5.67E-02		-6.02E-01	6.13E-01		-1.67E+00	1.41E-01		Unigene103999_All//gi|229893912|gb|ACQ90301.1|//1.00E-34//squalene epoxidase [Gynostemma pentaphyllum]	Unigene103999_All//4.00E-33//AT4G37760| SQE3 (squalene epoxidase 3); squalene monooxygenase	Unigene103999_All//6.00E-101//gi|48795641|gb|CO096955.1|CO096955		ko00100|Steroid biosynthesis		nr +
Unigene1040_All	2495	20.07	6.30	11.01	37.52	33.66	10.28	21.11	8.74	8.69	-1.67E+00	2.98E-80	Down	-8.66E-01	9.17E-28		-1.56E-01	3.07E-03			-1.87E+00	6.92E-190	Down	-1.27E+00	1.10E-68	Down	-1.28E+00	1.70E-71	Down	Unigene1040_All//gi|269980442|gb|AC256416.1|//0.00E+00//ankyrin-like protein [Vitis vinifera]	Unigene1040_All//0.00E+00//AT3G01750| ankyrin repeat family protein	Unigene1040_All//0.00E+00//TC151204				nr +
Unigene10400_All	551	0.38	1.10	0.10	4.34	3.87	0.25	0.15	0.83	1.23	1.54E+00	1.22E-01		-1.98E+00	3.82E-01		-1.63E-01	7.23E-01			-4.14E+00	1.49E-11	Down	2.44E+00	3.75E-02		3.00E+00	2.00E-03		Unigene10400_All//gi|15233416|ref|NP_193816.1|//9.00E-32//FAD-binding domain-containing protein [Arabidopsis thaliana] >gi|5262224|emb|CAB45850.1| reticuline oxidase-like protein [Arabidopsis thaliana] >gi|7268880|emb|CAB79084.1| reticuline oxidase-like protein [Arabidopsis thaliana] >gi|222424693|dbj|BAH20300.1| AT4G20840 [Arabidopsis thaliana]	Unigene10400_All//4.00E-41//AT4G20840| FAD-binding domain-containing protein	Unigene10400_All//0.00E+00//TC153608			GO:0005576//GO:0005618//GO:0006950//GO:0016020//GO:0043231	nr -
Unigene10401_All	349	0.00	2.61	1.07	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.62E-05	Up	1.01E+01	2.51E-02		null	null			null	null		null	null		null	null		Unigene10401_All//sp|P13395|SPTCA_DROME//6.00E-61//Spectrin alpha chain 05-Drosophila melanogaster GN=alpha-Spec PE=1 SV=2	Unigene10401_All//6.00E-05//AT5G37780| CAM1 (CALMODULIN 1); calcium ion binding			ko04626|Plant-pathogen interaction		swissprot -
Unigene10405_All	618	0.25	0.33	2.84	0.00	0.67	0.07	0.00	0.00	0.00	3.69E-01	8.17E-01		3.48E+00	8.87E-07	Up	9.39E+00	1.25E-02			6.19E+00	7.04E-01		null	null		null	null		Unigene10405_All//gi|168069625|ref|XP_001786518.1|//1.00E-15//sensory histidine protein kinase [Physcomitrella patens subsp. patens] >gi|162661105|gb|EDQ48669.1| sensory histidine protein kinase [Physcomitrella patens subsp. patens]	Unigene10405_All//4.00E-09//AT5G10720| AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase		Orphans		GO:0016301//GO:0044237//GO:0044238	nr -
Unigene104056_All	549	0.00	0.46	4.75	0.00	0.00	1.15	0.00	0.00	0.00	8.85E+00	7.89E-02		1.22E+01	2.12E-14	Up	null	null			1.02E+01	7.60E-04	Up	null	null		null	null		Unigene104056_All//gi|56900734|gb|AAW31662.1|//4.00E-78//ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit [Amsopiptanthus mongolicus]	Unigene104056_All//4.00E-77//AT5G38430| ribulose bisphosphate carboxylase small chain 1B / RuBisCO small subunit 1B (RBCS-1B) (ATS1B)	Unigene104056_All//1.00E-20//gi|109886204|gb|DW515174.1|DW515174		ko00710|Carbon fixation in photosynthetic organisms//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene10406_All	823	0.13	132.18	103.14	0.36	0.54	0.66	0.36	0.10	0.48	1.00E+01	0.00E+00	Up	9.66E+00	0.00E+00	Up	5.83E-01	6.26E-01			8.58E-01	4.23E-01		-1.82E+00	2.11E-01		4.29E-01	6.62E-01		Unigene10406_All//gi|150406463|ref|XP_001315116.1|//7.00E-56//cytochrome c oxidase subunit 2 [Chlorokybus atmophyticus] >gi|126507700|gb|AB015097.1| cytochrome c oxidase subunit 2 [Chlorokybus atmophyticus]	Unigene10406_All//4.00E-35//ATMG00160| cytochrome c oxidase subunit 2			ko00190|Oxidative phosphorylation	GO:0016020//GO:0046872//GO:0055114	nr -
Unigene104075_All	790	29.21	19.05	21.70	14.69	11.51	6.92	2.03	1.53	0.66	-6.17E-01	6.10E-08		-4.28E-01	2.90E-04		-3.53E-01	3.16E-02			-1.09E+00	6.70E-11	Down	-4.07E-01	3.95E-01		-1.63E+00	6.02E-04	Down	Unigene104075_All//gi|297727877|ref|NP_001176302.1|//6.00E-10//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1| Os11g0106066 [Oryza sativa Japonica Group]		Unigene104075_All//1.00E-46//EST95234				nr -
Unigene10408_All	824	0.00	15.86	4.85	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	5.01E-75	Up	1.22E+01	3.83E-22	Up	null	null			null	null		null	null		null	null		Unigene10408_All//gi|255081672|ref|XP_002508058.1|//8.00E-71//peptidylprolyl isomerase, precursor [Micromonas sp. RCC299] >gi|226523334|gb|ACO69316.1| peptidylprolyl isomerase, precursor [Micromonas sp. RCC299]	Unigene10408_All//6.00E-50//AT5G13120| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein				GO:0016853//GO:0031410//GO:0043231	nr -
Unigene104081_All	268	0.00	0.00	0.00	1.12	1.03	9.61	0.95	3.28	1.19	null	null		null	null		-1.18E-01	9.01E-01			3.11E+00	1.37E-09	Up	1.79E+00	1.27E-02		3.29E-01	7.64E-01		Unigene104081_All//gi|22329131|ref|NP_195096.2|//5.00E-18//CBS domain-containing protein [Arabidopsis thaliana] >gi|17381276|gb|AAL36056.1| AT4g33700/T16L1_190 [Arabidopsis thaliana] >gi|20856058|gb|AAM26645.1| AT4g33700/T16L1_190 [Arabidopsis thaliana]	Unigene104081_All//2.00E-19//AT4G33700| CBS domain-containing protein	Unigene104081_All//7.00E-42//TC133787				nr +
Unigene104087_All	216	1.45	10.56	1.48	1.15	2.23	1.67	10.96	12.19	49.25	2.86E+00	1.28E-07	Up	2.54E-02	1.00E+00		9.53E-01	4.24E-01			5.37E-01	6.95E-01		1.53E-01	6.76E-01		2.17E+00	1.44E-30	Up			Unigene104087_All//2.00E-63//TC139645				
Unigene10409_All	278	0.00	15.31	4.02	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	3.04E-24	Up	1.20E+01	3.44E-06	Up	null	null			null	null		null	null		null	null								
Unigene104096_All	237	0.44	7.06	0.22	0.00	0.00	1.14	0.00	0.00	0.00	4.00E+00	2.08E-07	Up	-9.74E-01	7.23E-01		null	null			1.02E-01	7.06E-02		null	null		null	null				Unigene104096_All//3.00E-19//FL576574				
Unigene1041_All	2453	10.69	7.06	6.58	6.58	14.35	10.11	0.43	1.01	0.96	-5.97E-01	1.85E-08		-7.00E-01	1.84E-10		1.12E+00	1.75E-36	Up	6.19E-01	6.17E-09		1.22E+00	9.01E-04	Up	1.15E+00	1.66E-03		Unigene1041_All//gi|269980442|gb|AC256416.1|//0.00E+00//ankyrin-like protein [Vitis vinifera]	Unigene1041_All//8.00E-180//AT3G01750| ankyrin repeat family protein	Unigene1041_All//0.00E+00//TC151607				nr -
Unigene10411_All	578	2.99	0.79	3.41	0.95	0.71	0.47	1.02	1.16	0.14	-1.92E+00	4.67E-04	Down	1.90E-01	6.77E-01		-4.07E-01	6.58E-01			-1.02E+00	3.30E-01		1.76E-01	8.15E-01		-2.89E+00	4.54E-03								
Unigene10412_All	384	0.00	7.26	2.36	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	7.43E-16	Up	1.12E+01	4.71E-05	Up	null	null			null	null		null	null		null	null		Unigene10412_All//sp|Q69566|US8_HHV6U//1.00E-09//Uncharacterized protein US8 OS=Human herpesvirus 6A (strain Uganda-1102) GN=US8 PE=4 SV=1						swissprot -
Unigene10414_All	741	0.00	0.00	0.00	0.40	0.28	0.24	7.70	2.03	1.29	null	null		null	null		-5.33E-01	6.79E-01			-7.27E-01	6.39E-01		-1.92E+00	3.41E-14	Down	-2.58E+00	9.98E-21	Down			Unigene10414_All//2.00E-13//TC166793				
Unigene10415_All	564	0.00	0.00	0.00	0.00	0.00	0.00	1.80	5.48	0.00	null	null		null	null		null	null			null	null		1.61E+00	2.00E-06	Up	-1.08E+01	1.35E-07	Down							
Unigene10418_All	385	10.60	11.84	13.42	26.27	18.60	26.16	322.98	424.80	678.29	1.60E-01	6.18E-01		3.40E-01	2.33E-01		-4.98E-01	3.42E-03			-5.80E-03	9.71E-01		3.95E-01	2.21E-28		1.07E+00	7.23E-262	Up			Unigene10418_All//1.00E-152//gi|164253602|gb|ES824425.1|ES824425				
Unigene104194_All	325	27.05	2.65	4.26	28.36	11.87	10.56	18.34	1.80	0.74	-3.35E+00	1.86E-32	Down	-2.67E+00	7.87E-25	Down	-1.26E+00	2.93E-12	Down	-1.42E+00	4.12E-13	Down	-3.35E+00	4.94E-27	Down	-4.64E+00	1.63E-35	Down	Unigene104194_All//gi|15236175|ref|NP_194362.1|//2.00E-07//AGP13 (arabinogalactan protein 13) [Arabidopsis thaliana] >gi|75207711|sp|Q9SYA3.1|AGP13_ARATH RecName: Full=Arabinogalactan peptide 13; Short=AG-peptide 13; Flags: Precursor >gi|10880503|gb|AAG24281.1|AF195894_1 arabinogalactan protein [Arabidopsis thaliana] >gi|89111816|gb|ABD60680.1| At4g26320 [Arabidopsis thaliana]		Unigene104194_All//5.00E-71//gi|21094474|gb|BQ406799.1|BQ406799				nr -
Unigene104197_All	334	0.00	0.15	0.00	0.30	0.41	0.27	6.46	46.30	1.79	7.25E+00	6.23E-01		null	null		4.67E-01	8.78E-01			-1.42E-01	9.53E-01		2.84E+00	7.50E-59	Up	-1.85E+00	8.47E-06	Down	Unigene104197_All//gi|15220954|ref|NP_174363.1|//1.00E-32//FAD-binding domain-containing protein [Arabidopsis thaliana] >gi|16323167|gb|AAL15318.1| At1g30760/T518_22 [Arabidopsis thaliana] >gi|28416457|gb|AAO42759.1| At1g30760/T518_22 [Arabidopsis thaliana]	Unigene104197_All//5.00E-34//AT1G30760| FAD-binding domain-containing protein	Unigene104197_All//6.00E-09//TC166754				nr +
Unigene1042_All	3284	6.21	62.55	13.18	8.72	35.65	50.99	29.21	161.88	260.77	3.33E+00	0.00E+00	Up	1.09E+00	7.01E-35	Up	2.03E+00	5.48E-285	Up	2.55E+00	0.00E+00	Up	2.47E+00	0.00E+00	Up	3.16E+00	0.00E+00	Up	Unigene1042_All//gi|15224213|ref|NP_179460.1|//0.00E+00//ATTPS11; transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75216907|sp|Q9ZV48.1|TPS11_ARATH RecName: Full=Probable alpha,alpha-trehalose-phosphate synthase [UDP-forming] 11; AltName: Full=Trehalose-6-phosphate synthase 11; Short=AtTPS11	Unigene1042_All//0.00E+00//AT2G18700| ATTPS11; transferase, transferring glycosyl groups	Unigene1042_All//0.00E+00//TC176400		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0019203//GO:0035251//GO:0043231	nr +

Unigene10420_A11	671	0.00	0.00	0.00	0.00	0.00	0.00	1.76	4.98	0.00	null	null		null	null		null	null		null	null		1.50E+00	2.73E-06	Up	-1.08E+01	8.15E-09	Down	Unigene10420_A11//gi|115469274|ref|NP_001058236.1|//3.00E-19//0s06g0652600 [Oryza sativa Japonica Group] >gi|51535038|dbj|BAD37409.1| fibroin heavy chain precursor-like [Oryza sativa Japonica Group] >gi|113596276|dbj|BAF20150.1| Os06g0652600 [Oryza sativa Japonica Group]				ko03040|Spliceosome//ko03018|RNA degradation	GO:0044464	nr +
Unigene10210_A11	261	3.61	2.14	2.04	7.44	2.37	4.50	1.94	1.76	0.61	-7.57E-01	2.86E-01		-8.23E-01	2.71E-01		-1.65E+00	2.73E-04	Down	-7.26E-01	1.27E-01		-1.42E-01	8.76E-01		-1.67E+00	7.78E-02				Unigene104210_A11//1.00E-74//DW498863					
Unigene10422_A11	393	0.27	0.52	0.00	3.80	3.86	1.38	2.15	0.21	0.30	9.54E-01	6.23E-01		-8.06E+00	4.00E-01		1.99E-02	9.85E-01		-1.46E+00	8.90E-03		-3.34E+00	2.52E-04	Down	-2.82E+00	5.38E-04	Down	Unigene10422_A11//gi|124360202|gb|ABN08215.1|//1.00E-67//Zinc finger, CCCH-type [Medicago truncatula]	Unigene10422_A11//6.00E-68//AT2G41900| zinc finger (CCCH-type) family protein	Unigene10422_A11//4.00E-32//TC132093	C3H		GO:0001071//GO:0010468//GO:0044424//GO:0046914	nr +
Unigene104239_A11	267	3.33	10.44	7.18	13.99	13.93	11.16	9.03	7.04	10.30	1.65E+00	4.82E-05	Up	1.11E+00	2.53E-02		-6.60E-03	9.73E-01		-3.26E-01	3.52E-01		-3.58E-01	3.67E-01		1.90E-01	6.15E-01				Unigene104239_A11//8.00E-88//gi|13243815|gb|BE053182.2|BE053182					
Unigene10425_A11	734	0.00	5.11	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.40E-21	Up	1.05E+01	6.63E-06	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene10427_A11	438	0.00	0.58	0.24	0.00	0.24	0.21	0.19	2.29	0.18	9.18E+00	7.89E-02		7.93E+00	4.03E-01		7.88E+00	4.59E-01		7.69E+00	4.82E-01		3.57E+00	3.08E-05	Up	-8.62E-02	9.74E-01		Unigene10427_A11//gi|267124|sp|P29449.1|TRXH1_TOBAC//2.00E-06//RecName: Full=Thioredoxin H-type 1; Short=Trx-H1 >gi|20047|emb|CAA41415.1| thioredoxin [Nicotiana tabacum]		Unigene10427_A11//3.00E-33//EX167848				nr -
Unigene104270_A11	402	0.00	0.00	0.00	0.00	0.09	4.27	0.00	0.00	0.00	null	null		null	null		6.42E+00	8.40E-01		1.21E+01	3.12E-10	Up	null	null		null	null		Unigene104270_A11//gi|146160694|gb|ABQ08576.1|//3.00E-06//alpha-gliadin [Australopyrum retrofractum]				ko00760|Nicotinate and nicotinamide metabolism		nr -
Unigene10428_A11	337	0.00	9.02	0.00	0.59	1.23	1.88	0.00	0.00	1.30	1.31E+01	2.68E-17	Up	null	null		1.05E+00	4.26E-01		1.67E+00	9.80E-02		null	null		1.03E+01	2.14E-03		Unigene10428_A11//gi|2245113|emb|CAB10535.1|//9.00E-15//glycerol-3-phosphate permease like protein [Arabidopsis thaliana] >gi|7268507|emb|CAB78758.1| glycerol-3-phosphate permease like protein [Arabidopsis thaliana]	Unigene10428_A11//4.00E-16//AT4G17550| transporter-related				GO:0006810//GO:0009987//GO:0043231	nr +
Unigene10429_A11	980	0.11	0.31	0.33	0.81	0.70	0.23	4.27	4.65	1.22	1.54E+00	3.24E-01		1.61E+00	3.05E-01		-2.11E-01	8.06E-01		-1.82E+00	3.32E-02		1.22E-01	6.54E-01		-1.81E+00	3.56E-10	Down	Unigene10429_A11//gi|44888124|sp|P93308.1|ME30_ARATH//2.00E-30//RecName: Full=Uncharacterized mitochondrial protein AtMg00530; AltName: Full=ORF109	Unigene10429_A11//3.00E-27//ATMG00530| hypothetical protein	Unigene10429_A11//0.00E+00//gi|109854544|gb|DW483523.1|DW483523			GO:0043231	nr +
Unigene10430_A11	582	0.27	0.09	0.09	0.51	0.12	0.31	1.24	2.37	4.38	-1.63E+00	4.89E-01		-1.56E+00	5.34E-01		-2.12E+00	1.66E-01		-7.26E-01	6.39E-01		9.40E-01	6.71E-02	Up	1.83E+00	1.63E-06	Up			Unigene10430_A11//9.00E-25//TC149710					
Unigene10431_A11	726	0.00	0.00	0.00	0.00	0.09	0.00	0.82	1.73	5.43	null	null		null	null		6.57E+00	6.16E-01		null	null		1.08E+00	4.70E-02		2.74E+00	3.14E-15	Up	Unigene10431_A11//gi|284028888|gb|AD866335.1|//4.00E-40//CC-NBS-LRR protein [Quercus suber]	Unigene10431_A11//4.00E-17//AT3G14460| disease resistance protein (NBS-LRR class)_putative					nr +
Unigene10310_A11	274	72.56	40.50	49.95	119.99	131.83	166.81	144.89	79.93	64.70	-8.41E-01	2.18E-11		-5.39E-01	2.39E-05		1.36E-01	1.68E-01		4.75E-01	4.07E-10		-8.58E-01	1.11E-27		-1.16E+00	1.52E-46	Down	Unigene10310_A11//gi|195620934|gb|ACG32297.1|//6.00E-36//60S ribosomal protein L23 [Zea mays]	Unigene10310_A11//1.00E-36//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene104310_A11//6.00E-135//TC154590		ko03010|Ribosome		nr -
Unigene10330_A11	277	5.10	7.87	6.92	20.32	14.92	7.83	3.51	2.87	3.02	6.25E-01	1.50E-01		4.40E-01	3.86E-01		-4.46E-01	7.15E-02		-1.38E+00	7.40E-08	Down	-2.92E-01	6.31E-01		-2.17E-01	7.07E-01				Unigene104330_A11//7.00E-141//TC137783					ESTscan -
Unigene104332_A11	307	0.68	14.19	3.99	0.49	0.67	6.18	0.28	0.27	1.17	4.38E+00	1.10E-19	Up	2.55E+00	8.25E-04	Up	4.67E-01	8.26E-01		3.67E+00	3.48E-08	Up	-1.63E-02	1.02E+00		2.08E+00	1.01E-01		Unigene104332_A11//gi|44681328|gb|AAS47604.1|//5.00E-24//At4g15670 [Arabidopsis thaliana] >gi|45773840|gb|AAS67624.1| At4g15670 [Arabidopsis thaliana]	Unigene104332_A11//3.00E-25//AT5G18600| glutaredoxin family protein	Unigene104332_A11//4.00E-56//gi|109866735|gb|DW495711.1|DW495711				nr -
Unigene104349_A11	239	0.00	0.42	0.00	0.00	0.29	1.70	25.12	55.44	226.70	8.73E+00	3.91E-01		null	null		8.17E+00	6.16E-01		1.07E+01	1.36E-02		1.14E+00	3.57E-15	Up	3.17E+00	8.94E-233	Up	Unigene104349_A11//gi|224092400|ref|XP_002309592.1|//5.00E-14//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222855568|gb|EEE93115.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene104349_A11//1.00E-13//AT1G32800| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene104349_A11//2.00E-82//TC144167				nr -
Unigene10436_A11	629	0.00	10.47	8.21	0.00	0.00	0.14	0.00	0.00	0.00	1.34E+01	1.26E-37	Up	1.30E+01	9.62E-29	Up	null	null		7.17E+00	4.82E-01		null	null		null	null		Unigene10436_A11//sp|P08727|K1C19_HUMAN//3.00E-90//Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=3						swissprot -
Unigene104378_A11	241	0.22	3.78	0.44	0.83	3.43	0.94	0.35	0.35	0.33	4.12E+00	2.34E-04	Up	1.03E+00	7.05E-01		2.05E+00	1.79E-02		1.81E-01	9.36E-01		-1.65E-02	1.02E+00		-8.60E-02	9.74E-01									
Unigene10439_A11	750	0.00	7.30	5.40	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	3.25E-31	Up	1.24E+01	1.92E-22	Up	null	null		null	null		null	null		null	null		Unigene10439_A11//gi|300147461|gb|EFJ14125.1|//3.00E-06//hypothetical protein SELMODRAFT_446044 [Selaginella moellendorffii]	Unigene10439_A11//6.00E-06//AT1G56040| binding / protein binding / ubiquitin-protein ligase					nr +
Unigene104391_A11	280	0.75	0.00	0.76	0.00	0.74	2.90	0.45	0.00	0.28	-9.55E+00	1.23E-01		2.54E-02	1.00E+00		9.53E+00	1.57E-01		1.15E+01	6.96E-05	Up	-8.82E+00	2.37E-01		-6.71E-01	7.21E-01		Unigene104391_A11//gi|297842799|ref|XP_002889281.1|//4.00E-23//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335122|gb|EFH65540.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene104391_A11//3.00E-24//AT1G80640| protein kinase family protein	Unigene104391_A11//4.00E-96//TC158373		ko04626|Plant-pathogen interaction		nr -
Unigene10441_A11	835	0.00	48.18	12.88	0.00	0.00	0.00	0.00	0.00	0.00	1.56E+01	3.15E-232	Up	1.37E+01	2.06E-60	Up	null	null		null	null		null	null		null	null		Unigene10441_A11//gi|195611912|gb|ACG27786.1|//2.00E-79//40S ribosomal protein SA [Zea mays]	Unigene10441_A11//3.00E-73//AT1G72370| P40; structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr +
Unigene10422_A11	496	0.63	0.51	0.32	2.81	1.04	0.55	2.73	1.18	0.96	-3.09E-01	7.89E-01		-9.75E-01	5.06E-01		-1.43E+00	8.65E-03		-2.36E+00	2.38E-04	Down	-1.21E+00	2.08E-02		-1.50E+00	3.72E-03				Unigene104422_A11//7.00E-127//TC158572					
Unigene10443_A11	482	0.98	0.53	1.99	0.52	2.36	4.69	0.00	0.00	0.17	-8.94E-01	3.89E-01		1.03E+00	1.68E-01		2.19E+00	2.16E-03		3.18E+00	1.22E-08	Up	null	null		7.37E+00	4.06E-01		Unigene10443_A11//gi|224060417|ref|XP_002300189.1|//7.00E-57//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222847447|gb|EEE84994.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene10443_A11//8.00E-35//AT1G17840| WBC11 (WHITE-BROWN COMPLEX HOMOLOG PROTEIN 11); ATPase, coupled to transmembrane movement of substances / fatty acid transporter	Unigene10443_A11//0.00E+00//gi|48880748|gb|CO131770.1|CO131770		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015604//GO:0017111//GO:0032559//GO:0044464	nr +
Unigene104438_A11	620	0.17	0.08	0.09	0.16	0.06	0.07	1.98	0.47	0.32	-1.05E+00	6.86E-01		-9.75E-01	7.22E-01		-1.53E+00	5.89E-01		-1.14E+00	6.79E-01		-2.07E+00	6.67E-04	Down	-2.62E+00	4.02E-05	Down	Unigene104438_A11//gi|297818614|ref|XP_002877190.1|//4.00E-15//ATEX07OE1 [Arabidopsis lyrata subsp. lyrata] >gi|297323028|gb|EFH53449.1| ATEX07OE1 [Arabidopsis lyrata subsp. lyrata]	Unigene104438_A11//3.00E-15//AT3G29400| ATEX07OE1 (exocyst subunit EX070 family protein E1); protein binding	Unigene104438_A11//0.00E+00//TC146233				nr -
Unigene10445_A11	619	1.35	0.74	1.89	8.77	3.73	2.19	2.19	0.88	0.51	-8.76E-01	2.47E-01		4.85E-01	4.47E-01		-1.23E+00	3.00E-07	Down	-2.00E+00	1.58E-12	Down	-1.32E+00	1.25E-02		-2.09E+00	1.85E-04	Down			Unigene10445_A11//3.00E-12//ES830995					
Unigene10446_A11	595	0.79	0.17	0.81	0.50	3.65	0.76	1.07	0.21	0.27	-2.22E+00	7.77E-02		2.55E-02	1.00E+00		2.86E+00	5.97E-08	Up	5.96E-01	6.40E-01		-2.34E+00	1.27E-02		-1.99E+00	2.04E-02		Unigene10446_A11//gi|15232013|ref|NP_187520.1|//2.00E-35//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene10446_A11//1.00E-36//AT3G09080| transducin family protein / WD-40 repeat family protein	Unigene10446_A11//0.00E+00//ES850458				nr +
Unigene10447_A11	335	0.00	14.82	2.54	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	2.63E-28	Up	1.13E+01	9.03E-05	Up	null	null		null	null		null	null		null	null		Unigene10447_A11//gi|226456844|gb|EEH54144.1|//1.00E-25//histone H4 [Micromonas pusilla CCMP1545]	Unigene10447_A11//6.00E-27//AT5G59970| histone H4	Unigene10447_A11//1.00E-16//TC167353			GO:0000785//GO:0003676//GO:0005856//GO:0008092//GO:0034728//GO:0043231	nr -
Unigene104472_A11	587	4.10	3.45	1.18	3.73	2.70	4.23	3.75	2.21	1.83	-2.48E-01	5.63E-01		-1.80E+00	1.11E-04	Down	-4.69E-01	2.94E-01		1.81E-01	6.97E-01		-7.63E-01	4.86E-02		-1.03E+00	5.87E-03		Unigene104472_A11//gi|7330785|gb|AAF60252.1|AF204677_1//2.00E-59//guanylate kinase [Arabidopsis thaliana]	Unigene104472_A11//3.00E-52//AT3G57550| AGK2 (GUANYLATE KINASE); guanylate kinase	Unigene104472_A11//0.00E+00//EX168696		ko00230|Purine metabolism	GO:0009117//GO:0016776//GO:0032559//GO:0044424	nr +
Unigene10448_A11	479	0.00	0.00	0.00	0.00	0.29	0.19	0.26	1.83	6.15	null	null		null	null		8.17E+00	3.20E-01		7.56E+00	4.82E-01		2.79E+00	6.97E-04	Up	4.54E+00	3.38E-17	Up	Unigene10448_A11//gi|6017938|gb|AAF01694.1|AF181456_1//7.00E-13//dehydrin [Hordeum vulgare subsp. vulgare]						nr +
Unigene10449_A11	483	0.00	0.00	0.00	0.00	0.00	0.00	5.34	0.61	2.14	null	null		null	null		null	null		null	null		-3.14E+00	2.22E-11	Down	-1.32E+00	1.79E-04	Down	Unigene10449_A11//gi|55168340|gb|AAV44205.1|//3.00E-12//unknow protein [Oryza sativa Japonica Group]		Unigene10449_A11//1.00E-17//TC149394				nr +
Unigene104511_A11	250	0.21	0.00	0.00	0.60	0.83	0.18	3.55	0.50	0.48	-7.71E+00	6.21E-01		-7.71E+00	6.34E-01		4.67E-01	8.26E-01		-1.73E+00	5.02E-01		-2.82E+00	5.65E-04	Down	-2.89E+00	3.05E-04	Down								
Unigene104515_A11	277	0.19	0.37	1.35	1.44	0.25	1.63	8.70	15.99	27.04	9.53E-01	7.28E-01		2.83E+00	9.32E-02		-2.53E+00	5.80E-02		1.81E-01	8.84E-01		8.78E-01	6.29E-04	Up	1.64E+00	3.49E-15	Up			Unigene104515_A11//2.00E-60//FL576534					
Unigene104518_A11	306	0.00	0.33	0.00	0.00	0.00	2.66	0.83	0.00	0.13	8.37E+00	3.91E-01		null	null		null	null		1.14E+01	6.96E-05	Up	-9.70E+00	4.06E-02		-2.67E+00	1.15E-01									
Unigene10452_A11	452	0.00	5.72	3.30	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.06E-14	Up	1.17E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene10452_A11//gi|297798734|ref|XP_002867251.1|//1.00E-43//ATP synthase family [Arabidopsis lyrata subsp. lyrata] >gi|297313087|gb|EFH43510.1| ATP synthase family [Arabidopsis lyrata subsp. lyrata]	Unigene10452_A11//1.00E-37//AT4G32260| ATP synthase family			ko00190|Oxidative phosphorylation//ko00195|Photosynthesis	GO:0006754//GO:0006818//GO:0006952//GO:0009526//GO:0009534//GO:0015077//GO:0031224//GO:0033177	nr -
Unigene10453_A11	493	0.00	2.78	1.30	0.00	0.14	0.09	0.00	0.00	0.00	1.14E+01	7.80E-08	Up	1.03E+01	1.16E-03		7.13E+00	6.16E-01		6.52E+00	7.04E-01		null	null		null	null		Unigene10453_A11//sp|Q5RC60|TIMP1_PONAB//2.00E-68//Metalloproteinase inhibitor 1 OS=Pongo abelii GN=TIMP1 PE=2 SV=1						swissprot -
Unigene104556_A11	614	0.00	0.00	0.00	0.16	0.22	1.69	0.48	0.14	0.00	null	null		null	null		4.67E-01	8.78E-01		3.38E+00	2.04E-04	Up	-1.82E+00	2.11E-01		-8.91E+00	1.59E-02		Unigene104556_A11//gi|296081092|emb|CBI18286.3|//3.00E-06//unnamed protein product [Vitis vinifera]		Unigene104556_A11//4.00E-27//DT462277				nr -
Unigene104566_A11	364	0.00	0.00	0.00	0.00	0.00	0.00	6.27	0.00	0.00	null	null		null	null		null	null		null	null		-1.26E+01	3.78E-16	Down	-1.26E+01	8.15E-17	Down	Unigene104566_A11//gi|53828151|gb|AAU94355.1|//2.00E-31//iron reductase [Pisum sativum]	Unigene104566_A11//4.00E-16//AT1G23020| FRO3; ferric-chelate reductase	Unigene104566_A11//1.00E-22//C0089158			GO:0006826//GO:0008152//GO:0016723//GO:0030554//GO:0031224//GO:0046914//GO:0050664//GO:0051707//GO:0055066	nr -
Unigene104568_A11	251	0.00	0.00	0.21	0.40	0.00	0.00	4.55	0.00	0.63	null	null		7.73E+00	6.42E-01		-8.63E+00	3.18E-01		-8.63E+00	4.06E-01		-1.22E+01	3.89E-08	Down	-2.84E+00	3.60E-05	Down	Unigene104568_A11//gi|224120220|ref|XP_002330994.1|//3.00E-22//cytochrome P450 [Populus trichocarpa] >gi|222872924|gb|EEF10055.1| cytochrome P450 [Populus trichocarpa]	Unigene104568_A11//2.00E-22//AT2G42250| CYP712A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene104568_A11//6.00E-70//ES837654			GO:0005506//GO:0008152//GO:0016709//GO:0044464	nr +
Unigene104571_A11	391	1.34	0.00	0.14	0.00	0.18	1.85	0.11	0.11	0.00	-1.04E+01	2.93E-03		-3.30E+00	2.40E-02		7.46E+00	6.16E-01		1.09E+01	2.31E-04	Up	-1.61E-02	1.01E+00		-6.76E+00	6.18E-01		Unigene104571_A11//gi|9294523|dbj|BAB02785.1|//3.00E-43//protein transport protein Sec23 [Arabidopsis thaliana]	Unigene104571_A11//1.00E-44//AT3G23660| transport protein, putative	Unigene104571_A11//1.00E-96//TC133366			GO:0012507//GO:0015031//GO:0046914//GO:0048193	nr +
Unigene104579_A11	286	3.48	9.92	2.98	2.96	3.85	4.58	0.30	0.58	0.84	1.51E+00	1.25E-04	Up	-2.23E-01	7.34E-01		3.80E-01	6.01E-01		6.29E-01	3.15E-01		9.83E-01	6.35E-01		1.50E+00	3.39E-01		Unigene104579_A11//gi|196196276|gb|ACG76109.1|//2.00E-18//pathogenesis-induced protein [Arachis hypogaea]	Unigene104579_A11//2.00E-16//AT1G01360| unknown protein	Unigene104579_A11//6.00E-61//C0084264				nr +

Unigene10459_All	349	0.00	0.00	0.00	0.29	0.00	0.00	1.94	0.12	1.71	null	null		null	null		-8.16E+00	3.18E-01		-8.16E+00	4.06E-01		-4.02E+00	5.36E-04	Down	-1.79E-01	7.94E-01		Unigene10459_All//gi|255586731|ref|XP_002533988.1|//1.00E-36//ice binding protein, putative [Ricinus communis] >gi|223526023|gb|EEF28395.1| ice binding protein, putative [Ricinus communis]	Unigene10459_All//3.00E-22//AT5G57770| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Pleckstrin-like, plant (InterPro:IPR013666), Protein of unknown function DUF828, plant (InterPro:IPR008546); Has 104 Blast hits to 104 proteins in 9 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 102; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr +
Unigene104598_All	250	0.84	0.00	0.21	6.38	2.75	1.63	0.17	0.00	0.00	-9.71E+00	1.23E-01		-1.97E+00	3.82E-01		-1.21E+00	1.52E-02		-1.97E+00	4.88E-04	Down	-7.40E+00	6.64E-01		-7.40E+00	6.18E-01			Unigene104598_All//4.00E-71//DT048741					
Unigene104611_All	258	0.00	0.00	0.00	3.67	1.87	0.18	0.33	0.00	0.00	null	null		null	null		-9.73E-01	1.60E-01		-4.39E+00	5.97E-05	Down	-8.36E+00	4.08E-01		-8.36E+00	3.62E-01			Unigene104611_All//2.00E-76//gi|3326234|gb|AI055120.1|AI055120					nr -
Unigene104622_All	224	0.00	0.00	0.71	0.22	0.46	0.81	5.10	0.93	0.53	null	null		9.48E+00	2.40E-01		1.05E+00	8.10E-01		1.86E+00	4.59E-01		-2.45E+00	2.46E-04	Down	-3.26E+00	8.94E-06	Down		Unigene104622_All//2.00E-66//TC154279					
Unigene10463_All	378	0.14	0.13	0.28	0.79	0.18	0.48	2.01	6.63	11.38	-4.66E-02	9.88E-01		1.03E+00	7.05E-01		-2.12E+00	1.66E-01		-7.26E-01	6.39E-01		1.72E+00	8.26E-06	Up	2.50E+00	4.72E-15	Up		Unigene10463_All//1.00E-10//BQ413454					
Unigene104641_All	722	0.00	0.00	0.00	3.31	5.20	2.13	1.52	0.17	0.11	null	null		null	null		6.51E-01	3.83E-02		-6.39E-01	1.31E-01		-3.13E+00	3.47E-05	Down	-3.79E+00	3.27E-06	Down	Unigene104641_All//gi|224090738|ref|XP_002309069.1|//1.00E-100//laccase 110c [Populus trichocarpa] >gi|222855045|gb|EEE92592.1| laccase 110c [Populus trichocarpa]	Unigene104641_All//1.00E-83//AT5G60020| LAC17 (laccase 17); laccase	Unigene104641_All//0.00E+00//gi|109859138|gb|DW488117.1|DW488117		ko00910|Nitrogen metabolism/ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr +
Unigene104648_All	304	1.20	2.50	0.00	0.82	1.25	6.39	0.28	0.55	0.00	1.05E+00	2.05E-01		-1.02E+01	2.79E-02		6.05E-01	6.59E-01		2.96E+00	4.85E-07	Up	9.83E-01	6.35E-01		-8.12E+00	3.62E-01			Unigene104648_All//1.00E-12//AW187099					
Unigene10467_All	469	0.45	0.65	0.57	1.49	0.59	0.67	0.99	4.55	1.10	5.39E-01	6.72E-01		3.47E-01	7.97E-01		-1.34E+00	1.09E-01		-1.14E+00	2.01E-01		2.20E+00	1.16E-06	Up	1.55E-01	8.60E-01			Unigene10467_All//0.00E+00//TC137224					
Unigene10468_All	316	0.00	0.00	0.00	0.00	0.00	0.00	1.87	3.04	0.00	null	null		null	null		null	null		null	null		7.00E-01	2.78E-01		-1.09E+01	1.42E-04	Down								ESTscan -
Unigene104697_All	359	5.98	14.26	7.71	10.27	14.96	17.99	10.36	22.12	24.97	1.25E+00	5.19E-06	Up	3.68E-01	3.75E-01		5.43E-01	3.31E-02		8.09E-01	4.14E-04		1.09E+00	7.67E-09	Up	1.27E+00	1.35E-12	Up	Unigene104697_All//gi|224058435|ref|XP_002299508.1|//6.00E-06//predicted protein [Populus trichocarpa] >gi|222846766|gb|EEE84313.1| predicted protein [Populus trichocarpa]	Unigene104697_All//4.00E-05//AT1G01490| heavy-metal-associated domain-containing protein	Unigene104697_All//9.00E-73//TC164512					nr -
Unigene10470_All	339	0.15	2.69	0.47	0.29	0.41	0.80	0.37	0.25	1.06	4.12E+00	2.34E-04	Up	1.61E+00	5.12E-01		4.67E-01	8.78E-01		1.44E+00	4.10E-01		-6.02E-01	7.68E-01		1.50E+00	2.04E-01			Unigene10470_All//4.00E-07//TC161099					
Unigene104704_All	215	1.22	0.71	5.70	0.93	2.08	6.72	0.20	1.56	0.00	-7.83E-01	6.20E-01		2.23E+00	2.23E-03		1.17E+00	3.47E-01		2.86E+00	3.35E-05	Up	2.98E+00	5.74E-02		-7.62E+00	6.18E-01			Unigene104704_All//3.00E-19//TC133986					ESTscan -
Unigene104720_All	312	12.41	5.52	17.75	3.03	2.54	3.04	0.00	0.00	0.00	-1.17E+00	2.34E-04	Down	5.16E-01	5.24E-02		-2.57E-01	7.27E-01		2.90E-03	9.98E-01		null	null		null	null		Unigene104720_All//gi|19184|emb|CAA43590.1|//6.00E-07//Type I (26 kD) CF29 polypeptide [Solanum lycopersicum]	Unigene104720_All//2.00E-05//AT4G10340| LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding	Unigene104720_All//3.00E-20//EX167600		ko00196|Photosynthesis - antenna proteins	GO:0044237//GO:0044464	nr -
Unigene10473_All	568	0.00	5.17	1.22	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.01E-16	Up	1.03E+01	6.17E-04	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene104760_All	230	0.00	0.00	0.23	0.43	0.60	0.79	6.99	52.34	10.74	null	null		7.85E+00	6.42E-01		4.67E-01	8.78E-01		8.59E-01	6.97E-01		2.91E+00	5.45E-47	Up	6.21E-01	7.63E-02		Unigene104760_All//gi|239784432|dbj|BAC21263.1|//3.00E-12//glutathione S-transferase [Cucurbita maxima]		Unigene104760_All//1.00E-30//gi|164314276|gb|ES842964.1|ES842964	ko00480|Glutathione metabolism	GO:0016740//GO:0016846	nr +
Unigene104761_All	315	0.00	0.00	0.17	4.90	4.04	1.86	2.68	0.27	0.89	null	null		7.40E+00	6.42E-01		-2.77E-01	5.98E-01		-1.40E+00	1.06E-02		-3.34E+00	2.52E-04	Down	-1.60E+00	2.02E-02			Unigene104761_All//1.00E-46//gi|109836538|gb|DW235099.1|DW235099					
Unigene104787_All	352	1.34	5.18	1.82	0.71	1.47	1.80	1.08	1.07	1.13	1.95E+00	2.77E-04	Up	4.41E-01	6.23E-01		1.05E+00	3.49E-01		1.34E+00	1.74E-01		-1.66E-02	1.02E+00		6.63E-02	9.66E-01		Unigene104787_All//gi|6664314|gb|AAF22896.1|AC006932_13//8.00E-12//T2767.21 [Arabidopsis thaliana]	Unigene104787_All//1.00E-15//AT1G08530| unknown protein	Unigene104787_All//2.00E-120//TC152997			GO:0043231	nr -
Unigene10480_All	291	7.01	32.21	25.25	75.66	61.06	57.58	353.35	284.38	143.88	2.20E+00	5.48E-22	Up	1.85E+00	1.64E-13	Up	-3.09E-01	6.24E-03		-3.94E-01	6.26E-04		-3.13E-01	4.91E-12		-1.30E+00	2.92E-141	Down		Unigene10480_All//2.00E-138//gi|109838778|gb|DW237339.1|DW237339					
Unigene104806_All	495	0.42	0.82	2.80	1.51	0.42	0.91	0.17	0.17	0.16	9.54E-01	4.14E-01		2.73E+00	1.78E-04	Up	-1.85E+00	2.53E-02		-7.26E-01	3.90E-01		-1.61E-02	1.02E+00		-8.52E-02	9.74E-01			Unigene104806_All//1.00E-149//gi|21096576|gb|BQ408889.1|BQ408889					
Unigene10482_All	412	0.00	0.00	0.00	0.00	0.00	0.00	6.57	3.04	0.00	null	null		null	null		null	null		null	null		-1.11E+00	1.31E-03		-1.27E+01	6.55E-20	Down	Unigene10482_All//gi|145408590|ref|YP_001152214.1|//8.00E-06//ORF124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| ORF124 [Pinus koraiensis]		Unigene10482_All//4.00E-23//gi|11207717|gb|BF276647.1|BF276647				nr -
Unigene104832_All	298	0.53	0.34	1.25	7.36	15.25	4.55	2.84	0.00	0.00	-6.31E-01	7.29E-01		1.25E+00	3.66E-01		1.05E+00	1.21E-04	Up	-6.94E-01	1.18E-01		-1.15E-01	4.39E-06	Down	-1.15E-01	2.21E-06	Down		Unigene104832_All//3.00E-134//ES851582					
Unigene104833_All	309	34.20	13.45	37.57	23.70	22.18	10.09	0.96	0.68	0.52	-1.35E+00	6.78E-13	Down	1.35E-01	4.79E-01		-9.57E-02	7.14E-01		-1.23E+00	1.49E-08	Down	-5.02E-01	6.78E-01		-8.93E-01	4.71E-01			Unigene104833_All//2.00E-110//TC174668					
Unigene10484_All	373	0.56	2.45	4.00	8.15	8.68	6.54	0.45	0.22	0.00	2.12E+00	1.04E-02		2.83E+00	6.17E-05	Up	9.12E-02	8.23E-01		-3.17E-01	4.17E-01		-1.02E+00	6.16E-01		-8.82E+00	1.09E-01			Unigene10484_All//2.00E-67//gi|13247536|gb|BF270981.2|BF270981					
Unigene104856_All	269	0.39	0.00	0.00	0.19	0.38	0.17	2.67	0.16	0.59	-8.60E+00	3.77E-01		-8.60E+00	3.99E-01		1.05E+00	8.10E-01		-1.42E-01	9.57E-01		-4.10E+00	2.92E-04	Down	-2.17E+00	7.76E-03		Unigene104856_All//gi|19570247|dbj|BAB86283.1|//6.00E-28//kinesin-like protein NACK1 [Nicotiana tabacum]	Unigene104856_All//7.00E-27//AT1G18370| HIK (HINKEL); ATP binding / microtubule motor				GO:0000226//GO:0003774//GO:0007349//GO:0009536//GO:0015630//GO:0032559//GO:0033206//GO:0046914//GO:0048229	nr +
Unigene104865_All	266	0.39	0.00	1.20	0.00	1.42	2.89	0.95	0.00	0.60	-8.62E+00	3.77E-01		1.61E+00	3.05E-01		1.05E+01	1.96E-02		1.15E+01	1.27E-04	Up	-9.90E+00	4.06E-02		-6.71E-01	6.06E-01		Unigene104865_All//gi|186501175|ref|NP_179383.2|//8.00E-35//binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor [Arabidopsis thaliana]	Unigene104865_All//3.00E-36//AT2G17930| binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor	Unigene104865_All//2.00E-141//TC142236			GO:0016772	nr +
Unigene10487_All	286	0.00	0.00	0.00	0.00	0.00	0.00	217.46	79.21	21.17	null	null		null	null		null	null		null	null		-1.46E+00	1.65E-99	Down	-3.36E+00	6.57E-287	Down								
Unigene10489_All	362	0.87	0.14	3.97	1.24	0.00	0.00	0.00	0.00	0.00	-2.63E+00	1.31E-01		2.20E+00	8.73E-04	Up	-1.03E+01	2.00E-03		-1.03E+01	5.79E-03		null	null		null	null		Unigene10489_All//COG4784//1.00E-25//Putative Zn-dependent protease						cog -
Unigene104908_All	274	2.29	2.03	1.75	4.73	5.66	2.47	5.25	6.25	1.16	-1.72E-01	8.29E-01		-3.90E-01	6.46E-01		2.59E-01	6.64E-01		-9.35E-01	1.22E-01		2.54E-01	6.22E-01		-2.17E+00	6.89E-05	Down			Unigene104908_All//7.00E-73//ES847924					
Unigene104912_All	236	190.88	117.44	217.96	24.27	22.18	8.80	0.18	0.35	0.00	-7.01E-01	2.76E-18		1.91E-01	1.68E-02		-1.30E-01	6.34E-01		-1.46E+00	1.08E-08	Down	9.83E-01	7.33E-01		-7.49E+00	6.18E-01			Unigene104912_All//6.00E-107//gi|84145839|gb|DN760081.1|DN760081					
Unigene104917_All	446	1.06	0.68	1.19	1.90	0.77	2.23	5.97	1.78	1.79	-6.31E-01	5.54E-01		1.77E-01	8.45E-01		-1.30E+00	8.01E-02		2.31E-01	7.41E-01		-1.75E+00	2.99E-06	Down	-1.74E+00	1.78E-06	Down	Unigene104917_All//gi|225440831|ref|XP_002282071.1|//2.00E-15//PREDICTED: similar to ubiquitin fusion protein [Vitis vinifera] >gi|71040673|gb|AAZ20285.1| ubiquitin fusion protein [Arachis hypogaea] >gi|192910738|gb|ACF06477.1| ubiquitin fusion protein [Elaeis guineensis] >gi|284433784|gb|AD885098.1| ubiquitin C variant [Jatropha curcas]	Unigene104917_All//2.00E-16//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene104917_All//2.00E-154//gi|84164961|gb|DR453609.1|DR453609		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0031981//GO:0032446	nr +
Unigene10493_All	272	0.00	0.00	0.00	0.00	0.00	0.00	2.80	0.92	0.00	null	null		null	null		null	null		null	null		-1.60E+00	3.70E-02		-1.15E+01	8.89E-06	Down	Unigene10493_All//gi|159489791|ref|XP_001702878.1|//3.00E-18//ribosomal protein L38, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|27497793|gb|AA013217.1| 60S ribosomal protein L38 [Chlamydomonas reinhardtii] >gi|158271006|gb|ED096835.1| ribosomal protein L38 [Chlamydomonas reinhardtii]	Unigene10493_All//4.00E-19//AT3G59540| 60S ribosomal protein L38 (RPL38B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +
Unigene104932_All	487	0.43	3.95	0.87	0.20	0.14	2.97	1.48	3.18	1.31	3.20E+00	3.42E-07	Up	1.03E+00	3.97E-01		-5.33E-01	8.20E-01		3.86E+00	1.51E-06	Up	1.11E+00	2.15E-02		-1.73E-01	7.94E-01		Unigene104932_All//gi|109631652|gb|ABG36000.1|//3.00E-31//glutathione peroxidase [Helianthus annuus] >gi|109631654|gb|ABG36001.1| glutathione peroxidase [Helianthus annuus]	Unigene104932_All//1.00E-26//AT1G48130| ATPER1; antioxidant/ thioredoxin peroxidase	Unigene104932_All//1.00E-168//gi|109871672|gb|DW500648.1|DW500648		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0008152//GO:0016209//GO:0016705//GO:0019725//GO:0043231	nr +
Unigene104194_All	343	0.00	4.87	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.54E-09	Up	9.60E+00	8.04E-02		null	null		null	null		null	null		null	null		Unigene10494_All//sp|P40092|SP11_YEAST//7.00E-09//Uncharacterized cell wall protein SP11 OS=Saccharomyces cerevisiae GN=SP11 PE=2 SV=1						swissprot -
Unigene10496_All	398	0.00	0.00	0.00	0.63	0.95	0.00	2.76	1.47	0.60	null	null		null	null		6.05E-01	6.59E-01		-9.29E+00	7.36E-02		-9.10E-01	1.24E-01		-2.20E+00	5.66E-04	Down	Unigene10496_All//gi|224129122|ref|XP_002320506.1|//3.00E-19//f-box family protein [Populus trichocarpa] >gi|222861279|gb|EEE98821.1| f-box family protein [Populus trichocarpa]	Unigene10496_All//3.00E-11//AT3G07870| F-box family protein					nr -
Unigene104966_All	793	1.06	1344.50	787.60	0.38	0.09	3.82	2.03	2.27	1.51	1.03E+01	0.00E+00	Up	9.54E+00	0.00E+00	Up	-2.12E+00	1.66E-01		3.34E+00	6.20E-12	Up	1.62E-01	7.18E-01		-4.27E-01	3.59E-01		Unigene104966_All//gi|145408594|ref|YP_001152218.1|//3.00E-15//ORF82c [Pinus koraiensis] >gi|145048843|gb|ABP35459.1| ORF82c [Pinus koraiensis]		Unigene104966_All//1.00E-92//TC171825			GO:0009536	nr +
Unigene10498_All	332	0.00	3.36	3.37	0.00	0.00	0.00	0.00	0.00	0.12	1.17E+01	2.00E-06	Up	1.17E+01	3.44E-06	Up	null	null		null	null		null	null		6.91E+00	6.48E-01								
Unigene104980_All	310	11.65	9.81	15.46	20.57	19.55	20.11	44.33	25.08	18.38	-2.48E-01	4.59E-01		4.09E-01	1.62E-01		-7.32E-02	8.11E-01		-3.29E-02	9.14E-01		-8.22E-01	1.86E-09		-1.27E+00	4.74E-19	Down	Unigene104980_All//gi|225464952|ref|XP_002274218.1|//2.00E-09//PREDICTED: similar to ribosomal protein L10a [Vitis vinifera]	Unigene104980_All//5.00E-09//AT2G27530| PGY1 (PIGGYBACK1); RNA binding / structural constituent of ribosome	Unigene104980_All//7.00E-138//gi|13245690|gb|BE055045.2|BE055045		ko03010|Ribosome		nr +
Unigene104982_All	254	0.82	1.00	3.14	0.39	1.76	2.13	3.50	0.49	1.73	2.76E-01	8.44E-01		1.93E+00	3.42E-02		2.17E+00	1.06E-01		2.44E+00	4.41E-02		-2.82E+00	5.65E-04	Down	-1.02E+00	1.09E-01		Unigene104982_All//gi|26451087|dbj|BAC42648.1|//4.00E-15//GPI-anchored protein [Arabidopsis thaliana] >gi|28416735|gb|AA042898.1| At5g63500 [Arabidopsis thaliana]	Unigene104982_All//6.00E-17//AT3G48860| unknown protein	Unigene104982_All//1.00E-21//gi|31073375|gb|CA993654.1|CA993654			GO:0031224	nr -
Unigene104988_All	443	0.24	0.23	0.24	0.00	0.86	2.24	0.48	0.94	0.36	-4.59E-02	9.91E-01		2.54E-02	1.00E+00		9.74E+00	1.96E-02		1.11E+01	6.15E-06	Up	9.83E-01	3.73E-01		-4.08E-01	7.56E-01		Unigene104988_All//gi|149391295|gb|ABR25665.1|//2.00E-54//cbs domain containing protein, expressed [Oryza sativa Indica Group]	Unigene104988_All//3.00E-55//AT2G14520| CBS domain-containing protein	Unigene104988_All//2.00E-56//TC172662			GO:0031410	nr +
Unigene104998_All	252	5.40	0.60	0.85	12.45	9.57	8.24	43.29	22.56	13.12	-3.16E+00	2.85E-05	Down	-2.68E+00	2.60E-04	Down	-3.81E-01	3.03E-01		-5.95E-01	9.66E-02		-9.40E-01	1.97E-09		-1.72E+00	1.43E-23	Down	Unigene104998_All//gi|195618310|gb|ACG30985.1|//6.00E-06//60S acidic ribosomal protein P1 [Zea mays] >gi|195625300|gb|ACG34480.1| 60S acidic ribosomal protein P1 [Zea mays]		Unigene104998_All//3.00E-133//gi|21089661|gb|BQ401986.1|BQ401986		ko03010|Ribosome		nr -
Unigene1050_All	2881	5.43	0.97	2.62	88.13	71.68	64.87	31.61	6.34	9.04	-2.49E+00	2.54E-42	Down	-1.05E+00	2.82E-12	Down	-2.98E-01	1.71E-25		-4.42E-01	3.39E-47		-2.32E+00	8.41E-274	Down	-1.81E+00	1.05E-203	Down	Unigene1050_All//gi|224130916|ref|XP_002320956.1|//0.00E+00//anion exchanger family protein [Populus trichocarpa] >gi|222861729|gb|EEE99271.1| anion exchanger family protein [Populus trichocarpa]	Unigene1050_All//0.00E+00//AT2G47160| BOR1 (REQUIRES HIGH BORON 1); anion exchanger/ boron transporter	Unigene1050_All//0.00E+00//CO074020			GO:0006811//GO:0010035//GO:0015301//GO:0015562//GO:0031224//GO:0043231//GO:0043673//GO:0044459	nr -

Unigene10500_All	428	0.00	0.00	0.00	0.00	0.00	0.00	1.78	1.86	0.00	null	null		null	null		null	null		null	null		6.14E-02	9.50E-01		-1.08E+01	8.89E-06	Down	Unigene10500_All//gi|300267444|gb|EFJ51627.1|//2.00E-23//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene10500_All//1.00E-21//AT3G04770| RPSAb (40S ribosomal protein SA B); structural constituent of ribosome			ko03010|Ribosome	GO:0005737//GO:0030529	nr +
Unigene105022_All	596	34.41	12.33	36.54	4.01	3.18	1.21	1.21	1.68	0.27	-1.48E+00	5.85E-28	Down	8.66E-02	5.43E-01		-3.36E-01	4.41E-01		-1.73E+00	6.61E-05	Down	4.81E-01	4.46E-01		-2.17E+00	7.76E-03		Unigene105022_All//gi|87241054|gb|ABB32912.1|//5.00E-38//Ferric reductase-like transmembrane component [Medicago truncatula]	Unigene105022_All//6.00E-30//AT5G49730| ATFRO6 (FERRIC REDUCTION OXIDASE 6); ferric-chelate reductase/ oxidoreductase	Unigene105022_All//0.00E+00//DW504224			GO:0005488//GO:0009314//GO:0016020//GO:0016723	nr -
Unigene10503_All	1095	0.00	0.00	0.00	0.05	0.19	0.25	0.66	1.41	4.04	null	null		null	null		2.05E+00	3.95E-01		2.44E+00	2.22E-01		1.11E+00	2.15E-02		2.62E+00	2.98E-16	Up	Unigene10503_All//gi|14330716|emb|CAC40826.1|//1.00E-42//Rcr4V2 protein [Malus floribunda]	Unigene10503_All//1.00E-29//AT2G34930| disease resistance family protein					nr +
Unigene10507_All	381	0.41	0.00	0.00	0.00	0.00	0.00	2.89	1.10	0.21	-8.69E+00	2.17E-01		-8.69E+00	2.46E-01		null	null		null	null		-1.40E+00	2.04E-02		-3.79E+00	3.27E-06	Down							
Unigene10509_All	482	0.87	1.68	0.77	3.93	3.72	1.03	0.70	0.35	0.50	9.54E-01	2.26E-01		-1.67E-01	8.79E-01		-8.02E-02	8.58E-01		-1.93E+00	1.45E-04	Down	-1.02E+00	4.00E-01		-5.01E-01	6.50E-01			Unigene10509_All//3.00E-135//DW519316				
Unigene1051_All	2081	12.22	14.88	14.25	25.28	26.58	38.07	51.54	46.48	20.01	2.84E-01	4.02E-03		2.22E-01	4.09E-02		7.22E-02	4.13E-01		5.91E-01	4.64E-25		-1.49E-01	1.21E-03		-1.37E+00	1.34E-159	Down	Unigene1051_All//gi|28380080|sp|Q9CSF1.1|FSY_ARATH//1.00E-170//RecName: Full=Probable eukaryotic translation initiation factor 5-1; Short=eIF-5 1	Unigene1051_All//4.00E-142//AT1G36730| eukaryotic translation initiation factor 5, putative / eIF-5, putative	Unigene1051_All//0.00E+00//TC149110			GO:0006412//GO:0008135	nr -
Unigene105108_All	298	0.18	0.00	0.00	4.18	2.20	0.76	0.00	0.00	0.27	-7.46E+00	6.21E-01		-7.46E+00	6.34E-01		-9.29E-01	1.11E-01		-2.46E+00	4.15E-04	Down	null	null		8.06E+00	4.06E-01		Unigene105108_All//gi|22329014|ref|NP_194662.2|//5.00E-24//DER1 (DERLIN-1) [Arabidopsis thaliana] >gi|75161705|sp|Q8VZU9.1|DERL1_ARATH RecName: Full=Derlin-1; AltName: Full=AtDerlin1-1	Unigene105108_All//2.00E-25//AT4G29330| DER1 (DERLIN-1)	Unigene105108_All//9.00E-08//DR459372			GO:0019538//GO:0043231//GO:0044425	nr +
Unigene10511_All	398	0.00	4.71	2.81	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.11E-10	Up	1.15E+01	3.44E-06	Up	null	null		null	null		null	null		null	null								
Unigene105113_All	296	2.65	0.17	1.62	1.85	1.63	1.53	0.14	0.56	0.81	-3.95E+00	8.54E-04	Down	-7.12E-01	3.89E-01		-1.85E-01	8.25E-01		-2.79E-01	7.57E-01		1.98E+00	3.80E-01		2.50E+00	1.59E-01		Unigene105113_All//gi|18396347|ref|NP_564285.1|//2.00E-16//NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding [Arabidopsis thaliana] >gi|9802536|gb|AAF99738.1|AC004557_17 F17L21.25 [Arabidopsis thaliana] >gi|16226498|gb|AAL16183.1|AF424815_1 At1g27460/F17L21_26 [Arabidopsis thaliana] >gi|33589668|gb|AAQ22600.1|At1g27460/F17L21_26 [Arabidopsis thaliana]	Unigene105113_All//7.00E-18//AT1G27460| NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding	Unigene105113_All//1.00E-108//TC142974			GO:0005515//GO:0016020	nr +
Unigene10512_All	430	0.00	0.47	1.24	0.00	1.20	2.00	0.98	0.29	2.78	8.88E+00	1.37E-01		1.03E+01	4.05E-03		1.02E+01	3.22E-03		1.10E+01	3.79E-05	Up	-1.75E+00	1.24E-01		1.50E+00	7.56E-03		Unigene10512_All//gi|225432404|ref|XP_002276907.1|//2.00E-11//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene10512_All//2.00E-49//gi|109864441|gb|DW493417.1|DW493417				nr +
Unigene105124_All	495	0.42	0.00	1.18	2.92	2.09	2.10	1.03	0.00	0.32	-8.72E+00	1.23E-01		1.48E+00	1.53E-01		-4.84E-01	3.92E-01		-4.76E-01	4.15E-01		-1.00E+01	8.91E-04	Down	-1.67E+00	7.78E-02		Unigene105124_All//gi|118481019|gb|ABK92463.1|//4.00E-15//unknown [Populus trichocarpa]	Unigene105124_All//4.00E-08//AT2G40480| unknown protein	Unigene105124_All//4.00E-14//TC165937				nr +
Unigene105128_All	317	0.00	0.16	0.00	0.16	0.00	1.42	0.27	0.79	2.76	7.32E+00	6.22E-01		null	null		-7.30E+00	5.64E-01		3.18E+00	3.79E-02		1.57E+00	3.27E-01		3.37E+00	1.32E-04	Up	Unigene105128_All//gi|297819958|ref|XP_002877862.1|//4.00E-21//U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297323700|gb|EFH54121.1| U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene105128_All//2.00E-22//AT3G52450| PUB22 (PLANT U-BOX 22); ubiquitin-protein ligase			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0002252//GO:0006950//GO:0016567//GO:0019787//GO:0043234//GO:0044444	nr +
Unigene10514_All	478	0.00	0.00	0.00	2.29	1.80	0.38	1.06	0.26	0.67	null	null		null	null		-3.48E-01	5.97E-01		-2.60E+00	7.14E-04	Down	-2.02E+00	5.21E-02		-6.71E-01	4.49E-01		Unigene10514_All//gi|297605832|ref|NP_001057661.2|//7.00E-16//Os06g0484800 [Oryza sativa Japonica Group] >gi|255677053|dbj|BAF19575.2|Os06g0484800 [Oryza sativa Japonica Group]						nr -
Unigene10515_All	342	0.00	0.00	0.00	0.00	0.00	0.00	3.83	3.79	0.00	null	null		null	null		null	null		null	null		-1.66E-02	1.01E+00		-1.19E+01	9.86E-10	Down			Unigene10515_All//4.00E-10//TC139311				
Unigene105161_All	568	0.00	1.78	0.00	0.18	0.36	1.67	0.00	0.66	1.05	1.08E+01	7.26E-06	Up	null	null		1.05E+00	6.13E-01		3.25E+00	5.84E-04	Up	9.37E+00	6.87E-03		1.00E+01	1.76E-04	Up	Unigene105161_All//gi|224082932|ref|XP_002306897.1|//1.00E-48//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222856346|gb|EEE93893.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene105161_All//1.00E-42//AT1G75490| DNA binding / transcription factor	Unigene105161_All//3.00E-52//TC178922	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0009743//GO:0010468//GO:0043231	nr +
Unigene10517_All	250	0.21	0.00	0.00	0.00	0.28	0.00	13.53	26.75	224.85	-7.71E+00	6.21E-01		-7.71E+00	6.34E-01		8.11E+00	6.16E-01		null	null		9.83E-01	1.72E-06		4.05E+00	1.65E-296	Up	Unigene10517_All//gi|255575021|ref|XP_002528416.1|//9.00E-13//amino acid transporter, putative [Ricinus communis] >gi|223532152|gb|EEF33958.1| amino acid transporter, putative [Ricinus communis]					GO:0031224	nr +
Unigene105188_All	486	0.65	1.25	0.00	1.33	1.70	2.42	0.09	1.12	1.56	9.54E-01	3.14E-01		-9.34E+00	4.93E-02		3.52E-01	6.87E-01		8.59E-01	1.95E-01		3.68E+00	3.69E-03		4.16E+00	1.34E-04	Up	Unigene105188_All//gi|79474118|ref|NP_193133.3|//3.00E-54//zinc ion binding [Arabidopsis thaliana]	Unigene105188_All//1.00E-55//AT4G13970| zinc ion binding				GO:0046914	nr -
Unigene10519_All	394	0.27	2.44	0.81	1.52	0.52	0.11	2.15	0.95	1.21	3.20E+00	6.55E-04	Up	1.61E+00	3.05E-01		-1.53E+00	1.01E-01		-3.73E+00	4.96E-03		-1.17E+00	9.29E-02		-8.23E-01	2.07E-01			Unigene10519_All//0.00E+00//TC173046				
Unigene105205_All	567	0.00	0.00	0.19	0.79	0.97	0.40	15.36	0.96	0.49	null	null		7.55E+00	4.03E-01		2.97E-01	8.18E-01		-9.89E-01	3.94E-01		-4.00E+00	2.65E-45	Down	-4.97E+00	1.25E-53	Down	Unigene105205_All//gi|224120220|ref|XP_002330994.1|//7.00E-63//cytochrome P450 [Populus trichocarpa] >gi|222872924|gb|EEF10055.1| cytochrome P450 [Populus trichocarpa]	Unigene105205_All//1.00E-55//AT2G42250| CYP712A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene105205_All//2.00E-158//gi|48750763|gb|CO081282.1|CO081282		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016709//GO:0044464	nr +
Unigene105206_All	340	0.92	0.00	0.31	3.52	0.81	0.80	1.74	0.25	0.00	-9.85E+00	3.67E-02		-1.56E+00	3.30E-01		-2.12E+00	8.56E-04	Down	-2.14E+00	1.81E-03		-2.82E+00	7.18E-03		-1.08E+01	1.42E-04	Down							
Unigene105230_All	327	0.48	0.16	0.00	0.61	1.05	1.66	4.91	3.07	0.85	-1.63E+00	4.89E-01		-8.91E+00	2.46E-01		7.89E-01	5.96E-01		1.44E+00	1.93E-01		-6.80E-01	1.47E-01		-2.53E+00	2.96E-06	Down		Unigene105230_All//2.00E-67//gi|18098905|gb|BM358159.1|BM358159				
Unigene105235_All	741	0.14	0.00	0.07	0.20	0.05	0.00	0.68	0.00	0.00	-7.14E+00	3.77E-01		-9.74E-01	7.22E-01		-2.12E+00	3.88E-01		-7.66E+00	2.35E-01		-9.42E+00	8.91E-04	Down	-9.42E+00	5.56E-04	Down	Unigene105235_All//gi|224140225|ref|XP_002323485.1|//5.00E-81//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222868115|gb|EEF05246.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene105235_All//8.00E-69//AT2G36910| ABCB1 (ATP BINDING CASSETTE SUBFAMILY B1); ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter/ calmodulin binding			ko02010|ABC transporters	GO:0005515//GO:0009630//GO:0009639//GO:0009725//GO:0015562//GO:0022891//GO:0031224//GO:0032535//GO:0032559//GO:0042626//GO:0043231//GO:0043479//GO:0048437//GO:0051707//GO:0060918	nr -
Unigene105249_All	810	0.13	0.00	0.13	0.06	0.38	2.84	0.00	0.00	0.30	-7.01E+00	3.77E-01		2.55E-02	1.00E+00		2.64E+00	1.61E-01		5.53E+00	2.12E-12	Up	null	null		8.21E+00	4.41E-02								
Unigene105254_All	655	4.79	9.98	9.02	3.80	3.31	3.17	0.13	0.06	0.12	1.06E+00	7.00E-06	Up	9.13E-01	3.35E-04		-1.99E-01	6.31E-01		-2.62E-01	5.66E-01		-1.02E+00	7.27E-01		-8.63E-02	9.74E-01				Unigene105254_All//1.00E-131//gi|78333874|gb|DT554148.1|DT554148				
Unigene10526_All	302	1.73	7.89	7.93	0.99	1.14	0.75	2.52	0.42	0.66	2.19E+00	4.62E-06	Up	2.20E+00	7.43E-06	Up	2.04E-01	9.02E-01		-4.05E-01	7.52E-01		-2.60E+00	2.81E-03		-1.93E+00	1.14E-02				Unigene10526_All//3.00E-109//gi|21102508|gb|BQ414821.1|BQ414821				
Unigene105280_All	301	8.00	10.44	10.79	8.44	5.38	2.85	2.25	0.97	0.40	3.84E-01	2.87E-01		4.33E-01	2.39E-01		-6.51E-01	9.08E-02		-1.57E+00	1.37E-04	Down	-1.21E+00	1.34E-01		-2.50E+00	4.79E-03			Unigene105280_All//9.00E-88//TC149505				
Unigene10529_All	293	0.36	0.00	1.27	0.17	0.00	0.00	6.06	3.14	1.22	-8.48E+00	3.77E-01		1.83E+00	2.13E-01		-7.41E+00	5.64E-01		-7.41E+00	6.46E-01		-9.50E-01	3.09E-02		-2.31E+00	3.08E-06	Down	Unigene10529_All//gi|115447285|ref|NP_001047422.1|//4.00E-19//Os02g0614100 [Oryza sativa Japonica Group] >gi|113536953|dbj|BAF09336.1|Os02g0614100 [Oryza sativa Japonica Group]	Unigene10529_All//5.00E-11//AT4G32272| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter-related (TAIR:AT4G31600.1); Has 1302 Blast hits to 1300 proteins in 174 species: Archae - 0; Bacteria - 4; Metazoa - 376; Fungi - 239; Plants - 567; Viruses - 0; Other Eukaryotes - 116 (source: NCBI BLink).	Unigene10529_All//3.00E-94//TC175087			GO:0031224	nr +
Unigene1053_All	1096	2.24	3.98	0.97	1.18	2.04	1.69	1.62	7.59	3.93	8.25E-01	4.54E-03		-1.21E+00	5.14E-03		7.89E-01	6.64E-02		5.16E-01	3.15E-01		2.23E+00	2.37E-24	Up	1.28E+00	1.51E-06	Up	Unigene1053_All//gi|90900944|gb|AB501834.1|//1.00E-82//NAK-type protein kinase [Nicotiana tabacum]	Unigene1053_All//2.00E-54//AT2G39110| protein kinase, putative	Unigene1053_All//0.00E+00//CO113128			GO:0004672//GO:0006464//GO:0032559	nr +
Unigene10530_All	1110	0.00	0.00	0.00	0.00	0.00	0.00	4.72	1.51	0.50	null	null		null	null		null	null		null	null		-1.65E+00	9.64E-11	Down	-3.23E+00	6.29E-24	Down	Unigene10530_All//gi|27544010|dbj|BAC54829.1|//5.00E-67//vacuolar processing enzyme-2 [Nicotiana tabacum]	Unigene10530_All//2.00E-65//AT2G25940| ALPHA-VPE (alpha-vacuolar processing enzyme); cysteine-type endopeptidase				GO:0004175//GO:0016485	nr -
Unigene105308_All	361	0.72	0.84	3.69	2.48	0.86	1.25	0.23	0.00	0.00	2.17E-01	8.65E-01		2.35E+00	8.68E-04	Up	-1.53E+00	3.38E-02		-9.89E-01	1.96E-01		-7.87E+00	4.08E-01		-7.87E+00	3.62E-01								
Unigene105325_All	691	0.53	0.44	0.46	1.37	1.45	3.66	0.98	0.00	0.52	-2.69E-01	8.01E-01		-1.97E-01	8.66E-01		7.74E-02	9.37E-01		1.42E+00	5.71E-04	Up	-9.94E+00	6.35E-05	Down	-9.16E-01	2.21E-01		Unigene105325_All//gi|14334057|gb|AAK60517.1|AF332974_1//8.00E-53//P450 monooxygenase [Gossypium arboreum]	Unigene105325_All//2.00E-32//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene105325_All//1.00E-119//ES819299		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0016491	nr -
Unigene10533_All	562	0.00	0.00	0.00	0.00	0.00	0.00	3.01	2.60	0.43	null	null		null	null		null	null		null	null		-2.09E-01	6.45E-01		-2.82E+00	2.86E-07	Down	Unigene10533_All//gi|116222259|gb|ABJ80993.1|//7.00E-86//beta tubulin [Goniomonas truncata]	Unigene10533_All//1.00E-82//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene10533_All//4.00E-11//gi|48790617|gb|CO091931.1|CO091931		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene105331_All	833	0.06	0.37	0.38	0.00	0.08	11.66	0.00	0.00	0.00	2.54E+00	1.51E-01		2.61E+00	1.46E-01		6.37E+00	6.16E-01		1.35E+01	3.50E-59	Up	null	null		null	null		Unigene105331_All//sp|Q7ZIM0|VIT1_SOLIN//1.00E-59//Vitellogenin-1 OS=Solenopsis invicta PE=2 SV=1						swissprot -
Unigene105333_All	535	2.25	5.78	5.08	3.63	4.31	2.79	0.40	1.02	0.30	1.36E+00	2.28E-04	Up	1.17E+00	3.80E-03		2.48E-01	6.08E-01		-3.82E-01	4.51E-01		1.36E+00	1.44E-01		-4.07E-01	7.56E-01			Unigene105333_All//1.00E-165//gi|8165968|gb|DR456416.1|DR456416				
Unigene105373_All	592	0.18	0.00	0.00	0.08	0.06	0.15	0.00	1.41	0.00	-7.47E+00	3.77E-01		-7.47E+00	3.99E-01		-5.31E-01	8.29E-01		8.60E-01	7.97E-01		1.05E+01	5.54E-06	Up	null	null		Unigene105373_All//gi|297829824|ref|XP_002882794.1|//3.00E-56//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328634|gb|EFH59053.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene105373_All//2.00E-57//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene105373_All//2.00E-16//TC134433		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0008152//GO:0016701//GO:0016706	nr -
Unigene10539_All	397	0.00	0.00	0.00	0.00	0.00	0.00	2.13	1.58	0.00	null	null		null	null		null	null		null	null		-4.32E-01	5.47E-01		-1.11E+01	2.21E-06	Down	Unigene10539_All//sp|P34121|COAA_DICDI//9.00E-17//Coactosin OS=Dictyostelium discoideum GN=coaA PE=1 SV=1						swissprot +
Unigene105402_All	407	0.13	0.00	0.00	0.00	0.17	1.66	0.73	0.10	0.78	-7.01E+00	6.21E-01		-7.01E+00	6.34E-01		7.40E+00	6.16E-01		1.07E+01	4.19E-04	Up	-2.82E+00	8.87E-02		1.07E-01	9.46E-01								
Unigene105414_All	419	3.12	0.24	1.40	4.16	3.21	0.86	0.61	0.20	0.00	-3.69E+00	1.09E-05	Down	-1.16E+00	6.45E-02		-3.77E-01	4.65E-01		-2.27E+00	4.53E-05	Down	-1.60E+00	3.11E-01		-9.24E+00	3.06E-02		Unigene105414_All//gi|30678256|ref|NP_171720.2|//2.00E-08//ferredoxin-related [Arabidopsis thaliana]	Unigene105414_All//6.00E-09//AT1G02180| ferredoxin-related	Unigene105414_All//6.00E-90//BG440260				nr +
Unigene105542_All	491	0.00	0.00	0.00	0.00	0.00	0.00	5.43	1.45	3.25	null	null		null	null		null	null		null	null		-1.91E+00	6.07E-07	Down	-7.41E-01	2.52E-02			Unigene105542_All//2.00E-12//DR461796				

Unigene105426_All	754	0.07	1.21	0.57	0.26	0.27	0.78	0.67	0.11	0.11	4.12E+00	2.34E-04	Up	3.03E+00	5.74E-02		5.20E-02	9.89E-01		1.56E+00	1.36E-01		-2.60E+00	2.05E-02		-2.67E+00	1.38E-02		Unigene105426_All//gi|226499346|ref|NP_001149805.1//1.00E-47//CUE domain containing protein [Zea mays] >gi|195634781|gb|ACG36859.1| CUE domain containing protein [Zea mays]	Unigene105426_All//6.00E-35//AT5G32440| LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin system component Cue (InterPro:IPR003892); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80040.1); Has 303 Blast hits to 289 proteins in 67 species: Archae - 0; Bacteria - 2; Metazoa - 74; Fungi - 21; Plants - 93; Viruses - 0; Other Eukaryotes - 113 (source: NCBI BLink).	Unigene105426_All//0.00E+00//gi|21097417|gb|BQ409730.1|BQ409730			GO:0043231	nr +
Unigene10543_All	318	0.00	0.00	0.00	0.00	0.00	0.00	3.19	0.26	0.75	null	null		null	null		null	null		null	null		-3.60E+00	2.38E-05	Down	-2.09E+00	1.53E-03								
Unigene105439_All	454	6.57	23.77	11.26	23.59	15.02	16.31	9.22	8.75	7.55	1.86E+00	2.37E-20	Up	7.78E-01	4.78E-03		-6.52E-01	5.09E-05		-5.32E-01	1.94E-03		-7.61E-02	7.94E-01		-2.89E-01	2.89E-01				Unigene105439_All//2.00E-71//gi|164311793|gb|ES851073.1|ES851073				
Unigene10544_All	212	0.00	1.67	0.50	3.99	0.32	1.49	1.20	0.79	0.75	1.07E+01	2.47E-02		8.97E+00	4.03E-01		-3.62E+00	1.47E-04	Down	-1.42E+00	7.34E-02		-6.02E-01	6.48E-01		-6.71E-01	6.06E-01								
Unigene105450_All	482	3.15	0.84	0.33	2.07	0.29	1.22	2.28	0.87	1.41	-1.90E+00	1.25E-03		-3.25E+00	1.40E-05	Down	-2.85E+00	2.37E-04	Down	-7.63E-01	2.89E-01		-1.40E+00	2.04E-02		-6.99E-01	2.11E-01		Unigene105450_All//gi|222424070|dbj|BAH19995.1//5.00E-19//AT4G28760 [Arabidopsis thaliana]	Unigene105450_All//7.00E-12//AT4G28760| unknown protein	Unigene105450_All//7.00E-59//gi|78343612|gb|DT563886.1|DT563886			GO:0005488	nr -
Unigene105454_All	484	0.43	0.00	0.00	0.00	0.64	1.31	0.09	0.00	0.00	-8.76E+00	1.23E-01		-8.76E+00	1.47E-01		9.32E+00	4.55E-02		1.04E+01	7.60E-04	Up	-6.45E+00	6.64E-01		-6.45E+00	6.18E-01		Unigene105454_All//gi|225458882|ref|XP_002283431.1//4.00E-09//PREDICTED: hypothetical protein [Vitis vinifera] >gi|302142175|emb|CBI19378.3| unnamed protein product [Vitis vinifera]	Unigene105454_All//6.00E-06//AT1G10140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031279 (InterPro:IPR016972); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G58420.1); Has 38 Blast hits to 38 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene105454_All//0.00E+00//DW512687				nr +
Unigene105469_All	585	0.72	0.78	0.46	0.43	0.82	1.62	0.94	0.00	0.14	1.24E-01	9.11E-01		-6.53E-01	5.94E-01		9.53E-01	4.24E-01		1.93E+00	1.48E-02		-9.88E+00	4.62E-04	Down	-2.79E+00	7.97E-03		Unigene105469_All//gi|18406084|ref|NP_565988.1//9.00E-20//PAR1 (PHY RAPIDLY REGULATED 1) [Arabidopsis thaliana] >gi|4512668|gb|AAD21722.1| expressed protein [Arabidopsis thaliana] >gi|83776541|tpe|CAJ55345.1| TPA: helix-loop-helix protein [Arabidopsis thaliana]	Unigene105469_All//4.00E-17//AT2G42870| PAR1 (PHY RAPIDLY REGULATED 1)	Unigene105469_All//4.00E-119//TC160093				nr +
Unigene10547_All	230	0.00	6.17	2.08	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	4.06E-08	Up	1.10E+01	7.50E-03		null	null		null	null		null	null		null	null								ESTscan -
Unigene105471_All	605	1.38	1.42	1.76	2.55	1.42	1.34	2.10	0.35	2.11	4.12E-02	9.74E-01		3.47E-01	6.29E-01		-8.43E-01	1.01E-01		-9.26E-01	8.58E-02		-2.60E+00	5.14E-05	Down	7.30E-03	9.89E-01		Unigene105471_All//gi|240254425|ref|NP_178255.4//7.00E-42//ATP binding / kinase [Arabidopsis thaliana]	Unigene105471_All//4.00E-43//AT2G01460| ATP binding / kinase	Unigene105471_All//0.00E+00//ES849346				nr +
Unigene105490_All	200	1.31	2.03	3.46	1.00	1.55	6.10	1.27	1.67	3.98	6.32E-01	6.01E-01		1.40E+00	1.39E-01		6.37E-01	6.95E-01		2.61E+00	3.93E-04	Up	3.98E-01	7.24E-01		1.65E+00	2.32E-02			Unigene105490_All//5.00E-107//TC170854				
Unigene1055_All	367	4.28	1.52	4.21	13.98	15.95	16.61	3.80	2.73	1.09	-1.49E+00	6.73E-03		-2.35E-02	9.87E-01		1.90E-01	5.20E-01		2.49E-01	3.65E-01		-4.76E-01	3.74E-01		-1.81E+00	6.10E-04	Down	Unigene1055_All//gi|85069287|gb|ABC69715.1|//1.00E-35//auxin response factor 4 [Solanum lycopersicum]	Unigene1055_All//7.00E-22//AT5G60450| ARF4 (AUXIN RESPONSE FACTOR 4); transcription factor	Unigene1055_All//6.00E-142//gi|48807809|gb|CO109123.1|CO109123	ARF		GO:0001708//GO:0005488//GO:0006350//GO:0009725//GO:0009791//GO:0010468	nr +
Unigene105501_All	200	31.65	11.15	13.31	61.52	56.65	58.94	42.70	13.79	20.12	-1.51E+00	2.36E-09	Down	-1.25E+00	7.17E-07	Down	-1.19E-01	5.52E-01		-6.19E-02	7.36E-01		-1.63E+00	9.33E-17	Down	-1.09E+00	1.11E-09	Down			Unigene105501_All//3.00E-96//gi|13248510|gb|BF277159.2|BF277159				
Unigene10553_All	264	0.00	0.00	0.00	9.06	3.39	1.03	0.80	0.00	0.00	null	null		null	null		-1.42E+00	3.12E-04	Down	-3.14E+00	2.53E-09	Down	-9.65E+00	7.48E-02		-9.65E+00	5.84E-02		Unigene10553_All//gi|186509725|ref|NP_001118863.1|//1.00E-11//WOX11 (WUSCHEL related homeobox 11); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene10553_All//5.00E-13//AT3G03660| WOX11 (WUSCHEL related homeobox 11); DNA binding / transcription factor	Unigene10553_All//7.00E-110//TC173647	HB		GO:0001071//GO:0003677//GO:0006351//GO:0009536//GO:0010468	nr -
Unigene10554_All	284	0.00	0.00	0.00	7.19	2.06	1.27	0.15	0.00	0.14	null	null		null	null		-1.80E+00	5.35E-05	Down	-2.50E+00	1.87E-06	Down	-7.22E+00	6.64E-01		-8.58E-02	9.74E-01								
Unigene10555_All	394	0.00	12.86	6.76	0.00	0.00	0.23	0.00	0.00	0.00	1.37E+01	6.88E-29	Up	1.27E+01	1.07E-14	Up	null	null		7.84E+00	4.81E-01		null	null		null	null		Unigene10555_All//gi|14423905|sp|Q9XGL4.1|RL31_CYAPA//1.00E-44//RecName: Full=60S ribosomal protein L31 >gi|51237327|emb|CAB45375.1| ribosomal protein L31 [Cyanophora paradoxa]	Unigene10555_All//1.00E-29//AT4G26230| 60S ribosomal protein L31 (RPL31B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0044267	nr +
Unigene10556_All	344	0.00	1.03	0.31	0.00	0.60	0.13	0.49	2.92	4.40	1.00E+01	2.47E-02		8.27E+00	4.03E-01		9.23E+00	1.57E-01		7.04E+00	7.03E-01		2.57E+00	4.79E-04	Up	3.16E+00	4.04E-07	Up	Unigene10556_All//gi|30679545|ref|NP_179190.2|//2.00E-13//phox (PX) domain-containing protein [Arabidopsis thaliana]	Unigene10556_All//7.00E-15//AT2G15900| phox (PX) domain-containing protein					nr +
Unigene105576_All	203	0.00	0.75	0.00	0.00	0.00	0.45	1.46	4.74	10.01	9.55E+00	2.37E-01		null	null		null	null		8.80E+00	4.81E-01		1.70E+00	1.17E-02		2.78E+00	2.59E-08	Up							
Unigene10558_All	422	0.62	3.96	1.26	2.83	2.28	1.28	0.00	0.00	0.00	2.68E+00	1.99E-05	Up	1.03E+00	3.42E-01		-3.10E-01	6.07E-01		-1.14E+00	7.15E-02		null	null		null	null		Unigene10558_All//gi|13877599|gb|AK43877.1|AF370500_1//2.00E-32//Unknown protein [Arabidopsis thaliana] >gi|28059703|gb|AAO30085.1| Unknown protein [Arabidopsis thaliana]	Unigene10558_All//1.00E-33//AT2G40150| INVOLVED IN: biological_process unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF231, plant (InterPro:IPR004253); BEST Arabidopsis thaliana protein match is: ESK1 (ESKIMO 1) (TAIR:AT3G55990.1); Has 712 Blast hits to 693 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 712; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene10558_All//7.00E-68//EE592863			GO:0006970//GO:0009409//GO:0010557	nr +
Unigene105591_All	203	61.08	29.20	32.53	74.11	66.50	120.36	70.81	54.77	36.50	-1.06E+00	1.40E-10	Down	-9.09E-01	6.29E-08		-1.56E-01	3.32E-01		7.00E-01	8.88E-11		-3.71E-01	5.57E-03		-9.56E-01	6.86E-13		Unigene105591_All//gi|13877126|gb|AAK43709.1|AF358665_1//7.00E-07//ribosomal protein L32 [Mercurialis annua] >gi|13899053|gb|AAK48948.1|AF370436_1 ribosomal protein L32 [Mercurialis annua] >gi|13899055|gb|AAK48949.1|AF370437_1 ribosomal protein L32 [Mercurialis annua] >gi|13899057|gb|AAK48950.1|AF370438_1 ribosomal protein L32 [Mercurialis annua]		Unigene105591_All//5.00E-70//TC152244		ko03010|Ribosome		nr +
Unigene1056_All	3063	9.60	5.14	4.17	28.02	29.16	36.67	7.73	4.64	3.00	-9.00E-01	2.29E-18		-1.20E+00	5.95E-28	Down	5.76E-02	4.00E-01		3.88E-01	1.13E-16		-7.37E-01	3.90E-13		-1.36E+00	8.27E-36	Down	Unigene1056_All//gi|85069287|gb|ABC69715.1|//0.00E+00//auxin response factor 4 [Solanum lycopersicum]	Unigene1056_All//0.00E+00//AT5G60450| ARF4 (AUXIN RESPONSE FACTOR 4); transcription factor	Unigene1056_All//0.00E+00//gi|48807809|gb|CO109123.1|CO109123	ARF		GO:0001071//GO:0001708//GO:0003676//GO:0005515//GO:0006351//GO:0009755//GO:0009791//GO:0010468//GO:0043231	nr +
Unigene10562_All	1852	0.00	0.22	0.23	0.27	0.37	0.54	0.23	0.43	3.61	7.77E+00	1.36E-02		7.85E+00	1.39E-02		4.67E-01	6.12E-01		9.96E-01	1.72E-01		9.09E-01	2.11E-01		3.98E+00	2.69E-35	Up	Unigene10562_All//gi|195619326|gb|ACG31493.1|//3.00E-18//harpin-induced protein [Zea mays]	Unigene10562_All//2.00E-14//AT2G01080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54200.1); Has 388 Blast hits to 387 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 386; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene10562_All//6.00E-10//TC149098				nr -
Unigene105620_All	204	0.00	1.49	0.00	0.00	1.01	3.54	0.00	0.00	0.20	1.05E+01	4.45E-02		null	null		9.98E+00	1.57E-01		1.18E+01	2.31E-04	Up	null	null		7.61E+00	6.48E-01								
Unigene10563_All	339	1.23	0.90	1.26	2.65	2.64	0.40	2.62	0.74	0.35	-4.61E-01	6.50E-01		2.54E-02	1.00E+00		-2.10E-03	9.78E-01		-2.73E+00	2.06E-03		-1.82E+00	1.08E-02		-2.89E+00	3.05E-04	Down	Unigene10563_All//gi|297818068|ref|XP_002876917.1|//8.00E-27//nsp-interacting kinase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297322755|gb|EFH53176.1| nsp-interacting kinase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene10563_All//3.00E-24//AT3G25560| NIK2 (NSP-INTERACTING KINASE 2); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene105633_All	204	2.31	4.97	9.14	9.03	5.06	5.76	1.24	0.41	1.76	1.11E+00	1.13E-01		1.98E+00	3.17E-04	Up	-8.35E-01	7.02E-02		-6.50E-01	1.92E-01		-1.60E+00	3.11E-01		4.99E-01	6.28E-01		Unigene105633_All//gi|224130518|ref|XP_002328629.1|//1.00E-10//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222838611|gb|EEE76976.1| tir-nbs-lrr resistance protein [Populus trichocarpa]		Unigene105633_All//2.00E-63//TC135081				nr +
Unigene105635_All	204	46.68	79.48	44.90	63.98	75.96	97.63	195.86	261.02	83.19	7.68E-01	3.72E-08		-5.61E-02	7.81E-01		2.48E-01	9.59E-02		6.10E-01	3.98E-07		4.14E-01	1.27E-10		-1.24E+00	1.92E-51	Down	Unigene105635_All//gi|38194890|gb|AAR13288.1|//4.00E-17//Anx1 [Gossypium hirsutum]	Unigene105635_All//1.00E-12//AT5G65020| ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding	Unigene105635_All//2.00E-106//TC139742				nr -
Unigene10564_All	426	0.25	13.92	3.25	0.00	0.00	0.00	0.00	0.00	0.00	5.82E+00	1.27E-30	Up	3.73E+00	1.05E-05	Up	null	null		null	null		null	null		null	null		Unigene10564_All//gi|115441859|ref|NP_001045209.1|//3.00E-10//Os01g0919200 [Oryza sativa Japonica Group] >gi|57899841|dbj|BAD87625.1| fibroin heavy chain Fib-H-like [Oryza sativa Japonica Group] >gi|113534740|dbj|BAF07123.1| Os01g0919200 [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr +
Unigene10568_All	276	0.00	0.37	0.00	2.35	0.12	1.15	0.31	0.91	0.43	8.52E+00	3.91E-01		null	null		-4.23E+00	5.94E-04	Down	-1.03E+00	2.68E-01		1.57E+00	3.27E-01		4.99E-01	8.09E-01								
Unigene10569_All	340	2.31	2.09	0.63	3.52	4.25	2.79	26.24	21.76	5.39	-1.46E-01	8.37E-01		-1.88E+00	4.13E-02		2.75E-01	6.54E-01		-3.34E-01	6.39E-01		-2.70E-01	1.41E-01		-2.28E+00	8.16E-28	Down			Unigene10569_All//3.00E-85//BQ402008				

Unigene1057_A11	999	0.68	0.10	0.00	4.64	6.03	2.76	14.94	10.96	3.43	-2.75E+00	1.06E-02		-9.41E+00	7.65E-04	Down	3.79E-01	1.31E-01		-7.50E-01	6.84E-03		-4.47E-01	5.50E-04		-2.12E+00	4.64E-42	Down	Unigene1057_A11//gi|224126613|ref|XP_002329598.1|//1.00E-108//cationic amino acid transporter [Populus trichocarpa] >gi|222870307|gb|EEF07438.1| cationic amino acid transporter [Populus trichocarpa]	Unigene1057_A11//2.00E-63//AT5G04770| CAT6 (CATIONIC AMINO ACID TRANSPORTER 6); amino acid transmembrane transporter/ basic amino acid transmembrane transporter/ cationic amino acid transmembrane transporter	Unigene1057_A11//5.00E-77//TC146944			GO:0006810//GO:0015171//GO:0016020//GO:0043231//GO:0051707	nr -
Unigene105701_A11	207	21.99	8.81	14.15	15.64	13.31	14.18	44.73	9.49	8.66	-1.32E+00	7.66E-06	Down	-6.36E-01	3.20E-02		-2.33E-01	5.57E-01		-1.41E-01	6.92E-01		-2.24E+00	3.07E-27	Down	-2.37E+00	4.10E-30	Down			Unigene105701_A11//1.00E-76//gi|21089134|gb|BQ401447.1|BQ401447				
Unigene10572_A11	301	0.00	0.00	0.00	0.17	0.00	0.00	3.09	1.67	0.40	null	null		null	null		-7.37E+00	5.64E-01		-7.37E+00	6.45E-01		-8.91E-01	1.72E-01		-2.96E+00	1.72E-04	Down	Unigene10572_A11//gi|297810727|ref|XP_002873247.1|//3.00E-09//carboxy-lyase [Arabidopsis lyrata subsp. lyrata] >gi|297319084|gb|EFH49506.1| carboxy-lyase [Arabidopsis lyrata subsp. lyrata]	Unigene10572_A11//2.00E-10//AT5G06300| carboxy-lyase					nr +
Unigene105733_A11	209	3.25	5.33	4.33	0.95	2.31	2.81	1.01	3.40	10.29	7.13E-01	2.69E-01		4.12E-01	5.94E-01		1.27E+00	2.92E-01		1.56E+00	1.36E-01		1.75E+00	3.21E-02		3.35E+00	2.59E-10	Up			Unigene105733_A11//3.00E-22//EX169656				
Unigene105742_A11	209	0.25	4.61	1.53	0.00	0.49	1.30	0.20	0.20	0.38	4.20E+00	1.29E-04	Up	2.61E+00	1.46E-01		8.95E+00	4.59E-01		1.03E+01	7.06E-02		-1.65E-02	1.01E+00		9.14E-01	7.52E-01		Unigene105742_A11//gi|297803414|ref|XP_002869591.1|//2.00E-20//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315427|gb|EFH45850.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene105742_A11//8.00E-22//AT4G26790| GDSL-motif lipase/hydrolase family protein	Unigene105742_A11//3.00E-108//C0090421				nr +
Unigene105744_A11	209	65.34	36.12	30.83	98.91	74.47	105.02	242.55	117.19	98.17	-8.55E-01	2.82E-08		-1.08E+00	2.39E-11	Down	-4.10E-01	2.96E-04		8.64E-02	5.64E-01		-1.05E+00	7.81E-49	Down	-1.31E+00	8.69E-71	Down	Unigene105744_A11//gi|73761683|gb|AAZ83341.1|//6.00E-36//ubiquitin extension protein [Gossypium hirsutum]	Unigene105744_A11//1.00E-24//AT2G47110| UBQ6; protein binding	Unigene105744_A11//2.00E-100//ES822113		ko03010|Ribosome		nr -
Unigene105748_A11	209	0.25	2.18	0.00	0.00	0.49	3.67	0.00	0.20	0.19	3.12E+00	3.58E-02		-7.97E+00	6.33E-01		8.95E+00	4.59E-01		1.18E+01	1.27E-04	Up	7.64E+00	6.38E-01		7.57E+00	6.48E-01									
Unigene105759_A11	210	0.75	0.00	0.00	101.76	89.53	41.08	0.40	0.60	0.00	-9.55E+00	2.17E-01		-9.55E+00	2.46E-01		-1.85E-01	1.48E-01		-1.31E+00	4.01E-26	Down	5.68E-01	7.83E-01		-8.65E+00	3.61E-01		Unigene105759_A11//gi|186510343|ref|NP_001078202.2|//1.00E-26//LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4) [Arabidopsis thaliana]	Unigene105759_A11//6.00E-28//AT3G23290| LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4)	Unigene105759_A11//2.00E-103//TC160625				nr +
Unigene105761_A11	210	0.75	0.00	0.00	0.00	0.16	3.01	0.40	0.20	0.00	-9.55E+00	2.17E-01		-9.55E+00	2.46E-01		7.36E+00	8.40E-01		1.16E+01	7.60E-04	Up	-1.02E+00	7.27E-01		-8.65E+00	3.61E-01				Unigene105761_A11//7.00E-91//A1728016				ESTscan +
Unigene105767_A11	210	1.00	1.93	4.82	0.47	1.80	6.45	0.00	0.60	1.52	9.54E-01	4.14E-01		2.22E+00	5.77E-03		1.93E+00	1.94E-01		3.77E+00	4.57E-06	Up	9.22E+00	2.41E-01		1.06E+01	1.34E-02									
Unigene105773_A11	211	20.09	5.04	6.81	12.75	10.93	33.18	58.91	27.73	19.26	-1.99E+00	2.96E-09	Down	-1.56E+00	1.86E-06	Down	-2.22E-01	5.93E-01		1.38E+00	1.72E-09	Up	-1.09E+00	2.80E-13	Down	-1.61E+00	1.95E-24	Down			Unigene105773_A11//9.00E-41//gi|78330471|gb|DT550745.1|DT550745				
Unigene105778_A11	211	0.25	4.08	0.50	4.25	3.10	1.50	2.40	0.79	1.32	4.04E+00	4.20E-04	Up	1.03E+00	7.05E-01		-4.55E-01	5.58E-01		-1.50E+00	5.09E-02		-1.60E+00	1.07E-01		-8.63E-01	3.39E-01				Unigene105778_A11//6.00E-14//ES803332				
Unigene105779_A11	211	0.00	0.24	0.00	0.00	0.33	4.28	0.20	0.00	0.57	7.91E+00	6.22E-01		null	null		8.35E+00	6.16E-01		1.21E+01	2.07E-05	Up	-7.65E+00	6.63E-01		1.50E+00	5.59E-01		Unigene105729_A11//gi|297809467|ref|XP_002872617.1|//5.00E-14//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297318454|gb|EFH48876.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene105779_A11//4.00E-15//AT4G11690| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene105579_A11	235	0.00	0.22	0.00	0.21	0.59	0.19	9.00	2.85	5.26	7.75E+00	6.22E-01		null	null		1.47E+00	6.20E-01		-1.42E-01	9.57E-01		-1.66E+00	7.98E-05	Down	-7.76E-01	4.06E-02				Unigene105579_A11//2.00E-38//DW480207				
Unigene105797_A11	212	0.00	1.43	0.25	2.11	0.16	2.13	312.91	200.30	856.91	1.05E+01	4.45E-02		7.97E+00	6.41E-01		-3.70E+00	1.07E-02		1.05E-02	1.00E+00		-6.44E-01	5.14E-28		1.45E+00	8.66E-294	Up	Unigene105797_A11//gi|40218371|gb|AAR83118.1|//8.00E-38//secretory laccase [Gossypium arboreum]	Unigene105797_A11//7.00E-23//AT5G48100| TT10 (TRANSPARENT TESTA 10); copper ion binding / laccase	Unigene105797_A11//6.00E-116//TC137114		ko00053|Ascorbate and aldarate metabolism		nr +
Unigene1058_A11	2372	0.66	0.90	0.81	13.00	10.12	9.90	16.81	7.47	5.29	4.39E-01	3.33E-01		2.89E-01	5.72E-01		-3.62E-01	6.65E-05		-3.93E-01	3.44E-05		-1.17E+00	8.03E-46	Down	-1.67E+00	3.36E-80	Down	Unigene1058_A11//gi|224137956|ref|XP_002326482.1|//0.00E+00//cationic amino acid transporter [Populus trichocarpa] >gi|222833804|gb|EEE72281.1| cationic amino acid transporter [Populus trichocarpa]	Unigene1058_A11//2.00E-128//AT5G04770| CAT6 (CATIONIC AMINO ACID TRANSPORTER 6); amino acid transmembrane transporter/ basic amino acid transmembrane transporter/ cationic amino acid transmembrane transporter	Unigene1058_A11//6.00E-60//TC146944			GO:0005275//GO:0015837//GO:0031224//GO:0043231	nr -
Unigene10580_A11	287	55.60	550.48	210.59	33.33	81.95	117.08	29.46	78.20	120.21	3.31E+00	0.00E+00	Up	1.92E+00	1.20E-113	Up	1.30E+00	1.60E-30	Up	1.81E+00	2.28E-64	Up	1.41E+00	1.49E-34	Up	2.03E+00	1.50E-89	Up	Unigene10580_A11//gi|210062232|gb|ACJ06163.1|//7.00E-18//HVA22E [Arabidopsis thaliana]	Unigene10580_A11//3.00E-19//AT5G50720| ATHVA22E	Unigene10580_A11//7.00E-104//TC166347			GO:0031224//GO:0050896	nr -
Unigene105815_A11	213	259.39	338.03	364.00	402.26	333.20	396.50	311.64	248.81	130.36	3.82E-01	4.63E-10		4.89E-01	6.69E-16		-2.72E-01	1.46E-07		-2.08E-02	7.64E-01		-3.25E-01	1.41E-08		-1.26E+00	2.90E-87	Down	Unigene105815_A11//gi|225427492|ref|XP_002263421.1|//3.00E-13//PREDICTED: similar to Os03g0576600 [Vitis vinifera]		Unigene105815_A11//3.00E-102//gi|84164696|gb|DR453344.1|DR453344				nr +
Unigene105816_A11	213	2899.75	970.33	3168.25	428.68	469.32	300.24	0.00	0.00	0.00	-1.58E+00	0.00E+00	Down	1.28E-01	6.28E-11		1.31E-01	1.34E-02		-5.14E-01	1.18E-22		null	null		null	null				Unigene105816_A11//2.00E-69//gi|21093041|gb|BQ405354.1|BQ405354				
Unigene10584_A11	274	0.57	1.11	0.39	2.18	4.02	4.45	4.17	0.31	0.44	9.54E-01	5.04E-01		-5.60E-01	7.77E-01		8.82E-01	1.94E-01		1.03E+00	1.07E-01		-3.77E+00	3.90E-06	Down	-3.26E+00	8.94E-06	Down								
Unigene105840_A11	215	0.97	2.59	0.99	3.71	4.00	15.75	4.33	4.28	11.12	1.41E+00	1.69E-01		2.54E-02	1.00E+00		1.11E-01	9.04E-01		2.09E+00	3.11E-08	Up	-1.66E-02	1.02E+00		1.36E+00	2.45E-04	Up	Unigene105840_A11//gi|15233476|ref|NP_192343.1|//2.00E-21//early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana] >gi|30679712|ref|NP_849296.1| early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana] >gi|30679715|ref|NP_849297.1| early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana]	Unigene105840_A11//5.00E-23//AT1G11960| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF221 (InterPro:IPR003864); BEST Arabidopsis thaliana protein match is: early-responsive to dehydration protein-related / ERD protein-related (TAIR:AT1G62320.1); Has 746 Blast hits to 706 proteins in 111 species: Archae - 0; Bacteria - 4; Metazoa - 131; Fungi - 370; Plants - 224; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink).	Unigene105840_A11//1.00E-36//TC131090				nr -
Unigene105841_A11	215	8.76	5.42	1.24	18.54	14.25	15.33	8.65	5.64	6.67	-6.93E-01	1.39E-01		-2.82E+00	5.01E-06	Down	-3.79E-01	2.27E-01		-2.74E-01	4.20E-01		-6.18E-01	1.52E-01		-3.75E-01	3.77E-01				Unigene105841_A11//3.00E-99//TC132167				
Unigene105844_A11	215	0.00	0.00	0.50	0.00	0.16	9.45	0.00	0.00	0.00	null	null		8.95E+00	4.02E-01		7.32E+00	8.40E-01		1.32E+01	3.89E-12	Up	null	null		null	null		Unigene105844_A11//sp|Q9U8M0|VIT1_PERAM//2.00E-11//Vitellogenin-1 OS=Periplaneta americana GN=VG2 PE=2 SV=1						swissprot +
Unigene105859_A11	216	0.00	0.00	0.00	0.00	0.64	2.93	0.20	0.19	0.00	null	null		null	null		9.32E+00	3.20E-01		1.15E+01	7.60E-04	Up	-1.63E-02	1.01E+00		-7.61E+00	6.18E-01		Unigene105859_A11//gi|15226939|ref|NP_178341.1|//3.00E-10//AtPP2-B10 (Phloem protein 2-B10); carbohydrate binding [Arabidopsis thaliana] >gi|75288076|sp|Q9ZVQ6.1|P2B10_ARATH RecName: Full=F-box protein PP2-B10; AltName: Full=Protein PHLOEM PROTEIN 2-LIKE B10; Short=AtPP2-B10 >gi|107738391|gb|ABF83689.1| At2g02360 [Arabidopsis thaliana]	Unigene105859_A11//1.00E-11//AT2G02360| AtPP2-B10 (Phloem protein 2-B10); carbohydrate binding	Unigene105859_A11//7.00E-54//gi|109843286|gb|DW241844.1|DW241844				nr -
Unigene10586_A11	430	0.00	0.35	0.00	1.16	1.04	0.11	1.18	0.00	0.56	8.47E+00	2.37E-01		null	null		-1.54E-01	8.50E-01		-3.46E+00	1.61E-02		-1.02E+01	8.91E-04	Down	-1.09E+00	2.28E-01		Unigene10586_A11//gi|297721755|ref|NP_001173241.1|//2.00E-75//Os03g0119966 [Oryza sativa Japonica Group] >gi|27452910|gb|AA015294.1| Hypothetical protein [Oryza sativa Japonica Group] >gi|217415974|dbj|BAH03170.1| NAC protein [Oryza sativa Japonica Group] >gi|255674164|dbj|BAH91969.1| Os03g0119966 [Oryza sativa Japonica Group]	Unigene10586_A11//4.00E-75//AT1G65910| anac028 (Arabidopsis NAC domain containing protein 28); transcription factor		NAC		GO:0001071//GO:0003676//GO:0010468//GO:0032501	nr +
Unigene105860_A11	216	40.69	26.98	24.16	30.90	36.67	61.05	57.35	34.83	18.63	-5.93E-01	2.26E-03		-7.52E-01	1.99E-04		2.47E-01	2.86E-01		9.82E-01	2.18E-10		-7.20E-01	5.27E-07		-1.62E+00	1.50E-24	Down			Unigene105860_A11//2.00E-94//TC156390				
Unigene10588_A11	313	199.42	160.26	218.27	6.37	14.74	4.47	0.00	0.00	0.00	-3.15E-01	2.01E-06		1.30E-01	6.83E-02		1.21E+00	9.95E-06	Up	-5.09E-01	2.94E-01		null	null		null	null				Unigene10588_A11//4.00E-155//gi|164342758|gb|ES843169.1|ES843169				
Unigene105883_A11	217	126.82	328.53	286.37	92.28	150.91	83.46	0.00	0.96	0.00	1.37E+00	6.61E-85	Up	1.18E+00	1.22E-56	Up	7.10E-01	6.26E-16		-1.45E-01	3.13E-01		9.91E+00	7.87E-02		null	null				Unigene105883_A11//5.00E-98//DR515441				
Unigene105889_A11	445	0.00	6.15	2.99	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.44E-15	Up	1.15E+01	2.40E-07	Up	null	null		null	null		null	null		null	null									
Unigene105896_A11	218	764.65	322.84	795.09	112.65	160.49	55.31	0.19	0.38	0.55	-1.24E+00	1.36E-170	Down	5.63E-02	2.36E-01		5.11E-01	1.14E-09		-1.03E+00	1.88E-20	Down	9.84E-01	7.33E-01		1.50E+00	5.59E-01		Unigene105896_A11//gi|1345698|sp|P27518.2|CB21_GOSHI//7.00E-28//RecName: Full=Chlorophyll a-b binding protein 151, chloroplastic; AltName: Full=LHCII type II CAB-151; Short=LHCP; Flags: Precursor >gi|452314|emb|CAA38025.1| chlorophyll ab binding protein [Gossypium hirsutum]	Unigene105896_A11//3.00E-27//AT3G27690| LHCB2.3; chlorophyll binding	Unigene105896_A11//4.00E-80//ES834749		ko00196|Photosynthesis - antenna proteins		nr +
Unigene1059_A11	1930	0.03	0.11	0.00	2.01	1.39	1.26	5.87	3.03	1.67	1.95E+00	3.76E-01		-4.76E+00	6.33E-01		-5.33E-01	7.95E-02		-6.72E-01	3.04E-02		-9.53E-01	5.66E-10		-1.81E+00	3.45E-26	Down	Unigene1059_A11//gi|224137956|ref|XP_002326482.1|//0.00E+00//cationic amino acid transporter [Populus trichocarpa] >gi|222833804|gb|EEE72281.1| cationic amino acid transporter [Populus trichocarpa]	Unigene1059_A11//3.00E-142//AT5G04770| CAT6 (CATIONIC AMINO ACID TRANSPORTER 6); amino acid transmembrane transporter/ basic amino acid transmembrane transporter/ cationic amino acid transmembrane transporter	Unigene1059_A11//9.00E-77//TC146944			GO:0005275//GO:0015837//GO:0031224//GO:0043231	nr +
Unigene105905_A11	218	0.24	2.79	0.00	3.43	7.11	10.98	1.16	1.73	1.64	3.54E+00	7.25E-03		-7.91E+00	6.33E-01		1.05E+00	5.02E-02		1.68E+00	1.19E-04	Up	5.68E-01	6.38E-01		4.99E-01	6.28E-01									
Unigene10591_A11	373	0.84	1.36	6.00	3.34	2.22	2.66	0.34	0.67	0.11	6.91E-01	4.99E-01		2.83E+00	4.06E-07	Up	-5.92E-01	3.18E-01		-3.26E-01	6.41E-01		9.83E-01	5.18E-01		-1.67E+00	4.78E-01		Unigene10591_A11//gi|50512300|gb|AAT77547.1|//6.00E-20//9A [Solanum pimpinellifolium]	Unigene10591_A11//2.00E-17//AT3G11080| AtRLP35 (Receptor Like Protein 35); kinase/ protein binding					nr +
Unigene105912_A11	219	83.38	23.60	83.16	19.79	20.28	8.46	0.00	0.00	0.18	-1.82E+00	2.44E-33	Down	-3.80E-03	1.00E+00		3.56E-02	9.25E-01		-1.23E+00	2.67E-05	Down	null	null		7.51E+00	6.48E-01				Unigene105912_A11//3.00E-102//TC132557				
Unigene105917_A11	219	7.17	6.25	5.59	12.06	14.78	11.55	1.35	6.68	0.91	-1.98E-01	6.85E-01		-3.58E-01	5.20E-01		2.94E-01	4.54E-01		-6.20E-02	8.91E-01		2.31E+00	4.93E-05	Up	-5.71E-01	6.28E-01		Unigene105917_A11//gi|195625106|gb|ACG34383.1|//2.00E-08//mannose-1-phosphate guanyltransferase [Zea mays]		Unigene105917_A11//6.00E-73//TC166316				nr +
Unigene105924_A11	219	0.00	0.00	0.00	0.00	0.16	12.17	0.00	0.00	0.00	null	null		null	null		7.30E+00	8.40E-01		1.36E+01	5.75E-16	Up	null	null		null	null									ESTscan -
Unigene105938_A11	220	1.43	0.00	0.00	1.81	2.97	7.39	2.50	0.57	0.54	-1.05E+01	3.67E-02		-1.05E+01	4.93E-02		7.15E-01	4.65E-01		2.03E+00	3.98E-04	Up	-2.13E+00	3.32E-02		-2.20E+00	2.24E-02		Unigene105938_A11//gi|297793507|ref|XP_002864638.1|//8.00E-27//protein-s-isoprenylcysteine O-methyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297310473|gb|EFH40897.1| protein-s-isoprenylcysteine O-methyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene105938_A11//2.00E-28//AT5G39500| unknown protein	Unigene105938_A11//2.00E-51//ES841908				nr +
Unigene10594_A11	240	1.09	1.27	0.67	3.53	3.30	0.19	0.18	0.17	0.00	2.17E-01	8.65E-01		-7.12E-01	6.22E-01		-9.66E-02	8.77E-01		-4.23E+00	2.18E-04	Down	-1.73E-02	1.01E+00		-7.46E+00	6.18E-01				Unigene10594_A11//1.00E-55//ES839899				

Unigene105942_All	220	119.39	299.41	236.96	102.35	140.40	112.91	0.38	0.00	0.18	1.33E+00	1.79E-74	Up	9.89E-01	4.70E-36		4.56E-01	4.22E-07		1.42E-01	2.65E-01		-8.59E+00	4.07E-01		-1.09E+00	6.78E-01		Unigene105942_All//gi|15294284|gb|AAK96319.1|AF410333_1//5.00E-07//AT3g62730/F26K9_160 [Arabidopsis thaliana] >gi|20147275|gb|AAM10351.1|AT3g62730/F26K9_160 [Arabidopsis thaliana]		Unigene105942_All//4.00E-83//TC159115				nr -
Unigene105946_All	220	0.95	1.38	8.23	3.62	2.97	5.75	0.19	0.57	0.36	5.39E-01	6.72E-01		3.11E+00	2.28E-06	Up	-2.85E-01	7.21E-01		6.66E-01	2.99E-01		1.57E+00	5.46E-01		9.14E-01	7.51E-01										ESTscan +
Unigene105952_All	221	27.46	19.95	24.58	23.89	23.37	25.14	13.01	12.86	5.23	-4.61E-01	5.74E-02		-1.60E-01	5.64E-01		-3.18E-02	9.10E-01		7.32E-02	7.93E-01		-1.66E-02	9.95E-01		-1.32E+00	6.99E-05	Down			Unigene105952_All//7.00E-51//TC155713					
Unigene105963_All	221	0.47	4.13	1.45	1.35	1.71	4.09	13.58	3.97	10.82	3.12E+00	1.14E-03		1.61E+00	3.05E-01		3.42E-01	8.36E-01		1.60E+00	4.34E-02		-1.77E+00	4.38E-07	Down	-3.29E-01	3.14E-01				Unigene105963_All//1.00E-67//gi|164369257|gb|ESS50707.1|ESS50707					
Unigene10598_All	224	0.47	0.00	0.24	0.44	0.00	0.81	80.03	50.19	866.49	-8.87E+00	3.77E-01		-9.75E-01	7.22E-01		-8.80E+00	3.17E-01		8.59E-01	6.96E-01		-6.73E-01	8.76E-09		3.44E+00	0.00E+00	Up	Unigene10598_All//gi|3970689|emb|CAA77191.1|//1.00E-14//(+)-delta-cadinene synthase [Gossypium arboreum]		Unigene10598_All//3.00E-13//gi|73861227|gb|DT463966.1|DT463966			GO:0010334//GO:0046872	nr +
Unigene1060_All	1955	0.08	0.10	0.19	3.67	2.29	2.73	4.84	0.98	1.57	3.69E-01	8.17E-01		1.25E+00	3.66E-01		-6.80E-01	8.16E-04		-4.29E-01	5.54E-02		-2.30E+00	8.60E-29	Down	-1.63E+00	4.92E-19	Down	Unigene1060_All//gi|224137956|ref|XP_002326482.1|//0.00E+00//cationic amino acid transporter [Populus trichocarpa] >gi|222833804|gb|EEE72281.1|cationic amino acid transporter [Populus trichocarpa]	Unigene1060_All//9.00E-144//AT5G04770| CAT6 (CATIONIC AMINO ACID TRANSPORTER 6); amino acid transmembrane transporter/ basic amino acid transmembrane transporter/ cationic amino acid transmembrane transporter	Unigene1060_All//1.00E-72//TC146944			GO:0005275//GO:0015837//GO:0031224//GO:0043231	nr +
Unigene10600_All	453	0.00	0.11	0.00	0.55	0.15	0.30	0.09	0.28	2.11	6.81E+00	6.22E-01		null	null		-1.85E+00	2.76E-01		-8.78E-01	6.17E-01		1.57E+00	5.46E-01		4.50E+00	6.81E-06	Up			Unigene10600_All//4.00E-29//TC170757					ESTscan +
Unigene106005_All	224	201.34	86.41	212.29	26.24	32.28	13.91	0.94	0.56	1.25	-1.22E+00	3.05E-45	Down	7.64E-02	3.96E-01		2.99E-01	2.00E-01		-9.16E-01	1.41E-04		-7.54E-01	6.33E-01		4.00E-01	7.43E-01				Unigene106005_All//3.00E-87//gi|164293551|gb|ES810014.1|ES810014					
Unigene106024_All	226	0.00	0.00	0.00	0.00	0.30	3.00	0.00	0.18	1.76	null	null		null	null		8.25E+00	6.16E-01		1.15E+01	4.19E-04	Up	7.53E+00	6.38E-01		1.08E+01	3.97E-03									
Unigene10603_All	428	0.24	2.25	0.00	0.35	1.45	0.11	0.20	0.00	0.00	3.20E+00	6.55E-04	Up	-7.93E+00	3.99E-01		2.05E+00	5.13E-02		-1.73E+00	5.02E-01		-7.63E+00	4.07E-01		-7.63E+00	3.61E-01		Unigene10603_All//gi|300507129|gb|ADK23940.1|//4.00E-29//KASII [Gossypium hirsutum]		Unigene10603_All//2.00E-12//gi|48829336|gb|CO127726.1|CO127726	ko00061|Fatty acid biosynthesis	GO:0008152//GO:0016747	nr +
Unigene106036_All	226	0.00	0.00	0.71	0.00	0.00	4.40	0.56	0.37	0.00	null	null		9.47E+00	2.40E-01		null	null		1.21E+01	6.15E-06	Up	-6.01E-01	7.68E-01		-9.13E+00	2.01E-01		Unigene106036_All//gi|302128114|dbj|BAJ13478.1|//5.00E-28//actin 1 [Guillardia theta]	Unigene106036_All//2.00E-28//AT3G18780| ACT2 (ACTIN 2); structural constituent of cytoskeleton	Unigene106036_All//1.00E-27//gi|31406833|gb|CD485868.1|CD485868	ko04145|Phagosome		nr -
Unigene106605_All	530	0.00	0.00	0.00	0.00	0.00	0.00	2.39	4.02	0.08	null	null		null	null		null	null		null	null		7.49E-01	5.78E-02		-4.99E+00	3.13E-08	Down	Unigene10605_All//gi|195624710|gb|ACG34185.1|//7.00E-69//60S ribosomal protein L10-3 [Zea mays]	Unigene10605_All//1.00E-68//AT1G14320| SAC52 (SUPPRESSOR OF ACAULIS 52); structural constituent of ribosome	Unigene10605_All//2.00E-13//ES822876	ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene10606_All	525	0.00	2.03	0.81	0.19	0.46	1.12	1.53	1.19	3.57	1.10E+01	3.82E-06	Up	9.66E+00	1.39E-02		1.27E+00	5.32E-01		2.56E+00	2.87E-02		-3.58E-01	6.49E-01		1.22E+00	3.68E-03				Unigene10606_All//3.00E-70//gi|78339929|gb|DT560203.1|DT560203					
Unigene106066_All	228	0.92	0.22	0.47	0.22	0.15	0.59	2.60	0.00	1.22	-2.05E+00	3.34E-01		-9.75E-01	6.22E-01		-5.33E-01	8.29E-01		1.44E+00	6.40E-01		-1.13E+01	2.40E-04	Down	-1.09E+00	1.86E-01				Unigene106066_All//7.00E-119//TC175066					
Unigene106097_All	230	0.23	3.97	0.00	0.65	1.20	0.79	0.55	0.18	0.35	4.12E+00	2.34E-04	Up	-7.83E+00	6.33E-01		8.82E-01	5.95E-01		2.74E-01	9.06E-01		-1.60E+00	5.35E-01		-6.71E-01	7.21E-01		Unigene106097_All//gi|15235982|ref|NP_195678.1|//4.00E-07//SAP domain-containing protein [Arabidopsis thaliana] >gi|145334269|ref|NP_001078515.1|SAP domain-containing protein [Arabidopsis thaliana]	Unigene106097_All//2.00E-08//AT4G39680| SAP domain-containing protein	Unigene106097_All//3.00E-115//TC177371				nr -
Unigene106112_All	231	0.45	3.29	1.61	0.86	1.79	0.98	91.88	11.58	15.00	2.86E+00	5.51E-03		1.83E+00	2.13E-01		1.05E+00	4.26E-01		1.81E-01	9.36E-01		-2.99E+00	4.67E-85	Down	-2.61E+00	3.35E-76	Down			Unigene106112_All//1.00E-114//gi|164365935|gb|ES812563.1|ES812563					
Unigene106120_All	231	0.00	0.00	0.00	0.00	0.00	3.52	0.00	0.00	0.00	null	null		null	null		null	null		1.18E+01	6.95E-05	Up	null	null		null	null		Unigene106120_All//gi|160898912|ref|YP_001564494.1|//8.00E-06//CshD family protein [Delftia acidovorans SPH-1] >gi|160364496|gb|ABX36109.1| CshD family protein [Delftia acidovorans SPH-1]						nr -
Unigene10614_All	203	92.27	40.93	72.66	60.86	76.67	41.60	2.08	0.62	0.79	-1.17E+00	4.42E-18	Down	-3.45E-01	1.08E-02		3.33E-01	1.78E-02		-5.49E-01	4.96E-04		-1.75E+00	1.24E-01		-1.41E+00	1.74E-01		Unigene10614_All//gi|228481103|gb|ACQ42250.1|//2.00E-29//blue light photoreceptor [Fragaria x ananassa]	Unigene10614_All//2.00E-27//AT3G45780| PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase	Unigene10614_All//3.00E-111//TC143876			GO:0004673//GO:0004674//GO:0005515//GO:0006351//GO:0006468//GO:0009416//GO:0009606//GO:0009881//GO:0009902//GO:0010118//GO:0010360//GO:0015992//GO:0023060//GO:0032559//GO:0043231//GO:0044459	nr +
Unigene106146_All	232	252.13	104.18	167.78	57.54	90.39	46.53	0.00	0.36	0.00	-1.28E+00	1.32E-62	Down	-5.88E-01	1.07E-16		6.52E-01	5.44E-09		-3.07E-01	5.64E-02		8.49E+00	4.04E-01		null	null				Unigene106146_All//2.00E-128//TC141493					
Unigene106152_All	233	0.22	0.65	4.80	3.63	3.84	2.52	0.18	1.61	0.68	1.54E+00	5.32E-01		4.42E+00	3.51E-05	Up	8.03E-02	9.41E-01		-5.28E-01	5.03E-01		3.15E+00	3.41E-02		1.91E+00	3.78E-01				Unigene106152_All//8.00E-57//ES821800					
Unigene106165_All	233	6.74	98.29	11.20	7.48	7.83	21.90	72.95	208.26	60.70	3.87E+00	1.63E-93	Up	7.33E-01	7.42E-02		6.60E-02	9.10E-01		1.55E+00	2.74E-08	Up	1.51E+00	4.06E-82	Up	-2.65E-01	2.80E-02		Unigene106165_All//gi|225426282|ref|XP_002266388.1|//8.00E-16//PREDICTED: similar to B2 protein [Vitis vinifera]	Unigene106165_All//4.00E-13//AT3G27090| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G42050.1); Has 642 Blast hits to 564 proteins in 35 species: Archae - 0; Bacteria - 2; Metazoa - 12; Fungi - 0; Plants - 155; Viruses - 0; Other Eukaryotes - 473 (source: NCBI BLink).	Unigene106165_All//5.00E-89//DR461377				nr +
Unigene10617_All	574	1.19	0.18	0.00	0.09	0.42	0.16	2.58	1.02	1.04	-2.75E+00	1.06E-02		-1.02E+01	7.65E-04	Down	2.27E+00	3.05E-01		8.59E-01	7.97E-01		-1.34E+00	7.48E-03		-1.31E+00	6.57E-03		Unigene10617_All//gi|124359380|gb|ABN05846.1|//4.00E-06//Tetratricopeptide-like helical [Medicago truncatula]		Unigene10617_All//2.00E-13//TC136777				nr -
Unigene106174_All	234	107.55	221.73	175.68	92.82	144.95	102.68	51.13	66.98	64.35	1.04E+00	2.18E-40	Up	7.08E-01	2.27E-16		6.43E-01	6.05E-14		1.46E-01	2.57E-01		3.90E-01	2.13E-03		3.32E-01	9.08E-03		Unigene106174_All//gi|151368154|gb|ABS10812.1|//2.00E-23//DNA binding protein-like protein [Gossypium arboreum]		Unigene106174_All//7.00E-125//TC132469				nr +
Unigene106178_All	234	0.22	1.30	1.82	1.70	13.10	8.88	1.63	0.18	0.34	2.54E+00	1.51E-01		3.03E+00	5.74E-02		2.94E+00	2.00E-11	Up	2.38E+00	4.55E-06	Up	-3.19E+00	3.12E-02		-2.26E+00	6.50E-02									
Unigene106195_All	235	0.22	3.67	1.13	0.21	0.29	0.96	0.18	1.07	1.19	4.04E+00	4.20E-04	Up	2.35E+00	2.40E-01		4.67E-01	9.61E-01		2.18E+00	3.23E-01		2.57E+00	1.53E-01		2.72E+00	9.95E-02				Unigene106195_All//2.00E-36//TC157213					
Unigene106196_All	235	34.73	8.19	15.86	61.26	31.65	24.98	4.50	1.42	2.20	-2.08E+00	3.83E-18	Down	-1.13E+00	1.68E-07	Down	-9.53E-01	3.66E-12		-1.29E+00	1.80E-17	Down	-1.66E+00	8.55E-03		-1.03E+00	7.30E-02				Unigene106196_All//1.00E-86//TC153940					ESTscan +
Unigene106228_All	237	0.00	1.92	0.45	1.05	1.02	3.43	2.68	8.29	5.72	1.09E+01	7.44E-03		8.81E+00	4.02E-01		-4.72E-02	9.52E-01		1.71E+00	4.57E-02		1.63E+00	1.97E-04	Up	1.09E+00	2.95E-02				Unigene106228_All//2.00E-131//TC164875					
Unigene106270_All	239	14.45	6.15	31.86	82.54	131.55	52.72	78.37	11.54	45.84	-1.23E+00	3.00E-04	Down	1.14E+00	3.76E-07	Up	6.72E-01	5.62E-14		-6.47E-01	7.89E-08		-2.76E+00	2.71E-69	Down	-7.74E-01	8.45E-12		Unigene106270_All//gi|50313462|gb|AAT74601.1|//4.00E-23//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene106270_All//7.00E-17//AT3G23510| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene106270_All//3.00E-78//TC129560				nr +
Unigene106628_All	273	0.38	0.00	0.00	2.37	0.13	1.99	0.62	0.61	0.44	-8.58E+00	3.77E-01		-8.58E+00	3.99E-01		-4.23E+00	5.94E-04	Down	-2.57E-01	7.57E-01		-1.66E-02	1.02E+00		-5.01E-01	7.47E-01		Unigene106628_All//gi|186898205|gb|ACC93947.1|//6.00E-44//heat-shock protein 70 [Hevea brasiliensis]	Unigene106628_All//5.00E-27//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene106628_All//7.00E-67//TC165936	ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0000302//GO:0009642//GO:0010038//GO:0016020//GO:0016628//GO:0019899//GO:0030312//GO:0032146//GO:0032559//GO:0043231//GO:0051707	nr +
Unigene106295_All	241	0.00	0.00	0.00	0.83	0.00	0.75	0.00	0.69	2.98	null	null		null	null		-9.69E+00	8.48E-02		-1.41E-01	9.35E-01		9.44E+00	1.39E-01		1.15E+01	2.63E-05	Up	Unigene106295_All//gi|255587535|ref|XP_002534305.1|//2.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223525538|gb|EEF28080.1|conserved hypothetical protein [Ricinus communis]		Unigene106295_All//1.00E-126//gi|109889377|gb|DW518345.1|DW518345				nr -
Unigene1063_All	1193	8.55	17.20	12.68	12.61	15.99	15.07	8.15	12.26	11.59	1.01E+00	1.48E-15	Up	5.68E-01	1.32E-04		3.43E-01	5.44E-03		2.57E-01	6.41E-02		5.89E-01	6.10E-06		5.08E-01	1.12E-04		Unigene1063_All//gi|42572315|ref|NP_974253.1|//8.00E-68//HhH-GPD base excision DNA repair family protein [Arabidopsis thaliana] >gi|114050633|gb|ABI49466.1|At3g07930 [Arabidopsis thaliana]	Unigene1063_All//4.00E-69//AT3G07930| HhH-GPD base excision DNA repair family protein	Unigene1063_All//0.00E+00//TC169474	ko03410|Base excision repair	GO:0006281	nr +
Unigene106308_All	242	33.73	13.61	14.96	64.84	64.46	79.13	357.81	147.49	194.58	-1.31E+00	9.81E-10	Down	-1.17E+00	6.59E-08	Down	-8.50E-03	9.54E-01		2.87E-01	2.81E-02		-1.28E+00	2.39E-113	Down	-8.79E-01	1.48E-63		Unigene106308_All//gi|78191410|gb|ABB29926.1|//1.00E-35//fructose-bisphosphate aldolase-like [Solanum tuberosum]	Unigene106308_All//2.00E-34//AT5G03690| fructose-bisphosphate aldolase, putative	Unigene106308_All//2.00E-134//gi|11201622|gb|BF270531.1|BF270531	ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene106326_All	243	0.22	0.00	1.31	0.21	1.13	10.04	0.35	1.55	0.66	-7.75E+00	6.20E-01		2.61E+00	1.46E-01		2.47E+00	2.23E-01		5.61E+00	3.38E-13	Up	2.15E+00	9.46E-02		9.14E-01	6.25E-01				Unigene106326_All//3.00E-07//TC168359					
Unigene10633_All	592	0.00	0.00	0.00	0.00	0.00	0.00	2.14	12.85	0.34	null	null		null	null		null	null		null	null		2.58E+00	1.82E-26	Up	-2.67E+00	2.31E-05	Down	Unigene10633_All//gi|38640722|gb|AAR25996.1|//5.00E-06//cytochrome P450 monooxygenase [Pyrus communis]		Unigene10633_All//1.00E-36//gi|73864682|gb|DT467421.1|DT467421				nr -
Unigene106358_All	246	0.85	2.47	1.08	0.41	0.84	0.37	0.69	0.34	5.18	1.54E+00	1.22E-01		3.47E-01	7.97E-01		1.05E+00	6.13E-01		-1.41E-01	9.53E-01		-1.02E+00	6.15E-01		2.91E+00	1.05E-05	Up	Unigene106358_All//gi|55168340|gb|AAV44205.1|//3.00E-06//unknown protein [Oryza sativa Japonica Group]		Unigene106358_All//1.00E-31//TC139311				nr -
Unigene106636_All	345	0.00	0.73	0.62	1.30	0.20	0.52	1.59	0.00	2.77	9.52E+00	7.89E-02		9.27E+00	1.42E-01		-2.70E+00	3.24E-02		-1.31E+00	2.73E-01		-1.06E+01	4.62E-04	Down	7.99E-01	1.95E-01				Unigene106636_All//3.00E-128//TC179309					
Unigene106360_All	246	0.00	0.62	0.00	2.84	0.00	2.39	0.17	0.34	0.16	9.22E+00	2.37E-01		null	null		-1.15E+01	3.44E-05	Down	-2.48E-01	7.56E-01		9.83E-01	7.33E-01		-8.65E-02	9.74E-01									
Unigene10637_All	420	0.00	2.53	1.78	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.82E-06	Up	1.08E+01	3.28E-04	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene106378_All	247	0.42	640.65	459.20	0.40	0.00	2.56	0.34	0.17	0.00	1.06E+01	0.00E+00	Up	1.01E+01	0.00E+00	Up	-8.66E+00	3.17E-01		2.67E+00	1.83E-02		-1.02E+00	7.26E-01		-8.42E+00	3.61E-01									
Unigene1064_All	1263	1.04	2.85	1.31	2.45	2.84	2.00	0.87	1.36	2.71	1.46E+00	2.10E-05	Up	3.36E-01	5.35E-01		2.14E-01	5.76E-01		-2.88E-01	4.68E-01		6.41E-01	1.57E-01		1.64E+00	2.03E-07	Up	Unigene1064_All//gi|42572313|ref|NP_974252.1|//2.00E-28//HhH-GPD base excision DNA repair family protein [Arabidopsis thaliana]	Unigene1064_All//1.00E-29//AT3G07930| HhH-GPD base excision DNA repair family protein	Unigene1064_All//0.00E+00//TC169474	ko03410|Base excision repair		nr -
Unigene10641_All	774	0.00	0.00	0.00	0.51	0.98	0.41	0.33	3.29	0.82	null	null		null	null		9.27E-01	2.97E-01		-3.34E-01	7.57E-01		3.33E+00	8.60E-12	Up	1.33E+00	1.00E-01		Unigene10641_All//gi|18404500|ref|NP_566763.1|//2.00E-65//auxin-responsive family protein [Arabidopsis thaliana] >gi|79313415|ref|NP_001030764.1|auxin-responsive family protein [Arabidopsis thaliana] >gi|16323200|gb|AAL15334.1|AT3g25290/MJL12_25 [Arabidopsis thaliana] >gi|250900093|gb|AAN72226.1|At3g25290/MJL12_25 [Arabidopsis thaliana]	Unigene10641_All//3.00E-63//AT3G25290| auxin-responsive family protein	Unigene10641_All//3.00E-62//gi|78325030|gb|DT545304.1|DT545304		GO:0016020	nr +
Unigene106413_All	250	0.00	0.00	0.00	1.00	0.69	1.99	0.85	3.34	4.30	null	null		null	null		-5.33E-01	7.13E-01		9.96E-01	3.94E-01		1.98E+00	8.88E-03		2.35E+00	4.46E-04	Up	Unigene106413_All//gi|115472687|ref|NP_001059942.1|//9.00E-28//Os07g0551300 [Oryza sativa Japonica Group] >gi|113611478|dbj|BAF21856.1|Os07g0551300 [Oryza sativa Japonica Group]	Unigene106413_All//7.00E-28//AT4G21390| B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding	Unigene106413_All//5.00E-12//DT469086	ko04626|Plant-pathogen interaction		nr +
Unigene106642_All	482	0.00	0.32	0.00	0.00	0.00	0.00	1.75	4.77	0.91	8.30E+00	2.37E-01		null	null		null	null		null	null		1.44E+00	2.32E-04	Up	-9.48E-01	1.47E-01		Unigene106642_All//gi|7267528|emb|CAB78010.1|//2.00E-06//receptor protein kinase-like protein [Arabidopsis thaliana] >gi|7321074|emb|CAB82121.1|receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene106642_All//1.00E-07//AT4G08850| kinase			GO:0004672//GO:0005488	nr -

Unigene106643_All	411	1.78	0.00	0.39	1.33	0.59	0.00	0.00	0.31	0.00	-1.08E+01	2.11E-04	Down	-2.20E+00	2.77E-02		-1.18E+00	2.25E-01		-1.04E+01	1.52E-03		8.25E+00	2.41E-01		null	null		Unigene10643_All//gi|225456658|ref|XP_002271524.1|//7.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene10643_All//1.00E-07//TC144614				nr -
Unigene106448_All	253	16.54	8.21	27.15	3.15	1.77	1.96	0.17	0.00	0.16	-1.01E+00	7.51E-04	Down	7.15E-01	2.12E-03		-8.32E-01	2.88E-01		-6.82E-01	4.05E-01		-7.38E+00	6.63E-01		-8.54E-02	9.74E-01		Unigene106448_All//1.00E-12//AT1G48600| phosphoethanolamine N-methyltransferase [Gossypium hirsutum]	Unigene106448_All//1.00E-52//TC162345		ko00564|Glycerophospholipid metabolism		nr -
Unigene10645_All	308	0.00	2.80	2.59	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.95E-05	Up	1.13E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene10645_All//sp|Q8VHX6|FLNC_MOUSE//9.00E-31//Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3					swissprot -
Unigene106472_All	255	0.00	2.98	0.63	0.59	1.35	3.01	0.33	0.00	0.00	1.15E+01	1.77E-04	Up	9.29E+00	2.40E-01		1.20E+00	4.26E-01		2.36E+00	1.34E-02		-8.37E+00	4.07E-01		-8.37E+00	3.61E-01								
Unigene106474_All	255	13.54	4.97	14.83	51.18	42.40	44.28	117.39	79.00	58.43	-1.45E+00	3.41E-05	Down	1.31E-01	6.90E-01		-2.72E-01	8.87E-02		-2.09E-01	2.32E-01		-5.71E-01	9.53E-11		-1.01E+00	4.26E-28	Down	Unigene106474_All//gi|297611781|ref|NP_001067845.2|//1.00E-30//Os11g0455500 [Oryza sativa Japonica Group] >gi|255680068|dbj|BAF28208.2| Os11g0455500 [Oryza sativa Japonica Group]	Unigene106474_All//2.00E-28//AT4G13940| MEE58 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding	Unigene106474_All//1.00E-101//gi|164369275|gb|EV484110.1|EV484110	ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -
Unigene106652_All	435	0.00	3.38	2.45	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.11E-08	Up	1.13E+01	6.63E-06	Up	null	null		null	null		null	null		null	null		Unigene106652_All//gi|300260006|gb|EFJ14228.1|//2.00E-14//RWP-RK domain-containing transcription factor [Volvox carteri f. nagariensis]				GO:0005488//GO:0017111//GO:0044464	nr +
Unigene106520_All	262	0.00	0.77	0.00	0.00	0.13	2.76	0.00	0.00	0.00	9.60E+00	1.37E-01		null	null		7.04E+00	8.39E-01		1.14E+01	2.31E-04	Up	null	null		null	null		Unigene106520_All//gi|15218349|ref|NP_177355.1|//3.00E-09//late embryogenesis abundant domain-containing protein / LEA domain-containing protein [Arabidopsis thaliana]					nr -
Unigene106525_All	262	0.00	42.16	1.63	0.00	0.00	0.52	0.00	0.16	0.00	1.54E+01	2.52E-63	Up	1.07E+01	1.39E-02		null	null		9.01E+00	3.12E-01		7.32E+00	6.38E-01		null	null		Unigene106525_All//gi|187610416|gb|ACD13462.1|//1.00E-23//raffinose synthase 3 [Glycine max]	Unigene106525_All//1.00E-19//AT5G40390| SIP1 (seed imbibition 1-like); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compounds		ko00052|Galactose metabolism		nr +
Unigene106530_All	263	6.96	0.39	3.24	8.90	6.02	5.84	0.00	0.00	0.00	-4.18E+00	2.18E-08	Down	-1.10E+00	3.06E-02		-5.64E-01	1.69E-01		-6.09E-01	1.55E-01		null	null		null	null									
Unigene106539_All	263	0.80	5.78	2.23	3.98	3.93	3.43	0.00	0.00	0.45	2.86E+00	2.69E-05	Up	1.48E+00	1.53E-01		-1.81E-02	9.61E-01		-2.12E-01	7.44E-01		null	null		8.83E+00	2.44E-01									
Unigene106542_All	264	105.24	85.41	137.97	10.00	4.83	1.37	0.64	0.32	0.00	-3.01E-01	3.97E-03		3.91E-01	2.01E-05		-1.05E+00	4.04E-03		-2.87E+00	2.04E-09	Down	-1.02E+00	6.15E-01		-9.32E+00	1.09E-01				Unigene106542_All//4.00E-133//TC140158				
Unigene106544_All	264	0.00	0.00	0.00	0.00	0.78	0.86	0.48	0.95	4.53	null	null		null	null		9.61E+00	1.57E-01		9.74E+00	1.19E-01		9.83E-01	5.18E-01		3.24E+00	7.29E-06	Up							
Unigene106548_All	264	0.00	0.00	0.20	0.00	0.65	2.57	0.00	0.16	0.00	null	null		7.66E+00	6.41E-01		9.35E+00	2.28E-01		1.13E+01	4.19E-04	Up	7.31E+00	6.38E-01		null	null		Unigene106548_All//gi|207693265|gb|ACI25287.1|//4.00E-20//ARM repeat containing protein [Populus trichocarpa]	Unigene106548_All//1.00E-20//AT5G66200| ARO2 (ARMADILLO REPEAT ONLY 2); binding	Unigene106548_All//3.00E-140//EX165874			nr -
Unigene106560_All	267	0.39	3.04	0.80	0.00	0.64	5.58	0.63	0.00	0.00	2.95E+00	3.29E-03		1.03E+00	5.92E-01		9.33E+00	2.28E-01		1.24E+01	7.04E-09	Up	-9.31E+00	1.35E-01		-9.31E+00	1.09E-01		Unigene106560_All//gi|297811437|ref|XP_002873602.1|//4.00E-17//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319439|gb|EFH49861.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene106560_All//4.00E-18//AT5G13170| SAG29 (SENESCENCE-ASSOCIATED PROTEIN 29)	Unigene106560_All//1.00E-129//TC176027			nr +
Unigene106569_All	269	0.00	0.38	0.59	0.00	0.26	3.02	0.16	0.16	0.00	8.56E+00	3.91E-01		9.21E+00	2.40E-01		8.00E+00	6.16E-01		1.16E+01	6.95E-05	Up	-1.66E-02	1.01E+00		-7.30E+00	6.17E-01		Unigene106569_All//gi|15218927|ref|NP_176191.1|//9.00E-18//ALA3 (Aminophospholipid ATPase3); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / phospholipid transporter [Arabidopsis thaliana] >gi|30316321|sp|Q9XIE6.2|ALA3_ARATH RecName: Full=Phospholipid-transporting ATPase 3; Short=AtALA3; AltName: Full=Aminophospholipid flippase 3 >gi|20147219|gb|AAM10325.1| At1g59820/F23H11_14 [Arabidopsis thaliana]	Unigene106569_All//4.00E-19//AT1G59820| ALA3 (Aminophospholipid ATPase3); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / phospholipid transporter				nr -
Unigene106570_All	269	94.53	30.14	45.33	161.85	141.71	162.19	106.88	44.28	53.91	-1.65E+00	2.94E-40	Down	-1.06E+00	6.57E-20	Down	-1.92E-01	1.82E-02		3.00E-03	9.73E-01		-1.27E+00	8.20E-38	Down	-9.87E-01	3.32E-26			Unigene106570_All//7.00E-113//TC134569				
Unigene106571_All	269	0.19	0.38	1.58	2.96	0.00	3.02	1.10	0.00	0.30	9.54E-01	7.28E-01		3.03E+00	5.74E-02		-1.15E+01	6.49E-06	Down	2.85E-02	9.71E-01		-1.01E+01	2.19E-02		-1.89E+00	1.68E-01		Unigene106571_All//gi|255578137|ref|XP_002529938.1|//3.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223530568|gb|EEF32446.1| conserved hypothetical protein [Ricinus communis]		Unigene106571_All//5.00E-89//EX164741			nr -
Unigene106575_All	270	1.94	0.75	1.78	1.29	2.17	2.84	4.85	2.01	1.33	-1.37E+00	1.97E-01		-1.27E-01	8.98E-01		7.47E-01	4.82E-01		1.14E+00	1.89E-01		-1.27E+00	1.77E-02		-1.87E+00	6.93E-04	Down		Unigene106575_All//5.00E-151//TC174841				
Unigene10658_All	785	0.00	1.03	0.00	0.00	1.32	0.86	0.00	0.05	0.00	1.00E+01	9.39E-05	Up	null	null		1.04E+01	2.35E-06	Up	9.75E+00	4.19E-04	Up	5.73E+00	6.38E-01		null	null		Unigene10658_All//gi|6686397|gb|AAF23831.1|AC007234_3//1.00E-20//F1E22.12 [Arabidopsis thaliana]	Unigene10658_All//3.00E-10//AT3G25270| nucleic acid binding			GO:0005488	nr -
Unigene106580_All	270	0.39	0.00	0.39	0.74	1.53	5.85	1.25	0.77	0.89	-8.60E+00	3.77E-01		2.51E-02	1.00E+00		1.05E+00	4.26E-01		2.99E+00	7.31E-06	Up	-6.95E-01	5.78E-01		-5.01E-01	6.50E-01			Unigene106580_All//4.00E-68//ES801598				
Unigene106586_All	271	626.50	436.95	625.25	247.42	215.00	120.66	427.95	291.95	286.07	-5.20E-01	1.88E-39		-2.90E-03	9.73E-01		-2.03E-01	1.03E-03		-1.04E+00	8.65E-56	Down	-5.52E-01	6.85E-37		-5.81E-01	1.51E-41		Unigene106586_All//gi|148807173|gb|ABR13296.1|//9.00E-07//unknown protein [Prunus dulcis]		Unigene106586_All//5.00E-83//TC144875			nr -
Unigene106593_All	272	1.15	2.79	5.48	4.76	4.94	4.98	0.78	0.31	1.90	1.28E+00	1.28E-01		2.25E+00	5.49E-04	Up	5.23E-02	9.57E-01		6.50E-02	9.34E-01		-1.34E+00	4.31E-01		1.29E+00	1.59E-01								
Unigene106597_All	272	0.58	4.47	2.15	5.68	3.42	4.65	2.18	2.77	2.64	2.95E+00	1.75E-04	Up	1.90E+00	8.48E-02		-7.32E-01	1.59E-01		-2.88E-01	6.38E-01		3.46E-01	6.20E-01		2.77E-01	6.90E-01			Unigene106597_All//2.00E-70//gi|13246583|gb|BE054988.2|BE054988				
Unigene106598_All	272	766.92	355.99	626.27	96.70	91.41	56.12	0.47	0.15	0.29	-1.11E+00	2.93E-177	Down	-2.92E-01	2.39E-16		-8.12E-02	5.52E-01		-7.85E-01	4.15E-14		-1.60E+00	5.35E-01		-6.71E-01	7.21E-01		Unigene106598_All//6.00E-46//AT2G05070| LHCB2.2; chlorophyll binding	Unigene106598_All//3.00E-152//TC135194		ko00196|Photosynthesis - antenna proteins		nr -
Unigene1066_All	819	13.61	14.54	21.00	15.02	15.64	17.37	43.21	24.29	19.07	9.55E-02	5.91E-01		6.26E-01	5.76E-06		5.81E-02	7.98E-01		2.09E-01	2.09E-01		-8.31E-01	1.76E-23		-1.18E+00	1.53E-42	Down	Unigene1066_All//gi|295687233|gb|AD627842.1|//1.00E-126//transaldolase [Gossypium hirsutum]	Unigene1066_All//4.00E-71//AT1G12230| transaldolase, putative	Unigene1066_All//0.00E+00//TC142315	ko00030|Pentose phosphate pathway	GO:0009536//GO:0016744//GO:0044238//GO:0046914	nr -
Unigene106600_All	272	0.19	15.83	1.17	0.37	0.13	0.66	0.31	0.00	0.00	6.36E+00	6.39E-23	Up	2.61E+00	1.46E-01		-1.53E+00	5.89E-01		8.59E-01	6.96E-01		-8.28E+00	4.07E-01		-8.28E+00	3.61E-01		Unigene106600_All//gi|62420870|tpg|DAA01542.1|//5.00E-30//TPA: TPA_exp: alpha-dioxygenase 3 [Lycopersicon esculentum]	Unigene106600_All//5.00E-28//AT1G73680| pathogen-responsive alpha-dioxygenase, putative	Unigene106600_All//2.00E-125//TC167331	ko00592|alpha-Linolenic acid metabolism		nr -
Unigene106603_All	273	0.38	0.37	0.20	0.18	1.01	3.14	0.93	0.61	0.15	-4.63E-02	9.91E-01		-9.74E-01	7.22E-01		2.47E+00	2.23E-01		4.11E+00	3.41E-04	Up	-6.02E-01	6.48E-01		-2.67E+00	1.15E-01		Unigene106603_All//gi|224062025|ref|XP_002300717.1|//8.00E-41//SAUR family protein [Populus trichocarpa] >gi|222842443|gb|EEE79990.1| SAUR family protein [Populus trichocarpa]	Unigene106603_All//1.00E-39//AT1G75580| auxin-responsive protein, putative	Unigene106603_All//7.00E-141//TC157705			nr +
Unigene106609_All	273	11.88	0.00	0.39	11.50	2.65	1.65	4.03	1.53	5.11	-1.35E+01	9.73E-19	Down	-4.93E+00	3.88E-15	Down	-2.12E+00	4.75E-09	Down	-2.80E+00	7.93E-11	Down	-1.40E+00	2.04E-02		3.43E-01	5.03E-01		Unigene106609_All//gi|224115708|ref|XP_002317102.1|//7.00E-10//predicted protein [Populus trichocarpa] >gi|222860167|gb|EEE97714.1| predicted protein [Populus trichocarpa]		Unigene106609_All//4.00E-133//ES815751			nr +
Unigene10661_All	478	0.77	0.32	0.89	4.38	2.67	1.04	1.24	0.70	2.00	-1.27E+00	3.36E-01		2.18E-01	8.31E-01		-7.16E-01	9.63E-02		-2.07E+00	2.11E-05	Down	-8.24E-01	3.48E-01		6.92E-01	2.60E-01		Unigene10661_All//gi|224073274|ref|XP_002304055.1|//1.00E-30//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222841487|gb|EEE79034.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene10661_All//6.00E-18//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene10661_All//2.00E-161//gi|109863388|gb|DW492365.1|DW492365	ko04626|Plant-pathogen interaction	GO:0005488//GO:0009987	nr +
Unigene10662_All	882	2.85	0.23	1.51	0.34	0.23	0.20	0.00	0.00	0.00	-3.63E+00	2.75E-10	Down	-9.16E-01	2.91E-02		-5.33E-01	6.79E-01		-7.27E-01	6.39E-01		null	null		null	null		Unigene10662_All//gi|224127726|ref|XP_002329162.1|//5.00E-15//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene10662_All//4.00E-05//AT4G19530| disease resistance protein (TIR-NBS-LRR class), putative	Unigene10662_All//6.00E-73//TC178046		GO:0005488	nr +
Unigene106629_All	277	3.40	0.00	0.00	0.36	0.62	0.82	0.46	0.75	1.44	-1.17E+01	1.46E-05	Down	-1.17E+01	3.35E-05	Down	7.89E-01	7.72E-01		1.18E+00	5.50E-01		7.20E-01	6.32E-01		1.65E+00	1.41E-01		Unigene106629_All//gi|195621024|gb|ACG32342.1|//5.00E-18//histone mRNA exonuclease 1 [Zea mays]	Unigene106629_All//1.00E-17//AT3G15140| exonuclease family protein	Unigene106629_All//2.00E-110//TC143702			nr +
Unigene10663_All	746	0.00	0.00	0.00	0.00	0.00	0.00	1.76	2.41	0.11	null	null		null	null		null	null		null	null		4.55E-01	3.20E-01		-4.04E+00	1.35E-07	Down	Unigene10663_All//gi|80973464|gb|ABB53473.1|//5.00E-86//GDP-mannose pyrophosphorylase [Malpighia glabra] >gi|161898831|gb|ABX80393.1| GDP-mannose pyrophosphorylase [Malpighia glabra]	Unigene10663_All//9.00E-86//AT2G39770| CYT1 (CYTOKINESIS DEFECTIVE 1); mannose-1-phosphate guanylyltransferase/ nucleotidyltransferase		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism	GO:0008152//GO:0008905//GO:0043231	nr -
Unigene10664_All	693	0.00	0.00	0.00	0.00	0.00	0.00	25.69	2.35	0.52	null	null		null	null		null	null		null	null		-3.45E+00	1.05E-81	Down	-5.63E+00	6.87E-116	Down	Unigene10664_All//gi|226501140|ref|NP_001152197.1|//9.00E-11//LOC100285835 [Zea mays] >gi|195653721|gb|ACG46328.1| keratin-associated protein 5-4 [Zea mays]	Unigene10664_All//2.00E-07//AT1G05660| ATNFXL2; protein binding / transcription factor/ zinc ion binding		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko03020|RNA polymerase		nr +
Unigene10665_All	267	0.00	0.00	0.20	4.66	4.13	1.01	0.95	26.46	1.19	null	null		7.64E+00	6.41E-01		-1.77E-01	7.95E-01		-2.20E+00	1.10E-03		4.80E+00	3.93E-41	Up	3.29E-01	7.64E-01			Unigene10665_All//2.00E-45//gi|13244098|gb|BE053719.2|BE053719				
Unigene106654_All	283	0.18	0.36	2.07	0.00	0.00	10.21	0.00	0.00	0.00	9.54E-01	7.28E-01		3.48E+00	1.21E-02		null	null		1.33E+01	2.44E-17	Up	null	null		null	null		Unigene106654_All//sp|Q9U8M0|VITI_PERAM//1.00E-07//Vitellogenin-1 OS=Periplaneta americana GN=VG2 PE=2 SV=1					swissprot +
Unigene10666_All	441	0.00	0.11	0.00	0.11	0.31	1.13	1.73	0.47	0.00	6.84E+00	6.22E-01		null	null		1.47E+00	6.20E-01		3.32E+00	2.31E-02		-1.86E+00	1.82E-02		-1.08E+01	8.89E-06	Down							
Unigene106662_All	284	0.00	0.00	0.00	0.00	0.12	2.54	0.60	0.29	0.56	null	null		null	null		6.92E+00	8.39E-01		1.13E+01	2.31E-04	Up	-1.02E+00	6.15E-01		-8.58E-02	9.66E-01		Unigene106662_All//gi|15237835|ref|NP_200728.1|//4.00E-36//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene106662_All//2.00E-37//AT5G59200| pentatricopeptide (PPR) repeat-containing protein				nr -
Unigene10667_All	287	0.00	0.00	0.00	0.00	0.00	0.00	2.06	2.91	0.00	null	null		null	null		null	null		null	null		4.98E-01	4.86E-01		-1.10E+01	1.42E-04	Down	Unigene10667_All//gi|159462882|ref|XP_001689671.1|//3.00E-06//polyadenylate-binding protein RB47 [Chlamydomonas reinhardtii] >gi|158283659|gb|EDP09409.1| polyadenylate-binding protein RB47 [Chlamydomonas reinhardtii]				GO:0005488	nr -
Unigene106672_All	287	1.28	2.12	3.15	5.38	2.52	41.23	50.24	20.10	20.96	7.31E-01	4.16E-01		1.31E+00	9.77E-02		-1.09E+00	3.11E-02		2.94E+00	1.42E-40	Up	-1.32E+00	1.63E-20	Down	-1.26E+00	9.90E-20	Down			Unigene10672_All//3.00E-44//gi|78334472|gb|DT554746.1|DT554746				

Unigene106673_All	288	0.36	0.35	0.00	0.35	2.03	3.45	0.59	0.00	0.83	-4.60E-02	9.91E-01			-8.51E+00	3.99E-01		2.55E+00	2.84E-02		3.32E+00	3.47E-04	Up	-9.20E+00	1.35E-01		4.99E-01	7.08E-01		Unigene106673_All//gi|297836510|ref|XP_002886137.1|//4.00E-34//FAT domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331977|gb|EFH62396.1| FAT domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene106673_All//1.00E-34//AT2G17930| binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor				nr -
Unigene106695_All	292	0.00	0.00	2.55	0.34	0.24	1.39	0.43	0.43	0.55	null	null			1.13E+01	3.28E-04	Up	-5.32E-01	8.19E-01		2.03E+00	1.49E-01		-1.67E-02	1.02E+00		3.29E-01	8.52E-01		Unigene106695_All//gi|225442485|ref|XP_002278313.1|//1.00E-44//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene106695_All//4.00E-45//AT1G59870| PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	Unigene106695_All//8.00E-08//gi|78354132|gb|DT574406.1|DT574406		ko02010|ABC transporters		nr -
Unigene10670_All	252	2.08	11.66	5.49	5.53	4.37	6.45	20.30	15.09	10.91	2.49E+00	2.11E-08	Up	1.40E+00	2.28E-02		-3.40E-01	5.62E-01		2.21E-01	6.77E-01		-4.28E-01	7.84E-02		-8.96E-01	1.02E-04					Unigene10670_All//1.00E-61//TC140097				
Unigene10701_All	294	252.53	294.37	287.44	142.33	97.80	53.15	0.29	0.57	0.27	2.21E-01	9.00E-05		1.87E-01	1.95E-03		-5.41E-01	5.15E-13		-1.42E+00	1.99E-57	Down	9.83E-01	6.35E-01		-8.58E-02	9.74E-01					Unigene10701_All//1.00E-148//TC114944				
Unigene10671_All	346	0.00	0.00	0.00	0.58	0.00	0.26	4.52	1.09	2.19	null	null		null	null		-9.17E+00	8.48E-02		-1.14E+00	5.70E-01		-2.06E+00	9.44E-05	Down	-1.05E+00	2.17E-02					Unigene10671_All//8.00E-24//DF464488				
Unigene10673_All	337	0.62	1.05	0.00	2.07	3.68	2.81	1.88	0.00	0.00	7.61E-01	5.57E-01		-9.28E+00	1.47E-01		8.30E-01	1.88E-01		4.44E-01	5.74E-01		-1.09E+01	1.24E-04	Down	-1.09E+01	7.13E-05	Down	Unigene10673_All//gi|27476088|gb|AA017019.1|//2.00E-10//Hypothetical protein [Oryza sativa Japonica Group]	Unigene10673_All//3.00E-10//AT2G22610| kinesin motor protein-related				GO:0000166//GO:0003774	nr +
Unigene106734_All	305	2.06	0.00	1.22	0.65	0.79	0.74	0.14	0.27	0.26	-1.10E+01	7.92E-04	Down	-7.52E-01	4.11E-01		2.75E-01	8.95E-01		1.81E-01	9.35E-01		9.84E-01	7.33E-01		9.14E-01	7.51E-01					Unigene106734_All//3.00E-07//DR462295				
Unigene106746_All	309	0.51	0.33	0.52	0.00	0.45	0.73	6.43	0.41	1.42	-6.31E-01	7.28E-01		2.53E-02	1.00E+00		8.80E+00	3.20E-01		9.51E+00	1.19E-01		-3.99E+00	1.09E-10	Down	-2.18E+00	1.75E-06	Down	Unigene106746_All//gi|84688912|gb|ABG61505.1|//4.00E-16//AGO4-2 [Nicotiana benthamiana]	Unigene106746_All//2.00E-12//AT5G21150| PAZ domain-containing protein / piwi domain-containing protein	Unigene106746_All//8.00E-70//gi|48807247|gb|CO108561.1|CO108561				nr -
Unigene106764_All	315	0.00	0.32	0.00	0.32	2.84	1.72	0.00	0.00	0.00	8.33E+00	3.90E-01		null	null		3.17E+00	8.78E-04	Up	2.44E+00	4.41E-02		null	null		null	null					Unigene106764_All//8.00E-05//AT4G10265| wound-responsive protein, putative	Unigene106764_All//1.00E-105//gi|109876398|gb|DW505572.1|DW505572				
Unigene106767_All	317	1.49	0.80	0.34	0.16	1.63	2.85	0.67	0.66	1.13	-8.94E-01	3.89E-01		-2.14E+00	1.03E-01		3.37E+00	1.82E-02		4.18E+00	1.95E-04	Up	-1.68E-02	1.02E+00		7.62E-01	5.00E-01		Unigene106767_All//gi|15228991|ref|NP_191228.1|//2.00E-17//CIP111 (CAM INTERACTING PROTEIN 111); ATPase/ calmodulin binding [Arabidopsis thaliana] >gi|9662988|emb|CAC00732.1| calmodulin-binding protein [Arabidopsis thaliana]	Unigene106767_All//8.00E-19//AT3G56690| CIP111 (CAM INTERACTING PROTEIN 111); ATPase/ calmodulin binding				nr -
Unigene106777_All	327	0.00	0.00	0.00	0.00	0.63	2.76	1.81	0.77	1.95	null	null		null	null		9.30E+00	1.57E-01		1.14E+01	2.07E-05	Up	-1.24E+00	1.54E-01		1.07E-01	9.02E-01		Unigene106777_All//gi|42565171|ref|NP_189132.2|//2.00E-17//DNA binding [Arabidopsis thaliana]	Unigene106777_All//8.00E-19//AT3G24880| DNA binding				nr +
Unigene10678_All	647	0.00	0.08	0.00	0.69	0.16	0.42	0.00	0.00	2.89	6.29E+00	6.22E-01		null	null		-2.12E+00	7.28E-02		-7.26E-01	5.33E-01		null	null		1.15E+01	1.95E-13	Up	Unigene10678_All//gi|87240526|gb|ABD32384.1|//7.00E-28//Peptidase A1, pepsin [Medicago truncatula]	Unigene10678_All//1.00E-16//AT1G03220| extracellular dermal glycoprotein, putative / EDGP, putative	Unigene10678_All//1.00E-135//TC176754			GO:0005618//GO:0006970//GO:0016020	nr -
Unigene10679_All	270	1.55	3.38	7.10	20.29	15.43	17.73	5.79	3.72	3.98	1.12E+00	1.30E-01		2.20E+00	8.21E-05	Up	-3.95E-01	1.23E-01		-1.95E-01	5.01E-01		-6.41E-01	1.82E-01		-5.40E-01	2.40E-01		Unigene10679_All//gi|147802546|emb|CAN77665.1|//4.00E-06//hypothetical protein [Vitis vinifera]		Unigene10679_All//2.00E-61//ES823904				nr +
Unigene106796_All	342	0.00	0.44	0.00	0.00	0.00	3.43	0.00	0.00	0.00	8.80E+00	2.37E-01		null	null		null	null		1.17E+01	5.32E-07	Up	null	null		null	null										ESTscan +
Unigene106799_All	346	0.00	0.00	0.00	0.00	0.00	3.13	0.00	0.00	0.00	null	null		null	null		null	null		1.16E+01	1.82E-06	Up	null	null		null	null		Unigene106799_All//gi|30696750|ref|NP_176463.2|//2.00E-07//invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana] >gi|6630459|gb|AAF19547.1|AC007190_15 F23N19.12 [Arabidopsis thaliana]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene10680_All	319	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.06	1.25	null	null		null	null		null	null		null	null		1.20E+01	3.67E-09	Up	1.03E+01	3.97E-03											
Unigene106801_All	346	0.00	1.76	1.23	0.58	0.30	7.70	0.12	0.00	0.46	1.08E+01	1.17E-03		1.03E+01	1.39E-02		-9.48E-01	5.88E-01		3.74E+00	1.56E-11	Up	-6.93E+00	6.63E-01		1.91E+00	3.78E-01		Unigene106801_All//gi|297807543|ref|XP_002871655.1|//5.00E-22//amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317492|gb|EFH47914.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata]	Unigene106801_All//9.00E-23//AT5G15240| amino acid transporter family protein	Unigene106801_All//5.00E-167//gi|48826851|gb|CO125241.1|CO125241				nr +
Unigene106810_All	358	7901.32	3489.26	7207.19	190.63	308.86	168.67	0.00	0.23	0.00	-1.18E+00	0.00E+00	Down	-1.33E-01	3.49E-47		6.96E-01	2.54E-51		-1.77E-01	6.91E-03		7.87E+00	4.03E-01		null	null		Unigene106810_All//gi|12620881|gb|AAG61120.1|//1.00E-65//ribulose-1,5-bisphosphate carboxylase/oxygenase activase 1 [Gossypium hirsutum]	Unigene106810_All//3.00E-54//AT2G39730| RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	Unigene106810_All//0.00E+00//EX168151				nr +
Unigene106812_All	362	0.00	2.24	0.00	0.00	0.57	2.62	0.82	0.35	0.99	1.11E+01	9.39E-05	Up	null	null		9.16E+00	1.57E-01		1.14E+01	1.13E-05	Up	-1.24E+00	3.73E-01		2.77E-01	7.88E-01		Unigene106812_All//gi|225465575|ref|XP_002263953.1|//5.00E-08//PREDICTED: hypothetical protein [Vitis vinifera] >gi|147865101|emb|CAN79390.1| hypothetical protein [Vitis vinifera]				ko03040|Spliceosome		nr -
Unigene10682_All	491	0.00	0.00	0.00	0.00	0.00	0.00	3.10	2.21	0.00	null	null		null	null		null	null		null	null		-4.86E-01	3.35E-01		-1.16E+01	2.88E-11	Down	Unigene10682_All//gi|15241051|ref|NP_198129.1|//2.00E-37//60S ribosomal protein L22 (RPL22C) [Arabidopsis thaliana] >gi|17865557|sp|Q9FE58.1|RL223_ARATH RecName: Full=60S ribosomal protein L22-3 >gi|11692938|gb|AAG40072.1|AF324721_1 TIG16 [Arabidopsis thaliana] >gi|21554057|gb|AAM63138.1| 60S ribosomal protein L22-like [Arabidopsis thaliana] >gi|27808502|gb|AAO24531.1| At5g27770 [Arabidopsis thaliana] >gi|110736618|dbj|BAF00273.1| 60S ribosomal protein L22 - like [Arabidopsis thaliana]	Unigene10682_All//1.00E-25//AT5G27770| 60S ribosomal protein L22 (RPL22C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene106820_All	371	0.00	0.00	0.00	0.00	0.00	0.37	8.66	0.79	1.07	null	null		null	null		null	null		8.51E+00	3.12E-01		-3.46E+00	3.09E-15	Down	-3.01E+00	5.32E-14	Down	Unigene106820_All//gi|1743354|emb|CAA71003.1|//6.00E-35//aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]	Unigene106820_All//3.00E-34//AT3G48000| ALDH2B4 (ALDEHYDE DEHYDROGENASE 2B4); 3-chloroallyl aldehyde dehydrogenase/ ATP binding / aldehyde dehydrogenase (NAD)	Unigene106820_All//4.00E-35//EG702325		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr -
Unigene106829_All	377	2.22	11.56	3.67	25.11	65.49	38.93	0.79	2.66	3.80	2.38E+00	1.47E-11	Up	7.26E-01	2.28E-01		1.38E+00	3.11E-35	Up	6.33E-01	9.30E-06		1.76E+00	7.67E-03		2.28E+00	4.94E-05	Up	Unigene106829_All//gi|15241290|ref|NP_197519.1|//3.00E-23//binding [Arabidopsis thaliana]	Unigene106829_All//1.00E-24//AT5G20190| binding	Unigene106829_All//5.00E-84//TC165464				nr -
Unigene106832_All	387	0.14	0.00	0.00	0.00	0.00	2.45	0.00	0.00	0.10	-7.08E+00	6.20E-01		-7.08E+00	6.33E-01		null	null		1.13E+01	1.13E-05	Up	null	null		6.69E+00	6.48E-01		Unigene106832_All//gi|5231127|gb|AAD41083.1|AF151961_1|//5.00E-61//1-aminocyclopropane-1-carboxylic acid synthase [Vigna radiata]	Unigene106832_All//9.00E-55//AT3G49700| ACS9 (1-AMINACYCLOPROPANE-1-CARBOXYLATE SYNTHASE 9); 1-aminocyclopropane-1-carboxylate synthase			ko00270|Cysteine and methionine metabolism		nr +
Unigene106834_All	388	0.00	0.52	0.00	0.51	1.33	3.96	0.44	0.32	0.00	9.03E+00	1.37E-01		null	null		1.37E+00	2.26E-01		2.95E+00	1.22E-05	Up	-4.32E-01	7.94E-01		-8.77E+00	1.09E-01		Unigene106834_All//gi|3121837|sp|O04940.1|CDS1_SOLTU//1.00E-53//RecName: Full=Phosphatidate cytidylyltransferase; AltName: Full=CDP-diglyceride pyrophosphorylase; AltName: Full=CDP-diglyceride synthase; AltName: Full=CDP-diacylglycerol synthase; Short=CDS; AltName: Full=CTP:phosphatidate cytidylyltransferase; AltName: Full=CDP-DG synthase; AltName: Full=CDP-DAG synthase >gi|2182104|emb|CAA63004.1| CDP-diacylglycerol synthetase [Solanum tuberosum]	Unigene106834_All//7.00E-50//AT4G22340| phosphatidate cytidylyltransferase, putative / CDP-diglyceride synthetase, putative	Unigene106834_All//1.00E-103//CO498072		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism		nr -
Unigene106836_All	389	0.81	0.00	1.10	0.38	1.68	3.25	0.00	0.11	0.10	-9.66E+00	3.67E-02		4.40E-01	6.77E-01		2.13E+00	3.78E-02		3.08E+00	6.55E-05	Up	6.75E+00	6.38E-01		6.68E+00	6.48E-01										
Unigene106838_All	395	0.00	1.67	0.00	1.01	0.96	2.97	1.50	1.38	0.81	1.07E+01	6.26E-04	Up	null	null		-7.32E-02	9.26E-01		1.56E+00	1.95E-02		-1.24E-01	8.84E-01		-8.93E-01	2.72E-01					Unigene106838_All//5.00E-07//TC140528				
Unigene10684_All	500	0.00	0.00	0.00	0.00	0.00	0.00	1.86	2.84	0.16	null	null		null	null		null	null		null	null		6.11E-01	2.36E-01		-3.54E+00	3.97E-05	Down	Unigene10684_All//gi|145353927|ref|XP_001421249.1|//1.00E-07//predicted protein [Ostreococcus lucimarinus CCE9901] >gi|145354001|ref|XP_001421285.1| predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144581486|gb|ABO99542.1| predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144581522|gb|ABO99578.1| predicted protein [Ostreococcus lucimarinus CCE9901]						nr +
Unigene106841_All	398	1.84	0.00	0.13	0.38	0.61	0.57	0.64	0.00	0.20	-1.08E+01	2.11E-04	Down	-3.78E+00	2.79E-03		6.90E-01	7.32E-01		5.96E-01	7.22E-01		-9.32E+00	4.06E-02		-1.67E+00	2.57E-01		Unigene106841_All//gi|52789958|gb|AAU87582.1|//7.00E-60//MADS9 protein [Gossypium hirsutum]	Unigene106841_All//6.00E-14//AT5G13790| AGL15 (AGAMOUS-LIKE 15); DNA binding / transcription factor	Unigene106841_All//2.00E-154//TC129654	MADS			nr -
Unigene106842_All	398	0.00	0.00	0.27	0.00	0.00	10.89	0.00	0.00	0.00	null	null		8.06E+00	4.02E-01		null	null		1.34E+01	3.67E-26	Up	null	null		null	null		Unigene106842_All//sp|Q16927|VIT1_AEDAE//2.00E-17//Vitellogenin-A1 OS=Aedes aegypti GN=VGA1 PE=1 SV=2						swissprot -

Unigene106844_All	406	0.52	0.50	0.52	0.12	0.59	2.89	1.15	0.21	1.57	-4.64E-02	9.89E-01		2.52E-02	1.00E+00		2.27E+00	3.05E-01		4.56E+00	6.41E-06	Up	-2.48E+00	3.38E-02		4.55E-01	5.78E-01		Unigene106844_All//gi|297841629|ref|XP_002888696.1|//4.00E-38//prolyl oligopeptidase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334537|gb|EFH64955.1| prolyl oligopeptidase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene106844_All//4.00E-37//AT1G69020| prolyl oligopeptidase family protein				nr -
Unigene106847_All	411	0.00	0.00	0.00	0.12	0.34	2.09	0.51	0.71	0.29	null	null		null	null		1.47E+00	6.20E-01		4.11E+00	3.41E-04	Up	4.69E-01	7.07E-01		-8.23E-01	6.00E-01		Unigene106847_All//gi|115488208|ref|NP_001066591.1|//1.00E-10//Os12g0288000 [Oryza sativa Japonica Group] >gi|77534969|gb|ABA97765.1| Integral membrane protein DUF6 containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113649098|dbj|BAF29610.1| Os12g0288000 [Oryza sativa Japonica Group]	Unigene106847_All//3.00E-08//AT5G64700| nodulin MtN21 family protein	Unigene106847_All//2.00E-34//TC144438			nr -
Unigene106850_All	418	2.38	2007.38	1212.27	0.36	0.33	10.16	0.51	0.20	0.10	9.72E+00	0.00E+00	Up	8.99E+00	0.00E+00	Up	-1.18E-01	9.11E-01		4.83E+00	1.91E-21	Up	-1.34E+00	4.31E-01		-2.41E+00	1.95E-01					Unigene106850_All//9.00E-21//TC149074				
Unigene106851_All	421	0.75	0.00	0.00	0.00	0.00	7.94	0.00	0.10	0.28	-9.54E+00	3.67E-02		-9.54E+00	4.93E-02		null	null		1.30E+01	4.33E-20	Up	6.63E+00	6.38E-01		8.15E+00	2.44E-01		Unigene106851_All//gi|224127212|ref|XP_002320015.1|//8.00E-59//1-aminocyclopropane-1-carboxylate [Populus trichocarpa] >gi|222860788|gb|EEE98330.1| 1-aminocyclopropane-1-carboxylate [Populus trichocarpa]	Unigene106851_All//2.00E-57//AT5G65800| ACS5 (ACC SYNTHASE 5); 1-aminocyclopropane-1-carboxylate synthase			ko00270|Cysteine and methionine metabolism	nr -
Unigene106852_All	422	0.99	0.48	3.91	0.35	0.57	0.43	0.00	0.00	0.00	-1.05E+00	3.66E-01		1.98E+00	8.06E-04	Up	6.90E-01	7.32E-01		2.74E-01	9.06E-01		null	null		null	null		Unigene106852_All//gi|291506702|gb|ADE08783.1|//1.00E-29//phytochrome interacting factor 4 [Arabidopsis thaliana] >gi|291506704|gb|ADE08784.1| phytochrome interacting factor 4 [Arabidopsis thaliana] >gi|291506706|gb|ADE08785.1| phytochrome interacting factor 4 [Arabidopsis thaliana] >gi|291506708|gb|ADE08786.1| phytochrome interacting factor 4 [Arabidopsis thaliana] >gi|291506710|gb|ADE08787.1| phytochrome interacting factor 4 [Arabidopsis thaliana] >gi|291506712|gb|ADE08788.1| phytochrome interacting factor 4 [Arabidopsis thaliana]	Unigene106852_All//8.00E-29//AT2G43010| PIF4 (phytochrome interacting factor 4); DNA binding / protein binding / transcription factor	Unigene106852_All//5.00E-10//TC178874	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	nr -
Unigene106856_All	432	0.00	0.23	0.49	0.92	1.91	5.85	0.00	0.00	0.00	7.87E+00	3.90E-01		8.95E+00	1.42E-01		1.05E+00	1.99E-01		2.67E+00	3.65E-08	Up	null	null		null	null		Unigene106856_All//gi|297850352|ref|XP_002893057.1|//1.00E-33//S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297338899|gb|EFH69316.1| S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene106856_All//1.00E-33//AT1G19640| JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate O-methyltransferase			ko00592|alpha-Linolenic acid metabolism	nr +
Unigene106857_All	434	0.00	0.23	0.74	0.69	0.00	4.16	0.19	0.29	0.00	7.87E+00	3.90E-01		9.52E+00	4.54E-02		-9.43E+00	2.02E-02		2.60E+00	7.99E-06	Up	5.69E-01	7.83E-01		-7.61E+00	3.61E-01		Unigene106857_All//gi|21536895|gb|AAM61227.1|//3.00E-64//amino acid transport protein AAP2 [Arabidopsis thaliana]	Unigene106857_All//2.00E-65//AT5G09220| AAP2 (AMINO ACID PERMEASE 2); amino acid transmembrane transporter	Unigene106857_All//0.00E+00//gi|48814445|gb|CO115758.1|CO115758			nr -
Unigene106865_All	460	2.27	0.99	0.23	0.65	0.97	3.73	0.00	0.36	0.09	-1.20E+00	7.76E-02		-3.30E+00	4.59E-04	Down	5.83E-01	6.26E-01		2.52E+00	2.09E-05	Up	8.51E+00	1.39E-01		6.44E+00	6.48E-01									
Unigene106868_All	472	0.00	1.83	0.45	1.27	0.80	0.29	0.09	0.27	0.51	1.08E+01	4.95E-05	Up	8.82E+00	1.42E-01		-6.58E-01	4.78E-01		-2.14E+00	4.39E-02		1.57E+00	5.46E-01		2.50E+00	1.59E-01					Unigene106868_All//0.00E+00//gi|164288680|gb|ES800533.1|ES800533				ESTscan -
Unigene106869_All	492	0.43	5.87	2.06	0.20	0.91	4.31	0.17	0.34	0.32	3.79E+00	5.53E-12	Up	2.27E+00	5.77E-03		2.17E+00	1.06E-01		4.41E+00	2.73E-10	Up	9.83E-01	6.35E-01		9.14E-01	6.25E-01		Unigene106869_All//gi|292668975|gb|ADE41142.1|//6.00E-42//AP2 domain class transcription factor [Malus x domestica]	Unigene106869_All//3.00E-24//AT5G11590| TINY2 (TINY2); DNA binding / transcription factor	Unigene106869_All//0.00E+00//TC178420	AP2-EREBP		nr +
Unigene10687_All	465	0.00	3.92	3.78	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.14E-10	Up	1.19E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene10687_All//gi|15021748|gb|AAK77901.1|AF397029_1|//3.00E-15//root nodule extensin [Pisum sativum]				ko03040|Spliceosome//ko04144|Endocytosis	nr +
Unigene106870_All	507	0.00	0.00	0.00	0.00	0.00	1.78	0.00	0.00	0.00	null	null		null	null		null	null		1.08E+01	2.07E-05	Up	null	null		null	null									
Unigene106871_All	507	0.00	0.00	0.00	0.00	0.27	3.83	0.00	0.00	0.00	null	null		null	null		8.09E+00	3.20E-01		1.19E+01	1.36E-11	Up	null	null		null	null		Unigene106871_All//sp|P08171|EST6_DROME//9.00E-09//Esterase-6 OS=Drosophila melanogaster GN=Est-6 PE=1 SV=2						swissprot +
Unigene106875_All	543	0.29	0.09	0.00	0.28	0.06	3.41	0.16	0.23	0.15	-1.63E+00	4.89E-01		-8.18E+00	2.46E-01		-2.12E+00	3.87E-01		3.63E+00	6.06E-08	Up	5.69E-01	7.83E-01		-8.59E-02	9.74E-01		Unigene106875_All//gi|224053975|ref|XP_002298066.1|//1.00E-38//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222845324|gb|EEE82871.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene106875_All//2.00E-26//AT1G12630| DNA binding / transcription activator/ transcription factor	Unigene106875_All//8.00E-130//TC163291	AP2-EREBP		nr -
Unigene106876_All	573	0.00	0.18	0.00	0.00	0.12	7.09	0.00	0.00	0.00	7.47E+00	3.90E-01		null	null		6.91E+00	6.15E-01		1.28E+01	1.68E-24	Up	null	null		null	null		Unigene106876_All//sp|Q05808|VIT_ANTGR//3.00E-31//Vitellogenin OS=Anthonomus grandis GN=VTG PE=4 SV=1						swissprot +
Unigene106877_All	600	0.17	1.35	0.62	0.66	1.89	3.76	0.00	0.00	0.00	2.95E+00	3.29E-03		1.83E+00	2.13E-01		1.51E+00	2.36E-02		2.50E+00	6.84E-07	Up	null	null		null	null		Unigene106877_All//gi|87241322|gb|ABD33180.1|//5.00E-29//TGF-beta receptor, type I/II extracellular region [Medicago truncatula]	Unigene106877_All//1.00E-27//AT1G33440| proton-dependent oligopeptide transport (POT) family protein	Unigene106877_All//0.00E+00//C0119167			nr +
Unigene106882_All	446	0.00	0.00	0.00	0.00	0.00	0.00	21.23	1.31	1.07	null	null		null	null		null	null		null	null		-4.02E+00	2.42E-49	Down	-4.31E+00	1.36E-53	Down								
Unigene106883_All	232	0.00	0.00	1.84	0.21	0.00	0.00	3.28	2.16	8.59	null	null		1.08E+01	1.38E-02		-7.75E+00	5.64E-01		-7.75E+00	6.45E-01		-6.02E-01	4.12E-01		1.39E+00	7.70E-04	Up	Unigene106883_All//gi|15219445|ref|NP_178085.1|//7.00E-20//RF01 (RESISTANCE TO FUSARIUM OXYSPORUM 1); kinase [Arabidopsis thaliana] >gi|75247675|sp|Q8RY17.1|WAKL1_ARATH RecName: Full=Wall-associated receptor kinase-like 22; Flags: Precursor >gi|19310447|gb|AAL84959.1| At1g79670/F20B17_27 [Arabidopsis thaliana]	Unigene106883_All//3.00E-21//AT1G79670| RF01 (RESISTANCE TO FUSARIUM OXYSPORUM 1); kinase	Unigene106883_All//1.00E-43//DT462731		ko04626|Plant-pathogen interaction	nr -
Unigene106884_All	641	0.00	0.00	0.00	0.00	0.00	0.00	2.84	0.72	0.44	null	null		null	null		null	null		null	null		-1.98E+00	3.39E-05	Down	-2.70E+00	1.86E-07	Down	Unigene106884_All//gi|157011451|gb|ABV00887.1|//1.00E-100//actin [Rhodomonas sp. CCMP768]	Unigene106884_All//2.00E-97//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene106884_All//4.00E-33//gi|5045286|gb|AI726434.1|AI726434			nr -
Unigene106886_All	379	0.00	0.00	0.00	0.00	0.00	0.00	1.78	0.00	0.00	null	null		null	null		null	null		null	null		-1.08E+01	6.35E-05	Down	-1.08E+01	3.57E-05	Down	Unigene106886_All//gi|253998300|ref|YP_003050363.1|//1.00E-08//cold-shock DNA-binding domain protein [Methylovorus sp. SIP3-4] >gi|253984979|gb|ACT49836.1| cold-shock DNA-binding domain protein [Methylovorus sp. SIP3-4]	Unigene106886_All//4.00E-07//AT4G36020| CSDP1 (cold shock domain protein 1); RNA binding / double-stranded DNA binding / nucleic acid binding / single-stranded DNA binding		CSD		nr +
Unigene106887_All	292	0.00	0.00	0.00	0.00	0.00	0.00	2.75	1.00	0.00	null	null		null	null		null	null		null	null		-1.46E+00	4.65E-02		-1.14E+01	4.43E-06	Down								
Unigene106888_All	595	0.00	0.00	0.00	0.00	0.00	0.00	5.12	0.56	0.20	null	null		null	null		null	null		null	null		-3.19E+00	1.70E-13	Down	-4.67E+00	1.91E-18	Down	Unigene106888_All//gi|300266840|gb|EFJ51026.1|//8.00E-46//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene106888_All//5.00E-41//AT3G02560| 40S ribosomal protein S7 (RPS7B)			ko03010|Ribosome	nr -
Unigene10689_All	443	1.89	1.14	0.48	1.24	0.62	1.63	2.58	0.38	1.08	-7.24E-01	3.48E-01		-1.97E+00	2.71E-02		-9.92E-01	3.13E-01		3.99E-01	6.52E-01		-2.77E+00	7.62E-05	Down	-1.26E+00	2.42E-02									
Unigene106890_All	485	0.00	0.00	0.00	0.00	0.00	0.00	2.44	0.17	0.00	null	null		null	null		null	null		null	null		-3.82E+00	2.12E-06	Down	-1.13E+01	8.15E-09	Down								
Unigene106892_All	430	0.00	0.00	0.00	0.00	0.00	0.00	6.29	1.07	0.56	null	null		null	null		null	null		null	null		-2.56E+00	9.03E-10	Down	-3.50E+00	1.50E-13	Down								ESTscan -
Unigene106893_All	807	0.00	0.00	0.00	0.00	0.00	0.00	3.41	0.67	0.25	null	null		null	null		null	null		null	null		-2.34E+00	5.13E-09	Down	-3.79E+00	1.33E-14	Down	Unigene106893_All//gi|300267515|gb|EFJ51698.1|//4.00E-79//ADP/ATP carrier protein, probably mitochondrial [Volvox carteri f. nagariensis]	Unigene106893_All//2.00E-72//AT4G28390| AAC3 (ADP/ATP CARRIER 3); ATP:ADP antiporter/ binding	Unigene106893_All//1.00E-06//EV483520			nr -
Unigene106894_All	268	0.00	0.00	0.00	0.00	0.00	0.00	2.84	0.31	0.00	null	null		null	null		null	null		null	null		-3.19E+00	7.93E-04	Down	-1.15E+01	8.89E-06	Down	Unigene106894_All//gi|298709974|emb|CBJ31696.1|//2.00E-27//Ribosomal protein S23, component of cytosolic 80S ribosome and 40S small subunit [Ectocarpus siliculosus]	Unigene106894_All//4.00E-23//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene106894_All//2.00E-20//CD486290		ko03010|Ribosome	nr -
Unigene106896_All	205	0.00	0.00	0.00	0.00	0.00	0.00	3.51	0.20	0.00	null	null		null	null		null	null		null	null		-4.10E+00	2.92E-04	Down	-1.18E+01	1.78E-05	Down	Unigene106896_All//gi|116059767|emb|CAL55474.1|//6.00E-22//ribosomal protein L18 (ISS) [Ostreococcus tauri]	Unigene106896_All//1.00E-19//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome			ko03010|Ribosome	nr -
Unigene106898_All	399	0.00	0.00	0.00	0.00	0.00	0.00	5.83	0.21	0.10	null	null		null	null		null	null		null	null		-4.80E+00	7.37E-14	Down	-5.87E+00	1.13E-15	Down	Unigene106898_All//gi|32400871|gb|AAP80667.1|AF179048_1|//5.00E-55//ribosomal Pr 117 [Triticum aestivum]	Unigene106898_All//4.00E-56//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene106898_All//5.00E-13//TC156592		ko03010|Ribosome	nr -
Unigene10690_All	593	0.00	4.53	1.62	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.81E-15	Up	1.07E+01	2.46E-05	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene106901_All	269	0.00	0.00	0.00	0.00	0.00	0.00	2.67	0.47	0.00	null	null		null	null		null	null		null	null		-2.52E+00	4.69E-03		-1.14E+01	1.78E-05	Down								ESTscan +
Unigene106902_All	848	0.00	0.00	0.00	0.00	0.24	0.05	11.77	0.59	0.52	null	null		null	null		7.93E+00	1.57E-01		5.74E+00	7.03E-01		-4.31E+00	1.38E-54	Down	-4.51E+00	4.25E-58	Down	Unigene106902_All//gi|117622276|gb|ABK51384.1|//1.00E-08//IMP dehydrogenase/GMP reductase [Hevea brasiliensis]					nr -
Unigene106903_All	577	0.00	0.00	0.00	0.00	0.00	0.00	3.30	0.14	0.00	null	null		null	null		null	null		null	null		-4.51E+00	4.75E-11	Down	-1.17E+01	4.91E-14	Down	Unigene106903_All//gi|83582438|emb|CAJ45370.1|//3.00E-65//40S ribosomal protein S5 [Chlamydomonas sp. ICE-L]	Unigene106903_All//3.00E-64//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome			ko03010|Ribosome	nr +
Unigene106904_All	531	0.00	0.00	0.00	0.00	0.00	0.00	3.34	0.08	0.08	null	null		null	null		null	null		null	null		-5.41E+00	2.97E-11	Down	-5.48E+00	8.92E-12	Down								ESTscan -
Unigene106907_All	383	1.09	2.12	2.64	2.99	2.97	2.00	2.76	6.88	2.08	9.54E-01	2.26E-01		1.27E+00	8.36E-02		-1.19E-02	9.64E-01		-5.78E-01	3.98E-01		1.32E+00	2.33E-04	Up	-4.08E-01	4.85E-01					Unigene106907_All//2.00E-101//TC162510				
Unigene106908_All	505	0.00	0.00	0.00	0.00	0.00	0.00	2.68	1.57	0.39	null	null		null	null		null	null		null	null		-7.69E-01	1.39E-01		-2.76E+00	7.51E-06	Down	Unigene106908_All//gi|34761728|gb|AAQ82037.1|//3.00E-15//gag/pol polyprotein [Pisum sativum]		Unigene106908_All//3.00E-36//FL576545			nr +
Unigene106909_All	693	0.00	0.00	0.00	0.00	0.00	0.00	2.38	0.24	0.00	null	null		null	null		null	null		null	null		-3.30E+00	8.31E-08	Down	-1.12E+01	3.45E-12	Down								ESTscan -
Unigene106911_All	403	0.00	0.25	0.00	0.00	0.26	0.34	55.81	46.15	417.66	7.97E+00	3.90E-01		null	null		8.00E+00	4.58E-01		8.39E+00	3.12E-01		-2.74E-01	9.77E-03		2.90E+00	0.00E+00	Up	Unigene106911_All//gi|3970689|emb|CAA77191.1|//1.00E-36//(+)-delta-cadinene synthase [Gossypium arboreum]	Unigene106911_All//7.00E-13//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene106911_All//2.00E-74//gi|84158582|gb|DN827629.1|DN827629		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis	nr -
Unigene106913_All	772	0.00	0.00	0.00	0.00	0.00	0.00	7.23	0.43	0.36	null	null		null	null		null	null		null	null		-4.06E+00	1.68E-29	Down	-4.32E+00	7.14E-32	Down	Unigene106913_All//gi|192910762|gb|ACF06489.1|//5.00E-68//ribosomal protein L10a [Elaeis guineensis]	Unigene106913_All//1.00E-61//AT1G08360| 60S ribosomal protein L10A (RPL10aA)	Unigene106913_All//6.00E-11//CD486329		ko03010|Ribosome	nr +

Unigene106914_All	597	0.00	0.00	0.00	0.00	0.00	0.00	5.03	0.00	0.40	null	null		null	null		null	null		null	null		-1.23E+01	3.14E-21	Down	-3.65E+00	1.83E-15	Down	Unigene106914_All//gi|298704815|emb|CBJ48963.1|/8.00E-74//Arf1, ARF family GTPase [Ectocarpus siliculosus]	Unigene106914_All//4.00E-72//AT3G62290| ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding	Unigene106914_All//2.00E-41//gi|78322862|gb|DT543136.1|DT543136				nr -
Unigene106925_All	237	0.00	0.00	0.00	0.00	0.00	0.00	2.14	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	8.91E-04	Down	-1.11E+01	5.56E-04	Down									
Unigene106929_All	367	0.00	0.00	0.00	0.00	0.00	0.00	2.76	1.03	0.22	null	null		null	null		null	null		null	null		-1.43E+00	2.36E-02	Down	-3.67E+00	1.15E-05	Down									
Unigene106932_All	383	0.00	0.26	0.00	0.00	0.00	0.00	1.77	0.11	0.21	8.05E+00	3.90E-01		null	null		null	null		null	null		-4.02E+00	5.36E-04	Down	-3.09E+00	1.45E-03										
Unigene106935_All	578	0.00	0.00	0.00	0.00	0.00	0.00	1.98	1.01	0.07	null	null		null	null		null	null		null	null		-9.64E-01	9.33E-02		-4.84E+00	2.34E-07	Down									
Unigene106940_All	361	0.58	0.00	0.00	0.00	0.00	0.00	7.26	1.62	7.06	-9.18E+00	1.23E-01		-9.18E+00	1.47E-01		null	null		-2.16E+00	6.42E-08	Down	-4.00E-02	9.23E-01													
Unigene106943_All	433	0.00	0.35	0.37	1.15	0.16	0.21	2.05	0.48	0.18	8.46E+00	2.27E-01		8.53E+00	2.40E-01		-2.88E+00	1.78E-02		-2.46E+00	4.83E-02		-2.09E+00	4.71E-03		-3.48E+00	7.34E-05	Down									
Unigene106955_All	265	0.00	6.50	3.22	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	8.00E-10	Up	1.17E+01	9.03E-05	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene106956_All	400	0.00	0.00	0.00	0.00	0.00	0.00	2.11	0.84	0.10	null	null		null	null		null	null		null	null		-1.34E+00	5.68E-02		-4.41E+00	2.37E-05	Down									ESTscan +
Unigene106957_All	596	0.00	0.00	0.00	0.00	0.00	0.00	2.06	2.17	0.00	null	null		null	null		null	null		null	null		7.95E-02	8.90E-01		-1.10E+01	4.03E-09	Down	Unigene106957_All//gi|300266545|gb|EFJ50732.1|//9.00E-54//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene106957_All//3.00E-42//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene106959_All	1475	0.00	0.00	0.00	0.00	0.00	0.00	6.36	5.41	0.35	null	null		null	null		null	null		null	null		-2.34E-01	2.03E-01		-4.18E+00	4.76E-52	Down	Unigene106959_All//gi|226347409|gb|ACO50115.1|//0.00E+00//elongation factor 1 alpha [Peranema trichophorum]	Unigene106959_All//1.00E-130//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene106959_All//1.00E-72//TC166357				nr -
Unigene106696_All	451	0.00	0.00	0.00	0.00	0.00	0.00	2.81	2.22	0.35	null	null		null	null		null	null		null	null		-3.39E-01	5.58E-01		-2.99E+00	6.36E-06	Down	Unigene10696_All//gi|167859793|gb|ACA04850.1|//7.00E-14//senescence-associated protein [Picea abies]		Unigene10696_All//4.00E-17//gi|84158108|gb|DN827155.1|DN827155				nr +
Unigene106972_All	270	0.00	0.00	0.00	5.90	2.17	1.51	30.85	2.48	23.76	null	null		null	null		-1.45E+00	4.07E-03		-1.97E+00	4.88E-04	Down	-3.64E+00	2.76E-40	Down	-3.77E-01	3.26E-02					Unigene106972_All//3.00E-47//ES827343				
Unigene106979_All	236	0.89	0.86	1.35	2.53	2.19	2.87	12.36	145.40	21.44	-4.63E-02	9.89E-01		6.10E-01	6.25E-01		-2.11E-01	8.23E-01		1.81E-01	8.45E-01		3.56E+00	9.98E-161	Up	7.94E-01	5.98E-04		Unigene106979_All//gi|23978432|dbj|BAC21263.1|//7.00E-28//glutathione S-transferase [Cucurbita maxima]	Unigene106979_All//1.00E-20//AT2G29450| ATGSTU5 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 5); glutathione binding / glutathione transferase	Unigene106979_All//2.00E-69//gi|62295949|gb|DN779339.1|DN779339		ko00480|Glutathione metabolism	GO:0016765//GO:0016846//GO:0044424	nr +
Unigene106981_All	679	0.00	0.00	0.00	0.00	0.00	0.00	3.30	0.43	0.18	null	null		null	null		null	null		null	null		-2.94E+00	2.19E-09	Down	-4.23E+00	6.02E-13	Down	Unigene106981_All//gi|226500076|ref|NP_001150681.1|/3.00E-17//LOC100284314 [Zea mays] >gi|195641032|gb|ACG39984.1| zinc finger protein hangover [Zea mays]				ko04120|Ubiquitin mediated proteolysis		nr -
Unigene106982_All	799	0.00	0.00	0.00	0.00	0.13	0.00	0.32	0.68	1.65	null	null		null	null		7.01E+00	4.58E-01		null	null		1.10E+00	2.36E-01		2.37E+00	7.20E-05	Up	Unigene106982_All//gi|224074393|ref|XP_002304363.1|/5.00E-67//acyl:coa ligase [Populus trichocarpa] >gi|222841795|gb|EEE79342.1| acyl:coa ligase [Populus trichocarpa]	Unigene106982_All//1.00E-39//AT4G19010| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene106982_All//1.00E-163//gi|13352404|gb|BG442752.1|BG442752		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0016405	nr -
Unigene106986_All	288	0.00	0.00	0.00	0.00	0.00	0.00	3.38	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	5.84E-07	Down	-1.17E+01	2.72E-07	Down									
Unigene106989_All	288	0.00	0.00	0.00	0.00	0.00	0.00	3.08	0.44	0.00	null	null		null	null		null	null		null	null		-2.82E+00	5.65E-04	Down	-1.16E+01	1.10E-06	Down	Unigene106989_All//gi|73761683|gb|AAZ83341.1|//3.00E-33//ubiquitin extension protein [Gossypium hirsutum]	Unigene106989_All//6.00E-19//AT3G62250| UBQ5 (ubiquitin 5); protein binding / structural constituent of ribosome	Unigene106989_All//1.00E-09//gi|164316986|gb|EV492026.1|EV492026		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0010467//GO:0015935//GO:0016567//GO:0019941	nr +
Unigene106699_All	274	0.19	9.06	0.78	0.18	0.88	0.49	0.31	0.15	1.02	5.57E+00	9.50E-13	Up	2.03E+00	3.62E-01		2.27E+00	3.05E-01		1.44E+00	6.39E-01		-1.02E+00	7.26E-01		1.72E+00	2.30E-01					Unigene10699_All//3.00E-29//CO111688				
Unigene1070_All	1487	10.56	4.97	8.49	12.23	13.94	15.22	6.20	6.97	14.57	-1.09E+00	1.41E-13	Down	-3.15E-01	3.77E-02		1.89E-01	1.51E-01		3.16E-01	6.81E-03		1.69E-01	3.57E-01		1.23E+00	5.20E-28	Up	Unigene1070_All//gi|90399346|emb|CAH68425.1|//2.00E-93//H0811D08.10 [Oryza sativa (indica cultivar-group)]	Unigene1070_All//1.00E-61//AT5G10790| UBP22 (UBIQUITIN-SPECIFIC PROTEASE 22); ubiquitin thiolesterase/ ubiquitin-specific protease/ zinc ion binding	Unigene1070_All//0.00E+00//gi|78338363|gb|DT588637.1|DT588637			GO:0008233//GO:0043231	nr -
Unigene10701_All	477	1.97	0.21	0.89	4.70	3.75	4.73	0.18	0.35	1.00	-3.22E+00	6.77E-04	Down	-1.14E+00	1.38E-01		-3.24E-01	4.77E-01		1.06E-02	9.82E-01		9.83E-01	6.35E-01		2.50E+00	2.52E-02		Unigene10701_All//gi|21322711|emb|CAD22154.1|//2.00E-40//pherophorin-dz1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome		nr -
Unigene107016_All	238	0.00	0.00	0.00	0.00	0.00	0.00	2.13	0.00	0.33	null	null		null	null		null	null		null	null		-1.11E+01	8.91E-04	Down	-2.67E+00	1.37E-02										
Unigene107032_All	390	0.00	0.00	0.00	0.00	0.00	0.00	1.73	1.18	0.00	null	null		null	null		null	null		null	null		-5.57E-01	4.89E-01		-1.08E+01	3.57E-05	Down	Unigene107032_All//gi|226462262|gb|EEH59554.1|//2.00E-32//60S ribosomal protein L35 [Micromonas pusilla CCMP1545]	Unigene107032_All//3.00E-32//AT5G02610| 60S ribosomal protein L35 (RPL35D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene10704_All	297	0.00	0.68	0.00	0.00	0.00	0.15	0.00	1.97	2.68	9.41E+00	1.37E-01		null	null		null	null		7.25E+00	7.03E-01		1.09E+01	2.81E-04	Up	1.14E+01	7.36E-06	Up									
Unigene107043_All	300	0.00	0.00	0.00	0.00	0.11	0.00	2.68	0.14	0.00	null	null		null	null		6.84E+00	8.39E-01		null	null		-4.26E+00	8.48E-05	Down	-1.14E+01	4.43E-06	Down	Unigene107043_All//gi|44917549|gb|AAS49099.1|//2.00E-13//At2g37380 [Arabidopsis thaliana]	Unigene107043_All//2.00E-16//AT2G39370| unknown protein	Unigene107043_All//4.00E-10//TC160952				nr +
Unigene107048_All	552	0.00	0.00	0.00	0.00	0.00	0.00	2.53	0.08	0.14	null	null		null	null		null	null		null	null		-5.06E+00	1.10E-08	Down	-4.13E+00	3.70E-08	Down									
Unigene107050_All	326	0.48	0.78	0.00	0.46	0.63	0.83	2.46	0.00	1.10	6.91E-01	6.27E-01		-8.91E+00	2.46E-01		4.67E-01	8.26E-01		8.59E-01	6.31E-01		-1.13E+01	8.58E-06	Down	-1.16E+00	8.85E-02		Unigene107050_All//gi|297834848|ref|XP_002885306.1|//2.00E-48//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331146|gb|EFH61565.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene107050_All//3.00E-40//AT3G19300| protein kinase family protein	Unigene107050_All//1.00E-179//ES800996		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016020//GO:0031410//GO:0032559	nr +
Unigene107061_All	257	0.00	0.00	0.00	0.00	0.00	0.00	2.14	0.00	0.31	null	null		null	null		null	null		null	null		-1.11E+01	4.62E-04	Down	-2.79E+00	7.97E-03		Unigene107061_All//gi|145345768|ref|XP_001417372.1|//2.00E-20//Ribosomal protein S17, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901] >gi|145375599|gb|ABO95665.1| Ribosomal protein S17, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901]	Unigene107061_All//1.00E-20//AT5G04800| 40S ribosomal protein S17 (RPS17D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene107064_All	497	0.00	0.00	0.00	0.00	0.00	0.00	2.64	0.00	0.08	null	null		null	null		null	null		null	null		-1.14E+01	2.56E-09	Down	-5.04E+00	1.60E-08	Down	Unigene107064_All//gi|209967441|gb|ACJ02349.1|//2.00E-21//60S ribosomal protein L35a [Vernicia fordii]	Unigene107064_All//2.00E-20//AT1G41880| 60S ribosomal protein L35a (RPL35aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +
Unigene107068_All	207	0.00	0.00	0.00	0.00	0.00	0.00	3.06	0.20	0.00	null	null		null	null		null	null		null	null		-3.92E+00	9.81E-04	Down	-1.16E+01	7.13E-05	Down	Unigene107068_All//gi|126566038|gb|AB020848.1|//1.00E-07//cytochrome P450-like TBP protein [Lilium longiflorum]		Unigene107068_All//9.00E-07//EV495741				nr -
Unigene10707_All	278	0.38	0.00	1.53	2.87	0.12	0.16	0.30	0.00	0.00	-8.56E+00	3.76E-01		2.03E+00	1.40E-01		-4.53E+00	6.06E-05	Down	-4.14E+00	4.13E-04	Down	-8.25E+00	4.07E-01		-8.25E+00	3.61E-01									
Unigene107071_All	284	104.64	101.70	87.56	4.03	6.79	10.02	2.38	0.74	1.26	-4.12E-02	7.09E-01		-2.57E-01	1.57E-02		7.51E-01	1.14E-01		1.31E+00	5.61E-04	Up	-1.69E+00	4.19E-02		-9.16E-01	2.21E-01		Unigene107071_All//gi|55168340|gb|AAV44205.1|//7.00E-10//unknow protein [Oryza sativa Japonica Group]		Unigene107071_All//1.00E-80//TC147077				nr -
Unigene107076_All	499	0.00	0.00	0.00	0.00	0.00	0.00	1.27	1.93	0.00	null	null		null	null		null	null		null	null		6.00E-01	3.67E-01		-1.03E+01	7.12E-05	Down	Unigene107076_All//gi|212275977|ref|NP_001130697.1|//3.00E-16//hypothetical protein LOC100191800 [Zea mays] >gi|194689862|gb|ACF79015.1| unknown [Zea mays]						nr -
Unigene10708_All	358	17.10	8.35	11.90	22.40	22.99	25.86	5.31	2.80	5.68	-1.03E+00	2.07E-05	Down	-5.23E-01	3.79E-02		3.73E-02	8.80E-01		2.07E-01	3.43E-01		-9.24E-01	2.84E-02		9.48E-02	8.12E-01					Unigene10708_All//7.00E-15//gi|109890883|gb|DN519846.1|DN519846				
Unigene107081_All	352	0.00	0.00	0.00	0.00	0.00	0.00	2.76	0.59	0.00	null	null		null	null		null	null		null	null		-2.22E+00	1.82E-03		-1.14E+01	2.72E-07	Down									
Unigene107084_All	1125	0.00	0.00	0.00	0.00	0.00	0.00	4.59	0.04	0.11	null	null		null	null		null	null		null	null		-6.95E+00	9.46E-35	Down	-5.43E+00	2.57E-33	Down	Unigene107084_All//gi|115463079|ref|NP_001055139.1|//2.00E-99//Os05g0302700 [Oryza sativa Japonica Group] >gi|113578690|dbj|BAF17053.1| Os05g0302700 [Oryza sativa Japonica Group]	Unigene107084_All//2.00E-80//AT5G13490| AAC2 (ADP/ATP carrier 2); ATP:ADP antiporter/ binding	Unigene107084_All//4.00E-13//TC167393			GO:0006810//GO:0019866//GO:0031224//GO:0043231	nr -
Unigene107088_All	462	0.00	0.00	0.00	0.00	0.00	0.00	2.10	0.54	0.00	null	null		null	null		null	null		null	null		-1.96E+00	4.44E-03		-1.10E+01	2.72E-07	Down									ESTscan -
Unigene107104_All	363	0.00	0.00	0.00	0.00	0.00	0.00	1.98	0.12	0.00	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-1.10E+01	1.78E-05	Down	Unigene107104_All//gi|297834842|ref|XP_002875304.1|//2.00E-09//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321142|gb|EFH51563.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene107104_All//2.00E-09//AT5G66330| leucine-rich repeat family protein	Unigene107104_All//8.00E-55//gi|78335416|gb|DT555690.1|DT555690				nr -
Unigene107106_All	237	0.00	0.00	0.00	0.84	0.00	0.00	2.14	0.71	0.00	null	null		null	null		-9.72E+00	8.48E-02		-9.72E+00	1.34E-01		-1.60E+00	1.07E-01		-1.11E+01	5.56E-04	Down	Unigene107106_All//gi|124360490|gb|ABN08500.1|//2.00E-13//Protein kinase [Medicago truncatula]	Unigene107106_All//3.00E-09//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488	nr -
Unigene107107_All	458	0.00	0.00	0.00	0.00	0.08	0.10	5.17	0.37	0.35	null	null		null	null		6.23E+00	8.39E-01		6.62E+00	7.03E-01		-3.82E+00	2.79E-12	Down	-3.89E+00	6.40E-13	Down				Unigene107107_All//2.00E-25//gi|195983575|gb|FL577381.1|FL577381					
Unigene10711_All	310	3.54	0.00	2.23	0.48	0.33	0.58	0.55	0.13	0.51	-1.18E+01	1.95E-06	Down	-6.67E-01	3.35E-01		-5.33E-01	7.86E-01		2.74E-01	9.06E-01		-2.02E+00	3.68E-01		-8.61E-02	9.66E-01										
Unigene10711_All	553	0.00	0.00	0.00	0.09	0.00	0.00	2.14	0.91	0.36	null	null		null	null		-6.49E+00	5.64E-01		-6.49E+00	6.45E-01		-1.24E+00	2.93E-02		-2.57E+00	6.98E-05	Down				Unigene107111_All//3.00E-21//TC132835				
Unigene107113_All	280	0.00	0.00	0.00	0.00	0.00	0.00	2.42	0.15	0.00	null	null		null	null		null	null		null	null		-4.02E+00	5.36E-04	Down	-1.12E+01	3.57E-05	Down	Unigene107113_All//gi|116222125|gb|ABJ80933.1|//4.00E-38//actin [Leucocryptos marina]	Unigene107113_All//3.00E-33//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene107113_All//1.00E-15//gi|5049214|gb|AI730362.1|AI730362			GO:0032559//GO:0043232	nr +
Unigene107114_All	272	0.00	0.00	0.00	0.00	0.00	0.00	7.46	0.00	0.88	null	null		null	null		null	null		null	null		-1.29E+01	2.32E-14	Down	-3.09E+00	2.66E-09	Down	Unigene107114_All//gi|37901017|gb|AAP46148.1|//2.00E-45//actin 2 [Pseudo-nitzschia multiseries] >gi|37935564|gb|AAP46147.1| actin 1 [Pseudo-nitzschia multiseries]	Unigene107114_All//2.00E-43//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene107114_All//9.00E-20//gi|31406833|gb|CD485868.1|CD485868		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008092//GO:0012501//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0048747//GO:0051707//GO:0060415	nr -
Unigene10712_All	361	0.00	4.77	1.48	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	8.00E-10	Up	1.05E+01	4.05E-03		null	null		null	null		null	null		null	null		Unigene10712_All//gi|226530890|ref|NP_001151865.1|//1.00E-44//serine hydroxymethyltransferase [Zea mays] >gi|195650403|gb|ACG44669.1| serine hydroxymethyltransferase [Zea mays]	Unigene10712_All//2.00E-41//AT5G26780| SHM2 (SERINE HYDROXYMETHYLTRANSFERASE 2); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding			ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate	GO:0009069//GO:0016742//GO:0043231//GO:0048037	nr -

Unigene107123_All	241	0.00	0.00	0.00	0.00	0.14	0.00	4.04	3.47	11.57	null	null		null	null		7.16E+00	8.39E-01		null	null		-2.18E-01	7.24E-01		1.52E+00	1.22E-05	Up	Unigene107123_All//gi|15217709|ref|NP_176647.1|//9.00E-30//ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase [Arabidopsis thaliana] >gi|6633821|gb|AAF19680.1|AC009519_14 F19J9.23 [Arabidopsis thaliana] >gi|16226491|gb|AAL16181.1|AF428413_1 At1g64660/F1N19_22 [Arabidopsis thaliana] >gi|15450932|gb|AAK96737.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana] >gi|30387333|gb|AAP31932.1| At1g64660 [Arabidopsis thaliana] >gi|10740851|dbj|BAE98522.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana]	Unigene107123_All//4.00E-31//AT1G64660| ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase	Unigene107123_All//1.00E-49//TC130861		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0009087//GO:0016765//GO:0016846//GO:0044444//GO:0048037	nr -
Unigene107128_All	512	0.61	0.00	0.31	4.38	2.42	2.82	6.94	1.71	3.73	-9.26E+00	3.67E-02		-9.75E-01	5.06E-01		-8.55E-01	3.58E-02		-6.33E-01	1.48E-01		-2.02E+00	1.20E-09	Down	-8.93E-01	1.57E-03		Unigene107128_All//gi|302142868|emb|CBI20163.3|//5.00E-09//unnamed protein product [Vitis vinifera]		Unigene107128_All//2.00E-161//C0094931				nr +
Unigene107113_All	299	0.35	1.19	0.18	0.50	1.04	1.81	3.25	7.27	9.46	1.76E+00	2.18E-01		-9.75E-01	7.22E-01		1.05E+00	5.32E-01		1.86E+00	1.03E-01		1.16E+00	3.26E-03		1.54E+00	8.34E-06	Up	Unigene107113_All//gi|114199050|gb|AB154120.1|//4.00E-24//caffeic acid O-methyltransferase [Malus x domestica]	Unigene107113_All//6.00E-24//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene107113_All//8.00E-36//A1055471		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005515//GO:0008171//GO:0009699	nr +
Unigene107136_All	761	0.00	0.00	0.00	0.00	0.00	0.00	2.00	2.14	0.10	null	null		null	null		null	null		null	null		9.89E-02	8.36E-01		-4.26E+00	5.22E-09	Down	Unigene107136_All//gi|7208784|emb|CAB76914.1|//2.00E-26//60S ribosomal protein L6 [Cicer arietinum]	Unigene107136_All//9.00E-15//AT1G74060| 60S ribosomal protein L6 (RPL6B)			ko03010|Ribosome	GO:0005488//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene107138_All	235	0.45	0.65	1.13	0.64	0.88	0.19	2.88	0.18	0.00	5.39E-01	7.80E-01		1.35E+00	4.09E-01		4.67E-01	8.26E-01		-1.73E+00	5.02E-01		-4.02E+00	5.36E-04	Down	-1.15E+01	3.57E-05	Down	Unigene107138_All//gi|105922786|gb|ABF81437.1|//7.00E-08//TIR-NBS-LRR-TIR type disease resistance protein [Populus trichocarpa]	Unigene107138_All//4.00E-05//AT1G27180| disease resistance protein (TIR-NBS-LRR class), putative	Unigene107138_All//9.00E-29//gi|48807031|gb|CO108345.1|CO108345			GO:0000166//GO:0006952//GO:0009987	nr -
Unigene107140_All	387	2.16	0.65	0.00	0.77	0.53	1.52	2.84	1.08	1.24	-1.72E+00	3.63E-02		-1.11E+01	1.19E-04	Down	-5.33E-01	6.79E-01		9.74E-01	3.46E-01		-1.40E+00	2.04E-02		-1.20E+00	3.41E-02					Unigene107140_All//3.00E-76//BG440255				
Unigene107141_All	255	0.00	0.00	0.00	0.00	0.00	0.00	3.15	0.00	0.00	null	null		null	null		null	null		null	null		-1.16E+01	8.58E-06	Down	-1.16E+01	4.43E-06	Down								
Unigene107156_All	507	0.21	0.10	0.63	0.20	0.27	0.36	2.34	1.48	0.16	-1.05E+00	6.86E-01		1.61E+00	3.05E-01		4.68E-01	8.78E-01		8.59E-01	6.96E-01		-6.54E-01	2.47E-01		-3.89E+00	9.21E-07	Down								
Unigene107158_All	493	0.00	0.00	0.00	0.00	0.00	0.00	4.97	0.59	1.62	null	null		null	null		null	null		null	null		-3.07E+00	1.26E-10	Down	-1.62E+00	1.55E-05	Down								
Unigene107159_All	341	0.00	0.00	0.00	0.00	0.00	0.00	2.36	1.96	0.00	null	null		null	null		null	null		null	null		-2.65E-01	7.05E-01		-1.12E+01	4.43E-06	Down			Unigene107159_All//4.00E-10//gi|13246915|gb|BE052560.2|BE052560				kegg -
Unigene107160_All	310	0.34	0.00	0.00	0.00	0.00	0.00	1.91	0.00	0.00	-8.40E+00	3.76E-01		-8.40E+00	3.99E-01		null	null		null	null		-1.09E+01	2.40E-04	Down	-1.09E+01	1.42E-04	Down								
Unigene107166_All	1000	0.16	0.15	0.11	0.60	0.55	0.77	1.06	0.17	0.20	-4.67E-02	9.90E-01		-5.60E-01	7.76E-01		-1.18E-01	8.76E-01		3.61E-01	6.80E-01		-2.66E+00	2.25E-04	Down	-2.41E+00	3.46E-04	Down	Unigene107166_All//gi|297820436|ref|XP_002878101.1|//1.00E-39//CIP111 [Arabidopsis lyrata subsp. lyrata] >gi|297323939|gb|EFH54360.1| CIP111 [Arabidopsis lyrata subsp. lyrata]	Unigene107166_All//1.00E-32//AT3G56690| CIP111 (CAM INTERACTING PROTEIN 111); ATPase/ calmodulin binding	Unigene107166_All//0.00E+00//TC173047		ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0009534//GO:0017111	nr -
Unigene107168_All	564	0.00	0.09	0.00	0.09	0.12	0.32	1.72	0.52	0.14	6.49E+00	6.22E-01		null	null		4.68E-01	9.61E-01		1.86E+00	4.59E-01		-1.73E+00	9.67E-03		-3.61E+00	2.14E-05	Down								
Unigene107717_All	274	102.73	130.93	103.58	147.81	170.42	157.25	59.41	61.93	134.93	3.50E-01	9.67E-05		1.19E-02	9.33E-01		2.05E-01	8.00E-03		8.93E-02	3.76E-01		6.00E-02	6.72E-01		1.18E+00	3.07E-44	Up	Unigene107717_All//gi|227204481|dbj|BAH57092.1|//6.00E-17//AT4G10970 [Arabidopsis thaliana]	Unigene107717_All//3.00E-14//AT4G10970| unknown protein	Unigene107717_All//2.00E-153//TC154089				nr +
Unigene107173_All	821	0.00	0.00	0.00	0.00	0.00	0.00	4.02	0.00	0.19	null	null		null	null		null	null		null	null		-1.20E+01	2.53E-23	Down	-4.37E+00	3.47E-19	Down								ESTscan -
Unigene107176_All	448	0.00	0.00	0.00	0.00	0.00	0.00	2.64	0.37	0.27	null	null		null	null		null	null		null	null		-2.82E+00	4.41E-05	Down	-3.31E+00	4.89E-06	Down	Unigene107176_All//gi|224004980|ref|XP_002296141.1|//7.00E-32//RL3, ribosomal protein 3, 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335] >gi|209586173|gb|ACI64858.1| RL3, ribosomal protein 3, 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335]	Unigene107176_All//1.00E-31//AT1G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome			ko03010|Ribosome	GO:0030529	nr -
Unigene107179_All	1445	0.00	0.00	0.00	0.07	0.05	0.00	2.84	1.36	0.58	null	null		null	null		-5.31E-01	8.19E-01		-6.11E+00	4.06E-01		-1.06E+00	9.14E-05	Down	-2.29E+00	2.79E-13	Down	Unigene107179_All//gi|283132365|dbj|BAI63588.1|//1.00E-128//leucine rich repeat protein [Lotus japonicus]	Unigene107179_All//2.00E-108//AT2G19330| leucine-rich repeat family protein			ko04626|Plant-pathogen interaction		nr -
Unigene107192_All	1107	0.00	0.00	0.00	0.00	0.06	0.04	0.23	0.15	1.01	null	null		null	null		5.96E+00	6.15E-01		5.35E+00	7.03E-01		-6.02E-01	6.48E-01		2.14E+00	7.62E-04	Up	Unigene107192_All//gi|297802268|ref|XP_002869018.1|//2.00E-61//GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314854|gb|EFH45277.1| GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene107192_All//2.00E-79//AT4G36830| GNS1/SUR4 membrane family protein	Unigene107192_All//3.00E-10//TC171527				nr +
Unigene107197_All	953	0.05	0.00	0.00	0.00	0.00	0.00	11.80	1.62	0.92	-5.78E+00	6.20E-01		-5.78E+00	6.33E-01		null	null		null	null		-2.86E+00	2.01E-43	Down	-3.68E+00	1.35E-56	Down	Unigene107197_All//gi|34761723|gb|AAQ82034.1|//3.00E-10//unknown [Pisum sativum]		Unigene107197_All//6.00E-70//TC161176				nr -
Unigene107201_All	391	0.00	0.00	0.00	0.00	0.00	0.00	4.87	0.21	0.00	null	null		null	null		null	null		null	null		-4.51E+00	4.75E-11	Down	-1.22E+01	4.91E-14	Down								ESTscan +
Unigene107202_All	444	0.00	0.00	0.00	0.00	0.00	0.00	1.14	0.09	0.00	null	null		null	null		null	null		null	null		-3.60E+00	5.78E-03		-1.02E+01	5.56E-04	Down	Unigene107202_All//gi|226347429|gb|ACO50125.1|//4.00E-60//elongation factor 1 alpha [Entosiphon sulcatum]	Unigene107202_All//5.00E-56//AT5G60390| elongation factor 1-alpha / EF-1-alpha				GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene107205_All	647	0.00	0.00	0.00	0.00	0.00	0.00	3.79	0.00	0.00	null	null		null	null		null	null		null	null		-1.19E+01	2.41E-17	Down	-1.19E+01	4.73E-18	Down	Unigene107205_All//gi|81157943|dbj|BAE48222.1|//1.00E-59//elongation factor 2 [Chlorella pyrenoidosa]	Unigene107205_All//4.00E-56//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding				GO:0000166//GO:0016787	nr +
Unigene107206_All	334	0.00	0.00	0.00	0.00	0.00	0.00	4.05	0.00	0.12	null	null		null	null		null	null		null	null		-1.20E+01	1.30E-09	Down	-5.09E+00	8.12E-09	Down	Unigene107206_All//gi|145354676|ref|XP_001421604.1|//2.00E-13//Ribosomal protein S21, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901] >gi|144581842|gb|ABO99897.1| Ribosomal protein S21, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901]	Unigene107206_All//4.00E-11//AT5G27700| structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0031410	nr +
Unigene107214_All	395	0.00	0.00	0.00	0.00	0.00	0.00	2.03	0.21	0.00	null	null		null	null		null	null		null	null		-3.26E+00	4.49E-04	Down	-1.10E+01	4.43E-06	Down	Unigene107214_All//gi|223996063|ref|XP_002287705.1|//2.00E-29//RL12, ribosomal protein 11 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335] >gi|220976821|gb|EED95148.1| RL12, ribosomal protein 11 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335]	Unigene107214_All//4.00E-29//AT5G60670| 60S ribosomal protein L12 (RPL12C)			ko03010|Ribosome		nr -
Unigene107220_All	222	5.66	0.68	0.24	4.26	3.88	3.26	1.71	0.19	0.72	-3.05E+00	9.00E-05	Down	-4.56E+00	8.14E-06	Down	-1.37E-01	8.18E-01		-3.89E-01	6.28E-01		-3.19E+00	3.12E-02		-1.26E+00	2.48E-01									
Unigene107225_All	442	0.00	0.00	0.00	0.00	0.00	0.00	1.91	0.38	0.00	null	null		null	null		null	null		null	null		-2.34E+00	2.96E-03		-1.09E+01	2.21E-06	Down	Unigene107225_All//gi|195652927|gb|ACG45931.1|//4.00E-29//60S ribosomal protein L22-2 [Zea mays]	Unigene107225_All//2.00E-17//AT5G27770| 60S ribosomal protein L22 (RPL22C)			ko03010|Ribosome	GO:0015934//GO:0016020//GO:0031981	nr +
Unigene107231_All	339	0.46	0.00	0.00	0.44	0.61	0.27	2.49	0.62	0.24	-8.85E+00	2.17E-01		-8.85E+00	2.46E-01		4.68E-01	8.26E-01		-7.26E-01	7.17E-01		-2.02E+00	7.45E-03		-3.41E+00	1.35E-04	Down	Unigene107231_All//gi|2790705|gb|AA026688.1|AF478375_1//2.00E-15//gag-pol polyprotein [Vitis vinifera]		Unigene107231_All//3.00E-20//TC140327			GO:0003676//GO:0003824//GO:0006259//GO:0046872	nr +
Unigene107239_All	528	0.00	0.00	0.00	0.00	0.00	0.00	2.40	0.16	0.00	null	null		null	null		null	null		null	null		-3.92E+00	6.20E-07	Down	-1.12E+01	1.99E-09	Down	Unigene107239_All//gi|115453465|ref|NP_001050333.1|//4.00E-20//Os03g0406200 [Oryza sativa Japonica Group] >gi|90101284|sp|Q40682.3|EF1D2_ORYSJ RecName: Full=Elongation factor 1-delta 2; Short=EF-1-delta 2; AltName: Full=Elongation factor 1B-beta 2; AltName: Full=eEF-1B beta 2 >gi|3894214|dbj|BAA34598.1| elongation factor 1 beta 2 [Oryza sativa Japonica Group] >gi|3894216|dbj|BAA34599.1| elongation factor 1 beta 2 [Oryza sativa Japonica Group] >gi|53370742|gb|AAU89237.1| elongation factor 1 beta 2 [Oryza sativa Japonica Group] >gi|108708724|gb|ABF96519.1| EF-1 guanine nucleotide exchange domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548804|dbj|BAF12247.1| Os03g0406200 [Oryza sativa Japonica Group]	Unigene107239_All//3.00E-11//AT2G18110| elongation factor 1-beta, putative / EF-1-beta, putative				GO:0006412//GO:0008135//GO:0043234	nr +
Unigene107724_All	291	0.00	0.70	0.00	2.23	0.95	0.47	2.18	0.14	0.00	9.44E+00	1.37E-01		null	null		-1.23E+00	1.60E-01		-2.26E+00	2.76E-02		-3.92E+00	9.81E-04	Down	-1.11E+01	7.12E-05	Down			Unigene107724_All//5.00E-37//DT049198				ESTscan -
Unigene107242_All	230	0.46	0.00	2.55	2.38	2.40	1.77	49.45	35.98	23.21	-8.83E+00	3.76E-01		2.48E+00	3.76E-02		7.90E-03	9.83E-01		-4.31E-01	6.67E-01		-4.59E-01	2.36E-03		-1.09E+00	1.08E-12	Down	Unigene107242_All//gi|163943787|gb|ABY49018.1|//2.00E-07//GA2-oxidase [Leersia tisserantii]	Unigene107242_All//5.00E-07//AT1G78440| ATGA2OX1 (gibberellin 2-oxidase 1); gibberellin 2-beta-dioxygenase	Unigene107242_All//3.00E-59//TC139925		ko00904|Diterpenoid biosynthesis	GO:0016706	nr +
Unigene107248_All	439	0.00	0.00	0.00	0.00	0.00	0.00	2.02	0.57	0.18	null	null		null	null		null	null		null	null		-1.82E+00	1.08E-02		-3.48E+00	7.34E-05	Down								
Unigene107725_All	457	2.29	0.00	1.86	2.07	2.86	0.79	0.19	0.09	0.00	-1.12E+01	3.80E-06	Down	-2.97E-01	6.42E-01		4.67E-01	4.71E-01		-1.39E+00	6.08E-02		-1.02E+00	7.26E-01		-7.53E+00	3.61E-01									
Unigene107256_All	438	0.12	0.12	0.36	0.23	0.00	0.21	3.67	0.95	1.73	-4.66E-02	9.87E-01		1.61E+00	5.12E-01		-7.83E+00	3.17E-01		-1.42E-01	9.53E-01		-1.94E+00	1.42E-04	Down	-1.09E+00	1.58E-02									
Unigene107268_All	373	0.00	6.52	0.71	0.00	0.55	1.82	0.34	0.22	0.21	1.27E+01	7.73E-14	Up	9.48E+00	8.04E-02		9.11E+00	1.57E-01		1.08E+01	4.19E-04	Up	-6.02E-01	7.68E-01		-6.71E-01	7.21E-01		Unigene107268_All//gi|4336434|gb|AAD17804.1|//2.00E-09//nodule-enhanced protein phosphatase type 2C [Lotus japonicus]	Unigene107268_All//3.00E-08//AT5G59220| protein phosphatase 2C, putative / PP2C, putative				GO:0016787	nr -
Unigene107270_All	213	0.00	0.24	0.25	0.47	0.49	0.00	5.36	0.78	3.18	7.89E+00	6.22E-01		7.97E+00	6.41E-01		5.24E-02	9.68E-01		-8.87E+00	4.05E-01		-2.77E+00	7.62E-05	Down	-7.53E-01	1.68E-01				Unigene107270_All//4.00E-83//gi|73863243|gb|DT465982.1|DT465982				ESTscan -
Unigene107277_All	251	1.25	1.21	0.85	8.14	6.59	0.36	0.51	0.33	0.63	-4.63E-02	9.83E-01		-5.60E-01	6.64E-01		-3.05E-01	5.37E-01		-4.50E+00	2.02E-10	Down	-6.02E-01	7.68E-01		3.29E-01	8.52E-01				Unigene107277_All//1.00E-71//DW504295				

Unigene107278_All	239	0.00	0.00	0.00	0.00	0.14	0.38	2.30	0.52	0.00	null	null		null	null		7.17E+00	8.39E-01		8.56E+00	4.81E-01		-2.13E+00	3.32E-02		-1.12E+01	2.81E-04	Down	Unigene107278_All//gi|115472361|ref|NP_001059779.1|//4.00E-12//Os07g0516000 [Oryza sativa Japonica Group] >gi|34393670|dbj|BAC83370.1| alpha-rhamnosidase-like protein [Oryza sativa Japonica Group] >gi|50508733|dbj|BAD31309.1| alpha-rhamnosidase-like protein [Oryza sativa Japonica Group] >gi|113611315|dbj|BAF21693.1| Os07g0516000 [Oryza sativa Japonica Group]	Unigene107278_All//3.00E-12//AT1G57700| RNR/Asp-box repeat family protein	Unigene107278_All//6.00E-33//gi|78325962|gb|DT546236.1|DT546236				nr -
Unigene107279_All	287	0.00	0.00	0.00	0.00	0.00	0.00	1.77	0.44	0.00	null	null		null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.08E+01	5.56E-04	Down	Unigene107279_All//sp|Q9Y197|OAZ2_DANRE//7.00E-07//Ornithine decarboxylase antizyme 2 OS=Danio rerio GN=oaz2 PE=2 SV=1						swissprot +
Unigene10728_All	308	64.04	162.54	115.49	48.04	48.19	47.66	209.34	252.95	101.28	1.34E+00	7.13E-58	Up	8.51E-01	2.40E-19		4.60E-03	9.83E-01		-1.14E-02	9.52E-01		2.73E-01	2.31E-07		-1.05E+00	1.84E-63	Down	Unigene10728_All//gi|225440392|ref|XP_002267559.1|//4.00E-16//PREDICTED: ripening-related protein-like [Vitis vinifera]	Unigene10728_All//3.00E-14//AT5G02230| haloacid dehalogenase-like hydrolase family protein	Unigene10728_All//4.00E-127//gi|73861720|gb|DT464459.1|DT464459			GO:0003824	nr -
Unigene107285_All	224	0.00	0.00	0.00	0.22	0.00	0.20	2.27	0.56	0.00	null	null		null	null		-7.80E+00	5.64E-01		-1.42E-01	9.57E-01		-2.02E+00	5.21E-02		-1.11E+01	5.56E-04	Down							
Unigene107286_All	228	0.00	0.00	0.00	0.00	0.00	0.00	2.78	1.28	0.17	null	null		null	null		null	null		null	null		-1.12E+00	1.80E-01		-3.99E+00	5.83E-04	Down	Unigene107286_All//gi|110737394|dbj|BAF00641.1|//2.00E-31//ATPase [Arabidopsis thaliana]	Unigene107286_All//7.00E-33//AT5G04930| ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism				GO:0005548//GO:0006869//GO:0009206//GO:0031224//GO:0032559//GO:0042625//GO:0046872	nr +
Unigene107288_All	401	0.00	0.00	0.00	0.00	0.00	0.00	1.48	1.04	0.00	null	null		null	null		null	null		null	null		-5.02E-01	5.74E-01		-1.05E+01	1.42E-04	Down	Unigene107288_All//gi|298711973|emb|CBJ32915.1|//6.00E-25//ribosomal protein L35 [Ectocarpus siliculosus]	Unigene107288_All//7.00E-26//AT1G74270| 60S ribosomal protein L35a (RPL35aC)			ko03010|Ribosome	GO:0009987//GO:0015934//GO:0043231	nr -
Unigene107296_All	477	0.00	0.00	0.00	0.00	0.00	0.00	2.84	0.44	0.00	null	null		null	null		null	null		null	null		-2.69E+00	1.77E-05	Down	-1.15E+01	4.86E-10	Down	Unigene107296_All//gi|301105230|ref|XP_002901699.1|//1.00E-51//40S ribosomal protein S11 [Phytophthora infestans T30-4] >gi|262100703|gb|EEY58755.1| 40S ribosomal protein S11 [Phytophthora infestans T30-4]	Unigene107296_All//1.00E-47//AT3G48930| EMB1080 (embryo defective 1080); structural constituent of ribosome			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0003312	nr +
Unigene107298_All	242	42.38	35.18	26.85	47.96	70.72	83.61	80.02	744.21	90.21	-2.69E-01	1.49E-01		-6.59E-01	3.72E-04		5.60E-01	8.19E-06		8.02E-01	2.85E-11		3.22E+00	0.00E+00	Up	1.73E-01	1.15E-01		Unigene107298_All//gi|297610489|ref|NP_001064615.2|//2.00E-18//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene107298_All//2.00E-13//AT1G60690| aldo/keto reductase family protein	Unigene107298_All//3.00E-81//DR044167			GO:0004033//GO:0008152	nr +
Unigene107299_All	570	0.00	0.00	0.00	0.00	0.00	0.00	2.89	0.59	0.21	null	null		null	null		null	null		null	null		-2.30E+00	1.36E-05	Down	-3.79E+00	5.22E-09	Down	Unigene107299_All//gi|260516654|gb|ACX43954.1|//3.00E-39//cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516656|gb|ACX43955.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516658|gb|ACX43956.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516660|gb|ACX43957.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516662|gb|ACX43958.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516664|gb|ACX43959.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516666|gb|ACX43960.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516668|gb|ACX43961.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516670|gb|ACX43962.1| cysteine protease 2 [Brachiaria hybrid cultivar]	Unigene107299_All//1.00E-37//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase				GO:0005488//GO:0009725//GO:0032502//GO:0043231//GO:0070011	nr -
Unigene10730_All	503	0.52	0.10	4.66	0.20	0.89	0.00	0.00	0.00	0.00	-2.37E+00	2.14E-01		3.16E+00	3.28E-08	Up	2.17E+00	1.06E-01		-7.63E+00	4.05E-01		null	null		null	null		Unigene10730_All//gi|56130780|ref|YP_145683.1|//9.00E-12//two component response transcription regulator [Ralstonia metallidurans CH34] >gi|94152513|ref|YP_581920.1| regulator protein CopR [Cupriavidus metallidurans CH34] >gi|10047062|emb|CAC07978.1| CopR protein [Ralstonia metallidurans CH34] >gi|56068770|emb|CAI11332.1| two component response transcription regulator [Ralstonia metallidurans CH34] >gi|93358883|gb|ABF12970.1| CopR regulator from the two components sensor/regulator family involved in Cu(II)/Cu(I) resistance [Cupriavidus metallidurans CH34]					GO:0005622//GO:0006350	nr -
Unigene107300_All	502	0.00	0.00	0.00	0.00	0.00	0.00	3.87	0.17	0.95	null	null		null	null		null	null		null	null		-4.54E+00	2.49E-11	Down	-2.02E+00	7.23E-06	Down	Unigene107300_All//gi|188496902|dbj|BAG32350.1|//1.00E-12//glucan binding protein-2 [Actinophrys sol]						nr +
Unigene107302_All	244	0.00	0.00	0.00	0.00	0.00	0.00	3.29	1.03	0.33	null	null		null	null		null	null		null	null		-1.68E+00	2.46E-02		-3.33E+00	2.47E-04	Down							
Unigene10731_All	275	0.57	0.00	0.00	4.53	2.50	0.00	0.15	0.00	0.14	-9.16E+00	2.17E-01		-9.16E+00	2.46E-01		-8.55E-01	1.47E-01		-1.21E+01	8.65E-08	Down	-7.26E+00	6.63E-01		-8.51E-02	9.73E-01				Unigene10731_All//3.00E-118//TC158907				
Unigene107315_All	236	0.00	0.00	0.00	0.00	0.00	0.00	3.05	0.00	0.00	null	null		null	null		null	null		null	null		-1.16E+01	3.27E-05	Down	-1.16E+01	1.78E-05	Down							ESTscan +
Unigene107317_All	359	0.73	0.00	0.74	1.80	0.38	0.13	4.24	1.16	0.55	-9.51E+00	6.72E-02		2.53E-02	1.00E+00		-2.23E+00	1.79E-02		-3.84E+00	2.70E-03		-1.86E+00	3.50E-04	Down	-2.93E+00	7.58E-07	Down			Unigene107317_All//1.00E-90//ES850878				
Unigene107328_All	244	0.00	0.00	0.00	0.00	0.00	0.00	2.08	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	8.91E-04	Down	-1.10E+01	5.56E-04	Down	Unigene107328_All//sp|Q9PLI5|Y114_CHLMU//1.00E-06//Uncharacterized protein TC_0114 OS=Chlamydia muridarum GN=TC_0114 PE=4 SV=2						swissprot +
Unigene107329_All	264	0.00	0.00	0.00	0.75	0.00	0.00	4.64	5.07	0.91	null	null		null	null		-9.56E+00	8.48E-02		-9.56E+00	1.34E-01		1.25E-01	8.14E-01		-2.36E+00	1.22E-04	Down							
Unigene107333_All	257	0.00	0.00	0.00	0.39	0.00	0.35	85.22	47.00	242.75	null	null		null	null		-8.60E+00	3.17E-01		-1.41E-01	9.53E-01		-8.59E-01	1.19E-15		1.51E+00	2.99E-107	Up	Unigene107333_All//gi|40218371|gb|AAR83118.1|//2.00E-47//secretory laccase [Gossypium arboreum]	Unigene107333_All//1.00E-31//AT5G09360| LAC14 (laccase 14); laccase	Unigene107333_All//8.00E-122//TC137114		ko00910|Nitrogen metabolism/ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr +
Unigene107337_All	338	0.00	0.00	0.00	0.00	0.00	0.00	8.26	3.71	0.24	null	null		null	null		null	null		null	null		-1.15E+00	6.98E-04	Down	-5.13E+00	9.17E-18	Down	Unigene107337_All//gi|2894308|emb|CAA11269.1|//3.00E-38//polyubiquitin [Nicotiana tabacum]	Unigene107337_All//5.00E-34//AT4G05320| UBQ10 (POLYUBIQUITIN 10); protein binding	Unigene107337_All//4.00E-41//BF277514			GO:0031410//GO:0043231	nr -
Unigene107338_All	512	0.00	0.00	0.00	0.00	0.00	0.00	3.96	1.80	0.16	null	null		null	null		null	null		null	null		-1.14E+00	5.27E-03		-4.67E+00	1.83E-12	Down							
Unigene107345_All	527	0.20	0.00	0.00	0.28	1.05	0.17	4.41	0.48	0.45	-7.63E+00	3.76E-01		-7.63E+00	3.98E-01		1.88E+00	9.42E-02		-7.27E-01	7.17E-01		-3.21E+00	1.59E-10	Down	-3.28E+00	3.91E-11	Down	Unigene107345_All//gi|28466815|gb|AAO41016.1|//1.00E-08//At1g11655 [Arabidopsis thaliana]		Unigene107345_All//7.00E-22//DW518236				nr +
Unigene107348_All	497	0.21	0.41	0.21	2.00	0.14	0.36	1.70	0.59	0.64	9.54E-01	6.22E-01		2.58E-02	1.00E+00		-3.85E+00	1.61E-05	Down	-2.46E+00	2.07E-03		-1.53E+00	3.21E-02		-1.41E+00	3.70E-02		Unigene107348_All//gi|18415647|ref|NP_568185.1|//4.00E-14//mitochondrial transcription termination factor family protein / mTERF family protein [Arabidopsis thaliana]	Unigene107348_All//1.00E-15//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein				GO:0044464	nr -
Unigene107350_All	496	0.00	0.00	0.00	0.00	0.00	0.00	1.62	0.00	0.16	null	null		null	null		null	null		null	null		-1.07E+01	8.58E-06	Down	-3.33E+00	2.47E-04	Down							
Unigene107351_All	383	0.41	0.00	0.28	0.00	0.00	0.00	4.19	0.98	4.68	-8.68E+00	2.17E-01		-5.59E-01	7.76E-01		null	null		null	null		-2.09E+00	5.87E-05	Down	1.58E-01	7.12E-01		Unigene107351_All//gi|73624747|gb|AAZ79231.1|//6.00E-14//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene107351_All//1.00E-10//AT4G24000| ATCSLG2; cellulose synthase/ transferase/ transferase, transferring glycosyl groups				GO:0009987//GO:0016020//GO:0016757	nr +
Unigene107354_All	395	0.93	0.51	0.54	1.64	1.05	0.57	1.93	0.00	0.30	-8.54E-01	4.89E-01		-7.82E-01	5.53E-01		-6.48E-01	4.60E-01		-1.52E+00	1.12E-01		-1.09E+01	1.68E-05	Down	-2.67E+00	1.64E-03		Unigene107354_All//gi|240255876|ref|NP_193313.5|//1.00E-51//ATVAMP724 [Arabidopsis thaliana]	Unigene107354_All//3.00E-52//AT4G15780| ATVAMP724	Unigene107354_All//2.00E-169//TC163824			GO:0006810//GO:0031224	nr -
Unigene107361_All	289	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.43	0.00	null	null		null	null		null	null		null	null		-2.24E+00	2.07E-02		-1.10E+01	1.42E-04	Down	Unigene107361_All//gi|298713802|emb|CBJ27174.1|//4.00E-10//phosphatase PP1 [Ectocarpus siliculosus]	Unigene107361_All//2.00E-05//AT1G64040| TOPP3; protein serine/threonine phosphatase				GO:0016791	nr -
Unigene107362_All	499	0.00	0.00	0.00	0.00	0.00	0.00	1.69	0.34	0.24	null	null		null	null		null	null		null	null		-2.34E+00	2.96E-03		-2.82E+00	5.38E-04	Down	Unigene107362_All//gi|288310312|gb|ADC45395.1|//1.00E-43//HSP90-1 [Glycine max]	Unigene107362_All//2.00E-36//AT5G56010| HSP81-3; ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0006950//GO:0016020//GO:0031981//GO:0032559//GO:0044267//GO:0044444//GO:0051592	nr +
Unigene107363_All	228	0.00	0.00	0.00	0.00	0.00	0.00	2.41	0.73	0.00	null	null		null	null		null	null		null	null		-1.72E+00	7.24E-02		-1.12E+01	2.81E-04	Down	Unigene107363_All//gi|26190436|emb|CAD45251.1|//4.00E-06//barley B recombinant [Hordeum vulgare]					GO:0005488	nr -
Unigene107364_All	594	0.26	0.77	0.63	0.84	0.87	1.22	4.06	0.99	1.48	1.54E+00	1.96E-01		1.25E+00	3.66E-01		5.24E-02	9.80E-01		5.37E-01	5.61E-01		-2.04E+00	7.09E-07	Down	-1.46E+00	8.41E-05	Down	Unigene107364_All//gi|108864347|gb|ABA95307.2|//7.00E-47//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene107364_All//3.00E-41//AT5G53900| unknown protein	Unigene107364_All//1.00E-82//gi|78323562|gb|DT543836.1|DT543836				nr -
Unigene10737_All	400	0.00	3.93	2.26	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.71E-09	Up	1.11E+01	4.71E-05	Up	null	null		null	null		null	null		null	null		Unigene10737_All//gi|301121760|ref|XP_002908607.1|//1.00E-30//succinyl-CoA ligase subunit alpha, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262103638|gb|EEY61690.1| succinyl-CoA ligase subunit alpha, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene10737_All//5.00E-27//AT5G23250| succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative			ko00020|Citrate cycle (TCA cycle)//ko00640|Propanoate metabolism	GO:0004774//GO:0009060//GO:0043231//GO:0046912	nr +
Unigene107372_All	291	0.18	0.00	0.00	0.00	0.12	0.00	1.74	0.00	0.68	-7.49E+00	6.20E-01		-7.49E+00	6.32E-01		6.89E+00	8.39E-01		null	null		-1.08E+01	8.91E-04	Down	-1.35E+00	1.40E-01		Unigene107372_All//gi|115469532|ref|NP_001058365.1|//6.00E-16//Os06g0678800 [Oryza sativa Japonica Group] >gi|113596405|dbj|BAF20279.1| Os06g0678800 [Oryza sativa Japonica Group]	Unigene107372_All//4.00E-12//AT4G22010| sks4 (SKU5 Similar 4); copper ion binding / oxidoreductase	Unigene107372_All//8.00E-36//gi|164305746|gb|EV495235.1|EV495235		ko00053|Ascorbate and aldarate metabolism	GO:0031410	nr +
Unigene107385_All	233	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.18	0.00	null	null		null	null		null	null		null	null		-3.60E+00	5.78E-03		-1.11E+01	5.56E-04	Down							

Unigene1074_All	1273	15.08	20.26	19.70	48.09	58.32	50.24	10.50	69.47	4.13	4.26E-01	7.04E-05		3.85E-01	6.64E-04		2.78E-01	8.20E-07		6.29E-02	4.53E-01		2.73E+00	0.00E+00	Up	-1.35E+00	3.45E-20	Down	Unigene1074_All//gi|57229665|gb|AAW45741.1|//0.00E+00//sinapyl alcohol dehydrogenase-like protein [Populus tremula x Populus tremuloides]	Unigene1074_All//8.00E-116//AT4G37970| CAD6 (CINNAMYL ALCOHOL DEHYDROGENASE 6); binding / catalytic/ oxidoreductase/ zinc ion binding	Unigene1074_All//0.00E+00//TC154710		ko00940|Phenylpropanoid biosynthesis	GO:0003824//GO:0008152//GO:0046914	nr +
Unigene10740_All	416	0.00	0.00	0.00	0.12	0.00	0.00	5.89	5.63	0.86	null	null		null	null		-6.90E+00	5.64E-01		-6.90E+00	6.45E-01		-6.73E-02	8.65E-01		-2.77E+00	4.81E-10	Down			Unigene10740_All//3.00E-08//TC158843				
Unigene107402_All	735	0.00	0.00	0.00	0.00	0.00	0.00	4.60	2.45	0.92	null	null		null	null		null	null		null	null		-9.12E-01	2.38E-03		-2.32E+00	3.08E-11	Down	Unigene107402_All//gi|238014838|gb|ACH38454.1|//1.00E-07//unknown [Zea mays]		Unigene107402_All//3.00E-22//TC146753				nr +
Unigene107407_All	265	14.02	4.40	7.03	1.50	3.51	2.22	1.28	0.16	0.00	-1.67E+00	1.25E-06	Down	-9.95E-01	2.95E-03		1.22E+00	1.05E-01		5.59E-01	6.01E-01		-3.02E+00	5.31E-02		-1.03E+01	8.18E-03		Unigene107407_All//gi|18400342|ref|NP_565556.1|//7.00E-15//YCF37 (Arabidopsis homolog of Synechocystis YCF37) [Arabidopsis thaliana] >gi|3152615|gb|AAC17094.1| expressed protein [Arabidopsis thaliana] >gi|16648702|gb|AAL25543.1| At2g23670/F26B6.32 [Arabidopsis thaliana] >gi|20197003|gb|AAM14867.1| expressed protein [Arabidopsis thaliana] >gi|20334912|gb|AAM16212.1| At2g23670/F26B6.32 [Arabidopsis thaliana] >gi|206748360|gb|ACI22363.1| YCF37-like protein [Arabidopsis thaliana]	Unigene107407_All//1.00E-07//AT2G23670| YCF37 (Arabidopsis homolog of Synechocystis YCF37)	Unigene107407_All//2.00E-67//TC158076			GO:0009534	nr -
Unigene107411_All	227	0.00	2.01	3.05	1.98	2.43	1.19	0.93	0.00	0.88	1.10E+01	7.44E-03		1.16E+01	6.17E-04	Up	2.97E-01	8.18E-01		-7.26E-01	5.33E-01		-9.86E+00	7.48E-02		-8.58E-02	9.61E-01									
Unigene107413_All	221	0.95	1.83	1.69	0.68	0.47	2.25	3.25	8.89	8.83	9.54E-01	4.14E-01		8.33E-01	5.16E-01		-5.33E-01	7.86E-01		1.73E+00	1.45E-01		1.45E+00	7.26E-04	Up	1.44E+00	6.00E-04	Up			Unigene107413_All//7.00E-11//TC158642				
Unigene107416_All	509	0.62	0.40	0.00	0.10	0.14	0.00	1.74	0.00	0.08	-6.31E-01	6.22E-01		-9.27E+00	4.93E-02		4.67E-01	9.61E-01		-6.61E+00	6.45E-01		-1.08E+01	2.24E-06	Down	-4.48E+00	1.24E-05	Down	Unigene107416_All//gi|15229025|ref|NP_190449.1|//8.00E-24//sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	Unigene107416_All//5.00E-25//AT3G48800| sterile alpha motif (SAM) domain-containing protein	Unigene107416_All//3.00E-129//TC176975				nr -
Unigene107417_All	388	0.00	0.00	0.00	0.00	0.00	0.00	3.92	0.75	0.00	null	null		null	null		null	null		null	null		-2.38E+00	2.15E-05	Down	-1.19E+01	2.88E-11	Down								
Unigene107424_All	295	0.00	0.00	0.00	0.00	0.00	0.00	3.58	0.57	0.00	null	null		null	null		null	null		null	null		-2.66E+00	2.25E-04	Down	-1.18E+01	6.73E-08	Down	Unigene107424_All//gi|300266716|gb|EFJ50902.1|//3.00E-14//elongation factor 2 (EF-2, EF-TU) [Volvox carteri f. nagariensis]	Unigene107424_All//2.00E-15//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding				GO:0000166//GO:0006950//GO:0008135//GO:0009536//GO:0016020//GO:0016787//GO:0031981//GO:0046914	nr -
Unigene107430_All	502	0.00	0.30	0.00	0.30	0.00	0.18	1.60	1.58	6.11	8.24E+00	2.36E-01		null	null		-8.22E+00	1.66E-01		-7.27E-01	7.17E-01		-1.66E-02	1.02E+00		1.93E+00	3.29E-08	Up	Unigene107430_All//gi|115472685|ref|NP_001059941.1|//3.00E-45//Os07g0550900 [Oryza sativa Japonica Group] >gi|113611477|dbj|BAF21855.1| Os07g0550900 [Oryza sativa Japonica Group]	Unigene107430_All//2.00E-46//AT4G27300| S-locus protein kinase, putative	Unigene107430_All//2.00E-28//gi|164366409|gb|ESR02621.1|ESR02621		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr -
Unigene107437_All	489	0.00	0.00	0.00	0.00	0.00	0.00	1.38	0.26	0.00	null	null		null	null		null	null		null	null		-2.43E+00	7.77E-03		-1.04E+01	3.57E-05	Down								ESTscan +
Unigene107438_All	581	0.00	0.00	0.00	0.00	0.00	0.00	2.69	0.43	0.00	null	null		null	null		null	null		null	null		-2.64E+00	4.08E-06	Down	-1.14E+01	1.42E-11	Down								
Unigene107444_All	616	0.00	0.16	0.52	0.00	0.56	0.00	2.33	0.14	0.97	7.36E+00	3.90E-01		9.02E+00	4.54E-02		9.13E+00	3.02E-02		null	null		-4.10E+00	5.15E-08	Down	-1.22E+00	9.34E-03									
Unigene107449_All	339	0.00	0.00	0.00	0.00	0.00	0.00	2.49	0.12	0.00	null	null		null	null		null	null		null	null		-4.34E+00	4.56E-05	Down	-1.13E+01	2.21E-06	Down								ESTscan -
Unigene107450_All	879	0.24	0.06	0.00	0.17	0.04	0.15	2.02	0.52	0.41	-2.05E+00	3.34E-01		-7.90E+00	1.47E-01		-2.12E+00	3.87E-01		-1.42E-01	9.44E-01		-1.95E+00	5.37E-05	Down	-2.31E+00	3.08E-06	Down								ESTscan -
Unigene107451_All	867	0.00	0.00	0.00	0.00	0.00	0.00	2.39	0.05	0.05	null	null		null	null		null	null		null	null		-5.63E+00	2.86E-13	Down	-5.70E+00	7.21E-14	Down	Unigene107451_All//gi|301122631|ref|XP_002969042.1|//2.00E-63//40S ribosomal protein S6 [Phytophthora infestans T30-4] >gi|262099804|gb|EEY57856.1| 40S ribosomal protein S6 [Phytophthora infestans T30-4]	Unigene107451_All//9.00E-58//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome	Unigene107451_All//3.00E-16//CD486323		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0016020	nr -
Unigene107452_All	837	0.00	0.00	0.00	0.12	0.29	0.11	5.66	0.85	1.05	null	null		null	null		1.28E+00	5.32E-01		-1.41E-01	9.53E-01		-2.74E+00	8.02E-18	Down	-2.43E+00	2.86E-16	Down	Unigene107452_All//gi|15222073|ref|NP_175349.1|//2.00E-56//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68566178|sp|Q6NQG7.1|ATL1L_ARATH RecName: Full=RING-H2 finger protein ATL1L >gi|34365601|gb|AAQ65112.1| At1g49230 [Arabidopsis thaliana]	Unigene107452_All//2.00E-48//AT1G49230| zinc finger (C3HC4-type RING finger) family protein	Unigene107452_All//0.00E+00//TC137887		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0019787//GO:0032446//GO:0046914	nr +
Unigene107455_All	610	0.00	0.00	0.00	0.00	0.00	0.00	5.13	1.30	0.98	null	null		null	null		null	null		null	null		-1.98E+00	2.16E-08	Down	-2.39E+00	8.62E-11	Down	Unigene107455_All//gi|118572295|sp|Q8LB19.2|EDL16_ARATH//2.00E-25//RecName: Full=Sugar transporter ERD6-like 16 >gi|17381265|gb|AAL36051.1| AT5g18840/F17K4_90 [Arabidopsis thaliana] >gi|23309019|gb|AAN18269.1| At5g18840/F17K4_90 [Arabidopsis thaliana]	Unigene107455_All//1.00E-26//AT5G18840| sugar transporter, putative	Unigene107455_All//2.00E-10//TC145455			GO:0006810//GO:0016020//GO:0022891	nr -
Unigene107456_All	460	0.00	0.00	0.00	0.00	0.00	0.00	2.21	0.00	0.61	null	null		null	null		null	null		null	null		-1.11E+01	2.97E-07	Down	-1.86E+00	3.54E-03		Unigene107456_All//gi|3834323|gb|AC83039.1|//2.00E-40//P9K20.25 [Arabidopsis thaliana]	Unigene107456_All//2.00E-41//AT1G78710| unknown protein	Unigene107456_All//1.00E-162//gi|109862280|gb|DW491257.1|DW491257				nr -
Unigene107748_All	243	30.36	927.27	324.98	95.94	221.21	295.70	0.00	0.17	0.00	4.93E+00	0.00E+00	Up	3.42E+00	2.61E-285	Up	1.21E+00	5.10E-62	Up	1.62E+00	1.01E-117	Up	7.43E+00	6.38E-01		null	null		Unigene107748_All//gi|6723687|emb|CAB67122.1|//1.00E-12//cell wall protein [Nicotiana tabacum] >gi|270313156|gb|ACZ73645.1| glycine-rich protein precursor [Nicotiana tabacum]		Unigene107748_All//1.00E-129//TC169148				nr +
Unigene107487_All	357	13.34	220.56	27.30	20.09	35.98	54.40	80.77	165.66	128.22	4.05E+00	0.00E+00	Up	1.03E+00	9.76E-08	Up	8.40E-01	1.46E-08		1.44E+00	6.41E-27	Up	1.04E+00	1.29E-55	Up	6.67E-01	2.56E-21		Unigene107487_All//gi|13161401|dbj|BAB33035.1|//5.00E-17//CPRD48 [Vigna unguiculata]	Unigene107487_All//2.00E-16//AT5G42050| FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013089), Kelch related (InterPro:IPR013089); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27090.1); Has 5084 Blast hits to 2870 proteins in 85 species: Archae - 0; Bacteria - 24; Metazoa - 270; Fungi - 58; Plants - 157; Viruses - 8; Other Eukaryotes - 4567 (source: NCBI BLink).	Unigene107487_All//2.00E-147//TC138767				nr +
Unigene107488_All	1293	0.49	0.55	0.58	0.08	0.21	0.07	0.46	0.78	1.45	1.76E-01	8.17E-01		2.48E-01	7.45E-01		1.47E+00	4.20E-01		-1.41E-01	9.53E-01		7.61E-01	2.28E-01		1.66E+00	1.72E-04	Up	Unigene107488_All//gi|15221299|ref|NP_176986.1|//3.00E-29//zinc finger (B-box type) family protein [Arabidopsis thaliana] >gi|17433041|sp|Q9C9F4.1|COL5_ARATH RecName: Full=Putative zinc finger protein At1g68190	Unigene107488_All//2.00E-31//AT1G68190| zinc finger (B-box type) family protein	Unigene107488_All//0.00E+00//TC157110	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene10749_All	430	0.00	0.00	0.00	0.00	0.00	0.00	3.93	3.69	1.30	null	null		null	null		null	null		null	null		-9.06E-02	8.48E-01		-1.60E+00	5.13E-04	Down			Unigene10749_All//3.00E-27//ES810763				
Unigene107493_All	662	0.00	0.00	0.00	0.00	0.00	0.00	3.13	3.22	0.00	null	null		null	null		null	null		null	null		4.11E-02	9.39E-01		-1.16E+01	2.86E-15	Down	Unigene107493_All//gi|192910824|gb|ACF06520.1|//3.00E-64//60S ribosomal protein L7 [Elaeis guineensis]	Unigene107493_All//1.00E-56//AT3G13580| 60S ribosomal protein L7 (RPL7D)			ko03010|Ribosome		nr -
Unigene107494_All	233	0.00	0.00	0.00	0.00	0.00	0.00	2.54	1.44	0.00	null	null		null	null		null	null		null	null		-8.24E-01	3.48E-01		-1.13E+01	1.42E-04	Down	Unigene107494_All//gi|29539344|dbj|BAC67673.1|//6.00E-14//ribosomal protein S8 [Cyanidioschyzon merolae]	Unigene107494_All//6.00E-13//AT5G20290| 40S ribosomal protein S8 (RPS8A)			ko03010|Ribosome		nr -
Unigene107495_All	392	0.00	0.00	0.00	0.00	0.00	0.00	8.95	0.64	0.20	null	null		null	null		null	null		null	null		-3.81E+00	6.87E-18	Down	-5.46E+00	7.62E-23	Down								
Unigene107501_All	256	0.00	0.00	0.00	0.00	0.00	0.00	2.31	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	2.40E-04	Down	-1.12E+01	1.42E-04	Down								
Unigene107504_All	254	0.00	0.00	0.00	0.00	0.00	0.00	3.50	0.00	0.31	null	null		null	null		null	null		null	null		-1.18E+01	2.24E-06	Down	-3.48E+00	7.34E-05	Down	Unigene107504_All//gi|159471131|ref|XP_001693710.1|//3.00E-06//ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|269969596|sp|A8HS48.1|RS3A_CHLRE RecName: Full=40S ribosomal protein S3a >gi|158283213|gb|EDP08964.1| ribosomal protein S3a [Chlamydomonas reinhardtii]				ko03010|Ribosome		nr +
Unigene107509_All	402	0.00	0.00	0.00	0.00	0.00	0.00	2.31	1.46	0.00	null	null		null	null		null	null		null	null		-6.69E-01	3.12E-01		-1.12E+01	5.48E-07	Down	Unigene107509_All//gi|195615414|gb|ACG29537.1|//1.00E-33//60S ribosomal protein L23a [Zea mays] >gi|195641834|gb|ACG40385.1| 60S ribosomal protein L23a [Zea mays] >gi|195645532|gb|ACG42234.1| 60S ribosomal protein L23a [Zea mays]	Unigene107509_All//2.00E-30//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene107509_All//1.00E-13//DW502458		ko03010|Ribosome		nr +
Unigene10751_All	441	1.31	0.57	0.12	3.16	1.64	0.72	0.38	0.85	0.81	-1.18E+00	2.26E-01		-3.43E+00	1.41E-02		-9.48E-01	8.16E-02		-2.14E+00	6.16E-04	Down	1.15E+00	3.28E-01		1.08E+00	3.50E-01		Unigene10751_All//gi|124359292|gb|ABD28429.2|//3.00E-52//Regulator of chromosome condensation/beta-lactamase-inhibitor protein II [Medicago truncatula]	Unigene10751_All//5.00E-45//AT3G03790| ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein					nr +
Unigene107517_All	309	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.14	1.29	null	null		null	null		null	null		null	null		-3.92E+00	9.81E-04	Down	-6.71E-01	3.86E-01									
Unigene107518_All	267	0.00	0.00	0.00	0.00	0.00	0.00	2.38	0.31	0.00	null	null		null	null		null	null		null	null		-2.92E+00	4.20E-03		-1.12E+01	7.12E-05	Down	Unigene107518_All//gi|60543080|dbj|BAD90789.1|//8.00E-22//histone 3 [Marchantia polymorpha]	Unigene107518_All//2.00E-20//AT1G75600| histone H3.2, putative					nr +
Unigene107519_All	264	0.00	0.00	0.00	0.00	0.00	0.00	2.40	0.00	0.30	null	null		null	null		null	null		null	null		-1.12E+01	1.24E-04	Down	-2.99E+00	2.58E-03									
Unigene107521_All	444	0.00	0.00	0.00	0.00	0.08	0.00	2.10	0.09	0.63	null	null		null	null		6.28E+00	8.39E-01		null	null		-4.48E+00	1.30E-05	Down	-1.74E+00	8.55E-03				Unigene107521_All//2.00E-126//CO128086					
Unigene107532_All	369	0.00	0.00	0.00	0.00	0.00	0.00	6.07	1.02	0.54	null	null		null	null		null	null		null	null		-2.57E+00	2.90E-08	Down	-3.49E+00	2.61E-11	Down	Unigene107532_All//gi|10802935|gb|AAG23683.1|AF288091_28//2.00E-20//apocytochrome b [Thraustochytrium aureum]	Unigene107532_All//1.00E-14//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.				ko00190|Oxidative phosphorylation		nr +
Unigene107537_All	259	0.81	0.00	0.00	0.19	0.13	0.35	5.22	0.32	0.77	-9.66E+00	1.23E-01		-9.66E+00	1.47E-01		-5.32E-01	8.28E-01		8.59E-01	7.97E-01		-4.02E+00	1.80E-07	Down	-2.76E+00	7.51E-06	Down			Unigene107537_All//6.00E-24//TC140227				

Unigene107544_All	240	0.00	0.00	0.00	0.00	0.00	0.00	2.99	0.17	0.00	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-1.15E+01	1.78E-05	Down	Unigene107544_All//gi|6094014|sp|O82528.1|RL15_PETHY//5.00E-11//RecName: Full=60S ribosomal protein L15 >gi|3608479|gb|AAD13389.1| ribosomal protein L15 [Petunia x hybrida]	Unigene107544_All//1.00E-08//AT4G16720| 60S ribosomal protein L15 (RPL15A)			ko03010|Ribosome		nr -
Unigene107546_All	363	0.00	0.00	0.00	0.00	0.00	0.00	2.33	0.12	0.00	null	null		null	null		null	null		null	null		-4.34E+00	4.56E-05	Down	-1.12E+01	2.21E-06	Down	Unigene107546_All//gi|226502949|ref|NP_001149726.1|/2.00E-35//60S ribosomal protein L5-1 [Zea mays] >gi|195629822|gb|ACG36552.1| 60S ribosomal protein L5-1 [Zea mays]	Unigene107546_All//3.00E-30//AT3G25520| ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); 5S rRNA binding / structural constituent of ribosome			ko03010|Ribosome		nr -
Unigene107553_All	232	0.00	0.00	0.00	0.00	0.00	0.00	5.47	1.62	0.34	null	null		null	null		null	null		null	null		-1.75E+00	2.19E-03		-3.99E+00	2.56E-07	Down							ESTscan +
Unigene10756_All	489	0.00	9.53	4.90	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.46E-26	Up	1.23E+01	3.24E-13	Up	null	null		null	null		null	null		null	null								
Unigene107564_All	372	0.00	0.00	0.00	0.00	0.00	0.00	2.50	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	1.15E-06	Down	-1.13E+01	5.48E-07	Down							
Unigene107569_All	273	269.46	298.45	201.69	64.23	100.53	93.30	19.67	198.57	99.82	1.47E-01	1.50E-02		-4.18E-01	1.76E-11		6.46E-01	1.86E-11		5.39E-01	2.80E-07		3.34E+00	7.83E-240	Up	2.34E+00	9.28E-85	Up	Unigene107569_All//gi|255647586|gb|ACU24256.1|//2.00E-16//unknown [Glycine max]		Unigene107569_All//3.00E-66//gi|109847166|gb|DW476146.1|DW476146				nr -
Unigene10757_All	356	0.00	39.85	18.55	0.00	0.00	0.00	0.00	0.00	0.00	1.53E+01	1.82E-81	Up	1.42E+01	7.37E-37	Up	null	null		null	null		null	null		null	null		Unigene10757_All//gi|224005945|ref|XP_002291933.1|//1.00E-18//trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972452|gb|EED90784.1| trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]					GO:0016787	nr +
Unigene107570_All	611	0.00	0.00	0.00	0.00	0.00	15.02	1.78	14.54	null	null			null	null		null	null		null	null		-3.08E+00	3.41E-38	Down	-4.65E-02	7.99E-01		Unigene107570_All//gi|15233696|ref|NP_195527.1|/6.00E-18//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565341|sp|Q9SZL4.1|ATL4N_ARATH RecName: Full=RING-H2 finger protein ATL4N; Flags: Precursor >gi|124301120|gb|ABN04812.1| At4g38140 [Arabidopsis thaliana]	Unigene107570_All//3.00E-19//AT4G38140| zinc finger (C3HC4-type RING finger) family protein			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene107577_All	271	0.00	0.00	0.00	0.00	0.00	0.00	2.81	0.00	0.00	null	null		null	null		null	null		null	null		-1.15E+01	1.68E-05	Down	-1.15E+01	8.89E-06	Down	Unigene107577_All//gi|1256830|gb|AAB68374.1|/2.00E-06//cysteine endopeptidase 1 [Phaseolus vulgaris] >gi|2959418|emb|CAA12118.1| cysteine protease [Phaseolus vulgaris]	Unigene107577_All//5.00E-05//AT3G45310| cysteine proteinase, putative					nr -
Unigene107758_All	991	0.00	0.36	0.54	6.48	8.41	3.24	0.26	0.00	0.24	8.48E+00	2.47E-02		9.07E+00	4.05E-03		3.75E-01	6.65E-02		-1.00E+00	1.24E-05	Down	-8.00E+00	4.06E-02		-8.59E-02	9.57E-01		Unigene107758_All//gi|75296458|sp|Q7XSK0.2|BGL18_ORYSJ//3.00E-58//RecName: Full=Beta-glucosidase 18; Short=Osbglu18; Flags: Precursor >gi|38345329|emb|CAE54546.1| OSJNBa0004N05.26 [Oryza sativa (japonica cultivar-group)] >gi|38345687|emb|CAE01910.2| OSJNBb0070J16.3 [Oryza sativa (japonica cultivar-group)] >gi|116310833|emb|CAH67620.1| OS1GBa0140J09.1 [Oryza sativa (indica cultivar-group)]	Unigene107758_All//4.00E-56//AT4G21760| BGLU47 (Beta-glucosidase 47); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene107758_All//0.00E+00//CO109603		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0008422//GO:0009699//GO:0031410//GO:0043167	nr +
Unigene107582_All	929	0.00	0.00	0.00	0.00	0.00	0.00	4.82	1.75	0.09	null	null		null	null		null	null		null	null		-1.46E+00	6.61E-08	Down	-5.81E+00	8.77E-30	Down	Unigene107582_All//gi|115465379|ref|NP_001056289.1|/1.00E-55//Os05g0557500 [Oryza sativa Japonica Group] >gi|113579840|dbj|BAF18203.1| Os05g0557500 [Oryza sativa Japonica Group]	Unigene107582_All//5.00E-55//AT4G21700| unknown protein	Unigene107582_All//1.00E-117//CO096440				nr +
Unigene107584_All	308	0.00	0.00	0.00	0.00	0.00	0.00	1.92	0.68	0.00	null	null		null	null		null	null		null	null		-1.50E+00	9.14E-02		-1.09E+01	1.42E-04	Down	Unigene107584_All//sp|Q5SA42|DD3_DICDU//2.00E-14//Protein DD3-3 OS=Dictyostelium discoideum GN=DD3-3 PE=2 SV=1						swissprot -
Unigene107585_All	227	0.00	0.00	0.00	0.00	0.00	0.00	3.54	0.18	0.35	null	null		null	null		null	null		null	null		-4.26E+00	8.48E-05	Down	-3.33E+00	2.47E-04	Down							
Unigene107598_All	252	0.00	0.00	0.00	0.00	0.00	0.00	9.06	10.12	0.16	null	null		null	null		null	null		null	null		1.59E-01	6.69E-01		-5.84E+00	2.26E-15	Down	Unigene107598_All//gi|145408590|ref|YP_001152214.1|/3.00E-14//O8F124 [Pinus koraiensis] >gi|145048839|gb|ABF35456.1| O8F124 [Pinus koraiensis]		Unigene107598_All//3.00E-38//gi|11208796|gb|BF277726.1|BF277726				nr +
Unigene1076_All	1674	0.16	3.21	1.08	4.20	6.40	4.86	2.00	14.18	0.36	4.36E+00	4.15E-24	Up	2.79E+00	8.64E-06	Up	6.09E-01	2.23E-04		2.11E-01	3.75E-01		2.83E+00	1.34E-89	Up	-2.48E+00	5.85E-12	Down	Unigene1076_All//gi|57229665|gb|AAW45741.1|/1.00E-179//sinapyl alcohol dehydrogenase-like protein [Populus tremula x Populus tremuloides]	Unigene1076_All//2.00E-111//AT4G37970| CAD6 (CINNAMYL ALCOHOL DEHYDROGENASE 6); binding / catalytic/ oxidoreductase/ zinc ion binding	Unigene1076_All//0.00E+00//TC154710		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene10760_All	452	0.00	0.00	0.00	0.00	0.00	0.00	5.05	2.59	0.62	null	null		null	null		null	null		null	null		-9.64E-01	1.09E-02		-3.03E+00	3.22E-10	Down			Unigene10760_All//2.00E-19//TC149074				
Unigene107612_All	295	0.00	0.00	0.00	0.00	0.00	0.00	1.72	0.00	0.00	null	null		null	null		null	null		null	null		-1.07E+01	8.91E-04	Down	-1.07E+01	5.56E-04	Down	Unigene107612_All//gi|255085060|ref|XP_002504961.1|/7.00E-10//COMPASS/Set1C complex protein [Micromonas sp. RCC299] >gi|226520230|gb|ACO66219.1| COMPASS/Set1C complex protein [Micromonas sp. RCC299]				ko03040|Spliceosome		nr +
Unigene107615_All	252	0.00	0.00	0.00	0.20	0.14	0.00	2.35	0.00	0.16	null	null		null	null		-5.33E-01	8.28E-01		-7.63E+00	6.45E-01		-1.12E+01	2.40E-04	Down	-3.89E+00	1.10E-03		Unigene107615_All//gi|224136035|ref|XP_002322223.1|/3.00E-26//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222869219|gb|EEF06350.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene107615_All//2.00E-22//AT5G50300| xanthine/uracil/vitamin C permease family protein					nr +
Unigene107622_All	243	0.22	1.25	0.00	0.00	0.14	0.00	2.09	0.00	0.00	2.54E+00	1.51E-01		-7.75E+00	6.32E-01		7.15E+00	8.38E-01		null	null		-1.10E+01	8.91E-04	Down	-1.10E+01	5.56E-04	Down			Unigene107622_All//2.00E-14//FL577038				
Unigene10764_All	464	0.00	0.00	0.00	2.68	1.19	0.49	0.18	0.00	1.20	null	null		null	null		-1.18E+00	4.23E-02		-2.46E+00	4.15E-04	Down	-7.51E+00	4.07E-01		2.72E+00	9.38E-03		Unigene10764_All//gi|297834560|ref|XP_002885162.1|/6.00E-24//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331002|gb|EFH01421.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene10764_All//3.00E-24//AT3G16690| nodulin MtN3 family protein				GO:0031224	nr -
Unigene107652_All	239	0.00	0.00	0.00	0.00	0.00	0.00	1.42	0.87	10.33	null	null		null	null		null	null		null	null		-6.95E-01	5.78E-01		2.87E+00	2.95E-10	Up							
Unigene107656_All	1286	0.00	0.00	0.00	0.00	0.00	0.00	3.95	1.27	0.31	null	null		null	null		null	null		null	null		-1.64E+00	2.49E-10	Down	-3.67E+00	8.13E-26	Down	Unigene107656_All//gi|1706590|sp|P50257.1|EF1AS_PORPU//1.00E-102//RecName: Full=Elongation factor 1-alpha S; Short=EF-1-alpha S; AltName: Full=Sporophyte-specific EF-1-alpha >gi|476149|gb|AAA61790.1| EF1-alpha [Porphyra purpurea]	Unigene107656_All//2.00E-123//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene107656_All//1.00E-13//BF275715				nr -
Unigene107659_All	247	37.28	8.21	21.99	7.87	10.73	6.95	1.20	0.34	0.00	-2.18E+00	1.38E-21	Down	-7.62E-01	1.10E-04		4.49E-01	2.82E-01		-1.79E-01	7.02E-01		-1.82E+00	2.11E-01		-1.02E+01	1.59E-02		Unigene107659_All//gi|210061121|gb|ACJ05633.1|//5.00E-10//squalene epoxidase 1 [Nigella sativa]	Unigene107659_All//7.00E-05//AT5G24160| SQE6 (SQUALENE MONOXYGENASE 6); FAD binding / oxidoreductase/ squalene monooxygenase	Unigene107659_All//1.00E-58//CO083658		ko00100|Steroid biosynthesis		nr +
Unigene107661_All	960	0.00	0.00	0.00	0.00	0.00	0.00	3.79	0.00	3.57	null	null		null	null		null	null		null	null		-1.19E+01	1.01E-25	Down	-8.58E-02	7.66E-01		Unigene107661_All//gi|225442485|ref|XP_002278313.1|/2.00E-86//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene107661_All//5.00E-70//AT1G15210| PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATPase, coupled to transmembrane movement of substances					nr -
Unigene107663_All	385	0.00	0.00	0.00	0.00	0.00	0.00	6.37	1.30	0.31	null	null		null	null		null	null		null	null		-2.29E+00	6.20E-08	Down	-4.36E+00	2.22E-14	Down	Unigene107663_All//gi|11466301|ref|NP_051129.1|//2.00E-20//cytochrome c oxidase subunit 3 [Cafeteria roenbergensis] >gi|61890083|gb|AAP05780.1|AF193903_3 cytochrome c oxidase subunit 3 [Cafeteria roenbergensis]	Unigene107663_All//1.00E-07//ATMG00730| Encodes cytochrome c oxidase subunit 3.			ko00190|Oxidative phosphorylation		nr -
Unigene107669_All	283	0.00	0.00	0.00	0.00	0.00	0.00	2.09	0.59	0.00	null	null		null	null		null	null		null	null		-1.82E+00	4.72E-02		-1.10E+01	1.42E-04	Down							
Unigene107673_All	426	0.00	0.36	0.00	0.35	0.16	0.21	1.99	0.20	0.75	8.48E+00	2.36E-01		null	null		-1.12E+00	5.85E-01		-7.27E-01	7.17E-01		-3.34E+00	2.52E-04	Down	-1.41E+00	3.70E-02								
Unigene107684_All	626	0.00	0.00	0.00	0.00	0.17	0.00	2.03	0.40	0.45	null	null		null	null		7.37E+00	4.58E-01		null	null		-2.34E+00	1.56E-04	Down	-2.19E+00	1.97E-04	Down	Unigene107684_All//gi|108710987|gb|ABF98782.1|//2.00E-17//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene107684_All//5.00E-33//AT5G42655| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: disease resistance-responsive family protein (TAIR:AT5G42500.1); Has 121 Blast hits to 121 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 121; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene107684_All//9.00E-25//gi|21098523|gb|BQ410848.1|BQ410848				nr +
Unigene107688_All	233	0.00	0.00	0.00	0.00	0.00	0.00	6.90	2.69	0.85	null	null		null	null		null	null		null	null		-1.36E+00	4.47E-03		-3.01E+00	2.36E-07	Down	Unigene107688_All//gi|4139170|gb|AAD03711.1|//2.00E-38//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene107688_All//5.00E-36//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene107688_All//1.00E-43//TC166357				nr -
Unigene10769_All	436	0.00	6.97	2.93	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.67E-17	Up	1.15E+01	4.69E-07	Up	null	null		null	null		null	null		null	null		Unigene10769_All//sp|P06002|OPS1_DROME//2.00E-40//Opsin Rh1 OS=Drosophila melanogaster GN=ninaE PE=1 SV=1						swissprot -
Unigene107690_All	312	0.00	0.00	0.00	0.00	0.00	0.00	2.44	0.40	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.81E-03		-1.13E+01	8.89E-06	Down	Unigene107690_All//gi|300263896|gb|EFJ48094.1|//6.00E-33//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene107690_All//3.00E-30//AT3G13580| 60S ribosomal protein L7 (RPL7D)	Unigene107690_All//4.00E-07//gi|21100940|gb|BQ413253.1|BQ413253		ko03010|Ribosome		nr -

Unigene107693_All	398	0.00	0.00	0.00	0.00	0.00	0.00	25.92	39.59	151.15	null	null		null	null		null	null		null	null		6.11E-01	1.04E-06		2.54E+00	4.88E-205	Up	Unigene107693_All//gi|224127083|ref|XP_002329388.1|//2.00E-08//predicted protein [Populus trichocarpa] >gi|222870438|gb|EEF07569.1| predicted protein [Populus trichocarpa]		Unigene107693_All//4.00E-78//TC175720				nr +
Unigene107695_All	356	0.00	0.00	0.00	0.00	0.00	0.00	1.66	0.70	0.00	null	null		null	null		null	null		null	null		-1.24E+00	1.54E-01		-1.07E+01	1.42E-04	Down	Unigene107695_All//gi|300123728|emb|CBK25000.2|//5.00E-24//Ribosomal protein L18a [Blastocystis hominis] >gi|300175241|emb|CBK20552.2| Ribosomal protein L18a [Blastocystis hominis]	Unigene107695_All//1.00E-17//AT2G34480| 60S ribosomal protein L18A (RPL18aB)			ko03010|Ribosome		nr -
Unigene1077_All	584	0.63	0.69	3.83	1.88	1.42	0.85	0.94	0.21	0.75	1.46E-01	8.98E-01		2.61E+00	1.40E-06	Up	-4.07E-01	5.61E-01		-1.14E+00	8.74E-02		-2.13E+00	3.32E-02		-3.27E-01	6.72E-01		Unigene1077_All//gi|224089188|ref|XP_002308654.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222854630|gb|EEE92177.1| predicted protein [Populus trichocarpa]		Unigene1077_All//6.00E-146//gi|78350462|gb|DT570736.1|DT570736				nr -
Unigene107708_All	558	0.00	1.18	0.29	0.18	0.19	0.65	0.15	0.22	0.07	1.02E+01	6.26E-04	Up	8.16E+00	2.40E-01		5.24E-02	9.68E-01		1.86E+00	2.20E-01		5.69E-01	7.83E-01		-1.09E+00	6.77E-01		Unigene107708_All//gi|224134959|ref|XP_002327532.1|//6.00E-13//f-box family protein [Populus trichocarpa] >gi|222836086|gb|EEE74507.1| f-box family protein [Populus trichocarpa]		Unigene107708_All//0.00E+00//TC178035				nr +
Unigene10771_All	321	0.00	0.95	1.16	0.00	0.11	0.00	115.38	321.61	385.11	9.89E+00	4.45E-02		1.02E+01	2.50E-02		6.75E+00	8.38E-01		null	null		1.48E+00	3.94E-168	Up	1.74E+00	2.87E-259	Up	Unigene10771_All//gi|197312909|gb|ACH63235.1|//2.00E-37//alcohol dehydrogenase [Rheum australe]	Unigene10771_All//3.00E-35//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene10771_All//8.00E-36//gi|13355011|gb|BG445359.1|BG445359		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0004030//GO:0009698	nr -
Unigene107727_All	211	13.39	12.49	34.83	30.22	23.01	29.32	1.60	2.18	1.89	-1.01E-01	7.77E-01		1.38E+00	4.50E-09	Up	-3.93E-01	9.17E-02		-4.34E-02	8.79E-01		4.43E-01	6.32E-01		2.36E-01	8.05E-01					Unigene107727_All//3.00E-37//TC163844				
Unigene107728_All	322	0.00	0.00	0.00	0.00	0.00	2.49	0.65	0.00	null	null			null	null		null	null		null	null		-1.94E+00	1.17E-02		-1.13E+01	4.43E-06	Down								ESTscan -
Unigene10774_All	490	0.11	0.41	0.98	1.63	6.32	4.89	0.09	0.09	0.00	1.95E+00	3.76E-01		3.20E+00	3.48E-02		1.96E+00	1.92E-07	Up	1.59E+00	2.41E-04	Up	-1.68E-02	1.01E+00		-6.43E+00	6.17E-01									
Unigene107743_All	926	0.00	0.00	0.00	0.11	0.00	0.20	7.08	0.54	1.12	null	null		null	null		-6.75E+00	3.17E-01		8.59E-01	6.96E-01		-3.71E+00	2.73E-32	Down	-2.66E+00	1.61E-24	Down	Unigene107743_All//sp|Q5VU43|MYOME_HUMAN//7.00E-07//Myomegalin OS=Homo sapiens GN=PDE4DIP PE=2 SV=1		Unigene107743_All//2.00E-125//TC161176				swissprot +
Unigene107753_All	1494	0.00	0.00	0.00	0.00	0.00	0.00	4.47	1.15	0.48	null	null		null	null		null	null		null	null		-1.96E+00	6.48E-17	Down	-3.22E+00	3.45E-30	Down	Unigene107753_All//gi|8928433|sp|Q92581.1|TB81_CYAPA//0.00E+00//RecName: Full=Tubulin beta-1 chain; AltName: Full=Beta-1-tubulin >gi|413917|gb|AAD03712.1| beta 1 tubulin [Cyanophora paradoxa]	Unigene107753_All//0.00E+00//AT5G12250| TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton	Unigene107753_All//2.00E-43//TC130221		ko04145|Phagosome		nr +
Unigene107754_All	245	0.00	2.69	4.35	6.91	34.15	44.43	0.35	0.00	0.33	1.14E+01	6.26E-04	Up	1.21E+01	6.63E-06	Up	2.30E+00	8.18E-24	Up	2.68E+00	5.27E-34	Up	-8.43E+00	4.07E-01		-8.57E-02	9.74E-01		Unigene107754_All//gi|30725324|gb|AAP37684.1|//2.00E-13//At3g01680 [Arabidopsis thaliana]	Unigene107754_All//9.00E-15//AT3G01680| unknown protein	Unigene107754_All//6.00E-101//TC134810				nr +
Unigene107757_All	360	0.00	0.00	0.00	0.00	0.00	0.00	3.29	1.04	0.44	null	null		null	null		null	null		null	null		-1.65E+00	5.03E-03		-2.89E+00	2.03E-05	Down	Unigene107757_All//gi|29539344|dbj|BAC67673.1|//8.00E-32//ribosomal protein S8 [Cyanidioschyzon merolae]	Unigene107757_All//1.00E-32//AT5G20290| 40S ribosomal protein S8 (RPS8A)			ko03010|Ribosome		nr -
Unigene10776_All	223	0.00	6.59	1.19	0.00	0.31	0.00	0.00	0.00	0.00	1.27E+01	2.11E-08	Up	1.02E+01	8.03E-02		8.27E+00	6.15E-01		null	null		null	null		null	null									
Unigene107764_All	1104	0.09	0.00	0.10	0.63	0.47	0.16	4.02	0.57	0.14	-6.57E+00	3.76E-01		2.56E-02	1.00E+00		-4.33E-01	6.06E-01		-1.95E+00	3.91E-02		-2.82E+00	2.72E-17	Down	-4.80E+00	4.46E-27	Down	Unigene107764_All//gi|224069166|ref|XP_002302916.1|//1.00E-104//GRAS family protein [Populus trichocarpa] >gi|222844642|gb|EEE82189.1| GRAS family protein [Populus trichocarpa]	Unigene107764_All//3.00E-89//AT4G08250| scarecrow transcription factor family protein	Unigene107764_All//0.00E+00//gi|21099408|gb|BQ411721.1|BQ411721	GRAS			nr -
Unigene10777_All	243	0.22	0.00	0.00	6.56	2.27	0.00	0.00	0.00	0.00	-7.75E+00	6.20E-01		-7.75E+00	6.32E-01		-1.53E+00	2.44E-03		-1.27E+01	5.79E-10	Down	null	null		null	null									
Unigene10771_All	222	0.00	0.00	0.00	0.00	0.00	0.00	2.29	0.38	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.05E-02		-1.12E+01	5.56E-04	Down								ESTscan +
Unigene10772_All	300	0.00	0.00	0.00	0.00	0.00	0.00	3.95	0.70	0.00	null	null		null	null		null	null		null	null		-2.50E+00	1.47E-04	Down	-1.19E+01	8.15E-09	Down								
Unigene107775_All	241	0.65	0.63	0.88	1.45	1.86	1.31	1.75	0.35	6.45	-4.64E-02	9.90E-01		4.40E-01	7.76E-01		3.60E-01	8.07E-01		-1.41E-01	9.12E-01		-2.34E+00	5.47E-02		1.88E+00	2.07E-04	Up	Unigene107775_All//gi|212717129|gb|ACJ37406.1|//9.00E-13//stress-induced receptor-like kinase [Glycine max]	Unigene107775_All//7.00E-05//AT4G32300| SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase	Unigene107775_All//3.00E-75//ES826968				nr +
Unigene107776_All	318	0.00	0.00	0.00	0.00	0.00	0.00	1.86	1.05	0.00	null	null		null	null		null	null		null	null		-8.24E-01	3.48E-01		-1.09E+01	1.42E-04	Down	Unigene107776_All//gi|192910756|gb|ACF06486.1|//6.00E-35//60S ribosomal protein L11 [Elaeis guineensis] >gi|192910758|gb|ACF06487.1| 60S ribosomal protein L11 [Elaeis guineensis]	Unigene107776_All//7.00E-25//AT5G45775| 60S ribosomal protein L11 (RPL11D)	Unigene107776_All//1.00E-09//TC154176		ko03010|Ribosome		nr -
Unigene107779_All	238	0.00	0.00	0.00	0.00	0.00	0.00	2.84	0.00	0.00	null	null		null	null		null	null		null	null		-1.15E+01	6.35E-05	Down	-1.15E+01	3.57E-05	Down								ESTscan +
Unigene107790_All	347	0.45	1.75	0.92	0.43	0.00	0.26	4.02	0.36	0.46	1.95E+00	6.04E-02		1.03E+00	4.71E-01		-8.75E+00	1.66E-01		-7.27E-01	7.17E-01		-3.48E+00	5.80E-07	Down	-3.13E+00	1.09E-06	Down			Unigene107790_All//1.00E-47//TC138513				
Unigene107793_All	231	0.00	0.00	0.00	0.00	0.00	0.00	2.93	0.54	0.00	null	null		null	null		null	null		null	null		-2.43E+00	7.77E-03		-1.15E+01	3.57E-05	Down	Unigene107793_All//gi|15224284|ref|NP_181874.1|//4.00E-15//60S ribosomal protein L38 (RPL38A) [Arabidopsis thaliana] >gi|15231705|ref|NP_191513.1| 60S ribosomal protein L38 (RPL38B) [Arabidopsis thaliana] >gi|297820788|ref|XP_002878277.1| 60S ribosomal protein L38 [Arabidopsis lyrata subsp. lyrata] >gi|297828045|ref|XP_002881905.1| 60S ribosomal protein L38 [Arabidopsis lyrata subsp. lyrata] >gi|3122724|sp|O22860.1|RL38_ARATH RecName: Full=60S ribosomal protein L38 >gi|13605720|gb|AAX32853.1|AF36184 1_1 AT3g59540/T16L24_90 [Arabidopsis thaliana] >gi|2289009|gb|AAB64338.1| 60S ribosomal protein L38 [Arabidopsis thaliana] >gi|6996290|emb|CAB75451.1| 60S RIBOSOMAL PROTEIN L38-like protein [Arabidopsis thaliana] >gi|21593879|gb|AAM65846.1| 60S RIBOSOMAL PROTEIN L38-like protein [Arabidopsis thaliana] >gi|23507723|gb|AAX38690.1| At3g59540/T16L24_90 [Arabidopsis	Unigene107793_All//2.00E-16//AT3G59540| 60S ribosomal protein L38 (RPL38B)			ko03010|Ribosome		nr -
Unigene107803_All	446	0.00	0.00	0.00	0.00	0.00	12.13	3.09	0.98	null	null		null	null		null	null		null	null		-1.97E+00	6.32E-14	Down	-3.63E+00	3.14E-27	Down	Unigene107803_All//gi|18076136|emb|CAC80486.1|//5.00E-49//cytochrome oxidase subunit I [Musa acuminata]	Unigene107803_All//1.00E-46//ATMG01360| cytochrome c oxidase subunit I	Unigene107803_All//3.00E-08//EX172657		ko00190|Oxidative phosphorylation		nr -
Unigene10781_All	470	0.45	2.48	1.36	5.51	3.44	2.79	0.81	0.71	0.34	2.48E+00	9.80E-04	Up	1.61E+00	1.11E-01		-6.79E-01	7.37E-02		-9.84E-01	1.20E-02		-1.87E-01	8.57E-01		-1.26E+00	2.48E-01		Unigene10781_All//gi|297846424|ref|XP_002891093.1|//1.00E-55//phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336935|gb|EFH67352.1| phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene10781_All//9.00E-44//AT1G34260| phosphatidylinositol-4-phosphate 5-kinase family protein	Unigene10781_All//5.00E-75//CA993882		ko04145|Phagosome//ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0016307//GO:0019538//GO:0030384//GO:0032559	nr +
Unigene107810_All	442	0.00	0.00	0.00	0.00	0.00	0.10	1.53	1.42	0.09	null	null		null	null		null	null		6.68E+00	7.03E-01		-1.10E-01	8.90E-01		-4.09E+00	3.10E-04	Down								
Unigene10782_All	546	0.00	0.00	0.00	0.00	0.00	0.00	2.01	2.37	0.00	null	null		null	null		null	null		null	null		2.37E-01	6.52E-01		-1.10E+01	3.33E-08	Down	Unigene10782_All//gi|297829134|ref|XP_002882469.1|//6.00E-25//dual specificity protein phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328289|gb|EFH58708.1| dual specificity protein phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene10782_All//1.00E-25//AT3G06110| MKP2 (MAPK PHOSPHATASE 2); MAP kinase phosphatase/ protein tyrosine/serine/threonine phosphatase				GO:0004721//GO:0005515//GO:0016020//GO:0042221//GO:0043231//GO:0043405	nr +
Unigene107820_All	409	0.00	0.00	0.00	0.24	0.00	0.00	1.65	0.10	0.39	null	null		null	null		-7.93E+00	3.17E-01		-7.93E+00	4.05E-01		-4.02E+00	5.36E-04	Down	-2.09E+00	1.27E-02									
Unigene107821_All	255	0.00	0.00	0.00	0.00	0.00	0.00	2.32	0.49	0.00	null	null		null	null		null	null		null	null		-2.24E+00	2.07E-02		-1.12E+01	1.42E-04	Down								
Unigene107826_All	296	0.53	0.17	0.90	2.19	0.23	0.00	0.86	0.00	0.00	-1.63E+00	4.89E-01		7.62E-01	6.44E-01		-3.23E+00	2.49E-03		-1.11E+01	3.90E-04	Down	-9.74E+00	4.06E-02		-9.74E+00	3.06E-02		Unigene107826_All//gi|73921149|sp|Q9LV66.1|YS848_ARATH//6.00E-06//RecName: Full=Uncharacterized protein At5g48480	Unigene107826_All//2.00E-07//AT5G48480| unknown protein	Unigene107826_All//1.00E-77//TC151304				nr +
Unigene107828_All	269	0.78	0.00	0.00	0.19	0.00	0.00	2.04	0.00	0.00	-9.60E+00	1.23E-01		-9.60E+00	1.47E-01		-7.53E+00	5.63E-01		-7.53E+00	6.45E-01		-1.10E+01	4.62E-04	Down	-1.10E+01	2.81E-04	Down								
Unigene10783_All	469	0.00	8.21	2.38	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	6.33E-22	Up	1.12E+01	3.44E-06	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene107837_All	230	0.00	0.00	0.00	0.00	0.00	0.00	2.76	0.73	0.00	null	null		null	null		null	null		null	null		-1.92E+00	3.10E-02		-1.14E+01	7.12E-05	Down			Unigene107837_All//7.00E-17//TC147981				
Unigene107838_All	266	0.00	0.00	0.00	0.00	0.00	0.00	2.38	0.00	0.60	null	null		null	null		null	null		null	null		-1.12E+01	1.24E-04	Down	-1.99E+00	2.04E-02									
Unigene10784_All	367	7.41	3.45	2.47	4.75	2.81	1.85	1.84	1.14	1.63	-1.10E+00	4.26E-03		-1.59E+00	1.72E-04	Down	-7.55E-01	1.15E-01		-1.36E+00	6.97E-03		-6.95E-01	3.94E-01		-1.79E-01	7.94E-01				Unigene10784_All//8.00E-166//TC171472				
Unigene10785_All	343	0.00	0.30	0.00	0.00	0.00	0.00	0.74	2.80	5.58	8.21E+00	3.90E-01		null	null		null	null		null	null		1.92E+00	5.42E-03		2.91E+00	3.25E-08	Up								
Unigene107856_All	410	0.00	0.00	0.00	0.00	0.00	0.00	1.75	0.41	0.19	null	null		null	null		null	null		null	null		-2.10E+00	1.25E-02		-3.17E+00	8.09E-04	Down	Unigene107856_All//gi|300259453|gb|EFJ43680.1|//2.00E-17//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene107856_All//2.00E-14//AT4G25740| 40S ribosomal protein S10 (RPS10A)			ko03010|Ribosome		nr -
Unigene10786_All	360	2.03	1.41	1.18	1.11	0.19	1.51	0.23	6.85	2.77	-5.32E-01	5.13E-01		-7.82E-01	3.80E-01		-2.53E+00	5.80E-02		4.44E-01	6.78E-01		4.87E+00	1.04E-14	Up	3.56E+00	2.43E-05	Up	Unigene10786_All//gi|297804080|ref|XP_002869924.1|//1.00E-25//FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315760|gb|EFH46183.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene10786_All//1.00E-22//AT4G20840| FAD-binding domain-containing protein	Unigene10786_All//3.00E-23//TC163182			GO:0005576//GO:0005618//GO:0006950//GO:0016020//GO:0016491//GO:0043231	nr -

Unigene10787_All	402	0.00	0.00	0.00	0.00	0.00	0.00	3.37	3.64	0.20	null	null		null	null		null	null		null	null		1.13E-01	8.23E-01		-4.09E+00	7.07E-08	Down	Unigene10787_All//gi|195619738|gb|ACG31699.1|//5.00E-32//60S ribosomal protein L4 [Zea mays]	Unigene10787_All//6.00E-28//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)			ko03010|Ribosome	GO:0005622	nr -
Unigene107876_All	388	0.00	0.00	0.00	0.00	0.00	0.00	1.85	1.72	0.00	null	null		null	null		null	null		null	null		-1.04E-01	8.93E-01		-1.09E+01	1.78E-05	Down			Unigene107876_All//6.00E-145//ES842468					
Unigene107882_All	228	0.00	0.00	0.00	0.00	0.00	0.00	6.49	1.47	8.56	null	null		null	null		null	null		null	null		-2.15E+00	9.69E-05	Down	4.00E-01	3.41E-01		Unigene107882_All//gi|125887|sp|P13447.1|LAT52_SOLLC//2.00E-10//RecName: Full=Anther-specific protein LAT52; Flags: Precursor >gi|295812|emb|CAA33854.1| LAT52 [Solanum lycopersicum]	Unigene107882_All//1.00E-08//AT4G18596| pollen Ole e 1 allergen and extensin family protein	Unigene107882_All//5.00E-67//TC149258				nr +
Unigene107889_All	237	0.00	0.00	0.00	3.15	1.60	0.19	1.07	0.71	0.67	null	null		null	null		-9.80E-01	2.23E-01		-4.05E+00	7.76E-04	Down	-6.02E-01	6.48E-01		-6.71E-01	6.06E-01									
Unigene10789_All	311	0.00	15.31	11.30	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	3.83E-27	Up	1.35E+01	1.87E-19	Up	null	null		null	null		null	null		null	null		Unigene10789_All//gi|1173043|sp|P46291.1|RL38_SOLLC//4.00E-25//RecName: Full=60S ribosomal protein L38 >gi|313027|emb|CAA49599.1| ribosomal protein L38 [Solanum lycopersicum] >gi|77745467|gb|ABB02632.1| ribosomal protein L38-like [Solanum tuberosum]	Unigene10789_All//2.00E-15//AT3G39540| 60S ribosomal protein L38 (RPL38B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +
Unigene107893_All	247	0.00	0.00	0.00	0.20	0.00	0.00	2.05	0.00	0.97	null	null		null	null		-7.66E+00	5.63E-01		-7.66E+00	6.45E-01		-1.10E+01	8.91E-04	Down	-1.09E+00	2.28E-01		Unigene107893_All//gi|4206110|gb|AAD11424.1|//5.00E-07//cytochrome [Mesembryanthemum crystallinum]							nr -
Unigene107897_All	448	0.00	0.00	0.00	0.00	0.00	0.00	1.60	0.00	0.09	null	null		null	null		null	null		null	null		-1.06E+01	3.27E-05	Down	-4.17E+00	1.65E-04	Down								ESTscan -
Unigene1079_All	2873	29.37	22.50	24.15	29.67	19.37	14.43	74.41	71.01	26.75	-3.84E-01	8.50E-12		-2.83E-01	1.27E-06		-6.15E-01	8.92E-33		-1.04E+00	3.27E-71	Down	-6.74E-02	5.16E-02		-1.48E+00	0.00E+00	Down	Unigene1079_All//gi|187940724|gb|ACD39463.1|//1.00E-170//BEL30 protein [Solanum etuberosum]	Unigene1079_All//5.00E-117//AT4G34610| BLH6 (BELL1-LIKE HOMEODOMAIN 6); DNA binding / transcription factor	Unigene1079_All//0.00E+00//TC144172	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene107904_All	393	0.00	0.00	0.14	0.00	0.00	0.00	2.15	0.21	0.20	null	null		7.08E+00	6.41E-01		null	null		null	null		-3.34E+00	2.52E-04	Down	-3.41E+00	1.35E-04	Down								
Unigene107918_All	273	0.00	0.00	0.00	0.18	0.00	0.33	1.86	0.00	0.15	null	null		null	null		-7.51E+00	5.63E-01		8.59E-01	7.97E-01		-1.09E+01	8.91E-04	Down	-3.67E+00	3.75E-03				Unigene107918_All//8.00E-119//TC143380					
Unigene107919_All	238	0.00	0.00	0.00	0.00	0.14	0.00	3.02	0.18	0.67	null	null		null	null		7.18E+00	8.38E-01		null	null		-4.10E+00	2.91E-04	Down	-2.17E+00	7.76E-03									
Unigene107926_All	633	0.25	0.24	0.34	0.47	0.27	0.00	1.67	0.99	0.19	-4.67E-02	9.90E-01		4.40E-01	7.76E-01		-7.96E-01	5.57E-01		-8.88E+00	4.01E-02		-7.54E-01	2.17E-01		-3.14E+00	2.97E-05	Down	Unigene107926_All//gi|108864366|gb|ABA93633.2|//8.00E-08//Protein kinase domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]							nr +
Unigene107934_All	529	0.00	0.00	0.20	0.75	0.07	0.17	2.24	0.40	0.30	null	null		7.65E+00	4.02E-01		-3.53E+00	2.10E-02		-2.14E+00	1.26E-01		-2.50E+00	1.47E-04	Down	-2.89E+00	2.03E-05	Down								
Unigene10794_All	358	1.02	5.94	5.06	0.14	1.25	0.38	1.54	0.58	0.00	2.54E+00	2.15E-06	Up	2.31E+00	8.14E-05	Up	3.17E+00	3.95E-02		1.44E+00	6.39E-01		-1.40E+00	1.35E-01		-1.06E+01	2.81E-04	Down		Unigene10794_All//3.00E-05//AT3G53880| aldo/keto reductase family protein	Unigene10794_All//3.00E-14//gi|48805189|gb|CO106503.1|CO106503					
Unigene107942_All	296	0.00	0.00	0.00	0.00	0.00	0.00	2.14	0.00	0.13	null	null		null	null		null	null		null	null		-1.11E+01	1.24E-04	Down	-3.99E+00	5.83E-04	Down								
Unigene107947_All	224	0.70	0.00	0.00	1.78	0.46	0.00	2.83	0.19	0.18	-9.45E+00	2.17E-01		-9.45E+00	2.46E-01		-1.95E+00	1.19E-01		-1.08E+01	1.11E-02		-3.92E+00	9.81E-04	Down	-3.99E+00	5.83E-04	Down								
Unigene10795_All	445	0.35	0.00	0.00	5.49	4.26	0.91	1.24	0.19	0.18	-8.46E+00	2.17E-01		-8.46E+00	2.46E-01		-3.66E-01	3.91E-01		-2.59E+00	6.96E-08	Down	-2.72E+00	1.22E-02		-2.79E+00	7.97E-03		Unigene10795_All//gi|122209356|sp|Q2V313.1|EPFL4_ARATH//3.00E-26//RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 4; Short=EPF-like protein 4; Flags: Precursor	Unigene10795_All//1.00E-14//AT3G22820| allergen-related	Unigene10795_All//0.00E+00//CO071488			GO:0009791//GO:0009913	nr -
Unigene107956_All	336	12.77	7.54	16.48	23.42	23.78	17.88	34.48	13.68	15.41	-7.60E-01	9.33E-03		3.68E-01	1.77E-01		2.15E-02	9.45E-01		-3.90E-01	6.96E-02		-1.33E+00	7.46E-17	Down	-1.16E+00	3.51E-14	Down	Unigene107956_All//gi|47026989|gb|AAT08712.1|//9.00E-13//nucleoside diphosphate kinase [Hyacinthus orientalis]	Unigene107956_All//9.00E-13//AT4G09320| NDPK1; ATP binding / nucleoside diphosphate kinase	Unigene107956_All//6.00E-74//gi|109828864|gb|DW227483.1|DW227483		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism		nr -
Unigene107957_All	551	0.00	0.00	0.00	0.45	0.06	0.00	2.46	0.76	0.58	null	null		null	null		-2.85E+00	1.37E-01		-8.82E+00	7.36E-02		-1.69E+00	1.96E-03		-2.09E+00	1.85E-04	Down	Unigene107957_All//gi|15225548|ref|NP_182094.1|//5.00E-79//sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	Unigene107957_All//3.00E-80//AT2G45700| sterile alpha motif (SAM) domain-containing protein	Unigene107957_All//0.00E+00//TC179553				nr -
Unigene107962_All	733	0.00	0.00	0.00	0.00	0.00	0.00	7.15	0.11	0.76	null	null		null	null		null	null		null	null		-5.97E+00	7.48E-34	Down	-3.23E+00	6.29E-24	Down	Unigene107962_All//gi|115474639|ref|NP_001060916.1|//4.00E-46//Os08g0129600 [Oryza sativa Japonica Group] >gi|29467327|dbj|BAC66716.1| proline-rich protein family-like [Oryza sativa Japonica Group] >gi|113622885|dbj|BAF22830.1| Os08g0129600 [Oryza sativa Japonica Group]	Unigene107962_All//3.00E-36//AT3G25690| CHUP1 (CHLOROPLAST UNUSUAL POSITIONING 1)	Unigene107962_All//1.00E-70//TC132881				nr -
Unigene107984_All	249	0.00	0.00	0.00	0.60	0.55	0.00	3.40	0.17	0.16	null	null		null	null		-1.18E-01	9.11E-01		-9.23E+00	2.35E-01		-4.34E+00	4.56E-05	Down	-4.41E+00	2.37E-05	Down			Unigene107984_All//8.00E-51//TC140956					
Unigene107989_All	624	0.00	0.00	0.00	0.00	0.00	0.00	2.44	0.60	0.13	null	null		null	null		null	null		null	null		-2.02E+00	1.51E-04	Down	-4.26E+00	5.22E-09	Down			Unigene107989_All//9.00E-19//TC142576					
Unigene10799_All	266	0.00	4.38	2.80	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	1.15E+01	3.28E-04	Up	null	null		null	null		null	null		null	null									
Unigene107998_All	448	0.00	0.00	0.00	0.00	0.00	0.00	1.51	0.00	0.09	null	null		null	null		null	null		null	null		-1.06E+01	6.35E-05	Down	-4.09E+00	3.10E-04	Down	Unigene107998_All//gi|222874561|gb|EEF11692.1|//5.00E-09//predicted protein [Populus trichocarpa]							nr +
Unigene10801_All	354	0.00	10.59	6.92	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.40E-21	Up	1.28E+01	1.64E-13	Up	null	null		null	null		null	null		null	null		Unigene10801_All//gi|255089517|ref|XP_002506680.1|//4.00E-33//ribosomal protein L37ae [Micromonas sp. RCC299] >gi|226457652|gb|EEH54951.1| ribosomal protein L37ae [Micromonas pusilla CCMP1545] >gi|226521953|gb|ACO67938.1| ribosomal protein L37ae [Micromonas sp. RCC299]	Unigene10801_All//2.00E-33//AT3G60245| 60S ribosomal protein L37a (RPL37aC)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613//GO:0043169//GO:0043231	nr -
Unigene108015_All	404	0.00	0.00	0.00	0.25	0.26	0.00	5.02	1.14	1.08	null	null		null	null		5.23E-02	9.68E-01		-7.95E+00	4.05E-01		-2.14E+00	3.19E-06	Down	-2.21E+00	1.05E-06	Down	Unigene108015_All//gi|224112451|ref|XP_002332774.1|//3.00E-09//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834669|gb|EEE73132.1| cc-nbs-lrr resistance protein [Populus trichocarpa]							nr -
Unigene108016_All	458	0.00	0.00	0.00	0.00	0.00	0.00	1.94	0.09	0.17	null	null		null	null		null	null		null	null		-4.41E+00	2.44E-05	Down	-3.48E+00	7.34E-05	Down	Unigene108016_All//gi|300267685|gb|EFJ51868.1|//9.00E-14//dynein heavy chain 4 [Volvox carteri f. nagariensis]				ko04141|Protein processing in endoplasmic reticulum//ko03420|Nucleotide excision repair		nr -
Unigene108017_All	449	0.00	0.00	0.00	0.11	0.00	0.00	5.08	3.54	0.62	null	null		null	null		-6.79E+00	5.63E-01		-6.79E+00	6.45E-01		-5.24E-01	1.77E-01		-3.03E+00	3.22E-10	Down			Unigene108017_All//6.00E-22//TC149187					
Unigene108037_All	425	0.00	0.00	0.00	0.00	0.00	0.00	1.89	0.49	0.09	null	null		null	null		null	null		null	null		-1.94E+00	1.17E-02		-4.33E+00	4.54E-05	Down	Unigene108037_All//gi|9979193|sp|Q92KU0.1|TCTP_PSEMZ//4.00E-06//RecName: Full=Translationally-controlled tumor protein homolog; Short=TCTP >gi|3850844|emb|CAA10048.1| TCTP-like protein [Pseudotsuga menziesii]	Unigene108037_All//3.00E-05//AT3G16640| TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN)					nr -
Unigene108040_All	461	0.23	0.00	0.23	0.00	0.75	0.20	1.65	0.18	0.95	-7.83E+00	3.76E-01		2.52E-02	1.00E+00		9.55E+00	3.02E-02		7.61E+00	4.81E-01		-3.19E+00	7.93E-04	Down	-7.96E-01	2.52E-01		Unigene108040_All//gi|145358569|ref|NP_198529.3|//1.00E-17//binding [Arabidopsis thaliana]	Unigene108040_All//7.00E-14//AT5G37130| binding	Unigene108040_All//2.00E-163//TC134980				nr -
Unigene108046_All	383	0.14	1.19	0.56	0.13	0.18	0.00	0.33	0.11	2.39	3.12E+00	3.58E-02		2.03E+00	3.62E-01		4.67E-01	9.61E-01		-7.02E+00	6.45E-01		-1.60E+00	5.35E-01		2.85E+00	3.18E-04	Up	Unigene108046_All//gi|15222311|ref|NP_172195.1|//1.00E-18//MAPKKK13; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|8954031|gb|AAF82205.1|AC067971_13 Strong similarity to a protein kinase homolog F23F1.4 gi|7488253 from Arabidopsis thaliana BAC F23F1 gb|AC004680. It contains a eukaryotic protein kinase domain PF|00069. ESTs gb|F13903 and gb|F13904 come from this gene	Unigene108046_All//6.00E-20//AT1G07150| MAPKKK13; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene108046_All//2.00E-142//TC161841				nr +
Unigene108050_All	491	0.00	0.00	0.00	0.00	0.00	0.00	5.34	0.26	0.65	null	null		null	null		null	null		null	null		-4.39E+00	8.13E-15	Down	-3.04E+00	1.19E-11	Down	Unigene108050_All//gi|226496173|ref|NP_001152735.1|//7.00E-06//phytosulfokines 4 [Zea mays] >gi|195659479|gb|ACG49207.1| phytosulfokines 4 precursor [Zea mays]	Unigene108050_All//2.00E-05//AT3G49780| ATPSK4 (PHYTOSULFOKINE 4 PRECURSOR); growth factor					nr -
Unigene108057_All	300	0.00	0.00	0.00	0.33	0.00	0.00	6.34	5.85	0.66	null	null		null	null		-8.38E+00	3.17E-01		-8.38E+00	4.05E-01		-1.16E-01	7.89E-01		-3.26E+00	3.59E-09	Down			Unigene108057_All//1.00E-19//TC134836					
Unigene108058_All	224	0.00	0.00	0.00	0.00	0.00	0.20	3.02	1.68	0.00	null	null		null	null		null	null		7.66E+00	7.03E-01		-8.47E-01	2.88E-01		-1.16E+01	3.57E-05	Down			Unigene108058_All//3.00E-07//EX169661					
Unigene10806_All	231	0.00	3.29	4.38	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.77E-04	Up	1.21E+01	1.28E-05	Up	null	null		null	null		null	null		null	null		Unigene10806_All//sp|O00322|UPK1A_HUMAN//1.00E-12//Uroplakin-1a OS=Homo sapiens GN=UPK1A PE=2 SV=1							swissprot +
Unigene108067_All	335	0.00	0.00	0.00	0.00	0.00	0.00	2.15	0.00	0.36	null	null		null	null		null	null		null	null		-1.11E+01	3.27E-05	Down	-2.59E+00	2.81E-03		Unigene108067_All//sp|Q8BP40|PPA6_MOUSE//3.00E-06//Lysophosphatidic acid phosphatase type 6 OS=Mus musculus GN=Acp6 PE=2 SV=1							swissprot +
Unigene108076_All	333	0.00	0.00	0.00	0.00	0.00	0.00	2.67	0.38	0.00	null	null		null	null		null	null		null	null		-2.82E+00	5.65E-04	Down	-1.14E+01	1.10E-06	Down			Unigene108076_All//4.00E-07//gi|48746449|gb|CO076968.1|CO076968					
Unigene108087_All	294	0.00	0.00	0.00	0.00	0.00	0.00	2.01	0.85	0.00	null	null		null	null		null	null		null	null		-1.24E+00	1.54E-01		-1.10E+01	1.42E-04	Down	Unigene108087_All//gi|223994173|ref|XP_002286770.1|//4.00E-10//udp-d-glucose 6-dehydrogenase [Thalassiosira pseudonana CCMP1335] >gi|220978085|gb|EED96411.1| udp-d-glucose 6-dehydrogenase [Thalassiosira pseudonana CCMP1335]				ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene108089_All	428	0.00	0.00	0.00	0.00	0.00	0.00	2.57	0.29	0.00	null	null		null	null		null	null		null	null		-3.13E+00	3.47E-05	Down	-1.13E+01	3.33E-08	Down	Unigene108089_All//gi|297829496|ref|XP_002882630.1|//1.00E-21//60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata] >gi|297328470|gb|EFH58889.1| 60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata]	Unigene108089_All//4.00E-22//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)			ko03010|Ribosome		nr -
Unigene10809_All	356	0.00	0.00	0.00	0.00	0.00	0.00	9.74	6.69	0.22	null	null		null	null		null	null		null	null		-5.41E-01	7.19E-02		-5.44E+00	1.52E-22	Down			Unigene10809_All//8.00E-27//gi|109850443|gb|DW479422.1|DW479422					
Unigene108104_All	595	0.18	0.94	0.54	0.25	0.17	0.15	3.41	1.19	0.67	2.41E+00	3.93E-02		1.61E+00	3.05E-01		-5.33E-01	7.86E-01		-7.27E-01	7.17E-01		-1.51E+00	3.50E-04	Down	-2.35E+00	3.80E-07	Down								
Unigene108108_All	662	0.00	0.00	0.00	0.00	0.00	0.00	6.20	1.77	0.00	null	null		null	null		null	null		null	null		-1.81E+00	1.21E-09	Down	-1.26E+01	3.74E-30	Down			Unigene108108_All//2.00E-35//TC175328					
Unigene108114_All	262	30.75	15.08	12.40	19.96	13.80	12.24	2.10	74.98	0.61	-1.03E+00	8.45E-07	Down	-1.31E+00	3.61E-09	Down	-5.33E-01	3.49E-02		-7.06E-01	6.29E-03		5.16E+00	3.33E-118	Up	-1.79E+00	5.07E-02		Unigene108114_All//gi|146148631|gb|ABQ02258.1|//4.00E-34//O-glucosyltransferase 3 [Vitis labrusca]	Unigene108114_All//2.00E-28//AT1G05560| UGT75B1 (UDP-GLUCOSYLTRANSFERASE 75B1); UDP-glucose:4-aminobenzoate acylglucosyltransferase/ UDP-glucosyltransferase/ UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring glycosyl groups	Unigene108114_All//9.00E-131//gi|109838326|gb|DW236887.1|DW236887		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00908|Zeatin biosynthesis//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr -

Unigene10812_All	332	0.00	6.72	4.49	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.09E-12	Up	1.21E+01	3.22E-08	Up	null	null		null	null		null		null	null		Unigene10812_All//gi|297600424|ref|NP_001049175.2|//2.00E-14//0s03g0182700 [Oryza sativa Japonica Group] >gi|23396617|sp|Q94HF1.1|EIF3K_ORYSJ RecName: Full=Eukaryotic translation initiation factor 3 subunit K; Short=eIF3k; AltName: Full=eIF-3 p25 >gi|15217293|gb|AAK92637.1|AC079633_17 Unknown protein [Oryza sativa Japonica Group] >gi|108706532|gb|ABF94327.1| Eukaryotic translation initiation factor 3 subunit 11 family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255674253|dbj|BAF11089.2|Os03g0182700 [Oryza sativa Japonica Group]	Unigene10812_All//1.00E-10//AT4G33250| EIF3K (EUKARYOTIC TRANSLATION INITIATION FACTOR 3K); translation initiation factor					nr +
Unigene108122_All	397	0.00	0.00	0.00	0.00	0.00	0.00	1.28	0.42	0.00	null	null		null	null		null	null		null	null		-1.60E+00	1.07E-01		-1.03E+01	5.56E-04	Down	Unigene108122_All//gi|225685853|dbj|BAE30213.1|//2.00E-30//methionine S-adenosyl transferase [Cylindrotheca closterium]	Unigene108122_All//4.00E-29//AT2G36880| MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase	Unigene108122_All//5.00E-07//ES821717		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -
Unigene108123_All	405	1.03	0.00	0.26	0.49	0.34	1.56	3.45	0.10	0.20	-1.00E+01	1.05E-02		-1.97E+00	1.51E-01		-5.33E-01	7.49E-01		1.67E+00	9.80E-02		-5.06E+00	1.10E-08	Down	-4.13E+00	3.70E-08	Down	Unigene108123_All//gi|224101205|ref|XP_002312184.1|//1.00E-42//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222852004|gb|EEE89551.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene108123_All//6.00E-35//AT3G42670| CHR38 (CHROMATIN REMODELING 38); ATP binding / DNA binding / helicase/ nucleic acid binding					nr +
Unigene108131_All	949	0.00	0.00	0.00	0.00	0.00	0.00	2.76	0.18	0.17	null	null		null	null		null	null		null	null		-3.97E+00	6.69E-14	Down	-4.04E+00	1.31E-14	Down	Unigene108131_All//gi|301121570|ref|XP_002908512.1|//1.00E-39//40S ribosomal protein SA [Phytophthora infestans T30-4] >gi|262103543|gb|EEY61595.1| 40S ribosomal protein SA [Phytophthora infestans T30-4]	Unigene108131_All//6.00E-32//AT1G72370| P40; structural constituent of ribosome	Unigene108131_All//3.00E-07//gi|109823896|gb|DW008744.1|DW008744		ko03010|Ribosome		nr -
Unigene108132_All	368	0.00	0.00	0.00	0.00	0.00	0.00	3.10	0.00	0.43	null	null		null	null		null	null		null	null		-1.16E+01	3.89E-08	Down	-2.84E+00	3.60E-05	Down	Unigene108132_All//gi|300266605|gb|EFJ50792.1|//5.00E-34//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene108132_All//9.00E-34//AT1G77940| 60S ribosomal protein L30 (RPL30B)			ko03010|Ribosome		nr +
Unigene108136_All	224	0.00	0.00	0.00	0.00	0.00	0.00	2.45	0.56	0.00	null	null		null	null		null	null		null	null		-2.13E+00	3.32E-02		-1.13E+01	2.81E-04	Down	Unigene108136_All//gi|74272607|gb|ABA01099.1|//9.00E-18//40S ribosomal protein S3 [Chlamydomonas incerta]	Unigene108136_All//3.00E-10//AT2G31610| 40S ribosomal protein S3 (RPS3A)			ko03010|Ribosome		nr -
Unigene108137_All	257	0.00	0.00	0.00	0.00	0.00	0.00	1.97	0.49	0.00	null	null		null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.09E+01	5.56E-04	Down	Unigene108137_All//gi|116061096|emb|CAL56484.1|//4.00E-31//GTP-binding regulatory protein beta chain homolog-Ch (ISS) [Ostreococcus tauri]	Unigene108137_All//2.00E-28//AT1G48630| RACK1B_AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding					nr +
Unigene10814_All	216	0.00	5.16	1.97	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.00E-06	Up	1.09E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene10814_All//gi|225469312|ref|XP_002267662.1|//6.00E-06//PREDICTED: similar to L-idonate dehydrogenase [Vitis vinifera]	Unigene10814_All//4.00E-07//AT5G51970| sorbitol dehydrogenase, putative / L-iditol 2-dehydrogenase, putative			ko00051|Fructose and mannose metabolism	GO:0008152//GO:0016491//GO:0046914	nr -
Unigene108140_All	569	0.00	0.00	0.00	0.00	0.00	0.00	1.86	0.07	0.00	null	null		null	null		null	null		null	null		-4.66E+00	1.94E-06	Down	-1.09E+01	6.73E-08	Down	Unigene108140_All//gi|189081811|sp|A8CEP3.1|CALM_SACJA//7.00E-44//RecName: Full=Calmodulin; Short=CaM >gi|157888809|dbj|BAF80878.1| calmodulin [Saccharina japonica] >gi|298713212|emb|CBJ33511.1| Calcium-binding protein [Ectocarpus siliculosus]	Unigene108140_All//2.00E-43//AT2G27030| CAM8 (CALMODULIN 5); calcium ion binding	Unigene108140_All//3.00E-15//CD485888		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene108142_All	419	0.00	0.00	0.00	0.00	0.00	0.00	1.92	0.20	0.76	null	null		null	null		null	null		null	null		-3.26E+00	4.49E-04	Down	-1.33E+00	5.40E-02						Unigene108142_All//6.00E-28//gi|48805733|gb|CO107047.1|CO107047					
Unigene10815_All	330	1.59	11.52	4.68	1.96	4.38	5.20	5.12	6.84	12.80	2.86E+00	2.76E-12	Up	1.56E+00	7.60E-03		1.16E+00	3.97E-02		1.41E+00	6.85E-03		4.16E-01	3.00E-01		1.32E+00	9.76E-07	Up	Unigene10815_All//gi|297792833|ref|XP_002864301.1|//4.00E-09//homogentisate 1,2-dioxygenase [Arabidopsis lyrata subsp. lyrata] >gi|297310136|gb|EFH40560.1| homogentisate 1,2-dioxygenase [Arabidopsis lyrata subsp. lyrata]	Unigene10815_All//2.00E-10//AT5G54080| HGO (HOMOGENTISATE 1,2-DIOXYGENASE); homogentisate 1,2-dioxygenase	Unigene10815_All//5.00E-59//TC155472		ko00350|Tyrosine metabolism		nr +
Unigene108164_All	540	0.00	0.00	0.00	0.00	0.00	0.00	6.89	16.56	1.18	null	null		null	null		null	null		null	null		1.27E+00	3.27E-12	Up	-2.55E+00	1.37E-13	Down	Unigene108164_All//gi|238014838|gb|ACR38454.1|//6.00E-15//unknown [Zea mays]		Unigene108164_All//6.00E-38//TC146753				nr -
Unigene10817_All	323	1.94	0.63	16.65	3.08	0.21	0.00	0.26	0.00	0.00	-1.63E+00	9.23E-02		3.10E+00	6.25E-18	Up	-3.85E+00	1.61E-05	Down	-1.16E+01	2.97E-06	Down	-8.03E+00	4.07E-01		-8.03E+00	3.61E-01		Unigene10817_All//gi|5814093|gb|AAD52097.1|AF088885_1/3.00E-19//receptor-like kinase CHRK1 [Nicotiana tabacum]	Unigene10817_All//1.00E-15//AT4G19810| glycosyl hydrolase family 18 protein				GO:0004553//GO:0004672//GO:0006026//GO:0006464//GO:0030312//GO:0032559//GO:0043167	nr -
Unigene108171_All	514	0.00	0.00	0.00	0.00	0.00	0.00	3.04	1.79	0.47	null	null		null	null		null	null		null	null		-7.67E-01	1.07E-01		-2.71E+00	1.57E-06	Down	Unigene108171_All//gi|171452356|dbj|BAG15869.1|//2.00E-33//ankyrin repeat protein [Bruguiera gymnorhiza]	Unigene108171_All//2.00E-22//AT1G14480| protein binding					nr -
Unigene108186_All	275	0.00	0.00	0.00	0.18	0.00	0.00	2.46	0.00	0.14	null	null		null	null		-7.50E+00	5.63E-01		-7.50E+00	6.43E-01		-1.13E+01	6.34E-05	Down	-4.09E+00	3.10E-04	Down			Unigene108186_All//3.00E-07//TC175182				
Unigene108195_All	309	218.77	91.34	151.13	158.47	229.23	100.70	0.14	0.27	0.26	-1.26E+00	6.18E-71	Down	-5.34E-01	3.13E-16		5.33E-01	1.29E-20		-6.54E-01	7.21E-19		9.84E-01	7.33E-01		9.15E-01	7.51E-01		Unigene108195_All//gi|6959488|gb|AAF33112.1|AF181683_1/4.00E-38//RPT2 [Arabidopsis thaliana]	Unigene108195_All//2.00E-39//AT2G30520| RPT2 (ROOT PHOTOTROPISM 2); protein binding	Unigene108195_All//2.00E-95//EX168571				nr -
Unigene1082_All	466	4.04	0.98	3.20	4.49	6.80	4.94	2.09	1.97	1.28	-2.05E+00	1.17E-04	Down	-3.37E-01	5.04E-01		5.99E-01	8.91E-02		1.39E-01	7.56E-01		-8.08E-02	9.06E-01		-7.02E-01	2.43E-01		Unigene1082_All//gi|5733885|gb|AAD49773.1|AC007932_21//1.00E-25//ESTs gb|T22141 and gb|H37217 come from this gene [Arabidopsis thaliana]	Unigene1082_All//6.00E-12//AT3G17430| phosphate translocator-related	Unigene1082_All//1.00E-152//TC140046			GO:0031224//GO:0031410	nr -
Unigene108820_All	328	6.06	10.81	4.55	9.87	8.61	8.67	11.60	7.52	5.47	8.35E-01	1.08E-02		-4.15E-01	3.93E-01		-1.98E-01	6.03E-01		-1.87E-01	6.20E-01		-6.26E-01	2.59E-02		-1.09E+00	8.46E-05	Down			Unigene108820_All//7.00E-55//gi|109828667|gb|DW227288.1|DW227288				
Unigene108208_All	495	0.00	0.00	0.00	0.00	0.00	0.00	4.01	0.25	0.80	null	null		null	null		null	null		null	null		-3.99E+00	1.09E-10	Down	-2.32E+00	6.40E-07	Down	Unigene108208_All//gi|224000567|ref|XP_002289956.1|//3.00E-60//ubiquitin-conjugating enzyme e2-16kda, ubiquitin protein ligase [Thalassiosira pseudonana CCMP1335] >gi|220975164|gb|EED93493.1| ubiquitin-conjugating enzyme e2-16kda, ubiquitin protein ligase [Thalassiosira pseudonana CCMP1335]	Unigene108208_All//2.00E-46//AT5G56150| UBC30 (ubiquitin-conjugating enzyme 30); ubiquitin-protein ligase			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene10821_All	386	0.00	5.51	0.83	2.19	2.77	1.17	3.07	5.52	4.13	1.24E+01	4.10E-12	Up	9.69E+00	4.54E-02		3.34E-01	6.42E-01		-9.07E-01	2.47E-01		8.48E-01	3.14E-02		4.29E-01	3.53E-01		Unigene10821_All//gi|297832174|ref|XP_002883969.1|//8.00E-18//myo-inositol oxygenase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297329809|gb|EFH60228.1| myo-inositol oxygenase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene10821_All//6.00E-17//AT5G56640| MIOX5; inositol oxygenase/ iron ion binding	Unigene10821_All//6.00E-99//ES827071		ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0006020//GO:0016701//GO:0044424//GO:0046914	nr -
Unigene108212_All	340	0.00	0.00	0.00	0.00	0.00	0.00	2.24	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	1.68E-05	Down	-1.11E+01	8.89E-06	Down	Unigene108212_All//gi|224008993|ref|XP_002293455.1|//6.00E-22//vacuolar proton pump alpha subunit [Thalassiosira pseudonana CCMP1335] >gi|220970855|gb|EED89191.1| vacuolar proton pump alpha subunit [Thalassiosira pseudonana CCMP1335]	Unigene108212_All//1.00E-13//AT1G78900| VHA-A (VACUOLAR ATP SYNTHASE SUBUNIT A); ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism / hydrolase, acting on acid anhydrides, catalyzing transmembrane movement of substances / proton-transporting ATPase, rotational mechanism			ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr +
Unigene108214_All	403	2.47	0.50	0.00	2.84	2.82	1.12	4.51	1.56	0.99	-2.29E+00	4.05E-03		-1.13E+01	1.77E-05	Down	-1.18E-02	9.64E-01		-1.34E+00	4.01E-02		-1.54E+00	6.84E-04	Down	-2.19E+00	5.01E-06	Down	Unigene108214_All//gi|195626560|gb|ACG35110.1|//6.00E-17//cytochrome c oxidase copper chaperone [Zea mays]	Unigene108214_All//7.00E-18//AT3G15352| ATCOX17; copper chaperone	Unigene108214_All//0.00E+00//gi|84167290|gb|DR455938.1|DR455938		ko00190|Oxidative phosphorylation		nr -
Unigene108229_All	491	0.00	0.00	0.00	0.00	0.00	0.00	1.64	0.17	0.16	null	null		null	null		null	null		null	null		-3.27E+00	4.49E-04	Down	-3.33E+00	2.47E-04	Down	Unigene108229_All//gi|29539334|dbj|BAC67668.1|//8.00E-50//elongation factor-2 [Cyanidioschyzon merolae]	Unigene108229_All//3.00E-41//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding					nr -
Unigene10823_All	482	0.00	7.99	5.97	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	6.32E-22	Up	1.25E+01	6.96E-16	Up	null	null		null	null		null	null		null	null		Unigene10823_All//gi|156554296|ref|XP_001602465.1|//4.00E-67//PREDICTED: similar to S14e ribosomal protein [Nasonia vitripennis]	Unigene10823_All//1.00E-58//AT2G36160| 40S ribosomal protein S14 (RPS14A)	Unigene10823_All//7.00E-19//TC154908		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0030529	nr -
Unigene108237_All	576	0.00	0.00	0.00	0.52	0.18	0.00	2.72	0.15	0.14	null	null		null	null		-1.53E+00	2.98E-01		-9.02E+00	4.01E-02		-4.23E+00	7.78E-09	Down	-4.30E+00	2.71E-09	Down	Unigene108237_All//gi|25991350|gb|AAN76811.1|AF453448_1/3.00E-23//PEP carboxylase kinase [Solanum tuberosum] >gi|33329260|gb|AAQ10030.1| PEPC kinase 1a [Solanum tuberosum]	Unigene108237_All//4.00E-23//AT1G08650| PPCK1 (PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE); kinase/ protein serine/threonine kinase	Unigene108237_All//1.00E-42//TC132996		ko04626|Plant-pathogen interaction		nr -
Unigene108242_All	241	0.00	0.00	0.00	0.00	0.00	0.00	2.98	0.35	0.33	null	null		null	null		null	null		null	null		-3.10E+00	1.40E-03		-3.17E+00	8.09E-04	Down	Unigene108242_All//gi|297728401|ref|NP_001176564.1|//6.00E-16//Os11g0521000 [Oryza sativa Japonica Group] >gi|77551166|gb|ABA93963.1| GDSL-like Lipase/Acylhydrolase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255680130|dbj|BAH95292.1|Os11g0521000 [Oryza sativa Japonica Group]	Unigene108242_All//2.00E-16//AT5G03980| GDSL-motif lipase/hydrolase family protein					nr -
Unigene108247_All	299	0.00	0.17	0.53	0.00	0.00	0.15	0.42	0.00	3.06	7.41E+00	6.21E-01		9.06E+00	2.40E-01		null	null		7.24E+00	7.03E-01		-8.73E+00	2.36E-01		2.85E+00	3.18E-04	Up	Unigene108247_All//gi|18405138|ref|NP_565911.1|//2.00E-15//aspartyl protease family protein [Arabidopsis thaliana] >gi|20196976|gb|AAB87120.2| expressed protein [Arabidopsis thaliana] >gi|20197046|gb|AAM14894.1| expressed protein [Arabidopsis thaliana]	Unigene108247_All//1.00E-16//AT2G39710| aspartyl protease family protein					nr +

Unigene10825_All	416	0.00	7.31	8.06	0.00	0.17	0.00	0.00	0.00	0.00	1.28E+01	2.67E-17	Up	1.30E+01	1.47E-18	Up	7.37E+00	6.15E-01		null	null		null	null		null	null		Unigene10825_All//sp|P35749|MYH11_HUMAN//6.00E-29//Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3							swissprot +
Unigene108255_All	309	0.00	0.00	0.00	0.00	0.00	0.00	6.57	0.41	0.26	null	null		null	null		null	null		null	null		-4.02E+00	5.83E-11	Down	-4.67E+00	1.83E-12	Down	Unigene108255_All//gi|6012952|emb|CAB57309.1|//9.00E-15//60S ribosomal protein L6 (YL 16 like) [Cyanophora paradoxa]				ko03010|Ribosome		nr -
Unigene108256_All	248	0.63	1.84	0.21	1.61	0.69	0.55	9.89	4.38	3.05	1.54E+00	1.96E-01		-1.56E+00	5.34E-01		-1.21E+00	3.14E-01		-1.56E+00	2.31E-01		-1.17E+00	1.40E-03		-1.70E+00	7.66E-06	Down	Unigene108256_All//gi|297810879|ref|XP_002873323.1|//5.00E-06//predicted protein [Arabidopsis lyrata subsp. lyrata] >gi|297319160|gb|EFH49582.1| predicted protein [Arabidopsis lyrata subsp. lyrata]		Unigene108256_All//1.00E-31//ES819093				nr +
Unigene108258_All	599	0.00	0.00	0.00	0.00	0.00	0.00	2.96	2.79	0.00	null	null		null	null		null	null		null	null		-8.71E-02	8.50E-01		-1.15E+01	4.12E-13	Down	Unigene108258_All//gi|115484761|ref|NP_001067524.1|//2.00E-54//Os11g0220800 [Oryza sativa Japonica Group] >gi|122240410|sp|Q0ITS8.1|RL101_ORYSJ RecName: Full=60S ribosomal protein L10-1; AltName: Full=Putative tumor suppressor SC34; AltName: Full=Protein QM >gi|158513712|sp|A2ZCQ7.2|RL101_ORYSI RecName: Full=60S ribosomal protein L10-1; AltName: Full=Putative tumor suppressor SC34; AltName: Full=Protein QM >gi|113644746|dbj|BAF27887.1| Os11g0220800 [Oryza sativa Japonica Group]	Unigene108258_All//1.00E-53//ATI666580| 60S ribosomal protein L10 (RPL10C)	Unigene108258_All//3.00E-15//CD485839		ko03010|Ribosome		nr -
Unigene10826_All	452	1.85	0.22	0.00	2.65	2.13	0.80	1.50	0.74	0.62	-3.05E+00	2.11E-03		-1.09E+01	1.19E-04	Down	-3.10E-01	6.07E-01		-1.73E+00	8.52E-03		-1.02E+00	2.04E-01		-1.28E+00	9.49E-02		Unigene10826_All//gi|224054508|ref|XP_002298295.1|//2.00E-13//predicted protein [Populus trichocarpa] >gi|222845553|gb|EEE83100.1| predicted protein [Populus trichocarpa]		Unigene10826_All//1.00E-16//ES852406				nr -
Unigene108265_All	246	0.00	0.00	0.00	0.00	0.00	0.00	2.06	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	8.91E-04	Down	-1.10E+01	5.56E-04	Down		Unigene108265_All//5.00E-07//ATI648590| C2 domain-containing protein					ESTscan +
Unigene10827_All	920	0.00	0.00	0.00	0.00	0.00	0.00	4.69	1.00	0.69	null	null		null	null		null	null		null	null		-2.23E+00	5.09E-13	Down	-2.76E+00	5.24E-17	Down	Unigene10827_All//sp|P28770|EPD1_ONCMY//1.00E-21//Ependymin-1 OS=Oncorhynchus mykiss GN=epd1 PE=1 SV=1						swissprot +
Unigene108272_All	250	0.00	0.00	0.00	0.00	0.00	0.00	1.52	6.02	22.95	null	null		null	null		null	null		null	null		1.98E+00	2.06E-04	Up	3.91E+00	6.01E-30	Up								
Unigene108274_All	642	0.00	0.00	0.00	0.00	0.00	0.00	2.50	0.72	0.00	null	null		null	null		null	null		null	null		-1.81E+00	3.20E-04	Down	-1.13E+01	7.00E-12	Down	Unigene108274_All//gi|159480690|ref|XP_001698415.1|//2.00E-07//basal body protein [Chlamydomonas reinhardtii] >gi|158282155|gb|EDF07908.1| basal body protein [Chlamydomonas reinhardtii]	Unigene108274_All//6.00E-06//ATI635250| HUB2 (HISTONE MONO-UBIQUITINATION 2); protein binding / zinc ion binding					nr -
Unigene108278_All	395	0.00	0.00	0.13	0.38	0.09	0.23	2.35	0.42	0.20	null	null		7.07E+00	6.41E-01		-2.12E+00	3.87E-01		-7.26E-01	7.17E-01		-2.48E+00	1.07E-03		-3.55E+00	3.97E-05	Down	Unigene108278_All//gi|38605802|emb|CAE05270.2|//2.00E-06//OSJNBa0014023.4 [Oryza sativa (japonica cultivar-group)]						nr +
Unigene108279_All	476	0.44	0.96	1.68	0.42	0.00	0.00	2.49	1.40	0.42	1.12E+00	3.28E-01		1.93E+00	3.42E-02		-8.71E+00	8.47E-02		-8.71E+00	1.34E-01		-8.24E-01	1.42E-01		-2.57E+00	6.98E-05	Down	Unigene108279_All//gi|187940732|gb|ACD39467.1|//5.00E-06//BEL30 protein [Solanum palustre]	Unigene108279_All//2.00E-06//AT4G34610| BLH8 (BELL1-LIKE HOMEODOMAIN 6); DNA binding / transcription factor	Unigene108279_All//4.00E-17//gi|164305110|gb|ES808607.1|ES808607	HB			nr -
Unigene108285_All	439	2342.88	1085.53	2076.02	319.31	349.45	224.69	3.27	1.24	0.82	-1.11E+00	0.00E+00	Down	-1.75E-01	1.96E-29		1.30E-01	1.38E-03		-5.07E-01	1.12E-33		-1.40E+00	6.15E-03		-2.00E+00	1.70E-04	Down	Unigene108285_All//gi|5738542|emb|CAB53034.1|//2.00E-42//photosystem I subunit XI precursor [Arabidopsis thaliana]	Unigene108285_All//2.00E-43//AT4G12800| PSAL (photosystem I subunit L)	Unigene108285_All//0.00E+00//TC136126		ko00195|Photosynthesis		nr +
Unigene10829_All	361	0.58	0.42	0.15	1.38	2.48	0.50	1.99	0.00	0.33	-4.61E-01	7.58E-01		-1.97E+00	3.82E-01		8.46E-01	2.87E-01		-1.46E+00	1.93E-01		-1.10E+01	3.27E-05	Down	-2.59E+00	2.81E-03									ESTscan +
Unigene108291_All	381	0.00	0.00	0.00	0.00	0.00	0.00	2.44	0.55	0.21	null	null		null	null		null	null		null	null		-2.15E+00	2.95E-03		-3.55E+00	3.97E-05	Down	Unigene108291_All//gi|301123509|ref|XP_002909481.1|//1.00E-27//60S ribosomal protein L21-1 [Phytophthora infestans T30-4] >gi|262100243|gb|EEY58295.1| 60S ribosomal protein L21-1 [Phytophthora infestans T30-4]	Unigene108291_All//9.00E-28//ATI609690| 60S ribosomal protein L21 (RPL21C)			ko03010|Ribosome		nr -
Unigene10830_All	288	0.18	2.46	0.74	0.00	0.96	2.51	0.88	2.03	1.11	3.76E+00	2.36E-03		2.03E+00	3.62E-01		9.90E+00	7.03E-02		1.13E+01	2.31E-04	Up	1.21E+00	1.71E-01		3.29E-01	7.64E-01									
Unigene108301_All	449	0.00	0.00	0.00	0.00	0.00	0.00	5.56	1.68	0.80	null	null		null	null		null	null		null	null		-1.73E+00	7.81E-06	Down	-2.80E+00	2.72E-10	Down			Unigene108301_All//5.00E-10//TC135460					
Unigene10831_All	912	0.00	0.44	0.58	0.22	0.57	0.00	0.60	1.74	3.63	8.80E+00	1.36E-02		9.19E+00	4.05E-03		1.37E+00	2.26E-01		-7.77E+00	1.34E-01		1.53E+00	1.78E-03		2.59E+00	3.51E-12	Up			Unigene10831_All//1.00E-40//TC168132					
Unigene108314_All	413	0.89	0.00	0.00	0.00	0.42	0.44	1.33	0.51	0.00	-9.79E+00	1.97E-02		-9.79E+00	2.79E-02		8.70E+00	2.28E-01		8.77E+00	1.95E-01		-1.40E+00	1.35E-01		-1.04E+01	2.81E-04	Down								
Unigene108316_All	394	0.00	0.00	0.00	0.00	0.00	0.00	3.43	0.74	0.40	null	null		null	null		null	null		null	null		-2.21E+00	1.58E-04	Down	-3.09E+00	1.97E-06	Down	Unigene108316_All//gi|34105768|gb|AAQ62075.1|//5.00E-35//ribosomal protein L3 [Triticum aestivum] >gi|34105770|gb|AAQ62076.1| ribosomal protein L3 [Triticum aestivum] >gi|34105774|gb|AAQ62078.1| ribosomal protein L3 [Triticum aestivum] >gi|118152389|gb|ABK63938.1| ribosomal protein L3-B3 [Triticum aestivum] >gi|118152400|gb|ABK63944.1| ribosomal protein L3-B1 [Triticum aestivum] >gi|146141392|tpg|DAA01144.1| TPA_inf: ribosomal protein L3B-3 [Triticum aestivum] >gi|146141396|tpg|DAA01146.1| TPA_inf: ribosomal protein L3B-1 [Triticum aestivum]	Unigene108316_All//2.00E-27//ATI6G1880| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene108316_All//5.00E-07//gi|78348789|gb|DT569063.1|DT569063		ko03010|Ribosome		nr +
Unigene10832_All	333	0.00	172.09	102.82	0.30	0.00	0.54	0.00	0.00	0.00	1.74E+01	0.00E+00	Up	1.66E+01	2.77E-194	Up	-8.23E+00	3.17E-01		8.59E-01	6.96E-01		null	null		null	null										
Unigene108325_All	423	0.25	0.48	0.00	0.24	0.65	0.11	2.90	1.58	0.19	9.54E-01	6.22E-01		-7.95E+00	3.98E-01		1.47E+00	4.20E-01		-1.14E+00	6.79E-01		-8.75E-01	1.13E-01		-3.94E+00	4.86E-07	Down			Unigene108325_All//1.00E-50//TC154322					
Unigene10833_All	367	2.85	1.38	1.89	3.66	1.97	0.49	0.23	0.00	0.22	-1.03E+00	1.20E-01		-5.96E-01	3.93E-01		-8.95E-01	1.07E-01		-2.90E+00	4.29E-05	Down	-7.85E+00	4.07E-01		-8.58E-02	9.73E-01				Unigene10833_All//8.00E-18//ES831804					
Unigene108331_All	225	0.00	0.45	0.47	0.22	0.00	0.20	4.89	2.23	1.06	8.82E+00	3.90E-01		8.89E+00	4.02E-01		-7.79E+00	5.63E-01		-1.42E-01	9.56E-01		-1.13E+00	5.52E-02		-2.20E+00	5.66E-04	Down			Unigene108331_All//2.00E-14//CO123936					
Unigene108332_All	765	0.68	0.60	0.14	0.72	0.41	0.18	2.32	0.49	0.52	-1.98E-01	8.20E-01		-2.30E+00	6.77E-02		-8.22E-01	3.96E-01		-2.02E+00	7.06E-02		-2.24E+00	8.44E-06	Down	-2.16E+00	8.30E-06	Down			Unigene108332_All//1.00E-92//TC165104					
Unigene108333_All	1798	0.00	0.00	0.00	0.06	0.00	0.00	4.47	0.51	0.18	null	null		null	null		-5.79E+00	3.17E-01		-5.79E+00	4.05E-01		-3.13E+00	5.01E-34	Down	-4.66E+00	8.88E-48	Down	Unigene108333_All//gi|18147592|dbj|BAB83086.1|//0.00E+00//cycloartenol synthase [Betula platyphylla]	Unigene108333_All//0.00E+00//AT2G07050| CAS1 (cycloartenol synthase 1); cycloartenol synthase	Unigene108333_All//2.00E-25//CB350491		ko00100|Steroid biosynthesis		nr -
Unigene10834_All	763	0.82	0.00	0.07	0.13	0.27	0.12	0.11	5.92	3.24	-9.68E+00	7.92E-04	Down	-3.56E+00	8.32E-03		1.05E+00	6.13E-01		-1.42E-01	9.53E-01		5.74E+00	1.24E-28	Up	4.87E+00	5.00E-15	Up	Unigene10834_All//gi|75326590|sp|Q76312.1|PDR1_TOBAC//1.00E-102//RecName: Full=Pleiotropic drug resistance protein 1; AltName: Full=NtPDR1 >gi|410524472|dbj|BAD07483.1| PDR-type ABC transporter 1 [Nicotiana tabacum]	Unigene10834_All//1.00E-101//ATI6G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene10834_All//0.00E+00//TC147767		ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene108340_All	312	0.00	0.00	0.00	0.00	0.00	0.00	2.98	0.00	0.00	null	null		null	null		null	null		null	null		-1.15E+01	1.15E-06	Down	-1.15E+01	5.48E-07	Down	Unigene108340_All//sp|Q58A42|DD3_DICDI//1.00E-16//Protein DD3-3 OS=Dictyostelium discoideum GN=DD3-3 PE=2 SV=1						swissprot -
Unigene108341_All	1039	0.00	0.00	0.00	0.00	0.00	0.00	6.31	0.08	0.00	null	null		null	null		null	null		null	null		-6.29E+00	5.49E-43	Down	-1.26E+01	3.26E-48	Down	Unigene108341_All//gi|19698452|gb|AAL93154.1|AF485268_1//1.00E-137//bacterial-induced class III peroxidase [Gossypium hirsutum]	Unigene108341_All//1.00E-102//AT2G41480| electron carrier/ heme binding / peroxidase	Unigene108341_All//6.00E-135//TC147787		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene108350_All	935	0.00	0.00	0.00	0.00	0.00	0.00	2.58	0.58	1.02	null	null		null	null		null	null		null	null		-2.15E+00	2.78E-07	Down	-1.33E+00	2.65E-04	Down	Unigene108350_All//gi|297806151|ref|XP_002870959.1|//1.00E-95//amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316796|gb|EFH47218.1| amino acid transporter family protein [Arabidopsis lyrata subsp. lyrata]	Unigene108350_All//9.00E-87//AT5G02180| amino acid transporter family protein					nr +
Unigene108355_All	420	0.00	0.00	0.00	0.00	0.00	0.00	3.22	0.80	0.66	null	null		null	null		null	null		null	null		-2.02E+00	4.01E-04	Down	-2.28E+00	7.13E-05	Down								
Unigene108360_All	355	0.00	0.00	0.00	0.28	0.00	0.13	2.38	0.24	1.01	null	null		null	null		-8.13E+00	3.17E-01		-1.14E+00	6.79E-01		-3.34E+00	2.52E-04	Down	-1.24E+00	6.26E-02										
Unigene108363_All	320	0.00	0.00	0.00	0.00	0.00	0.00	13.87	37.35	1.37	null	null		null	null		null	null		null	null		1.43E+00	3.60E-19	Up	-3.34E+00	5.76E-21	Down			Unigene108363_All//2.00E-08//ES810763					
Unigene108369_All	466	0.00	0.00	0.00	0.00	0.00	0.00	1.63	0.18	13.34	null	null		null	null		null	null		null	null		-3.19E+00	7.93E-04	Down	3.03E+00	4.22E-26	Up								
Unigene10837_All	368	0.14	0.00	0.00	4.60	0.37	3.31	0.00	0.00	0.00	-7.15E+00	6.19E-01		-7.15E+00	6.32E-01		-3.62E+00	1.02E-08	Down	-4.74E-01	3.86E-01		null	null		null	null		Unigene10837_All//gi|115477821|ref|NP_001062506.1|//3.00E-20//Os08g0560000 [Oryza sativa Japonica Group] >gi|113624475|dbj|BAF24420.1| Os08g0560000 [Oryza sativa Japonica Group]	Unigene10837_All//1.00E-20//AT2G36690| oxidoreductase, 2OG-Fe(II) oxygenase family protein			ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis	GO:0008152//GO:0016706	nr +
Unigene108376_All	529	0.00	0.00	0.00	0.00	0.00	0.00	2.80	1.50	0.00	null	null		null	null		null	null		null	null		-8.98E-01	6.74E-02		-1.14E+01	5.85E-11	Down	Unigene108376_All//gi|2500261|sp|P93099.1|RL13A_CYAPA//7.00E-41//RecName: Full=60S ribosomal protein L13a >gi|1743007|emb|CAA71090.1| ribosomal protein L13a [Cyanophora paradoxa]	Unigene108376_All//3.00E-37//AT4G13170| 60S ribosomal protein L13A (RPL13aC)			ko03010|Ribosome		nr +
Unigene108380_All	496	0.00	0.00	0.00	0.00	0.00	0.00	1.62	0.17	0.40	null	null		null	null		null	null		null	null		-3.26E+00	4.49E-04	Down	-2.01E+00	7.11E-03		Unigene108380_All//gi|15242647|ref|NP_198848.1|//1.00E-09//DC1 domain-containing protein [Arabidopsis thaliana] >gi|10178142|dbj|BAB11587.1| CHP-rich zinc finger protein-like [Arabidopsis thaliana]	Unigene108380_All//6.00E-11//AT5G40320| DC1 domain-containing protein	Unigene108380_All//3.00E-101//CO075261				nr +
Unigene108381_All	589	0.00	0.00	0.00	0.00	0.00	0.00	4.88	0.28	0.27	null	null		null	null		null	null		null	null		-4.10E+00	1.53E-15	Down	-4.17E+00	2.58E-16	Down	Unigene108381_All//gi|157503121|gb|ABV58643.1|//2.00E-37//ubquitin [Catharanthus roseus]	Unigene108381_All//2.00E-24//AT1G65350| UBQ13; protein binding	Unigene108381_All//2.00E-25//TC164984		ko03010|Ribosome		nr +
Unigene108383_All	379	0.00	0.00	0.00	0.13	0.00	0.36	2.57	0.22	0.00	null	null		null	null		-7.04E+00	5.63E-01		1.44E+00	6.39E-01		-3.54E+00	4.32E-05	Down	-1.13E+01	2.72E-07	Down								

Unigene108386_All	391	0.00	0.00	0.00	0.25	0.18	0.12	1.62	0.32	0.00	null	null		null	null		-5.33E-01	8.19E-01		-1.14E+00	6.79E-01		-2.34E+00	1.27E-02		-1.07E+01	7.12E-05	Down	Unigene108386_All//gi|15233062|ref|NP_191681.1|//1.00E-24//short-chain dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] >gi|75311801|sp|Q9M2E2.1|SDR1_ARATH RecName: Full=(+)-neomenthol dehydrogenase; AltName: Full=Menthone:neomenthol reductase; AltName: Full=Short-chain dehydrogenase/reductase 1; Short=AtSDR1	Unigene108386_All//1.00E-25//AT3G61220| short-chain dehydrogenase/reductase (SDR) family protein	Unigene108386_All//4.00E-174//ES839198				nr +
Unigene10839_All	259	0.00	11.74	2.88	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	2.67E-17	Up	1.15E+01	3.28E-04	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene108393_All	875	0.06	0.00	0.00	0.00	0.08	0.00	9.91	1.58	0.14	-5.90E+00	6.19E-01		-5.90E+00	6.32E-01		6.30E+00	6.15E-01		null	null		-2.65E+00	5.14E-31	Down	-6.18E+00	1.58E-58	Down							
Unigene108396_All	368	0.00	0.00	0.00	0.00	0.00	0.00	1.49	1.36	0.00	null	null		null	null		null	null		null	null		-1.32E-01	8.80E-01		-1.05E+01	2.81E-04	Down							
Unigene108397_All	321	0.00	0.00	0.00	0.00	0.00	0.00	2.50	0.65	0.00	null	null		null	null		null	null		null	null		-1.94E+00	1.17E-02		-1.13E+01	4.43E-06	Down							ESTscan +
Unigene108398_All	275	8.18	2.76	4.84	17.21	14.78	19.05	7.69	3.50	8.69	-1.57E+00	5.19E-04	Down	-7.57E-01	9.06E-02		-2.20E-01	4.78E-01		1.47E-01	6.22E-01		-1.14E+00	4.42E-03		1.77E-01	6.46E-01								
Unigene10841_All	434	0.72	0.23	0.00	1.72	1.82	1.04	5.75	0.67	0.64	-1.63E+00	2.77E-01		-9.50E+00	4.93E-02		8.40E-02	9.45E-01		-7.26E-01	3.90E-01		-3.09E+00	7.09E-11	Down	-3.16E+00	1.62E-11	Down	Unigene10841_All//gi|46359653|dbj|BAD15331.1|//3.00E-42//cytochrome P450 [Panax ginseng]	Unigene10841_All//1.00E-31//AT2G45570| CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene10841_All//0.00E+00//TC135966		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0003676//GO:0005506//GO:0006259//GO:0016709	nr -
Unigene108423_All	523	0.00	0.00	0.00	0.00	0.00	0.00	1.86	1.36	0.00	null	null		null	null		null	null		null	null		-4.53E-01	4.90E-01		-1.09E+01	2.72E-07	Down	Unigene108423_All//gi|301095349|ref|XP_002896775.1|//6.00E-26//60S acidic ribosomal protein P0 [Phytophthora infestans T30-4] >gi|262108658|gb|EEY66710.1| 60S acidic ribosomal protein P0 [Phytophthora infestans T30-4]	Unigene108423_All//2.00E-23//AT2G40010| 60S acidic ribosomal protein P0 (RPP0A)			ko03010|Ribosome		nr +
Unigene10843_All	285	0.00	0.00	0.00	0.00	0.00	0.00	1.78	1.76	0.00	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		-1.08E+01	5.56E-04	Down							
Unigene10844_All	360	0.73	0.00	0.30	0.00	0.19	0.50	5.29	1.97	0.66	-9.51E+00	6.72E-02		-1.30E+00	4.37E-01		7.58E+00	6.15E-01		8.97E+00	1.95E-01		-1.42E+00	1.09E-03		-2.99E+00	1.57E-08	Down					ko00910|Nitrogen metabolism		kegg -
Unigene108448_All	1989	0.11	0.00	0.00	0.05	0.03	0.00	1.51	3.13	1.12	-6.72E+00	1.23E-01		-6.72E+00	1.47E-01		-5.34E-01	8.19E-01		-5.65E+00	4.05E-01		1.05E+00	1.00E-06	Up	-4.28E-01	1.78E-01		Unigene108448_All//gi|297827551|ref|XP_002881658.1|//8.00E-22//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327497|gb|EFH57917.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene108448_All//7.00E-22//AT2G39490| F-box family protein	Unigene108448_All//5.00E-23//TC177932				nr +
Unigene108452_All	341	0.00	0.00	0.00	0.00	0.00	0.00	6.08	1.72	3.04	null	null		null	null		null	null		null	null		-1.82E+00	2.74E-05	Down	-1.00E+00	9.64E-03		Unigene108452_All//gi|226453532|gb|EEH50843.1|//1.00E-10//predicted protein [Micromonas pusilla CCMP1545]		Unigene108452_All//6.00E-37//gi|45395442|gb|CK988291.1|CK988291				nr -
Unigene108457_All	237	0.00	0.00	0.00	0.00	0.00	0.00	4.64	6.88	0.00	null	null		null	null		null	null		null	null		5.68E-01	2.34E-01		-1.22E+01	3.33E-08	Down							
Unigene108459_All	527	0.00	0.00	0.00	0.00	0.00	0.00	2.65	3.09	0.00	null	null		null	null		null	null		null	null		2.24E-01	6.27E-01		-1.14E+01	2.40E-10	Down	Unigene108459_All//gi|159469668|ref|XP_001692985.1|//2.00E-65//ribosomal protein L8, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|158277787|gb|EDP03554.1| ribosomal protein L8 [Chlamydomonas reinhardtii]	Unigene108459_All//4.00E-61//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene108459_All//4.00E-14//ES836532		ko03010|Ribosome		nr +
Unigene108463_All	362	0.00	0.00	0.00	0.00	0.00	0.00	1.40	0.23	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.05E-02		-1.05E+01	5.56E-04	Down	Unigene108463_All//gi|38230174|gb|AAR14182.1|//6.00E-32//Rho family GTPase [Fucus distichus]	Unigene108463_All//4.00E-30//AT4G35020| ARAC3 (ARABIDOPSIS RAC-LIKE 3); GTP binding / GTPase			ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity	GO:0015630//GO:0016020//GO:0017111//GO:0031981//GO:0032561//GO:0035556	nr -
Unigene108466_All	429	0.00	0.00	0.00	0.00	0.00	0.00	1.18	0.97	0.00	null	null		null	null		null	null		null	null		-2.80E-01	7.49E-01		-1.02E+01	5.56E-04	Down	Unigene108466_All//gi|159468233|ref|XP_001692287.1|//3.00E-42//elongation factor EF-3 [Chlamydomonas reinhardtii] >gi|158278473|gb|EDP04237.1| elongation factor EF-3 [Chlamydomonas reinhardtii]	Unigene108466_All//4.00E-14//AT3G54540| ATGCN4; transporter	Unigene108466_All//1.00E-10//TC134087			GO:0000166//GO:0003676//GO:0017111//GO:0043232//GO:0051276	nr -
Unigene108469_All	251	0.00	0.00	0.00	0.00	0.00	0.00	2.53	2.16	0.00	null	null		null	null		null	null		null	null		-2.23E-01	7.74E-01		-1.13E+01	7.12E-05	Down	Unigene108469_All//gi|301102985|ref|XP_002900579.1|//2.00E-06//RNA polymerase-associated protein RTF1 [Phytophthora infestans T30-4] >gi|262101842|gb|EEY59894.1| RNA polymerase-associated protein RTF1 [Phytophthora infestans T30-4]					GO:0003676//GO:0006259//GO:0006351//GO:0006464//GO:0043231	nr -
Unigene108474_All	300	0.35	0.00	0.18	0.17	0.23	0.15	1.83	0.00	0.27	-8.45E+00	3.76E-01		-9.75E-01	7.22E-01		4.68E-01	9.61E-01		-1.41E-01	9.56E-01		-1.08E+01	4.62E-04	Down	-2.79E+00	7.97E-03								
Unigene10848_All	615	0.00	20.68	6.93	0.00	0.00	0.00	0.00	0.00	0.00	1.43E+01	5.60E-73	Up	1.28E+01	1.22E-23	Up	null	null		null	null		null	null		null	null		Unigene10848_All//gi|297844300|ref|XP_002890031.1|//2.00E-51//eukaryotic translation initiation factor 5A-1 [Arabidopsis lyrata subsp. lyrata] >gi|297335873|gb|EFH66290.1| eukaryotic translation initiation factor 5A-1 [Arabidopsis lyrata subsp. lyrata]	Unigene10848_All//4.00E-52//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor				GO:0006448//GO:0006449//GO:0008135//GO:0010087//GO:0018205//GO:0043021	nr +
Unigene108480_All	342	0.00	0.00	0.00	0.00	0.00	0.00	3.21	0.49	0.47	null	null		null	null		null	null		null	null		-2.72E+00	1.31E-04	Down	-2.79E+00	6.37E-05	Down	Unigene108480_All//gi|9653250|ref|NP_062496.1|//1.00E-07//NADH dehydrogenase subunit 4 [Chondrus crispus] >gi|1352567|sp|P48915.1|NU4M_CHOCR RecName: Full=NADH-ubiquinone oxidoreductase chain 4; AltName: Full=NADH dehydrogenase subunit 4 >gi|1334501|emb|CAA87623.1| NADH dehydrogenase (ubiquinone), subunit 4 [Chondrus crispus]	Unigene108480_All//1.00E-07//AT3G03070| NDH4 (NADH DEHYDROGENASE 4); NADH dehydrogenase (ubiquinone)				GO:0016491//GO:0022904//GO:0043231//GO:0044425	nr -
Unigene108486_All	252	0.00	0.00	0.00	0.00	0.00	0.00	3.86	0.00	0.47	null	null		null	null		null	null		null	null		-1.19E+01	5.84E-07	Down	-3.02E+00	9.61E-05	Down							
Unigene10849_All	524	0.00	5.71	1.12	0.00	0.00	0.00	0.08	0.00	0.00	1.25E+01	5.19E-17	Up	1.01E+01	2.17E-03		null	null		null	null		-6.33E+00	6.62E-01		-6.33E+00	6.17E-01		Unigene10849_All//gi|7248459|gb|AAF43497.1|AF134579_1//4.00E-09//arabinogalactan protein [Zea mays]	Unigene10849_All//9.00E-08//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase				GO:0000902//GO:0005975//GO:0006884//GO:0010033//GO:0016020	nr -
Unigene108494_All	470	0.00	0.00	0.00	0.00	0.00	0.00	2.16	0.62	0.08	null	null		null	null		null	null		null	null		-1.79E+00	6.30E-03		-4.67E+00	1.72E-06	Down	Unigene108494_All//gi|247421835|gb|ACS96445.1|//1.00E-52//S18.A ribosomal protein [Jatropha curcas]	Unigene108494_All//1.00E-47//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006412//GO:0015935//GO:0016020//GO:0003012//GO:0031981	nr +
Unigene1085_All	3274	1.68	3.73	1.76	1.99	2.60	2.30	1.98	4.49	5.48	1.15E+00	1.08E-11	Up	6.60E-02	8.01E-01		3.82E-01	5.68E-02		2.09E-01	3.87E-01		1.19E+00	9.67E-18	Up	1.47E+00	3.08E-30	Up	Unigene1085_All//gi|15234064|ref|NP_192018.1|//2.00E-86//extra-large G-protein-related [Arabidopsis thaliana] >gi|79329014|gb|AAL47466.1| AT4g01090/F2N1_13 [Arabidopsis thaliana] >gi|20334762|gb|AAM16242.1| AT4g01090/F2N1_13 [Arabidopsis thaliana] >gi|222424660|dbj|BAH20284.1| AT4G01090 [Arabidopsis thaliana]	Unigene1085_All//5.00E-112//AT2G46380| unknown protein	Unigene1085_All//0.00E+00//gi|13351545|gb|BG441893.1|BG441893				nr -
Unigene108500_All	462	0.00	0.00	0.00	0.00	0.07	0.00	8.69	6.15	3.62	null	null		null	null		6.22E+00	8.38E-01		null	null		-4.99E-01	7.18E-02		-1.26E+00	3.83E-06	Down			Unigene108500_All//4.00E-131//gi|78352234|gb|DT572508.1|DT572508				
Unigene108501_All	598	0.35	0.17	0.09	0.25	0.17	0.00	2.26	0.77	0.33	-1.05E+00	5.65E-01		-1.98E+00	3.82E-01		-5.32E-01	7.86E-01		-7.97E+00	2.35E-01		-1.56E+00	3.85E-03		-2.76E+00	7.51E-06	Down			Unigene108501_All//6.00E-26//DW512828				
Unigene108511_All	359	0.00	0.42	0.00	0.14	0.19	0.13	2.71	0.12	0.22	8.73E+00	2.36E-01		null	null		4.67E-01	9.61E-01		-1.42E-01	9.56E-01		-4.54E+00	6.92E-06	Down	-3.61E+00	2.14E-05	Down	Unigene108511_All//gi|19715597|gb|AAL91622.1|//5.00E-16//At2g23450/F26B6.10 [Arabidopsis thaliana] >gi|23463045|gb|AAX33192.1| At2g23450/F26B6.10 [Arabidopsis thaliana]	Unigene108511_All//2.00E-17//AT2G23450| protein kinase family protein				GO:0000166//GO:0004672//GO:0008152	nr +
Unigene108513_All	570	0.00	0.00	0.00	0.00	0.00	0.00	3.63	5.28	0.56	null	null		null	null		null	null		null	null		5.39E-01	9.97E-02		-2.70E+00	2.21E-08	Down	Unigene108513_All//gi|212717149|gb|ACJ37416.1|//1.00E-31//stress-induced receptor-like kinase [Glycine max]	Unigene108513_All//5.00E-23//AT5G39020| protein kinase family protein	Unigene108513_All//2.00E-170//C0081306			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene108517_All	242	0.00	0.00	0.00	0.00	0.00	0.00	2.10	0.52	0.00	null	null		null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.10E+01	5.56E-04	Down							
Unigene108852_All	254	0.00	0.00	0.00	0.00	0.00	0.00	0.67	2.14	4.55	null	null		null	null		null	null		null	null		1.68E+00	7.92E-02		2.77E+00	5.09E-05	Up							
Unigene108524_All	438	0.00	0.00	0.00	0.00	0.00	0.00	2.22	0.38	1.09	null	null		null	null		null	null		null	null		-2.54E+00	6.42E-04	Down	-1.02E+00	9.02E-02		Unigene108524_All//gi|255569613|ref|XP_002525772.1|//4.00E-06//conserved hypothetical protein [Ricinus communis] >gi|255569615|ref|XP_002525773.1| conserved hypothetical protein [Ricinus communis] >gi|223534922|gb|EEF36608.1| conserved hypothetical protein [Ricinus communis] >gi|223534923|gb|EEF36609.1| conserved hypothetical protein [Ricinus communis]	Unigene108524_All//4.00E-06//AT4G10270| wound-responsive family protein	Unigene108524_All//2.00E-09//ES791233				nr -
Unigene10853_All	528	0.00	0.00	0.00	0.00	0.00	0.00	3.92	2.14	0.00	null	null		null	null		null	null		null	null		-8.76E-01	2.86E-02		-1.19E+01	2.86E-15	Down							
Unigene108533_All	274	0.00	0.00	0.00	0.00	0.00	0.00	0.31	0.00	16.72	null	null		null	null		null	null		null	null		-8.27E+00	4.06E-01		5.76E+00	1.34E-29	Up	Unigene108533_All//gi|74273615|gb|ABA01475.1|//2.00E-33//1-aminocyclopropane-1-carboxylate synthase ACS6 [Gossypium hirsutum]	Unigene108533_All//8.00E-25//AT1G01480| ACS2; 1-aminocyclopropane-1-carboxylate synthase	Unigene108533_All//8.00E-08//ES822034		ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016740//GO:0016831//GO:0016846//GO:0048037	nr +
Unigene108541_All	994	4796.46	3980.56	5932.28	912.54	1274.11	754.10	8.72	4.54	0.76	-2.69E-01	0.00E+00		3.07E-01	0.00E+00		4.82E-01	4.93E-304		-2.75E-01	6.65E-69		-9.41E-01	1.14E-07		-3.52E+00	3.85E-42	Down	Unigene108541_All//gi|22412190|ref|XP_002330127.1|//1.00E-128//light-harvesting complex I protein Lhca4 [Populus trichocarpa] >gi|222871261|gb|EEF08392.1| light-harvesting complex I protein Lhca4 [Populus trichocarpa]	Unigene108541_All//7.00E-120//AT3G47470| LHCA4 (LIGHT-HARVESTING CHLOROPHYLL-PROTEIN COMPLEX I SUBUNIT A4); chlorophyll binding	Unigene108541_All//0.00E+00//gi|48752319|gb|CO082838.1|CO082838		ko00196|Photosynthesis - antenna proteins		nr +
Unigene108545_All	442	0.00	0.00	0.00	0.00	0.00	0.00	2.20	0.09	0.00	null	null		null	null		null	null		null	null		-4.54E+00	6.92E-06	Down	-1.11E+01	2.72E-07	Down	Unigene108545_All//gi|27450759|gb|AA014682.1|AF508263_1//2.00E-62//actin [Pyrocystis lunula]	Unigene108545_All//7.00E-54//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene108545_All//1.00E-26//gi|109842528|gb|DW241088.1|DW241088			GO:0032559//GO:0043232	nr +
Unigene108855_All	480	0.00	8.23	4.88	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.67E-22	Up	1.23E+01	6.41E-13	Up	null	null		null	null		null	null		null	null								
Unigene108566_All	226	0.00	0.00	0.00	0.00	0.00	0.00	2.43	0.18	0.00	null	null		null	null		null	null		null	null		-3.72E+00	3.23E-03		-1.12E+01	2.81E-04	Down	Unigene108566_All//gi|73761683|gb|AAZ83341.1|//2.00E-29//ubiquitin extension protein [Gossypium hirsutum]	Unigene108566_All//7.00E-13//AT2G47110| UBQ6; protein binding	Unigene108566_All//6.00E-08//DN780054		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +

Unigene108567_All	717	0.00	0.00	0.00	0.00	0.10	0.00	3.83	0.52	2.22	null	null		null	null		6.59E+00	6.15E-01		null	null		-2.87E+00	4.04E-11	Down	-7.86E-01	1.58E-02		Unigene108567_All//gi|42568648|ref|NP_200715.2|//3.00E-90//glycosyl transferase family 1 protein [Arabidopsis thaliana]	Unigene108567_All//3.00E-84//AT5G59070| glycosyl transferase family 1 protein					nr -
Unigene10857_All	360	1.16	0.84	2.96	2.91	1.34	0.25	0.00	0.00	0.11	-4.61E-01	6.50E-01		1.35E+00	6.01E-02		-1.12E+00	8.44E-02		-3.53E+00	9.34E-05	Down	null	null		6.79E+00	6.47E-01									
Unigene108590_All	361	0.00	0.00	0.00	0.00	0.00	0.00	10.07	1.62	0.22	null	null		null	null		null	null		null	null		-2.64E+00	2.59E-13	Down	-5.51E+00	9.56E-24	Down			Unigene108590_All//4.00E-10//TC135251					
Unigene108596_All	433	0.00	0.00	0.00	0.00	0.00	0.00	1.86	0.19	0.28	null	null		null	null		null	null		null	null		-3.26E+00	4.49E-04	Down	-2.75E+00	9.43E-04	Down	Unigene108596_All//gi|32401352|gb|AAP80848.1|//3.00E-17//protein disulfide isomerase 2 precursor [Griffithsia japonica]	Unigene108596_All//3.00E-15//AT1G77510| ATPDIL1-2 (PDI-LIKE 1-2); protein disulfide isomerase			ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene108599_All	215	0.00	0.24	0.00	0.00	0.00	0.00	3.74	0.39	0.37	7.88E+00	6.21E-01		null	null		null	null		null	null		-3.26E+00	4.48E-04	Down	-3.33E+00	2.47E-04	Down								
Unigene10860_All	420	0.00	15.92	3.93	0.00	0.16	0.00	0.00	0.00	0.00	1.40E+01	3.29E-38	Up	1.19E+01	4.31E-09	Up	7.36E+00	6.15E-01		null	null		null	null		null	null									
Unigene108600_All	508	0.21	0.00	0.00	0.00	0.00	0.27	2.83	0.41	1.02	-7.69E+00	3.76E-01		-7.69E+00	3.98E-01		null	null		8.06E+00	3.12E-01		-2.78E+00	5.95E-06	Down	-1.47E+00	3.09E-03		Unigene108600_All//gi|297806927|ref|XP_002871347.1|//4.00E-50//positive transcription elongation factor/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297317184|gb|EFH47606.1| positive transcription elongation factor/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene108600_All//3.00E-51//AT5G08565| positive transcription elongation factor/ zinc ion binding	Unigene108600_All//5.00E-103//TC154168			GO:0003711//GO:0008135//GO:0010557//GO:0043231//GO:0046914	nr +
Unigene10861_All	394	0.00	0.00	0.00	0.00	0.00	4.40	8.06	0.00	null	null	null		null	null		null	null		null	null		8.74E-01	5.01E-03		-1.21E+01	8.37E-13	Down	Unigene10861_All//gi|66270183|gb|AY43421.1|//6.00E-33//ribosomal protein L34 [Phytophthora infestans]	Unigene10861_All//1.00E-30//AT1G26880| 60S ribosomal protein L34 (RPL34A)			ko03010|Ribosome	GO:0043231	nr +
Unigene108618_All	245	0.00	0.00	0.00	0.00	0.00	0.00	2.42	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	2.40E-04	Down	-1.12E+01	1.42E-04	Down								
Unigene10862_All	342	0.31	0.00	1.09	1.60	2.52	0.00	1.98	1.71	0.00	-8.26E+00	3.76E-01		1.83E+00	2.13E-01		6.52E-01	4.25E-01		-1.06E+01	1.52E-03		-2.09E-01	7.82E-01		-1.09E+01	3.57E-05	Down			Unigene10862_All//5.00E-176//ES836338					
Unigene108620_All	459	0.00	0.00	0.00	0.22	0.00	0.00	2.86	0.27	1.39	null	null		null	null		-7.76E+00	3.17E-01		-7.76E+00	4.05E-01		-3.39E+00	1.90E-06	Down	-1.04E+00	3.96E-02		Unigene108620_All//gi|15239274|ref|NP_201416.1|//1.00E-46//glycosyl hydrolase family 38 protein [Arabidopsis thaliana] >gi|10177130|dbj|BAB10420.1| alpha-mannosidase [Arabidopsis thaliana]	Unigene108620_All//7.00E-48//AT5G66150| glycosyl hydrolase family 38 protein	Unigene108620_All//1.00E-174//TC178171		ko00511|Other glycan degradation	GO:0003676//GO:0005618//GO:0006259//GO:0019923//GO:0016020//GO:0019318//GO:0031410//GO:0043231//GO:0046914	nr +
Unigene108626_All	291	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	1.24E-04	Down	-1.11E+01	7.12E-05	Down								ESTscan -
Unigene108637_All	247	0.00	0.00	0.00	0.00	0.00	0.00	2.40	1.02	0.00	null	null		null	null		null	null		null	null		-1.24E+00	1.54E-01		-1.12E+01	1.42E-04	Down	Unigene108637_All//gi|145344332|ref|XP_001416689.1|//9.00E-10//Cytosolic 80S ribosomal protein L39; Cytosolic 60S large ribosomal protein L39 [Ostreococcus lucimarinus CCE9901] >gi|144576915|gb|ABO94982.1| Cytosolic 80S ribosomal protein L39; Cytosolic 60S large ribosomal protein L39 [Ostreococcus lucimarinus CCE9901]	Unigene108637_All//3.00E-09//AT4G31985| 60S ribosomal protein L39 (RPL39C)			ko03010|Ribosome		nr +
Unigene10864_All	425	0.00	0.00	0.00	0.00	0.00	0.00	2.39	2.66	0.00	null	null		null	null		null	null		null	null		1.53E-01	7.89E-01		-1.12E+01	1.35E-07	Down	Unigene10864_All//gi|299472847|emb|CBN80416.1|//1.00E-07//EsV-1-116 [Ectocarpus siliculosus]						nr -
Unigene108642_All	302	59.08	20.97	50.08	27.38	35.23	24.82	2.66	0.14	0.40	-1.49E+00	9.99E-25	Down	-2.39E-01	9.88E-02		3.64E-01	3.88E-02		-1.41E-01	5.63E-01		-4.26E+00	8.48E-05	Down	-2.75E+00	9.43E-04	Down	Unigene108642_All//gi|62945915|gb|AAY22200.1|//3.00E-28//squalene monooxygenase [Datura inoxia]	Unigene108642_All//3.00E-28//AT2G22830| SQE2 (squalene epoxidase 2); FAD binding / oxidoreductase/ squalene monooxygenase	Unigene108642_All//1.00E-148//TC155314		ko00100|Steroid biosynthesis	GO:0004497//GO:0008152//GO:0030554//GO:0031224	nr +
Unigene108652_All	327	0.32	8.68	1.14	0.00	0.11	0.41	0.39	0.51	0.24	4.76E+00	1.45E-13	Up	1.83E+00	2.13E-01		6.72E+00	8.38E-01		8.69E+00	3.12E-01		3.99E-01	8.15E-01		-6.71E-01	7.21E-01		Unigene108652_All//gi|20197247|gb|AAM14995.1|//5.00E-08//Expressed protein [Arabidopsis thaliana]	Unigene108652_All//2.00E-09//AT2G38465| unknown protein				GO:0016020	nr +
Unigene108654_All	766	0.00	0.00	0.00	0.00	0.00	0.00	2.76	0.82	0.94	null	null		null	null		null	null		null	null		-1.75E+00	3.84E-05	Down	-1.56E+00	1.14E-04	Down	Unigene108654_All//gi|224072801|ref|XP_002303888.1|//4.00E-86//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222841320|gb|EEE78867.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene108654_All//9.00E-63//AT1G51190| PLT2 (PLETHORA 2); transcription factor	Unigene108654_All//1.00E-12//ES821430	AP2-EREBP		GO:0006350//GO:0010468//GO:0016491//GO:0043231//GO:0048513	nr +
Unigene10866_All	326	0.00	170.19	74.65	0.00	0.00	0.00	0.00	0.00	0.00	1.74E+01	0.00E+00	Up	1.62E+01	9.83E-138	Up	null	null		null	null		null	null		null	null									
Unigene108673_All	445	0.00	0.00	0.00	0.00	0.00	0.00	2.09	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	1.15E-06	Down	-1.10E+01	5.48E-07	Down	Unigene108673_All//gi|300294856|gb|ADJ96635.1|//1.00E-45//S-adenosyl homocysteine hydrolase [Dunaliella salina]	Unigene108673_All//1.00E-40//AT4G13940| MEE58 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding			ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0008152//GO:0016787	nr -
Unigene10868_All	270	0.39	0.00	0.39	0.37	3.83	1.34	0.31	0.31	0.15	-8.60E+00	3.76E-01		2.51E-02	1.00E+00		3.37E+00	1.64E-04	Up	1.86E+00	2.20E-01		-1.67E-02	1.02E+00		-1.09E+00	6.77E-01									
Unigene108681_All	414	0.00	0.00	0.00	0.00	0.00	0.00	2.55	1.92	0.00	null	null		null	null		null	null		null	null		-4.13E-01	5.15E-01		-1.13E+01	6.73E-08	Down								
Unigene108685_All	281	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.45	0.00	null	null		null	null		null	null		null	null		-2.13E+00	3.32E-02		-1.09E+01	2.81E-04	Down								
Unigene108698_All	248	0.00	0.00	0.00	0.80	0.14	0.18	2.73	0.17	0.32	null	null		null	null		-2.53E+00	2.34E-01		-2.14E+00	3.48E-01		-4.02E+00	5.36E-04	Down	-3.09E+00	1.45E-03									
Unigene108689_All	555	0.00	0.00	0.00	1.17	0.12	0.16	1.45	0.15	2.08	null	null		null	null		-3.23E+00	2.49E-03		-2.84E+00	1.02E-02		-3.26E+00	4.48E-04	Down	5.24E-01	3.53E-01		Unigene108689_All//gi|297727877|ref|NP_001176302.1|//6.00E-23//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1| Os11g0106066 [Oryza sativa Japonica Group]	Unigene108689_All//2.00E-05//AT1G43760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015700), Endonuclease/exonuclease/phosphatase (InterPro:IPR005135); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40390.1); Has 2614 Blast hits to 2551 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 1517; Fungi - 2; Plants - 1086; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene108689_All//2.00E-16//TC145821				nr -
Unigene108696_All	949	0.00	0.00	0.00	0.00	0.00	0.00	5.12	0.31	0.13	null	null		null	null		null	null		null	null		-4.05E+00	9.81E-26	Down	-5.35E+00	3.27E-31	Down	Unigene108696_All//gi|146216004|gb|ABQ10204.1|//3.00E-55//cysteine protease Cp6 [Actinidia deliciosa]	Unigene108696_All//2.00E-44//AT4G23520| cysteine proteinase, putative				GO:0070011	nr +
Unigene10870_All	392	0.00	0.00	0.00	0.00	0.00	0.00	2.70	2.56	0.00	null	null		null	null		null	null		null	null		-7.55E-02	9.09E-01		-1.14E+01	6.73E-08	Down	Unigene10870_All//gi|226503351|ref|NP_001156284.1|//2.00E-47//60S ribosomal protein L23a [Zea mays] >gi|195638090|gb|ACG38513.1| 60S ribosomal protein L23a [Zea mays]	Unigene10870_All//5.00E-45//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene10870_All//2.00E-15//ES840224		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene108708_All	400	0.26	0.00	0.40	0.12	0.69	0.11	1.27	0.00	1.00	-8.03E+00	3.76E-01		6.11E-01	7.49E-01		2.47E+00	2.23E-01		-1.41E-01	9.56E-01		-1.03E+01	8.91E-04	Down	-3.49E-01	6.73E-01		Unigene108708_All//gi|22128591|gb|AAM52341.1|//2.00E-06//Fertility restorer-like protein [Petunia x hybrida]	Unigene108708_All//2.00E-05//AT1G62590| pentatricopeptide (PPR) repeat-containing protein	Unigene108708_All//2.00E-30//BF268954			GO:0003676//GO:0006260//GO:0034061	nr +
Unigene10871_All	344	3.65	2.65	1.55	21.43	5.71	3.81	8.48	12.39	2.78	-4.61E-01	4.32E-01		-1.24E+00	5.53E-02		-1.91E+00	4.67E-18	Down	-2.49E+00	6.41E-22	Down	5.47E-01	3.91E-02		-1.61E+00	2.29E-06	Down			Unigene10871_All//3.00E-48//FL577497					
Unigene108718_All	300	0.00	0.00	0.00	0.00	0.00	0.00	23.54	9.89	3.85	null	null		null	null		null	null		null	null		-1.25E+00	1.17E-09	Down	-2.61E+00	7.96E-26	Down								
Unigene108722_All	725	0.00	0.00	0.00	0.00	0.00	0.00	7.70	6.05	1.65	null	null		null	null		null	null		null	null		-3.47E-01	1.41E-01		-2.22E+00	3.73E-17	Down	Unigene108722_All//gi|298706692|emb|CBJ34222.1|//6.00E-20//conserved unknown protein [Ectocarpus siliculosus] >gi|298713886|emb|CBJ33762.1| conserved unknown protein [Ectocarpus siliculosus]		Unigene108722_All//6.00E-48//gi|78352089|gb|DT572363.1|DT572363				nr -
Unigene108729_All	554	0.00	0.00	0.00	0.00	0.00	0.00	4.73	0.15	0.36	null	null		null	null		null	null		null	null		-4.97E+00	7.56E-16	Down	-3.72E+00	9.00E-14	Down	Unigene108729_All//gi|118152392|gb|ABR63940.1|//2.00E-63//ribosomal protein L3-A2-II [Triticum aestivum]	Unigene108729_All//4.00E-54//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene10873_All	352	0.00	0.00	0.00	0.00	0.00	0.00	0.24	1.90	5.21	null	null		null	null		null	null		null	null		2.98E+00	2.86E-03		4.44E+00	9.60E-11	Up			Unigene10873_All//3.00E-51//TC140526					
Unigene10734_All	378	0.00	0.00	0.00	0.53	0.36	0.24	3.02	0.00	0.11	null	null		null	null		-5.33E-01	7.49E-01		-1.14E+00	5.70E-01		-1.16E+01	3.89E-08	Down	-4.84E+00	2.34E-07	Down								
Unigene108736_All	538	0.19	0.00	0.00	0.09	0.06	0.00	1.96	0.78	0.30	-7.60E+00	3.76E-01		-7.60E+00	3.98E-01		-5.33E-01	8.28E-01		-6.53E+00	6.44E-01		-1.34E+00	2.90E-02		-2.73E+00	1.12E-04	Down	Unigene108736_All//gi|297596537|ref|NP_001042723.2|//2.00E-15//Os01g0275900 [Oryza sativa Japonica Group] >gi|255673109|dbj|BAF04637.2| Os01g0275900 [Oryza sativa Japonica Group]		Unigene108736_All//8.00E-62//gi|109881497|gb|DW510467.1|DW510467				nr -
Unigene10875_All	1625	0.00	0.00	0.00	0.43	0.04	0.14	5.57	0.46	0.71	null	null		null	null		-3.34E+00	1.25E-03		-1.63E+00	7.45E-02		-3.59E+00	3.22E-43	Down	-2.97E+00	1.32E-37	Down	Unigene10875_All//gi|115447863|ref|NP_001047711.1|//1.00E-127//Os02g0673100 [Oryza sativa Japonica Group] >gi|50251239|dbj|BAD27825.1| aluminum-activated malate transporter-like [Oryza sativa Japonica Group] >gi|50253199|dbj|BAD29455.1| aluminum-activated malate transporter-like [Oryza sativa Japonica Group] >gi|113537242|dbj|BAF09625.1| Os02g0673100 [Oryza sativa Japonica Group]	Unigene10875_All//1.00E-108//AT4G00910| unknown protein	Unigene10875_All//2.00E-46//FL576764				nr +
Unigene108753_All	551	0.00	0.00	0.00	0.00	0.00	0.00	2.30	0.53	0.14	null	null		null	null		null	null		null	null		-2.12E+00	4.17E-04	Down	-3.99E+00	2.56E-07	Down	Unigene108753_All//gi|255070117|ref|XP_002507140.1|//9.00E-18//60S ribosomal protein L36 [Micromonas sp. RCC299] >gi|226522415|gb|ACO68398.1| 60S ribosomal protein L36 [Micromonas sp. RCC299]	Unigene108753_All//3.00E-17//AT2G37600| 60S ribosomal protein L36 (RPL36A)			ko03010|Ribosome	GO:0009536//GO:0010467//GO:0015934	nr -
Unigene108772_All	284	0.18	0.00	0.00	0.88	0.12	0.00	2.53	0.88	0.00	-7.53E+00	6.19E-01		-7.53E+00	6.32E-01		-2.85E+00	1.37E-01		-9.78E+00	7.36E-02		-1.52E+00	5.42E-02		-1.13E+01	1.78E-05	Down			Unigene108772_All//1.00E-31//TC167240					
Unigene108787_All	245	0.00	0.00	0.00	0.00	0.00	0.00	2.42	1.36	0.00	null	null		null	null		null	null		null	null		-8.24E-01	3.48E-01		-1.12E+01	1.42E-04	Down	Unigene108787_All//gi|192910762|gb|ACF06489.1|//1.00E-23//ribosomal protein L10A [Elaeis guineensis]	Unigene108787_All//6.00E-15//AT5G22440| 60S ribosomal protein L10A (RPL10aC)			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene10879_All	518	6.97	14.48	2.47	29.52	30.11	55.80	110.68	79.32	214.42	1.05E+00	1.34E-06	Up	-1.50E+00	2.51E-05	Down	2.86E-02	8.72E-01		9.18E-01	8.33E-20		-4.81E-01	1.05E-14		9.54E-01	1.25E-92		Unigene10879_All//gi|45861745|gb|AS78671.1|//1.00E-70//actin [Capsicum annuum]	Unigene10879_All//7.00E-71//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene10879_All//0.00E+00//TC140485		ko04145|Phagosome	GO:0032559//GO:0043232	nr +
Unigene108791_All	292	0.00	0.00	0.00	0.00	0.00	0.00	2.32	0.14	0.14	null	null		null	null		null	null		null	null		-4.02E+00	5.36E-04	Down	-4.09E+00	3.10E-04	Down	Unigene108791_All//gi|75321780|sp|Q5W274.1|PDR3_TOBAC//5.00E-19//RecName: Full=Pleiotropic drug resistance protein 3; AltName: Full=NtPDR3 >gi|55056942|emb|CAH39853.1| PDR-like ABC transporter [Nicotiana tabacum]	Unigene108791_All//6.00E-19//AT1G15210| PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATPase, coupled to transmembrane movement of substances				GO:0000166//GO:0016020//GO:0017111	nr +
Unigene108794_All	283	1.11	1.07	0.19	2.82	5.96	1.44	42.58	5.91	2.39	-4.63E-02	9.85E-01		-2.56E+00	1.59E-01		1.08E+00	3.35E-02		-9.72E-01	2.30E-01		-2.85E+00	2.89E-46	Down	-4.15E+00	2.28E-66	Down			Unigene108794_All//5.00E-09//TC156509					

Unigene108795_All	234	0.00	0.00	0.00	0.00	0.00	0.00	2.35	0.36	0.00	null	null		null	null		null	null		null	null		-2.72E+00	1.22E-02		-1.12E+01	2.81E-04	Down								ESTscan +
Unigene108804_All	246	0.00	0.00	0.00	0.00	0.14	0.00	3.27	0.00	0.32	null	null		null	null		7.13E+00	8.38E-01		null	null		-1.17E+01	8.58E-06	Down	-3.33E+00	2.47E-04	Down								
Unigene108806_All	437	0.00	0.00	0.00	0.00	0.00	0.00	2.32	3.06	0.36	null	null		null	null		null	null		null	null		3.98E-01	4.64E-01		-2.67E+00	1.94E-04	Down								
Unigene10881_All	347	0.00	0.15	1.38	0.57	0.20	0.91	46.06	135.14	215.73	7.19E+00	6.21E-01		1.04E+01	7.50E-03		-1.53E+00	4.16E-01		6.66E-01	6.48E-01		1.55E+00	2.02E-82	Up	2.23E+00	7.15E-218	Up	Unigene10881_All//gi|115467322|ref|NP_001057260.1|//1.00E-11//Os06g0239200 [Oryza sativa Japonica Group] >gi|113595300|dbj|BAF19174.1| Os06g0239200 [Oryza sativa Japonica Group]	Unigene10881_All//1.00E-10//AT3G48180| unknown protein						nr -
Unigene10882_All	293	3.57	0.35	0.36	2.04	0.59	1.08	0.58	0.14	0.00	-3.37E+00	2.13E-04	Down	-3.30E+00	4.59E-04	Down	-1.80E+00	5.87E-02		-9.19E-01	3.52E-01		-2.02E+00	3.68E-01		-9.17E+00	1.09E-01		Unigene10882_All//gi|147866156|emb|CAN84129.1|//2.00E-07//hypothetical protein [Vitis vinifera]	Unigene10882_All//2.00E-06//AT5G05330| DNA binding	Unigene10882_All//5.00E-71//ES827558				nr -
Unigene10883_All	380	3.17	0.13	3.78	1.84	2.45	1.78	0.78	0.22	0.31	-4.57E+00	5.88E-06	Down	2.57E-01	6.28E-01		4.15E-01	6.06E-01		-4.19E-02	9.45E-01		-1.82E+00	2.11E-01		-1.31E+00	3.13E-01									
Unigene108833_All	302	0.35	0.00	0.00	0.33	0.11	0.15	2.10	0.00	0.40	-8.44E+00	3.76E-01		-8.44E+00	3.98E-01		-1.53E+00	5.88E-01		-1.14E+00	6.79E-01		-1.10E+01	1.24E-04	Down	-2.41E+00	8.12E-03		Unigene108833_All//gi|297847636|ref|XP_002891699.1|//1.00E-36//glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata] >gi|297337541|gb|EFH67958.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata]	Unigene108833_All//4.00E-35//AT1G52420| glycosyl transferase family 1 protein	Unigene108833_All//6.00E-92//TC173745			GO:0008152//GO:0009536//GO:0016740	nr -
Unigene108884_All	449	1.86	1.35	1.54	11.43	11.50	11.37	2.73	5.03	6.48	-4.61E-01	5.43E-01		-2.74E-01	7.05E-01		9.70E-03	9.80E-01		-7.70E-03	9.72E-01		8.80E-01	2.08E-02		1.25E+00	1.47E-04	Up			Unigene10884_All//1.00E-109//DW498751					ESTscan -
Unigene108849_All	634	0.00	0.00	0.00	0.00	0.00	0.00	2.07	0.00	0.88	null	null		null	null		null	null		null	null		-1.10E+01	2.56E-09	Down	-1.23E+00	1.61E-02		Unigene108849_All//gi|4559334|gb|AAD22996.1|//2.00E-50//expressed protein [Arabidopsis thaliana]	Unigene108849_All//4.00E-52//AT2G42570| unknown protein	Unigene108849_All//7.00E-180//gi|78354609|gb|DT574883.1|DT574883			GO:0031410	nr +
Unigene108850_All	396	0.00	2.94	0.00	0.00	0.26	0.11	0.43	0.42	3.12	1.15E+01	1.05E-06	Up	null	null		8.03E+00	4.58E-01		6.83E+00	7.02E-01		-1.66E-02	1.02E+00		2.87E+00	1.78E-05	Up	Unigene108850_All//gi|296081324|emb|CBI17706.3|//4.00E-07//unnamed protein product [Vitis vinifera]	Unigene108850_All//1.00E-06//AT5G55850| NOI	Unigene108850_All//8.00E-55//TC163606				nr +
Unigene108851_All	1062	0.00	0.00	0.00	0.00	0.00	0.00	13.06	0.94	0.26	null	null		null	null		null	null		null	null		-3.79E+00	6.19E-69	Down	-5.64E+00	2.30E-90	Down	Unigene108851_All//gi|149392583|gb|ABR26094.1|//8.00E-06//retrotransposon protein [Oryza sativa Indica Group]		Unigene108851_All//7.00E-27//TC146107				nr -
Unigene108867_All	348	0.00	0.00	0.00	0.00	0.00	0.00	2.55	0.72	0.46	null	null		null	null		null	null		null	null		-1.82E+00	1.08E-02		-2.48E+00	9.93E-04	Down	Unigene108867_All//gi|145349279|ref|XP_001419064.1|//8.00E-13//Ribosomal protein S30, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901] >gi|144579295|gb|AB097357.1| Ribosomal protein S30, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901]	Unigene108867_All//8.00E-11//AT5G56670| 40S ribosomal protein S30 (RPS30C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene10887_All	663	0.00	5.12	3.77	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.55E-19	Up	1.19E+01	8.33E-14	Up	null	null		null	null		null	null		null	null		Unigene10887_All//gi|159483795|ref|XP_001699946.1|//4.00E-07//gamete-specific transcription factor [Chlamydomonas reinhardtii] >gi|158281888|gb|EDF07642.1| gamete-specific transcription factor [Chlamydomonas reinhardtii]		Unigene10887_All//8.00E-07//gi|78326393|gb|DT546667.1|DT546667				nr -
Unigene108870_All	267	0.00	0.00	0.00	0.00	0.00	0.00	1.27	9.08	1.34	null	null		null	null		null	null		null	null		2.84E+00	9.30E-10	Up	8.42E-02	9.58E-01			Unigene108870_All//9.00E-05//AT3G13784| AtcwINV5 (Arabidopsis thaliana cell wall invertase 5); hydrolase, hydrolyzing O-glycosyl compounds	Unigene108870_All//8.00E-14//TC175966				
Unigene108872_All	408	0.00	0.00	0.00	0.00	0.00	0.00	2.07	1.43	0.00	null	null		null	null		null	null		null	null		-5.31E-01	4.45E-01		-1.10E+01	2.21E-06	Down	Unigene108872_All//gi|301105188|ref|XP_002901678.1|//3.00E-30//60S ribosomal protein L32-1 [Phytophthora infestans T30-4] >gi|262100682|gb|EEY58734.1| 60S ribosomal protein L32-1 [Phytophthora infestans T30-4]	Unigene108872_All//3.00E-29//AT4G18100| 60S ribosomal protein L32 (RPL32A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene108874_All	692	0.00	0.00	0.00	0.00	0.00	0.00	2.44	0.91	0.00	null	null		null	null		null	null		null	null		-1.43E+00	2.16E-03		-1.13E+01	1.70E-12	Down	Unigene108874_All//gi|301111866|ref|XP_002905012.1|//4.00E-40//major vault protein [Phytophthora infestans T30-4] >gi|262095342|gb|EEY53394.1| major vault protein [Phytophthora infestans T30-4]						nr +
Unigene108877_All	285	0.00	0.00	0.00	0.00	0.00	0.00	4.60	10.12	0.00	null	null		null	null		null	null		null	null		1.14E+00	6.59E-04	Up	-1.22E+01	9.85E-10	Down								
Unigene108878_All	248	0.00	0.00	0.00	0.00	0.00	0.00	2.56	0.00	0.32	null	null		null	null		null	null		null	null		-1.13E+01	1.24E-04	Down	-2.99E+00	2.58E-03									ESTscan +
Unigene108879_All	370	0.00	0.00	0.00	0.00	0.00	0.00	1.60	0.00	0.00	null	null		null	null		null	null		null	null		-1.06E+01	2.40E-04	Down	-1.06E+01	1.42E-04	Down								
Unigene10888_All	948	0.00	0.00	0.00	0.00	0.00	0.00	0.45	0.75	5.34	null	null		null	null		null	null		null	null		7.49E-01	3.41E-01		3.58E+00	9.62E-25	Up	Unigene10888_All//gi|297607204|ref|NP_001059610.2|//9.00E-11//Os07g0471900 [Oryza sativa Japonica Group] >gi|255677757|dbj|BAF21524.2| Os07g0471900 [Oryza sativa Japonica Group]	Unigene10888_All//4.00E-10//AT3G20640| ethylene-responsive protein -related	Unigene10888_All//8.00E-57//TC160843	bHLH		GO:0010468//GO:0043231	nr +
Unigene108883_All	410	0.00	0.00	0.00	0.00	0.00	0.00	3.20	0.51	0.00	null	null		null	null		null	null		null	null		-2.65E+00	3.03E-05	Down	-1.16E+01	9.85E-10	Down			Unigene108883_All//1.00E-13//DW489120					
Unigene1089_All	2875	1.64	2.15	2.22	2.34	2.37	2.98	9.51	15.06	22.61	3.93E-01	1.07E-01		4.40E-01	7.68E-02		1.98E-02	9.58E-01		3.52E-01	9.03E-02		6.63E-01	1.69E-19		1.25E+00	6.65E-84	Up	Unigene1089_All//gi|37703718|gb|AAR01224.1|//1.00E-20//cyclin T1 [Medicago truncatula]	Unigene1089_All//2.00E-06//AT5G45190| cyclin family protein	Unigene1089_All//0.00E+00//TC153765			GO:0000904//GO:0007049//GO:0009791//GO:0048827//GO:0050789//GO:0051707	nr -
Unigene108903_All	397	0.00	0.00	0.00	0.00	0.00	0.00	1.81	0.53	0.00	null	null		null	null		null	null		null	null		-1.78E+00	2.79E-02		-1.08E+01	1.78E-05	Down	Unigene108903_All//gi|301114000|ref|XP_002998770.1|//6.00E-38//cell division control protein 42 [Phytophthora infestans T30-4] >gi|262112071|gb|EEY70123.1| cell division control protein 42 [Phytophthora infestans T30-4]	Unigene108903_All//7.00E-28//AT1G20090| ROP2 (RHO-RELATED PROTEIN FROM PLANTS 2); GTP binding			ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity	GO:0000904//GO:0007010//GO:0009314//GO:0010118//GO:0016020//GO:0031981//GO:0032561//GO:0035556//GO:0044444	nr -
Unigene108914_All	379	4.00	0.13	1.26	2.76	3.00	2.50	14.06	6.84	3.89	-4.90E+00	1.23E-07	Down	-1.66E+00	5.58E-03		1.19E-01	8.71E-01		-1.41E-01	8.32E-01		-1.04E+00	8.91E-06	Down	-1.85E+00	3.94E-13	Down			Unigene108914_All//1.00E-118//TC162854					
Unigene108937_All	228	0.00	0.00	0.00	0.00	0.00	0.00	6.49	6.23	0.70	null	null		null	null		null	null		null	null		-5.85E-02	9.19E-01		-3.22E+00	3.28E-07	Down	Unigene108937_All//sp|Q8TGM6|TAR1_YEAST//1.00E-06//Protein TAR1 OS=Saccharomyces cerevisiae GN=TAR1 PE=2 SV=1		Unigene108937_All//1.00E-18//TC146753				swissprot -
Unigene108945_All	217	0.00	0.00	0.00	0.00	0.00	0.00	2.34	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	8.91E-04	Down	-1.12E+01	5.56E-04	Down	Unigene108945_All//gi|300266716|gb|EFJ50902.1|//2.00E-21//elongation factor 2 (EF-2, EF-TU) [Volvox carteri f. nagariensis]	Unigene108945_All//2.00E-21//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding				GO:0008135//GO:0017111//GO:0032561	nr +
Unigene10895_All	244	43.74	12.67	73.98	105.14	152.28	116.24	175.88	45.39	62.53	-1.79E+00	2.67E-19	Down	7.58E-01	1.97E-08		5.34E-01	4.49E-11		1.45E-01	2.17E-01		-1.95E+00	4.32E-104	Down	-1.49E+00	1.98E-73	Down	Unigene10895_All//gi|50313462|gb|AAT74601.1|//9.00E-42//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene10895_All//1.00E-26//AT3G23510| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene10895_All//5.00E-129//TC129559			GO:0006629//GO:0008757	nr +
Unigene108954_All	231	0.00	0.00	0.00	0.00	0.00	0.00	2.93	0.72	0.00	null	null		null	null		null	null		null	null		-2.02E+00	1.98E-02		-1.15E+01	3.57E-05	Down	Unigene108954_All//gi|301105535|ref|XP_002901851.1|//2.00E-06//villin-like protein [Phytophthora infestans T30-4] >gi|262099189|gb|EEY57241.1| villin-like protein [Phytophthora infestans T30-4]	Unigene108954_All//7.00E-05//AT3G57410| VLN3 (VILLIN 3); actin binding					nr -
Unigene108955_All	360	0.00	0.00	0.00	0.00	0.00	0.00	2.58	0.93	0.00	null	null		null	null		null	null		null	null		-1.48E+00	2.77E-02		-1.13E+01	5.48E-07	Down	Unigene108955_All//gi|223994887|ref|XP_002287127.1|//3.00E-38//RS18, ribosomal protein 18 40S small ribosomal subunit [Thalassiosira pseudonana CCMP1335] >gi|220976243|gb|EEP94570.1| RS18, ribosomal protein 18 40S small ribosomal subunit [Thalassiosira pseudonana CCMP1335]	Unigene108955_All//8.00E-38//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006412//GO:0015935//GO:0016020//GO:0003012//GO:0031981	nr +
Unigene108956_All	240	0.00	0.00	0.00	0.00	0.00	0.00	0.53	0.70	5.31	null	null		null	null		null	null		null	null		3.98E-01	8.15E-01		3.33E+00	2.39E-06	Up								
Unigene108896_All	403	2.47	0.25	2.38	3.83	3.50	2.47	0.94	0.62	2.17	-3.29E+00	3.81E-04	Down	-5.26E-02	9.54E-01		-1.29E-01	8.32E-01		-6.36E-01	2.47E-01		-6.02E-01	6.13E-01		1.20E+00	6.68E-02		Unigene108896_All//gi|225447735|ref|XP_002262698.1|//3.00E-45//PREDICTED: similar to somatic embryogenesis receptor-like kinase 3 [Vitis vinifera]	Unigene108896_All//3.00E-34//AT4G33430| BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE); kinase/ protein binding / protein heterodimerization/ protein serine/threonine kinase	Unigene108896_All//6.00E-62//TC146742		ko04626|Plant-pathogen interaction	GO:0002239//GO:0004713//GO:0004871//GO:0006464//GO:0006952//GO:0009555//GO:0016628//GO:0031224//GO:0032559//GO:0032991//GO:0040007//GO:0043231//GO:0043401//GO:0046983	nr +
Unigene108961_All	621	0.00	0.00	0.00	0.00	0.00	0.00	1.36	0.67	0.06	null	null		null	null		null	null		null	null		-1.02E+00	1.41E-01		-4.41E+00	2.37E-05	Down	Unigene108961_All//gi|298715057|emb|CBJ27764.1|//2.00E-09//delta protein [Ectocarpus siliculosus]				ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene10897_All	316	20469.36	7123.71	20124.62	2439.64	2547.67	1786.53	3.61	2.38	0.88	-1.52E+00	0.00E+00	Down	-2.45E-02	1.82E-04		6.25E-02	2.72E-04		-4.50E-01	7.83E-147		-6.02E-01	3.08E-01		-2.03E+00	8.64E-04	Down	Unigene10897_All//gi|29468504|gb|AA085557.1|//2.00E-39//photosystem I subunit XI [Nicotiana attenuata]	Unigene10897_All//5.00E-37//AT4G12800| PSAL (photosystem I subunit L)	Unigene10897_All//1.00E-173//TC136126		ko00195|Photosynthesis	GO:0006091//GO:0009522//GO:0009526//GO:0009534//GO:0009570//GO:0031224	nr -
Unigene108970_All	307	0.00	0.00	0.00	0.00	0.00	0.00	2.20	0.54	0.00	null	null		null	null		null	null		null	null		-2.02E+00	1.98E-02		-1.11E+01	3.57E-05	Down	Unigene108970_All//gi|4501883|ref|NP_001604.1|//2.00E-32//actin, aortic smooth muscle [Homo sapiens] >gi|6671507|ref|NP_031418.1| actin, aortic smooth muscle [Mus musculus] >gi|78045238|ref|NP_001029674.1| actin, aortic smooth muscle [Bos taurus] >gi|110625958|ref|NP_112266.1| actin, aortic smooth muscle [Rattus norvegicus] >gi|156119362|ref|NP_001095152.1| actin, aortic smooth muscle [Oryctolagus cuniculus] >gi|197097944|ref|NP_001126814.1| actin, aortic smooth muscle [Pongo abelii] >gi|213688375|ref|NP_001135417.1| actin, aortic smooth muscle [Homo sapiens] >gi|257470979|ref|NP_001158122.1| actin, aortic smooth muscle [Sus scrofa] >gi|73996085|ref|XP_534781.2| PREDICTED: similar to Actin, aortic smooth muscle (Alpha-actin 2) [Canis familiaris] >gi|114631685|ref|XP_521550.2|	Unigene108970_All//2.00E-29//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene108970_All//4.00E-19//TC140956		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008015//GO:0008092//GO:0012501//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0048747//GO:0051707//GO:0060415	nr +

Unigene108978_All	433	0.00	0.00	0.00	0.00	0.00	0.00	1.37	0.39	0.00	null	null		null	null		null	null		null	null		-1.82E+00	4.72E-02		-1.04E+01	1.42E-04	Down	Unigene108978_All//gi|219118192|ref|XP_002179876.1|//5.00E-09//coronin like protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|217408929|gb|EEC48862.1| coronin like protein [Phaeodactylum tricornutum CCAP 1055/1]						nr +
Unigene10898_All	422	0.00	0.36	0.00	0.12	0.98	0.11	0.70	0.50	8.59	8.49E+00	2.36E-01		null	null		3.05E+00	5.68E-02		-1.41E-01	9.56E-01		-5.02E-01	6.78E-01		3.61E+00	4.95E-18	Up	Unigene10898_All//gi|224054334|ref|XP_002298208.1|//3.00E-16//amino acid transporter [Populus trichocarpa] >gi|222845466|gb|EEE83013.1| amino acid transporter [Populus trichocarpa]	Unigene10898_All//3.00E-16//AT1G80510| amino acid transporter family protein	Unigene10898_All//2.00E-09//TC168546				nr -
Unigene108980_All	418	0.25	0.36	0.13	0.72	0.16	0.86	2.63	0.40	0.57	5.39E-01	7.80E-01		-9.74E-01	7.22E-01		-2.12E+00	1.66E-01		2.74E-01	8.33E-01		-2.72E+00	1.31E-04	Down	-2.20E+00	5.66E-04	Down		Unigene108980_All//5.00E-07//EX172114				
Unigene108994_All	681	0.00	0.15	0.00	0.15	0.15	0.07	3.29	0.12	0.00	7.22E+00	3.90E-01		null	null		5.23E-02	9.68E-01		-1.14E+00	6.79E-01		-4.75E+00	2.70E-13	Down	-1.17E+01	1.66E-16	Down	Unigene108994_All//gi|224052970|ref|XP_002297642.1|//2.00E-79//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222844900|gb|EEE82447.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene108994_All//2.00E-78//AT1G55290| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene108994_All//3.00E-34//TC178591		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0009699//GO:0012501//GO:0016701//GO:0016706	nr -
Unigene108997_All	403	0.39	0.00	0.26	0.25	0.17	0.11	1.78	0.10	0.49	-8.61E+00	2.17E-01		-5.59E-01	7.76E-01		-5.33E-01	8.19E-01		-1.14E+00	6.79E-01		-4.10E+00	2.91E-04	Down	-1.85E+00	1.79E-02		Unigene108997_All//gi|115471355|ref|NP_001059276.1|//2.00E-47//Os07g0243200 [Oryza sativa Japonica Group] >gi|113610812|dbj|BAF21190.1| Os07g0243200 [Oryza sativa Japonica Group]	Unigene108997_All//6.00E-48//AT1G27680| APL2 (ADPGLC-PPASE LARGE SUBUNIT); glucose-1-phosphate adenylyltransferase	Unigene108997_All//2.00E-176//ES801523		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0070566	nr -
Unigene1090_All	981	5.97	8.94	5.81	20.26	35.45	52.30	4.05	11.12	7.47	5.81E-01	2.90E-03		-4.05E-02	8.83E-01		8.07E-01	5.35E-21		1.37E+00	2.15E-65	Up	1.46E+00	4.73E-18	Up	8.83E-01	3.31E-06		Unigene10_90_All//gi|42571559|ref|NP_973870.1|//1.00E-111//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|87789995|gb|AAF79910.1|AC022472_19 Contains similarity to SCUTL1 mRNA from Vitis vinifera gb|AF195653 and is a member of the thaumatin family PF|00314. EST gb|AI995819 comes from this gene [Arabidopsis thaliana]	Unigene10_90_All//7.00E-111//AT1G20030| pathogenesis-related thaumatin family protein	Unigene10_90_All//0.00E+00//CO118480				nr +
Unigene10900_All	285	135.85	67.38	71.37	244.35	265.33	200.30	214.66	70.69	75.20	-1.01E+00	6.14E-29	Down	-9.29E-01	3.18E-24		1.19E-01	6.43E-02		-2.87E-01	2.67E-06		-1.60E+00	1.53E-112	Down	-1.51E+00	1.52E-106	Down	Unigene10900_All//gi|295389384|dbj|BAJ06362.1|//3.00E-50//alpha-tubulin [Alopecurus aequalis]	Unigene10900_All//1.00E-51//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene10900_All//6.00E-160//EX171166		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene109001_All	261	0.00	0.00	0.00	0.00	0.00	0.00	2.59	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	6.34E-05	Down	-1.13E+01	3.57E-05	Down							
Unigene109002_All	536	0.00	0.00	0.00	0.00	0.00	0.00	3.47	2.81	0.00	null	null		null	null		null	null		null	null		-3.06E-01	5.09E-01		-1.18E+01	9.97E-14	Down	Unigene109002_All//gi|195641182|gb|ACG40059.1|//2.00E-33//60S ribosomal protein L21 [Zea mays]	Unigene109002_All//1.00E-33//AT1G09690| 60S ribosomal protein L21 (RPL21C)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr +
Unigene10901_All	360	0.00	0.00	0.00	0.00	0.00	0.00	2.35	1.74	0.00	null	null		null	null		null	null		null	null		-4.32E-01	5.47E-01		-1.12E+01	2.21E-06	Down							ESTscan +
Unigene109011_All	333	0.00	0.00	0.00	0.15	0.00	0.00	36.31	47.32	11.72	null	null		null	null		-7.23E+00	5.63E-01		-7.23E+00	6.44E-01		3.82E-01	2.56E-03		-1.63E+00	3.66E-24	Down	Unigene109011_All//gi|161778780|gb|ABX79341.1|//2.00E-36//cysteine protease [Vitis vinifera]	Unigene109011_All//2.00E-35//AT2G21430| cysteine proteinase A494, putative / thiol protease, putative	Unigene109011_All//8.00E-67//gi|109856138|gb|DW485117.1|DW485117			GO:0004175//GO:0019538	nr -
Unigene109012_All	314	0.00	0.00	0.00	0.00	0.00	0.00	2.02	0.40	0.13	null	null		null	null		null	null		null	null		-2.34E+00	1.27E-02		-3.99E+00	5.82E-04	Down	Unigene109012_All//gi|300120011|emb|CBK19565.2|//2.00E-06//unnamed protein product [Blastocystis hominis]					GO:0043231	nr -
Unigene109014_All	277	0.38	0.00	0.00	0.54	0.00	0.49	2.14	0.00	0.72	-8.56E+00	3.76E-01		-8.56E+00	3.98E-01		-9.08E+00	1.66E-01		-1.42E-01	9.44E-01		-1.11E+01	2.40E-04	Down	-1.57E+00	6.49E-02		Unigene109014_All//gi|225427898|ref|XP_002276690.1|//4.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]						nr +
Unigene109019_All	586	0.09	0.26	0.18	0.26	0.53	0.00	1.52	0.00	0.34	1.54E+00	5.32E-01		1.02E+00	7.04E-01		1.05E+00	5.32E-01		-7.99E+00	2.35E-01		-1.06E+01	2.24E-06	Down	-2.16E+00	2.68E-03		Unigene109019_All//gi|297601293|ref|NP_001050632.2|//6.00E-24//Os03g0604600 [Oryza sativa Japonica Group] >gi|255674692|dbj|BAF12546.2| Os03g0604600 [Oryza sativa Japonica Group]	Unigene109019_All//2.00E-20//AT1G49870| LOCATED IN: chloroplast; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; BEST Arabidopsis thaliana protein match is: MBD10; DNA binding / methyl-CpG binding (TAIR:AT1G15340.1); Has 5602 Blast hits to 4205 proteins in 368 species: Archae - 30; Bacteria - 406; Metazoa - 2889; Fungi - 302; Plants - 153; Viruses - 8; Other Eukaryotes - 1814 (source: NCBI BLink).					GO:0043231	nr +
Unigene10902_All	307	0.00	6.77	5.55	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	7.95E-12	Up	1.24E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene10902_All//sp|P00995|ISK1_HUMAN//7.00E-35//Pancreatic secretory trypsin inhibitor OS=Homo sapiens GN=SPINK1 PE=1 SV=2						swissprot -
Unigene109024_All	354	0.00	0.00	0.00	0.00	0.00	0.00	2.27	0.47	0.00	null	null		null	null		null	null		null	null		-2.26E+00	4.82E-03		-1.11E+01	4.43E-06	Down	Unigene109024_All//gi|15229438|ref|NP_188981.1|//2.00E-34//60S ribosomal protein L36a/L44 (RPL36aA) [Arabidopsis thaliana] >gi|15236469|ref|NP_193168.1| 60S ribosomal protein L36a/L44 (RPL36aB) [Arabidopsis thaliana] >gi|297800816|ref|XP_002868292.1| 60S ribosomal protein L36a/L44 [Arabidopsis lyrata subsp. lyrata] >gi|297831094|ref|XP_002883429.1| 60S ribosomal protein L36a/L44 [Arabidopsis lyrata subsp. lyrata] >gi|3122753|sp|O23290.3|RL36A_ARATH RecName: Full=60S ribosomal protein L36a >gi|2244789|emb|CAB10211.1| ribosomal protein [Arabidopsis thaliana] >gi|7268137|emb|CAB78474.1| ribosomal protein [Arabidopsis thaliana] >gi|11994324|dbj|BAB02283.1| 60S ribosomal protein L44-like [Arabidopsis thaliana] >gi|17065558|gb|AAL32933.1| 60S ribosomal protein L44-like [Arabidopsis thaliana] >gi|17473681|gb|AAL38297.1| ribosomal protein [Arabidopsis	Unigene109024_All//1.00E-35//AT4G14320| 60S ribosomal protein L36a/L44 (RPL36aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934	nr +
Unigene109039_All	431	0.00	0.00	0.00	0.00	0.00	0.00	4.32	1.36	2.03	null	null		null	null		null	null		null	null		-1.67E+00	2.33E-04	Down	-1.09E+00	8.60E-03								
Unigene10904_All	270	1.74	4.13	1.18	0.55	0.26	0.67	3.45	9.75	4.13	1.24E+00	6.10E-02		-5.60E-01	6.28E-01		-1.12E+00	5.85E-01		2.74E-01	9.05E-01		1.50E+00	3.94E-05	Up	2.62E-01	6.28E-01				Unigene10904_All//2.00E-51//gi|164300495|gb|ES814990.1|ES814990				
Unigene109048_All	420	0.00	0.00	0.00	0.00	0.00	0.00	3.52	0.70	0.47	null	null		null	null		null	null		null	null		-2.34E+00	3.57E-05	Down	-2.89E+00	1.35E-06	Down	Unigene109048_All//gi|226505998|ref|NP_001146929.1|//3.00E-35//60S ribosomal protein L7a [Zea mays] >gi|195605318|gb|ACG24489.1| 60S ribosomal protein L7a [Zea mays]	Unigene109048_All//1.00E-23//AT3G62870| 60S ribosomal protein L7A (RPL7aB)			ko03010|Ribosome	GO:0005198//GO:0005488//GO:0010467//GO:0022613//GO:0030529	nr -
Unigene10905_All	992	0.00	4.60	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.54E-26	Up	1.07E+01	8.44E-09	Up	null	null		null	null		null	null		null	null		Unigene10905_All//gi|300267271|gb|EFJ51455.1|//7.00E-09//CCCH zinc finger protein [Volvox carteri f. nagariensis]					GO:0005488//GO:0044238//GO:0044260	nr -
Unigene109058_All	535	0.00	0.00	0.00	0.00	0.00	0.00	5.22	1.64	0.97	null	null		null	null		null	null		null	null		-1.67E+00	3.67E-06	Down	-2.43E+00	6.89E-10	Down	Unigene109058_All//gi|45477151|sp|Q8RXA8.1|NDK4_SPIOL//3.00E-31//RecName: Full=Nucleoside diphosphate kinase 4, chloroplastic; AltName: Full=Nucleoside diphosphate kinase IV; Short=NDP kinase IV; Short=NDK IV; AltName: Full=Nucleoside diphosphate kinase III; Flags: Precursor >gi|196990051|gb|AAL91136.1| nucleoside diphosphate kinase III [Spinacia oleracea]	Unigene109058_All//1.00E-31//AT4G23900| nucleoside diphosphate kinase 4 (NDK4)			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism	GO:0009117//GO:0043231//GO:0044444//GO:0046914	nr +
Unigene109061_All	270	0.00	0.00	0.00	0.00	0.00	0.00	2.19	0.31	0.00	null	null		null	null		null	null		null	null		-2.82E+00	7.18E-03		-1.11E+01	1.42E-04	Down	Unigene109061_All//gi|301115128|ref|XP_002965292.1|//9.00E-07//RIB72 protein [Phytophthora infestans T30-4] >gi|262110081|gb|EEY68133.1| RIB72 protein [Phytophthora infestans T30-4]						nr +
Unigene10907_All	278	0.38	0.00	0.00	2.51	0.12	1.62	0.30	0.15	0.57	-8.56E+00	3.76E-01		-8.56E+00	3.98E-01		-4.34E+00	2.80E-04	Down	-6.27E-01	4.76E-01		-1.02E+00	7.26E-01		9.14E-01	6.25E-01		Unigene10907_All//gi|224102125|ref|XP_002312557.1|//2.00E-38//autoinhibited calcium ATPase [Populus trichocarpa] >gi|222852377|gb|EEE89924.1| autoinhibited calcium ATPase [Populus trichocarpa]	Unigene10907_All//7.00E-34//AT3G63380| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12)	Unigene10907_All//8.00E-08//TC163603			GO:0009206//GO:0019829//GO:0031224//GO:0032559//GO:0046873//GO:0070838	nr -
Unigene109072_All	372	0.00	0.00	0.00	0.13	0.00	0.00	1.59	0.00	0.00	null	null		null	null		-7.07E+00	5.63E-01		-7.07E+00	6.44E-01		-1.06E+01	2.40E-04	Down	-1.06E+01	1.42E-04	Down	Unigene109072_All//gi|55168340|gb|AAV44205.1|//3.00E-17//unknow protein [Oryza sativa Japonica Group]		Unigene109072_All//2.00E-27//TC149394				nr -
Unigene109075_All	276	0.95	2.57	3.47	16.42	3.12	3.76	3.22	2.73	0.72	1.44E+00	1.06E-01		1.87E+00	2.06E-02		-2.40E+00	5.62E-15	Down	-2.13E+00	2.40E-11	Down	-2.39E-01	7.21E-01		-2.16E+00	2.68E-03				Unigene109075_All//1.00E-86//DW499907				

Unigene10908_All	997	0.00	0.00	0.00	0.00	0.00	0.00	3.01	1.22	0.12	null	null		null	null		null	null		null	null		-1.31E+00	7.84E-05	Down	-4.65E+00	3.75E-18	Down	Unigene10908_All//gi|115474653|ref|NP_001060923.1|//1.00E-65//0s08g0130500 [Oryza sativa Japonica Group] >gi|730580|sp|P41095.3|RLA0_ORYSJ RecName: Full=60S acidic ribosomal protein P0 >gi|455401|dbj|BAA01668.1| acidic ribosomal protein P0 [Oryza sativa Japonica Group] >gi|29467534|dbj|BAC66723.1| 60S acidic ribosomal protein P0 [Oryza sativa Japonica Group] >gi|113622892|dbj|BAF22837.1| Os08g0130500 [Oryza sativa Japonica Group]	Unigene10908_All//4.00E-52//AT2G40010| 60S acidic ribosomal protein P0 (RPP0A)			ko03010|Ribosome	GO:0005198//GO:0006412//GO:0030529	nr +
Unigene109086_All	260	0.00	0.00	0.00	0.00	0.00	0.00	1.95	0.00	0.15	null	null		null	null		null	null		null	null		-1.09E+01	8.90E-04	Down	-3.67E+00	3.75E-03		Unigene109086_All//sp|Q55FT1|DPYD_DICDI//4.00E-08//Dihydropyrimidine dehydrogenase [NADP+] OS=Dictyostelium discoideum GN=pydl PE=2 SV=1							swissprot +
Unigene109090_All	342	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	0.00	null	null		null	null		null	null		null	null		-1.07E+01	4.62E-04	Down	-1.07E+01	2.81E-04	Down	Unigene109090_All//gi|94958151|gb|ABF47216.1|//1.00E-15//cathepsin B [Nicotiana benthamiana]	Unigene109090_All//3.00E-14//AT1G02300| cathepsin B-like cysteine protease, putative				GO:0008233	nr +
Unigene1091_All	801	0.39	0.63	1.20	4.29	6.88	4.85	0.42	2.56	0.80	6.91E-01	4.99E-01		1.61E+00	4.07E-02		6.81E-01	5.50E-03		1.76E-01	6.08E-01		2.60E+00	1.19E-07	Up	9.14E-01	2.47E-01		Unigene1091_All//gi|118485842|gb|ABR94768.1|//2.00E-08//unknown [Populus trichocarpa]		Unigene1091_All//1.00E-117//CO118480				nr -
Unigene10910_All	292	0.00	0.00	3.65	4.44	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	6.63E-06	Up	-1.21E+01	1.33E-09	Down	-1.21E+01	4.24E-08	Down	null	null		null	null		Unigene10910_All//gi|548587|sp|P04284.2|PR06_SOLLC//3.00E-51//RecName: Full=Pathogenesis-related leaf protein 6; Short=P6; AltName: Full=Ethylene-induced protein P1; AltName: Full=P14; AltName: Full=P14A; AltName: Full=PR protein; Flags: Precursor >gi|19285|emb|CAA48672.1| P1(p14) protein [Solanum lycopersicum] >gi|170490|gb|AAA03616.1| pathogenesis-related protein P6 [Solanum lycopersicum] >gi|2529165|emb|CAA70042.1| PR protein [Solanum lycopersicum]	Unigene10910_All//5.00E-24//AT2G14580| ATPRB1			ko04626|Plant-pathogen interaction	GO:0001906//GO:0006952	nr -
Unigene109104_All	459	1.37	0.77	2.09	0.54	0.83	2.95	1.11	0.27	0.43	-8.24E-01	3.75E-01		6.10E-01	3.86E-01		6.05E-01	6.59E-01		2.44E+00	2.97E-04	Up	-2.02E+00	5.21E-02		-1.35E+00	1.40E-01				Unigene109104_All//1.00E-94//ES837091				
Unigene109107_All	525	0.20	0.00	0.00	0.00	0.00	0.00	2.42	0.00	0.68	-7.64E+00	3.76E-01		-7.64E+00	3.98E-01		null	null		null	null		-1.12E+01	5.06E-09	Down	-1.82E+00	1.09E-03		Unigene109107_All//gi|18265373|dbj|BAB84015.1|//3.00E-43//polyprotein [Arabidopsis thaliana]	Unigene109107_All//1.00E-28//ATMG00810| hypothetical protein	Unigene109107_All//1.00E-29//EX169483			GO:0003676	nr -
Unigene109109_All	245	0.00	0.00	0.00	0.00	0.00	0.00	3.28	0.17	0.33	null	null		null	null		null	null		null	null		-4.26E+00	8.48E-05	Down	-3.33E+00	2.47E-04	Down							
Unigene10911_All	411	0.00	2.10	2.33	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	4.95E-05	Up	1.12E+01	2.46E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene109116_All	1080	0.68	0.23	0.00	0.32	0.41	0.08	1.72	0.35	0.30	-1.53E+00	7.78E-02		-9.41E+00	4.13E-04	Down	3.60E-01	8.07E-01		-1.95E+00	1.96E-01		-2.31E+00	3.11E-06	Down	-2.55E+00	3.55E-07	Down	Unigene109116_All//gi|30694495|ref|NP_849787.1|//3.00E-40//WNK7; kinase/ protein kinase [Arabidopsis thaliana] >gi|75246559|sp|Q8LST2.1|WNK7_ARATH RecName: Full=Probable serine/threonine-protein kinase WNK7; Short=AtWNK7; AltName: Full=Protein kinase with no lysine 7 >gi|21039014|dbj|BAB92986.1| protein kinase [Arabidopsis thaliana] >gi|222423633|dbj|BAH19785.1| AT1G49160 [Arabidopsis thaliana]	Unigene109116_All//7.00E-37//AT3G18750| WNK6 (WITH NO K (=LYSINE) 6); kinase/ protein kinase	Unigene109116_All//1.00E-49//TC164044		ko04712|Circadian rhythm - plant	GO:0004702//GO:0006464//GO:0032559	nr -
Unigene10912_All	319	0.00	9.69	3.17	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.38E-17	Up	1.16E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene10912_All//gi|301105781|ref|XP_002901974.1|//4.00E-13//DnaJ subfamily C protein [Phytophthora infestans T30-4] >gi|262099312|gb|EEY57364.1| DnaJ subfamily C protein [Phytophthora infestans T30-4]				ko04141|Protein processing in endoplasmic reticulum	GO:0005515	nr -
Unigene109125_All	258	0.00	0.00	0.00	0.00	0.00	0.00	3.61	0.32	0.00	null	null		null	null		null	null		null	null		-3.48E+00	7.79E-05	Down	-1.18E+01	5.48E-07	Down							ESTscan +
Unigene109126_All	428	1.34	0.95	1.12	1.63	0.64	0.21	1.98	0.68	0.28	-5.06E-01	6.00E-01		-2.64E-01	7.67E-01		-1.34E+00	1.09E-01		-2.95E+00	5.84E-03		-1.53E+00	3.21E-02		-2.82E+00	5.38E-04	Down	Unigene109126_All//gi|124359162|gb|ABN05685.1|//7.00E-10//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene109126_All//3.00E-05//AT3G09510| nucleic acid binding	Unigene109126_All//2.00E-43//ES818849				nr +
Unigene10913_All	364	0.00	2.51	5.71	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	2.62E-05	Up	1.25E+01	1.93E-11	Up	null	null		null	null		null	null		null	null		Unigene10913_All//gi|9858814|gb|AAG01147.1|AF283816|//3.00E-32//calreticulin [Pinus taeda]	Unigene10913_All//5.00E-27//AT1G09210| calreticulin 2 (CRT2)			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	GO:0006874//GO:0031410//GO:0044432//GO:0046872	nr -
Unigene109131_All	1836	0.00	0.00	0.00	0.11	0.00	0.00	2.16	2.85	4.51	null	null		null	null		-6.76E+00	8.47E-02		-6.76E+00	1.34E-01		3.95E-01	1.03E-01		1.06E+00	5.06E-09	Up	Unigene109131_All//gi|115435462|ref|NP_001042489.1|//1.00E-142//0s01g0229700 [Oryza sativa Japonica Group] >gi|113532020|dbj|BAF04403.1| Os01g0229700 [Oryza sativa Japonica Group]	Unigene109131_All//1.00E-35//AT3G06880| nucleotide binding	Unigene109131_All//0.00E+00//gi|164312745|gb|ES848791.1|ES848791		ko03040|Spliceosome	GO:0019787//GO:0032446//GO:0043234//GO:0005886	nr -
Unigene109134_All	252	0.00	0.00	0.00	0.00	0.00	0.00	3.52	1.00	0.16	null	null		null	null		null	null		null	null		-1.82E+00	1.08E-02		-4.48E+00	1.23E-05	Down	Unigene109134_All//gi|300261259|gb|EFJ45473.1|//1.00E-25//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene109134_All//2.00E-25//AT5G60670| 60S ribosomal protein L12 (RPL12C)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene109137_All	623	0.00	0.00	0.00	0.00	0.00	0.00	7.13	5.50	0.19	null	null		null	null		null	null		null	null		-3.73E-01	1.64E-01		-5.22E+00	3.22E-28	Down	Unigene109137_All//gi|253759791|ref|XP_002488947.1|//1.00E-10//hypothetical protein SORBIDRAFT_1368s002010 [Sorghum bicolor] >gi|241947119|gb|EES20264.1| hypothetical protein SORBIDRAFT_1368s002010 [Sorghum bicolor]		Unigene109137_All//4.00E-36//TC148521				nr +
Unigene109138_All	297	0.00	0.00	0.00	0.00	0.00	0.00	2.42	0.42	0.00	null	null		null	null		null	null		null	null		-2.52E+00	4.69E-03		-1.12E+01	1.78E-05	Down							
Unigene109142_All	476	0.00	0.00	0.00	0.00	0.00	0.00	1.51	0.09	0.00	null	null		null	null		null	3.14E-01		null	null		-4.10E+00	2.91E-04	Down	-1.06E+01	1.78E-05	Down	Unigene109142_All//gi|297801916|ref|XP_002868842.1|//3.00E-11//patched family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316628|gb|EFH45104.1| patched family protein [Arabidopsis lyrata subsp. lyrata]						nr +
Unigene109144_All	241	0.00	0.00	0.00	0.41	0.14	0.00	4.39	1.73	0.17	null	null		null	null		-1.53E+00	5.88E-01		-8.69E+00	4.05E-01		-1.34E+00	2.90E-02		-4.73E+00	8.85E-07	Down							
Unigene109146_All	395	0.00	0.00	0.00	0.00	0.00	0.00	2.68	0.00	0.10	null	null		null	null		null	null		null	null		-1.14E+01	1.51E-07	Down	-4.73E+00	8.85E-07	Down	Unigene109146_All//gi|223452518|gb|ACM89586.1|//2.00E-28//leucine-rich repeat family protein [Glycine max]	Unigene109146_All//7.00E-27//AT5G66330| leucine-rich repeat family protein	Unigene109146_All//3.00E-153//gi|78335416|gb|DT555690.1|DT555690			GO:0016491//GO:0023060	nr +
Unigene10915_All	294	3.03	0.00	3.62	0.34	0.00	0.00	0.58	0.57	0.41	-1.16E+01	2.86E-05	Down	2.60E-01	6.82E-01		-8.40E+00	3.17E-01		-8.40E+00	4.05E-01		-1.66E-02	1.02E+00		-5.01E-01	7.47E-01				Unigene10915_All//3.00E-07//TC153528				
Unigene109158_All	1047	0.00	0.00	0.00	0.10	0.00	0.09	0.44	0.40	1.98	null	null		null	null		-6.57E+00	3.17E-01		-1.42E-01	9.53E-01		-1.54E-01	8.70E-01		2.16E+00	1.54E-06	Up							
Unigene10916_All	923	0.00	0.00	0.00	0.00	0.00	0.00	6.73	1.95	0.86	null	null		null	null		null	null		null	null		-1.79E+00	4.95E-14	Down	-2.96E+00	5.25E-26	Down	Unigene10916_All//gi|3377952|emb|CAA08906.1|//1.00E-64//cysteine proteinase [Cicer arietinum]	Unigene10916_All//1.00E-60//AT4G35350| XCP1 (XYLEM CYSTEINE PEPTIDASE 1); cysteine-type endopeptidase/ cysteine-type peptidase				GO:0016787	nr +
Unigene109161_All	279	70.70	52.49	26.53	93.20	131.57	117.20	72.13	1093.73	156.93	-4.30E-01	5.39E-04		-1.41E+00	3.68E-24	Down	4.97E-01	1.13E-09		3.31E-01	3.96E-04		3.92E+00	0.00E+00	Up	1.12E+00	5.40E-48	Up	Unigene109161_All//gi|59896631|gb|AAX11684.1|//8.00E-06//perakine reductase [Rauvolfia serpentina]		Unigene109161_All//5.00E-154//TC135928			GO:0003824//GO:0008152	nr +
Unigene109163_All	397	0.00	0.00	0.00	0.00	0.00	0.00	2.34	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	1.15E-06	Down	-1.12E+01	5.48E-07	Down			Unigene109163_All//5.00E-07//ES792745				
Unigene109164_All	297	0.00	0.00	0.00	0.00	0.00	0.00	1.71	0.56	0.00	null	null		null	null		null	null		null	null		-1.60E+00	1.07E-01		-1.07E+01	5.56E-04	Down			Unigene109164_All//9.00E-08//TC159777				
Unigene109167_All	462	0.00	0.00	0.00	0.00	0.00	0.00	2.47	0.09	0.09	null	null		null	null		null	null		null	null		-4.77E+00	5.39E-07	Down	-4.84E+00	2.34E-07	Down							
Unigene109175_All	233	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	2.56	null	null		null	null		null	null		null	null		7.49E+00	6.38E-01		1.13E+01	1.76E-04	Up	Unigene109175_All//gi|15235905|ref|NP_194034.1|//2.00E-06//MATE efflux protein-related [Arabidopsis thaliana]						nr +
Unigene109177_All	431	0.00	0.00	0.00	0.00	0.00	0.00	1.37	1.26	0.00	null	null		null	null		null	null		null	null		-1.24E-01	8.84E-01		-1.04E+01	1.42E-04	Down	Unigene109177_All//gi|111379068|gb|ABR09321.1|//6.00E-11//leucine rich protein [Arachis hypogaea]		Unigene109177_All//3.00E-08//DW479423				nr -
Unigene109182_All	385	0.00	0.00	0.00	0.00	0.00	0.00	3.07	0.54	0.31	null	null		null	null		null	null		null	null		-2.50E+00	1.47E-04	Down	-3.31E+00	4.89E-06	Down	Unigene109182_All//gi|3885515|gb|AAC17928.1|//7.00E-18//similar to ribosomal protein S26 [Medicago sativa]	Unigene109182_All//2.00E-12//AT3G56340| 40S ribosomal protein S26 (RPS26C)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935	nr -
Unigene109185_All	711	0.22	0.00	0.00	1.05	0.19	0.19	4.16	0.12	0.50	-7.79E+00	2.17E-01		-7.79E+00	2.46E-01		-2.44E+00	5.60E-03		-2.46E+00	1.02E-02		-5.15E+00	3.87E-18	Down	-3.05E+00	4.39E-13	Down			Unigene109185_All//7.00E-63//CO490797				
Unigene109186_All	403	0.00	0.00	0.00	0.00	0.00	0.00	2.62	0.52	0.20	null	null		null	null		null	null		null	null		-2.34E+00	6.78E-04	Down	-3.73E+00	6.14E-06	Down							
Unigene109189_All	288	0.00	0.00	0.00	0.00	0.00	0.00	1.17	5.81	0.00	null	null		null	null		null	null		null	null		2.31E+00	1.19E-05	Up	-1.02E+01	8.17E-03								
Unigene109196_All	285	0.00	0.00	0.00	0.00	0.00	0.00	2.67	0.00	0.84	null	null		null	null		null	null		null	null		-1.14E+01	1.68E-05	Down	-1.67E+00	2.39E-02		Unigene109196_All//gi|224141315|ref|XP_002324019.1|//2.00E-20//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222867021|gb|EEF04152.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene109196_All//2.00E-21//AT3G28390| PGP18 (P-GLYCOPROTEIN 18); ATPase, coupled to transmembrane movement of substances			ko02010|ABC transporters	GO:0006810//GO:0031224//GO:0032559//GO:0042626	nr +
Unigene109204_All	272	0.00	0.00	0.00	0.00	0.00	0.00	2.18	1.84	0.00	null	null		null	null		null	null		null	null		-2.39E-01	7.65E-01		-1.11E+01	1.42E-04	Down	Unigene109204_All//gi|297838233|ref|XP_002886998.1|//7.00E-07//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332839|gb|EFH63257.1| expressed protein [Arabidopsis lyrata subsp. lyrata]					GO:0016462//GO:0032559	nr -
Unigene109209_All	433	0.12	0.12	1.97	0.12	0.00	0.00	0.88	0.00	0.09	-4.61E-02	9.87E-01		4.03E+00	7.02E-04	Up	-6.85E+00	5.62E-01		-6.85E+00	6.44E-01		-9.78E+00	6.19E-03		-3.26E+00	2.22E-02		Unigene109209_All//gi|4894211|gb|AAD32302.1|//1.00E-36//ribonucleotide reductase small subunit [Glycine max]	Unigene109209_All//6.00E-37//AT3G23580| RNR2A (RIBONUCLEOTIDE REDUCTASE 2A); ribonucleoside-diphosphate reductase	Unigene109209_All//4.00E-131//gi|164251877|gb|ES849561.1|ES849561		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism	GO:0006259//GO:0007049//GO:0009132//GO:0016728//GO:0016757//GO:0031241//GO:0032501//GO:0043234//GO:0046872	nr +
Unigene109225_All	263	0.00	0.00	0.00	0.00	0.00	0.00	2.09	0.32	0.00	null	null		null	null		null	null		null	null		-2.72E+00	1.22E-02		-1.10E+01	2.81E-04	Down							
Unigene109231_All	324	0.32	0.00	0.00	0.00	0.74	0.14	2.48	0.52	0.37	-8.34E+00	3.76E-01		-8.34E+00	3.98E-01		9.54E+00	1.04E-01		7.12E+00	7.02E-01		-2.26E+00	4.82E-03		-2.75E+00	9.43E-04	Down							
Unigene109234_All	427	0.00	0.00	0.00	0.00	0.00	0.00	4.75	0.59	1.03	null	null		null	null		null	null		null	null		-3.02E+00	9.07E-09	Down	-2.21E+00	1.05E-06	Down			Unigene109234_All//3.00E-14//TC150240				

Unigene109243_All	545	0.00	0.00	0.00	0.00	0.00	0.00	2.95	0.00	0.15	null	null		null	null		null	null		null	null		-1.15E+01	2.17E-11	Down	-4.33E+00	1.41E-09	Down	Unigene109243_All//gi|159464339|ref|XP_001690399.1|//2.00E-06//fibrocystin-L-like protein [Chlamydomonas reinhardtii] >gi|158279899|gb|EDP05658.1| fibrocystin-L-like protein [Chlamydomonas reinhardtii]					GO:0044464	nr +
Unigene109245_All	492	0.00	0.00	0.00	0.00	0.00	0.00	2.58	1.10	0.65	null	null		null	null		null	null		null	null		-1.22E+00	2.45E-02		-1.99E+00	4.87E-04	Down	Unigene109245_All//gi|159479982|ref|XP_001698065.1|//4.00E-50//receptor of activated protein kinase C 1 [Chlamydomonas reinhardtii] >gi|121026|sp|P25387.1|GBLP_CHLRE RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein >gi|158273864|gb|EDO99650.1| receptor of activated protein kinase C 1 [Chlamydomonas reinhardtii]	Unigene109245_All//4.00E-46//AT1G18080| ATARCA; nucleotide binding			ko03040|Spliceosome//ko03022|Basal transcription factors	GO:0004683//GO:0004871	nr +
Unigene109247_All	342	0.00	0.00	0.00	0.00	0.00	0.00	3.21	0.98	0.00	null	null		null	null		null	null		null	null		-1.72E+00	5.68E-03		-1.17E+01	3.33E-08	Down	Unigene109247_All//gi|13359451|dbj|BAB33421.1|//7.00E-07//putative senescence-associated protein [Pisum sativum]		Unigene109247_All//1.00E-10//gi|84157990|gb|DN827037.1|DN827037				nr -
Unigene10925_All	209	40.55	81.46	49.43	53.87	46.30	58.99	70.00	49.99	52.04	1.01E+00	5.39E-13	Up	2.86E-01	1.42E-01		-2.18E-01	2.33E-01		1.31E-01	4.98E-01		-4.86E-01	1.97E-04		-4.28E-01	7.83E-04		Unigene10925_All//gi|195641908|gb|ACG49422.1|//7.00E-07//cytochrome b5 [Zea mays]	Unigene10925_All//9.00E-07//AT5G53560| CB5-E (CYTOCHROME B5 ISOFORM E); heme binding	Unigene10925_All//8.00E-103//TC157945			GO:0005506//GO:0008152//GO:0008940//GO:0016020	nr +
Unigene109251_All	344	0.00	0.00	0.00	0.43	0.10	0.00	1.47	0.24	0.00	null	null		null	null		-2.12E+00	3.87E-01		-8.76E+00	2.35E-01		-2.60E+00	2.05E-02		-1.05E+01	5.56E-04	Down			Unigene109251_All//9.00E-70//gi|21098584|gb|BQ410897.1|BQ410897				
Unigene109252_All	369	0.00	0.00	0.00	0.27	0.00	0.00	1.72	0.34	0.00	null	null		null	null		-8.08E+00	3.17E-01		-8.08E+00	4.05E-01		-2.34E+00	1.27E-02		-1.07E+01	7.12E-05	Down	Unigene109252_All//gi|164564729|dbj|BAF98211.1|//4.00E-13//CM0216.240.nc [Lotus japonicus]	Unigene109252_All//3.00E-07//AT3G51400| unknown protein					nr +
Unigene109253_All	248	0.00	0.00	0.00	0.00	0.00	0.00	2.22	0.34	0.00	null	null		null	null		null	null		null	null		-2.72E+00	1.22E-02		-1.11E+01	2.81E-04	Down							
Unigene109256_All	645	0.00	0.39	0.33	0.31	0.32	0.63	1.97	0.39	1.24	8.62E+00	7.88E-02		8.37E+00	1.42E-01		5.23E-02	9.89E-01		1.03E+00	4.29E-01		-2.34E+00	1.56E-04	Down	-6.71E-01	1.95E-01		Unigene109256_All//gi|297800328|ref|XP_002868048.1|//1.00E-39//tRNA/rRNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313884|gb|EFH44307.1| tRNA/rRNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene109256_All//9.00E-36//AT1G17610| tRNA/rRNA methyltransferase (SpoU) family protein				GO:0003676//GO:0008168//GO:0010467	nr +
Unigene109261_All	463	0.00	0.00	0.00	0.00	0.00	0.00	1.37	0.72	0.00	null	null		null	null		null	null		null	null		-9.24E-01	2.63E-01		-1.04E+01	7.12E-05	Down			Unigene109261_All//4.00E-17//ES794483				
Unigene109269_All	402	0.00	0.00	0.00	0.00	0.00	0.00	3.89	1.04	0.20	null	null		null	null		null	null		null	null		-1.90E+00	2.25E-04	Down	-4.30E+00	2.71E-09	Down	Unigene109269_All//sp|Q86HV8|CTNC_DICDI//1.00E-12//Countin-3 OS=Dictyostelium discoideum GN=ctnC PE=2 SV=1						swissprot -
Unigene109271_All	656	0.00	0.00	0.00	0.00	0.00	0.00	3.22	0.13	0.12	null	null		null	null		null	null		null	null		-4.66E+00	1.89E-12	Down	-4.73E+00	4.77E-13	Down	Unigene109271_All//gi|225463468|ref|XP_002276545.1|//8.00E-43//PREDICTED: similar to RPL18AA (60S RIBOSOMAL PROTEIN L18A-1); structural constituent of ribosome isoform 2 [Vitis vinifera]	Unigene109271_All//4.00E-42//AT2G34480| 60S ribosomal protein L18A (RPL18aB)			ko03010|Ribosome		nr -
Unigene109272_All	246	11.91	2.88	11.91	4.05	2.38	7.89	0.52	0.17	0.16	-2.05E+00	7.98E-07	Down	-6.00E-04	9.99E-01		-7.67E-01	2.60E-01		9.63E-01	4.20E-02		-1.60E+00	5.35E-01		-1.67E+00	4.78E-01				Unigene109272_All//7.00E-39//gi|48876282|gb|CO129804.1|CO129804				
Unigene109280_All	1083	0.05	0.28	0.00	0.18	0.25	0.08	0.90	0.00	0.52	2.54E+00	1.51E-01		-5.59E+00	6.32E-01		4.67E-01	8.17E-01		-1.14E+00	5.70E-01		-9.81E+00	5.84E-07	Down	-8.02E-01	1.83E-01		Unigene109280_All//1.00E-74//AT5G58530| lectin protein kinase, putative		Unigene109280_All//4.00E-90//CO115789		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016020//GO:0030246//GO:0031410//GO:0032559//GO:0046914	nr -
Unigene109281_All	265	0.39	0.00	0.40	0.38	0.00	0.00	1.91	0.00	0.15	-8.63E+00	3.76E-01		2.53E-02	1.00E+00		-8.55E+00	3.17E-01		-8.55E+00	4.05E-01		-1.09E+01	8.90E-04	Down	-3.67E+00	3.75E-03								
Unigene109284_All	595	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.07	1.21	null	null		null	null		null	null		null	null		-1.84E-02	1.01E+00		4.08E+00	2.41E-04	Up	Unigene109284_All//gi|86155935|gb|ABC86705.1|//1.00E-14//R111 [Coffea arabica]	Unigene109284_All//9.00E-13//AT5G12010| unknown protein	Unigene109284_All//0.00E+00//TC140933			GO:0009536	nr +
Unigene109294_All	399	0.00	0.00	0.00	0.00	0.00	0.00	2.65	0.10	0.00	null	null		null	null		null	null		null	null		-4.66E+00	1.94E-06	Down	-1.14E+01	6.72E-08	Down	Unigene109294_All//gi|3059122|emb|CAA06030.1|//2.00E-50//glyceraldehyde-3-phosphate dehydrogenase [Marsilea quadrifolia]	Unigene109294_All//1.00E-49//AT1G79530| GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene109294_All//1.00E-16//gi|84169252|gb|DR457900.1|DR457900		ko00010|Glycolysis / Gluconeogenesis	GO:0000166//GO:0006007//GO:0008943//GO:0043231	nr +
Unigene109295_All	386	0.00	0.00	0.00	0.00	0.00	0.00	3.51	0.11	0.00	null	null		null	null		null	null		null	null		-5.02E+00	2.11E-08	Down	-1.18E+01	4.86E-10	Down	Unigene109295_All//gi|12229935|sp|Q9SMI3.1|RS12_CYAPA//6.00E-29//RecName: Full=40S ribosomal protein S12 >gi|6012956|emb|CAB57311.1| 40s ribosomal protein S12 [Cyanophora paradoxa]	Unigene109295_All//5.00E-20//AT2G32060| 40S ribosomal protein S12 (RPS12C)			ko03010|Ribosome	GO:0030529//GO:0043229//GO:0044444	nr +
Unigene1093_All	1433	11.79	6.22	7.36	11.54	8.80	6.02	3.22	0.26	0.75	-9.22E-01	2.59E-11		-6.81E-01	1.10E-06		-3.92E-01	2.56E-03		-9.39E-01	3.96E-12		-3.61E+00	2.07E-22	Down	-2.10E+00	2.30E-13	Down	Unigene1093_All//gi|227204257|dbj|BAH56980.1|//1.00E-102//AT1G75800 [Arabidopsis thaliana]	Unigene1093_All//9.00E-103//AT1G20030| pathogenesis-related thaumatin family protein	Unigene1093_All//0.00E+00//gi|78323547|gb|DT543821.1|DT543821				nr +
Unigene10930_All	599	0.35	1.10	2.67	0.58	0.40	0.30	0.00	0.00	0.00	1.65E+00	8.14E-02		2.93E+00	2.09E-05	Up	-5.33E-01	6.46E-01		-9.49E-01	4.81E-01		null	null		null	null		Unigene10930_All//gi|255591021|ref|XP_002535422.1|//3.00E-30//conserved hypothetical protein [Ricinus communis] >gi|223523171|gb|EEF26965.1| conserved hypothetical protein [Ricinus communis]	Unigene10930_All//2.00E-05//AT4G03140| binding / catalytic/ oxidoreductase				GO:0003824	nr -
Unigene109305_All	324	0.00	0.00	0.00	0.00	0.00	0.00	10.57	5.16	14.26	null	null		null	null		null	null		null	null		-1.03E+00	5.63E-04	Down	4.32E-01	8.00E-02		Unigene109305_All//gi|15230603|ref|NP_190094.1|//9.00E-23//sulfotransferase family protein [Arabidopsis thaliana] >gi|6911846|emb|CAB72146.1| sulfotransferase-like protein [Arabidopsis thaliana] >gi|50198823|gb|AAT70444.1| At3g45080 [Arabidopsis thaliana] >gi|52421317|gb|AAU45228.1| At3g45080 [Arabidopsis thaliana]	Unigene109305_All//4.00E-24//AT3G45080| sulfotransferase family protein	Unigene109305_All//1.00E-99//gi|48804834|gb|CO106148.1|CO106148		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0008146	nr -
Unigene109307_All	479	0.11	0.00	0.00	0.83	0.22	0.00	2.03	0.44	0.17	-6.77E+00	6.19E-01		-6.77E+00	6.32E-01		-1.95E+00	1.19E-01		-9.70E+00	1.11E-02		-2.22E+00	1.82E-03		-3.61E+00	2.14E-05	Down							
Unigene10931_All	237	0.00	0.00	0.00	0.00	0.00	0.00	0.18	1.23	2.86	null	null		null	null		null	null		null	null		2.79E+00	9.49E-02		4.00E+00	4.30E-04	Up							
Unigene109313_All	241	0.00	0.00	0.00	0.00	0.00	0.00	2.28	0.17	0.00	null	null		null	null		null	null		null	null		-3.72E+00	3.23E-03		-1.12E+01	2.81E-04	Down							
Unigene109318_All	1489	0.00	0.00	0.00	0.13	0.00	0.00	3.55	2.58	1.26	null	null		null	null		-7.06E+00	8.47E-02		-7.06E+00	1.34E-01		-4.59E-01	5.23E-02		-1.50E+00	7.58E-10	Down	Unigene109318_All//gi|225425912|ref|XP_002267341.1|//1.00E-107//PREDICTED: similar to F21J9.9 [Vitis vinifera]	Unigene109318_All//4.00E-94//AT1G24430| transferase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene109318_All//0.00E+00//TC142154		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016740	nr +
Unigene10932_All	328	0.00	0.77	0.00	0.30	0.52	0.55	3.22	2.04	0.49	9.59E+00	7.88E-02		null	null		7.89E-01	7.72E-01		8.59E-01	6.96E-01		-6.61E-01	2.78E-01		-2.73E+00	1.12E-04	Down							
Unigene109324_All	910	0.00	0.00	0.00	0.60	0.26	0.15	4.83	0.37	0.31	null	null		null	null		-1.18E+00	2.25E-01		-2.02E+00	7.06E-02		-3.72E+00	6.99E-22	Down	-3.98E+00	7.42E-24	Down	Unigene109324_All//gi|288559104|sp|B9GXD6.1|U497E_POPTR//1.00E-55//RecName: Full=UPF0497 membrane protein 14	Unigene109324_All//5.00E-38//AT3G16300| integral membrane family protein	Unigene109324_All//0.00E+00//TC173483			GO:0016020	nr +
Unigene109326_All	1230	0.09	0.08	0.00	0.04	0.22	0.07	6.29	0.51	3.14	-4.65E-02	9.91E-01		-6.41E+00	3.98E-01		2.47E+00	2.23E-01		8.58E-01	7.97E-01		-3.63E+00	2.38E-37	Down	-1.00E+00	7.22E-08	Down	Unigene109326_All//gi|17979520|gb|AAL50095.1|//1.00E-125//At2g41800/T11A7.10 [Arabidopsis thaliana] >gi|20453311|gb|AAM19894.1| At2g41800/T11A7.10 [Arabidopsis thaliana]	Unigene109326_All//3.00E-132//AT2G41810| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41800.1); Has 161 Blast hits to 157 proteins in 12 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 159; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene109326_All//0.00E+00//gi|78342877|gb|DT563151.1|DT563151				GO:0005618	nr -
Unigene109328_All	264	0.00	0.00	0.00	0.00	0.00	0.00	1.92	0.00	0.00	null	null		null	null		null	null		null	null		-1.09E+01	8.90E-04	Down	-1.09E+01	5.56E-04	Down	Unigene109328_All//gi|227059902|gb|ACP18969.1|//2.00E-08//calcium binding protein [Euglena gracilis]	Unigene109328_All//2.00E-09//AT2G41100| TCH3 (TOUCH 3); calcium ion binding			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0009612//GO:0009642//GO:0016020//GO:0046872	nr +
Unigene109329_All	403	0.00	0.00	0.00	0.00	0.00	0.00	2.31	0.31	0.00	null	null		null	null		null	null		null	null		-2.89E+00	3.28E-04	Down	-1.12E+01	5.48E-07	Down							
Unigene10933_All	469	0.56	0.97	1.25	1.59	1.25	2.79	3.34	3.39	13.85	8.02E-01	4.60E-01		1.16E+00	2.47E-01		-3.52E-01	6.51E-01		8.10E-01	1.91E-01		2.18E-02	9.98E-01		2.05E+00	9.12E-18	Up							
Unigene109336_All	800	0.00	0.00	0.00	0.00	0.00	0.00	6.24	0.37	0.10	null	null		null	null		null	null		null	null		-4.09E+00	1.46E-26	Down	-5.97E+00	2.00E-33	Down	Unigene109336_All//gi|297820480|ref|XP_002878123.1|//6.00E-27//OBP3-responsive gene 3 [Arabidopsis lyrata subsp. lyrata] >gi|297323961|gb|EFH54382.1| OBP3-responsive gene 3 [Arabidopsis lyrata subsp. lyrata]	Unigene109336_All//1.00E-22//AT3G56970| BHLH038; DNA binding / transcription factor		bHLH		GO:0005488//GO:0006950//GO:0010468	nr +
Unigene10934_All	1536	0.00	0.00	0.35	0.00	0.00	0.06	0.28	0.84	6.04	null	null		8.44E+00	4.05E-03		null	null		5.88E+00	4.81E-01		1.62E+00	3.75E-03		4.46E+00	1.58E-52	Up	Unigene10934_All//gi|124360549|gb|ABD33126.2|//2.00E-24//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene10934_All//5.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative				GO:0003676//GO:0016772//GO:0044238//GO:0044260	nr -
Unigene109348_All	335	0.00	0.00	0.00	0.00	0.00	0.00	1.51	0.00	0.36	null	null		null	null		null	null		null	null		-1.06E+01	8.90E-04	Down	-2.09E+00	3.65E-02		Unigene109348_All//gi|15778156|dbj|BAB68528.1|//2.00E-29//14-3-3 protein [Nicotiana tabacum]	Unigene109348_All//2.00E-29//AT1G22300| GRF10 (GENERAL REGULATORY FACTOR 10); ATP binding / protein binding / protein phosphorylated amino acid binding	Unigene109348_All//4.00E-10//DV849765				nr -
Unigene109354_All	311	0.00	0.00	0.00	0.00	0.00	0.00	1.90	0.00	0.13	null	null		null	null		null	null		null	null		-1.09E+01	2.40E-04	Down	-3.89E+00	1.10E-03		Unigene109354_All//gi|37625025|gb|AAQ86336.1|//3.00E-20//ribosomal protein L38 [Nicotiana tabacum]	Unigene109354_All//9.00E-18//AT1G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	Unigene109354_All//9.00E-11//TC149894		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene109357_All	737	0.00	0.00	0.00	0.34	0.28	0.00	3.27	0.74	0.16	null	null		null	null		-2.70E-01	8.23E-01		-8.40E+00	7.36E-02		-2.15E+00	2.78E-07	Down	-4.33E+00	4.31E-14	Down	Unigene109357_All//gi|297835706|ref|XP_002885735.1|//9.00E-57//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331575|gb|EFH61994.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene109357_All//2.00E-51//AT2G04100| MATE efflux family protein	Unigene109357_All//3.00E-151//gi|5044469|gb|AI725617.1|AI725617			GO:0006810//GO:0022857//GO:0044464	nr +

Unigene109364_All	340	0.00	0.00	0.00	0.00	0.00	0.00	1.74	0.00	0.00	null	null		null	null		null	null		null	null		-1.08E+01	2.40E-04	Down	-1.08E+01	1.42E-04	Down	Unigene109364_All//sp|Q9ZZM3|NU5M_SALSA//7.00E-33//NADH-ubiquinone oxidoreductase chain 5 OS=Salmo salar GN=MT-ND5 PE=3 SV=1						swissprot +
Unigene109376_All	341	0.00	0.00	0.00	0.00	0.00	0.00	1.74	0.00	0.00	null	null		null	null		null	null		null	null		-1.08E+01	2.40E-04	Down	-1.08E+01	1.42E-04	Down							ESTscan -
Unigene109381_All	525	0.00	0.00	0.00	0.00	0.00	0.00	1.53	0.08	0.08	null	null		null	null		null	null		null	null		-4.26E+00	8.48E-05	Down	-4.33E+00	4.54E-05	Down	Unigene109381_All//gi|159464339|ref|XP_001690399.1|//3.00E-15//fibrocystin-L-like protein [Chlamydomonas reinhardtii] >gi|158279899|gb|EDP05658.1| fibrocystin-L-like protein [Chlamydomonas reinhardtii]						nr -
Unigene109383_All	486	0.00	0.00	0.00	0.00	0.00	0.00	2.44	0.60	0.33	null	null		null	null		null	null		null	null		-2.02E+00	1.06E-03		-2.89E+00	2.03E-05	Down	Unigene109383_All//gi|157060284|dbj|BAF79872.1|//3.00E-42//actin [Lobosphaeropsis lobophora]	Unigene109383_All//3.00E-34//AT3G18780| ACT2 (ACTIN 2); structural constituent of cytoskeleton	Unigene109383_All//1.00E-07//EX164549		ko04145|Phagosome	GO:0032559//GO:0043232	nr -
Unigene109385_All	767	0.00	0.00	0.00	0.00	0.00	0.00	2.37	0.16	0.36	null	null		null	null		null	null		null	null		-3.86E+00	1.31E-09	Down	-2.70E+00	1.86E-07	Down	Unigene109385_All//gi|84508536|ref|XP_448700.1|//2.00E-95//cytochrome c oxidase subunit 1 [Dictyota dichotoma] >gi|45925704|gb|AAS79085.1| cytochrome oxidase subunit I [Dictyota dichotoma]	Unigene109385_All//4.00E-77//ATMG01360| cytochrome c oxidase subunit I	Unigene109385_All//2.00E-07//EX167412		ko00190|Oxidative phosphorylation	GO:0005506//GO:0015002//GO:0019866//GO:0031224//GO:0043231//GO:0045433//GO:0051234	nr -
Unigene109388_All	610	0.09	0.00	0.00	0.16	0.00	0.15	0.90	0.00	1.96	-6.42E+00	6.19E-01		-6.42E+00	6.32E-01		-7.35E+00	3.17E-01		-1.41E-01	9.53E-01		-9.82E+00	4.62E-04	Down	1.12E+00	3.88E-02		Unigene109388_All//gi|147771776|emb|CAN66777.1|//6.00E-15//hypothetical protein [Vitis vinifera]						nr -
Unigene109939_All	410	2.68	6.92	5.45	3.89	3.44	2.09	2.99	2.75	2.14	1.37E+00	4.19E-04	Up	1.03E+00	2.31E-02		-1.75E-01	7.68E-01		-8.94E-01	9.15E-02		-1.20E-01	8.28E-01		-4.84E-01	3.61E-01		Unigene10939_All//gi|224993380|gb|ACN76469.1|//1.00E-08//CBL-interacting protein kinase 12 [Populus euphratica]	Unigene10939_All//3.00E-07//AT1G01140| CIPK9 (CBL-INTERACTING PROTEIN KINASE 9); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene10939_All//8.00E-86//gi|78328960|gb|DT549234.1|DT549234				nr +
Unigene109390_All	354	0.00	0.00	0.00	0.00	0.00	0.00	2.75	0.00	0.34	null	null		null	null		null	null		null	null		-1.14E+01	5.84E-07	Down	-3.02E+00	9.61E-05	Down	Unigene109390_All//gi|188496902|dbj|BAG32350.1|//1.00E-07//glucan binding protein-2 [Actinophrys sol]						nr -
Unigene109396_All	960	1.42	1.32	0.33	6.69	3.95	3.20	0.53	0.52	0.79	-1.03E-01	8.47E-01		-2.09E+00	1.95E-03		-7.63E-01	4.08E-04		-1.07E+00	3.80E-06	Down	-1.67E-02	1.02E+00		5.77E-01	4.12E-01		Unigene109396_All//gi|22326632|ref|NP_196289.2|//6.00E-70//HAT14 (HOMEOBOX FROM ARABIDOPSIS THALIANA); DNA binding / transcription factor [Arabidopsis thaliana] >gi|90101577|sp|P46665.3|HAT14_ARATH RecName: Full=Homeobox-leucine zipper protein HAT14; AltName: Full=Homeodomain-leucine zipper protein HAT14; Short=HD-ZIP protein 14 >gi|110743069|dbj|BAE99427.1| homeobox protein [Arabidopsis thaliana] >gi|167320916|emb|CAD24012.2| homeodomain-leucine zipper protein HAT14 [Arabidopsis thaliana]	Unigene109396_All//9.00E-58//AT5G06710| HAT14 (HOMEOBOX FROM ARABIDOPSIS THALIANA); DNA binding / transcription factor	Unigene109396_All//0.00E+00//ES802659	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0030528//GO:0043231	nr -
Unigene1094_All	1254	4.59	7.03	5.18	13.63	20.79	43.61	2.80	6.37	4.70	6.15E-01	1.53E-03		1.75E-01	5.05E-01		6.09E-01	7.02E-10		1.68E+00	5.55E-94	Up	1.19E+00	5.38E-10	Up	7.49E-01	4.13E-04		Unigene1094_All//gi|42571559|ref|NP_973870.1|//1.00E-117//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|8778995|gb|AAF79910.1|AC022472_19 Contains similarity to SCUTL1 mRNA from Vitis vinifera gb|AF195653 and is a member of the thaumatin family PF|00314. EST gb|AI995819 comes from this gene [Arabidopsis thaliana]	Unigene1094_All//8.00E-118//AT1G20030| pathogenesis-related thaumatin family protein	Unigene1094_All//0.00E+00//TC132485				nr +
Unigene10940_All	282	0.00	0.00	0.00	0.00	0.00	0.00	4.50	5.34	0.71	null	null		null	null		null	null		null	null		2.46E-01	6.67E-01		-2.67E+00	2.31E-05	Down			Unigene10940_All//1.00E-12//TC155558				
Unigene109400_All	918	0.63	0.00	0.12	0.22	0.00	0.30	1.43	0.73	0.09	-9.29E+00	1.52E-03		-2.43E+00	4.40E-02		-7.76E+00	8.47E-02		4.43E-01	7.64E-01		-9.71E-01	6.64E-02		-4.04E+00	1.35E-07	Down	Unigene109400_All//gi|145332393|ref|NP_001078153.1|//2.00E-122//RTFL10 (ROTUNDIFOLIA LIKE 10) [Arabidopsis thaliana] >gi|42822071|tpg|BAA02290.1| TPA_exp: DVL19 [Arabidopsis thaliana]	Unigene109400_All//4.00E-113//AT3G14362| RTFL10 (ROTUNDIFOLIA LIKE 10)				GO:0048513	nr -
Unigene109402_All	566	0.00	0.00	0.00	0.00	0.00	0.00	1.42	0.52	0.00	null	null		null	null		null	null		null	null		-1.46E+00	4.65E-02		-1.05E+01	4.43E-06	Down	Unigene109402_All//gi|21362874|sp|Q9AFT5.1|RL18A_CASSA//3.00E-29//RecName: Full=60S ribosomal protein L18a >gi|13430184|gb|AAK25759.1|AF343839_1 ribosomal protein L18a [Castanea sativa]	Unigene109402_All//6.00E-29//AT3G14600| 60S ribosomal protein L18A (RPL18aC)			ko03010|Ribosome	GO:0009987//GO:0015934	nr +
Unigene109419_All	407	0.00	0.00	0.00	0.00	0.08	0.00	0.93	0.21	3.82	null	null		null	null		6.40E+00	8.37E-01		null	null		-2.19E+00	8.77E-02		2.03E+00	8.65E-05	Up							
Unigene109420_All	292	0.00	2.43	0.00	0.00	0.00	0.00	0.58	0.14	0.14	1.12E+01	3.33E-04	Up	null	null		null	null		null	null		-2.02E+00	3.68E-01		-2.09E+00	3.14E-01								
Unigene109421_All	619	0.51	0.49	0.95	0.48	0.17	0.00	1.57	0.20	0.45	-4.63E-02	9.85E-01		9.00E-01	3.77E-01		-1.53E+00	2.98E-01		-8.92E+00	4.01E-02		-2.96E+00	1.89E-04	Down	-1.80E+00	5.53E-03		Unigene109421_All//gi|15242739|ref|NP_195957.1|//5.00E-22//acylphosphatase family [Arabidopsis thaliana]	Unigene109421_All//6.00E-28//AT5G03370| acylphosphatase family	Unigene109421_All//7.00E-115//TC154406		ko00620|Pyruvate metabolism	GO:0016787//GO:0043231	nr -
Unigene109422_All	350	0.00	0.00	0.00	0.00	0.00	0.00	2.17	1.19	0.00	null	null		null	null		null	null		null	null		-8.65E-01	2.39E-01		-1.11E+01	8.89E-06	Down	Unigene109422_All//gi|37625523|gb|AAQ96375.1|//9.00E-29//60S ribosomal protein L13 [Solanum palustre]	Unigene109422_All//2.00E-23//AT3G49010| ATRBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome			ko03010|Ribosome	GO:0030529	nr -
Unigene109425_All	255	0.00	0.00	0.00	0.00	0.14	0.18	2.32	0.66	0.00	null	null		null	null		7.08E+00	8.37E-01		7.47E+00	7.02E-01		-1.82E+00	4.72E-02		-1.12E+01	1.42E-04	Down		Unigene109425_All//7.00E-65//AT3G13870| RHD2 (ROOT HAIR DEFECTIVE 3); GTP binding	Unigene109425_All//3.00E-22//DW478609				
Unigene109427_All	244	0.00	0.00	0.00	0.00	0.00	0.00	6.93	2.74	0.00	null	null		null	null		null	null		null	null		-1.34E+00	3.80E-03		-1.28E+01	1.70E-12	Down	Unigene109427_All//gi|302128114|dbj|BAJ13478.1|//5.00E-30//actin 1 [Guillardia theta]	Unigene109427_All//6.00E-30//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene109427_All//9.00E-29//gi|31406833|gb|CD485868.1|CD485868		ko04145|Phagosome	GO:0000267//GO:0000015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008015//GO:0008092//GO:0012501//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0048747//GO:0051707//GO:0060415	nr -
Unigene109428_All	258	0.00	0.00	0.00	0.00	0.00	0.00	5.08	0.97	0.00	null	null		null	null		null	null		null	null		-2.39E+00	9.40E-05	Down	-1.23E+01	9.85E-10	Down	Unigene109428_All//gi|76161004|gb|ABA40465.1|//2.00E-20//ribosomal protein S27-like protein [Solanum tuberosum]	Unigene109428_All//5.00E-21//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043169	nr +
Unigene109430_All	984	0.00	0.00	0.00	0.30	0.00	0.00	2.41	0.34	6.64	null	null		null	null		-8.25E+00	2.02E-02		-8.25E+00	4.01E-02		-2.82E+00	1.60E-09	Down	1.46E+00	1.70E-11	Up	Unigene109430_All//gi|158934007|emb|CAJ40777.1|//4.00E-93//alpha galactosidase precursor [Coffea arabica]	Unigene109430_All//4.00E-95//AT2G42570| unknown protein	Unigene109430_All//5.00E-80//TC144190				nr +
Unigene109437_All	315	0.00	0.00	0.00	0.00	0.00	0.00	1.74	0.00	0.00	null	null		null	null		null	null		null	null		-1.08E+01	4.62E-04	Down	-1.08E+01	2.81E-04	Down	Unigene109437_All//gi|17221648|dbj|BAB78478.1|//9.00E-15//preproMP73 [Cucurbita maxima]				ko03040|Spliceosome		nr +
Unigene109438_All	477	0.00	0.21	0.00	0.31	0.00	0.38	3.55	0.35	0.17	7.73E+00	3.90E-01		null	null		-8.29E+00	1.66E-01		2.74E-01	9.05E-01		-3.34E+00	4.60E-08	Down	-4.41E+00	3.76E-10	Down			Unigene109438_All//4.00E-20//ES817207				
Unigene109439_All	988	0.00	0.00	0.00	0.00	0.00	0.00	2.10	2.83	0.00	null	null		null	null		null	null		null	null		4.35E-01	2.16E-01		-1.10E+01	2.86E-15	Down							
Unigene109441_All	415	0.13	0.37	0.51	0.48	0.17	0.76	76.41	86.21	256.31	1.54E+00	5.32E-01		2.03E+00	3.62E-01		-1.53E+00	4.16E-01		6.66E-01	6.48E-01		1.74E-01	4.20E-02		1.75E+00	1.84E-224	Up			Unigene109441_All//1.00E-26//gi|164320070|gb|EV494852.1|EV494852				
Unigene109445_All	528	0.00	0.00	0.00	0.00	0.00	0.00	2.08	0.32	0.23	null	null		null	null		null	null		null	null		-2.72E+00	1.31E-04	Down	-3.20E+00	1.63E-05	Down	Unigene109445_All//gi|162458045|ref|NP_001105804.1|//2.00E-25//protein disulfide isomerase [Zea mays] >gi|59861273|gb|AAX09966.1| protein disulfide isomerase [Zea mays]	Unigene109445_All//3.00E-24//AT1G04980| ATPDIL2-2 (PDI-LIKE 2-2); protein disulfide isomerase	Unigene109445_All//6.00E-07//TC132722		ko04141|Protein processing in endoplasmic reticulum	GO:0016020//GO:0033554//GO:0043231//GO:0044444	nr -
Unigene109449_All	442	0.00	0.11	0.00	0.00	0.31	0.20	1.82	0.09	0.72	6.84E+00	6.21E-01		null	null		8.28E+00	3.20E-01		7.68E+00	4.81E-01		-4.26E+00	8.48E-05	Down	-1.33E+00	5.40E-02								
Unigene109464_All	594	0.18	0.00	0.18	0.25	0.12	0.15	1.85	0.28	1.81	-7.46E+00	3.76E-01		2.52E-02	1.00E+00		-1.12E+00	5.85E-01		-7.26E-01	7.17E-01		-2.72E+00	1.31E-04	Down	-3.14E-02	9.69E-01								
Unigene109467_All	256	0.00	0.00	0.00	0.00	0.00	0.00	2.81	0.82	0.00	null	null		null	null		null	null		null	null		-1.78E+00	2.79E-02		-1.15E+01	1.78E-05	Down	Unigene109467_All//gi|254933819|gb|ACT87559.1|//4.00E-13//60S ribosomal protein L22 [Karlodinium veneficum]				ko03010|Ribosome		nr +
Unigene109472_All	261	0.00	0.00	0.00	0.00	0.00	0.00	2.75	0.64	0.00	null	null		null	null		null	null		null	null		-2.10E+00	1.25E-02		-1.14E+01	1.78E-05	Down	Unigene109472_All//gi|301111866|ref|NP_002965012.1|//4.00E-13//major vault protein [Phytophthora infestans T30-4] >gi|262095342|gb|EEY53394.1| major vault protein [Phytophthora infestans T30-4]						nr +
Unigene109488_All	474	0.00	0.00	0.00	0.00	0.00	0.00	3.75	1.94	0.00	null	null		null	null		null	null		null	null		-9.50E-01	3.09E-02		-1.19E+01	4.12E-13	Down	Unigene109488_All//gi|4204761|gb|AAD11482.1|//1.00E-24//peroxidase precursor [Glycine max]	Unigene109488_All//5.00E-22//AT1G05260| RC13 (RARE COLD INDUCIBLE GENE 3); peroxidase	Unigene109488_All//3.00E-104//DN817536		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene10949_All	288	6.54	3.87	2.96	9.17	5.86	2.82	3.82	2.61	0.55	-7.57E-01	1.10E-01		-1.14E+00	2.33E-02		-6.46E-01	8.50E-02		-1.70E+00	3.01E-05	Down	-5.47E-01	3.72E-01		-2.79E+00	6.37E-05	Down			Unigene10949_All//3.00E-07//GE653421				
Unigene109491_All	264	0.00	0.00	0.00	0.00	0.00	0.00	3.36	1.58	0.15	null	null		null	null		null	null		null	null		-1.09E+00	1.07E-01		-4.48E+00	1.23E-05	Down			Unigene109491_All//2.00E-08//gi|11208818|gb|BF277548.1|BF277548				
Unigene109492_All	456	0.00	0.00	0.00	0.00	0.00	0.00	1.67	0.00	0.00	null	null		null	null		null	null		null	null		-1.07E+01	1.68E-05	Down	-1.01E+01	8.89E-06	Down							ESTscan -
Unigene109495_All	396	0.00	0.00	0.00	1.13	1.65	2.85	1.92	0.21	0.91	null	null		null	null		5.45E-01	5.86E-01		1.33E+00	4.77E-02		-3.19E+00	7.93E-04	Down	-1.09E+00	1.21E-01								
Unigene109497_All	263	0.00	0.00	0.00	0.00	0.00	0.00	1.93	0.16	0.00	null	null		null	null		null	null		null	null		-3.60E+00	5.78E-03		-1.09E+01	5.56E-04	Down	Unigene109497_All//gi|4139170|gb|AAD03711.1|//1.00E-31//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene109497_All//5.00E-31//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene109497_All//6.00E-27//TC166357				nr +
Unigene10950_All	478	0.66	0.00	0.00	4.38	2.02	1.42	0.35	0.00	0.08	-9.36E+00	3.67E-02		-9.36E+00	4.93E-02		-1.12E+00	8.02E-03		-1.63E+00	4.42E-04	Down	-8.47E+00	1.35E-01		-2.09E+00	3.14E-01		Unigene10950_All//gi|42567435|ref|NP_195315.2|//2.00E-11//FD: DNA binding / protein binding / transcription activator/ transcription factor [Arabidopsis thaliana]						nr -
Unigene109510_All	271	0.00	0.00	0.00	0.00	0.00	0.00	2.50	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	6.34E-05	Down	-1.13E+01	3.57E-05	Down							
Unigene109511_All	260	0.00	0.00	0.00	0.00	0.00	0.00	2.28	0.64	0.00	null	null		null	null		null	null		null	null		-1.82E+00	4.72E-02		-1.12E+01	1.42E-04	Down							ESTscan -
Unigene109513_All	284	0.00	0.00	0.00	0.00	0.12	0.00	1.94	0.00	0.42	null	null		null	null		6.92E+00	8.37E-01		null	null		-1.09E+01	4.62E-04	Down	-2.20E+00	2.24E-02		Unigene109513_All//gi|224087080|ref|XP_002308057.1|//2.00E-08//predicted protein [Populus trichocarpa] >gi|222854033|gb|EEE91580.1| predicted protein [Populus trichocarpa]	Unigene109513_All//5.00E-06//AT5G35200| epsin N-terminal homology (ENTH) domain-containing protein	Unigene109513_All//3.00E-13//TC132781				nr -
Unigene109516_All	462	0.00	0.00	0.00	0.00	0.00	0.20	2.10	0.54	0.17	null	null		null	null		null	null		7.61E+00	4.81E-01		-1.96E+00	4.44E-03		-3.61E+00	2.14E-05	Down			Unigene109516_All//3.00E-67//TC167240				

Unigene109518_All	567	0.00	0.00	0.00	0.18	0.00	0.00	2.24	0.74	0.42	null	null		null	null		-7.46E+00	3.16E-01		-7.46E+00	4.05E-01		-1.60E+00	4.42E-03		-2.41E+00	7.19E-05	Down	Unigene109518_All//gi|297610489|ref|NP_00106461 5.2|//5.00E-37//0s10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene109518_All//3.00E-25//AT1G60680| aldo/keto reductase family protein			ko00053|Ascorbate and aldarate metabolism		nr -
Unigene109528_All	217	0.00	0.00	0.00	0.00	0.00	0.00	5.26	0.00	0.00	null	null		null	null		null	null		null	null		-1.24E+01	3.89E-08	Down	-1.24E+01	1.65E-08	Down							ESTscan -
Unigene109954_All	405	6.59	7.26	5.65	1.23	0.34	0.22	0.21	0.52	2.16	1.39E-01	6.97E-01		-2.21E-01	6.16E-01		-1.85E+00	8.44E-02		-2.46E+00	4.83E-02		1.31E+00	4.48E-01		3.37E+00	1.32E-04	Up			Unigene109954_All//4.00E-66//TC170579				
Unigene109544_All	251	0.00	0.00	0.00	0.00	0.00	0.00	2.36	0.67	0.00	null	null		null	null		null	null		null	null		-1.82E+00	4.72E-02		-1.12E+01	1.42E-04	Down	Unigene109544_All//sp|O70370|CATS_MOUSE|9.00E-09//Cathepsin S OS=Mus musculus GN=Ctss PE=2 SV=1						swissprot -
Unigene109546_All	502	0.00	0.00	0.00	0.00	0.00	0.00	2.53	0.83	0.00	null	null		null	null		null	null		null	null		-1.60E+00	4.42E-03		-1.13E+01	1.99E-09	Down	Unigene109546_All//gi|226490975|ref|NP_001147262.1|//1.00E-36//60S ribosomal protein L13a-2 [Zea mays] >gi|195609234|gb|ACG26447.1| 60S ribosomal protein L13a-2 [Zea mays]	Unigene109546_All//3.00E-17//AT3G07110| 60S ribosomal protein L13A (RPL13aA)			ko03010|Ribosome		nr -
Unigene109547_All	280	0.75	1.45	0.76	1.42	3.69	3.23	3.47	0.30	3.98	9.54E-01	4.14E-01		2.54E-02	1.00E+00		1.37E+00	5.14E-02		1.18E+00	1.29E-01		-3.54E+00	4.32E-05	Down	1.98E-01	7.17E-01		Unigene109547_All//gi|225454244|ref|XP_002274479.1|//5.00E-39//PREDICTED: similar to 2-oxo acid dehydrogenase, lipoyl-binding site [Vitis vinifera]	Unigene109547_All//3.00E-31//AT4G00450| CRP (CRYPTIC PRECOCIOUS)	Unigene109547_All//6.00E-135//TC136182				nr -
Unigene109548_All	227	0.00	0.00	0.00	0.00	0.00	0.00	5.40	1.84	0.18	null	null		null	null		null	null		null	null		-1.55E+00	6.55E-03		-4.94E+00	6.14E-08	Down	Unigene109548_All//gi|297792603|ref|XP_002864186.1|//5.00E-28//heat shock protein 81-1 [Arabidopsis lyrata subsp. lyrata] >gi|297310021|gb|EFH40445.1| heat shock protein 81-1 [Arabidopsis lyrata subsp. lyrata]	Unigene109548_All//2.00E-29//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene109552_All	276	0.00	0.00	0.00	0.18	0.00	0.00	2.14	1.21	0.00	null	null		null	null		-7.50E+00	5.62E-01		-7.50E+00	6.44E-01		-8.24E-01	3.48E-01		-1.11E+01	1.42E-04	Down	Unigene109552_All//gi|297720735|ref|NP_001172729.1|//6.00E-22//0s01g0935200 [Oryza sativa Japonica Group] >gi|148921414|dbj|BAF64446.1| HAP3 subunit of HAP complex [Oryza sativa Japonica Group] >gi|255674039|dbj|BAH91459.1| Os01g0935200 [Oryza sativa Japonica Group]	Unigene109552_All//6.00E-22//AT2G38880| NF-YB1 (NUCLEAR FACTOR Y, SUBUNIT B1); transcription factor		CCAAT			nr +
Unigene109563_All	993	0.00	0.00	0.00	0.00	0.00	0.05	2.43	0.29	0.84	null	null		null	null		null	null		5.51E+00	7.02E-01		-3.04E+00	2.24E-10	Down	-1.53E+00	4.53E-05	Down	Unigene109563_All//gi|15236579|ref|NP_194919.1|//2.00E-45//transferase family protein [Arabidopsis thaliana] >gi|15450359|gb|AAO36473.1| AT4g31910/F11C18_110 [Arabidopsis thaliana] >gi|22655040|gb|AAM98111.1| At4g31910/F11C18_110 [Arabidopsis thaliana]	Unigene109563_All//8.00E-41//AT4G31910| transferase family protein			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene109567_All	517	0.00	0.00	0.00	0.00	0.00	0.00	4.91	1.37	0.00	null	null		null	null		null	null		null	null		-1.84E+00	2.33E-06	Down	-1.23E+01	1.14E-18	Down							
Unigene10957_All	301	0.00	3.87	0.00	0.99	1.49	0.60	0.00	0.00	0.00	1.19E+01	1.05E-06	Up	null	null		5.83E-01	6.26E-01		-7.26E-01	6.39E-01		null	null		null	null		Unigene10957_All//gi|224103919|ref|XP_002313244.1|//6.00E-27//ZIP transporter [Populus trichocarpa] >gi|222849652|gb|EEE87199.1| ZIP transporter [Populus trichocarpa]	Unigene10957_All//3.00E-22//AT2G30080| ZIP6; cation transmembrane transporter/ metal ion transmembrane transporter	Unigene10957_All//2.00E-122//C0088688			GO:0000041//GO:0008152//GO:0015082//GO:0016628//GO:0031224//GO:0046914//GO:0051707	nr -
Unigene109574_All	270	0.00	0.00	0.00	0.00	0.00	0.00	2.66	0.00	0.00	null	null		null	null		null	null		null	null		-1.14E+01	3.27E-05	Down	-1.14E+01	1.78E-05	Down							ESTscan -
Unigene109575_All	484	0.00	0.00	0.00	0.00	0.00	0.00	7.51	0.00	0.08	null	null		null	null		null	null		null	null		-1.29E+01	1.01E-25	Down	-6.51E+00	4.29E-25	Down	Unigene109575_All//gi|289586042|gb|ADO18814.1|//6.00E-27//hybrid proline-rich protein [Cajanus cajan]	Unigene109575_All//6.00E-17//AT4G12480| pEARLI 1; lipid binding	Unigene109575_All//2.00E-25//gi|72270150|gb|DT047511.1|DT047511				nr +
Unigene109580_All	617	0.17	0.00	0.00	0.16	0.00	0.00	1.71	0.34	0.32	-7.41E+00	3.76E-01		-7.41E+00	3.98E-01		-7.34E+00	3.16E-01		-7.34E+00	4.05E-01		-2.34E+00	6.78E-04	Down	-2.41E+00	3.46E-04	Down	Unigene109580_All//gi|87240699|gb|ABR02552.1|//7.00E-11//Tetratricopeptide-like helical [Medicago truncatula]	Unigene109580_All//1.00E-11//AT2G22070| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene109588_All	265	1.38	0.00	0.60	4.51	11.70	0.85	1.28	0.16	0.00	-1.04E+01	1.97E-02		-1.20E+00	3.96E-01		1.37E+00	9.45E-05	Up	-2.40E+00	7.07E-04	Down	-3.02E+00	5.31E-02		-1.03E+01	8.17E-03		Unigene109588_All//gi|255550325|ref|XP_002516213.1|//8.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223541699|gb|EEF46215.1| conserved hypothetical protein [Ricinus communis]		Unigene109588_All//1.00E-61//gi|109867016|gb|DW495992.1|DW495992				nr +
Unigene10959_All	408	0.00	17.39	12.40	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	1.53E-40	Up	1.36E+01	3.83E-28	Up	null	null		null	null		null	null		null	null								
Unigene109593_All	539	0.00	0.00	0.00	0.00	0.00	0.00	2.27	0.54	0.89	null	null		null	null		null	null		null	null		-2.07E+00	6.67E-04	Down	-1.36E+00	1.18E-02		Unigene109593_All//gi|5302802|emb|CAB46043.1|//3.00E-41//retrotransposon like protein [Arabidopsis thaliana] >gi|7268438|emb|CAB80958.1| retrotransposon like protein [Arabidopsis thaliana]	Unigene109593_All//2.00E-05//ATMG00710| hypothetical protein					nr -
Unigene109597_All	248	0.00	0.00	0.00	0.00	0.00	0.00	3.92	1.69	0.16	null	null		null	null		null	null		null	null		-1.22E+00	5.68E-02		-4.61E+00	3.32E-06	Down	Unigene109597_All//gi|224062999|ref|XP_002300962.1|//4.00E-28//1-aminocyclopropane-1-carboxylate [Populus trichocarpa] >gi|222842688|gb|EEE80235.1| 1-aminocyclopropane-1-carboxylate [Populus trichocarpa]	Unigene109597_All//1.00E-21//AT1G77330| 1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative			ko00270|Cysteine and methionine metabolism		nr -
Unigene109960_All	310	0.68	3.11	4.81	0.48	0.22	0.00	0.00	0.00	0.00	2.20E+00	6.58E-03		2.83E+00	6.17E-05	Up	-1.12E+00	5.85E-01		-8.91E+00	2.34E-01		null	null		null	null								
Unigene109600_All	513	0.00	0.00	0.00	0.00	0.00	0.00	1.98	1.79	0.16	null	null		null	null		null	null		null	null		-1.42E-01	8.11E-01		-3.67E+00	1.15E-05	Down	Unigene109600_All//sp|Q86955|DOKA_DICDI//4.00E-07//Hybrid signal transduction protein dokA OS=Dictyostelium discoideum GN=dokA PE=1 SV=1						swissprot +
Unigene109601_All	255	0.00	0.00	0.00	0.00	0.00	0.00	2.16	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	4.62E-04	Down	-1.11E+01	2.81E-04	Down							
Unigene109604_All	372	0.00	0.00	0.00	0.00	0.00	0.00	2.16	0.90	0.00	null	null		null	null		null	null		null	null		-1.26E+00	7.98E-02		-1.11E+01	4.43E-06	Down							ESTscan +
Unigene109605_All	629	0.00	0.00	0.00	0.00	0.00	0.00	1.81	0.00	0.00	null	null		null	null		null	null		null	null		-1.08E+01	3.89E-08	Down	-1.08E+01	1.65E-08	Down	Unigene109605_All//gi|226497590|ref|NP_001148801.1|//5.00E-43//60S ribosomal protein L7a [Zea mays] >gi|195622244|gb|ACG32952.1| 60S ribosomal protein L7a [Zea mays]	Unigene109605_All//7.00E-38//AT2G17610| 60S ribosomal protein L7A (RPL7aA)			ko03010|Ribosome		nr +
Unigene109962_All	297	0.00	0.00	0.18	1.01	0.93	0.30	3.70	8.02	24.82	null	null		7.49E+00	6.40E-01		-1.18E-01	9.01E-01		-1.73E+00	2.90E-01		1.12E+00	2.75E-03		2.75E+00	6.25E-28	Up			Unigene109962_All//4.00E-28//C0103704				
Unigene109621_All	448	0.00	0.00	0.00	0.44	0.23	0.20	2.27	0.56	0.00	null	null		null	null		-9.48E-01	5.88E-01		-1.14E+00	5.70E-01		-2.02E+00	2.83E-03		-1.11E+01	1.35E-07	Down	Unigene109621_All//gi|145340316|ref|NP_193430.3|//2.00E-39//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|110738029|dbj|BAF00949.1| kinase like protein [Arabidopsis thaliana]	Unigene109621_All//1.00E-40//AT4G16970| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene109621_All//7.00E-62//ES834303				nr -
Unigene109622_All	264	0.00	0.00	0.00	0.00	0.00	0.00	1.92	0.48	0.00	null	null		null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.09E+01	5.56E-04	Down			Unigene109622_All//2.00E-36//TC169484				
Unigene109623_All	204	0.00	0.00	0.00	0.00	0.00	0.00	2.90	0.41	8.98	null	null		null	null		null	null		null	null		-2.82E+00	7.18E-03		1.63E+00	2.55E-04	Up							
Unigene109625_All	472	0.00	0.00	0.00	0.00	0.07	0.00	1.88	0.00	0.00	null	null		null	null		6.19E+00	8.37E-01		null	null		-1.09E+01	2.24E-06	Down	-1.09E+01	1.10E-06	Down							
Unigene109628_All	500	0.00	0.20	0.43	0.40	0.21	0.09	1.94	2.26	0.32	7.66E+00	3.90E-01		8.73E+00	1.42E-01		-9.48E-01	5.88E-01		-2.14E+00	3.48E-01		2.15E-01	7.15E-01		-2.61E+00	3.36E-04	Down							
Unigene109636_All	224	0.00	0.00	0.00	0.67	0.77	0.40	4.72	2.99	0.36	null	null		null	null		2.01E-01	9.50E-01		-7.27E-01	7.17E-01		-6.61E-01	2.78E-01		-3.73E+00	6.14E-06	Down							
Unigene10964_All	773	0.00	6.82	2.48	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	4.74E-30	Up	1.13E+01	1.47E-10	Up	null	null		null	null		null	null		null	null		Unigene10964_All//gi|195636372|gb|ACG37654.1|//2.00E-24//eukaryotic initiation factor 5C CG2922-PF, isoform F [Zea mays]	Unigene10964_All//7.00E-20//AT5G36230| eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein				GO:0044464	nr -
Unigene109965_All	448	0.47	1.13	3.21	0.56	0.46	0.00	0.00	0.00	0.00	1.28E+00	2.31E-01		2.78E+00	1.05E-04	Up	-2.70E-01	8.23E-01		-9.12E+00	7.36E-02		null	null		null	null								ESTscan -
Unigene109651_All	508	0.00	0.00	0.00	0.00	0.00	0.00	1.50	0.16	0.08	null	null		null	null		null	null		null	null		-3.19E+00	7.93E-04	Down	-4.26E+00	8.66E-05	Down	Unigene109651_All//gi|15231294|ref|NP_187969.1|//2.00E-21//calmodulin-binding family protein [Arabidopsis thaliana]	Unigene109651_All//7.00E-23//AT3G13600| calmodulin-binding family protein					nr +
Unigene109657_All	324	0.00	0.00	0.00	0.00	0.00	0.00	2.09	0.39	0.12	null	null		null	null		null	null		null	null		-2.43E+00	7.77E-03		-4.09E+00	3.10E-04	Down	Unigene109657_All//gi|159466892|ref|XP_001691632.1|//2.00E-37//beta subunit of mitochondrial ATP synthase [Chlamydomonas reinhardtii] >gi|384796|sp|P38482.1|ATPBM_CHLRE RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor >gi|18123|emb|CAA43808.1| H(+)-transporting ATP synthase; beta subunit of mitochondrial ATP synthase [Chlamydomonas reinhardtii] >gi|158278978|gb|EDP04740.1| beta subunit of mitochondrial ATP synthase [Chlamydomonas reinhardtii]	Unigene109657_All//1.00E-36//AT5G08680| ATP synthase beta chain, mitochondrial, putative			ko00190|Oxidative phosphorylation		nr -
Unigene109658_All	480	0.00	0.00	0.00	0.00	0.00	0.00	2.47	1.31	0.17	null	null		null	null		null	null		null	null		-9.17E-01	1.03E-01		-3.89E+00	9.21E-07	Down							ESTscan +
Unigene109665_All	1174	0.13	0.35	0.36	0.51	0.21	0.15	5.08	3.06	1.59	1.37E+00	2.74E-01		1.44E+00	2.53E-01		-1.31E+00	1.56E-01		-1.73E+00	9.04E-02		-7.30E-01	7.15E-04		-1.67E+00	9.54E-13	Down			Unigene109665_All//1.00E-13//TC178515				
Unigene109666_All	278	0.00	0.00	0.00	0.00	0.00	0.00	2.43	1.50	0.00	null	null		null	null		null	null		null	null		-6.95E-01	3.94E-01		-1.12E+01	3.57E-05	Down	Unigene109666_All//gi|197312883|gb|ACH63222.1|//2.00E-10//actin depolymerizing factor [Rheum australe]	Unigene109666_All//3.00E-10//AT5G59890| ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); actin binding					nr -
Unigene109667_All	246	0.00	0.00	0.00	0.00	0.00	0.00	2.23	0.68	0.00	null	null		null	null		null	null		null	null		-1.72E+00	7.23E-02		-1.11E+01	2.81E-04	Down	Unigene109667_All//gi|146216004|gb|ABQ10204.1|//3.00E-10//cysteine protease Cp6 [Actinidia deliciosa]	Unigene109667_All//3.00E-09//AT4G35350| XCP1 (XYLEM CYSTEINE PEPTIDASE 1); cysteine-type endopeptidase/ cysteine-type peptidase					nr -
Unigene109668_All	312	0.00	0.00	0.17	0.16	0.11	0.00	2.03	0.00	0.89	null	null		7.42E+00	6.40E-01		-5.33E-01	8.28E-01		-7.32E+00	6.44E-01		-1.10E+01	1.24E-04	Down	-1.19E+00	1.33E-01				Unigene109668_All//6.00E-09//FL577058				
Unigene109670_All	469	0.11	0.11	0.00	1.17	0.88	0.29	2.07	0.27	0.25	-4.73E-02	9.87E-01		-6.80E+00	6.31E-01		-4.07E-01	6.58E-01		-2.02E+00	7.06E-02		-2.95E+00	1.89E-04	Down	-3.02E+00	9.61E-05	Down	Unigene109670_All//gi|224126937|ref|XP_002319964.1|//1.00E-12//predicted protein [Populus trichocarpa] >gi|222858340|gb|EEE95887.1| predicted protein [Populus trichocarpa]						nr -
Unigene109672_All	394	0.00	0.00	0.00	0.00	0.00	0.00	1.29	1.91	0.00	null	null		null	null		null	null		null	null		5.68E-01	4.47E-01		-1.03E+01	5.56E-04	Down	Unigene109672_All//gi|14423905|sp|Q9XGL4.1|RL31_CYAPA//1.00E-24//RecName: Full=60S ribosomal protein L31 >gi|5123727|emb|CAB45375.1| ribosomal protein L31 [Cyanophora paradoxa]	Unigene109672_All//2.00E-18//AT5G56710| 60S ribosomal protein L31 (RPL31C)			ko03010|Ribosome		nr +
Unigene109673_All	272	0.00	0.00	0.00	0.00	0.00	0.00	1.87	0.00	0.29	null	null		null	null		null	null		null	null		-1.09E+01	8.90E-04	Down	-2.67E+00	1.37E-02								ESTscan -

Unigene109676_All	407	0.00	0.00	0.00	0.00	0.00	0.00	1.45	0.62	0.00	null	null		null	null		null	null		null	null		-1.24E+00	1.54E-01		-1.05E+01	1.42E-04	Down	Unigene109676_All//gi|226493187|ref|NP_001148445.1//6.00E-19//actin-depolymerizing factor [Zea mays] >gi|195619314|gb|ACG31487.1| actin-depolymerizing factor [Zea mays]	Unigene109676_All//7.00E-18//AT4G25590| ADF7 (actin depolymerizing factor 7); actin binding					nr -
Unigene109677_All	519	0.00	0.00	0.00	0.00	0.00	0.00	0.98	1.45	0.00	null	null		null	null		null	null		null	null		5.68E-01	4.47E-01		-9.93E+00	5.55E-04	Down	Unigene109677_All//gi|116056034|emb|CAL58567.1|//2.00E-15//Nucleolar GTPase/ATPase p130 (ISS) [Ostreococcus tauri]						nr +
Unigene109678_All	442	0.00	0.00	0.00	0.00	0.00	0.00	5.74	0.47	0.72	null	null		null	null		null	null		null	null		-3.60E+00	1.51E-12	Down	-2.99E+00	3.88E-11	Down	Unigene109678_All//gi|301105188|ref|XP_002901678.1//1.00E-31//60S ribosomal protein L32-1 [Phytophthora infestans T30-4] >gi|262100682|gb|EEY58734.1| 60S ribosomal protein L32-1 [Phytophthora infestans T30-4]	Unigene109678_All//5.00E-26//AT4G18100| 60S ribosomal protein L32 (RPL32A)			ko03010|Ribosome		nr +
Unigene10968_All	357	1.61	3.12	7.31	0.56	1.16	1.14	0.24	0.00	0.00	9.54E-01	1.40E-01		2.18E+00	2.86E-06	Up	1.05E+00	4.26E-01		1.03E+00	4.29E-01		-7.89E+00	4.06E-01		-7.89E+00	3.60E-01				Unigene10968_All//0.00E+00//BQ403264				
Unigene109680_All	426	0.00	0.00	0.00	0.00	0.00	0.00	2.98	0.10	0.00	null	null		null	null		null	null		null	null		-4.92E+00	7.77E-08	Down	-1.15E+01	1.99E-09	Down	Unigene109680_All//gi|298713887|emb|CBJ33763.1|//3.00E-09//conserved unknown protein [Ectocarpus siliculosus]		Unigene109680_All//4.00E-20//TC146753				nr +
Unigene109682_All	424	0.00	0.00	0.00	0.00	0.00	0.00	1.79	0.10	0.00	null	null		null	null		null	null		null	null		-4.19E+00	1.58E-04	Down	-1.08E+01	8.89E-06	Down	Unigene109682_All//gi|110006646|gb|ABG37650.2|//3.00E-16//CCHC-type integrase [Populus trichocarpa]						nr -
Unigene109684_All	308	0.00	0.00	0.17	0.00	0.00	0.00	3.16	0.81	0.65	null	null		7.43E+00	6.40E-01		null	null		null	null		-1.96E+00	4.44E-03		-2.29E+00	9.84E-04	Down	Unigene109684_All//gi|149392539|gb|ABR26072.1|//1.00E-14//imp biosynthesis protein [Oryza sativa Indica Group]		Unigene109684_All//4.00E-50//gi|78354813|gb|DT575087.1|DT575087				nr +
Unigene109686_All	415	0.00	0.00	0.00	0.00	0.00	0.00	5.91	0.40	0.00	null	null		null	null		null	null		null	null		-3.87E+00	8.08E-13	Down	-1.25E+01	4.73E-18	Down	Unigene109686_All//gi|116057495|emb|CAL51922.1|//1.00E-43//Putative 40S ribosomal protein S17 (ISS) [Ostreococcus tauri]	Unigene109686_All//4.00E-39//AT5G04800| 40S ribosomal protein S17 (RPS17D)			ko03010|Ribosome		nr +
Unigene10969_All	473	0.00	7.28	2.59	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.31E-19	Up	1.13E+01	9.13E-07	Up	null	null		null	null		null	null		null	null		Unigene10969_All//gi|56236114|gb|AAV84513.1|//3.00E-09//At5g67490 [Arabidopsis thaliana] >gi|56381905|gb|AAV85671.1| At5g67490 [Arabidopsis thaliana] >gi|114050697|gb|ABI49498.1| At5g67490 [Arabidopsis thaliana]	Unigene10969_All//2.00E-10//AT5G67490| unknown protein					nr -
Unigene109693_All	318	0.16	0.00	0.00	0.63	0.87	0.14	3.06	0.26	0.25	-7.36E+00	6.19E-01		-7.36E+00	6.31E-01		4.67E-01	8.17E-01		-2.14E+00	3.48E-01		-3.54E+00	4.32E-05	Down	-3.61E+00	2.14E-05	Down			Unigene109693_All//4.00E-07//TC138616				
Unigene109698_All	590	0.00	0.00	0.00	0.00	0.00	0.00	1.58	0.00	0.47	null	null		null	null		null	null		null	null		-1.06E+01	1.15E-06	Down	-1.74E+00	8.54E-03		Unigene109698_All//gi|119714|sp|P13983.1|EXTN_TOBAC//2.00E-09//RecName: Full=Extensin; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor				ko03040|Spliceosome		nr +
Unigene109699_All	270	0.00	0.00	0.00	0.00	0.00	0.00	1.88	0.31	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.05E-02		-1.09E+01	5.55E-04	Down								ESTscan +
Unigene10970_All	334	0.00	19.27	9.73	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	9.43E-37	Up	1.32E+01	5.81E-18	Up	null	null		null	null		null	null		null	null								
Unigene109703_All	405	0.39	0.38	0.13	0.74	0.77	0.22	1.98	0.72	0.20	-4.65E-02	9.90E-01		-1.56E+00	5.34E-01		5.22E-02	9.99E-01		-1.73E+00	2.89E-01		-1.46E+00	4.65E-02		-3.33E+00	2.47E-04	Down			Unigene109703_All//2.00E-169//TC179467				
Unigene109708_All	238	0.00	0.00	0.00	0.21	0.00	0.19	1.60	0.35	19.25	null	null		null	null		-7.71E+00	5.62E-01		-1.41E-01	9.56E-01		-2.19E+00	8.76E-02		3.59E+00	1.66E-22	Up	Unigene109708_All//gi|115472809|ref|NP_001060003.1|//4.00E-20//Os07g0564500 [Oryza sativa Japonica Group] >gi|113611539|dbj|BAF21917.1| Os07g0564500 [Oryza sativa Japonica Group]	Unigene109708_All//2.00E-20//AT2G29990| NDA2 (ALTERNATIVE NAD(P)H DEHYDROGENASE 2); FAD binding / NADH dehydrogenase/ oxidoreductase	Unigene109708_All//4.00E-80//gi|164352536|gb|EX166155.1|EX166155		ko00190|Oxidative phosphorylation		nr +
Unigene10971_All	399	0.13	0.38	0.00	2.50	0.95	0.45	2.54	0.94	0.50	1.54E+00	5.32E-01		-7.03E+00	6.31E-01		-1.40E+00	3.79E-02		-2.46E+00	2.07E-03		-1.43E+00	2.36E-02		-2.35E+00	5.84E-04	Down			Unigene10971_All//3.00E-156//AW187287				
Unigene109712_All	301	0.00	0.34	0.00	0.00	0.00	0.00	7.16	2.36	0.40	8.40E+00	3.90E-01		null	null		null	null		null	null		-1.60E+00	1.06E-04	Down	-4.17E+00	2.24E-12	Down								
Unigene109719_All	243	0.00	0.00	0.00	0.00	0.00	0.00	4.87	2.75	0.66	null	null		null	null		null	null		null	null		-8.24E-01	1.42E-01		-2.89E+00	2.03E-05	Down	Unigene109719_All//gi|20378861|gb|AAM21011.1|AF469073_1//1.00E-23//NBS resistance protein-like protein [Gossypium hirsutum]	Unigene109719_All//1.00E-12//AT4G11170| disease resistance protein (TIR-NBS-LRR class), putative	Unigene109719_All//8.00E-88//TC177530				nr +
Unigene109728_All	447	0.23	1.02	0.00	0.45	0.00	0.51	2.93	0.84	0.80	2.12E+00	9.60E-02		-7.87E+00	3.98E-01		-8.80E+00	8.47E-02		1.81E-01	9.35E-01		-1.80E+00	1.43E-03		-1.87E+00	6.93E-04	Down	Unigene109728_All//gi|224144987|ref|XP_002325485.1|//6.00E-50//cytochrome P450 [Populus trichocarpa] >gi|222862360|gb|EEE99866.1| cytochrome P450 [Populus trichocarpa]	Unigene109728_All//4.00E-36//AT5G36110| CYP71B31; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00906|Carotenoid biosynthesis		nr -
Unigene10973_All	511	0.00	4.96	1.67	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.05E-14	Up	1.07E+01	9.03E-05	Up	null	null		null	null		null	null		null	null		Unigene10973_All//gi|Q8VEL2|MTMRE_MOUSE//3.00E-26//Myotubularin-related protein 14 OS=Mus musculus GN=Mtmr14 PE=2 SV=2						swissprot +
Unigene109733_All	234	0.00	0.00	0.00	0.00	0.00	0.00	6.14	3.04	0.34	null	null		null	null		null	null		null	null		-1.02E+00	4.18E-02		-4.17E+00	1.93E-08	Down	Unigene109733_All//gi|66270081|gb|AAV43370.1|//7.00E-20//cathepsin-like cysteine protease [Phytophthora infestans]	Unigene109733_All//2.00E-18//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase					nr -
Unigene109739_All	263	0.00	0.00	0.00	0.00	0.00	0.00	2.25	2.07	0.00	null	null		null	null		null	null		null	null		-1.24E-01	8.84E-01		-1.11E+01	1.41E-04	Down	Unigene109739_All//gi|257219572|gb|ACV50439.1|//5.00E-29//ribosomal protein L15 [Jatropha curcas]	Unigene109739_All//2.00E-19//AT4G16720| 60S ribosomal protein L15 (RPL15A)			ko03010|Ribosome		nr +
Unigene10974_All	353	0.00	0.00	0.00	0.00	0.00	0.77	0.96	2.84	4.06	null	null		null	null		null	null		9.58E+00	7.04E-02		1.57E+00	1.54E-02		2.08E+00	1.33E-04	Up								
Unigene109742_All	477	0.00	0.00	0.00	0.00	0.00	0.00	2.57	0.00	0.17	null	null		null	null		null	null		null	null		-1.13E+01	9.98E-09	Down	-3.94E+00	4.86E-07	Down	Unigene109742_All//gi|15229631|ref|NP_190560.1|//5.00E-34//60S ribosomal protein L26 (RPL26A) [Arabidopsis thaliana] >gi|297816242|ref|XP_002876004.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|27735242|sp|P51414.2|RL261_ARATH RecName: Full=60S ribosomal protein L26-1 >gi|6723436|emb|CAB66929.1| 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana] >gi|297321842|gb|EFH52263.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene109742_All//2.00E-35//AT3G49910| 60S ribosomal protein L26 (RPL26A)			ko03010|Ribosome		nr -
Unigene10975_All	200	1.31	0.00	0.00	0.75	0.00	1.58	0.85	5.22	0.20	-1.04E+01	6.72E-02		-1.04E+01	8.59E-02		-9.55E+00	1.66E-01		1.08E+00	4.76E-01		2.63E+00	2.86E-04	Up	-2.09E+00	3.14E-01				Unigene10975_All//3.00E-62//TC178153				
Unigene109753_All	387	0.14	0.13	0.00	0.77	0.00	0.00	2.73	1.40	0.62	-4.66E-02	9.87E-01		-7.08E+00	6.31E-01		-9.59E+00	2.02E-02		-9.59E+00	4.01E-02		-9.60E-01	1.12E-01		-2.14E+00	9.36E-04	Down	Unigene109753_All//gi|223452335|gb|ACM89495.1|//7.00E-15//protein kinase family protein [Glycine max]	Unigene109753_All//5.00E-11//AT2G18890| protein kinase family protein	Unigene109753_All//1.00E-75//TC160556		ko04626|Plant-pathogen interaction		nr -
Unigene109755_All	406	0.00	0.00	0.00	0.00	0.00	0.00	4.89	0.93	0.79	null	null		null	null		null	null		null	null		-2.40E+00	6.76E-07	Down	-2.64E+00	6.80E-08	Down								
Unigene109758_All	250	0.00	0.00	0.00	1.39	0.55	0.90	3.89	1.00	0.00	null	null		null	null		-1.34E+00	3.08E-01		-6.27E-01	6.21E-01		-1.96E+00	4.44E-03		-1.19E+01	2.72E-07	Down								
Unigene10976_All	384	0.00	0.00	0.00	0.26	1.61	1.65	21.47	9.80	1.97	null	null		null	null		2.64E+00	1.99E-02		2.67E+00	1.83E-02		-1.13E+00	1.22E-09	Down	-3.45E+00	2.06E-39	Down			Unigene10976_All//2.00E-178//DW510669				
Unigene109768_All	307	0.00	0.00	0.00	0.00	0.00	0.00	3.31	0.41	0.26	null	null		null	null		null	null		null	null		-3.02E+00	1.08E-04	Down	-3.67E+00	1.15E-05	Down	Unigene109768_All//gi|15231294|ref|NP_187969.1|//2.00E-46//calmodulin-binding family protein [Arabidopsis thaliana]	Unigene109768_All//5.00E-45//AT3G13600| calmodulin-binding family protein	Unigene109768_All//4.00E-47//gi|73861130|gb|DT463869.1|DT463869				nr +
Unigene10977_All	336	5.29	2.41	0.00	0.59	1.84	0.27	1.26	0.87	0.83	-1.13E+00	2.21E-02		-1.24E+01	1.03E-09	Down	1.64E+00	1.06E-01		-1.14E+00	5.70E-01		-5.31E-01	6.34E-01		-6.00E-01	5.53E-01		Unigene10977_All//gi|32171918|sp|Q9LXB4.1|Y5620_ARATH//3.00E-17//RecName: Full=Putative RNA methyltransferase At5g10620	Unigene10977_All//1.00E-18//AT5G10620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: SPOUT methyltransferase, predicted (InterPro:IPR003742); Has 3142 Blast hits to 3142 proteins in 1101 species: Archae - 27; Bacteria - 2338; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 755 (source: NCBI BLink).	Unigene10977_All//6.00E-120//gi|164321360|gb|ES846517.1|ES846517			GO:0006364//GO:0008168//GO:0009536	nr +
Unigene109773_All	325	0.00	0.00	0.00	0.00	0.00	0.00	2.99	0.13	0.00	null	null		null	null		null	null		null	null		-4.54E+00	6.92E-06	Down	-1.15E+01	2.72E-07	Down	Unigene109773_All//gi|301120388|ref|XP_002907921.1|//1.00E-11//polyadenylate-binding protein 1-B [Phytophthora infestans T30-4] >gi|262102962|gb|EEY61004.1| polyadenylate-binding protein 1-B [Phytophthora infestans T30-4]	Unigene109773_All//1.00E-11//AT1G71770| PAB5 (POLY(A)-BINDING PROTEIN 5); RNA binding / poly(A) binding / translation initiation factor					nr -
Unigene109776_All	425	0.00	0.00	0.00	0.00	0.00	0.00	3.68	0.89	1.31	null	null		null	null		null	null		null	null		-2.06E+00	9.44E-05	Down	-1.49E+00	1.74E-03									
Unigene109978_All	345	5.16	4.70	0.62	2.60	5.29	4.84	1.23	0.00	0.00	-1.34E-01	7.71E-01		-3.06E+00	3.82E-06	Down	1.03E+00	3.41E-02		8.98E-01	8.51E-02		-1.03E+01	3.26E-03		-1.03E+01	2.15E-03		Unigene109978_All//gi|30684447|ref|NP_193591.2|//2.00E-15//proline-rich family protein [Arabidopsis thaliana] >gi|22135814|gb|AAM91093.1| AT4g18560/F28J12_220 [Arabidopsis thaliana] >gi|28416477|gb|AAO42769.1| At4g18560/F28J12_220 [Arabidopsis thaliana]		Unigene109978_All//1.00E-90//gi|78331756|gb|DT552030.1|DT552030			GO:0043231	nr +
Unigene109780_All	257	0.41	1.18	0.00	0.00	0.13	0.00	3.62	0.00	2.33	1.54E+00	3.24E-01		-8.67E+00	3.98E-01		7.07E+00	8.37E-01		null	null		-1.18E+01	1.15E-06	Down	-6.38E-01	3.08E-01									
Unigene109781_All	279	2.81	0.00	3.05	3.21	0.74	1.30	2.27	0.60	0.00	-1.15E+01	1.09E-04	Down	1.19E-01	8.69E-01		-2.12E+00	5.22E-03		-1.31E+00	8.52E-02		-1.92E+00	3.09E-02		-1.12E+01	7.12E-05	Down	Unigene109781_All//gi|224092091|ref|XP_002309468.1|//3.00E-26//cytokinin oxidase [Populus trichocarpa] >gi|222855444|gb|EEE92991.1| cytokinin oxidase [Populus trichocarpa]	Unigene109781_All//2.00E-24//AT5G21482| CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase	Unigene109781_All//3.00E-121//ES790738		ko00908|Zeatin biosynthesis		nr +
Unigene109786_All	405	0.26	0.00	0.00	0.00	0.00	0.00	3.03	0.62	0.49	-8.01E+00	3.76E-01		-8.01E+00	3.98E-01		null	null		null	null		-2.29E+00	2.57E-04	Down	-2.62E+00	4.02E-05	Down	Unigene109786_All//gi|291197511|emb|CAZ68124.1|//3.00E-29//ATP binding / protein kinase/ protein tyrosine kinase [Arabidopsis halleri subsp. halleri]	Unigene109786_All//3.00E-24//AT2G46850| ATP binding / protein kinase/ protein tyrosine kinase					nr -
Unigene109799_All	317	0.00	0.00	0.00	0.00	0.00	0.00	1.87	1.19	0.00	null	null		null	null		null	null		null	null		-6.54E-01	4.45E-01		-1.09E+01	1.41E-04	Down	Unigene109799_All//gi|1015937|emb|CAA62943.1|//2.00E-10//extensin class 1 protein [Vigna unguiculata]				ko03040|Spliceosome		nr -
Unigene109801_All	430	0.00	0.00	0.00	0.00	0.00	0.00	2.85	0.49	0.56	null	null		null	null		null	null		null	null		-2.55E+00	8.71E-05	Down	-2.36E+00	1.22E-04	Down	Unigene109801_All//gi|297829824|ref|XP_002882794.1|//2.00E-27//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328634|gb|EFH59053.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene109801_All//1.00E-28//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein					nr +

Unigene109811_All	606	0.00	0.00	0.00	0.00	0.00	0.00	5.51	0.14	0.07	null	null		null	null		null	null		null	null		-5.32E+00	9.93E-21	Down	-6.39E+00	5.88E-23	Down	Unigene109811_All//gi|15824574|gb|AAL09401.1|AF307336_1//2.00E-41//ribosomal protein [Petunia x hybrida]	Unigene109811_All//3.00E-42//AT1G27400| 60S ribosomal protein L17 (RPL17A)			ko03010|Ribosome		nr -
Unigene109813_All	353	0.00	0.00	0.00	0.00	0.00	0.00	1.92	0.00	0.34	null	null		null	null		null	null		null	null		-1.09E+01	6.34E-05	Down	-2.50E+00	4.79E-03		Unigene109813_All//sp|Q4JQH8|NU4M_TETNG//1.00E-26//NADH-ubiquinone oxidoreductase chain 4 OS=Tetraodon nigroviridis GN=MT-ND4 PE=3 SV=1						swissprot -
Unigene109815_All	570	0.00	0.00	0.00	0.00	0.00	0.00	3.19	1.17	0.00	null	null		null	null		null	null		null	null		-1.44E+00	1.28E-03		-1.16E+01	2.03E-13	Down							
Unigene109817_All	396	0.00	0.00	0.00	0.00	0.00	0.00	1.71	0.63	0.00	null	null		null	null		null	null		null	null		-1.43E+00	7.84E-02		-1.07E+01	3.57E-05	Down							
Unigene109820_All	492	0.00	0.00	0.00	0.00	0.00	0.00	2.23	1.61	0.00	null	null		null	null		null	null		null	null		-4.69E-01	4.31E-01		-1.11E+01	3.33E-08	Down	Unigene109820_All//gi|160330969|ref|XP_001712192.1|//2.00E-67//ef2 [Hemiselmis andersenii] >gi|159765639|gb|ABW97867.1| ef2 [Hemiselmis andersenii]	Unigene109820_All//3.00E-65//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene109820_All//1.00E-07//ES850809				nr -
Unigene109821_All	279	0.00	0.18	0.00	0.00	0.00	0.49	1.97	0.00	0.43	7.50E+00	6.21E-01		null	null		null	null		8.92E+00	3.12E-01		-1.09E+01	4.62E-04	Down	-2.20E+00	2.24E-02		Unigene109821_All//gi|30684540|ref|NP_193617.2|//8.00E-38//ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene109821_All//3.00E-39//AT4G18820| ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding					nr +
Unigene109822_All	265	0.00	0.76	0.00	0.00	0.26	0.00	3.35	0.79	0.45	9.58E+00	1.37E-01		null	null		8.02E+00	6.15E-01		null	null		-2.09E+00	4.71E-03		-2.89E+00	3.05E-04	Down	Unigene109822_All//gi|256016311|gb|ACU56981.1|//1.00E-28//importin alpha [Citrus sinensis]	Unigene109822_All//5.00E-26//AT1G09270| IMPA-4 (IMPORTIN ALPHA ISOFORM 4); binding / protein transporter	Unigene109822_All//3.00E-07//TC168025				nr +
Unigene109830_All	370	0.00	0.00	0.00	0.27	0.09	0.00	3.54	0.34	0.54	null	null		null	null		-1.53E+00	5.88E-01		-8.07E+00	4.05E-01		-3.39E+00	1.90E-06	Down	-2.72E+00	1.32E-05	Down	Unigene109830_All//gi|224126161|ref|XP_002319770.1|//1.00E-27//cytochrome P450 [Populus trichocarpa] >gi|222858146|gb|EEE95693.1| cytochrome P450 [Populus trichocarpa]	Unigene109830_All//5.00E-16//AT2G27690| CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene109830_All//0.00E+00//gi|84167351|gb|DR455999.1|DR455999		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene109831_All	335	0.00	1.21	0.00	1.04	0.82	0.67	2.52	0.25	0.48	1.02E+01	1.36E-02		null	null		-3.40E-01	7.86E-01		-6.27E-01	6.21E-01		-3.34E+00	2.51E-04	Down	-2.41E+00	1.68E-03		Unigene109831_All//gi|148524775|dbj|BAF63395.1|//5.00E-22//kinetochore protein [Olimarabidopsis pumila]	Unigene109831_All//5.00E-23//AT3G54630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Kinetochore protein Ndc80 (InterPro:IPR005550); Has 19800 Blast hits to 12108 proteins in 815 species: Archae - 345; Bacteria - 1709; Metazoa - 11031; Fungi - 1499; Plants - 797; Viruses - 39; Other Eukaryotes - 4380 (source: NCBI BLink).	Unigene109831_All//6.00E-43//C0109061				nr +
Unigene109832_All	396	0.00	0.00	0.00	0.00	0.00	0.00	2.67	0.00	0.00	null	null		null	null		null	null		null	null		-1.14E+01	1.51E-07	Down	-1.14E+01	6.72E-08	Down	Unigene109832_All//gi|66270183|gb|AAY43421.1|//5.00E-27//ribosomal protein L34 [Phytophthora infestans]	Unigene109832_All//7.00E-19//AT1G26880| 60S ribosomal protein L34 (RPL34A)			ko03010|Ribosome		nr +
Unigene109843_All	469	0.89	0.11	0.00	0.74	0.29	0.48	2.79	0.62	0.25	-3.05E+00	4.65E-02		-9.80E+00	1.56E-02		-1.34E+00	3.08E-01		-6.27E-01	6.21E-01		-2.16E+00	2.57E-04	Down	-3.46E+00	7.84E-07	Down	Unigene109843_All//gi|224144987|ref|XP_002325485.1|//5.00E-26//cytochrome P450 [Populus trichocarpa] >gi|222862360|gb|EEE99866.1| cytochrome P450 [Populus trichocarpa]	Unigene109843_All//2.00E-07//AT2G42850| CYP718; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding					nr +
Unigene109846_All	664	1.26	0.15	0.00	1.95	1.82	1.09	2.42	1.07	0.90	-3.05E+00	2.11E-03		-1.03E+01	1.19E-04	Down	-1.04E-01	8.43E-01		-8.42E-01	1.64E-01		-1.18E+00	1.24E-02		-1.43E+00	2.13E-03		Unigene109846_All//gi|30685150|ref|NP_188529.2|//5.00E-21//VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor [Arabidopsis thaliana] >gi|75153628|sp|Q8L3W1.1|VRN1_ARATH RecName: Full=B3 domain-containing transcription factor VRN1; AltName: Full=Protein VERNALIZATION 1 >gi|21734794|gb|AAW76972.1|AF289051_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|21734796|gb|AAW76973.1|AF289052_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|89000959|gb|ABD59069.1| At3g18990 [Arabidopsis thaliana]	Unigene109846_All//3.00E-22//AT3G18990| VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor	Unigene109846_All//0.00E+00//ES832924	ABI3VP1			nr +
Unigene109848_All	359	0.00	0.00	0.00	0.00	0.00	0.00	1.77	0.58	0.00	null	null		null	null		null	null		null	null		-1.60E+00	6.27E-02		-1.08E+01	7.12E-05	Down	Unigene109848_All//gi|226495717|ref|NP_001152730.1|//5.00E-19//60S ribosomal protein L13-2 [Zea mays] >gi|195659423|gb|ACG49179.1| 60S ribosomal protein L13-2 [Zea mays]	Unigene109848_All//2.00E-19//AT5G23900| 60S ribosomal protein L13 (RPL13D)			ko03010|Ribosome		nr +
Unigene109849_All	241	0.00	0.00	0.00	0.00	0.00	0.00	2.81	0.35	0.17	null	null		null	null		null	null		null	null		-3.02E+00	2.44E-03		-4.09E+00	3.10E-04	Down							
Unigene109851_All	337	0.00	0.00	0.00	0.00	0.00	0.00	2.76	0.74	0.35	null	null		null	null		null	null		null	null		-1.89E+00	6.92E-03		-2.96E+00	1.72E-04	Down	Unigene109851_All//gi|283795057|ref|YP_003359473.1|//2.00E-17//cytochrome c oxidase subunit I [Synedra acus] >gi|261279713|gb|ACX62021.1| cytochrome c oxidase subunit I [Synedra acus]	Unigene109851_All//3.00E-13//ATMG01360| cytochrome c oxidase subunit 1			ko00190|Oxidative phosphorylation		nr +
Unigene109852_All	358	0.00	0.00	0.00	0.00	0.00	0.00	2.13	0.35	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.81E-03		-1.11E+01	8.89E-06	Down			Unigene109852_All//2.00E-12//gi|109859885|gb|DW488864.1|DW488864				
Unigene109853_All	866	0.06	0.00	0.00	0.12	0.04	0.21	4.78	0.92	0.05	-5.92E+00	6.19E-01		-5.92E+00	6.31E-01		-1.53E+00	5.88E-01		8.59E-01	6.96E-01		-2.38E+00	1.60E-13	Down	-6.70E+00	9.12E-29	Down	Unigene109853_All//gi|257219564|gb|ACV50435.1|//2.00E-82//A1-induced protein [Jatropha curcas]	Unigene109853_All//3.00E-78//AT5G19140| A1LP1	Unigene109853_All//0.00E+00//DT047684				nr +
Unigene109855_All	1188	0.00	0.00	0.00	0.00	0.00	0.00	3.24	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	3.21E-27	Down	-1.17E+01	2.75E-28	Down	Unigene109855_All//gi|4139170|gb|AD03711.1|//1.00E-173//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene109855_All//1.00E-165//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene109855_All//2.00E-12//TC166357				nr -
Unigene109856_All	289	0.00	0.00	0.00	0.00	0.00	0.00	2.63	0.00	0.14	null	null		null	null		null	null		null	null		-1.14E+01	1.68E-05	Down	-4.26E+00	8.66E-05	Down							
Unigene109861_All	256	0.00	0.00	0.00	0.00	0.00	0.00	2.31	0.16	0.00	null	null		null	null		null	null		null	null		-3.82E+00	1.79E-03		-1.12E+01	1.41E-04	Down							ESTscan -
Unigene109864_All	654	0.00	0.00	0.00	0.00	0.00	0.00	4.53	0.70	0.43	null	null		null	null		null	null		null	null		-2.69E+00	3.55E-11	Down	-3.41E+00	1.95E-14	Down	Unigene109864_All//gi|14029020|gb|AAK52561.1|AC079853_14/8.00E-20//Putative retroelement pol polyprotein [Oryza sativa Japonica Group]						nr +
Unigene109865_All	328	0.00	0.00	0.00	0.00	0.00	0.00	1.93	1.15	0.00	null	null		null	null		null	null		null	null		-7.54E-01	3.73E-01		-1.09E+01	7.12E-05	Down	Unigene109865_All//gi|300267215|gb|EFJ51399.1|//2.00E-17//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene109865_All//5.00E-18//AT1G07070| 60S ribosomal protein L35a (RPL35aA)			ko03010|Ribosome		nr -
Unigene10987_All	760	5.44	1.60	0.70	0.59	1.04	0.95	0.33	0.17	0.31	-1.77E+00	8.51E-08	Down	-2.96E+00	3.32E-13	Down	8.21E-01	3.28E-01		6.89E-01	4.48E-01		-1.02E+00	4.95E-01		-8.59E-02	9.57E-01		Unigene10987_All//gi|157863714|gb|ABV90878.1|//3.00E-74//inositol-1,4,5-triphosphate-5-phosphatase [Solanum lycopersicum]	Unigene10987_All//7.00E-17//AT5G19890| endonuclease/exonuclease/phosphatase family protein	Unigene10987_All//7.00E-171//TC169894			GO:0046030	nr +
Unigene109871_All	323	0.00	0.00	0.00	0.00	0.00	0.00	2.23	2.85	0.25	null	null		null	null		null	null		null	null		3.55E-01	6.21E-01		-3.17E+00	8.09E-04	Down			Unigene109871_All//6.00E-12//TC174779				
Unigene109874_All	976	0.00	0.00	0.00	0.00	0.00	0.00	3.99	0.09	0.04	null	null		null	null		null	null		null	null		-5.54E+00	1.70E-24	Down	-6.61E+00	6.27E-27	Down	Unigene109874_All//gi|226505998|ref|NP_001146929.1|//2.00E-59//60S ribosomal protein L7a [Zea mays] >gi|195605318|gb|ACG24489.1| 60S ribosomal protein L7a [Zea mays]	Unigene109874_All//2.00E-55//AT2G47610| 60S ribosomal protein L7A (RPL7aA)			ko03010|Ribosome		nr -
Unigene109878_All	477	0.33	0.85	0.67	0.52	0.94	0.00	3.72	1.14	3.67	1.37E+00	2.74E-01		1.03E+00	4.71E-01		8.46E-01	5.14E-01		-9.03E+00	7.35E-02		-1.71E+00	2.61E-04	Down	-1.87E-02	9.70E-01				Unigene109878_All//6.00E-07//TC168693				
Unigene109897_All	339	0.00	0.00	0.00	0.00	0.00	0.00	3.37	0.99	0.00	null	null		null	null		null	null		null	null		-1.77E+00	3.71E-03		-1.17E+01	1.65E-08	Down			Unigene109897_All//4.00E-07//C0126363				
Unigene1099_All	3340	11.23	40.07	16.25	9.02	11.77	40.88	10.75	16.36	22.03	1.83E+00	1.43E-241	Up	5.33E-01	3.98E-13		3.84E-01	1.28E-06		2.18E+00	0.00E+00	Up	6.06E-01	6.51E-21		1.04E+00	1.83E-70	Up	Unigene1099_All//225449372|ref|XP_002282355.1|//0.00E+00//PREDICTED: pyrroline-5-carboxylate synthetase [Vitis vinifera]	Unigene1099_All//0.00E+00//AT2G39800| P5CS1 (DELTA1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1); delta1-pyrroline-5-carboxylate synthetase	Unigene1099_All//0.00E+00//TC155874		ko00330|Arginine and proline metabolism	GO:0006560//GO:0016620//GO:0016774//GO:0032559//GO:0044424	nr -
Unigene109902_All	537	0.00	0.00	0.00	0.00	0.00	0.00	5.12	0.31	0.00	null	null		null	null		null	null		null	null		-4.04E+00	1.02E-14	Down	-1.23E+01	3.21E-20	Down	Unigene109902_All//gi|247421835|gb|ACS96445.1|//3.00E-48//S18.A ribosomal protein [Jatropha curcas]	Unigene109902_All//7.00E-49//AT4G08800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome	Unigene109902_All//4.00E-11//BM360106		ko03010|Ribosome		nr -
Unigene109904_All	388	0.00	0.00	0.00	0.00	0.00	0.00	2.94	3.45	0.00	null	null		null	null		null	null		null	null		2.29E-01	6.60E-01		-1.15E+01	1.65E-08	Down	Unigene109904_All//gi|195626686|gb|ACG35173.1|//5.00E-37//60S ribosomal protein L12 [Zea mays]	Unigene109904_All//3.00E-36//AT2G37190| 60S ribosomal protein L12 (RPL12A)			ko03010|Ribosome		nr -
Unigene109906_All	517	0.00	0.00	0.00	0.00	0.00	0.00	2.04	1.54	0.31	null	null		null	null		null	null		null	null		-4.13E-01	5.15E-01		-2.73E+00	1.12E-04	Down							
Unigene109909_All	491	0.00	0.00	0.22	1.01	0.14	0.00	1.89	0.00	0.00	null	null		7.76E+00	4.02E-01		-2.85E+00	1.78E-02		-9.99E+00	2.98E-03		-1.09E+01	1.15E-06	Down	-1.09E+01	5.48E-07	Down	Unigene109909_All//gi|297819644|ref|XP_002877705.1|//1.00E-56//U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297323543|gb|EFH53964.1| U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene109909_All//3.00E-53//AT3G49810| U-box domain-containing protein	Unigene109909_All//0.00E+00//gi|3325662|gb|AI054548.1|AI054548				nr +
Unigene109914_All	256	0.20	0.40	0.42	0.00	0.54	1.06	2.64	2.45	0.16	9.54E-01	7.27E-01		1.03E+00	7.04E-01		9.07E+00	3.20E-01		1.00E+01	7.04E-02		-1.10E-01	8.90E-01		-4.09E+00	3.10E-04	Down							
Unigene10992_All	431	0.61	0.00	0.00	0.46	1.36	0.73	2.55	0.78	0.46	-9.25E+00	6.72E-02		-9.25E+00	8.59E-02		1.55E+00	1.41E-01		6.66E-01	6.48E-01		-1.72E+00	5.68E-03		-2.46E+00	2.04E-04	Down			Unigene10992_All//1.00E-90//ES817369				ESTscan -
Unigene109921_All	527	0.00	0.00	0.00	0.00	0.00	0.00	1.93	1.11	0.00	null	null		null	null		null	null		null	null		-7.94E-01	2.03E-01		-1.09E+01	1.35E-07	Down	Unigene109921_All//gi|81074776|gb|AB85537A.1|//1.00E-62//ribosomal protein L2-like [Solanum tuberosum]	Unigene109921_All//7.00E-57//AT2G18020| EMB2296 (embryo defective 2296); structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene109928_All	368	0.00	0.00	0.00	0.00	0.00	0.00	2.30	1.25	0.00	null	null		null	null		null	null		null	null		-8.79E-01	2.07E-01		-1.12E+01	2.21E-06	Down	Unigene109928_All//gi|42565379|gb|AAS20966.1|//1.00E-26//60s acidic ribosomal protein [Hyacinthus orientalis]	Unigene109928_All//3.00E-15//AT3G44590| 60S acidic ribosomal protein P2 (RPP2D)	Unigene109928_All//7.00E-09//CD486354		ko03010|Ribosome		nr -
Unigene10993_All	474	0.00	4.38	2.13	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.95E-12	Up	1.11E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene10993_All//224000485|ref|XP_002289915.1|//1.00E-21//ran binding protein 7 [Thalassiosira pseudonana CCMP1335] >gi|220975123|gb|EED93452.1| ran binding protein 7 [Thalassiosira pseudonana CCMP1335]	Unigene10993_All//2.00E-21//AT2G31660| SAR2 (SUPER SENSITIVE TO ABA AND DROUGHT2); binding / protein transporter					nr +
Unigene109935_All	395	0.00	0.00	0.00	0.00	0.00	0.00	1.28	0.32	0.00	null	null		null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.03E+01	5.55E-04	Down							
Unigene109937_All	900	0.12	0.11	0.24	0.11	0.00	0.00	3.81	1.49	0.80	-4.66E-02	9.91E-01		1.03E+00	5.92E-01		-6.79E+00	3.16E-01		-6.79E+00	4.05E-01		-1.36E+00	1.16E-05	Down	-2.26E+00	5.16E-11	Down	Unigene109937_All//gi|164564743|dbj|BAF98224.1|//2.00E-63//CM0216.420.nc [Lotus japonicus]	Unigene109937_All//3.00E-56//AT2G21540| SFH3 (SEC14-LIKE 3); phosphatidylinositol transporter	Unigene109937_All//0.00E+00//TC131079				nr -

Unigene109939_All	430	0.49	0.00	0.37	1.16	0.48	0.21	2.46	0.58	0.28	-8.93E+00	1.23E-01		-3.90E-01	8.08E-01		-1.27E+00	2.22E-01		-2.46E+00	4.83E-02		-2.08E+00	1.78E-03		-3.15E+00	2.97E-05	Down	Unigene109939_All//gi|124359162|gb|AB|AY05685.1|//4.00E-09//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene109939_All//2.00E-77//TC176279				nr +
Unigene109940_All	291	0.00	0.00	0.55	0.17	0.00	0.31	1.74	0.00	0.27	null	null		9.10E+00	2.40E-01		-7.42E+00	5.62E-01		8.58E-01	7.96E-01		-1.08E+01	8.90E-04	Down	-2.67E+00	1.37E-02		Unigene109940_All//gi|224144987|ref|XP_002325485.1|//8.00E-11//cytochrome P450 [Populus trichocarpa] >gi|222862360|gb|EEE99866.1| cytochrome P450 [Populus trichocarpa]	Unigene109940_All//2.00E-07//AT1G12740| CYP87A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene109940_All//8.00E-08//gi|78336333|gb|DT556607.1|DT556607				nr -
Unigene109943_All	263	0.00	0.00	0.00	0.00	0.00	0.00	2.09	1.27	0.00	null	null		null	null		null	null		null	null		-7.17E-01	4.22E-01		-1.10E+01	2.81E-04	Down	Unigene109943_All//gi|192910912|gb|ACF06564.1|//7.00E-20//ribosomal protein L15 [Elaeis guineensis]	Unigene109943_All//8.00E-16//AT4G16720| 60S ribosomal protein L15 (RPL15A)			ko03010|Ribosome		nr +
Unigene109944_All	321	0.00	0.00	0.00	0.00	0.00	0.00	5.80	0.26	0.50	null	null		null	null		null	null		null	null		-4.48E+00	9.04E-11	Down	-3.55E+00	1.31E-09	Down	Unigene109944_All//gi|161015596|gb|ABX55852.1|//2.00E-42//actin [Spumella-like flagellate JBC/S24]	Unigene109944_All//1.00E-40//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene109944_All//2.00E-46//TC153744				nr +
Unigene109946_All	391	0.00	0.13	0.00	0.00	0.00	0.00	3.46	1.60	0.31	7.02E+00	6.21E-01		null	null		null	null		null	null		-1.11E+00	3.31E-02		-3.50E+00	4.24E-07	Down	Unigene109946_All//gi|224096760|ref|XP_002334672.1|//7.00E-13//cytochrome P450 [Populus trichocarpa] >gi|222874188|gb|EEF11319.1| cytochrome P450 [Populus trichocarpa]	Unigene109946_All//2.00E-10//AT4G36220| FAH1 (FERULIC ACID 5-HYDROXYLASE 1); ferulate 5-hydroxylase/ monooxygenase			ko00940|Phenylpropanoid biosynthesis		nr +
Unigene109949_All	354	0.15	0.00	0.15	0.14	0.00	0.00	2.15	0.00	0.68	-7.21E+00	6.19E-01		2.52E-02	9.97E-01		-7.14E+00	5.62E-01		-7.14E+00	6.43E-01		-1.11E+01	1.68E-05	Down	-1.67E+00	2.39E-02		Unigene109949_All//gi|186513260|ref|NP_194210.2|//3.00E-17//ATP binding / DNA binding / DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|186513264|ref|NP_001119046.1| ATP binding / DNA binding / DNA-directed DNA polymerase [Arabidopsis thaliana]	Unigene109949_All//1.00E-18//AT4G24790| ATP binding / DNA binding / DNA-directed DNA polymerase					nr +
Unigene109958_All	384	0.00	0.00	0.00	0.00	0.00	0.00	1.98	0.87	0.00	null	null		null	null		null	null		null	null		-1.19E+00	1.12E-01		-1.10E+01	8.88E-06	Down	Unigene109958_All//gi|195618210|gb|AC320935.1|//4.00E-20//60S ribosomal protein L21 [Zea mays]	Unigene109958_All//4.00E-20//AT1G57860| 60S ribosomal protein L21	Unigene109958_All//4.00E-07//CD485725		ko03010|Ribosome		nr +
Unigene109972_All	587	0.00	0.00	0.00	0.00	0.00	0.00	6.27	1.57	0.07	null	null		null	null		null	null		null	null		-2.00E+00	7.24E-10	Down	-6.53E+00	2.12E-25	Down	Unigene109972_All//gi|208964722|gb|AC131551.1|//5.00E-76//heat shock protein 90-2 [Glycine max]	Unigene109972_All//5.00E-66//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene109972_All//3.00E-12//TC173881		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene109975_All	355	0.00	0.00	0.00	0.00	0.00	0.00	4.17	0.47	0.22	null	null		null	null		null	null		null	null		-3.15E+00	8.54E-07	Down	-4.22E+00	1.00E-08	Down	Unigene109975_All//gi|15230008|ref|NP_187207.1|//2.00E-23//60S ribosomal protein L22-2 (RPL22B) [Arabidopsis thaliana] >gi|42572267|ref|NP_974229.1| 60S ribosomal protein L22-2 (RPL22B) [Arabidopsis thaliana] >gi|145331980|ref|NP_001078112.1| 60S ribosomal protein L22-2 (RPL22B) [Arabidopsis thaliana] >gi|17865568|sp|Q9M9V1.1|RL222_ARATH RecName: Full=60S ribosomal protein L22-2 >gi|215956684|gb|AAM66123.1| 60S ribosomal protein L22-2 [Arabidopsis thaliana] >gi|30102826|gb|AAP21331.1| At3g05560 [Arabidopsis thaliana]	Unigene109975_All//2.00E-14//AT3G05560| 60S ribosomal protein L22-2 (RPL22B)			ko03010|Ribosome		nr +
Unigene109978_All	696	0.00	0.00	0.00	0.00	0.00	0.00	3.58	1.14	0.74	null	null		null	null		null	null		null	null		-1.65E+00	1.62E-05	Down	-2.27E+00	2.76E-08	Down									
Unigene109982_All	221	0.00	0.00	0.00	0.00	0.00	0.00	2.87	6.62	0.18	null	null		null	null		null	null		null	null		1.21E+00	1.59E-02		-3.99E+00	5.82E-04	Down									
Unigene109983_All	428	0.00	0.00	0.00	0.00	0.00	0.00	10.97	1.66	2.14	null	null		null	null		null	null		null	null		-2.72E+00	1.39E-17	Down	-2.36E+00	1.47E-15	Down									
Unigene109985_All	342	0.92	1.19	0.00	0.44	0.30	0.79	3.71	1.83	0.35	3.69E-01	7.24E-01		-9.84E+00	4.93E-02		-5.33E-01	7.86E-01		8.58E-01	6.31E-01		-1.02E+00	5.93E-02		-3.41E+00	1.45E-06	Down	Unigene109985_All//gi|42568453|ref|NP_199910.2|//7.00E-15//WD-40 repeat family protein [Arabidopsis thaliana]	Unigene109985_All//4.00E-12//AT5G50970| WD-40 repeat family protein	Unigene109985_All//2.00E-157//TC151162				nr +
Unigene109986_All	382	1.10	0.27	0.14	0.65	0.27	0.47	3.21	2.19	0.52	-2.05E+00	1.21E-01		-2.97E+00	6.46E-02		-1.27E+00	4.24E-01		-4.63E-01	7.45E-01		-5.53E-01	3.30E-01		-2.62E+00	4.02E-05	Down	Unigene109986_All//gi|297809813|ref|XP_002872790.1|//2.00E-21//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318627|gb|EFH49049.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene109986_All//1.00E-21//AT4G03230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding			ko04626|Plant-pathogen interaction		nr -
Unigene109987_All	682	0.00	0.00	0.00	0.00	0.00	0.00	2.67	0.61	0.00	null	null		null	null		null	null		null	null		-2.12E+00	1.37E-05	Down	-1.14E+01	2.03E-13	Down									ESTscan -
Unigene109988_All	582	0.00	0.00	0.00	0.00	0.00	0.00	2.83	0.14	0.41	null	null		null	null		null	null		null	null		-4.30E+00	2.19E-09	Down	-2.79E+00	5.06E-07	Down	Unigene109988_All//gi|157313320|gb|ABV32553.1|//6.00E-65//endopolygalacturonase [Prunus persica]	Unigene109988_All//1.00E-53//AT3G59850| polygalacturonase, putative / pectinase, putative	Unigene109988_All//0.00E+00//CO1111186		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene109991_All	276	0.00	0.00	0.00	0.00	0.00	0.00	3.06	0.91	0.00	null	null		null	null		null	null		null	null		-1.75E+00	1.64E-02		-1.16E+01	2.21E-06	Down	Unigene109991_All//gi|192913040|gb|ACF06628.1|//2.00E-22//structural constituent of ribosome [Elaeis guineensis]	Unigene109991_All//7.00E-22//AT3G04920| 40S ribosomal protein S24 (RPS24A)			ko03010|Ribosome		nr +
Unigene109992_All	265	0.00	0.00	0.00	0.00	0.00	0.00	0.64	4.57	0.00	null	null		null	null		null	null		null	null		2.84E+00	3.39E-05	Up	-9.32E+00	1.09E-01		Unigene109992_All//gi|3426064|emb|CAA07575.1|//2.00E-10//monooxygenase [Arabidopsis thaliana] >gi|4467141|emb|CAB37510.1| monooxygenase 2 (MO2) [Arabidopsis thaliana] >gi|7270837|emb|CAB80518.1| monooxygenase 2 (MO2) [Arabidopsis thaliana]	Unigene109992_All//7.00E-12//AT4G38510| monooxygenase, putative (MO2)	Unigene109992_All//1.00E-15//DW488507				nr +
Unigene109993_All	1307	0.00	0.00	0.00	0.00	0.00	0.00	2.94	4.35	0.09	null	null		null	null		null	null		null	null		5.63E-01	1.17E-02		-5.01E+00	4.76E-24	Down	Unigene109993_All//gi|297721715|ref|NP_001173220.1|//4.00E-12//Os02g0832150 [Oryza sativa Japonica Group] >gi|255671379|dbj|BAH91949.1| Os02g0832150 [Oryza sativa Japonica Group]	Unigene109993_All//3.00E-12//AT4G32600| zinc finger (C3HC4-type RING finger) family protein					nr +
Unigene109997_All	264	0.00	0.00	0.00	0.00	0.00	0.00	1.92	0.32	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.05E-02		-1.09E+01	5.55E-04	Down									
Unigene109998_All	361	0.00	0.00	0.00	0.00	0.00	0.00	2.58	0.58	0.11	null	null		null	null		null	null		null	null		-2.15E+00	2.95E-03		-4.54E+00	6.41E-06	Down			Unigene109998_All//3.00E-82//TC142701				
Unigene11_All	3832	4.74	1.81	1.64	22.52	19.26	9.57	10.03	2.33	4.00	-1.39E+00	1.43E-22	Down	-1.53E+00	5.28E-25	Down	-2.26E-01	1.72E-05		-1.23E+00	6.11E-95	Down	-2.10E+00	1.19E-102	Down	-1.33E+00	3.72E-55	Down	Unigene11_All//gi|15231259|ref|NP_190171.1|//0.00E+00//kinesin motor protein-related [Arabidopsis thaliana] >gi|7339486|emb|CAB82809.1| kinesin-related protein-like [Arabidopsis thaliana]	Unigene11_All//0.00E+00//AT3G45850| kinesin motor protein-related	Unigene11_All//0.00E+00//TC155062				nr +
Unigene1100_All	462	0.00	0.33	0.00	1.51	0.75	2.05	7.05	10.95	27.68	8.36E+00	2.36E-01		null	null		-1.02E+00	2.25E-01		4.44E-01	5.74E-01		6.35E-01	7.52E-03		1.97E+00	1.54E-32	Up	Unigene1100_All//gi|15237207|ref|NP_197091.1|//1.00E-49//glycosyl hydrolase family 81 protein [Arabidopsis thaliana] Unigene1100_All//gi|15237207|ref|NP_197091.1|//1.00E-49//glycosyl hydrolase family 81 protein [Arabidopsis thaliana]	Unigene1100_All//7.00E-51//AT5G18570| glycosyl hydrolase family 81 protein	Unigene1100_All//2.00E-148//gi|84168686|gb|DR457334.1|DR457334			GO:0008152//GO:0016798	nr -
Unigene110000_All	334	0.00	0.91	0.96	3.73	1.24	0.68	3.16	2.50	0.00	9.83E+00	4.45E-02		9.90E+00	4.54E-02		-1.59E+00	7.06E-03		-2.46E+00	4.15E-04	Down	-3.39E-01	6.10E-01		-1.16E+01	6.72E-08	Down	Unigene110000_All//gi|225016141|gb|ACN78965.1|//3.00E-06//Rpp4 candidate 1 [Glycine max]		Unigene110000_All//9.00E-116//ES810366				nr -
Unigene110003_All	732	0.00	0.00	0.00	0.00	0.00	0.00	2.77	0.34	0.44	null	null		null	null		null	null		null	null		-3.02E+00	9.07E-09	Down	-2.67E+00	3.89E-08	Down									
Unigene110007_All	516	0.20	0.00	0.00	0.39	0.27	0.96	2.95	0.65	1.00	-7.66E+00	3.76E-01		-7.66E+00	3.98E-01		-5.33E-01	7.49E-01		1.32E+00	2.52E-01		-2.19E+00	5.96E-05	Down	-1.56E+00	1.38E-03				Unigene110007_All//7.00E-170//AW187731				
Unigene110011_All	1620	0.65	0.06	0.07	0.15	0.09	0.08	11.98	7.56	8.75	-3.37E+00	2.13E-04	Down	-3.30E+00	4.59E-04	Down	-8.55E-01	5.74E-01		-8.79E-01	6.17E-01		-6.64E-01	3.05E-09		-4.52E-01	3.23E-05		Unigene110011_All//gi|3152398|gb|AAC17079.1|//1.00E-155//Contains similarity to C2-HC type zinc finger protein C.e-MyT1 gb|U67079 from C. elegans and to hypersensitivity-related gene 201 isolog T28M21.14 from A. thaliana BAC gb|AF002109 [Arabidopsis thaliana]	Unigene110011_All//1.00E-150//AT1G78990| transferase family protein	Unigene110011_All//0.00E+00//DW488553		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene110013_All	365	0.00	0.00	0.00	0.00	0.00	0.00	4.75	0.23	0.22	null	null		null	null		null	null		null	null		-4.37E+00	6.16E-10	Down	-4.44E+00	1.94E-10	Down	Unigene110013_All//gi|159465565|ref|XP_001690993.1|//2.00E-30//ribosomal protein S23, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158279679|gb|EDP05439.1| ribosomal protein S23, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii]	Unigene110013_All//5.00E-20//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene110013_All//7.00E-09//TC139937		ko03010|Ribosome		nr +
Unigene110016_All	302	0.00	0.00	0.00	0.33	0.00	0.00	2.38	0.14	0.40	null	null		null	null		-8.37E+00	3.16E-01		-8.37E+00	4.05E-01		-4.10E+00	2.91E-04	Down	-2.59E+00	2.81E-03		Unigene110016_All//gi|4914318|gb|AAD32866.1|AC005489_4//2.00E-07//F14N23.4 [Arabidopsis thaliana]	Unigene110016_All//2.00E-06//AT1G40390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Endonuclease/exonuclease/phosphatase (InterPro:IPR005135), RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43760.1); Has 480 Blast hits to 479 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 480; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).						nr -
Unigene110017_All	254	1.03	0.40	0.42	0.00	0.27	0.00	16.48	8.56	4.08	-1.37E+00	3.83E-01		-1.30E+00	4.37E-01		8.08E+00	6.15E-01		null	null		-9.46E-01	3.80E-04		-2.01E+00	1.26E-11	Down			Unigene110017_All//6.00E-107//ES801549				
Unigene110024_All	517	0.00	0.29	0.00	0.19	0.07	0.09	1.88	0.24	0.31	8.20E+00	2.36E-01		null	null		-1.53E+00	5.88E-01		-1.14E+00	6.79E-01		-2.96E+00	1.89E-04	Down	-2.61E+00	3.36E-04	Down	Unigene110024_All//gi|15239682|ref|NP_200273.1|//6.00E-21//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene110024_All//1.00E-22//AT5G54620| ankyrin repeat family protein					nr -
Unigene11003_All	395	0.13	0.13	0.40	0.63	0.52	0.11	2.35	2.22	0.20	-4.65E-02	9.87E-01		1.61E+00	5.12E-01		-2.70E-01	8.23E-01		-2.46E+00	2.24E-01		-8.37E-02	9.05E-01		-3.55E+00	3.97E-05	Down			Unigene11003_All//4.00E-23//FL577168				

Unigene110032_All	341	0.00	0.00	0.00	0.00	0.00	0.00	3.10	0.98	0.00	null	null		null	null		null	null		null	null		-1.66E+00	8.55E-03		-1.16E+01	6.72E-08	Down	Unigene110032_All//gi|37780051|gb|AAP32198.1|//1.00E-25//cysteine protease 12 [Trifolium repens]	Unigene110032_All//2.00E-25//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type_peptidase					nr -
Unigene110033_All	573	0.18	0.00	0.00	0.35	0.24	0.16	2.21	0.22	0.63	-7.51E+00	3.76E-01		-7.51E+00	3.98E-01		-5.32E-01	7.49E-01		-1.14E+00	5.70E-01		-3.34E+00	3.42E-06	Down	-1.82E+00	1.09E-03	Down	Unigene110033_All//gi|224061531|ref|XP_002300526.1|//8.00E-54//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222847784|gb|EEE85331.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene110033_All//3.00E-10//AT5G19790| RAP2.11 (related to AP2 11); DNA binding / transcription factor	Unigene110033_All//0.00E+00//gi|78329508|gb|DT549782.1|DT549782	AP2-EREBP			nr +
Unigene110034_All	251	0.00	0.00	0.00	0.00	0.00	0.00	2.36	1.33	0.00	null	null		null	null		null	null		null	null		-8.24E-01	3.48E-01		-1.12E+01	1.41E-04	Down	Unigene110034_All//gi|116061061|emb|CAL56449.1|//8.00E-38//GTP-binding protein (ISS) [Ostreococcus tauri]	Unigene110034_All//3.00E-36//AT5G20010| RAN-1; GTP binding / GTPase/ protein binding	Unigene110034_All//2.00E-08//ES831931				nr -
Unigene110035_All	654	0.00	0.00	0.00	0.00	0.00	0.00	3.56	0.38	0.61	null	null		null	null		null	null		null	null		-3.21E+00	1.59E-10	Down	-2.55E+00	8.83E-09	Down	Unigene110035_All//sp|P10414|TPM2_YEAST//7.00E-06//Tropomyosin-2 OS=Saccharomyces cerevisiae GN=TPM2 PE=1 SV=1						swissprot -
Unigene110037_All	259	0.00	0.00	0.00	0.00	0.00	0.00	3.26	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	4.39E-06	Down	-1.17E+01	2.21E-06	Down								
Unigene110038_All	700	0.00	0.00	0.00	0.00	0.00	0.00	2.72	0.36	0.46	null	null		null	null		null	null		null	null		-2.92E+00	4.98E-08	Down	-2.58E+00	2.06E-07	Down	Unigene110038_All//gi|224118242|ref|XP_002331505.1|//9.00E-25//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222873841|gb|EEF10972.1| NAC domain protein, IPR003441 [Populus trichocarpa]						nr -
Unigene110046_All	372	0.00	0.00	0.00	0.00	0.00	0.00	1.82	0.79	0.00	null	null		null	null		null	null		null	null		-1.21E+00	1.34E-01		-1.08E+01	3.57E-05	Down	Unigene110046_All//gi|156554296|ref|XP_001602465.1|//5.00E-28//PREDICTED: similar to S14e ribosomal protein [Nasonia vitripennis]	Unigene110046_All//2.00E-27//AT3G11510| 40S ribosomal protein S14 (RPS14B)	Unigene110046_All//7.00E-12//CD485874		ko03010|Ribosome		nr +
Unigene110051_All	528	0.00	0.00	0.00	0.00	0.00	0.00	3.12	0.16	0.00	null	null		null	null		null	null		null	null		-4.30E+00	2.19E-09	Down	-1.16E+01	3.45E-12	Down	Unigene110051_All//gi|226495867|ref|NP_001151716.1|//1.00E-13//LOC100285352 [Zea mays] >gi|195649275|gb|ACG44105.1| actin-depolymerizing factor [Zea mays]	Unigene110051_All//6.00E-13//AT5G22360| ADF10 (ACTIN DEPOLYMERIZING FACTOR 10); actin binding					nr +
Unigene110055_All	415	0.00	0.00	0.00	0.00	0.00	0.00	5.09	0.91	0.67	null	null		null	null		null	null		null	null		-2.49E+00	1.42E-07	Down	-2.92E+00	3.37E-09	Down			Unigene110055_All//5.00E-124//gi|189098583|gb|FG551735.1|FG551735				
Unigene110056_All	932	0.00	0.00	0.00	0.21	0.22	0.00	3.67	1.08	1.92	null	null		null	null		5.23E-02	9.89E-01		-7.74E+00	1.34E-01		-1.77E+00	5.77E-08	Down	-9.34E-01	1.23E-03	Down	Unigene110056_All//gi|297810727|ref|XP_002873247.1|//1.00E-105//carboxy-lyase [Arabidopsis lyrata subsp. lyrata] >gi|297319084|gb|EFH49506.1| carboxy-lyase [Arabidopsis lyrata subsp. lyrata]	Unigene110056_All//6.00E-94//AT5G06300| carboxy-lyase	Unigene110056_All//6.00E-33//ES812867				nr +
Unigene110059_All	298	0.00	0.00	0.00	0.00	0.00	0.00	4.26	0.56	0.80	null	null		null	null		null	null		null	null		-2.92E+00	1.46E-05	Down	-2.41E+00	7.19E-05	Down								
Unigene110065_All	507	0.00	0.00	0.00	0.00	0.00	0.00	1.92	0.41	0.00	null	null		null	null		null	null		null	null		-2.22E+00	1.82E-03		-1.09E+01	2.72E-07	Down	Unigene110065_All//gi|226494632|ref|NP_001152668.1|//6.00E-48//elongation factor 1-alpha [Zea mays] >gi|195658719|gb|ACG48827.1| elongation factor 1-alpha [Zea mays]	Unigene110065_All//7.00E-45//AT5G60390| elongation factor 1-alpha / EF-1-alpha					nr -
Unigene110071_All	224	0.23	0.00	0.00	0.22	0.31	0.00	3.59	0.37	0.89	-7.87E+00	6.19E-01		-7.87E+00	6.31E-01		4.67E-01	9.61E-01		-7.80E+00	6.43E-01		-3.26E+00	4.48E-04	Down	-2.01E+00	7.11E-03				Unigene110071_All//2.00E-39//DW510835				
Unigene110073_All	498	0.00	0.00	0.00	0.00	0.00	0.00	1.27	0.76	0.00	null	null		null	null		null	null		null	null		-7.54E-01	3.73E-01		-1.03E+01	7.12E-05	Down	Unigene110073_All//gi|159465349|ref|XP_001690885.1|//3.00E-37//ribosomal protein L18, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|158279571|gb|EDP05331.1| ribosomal protein L18, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii]	Unigene110073_All//2.00E-35//AT5G27850| 60S ribosomal protein L18 (RPL18C)			ko03010|Ribosome		nr -
Unigene110077_All	397	0.00	0.00	0.00	0.00	0.00	0.00	2.56	0.21	0.00	null	null		null	null		null	null		null	null		-3.60E+00	2.38E-05	Down	-1.13E+01	1.35E-07	Down								
Unigene11008_All	647	0.00	0.00	0.00	0.00	0.00	0.00	11.63	1.55	1.35	null	null		null	null		null	null		null	null		-2.91E+00	9.92E-30	Down	-3.10E+00	9.26E-33	Down	Unigene11008_All//gi|30683788|ref|NP_850114.1|//4.00E-42//FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor [Arabidopsis thaliana] >gi|122242304|sp|Q9VTX4.1|FIT_ARATH RecName: Full=Transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR; AltName: Full=Transcription factor EN 43; AltName: Full=Transcription factor Fe-DEFICIENCY INDUCED TRANSCRIPTION FACTOR 1; AltName: Full=FER-LIKE REGULATOR OF IRON UPTAKE; AltName: Full=bHLH transcription factor bHLH029; AltName: Full=Basic helix-loop-helix protein 29; Short=bHLH 29; Short=AtbHLH29 >gi|111074360|gb|ABH04553.1| At2g28160 [Arabidopsis thaliana]	Unigene11008_All//4.00E-26//AT2G28160| FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor	Unigene11008_All//0.00E+00//CA994022	bHLH	ko04626|Plant-pathogen interaction	GO:0005515//GO:0006826//GO:0010038//GO:0010468//GO:0043231	nr -
Unigene110080_All	1010	0.00	0.20	0.00	0.00	0.00	0.00	4.31	1.32	1.38	7.65E+00	1.37E-01		null	null		null	null		null	null		-1.70E+00	1.94E-09	Down	-1.64E+00	2.46E-09	Down	Unigene110080_All//gi|79570100|ref|NP_181364.2|//5.00E-33//DNA binding / transcription factor [Arabidopsis thaliana]	Unigene110080_All//4.00E-35//AT2G38300| DNA binding / transcription factor		G2-like			nr +
Unigene110081_All	583	0.00	0.00	0.00	0.00	0.12	0.08	1.89	5.23	0.21	null	null		null	null		6.88E+00	6.15E-01		6.28E+00	7.02E-01		1.47E+00	1.10E-05	Up	-3.20E+00	1.63E-05	Down	Unigene110081_All//gi|186501250|ref|NP_849973.3|//4.00E-45//metal ion binding [Arabidopsis thaliana]	Unigene110081_All//7.00E-47//AT2G18196| metal ion binding	Unigene110081_All//2.00E-56//DN800214				nr +
Unigene110084_All	262	0.00	0.00	0.00	0.95	0.13	0.34	2.42	0.00	0.15	null	null		null	null		-2.86E+00	1.37E-01		-1.46E+00	4.07E-01		-1.12E+01	1.23E-04	Down	-3.99E+00	5.82E-04	Down								
Unigene110085_All	382	0.00	0.00	0.00	0.00	0.00	0.00	1.77	0.11	0.42	null	null		null	null		null	null		null	null		-4.02E+00	5.36E-04	Down	-2.09E+00	1.27E-02									
Unigene110086_All	806	0.00	0.00	0.00	0.31	0.60	0.28	13.69	0.57	0.30	null	null		null	null		9.53E-01	4.24E-01		-1.41E-01	9.29E-01		-4.59E+00	1.14E-62	Down	-5.53E+00	2.17E-71	Down	Unigene110086_All//gi|297805842|ref|XP_002870805.1|//1.00E-105//ATTAP2 [Arabidopsis lyrata subsp. lyrata] >gi|297316641|gb|EFH47064.1| ATTAP2 [Arabidopsis lyrata subsp. lyrata]	Unigene110086_All//9.00E-82//AT5G39040| ATTAP2; ATPase, coupled to transmembrane movement of substances / transporter	Unigene110086_All//7.00E-91//TC135398		ko02010|ABC transporters		nr +
Unigene110097_All	269	0.00	0.00	0.00	0.00	0.00	0.00	1.89	0.47	0.00	null	null		null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.09E+01	5.55E-04	Down	Unigene110097_All//gi|15226694|ref|NP_181583.1|//2.00E-19//40S ribosomal protein S26 (RPS26A) [Arabidopsis thaliana] >gi|115502826|sp|Q8LPJ7.2|RS262_ARATH RecName: Full=40S ribosomal protein S26-2 >gi|2651314|gb|AAB87594.1| 40S ribosomal protein S26 [Arabidopsis thaliana] >gi|21554493|gb|AAM63871.1| 40S ribosomal protein S26 [Arabidopsis thaliana] >gi|56236112|gb|AAV84512.1| At2g40510 [Arabidopsis thaliana] >gi|111074312|gb|ABH04529.1| At2g40510 [Arabidopsis thaliana]	Unigene110097_All//9.00E-18//AT3G56340| 40S ribosomal protein S26 (RPS26C)			ko03010|Ribosome		nr -
Unigene110098_All	258	0.00	0.00	0.00	0.00	0.00	0.00	2.13	0.16	0.00	null	null		null	null		null	null		null	null		-3.72E+00	3.23E-03		-1.11E+01	2.81E-04	Down	Unigene110098_All//gi|156763856|emb|CAO99130.1|//5.00E-24//berberine bridge enzyme like protein [Nicotiana tabacum]	Unigene110098_All//1.00E-12//AT2G34790| MEE23 (MATERNAL EFFECT EMBRYO ARREST 23); FAD binding / catalytic/ electron carrier/ oxidoreductase					nr -
Unigene1101_All	287	0.00	0.00	0.00	0.52	0.48	0.63	2.80	5.10	9.72	null	null		null	null		-1.18E-01	9.11E-01		2.74E-01	9.05E-01		8.65E-01	8.03E-02		1.80E+00	6.57E-07	Up	Unigene1101_All//gi|81250791|gb|AB069785.1|//6.00E-39//beta-glucan-binding protein 5 [Medicago truncatula]	Unigene1101_All//3.00E-28//AT1G18310| glycosyl hydrolase family 81 protein	Unigene1101_All//1.00E-114//gi|164309730|gb|EV483652.1|EV483652			GO:0004553//GO:0004871//GO:0009056	nr +
Unigene11010_All	635	0.00	0.00	0.00	0.00	0.00	0.00	1.20	1.38	7.65	null	null		null	null		null	null		null	null		2.06E-01	7.54E-01		2.68E+00	3.58E-18	Up	Unigene11010_All//gi|297850310|ref|XP_002893036.1|//4.00E-31//flavin-dependent monooxygenase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297338878|gb|EFH69295.1| flavin-dependent monooxygenase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene11010_All//6.00E-32//AT1G19250| FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase			ko00380|Tryptophan metabolism	GO:0002218//GO:0005789//GO:0008152//GO:0009814//GO:0016709//GO:0030545//GO:0033554	nr +
Unigene110101_All	258	0.61	0.00	0.21	0.39	0.40	0.00	2.29	0.00	0.15	-9.25E+00	2.17E-01		-1.56E+00	5.34E-01		5.21E-02	9.68E-01		-8.59E+00	4.05E-01		-1.12E+01	2.40E-04	Down	-3.89E+00	1.10E-03				Unigene110101_All//2.00E-60//DR456209					ESTscan +
Unigene110103_All	321	0.00	0.00	0.00	0.00	0.00	0.00	4.08	0.00	0.00	null	null		null	null		null	null		null	null		-1.20E+01	2.56E-09	Down	-1.20E+01	9.85E-10	Down	Unigene110103_All//gi|51315784|sp|Q7Y1X1.1|EST_HEVBR//2.00E-10//RecName: Full=Esterase; AltName: Full=Early nodule-specific protein homolog; AltName: Full=Latex allergen Hev b 13; AltName: Allergen=Hev b 13; Flags: Precursor >gi|30909057|gb|AAP37470.1| ENSP-like protein [Hevea brasiliensis]	Unigene110103_All//3.00E-09//AT5G14450| GDSL-motif lipase/hydrolase family protein	Unigene110103_All//3.00E-57//DR453903				nr +
Unigene110106_All	285	0.00	0.00	0.00	0.00	0.00	0.00	2.08	0.29	0.00	null	null		null	null		null	null		null	null		-2.82E+00	7.18E-03		-1.10E+01	1.41E-04	Down	Unigene110106_All//gi|300262703|gb|EFJ46908.1|//2.00E-06//metalloproteinase, extracellular matrix glycoprotein VMP6 [Volvox carteri f. nagariensis]						nr -
Unigene110109_All	247	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.17	0.00	null	null		null	null		null	null		null	null		-3.60E+00	5.78E-03		-1.10E+01	5.55E-04	Down								ESTscan +
Unigene110110_All	261	0.00	0.00	0.00	0.00	0.00	0.17	1.94	0.80	0.00	null	null		null	null		null	null		7.43E+00	7.02E-01		-1.28E+00	1.86E-01		-1.09E+01	5.55E-04	Down			Unigene110110_All//3.00E-56//gi|84165786|gb|DR454434.1|DR454434				
Unigene110112_All	298	0.00	0.00	1.61	0.00	0.00	0.00	2.13	0.70	0.13	null	null		1.07E+01	7.49E-03		null	null		null	null		-1.60E+00	6.27E-02		-3.99E+00	5.82E-04	Down			Unigene110112_All//3.00E-07//DW500060				
Unigene110113_All	480	0.00	0.00	0.00	0.00	0.00	0.00	1.76	1.22	0.00	null	null		null	null		null	null		null	null		-5.31E-01	4.45E-01		-1.08E+01	2.21E-06	Down			Unigene110113_All//3.00E-24//gi|109856915|gb|DW485894.1|DW485894				
Unigene110115_All	631	0.00	0.00	0.00	0.00	0.00	0.00	0.87	2.12	0.00	null	null		null	null		null	null		null	null		1.28E+00	1.56E-02		-9.77E+00	2.81E-04	Down								

Unigene110119_All	250	0.00	0.00	0.00	0.00	0.00	0.00	2.03	1.84	0.00	null	null		null	null		null	null		null	null		-1.42E-01	8.76E-01		-1.10E+01	5.55E-04	Down	Unigene110119_All//gi|301097804|ref|XP_002897996.1//3.00E-30//60S ribosomal protein L5 [Phytophthora infestans T30-4] >gi|262106441|gb|EEY64493.1| 60S ribosomal protein L5 [Phytophthora infestans T30-4]	Unigene110119_All//4.00E-29//AT3G25520| ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); 5S rRNA binding / structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene11012_All	259	16.16	20.35	7.61	18.08	22.34	31.21	31.83	20.82	25.53	3.32E-01	2.18E-01		-1.09E+00	5.41E-04	Down	3.05E-01	2.57E-01		7.88E-01	8.89E-05		-6.13E-01	6.38E-04		-3.18E-01	7.78E-02				Unigene11012_All//4.00E-62//TC168595				
Unigene110121_All	288	0.00	0.00	0.00	0.00	0.00	0.16	1.76	0.44	0.00	null	null		null	null		null	null		7.29E+00	7.02E-01		-2.02E+00	5.21E-02		-1.08E+01	5.55E-04	Down							
Unigene110123_All	397	0.00	0.00	0.00	0.00	0.00	0.00	2.88	0.00	0.00	null	null		null	null		null	null		null	null		-1.15E+01	3.89E-08	Down	-1.15E+01	1.65E-08	Down	Unigene110123_All//gi|109939734|sp|P25776.2|ORYA_ORYSJ//5.00E-24//RecName: Full=Oryzain alpha chain; Flags: Precursor >gi|78192122|gb|ABB30151.1| oryzain alpha [Oryza sativa Japonica Group]	Unigene110123_All//9.00E-24//AT1G06260| cysteine proteinase, putative					nr -
Unigene110131_All	1894	0.00	0.05	0.00	0.00	0.00	0.00	1.16	1.54	0.17	5.74E+00	3.90E-01		null	null		null	null		null	null		4.12E-01	2.32E-01		-2.79E+00	4.04E-09	Down	Unigene110131_All//gi|115466826|ref|NP_001057012.1//1.00E-132//Os06g0186700 [Oryza sativa Japonica Group] >gi|55773865|dbj|BAD72450.1| integral membrane transporter-like protein [Oryza sativa Japonica Group] >gi|113595052|dbj|BAF18926.1| Os06g0186700 [Oryza sativa Japonica Group]	Unigene110131_All//2.00E-125//AT5G25050| integral membrane transporter family protein					nr +
Unigene110134_All	333	2.20	2.28	0.00	1.20	1.65	0.81	10.54	7.15	8.37	5.32E-02	9.63E-01		-1.11E+01	4.13E-04	Down	4.67E-01	6.68E-01		-5.56E-01	6.38E-01		-5.59E-01	5.99E-02		-3.32E-01	2.62E-01		Unigene110134_All//gi|17933310|gb|AAL82337.1|AF446365.1//1.00E-36//At1g10950/T19D16_13 [Arabidopsis thaliana] >gi|15451172|gb|AAK96857.1| endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana] >gi|20148415|gb|AAM10098.1| endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]	Unigene110134_All//6.00E-38//AT1G10950| endomembrane protein 70, putative	Unigene110134_All//1.00E-96//TC147189				nr +
Unigene11014_All	604	0.00	0.84	0.26	2.39	3.25	0.30	0.56	0.28	0.13	9.71E+00	4.05E-03		8.05E+00	2.40E-01		4.42E-01	3.82E-01		-3.00E+00	1.34E-05	Down	-1.02E+00	4.00E-01		-2.09E+00	1.07E-01		Unigene11014_All//gi|297832296|ref|XP_002884030.1//3.00E-37//tetracycline transporter [Arabidopsis lyrata subsp. lyrata] >gi|297329870|gb|EFH60289.1| tetracycline transporter [Arabidopsis lyrata subsp. lyrata]	Unigene11014_All//1.00E-51//AT5G42210| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Major facilitator superfamily MFS-1 (InterPro:IPR011701), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: tetracycline transporter (TAIR:AT2G16990.2); Has 985 Blast hits to 984 proteins in 348 species: Archae - 2; Bacteria - 541; Metazoa - 251; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 152 (source: NCBI BLink).	Unigene11014_All//0.00E+00//TC134017			GO:0006810//GO:0031410	nr +
Unigene110142_All	345	0.00	0.00	0.00	0.00	0.00	0.00	2.08	0.00	0.23	null	null		null	null		null	null		null	null		-1.10E+01	3.27E-05	Down	-3.17E+00	8.09E-04	Down							
Unigene110147_All	725	0.00	0.00	0.00	0.00	0.05	0.19	3.09	1.04	0.27	null	null		null	null		5.57E+00	8.37E-01		7.55E+00	3.12E-01		-1.57E+00	9.33E-05	Down	-3.49E+00	2.61E-11	Down							
Unigene11015_All	314	0.00	5.49	4.75	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.99E-10	Up	1.22E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene11015_All//gi|301095248|ref|XP_002896725.1//6.00E-06//enoyl-CoA hydratase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262108786|gb|EEY66838.1| enoyl-CoA hydratase, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene11015_All//3.00E-05//AT2G30660| 3-hydroxyisobutyryl-coenzyme A hydrolase, putative / CoA-thioester hydrolase, putative					nr -
Unigene110161_All	268	0.00	0.00	0.00	0.00	0.00	0.00	8.36	16.84	6.39	null	null		null	null		null	null		null	null		1.01E+00	8.10E-05	Up	-3.88E-01	3.12E-01				Unigene110161_All//2.00E-33//gi|109886409|gb|DW515379.1|DW515379				
Unigene110162_All	266	0.00	0.00	0.00	0.00	0.26	0.00	3.02	0.00	0.15	null	null		null	null		8.02E+00	6.15E-01		null	null		-1.16E+01	8.58E-06	Down	-4.33E+00	4.54E-05	Down			Unigene110162_All//6.00E-24//FL576545				ESTscan +
Unigene110170_All	404	0.00	0.00	0.00	0.00	0.00	0.22	2.41	1.97	0.20	null	null		null	null		null	null		7.80E+00	4.81E-01		-2.92E-01	6.31E-01		-3.61E+00	2.14E-05	Down			Unigene110170_All//2.00E-32//DN501068				
Unigene110172_All	300	0.00	0.00	0.00	0.00	0.00	0.00	2.96	0.42	0.00	null	null		null	null		null	null		null	null		-2.82E+00	5.65E-04	Down	-1.15E+01	1.10E-06	Down	Unigene110172_All//gi|300264920|gb|EFJ49114.1|//4.00E-06//hypothetical protein VOLCADRAFT_117426 [Volvox carteri f. nagariensis]						nr -
Unigene110175_All	240	0.00	0.00	0.00	0.00	0.14	0.00	13.39	3.66	5.81	null	null		null	null		7.16E+00	8.37E-01		null	null		-1.87E+00	4.78E-08	Down	-1.20E+00	8.77E-05	Down							
Unigene110178_All	273	0.00	0.00	0.00	0.00	0.00	0.00	2.32	0.77	0.00	null	null		null	null		null	null		null	null		-1.60E+00	6.27E-02		-1.12E+01	7.12E-05	Down							
Unigene110179_All	365	0.00	0.00	0.00	0.00	0.00	0.00	2.55	0.23	0.00	null	null		null	null		null	null		null	null		-3.48E+00	7.79E-05	Down	-1.13E+01	5.48E-07	Down	Unigene110179_All//gi|76161008|gb|ABA40467.1|//3.00E-17//glycoprotein-like protein [Solanum tuberosum]	Unigene110179_All//9.00E-18//AT4G27090| 60S ribosomal protein L14 (RPL14B)			ko03010|Ribosome		nr +
Unigene11018_All	405	1.42	3.25	2.37	1.72	2.55	2.56	3.97	1.03	3.64	1.19E+00	4.50E-02		7.36E-01	3.23E-01		5.67E-01	4.46E-01		5.75E-01	4.27E-01		-1.94E+00	1.42E-04	Down	-1.24E-01	7.77E-01		Unigene11018_All//gi|224064045|ref|XP_002301364.1|//3.00E-39//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222843090|gb|EEE90637.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene11018_All//3.00E-30//AT2G46020| transcription regulatory protein SNF2, putative				GO:0003676//GO:0006338//GO:0010160//GO:0010468//GO:0016818//GO:0043231//GO:0043234//GO:0044444	nr +
Unigene110180_All	354	0.00	0.00	0.00	0.00	0.00	0.00	2.15	0.24	0.11	null	null		null	null		null	null		null	null		-3.19E+00	7.93E-04	Down	-4.26E+00	8.66E-05	Down							ESTscan +
Unigene110181_All	261	0.00	0.00	0.00	0.00	0.00	0.00	2.11	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	4.62E-04	Down	-1.10E+01	2.81E-04	Down	Unigene110181_All//gi|159483211|ref|XP_001699654.1|//1.00E-20//ribosomal protein L27a, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|158281596|gb|EDP07350.1| ribosomal protein L27a, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii]	Unigene110181_All//3.00E-20//AT1G70600| structural constituent of ribosome			ko03010|Ribosome		nr -
Unigene110182_All	516	0.00	0.00	0.00	0.00	0.00	0.00	2.29	0.24	0.23	null	null		null	null		null	null		null	null		-3.24E+00	1.10E-05	Down	-3.31E+00	4.89E-06	Down							
Unigene110184_All	557	0.00	0.00	0.00	0.00	0.00	0.16	0.53	0.23	3.43	null	null		null	null		null	null		7.34E+00	4.80E-01		-1.24E+00	3.73E-01		2.69E+00	1.24E-07	Up	Unigene110184_All//gi|145335895|ref|NP_173359.3|//4.00E-68//FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase [Arabidopsis thaliana] >gi|75174733|sp|Q9LMA1.1|FMO1_ARATH RecName: Full=Probable flavin-containing monooxygenase 1 >gi|8954062|gb|AAF82235.1|AC069143_11 Contains similarity to a dimethylaniline monooxygenase (N-oxide forming) 2 (pulmonary flavin-containing monooxygenase 2) (FMO 2) (Dimethylaniline oxidase 2) (FMO 1B1) from Oryctolagus cuniculus gi|120434 and contains a flavin-binding monooxygenase-like PF|00743 domain [Arabidopsis thaliana]	Unigene110184_All//8.00E-70//AT1G19250| FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase					nr +
Unigene110186_All	901	0.00	0.00	0.00	0.00	0.00	0.00	4.55	0.05	0.04	null	null		null	null		null	null		null	null		-6.62E+00	2.45E-27	Down	-6.69E+00	1.85E-28	Down	Unigene110186_All//gi|4139170|gb|AAD03711.1|//1.00E-129//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene110186_All//3.00E-123//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene110186_All//8.00E-20//TC170429				nr -
Unigene110187_All	276	0.00	0.00	0.00	0.00	0.00	0.00	1.84	0.30	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.05E-02		-1.08E+01	5.55E-04	Down							
Unigene110193_All	476	0.00	0.00	0.00	0.00	0.00	0.00	2.22	1.05	0.00	null	null		null	null		null	null		null	null		-1.08E+00	7.50E-02		-1.11E+01	6.72E-08	Down	Unigene110193_All//gi|9188543|dbj|BAA99561.1|//2.00E-34//alpha-tubulin [Chlorella vulgaris]	Unigene110193_All//8.00E-24//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene110193_All//9.00E-09//gi|54122405|gb|CO497914.1|CO497914		ko04145|Phagosome		nr +
Unigene110196_All	509	0.00	1.19	0.21	0.00	0.34	0.35	2.33	0.41	0.63	1.02E+01	1.17E-03		7.71E+00	4.02E-01		8.40E+00	2.27E-01		8.47E+00	1.95E-01		-2.50E+00	1.47E-04	Down	-1.89E+00	1.24E-03		Unigene110196_All//gi|224077504|ref|XP_002305276.1|//3.00E-15//GRAS domain protein [Populus trichocarpa] >gi|222848240|gb|EEE85787.1| GRAS domain protein [Populus trichocarpa]		Unigene110196_All//1.00E-112//TC153520				nr -
Unigene110197_All	246	0.00	0.00	0.00	0.00	0.00	0.00	3.27	0.34	0.65	null	null		null	null		null	null		null	null		-3.26E+00	4.48E-04	Down	-2.33E+00	2.82E-03								ESTscan -
Unigene110199_All	279	0.00	0.00	0.00	0.00	0.00	0.00	1.97	0.15	0.00	null	null		null	null		null	null		null	null		-3.72E+00	3.23E-03		-1.09E+01	2.81E-04	Down	Unigene110199_All//gi|224000593|ref|XP_002289969.1|//7.00E-14//the actin binding protein cofilin-like protein [Thalassiosira pseudonana CCMP1335] >gi|220975177|gb|EED93506.1| the actin binding protein cofilin-like protein [Thalassiosira pseudonana CCMP1335]	Unigene110199_All//4.00E-12//AT2G16700| ADF5 (ACTIN DEPOLYMERIZING FACTOR 5); actin binding					nr +
Unigene110202_All	542	0.00	0.00	0.00	0.00	0.00	0.00	1.95	0.69	0.44	null	null		null	null		null	null		null	null		-1.49E+00	1.64E-02		-2.14E+00	9.36E-04	Down							ESTscan -
Unigene110205_All	353	0.74	0.00	0.00	1.27	0.39	0.00	2.40	0.95	0.23	-9.53E+00	6.72E-02		-9.53E+00	8.59E-02		-1.70E+00	1.35E-01		-1.03E+01	5.79E-03		-1.34E+00	5.68E-02		-3.41E+00	1.35E-04	Down			Unigene110205_All//4.00E-07//C0105291				
Unigene110206_All	224	0.00	0.00	0.00	0.00	0.00	0.00	2.27	0.19	0.00	null	null		null	null		null	null		null	null		-3.60E+00	5.78E-03		-1.11E+01	5.55E-04	Down	Unigene110206_All//gi|300508148|dbj|BAJ10906.1|//7.00E-23//elongation factor like [Grateloupia subpectinata]						nr +
Unigene110210_All	272	0.00	0.00	0.00	0.00	0.00	0.00	2.49	0.15	0.00	null	null		null	null		null	null		null	null		-4.02E+00	5.36E-04	Down	-1.13E+01	3.57E-05	Down	Unigene110210_All//gi|116222123|gb|ABJ80932.1|//2.00E-36//actin [Leucocryptos marina]	Unigene110210_All//7.00E-33//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton			ko04145|Phagosome		nr -

Unigene110212_All	275	0.00	0.00	0.00	0.00	0.00	0.00	1.85	1.06	0.00	null	null		null	null		null	null		null	null		-7.94E-01	4.02E-01		-1.08E+01	5.55E-04	Down	Unigene110212_All//gi|253760977|ref|XP_002489033.1|//7.00E-07//hypothetical protein SORBIDRAFT_0351s002020 [Sorghum bicolor] >gi|241947330|gb|EES20475.1| hypothetical protein SORBIDRAFT_0351s002020 [Sorghum bicolor]		Unigene110212_All//3.00E-16//EX170698				nr +
Unigene11022_All	2745	0.50	1.22	0.95	2.09	2.95	3.06	3.17	2.12	4.17	1.30E+00	2.16E-04	Up	9.40E-01	2.21E-02		4.98E-01	1.24E-02		5.52E-01	5.55E-03		-5.84E-01	7.91E-04		3.93E-01	7.68E-03		Unigene11022_All//gi|224064045|ref|XP_002301364.1|//0.00E+00//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222843090|gb|EEE80637.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene11022_All//4.00E-137//AT2G46020| transcription regulatory protein SNF2, putative	Unigene11022_All//0.00E+00//ES845478			GO:0003676//GO:0006338//GO:0010160//GO:0010468//GO:0016818//GO:0043231//GO:0043234//GO:0044444	nr +
Unigene110220_All	880	0.00	0.00	0.00	0.00	0.00	0.10	2.31	0.57	0.81	null	null		null	null		null	null		6.68E+00	4.80E-01		-2.02E+00	8.03E-06	Down	-1.50E+00	2.57E-04	Down	Unigene110220_All//gi|159138929|gb|ABW89464.1|//5.00E-89//glutamine synthetase [Gossypium hirsutum] >gi|159138931|gb|ABW89465.1| glutamine synthetase [Gossypium hirsutum]	Unigene110220_All//5.00E-86//AT5G16570| GLN1;4; glutamate-ammonia ligase	Unigene110220_All//0.00E+00//gi|78342884|gb|DT563158.1|DT563158		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene110224_All	566	0.00	0.00	0.00	0.09	0.00	0.00	2.69	1.18	0.84	null	null		null	null		-6.46E+00	5.62E-01		-6.46E+00	6.43E-01		-1.19E+00	1.47E-02		-1.67E+00	7.06E-04	Down			Unigene110224_All//1.00E-54//DV849456					
Unigene11023_All	2339	1.23	2.56	2.85	4.32	4.53	4.44	5.42	3.11	6.27	1.06E+00	1.98E-05	Up	1.21E+00	6.90E-07	Up	6.88E-02	7.79E-01		3.88E-02	8.59E-01		-8.03E-01	1.79E-08		2.09E-01	1.22E-01		Unigene11023_All//gi|224064045|ref|XP_002301364.1|//0.00E+00//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222843090|gb|EEE80637.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene11023_All//0.00E+00//AT2G46020| transcription regulatory protein SNF2, putative	Unigene11023_All//3.00E-77//ES845478			GO:0003676//GO:0006338//GO:0010160//GO:0010468//GO:0017111//GO:0032559//GO:0043231//GO:0043234//GO:0044444	nr -
Unigene110233_All	463	0.00	0.00	0.00	0.00	0.00	0.00	2.74	0.90	0.00	null	null		null	null		null	null		null	null		-1.60E+00	4.42E-03		-1.14E+01	1.99E-09	Down	Unigene110233_All//gi|42569129|ref|NP_179444.2|//2.00E-14//cupin family protein [Arabidopsis thaliana]				ko03040|Spliceosome		nr -
Unigene110235_All	299	0.00	0.00	0.00	0.00	0.23	0.00	4.67	0.28	1.20	null	null		null	null		7.85E+00	6.15E-01		null	null		-4.06E+00	9.64E-08	Down	-1.96E+00	2.74E-04	Down								
Unigene110237_All	946	0.00	0.00	0.00	0.00	0.00	0.00	2.23	0.27	0.00	null	null		null	null		null	null		null	null		-3.08E+00	2.88E-09	Down	-1.11E+01	1.40E-15	Down	Unigene110237_All//gi|50508930|dbj|BAD31835.1|//2.00E-07//putative high-affinity potassium transporter [Oryza sativa Japonica Group] >gi|215694830|dbj|BAG90021.1| unnamed protein product [Oryza sativa Japonica Group]						nr -
Unigene110238_All	402	0.65	0.50	0.53	0.25	0.60	0.11	3.37	0.52	0.99	-3.68E-01	7.79E-01		-2.97E-01	8.32E-01		1.27E+00	5.32E-01		-1.14E+00	6.79E-01		-2.69E+00	1.77E-05	Down	-1.76E+00	9.57E-04	Down	Unigene110238_All//gi|145334291|ref|NP_001078527.1|//9.00E-20//DME (DEMETER); DNA N-glycosylase/ DNA-(apurinic or apyrimidinic site) lyase [Arabidopsis thaliana] >gi|108935833|sp|Q8LK56.2|DME_ARATH RecName: Full=Transcriptional activator DEMETER; AltName: Full=DNA glycosylase-related protein DME >gi|84782664|gb|ABC61677.1| DNA glycosylase DEMETER [Arabidopsis thaliana]	Unigene110238_All//1.00E-18//AT5G04560| DME (DEMETER); DNA N-glycosylase/ DNA-(apurinic or apyrimidinic site) lyase			ko03410|Base excision repair		nr -
Unigene110240_All	623	0.08	0.00	0.00	0.40	0.28	0.87	11.20	3.02	4.86	-6.39E+00	6.18E-01		-6.39E+00	6.31E-01		-5.33E-01	7.13E-01		1.12E+00	3.05E-01		-1.89E+00	8.16E-17	Down	-1.20E+00	2.30E-09	Down	Unigene110240_All//gi|224128414|ref|XP_002329156.1|//3.00E-26//nbs-lrr resistance protein [Populus trichocarpa] >gi|222869825|gb|EEF06956.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene110240_All//1.00E-09//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene110240_All//2.00E-47//C0080429		ko04626|Plant-pathogen interaction		nr +
Unigene110242_All	1635	0.00	0.00	0.00	0.00	0.00	0.00	3.36	2.89	0.05	null	null		null	null		null	null		null	null		-2.19E-01	3.98E-01		-6.11E+00	4.43E-37	Down	Unigene110242_All//gi|115463921|ref|NP_001055560.1|//1.00E-120//0s05g0417100 [Oryza sativa Japonica Group] >gi|113579111|dbj|BAF17474.1| 0s05g0417100 [Oryza sativa Japonica Group]	Unigene110242_All//3.00E-116//AT5G36950| DegP10 (DegP protease 10); catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase					nr -
Unigene110246_All	306	0.51	0.17	0.00	0.33	0.56	0.44	1.80	0.55	0.00	-1.63E+00	4.89E-01		-9.00E+00	2.46E-01		7.89E-01	7.72E-01		4.44E-01	8.62E-01		-1.72E+00	7.23E-02		-1.08E+01	2.81E-04	Down								
Unigene110253_All	448	0.00	0.00	0.00	0.00	0.00	0.00	1.23	0.00	4.36	null	null		null	null		null	null		null	null		-1.03E+01	4.62E-04	Down	1.83E+00	3.51E-05	Up	Unigene110253_All//gi|68299217|emb|CAJ13709.1|//6.00E-19//glutathione S-transferase 12 [Capsicum chinense]	Unigene110253_All//4.00E-11//AT5G62480| ATGSTU9 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 9); glutathione transferase			ko00480|Glutathione metabolism		nr +
Unigene110256_All	422	0.00	0.00	0.50	0.47	0.00	0.00	4.21	2.87	0.85	null	null		8.98E+00	1.42E-01		-8.88E+00	8.47E-02		-8.88E+00	1.34E-01		-5.51E-01	2.24E-01		-2.31E+00	3.08E-06	Down								
Unigene110257_All	405	0.00	0.00	0.00	0.00	0.00	0.00	1.88	1.03	0.10	null	null		null	null		null	null		null	null		-8.65E-01	2.39E-01		-4.26E+00	8.66E-05	Down								
Unigene110258_All	405	0.00	0.00	0.00	0.12	0.00	0.11	5.32	1.65	21.15	null	null		null	null		-6.94E+00	5.62E-01		-1.42E-01	9.56E-01		-1.69E+00	5.26E-05	Down	1.99E+00	2.74E-22	Up			Unigene110258_All//1.00E-100//gi|195983813|gb|FL576553.1|FL576553					
Unigene110259_All	272	0.00	0.00	0.00	0.00	0.00	0.00	2.49	1.08	0.00	null	null		null	null		null	null		null	null		-1.21E+00	1.34E-01		-1.13E+01	3.57E-05	Down			Unigene110259_All//5.00E-15//DW479423					ESTscan -
Unigene110266_All	264	0.00	0.00	0.00	0.00	0.00	0.00	2.88	0.32	0.00	null	null		null	null		null	null		null	null		-3.19E+00	7.93E-04	Down	-1.15E+01	8.88E-06	Down								
Unigene110268_All	337	0.00	0.00	0.00	0.00	0.00	0.00	2.01	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	6.34E-05	Down	-1.10E+01	3.57E-05	Down	Unigene110268_All//gi|42569129|ref|NP_179444.2|//4.00E-11//cupin family protein [Arabidopsis thaliana]						nr -
Unigene11027_All	940	1.78	1.62	4.65	6.78	4.47	5.57	4.18	2.13	4.87	-1.39E-01	7.69E-01		1.38E+00	1.09E-05	Up	-6.02E-01	6.30E-03		-2.83E-01	2.70E-01		-9.71E-01	4.39E-04		2.21E-01	3.99E-01		Unigene11027_All//gi|186510768|ref|NP_190388.2|//5.00E-46//DNA binding / protein binding / transcription regulator [Arabidopsis thaliana] >gi|186510770|ref|NP_850669.2| DNA binding / protein binding / transcription regulator [Arabidopsis thaliana]	Unigene11027_All//1.00E-47//AT3G48050| DNA binding / protein binding / transcription regulator	Unigene11027_All//0.00E+00//gi|73866001|gb|DT468739.1|DT468739				nr -
Unigene110279_All	296	0.00	0.00	0.00	0.34	0.00	0.00	1.86	0.00	0.00	null	null		null	null		-8.39E+00	3.16E-01		-8.39E+00	4.05E-01		-1.09E+01	4.62E-04	Down	-1.09E+01	2.81E-04	Down								
Unigene110282_All	290	0.00	0.00	0.00	0.00	0.00	0.00	1.90	0.00	0.27	null	null		null	null		null	null		null	null		-1.09E+01	4.62E-04	Down	-2.79E+00	7.96E-03		Unigene110282_All//gi|15234663|ref|NP_192431.1|//6.00E-13//harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana]	Unigene110282_All//2.00E-14//AT4G05220| harpin-induced protein-related / HIN1-related / harpin-responsive protein-related					nr -
Unigene110284_All	509	0.00	0.00	0.00	0.00	0.00	0.00	2.82	1.07	0.16	null	null		null	null		null	null		null	null		-1.40E+00	6.15E-03		-4.17E+00	1.93E-08	Down	Unigene110284_All//gi|226505998|ref|NP_001146929.1|//1.00E-30//60S ribosomal protein L7a [Zea mays] >gi|195605318|gb|ACG24489.1| 60S ribosomal protein L7a [Zea mays]	Unigene110284_All//3.00E-26//AT2G47610| 60S ribosomal protein L7A (RPL7AA)			ko03010|Ribosome		nr -
Unigene110286_All	448	0.23	0.00	0.12	0.00	1.00	0.40	4.06	0.19	0.36	-7.87E+00	3.76E-01		-9.74E-01	7.22E-01		9.96E+00	8.02E-03		8.66E+00	1.95E-01		-4.44E+00	1.72E-10	Down	-3.51E+00	2.43E-09	Down								
Unigene110287_All	1443	0.00	0.00	0.00	0.00	0.00	0.00	11.08	0.00	0.47	null	null		null	null		null	null		null	null		-1.34E+01	9.31E-114	Down	-4.56E+00	2.00E-93	Down								
Unigene110289_All	365	0.00	0.00	0.00	0.00	0.00	0.00	2.09	0.23	0.00	null	null		null	null		null	null		null	null		-3.19E+00	7.93E-04	Down	-1.10E+01	8.88E-06	Down	Unigene110289_All//gi|205364757|gb|AC104578.1|//2.00E-20//cysteine protease-like protein [Robinia pseudoacacia]	Unigene110289_All//2.00E-20//AT4G16190| cysteine proteinase, putative					nr -
Unigene11029_All	726	5.98	18.63	5.13	12.63	13.38	14.43	6.76	8.52	15.20	1.64E+00	1.96E-21	Up	-2.20E-01	4.94E-01		8.33E-02	7.30E-01		1.93E-01	3.48E-01		3.35E-01	1.33E-01		1.17E+00	1.38E-13	Up	Unigene11029_All//gi|186510768|ref|NP_190388.2|//1.00E-22//DNA binding / protein binding / transcription regulator [Arabidopsis thaliana] >gi|186510770|ref|NP_850669.2| DNA binding / protein binding / transcription regulator [Arabidopsis thaliana]	Unigene11029_All//1.00E-17//AT3G48050| DNA binding / protein binding / transcription regulator	Unigene11029_All//1.00E-36//AW187392			GO:0003676//GO:0006351//GO:0030528	nr +
Unigene110292_All	425	0.00	0.00	0.00	0.00	0.00	0.21	0.50	3.64	1.03	null	null		null	null		null	null		7.73E+00	4.80E-01		2.87E+00	1.64E-06	Up	1.05E+00	2.98E-01		Unigene110292_All//gi|13940209|emb|CAC37922.1|//3.00E-27//fructan 1-exohydrolase IIa [Cichorium intybus] >gi|32492892|gb|AAP85536.1| fructan 1-exohydrolase IIa [Cichorium intybus]	Unigene110292_All//4.00E-26//AT5G11920| AtcwINV6 (6-&1-fructan exohydrolase); hydrolase, hydrolyzing O-glycosyl compounds / inulinase/ levanase	Unigene110292_All//6.00E-59//TC152854		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr +
Unigene11030_All	1205	1.61	3.53	3.18	5.08	5.12	8.66	4.74	3.71	15.31	1.14E+00	1.62E-04	Up	9.86E-01	2.63E-03		8.60E-03	9.80E-01		7.68E-01	9.76E-06		-3.52E-01	1.33E-01		1.69E+00	6.59E-38	Up	Unigene11030_All//gi|186510768|ref|NP_190388.2|//8.00E-82//DNA binding / protein binding / transcription regulator [Arabidopsis thaliana] >gi|186510770|ref|NP_850669.2| DNA binding / protein binding / transcription regulator [Arabidopsis thaliana]	Unigene11030_All//2.00E-80//AT3G48050| DNA binding / protein binding / transcription regulator	Unigene11030_All//5.00E-25//AW187169			GO:0006351//GO:0008135//GO:0030528//GO:0043231	nr -
Unigene110300_All	1037	0.20	0.00	0.10	0.29	0.10	0.30	2.04	0.04	0.54	-7.66E+00	1.23E-01		-9.75E-01	6.21E-01		-1.53E+00	2.98E-01		8.13E-02	9.50E-01		-5.66E+00	1.47E-13	Down	-1.92E+00	5.97E-06	Down	Unigene110300_All//gi|115451409|ref|NP_001049305.1|//1.00E-09//0s03g0203100 [Oryza sativa Japonica Group] >gi|108706728|gb|ABF94523.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547776|dbj|BAF11219.1| 0s03g0203100 [Oryza sativa Japonica Group]	Unigene110300_All//4.00E-35//AT4G30150| EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Nucleolar 27S pre-rRNA processing, Urb2/Npa2 (InterPro:IPR018849); Has 31 Blast hits to 27 proteins in 14 species: Archae - 0; Bacteria - 2; Metazoa - 3; Fungi - 0; Plants - 19; Viruses - 3; Other Eukaryotes - 4 (source: NCBI BLink).						nr +
Unigene110302_All	267	0.39	0.00	0.00	0.93	0.00	1.01	2.38	0.00	0.75	-8.61E+00	3.76E-01		-8.61E+00	3.98E-01		-9.87E+00	4.19E-02		1.22E-01	9.44E-01		-1.12E+01	1.23E-04	Down	-1.67E+00	4.29E-02		Unigene110302_All//gi|115455297|ref|NP_001051249.1|//3.00E-22//0s03g0746400 [Oryza sativa Japonica Group] >gi|113549720|dbj|BAF13163.1| 0s03g0746400 [Oryza sativa Japonica Group]	Unigene110302_All//2.00E-23//AT3G22670| pentatricopeptide (PPR) repeat-containing protein	Unigene110302_All//4.00E-145//TC174147				nr +
Unigene110307_All	267	0.20	0.00	0.00	0.00	0.00	0.00	2.38	0.00	0.15	-7.61E+00	6.18E-01		-7.61E+00	6.31E-01		null	null		null	null		-1.12E+01	1.23E-04	Down	-3.99E+00	5.82E-04	Down								
Unigene110308_All	319	0.00	0.00	0.00	0.00	0.00	0.00	1.72	0.00	0.00	null	null		null	null		null	null		null	null		-1.08E+01	4.62E-04	Down	-1.08E+01	2.81E-04	Down								
Unigene110313_All	276	0.00	0.00	0.00	0.18	0.00	0.00	4.44	0.30	1.15	null	null		null	null		-7.50E+00	5.62E-01		-7.50E+00	6.43E-01		-3.87E+00	1.15E-06	Down	-1.94E+00	7.80E-04	Down								
Unigene110315_All	360	465.51	192.26	505.14	165.36	225.55	318.53	598.26	282.01	292.37	-1.28E+00	2.16E-178	Down	1.18E-01	4.01E-03		4.48E-01	2.64E-17		9.46E-01	6.13E-81		-1.09E+00	1.60E-216	Down	-1.03E+00	2.55E-205	Down	Unigene110315_All//gi|292653525|gb|ADE34280.1|//2.00E-23//aquaporin PIP1;11 [Gossypium hirsutum]	Unigene110315_All//3.00E-23//AT2G45960| PIP1B (NAMED PLASMA MEMBRANE INTRINSIC PROTEIN 1B); water channel	Unigene110315_All//2.00E-138//TC165394				nr +
Unigene110317_All	294	0.00	0.00	0.00	0.00	0.00	0.00	1.87	0.00	0.27	null	null		null	null		null	null		null	null		-1.09E+01	4.62E-04	Down	-2.79E+00	7.96E-03									
Unigene110322_All	559	0.00	0.00	0.00	0.00	0.00	0.00	1.66	0.15	0.00	null	null		null	null		null	null		null	null		-3.48E+00	7.79E-05	Down	-1.07E+01	5.48E-07	Down								ESTscan -

Unigene110327_All	505	0.73	0.20	2.00	0.20	0.48	0.00	4.35	0.91	0.55	-1.85E+00	1.87E-01		1.47E+00	4.95E-02		1.27E+00	5.32E-01		-7.62E+00	4.05E-01		-2.26E+00	4.47E-07	Down	-2.98E+00	1.05E-09	Down	Unigene110327_All//gi|224142499|ref|XP_002324594.1|//1.00E-06//predicted protein [Populus trichocarpa] >gi|222866028|gb|EEF03159.1| predicted protein [Populus trichocarpa]		Unigene110327_All//1.00E-17//TC175191				nr +
Unigene110335_All	261	0.00	0.00	0.20	0.19	0.00	0.35	2.43	0.48	0.00	null	null		7.67E+00	6.40E-01		-7.58E+00	5.62E-01		8.58E-01	7.96E-01		-2.34E+00	1.27E-02		-1.12E+01	7.12E-05	Down			Unigene110335_All//4.00E-22//gi|164357674|gb|ES820724.1|ES820724				
Unigene110338_All	269	0.00	0.00	0.00	0.00	0.00	0.00	4.56	0.78	0.30	null	null		null	null		null	null		null	null		-2.55E+00	8.71E-05	Down	-3.94E+00	4.86E-07	Down			Unigene110338_All//2.00E-08//gi|109850443|gb|DW479422.1|DW479422				
Unigene110341_All	274	0.00	0.00	0.00	0.00	0.00	0.00	2.78	0.00	0.00	null	null		null	null		null	null		null	null		-1.14E+01	1.68E-05	Down	-1.14E+01	8.88E-06	Down							
Unigene110342_All	266	0.59	0.57	0.80	0.56	0.26	0.00	3.34	2.04	0.45	-4.62E-02	9.90E-01		4.41E-01	7.76E-01		-1.12E+00	5.85E-01		-9.13E+00	2.34E-01		-7.09E-01	2.97E-01		-2.89E+00	3.05E-04	Down							
Unigene110343_All	578	0.00	0.00	0.00	0.00	0.00	0.00	2.56	2.82	0.00	null	null		null	null		null	null		null	null		1.40E-01	7.67E-01		-1.13E+01	5.85E-11	Down	Unigene110343_All//gi|302128114|db|BAJ13478.1|//1.00E-59//actin 1 [Guillardia theta]	Unigene110343_All//7.00E-58//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene110343_All//7.00E-13//TC153744				nr +
Unigene110344_All	457	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.00	0.17	null	null		null	null		null	null		null	null		-1.10E+01	1.15E-06	Down	-3.55E+00	3.97E-05	Down							
Unigene110352_All	407	0.39	0.00	0.00	0.12	0.51	0.00	1.45	0.00	0.10	-8.59E+00	2.17E-01		-8.59E+00	2.46E-01		2.05E+00	3.95E-01		-6.94E+00	6.43E-01		-1.05E+01	2.40E-04	Down	-3.89E+00	1.10E-03		Unigene110352_All//gi|226530818|ref|NP_001148776.1|//1.00E-18//cysteine-type peptidase [Zea mays] >gi|195622072|gb|ACG32866.1| cysteine-type peptidase [Zea mays]	Unigene110352_All//9.00E-18//AT5G04250| OTU-like cysteine protease family protein	Unigene110352_All//6.00E-136//TC174360				nr -
Unigene110353_All	687	0.00	0.00	0.00	0.00	0.00	0.00	4.31	0.12	0.23	null	null		null	null		null	null		null	null		-5.15E+00	3.87E-18	Down	-4.21E+00	6.93E-17	Down	Unigene110353_All//gi|297811659|ref|XP_002873713.1|//3.00E-63//40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata] >gi|297319550|gb|EFH49972.1| 40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata]	Unigene110353_All//5.00E-50//AT5G15200| 40S ribosomal protein S9 (RPS9B)			ko03010|Ribosome		nr +
Unigene110356_All	351	0.00	0.00	0.00	1.70	0.78	1.03	3.98	0.60	0.34	null	null		null	null		-1.12E+00	2.26E-01		-7.26E-01	4.60E-01		-2.74E+00	1.03E-05	Down	-3.55E+00	2.28E-07	Down	Unigene110356_All//gi|297596229|ref|NP_00102217.2|//3.00E-08//Os01g0182300 [Oryza sativa Japonica Group] >gi|255672942|dbj|BAF04131.2| Os01g0182300 [Oryza sativa Japonica Group]						nr -
Unigene110357_All	225	0.00	0.00	0.24	1.55	0.46	0.40	2.25	0.19	0.00	null	null		7.89E+00	6.40E-01		-1.76E+00	1.90E-01		-1.95E+00	1.96E-01		-3.60E+00	5.78E-03		-1.11E+01	5.55E-04	Down			Unigene110357_All//5.00E-21//TC176559				
Unigene11036_All	1023	3.58	1.68	2.71	8.62	10.20	10.90	10.25	2.94	6.35	-1.09E+00	8.27E-04	Down	-4.04E-01	2.42E-01		2.43E-01	2.08E-01		3.39E-01	5.60E-02		-1.80E+00	2.43E-23	Down	-6.91E-01	6.51E-06		Unigene11036_All|gi|225438627|ref|XP_002276798.1|//1.00E-161//PREDICTED: similar to binding [Vitis vinifera]	Unigene11036_All//3.00E-147//AT2G22125| binding	Unigene11036_All//0.00E+00//TC133396				nr -
Unigene110360_All	343	0.00	0.15	0.16	1.74	0.60	0.00	1.23	0.00	0.93	7.21E+00	6.21E-01		7.28E+00	6.40E-01		-1.53E+00	1.01E-01		-1.08E+01	7.71E-04	Down	-1.03E+01	3.26E-03		-4.08E-01	6.54E-01		Unigene110360_All//gi|57834114|emb|CAE05707.2|//2.00E-24//OSJNBa0065J09.3 [Oryza sativa (japonica cultivar-group)]						nr +
Unigene110364_All	243	0.43	0.00	0.00	0.00	0.00	0.00	4.00	0.00	0.33	-8.75E+00	3.76E-01		-8.75E+00	3.98E-01		null	null		null	null		-1.20E+01	5.84E-07	Down	-3.61E+00	2.14E-05	Down	Unigene110364_All//gi|9759032|dbj|BAB09401.1|//1.00E-13//transmembrane transport protein-like [Arabidopsis thaliana]	Unigene110364_All//5.00E-15//AT5G50300| xanthine/uracil/vitamin C permease family protein					nr -
Unigene110366_All	374	0.00	0.00	0.00	0.00	0.00	0.00	2.94	0.89	0.32	null	null		null	null		null	null		null	null		-1.72E+00	5.68E-03		-3.20E+00	1.63E-05	Down							
Unigene11037_All	635	1.32	0.48	1.51	2.12	6.13	3.41	5.93	1.71	2.82	-1.46E+00	6.69E-02		1.95E-01	7.70E-01		1.53E+00	9.42E-07	Up	6.89E-01	1.28E-01		-1.79E+00	8.35E-09	Down	-1.07E+00	1.16E-04	Down	Unigene11037_All|gi|225438627|ref|XP_002276798.1|//3.00E-94//PREDICTED: similar to binding [Vitis vinifera]	Unigene11037_All//7.00E-83//AT2G22125| binding	Unigene11037_All//0.00E+00//TC133396				nr -
Unigene110370_All	326	0.32	0.78	3.10	0.61	0.53	0.28	1.82	0.77	0.49	1.28E+00	4.36E-01		3.27E+00	5.93E-04	Up	-2.11E-01	8.59E-01		-1.14E+00	5.70E-01		-1.24E+00	1.54E-01		-1.89E+00	3.22E-02		Unigene110370_All|gi|255541236|ref|XP_002511682.1|//7.00E-07//beta-tubulin cofactor d, putative [Ricinus communis] >gi|223548862|gb|EEF50351.1| beta-tubulin cofactor d, putative [Ricinus communis]	Unigene110370_All//5.00E-05//AT3G60740| TTN1 (TITAN 1); tubulin binding	Unigene110370_All//1.00E-47//gi|73847702|gb|DT456722.1|DT456722				nr +
Unigene110372_All	344	0.00	0.00	0.00	0.00	0.00	0.00	2.21	0.49	0.23	null	null		null	null		null	null		null	null		-2.19E+00	7.78E-03		-3.26E+00	4.48E-04	Down							ESTscan -
Unigene11038_All	608	0.86	0.67	0.70	2.87	2.10	4.23	3.48	0.28	0.46	-3.68E-01	6.83E-01		-2.96E-01	7.50E-01		-4.53E-01	3.73E-01		5.62E-01	1.74E-01		-3.66E+00	1.12E-10	Down	-2.92E+00	3.37E-09	Down	Unigene11038_All|gi|225438627|ref|XP_002276798.1|//2.00E-93//PREDICTED: similar to binding [Vitis vinifera]	Unigene11038_All//1.00E-78//AT2G22125| binding	Unigene11038_All//0.00E+00//TC142058			GO:0043231	nr +
Unigene110380_All	268	0.00	0.00	0.00	0.00	0.00	0.00	3.79	0.00	0.59	null	null		null	null		null	null		null	null		-1.19E+01	2.97E-07	Down	-2.67E+00	1.94E-04	Down							
Unigene110381_All	1570	0.33	0.39	1.22	0.10	0.13	0.43	1.62	1.22	0.53	2.17E-01	7.93E-01		1.87E+00	4.53E-04	Up	4.67E-01	8.26E-01		2.18E+00	3.14E-02		-4.00E-01	2.85E-01		-1.60E+00	1.31E-05	Down							
Unigene110385_All	304	513.40	1507.92	676.13	78.82	157.90	305.89	67.87	173.23	214.26	1.55E+00	0.00E+00	Up	3.97E-01	2.88E-28		1.00E+00	2.57E-41	Up	1.96E+00	7.56E-197	Up	1.35E+00	2.98E-75	Up	1.66E+00	4.06E-128	Up	Unigene110385_All//gi|73761689|gb|AAZ83344.1|//4.00E-31//ACC oxidase 3 [Gossypium hirsutum]	Unigene110385_All//1.00E-24//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene110385_All//2.00E-159//TC134764		ko00270|Cysteine and methionine metabolism		nr +
Unigene110386_All	760	0.00	0.00	0.00	0.20	0.09	0.06	7.01	0.93	4.19	null	null		null	null		-1.12E+00	5.85E-01		-1.73E+00	5.02E-01		-2.91E+00	3.18E-21	Down	-7.41E-01	9.05E-04		Unigene110386_All|gi|224069338|ref|XP_002302959.1|//1.00E-13//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222844685|gb|EEE82232.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene110386_All//1.00E-06//AT1G69545| leucine-rich repeat family protein	Unigene110386_All//2.00E-85//ES801940				nr -
Unigene11039_All	1073	9.26	3.02	6.15	22.38	21.18	15.78	18.68	6.23	10.40	-1.62E+00	9.99E-16	Down	-5.90E-01	1.76E-03		-7.92E-02	5.67E-01		-5.04E-01	3.16E-06		-1.58E+00	9.88E-37	Down	-8.45E-01	1.78E-14		Unigene11039_All|gi|225438627|ref|XP_002276798.1|//1.00E-171//PREDICTED: similar to binding [Vitis vinifera]	Unigene11039_All//4.00E-150//AT2G22125| binding	Unigene11039_All//0.00E+00//TC133396				nr -
Unigene110393_All	416	0.00	0.00	0.00	0.00	0.00	0.00	2.03	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	4.39E-06	Down	-1.10E+01	2.21E-06	Down							ESTscan -
Unigene110399_All	314	0.00	0.00	0.00	0.00	0.00	0.00	2.29	0.53	0.00	null	null		null	null		null	null		null	null		-2.10E+00	1.25E-02		-1.12E+01	1.78E-05	Down	Unigene110399_All//gi|146454510|gb|ABQ41921.1|//3.00E-33//60S ribosomal protein large subunit 9 [Sonneratia caseolaris] >gi|156633898|gb|ABL90948.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633900|gb|ABL90949.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633902|gb|ABL90950.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633904|gb|ABL90951.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633906|gb|ABL90952.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633908|gb|ABL90953.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633910|gb|ABL90954.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633912|gb|ABL90955.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633914|gb|ABL90956.1| ribosomal protein L9 [Sonneratia	Unigene110399_All//6.00E-32//AT4G10450| 60S ribosomal protein L9 (RPL9OD)			ko03010|Ribosome		nr -
Unigene11040_All	1917	2.10	2.19	1.94	5.61	5.86	6.15	4.39	1.72	2.87	6.19E-02	8.39E-01		-1.12E-01	7.18E-01		6.12E-02	8.03E-01		1.32E-01	5.05E-01		-1.35E+00	1.12E-12	Down	-6.14E-01	3.71E-04		Unigene11040_All|gi|225438627|ref|XP_002276798.1|//0.00E+00//PREDICTED: similar to binding [Vitis vinifera]	Unigene11040_All//0.00E+00//AT2G22125| binding	Unigene11040_All//0.00E+00//TC142058				nr +
Unigene110400_All	898	0.82	2.09	0.83	2.77	1.80	2.06	1.18	0.37	0.27	1.36E+00	5.88E-03		2.54E-02	9.95E-01		-6.22E-01	1.12E-01		-4.28E-01	3.21E-01		-1.66E+00	8.55E-03		-2.14E+00	9.36E-04	Down			Unigene110400_All//3.00E-161//gi|84172254|gb|DR460902.1|DR460902				
Unigene11041_All	5663	6.25	3.44	3.71	11.56	10.34	10.08	15.18	4.94	7.01	-8.64E-01	1.45E-20		-7.52E-01	1.14E-15		-1.61E-01	1.36E-02		-1.97E-01	2.74E-03		-1.62E+00	4.55E-160	Down	-1.12E+00	2.81E-93	Down	Unigene11041_All|gi|225438627|ref|XP_002276798.1|//0.00E+00//PREDICTED: similar to binding [Vitis vinifera]	Unigene11041_All//0.00E+00//AT2G22125| binding	Unigene11041_All//0.00E+00//TC133396				nr -
Unigene110411_All	858	0.00	0.00	0.19	0.00	0.04	0.00	0.79	0.15	0.05	null	null		7.54E+00	2.40E-01		5.33E+00	8.37E-01		null	null		-2.43E+00	7.77E-03		-4.09E+00	3.10E-04	Down	Unigene110411_All|gi|4249380|gb|AA014477.1|//1.00E-36//ESTs gb|Z37637, gb|AA042498 and gb|AA042269 come from this gene [Arabidopsis thaliana]	Unigene110411_All//7.00E-38//AT1G60010| unknown protein	Unigene110411_All//0.00E+00//TC164121				nr -
Unigene110413_All	627	0.08	1.37	0.59	0.24	1.26	1.15	1.15	0.53	0.95	4.04E+00	4.20E-04	Up	2.83E+00	9.31E-02		2.41E+00	9.58E-03		2.27E+00	2.08E-02		-1.10E+00	1.49E-01		-2.66E-01	6.93E-01				Unigene110413_All//7.00E-07//DN803899				
Unigene110414_All	598	0.00	0.00	0.00	0.00	0.00	0.00	3.82	5.94	0.13	null	null		null	null		null	null		null	null		6.38E-01	2.95E-02		-4.84E+00	3.22E-14	Down	Unigene110414_All//gi|238014838|gb|ACR38454.1|//2.00E-13//unknown [Zea mays]		Unigene110414_All//4.00E-27//ES850594				nr -
Unigene110418_All	301	0.00	0.00	0.00	0.00	0.00	0.00	1.83	0.00	0.40	null	null		null	null		null	null		null	null		-1.08E+01	4.62E-04	Down	-2.20E+00	2.24E-02								
Unigene11042_All	6962	6.76	4.24	4.16	15.66	14.53	12.62	17.51	5.15	8.70	-6.75E-01	6.42E-18		-7.01E-01	2.56E-18		-1.08E-01	3.72E-02		-3.11E-01	5.86E-11		-1.77E+00	1.50E-256	Down	-1.01E+00	5.13E-112	Down	Unigene11042_All|gi|225438627|ref|XP_002276798.1|//0.00E+00//PREDICTED: similar to binding [Vitis vinifera]	Unigene11042_All//0.00E+00//AT2G22125| binding	Unigene11042_All//0.00E+00//TC133396			GO:0003824	nr -
Unigene110421_All	263	0.00	0.00	0.00	0.00	0.00	0.00	3.38	0.64	0.30	null	null		null	null		null	null		null	null		-2.41E+00	1.79E-03		-3.48E+00	7.34E-05	Down	Unigene110421_All|gi|255071745|ref|XP_002499547.1|//8.00E-29//ribosomal protein L37e [Micromonas sp. RCC299] >gi|226514809|gb|ACO60805.1| ribosomal protein L37e [Micromonas sp. RCC299]	Unigene110421_All//2.00E-28//AT1G52300| 60S ribosomal protein L37 (RPL37B)			ko03010|Ribosome		nr -
Unigene110427_All	413	0.51	0.00	0.26	0.24	0.33	0.44	1.54	0.20	0.00	-8.99E+00	1.23E-01		-9.74E-01	6.21E-01		4.68E-01	8.78E-01		8.59E-01	6.96E-01		-2.92E+00	4.20E-03		-1.06E+01	7.12E-05	Down							
Unigene110428_All	340	0.00	0.00	0.00	0.29	0.00	0.00	3.36	0.49	0.12	null	null		null	null		-8.19E+00	3.16E-01		-8.19E+00	4.04E-01		-2.77E+00	7.62E-05	Down	-4.84E+00	2.34E-07	Down	Unigene110428_All//gi|75100616|sp|Q82318.1|Y2579_ARATH//2.00E-13//RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase At2g25790; Flags: Precursor >gi|224589523|gb|ACN59295.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene110428_All//7.00E-12//AT2G25790| leucine-rich repeat transmembrane protein kinase, putative	Unigene110428_All//7.00E-92//TC179552		ko04626|Plant-pathogen interaction		nr +
Unigene110437_All	310	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.13	0.13	null	null		null	null		null	null		null	null		-3.92E+00	9.81E-04	Down	-3.99E+00	5.82E-04	Down							
Unigene110439_All	592	0.00	0.00	0.00	0.00	0.00	0.00	3.43	1.84	0.34	null	null		null	null		null	null		null	null		-9.01E-01	2.61E-02		-3.35E+00	5.75E-10	Down							
Unigene110440_All	473	0.00	0.00	0.00	0.21	0.07	0.00	3.49	0.00	0.25	null	null		null	null		-1.53E+00	5.88E-01		-7.72E+00	4.04E-01		-1.18E+01	1.09E-11	Down	-3.79E+00	5.22E-09	Down	Unigene110440_All|gi|240255605|ref|NP_001030839.5|//2.00E-39//ET01 (ETHYLENE OVERPRODUCER 1); protein binding, bridging [Arabidopsis thaliana]	Unigene110440_All//2.00E-40//AT3G51770| ET01 (ETHYLENE OVERPRODUCER 1); protein binding, bridging					nr -
Unigene110441_All	407	30.34	8.59	12.82	40.88	19.12	10.43	10.39	7.70	4.60	-1.82E+00	9.37E-23	Down	-1.24E+00	1.11E-12	Down	-1.10E+00	1.51E-17	Down	-1.97E+00	1.37E-36	Down	-4.32E-01	1.13E-01		-1.18E+00	7.98E-06	Down			Unigene110441_All//3.00E-70//TC171513				
Unigene110443_All	310	0.34	0.00	0.86	0.80	0.22	0.29	1.64	0.81	0.00	-8.40E+00	3.76E-01		1.35E+00	4.09E-01		-1.85E+00	2.76E-01		-1.46E+00	4.07E-01		-1.02E+00	2.88E-01		-1.07E+01	5.55E-04	Down							

Unigene110444_All	380	0.14	0.00	0.42	3.80	2.54	1.55	9.35	4.18	1.05	-7.11E+00	6.18E-01		1.61E+00	5.12E-01		-5.83E-01	2.98E-01		-1.30E+00	2.16E-02		-1.16E+00	9.24E-05	Down	-3.16E+00	4.42E-16	Down	Unigene110444_All//gi|4733946|gb|AAD28641.1|/6.00E-17//sucrose synthase [Gossypium hirsutum]	Unigene110444_All//1.00E-14//AT4G02280| SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups	Unigene110444_All//3.00E-54//TC150792		ko00500|Starch and sucrose metabolism		nr -
Unigene110445_All	568	0.00	0.00	0.00	0.09	0.06	0.00	4.09	0.88	0.56	null	null		null	null		-5.33E-01	8.28E-01		-6.45E+00	6.43E-01		-2.21E+00	2.77E-07	Down	-2.87E+00	7.21E-10	Down			Unigene110445_All//2.00E-145//TC132634					
Unigene110447_All	459	0.00	0.00	0.00	0.00	0.00	0.00	1.66	0.00	0.09	null	null		null	null		null	null		null	null		-1.07E+01	1.68E-05	Down	-4.26E+00	8.66E-05	Down	Unigene110447_All//gi|300265162|gb|EFJ49355.1|//4.00E-29//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene110447_All//3.00E-27//AT3G25520| ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); 5S rRNA binding / structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene110448_All	310	1.01	0.98	0.34	0.16	0.56	0.29	2.86	0.40	0.64	-4.63E-02	9.85E-01		-1.56E+00	3.30E-01		1.79E+00	5.21E-01		8.59E-01	7.96E-01		-2.82E+00	5.65E-04	Down	-2.16E+00	2.68E-03		Unigene110448_All//gi|12322008|gb|AAG51046.1|AC069473_8//1.00E-21//gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] >gi|109981388|dbj|BAB93109.1| retroelement pol polyprotein [Arabidopsis thaliana]						nr -
Unigene110449_All	324	0.00	0.00	0.00	0.00	0.21	0.00	2.87	9.55	6.89	null	null		null	null		7.73E+00	6.14E-01		null	null		1.73E+00	4.69E-07	Up	1.26E+00	9.46E-04	Up		Unigene110449_All//2.00E-65//AT5G18170| GDH1 (GLUTAMATE DEHYDROGENASE 1); ATP binding / glutamate dehydrogenase [NAD(P)+]/ oxidoreductase	Unigene110449_All//8.00E-64//EST91234		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		kegg -
Unigene11045_All	547	0.67	1.76	0.97	0.18	0.82	2.15	1.47	1.15	1.68	1.39E+00	5.77E-02		5.40E-01	6.10E-01		2.17E+00	1.06E-01		3.56E+00	4.10E-05	Up	-3.58E-01	6.49E-01		1.90E-01	7.54E-01		Unigene11045_All//gi|30679594|ref|NP_195851.2|//6.00E-74//PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene11045_All//3.00E-75//AT5G02310| PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase				GO:0019787//GO:0046914	nr -
Unigene110450_All	282	0.00	0.00	0.00	0.00	0.00	0.00	2.25	0.15	0.42	null	null		null	null		null	null		null	null		-3.92E+00	9.81E-04	Down	-2.41E+00	8.12E-03		Unigene110450_All//sp|P26262|KLKB1_MOUSE//5.00E-06//Plasma kallikrein OS=Mus musculus GN=Klkb1 PE=1 SV=1						swissprot -
Unigene110451_All	576	0.00	0.00	0.00	0.17	0.24	0.16	6.61	10.67	24.42	null	null		null	null		4.67E-01	8.78E-01		-1.42E-01	9.52E-01		6.91E-01	1.12E-03		1.89E+00	1.20E-33	Up	Unigene110451_All//gi|115483761|ref|NP_001065542.1|//6.00E-38//Os11g0106900 [Oryza sativa Japonica Group] >gi|115486902|ref|NP_001065938.1| Os12g0106200 [Oryza sativa Japonica Group] >gi|113644246|dbj|BAF27387.1| Os11g0106900 [Oryza sativa Japonica Group] >gi|113648445|dbj|BAF28957.1| Os12g0106200 [Oryza sativa Japonica Group]	Unigene110451_All//4.00E-31//AT1G07900| LBD1 (LOB DOMAIN-CONTAINING PROTEIN 1)	Unigene110451_All//0.00E+00//TC178840		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene110458_All	774	0.00	0.00	0.14	0.13	0.09	0.41	5.79	0.38	2.11	null	null		7.10E+00	4.02E-01		-5.32E-01	8.19E-01		1.67E+00	3.09E-01		-3.94E+00	2.86E-23	Down	-1.46E+00	3.57E-08	Down	Unigene110458_All//gi|57222232|gb|AAK39023.1|//2.00E-78//At3g27230 [Arabidopsis thaliana] >gi|63003758|gb|AAY25408.1| At3g27230 [Arabidopsis thaliana]	Unigene110458_All//4.00E-82//AT5G40830| methyltransferase	Unigene110458_All//3.00E-56//gi|48744105|gb|CO074624.1|CO074624				nr -
Unigene110459_All	490	0.00	0.00	0.00	0.00	0.00	0.00	15.19	1.11	0.41	null	null		null	null		null	null		null	null		-3.78E+00	4.05E-37	Down	-5.22E+00	4.72E-47	Down	Unigene110459_All//gi|5080804|gb|AAD39313.1|AC007258_2//3.00E-29//Hypothetical protein [Arabidopsis thaliana] >gi|15010642|gb|AAK73980.1| At1g59710/T30E16_31 [Arabidopsis thaliana] >gi|22137290|gb|AAM91490.1| At1g59710/T30E16_31 [Arabidopsis thaliana]	Unigene110459_All//2.00E-30//AT1G59710| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27100.1); Has 119 Blast hits to 107 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 119; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene110459_All//2.00E-59//TC162219				nr +
Unigene110461_All	241	7.82	10.72	15.02	15.50	3.57	13.87	1.23	1.39	0.66	4.56E-01	2.50E-01		9.43E-01	5.28E-03		-2.12E+00	1.11E-10	Down	-1.61E-01	6.52E-01		1.76E-01	8.81E-01		-8.93E-01	4.71E-01				Unigene110461_All//7.00E-42//gi|78341252|gb|DT561526.1|DT561526					
Unigene110465_All	613	0.00	0.00	0.00	0.00	0.00	0.00	3.10	0.48	0.00	null	null		null	null		null	null		null	null		-2.70E+00	1.87E-07	Down	-1.16E+01	4.91E-14	Down								ESTscan +
Unigene110470_All	539	0.00	0.00	0.00	0.18	0.00	0.00	3.22	0.16	0.30	null	null		null	null		-7.53E+00	3.16E-01		-7.53E+00	4.04E-01		-4.37E+00	6.16E-10	Down	-3.44E+00	8.42E-09	Down								
Unigene110474_All	270	0.00	0.00	0.00	0.00	0.00	0.00	2.35	0.46	0.00	null	null		null	null		null	null		null	null		-2.34E+00	1.27E-02		-1.12E+01	7.12E-05	Down	Unigene110474_All//gi|81237625|gb|AAX77224.2|//3.00E-17//14-3-3 protein [Dunaliella salina] >gi|157062258|gb|ABV03825.1| 14-3-3 protein [Dunaliella salina]	Unigene110474_All//1.00E-15//AT5G38480| GRF3 (GENERAL REGULATORY FACTOR 3); ATP binding / protein binding / protein phosphorylated amino acid binding	Unigene110474_All//9.00E-20//DV849765				nr -
Unigene110478_All	495	0.00	0.00	0.00	0.00	0.21	0.00	4.27	1.60	0.08	null	null		null	null		7.71E+00	4.58E-01		null	null		-1.41E+00	5.54E-04	Down	-5.73E+00	3.61E-14	Down	Unigene110478_All//gi|224365602|gb|ACN41354.1|//6.00E-30//LR34 [Triticum aestivum]	Unigene110478_All//2.00E-30//AT2G37280| PDR5 (PLEIOTROPIC DRUG RESISTANCE 5); ATPase, coupled to transmembrane movement of substances					nr +
Unigene110483_All	330	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.13	0.00	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-1.11E+01	1.78E-05	Down	Unigene110483_All//gi|195640868|gb|ACG39902.1|//6.00E-08//36.4 kDa proline-rich protein [Zea mays]				ko04626|Plant-pathogen interaction//ko03040|Spliceosome		nr +
Unigene110484_All	617	0.00	0.00	0.00	0.00	0.00	0.00	3.84	0.41	0.13	null	null		null	null		null	null		null	null		-3.24E+00	8.82E-11	Down	-4.89E+00	8.31E-15	Down	Unigene110484_All//gi|299471658|emb|CBN76880.1|//1.00E-27//chp-1 / RAR1 homologue [Ectocarpus siliculosus]	Unigene110484_All//3.00E-13//AT5G51700| PBS2 (PPHB SUSCEPTIBLE 2); protein binding / zinc ion binding			ko04626|Plant-pathogen interaction		nr -
Unigene110487_All	250	6.91	15.00	8.95	32.88	27.00	30.71	4.40	3.51	4.14	1.12E+00	5.36E-04	Up	3.73E-01	3.96E-01		-2.84E-01	1.77E-01		-9.83E-02	6.90E-01		-3.25E-01	6.15E-01		-8.58E-02	8.84E-01				Unigene110487_All//4.00E-43//TC161899					
Unigene11049_All	4497	0.15	0.18	0.31	0.22	0.25	0.15	0.75	1.68	1.02	2.54E-01	7.26E-01		1.03E+00	8.63E-02		1.46E-01	8.37E-01		-5.57E-01	4.47E-01		1.16E+00	3.12E-09	Up	4.38E-01	7.78E-02		Unigene11049_All//gi|30679594|ref|NP_195851.2|//0.00E+00//PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene11049_All//0.00E+00//AT5G02310| PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase	Unigene11049_All//0.00E+00//TC138549			GO:0003824	nr -
Unigene110496_All	295	0.00	0.00	0.00	0.00	0.00	0.00	1.72	0.00	0.00	null	null		null	null		null	null		null	null		-1.07E+01	8.90E-04	Down	-1.07E+01	5.55E-04	Down	Unigene110496_All//gi|226347409|gb|ACO50115.1|//2.00E-42//elongation factor 1 alpha [Peranema trichophorum]	Unigene110496_All//4.00E-32//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene110496_All//6.00E-18//TC129595				nr -
Unigene110501_All	307	0.34	0.50	0.17	0.32	0.00	0.00	7.99	4.36	0.91	5.38E-01	7.80E-01		-9.74E-01	7.22E-01		-8.34E+00	3.16E-01		-8.34E+00	4.04E-01		-8.75E-01	1.57E-02		-3.14E+00	2.96E-11	Down			Unigene110501_All//7.00E-21//TC152267					
Unigene110505_All	410	0.00	0.00	0.00	0.00	0.00	0.00	2.47	3.06	0.00	null	null		null	null		null	null		null	null		3.05E-01	6.11E-01		-1.13E+01	1.35E-07	Down	Unigene110505_All//gi|20140684|sp|Q94486.1|TCTP_BRAOL//6.00E-13//RecName: Full=Translationally-controlled tumor protein homolog; Short=TCTP >gi|16033628|gb|AAL13303.1|AF418663_1 translationally controlled tumor protein [Brassica oleracea]	Unigene110505_All//1.00E-11//AT3G16640| TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN)					nr -
Unigene11051_All	1128	1.67	3.59	3.92	3.71	4.15	5.53	8.32	13.04	23.42	1.11E+00	3.41E-04	Up	1.23E+00	6.31E-05	Up	1.63E-01	6.07E-01		5.75E-01	1.56E-02		6.48E-01	6.26E-07		1.49E+00	4.13E-45	Up	Unigene11051_All//gi|190148357|gb|ACE63261.1|//0.00E+00//histidine kinase 3 [Betula pendula]	Unigene11051_All//2.00E-169//AT1G27320| AHK3 (ARABIDOPSIS HISTIDINE KINASE 3); cytokinin receptor/ osmosensor/ protein histidine kinase	Unigene11051_All//0.00E+00//TC179474	Orphans		GO:0004673//GO:0004871//GO:0006351//GO:0006468//GO:0023060//GO:0032559//GO:0044464	nr -
Unigene110515_All	765	0.00	0.00	0.00	0.00	0.00	0.00	0.88	0.66	2.40	null	null		null	null		null	null		null	null		-4.32E-01	6.12E-01		1.44E+00	9.58E-04	Up	Unigene110515_All//gi|300157379|gb|EFJ24005.1|//2.00E-62//ubiquitin-protein ligase, PUB17 [Selaginella moellendorffii]	Unigene110515_All//5.00E-48//AT3G54850| PUB14; ubiquitin-protein ligase			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene110516_All	625	0.00	0.00	0.00	0.00	0.00	0.00	2.23	0.40	0.57	null	null		null	null		null	null		null	null		-2.48E+00	3.36E-05	Down	-1.96E+00	2.74E-04	Down	Unigene110516_AllI//gi|223452532|gb|ACM89593.1|//5.00E-86//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene110516_AllI//7.00E-81//AT1G34110| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction		nr +
Unigene110052_All	3040	6.06	10.78	10.44	10.67	13.99	16.61	18.26	29.52	38.27	8.32E-01	7.03E-18		7.85E-01	3.54E-15		3.91E-01	2.39E-07		6.39E-01	1.61E-18		6.93E-01	1.08E-42		1.07E+00	1.74E-116	Up	Unigene11052_All//gi|190148357|gb|ACE63261.1|//0.00E+00//histidine kinase 3 [Betula pendula]	Unigene11052_All//0.00E+00//AT1G27320| AHK3 (ARABIDOPSIS HISTIDINE KINASE 3); cytokinin receptor/ osmosensor/ protein histidine kinase	Unigene11052_All//0.00E+00//TC179474	Orphans	ko04712|Circadian rhythm - plant	GO:0004673//GO:0004888//GO:0006351//GO:0006468//GO:0006826//GO:0006952//GO:0006970//GO:0009267//GO:0009409//GO:0009737//GO:0009744//GO:0009755//GO:0009845//GO:0009888//GO:0009908//GO:0010260//GO:0015996//GO:0016020//GO:0016791//GO:0019901//GO:0023060//GO:0032559//GO:0040007//GO:2000026	nr +
Unigene110524_All	493	0.00	0.00	0.00	0.00	0.00	0.00	5.15	0.17	0.00	null	null		null	null		null	null		null	null		-4.92E+00	2.81E-15	Down	-1.23E+01	1.14E-18	Down	Unigene110524_All//gi|297824403|ref|XP_002880084.1|//9.00E-59//60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata] >gi|297325923|gb|EFH56343.1| 60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata]	Unigene110524_All//5.00E-60//AT2G44120| 60S ribosomal protein L7 (RPL7C)	Unigene110524_All//4.00E-08//TC131081		ko03010|Ribosome		nr +
Unigene110529_All	522	0.00	0.00	0.00	0.00	0.00	0.00	2.27	0.32	0.00	null	null		null	null		null	null		null	null		-2.82E+00	4.41E-05	Down	-1.11E+01	8.15E-09	Down	Unigene110529_All//gi|159462862|ref|XP_001689661.1|//2.00E-60//calreticulin 2, calcium-binding protein [Chlamydomonas reinhardtii] >gi|11131843|sp|Q9STD3.1|CALR_CHLRE RecName: Full=Calreticulin; Flags: Precursor >gi|5830186|emb|CAB54526.1| calreticulin [Chlamydomonas reinhardtii] >gi|158283649|gb|EDP09399.1| calreticulin 2, calcium-binding protein [Chlamydomonas reinhardtii]	Unigene110529_All//6.00E-43//AT1G09210| calreticulin 2 (CRT2)			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr -
Unigene110053_All	4147	4.24	20.22	13.02	5.57	12.81	14.22	4.83	12.00	18.52	2.25E+00	5.43E-198	Up	1.62E+00	4.91E-80	Up	1.20E+00	5.78E-61	Up	1.35E+00	9.49E-74	Up	1.31E+00	4.72E-68	Up	1.94E+00	5.18E-187	Up	Unigene11053_All//gi|190148361|gb|ACE63263.1|//0.00E+00//histidine kinase 3B [Populus trichocarpa]	Unigene11053_All//0.00E+00//AT1G27320| AHK3 (ARABIDOPSIS HISTIDINE KINASE 3); cytokinin receptor/ osmosensor/ protein histidine kinase	Unigene11053_All//0.00E+00//ES839435	Orphans		GO:0004673//GO:0004888//GO:0006351//GO:0006468//GO:0006826//GO:0006952//GO:0006970//GO:0009267//GO:0009409//GO:0009737//GO:0009744//GO:0009755//GO:0009845//GO:0009888//GO:0009908//GO:0010260//GO:0015996//GO:0016020//GO:0016791//GO:0019901//GO:0023060//GO:0032559//GO:0040007//GO:0043231//GO:2000026	nr -
Unigene110536_All	496	0.00	0.00	0.00	0.00	0.00	0.00	2.30	0.42	0.00	null	null		null	null		null	null		null	null		-2.45E+00	2.46E-04	Down	-1.12E+01	1.65E-08	Down	Unigene110536_All//gi|186898205|gb|ACC93947.1|//4.00E-58//heat-shock protein 70 [Hevea brasiliensis]	Unigene110536_All//5.00E-55//AT5G09440| heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	Unigene110536_All//4.00E-23//ES849176		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -

Unigene110537_All	360	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	3.27E-05	Down	-1.10E+01	1.78E-05	Down	Unigene110537_All//gi|299470507|emb|CBN78498.1|//3.00E-07//carnitine/acylcarnitine carrier protein [Ectocarpus siliculosus]	Unigene110537_All//5.00E-05//AT1G25380| mitochondrial substrate carrier family protein					nr -
Unigene110539_All	1050	0.00	0.00	0.00	0.00	0.09	6.85	0.08	0.46	null	null		null	null		null	null		6.43E+00	4.80E-01		-6.43E+00	2.00E-47	Down	-3.91E+00	3.94E-38	Down	Unigene110539_All//gi|194136583|gb|ACF33514.1|//6.00E-81//salicylic acid methyl transferase-like protein [Glycine max]	Unigene110539_All//2.00E-75//AT5G38020| S-adenosyl-L-methionine:carboxyl methyltransferase family protein			ko00592|alpha-Linolenic acid metabolism		nr -
Unigene110054_All	4216	6.17	8.81	6.64	9.23	9.62	10.71	15.08	29.40	52.60	5.14E-01	4.58E-09		1.07E-01	3.91E-01		6.03E-02	5.79E-01		2.15E-01	8.17E-03		9.63E-01	1.29E-102		1.80E+00	0.00E+00	Up	Unigene110054_All//gi|190148357|gb|ACE83261.1|//0.00E+00//histidine kinase 3 [Betula pendula]	Unigene110054_All//0.00E+00//AT1G27320| AHK3 (ARABIDOPSIS HISTIDINE KINASE 3); cytokinin receptor/ osmosensor/ protein histidine kinase	Unigene110054_All//0.00E+00//TC179474	Orphans	ko04712|Circadian rhythm - plant	GO:0004673//GO:0004888//GO:0006351//GO:0006468//GO:0006826//GO:0006952//GO:0006970//GO:0009267//GO:0009409//GO:0009737//GO:0009744//GO:0009755//GO:0009845//GO:0009888//GO:0009908//GO:0010260//GO:0015996//GO:0016020//GO:0016791//GO:0019901//GO:0023060//GO:0032559//GO:0040007//GO:2000026	nr +
Unigene110543_All	303	0.00	0.00	0.00	0.00	0.00	0.00	2.37	0.69	0.00	null	null		null	null		null	null		null	null		-1.78E+00	2.79E-02		-1.12E+01	1.78E-05	Down							
Unigene110544_All	530	0.00	0.00	0.00	0.00	0.00	0.00	3.03	2.21	0.00	null	null		null	null		null	null		null	null		-4.57E-01	3.54E-01		-1.16E+01	7.00E-12	Down	Unigene110544_All//gi|145353601|ref|XP_001421096.1|//3.00E-58//Receptor of activated protein kinase C 1A, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|145357301|ref|XP_001422858.1| Receptor of activated protein kinase C 1B, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|144581332|gb|ABO99389.1| Receptor of activated protein kinase C 1A, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|144583102|gb|ABP01217.1| Receptor of activated protein kinase C 1B, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901]	Unigene110544_All//1.00E-52//AT1G48630| RACK1B_AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding	Unigene110544_All//2.00E-13//gi|78353144|gb|DT573418.1|DT573418		ko03040|Spliceosome//ko03022|Basal transcription factors		nr -
Unigene110545_All	642	0.00	0.00	0.00	0.00	0.00	0.00	6.72	7.62	0.74	null	null		null	null		null	null		null	null		1.81E-01	5.18E-01		-3.17E+00	1.79E-19	Down							
Unigene110546_All	416	0.00	0.00	0.00	0.00	0.00	0.11	6.20	0.10	0.29	null	null		null	null		null	null		6.76E+00	7.02E-01		-5.95E+00	9.35E-17	Down	-4.43E+00	3.02E-15	Down	Unigene110546_All//gi|224141527|ref|XP_002324121.1|//9.00E-20//ABC transporter family protein [Populus trichocarpa] >gi|222867123|gb|EEF04254.1| ABC transporter family protein [Populus trichocarpa]	Unigene110546_All//2.00E-19//AT5G39040| ATTAP2: ATPase, coupled to transmembrane movement of substances / transporter	Unigene110546_All//1.00E-10//TC135398				nr -
Unigene110549_All	441	0.83	0.00	0.00	0.23	1.09	0.00	1.73	0.00	0.90	-9.70E+00	1.97E-02		-9.70E+00	2.79E-02		2.27E+00	7.83E-02		-7.82E+00	4.04E-01		-1.08E+01	1.68E-05	Down	-9.34E-01	1.82E-01		Unigene110549_All//gi|145336239|ref|NP_174256.2|//6.00E-62//nuclease [Arabidopsis thaliana]	Unigene110549_All//4.00E-63//AT1G29630| nuclease			ko03430|Mismatch repair		nr +
Unigene110551_All	1188	0.00	0.00	0.00	0.00	0.00	0.00	3.45	0.32	0.50	null	null		null	null		null	null		null	null		-3.45E+00	3.04E-19	Down	-2.78E+00	2.48E-16	Down	Unigene110551_All//gi|297824859|ref|XP_002880312.1|//1.00E-120//pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326151|gb|EFH56571.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene110551_All//3.00E-112//AT1G02810| pectinesterase family protein	Unigene110551_All//0.00E+00//TC135702		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene110553_All	315	0.00	0.00	0.00	0.00	0.00	0.00	2.42	0.40	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.81E-03		-1.12E+01	8.88E-06	Down	Unigene110553_All//gi|160339969|ref|XP_001712192.1|//7.00E-29//ef2 [Hemiselmis andersenii] >gi|159765639|gb|ABW97867.1| ef2 [Hemiselmis andersenii]	Unigene110553_All//1.00E-27//AT1G56070| LOS1: copper ion binding / translation elongation factor/ translation factor, nucleic acid binding					nr +
Unigene110056_All	3466	102.74	46.09	56.15	159.60	157.59	105.74	45.12	12.71	16.28	-1.16E+00	0.00E+00	Down	-8.72E-01	2.89E-197		-1.83E-02	5.30E-01		-5.94E-01	4.55E-175		-1.83E+00	0.00E+00	Down	-1.47E+00	4.03E-260	Down	Unigene110056_All//gi|297825203|ref|XP_002880484.1|//0.00E+00//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326323|gb|EFH56743.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene110056_All//0.00E+00//AT2G23140| binding / ubiquitin-protein ligase	Unigene110056_All//0.00E+00//TC140444		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0016874	nr -
Unigene110561_All	249	0.00	0.00	0.00	0.00	0.00	0.00	3.40	0.34	0.32	null	null		null	null		null	null		null	null		-3.34E+00	2.51E-04	Down	-3.41E+00	1.35E-04	Down	Unigene110561_All//gi|44662866|gb|AAS47512.1|//1.00E-12//ribosomal protein L37 [Glycine max]				ko03010|Ribosome		nr -
Unigene110569_All	534	0.00	0.00	0.00	0.00	0.00	0.00	3.09	0.39	0.37	null	null		null	null		null	null		null	null		-2.98E+00	3.67E-07	Down	-3.05E+00	1.31E-07	Down	Unigene110569_All//gi|300266999|gb|EFJ51184.1|//3.00E-32//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene110569_All//5.00E-31//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)			ko03010|Ribosome		nr +
Unigene110057_All	2242	0.68	0.59	0.81	1.78	1.61	1.47	3.15	5.33	13.93	-2.04E-01	6.81E-01		2.55E-01	6.40E-01		-1.40E-01	6.82E-01		-2.74E-01	4.20E-01		7.60E-01	2.28E-07		2.15E+00	4.10E-87	Up	Unigene110057_All//gi|297825203|ref|XP_002880484.1|//1.00E-159//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326323|gb|EFH56743.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene110057_All//3.00E-150//AT2G23140| binding / ubiquitin-protein ligase	Unigene110057_All//0.00E+00//gi|78340263|gb|DT560537.1|DT560537				nr +
Unigene110571_All	1033	0.05	0.00	0.00	0.14	0.13	0.04	5.69	0.73	0.73	-5.66E+00	6.18E-01		-5.66E+00	6.31E-01		-1.18E-01	9.11E-01		-1.73E+00	5.02E-01		-2.97E+00	8.14E-24	Down	-2.96E+00	1.42E-24	Down	Unigene110571_All//gi|9759032|dbj|BAB09401.1|//1.00E-127//transmembrane transport protein-like [Arabidopsis thaliana]	Unigene110571_All//1.00E-110//AT5G50300| xanthine/uracil/vitamin C permease family protein					nr +
Unigene110572_All	388	0.27	0.39	0.69	1.67	0.18	0.81	1.85	0.86	0.10	5.39E-01	7.80E-01		1.35E+00	4.09E-01		-3.23E+00	2.49E-03		-1.03E+00	2.68E-01		-1.10E+00	1.49E-01		-4.17E+00	1.65E-04	Down	Unigene110572_All//gi|297836510|ref|XP_002886137.1|//2.00E-65//FAT domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331977|gb|EFH62396.1| FAT domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene110572_All//1.00E-66//AT4G36080| FAT domain-containing protein / phosphatidylinositol 3- and 4-kinase family protein	Unigene110572_All//0.00E+00//C0110904				nr +
Unigene110575_All	668	0.00	0.00	0.00	0.00	0.00	0.00	2.22	0.44	0.42	null	null		null	null		null	null		null	null		-2.34E+00	3.57E-05	Down	-2.41E+00	1.48E-05	Down	Unigene110575_All//gi|183229550|gb|ACC60273.1|//2.00E-55//aluminum-activated malate transporter [Glycine max]	Unigene110575_All//6.00E-53//AT3G11680| unknown protein					nr -
Unigene110577_All	595	0.00	0.00	0.00	0.00	0.00	0.00	2.49	0.56	0.33	null	null		null	null		null	null		null	null		-2.15E+00	9.69E-05	Down	-2.89E+00	1.35E-06	Down	Unigene110577_All//gi|146454508|gb|ABQ41920.1|//4.00E-45//60S ribosomal protein large subunit 9 [Sonneratia alba] >gi|156633690|gb|ABU90844.1| ribosomal protein L9 [Sonneratia alba] >gi|156633692|gb|ABU90845.1| ribosomal protein L9 [Sonneratia alba] >gi|156633694|gb|ABU90846.1| ribosomal protein L9 [Sonneratia alba] >gi|156633696|gb|ABU90847.1| ribosomal protein L9 [Sonneratia alba] >gi|156633698|gb|ABU90848.1| ribosomal protein L9 [Sonneratia alba] >gi|156633700|gb|ABU90849.1| ribosomal protein L9 [Sonneratia alba] >gi|156633702|gb|ABU90850.1| ribosomal protein L9 [Sonneratia alba] >gi|156633704|gb|ABU90851.1| ribosomal protein L9 [Sonneratia alba] >gi|156633706|gb|ABU90852.1| ribosomal protein L9 [Sonneratia alba] >gi|156633708|gb|ABU90853.1| ribosomal protein L9 [Sonneratia alba] >gi|156633710|gb|ABU90854.1| ribosomal protein L9 [Sonneratia alba] >gi|156633712|gb|ABU90855.1| ribosomal protein L9 [Sonneratia alba] >gi|156633714|gb|ABU90856.1| ribosomal protein L9 [Sonneratia	Unigene110577_All//2.00E-42//AT1G33140| PGY2 (PIGGYBACK2); structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene110578_All	677	0.00	2.25	0.31	0.74	0.36	0.00	1.44	0.86	0.94	1.11E+01	1.10E-08	Up	8.30E+00	1.42E-01		-1.05E+00	3.15E-01		-9.52E+00	2.98E-03		-7.33E-01	2.48E-01		-6.09E-01	3.16E-01				Unigene110578_All//1.00E-08//FL576999					
Unigene110579_All	366	2.14	2.91	1.45	3.27	3.01	3.95	8.78	16.10	18.72	4.39E-01	5.07E-01		-5.60E-01	4.96E-01		-1.18E-01	8.27E-01		2.74E-01	6.49E-01		8.75E-01	6.26E-05		1.09E+00	6.01E-08	Up			Unigene110579_All//6.00E-74//TC142193					
Unigene110582_All	448	0.00	0.00	0.00	0.11	0.00	0.00	3.87	1.96	0.44	null	null		null	null		-6.80E+00	5.62E-01		-6.80E+00	6.43E-01		-9.82E-01	2.77E-02		-3.12E+00	3.99E-08	Down			Unigene110582_All//0.00E+00//gi|109883187|gb|DW512157.1|DW512157					ESTscan +
Unigene110583_All	278	0.00	0.00	0.00	0.00	0.00	0.00	1.83	0.00	0.00	null	null		null	null		null	null		null	null		-1.08E+01	8.90E-04	Down	-1.08E+01	5.55E-04	Down	Unigene110583_All//gi|159474294|ref|XP_001695264.1|//1.00E-16//heat shock protein 90A [Chlamydomonas reinhardtii] >gi|158276198|gb|EDP01972.1| heat shock protein 90A [Chlamydomonas reinhardtii]	Unigene110583_All//3.00E-13//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene110597_All	438	0.00	0.00	0.00	0.00	0.00	0.00	2.32	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	2.97E-07	Down	-1.12E+01	1.35E-07	Down							ESTscan -
Unigene110598_All	252	0.00	0.00	0.00	0.00	0.00	0.00	1.68	13.27	1.26	null	null		null	null		null	null		null	null		2.98E+00	7.53E-14	Up	-4.08E-01	6.54E-01								
Unigene110604_All	257	0.00	0.00	0.00	0.00	0.00	0.00	4.94	4.39	0.00	null	null		null	null		null	null		null	null		-1.69E-01	7.53E-01		-1.23E+01	1.99E-09	Down	Unigene110604_All//gi|27450759|gb|AA014682.1|AF508263_1//7.00E-20//actin [Pyrocystis lunula]	Unigene110604_All//2.00E-20//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene110604_All//1.00E-21//gi|31406833|gb|CD485868.1|CD485868		ko04145|Phagosome		nr -
Unigene110606_All	447	0.00	0.00	0.00	0.00	0.00	0.00	1.23	0.19	0.00	null	null		null	null		null	null		null	null		-2.72E+00	1.22E-02		-1.03E+01	2.81E-04	Down	Unigene110606_All//gi|297842159|ref|XP_002888961.1|//2.00E-16//60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata] >gi|297334802|gb|EFH65220.1| 60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata]	Unigene110606_All//1.00E-10//AT1G74060| 60S ribosomal protein L6 (RPL6B)	Unigene110606_All//8.00E-09//TC147093		ko03010|Ribosome		nr +
Unigene110608_All	471	0.00	0.00	0.00	0.00	0.00	0.00	3.23	0.09	0.25	null	null		null	null		null	null		null	null		-5.19E+00	1.55E-09	Down	-3.67E+00	3.49E-08	Down	Unigene110608_All//gi|297812535|ref|XP_002874151.1|//5.00E-10//60S ribosomal protein L13 [Arabidopsis lyrata subsp. lyrata] >gi|297319988|gb|EFH50410.1| 60S ribosomal protein L13 [Arabidopsis lyrata subsp. lyrata]	Unigene110608_All//4.00E-11//AT5G23900| 60S ribosomal protein L13 (RPL13D)			ko03010|Ribosome		nr -

Unigene11061_All	3271	0.99	2.37	0.75	6.69	5.26	7.75	28.15	16.99	31.89	1.26E+00	1.01E-08	Up	-4.05E-01	2.71E-01		-3.45E-01	2.02E-03		2.12E-01	6.78E-02		-7.28E-01	9.34E-48		1.80E-01	6.51E-05		Unigene11061_All//gi|301119757|ref|XP_002907606.1|/1.00E-19//NUK6 [Phytophthora infestans T30-4] >gi|262106118|gb|EEY64170.1| NUK6 [Phytophthora infestans T30-4]	Unigene11061_All//4.00E-13//AT2G22795| unknown protein	Unigene11061_All//0.00E+00//TC174208				nr -
Unigene110614_All	427	0.00	0.00	0.00	0.00	0.00	0.00	1.78	0.10	0.09	null	null		null	null		null	null		null	null		-4.19E+00	1.58E-04	Down	-4.26E+00	8.66E-05	Down									
Unigene110616_All	533	0.00	0.00	0.00	0.00	0.00	0.00	4.84	0.24	0.00	null	null		null	null		null	null		null	null		-4.36E+00	1.54E-14	Down	-1.22E+01	5.57E-19	Down	Unigene110616_All//gi|301122321|ref|XP_002908887.1|/2.00E-40//40S ribosomal protein S10 [Phytophthora infestans T30-4] >gi|66270167|gb|AAY43413.1| ribosomal protein S10 [Phytophthora infestans] >gi|262099649|gb|EEY57701.1| 40S ribosomal protein S10 [Phytophthora infestans T30-4]	Unigene110616_All//2.00E-25//AT4G25740| 40S ribosomal protein S10 (RPS10A)			ko03010|Ribosome		nr -
Unigene110617_All	324	0.00	0.00	0.00	0.00	0.00	0.00	7.70	0.90	0.74	null	null		null	null		null	null		null	null		-3.09E+00	7.09E-11	Down	-3.38E+00	3.35E-12	Down									
Unigene110619_All	297	0.00	0.00	0.00	0.17	0.23	0.00	4.70	0.00	0.67	null	null		null	null		4.68E-01	9.60E-01		-7.39E+00	6.43E-01		-1.22E+01	6.58E-10	Down	-2.81E+00	4.26E-06	Down			Unigene110619_All//4.00E-13//gi|84168982|gb|DR457630.1|DR457630					
Unigene110062_All	2638	1.39	4.17	0.99	9.14	8.71	12.09	32.74	17.97	37.32	1.59E+00	8.95E-17	Up	-4.89E-01	1.48E-01		-7.00E-02	6.17E-01		4.03E-01	1.52E-05		-8.66E-01	3.59E-60		1.89E-01	4.62E-05		Unigene11062_All//gi|89357137|gb|ABD72304.1|/2.00E-24//apple fruit acidity-related protein [Malus x domestica]	Unigene11062_All//8.00E-26//AT2G22795| unknown protein	Unigene11062_All//0.00E+00//TC164203		ko03040|Spliceosome		nr +
Unigene110621_All	484	0.00	0.00	0.00	0.00	0.00	0.00	2.88	0.00	0.00	null	null		null	null		null	null		null	null		-1.15E+01	6.58E-10	Down	-1.15E+01	2.40E-10	Down	Unigene110621_All//gi|227206418|dbj|BAH57264.1|/3.00E-06//AT2G40070 [Arabidopsis thaliana]							nr +
Unigene110623_All	507	0.00	0.00	0.00	0.00	0.00	0.00	3.09	0.00	0.00	null	null		null	null		null	null		null	null		-1.16E+01	4.29E-11	Down	-1.16E+01	1.42E-11	Down	Unigene110623_All//gi|148727870|gb|ABR08570.1|/2.00E-08//proline-rich protein [Oryza sativa Japonica Group]	Unigene110623_All//5.00E-06//AT4G02270| pollen Ole e 1 allergen and extensin family protein	Unigene110623_All//6.00E-10//BG444324				nr -
Unigene110624_All	340	0.00	0.00	0.00	0.00	0.00	0.00	1.74	0.00	0.12	null	null		null	null		null	null		null	null		-1.08E+01	2.39E-04	Down	-3.89E+00	1.10E-03									ESTscan -
Unigene110625_All	313	0.00	0.00	0.00	0.00	0.00	0.00	2.16	0.27	0.00	null	null		null	null		null	null		null	null		-3.02E+00	2.43E-03		-1.11E+01	3.57E-05	Down	Unigene110625_All//gi|58801147|dbj|BAD88506.1|/5.00E-86//beta-tubulin [Protosaplina japonica]	Unigene110625_All//3.00E-38//AT5G62700| TUB3; GTP binding / GTPase/ structural molecule	Unigene110625_All//2.00E-18//gi|78323375|gb|DT543649.1|DT543649		ko04145|Phagosome		nr -
Unigene110626_All	264	11.10	1.34	3.63	13.59	15.13	8.72	4.16	2.37	1.81	-3.05E+00	2.74E-10	Down	-1.61E+00	7.17E-05	Down	1.55E-01	6.62E-01		-6.39E-01	5.07E-02		-8.10E-01	1.69E-01		-1.20E+00	3.41E-02				Unigene110626_All//5.00E-46//TC169420					
Unigene110629_All	373	0.00	0.00	0.00	0.00	0.00	0.00	2.15	0.56	0.00	null	null		null	null		null	null		null	null		-1.94E+00	1.17E-02		-1.11E+01	4.43E-06	Down			Unigene110629_All//7.00E-09//TC149074					ESTscan -
Unigene11063_All	7254	3.94	9.44	2.31	19.15	17.71	24.31	56.80	35.01	60.52	1.26E+00	1.06E-71	Up	-7.73E-01	2.39E-13		-1.13E-01	1.08E-02		3.45E-01	7.95E-21		-6.98E-01	3.61E-196		9.14E-02	2.05E-05		Unigene11063_All//gi|38344252|emb|CAE04334.2|/2.00E-41//OSJNBa0008M17.5 [Oryza sativa (japonica cultivar-group)]	Unigene11063_All//6.00E-18//AT5G40450| unknown protein	Unigene11063_All//0.00E+00//TC156877		ko03040|Spliceosome		nr +
Unigene110638_All	504	0.00	0.00	0.00	0.00	0.00	0.00	1.93	0.66	0.00	null	null		null	null		null	null		null	null		-1.54E+00	1.90E-02		-1.09E+01	2.72E-07	Down	Unigene110638_All//gi|255073061|ref|XP_002500205.1|/2.00E-23//profilin [Micromonas sp. RCC299] >gi|226515467|gb|ACO61463.1| profilin [Micromonas sp. RCC299]	Unigene110638_All//1.00E-14//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding					nr +
Unigene110640_All	365	0.00	0.00	0.00	0.14	0.00	0.00	2.20	0.69	0.33	null	null		null	null		-7.09E+00	5.62E-01		-7.09E+00	6.43E-01		-1.68E+00	2.46E-02		-2.75E+00	9.43E-04	Down			Unigene110640_All//3.00E-23//TC142576					
Unigene110644_All	399	0.00	0.00	0.00	0.00	0.00	0.00	1.80	0.10	0.20	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-3.17E+00	8.09E-04	Down	Unigene110644_All//gi|240254117|ref|NP_173393.5|/1.00E-35//CYP722A1: electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	Unigene110644_All//7.00E-37//AT1G19630| CYP722A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00906|Carotenoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene110647_All	316	0.00	0.00	0.00	0.00	0.00	0.00	2.41	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	1.68E-05	Down	-1.12E+01	8.88E-06	Down	Unigene110647_All//gi|11131946|sp|Q92XY3.1|CALR_EUGGR//3.00E-14//RecName: Full=Calreticulin; Flags: Precursor >gi|3970687|emb|CAA70945.1| calreticulin precursor [Euglena gracilis]	Unigene110647_All//2.00E-05//AT1G56340| CRT1 (CALRETICULIN 1); calcium ion binding / unfolded protein binding			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr -
Unigene110648_All	571	0.00	0.00	0.00	0.00	0.00	0.00	11.18	3.73	1.88	null	null		null	null		null	null		null	null		-1.58E+00	3.20E-12	Down	-2.57E+00	5.17E-23	Down	Unigene110648_All//gi|20197696|gb|AAM15209.1|/1.00E-14//senescence-associated protein [Arabidopsis thaliana] >gi|20197726|gb|AAM15226.1| senescence-associated protein [Arabidopsis thaliana]	Unigene110648_All//3.00E-16//AT2G21045| INVOLVED IN: aging; EXPRESSED IN: hypocotyl, root; CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66170.2); Has 1919 Blast hits to 1917 proteins in 542 species: Archae - 34; Bacteria - 1258; Metazoa - 17; Fungi - 21; Plants - 115; Viruses - 0; Other Eukaryotes - 474 (source: NCBI BLink).					nr +
Unigene110649_All	372	0.00	0.00	0.00	0.00	0.00	0.00	2.84	0.67	0.43	null	null		null	null		null	null		null	null		-2.08E+00	1.78E-03		-2.73E+00	1.12E-04	Down	Unigene110649_All//gi|116058914|emb|CAL54621.1|/9.00E-10//calcineurin B regulatory subunit (ISS) [Ostreococcus tauri]	Unigene110649_All//4.00E-07//AT5G37780| CAM1 (CALMODULIN 1); calcium ion binding			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene11065_All	1054	2.48	1.54	2.83	3.36	4.12	3.99	4.09	1.31	1.21	-6.90E-01	7.70E-02		1.89E-01	6.29E-01		2.95E-01	3.59E-01		2.48E-01	4.68E-01		-1.64E+00	6.08E-09	Down	-1.76E+00	4.29E-10	Down	Unigene11065_All//gi|115455129|ref|NP_001051165.1|/1.00E-126//Os03g0731500 [Oryza sativa Japonica Group] >gi|113549636|dbj|BAF13079.1| Os03g0731500 [Oryza sativa Japonica Group]	Unigene11065_All//2.00E-124//AT5G42620| metalloendopeptidase/ zinc ion binding	Unigene11065_All//9.00E-162//EE592770				nr -
Unigene110650_All	357	0.15	0.00	0.15	0.00	0.19	0.25	2.61	0.12	0.22	-7.20E+00	6.18E-01		2.54E-02	9.96E-01		7.59E+00	6.14E-01		7.98E+00	4.80E-01		-4.48E+00	1.30E-05	Down	-3.55E+00	3.97E-05	Down	Unigene110650_All//gi|222424691|dbj|BAH20299.1|/7.00E-26//AT5G25770 [Arabidopsis thaliana]	Unigene110650_All//9.00E-26//AT5G25770| unknown protein	Unigene110650_All//2.00E-77//gi|164318181|gb|ES792606.1|ES792606				nr +
Unigene110652_All	301	0.17	0.00	0.53	0.17	0.34	0.00	1.83	0.69	0.00	-7.44E+00	6.18E-01		1.61E+00	5.12E-01		1.05E+00	8.09E-01		-7.37E+00	6.43E-01		-1.40E+00	1.35E-01		-1.08E+01	2.81E-04	Down								
Unigene110653_All	459	0.00	0.00	0.00	0.00	0.00	0.30	1.93	0.73	0.00	null	null		null	null		null	null		8.21E+00	3.12E-01		-1.41E+00	4.01E-02		-1.09E+01	1.10E-06	Down	Unigene110653_All//gi|7768153|emb|CAB90634.1|/7.00E-41//protein phosphatase 2C (PP2C) [Fagus sylvatica]	Unigene110653_All//2.00E-40//AT5G66080| protein phosphatase 2C family protein / PP2C family protein	Unigene110653_All//7.00E-62//TC150159				nr -
Unigene110656_All	1049	0.00	0.10	0.00	0.19	0.13	0.34	6.69	2.83	1.06	6.59E+00	3.90E-01		null	null		-5.32E-01	7.49E-01		8.59E-01	5.42E-01		-1.24E+00	1.64E-09	Down	-2.65E+00	4.03E-26	Down	Unigene110656_All//gi|30690333|ref|NP_195265.2|/1.00E-84//AGF1 (AT-hook protein of GA feedback 1); transcription factor [Arabidopsis thaliana] >gi|50198777|gb|AAT70422.1| At4g35390 [Arabidopsis thaliana] >gi|53828597|gb|AAU94408.1| At4g35390 [Arabidopsis thaliana] >gi|119657394|tpd|FAA00296.1| TPA: AT-hook motif nuclear localized protein 25 [Arabidopsis thaliana]	Unigene110656_All//8.00E-44//AT4G35390| AGF1 (AT-hook protein of GA feedback 1); transcription factor	Unigene110656_All//0.00E+00//gi|78324579|gb|DT544853.1|DT544853				nr +
Unigene110660_All	349	1.20	0.58	2.75	1.28	1.97	0.91	7.87	2.16	5.37	-1.05E+00	3.66E-01		1.20E+00	1.15E-01		6.19E-01	5.30E-01		-5.04E-01	6.49E-01		-1.87E+00	5.66E-07	Down	-5.51E-01	9.22E-02		Unigene110660_All//gi|17017951|emb|CAC84117.1|/4.00E-18//3'(2'),5'-bisphosphate nucleotidase [Gossypium hirsutum]		Unigene110660_All//5.00E-90//TC158033		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism		nr -
Unigene110662_All	326	0.00	0.00	0.00	0.00	0.00	0.00	2.59	0.13	0.12	null	null		null	null		null	null		null	null		-4.34E+00	4.55E-05	Down	-4.41E+00	2.37E-05	Down									ESTscan +
Unigene110666_All	355	0.59	0.71	0.00	0.28	0.00	0.89	2.98	0.47	0.90	2.76E-01	8.44E-01		-9.20E+00	1.47E-01		-8.13E+00	3.16E-01		1.67E+00	3.09E-01		-2.66E+00	2.25E-04	Down	-1.73E+00	4.76E-03		Unigene110666_All//gi|224110076|ref|XP_002315406.1|/1.00E-47//aminophospholipid ATPase [Populus trichocarpa] >gi|222864446|gb|EEF01577.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene110666_All//2.00E-46//AT5G04930| ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism					nr -
Unigene110679_All	241	0.87	9.25	5.74	0.41	0.43	1.69	0.00	0.00	0.00	3.41E+00	1.13E-08	Up	2.73E+00	1.78E-04	Up	5.24E-02	9.68E-01		2.03E+00	1.49E-01		null	null		null	null		Unigene110679_All//gi|18397470|ref|NP_564354.1|/4.00E-22//ERD4 (early-responsive to dehydration 4) [Arabidopsis thaliana]	Unigene110679_All//8.00E-19//AT1G30360| ERD4 (early-responsive to dehydration 4)	Unigene110679_All//9.00E-106//gi|199882488|gb|DW511458.1|DW511458				nr -
Unigene110681_All	217	5.06	2.57	7.61	18.59	13.17	14.57	160.74	113.64	36.35	-9.79E-01	1.34E-01		5.87E-01	2.72E-01		-4.98E-01	9.62E-02		-3.52E-01	2.86E-01		-5.00E-01	6.51E-10		-2.14E+00	1.71E-98	Down	Unigene110681_All//gi|211906506|gb|ACJ11746.1|/7.00E-12//luminal binding protein [Gossypium hirsutum]	Unigene110681_All//5.00E-14//AT5G42020| BIP2; ATP binding	Unigene110681_All//4.00E-49//ES837705		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr -
Unigene110684_All	337	0.16	0.00	0.00	0.00	0.00	0.00	3.26	0.74	0.24	-7.28E+00	6.18E-01		-7.28E+00	6.31E-01		null	null		null	null		-2.13E+00	1.11E-03		-3.79E+00	3.27E-06	Down	Unigene110684_All//gi|15226168|ref|NP_178215.1|/8.00E-11//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene110684_All//3.00E-12//AT2G01050| nucleic acid binding / zinc ion binding					nr -
Unigene110686_All	279	0.00	0.00	0.00	0.00	0.00	0.00	3.33	0.60	0.29	null	null		null	null		null	null		null	null		-2.48E+00	1.07E-03		-3.55E+00	3.97E-05	Down									ESTscan -
Unigene110688_All	356	0.00	0.00	0.00	0.00	0.00	0.00	2.26	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	8.58E-06	Down	-1.11E+01	4.43E-06	Down									ESTscan +
Unigene11069_All	3171	7.05	5.42	5.98	12.27	18.70	10.95	24.85	9.71	21.90	-3.79E-01	1.13E-03		-2.37E-01	6.17E-02		6.08E-01	7.50E-22		-1.64E-01	7.83E-02		-1.36E+00	6.76E-113	Down	-1.83E-01	4.89E-04		Unigene11069_All//gi|297795237|ref|XP_002865503.1|/0.00E+00//metalloendopeptidase/ metallopeptidase/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297311338|gb|EFH41762.1| metalloendopeptidase/ metallopeptidase/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene11069_All//0.00E+00//AT5G42620| metalloendopeptidase/ zinc ion binding	Unigene11069_All//0.00E+00//TC167388			GO:0004175//GO:0009987//GO:0019538//GO:0044464//GO:0046914	nr +
Unigene110694_All	287	0.00	0.00	0.00	0.00	0.00	0.00	1.77	0.29	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.05E-02		-1.08E+01	5.55E-04	Down									ESTscan +
Unigene110695_All	231	0.00	0.00	0.00	0.00	0.00	0.00	2.75	0.72	0.17	null	null		null	null		null	null		null	null		-1.92E+00	3.09E-02		-3.99E+00	5.82E-04	Down	Unigene110695_All//gi|145408590|ref|YP_001152214.1|/2.00E-07//ORF124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| ORF124 [Pinus koraiensis]							nr +
Unigene110696_All	211	0.00	0.00	0.00	0.00	0.00	0.00	5.81	0.40	0.00	null	null		null	null		null	null		null	null		-3.87E+00	1.15E-06	Down	-1.25E+01	4.03E-09	Down	Unigene110696_All//sp|Q86IV5|CTNA_DICDI//2.00E-06//Countin-1 OS=Dictyostelium discoideum GN=ctnA PE=1 SV=1							swissprot -
Unigene110697_All	261	0.00	0.00	0.00	0.00	0.79	0.00	2.75	0.00	0.00	null	null		null	null		9.63E+00	1.57E-01		null	null		-1.14E+01	3.27E-05	Down	-1.14E+01	1.78E-05	Down			Unigene110697_All//2.00E-76//TC174148					ESTscan -
Unigene110704_All	233	0.00	0.00	0.00	0.00	0.00	0.00	4.54	3.41	0.00	null	null		null	null		null	null		null	null		-4.13E-01	5.15E-01		-1.21E+01	6.72E-08	Down			Unigene110704_All//4.00E-09//gi|78348172|gb|DT568446.1|DT568446					

Unigene110707_All	564	0.00	0.00	0.00	0.00	0.18	0.08	2.55	0.15	0.92	null	null		null	null		7.52E+00	4.58E-01		6.32E+00	7.02E-01		-4.10E+00	5.15E-08	Down	-1.47E+00	3.09E-03		Unigene110707_All//gi|115446137|ref|NP_001046848.1|//8.00E-39//Os02g0479300 [Oryza sativa Japonica Group] >gi|47848144|dbj|BAD21925.1| XTP3-transactivated protein A-like [Oryza sativa Japonica Group] >gi|47848239|dbj|BAD22064.1| XTP3-transactivated protein A-like [Oryza sativa Japonica Group] >gi|113536379|dbj|BAF08762.1| Os02g0479300 [Oryza sativa Japonica Group]	Unigene110707_All//7.00E-28//AT3G25400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: NTP Pyrophosphohydrolase MazG-related, RS21-C6 (InterPro:IPR011394), EAR (InterPro:IPR009039), NTP pyrophosphohydrolase MazG, putative catalytic core (InterPro:IPR004518); Has 572 Blast hits to 572 proteins in 181 species: Archae - 11; Bacteria - 286; Metazoa - 71; Fungi - 1; Plants - 31; Viruses - 0; Other Eukaryotes - 172 (source: NCBI BLink).	Unigene110707_All//4.00E-39//DW519333				nr -
Unigene110708_All	392	1.33	0.00	0.68	0.64	0.18	0.00	3.24	0.64	2.54	-1.04E+01	2.93E-03		-9.75E-01	3.77E-01		-1.85E+00	2.76E-01		-9.31E+00	7.35E-02		-2.34E+00	1.56E-04	Down	-3.49E-01	5.15E-01		Unigene110708_All//gi|242199346|gb|ACS87994.1|//4.00E-11//UDP-glucosyltransferase family 1 protein [Citrus sinensis]	Unigene110708_All//2.00E-07//AT1G78270| AtUGT85A4 (UDP-glucosyl transferase 85A4); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring hexosyl groups	Unigene110708_All//4.00E-60//gi|48819923|gb|CO121236.1|CO121236				nr +
Unigene110714_All	284	0.00	0.00	0.00	0.00	0.00	0.00	3.72	1.62	0.00	null	null		null	null		null	null		null	null		-1.20E+00	4.79E-02		-1.19E+01	6.72E-08	Down	Unigene110714_All//gi|116056464|emb|CAL52753.1|//4.00E-32//ribosomal protein S20 (ISS) [Ostreococcus tauri]	Unigene110714_All//1.00E-31//AT5G62300| 40S ribosomal protein S20 (RPS20C)				ko03010|Ribosome		nr -
Unigene110717_All	304	1.03	0.00	0.88	0.98	0.45	0.45	9.32	29.83	8.39	-1.00E+01	3.66E-02		-2.38E-01	8.50E-01		-1.12E+00	4.24E-01		-1.14E+00	4.58E-01		1.68E+00	1.98E-18	Up	-1.52E-01	6.44E-01					Unigene110717_All//2.00E-14//gi|3326594|gb|AI055480.1|AI055480				
Unigene110719_All	1481	0.00	0.00	0.00	0.00	0.00	0.00	2.14	1.89	0.16	null	null		null	null		null	null		null	null		-1.79E-01	6.32E-01		-3.73E+00	1.43E-16	Down	Unigene110719_All//gi|260446989|emb|CBG76271.1|//6.00E-44//OO_Ba0005L10-OO_Ba0081K17.22 [Oryza officinalis]	Unigene110719_All//1.00E-42//AT2G44570| AtGH9B12 (Arabidopsis thaliana glycosyl hydrolase 9B12); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds				ko00500|Starch and sucrose metabolism		nr -
Unigene110721_All	362	0.00	0.00	0.00	0.00	0.00	0.00	1.75	0.92	0.00	null	null		null	null		null	null		null	null		-9.23E-01	2.63E-01		-1.08E+01	7.12E-05	Down	Unigene110721_All//gi|301111866|ref|XP_002905012.1|//2.00E-27//major vault protein [Phytophthora infestans T30-4] >gi|262096342|gb|EEY53394.1| major vault protein [Phytophthora infestans T30-4]						nr +
Unigene110723_All	623	0.00	0.00	0.00	0.00	0.06	0.22	1.63	0.27	0.13	null	null		null	null		5.79E+00	8.37E-01		7.76E+00	3.12E-01		-2.60E+00	3.81E-04	Down	-3.67E+00	1.15E-05	Down	Unigene110723_All//gi|292668903|gb|ADE41106.1|//3.00E-11//AP2 domain class transcription factor [Malus x domestica]	Unigene110723_All//1.00E-08//AT4G27950| CRF4 (CYTOKININ RESPONSE FACTOR 4); DNA binding / transcription factor	Unigene110723_All//2.00E-66//gi|84169116|gb|DR457764.1|DR457764	AP2-EREBP			nr +
Unigene110724_All	671	0.00	0.00	0.00	0.00	0.00	0.00	3.09	0.12	0.06	null	null		null	null		null	null		null	null		-4.63E+00	3.60E-12	Down	-5.70E+00	7.21E-14	Down	Unigene110724_All//gi|2388584|gb|AB71465.1|//5.00E-08//EST gb|ATTS1136 comes from this gene [Arabidopsis thaliana]						nr +
Unigene110734_All	316	4.14	1.76	2.19	2.84	2.18	1.72	4.28	1.19	0.38	-1.23E+00	3.96E-02		-9.18E-01	1.38E-01		-3.81E-01	6.05E-01		-7.26E-01	3.45E-01		-1.85E+00	9.22E-04	Down	-3.50E+00	4.24E-07	Down				Unigene110734_All//4.00E-121//ES818844				
Unigene110736_All	531	0.00	0.00	0.00	0.00	0.00	0.00	3.90	0.31	0.00	null	null		null	null		null	null		null	null		-3.63E+00	2.06E-10	Down	-1.19E+01	2.86E-15	Down								
Unigene110743_All	419	0.00	0.00	0.00	0.00	0.00	0.00	2.52	0.40	0.00	null	null		null	null		null	null		null	null		-2.66E+00	2.25E-04	Down	-1.13E+01	6.72E-08	Down	Unigene110743_All//gi|224139376|ref|XP_002323082.1|//3.00E-45//cytochrome P450 [Populus trichocarpa] >gi|222867712|gb|EEF04843.1| cytochrome P450 [Populus trichocarpa]	Unigene110743_All//3.00E-36//AT5G25120| CYP71B11; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene110743_All//1.00E-118//CO115885		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene110744_All	536	0.00	0.00	0.00	0.00	0.00	0.00	2.68	0.47	0.30	null	null		null	null		null	null		null	null		-2.52E+00	2.00E-05	Down	-3.17E+00	5.96E-07	Down								
Unigene110748_All	267	0.20	0.76	0.00	0.00	0.39	0.17	18.69	3.60	3.28	1.95E+00	3.76E-01		-7.61E+00	6.31E-01		8.60E+00	4.58E-01		7.40E+00	7.02E-01		-2.38E+00	4.42E-16	Down	-2.51E+00	1.10E-17	Down								
Unigene110749_All	651	0.00	0.00	0.00	0.46	0.05	0.14	3.18	0.00	0.55	null	null		null	null		-3.12E+00	7.57E-02		-1.73E+00	2.89E-01		-1.16E+01	1.17E-14	Down	-2.53E+00	7.37E-08	Down	Unigene110749_All//gi|297824857|ref|XP_002880311.1|//1.00E-37//pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326150|gb|EFH56570.1| pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene110749_All//6.00E-38//AT2G47540| pollen Ole e 1 allergen and extensin family protein					nr +
Unigene110752_All	571	0.00	0.00	0.00	0.00	0.00	0.08	1.41	0.00	1.60	null	null		null	null		null	null		6.31E+00	7.02E-01		-1.05E+01	8.58E-06	Down	1.90E-01	7.54E-01					Unigene110752_All//1.00E-159//DR459330				
Unigene110757_All	657	0.00	0.00	0.00	0.00	0.00	0.00	3.60	1.08	0.00	null	null		null	null		null	null		null	null		-1.74E+00	1.33E-05	Down	-1.18E+01	1.96E-17	Down	Unigene110757_All//gi|298711872|emb|CBJ32893.1|//6.00E-93//EEF1A2, eukaryotic translation elongation factor 1 alpha [Ectocarpus siliculosus] >gi|298711873|emb|CBJ32894.1| EEF1A1, eukaryotic translation elongation factor 1 alpha [Ectocarpus siliculosus]	Unigene110757_All//4.00E-88//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene110757_All//1.00E-24//gi|13354929|gb|BG445277.1|BG445277				nr -
Unigene110758_All	304	0.00	0.00	0.00	0.00	0.00	0.00	1.95	0.96	0.00	null	null		null	null		null	null		null	null		-1.02E+00	2.40E-01		-1.09E+01	1.41E-04	Down	Unigene110758_All//gi|256427002|gb|ACU81074.1|//4.00E-44//ubiquitin extension protein [Jatropha curcas]	Unigene110758_All//2.00E-35//AT3G62250| UBQ5 (ubiquitin 5); protein binding / structural constituent of ribosome	Unigene110758_All//2.00E-27//BM359461		ko03010|Ribosome		nr +
Unigene110762_All	500	0.00	0.00	0.00	0.00	0.00	0.00	2.62	0.08	0.00	null	null		null	null		null	null		null	null		-4.97E+00	4.05E-08	Down	-1.14E+01	9.85E-10	Down	Unigene110762_All//gi|300267685|gb|EFJ51868.1|//2.00E-09//dynein heavy chain 4 [Volvox carteri f. nagariensis]	Unigene110762_All//2.00E-05//AT2G43580| chitinase, putative					nr -
Unigene110769_All	1320	0.00	0.00	0.16	0.15	0.00	0.14	4.07	0.66	4.04	null	null		7.33E+00	1.42E-01		-7.24E+00	8.47E-02		-1.41E-01	9.35E-01		-2.61E+00	3.63E-19	Down	-8.40E-03	9.65E-01		Unigene110769_All//gi|18402992|ref|NP_566685.1|//4.00E-70//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|29029088|gb|AAO64923.1| At3g21420 [Arabidopsis thaliana]	Unigene110769_All//4.00E-71//AT3G21420| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene110769_All//1.00E-44//gi|31073529|gb|CA993808.1|CA993808		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr +
Unigene110771_All	315	1.00	3.38	0.00	0.47	1.86	1.00	4.70	3.85	1.26	1.76E+00	1.43E-02		-9.96E+00	4.93E-02		1.97E+00	7.04E-02		1.08E+00	4.76E-01		-2.88E-01	6.00E-01		-1.89E+00	2.45E-04	Down		Unigene110771_All//2.00E-05//AT3G53570| AFC1 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene110771_All//2.00E-144//gi|164309664|gb|ES844604.1|ES844604				kegg -
Unigene110772_All	275	0.00	0.00	0.00	0.00	0.00	0.00	2.15	0.76	0.00	null	null		null	null		null	null		null	null		-1.50E+00	9.14E-02		-1.11E+01	1.41E-04	Down	Unigene110772_All//gi|258598734|gb|ACV83439.1|//2.00E-29//QM-like protein [Zea mays]	Unigene110772_All//3.00E-30//AT1G66580| 60S ribosomal protein L10 (RPL10C)			ko03010|Ribosome		nr -
Unigene110778_All	456	4.93	10.67	5.14	2.51	8.38	5.05	0.09	0.28	0.35	1.11E+00	6.62E-05	Up	5.86E-02	8.94E-01		1.74E+00	7.96E-08	Up	1.01E+00	1.82E-02		1.57E+00	5.46E-01		1.91E+00	3.78E-01		Unigene110778_All//gi|194466223|gb|ACF74342.1|//2.00E-33//gonadotropin beta chain [Arachis hypogaea]	Unigene110778_All//1.00E-21//AT5G14920| gibberellin-regulated family protein	Unigene110778_All//9.00E-160//TC176495				nr +
Unigene110783_All	363	0.00	0.00	0.00	0.00	0.00	0.00	2.80	0.35	0.33	null	null		null	null		null	null		null	null		-3.02E+00	1.08E-04	Down	-3.09E+00	5.36E-05	Down	Unigene110783_All//gi|6831602|sp|Q90XHE4.1|RL37A_GOSHI//2.00E-31//RecName: Full=60S ribosomal protein L37a >gi|4741896|gb|AAD28753.1|AF127042_1 60S ribosomal protein L37a [Gossypium hirsutum]	Unigene110783_All//1.00E-31//AT5G60245| 60S ribosomal protein L37a (RPL37aC)			ko03010|Ribosome		nr -
Unigene110786_All	367	0.00	0.00	0.00	0.00	0.00	0.00	4.38	0.11	0.22	null	null		null	null		null	null		null	null		-5.26E+00	4.17E-10	Down	-4.33E+00	1.41E-09	Down	Unigene110786_All//gi|297827841|ref|XP_002881803.1|//6.00E-20//40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata] >gi|297327642|gb|EFH58062.1| 40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata]	Unigene110786_All//3.00E-21//AT1G58684| 40S ribosomal protein S2, putative			ko03010|Ribosome		nr +
Unigene110787_All	316	0.00	0.00	0.00	0.00	0.00	0.00	2.94	1.06	0.13	null	null		null	null		null	null		null	null		-1.48E+00	2.77E-02		-4.54E+00	6.41E-06	Down	Unigene110787_All//gi|300266840|gb|EFJ51026.1|//2.00E-23//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene110787_All//3.00E-23//AT1G48830| 40S ribosomal protein S7 (RPS7A)			ko03010|Ribosome		nr +
Unigene110789_All	313	0.00	0.81	1.36	0.32	0.44	0.29	1.76	0.53	0.00	9.66E+00	7.88E-02		1.04E+01	1.38E-02		4.67E-01	8.78E-01		-1.41E-01	9.52E-01		-1.72E+00	7.23E-02		-1.08E+01	2.81E-04	Down	Unigene110789_All//gi|115450411|ref|NP_001048896.1|//3.00E-23//Os03g0123600 [Oryza sativa Japonica Group] >gi|113547277|dbj|BAF10720.1| Os03g0123600 [Oryza sativa Japonica Group]	Unigene110789_All//3.00E-24//AT5G41390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function Cys-rich (InterPro:IPR006461); BEST Arabidopsis thaliana protein match is: proline-rich family protein (TAIR:AT1G63830.2); Has 12019 Blast hits to 5816 proteins in 448 species: Archae - 6; Bacteria - 1151; Metazoa - 4980; Fungi - 1500; Plants - 2685; Viruses - 338; Other Eukaryotes - 1439 (source: NCBI BLink).	Unigene110789_All//1.00E-114//gi|21094210|gb|BQ406523.1|BQ406523				nr -
Unigene110794_All	495	0.00	0.00	0.00	0.00	0.00	0.00	2.65	0.76	0.00	null	null		null	null		null	null		null	null		-1.80E+00	1.43E-03		-1.14E+01	9.85E-10	Down	Unigene110794_All//gi|226460767|gb|EEH58061.1|//2.00E-21//profilin [Micromonas pusilla CCMP1545]	Unigene110794_All//3.00E-10//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding					nr -
Unigene110795_All	422	0.00	0.00	0.00	0.00	0.00	0.00	2.50	1.88	0.47	null	null		null	null		null	null		null	null		-4.13E-01	5.15E-01		-2.41E+00	3.46E-04	Down	Unigene110795_All//gi|115440955|ref|NP_001044757.1|//2.00E-30//Os01g0840100 [Oryza sativa Japonica Group] >gi|113534288|dbj|BAF06671.1| Os01g0840100 [Oryza sativa Japonica Group]	Unigene110795_All//2.00E-22//AT5G09440| heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr +
Unigene110803_All	369	0.00	0.00	0.00	0.00	0.00	0.00	2.64	0.11	0.00	null	null		null	null		null	null		null	null		-4.54E+00	6.92E-06	Down	-1.14E+01	2.72E-07	Down	Unigene110803_All//gi|48431269|gb|AAT44124.1|//1.00E-30//F3H-like protein [Saussurea medusa]	Unigene110803_All//6.00E-23//AT2G44800| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene110803_All//4.00E-112//DW479710		ko00941|Flavonoid biosynthesis		nr +
Unigene110805_All	495	0.00	0.00	0.00	0.50	0.00	0.00	2.99	0.68	0.80	null	null		null	null		-8.98E+00	4.19E-02		-8.98E+00	7.35E-02		-2.15E+00	9.69E-05	Down	-1.89E+00	2.45E-04	Down								
Unigene110807_All	339	0.00	0.00	0.00	0.00	0.00	0.00	2.25	0.37	0.24	null	null		null	null		null	null		null	null		-2.60E+00	2.81E-03		-3.26E+00	4.48E-04	Down	Unigene110807_All//gi|260766526|gb|ACX50285.1|//1.00E-20//cytochrome oxidase subunit I [Guillardia theta]	Unigene110807_All//9.00E-18//ATMG01360| cytochrome c oxidase subunit I			ko00190|Oxidative phosphorylation		nr -

Unigene110808_All	251	0.00	0.00	0.00	0.00	0.00	0.00	3.03	0.33	0.00	null	null		null	null		null	null		null	null		-3.19E+00	7.93E-04	Down	-1.16E+01	8.88E-06	Down	Unigene110808_All//gi|115451757|ref|NP_001049479.1|//5.00E-27//Os03g0234200 [Oryza sativa Japonica Group] >gi|303857|dbj|BAA02154.1| ubiquitin/ribosomal polyprotein [Oryza sativa Japonica Group] >gi|13358806|dbj|BAB33149.1| ubiquitin fused to ribosomal protein L40 [Oryza sativa] >gi|13358808|dbj|BAB33150.1| ubiquitin fused to ribosomal protein L40 [Oryza sativa] >gi|52077170|dbj|BAD46215.1| ubiquitin / ribosomal protein CEP52 [Oryza sativa Japonica Group] >gi|113547950|dbj|BAF11393.1| Os03g0234200 [Oryza sativa Japonica Group]	Unigene110808_All//1.00E-22//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene110808_All//2.00E-26//DW500399		ko03010|Ribosome		nr +
Unigene110813_All	251	0.00	0.00	0.00	0.00	0.00	3.20	0.50	0.48	null	null		null	null		null	null		null	null		-2.68E+00	1.67E-03		-2.75E+00	9.43E-04	Down	Unigene110813_All//gi|14423905|sp|Q8VGL4.1|RL31_CYAPA//2.00E-30//RecName: Full=60S ribosomal protein L31 >gi|5123727|emb|CAB45375.1| ribosomal protein L31 [Cyanophora paradoxa]	Unigene110813_All//2.00E-30//AT5G56710| 60S ribosomal protein L31 (RPL31C)		ko03010|Ribosome		nr +
Unigene110815_All	619	0.00	0.00	0.17	0.08	0.06	0.00	3.21	2.36	77.94	null	null		7.43E+00	4.02E-01		-5.34E-01	8.28E-01		-6.33E+00	6.43E-01		-4.42E-01	3.06E-01		4.60E+00	1.01E-276	Up							
Unigene110819_All	571	0.00	0.09	0.00	0.00	0.36	0.00	2.96	0.73	0.70	6.47E+00	6.21E-01		null	null		8.50E+00	1.57E-01		null	null		-2.02E+00	5.66E-05	Down	-2.09E+00	2.24E-05	Down	Unigene110819_All//gi|15234416|ref|NP_192948.1|//4.00E-33//SMO1-1 (STEROL-4ALPHA-METHYL OXIDASE 1-1); 4,4-dimethyl-9beta,19-cyclopropylsterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase/ catalytic [Arabidopsis thaliana] >gi|21928127|gb|AAN78091.1| AT4g12110/F16J13_180 [Arabidopsis thaliana] >gi|23308291|gb|AAN18115.1| At4g12110/F16J13_180 [Arabidopsis thaliana]	Unigene110819_All//3.00E-27//AT4G12110| SMO1-1 (STEROL-4ALPHA-METHYL OXIDASE 1-1); 4,4-dimethyl-9beta,19-cyclopropylsterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase/ catalytic	Unigene110819_All//0.00E+00//DW512447		ko00100|Steroid biosynthesis		nr -
Unigene110820_All	330	0.00	0.00	0.00	0.00	0.00	0.00	4.10	7.22	0.00	null	null		null	null		null	null		null	null		8.16E-01	2.69E-02		-1.20E+01	4.86E-10	Down	Unigene110820_All//gi|255084545|ref|XP_002508847.1|//4.00E-41//ribosomal protein L44 [Micromonas sp. RCC299] >gi|226524124|gb|ACO70105.1| ribosomal protein L44 [Micromonas sp. RCC299]	Unigene110820_All//3.00E-41//AT4G14320| 60S ribosomal protein L36a/L44 (RPL36aB)	Unigene110820_All//4.00E-19//TC176118		ko03010|Ribosome		nr -
Unigene110821_All	414	8.47	26.93	11.06	27.07	27.45	40.04	36.15	50.18	24.15	1.67E+00	3.15E-18	Up	3.86E-01	2.08E-01		1.99E-02	9.34E-01		5.65E-01	2.35E-05		4.73E-01	1.06E-05		-5.82E-01	3.62E-06		Unigene110821_All//gi|22327990|ref|NP_200888.2|//1.00E-07//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|28416657|gb|AAO42859.1| At5g60800 [Arabidopsis thaliana]	Unigene110821_All//2.00E-06//AT5G60800| heavy-metal-associated domain-containing protein	Unigene110821_All//2.00E-120//gi|78345451|gb|DT565725.1|DT565725				nr +
Unigene110822_All	529	0.00	0.19	0.00	0.19	1.11	0.17	2.80	0.16	1.05	7.58E+00	3.90E-01		null	null		2.56E+00	2.84E-02		-1.41E-01	9.52E-01		-4.15E+00	2.75E-08	Down	-1.41E+00	3.79E-03		Unigene110822_All//gi|219292220|dbj|BAC06184.1|//2.00E-69//110 kDa 4SNc-Tudor domain protein [Pisum sativum]	Unigene110822_All//2.00E-65//AT5G07350| tudor domain-containing protein / nuclease family protein	Unigene110822_All//3.00E-144//gi|84173243|gb|DR461891.1|DR461891				nr -
Unigene110824_All	705	0.00	0.00	0.00	0.00	0.00	0.00	5.34	0.47	0.79	null	null		null	null		null	null		null	null		-3.49E+00	6.76E-18	Down	-2.75E+00	6.54E-15	Down							
Unigene110825_All	212	0.00	0.00	0.00	0.00	0.00	0.00	4.19	0.59	0.00	null	null		null	null		null	null		null	null		-2.82E+00	5.65E-04	Down	-1.20E+01	1.10E-06	Down	Unigene110825_All//gi|94692251|gb|ABF46833.1|//3.00E-33//actin [Labyrinthula terrestris]	Unigene110825_All//5.00E-32//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene110825_All//3.00E-22//gi|5045730|gb|AI726878.1|AI726878		ko04145|Phagosome		nr +
Unigene110826_All	591	0.00	0.00	0.00	0.00	0.00	0.00	4.36	0.21	0.13	null	null		null	null		null	null		null	null		-4.36E+00	1.54E-14	Down	-5.02E+00	2.78E-16	Down	Unigene110826_All//gi|159489312|ref|XP_001702641.1|//2.00E-68//ribosomal protein L3, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|158280663|gb|EDF06420.1| ribosomal protein L3, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii]	Unigene110826_All//2.00E-50//AT1G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	Unigene110826_All//7.00E-10//ES848354		ko03010|Ribosome		nr +
Unigene110828_All	547	0.00	0.00	0.00	0.00	0.00	0.00	1.78	0.08	0.00	null	null		null	null		null	null		null	null		-4.54E+00	6.92E-06	Down	-1.08E+01	2.72E-07	Down		Unigene110828_All//2.00E-05//AT5G15090| VDAC3 (VOLTAGE DEPENDENT ANION CHANNEL 3); voltage-gated anion channel					ESTscan +
Unigene110829_All	395	0.13	0.00	0.00	0.38	0.17	0.23	2.03	0.11	0.81	-7.05E+00	6.18E-01		-7.05E+00	6.31E-01		-1.12E+00	5.85E-01		-7.26E-01	7.16E-01		-4.26E+00	8.48E-05	Down	-1.33E+00	5.40E-02		Unigene110829_All//gi|30699453|ref|NP_850983.1|//1.00E-30//SGB1 (SUPPRESSOR OF G PROTEIN BETA1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|30699455|ref|NP_178100.3| SGB1 (SUPPRESSOR OF G PROTEIN BETA1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|117940111|sp|Q2V4B9.2|PLST3_ARATH RecName: Full=Probable plastidic glucose transporter 3 >gi|222424748|dbj|BAH20327.1| AT1G79820 [Arabidopsis thaliana]	Unigene110829_All//2.00E-40//AT1G79820| SGB1 (SUPPRESSOR OF G PROTEIN BETA1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene110829_All//2.00E-40//CO109110				nr +
Unigene110834_All	415	0.00	0.00	0.00	0.00	0.00	0.00	6.52	1.31	0.38	null	null		null	null		null	null		null	null		-2.32E+00	8.55E-09	Down	-4.09E+00	3.55E-15	Down	Unigene110834_All//gi|145408595|ref|YP_001152219.1|//1.00E-15//O8F58f [Pinus koraiensis] >gi|145048844|gb|ABF35460.1| O8F58f [Pinus koraiensis]		Unigene110834_All//4.00E-29//TC150009				nr -
Unigene110836_All	433	17.40	6.79	5.41	29.91	14.79	20.13	49.21	17.95	23.65	-1.36E+00	1.59E-09	Down	-1.69E+00	3.35E-12	Down	-1.02E+00	3.47E-12	Down	-5.71E-01	1.88E-04		-1.45E+00	1.63E-34	Down	-1.06E+00	6.71E-22	Down	Unigene110836_All//gi|73761683|gb|AAZ83341.1|//6.00E-30//ubiquitin extension protein [Gossypium hirsutum]	Unigene110836_All//5.00E-27//AT2G47110| UBQ6; protein binding	Unigene110836_All//0.00E+00//gi|164334010|gb|ES806164.1|ES806164		ko03010|Ribosome		nr +
Unigene110839_All	394	0.00	0.00	0.00	0.76	0.52	0.00	2.47	0.21	1.42	null	null		null	null		-5.33E-01	6.79E-01		-9.57E+00	4.01E-02		-3.54E+00	4.32E-05	Down	-8.02E-01	1.83E-01		Unigene110839_All//gi|115451357|ref|NP_001049279.1|//4.00E-56//Os03g0198500 [Oryza sativa Japonica Group] >gi|113547750|dbj|BAF11193.1| Os03g0198500 [Oryza sativa Japonica Group]	Unigene110839_All//4.00E-52//AT1G47740| unknown protein	Unigene110839_All//0.00E+00//TC156499				nr +
Unigene110841_All	587	2634.40	2034.29	3068.81	421.68	567.39	385.70	2.81	0.78	0.75	-3.73E-01	5.91E-192		2.20E-01	4.45E-80		4.28E-01	1.74E-64		-1.29E-01	6.20E-05		-1.84E+00	2.07E-04	Down	-1.91E+00	8.63E-05	Down	Unigene110841_All//gi|224100797|ref|XP_002312019.1|//3.00E-55//light-harvesting complex I protein Lhca1 [Populus trichocarpa] >gi|222861839|gb|EEE89386.1| light-harvesting complex I protein Lhca1 [Populus trichocarpa]	Unigene110841_All//2.00E-51//AT3G54890| LHCA1; chlorophyll binding	Unigene110841_All//0.00E+00//TC132114		ko00196|Photosynthesis - antenna proteins		nr +
Unigene110845_All	454	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.92	0.26	null	null		null	null		null	null		null	null		-1.15E+00	7.87E-02		-2.96E+00	1.72E-04	Down	Unigene110845_All//gi|4115918|gb|AAO03429.1|//2.00E-33//similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]	Unigene110845_All//8.00E-32//AT5G13850| NACA3 (NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX SUBUNIT ALPHA-LIKE PROTEIN 3)					nr +
Unigene110847_All	271	0.00	0.00	0.00	0.00	0.00	0.00	2.50	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	6.34E-05	Down	-1.13E+01	3.57E-05	Down							ESTscan -
Unigene110848_All	377	0.00	0.00	0.00	0.00	0.00	0.00	6.50	1.00	0.63	null	null		null	null		null	null		null	null		-2.70E+00	1.95E-09	Down	-3.36E+00	6.21E-12	Down	Unigene110848_All//gi|238014838|gb|ACR38454.1|//8.00E-17//unknown [Zea mays]		Unigene110848_All//6.00E-28//TC143817				nr -
Unigene11085_All	725	7.14	5.73	6.17	9.69	8.64	4.73	31.55	28.59	23.96	-3.18E-01	2.39E-01		-2.12E-01	4.64E-01		-1.64E-01	5.31E-01		-1.03E+00	2.31E-06	Down	-1.42E-01	2.24E-01		-3.97E-01	6.78E-05		Unigene11085_All//gi|15233656|ref|NP_194133.1|//2.00E-36//NLP7 (NIN LIKE PROTEIN 7); transcription factor [Arabidopsis thaliana]	Unigene110085_All//0.00E+00//gi|73850762|gb|DT459782.1|DT459782	RWP-RK		GO:0006950//GO:0009987//GO:0010035//GO:0042126//GO:0043231	nr -
Unigene110853_All	417	0.00	0.00	0.00	0.00	0.00	0.00	2.94	0.40	18.06	null	null		null	null		null	null		null	null		-2.87E+00	2.54E-05	Down	2.62E+00	3.95E-27	Up	Unigene110853_All//gi|28300299|gb|AAO37645.1|//6.00E-30//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene110853_All//1.00E-18//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene110853_All//5.00E-87//TC177573		ko04626|Plant-pathogen interaction		nr -
Unigene110854_All	590	0.00	0.00	0.00	0.00	0.00	0.00	2.65	0.50	0.00	null	null		null	null		null	null		null	null		-2.42E+00	1.29E-05	Down	-1.14E+01	1.42E-11	Down	Unigene110854_All//gi|192910756|gb|ACF06486.1|//2.00E-57//60S ribosomal protein L11 [Elaeis guineensis] >gi|192910758|gb|ACF06487.1| 60S ribosomal protein L11 [Elaeis guineensis]	Unigene110854_All//2.00E-57//AT5G45775| 60S ribosomal protein L11 (RPL11D)			ko03010|Ribosome		nr -
Unigene110857_All	277	0.00	0.00	0.00	0.00	0.00	0.00	4.73	0.00	0.14	null	null		null	null		null	null		null	null		-1.22E+01	2.56E-09	Down	-5.04E+00	1.60E-08	Down							ESTscan +
Unigene110086_All	717	2.41	9.89	3.94	7.99	8.12	12.16	13.74	25.53	23.78	2.04E+00	2.53E-15	Up	7.09E-01	7.03E-02		2.27E-02	9.55E-01		6.06E-01	1.75E-03		8.94E-01	4.45E-14		7.92E-01	3.72E-11		Unigene110086_All//gi|297803722|ref|XP_002869745.1|//3.00E-39//RWP-RK domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315581|gb|EFH46004.1| RWP-RK domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene110086_All//4.00E-40//AT4G24020| NLP7 (NIN LIKE PROTEIN 7); transcription factor	Unigene110086_All//0.00E+00//TC134183	RWP-RK		GO:0006950//GO:0009987//GO:0010035//GO:0042126//GO:0043231	nr +
Unigene110861_All	302	173.59	76.51	232.04	73.57	98.86	35.89	0.84	0.28	0.66	-1.18E+00	6.36E-50	Down	4.19E-01	5.18E-11		4.26E-01	3.83E-06		-1.04E+00	7.99E-19	Down	-1.60E+00	3.11E-01		-3.49E-01	7.67E-01		Unigene110861_All//gi|222422857|dbj|BAH19415.1|//2.00E-08//AT4G25080 [Arabidopsis thaliana]		Unigene110861_All//3.00E-81//TC132357				nr +
Unigene110862_All	434	0.00	0.00	0.00	0.00	0.00	0.00	3.31	0.19	0.00	null	null		null	null		null	null		null	null		-4.10E+00	5.15E-08	Down	-1.17E+01	1.19E-10	Down							
Unigene110866_All	1029	0.31	0.30	0.00	0.39	0.54	0.70	2.75	0.93	0.89	-4.66E-02	9.85E-01		-8.25E+00	4.93E-02		4.67E-01	6.68E-01		8.58E-01	3.42E-01		-1.56E+00	9.71E-06	Down	-1.63E+00	2.69E-06	Down	Unigene110866_All//gi|4971998|emb|CAB43864.1|//1.00E-100//polynucleotide phosphorylase [Arabidopsis thaliana] >gi|4972000|emb|CAB43865.1| polynucleotide phosphorylase [Arabidopsis thaliana] >gi|7573307|emb|CAB87625.1| polynucleotide phosphorylase [Arabidopsis thaliana]	Unigene110866_All//3.00E-101//AT5G14580| polyribonucleotide nucleotidyltransferase, putative	Unigene110866_All//0.00E+00//TC170267		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03018|RNA degradation		nr +

Unigene110867_All	432	0.00	0.00	0.00	0.00	0.00	0.00	5.38	0.10	0.18	null	null		null	null		null	null		null	null		-5.80E+00	5.23E-15	Down	-4.87E+00	1.64E-14	Down	Unigene110867_All//gi|301095995|ref|XP_002897096.1//2.00E-54//40S ribosomal protein S15a [Phytophthora infestans T30-4] >gi|262107415|gb|EEY65467.1| 40S ribosomal protein S15a [Phytophthora infestans T30-4]	Unigene110867_All//8.00E-48//AT5G59850| 40S ribosomal protein S15A (RPS15aF)			ko03010|Ribosome		nr -
Unigene110868_All	415	0.00	0.00	0.00	0.00	0.00	0.00	1.63	0.10	0.00	null	null		null	null		null	null		null	null		-4.02E+00	5.36E-04	Down	-1.07E+01	3.57E-05	Down	Unigene110868_All//gi|226493384|ref|NP_001150104.1//8.00E-32//LOC100283733 [Zea mays] >gi|195636758|gb|ACG37847.1| xaa-Pro dipeptidase [Zea mays]	Unigene110868_All//3.00E-26//AT4G29490| aminopeptidase/ manganese ion binding					nr -
Unigene110874_All	340	0.00	0.00	0.00	0.00	0.00	0.00	3.23	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	7.67E-08	Down	-1.17E+01	3.33E-08	Down	Unigene110874_All//gi|223995041|ref|XP_002287204.1//3.00E-33//v-type ATPase [Thalassiosira pseudonana CCMP1335] >gi|223996057|ref|XP_002287702.1| vacuolar ATP synthase [Thalassiosira pseudonana CCMP1335] >gi|220976320|gb|EED94647.1| v-type ATPase [Thalassiosira pseudonana CCMP1335] >gi|220976818|gb|EED95145.1| vacuolar ATP synthase [Thalassiosira pseudonana CCMP1335]	Unigene110874_All//2.00E-20//AT4G34720| AVA-P1: ATPase/ proton-transporting ATPase, rotational mechanism			ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr +
Unigene110875_All	397	0.00	0.00	0.00	0.00	0.00	0.00	10.54	4.00	1.10	null	null		null	null		null	null		null	null		-1.40E+00	5.05E-07	Down	-3.26E+00	2.32E-19	Down								
Unigene110876_All	399	0.00	0.00	0.00	0.00	0.00	0.00	2.01	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	8.58E-06	Down	-1.10E+01	4.43E-06	Down	Unigene110876_All//gi|1706586|sp|P50256.1|EF1AC_PORPU//6.00E-24//RecName: Full=Elongation factor 1-alpha C; Short=EF-1-alpha C >gi|476155|gb|AAA61763.1| EF1-alpha [Porphyra purpurea]	Unigene110876_All//3.00E-21//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene110876_All//5.00E-13//CD809343				nr -
Unigene110877_All	298	0.00	0.00	0.00	0.00	0.00	0.00	2.13	0.00	0.27	null	null		null	null		null	null		null	null		-1.11E+01	1.23E-04	Down	-2.99E+00	2.58E-03		Unigene110877_All//sp|P22549|PDE_DICDI//9.00E-06//Cyclic nucleotide phosphodiesterase inhibitor OS=Dictyostelium discoideum GN=pdiA PE=1 SV=1						swissprot +
Unigene110879_All	908	0.35	0.00	0.12	0.16	0.23	0.00	4.52	0.46	6.01	-8.43E+00	3.66E-02		-1.56E+00	3.30E-01		4.67E-01	8.26E-01		-7.36E+00	2.34E-01		-3.29E+00	1.63E-18	Down	4.12E-01	6.65E-02		Unigene110879_All//gi|24461866|gb|AAM22553.1|AF506028_20//2.00E-37//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene110879_All//4.00E-102//gi|48775674|gb|CO085040.1|CO085040			ko04626|Plant-pathogen interaction		nr +
Unigene110881_All	651	0.16	0.00	0.00	0.38	0.26	0.14	2.40	0.06	0.06	-7.33E+00	3.76E-01		-7.33E+00	3.98E-01		-5.33E-01	7.13E-01		-1.46E+00	4.07E-01		-5.23E+00	8.04E-10	Down	-5.30E+00	2.73E-10	Down	Unigene110881_All//gi|58294490|gb|AAW70161.1|//1.00E-33//GEX2 [Arabidopsis thaliana]	Unigene110881_All//2.00E-35//AT5G49150| GEX2 (GAMETE EXPRESSED 2)	Unigene110881_All//0.00E+00//gi|164365009|gb|ES831842.1|ES831842				nr -
Unigene110883_All	332	0.00	0.00	0.00	0.00	0.00	0.00	5.22	0.25	1.08	null	null		null	null		null	null		null	null		-4.37E+00	6.16E-10	Down	-2.27E+00	5.17E-06	Down	Unigene110883_All//gi|225444704|ref|XP_002278093.1//6.00E-41//PREDICTED: similar to aldehyde dehydrogenase family 7 member A1 [Vitis vinifera]	Unigene110883_All//4.00E-42//AT1G54100| ALDH7B4 (Aldehyde Dehydrogenase 7B4); 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase			ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00350|Tyrosine metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr -
Unigene110886_All	346	2.27	1.61	0.92	1.58	0.90	0.39	5.99	1.93	3.91	-4.94E-01	5.30E-01		-1.30E+00	1.38E-01		-8.22E-01	3.96E-01		-2.02E+00	7.05E-02		-1.63E+00	1.21E-04	Down	-6.13E-01	1.11E-01		Unigene110886_All//gi|18405757|ref|NP_564717.1//8.00E-12//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|30102878|gb|AAP21357.1| At1g56300 [Arabidopsis thaliana]	Unigene110886_All//3.00E-13//AT1G56300| DNAJ heat shock N-terminal domain-containing protein	Unigene110886_All//1.00E-90//TC144885				nr -
Unigene110887_All	609	0.00	0.00	0.00	0.00	0.00	0.00	3.47	1.03	0.00	null	null		null	null		null	null		null	null		-1.75E+00	3.84E-05	Down	-1.18E+01	1.40E-15	Down								
Unigene110888_All	460	0.00	0.00	0.35	0.22	0.07	0.20	2.48	0.27	0.26	null	null		8.44E+00	2.40E-01		-1.53E+00	5.88E-01		-1.41E-01	9.52E-01		-3.19E+00	1.96E-05	Down	-3.26E+00	8.94E-06	Down								
Unigene110889_All	453	2.08	6.38	1.41	1.54	1.22	0.50	2.71	2.86	0.35	1.62E+00	4.40E-05	Up	-5.60E-01	4.39E-01		-3.40E-01	6.80E-01		-1.63E+00	7.45E-02		7.96E-02	8.90E-01		-2.94E+00	1.14E-05	Down			Unigene110889_All//4.00E-131//TC178548					
Unigene110890_All	461	0.34	0.00	0.58	0.00	0.07	0.20	2.84	0.63	0.60	-8.41E+00	2.17E-01		7.62E-01	6.44E-01		6.22E+00	8.37E-01		7.61E+00	4.80E-01		-2.16E+00	2.57E-04	Down	-2.23E+00	1.19E-04	Down			Unigene110890_All//5.00E-07//TC178893					
Unigene110891_All	276	0.00	0.00	0.00	0.18	0.25	0.16	1.84	0.30	0.00	null	null		null	null		4.67E-01	9.60E-01		-1.42E-01	9.56E-01		-2.60E+00	2.05E-02		-1.08E+01	5.55E-04	Down			Unigene110891_All//3.00E-32//gi|164346740|gb|ES822710.1|ES822710					
Unigene110892_All	320	0.16	0.00	0.17	0.62	0.65	0.28	2.11	0.00	0.50	-7.35E+00	6.18E-01		2.54E-02	9.96E-01		5.23E-02	9.89E-01		-1.14E+00	5.70E-01		-1.10E+01	6.34E-05	Down	-2.09E+00	1.27E-02		Unigene110892_All//gi|195633079|gb|ACG36723.1|//5.00E-08//transcriptional activator FHA1 [Zea mays] >gi|195637976|gb|ACG38456.1| transcriptional activator FHA1 [Zea mays] >gi|195648198|gb|ACG43567.1| transcriptional activator FHA1 [Zea mays]	Unigene110892_All//6.00E-14//AT3G07220| transcriptional activator, putative	Unigene110892_All//4.00E-50//DT049758				nr +
Unigene110895_All	402	0.00	0.00	0.00	1.36	1.28	0.22	6.84	0.21	0.69	null	null		null	null		-8.52E-02	9.07E-01		-2.60E+00	2.93E-02		-5.04E+00	1.05E-16	Down	-3.30E+00	4.24E-13	Down	Unigene110895_All//gi|18411885|ref|NP_565175.1|//4.00E-17//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|21537200|gb|AAM61541.1| RNA recognition motif-containing protein SEB-4 [Arabidopsis thaliana] >gi|124300976|gb|ABN04740.1| At1g78260 [Arabidopsis thaliana]	Unigene110895_All//2.00E-18//AT1G78260| RNA recognition motif (RRM)-containing protein	Unigene110895_All//8.00E-120//gi|78345885|gb|DT566159.1|DT566159				nr -
Unigene110896_All	448	0.00	0.00	0.00	0.00	0.00	0.00	2.27	2.24	24.10	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		3.41E+00	5.22E-50	Up								
Unigene110897_All	519	0.00	0.98	0.00	0.10	0.00	0.44	1.47	0.00	0.38	9.93E+00	4.05E-03		null	null		-6.59E+00	5.62E-01		2.18E+00	3.23E-01		-1.05E+01	1.68E-05	Down	-1.93E+00	1.14E-02									
Unigene110899_All	421	0.00	0.00	0.00	0.36	0.16	0.00	2.61	0.89	0.00	null	null		null	null		-1.12E+00	5.85E-01		-8.47E+00	2.34E-01		-1.55E+00	1.12E-02		-1.14E+01	3.33E-08	Down	Unigene110899_All//gi|115462287|ref|NP_001054743.1|//9.00E-19//Os05g0164900 [Oryza sativa Japonica Group] >gi|113578294|dbj|BAF16657.1| Os05g0164900 [Oryza sativa Japonica Group]	Unigene110899_All//9.00E-22//AT5G01660| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Kelch repeat type 1 (InterPro:IPR006652), Galactose oxidase/kelch, beta-propeller (InterPro:IPR011043), Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089), Kelch-type beta propeller (InterPro:IPR015915); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11000.2); Has 12390 Blast hits to 5423 proteins in 323 species: Archae - 22; Bacteria - 787; Metazoa - 8729; Fungi - 223; Plants - 966; Viruses - 639; Other Eukaryotes - 1024 (source: NCBI BLink).						nr +
Unigene1109_All	1236	3.81	1.80	4.39	5.88	5.85	7.45	19.12	25.60	14.12	-1.08E+00	1.32E-04	Down	2.06E-01	4.64E-01		-8.20E-03	9.69E-01		3.41E-01	8.70E-02		4.21E-01	8.12E-07		-4.38E-01	7.54E-06		Unigene1109_All//gi|15220976|ref|NP_172253.1|//1.00E-176//ATMPK8; MAP kinase [Arabidopsis thaliana] >gi|30685711|ref|NP_849685.1| ATMPK8; MAP kinase [Arabidopsis thaliana] >gi|110287680|sp|Q9LM33.2|MPK8_ARATH RecName: Full=Mitogen-activated protein kinase 8; Short=MAP kinase 8; Short=AtMPK8 >gi|9719729|gb|AAF97831.1|AC034107_14 Strong similarity (practically identical) to ATMPK8 gene from Arabidopsis thaliana gb|AB038693 and contains a eukaryotic protein kinase PF|00069 domain. ESTs gb|AV526779, gb|AV527934, gb|AV540522, gb|T22988, gb|R90476, gb|Z24497, gb|N97150, gb|AA713291, gb|AI100188 come from this gene	Unigene1109_All//8.00E-155//AT1G18150| ATMPK8; MAP kinase	Unigene1109_All//0.00E+00//TC176812		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene110900_All	347	0.00	0.00	0.00	0.00	0.00	0.13	25.59	0.36	0.00	null	null		null	null		null	null		7.02E+00	7.02E-01		-6.15E+00	9.52E-58	Down	-1.46E+01	2.26E-65	Down	Unigene110900_All//gi|84514187|gb|ABC39102.1|//1.00E-26//cytochrome P450 monooxygenase CYP706A12 [Medicago truncatula]	Unigene110900_All//6.00E-21//AT5G44620| CYP706A3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene110900_All//3.00E-91//TC134420		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene110905_All	410	0.00	0.00	0.00	0.00	0.00	0.00	1.55	0.00	0.19	null	null		null	null		null	null		null	null		-1.06E+01	1.23E-04	Down	-2.99E+00	2.58E-03		Unigene110905_All//gi|219110933|ref|XP_002177218.1|//4.00E-34//gelsolin [Phaeodactylum tricornutum CCAP 1055/1] >gi|217411753|gb|EEC51681.1| gelsolin [Phaeodactylum tricornutum CCAP 1055/1]	Unigene110905_All//1.00E-31//AT2G41740| VLN2 (VILLIN 2); actin binding					nr -

Unigene110909_All	287	0.00	0.00	0.00	0.00	0.00	0.00	8.25	1.46	0.28	null	null		null	null		null	null		null	null		-2.50E+00	1.92E-08	Down	-4.89E+00	8.31E-15	Down	Unigene110909_All//gi|224085888|ref|XP_002307727.1|//1.00E-26//tubulin, beta chain [Populus trichocarpa] >gi|222857176|gb|EEE94723.1| tubulin, beta chain [Populus trichocarpa]	Unigene110909_All//9.00E-23//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene110909_All//7.00E-33//TC166231		ko04145|Phagosome		nr -
Unigene11091_All	3281	1.82	4.34	2.63	4.78	3.97	6.41	12.54	17.02	21.37	1.26E+00	2.39E-15	Up	5.32E-01	9.54E-03		-2.70E-01	5.88E-02		4.24E-01	3.33E-04		4.41E-01	2.40E-12		7.69E-01	4.72E-41		Unigene11091_All//gi|15217662|ref|NP_176634.1|//0.00E+00//RWP-RK domain-containing protein [Arabidopsis thaliana]	Unigene11091_All//0.00E+00//AT1G64530| RWP-RK domain-containing protein	Unigene11091_All//0.00E+00//TC177468	RWP-RK		GO:0006950//GO:0009987//GO:0010035//GO:0042126//GO:0043231	nr -
Unigene110911_All	383	0.00	0.00	0.00	0.00	0.00	0.00	1.66	1.31	0.10	null	null		null	null		null	null		null	null		-3.39E-01	6.63E-01		-3.99E+00	5.82E-04	Down	Unigene110911_All//gi|223992823|ref|XP_002286095.1|//3.00E-46//guanine nucleotide binding protein beta subunit-like protein [Thalassiosira pseudonana CCMP1335] >gi|220977410|gb|EED95736.1| guanine nucleotide binding protein beta subunit-like protein [Thalassiosira pseudonana CCMP1335]	Unigene110911_All//2.00E-43//AT1G18080| ATARCA; nucleotide binding			ko03022|Basal transcription factors		nr +
Unigene110915_All	363	0.00	0.00	0.00	0.00	0.00	0.00	1.98	0.23	0.00	null	null		null	null		null	null		null	null		-3.10E+00	1.40E-03		-1.10E+01	1.78E-05	Down	Unigene110915_All//gi|262360187|gb|ACY38051.2|//2.00E-19//cysteine proteinase C1A [Dactylis glomerata]	Unigene110915_All//5.00E-19//AT5G50260| cysteine proteinase, putative					nr -
Unigene110917_All	317	0.00	0.00	0.63	0.00	0.14	1.87	0.00	0.00	null	null		null	null		-9.30E+00	8.47E-02		-2.14E+00	3.48E-01		-1.09E+01	2.39E-04	Down	-1.09E+01	1.41E-04	Down	Unigene110917_All//gi|115468064|ref|NP_001057631.1|//1.00E-31//Os06g0174300 [Oryza sativa Japonica Group] >gi|113595671|dbj|BAF19545.1| Os06g0174300 [Oryza sativa Japonica Group]	Unigene110917_All//1.00E-44//AT3G05390| unknown protein					nr -
Unigene110919_All	342	0.00	0.00	0.16	0.00	0.00	0.00	5.44	0.73	0.70	null	null		7.28E+00	6.40E-01		null	null		null	null		-2.89E+00	8.76E-08	Down	-2.96E+00	2.82E-08	Down	Unigene110919_All//gi|7105717|gb|AB84202.2|//1.00E-09//plasma membrane proton ATPase [Kosteletzkya virginica]	Unigene110919_All//4.00E-10//AT2G24520| AHA5 (Arabidopsis H(+)-ATPase 5); ATPase	Unigene110919_All//7.00E-21//C0113495		ko00190|Oxidative phosphorylation		nr -
Unigene110925_All	399	0.00	0.00	0.00	0.00	0.09	0.11	0.32	5.55	0.80	null	null		null	null		6.43E+00	8.37E-01		6.82E+00	7.02E-01		4.13E+00	4.45E-12	Up	1.33E+00	2.93E-01		Unigene110925_All//gi|224083966|ref|XP_002307190.1|//2.00E-13//predicted protein [Populus trichocarpa] >gi|222856639|gb|EEE94186.1| predicted protein [Populus trichocarpa]						nr +
Unigene110926_All	496	0.00	0.00	0.21	0.00	0.07	0.00	2.30	0.51	0.96	null	null		7.75E+00	4.02E-01		6.12E+00	8.37E-01		null	null		-2.19E+00	6.84E-04	Down	-1.26E+00	2.42E-02		Unigene110926_All//gi|79390803|ref|NP_187087.2|//4.00E-23//PDLP4 (PLASMODESMATA-LOCATED PROTEIN 4) [Arabidopsis thaliana] >gi|158563987|sp|Q6E263.2|CRR39_ARATH RecName: Full=Cysteine-rich repeat secretory protein 39; Flags: Precursor	Unigene110926_All//6.00E-19//AT3G04370| PDLP4 (PLASMODESMATA-LOCATED PROTEIN 4)					nr +
Unigene110928_All	361	0.00	0.00	0.00	0.00	0.00	0.00	6.79	3.47	2.98	null	null		null	null		null	null		null	null		-9.68E-01	7.64E-03		-1.19E+00	8.55E-04	Down			Unigene110928_All//5.00E-28//BG445269				
Unigene11093_All	4362	4.21	1.85	3.64	9.52	8.94	6.21	10.79	4.96	5.93	-1.19E+00	4.07E-18	Down	-2.11E-01	1.43E-01		-9.19E-02	3.43E-01		-6.17E-01	1.52E-14		-1.12E+00	2.33E-50	Down	-8.64E-01	5.50E-34		Unigene11093_All//gi|42570286|ref|NP_849997.2|//0.00E+00//CLASP (CLIP-ASSOCIATED PROTEIN); binding [Arabidopsis thaliana]	Unigene11093_All//0.00E+00//AT2G20190| CLASP (CLIP-ASSOCIATED PROTEIN); binding	Unigene11093_All//0.00E+00//TC176731			GO:0000087//GO:0005819//GO:0016020//GO:0031617//GO:0040007	nr -
Unigene110931_All	255	3.28	2.78	1.25	2.93	4.05	10.45	3.15	2.62	3.12	-2.39E-01	7.25E-01		-1.39E+00	9.66E-02		4.67E-01	5.51E-01		1.83E+00	1.12E-05	Up	-2.65E-01	7.05E-01		-1.18E-02	9.78E-01				Unigene110931_All//8.00E-14//DT463109				
Unigene110932_All	622	0.00	0.00	0.00	0.00	0.00	0.00	1.09	0.94	0.00	null	null		null	null		null	null		null	null		-2.09E-01	7.82E-01		-1.01E+01	3.57E-05	Down							ESTscan -
Unigene110934_All	378	0.00	0.00	0.00	0.00	0.00	0.00	2.91	0.33	0.74	null	null		null	null		null	null		null	null		-3.13E+00	3.47E-05	Down	-1.98E+00	1.39E-03		Unigene110934_All//gi|110430668|gb|AB673458.1|//7.00E-20//AP2 domain-containing protein [Oryza brachyantha]	Unigene110934_All//2.00E-18//AT5G19790| RAP2.11 (related to AP2 11); DNA binding / transcription factor		AP2-EREBP			nr +
Unigene110937_All	379	0.00	0.00	0.00	0.00	0.18	0.48	4.46	0.77	0.95	null	null		null	null		7.51E+00	6.14E-01		8.90E+00	1.95E-01		-2.53E+00	2.71E-06	Down	-2.24E+00	8.65E-06	Down			Unigene110937_All//2.00E-68//DW515284				
Unigene110948_All	405	0.00	0.00	0.00	0.00	0.00	0.00	2.82	0.93	0.10	null	null		null	null		null	null		null	null		-1.60E+00	7.51E-03		-4.84E+00	2.34E-07	Down	Unigene110948_All//gi|2780194|emb|CAA05979.1|//2.00E-15//adenine nucleotide translocator [Lupinus albus]	Unigene110948_All//2.00E-16//AT5G13490| AAC2 (ADP/ATP carrier 2); ATP:ADP antiporter/ binding					nr +
Unigene110995_All	841	7.90	9.22	10.64	12.26	14.13	8.32	16.44	11.53	7.15	2.22E-01	3.28E-01		4.29E-01	3.57E-02		2.04E-01	2.70E-01		-5.59E-01	1.41E-03		-5.12E-01	1.40E-04		-1.20E+00	1.30E-17	Down	Unigene110995_All//gi|49523817|emb|CAF18249.1|//1.00E-148//SEU3A protein [Antirrhinum majus]	Unigene110995_All//8.00E-148//AT1G43850| SEU (seuss); DNA binding / protein binding / protein heterodimerization/ transcription cofactor	Unigene110995_All//0.00E+00//gi|84148586|gb|DN779886.1|DN779886				nr +
Unigene110952_All	294	0.00	2.24	0.18	0.85	1.29	0.77	0.43	0.14	0.00	1.11E+01	6.26E-04	Up	7.50E+00	6.40E-01		6.05E-01	6.59E-01		-1.41E-01	9.29E-01		-1.60E+00	5.35E-01		-8.75E+00	2.00E-01		Unigene110952_All//gi|15219557|ref|NP_171875.1|//1.00E-06//SOM (SOMNUS); nucleic acid binding / transcription factor [Arabidopsis thaliana] >gi|75268098|sp|Q9ZWA1.1|C3H2_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 2; Short=AtC3H2; AltName: Full=Protein SOMNUS; Short=SOM >gi|4204308|gb|AAD10689.1| Hypothetical protein [Arabidopsis thaliana]	Unigene110952_All//6.00E-06//AT5G44260| zinc finger (CCCH-type) family protein	Unigene110952_All//3.00E-72//TC129629	C3H			nr +
Unigene110953_All	822	0.00	0.00	0.00	0.00	0.00	0.00	2.78	1.17	0.44	null	null		null	null		null	null		null	null		-1.25E+00	1.20E-03		-2.67E+00	4.62E-09	Down	Unigene110953_All|gi|1706740|sp|P52837.1|F4ST_FLACH//4.00E-50//RecName: Full=Flavonol 4'-sulfotransferase; Short=F4-ST >gi|168169|gb|AAA33343.1| flavonol 4'-sulfotransferase [Flaveria chlorae folia]	Unigene110953_All//1.00E-50//AT1G18590| SOT17 (SULFOTRANSFERASE 17); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene110953_All//4.00E-12//EX167975		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr -
Unigene110955_All	371	0.00	0.00	0.00	0.00	0.00	0.00	2.39	0.79	0.11	null	null		null	null		null	null		null	null		-1.60E+00	2.18E-02		-4.48E+00	1.23E-05	Down							ESTscan +
Unigene110956_All	335	0.31	0.30	0.16	0.00	1.03	0.67	1.89	0.12	0.36	-4.65E-02	9.91E-01		-9.74E-01	7.22E-01		1.00E+01	3.02E-02		9.40E+00	1.19E-01		-3.92E+00	9.81E-04	Down	-2.41E+00	8.12E-03				Unigene110956_All//2.00E-08//DR461672				
Unigene110957_All	375	0.00	0.00	0.00	0.00	0.00	0.00	5.07	0.00	0.00	null	null		null	null		null	null		null	null		-1.23E+01	1.81E-13	Down	-1.23E+01	4.91E-14	Down							ESTscan +
Unigene110958_All	218	0.00	0.00	0.00	0.91	0.00	0.00	2.72	0.00	0.00	null	null		null	null		-9.84E+00	8.47E-02		-9.84E+00	1.34E-01		-1.14E+01	2.39E-04	Down	-1.14E+01	1.41E-04	Down	Unigene110958_All//gi|297607012|ref|NP_001059355.2|//9.00E-07//Os07g0273700 [Oryza sativa Japonica Group] >gi|255677660|dbj|BAF21269.2| Os07g0273700 [Oryza sativa Japonica Group]		Unigene110958_All//2.00E-11//TC168228				nr -
Unigene110959_All	296	0.00	0.00	0.00	0.00	0.00	0.00	1.71	0.00	0.00	null	null		null	null		null	null		null	null		-1.07E+01	8.90E-04	Down	-1.07E+01	5.55E-04	Down	Unigene110959_All//gi|116056464|emb|CAL32753.1|//1.00E-21//ribosomal protein S20 (ISS) [Ostreococcus tauri]	Unigene110959_All//3.00E-21//AT5G62300| 40S ribosomal protein S20 (RPS20C)			ko03010|Ribosome		nr -
Unigene110962_All	255	0.00	0.00	0.00	0.00	0.00	0.00	6.13	1.48	1.56	null	null		null	null		null	null		null	null		-2.06E+00	9.44E-05	Down	-1.97E+00	9.58E-05	Down			Unigene110962_All//3.00E-10//TC167637				
Unigene110965_All	215	0.97	0.00	0.00	2.78	3.68	2.94	3.34	0.97	0.37	-9.93E+00	1.23E-01		-9.93E+00	1.46E-01		4.06E-01	6.32E-01		8.10E-02	9.45E-01		-1.78E+00	2.79E-02		-3.17E+00	8.09E-04	Down	Unigene110965_All|gi|224152830|ref|XP_002337280.1|//7.00E-12//BED finger-nhs-1rr resistance protein [Populus trichocarpa] >gi|222838678|gb|EEE77043.1| BED finger-nhs-1rr resistance protein [Populus trichocarpa]	Unigene110965_All//5.00E-10//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene110965_All//4.00E-92//DT463318		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene110967_All	468	0.00	0.22	1.02	0.00	0.00	0.19	1.63	0.36	0.00	7.76E+00	3.90E-01		1.00E+01	7.49E-03		null	null		7.59E+00	4.80E-01		-2.19E+00	7.78E-03		-1.07E+01	8.88E-06	Down			Unigene110967_All//8.00E-145//ES806643				
Unigene110969_All	481	0.00	0.00	0.00	0.00	0.00	0.00	1.14	0.70	0.00	null	null		null	null		null	null		null	null		-7.17E-01	4.22E-01		-1.02E+01	2.81E-04	Down	Unigene110969_All//gi|40287526|gb|AAR83877.1|//6.00E-33//60S ribosomal protein L19 [Capsicum annuum]	Unigene110969_All//7.00E-26//AT3G16780| 60S ribosomal protein L19 (RPL19B)	Unigene110969_All//1.00E-07//TC132886		ko03010|Ribosome	GO:0043231	nr -
Unigene110972_All	672	0.08	0.00	0.16	0.15	0.15	0.07	10.76	0.87	1.84	-6.28E+00	6.18E-01		1.02E+00	7.04E-01		5.16E-02	9.68E-01		-1.14E+00	6.78E-01		-3.63E+00	5.99E-35	Down	-2.55E+00	9.72E-26	Down	Unigene110972_All|gi|109900626|gb|ABG47806.1|//1.00E-42//pectin methlyesterase inhibitor protein 1 [Capsicum annuum] >gi|110631514|gb|ABG81102.1| pectin methlyesterase inhibitor protein 1 [Capsicum annuum]	Unigene110972_All//2.00E-36//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene110972_All//1.00E-14//DW502487		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene110974_All	516	0.00	0.00	0.00	0.00	0.00	0.00	2.54	0.08	0.00	null	null		null	null		null	null		null	null		-4.97E+00	4.05E-08	Down	-1.13E+01	9.85E-10	Down	Unigene110974_All|gi|301093349|ref|XP_002896775.1|//1.00E-34//60S acidic ribosomal protein P0 [Phytophthora infestans T30-4] >gi|262108658|gb|EEY66710.1| 60S acidic ribosomal protein P0 [Phytophthora infestans T30-4]	Unigene110974_All//8.00E-31//AT2G40010| 60S acidic ribosomal protein P0 (RPP0A)			ko03010|Ribosome	GO:0005198//GO:0006412//GO:0030529	nr -
Unigene110976_All	405	0.00	0.00	0.00	0.00	0.00	0.00	3.55	0.10	0.00	null	null		null	null		null	null		null	null		-5.10E+00	5.72E-09	Down	-1.18E+01	1.19E-10	Down	Unigene110976_All|gi|6094086|sp|O65353.1|RL5_HELAN//2.00E-40//RecName: Full=60S ribosomal protein L5 >gi|3153904|gb|AAC17448.1| RPL5A-related protein [Helianthus annuus]	Unigene110976_All//1.00E-17//AT3G25520| ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); 5S rRNA binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003002//GO:0005198//GO:0009536//GO:0009887//GO:0010467//GO:0015934//GO:0016020//GO:0019843//GO:0022613//GO:0031981//GO:0046914//GO:0051169//GO:0065003	nr -
Unigene110977_All	462	0.00	0.00	0.00	0.00	0.00	0.00	2.29	12.57	0.00	null	null		null	null		null	null		null	null		2.46E+00	2.75E-19	Up	-1.12E+01	6.72E-08	Down							
Unigene110978_All	707	0.00	0.00	0.00	0.00	0.00	0.00	2.81	0.77	0.11	null	null		null	null		null	null		null	null		-1.87E+00	2.98E-05	Down	-4.64E+00	3.57E-12	Down	Unigene110978_All//gi|159471131|ref|XP_001693710.1|//4.00E-78//ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|269969596|sp|A8HS48.1|RS3A_CHLRE RecName: Full=40S ribosomal protein S3a >gi|158283213|gb|EDP08964.1| ribosomal protein S3a [Chlamydomonas reinhardtii]	Unigene110978_All//2.00E-63//AT4G34670| 40S ribosomal protein S3A (RPS3aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr -
Unigene110980_All	1651	0.00	0.00	0.00	0.06	0.00	0.00	4.00	1.16	1.11	null	null		null	null		-5.91E+00	3.16E-01		-5.91E+00	4.04E-01		-1.78E+00	1.01E-14	Down	-1.85E+00	5.42E-16	Down	Unigene110980_All//gi|156447779|gb|ABU63668.1|//1.00E-95//CYCLOPS [Lotus japonicus]						nr -
Unigene110981_All	411	0.00	0.00	0.00	0.00	0.00	0.00	2.67	0.71	0.19	null	null		null	null		null	null		null	null		-1.91E+00	2.64E-03		-3.79E+00	3.27E-06	Down							ESTscan +
Unigene110983_All	319	0.00	0.00	0.00	0.00	0.00	0.00	2.78	0.66	0.00	null	null		null	null		null	null		null	null		-2.09E+00	4.71E-03		-1.14E+01	1.10E-06	Down	Unigene110983_All//gi|247421835|gb|ACS96445.1|//1.00E-34//S18.A ribosomal protein [Jatropha curcas]	Unigene110983_All//8.00E-30//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006412//GO:0015935//GO:0016020//GO:0003012//GO:0031981	nr +

Unigene110985_All	272	18.85	54.77	24.47	11.72	13.17	25.74	10.88	22.28	10.11	1.54E+00	1.56E-21	Up	3.77E-01	1.28E-01		1.68E-01	6.54E-01		1.13E+00	3.58E-07	Up	1.03E+00	2.12E-06	Up	-1.07E-01	7.47E-01		Unigene110985_All//gi|224144535|ref|XP_002323324.1|//5.00E-10//cytochrome P450 [Populus trichocarpa] >gi|222862199|gb|EEE99705.1| cytochrome P450 [Populus trichocarpa]	Unigene110985_All//3.00E-065//AT5G23190| CYP96B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene110985_All//9.00E-60//TC133857			GO:0005506//GO:0016491	nr -
Unigene110986_All	1899	0.00	0.00	0.00	0.10	0.00	0.00	7.95	0.04	0.04	null	null		null	null		-6.71E+00	8.47E-02		-6.71E+00	1.34E-01		-7.50E+00	3.26E-103	Down	-7.56E+00	4.12E-107	Down	Unigene110986_All//gi|224119978|ref|XP_002331107.1|//1.00E-157//cytochrome P450 [Populus trichocarpa] >gi|222872835|gb|EEF09966.1| cytochrome P450 [Populus trichocarpa]	Unigene110986_All//5.00E-139//AT4G37310| CYP81H1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene110986_All//6.00E-16//TC178809		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene110990_All	427	0.00	0.00	0.00	0.00	0.00	0.00	3.37	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	3.33E-10	Down	-1.17E+01	1.19E-10	Down	Unigene110990_All//sp|P60372|KR104_HUMAN//7.00E-07//Keratin-associated protein 10-4 OS=Homo sapiens GN=KRTAP10-4 PE=2 SV=1						swissprot +
Unigene110991_All	817	0.38	0.37	0.26	0.24	0.00	0.17	1.24	2.46	5.02	-4.62E-02	9.85E-01		-5.60E-01	6.64E-01		-7.93E+00	8.47E-02		-5.57E-01	7.33E-01		9.83E-01	1.63E-02		2.02E+00	2.88E-11	Up	Unigene110991_All//gi|223452359|gb|ACM89507.1|//5.00E-89//NAK-type protein kinase [Glycine max]	Unigene110991_All//4.00E-76//AT5G47070| protein kinase, putative	Unigene110991_All//1.00E-55//ES808920		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0016020	nr +
Unigene110994_All	332	0.00	0.00	0.00	0.00	0.00	0.00	1.91	1.51	0.00	null	null		null	null		null	null		null	null		-3.39E-01	6.63E-01		-1.09E+01	7.12E-05	Down	Unigene110994_All//gi|115436514|ref|NP_001043015.1|//2.00E-28//Os01g0358400 [Oryza sativa Japonica Group] >gi|113532546|dbj|BAF04929.1| Os01g0358400 [Oryza sativa Japonica Group] >gi|149391309|gb|ABR25672.1| 40S ribosomal protein S4 [Oryza sativa Indica Group]	Unigene110994_All//2.00E-28//AT5G58420| 40S ribosomal protein S4 (RPS4D)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr -
Unigene110995_All	497	0.00	0.00	0.00	0.00	0.00	0.00	4.59	0.00	0.64	null	null		null	null		null	null		null	null		-1.22E+01	3.78E-16	Down	-2.84E+00	1.28E-09	Down								
Unigene110996_All	439	0.00	0.00	0.00	0.00	0.00	0.00	2.70	0.38	0.09	null	null		null	null		null	null		null	null		-2.82E+00	4.41E-05	Down	-4.89E+00	1.20E-07	Down	Unigene110996_All//gi|15809990|gb|AAL06922.1|//3.00E-10//AT5g60530/muf9_180 [Arabidopsis thaliana]				ko03040|Spliceosome		nr -
Unigene110997_All	339	0.00	0.00	0.00	0.00	0.00	0.00	2.99	0.49	0.24	null	null		null	null		null	null		null	null		-2.60E+00	3.81E-04	Down	-3.67E+00	1.15E-05	Down	Unigene110997_All//gi|255103522|gb|ACH70610.1|//5.00E-49//alpha tubulin [Ulva fasciata]	Unigene110997_All//7.00E-49//AT1G50010| TUA2; structural constituent of cytoskeleton	Unigene110997_All//7.00E-12//gi|164334548|gb|EV483418.1|EV483418		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene111_All	12603	1.17	5.72	2.68	2.80	4.02	4.35	8.92	22.25	23.52	2.28E+00	4.63E-173	Up	1.19E+00	1.07E-31	Up	5.20E-01	2.96E-14		6.35E-01	7.90E-20		1.32E+00	0.00E+00	Up	1.40E+00	0.00E+00	Up	Unigene111_All//gi|225432116|ref|XP_002274451.1|//0.00E+00//PREDICTED: similar to vacuolar protein sorting 13C protein-like [Vitis vinifera]	Unigene111_All//0.00E+00//AT4G17140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pleckstrin homology (InterPro:IPR001849); BEST Arabidopsis thaliana protein match is: phosphoinositide binding (TAIR:AT1G48090.2); Has 1924 Blast hits to 1182 proteins in 161 species: Archae - 0; Bacteria - 16; Metazoa - 911; Fungi - 304; Plants - 271; Viruses - 0; Other Eukaryotes - 422 (source: NCBI BLink).	Unigene111_All//0.00E+00//TC169119				nr +
Unigene1110_All	1325	5.05	2.49	3.46	4.77	6.19	8.15	19.82	21.45	21.68	-1.02E+00	9.20E-06	Down	-5.48E-01	2.14E-02		3.74E-01	7.04E-02		7.71E-01	6.02E-06		1.14E-01	2.78E-01		1.30E-01	1.86E-01		Unigene1110_All//gi|15220976|ref|NP_173253.1|//0.00E+00//ATMPK8; MAP kinase [Arabidopsis thaliana] >gi|30685711|ref|NP_849685.1| ATMPK8; MAP kinase [Arabidopsis thaliana] >gi|110287680|sp|Q9LM33.2|MPK8_ARATH RecName: Full=Mitogen-activated protein kinase 8; Short=MAP kinase 8; Short=AtMPK8 >gi|97179729|gb|AAP97831.1|AC034107_14 Strong similarity (practically identical) to ATMPK8 gene from Arabidopsis thaliana gb|AB038693 and contains a eukaryotic protein kinase PF|00069 domain. ESTs gb|AV526779, gb|AV527934, gb|AV540522, gb|T22988, gb|R90476, gb|224497, gb|N97150, gb|AA713291, gb|AI100188 come from this gene	Unigene1110_All//4.00E-165//AT1G18150| ATMPK8; MAP kinase	Unigene1110_All//0.00E+00//TC176812		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0016020//GO:0023060//GO:0032559	nr -
Unigene1100_All	370	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.68	2.05	null	null		null	null		null	null		null	null		1.57E+00	3.27E-01		3.16E+00	6.83E-04	Up	Unigene1100_All//gi|297722553|ref|NP_001173640.1|//2.00E-27//Os03g0744650 [Oryza sativa Japonica Group] >gi|255674888|dbj|BAH92368.1| Os03g0744650 [Oryza sativa Japonica Group]	Unigene1100_All//1.00E-28//AT1G03060| WD-40 repeat family protein / beige-related	Unigene1100_All//5.00E-93//TC145957			GO:0046914	nr -
Unigene111000_All	336	0.00	0.00	0.00	0.00	0.00	0.00	2.14	0.00	0.24	null	null		null	null		null	null		null	null		-1.11E+01	3.27E-05	Down	-3.17E+00	8.09E-04	Down								ESTscan -
Unigene111002_All	305	0.00	0.00	0.00	0.00	0.00	0.00	3.60	0.69	0.26	null	null		null	null		null	null		null	null		-2.40E+00	4.11E-04	Down	-3.79E+00	3.27E-06	Down	Unigene111002_All//gi|159476204|ref|XP_001696201.1|//3.00E-18//ribosomal protein S8, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158282426|gb|EDF08178.1| ribosomal protein S8 [Chlamydomonas reinhardtii]	Unigene111002_All//8.00E-17//AT5G39240| 40S ribosomal protein S8 (RPS8B)			ko03010|Ribosome	GO:0030529//GO:0043229//GO:0044444	nr -
Unigene111011_All	405	0.00	0.00	0.00	0.00	0.00	0.00	8.14	2.27	0.49	null	null		null	null		null	null		null	null		-1.84E+00	4.43E-08	Down	-4.05E+00	2.95E-18	Down	Unigene111011_All//gi|238014838|gb|ACR38454.1|//1.00E-21//unknown [Zea mays]		Unigene111011_All//0.00E+00//TC146753				nr -
Unigene111013_All	666	0.00	0.00	0.00	0.00	0.00	0.00	1.71	0.44	0.00	null	null		null	null		null	null		null	null		-1.96E+00	1.69E-03		-1.07E+01	1.65E-08	Down	Unigene111013_All//sp|Q58842|DD3_DICDI//9.00E-29//Protein DD3-3 OS=Dictyostelium discoideum GN=DD3-3 PE=2 SV=1						swissprot +
Unigene111014_All	370	0.00	0.00	0.00	0.13	0.00	0.00	3.43	0.90	1.29	null	null		null	null		-7.07E+00	5.62E-01		-7.07E+00	6.43E-01		-1.92E+00	9.98E-04	Down	-1.41E+00	8.06E-03				Unigene111014_All//1.00E-133//TC138525				
Unigene111015_All	435	0.00	0.00	0.00	0.00	0.00	0.00	4.18	0.77	0.64	null	null		null	null		null	null		null	null		-2.44E+00	1.77E-06	Down	-2.70E+00	1.86E-07	Down	Unigene111015_All//gi|297838233|ref|XP_002886998.1|//7.00E-07//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332839|gb|EFH63257.1| expressed protein [Arabidopsis lyrata subsp. lyrata]				ko03040|Spliceosome	GO:0005488	nr +
Unigene111022_All	272	0.00	0.37	0.20	1.28	0.76	0.50	3.89	1.23	0.88	8.54E+00	3.90E-01		7.61E+00	6.40E-01		-7.55E-01	5.67E-01		-1.36E+00	3.37E-01		-1.66E+00	8.55E-03		-2.14E+00	9.36E-04	Down								
Unigene111024_All	487	0.00	0.00	0.00	0.00	0.00	0.00	2.43	0.26	0.16	null	null		null	null		null	null		null	null		-3.24E+00	1.10E-05	Down	-3.89E+00	9.21E-07	Down								
Unigene111026_All	352	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.95	0.45	null	null		null	null		null	null		null	null		-1.66E+00	8.55E-03		-2.73E+00	1.12E-04	Down								
Unigene111028_All	543	0.00	0.00	0.00	0.00	0.00	0.00	5.61	0.00	0.07	null	null		null	null		null	null		null	null		-1.25E+01	1.58E-21	Down	-6.26E+00	7.97E-21	Down								
Unigene111029_All	583	0.00	0.00	0.00	0.00	0.00	0.00	2.83	0.57	2.32	null	null		null	null		null	null		null	null		-2.30E+00	1.36E-05	Down	-2.84E-01	5.50E-01									
Unigene111030_All	296	39.42	85.93	53.25	143.89	255.71	234.06	58.42	120.59	63.80	1.12E+00	1.18E-22	Up	4.34E-01	3.09E-03		8.30E-01	1.67E-47		7.02E-01	1.18E-29		1.05E+00	2.30E-34	Up	1.27E-01	3.12E-01		Unigene111030_All//gi|148645857|gb|ABR01221.1|//2.00E-30//MYB8 [Gossypium hirsutum]	Unigene111030_All//7.00E-30//AT4G38620| MYB4; DNA binding / transcription factor	Unigene111030_All//2.00E-91//TC167380	MYB		GO:0001071//GO:0003676//GO:0006350//GO:0009411//GO:0009719//GO:0010033//GO:0010468//GO:0043231	nr +
Unigene111033_All	373	0.00	0.00	0.00	0.00	0.00	0.00	4.31	0.34	0.21	null	null		null	null		null	null		null	null		-3.68E+00	2.83E-08	Down	-4.33E+00	1.41E-09	Down	Unigene111033_All//gi|238632211|gb|ACR50977.1|//1.00E-31//60s ribosomal protein L21 [Lycoris radiata]	Unigene111033_All//9.00E-31//AT1G09690| 60S ribosomal protein L21 (RPL21C)	Unigene111033_All//3.00E-08//TC169130		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr +
Unigene111038_All	811	0.00	0.37	0.00	0.00	0.00	0.00	4.59	0.41	0.69	8.55E+00	4.45E-02		null	null		null	null		null	null		-3.48E+00	1.24E-17	Down	-2.74E+00	1.16E-14	Down	Unigene111038_All//gi|297825707|ref|XP_002880736.1|//1.00E-53//bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326575|gb|EFH56995.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata]	Unigene111038_All//2.00E-54//AT2G26040| Bet v I allergen family protein				GO:0004871//GO:0009755//GO:0042802	nr +
Unigene111040_All	406	0.00	0.00	0.00	0.00	0.00	0.00	4.69	0.31	0.49	null	null		null	null		null	null		null	null		-3.92E+00	3.80E-10	Down	-3.26E+00	3.59E-09	Down	Unigene111040_All//gi|238617665|gb|ACR46954.1|//6.00E-69//alpha-tubulin [Rhodochaete parvula]	Unigene111040_All//1.00E-67//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene111040_All//1.00E-47//gi|11208953|gb|BF277883.1|BF277883		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene111042_All	278	0.00	0.00	0.00	0.00	0.00	0.00	2.28	0.15	0.00	null	null		null	null		null	null		null	null		-3.92E+00	9.81E-04	Down	-1.12E+01	7.12E-05	Down	Unigene111042_All//gi|124365534|gb|ABN09768.1|//1.00E-07//Cyclin-like F-box; Calcium-binding EF-hand [Medicago truncatula]					GO:0005488	nr +
Unigene111045_All	471	0.56	0.00	0.23	0.21	0.15	0.00	2.87	0.00	0.00	-9.12E+00	6.72E-02		-1.30E+00	4.37E-01		-5.33E-01	8.19E-01		-7.72E+00	4.04E-01		-1.15E+01	1.30E-09	Down	-1.15E+01	4.86E-10	Down	Unigene111045_All//gi|224094135|ref|XP_002310080.1|//2.00E-60//glycosyl hydrolase family 9 [Populus trichocarpa] >gi|222852983|gb|EEE90530.1| glycosyl hydrolase family 9 [Populus trichocarpa]	Unigene111045_All//2.00E-59//AT1G48930| AtGH9C1 (Arabidopsis thaliana glycosyl hydrolase 9C1); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene111045_All//0.00E+00//EST90572		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0005488//GO:0031410//GO:0044238	nr +
Unigene111048_All	430	0.00	0.00	0.00	0.00	0.00	0.00	2.75	0.19	0.09	null	null		null	null		null	null		null	null		-3.82E+00	2.12E-06	Down	-4.89E+00	1.20E-07	Down	Unigene111048_All//gi|11131946|sp|Q9ZNY3.1|CALR_EUGGR//3.00E-06//RecName: Full=Calreticulin; Flags: Precursor >gi|3970687|emb|CAA70945.1| calreticulin precursor [Euglena gracilis]				ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko00010|Glycolysis / Gluconeogenesis	GO:0005488//GO:0005622	nr +
Unigene111053_All	483	0.22	0.42	0.00	0.52	0.29	0.19	1.93	0.95	0.33	9.54E-01	6.22E-01		-7.76E+00	3.98E-01		-8.55E-01	5.74E-01		-1.46E+00	4.07E-01		-1.02E+00	1.21E-01		-2.55E+00	5.79E-04	Down			Unigene111053_All//1.00E-10//ESS39853				
Unigene111055_All	679	0.00	0.00	0.00	0.00	0.00	0.00	3.36	0.43	0.41	null	null		null	null		null	null		null	null		-2.96E+00	1.24E-09	Down	-3.03E+00	3.22E-10	Down			Unigene111055_All//2.00E-35//CF932145				
Unigene111056_All	362	0.00	0.00	0.00	0.00	0.00	0.00	4.09	0.23	0.55	null	null		null	null		null	null		null	null		-4.15E+00	2.75E-08	Down	-2.89E+00	1.35E-06	Down	Unigene111056_All//gi|226459877|gb|EEH57172.1|//3.00E-18//ribosomal protein [Micromonas pusilla CCMP1545]	Unigene111056_All//2.00E-06//AT5G56670| 40S ribosomal protein S30 (RPS30C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0031981	nr -
Unigene111060_All	617	0.00	0.00	0.00	0.00	0.00	0.00	1.71	0.07	0.00	null	null		null	null		null	null		null	null		-4.66E+00	1.94E-06	Down	-1.07E+01	6.72E-08	Down	Unigene111060_All//gi|70663983|emb|CAE04677.2|//3.00E-06//OSJNB0018A10.6 [Oryza sativa (japonica cultivar-group)]					GO:0005488	nr -
Unigene111063_All	359	0.00	0.00	0.00	0.00	0.00	0.00	8.01	4.42	3.22	null	null		null	null		null	null		null	null		-8.56E-01	9.39E-03		-1.32E+00	6.99E-05	Down			Unigene111063_All//3.00E-23//TC142576				
Unigene111064_All	528	0.00	0.00	0.00	0.00	0.00	0.00	2.96	0.08	0.00	null	null		null	null		null	null		null	null		-5.23E+00	8.04E-10	Down	-1.15E+01	1.42E-11	Down	Unigene111064_All//gi|195605794|gb|ACG24727.1|//6.00E-30//40S ribosomal protein S26 [Zea mays] >gi|195610710|gb|ACG27185.1| 40S ribosomal protein S26 [Zea mays]	Unigene111064_All//1.00E-24//AT3G56340| 40S ribosomal protein S26 (RPS26C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene111067_All	364	0.29	0.14	0.00	0.55	0.57	0.12	2.09	0.11	0.11	-1.05E+00	6.85E-01		-8.17E+00	3.98E-01		5.23E-02	9.89E-01		-2.14E+00	3.48E-01		-4.19E+00	1.58E-04	Down	-4.26E+00	8.66E-05	Down								
Unigene111068_All	238	0.00	0.00	0.00	0.00	0.00	0.00	3.55	1.05	0.00	null	null		null	null		null	null		null	null		-1.75E+00	1.64E-02		-1.18E+01	2.21E-06	Down			Unigene111068_All//5.00E-15//gi|109848340|gb|DW477320.1|DW477320				

Unigene11107_All	990	2.11	0.72	0.91	1.56	2.09	3.01	3.25	2.07	1.69	-1.56E+00	8.94E-04	Down	-1.21E+00	1.09E-02		4.20E-01	3.93E-01		9.49E-01	9.14E-03		-6.50E-01	3.63E-02		-9.42E-01	1.69E-03		Unigene11107_All//gi|297838455|ref|XP_002887109.1|//1.00E-134//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332950|gb|EFH63368.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11107_All//7.00E-135//AT1G67190| F-box family protein	Unigene11107_All//0.00E+00//TC178032				nr +
Unigene111070_All	476	0.00	0.53	0.00	0.00	0.07	1.14	52.32	128.72	91.06	9.06E+00	7.88E-02		null	null		6.18E+00	8.37E-01		1.02E+01	2.46E-03		1.30E+00	2.93E-82	Up	8.00E-01	1.97E-27		Unigene111070_All//gi|603890|emb|CAA87073.1|//8.00E-17//pathogenesis-related protein PR-6 type [Sambucus nigra]	Unigene111070_All//2.00E-16//AT2G38870| protease inhibitor, putative				GO:0004866//GO:0006952//GO:0030312	nr -
Unigene111073_All	342	0.31	0.00	0.47	1.02	0.30	0.66	4.45	0.49	0.82	-8.26E+00	3.76E-01		6.10E-01	7.49E-01		-1.75E+00	1.90E-01		-6.27E-01	6.21E-01		-3.19E+00	4.80E-07	Down	-2.45E+00	8.71E-06	Down									
Unigene111074_All	305	0.00	0.00	0.00	0.00	0.00	0.00	2.63	0.00	0.39	null	null		null	null		null	null		null	null		-1.14E+01	8.58E-06	Down	-2.75E+00	9.43E-04	Down	Unigene111074_All//gi|300265001|gb|EFJ49194.1|//1.00E-11//molecular chaperone [Volvox carteri f. nagariensis]	Unigene111074_All//1.00E-10//AT3G44110| ATJ3; protein binding			ko04141|Protein processing in endoplasmic reticulum	GO:0005488	nr -
Unigene111077_All	238	0.88	0.00	0.00	1.26	0.29	1.14	2.84	0.18	0.33	-9.78E+00	1.23E-01		-9.78E+00	1.46E-01		-2.12E+00	1.66E-01		-1.41E-01	9.21E-01		-4.02E+00	5.36E-04	Down	-3.09E+00	1.45E-03		Unigene111077_All//gi|224058355|ref|XP_002299486.1|//1.00E-11//high mobility group family [Populus trichocarpa] >gi|222846744|gb|EEE84291.1| high mobility group family [Populus trichocarpa]		Unigene111077_All//7.00E-42//TC163360				nr +
Unigene111079_All	380	0.00	0.00	0.00	0.00	0.00	0.00	2.11	0.11	0.00	null	null		null	null		null	null		null	null		-4.26E+00	8.48E-05	Down	-1.10E+01	4.43E-06	Down	Unigene111079_All//gi|301112246|ref|XP_002905202.1|//7.00E-10//60S ribosomal protein L7 [Phytophthora infestans T30-4] >gi|262095532|gb|EEY53584.1| 60S ribosomal protein L7 [Phytophthora infestans T30-4]	Unigene111079_All//2.00E-07//AT2G01250| 60S ribosomal protein L7 (RPL7B)			ko03010|Ribosome	GO:0005488//GO:0009536//GO:0015934//GO:0016020//GO:0030312	nr +
Unigene111081_All	345	0.00	0.00	0.00	0.87	0.30	0.13	2.70	1.21	0.35	null	null		null	null		-1.53E+00	2.98E-01		-2.73E+00	1.37E-01		-1.15E+00	7.87E-02		-2.96E+00	1.72E-04	Down			Unigene111081_All//2.00E-24//TC178046					
Unigene111082_All	439	0.00	0.00	0.00	0.00	0.00	0.00	3.18	0.29	0.36	null	null		null	null		null	null		null	null		-3.48E+00	5.80E-07	Down	-3.13E+00	1.09E-06	Down	Unigene111082_All//gi|148646851|gb|ABR01233.1|//3.00E-84//60S ribosomal protein L10a [Chlorella vulgaris] >gi|148646859|gb|ABR01237.1| 60S ribosomal protein L10a [Chlorella vulgaris] >gi|148646863|gb|ABR01239.1| 60S ribosomal protein L10a [Chlorella vulgaris]	Unigene111082_All//6.00E-35//AT5G22440| 60S ribosomal protein L10A (RPL10aC)			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene111085_All	1146	0.00	0.00	0.00	0.00	0.00	0.00	3.03	1.20	0.10	null	null		null	null		null	null		null	null		-1.33E+00	1.42E-05	Down	-4.86E+00	2.19E-21	Down	Unigene111085_All//gi|301111776|ref|XP_002904967.1|//1.00E-103//60S ribosomal protein L4 [Phytophthora infestans T30-4] >gi|262095297|gb|EEY53349.1| 60S ribosomal protein L4 [Phytophthora infestans T30-4]	Unigene111085_All//8.00E-95//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)	Unigene111085_All//2.00E-17//BQ405438		ko03010|Ribosome		nr -
Unigene111086_All	267	0.00	0.00	0.00	0.00	0.00	0.00	4.43	0.31	0.15	null	null		null	null		null	null		null	null		-3.82E+00	2.12E-06	Down	-4.89E+00	1.20E-07	Down	Unigene111086_All//gi|116222111|gb|AEJ80926.1|//2.00E-48//actin [Synura sphagnicola]	Unigene111086_All//4.00E-47//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene111086_All//3.00E-47//TC135405		ko04145|Phagosome	GO:0032559//GO:0043232	nr +
Unigene111089_All	859	0.79	0.41	0.43	0.23	0.52	0.89	2.90	0.39	0.93	-9.39E-01	2.77E-01		-8.68E-01	3.51E-01		1.17E+00	3.47E-01		1.95E+00	3.23E-02		-2.90E+00	2.98E-10	Down	-1.65E+00	1.01E-05	Down	Unigene111089_All//gi|283362114|dbj|BAI65910.1|//1.00E-74//UDP-sugar:glycosyltransferase [Forsythia x intermedia]	Unigene111089_All//6.00E-60//AT3G16520| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene111089_All//0.00E+00//TC133049		ko00940|Phenylpropanoid biosynthesis	GO:0035251	nr -
Unigene11109_All	2523	8.09	8.52	8.23	23.69	23.64	20.26	20.44	14.58	9.38	7.43E-02	6.05E-01		2.54E-02	8.56E-01		-3.30E-03	9.63E-01		-2.26E-01	9.50E-04		-4.88E-01	1.17E-13		-1.12E+00	4.83E-57	Down	Unigene11109_All//gi|22329659|ref|NP_173305.2|//0.00E+00//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|17979007|gb|AAL47463.1|At1g18700/F6A14_19 [Arabidopsis thaliana] >gi|23506111|gb|AAN28915.1|At1g18700/F6A14_19 [Arabidopsis thaliana]	Unigene11109_All//0.00E+00//AT1G18700| DNAJ heat shock N-terminal domain-containing protein	Unigene11109_All//0.00E+00//TC153985			GO:0005515//GO:0043231//GO:0050896	nr -
Unigene111092_All	241	1.30	0.42	2.21	1.03	2.57	1.31	6.32	1.91	3.14	-1.63E+00	2.77E-01		7.62E-01	4.53E-01		1.32E+00	1.88E-01		3.44E-01	7.97E-01		-1.73E+00	7.56E-04	Down	-1.01E+00	2.94E-02					Unigene111092_All//1.00E-58//FL576420					
Unigene111096_All	388	0.13	0.00	0.00	0.26	0.00	0.00	1.96	0.11	0.10	-7.07E+00	6.18E-01		-7.07E+00	6.31E-01		-8.00E+00	3.16E-01		-8.00E+00	4.04E-01		-4.19E+00	1.58E-04	Down	-4.26E+00	8.65E-05	Down				Unigene111096_All//1.00E-07//FL577589					
Unigene111097_All	374	0.28	0.27	0.00	0.40	0.09	0.24	2.94	0.78	0.43	-4.61E-02	9.91E-01		-8.13E+00	3.98E-01		-2.12E+00	3.87E-01		-7.27E-01	7.16E-01		-1.91E+00	2.64E-03		-2.79E+00	6.37E-05	Down				Unigene111097_All//8.00E-15//EX170653					
Unigene111098_All	789	0.13	0.00	0.00	0.00	0.00	0.00	2.57	0.05	0.45	-7.05E+00	3.76E-01		-7.05E+00	3.98E-01		null	null		null	null		-5.60E+00	5.56E-13	Down	-2.50E+00	1.27E-07	Down	Unigene111098_All//gi|124360457|gb|ABN08467.1|//3.00E-40//Rhea peroxidase, plant/fungal/bacterial [Medicago truncatula]	Unigene111098_All//9.00E-37//AT4G26010| peroxidase, putative	Unigene111098_All//1.00E-30//BE053812		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0006464//GO:0009755//GO:0016020//GO:0023060//GO:0032559//GO:0043231//GO:0044444	nr +
Unigene1111_All	2460	3.30	2.53	2.88	6.68	3.12	2.90	9.40	2.87	3.06	-3.80E-01	6.74E-02		-1.95E-01	3.96E-01		-1.10E+00	2.16E-17	Down	-1.20E+00	8.38E-18	Down	-1.71E+00	3.78E-47	Down	-1.62E+00	5.92E-45	Down	Unigene1111_All//gi|9294059|dbj|BAB02016.1|//0.00E+00//MAP kinase [Arabidopsis thaliana]	Unigene1111_All//0.00E+00//AT3G18040| MPK9 (MAP KINASE 9); MAP kinase	Unigene1111_All//0.00E+00//TC173934		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene111106_All	495	0.00	0.00	0.00	0.00	0.00	0.00	3.50	0.17	0.64	null	null		null	null		null	null		null	null		-4.37E+00	6.16E-10	Down	-2.44E+00	1.80E-06	Down									
Unigene111108_All	632	0.00	0.00	0.00	0.00	0.00	0.00	2.81	0.13	0.13	null	null		null	null		null	null		null	null		-4.41E+00	3.25E-10	Down	-4.48E+00	1.00E-10	Down	Unigene11108_All//gi|2500261|sp|P93099.1|RL13A_CYAPA//2.00E-47//RecName: Full=60S ribosomal protein L13a >gi|1743007|emb|CAA71090.1| ribosomal protein L13a [Cyanophora paradoxa]	Unigene111108_All//7.00E-41//AT3G24830| 60S ribosomal protein L13A (RPL13aB)			ko03010|Ribosome	GO:0030529	nr +
Unigene111112_All	317	0.00	0.00	0.00	0.00	0.00	0.00	2.13	0.00	0.25	null	null		null	null		null	null		null	null		-1.11E+01	6.34E-05	Down	-3.09E+00	1.45E-03		Unigene111112_All//gi|18379010|ref|NP_563662.1|//3.00E-44//pectinesterase family protein [Arabidopsis thaliana] >gi|75313808|sp|Q9SRX4.1|PME7_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 7; Includes: RecName: Full=Pectinesterase inhibitor 7; AltName: Full=Pectin methylesterase inhibitor 7; Includes: RecName: Full=Pectinesterase 7; Short=PE 7; AltName: Full=Pectin methylesterase 7; AltName: Full=Pectin methylesterase 1; Short=AtPME1; Flags: Precursor >gi|6056422|gb|AAF02886.1|AC009525_20 Similar to pectinesterases [Arabidopsis thaliana] >gi|133778888|gb|ABO38784.1|At1g02810 [Arabidopsis thaliana]	Unigene111112_All//2.00E-39//AT1G02810| pectinesterase family protein	Unigene111112_All//5.00E-62//TC138774		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0030234//GO:0031410//GO:0071555	nr -
Unigene111113_All	307	0.00	0.00	0.00	0.00	0.00	0.00	2.07	0.00	0.26	null	null		null	null		null	null		null	null		-1.10E+01	1.23E-04	Down	-2.99E+00	2.58E-03										
Unigene111115_All	420	0.00	0.00	0.00	0.12	0.00	0.00	2.32	0.20	0.09	null	null		null	null		-6.89E+00	5.62E-01		-6.89E+00	6.43E-01		-3.54E+00	4.32E-05	Down	-4.61E+00	3.32E-06	Down			Unigene111115_All//7.00E-34//FL576545					
Unigene111117_All	266	0.00	0.00	0.00	0.00	0.00	0.00	4.93	0.47	0.45	null	null		null	null		null	null		null	null		-3.39E+00	1.90E-06	Down	-3.46E+00	7.84E-07	Down	Unigene111117_All//gi|302128114|dbj|BAJ13478.1|//3.00E-18//actin 1 [Guillardia theta]	Unigene111117_All//5.00E-19//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene111117_All//2.00E-08//TC135405		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0006950//GO:0007015//GO:0008015//GO:0008092//GO:0009314//GO:0009725//GO:0009913//GO:0012501//GO:0016020//GO:0017111//GO:0030017//GO:0030239//GO:0030312//GO:0031981//GO:0032432//GO:0032559//GO:0048588//GO:0048747//GO:0051707//GO:0060415	nr -
Unigene111119_All	424	0.00	0.00	0.00	0.24	0.08	0.00	1.70	0.79	0.09	null	null		null	null		-1.53E+00	5.88E-01		-7.88E+00	4.04E-01		-1.10E+00	1.49E-01		-4.17E+00	1.65E-04	Down	Unigene111119_All//gi|145334909|ref|NP_001078800.1|//4.00E-32//TGA1; DNA binding / calmodulin binding / transcription factor [Arabidopsis thaliana]	Unigene111119_All//2.00E-33//AT5G65210| TGA1; DNA binding / calmodulin binding / transcription factor	Unigene111119_All//9.00E-18//TC148920	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0006952//GO:0043231	nr +
Unigene111120_All	479	0.00	0.00	0.00	0.00	0.00	0.00	3.71	0.79	0.42	null	null		null	null		null	null		null	null		-2.24E+00	8.44E-06	Down	-3.16E+00	2.19E-08	Down	Unigene111120_All//gi|12580867|emb|CAC27142.1|//3.00E-31//60S ribosomal protein L13E [Picea abies]	Unigene111120_All//6.00E-27//AT3G49010| ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome			ko03010|Ribosome	GO:0005622	nr -
Unigene111123_All	880	0.00	0.00	0.00	0.00	0.00	0.00	6.20	2.09	10.68	null	null		null	null		null	null		null	null		-1.57E+00	2.00E-10	Down	7.86E-01	1.77E-06		Unigene111123_All//gi|73624747|gb|AAZ79231.1|//1.00E-81//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene111123_All//9.00E-75//AT4G23990| ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	Unigene111123_All//4.00E-12//TC160226			GO:0009987//GO:0016020//GO:0016757	nr -
Unigene111124_All	455	0.00	0.00	0.00	0.00	0.30	0.00	3.53	0.92	0.18	null	null		null	null		8.24E+00	3.20E-01		null	null		-1.94E+00	1.42E-04	Down	-4.33E+00	1.41E-09	Down	Unigene111124_All//gi|15718687|ref|NP_000996.2|//1.00E-33//40S ribosomal protein S3 [Homo sapiens] >gi|77404290|ref|NP_001029219.1|40S ribosomal protein S3 [Bos taurus] >gi|113205854|ref|NP_001038066.1|40S ribosomal protein S3 [Sus scrofa] >gi|109107963|ref|XP_001086020.1|PREDICTED: 40S ribosomal protein S3 [Macaca mulatta] >gi|417719|sp|P23396.2|RS3_HUMAN RecName: Full=40S ribosomal protein S3 >gi|91207641|sp|Q3T169.1|RS3_BOVIN RecName: Full=40S ribosomal protein S3 >gi|115502828|sp|Q0ZSU2.1|RS3_PIG RecName: Full=40S ribosomal protein S3 >gi|187609257|pdb|2ZKQ|C Chain c, Structure Of A Mammalian Ribosomal 40s Subunit Within An 80s Complex Obtained By Docking Homology Models Of The Rna And Proteins Into An 8.7 A Cryo-Em Map >gi|555941|gb|AAB60336.1|ribosomal protein S3 [Homo	Unigene111124_All//5.00E-22//AT3G53870| 40S ribosomal protein S3 (RPS3B)			ko03010|Ribosome	GO:0001726//GO:0003677//GO:0003723//GO:0004518//GO:0005198//GO:0006282//GO:0006412//GO:0008134//GO:0012502//GO:0015935//GO:0016835//GO:0019900//GO:0043231//GO:0043280//GO:0043433//GO:0051540	nr +
Unigene111125_All	250	0.00	0.00	0.00	0.00	0.00	0.00	2.88	1.34	0.00	null	null		null	null		null	null		null	null		-1.10E+00	1.49E-01		-1.15E+01	1.78E-05	Down			Unigene111125_All//3.00E-16//DW479423					
Unigene111128_All	319	0.00	0.00	0.00	0.00	0.00	0.00	0.27	0.00	24.10	null	null		null	null		null	null		null	null		-8.05E+00	4.06E-01		6.51E+00	1.85E-51	Up			Unigene111128_All//4.00E-90//TC133844					
Unigene111131_All	261	0.80	0.00	1.02	1.34	0.26	0.17	6.64	1.60	1.53	-9.65E+00	1.23E-01		3.47E-01	7.97E-01		-2.34E+00	1.01E-01		-2.95E+00	8.31E-02		-2.05E+00	3.55E-05	Down	-2.12E+00	1.37E-05	Down			Unigene111131_All//2.00E-138//DW519828					
Unigene111132_All	254	0.00	0.00	0.00	0.00	0.00	0.00	3.50	0.16	0.78	null	null		null	null		null	null		null	null		-4.41E+00	2.44E-05	Down	-2.16E+00	2.68E-03										

Unigene111133_All	371	0.00	0.00	0.00	0.00	0.00	1.37	0.45	0.00	null	null		null	null		null	null		null	null		-1.60E+00	1.07E-01		-1.04E+01	5.55E-04	Down	Unigene111133_All//gi|219116705|ref|XP_002179147.1//8.00E-06//nad-dependent epimerase/dehydratase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217409038|gb|EEC48970.1| nad-dependent epimerase/dehydratase [Phaeodactylum tricornutum CCAP 1055/1]						nr -
Unigene111134_All	626	0.17	0.00	0.00	0.08	0.22	0.14	2.97	0.00	0.76	-7.39E+00	3.76E-01		-7.39E+00	3.98E-01		1.47E+00	6.20E-01		8.58E-01	7.96E-01		-1.15E+01	3.59E-13	Down	-1.96E+00	1.89E-05	Down								ESTscan +
Unigene111139_All	721	0.00	0.00	0.00	0.00	0.00	0.00	2.11	1.10	0.44	null	null		null	null		null	null		null	null		-9.39E-01	5.17E-02		-2.26E+00	2.48E-05	Down	Unigene111139_All//gi|227438273|gb|ACP30626.1|//7.00E-25//disease resistance protein [Brassica rapa subsp. pekinensis]	Unigene111139_All//4.00E-25//AT4G12010| disease resistance protein (TIR-NBS-LRR class), putative				GO:0005488//GO:0009987	nr +
Unigene111140_All	276	0.95	0.18	0.00	0.18	0.25	0.00	1.84	0.30	0.00	-2.37E+00	2.14E-01		-9.89E+00	8.59E-02		4.67E-01	9.60E-01		-7.50E+00	6.43E-01		-2.60E+00	2.05E-02		-1.08E+01	5.55E-04	Down								
Unigene111143_All	395	0.00	0.00	0.00	0.00	0.00	0.00	4.60	0.74	0.00	null	null		null	null		null	null		null	null		-2.64E+00	5.50E-07	Down	-1.22E+01	2.03E-13	Down								
Unigene111150_All	275	0.00	0.00	0.58	0.18	0.50	0.00	2.00	0.15	0.00	null	null		9.18E+00	2.40E-01		1.47E+00	6.20E-01		-7.50E+00	6.43E-01		-3.72E+00	3.23E-03		-1.10E+01	2.81E-04	Down								
Unigene111155_All	288	0.00	0.00	0.00	0.00	0.00	0.00	1.91	0.00	0.14	null	null		null	null		null	null		null	null		-1.09E+01	4.62E-04	Down	-3.79E+00	2.03E-03		Unigene111155_All//gi|4139170|gb|AAD03711.1|//5.00E-36//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene111155_All//8.00E-33//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene111155_All//2.00E-08//DR462623			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene111157_All	498	0.00	0.00	0.00	0.10	0.00	0.09	1.95	0.34	0.24	null	null		null	null		-6.64E+00	5.62E-01		-1.41E-01	9.56E-01		-2.54E+00	6.42E-04	Down	-3.02E+00	9.61E-05	Down	Unigene111157_All//gi|224589412|gb|ACN59240.1|//4.00E-62//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene111157_All//2.00E-40//AT1G34110| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0016301	nr -
Unigene111162_All	520	0.00	0.00	0.00	0.00	0.00	0.00	2.20	0.72	0.00	null	null		null	null		null	null		null	null		-1.60E+00	7.51E-03		-1.11E+01	1.65E-08	Down	Unigene111162_All//sp|P63240|NEC1_MUSCO//3.00E-41//Neuroendocrine convertase 1 OS=Mus cookii GN=Pcsk1 PE=2 SV=1						swissprot -
Unigene111163_All	299	0.00	0.00	0.00	0.00	0.00	0.00	1.98	0.00	0.13	null	null		null	null		null	null		null	null		-1.10E+01	2.39E-04	Down	-3.89E+00	1.09E-03		Unigene111163_All//gi|224078614|ref|XP_002305575.1|//6.00E-22//predicted protein [Populus trichocarpa] >gi|222848539|gb|EEE86086.1| predicted protein [Populus trichocarpa]						nr +
Unigene111166_All	318	0.00	0.00	0.17	0.63	0.00	0.14	1.73	0.00	0.13	null	null		7.39E+00	6.40E-01		-9.29E+00	8.47E-02		-2.14E+00	3.47E-01		-1.08E+01	4.62E-04	Down	-3.79E+00	2.03E-03		Unigene111166_All//gi|260177090|gb|ACX33888.1|//3.00E-37//flavin monooxygenase-like protein [Solanum lycopersicum]	Unigene111166_All//1.00E-35//AT5G43890| YUCCA5; monooxygenase	Unigene111166_All//3.00E-20//gi|78348897|gb|DT569171.1|DT569171		ko00380|Tryptophan metabolism	GO:0009850//GO:0016709//GO:0030554	nr -
Unigene111174_All	327	0.00	0.00	0.00	0.00	0.00	0.00	1.68	0.00	0.00	null	null		null	null		null	null		null	null		-1.07E+01	4.62E-04	Down	-1.07E+01	2.81E-04	Down								ESTscan -
Unigene111175_All	319	0.16	0.00	0.33	0.78	0.32	0.57	2.39	0.13	0.25	-7.36E+00	6.18E-01		1.03E+00	7.04E-01		-1.27E+00	4.24E-01		-4.63E-01	7.45E-01		-4.19E+00	1.58E-04	Down	-3.26E+00	4.48E-04	Down								
Unigene111177_All	639	0.00	0.00	0.00	0.00	0.00	0.00	2.85	0.00	0.19	null	null		null	null		null	null		null	null		-1.15E+01	7.10E-13	Down	-3.93E+00	4.04E-10	Down	Unigene111177_All//gi|110589651|gb|AB677330.1|//4.00E-76//Hsp90 [Entosiphon sulcatum]	Unigene111177_All//3.00E-64//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr +
Unigene111118_All	398	3.16	0.64	6.96	7.38	7.44	9.08	3.61	4.10	5.00	-2.31E+00	9.22E-04	Down	1.14E+00	4.31E-03		1.10E-02	9.89E-01		2.98E-01	4.07E-01		1.81E-01	7.06E-01		4.71E-01	2.45E-01		Unigene111118_All//gi|15450488|gb|AB96537.1|//3.00E-06//At2g36480/F1011.11 [Arabidopsis thaliana] >gi|16974461|gb|AAL31234.1| At2g36480/F1011.11 [Arabidopsis thaliana] >gi|20197924|gb|AAM15315.1| Expressed protein [Arabidopsis thaliana]	Unigene111118_All//1.00E-07//AT2G36485| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: ENTH/VHS (InterPro:IPR008942); BEST Arabidopsis thaliana protein match is: PCFS4 (PCF11P-SIMILAR PROTEIN 4); zinc ion binding (TAIR:AT4G04885.1); Has 87 Blast hits to 87 proteins in 38 species: Archae - 0; Bacteria - 0; Metazoa - 30; Fungi - 33; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene111118_All//5.00E-152//TC177315				nr -
Unigene111180_All	613	0.00	0.25	0.00	0.00	0.00	0.00	1.66	0.41	0.26	7.95E+00	2.36E-01		null	null		null	null		null	null		-2.02E+00	2.83E-03		-2.67E+00	1.94E-04	Down			Unigene111180_All//1.00E-14//TC168901					
Unigene111181_All	305	0.00	0.00	0.00	0.00	0.00	0.00	3.74	1.51	0.00	null	null		null	null		null	null		null	null		-1.31E+00	2.45E-02		-1.19E+01	1.65E-08	Down	Unigene111181_All//gi|115477126|ref|NP_001062159.1|/4.00E-48//Os08g0500700 [Oryza sativa Japonica Group] >gi|113624128|dbj|BAF24073.1| Os08g0500700 [Oryza sativa Japonica Group]	Unigene111181_All//6.00E-40//AT5G56010| HSP81-3; ATP binding / unfolded protein binding	Unigene111181_All//9.00E-42//gi|11208934|gb|BF277864.1|BF277864		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr +
Unigene111189_All	310	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	6.34E-05	Down	-1.11E+01	3.57E-05	Down	Unigene111189_All//gi|27764533|gb|AAO23064.1|//7.00E-07//ent-kaurenoic acid oxidase [Pisum sativum]	Unigene111189_All//2.00E-06//AT1G05160| CYP88A3 (CYTOCHROME P450 88 A3); ent-kaurenoate oxidase/ oxygen binding			ko00904|Diterpenoid biosynthesis		nr -
Unigene111194_All	690	0.61	0.00	1.39	0.58	0.40	0.46	4.04	1.76	0.64	-9.24E+00	1.05E-02		1.20E+00	1.15E-01		-5.33E-01	6.16E-01		-3.34E-01	7.57E-01		-1.20E+00	4.34E-04	Down	-2.67E+00	6.57E-11	Down	Unigene111194_All//gi|222423130|dbj|BAH19544.1|//2.00E-14//AT4G21215 [Arabidopsis thaliana]	Unigene111194_All//4.00E-16//AT4G21215| unknown protein	Unigene111194_All//9.00E-16//DW236374				nr -
Unigene111195_All	794	0.00	0.26	0.13	0.00	0.09	0.00	3.51	0.00	0.30	8.00E+00	1.37E-01		7.07E+00	4.01E-01		6.44E+00	6.14E-01		null	null		-1.18E+01	9.81E-20	Down	-3.55E+00	4.30E-14	Down	Unigene111195_All//gi|38564292|gb|AAR23725.1|//2.00E-47//At5g62280 [Arabidopsis thaliana] >gi|45592914|gb|AAS68111.1| At5g62280 [Arabidopsis thaliana]	Unigene111195_All//2.00E-49//AT5G62280| unknown protein					nr +
Unigene111197_All	590	0.00	0.00	0.00	0.00	0.00	0.00	2.51	0.57	0.47	null	null		null	null		null	null		null	null		-2.15E+00	9.69E-05	Down	-2.41E+00	1.48E-05	Down	Unigene111197_All//gi|15223002|ref|NP_172848.1|//6.00E-42//ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor [Arabidopsis thaliana] >gi|20138796|sp|Q9XI91.1|IF5A1_ARATH RecName: Full=Eukaryotic translation initiation factor 5A-1; Short=eIF-5A-1 >gi|5080771|gb|AAD39281.1|AC007576_4 initiation factor 5A-4 [Arabidopsis thaliana] >gi|12407785|gb|AAG53646.1|AF296082_1 eukaryotic translation initiation factor 5A [Arabidopsis thaliana]	Unigene111197_All//1.00E-43//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor				GO:0006417//GO:0008135//GO:0010087	nr -
Unigene1112_All	2717	2.33	1.94	1.67	2.59	2.92	2.63	11.19	3.35	4.18	-2.65E-01	2.84E-01		-4.84E-01	5.03E-02		1.73E-01	4.79E-01		2.29E-02	9.42E-01		-1.74E+00	4.18E-63	Down	-1.42E+00	1.23E-48	Down	Unigene1112_All//gi|30689234|ref|NP_850382.1|//0.00E+00//NPG1 (no pollen germination 1); calmodulin binding [Arabidopsis thaliana] >gi|27450574|gb|AAO14644.1|AF474176_1 pollen-specific calmodulin-binding protein [Arabidopsis thaliana] >gi|209529807|gb|ACI49798.1| At2g43040 [Arabidopsis thaliana]	Unigene1112_All//0.00E+00//AT2G43040| NPG1 (no pollen germination 1); calmodulin binding	Unigene1112_All//0.00E+00//TC145967			GO:0005515//GO:0016740	nr +
Unigene111201_All	324	0.00	0.00	0.00	0.00	0.00	0.00	2.74	1.03	0.12	null	null		null	null		null	null		null	null		-1.41E+00	4.01E-02		-4.48E+00	1.23E-05	Down	Unigene111201_All//gi|81159226|gb|ABB55890.1|//3.00E-41//heat shock protein 90 [Proteomonas sulcata]	Unigene111201_All//2.00E-42//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0006952//GO:0010035//GO:0016020//GO:0030312//GO:0032559//GO:0044267//GO:0044444	nr -
Unigene111202_All	450	0.00	0.00	0.00	0.00	0.00	0.00	1.50	0.00	0.00	null	null		null	null		null	null		null	null		-1.06E+01	6.34E-05	Down	-1.06E+01	3.57E-05	Down								ESTscan +
Unigene111207_All	324	0.32	0.63	0.82	4.92	1.28	0.56	1.70	1.03	0.61	9.54E-01	6.22E-01		1.35E+00	4.09E-01		-1.95E+00	2.04E-04	Down	-3.14E+00	2.25E-06	Down	-7.17E-01	4.22E-01		-1.46E+00	9.76E-02									
Unigene111210_All	300	0.00	0.00	0.00	0.00	0.00	0.00	1.83	1.11	0.00	null	null		null	null		null	null		null	null		-7.17E-01	4.22E-01		-1.08E+01	2.81E-04	Down	Unigene111210_All//sp|P18426|SCR11_OMMSL//4.00E-06//S-crystallin SL11 OS=Ommastrephes sloanei PE=2 SV=1						swissprot +
Unigene111211_All	331	0.00	0.00	0.00	0.00	0.00	0.00	2.68	0.25	0.00	null	null		null	null		null	null		null	null		-3.41E+00	1.40E-04	Down	-1.14E+01	1.10E-06	Down	Unigene111211_All//gi|298708862|emb|CBJ30820.1|//6.00E-17//40S ribosomal protein S28 [Ectocarpus siliculosus]	Unigene111211_All//3.00E-09//AT5G03850| 40S ribosomal protein S28 (RPS28B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene111212_All	274	0.00	0.00	0.00	0.00	0.00	0.00	3.39	1.07	0.15	null	null		null	null		null	null		null	null		-1.67E+00	1.45E-02		-4.55E+00	6.41E-06	Down	Unigene111212_All//gi|288300146|gb|ADC45376.1|//5.00E-32//actin [Cleistogenes songorica]	Unigene111212_All//1.00E-30//AT5G59370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene111212_All//1.00E-21//gi|50469957|gb|AI728105.1|AI728105		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008015//GO:0008092//GO:0012501;//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0042995//GO:0048747//GO:0051707//GO:0060415	nr -
Unigene111213_All	450	0.81	1.91	0.24	0.66	0.46	0.00	2.07	0.28	0.44	1.23E+00	1.12E-01		-1.78E+00	2.34E-01		-5.33E-01	6.79E-01		-9.38E+00	4.01E-02		-2.89E+00	3.28E-04	Down	-2.22E+00	1.63E-03		Unigene111213_All//gi|115478484|ref|NP_001062837.1|//3.00E-09//Os09g0311600 [Oryza sativa Japonica Group] >gi|113631070|dbj|BAF24751.1| Os09g0311600 [Oryza sativa Japonica Group]	Unigene111213_All//1.00E-07//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene111213_All//3.00E-150//CO097771		ko04626|Plant-pathogen interaction	GO:0005488	nr -
Unigene111214_All	419	0.00	0.00	0.00	0.00	0.00	0.00	3.43	0.70	0.19	null	null		null	null		null	null		null	null		-2.30E+00	5.90E-05	Down	-4.17E+00	1.93E-08	Down	Unigene111214_All//gi|145344703|ref|XP_001416866.1|//1.00E-35//Ribosomal protein S20, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901] >gi|144577092|gb|ABO95159.1| Ribosomal protein S20, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901]	Unigene111214_All//4.00E-31//AT5G62300| 40S ribosomal protein S20 (RPS20C)			ko03010|Ribosome	GO:0003676//GO:0004622//GO:0005198//GO:0006464//GO:0010467//GO:0032559//GO:0033279	nr +
Unigene111216_All	278	0.00	0.00	0.00	0.00	0.00	0.00	8.82	4.36	21.64	null	null		null	null		null	null		null	null		-1.02E+00	5.18E-03		1.29E+00	5.47E-09	Up								
Unigene111122_All	972	1.99	4.22	3.94	5.53	4.61	4.46	4.31	3.74	5.41	1.08E+00	3.96E-04	Up	9.86E-01	2.63E-03		-2.65E-01	3.33E-01		-3.11E-01	2.67E-01		-2.03E-01	5.00E-01		3.29E-01	1.61E-01		Unigene111122_All//gi|115480719|ref|NP_001063953.1|//5.00E-61//Os09g0566100 [Oryza sativa Japonica Group] >gi|113632186|dbj|BAF25867.1| Os09g0566100 [Oryza sativa Japonica Group]	Unigene111122_All//1.00E-45//AT2G36480| zinc finger (C2H2-type) family protein	Unigene111122_All//0.00E+00//TC177315			GO:0046914	nr -
Unigene111220_All	333	0.00	0.00	0.00	0.00	0.00	0.00	4.19	1.88	0.96	null	null		null	null		null	null		null	null		-1.15E+00	2.40E-02		-2.13E+00	1.13E-04	Down								
Unigene111225_All	337	0.00	0.00	0.00	0.00	0.00	0.00	1.88	0.12	0.00	null	null		null	null		null	null		null	null		-3.92E+00	9.81E-04	Down	-1.09E+01	7.12E-05	Down	Unigene111225_All//gi|224103789|ref|XP_002313194.1|//6.00E-52//tubulin alpha-5 chain [Populus trichocarpa] >gi|222849602|gb|EEE87149.1| tubulin alpha-5 chain [Populus trichocarpa]	Unigene111225_All//3.00E-53//AT1G50010| TUA2; structural constituent of cytoskeleton	Unigene111225_All//1.00E-28//gi|109864583|gb|DW493559.1|DW493559		ko04145|Phagosome	GO:0006970//GO:0007017//GO:0009536//GO:0009629//GO:0010038//GO:0015630//GO:0016020//GO:0017111//GO:0030312//GO:0032561//GO:0043234//GO:0043623	nr +
Unigene111226_All	1265	0.00	0.00	0.00	0.00	0.00	0.00	2.71	0.10	0.28	null	null		null	null		null	null		null	null		-4.77E+00	3.63E-20	Down	-3.26E+00	5.76E-16	Down	Unigene111226_All//gi|298715057|emb|CBJ27764.1|//6.00E-08//delta protein [Ectocarpus siliculosus]					GO:0044464	nr +
Unigene111227_All	562	0.74	0.00	0.47	0.00	0.18	0.16	1.20	0.60	0.07	-9.54E+00	1.05E-02		-6.53E-01	5.94E-01		7.52E+00	4.58E-01		7.33E+00	4.80E-01		-1.02E+00	2.04E-01		-4.09E+00	3.10E-04	Down			Unigene111227_All//1.00E-08//ES832462					

Unigene111229_All	597	0.00	0.00	0.00	0.00	0.12	0.00	9.77	0.84	1.60	null	null		null	null		6.85E+00	6.14E-01		null	null		-3.54E+00	9.45E-28	Down	-2.61E+00	1.87E-21	Down	Unigene111229_All//gi|18418598|ref|NP_567979.1|//3.00E-56//cyclase family protein [Arabidopsis thaliana] >gi|13937204|gb|AAK50095.1|AF37295 6_1 AT4g35220/F23E12_220 [Arabidopsis thaliana] >gi|18491127|gb|AAL69532.1| AT4g35220/F23E12_220 [Arabidopsis thaliana]	Unigene111229_All//2.00E-57//AT4G35220| cyclase family protein	Unigene111229_All//1.00E-128//TC158981			GO:0031410	nr -
Unigene111230_All	345	1.21	2.94	1.39	1.16	1.40	0.92	1.59	5.21	2.08	1.28E+00	6.99E-02		1.95E-01	8.39E-01		2.75E-01	8.20E-01		-3.34E-01	7.57E-01		1.71E+00	2.41E-04	Up	3.84E-01	5.96E-01		Unigene111230_All//gi|224071337|ref|XP_002303411.1|//8.00E-14//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222840843|gb|EEE78390.1| oligopeptide transporter OPT family [Populus trichocarpa]	Unigene111230_All//1.00E-13//AT4G10770| OPT7 (OLIGOPEPTIDE TRANSPORTER 7); oligopeptide transporter				GO:0015197//GO:0015833//GO:0044464	nr -
Unigene111231_All	301	0.00	0.00	0.00	0.00	0.00	0.00	2.39	2.08	0.13	null	null		null	null		null	null		null	null		-1.97E-01	7.84E-01		-4.17E+00	1.64E-04	Down								
Unigene111233_All	537	0.00	0.00	0.00	0.00	0.00	0.00	4.02	0.16	0.22	null	null		null	null		null	null		null	null		-4.69E+00	9.88E-13	Down	-4.17E+00	2.24E-12	Down	Unigene111233_All//gi|297833676|ref|XP_002884720.1|//4.00E-26//60S acidic ribosomal protein P0 [Arabidopsis lyrata subsp. lyrata] >gi|297330560|gb|EFH60979.1| 60S acidic ribosomal protein P0 [Arabidopsis lyrata subsp. lyrata]	Unigene111233_All//9.00E-22//AT3G11250| 60S acidic ribosomal protein P0 (RPP0C)			ko03010|Ribosome	GO:0005840//GO:0006412//GO:0006970//GO:0009536//GO:0010038//GO:0016020//GO:0031981//GO:0046914	nr -
Unigene111234_All	287	2.19	0.00	0.74	2.95	0.72	1.10	1.62	0.29	0.83	-1.11E+01	7.92E-04	Down	-1.56E+00	1.29E-01		-2.04E+00	9.05E-03		-1.42E+00	7.34E-02		-2.48E+00	3.38E-02		-9.60E-01	3.13E-01		Unigene111234_All//gi|15240353|ref|NP_200987.1|//3.00E-44//calnexin 1 (CNX1) [Arabidopsis thaliana] >gi|231683|sp|P29402.1|CALXI_ARATH RecName: Full=Calnexin homolog 1; Flags: Precursor >gi|16211|emb|CAA79144.1| calnexin homolog [Arabidopsis thaliana] >gi|10176872|dbj|BAB10079.1| calnexin homolog precursor [Arabidopsis thaliana] >gi|16649021|gb|AAL24362.1| calnexin homolog precursor [Arabidopsis thaliana] >gi|21387169|gb|AAM47988.1| calnexin-like protein precursor [Arabidopsis thaliana] >gi|21555674|gb|AAM63911.1| calnexin-like protein [Arabidopsis thaliana]	Unigene111234_All//1.00E-45//AT5G61790| calnexin 1 (CNX1)	Unigene111234_All//5.00E-154//TC161906		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	GO:0005515//GO:0009536//GO:0030246//GO:0031090//GO:0031224//GO:0044267//GO:0046872	nr -
Unigene111235_All	332	0.00	0.00	0.00	0.00	0.52	0.54	1.78	0.63	0.00	null	null		null	null		9.02E+00	2.27E-01		9.09E+00	1.95E-01		-1.50E+00	9.14E-02		-1.08E+01	1.41E-04	Down	Unigene111235_All//gi|159031811|dbj|BAF91877.1|//5.00E-33//polyamine oxidase [Nicotiana benthamiana]	Unigene111235_All//2.00E-31//AT5G13700| ATPAO1 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 1); FAD binding / polyamine oxidase	Unigene111235_All//5.00E-71//gi|78327583|gb|DT547857.1|DT547857			GO:0008152//GO:0016647	nr +
Unigene111236_All	424	0.00	0.00	0.00	0.00	0.00	0.00	1.40	0.00	0.00	null	null		null	null		null	null		null	null		-1.04E+01	2.39E-04	Down	-1.04E+01	1.41E-04	Down	Unigene111236_All//sp|Q5LWL4|IF2_SILPO//4.00E-06//Translation initiation factor IF-2 OS=Silicibacter pomeroyi GN=infB PE=3 SV=1						swissprot +
Unigene111238_All	290	0.00	0.00	0.00	0.00	0.24	0.00	3.50	0.43	1.51	null	null		null	null		7.89E+00	6.14E-01		null	null		-3.02E+00	1.08E-04	Down	-1.21E+00	4.17E-02		Unigene111238_All//gi|115435928|ref|NP_001042722.1|//2.00E-09//Os01g0275600 [Oryza sativa Japonica Group] >gi|75200337|sp|Q9SDG8.1|AGO4A_ORYSJ RecName: Full=Protein argonaute 4A; Short=OsAGO4a >gi|113332253|dbj|BAF04636.1| Os01g0275600 [Oryza sativa Japonica Group]	Unigene111238_All//1.00E-08//AT5G21150| PAZ domain-containing protein / piwi domain-containing protein	Unigene111238_All//1.00E-37//gi|109838370|gb|DW236931.1|DW236931			GO:0003676	nr -
Unigene111244_All	497	0.00	0.00	0.00	0.00	0.00	0.00	8.17	0.17	0.00	null	null		null	null		null	null		null	null		-5.60E+00	1.17E-25	Down	-1.30E+01	7.66E-30	Down			Unigene111244_All//4.00E-11//ES809074				
Unigene111245_All	311	0.17	0.49	0.00	0.00	0.22	0.00	3.26	0.00	0.90	1.54E+00	5.32E-01		-7.39E+00	6.31E-01		7.79E+00	6.14E-01		null	null		-1.17E+01	2.97E-07	Down	-1.86E+00	3.54E-03		Unigene111245_All//gi|83853831|gb|ABC47863.1|//5.00E-19//Heat shock transcription factor (HSF) [Glycine max]	Unigene111245_All//3.00E-09//AT1G46264| AT-HSFB4; DNA binding / transcription factor	Unigene111245_All//2.00E-08//TC156804	HSF		GO:0001071//GO:0003677//GO:0006351//GO:0043231//GO:0050896//GO:0051301	nr +
Unigene111246_All	422	0.37	0.00	0.50	0.00	1.47	2.14	2.20	1.19	0.38	-8.54E+00	2.17E-01		4.41E-01	7.76E-01		1.05E+01	7.90E-04	Up	1.11E+01	2.07E-05	Up	-8.91E-01	1.72E-01		-2.55E+00	5.79E-04	Down			Unigene111246_All//3.00E-122//TC163108				
Unigene111248_All	326	0.00	0.00	0.00	0.00	0.00	0.00	2.85	0.13	0.12	null	null		null	null		null	null		null	null		-4.48E+00	1.30E-05	Down	-4.55E+00	6.41E-06	Down	Unigene111248_All//gi|300175324|emb|CBK20635.2|//1.00E-12//Ribosomal protein S28e [Blastocystis hominis]	Unigene111248_All//3.00E-07//AT5G64140| RPS28 (RIBOSOMAL PROTEIN S28); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene111249_All	335	0.00	0.00	0.00	0.00	0.00	0.00	4.29	0.25	0.24	null	null		null	null		null	null		null	null		-4.10E+00	5.15E-08	Down	-4.17E+00	1.93E-08	Down								
Unigene111251_All	311	0.00	0.00	0.00	0.00	0.00	0.00	1.90	0.27	0.00	null	null		null	null		null	null		null	null		-2.82E+00	7.18E-03		-1.09E+01	1.41E-04	Down	Unigene111251_All//gi|238481396|ref|NP_198107.2|//1.00E-25//ATP binding / microtubule motor [Arabidopsis thaliana]	Unigene111251_All//1.00E-26//AT5G27550| ATP binding / microtubule motor				GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr +
Unigene111252_All	406	0.00	0.00	0.00	0.00	0.00	0.00	3.96	0.51	0.00	null	null		null	null		null	null		null	null		-2.94E+00	6.45E-07	Down	-1.20E+01	7.00E-12	Down	Unigene111252_All//gi|1174592|sp|P46259.1|TBA1_PEA//6.00E-50//RecName: Full=Tubulin alpha-1 chain >gi|525332|gb|AAA79910.1| alpha-tubulin [Pisum sativum]	Unigene111252_All//2.00E-47//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene111252_All//1.00E-35//gi|84148110|gb|DN762352.1|DN762352		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene111253_All	1446	0.00	0.00	0.00	0.00	0.00	0.00	26.99	3.18	4.19	null	null		null	null		null	null		null	null		-3.09E+00	4.97E-161	Down	-2.69E+00	6.47E-144	Down	Unigene111253_All//gi|297841521|ref|XP_002888642.1|//2.00E-85//S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334483|gb|EFH64901.1| S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene111253_All//5.00E-85//AT1G68040| S-adenosyl-L-methionine:carboxyl methyltransferase family protein			ko00592|alpha-Linolenic acid metabolism	GO:0008168	nr +
Unigene111255_All	342	0.00	0.00	0.00	0.00	0.00	0.00	5.69	2.93	0.23	null	null		null	null		null	null		null	null		-9.55E-01	2.18E-02		-4.61E+00	6.97E-12	Down	Unigene111255_All//gi|7799051|emb|CAB98826.1|//1.00E-26//ubiquitin [Cyanidium caldarium]	Unigene111255_All//1.00E-13//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene111255_All//1.00E-13//ES829082		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0016209//GO:0030529//GO:0046914	nr +
Unigene111256_All	429	0.00	0.00	0.37	0.35	0.00	0.11	2.76	0.10	0.09	null	null		8.54E+00	2.40E-01		-8.44E+00	1.66E-01		-1.73E+00	5.02E-01		-4.82E+00	2.84E-07	Down	-4.89E+00	1.20E-07	Down			Unigene111256_All//2.00E-37//TC166761				
Unigene111259_All	422	0.00	0.00	0.00	0.00	0.00	0.00	10.42	1.68	1.13	null	null		null	null		null	null		null	null		-2.63E+00	6.39E-16	Down	-3.20E+00	5.31E-20	Down			Unigene111259_All//8.00E-86//C0091281				
Unigene111260_All	400	5.49	0.38	0.00	2.49	1.38	0.34	12.90	7.52	6.77	-3.85E+00	1.84E-09	Down	-1.24E+01	5.21E-12	Down	-8.55E-01	2.05E-01		-2.88E+00	6.76E-04	Down	-7.77E-01	9.16E-04		-9.29E-01	5.42E-05				Unigene111260_All//5.00E-121//gi|48749456|gb|C0079975.1|C0079975				
Unigene111262_All	376	0.00	0.00	0.00	0.53	0.00	0.00	2.81	0.33	0.21	null	null		null	null		-9.05E+00	8.47E-02		-9.05E+00	1.34E-01		-3.08E+00	6.12E-05	Down	-3.73E+00	6.14E-06	Down	Unigene111262_All//gi|224121846|ref|XP_002318687.1|//3.00E-29//cytochrome P450 [Populus trichocarpa] >gi|222859360|gb|EEE96907.1| cytochrome P450 [Populus trichocarpa]	Unigene111262_All//4.00E-19//AT3G48300| CYP71A23; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene111262_All//2.00E-49//C0115886		ko00941|Flavonoid biosynthesis//ko00380|Tryptophan metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506//GO:0016020	nr +
Unigene111263_All	357	0.00	0.00	0.00	0.00	0.00	0.00	2.37	0.59	0.00	null	null		null	null		null	null		null	null		-2.02E+00	7.45E-03		-1.12E+01	2.21E-06	Down	Unigene111263_All//gi|17221648|dbj|BAB78478.1|//2.00E-18//preproMPT3 [Cucurbita maxima]				ko03040|Spliceosome		nr +
Unigene111267_All	348	0.00	0.00	0.00	0.00	0.00	0.00	2.55	0.24	0.11	null	null		null	null		null	null		null	null		-3.41E+00	1.40E-04	Down	-4.48E+00	1.23E-05	Down	Unigene111267_All//gi|30694961|ref|NP_849791.1|//4.00E-15//myosin-related [Arabidopsis thaliana]	Unigene111267_All//4.00E-09//AT1G51405| myosin-related				GO:0043231	nr +
Unigene111271_All	612	0.34	1.74	0.00	0.49	0.00	0.59	3.32	0.82	1.11	2.35E+00	2.58E-03		-8.42E+00	1.46E-01		-8.93E+00	2.02E-02		2.74E-01	8.33E-01		-2.02E+00	8.03E-06	Down	-1.58E+00	1.35E-04	Down	Unigene111271_All//gi|28950899|gb|AA063373.1|//2.00E-51//At2g27770 [Arabidopsis thaliana]	Unigene111271_All//1.00E-52//AT2G27770| unknown protein	Unigene111271_All//0.00E+00//TC139105			GO:0005622//GO:0008152	nr +
Unigene111274_All	464	0.00	0.00	0.00	0.00	0.00	0.00	5.65	0.18	0.00	null	null		null	null		null	null		null	null		-4.97E+00	7.56E-16	Down	-1.25E+01	2.73E-19	Down	Unigene111274_All//gi|192913040|gb|ACF06628.1|//3.00E-33//structural constituent of ribosome [Elaeis guineensis]	Unigene111274_All//4.00E-24//AT3G04920| 40S ribosomal protein S24 (RPS24A)			ko03010|Ribosome	GO:0030529	nr +
Unigene111276_All	367	0.00	0.00	0.00	0.00	0.00	0.00	6.80	0.57	3.15	null	null		null	null		null	null		null	null		-3.58E+00	2.77E-12	Down	-1.11E+00	1.54E-03									
Unigene111279_All	317	0.00	0.00	0.00	0.00	0.00	0.00	2.00	0.53	0.00	null	null		null	null		null	null		null	null		-1.92E+00	3.09E-02		-1.10E+01	7.12E-05	Down	Unigene111279_All//gi|99029149|gb|ABF60862.1|//5.00E-14//GRSF [Lilium longiflorum]	Unigene111279_All//4.00E-14//AT4G24770| RBP31 (31-KDA RNA BINDING PROTEIN); RNA binding / poly(U) binding			ko03040|Spliceosome	GO:0006952//GO:0008187//GO:0009526//GO:0009532//GO:0009534//GO:0010467//GO:0016070	nr +
Unigene111281_All	326	0.00	0.00	0.00	0.00	0.00	0.42	4.67	0.51	0.73	null	null		null	null		null	null		8.70E+00	3.12E-01		-3.19E+00	4.80E-07	Down	-2.67E+00	2.74E-06	Down	Unigene111281_All//gi|13111324|dbj|BAB32793.1|//1.00E-50//110 kDa 4SNc-Tudor domain protein [Pisum sativum]	Unigene111281_All//5.00E-45//AT5G07350| tudor domain-containing protein / nuclease family protein	Unigene111281_All//3.00E-85//TC152035			GO:0005488//GO:0016787//GO:0031332//GO:0035194	nr +
Unigene111283_All	507	0.62	0.50	0.00	0.20	0.14	0.45	2.34	1.15	0.55	-3.09E-01	7.89E-01		-9.27E+00	4.93E-02		-5.33E-01	8.18E-01		1.18E+00	5.50E-01		-1.02E+00	7.15E-02		-2.09E+00	5.32E-04	Down							ESTscan -
Unigene111284_All	754	0.00	0.00	0.00	0.00	0.00	0.00	3.87	0.22	0.16	null	null		null	null		null	null		null	null		-4.13E+00	8.13E-16	Down	-4.61E+00	1.44E-17	Down	Unigene111284_All//gi|29427830|sp|Q8LPB4.1|PSKR1_DAUCA//5.00E-70//RecName: Full=Phytosulfokine receptor 1; Short=DcPSKR1; AltName: Full=Phytosulfokine LRR receptor kinase 1; Flags: Precursor >gi|21623969|dbj|BAC00995.1| phytosulfokine receptor [Daucus carota]	Unigene111284_All//3.00E-67//AT2G02220| PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase				GO:0003824//GO:0004872//GO:0005488	nr +
Unigene111288_All	874	0.18	0.06	0.00	0.00	0.00	0.00	2.18	0.91	0.59	-1.63E+00	4.89E-01		-7.49E+00	2.46E-01		null	null		null	null		-1.26E+00	3.27E-03		-1.88E+00	2.70E-05	Down	Unigene111288_All//gi|224074241|ref|XP_002304316.1|//1.00E-132//GRAS family transcription factor [Populus trichocarpa] >gi|222841748|gb|EEE79295.1| GRAS family transcription factor [Populus trichocarpa]	Unigene111288_All//2.00E-91//AT3G49950| scarecrow transcription factor family protein			GRAS	GO:0010468	nr -
Unigene111292_All	378	0.00	0.00	0.00	0.00	0.00	0.00	2.01	0.33	0.11	null	null		null	null		null	null		null	null		-2.60E+00	2.81E-03		-4.26E+00	8.65E-05	Down	Unigene111292_All//gi|224002995|ref|XP_002291169.1|//7.00E-37//translation factor tu domain 2 [Thalassiosira pseudonana CCMP1335] >gi|220972945|gb|EED91276.1| translation factor tu domain 2 [Thalassiosira pseudonana CCMP1335]	Unigene111292_All//2.00E-20//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene111292_All//7.00E-12//TC148998			GO:0008135//GO:0017111//GO:0032561	nr +
Unigene111294_All	308	1.19	0.00	0.35	1.13	0.22	1.32	3.98	1.63	0.52	-1.02E+01	1.97E-02		-1.78E+00	2.34E-01		-2.34E+00	1.01E-01		2.21E-01	8.63E-01		-1.29E+00	2.09E-02		-2.94E+00	1.14E-05	Down			Unigene111294_All//3.00E-109//ES845374				
Unigene111297_All	616	0.00	0.16	0.43	0.08	0.22	0.07	4.60	1.02	1.16	7.36E+00	3.90E-01		8.76E+00	8.03E-02		1.47E+00	6.20E-01		-1.42E-01	9.56E-01		-2.18E+00	1.48E-08	Down	-1.98E+00	5.62E-08	Down	Unigene111297_All//gi|38603902|gb|AAR24696.1|//1.00E-31//At4g32870 [Arabidopsis thaliana] >gi|38603986|gb|AAR24736.1| At4g32870 [Arabidopsis thaliana]	Unigene111297_All//2.00E-33//AT4G32870| unknown protein	Unigene111297_All//0.00E+00//TC146635				nr +
Unigene111298_All	541	0.00	0.00	0.00	0.00	0.00	0.00	3.83	0.46	0.29	null	null		null	null		null	null		null	null		-3.05E+00	5.12E-09	Down	-3.70E+00	5.61E-11	Down								
Unigene111299_All	533	0.00	0.00	0.00	0.00	0.00	0.00	3.25	1.57	0.00	null	null		null	null		null	null		null	null		-1.05E+00	1.87E-02		-1.17E+01	8.37E-13	Down	Unigene111299_All//gi|116222141|gb|ABJ80944.1|//1.00E-71//Hsp90 [Cyanophora paradoxa]	Unigene111299_All//3.00E-55//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene111299_All//8.00E-22//EV499016		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr +

Unigene111300_All	568	0.00	0.00	0.00	0.00	0.00	0.00	2.53	0.15	0.21	null	null		null	null		null	null		null	null		-4.10E+00	5.15E-08	Down	-3.59E+00	1.22E-07	Down	Unigene111300_All//gi|195655421|gb|ACG47178.1|//1.00E-17//GSDL-motif lipase [Zea mays]	Unigene111300_All//2.00E-13//AT2G23540| GDSL-motif lipase/hydrolase family protein				GO:0031410	nr +
Unigene111304_All	389	0.00	0.00	0.00	0.00	0.00	0.00	2.28	0.64	0.00	null	null		null	null		null	null		null	null		-1.82E+00	1.08E-02		-1.12E+01	1.10E-06	Down	Unigene111304_All//gi|301105230|ref|XP_002901699.1|//4.00E-39//40S ribosomal protein S11 [Phytophthora infestans T30-4] >gi|262100703|gb|EEY58755.1| 40S ribosomal protein S11 [Phytophthora infestans T30-4]	Unigene111304_All//3.00E-39//AT3G48930| EMB1080 (embryo defective 1080); structural constituent of ribosome			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0015935//GO:0030312	nr -
Unigene111305_All	355	0.00	0.00	0.00	0.28	0.00	0.00	1.91	0.94	0.11	null	null		null	null		-8.13E+00	3.16E-01		-8.13E+00	4.04E-01		-1.02E+00	2.04E-01		-4.09E+00	3.10E-04	Down							
Unigene111306_All	957	0.00	0.00	0.00	0.00	0.00	0.00	3.49	0.52	0.46	null	null		null	null		null	null		null	null		-2.74E+00	9.26E-13	Down	-2.93E+00	3.76E-14	Down	Unigene111306_All//gi|297853194|ref|XP_002894478.1|//3.00E-83//ALDH7B4 [Arabidopsis lyrata subsp. lyrata] >gi|297340320|gb|EFH70737.1| ALDH7B4 [Arabidopsis lyrata subsp. lyrata]	Unigene111306_All//6.00E-48//AT1G54100| ALDH7B4 (Aldehyde Dehydrogenase 7B4); 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase			ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00350|Tyrosine metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0004030//GO:0006970//GO:0009414//GO:0009725//GO:0044237	nr -
Unigene111307_All	353	0.00	0.00	0.00	0.00	0.00	0.00	2.28	0.95	0.00	null	null		null	null		null	null		null	null		-1.26E+00	7.98E-02		-1.12E+01	4.43E-06	Down	Unigene111307_All//gi|192912958|gb|ACF06587.1|//7.00E-20//actin depolymerizing factor [Elaeis guineensis]	Unigene111307_All//2.00E-19//AT5G52360| ADF10 (ACTIN DEPOLYMERIZING FACTOR 10); actin binding				GO:0046872	nr +
Unigene111308_All	730	0.14	0.42	0.44	0.68	0.19	0.68	6.14	1.77	3.55	1.54E+00	3.24E-01		1.61E+00	3.05E-01		-1.85E+00	8.44E-02		-4.00E-03	9.87E-01		-1.79E+00	2.48E-10	Down	-7.91E-01	1.32E-03				Unigene111308_All//5.00E-67//TC140052				
Unigene111309_All	406	0.00	0.00	0.00	0.00	0.00	0.00	1.35	0.00	0.00	null	null		null	null		null	null		null	null		-1.04E+01	4.62E-04	Down	-1.04E+01	2.81E-04	Down							
Unigene111311_All	378	0.00	0.00	0.00	0.00	0.00	0.00	3.69	0.00	0.11	null	null		null	null		null	null		null	null		-1.18E+01	6.58E-10	Down	-5.13E+00	4.13E-09	Down	Unigene111311_All//gi|226501140|ref|NP_001152197.1|//3.00E-06//LOC100285835 [Zea mays] >gi|195653721|gb|ACG46328.1| keratin-associated protein 5-4 [Zea mays]						nr +
Unigene111312_All	402	0.00	0.00	0.00	0.00	0.00	0.00	1.79	0.00	0.00	null	null		null	null		null	null		null	null		-1.08E+01	3.27E-05	Down	-1.08E+01	1.78E-05	Down	Unigene111312_All//gi|115436514|ref|NP_001043015.1|//8.00E-32//Os01g0358400 [Oryza sativa Japonica Group] >gi|113532546|db|BAF04929.1| Os01g0358400 [Oryza sativa Japonica Group] >gi|149391309|gb|ABR25672.1| 40S ribosomal protein S4 [Oryza sativa Indica Group]	Unigene111312_All//7.00E-29//AT5G58420| 40S ribosomal protein S4 (RPS4D)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene111313_All	386	0.00	0.00	0.00	0.00	0.00	0.00	2.41	0.54	0.00	null	null		null	null		null	null		null	null		-2.15E+00	2.95E-03		-1.12E+01	5.48E-07	Down	Unigene111313_All//gi|222446462|dbj|BAH20861.1|//5.00E-07//NBS-LRR disease resistance protein [Oryza sativa Japonica Group] >gi|222446464|dbj|BAH20862.1| NBS-LRR disease resistance protein [Oryza sativa Japonica Group]	Unigene111313_All//3.00E-08//AT2G17440| leucine-rich repeat family protein					nr +
Unigene111314_All	374	0.00	0.00	0.00	0.00	0.00	0.00	2.60	0.56	0.00	null	null		null	null		null	null		null	null		-2.22E+00	1.82E-03		-1.13E+01	2.72E-07	Down	Unigene111314_All//gi|301111866|ref|XP_002905012.1|//1.00E-12//major vault protein [Phytophthora infestans T30-4] >gi|262095342|gb|EEY53394.1| major vault protein [Phytophthora infestans T30-4]						nr +
Unigene111315_All	358	0.00	0.00	1.04	0.56	0.19	0.13	1.77	0.12	0.89	null	null		1.00E+01	2.50E-02		-1.53E+00	4.16E-01		-2.14E+00	3.47E-01		-3.92E+00	9.81E-04	Down	-9.93E-01	2.02E-01		Unigene111315_All//gi|240255538|ref|NP_190402.6|//2.00E-30//ATM (ATAXIA-TELANGIECTASIA MUTATED); 1-phosphatidylinositol-3-phosphate 5-kinase [Arabidopsis thaliana]	Unigene111315_All//6.00E-32//AT3G48190| ATM (ATAXIA-TELANGIECTASIA MUTATED); 1-phosphatidylinositol-3-phosphate 5-kinase				GO:0016772//GO:0032559	nr +
Unigene111316_All	351	0.30	0.43	0.00	2.27	0.69	1.80	6.38	4.41	2.61	5.39E-01	7.80E-01		-8.22E+00	3.98E-01		-1.73E+00	2.86E-02		-3.34E-01	6.86E-01		-5.35E-01	1.71E-01		-1.29E+00	6.63E-04	Down			Unigene111316_All//4.00E-112//TC178205				
Unigene111317_All	545	0.19	0.00	0.00	0.37	0.19	0.41	6.44	1.15	0.73	-7.59E+00	3.76E-01		-7.59E+00	3.98E-01		-9.47E-01	5.88E-01		1.80E-01	9.35E-01		-2.48E+00	4.26E-12	Down	-3.14E+00	8.08E-16	Down	Unigene111317_All//gi|225468852|ref|XP_002266296.1|//1.00E-06//PREDICTED: hypothetical protein isoform 2 [Vitis vinifera]		Unigene111317_All//1.00E-14//gi|48803105|gb|CO104419.1|CO104419			GO:0008152//GO:0016491	nr +
Unigene111318_All	383	0.00	0.00	0.00	0.00	0.00	0.00	2.10	0.11	0.42	null	null		null	null		null	null		null	null		-4.26E+00	8.48E-05	Down	-2.33E+00	2.82E-03								
Unigene111319_All	387	28.26	27.50	28.48	96.67	109.98	77.14	1.31	0.00	0.21	-3.94E-02	8.31E-01		1.15E-02	9.72E-01		1.86E-01	2.60E-02		-3.26E-01	1.57E-04		-1.04E+01	8.90E-04	Down	-2.67E+00	1.37E-02		Unigene111319_All//gi|297825869|ref|XP_002880817.1|//2.00E-48//nitrate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326656|gb|EFH57076.1| nitrate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene111319_All//3.00E-49//AT2G26690| nitrate transporter (NTP2)	Unigene111319_All//3.00E-147//TC140606			GO:0006950//GO:0009719//GO:0015833//GO:0031224	nr -
Unigene111320_All	330	0.00	0.00	0.00	0.00	0.00	0.00	2.95	3.42	0.48	null	null		null	null		null	null		null	null		2.15E-01	7.15E-01		-2.61E+00	3.36E-04	Down			Unigene111320_All//7.00E-15//ES843311				
Unigene111322_All	391	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.11	0.41	null	null		null	null		null	null		null	null		-4.26E+00	8.48E-05	Down	-2.33E+00	2.82E-03		Unigene111322_All//gi|15242725|ref|NP_195956.1|//4.00E-12//DC1 domain-containing protein [Arabidopsis thaliana]	Unigene111322_All//9.00E-14//AT4G13992| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular signaling cascade; LOCATED IN: mitochondrion; CONTAINS InterPro DOMAIN/s: Protein kinase C, phorbol ester/diacylglycerol binding (InterPro:IPR002219), DC1 (InterPro:IPR004146), C1-like (InterPro:IPR011424); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT4G16015.1); Has 1471 Blast hits to 614 proteins in 36 species: Archae - 0; Bacteria - 0; Metazoa - 87; Fungi - 0; Plants - 1295; Viruses - 0; Other Eukaryotes - 89 (source: NCBI BLink).					nr +
Unigene111327_All	387	0.00	0.00	0.00	0.00	0.00	0.00	2.19	3.56	8.13	null	null		null	null		null	null		null	null		7.06E-01	1.71E-01		1.90E+00	3.27E-08	Up							
Unigene111328_All	629	0.08	0.00	0.51	0.32	0.22	0.50	3.70	0.53	0.57	-6.38E+00	6.18E-01		2.61E+00	1.46E-01		-5.33E-01	7.49E-01		6.66E-01	6.48E-01		-2.80E+00	2.78E-09	Down	-2.70E+00	2.63E-09	Down	Unigene111328_All//gi|255582386|ref|XP_002531982.1|//9.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223528379|gb|EEF30418.1| conserved hypothetical protein [Ricinus communis]			Unigene111328_All//6.00E-66//ES815114				nr -
Unigene111329_All	742	0.14	0.00	0.00	0.13	0.19	0.91	5.24	0.96	0.97	-7.14E+00	3.76E-01		-7.14E+00	3.98E-01		4.67E-01	8.78E-01		2.77E+00	1.14E-02		-2.45E+00	3.80E-13	Down	-2.44E+00	1.54E-13	Down	Unigene111329_All//gi|48310064|gb|AAT41746.1|//6.00E-27//At4g28840 [Arabidopsis thaliana] >gi|50198849|gb|AAT70453.1| At4g28840 [Arabidopsis thaliana]	Unigene111329_All//1.00E-17//AT4G28840| unknown protein	Unigene111329_All//0.00E+00//gi|109870952|gb|DW499928.1|DW499928				nr +
Unigene111333_All	547	0.00	0.00	0.00	0.00	0.00	0.00	10.05	1.60	2.84	null	null		null	null		null	null		null	null		-2.65E+00	7.13E-20	Down	-1.82E+00	3.11E-13	Down							
Unigene111335_All	852	0.00	0.00	0.00	0.00	0.00	0.00	3.62	0.34	0.37	null	null		null	null		null	null		null	null		-3.40E+00	1.87E-14	Down	-3.28E+00	1.57E-14	Down	Unigene111335_All//gi|164564727|dbj|BAF98210.1|//3.00E-66//CM0216.210.nc [Lotus japonicus]	Unigene111335_All//8.00E-36//AT2G17080| unknown protein					nr -
Unigene111336_All	424	0.00	0.72	0.38	0.24	0.00	0.11	2.09	0.20	0.56	9.49E+00	4.45E-02		8.56E+00	2.40E-01		-7.88E+00	3.16E-01		-1.14E+00	6.78E-01		-3.41E+00	1.40E-04	Down	-1.89E+00	6.34E-03		Unigene111336_All//gi|223452393|gb|ACN89524.1|//9.00E-09//FERONIA receptor-like kinase [Glycine max]	Unigene111336_All//1.00E-06//AT5G28680| protein kinase family protein					nr -
Unigene111338_All	416	0.00	0.00	0.00	0.00	0.00	0.00	2.24	1.51	0.00	null	null		null	null		null	null		null	null		-5.69E-01	4.02E-01		-1.11E+01	5.48E-07	Down	Unigene111338_All//gi|301120388|ref|XP_002907921.1|//5.00E-08//polyadenylate-binding protein 1-B [Phytophthora infestans T30-4] >gi|262102952|gb|EEY61004.1| polyadenylate-binding protein 1-B [Phytophthora infestans T30-4]	Unigene111338_All//8.00E-07//AT2G23350| PAB4 (POLY(A) BINDING PROTEIN 4); RNA binding / translation initiation factor			ko03040|Spliceosome		nr -
Unigene111339_All	385	0.00	0.00	0.00	0.00	0.00	0.00	2.64	0.00	0.00	null	null		null	null		null	null		null	null		-1.14E+01	2.97E-07	Down	-1.14E+01	1.35E-07	Down	Unigene111339_All//gi|164564735|dbj|BAF98217.1|//2.00E-12//CM0216.330.nc [Lotus japonicus]						nr -
Unigene11134_All	2325	9.56	6.73	8.66	21.79	17.58	14.88	15.11	10.30	5.93	-5.06E-01	1.24E-05		-1.44E-01	2.86E-01		-3.10E-01	7.12E-06		-5.50E-01	1.85E-14		-5.53E-01	8.37E-12		-1.35E+00	6.27E-52	Down	Unigene11134_All//gi|115445577|ref|NP_001046568.1|//0.00E+00//Os02g0283800 [Oryza sativa Japonica Group] >gi|113536099|dbj|BAF08482.1| Os02g0283800 [Oryza sativa Japonica Group]	Unigene11134_All//0.00E+00//AT5G10290| leucine-rich repeat family protein / protein kinase family protein	Unigene11134_All//0.00E+00//ES829580			GO:0004672//GO:0006464//GO:0031224//GO:0032559//GO:0043231	nr -
Unigene111341_All	396	0.00	0.00	0.00	0.00	0.00	0.00	2.67	0.00	0.00	null	null		null	null		null	null		null	null		-1.14E+01	1.51E-07	Down	-1.14E+01	6.72E-08	Down	Unigene111341_All//gi|159487004|ref|XP_001701526.1|//2.00E-08//glyoxal or galactose oxidase [Chlamydomonas reinhardtii] >gi|158271587|gb|EDO97403.1| glyoxal or galactose oxidase [Chlamydomonas reinhardtii]				ko03430|Mismatch repair		nr +
Unigene111344_All	497	0.00	0.00	0.00	0.00	0.00	0.00	1.87	4.46	0.16	null	null		null	null		null	null		null	null		1.25E+00	1.44E-03		-3.55E+00	3.97E-05	Down			Unigene111344_All//2.00E-10//TC135460				
Unigene111345_All	1743	0.06	0.00	0.00	0.00	0.00	0.10	9.53	1.06	6.51	-5.91E+00	3.76E-01		-5.91E+00	3.98E-01		null	null		6.69E+00	1.95E-01		-3.18E+00	8.83E-71	Down	-5.49E-01	3.58E-06		Unigene111345_All//gi|224120220|ref|XP_002330994.1|//1.00E-143//cytochrome P450 [Populus trichocarpa] >gi|222872924|gb|EEF10055.1| cytochrome P450 [Populus trichocarpa]	Unigene111345_All//5.00E-130//AT5G06905| CYP71A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene111345_All//1.00E-07//TC137811		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene111346_All	409	0.00	0.00	0.00	0.00	0.00	0.00	2.69	0.92	0.10	null	null		null	null		null	null		null	null		-1.55E+00	1.12E-02		-4.79E+00	4.55E-07	Down	Unigene111346_All//gi|298711489|emb|CBJ26577.1|//5.00E-24//40S ribosomal protein S17 [Ectocarpus siliculosus]	Unigene111346_All//2.00E-19//AT5G04800| 40S ribosomal protein S17 (RPS17D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -

Unigene111347_All	582	0.00	0.00	0.00	0.00	0.00	0.00	10.32	0.14	2.05	null	null		null	null		null	null		null	null		-6.17E+00	3.77E-39	Down	-2.33E+00	2.04E-19	Down	Unigene111347_All//gi|15235406|ref|NP_192992.1|//4.00E-06//AIR1: lipid binding [Arabidopsis thaliana] >gi|15294192|gb|AAK95273.1|AF410287_1 AT4g12550/T1P17_140 [Arabidopsis thaliana] >gi|20147277|gb|AAM10352.1|AT4g12550/T1P17_140 [Arabidopsis thaliana]							nr -
Unigene111348_All	791	0.00	0.00	0.00	0.00	0.00	0.00	9.78	2.64	5.09	null	null		null	null		null	null		null	null		-1.89E+00	1.55E-18	Down	-9.43E-01	3.31E-07		Unigene111348_All//gi|288559172|sp|B9HBX2.1|U4978_POPTR//2.00E-68//RecName: Full=UPF0497 membrane protein 8	Unigene111348_All//6.00E-47//AT5G06200| integral membrane family protein					GO:0031224	nr -
Unigene111350_All	589	0.09	0.00	0.18	0.85	0.47	0.31	3.73	0.57	1.08	-6.47E+00	6.18E-01		1.03E+00	7.04E-01		-8.55E-01	4.07E-01		-1.46E+00	1.93E-01		-2.72E+00	1.45E-08	Down	-1.79E+00	1.17E-05	Down	Unigene111350_All//gi|3582434|dbj|BAA33062.1|//8.00E-62//low-molecular-weight heat shock protein [Cuscuta japonica]	Unigene111350_All//1.00E-43//AT5G59720| HSP18.2 (heat shock protein 18.2)	Unigene111350_All//0.00E+00//gi|109829300|gb|DW227888.1|DW227888			GO:0050896	nr +
Unigene111351_All	431	0.49	0.00	0.00	0.12	0.08	0.00	3.04	1.84	0.65	-8.92E+00	1.23E-01		-8.92E+00	1.46E-01		-5.33E-01	8.28E-01		-6.85E+00	6.43E-01		-7.23E-01	1.73E-01		-2.23E+00	1.19E-04	Down			Unigene111351_All//1.00E-124//gi|48794438|gb|CO095752.1|CO095752					
Unigene111352_All	724	2.31	0.28	3.31	2.75	2.05	1.93	0.58	0.00	0.17	-3.05E+00	3.81E-06	Down	5.17E-01	2.32E-01		-4.28E-01	3.61E-01		-5.09E-01	2.94E-01		-9.19E+00	3.25E-03		-1.82E+00	9.22E-02				Unigene111352_All//6.00E-08//TC133829					
Unigene111355_All	437	0.24	1.39	0.49	0.80	0.55	0.83	2.52	0.67	0.36	2.54E+00	2.46E-02		1.03E+00	5.92E-01		-5.33E-01	6.46E-01		5.13E-02	9.69E-01		-1.91E+00	2.64E-03		-2.79E+00	6.37E-05	Down	Unigene111355_All//gi|297814241|ref|XP_002875004.1|//1.00E-36//transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297320841|gb|EFH51263.1| transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene111355_All//1.00E-36//AT4G00990| transcription factor jumonji (jmjC) domain-containing protein	Unigene111355_All//9.00E-92//CA993153			GO:0005488	nr -
Unigene111356_All	614	0.00	0.00	0.00	0.00	0.00	0.00	9.57	0.88	0.32	null	null		null	null		null	null		null	null		-3.44E+00	3.00E-27	Down	-4.88E+00	5.10E-36	Down			Unigene111356_All//2.00E-13//TC146753					
Unigene111358_All	375	0.00	0.00	0.00	0.00	0.00	0.00	9.70	0.89	3.40	null	null		null	null		null	null		null	null		-3.44E+00	4.14E-17	Down	-1.51E+00	3.92E-07	Down	Unigene111358_All//gi|300263568|gb|EFJ47768.1|//6.00E-06//hypothetical protein VOLCADRAFT_117787 [Volvox carteri f. nagariensis]							nr +
Unigene11136_All	2603	13.33	6.93	10.72	15.25	16.22	16.19	17.57	8.32	10.68	-9.43E-01	3.06E-23		-3.14E-01	1.02E-03		8.86E-02	3.71E-01		8.59E-02	3.89E-01		-1.08E+00	3.57E-46	Down	-7.18E-01	2.82E-24		Unigene11136_All//gi|297811131|ref|XP_002873449.1|//0.00E+00//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319286|gb|EFH49708.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11136_All//0.00E+00//AT5G10290| leucine-rich repeat family protein / protein kinase family protein	Unigene11136_All//0.00E+00//TC157415		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0031224//GO:0032559//GO:0043231	nr -
Unigene111360_All	594	0.00	0.00	0.00	0.00	0.00	0.00	3.20	1.48	0.00	null	null		null	null		null	null		null	null		-1.12E+00	8.54E-03		-1.16E+01	4.91E-14	Down	Unigene111360_All//gi|195626686|gb|ACG35173.1|//7.00E-58//60S ribosomal protein L12 [Zea mays]	Unigene111360_All//2.00E-57//AT2G37190| 60S ribosomal protein L12 (RPL12A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene111362_All	485	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.09	0.00	null	null		null	null		null	null		null	null		-4.66E+00	1.94E-06	Down	-1.11E+01	6.72E-08	Down								
Unigene111363_All	448	0.00	0.00	0.00	0.67	0.08	0.20	2.55	1.21	0.44	null	null		null	null		-3.12E+00	7.57E-02		-1.73E+00	2.89E-01		-1.07E+00	6.31E-02		-2.52E+00	1.20E-04	Down								
Unigene111365_All	711	0.00	0.00	0.00	0.00	0.00	0.00	4.10	0.29	0.22	null	null		null	null		null	null		null	null		-3.80E+00	6.00E-15	Down	-4.19E+00	1.34E-16	Down	Unigene111365_All//gi|301108189|ref|XP_002903176.1|//1.00E-70//60S ribosomal protein L19-1 [Phytophthora infestans T30-4] >gi|262097548|gb|EEY55600.1| 60S ribosomal protein L19-1 [Phytophthora infestans T30-4]	Unigene111365_All//3.00E-57//AT4G02230| 60S ribosomal protein L19 (RPL19C)	Unigene111365_All//1.00E-11//gi|109861980|gb|DW490957.1|DW490957		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr -
Unigene111367_All	458	0.00	0.00	0.23	0.44	0.15	0.59	1.94	0.37	0.26	null	null		7.86E+00	4.01E-01		-1.53E+00	4.16E-01		4.44E-01	7.64E-01		-2.41E+00	1.79E-03		-2.89E+00	3.05E-04	Down	Unigene111367_All//gi|224143299|ref|XP_002324908.1|//1.00E-10//predicted protein [Populus trichocarpa] >gi|222866342|gb|EEF03473.1| predicted protein [Populus trichocarpa]							nr -
Unigene111368_All	775	0.74	0.20	0.21	0.06	0.27	0.41	2.73	1.02	0.62	-1.92E+00	7.01E-02		-1.85E+00	9.62E-02		2.05E+00	3.95E-01		2.67E+00	1.45E-01		-1.41E+00	5.54E-04	Down	-2.14E+00	1.01E-06	Down			Unigene111368_All//1.00E-163//TC150789					
Unigene111369_All	699	0.00	0.00	0.00	0.00	0.00	0.00	2.66	2.03	0.00	null	null		null	null		null	null		null	null		-3.89E-01	3.99E-01		-1.14E+01	9.97E-14	Down	Unigene111369_All//gi|195622794|gb|ACG33227.1|//1.00E-48//60S ribosomal protein L9 [Zea mays]	Unigene111369_All//2.00E-48//AT4G10450| 60S ribosomal protein L9 (RPL9OD)			ko03010|Ribosome	GO:0005622	nr -
Unigene11137_All	436	0.60	0.58	0.49	0.46	1.03	3.31	5.04	10.93	11.15	-4.62E-02	9.87E-01		-2.97E-01	8.32E-01		1.17E+00	3.47E-01		2.86E+00	3.35E-05	Up	1.12E+00	8.86E-06	Up	1.14E+00	2.82E-06	Up	Unigene11137_All//gi|297824921|ref|XP_002880343.1|//6.00E-46//structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata] >gi|297326182|gb|EFH56602.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	Unigene11137_All//2.00E-45//AT3G23590| RFR1 (REF4-related 1)	Unigene11137_All//2.00E-95//gi|78342988|gb|DT563262.1|DT563262				nr -
Unigene111370_All	419	0.00	0.00	0.00	0.00	0.00	0.00	2.42	1.10	0.00	null	null		null	null		null	null		null	null		-1.14E+00	6.62E-02		-1.12E+01	1.35E-07	Down	Unigene111370_All//gi|1354041|sp|P11481.1|TBA1_VOLCA//9.00E-66//RecName: Full=Tubulin alpha-1/alpha-2 chain >gi|22001|emb|CAA31326.1| alpha-1 tubulin [Volvox carteri f. nagariensis] >gi|404089|gb|AAA99438.1| alpha-2 tubulin [Volvox carteri] >gi|300257467|gb|EFJ41715.1| alpha tubulin [Volvox carteri f. nagariensis] >gi|300263702|gb|EFJ47901.1| alpha tubulin [Volvox carteri f. nagariensis]	Unigene111370_All//2.00E-65//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene111370_All//6.00E-22//ES832636		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene111371_All	428	1.47	0.12	0.12	1.05	0.32	0.42	1.88	0.39	0.28	-3.63E+00	5.07E-03		-3.56E+00	8.32E-03		-1.70E+00	1.35E-01		-1.31E+00	2.73E-01		-2.26E+00	4.82E-03		-2.75E+00	9.43E-04	Down			Unigene111371_All//1.00E-07//DW500060					
Unigene111373_All	801	0.00	0.00	0.00	0.00	0.00	0.00	0.79	1.04	0.00	null	null		null	null		null	null		null	null		3.98E-01	5.94E-01		-9.63E+00	7.12E-05	Down	Unigene111373_All//gi|298706583|emb|CBJ29542.1|//7.00E-23//ankyrin repeat protein [Ectocarpus siliculosus]	Unigene111373_All//5.00E-19//AT5G14230| protein binding					nr +
Unigene111375_All	683	0.00	0.00	0.00	0.00	0.00	0.00	4.70	0.67	0.35	null	null		null	null		null	null		null	null		-2.81E+00	1.30E-12	Down	-3.75E+00	7.58E-17	Down	Unigene111375_All//gi|49147195|ref|YP_025788.1|//3.00E-20//ATP synthase F0 subunit 6 [Pseudendoclonium akinetum] >gi|33439210|gb|AAQ18747.1| ATP synthase F0 subunit 6 [Pseudendoclonium akinetum]				ko00190|Oxidative phosphorylation	GO:0006754//GO:0015992//GO:0016020//GO:0044424	nr +
Unigene111377_All	449	0.00	0.34	0.24	1.22	0.15	0.00	1.98	0.74	0.27	8.40E+00	2.36E-01		7.89E+00	4.01E-01		-2.99E+00	9.39E-03		-1.03E+01	1.52E-03		-1.41E+00	4.01E-02		-2.89E+00	3.04E-04	Down								ESTscan -
Unigene111378_All	376	0.42	1.08	0.57	0.53	0.82	0.12	8.88	0.67	1.27	1.37E+00	2.74E-01		4.40E-01	7.76E-01		6.37E-01	6.95E-01		-2.14E+00	3.47E-01		-3.74E+00	8.20E-17	Down	-2.80E+00	1.46E-13	Down	Unigene111378_All//gi|224139620|ref|XP_002323196.1|//4.00E-08//argonaute protein group [Populus trichocarpa] >gi|222867826|gb|EEF04957.1| argonaute protein group [Populus trichocarpa]		Unigene111378_All//2.00E-09//TC138448				nr -
Unigene11138_All	1105	0.19	0.37	0.87	0.90	2.68	3.60	6.16	8.70	14.82	9.54E-01	4.14E-01		2.20E+00	9.10E-03		1.57E+00	2.01E-05	Up	2.00E+00	4.55E-09	Up	4.98E-01	2.63E-03		1.27E+00	3.10E-22	Up	Unigene11138_All//gi|297824921|ref|XP_002880343.1|//1.00E-68//structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata] >gi|297326182|gb|EFH56602.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	Unigene11138_All//1.00E-69//AT2G48110| REF4 (REDUCED EPIDERMAL FLUORESCENCE 4)	Unigene11138_All//0.00E+00//TC138318				nr +
Unigene111380_All	503	0.00	0.00	0.00	0.00	0.00	0.00	3.11	0.50	0.00	null	null		null	null		null	null		null	null		-2.64E+00	4.08E-06	Down	-1.16E+01	1.42E-11	Down	Unigene111380_All//gi|1706581|sp|P54959.1|EF1A_BLAHO//2.00E-66//RecName: Full=Elongation factor 1-alpha; Short=EF-1-alpha >gi|984790|dbj|BAA10962.1| elongation factor 1alpha [Blastocystis hominis]	Unigene111380_All//2.00E-47//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene111380_All//4.00E-17//TC166357			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene111381_All	398	0.00	0.00	0.00	0.00	0.00	0.00	8.29	0.53	0.60	null	null		null	null		null	null		null	null		-3.98E+00	2.17E-17	Down	-3.79E+00	2.10E-17	Down	Unigene111381_All//gi|27923849|sp|Q945U1.1|RS15_ELAOL//7.00E-42//RecName: Full=40S ribosomal protein S15 >gi|15425963|gb|AAK97632.1| 40S ribosomal protein S15 [Elaeis oleifera] >gi|192910788|gb|ACF06502.1| 40S ribosomal protein S15 [Elaeis guineensis]	Unigene111381_All//5.00E-32//AT5G09560| 40S ribosomal protein S15 (RPS15C)	Unigene111381_All//5.00E-07//BG444152		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene111385_All	449	0.00	0.11	0.47	1.11	1.00	0.50	3.48	1.30	0.44	6.82E+00	6.21E-01		8.89E+00	1.42E-01		-1.54E-01	8.50E-01		-1.14E+00	3.07E-01		-1.42E+00	3.64E-03		-2.97E+00	4.24E-07	Down								
Unigene111386_All	831	0.00	0.00	0.00	0.00	0.04	0.11	3.61	0.25	0.62	null	null		null	null		5.37E+00	8.37E-01		6.76E+00	4.80E-01		-3.84E+00	1.74E-15	Down	-2.54E+00	4.57E-11	Down	Unigene111386_All//gi|260401291|gb|ACX37122.1|//4.00E-06//ORF1 [Pisum sativum]		Unigene111386_All//1.00E-09//FL577667				nr -
Unigene111387_All	422	0.00	0.00	0.00	0.00	0.00	0.00	3.01	0.10	0.19	null	null		null	null		null	null		null	null		-4.92E+00	7.77E-08	Down	-3.99E+00	2.56E-07	Down	Unigene111387_All//sp|Q92954|PRG4_HUMAN//2.00E-06//Proteoglycan 4 OS=Homo sapiens GN=PRG4 PE=1 SV=2							swissprot +
Unigene111389_All	471	0.00	0.00	0.00	0.00	0.00	0.00	2.33	0.18	0.00	null	null		null	null		null	null		null	null		-3.72E+00	7.15E-06	Down	-1.12E+01	3.33E-08	Down	Unigene111389_All//gi|223995731|ref|XP_002287539.1|//7.00E-52//cyclophilin-type peptidyl-prolyl cis-trans isomerase [Thalassiosira pseudonana CCMP1335] >gi|220976655|gb|EED94982.1| cyclophilin-type peptidyl-prolyl cis-trans isomerase [Thalassiosira pseudonana CCMP1335]	Unigene111389_All//3.00E-42//AT2G29960| CYP5 (CYCLOPHILIN 5); peptidyl-prolyl cis-trans isomerase	Unigene111389_All//7.00E-25//gi|78351431|gb|DT571705.1|DT571705			GO:0016859//GO:0044267	nr +
Unigene111393_All	506	0.00	0.00	0.00	0.00	0.00	0.00	1.67	0.08	0.00	null	null		null	null		null	null		null	null		-4.34E+00	4.55E-05	Down	-1.07E+01	2.21E-06	Down	Unigene111393_All//gi|266706161|gb|ACY78390.1|//2.00E-10//protein tyrosine phosphatase 1 [Phaleanopsis amabilis]	Unigene111393_All//9.00E-08//AT1G71860| PTP1 (PROTEIN TYROSINE PHOSPHATASE 1); protein tyrosine phosphatase				GO:0016791	nr -
Unigene111395_All	1181	0.00	0.00	0.00	0.00	0.00	0.00	9.42	0.07	0.00	null	null		null	null		null	null		null	null		-7.06E+00	4.36E-75	Down	-1.32E+01	6.27E-82	Down								ESTscan -
Unigene111397_All	452	0.00	0.00	0.00	0.00	0.00	0.00	8.33	0.00	0.35	null	null		null	null		null	null		null	null		-1.30E+01	1.28E-26	Down	-4.56E+00	2.21E-22	Down	Unigene111397_All//gi|301117182|ref|XP_002906319.1|//2.00E-41//60S ribosomal protein L27 [Phytophthora infestans T30-4] >gi|262107668|gb|EE165720.1| 60S ribosomal protein L27 [Phytophthora infestans T30-4]	Unigene111397_All//4.00E-31//AT3G22230| 60S ribosomal protein L27 (RPL27B)	Unigene111397_All//2.00E-09//gi|78337699|gb|DT557973.1|DT557973		ko03010|Ribosome	GO:0030529	nr +
Unigene111398_All	528	0.40	0.29	0.00	1.13	0.20	0.17	2.24	0.95	0.53	-4.61E-01	7.58E-01		-8.63E+00	1.46E-01		-2.53E+00	1.36E-02		-2.73E+00	1.74E-02		-1.24E+00	2.93E-02		-2.09E+00	5.32E-04	Down			Unigene111398_All//6.00E-07//TC141683					

Unigene111399_All	492	0.00	0.00	0.00	0.00	0.00	0.00	2.75	1.61	0.65	null	null		null	null		null	null		null	null		-7.69E-01	1.39E-01		-2.09E+00	1.85E-04	Down	Unigene111399_All//gi|297824773|ref|XP_002880269.1|//7.00E-32//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297326108|gb|EFH56528.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene111399_All//7.00E-31//AT2G46850| ATP binding / protein kinase/ protein tyrosine kinase				GO:0004672//GO:0006464//GO:0032559	nr -
Unigene111400_All	494	0.00	0.00	0.00	0.00	0.00	0.00	2.65	0.17	2.10	null	null		null	null		null	null		null	null		-3.97E+00	3.35E-07	Down	-3.40E-01	5.21E-01		Unigene111400_All//gi|164564727|dbj|BAF98210.1|//6.00E-33//CM0216.210.nc [Lotus japonicus]	Unigene111400_All//6.00E-19//AT4G35200| unknown protein					nr -
Unigene111401_All	1262	0.08	0.16	0.08	0.28	0.00	0.07	3.55	2.29	1.58	9.54E-01	6.22E-01		2.59E-02	1.00E+00		-8.11E+00	9.46E-03		-1.95E+00	1.96E-01		-6.36E-01	1.26E-02		-1.17E+00	4.38E-06	Down							
Unigene111402_All	817	0.00	0.00	0.00	0.00	0.00	0.00	3.57	0.46	0.39	null	null		null	null		null	null		null	null		-2.96E+00	4.23E-12	Down	-3.19E+00	1.79E-13	Down	Unigene111402_All//gi|115489150|ref|XP_001067062.1|//9.00E-95//Os12g0567700 [Oryza sativa Japonica Group] >gi|113649569|dbj|BAF30081.1| Os12g0567700 [Oryza sativa Japonica Group]	Unigene111402_All//2.00E-88//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene111402_All//3.00E-10//gi|78337755|gb|DT558029.1|DT558029		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0043231	nr -
Unigene111404_All	490	0.00	0.00	0.00	0.00	0.00	0.00	6.47	1.28	1.54	null	null		null	null		null	null		null	null		-2.34E+00	2.70E-10	Down	-2.07E+00	2.80E-09	Down	Unigene111404_All//gi|224140285|ref|XP_002323513.1|//1.00E-17//amino acid transporter [Populus trichocarpa] >gi|222868143|gb|EEF05274.1| amino acid transporter [Populus trichocarpa]	Unigene111404_All//2.00E-16//AT5G02170| amino acid transporter family protein				GO:0005275//GO:0009536//GO:0016020	nr +
Unigene111405_All	575	0.00	0.00	0.00	0.26	0.12	0.16	2.43	0.07	1.52	null	null		null	null		-1.12E+00	5.85E-01		-7.26E-01	7.16E-01		-5.06E+00	1.10E-08	Down	-6.71E-01	1.68E-01		Unigene111405_All//gi|116310721|emb|CAM67518.1|//1.00E-29//OS1G0a0092E01.13 [Oryza sativa (indica cultivar-group)]	Unigene111405_All//3.00E-18//AT5G57770| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Pleckstrin-like, plant (InterPro:IPR013666), Protein of unknown function DUF828, plant (InterPro:IPR008546); Has 104 Blast hits to 104 proteins in 9 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 102; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene111405_All//1.00E-69//CA993859				nr -
Unigene111406_All	651	0.00	0.00	0.00	0.00	0.00	0.00	2.27	0.06	0.24	null	null		null	null		null	null		null	null		-5.15E+00	2.98E-09	Down	-3.22E+00	3.28E-07	Down	Unigene111406_All//gi|15237193|ref|NP_197691.1|//1.00E-22//MYB37 (MYB DOMAIN PROTEIN 37); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75333792|sp|Q9FG68.1|RAX1_ARATH RecName: Full=Transcription factor RAX1; AltName: Full=Protein REGULATOR OF AXILLARY MERISTEMS 1; AltName: Full=Myb-related protein 37; Short=AtMYB37 >gi|9758402|dbj|BAB08873.1| myb-related transcription factor-like [Arabidopsis thaliana] >gi|18072740|emb|CAC80101.1| R2R3-MYB transcription factor [Arabidopsis thaliana] >gi|41619420|gb|AAS10098.1| MYB transcription factor [Arabidopsis thaliana] >gi|51969156|dbj|BAD43270.1| myb like transcription factor (MYB37) [Arabidopsis thaliana] >gi|918068896|gb|ABE66175.1| myb family transcription factor [Arabidopsis thaliana]	Unigene111406_All//5.00E-23//AT5G23000| MYB37 (MYB DOMAIN PROTEIN 37); DNA binding / transcription factor		MYB		GO:0006350//GO:0010468	nr -
Unigene111407_All	539	0.29	0.19	1.28	0.18	0.00	0.17	4.16	1.01	0.07	-6.31E-01	7.28E-01		2.14E+00	3.67E-02		-7.53E+00	3.16E-01		-1.41E-01	9.52E-01		-2.04E+00	1.89E-06	Down	-5.81E+00	4.52E-15	Down							
Unigene111409_All	562	0.00	0.00	0.00	0.00	0.00	0.00	3.76	0.00	0.07	null	null		null	null		null	null		null	null		-1.19E+01	5.89E-15	Down	-5.73E+00	3.61E-14	Down							ESTscan -
Unigene111411_All	553	0.00	0.00	0.00	0.00	0.00	0.00	2.37	1.13	0.14	null	null		null	null		null	null		null	null		-1.06E+00	4.42E-02		-4.04E+00	1.35E-07	Down							ESTscan +
Unigene111412_All	542	0.00	0.00	0.00	0.00	0.00	0.00	2.50	0.54	0.07	null	null		null	null		null	null		null	null		-2.21E+00	1.58E-04	Down	-5.09E+00	8.12E-09	Down	Unigene111412_All//gi|297809931|ref|XP_002872849.1|//2.00E-32//60S ribosomal protein L19 [Arabidopsis lyrata subsp. lyrata] >gi|297318686|gb|EFH49108.1| 60S ribosomal protein L19 [Arabidopsis lyrata subsp. lyrata]	Unigene111412_All//1.00E-14//AT4G02230| 60S ribosomal protein L19 (RPL19C)			ko03010|Ribosome	GO:0005198//GO:0009987//GO:0010467//GO:0015934//GO:0016020//GO:0003198 1	nr +
Unigene111414_All	592	0.18	0.00	0.81	1.26	0.52	0.69	2.79	0.35	0.13	-7.47E+00	3.76E-01		2.19E+00	9.15E-02		-1.27E+00	1.12E-01		-8.78E-01	3.08E-01		-2.98E+00	3.67E-07	Down	-4.37E+00	7.28E-10	Down	Unigene111414_All//gi|15230954|ref|NP_189226.1|//3.00E-59//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene111414_All//1.00E-60//AT3G25970| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene111415_All	564	0.28	0.00	0.66	8.04	5.37	3.36	10.79	2.37	5.93	-8.12E+00	2.16E-01		1.25E+00	3.66E-01		-5.81E-01	3.32E-02		-1.26E+00	1.07E-05	Down	-2.19E+00	1.13E-17	Down	-8.63E-01	3.59E-05		Unigene111415_All//gi|211906540|gb|ACJ11763.1|//1.00E-23//class III peroxidase [Gossypium hirsutum]	Unigene111415_All//6.00E-19//AT4G30170| peroxidase, putative	Unigene111415_All//1.00E-94//TC133431		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209//GO:0031410	nr -
Unigene111417_All	623	0.84	0.00	0.17	0.16	0.11	0.00	14.66	7.92	0.58	-9.71E+00	2.93E-03		-2.30E+00	6.77E-02		-5.33E-01	8.18E-01		-7.32E+00	4.04E-01		-8.89E-01	2.25E-07		-4.67E+00	2.38E-54	Down	Unigene111417_All//gi|18397934|ref|NP_565380.1|//8.00E-26//glycine-rich protein [Arabidopsis thaliana] >gi|15294186|gb|AAK95270.1|AF410284_1 At2g15780/F19G14.22 [Arabidopsis thaliana] >gi|3306253|gb|AAD41986.1| expressed protein [Arabidopsis thaliana] >gi|20147265|gb|AAM10346.1| At2g15780/F19G14.22 [Arabidopsis thaliana]	Unigene111417_All//4.00E-27//AT2G15780| glycine-rich protein					nr +
Unigene111418_All	1206	1.30	0.59	1.10	0.95	0.40	0.34	1.33	0.55	0.40	-1.15E+00	3.18E-02		-2.38E-01	6.42E-01		-1.25E+00	4.15E-02		-1.50E+00	2.37E-02		-1.26E+00	7.61E-03		-1.75E+00	2.97E-04	Down	Unigene111418_All//gi|297389604|ref|XP_002862749.1|//2.00E-83//myb family transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297308457|gb|EFH39007.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene111418_All//2.00E-58//AT5G45420| myb family transcription factor	Unigene111418_All//0.00E+00//TC143540	MYB-related		GO:0016020//GO:0043231	nr +
Unigene111420_All	603	0.00	0.00	0.00	0.00	0.00	0.00	4.07	0.07	0.00	null	null		null	null		null	null		null	null		-5.87E+00	7.01E-16	Down	-1.20E+01	4.73E-18	Down	Unigene111420_All//gi|159476204|ref|XP_001696201.1|//9.00E-48//ribosomal protein S8, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158282426|gb|EDP08178.1| ribosomal protein S8 [Chlamydomonas reinhardtii]	Unigene111420_All//4.00E-43//AT5G59240| 40S ribosomal protein S8 (RPS8B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0030529	nr -
Unigene111421_All	1158	0.00	0.00	0.00	0.00	0.00	0.00	7.74	0.07	0.38	null	null		null	null		null	null		null	null		-6.74E+00	6.86E-60	Down	-4.35E+00	4.18E-51	Down	Unigene111421_All//gi|169137009|gb|ABS86614.2|//1.00E-10//latex protein [Morus alba]	Unigene111421_All//5.00E-05//AT3G04720| PR4 (PATHOGENESIS-RELATED 4); chitin binding					nr +
Unigene111423_All	1413	0.00	0.00	0.00	0.00	0.00	0.00	3.56	0.12	0.06	null	null		null	null		null	null		null	null		-4.91E+00	6.78E-30	Down	-5.98E+00	9.91E-34	Down	Unigene111423_All//gi|298705968|emb|CBJ29089.1|//5.00E-38//WRKN repeat variant family protein [Ectocarpus siliculosus]	Unigene111423_All//1.00E-29//AT1G60890| phosphatidylinositol-4-phosphate 5-kinase family protein			ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0003779//GO:0016307	nr +
Unigene111425_All	735	0.00	0.00	0.00	0.00	0.00	0.00	8.46	0.11	1.14	null	null		null	null		null	null		null	null		-6.22E+00	1.26E-40	Down	-2.89E+00	2.15E-25	Down	Unigene111425_All//gi|18414906|ref|NP_568156.1|//4.00E-46//pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] >gi|111074158|gb|ABH04452.1| At5g05500 [Arabidopsis thaliana]	Unigene111425_All//1.00E-46//AT5G05500| pollen Ole e 1 allergen and extensin family protein				GO:0044464	nr +
Unigene111426_All	832	0.00	0.00	0.00	0.00	0.00	0.00	1.27	0.20	1.05	null	null		null	null		null	null		null	null		-2.66E+00	2.25E-04	Down	-2.70E-01	6.43E-01		Unigene111426_All//gi|15230628|ref|NP_187896.1|//2.00E-55//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|918006419|gb|ABE65937.1| oxidoreductase 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	Unigene111426_All//2.00E-50//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene111426_All//1.00E-104//TC134433		ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016701//GO:0016706	nr +
Unigene111427_All	849	0.00	0.00	0.00	0.00	0.00	0.00	4.18	0.89	0.70	null	null		null	null		null	null		null	null		-2.24E+00	6.71E-11	Down	-2.57E+00	3.78E-13	Down	Unigene111427_All//gi|226510214|ref|NP_001149016.1|//9.00E-14//dnaJ subfamily B member 5 [Zea mays] >gi|195624008|gb|ACG33834.1| dnaJ subfamily B member 5 [Zea mays]	Unigene111427_All//2.00E-12//AT4G28480| DNAJ heat shock family protein				GO:0005515//GO:0031410	nr +
Unigene11143_All	1661	3.24	7.23	4.81	5.19	4.87	4.30	19.80	27.73	28.95	1.16E+00	1.45E-11	Up	5.68E-01	8.03E-03		-9.08E-02	7.04E-01		-2.72E-01	2.06E-01		4.86E-01	3.50E-12		5.48E-01	5.34E-16		Unigene11143_All//gi|3776567|gb|AAC64884.1|//0.00E+00//Strong similarity to F21B7.33 gi|2809264 from A. thaliana BAC gb|AC002560. EST gb|N65119 comes from this gene [Arabidopsis thaliana]	Unigene11143_All//4.00E-180//AT1G54710| AtATG18h	Unigene11143_All//0.00E+00//DN780615			GO:0006464//GO:0006950//GO:0009536//GO:0016301//GO:0032559	nr +
Unigene111430_All	1749	0.00	0.00	0.00	0.00	0.00	0.00	15.81	0.43	0.66	null	null		null	null		null	null		null	null		-5.20E+00	1.01E-167	Down	-4.58E+00	8.55E-162	Down	Unigene111430_All//gi|224113191|ref|XP_002332632.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222832859|gb|EEE71336.1| cytochrome P450 [Populus trichocarpa]	Unigene111430_All//0.00E+00//AT3G52970| CYP7561; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr -
Unigene111433_All	200	0.00	0.00	0.00	0.00	0.00	0.00	4.23	0.21	1.79	null	null		null	null		null	null		null	null		-4.34E+00	4.55E-05	Down	-1.24E+00	6.26E-02								
Unigene111436_All	200	0.00	0.00	0.00	0.25	0.69	0.00	4.86	0.00	0.00	null	null		null	null		1.47E+00	6.20E-01		-7.96E+00	6.43E-01		-1.22E+01	5.84E-07	Down	-1.22E+01	2.72E-07	Down			Unigene111436_All//9.00E-13//EX169598				
Unigene11144_All	3708	2.03	8.53	2.38	3.24	2.93	3.78	17.23	32.65	52.09	2.07E+00	2.41E-67	Up	2.31E-01	2.89E-01		-1.42E-01	4.52E-01		2.22E-01	1.84E-01		9.22E-01	2.55E-93		1.60E+00	0.00E+00	Up	Unigene11144_All//gi|18405032|ref|NP_564664.1|//0.00E+00//AtATG18h [Arabidopsis thaliana]	Unigene11144_All//0.00E+00//AT1G54710| AtATG18h	Unigene11144_All//0.00E+00//DN780615			GO:0000166//GO:0006950//GO:0043231	nr +
Unigene11145_All	3079	3.31	7.85	4.00	3.64	4.42	4.08	20.35	23.81	23.43	1.24E+00	3.41E-25	Up	2.70E-01	1.31E-01		2.79E-01	7.71E-02		1.64E-01	3.93E-01		2.27E-01	3.93E-05		2.03E-01	1.98E-04		Unigene11145_All//gi|18405032|ref|NP_564664.1|//0.00E+00//AtATG18h [Arabidopsis thaliana]	Unigene11145_All//0.00E+00//AT1G54710| AtATG18h	Unigene11145_All//0.00E+00//CO083391			GO:0000166//GO:0006950//GO:0043231	nr -

Unigene111458_A11	200	8.89	3.55	3.20	14.20	6.20	6.32	32.98	22.57	27.29	-1.33E+00	8.42E-03		-1.48E+00	5.78E-03		-1.20E+00	6.51E-04	Down	-1.17E+00	1.74E-03		-5.47E-01	7.52E-03		-2.73E-01	1.94E-01		Unigene111458_A11//gi|15234480|ref|NP_192395.1|//9.00E-31//DER2.2 (DERLIN-2.2) [Arabidopsis thaliana] >gi|75216465|sp|Q9ZS88.1|DER22_ARATH RecName: Full=Derlin-2.2; AltName: Full=AtDerlin2-2 >gi|14488073|gb|AAK63857.1|AF38928_1_AT4g04860/T4B21_2 [Arabidopsis thaliana] >gi|4115936|gb|AAD03446.1| T4B21.2 gene product [Arabidopsis thaliana] >gi|20147127|gb|AAM10280.1|AT4g04860/T4B21_2 [Arabidopsis thaliana]	Unigene111458_A11//5.00E-23//AT4G04860| DER2.2 (DERLIN-2.2)	Unigene111458_A11//5.00E-107//TC135552			GO:0019538//GO:0031090//GO:0031224//GO:0043231//GO:0050896	nr -
Unigene111459_A11	200	0.00	0.00	0.00	0.00	0.00	0.00	3.17	0.00	0.00	null	null		null	null		null	null		null	null		-1.16E+01	1.23E-04	Down	-1.16E+01	7.12E-05	Down	Unigene111459_A11//gi|300521738|gb|ADK26058.1|//4.00E-15//drought resistance protein [Glycine max]	Unigene111459_A11//2.00E-12//AT4G02270| pollen Ole e 1 allergen and extensin family protein					nr +
Unigene111464_A11	201	0.26	0.00	0.26	0.00	0.34	0.67	2.94	0.00	0.40	-8.02E+00	6.18E-01		2.53E-02	9.96E-01		8.42E+00	6.14E-01		9.40E+00	3.12E-01		-1.15E+01	2.39E-04	Down	-2.89E+00	4.54E-03				Unigene111464_A11//8.00E-106//gi|109884320|gb|DW513290.1|DW513290				
Unigene111466_A11	201	0.00	0.00	0.00	0.00	0.00	0.00	2.94	0.00	0.00	null	null		null	null		null	null		null	null		-1.15E+01	2.39E-04	Down	-1.15E+01	1.41E-04	Down	Unigene111466_A11//gi|10443488|gb|AAG17477.1|AF106846_1//3.00E-20//QM protein [Oryza sativa (Indica Group)]	Unigene111466_A11//1.00E-20//AT1G14320| SAC52 (SUPPRESSOR OF ACAULIS 52); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene111483_A11	201	0.00	0.00	0.00	0.00	0.00	0.00	3.37	0.62	0.00	null	null		null	null		null	null		null	null		-2.43E+00	7.77E-03		-1.17E+01	3.57E-05	Down	Unigene111483_A11//gi|300256601|gb|EFJ40863.1|//8.00E-06//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]				ko03010|Ribosome		nr -
Unigene111485_A11	201	0.00	0.00	0.00	0.00	0.00	0.00	9.05	0.00	0.20	null	null		null	null		null	null		null	null		-1.31E+01	7.16E-13	Down	-5.51E+00	4.49E-12	Down				Unigene111485_A11//2.00E-07//TC142576				
Unigene111487_A11	201	0.52	0.00	0.00	1.49	0.34	0.00	2.52	0.62	0.00	-9.02E+00	3.76E-01		-9.02E+00	3.98E-01		-2.12E+00	1.66E-01		-1.03E-01	4.01E-02		-2.02E+00	5.21E-02		-1.13E+01	5.55E-04	Down							
Unigene111490_A11	201	0.00	0.00	0.00	0.00	0.00	0.00	16.41	1.04	0.59	null	null		null	null		null	null		null	null		-3.98E+00	2.17E-17	Down	-4.79E+00	3.31E-20	Down							
Unigene111500_A11	202	0.00	0.00	0.00	0.00	0.00	0.00	2.72	0.21	0.00	null	null		null	null		null	null		null	null		-3.72E+00	3.23E-03		-1.14E+01	2.81E-04	Down							ESTscan -
Unigene111509_A11	202	0.00	0.00	0.00	0.00	0.00	0.00	2.72	0.21	0.00	null	null		null	null		null	null		null	null		-3.72E+00	3.23E-03		-1.14E+01	2.81E-04	Down							ESTscan -
Unigene11151_A11	593	2.82	0.17	1.98	4.20	5.05	3.20	4.28	1.76	1.68	-4.05E+00	1.45E-07	Down	-5.15E-01	3.44E-01		2.66E-01	5.31E-01		-3.93E-01	3.72E-01		-1.28E+00	4.33E-04	Down	-1.35E+00	1.51E-04	Down	Unigene11151_A11//gi|2444174|gb|AA871526.1|//3.00E-90//unconventional myosin [Helianthus annuus]	Unigene11151_A11//2.00E-89//AT1G50360| VIIIA; motor	Unigene11151_A11//0.00E+00//ES791939			GO:0015629//GO:0017111//GO:0032559//GO:0043231	nr +
Unigene11152_A11	907	2.77	0.61	0.88	5.11	5.73	2.64	2.75	1.29	2.72	-2.17E+00	2.32E-06	Down	-1.65E+00	2.09E-04	Down	1.67E-01	5.88E-01		-9.53E-01	5.76E-04		-1.09E+00	2.53E-03		-1.42E-02	9.75E-01		Unigene11152_A11//gi|6491702|emb|CAB61875.1|//1.00E-78//myosin [Arabidopsis thaliana]	Unigene11152_A11//6.00E-80//AT3G19960| ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor	Unigene11152_A11//0.00E+00//gi|48777324|gb|C00866690.1|C00866690			GO:0015405//GO:0015629//GO:0017111//GO:0030029//GO:0031224//GO:0032559//GO:0043231//GO:0044444//GO:0051234	nr -
Unigene11528_A11	203	0.00	0.00	0.00	0.00	0.17	0.00	121.22	72.27	328.33	null	null		null	null		7.41E+00	8.36E-01		null	null		-7.46E-01	6.55E-14		1.44E+00	1.77E-106	Up	Unigene11528_A11//gi|40218371|gb|AAR83118.1|//4.00E-19//secretory laccase [Gossypium arboreum]	Unigene11528_A11//3.00E-05//AT5G03260| LAC11 (laccase 11); laccase	Unigene11528_A11//2.00E-63//TC137114			GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr +
Unigene11153_A11	1756	1.52	0.87	4.03	6.07	5.26	4.09	4.43	1.40	3.56	-8.12E-01	3.53E-02		1.41E+00	4.99E-09	Up	-2.08E-01	2.81E-01		-5.70E-01	8.81E-04		-1.66E+00	1.12E-15	Down	-3.15E-01	9.23E-02		Unigene11153_A11//gi|116047919|gb|ABJ53200.1|//0.00E+00//myosin VIII-1 [Nicotiana benthamiana]	Unigene11153_A11//0.00E+00//AT3G19960| ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor	Unigene11153_A11//0.00E+00//C0099686			GO:0015405//GO:0015629//GO:0017111//GO:0030029//GO:0031224//GO:0032559//GO:0044444//GO:0051234	nr -
Unigene11154_A11	2360	8.27	3.13	5.03	12.66	14.45	10.05	10.68	6.64	4.63	-1.40E+00	1.59E-24	Down	-7.17E-01	2.88E-08		1.90E-01	4.66E-02		-3.34E-01	6.45E-04		-6.85E-01	2.29E-12		-1.21E+00	1.26E-31	Down	Unigene11154_A11//gi|116047919|gb|ABJ53200.1|//0.00E+00//myosin VIII-1 [Nicotiana benthamiana]	Unigene11154_A11//0.00E+00//AT3G19960| ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor	Unigene11154_A11//0.00E+00//gi|164335094|gb|ES790869.1|ES790869			GO:0015405//GO:0015629//GO:0017111//GO:0030029//GO:0031224//GO:0032559//GO:0044444//GO:0051234	nr -
Unigene111549_A11	204	0.00	0.00	0.00	0.00	0.00	0.66	3.52	0.61	0.39	null	null		null	null		null	null		9.38E+00	3.12E-01		-2.52E+00	4.69E-03		-3.17E+00	8.09E-04	Down							
Unigene111563_A11	204	0.00	0.00	0.00	0.00	0.00	0.00	3.11	1.43	0.00	null	null		null	null		null	null		null	null		-1.12E+00	1.80E-01		-1.16E+01	7.12E-05	Down	Unigene111563_A11//sp|Q6CQE5|TAR1_KLULA//4.00E-18//Protein TAR1 OS=Kluyveromyces lactis GN=TAR1-A PE=4 SV=2		Unigene111563_A11//2.00E-17//TC133518				swissprot +
Unigene111581_A11	205	0.00	0.00	0.00	0.24	0.17	0.00	2.68	1.43	0.00	null	null		null	null		-5.33E-01	8.28E-01		-7.92E+00	6.43E-01		-9.10E-01	3.19E-01		-1.14E+01	2.81E-04	Down							
Unigene111583_A11	205	0.00	0.00	0.00	0.00	0.00	0.00	3.30	0.82	0.00	null	null		null	null		null	null		null	null		-2.02E+00	1.98E-02		-1.17E+01	3.57E-05	Down							ESTscan -
Unigene111584_A11	205	0.00	0.00	0.00	0.00	0.00	0.00	3.92	0.61	0.58	null	null		null	null		null	null		null	null		-2.68E+00	1.67E-03		-2.75E+00	9.43E-04	Down							
Unigene11159_A11	468	0.67	0.65	1.48	2.24	1.03	0.87	5.87	2.32	0.77	-4.63E-02	9.85E-01		1.14E+00	2.18E-01		-1.12E+00	8.44E-02		-1.36E+00	4.89E-02		-1.34E+00	1.28E-04	Down	-2.94E+00	8.38E-12	Down				Unigene11159_A11//3.00E-95//gi|163424276|gb|ES793425.1|ES793425				
Unigene111592_A11	205	0.00	0.00	0.00	0.00	0.00	0.00	2.68	0.82	0.00	null	null		null	null		null	null		null	null		-1.72E+00	7.23E-02		-1.14E+01	2.81E-04	Down							ESTscan -
Unigene111595_A11	205	0.00	0.00	0.00	0.00	0.00	0.00	2.47	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	8.90E-04	Down	-1.13E+01	5.55E-04	Down							
Unigene11160_A11	472	6.32	2.58	4.63	1.90	1.53	0.67	3.40	1.42	0.68	-1.29E+00	5.17E-04	Down	-4.50E-01	2.44E-01		-3.10E-01	6.65E-01		-1.50E+00	5.09E-02		-1.26E+00	7.61E-03		-2.33E+00	8.81E-06	Down				Unigene11160_A11//0.00E+00//gi|164350365|gb|ES847900.1|ES847900				
Unigene11161_A11	3991	6.19	2.83	4.55	2.85	2.79	1.54	2.07	0.81	0.64	-1.13E+00	3.19E-22	Down	-4.44E-01	9.25E-05		-3.02E-02	8.77E-01		-8.87E-01	8.34E-08		-1.36E+00	1.54E-12	Down	-1.69E+00	1.29E-17	Down	Unigene11161_A11//gi|224131798|ref|XP_002321181.1|//0.00E+00//histidine kinase cytokinin receptor [Populus trichocarpa] >gi|222861954|gb|EEE99496.1|histidine kinase cytokinin receptor [Populus trichocarpa]	Unigene11161_A11//0.00E+00//AT2G01830| WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase	Unigene11161_A11//0.00E+00//TC168551	Orphans		GO:0006351//GO:0006468//GO:0006952//GO:0009267//GO:0009744//GO:0009755//GO:0009784//GO:0009845//GO:0010015//GO:0010260//GO:0015698//GO:0016791//GO:0019901//GO:0023060//GO:0032559//GO:0044464//GO:2000026	nr +
Unigene11162_A11	5162	6.69	3.61	5.02	11.92	9.29	6.82	12.98	5.57	4.92	-8.89E-01	5.17E-21		-4.13E-01	1.17E-05		-3.60E-01	3.89E-09		-8.04E-01	1.33E-33		-1.22E+00	9.04E-82	Down	-1.40E+00	1.03E-103	Down	Unigene11162_A11//gi|190148355|gb|ACE63260.1|//0.00E+00//histidine kinase 2 [Betula pendula]	Unigene11162_A11//0.00E+00//AT5G35750| AHK2 (ARABIDOPSIS HISTIDINE KINASE 2); cytokinin receptor/ osmosensor/ protein histidine kinase	Unigene11162_A11//0.00E+00//TC177777	Orphans		GO:0004673//GO:0004888//GO:0006351//GO:0006468//GO:0006826//GO:0006952//GO:0006970//GO:0009267//GO:0009409//GO:0009737//GO:0009744//GO:0009755//GO:0009845//GO:0009888//GO:0009908//GO:0010260//GO:0015996//GO:0016020//GO:0016791//GO:0019901//GO:0023060//GO:0032559//GO:0040007//GO:2000026	nr -
Unigene111627_A11	207	0.00	0.00	0.00	0.00	0.00	0.00	2.45	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	8.90E-04	Down	-1.13E+01	5.55E-04	Down	Unigene111627_A11//gi|18411538|ref|NP_567096.1|//1.00E-24//60S ribosomal protein L37a (RPL37aC) [Arabidopsis thaliana] >gi|297817320|ref|XP_002876543.1| 60S ribosomal protein L37a [Arabidopsis lyrata subsp. lyrata] >gi|752417667|sp|Q8RUI5.1|RS37C_ARATH RecName: Full=60S ribosomal protein L37a-2 >gi|21593754|gb|AAM65721.1| 60S ribosomal protein L37a [Arabidopsis thaliana] >gi|297322381|gb|EFH52802.1| 60S ribosomal protein L37a [Arabidopsis lyrata subsp. lyrata]	Unigene111627_A11//3.00E-15//AT3G60245| 60S ribosomal protein L37a (RPL37aC)	Unigene111627_A11//9.00E-10//ES845699		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613//GO:0043169	nr +
Unigene111629_A11	207	0.00	0.00	0.00	0.00	0.00	0.00	4.49	0.61	0.19	null	null		null	null		null	null		null	null		-2.89E+00	3.28E-04	Down	-4.54E+00	6.41E-06	Down								
Unigene111644_A11	207	0.00	0.00	0.00	0.00	0.00	0.00	2.45	0.00	0.58	null	null		null	null		null	null		null	null		-1.13E+01	8.90E-04	Down	-2.09E+00	3.65E-02									
Unigene11166_A11	695	3.39	1.31	2.83	3.94	3.86	5.33	4.87	3.61	2.06	-1.37E+00	1.46E-03		-2.57E-01	5.77E-01		-2.86E-02	9.44E-01		4.35E-01	2.01E-01		-4.32E-01	1.65E-01		-1.24E+00	3.60E-05	Down	Unigene11166_A11//gi|18401324|ref|NP_565636.1|//8.00E-70//FRS3 (FAR1-related sequence 3); zinc ion binding [Arabidopsis thaliana] >gi|30683396|ref|NP_850098.1| FRS3 (FAR1-related sequence 3); zinc ion binding [Arabidopsis thaliana] >gi|75216958|sp|Q9ZVC9.2|FRS3_ARATH RecName: Full=Protein FAR1-RELATED SEQUENCE 3 >gi|15982769|gb|AAL09732.1|At2g27110/T20P8.16 [Arabidopsis thaliana] >gi|20197414|gb|AAC77869.2| Mutator-like transposase [Arabidopsis thaliana] >gi|27363374|gb|AAO11606.1|At2g27110/T20P8.16 [Arabidopsis thaliana]	Unigene11166_A11//4.00E-71//AT2G27110| FRS3 (FAR1-related sequence 3); zinc ion binding	Unigene11166_A11//0.00E+00//EX166588			GO:0009416//GO:0046914	nr -
Unigene111669_A11	208	0.00	0.00	0.00	0.00	0.00	0.00	17.07	14.47	0.00	null	null		null	null		null	null		null	null		-2.39E-01	4.55E-01		-1.41E+01	4.09E-26	Down								
Unigene111674_A11	208	0.00	0.00	0.00	2.63	0.33	0.22	19.92	5.02	5.75	null	null		null	null		-2.99E+00	9.39E-03		-3.60E+00	8.98E-03		-1.99E+00	6.14E-11	Down	-1.79E+00	5.60E-10	Down			Unigene111674_A11//4.00E-80//gi|109827560|gb|DW226236.1|DW226236				
Unigene11168_A11	700	0.75	2.61	0.68	0.57	1.87	1.74	1.87	2.27	4.55	1.80E+00	6.20E-04	Up	-1.27E-01	8.98E-01		1.72E+00	5.60E-03		1.61E+00	1.36E-02		2.77E-01	6.01E-01		1.28E+00	4.26E-05	Up	Unigene11168_A11//gi|224057200|ref|XP_002299169.1|//5.00E-21//predicted protein [Populus trichocarpa] >gi|222846427|gb|EEE83974.1|predicted protein [Populus trichocarpa]					GO:0004713//GO:0006464//GO:0032559	nr +
Unigene111685_A11	209	0.00	0.00	0.00	0.00	0.00	0.00	4.65	5.00	0.00	null	null		null	null		null	null		null	null		1.04E-01	8.68E-01		-1.22E+01	2.72E-07	Down								ESTscan +
Unigene111686_A11	209	0.00	0.00	0.00	0.48	0.16	0.00	2.83	0.00	0.00	null	null		null	null		-1.53E+00	5.88E-01		-8.90E+00	4.04E-01		-1.15E+01	2.39E-04	Down	-1.15E+01	1.41E-04	Down								
Unigene11169_A11	602	0.17	0.00	0.00	1.49	0.80	1.20	0.42	1.32	2.91	-7.44E+00	3.76E-01		-7.44E+00	3.98E-01		-8.95E-01	2.14E-01		-3.11E-01	6.88E-01		1.65E+00	2.88E-02		2.79E+00	2.72E-07	Up	Unigene11169_A11//gi|297793187|ref|XP_002864478.1|//5.00E-43//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310313|gb|EFH40737.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11169_A11//3.00E-44//AT5G56790| protein kinase family protein	Unigene11169_A11//0.00E+00//A1726378		ko04626|Plant-pathogen interaction	GO:0004713	nr +
Unigene111694_A11	209	0.00	0.00	0.00	0.00	0.00	0.00	41.27	28.00	0.00	null	null		null	null		null	null		null	null		-5.60E-01	1.40E-03		-1.53E+01	1.70E-63	Down	Unigene111694_A11//gi|168069582|ref|XP_001786502.1|//2.00E-12//predicted protein [Physcomitrella patens subsp. patens] >gi|162661153|gb|EDQ48685.1|predicted protein [Physcomitrella patens subsp. patens]		Unigene111694_A11//2.00E-20//gi|109830702|gb|DW229261.1|DW229261				nr -
Unigene111700_A11	210	0.00	0.00	0.00	0.47	0.00	0.65	5.44	1.39	1.14	null	null		null	null		-8.89E+00	3.16E-01		4.44E-01	8.62E-01		-1.96E+00	1.69E-03		-2.26E+00	3.40E-04	Down			Unigene111700_A11//1.00E-09//DW520090				
Unigene11171_A11	1896	0.00	0.61	0.11	0.42	0.42	0.31	0.78	0.66	1.47	9.26E+00	1.05E-06	Up	6.81E+00	1.42E-01		-9.30E-03	9.67E-01		-4.41E-01	6.14E-01		-2.39E-01	6.20E-01		9.14E-01	5.09E-03		Unigene11171_A11//gi|53791527|dbj|BAD52649.1|//9.00E-44//dual-specific kinase DSK1-like [Oryza sativa Japonica Group] >gi|53793414|dbj|BAD53117.1| dual-specific kinase DSK1-like [Oryza sativa Japonica Group]	Unigene11171_A11//5.00E-44//AT5G56790| protein kinase family protein	Unigene11171_A11//0.00E+00//TC170196		ko04626|Plant-pathogen interaction	GO:0004672	nr -
Unigene111714_A11	210	0.00	0.00	0.00	0.00	0.00	0.00	3.22	1.59	0.19	null	null		null	null		null	null		null	null		-1.02E+00	2.04E-01		-4.09E+00	3.10E-04	Down								
Unigene111721_A11	211	0.00	0.00	0.00	0.00	0.00	0.00	3.81	8.32	0.57	null	null		null	null		null	null		null	null		1.13E+00	1.16E-02		-2.75E+00	9.43E-04	Down								
Unigene111734_A11	212	0.00	0.00	0.00	0.00	0.00	0.00	2.39	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	8.90E-04	Down	-1.12E+01	5.55E-04	Down								ESTscan -
Unigene111739_A11	212	0.00	0.00	0.00	0.00	0.49	0.00	2.19	2.56	7.70	null	null		null	null		8.93E+00	4.58E-01		null	null		2.24E-01	7.92E-01		1.81E+00	2.01E-04	Up			Unigene111739_A11//7.00E-54//DW519317				
Unigene111751_A11	213	15.23	5.23	11.50	14.50	20.69	17.81	2.98	4.12	6.17	-1.54E+00	2.52E-05	Down	-4.05E-01	2.71E-01		5.13E-01	7.85E-02		2.97E-01	3.94E-01		4.69E-01	5.04E-01		1.05E+00	3.92E-02		Unigene111751_A11//gi|227438229|gb|ACP30604.1|//6.00E-06//disease resistance protein [Brassica rapa subsp. pekinensis]	Unigene111751_A11//1.00E-06//AT5G40910| disease resistance protein (TIR-NBS-LRR class), putative					nr +

Unigene111755_All	213	0.49	0.24	0.00	0.47	2.26	0.42	8.93	0.20	1.68	-1.05E+00	6.85E-01			-8.94E+00	3.98E-01		2.27E+00	7.83E-02		-1.41E-01	9.52E-01		-5.51E+00	4.08E-12	Down	-2.41E+00	6.35E-07	Down	Unigene111755_All//gi|297813757|ref|XP_002874762.1|//7.00E-18//At4g12320 [Arabidopsis lyrata subsp. lyrata] >gi|297320599|gb|EFH51021.1| At4g12320 [Arabidopsis lyrata subsp. lyrata]	Unigene111755_All//4.00E-09//AT4G12300| CYP706A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene111755_All//3.00E-93//TC134420		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506//GO:0008152//GO:0044464	nr +
Unigene111757_All	213	0.00	0.48	1.25	0.00	1.13	0.64	3.77	0.59	0.00	8.89E+00	3.90E-01			1.03E+01	8.03E-02		1.01E+01	1.04E-01		9.31E+00	3.12E-01		-2.68E+00	1.67E-03		-1.19E+01	4.43E-06	Down	Unigene111757_All//gi|224146449|ref|XP_002326011.1|//1.00E-13//predicted protein [Populus trichocarpa] >gi|222862886|gb|EEF00393.1| predicted protein [Populus trichocarpa]		Unigene111757_All//6.00E-48//TC175290			GO:0005488//GO:0016307//GO:0044237//GO:0044238	nr +
Unigene111774_All	214	0.24	0.24	0.50	0.93	0.64	0.63	2.37	0.00	0.93	-4.62E-02	9.86E-01			1.03E+00	7.04E-01		-5.33E-01	7.49E-01		-5.57E-01	7.33E-01		-1.12E+01	8.90E-04	Down	-1.35E+00	1.40E-01		Unigene111774_All//gi|15237312|ref|NP_197731.1|//5.00E-16//disease resistance family protein / LRR family protein [Arabidopsis thaliana] >gi|9759078|dbj|BAB09556.1| disease resistance protein-like [Arabidopsis thaliana]	Unigene111774_All//3.00E-13//AT5G23400| disease resistance family protein / LRR family protein	Unigene111774_All//2.00E-115//TC175205			GO:0006950//GO:0016491//GO:0023060//GO:0030312//GO:0031410	nr -
Unigene111781_All	214	0.00	0.00	0.00	0.00	0.00	0.00	2.77	0.00	0.00	null	null			null	null		null	null		null	null		-1.14E+01	2.39E-04	Down	-1.14E+01	1.41E-04	Down	Unigene111781_All//gi|116048190|gb|ABJ53283.1|//7.00E-28//S-adenosyl-L-homocysteine hydrolase [Ligularia fischeri]	Unigene111781_All//4.00E-28//AT3G23810| SAHH2 (S-ADENOSYL-L-HOMOCYSTEINE (SAH) HYDROLASE 2); adenosylhomocysteinase/ binding / catalytic	Unigene111781_All//4.00E-12//gi|5048510|gb|AI729658.1|AI729658		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0016802//GO:0044237	nr -
Unigene111789_All	214	0.00	3.08	0.00	0.47	0.00	0.84	0.99	0.00	0.56	1.16E+01	6.26E-04	Up	null	null	null		-8.86E+00	3.16E-01		8.59E-01	6.96E-01		-9.95E+00	7.46E-02		-8.23E-01	6.00E-01		Unigene111789_All//gi|208429106|gb|ACI26722.1|//4.00E-16//receptor-like kinase [Nicotiana glutinosa]	Unigene111789_All//1.00E-05//AT4G32300| SRF-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase	Unigene111789_All//1.00E-117//TC178969			GO:0004674//GO:0004871//GO:0006464//GO:0031410//GO:0032559	nr +
Unigene111179_All	2663	6.96	3.58	3.14	12.96	11.42	10.35	15.77	9.01	8.35	-9.59E-01	4.15E-13			-1.15E+00	1.40E-16	Down	-1.83E-01	5.25E-02		-3.26E-01	3.11E-04		-8.07E-01	2.07E-26		-9.17E-01	1.42E-33		Unigene111179_All//gi|15231445|ref|NP_190235.1|//0.00E+00//PUB13 (PLANT U-BOX 13; ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75266129|sp|Q9SNC6.1|PUB13_ARATH RecName: Full=U-box domain-containing protein 13; AltName: Full=Plant U-box protein 13 >gi|6523054|emb|CAB62321.1| arm repeat containing protein homolog [Arabidopsis thaliana] >gi|145966007|gb|AAK68731.1| arm repeat containing protein homolog [Arabidopsis thaliana] >gi|22136270|gb|AAM91213.1| arm repeat containing protein homolog [Arabidopsis thaliana]	Unigene111179_All//0.00E+00//AT3G46510| PUB13 (PLANT U-BOX 13); ubiquitin-protein ligase	Unigene111179_All//0.00E+00//TC171950		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0019787//GO:0032446//GO:0043231//GO:0043234//GO:0044444	nr +
Unigene111795_All	214	6.85	2.60	7.47	12.80	12.87	20.05	51.76	14.65	15.45	-1.39E+00	1.39E-02			1.25E-01	8.06E-01		7.90E-03	9.95E-01		6.47E-01	2.87E-02		-1.82E+00	5.48E-25	Down	-1.74E+00	2.43E-24	Down	Unigene111795_All//gi|225431804|ref|XP_002272727.1|//1.00E-11//PREDICTED: similar to 60S ribosomal protein L19 [Vitis vinifera]		Unigene111795_All//3.00E-50//ES836772		ko03010|Ribosome		nr +
Unigene111798_All	215	0.00	0.00	0.00	0.00	0.00	0.00	2.56	0.00	0.00	null	null			null	null		null	null		null	null		-1.13E+01	4.62E-04	Down	-1.13E+01	2.81E-04	Down									
Unigene111802_All	215	0.00	0.00	0.00	0.00	0.00	0.00	2.36	1.17	0.00	null	null			null	null		null	null		null	null		-1.02E+00	2.88E-01		-1.12E+01	5.55E-04	Down									ESTscan -
Unigene111805_All	215	0.00	0.00	0.00	0.00	0.00	0.00	2.56	0.97	0.00	null	null			null	null		null	null		null	null		-1.40E+00	1.35E-01		-1.13E+01	2.81E-04	Down	Unigene111805_All//gi|300137372|gb|EFJ04348.1|//5.00E-11//hypothetical protein SELMODRAFT_138833 [Selaginella moellendorffii]		Unigene111805_All//1.00E-15//TC148521				nr -
Unigene111807_All	215	0.00	0.00	0.00	1.39	1.76	0.00	3.74	0.58	0.00	null	null			null	null		3.42E-01	8.36E-01		-1.04E+01	4.01E-02		-2.68E+00	1.67E-03		-1.19E+01	4.43E-06	Down			Unigene111807_All//2.00E-07//ES810950					
Unigene111809_All	215	0.49	0.24	0.00	0.93	1.44	0.21	32.45	12.64	15.01	-1.05E+00	6.85E-01			-8.93E+00	3.98E-01		6.37E-01	6.95E-01		-2.14E+00	3.47E-01		-1.36E+00	9.07E-11	Down	-1.11E+00	2.35E-08	Down	Unigene111809_All//gi|115480625|ref|NP_001063906.1|//6.00E-35//Os09g0557800 [Oryza sativa Japonica Group] >gi|113632139|dbj|BAF25820.1| Os09g0557800 [Oryza sativa Japonica Group]	Unigene111809_All//5.00E-30//AT5G25100| endomembrane protein 70, putative	Unigene111809_All//2.00E-82//TC142008			GO:0031224//GO:0031410//GO:0043231	nr -
Unigene11181_All	4217	2.43	9.29	3.75	2.67	2.28	2.15	10.03	9.92	5.73	1.93E+00	3.09E-76	Up	6.25E-01	1.56E-05		-2.29E-01	2.09E-01		-3.11E-01	8.05E-02		-1.52E-02	8.73E-01		-8.06E-01	2.68E-27		Unigene11181_All//gi|255545642|ref|XP_002513881.1|//0.00E+00//Homomeric Acetyl-CoA Carboxylase (Hom-ACCase) [Ricinus communis] >gi|223546967|gb|EEF48464.1| Homomeric Acetyl-CoA Carboxylase (Hom-ACCase) [Ricinus communis]	Unigene11181_All//0.00E+00//AT1G36180| ACC2 (ACETYL-COA CARBOXYLASE 2); acetyl-CoA carboxylase	Unigene11181_All//0.00E+00//TC150892		ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis	GO:0003006//GO:0006633//GO:0009725//GO:0016020//GO:0016421//GO:0019899//GO:0030312//GO:0032559//GO:0043231//GO:0048507	nr +
Unigene111810_All	215	0.00	0.00	0.00	0.00	0.00	0.00	2.36	0.00	0.00	null	null			null	null		null	null		null	null		-1.12E+01	8.90E-04	Down	-1.12E+01	5.55E-04	Down	Unigene111810_All//gi|255103522|gb|ACH70610.1|//4.00E-16//alpha tubulin [Ulva fasciata]	Unigene111810_All//4.00E-17//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene111810_All//2.00E-17//gi|54115762|gb|CO491271.1|CO491271		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene111811_All	215	0.00	0.00	0.00	0.00	0.00	0.00	2.56	0.00	1.48	null	null			null	null		null	null		null	null		-1.13E+01	4.62E-04	Down	-7.86E-01	3.62E-01									
Unigene111812_All	215	3.16	1.89	3.72	5.33	3.84	0.84	7.28	2.33	12.79	-7.47E-01	3.80E-01			2.32E-01	7.49E-01		-4.71E-01	4.64E-01		-2.67E+00	4.12E-04	Down	-1.64E+00	1.02E-03		8.13E-01	1.31E-02				Unigene111812_All//4.00E-46//TC169760					
Unigene111815_All	216	3.88	2.35	0.49	2.31	2.87	1.88	4.89	0.97	1.66	-7.24E-01	3.48E-01			-2.97E+00	3.83E-03		3.15E-01	7.84E-01		-2.93E-01	7.57E-01		-2.34E+00	6.78E-04	Down	-1.56E+00	9.40E-03				Unigene111815_All//2.00E-51//TC154650					
Unigene11182_All	7246	9.35	34.07	18.01	9.88	12.26	16.22	29.23	14.67	16.89	1.87E+00	0.00E+00	Up	9.46E-01	2.90E-83		3.11E-01	8.29E-10		7.16E-01	1.10E-51		-9.95E-01	1.16E-184		-7.91E-01	5.91E-129		Unigene11182_All//gi|255545642|ref|XP_002513881.1|//0.00E+00//Homomeric Acetyl-CoA Carboxylase (Hom-ACCase) [Ricinus communis] >gi|223546967|gb|EEF48464.1| Homomeric Acetyl-CoA Carboxylase (Hom-ACCase) [Ricinus communis]	Unigene11182_All//0.00E+00//AT1G36180| ACC1 (ACETYL-COENZYME A CARBOXYLASE 1); acetyl-CoA carboxylase	Unigene11182_All//0.00E+00//TC161428		ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis	GO:0003006//GO:0006633//GO:0009317//GO:0009725//GO:0016020//GO:0016421//GO:0019899//GO:0030312//GO:0032559//GO:0043231//GO:0048507	nr +
Unigene111827_All	216	139.04	815.40	501.68	244.46	264.16	876.71	52.65	105.07	50.17	2.55E+00	0.00E+00	Up	1.85E+00	1.04E-193	Up	1.12E-01	1.53E-01		1.84E+00	0.00E+00	Up	9.97E-01	1.56E-20		-6.98E-02	6.70E-01				Unigene111827_All//9.00E-78//DW510023					
Unigene111833_All	216	0.00	0.00	0.00	0.00	0.00	0.00	2.35	0.19	0.00	null	null			null	null		null	null		null	null		-3.60E+00	5.77E-03		-1.12E+01	5.55E-04	Down	Unigene111833_All//gi|241865275|gb|ACS68715.1|//2.00E-23//40S RPS3B [Sonneratia alba] >gi|241865508|gb|ACS68786.1| RPS3B [Sonneratia alba]	Unigene111833_All//3.00E-17//AT5G35530| 40S ribosomal protein S3 (RPS3C)			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene111841_All	217	9.16	5.14	5.40	27.09	25.23	25.81	44.81	46.42	12.85	-8.35E-01	6.77E-02		-7.63E-01	1.14E-01		-1.02E-01	7.31E-01		-6.99E-02	7.91E-01		5.08E-02	7.84E-01		-1.80E+00	1.98E-22	Down	Unigene111841_All//gi|57639078|gb|AAW55475.1|//2.00E-10//ER-binding protein [Malus pumila]	Unigene111841_All//1.00E-05//AT5G42020| BIP2; ATP binding	Unigene111841_All//1.00E-117//BG440344		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0008152//GO:0016628//GO:0032559//GO:0044432//GO:0050896	nr +
Unigene111849_All	217	0.00	0.00	0.00	0.00	0.00	0.00	4.68	2.50	0.73	null	null			null	null		null	null		null	null		-9.01E-01	1.44E-01		-2.67E+00	1.94E-04	Down			Unigene111849_All//3.00E-22//TC154893					
Unigene111852_All	217	0.24	0.47	0.74	0.23	3.65	0.42	1.95	2.31	1.47	9.54E-01	7.27E-01		1.61E+00	5.12E-01		3.99E+00	6.32E-04	Up	8.59E-01	7.96E-01		2.46E-01	7.84E-01		-4.08E-01	6.54E-01				Unigene111852_All//1.00E-86//TC155814					
Unigene111855_All	218	0.00	0.00	0.00	0.00	0.00	0.00	9.31	0.77	6.76	null	null			null	null		null	null		null	null		-3.60E+00	3.79E-10	Down	-4.61E-01	2.45E-01				Unigene111855_All//2.00E-07//TC158875					
Unigene11186_All	2915	1.87	1.32	0.90	1.73	3.24	2.54	1.29	1.45	2.35	-4.99E-01	5.24E-02		-1.06E+00	8.56E-05	Down	9.07E-01	3.15E-07		5.58E-01	9.33E-03		1.66E-01	6.01E-01		8.65E-01	1.10E-05		Unigene11186_All//gi|9294523|dbj|BAB02785.1|//0.00E+00//protein transport protein Sec23 [Arabidopsis thaliana]	Unigene11186_All//0.00E+00//AT3G23660| transport protein, putative	Unigene11186_All//0.00E+00//TC132777			GO:0012507//GO:0015031//GO:0046914//GO:0048193	nr +
Unigene111870_All	219	0.00	0.00	0.00	0.00	0.00	0.00	4.63	0.57	0.73	null	null			null	null		null	null		null	null		-3.02E+00	1.08E-04	Down	-2.67E+00	1.94E-04	Down	Unigene111870_All//gi|164521173|gb|ABY60448.1|//5.00E-15//ribosomal protein S25 [Adonis aestivalis var. palaestina]	Unigene111870_All//5.00E-06//AT4G34555| 40S ribosomal protein S25, putative			ko03010|Ribosome	GO:0030529//GO:0043231	nr -
Unigene111874_All	219	0.00	0.00	0.00	0.00	0.00	0.00	5.21	0.76	0.18	null	null			null	null		null	null		null	null		-2.77E+00	7.62E-05	Down	-4.84E+00	2.34E-07	Down			Unigene111874_All//3.00E-10//TC161862					
Unigene111889_All	1019	4.36	5.27	6.06	14.76	15.51	10.15	10.66	6.69	4.65	2.72E-01	3.23E-01		4.74E-01	5.91E-02		7.13E-02	6.90E-01		-5.41E-01	1.21E-04		-6.74E-01	1.19E-05		-1.20E+00	5.82E-14	Down	Unigene111889_All//gi|240256264|ref|NP_196285.5|//2.00E-61//ATP binding / microtubule motor [Arabidopsis thaliana]	Unigene111889_All//1.00E-56//AT5G06670| ATP binding / microtubule motor	Unigene111889_All//0.00E+00//gi|164341533|gb|ES851792.1|ES851792			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr +
Unigene111894_All	220	96.08	36.39	45.75	688.12	473.49	1052.72	144.33	121.78	64.65	-1.40E+00	1.55E-26	Down	-1.07E+00	6.62E-17	Down	-5.39E-01	9.41E-46		6.13E-01	2.60E-77		-2.45E-01	5.31E-03		-1.16E+00	3.50E-37	Down	Unigene111894_All//gi|255559090|ref|XP_002520567.1|//6.00E-09//Repetitive proline-rich cell wall protein 2 precursor, putative [Ricinus communis] >gi|223540227|gb|EEF41800.1| Repetitive proline-rich cell wall protein 2 precursor, putative [Ricinus communis]		Unigene111894_All//2.00E-100//TC134791				nr +
Unigene111900_All	221	0.00	0.00	0.00	0.00	0.00	0.00	2.30	0.57	0.00	null	null			null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.12E+01	5.55E-04	Down			Unigene111900_All//2.00E-07//FL684464					
Unigene111901_All	221	0.00	0.23	0.00	0.00	0.00	0.00	2.87	0.38	0.00	7.84E+00	6.20E-01			null	null		null	null		null	null		-2.92E+00	4.20E-03		-1.15E+01	7.12E-05	Down			Unigene111901_All//3.00E-10//FL576920					
Unigene111905_All	221	0.00	0.00	0.00	0.00	0.00	0.00	3.06	0.19	0.00	null	null			null	null		null	null		null	null		-4.02E+00	5.36E-04	Down	-1.16E+01	3.57E-05	Down								ESTscan -
Unigene111908_All	221	0.00	0.00	0.00	0.00	0.00	0.00	2.30	0.57	0.00	null	null			null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.12E+01	5.55E-04	Down								ESTscan -
Unigene11191_All	3593	0.95	2.06	1.63	3.24	4.34	3.23	2.27	1.74	1.92	1.12E+00	4.12E-07	Up	7.85E-01	2.10E-03		4.20E-01	1.97E-03		-6.10E-03	9.69E-01		-3.80E-01	4.06E-02		-2.44E-01	1.95E-01		Unigene11191_All//gi|22331006|ref|NP_187809.2|//0.00E+00//kinesin motor protein-related [Arabidopsis thaliana]	Unigene11191_All//0.00E+00//AT3G12020| kinesin motor protein-related	Unigene11191_All//0.00E+00//gi|78340671|gb|DT560945.1|DT560945			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr +
Unigene111911_All	221	0.00	0.00	0.00	0.00	0.00	0.00	2.68	0.00	0.00	null	null			null	null		null	null		null	null		-1.14E+01	2.39E-04	Down	-1.14E+01	1.41E-04	Down									
Unigene111913_All	222	18.85	41.08	14.87	43.53	49.17	38.86	94.46	147.60	226.11	1.12E+00	1.31E-08	Up	-3.42E-01	2.90E-01		1.76E-01	3.81E-01		-1.64E-01	4.54E-01		6.44E-01	2.94E-14		1.26E+00	8.64E-66	Up	Unigene111913_All//gi|294987233|gb|ADF56051.1|//5.00E-23//homeobox-leucine zipper protein [Cucumis sativus]	Unigene111913_All//1.00E-08//AT2G22800| HAT9; DNA binding / transcription factor	Unigene111913_All//1.00E-117//TC143756	HB		GO:0001071//GO:0003677//GO:0006351//GO:0009725//GO:0010468//GO:0043231	nr +
Unigene111924_All	222	12.49	11.87	9.11	18.62	9.00	14.44	18.66	18.26	8.97	-7.38E-02	8.43E-01		-4.55E-01	2.54E-01		-1.05E+00	1.71E-04	Down	-3.67E-01	2.52E-01		-3.14E-02	9.30E-01		-1.06E+00	5.80E-05	Down			Unigene111924_All//3.00E-59//gi|21091992|gb|BQ404305.1|BQ404305					
Unigene111934_All	223	0.00	0.00	0.00	0.00	0.00	0.00	2.84	0.56	0.18	null	null			null	null		null	null		null	null		-2.34E+00	1.27E-02		-3.99E+00	5.82E-04	Down	Unigene111934_All//gi|297600719|ref|NP_001049719.2|//6.00E-22//Os03g0277300 [Oryza sativa Japonica Group] >gi|253674402|dbj|BAF11633.2| Os03g0277300 [Oryza sativa Japonica Group]	Unigene111934_All//1.00E-11//AT3G09440| heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0000302//GO:0009642//GO:0010038//GO:0016020//GO:0016628//GO:0019899//GO:0030312//GO:0032446//GO:0032559//GO:0043231//GO:0051707	nr +
Unigene11194_All	699	6.21	3.91	3.58	11.62	4.98	8.21	10.65	8.85	7.01	-6.66E-01	2.17E-02		-7.95E-01	8.80E-03		-1.22E+00	2.02E-10	Down	-5.01E-01	1.38E-02		-2.67E-01	1.97E-01		-6.03E-01	1.10E-03		Unigene11194_All//gi|113208238|dbj|BAF03523.1|//5.00E-44//CCS1 mRNA stability 1 [Arabidopsis thaliana]	Unigene11194_All//2.00E-33//AT2G25320| LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: TRAF-like (InterPro:IPR008974), MATH (InterPro:IPR002083); BEST Arabidopsis thaliana protein match is: meprin and TRAF homology domain-containing protein / MATH domain-containing protein (TAIR:AT2G25330.1); Has 59993 Blast hits to 32072 proteins in 1426 species: Archae - 584; Bacteria - 5166; Metazoa - 31897; Fungi - 4070; Plants - 2329; Viruses - 207; Other Eukaryotes - 15740 (source: NCBI BLink).	Unigene11194_All//0.00E+00//gi|164338975|gb|EX172487.1|EX172487			GO:0001071//GO:0006351//GO:0031406//GO:0043231//GO:0048037	nr +
Unigene111944_All	224	0.00	0.00	0.00	0.00	0.00	0.00	3.40	0.56	0.00	null	null			null	null		null	null		null	null		-2.60E+00	2.81E-03		-1.17E+01	8.88E-06	Down	Unigene111944_All//gi|116222089|gb|ABJ88015.1|//7.00E-36//actin [Goniomonas truncata]	Unigene111944_All//1.00E-36//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene111944_All//2.00E-39//TC153744		ko04145|Phagosome	GO:0032559//GO:0043232	nr +

Unigene111948_All	224	0.00	0.00	0.00	0.00	0.00	0.00	2.27	0.75	0.00	null	null		null	null		null	null		null	null		-1.60E+00	1.07E-01		-1.11E+01	5.55E-04	Down	Unigene111948_All//gi|2894308|emb|CAA11269.1|//4.00E-33//polyubiquitin [Nicotiana tabacum]	Unigene111948_All//2.00E-33//AT5G03240| UBQ3 (POLYUBIQUITIN 3) ; protein binding	Unigene111948_All//1.00E-30//gi|109826718|gb|DW225428.1|DW225428			GO:0043231	nr +
Unigene111954_All	225	0.00	0.00	0.00	0.00	0.00	0.00	3.38	1.30	0.00	null	null		null	null		null	null		null	null		-1.38E+00	6.73E-02		-1.17E+01	8.88E-06	Down	Unigene111954_All//gi|299470875|emb|CBN78824.1|//6.00E-09//Protein for assembly of pre-ribosomal particles containing 18S rRNA [Ectocarpus siliculosus]	Unigene111954_All//9.00E-05//AT5G50250| 31 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein RNP-T, putative / RNA-binding protein 1/2/3, putative / RNA-binding protein cp31, putative				GO:0005488	nr -
Unigene111958_All	225	0.00	0.00	0.00	0.00	0.00	0.00	3.19	0.00	0.18	null	null		null	null		null	null		null	null		-1.16E+01	3.27E-05	Down	-4.17E+00	1.64E-04	Down	Unigene111958_All//gi|17979018|gb|AAL49957.1|//8.00E-06//GTP cyclohydrolase I [Solanum lycopersicum]	Unigene111958_All//9.00E-05//AT3G07270| GTP cyclohydrolase I			ko00790|Folate biosynthesis	GO:0003933	nr -
Unigene111960_All	225	0.00	0.00	0.00	0.89	0.15	0.40	3.01	0.37	0.18	null	null		null	null		-2.53E+00	2.34E-01		-1.14E+00	5.70E-01		-3.02E+00	2.43E-03		-4.09E+00	3.10E-04	Down			Unigene111960_All//5.00E-18//gi|78329277|gb|DT549551.1|DT549551				
Unigene111967_All	226	340.55	183.17	81.05	225.71	195.64	123.90	208.22	52.52	53.94	-8.95E-01	2.06E-46		-2.07E+00	4.11E-159	Down	-2.06E-01	4.50E-03		-8.65E-01	1.32E-31		-1.99E+00	1.23E-116	Down	-1.95E+00	4.35E-117	Down			Unigene111967_All//1.00E-120//gi|21098593|gb|BQ410906.1|BQ410906				
Unigene111197_All	805	0.13	0.63	0.46	1.61	1.28	1.18	0.84	1.56	3.51	2.28E+00	6.23E-02		1.83E+00	2.13E-01		-3.26E-01	5.86E-01		-4.50E-01	4.84E-01		8.90E-01	1.02E-01		2.06E+00	3.11E-08	Up	Unigene111197_All//gi|297812493|ref|XP_002874130.1|//2.00E-21//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319967|gb|EFH50389.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene111197_All//1.00E-22//AT5G23430| transducin family protein / WD-40 repeat family protein				GO:0004468//GO:0005488//GO:0031461	nr +
Unigene111971_All	226	0.93	0.00	0.00	0.22	0.00	0.00	5.43	1.11	1.06	-9.85E+00	1.23E-01		-9.85E+00	1.46E-01		-7.78E+00	5.61E-01		-7.78E+00	6.43E-01		-2.29E+00	2.57E-04	Down	-2.36E+00	1.22E-04	Down			Unigene111971_All//7.00E-17//TC142701				
Unigene111973_All	226	0.00	0.00	0.00	0.00	0.00	0.00	3.18	0.37	0.35	null	null		null	null		null	null		null	null		-3.10E+00	1.40E-03		-3.17E+00	8.09E-04	Down							
Unigene111987_All	227	0.46	0.00	0.94	0.00	0.00	0.00	2.79	0.74	0.18	-8.85E+00	3.75E-01		1.03E+00	5.92E-01		null	null		null	null		-1.92E+00	3.09E-02		-3.99E+00	5.82E-04	Down							
Unigene111991_All	227	0.00	0.00	0.00	0.00	0.00	0.00	18.44	1.29	1.23	null	null		null	null		null	null		null	null		-3.84E+00	2.28E-21	Down	-3.91E+00	1.91E-22	Down							
Unigene111995_All	227	42.87	20.31	20.88	37.09	33.07	64.86	85.49	45.85	33.35	-1.08E+00	1.25E-08	Down	-1.04E+00	9.21E-08	Down	-1.65E-01	4.71E-01		8.06E-01	1.89E-08		-8.99E-01	5.01E-15		-1.36E+00	2.39E-29	Down	Unigene111995_All//gi|81076822|gb|ABB53598.1|//3.00E-17//40S ribosomal protein S10-like [Solanum tuberosum]	Unigene111995_All//1.00E-15//AT5G52650| 40S ribosomal protein S10 (RPS10C)	Unigene111995_All//8.00E-103//TC134619		ko03010|Ribosome	GO:0030529	nr -
Unigene1120_All	2739	2.18	1.46	2.53	2.66	3.91	3.10	3.75	1.85	3.62	-5.75E-01	1.77E-02		2.15E-01	3.87E-01		5.58E-01	7.59E-04		2.23E-01	3.23E-01		-1.02E+00	3.87E-10	Down	-5.06E-02	7.67E-01		Unigene1120_All//gi|297796671|ref|XP_002866220.1|//0.00E+00//mitochondrial bifunctional diaminopelargonate synthetase [Arabidopsis lyrata subsp. lyrata] >gi|297312055|gb|EFH42479.1| mitochondrial bifunctional diaminopelargonate synthetase [Arabidopsis lyrata subsp. lyrata]	Unigene1120_All//6.00E-137//AT5G57590| BIO1 (biotin auxotroph 1); adenosylmethionine-8-amino-7-oxononanoate transaminase	Unigene1120_All//0.00E+00//gi|164345713|gb|ES826238.1|ES826238		ko00780|Biotin metabolism	GO:0016769//GO:0048037	nr -
Unigene11200_All	2538	1.63	1.90	1.93	4.14	5.06	3.10	6.03	2.72	2.70	2.20E-01	4.43E-01		2.45E-01	3.97E-01		2.89E-01	7.56E-02		-4.20E-01	1.83E-02		-1.15E+00	1.26E-17	Down	-1.16E+00	2.12E-18	Down	Unigene11200_All//gi|297812493|ref|XP_002874130.1|//1.00E-160//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319967|gb|EFH50389.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11200_All//4.00E-79//AT5G23430| transducin family protein / WD-40 repeat family protein	Unigene11200_All//0.00E+00//EX167732				nr -
Unigene112000_All	228	0.00	3.11	0.00	0.87	0.00	0.40	2.41	1.83	0.17	1.16E+01	3.33E-04	Up	null	null		-9.77E+00	8.47E-02		-1.14E+00	5.70E-01		-3.95E-01	6.34E-01		-3.79E+00	2.03E-03				Unigene112000_All//3.00E-07//BF270264				
Unigene112003_All	228	0.00	0.00	0.00	0.00	0.00	0.00	3.34	0.00	0.17	null	null		null	null		null	null		null	null		-1.17E+01	1.68E-05	Down	-4.26E+00	8.63E-05	Down							
Unigene112008_All	228	0.00	0.00	0.00	1.75	0.00	0.00	2.23	0.00	0.00	null	null		null	null		-1.08E+01	4.39E-03		-1.08E+01	1.11E-02		-1.11E+01	8.90E-04	Down	-1.11E+01	5.55E-04	Down							ESTscan +
Unigene112010_All	228	0.00	0.00	0.00	0.00	0.00	0.00	3.15	0.18	1.05	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-1.59E+00	3.62E-02		Unigene112010_All//gi|112455658|gb|AB118985.1|//4.00E-12//molecular chaperone DjA2 [Allium ampeloprasum]	Unigene112010_All//4.00E-12//AT5G22060| ATJ2; protein binding			ko04141|Protein processing in endoplasmic reticulum	GO:0005488	nr -
Unigene112011_All	228	0.00	0.00	0.00	0.00	0.00	0.00	2.60	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	2.39E-04	Down	-1.13E+01	1.41E-04	Down	Unigene112011_All//gi|283136138|gb|ADB11388.1|//5.00E-08//gamma class glutathione transferase EF1Bgamma3 [Populus trichocarpa]	Unigene112011_All//1.00E-05//AT1G57720| elongation factor 1B-gamma, putative / eEF-1B gamma, putative					nr +
Unigene112202_All	687	2.67	3.61	1.24	4.13	4.31	3.68	3.63	0.61	1.80	4.39E-01	2.84E-01		-1.10E+00	3.06E-02		6.07E-02	8.91E-01		-1.67E-01	6.96E-01		-2.58E+00	3.91E-09	Down	-1.01E+00	3.56E-03		Unigene112202_All//gi|75221490|sp|Q43715.1|TOC75_PEA//2.00E-90//RecName: Full=Protein TOC75, chloroplastic; AltName: Full=75 kDa translocon at the outer-envelope membrane of chloroplasts; AltName: Full=Import intermediate-associated protein of 75 kDa; AltName: Full=75 kDa chloroplast outer envelope protein; Flags: Precursor >gi|576507|gb|AAA53275.1| outer membrane protein [Pisum sativum] >gi|633607|emb|CAA58720.1| chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]	Unigene112202_All//2.00E-64//AT3G46740| TOC75-III (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene112202_All//3.00E-154//gi|78347599|gb|DT567873.1|DT567873			GO:0006605//GO:0008320//GO:0009653//GO:0009657//GO:0009707//GO:0031224	nr -
Unigene112022_All	229	2.74	8.41	4.88	3.48	2.86	4.34	9.79	12.59	3.48	1.62E+00	1.18E-03		8.33E-01	2.23E-01		-2.85E-01	7.21E-01		3.18E-01	6.73E-01		3.64E-01	3.01E-01		-1.49E+00	1.21E-04	Down			Unigene112022_All//2.00E-66//DW499434				
Unigene112024_All	229	0.23	0.00	0.00	0.87	0.60	0.00	2.77	0.18	0.52	-7.84E+00	6.18E-01		-7.84E+00	6.30E-01		-5.33E-01	7.49E-01		-9.77E+00	1.34E-01		-3.92E+00	9.81E-04	Down	-2.41E+00	8.12E-03		Unigene112024_All//gi|224119534|ref|XP_002318098.1|//6.00E-11//predicted protein [Populus trichocarpa] >gi|222858771|gb|EEE96318.1| predicted protein [Populus trichocarpa]		Unigene112024_All//7.00E-122//gi|109870617|gb|DW499593.1|DW499593			GO:0003824	nr -
Unigene112025_All	229	0.00	0.00	0.00	0.00	0.00	0.00	2.77	0.00	0.35	null	null		null	null		null	null		null	null		-1.14E+01	1.23E-04	Down	-2.99E+00	2.58E-03		Unigene112025_All//gi|222424342|dbj|BAH20127.1|//2.00E-09//AT5G35530 [Arabidopsis thaliana]				ko03010|Ribosome	GO:0005198//GO:0006970//GO:0010467//GO:0015935//GO:0031981	nr +
Unigene112026_All	230	0.00	0.00	0.00	0.00	0.00	0.00	2.39	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	4.61E-04	Down	-1.12E+01	2.81E-04	Down	Unigene112026_All//gi|6012952|emb|CAB57309.1|//4.00E-11//60S ribosomal protein L6 (YL 16 like) [Cyanophora paradoxa]	Unigene112026_All//7.00E-07//AT1G18540| 60S ribosomal protein L6 (RPL6A)			ko03010|Ribosome	GO:0005488//GO:0009536//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene112027_All	230	0.00	0.00	0.00	0.00	0.00	0.00	2.76	0.00	0.35	null	null		null	null		null	null		null	null		-1.14E+01	1.23E-04	Down	-2.99E+00	2.58E-03								
Unigene11203_All	2343	17.95	11.20	8.45	11.01	11.74	11.58	13.52	6.07	8.48	-6.81E-01	2.64E-16		-1.09E+00	6.80E-34	Down	9.26E-02	4.67E-01		7.30E-02	5.96E-01		-1.16E+00	6.87E-36	Down	-6.72E-01	2.75E-15		Unigene11203_All//gi|15232625|ref|NP_190258.1|//0.00E+00//TOC75-III (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter [Arabidopsis thaliana] >gi|75207662|sp|Q9STE8.1|TC753_ARATH RecName: Full=Protein TOC75-3, chloroplastic; AltName: Full=75 kDa translocon at the outer-envelope-membrane of chloroplasts 3; Short=AtTOC75-III; Flags: Precursor >gi|5541685|emb|CAB51191.1| chloroplast import-associated channel homolog [Arabidopsis thaliana] >gi|22022564|gb|AAM83239.1| AT3g46740/T6H20_230 [Arabidopsis thaliana] >gi|30102496|gb|AAP211166.1| At3g46740/T6H20_230 [Arabidopsis thaliana]	Unigene11203_All//0.00E+00//AT3G46740| TOC75-III (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene11203_All//0.00E+00//TC163188			GO:0006605//GO:0008320//GO:0009653//GO:0009657//GO:0009707//GO:0031224	nr -
Unigene112039_All	231	0.00	0.00	0.00	0.00	0.00	0.00	2.75	0.00	0.00	null	null		null	null		null	null		null	null		-1.14E+01	1.23E-04	Down	-1.14E+01	7.12E-05	Down	Unigene112039_All//gi|297820548|ref|XP_002878157.1|//1.00E-28//40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata] >gi|297323995|gb|EFH54416.1| 40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata]	Unigene112039_All//4.00E-30//AT3G57490| 40S ribosomal protein S2 (RPS2D)			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr +
Unigene11204_All	2815	11.62	4.84	4.39	13.68	14.06	15.69	12.48	5.45	6.62	-1.26E+00	9.17E-35	Down	-1.40E+00	2.44E-39	Down	3.92E-02	7.42E-01		1.98E-01	1.79E-02		-1.20E+00	7.02E-42	Down	-9.14E-01	4.40E-28		Unigene11204_All//gi|15232625|ref|NP_190258.1|//0.00E+00//TOC75-III (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter [Arabidopsis thaliana] >gi|75207662|sp|Q9STE8.1|TC753_ARATH RecName: Full=Protein TOC75-3, chloroplastic; AltName: Full=75 kDa translocon at the outer-envelope-membrane of chloroplasts 3; Short=AtTOC75-III; Flags: Precursor >gi|5541685|emb|CAB51191.1| chloroplast import-associated channel homolog [Arabidopsis thaliana] >gi|22022564|gb|AAM83239.1| AT3g46740/T6H20_230 [Arabidopsis thaliana] >gi|30102496|gb|AAP211166.1| At3g46740/T6H20_230 [Arabidopsis thaliana]	Unigene11204_All//0.00E+00//AT3G46740| TOC75-III (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene11204_All//0.00E+00//TC144595			GO:0006605//GO:0008320//GO:0009653//GO:0009657//GO:0009707//GO:0031224	nr -
Unigene112040_All	231	118.91	53.96	77.92	161.09	149.67	169.90	178.82	107.11	104.51	-1.14E+00	4.86E-25	Down	-6.10E-01	1.04E-08		-1.06E-01	3.05E-01		7.68E-02	4.81E-01		-7.39E-01	1.92E-22		-7.75E-01	5.42E-25		Unigene112040_All//gi|192912962|gb|ACF06589.1|//2.00E-31//ribosomal protein [Elaeis guineensis]	Unigene112040_All//3.00E-32//AT1G67430| 60S ribosomal protein L17 (RPL17B)	Unigene112040_All//3.00E-118//TC164010		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0016787//GO:0019538//GO:0033279	nr -
Unigene112045_All	231	1.36	1.10	0.46	1.29	1.34	0.78	9.88	5.97	2.76	-3.09E-01	7.89E-01		-1.56E+00	3.30E-01		5.22E-02	9.99E-01		-7.27E-01	6.39E-01		-7.27E-01	5.48E-02		-1.84E+00	4.73E-06	Down			Unigene112045_All//9.00E-109//gi|109861542|gb|DW490519.1|DW490519				
Unigene11205_All	2883	7.19	4.83	3.80	8.10	7.13	6.89	5.87	2.29	3.98	-5.72E-01	2.02E-06		-9.18E-01	5.46E-13		-1.85E-01	1.26E-01		-2.34E-01	5.00E-02		-1.36E+00	7.18E-25	Down	-5.60E-01	1.89E-06		Unigene11205_All//gi|297819256|ref|XP_002877511.1|//0.00E+00//translocon outer membrane complex 75-III [Arabidopsis lyrata subsp. lyrata] >gi|297323349|gb|EFH53770.1| translocon outer membrane complex 75-III [Arabidopsis lyrata subsp. lyrata]	Unigene11205_All//0.00E+00//AT3G46740| TOC75-III (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene11205_All//0.00E+00//TC144595			GO:0006605//GO:0008320//GO:0009653//GO:0009657//GO:0009707//GO:0031224	nr +
Unigene112054_All	231	0.00	0.00	0.00	0.00	0.00	0.00	4.21	0.18	0.00	null	null		null	null		null	null		null	null		-4.54E+00	6.92E-06	Down	-1.20E+01	2.72E-07	Down			Unigene112054_All//6.00E-110//CK640449				
Unigene112068_All	232	0.00	0.00	0.00	0.00	0.00	0.00	2.19	0.72	0.00	null	null		null	null		null	null		null	null		-1.60E+00	1.07E-01		-1.11E+01	5.55E-04	Down	Unigene112068_All//gi|297735100|emb|CBI17462.3|//2.00E-23//unnamed protein product [Vitis vinifera]	Unigene112068_All//1.00E-05//AT1G19630| CYP722A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding				GO:0005506//GO:0008152//GO:0016491	nr -

Unigene112070_All	233	0.00	0.00	0.00	0.00	0.00	0.00	2.72	0.18	0.68	null	null		null	null		null	null		null	null		-3.92E+00	9.81E-04	Down	-1.99E+00	2.04E-02		Unigene112070_All//gi|224085587|ref|XP_002307628.1|//4.00E-21//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222857077|gb|EEE94624.1| glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene112070_All//2.00E-19//AT5G47780| GAUT4 (Galacturonosyltransferase 4); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups	Unigene112070_All//2.00E-26//TC169308			GO:0016740	nr +
Unigene112076_All	233	416.10	307.93	398.58	83.38	126.80	87.42	29.22	46.10	67.20	-4.34E-01	1.18E-16		-6.21E-02	3.42E-01		6.05E-01	5.41E-11		6.83E-02	6.53E-01		6.58E-01	2.12E-05		1.20E+00	1.09E-19	Up	Unigene112076_All//gi|115450991|ref|NP_001049096.1|//8.00E-35//Os03g0169100 (Oryza sativa Japonica Group) >gi|109940150|sp|Q9ZTP5.2|RPE_ORYSJ RecName: Full=Ribulose-phosphate 3-epimerase, chloroplastic; AltName: Full=Pentose-5-phosphate 3-epimerase; Short=PPE; AltName: Full=RSP3E; Short=RPE; Flags: Precursor >gi|19071636|gb|AAL84303.1|AC073556_20 ribulose-5-phosphate-3-epimerase [Oryza sativa Japonica Group] >gi|113547567|dbj|BAF11010.1| Os03g0169100 (Oryza sativa Japonica Group)	Unigene112076_All//8.00E-35//AT5G61410| RPE; catalytic/ ribulose-phosphate 3-epimerase	Unigene112076_All//5.00E-129//gi|164350992|gb|ES831405.1|ES831405		ko00710|Carbon fixation in photosynthetic organisms//ko00040|Pentose and glucuronate interconversions//ko00030|Pentose phosphate pathway	GO:0003006//GO:0005488//GO:0005576//GO:0006007//GO:0006950//GO:0009526//GO:0009532//GO:0009534//GO:0015977//GO:0016857//GO:0051707	nr -
Unigene112080_All	233	0.00	0.00	0.00	0.00	0.00	0.00	3.27	1.79	0.00	null	null		null	null		null	null		null	null		-8.65E-01	2.39E-01		-1.17E+01	8.88E-06	Down	Unigene112080_All//sp|P42312|NUPG_BACSU//4.00E-08//Purine nucleoside transport protein nupG OS=Bacillus subtilis GN=nupG PE=1 SV=2							swissprot -
Unigene112081_All	233	23.80	26.31	12.11	16.68	17.29	10.47	98.53	48.79	37.79	1.45E-01	5.93E-01		-9.75E-01	2.41E-04		5.23E-02	8.88E-01		-6.72E-01	3.04E-02		-1.01E+00	2.31E-21	Down	-1.38E+00	1.74E-35	Down			Unigene112081_All//4.00E-114//TC163662				
Unigene112084_All	233	4.72	0.65	3.66	2.35	0.44	0.58	2.36	5.38	0.68	-2.85E+00	4.77E-04	Down	-3.67E-01	6.01E-01		-2.41E+00	2.44E-02		-2.02E+00	7.05E-02		1.19E+00	3.01E-02		-1.79E+00	5.07E-02		Unigene112084_All//gi|2677828|gb|AAB97142.1|/5.00E-11//cysteine protease [Prunus armeniaca]	Unigene112084_All//1.00E-111//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase	Unigene112084_All//7.00E-54//TC140087			GO:0004175//GO:0005488//GO:0009725//GO:0019538//GO:0032502//GO:0043231	nr +
Unigene112093_All	234	0.00	0.00	0.00	0.00	0.00	0.00	4.52	1.25	0.00	null	null		null	null		null	null		null	null		-1.85E+00	4.09E-03		-1.21E+01	6.72E-08	Down							
Unigene112099_All	234	0.00	1.08	1.37	2.34	0.00	1.74	2.53	2.86	0.68	1.01E+01	7.88E-02		1.04E+01	4.53E-02		-1.12E+01	4.01E-04	Down	-4.31E-01	6.67E-01		1.76E-01	8.15E-01		-1.89E+00	3.22E-02				Unigene112099_All//3.00E-07//TC148696				
Unigene11210_All	826	31.23	10.61	21.47	3.02	5.42	3.61	2.56	1.52	2.65	-1.56E+00	1.27E-37	Down	-5.41E-01	9.32E-07		8.46E-01	2.16E-03		2.59E-01	5.30E-01		-7.54E-01	5.72E-02		5.17E-02	9.10E-01		Unigene11210_All//gi|259130061|gb|ACV95483.1|//1.00E-73//TCP4 [Citrus trifoliata]	Unigene11210_All//8.00E-57//AT3G15030| TCP4 (TCP family transcription factor 4); transcription factor	Unigene11210_All//0.00E+00//TC147925	TCP		GO:0003006//GO:0003676//GO:0009887//GO:0010468//GO:0040034//GO:0048827//GO:0048869	nr -
Unigene112100_All	234	0.00	0.00	0.00	0.00	0.00	0.00	3.79	0.89	0.17	null	null		null	null		null	null		null	null		-2.09E+00	4.71E-03		-4.48E+00	1.23E-05	Down	Unigene112100_All//gi|297833728|ref|XP_002884746.1|//1.00E-30//40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata] >gi|297330586|gb|EFH61005.1| 40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata]	Unigene112100_All//5.00E-32//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene112100_All//7.00E-11//DV850314		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene112117_All	235	0.00	0.00	0.00	0.00	0.00	0.00	3.42	0.71	0.00	null	null		null	null		null	null		null	null		-2.26E+00	4.82E-03		-1.17E+01	4.43E-06	Down	Unigene112117_All//gi|1545805|dbj|BAA10929.1|//8.00E-09//cytochrome P450 like_TBP [Nicotiana tabacum]		Unigene112117_All//4.00E-09//EV495741				nr +
Unigene112118_All	235	0.00	0.00	0.00	0.00	0.00	0.00	4.14	0.00	0.00	null	null		null	null		null	null		null	null		-1.20E+01	5.84E-07	Down	-1.20E+01	2.72E-07	Down							
Unigene112212_All	2264	15.25	8.75	12.37	1.01	1.16	1.00	2.00	0.35	0.33	-8.02E-01	9.81E-18		-3.02E-01	1.67E-03		1.92E-01	6.70E-01		-2.11E-02	9.50E-01		-2.51E+00	1.45E-15	Down	-2.58E+00	1.34E-16	Down	Unigene112212_All//gi|295841589|dbj|BAJ07175.1|//1.00E-119//MdTCP4A [Malus x domestica]	Unigene112212_All//5.00E-82//AT3G15030| TCP4 (TCP family transcription factor 4); transcription factor	Unigene112212_All//0.00E+00//TC144631	TCP		GO:0009887//GO:0040034//GO:0048827//GO:0048869	nr -
Unigene112121_All	236	0.00	0.00	0.00	0.42	0.00	0.00	2.33	0.89	0.00	null	null		null	null		-8.72E+00	3.16E-01		-8.72E+00	4.04E-01		-1.40E+00	1.35E-01		-1.12E+01	2.81E-04	Down							
Unigene112123_All	236	0.00	0.00	0.00	0.00	0.00	0.00	2.51	0.35	0.00	null	null		null	null		null	null		null	null		-2.82E+00	7.18E-03		-1.13E+01	1.41E-04	Down	Unigene112123_All//gi|159465349|ref|XP_001690885.1|//2.00E-24//ribosomal protein L18, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|158279571|gb|EDP05331.1| ribosomal protein L18, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii]	Unigene112123_All//7.00E-20//AT5G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene11213_All	2023	21.62	10.29	13.35	2.29	3.32	1.88	1.90	1.57	1.20	-1.07E+00	1.04E-35	Down	-6.96E-01	7.27E-17		5.36E-01	1.59E-02		-2.88E-01	3.57E-01		-2.77E-01	3.72E-01		-6.63E-01	1.35E-02		Unigene11213_All//gi|259130061|gb|ACV95483.1|//1.00E-123//TCP4 [Citrus trifoliata]	Unigene11213_All//9.00E-80//AT3G15030| TCP4 (TCP family transcription factor 4); transcription factor	Unigene11213_All//0.00E+00//TC147925	TCP		GO:0009887//GO:0010468//GO:0040034//GO:0048827//GO:0048869	nr +
Unigene11214_All	2261	62.29	22.77	41.99	6.15	5.74	3.44	4.60	2.42	2.22	-1.45E+00	8.24E-183	Down	-5.69E-01	3.15E-37		-9.84E-02	5.82E-01		-8.39E-01	1.27E-08		-9.26E-01	8.10E-09		-1.05E+00	4.82E-11	Down	Unigene11214_All//gi|37783285|gb|AA043102.1|//1.00E-112//mutant cincinnata [Antirrhinum majus]	Unigene11214_All//2.00E-86//AT3G15030| TCP4 (TCP family transcription factor 4); transcription factor	Unigene11214_All//0.00E+00//TC136853	TCP		GO:0003006//GO:0003676//GO:0009887//GO:0040034//GO:0048827//GO:0048869	nr +
Unigene112141_All	237	0.00	0.00	0.00	0.00	0.00	0.00	8.21	0.71	0.67	null	null		null	null		null	null		null	null		-3.54E+00	1.27E-09	Down	-3.61E+00	3.72E-10	Down							ESTscan -
Unigene112143_All	237	0.00	0.00	0.00	0.00	0.15	0.00	3.21	1.06	0.00	null	null		null	null		7.18E+00	8.36E-01		null	null		-1.60E+00	3.70E-02		-1.16E+01	8.88E-06	Down	Unigene112143_All//gi|18404062|ref|NP_565836.1|//1.00E-17//ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A) [Arabidopsis thaliana] >gi|18409639|ref|NP_566969.1| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome [Arabidopsis thaliana] >gi|166930|gb|AAA32904.1| ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi|166932|gb|AAA32905.1| ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi|4886268|emb|CAB43405.1| ubiquitin / ribosomal protein CEP52 [Arabidopsis thaliana] >gi|20198116|gb|AAM15407.1| ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi|21553955|gb|AAM63036.1| ubiquitin extension protein UBQ1 [Arabidopsis thaliana] >gi|222424333|dbj|BAH20123.1| AT2G36170 [Arabidopsis thaliana]	Unigene112143_All//5.00E-19//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0031981//GO:0032446	nr -
Unigene112147_All	237	0.00	0.00	0.00	0.00	0.00	0.00	2.50	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	2.39E-04	Down	-1.13E+01	1.41E-04	Down	Unigene112147_All//sp|Q35920|ATP6_SALSA//1.00E-07//ATP synthase subunit a OS=Salmo salar GN=mt-atp6 PE=3 SV=3							swissprot -
Unigene11215_All	966	5.25	2.99	2.98	7.37	4.85	5.75	10.11	5.49	3.84	-8.13E-01	2.22E-03		-8.20E-01	3.14E-03		-6.05E-01	3.30E-03		-3.59E-01	1.21E-01		-8.80E-01	1.04E-07		-1.40E+00	7.45E-16	Down	Unigene11215_All//gi|15221423|ref|NP_172112.1|//1.00E-123//MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding [Arabidopsis thaliana] >gi|30679607|ref|NP_849600.1| MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding [Arabidopsis thaliana] >gi|8844127|gb|AAF80219.1|AC025290_8 Contains similarity to an U5 snRNP-specific protein 116 kD from Homo sapiens gi|4759280 and contains elongation factor G C-terminus PF|00679 and is a member of the elongation factor Tu family PF|00009 [Arabidopsis thaliana] >gi|110741512|dbj|BAE98706.1| elongation factor like protein [Arabidopsis thaliana]	Unigene11215_All//7.00E-125//AT1G06220| MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding	Unigene11215_All//0.00E+00//TC153558		ko03040|Spliceosome		nr +
Unigene112150_All	237	0.00	0.00	0.00	0.00	0.00	0.00	17.13	1.06	0.34	null	null		null	null		null	null		null	null		-4.02E+00	2.01E-21	Down	-5.67E+00	9.26E-27	Down			Unigene112150_All//4.00E-09//CD809343				
Unigene11216_All	994	8.95	5.35	3.11	9.67	6.93	8.81	15.70	8.75	6.61	-7.41E-01	1.24E-04		-1.53E+00	1.77E-12	Down	-4.81E-01	6.23E-03		-1.34E-01	5.50E-01		-8.44E-01	4.45E-11		-1.25E+00	6.34E-21	Down	Unigene11216_All//gi|15221423|ref|NP_172112.1|//1.00E-127//MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding [Arabidopsis thaliana] >gi|30679607|ref|NP_849600.1| MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding [Arabidopsis thaliana] >gi|8844127|gb|AAF80219.1|AC025290_8 Contains similarity to an U5 snRNP-specific protein 116 kD from Homo sapiens gi|4759280 and contains elongation factor G C-terminus PF|00679 and is a member of the elongation factor Tu family PF|00009 [Arabidopsis thaliana] >gi|110741512|dbj|BAE98706.1| elongation factor like protein [Arabidopsis thaliana]	Unigene11216_All//1.00E-128//AT1G06220| MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding	Unigene11216_All//0.00E+00//gi|48778046|gb|CO087412.1|CO087412		ko03040|Spliceosome		nr -
Unigene11217_All	1411	1.97	2.01	1.85	2.47	3.64	3.55	5.33	2.22	2.88	3.32E-02	9.46E-01		-8.78E-02	8.19E-01		5.57E-01	3.32E-02		5.24E-01	5.63E-02		-1.26E+00	2.14E-10	Down	-8.89E-01	1.88E-06		Unigene11217_All//gi|110741074|dbj|BAE98631.1|//0.00E+00//elongation factor like protein [Arabidopsis thaliana]	Unigene11217_All//0.00E+00//AT1G06220| MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding	Unigene11217_All//0.00E+00//DW481638		ko03040|Spliceosome	GO:0003006//GO:0003723//GO:0016020//GO:0016604//GO:0017111//GO:0030312//GO:0032561//GO:0032991//GO:0045595	nr +
Unigene112172_All	238	0.00	0.00	0.00	1.05	0.14	0.38	3.38	0.00	0.50	null	null		null	null		-2.85E+00	1.37E-01		-1.46E+00	4.07E-01		-1.17E+01	8.58E-06	Down	-2.75E+00	9.43E-04	Down							
Unigene112173_All	238	0.00	0.00	0.00	0.00	0.00	0.00	2.31	0.35	0.00	null	null		null	null		null	null		null	null		-2.72E+00	1.22E-02		-1.12E+01	2.81E-04	Down							

Unigene11218_All	2243	4.76	4.04	2.71	5.29	5.34	7.55	12.03	4.23	5.12	-2.35E-01	2.09E-01		-8.14E-01	7.29E-06		1.54E-02	9.53E-01		5.15E-01	1.00E-04		-1.51E+00	8.28E-46	Down	-1.23E+00	6.19E-35	Down	Unigene11218_All//gi|15221423|ref|NP_172112.1|//0.00E+00//MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding [Arabidopsis thaliana] >gi|30679607|ref|NP_849600.1| MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding [Arabidopsis thaliana] >gi|88441277|gb|AAF80219.1|AC025290_8 Contains similarity to an U5 snRNP-specific protein 116 kD from Homo sapiens gi|4759280 and contains elongation factor G C-terminus PF|00679 and is a member of the elongation factor Tu family PF|00009 [Arabidopsis thaliana] >gi|110741512|dbj|BAE98706.1| elongation factor like protein [Arabidopsis thaliana]	Unigene11218_All//0.00E+00//AT1G06220| MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding	Unigene11218_All//0.00E+00//TC158929		ko03040|Spliceosome	GO:0003006//GO:0008135//GO:0016020//GO:0016604//GO:0017111//GO:0003012//GO:0032561//GO:0032991//GO:0045595	nr +
Unigene112180_All	239	0.00	0.00	0.00	0.00	0.00	0.00	4.60	1.22	0.00	null	null		null	null		null	null		null	null		-1.91E+00	2.64E-03		-1.22E+01	3.33E-08	Down		Unigene112180_All//5.00E-05//AT2G40935| unknown protein					ESTscan +
Unigene112181_All	239	0.00	0.00	0.00	0.00	0.00	0.00	2.48	0.00	0.17	null	null		null	null		null	null		null	null		-1.13E+01	2.39E-04	Down	-3.89E+00	1.09E-03		Unigene112181_All//gi|50843988|gb|AAT84169.1|//3.00E-23//60S ribosomal protein L27 [Chara globularis]	Unigene112181_All//1.00E-15//AT4G15000| 60S ribosomal protein L27 (RPL27C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene112189_All	240	0.00	0.00	0.00	0.21	0.00	0.00	5.81	1.39	1.83	null	null		null	null		-7.70E+00	5.61E-01		-7.70E+00	6.42E-01		-2.06E+00	2.51E-04	Down	-1.67E+00	1.27E-03									
Unigene11219_All	2177	5.96	3.84	3.35	6.45	5.33	7.78	10.78	3.76	5.62	-6.34E-01	4.86E-05		-8.31E-01	3.43E-07		-2.76E-01	7.05E-02		2.70E-01	5.84E-02		-1.52E+00	2.31E-40	Down	-9.40E-01	6.27E-20		Unigene11219_All//gi|110741074|dbj|BAE98631.1|//0.00E+00//elongation factor like protein [Arabidopsis thaliana]	Unigene11219_All//0.00E+00//AT1G06220| MEE5 (MATERNAL EFFECT EMBRYO ARREST 5); GTP binding / GTPase/ translation elongation factor/ translation factor, nucleic acid binding	Unigene11219_All//0.00E+00//DW481638		ko03040|Spliceosome	GO:0003006//GO:0008135//GO:0016020//GO:0016604//GO:0017111//GO:0003012//GO:0032561//GO:0032991//GO:0045595	nr -
Unigene1122_All	2099	12.69	20.40	15.12	1.69	4.02	4.86	78.90	44.86	79.92	6.85E-01	1.01E-16		2.53E-01	1.36E-02		1.25E+00	1.31E-10	Up	1.53E+00	1.00E-15	Up	-8.15E-01	2.35E-103		1.86E-02	6.60E-01		Unigene1122_All//gi|56157408|gb|AAV80420.1|//4.00E-62//Prf interactor 30137 [Solanum lycopersicum]	Unigene1122_All//2.00E-41//AT2G27230| LHW (LONESOME HIGHWAY); protein homodimerization/ transcription activator/ transcription factor	Unigene1122_All//2.00E-114//TC150417	bHLH			nr +
Unigene112208_All	241	0.00	4.20	0.00	0.62	0.57	1.87	3.33	3.47	1.65	1.20E+01	7.26E-06	Up	null	null		-1.18E-01	9.11E-01		1.60E+00	2.05E-01		5.74E-02	9.54E-01		-1.01E+00	1.35E-01									
Unigene112209_All	241	0.00	0.00	0.00	0.00	0.00	0.00	2.46	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	2.39E-04	Down	-1.13E+01	1.41E-04	Down	Unigene112209_All//gi|115454357|ref|NP_001050779.1|//2.00E-23//Os03g0648400 [Oryza sativa Japonica Group] >gi|29867357|gb|AAO72551.1| DNAJ-like protein [Oryza sativa Japonica Group] >gi|113549250|dbj|BAF12693.1| Os03g0648400 [Oryza sativa Japonica Group] >gi|169244473|gb|ACA50510.1| DnaJ protein [Oryza sativa Japonica Group]	Unigene112209_All//1.00E-23//AT5G22060| ATJ2; protein binding			ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0006950//GO:0032559//GO:0043169//GO:0044267//GO:0044424	nr +
Unigene112214_All	241	0.00	0.00	0.00	0.00	0.00	0.00	2.98	0.17	0.17	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-4.17E+00	1.64E-04	Down	Unigene112214_All//gi|226507440|ref|NP_001152131.1|//1.00E-23//LOC100285769 [Zea mays] >gi|195653083|gb|ACG46009.1| 60S ribosomal protein L30 [Zea mays]	Unigene112214_All//2.00E-22//AT3G18740| 60S ribosomal protein L30 (RPL30C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene11222_All	986	8.49	5.24	6.59	12.02	14.95	16.12	19.98	9.07	9.90	-6.96E-01	4.92E-04		-3.66E-01	8.85E-02		3.14E-01	3.25E-02		4.23E-01	2.37E-03		-1.14E+00	3.95E-22	Down	-1.01E+00	5.31E-19	Down	Unigene11222_All//gi|146286094|sp|Q0WK26.2|COPG_ARATH//1.00E-140//RecName: Full=Coatomer subunit gamma; AltName: Full=Gamma-coat protein; Short=Gamma-COP >gi|222424705|dbj|BAH20306.1| AT4G34450 [Arabidopsis thaliana]	Unigene11222_All//5.00E-136//AT4G34450| coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	Unigene11222_All//0.00E+00//gi|78337737|gb|DT558011.1|DT558011			nr +
Unigene11223_All	1525	4.87	2.86	3.04	10.91	7.07	7.26	16.50	8.55	7.78	-7.70E-01	3.23E-04		-6.81E-01	2.19E-03		-6.26E-01	5.32E-07		-5.89E-01	8.86E-06		-9.48E-01	5.92E-21		-1.08E+00	1.09E-26	Down	Unigene11223_All//gi|146286094|sp|Q0WK26.2|COPG_ARATH//0.00E+00//RecName: Full=Coatomer subunit gamma; AltName: Full=Gamma-coat protein; Short=Gamma-COP >gi|222424705|dbj|BAH20306.1| AT4G34450 [Arabidopsis thaliana]	Unigene11223_All//0.00E+00//AT4G34450| coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	Unigene11223_All//0.00E+00//gi|109854135|gb|DW483114.1|DW483114			GO:0005515//GO:0009536//GO:0015031//GO:0030120	nr -
Unigene112235_All	243	0.43	0.00	0.00	1.23	0.71	0.19	3.65	1.55	0.66	-8.75E+00	3.75E-01		-8.75E+00	3.97E-01		-7.96E-01	5.57E-01		-2.73E+00	1.37E-01		-1.24E+00	6.79E-02		-2.48E+00	9.93E-04	Down							
Unigene112236_All	243	0.00	0.00	0.00	0.00	0.00	0.00	2.78	0.52	0.00	null	null		null	null		null	null		null	null		-2.43E+00	7.77E-03		-1.14E+01	3.57E-05	Down			Unigene112236_All//2.00E-11//ES843311				
Unigene112238_All	244	0.00	0.00	0.00	0.00	0.00	0.00	3.47	0.17	0.49	null	null		null	null		null	null		null	null		-4.34E+00	4.55E-05	Down	-2.82E+00	5.38E-04	Down			Unigene112238_All//1.00E-12//CD486305				
Unigene11224_All	1408	11.37	6.55	5.22	24.27	21.86	18.93	27.48	15.14	12.17	-7.96E-01	1.49E-08		-1.12E+00	5.97E-14	Down	-1.51E-01	1.30E-01		-3.59E-01	6.67E-05		-8.60E-01	4.37E-27		-1.18E+00	4.04E-46	Down	Unigene11224_All//gi|146286094|sp|Q0WK26.2|COPG_ARATH//0.00E+00//RecName: Full=Coatomer subunit gamma; AltName: Full=Gamma-coat protein; Short=Gamma-COP >gi|222424705|dbj|BAH20306.1| AT4G34450 [Arabidopsis thaliana]	Unigene11224_All//0.00E+00//AT4G34450| coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	Unigene11224_All//0.00E+00//TC140277			GO:0005515//GO:0009536//GO:0015031//GO:0030120	nr +
Unigene112247_All	245	0.00	0.00	0.00	0.00	0.00	0.00	2.59	0.00	0.16	null	null		null	null		null	null		null	null		-1.13E+01	1.23E-04	Down	-3.99E+00	5.82E-04	Down	Unigene112247_All//gi|260516678|gb|ACX43965.1|//4.00E-24//cysteine protease 1 [Brachiaria hybrid cultivar]	Unigene112247_All//1.00E-23//AT5G43060| cysteine proteinase, putative / thiol protease, putative				GO:0004175//GO:0005488//GO:0006970//GO:0019538//GO:0043231	nr -
Unigene11225_All	2015	17.89	10.84	8.96	33.62	26.83	26.25	34.56	19.81	13.86	-7.23E-01	1.40E-15		-9.98E-01	2.13E-25		-3.26E-01	2.29E-08		-3.57E-01	5.84E-09		-8.03E-01	7.30E-43		-1.32E+00	1.94E-98	Down	Unigene11225_All//gi|195613770|gb|ACG28715.1|//0.00E+00//coatomer subunit gamma [Zea mays]	Unigene11225_All//0.00E+00//AT4G34450| coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	Unigene11225_All//0.00E+00//TC149588			GO:0005515//GO:0009536//GO:0015031//GO:0030120	nr -
Unigene112252_All	245	0.00	0.00	0.41	0.28	0.00	2.24	0.00	0.65	null	null		null	null		-5.33E-01	8.18E-01		-8.67E+00	4.04E-01		-1.11E+01	4.61E-04	Down	-1.79E+00	5.07E-02		Unigene112252_All//gi|159025723|emb|CAN88862.1|//6.00E-22//D5-type cyclin [Populus trichocarpa]	Unigene112252_All//6.00E-06//AT2G22490| CYCD2;1 (Cyclin D2;1); cyclin-dependent protein kinase regulator/ protein binding	Unigene112252_All//4.00E-09//ES821171			GO:0009987//GO:0043231	nr +
Unigene112253_All	245	0.00	0.00	0.00	0.00	0.00	0.00	4.49	0.17	0.33	null	null		null	null		null	null		null	null		-4.72E+00	1.02E-06	Down	-3.79E+00	3.27E-06	Down	Unigene112253_All//gi|116059767|emb|CAL55474.1|//6.00E-32//ribosomal protein L18 (ISS) [Ostreococcus tauri]	Unigene112253_All//4.00E-28//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene112254_All	245	0.00	0.00	0.00	0.81	2.53	0.74	23.30	1.19	0.49	null	null		null	null		1.64E+00	1.06E-01		-1.41E-01	9.35E-01		-4.29E+00	2.81E-31	Down	-5.58E+00	3.08E-37	Down	Unigene112254_All//gi|22327455|ref|NP_198720.2|//1.00E-32//ATTAP2; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana] >gi|122246555|sp|Q0WML0.1|AR27B_ARATH RecName: Full=ABC transporter B family member 27; Short=ABC transporter ABCB.27; Short=AtABCB27; AltName: Full=Antigen peptide transporter-like 2; AltName: Full=Transporter associated with antigen processing-like protein 2; Short=AtTAP2; AltName: Full=Aluminum tolerance-related ATP-binding cassette transporter >gi|109690059|gb|ABG37923.1| aluminum tolerance-related ABC transporter [Arabidopsis thaliana] >gi|110739463|dbj|BAF01641.1| transporter associated with antigen processing-like protein [Arabidopsis thaliana]	Unigene112254_All//5.00E-34//AT5G39040| ATTAP2; ATPase, coupled to transmembrane movement of substances / transporter	Unigene112254_All//2.00E-45//TC135398		ko02010|ABC transporters	GO:0006810//GO:0031224//GO:0032559//GO:0042626//GO:0043234	nr +
Unigene11226_All	3116	10.36	5.46	6.19	19.90	14.81	15.15	24.48	12.80	11.28	-9.23E-01	6.23E-21		-7.44E-01	4.38E-14		-4.27E-01	1.86E-12		-3.94E-01	8.69E-10		-9.36E-01	1.45E-60		-1.12E+00	3.24E-83	Down	Unigene11226_All//gi|146286094|sp|Q0WK26.2|COPG_ARATH//0.00E+00//RecName: Full=Coatomer subunit gamma; AltName: Full=Gamma-coat protein; Short=Gamma-COP >gi|222424705|dbj|BAH20306.1| AT4G34450 [Arabidopsis thaliana]	Unigene11226_All//0.00E+00//AT4G34450| coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	Unigene11226_All//0.00E+00//TC166622			GO:0005515//GO:0009536//GO:0015031//GO:0030120	nr +
Unigene112263_All	246	0.00	0.00	0.00	0.00	0.00	0.00	5.84	1.53	0.81	null	null		null	null		null	null		null	null		-1.93E+00	3.78E-04	Down	-2.85E+00	2.40E-06	Down								ESTscan -
Unigene112270_All	247	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	8.90E-04	Down	-1.10E+01	5.55E-04	Down	Unigene112270_All//gi|219124680|ref|XP_002182626.1|//2.00E-13//14-3-3-like protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|217465972|gb|EEC43913.1| 14-3-3-like protein [Phaeodactylum tricornutum CCAP 1055/1]	Unigene112270_All//3.00E-13//AT2G42590| GRF9 (GENERAL REGULATORY FACTOR 9); calcium ion binding / protein binding / protein phosphorylated amino acid binding				GO:0005515//GO:0009532//GO:0016020//GO:0046872	nr -
Unigene112272_All	247	0.00	0.00	0.00	0.20	0.14	0.37	2.05	0.17	0.00	null	null		null	null		-5.33E-01	8.27E-01		8.58E-01	7.96E-01		-3.60E+00	5.77E-03		-1.10E+01	5.55E-04	Down	Unigene112272_All//gi|224082258|ref|XP_002306621.1|//9.00E-31//GRAS family transcription factor [Populus trichocarpa] >gi|222856070|gb|EEE93617.1| GRAS family transcription factor [Populus trichocarpa]	Unigene112272_All//5.00E-11//AT4G08250| scarecrow transcription factor family protein		GRAS		GO:0005634//GO:0010468	nr +
Unigene11228_All	742	12.13	8.60	9.26	26.65	26.45	26.23	17.78	13.01	6.82	-4.95E-01	1.02E-02		-3.90E-01	5.73E-02		-1.08E-02	9.51E-01		-2.29E-02	8.91E-01		-4.50E-01	1.16E-03		-1.38E+00	9.26E-21	Down	Unigene11228_All//gi|240255711|ref|NP_192030.4|//1.00E-70//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene11228_All//2.00E-63//AT4G01210| transferase, transferring glycosyl groups	Unigene11228_All//0.00E+00//TC156636			GO:0003824//GO:0008152	nr -
Unigene112280_All	247	0.00	0.00	0.00	0.00	0.00	0.00	2.23	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	4.61E-04	Down	-1.11E+01	2.81E-04	Down	Unigene112280_All//gi|6831610|sp|O48513.1|RL13_CHLSW//2.00E-21//RecName: Full=60S ribosomal protein L13; AltName: Full=BBC1 protein homolog >gi|2662188|dbj|BAA23724.1| BBC1 protein [Chlamydomonas sp. W80]	Unigene112280_All//5.00E-22//AT3G49010| ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +
Unigene112283_All	248	0.00	0.00	0.00	0.00	0.00	0.00	2.73	0.34	0.00	null	null		null	null		null	null		null	null		-3.02E+00	2.43E-03		-1.14E+01	3.57E-05	Down	Unigene112283_All//gi|6525111|gb|AF15333.1|AF181949.1|//2.00E-15//cytochrome oxidase subunit 2 [Lespedeza formosa]	Unigene112283_All//2.00E-14//ATMG00160| cytochrome c oxidase subunit 2			ko00190|Oxidative phosphorylation	GO:0005506//GO:0015002//GO:0019866//GO:0022900//GO:0031224//GO:0045231//GO:0051234	nr -
Unigene112285_All	248	0.00	0.00	0.00	0.00	0.00	0.00	3.07	1.85	0.00	null	null		null	null		null	null		null	null		-7.27E-01	3.32E-01		-1.16E+01	8.88E-06	Down	Unigene112285_All//gi|298712420|emb|CRI33198.1|//2.00E-17//histone H4 [Ectocarpus siliculosus]	Unigene112285_All//3.00E-08//AT5G59970| histone H4	Unigene112285_All//2.00E-23//BQ408984			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr +
Unigene112286_All	248	0.00	0.00	0.21	0.40	0.14	0.36	4.43	0.84	1.77	null	null		7.75E+00	6.40E-01		-1.53E+00	5.88E-01		-1.41E-01	9.52E-01		-2.40E+00	4.11E-04	Down	-1.33E+00	2.07E-02									

Unigene11229_All	3570	1.38	0.79	1.48	2.53	2.00	1.70	2.87	1.44	0.79	-7.94E-01	3.37E-03		1.00E-01	7.16E-01		-3.39E-01	7.96E-02		-5.75E-01	2.35E-03		-9.93E-01	1.16E-09		-1.86E+00	1.78E-24	Down	Unigene11229_All//gi|240255711|ref|NP_192030.4|//0.00E+00//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene11229_All//0.00E+00//AT4G01210| transferase, transferring glycosyl groups	Unigene11229_All//0.00E+00//gi|73943845|gb|DT527153.1|DT527153				nr -
Unigene1123_All	1141	5.18	2.93	3.50	7.03	4.98	3.88	18.12	14.03	8.03	-8.22E-01	7.50E-04		-5.66E-01	2.68E-02		-4.97E-01	1.10E-02		-8.58E-01	1.95E-05		-3.69E-01	6.74E-04		-1.17E+00	5.04E-25	Down	Unigene1123_All//gi|62321656|dbj|BAD95276.1|//1.00E-147//DNA ligase like protein [Arabidopsis thaliana]	Unigene1123_All//8.00E-133//AT1G08130| ATLIG1 (ARABIDOPSIS THALIANA DNA LIGASE 1); ATP binding / DNA binding / DNA ligase (ATP)	Unigene1123_All//0.00E+00//TC162781		ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03430|Mismatch repair		nr +
Unigene112300_All	249	1.05	0.20	2.14	0.80	0.41	0.00	2.21	0.00	0.64	-2.37E+00	2.14E-01		1.03E+00	3.42E-01		-9.48E-01	5.88E-01		-9.64E+00	1.34E-01		-1.11E+01	4.61E-04	Down	-1.79E+00	5.07E-02					Unigene112300_All//2.00E-82//C0110844				
Unigene112301_All	249	0.00	0.00	0.00	0.00	0.00	0.00	2.38	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	2.39E-04	Down	-1.12E+01	1.41E-04	Down	Unigene112301_All//gi|195623470|gb|ACG33565.1|//1.00E-28//40S ribosomal protein S24 [Zea mays]	Unigene112301_All//2.00E-26//AT3G04920| 40S ribosomal protein S24 (RPS24A)			ko03010|Ribosome	GO:0005198//GO:0005488//GO:0010467//GO:0030529	nr -
Unigene112302_All	250	0.00	0.00	0.21	0.00	0.00	0.36	3.04	0.17	0.00	null	null		7.73E+00	6.40E-01		null	null		8.50E+00	4.80E-01		-4.19E+00	1.58E-04	Down	-1.16E+01	8.88E-06	Down								
Unigene112304_All	250	59.23	31.21	24.71	99.83	75.62	51.31	44.99	22.74	40.95	-9.24E-01	4.83E-10		-1.26E+00	2.00E-15	Down	-4.01E-01	7.92E-05		-9.60E-01	1.14E-18		-9.84E-01	2.11E-10		-1.36E-01	4.10E-01		Unigene112304_All//gi|15235668|ref|NP_193070.1|//1.00E-13//leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] >gi|75337952|sp|Q9T0K5.1|LRX3_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 3; Short=LRR/EXTENSIN3; Short=AtLRX3; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|4584539|emb|CAB40769.1|extensin-like protein [Arabidopsis thaliana] >gi|7268037|emb|CAB78376.1|extensin-like protein [Arabidopsis thaliana]		Unigene112304_All//4.00E-99//BQ407414				GO:0005198//GO:0005488//GO:0005618//GO:0016491//GO:0031410	nr +
Unigene112305_All	250	0.00	0.00	0.00	0.00	0.00	0.00	3.21	0.00	0.16	null	null		null	null		null	null		null	null		-1.16E+01	8.58E-06	Down	-4.33E+00	4.54E-05	Down								ESTscan -
Unigene112309_All	250	0.00	0.00	0.00	0.00	0.00	0.00	57.16	1.34	0.96	null	null		null	null		null	null		null	null		-5.42E+00	1.98E-88	Down	-5.90E+00	8.40E-95	Down	Unigene112309_All//gi|224084948|ref|XP_002307453.1|//5.00E-26//nramp transporter [Populus trichocarpa] >gi|222856902|gb|EEE94419.1| nramp transporter [Populus trichocarpa]	Unigene112309_All//5.00E-18//AT1G80830| NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter	Unigene112309_All//6.00E-33//BN804497			GO:0044464//GO:0051234	nr +
Unigene112310_All	250	0.00	0.00	0.00	0.00	0.00	0.00	2.03	0.50	0.00	null	null		null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.10E+01	5.55E-04	Down								ESTscan +
Unigene112311_All	250	0.00	0.00	0.00	0.40	0.41	0.18	4.23	0.67	0.96	null	null		null	null		5.23E-02	9.68E-01		-1.14E+00	6.78E-01		-2.66E+00	2.25E-04	Down	-2.14E+00	9.36E-04	Down			Unigene112311_All//3.00E-07//TC173050					
Unigene112312_All	250	0.63	0.61	0.85	1.00	0.69	0.72	2.71	0.00	0.96	-4.62E-02	9.89E-01		4.41E-01	7.76E-01		-5.33E-01	7.13E-01		-4.63E-01	7.45E-01		-1.14E+01	6.34E-05	Down	-1.50E+00	5.44E-02								
Unigene112314_All	250	0.00	0.00	0.00	0.00	0.00	0.00	3.21	0.00	0.00	null	null		null	null		null	null		null	null		-1.16E+01	8.58E-06	Down	-1.16E+01	4.43E-06	Down	Unigene112314_All//gi|115456397|ref|NP_001051799.1|//2.00E-22//Os03g0832200 [Oryza sativa Japonica Group] >gi|113550270|dbj|BAF13713.1|Os03g0832200 [Oryza sativa Japonica Group]	Unigene112314_All//8.00E-24//AT1G56340| CRT1 (CALRETICULIN 1); calcium ion binding / unfolded protein binding			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	GO:0005515//GO:0030246//GO:0031410//GO:0033554//GO:0042742//GO:0044267//GO:0044432//GO:0046872	nr +
Unigene112316_All	250	0.00	0.00	0.00	0.00	0.00	0.00	2.88	1.50	0.00	null	null		null	null		null	null		null	null		-9.34E-01	2.26E-01		-1.15E+01	1.78E-05	Down								
Unigene112319_All	250	0.00	0.00	0.00	0.00	0.00	0.00	2.03	0.33	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.05E-02		-1.10E+01	5.55E-04	Down	Unigene112319_All//gi|257815167|gb|ACV69975.1|//2.00E-20//14-3-3 protein [Solanum chacoense]	Unigene112319_All//1.00E-20//AT5G65430| GRF8 (GENERAL REGULATORY FACTOR 8); protein binding / protein phosphorylated amino acid binding					nr +
Unigene112322_All	251	0.00	0.00	0.00	0.00	0.00	0.00	2.02	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	8.90E-04	Down	-1.10E+01	5.55E-04	Down								ESTscan -
Unigene112324_All	251	0.00	0.00	0.00	0.00	0.00	0.00	9.26	9.82	0.95	null	null		null	null		null	null		-3.28E+00	3.91E-11	Down									Unigene112324_All//2.00E-08//TC142106				
Unigene112326_All	251	61.49	47.24	39.25	43.26	42.12	36.53	42.95	26.98	19.52	-3.81E-01	8.02E-03		-6.48E-01	1.02E-05		-3.88E-02	8.38E-01		-2.44E-01	1.98E-01		-6.71E-01	1.39E-05		-1.14E+00	7.43E-13	Down	Unigene112326_All//gi|238837063|gb|ACR61637.1|//3.00E-41//heteromeric acetyl-CoA biotin carboxylase [Jatropha curcas]	Unigene112326_All//2.00E-41//AT5G35360| CAC2; acetyl-CoA carboxylase/ biotin carboxylase	Unigene112326_All//3.00E-130//gi|164367339|gb|ES801692.1|ES801692		ko00280|Valine, leucine and isoleucine degradation	GO:0006631//GO:0009526//GO:0009532//GO:0016421//GO:0016879//GO:0019842//GO:0032559//GO:0043169	nr -
Unigene112327_All	251	0.63	0.00	0.99	0.00	0.54	2.02	0.00	0.16	-9.29E+00	2.16E-01		-9.29E+00	2.46E-01		-9.95E+00	4.19E-02		-8.78E-01	6.17E-01		-1.10E+01	8.90E-04	Down	-3.67E+00	3.75E-03		Unigene112327_All//gi|34365551|gb|AAQ65087.1|//1.00E-29//At4g14850 [Arabidopsis thaliana]	Unigene112327_All//9.00E-23//AT4G14850| LO11 (lovastatin insensitive 1)				GO:0006066//GO:0006084//GO:0006090//GO:0019222//GO:0043231//GO:0048513//GO:0070717	nr +
Unigene112328_All	251	0.00	0.00	0.00	0.55	0.00	2.19	0.50	16.98	null	null		null	null		9.10E+00	3.20E-01		null	null		-2.13E+00	3.31E-02		2.96E+00	1.08E-17	Up			Unigene112328_All//1.00E-105//FL577603				
Unigene112336_All	252	0.00	0.00	0.00	0.00	0.00	0.00	2.35	0.17	0.00	null	null		null	null		null	null		null	null		-3.82E+00	1.79E-03		-1.12E+01	1.41E-04	Down	Unigene112336_All//gi|301122571|ref|XP_002909012.1|//2.00E-06//rho GDP-dissociation inhibitor [Phytophthora infestans T30-4] >gi|262099774|gb|EEY57826.1| rho GDP-dissociation inhibitor [Phytophthora infestans T30-4]	Unigene112336_All//4.00E-05//AT1G12070| Rho GDP-dissociation inhibitor family protein					nr -
Unigene112337_All	252	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.33	0.00	null	null		null	null		null	null		null	null		-2.72E+00	1.22E-02		-1.11E+01	2.81E-04	Down								
Unigene112339_All	252	0.00	0.00	0.00	0.00	0.00	0.00	4.19	0.50	0.16	null	null		null	null		null	null		null	null		-3.08E+00	6.12E-05	Down	-4.73E+00	8.85E-07	Down	Unigene112339_All//gi|30683788|ref|NP_850114.1|//1.00E-13//FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor [Arabidopsis thaliana] >gi|122242304|sp|Q0V7X4.1|FIT_ARATH RecName: Full=Transcription factor FER-LIKE IRON DEFICIENCY-INDUCED TRANSCRIPTION FACTOR; AltName: Full=Transcription factor EN 43; AltName: Full=Transcription factor Fe-DEFICIENCY INDUCED TRANSCRIPTION FACTOR 1; AltName: Full=FER-LIKE REGULATOR OF IRON UPTAKE; AltName: Full=bHLH transcription factor bHLH029; AltName: Full=Basic helix-loop-helix protein 29; Short=bHLH 29; Short=AtbHLH29 >gi|111074360|gb|ABH04553.1|At2g28160 [Arabidopsis thaliana]	Unigene112339_All//1.00E-05//AT2G28160| FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor	Unigene112339_All//4.00E-34//CA994022	bHLH		GO:0005515//GO:0006826//GO:0010038//GO:0010468//GO:0043231	nr -
Unigene11234_All	1174	9.63	17.44	11.20	24.06	28.04	36.74	14.41	16.45	35.22	8.57E-01	5.20E-12		2.19E-01	2.13E-01		2.21E-01	1.99E-02		6.11E-01	9.98E-15		1.91E-01	1.19E-01		1.29E+00	2.15E-56	Up	Unigene11234_All//gi|297807481|ref|XP_002871624.1|//3.00E-44//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297317461|gb|EFH47883.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene11234_All//3.00E-44//AT5G14610| ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding / protein binding	Unigene11234_All//0.00E+00//TC179191		ko03040|Spliceosome	GO:0000166//GO:0016887	nr +
Unigene112347_All	253	0.00	0.00	0.00	0.00	0.00	0.00	2.34	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	2.39E-04	Down	-1.12E+01	1.41E-04	Down	Unigene112347_All//gi|99903571|gb|ABF68589.1|//5.00E-11//chloroplast sedoheptulose-1,7-bisphosphatase [Prymnesium parvum]	Unigene112347_All//5.00E-08//AT3G55800| SBPASE (sedoheptulose-bisphosphatase); phosphoric ester hydrolase/ sedoheptulose-bisphosphatase			ko00710|Carbon fixation in photosynthetic organisms	GO:0016787	nr +
Unigene112350_All	253	0.00	0.60	0.00	0.39	0.14	0.18	2.01	0.00	0.79	9.23E+00	2.36E-01		null	null		-1.53E+00	5.88E-01		-1.14E+00	6.78E-01		-1.10E+01	8.90E-04	Down	-1.35E+00	1.40E-01				Unigene112350_All//7.00E-110//EE592576				
Unigene112236_All	3977	1.63	1.58	1.22	12.58	24.19	12.63	11.12	3.07	10.42	-4.63E-02	8.47E-01		-4.21E-01	8.73E-02		9.44E-01	6.87E-75		6.00E-03	9.57E-01		-1.86E+00	3.30E-100	Down	-9.41E-02	2.37E-01		Unigene11236_All//gi|224140965|ref|XP_002323847.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222866649|gb|EEF03980.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene11236_All//0.00E+00//AT3G28860| ABCB19; ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter	Unigene11236_All//0.00E+00//TC144381		ko02010|ABC transporters	GO:0009630//GO:0009639//GO:0009725//GO:0009926//GO:0015562//GO:0032124//GO:0033410//GO:0032535//GO:0032559//GO:0042626//GO:0043234//GO:0043479//GO:0048437//GO:0048528	nr +
Unigene112360_All	254	0.00	0.00	0.00	0.00	0.00	0.00	2.33	0.33	0.00	null	null		null	null		null	null		null	null		-2.82E+00	7.18E-03		-1.12E+01	1.41E-04	Down	Unigene112360_All//gi|119638443|gb|ABL85034.1|//4.00E-09//ribosomal subunit 8E protein [Brachypodium sylvaticum]	Unigene112360_All//2.00E-06//AT5G20290| 40S ribosomal protein S8 (RPS8A)			ko03010|Ribosome	GO:0044424	nr +
Unigene112365_All	254	0.00	0.00	0.00	0.00	0.00	0.00	4.49	0.00	0.00	null	null		null	null		null	null		null	null		-1.21E+01	3.89E-08	Down	-1.21E+01	1.65E-08	Down								
Unigene112237_All	4421	1.60	0.73	0.73	9.15	11.18	6.62	19.27	5.00	17.97	-1.12E+00	7.12E-07	Down	-1.12E+00	1.70E-06	Down	2.89E-01	4.95E-05		-4.67E-01	8.21E-09		-1.95E+00	5.79E-205	Down	-1.01E-01	5.89E-02		Unigene112237_All//gi|162280537|gb|ABX82929.1|//0.00E+00//LO4 [Solanum pennellii]	Unigene112237_All//0.00E+00//AT3G28860| ABCB19; ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter	Unigene112237_All//0.00E+00//TC150081		ko02010|ABC transporters	GO:0009630//GO:0009639//GO:0009725//GO:0009926//GO:0015562//GO:0032124//GO:0033410//GO:0032535//GO:0032559//GO:0042626//GO:0043234//GO:0043479//GO:0048437//GO:0048528	nr +
Unigene112374_All	255	0.00	0.00	0.00	0.00	0.00	0.00	2.65	0.49	0.00	null	null		null	null		null	null		null	null		-2.43E+00	7.77E-03		-1.14E+01	3.56E-05	Down								
Unigene11238_All	568	2.12	2.32	1.69	3.86	2.55	4.45	5.73	2.35	4.49	1.31E-01	8.13E-01		-3.28E-01	6.27E-01		-6.00E-01	1.60E-01		2.07E-01	6.41E-01		-1.28E+00	4.79E-05	Down	-3.53E-01	2.51E-01		Unigene11238_All//gi|27923772|sp|Q9C641.1|EFGM_ARATH//7.00E-68//RecName: Full=Elongation factor G, mitochondrial; Short=EF-Gmt; AltName: Full=Elongation factor G 1, mitochondrial; Short=mEF-G 1; AltName: Full=Elongation factor G1; Flags: Precursor	Unigene11238_All//1.00E-69//AT2G45030| mitochondrial elongation factor, putative	Unigene11238_All//0.00E+00//ES825080			GO:0006412//GO:0008135//GO:0010038//GO:0017111//GO:0032559//GO:0032561//GO:0043231	nr -
Unigene112382_All	255	0.00	0.00	0.00	0.00	0.00	0.00	2.32	0.33	0.00	null	null		null	null		null	null		null	null		-2.82E+00	7.17E-03		-1.12E+01	1.41E-04	Down	Unigene112382_All//gi|109676342|gb|ABG37653.1|//5.00E-14//integrase [Populus trichocarpa]					GO:0003676	nr +
Unigene112385_All	256	0.00	0.00	0.00	0.00	0.00	0.00	2.48	1.31	0.16	null	null		null	null		null	null		null	null		-9.24E-01	2.63E-01		-3.99E+00	5.82E-04	Down	Unigene112385_All//gi|18404062|ref|NP_565836.1|//7.00E-39//ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A) [Arabidopsis thaliana] >gi|18409639|ref|NP_566969.1| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome [Arabidopsis thaliana] >gi|166930|gb|AAA32904.1|ubiquitin extension protein (UBQ1) [Arabidopsis thaliana] >gi|166932|gb|AAA32905.1|ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi|4886268|emb|CAB43405.1|ubiquitin / ribosomal protein CEP52 [Arabidopsis thaliana] >gi|20198116|gb|AAM15407.1|ubiquitin extension protein (UBQ2) [Arabidopsis thaliana] >gi|21553955|gb|AAM63036.1|ubiquitin extension protein UBQ1 [Arabidopsis thaliana] >gi|222424333|dbj|BAH20123.1|AT2G36170 [Arabidopsis thaliana]	Unigene112385_All//3.00E-40//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene112385_All//3.00E-10//TC154845		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0031981//GO:0032446	nr -
Unigene112386_All	256	0.00	0.00	0.00	0.00	0.00	0.00	4.29	0.00	0.16	null	null		null	null		null	null		null	null		-1.21E+01	7.67E-08	Down	-4.79E+00	4.55E-07	Down								

Unigene112391_All	256	0.41	1.98	0.83	0.19	0.00	0.00	10.40	4.57	1.40	2.28E+00	6.23E-02			1.03E+00	5.92E-01			-7.60E+00	5.61E-01			-7.60E+00	6.42E-01			-1.19E+00	7.13E-04	Down	-2.89E+00	2.70E-11	Down			Unigene112391_All//3.00E-10//FL576427				
Unigene112392_All	257	0.00	0.00	0.00	0.00	0.00	0.00	2.30	1.46	0.00	null	null			null	null			null	null			null	null			-6.54E-01	4.45E-01		-1.12E+01	1.41E-04	Down							ESTscan -
Unigene112394_All	257	0.00	0.00	0.00	0.00	0.00	0.00	16.95	0.81	9.15	null	null			null	null			null	null			null	null			-4.38E+00	2.65E-24	Down	-8.90E-01	4.13E-04			Unigene112394_All//gi|297746450|emb|CBI16506.3//8.00E-06//unnamed protein product [Vitis vinifera]	Unigene112394_All//4.00E-06//AT1G55290| oxidoreductase, 2OG-Fe(II) oxygenase family protein					nr +
Unigene112396_All	257	0.00	0.00	0.00	0.00	0.00	0.00	2.30	0.16	0.00	null	null			null	null			null	null			null	null			-3.82E+00	1.79E-03		-1.12E+01	1.41E-04	Down			Unigene112396_All//gi|301122571|ref|XP_002909012.1|//7.00E-10//rho GDP-dissociation inhibitor [Phytophthora infestans T30-4] >gi|262099774|gb|EEY57826.1| rho GDP-dissociation inhibitor [Phytophthora infestans T30-4]	Unigene112396_All//8.00E-09//AT3G07880| Rho GDP-dissociation inhibitor family protein				GO:0005488//GO:0005737//GO:0007265//GO:0008101//GO:0010769//GO:0031344//GO:0044459	nr -
Unigene112399_All	258	0.00	0.00	0.00	0.00	0.00	0.00	1.97	0.49	0.00	null	null			null	null			null	null			null	null			-2.02E+00	5.21E-02		-1.09E+01	5.55E-04	Down			Unigene112399_All//gi|87783383|gb|AF79401.1|AC068197_11//5.00E-11//F16A14.17 [Arabidopsis thaliana]	Unigene112399_All//2.00E-12//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor				GO:0006417//GO:0008135//GO:0010087	nr +
Unigene112401_All	258	0.41	0.79	0.00	0.00	0.80	0.00	4.26	0.81	0.77	9.54E-01	6.22E-01			-8.66E+00	3.97E-01			9.65E+00	1.57E-01			null	null			-2.40E+00	4.11E-04	Down	-2.46E+00	2.04E-04	Down			Unigene112401_All//2.00E-20//TC163295				
Unigene112402_All	258	0.00	0.00	0.00	0.00	0.00	0.00	3.61	1.13	0.31	null	null			null	null			null	null			null	null			-1.67E+00	1.45E-02		-3.55E+00	3.97E-05	Down			Unigene112402_All//gi|300254105|gb|EFJ39080.1|//2.00E-14//hypothetical protein VOLCADRAFT_85069 [Volvox carteri f. nagariensis]	Unigene112402_All//1.00E-18//gi|109830702|gb|DW229261.1|DW229261					nr +
Unigene112405_All	258	0.00	0.00	0.00	0.00	0.00	0.00	2.29	0.32	0.00	null	null			null	null			null	null			null	null			-2.82E+00	7.17E-03		-1.12E+01	1.41E-04	Down			Unigene112405_All//gi|297794223|ref|XP_002864996.1|//3.00E-22//60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|297310831|gb|EFH41255.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene112405_All//2.00E-22//AT5G67510| 60S ribosomal protein L26 (RPL26B)			ko03010|Ribosome	GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0043231	nr +
Unigene112407_All	259	0.00	0.00	0.00	0.00	0.00	0.00	3.43	0.00	0.00	null	null			null	null			null	null			null	null			-1.17E+01	2.24E-06	Down	-1.17E+01	1.10E-06	Down								
Unigene112408_All	259	0.00	0.00	0.00	1.54	0.27	0.52	2.78	0.32	0.00	null	null			null	null			-2.53E+00	5.80E-02			-1.56E+00	2.31E-01			-3.10E+00	1.40E-03		-1.14E+01	1.78E-05	Down			Unigene112408_All//5.00E-123//EV495313				
Unigene112409_All	259	0.00	0.00	0.00	0.00	0.00	0.00	3.26	0.32	0.31	null	null			null	null			null	null			null	null			-3.34E+00	2.51E-04	Down	-3.41E+00	1.35E-04	Down							ESTscan -
Unigene11241_All	1026	5.86	16.59	7.11	8.35	5.24	9.77	12.28	23.79	18.06	1.50E+00	1.20E-23	Up		2.78E-01	2.44E-01			-6.74E-01	2.32E-04			2.27E-01	2.65E-01			9.54E-01	1.55E-20		5.56E-01	7.03E-07				Unigene11241_All//gi|18391384|ref|NP_563905.1|//1.00E-133//KEU (keule); protein transporter [Arabidopsis thaliana] >gi|150421587|sp|Q9C5X3.2|KEULE_ARATH RecName: Full=SNARE-interacting protein KEULE	Unigene11241_All//1.00E-129//AT1G12360| KEU (keule); protein transporter	Unigene11241_All//1.00E-102//TC156564				nr -
Unigene112413_All	259	0.00	0.00	0.00	0.19	0.00	0.00	3.10	0.00	0.31	null	null			null	null			-7.59E+00	5.61E-01			-7.59E+00	6.42E-01			-1.16E+01	8.58E-06	Down	-3.33E+00	2.47E-04	Down			Unigene112413_All//gi|297596074|ref|NP_001041976.2|//6.00E-21//Os01g0139200 [Oryza sativa Japonica Group] >gi|255672859|dbj|BAF03890.2| Os01g0139200 [Oryza sativa Japonica Group]	Unigene112413_All//3.00E-20//AT3G18230 octicosapeptide/Phox/Bem1p (PB1) domain-containing protein				GO:0044444	nr -
Unigene112416_All	259	0.00	0.00	0.00	0.00	0.00	0.00	31.18	0.00	0.00	null	null			null	null			null	null			null	null			-1.49E+01	2.66E-57	Down	-1.49E+01	1.93E-59	Down			Unigene112416_All//gi|145408590|ref|YP_001152214.1|//3.00E-06//ORF124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| ORF124 [Pinus koraiensis]		Unigene112416_All//3.00E-16//BP275966				nr +
Unigene112419_All	259	0.00	0.00	0.38	0.27	0.35	3.43	0.97	268.87	null	null	null			null	null			-5.33E-01	8.18E-01			-1.41E-01	9.52E-01			-1.82E+00	1.08E-02		6.29E+00	0.00E+00	Up			Unigene112419_All//gi|114145390|dbj|BAF30984.1|//2.00E-09//basic helix-loop-helix protein [Nicotiana tabacum]	Unigene112419_All//1.00E-07//AT5G43650| basic helix-loop-helix (bHLH) family protein	Unigene112419_All//2.00E-141//DT465287	bHLH			nr -
Unigene112420_All	259	0.00	0.00	0.00	0.00	0.00	0.00	5.55	0.00	0.00	null	null			null	null			null	null			null	null			-1.24E+01	3.33E-10	Down	-1.24E+01	1.19E-10	Down			Unigene112420_All//gi|223997350|ref|XP_002288348.1|//5.00E-14//RL24, ribosomal protein 24 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335] >gi|220975456|gb|EED93784.1| RL24, ribosomal protein 24 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335]	Unigene112420_All//3.00E-09//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome			ko03010|Ribosome	GO:0009536//GO:0009755//GO:0015934//GO:0016020//GO:0031981//GO:0048438	nr +
Unigene112427_All	260	0.00	0.00	0.00	0.00	0.00	0.00	1.95	0.00	0.00	null	null			null	null			null	null			null	null			-1.09E+01	8.90E-04	Down	-1.09E+01	5.55E-04	Down								
Unigene112431_All	260	0.00	0.00	0.00	0.00	0.00	0.17	125.54	585.30	258.34	null	null			null	null			null	null			7.44E+00	7.01E-01			2.22E+00	0.00E+00	Up	1.04E+00	5.85E-65	Up			Unigene112431_All//gi|300077149|gb|ADJ66851.1|//2.00E-35//O-methyltransferase [Vitis vinifera]	Unigene112431_All//4.00E-29//AT1G51990| O-methyltransferase family 2 protein	Unigene112431_All//4.00E-102//TC157783		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0005515//GO:0008171	nr -
Unigene112436_All	260	0.00	0.00	0.00	0.00	0.00	0.69	3.41	0.80	0.15	null	null			null	null			null	null			9.44E+00	1.95E-01			-2.09E+00	4.71E-03		-4.48E+00	1.23E-05	Down				Unigene112436_All//3.00E-44//TC149496				
Unigene11244_All	763	8.50	4.52	8.65	14.56	11.96	10.18	7.81	2.90	5.90	-9.13E-01	8.80E-05			2.54E-02	9.31E-01			-2.84E-01	1.05E-01			-5.16E-01	2.18E-03			-1.43E+00	5.78E-10	Down	-4.05E-01	5.77E-02				Unigene11244_All//1.00E-52//AT1G24764| ATMAP70-2 (microtubule-associated proteins 70-2); microtubule binding	Unigene11244_All//0.00E+00//gi|78338135|gb|DT558409.1|DT558409			GO:0003002//GO:0006996//GO:0015631//GO:0016020//GO:0042546//GO:0055028	nr -
Unigene112442_All	261	0.20	0.97	0.82	0.19	0.53	1.73	2.43	0.96	0.15	2.28E+00	2.34E-01			2.03E+00	3.62E-01			1.47E+00	6.19E-01			3.18E+00	3.79E-02			-1.34E+00	1.13E-01		-3.99E+00	5.82E-04	Down				Unigene112442_All//1.00E-18//TC174009				
Unigene112449_All	262	0.00	0.00	0.00	0.00	0.00	0.00	2.90	2.39	0.00	null	null			null	null			null	null			null	null			-2.80E-01	6.96E-01		-1.15E+01	8.88E-06	Down								ESTscan -
Unigene11245_All	1365	6.17	3.93	4.17	15.73	10.32	7.38	13.85	4.10	5.63	-6.49E-01	1.10E-03			-5.64E-01	6.74E-03			-6.08E-01	1.92E-08			-1.09E+00	8.15E-20	Down		-1.75E+00	5.00E-40	Down	-1.30E+00	1.03E-26	Down			Unigene11245_All//gi|297849904|ref|XP_002892833.1|//1.00E-123//atmap70-4 [Arabidopsis lyrata subsp. lyrata] >gi|297338675|gb|EFH69092.1| atmap70-4 [Arabidopsis lyrata subsp. lyrata]	Unigene11245_All//7.00E-86//AT1G68060| ATMAP70-1 (microtubule-associated proteins 70-1); microtubule binding	Unigene11245_All//0.00E+00//TC135367				nr -
Unigene112454_All	263	0.00	0.00	0.00	0.00	0.00	0.00	3.70	0.32	0.61	null	null			null	null			null	null			null	null			-3.54E+00	4.32E-05	Down	-2.61E+00	3.36E-04	Down			Unigene112454_All//gi|292606435|gb|ADE34119.1|//9.00E-23//Superman-like protein PRASUP5 [Fragaria virginiana subsp. virginiana]	Unigene112454_All//9.00E-20//AT2G37740| ZFP10 (ZINC-FINGER PROTEIN 10); nucleic acid binding / transcription factor/ zinc ion binding	Unigene112454_All//3.00E-13//TC130397	C2H2		GO:0003824//GO:0008152//GO:0044464//GO:0046914	nr +
Unigene112457_All	263	0.00	0.00	0.00	0.00	0.00	0.00	2.57	0.00	0.00	null	null			null	null			null	null			null	null			-1.13E+01	6.34E-05	Down	-1.13E+01	3.56E-05	Down			Unigene112457_All//gi|59859758|gb|AAXM9601.1|//5.00E-39//elongation factor 1 alpha [Mallomonas rasilis]	Unigene112457_All//3.00E-34//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene112457_All//1.00E-28//EV494515			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene112458_All	263	0.00	0.00	0.00	2.84	0.39	0.17	2.09	0.16	0.15	null	null			null	null			-2.85E+00	2.09E-03			-4.05E+00	7.75E-04	Down		-3.72E+00	3.23E-03		-3.79E+00	2.03E-03									
Unigene112462_All	263	0.00	0.00	0.00	0.00	0.00	0.00	1.93	0.00	0.30	null	null			null	null			null	null			null	null			-1.09E+01	8.90E-04	Down	-2.67E+00	1.37E-02									ESTscan -
Unigene112463_All	263	0.00	0.00	0.00	0.00	0.00	0.00	3.54	0.95	0.30	null	null			null	null			null	null			null	null			-1.89E+00	6.92E-03		-3.55E+00	3.97E-05	Down			Unigene112463_All//gi|116734005|gb|ABX20083.1|//7.00E-26//elongation factor 2 [Amphiroa fragilissima]	Unigene112463_All//2.00E-23//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding				GO:0000166	nr -
Unigene112468_All	264	3.57	2.11	2.42	2.08	3.13	1.20	8.81	5.70	3.47	-7.57E-01	2.86E-01			-5.60E-01	4.39E-01			5.93E-01	4.93E-01			-7.94E-01	4.44E-01			-6.28E-01	9.58E-02		-1.34E+00	3.20E-04	Down				Unigene112468_All//4.00E-108//TC172388				
Unigene112470_All	264	0.00	1.73	1.41	1.89	0.26	1.03	2.88	0.95	0.30	1.08E+01	7.44E-03			1.05E+01	2.50E-02			-2.85E+00	1.78E-02			-8.78E-01	4.20E-01			-1.60E+00	3.70E-02		-3.26E+00	4.48E-04	Down								ESTscan +
Unigene112471_All	264	0.00	0.00	0.00	0.00	0.00	0.00	2.24	0.95	0.00	null	null			null	null			null	null			null	null			-1.24E+00	1.54E-01		-1.11E+01	1.41E-04	Down			Unigene112471_All//gi|226509811|ref|NP_001147421.1|//2.00E-11//60 ribosomal protein L14 [Zea mays] >gi|195611252|gb|ACG27456.1| 60 ribosomal protein L14 [Zea mays]	Unigene112471_All//6.00E-09//AT2G20450| 60S ribosomal protein L14 (RPL14A)			ko03010|Ribosome	GO:0030529//GO:0043229//GO:0044444	nr -
Unigene112473_All	265	0.39	0.19	0.00	1.88	0.00	0.34	2.39	0.47	1.05	-1.05E+00	6.85E-01			-8.63E+00	3.97E-01			-1.09E+01	8.99E-04	Down		-2.46E+00	4.83E-02			-2.34E+00	1.27E-02		-1.19E+00	1.33E-01									
Unigene112475_All	265	0.00	0.00	0.00	0.19	0.00	0.00	4.31	1.58	0.00	null	null			null	null			-7.55E+00	5.61E-01			-7.55E+00	6.42E-01			-1.45E+00	1.40E-02		-1.21E+01	1.65E-08	Down								
Unigene112477_All	265	0.00	0.00	0.00	0.00	0.00	0.00	2.39	0.16	0.00	null	null			null	null			null	null			null	null			-3.92E+00	9.81E-04	Down	-1.12E+01	7.12E-05	Down			Unigene112477_All//gi|32401334|gb|AAP80839.1|//1.00E-15//ribosomal S29-like protein [Griffithsia japonica]	Unigene112477_All//3.00E-16//AT4G33865| 40S ribosomal protein S29 (RPS29C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935	nr -
Unigene112478_All	265	0.00	0.00	0.00	0.00	0.00	0.00	2.71	0.00	0.00	null	null			null	null			null	null			null	null			-1.14E+01	3.27E-05	Down	-1.14E+01	1.78E-05	Down								
Unigene112248_All	654	0.56	2.17	1.22	0.84	1.95	2.28	4.40	3.64	11.03	1.95E+00	1.68E-03			1.12E+00	1.80E-01			1.22E+00	4.61E-02			1.44E+00	1.11E-02			-2.71E-01	4.47E-01		1.33E+00	5.65E-11	Up			Unigene112248_All//gi|224071385|ref|XP_002303434.1|//8.00E-66//jumonji domain protein [Populus trichocarpa] >gi|222840866|gb|EEE78413.1| jumonji domain protein [Populus trichocarpa]	Unigene112248_All//5.00E-44//AT5G46910| transcription factor jumonji (jmj) family protein	Unigene112248_All//0.00E+00//TC133454			GO:0009743//GO:0010468//GO:0043231	nr -
Unigene112484_All	266	0.00	0.00	0.00	0.00	0.00	0.00	2.38	0.16	0.00	null	null			null	null			null	null			null	null			-3.92E+00	9.81E-04	Down	-1.12E+01	7.12E-05	Down			Unigene112484_All//gi|297812013|ref|XP_002873890.1|//8.00E-30//40S ribosomal protein S16 [Arabidopsis lyrata subsp. lyrata] >gi|297319727|gb|EFH50149.1| 40S ribosomal protein S16 [Arabidopsis lyrata subsp. lyrata]	Unigene112484_All//1.00E-29//AT5G18380| 40S ribosomal protein S16 (RPS16C)	Unigene112484_All//8.00E-08//CD486142		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene112485_All	266	0.00	0.00	0.00	0.00	0.00	0.00	3.66	0.00	0.00	null	null			null	null			null	null			null	null			-1.18E+01	5.83E-07	Down	-1.18E+01	2.72E-07	Down			Unigene112485_All//gi|297812013|ref|XP_002873890.1|//3.00E-30//40S ribosomal protein S16 [Arabidopsis lyrata subsp. lyrata] >gi|297319727|gb|EFH50149.1| 40S ribosomal protein S16 [Arabidopsis lyrata subsp. lyrata]	Unigene112485_All//5.00E-30//AT5G18380| 40S ribosomal protein S16 (RPS16C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene11249_All	3651	1.62	2.97	2.42	5.83	7.55	5.83	7.85	5.38	20.57	8.75E-01	5.93E-07			5.80E-01	4.00E-03			3.75E-01	1.23E-04			1.00E-04	1.00E+00			-5.45E-01	1.47E-09		1.39E+00	6.58E-114	Up			Unigene11249_All//gi|224138208|ref|XP_002326545.1|//0.00E+00//jumonji domain protein [Populus trichocarpa] >gi|222833867|gb|EEE72344.1| jumonji domain protein [Populus trichocarpa]	Unigene11249_All//0.00E+00//AT5G46910| transcription factor jumonji (jmj) family protein	Unigene11249_All//0.00E+00//TC168243			GO:0001071//GO:0009743//GO:0010468	nr +
Unigene112495_All	268	0.39	0.38	0.99	0.00	0.26	0.67	2.05	1.09	0.00	-4.66E-02	9.90E-01			1.35E+00	4.09E-01			8.01E+00	6.14E-01			9.40E+00	1.95E-01			-9.10E-01	3.19E-01		-1.10E+01	2.81E-04	Down			Unigene112495_All//gi|15233100|ref|NP_188799.1|//1.00E-40//early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana]	Unigene112495_All//5.00E-42//AT3G21620| early-responsive to dehydration protein-related / ERD protein-related	Unigene112495_All//2.00E-20//TC156729			GO:0016020//GO:0031410	nr +
Unigene112499_All	268	0.00	0.00	0.00	0.00	0.00	0.00	2.52	0.00	0.00	null	null			null	null			null	null			null	null			-1.13E+01	6.34E-05	Down	-1.13E+01	3.56E-05	Down								

Unigene112250_All	3721	2.80	3.94	2.13	5.05	4.66	3.67	18.12	24.95	92.36	4.92E-01	7.76E-04		-3.92E-01	3.76E-02		-1.14E-01	4.47E-01		-4.61E-01	2.18E-04		4.61E-01	1.29E-21		2.35E+00	0.00E+00	Up	Unigene112250_All//gi|224138208|ref|XP_002326545.1|//0.00E+00//jumonji domain protein [Populus trichocarpa] >gi|222833867|gb|EEE72344.1| jumonji domain protein [Populus trichocarpa]	Unigene112250_All//0.00E+00//TC179033 (jmj) family protein	Unigene112250_All//0.00E+00//TC179033			GO:0001071//GO:0009743//GO:0010468//GO:0043231	nr -
Unigene112505_All	268	0.00	0.00	0.00	0.00	0.26	0.00	2.05	0.00	0.45	null	null		null	null		8.01E+00	6.14E-01		null	null		-1.10E+01	4.61E-04	Down	-2.20E+00	2.24E-02									
Unigene112506_All	268	0.00	0.00	0.00	0.00	0.00	0.00	5.21	0.31	0.00	null	null		null	null		null	null		null	null		-4.06E+00	9.64E-08	Down	-1.23E+01	2.40E-10	Down	Unigene112506_All//gi|300264478|gb|EFJ48674.1|//3.00E-18//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene112506_All//7.00E-17//AT5G06680| 60S ribosomal protein L29 (RPL29B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene112511_All	269	0.00	0.00	0.59	1.11	0.38	1.01	3.14	0.78	0.44	null	null		9.21E+00	2.39E-01		-1.53E+00	2.98E-01		-1.41E-01	9.21E-01		-2.02E+00	7.45E-03		-2.82E+00	5.38E-04	Down								
Unigene112515_All	270	0.19	0.00	0.00	0.00	0.00	0.00	2.19	0.00	0.00	-7.60E+00	6.17E-01		-7.60E+00	6.30E-01		null	null		null	null		-1.11E+01	2.39E-04	Down	-1.11E+01	1.41E-04	Down								
Unigene112518_All	270	0.00	0.00	0.00	0.00	0.00	0.00	5.32	1.86	0.15	null	null		null	null		null	null		null	null		-1.52E+00	3.35E-03		-5.17E+00	2.09E-09	Down								
Unigene112525_All	271	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.15	0.00	null	null		null	null		null	null		null	null		-3.82E+00	1.79E-03		-1.11E+01	1.41E-04	Down								
Unigene112528_All	271	0.19	0.37	0.39	0.92	0.25	0.00	1.87	0.00	0.59	9.53E-01	7.27E-01		1.03E+00	7.04E-01		-1.85E+00	2.75E-01		-9.84E+00	7.35E-02		-1.09E+01	8.90E-04	Down	-1.61E+00	7.28E-02			Unigene112528_All//9.00E-97//ES791525						
Unigene112534_All	272	0.00	0.00	0.00	1.47	0.38	0.33	2.95	0.31	1.03	null	null		null	null		-1.95E+00	1.19E-01		-2.14E+00	1.26E-01		-3.26E+00	4.48E-04	Down	-1.83E+00	3.04E-02									
Unigene112535_All	272	0.77	0.00	0.00	0.18	0.25	0.17	1.87	0.31	0.00	-9.59E+00	1.22E-01		-9.59E+00	1.46E-01		4.68E-01	9.60E-01		-1.41E-01	9.55E-01		-2.60E+00	2.05E-02		-1.09E+01	5.55E-04	Down	Unigene112535_All//gi|34365659|gb|AAQ65141.1|//9.00E-26//At5g37070 [Arabidopsis thaliana]	Unigene112535_All//4.00E-27//AT5G37070| unknown protein	Unigene112535_All//2.00E-23//gi|164248196|gb|ES810211.1|ES810211				nr +
Unigene112536_All	272	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.00	0.29	null	null		null	null		null	null		null	null		-1.11E+01	2.39E-04	Down	-2.89E+00	4.53E-03		Unigene112536_All//gi|87162909|gb|ABD28704.1|//6.00E-06//WD40-like [Medicago truncatula]	Unigene112536_All//5.00E-07//AT5G28350| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1339 (InterPro:IPR009771), WD40 repeat (InterPro:IPR001680), WD40/YVTN repeat-like (InterPro:IPR015943), Quinoprotein amine dehydrogenase, beta chain-like (InterPro:IPR011044); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G61480.1); Has 271 Blast hits to 226 proteins in 106 species: Archae - 0; Bacteria - 9; Metazoa - 133; Fungi - 64; Plants - 30; Viruses - 0; Other Eukaryotes - 35 (source: NCBI BLink).	Unigene112536_All//4.00E-22//BP275526				nr -
Unigene112538_All	272	0.00	0.00	0.00	0.00	0.00	0.00	2.80	0.00	0.15	null	null		null	null		null	null		null	null		-1.15E+01	1.68E-05	Down	-4.26E+00	8.65E-05	Down	Unigene112538_All//gi|186510913|ref|NP_190687.2|//5.00E-27//structural constituent of ribosome [Arabidopsis thaliana] >gi|67633686|gb|AAY78767.1| 60S ribosomal protein L8 [Arabidopsis thaliana]	Unigene112538_All//2.00E-28//AT3G51190| structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934	nr +
Unigene112539_All	272	0.19	0.75	0.00	0.18	0.63	0.17	2.18	0.00	0.00	1.95E+00	3.76E-01		-7.59E+00	6.30E-01		1.79E+00	5.21E-01		-1.41E-01	9.55E-01		-1.11E+01	2.39E-04	Down	-1.11E+01	1.41E-04	Down			Unigene112539_All//8.00E-11//DW512877					
Unigene11254_All	652	2.57	2.88	2.61	9.78	8.03	3.32	1.56	0.06	1.65	1.63E-01	7.23E-01		2.54E-02	9.79E-01		-2.85E-01	2.51E-01		-1.56E+00	1.83E-10	Down	-4.60E+00	3.67E-06	Down	8.42E-02	8.95E-01		Unigene11254_All//gi|3540180|gb|AAC34330.1|//4.00E-07//Unknown protein [Arabidopsis thaliana]	Unigene11254_All//2.00E-08//AT1G09980| INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF676, hydrolase-like (InterPro:IPR000755); BEST Arabidopsis thaliana protein match is: ZW18 (TAIR:AT1G58350.2); Has 342 Blast hits to 275 proteins in 70 species: Archae - 0; Bacteria - 0; Metazoa - 214; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 83 (source: NCBI BLink).	Unigene11254_All//1.00E-17//DW500858				nr -
Unigene112545_All	273	0.00	0.00	0.00	0.00	0.00	0.00	9.45	0.31	0.00	null	null		null	null		null	null		null	null		-4.95E+00	1.46E-15	Down	-1.32E+01	5.57E-19	Down								ESTscan +
Unigene112546_All	273	0.00	0.00	0.00	0.00	0.00	0.00	2.79	1.84	0.00	null	null		null	null		null	null		null	null		-6.02E-01	4.12E-01		-1.14E+01	8.88E-06	Down	Unigene112546_All//gi|27923848|sp|O65059.1|RS15_PICMA//4.00E-34//RecName: Full=40S ribosomal protein S15 >gi|2982268|gb|AAC32121.1| probable 40S ribosomal protein S15 [Picea mariana]	Unigene112546_All//4.00E-33//AT5G09510| 40S ribosomal protein S15 (RPS15D)			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene112548_All	273	0.00	0.93	0.00	2.19	0.76	0.33	4.18	0.00	0.58	9.86E+00	7.88E-02		null	null		-1.53E+00	1.01E-01		-2.73E+00	1.74E-02		-1.20E+01	3.89E-08	Down	-2.84E+00	3.60E-05	Down			Unigene112548_All//2.00E-42//gi|78347071|gb|DT567345.1|DT567345					
Unigene112550_All	274	0.00	0.00	0.00	0.00	0.00	0.00	4.01	0.31	0.29	null	null		null	null		null	null		null	null		-3.72E+00	7.15E-06	Down	-3.79E+00	3.27E-06	Down								ESTscan +
Unigene112552_All	274	0.00	0.00	0.00	0.00	0.00	0.00	2.31	0.15	0.00	null	null		null	null		null	null		null	null		-3.92E+00	9.81E-04	Down	-1.12E+01	7.12E-05	Down	Unigene112552_All//sp|P08016|EGGS_SCHMA//5.00E-07//Putative eggshell protein (Fragment) OS=Schistosoma mansoni PE=2 SV=1						swissprot +
Unigene112553_All	274	0.00	0.74	0.00	0.00	0.25	0.00	160.33	695.12	375.85	9.53E+00	1.37E-01		null	null		7.97E+00	6.14E-01		null	null		2.12E+00	0.00E+00	Up	1.23E+00	3.58E-129	Up	Unigene112553_All//gi|224103575|ref|XP_002334037.1|//5.00E-06//alkaloid o-methyltransferase related [Populus trichocarpa] >gi|224124568|ref|XP_002319364.1| alkaloid o-methyltransferase related [Populus trichocarpa] >gi|222839673|gb|EEE77996.1| alkaloid o-methyltransferase related [Populus trichocarpa] >gi|222857740|gb|EEE95287.1| alkaloid o-methyltransferase related [Populus trichocarpa]		Unigene112553_All//5.00E-46//TC157783				nr +
Unigene112554_All	274	0.00	2.40	0.00	0.00	0.00	0.00	2.78	0.15	0.00	1.12E+01	6.26E-04	Up	null	null		null	null		null	null		-4.19E+00	1.58E-04	Down	-1.14E+01	8.88E-06	Down			Unigene112554_All//1.00E-09//FL576816					
Unigene112555_All	274	0.00	0.00	0.00	0.00	0.00	0.00	1.85	0.00	0.15	null	null		null	null		null	null		null	null		-1.09E+01	8.90E-04	Down	-3.67E+00	3.75E-03									ESTscan -
Unigene112557_All	274	0.00	0.00	0.00	0.00	0.00	0.00	2.31	0.00	0.29	null	null		null	null		null	null		null	null		-1.12E+01	1.23E-04	Down	-2.99E+00	2.58E-03		Unigene112557_All//gi|1352831|sp|P48413.1|VATB_CYACA//2.00E-15//RecName: Full=V-type proton ATPase subunit B; Short=V-ATPase subunit B; AltName: Full=Vacuolar proton pump subunit B >gi|576664|gb|AAA85821.1| V-ATPase B subunit [Cyanidium caldarium]	Unigene112557_All//5.00E-16//AT4G38510| vacuolar ATP synthase subunit B, putative / V-ATPase B subunit, putative / vacuolar proton pump B subunit, putative / V-ATPase 57 kDa subunit, putative			ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0015078//GO:0015986//GO:0016469//GO:0016820	nr -
Unigene112558_All	274	0.00	0.00	0.00	0.00	0.00	0.00	4.63	1.07	0.00	null	null		null	null		null	null		null	null		-2.12E+00	4.17E-04	Down	-1.22E+01	1.99E-09	Down	Unigene112558_All//gi|297816820|ref|XP_002876293.1|//5.00E-14//60S ribosomal protein L23A [Arabidopsis lyrata subsp. lyrata] >gi|297322131|gb|EFH52552.1| 60S ribosomal protein L23A [Arabidopsis lyrata subsp. lyrata]	Unigene112558_All//8.00E-13//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome			ko03010|Ribosome	GO:0005488//GO:0043231	nr -
Unigene112559_All	275	0.00	0.00	0.77	0.00	0.63	0.16	2.61	0.30	0.29	null	null		9.60E+00	1.42E-01		9.29E+00	2.27E-01		7.36E+00	7.01E-01		-3.10E+00	1.40E-03		-3.17E+00	8.09E-04	Down	Unigene112559_All//gi|21952815|dbj|BAC06231.1|//4.00E-06//pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa Japonica Group]	Unigene112559_All//3.00E-07//AT3G49140| EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: EMB2758 (embryo defective 2758) (TAIR:AT4G33990.1); Has 45368 Blast hits to 16108 proteins in 635 species: Archae - 60; Bacteria - 10333; Metazoa - 8211; Fungi - 2499; Plants - 14806; Viruses - 492; Other Eukaryotes - 7967 (source: NCBI BLink).	Unigene112559_All//1.00E-151//DW008051			GO:0043231	nr +
Unigene11256_All	3070	0.44	0.56	0.36	0.76	1.30	1.00	0.85	0.14	0.53	3.41E-01	5.01E-01		-2.83E-01	6.05E-01		7.71E-01	9.48E-03		3.92E-01	3.12E-01		-2.65E+00	7.82E-10	Down	-6.83E-01	4.13E-02		Unigene11256_All//gi|18406260|ref|NP_564732.1|//0.00E+00//ZW18 [Arabidopsis thaliana] >gi|186491769|ref|NP_001117514.1| ZW18 [Arabidopsis thaliana] >gi|89799639|gb|AAP82253.1|AC008051_4 Identical to gene ZW18 from Arabidopsis thaliana gb|AB028199 >gi|6520167|dbj|BAA87940.1| ZW18 [Arabidopsis thaliana]	Unigene11256_All//0.00E+00//AT1G58350| ZW18	Unigene11256_All//0.00E+00//TC163281				nr -
Unigene112560_All	275	0.00	0.00	0.00	0.00	0.00	0.00	3.84	0.46	0.00	null	null		null	null		null	null		null	null		-3.08E+00	6.12E-05	Down	-1.19E+01	6.72E-08	Down	Unigene112560_All//gi|83582438|emb|CAJ45370.1|//7.00E-15//40S ribosomal protein S5 [Chlamydomonas sp. ICE-L]	Unigene112560_All//1.00E-12//AT3G11940| ATRPS5A (RIBOSOMAL PROTEIN 5A); structural constituent of ribosome			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr +
Unigene112562_All	275	0.00	0.00	0.00	0.00	0.00	0.00	1.85	0.46	0.00	null	null		null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.08E+01	5.55E-04	Down								ESTscan +
Unigene112566_All	276	0.00	0.00	0.00	0.72	0.62	0.82	2.60	0.15	2.31	null	null		null	null		-2.11E-01	8.59E-01		1.81E-01	9.35E-01		-4.10E+00	2.91E-04	Down	-1.73E-01	7.94E-01		Unigene112566_All//gi|296087024|emb|CBI33287.3|//1.00E-15//unnamed protein product [Vitis vinifera]						nr +
Unigene112567_All	276	0.00	0.00	0.00	0.00	0.00	0.00	1.99	0.00	0.14	null	null		null	null		null	null		null	null		-1.10E+01	4.61E-04	Down	-3.79E+00	2.03E-03									ESTscan -
Unigene112569_All	276	0.00	0.00	0.00	0.00	0.00	0.00	2.30	0.30	0.00	null	null		null	null		null	null		null	null		-2.92E+00	4.20E-03		-1.12E+01	7.12E-05	Down	Unigene112569_All//gi|8096269|dbj|BAA85789.1|//3.00E-12//RED [Nicotiana tabacum]				ko03040|Spliceosome	GO:0005488	nr +
Unigene112572_All	277	0.00	0.00	0.00	0.00	0.00	0.00	11.45	0.00	0.29	null	null		null	null		null	null		null	null		-1.35E+01	2.00E-22	Down	-5.31E+00	1.91E-20	Down								
Unigene112573_All	277	0.00	0.00	0.00	0.00	0.00	0.00	2.75	0.00	0.00	null	null		null	null		null	null		null	null		-1.14E+01	1.68E-05	Down	-1.14E+01	8.88E-06	Down	Unigene112573_All//gi|162459555|ref|NP_001105685.1|//7.00E-10//cysteine proteinase 1 precursor [Zea mays] >gi|1706260|sp|Q10716.1|CYSP1_MAIZE RecName: Full=Cysteine proteinase 1; Flags: Precursor >gi|643597|dbj|BAA08244.1| cysteine proteinase [Zea mays]	Unigene112573_All//9.00E-10//AT4G16190| cysteine proteinase, putative				GO:0008233//GO:0031410//GO:0043231	nr +

Unigene112575_All	277	0.00	0.00	0.00	0.00	0.00	0.00	2.44	0.60	0.14	null	null		null	null		null	null		null	null		-2.02E+00	1.98E-02		-4.09E+00	3.10E-04	Down	Unigene112575_All//gi|159479072|ref|XP_001697622.1|//4.00E-09//cysteine endopeptidase [Chlamydomonas reinhardtii] >gi|158274232|gb|EDP00016.1| cysteine endopeptidase [Chlamydomonas reinhardtii]	Unigene112575_All//1.00E-08//AT3G19390| cysteine proteinase, putative / thiol protease, putative				GO:0016787	nr -
Unigene112576_All	277	0.00	0.00	0.00	0.00	0.00	0.00	2.59	0.15	0.00	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-1.13E+01	1.78E-05	Down							
Unigene112577_All	277	0.19	0.55	0.00	0.90	0.12	0.82	2.90	0.91	0.29	1.54E+00	5.32E-01		-7.56E+00	6.30E-01		-2.85E+00	1.37E-01		-1.42E-01	9.29E-01		-1.68E+00	2.46E-02		-3.33E+00	2.47E-04	Down							
Unigene112579_All	277	0.00	0.18	1.73	0.18	0.25	0.00	2.14	0.60	0.00	7.51E+00	6.20E-01		1.08E+01	7.49E-03		4.67E-01	9.60E-01		-7.49E+00	6.42E-01		-1.82E+00	4.72E-02		-1.11E+01	1.41E-04	Down		Unigene112579_All//3.00E-07//TC132286					
Unigene112586_All	278	0.00	0.00	0.00	0.00	0.00	0.00	5.78	0.00	0.72	null	null		null	null		null	null		null	null		-1.25E+01	2.17E-11	Down	-3.01E+00	2.36E-07	Down	Unigene112586_All//gi|145340168|ref|NP_567399.2|//9.00E-10//EDA21 (embryo sac development arrest 21) [Arabidopsis thaliana] >gi|254767752|sp|Q56XC2.2|DEF37_ARATH RecName: Full=Defensin-like protein 37; AltName: Full=Protein EMBRYO SAC DEVELOPMENT ARREST 21; Flags: Precursor	Unigene112586_All//4.00E-11//AT4G13235| EDA21 (embryo sac development arrest 21)					nr +
Unigene112587_All	278	0.00	0.00	0.00	0.00	0.00	0.00	4.26	0.75	0.72	null	null		null	null		null	null		null	null		-2.50E+00	1.47E-04	Down	-2.57E+00	6.98E-05	Down	Unigene112587_All//gi|13235641|emb|CAC33768.1|//6.00E-12//S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase [Stephanotis floribunda]	Unigene112587_All//2.00E-12//AT5G38020| S-adenosyl-L-methionine:carboxyl methyltransferase family protein			ko00592|alpha-Linolenic acid metabolism	GO:0016740	nr +
Unigene112588_All	279	0.00	0.00	0.00	0.00	0.00	0.00	2.27	0.60	0.14	null	null		null	null		null	null		null	null		-1.92E+00	3.09E-02		-3.99E+00	5.82E-04	Down							
Unigene112589_All	279	0.19	0.00	0.00	0.54	0.62	0.16	2.73	2.10	0.29	-7.55E+00	6.17E-01		-7.55E+00	6.30E-01		2.01E-01	9.50E-01		-1.73E+00	5.02E-01		-3.79E-01	6.35E-01		-3.26E+00	4.48E-04	Down							
Unigene112590_All	279	0.00	0.00	0.19	0.00	0.49	0.00	2.58	0.45	0.14	null	null		7.58E+00	6.40E-01		8.95E+00	3.20E-01		null	null		-2.52E+00	4.69E-03		-4.17E+00	1.64E-04	Down							
Unigene112592_All	279	0.00	0.00	0.00	0.00	0.00	0.00	3.49	0.60	0.57	null	null		null	null		null	null		null	null		-2.54E+00	6.42E-04	Down	-2.61E+00	3.35E-04	Down	Unigene112592_All//gi|11465865|ref|NP_066414.1|//3.00E-13//cytochrome c oxidase subunit 2 [Ochromonas danica] >gi|10505198|gb|AAG18380.1|AF287134_5 cytochrome c oxidase subunit 2 [Ochromonas danica]				ko00190|Oxidative phosphorylation	GO:0016020//GO:0046872//GO:0055114	nr +
Unigene112599_All	280	0.00	0.00	0.00	0.00	0.00	0.00	2.27	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	1.23E-04	Down	-1.11E+01	7.12E-05	Down							ESTscan +
Unigene1126_All	302	23.56	11.58	19.22	18.80	16.76	25.12	15.82	9.69	5.67	-1.03E+00	4.41E-06	Down	-2.94E-01	2.29E-01		-1.66E-01	5.60E-01		4.18E-01	5.56E-02		-7.08E-01	3.87E-03		-1.48E+00	7.60E-09	Down	Unigene1126_All//gi|145910320|gb|AB958813.1|//1.00E-18//chloroplast biotin carboxylase [Gossypium hirsutum]	Unigene1126_All//4.00E-08//AT5G35360| CAC2; acetyl-CoA carboxylase/ biotin carboxylase	Unigene1126_All//8.00E-113//ES836895			GO:0006631//GO:0009526//GO:0009532//GO:0016421//GO:0016879//GO:0019842//GO:0032559//GO:0043169	nr -
Unigene112600_All	280	0.00	0.00	0.00	0.00	0.00	0.00	2.27	1.04	0.14	null	null		null	null		null	null		null	null		-1.12E+00	1.80E-01		-3.99E+00	5.82E-04	Down	Unigene112600_All//gi|192910710|gb|ACF06463.1|//3.00E-20//actin depolymerizing factor [Elaeis guineensis]	Unigene112600_All//2.00E-20//AT3G46010| ADF1 (ACTIN DEPOLYMERIZING FACTOR 1); actin binding				GO:0008092//GO:0030036//GO:0044464	nr +
Unigene112603_All	280	0.19	0.00	0.00	0.00	0.12	0.65	2.57	0.60	0.28	-7.55E+00	6.17E-01		-7.55E+00	6.30E-01		6.94E+00	8.36E-01		9.33E+00	1.95E-01		-2.10E+00	1.25E-02		-3.17E+00	8.09E-04	Down							
Unigene112605_All	280	0.37	0.00	0.00	0.18	0.00	0.00	2.57	2.39	0.28	-8.55E+00	3.75E-01		-8.55E+00	3.97E-01		-7.47E+00	5.61E-01		-7.47E+00	6.42E-01		-1.04E-01	8.93E-01		-3.17E+00	8.09E-04	Down		Unigene112605_All//6.00E-24//FL577251					
Unigene112608_All	280	0.00	0.00	0.00	0.00	0.00	0.00	2.72	1.19	0.00	null	null		null	null		null	null		null	null		-1.19E+00	1.12E-01		-1.14E+01	8.88E-06	Down	Unigene112608_All//gi|115462177|ref|NP_001054688.1|//1.00E-26//Os05g0155100 [Oryza sativa Japonica Group] >gi|54291850|gb|AAV32218.1| cytoplasmic ribosomal protein L18 [Oryza sativa Japonica Group] >gi|113578239|dbj|BAF16602.1| Os05g0155100 [Oryza sativa Japonica Group] >gi|149392184|gb|ABR25945.1| 60S ribosomal protein L18 [Oryza sativa Indica Group]	Unigene112608_All//2.00E-26//AT5G27850| 60S ribosomal protein L18 (RPL18C)			ko03010|Ribosome	GO:0030529	nr +
Unigene112610_All	281	0.00	0.00	0.00	0.00	0.00	0.00	1.96	0.00	0.00	null	null		null	null		null	null		null	null		-1.09E+01	4.61E-04	Down	-1.09E+01	2.81E-04	Down							
Unigene112615_All	281	0.00	0.00	0.00	0.00	0.00	0.00	2.11	0.15	0.00	null	null		null	null		null	null		null	null		-3.82E+00	1.79E-03		-1.10E+01	1.41E-04	Down	Unigene112615_All//gi|116055471|emb|CAL58139.1|//7.00E-23//Ribosomal protein RPL1/RPL2/RL4L4 (ISS) [Ostreococcus tauri]	Unigene112615_All//5.00E-22//AT5G09630| 60S ribosomal protein L4/L1 (RPL4A)			ko03010|Ribosome	GO:0030529	nr +
Unigene112618_All	282	0.00	0.00	0.00	0.00	0.00	0.00	1.95	0.89	0.00	null	null		null	null		null	null		null	null		-1.13E+00	2.18E-01		-1.09E+01	2.81E-04	Down	Unigene112618_All//gi|112253589|gb|AB114381.1|//5.00E-06//ribosomal protein S30 [Pfiesteria piscicida]						nr +
Unigene112619_All	282	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.30	0.14	null	null		null	null		null	null		null	null		-3.34E+00	2.51E-04	Down	-4.41E+00	2.37E-05	Down	Unigene112619_All//gi|192910698|gb|ACF06457.1|//2.00E-25//60S ribosomal protein L35 [Elaeis guineensis]	Unigene112619_All//8.00E-25//AT5G02610| 60S ribosomal protein L35 (RPL35D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr +
Unigene112262_All	254	1.03	3.59	0.42	7.26	4.20	3.38	10.15	3.95	2.82	1.80E+00	2.33E-02		-1.30E+00	4.37E-01		-7.88E-01	8.70E-02		-1.10E+00	2.24E-02		-1.36E+00	1.76E-04	Down	-1.85E+00	9.39E-07	Down			Unigene112262_All//1.00E-138//gi|164363932|gb|ES810591.1|ES810591				
Unigene112620_All	282	0.37	0.36	0.00	0.88	0.49	0.16	4.50	1.19	0.28	-4.62E-02	9.90E-01		-8.54E+00	3.97E-01		-8.55E-01	5.74E-01		-2.46E+00	2.24E-01		-1.92E+00	9.98E-04	Down	-3.99E+00	2.56E-07	Down							
Unigene112621_All	282	9.09	2.52	6.99	14.66	8.79	23.22	15.59	6.97	7.20	-1.85E+00	2.00E-05	Down	-3.80E-01	3.81E-01		-7.38E-01	8.92E-03		6.64E-01	3.67E-03		-1.16E+00	1.03E-05	Down	-1.11E+00	1.33E-05	Down	Unigene112621_All//gi|71370259|gb|AAZ30377.1|//6.00E-20//PHB2 [Nicotiana benthamiana]	Unigene112621_All//1.00E-08//AT4G28510| ATPHB1 (PROHIBITIN 1)	Unigene112621_All//7.00E-101//TC153736			GO:0030964//GO:0043231//GO:0050896	nr +
Unigene112622_All	282	0.00	0.00	0.00	0.00	0.12	0.32	1.95	0.00	0.28	null	null		null	null		6.93E+00	8.36E-01		8.32E+00	4.80E-01		-1.09E+01	4.61E-04	Down	-2.79E+00	7.96E-03								
Unigene112623_All	282	0.00	0.00	0.00	0.00	0.00	0.00	3.15	0.00	0.57	null	null		null	null		null	null		null	null		-1.16E+01	2.24E-06	Down	-2.48E+00	9.93E-04	Down	Unigene112623_All//gi|297796871|ref|XP_002886320.1|//1.00E-29//glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata] >gi|297312155|gb|EFH42579.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata]	Unigene112623_All//5.00E-31//AT5G39070| glycosyl transferase family 1 protein				GO:0008152//GO:0016740	nr -
Unigene112624_All	283	0.18	0.00	0.38	0.88	0.49	0.00	5.23	1.48	1.97	-7.53E+00	6.17E-01		1.03E+00	7.04E-01		-8.55E-01	5.74E-01		-9.78E+00	7.35E-02		-1.82E+00	5.43E-04	Down	-1.41E+00	3.79E-03			Unigene112624_All//1.00E-120//CO122161					
Unigene112628_All	283	0.37	0.36	0.00	0.18	0.24	0.00	3.29	0.44	0.00	-4.64E-02	9.90E-01		-8.53E+00	3.97E-01		4.68E-01	9.60E-01		-7.46E+00	6.42E-01		-2.89E+00	3.28E-04	Down	-1.17E+01	5.48E-07	Down		Unigene112628_All//4.00E-16//TC150436					
Unigene112630_All	283	0.00	0.00	0.00	0.00	0.00	0.00	3.29	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	1.15E-06	Down	-1.17E+01	5.48E-07	Down							
Unigene112631_All	283	0.00	0.00	0.00	0.00	0.00	0.00	1.79	1.62	0.00	null	null		null	null		null	null		null	null		-1.42E-01	8.76E-01		-1.08E+01	5.55E-04	Down			Unigene112631_All//8.00E-11//gi|109856915|gb|DW485894.1|DW485894				
Unigene112633_All	283	0.00	0.00	0.00	0.00	0.00	0.00	6.27	0.89	0.00	null	null		null	null		null	null		null	null		-2.82E+00	2.67E-07	Down	-1.26E+01	4.12E-13	Down	Unigene112633_All//gi|223996813|ref|XP_002288080.1|//1.00E-13//RS4, ribosomal protein 4 [Thalassiosira pseudonana CCMP1335] >gi|220977196|gb|EED95523.1| RS4, ribosomal protein 4 [Thalassiosira pseudonana CCMP1335]	Unigene112633_All//9.00E-13//AT5G07090| 40S ribosomal protein S4 (RPS4B)			ko03010|Ribosome	GO:0003676//GO:0030529	nr -
Unigene112634_All	284	0.00	0.00	0.00	0.00	0.00	0.00	2.68	0.00	0.00	null	null		null	null		null	null		null	null		-1.14E+01	1.68E-05	Down	-1.14E+01	8.88E-06	Down	Unigene112634_All//gi|115439475|ref|NP_001044017.1|//2.00E-13//Os01g0706500 [Oryza sativa Japonica Group] >gi|113533548|dbj|BAF05931.1| Os01g0706500 [Oryza sativa Japonica Group]	Unigene112634_All//2.00E-11//AT2G19730| 60S ribosomal protein L28 (RPL28A)			ko03010|Ribosome		nr +
Unigene112638_All	284	0.18	0.71	0.00	0.18	0.00	0.32	3.28	0.29	0.42	1.95E+00	3.75E-01		-7.53E+00	6.30E-01		-7.45E+00	5.61E-01		8.59E-01	7.96E-01		-3.48E+00	7.79E-05	Down	-2.96E+00	1.72E-04	Down		Unigene112638_All//9.00E-85//ES804248					
Unigene112641_All	284	0.00	0.00	0.00	0.00	0.00	0.00	2.08	0.29	0.00	null	null		null	null		null	null		null	null		-2.82E+00	7.17E-03		-1.10E+01	1.41E-04	Down	Unigene112641_All//gi|195637410|gb|ACG38173.1|//1.00E-38//40S ribosomal protein S3 [Zea mays]	Unigene112641_All//2.00E-38//AT5G35530| 40S ribosomal protein S3 (RPS3C)			ko03010|Ribosome	GO:0001726//GO:0003677//GO:0003723//GO:0004518//GO:0005198//GO:0006682//GO:0006412//GO:0008134//GO:0012502//GO:0015935//GO:0016835//GO:0019900//GO:0043231//GO:0043280//GO:0043433//GO:0051540	nr +
Unigene112645_All	285	0.00	0.53	0.00	1.75	0.00	0.32	1.78	0.44	0.14	9.06E+00	2.36E-01		null	null		-1.08E+01	8.99E-04	Down	-2.46E+00	4.83E-02		-2.02E+00	5.21E-02		-3.67E+00	3.75E-03			Unigene112645_All//3.00E-07//gi|21091495|gb|BQ403808.1|BQ403808					
Unigene112646_All	285	0.00	0.00	0.00	0.35	0.36	0.48	1.78	0.00	0.00	null	null		null	null		5.23E-02	9.68E-01		4.43E-01	8.62E-01		-1.08E+01	8.90E-04	Down	-1.08E+01	5.55E-04	Down	Unigene112646_All//gi|297795265|ref|XP_002865517.1|//3.00E-30//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297311352|gb|EFH41776.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene112646_All//4.00E-30//AT5G42450| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene112653_All	286	0.00	0.00	0.00	0.35	0.00	0.00	11.09	3.65	0.14	null	null		null	null		-8.44E+00	3.16E-01		-8.44E+00	4.04E-01		-1.60E+00	1.50E-06	Down	-6.31E+00	9.72E-22	Down		Unigene112653_All//9.00E-14//gi|109850443|gb|DW479422.1|DW479422					
Unigene112659_All	287	0.00	2.47	0.00	0.69	0.24	0.00	1.77	0.29	0.00	1.13E+01	3.33E-04	Up	null	null		-1.53E+00	4.16E-01		-9.44E+00	1.34E-01		-2.60E+00	2.05E-02		-1.08E+01	5.55E-04	Down	Unigene112659_All//gi|8493588|gb|AAF35811.1|AC011000_14//2.00E-11//F16P17.15 [Arabidopsis thaliana]	Unigene112659_All//3.00E-15//AT4G11950| unknown protein	Unigene112659_All//4.00E-56//AI726683			GO:0044464	nr +
Unigene112664_All	287	0.00	0.71	0.00	2.43	0.60	0.31	2.95	1.46	0.28	9.46E+00	1.37E-01		null	null		-2.02E+00	2.15E-02		-2.95E+00	5.84E-03		-1.02E+00	1.41E-01		-3.41E+00	1.35E-04	Down							ESTscan -
Unigene112665_All	288	0.00	0.00	0.00	0.00	0.00	0.00	2.64	0.29	0.69	null	null		null	null		null	null		null	null		-3.19E+00	7.93E-04	Down	-1.93E+00	1.14E-02								
Unigene112666_All	288	0.36	0.88	0.00	0.69	0.12	0.47	2.20	1.74	0.00	1.28E+00	4.35E-01		-8.51E+00	3.97E-01		-2.53E+00	2.54E-01		-5.56E-01	7.33E-01		-3.39E-01	6.63E-01		-1.11E+01	7.12E-05	Down		Unigene112666_All//3.00E-07//ES798867					
Unigene112667_All	288	0.00	0.00	0.00	0.00	0.00	0.00	4.40	1.02	0.00	null	null		null	null		null	null		null	null		-2.12E+00	4.17E-04	Down	-1.21E+01	1.99E-09	Down	Unigene112667_All//gi|116057495|emb|CAL51922.1|//4.00E-33//Putative 40S ribosomal protein S17 (ISS) [Ostreococcus tauri]	Unigene112667_All//4.00E-34//AT5G04800| 40S ribosomal protein S17 (RPS17D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935	nr -
Unigene112669_All	288	0.00	0.00	0.00	0.00	0.00	0.00	2.20	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	1.23E-04	Down	-1.11E+01	7.12E-05	Down	Unigene112669_All//gi|157093587|gb|ABV22448.1|//6.00E-17//60S ribosomal protein L21 [Oxyrrhis marina] >gi|157093591|gb|ABV22450.1| ribosomal protein L21 [Oxyrrhis marina]	Unigene112669_All//3.00E-16//AT1G57860| 60S ribosomal protein L21			ko03010|Ribosome	GO:0005622	nr -
Unigene112671_All	289	0.36	0.00	0.00	0.00	0.24	0.00	2.34	1.30	0.00	-8.50E+00	3.75E-01		-8.50E+00	3.97E-01		7.90E+00	6.14E-01		null	null		-8.47E-01	2.88E-01		-1.12E+01	3.56E-05	Down							
Unigene112672_All	289	0.00	0.00	0.00	0.00	0.00	0.00	2.63	0.58	0.00	null	null		null	null		null	null		null	null		-2.19E+00	7.78E-03		-1.14E+01	8.88E-06	Down							ESTscan +
Unigene112675_All	289	0.00	0.00	1.11	1.55	0.48	0.78	2.34	0.14	0.55	null	null		1.01E+01	4.53E-02		-1.70E+00	1.35E-01		-9.89E-01	3.94E-01		-4.02E+00	5.36E-04	Down	-2.09E+00	1.27E-02		Unigene112675_All//gi|225442190|ref|XP_002274489.1|//2.00E-27//PREDICTED: similar to midasin-related [Vitis vinifera]	Unigene112675_All//5.00E-22//AT1G67120| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / transcription factor binding				GO:0005515//GO:0016043//GO:0017111//GO:0030554//GO:0043231//GO:0044438//GO:0044260	nr +
Unigene112677_All	290	0.00	0.00	0.00	0.00	0.00	0.00	2.48	1.44	0.00	null	null		null	null		null	null		null	null		-7.82E-01	3.11E-01		-1.13E+01	1.78E-05	Down	Unigene112677_All//gi|289065194|ref|YP_003434246.1|//1.00E-19//ATP synthase F0 subunit 9 [Chattonella marina] >gi|288871906|dbj|BAI70593.1| ATP synthase F0 subunit 9 [Chattonella marina]	Unigene112677_All//2.00E-06//ATMG01080| subunit 9 of mitochondrial F0-ATPase			ko00190|Oxidative phosphorylation	GO:0000166//GO:0005739//GO:0006754//GO:0006818//GO:0015078//GO:0031224//GO:0033177	nr -
Unigene112681_All	290	0.00	0.00	0.00	0.00	0.00	0.00	3.35	0.58	0.69	null	null		null	null		null	null		null	null		-2.54E+00	6.41E-04	Down	-2.29E+00	9.84E-04	Down							ESTscan -
Unigene112682_All	290	0.18	0.00	0.00	0.17	0.00	0.00	4.08	2.02	0.55	-7.50E+00	6.17E-01		-7.50E+00	6.30E-01		-7.42E+00	5.61E-01		-7.42E+00	6.42E-01		-1.02E+00	7.15E-02		-2.89E+00	2.03E-05	Down							
Unigene112684_All	290	0.00	0.00	0.00	0.00	0.00	0.00	2.19	0.00	0.69	null	null		null	null		null	null		null	null		-1.11E+01	1.23E-04	Down	-1.67E+00	4.29E-02								ESTscan -
Unigene112688_All	291	0.36	0.00	0.00	0.00	0.00	0.00	4.36	0.72	3.15	-8.49E+00	3.75E-01		-8.49E+00	3.97E-01		null	null		null	null		-2.60E+00	5.14E-05	Down	-4.69E-01	3.69E-01								
Unigene112690_All	291	0.00	0.00	0.00	0.00	0.00	0.00	3.63	1.29	0.00	null	null		null	null		null	null		null	null		-1.49E+00	1.64E-02		-1.18E+01	6.72E-08	Down	Unigene112690_All//gi|112253669|gb|AB114419.1|//3.00E-27//heat shock protein 90 [Karlodinium micrum]	Unigene112690_All//3.00E-21//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005488	nr -

Unigene112692_All	292	0.00	0.00	0.00	0.00	0.00	0.00	2.61	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	1.68E-05	Down	-1.13E+01	8.88E-06	Down	Unigene112692_All//gi|297833766|ref|XP_002884765.1|//4.00E-18//pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330605|gb|EFH61024.1| pollen ole e 1 allergen and extensin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene112692_All//2.00E-18//AT3G09925| pollen Ole e 1 allergen and extensin family protein				GO:0044464	nr -
Unigene112694_All	292	0.00	0.00	0.00	0.00	0.00	0.00	4.05	0.57	0.27	null	null		null	null		null	null		null	null		-2.82E+00	4.41E-05	Down	-3.89E+00	9.21E-07	Down	Unigene112694_All//gi|117940159|sp|P50051.2|ERD6_ARATH//6.00E-25//RecName: Full=Sugar transporter ERD6-like 7	Unigene112694_All//2.00E-26//AT2G48020| sugar transporter, putative				GO:0006810//GO:0009536//GO:0016020//GO:0016491//GO:0022891	nr +
Unigene112698_All	293	0.00	0.00	0.00	0.00	0.00	0.00	3.90	0.43	0.14	null	null		null	null		null	null		null	null		-3.19E+00	1.96E-05	Down	-4.84E+00	2.34E-07	Down	Unigene112698_All//gi|255076213|ref|XP_002501781.1|//8.00E-27//histone H2B [Micromonas sp. RCC299] >gi|226517045|gb|ACO63039.1| histone H2B [Micromonas sp. RCC299]	Unigene112698_All//8.00E-24//AT3G09480| histone H2B, putative				GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr +
Unigene112699_All	293	0.00	0.00	0.00	0.00	0.00	0.00	1.88	0.00	0.00	null	null		null	null		null	null		null	null		-1.09E+01	4.61E-04	Down	-1.09E+01	2.81E-04	Down									ESTscan +
Unigene1127_All	952	21.93	18.26	23.94	20.62	22.10	23.10	27.58	13.17	13.56	-2.65E-01	3.37E-02		1.27E-01	3.57E-01		1.00E-01	5.07E-01		1.64E-01	2.19E-01		-1.07E+00	2.48E-26	Down	-1.02E+00	1.85E-25	Down	Unigene1127_All//gi|145910320|gb|AB798813.1|//1.00E-115//chloroplast biotin carboxylase [Gossypium hirsutum]	Unigene1127_All//3.00E-89//AT5G35360| CAC2; acetyl-CoA carboxylase/ biotin carboxylase	Unigene1127_All//0.00E+00//gi|78323863|gb|DT544137.1|DT544137		ko00280|Valine, leucine and isoleucine degradation	GO:0006631//GO:0009526//GO:0009532//GO:0016421//GO:0016879//GO:0019842//GO:0032559//GO:0043169	nr -
Unigene11270_All	317	2.64	0.32	0.00	1.73	0.33	1.42	10.54	2.24	3.77	-3.05E+00	2.11E-03		-1.14E+01	1.19E-04	Down	-2.41E+00	2.44E-02		-2.79E-01	7.57E-01		-2.23E+00	2.92E-10	Down	-1.48E+00	1.86E-06	Down			Unigene11270_All//8.00E-70//TC154667		ko00230|Purine metabolism		kegg -
Unigene112700_All	293	0.00	0.00	0.00	0.00	0.00	0.00	1.73	0.29	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.05E-02		-1.08E+01	5.55E-04	Down	Unigene112700_All//gi|224004780|ref|XP_002296041.1|//1.00E-40//F-type H-ATPase beta subunit [Thalassiosira pseudonana CCMP1335] >gi|209586073|gb|ACI64758.1| F-type H-ATPase beta subunit [Thalassiosira pseudonana CCMP1335]	Unigene112700_All//3.00E-39//AT5G08690| ATP synthase beta chain 2, mitochondrial			ko00190|Oxidative phosphorylation	GO:0005746//GO:0005753//GO:0008187//GO:0009526//GO:0010038//GO:0015078//GO:0015662//GO:0015986//GO:0019829//GO:0031981//GO:0032559//GO:0033178//GO:0046914	nr -
Unigene112701_All	293	0.71	0.00	1.82	1.36	1.88	0.31	2.89	0.29	1.22	-9.48E+00	1.22E-01		1.35E+00	2.25E-01		4.67E-01	6.68E-01		-2.14E+00	1.26E-01		-3.34E+00	2.51E-04	Down	-1.24E+00	6.26E-02									
Unigene112702_All	293	2.50	4.50	0.91	7.65	4.00	6.78	9.38	614.53	56.29	8.47E-01	1.46E-01		-1.46E+00	1.12E-01		-9.37E-01	2.06E-02		-1.74E-01	6.85E-01		6.03E+00	0.00E+00	Up	2.59E+00	9.83E-58	Up	Unigene112702_All//gi|297242517|gb|ADI24922.1|//2.00E-31//pirin [Carica papaya]	Unigene112702_All//6.00E-24//AT1G56590| pirin, putative	Unigene112702_All//4.00E-121//DW507929			GO:0005515//GO:0043231	nr +
Unigene112703_All	293	0.00	0.00	0.00	0.00	0.00	0.00	3.46	0.00	0.68	null	null		null	null		null	null		null	null		-1.18E+01	2.97E-07	Down	-2.35E+00	5.84E-04	Down									
Unigene112705_All	293	0.71	0.35	0.00	1.02	0.71	0.77	2.89	0.00	0.14	-1.05E+00	5.65E-01		-9.48E+00	1.46E-01		-5.33E-01	6.79E-01		-4.05E-01	7.52E-01		-1.15E+01	4.39E-06	Down	-4.41E+00	2.37E-05	Down	Unigene112705_All//gi|15231488|ref|NP_187419.1|//2.00E-36//exostosin family protein [Arabidopsis thaliana] >gi|75207507|sp|Q9SSE8.1|GLT1_ARATH RecName: Full=Probable glycosyltransferase At3g07620	Unigene112705_All//1.00E-37//AT3G07620| exostosin family protein				GO:0008375//GO:0044464	nr +
Unigene112706_All	293	0.00	0.00	0.00	0.00	0.00	0.00	1.88	0.00	0.00	null	null		null	null		null	null		null	null		-1.09E+01	4.61E-04	Down	-1.09E+01	2.81E-04	Down	Unigene112706_All//gi|297826751|ref|XP_002881258.1|//1.00E-17//gamma subunit of mitochondrial F1-ATPase [Arabidopsis lyrata subsp. lyrata] >gi|297327097|gb|EFH57517.1| gamma subunit of mitochondrial F1-ATPase [Arabidopsis lyrata subsp. lyrata]	Unigene112706_All//8.00E-16//AT2G33040| ATP synthase gamma chain, mitochondrial (ATPC)			ko00190|Oxidative phosphorylation	GO:0006754//GO:0006818//GO:0015078//GO:0019829//GO:0032559//GO:0033178//GO:0043231	nr +
Unigene112707_All	294	0.00	0.00	0.00	0.00	0.00	0.00	2.01	0.57	0.00	null	null		null	null		null	null		null	null		-1.82E+00	4.72E-02		-1.10E+01	1.41E-04	Down	Unigene112707_All//gi|226457105|gb|EEH54405.1|//2.00E-10//MIF4G and MA3 domain-containing protein [Micromonas pusilla CCMP1545]					GO:0003676//GO:0004672//GO:0006464//GO:0032559//GO:0043231	nr -
Unigene112708_All	294	0.00	0.00	0.00	0.68	0.12	0.00	1.73	0.14	0.00	null	null		null	null		-2.53E+00	2.34E-01		-9.40E+00	1.34E-01		-3.60E+00	5.77E-03		-1.08E+01	5.55E-04	Down									
Unigene112709_All	294	0.00	0.00	0.00	0.00	0.00	0.00	2.44	0.57	0.00	null	null		null	null		null	null		null	null		-2.10E+00	1.25E-02		-1.13E+01	1.78E-05	Down	Unigene112709_All//gi|57115501|gb|AAW33059.1|//1.00E-30//apocytochrome B [Plantago rugelii]	Unigene112709_All//7.00E-26//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.			ko00190|Oxidative phosphorylation	GO:0003824//GO:0022900//GO:0043231//GO:0044260//GO:0044425//GO:0090304	nr -
Unigene11271_All	665	3.62	0.84	0.72	5.54	2.07	2.78	7.82	2.70	3.77	-2.11E+00	6.17E-06	Down	-2.33E+00	3.17E-06	Down	-1.42E+00	3.29E-06	Down	-9.93E-01	1.72E-03		-1.53E+00	1.13E-09	Down	-1.05E+00	5.78E-06	Down	Unigene11271_All//gi|186495325|ref|NP_177566.3|//3.00E-50//PUR4 (purine biosynthesis 4); ATP binding / catalytic/ phosphoribosylformylglycinamidine synthase [Arabidopsis thaliana]	Unigene11271_All//2.00E-51//AT1G74260| PUR4 (purine biosynthesis 4); ATP binding / catalytic/ phosphoribosylformylglycinamidine synthase			ko00230|Purine metabolism	GO:0006188//GO:0016884//GO:0043231	nr +
Unigene112710_All	294	0.00	0.00	0.00	0.00	0.00	2.16	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	1.23E-04	Down	-1.11E+01	7.11E-05	Down	Unigene112710_All//gi|74272615|gb|AB401103.1|//3.00E-33//mitochondrial ADP/ATP translocator [Chlamydomonas incerta]	Unigene112710_All//5.00E-32//AT5G13490| AAC2 (ADP/ATP carrier 2); ATP:ADP antiporter/ binding	Unigene112710_All//3.00E-10//EX172555			GO:0006862//GO:0009526//GO:0009987//GO:0015300//GO:0019866//GO:0030312//GO:0031224//GO:0031981//GO:0046914	nr -
Unigene112712_All	294	0.00	0.00	0.00	0.00	0.00	0.00	2.44	0.14	0.54	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-2.17E+00	7.76E-03										ESTscan +
Unigene112714_All	294	0.00	0.00	0.00	0.00	0.00	0.00	1.87	0.85	0.00	null	null		null	null		null	null		null	null		-1.13E+00	2.18E-01		-1.09E+01	2.81E-04	Down	Unigene112714_All//gi|164652934|gb|ABY65000.1|//5.00E-36//14-3-3a protein [Gossypium hirsutum]	Unigene112714_All//6.00E-35//AT1G22300| GRF10 (GENERAL REGULATORY FACTOR 10); ATP binding / protein binding / protein phosphorylated amino acid binding	Unigene112714_All//2.00E-18//gi|48792798|gb|CO094112.1|CO094112			GO:0005515	nr +
Unigene112715_All	294	0.00	0.00	0.00	0.00	0.23	0.00	5.61	1.56	1.90	null	null		null	null		7.87E+00	6.14E-01		null	null		-1.84E+00	2.07E-04	Down	-1.56E+00	7.74E-04	Down									
Unigene112718_All	295	0.00	0.00	0.00	0.00	0.00	0.00	3.01	1.70	0.00	null	null		null	null		null	null		null	null		-8.24E-01	2.24E-01		-1.16E+01	1.10E-06	Down	Unigene112718_All//gi|159470055|ref|XP_001693175.1|//2.00E-15//ribosomal protein L29, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|158277433|gb|EDP03201.1| ribosomal protein L29 [Chlamydomonas reinhardtii]	Unigene112718_All//1.00E-12//AT3G06700| 60S ribosomal protein L29 (RPL29A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613//GO:0031981	nr -
Unigene11272_All	1299	4.35	2.46	1.97	5.60	4.75	5.35	13.18	7.05	7.12	-8.24E-01	9.97E-04		-1.14E+00	1.68E-05	Down	-2.39E-01	3.18E-01		-6.44E-02	7.94E-01		-9.04E-01	1.82E-13		-8.90E-01	1.49E-13		Unigene11272_All//gi|225449428|ref|XP_002277973.1|//0.00E+00//PREDICTED: similar to phosphoribosylformylglycinamidine synthase [Vitis vinifera]	Unigene11272_All//0.00E+00//AT1G74260| PUR4 (purine biosynthesis 4); ATP binding / catalytic/ phosphoribosylformylglycinamidine synthase	Unigene11272_All//0.00E+00//TC136476		ko00230|Purine metabolism	GO:0006188//GO:0016884//GO:0043231	nr -
Unigene112720_All	295	0.00	0.00	0.00	0.00	0.00	0.00	2.72	0.28	0.00	null	null		null	null		null	null		null	null		-3.26E+00	4.48E-04	Down	-1.14E+01	4.43E-06	Down									
Unigene112722_All	296	0.00	0.00	0.00	0.00	0.00	0.00	2.71	0.00	0.00	null	null		null	null		null	null		null	null		-1.14E+01	8.58E-06	Down	-1.14E+01	4.43E-06	Down									ESTscan +
Unigene112725_All	296	0.00	0.00	0.00	0.00	0.00	0.00	1.86	0.71	0.00	null	null		null	null		null	null		null	null		-1.40E+00	1.34E-01		-1.09E+01	2.81E-04	Down	Unigene112725_All//gi|297843614|ref|XP_002889688.1|//2.00E-29//60S ribosomal protein L10A [Arabidopsis lyrata subsp. lyrata] >gi|297335530|gb|EFH65947.1| 60S ribosomal protein L10A [Arabidopsis lyrata subsp. lyrata]	Unigene112725_All//7.00E-31//AT5G22440| 60S ribosomal protein L10A (RPL10aC)			ko03010|Ribosome	GO:0003002//GO:0003676//GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0031981//GO:0048513	nr -
Unigene112727_All	297	0.00	0.00	0.00	0.00	0.00	0.00	1.71	2.39	0.00	null	null		null	null		null	null		null	null		4.86E-01	5.42E-01		-1.07E+01	5.55E-04	Down	Unigene112727_All//gi|297836874|ref|XP_002886319.1|//1.00E-08//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332159|gb|EFH62578.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene112727_All//1.00E-12//DW506003				nr +
Unigene112728_All	297	0.00	0.00	0.00	0.00	0.00	0.00	2.14	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	1.23E-04	Down	-1.11E+01	7.11E-05	Down	Unigene112728_All//gi|260401292|gb|ACX37123.1|//2.00E-22//gag-pro [Pisum sativum]					GO:0003676//GO:0003824//GO:0043170//GO:0044238	nr -
Unigene11273_All	1135	4.10	0.49	1.78	3.99	2.73	3.34	6.89	1.55	2.28	-3.06E+00	4.37E-16	Down	-1.20E+00	5.57E-05	Down	-5.49E-01	4.55E-02		-2.57E-01	4.17E-01		-2.16E+00	4.09E-22	Down	-1.59E+00	1.88E-15	Down	Unigene11273_All//gi|225449428|ref|XP_002277973.1|//1.00E-180//PREDICTED: similar to phosphoribosylformylglycinamidine synthase [Vitis vinifera]	Unigene11273_All//2.00E-162//AT1G74260| PUR4 (purine biosynthesis 4); ATP binding / catalytic/ phosphoribosylformylglycinamidine synthase	Unigene11273_All//0.00E+00//TC136476		ko00230|Purine metabolism		nr +
Unigene112731_All	297	0.00	0.00	0.00	0.00	0.00	0.30	1.71	0.99	0.00	null	null		null	null		null	null		8.25E+00	4.80E-01		-7.94E-01	4.02E-01		-1.07E+01	5.55E-04	Down	Unigene112731_All//gi|63334283|gb|AAY40471.1|//4.00E-14//LITAF-domain-containing protein [Pisum sativum]	Unigene112731_All//2.00E-14//AT5G13190| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: LPS-induced tumor necrosis factor alpha factor (InterPro:IPR006629); Has 21 Blast hits to 21 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene112731_All//3.00E-26//ES802320				nr +
Unigene112732_All	298	0.00	0.00	0.00	0.00	0.00	0.00	2.84	0.00	0.00	null	null		null	null		null	null		null	null		-1.15E+01	4.39E-06	Down	-1.15E+01	2.21E-06	Down									ESTscan -
Unigene112737_All	298	0.00	0.00	0.00	0.00	0.00	0.00	3.41	0.28	0.94	null	null		null	null		null	null		null	null		-3.60E+00	2.38E-05	Down	-1.86E+00	3.54E-03										
Unigene112738_All	298	0.00	0.00	0.00	0.00	0.00	0.00	3.12	0.00	0.27	null	null		null	null		null	null		null	null		-1.16E+01	1.15E-06	Down	-3.55E+00	3.97E-05	Down									
Unigene11274_All	4903	3.44	2.10	2.60	7.52	6.38	7.32	11.50	5.59	6.69	-7.12E-01	1.59E-07		-4.05E-01	4.34E-03		-2.36E-01	6.35E-03		-3.80E-02	7.19E-01		-1.04E+00	1.67E-53	Down	-7.83E-01	2.31E-34		Unigene11274_All//gi|186495325|ref|NP_177566.3|//0.00E+00//PUR4 (purine biosynthesis 4); ATP binding / catalytic/ phosphoribosylformylglycinamidine synthase [Arabidopsis thaliana]	Unigene11274_All//0.00E+00//AT1G74260| PUR4 (purine biosynthesis 4); ATP binding / catalytic/ phosphoribosylformylglycinamidine synthase	Unigene11274_All//0.00E+00//TC136476		ko00230|Purine metabolism	GO:0006188//GO:0016884//GO:0043231	nr +
Unigene112742_All	299	0.18	0.34	0.00	1.17	0.23	0.00	2.97	0.28	0.13	9.54E-01	7.27E-01		-7.45E+00	6.30E-01		-2.34E+00	1.01E-01		-1.02E+01	2.13E-02		-3.41E+00	1.40E-04	Down	-4.48E+00	1.23E-05	Down			Unigene112742_All//6.00E-18//CO119622					
Unigene112743_All	300	0.00	0.00	0.00	0.00	0.00	0.00	2.54	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	1.68E-05	Down	-1.13E+01	8.88E-06	Down	Unigene112743_All//gi|25453222|sp|Q9SY33.1|PER7_ARATH//1.00E-23//RecName: Full=Peroxidase 7; Short=Atperox P7; AltName: Full=ATP30; Flags: Precursor >gi|4926834|gb|AAD32944.1|AC004135_19 T17H7.19 [Arabidopsis thaliana] >gi|9758387|gb|AAF98194.1|AC000107_17 F17P8.26 [Arabidopsis thaliana]	Unigene112743_All//4.00E-25//AT1G30870| cationic peroxidase, putative			ko00940|Phenylpropanoid biosynthesis/ko00360|Phenylalanine metabolism	GO:0003824//GO:0016209//GO:0031410//GO:0046872	nr -
Unigene112745_All	300	0.00	0.00	0.00	0.00	0.00	0.00	2.11	0.28	0.00	null	null		null	null		null	null		null	null		-2.92E+00	4.20E-03		-1.10E+01	7.11E-05	Down									ESTscan +
Unigene112746_All	300	0.00	0.00	0.00	0.00	0.00	0.00	2.54	1.11	0.00	null	null		null	null		null	null		null	null		-1.19E+00	1.12E-01		-1.13E+01	8.88E-06	Down	Unigene112746_All//gi|226460767|gb|EEH58061.1|//8.00E-14//profilin [Micromonas pusilla CCMP1545]	Unigene112746_All//2.00E-12//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding					nr +
Unigene112747_All	300	0.17	0.00	0.71	0.66	0.11	0.15	3.81	0.70	0.40	-7.45E+00	6.17E-01		2.03E+00	3.62E-01		-2.53E+00	2.34E-01		-2.14E+00	3.47E-01		-2.45E+00	2.46E-04	Down	-3.26E+00	8.94E-06	Down									

Unigene11275_All	607	2.50	3.34	1.93	4.10	3.69	4.76	10.24	13.08	4.20	4.18E-01	3.77E-01		-3.73E-01	5.09E-01		-1.54E-01	7.36E-01		2.15E-01	6.36E-01		3.54E-01	6.38E-02		-1.29E+00	2.98E-09	Down	Unigene11275_All//gi|15450511|gb|AAK96548.1|//3.00E-27//At2g46420/F11C10.11 [Arabidopsis thaliana] >gi|20197824|gb|AAD23044.2| expressed protein [Arabidopsis thaliana] >gi|27363256|gb|AAO11547.1| At2g46420/F11C10.11 [Arabidopsis thaliana]	Unigene11275_All//2.00E-28//AT2G46420| unknown protein	Unigene11275_All//0.00E+00//TC179077				nr -
Unigene112750_All	300	0.00	0.00	0.00	0.00	0.00	0.00	3.81	1.39	0.80	null	null		null	null		null	null		null	null		-1.45E+00	1.40E-02		-2.26E+00	3.40E-04	Down	Unigene112750_All//gi|87241351|gb|ABD33209.1|//1.00E-08//Ribonuclease H [Medicago truncatula]					GO:0003824	nr +
Unigene112751_All	301	0.00	0.00	0.00	0.00	0.00	0.00	2.39	0.00	0.00	null	null		null	null		null	null		null	null		-1.12E+01	3.27E-05	Down	-1.12E+01	1.78E-05	Down								ESTscan -
Unigene112753_All	301	0.00	0.00	0.00	0.00	0.23	0.30	4.49	0.42	0.79	null	null		null	null		7.84E+00	6.14E-01		8.23E+00	4.80E-01		-3.43E+00	1.05E-06	Down	-2.50E+00	2.46E-05	Down								
Unigene112755_All	301	0.00	0.84	0.35	0.33	0.34	0.15	2.67	0.28	0.66	9.72E+00	7.88E-02		8.47E+00	4.01E-01		5.22E-02	9.68E-01		-1.14E+00	6.78E-01		-3.26E+00	4.48E-04	Down	-2.01E+00	7.11E-03		Unigene112755_All//gi|51968638|dbj|BAD43011.1|//8.00E-33//peroxidase ATP23a [Arabidopsis thaliana]	Unigene112755_All//3.00E-34//AT1G68850| peroxidase, putative	Unigene112755_All//2.00E-162//gi|31073240|gb|CAI993519.1|CAI993519		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950 //GO:0008152//GO:0016209//GO:0044464	nr -
Unigene112757_All	302	0.00	0.00	0.00	0.00	0.00	0.00	2.80	0.42	0.13	null	null		null	null		null	null		null	null		-2.75E+00	9.73E-04	Down	-4.41E+00	2.37E-05	Down	Unigene112757_All//gi|6688812|emb|CAB65281.1|//5.00E-40//L3 Ribosomal protein [Medicago sativa subsp. x varia]	Unigene112757_All//7.00E-41//AT1G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	Unigene112757_All//2.00E-08//TC135599		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0010467 //GO:0015934//GO:0016020//GO:0019019//GO:0030312//GO:0031981	nr +
Unigene112758_All	302	0.00	0.00	0.00	0.00	0.00	0.00	1.68	0.28	0.00	null	null		null	null		null	null		null	null		-2.60E+00	2.05E-02		-1.07E+01	5.54E-04	Down			Unigene112758_All//3.00E-07//DW479710					
Unigene11276_All	1253	16.95	6.11	7.65	11.13	6.98	6.27	6.95	3.10	2.77	-1.47E+00	1.04E-28	Down	-1.15E+00	6.11E-19	Down	-6.73E-01	1.06E-06		-8.28E-01	1.84E-08		-1.16E+00	1.47E-10	Down	-1.33E+00	3.07E-13	Down	Unigene11276_All//gi|113205376|gb|AAU93592.2|//1.00E-144//uncharacterized plant-specific domain TIGR01589 family protein [Solanum demissum]	Unigene11276_All//9.00E-136//AT2G46420| unknown protein	Unigene11276_All//0.00E+00//TC145959				nr -
Unigene112760_All	302	0.00	0.00	0.00	0.00	0.00	0.00	2.24	0.28	0.00	null	null		null	null		null	null		null	null		-3.02E+00	2.43E-03		-1.11E+01	3.56E-05	Down	Unigene112760_All//gi|1173256|sp|P46299.1|RS4_GOSHI//3.00E-36//RecName: Full=40S ribosomal protein S4 >gi|488739|emb|CAA55882.1| ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene112760_All//2.00E-37//AT5G07090| 40S ribosomal protein S4 (RPS4B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536 //GO:0010467//GO:0015935//GO:0016020//GO:0031981	nr +
Unigene112761_All	303	0.00	0.00	0.00	0.00	0.00	0.00	2.51	0.83	0.13	null	null		null	null		null	null		null	null		-1.60E+00	3.70E-02		-4.26E+00	8.65E-05	Down								
Unigene112763_All	303	0.00	0.00	0.00	0.00	0.00	0.00	9.21	0.28	0.13	null	null		null	null		null	null		null	null		-5.06E+00	5.44E-17	Down	-6.13E+00	5.32E-19	Down	Unigene112763_All//gi|300261783|gb|EFJ45994.1|//7.00E-18//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene112763_All//5.00E-16//AT4G39200| 40S ribosomal protein S25 (RPS25E)			ko03010|Ribosome	GO:0010467//GO:0015935	nr -
Unigene112766_All	304	0.00	0.00	0.00	0.00	0.00	0.00	2.36	0.00	0.39	null	null		null	null		null	null		null	null		-1.12E+01	3.27E-05	Down	-2.59E+00	2.81E-03									
Unigene112767_All	304	0.00	0.00	0.00	0.00	0.00	0.00	2.36	0.14	1.18	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-1.00E+00	1.66E-01									ESTscan +
Unigene112768_All	305	0.00	0.00	0.00	0.00	0.00	0.00	2.22	0.00	0.52	null	null		null	null		null	null		null	null		-1.11E+01	6.34E-05	Down	-2.09E+00	1.27E-02		Unigene112768_All//gi|9256636|ref|NP_061348.1|//5.00E-07//60S ribosomal protein L41 [Mus musculus] >gi|10863875|ref|NP_066927.1| 60S ribosomal protein L41 [Homo sapiens] >gi|20806115|ref|NP_620783.1| 60S ribosomal protein L41 [Rattus norvegicus] >gi|78217384|ref|NP_001030344.1| 60S ribosomal protein L41 [Homo sapiens] >gi|114326422|ref|NP_001041622.1| 60S ribosomal protein L41 [Felis catus] >gi|197100322|ref|NP_001124641.1| 60S ribosomal protein L41 [Pongo abelii] >gi|159476032|ref|XP_001696118.1| ribosomal protein L41, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|51701777|sp|Q6YLX4.1|RL41_CYPCA RecName: Full=60S ribosomal protein L41 >gi|51701779|sp|Q71H53.1|RL41_EPIC0 RecName: Full=60S ribosomal protein L41				ko03010|Ribosome		nr -
Unigene11277_All	1094	11.96	6.48	4.92	5.60	5.57	3.76	7.19	3.67	2.37	-8.83E-01	2.32E-08		-1.28E+00	4.89E-14	Down	-7.60E-03	9.67E-01		-5.76E-01	1.56E-02		-9.71E-01	2.32E-07		-1.60E+00	1.24E-15	Down	Unigene11277_All//gi|113205376|gb|AAU93592.2|//1.00E-111//uncharacterized plant-specific domain TIGR01589 family protein [Solanum demissum]	Unigene11277_All//5.00E-102//AT2G46420| unknown protein	Unigene11277_All//0.00E+00//TC129816				nr +
Unigene112772_All	306	0.00	0.00	0.00	0.00	0.00	0.00	3.18	0.00	0.00	null	null		null	null		null	null		null	null		-1.16E+01	5.83E-07	Down	-1.16E+01	2.72E-07	Down	Unigene112772_All//gi|159469668|ref|XP_001692985.1|//3.00E-41//ribosomal protein L8, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|158277787|gb|EDP03554.1| ribosomal protein L8 [Chlamydomonas reinhardtii]	Unigene112772_All//2.00E-38//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene112772_All//6.00E-09//ES817671		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene112773_All	306	0.00	0.00	0.00	0.00	0.00	0.00	3.18	1.09	0.39	null	null		null	null		null	null		null	null		-1.54E+00	1.90E-02		-3.02E+00	9.61E-05	Down	Unigene112773_All//gi|298709870|emb|CBJ26210.1|//3.00E-36//Ribosomal protein S27 [Ectocarpus siliculosus]	Unigene112773_All//2.00E-35//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935 //GO:0016020//GO:0022613//GO:0030312//GO:0043169	nr -
Unigene112776_All	306	0.00	0.00	0.00	0.00	0.00	0.00	3.04	0.00	0.00	null	null		null	null		null	null		null	null		-1.16E+01	1.15E-06	Down	-1.16E+01	5.48E-07	Down	Unigene112776_All//gi|6687299|emb|CAB64903.1|//2.00E-29//40S ribosomal protein S9 [Cynanophora paradoxa]	Unigene112776_All//6.00E-17//AT5G15200| 40S ribosomal protein S9 (RPS9B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467 //GO:0033279	nr -
Unigene112779_All	307	0.00	0.00	0.00	0.00	0.00	0.00	3.17	0.00	0.00	null	null		null	null		null	null		null	null		-1.16E+01	5.83E-07	Down	-1.16E+01	2.72E-07	Down								ESTscan -
Unigene112780_All	307	0.00	0.00	0.00	0.00	0.00	0.00	2.62	0.54	0.13	null	null		null	null		null	null		null	null		-2.26E+00	4.82E-03		-4.33E+00	4.54E-05	Down	Unigene112780_All//gi|219119576|ref|XP_002180545.1|//2.00E-18//ornithine decarboxylase 2 [Phaeodactylum tricornutum CCAP 1055/1] >gi|217408018|gb|EEC47953.1| ornithine decarboxylase 2 [Phaeodactylum tricornutum CCAP 1055/1]				ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism	GO:0006595//GO:0016831	nr -
Unigene112783_All	308	0.00	0.00	0.00	0.00	0.00	0.29	33.63	2.17	2.59	null	null		null	null		null	null		8.20E+00	4.80E-01		-3.95E+00	2.66E-53	Down	-3.70E+00	2.15E-52	Down			Unigene112783_All//6.00E-46//gi|109887275|gb|DW516244.1|DW516244				
Unigene112784_All	308	0.00	0.00	0.00	0.00	0.00	0.00	3.29	0.14	0.00	null	null		null	null		null	null		null	null		-4.60E+00	3.67E-06	Down	-1.17E+01	1.35E-07	Down	Unigene112784_All//gi|226454387|gb|EEH51693.1|//6.00E-16//predicted protein [Micromonas pusilla CCMP1545]						nr -
Unigene112785_All	309	0.00	0.00	0.00	0.00	0.00	0.00	2.33	0.54	0.00	null	null		null	null		null	null		null	null		-2.10E+00	1.25E-02		-1.12E+01	1.78E-05	Down	Unigene112785_All//gi|145408590|ref|YP_001152214.1|//4.00E-06//ORF124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| ORF124 [Pinus koraiensis]		Unigene112785_All//6.00E-15//TC178045				nr +
Unigene112787_All	309	0.00	0.00	0.00	0.00	0.00	0.00	3.28	0.68	0.13	null	null		null	null		null	null		null	null		-2.28E+00	1.11E-03		-4.67E+00	1.72E-06	Down								
Unigene112788_All	309	0.34	0.33	0.00	1.29	0.33	0.00	3.83	0.81	0.39	-4.59E-02	9.90E-01		-8.40E+00	3.97E-01		-1.95E+00	1.19E-01		-1.03E+01	1.11E-02		-2.24E+00	4.21E-04	Down	-3.31E+00	4.89E-06	Down			Unigene112788_All//4.00E-07//TC177115					
Unigene11279_All	1853	1.07	2.79	0.66	1.64	3.03	4.02	1.73	2.48	3.40	1.38E+00	7.08E-07	Up	-6.99E-01	1.44E-01		8.85E-01	2.29E-04		1.29E+00	3.47E-09	Up	5.17E-01	4.21E-02		9.70E-01	3.16E-06		Unigene11279_All//gi|15450511|gb|AAK96548.1|//1.00E-143//At2g46420/F11C10.11 [Arabidopsis thaliana] >gi|20197824|gb|AAD23044.2| expressed protein [Arabidopsis thaliana] >gi|27363256|gb|AAO11547.1| At2g46420/F11C10.11 [Arabidopsis thaliana]	Unigene11279_All//1.00E-142//AT2G46420| unknown protein	Unigene11279_All//0.00E+00//TC145959				nr -
Unigene112791_All	309	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	1.23E-04	Down	-1.10E+01	7.11E-05	Down	Unigene112791_All//gi|298710912|emb|CBJ49265.1|//6.00E-35//3-ketoacyl-CoA thiolase [Ectocarpus siliculosus]	Unigene112791_All//6.00E-32//AT1G04710| PKT4 (PEROXISOMAL 3-KETOACYL-COA THIOLASE 4); acetyl-CoA C-acyltransferase/ catalytic			ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids	GO:0006950//GO:0009062//GO:0009536 //GO:0009657//GO:0009694//GO:0016020//GO:0016108//GO:0031981//GO:0042579	nr -
Unigene112793_All	310	0.00	0.00	0.00	0.00	0.00	0.00	4.50	0.94	0.64	null	null		null	null		null	null		null	null		-2.25E+00	9.69E-05	Down	-2.81E+00	4.26E-06	Down	Unigene112793_All//gi|10802935|gb|AAG23683.1|AF288091_28//4.00E-29//apocytochrome b [Thraustochytrium aureum]	Unigene112793_All//2.00E-18//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a submit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.			ko00190|Oxidative phosphorylation	GO:0003824//GO:0005488//GO:0022900 //GO:0043231//GO:0044425	nr +
Unigene112794_All	310	1.18	0.82	0.86	0.96	2.11	0.87	4.23	3.24	1.16	-5.32E-01	6.27E-01		-4.60E-01	6.97E-01		1.13E+00	2.38E-01		-1.41E-01	9.21E-01		-3.86E-01	4.87E-01		-1.87E+00	6.93E-04	Down	Unigene112794_All//gi|147857564|emb|CAN82884.1|//4.00E-08//hypothetical protein [Vitis vinifera]	Unigene112794_All//2.00E-05//AT3G60360| EDA14 (EMBRYO SAC DEVELOPMENT ARREST 14)	Unigene112794_All//4.00E-118//ES793613			GO:0030684//GO:0042254	nr -
Unigene112795_All	311	0.00	0.00	0.00	0.00	0.00	0.00	1.90	0.27	0.00	null	null		null	null		null	null		null	null		-2.82E+00	7.17E-03		-1.09E+01	1.41E-04	Down	Unigene112795_All//gi|226531524|ref|NP_001148960.1|//3.00E-20//ATP-dependent RNA helicase dbh1 [Zea mays] >gi|195622636|gb|ACG33648.1| ATP-dependent RNA helicase dbh1 [Zea mays]	Unigene112795_All//3.00E-21//AT4G00660| DEAD/DEAH box helicase, putative			ko03018|RNA degradation	GO:0032559//GO:0042623	nr -
Unigene112796_All	312	0.00	0.00	0.00	0.00	0.00	0.00	2.17	0.00	0.38	null	null		null	null		null	null		null	null		-1.11E+01	6.34E-05	Down	-2.50E+00	4.78E-03		Unigene112796_All//gi|301105535|ref|XP_002901851.1|//1.00E-10//villin-like protein [Phytophthora infestans T30-4] >gi|262099189|gb|EEY57241.1| villin-like protein [Phytophthora infestans T30-4]	Unigene112796_All//1.00E-07//AT3G57410| VLN3 (VILLIN 3); actin binding					nr -

Unigene112798_All	313	1144.87	389.65	570.44	2096.33	2781.45	1844.92	2.43	0.27	0.51	-1.55E+00	0.00E+00	Down	-1.01E+00	5.23E-252	Down	4.08E-01	4.46E-154		-1.84E-01	2.00E-23		-3.19E+00	7.93E-04	Down	-2.26E+00	4.68E-03		Unigene112798_All//gi|155966601|gb|ABU41235.1|//9.00E-45//xyloglucan endotransglycosylase [Gossypium hirsutum] >gi|166343773|gb|ABY86634.1| xyloglucan endotransglycosylase/hydrolase [Gossypium arboreum]	Unigene112798_All//2.00E-35//AT5G65730| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene112798_All//3.00E-174//gi|11202308|gb|BF271313.1|BF271313			GO:0005576//GO:0016758//GO:0016798//GO:0030312//GO:0044042	nr -
Unigene1128_All	1260	48.58	40.94	54.52	26.88	32.47	28.39	32.41	20.00	13.15	-2.47E-01	2.75E-04		1.66E-01	1.57E-02		2.72E-01	6.84E-04		7.86E-02	4.79E-01		-6.97E-01	4.44E-20		-1.30E+00	5.97E-57	Down	Unigene1128_All//gi|145910320|gb|A8P98813.1|//0.00E+00//chloroplast biotin carboxylase [Gossypium hirsutum]	Unigene1128_All//3.00E-162//AT5G35360| CAC2; acetyl-CoA carboxylase/ biotin carboxylase	Unigene1128_All//0.00E+00//TC158265		ko00280|Valine, leucine and isoleucine degradation	GO:0003824//GO:0019842//GO:0032559	nr -
Unigene11280_All	1603	3.75	4.11	3.72	4.79	4.19	3.27	2.72	0.81	1.39	1.31E-01	6.20E-01		-1.27E-02	9.83E-01		-1.92E-01	4.19E-01		-5.50E-01	8.47E-03		-1.75E+00	9.14E-10	Down	-9.65E-01	1.41E-04		Unigene11280_All//gi|113205376|gb|AAW93592.2|//1.00E-144//uncharacterized plant-specific domain TIGR01589 family protein [Solanum demissum]	Unigene11280_All//2.00E-141//AT2G46120| unknown protein	Unigene11280_All//0.00E+00//TC145959				nr -
Unigene112802_All	313	0.00	0.00	0.00	0.00	0.00	0.00	49.71	0.00	0.89	null	null		null	null		null	null		null	null		-1.56E+01	9.81E-111	Down	-5.80E+00	1.55E-102	Down								
Unigene112803_All	314	0.00	0.00	0.00	0.00	0.00	0.00	1.89	0.27	0.00	null	null		null	null		null	null		null	null		-2.82E+00	7.17E-03		-1.09E+01	1.41E-04	Down								ESTscan -
Unigene112804_All	314	0.00	0.00	0.00	0.00	0.00	0.00	3.23	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	2.97E-07	Down	-1.17E+01	1.35E-07	Down	Unigene112804_All//gi|115477976|ref|NP_001062583.1|//2.00E-26//0s09g0115400 [Oryza sativa Japonica Group] >gi|113630816|dbj|BAF24497.1| Os09g0115400 [Oryza sativa Japonica Group] >gi|169244485|gb|ACA50516.1| poly(A)-binding protein [Oryza sativa Japonica Group]	Unigene112804_All//7.00E-25//AT4G34110| PAB2 (POLY(A) BINDING 2); RNA binding / translation initiation factor				GO:0003723//GO:0006970	nr -
Unigene112805_All	314	0.33	0.97	0.34	0.00	0.66	0.00	3.37	0.53	0.89	1.54E+00	3.24E-01		2.53E-02	1.00E+00		9.36E+00	1.57E-01		null	null		-2.66E+00	2.25E-04	Down	-1.92E+00	2.21E-03									
Unigene112806_All	314	0.00	0.00	0.00	0.00	0.00	0.00	1.89	1.06	0.00	null	null		null	null		null	null		null	null		-8.24E-01	3.48E-01		-1.09E+01	1.41E-04	Down	Unigene112806_All//gi|298707517|emb|CBJ30119.1|//9.00E-23//14-3-3-like protein [Ectocarpus siliculosus]	Unigene112806_All//5.00E-23//AT5G38480| GRF3 (GENERAL REGULATORY FACTOR 3); ATP binding / protein binding / protein phosphorylated amino acid binding				GO:0009536//GO:0016020//GO:0030312//GO:0032559	nr -
Unigene112807_All	315	0.00	0.00	0.00	0.00	0.00	0.00	4.30	0.53	0.51	null	null		null	null		null	null		null	null		-3.02E+00	4.74E-06	Down	-3.09E+00	1.97E-06	Down	Unigene112807_All//gi|260516674|gb|ACX43964.1|//2.00E-22//cysteine protease 4 [Brachiaria hybrid cultivar]	Unigene112807_All//1.00E-20//AT3G19390| cysteine proteinase, putative / thiol protease, putative				GO:0008233	nr +
Unigene112808_All	315	0.00	0.00	0.00	0.00	0.00	0.00	3.22	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	2.97E-07	Down	-1.17E+01	1.35E-07	Down	Unigene112808_All//gi|260516678|gb|ACX43965.1|//3.00E-24//cysteine protease 1 [Brachiaria hybrid cultivar]	Unigene112808_All//4.00E-23//AT1G09850| XBCP3 (xylem bark cysteine peptidase 3); cysteine-type endopeptidase/ cysteine-type peptidase				GO:0008233	nr +
Unigene112809_All	315	0.00	0.00	0.00	0.00	0.00	0.00	15.17	0.00	3.04	null	null		null	null		null	null		null	null		-1.39E+01	7.94E-34	Down	-2.32E+00	1.49E-15	Down			Unigene112809_All//2.00E-15//TC148479					
Unigene11281_All	3463	1.78	1.73	2.69	74.01	72.43	64.01	10.77	8.50	5.10	-4.63E-02	8.52E-01		5.94E-01	2.38E-03		-3.11E-02	4.45E-01		-2.09E-01	5.14E-12		-3.42E-01	1.28E-05		-1.08E+00	6.81E-39	Down	Unigene11281_All//0.00E+00//AT5G17420| IRX3 (IRREGULAR XYLEM 3); cellulose synthase	Unigene11281_All//0.00E+00//TC170081				GO:0009250//GO:0009536//GO:0009832//GO:0010395//GO:0016759//GO:0031224//GO:0042545//GO:0046914	nr +
Unigene112810_All	316	0.17	0.00	0.17	0.79	1.31	0.00	1.61	0.00	0.25	-7.37E+00	6.17E-01		2.50E-02	9.96E-01		7.30E-01	5.87E-01		-9.62E+00	7.35E-02		-1.06E+01	8.89E-04	Down	-2.67E+00	1.37E-02		Unigene112810_All//gi|224129022|ref|XP_002320481.1|//7.00E-41//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222861254|gb|EEE98796.1| nucleobase ascorbate transporter [Populus trichocarpa]	Unigene112810_All//3.00E-41//AT2G05760| xanthine/uracil permease family protein	Unigene112810_All//3.00E-57//gi|78348668|gb|DT568942.1|DT568942			GO:0005215//GO:0006810//GO:0044464	nr +
Unigene112814_All	318	0.00	0.00	0.31	0.22	0.00	2.39	0.00	0.38	null	null		null	null		-5.33E-01	8.18E-01		-8.29E+00	4.04E-01		-1.12E+01	1.68E-05	Down	-2.67E+00	1.64E-03		Unigene112814_All//gi|115468064|ref|NP_001057631.1|//2.00E-13//0s06g0174300 [Oryza sativa Japonica Group] >gi|113595671|dbj|BAF19545.1| Os06g0174300 [Oryza sativa Japonica Group]	Unigene112814_All//2.00E-29//AT3G05390| unknown protein				GO:0031410//GO:0043231	nr -
Unigene112816_All	318	0.00	0.00	0.00	0.22	0.85	2.53	0.39	0.13	null	null		null	null		7.76E+00	6.14E-01		9.73E+00	7.04E-02		-2.68E+00	1.67E-03		-4.33E+00	4.54E-05	Down	Unigene112816_All//gi|224064756|ref|XP_002301547.1|//1.00E-48//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222843273|gb|EEE80820.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene112816_All//3.00E-49//AT2G47000| ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase	Unigene112816_All//3.00E-91//TC135162		ko02010|ABC transporters	GO:0009606//GO:0009734//GO:0009926//GO:0015114//GO:0031224//GO:0032559//GO:0042626//GO:0048588	nr -
Unigene112817_All	318	0.00	0.00	0.00	0.00	0.00	2.66	0.00	0.00	null	null		null	null					null	null		-1.14E+01	4.39E-06	Down	-1.14E+01	2.21E-06	Down	Unigene112817_All//gi|301105230|ref|XP_002901699.1|//7.00E-34//40S ribosomal protein S11 [Phytophthora infestans T30-4] >gi|262100703|gb|EEY58755.1| 40S ribosomal protein S11 [Phytophthora infestans T30-4]	Unigene112817_All//1.00E-28//AT4G30800| 40S ribosomal protein S11 (RPS11B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0003012	nr +
Unigene112818_All	318	0.00	0.00	0.00	0.16	0.00	0.00	2.26	0.00	0.13	null	null		null	null		-7.29E+00	5.61E-01		-7.29E+00	6.42E-01		-1.11E+01	3.27E-05	Down	-4.17E+00	1.64E-04	Down								
Unigene112819_All	318	0.00	0.00	0.00	0.00	0.00	0.00	5.05	0.26	0.38	null	null		null	null		null	null		null	null		-4.26E+00	4.13E-09	Down	-3.75E+00	9.85E-09	Down								
Unigene11282_All	2868	2.23	2.54	4.44	66.04	59.23	62.80	17.47	8.79	7.60	1.93E-01	3.95E-01		9.96E-01	2.38E-09		-1.57E-01	6.40E-06		-7.25E-02	8.16E-02		-9.91E-01	5.14E-44		-1.20E+00	1.58E-61	Down	Unigene11282_All//gi|67003911|gb|AY660845.1|//0.00E+00//cellulose synthase 3 [Eucalyptus grandis]	Unigene11282_All//0.00E+00//AT5G17420| IRX3 (IRREGULAR XYLEM 3); cellulose synthase	Unigene11282_All//0.00E+00//TC172422			GO:0009250//GO:0009536//GO:0009832//GO:0010395//GO:0016759//GO:0031224//GO:0042545//GO:0046914	nr +
Unigene112821_All	319	0.00	0.00	0.00	0.00	0.00	0.00	1.86	0.00	0.00	null	null		null	null		null	null		null	null		-1.09E+01	2.39E-04	Down	-1.09E+01	1.41E-04	Down	Unigene112821_All//gi|38230174|gb|AAR14182.1|//1.00E-53//Rho family GTPase [Fucus distichus]	Unigene112821_All//5.00E-45//AT4G35020| ARAC3 (ARABIDOPSIS RAC-LIKE 3); GTP binding / GTPase			ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity	GO:0032561//GO:0035556//GO:0044424	nr +
Unigene112822_All	319	0.00	0.00	0.00	0.00	0.00	0.00	2.65	0.13	0.12	null	null		null	null		null	null		null	null		-4.34E+00	4.55E-05	Down	-4.41E+00	2.37E-05	Down	Unigene112822_All//gi|159483149|ref|XP_001699625.1|//1.00E-07//membrane protein [Chlamydomonas reinhardtii] >gi|158272730|gb|ED098527.1| membrane protein [Chlamydomonas reinhardtii]	Unigene112822_All//9.00E-05//AT1G14880| unknown protein					nr +
Unigene112823_All	319	0.00	0.00	0.00	0.00	0.00	0.00	4.64	0.79	0.00	null	null		null	null		null	null		null	null		-2.56E+00	1.18E-05	Down	-1.22E+01	5.85E-11	Down								ESTscan +
Unigene112824_All	319	0.00	0.00	0.00	0.00	0.00	0.00	2.25	0.00	0.12	null	null		null	null		null	null		null	null		-1.11E+01	3.27E-05	Down	-4.17E+00	1.64E-04	Down								ESTscan +
Unigene112826_All	320	0.00	0.00	0.00	0.00	0.00	0.00	2.25	0.13	0.12	null	null		null	null		null	null		null	null		-4.10E+00	2.91E-04	Down	-4.17E+00	1.64E-04	Down								ESTscan -
Unigene112827_All	320	0.00	0.00	0.00	0.00	0.00	0.00	2.25	1.44	0.00	null	null		null	null		null	null		null	null		-6.45E-01	4.01E-01		-1.11E+01	1.78E-05	Down	Unigene112827_All//gi|75330275|sp|Q8LPC4.1|EF1A_PORYE//3.00E-47//RecName: Full=Elongation factor 1-alpha; Short=EF-1-alpha >gi|213201072|dbj|BAB96818.1| elongation factor 1-alpha [Porphyra yezoensis] >gi|317450924|dbj|BAC77640.1| elongation factor-1a [Porphyra yezoensis]	Unigene112827_All//1.00E-43//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene112827_All//4.00E-10//EX171978			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene112829_All	320	0.00	0.00	0.00	0.00	0.00	0.00	3.30	0.00	0.12	null	null		null	null		null	null		null	null		-1.17E+01	1.51E-07	Down	-4.73E+00	8.85E-07	Down								ESTscan +
Unigene112834_All	322	0.00	0.00	0.00	0.00	0.00	0.00	3.94	0.26	0.25	null	null		null	null		null	null		null	null		-3.92E+00	6.20E-07	Down	-3.99E+00	2.56E-07	Down	Unigene112834_All//sp|Q55CE0|MKCF_DICDI//1.00E-06//Probable serine/threonine-protein kinase mkcF OS=Dictyostelium discoideum GN=mkcF PE=3 SV=1						swissprot +
Unigene112835_All	322	0.00	0.00	0.00	0.00	0.00	0.00	1.97	0.00	0.00	null	null		null	null		null	null		null	null		-1.09E+01	1.23E-04	Down	-1.09E+01	7.11E-05	Down	Unigene112835_All//gi|14275758|emb|CAC40035.1|//4.00E-16//P-type ATPase [Hordeum vulgare]	Unigene112835_All//9.00E-15//AT3G22910| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA13)				GO:0006464//GO:0006812//GO:0016020//GO:0016301//GO:0032559//GO:0042625//GO:0043231//GO:0046873	nr +
Unigene112836_All	322	0.00	0.00	0.00	0.00	0.00	0.00	4.33	0.26	0.00	null	null		null	null		null	null		null	null		-4.06E+00	9.64E-08	Down	-1.21E+01	2.40E-10	Down								
Unigene112837_All	322	0.00	0.00	0.00	0.00	0.00	0.00	2.23	0.26	0.25	null	null		null	null		null	null		null	null		-3.10E+00	1.40E-03		-3.17E+00	8.09E-04	Down	Unigene112837_All//gi|301016726|dbj|BAJ11784.1|//2.00E-07//dehydration responsive protein [Corchorus olitorius]		Unigene112837_All//3.00E-38//TC171825				nr +
Unigene112838_All	322	0.00	0.00	0.00	0.00	0.00	0.00	2.10	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	6.34E-05	Down	-1.10E+01	3.56E-05	Down	Unigene112838_All//gi|297600719|ref|NP_001049719.2|//3.00E-45//Os03g0277300 [Oryza sativa Japonica Group] >gi|255674402|dbj|BAF11633.2| Os03g0277300 [Oryza sativa Japonica Group]	Unigene112838_All//8.00E-35//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene112838_All//4.00E-13//EX164279		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr +
Unigene11284_All	1162	0.77	1.31	1.10	1.76	3.67	3.58	5.09	2.73	7.23	7.73E-01	1.48E-01		5.23E-01	3.99E-01		1.06E+00	1.83E-04	Up	1.02E+00	6.01E-04	Up	-8.98E-01	3.86E-05		5.06E-01	3.54E-03		Unigene11284_All//gi|297797804|ref|XP_002866786.1|//1.00E-166//guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312622|gb|EFH43045.1| guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11284_All//2.00E-161//AT4G38200| guanine nucleotide exchange family protein	Unigene11284_All//1.00E-22//gi|13244082|gb|BE053450.2|BE053450		ko04626|Plant-pathogen interaction		nr -
Unigene112842_All	324	0.32	0.00	0.00	1.38	0.43	0.14	3.78	0.00	0.00	-8.34E+00	3.75E-01		-8.34E+00	3.97E-01		-1.70E+00	1.35E-01		-3.31E+00	2.84E-02		-1.19E+01	9.98E-09	Down	-1.19E+01	4.03E-09	Down	Unigene112842_All//gi|302141968|emb|CBI19171.3|//1.00E-06//unnamed protein product [Vitis vinifera]	Unigene112842_All//7.00E-07//AT1G78260| RNA recognition motif (RRM)-containing protein	Unigene112842_All//1.00E-158//gi|78336615|gb|DT556889.1|DT556889				nr +
Unigene112843_All	324	0.00	0.00	0.00	0.00	0.00	0.00	1.57	0.39	0.00	null	null		null	null		null	null		null	null		-2.02E+00	5.21E-02		-1.06E+01	5.54E-04	Down								ESTscan -
Unigene112844_All	324	0.00	0.00	0.00	0.00	0.00	0.00	3.13	1.16	0.00	null	null		null	null		null	null		null	null		-1.43E+00	2.36E-02		-1.16E+01	1.35E-07	Down	Unigene112844_All//gi|40809693|dbj|BAD07266.1|//2.00E-51//beta-tubulin [Opalina sp. Rs1]	Unigene112844_All//1.00E-49//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene112844_All//9.00E-08//TC147024		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene112849_All	325	0.00	0.00	0.00	0.92	0.42	0.00	2.60	2.31	0.37	null	null		null	null		-1.12E+00	4.24E-01		-9.84E+00	4.01E-02		-1.69E-01	7.99E-01		-2.82E+00	5.38E-04	Down								
Unigene112851_All	326	0.00	0.00	0.00	0.00	0.00	0.00	3.63	2.05	0.00	null	null		null	null		null	null		null	null		-8.24E-01	1.42E-01		-1.18E+01	8.15E-09	Down	Unigene112851_All//gi|145353890|ref|XP_001421232.1|//5.00E-43//Ribosomal protein L27aA, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901] >gi|145353965|ref|XP_001421267.1| Ribosomal protein L27aB, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901] >gi|144581469|gb|AB099525.1| Ribosomal protein L27aA, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901] >gi|144581504|gb|AB099560.1| Ribosomal protein L27aB, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901]	Unigene112851_All//3.00E-35//AT1G70600| structural constituent of ribosome	Unigene112851_All//6.00E-12//CD486164		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene112854_All	327	0.00	0.00	0.00	0.00	0.00	0.00	3.23	0.26	0.00	null	null		null	null		null	null		null	null		-3.66E+00	1.31E-05	Down	-1.17E+01	6.72E-08	Down								ESTscan -

Unigene112855_All	328	0.00	0.00	0.00	0.00	0.00	0.00	2.19	0.00	0.12	null	null		null	null		null	null		null	null		-1.11E+01	3.27E-05	Down	-4.17E+00	1.64E-04	Down	Unigene112855_All//gi|192910898|gb|ACF06557.1|//1.00E-12//translationally controlled tumor protein [Elaeis guineensis]	Unigene112855_All//2.00E-13//AT3G05540| INVOLVED IN: biological_process unknown; LOCATED IN: cytoplasm; CONTAINS InterPro DOMAIN/s: Translationally controlled tumour protein (InterPro:IPR018105), Translationally controlled tumour-associated TCTP (InterPro:IPR001983), Mss4/translationally controlled tumour-associated TCTP (InterPro:IPR011323), Translationally controlled tumour protein, conserved site (InterPro:IPR018103), Mss4-like (InterPro:IPR011057); BEST Arabidopsis thaliana protein match is: TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN) (TAIR:AT3G16640.1); Has 640 Blast hits to 640 proteins in 231 species: Archae - 0; Bacteria - 0; Metazoa - 343; Fungi - 110; Plants - 105; Viruses - 0; Other Eukaryotes - 82 (source: NCBI BLink).					nr +
Unigene112857_All	328	0.00	0.00	0.00	0.00	0.00	0.28	1.29	1.78	7.89	null	null		null	null		null	null		8.11E+00	4.80E-01		4.69E-01	6.13E-01		2.61E+00	8.54E-10	Up			Unigene112857_All//4.00E-07//BQ402741				
Unigene112859_All	328	0.00	0.00	0.00	0.00	0.00	0.00	4.64	1.66	1.09	null	null		null	null		null	null		null	null		-1.49E+00	2.91E-03		-2.09E+00	6.46E-05	Down	Unigene112859_All//gi|297811659|ref|XP_002873713.1|//7.00E-41//40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata] >gi|297319550|gb|EFH49972.1| 40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata]	Unigene112859_All//7.00E-42//AT5G15200| 40S ribosomal protein S9 (RPS9B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr +
Unigene112860_All	329	0.00	0.00	0.00	0.00	0.00	0.00	2.06	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	6.34E-05	Down	-1.10E+01	3.56E-05	Down	Unigene112860_All//gi|115445077|ref|NP_001046318.1|//2.00E-17//Os02g0220600 [Oryza sativa Japonica Group] >gi|13626515|sp|Q9ZR17.1|EF1G1_ORYSJ RecName: Full=Elongation factor 1-gamma 1; Short=EF-1-gamma 1; AltName: Full=eEF-1B gamma 1 >gi|3868758|dbj|BAA34206.1| elongation factor 1B gamma [Oryza sativa] >gi|46806491|dbj|BAD17615.1| Elongation factor 1-gamma [Oryza sativa Japonica Group] >gi|113535849|dbj|BAF08232.1| Os02g0220600 [Oryza sativa Japonica Group]	Unigene112860_All//1.00E-07//AT1G57720| elongation factor 1B-gamma, putative / eEF-1B gamma, putative				GO:0006412	nr -
Unigene112861_All	330	0.00	0.00	0.00	0.00	0.00	0.00	2.43	0.76	0.00	null	null		null	null		null	null		null	null		-1.68E+00	2.46E-02		-1.12E+01	4.43E-06	Down	Unigene112861_All//gi|297842161|ref|XP_002888962.1|//3.00E-25//60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata] >gi|297334803|gb|EFH65221.1| 60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata]	Unigene112861_All//7.00E-26//AT1G74060| 60S ribosomal protein L6 (RPL6B)			ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene112862_All	330	20.45	7.06	21.46	1.36	0.94	6.30	0.64	0.25	0.24	-1.53E+00	3.57E-10	Down	6.95E-02	7.70E-01		-5.33E-01	5.96E-01		2.21E+00	1.30E-05	Up	-1.34E+00	4.30E-01		-1.41E+00	3.80E-01		Unigene112862_All//gi|297794051|ref|XP_002864910.1|//3.00E-15//C/VIF2 [Arabidopsis lyrata subsp. lyrata] >gi|297310745|gb|EFH41169.1| C/VIF2 [Arabidopsis lyrata subsp. lyrata]	Unigene112862_All//5.00E-15//AT5G44620| C/VIF2 (CELL WALL / VACUOLAR INHIBITOR OF FRUCTOSIDASE 2); enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor	Unigene112862_All//7.00E-89//TC166594			GO:0004091//GO:0004857//GO:0031410	nr -
Unigene112863_All	330	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.00	0.00	null	null		null	null		null	null		null	null		-1.10E+01	6.34E-05	Down	-1.10E+01	3.56E-05	Down			Unigene112863_All//3.00E-63//TC161176					ESTscan -
Unigene112865_All	331	0.00	0.00	0.00	0.00	0.00	0.00	2.17	0.38	0.00	null	null		null	null		null	null		null	null		-2.52E+00	4.69E-03		-1.11E+01	1.78E-05	Down	Unigene112865_All//gi|2500261|sp|P93099.1|RL13A_CYAPA//2.00E-23//RecName: Full=60S ribosomal protein L13a >gi|1743007|emb|CAA71090.1| ribosomal protein L13a [Cyanophora paradoxa]	Unigene112865_All//2.00E-19//AT3G07110| 60S ribosomal protein L13A (RPL13aA)			ko03010|Ribosome	GO:0009536//GO:0015934//GO:0031981	nr -
Unigene112866_All	331	0.00	0.00	0.00	0.75	0.62	0.14	2.04	0.00	0.24	null	null		null	null		-2.70E-01	8.23E-01		-2.46E+00	2.24E-01		-1.10E+01	6.34E-05	Down	-3.09E+00	1.45E-03		Unigene112866_All//gi|18411885|ref|NP_565175.1|//1.00E-31//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|21537200|gb|AAM61541.1| RNA recognition motif-containing protein SEB-4 [Arabidopsis thaliana] >gi|124300976|gb|ABN04740.1| At1g78260 [Arabidopsis thaliana]	Unigene112866_All//6.00E-22//AT1G22330| RNA binding / nucleic acid binding / nucleotide binding	Unigene112866_All//0.00E+00//EE592791			GO:0003676	nr +
Unigene112868_All	331	2.37	0.00	0.00	0.30	0.00	0.00	2.94	0.38	0.72	-1.12E+01	1.09E-04	Down	-1.12E+01	2.22E-04	Down	-8.23E+00	3.16E-01		-8.23E+00	4.04E-01		-2.96E+00	1.89E-04	Down	-2.02E+00	2.47E-03		Unigene112868_All//gi|15219665|ref|NP_171911.1|//2.00E-29//C2 domain-containing protein [Arabidopsis thaliana] >gi|3142295|gb|AAC16746.1| Strong similarity to phosphoribosylanthranilate transferase gb|D86180 from Pisum sativum [Arabidopsis thaliana]	Unigene112868_All//9.00E-31//AT1G04150| C2 domain-containing protein	Unigene112868_All//3.00E-180//gi|109832103|gb|DW230662.1|DW230662			GO:0016740//GO:0044464	nr -
Unigene112869_All	331	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.25	0.00	null	null		null	null		null	null		null	null		-3.02E+00	2.43E-03		-1.10E+01	3.56E-05	Down	Unigene112869_All//gi|58801147|dbj|BAD89506.1|//3.00E-52//beta-tubulin [Protopeplina japonica]	Unigene112869_All//3.00E-51//AT1G20010| TUB5; structural constituent of cytoskeleton	Unigene112869_All//1.00E-16//gi|13350074|gb|BG440423.1|BG440423		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene112870_All	331	1.11	0.00	1.61	0.00	0.62	0.27	3.19	1.01	0.60	-1.01E+01	1.97E-02		5.40E-01	6.10E-01		9.29E+00	1.57E-01		8.09E+00	4.80E-01		-1.66E+00	8.55E-03		-2.41E+00	3.46E-04	Down								
Unigene112874_All	333	0.00	0.00	0.00	0.00	0.00	0.00	1.65	0.00	0.00	null	null		null	null		null	null		null	null		-1.07E+01	4.61E-04	Down	-1.07E+01	2.81E-04	Down	Unigene112874_All//gi|224054418|ref|XP_002298250.1|//6.00E-36//histidine phosphotransfer protein [Populus trichocarpa] >gi|222845508|gb|EEE83055.1| histidine phosphotransfer protein [Populus trichocarpa]	Unigene112874_All//1.00E-30//AT1G80100| AHP6 (ARABIDOPSIS HISTIDINE PHOSPHOTRANSFER PROTEIN 6); histidine phosphotransfer kinase/ transferase, transferring phosphorus-containing groups				GO:0004871//GO:0008152//GO:0009736//GO:0010087//GO:0016628//GO:0016740//GO:0023060//GO:0043231	nr +
Unigene112875_All	333	0.00	0.00	0.00	0.00	0.00	0.00	3.17	0.13	0.96	null	null		null	null		null	null		null	null		-4.66E+00	1.94E-06	Down	-1.73E+00	4.76E-03		Unigene112875_All//gi|297838323|ref|XP_002887043.1|//2.00E-21//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332884|gb|EFH63302.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene112875_All//9.00E-23//AT1G66470| basic helix-loop-helix (bHLH) family protein		bHLH		GO:0010468//GO:0043231	nr -
Unigene112876_All	333	0.00	0.00	0.00	0.00	0.00	0.27	2.67	0.25	0.00	null	null		null	null		null	null		8.08E+00	4.80E-01		-3.41E+00	1.40E-04	Down	-1.14E+01	1.10E-06	Down	Unigene112876_All//gi|15231435|ref|NP_187383.1|//1.00E-23//GTP cyclohydrolase I [Arabidopsis thaliana] >gi|6642638|gb|AAF20219.1|AC012395_6 GTP cyclohydrolase I [Arabidopsis thaliana] >gi|20466832|gb|AAM20733.1| GTP cyclohydrolase I [Arabidopsis thaliana] >gi|30387557|gb|AAP31944.1| At3g07270 [Arabidopsis thaliana]	Unigene112876_All//6.00E-25//AT3G07270| GTP cyclohydrolase I	Unigene112876_All//4.00E-38//TC145472		ko00790|Folate biosynthesis	GO:0003933//GO:0009396//GO:0044424	nr +
Unigene112878_All	334	0.00	0.00	0.00	0.00	0.00	0.00	1.77	0.50	0.00	null	null		null	null		null	null		null	null		-1.82E+00	4.72E-02		-1.08E+01	1.41E-04	Down	Unigene112878_All//gi|226505998|ref|NP_001146929.1|//4.00E-39//60S ribosomal protein L7a [Zea mays] >gi|195605318|gb|ACG24489.1| 60S ribosomal protein L7a [Zea mays]	Unigene112878_All//7.00E-36//AT2G47610| 60S ribosomal protein L7A (RPL7aA)			ko03010|Ribosome	GO:0022613//GO:0030529//GO:0046914	nr -
Unigene11288_All	1363	3.72	2.23	3.52	6.51	6.82	4.71	7.60	4.17	3.57	-7.39E-01	5.36E-03		-8.27E-02	7.70E-01		6.84E-02	7.99E-01		-4.67E-01	1.63E-02		-8.66E-01	6.20E-08		-1.09E+00	1.20E-11	Down	Unigene11288_All//gi|58342485|gb|AAD53877.1|AF175124_1//1.00E-175//SINAH1 protein [Gossypium hirsutum]	Unigene11288_All//2.00E-156//AT4G27880| seven in absentia (SINA) family protein	Unigene11288_All//0.00E+00//TC132499		ko04120|Ubiquitin mediated proteolysis	GO:0019787//GO:0019941//GO:0032446//GO:0032501//GO:0043231//GO:0046914	nr +
Unigene112883_All	336	0.00	0.00	0.00	0.00	0.10	0.00	3.52	0.12	0.47	null	null		null	null		6.68E+00	8.36E-01		null	null		-4.82E+00	2.84E-07	Down	-2.89E+00	2.03E-05	Down	Unigene112883_All//gi|113205247|gb|AAT39965.2|//2.00E-06//hypothetical protein SDM1_29t00005 [Solanum demissum]		Unigene112883_All//1.00E-161//FL577203				nr -
Unigene112884_All	336	0.00	0.00	0.00	0.00	0.00	0.00	4.91	0.37	0.00	null	null		null	null		null	null		null	null		-3.72E+00	1.53E-08	Down	-1.23E+01	3.45E-12	Down								ESTscan -
Unigene112885_All	337	0.00	0.00	0.00	0.00	0.00	0.00	3.14	0.12	0.00	null	null		null	null		null	null		null	null		-4.66E+00	1.94E-06	Down	-1.16E+01	6.72E-08	Down	Unigene112885_All//gi|20340229|gb|AAM19701.1|AF499714_1//5.00E-40//14-3-3-like protein [Thellungiella halophila]	Unigene112885_All//6.00E-41//AT4G09000| 14-3-3-like protein GF14 chi / general regulatory factor 1 (GRF1)	Unigene112885_All//4.00E-10//ES846360			GO:0005576//GO:0009536//GO:0010038//GO:0016020//GO:0051219	nr +
Unigene112886_All	337	0.00	0.00	0.00	0.00	0.00	0.00	3.26	0.37	0.00	null	null		null	null		null	null		null	null		-3.13E+00	3.47E-05	Down	-1.17E+01	3.33E-08	Down	Unigene112886_All//gi|15222073|ref|NP_175349.1|//7.00E-26//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565178|sp|Q6NQG7.1|ATL1L_ARATH RecName: Full=RING-H2 finger protein ATL1L >gi|34365601|gb|AAQ65112.1| At1g49230 [Arabidopsis thaliana]	Unigene112886_All//3.00E-27//AT1G49230| zinc finger (C3HC4-type RING finger) family protein	Unigene112886_All//8.00E-98//gi|109874979|gb|DW503953.1|DW503953			GO:0019787//GO:0032446//GO:0046872	nr -
Unigene112888_All	338	0.00	0.00	0.00	0.00	0.00	0.00	3.00	1.98	0.00	null	null		null	null		null	null		null	null		-6.02E-01	3.45E-01		-1.16E+01	1.35E-07	Down								ESTscan -
Unigene112894_All	339	0.00	0.00	0.00	0.00	0.10	0.00	2.37	0.00	0.00	null	null		null	null		6.67E+00	8.36E-01		null	null		-1.12E+01	8.58E-06	Down	-1.12E+01	4.43E-06	Down	Unigene112894_All//gi|297804022|ref|XP_002869895.1|//2.00E-33//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315731|gb|EFH46154.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene112894_All//8.00E-35//AT4G21300| pentatricopeptide (PPR) repeat-containing protein				GO:0043231	nr +
Unigene112895_All	339	0.00	0.00	0.00	0.00	0.00	0.00	2.74	0.74	0.00	null	null		null	null		null	null		null	null		-1.89E+00	6.92E-03		-1.14E+01	5.48E-07	Down	Unigene112895_All//gi|301111866|ref|XP_002905012.1|//3.00E-29//major vault protein [Phytophthora infestans T30-4] >gi|262096342|gb|EEY53394.1| major vault protein [Phytophthora infestans T30-4]						nr -
Unigene112896_All	340	0.00	0.00	0.00	0.00	0.00	0.00	1.74	0.00	0.00	null	null		null	null		null	null		null	null		-1.08E+01	2.39E-04	Down	-1.08E+01	1.41E-04	Down								

Unigene112898_All	341	0.15	0.00	0.00	0.29	0.50	0.26	5.83	1.10	0.35	-7.26E+00	6.17E-01			-7.26E+00	6.30E-01			7.89E-01	7.71E-01			-1.42E-01	9.52E-01			-2.40E+00	6.76E-07	Down	-4.06E+00	3.04E-11	Down			Unigene112898_All//4.00E-13//gi|164295307|gb|ES844568.1|ES844568				
Unigene112899_All	341	0.00	0.00	0.00	0.15	0.10	0.13	3.97	1.59	1.05	null	null			null	null			-5.33E-01	8.27E-01			-1.42E-01	9.55E-01			-1.32E+00	1.25E-02		-1.92E+00	4.37E-04	Down			Unigene112899_All//3.00E-14//gi|21103053|gb|BQ415366.1|BQ415366				
Unigene112900_All	342	0.00	0.00	0.00	0.00	0.00	0.00	4.82	0.00	0.23	null	null			null	null			null	null			null	null			-1.22E+01	1.09E-11	Down	-4.37E+00	7.28E-10	Down	Unigene112900_All//gi|224140765|ref|XP_002323749.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222866751|gb|EEF03882.1| predicted protein [Populus trichocarpa]		Unigene112900_All//5.00E-142//CA992640				nr -
Unigene112901_All	342	0.00	0.00	0.00	0.00	0.00	0.00	3.09	0.12	0.35	null	null			null	null			null	null			null	null			-4.66E+00	1.94E-06	Down	-3.14E+00	2.97E-05	Down	Unigene112901_All//gi|164652938|gb|ABY65002.1|//7.00E-31//14-3-3c protein [Gossypium hirsutum]	Unigene112901_All//2.00E-26//AT2G42590| GRF9 (GENERAL REGULATORY FACTOR 9); calcium ion binding / protein binding / protein phosphorylated amino acid binding				GO:0009532//GO:0016020//GO:0046872	nr -
Unigene112902_All	343	0.00	0.00	0.00	0.00	0.00	0.00	2.47	1.58	0.00	null	null			null	null			null	null			null	null			-6.38E-01	3.70E-01		-1.13E+01	2.21E-06	Down							
Unigene112903_All	343	0.00	0.00	0.00	0.00	0.00	0.00	1.97	0.24	0.00	null	null			null	null			null	null			null	null			-3.02E+00	2.43E-03		-1.09E+01	3.56E-05	Down							
Unigene112904_All	344	0.00	0.00	0.00	0.00	0.00	0.00	1.60	0.00	0.00	null	null			null	null			null	null			null	null			-1.06E+01	4.61E-04	Down	-1.06E+01	2.81E-04	Down							
Unigene112906_All	344	0.46	0.00	0.00	0.00	0.40	0.00	2.83	0.97	0.46	-8.83E+00	2.16E-01			-8.83E+00	2.46E-01			8.65E+00	3.20E-01			null	null			-1.34E+00	1.90E-02		-2.61E+00	3.35E-04	Down							
Unigene112907_All	346	0.00	0.29	0.00	0.29	0.90	0.00	3.30	0.72	1.61	8.19E+00	3.90E-01			null	null			1.64E+00	3.22E-01			-8.17E+00	4.04E-01			-2.19E+00	6.84E-04	Down	-1.03E+00	5.95E-02							
Unigene112908_All	346	0.00	0.00	0.00	0.72	0.70	0.00	2.08	0.48	0.23	null	null			null	null			-4.73E-02	9.52E-01			-9.49E+00	7.35E-02			-2.10E+00	1.25E-02		-3.17E+00	8.09E-04	Down							
Unigene112909_All	346	0.00	0.00	0.00	0.00	0.00	0.00	2.69	0.00	0.00	null	null			null	null			null	null			null	null			-1.14E+01	1.15E-06	Down	-1.14E+01	5.48E-07	Down							ESTscan -
Unigene112910_All	346	0.00	0.00	0.00	0.00	0.00	0.00	10.39	0.00	0.92	null	null			null	null			null	null			null	null			-1.33E+01	2.02E-25	Down	-3.50E+00	9.26E-18	Down	Unigene112910_All//gi|115480900|ref|NP_001064043.1|//2.00E-16//Os10g0113000 [Oryza sativa Japonica Group] >gi|73621239|sp|Q7G764.1|NAD01_ORYSJ RecName: Full=Probable NAD(P)H-dependent oxidoreductase 1 >gi|14029046|gb|AAK52587.1|AC07968 5_18 Putative NADPH-dependent oxidoreductase [Oryza sativa Japonica Group] >gi|21263197|gb|AAM44874.1|AC09869 4_13 Putative NADPH-dependent oxidoreductase [Oryza sativa Japonica Group] >gi|113638652|dbj|BAF25957.1| Os10g0113000 [Oryza sativa Japonica Group]	Unigene112910_All//5.00E-12//AT1G59960| aldo/keto reductase, putative	Unigene112910_All//8.00E-67//BQ410950		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism	GO:0008152//GO:0016747	nr +
Unigene112913_All	347	0.00	0.00	0.00	0.14	0.20	1.17	2.56	0.00	0.69	null	null			null	null			4.67E-01	9.60E-01			3.03E+00	6.03E-02			-1.13E+01	2.24E-06	Down	-1.89E+00	6.34E-03	Down	Unigene112913_All//gi|297609225|ref|NP_001063856.2|//1.00E-15//Os09g0321200 [Oryza sativa Japonica Group] >gi|255678772|dbj|BAF24770.2| Os09g0321200 [Oryza sativa Japonica Group]					GO:0046872	nr -
Unigene112914_All	347	0.00	0.00	0.00	0.00	0.00	0.00	5.00	0.36	0.46	null	null			null	null			null	null			null	null			-3.79E+00	4.50E-09	Down	-3.44E+00	8.41E-09	Down	Unigene112914_All//sp|O15162|PLS1_HUMAN//3.00E-06//Phospholipid scramblase 1 OS=Homo sapiens GN=PLSCR1 PE=1 SV=1						swissprot +
Unigene112915_All	348	0.00	0.00	0.00	0.00	0.00	0.00	2.55	1.08	0.00	null	null			null	null			null	null			null	null			-1.24E+00	6.79E-02		-1.13E+01	1.10E-06	Down	Unigene112915_All//gi|195621288|gb|ACG32474.1|//2.00E-27//eukaryotic translation initiation factor 5A-1/2 [Zea mays]	Unigene112915_All//6.00E-27//AT1G26630| FBR12 (FUMONISIN B1-RESISTANT12); translation initiation factor				GO:0006448//GO:0006449//GO:0006952//GO:0008135//GO:0010038//GO:0012501//GO:0018205//GO:0043021//GO:0043231//GO:0051707	nr -
Unigene112916_All	348	0.00	0.00	0.00	0.00	0.00	0.00	2.55	0.60	0.11	null	null			null	null			null	null			null	null			-2.09E+00	4.71E-03		-4.48E+00	1.23E-05	Down							ESTscan +
Unigene112918_All	349	0.00	0.00	0.00	0.00	0.00	0.00	3.39	1.68	0.68	null	null			null	null			null	null			null	null			-1.02E+00	7.15E-02		-2.31E+00	2.04E-04	Down							
Unigene112919_All	349	0.00	0.00	0.00	0.00	0.00	0.00	2.79	0.00	0.00	null	null			null	null			null	null			null	null			-1.14E+01	5.83E-07	Down	-1.14E+01	2.72E-07	Down	Unigene112919_All//gi|298715853|emb|CBJ28318.1|//5.00E-06//hypothetical protein [Ectocarpus siliculosus]						nr +
Unigene112920_All	351	0.00	0.00	0.00	0.00	0.00	0.00	3.61	1.91	0.23	null	null			null	null			null	null			null	null			-9.24E-01	8.68E-02		-3.99E+00	2.56E-07	Down	Unigene112920_All//gi|145324164|ref|NP_001077671.1|//3.00E-38//ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome [Arabidopsis thaliana]	Unigene112920_All//1.00E-39//AT1G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	Unigene112920_All//4.00E-10//gi|11200269|gb|BF269274.1|BF269274		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0019219//GO:0003312//GO:0031981	nr -
Unigene112921_All	351	0.00	0.00	0.00	0.00	0.00	0.00	2.77	0.00	0.34	null	null			null	null			null	null			null	null			-1.14E+01	5.83E-07	Down	-3.02E+00	9.61E-05	Down							ESTscan -
Unigene112923_All	351	0.00	1.30	2.12	0.43	0.10	0.00	1.93	1.07	0.45	1.03E+01	7.44E-03		Up	-2.12E+00	3.28E-04		Up	-2.12E+00	3.87E-01			-8.73E+00	2.34E-01			-8.47E-01	2.88E-01		-2.09E+00	1.27E-02				Unigene112923_All//1.00E-22//TC145384				
Unigene112925_All	353	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.83	0.11	null	null			null	null			null	null			null	null			-1.30E+00	9.45E-02		-4.17E+00	1.64E-04	Down	Unigene112925_All//gi|192910698|gb|ACF06457.1|//6.00E-22//60S ribosomal protein L35 [Elaeis guineensis]	Unigene112925_All//7.00E-18//AT5G02610| 60S ribosomal protein L35 (RPL35D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr -
Unigene112926_All	353	97.97	67.89	51.89	94.27	69.85	20.21	63.24	13.14	29.46	-5.29E-01	6.34E-09			-9.17E-01	2.99E-21			-4.33E-01	4.22E-07			-2.22E+00	6.46E-85		Down	-2.27E+00	9.71E-66	Down	-1.10E+00	1.94E-24	Down	Unigene112926_All//gi|87241442|gb|ABD33300.1|//5.00E-11//Gibberellin regulated protein [Medicago truncatula]	Unigene112926_All//1.00E-11//AT5G15230| GASA4 (GAST1 PROTEIN HOMOLOG 4)	Unigene112926_All//8.00E-135//TC175750				nr +
Unigene112293_All	1005	2.60	3.28	2.65	3.57	2.54	2.20	5.68	2.66	3.29	3.32E-01	3.58E-01			2.54E-02	9.67E-01			-4.93E-01	1.26E-01			-6.97E-01	3.23E-02			-1.09E+00	1.39E-06	Down	-7.88E-01	2.56E-04		Unigene112293_All//gi|28950779|gb|AA063313.1|//3.00E-98//At4g16060 [Arabidopsis thaliana]	Unigene112293_All//5.00E-96//AT4G16060| unknown protein	Unigene112293_All//0.00E+00//TC177353			GO:0043231	nr -
Unigene112930_All	354	0.00	0.00	0.00	0.00	0.00	0.00	4.18	0.47	0.00	null	null			null	null			null	null			null	null			-3.15E+00	8.54E-07	Down	-1.20E+01	5.85E-11	Down			Unigene112930_All//7.00E-15//DR455073				
Unigene112932_All	355	0.00	0.00	0.00	0.00	0.00	0.00	3.57	0.00	0.22	null	null			null	null			null	null			null	null			-1.18E+01	5.06E-09	Down	-3.99E+00	2.56E-07	Down							ESTscan -
Unigene112933_All	355	0.29	0.00	0.00	1.12	0.49	0.51	1.67	0.35	0.00	-8.20E+00	3.75E-01			-8.20E+00	3.97E-01			-1.21E+00	3.14E-01			-1.14E+00	3.80E-01			-2.24E+00	2.07E-02		-1.07E+01	1.41E-04	Down							
Unigene112935_All	356	0.00	0.00	0.00	0.00	0.00	0.00	2.73	1.41	0.45	null	null			null	null			null	null			null	null			-9.55E-01	1.35E-01		-2.61E+00	3.35E-04	Down							
Unigene112936_All	357	0.00	0.00	0.00	0.00	0.00	0.00	5.57	1.17	0.78	null	null			null	null			null	null			null	null			-2.25E+00	1.94E-06	Down	-2.83E+00	1.91E-08	Down							
Unigene112938_All	357	0.00	0.00	0.00	0.00	0.00	0.00	1.78	0.82	0.00	null	null			null	null			null	null			null	null			-1.12E+00	1.80E-01		-1.08E+01	7.11E-05	Down			Unigene112938_All//3.00E-08//TC178941				ESTscan -
Unigene112939_All	358	0.00	0.00	0.00	0.28	0.00	0.00	3.07	0.35	0.89	null	null			null	null			-8.12E+00	3.16E-01			-8.12E+00	4.04E-01			-3.13E+00	3.47E-05	Down	-1.79E+00	3.08E-03		Unigene112939_All//gi|187940311|gb|ACD39386.1|//2.00E-53//NAC domain protein [Glycine max]	Unigene112939_All//3.00E-49//AT1G26870| FEZ (FEZ); transcription factor	Unigene112939_All//1.00E-10//DW224083	NAC		GO:0001071//GO:0003676//GO:0009725//GO:0009786//GO:0010468//GO:0017145//GO:0043231//GO:0048856	nr +
Unigene112294_All	1452	0.86	2.65	0.62	3.47	3.58	3.11	2.42	1.76	2.66	1.62E+00	1.62E-06		Up	-4.72E-01	4.42E-01			4.75E-02	8.80E-01			-1.56E-01	6.38E-01			-4.61E-01	1.29E-01		1.39E-01	6.43E-01		Unigene112294_All//gi|22328699|ref|NP_567482.2|//1.00E-172//lipase class 3 family protein [Arabidopsis thaliana]	Unigene112294_All//2.00E-142//AT4G16070| lipase class 3 family protein	Unigene112294_All//0.00E+00//gi|78338930|gb|DT559204.1|DT559204			GO:0004091//GO:0006629	nr +
Unigene112940_All	358	0.00	0.00	0.00	0.00	0.00	0.00	2.36	0.35	0.00	null	null			null	null			null	null			null	null			-2.75E+00	9.73E-04	Down	-1.12E+01	2.21E-06	Down	Unigene112940_All//gi|301111414|ref|XP_002904786.1|//1.00E-41//ribosomal protein L27 [Phytophthora infestans T30-4] >gi|66270187|gb|AAY43423.1| ribosomal protein L27 [Phytophthora infestans] >gi|262095116|gb|EEY53168.1| ribosomal protein L27 [Phytophthora infestans T30-4]	Unigene112940_All//2.00E-39//AT1G70600| structural constituent of ribosome	Unigene112940_All//7.00E-12//DW504561		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene112941_All	358	1.02	1.13	0.60	1.11	0.19	0.00	4.96	1.17	0.89	1.47E-01	8.98E-01			-7.82E-01	5.53E-01			-2.53E+00	5.80E-02			-1.01E+01	1.11E-02			-2.09E+00	2.21E-05	Down	-2.48E+00	1.05E-06	Down	Unigene112941_All//gi|31559433|emb|CAD35533.1|//5.00E-14//major latex protein homologue [Datisca glomerata]	Unigene112941_All//7.00E-15//AT1G23120| major latex protein-related / MLP-related	Unigene112941_All//0.00E+00//gi|109883067|gb|DW512037.1|DW512037				nr +
Unigene112944_All	360	0.00	0.00	0.30	0.00	0.00	0.00	3.76	0.58	0.33	null	null			8.21E+00	4.01E-01			null	null			null	null			-2.69E+00	1.77E-05	Down	-3.50E+00	4.24E-07	Down	Unigene112944_All//gi|119507465|dbj|BAF42040.1|//2.00E-52//pectin methylesterase 3 [Pyrus communis]	Unigene112944_All//1.00E-49//AT4G02330| ATPMEPCRB; pectinesterase	Unigene112944_All//3.00E-60//TC138774		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0030234//GO:0071555	nr -
Unigene112947_All	362	0.00	0.00	0.00	0.00	0.00	0.00	2.57	0.00	0.00	null	null			null	null			null	null			null	null			-1.13E+01	1.14E-06	Down	-1.13E+01	5.48E-07	Down							ESTscan -
Unigene112949_All	362	0.00	0.00	0.00	0.00	0.00	0.00	3.15	0.35	0.00	null	null			null	null			null	null			null	null			-3.19E+00	1.96E-05	Down	-1.16E+01	1.65E-08	Down	Unigene112949_All//gi|226510343|ref|NP_001151730.1|//4.00E-46//40S ribosomal protein S15 [Zea mays] >gi|195649383|gb|ACG44159.1| 40S ribosomal protein S15 [Zea mays]	Unigene112949_All//6.00E-36//AT5G09500| 40S ribosomal protein S15 (RPS15C)	Unigene112949_All//2.00E-09//BG444152		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene112295_All	759	0.69	1.13	1.05	0.98	1.54	2.26	2.73	0.72	1.47	7.19E-01	3.48E-01			6.11E-01	4.41E-01			6.48E-01	3.26E-01			1.20E+00	1.97E-02			-1.93E+00	1.21E-05	Down	-8.93E-01	2.02E-02		Unigene112295_All//gi|115463405|ref|NP_001055302.1|//8.00E-21//Os05g0358400 [Oryza sativa Japonica Group] >gi|113578853|dbj|BAF17216.1| Os05g0358400 [Oryza sativa Japonica Group]	Unigene112295_All//1.00E-16//AT4G16060| unknown protein	Unigene112295_All//3.00E-90//TC177353			GO:0043231	nr -
Unigene112950_All	365	0.00	0.69	1.02	0.55	0.19	0.87	3.01	0.69	0.22	9.44E+00	7.88E-02			1.00E+01	2.50E-02			-1.53E+00	4.16E-01			6.66E-01	6.48E-01			-2.13E+00	1.11E-03		-3.79E+00	3.27E-06	Down			Unigene112950_All//4.00E-07//TC164828				
Unigene112952_All	368	0.00	0.00	0.00	0.54	0.00	0.00	1.84	0.00	0.22	null	null			null	null			-9.08E+00	8.46E-02			-9.08E+00	1.34E-01			-1.08E+01	6.34E-05	Down	-3.09E+00	1.45E-03		Unigene112952_All//gi|224078614|ref|XP_002305575.1|//6.00E-64//predicted protein [Populus trichocarpa] >gi|222848539|gb|EEE86086.1| predicted protein [Populus trichocarpa]						nr -
Unigene112953_All	368	0.28	0.00	0.00	0.27	0.09	0.12	2.30	0.11	0.87	-8.15E+00	3.75E-01			-8.15E+00	3.97E-01			-1.53E+00	5.88E-01			-1.14E+00	6.78E-01			-4.34E+00	4.55E-05	Down	-1.41E+00	3.70E-02		Unigene112953_All//gi|15233503|ref|NP_193195.1|//1.00E-30//emb2739 (embryo defective 2739) [Arabidopsis thaliana]	Unigene112953_All//5.00E-32//AT4G14590| emb2739 (embryo defective 2739)	Unigene112953_All//3.00E-91//ES802105			GO:0003006	nr -
Unigene112954_All	369	0.00	0.00	0.00	0.00	0.00	0.00	4.93	1.25	0.43	null	null			null	null			null	null			null	null			-1.98E+00	3.39E-05	Down	-3.51E+00	2.43E-09	Down							
Unigene112955_All	369	0.43	0.82	0.29	1.49	0.65	0.61	3.21	0.57	1.30	9.54E-01	5.04E-01			-5.60E-01	7.76E-01			-1.18E+00	2.25E-01			-1.28E+00	2.24E-01			-2.50E+00	1.47E-04	Down	-1.31E+00	1.69E-02		Unigene112955_All//gi|22327146|ref|NP_198205.2|//2.00E-55//FRS10 (FAR1-related sequence 10); zinc ion binding [Arabidopsis thaliana] >gi|257051024|sp|Q9LKR4.2|FRS10_ARATH RecName: Full=Putative protein FAR1-RELATED SEQUENCE 10	Unigene112955_All//1.00E-56//AT5G28530| FRS10 (FAR1-related sequence 10); zinc ion binding				GO:0046914	nr +
Unigene112958_All	371	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.11	0.00	null	null			null	null			null	null			null	null			-4.19E+00	1.57E-04	Down	-1.10E+01	8.88E-06	Down	Unigene112958_All//gi|116057156|emb|CAL51583.1|//1.00E-36//ribosomal L9-like protein (YSS) [Ostreococcus tauri]	Unigene112958_All//3.00E-33//AT1G33140| PGY2 (PIGGYBACK2); structural constituent of ribosome	Unigene112958_All//5.00E-13//TC152661		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene112959_All	372	0.14	0.00	0.00	0.00	0.37	0.73	2.73	1.12	0.54	-7.14E+00	6.17E-01			-7.14E+00	6.30E-01			8.53E+00	3.20E-01			9.51E+00	7.04E-02			-1.28E+00	4.06E-02		-2.35E+00	5.84E-04	Down							
Unigene112961_All	373	0.00	0.00	0.00	0.00	0.46	0.00	5.10	0.78	0.85	null	null			null	null			8.85E+00	2.27E-01			null	null			-2.70E+00	1.87E-07	Down	-2.58E+00	2.06E-07	Down			Unigene112961_All//3.00E-125//TC172393				
Unigene112962_All	373	0.00	0.00	0.00	0.40	0.46	0.00	3.51	0.90	0.75	null	null			null	null			2.04E-01	9.50E-01			-8.65E+00	2.34E-01			-1.97E+00	6.34E-04	Down	-2.23E+00	1.19E-04	Down							
Unigene112963_All	375	0.00	0.00	0.57	0.00	0.00	0.00	2.48	0.22	0.00	null	null			9.15E+00	1.42E-01			null	null			null	null			-3.48E+00	7.79E-05	Down	-1.13E+01	5.48E-07	Down	Unigene112963_All//gi|225461437|ref|XP_002282367.1|//1.00E-08//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene112963_All//3.00E-73//TC147141				nr +
Unigene112964_All	375	0.14	0.27	0.00	0.53	0.73	0.60	2.03	0.67	0.21	9.54E-01	7.27E-01			-7.12E+00	6.30E-01			4.67E-01	8.17E-01			1.80E-01	9.35E-01			-1.60E+00	3.70E-02		-3.26E+00	4.48E-04	Down	Unigene112964_All//gi|115461308|ref|NP_001054254.1|//2.00E-24//Os04g0676200 (Oryza sativa Japonica Group) >gi|113565825|dbj|BAF16168.1| Os04g0676200 [Oryza sativa Japonica Group]	Unigene112964_All//4.00E-16//AT1G03540| pentatricopeptide (PPR) repeat-containing protein				GO:0043231	nr +
Unigene112965_All	375	0.00	0.00	0.00	0.00	0.00	0.00	4.51	0.22	1.81	null	null			null	null			null	null			null	null			-4.34E+00	1.16E-09	Down	-1.32E+00	3.08E-03									ESTscan +
Unigene112966_All	376	0.56	0.27	0.00	0.00	0.27	0.12	4.27	0.89	0.42	-1.05E+00	5.65E-01			-9.12E+00	1.46E-01			8.10E+00	4.58E-01			6.91E+00	7.01E-01			-2.26E+00	2.23E-05	Down	-3.33E+00	5.33E-08	Down			Unigene112966_All//4.00E-07//TC164796				
Unigene112968_All	377	0.00	0.00	0.00	0.00	0.00	0.00	5.27	0.11	0.53	null	null			null	null			null	null			null	null			-5.57E+00	1.08E-12	Down	-3.32E+00	1.06E-09	Down			Unigene112968_All//5.00E-13//TC149394				
Unigene112971_All	382	0.00	0.00	0.00	0.00	0.00	0.00	2.10	1.53	0.31	null	null			null	null			null	null			null	null			-4.57E-01	5.36E-01		-2.75E+00	9.43E-04	Down	Unigene112971_All//gi|164449276|gb|ABY56104.1|//8.00E-51//ribosomal protein [Cucumis sativus]	Unigene112971_All//1.00E-51//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene112971_All//4.00E-07//TC164532		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0010467//GO:0015934//GO:0031981	nr +

Unigene112972_All	382	0.00	0.00	0.00	0.00	0.00	0.00	2.55	0.22	0.00	null	null		null	null		null	null		null	null		-3.54E+00	4.32E-05	Down	-1.13E+01	2.72E-07	Down	Unigene112972_All//gi|159471131|ref|XP_001693710.1|//2.00E-44//ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|269969596|sp|A8HS48.1|RS3A_CHLRE RecName: Full=40S ribosomal protein S3a >gi|158283213|gb|EDF08964.1| ribosomal protein S3a [Chlamydomonas reinhardtii]	Unigene112972_All//2.00E-39//AT4G34670| 40S ribosomal protein S3A (RPS3aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene112973_All	384	0.00	0.00	0.00	0.00	0.00	0.00	7.27	1.52	0.52	null	null		null	null		null	null		null	null		-2.25E+00	8.87E-09	Down	-3.81E+00	6.99E-15	Down	Unigene112973_All//gi|74325167|ref|XP_316386.1|//9.00E-31//cytochrome oxidase subunit I [Thalassiosira pseudonana] >gi|74100233|gb|AAZ99394.1| cytochrome oxidase subunit I [Thalassiosira pseudonana]	Unigene112973_All//3.00E-19//ATMG01360| cytochrome c oxidase subunit I			ko00190|Oxidative phosphorylation	GO:0005506//GO:0008091//GO:0016491//GO:0043231//GO:0044425	nr -
Unigene112975_All	385	0.00	0.00	0.00	0.00	0.00	0.00	1.65	0.33	0.00	null	null		null	null		null	null		-2.34E+00	1.27E-02		-1.07E+01	7.11E-05	Down	Unigene112975_All//gi|57471702|gb|AAW50982.1|//8.00E-51//ribosomal protein L10A [Triticum aestivum]	Unigene112975_All//1.00E-38//AT5G22440| 60S ribosomal protein L10A (RPL10aC)	Unigene112975_All//1.00E-07//TC157648		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015934//GO:0016020	nr -
Unigene112976_All	386	0.00	0.00	0.00	0.00	0.00	0.00	2.41	1.73	0.41	null	null		null	null		null	null		-4.76E-01	4.76E-01		-2.55E+00	5.79E-04	Down				Unigene112976_All//7.00E-37//C0075999					
Unigene112977_All	386	0.81	0.00	0.14	1.55	0.36	0.70	2.52	0.00	0.93	-9.67E+00	3.66E-02		-2.56E+00	1.59E-01		-2.12E+00	3.06E-02		-1.14E+00	2.43E-01		-1.13E+01	5.83E-07	Down	-1.44E+00	2.09E-02		Unigene112977_All//gi|297606758|ref|NP_001058915.2|//3.00E-11//Os07g0154400 [Oryza sativa Japonica Group] >gi|255677527|dbj|BAF20829.2| Os07g0154400 [Oryza sativa Japonica Group]	Unigene112977_All//5.00E-20//AT4G14970| unknown protein					nr -
Unigene112978_All	387	0.00	0.00	0.00	0.00	0.00	0.00	3.50	0.32	1.13	null	null		null	null		null	null		null	null		-3.43E+00	1.05E-06	Down	-1.63E+00	1.95E-03				Unigene112978_All//1.00E-13//TC134836					
Unigene112980_All	388	0.00	0.00	0.00	0.77	0.53	0.00	1.74	0.00	0.31	null	null		null	null		-5.33E-01	6.79E-01		-9.59E+00	4.01E-02		-1.08E+01	6.34E-05	Down	-2.50E+00	4.78E-03		Unigene112980_All//sp|Q8CF90|MAFA_MOUSE//7.00E-06//Transcription factor MafA OS=Mus musculus GN=Mafa PE=1 SV=1		Unigene112980_All//6.00E-65//TC151886				swissprot -
Unigene112981_All	390	0.00	0.00	0.00	0.00	0.00	0.00	6.29	0.21	0.20	null	null		null	null		null	null		null	null		-4.87E+00	1.04E-14	Down	-4.94E+00	2.14E-15	Down	Unigene112981_All//gi|300258120|gb|EFJ42360.1|//4.00E-45//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene112981_All//1.00E-42//AT1G23290| RPL27AB; structural constituent of ribosome	Unigene112981_All//1.00E-13//TC169611		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene112982_All	391	0.00	0.00	0.00	0.00	0.00	0.00	3.14	0.43	0.20	null	null		null	null		null	null		null	null		-2.87E+00	2.54E-05	Down	-3.94E+00	4.86E-07	Down	Unigene112982_All//gi|301119741|ref|XP_002907598.1|//1.00E-29//60S ribosomal protein L23a [Phytophthora infestans T30-4] >gi|262106110|gb|EEY64182.1| 60S ribosomal protein L23a [Phytophthora infestans T30-4]	Unigene112982_All//1.00E-28//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene112982_All//7.00E-09//BG441496		ko03010|Ribosome	GO:0001071//GO:0003723//GO:0005198//GO:0006351//GO:0030529//GO:0043234	nr -
Unigene112983_All	392	0.00	0.00	0.00	0.00	0.00	0.00	3.34	0.43	0.00	null	null		null	null		null	null		null	null		-2.97E+00	8.34E-06	Down	-1.17E+01	9.85E-10	Down								
Unigene112984_All	398	0.00	0.00	0.00	0.00	0.00	0.00	32.83	1.47	0.00	null	null		null	null		null	null		null	null		-4.48E+00	4.33E-73	Down	-1.50E+01	2.58E-96	Down	Unigene112984_All//gi|224125106|ref|XP_002329895.1|//3.00E-28//cytochrome P450 [Populus trichocarpa] >gi|222871132|gb|EEF08263.1| cytochrome P450 [Populus trichocarpa]	Unigene112984_All//2.00E-26//AT4G22690| CYP706A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene112984_All//2.00E-86//TC137030		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506//GO:0016020	nr +
Unigene112985_All	399	0.00	0.00	0.00	0.00	0.00	0.00	4.45	0.73	0.00	null	null		null	null		null	null		null	null		-2.60E+00	9.40E-07	Down	-1.21E+01	4.12E-13	Down			Unigene112985_All//8.00E-18//ES794483					
Unigene112986_All	399	0.00	0.00	0.00	0.00	0.00	0.00	4.87	1.05	0.70	null	null		null	null		null	null		null	null		-2.22E+00	3.19E-06	Down	-2.80E+00	3.40E-08	Down								
Unigene112987_All	399	0.00	0.00	0.00	0.00	0.00	0.00	3.28	0.21	0.00	null	null		null	null		null	null		null	null		-3.97E+00	3.35E-07	Down	-1.17E+01	9.85E-10	Down								ESTscan -
Unigene112988_All	402	0.00	0.00	0.00	0.00	0.00	0.00	3.68	2.29	0.20	null	null		null	null		null	null		null	null		-6.87E-01	1.64E-01		-4.22E+00	1.00E-08	Down			Unigene112988_All//9.00E-21//ES825902					
Unigene112990_All	402	0.00	0.00	0.00	0.00	0.00	0.00	3.58	0.73	0.00	null	null		null	null		null	null		null	null		-2.30E+00	5.89E-05	Down	-1.18E+01	1.19E-10	Down	Unigene112990_All//gi|255977225|dbj|BAB97104.1|//1.00E-57//heat shock protein Hsp70 [Glaucocystis nostochinearum]	Unigene112990_All//6.00E-55//AT1G16030| Hsp70b (heat shock protein 70B); ATP binding	Unigene112990_All//9.00E-21//TC169169		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr -
Unigene112991_All	403	0.00	0.00	0.00	0.00	0.00	0.00	1.78	0.00	0.69	null	null		null	null		null	null		null	null		-1.08E+01	3.27E-05	Down	-1.37E+00	6.51E-02		Unigene112991_All//gi|55831356|gb|AAV46572.1|//2.00E-29//lipase [Ricinus communis]	Unigene112991_All//2.00E-25//AT5G42930| triacylglycerol lipase				GO:0016787	nr +
Unigene112992_All	403	0.00	0.00	0.00	0.00	0.00	0.00	1.57	0.00	0.00	null	null		null	null		null	null		null	null		-1.06E+01	1.23E-04	Down	-1.06E+01	7.11E-05	Down	Unigene112992_All//gi|4139170|gb|AB003711.1|//5.00E-46//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene112992_All//8.00E-44//AT5G60390| elongation factor 1-alpha / EF-1-alpha				GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene112994_All	406	0.00	0.00	0.00	0.00	0.00	0.00	2.92	0.00	0.00	null	null		null	null		null	null		null	null		-1.15E+01	1.97E-08	Down	-1.15E+01	8.15E-09	Down	Unigene112994_All//gi|301101263|ref|XP_002899720.1|//9.00E-37//40S ribosomal protein S4 [Phytophthora infestans T30-4] >gi|262102722|gb|EEY60774.1| 40S ribosomal protein S4 [Phytophthora infestans T30-4]	Unigene112994_All//1.00E-35//AT5G58420| 40S ribosomal protein S4 (RPS4D)			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene112995_All	408	0.00	0.00	0.00	0.00	0.00	0.00	7.36	0.82	0.68	null	null		null	null		null	null		null	null		-3.17E+00	3.04E-13	Down	-3.43E+00	1.05E-14	Down	Unigene112995_All//gi|225429199|ref|XP_002276272.1|//3.00E-06//PREDICTED: hypothetical protein [Vitis vinifera] >gi|147769903|emb|CAN65538.1| hypothetical protein [Vitis vinifera] >gi|297736408|emb|CBI25131.3| unnamed protein product [Vitis vinifera]	Unigene112995_All//9.00E-06//AT3G49780| ATPSK4 (PHYTOSULFOKINE 4 PRECURSOR); growth factor					nr -
Unigene112996_All	408	0.00	0.00	0.00	0.00	0.00	0.00	2.59	0.20	0.20	null	null		null	null		null	null		null	null		-3.66E+00	1.31E-05	Down	-3.73E+00	6.14E-06	Down								
Unigene112997_All	408	0.00	0.00	0.00	0.24	0.00	0.00	6.63	1.64	1.07	null	null		null	null		-7.93E+00	3.16E-01		-7.93E+00	4.04E-01		-2.02E+00	1.61E-07	Down	-2.63E+00	2.01E-10	Down								
Unigene112999_All	411	0.00	0.00	0.00	0.00	0.00	0.00	3.39	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	6.58E-10	Down	-1.17E+01	2.40E-10	Down	Unigene112999_All//gi|54039313|sp|P62302.1|RS13_SOYBN//7.00E-44//RecName: Full=40S ribosomal protein S13 >gi|44662862|gb|AAS47510.1| ribosomal protein S13 [Glycine max] >gi|161367348|gb|ABX71080.1| ribosomal protein S13 [Glycine max]	Unigene112999_All//2.00E-43//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene112999_All//5.00E-10//TC137925		ko03010|Ribosome	GO:0000904//GO:0005198//GO:0009887//GO:0010467//GO:0015935//GO:0031981//GO:0033205	nr -
Unigene113001_All	411	0.00	0.00	0.00	0.97	0.59	0.44	4.01	0.10	0.68	null	null		null	null		-7.25E-01	5.47E-01		-1.14E+00	3.80E-01		-5.30E+00	2.16E-10	Down	-2.56E+00	1.72E-06	Down	Unigene113001_All//gi|115470965|ref|NP_001059081.1|//8.00E-43//Os07g0188700 [Oryza sativa Japonica Group] >gi|113610617|dbj|BAF20995.1| Os07g0188700 [Oryza sativa Japonica Group]	Unigene113001_All//1.00E-39//AT5G03795| LOCATED IN: membrane; EXPRESSED IN: embryo, sepal, flower; EXPRESSED DURING: C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Exostosin-like (InterPro:IPR004263); BEST Arabidopsis thaliana protein match is: exostosin family protein (TAIR:AT3G07620.1); Has 866 Blast hits to 860 proteins in 87 species: Archae - 0; Bacteria - 9; Metazoa - 265; Fungi - 4; Plants - 504; Viruses - 0; Other Eukaryotes - 84 (source: NCBI BLink).				GO:0008375//GO:0044464	nr +
Unigene113002_All	412	0.00	0.00	0.00	0.00	0.00	0.00	4.10	1.22	0.00	null	null		null	null		null	null		null	null		-1.75E+00	2.90E-04	Down	-1.20E+01	1.70E-12	Down	Unigene113002_All//gi|192910698|gb|ACF06457.1|//5.00E-37//60S ribosomal protein L35 [Elaeis guineensis]	Unigene113002_All//6.00E-36//AT3G55170| 60S ribosomal protein L35 (RPL35C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613//GO:0031981	nr +
Unigene113003_All	414	0.00	0.00	0.00	0.00	0.00	0.00	3.68	0.00	0.10	null	null		null	null		null	null		null	null		-1.18E+01	8.51E-11	Down	-5.26E+00	5.39E-10	Down								
Unigene113004_All	418	0.00	0.00	0.00	0.00	0.00	0.00	1.62	0.00	0.00	null	null		null	null		null	null		null	null		-1.07E+01	6.34E-05	Down	-1.07E+01	3.56E-05	Down								ESTscan +
Unigene113005_All	418	0.00	0.00	0.00	0.00	0.00	0.00	4.25	0.10	0.38	null	null		null	null		null	null		null	null		-5.41E+00	2.97E-11	Down	-3.48E+00	4.53E-09	Down								ESTscan +
Unigene113006_All	418	0.00	0.00	0.00	0.00	0.00	0.00	6.07	2.10	0.57	null	null		null	null		null	null		null	null		-1.53E+00	4.18E-05	Down	-3.41E+00	1.81E-12	Down	Unigene113006_All//gi|300262307|gb|EFJ46514.1|//3.00E-17//hypothetical protein VOLCADRAFT_93060 [Volvox carteri f. nagariensis]						nr +
Unigene113007_All	419	0.12	0.00	0.00	0.24	0.25	0.00	3.33	0.20	0.48	-6.96E+00	6.17E-01		-6.96E+00	6.30E-01		5.24E-02	9.68E-01		-7.89E+00	4.04E-01		-4.06E+00	9.64E-08	Down	-2.81E+00	4.25E-06	Down	Unigene113007_All//gi|240254545|ref|NP_180360.4|//2.00E-46//binding [Arabidopsis thaliana]	Unigene113007_All//1.00E-47//AT2G27930| binding	Unigene113007_All//7.00E-111//TC179204	PLATZ			nr -
Unigene113009_All	419	0.50	0.73	1.27	0.36	0.82	0.00	2.72	1.10	0.29	5.39E-01	6.72E-01		1.35E+00	2.25E-01		1.20E+00	4.26E-01		-8.48E+00	2.34E-01		-1.31E+00	2.45E-02		-3.26E+00	8.94E-06	Down			Unigene113009_All//1.00E-127//TC163926					
Unigene113010_All	421	0.00	0.00	0.00	0.47	0.16	0.21	3.31	0.79	0.47	null	null		null	null		-1.53E+00	4.16E-01		-1.14E+00	5.70E-01		-2.06E+00	2.51E-04	Down	-2.81E+00	4.25E-06	Down	Unigene113010_All//gi|115464229|ref|NP_001055714.1|//8.00E-08//Os05g0453300 [Oryza sativa Japonica Group] >gi|113579265|dbj|BAF17628.1| Os05g0453300 [Oryza sativa Japonica Group]	Unigene113010_All//2.00E-13//AT4G02830| unknown protein					nr +
Unigene113011_All	422	0.00	0.00	0.00	0.00	0.00	0.00	3.31	0.69	0.19	null	null		null	null		null	null		null	null		-2.25E+00	9.69E-05	Down	-4.13E+00	3.70E-08	Down	Unigene113011_All//gi|116055804|emb|CAL57889.1|//2.00E-10//Protein required for actin cytoskeleton organization and cell cycle progression (ISS) [Ostreococcus tauri]				ko03040|Spliceosome	GO:0005488//GO:0016787	nr -
Unigene113012_All	425	0.00	0.00	0.00	0.00	0.00	0.11	2.19	0.20	0.66	null	null		null	null		null	null		6.73E+00	7.01E-01		-3.48E+00	7.79E-05	Down	-1.74E+00	8.54E-03		Unigene113012_All//gi|15223264|ref|NP_172335.1|//1.00E-29//CLAVATA1 receptor kinase (CLV1) [Arabidopsis thaliana] >gi|9802553|gb|AAF99755.1|AC003981_5 F22013.7 [Arabidopsis thaliana] >gi|224589384|gb|ACN59226.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene113012_All//7.00E-31//AT1G08590| CLAVATA1 receptor kinase (CLV1)			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152//GO:0016020	nr -
Unigene113013_All	426	0.00	0.00	0.00	0.00	0.00	0.00	3.18	1.28	0.00	null	null		null	null		null	null		null	null		-1.32E+00	1.25E-02		-1.16E+01	4.86E-10	Down	Unigene113013_All//gi|299472847|emb|CBN80416.1|//3.00E-22//EsV-1-116 [Ectocarpus siliculosus]						nr -
Unigene113014_All	429	0.00	0.00	0.00	0.00	0.00	0.00	4.04	12.57	0.19	null	null		null	null		null	null		null	null		1.64E+00	6.75E-11	Up	-4.44E+00	1.94E-10	Down	Unigene113014_All//gi|145334271|ref|NP_001078516.1|//6.00E-57//histone H3.2 [Arabidopsis thaliana]	Unigene113014_All//4.00E-58//AT4G40030| histone H3.2	Unigene113014_All//8.00E-09//CD485766			GO:0000785//GO:0003676//GO:0009536//GO:0034728	nr +
Unigene113015_All	429	0.00	0.00	0.00	0.00	0.00	0.00	6.01	0.00	0.74	null	null		null	null		null	null		null	null		-1.26E+01	3.07E-18	Down	-3.02E+00	2.15E-11	Down								

Unigene113016_All	430	0.00	0.00	0.00	0.00	0.00	0.00	2.26	0.29	0.37	null	null		null	null		null	null		null	null		-2.96E+00	1.89E-04	Down	-2.61E+00	3.35E-04	Down	Unigene113016_All//gi|41203466|ref|NP_957726.1|//3.00E-28//NADH dehydrogenase subunit 4 [Emiliania huxleyi] >gi|33114152|gb|AAP94708.1| NADH dehydrogenase subunit 4 [Emiliania huxleyi]	Unigene113016_All//3.00E-22//ATMG00580| NADH dehydrogenase subunit 4			ko00190|Oxidative phosphorylation	GO:0016020//GO:0055114	nr -
Unigene113017_All	430	0.00	0.00	0.00	0.00	0.00	0.00	3.74	0.19	1.11	null	null		null	null		null	null		null	null		-4.26E+00	4.13E-09	Down	-1.75E+00	2.97E-04	Down								
Unigene113018_All	431	0.00	0.00	0.00	0.00	0.00	0.00	5.30	0.19	0.00	null	null		null	null		null	null		null	null		-4.77E+00	1.41E-13	Down	-1.24E+01	8.15E-17	Down	Unigene113018_All//gi|300265437|gb|EFJ49628.1|//6.00E-48//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene113018_All//6.00E-45//AT4G34670| 40S ribosomal protein S3A (RPS3aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene113019_All	431	0.00	0.00	0.00	0.00	0.00	0.00	2.16	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	1.14E-06	Down	-1.11E+01	5.48E-07	Down								
Unigene113020_All	434	0.00	0.00	0.00	0.00	0.16	0.00	3.02	0.19	0.55	null	null		null	null		7.31E+00	6.14E-01		null	null		-3.97E+00	3.35E-07	Down	-2.45E+00	4.22E-05	Down			Unigene113020_All//4.00E-103//TC165744					
Unigene113022_All	437	0.00	0.00	0.00	0.00	0.00	0.00	2.42	0.57	0.00	null	null		null	null		null	null		null	null		-2.08E+00	1.78E-03		-1.12E+01	6.72E-08	Down								ESTscan -
Unigene113025_All	440	0.00	0.00	0.00	0.00	0.00	0.00	3.84	0.19	0.00	null	null		null	null		null	null		null	null		-4.34E+00	1.16E-09	Down	-1.19E+01	1.70E-12	Down	Unigene113025_All//gi|18087805|ref|NP_032329.2|//2.00E-51//40S ribosomal protein S2 [Mus musculus] >gi|78126159|ref|NP_114026.3| 40S ribosomal protein S2 [Rattus norvegicus] >gi|133914|sp|P27952.1|RS2_RAT RecName: Full=40S ribosomal protein S2 >gi|46397787|sp|P25444.3|RS2_MOUSE RecName: Full=40S ribosomal protein S2; AltName: Full=40S ribosomal protein S4; AltName: Full=Protein LLRep3 >gi|10179940|gb|AAG13953.1|AF283559_1 ribosomal protein S2 [Mus musculus] >gi|57718|emb|CAA40679.1| ribosomal protein S2 [Rattus rattus] >gi|12805427|gb|AAH02186.1| Ribosomal protein S2 [Mus musculus] >gi|56971737|gb|AAH87956.1| Ribosomal protein S2 [Mus musculus] >gi|61402217|gb|AAH91730.1| Ribosomal protein S2 [Mus musculus]	Unigene113025_All//1.00E-48//AT1G58684| 40S ribosomal protein S2, putative	Unigene113025_All//4.00E-17//DW519163		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006413//GO:0009536//GO:0015935//GO:0016020//GO:0017134//GO:0030312//GO:0031981//GO:0042257	nr +
Unigene113026_All	446	0.00	0.00	0.00	0.00	0.00	0.00	4.46	0.00	0.54	null	null		null	null		null	null		null	null		-1.21E+01	4.61E-14	Down	-3.06E+00	4.82E-09	Down	Unigene113026_All//gi|114432130|gb|ABI74673.1|//4.00E-08//suppressor of necrosis 1 [Phytophthora infestans]				ko03040|Spliceosome		nr +
Unigene113027_All	446	0.00	0.00	0.00	0.00	0.00	0.00	9.95	0.56	0.00	null	null		null	null		null	null		null	null		-4.15E+00	6.72E-24	Down	-1.33E+01	1.22E-32	Down			Unigene113027_All//3.00E-08//gi|11207717|gb|BF276647.1|BF276647				
Unigene113028_All	446	0.00	0.00	0.00	0.00	0.00	0.00	3.32	0.84	1.25	null	null		null	null		null	null		null	null		-1.98E+00	2.39E-04	Down	-1.41E+00	3.79E-03		Unigene113028_All//gi|115466618|ref|NP_001056908.1|//6.00E-36//Os06g0165500 [Oryza sativa Japonica Group] >gi|113594948|dbj|BAF18822.1| Os06g0165500 [Oryza sativa Japonica Group]	Unigene113028_All//3.00E-14//AT1G78830| curculin-like (mannose-binding) lectin family protein				GO:0000166//GO:0004672//GO:0009987	nr -
Unigene113030_All	449	0.00	0.00	0.00	0.00	0.00	0.00	2.17	0.19	0.18	null	null		null	null		null	null		null	null		-3.54E+00	4.32E-05	Down	-3.61E+00	2.14E-05	Down	Unigene113030_All//gi|5669638|gb|AAD46404.1|AF096248_1//3.00E-34//ethylene-responsive RNA helicase [Solanum lycopersicum]	Unigene113030_All//1.00E-34//AT3G06480| DEAD box RNA helicase, putative			ko03040|Spliceosome	GO:0032559//GO:0042623//GO:0043231	nr +
Unigene113031_All	449	0.00	0.00	0.00	0.00	0.00	0.00	2.64	0.09	0.53	null	null		null	null		null	null		null	null		-4.82E+00	2.83E-07	Down	-2.31E+00	2.04E-04	Down	Unigene113031_All//gi|2388584|gb|AAB71465.1|//5.00E-09//EST gb|ATTS1136 comes from this gene [Arabidopsis thaliana]	Unigene113031_All//4.00E-07//AT4G33740| unknown protein				GO:0003824	nr +
Unigene113032_All	450	0.23	0.00	0.00	0.22	0.00	0.20	4.04	0.00	1.42	-7.86E+00	3.75E-01		-7.86E+00	3.97E-01		-7.79E+00	3.16E-01		-1.42E-01	9.52E-01		-1.20E+01	7.10E-13	Down	-1.51E+00	5.47E-04	Down	Unigene113032_All//gi|30687119|ref|NP_181275.2|//2.00E-26//heavy-metal-associated domain-containing protein [Arabidopsis thaliana]	Unigene113032_All//1.00E-27//AT2G37390| heavy-metal-associated domain-containing protein	Unigene113032_All//2.00E-126//TC177472			GO:0006812//GO:0043169	nr -
Unigene113033_All	451	0.00	0.00	0.00	0.00	0.00	0.00	5.72	0.19	0.00	null	null		null	null		null	null		null	null		-4.95E+00	1.46E-15	Down	-1.25E+01	5.57E-19	Down	Unigene113033_All//gi|2500354|sp|P93847.1|RL10_SOLME//3.00E-57//RecName: Full=60S ribosomal protein L10; AltName: Full=QM >gi|1902894|dbj|BAA19462.1| QM family protein [Solanum melongena]	Unigene113033_All//5.00E-54//AT1G66580| 60S ribosomal protein L10 (RPL10C)	Unigene113033_All//4.00E-11//TC145515		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0016787//GO:0030529//GO:0044238//GO:0044229	nr -
Unigene113034_All	457	0.57	0.00	0.00	1.64	1.51	0.20	3.24	0.82	0.52	-9.16E+00	6.72E-02		-9.16E+00	8.59E-02		-1.18E-01	8.62E-01		-3.05E+00	3.33E-03		-1.98E+00	2.39E-04	Down	-2.63E+00	4.77E-06	Down			Unigene113034_All//2.00E-77//TC158640				
Unigene113035_All	463	0.34	0.00	0.12	0.54	0.00	0.00	6.76	0.99	0.52	-8.41E+00	2.16E-01		-1.56E+00	5.34E-01		-9.07E+00	4.19E-02		-9.07E+00	7.35E-02		-2.77E+00	3.94E-12	Down	-3.71E+00	2.72E-16	Down								
Unigene113036_All	465	0.00	0.00	0.00	0.00	0.00	0.00	4.18	0.72	0.51	null	null		null	null		null	null		null	null		-2.54E+00	3.67E-07	Down	-3.02E+00	8.70E-09	Down	Unigene113036_All//gi|115448105|ref|NP_001047832.1|//1.00E-44//Os02g0699600 [Oryza sativa Japonica Group] >gi|113537363|dbj|BAF09746.1| Os02g0699600 [Oryza sativa Japonica Group]	Unigene113036_All//5.00E-44//AT2G37190| 60S ribosomal protein L12 (RPL12A)			ko03010|Ribosome	GO:0005198//GO:0006950//GO:0009536//GO:0010467//GO:0015934//GO:0022613//GO:0031981//GO:0046914	nr -
Unigene113037_All	466	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.00	0.09	null	null		null	null		null	null		null	null		-1.11E+01	2.97E-07	Down	-4.67E+00	1.72E-06	Down	Unigene113037_All//gi|224009247|ref|XP_002293582.1|//2.00E-15//calcium transporting rt-atpase [Thalassiosira pseudonana CCMP1335] >gi|220970982|gb|EED89318.1| calcium transporting rt-atpase [Thalassiosira pseudonana CCMP1335]	Unigene113037_All//5.00E-14//AT5G57110| ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFORM 8); calcium-transporting ATPase/ calmodulin binding / protein self-association				GO:0005515//GO:0006810//GO:0016020//GO:0019829//GO:0051707	nr +
Unigene113038_All	468	0.56	0.00	0.68	0.21	0.15	0.00	4.88	1.61	1.19	-9.13E+00	6.72E-02		2.88E-01	8.10E-01		-5.32E-01	8.18E-01		-7.73E+00	4.04E-01		-1.60E+00	6.24E-05	Down	-2.03E+00	8.82E-07	Down			Unigene113038_All//1.00E-10//BQ405485				
Unigene113039_All	469	0.00	0.00	0.00	0.00	0.00	0.00	2.88	1.34	0.00	null	null		null	null		null	null		null	null		-1.11E+00	3.31E-02		-1.15E+01	4.86E-10	Down	Unigene113039_All//gi|115452955|ref|NP_001050078.1|//3.00E-32//Os03g0343500 [Oryza sativa Japonica Group] >gi|42733478|dbj|BAD11336.1| BRI1-KD interacting protein 108 [Oryza sativa Japonica Group] >gi|113548549|dbj|BAF11992.1| Os03g0343500 [Oryza sativa Japonica Group]	Unigene113039_All//3.00E-29//AT3G05560| 60S ribosomal protein L22-2 (RPL22B)			ko03010|Ribosome	GO:0005622	nr -
Unigene113040_All	470	0.56	0.65	0.23	1.48	0.88	0.19	2.34	1.07	0.51	2.17E-01	8.65E-01		-1.30E+00	4.37E-01		-7.55E-01	3.69E-01		-2.95E+00	5.84E-03		-1.13E+00	5.52E-02		-2.20E+00	5.66E-04	Down			Unigene113040_All//6.00E-07//ES810824				
Unigene113041_All	471	0.00	0.00	0.00	0.00	0.00	0.00	2.60	0.44	0.00	null	null		null	null		null	null		null	null		-2.55E+00	8.70E-05	Down	-1.13E+01	4.03E-09	Down	Unigene113041_All//gi|15219950|ref|NP_173692.1|//8.00E-59//PFL (POINTED FIRST LEAVES); RNA binding / nucleic acid binding / structural constituent of ribosome [Arabidopsis thaliana] >gi|15234790|ref|NP_192718.1| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome [Arabidopsis thaliana] >gi|18399100|ref|NP_564434.1| 40S ribosomal protein S18 (RPS18B) [Arabidopsis thaliana] >gi|464707|sp|P34788.1|RS18_ARATH RecName: Full=40S ribosomal protein S18 >gi|10086474|gb|AAG12534.1|AC015446_15 ribosomal protein S18 [Arabidopsis thaliana] >gi|10092450|gb|AAG12853.1|AC007926_10 40S ribosomal protein S18; 25853-24673 [Arabidopsis thaliana] >gi|14423408|gb|AAK62386.1|AF384691_1 S18.A ribosomal protein [Arabidopsis thaliana] >gi|15724158|gb|AAL06471.1|AF411781_1 At1g22780/T22J18_5 [Arabidopsis thaliana] >gi|405613|emb|CAA80684.1|	Unigene113041_All//7.00E-51//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006412//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr +
Unigene113042_All	472	0.00	0.00	0.00	0.00	0.00	0.00	4.30	0.35	0.84	null	null		null	null		null	null		null	null		-3.60E+00	3.79E-10	Down	-2.35E+00	3.80E-07	Down	Unigene113042_All//gi|293336485|ref|NP_001170475.1|//2.00E-63//heat shock protein 90 [Zea mays] >gi|225903795|gb|ACO35045.1| heat shock protein 90 [Zea mays]	Unigene113042_All//1.00E-40//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene113042_All//4.00E-23//gi|164289322|gb|ES826064.1|ES826064		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr +
Unigene113043_All	479	0.00	0.00	0.00	0.00	0.00	0.00	4.06	1.22	0.75	null	null		null	null		null	null		null	null		-1.73E+00	1.00E-04	Down	-2.44E+00	3.73E-07	Down								ESTscan -
Unigene113045_All	485	0.00	0.00	0.00	0.00	0.00	0.00	1.92	0.17	0.00	null	null		null	null		null	null		null	null		-3.48E+00	7.79E-05	Down	-1.09E+01	5.48E-07	Down	Unigene113045_All//gi|15239409|ref|NP_200875.1|//4.00E-52//60S ribosomal protein L12 (RPL12C) [Arabidopsis thaliana] >gi|75309019|sp|Q9FF52.1|RL123_ARATH RecName: Full=60S ribosomal protein L12-3 >gi|9759331|dbj|BAB09840.1| 60S ribosomal protein L12 [Arabidopsis thaliana] >gi|14517558|gb|AAK62669.1| AT5g60670/mup24_80 [Arabidopsis thaliana] >gi|18700232|gb|AAL77726.1| AT5g60670/mup24_80 [Arabidopsis thaliana] >gi|21593741|gb|AAM65708.1| 60S ribosomal protein L12-like [Arabidopsis thaliana]	Unigene113045_All//3.00E-53//AT5G60670| 60S ribosomal protein L12 (RPL12C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +
Unigene113046_All	492	0.11	0.00	0.00	0.00	0.28	2.02	1.63	0.76	0.89	-6.73E+00	6.17E-01		-6.73E+00	6.30E-01		8.13E+00	3.20E-01		1.10E+01	6.15E-06	Up	-1.09E+00	1.29E-01		-8.74E-01	1.96E-01								
Unigene113048_All	495	0.00	0.00	0.00	0.00	0.00	0.00	1.88	0.17	0.24	null	null		null	null		null	null		null	null		-3.48E+00	7.79E-05	Down	-2.96E+00	1.72E-04	Down								
Unigene113049_All	501	0.00	0.00	0.00	0.00	0.00	0.00	4.05	0.42	1.03	null	null		null	null		null	null		null	null		-3.28E+00	2.01E-09	Down	-1.97E+00	6.60E-06	Down	Unigene113049_All//gi|32400971|gb|AF980691.1|//2.00E-69//ubiquitin-conjugating enzyme [Griffithsia japonica]	Unigene113049_All//1.00E-59//AT3G08690| UBC11 (UBIQUITIN-CONJUGATING ENZYME 11); ubiquitin-protein ligase	Unigene113049_All//2.00E-10//ES828592		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0006461//GO:0019787//GO:0019941//GO:0060255	nr +

Unigene11305_All	3343	9.31	19.43	11.99	26.72	27.60	27.55	32.14	52.46	94.44	1.06E+00	9.55E-52	Up	3.65E-01	2.76E-05		4.66E-02	5.15E-01		4.41E-02	5.35E-01		7.07E-01	1.25E-85		1.56E+00	0.00E+00	Up	Unigene11305_All//gi|47834701|gb|AAT39004.1|//0.00E+00//AML1 [Citrus unshiu]	Unigene11305_All//0.00E+00//AT1G29400| AML5 (ARABIDOPSIS ME12-LIKE PROTEIN 5); RNA binding / nucleic acid binding / nucleotide binding	Unigene11305_All//0.00E+00//TC150073		ko03040|Spliceosome	GO:0003676	nr +
Unigene113050_All	501	0.00	0.00	0.00	0.00	0.00	0.00	1.69	0.00	0.00	null	null		null	null		null	null		null	null		-1.07E+01	4.39E-06	Down	-1.07E+01	2.21E-06	Down	Unigene113050_All//gi|57472005|gb|AAW51128.1|//2.00E-11//minus agglutinin [Chlamydomonas incerta]	Unigene113050_All//3.00E-12//AT3G44100| MD-2-related lipid recognition domain-containing protein / ML domain-containing protein			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003824//GO:0016020//GO:0030312//GO:0043231	nr -
Unigene113051_All	510	0.00	0.00	0.00	0.00	0.00	0.00	2.24	0.57	0.00	null	null		null	null		null	null		null	null		-1.96E+00	1.69E-03		-1.11E+01	1.65E-08	Down	Unigene113051_All//gi|152003979|gb|ABS19813.1|//9.00E-49//eukaryotic initiation factor 4A [Lolium perenne]	Unigene113051_All//4.00E-42//AT3G13920| EIF4A1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 4A1); ATP-dependent helicase/ translation initiation factor				GO:0003676//GO:0032559//GO:0042623	nr +
Unigene113052_All	518	0.51	0.78	0.31	0.96	0.53	0.35	3.59	4.68	1.23	6.32E-01	6.01E-01		-7.12E-01	6.22E-01		-8.55E-01	4.07E-01		-1.46E+00	1.93E-01		3.82E-01	3.27E-01		-1.55E+00	3.64E-04	Down		Unigene113052_All//6.00E-07//TC155745					
Unigene113053_All	519	0.00	0.10	0.41	0.96	0.07	0.78	4.48	0.97	1.07	6.61E+00	6.20E-01		8.68E+00	1.42E-01		-3.86E+00	5.32E-03		-2.93E-01	7.57E-01		-2.21E+00	2.77E-07	Down	-2.06E+00	5.41E-07	Down							
Unigene113054_All	524	0.00	0.00	0.00	0.19	0.00	0.00	2.58	0.48	1.29	null	null		null	null		-7.57E+00	3.16E-01		-7.57E+00	4.04E-01		-2.43E+00	5.63E-05	Down	-9.98E-01	4.39E-02		Unigene113054_All//gi|297830832|ref|XP_002883298.1|//3.00E-17//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329138|gb|EFH59557.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene113054_All//2.00E-18//AT3G21330| basic helix-loop-helix (bHLH) family protein		bHLH		GO:0001071//GO:0010468//GO:0043231	nr -
Unigene113055_All	525	0.00	0.00	0.00	0.00	0.00	0.00	5.07	0.32	0.30	null	null		null	null		null	null		null	null		-3.99E+00	3.57E-14	Down	-4.06E+00	6.84E-15	Down	Unigene113055_All//gi|61656129|gb|AAX49367.1|//4.00E-31//At2g38640 [Arabidopsis thaliana]	Unigene113055_All//1.00E-30//AT5G41590| unknown protein					nr -
Unigene113056_All	525	0.20	0.29	1.01	0.28	0.33	1.29	2.98	0.16	0.91	5.39E-01	7.80E-01		2.35E+00	5.88E-02		2.04E-01	9.50E-01		2.18E+00	3.14E-02		-4.23E+00	7.78E-09	Down	-1.71E+00	4.59E-04	Down	Unigene113056_All//gi|297812057|ref|XP_002873912.1|//4.00E-38//EMB3013 [Arabidopsis lyrata subsp. lyrata] >gi|297319749|gb|EFH50171.1| EMB3013 [Arabidopsis lyrata subsp. lyrata]	Unigene113056_All//9.00E-38//AT5G18700| EMB3013 (embryo defective 3013); ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene113056_All//0.00E+00//TC152167			GO:0004672//GO:0005488	nr -
Unigene113058_All	536	0.20	1.13	0.00	1.12	0.90	0.25	2.76	0.55	0.67	2.54E+00	2.46E-02		-7.61E+00	3.97E-01		-3.10E-01	7.41E-01		-2.14E+00	4.39E-02		-2.34E+00	3.57E-05	Down	-2.05E+00	1.05E-04	Down							
Unigene113059_All	538	0.00	0.00	0.00	0.00	0.00	0.00	3.22	0.78	0.00	null	null		null	null		null	null		null	null		-2.05E+00	3.55E-05	Down	-1.17E+01	8.37E-13	Down	Unigene113059_All//gi|37625023|gb|AAQ96335.1|//7.00E-66//ribosomal protein L3A [Nicotiana tabacum]	Unigene113059_All//3.00E-65//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene113059_All//6.00E-07//TC149894		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene11306_All	1990	6.52	1.94	4.04	10.89	10.28	12.23	19.46	13.97	25.99	-1.75E+00	1.09E-22	Down	-6.90E-01	2.02E-05		-8.32E-02	5.68E-01		1.68E-01	1.79E-01		-4.79E-01	3.95E-10		4.17E-01	9.27E-11		Unigene11306_All//gi|115478695|ref|NP_001062941.1|//1.00E-141//Os09g0346700 [Oryza sativa Japonica Group] >gi|113631174|dbj|BAF24855.1| Os09g0346700 [Oryza sativa Japonica Group]	Unigene11306_All//0.00E+00//AT2G25800| INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Munc13 homology 1 (InterPro:IPR014770), Protein of unknown function DUF810 (InterPro:IPR008528), Munc13 homology 2 (InterPro:IPR014772); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G20010.2); Has 242 Blast hits to 156 proteins in 35 species: Archae - 0; Bacteria - 8; Metazoa - 36; Fungi - 18; Plants - 94; Viruses - 0; Other Eukaryotes - 86 (source: NCBI BLink).	Unigene11306_All//0.00E+00//TC133767				nr +
Unigene113060_All	547	0.48	0.65	0.19	0.18	0.19	0.33	3.17	1.15	1.09	4.39E-01	7.01E-01		-1.30E+00	4.37E-01		5.29E-02	9.68E-01		8.59E-01	6.96E-01		-1.47E+00	1.48E-03		-1.54E+00	6.50E-04	Down	Unigene113060_All//gi|297833840|ref|XP_002884802.1|//6.00E-68//glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata] >gi|297330642|gb|EFH61061.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata]	Unigene113060_All//9.00E-68//AT3G10630| glycosyl transferase family 1 protein	Unigene113060_All//0.00E+00//ES809782			GO:0008152//GO:0016740//GO:0043231	nr -
Unigene113061_All	555	0.19	0.00	0.00	0.00	0.00	0.00	4.65	1.05	0.86	-7.56E+00	3.75E-01		-7.56E+00	3.97E-01		null	null		null	null		-2.14E+00	1.05E-07	Down	-2.43E+00	3.32E-09	Down	Unigene113061_All//gi|53370641|gb|AAU89136.1|//5.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene113061_All//1.00E-51//ES797781			GO:0043231	nr -
Unigene113062_All	556	0.00	0.00	0.00	0.00	0.00	0.00	2.89	0.45	0.14	null	null		null	null		null	null		null	null		-2.68E+00	2.38E-06	Down	-4.33E+00	1.41E-09	Down	Unigene113062_All//gi|300175513|emb|CBK20824.2|//2.00E-15//unnamed protein product [Blastocystis hominis]						nr +
Unigene113063_All	556	0.00	0.00	0.00	0.00	0.00	0.00	3.57	0.75	0.07	null	null		null	null		null	null		null	null		-2.25E+00	1.94E-06	Down	-5.64E+00	2.87E-13	Down	Unigene113063_All//sp|P51880|FABP7_MOUSE//1.00E-22//Fatty acid-binding protein, brain OS=Mus musculus GN=Fabp7 PE=1 SV=2						swissprot +
Unigene113064_All	561	0.00	0.00	0.00	0.00	0.00	0.00	2.49	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	6.58E-10	Down	-1.13E+01	2.40E-10	Down	Unigene113064_All//gi|159459822|gb|AB096308.1|//8.00E-79//heat shock protein 90 [Vitis pseudoreticulata]	Unigene113064_All//1.00E-57//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr -
Unigene113065_All	562	0.00	0.00	0.00	0.00	0.00	0.00	3.46	2.45	0.07	null	null		null	null		null	null		null	null		-4.96E-01	2.44E-01		-5.61E+00	5.71E-13	Down	Unigene113065_All//gi|119713|sp|P24152.1|EXTN_SORBI//1.00E-06//RecName: Full=Extensin; AltName: Full=Proline-rich glycoprotein; Flags: Precursor >gi|21627|emb|CAA39485.1| hydroxyproline-rich glycoprotein [Sorghum bicolor]						nr -
Unigene113066_All	572	0.00	0.00	0.00	0.00	0.24	0.00	5.47	0.73	0.00	null	null		null	null		7.91E+00	3.20E-01		null	null		-2.90E+00	1.02E-12	Down	-1.24E+01	5.19E-23	Down							
Unigene113067_All	578	0.00	0.00	0.00	0.00	0.00	0.16	4.46	0.00	0.14	null	null		null	null		null	null		7.29E+00	4.80E-01		-1.21E+01	3.06E-18	Down	-5.02E+00	2.78E-16	Down			Unigene113067_All//7.00E-07//gi|21098785|gb|BQ411098.1|BQ411098					
Unigene113068_All	580	0.00	0.00	0.00	0.00	0.24	0.00	6.12	0.00	0.00	null	null		null	null		7.89E+00	3.20E-01		null	null		-1.26E+01	4.04E-25	Down	-1.26E+01	4.09E-26	Down							
Unigene113069_All	586	0.00	0.00	0.00	0.00	0.00	0.00	2.89	1.14	0.14	null	null		null	null		null	null		null	null		-1.34E+00	3.80E-03		-4.41E+00	3.76E-10	Down	Unigene113069_All//gi|6012952|emb|CAB57309.1|//4.00E-35//60S ribosomal protein L6 (YL 16 like) [Cyanophora paradoxa]	Unigene113069_All//6.00E-31//AT1G18540| 60S ribosomal protein L6 (RPL6A)			ko03010|Ribosome	GO:0009536//GO:0015934//GO:0016020	nr -
Unigene113070_All	599	0.00	0.00	0.00	0.00	0.00	0.00	2.54	0.28	0.20	null	null		null	null		null	null		null	null		-3.19E+00	4.80E-07	Down	-3.67E+00	3.49E-08	Down	Unigene113070_All//gi|116056635|emb|CAL52924.1|//2.00E-16//CCCH-type Zn-finger protein (ISS) [Ostreococcus tauri]	Unigene113070_All//9.00E-13//AT1G66810| zinc finger (CCCH-type) family protein		C3H		GO:0046872	nr +
Unigene113071_All	604	0.00	0.00	0.00	0.00	0.00	0.00	28.77	0.90	0.07	null	null		null	null		null	null		null	null		-5.00E+00	2.16E-103	Down	-8.77E+00	6.55E-126	Down	Unigene113071_All//gi|297807629|ref|XP_002871698.1|//1.00E-46//3-oxo-5-alpha-steroid 4-dehydrogenase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317535|gb|EFH47957.1| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene113071_All//9.00E-45//AT5G16010| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein	Unigene113071_All//2.00E-16//ES794235			GO:0009526//GO:0016020	nr +
Unigene113072_All	612	0.00	0.00	0.35	0.00	0.00	0.00	13.68	0.41	0.91	null	null		8.44E+00	1.42E-01		null	null		null	null		-5.06E+00	2.82E-50	Down	-3.91E+00	2.72E-44	Down	Unigene113072_All//gi|8778875|gb|AF79874.1|AC000348_27//3.00E-49//T7N9.16 [Arabidopsis thaliana]	Unigene113072_All//2.00E-50//AT1G27100| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G69900.1); Has 184 Blast hits to 118 proteins in 20 species: Archae - 0; Bacteria - 2; Metazoa - 3; Fungi - 8; Plants - 166; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene113072_All//3.00E-89//gi|109860727|gb|DW489706.1|DW489706				GO:0043231	nr +
Unigene113073_All	614	0.09	0.00	0.00	0.00	0.11	0.00	2.34	0.00	0.91	-6.41E+00	6.17E-01		-6.41E+00	6.30E-01		6.81E+00	6.14E-01		null	null		-1.12E+01	3.33E-10	Down	-1.37E+00	5.50E-03		Unigene113073_All//gi|224085587|ref|XP_002307628.1|//3.00E-82//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222857077|gb|EEE94624.1| glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene113073_All//2.00E-75//AT1G06780| GAUT6 (Galacturonosyltransferase 6); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups	Unigene113073_All//0.00E+00//gi|164343548|gb|ES825706.1|ES825706			GO:0008194//GO:0043231//GO:0045489	nr -
Unigene113074_All	625	0.00	0.00	0.00	0.00	0.11	0.07	2.71	0.00	0.06	null	null		null	null		6.78E+00	6.14E-01		6.18E+00	7.01E-01		-1.14E+01	5.52E-12	Down	-5.41E+00	3.52E-11	Down	Unigene113074_All//gi|300521738|gb|ADK26058.1|//9.00E-14//drought resistance protein [Glycine max]	Unigene113074_All//8.00E-13//AT2G47540| pollen Ole e 1 allergen and extensin family protein	Unigene113074_All//0.00E+00//BG444324				nr +
Unigene113075_All	630	0.00	0.00	0.00	0.00	0.00	0.00	4.03	0.13	0.70	null	null		null	null		null	null		null	null		-4.92E+00	2.81E-15	Down	-2.53E+00	1.83E-09	Down	Unigene113075_All//gi|168009836|ref|XP_001757611.1|//2.00E-06//argonaute family member [Physcomitrella patens subsp. patens] >gi|162691305|gb|EDQ77668.1| argonaute family member [Physcomitrella patens subsp. patens]						nr +
Unigene113076_All	630	0.00	0.00	0.00	0.00	0.00	0.00	2.68	0.07	0.00	null	null		null	null		null	null		null	null		-5.34E+00	1.11E-10	Down	-1.14E+01	1.70E-12	Down	Unigene113076_All//gi|70663909|emb|CAE01636.3|//2.00E-49//OSJNBa0029H02.21 [Oryza sativa (japonica cultivar-group)]	Unigene113076_All//5.00E-45//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene113077_All	631	0.00	0.00	0.00	0.16	0.00	0.00	5.23	0.60	0.38	null	null		null	null		-7.30E+00	3.16E-01		-7.30E+00	4.04E-01		-3.13E+00	2.40E-14	Down	-3.79E+00	2.10E-17	Down			Unigene113077_All//5.00E-119//AI728318					
Unigene113078_All	643	0.00	0.00	0.00	0.00	0.00	0.00	7.36	0.26	0.25	null	null		null	null		null	null		null	null		-4.82E+00	6.79E-28	Down	-4.89E+00	3.81E-29	Down	Unigene113078_All//gi|301095349|ref|XP_002896775.1|//3.00E-49//60S acidic ribosomal protein P0 [Phytophthora infestans T30-4] >gi|262108858|gb|EEY66710.1| 60S acidic ribosomal protein P0 [Phytophthora infestans T30-4]	Unigene113078_All//3.00E-42//AT2G40010| 60S acidic ribosomal protein P0 (RPP0A)			ko03010|Ribosome	GO:0005198//GO:0006412//GO:0030529	nr +
Unigene113079_All	652	0.00	0.00	0.00	0.00	0.00	0.00	2.40	0.90	0.00	null	null		null	null		null	null		null	null		-1.42E+00	3.64E-03		-1.12E+01	1.42E-11	Down							ESTscan -

Unigene113080_All	673	0.23	0.00	0.08	0.37	0.00	0.40	3.58	1.43	1.36	-7.87E+00	2.16E-01			-1.56E+00	5.34E-01			-8.53E+00	4.19E-02			1.21E-01	9.44E-01			-1.33E+00	4.24E-04	Down	-1.40E+00	1.51E-04	Down	Unigene113080_All//gi|140053482|gb|AB080459.1|//7.00E-07//RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H [Medicago truncatula]	Unigene113080_All//8.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative					nr +
Unigene113081_All	674	0.00	0.00	0.00	0.00	0.00	0.00	3.45	0.06	1.12	null	null			null	null			null	null			null	null			-5.80E+00	5.23E-15	Down	-1.62E+00	2.77E-05	Down	Unigene113081_All//gi|157093097|gb|ABV22203.1|//1.00E-33//skp1 family protein [Karlodinium micrum]	Unigene113081_All//7.00E-26//AT4G34210| ASK11 (ARABIDOPSIS SKP1-LIKE 11); protein binding / ubiquitin-protein ligase	Unigene113081_All//8.00E-07//TC174480		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene113082_All	683	0.00	0.00	0.00	0.00	0.00	0.00	5.32	0.86	0.00	null	null			null	null			null	null			null	null			-2.64E+00	2.59E-13	Down	-1.24E+01	9.77E-27	Down	Unigene113082_All//gi|223996425|ref|XP_002287886.1|//1.00E-11//predicted protein [Thalassiosira pseudonana CCMP1335] >gi|220977002|gb|EED95329.1| predicted protein [Thalassiosira pseudonana CCMP1335]						nr -
Unigene113083_All	725	0.87	0.00	0.00	0.82	0.57	1.12	2.86	0.81	0.00	-9.76E+00	7.92E-04	Down	-9.76E+00	1.41E-03			-5.33E-01	5.62E-01			4.44E-01	6.21E-01			-1.82E+00	2.74E-05	Down	-1.15E+01	2.86E-15	Down	Unigene113083_All//gi|124359343|gb|ABD28505.2|//1.00E-34//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene113083_All//6.00E-10//AT3G24255| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G23910.1); Has 2302 Blast hits to 2235 proteins in 74 species: Archae - 4; Bacteria - 15; Metazoa - 871; Fungi - 12; Plants - 1295; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).					nr -
Unigene113084_All	736	0.07	0.00	0.72	0.47	0.14	0.00	4.54	0.74	0.70	-6.15E+00	6.17E-01			3.35E+00	2.06E-02		-1.75E+00	1.90E-01		-8.89E+00	2.13E-02		-2.62E+00	3.28E-12	Down	-2.69E+00	5.32E-13	Down								
Unigene113085_All	773	0.00	0.00	0.00	0.00	0.00	0.00	11.81	0.00	0.00	null	null			null	null		null	null		null	null		-1.35E+01	7.72E-65	Down	-1.35E+01	3.03E-67	Down								ESTscan +
Unigene113086_All	847	0.00	0.00	0.00	0.00	0.00	0.00	3.94	0.35	0.33	null	null			null	null		null	null		null	null		-3.51E+00	5.04E-16	Down	-3.58E+00	6.98E-17	Down	Unigene113086_All//gi|159147901|dbj|BAF92024.1|//6.00E-29//aedolisin-like peptidase [Actinophrys sol]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003824	nr -
Unigene113087_All	852	0.55	0.54	0.56	0.88	0.61	0.32	2.73	0.59	0.98	-4.64E-02	9.78E-01			2.54E-02	1.00E+00		-5.33E-01	5.26E-01		-1.46E+00	9.04E-02		-2.21E+00	2.77E-07	Down	-1.47E+00	1.01E-04	Down	Unigene113087_All//gi|224111738|ref|XP_002315960.1|//1.00E-125//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222865000|gb|EEF02131.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene113087_All//2.00E-106//AT1G25580| ANAC008 (Arabidopsis NAC domain containing protein 8); transcription factor	Unigene113087_All//0.00E+00//TC139349	NAC		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene113088_All	876	0.00	0.00	0.00	0.00	0.00	0.00	33.01	0.86	0.91	null	null			null	null		null	null		null	null		-5.26E+00	1.85E-176	Down	-5.18E+00	3.91E-181	Down								
Unigene113089_All	888	0.00	0.00	0.00	0.00	0.00	0.00	22.38	0.38	0.63	null	null			null	null		null	null		null	null		-5.89E+00	3.34E-127	Down	-5.15E+00	3.15E-124	Down			Unigene113089_All//5.00E-15//TC171825					
Unigene113090_All	1053	0.00	0.00	0.00	0.00	0.20	0.00	9.92	0.32	0.49	null	null			null	null		7.62E+00	1.57E-01		null	null		-4.97E+00	4.98E-62	Down	-4.33E+00	2.86E-59	Down	Unigene113090_All//gi|224080564|ref|XP_002306164.1|//1.00E-119//aquaporin, MIP family, PIP subfamily [Populus trichocarpa] >gi|222849128|gb|EEE86675.1| aquaporin, MIP family, PIP subfamily [Populus trichocarpa]	Unigene113090_All//9.00E-22//AT1G17810| BETA-TIP (BETA-TONOPLAST INTRINSIC PROTEIN); water channel	Unigene113090_All//6.00E-15//gi|48791108|gb|C0092422.1|C0092422				nr -
Unigene113092_All	243	0.00	0.00	0.00	0.00	0.00	0.00	1.39	5.50	0.00	null	null			null	null		null	null		null	null		1.98E+00	5.28E-04	Up	-1.04E+01	8.15E-03									
Unigene113096_All	443	0.00	0.00	0.00	0.00	0.00	0.00	0.19	2.83	0.00	null	null			null	null		null	null		null	null		3.89E+00	8.57E-07	Up	-7.58E+00	3.60E-01		Unigene113096_All//gi|32401039|gb|AAP80725.1|//5.00E-51//histone H3.3 protein [Griffithsia japonica]	Unigene113096_All//2.00E-51//AT5G65360| histone H3				GO:0000785//GO:0003676//GO:0006810//GO:0009536//GO:0031224//GO:0034728	nr -
Unigene113097_All	1249	0.25	0.45	0.30	0.08	0.36	0.00	1.46	4.99	0.83	8.28E-01	3.81E-01			2.48E-01	8.23E-01		2.17E+00	1.06E-01		-6.32E+00	4.04E-01		1.78E+00	6.94E-14	Up	-8.12E-01	5.01E-02		Unigene113097_All//gi|8777580|dbj|BAA97098.1|//1.00E-07//unnamed protein product [Arabidopsis thaliana]		Unigene113097_All//4.00E-07//FL576859				nr -
Unigene113098_All	441	0.00	0.00	0.00	0.00	0.00	0.31	0.86	3.89	2.17	null	null			null	null		null	null		8.26E+00	3.12E-01		2.17E+00	2.00E-05	Up	1.33E+00	3.49E-02		Unigene113098_All//gi|115474457|ref|NP_001060825.1|//3.00E-11//Os08g0111200 [Oryza sativa Japonica Group] >gi|113622794|dbj|BAF22739.1| Os08g0111200 [Oryza sativa Japonica Group]	Unigene113098_All//3.00E-12//AT1G33700| catalytic/ glucosylceramidase				GO:0004553//GO:0006678//GO:0016020//GO:0043231	nr +
Unigene113100_All	364	0.00	0.00	0.00	0.00	0.00	0.00	1.84	0.22	null	null				null	null		null	null		null	null		1.08E+01	7.64E-05	Up	7.77E+00	4.06E-01		Unigene113100_All//gi|13486671|dbj|BAB39908.1|//1.00E-12//P0028E10.12 [Oryza sativa Japonica Group]	Unigene113100_All//7.00E-14//AT2G04865| unknown protein					nr +
Unigene113103_All	350	0.00	0.00	0.00	0.00	0.00	0.00	0.85	3.58	0.00	null	null			null	null		null	null		null	null		2.08E+00	5.41E-04	Up	-9.72E+00	1.58E-02		Unigene113103_All//gi|161015606|gb|ABX55855.1|//8.00E-56//actin [Spumella-like flagellate 1006]	Unigene113103_All//2.00E-54//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene113103_All//8.00E-27//gi|31406833|gb|CD485868.1|CD485868		ko04145|Phagosome	GO:0032559//GO:0043232	nr +
Unigene113106_All	421	0.12	0.24	0.63	0.24	0.33	0.11	0.50	3.18	0.47	9.53E-01	7.27E-01			2.35E+00	2.40E-01		4.68E-01	8.77E-01		-1.14E+00	6.78E-01		2.66E+00	2.41E-05	Up	-8.58E-02	9.61E-01		Unigene113106_All//gi|297330767|ref|XP_002884927.1|//6.00E-30//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330767|gb|EFH61186.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene113106_All//1.00E-24//AT3G12800| SDRB (SHORT-CHAIN DEHYDROGENASE-REDUCTASE B); binding / catalytic/ oxidoreductase	Unigene113106_All//6.00E-53//gi|48880901|gb|C0131923.1|C0131923		ko04146|Peroxisome	GO:0008152//GO:0016020//GO:0016491//GO:0042579	nr -
Unigene113107_All	571	0.27	0.44	0.09	0.00	1.09	0.47	1.04	2.56	0.56	6.91E-01	6.27E-01			-1.56E+00	5.34E-01		1.01E+01	7.90E-04	Up	8.89E+00	7.04E-02		1.31E+00	9.56E-03		-8.93E-01	2.72E-01		Unigene113107_All//gi|15187172|gb|AAK91322.1|AC090441_4//9.00E-39//Putative transposase protein [Oryza sativa Japonica Group]		Unigene113107_All//2.00E-87//ES819408				nr +
Unigene113110_All	231	0.00	0.00	0.00	0.00	0.60	0.00	1.10	6.15	0.86	null	null			null	null		9.22E+00	3.20E-01		null	null		2.49E+00	2.76E-05	Up	-3.49E-01	7.67E-01									
Unigene113111_All	412	0.25	0.98	0.00	0.24	0.00	0.11	0.00	3.45	0.10	1.95E+00	1.44E-01			-7.99E+00	3.97E-01		-7.92E+00	3.16E-01		-1.14E+00	6.78E-01		1.18E+01	4.93E-10	Up	6.60E+00	6.47E-01		Unigene113111_All//gi|18396059|ref|NP_564263.1|//1.00E-21//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|9295734|gb|AAF87040.1|AC006535_18 T24P13.19 [Arabidopsis thaliana] >gi|13605625|gb|AAK32806.1|AF36163 8_1 At1g26800/T24P13_21 [Arabidopsis thaliana] >gi|15450675|gb|AAK96609.1| At1g26800/T24P13_21 [Arabidopsis thaliana] >gi|15777873|gb|AAL05897.1| At1g26800/T24P13_21 [Arabidopsis thaliana]	Unigene113111_All//3.00E-21//AT1G26800| zinc finger (C3HC4-type RING finger) family protein	Unigene113111_All//0.00E+00//DW498401			GO:0046914	nr -
Unigene113112_All	809	0.00	0.00	0.00	0.00	0.00	0.22	1.41	7.39	39.15	null	null			null	null		null	null		7.80E+00	1.95E-01		2.39E+00	3.45E-19	Up	4.79E+00	4.18E-186	Up	Unigene113112_All//gi|224143055|ref|XP_002324836.1|//1.00E-22//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222866270|gb|EEF03401.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene113112_All//2.00E-17//AT4G03070| AOP1; oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene113112_All//0.00E+00//TC137085		ko00904|Diterpenoid biosynthesis	GO:0016491//GO:0044464	nr -
Unigene113115_All	291	216.12	143.48	234.23	172.89	197.14	152.87	10.03	11.49	21.22	-5.91E-01	7.76E-19			1.16E-01	1.11E-01		1.89E-01	6.23E-03		-1.78E-01	2.37E-02		1.97E-01	5.74E-01		1.08E+00	3.78E-07	Up			Unigene113115_All//6.00E-132//TC136859					
Unigene113122_All	223	0.00	0.00	0.00	0.00	0.00	0.00	7.02	4.31	1.25	null	null			null	null		null	null		null	null		-7.03E-01	1.40E-01		-2.49E+00	5.08E-06	Down			Unigene113122_All//1.00E-06//ES844746					ESTscan +
Unigene113132_All	380	0.00	0.00	0.00	0.00	0.00	0.00	0.11	2.09	0.00	null	null			null	null		null	null		null	null		4.23E+00	1.05E-04	Up	-6.80E+00	6.16E-01									
Unigene113139_All	358	10.67	0.28	2.97	37.43	18.37	24.47	0.83	1.63	0.45	-5.24E+00	3.06E-19	Down	-1.84E+00	2.98E-07	Down	-1.03E+00	8.30E-13	Down	-6.13E-01	4.21E-05		9.83E-01	2.59E-01		-8.93E-01	4.71E-01				Unigene113139_All//8.00E-64//TC162673					
Unigene113147_All	417	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.11	0.10	null	null			null	null		null	null		null	null		1.20E+01	4.48E-12	Up	6.58E+00	6.47E-01				Unigene113147_All//2.00E-27//TC153523					
Unigene113174_All	224	0.00	0.68	0.00	0.22	0.00	0.20	0.00	2.61	0.18	9.41E+00	2.36E-01			null	null		-7.80E+00	5.61E-01		-1.42E-01	9.55E-01		1.14E+01	2.81E-04	Up	7.47E+00	6.47E-01		Unigene113174_All//gi|260513724|gb|ACX42574.1|//8.00E-24//CONSTANS-like zinc finger protein [Glycine max]	Unigene113174_All//4.00E-14//AT3G21880| zinc finger (B-box type) family protein		C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0044464//GO:0046914	nr +
Unigene113185_All	304	0.00	0.00	0.00	0.00	0.00	0.00	2.50	6.74	2.75	null	null			null	null		null	null		null	null		1.43E+00	6.34E-04	Up	1.37E-01	8.36E-01		Unigene113185_All//gi|55168340|gb|AAV44205.1|//4.00E-14//unknow protein [Oryza sativa Japonica Group]		Unigene113185_All//4.00E-22//TC160192				nr -
Unigene113186_All	737	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.90	0.00	null	null			null	null		null	null		null	null		1.25E+01	1.33E-30	Up	null	null		Unigene113186_All//gi|8250119|emb|CAB93512.1|//4.00E-07//HSP17.7-a protein [Brassica oleracea var. alboglabra]	Unigene113186_All//1.00E-06//AT5G12030| AT-HSP17.6A (ARABIDOPSIS THALIANA HEAT SHOCK PROTEIN 17.6A); unfolded protein binding					nr -
Unigene113189_All	553	0.00	0.00	0.00	0.00	0.00	0.00	0.54	2.49	0.00	null	null			null	null		null	null		null	null		2.22E+00	1.31E-04	Up	-9.06E+00	1.58E-02		Unigene113189_All//gi|15237805|ref|NP_197756.1|//4.00E-40//LCB2; protein binding / serine C-palmitoyltransferase [Arabidopsis thaliana] >gi|79328575|ref|NP_001031932.1| LCB2; protein binding / serine C-palmitoyltransferase [Arabidopsis thaliana] >gi|8809693|dbj|BAA97234.1| serine palmitoyltransferase [Arabidopsis thaliana]	Unigene113189_All//2.00E-41//AT5G23670| LCB2; protein binding / serine C-palmitoyltransferase	Unigene113189_All//4.00E-08//gi|84169650|gb|DR458298.1|DR458298		ko00600|Sphingolipid metabolism	GO:0005488//GO:0006670//GO:0009639//GO:0016454//GO:0043231//GO:0048229	nr -
Unigene11319_All	4363	16.50	7.51	10.62	25.23	20.95	16.48	13.15	9.96	24.40	-1.13E+00	4.80E-64	Down	-6.36E-01	2.00E-23		-2.69E-01	2.35E-09		-6.15E-01	2.14E-37		-4.01E-01	9.65E-11		8.92E-01	2.24E-79		Unigene11319_All//gi|224128678|ref|XP_002329063.1|//0.00E+00//aminophospholipid ATPase [Populus trichocarpa] >gi|222839734|gb|EEE78057.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene11319_All//0.00E+00//AT1G17500| ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	Unigene11319_All//0.00E+00//TC144897			GO:0005548//GO:0006869//GO:0009206//GO:0031224//GO:0032559//GO:0042625//GO:0043231//GO:0046914	nr +
Unigene113199_All	206	27.94	15.74	21.46	45.95	40.95	52.18	99.13	48.09	59.76	-8.28E-01	8.33E-04		-3.81E-01	1.50E-01		-1.66E-01	4.39E-01		1.84E-01	3.71E-01		-1.04E+00	5.52E-20	Down	-7.30E-01	1.20E-11		Unigene113199_All//gi|209967441|gb|ACJ02349.1|//2.00E-12//60S ribosomal protein L35a [Vernicia fordii]	Unigene113199_All//1.00E-13//AT1G74270| 60S ribosomal protein L35a (RPL35aC)	Unigene113199_All//1.00E-79//TC155009		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +

Unigene11320_A11	1165	2.47	1.87	5.58	6.88	7.86	5.58	3.19	1.44	2.39	-4.01E-01	2.87E-01		1.17E+00	1.82E-06	Up	1.92E-01	3.84E-01		-3.02E-01	1.71E-01		-1.15E+00	6.53E-05	Down	-4.16E-01	1.38E-01		Unigene11320_A11//gi|160892401|gb|ABX52080.1|//4.00E-84//RRP6-like protein 2 [Arabidopsis thaliana]	Unigene11320_A11//6.00E-70//AT5G35910| 3'-5' exonuclease domain-containing protein / helicase and RNase D C-terminal domain-containing protein / HRDC domain-containing protein	Unigene11320_A11//0.00E+00//gi|109857934|gb|DW486913.1|DW486913		ko03018|RNA degradation	GO:0004527//GO:0005488//GO:0034641//GO:0043231	nr -
Unigene113207_A11	350	0.00	0.00	0.00	0.00	0.00	0.00	0.24	4.54	0.80	null	null		null	null		null	null		null	null		4.23E+00	6.26E-09	Up	1.72E+00	2.30E-01		Unigene113207_A11//gi|145408595|ref|YP_001152219.1|//4.00E-10//O8F58| [Pinus koraiensis] >gi|145048844|gb|ABF35460.1|O8F58| [Pinus koraiensis]		Unigene113207_A11//8.00E-24//TC150009			GO:0009536	nr +
Unigene113210_A11	230	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.91	0.69	null	null		null	null		null	null		null	null		1.15E+01	7.64E-05	Up	9.44E+00	1.40E-01		Unigene113210_A11//gi|54399516|gb|AAV34148.1|//5.00E-11//EF-1 alpha-like protein [Helicosporidium sp. ex Simulium jonesi]					GO:0008135//GO:0017111//GO:0032561	nr -
Unigene113211_A11	246	0.00	0.00	0.00	0.00	0.00	0.00	0.17	2.89	0.81	null	null		null	null		null	null		null	null		4.07E+00	3.51E-04	Up	2.24E+00	2.49E-01									
Unigene113212_A11	464	0.00	0.00	0.00	0.00	0.00	0.00	2.73	6.76	0.09	null	null		null	null		null	null		null	null		1.31E+00	5.51E-05	Up	-4.99E+00	3.13E-08	Down	Unigene113212_A11//gi|300137035|gb|EFJ04209.1|//2.00E-17//hypothetical protein SELMODRAFT_139061 [Selaginella moellendorffii]		Unigene113212_A11//1.00E-41//TC148521				nr +
Unigene11323_A11	1486	7.50	9.31	9.53	15.29	13.49	6.44	8.08	6.27	3.54	3.12E-01	4.44E-02		3.46E-01	2.94E-02		-1.81E-01	1.44E-01		-1.25E+00	9.83E-26	Down	-3.66E-01	1.39E-02		-1.19E+00	3.12E-15	Down	Unigene11323_A11//gi|6056391|gb|AAF02855.1|AC009324_4//2.00E-22//Similar to retrotransposon proteins [Arabidopsis thaliana]	Unigene11323_A11//3.00E-05//AT5G48050| unknown protein	Unigene11323_A11//2.00E-86//TC176628				nr -
Unigene113231_A11	380	0.00	0.53	0.84	0.52	0.00	0.00	0.22	6.49	6.08	9.06E+00	1.37E-01		9.72E+00	4.53E-02		-9.03E+00	8.46E-02		-9.03E+00	1.34E-01		4.87E+00	1.04E-14	Up	4.77E+00	6.01E-14	Up								
Unigene113237_A11	270	0.00	0.00	0.00	0.00	0.00	0.00	0.78	3.25	4.28	null	null		null	null		null	null		null	null		2.05E+00	5.68E-03		2.45E+00	1.69E-04	Up								
Unigene11324_A11	278	3.76	8.75	16.09	10.57	8.79	6.01	1.37	1.95	0.72	1.22E+00	3.60E-03		2.10E+00	7.43E-10	Up	-2.66E-01	5.14E-01		-8.15E-01	2.52E-02		5.14E-01	5.89E-01		-9.34E-01	3.80E-01				Unigene11324_A11//4.00E-16//TC176628					
Unigene113240_A11	456	0.00	0.00	0.00	0.11	0.00	0.00	0.19	2.20	0.61	null	null		null	null		-6.77E+00	5.61E-01		-6.77E+00	6.42E-01		3.57E+00	3.08E-05	Up	1.72E+00	2.30E-01				Unigene113240_A11//1.00E-87//gi|73848529|gb|DT457549.1|DT457549					
Unigene113251_A11	425	0.00	0.00	0.00	0.00	0.00	0.00	3.28	14.26	1.97	null	null		null	null		null	null		null	null		2.12E+00	6.79E-17	Up	-7.38E-01	1.28E-01		Unigene113251_A11//gi|238014838|gb|ACR38454.1|//1.00E-13//unknown [Zea mays]		Unigene113251_A11//4.00E-23//ES850594				nr +
Unigene11326_A11	5065	3.06	6.24	4.46	6.16	5.28	4.13	6.89	7.53	5.05	1.03E+00	2.34E-24	Up	5.44E-01	4.55E-06		-2.21E-01	2.26E-02		-5.77E-01	6.88E-10		1.28E-01	1.39E-01		-4.48E-01	1.65E-08		Unigene11326_A11//gi|7444442|pir||T02087//0.00E+00//gag/pol polyprotein - maize retrotransposon Hopscotch >gi|531389|gb|AAA57005.1| copia-like retrotransposon Hopscotch polyprotein [Zea mays]	Unigene11326_A11//2.00E-82//AT4G23160| protein kinase family protein	Unigene11326_A11//0.00E+00//TC165869				nr -
Unigene113268_A11	219	0.00	0.23	0.00	0.00	0.00	0.00	0.77	6.49	0.73	7.85E+00	6.20E-01		null	null		null	null		null	null		3.07E+00	2.15E-06	Up	-8.58E-02	9.66E-01				Unigene113268_A11//2.00E-07//TC165900					
Unigene11327_A11	484	3.68	7.43	3.41	8.34	8.18	7.56	7.86	6.48	3.79	1.02E+00	1.97E-03		-1.08E-01	8.24E-01		-2.70E-02	9.36E-01		-1.41E-01	6.90E-01		-2.80E-01	3.68E-01		-1.05E+00	1.29E-04	Down	Unigene11327_A11//gi|41056592|gb|AB98738.1|//2.00E-55//signal peptide peptidase [Galega orientalis]	Unigene11327_A11//3.00E-55//AT2G03120| ATSPP (ARABIDOPSIS SIGNAL PEPTIDE PEPTIDASE); aspartic-type endopeptidase	Unigene11327_A11//0.00E+00//TC140648			GO:0004175//GO:0031224//GO:0031410	nr -
Unigene113277_A11	207	0.00	0.00	0.00	0.24	0.00	0.00	4.09	7.47	0.38	null	null		null	null		-7.91E+00	5.61E-01		-7.91E+00	6.42E-01		8.71E-01	6.92E-02		-3.41E+00	1.35E-04	Down								
Unigene11328_A11	500	1.05	2.33	1.28	1.20	1.93	1.45	18.27	20.23	8.29	1.16E+00	7.15E-02		2.89E-01	7.25E-01		6.90E-01	3.61E-01		2.74E-01	7.43E-01		1.47E-01	4.24E-01		-1.14E+00	4.61E-11	Down	Unigene11328_A11//gi|41056592|gb|AB98738.1|//5.00E-37//signal peptide peptidase [Galega orientalis]	Unigene11328_A11//3.00E-33//AT2G03120| ATSPP (ARABIDOPSIS SIGNAL PEPTIDE PEPTIDASE); aspartic-type endopeptidase	Unigene11328_A11//0.00E+00//TC131602			GO:0004175//GO:0031224//GO:0031410	nr +
Unigene113286_A11	220	0.24	0.69	0.48	0.45	1.88	1.64	0.77	5.13	0.54	1.54E+00	5.32E-01		1.03E+00	7.04E-01		2.05E+00	1.47E-01		1.86E+00	2.20E-01		2.74E+00	9.94E-05	Up	-5.01E-01	7.47E-01									
Unigene11329_A11	599	1.75	2.37	1.78	1.75	3.33	2.04	7.34	4.81	2.46	4.39E-01	4.26E-01		2.55E-02	9.89E-01		9.33E-01	4.16E-02		2.21E-01	7.22E-01		-6.09E-01	1.86E-02		-1.58E+00	6.31E-09	Down	Unigene11329_A11//gi|297814610|ref|XP_002875188.1|//3.00E-62//signal peptide peptidase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321026|gb|EFH51447.1| signal peptide peptidase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11329_A11//4.00E-55//AT2G03120| ATSPP (ARABIDOPSIS SIGNAL PEPTIDE PEPTIDASE); aspartic-type endopeptidase	Unigene11329_A11//0.00E+00//TC140648			GO:0004175//GO:0031224//GO:0031410	nr -
Unigene113295_A11	228	0.00	0.00	0.00	0.00	0.00	0.00	21.51	1.28	0.00	null	null		null	null		null	null		null	null		-4.07E+00	5.20E-26	Down	-1.44E+01	4.60E-36	Down	Unigene113295_A11//gi|15237245|ref|NP_197105.1|//1.00E-08//3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein [Arabidopsis thaliana] >gi|14190513|gb|AAK55737.1|AF38065_1_AT5g16010/F1N13_150 [Arabidopsis thaliana] >gi|9755647|emb|CAC01800.1| steroid 5alpha-reductase-like protein [Arabidopsis thaliana] >gi|24797018|gb|AAN64521.1| At5g16010/F1N13_150 [Arabidopsis thaliana]	Unigene113295_A11//8.00E-10//AT5G16010| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein					nr +
Unigene11330_A11	1427	0.81	2.24	1.27	4.01	3.35	2.72	4.80	3.95	1.65	1.47E+00	6.16E-05	Up	6.53E-01	2.02E-01		-2.59E-01	3.26E-01		-5.61E-01	2.42E-02		-2.80E-01	1.95E-01		-1.54E+00	4.89E-13	Down	Unigene11330_A11//gi|18395487|ref|NP_565294.1|//1.00E-161//ATSPP (ARABIDOPSIS SIGNAL PEPTIDE PEPTIDASE); aspartic-type endopeptidase [Arabidopsis thaliana] >gi|3548818|gb|AAC34490.1| expressed protein [Arabidopsis thaliana]	Unigene11330_A11//7.00E-154//AT2G03120| ATSPP (ARABIDOPSIS SIGNAL PEPTIDE PEPTIDASE); aspartic-type endopeptidase	Unigene11330_A11//0.00E+00//TC140648				nr +
Unigene113310_A11	265	0.00	0.00	0.00	0.38	0.65	0.17	0.16	3.15	1.05	null	null		null	null		7.89E-01	7.71E-01		-1.14E+00	6.78E-01		4.31E+00	5.68E-05	Up	2.72E+00	9.95E-02				Unigene113310_A11//1.00E-09//TC152940					
Unigene113312_A11	217	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.47	0.00	null	null		null	null		null	null		null	null		1.18E+01	2.07E-05	Up	null	null		Unigene113312_A11//gi|297794223|ref|XP_002864996.1|//3.00E-13//60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|297310831|gb|EFH41255.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene113312_A11//4.00E-13//AT5G67510| 60S ribosomal protein L26 (RPL26B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279//GO:0043231	nr -
Unigene113315_A11	370	0.00	0.68	0.00	0.67	0.00	0.37	1.26	6.10	2.26	9.42E+00	7.88E-02		null	null		-9.39E+00	4.19E-02		-8.78E-01	6.17E-01		2.28E+00	2.69E-07	Up	8.47E-01	2.03E-01		Unigene113315_A11//gi|254212161|gb|ACT65738.1|//6.00E-14//QM [Nicotiana benthamiana]	Unigene113315_A11//3.00E-12//AT1G26910| 60S ribosomal protein L10 (RPL10B)	Unigene113315_A11//4.00E-112//CO093073		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene11333_A11	2747	4.42	4.91	4.89	10.16	9.25	10.74	33.38	24.22	14.00	1.51E-01	3.68E-01		1.45E-01	4.00E-01		-1.35E-01	2.44E-01		8.03E-02	5.20E-01		-4.63E-01	1.59E-21		-1.25E+00	8.64E-120	Down	Unigene11333_A11//gi|15215736|gb|AB91413.1|//0.00E+00//AT5g19690/T29J13_110 [Arabidopsis thaliana] >gi|16974315|gb|AL31142.1| AT5g19690/T29J13_110 [Arabidopsis thaliana]	Unigene11333_A11//0.00E+00//AT5G19690| STT3A (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE A); oligosaccharyl transferase	Unigene11333_A11//0.00E+00//gi|73862681|gb|DT465420.1|DT465420		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0006464//GO:0006970//GO:0016020//GO:0043231	nr +
Unigene113337_A11	212	0.00	0.00	0.00	0.00	0.00	0.00	0.40	3.94	0.00	null	null		null	null		null	null		null	null		3.31E+00	3.10E-04	Up	-8.64E+00	3.60E-01		Unigene113337_A11//sp|P23403|RS20_XENLA//2.00E-07//40S ribosomal protein S20 OS=Xenopus laevis GN=rps20 PE=3 SV=1	Unigene113337_A11//9.00E-05//AT5G62300| 40S ribosomal protein S20 (RPS20C)			ko03010|Ribosome		swissprot +
Unigene113341_A11	244	0.00	0.00	0.00	0.00	0.00	0.00	2.77	1.03	11.10	null	null		null	null		null	null		null	null		-1.43E+00	7.84E-02		2.00E+00	1.20E-07	Up								
Unigene113354_A11	544	0.00	0.00	0.00	0.00	0.00	0.00	1.01	3.30	0.00	null	null		null	null		null	null		null	null		1.71E+00	2.41E-04	Up	-9.98E+00	2.81E-04	Down	Unigene113354_A11//gi|301117174|ref|XP_002906315.1|//1.00E-32//60S ribosomal protein L35a-4 [Phytophthora infestans T30-4] >gi|66270185|gb|AAY43422.1| ribosomal protein L35 [Phytophthora infestans] >gi|262107664|gb|EEY65716.1| 60S ribosomal protein L35a-4 [Phytophthora infestans T30-4]	Unigene113354_A11//1.00E-29//AT3G55750| 60S ribosomal protein L35a (RPL35aD)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr -
Unigene11336_A11	2972	1.43	1.18	2.19	3.08	2.39	2.77	8.28	5.74	2.45	-2.78E-01	3.63E-01		6.16E-01	1.05E-02		-3.70E-01	4.93E-02		-1.57E-01	4.76E-01		-5.29E-01	6.36E-08		-1.76E+00	1.74E-53	Down	Unigene11336_A11//gi|18419993|ref|NP_568380.1|//0.00E+00//STT3A (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE A); oligosaccharyl transferase [Arabidopsis thaliana]	Unigene11336_A11//0.00E+00//AT5G19690| STT3A (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE A); oligosaccharyl transferase	Unigene11336_A11//0.00E+00//TC142353		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0006464//GO:0006970//GO:0016020//GO:0043231	nr +
Unigene113364_A11	289	0.18	0.18	0.37	0.00	0.00	0.00	2.19	3.18	0.00	-4.62E-02	9.86E-01		1.03E+00	7.04E-01		null	null		null	null		5.36E-01	4.18E-01		-1.11E+01	7.11E-05	Down								
Unigene113367_A11	254	0.00	0.00	0.00	0.00	0.00	0.00	2.50	2.63	0.00	null	null		null	null		null	null		null	null		7.65E-02	9.37E-01		-1.13E+01	7.11E-05	Down	Unigene113367_A11//gi|2894308|emb|CAA11269.1|//1.00E-40//polyubiquitin [Nicotiana tabacum]	Unigene113367_A11//6.00E-41//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene113367_A11//2.00E-42//BM359461			GO:0043231	nr -
Unigene113373_A11	427	0.00	0.00	0.00	0.00	0.00	0.00	1.49	1.66	0.00	null	null		null	null		null	null		null	null		1.64E-01	8.24E-01		-1.05E+01	7.11E-05	Down								ESTscan -
Unigene113377_A11	535	0.00	0.00	0.00	0.00	0.00	0.00	0.55	2.58	0.00	null	null		null	null		null	null		null	null		2.22E+00	1.31E-04	Up	-9.11E+00	1.58E-02		Unigene113377_A11//gi|301092807|ref|XP_002997255.1|//4.00E-34//Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4] >gi|262111436|gb|EEY69488.1| Mitochondrial Carrier (MC) Family [Phytophthora infestans T30-4]	Unigene113377_A11//1.00E-32//AT5G14040| mitochondrial phosphate transporter				GO:0016020	nr -
Unigene113384_A11	505	0.00	0.00	0.00	0.00	0.00	0.00	1.09	2.48	0.00	null	null		null	null		null	null		null	null		1.19E+00	3.01E-02		-1.01E+01	2.81E-04	Down	Unigene113384_A11//gi|159477048|ref|XP_001696623.1|//6.00E-11//serine/threonine phosphatase, family 2C [Chlamydomonas reinhardtii] >gi|158282848|gb|EDP08600.1| serine/threonine phosphatase, family 2C [Chlamydomonas reinhardtii]	Unigene113384_A11//2.00E-09//AT4G33500| protein phosphatase 2C-related / PP2C-related				GO:0003824//GO:0009536	nr +
Unigene11341_A11	2782	22.46	84.20	51.49	25.34	41.21	53.18	23.10	26.04	34.15	1.91E+00	0.00E+00	Up	1.20E+00	4.44E-134	Up	7.02E-01	6.33E-54		1.07E+00	1.08E-127	Up	1.73E-01	2.40E-03		5.64E-01	2.40E-32		Unigene11341_A11//gi|30689342|ref|NP_850393.1|//1.00E-142//INT1 (INOSITOL TRANSPORTER 1); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|75331205|sp|Q8VZ86.1|INT1_ARATH RecName: Full=Probable inositol transporter 1 >gi|84617967|emb|CAJ00303.1| inositol transporter 1 [Arabidopsis thaliana]	Unigene11341_A11//9.00E-113//AT2G43330| INT1 (INOSITOL TRANSPORTER 1); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen symporter	Unigene11341_A11//0.00E+00//TC168474			GO:0006810//GO:0022857//GO:0031224	nr -
Unigene113412_A11	844	0.00	0.00	0.00	0.00	0.00	0.00	2.50	5.30	0.66	null	null		null	null		null	null		null	null		1.08E+00	3.06E-05	Up	-1.92E+00	5.97E-06	Down	Unigene113412_A11//gi|253761439|ref|XP_002489117.1|//3.00E-14//hypothetical protein SORBIDRAFT_0057s002150 [Sorghum bicolor] >gi|241947368|gb|EES20513.1| hypothetical protein SORBIDRAFT_0057s002150 [Sorghum bicolor]		Unigene113412_A11//5.00E-27//ES850594				nr +
Unigene113414_A11	1149	0.41	0.09	0.00	0.00	0.15	0.16	1.40	3.64	1.04	-2.22E+00	7.77E-02		-8.68E+00	8.66E-03		7.23E+00	2.27E-01		7.30E+00	1.95E-01		1.38E+00	7.10E-07	Up	-4.27E-01	3.59E-01									

Unigene113417_All	290	0.00	0.00	0.00	0.00	0.00	0.00	0.15	2.16	2.20	null	null		null	null		null	null		null	null		3.89E+00	1.15E-03		3.91E+00	7.66E-04	Up	Unigene113417_All//gi|297610014|ref|NP_001060026.2|//4.00E-09//Os10g0106900 [Oryza sativa Japonica Group] >gi|255679164|dbj|BAF25940.2|Os10g0106900 [Oryza sativa Japonica Group]					GO:0003676//GO:0006259//GO:0006810//GO:0016020//GO:0016209//GO:0046872	nr +
Unigene113423_All	280	0.19	0.36	0.00	0.00	0.00	0.00	333.71	379.00	754.80	9.53E-01	7.27E-01		-7.55E+00	6.30E-01		null	null		null	null		1.84E-01	5.52E-05		1.18E+00	4.65E-247	Up	Unigene113423_All//gi|242070913|ref|XP_002450733.1|//4.00E-16//hypothetical protein SORBIDRAFT_05g016477 [Sorghum bicolor] >gi|241936576|gb|EES09721.1|hypothetical protein SORBIDRAFT_05g016477 [Sorghum bicolor]		Unigene113423_All//4.00E-56//ES810795				nr -
Unigene113427_All	367	0.00	0.00	0.00	0.00	0.00	0.00	1.61	2.73	0.00	null	null		null	null		null	null		null	null		7.61E-01	2.28E-01		-1.07E+01	1.41E-04	Down	Unigene113427_All//gi|160330969|ref|XP_001712192.1|//2.00E-37//ef2 [Hemiselmis andersenii] >gi|159765639|gb|ABW97867.1| ef2 [Hemiselmis andersenii]	Unigene113427_All//1.00E-24//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene113427_All//1.00E-07//gi|78340849|gb|DT561123.1|DT561123			GO:0008135//GO:0017111//GO:0032561	nr +
Unigene11343_All	1871	2.68	1.68	1.59	6.04	6.13	3.81	5.31	3.02	2.17	-6.77E-01	1.12E-02		-7.52E-01	7.07E-03		2.02E-02	9.32E-01		-6.64E-01	5.52E-05		-8.16E-01	5.44E-07		-1.29E+00	2.45E-14	Down	Unigene11343_All//gi|83319215|dbj|BAE53712.1|//2.00E-72//At3g21480 [Arabidopsis thaliana]	Unigene11343_All//8.00E-73//AT3G21480| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: intracellular; CONTAINS InterPro DOMAIN/s: BRCT (InterPro:IPR001357); BEST Arabidopsis thaliana protein match is: transcription coactivator (TAIR:AT4G03130.1); Has 489 Blast hits to 455 proteins in 115 species: Archae - 2; Bacteria - 37; Metazoa - 270; Fungi - 30; Plants - 45; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).	Unigene11343_All//0.00E+00//ES830964				nr -
Unigene113433_All	503	0.00	0.00	0.00	0.00	0.09	0.50	11.72	0.32	null	null		null	null		null	null		6.49E+00	7.01E-01		4.54E+00	2.65E-33	Up	-6.71E-01	6.06E-01		Unigene113433_All//gi|224085625|ref|XP_002307640.1|//6.00E-42//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222857089|gb|EEE94636.1| AP2/EBP domain-containing transcription factor [Populus trichocarpa]	Unigene113433_All//8.00E-20//AT3G23230| ethylene-responsive factor, putative	Unigene113433_All//1.00E-171//DT461789	AP2-EREBP		GO:0000160//GO:0000071//GO:0006351//GO:0009743//GO:0010468//GO:0043231	nr -
Unigene11344_All	3341	2.27	1.71	1.43	3.03	3.28	3.26	3.80	1.81	1.63	-4.06E-01	5.91E-02		-6.63E-01	2.59E-03		1.15E-01	5.83E-01		1.06E-01	6.38E-01		-1.07E+00	3.96E-13	Down	-1.22E+00	1.48E-16	Down	Unigene11344_All//gi|83319215|dbj|BAE53712.1|//1.00E-55//At3g21480 [Arabidopsis thaliana]	Unigene11344_All//2.00E-48//AT3G21480| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: intracellular; CONTAINS InterPro DOMAIN/s: BRCT (InterPro:IPR001357); BEST Arabidopsis thaliana protein match is: transcription coactivator (TAIR:AT4G03130.1); Has 489 Blast hits to 455 proteins in 115 species: Archae - 2; Bacteria - 37; Metazoa - 270; Fungi - 30; Plants - 45; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).	Unigene11344_All//0.00E+00//ES825416				nr -
Unigene113444_All	479	0.00	0.00	0.00	0.00	0.14	0.00	19.77	4.89	5.49	null	null		null	null		7.17E+00	6.14E-01		null	null		-2.02E+00	1.69E-24	Down	-1.85E+00	1.28E-22	Down	Unigene113444_All//gi|124361039|gb|ABN09011.1|//2.00E-36//General substrate transporter; Sugar transporter superfamily [Medicago truncatula]	Unigene113444_All//2.00E-37//AT4G04750| carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene113444_All//4.00E-125//gi|48820844|gb|CO122157.1|CO122157			GO:0005215//GO:0006810	nr -
Unigene11345_All	1563	8.80	6.39	6.95	14.37	13.79	14.74	15.69	6.12	4.82	-4.63E-01	2.26E-03		-3.41E-01	3.55E-02		-5.96E-02	6.78E-01		3.60E-02	7.89E-01		-1.36E+00	9.82E-36	Down	-1.70E+00	3.78E-51	Down	Unigene11345_All//gi|186528371|ref|NP_198994.2|//9.00E-62//CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding [Arabidopsis thaliana]	Unigene11345_All//5.00E-63//AT5G41790| CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding	Unigene11345_All//0.00E+00//gi|84146467|gb|DN760709.1|DN760709				nr -
Unigene113454_All	406	0.00	0.00	0.00	0.00	0.00	0.00	1.56	1.54	0.00	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		-1.06E+01	7.11E-05	Down							ESTscan +
Unigene11346_All	320	0.00	0.32	0.17	0.16	0.22	0.28	2.91	1.31	0.37	8.31E+00	3.89E-01		7.38E+00	6.39E-01		4.67E-01	9.60E-01		8.59E-01	7.96E-01		-1.15E+00	7.87E-02		-2.96E+00	1.72E-04	Down	Unigene11346_All//gi|186528371|ref|NP_198994.2|//2.00E-11//CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding [Arabidopsis thaliana]	Unigene11346_All//7.00E-13//AT5G41790| CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding	Unigene11346_All//2.00E-122//gi|21101346|gb|BQ413659.1|BQ413659			GO:0010038//GO:0016020//GO:0043231	nr -
Unigene113460_All	673	0.00	0.00	0.00	0.00	0.00	0.00	0.38	2.98	0.89	null	null		null	null		null	null		null	null		2.98E+00	1.47E-08	Up	1.24E+00	1.39E-01		Unigene113460_All//gi|55168340|gb|AAV44205.1|//5.00E-28//unknow protein [Oryza sativa Japonica Group]		Unigene113460_All//3.00E-28//TC149394				nr -
Unigene113461_All	220	0.00	0.00	0.00	0.00	0.00	0.00	11.34	1.33	0.00	null	null		null	null		null	null		null	null		-3.09E+00	7.09E-11	Down	-1.35E+01	2.32E-18	Down			Unigene113461_All//1.00E-15//TC134836				
Unigene113464_All	528	0.00	0.00	0.00	0.00	0.00	0.00	3.52	12.19	0.00	null	null		null	null		null	null		null	null		1.79E+00	1.77E-14	Up	-1.18E+01	9.96E-14	Down							
Unigene11347_All	627	0.42	1.13	3.31	4.45	7.52	7.06	3.30	2.27	2.41	1.44E+00	1.06E-01		2.99E+00	5.58E-07	Up	7.58E-01	4.71E-03		6.66E-01	2.14E-02		-5.44E-01	1.85E-01		-4.53E-01	2.48E-01		Unigene11347_All//gi|186528371|ref|NP_198994.2|//5.00E-27//CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding [Arabidopsis thaliana]	Unigene11347_All//2.00E-22//AT5G41790| CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding	Unigene11347_All//4.00E-70//TC144925			GO:0016020//GO:0043231	nr +
Unigene113474_All	236	12.86	27.70	11.73	92.66	63.33	24.11	1.07	2.30	0.84	1.11E+00	2.90E-06	Up	-1.32E-01	7.19E-01		-5.49E-01	3.12E-07		-1.94E+00	4.84E-47	Down	1.10E+00	2.36E-01		-3.49E-01	7.67E-01		Unigene113474_All//gi|42571085|ref|NP_973616.1|//2.00E-11//ROT4 (ROTUNDIFOLIA4) [Arabidopsis thaliana] >gi|42822065|tpg|DAA02287.1|TPA_exp: DVL16 [Arabidopsis thaliana] >gi|109134191|gb|ABG25093.1|At2g36985 [Arabidopsis thaliana]	Unigene113474_All//6.00E-13//AT2G36985| ROT4 (ROTUNDIFOLIA4)	Unigene113474_All//4.00E-34//ES850629			GO:0008283//GO:0016020//GO:0048513	nr -
Unigene11348_All	2930	10.84	20.27	11.74	11.43	11.80	10.65	19.90	9.71	6.44	9.03E-01	2.10E-36		1.15E-01	2.84E-01		4.66E-02	7.01E-01		-1.01E-01	3.76E-01		-1.03E+00	9.26E-55	Down	-1.63E+00	8.25E-113	Down	Unigene11348_All//gi|186528371|ref|NP_198994.2|//1.00E-113//CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding [Arabidopsis thaliana]	Unigene11348_All//8.00E-87//AT5G41790| CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding	Unigene11348_All//0.00E+00//gi|164252827|gb|ES843361.1|ES843361			GO:0044464	nr +
Unigene113484_All	238	0.00	4.05	1.34	0.42	0.00	0.00	0.00	2.11	2.34	1.20E+01	1.38E-05	Up	1.04E+01	4.53E-02		-8.71E+00	3.16E-01		-8.71E+00	4.04E-01		1.10E+01	1.02E-03		1.12E+01	3.28E-04	Up							
Unigene11349_All	4757	6.09	4.78	4.75	8.86	9.06	9.67	13.42	5.84	3.91	-3.50E-01	5.41E-04		-3.60E-01	5.87E-04		3.17E-02	7.93E-01		1.26E-01	1.58E-01		-1.20E+00	7.38E-76	Down	-1.78E+00	4.26E-140	Down	Unigene11349_All//gi|186528371|ref|NP_198994.2|//1.00E-95//CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding [Arabidopsis thaliana]	Unigene11349_All//4.00E-85//AT5G41790| CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding	Unigene11349_All//0.00E+00//TC146762			GO:0044464	nr -
Unigene11350_All	208	0.00	0.00	0.00	0.96	0.66	0.43	2.03	20.09	6.51	null	null		null	null		-5.33E-01	7.49E-01		-1.14E+00	5.70E-01		3.31E+00	7.69E-19	Up	1.68E+00	1.63E-03		Unigene11350_All//gi|224054398|ref|XP_002298240.1|//1.00E-26//ABC transporter family, pleiotropic drug resistance protein [Populus trichocarpa] >gi|222845498|gb|EEE83045.1| ABC transporter family, pleiotropic drug resistance protein [Populus trichocarpa]	Unigene11350_All//1.00E-22//AT1G15210| PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATPase, coupled to transmembrane movement of substances	Unigene11350_All//8.00E-103//gi|73859385|gb|DT462124.1|DT462124				nr +
Unigene113507_All	406	0.00	0.00	0.00	0.00	0.00	0.00	0.42	2.57	0.00	null	null		null	null		null	null		null	null		2.63E+00	2.86E-04	Up	-8.70E+00	1.09E-01		Unigene113507_All//gi|247421835|gb|ACS96445.1|//2.00E-27//S18 A ribosomal protein [Jatropha curcas]	Unigene113507_All//1.00E-28//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome	Unigene113507_All//5.00E-10//ES845901		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006412//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr +
Unigene11351_All	281	0.19	0.72	1.52	0.18	1.96	0.96	12.04	41.80	31.47	1.95E+00	3.75E-01		3.03E+00	5.73E-02		3.47E+00	1.22E-02		2.44E+00	2.22E-01		1.80E+00	6.75E-26	Up	1.39E+00	3.96E-14	Up	Unigene11351_All//gi|224054398|ref|XP_002298240.1|//2.00E-43//ABC transporter family, pleiotropic drug resistance protein [Populus trichocarpa] >gi|222845498|gb|EEE83045.1| ABC transporter family, pleiotropic drug resistance protein [Populus trichocarpa]	Unigene11351_All//4.00E-43//AT1G15210| PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATPase, coupled to transmembrane movement of substances			ko03040|Spliceosome//ko02010|ABC transporters	GO:0000041//GO:0009526//GO:0009814//GO:0015082//GO:0015604//GO:0015893//GO:0016020//GO:0019762//GO:0032559//GO:0042626//GO:0050832//GO:0052482//GO:0071365	nr -
Unigene11352_All	463	1.24	0.77	1.38	1.08	3.27	4.97	187.29	236.24	557.83	-6.98E-01	4.50E-01		1.51E-01	8.56E-01		1.60E+00	4.07E-03		2.21E+00	3.75E-06	Up	3.35E-01	2.42E-14		1.57E+00	0.00E+00	Up	Unigene11352_All//gi|256538309|gb|ACU82514.1|//2.00E-72//pleiotropic drug resistance protein [Cucumis sativus]	Unigene11352_All//5.00E-73//AT1G15210| PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATPase, coupled to transmembrane movement of substances			ko03040|Spliceosome//ko02010|ABC transporters	GO:0000041//GO:0009526//GO:0009814//GO:0015082//GO:0015604//GO:0015893//GO:0016020//GO:0017111//GO:0019762//GO:0032559//GO:0050832//GO:0052482//GO:0071365	nr +
Unigene11353_All	877	0.18	0.58	0.30	0.45	1.45	2.37	136.96	174.52	354.91	1.69E+00	1.34E-01		7.62E-01	6.44E-01		1.68E+00	7.61E-03		2.38E+00	4.55E-06	Up	3.50E-01	2.55E-21		1.37E+00	0.00E+00	Up	Unigene11353_All//gi|225442485|ref|XP_002278313.1|//1.00E-153//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene11353_All//1.00E-144//AT1G15210| PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATPase, coupled to transmembrane movement of substances	Unigene11353_All//0.00E+00//TC177387		ko03040|Spliceosome//ko02010|ABC transporters		nr +
Unigene113535_All	339	0.31	2.69	0.00	1.32	0.61	0.93	1.75	7.77	1.41	3.12E+00	1.14E-03		-8.27E+00	3.97E-01		-1.12E+00	3.15E-01		-5.04E-01	6.49E-01		2.15E+00	6.92E-08	Up	-3.08E-01	6.79E-01				Unigene113535_All//3.00E-51//TC160704				
Unigene113539_All	669	0.00	0.00	0.00	0.15	0.31	0.00	0.13	2.94	0.54	null	null		null	null		1.05E+00	6.13E-01		-7.22E+00	4.03E-01		4.54E+00	2.20E-11	Up	2.08E+00	1.01E-01			Unigene113539_All//1.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative					
Unigene11354_All	4943	2.89	5.29	2.68	5.22	5.25	6.41	101.23	169.58	248.74	8.72E-01	1.47E-15		-1.07E-01	5.44E-01		8.90E-03	9.62E-01		2.97E-01	1.99E-03		7.44E-01	0.00E+00		1.30E+00	0.00E+00	Up	Unigene11354_All//gi|225442485|ref|XP_002278313.1|//0.00E+00//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene11354_All//0.00E+00//AT1G59870| PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	Unigene11354_All//0.00E+00//TC136716		ko03040|Spliceosome//ko02010|ABC transporters	GO:0000041//GO:0009526//GO:0009814//GO:0015082//GO:0015893//GO:0016020//GO:0016887//GO:0019762//GO:0050832//GO:0052482//GO:0071365	nr +
Unigene11355_All	2113	0.10	0.05	0.15	3.35	2.40	4.02	12.39	6.17	27.00	-1.04E+00	5.65E-01		6.11E-01	6.25E-01		-4.83E-01	2.28E-02		2.63E-01	2.32E-01		-1.01E+00	6.73E-24	Down	1.12E+00	1.61E-62	Up	Unigene11355_All//gi|253740260|gb|ACT34764.1|//0.00E+00//subtilisin-like protease preproenzyme [Nicotiana tabacum]	Unigene11355_All//2.00E-146//AT5G67090| subtilase family protein	Unigene11355_All//0.00E+00//TC139051			GO:0008152//GO:0016491//GO:0031410//GO:0070011	nr -
Unigene113550_All	456	0.11	0.33	0.00	0.44	0.91	0.00	0.74	2.02	4.19	1.54E+00	5.32E-01		-6.84E+00	6.30E-01		1.05E+00	4.26E-01		-8.77E+00	1.34E-01		1.44E+00	3.26E-02		2.50E+00	4.21E-07	Up			Unigene113550_All//5.00E-07//TC179376				
Unigene113558_All	492	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.63	0.00	null	null		null	null		null	null		null	null		1.14E+01	3.67E-09	Up	null	null		Unigene113558_All//gi|1350517|gb|AAB01561.1|//2.00E-06//heat shock protein 17.0 [Picea glauca]	Unigene113558_All//2.00E-05//AT1G07400| 17.8 kDa class I heat shock protein (HSP17.8-CI)					nr -

Unigene11356_All	2618	184.46	32.38	88.80	44.79	56.48	34.40	55.96	113.00	65.11	-2.51E+00	0.00E+00	Down	-1.05E+00	0.00E+00	Down	3.35E-01	2.60E-18		-3.81E-01	7.00E-17		1.01E+00	1.18E-265	Up	2.19E-01	1.78E-10		Unigene11356_All//gi|253740260|gb|ACT34764.1|//0.00E+00//subtilisin-like protease preproenzyme [Nicotiana tabacum]	Unigene11356_All//3.00E-167//AT5G67090| subtilase family protein	Unigene11356_All//0.00E+00//TC139051			GO:0004175//GO:0005515//GO:0016628//GO:0019538//GO:0004092	nr -
Unigene113563_All	361	0.00	0.00	0.00	0.00	0.00	0.00	0.23	5.79	0.66	null	null		null	null		null	null		null	null		4.63E+00	3.28E-12	Up	1.50E+00	3.39E-01		Unigene113563_All//gi|145048582|ref|YP_001152206.1|//1.00E-10//08F137 [Pinus koraiensis] >gi|145048831|gb|ABP35449.1|08F137 [Pinus koraiensis]		Unigene113563_All//1.00E-25//gi|109823694|gb|DW008546.1|DW008546			GO:0009536	nr +
Unigene113569_All	261	246.77	101.92	139.96	363.20	545.56	413.57	455.52	174.87	180.11	-1.28E+00	6.41E-69	Down	-8.18E-01	2.45E-32		5.87E-01	6.56E-49		1.87E-01	1.59E-04		-1.38E+00	5.46E-175	Down	-1.34E+00	1.54E-171	Down	Unigene113569_All//gi|223469631|gb|ACM00156.1|//5.00E-15//40S ribosomal protein S15-like protein [Jatropha curcas]	Unigene113569_All//1.00E-12//AT5G09500| 40S ribosomal protein S15 (RPS15C)	Unigene113569_All//4.00E-99//TC171659	ko03010|Ribosome		GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene11357_All	804	0.26	0.76	0.99	1.18	1.37	0.90	1.58	1.35	3.62	1.54E+00	1.22E-01		1.93E+00	3.42E-02		2.19E-01	7.93E-01		-3.89E-01	6.28E-01		-2.23E-01	6.77E-01		1.20E+00	2.46E-04	Up	Unigene11357_All//gi|22328551|ref|NP_192745.2|//2.00E-21//KH domain-containing protein [Arabidopsis thaliana]	Unigene11357_All//1.00E-11//AT4G10070| KH domain-containing protein	Unigene11357_All//1.00E-169//gi|78338319|gb|DT558593.1|DT558593			GO:0003676	nr +
Unigene113578_All	236	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.83	0.00	null	null		null	null		null	null		null	null		1.15E+01	7.64E-05	Up	null	null									
Unigene113579_All	667	0.00	0.00	0.00	0.00	0.00	0.00	0.89	2.13	0.00	null	null		null	null		null	null		null	null		1.26E+00	1.33E-02		-9.79E+00	1.41E-04	Down	Unigene113579_All//gi|115464309|ref|NP_001055754.1|//2.00E-84//Os05g0460000 [Oryza sativa Japonica Group] >gi|113579305|dbj|BAF17668.1|Os05g0460000 [Oryza sativa Japonica Group]	Unigene113579_All//8.00E-83//AT1G56410| ERD2 (EARLY-RESPONSIVE TO DEHYDRATION 2); ATP binding	Unigene113579_All//8.00E-07//TC142196	ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr +
Unigene113594_All	489	0.54	0.93	0.22	1.43	0.77	0.09	0.43	2.31	1.47	8.02E-01	4.60E-01		-1.30E+00	4.37E-01		-8.81E-01	3.00E-01		-3.95E+00	1.46E-03		2.42E+00	3.17E-04	Up	1.76E+00	2.48E-02				Unigene113594_All//6.00E-07//AT729024				
Unigene113608_All	310	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.83	0.00	null	null		null	null		null	null		null	null		1.15E+01	2.86E-06	Up	null	null									ESTscan -
Unigene113622_All	259	67.88	59.67	41.12	61.16	58.23	61.55	15.51	7.26	12.61	-1.86E-01	1.95E-01		-7.23E-01	1.27E-07		-7.08E-02	6.80E-01		9.20E-03	9.50E-01		-1.09E+00	7.04E-05	Down	-2.98E-01	2.83E-01				Unigene113622_All//5.00E-92//gi|210939319|gb|BQ406232.1|BQ406232				
Unigene11363_All	2366	3.38	2.48	1.60	7.54	8.43	6.28	8.20	5.79	8.18	-4.46E-01	3.15E-02		-1.08E+00	6.51E-07	Down	1.61E-01	2.48E-01		-2.63E-01	5.64E-02		-5.01E-01	6.69E-06		-3.30E-03	9.73E-01		Unigene11363_All//gi|115466596|ref|NP_001056897.1|//0.00E+00//Os06g0163500 [Oryza sativa Japonica Group] >gi|113594937|dbj|BAF18811.1|Os06g0163500 [Oryza sativa Japonica Group]	Unigene11363_All//0.00E+00//AT5G19660| S1P (SITE-1 PROTEASE); endopeptidase/ serine-type endopeptidase	Unigene11363_All//0.00E+00//gi|164284100|gb|ES816654.1|ES816654	ko04141|Protein processing in endoplasmic reticulum		GO:0004175//GO:0006972//GO:0019538//GO:0043231	nr +
Unigene113631_All	243	0.00	0.00	0.00	0.00	0.00	0.00	2.26	1.20	0.00	null	null		null	null		null	null		null	null		-9.10E-01	3.19E-01		-1.11E+01	2.81E-04	Down								ESTscan +
Unigene113645_All	277	0.00	0.00	0.00	0.00	0.00	0.00	3.36	11.92	4.89	null	null		null	null		null	null		null	null		1.83E+00	5.46E-08	Up	5.42E-01	2.85E-01				Unigene113645_All//5.00E-49//TC142576				
Unigene11365_All	1046	11.00	8.43	9.93	41.72	32.69	31.69	18.67	8.83	6.89	-3.85E-01	2.35E-02		-1.49E-01	4.30E-01		-3.52E-01	2.19E-06		-3.97E-01	3.66E-07		-1.08E+00	3.26E-20	Down	-1.44E+00	4.07E-32	Down	Unigene11365_All//gi|17978924|gb|AAL47429.1|//1.00E-85//AT5g65290/K9E15_7 [Arabidopsis thaliana]	Unigene11365_All//3.00E-84//AT5G45290| zinc finger (C3HC4-type RING finger) family protein	Unigene11365_All//0.00E+00//TC133491			GO:0009536//GO:0046914	nr -
Unigene113660_All	1389	0.00	0.00	0.00	0.00	0.00	0.00	0.03	5.99	0.00	null	null		null	null		null	null		null	null		7.62E+00	9.90E-57	Up	-4.93E+00	6.16E-01		Unigene113660_All//gi|253759874|ref|XP_002488951.1|//2.00E-14//hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor] >gi|241947058|gb|EES20203.1|hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor]		Unigene113660_All//4.00E-41//gi|78352089|gb|DT572363.1|DT572363				nr +
Unigene113664_All	223	0.00	0.00	0.00	0.00	0.00	0.00	9.86	1.12	3.93	null	null		null	null		null	null		null	null		-3.13E+00	9.10E-10	Down	-1.33E+00	5.61E-04	Down	Unigene113664_All//gi|15232607|ref|NP_187533.1|//3.00E-09//LAC7 (laccase 7); laccase [Arabidopsis thaliana] >gi|75337548|sp|Q9SR40.1|LAC7_ARATH RecName: Full=Laccase-7; AltName: Full=Benzenediol:oxygen oxidoreductase 7; AltName: Full=Urishiol oxidase 7; AltName: Full=Diphenol oxidase 7; Flags: Precursor	Unigene113664_All//3.00E-09//AT3G09220| LAC7 (laccase 7); laccase				GO:0005576//GO:0009808//GO:0016682//GO:0031410//GO:0046914	nr -
Unigene113668_All	374	0.14	0.81	0.00	0.00	0.28	0.60	0.57	2.79	0.96	2.54E+00	1.51E-01		-7.13E+00	6.30E-01		8.11E+00	4.58E-01		9.24E+00	1.19E-01		2.31E+00	8.56E-04	Up	7.62E-01	5.00E-01		Unigene113668_All//gi|20245|emb|CAA38315.1|//5.00E-21//Glycine-rich protein [Oryza sativa (indica cultivar-group)] >gi|1167657|gb|AAA85863.1|glycine-rich cell wall protein [Oryza sativa]				ko03040|Spliceosome	GO:0031410	nr +
Unigene113669_All	534	0.20	1.33	0.80	0.47	0.19	0.34	1.35	5.40	0.97	2.76E+00	9.15E-03		2.03E+00	1.40E-01		-1.27E+00	4.24E-01		-4.63E-01	7.45E-01		2.00E+00	6.86E-08	Up	-4.73E-01	5.20E-01		Unigene113669_All//gi|186506016|gb|AAL75907.1|//7.00E-35//AT4g03420/F9H3_4 [Arabidopsis thaliana] >gi|20452247|gb|AAM19862.1|AT4g03420/F9H3_4 [Arabidopsis thaliana]	Unigene113669_All//3.00E-29//AT4G03420| unknown protein	Unigene113669_All//1.00E-69//TC143805				nr +
Unigene113673_All	448	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.31	0.00	null	null		null	null		null	null		null	null		1.04E+01	2.81E-04	Up	null	null		Unigene113673_All//gi|219119111|ref|XP_002180322.1|//2.00E-41//glutathione reductase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217408579|gb|EEC48513.1|glutathione reductase [Phaeodactylum tricornutum CCAP 1055/1]	Unigene113673_All//2.00E-23//AT3G54660| GR (GLUTATHIONE REDUCTASE); ATP binding / glutathione-disulfide reductase		ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism	GO:0006790//GO:0015038//GO:0016651//GO:0019725//GO:0030554//GO:0044424	nr +
Unigene113677_All	209	0.00	0.00	0.00	4.77	0.82	0.00	0.81	1.80	0.19	null	null		null	null		-2.53E+00	6.75E-04	Down	-1.22E+01	2.97E-06	Down	1.15E+00	3.28E-01		-2.09E+00	3.14E-01				Unigene113677_All//2.00E-23//DW517725				
Unigene113681_All	372	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.47	0.00	null	null		null	null		null	null		null	null		1.13E+01	1.48E-06	Up	null	null									
Unigene113685_All	244	3.86	0.21	0.87	1.02	0.56	0.93	0.52	0.34	0.16	-4.22E+00	1.36E-04	Down	-2.14E+00	1.16E-02		-8.55E-01	5.74E-01		-1.41E-01	9.29E-01		-6.01E-01	7.67E-01		-1.67E+00	4.78E-01		Unigene113685_All//gi|222424875|dbj|BAH20389.1|//2.00E-16//AT3G53950 [Arabidopsis thaliana]	Unigene113685_All//6.00E-29//AT3G53950| glyoxal oxidase-related	Unigene113685_All//3.00E-50//EST99287			GO:0044464	nr +
Unigene113689_All	230	26.16	6.39	10.42	38.55	34.88	57.93	82.72	28.35	46.42	-2.03E+00	3.69E-13	Down	-1.33E+00	3.82E-07	Down	-1.44E-01	5.36E-01		5.87E-01	1.02E-04		-1.55E+00	1.04E-33	Down	-8.34E-01	1.74E-13		Unigene113689_All//gi|38327504|gb|AAR17783.1|//2.00E-27//ribosomal protein L3 [Solanum lycopersicum]	Unigene113689_All//3.00E-28//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene113689_All//3.00E-127//gi|13352685|gb|BG443033.1|BG443033	ko03010|Ribosome		GO:0005198//GO:0010467//GO:0015934	nr +
Unigene113692_All	228	27.31	19.56	19.62	16.39	21.14	38.82	20.21	23.10	28.66	-4.82E-01	4.37E-02		-4.77E-01	5.69E-02		3.68E-01	2.07E-01		1.24E+00	3.35E-10	Up	1.93E-01	4.62E-01		5.04E-01	1.20E-02		Unigene113692_All//gi|149390510|gb|ABR25316.1|//7.00E-09//splicing factor [Oryza sativa Indica Group]	Unigene113692_All//7.00E-10//AT3G53500| zinc knuckle (CCHC-type) family protein	Unigene113692_All//8.00E-100//gi|78328880|gb|DT549154.1|DT549154	ko03040|Spliceosome		GO:0000398//GO:0016604//GO:0046914	nr -
Unigene1137_All	4133	4.05	9.95	6.56	3.63	5.26	5.18	9.05	17.74	28.87	1.30E+00	3.41E-45	Up	6.95E-01	1.11E-10		5.35E-01	1.05E-06		5.14E-01	9.02E-06		9.70E-01	9.60E-62		1.67E+00	4.90E-237	Up	Unigene1137_All//gi|3201682|gb|AAC19353.1|//0.00E+00//extra-large G-protein [Arabidopsis thaliana]	Unigene1137_All//0.00E+00//AT2G23460| XLG1 (EXTRA-LARGE G-PROTEIN 1); guanyl nucleotide binding / signal transducer	Unigene1137_All//0.00E+00//TC178714	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		GO:0009725//GO:0009746//GO:0019001//GO:0023052//GO:0034285//GO:0043231	nr -
Unigene113707_All	223	0.00	0.00	0.00	0.00	0.00	0.41	0.00	2.62	1.25	null	null		null	null		null	null		8.66E+00	4.80E-01		1.14E+01	2.81E-04	Up	1.03E+01	2.44E-02									
Unigene113728_All	366	0.29	0.00	0.00	2.45	1.32	1.48	0.35	3.20	0.54	-8.16E+00	3.75E-01		-8.16E+00	3.97E-01		-8.95E-01	2.14E-01		-7.26E-01	3.45E-01		3.21E+00	1.47E-05	Up	6.51E-01	6.66E-01		Unigene113728_All//gi|209970618|gb|ACJ03070.1|//1.00E-21//M18-S3Bp [Malus floribunda]	Unigene113728_All//2.00E-11//AT5G23400| disease resistance family protein / LRR family protein	Unigene113728_All//9.00E-107//ES844034			GO:0003824	nr -
Unigene113731_All	460	0.00	0.00	0.00	0.22	0.15	0.00	0.64	5.27	0.95	null	null		null	null		-5.33E-01	8.18E-01		-7.76E+00	4.03E-01		3.03E+00	2.27E-10	Up	5.66E-01	5.78E-01				Unigene113731_All//3.00E-08//DT468975				
Unigene113732_All	208	0.00	0.00	0.00	0.00	0.00	0.00	0.41	4.22	0.00	null	null		null	null		null	null		null	null		3.38E+00	1.75E-04	Up	-8.67E+00	3.60E-01									
Unigene113754_All	236	0.00	0.00	0.00	0.00	0.00	0.00	9.85	1.06	9.79	null	null		null	null		null	null		null	null		-3.21E+00	1.59E-10	Down	-9.20E-03	9.73E-01									
Unigene113755_All	381	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.85	0.00	null	null		null	null		null	null		null	null		1.15E+01	1.04E-07	Up	null	null		Unigene113755_All//gi|301120398|ref|XP_002907926.1|//4.00E-16//aldehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262102957|gb|EE161009.1|aldehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene113755_All//2.00E-11//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase			ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0009698//GO:0016620	nr -
Unigene113756_All	224	0.00	0.00	0.00	0.00	0.00	0.00	3.02	10.82	0.00	null	null		null	null		null	null		null	null		1.84E+00	4.09E-06	Up	-1.16E+01	3.56E-05	Down	Unigene113756_All//gi|49532956|dbj|BAD26579.1|//1.00E-10//cytochrome P450 like_TBP [Citrullus lanatus]		Unigene113756_All//1.00E-36//gi|50505563|gb|AT731711.1|AT731711				nr +
Unigene113765_All	217	0.72	0.47	0.49	1.15	0.16	0.00	4.29	7.32	10.46	-6.31E-01	7.28E-01		-5.60E-01	7.76E-01		-2.85E+00	1.37E-01		-1.02E+01	7.35E-02		7.72E-01	1.02E-01		1.29E+00	6.77E-04	Up	Unigene113765_All//gi|37906506|gb|AAP49697.1|//9.00E-07//cytochrome P-450-like protein [Vitis vinifera]	Unigene113765_All//4.00E-07//AT2G25160| CYP82F1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene113765_All//4.00E-37//ES834213			GO:0005506//GO:0016709	nr -
Unigene113792_All	301	0.00	0.00	0.00	0.00	0.15	6.18	0.00	0.93	null	null			null	null		null	null		7.23E+00	7.01E-01		-1.26E+01	3.59E-13	Down	-2.74E+00	1.06E-07	Down	Unigene113792_All//gi|15232058|ref|NP_186768.1|//1.00E-27//peroxidase 27 (PER27) (P27) (PRXR7) [Arabidopsis thaliana] >gi|25453197|sp|Q43735.1|PER27_ARATH RecName: Full=Peroxidase 27; Short=Atperox P27; AltName: Full=PRXR7; AltName: Full=ATP12a; Flags: Precursor >gi|1402916|emb|CAA66963.1|peroxidase [Arabidopsis thaliana] >gi|1429217|emb|CAA67311.1|peroxidase ATP12a [Arabidopsis thaliana]	Unigene113792_All//8.00E-24//AT1G05250| peroxidase, putative		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209//GO:0044464	nr +
Unigene113795_All	339	0.00	0.00	0.00	0.00	0.00	0.00	0.12	2.34	0.00	null	null		null	null		null	null		null	null		4.23E+00	1.05E-04	Up	-6.96E+00	6.16E-01		Unigene113795_All//gi|299473653|emb|CBN78047.1|//1.00E-19//flagellar associated protein, quinone reductase-like protein [Ectocarpus siliculosus]	Unigene113795_All//2.00E-17//AT5G54500| FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor				GO:0016491	nr +
Unigene1138_All	375	1.40	12.03	3.41	2.92	4.87	8.19	1.35	1.11	2.12	3.11E+00	1.19E-15	Up	1.29E+00	4.48E-02		7.36E-01	1.37E-01		1.49E+00	5.72E-05	Up	-2.80E-01	7.49E-01		6.51E-01	3.53E-01		Unigene1138_All//gi|18409320|ref|NP_566948.1|//2.00E-07//aspartyl protease family protein [Arabidopsis thaliana]	Unigene1138_All//1.00E-07//AT3G51330| aspartyl protease family protein	Unigene1138_All//8.00E-89//TC146833				nr -
Unigene113800_All	640	1.14	0.87	1.41	2.96	1.61	2.05	3.50	0.85	1.37	-3.94E-01	6.11E-01		3.06E-01	6.57E-01		-8.74E-01	5.25E-02		-5.31E-01	2.87E-01		-2.04E+00	1.89E-06	Down	-1.35E+00	3.87E-04	Down			Unigene113800_All//0.00E+00//TC142481				

Unigene113802_A11	782	0.00	0.00	0.00	0.00	0.00	0.00	1.51	2.51	0.10	null	null		null	null		null	null		null	null		7.31E-01	7.85E-02		-3.89E+00	9.21E-07	Down	Unigene113802_A11//gi|301112246|ref|XP_002905202.1|//7.00E-64//60S ribosomal protein L7 [Phytophthora infestans T30-4] >gi|262095532|gb|EEY53584.1| 60S ribosomal protein L7 [Phytophthora infestans T30-4]	Unigene113802_A11//1.00E-54//AT3G13580| 60S ribosomal protein L7 (RPL7D)			ko03010|Ribosome	GO:0005840	nr -
Unigene113806_A11	426	0.00	0.00	0.00	0.00	0.00	0.00	3.14	0.00	null	null		null	null		null	null		null	null		1.16E+01	1.88E-09	Up	null	null										ESTscan -
Unigene113808_A11	354	0.00	0.00	0.00	0.00	0.19	0.00	0.00	2.95	0.56	null	null		null	null		7.60E+00	6.14E-01		null	null		1.15E+01	2.02E-07	Up	9.14E+00	7.91E-02		Unigene113808_A11//gi|297831428|ref|XP_002883596.1|//2.00E-39//oxidative signal-inducible1 [Arabidopsis lyrata subsp. lyrata] >gi|297329436|gb|EFH59855.1| oxidative signal-inducible1 [Arabidopsis lyrata subsp. lyrata]	Unigene113808_A11//2.00E-40//AT4G13000| protein kinase family protein	Unigene113808_A11//8.00E-169//TC142650			GO:0004674//GO:0006464//GO:0032559	nr -
Unigene11382_A11	2567	2.91	2.94	3.84	7.08	6.33	5.44	4.73	2.46	2.10	1.31E-02	9.75E-01		3.97E-01	4.14E-02		-1.62E-01	2.68E-01		-3.82E-01	3.17E-03		-9.43E-01	1.90E-10		-1.17E+00	4.74E-15	Down	Unigene11382_A11//gi|116008248|gb|ABJ51934.1|//0.00E+00//sucrose transporter 2A [Hevea brasiliensis]	Unigene11382_A11//0.00E+00//AT2G02860| SUT2 (SUCROSE TRANSPORTER 2); carbohydrate transmembrane transporter/ sucrose transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter	Unigene11382_A11//0.00E+00//gi|164252069|gb|ES790405.1|ES790405			GO:0005351//GO:0006950//GO:0015154//GO:0015766//GO:0016021	nr -
Unigene113824_A11	580	0.00	0.00	0.00	0.09	0.30	0.00	0.51	2.74	3.30	null	null		null	null		1.79E+00	5.21E-01		-6.42E+00	6.42E-01		2.42E+00	1.10E-05	Up	2.69E+00	1.24E-07	Up								
Unigene113826_A11	356	6.91	1.00	2.69	20.15	23.12	9.90	9.03	3.99	1.68	-2.79E+00	4.57E-08	Down	-1.36E+00	1.89E-03		1.98E-01	3.93E-01		-1.03E+00	2.04E-06	Down	-1.18E+00	1.84E-04	Down	-2.43E+00	2.96E-11	Down			Unigene113826_A11//2.00E-52//TC175539					
Unigene11384_A11	2951	7.64	9.58	7.98	11.33	12.63	25.63	12.09	15.48	19.99	3.26E-01	1.53E-03		6.18E-02	6.23E-01		1.57E-01	9.62E-02		1.18E+00	2.15E-76	Up	3.56E-01	3.60E-07		7.25E-01	2.05E-31		Unigene11384_A11//gi|297851224|ref|XP_002890493.1|//0.00E+00//U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297339335|gb|EFH69752.1| U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene11384_A11//0.00E+00//AT1G24330| armadillo/beta-catenin repeat family protein / U-box domain-containing family protein	Unigene11384_A11//0.00E+00//DT460925			GO:0005488//GO:0019787//GO:0032446//GO:0043234	nr -
Unigene113845_A11	830	0.00	0.00	0.00	0.00	0.00	0.00	1.27	3.12	0.00	null	null		null	null		null	null		null	null		1.29E+00	3.28E-04	Up	-1.03E+01	6.72E-08	Down	Unigene113845_A11//gi|301121570|ref|XP_002908512.1|//3.00E-87//40S ribosomal protein SA [Phytophthora infestans T30-4] >gi|262103543|gb|EEY61595.1| 40S ribosomal protein SA [Phytophthora infestans T30-4]	Unigene113845_A11//1.00E-70//AT3G04770| RPSAb (40S ribosomal protein SA B); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr +
Unigene113859_A11	298	0.00	0.00	0.00	0.00	0.00	0.00	1.99	3.23	0.00	null	null		null	null		null	null		null	null		7.00E-01	2.78E-01		-1.10E+01	1.41E-04	Down	Unigene113859_A11//gi|145340549|ref|XP_001415385.1|//3.00E-29//Ribosomal protein L3, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901] >gi|144575608|gb|ABO93677.1| Ribosomal protein L3, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901]	Unigene113859_A11//1.00E-27//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934	nr -
Unigene11386_A11	1938	0.84	0.84	0.49	2.93	1.63	1.35	2.97	4.46	4.71	-5.00E-04	9.97E-01		-7.59E-01	1.59E-01		-8.42E-01	2.74E-04		-1.12E+00	6.85E-06	Down	5.89E-01	7.47E-04		6.66E-01	5.92E-05		Unigene11386_A11//gi|297795477|ref|XP_002865623.1|//1.00E-109//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311458|gb|EFH41882.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11386_A11//1.00E-48//AT5G48250| zinc finger (B-box type) family protein	Unigene11386_A11//0.00E+00//gi|78341395|gb|DT561669.1|DT561669	C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0001071//GO:0010468//GO:0043231//GO:0048581	nr +
Unigene113862_A11	449	0.00	0.00	0.00	0.00	0.00	0.00	1.51	1.77	0.00	null	null		null	null		null	null		null	null		2.31E-01	7.35E-01		-1.06E+01	3.56E-05	Down	Unigene113862_A11//gi|299472847|emb|CBN80416.1|//5.00E-14//EsV-1-116 [Ectocarpus siliculosus]						nr +
Unigene113863_A11	398	0.00	0.00	0.00	0.00	0.00	0.00	0.42	2.73	0.00	null	null		null	null		null	null		null	null		2.68E+00	1.69E-04	Up	-8.73E+00	1.09E-01		Unigene113863_A11//gi|729618|sp|Q03682.1|BIP2_TOBAC//3.00E-26//RecName: Full=Luminal-binding protein 2; Short=BiP 2; AltName: Full=78 kDa glucose-regulated protein homolog 2; Short=GRP-78-2 >gi|19807|emb|CAA42661.1| luminal binding protein (BiP) [Nicotiana tabacum]	Unigene113863_A11//2.00E-22//AT5G28540| BIP1; ATP binding	Unigene113863_A11//1.00E-10//TC157469		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0000166//GO:0005783	nr -
Unigene113871_A11	248	0.21	0.00	0.00	0.40	0.00	0.00	0.17	3.20	0.48	-7.72E+00	6.17E-01		-7.72E+00	6.30E-01		-8.65E+00	3.15E-01		-8.65E+00	4.03E-01		4.23E+00	1.05E-04	Up	1.50E+00	5.59E-01		Unigene113871_A11//gi|224115116|ref|XP_002316944.1|//5.00E-09//predicted protein [Populus trichocarpa] >gi|222860009|gb|EEE97556.1| predicted protein [Populus trichocarpa]	Unigene113871_A11//7.00E-05//AT4G21380| ARK3 (A. THALIANA RECEPTOR KINASE 3); kinase/ transmembrane receptor protein serine/threonine kinase				GO:0004713//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr -
Unigene1139_A11	1880	33.20	114.19	35.32	38.53	44.95	68.39	13.74	13.87	15.55	1.78E+00	0.00E+00	Up	8.93E-02	2.42E-01		2.22E-01	3.30E-05		8.28E-01	1.52E-72		1.37E-02	9.20E-01		1.79E-01	5.31E-02		Unigene1139_A11//gi|30680102|ref|NP_849967.1|//1.00E-176//aspartyl protease family protein [Arabidopsis thaliana] >gi|22655368|gb|AAM98276.1| At2g17760/At2g17760 [Arabidopsis thaliana]	Unigene1139_A11//8.00E-169//AT2G17760| aspartyl protease family protein	Unigene1139_A11//0.00E+00//TC149049			GO:0008233	nr +
Unigene113902_A11	336	0.16	1.66	0.79	0.59	0.61	2.02	0.25	4.35	1.07	3.41E+00	1.24E-02		2.35E+00	2.40E-01		5.23E-02	9.89E-01		1.77E+00	6.95E-02		4.11E+00	4.02E-08	Up	2.08E+00	1.01E-01									
Unigene113915_A11	283	0.18	0.36	0.00	1.23	0.12	0.32	1.94	2.51	0.00	9.54E-01	7.27E-01		-7.53E+00	6.30E-01		-3.34E+00	4.07E-02		-1.95E+00	1.96E-01		3.70E-01	6.67E-01		-1.09E+01	2.81E-04	Down			Unigene113915_A11//1.00E-111//gi|164273610|gb|ES842137.1|ES842137					
Unigene11392_A11	543	0.00	0.00	0.00	1.38	0.00	0.67	0.00	0.54	0.29	null	null		null	null		-1.04E+01	1.50E-05	Down	-1.05E+00	2.21E-01		9.07E+00	2.36E-02		8.20E+00	1.40E-01		Unigene11392_A11//gi|224130846|ref|XP_002320939.1|//1.00E-46//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222861712|gb|EEE99254.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene11392_A11//5.00E-34//AT1G02520| PGP11 (P-GLYCOPROTEIN 11); ATPase, coupled to transmembrane movement of substances	Unigene11392_A11//5.00E-23//TC138934		ko02010|ABC transporters	GO:0006810//GO:0031224//GO:0032559//GO:0042626	nr +
Unigene113920_A11	440	0.12	0.00	0.00	0.00	0.00	0.00	0.38	8.64	0.91	-6.89E+00	6.17E-01		-6.89E+00	6.30E-01		null	null		null	null		4.49E+00	1.65E-21	Up	1.24E+00	2.51E-01									
Unigene113921_A11	225	0.00	0.00	0.00	0.00	0.00	0.00	0.19	2.97	0.35	null	null		null	null		null	null		null	null		3.98E+00	6.38E-04	Up	9.14E-01	7.51E-01		Unigene113921_A11//gi|29028782|gb|AA064770.1|//9.00E-07//At5g02580 [Arabidopsis thaliana]	Unigene113921_A11//2.00E-06//AT5G02580| unknown protein	Unigene113921_A11//7.00E-14//TC157651				nr -
Unigene113922_A11	476	0.22	0.53	1.12	0.00	0.94	0.38	0.36	4.13	0.25	1.28E+00	4.35E-01		2.35E+00	5.88E-02		9.88E+00	8.01E-03		8.57E+00	1.95E-01		3.54E+00	1.14E-09	Up	-5.01E-01	7.47E-01		Unigene113922_A11//gi|159138935|gb|ABW89467.1|//2.00E-57//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene113922_A11//4.00E-40//AT2G29500| 17.6 kDa class I small heat shock protein (HSP17.6B-CI)	Unigene113922_A11//2.00E-111//TC144617			GO:0044424//GO:0050896	nr -
Unigene113923_A11	300	0.35	0.68	0.36	3.82	1.03	0.00	0.28	0.56	0.27	9.54E-01	6.22E-01		2.54E-02	1.00E+00		-1.89E+00	3.06E-03		-1.19E+01	3.58E-07	Down	9.83E-01	6.34E-01		-8.59E-02	9.73E-01				Unigene113923_A11//6.00E-21//ES821095					
Unigene11393_A11	1169	0.49	0.35	1.09	3.79	1.38	2.28	54.29	88.38	201.54	-5.05E-01	6.00E-01		1.15E+00	6.95E-02		-1.45E+00	1.33E-07	Down	-7.35E-01	9.99E-03		7.03E-01	2.70E-50		1.89E+00	0.00E+00	Up	Unigene11393_A11//gi|224130846|ref|XP_002320939.1|//1.00E-168//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222861712|gb|EEE99254.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene11393_A11//3.00E-156//AT1G02520| PGP11 (P-GLYCOPROTEIN 11); ATPase, coupled to transmembrane movement of substances	Unigene11393_A11//4.00E-87//gi|109856091|gb|DW485070.1|DW485070		ko02010|ABC transporters		nr +
Unigene113933_A11	227	0.00	0.45	0.47	0.00	0.00	0.00	0.00	2.39	1.23	8.80E+00	3.89E-01		8.87E+00	4.01E-01		null	null		null	null		1.12E+01	5.37E-04	Up	1.03E+01	2.44E-02									
Unigene113934_A11	269	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.78	2.07	null	null		null	null		null	null		null	null		9.60E+00	7.87E-02		1.10E+01	3.28E-04	Up	Unigene113934_A11//gi|224138866|ref|XP_002322921.1|//9.00E-10//aldose reductase with ABC domain [Populus trichocarpa] >gi|222867551|gb|EEF04682.1| aldose reductase with ABC domain [Populus trichocarpa]		Unigene113934_A11//4.00E-34//DR460967				nr -
Unigene113935_A11	239	0.00	0.00	0.89	0.42	0.00	0.00	0.88	3.32	16.67	null	null		9.80E+00	1.42E-01		-8.70E+00	3.15E-01		-8.70E+00	4.03E-01		1.91E+00	1.37E-02		4.24E+00	4.01E-22	Up								
Unigene11394_A11	1843	0.88	2.67	1.04	8.89	3.94	3.77	145.70	308.63	416.00	1.60E+00	5.40E-08	Up	2.41E-01	6.24E-01		-1.17E+00	2.83E-19	Down	-1.24E+00	1.71E-18	Down	1.08E+00	0.00E+00	Up	1.51E+00	0.00E+00	Up	Unigene11394_A11//gi|224130858|ref|XP_002320942.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222861715|gb|EEE99257.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene11394_A11//0.00E+00//AT3G62150| PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances	Unigene11394_A11//0.00E+00//TC168072		ko02010|ABC transporters	GO:0000166//GO:0009606//GO:0009734//GO:0009926//GO:0016020//GO:0042626//GO:0048588	nr +
Unigene113947_A11	536	1.17	0.57	1.09	1.58	2.38	5.06	0.79	0.94	0.15	-1.05E+00	2.50E-01		-1.00E-01	9.15E-01		5.89E-01	3.55E-01		1.68E+00	3.55E-05	Up	2.46E-01	7.84E-01		-2.41E+00	3.94E-02				Unigene113947_A11//7.00E-90//DW510486					
Unigene11395_A11	3602	0.26	0.68	1.05	11.01	9.42	9.19	11.60	28.53	21.87	1.37E+00	1.23E-03		2.01E+00	5.43E-08	Up	-2.25E-01	6.87E-03		-2.60E-01	2.28E-03		1.30E+00	1.63E-137	Up	9.15E-01	1.58E-61		Unigene11395_A11//gi|224064756|ref|XP_002301547.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222843273|gb|EEE80820.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene11395_A11//0.00E+00//AT2G47000| ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase	Unigene11395_A11//0.00E+00//TC168072		ko02010|ABC transporters	GO:0009606//GO:0009734//GO:0009926//GO:0015114//GO:0031224//GO:0032559//GO:0042626//GO:0048588	nr +
Unigene113951_A11	694	0.00	0.00	0.00	0.00	0.00	0.00	1.40	4.58	0.11	null	null		null	null		null	null		null	null		1.71E+00	4.29E-07	Up	-3.61E+00	2.14E-05	Down			Unigene113951_A11//9.00E-13//ES848646					
Unigene113952_A11	399	0.00	0.00	0.00	0.00	0.00	0.00	4.03	7.86	0.50	null	null		null	null		null	null		null	null		9.64E-01	2.19E-03		-3.01E+00	2.36E-07	Down			Unigene113952_A11//3.00E-20//TC159777					
Unigene113955_A11	383	6.97	7.67	14.46	5.98	5.12	2.48	0.33	0.65	0.21	1.39E-01	6.97E-01		1.05E+00	7.79E-05	Up	-2.23E-01	6.06E-01		-1.27E+00	2.82E-03		9.83E-01	5.18E-01		-6.71E-01	7.20E-01				Unigene113955_A11//5.00E-127//TC169561					
Unigene113967_A11	212	0.00	0.00	0.75	0.00	0.00	0.00	16.55	10.05	0.19	null	null		9.56E+00	2.39E-01		null	null		null	null		-7.19E-01	1.42E-02		-6.46E+00	3.54E-24	Down	Unigene113967_A11//gi|116222089|gb|ABJ80915.1|//1.00E-34//actin [Goniomonas truncata]	Unigene113967_A11//1.00E-35//AT5G59370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene113967_A11//2.00E-66//TC153744		ko04145|Phagosome	GO:0032559//GO:0043232	nr -
Unigene113969_A11	1063	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.40	0.00	null	null		null	null		null	null		null	null		1.21E+01	5.77E-33	Up	null	null		Unigene113969_A11//gi|298704815|emb|CBJ48963.1|//6.00E-61//Arf1, ARF family GTPase [Ectocarpus siliculosus]	Unigene113969_A11//5.00E-61//AT3G62290| ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding	Unigene113969_A11//5.00E-12//TC157765			GO:0015031//GO:0032561//GO:0035556//GO:0043231	nr +
Unigene113973_A11	206	0.00	0.00	0.00	0.97	0.67	1.97	0.00	4.06	0.19	null	null		null	null		-5.33E-01	7.49E-01		1.03E+00	4.29E-01		1.20E+01	5.54E-06	Up	7.60E+00	6.47E-01				Unigene113973_A11//8.00E-75//TC157651					
Unigene113980_A11	235	0.22	0.00	0.00	0.00	0.00	0.38	114.79	66.34	231.74	-7.80E+00	6.17E-01		-7.80E+00	6.30E-01		null	null		8.59E+00	4.80E-01		-7.91E-01	1.07E-16		1.01E+00	1.33E-50	Up	Unigene113980_A11//gi|5802576|gb|AAD51718.1|//1.00E-23//(+)-delta-cadinene synthase [Gossypium arboreum]	Unigene113980_A11//2.00E-05//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene113980_A11//2.00E-72//ES834162			GO:0010334//GO:0046872	nr -
Unigene113992_A11	1553	0.00	0.00	0.00	0.00	0.00	0.00	1.33	4.17	0.10	null	null		null	null		null	null		null	null		1.64E+00	5.07E-13	Up	-3.70E+00	5.61E-11	Down	Unigene113992_A11//gi|115463921|ref|NP_001055560.1|//1.00E-123//Os05g0417100 [Oryza sativa Japonica Group] >gi|113579111|dbj|BAF17474.1| Os05g0417100 [Oryza sativa Japonica Group]	Unigene113992_A11//1.00E-117//AT5G36950| DegP10 (DegP protease 10); catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase					nr -
Unigene113997_A11	295	0.00	0.34	0.00	0.00	0.00	0.00	0.14	2.69	0.54	8.42E+00	3.89E-01		null	null		null	null		null	null		4.23E+00	1.05E-04	Up	1.91E+00	3.78E-01									

Unigene1140_All	1470	4.24	4.24	3.33	7.96	9.14	6.36	18.29	9.10	11.25	1.40E-03	9.96E-01			-3.46E-01	1.78E-01		1.98E-01	2.46E-01			-3.24E-01	6.03E-02		-1.01E+00	1.24E-24	Down	-7.02E-01	4.29E-14		Unigene1140_All|gi|71727712|gb|AAZ39949.1|//1.00E-175//serine/threonine protein kinase [Gossypium hirsutum]	Unigene1140_All//0.8.00E-155//AT5G08160| ATPK3; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene1140_All//0.00E+00//TC134593				nr -
Unigene114003_All	206	0.00	0.00	0.00	0.00	0.00	0.00	11.70	5.68	0.00	null	null			null	null		null	null			null	null		-1.04E+00	4.61E-03		-1.35E+01	9.62E-18	Down	Unigene114003_All|gi|158529884|gb|AB871681.1|//2.00E-27//actin [Glycyrrhiza uralensis]	Unigene114003_All//9.00E-29//AT5G59370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene114003_All//4.00E-24//TC153744		ko04145|Phagosome	GO:0032559//GO:0043232	nr +
Unigene114010_All	401	0.00	0.00	0.00	0.00	0.00	0.00	0.11	1.04	3.78	null	null			null	null		null	null			null	null		3.31E+00	2.00E-02		5.16E+00	1.25E-09	Up	Unigene114010_All//gi|145335895|ref|NP_173359.3|//3.00E-53//FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase [Arabidopsis thaliana] >gi|75174733|sp|Q9LMA1.1|FMO1_ARATH RecName: Full=Probable flavin-containing monooxygenase 1 >gi|8954062|gb|AAF82235.1|AC069143_11 Contains similarity to a dimethylaniline monooxygenase (N-oxide forming) 2 (pulmonary flavin-containing monooxygenase 2) (FMO 2) (Dimethylaniline oxidase 2) (FMO 1B1) from Oryctolagus cuniculus gi|120434 and contains a flavin-binding monooxygenase-like PF|00743 domain [Arabidopsis thaliana]	Unigene114010_All//2.00E-54//AT1G19250| FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase				GO:0002218//GO:0005789//GO:0008152//GO:0009841//GO:0016709//GO:0030554//GO:0033554	nr +
Unigene114022_All	348	0.00	0.00	0.00	0.00	0.00	0.00	19.07	12.13	2.86	null	null			null	null		null	null			null	null		-6.53E-01	1.29E-03		-2.74E+00	1.44E-25	Down								ESTscan +
Unigene114025_All	216	5.33	5.86	7.89	11.07	20.88	4.18	67.34	34.25	190.34	1.38E-01	8.05E-01			5.66E-01	2.83E-01		9.16E-01	8.40E-04			-1.40E+00	8.07E-04	Down	-9.75E-01	5.04E-13		1.50E+00	3.46E-70	Up	Unigene114025_All|gi|115338597|gb|AB194388.1|//1.00E-14//isopentyl diphosphate isomerase [Gossypium barbadense]		Unigene114025_All//4.00E-52//gi|73848414|gb|DT457434.1|DT457434			GO:0006720//GO:0016863	nr -
Unigene114030_All	210	0.25	1.45	0.00	0.00	0.00	0.00	9.87	22.29	0.57	2.54E+00	1.51E-01			-7.96E+00	6.30E-01		null	null			null	null		1.18E+00	4.06E-06	Up	-4.12E+00	8.26E-12	Down	Unigene114030_All|gi|168068200|ref|XP_001785975.1|//2.00E-21//predicted protein [Physcomitrella patens subsp. patens] >gi|162662338|gb|EDQ49215.1| predicted protein [Physcomitrella patens subsp. patens]		Unigene114030_All//2.00E-35//gi|78348172|gb|DT568446.1|DT568446				nr -
Unigene114049_All	338	0.00	0.00	0.00	0.59	1.02	0.27	0.00	5.69	0.24	null	null			null	null		7.89E-01	5.96E-01			-1.14E+00	5.70E-01		1.25E-01	1.55E-13	Up	7.88E+00	4.06E-01				Unigene114049_All//8.00E-98//DW509472				
Unigene114053_All	506	0.31	1.50	0.53	0.20	1.02	0.80	1.25	4.30	1.50	2.28E+00	1.60E-02			7.62E-01	6.44E-01		2.37E+00	5.64E-02			2.03E+00	1.49E-01		1.78E+00	2.47E-05	Up	2.55E-01	7.07E-01				Unigene114053_All//6.00E-07//TC133360				
Unigene114063_All	218	0.00	0.00	0.00	0.00	0.00	0.00	0.58	4.22	0.00	null	null			null	null		null	null			null	null		2.86E+00	4.09E-04	Up	-9.18E+00	2.00E-01		Unigene114063_All|gi|1350664|sp|P49627.1|RL13_TOBAC//3.00E-07//RecName: Full=60S ribosomal protein L13; AltName: Full=Clone 6.2.1 protein	Unigene114063_All//2.00E-06//AT3G49010| ATBBC1 (ARABIDOPSIS THALIANA BHEAST BASIC CONSERVED 1); structural constituent of ribosome		ko03010|Ribosome	GO:0005622	nr -
Unigene114066_All	497	0.00	21.92	11.46	0.10	0.07	0.18	2.81	3.87	3.45	1.44E+01	1.89E-62	Up	1.35E+01	9.59E-32	Up	-5.32E-01	8.27E-01		8.59E-01	7.96E-01				4.63E-01	2.89E-01		2.96E-01	5.24E-01		Unigene114066_All|gi|145088580|ref|YP_001152204.1|//1.00E-19//O8F64d [Pinus koraiensis] >gi|145048829|gb|ABP35447.1|O8F64d [Pinus koraiensis]		Unigene114066_All//4.00E-57//TC160492			GO:0009536	nr +
Unigene114068_All	296	0.00	0.00	0.00	0.00	0.00	0.00	1.71	1.98	0.00	null	null			null	null		null	null			null	null		2.06E-01	8.00E-01		-1.07E+01	5.54E-04	Down	Unigene114068_All|gi|297812013|ref|XP_002873890.1|//6.00E-33//40S ribosomal protein S16 [Arabidopsis lyrata subsp. lyrata] >gi|297319727|gb|EFH50149.1| 40S ribosomal protein S16 [Arabidopsis lyrata subsp. lyrata]	Unigene114068_All//1.00E-32//AT5G18380| 40S ribosomal protein S16 (RPS16C)		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene11407_All	1956	5.08	10.18	6.07	9.17	8.34	9.63	27.17	27.78	28.90	1.00E+00	5.61E-15	Up	2.56E-01	1.54E-01		-1.36E-01	3.69E-01		7.06E-02	6.56E-01				3.19E-02	6.88E-01		8.91E-02	1.97E-01		Unigene11407_All|gi|62857010|dbj|BAD95890.1|//0.00E+00//Ser/Thr protein kinase [Lotus japonicus]	Unigene11407_All//0.00E+00//AT4G24400| CIPK8 (CBL-INTERACTING PROTEIN KINASE 8); kinase/ protein kinase	Unigene11407_All//0.00E+00//TC164614		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0009746//GO:0010035//GO:0016020//GO:0023060//GO:0032559//GO:0048513	nr -
Unigene114075_All	305	0.00	0.00	0.00	0.00	0.00	0.30	2.08	8.91	96.66	null	null			null	null		null	null			8.21E+00	4.80E-01		2.10E+00	6.99E-08	Up	5.54E+00	5.62E-186	Up	Unigene114075_All|gi|115442351|ref|NP_001045455.1|//2.00E-133//Os01g0598700 [Oryza sativa Japonica Group] >gi|113534986|dbj|BAF07369.1|Os01g0598700 [Oryza sativa Japonica Group]	Unigene114075_All//8.00E-14//AT4G24290| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: NSL1 (necrotic spotted lesions 1) (TAIR:AT1G28380.1); Has 124 Blast hits to 124 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 41; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene114075_All//4.00E-93//DT466716			GO:0016020	nr -
Unigene11408_All	1688	0.37	0.42	0.28	1.15	1.39	1.95	2.63	0.79	1.53	1.76E-01	8.17E-01			-3.90E-01	6.46E-01		2.69E-01	5.74E-01			7.63E-01	2.66E-02		-1.73E+00	8.27E-10	Down	-7.78E-01	1.69E-03		Unigene11408_All|gi|115448237|ref|NP_001047898.1|//0.00E+00//Os02g0710900 [Oryza sativa Japonica Group] >gi|113537429|dbj|BAF09812.1|Os02g0710900 [Oryza sativa Japonica Group]	Unigene11408_All//0.00E+00//AT4G16660| heat shock protein 70, putative / HSP70, putative			ko04141|Protein processing in endoplasmic reticulum	GO:0008152//GO:0009536//GO:0016020//GO:0016628//GO:0031410//GO:0032559//GO:0050896	nr -
Unigene114080_All	583	0.00	0.00	0.00	0.00	0.00	0.00	0.51	2.22	0.00	null	null			null	null		null	null			null	null		2.13E+00	3.40E-04	Up	-8.99E+00	1.58E-02								ESTscan +
Unigene114083_All	638	0.00	0.00	0.00	0.00	0.00	0.00	2.12	2.10	0.37	null	null			null	null		null	null			null	null		-1.66E-02	1.01E+00		-2.50E+00	2.46E-05	Down	Unigene114083_All|gi|sp|Q86XX4|FRAS1_HUMAN//3.00E-06//Extracellular matrix protein FRAS1 OS=Homo sapiens GN=FRAS1 PE=2 SV=1						swissprot -
Unigene114085_All	401	0.26	3.16	1.46	4.10	3.61	3.27	1.16	0.94	1.09	3.60E+00	2.27E-05	Up	2.48E+00	3.75E-02		-1.85E-01	7.46E-01		-3.28E-01	5.64E-01				-3.06E-01	7.36E-01		-8.58E-02	9.34E-01				Unigene114085_All//8.00E-126//gi|18100915|gb|BM360169.1|BM360169					
Unigene11409_All	914	1.60	1.61	1.22	6.92	3.99	5.73	9.25	3.61	4.23	4.40E-03	9.94E-01			-3.90E-01	5.00E-01		-7.93E-01	2.63E-04			-2.72E-01	2.98E-01		-1.36E+00	7.81E-13	Down	-1.13E+00	3.60E-10	Down	Unigene11409_All|gi|110739797|dbj|BAF01805.1|//1.00E-67//HSP like protein [Arabidopsis thaliana]	Unigene11409_All//4.00E-59//AT4G16660| heat shock protein 70, putative / HSP70, putative	Unigene11409_All//0.00E+00//gi|11201306|gb|BF270311.1|BF270311		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03060|Protein export	GO:0009536//GO:0016020//GO:0016491//GO:0031410//GO:0032559	nr +
Unigene114097_All	330	0.00	0.00	0.00	0.00	0.00	0.00	1.67	3.29	0.00	null	null			null	null		null	null			null	null		9.83E-01	9.75E-02		-1.07E+01	2.81E-04	Down			Unigene114097_All//2.00E-09//TC154839					
Unigene1141_All	1545	6.84	14.10	9.03	13.51	11.28	13.71	23.23	22.16	13.82	1.04E+00	2.19E-17	Up	4.01E-01	1.15E-02		-2.61E-01	3.06E-02		2.12E-02	9.00E-01				-6.85E-02	4.93E-01		-7.49E-01	1.18E-20		Unigene1141_All|gi|71727712|gb|AAZ39949.1|//0.00E+00//serine/threonine protein kinase [Gossypium hirsutum]	Unigene1141_All//4.00E-178//AT5G08160| ATPK3; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene1141_All//0.00E+00//TC134693			GO:0004672//GO:0006464//GO:0032559	nr +
Unigene114103_All	568	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.21	0.00	null	null			null	null		null	null			null	null		1.11E+01	7.17E-09	Up	null	null		Unigene114103_All|gi|297719953|ref|NP_001172338.1|//3.00E-06//Os01g0363550 [Oryza sativa Japonica Group] >gi|255673227|dbj|BAH91068.1|Os01g0363550 [Oryza sativa Japonica Group]						nr -
Unigene114108_All	515	0.00	0.00	0.00	0.00	0.00	0.00	1.40	1.06	0.00	null	null			null	null		null	null			null	null		-4.04E-01	6.23E-01		-1.04E+01	1.78E-05	Down	Unigene114108_All|sp|Q86955|DOKA_DICDI//4.00E-07//Hybrid signal transduction protein dokA OS=Dictyostelium discoideum GN=dokA PE=1 SV=1						swissprot +
Unigene11411_All	5682	6.51	5.23	4.43	5.40	5.62	7.34	6.54	7.22	19.18	-3.17E-01	3.42E-04			-5.55E-01	8.64E-10		5.70E-02	6.26E-01			4.42E-01	3.30E-08		1.43E-01	7.84E-02		1.55E+00	2.47E-194	Up	Unigene11411_All|gi|297791025|ref|XP_002863397.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297309232|gb|EFH39656.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene11411_All//0.00E+00//AT5G46580| pentatricopeptide (PPR) repeat-containing protein	Unigene11411_All//0.00E+00//TC154377		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0009536//GO:0016787	nr -
Unigene114113_All	255	4.51	36.76	15.24	15.82	12.96	10.27	9.95	20.65	6.41	3.03E+00	3.88E-31	Up	1.76E+00	5.72E-07	Up	-2.88E-01	3.81E-01		-6.23E-01	4.08E-02		1.05E+00	8.10E-06	Up	-6.35E-01	6.30E-02					Unigene114113_All//1.00E-92//gi|164267296|gb|ES813703.1|ES813703				
Unigene114119_All	554	0.00	0.00	0.00	0.00	0.12	0.33	0.61	2.64	0.58	null	null			null	null		6.96E+00	6.13E-01			8.35E+00	1.95E-01		2.11E+00	1.32E-04	Up	-8.57E-02	9.47E-01				Unigene114119_All//7.00E-07//TC155021				
Unigene11412_All	1387	0.87	4.79	2.00	1.22	0.92	0.91	6.37	16.84	10.71	2.46E+00	5.97E-18	Up	1.20E+00	2.76E-03		-4.11E-01	4.28E-01		-4.22E-01	4.36E-01		1.40E+00	9.98E-36	Up	7.50E-01	4.85E-09					Unigene11412_All//0.00E+00//TC161569				
Unigene114126_All	866	0.06	0.35	0.18	0.17	0.32	0.00	0.98	2.90	0.64	2.54E+00	1.51E-01			1.61E+00	5.11E-01		8.82E-01	5.95E-01			-7.43E+00	2.34E-01		1.57E+00	3.40E-05	Up	-6.00E-01	3.58E-01		Unigene114126_All|gi|158829300|gb|ABR81175.1|//7.00E-12//non-LTR retrotransposon transposase [Arabidopsis cebennensis]						nr +
Unigene11413_All	2503	5.71	13.40	10.53	5.06	8.46	10.50	10.34	21.14	25.24	1.23E+00	3.73E-34	Up	8.84E-01	2.00E-15		7.43E-01	2.79E-11		1.05E+00	1.47E-22	Up	1.03E+00	1.65E-49	Up	1.29E+00	1.61E-85	Up	Unigene11413_All|gi|297843108|ref|XP_002889435.1|//1.00E-166//3-methylcrotonyl-CoA carboxylase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297335277|gb|EFH65694.1| 3-methylcrotonyl-CoA carboxylase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene11413_All//3.00E-167//AT1G03090| MCCA; methylcrotonoyl-CoA carboxylase	Unigene11413_All//0.00E+00//TC164785		ko00280|Valine, leucine and isoleucine degradation		nr -
Unigene114135_All	264	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.53	0.00	null	null			null	null		null	null			null	null		1.13E+01	7.64E-05	Up	null	null								
Unigene11414_All	3143	10.27	29.52	20.81	8.73	11.48	17.13	28.01	61.16	50.17	1.52E+00	9.93E-129	Up	1.02E+00	2.53E-47	Up	3.95E-01	2.03E-06		9.72E-01	5.52E-40		1.13E+00	4.09E-205	Up	8.41E-01	3.50E-106		Unigene11414_All|gi|297843108|ref|XP_002889435.1|//0.00E+00//3-methylcrotonyl-CoA carboxylase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297335277|gb|EFH65694.1| 3-methylcrotonyl-CoA carboxylase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene11414_All//0.00E+00//AT1G03090| MCCA; methylcrotonoyl-CoA carboxylase	Unigene11414_All//0.00E+00//TC164785		ko00280|Valine, leucine and isoleucine degradation	GO:0005840//GO:0006551//GO:0016421//GO:0019842//GO:0031980//GO:0032559//GO:0046914	nr -
Unigene114144_All	464	0.00	0.00	0.00	0.00	0.00	0.00	1.09	2.25	0.00	null	null			null	null		null	null			null	null		1.04E+00	8.75E-02		-1.01E+01	5.54E-04	Down	Unigene114144_All|gi|301122631|ref|XP_002909042.1|//5.00E-42//40S ribosomal protein S6 [Phytophthora infestans T30-4] >gi|262099804|gb|EEY57856.1| 40S ribosomal protein S6 [Phytophthora infestans T30-4]	Unigene114144_All//4.00E-28//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene114158_All	216	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.06	0.00	null	null			null	null		null	null			null	null		1.20E+01	2.86E-06	Up	null	null								
Unigene11417_All	436	32.40	14.76	23.69	49.24	28.99	22.58	2.72	3.26	4.20	-1.13E+00	3.76E-13	Down	-4.52E-01	3.83E-03		-7.65E-01	2.06E-12		-1.12E+00	9.30E-21	Down	2.64E-01	6.49E-01		6.30E-01	1.31E-01					Unigene11417_All//5.00E-121//gi|164344748|gb|EX166055.1|EX166055					ESTscan +
Unigene114170_All	246	0.00	0.00	0.00	0.00	0.00	0.18	0.17	3.40	0.00	null	null			null	null		null	null			7.52E+00	7.00E-01		4.31E+00	5.68E-05	Up	-7.43E+00	6.15E-01				Unigene114170_All//3.00E-127//DW498401					ESTscan -
Unigene11418_All	743	14.65	13.03	13.76	13.61	8.48	12.46	3.24	8.21	6.38	-1.69E-01	3.65E-01			-9.01E-02	6.28E-01		-6.82E-01	3.95E-05			-1.27E-01	5.65E-01		1.34E+00	2.65E-09	Up	9.76E-01	6.05E-05		Unigene11418_All|gi|53370641|gb|AAU89136.1|//7.00E-11//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene11418_All//0.00E+00//DW498283				nr +

Unigene114182_All	427	0.00	0.00	0.00	0.00	0.00	0.20	2.25	0.00	null	null		null	null		null	null		null	null		3.51E+00	5.50E-05	Up	-7.63E+00	3.60E-01		Unigene114182_All//gi|297814478|ref|XP_002875122.1|//6.00E-06//hypothetical protein ARALYDRAFT_904467 [Arabidopsis lyrata subsp. lyrata] >gi|297320960|gb|EFH51381.1| hypothetical protein ARALYDRAFT_904467 [Arabidopsis lyrata subsp. lyrata]	Unigene114182_All//7.00E-07//AT5G41210| ATGSTT1 (GLUTATHIONE S-TRANSFERASE THETA 1); glutathione transferase			ko00350|Tyrosine metabolism		nr -
Unigene114185_All	577	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.62	0.00	null	null		null	null		null	null		null	null		1.18E+01	1.05E-14	Up	null	null		Unigene114185_All//gi|150421627|sp|Q6Z982.3|PIRL2_ARATH//5.00E-27//RecName: Full=Pirin-like protein At2g43120 >gi|119360079|gb|ABL66768.1| At2g43120 [Arabidopsis thaliana]	Unigene114185_All//1.00E-28//AT2G43120| pirin, putative					GO:0005515//GO:0016020//GO:0043231	nr +
Unigene114186_All	327	0.00	0.00	0.00	0.00	0.00	0.00	2.97	3.45	0.24	null	null		null	null		null	null		null	null		2.15E-01	7.15E-01		-3.61E+00	2.14E-05	Down	Unigene114186_All//gi|257219570|gb|ACV50438.1|//9.00E-23//ribosomal protein L37 [Jatropha curcas]	Unigene114186_All//2.00E-08//AT1G52300| 60S ribosomal protein L37 (RPL37B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009987//GO:0010467//GO:0030529//GO:0043169//GO:0043231//GO:0043232	nr -
Unigene114188_All	257	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.60	0.78	null	null		null	null		null	null		null	null		1.13E+01	7.64E-05	Up	9.60E+00	7.91E-02										
Unigene114419_All	805	13.84	12.65	15.74	25.50	27.16	19.19	7.83	5.50	2.13	-1.30E-01	4.91E-01		1.86E-01	3.06E-01		9.14E-02	5.47E-01		-4.10E-01	6.09E-04		-5.08E-01	1.63E-02		-1.88E+00	1.21E-15	Down	Unigene11419_All//gi|297724159|ref|NP_001174443.1|//6.00E-06//0s05g0434000 [Oryza sativa Japonica Group] >gi|255676397|dbj|BAH93171.1| 0s05g0434000 [Oryza sativa Japonica Group]		Unigene11419_All//0.00E+00//BM357993				nr -
Unigene114201_All	387	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.62	0.00	null	null		null	null		null	null		null	null		1.07E+01	1.47E-04	Up	null	null										ESTscan +
Unigene114202_All	217	2.89	0.00	1.23	1.38	1.27	0.62	0.00	0.00	0.18	-1.15E+01	7.92E-04	Down	-1.24E+00	2.13E-01		-1.18E-01	9.01E-01		-1.14E+00	4.58E-01		null	null		7.52E+00	6.47E-01		Unigene114202_All//gi|3860321|emb|CAA10128.1|//1.00E-13//beta-galactosidase [Cicer arietinum]	Unigene114202_All//3.00E-10//AT4G26140| BGAL12 (beta-galactosidase 12); beta-galactosidase/ catalytic/ cation binding	Unigene114202_All//1.00E-49//C0496844		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation	GO:0031410	nr +
Unigene114204_All	437	0.00	0.00	0.00	0.00	0.00	0.00	1.16	3.06	0.00	null	null		null	null		null	null		null	null		1.40E+00	9.02E-03		-1.02E+01	5.54E-04	Down										ESTscan +
Unigene114209_All	245	14.74	2.28	6.09	14.84	18.13	15.30	28.65	11.43	24.88	-2.70E+00	3.87E-11	Down	-1.28E+00	2.41E-04	Down	2.89E-01	3.66E-01		4.38E-02	9.19E-01		-1.33E+00	1.95E-10	Down	-2.04E-01	3.36E-01		Unigene114209_All//gi|297606737|ref|NP_001058899.2|//2.00E-10//0s07g0150200 [Oryza sativa Japonica Group] >gi|255677517|dbj|BAF20813.2| 0s07g0150200 [Oryza sativa Japonica Group]	Unigene114209_All//6.00E-08//AT2G32060| 40S ribosomal protein S12 (RPS12C)	Unigene114209_All//4.00E-136//TC162854		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene11421_All	928	2.09	3.55	4.48	4.46	5.12	3.65	1.09	1.35	0.60	7.67E-01	2.46E-02		1.10E+00	4.78E-04	Up	2.01E-01	5.52E-01		-2.88E-01	3.98E-01		3.05E-01	6.11E-01		-8.64E-01	1.40E-01		Unigene11421_All//gi|115442463|ref|NP_001045511.1|//3.00E-06//0s01g0967700 [Oryza sativa Japonica Group] >gi|113535042|dbj|BAF07425.1| 0s01g0967700 [Oryza sativa Japonica Group]	Unigene11421_All//3.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene11421_All//0.00E+00//TC129954				nr +
Unigene114225_All	469	0.00	0.00	0.00	0.00	0.00	0.00	0.18	2.23	0.00	null	null		null	null		null	null		null	null		3.63E+00	1.71E-05	Up	-7.49E+00	3.60E-01		Unigene114225_All//sp|P15214|GST_PROMI//6.00E-16//Glutathione S-transferase GST-6.0 OS=Proteus mirabilis GN=gstB PE=1 SV=2						swissprot +
Unigene114236_All	793	0.00	0.00	0.00	0.00	0.00	0.00	0.43	3.74	0.00	null	null		null	null		null	null		null	null		3.13E+00	6.28E-13	Up	-8.74E+00	8.15E-03		Unigene114236_All//gi|192822681|gb|ACF06186.1|//2.00E-13//heat shock protein 20 [Fucus serratus]	Unigene114236_All//2.00E-13//AT1G07400| 17.8 kDa class I heat shock protein (HSP17.8-CI)				GO:0006950	nr -
Unigene11424_All	1185	0.71	0.64	1.12	2.23	2.91	2.78	6.21	2.96	5.04	-1.39E-01	8.39E-01		6.69E-01	2.69E-01		3.83E-01	2.92E-01		3.21E-01	3.94E-01		-1.07E+00	5.70E-08	Down	-3.00E-01	1.21E-01		Unigene11424_All//gi|9743334|gb|AAF97958.1|AC000103 8//8.00E-31//F21J9.12 [Arabidopsis thaliana]	Unigene11424_All//8.00E-25//AT1G24460| unknown protein					nr +
Unigene114247_All	271	2.70	3.37	3.54	11.95	10.55	4.17	15.91	11.72	14.26	3.16E-01	6.32E-01		3.88E-01	6.08E-01		-1.80E-01	6.16E-01		-1.52E+00	1.86E-05	Down	-4.41E-01	9.99E-02		-1.58E-01	5.86E-01		Unigene114247_All//gi|3281851|emb|CAA19746.1|//1.00E-09//RNA lariat debranching enzyme - like protein [Arabidopsis thaliana] >gi|7270080|emb|CAB79895.1| RNA lariat debranching enzyme-like protein [Arabidopsis thaliana]	Unigene114247_All//5.00E-11//AT4G31770| calcineurin-like phosphoesterase family protein	Unigene114247_All//7.00E-110//TC145739			GO:0003824	nr +
Unigene114252_All	239	0.00	0.00	0.00	0.00	0.00	0.00	1.59	5.77	0.00	null	null		null	null		null	null		null	null		1.86E+00	7.81E-04	Up	-1.06E+01	4.20E-03		Unigene114252_All//sp|P0C5Q0|YL54F_YEAST//7.00E-06//Uncharacterized protein YLR154W-F OS=Saccharomyces cerevisiae GN=YLR154W-F PE=2 SV=1		Unigene114252_All//8.00E-23//ES844801				swissprot -
Unigene114259_All	571	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.20	0.00	null	null		null	null		null	null		null	null		1.23E+01	7.12E-21	Up	null	null										ESTscan +
Unigene114260_All	379	0.00	0.00	0.00	0.39	0.64	0.00	0.00	2.10	0.00	null	null		null	null		6.90E-01	7.32E-01		-8.62E+00	2.34E-01		1.10E+01	1.07E-05	Up	null	null					Unigene114260_All//9.00E-30//TC155768					
Unigene114266_All	388	0.00	0.00	0.00	0.00	0.00	0.00	1.74	4.31	0.10	null	null		null	null		null	null		null	null		1.31E+00	5.02E-03		-4.09E+00	3.10E-04	Down	Unigene114266_All//gi|116222125|gb|ABJ80933.1|//2.00E-71//actin [Leucocryptos marina]	Unigene114266_All//8.00E-72//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene114266_All//2.00E-64//TC153744		ko04145|Phagosome	GO:0032559//GO:0043232	nr +
Unigene114270_All	350	0.00	0.00	0.00	0.28	0.00	0.00	0.60	2.99	1.25	null	null		null	null		-8.15E+00	3.15E-01		-8.15E+00	4.03E-01		2.31E+00	8.56E-04	Up	1.05E+00	2.98E-01		Unigene114270_All//gi|92897781|gb|ABE93893.1|//1.00E-16//Heavy metal transport/detoxification protein [Medicago truncatula]	Unigene114270_All//2.00E-08//AT1G01490| heavy-metal-associated domain-containing protein	Unigene114270_All//4.00E-07//EX165152			GO:0006812//GO:0043169	nr +
Unigene114278_All	330	0.00	0.00	0.00	0.00	0.00	0.00	0.26	2.53	0.12	null	null		null	null		null	null		null	null		3.31E+00	3.10E-04	Up	-1.09E+00	6.77E-01										
Unigene114285_All	227	12.22	4.46	15.25	16.68	27.46	16.12	6.71	4.23	2.46	-1.45E+00	2.37E-04	Down	3.20E-01	3.86E-01		7.19E-01	1.50E-03		-4.95E-02	8.98E-01		-6.63E-01	1.73E-01		-1.45E+00	2.57E-03					Unigene114285_All//2.00E-48//TC134423					
Unigene114288_All	755	0.14	0.00	0.00	0.40	0.41	0.66	0.95	3.49	0.95	-7.11E+00	3.75E-01		-7.11E+00	3.97E-01		5.22E-02	9.98E-01		7.33E-01	5.16E-01		1.87E+00	1.03E-06	Up	-3.30E-03	9.90E-01					Unigene114288_All//6.00E-08//gi|3325657|gb|AI054543.1|AI054543					
Unigene114294_All	388	0.00	0.00	0.00	0.00	0.00	0.00	1.85	1.18	0.10	null	null		null	null		null	null		null	null		-6.45E-01	4.01E-01		-4.17E+00	1.64E-04	Down				Unigene114294_All//2.00E-30//ES828348					
Unigene114296_All	490	1.71	1.65	1.85	0.51	0.28	0.46	1.21	5.20	0.81	-4.63E-02	9.64E-01		1.13E-01	8.72E-01		-8.55E-01	5.74E-01		-1.41E-01	9.29E-01		2.11E+00	1.80E-07	Up	-5.71E-01	4.78E-01		Unigene114296_All//gi|34014756|gb|AAQ56194.1|//2.00E-17//aminotransferase 1 [Cucumis melo]	Unigene114296_All//2.00E-11//AT2G13360| AGT (ALANINE:GLIOXYLATE AMINOTRANSFERASE); alanine:glyoxylate transaminase/ serine:glyoxylate transaminase/ serine:pyruvate transaminase	Unigene114296_All//2.00E-170//gi|48798267|gb|C0099581.1|C0099581		ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism	GO:0008483//GO:0048037	nr +
Unigene1143_All	3423	3.38	5.46	4.56	14.49	17.19	21.92	8.70	4.05	4.06	6.93E-01	6.70E-08		4.32E-01	3.42E-03		2.46E-01	1.67E-04		5.96E-01	3.60E-24		-1.10E+00	2.72E-31	Down	-1.10E+00	4.31E-32	Down	Unigene1143_All//gi|224058639|ref|XP_002299579.1|//1.00E-126//cytochrome P450 [Populus trichocarpa] >gi|222846837|gb|EEE84384.1| cytochrome P450 [Populus trichocarpa]	Unigene1143_All//2.00E-106//AT2G45570| CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene1143_All//0.00E+00//TC134926		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene11430_All	1542	6.58	3.15	7.29	2.62	2.68	1.20	0.05	0.05	0.10	-1.06E+00	9.19E-09	Down	1.47E-01	4.43E-01		3.44E-02	9.35E-01		-1.12E+00	2.00E-04	Down	-1.59E-02	1.01E+00		9.15E-01	6.25E-01		Unigene11430_All//gi|297814053|ref|XP_002874910.1|//3.00E-52//TOC159 [Arabidopsis lyrata subsp. lyrata] >gi|297320747|gb|EFH51169.1| TOC159 [Arabidopsis lyrata subsp. lyrata]	Unigene11430_All//5.00E-42//AT4G02510| TOC159 (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 159); transmembrane receptor	Unigene11430_All//0.00E+00//TC142232			GO:0006605//GO:0009527//GO:0017111//GO:0032555	nr +
Unigene114302_All	453	0.00	0.00	0.00	0.00	0.00	0.00	1.40	2.49	0.00	null	null		null	null		null	null		null	null		8.31E-01	1.51E-01		-1.05E+01	7.11E-05	Down	Unigene114302_All//gi|195605616|gb|ACG24638.1|//1.00E-06//translationally-controlled tumor protein [Zea mays] >gi|195622768|gb|ACG33214.1| translationally-controlled tumor protein [Zea mays]						nr +
Unigene114311_All	360	0.00	0.00	0.00	0.00	0.00	0.00	0.70	4.06	0.55	null	null		null	null		null	null		null	null		2.53E+00	1.65E-05	Up	-3.49E-01	7.67E-01										
Unigene114319_All	477	0.00	0.00	0.00	0.10	0.29	0.38	0.18	2.19	0.00	null	null		null	null		1.47E+00	6.19E-01		1.86E+00	4.59E-01		3.63E+00	1.71E-05	Up	-7.47E+00	3.60E-01										
Unigene11433_All	2843	5.23	4.76	2.55	196.96	202.97	199.61	30.53	37.24	15.69	-1.35E-01	3.86E-01		-1.04E+00	1.75E-11	Down	4.33E-02	5.70E-02		1.92E-02	4.86E-01		2.87E-01	1.45E-10		-9.60E-01	8.38E-74		Unigene11433_All//gi|258489633|gb|ACV72640.1|//0.00E+00//sucrose synthase 1 [Gossypium hirsutum]	Unigene11433_All//0.00E+00//AT3G43190| SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups	Unigene11433_All//0.00E+00//TC132647		ko00500|Starch and sucrose metabolism	GO:0005984//GO:0035251//GO:0044403	nr -
Unigene11435_All	2524	22.76	6.69	7.30	26.53	12.84	14.39	15.38	33.30	12.63	-1.77E+00	2.13E-99	Down	-1.64E+00	1.69E-86	Down	-1.05E+00	1.54E-64	Down	-8.83E-01	1.00E-42		1.11E+00	1.57E-88	Up	-2.84E-01	1.63E-04		Unigene11435_All//gi|211906466|gb|ACJ11726.1|//1.00E-173//serine hydroxymethyltransferase [Gossypium hirsutum]	Unigene11435_All//2.00E-161//AT4G13930| SHM4 (serine hydroxymethyltransferase 4); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene11435_All//0.00E+00//gi|78340525|gb|DT560799.1|DT560799		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr -
Unigene114350_All	276	0.00	0.00	0.00	0.00	0.00	0.00	1.99	1.82	0.00	null	null		null	null		null	null		null	null		-1.32E-01	8.80E-01		-1.10E+01	2.81E-04	Down				Unigene114350_All//6.00E-27//FL576679					
Unigene114365_All	233	0.00	0.43	0.00	0.21	0.59	0.39	0.73	5.56	1.71	8.76E+00	3.89E-01		null	null		1.47E+00	6.19E-01		8.59E-01	7.96E-01		2.94E+00	1.14E-05	Up	1.24E+00	2.51E-01		Unigene114365_All//gi|255540151|ref|XP_002511140.1|//4.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223550255|gb|EEF51742.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene114372_All	228	0.00	0.00	0.00	0.00	0.00	0.00	0.37	4.03	0.00	null	null		null	null		null	null		null	null		3.44E+00	9.84E-05	Up	-8.53E+00	3.60E-01										ESTscan -
Unigene114374_All	461	0.00	0.00	0.00	0.00	0.00	0.00	19.26	390.03	0.95	null	null		null	null		null	null		null	null		4.34E+00	0.00E+00	Up	-4.34E+00	1.59E-50	Down	Unigene114374_All//gi|1545805|dbj|BAA10929.1|//4.00E-12//cytochrome P450 like_TBP [Nicotiana tabacum]		Unigene114374_All//5.00E-41//gi|73864682|gb|DT467421.1|DT467421			GO:0016491//GO:0043231	nr -
Unigene114378_All	521	0.20	0.00	0.00	0.57	0.00	0.00	0.32	9.31	1.76	-7.65E+00	3.75E-01		-7.65E+00	3.97E-01		-9.16E+00	2.02E-02		-9.16E+00	4.00E-02		4.84E+00	1.77E-28	Up	2.44E+00	1.06E-03		Unigene114378_All//gi|297849980|ref|XP_002892871.1|//6.00E-72//ATPDR12/PDR12 [Arabidopsis lyrata subsp. lyrata] >gi|297338713|gb|EFH69130.1| ATPDR12/PDR12 [Arabidopsis lyrata subsp. lyrata]	Unigene114378_All//6.00E-60//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene114378_All//0.00E+00//TC164825		ko03040|Spliceosome	GO:0032559//GO:0042626//GO:0043231	nr -
Unigene11438_All	580	2.26	1.31	2.57	6.79	3.62	2.34	12.83	13.55	6.11	-7.83E-01	1.81E-01		1.89E-01	7.21E-01		-9.06E-01	1.64E-03		-1.54E+00	1.36E-06	Down	7.85E-02	7.15E-01		-1.07E+00	2.31E-08	Down				Unigene11438_All//5.00E-122//DR461849		ko04146|Peroxisome//ko00071|Fatty acid metabolism		kegg -
Unigene11439_All	674	5.05	6.69	8.22	8.65	4.19	6.16	4.01	3.16	3.01	4.07E-01	1.61E-01		7.04E-01	7.51E-03		-1.05E+00	4.84E-06	Down	-4.88E-01	5.04E-02		-3.44E-01	3.54E-01		-4.13E-01	2.22E-01					Unigene11439_All//6.00E-125//TC160702					
Unigene114400_All	709	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.12	0.00	null	null		null	null		null	null		null	null		1.16E+01	1.39E-15	Up	null	null										ESTscan -
Unigene114411_All	686	0.00	0.00	0.00	0.00	0.00	0.00	0.92	2.19	0.00	null	null		null	null		null	null		null	null		1.25E+00	1.16E-02		-9.85E+00	7.11E-05	Down	Unigene114411_All//gi|298706692|emb|CBJ34222.1|//5.00E-06//conserved unknown protein [Ectocarpus siliculosus] >gi|298713886|emb|CBJ33762.1| conserved unknown protein [Ectocarpus siliculosus]		Unigene114411_All//8.00E-07//ES794483				nr -
Unigene114416_All	296	0.00	0.00	0.00	0.00	0.00	0.00	1.71	5.65	0.00	null	null		null	null		null	null		null	null		1.72E+00	4.01E-04	Up	-1.07E+01	5.54E-04	Down										ESTscan +
Unigene114417_All	365	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.40	0.00	null	null		null	null		null	null		null	null		1.12E+01	2.86E-06	Up	null	null										ESTscan +
Unigene11442_All	2287	3.41	4.85	2.98	8.30	6.23	5.67	14.72	14.93	6.43	5.09E-01	2.93E-03		-1.94E-01	3.94E-01		-4.13E-01	5.18E-04		-5.50E-01	7.85E-06		2.09E-02	8.37E-01		-1.20E+00	2.71E-41	Down	Unigene11442_All//gi|62321026|dbj|BAD94085.1|//2.00E-10//A6 anther-specific protein [Arabidopsis thaliana]	Unigene11442_All//1.00E-11//AT4G14070| AAE15 (acyl-activating enzyme 15); long-chain-fatty-acid-[acyl-carrier-protein] ligase	Unigene11442_All//0.00E+00//gi|11204532|gb|BF273462.1|BF273462		ko04146|Peroxisome//ko00071|Fatty acid metabolism	GO:0006633//GO:0009526//GO:0015645	nr -

Unigene114421_All	373	0.00	0.00	0.00	0.13	0.00	0.00	0.11	1.90	0.00	null	null		null	null		-7.06E+00	5.60E-01		-7.06E+00	6.41E-01		4.07E+00	3.51E-04	Up	-6.83E+00	6.15E-01		Unigene114421_All//gi|224064011|ref|XP_002301347.1|//5.00E-37//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222843073|gb|EEE80620.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene114421_All//4.00E-38//AT3G53510| ABC transporter family protein			ko03040|Spliceosome	GO:0000166//GO:0015405//GO:0016020//GO:0017111//GO:0051707	nr +
Unigene114427_All	330	1.90	1.23	6.29	1.66	2.40	1.64	4.74	2.15	2.17	-6.31E-01	4.75E-01		1.73E+00	5.70E-04	Up	5.31E-01	5.40E-01		-1.59E-02	9.75E-01		-1.14E+00	1.72E-02		-1.13E+00	1.41E-02		Unigene114427_All//gi|30695682|ref|NP_191845.2|//1.00E-17//esterase/lipase/thioesterase family protein [Arabidopsis thaliana]	Unigene114427_All//6.00E-19//AT3G62860| esterase/lipase/thioesterase family protein	Unigene114427_All//2.00E-138//C0099437			GO:0004091//GO:0016020	nr +
Unigene114430_All	323	0.00	0.00	0.00	0.00	0.00	0.00	2.23	9.32	0.37	null	null		null	null		null	null		null	null		2.07E+00	1.69E-08	Up	-2.59E+00	2.81E-03		Unigene114430_All//gi|298706692|emb|CBJ34222.1|//2.00E-17//conserved unknown protein [Ectocarpus siliculosus] >gi|298713886|emb|CBJ33762.1| conserved unknown protein [Ectocarpus siliculosus]		Unigene114430_All//6.00E-40//gi|78348172|gb|DT568446.1|DT568446				nr -
Unigene114431_All	264	0.00	0.00	0.00	0.00	0.00	0.00	2.88	2.69	0.00	null	null		null	null		null	null		null	null		-9.91E-02	8.96E-01		-1.15E+01	8.87E-06	Down			Unigene114431_All//1.00E-15//TC134836				
Unigene114437_All	437	0.00	0.00	0.00	0.00	0.00	0.00	1.84	3.35	0.00	null	null		null	null		null	null		null	null		8.65E-01	8.03E-02		-1.08E+01	4.43E-06	Down	Unigene114437_All//gi|29539332|dbj|BAC67667.1|//1.00E-57//elongation factor-1alpha [Cyanidioschyzon merolae]	Unigene114437_All//9.00E-36//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene114437_All//4.00E-54//gi|11208772|gb|BF277702.1|BF277702			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene114438_All	552	0.00	0.00	0.00	0.00	0.00	0.00	3.75	4.85	0.43	null	null		null	null		null	null		null	null		3.69E-01	3.16E-01		-3.12E+00	1.46E-09	Down	Unigene114438_All//gi|4501883|ref|NP_001604.1|//4.00E-82//actin, aortic smooth muscle [Homo sapiens] >gi|6671507|ref|NP_031418.1| actin, aortic smooth muscle [Mus musculus] >gi|78045238|ref|NP_001029674.1| actin, aortic smooth muscle [Bos taurus] >gi|110625958|ref|NP_112266.1| actin, aortic smooth muscle [Rattus norvegicus] >gi|156119362|ref|NP_001095152.1| actin, aortic smooth muscle [Oryctolagus cuniculus] >gi|197097944|ref|NP_001126814.1| actin, aortic smooth muscle [Pongo abelii] >gi|213688375|ref|NP_001135417.1| actin, aortic smooth muscle [Homo sapiens] >gi|257470979|ref|NP_001158122.1| actin, aortic smooth muscle [Sus scrofa] >gi|73996085|ref|XP_534781.2| PREDICTED: similar to Actin, aortic smooth muscle (Alpha-actin 2) [Canis familiaris] >gi|114631685|ref|XP_521550.2|	Unigene114438_All//5.00E-76//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene114438_All//7.00E-16//TC155341		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008015//GO:0008092//GO:0012501//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0048747//GO:0051707//GO:0060415	nr -
Unigene11444_All	933	8.08	4.45	5.59	7.80	9.49	10.65	6.80	16.93	15.63	-8.59E-01	5.68E-05		-5.30E-01	1.73E-02		2.83E-01	1.68E-01		4.50E-01	1.41E-02		1.32E+00	3.06E-22	Up	1.20E+00	2.21E-18	Up	Unigene11444_All//gi|13937171|gb|AK50079.1|AF372939_1/9.00E-24//At1g63420/F2K11_19 [Arabidopsis thaliana] >gi|217008573|gb|AAM70560.1| At1g63420/F2K11_19 [Arabidopsis thaliana]	Unigene11444_All//9.00E-26//AT3G48980| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Lipopolysaccharide-modifying protein (InterPro:IPR006598), Protein of unknown function DUF821, CAP10-like (InterPro:IPR008539); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23850.1); Has 462 Blast hits to 458 proteins in 90 species: Archae - 0; Bacteria - 36; Metazoa - 203; Fungi - 74; Plants - 116; Viruses - 2; Other Eukaryotes - 31 (source: NCBI BLink).					nr +
Unigene114441_All	242	0.00	0.00	0.00	0.00	0.00	0.00	0.35	3.28	0.00	null	null		null	null		null	null		null	null		3.23E+00	5.44E-04	Up	-8.45E+00	3.60E-01		Unigene114441_All//gi|74272639|gb|ABA01115.1|//4.00E-08//mitochondrial carrier protein CR057 [Chlamydomonas incerta]	Unigene114441_All//1.00E-07//AT5G14040| mitochondrial phosphate transporter				GO:0016020//GO:0043231	nr +
Unigene11445_All	1477	3.33	1.30	4.65	5.70	6.81	9.88	5.47	10.13	9.28	-1.35E+00	1.86E-06	Down	4.82E-01	4.18E-02		2.56E-01	1.88E-01		7.93E-01	3.68E-08		8.90E-01	1.42E-11		7.63E-01	1.23E-08		Unigene11445_All//gi|48310551|gb|AT41837.1|//1.00E-100//At5g23850 [Arabidopsis thaliana]	Unigene11445_All//7.00E-105//AT3G61280| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Lipopolysaccharide-modifying protein (InterPro:IPR006598), Protein of unknown function DUF821, CAP10-like (InterPro:IPR008539); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61290.1); Has 467 Blast hits to 463 proteins in 98 species: Archae - 0; Bacteria - 38; Metazoa - 201; Fungi - 82; Plants - 115; Viruses - 4; Other Eukaryotes - 27 (source: NCBI BLink).	Unigene11445_All//0.00E+00//TC155101				nr +
Unigene114450_All	278	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.71	0.00	null	null		null	null		null	null		null	null		1.14E+01	2.07E-05	Up	null	null								ESTscan +
Unigene114451_All	396	0.00	0.00	0.00	0.00	0.00	0.00	0.11	1.79	0.00	null	null		null	null		null	null		null	null		4.07E+00	3.51E-04	Up	-6.74E+00	6.15E-01								ESTscan +
Unigene114454_All	362	0.00	0.00	0.00	0.00	0.00	0.00	0.12	2.08	0.00	null	null		null	null		null	null		null	null		4.15E+00	1.92E-04	Up	-6.87E+00	6.15E-01								ESTscan +
Unigene11446_All	4064	12.42	3.70	13.93	11.01	7.03	4.35	4.81	15.21	7.55	-1.75E+00	5.63E-86	Down	1.65E-01	3.28E-02		-6.46E-01	5.87E-19		-1.34E+00	3.43E-56	Down	1.66E+00	1.53E-119	Up	6.51E-01	5.05E-14		Unigene11446_All//gi|48310551|gb|AT41837.1|//1.00E-155//At5g23850 [Arabidopsis thaliana]	Unigene11446_All//1.00E-156//AT5G23850| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Lipopolysaccharide-modifying protein (InterPro:IPR006598), Protein of unknown function DUF821, CAP10-like (InterPro:IPR008539); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48980.1); Has 588 Blast hits to 567 proteins in 103 species: Archae - 2; Bacteria - 34; Metazoa - 301; Fungi - 69; Plants - 115; Viruses - 3; Other Eukaryotes - 64 (source: NCBI BLink).	Unigene11446_All//0.00E+00//TC155101				nr +
Unigene11447_All	395	5.17	1.67	2.70	11.60	9.42	5.83	10.70	2.43	6.76	-1.63E+00	6.88E-04	Down	-9.38E-01	4.84E-02		-3.01E-01	3.10E-01		-9.93E-01	3.71E-04		-2.14E+00	3.68E-12	Down	-6.64E-01	8.98E-03		Unigene11447_All//gi|16930439|gb|AL31905.1|AF419573_1/3.00E-25//AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|15912261|gb|AAL08264.1| AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|27764934|gb|AAO23588.1| At4g27720/T29A15_210 [Arabidopsis thaliana]	Unigene11447_All//5.00E-21//AT4G27720| LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G64650.1); Has 496 Blast hits to 491 proteins in 183 species: Archae - 5; Bacteria - 234; Metazoa - 75; Fungi - 33; Plants - 96; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink).	Unigene11447_All//2.00E-108//gi|48813868|gb|CO115181.1|CO115181				nr +
Unigene114477_All	285	0.00	0.00	0.00	0.00	0.48	0.16	0.74	11.88	1.40	null	null		null	null		8.92E+00	3.20E-01		7.31E+00	7.00E-01		4.00E+00	7.88E-18	Up	9.14E-01	3.86E-01								
Unigene114479_All	357	0.00	0.00	0.00	0.00	0.00	0.00	0.83	3.75	0.11	null	null		null	null		null	null		null	null		2.18E+00	2.12E-04	Up	-2.89E+00	6.77E-02		Unigene114479_All//gi|29539332|dbj|BAC67667.1|//2.00E-56//elongation factor-1alpha [Cyanidioschyzon merolae]	Unigene114479_All//5.00E-54//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene114479_All//9.00E-36//DR462623			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +

Unigene11448_All	1539	6.80	3.52	3.18	22.20	18.86	17.40	20.47	7.28	9.32	-9.49E-01	1.26E-07		-1.09E+00	5.52E-09	Down	-2.35E-01	9.38E-03		-3.52E-01	9.62E-05		-1.49E+00	1.52E-52	Down	-1.14E+00	1.02E-35	Down	Unigene11448_All//gi|16930439|gb|AL31905.1|AF419573_1//1.00E-136//AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|15912261|gb|AAL08264.1| AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|27764934|gb|AAO23588.1| At4g27720/T29A15_210 [Arabidopsis thaliana]	Unigene11448_All//6.00E-124//AT4G27720| LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G64650.1); Has 496 Blast hits to 491 proteins in 183 species: Archae - 5; Bacteria - 234; Metazoa - 75; Fungi - 33; Plants - 96; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink).	Unigene11448_All//0.00E+00//TC154478					nr -
Unigene114480_All	376	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.56	0.00	null	null		null	null		null	null		null	null		1.13E+01	7.61E-07	Up	null	null		Unigene114480_All//gi|193878342|gb|ACF25911.1|//5.00E-37//MLO-like protein 6 [Vitis vinifera]	Unigene114480_All//1.00E-23//AT3G28200| MLO12 (MILDEW RESISTANCE LOCUS O 12); calmodulin binding				GO:0009987//GO:0031224//GO:0050896	nr -
Unigene114488_All	211	0.74	1.44	0.00	0.24	0.65	0.64	42.88	12.08	13.97	9.54E-01	5.04E-01		-9.54E+00	2.46E-01		1.47E+00	6.19E-01		1.44E+00	6.39E-01		-1.83E+00	1.22E-20	Down	-1.62E+00	4.32E-18	Down			Unigene114488_All//2.00E-60//TC176131					
Unigene11449_All	678	6.10	4.86	4.95	22.63	21.18	23.11	10.54	4.32	6.40	-3.28E-01	2.92E-01		-3.01E-01	3.68E-01		-9.56E-02	5.88E-01		3.06E-02	8.65E-01		-1.29E+00	3.45E-10	Down	-7.19E-01	1.49E-04		Unigene11449_All//gi|16930439|gb|AL31905.1|AF419573_1//1.00E-68//AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|15912261|gb|AAL08264.1| AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|27764934|gb|AAO23588.1| At4g27720/T29A15_210 [Arabidopsis thaliana]	Unigene11449_All//1.00E-62//AT4G27720| LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G64650.1); Has 496 Blast hits to 491 proteins in 183 species: Archae - 5; Bacteria - 234; Metazoa - 75; Fungi - 33; Plants - 96; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink).	Unigene11449_All//0.00E+00//gi|13352221|gb|BG442569.1|BG442569					nr -
Unigene114498_All	690	0.00	0.07	0.00	0.00	0.00	0.00	1.04	1.64	3.06	6.20E+00	6.20E-01		null	null		null	null		null	null		6.51E-01	2.66E-01		1.55E+00	1.37E-04	Up								
Unigene11450_All	1312	0.48	1.20	0.32	2.09	2.15	2.07	4.83	1.50	1.70	1.32E+00	1.50E-02		-5.59E-01	5.54E-01		4.36E-02	9.32E-01		-1.58E-02	9.59E-01		-1.69E+00	2.85E-13	Down	-1.51E+00	9.39E-12	Down	Unigene11450_All//gi|16930439|gb|AL31905.1|AF419573_1//1.00E-147//AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|15912261|gb|AAL08264.1| AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|27764934|gb|AAO23588.1| At4g27720/T29A15_210 [Arabidopsis thaliana]	Unigene11450_All//3.00E-136//AT4G27720| LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G64650.1); Has 496 Blast hits to 491 proteins in 183 species: Archae - 5; Bacteria - 234; Metazoa - 75; Fungi - 33; Plants - 96; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink).	Unigene11450_All//0.00E+00//TC154478					nr -
Unigene114501_All	389	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.65	0.00	null	null		null	null		null	null		null	null		1.18E+01	4.93E-10	Up	null	null		Unigene114501_All//gi|297832702|ref|XP_002884233.1|//2.00E-08//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297836884|ref|XP_002886324.1| expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297836886|ref|XP_002886325.1| expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297836888|ref|XP_002886326.1| expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297330073|gb|EFH60492.1| expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332164|gb|EFH62583.1| expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332165|gb|EFH62584.1| expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332166|gb|EFH62585.1| expressed protein [Arabidopsis lyrata subsp. lyrata]					GO:0043231	nr -
Unigene114519_All	209	0.00	0.00	0.00	0.00	0.49	0.00	0.20	4.20	0.57	null	null		null	null		8.95E+00	4.57E-01		null	null		4.38E+00	3.08E-05	Up	1.50E+00	5.59E-01								
Unigene114520_All	366	0.00	0.00	0.00	0.00	0.00	0.00	1.39	2.85	0.00	null	null		null	null		null	null		null	null		1.04E+00	8.74E-02		-1.04E+01	5.54E-04	Down	Unigene114520_All//gi|300266999|gb|EFJ51184.1|//3.00E-24//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene114520_All//5.00E-10//AT5G02870| 60S ribosomal protein L4/L1 (RPL4D)			ko03010|Ribosome	GO:0005622	nr +
Unigene114522_All	351	0.00	0.43	0.61	0.99	1.47	0.90	6.38	4.05	2.27	8.76E+00	2.36E-01		9.25E+00	1.42E-01		5.67E-01	6.04E-01		-1.41E-01	9.12E-01		-6.57E-01	8.80E-02		-1.49E+00	1.21E-04	Down			Unigene114522_All//3.00E-42//ES840947					
Unigene114524_All	221	0.00	0.00	0.00	0.00	0.00	0.00	2.10	8.13	0.00	null	null		null	null		null	null		null	null		1.93E+00	4.90E-05	Up	-1.10E+01	1.09E-03									ESTscan -
Unigene114527_All	341	0.00	0.00	0.00	0.00	0.00	0.00	1.98	2.94	0.00	null	null		null	null		null	null		null	null		5.68E-01	3.79E-01		-1.10E+01	3.56E-05	Down	Unigene114527_All//gi|297842159|ref|XP_002888961.1|//5.00E-13//60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata] >gi|297334802|gb|EFH65220.1| 60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata]	Unigene114527_All//2.00E-06//AT1G18540| 60S ribosomal protein L6 (RPL6A)			ko03010|Ribosome	GO:0005488//GO:0009536//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene11454_All	1642	30.56	15.83	19.07	37.10	44.67	41.12	25.67	7.00	9.92	-9.49E-01	1.33E-33		-6.80E-01	1.63E-18		2.68E-01	2.65E-06		1.48E-01	2.91E-02		-1.87E+00	9.40E-97	Down	-1.37E+00	1.27E-63	Down	Unigene11454_All//gi|166343837|gb|AB986661.1|//0.00E+00//beta-tubulin 15 [Gossypium hirsutum]	Unigene11454_All//0.00E+00//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene11454_All//0.00E+00//TC130257		ko04145|Phagosome	GO:0006970//GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:00432 34//GO:0043623	nr +
Unigene11455_All	1710	9.49	6.22	6.66	18.47	24.31	19.07	9.10	2.54	5.06	-6.08E-01	1.04E-05		-5.09E-01	3.79E-04		3.96E-01	2.35E-07		4.61E-02	6.75E-01		-1.84E+00	2.86E-35	Down	-8.48E-01	1.70E-11		Unigene11455_All//gi|166343837|gb|AB986661.1|//0.00E+00//beta-tubulin 15 [Gossypium hirsutum]	Unigene11455_All//0.00E+00//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene11455_All//0.00E+00//TC130257		ko04145|Phagosome	GO:0006970//GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:00432 34//GO:0043623	nr -
Unigene114553_All	283	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.99	0.28	null	null		null	null		null	null		null	null		1.20E+01	5.32E-08	Up	8.14E+00	4.06E-01		Unigene114553_All//gi|55168340|gb|AAV44205.1|//4.00E-09//unknow protein [Oryza sativa Japonica Group]		Unigene114553_All//1.00E-12//BN780954				nr -
Unigene11456_All	1247	1.09	1.63	1.92	3.00	2.82	3.04	0.85	0.07	1.09	5.75E-01	2.12E-01		8.17E-01	5.74E-02		-8.90E-02	8.18E-01		2.21E-02	9.43E-01		-3.66E+00	1.31E-05	Down	3.58E-01	4.90E-01		Unigene11456_All//gi|166343837|gb|AB986661.1|//1.00E-128//beta-tubulin 15 [Gossypium hirsutum]	Unigene11456_All//1.00E-118//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene11456_All//0.00E+00//TC178061		ko04145|Phagosome		nr -
Unigene11457_All	1726	113.19	24.81	47.82	52.53	72.44	51.26	24.77	6.01	12.33	-2.19E+00	0.00E+00	Down	-1.24E+00	1.53E-193	Down	4.64E-01	3.60E-28		-3.52E-02	6.07E-01		-2.04E+00	5.57E-110	Down	-1.01E+00	9.56E-40	Down	Unigene11457_All//gi|166343837|gb|AB986661.1|//0.00E+00//beta-tubulin 15 [Gossypium hirsutum]	Unigene11457_All//0.00E+00//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene11457_All//0.00E+00//TC160116		ko04145|Phagosome	GO:0006970//GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:00432 34//GO:0043623	nr -
Unigene114570_All	594	0.97	1.62	0.27	2.43	0.70	1.06	0.14	0.63	0.74	7.42E-01	2.94E-01		-1.85E+00	9.62E-02		-1.81E+00	9.96E-04	Down	-1.19E+00	3.43E-02		2.15E+00	9.45E-02		2.37E+00	4.05E-02		Unigene114570_All//gi|15229185|ref|NP_190534.1|//6.00E-43//kinesin motor protein-related [Arabidopsis thaliana] >gi|6561965|emb|CAB62469.1| kinesin-like protein [Arabidopsis thaliana]	Unigene114570_All//1.00E-44//AT3G49650| kinesin motor protein-related	Unigene114570_All//4.00E-39//TC168718			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr -
Unigene114571_All	656	0.00	0.00	0.00	0.00	0.05	0.00	3.67	1.15	0.12	null	null		null	null		5.71E+00	8.35E-01		null	null		-1.68E+00	1.82E-05	Down	-4.92E+00	4.21E-15	Down	Unigene114571_All//gi|297851686|ref|XP_002893724.1|//4.00E-69//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339566|gb|EFH69983.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene114571_All//1.00E-60//AT1G32450| NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	Unigene114571_All//6.00E-29//TC160811			GO:0004871//GO:0015833//GO:0044464	nr -
Unigene114572_All	541	0.00	0.00	0.00	0.00	0.00	0.00	0.55	2.47	1.40	null	null		null	null		null	null		null	null		2.18E+00	2.12E-04	Up	1.35E+00	6.25E-02				Unigene114572_All//1.00E-137//ES822355					
Unigene114577_All	1680	0.00	0.00	0.00	0.06	0.00	0.00	0.91	4.98	0.66	null	null		null	null		-5.89E+00	3.15E-01		-5.89E+00	4.03E-01		2.46E+00	1.96E-27	Up	-4.48E-01	3.48E-01		Unigene114577_All//gi|145333011|ref|NP_001078371.1|//1.00E-51//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene114577_All//5.00E-53//AT4G10720| ankyrin repeat family protein				GO:0010033	nr +
Unigene114586_All	282	0.00	0.00	0.00	0.00	0.00	0.00	0.15	3.26	0.00	null	null		null	null		null	null		null	null		4.44E+00	1.66E-05	Up	-7.23E+00	6.15E-01									
Unigene114593_All	260	0.00	0.19	0.00	0.00	0.13	0.17	0.16	2.09	2.60	7.61E+00	6.20E-01		null	null		7.05E+00	8.35E-01		7.44E+00	7.00E-01		3.68E+00	3.69E-03		4.00E+00	4.30E-04	Up			Unigene114593_All//4.00E-31//AI055173					
Unigene114605_All	385	0.00	0.00	0.28	0.26	0.18	0.00	0.22	2.71	1.03	null	null		8.11E+00	4.01E-01		-5.33E-01	8.18E-01		-8.02E+00	4.03E-01		3.63E+00	1.71E-05	Up	2.24E+00	6.43E-02				Unigene114605_All//4.00E-100//DR462925					
Unigene114608_All	452	0.00	0.00	0.00	0.00	0.00	0.00	0.37	2.13	0.18	null	null		null	null		null	null		null	null		2.51E+00	8.00E-04	Up	-1.09E+00	5.53E-01									
Unigene114618_All	962	0.00	0.00	0.00	0.00	0.00	0.00	2.77	4.69	0.08	null	null		null	null		null	null		null	null		7.61E-01	2.68E-03		-5.06E+00	7.12E-17	Down	Unigene114618_All//gi|4139170|gb|AAD03711.1|//1.00E-151//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene114618_All//1.00E-146//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene114618_All//3.00E-32//TC166357				nr +
Unigene114629_All	943	0.11	0.00	0.00	2.91	3.87	3.98	0.58	1.86	0.34	-6.79E+00	3.75E-01		-6.79E+00	3.97E-01		4.14E-01	2.26E-01		4.52E-01	1.79E-01		1.68E+00	3.64E-04	Up	-7.86E-01	3.62E-01		Unigene114629_All//gi|30725324|gb|AAP37684.1|//2.00E-73//At3g01680 [Arabidopsis thaliana]	Unigene114629_All//2.00E-69//AT3G01880| unknown protein	Unigene114629_All//2.00E-66//TC158531				nr +
Unigene114642_All	376	0.00	0.00	0.28	0.00	0.00	0.00	3.37	2.11	0.42	null	null		8.15E+00	4.01E-01		null	null		null	null		-6.76E-01	2.18E-01		-2.99E+00	6.36E-06	Down			Unigene114642_All//8.00E-21//TC149074					
Unigene114644_All	247	0.85	3.08	2.80	17.95	30.11	13.35	14.38	13.03	6.45	1.86E+00	3.73E-02		1.73E+00	7.68E-02		7.47E-01	2.41E-04		-4.27E-01	1.56E-01		-1.42E-01	6.46E-01		-1.16E+00	6.35E-05	Down			Unigene114644_All//3.00E-56//gi|13248487|gb|BF277051.2|BF277051					
Unigene114653_All	237	0.00	0.00	0.00	0.00	0.00	0.00	0.71	4.23	0.00	null	null		null	null		null	null		null	null		2.57E+00	4.79E-04	Up	-9.48E+00	1.09E-01									
Unigene114657_All	420	0.00	0.00	0.00	0.00	0.00	0.00	2.52	2.49	0.57	null	null		null	null		null	null		null	null		-1.67E-02	1.01E+00		-2.14E+00	9.36E-04	Down								
Unigene11466_All	2335	4.71	2.91	3.95	7.64	7.89	6.48	6.05	3.22	2.76	-6.94E-01	5.12E-05		-2.54E-01	1.81E-01		4.69E-02	8.06E-01		-2.37E-01	9.12E-02		-9.09E-01	2.41E-11		-1.13E+00	2.18E-16	Down	Unigene11466_All//gi|73761697|gb|AZ83348.1|//0.00E+00//CDPK-related protein kinase [Gossypium hirsutum]	Unigene11466_All//0.00E+00//AT3G50530| CKK (CDPK-related kinase); ATP binding / calcium ion binding / calcium-dependent protein serine/threonine phosphatase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene11466_All//0.00E+00//TC129566			GO:0000901//GO:0000164//GO:0004722//GO:0006464//GO:0008092//GO:0008154//GO:0015629//GO:0016020//GO:0016049//GO:0032559//GO:0046872	nr -

Unigene114669_All	215	0.00	0.00	0.00	0.00	0.00	0.00	20.06	17.88	0.37	null	null		null	null		null	null		null	null		-1.66E-01	5.95E-01		-5.76E+00	1.43E-28	Down	Unigene114669_All//gi|238617627|gb|ACR46935.1|//1.00E-34//actin [Katablepharis japonica]	Unigene114669_All//3.00E-34//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene114669_All//8.00E-32//TC153744		ko04145|Phagosome	GO:0005198//GO:0015629//GO:0017111//GO:0032559	nr +
Unigene114679_All	733	0.00	0.00	0.00	0.00	0.00	0.00	1.50	0.91	0.16	null	null		null	null		null	null		null	null		-7.17E-01	2.30E-01		-3.20E+00	1.63E-05	Down	Unigene114679_All//gi|253759874|ref|XP_002488951.1|//5.00E-09//hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor] >gi|241947058|gb|EES20203.1| hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor]		Unigene114679_All//5.00E-30//TC148521				nr +
Unigene114682_All	440	0.00	0.00	0.00	0.00	0.00	0.00	0.19	1.71	0.00	null	null		null	null		null	null		null	null		3.15E+00	9.55E-04	Up	-7.59E+00	3.60E-01		Unigene114682_All//gi|145344920|ref|XP_001416972.1|//4.00E-06//NCS1 family transporter: cytosine/purines/uracil/thiamine/allantoin [Ostreococcus lucimarinus CCE9901] >gi|14457198|gb|AB095265.1| NCS1 family transporter: cytosine/purines/uracil/thiamine/allantoin [Ostreococcus lucimarinus CCE9901]						nr -
Unigene114697_All	825	0.13	0.12	0.13	0.36	1.00	0.00	0.82	0.51	0.00	-4.62E-02	9.90E-01		2.59E-02	1.00E+00		1.47E+00	7.56E-02		-8.50E+00	4.00E-02		-6.95E-01	3.94E-01		-9.68E+00	3.56E-05	Down	Unigene114697_All//gi|18398046|ref|NP_566318.1|//1.00E-122//3' exoribonuclease family domain 1-containing protein [Arabidopsis thaliana] >gi|30680427|ref|NP_850537.1| 3' exoribonuclease family domain 1-containing protein [Arabidopsis thaliana] >gi|11762184|gb|AAG40370.1|AF325018_1 AT3g07750 [Arabidopsis thaliana] >gi|56744222|gb|AAW28551.1| At3g07750 [Arabidopsis thaliana]	Unigene114697_All//7.00E-102//AT3G07750| 3' exoribonuclease family domain 1-containing protein	Unigene114697_All//5.00E-166//DT467685		ko03018|RNA degradation	GO:0003676//GO:0008408//GO:0010467	nr -
Unigene114706_All	1012	0.00	0.00	0.00	0.00	0.00	0.00	0.13	3.35	0.00	null	null		null	null		null	null		null	null		4.74E+00	8.91E-20	Up	-6.97E+00	2.00E-01		Unigene114706_All//gi|240254556|ref|NP_180668.4|//1.00E-30//triacylglycerol lipase [Arabidopsis thaliana]	Unigene114706_All//5.00E-32//AT2G31100| triacylglycerol lipase					nr -
Unigene114713_All	322	0.65	0.00	0.00	0.77	0.32	0.70	0.92	5.45	0.74	-9.34E+00	1.22E-01		-9.34E+00	1.46E-01		-1.27E+00	4.24E-01		-1.41E-01	9.29E-01		2.57E+00	1.41E-06	Up	-3.08E-01	7.75E-01				Unigene114713_All//4.00E-56//gi|109883973|gb|DW512943.1|DW512943				
Unigene114472_All	2242	11.48	2.62	3.75	25.82	15.42	28.42	25.44	8.13	8.24	-2.13E+00	1.98E-57	Down	-1.61E+00	5.02E-38	Down	-7.44E-01	3.29E-31		1.39E-01	5.14E-02		-1.65E+00	4.48E-109	Down	-1.63E+00	2.80E-110	Down	Unigene11472_All//gi|9758212|dbj|BAB08657.1|//0.00E+00//nucleolar protein-like [Arabidopsis thaliana]	Unigene11472_All//7.00E-180//AT4G26000| nucleolar protein, putative	Unigene11472_All//0.00E+00//TC151464			GO:0003676//GO:0008168//GO:0009887//GO:0031981//GO:0042254	nr -
Unigene114722_All	505	0.00	0.00	0.00	0.00	0.00	0.00	0.17	1.41	3.00	null	null		null	null		null	null		null	null		3.07E+00	1.67E-03		4.16E+00	1.21E-08	Up	Unigene114722_All//gi|38228693|emb|CAE54083.1|//1.00E-14//zinc finger protein [Fagus sylvatica]	Unigene114722_All//8.00E-16//AT2G17730| zinc finger (C3HC4-type RING finger) family protein				GO:0009743//GO:0046872	nr +
Unigene114747_All	801	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.05	0.00	null	null		null	null		null	null		null	null		1.26E+01	3.79E-34	Up	null	null		Unigene114747_All//gi|301100738|ref|XP_002899458.1|//2.00E-59//flavodoxin-like protein [Phytophthora infestans T30-4] >gi|262103766|gb|EEY61818.1| flavodoxin-like protein [Phytophthora infestans T30-4]	Unigene114747_All//2.00E-39//AT4G27270| quinone reductase family protein					nr -
Unigene114751_All	387	0.00	0.00	0.00	0.00	0.00	0.00	0.11	1.73	0.00	null	null		null	null		null	null		null	null		3.98E+00	6.38E-04	Up	-6.77E+00	6.15E-01		Unigene114751_All//gi|224000193|ref|XP_002289769.1|//5.00E-20//RL11A, ribosomal protein 11A 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335] >gi|220974977|gb|EED93306.1| RL11A, ribosomal protein 11A 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335]	Unigene114751_All//1.00E-17//AT5G45775| 60S ribosomal protein L11 (RPL11D)			ko03010|Ribosome	GO:0030529	nr +
Unigene114768_All	496	0.21	0.00	0.32	0.40	0.28	0.64	0.34	3.37	0.32	-7.72E+00	3.75E-01		6.10E-01	7.49E-01		-5.33E-01	7.49E-01		6.66E-01	6.48E-01		3.31E+00	6.98E-08	Up	-8.59E-02	9.66E-01									
Unigene11477_All	2260	12.80	8.92	8.58	32.51	28.49	38.01	64.73	26.39	28.72	-5.21E-01	2.08E-07		-5.78E-01	2.32E-08		-1.90E-01	1.26E-03		2.25E-01	4.80E-05		-1.29E+00	9.11E-195	Down	-1.17E+00	1.97E-171	Down	Unigene11477_All//gi|31711944|gb|AAP68328.1|//0.00E+00//At1g18070 [Arabidopsis thaliana]	Unigene11477_All//0.00E+00//AT1G18070| EF-1-alpha-related GTP-binding protein, putative	Unigene11477_All//0.00E+00//TC130151			GO:0004179//GO:0006412//GO:0008079//GO:0017111//GO:0032561//GO:0043231	nr +
Unigene114770_All	2705	0.00	0.00	0.00	0.00	0.00	0.00	0.30	1.16	0.21	null	null		null	null		null	null		null	null		1.96E+00	2.59E-08	Up	-5.26E-01	4.35E-01		Unigene114770_All//gi|240256087|ref|NP_194459.4|//0.00E+00//ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene114770_All//0.00E+00//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene114770_All//9.00E-10//TC151245		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0009987	nr -
Unigene114771_All	446	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.91	0.00	null	null		null	null		null	null		null	null		1.15E+01	3.67E-09	Up	null	null		Unigene114771_All//gi|150421627|sp|Q9ZW82.3|PIRL2_ARATH//2.00E-16//RecName: Full=Pirin-like protein At2g43120 >gi|195360079|gb|ABL66768.1| At2g43120 [Arabidopsis thaliana]	Unigene114771_All//1.00E-17//AT2G43120| pirin, putative				GO:0005515//GO:0016020//GO:0043231	nr +
Unigene114776_All	460	0.00	0.00	0.00	0.00	0.00	0.00	2.76	4.54	0.00	null	null		null	null		null	null		null	null		7.20E-01	7.28E-02		-1.14E+01	1.99E-09	Down	Unigene114776_All//gi|159470597|ref|XP_001693443.1|//3.00E-12//histone H1 [Chlamydomonas reinhardtii] >gi|158282946|gb|EDP08697.1| histone H1 [Chlamydomonas reinhardtii]					GO:0043229	nr +
Unigene11478_All	1350	2.44	4.43	0.55	4.98	5.25	5.42	4.64	8.24	9.27	8.59E-01	4.17E-04		-2.14E+00	1.39E-07	Down	7.70E-02	8.07E-01		1.22E-01	6.29E-01		8.29E-01	6.64E-08		9.99E-01	4.81E-12		Unigene11478_All//gi|297610410|ref|NP_001064488.2|//2.00E-95//Os10g0382300 [Oryza sativa Japonica Group] >gi|255679365|dbj|BAF26402.2| Os10g0382300 [Oryza sativa Japonica Group]	Unigene11478_All//2.00E-103//AT5G66810| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: CTLH, C-terminal to LisH motif (InterPro:IPR006595); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G61150.6); Has 214 Blast hits to 160 proteins in 56 species: Archae - 0; Bacteria - 0; Metazoa - 87; Fungi - 27; Plants - 86; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink).	Unigene11478_All//0.00E+00//TC164435			GO:0043231	nr -
Unigene114788_All	245	0.00	0.00	0.00	0.00	0.00	0.00	1.04	7.17	0.00	null	null		null	null		null	null		null	null		2.79E+00	4.04E-07	Up	-1.00E+01	3.04E-02				Unigene114788_All//1.00E-27//ES810763				ESTscan -
Unigene114790_All	463	0.00	0.00	0.00	0.00	0.00	0.00	0.82	4.24	0.60	null	null		null	null		null	null		null	null		2.37E+00	1.05E-06	Up	-4.49E-01	6.41E-01		Unigene114790_All//gi|15222073|ref|NP_173349.1|//1.00E-46//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565178|sp|Q6NQG7.1|ATL1L_ARATH RecName: Full=RING-H2 finger protein ATL1L >gi|34365601|gb|AAQ65112.1| At1g19230 [Arabidopsis thaliana]	Unigene114790_All//3.00E-44//AT1G19230| zinc finger (C3HC4-type RING finger) family protein				GO:0019787//GO:0032446//GO:0046914	nr -
Unigene114796_All	340	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.46	0.00	null	null		null	null		null	null		null	null		1.13E+01	5.54E-06	Up	null	null		Unigene114796_All//gi|301108545|ref|XP_002903354.1|//2.00E-10//mucin-like protein [Phytophthora infestans T30-4] >gi|262097726|gb|EEY55778.1| mucin-like protein [Phytophthora infestans T30-4]				ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko03022|Basal transcription factors	GO:0003824	nr -
Unigene11480_All	2294	1.05	3.51	1.74	1.74	2.51	3.19	4.48	14.98	12.00	1.74E+00	3.64E-14	Up	7.31E-01	2.21E-02		5.29E-01	3.08E-02		8.77E-01	4.00E-05		1.74E+00	2.99E-71	Up	1.42E+00	9.26E-44	Up	Unigene11480_All//gi|297610410|ref|NP_001064488.2|//0.00E+00//Os10g0382300 [Oryza sativa Japonica Group] >gi|255679365|dbj|BAF26402.2| Os10g0382300 [Oryza sativa Japonica Group]	Unigene11480_All//0.00E+00//AT5G66810| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: CTLH, C-terminal to LisH motif (InterPro:IPR006595); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G61150.6); Has 214 Blast hits to 160 proteins in 56 species: Archae - 0; Bacteria - 0; Metazoa - 87; Fungi - 27; Plants - 86; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink).	Unigene11480_All//0.00E+00//TC164435			GO:0043231	nr +
Unigene114802_All	349	0.00	0.00	0.00	0.00	0.00	0.00	2.67	2.63	0.34	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		-2.96E+00	1.72E-04	Down			Unigene114802_All//4.00E-10//TC142576				
Unigene11481_All	601	4.09	5.23	3.63	7.63	7.91	8.12	4.85	2.02	3.98	3.53E-01	3.35E-01		-1.72E-01	6.75E-01		5.23E-02	8.77E-01		8.99E-02	7.62E-01		-1.27E+00	1.57E-04	Down	-2.88E-01	3.88E-01				Unigene11481_All//0.00E+00//TC141993				ESTscan +
Unigene114811_All	311	0.00	0.00	0.00	0.00	0.00	0.00	5.03	4.84	0.00	null	null		null	null		null	null		null	null		-5.61E-02	9.21E-01		-1.23E+01	1.42E-11	Down	Unigene114811_All//gi|37901017|gb|AAP46148.1|//9.00E-53//actin 2 [Pseudo-nitzschia multiseries] >gi|37935564|gb|AAP46147.1| actin 1 [Pseudo-nitzschia multiseries]	Unigene114811_All//6.00E-51//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene114811_All//6.00E-46//TC153744		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008015//GO:0008092//GO:0012501//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0048747//GO:0051707//GO:0060115	nr +
Unigene114813_All	324	0.00	0.00	0.00	0.00	0.00	0.00	1.17	9.55	1.60	null	null		null	null		null	null		null	null		3.02E+00	5.11E-13	Up	4.45E-01	6.12E-01				Unigene114813_All//4.00E-07//DW479423				
Unigene114821_All	242	0.22	0.00	0.88	0.41	0.28	0.93	0.35	5.70	0.49	-7.76E+00	6.17E-01		2.03E+00	3.62E-01		-5.33E-01	8.18E-01		1.18E+00	5.50E-01		4.03E+00	1.38E-07	Up	4.99E-01	8.08E-01				Unigene114821_All//4.00E-111//DW514353				
Unigene114825_All	260	0.80	0.97	0.82	1.92	1.72	1.04	8.13	5.30	3.06	2.76E-01	8.44E-01		2.54E-02	1.00E+00		-1.54E-01	8.50E-01		-8.78E-01	4.20E-01		-6.16E-01	1.26E-01		-1.41E+00	3.88E-04	Down	Unigene114825_All//gi|154146804|emb|CAM84089.1|//3.00E-13//phosphoenolpyruvate carboxylase [Brachypodium pinnatum]	Unigene114825_All//1.00E-13//AT2G42600| ATPPC2 (PHOSPHOENOLPYRUVATE CARBOXYLASE 2); catalytic/ phosphoenolpruvate carboxylase	Unigene114825_All//2.00E-54//ES821747		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0004611//GO:0009060//GO:0044424//GO:0071704	nr -

Unigene114826_All	247	25.84	25.44	21.34	9.08	11.85	12.80	11.64	33.50	35.16	-2.28E-02	9.41E-01		-2.76E-01	2.84E-01		3.85E-01	3.24E-01		4.96E-01	1.81E-01		1.53E+00	8.39E-15	Up	1.59E+00	7.03E-17	Up	Unigene114826_All//gi|15223919|ref|NP_172939.1|//5.00E-14//atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase >gi|68565943|sp|Q9LQU5.1|NUD18_ARATH RecName: Full=Nudix hydrolase 18, mitochondrial; Short=AtNUDT18; Flags: Precursor >gi|8778216|gb|AAF79225.1|AC006917_10 F10B6.26 [Arabidopsis thaliana]	Unigene114826_All//2.00E-15//AT1G14860| atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase	Unigene114826_All//6.00E-73//gi|109889180|gb|DW518148.1|DW518148			GO:0016462	nr +
Unigene114828_All	244	0.43	0.00	0.00	0.82	0.42	0.00	0.17	0.51	3.10	-8.74E+00	3.75E-01		-8.74E+00	3.97E-01		-9.48E-01	5.88E-01		-9.67E+00	1.34E-01		1.57E+00	5.46E-01		4.16E+00	1.34E-04	Up									
Unigene114832_All	282	19.85	10.96	12.27	10.42	8.79	13.61	8.25	3.85	2.97	-8.57E-01	6.69E-04		-6.94E-01	8.13E-03		-2.45E-01	5.56E-01		3.85E-01	2.52E-01		-1.10E+00	3.58E-03		-1.47E+00	1.01E-04	Down	Unigene114832_All//gi|21780187|gb|AAM77651.1|AF522274.1//4.00E-17//cp10-like protein [Gossypium hirsutum]	Unigene114832_All//2.00E-07//AT5G20720| CPN20 (CHAPERONIN 20); calmodulin binding	Unigene114832_All//5.00E-74//gi|21092565|gb|BQ404878.1|BQ404878			GO:0005576//GO:0006950//GO:0009526//GO:0009532//GO:0009534//GO:0010038//GO:0032559//GO:0044267//GO:0046914	nr +
Unigene114839_All	255	23.80	6.16	7.10	120.53	69.82	37.02	28.52	13.11	19.53	-1.95E+00	1.35E-12	Down	-1.75E+00	2.07E-10	Down	-7.88E-11	1.71E-18		-1.70E+00	4.58E-55	Down	-1.12E+00	1.79E-08	Down	-5.46E-01	3.54E-03			Unigene114839_All//2.00E-70//TC167712						
Unigene11484_All	743	5.42	3.07	9.10	3.22	4.68	5.05	9.84	13.73	4.61	-8.21E-01	6.84E-03		7.47E-01	1.43E-03		5.41E-01	1.08E-01		6.49E-01	4.33E-02		4.80E-01	2.79E-03		-1.09E+00	1.64E-08	Down	Unigene11484_All//gi|15222119|ref|NP_172755.1|//1.00E-71//MATE efflux family protein [Arabidopsis thaliana] >gi|66792652|gb|AAY56428.1|At1g12950 [Arabidopsis thaliana]	Unigene11484_All//5.00E-73//AT1G12950| MATE efflux family protein	Unigene11484_All//0.00E+00//TC140107			GO:0015291//GO:0015893//GO:0016020//GO:0043231//GO:0051707	nr +
Unigene114840_All	588	0.00	0.00	0.00	0.00	0.00	0.00	1.37	2.20	0.00	null	null		null	null		null	null		null	null		6.90E-01	2.02E-01		-1.04E+01	4.43E-06	Down									ESTscan +
Unigene11485_All	1420	7.37	4.53	7.65	8.45	5.77	6.81	20.54	33.82	6.90	-7.01E-01	6.89E-05		5.40E-02	7.76E-01		-5.51E-01	2.87E-04		-3.13E-01	6.81E-02		7.19E-01	9.71E-25		-1.57E+00	3.09E-54	Down	Unigene11485_All//gi|297818202|ref|XP_002876984.1|//1.00E-165//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322822|gb|EFH53243.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11485_All//8.00E-162//AT3G26590| MATE efflux family protein	Unigene11485_All//0.00E+00//TC140107			GO:0015291//GO:0015893//GO:0044464	nr +
Unigene114856_All	455	0.00	0.00	0.00	0.00	0.00	0.00	4.46	5.05	0.09	null	null		null	null		null	null		null	null		1.80E-01	6.43E-01		-5.67E+00	1.44E-13	Down	Unigene114856_All//gi|6683481|dbj|BAA88231.1|//3.00E-46//wrpl5a [Citrullus lanatus]	Unigene114856_All//8.00E-47//AT5G59850| 40S ribosomal protein S15A (RPS15aF)		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:00432 31	nr +
Unigene11486_All	1112	6.73	4.37	6.85	9.00	6.19	6.50	16.08	24.99	6.41	-6.21E-01	3.52E-03		2.54E-02	9.23E-01		-5.40E-01	1.44E-03		-4.71E-01	9.21E-03		6.36E-01	5.60E-12		-1.33E+00	3.54E-26	Down	Unigene11486_All//gi|297818202|ref|XP_002876984.1|//2.00E-71//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322822|gb|EFH53243.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11486_All//6.00E-67//AT1G12950| MATE efflux family protein	Unigene11486_All//3.00E-78//gi|48778270|gb|C0087636.1|C0087636			GO:0015291//GO:0015893//GO:0016020//GO:0043231//GO:0051707	nr -
Unigene114861_All	374	0.00	0.00	0.00	0.13	0.00	0.48	0.00	2.46	0.21	null	null		null	null		-7.06E+00	5.60E-01		1.86E+00	4.59E-01		1.13E+01	1.48E-06	Up	7.73E+00	4.06E-01		Unigene114861_All//gi|296149177|gb|ADG96403.1|//4.00E-26//S-locus glycoprotein [Olea europaea]	Unigene114861_All//2.00E-20//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding				GO:0004674//GO:0004871//GO:0006464//GO:0008037//GO:0030246//GO:00325 59	nr +
Unigene114864_All	254	0.00	0.00	0.00	0.00	0.00	0.00	2.00	2.14	0.00	null	null		null	null		null	null		null	null		9.89E-02	9.21E-01		-1.10E+01	5.54E-04	Down	Unigene114864_All//gi|300256410|gb|EFJ40676.1|//2.00E-31//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene114864_All//2.00E-23//AT5G39850| 40S ribosomal protein S9 (RPS9C)		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935	nr -
Unigene114888_All	1980	7.45	3.38	4.09	10.49	6.94	10.70	10.85	4.96	7.87	-1.14E+00	7.86E-14	Down	-8.66E-01	1.26E-08		-5.96E-01	6.40E-08		2.81E-02	8.57E-01		-1.13E+00	1.05E-23	Down	-4.64E-01	6.75E-06		Unigene114888_All//gi|13623892|dbj|BAB41076.1|//0.00E+00//MAR-binding protein [Nicotiana tabacum]	Unigene114888_All//0.00E+00//AT3G05060| SAR DNA-binding protein, putative	Unigene114888_All//0.00E+00//gi|164274934|gb|ES818124.1|ES818124	ko03040|Spliceosome	GO:0003676//GO:0031981	nr -
Unigene114880_All	425	0.25	0.24	1.50	0.35	0.32	0.00	0.30	3.05	0.47	-4.64E-02	9.90E-01		2.61E+00	2.33E-02		-1.18E-01	9.11E-01		-8.46E+00	2.34E-01		3.35E+00	2.62E-06	Up	6.51E-01	6.66E-01										
Unigene114887_All	346	0.00	0.00	0.00	0.43	0.00	0.13	0.24	2.30	0.46	null	null		null	null		-8.75E+00	1.66E-01		-1.72E+00	5.02E-01		3.23E+00	5.44E-04	Up	9.14E-01	6.25E-01										
Unigene114888_All	294	0.18	0.52	0.00	0.34	0.23	0.61	0.00	0.85	2.17	1.54E+00	5.32E-01		-7.48E+00	6.29E-01		-5.33E-01	8.18E-01		8.59E-01	6.96E-01		9.74E+00	4.32E-02		1.11E+01	9.35E-05	Up			Unigene114888_All//2.00E-27//gi|84152253|gb|DN801608.1|DN801608						
Unigene114889_All	2084	16.07	7.83	9.22	27.70	21.89	33.68	56.56	31.61	31.62	-1.04E+00	3.74E-26	Down	-8.01E-01	1.76E-16		-3.40E-01	9.05E-08		2.82E-01	3.91E-06		-8.40E-01	1.13E-77		-8.39E-01	9.75E-80		Unigene114889_All//gi|13623892|dbj|BAB41076.1|//0.00E+00//MAR-binding protein [Nicotiana tabacum]	Unigene114889_All//0.00E+00//AT3G05060| SAR DNA-binding protein, putative	Unigene114889_All//0.00E+00//gi|164243931|gb|ES808355.1|ES808355	ko03040|Spliceosome	GO:0003676//GO:0031981	nr -
Unigene114890_All	427	0.00	0.00	0.00	0.00	0.00	0.00	2.97	2.06	0.19	null	null		null	null		null	null		null	null		-5.31E-01	3.43E-01		-3.99E+00	2.56E-07	Down	Unigene114890_All//gi|91885543|dbj|BAA89561.1|//2.00E-31//alpha-tubulin [Chlorella vulgaris]	Unigene114890_All//3.00E-23//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene114890_All//1.00E-26//gi|164280667|gb|ES792179.1|ES792179	ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene114891_All	471	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.00	null	null		null	null		null	null		null	null		1.10E+01	7.61E-07	Up	null	null		Unigene114891_All//gi|13516922|dbj|BAB40340.1|//1.00E-17//12-oxophytodienoic acid 10, 11-reductase [Pisum sativum] >gi|44917012|dbj|BAD12185.1| 12-oxophytodienoic acid 10,11-reductase [Pisum sativum]	Unigene114891_All//2.00E-17//AT1G17990| 12-oxophytodienoate reductase, putative		ko00592|alpha-Linolenic acid metabolism	GO:0003824	nr +
Unigene114892_All	357	0.00	0.43	0.15	0.28	0.48	0.13	0.12	1.99	0.33	8.73E+00	2.36E-01		7.22E+00	6.39E-01		7.89E-01	7.71E-01		-1.14E+00	6.78E-01		4.07E+00	3.51E-04	Up	1.50E+00	5.59E-01		Unigene114892_All//gi|15235767|ref|NP_193381.1|//7.00E-34//INT4 (INOSITOL TRANSPORTER 4); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|75318122|sp|Q23492.1|INT4_ARATH RecName: Full=Inositol transporter 4; AltName: Full=Myo-inositol-proton symporter INT4; AltName: Full=Protein INOSITOL TRANSPORTER 4 >gi|2245004|emb|CAB10424.1| membrane transporter like protein [Arabidopsis thaliana] >gi|7268398|emb|CAB78690.1| membrane transporter like protein [Arabidopsis thaliana] >gi|84617973|emb|CAJ00306.1| inositol transporter 4 [Arabidopsis thaliana]	Unigene114892_All//3.00E-35//AT4G16480| INT4 (INOSITOL TRANSPORTER 4); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen symporter				GO:0005365//GO:0008152//GO:0015791//GO:0016628//GO:0031224	nr +
Unigene1149_All	1362	3.65	1.90	2.31	6.91	5.64	4.01	5.03	0.37	2.25	-9.44E-01	4.94E-04		-6.62E-01	1.87E-02		-2.94E-01	1.28E-01		-7.85E-01	1.78E-05		-3.77E+00	3.54E-34	Down	-1.16E+00	1.02E-08	Down	Unigene1149_All//gi|15228248|ref|NP_187640.1|//1.00E-149//phosphate translocator-related [Arabidopsis thaliana]	Unigene1149_All//7.00E-140//AT3G10290| phosphate translocator-related	Unigene1149_All//0.00E+00//gi|48820927|gb|CO122240.1|CO122240				nr -
Unigene11490_All	407	1.80	6.72	13.87	2.94	5.67	3.99	1.66	1.95	2.06	1.90E+00	7.24E-06	Up	2.95E+00	6.60E-18	Up	9.49E-01	2.28E-02		4.44E-01	4.29E-01		2.31E-01	7.35E-01		3.07E-01	6.28E-01		Unigene11490_All//gi|297843644|ref|XP_002889703.1|//2.00E-09//thioredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335545|gb|EFH65962.1| thioredoxin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11490_All//3.00E-10//AT1G08570| ACHT4 (ATYPICAL CYS HIS RICH THIOREDOXIN 4); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	Unigene11490_All//3.00E-54//TC132912				nr -
Unigene114901_All	333	0.00	0.00	0.00	0.00	0.00	0.00	0.13	2.51	0.00	null	null		null	null		null	null		null	null		4.31E+00	5.68E-05	Up	-6.99E+00	6.15E-01		Unigene114901_All//gi|168070959|ref|XP_001786992.1|//3.00E-08//predicted protein [Physcomitrella patens subsp. patens] >gi|162659991|gb|EDQ48194.1| predicted protein [Physcomitrella patens subsp. patens]						nr -
Unigene114909_All	550	0.00	0.00	0.00	0.00	0.00	0.00	1.77	2.28	0.00	null	null		null	null		null	null		null	null		3.67E-01	5.29E-01		-1.08E+01	2.72E-07	Down									ESTscan -
Unigene11491_All	4312	21.19	49.76	32.34	38.87	42.82	35.88	22.99	12.24	19.37	1.23E+00	3.41E-215	Up	6.10E-01	8.31E-42		1.40E-01	1.09E-04		-1.16E-01	4.87E-03		-9.09E-01	7.70E-75		-2.47E-01	5.82E-08		Unigene11491_All//gi|18402209|ref|NP_564528.1|//0.00E+00//RKL1: ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|75338279|sp|Q9LF77.1|Y1848_ARATH RecName: Full=Probable inactive receptor kinase At1g48480; Flags: Precursor >gi|8778688|gb|AAF79696.1|AC020889_4 T1N15,9 [Arabidopsis thaliana] >gi|209529789|gb|ACI49789.1| At1g48480 [Arabidopsis thaliana] >gi|224589420|gb|ACN59214.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene11491_All//0.00E+00//AT1G48480| RKL1; ATP binding / kinase/ protein serine/threonine kinase	Unigene11491_All//0.00E+00//TC145693			GO:0004672//GO:0006464//GO:0007167//GO:0016491//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene114910_All	217	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12.33	0.92	null	null		null	null		null	null		null	null		1.36E+01	8.14E-19	Up	9.84E+00	7.90E-02				Unigene114910_All//1.00E-12//DT049550						
Unigene114914_All	239	0.00	0.00	0.00	0.00	0.00	0.00	1.24	7.52	0.50	null	null		null	null		null	null		null	null		2.60E+00	8.33E-07	Up	-1.31E+00	3.13E-01				Unigene114914_All//2.00E-51//gi|109883973|gb|DW512943.1|DW512943						
Unigene114919_All	216	134.92	113.54	56.21	247.23	118.29	201.98	484.26	351.59	112.14	-2.49E-01	1.59E-02		-1.26E+00	6.55E-30	Down	-1.06E+00	7.08E-53	Down	-2.92E-01	3.89E-05		-4.62E-01	2.38E-24		-2.11E+00	4.66E-288	Down			Unigene114919_All//9.00E-38//TC175475						
Unigene114921_All	318	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.84	0.00	null	null		null	null		null	null		null	null		1.08E-01	2.81E-04	Up	null	null										
Unigene114922_All	750	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.51	0.00	null	null		null	null		null	null		null	null		1.18E+01	1.60E-18	Up	null	null		Unigene114922_All//gi|298710310|emb|CBJ31931.1|//5.00E-12//putative transmembrane protein [Ectocarpus siliculosus]						nr +
Unigene114930_All	220	0.24	3.92	0.73	0.23	0.47	1.23	0.58	3.42	1.63	4.04E+00	4.20E-04	Up	1.61E+00	5.11E-01		1.05E+00	8.09E-01		2.44E+00	2.22E-01		2.57E+00	3.32E-03		1.50E+00	2.04E-01		Unigene114930_All//gi|18542927|gb|AAK00417.2|//6.00E-14//Putative inositol 1,3,4-trisphosphate 5/6-kinase [Oryza sativa Japonica Group]	Unigene114930_All//2.00E-14//AT4G08170| inositol 1,3,4-trisphosphate 5/6-kinase family protein	Unigene114930_All//2.00E-60//TC178237		ko04070|Phosphatidylinositol signaling system/ko00562|Inositol phosphate metabolism	GO:0006950//GO:0032559//GO:0043231//GO:0043647//GO:0046872//GO:0051765//GO:0051766	nr +
Unigene114937_All	257	3.66	7.10	5.59	2.33	3.89	4.92	2.30	6.83	2.64	9.54E-01	4.89E-02		6.10E-01	2.96E-01		7.40E-01	3.10E-01		1.08E+00	8.18E-02		1.57E+00	7.26E-04	Up	1.94E-01	7.87E-01				Unigene114937_All//5.00E-07//AT1G06210| VHS domain-containing protein / GAT domain-containing protein	Unigene114937_All//1.00E-65//ES843618				
Unigene114946_All	1172	0.09	0.09	0.00	0.09	0.00	0.00	1.08	3.71	2.82	-4.60E-02	9.90E-01		-6.48E+00	3.97E-01		-6.41E+00	3.15E-01		-6.41E+00	4.03E-01		1.78E+00	6.35E-10	Up	1.38E+00	8.62E-06	Up	Unigene114946_All//gi|238478527|ref|NP_001154349.1|//3.00E-22//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|259016409|sp|P0CSE2.2|Y1839_ARATH RecName: Full=Probable serine/threonine-protein kinase At1g18390; Flags: Precursor	Unigene114946_All//1.00E-23//AT1G18390| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase			GO:0004672//GO:0016020	nr -
Unigene114949_All	1050	0.00	0.00	0.00	0.00	0.00	0.04	0.40	2.07	0.49	null	null		null	null		null	null		5.43E+00	7.00E-01		2.36E+00	2.52E-07	Up	2.93E-01	7.27E-01		Unigene114949_All//gi|224124808|ref|XP_002319427.1|//1.00E-110//cytochrome P450 [Populus trichocarpa] >gi|222857803|gb|EEE95350.1| cytochrome P450 [Populus trichocarpa]	Unigene114949_All//4.00E-80//AT4G39950| CYP79B2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene114949_All//5.00E-09//TC176629		ko00460|Cyanoamino acid metabolism	GO:0002239//GO:0004497//GO:0005506//GO:0006091//GO:0006568//GO:0009536//GO:0009663//GO:0009700//GO:0044425//GO:0052482	nr -
Unigene114953_All	328	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.93	0.00	null	null		null	null		null	null		null	null		1.15E+01	7.61E-07	Up	null	null										
Unigene114958_All	400	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.78	0.00	null	null		null	null		null	null		null	null		1.08E+01	3.98E-05	Up	null	null										

Unigene11496_All	2646	3.74	1.24	3.02	12.93	10.58	9.81	4.15	1.33	0.72	-1.59E+00	2.99E-15	Down	-3.08E-01	1.23E-01		-2.90E-01	9.28E-04		-3.98E-01	8.31E-06		-1.65E+00	1.22E-21	Down	-2.52E+00	2.75E-38	Down	Unigene11496_All//gi|87240917|gb|AB032775.1|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene11496_All//3.00E-128//AT2G01820| leucine-rich repeat protein kinase, putative	Unigene11496_All//0.00E+00//TC159514			GO:0004672//GO:0006464//GO:0031224//GO:0032559	nr -
Unigene114962_All	746	0.00	0.00	0.00	0.00	0.00	0.00	3.06	15.74	0.21	null	null		null	null		null	null		null	null		2.36E+00	1.41E-36	Up	-3.84E+00	2.31E-12	Down	Unigene114962_All//gi|238014838|gb|ACR38454.1|//3.00E-14//unknown [Zea mays]		Unigene114962_All//4.00E-49//TC146753				nr -
Unigene11497_All	3060	4.07	2.37	5.26	7.98	8.00	8.06	4.15	1.54	1.34	-7.81E-01	1.20E-06		3.69E-01	1.20E-02		4.40E-03	9.76E-01		1.47E-02	9.31E-01		-1.43E+00	2.96E-20	Down	-1.63E+00	3.05E-25	Down	Unigene11497_All//gi|87240917|gb|AB032775.1|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene11497_All//0.00E+00//AT1G66150| TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase	Unigene11497_All//0.00E+00//gi|164239875|gb|ES827735.1|ES827735			GO:0004674//GO:0004871//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene114978_All	451	0.23	0.00	0.00	0.11	0.15	0.00	0.38	2.78	0.44	-7.86E+00	3.75E-01		-7.86E+00	3.97E-01		4.67E-01	9.60E-01		-6.79E+00	6.41E-01		2.89E+00	1.97E-05	Up	2.36E-01	8.84E-01				Unigene114978_All//4.00E-128//ES801465				
Unigene11498_All	1225	1.75	4.22	4.22	5.08	3.68	3.91	7.42	8.09	5.66	1.27E+00	3.74E-06	Up	1.27E+00	7.23E-06	Up	-4.65E-01	4.35E-02		-3.79E-01	1.28E-01		1.24E-01	5.28E-01		-3.91E-01	1.95E-02				Unigene11498_All//0.00E+00//TC179542				
Unigene114989_All	238	0.22	0.00	0.00	2.09	0.00	0.57	0.18	1.93	0.00	-7.78E+00	6.17E-01		-7.78E+00	6.29E-01		-1.10E+01	8.99E-04	Down	-1.88E+00	1.08E-01		3.44E+00	1.16E-02		-7.47E+00	6.15E-01				Unigene114989_All//4.00E-46//CO132540				
Unigene11499_All	1231	2.08	4.65	3.81	4.17	6.10	4.37	6.49	6.79	10.62	1.16E+00	5.95E-06	Up	8.70E-01	2.74E-03		5.49E-01	7.87E-03		6.69E-02	8.20E-01		6.50E-02	7.49E-01		7.10E-01	2.12E-07		Unigene11499_All//gi|297812189|ref|XP_002873978.1|//3.00E-46//agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319815|gb|EFH50237.1| agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene11499_All//4.00E-33//AT5G20030| agenet domain-containing protein	Unigene11499_All//5.00E-173//TC156483				nr +
Unigene1150_All	1368	3.48	1.07	1.67	4.73	4.10	2.71	5.72	1.34	2.80	-1.70E+00	1.99E-08	Down	-1.06E+00	2.88E-04	Down	-2.06E-01	4.24E-01		-8.06E-01	3.83E-04		-2.09E+00	2.84E-21	Down	-1.03E+00	2.65E-08	Down	Unigene1150_All//gi|15225248|ref|NP_187640.1|//1.00E-151//phosphate translocator-related [Arabidopsis thaliana]	Unigene1150_All//3.00E-131//AT5G41160| phosphate translocator-related	Unigene1150_All//0.00E+00//TC139348				nr +
Unigene115001_All	331	0.00	0.00	0.00	0.00	0.00	0.00	0.26	3.16	0.00	null	null		null	null		null	null		null	null		3.63E+00	1.71E-05	Up	-8.00E+00	3.60E-01		Unigene115001_All//gi|255070295|ref|XP_002507229.1|//2.00E-08//H+-or Na+-translocating f-type, v-type and A-type ATPase superfamily [Micromonas sp. RCC299] >gi|226522504|gb|ACO68487.1| H+-or Na+-translocating f-type, v-type and A-type ATPase superfamily [Micromonas sp. RCC299]	Unigene115001_All//3.00E-06//ATCG00480| chloroplast-encoded gene for beta subunit of ATP synthase			ko00190|Oxidative phosphorylation//ko00195|Photosynthesis	GO:0009534//GO:0015078//GO:0015662//GO:0019866//GO:0019829//GO:0032559//GO:0033178	nr -
Unigene115007_All	332	0.00	0.00	0.00	0.00	0.00	0.00	2.29	2.52	0.00	null	null		null	null		null	null		null	null		1.35E-01	8.42E-01		-1.12E+01	8.87E-06	Down									
Unigene11502_All	1271	1.56	0.96	1.89	3.02	3.20	2.10	4.36	2.37	2.04	-7.09E-01	1.20E-01		2.69E-01	5.47E-01		8.32E-02	8.15E-01		-5.26E-01	1.02E-01		-8.80E-01	9.99E-05		-1.10E+00	1.11E-06	Down	Unigene11502_All//gi|63087714|emb|CAI93172.1|//1.00E-122//beta-1,3-glucuronosyltransferase [Gossypium raimondii]	Unigene11502_All//1.00E-102//AT1G27600| glycosyl transferase family 43 protein	Unigene11502_All//0.00E+00//TC129656			GO:0015020//GO:0044464	nr +
Unigene115024_All	241	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.60	0.00	null	null		null	null		null	null		null	null		1.13E+01	1.47E-04	Up	null	null									
Unigene115027_All	442	0.36	0.23	0.00	0.23	0.00	0.00	0.67	2.84	1.26	-6.31E-01	7.28E-01		-8.47E+00	2.46E-01		-7.82E+00	3.15E-01		-7.82E+00	4.03E-01		2.08E+00	5.41E-04	Up	9.14E-01	2.89E-01				Unigene115027_All//8.00E-43//CO125212				
Unigene11503_All	1139	3.86	3.96	3.32	7.13	6.32	6.82	5.75	2.20	4.48	3.71E-02	9.10E-01		-2.17E-01	4.98E-01		-1.74E-01	4.48E-01		-6.39E-02	7.81E-01		-1.39E+00	1.98E-10	Down	-3.62E-01	7.55E-02		Unigene11503_All//gi|63087714|emb|CAI93172.1|//0.00E+00//beta-1,3-glucuronosyltransferase [Gossypium raimondii]	Unigene11503_All//5.00E-98//AT1G27600| glycosyl transferase family 43 protein	Unigene11503_All//0.00E+00//TC129656			GO:0015020//GO:0044464	nr -
Unigene115030_All	363	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.61	0.00	null	null		null	null		null	null		null	null		1.07E+01	2.81E-04	Up	null	null		Unigene115030_All//gi|18407264|ref|NP_566095.1|//8.00E-24//UBQ6; protein binding [Arabidopsis thaliana] >gi|14030651|gb|AAK53000.1|AF375416_1 At2g47110/F14M4.6 [Arabidopsis thaliana] >gi|166906|gb|AAA32907.1| ubiquitin extension protein (UBQ6) [Arabidopsis thaliana] >gi|3522953|gb|AAC34235.1| ubiquitin extension protein (UBQ6) [Arabidopsis thaliana] >gi|21593980|gb|AAM65909.1| ubiquitin extension protein (UBQ6) [Arabidopsis thaliana] >gi|22655410|gb|AAM98297.1| At2g47110/F14M4.6 [Arabidopsis thaliana] >gi|23505779|gb|AAN28749.1| At2g47110/F14M4.6 [Arabidopsis thaliana]	Unigene115030_All//4.00E-13//AT2G47110| UBQ6; protein binding			ko03010|Ribosome	GO:0015935//GO:0044267	nr +
Unigene115034_All	392	0.00	0.00	0.00	0.38	0.09	0.23	0.22	2.24	0.00	null	null		null	null		-2.12E+00	3.87E-01		-7.26E-01	7.16E-01		3.38E+00	1.75E-04	Up	-7.75E+00	3.60E-01		Unigene115034_All//gi|186532568|ref|NP_200663.2|//7.00E-18//EOL2 (ETO1-LIKE 2); binding / protein binding [Arabidopsis thaliana]	Unigene115034_All//4.00E-19//AT5G38550| EOL2 (ETO1-LIKE 2); binding / protein binding	Unigene115034_All//4.00E-41//TC171012			GO:0005488	nr +
Unigene115045_All	469	0.00	0.43	0.00	0.11	0.00	0.10	0.18	1.96	0.25	8.76E+00	1.37E-01		null	null		-6.73E+00	5.60E-01		-1.41E-01	9.55E-01		3.44E+00	9.84E-05	Up	4.99E-01	8.08E-01		Unigene115045_All//gi|255559276|ref|XP_002520658.1|//3.00E-14//conserved hypothetical protein [Ricinus communis] >gi|223540043|gb|EEF41620.1| conserved hypothetical protein [Ricinus communis]					GO:0005488	nr +
Unigene11505_All	1265	2.44	1.04	1.05	2.84	2.18	3.07	2.61	1.72	2.87	-1.23E+00	7.17E-04	Down	-1.21E+00	1.33E-03		-3.81E-01	2.58E-01		1.15E-01	7.31E-01		-6.02E-01	4.98E-02		1.37E-01	6.40E-01		Unigene11505_All//gi|63087714|emb|CAI93172.1|//1.00E-133//beta-1,3-glucuronosyltransferase [Gossypium raimondii]	Unigene11505_All//1.00E-112//AT1G27600| glycosyl transferase family 43 protein	Unigene11505_All//0.00E+00//TC167504			GO:0015020//GO:0044464	nr -
Unigene115050_All	401	0.00	0.13	0.00	0.37	0.00	1.13	0.21	2.92	0.10	6.98E+00	6.20E-01		null	null		-8.54E+00	1.66E-01		1.60E+00	2.05E-01		3.79E+00	2.86E-06	Up	-1.09E+00	6.77E-01				Unigene115050_All//9.00E-92//gi|109878692|gb|DW507662.1|DW507662				
Unigene115056_All	258	0.41	0.00	0.00	0.97	0.67	0.00	0.66	4.70	2.32	-8.66E+00	3.75E-01		-8.66E+00	3.97E-01		-5.33E-01	7.13E-01		-9.92E+00	7.35E-02		2.84E+00	3.39E-05	Up	1.82E+00	3.95E-02				Unigene115056_All//2.00E-131//DW511260				ESTscan -
Unigene11506_All	1603	2.48	1.33	1.73	3.92	3.20	2.93	2.95	1.96	1.44	-9.02E-01	3.29E-03		-5.22E-01	1.08E-01		-2.91E-01	2.42E-01		-4.18E-01	8.56E-02		-5.95E-01	1.63E-02		-1.04E+00	2.14E-05	Down	Unigene11506_All//gi|63087714|emb|CAI93172.1|//1.00E-113//beta-1,3-glucuronosyltransferase [Gossypium raimondii]	Unigene11506_All//1.00E-68//AT1G27600| glycosyl transferase family 43 protein	Unigene11506_All//0.00E+00//gi|78324411|gb|DT544685.1|DT544685			GO:0015020//GO:0044464	nr -
Unigene115063_All	417	0.00	0.00	0.00	0.00	0.00	0.00	1.42	4.21	0.00	null	null		null	null		null	null		null	null		1.57E+00	7.26E-04	Up	-1.05E+01	1.41E-04	Down	Unigene115063_All//gi|214003725|gb|ACJ60905.1|//2.00E-74//alpha tubulin [Betula pendula]	Unigene115063_All//1.00E-73//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene115063_All//6.00E-93//TC130219		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene115067_All	296	4.77	5.48	5.58	4.54	2.91	6.71	6.28	9.18	23.82	1.99E-01	6.82E-01		2.25E-01	6.52E-01		-6.44E-01	2.63E-01		5.63E-01	2.43E-01		5.46E-01	1.18E-01		1.92E+00	1.05E-17	Up			Unigene115067_All//2.00E-110//ES846306				
Unigene11507_All	725	12.34	4.19	2.50	16.56	15.91	15.51	15.69	9.34	8.30	-1.56E+00	1.60E-13	Down	-2.31E+00	1.97E-21	Down	-5.75E-02	7.98E-01		-9.43E-02	6.24E-01		-7.48E-01	6.72E-07		-9.19E-01	8.92E-10		Unigene11507_All//gi|297834468|ref|XP_002885116.1|//5.00E-68//glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata] >gi|297330956|gb|EFH61375.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata]	Unigene11507_All//2.00E-68//AT3G15940| glycosyl transferase family 1 protein	Unigene11507_All//0.00E+00//TC142889		ko00561|Glycerolipid metabolism	GO:0008152//GO:0009536//GO:0016740	nr +
Unigene115074_All	524	0.00	0.19	0.00	0.19	0.72	0.52	0.48	5.34	1.67	7.60E+00	3.89E-01		null	null		1.93E+00	1.94E-01		1.44E+00	4.09E-01		3.46E+00	2.53E-13	Up	1.79E+00	1.04E-02		Unigene115074_All//gi|1732406|gb|AB38748.1|//9.00E-44//S25-XP1 DNA binding protein [Nicotiana tabacum]	Unigene115074_All//8.00E-39//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene115074_All//3.00E-24//ES803928	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene115075_All	285	0.00	0.00	0.00	0.00	0.00	0.00	68.54	8.07	59.55	null	null		null	null		null	null		null	null		-3.09E+00	6.98E-81	Down	-2.03E-01	7.72E-02		Unigene115075_All//gi|791146|emb|CAA60020.1|//2.00E-44//extensin-like protein [Vigna unguiculata]						nr -
Unigene115077_All	362	0.00	0.00	0.00	0.00	0.00	0.00	2.57	4.85	0.44	null	null		null	null		null	null		null	null		9.16E-01	3.87E-02		-2.55E+00	5.79E-04	Down	Unigene115077_All//gi|145048590|ref|YP_001152214.1|//1.00E-07//O8F124 [Pinus koraiensis] >gi|145048839|gb|ABF35456.1| O8F124 [Pinus koraiensis]		Unigene115077_All//3.00E-17//TC149074				nr -
Unigene115078_All	276	0.00	0.00	0.00	0.00	0.00	0.00	0.31	2.73	0.58	null	null		null	null		null	null		null	null		3.15E+00	9.54E-04	Up	9.14E-01	6.25E-01									
Unigene115079_All	576	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.74	1.04	null	null		null	null		null	null		null	null		1.08E+01	3.93E-07	Up	1.00E+01	1.76E-04	Up	Unigene115079_All//gi|121077603|gb|ABM47305.1|//4.00E-06//nucleic acid binding protein [Volvox carteri f. nagariensis] >gi|300269119|gb|EFJ53299.1| nucleic acid binding protein [Volvox carteri f. nagariensis]	Unigene115079_All//1.00E-05//AT2G21060| ATGRP2B (GLYCINE-RICH PROTEIN 2B); DNA binding / nucleic acid binding / zinc ion binding		CSD			nr +
Unigene11508_All	2484	3.22	3.16	1.97	6.96	7.50	6.02	11.63	5.74	6.88	-2.76E-02	9.09E-01		-7.09E-01	8.87E-04		1.08E-01	4.99E-01		-2.10E-01	1.52E-01		-1.02E+00	7.35E-27	Down	-7.57E-01	4.56E-17		Unigene11508_All//gi|15233237|ref|NP_188215.1|//1.00E-121//glycosyl transferase family 1 protein [Arabidopsis thaliana] >gi|9294599|dbj|BAB02880.1| glycosyl transferases-like protein [Arabidopsis thaliana] >gi|20147191|gb|AAM10311.1| AT3g15940/MVC8_7 [Arabidopsis thaliana]	Unigene11508_All//2.00E-119//AT3G15940| glycosyl transferase family 1 protein	Unigene11508_All//0.00E+00//ES848925		ko00561|Glycerolipid metabolism		nr +
Unigene115080_All	229	0.00	0.44	0.00	0.22	0.00	0.39	8.68	13.69	2.78	8.79E+00	3.89E-01		null	null		-7.76E+00	5.60E-01		8.59E-01	7.96E-01		6.58E-01	3.70E-02		-1.64E+00	1.05E-04	Down	Unigene115080_All//gi|224111880|ref|XP_002316010.1|//2.00E-10//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene115080_All//3.00E-08//AT3G14690| CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene115080_All//1.00E-73//gi|109890708|gb|DW519672.1|DW519672			GO:0005506//GO:0008152//GO:0016634	nr -
Unigene115083_All	204	9.49	3.73	2.87	13.43	12.49	15.50	74.40	40.77	32.22	-1.35E+00	4.99E-03		-1.72E+00	9.79E-04	Down	-1.05E-01	8.15E-01		2.07E-01	6.32E-01		-8.68E-01	2.73E-11		-1.21E+00	2.07E-19	Down	Unigene115083_All//gi|8778823|gb|AF79822.1|AC026875_2//5.00E-15//T6D22.2 [Arabidopsis thaliana]	Unigene115083_All//4.00E-11//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene115083_All//5.00E-64//gi|78351725|gb|DT571999.1|DT571999			GO:0006412//GO:0008135//GO:0016772//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene115089_All	272	0.00	0.00	0.00	0.00	0.00	0.00	0.31	3.07	1.17	null	null		null	null		null	null		null	null		3.31E+00	3.10E-04	Up	1.91E+00	1.54E-01				Unigene115089_All//3.00E-16//CO092801				
Unigene11509_All	5030	3.18	1.88	1.93	8.69	6.92	5.63	6.88	1.85	3.60	-7.57E-01	6.59E-08		-7.24E-01	5.08E-07		-3.28E-01	1.17E-05		-6.26E-01	1.19E-15		-1.89E+00	1.16E-80	Down	-9.37E-01	7.97E-29		Unigene11509_All//gi|15233237|ref|NP_188215.1|//0.00E+00//glycosyl transferase family 1 protein [Arabidopsis thaliana] >gi|9294599|dbj|BAB02880.1| glycosyl transferases-like protein [Arabidopsis thaliana] >gi|20147191|gb|AAM10311.1| AT3g15940/MVC8_7 [Arabidopsis thaliana]	Unigene11509_All//0.00E+00//AT3G15940| glycosyl transferase family 1 protein	Unigene11509_All//0.00E+00//TC158791		ko00561|Glycerolipid metabolism	GO:0008152//GO:0016740	nr -
Unigene1151_All	2003	63.89	140.45	83.37	103.28	104.27	132.81	109.70	328.02	179.01	1.14E+00	5.13E-248	Up	3.84E-01	1.12E-21		1.37E-02	8.07E-01		3.63E-01	3.40E-34		1.58E+00	0.00E+00	Up	7.06E-01	4.82E-178		Unigene1151_All//gi|225446893|ref|XP_002284064.1|//0.00E+00//PREDICTED: similar to Citrate synthase, glyoxysomal [Vitis vinifera]	Unigene1151_All//0.00E+00//AT3G58750| CSY2 (citrate synthase 2); citrate (SI)-synthase	Unigene1151_All//0.00E+00//TC133360		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005777//GO:0009060//GO:0009062//GO:0016747//GO:0044262//GO:0046912	nr -
Unigene11510_All	1408	0.93	1.66	1.32	3.15	2.37	3.43	11.86	12.17	59.39	8.33E-01	4.59E-02		5.11E-01	3.12E-01		-4.09E-01	1.61E-01		1.24E-01	6.78E-01		3.71E-02	7.92E-01		2.32E+00	3.25E-256	Up	Unigene11510_All//gi|15226985|ref|NP_180455.1|//1.00E-121//PLL4 (POLTERGEIST LIKE 4); catalytic/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75216896|sp|Q9ZV25.1|P2C23_ARATH RecName: Full=Probable protein phosphatase 2C 23; Short=AtPP2C23; AltName: Full=Protein phosphatase 2C PLL4; Short=PP2C PLL4; AltName: Full=Protein POLTERGEIST-LIKE 4	Unigene11510_All//3.00E-96//AT1G07630| PLL5; catalytic/ protein serine/threonine phosphatase	Unigene11510_All//0.00E+00//TC139366				nr +

Unigene11511_All	2796	8.94	9.97	6.80	17.85	16.50	13.60	28.02	29.00	57.54	1.56E-01	1.61E-01			-3.96E-01	4.81E-04		-1.13E-01	1.72E-01		-3.92E-01	5.96E-08		4.96E-02	4.40E-01		1.04E+00	1.12E-153	Up	Unigene11511_All//gi|18390789|ref|NP_563791.1|//0.00E+00//PLL5; catalytic/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75180175|sp|Q9LQN6.1|P2C04_ARATH RecName: Full=Probable protein phosphatase 2C 4; Short=AtPP2C04; AltName: Full=Protein phosphatase 2C PLL5; Short=PP2C PLL5; AltName: Full=Protein POLTERGEIST-LIKE 5 >gi|8439909|gb|AAF75095.1|AC007583_31 It contains protein phosphatase 2C domain PF|00481. ESTs gb|H36120 and gb|36519 come from this gene [Arabidopsis thaliana]	Unigene11511_All//0.00E+00//AT1G07630| PLL5; catalytic/ protein serine/threonine phosphatase				GO:0004721//GO:0016020//GO:0048827	nr -
Unigene115112_All	296	0.00	0.00	0.00	0.00	0.00	0.00	12.43	2.26	2.15	null	null		null	null		null	null		null	null		-2.46E+00	1.66E-12	Down	-2.53E+00	2.37E-13	Down	Unigene115112_All//gi|20197696|gb|AAM15209.1|//1.00E-24//senescence-associated protein [Arabidopsis thaliana] >gi|20197726|gb|AAM15226.1| senescence-associated protein [Arabidopsis thaliana]	Unigene115112_All//5.00E-26//AT2G21045| INVOLVED IN: aging; EXPRESSED IN: hypocotyl, root; CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66170.2); Has 1919 Blast hits to 1917 proteins in 542 species: Archae - 34; Bacteria - 1258; Metazoa - 17; Fungi - 21; Plants - 115; Viruses - 0; Other Eukaryotes - 474 (source: NCBI BLink).				GO:0031410//GO:0032502	nr -
Unigene115115_All	339	0.00	0.00	0.00	0.00	0.00	0.00	11.35	14.06	30.44	null	null		null	null		null	null		null	null		3.09E-01	2.39E-01		1.42E+00	5.84E-17	Up	Unigene115115_All//gi|147791048|emb|CAN65763.1|//7.00E-07//hypothetical protein [Vitis vinifera]		Unigene115115_All//1.00E-65//ES810763				nr +
Unigene11512_All	444	0.59	1.03	1.92	1.23	2.02	1.73	4.57	1.60	2.60	8.02E-01	4.60E-01		1.70E+00	4.53E-02		7.08E-01	3.74E-01		4.87E-01	5.91E-01		-1.51E+00	3.50E-04	Down	-8.13E-01	3.63E-02		Unigene11512_All//gi|18402856|ref|NP_565734.1|//5.00E-33//integral membrane transporter family protein [Arabidopsis thaliana] >gi|20197619|gb|AAD15400.2| expressed protein [Arabidopsis thaliana]	Unigene11512_All//2.00E-32//AT2G32040| integral membrane transporter family protein	Unigene11512_All//0.00E+00//TC177047			GO:0008517//GO:0009526//GO:0051234	nr -
Unigene115123_All	286	0.00	0.00	0.00	0.00	0.00	1.26	0.00	4.09	0.42	null	null		null	null		null	null		1.03E+01	2.37E-02		1.20E+01	2.73E-08	Up	8.71E+00	2.43E-01		Unigene115123_All//gi|224096008|ref|XP_002310518.1|//2.00E-11//cation proton exchanger [Populus trichocarpa] >gi|222853421|gb|EEE90968.1| cation proton exchanger [Populus trichocarpa]	Unigene115123_All//2.00E-11//AT2G13620| ATCHX15; monovalent cation:proton antiporter/ sodium:hydrogen antiporter				GO:0006811//GO:0015078//GO:0015298//GO:0031224	nr -
Unigene115128_All	424	0.00	0.00	0.00	0.00	0.00	0.00	0.20	1.87	0.00	null	null		null	null		null	null		null	null		3.23E+00	5.44E-04	Up	-7.64E+00	3.60E-01		Unigene115128_All//gi|145408590|ref|YP_001152214.1|//9.00E-07//O8F124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| O8F124 [Pinus koraiensis]		Unigene115128_All//1.00E-07//TC134836				nr +
Unigene115129_All	385	0.00	0.00	0.00	0.00	0.00	0.55	3.15	0.00	null	null		null	null		null	null		null	null		2.52E+00	1.15E-04	Up	-9.10E+00	5.81E-02		Unigene115129_All//gi|159138763|gb|ABW89384.1|//6.00E-37//40S ribosomal protein S16 [Helianthus annuus] >gi|159138765|gb|ABW89385.1| 40S ribosomal protein S16 [Helianthus annuus] >gi|159138767|gb|ABW89386.1| 40S ribosomal protein S16 [Helianthus annuus] >gi|159138769|gb|ABW89387.1| 40S ribosomal protein S16 [Helianthus annuus] >gi|159138771|gb|ABW89388.1| 40S ribosomal protein S16 [Helianthus annuus] >gi|159138773|gb|ABW89389.1| 40S ribosomal protein S16 [Helianthus annuus] >gi|159138775|gb|ABW89390.1| 40S ribosomal protein S16 [Helianthus annuus] >gi|159138777|gb|ABW89391.1| 40S ribosomal protein S16 [Helianthus annuus] >gi|159138779|gb|ABW89392.1| 40S ribosomal protein S16 [Helianthus annuus] >gi|159138781|gb|ABW89393.1| 40S ribosomal protein S16 [Helianthus	Unigene115129_All//4.00E-37//AT2G09990| 40S ribosomal protein S16 (RPS16A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene115131_All	263	0.00	0.00	0.00	0.57	0.65	0.52	1.29	7.79	0.76	null	null		null	null		2.04E-01	9.50E-01		-1.41E-01	9.44E-01		2.60E+00	1.19E-07	Up	-7.64E-01	5.01E-01				Unigene115131_All//8.00E-48//TC144723				
Unigene115139_All	1059	0.00	0.38	0.20	0.47	0.49	0.34	1.52	6.59	0.71	8.58E+00	1.36E-02		7.65E+00	1.42E-01		5.24E-02	9.80E-01		-4.63E-01	6.59E-01		2.12E+00	2.36E-19	Up	-1.09E+00	1.58E-02		Unigene115139_All//gi|18404500|ref|NP_566763.1|//1.00E-95//auxin-responsive family protein [Arabidopsis thaliana] >gi|79313415|ref|NP_001030764.1| auxin-responsive family protein [Arabidopsis thaliana] >gi|16323200|gb|AAL15334.1| AT3g25290/MJL12_25 [Arabidopsis thaliana] >gi|25090093|gb|AAN72226.1| At3g25290/MJL12_25 [Arabidopsis thaliana]	Unigene115139_All//2.00E-81//AT3G25290| auxin-responsive family protein	Unigene115139_All//3.00E-81//TC146057			GO:0016020	nr +
Unigene115144_All	449	0.23	0.34	0.00	0.00	0.31	0.00	0.00	9.40	0.53	5.38E-01	7.80E-01		-7.86E+00	3.97E-01		8.26E+00	3.20E-01		null	null		1.32E+01	1.02E-29	Up	9.06E+00	4.40E-02		Unigene115144_All//gi|159138935|gb|ABR89467.1|//6.00E-42//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene115144_All//3.00E-32//AT1G07400| 17.8 kDa class I heat shock protein (HSP17.8-CI)	Unigene115144_All//0.00E+00//DT465134			GO:0044424//GO:0050896	nr -
Unigene115149_All	658	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.48	0.00	null	null		null	null		null	null		null	null		1.13E+01	1.71E-11	Up	null	null			Unigene115149_All//6.00E-05//AT3G18485| ILR2 (IAA-LEUCINE RESISTANT 2)					
Unigene115159_All	246	0.00	0.00	0.00	0.20	0.00	0.37	7.91	2.55	16.03	null	null		null	null		-7.66E+00	5.60E-01		8.59E-01	7.96E-01		-1.63E+00	2.06E-04	Down	1.02E+00	1.64E-04	Up			Unigene115159_All//2.00E-32//ES835202				
Unigene115162_All	371	0.56	0.14	0.57	1.88	0.74	0.00	3.30	2.37	2.15	-2.05E+00	3.34E-01		2.54E-02	1.00E+00		-1.34E+00	1.09E-01		-1.09E-01	1.96E-01	Down	-4.82E-01	4.08E-01		-6.22E-01	2.39E-01				Unigene115162_All//0.00E+00//TC141163				
Unigene115163_All	240	0.00	0.00	0.00	0.62	1.15	0.19	0.18	3.13	0.00	null	null		null	null		8.82E-01	5.95E-01		-1.73E+00	5.02E-01		4.15E+00	1.92E-04	Up	-7.46E+00	6.15E-01								
Unigene115167_All	460	0.23	0.00	0.00	0.32	0.00	0.29	0.18	1.73	0.95	-7.83E+00	3.75E-01		-7.83E+00	3.97E-01		-8.34E+00	1.66E-01		-1.42E-01	9.44E-01		3.23E+00	5.44E-04	Up	2.37E+00	4.05E-02								
Unigene115178_All	469	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.35	0.17	null	null		null	null		null	null		null	null		1.24E+01	1.22E-17	Up	7.41E+00	4.05E-01		Unigene115178_All//sp|P0A902|GST_ECOLI//2.00E-09//Glutathione S-transferase OS=Escherichia coli (strain K12) GN=gst PE=1 SV=1						swissprot +
Unigene11518_All	306	0.17	0.00	0.00	0.49	1.80	3.39	1.24	0.27	0.65	-7.42E+00	6.17E-01		-7.42E+00	6.29E-01		1.88E+00	9.42E-02		2.80E+00	8.13E-04	Up	-2.19E+00	8.76E-02		-9.34E-01	3.80E-01		Unigene11518_All//gi|115452841|ref|NP_001050021.1|//6.00E-19//0s03g0333100 [Oryza sativa Japonica Group] >gi|113548492|dbj|BAF11935.1| Os03g0333100 [Oryza sativa Japonica Group]	Unigene11518_All//8.00E-16//AT1G06720| INVOLVED IN: ribosome biogenesis; LOCATED IN: nucleus; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: AARP2CN (InterPro:IPR012948), Protein of unknown function DUF663 (InterPro:IPR007034); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G42440.1); Has 7944 Blast hits to 5342 proteins in 373 species: Archae - 33; Bacteria - 667; Metazoa - 2609; Fungi - 1045; Plants - 414; Viruses - 80; Other Eukaryotes - 3096 (source: NCBI BLink).	Unigene11518_All//4.00E-136//gi|109853645|gb|DW482624.1|DW482624			GO:0017111//GO:0032555	nr +
Unigene115181_All	247	0.21	0.41	0.22	0.00	1.39	0.73	0.00	2.54	2.10	9.54E-01	7.27E-01		2.57E-02	9.96E-01		1.04E+01	3.02E-02		9.51E+00	1.95E-01		1.13E+01	1.47E-04	Up	1.10E+01	6.14E-04	Up	Unigene115181_All//gi|59668640|emb|CAI53674.1|//3.00E-22//glutamate dehydrogenase 2 [Glycine max]	Unigene115181_All//4.00E-23//AT5G07440| GDH2 (GLUTAMATE DEHYDROGENASE 2); ATP binding / glutamate dehydrogenase [NAD(P)+]/ glutamate dehydrogenase/ oxidoreductase	Unigene115181_All//2.00E-79//gi|164272922|gb|EV489392.1|EV489392		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006519//GO:0006970//GO:0010038//GO:0016020//GO:0016639//GO:0019222//GO:0032559//GO:0043231//GO:0046914	nr +
Unigene115182_All	447	0.00	1.25	0.00	0.00	0.46	0.20	0.09	2.71	2.50	1.03E+01	2.19E-03		null	null		8.85E+00	1.57E-01		7.66E+00	4.80E-01		4.84E+00	2.06E-07	Up	4.72E+00	6.01E-07	Up			Unigene115182_All//5.00E-143//TC173956				
Unigene115185_All	573	0.00	0.00	0.00	0.00	0.00	0.00	1.18	0.95	0.00	null	null		null	null		null	null		null	null		-3.16E-01	6.74E-01		-1.02E+01	3.56E-05	Down	Unigene115185_All//gi|29539332|dbj|BAC67667.1|//4.00E-85//elongation factor-1alpha [Cyanidioschyzon merolae]	Unigene115185_All//3.00E-80//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene115185_All//4.00E-70//TC166357			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene115189_All	795	0.13	0.70	0.40	0.75	0.48	0.74	0.27	0.26	1.35	2.41E+00	3.93E-02		1.61E+00	3.05E-01		-6.58E-01	4.78E-01		-2.59E-02	9.64E-01		-1.64E-02	1.02E+00		2.35E+00	4.46E-04	Up	Unigene115189_All//gi|15229025|ref|NP_190449.1|//6.00E-36//sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	Unigene115189_All//1.00E-32//AT3G48800| sterile alpha motif (SAM) domain-containing protein	Unigene115189_All//0.00E+00//TC156752				nr -
Unigene11519_All	1229	2.60	0.70	1.43	6.44	4.48	5.73	5.95	2.72	4.89	-1.89E+00	1.03E-06	Down	-8.61E-01	1.81E-02		-5.24E-01	7.58E-03		-1.69E-01	4.78E-01		-1.13E+00	1.30E-08	Down	-2.82E-01	1.50E-01		Unigene11519_All//gi|7523707|gb|AAF63146.1|AC011001_16//1.00E-125//Putative membrane protein [Arabidopsis thaliana]	Unigene11519_All//9.00E-98//AT1G06720| INVOLVED IN: ribosome biogenesis; LOCATED IN: nucleus; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: AARP2CN (InterPro:IPR012948), Protein of unknown function DUF663 (InterPro:IPR007034); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G42440.1); Has 7944 Blast hits to 5342 proteins in 373 species: Archae - 33; Bacteria - 667; Metazoa - 2609; Fungi - 1045; Plants - 414; Viruses - 80; Other Eukaryotes - 3096 (source: NCBI BLink).	Unigene11519_All//4.00E-90//TC137970		ko04120|Ubiquitin mediated proteolysis		nr +

Unigene115191_All	455	0.00	0.56	0.00	0.00	0.00	0.00	0.28	2.20	0.18	9.12E+00	7.88E-02		null	null		null	null		null	null		2.98E+00	1.37E-04	Up	-6.71E-01	7.20E-01								
Unigene115193_All	263	0.00	0.00	0.00	0.00	0.00	0.00	1.93	2.86	0.00	null	null		null	null		null	null		null	null		5.68E-01	4.47E-01		-1.09E+01	5.54E-01	Down								
Unigene115194_All	397	0.00	0.00	0.00	0.00	0.00	0.00	1.28	4.74	1.81	null	null		null	null		null	null		null	null		1.89E+00	4.67E-05	Up	4.99E-01	5.01E-01								
Unigene115200_All	612	0.00	0.00	0.00	0.00	0.11	0.00	2.00	4.71	1.95	null	null		null	null		6.81E+00	6.13E-01		null	null		1.23E+00	2.50E-04	Up	-3.69E-02	9.60E-01		Unigene115200_All//gi|147765928|emb|CAN68977.1|//3.00E-07//hypothetical protein [Vitis vinifera]		Unigene115200_All//2.00E-07//FL576891				nr -
Unigene115204_All	508	0.00	0.00	0.00	0.00	0.00	0.00	0.58	2.72	2.12	null	null		null	null		null	null		null	null		2.22E+00	1.31E-04	Up	1.86E+00	2.85E-03								
Unigene115206_All	324	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.48	1.11	null	null		null	null		null	null		null	null		1.18E+01	5.32E-08	Up	1.01E+01	7.30E-03		Unigene115206_All//gi|30013669|gb|AAP03873.1|//5.00E-16//Avr9/Cf-9 rapidly elicited protein 141 [Nicotiana tabacum]	Unigene115206_All//8.00E-14//AT1G42540| ATGLR3.3; intracellular ligand-gated ion channel				GO:0004872//GO:0005215//GO:0031410//GO:0043231	nr -
Unigene115208_All	224	0.00	0.00	0.00	0.00	0.00	0.00	37.56	8.96	11.38	null	null		null	null		null	null		null	null		-2.07E+00	1.50E-22	Down	-1.72E+00	2.22E-18	Down	Unigene115208_All//gi|57867865|gb|AAW57312.1|//2.00E-29//alpha-tubulin [Ceratopteris richardii]	Unigene115208_All//3.00E-17//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene115208_All//1.00E-36//ES845326		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene115209_All	296	1.06	3.59	0.00	0.34	0.23	1.07	0.86	10.59	2.96	1.76E+00	1.43E-02		-1.01E+01	4.93E-02		-5.33E-01	8.18E-01		1.67E+00	3.09E-01		3.63E+00	2.13E-15	Up	1.79E+00	1.04E-02		Unigene115209_All//gi|89276799|gb|ABD66598.1|//6.00E-06//iron-binding protein [Pyrus pyrifolia]	Unigene115209_All//9.00E-07//AT3G11050| ATFER2 (ferritin 2); binding / ferric iron binding / oxidoreductase/ transition metal ion binding	Unigene115209_All//7.00E-33//gi|8381944|gb|BE054899.1|BE054899			GO:0046914	nr +
Unigene115212_All	284	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.65	0.00	null	null		null	null		null	null		null	null		1.14E+01	2.07E-05	Up	null	null								
Unigene115214_All	319	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.67	0.00	null	null		null	null		null	null		null	null		1.18E+01	2.73E-08	Up	null	null		Unigene115214_All//gi|300269136|gb|EFJ53316.1|//9.00E-07//hypothetical protein VOLCADRAFT_86475 [Volvox carteri f. nagariensis]					GO:0005488//GO:0017111	nr +
Unigene115217_All	352	0.00	0.00	0.00	0.00	0.00	0.00	1.44	2.02	0.00	null	null		null	null		null	null		null	null		4.86E-01	5.42E-01		-1.05E+01	5.54E-04	Down								ESTscan -
Unigene115222_All	1021	2.66	0.60	2.87	3.17	1.69	1.33	0.91	0.74	0.55	-2.16E+00	8.60E-07	Down	1.06E-01	7.77E-01		-9.11E-01	4.87E-03		-1.26E+00	2.89E-04	Down	-3.06E-01	6.21E-01		-7.38E-01	2.33E-01		Unigene115222_All//gi|240254315|ref|NP_001117543.1|//1.00E-107//peptidase M1 family protein [Arabidopsis thaliana]	Unigene115222_All//1.00E-107//AT1G63770| peptidase M1 family protein	Unigene115222_All//3.00E-106//gi|48812159|gb|CO113472.1|CO113472		ko00480|Glutathione metabolism	GO:0005576//GO:0009526//GO:0009532//GO:0010038//GO:0016020//GO:0070011	nr +
Unigene115233_All	327	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.05	0.00	null	null		null	null		null	null		null	null		1.10E+01	7.64E-05	Up	null	null		Unigene115233_All//sp|P73623|Y1773_SYNY3/2.00E-08//Pirin-like protein sll1773 OS=Synechocystis sp. (strain PCC 6803) GN=sll1773 PE=3 SV=1						swissprot -
Unigene115242_All	617	0.00	0.00	0.00	0.00	0.00	0.00	0.14	2.10	0.26	null	null		null	null		null	null		null	null		3.94E+00	4.68E-07	Up	9.14E-01	6.25E-01		Unigene115242_All//gi|2773251|gb|AAC15417.1|//2.00E-14//early nodulin [Mesckia amurensis]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene115243_All	541	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.71	0.00	null	null		null	null		null	null		null	null		1.19E+01	4.04E-14	Up	null	null		Unigene115243_All//gi|159487004|ref|XP_001701526.1|//3.00E-10//glyoxal or galactose oxidase [Chlamydomonas reinhardtii]>gi|158271587|gb|EDO97403.1| glyoxal or galactose oxidase [Chlamydomonas reinhardtii]					GO:0003824//GO:0005488	nr -
Unigene115254_All	610	0.09	0.50	0.09	0.16	0.11	0.00	0.14	2.60	0.59	2.54E+00	1.51E-01		2.50E-02	9.96E-01		-5.33E-01	8.18E-01		-7.35E+00	4.03E-01		4.23E+00	6.26E-09	Up	2.08E+00	1.01E-01		Unigene115254_All//gi|42566766|ref|NP_193135.2|//7.00E-48//exostosin family protein [Arabidopsis thaliana]	Unigene115254_All//4.00E-48//AT4G13990| exostosin family protein				GO:0016740//GO:0030312//GO:0031410	nr -
Unigene115259_All	680	0.00	0.00	0.00	0.00	0.00	0.07	0.37	2.03	1.23	null	null		null	null		null	null		6.05E+00	7.00E-01		2.44E+00	4.59E-05	Up	1.72E+00	1.56E-02		Unigene115259_All//gi|288310302|gb|ADC45390.1|//1.00E-45//branched chain amino acid transaminase [Cucumis melo]	Unigene115259_All//7.00E-42//AT3G49680| BCAT3 (BRANCHED-CHAIN AMINOTRANSFERASE 3); branched-chain-amino-acid transaminase/ catalytic	Unigene115259_All//3.00E-65//C0076800		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00970|Pantothenate and CoA biosynthesis	GO:0008152//GO:0008483//GO:0009536	nr -
Unigene115526_All	671	1.87	4.98	6.51	9.80	7.54	10.63	3.28	1.93	2.91	1.41E+00	6.99E-05	Up	1.80E+00	5.51E-08	Up	-3.77E-01	1.02E-01		1.18E-01	6.49E-01		-7.63E-01	4.86E-02		-1.72E-01	6.47E-01		Unigene115526_All//gi|124359654|gb|ABN06026.1|//4.00E-49//Peptidase, trypsin-like serine and cysteine proteases [Medicago truncatula]	Unigene115526_All//6.00E-41//AT5G45030| catalytic	Unigene115526_All//5.00E-153//TC159414			GO:0016787	nr -
Unigene115267_All	495	1.27	19.35	1.83	1.11	1.53	1.19	0.94	6.67	6.84	3.93E+00	8.66E-40	Up	5.28E-01	4.79E-01		4.67E-01	6.07E-01		9.96E-02	9.36E-01		2.83E+00	5.32E-13	Up	2.86E+00	8.82E-14	Up	Unigene115267_All//gi|297801100|ref|XP_002869939.1|//4.00E-12//CTP synthase [Arabidopsis lyrata subsp. lyrata]>gi|297315775|gb|EFH46198.1| CTP synthase [Arabidopsis lyrata subsp. lyrata]	Unigene115267_All//3.00E-12//AT4G20320| CTP synthase/ catalytic	Unigene115267_All//6.00E-81//DN817495		ko00240|Pyrimidine metabolism		nr +
Unigene115270_All	269	0.39	0.00	0.40	0.00	0.00	0.17	1.26	9.79	1.93	-8.60E+00	3.75E-01		2.54E-02	1.00E+00		null	null		7.39E+00	7.00E-01		2.96E+00	5.81E-11	Up	6.15E-01	4.94E-01					Unigene115270_All//6.00E-21//BF268625					
Unigene115271_All	432	0.00	0.00	0.00	0.00	0.00	0.00	2.25	1.16	0.09	null	null		null	null		null	null		null	null		-9.53E-01	1.35E-01		-4.61E+00	3.32E-06	Down								
Unigene115274_All	293	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.85	0.00	null	null		null	null		null	null		null	null		1.09E+01	5.37E-04	Up	null	null		Unigene115274_All//gi|116059710|emb|CAL55417.1|//1.00E-13//Pirin (ISS) [Ostreococcus tauri]	Unigene115274_All//3.00E-13//AT3G59260| pirin, putative				GO:0005515//GO:0016020	nr +
Unigene115275_All	702	0.00	0.00	0.00	0.00	0.00	0.00	1.26	2.20	0.11	null	null		null	null		null	null		null	null		8.01E-01	9.44E-02		-3.48E+00	7.34E-05	Down	Unigene115275_All//gi|57999636|dbj|BAD88438.1|//5.00E-31//60S ribosomal protein L6 CgRPL6 [Chara globularis]	Unigene115275_All//3.00E-17//AT1G74060| 60S ribosomal protein L6 (RPL6B)			ko03010|Ribosome	GO:0005488//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene115279_All	203	1.29	7.49	1.57	1.72	2.04	2.22	2.50	3.29	2.55	2.54E+00	9.21E-05	Up	2.88E-01	8.10E-01		2.45E-01	8.53E-01		3.73E-01	7.32E-01		3.98E-01	6.48E-01		2.97E-02	9.70E-01					Unigene115279_All//2.00E-07//TC168767					
Unigene115281_All	432	0.00	0.00	0.00	0.00	0.00	0.00	1.27	1.26	0.00	null	null		null	null		null	null		null	null		-1.67E-02	1.02E+00		-1.03E+01	2.81E-04	Down	Unigene115281_All//gi|226453529|gb|EEH50840.1|//3.00E-06//predicted protein [Micromonas pusilla CCMP1545]		Unigene115281_All//8.00E-12//ES794483				nr -
Unigene115283_All	580	1.08	0.00	0.46	0.17	0.12	0.31	0.87	4.68	0.89	-1.01E+01	7.92E-04	Down	-1.24E+00	2.13E-01		-5.33E-01	8.18E-01		8.59E-01	6.96E-01		2.42E+00	3.13E-09	Up	2.95E-02	9.70E-01									
Unigene115285_All	283	11.65	28.83	19.95	21.65	27.01	17.40	148.35	161.72	159.35	1.31E+00	1.16E-09	Up	7.76E-01	2.88E-03		3.19E-01	1.53E-01		-3.16E-01	2.24E-01		1.24E-01	1.12E-01		1.03E-01	1.84E-01					Unigene115285_All//2.00E-67//DW505711					
Unigene115289_All	276	14.03	54.89	49.01	14.08	15.72	21.11	6.74	11.36	29.73	1.97E+00	1.47E-30	Up	1.80E+00	1.19E-23	Up	1.59E-01	6.29E-01		5.84E-01	1.82E-02		7.53E-01	1.64E-02		2.14E+00	2.04E-23	Up				Unigene115289_All//2.00E-82//gi|48827491|gb|CO123881.1|CO123881					
Unigene115298_All	214	0.00	0.00	0.00	0.00	0.00	0.00	28.06	18.36	11.36	null	null		null	null		null	null		null	null		-6.12E-01	4.48E-03		-1.30E+00	3.72E-09	Down	Unigene115298_All//gi|255641066|gb|ACU20812.1|//3.00E-07//unknown [Glycine max]	Unigene115298_All//5.00E-05//AT5G06730| peroxidase, putative	Unigene115298_All//4.00E-40//TC166012				nr +
Unigene115302_All	685	0.00	0.00	0.00	0.00	0.00	0.00	0.86	2.93	0.23	null	null		null	null		null	null		null	null		1.76E+00	6.27E-05	Up	-1.89E+00	3.22E-02		Unigene115302_All//gi|224124808|ref|XP_002319427.1|//6.00E-80//cytochrome P450 [Populus trichocarpa]>gi|222857803|gb|EEE95350.1| cytochrome P450 [Populus trichocarpa]	Unigene115302_All//2.00E-75//AT4G39950| CYP79B2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00380|Tryptophan metabolism//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis	GO:0002239//GO:0005506//GO:0006568//GO:0009536//GO:0009683//GO:0009700//GO:0016491//GO:0031224//GO:0052482	nr -
Unigene115305_All	626	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.54	0.00	null	null		null	null		null	null		null	null		1.21E+01	5.42E-20	Up	null	null		Unigene115305_All//gi|301100736|ref|XP_002899457.1|//1.00E-48//flavodoxin-like protein [Phytophthora infestans T30-4]>gi|262103765|gb|EEY61817.1| flavodoxin-like protein [Phytophthora infestans T30-4]	Unigene115305_All//9.00E-42//AT4G27270| quinone reductase family protein					nr +
Unigene115312_All	252	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.65	0.00	null	null		null	null		null	null		null	null		1.14E+01	7.64E-05	Up	null	null									ESTscan +
Unigene115313_All	364	0.00	0.00	0.00	0.00	0.00	0.00	1.86	4.48	0.00	null	null		null	null		null	null		null	null		1.27E+00	7.03E-03		-1.09E+01	3.56E-05	Down	Unigene115313_All//gi|33590374|gb|AAQ22726.1|//4.00E-17//40S ribosomal protein S25 [Glycine max]	Unigene115313_All//2.00E-19//AT4G34555| 40S ribosomal protein S25, putative			ko03010|Ribosome	GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0031981	nr -
Unigene115317_All	492	0.00	0.00	0.00	0.61	0.14	0.00	9.71	5.27	0.40	null	null		null	null		-2.12E+00	1.66E-01		-9.25E+00	4.00E-02		-8.83E-01	3.32E-04		-4.58E+00	2.33E-28	Down	Unigene115317_All//gi|11994591|dbj|BAB02646.1|//9.00E-16//Ac transposase-like protein [Arabidopsis thaliana]		Unigene115317_All//2.00E-84//TC156042			GO:0003676	nr +
Unigene115318_All	241	0.00	0.00	0.00	0.00	0.14	0.00	2.11	0.35	0.00	null	null		null	null		7.16E+00	8.35E-01		null	null		-2.60E+00	2.05E-02		-1.10E+01	5.54E-04	Down								
Unigene115319_All	461	0.00	0.00	0.00	0.00	0.00	0.00	4.31	10.34	0.26	null	null		null	null		null	null		null	null		1.26E+00	7.63E-07	Up	-4.06E+00	3.04E-11	Down	Unigene115319_All//gi|238014838|gb|ACR38454.1|//8.00E-15//unknown [Zea mays]		Unigene115319_All//2.00E-16//TC152959				nr +
Unigene11532_All	1972	13.48	28.83	20.68	20.21	23.75	27.73	13.29	14.18	9.74	1.10E+00	7.67E-48	Up	6.18E-01	6.58E-13		2.33E-01	2.08E-03		4.57E-01	3.48E-11		9.31E-02	3.95E-01		-4.49E-01	1.18E-06		Unigene11532_All//gi|18409750|ref|NP_566977.1|//0.00E+00//SRPK4 (Ser/Arg-rich protein kinase 4); kinase/ protein kinase [Arabidopsis thaliana]	Unigene11532_All//0.00E+00//AT3G53030| SRPK4 (Ser/Arg-rich protein kinase 4); kinase/ protein kinase	Unigene11532_All//0.00E+00//gi|78336218|gb|DT556492.1|DT556492			GO:0004672//GO:0006464//GO:0006950//GO:0032559	nr +
Unigene115327_All	378	118.34	30.96	43.11	203.34	162.06	196.42	32.55	21.56	25.08	-1.93E+00	1.25E-87	Down	-1.46E+00	1.04E-56	Down	-3.27E-01	1.64E-09		-4.99E-02	5.12E-01		-5.94E-01	3.37E-05		-3.76E-01	7.76E-03		Unigene115327_All//gi|297842159|ref|XP_002888961.1|//1.00E-47//60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata]>gi|297334802|gb|EFH65220.1| 60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata]	Unigene115327_All//6.00E-40//AT1G74050| 60S ribosomal protein L6 (RPL6C)	Unigene115327_All//0.00E+00//gi|13247383|gb|BF270238.2|BF270238		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene115333_All	371	309.98	101.61	174.25	475.18	407.28	465.15	362.52	156.26	243.86	-1.61E+00	1.02E-173	Down	-8.31E-01	6.19E-59		-2.22E-01	2.26E-10		-3.08E-02	5.50E-01		-1.21E+00	4.61E-162	Down	-5.72E-01	1.03E-46		Unigene115333_All//gi|52783264|sp|Q9FUL4.1|RL24_PRUAV//2.00E-46//RecName: Full=60S ribosomal protein L24 >gi|10180025|gb|AAG13986.1|AF29882 7_1 60S ribosomal protein L24 [Prunus avium]	Unigene115333_All//6.00E-44//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome	Unigene115333_All//1.00E-179//gi|109866646|gb|DW495622.1|DW495622		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene115334_All	609	0.00	0.00	0.00	0.33	0.00	0.00	0.42	2.13	2.09	null	null		null	null		-8.35E+00	8.46E-02		-8.35E+00	1.34E-01		2.35E+00	1.25E-04	Up	2.33E+00	1.17E-04	Up	Unigene115334_All//gi|297849980|ref|XP_002892871.1|//3.00E-71//ATPDR12/PDR12 [Arabidopsis lyrata subsp. lyrata]>gi|297338713|gb|EFH69130.1| ATPDR12/PDR12 [Arabidopsis lyrata subsp. lyrata]	Unigene115334_All//1.00E-70//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene115334_All//0.00E+00//DT465573		ko03040|Spliceosome//ko02010|ABC transporters	GO:0009725//GO:0015893//GO:0016020//GO:0002891//GO:0030001//GO:0032559//GO:0042626//GO:0046864	nr -
Unigene115339_All	527	0.00	0.00	0.00	0.00	0.00	0.00	34.66	14.91	16.03	null	null		null	null		null	null		null	null		-1.22E+00	9.33E-23	Down	-1.11E+00	1.88E-20	Down				Unigene115339_All//1.00E-14//TC142576					
Unigene11534_All	2017	1.69	3.04	1.56	2.17	3.11	2.71	0.69	1.91	1.17	8.50E-01	3.94E-04		-1.14E-01	7.40E-01		5.16E-01	2.69E-02		3.18E-01	2.53E-01		1.46E+00	6.71E-07	Up	7.53E-01	3.61E-02		Unigene11534_All//gi|18409750|ref|NP_566977.1|//0.00E+00//SRPK4 (Ser/Arg-rich protein kinase 4); kinase/ protein kinase [Arabidopsis thaliana]	Unigene11534_All//0.00E+00//AT3G53030| SRPK4 (Ser/Arg-rich protein kinase 4); kinase/ protein kinase	Unigene11534_All//0.00E+00//TC175776			GO:0004672//GO:0006464//GO:0006950//GO:0032559	nr +
Unigene115350_All	343	0.00	0.00	0.00	0.00	0.00	0.00	0.62	5.00	1.28	null	null		null	null		null	null		null	null		3.02E+00	1.78E-07	Up	1.05E+00	2.98E-01		Unigene115350_All//gi|126566038|gb|ABR02848.1|//1.00E-20//cytochrome P450-like TBP protein [Lilium longiflorum]		Unigene115350_All//2.00E-36//gi|84158108|gb|DN827155.1|DN827155				nr +
Unigene115366_All	422	0.12	0.00	0.00	0.35	0.08	0.21	0.20	1.78	0.19	-6.95E+00	6.16E-01		-6.95E+00	6.29E-01		-2.12E+00	3.87E-01		-7.27E-01	7.16E-01		3.15E+00	9.54E-04	Up	-8.60E-02	9.73E-01									
Unigene115369_All	317	0.00	0.00	0.00	0.00	0.11	0.00	4.93	18.72	5.91	null	null		null	null		6.76E+00	8.35E-01		null	null		1.92E+00	1.07E-14	Up	2.59E-01	5.61E-01		Unigene115369_All//gi|75311691|sp|Q9LY51.1|PLCD7_ARATH//1.00E-09//RecName: Full=Phosphoinositide phospholipase C 7; AltName: Full=Phosphoinositide phospholipase PLC7; Short=PI-PLC7; Short=AtPLC7; Short=AtPLC10 >gi|7573489|emb|CAB57848.1| phosphoinositide-specific phospholipase C-like protein [Arabidopsis thaliana]	Unigene115369_All//6.00E-11//AT3G55940| phosphoinositide-specific phospholipase C, putative	Unigene115369_All//2.00E-24//TC146670		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene115379_All	589	0.36	0.52	1.18	0.76	0.29	0.31	0.36	6.24	0.95	5.39E-01	6.72E-01		1.73E+00	7.68E-02		-1.38E+00	2.16E-01		-1.31E+00	2.73E-01		4.12E+00	1.01E-19	Up	1.40E+00	1.12E-01		Unigene115379_All//gi|18652398|gb|AAL77102.1|AF472608_1//5.00E-54//carbohydrate oxidase [Lactuca sativa]	Unigene115379_All//8.00E-38//AT4G20800| FAD-binding domain-containing protein				GO:0016491	nr -

Unigene115394_All	403	0.00	0.00	0.00	0.12	0.34	0.67	0.73	3.11	0.20	null	null		null	null		1.47E+00	6.19E-01		2.44E+00	2.22E-01		2.08E+00	5.41E-04	Up	-1.89E+00	1.68E-01		Unigene115394_All//gi|15230158|ref|NP_188497.1|//9.00E-10//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene115394_All//5.00E-11//AT5G04730| unknown protein	Unigene115394_All//6.00E-25//TC178375				nr +
Unigene115397_All	260	0.00	0.00	0.00	0.00	0.00	0.00	11.55	3.54	0.61	null	null		null	null		null	null		null	null		-1.71E+00	9.31E-07	Down	-4.24E+00	3.58E-17	Down			Unigene115397_All//3.00E-10//TC146753				
Unigene115408_All	327	0.00	0.00	0.00	0.00	0.00	0.00	0.52	5.50	0.12	null	null		null	null		null	null		null	null		3.41E+00	1.21E-08	Up	-2.09E+00	3.14E-01									ESTscan +
Unigene115409_All	316	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.72	0.00	null	null		null	null		null	null		null	null		1.07E+01	5.37E-04	Up	null	null		Unigene115409_All//gi|220966698|gb|ACL97363.1|//3.00E-38//elongation factor-1 alpha [Ignatius tetrasporus]	Unigene115409_All//2.00E-36//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene115409_All//6.00E-49//CD809343			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene115417_All	441	0.00	0.00	0.00	0.00	0.00	0.00	1.05	4.55	0.00	null	null		null	null		null	null		null	null		2.11E+00	4.88E-06	Up	-1.00E+01	1.09E-03		Unigene115417_All//gi|1527001|gb|AB07724.1|//1.00E-20//Pn47p [Ipomoea nil]	Unigene115417_All//1.00E-20//AT4G18550| lipase class 3 family protein					nr +
Unigene115418_All	679	0.00	0.00	0.00	0.00	0.00	0.00	1.87	4.74	0.00	null	null		null	null		null	null		null	null		1.34E+00	2.74E-05	Up	-1.09E+01	1.99E-09	Down	Unigene115418_All//gi|116056034|emb|CAL58567.1|//3.00E-28//Nucleolar GTPase/ATPase p130 (ISS) [Ostreococcus tauri]						nr -
Unigene115542_All	5013	1.80	0.87	1.53	17.34	16.44	13.53	11.69	11.35	12.52	-1.05E+00	1.07E-07	Down	-2.31E-01	2.82E-01		-7.71E-02	2.33E-01		-3.58E-01	2.44E-11		-4.29E-02	6.08E-01		9.86E-02	1.24E-01		Unigene115542_All//gi|28268680|dbj|BAC56865.1|//0.00E+00//respiratory burst oxidase homolog [Nicotiana benthamiana]	Unigene115542_All//0.00E+00//AT5G51060| RHD2 (ROOT HAIR DEFECTIVE 2); NAD(P)H oxidase	Unigene115542_All//0.00E+00//gi|164283610|gb|ES818781.1|ES818781		ko04626|Plant-pathogen interaction	GO:0006950//GO:0008152//GO:0009913//GO:0010033//GO:0016021//GO:0016209//GO:0030554//GO:0046914//GO:0050664	nr -
Unigene115422_All	280	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.84	0.28	null	null		null	null		null	null		null	null		1.15E+01	1.07E-05	Up	8.15E+00	4.05E-01									ESTscan +
Unigene115423_All	352	0.00	0.00	0.00	0.00	0.00	0.00	3.48	14.60	0.00	null	null		null	null		null	null		null	null		2.07E+00	5.06E-14	Up	-1.18E+01	4.03E-09	Down								
Unigene115426_All	236	2.44	4.08	1.13	2.32	2.48	3.25	3.76	9.74	7.93	7.42E-01	2.94E-01		-1.11E+00	2.79E-01		9.54E-02	9.51E-01		4.87E-01	5.91E-01		1.37E+00	4.17E-04	Up	1.08E+00	9.46E-03				Unigene115426_All//1.00E-30//TC179380					
Unigene115442_All	326	20.06	86.57	76.44	60.05	52.81	63.73	29.96	39.23	21.87	2.11E+00	1.15E-61	Up	1.93E+00	2.64E-47	Up	-1.85E-01	1.65E-01		8.57E-02	5.81E-01		3.89E-01	6.35E-03		-4.54E-01	4.40E-03		Unigene115442_All//gi|224133362|ref|XP_002326841.1|//1.00E-06//predicted protein [Populus trichocarpa] >gi|118485601|gb|ABK94365.1| unknown [Populus trichocarpa] >gi|222835156|gb|EEE73591.1| predicted protein [Populus trichocarpa]		Unigene115442_All//5.00E-145//gi|164240695|gb|ES802406.1|ES802406				nr -
Unigene115448_All	343	1.98	5.91	3.73	2.47	3.41	2.37	2.84	8.65	4.65	1.58E+00	1.08E-03		9.10E-01	1.46E-01		4.67E-01	5.14E-01		-5.89E-02	9.44E-01		1.61E+00	3.33E-06	Up	7.13E-01	1.15E-01		Unigene115448_All//gi|297808579|ref|XP_002872173.1|//5.00E-15//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318010|gb|EFH48432.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene115448_All//7.00E-16//AT5G25560| zinc finger (C3HC4-type RING finger) family protein	Unigene115448_All//1.00E-41//EX167266		ko04120|Ubiquitin mediated proteolysis	GO:0046914	nr -
Unigene115545_All	2699	1.22	0.62	0.45	1.46	1.57	1.82	2.33	2.06	2.61	-9.79E-01	4.27E-03		-1.43E+00	1.22E-04	Down	1.06E-01	7.90E-01		3.23E-01	2.79E-01		-1.81E-01	4.45E-01		1.63E-01	4.47E-01		Unigene115545_All//gi|268044007|gb|ACY92092.1|//0.00E+00//HOS1 [Citrus trifoliata]	Unigene115545_All//1.00E-178//AT2G39810| HOS1; ubiquitin-protein ligase	Unigene115545_All//0.00E+00//CO096048			GO:0006350//GO:0006950//GO:0019787//GO:0032446//GO:0043231	nr -
Unigene115453_All	208	0.00	0.00	0.00	0.00	0.00	0.00	3.66	1.41	0.19	null	null		null	null		null	null		null	null		-1.38E+00	6.73E-02		-4.26E+00	8.65E-05	Down								
Unigene115455_All	526	0.00	0.00	0.00	1.04	0.39	0.09	0.64	13.75	1.51	null	null		null	null		-1.41E+00	1.53E-01		-3.60E+00	8.98E-03		4.42E+00	4.15E-40	Up	1.24E+00	7.69E-02		Unigene115455_All//gi|297242517|gb|ADI24922.1|//8.00E-06//pirin [Carica papaya]	Unigene115455_All//7.00E-07//AT1G56590| pirin, putative	Unigene115455_All//3.00E-18//DW507929				nr -
Unigene115456_All	1145	0.00	0.00	0.00	0.00	0.00	0.00	0.11	2.92	0.07	null	null		null	null		null	null		null	null		4.72E+00	1.69E-19	Up	-6.71E-01	7.20E-01		Unigene115456_All//gi|226495425|ref|NP_001148706.1|//6.00E-67//cysteine protease 1 [Zea mays] >gi|195621544|gb|ACG32602.1| cysteine protease 1 precursor [Zea mays]	Unigene115456_All//3.00E-64//AT5G43060| cysteine proteinase, putative / thiol protease, putative				GO:0016787	nr -
Unigene115457_All	713	0.00	0.00	0.00	0.00	0.00	0.00	1.25	3.11	0.00	null	null		null	null		null	null		null	null		1.32E+00	8.45E-04	Up	-1.03E+01	1.10E-06	Down								ESTscan -
Unigene115458_All	599	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.19	0.00	null	null		null	null		null	null		null	null		1.20E+01	1.22E-17	Up	null	null		Unigene115458_All//gi|226508392|ref|NP_001151699.1|//3.00E-07//LOC100285335 [Zea mays] >gi|195649099|gb|ACG44017.1| ABA induced plasma membrane protein PM19 [Zea mays]	Unigene115458_All//1.00E-06//AT5G18970| AMPM-19-like membrane family protein					nr -
Unigene115460_All	636	1.07	0.00	0.67	0.94	1.14	2.41	1.40	1.05	0.13	-1.01E+01	4.10E-04	Down	-6.75E-01	4.41E-01		2.75E-01	8.01E-01		1.36E+00	1.43E-02		-4.09E-01	5.62E-01		-3.48E+00	7.34E-05	Down	Unigene115460_All//gi|18401257|ref|NP_566559.1|//3.00E-20//APUM24 (Arabidopsis Pumilio 24); RNA binding / binding [Arabidopsis thaliana] >gi|15010674|gb|AAK73996.1| AT3g16810/K20I9_3 [Arabidopsis thaliana]	Unigene115460_All//2.00E-21//AT3G16810| APUM24 (Arabidopsis Pumilio 24); RNA binding / binding	Unigene115460_All//2.00E-170//CO097303			GO:0031981	nr +
Unigene115547_All	1120	2.85	0.54	1.47	2.36	1.72	2.74	2.45	1.79	1.92	-2.39E+00	9.11E-09	Down	-9.51E-01	9.11E-03		-4.53E-01	2.52E-01		2.18E-01	6.14E-01		-4.54E-01	1.98E-01		-3.53E-01	3.02E-01		Unigene115547_All//gi|15218495|ref|NP_177391.1|//9.00E-90//ATEXO70D1 (exocyst subunit EXO70 family protein D1); protein binding [Arabidopsis thaliana]	Unigene115547_All//3.00E-70//AT1G72470| ATEXO70D1 (exocyst subunit EXO70 family protein D1); protein binding	Unigene115547_All//0.00E+00//ES830101			GO:0016192//GO:0043231//GO:0043234//GO:0044444	nr -
Unigene115471_All	374	0.00	0.00	0.00	0.00	0.00	0.00	1.70	6.26	1.28	null	null		null	null		null	null		null	null		1.88E+00	4.35E-06	Up	-4.08E-01	6.19E-01				Unigene115471_All//2.00E-15//TC152786				
Unigene115474_All	278	0.00	0.00	0.00	0.00	0.00	0.00	2.28	2.10	0.14	null	null		null	null		null	null		null	null		-1.16E-01	8.88E-01		-3.99E+00	5.82E-04	Down			Unigene115474_All//1.00E-15//TC114001				
Unigene115477_All	254	0.00	0.00	0.00	0.00	0.14	0.00	46.94	33.07	103.83	null	null		null	null		7.08E+00	8.35E-01		null	null		-5.05E-01	5.48E-04		1.15E+00	3.07E-30	Up	Unigene115477_All//gi|147791048|emb|CAN65763.1|//1.00E-06//hypothetical protein [Vitis vinifera]		Unigene115477_All//3.00E-47//gi|73862963|gb|DT465702.1|DT465702				nr -
Unigene115479_All	414	0.00	0.00	0.00	0.24	0.17	0.00	0.10	1.41	2.79	null	null		null	null		-5.32E-01	8.18E-01		-7.91E+00	4.03E-01		3.79E+00	2.07E-03		4.77E+00	3.27E-07	Up								
Unigene115496_All	599	0.00	0.00	0.00	0.00	0.00	0.00	0.35	2.02	0.60	null	null		null	null		null	null		null	null		2.52E+00	1.15E-04	Up	7.62E-01	5.00E-01		Unigene115496_All//gi|115474815|ref|NP_001061004.1|//9.00E-29//Os08g0152500 [Oryza sativa Japonica Group] >gi|113622973|dbj|BAF22918.1| Os08g0152500 [Oryza sativa Japonica Group]	Unigene115496_All//1.00E-43//AT2G39170| unknown protein	Unigene115496_All//8.00E-19//TC170512				nr +
Unigene1155_All	734	0.29	0.00	0.15	0.61	1.13	1.78	4.38	1.08	2.66	-8.16E+00	1.22E-01		-9.74E-01	6.21E-01		8.82E-01	2.93E-01		1.55E+00	1.29E-02		-2.02E+00	8.50E-09	Down	-7.19E-01	1.56E-02		Unigene1155_All//gi|15912193|gb|AAL08230.1|//1.00E-113//AT4g22990/FZH19_170 [Arabidopsis thaliana]	Unigene1155_All//1.00E-112//AT4G22990| SPX (SYG1/Pho81/XPR1) domain-containing protein	Unigene1155_All//9.00E-121//CA994138				nr -
Unigene115509_All	452	0.00	0.56	0.47	0.00	0.08	0.00	0.37	2.22	1.23	9.13E+00	7.88E-02		8.88E+00	1.42E-01		6.25E+00	8.35E-01		null	null		2.57E+00	4.79E-04	Up	1.72E+00	5.92E-02				Unigene115509_All//4.00E-14//DR459122				
Unigene11551_All	1634	1.79	0.16	0.52	2.10	2.07	1.27	2.10	0.61	0.73	-3.53E+00	1.17E-11	Down	-1.78E+00	1.71E-05	Down	-2.64E-02	9.43E-01		-7.26E-01	2.91E-02		-1.77E+00	5.77E-08	Down	-1.52E+00	8.31E-07	Down	Unigene11551_All//gi|115469330|ref|NP_001058264.1|//1.00E-149//Os06g0659400 [Oryza sativa Japonica Group] >gi|51536173|dbj|BAD38346.1| lustrin A-like [Oryza sativa Japonica Group] >gi|52077362|dbj|BAD46402.1| lustrin A-like [Oryza sativa Japonica Group] >gi|113596304|dbj|BAF20178.1| Os06g0659400 [Oryza sativa Japonica Group]	Unigene11551_All//2.00E-167//AT5G20590| unknown protein	Unigene11551_All//0.00E+00//TC152473				nr -
Unigene115528_All	504	0.00	0.00	0.00	0.20	0.00	0.09	2.27	0.00	0.16	null	null		null	null		-7.63E+00	3.15E-01		-1.14E+00	6.78E-01		-1.11E+01	3.88E-08	Down	-3.84E+00	1.74E-06	Down	Unigene115528_All//gi|15233459|ref|NP_194643.1|//7.00E-53//MATE efflux protein-related [Arabidopsis thaliana]	Unigene115528_All//1.00E-42//AT4G29140| MATE efflux protein-related	Unigene115528_All//3.00E-104//TC170491				nr +
Unigene11553_All	596	1.14	4.51	2.59	2.26	1.79	4.17	60.94	57.22	46.26	1.98E+00	4.79E-06	Up	1.18E+00	3.71E-02		-3.33E-01	5.81E-01		8.85E-01	2.99E-02		-9.07E-02	3.46E-01		-3.98E-01	2.90E-07		Unigene11553_All//gi|225437164|ref|XP_002274787.1|//1.00E-77//PREDICTED: similar to type IIB calcium ATPase [Vitis vinifera]	Unigene11553_All//9.00E-64//AT3G63380| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12)	Unigene11553_All//0.00E+00//gi|78342403|gb|DT562677.1|DT562677			GO:0009206//GO:0019829//GO:0031224//GO:0032559//GO:0046873//GO:0070838	nr +
Unigene115532_All	437	0.00	0.00	0.00	0.00	0.00	0.00	0.10	1.82	0.18	null	null		null	null		null	null		null	null		4.23E+00	1.05E-04	Up	9.13E-01	7.51E-01		Unigene115532_All//gi|227908932|gb|ACO50134.2|//7.00E-57//elongation factor-like [Petalomonas cantuscygni]	Unigene115532_All//5.00E-18//AT5G60390| elongation factor 1-alpha / EF-1-alpha					nr -
Unigene115535_All	376	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.67	0.11	null	null		null	null		null	null		null	null		1.18E+01	9.64E-10	Up	6.73E+00	6.47E-01									ESTscan +
Unigene115539_All	293	0.00	0.00	0.00	0.00	0.00	0.00	2.31	2.43	0.14	null	null		null	null		null	null		null	null		7.08E-02	9.42E-01		-4.09E+00	3.10E-04	Down	Unigene115539_All//gi|8928433|sp|Q92581.1|TBB1_CYAPA//7.00E-34//RecName: Full=Tubulin beta-1 chain; AltName: Full=Beta-1-tubulin >gi|4139172|gb|AAD03712.1| beta 1 tubulin [Cyanophora paradoxa]	Unigene115539_All//1.00E-30//AT1G75780| TUB1; GTP binding / GTPase/ structural molecule	Unigene115539_All//1.00E-19//TC141009		ko04145|Phagosome		nr -
Unigene11554_All	4024	3.39	9.29	4.10	3.39	4.63	11.28	68.93	72.43	57.19	1.45E+00	8.84E-49	Up	2.74E-01	6.63E-02		4.49E-01	2.12E-04		1.73E+00	1.19E-81	Up	7.15E-02	1.24E-02		-2.69E-01	3.90E-24		Unigene11554_All//gi|225437164|ref|XP_002274787.1|//0.00E+00//PREDICTED: similar to type IIB calcium ATPase [Vitis vinifera]	Unigene11554_All//0.00E+00//AT3G63380| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12)	Unigene11554_All//0.00E+00//TC168651			GO:0005515//GO:0009206//GO:0019829//GO:0031224//GO:0032559//GO:0046873//GO:0070838	nr +
Unigene11555_All	2380	6.13	20.37	8.17	10.88	17.13	15.94	10.34	11.63	11.23	1.73E+00	3.70E-81	Up	4.13E-01	1.54E-03		6.54E-01	3.46E-17		5.51E-01	6.46E-11		1.69E-01	9.14E-02		1.20E-01	2.46E-01		Unigene11555_All//gi|115473603|ref|NP_001060600.1|//1.00E-115//Os07g0637200 [Oryza sativa Japonica Group] >gi|113611936|dbj|BAF22314.1| Os07g0637200 [Oryza sativa Japonica Group]	Unigene11555_All//8.00E-153//AT3G62200| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF537 (InterPro:IPR007491); BEST Arabidopsis thaliana protein match is: EDA32 (embryo sac development arrest 32) (TAIR:AT3G62210.1); Has 3380 Blast hits to 2820 proteins in 272 species: Archae - 0; Bacteria - 93; Metazoa - 1555; Fungi - 720; Plants - 473; Viruses - 42; Other Eukaryotes - 497 (source: NCBI BLink).	Unigene11555_All//0.00E+00//TC161332			GO:0000741	nr +
Unigene115551_All	625	0.00	0.00	0.00	0.00	0.00	0.00	1.62	2.74	0.00	null	null		null	null		null	null		null	null		7.56E-01	9.34E-02		-1.07E+01	1.35E-07	Down	Unigene115551_All//gi|166343843|gb|ABY86664.1|//1.00E-105//beta-tubulin 18 [Gossypium hirsutum]	Unigene115551_All//2.00E-86//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene115551_All//2.00E-41//TC148779		ko04145|Phagosome		nr -
Unigene115554_All	284	90.09	30.33	21.00	62.27	59.41	43.41	70.72	17.66	37.03	-1.57E+00	8.69E-38	Down	-2.10E+00	5.13E-54	Down	-6.77E-02	6.76E-01		-5.20E-01	5.05E-05		-2.00E+00	1.21E-50	Down	-9.33E-01	5.48E-17		Unigene115554_All//gi|166343845|gb|ABY86665.1|//1.00E-26//beta-tubulin 19 [Gossypium hirsutum]	Unigene115554_All//3.00E-26//AT5G62700| TUB3; GTP binding / GTPase/ structural molecule	Unigene115554_All//4.00E-124//gi|21094044|gb|BQ406369.1|BQ406369		ko04145|Phagosome		nr -
Unigene115555_All	308	0.00	0.00	0.00	0.00	0.00	0.00	0.82	3.94	0.00	null	null		null	null		null	null		null	null		2.26E+00	3.35E-04	Up	-9.69E+00	3.04E-02		Unigene115555_All//gi|13359451|dbj|BAB33421.1|//6.00E-06//putative senescence-associated protein [Pisum sativum]		Unigene115555_All//4.00E-07//TC143156				nr -
Unigene115558_All	415	0.00	0.00	0.00	0.00	0.00	0.00	0.61	3.32	1.44	null	null		null	null		null	null		null	null		2.44E+00	4.59E-05	Up	1.24E+00	1.39E-01				Unigene115558_All//5.00E-13//DT455935				
Unigene115569_All	222	0.00	12.10	0.72	1.57	5.74	0.20	1.71	5.27	8.08	1.36E+01	2.81E-15	Up	9.49E+00	2.39E-01		1.87E+00	3.47E-03		-2.95E+00	8.31E-02		1.62E+00	6.24E-03		2.24E+00	5.44E-06	Up			Unigene115569_All//2.00E-29//EX167763		ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism		kegg +
Unigene115570_All	523	0.00	0.00	0.00	0.00	0.00	0.00	0.97	1.44	0.00	null	null		null	null		null	null		null	null		5.68E-01	4.47E-01		-9.92E+00	5.54E-04	Down	Unigene115570_All//gi|12000413|gb|AAG40108.1|//1.00E-59//elongation factor 2 [Porphyra yezoensis]	Unigene115570_All//3.00E-54//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding					nr -

Unigene115574_All	530	1.28	0.29	1.31	2.54	0.91	1.45	7.58	3.71	1.58	-2.16E+00	2.84E-02		2.54E-02	9.96E-01		-1.48E+00	8.15E-03		-8.09E-01	1.73E-01		-1.03E+00	1.66E-04	Down	-2.26E+00	7.89E-13	Down	Unigene115574_All//gi|297824001|ref|XP_002879883.1|//2.00E-22//tRNA-binding region domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325722|gb|EFH56142.1| tRNA-binding region domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene115574_All//8.00E-23//AT2G40660| tRNA-binding region domain-containing protein	Unigene115574_All//0.00E+00//gi|21097965|gb|BQ410278.1|BQ410278		ko00450|Selenoamino acid metabolism//ko00970|Aminoacyl-tRNA biosynthesis		nr +
Unigene115576_All	295	0.00	0.17	0.00	0.84	0.23	0.00	0.43	0.57	5.13	7.42E+00	6.19E-01		null	null		-1.85E+00	2.75E-01		-9.72E+00	7.35E-02		3.98E-01	8.15E-01		3.58E+00	7.96E-08	Up				Unigene115576_All//4.00E-90//DR461288				
Unigene115577_All	1161	0.00	0.00	0.05	0.04	0.03	0.12	3.02	1.37	1.44	null	null		5.52E+00	6.39E-01		-5.31E-01	8.27E-01		1.44E+00	6.39E-01		-1.14E+00	1.27E-04	Down	-1.07E+00	2.11E-04	Down	Unigene115577_All//gi|3287835|sp|Q43714.1|DCS3_GOSAR//1.00E-108//RecName: Full=(+)-delta-cadinene synthase isozyme A; Short=D-cadinene synthase A >gi|1002523|gb|AAB41259.1| (+)-delta-cadinene synthase isozyme A [Gossypium arboreum] >gi|1217956|emb|CAA65289.1| (+)-delta-cadinene synthase [Gossypium arboreum]	Unigene115577_All//7.00E-67//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene115577_All//0.00E+00//TC142314		ko00904|Diterpenoid biosynthesis		nr -
Unigene115578_All	431	8.25	9.29	10.38	2.54	2.40	4.19	2.75	7.47	7.12	1.70E-01	6.21E-01		3.30E-01	2.89E-01		-8.52E-02	8.79E-01		7.21E-01	1.51E-01		1.44E+00	8.47E-06	Up	1.37E+00	2.17E-05	Up	Unigene115578_All//gi|85068668|gb|ABC69414.1|//7.00E-23//CYP72A57 [Nicotiana tabacum]	Unigene115578_All//2.00E-20//AT3G14690| CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene115578_All//9.00E-166//TC139184		ko00908|Zeatin biosynthesis//ko00591|Linoleic acid metabolism		nr +
Unigene11558_All	1662	16.09	7.99	8.30	19.69	19.81	18.80	25.69	11.42	12.63	-1.01E+00	3.62E-20	Down	-9.55E-01	1.10E-17		8.40E-03	9.58E-01		-6.65E-02	5.92E-01		-1.17E+00	4.77E-49	Down	-1.02E+00	7.81E-41	Down	Unigene11558_All//gi|297799222|ref|XP_002867495.1|//1.00E-150//band 7 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313331|gb|EFH43754.1| band 7 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11558_All//1.00E-144//AT4G27585| band 7 family protein	Unigene11558_All//0.00E+00//gi|78323484|gb|DT543758.1|DT543758				nr +
Unigene115580_All	241	0.00	0.00	0.00	0.00	0.00	0.00	272.10	40.06	3.97	null	null		null	null		null	null		null	null		-2.76E+00	2.32E-241	Down	-6.10E+00	0.00E+00	Down				Unigene115580_All//1.00E-12//TC142576				
Unigene115581_All	688	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.97	0.46	null	null		null	null		null	null		null	null		9.92E+00	7.64E-05	Up	8.86E+00	1.34E-02		Unigene115581_All//gi|296081204|emb|CBI18230.3|//3.00E-08//unnamed protein product [Vitis vinifera]			Unigene115581_All//0.00E+00//ES831270				nr -
Unigene115582_All	484	0.00	0.00	0.00	0.00	0.00	0.00	3.76	6.30	0.00	null	null		null	null		null	null		null	null		7.47E-01	1.92E-02		-1.19E+01	2.03E-13	Down	Unigene115582_All//gi|226503351|ref|NP_001148898.1|//2.00E-30//actin-depolymerizing factor [Zea mays] >gi|195623028|gb|ACG33344.1| actin-depolymerizing factor [Zea mays]	Unigene115582_All//2.00E-28//AT5G59890| ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); actin binding					nr -
Unigene115588_All	339	0.00	0.00	0.00	0.00	0.00	0.00	1.85	0.00	null	null	null		null	null		null	null		null	null		1.09E+01	1.47E-04	Up	null	null		Unigene115588_All//gi|148524155|gb|ABQ81936.1|//5.00E-24//elongation factor 1-alpha [Chara australis]	Unigene115588_All//4.00E-21//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene115588_All//1.00E-07//CD809343				nr +
Unigene115595_All	305	0.34	0.00	0.35	0.00	0.00	0.00	0.00	3.84	0.00	-8.42E+00	3.75E-01		2.54E-02	1.00E+00		null	null		null	null		1.19E+01	2.73E-08	Up	null	null		Unigene115595_All//gi|41390968|gb|AAS02074.1|//3.00E-48//auxin and ethylene responsive GH3-like protein [Capsicum chinense]	Unigene115595_All//5.00E-44//AT1G59500| GH3.4; indole-3-acetic acid amido synthetase	Unigene115595_All//2.00E-85//ES831098				nr +
Unigene115598_All	444	61.75	26.48	46.17	48.80	53.20	44.35	13.05	5.18	6.19	-1.22E+00	8.06E-28	Down	-4.19E-01	9.22E-05		1.25E-01	3.40E-01		-1.38E-01	3.19E-01		-1.33E+00	8.01E-09	Down	-1.08E+00	9.33E-07	Down				Unigene115598_All//8.00E-83//gi|11206634|gb|BF275564.1|BF275564				
Unigene1156_All	1618	76.96	107.70	86.36	78.32	75.47	91.16	39.28	114.82	77.73	4.85E-01	1.20E-35		1.66E-01	2.88E-04		-5.36E-02	3.27E-01		2.19E-01	9.24E-08		1.55E+00	0.00E+00	Up	9.85E-01	2.02E-110		Unigene1156_All//gi|18416049|ref|NP_567674.1|//0.00E+00//SPX (SYG1/Pho81/XPR1) domain-containing protein [Arabidopsis thaliana]	Unigene1156_All//0.00E+00//AT4G22990| SPX (SYG1/Pho81/XPR1) domain-containing protein	Unigene1156_All//0.00E+00//TC138350			GO:0006810//GO:0031090	nr -
Unigene115606_All	436	0.00	0.00	0.00	0.00	0.00	0.00	0.39	4.03	0.00	null	null		null	null		null	null		null	null		3.38E+00	2.17E-08	Up	-8.60E+00	1.08E-01		Unigene115606_All//gi|226347409|gb|ACO50115.1|//5.00E-63//elongation factor 1 alpha [Peranema trichophorum]	Unigene115606_All//9.00E-61//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene115606_All//1.00E-19//CD809343				nr +
Unigene115609_All	242	8.22	21.98	12.10	9.88	8.82	13.25	9.09	6.56	3.29	1.42E+00	2.42E-07	Up	5.59E-01	1.44E-01		-1.63E-01	7.23E-01		4.23E-01	2.54E-01		-4.69E-01	2.41E-01		-1.46E+00	1.79E-04	Down	Unigene115609_All//gi|4731573|gb|AAD28506.1|AF123265_1//6.00E-06//remorin 1 [Solanum lycopersicum]	Unigene115609_All//4.00E-07//AT2G45820| DNA-binding protein, putative	Unigene115609_All//3.00E-115//TC156235				nr -
Unigene11561_All	4843	352.40	168.44	344.81	128.34	158.34	134.87	13.22	10.29	7.87	-1.06E+00	0.00E+00	Down	-3.14E-02	2.10E-02		3.03E-01	7.11E-78		7.17E-02	3.11E-04		-3.62E-01	5.72E-10		-7.48E-01	5.67E-36		Unigene11561_All//gi|291419594|gb|ADE05291.1|//0.00E+00//magnesium chelatase H subunit [Vitis vinifera]	Unigene11561_All//0.00E+00//AT5G13630| GUN5 (GENOMES UNCOUPLED 5); magnesium chelatase	Unigene11561_All//0.00E+00//TC140684		ko00860|Porphyrin and chlorophyll metabolism	GO:0003676//GO:0006779//GO:0008408//GO:0009528//GO:0010467//GO:0043234//GO:0051003	nr -
Unigene115610_All	334	0.00	0.00	0.00	0.00	0.00	0.00	0.89	4.38	0.00	null	null		null	null		null	null		null	null		2.31E+00	4.93E-05	Up	-9.79E+00	1.58E-02		Unigene115610_All//gi|242039819|ref|XP_002467304.1|//6.00E-12//hypothetical protein SORBIDRAFT_01g024221 [Sorghum bicolor] >gi|241921158|gb|EER94302.1| hypothetical protein SORBIDRAFT_01g024221 [Sorghum bicolor]		Unigene115610_All//5.00E-25//TC176575				nr -
Unigene115611_All	412	7.24	8.85	8.66	15.36	14.04	13.26	36.64	15.62	18.28	2.91E-01	3.85E-01		2.59E-01	4.60E-01		-1.29E-01	6.15E-01		-2.11E-01	4.30E-01		-1.23E+00	3.02E-19	Down	-1.00E+00	1.53E-14	Down	Unigene115611_All//gi|12229923|sp|Q9M4T8.1|PSA5_SOYBN//5.00E-43//RecName: Full=Proteasome subunit alpha type-5; AltName: Full=20S proteasome alpha subunit E; AltName: Full=20S proteasome subunit alpha-5 >gi|7839485|gb|AAF70292.1|AF255338_1 20S proteasome subunit [Glycine max]	Unigene115611_All//1.00E-43//AT3G14290| PAE2; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene115611_All//4.00E-171//TC164836		ko03050|Proteasome		nr +
Unigene115613_All	606	0.35	3.09	0.35	1.07	1.08	0.67	0.70	4.21	0.66	3.16E+00	5.97E-07	Up	2.53E-02	1.00E+00		1.49E-02	9.92E-01		-6.72E-01	4.78E-01		2.59E+00	2.41E-09	Up	-8.58E-02	9.39E-01					Unigene115613_All//1.00E-14//TC177549				
Unigene115624_All	521	0.00	1.75	0.00	0.86	1.39	0.87	0.41	3.53	0.84	1.08E+01	2.62E-05	Up	null	null		6.90E-01	4.47E-01		1.07E-02	1.00E+00		3.12E+00	3.27E-08	Up	1.05E+00	2.98E-01		Unigene115624_All//gi|224093616|ref|XP_002309943.1|//2.00E-15//predicted protein [Populus trichocarpa] >gi|222852846|gb|EEE90393.1| predicted protein [Populus trichocarpa]						nr +
Unigene11563_All	3216	10.72	7.66	24.12	41.65	53.02	46.16	29.74	23.59	33.91	-4.86E-01	9.92E-08		1.17E+00	3.73E-70	Up	3.48E-01	1.11E-22		1.48E-01	4.78E-04		-3.34E-01	1.31E-12		1.89E-01	1.54E-05		Unigene11563_All//gi|22795064|gb|AAN05433.1|//0.00E+00//phospholipase D delta isoform 1a [Gossypium hirsutum]	Unigene11563_All//0.00E+00//AT4G35790| ATPLDDELTA; phospholipase D	Unigene11563_All//0.00E+00//TC1312269		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism	GO:0004620//GO:0006650//GO:0044464//GO:0046872	nr -
Unigene115630_All	599	0.09	0.00	0.00	0.33	0.00	0.30	0.00	3.07	0.13	-6.45E+00	6.16E-01		-6.45E+00	6.29E-01		-8.38E+00	8.46E-02		-1.41E-01	9.35E-01		1.16E+01	5.95E-13	Up	7.06E+00	4.05E-01									
Unigene115631_All	416	0.00	0.00	0.13	0.00	0.00	0.00	0.00	2.11	0.19	null	null		7.00E+00	6.39E-01		null	null		null	null		1.10E+01	2.86E-06	Up	7.58E+00	4.05E-01					Unigene115631_All//1.00E-53//FL576735				
Unigene115633_All	236	0.00	0.00	0.00	0.00	0.00	0.00	1.25	6.38	0.17	null	null		null	null		null	null		null	null		2.35E+00	3.01E-05	Up	-2.89E+00	6.77E-02					Unigene115633_All//3.00E-19//TC146753				
Unigene115637_All	593	0.00	0.00	0.00	0.00	0.00	0.00	1.21	2.04	0.00	null	null		null	null		null	null		null	null		7.54E-01	1.77E-01		-1.02E+01	1.78E-05	Down								
Unigene115638_All	532	0.00	0.00	0.00	0.00	0.00	0.00	0.08	2.51	0.00	null	null		null	null		null	null		null	null		4.98E+00	3.03E-08	Up	-6.31E+00	6.15E-01									
Unigene115645_All	302	0.00	0.00	0.00	0.00	0.00	0.00	1.96	1.52	0.00	null	null		null	null		null	null		null	null		-3.65E-01	6.49E-01		-1.09E+01	1.41E-04	Down	Unigene115645_All//gi|300268240|gb|EFJ52421.1|//1.00E-17//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene115645_All//6.00E-19//AT5G46430| 60S ribosomal protein L32 (RPL32B)			ko03010|Ribosome		nr -
Unigene115649_All	739	0.00	0.41	0.00	0.00	0.00	0.49	2.35	11.37	1.19	8.68E+00	4.44E-02		null	null		null	null		8.93E+00	2.37E-02		2.28E+00	3.08E-25	Up	-9.84E-01	2.16E-02		Unigene115649_All//gi|159488530|ref|XP_001702260.1|//2.00E-12//DEAH-box RNA helicase [Chlamydomonas reinhardtii] >gi|158271237|gb|EDO97061.1| DEAH-box RNA helicase [Chlamydomonas reinhardtii]		Unigene115649_All//7.00E-26//EX168464		ko03040|Spliceosome		nr -
Unigene115565_All	1076	6.27	5.13	0.99	20.18	24.19	10.41	9.23	6.37	5.26	-2.89E-01	2.21E-01		-2.66E+00	3.87E-19	Down	2.61E-01	1.40E-02		-9.55E-01	3.47E-16		-5.36E-01	9.35E-04		-8.13E-01	3.43E-07		Unigene115565_All//gi|224124160|ref|XP_002319260.1|//1.00E-132//GH3 family protein [Populus trichocarpa] >gi|222857636|gb|EEE95183.1| GH3 family protein [Populus trichocarpa]	Unigene115565_All//3.00E-131//AT5G54510| DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase	Unigene115565_All//0.00E+00//TC142322				nr -
Unigene115651_All	480	0.00	0.00	0.00	0.00	0.00	0.00	1.23	2.18	0.00	null	null		null	null		null	null		null	null		8.20E-01	1.79E-01		-1.03E+01	1.41E-04	Down	Unigene115651_All//gi|224003875|ref|XP_002291609.1|//2.00E-52//calreticulin-like protein [Thalassiosira pseudonana CCMP1335] >gi|220973385|gb|EED91716.1| calreticulin-like protein [Thalassiosira pseudonana CCMP1335]	Unigene115651_All//8.00E-39//AT1G56340| CRT1 (CALRETICULIN 1); calcium ion binding / unfolded protein binding			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr -
Unigene115653_All	798	0.00	0.00	0.00	0.00	0.00	0.00	1.27	3.09	0.10	null	null		null	null		null	null		null	null		1.28E+00	5.37E-04	Up	-3.67E+00	1.15E-05	Down	Unigene115653_All//gi|300264012|gb|EFJ48210.1|//1.00E-102//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene115653_All//8.00E-91//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene115653_All//2.00E-08//EV498577		ko03010|Ribosome		nr -
Unigene115654_All	489	4.81	7.15	10.45	13.04	14.15	6.74	27.32	43.16	12.38	5.70E-01	8.47E-02		1.12E+00	6.63E-05	Up	1.18E-01	6.54E-01		-9.52E-01	3.46E-05		6.60E-01	7.35E-10		-1.14E+00	8.38E-16	Down	Unigene115654_All//gi|166865124|gb|ABZ01817.1|//1.00E-33//cinnamyl alcohol dehydrogenase [Gossypium hirsutum]	Unigene115654_All//8.00E-29//AT4G34230| ATCAD5 (CINNAMYL ALCOHOL DEHYDROGENASE 5); cinnamyl-alcohol dehydrogenase	Unigene115654_All//4.00E-88//C0087836		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene115655_All	293	0.00	0.00	0.00	0.00	0.00	0.00	0.87	4.71	0.00	null	null		null	null		null	null		null	null		2.44E+00	4.59E-05	Up	-9.76E+00	3.04E-02					Unigene115655_All//9.00E-17//ES843311				
Unigene1566_All	2066	6.99	7.11	1.73	24.55	27.55	13.93	24.23	19.48	13.63	2.51E-02	8.82E-01		-2.02E+00	4.22E-29	Down	1.67E-01	1.96E-02		-8.18E-01	1.41E-28		-3.15E-01	2.49E-06		-8.30E-01	9.59E-34		Unigene1566_All//gi|224124160|ref|XP_002319260.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222857636|gb|EEE95183.1| GH3 family protein [Populus trichocarpa]	Unigene1566_All//0.00E+00//AT5G54510| DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase	Unigene1566_All//0.00E+00//TC142322			GO:0000902//GO:0009314//GO:0009536//GO:0009755//GO:0016881//GO:0048878	nr -
Unigene115661_All	471	0.00	0.00	0.00	0.00	0.00	0.00	0.54	8.52	0.00	null	null		null	null		null	null		null	null		3.98E+00	5.65E-21	Up	-9.07E+00	3.04E-02									
Unigene115663_All	411	0.00	0.00	0.00	0.12	0.00	0.00	0.31	9.15	0.10	null	null		null	null		-6.92E+00	5.60E-01		-6.92E+00	6.41E-01		4.89E+00	2.71E-22	Up	-1.67E+00	4.78E-01					Unigene115663_All//6.00E-173//gi|109835103|gb|DW233668.1|DW233668				
Unigene115666_All	565	0.00	0.00	0.19	0.00	0.00	0.00	0.45	3.25	0.00	null	null		7.56E+00	4.01E-01		null	null		null	null		2.86E+00	1.36E-07	Up	-8.81E+00	3.04E-02		Unigene115666_All//gi|224115056|ref|XP_002332226.1|//1.00E-46//GH3 family protein [Populus trichocarpa] >gi|222831839|gb|EEE70316.1| GH3 family protein [Populus trichocarpa]	Unigene115666_All//1.00E-44//AT2G23170| GH3.3; indole-3-acetic acid amido synthetase	Unigene115666_All//1.00E-63//ES805542				nr +

Unigene115669_All	375	0.28	1.35	0.00	0.00	0.00	0.24	0.34	3.34	0.21	2.28E+00	6.23E-02		-8.12E+00	3.97E-01		null	null		7.91E+00	4.79E-01		3.31E+00	4.67E-06	Up	-6.70E-01	7.20E-01		Unigene115669_All//gi|8778289|gb|AF79298.1|AC068602_21//1.00E-07//F14D16.29 [Arabidopsis thaliana]	Unigene115669_All//7.00E-08//AT1G19130| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF985 (InterPro:IPR009327), RmlC-like jelly roll fold (InterPro:IPR014710); Has 778 Blast hits to 778 proteins in 280 species: Archae - 8; Bacteria - 513; Metazoa - 2; Fungi - 16; Plants - 22; Viruses - 0; Other Eukaryotes - 217 (source: NCBI BLink).	Unigene115669_All//1.00E-72//AW187833				nr +
Unigene115671_All	611	0.09	0.17	0.70	0.57	0.17	0.37	1.04	3.28	0.13	9.55E-01	7.27E-01		3.03E+00	5.73E-02		-1.75E+00	1.90E-01		-6.27E-01	6.21E-01		1.66E+00	1.31E-04	Up	-2.99E+00	2.58E-03		Unigene115671_All//gi|17065180|gb|AAL32744.1|//8.00E-26//Unknown protein [Arabidopsis thaliana]	Unigene115671_All//2.00E-27//AT5G24460| unknown protein	Unigene115671_All//2.00E-10//DN801452				nr +
Unigene115674_All	300	0.00	0.00	0.00	0.00	0.00	0.00	0.28	2.79	0.00	null	null		null	null		null	null		null	null		3.31E+00	3.10E-04	Up	-8.14E+00	3.59E-01									
Unigene115680_All	510	0.00	0.00	0.00	0.00	0.00	0.00	1.16	1.15	0.00	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		-1.02E+01	1.41E-04	Down	Unigene115680_All//gi|255071427|ref|XP_002499387.1|//4.00E-51//sterol methyltransferase [Micromonas sp. RCC299] >gi|226514650|gb|ACO60646.1| sterol methyltransferase [Micromonas sp. RCC299]	Unigene115680_All//2.00E-49//AT5G13710| SMT1 (STEROL METHYLTRANSFERASE 1); sterol 24-C-methyltransferase	Unigene115680_All//4.00E-08//TC162556		ko00100|Steroid biosynthesis		nr +
Unigene115684_All	450	0.00	0.00	0.00	0.00	0.00	0.00	15.69	11.52	2.83	null	null		null	null		null	null		null	null		-4.46E-01	2.52E-02		-2.47E+00	2.82E-24	Down			Unigene115684_All//2.00E-25//TC146107				nr -
Unigene11569_All	2621	55.36	93.76	87.85	22.24	37.54	36.81	11.11	16.09	22.89	7.60E-01	7.65E-111		6.66E-01	2.57E-80		7.55E-01	1.36E-52		7.27E-01	1.17E-43		5.34E-01	3.58E-13		1.04E+00	3.16E-58	Up	Unigene11569_All//gi|297797507|ref|XP_002866638.1|//0.00E+00//AT6G54840| ATGCN5 (A. THALIANA GENERAL CONTROL NON-REPRESSIBLE 5); transporter >gi|297312473|gb|EFH42897.1| ATGCN5 [Arabidopsis lyrata subsp. lyrata]	Unigene11569_All//0.00E+00//AT5G64840| ATGCN5 (A. THALIANA GENERAL CONTROL NON-REPRESSIBLE 5); transporter	Unigene11569_All//0.00E+00//TC149541			GO:0016887//GO:0032559//GO:0043231	nr +
Unigene115693_All	443	0.00	0.00	0.00	0.00	0.00	0.00	1.24	3.49	0.00	null	null		null	null		null	null		null	null		1.49E+00	2.61E-03		-1.03E+01	2.81E-04	Down	Unigene115693_All//gi|224000193|ref|XP_002289769.1|//2.00E-46//RL11A, ribosomal protein 11A 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335] >gi|220974977|gb|EED93306.1| RL11A, ribosomal protein 11A 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335]	Unigene115693_All//9.00E-47//AT5G45775| 60S ribosomal protein L11 (RPL11D)			ko03010|Ribosome		nr +
Unigene115694_All	566	0.00	0.00	0.00	0.00	0.00	0.00	1.87	10.86	3.45	null	null		null	null		null	null		null	null		2.54E+00	4.24E-21	Up	8.85E-01	2.73E-02									
Unigene1157_All	727	0.00	0.00	0.07	0.14	0.28	0.37	13.20	5.75	7.40	null	null		6.19E+00	6.39E-01		1.05E+00	6.13E-01		1.44E+00	4.09E-01		-1.20E+00	4.45E-12	Down	-8.36E-01	2.83E-07		Unigene1157_All//gi|147826806|emb|CAN63950.1|//3.00E-10//hypothetical protein [Vitis vinifera]		Unigene1157_All//8.00E-72//TC171648			GO:0003676//GO:0000175//GO:0006260//GO:0006325//GO:0008168//GO:0008213//GO:0034061//GO:0043231//GO:0044427//GO:0046914	nr +
Unigene11570_All	2075	3.40	1.81	2.26	42.59	23.91	11.71	25.51	4.41	7.81	-9.14E-01	3.88E-05		-5.92E-01	1.01E-02		-8.33E-01	8.35E-58		-1.86E+00	1.13E-178	Down	-2.53E+00	8.23E-177	Down	-1.71E+00	8.99E-110	Down	Unigene11570_All//gi|224482639|gb|ACN50176.1|//0.00E+00//pectinesterase [Annona cherimola]	Unigene11570_All//0.00E+00//AT1G76160| sks5 (SKU5 Similar 5); copper ion binding / oxidoreductase	Unigene11570_All//0.00E+00//TC161343		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0004091//GO:0005576//GO:0005618//GO:0008152//GO:0016682//GO:0046914	nr +
Unigene115700_All	303	0.00	0.00	0.00	0.00	0.00	0.00	0.98	10.48	3.16	null	null		null	null		null	null		null	null		3.42E+00	6.83E-15	Up	1.69E+00	9.76E-03		Unigene115700_All//gi|195646322|gb|ACG42629.1|//2.00E-17//pirin-like protein [Zea mays]	Unigene115700_All//6.00E-14//AT2G43120| pirin, putative	Unigene115700_All//6.00E-83//TC141238				nr -
Unigene115703_All	794	0.26	1.47	1.01	1.32	0.39	0.00	0.80	9.37	1.05	2.48E+00	9.80E-04	Up	1.93E+00	3.42E-02		-1.76E+00	8.43E-03		-1.04E+01	1.47E-06	Down	3.55E+00	3.34E-35	Up	4.00E-01	5.65E-01		Unigene115703_All//gi|15222705|ref|NP_173966.1|//2.00E-66//FAD-binding domain-containing protein [Arabidopsis thaliana] >gi|9797756|gb|AAF98574.1|AC013427_17 Contains weak similarity to berberine bridge enzyme (bbe1) from Berberis stolonifera gb|AF049347 and contains a FAD binding PF|01565 domain [Arabidopsis thaliana]	Unigene115703_All//9.00E-68//AT1G26420| FAD-binding domain-containing protein	Unigene115703_All//2.00E-180//TC130360				nr +
Unigene115705_All	413	0.00	0.00	0.00	0.00	0.00	0.00	0.10	2.23	0.00	null	null		null	null		null	null		null	null		4.44E+00	1.66E-05	Up	-6.68E+00	6.15E-01									ESTscan -
Unigene11571_All	2213	18.72	5.61	5.49	19.34	17.47	29.18	43.29	5.40	17.19	-1.74E+00	2.95E-70	Down	-1.77E+00	1.46E-69	Down	-1.46E-01	9.20E-02		5.94E-01	9.88E-21		-3.00E+00	0.00E+00	Down	-1.33E+00	2.20E-137	Down	Unigene11571_All//gi|224061929|ref|XP_002300669.1|//0.00E+00//multicopper oxidase [Populus trichocarpa] >gi|222842395|gb|EEE79942.1| multicopper oxidase [Populus trichocarpa]	Unigene11571_All//0.00E+00//AT1G76160| sks5 (SKU5 Similar 5); copper ion binding / oxidoreductase	Unigene11571_All//0.00E+00//TC155372		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0004091//GO:0005576//GO:0005618//GO:0008152//GO:0016682//GO:0046914	nr +
Unigene115711_All	429	0.00	0.00	0.00	0.00	0.00	0.00	0.20	2.34	0.00	null	null		null	null		null	null		null	null		3.57E+00	3.08E-05	Up	-7.62E+00	3.59E-01									ESTscan +
Unigene115714_All	491	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19	0.00	null	null		null	null		null	null		null	null		1.02E+01	2.81E-04	Up	null	null		Unigene115714_All//sp|Q9GPH3|ATFC_BOMMO//1.00E-06//Activating transcription factor of chaperone OS=Bombyx mori GN=ATFC PE=2 SV=1						swissprot +
Unigene115716_All	797	0.00	0.00	0.00	0.00	0.00	0.00	1.38	6.14	0.60	null	null		null	null		null	null		null	null		2.15E+00	4.89E-14	Up	-1.20E+00	3.41E-02				Unigene115716_All//6.00E-08//TC160492				
Unigene115718_All	511	0.10	0.00	0.00	0.00	0.47	1.24	0.17	0.08	0.08	-6.68E+00	6.16E-01		-6.68E+00	6.29E-01		8.88E+00	1.04E-01		1.03E+01	7.60E-04	Up	-1.02E+00	7.26E-01		-1.09E+00	6.77E-01		Unigene115718_All//gi|212960417|gb|ACJ38666.1|//2.00E-78//cellulose synthase [Betula luminifera]	Unigene115718_All//2.00E-65//AT5G44030| CESA4 (CELLULOSE SYNTHASE A4); cellulose synthase/ transferase, transferring glycosyl groups	Unigene115718_All//4.00E-39//TC129590				nr +
Unigene115721_All	491	0.00	0.00	0.00	0.00	0.00	0.00	2.15	2.89	0.16	null	null		null	null		null	null		null	null		4.27E-01	4.07E-01		-3.73E+00	6.13E-06	Down	Unigene115721_All//gi|261887565|gb|ACY05960.1|//1.00E-82//alpha-tubulin [Haematococcus pluvialis]	Unigene115721_All//1.00E-69//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene115721_All//4.00E-17//ES829891		ko04145|Phagosome		nr +
Unigene115723_All	306	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.73	0.00	null	null		null	null		null	null		null	null		1.14E+01	5.54E-06	Up	null	null			Unigene115723_All//9.00E-05//AT5G37640| UBQ9; protein binding					
Unigene115725_All	915	0.00	0.00	0.00	0.00	0.00	0.00	0.05	3.29	0.00	null	null		null	null		null	null		null	null		6.15E+00	1.28E-19	Up	-5.53E+00	6.15E-01		Unigene115725_All//gi|301115724|ref|XP_002905591.1|//8.00E-19//kinesin-like protein [Phytophthora infestans T30-4] >gi|262110380|gb|EE168432.1| kinesin-like protein [Phytophthora infestans T30-4]	Unigene115725_All//1.00E-17//AT3G49650| kinesin motor protein-related					nr +
Unigene115733_All	813	0.26	0.12	0.33	0.12	0.30	0.22	0.88	4.73	1.27	-1.05E+00	5.65E-01		3.48E-01	7.97E-01		1.28E+00	5.32E-01		8.59E-01	6.96E-01		2.42E+00	9.00E-13	Up	5.27E-01	3.75E-01				Unigene115733_All//7.00E-23//TC153927				
Unigene115735_All	326	0.00	0.00	0.00	0.00	0.00	0.00	0.13	2.05	0.00	null	null		null	null		null	null		null	null		3.98E+00	6.38E-04	Up	-7.02E+00	6.15E-01		Unigene115735_All//gi|89276295|gb|ABD66504.1|//2.00E-18//actin depolymerizing factor 8 [Gossypium hirsutum] >gi|119388970|gb|AAY88048.2| actin depolymerizing factor [Gossypium hirsutum]	Unigene115735_All//8.00E-19//AT5G22360| ADF10 (ACTIN DEPOLYMERIZING FACTOR 10); actin binding					nr -
Unigene115737_All	614	0.00	0.00	0.00	0.00	0.00	0.00	1.38	10.55	0.26	null	null		null	null		null	null		null	null		2.94E+00	7.41E-26	Up	-2.41E+00	1.68E-03		Unigene115737_All//gi|186501250|ref|NP_849973.3|//9.00E-59//metal ion binding [Arabidopsis thaliana]	Unigene115737_All//5.00E-60//AT2G18196| metal ion binding	Unigene115737_All//2.00E-56//DN800214				nr +
Unigene115739_All	610	0.00	0.00	0.00	0.00	0.00	0.00	1.25	3.77	0.26	null	null		null	null		null	null		null	null		1.59E+00	6.35E-05	Up	-2.26E+00	4.68E-03		Unigene115739_All//gi|297842307|ref|XP_002889035.1|//7.00E-32//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334876|gb|EFH65294.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene115739_All//1.00E-28//AT1G75640| leucine-rich repeat family protein / protein kinase family protein			ko04626|Plant-pathogen interaction		nr +
Unigene115742_All	846	909.12	761.18	1391.68	169.87	218.74	174.14	1.15	0.84	0.05	-2.56E-01	2.06E-47		6.14E-01	0.00E+00		3.65E-01	9.09E-27		3.58E-02	5.17E-01		-4.53E-01	4.90E-01		-4.61E+00	3.32E-06	Down	Unigene115742_All//gi|224124190|ref|XP_002330127.1|//1.00E-122//light-harvesting complex I protein Lhca4 [Populus trichocarpa] >gi|222871261|gb|EEF08392.1| light-harvesting complex I protein Lhca4 [Populus trichocarpa]	Unigene115742_All//4.00E-122//AT3G47470| LHCA4 (LIGHT-HARVESTING CHLOROPHYLL-PROTEIN COMPLEX I SUBUNIT A4); chlorophyll binding	Unigene115742_All//0.00E+00//TC130501		ko00196|Photosynthesis - antenna proteins		nr -
Unigene11575_All	1936	13.11	12.30	8.50	28.56	27.39	23.72	30.64	15.70	13.85	-9.16E-02	4.53E-01		-6.25E-01	1.99E-08		-6.03E-02	5.10E-01		-2.68E-01	1.33E-04		-9.65E-01	9.69E-50		-1.15E+00	1.82E-67	Down	Unigene11575_All//gi|222423108|dbj|BAH19533.1|//1.00E-108//AT4G08310| [Arabidopsis thaliana]	Unigene11575_All//5.00E-78//AT4G08310| unknown protein	Unigene11575_All//0.00E+00//TC146538				nr -
Unigene115753_All	316	0.00	1.28	0.00	0.47	0.65	0.00	2.01	1.32	0.13	1.03E+01	1.36E-02		null	null		4.67E-01	8.25E-01		-8.89E+00	2.34E-01		-6.02E-01	4.67E-01		-3.99E+00	5.82E-04	Down								
Unigene115754_All	527	0.00	0.00	0.00	0.00	0.00	0.00	1.12	4.36	0.60	null	null		null	null		null	null		null	null		1.96E+00	2.90E-06	Up	-8.93E-01	2.72E-01				Unigene115754_All//3.00E-09//gi|84155251|gb|DN804606.1|DN804606				
Unigene115758_All	505	0.00	1.00	0.11	0.30	0.55	0.54	0.50	2.48	0.16	9.97E+00	4.05E-03		6.72E+00	6.39E-01		8.83E-01	5.95E-01		8.59E-01	6.31E-01		2.31E+00	2.06E-04	Up	-1.67E+00	2.56E-01									
Unigene115759_All	545	0.00	0.00	0.00	0.00	0.00	0.00	1.32	2.76	0.00	null	null		null	null		null	null		null	null		1.07E+00	2.90E-02		-1.04E+01	1.78E-05	Down	Unigene115759_All//gi|168056108|ref|XP_001780064.1|//4.00E-45//ATP-binding cassette transporter, subfamily G, member 3, group WBC protein PpABCG3 [Physcomitrella patens subsp. patens] >gi|162668562|gb|EDQ55167.1| ATP-binding cassette transporter, subfamily G, member 3, group WBC protein PpABCG3 [Physcomitrella patens subsp. patens]	Unigene115759_All//9.00E-44//AT2G39350| ADC transporter family protein			ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene115760_All	737	0.00	0.00	0.00	0.14	0.51	0.74	1.84	3.01	5.35	null	null		null	null		1.93E+00	1.94E-01		2.44E+00	4.41E-02		7.11E-01	6.62E-02		1.54E+00	8.71E-08	Up			Unigene115760_All//0.00E+00//BM358110				
Unigene115765_All	547	0.00	0.00	0.00	0.00	0.00	0.00	0.70	2.98	0.00	null	null		null	null		null	null		null	null		2.10E+00	5.14E-05	Up	-9.44E+00	4.20E-03									
Unigene115768_All	678	0.00	0.00	0.00	0.00	0.00	0.00	1.00	2.22	0.00	null	null		null	null		null	null		null	null		1.15E+00	1.87E-02		-9.96E+00	3.56E-05	Down								
Unigene115768_All	334	0.00	0.00	0.00	0.00	0.00	0.00	1.52	2.75	0.00	null	null		null	null		null	null		null	null		8.58E-01	1.95E-01		-1.06E+01	5.54E-04	Down	Unigene115768_All//gi|159465411|ref|XP_001690916.1|//7.00E-10//extracellular matrix protein [Chlamydomonas reinhardtii] >gi|158279602|gb|EDP05362.1| extracellular matrix protein [Chlamydomonas reinhardtii]				ko04141|Protein processing in endoplasmic reticulum//ko03420|Nucleotide excision repair		nr -
Unigene11577_All	406	15.46	28.08	11.67	1.47	1.70	2.67	0.62	6.28	1.08	8.61E-01	4.34E-07		-4.06E-01	1.08E-01		2.04E-01	8.21E-01		8.59E-01	2.17E-01		3.33E+00	8.60E-12	Up	7.89E-01	4.23E-01		Unigene11577_All//gi|224979415|gb|ACN72639.1|//3.00E-20//nitrate transporter [Malus hupehensis]	Unigene11577_All//5.00E-11//AT5G62680| proton-dependent oligopeptide transport (POT) family protein	Unigene11577_All//0.00E+00//gi|21100916|gb|BQ413229.1|BQ413229			GO:0015833//GO:0016020	nr +
Unigene115771_All	369	0.00	0.00	0.00	0.27	0.00	0.00	0.57	3.06	3.89	null	null		null	null		-8.08E+00	3.15E-01		-8.08E+00	4.03E-01		2.42E+00	3.17E-04	Up	2.76E+00	4.81E-06	Up			Unigene115771_All//2.00E-160//TC178436				
Unigene115777_All	368	0.00	0.00	0.00	0.00	0.00	0.00	2.18	2.95	0.00	null	null		null	null		null	null		null	null		4.36E-01	4.77E-01		-1.11E+01	4.43E-06	Down			Unigene115777_All//1.00E-28//gi|48805733|gb|CO107047.1|CO107047				
Unigene115786_All	370	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.28	0.00	null	null		null	null		null	null		null	null		1.17E+01	1.40E-08	Up	null	null									ESTscan -

Unigene115789_All	337	0.31	0.00	0.32	0.30	0.20	0.27	0.38	3.10	1.89	-8.28E+00	3.75E-01		2.53E-02	1.00E+00		-5.32E-01	8.18E-01		-1.41E-01	9.52E-01		3.04E+00	7.88E-05	Up	2.33E+00	1.05E-02		Unigene115789_All//gi|297829424|ref|XP_002882594.1//2.00E-32//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328434|gb|EFH58853.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene115789_All//2.00E-33//AT3G08970| ATERDJ3A; oxidoreductase	Unigene115789_All//6.00E-80//TC178503				nr -
Unigene11579_All	683	9.12	14.84	16.76	3.65	5.34	15.41	1.49	7.83	7.47	7.03E-01	9.34E-05		8.79E-01	5.15E-07		5.51E-01	8.96E-02		2.08E+00	2.03E-24	Up	2.40E+00	2.50E-17	Up	2.33E+00	2.27E-16	Up	Unigene11579_All//gi|11933400|dbj|BAB19757.1|//8.00E-33//nitrate transporter NRT1-2 [Glycine max]	Unigene11579_All//3.00E-31//AT1G18880| proton-dependent oligopeptide transport (POT) family protein	Unigene11579_All//1.00E-150//TC162742			GO:0015833//GO:0016020	nr -
Unigene115790_All	555	0.00	0.00	0.00	0.72	1.24	0.98	0.30	5.12	0.43	null	null		null	null		7.89E-01	4.04E-01		4.44E-01	6.78E-01		4.07E+00	3.20E-15	Up	4.99E-01	7.08E-01					Unigene115790_All//7.00E-07//ES824204				
Unigene115791_All	345	0.00	0.00	0.00	0.00	0.00	0.00	2.08	2.79	0.00	null	null		null	null		null	null		null	null		4.20E-01	5.31E-01		-1.10E+01	1.78E-05	Down	Unigene115791_All//gi|159473469|ref|XP_001694856.1//3.00E-23//acidic ribosomal protein P2 [Chlamydomonas reinhardtii] >gi|158276235|gb|EDP02008.1| acidic ribosomal protein P2 [Chlamydomonas reinhardtii]	Unigene115791_All//5.00E-16//AT2G27710| 60S acidic ribosomal protein P2 (RPP2B)			ko03010|Ribosome		nr -
Unigene115796_All	378	0.00	0.00	0.00	0.00	0.00	0.00	0.45	2.76	0.21	null	null		null	null		null	null		null	null		2.63E+00	2.86E-04	Up	-1.09E+00	5.53E-01									
Unigene115799_All	994	0.00	0.00	0.00	0.00	0.00	0.00	0.04	3.45	0.00	null	null		null	null		null	null		null	null		6.34E+00	1.66E-22	Up	-5.41E+00	6.15E-01		Unigene115799_All//gi|71143066|gb|AAZ23924.1|//6.00E-06//At2g40070 [Arabidopsis thaliana] >gi|110742086|dbj|BAE98974.1| En/Spm-like transposon protein [Arabidopsis thaliana]						nr -
Unigene115800_All	362	0.00	0.00	0.00	0.00	0.00	0.00	0.23	2.08	0.00	null	null		null	null		null	null		null	null		3.15E+00	9.54E-04	Up	-7.87E+00	3.59E-01									
Unigene115803_All	323	2.27	0.00	0.99	1.39	1.71	0.00	6.15	5.05	2.71	-1.11E+01	2.11E-04	Down	-1.20E+00	1.80E-01		2.97E-01	8.18E-01		-1.04E+01	5.79E-03		-2.86E-01	5.28E-01		-1.18E+00	3.26E-03					Unigene115803_All//2.00E-46//gi|109857439|gb|DW486418.1|DW486418				
Unigene115804_All	571	0.00	0.00	0.00	0.00	0.00	0.00	1.18	3.00	0.00	null	null		null	null		null	null		null	null		1.34E+00	3.54E-03		-1.02E+01	3.56E-05	Down	Unigene115804_All//gi|300266840|gb|EFJ51026.1|//2.00E-86//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene115804_All//3.00E-42//AT1G48830| 40S ribosomal protein S7 (RPS7A)			ko03010|Ribosome		nr -
Unigene115805_All	815	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.56	0.00	null	null		null	null		null	null		null	null		1.22E+01	3.56E-26	Up	null	null		Unigene115805_All//gi|294987218|gb|ADF56046.1|//9.00E-37//glutathione S-transferase [Grimmia pilifera]	Unigene115805_All//3.00E-07//AT2G30870| GSTF10 (HALIANA GLUTATHIONE S-TRANSFERASE PHI 10); copper ion binding / glutathione binding / glutathione transferase			ko00480|Glutathione metabolism		nr -
Unigene115809_All	372	0.00	0.00	0.00	0.00	0.00	0.00	0.68	3.82	0.32	null	null		null	null		null	null		null	null		2.49E+00	2.76E-05	Up	-1.09E+00	4.28E-01		Unigene115809_All//gi|300253702|gb|EFJ38959.1|//7.00E-12//hypothetical protein VOLCADRAFT_78580 [Volvox carteri f. nagariensis]		Unigene115809_All//4.00E-32//TC146753				nr -
Unigene11581_All	2304	23.50	30.00	26.35	10.27	14.83	29.64	4.20	25.63	17.93	3.52E-01	1.99E-08		1.65E-01	2.61E-02		5.30E-01	4.55E-10		1.53E+00	1.46E-102	Up	2.61E+00	2.14E-203	Up	2.09E+00	1.75E-111	Up	Unigene11581_All//gi|11933414|dbj|BAB19760.1|//0.00E+00//nitrate transporter NRT1-5 [Glycine max]	Unigene11581_All//1.00E-165//AT5G62680| proton-dependent oligopeptide transport (POT) family protein	Unigene11581_All//0.00E+00//TC159080				nr +
Unigene115811_All	500	0.00	0.00	0.00	0.00	0.00	0.72	15.05	10.11	75.61	null	null		null	null		null	null		9.50E+00	2.37E-02		-5.74E-01	2.46E-03		2.33E+00	1.87E-116	Up	Unigene115811_All//gi|224052970|ref|XP_002297642.1|//2.00E-47//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222841900|gb|EEE82447.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene115811_All//4.00E-42//AT3G13610| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene115811_All//2.00E-65//FL577006		ko00941|Flavonoid biosynthesis		nr -
Unigene115823_All	690	0.38	0.29	0.15	0.51	0.10	0.46	3.00	18.17	7.79	-3.68E-01	7.79E-01		-1.30E+00	4.37E-01		-2.34E+00	1.01E-01		-1.41E-01	9.12E-01		2.60E+00	1.92E-43	Up	1.38E+00	7.77E-09	Up	Unigene115823_All//gi|297610489|ref|NP_001064615.2|//6.00E-06//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene115823_All//5.00E-05//AT1G60690| aldo/keto reductase family protein	Unigene115823_All//0.00E+00//CD809346				nr +
Unigene115824_All	397	0.00	1.02	0.00	0.00	0.17	0.23	0.53	2.84	0.10	1.00E+01	1.36E-02		null	null		7.44E+00	6.13E-01		7.83E+00	4.79E-01		2.42E+00	3.17E-04	Up	-2.41E+00	1.95E-01									
Unigene115825_All	607	0.00	0.00	0.00	0.00	0.00	0.00	1.60	3.72	0.00	null	null		null	null		null	null		null	null		1.21E+00	1.71E-03		-1.06E+01	2.72E-07	Down	Unigene115825_All//gi|29691166|gb|AAO89237.1|//1.00E-66//adenosylhomocysteinase [Medicago truncatula]	Unigene115825_All//2.00E-66//AT4G13940| MES88 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding	Unigene115825_All//7.00E-07//gi|164343927|gb|ES810489.1|ES810489		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr +
Unigene115826_All	413	0.25	0.37	0.13	0.24	0.17	0.33	0.41	2.43	0.58	5.39E-01	7.80E-01		-9.75E-01	7.22E-01		-5.32E-01	8.18E-01		4.44E-01	8.62E-01		2.57E+00	4.79E-04	Up	4.99E-01	7.08E-01					Unigene115826_All//5.00E-07//TC175259				
Unigene115829_All	395	0.00	0.90	0.54	0.00	0.00	0.00	3.21	5.08	0.10	9.81E+00	2.47E-02		9.07E+00	1.42E-01		null	null		null	null		6.61E-01	1.09E-01		-4.99E+00	3.13E-08	Down	Unigene115829_All//gi|113289|sp|P26182.1|ACT_ACHBI|//7.00E-61//RecName: Full=Actin >gi|2290|emb|CAA42559.1| actin [Achlya bisexualis] >gi|78057820|gb|ABB17316.1| actin A [Peronospora viciae]	Unigene115829_All//8.00E-57//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene115829_All//6.00E-71//TC153744		ko04145|Phagosome		nr +
Unigene115830_All	399	0.00	0.76	0.27	0.00	0.00	1.02	0.42	2.51	0.00	9.57E+00	4.44E-02		8.06E+00	4.01E-01		null	null		9.99E+00	1.36E-02		2.57E+00	4.79E-04	Up	-8.73E+00	1.08E-01					Unigene115830_All//5.00E-19//TC175987				
Unigene115832_All	539	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.56	0.00	null	null		null	null		null	null		null	null		1.13E+01	9.64E-10	Up	null	null		Unigene115832_All//gi|269315884|gb|ACZ37068.1|//4.00E-16//thioredoxin h4 [Medicago truncatula]	Unigene115832_All//1.00E-10//AT1G59730| ATH7 (thioredoxin H-type 7)					nr +
Unigene115833_All	380	1.93	0.00	1.26	6.55	2.27	0.71	5.23	11.33	1.89	-1.09E+01	2.11E-04	Down	-6.12E-01	4.70E-01		-1.53E+00	7.55E-05	Down	-3.20E+00	7.46E-10	Down	1.12E+00	2.70E-05	Up	-1.47E+00	3.81E-04	Down	Unigene115833_All//gi|30697277|ref|NP_851226.1|//4.00E-31//MYB59 (MYB DOMAIN PROTEIN 59); DNA binding / transcription factor [Arabidopsis thaliana] >gi|68480112|gb|AAY97895.1| MYB transcription factor MYB59-2 [Arabidopsis thaliana]	Unigene115833_All//2.00E-32//AT5G59780| MYB59 (MYB DOMAIN PROTEIN 59); DNA binding / transcription factor	Unigene115833_All//1.00E-72//TC178283	MYB-related			nr +
Unigene115835_All	675	0.00	0.00	0.16	0.30	0.36	0.33	0.44	2.66	2.36	null	null		7.30E+00	4.01E-01		2.75E-01	8.95E-01		1.80E-01	9.35E-01		2.60E+00	8.33E-07	Up	2.43E+00	7.10E-06	Up	Unigene115835_All//gi|7671450|emb|CAB89390.1|//1.00E-55//lectin-like protein kinase-like [Arabidopsis thaliana] >gi|91806848|gb|ABE66151.1| lectin protein kinase [Arabidopsis thaliana]	Unigene115835_All//8.00E-57//AT5G10530| lectin protein kinase, putative	Unigene115835_All//1.00E-73//CA994027		ko04626|Plant-pathogen interaction		nr +
Unigene115836_All	629	0.33	0.81	0.25	0.00	0.11	0.36	0.27	3.06	0.57	1.28E+00	2.31E-01		-3.89E-01	8.08E-01		6.77E+00	6.13E-01		8.49E+00	1.19E-01		3.51E+00	2.06E-09	Up	1.08E+00	3.50E-01		Unigene115836_All//gi|15222705|ref|NP_173966.1|//7.00E-33//FAD-binding domain-containing protein [Arabidopsis thaliana] >gi|9797756|gb|AAP98574.1|AC013427_17 Contains weak similarity to berberine bridge enzyme (bbe1) from Berberis stolonifera gb|AF049347 and contains a FAD binding PF|01565 domain [Arabidopsis thaliana]	Unigene115836_All//1.00E-34//AT1G26420| FAD-binding domain-containing protein	Unigene115836_All//1.00E-73//TC130360				nr +
Unigene115837_All	600	0.00	0.00	0.00	0.00	0.06	0.00	0.99	3.41	1.59	null	null		null	null		5.84E+00	8.35E-01		null	null		1.79E+00	4.09E-05	Up	6.92E-01	2.60E-01					Unigene115837_All//0.00E+00//DN804072				
Unigene115840_All	794	0.26	0.00	0.00	0.06	0.09	0.00	1.33	3.05	0.20	-8.04E+00	1.22E-01		-8.04E+00	1.46E-01		4.68E-01	9.60E-01		-5.97E+00	6.41E-01		1.20E+00	1.25E-03		-2.73E+00	1.12E-04	Down								
Unigene115841_All	733	0.00	0.00	0.00	0.00	0.00	0.00	1.62	2.74	0.00	null	null		null	null		null	null		null	null		7.61E-01	6.33E-02		-1.07E+01	8.15E-09	Down	Unigene115841_All//gi|297829496|ref|XP_002882630.1|//2.00E-66//60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata] >gi|297328470|gb|EFH58889.1| 60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata]	Unigene115841_All//7.00E-46//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)			ko03010|Ribosome		nr -
Unigene115842_All	1184	0.00	0.00	0.00	0.00	0.00	0.00	0.79	1.24	0.07	null	null		null	null		null	null		null	null		6.53E-01	1.93E-01		-3.55E+00	3.97E-05	Down	Unigene115842_All//gi|297721715|ref|NP_001173220.1|//4.00E-12//Os02g0832150 [Oryza sativa Japonica Group] >gi|255671379|dbj|BAH91949.1| Os02g0832150 [Oryza sativa Japonica Group]	Unigene115842_All//3.00E-12//AT4G32600| zinc finger (C3HC4-type RING finger) family protein					nr -
Unigene115845_All	420	0.00	0.00	0.00	0.00	0.00	0.00	0.70	3.28	0.00	null	null		null	null		null	null		null	null		2.22E+00	1.31E-04	Up	-9.46E+00	1.58E-02		Unigene115845_All//gi|301121610|ref|XP_002908532.1|//2.00E-53//60S ribosomal protein L23 [Phytophthora infestans T30-4] >gi|66270163|gb|AAY43411.1| ribosomal protein L23 [Phytophthora infestans] >gi|262103563|gb|EEY61615.1| 60S ribosomal protein L23 [Phytophthora infestans T30-4]	Unigene115845_All//2.00E-52//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene115845_All//2.00E-18//TC174626		ko03010|Ribosome		nr -
Unigene115846_All	405	0.00	0.00	0.00	0.00	0.00	0.00	0.10	2.79	0.00	null	null		null	null		null	null		null	null		4.74E+00	7.27E-07	Up	-6.71E+00	6.15E-01		Unigene115846_All//gi|160331695|ref|XP_001712554.1|//1.00E-19//kin(snf2) [Hemiselmis andersenii] >gi|159766003|gb|ABW98229.1| kin(snf2) [Hemiselmis andersenii]	Unigene115846_All//6.00E-18//AT1G78290| serine/threonine protein kinase, putative			ko04140|Regulation of autophagy		nr +
Unigene115847_All	726	0.00	0.70	0.00	0.41	0.09	0.37	1.34	5.18	1.10	9.45E+00	4.05E-03		null	null		-2.12E+00	1.66E-01		-1.41E-01	9.21E-01		1.95E+00	9.38E-10	Up	-2.88E-01	6.35E-01		Unigene115847_All//gi|226713182|sp|A7R333.1|U497A_VITVI|//5.00E-46//RecName: Full=UPF0497 membrane protein 10	Unigene115847_All//6.00E-34//AT4G03540| integral membrane family protein					nr +
Unigene115848_All	872	0.18	0.17	0.00	0.40	0.04	0.78	1.21	7.43	1.87	-4.64E-02	9.89E-01		-7.49E+00	2.46E-01		-3.34E+00	4.07E-02		9.58E-01	3.09E-01		2.62E+00	6.16E-23	Up	6.28E-01	1.61E-01		Unigene115848_All//gi|115187640|gb|ABI84264.1|//2.00E-07//ubiquitin-conjugating enzyme [Arachis hypogaea]	Unigene115848_All//2.00E-07//AT3G53580| UBC14 (ubiquitin-conjugating enzyme 14); ubiquitin-protein ligase	Unigene115848_All//0.00E+00//gi|72273404|gb|DT049137.1|DT049137		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene115850_All	420	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.19	0.00	null	null		null	null		null	null		null	null		1.11E+01	1.48E-06	Up	null	null		Unigene115850_All//gi|299473653|emb|CBN78047.1|//1.00E-21//flagellar associated protein, quinone reductase-like protein [Ectocarpus siliculosus]	Unigene115850_All//7.00E-17//AT5G54500| FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor					nr +
Unigene115851_All	437	0.00	0.00	0.00	0.00	0.00	0.21	0.10	5.16	6.66	null	null		null	null		null	null		7.69E+00	4.79E-01		5.74E+00	1.88E-14	Up	6.10E+00	2.88E-19	Up								
Unigene115852_All	671	0.86	0.15	0.24	0.00	0.51	0.00	0.50	3.05	1.37	-2.51E+00	2.94E-02		-1.85E+00	9.62E-02		9.00E+00	3.02E-02		null	null		2.60E+00	1.19E-07	Up	1.44E+00	2.77E-02		Unigene115852_All//gi|124484395|dbj|BAF46308.1|//4.00E-07//leucine-rich repeat transmembrane protein kinase [Ipomoea nil]	Unigene115852_All//4.00E-08//AT5G01950| ATP binding / kinase/ protein serine/threonine kinase	Unigene115852_All//2.00E-35//gi|31072574|gb|CA992853.1|CA992853				nr -
Unigene115854_All	447	0.00	0.23	0.00	0.00	0.23	0.00	0.57	3.09	0.45	7.82E+00	3.89E-01		null	null		7.85E+00	4.57E-01		null	null		2.44E+00	4.59E-05	Up	-3.49E-01	7.67E-01					Unigene115854_All//4.00E-140//TC141652				
Unigene115859_All	438	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.62	0.00	null	null		null	null		null	null		null	null		1.07E+01	3.98E-05	Up	null	null		Unigene115859_All//gi|255598734|gb|ACV83439.1|//7.00E-54//QM-like protein [Zea mays]	Unigene115859_All//6.00E-53//AT1G66580| 60S ribosomal protein L10 (RPL10C)	Unigene115859_All//2.00E-58//CD485839		ko03010|Ribosome		nr -

Unigene115861_All	424	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.25	0.00	null	null		null	null		null	null		null	null		1.17E+01	9.64E-10	Up	null	null		Unigene115861_All//gi|159467345|ref|XP_001691852.1//3.00E-10//DEAD/DEAH box helicase [Chlamydomonas reinhardtii] >gi|158278579|gb|EDP04342.1| DEAD/DEAH box helicase [Chlamydomonas reinhardtii]						nr +
Unigene115862_All	459	0.00	0.00	1.04	0.22	0.15	0.20	0.83	3.37	0.78	null	null		1.00E+01	7.49E-03		-5.33E-01	8.18E-01		-1.42E-01	9.52E-01		2.02E+00	1.30E-04	Up	-8.59E-02	9.43E-01									
Unigene115863_All	430	0.00	0.00	0.00	0.00	0.00	0.00	0.79	4.08	1.30	null	null		null	null		null	null		null	null		2.38E+00	4.38E-06	Up	7.22E-01	3.99E-01		Unigene115863_All//gi|42567541|ref|NP_195692.2|//2.00E-16//binding [Arabidopsis thaliana] >gi|53749172|gb|AAU90071.1| At4g39820 [Arabidopsis thaliana]	Unigene115863_All//2.00E-16//AT4G39820| binding	Unigene115863_All//6.00E-22//gi|21090904|gb|BQ403217.1|BQ403217				nr -
Unigene115864_All	454	0.00	0.00	0.00	0.00	0.00	0.00	0.56	3.50	0.00	null	null		null	null		null	null		null	null		2.65E+00	3.44E-06	Up	-9.13E+00	3.04E-02		Unigene115864_All//sp|Q5SQX7|YL881_MIMIV//4.00E-07//Uncharacterized protein L881 OS=Acanthamoeba polyphaga mimivirus GN=MIMI_L881 PE=4 SV=1						swissprot +
Unigene115865_All	790	0.00	0.00	0.00	0.00	0.00	0.00	1.34	3.54	0.00	null	null		null	null		null	null		null	null		1.41E+00	5.57E-05	Up	-1.04E+01	6.72E-08	Down	Unigene115865_All//gi|81074776|gb|AB855374.1|//2.00E-92//ribosomal protein L2-like [Solanum tuberosum]	Unigene115865_All//1.00E-80//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene115865_All//2.00E-20//gi|78337755|gb|DT558029.1|DT558029		ko03010|Ribosome		nr -
Unigene115867_All	467	0.00	0.00	0.00	0.00	0.00	0.00	0.18	2.24	0.00	null	null		null	null		null	null		null	null		3.63E+00	1.71E-05	Up	-7.50E+00	3.59E-01									ESTscan -
Unigene115871_All	761	0.00	0.87	0.00	0.72	1.00	0.47	0.56	2.31	1.83	9.76E+00	6.26E-04	Up	null	null		4.67E-01	6.07E-01		-6.01E-01	5.66E-01		2.05E+00	3.20E-05	Up	1.72E+00	1.09E-03				Unigene115871_All//0.00E+00//CA993885					
Unigene115873_All	539	0.00	0.00	0.00	0.00	0.00	0.00	1.49	2.79	0.00	null	null		null	null		null	null		null	null		9.05E-01	6.27E-02		-1.05E+01	4.43E-06	Down	Unigene115873_All//gi|226501140|ref|NP_001152197.1|/3.00E-10//LOC100285835 [Zea mays] >gi|195653721|gb|ACG46328.1| keratin-associated protein 5-4 [Zea mays]						nr +
Unigene115874_All	493	0.00	0.00	0.00	0.00	0.00	0.00	2.14	5.34	0.16	null	null		null	null		null	null		null	null		1.32E+00	2.33E-04	Up	-3.73E+00	6.13E-06	Down	Unigene115874_All//gi|115467796|ref|NP_001057497.1|/2.00E-10//Os06g0316800 [Oryza sativa Japonica Group] >gi|113595537|dbj|BAF19411.1| Os06g0316800 [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr +
Unigene115875_All	775	0.00	0.00	0.00	0.00	0.00	0.00	0.11	2.64	0.00	null	null		null	null		null	null		null	null		4.60E+00	6.19E-12	Up	-6.77E+00	3.59E-01									ESTscan +
Unigene115876_All	515	0.20	0.49	0.00	0.00	0.07	0.18	0.33	1.79	4.87	1.28E+00	4.35E-01		-7.67E+00	3.97E-01		6.06E+00	8.35E-01		7.45E+00	4.79E-01		2.44E+00	1.33E-03		3.89E+00	2.29E-13	Up	Unigene115876_All//gi|297720115|ref|NP_001172419.1|/1.00E-08//Os01g0558700 [Oryza sativa Japonica Group] >gi|255673363|dbj|BAH91149.1| Os01g0558700 [Oryza sativa Japonica Group]		Unigene115876_All//0.00E+00//C0102469				nr +
Unigene115877_All	474	0.00	0.00	0.67	0.74	0.07	1.05	0.45	12.79	1.26	null	null		9.40E+00	4.53E-02		-3.34E+00	4.07E-02		5.11E-01	6.41E-01		4.84E+00	1.65E-35	Up	1.50E+00	7.88E-02		Unigene115877_All//8.00E-22//TNFR/CDC7/30/40/95 cysteine-rich region [Medicago truncatula]	Unigene115877_All//9.00E-14//AT1G12064| unknown protein	Unigene115877_All//1.00E-10//TC168397				nr +
Unigene115879_All	516	0.00	0.00	0.00	0.00	0.00	0.00	0.66	2.59	0.54	null	null		null	null		null	null		null	null		1.98E+00	5.28E-04	Up	-2.79E-01	7.81E-01		Unigene115879_All//gi|157093563|gb|ABV22436.1|//1.00E-36//cysteine proteinase [Oxyrrhis marina]	Unigene115879_All//7.00E-33//AT5G43060| cysteine proteinase, putative / thiol protease, putative					nr -
Unigene115880_All	1142	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.28	0.00	null	null		null	null		null	null		null	null		1.21E+01	1.92E-34	Up	null	null		Unigene115880_All//gi|1155068|emb|CAA64425.1|//3.00E-07//cell wall-plasma membrane linker protein [Brassica napus]						nr -
Unigene115881_All	548	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.05	0.00	null	null		null	null		null	null		null	null		1.16E+01	8.76E-12	Up	null	null		Unigene115881_All//gi|38325811|gb|AAR17078.1|//5.00E-71//heat shock protein 70-1 [Nicotiana tabacum]	Unigene115881_All//5.00E-41//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene115881_All//6.00E-07//EX170481		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr +
Unigene115882_All	3348	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.10	0.77	null	null		null	null		null	null		null	null		-2.10E+00	1.56E-04	Down	8.49E-01	1.25E-02		Unigene115882_All//gi|115435462|ref|NP_001042489.1|/0.00E+00//Os01g0229700 [Oryza sativa Japonica Group] >gi|113532020|dbj|BAF04403.1| Os01g0229700 [Oryza sativa Japonica Group]	Unigene115882_All//1.00E-46//AT3G06880| nucleotide binding	Unigene115882_All//0.00E+00//gi|164312745|gb|ES848791.1|ES848791		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene115886_All	564	0.00	0.00	0.00	0.00	0.00	0.00	0.60	2.74	0.07	null	null		null	null		null	null		null	null		2.19E+00	5.11E-05	Up	-3.09E+00	3.92E-02									
Unigene115887_All	530	0.00	0.00	0.00	0.00	0.00	0.00	0.56	3.39	0.00	null	null		null	null		null	null		null	null		2.60E+00	8.32E-07	Up	-9.13E+00	1.58E-02		Unigene115887_All//gi|298711872|emb|CBJ32893.1|//3.00E-72//EEF1A2, eukaryotic translation elongation factor 1 alpha [Ectocarpus siliculosus] >gi|298711873|emb|CBJ32894.1| EEF1A1, eukaryotic translation elongation factor 1 alpha [Ectocarpus siliculosus]	Unigene115887_All//1.00E-65//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene115887_All//3.00E-18//TC173271				nr -
Unigene115889_All	1158	0.00	0.00	0.00	0.00	0.00	0.00	0.62	0.00	0.00	null	null		null	null		null	null		null	null		-9.28E+00	3.27E-05	Down	-9.28E+00	1.78E-05	Down	Unigene115889_All//gi|297841521|ref|XP_002888642.1|/9.00E-80//S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334483|gb|EFH64901.1| S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene115889_All//1.00E-67//AT5G37990| S-adenosylmethionine-dependent methyltransferase/ methyltransferase			ko00592|alpha-Linolenic acid metabolism		nr -
Unigene115890_All	689	0.00	0.00	0.00	0.00	0.00	0.00	0.43	1.82	0.00	null	null		null	null		null	null		null	null		2.08E+00	5.41E-04	Up	-8.75E+00	1.58E-02		Unigene115890_All//gi|5902592|gb|AB055566.1|AF110784_1/1.00E-36//protein disulfide isomerase precursor [Volvox carteri f. nagariensis] >gi|300257635|gb|EFJ41881.1| protein disulfide isomerase 1 [Volvox carteri f. nagariensis]	Unigene115890_All//7.00E-37//AT5G60640| ATPDIL1-4 (PDI-LIKE 1-4); protein disulfide isomerase			ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene115892_All	686	0.00	0.00	0.00	0.00	0.00	0.00	1.85	2.13	0.00	null	null		null	null		null	null		null	null		2.06E-01	6.81E-01		-1.09E+01	1.99E-09	Down								
Unigene115893_All	756	0.00	0.00	0.00	0.00	0.00	0.00	0.78	3.48	0.00	null	null		null	null		null	null		null	null		2.15E+00	6.92E-08	Up	-9.61E+00	1.41E-04	Down	Unigene115893_All//gi|30687814|ref|NP_849698.1|//8.00E-74//GRF10 (GENERAL REGULATORY FACTOR 10); ATP binding / protein binding / protein phosphorylated amino acid binding [Arabidopsis thaliana] >gi|9392684|gb|AAF87261.1|AC068562_8 Identical to 14-3-3 protein GF14 epsilon (GRF10) from Arabidopsis thaliana gb|AF145302 and contains a 14-3-3 protein PF|00244 domain. ESTs gb|H37302, gb|T43075, gb|T88323, gb|T41936, gb|R87021, gb|N57965, gb|A1994245, gb|Z46557, gb|T20402, gb|T44175, gb|T88028 come from this gene >gi|222423202|dbj|BAH19578.1| AT1G22300 [Arabidopsis thaliana]	Unigene115893_All//2.00E-57//AT1G22300| GRF10 (GENERAL REGULATORY FACTOR 10); ATP binding / protein binding / protein phosphorylated amino acid binding					nr +
Unigene115894_All	776	0.00	0.00	0.00	0.00	0.00	0.00	0.11	5.22	0.10	null	null		null	null		null	null		null	null		5.58E+00	1.78E-25	Up	-8.59E-02	9.73E-01									ESTscan -
Unigene115895_All	834	0.00	0.00	0.00	0.00	0.00	0.00	0.15	3.46	0.00	null	null		null	null		null	null		null	null		4.51E+00	1.91E-16	Up	-7.25E+00	2.00E-01									ESTscan +
Unigene115896_All	830	0.00	0.00	0.00	0.00	0.00	0.00	0.87	1.36	0.00	null	null		null	null		null	null		null	null		6.51E-01	2.66E-01		-9.76E+00	1.78E-05	Down	Unigene115896_All//gi|299470262|emb|CBN79566.1|//5.00E-14//RecName: Full=Spherulin-4; Flags: Precursor [Ectocarpus siliculosus]						nr +
Unigene115897_All	1249	0.00	0.00	0.00	0.00	0.00	0.00	1.02	8.37	1.40	null	null		null	null		null	null		null	null		3.04E+00	8.82E-43	Up	4.67E-01	2.88E-01		Unigene115897_All//gi|15242438|ref|NP_196515.1|/2.00E-94//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|7671436|emb|CAB89377.1| periaxin-like protein [Arabidopsis thaliana]	Unigene115897_All//6.00E-05//AT1G10390| nucleoporin family protein	Unigene115897_All//4.00E-53//DW500838		ko03040|Spliceosome//ko03018|RNA degradation		nr +
Unigene1159_All	2546	0.49	0.08	0.08	1.15	0.95	2.00	8.57	5.91	8.23	-2.63E+00	3.16E-04	Down	-2.56E+00	6.99E-04	Down	-2.86E-01	4.66E-01		7.96E-01	2.52E-03		-5.36E-01	2.88E-07		-5.81E-02	6.35E-01		Unigene1159_All//gi|4235644|gb|AAD13304.1|//5.00E-51//polyprotein [Solanum lycopersicum]		Unigene1159_All//0.00E+00//TC171648			GO:0003676//GO:0006259//GO:0016740//GO:0019538//GO:0043229//GO:0046872	nr -
Unigene11590_All	2947	0.27	1.03	0.63	0.73	0.65	0.97	2.01	1.76	2.46	1.95E+00	1.22E-06	Up	1.25E+00	1.41E-02		-1.51E-01	7.68E-01		4.10E-01	3.09E-01		-1.92E-01	4.28E-01		2.93E-01	1.38E-01		Unigene11590_All//gi|15239902|ref|NP_199169.1|/1.00E-108//meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana] >gi|30694322|ref|NP_851125.1| meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana] >gi|19310439|gb|AAL84956.1| AT5g43560/K9D7_6 [Arabidopsis thaliana]	Unigene11590_All//3.00E-133//AT5G43560| meprin and TRAF homology domain-containing protein / MATH domain-containing protein	Unigene11590_All//0.00E+00//TC176246				nr -
Unigene115938_All	201	0.00	0.00	0.00	0.00	0.00	0.00	29.45	9.98	4.96	null	null		null	null		null	null		null	null		-1.56E+00	3.54E-11	Down	-2.57E+00	2.08E-21	Down								
Unigene115957_All	202	0.78	0.50	0.26	0.00	0.34	1.12	11.51	8.69	0.99	-6.31E-01	7.28E-01		-1.56E+00	5.34E-01		8.41E+00	6.13E-01		1.01E+01	1.19E-01		-4.06E-01	3.06E-01		-3.55E+00	7.48E-12	Down			Unigene115957_All//1.00E-101//gi|164354782|gb|ES805273.1|ES805273					
Unigene115964_All	202	0.00	0.00	0.00	0.00	0.00	0.00	23.02	3.72	0.99	null	null		null	null		null	null		null	null		-2.63E+00	8.61E-17	Down	-4.55E+00	1.75E-27	Down								
Unigene115965_All	202	0.00	0.50	0.79	0.25	0.00	0.00	2.09	8.90	3.75	8.97E+00	3.89E-01		9.63E+00	2.39E-01		-7.95E+00	5.60E-01		-7.95E+00	6.41E-01		2.09E+00	2.01E-05	Up	8.40E-01	2.38E-01				Unigene115965_All//1.00E-12//TC164872					
Unigene115967_All	202	0.00	0.00	0.00	0.00	0.00	0.00	2.72	0.83	0.00	null	null		null	null		null	null		null	null		-1.72E+00	7.23E-02		-1.14E+01	2.81E-04	Down	Unigene115967_All//gi|298706692|emb|CBJ34222.1|//1.00E-07//conserved unknown protein [Ectocarpus siliculosus] >gi|298713886|emb|CBJ33762.1| conserved unknown protein [Ectocarpus siliculosus]		Unigene115967_All//1.00E-15//TC148521				nr +
Unigene1160_All	1238	14.41	38.10	20.60	9.29	11.63	13.39	8.88	7.97	22.30	1.40E+00	3.20E-58	Up	5.16E-01	3.33E-06		3.23E-01	2.96E-02		5.27E-01	8.33E-05		-1.56E-01	3.84E-01		1.33E+00	1.15E-39	Up	Unigene1160_All//gi|15451126|gb|AAK96834.1|//1.00E-107//unknown protein [Arabidopsis thaliana]	Unigene1160_All//1.00E-108//AT1G70480| unknown protein	Unigene1160_All//0.00E+00//gi|78336205|gb|DT556479.1|DT556479			GO:0005488	nr -
Unigene116005_All	204	0.00	0.00	0.00	1.95	3.38	1.99	2.28	8.40	6.05	null	null		null	null		7.89E-01	4.04E-01		2.85E-02	9.85E-01		1.88E+00	1.20E-04	Up	1.41E+00	9.74E-03		Unigene116005_All//gi|6651292|gb|AAF22256.1|//8.00E-24//myb-related transcription factor [Pimpinella brachycarpa]	Unigene116005_All//1.00E-24//AT4G22680| MYB85 (myb domain protein 85); DNA binding / transcription activator/ transcription factor	Unigene116005_All//2.00E-51//gi|78326281|gb|DT546555.1|DT546555	MYB			nr -
Unigene116009_All	204	0.00	0.00	0.00	0.00	0.00	0.00	1.04	31.96	0.78	null	null		null	null		null	null		null	null		4.95E+00	1.31E-38	Up	-4.08E-01	7.56E-01									
Unigene116016_All	204	0.00	0.00	0.00	0.73	1.01	0.00	0.00	3.28	0.59	null	null		null	null		4.67E-01	8.25E-01		-9.52E+00	2.34E-01		1.17E-01	7.64E-05	Up	9.19E+00	2.43E-01				Unigene116016_All//1.00E-49//ES809411					
Unigene116041_All	205	0.00	0.00	0.00	0.00	0.00	0.00	59.81	15.09	2.53	null	null		null	null		null	null		null	null		-1.99E+00	6.50E-31	Down	-4.57E+00	8.01E-72	Down			Unigene116041_All//2.00E-07//TC171709					

Unigene11605_A11	2133	0.93	1.00	0.62	0.68	1.42	1.61	2.62	2.02	3.94	9.81E-02	8.17E-01		-5.79E-01	2.40E-01		1.07E+00	2.31E-03		1.25E+00	2.28E-04	Up	-3.75E-01	1.10E-01		5.91E-01	6.41E-04		Unigene11605_A11//gi|18390971|ref|NP_563834.1|//1.00E-169//SNF4 (HOMOLOG OF YEAST SUCROSE NONFERMENTING 4); protein kinase activator [Arabidopsis thaliana] >gi|16612255|gb|AAL27498.1|AF43982 6_1 At1g09020/F7G19_11 [Arabidopsis thaliana] >gi|23308443|gb|AAN18191.1| At1g09020/F7G19_11 [Arabidopsis thaliana] >gi|75037070|gb|ABA12450.1| AKINbetagamma [Arabidopsis thaliana]	Unigene11605_A11//9.00E-171//AT1G09020| SNF4 (HOMOLOG OF YEAST SUCROSE NONFERMENTING 4); protein kinase activator	Unigene11605_A11//0.00E+00//TC145866				nr +
Unigene116050_A11	206	0.00	0.00	0.00	0.00	0.33	0.00	0.00	4.06	0.39	null	null		null	null		8.39E+00	6.13E-01		null	null		1.20E+01	5.54E-06	Up	8.60E+00	4.05E-01				Unigene116050_A11//2.00E-07//FL576731				
Unigene11606_A11	662	5.85	5.05	6.68	11.89	12.28	9.14	10.03	6.06	4.21	-2.11E-01	5.23E-01		1.91E-01	5.57E-01		4.62E-02	8.49E-01		-3.79E-01	7.74E-02		-7.26E-01	3.45E-04		-1.25E+00	1.88E-09	Down			Unigene11606_A11//2.00E-90//DW504126				
Unigene116060_A11	206	123.44	59.03	109.86	30.71	41.12	33.76	0.41	1.62	0.58	-1.06E+00	7.19E-21	Down	-1.68E-01	1.68E-01		4.21E-01	3.36E-02		1.37E-01	6.32E-01		1.98E+00	1.45E-01		4.99E-01	8.08E-01		Unigene116060_A11//gi|21616072|emb|CAC87810.2|//1.00E-06//Tic62 protein [Pisum sativum]						nr +
Unigene116066_A11	207	1.01	0.73	0.77	2.41	2.16	1.53	4.90	2.22	0.19	-4.61E-01	7.58E-01		-3.90E-01	8.08E-01		-1.54E-01	8.50E-01		-6.56E-01	5.50E-01		-1.14E+00	6.62E-02		-4.67E+00	1.72E-06	Down			Unigene116066_A11//3.00E-93//gi|109889353|gb|DW518321.1|DW518321				
Unigene11609_A11	1581	5.66	1.06	1.68	17.39	12.22	8.00	26.37	11.95	19.20	-2.42E+00	1.09E-23	Down	-1.75E+00	4.09E-15	Down	-5.09E-01	7.16E-08		-1.12E+00	2.80E-26	Down	-1.14E+00	4.33E-16	Down	-4.58E-01	2.28E-10		Unigene11609_A11//gi|224092698|ref|XP_002309702.1|//2.00E-38//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222855628|gb|EEE93225.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene11609_A11//5.00E-07//AT1G69545| leucine-rich repeat family protein	Unigene11609_A11//0.00E+00//TC130797				nr -
Unigene116093_A11	208	0.00	0.49	0.00	0.00	0.00	0.00	1.22	6.23	31.41	8.93E+00	3.89E-01		null	null		null	null		null	null		2.35E+00	1.25E-04	Up	4.69E+00	3.16E-38	Up	Unigene116093_A11//gi|15234693|ref|NP_193934.1|//5.00E-08//F-box family protein [Arabidopsis thaliana]	Unigene116093_A11//2.00E-10//AT4G04480| LOCATED IN: chloroplast; EXPRESSED IN: flower, pollen tube; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT4G22030.1); Has 51 Blast hits to 51 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene1161_A11	1516	14.98	43.02	18.44	7.52	14.17	15.91	6.89	9.70	19.47	1.52E+00	1.47E-90	Up	3.00E-01	5.71E-03		9.14E-01	4.64E-16		1.08E+00	1.56E-21	Up	4.94E-01	1.42E-04		1.50E+00	1.23E-50	Up	Unigene1161_A11//gi|154511126|gb|AAK96834.1|//1.00E-103//Unknown protein [Arabidopsis thaliana]	Unigene1161_A11//6.00E-95//AT1G70480| unknown protein	Unigene1161_A11//0.00E+00//TC162925		GO:0005488		nr +
Unigene11610_A11	963	7.93	0.89	3.26	17.95	13.70	8.07	23.09	11.54	13.32	-3.15E+00	1.03E-26	Down	-1.28E+00	1.87E-08	Down	-3.90E-01	2.06E-03		-1.15E+00	1.67E-17	Down	-1.00E+00	2.80E-20	Down	-7.94E-01	1.99E-14		Unigene11610_A11//gi|224069142|ref|XP_002302910.1|//2.00E-20//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222844636|gb|EEE82183.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene11610_A11//6.00E-06//AT1G69545| leucine-rich repeat family protein	Unigene11610_A11//0.00E+00//TC130797				nr +
Unigene116102_A11	209	0.00	0.00	0.00	0.00	0.00	0.00	47.34	14.00	0.76	null	null		null	null		null	null		null	null		-1.76E+00	2.31E-21	Down	-5.96E+00	6.24E-66	Down								
Unigene116116_A11	209	0.00	0.00	0.00	0.24	0.00	0.00	1.42	8.40	1.72	null	null		null	null		-7.90E+00	5.60E-01		-7.90E+00	6.41E-01		2.57E+00	1.41E-06	Up	2.77E-01	7.87E-01				Unigene116116_A11//2.00E-85//TC141238				
Unigene11612_A11	2168	3.23	1.43	2.24	10.80	7.78	6.37	7.82	6.01	6.39	-1.18E+00	2.46E-07	Down	-5.33E-01	2.19E-02		-4.73E-01	5.52E-06		-7.61E-01	5.51E-12		-3.79E-01	1.81E-03		-2.90E-01	1.55E-02		Unigene11612_A11//gi|224092702|ref|XP_002309704.1|//9.00E-96//nbs-lrr resistance protein [Populus trichocarpa] >gi|222855680|gb|EEE93227.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene11612_A11//4.00E-40//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene11612_A11//0.00E+00//TC177573		ko04626|Plant-pathogen interaction		nr -
Unigene11613_A11	3840	20.11	43.32	19.84	57.87	79.86	67.38	48.34	71.30	115.88	1.11E+00	7.63E-141	Up	-1.93E-02	7.84E-01		4.65E-01	5.27E-69		2.20E-01	3.53E-13		5.61E-01	1.71E-88		1.26E+00	0.00E+00	Up	Unigene11613_A11//gi|224106445|ref|XP_002311468.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222850576|gb|EEE88123.1| GRAS family transcription factor [Populus trichocarpa]	Unigene11613_A11//1.00E-149//AT3G46600| scarecrow transcription factor family protein	Unigene11613_A11//0.00E+00//TC170524	GRAS	ko03018|RNA degradation		nr +
Unigene116131_A11	210	0.00	0.00	0.00	0.00	0.00	0.00	0.20	4.58	2.47	null	null		null	null		null	null		null	null		4.51E+00	8.92E-06	Up	3.61E+00	4.19E-03				Unigene116131_A11//2.00E-07//TC177400				
Unigene116147_A11	211	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.96	0.57	null	null		null	null		null	null		null	null		1.20E+01	5.54E-06	Up	9.15E+00	2.43E-01				Unigene116147_A11//2.00E-07//EX166575				
Unigene116157_A11	212	10.86	10.99	11.05	9.40	6.01	11.08	4.19	11.63	8.46	1.79E-02	9.86E-01		2.54E-02	9.71E-01		-6.45E-01	1.53E-01		2.37E-01	6.36E-01		1.47E+00	9.56E-05	Up	1.01E+00	1.67E-02				Unigene116157_A11//3.00E-65//TC145750				
Unigene116169_A11	212	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.34	0.00	null	null		null	null		null	null		null	null		1.21E+01	1.48E-06	Up	null	null									
Unigene116179_A11	213	0.00	0.00	0.00	0.00	0.00	0.21	1.39	2.94	6.73	null	null		null	null		null	null		7.73E+00	7.00E-01		1.08E+00	1.99E-01		2.28E+00	4.94E-05	Up			Unigene116179_A11//7.00E-51//TC150953				
Unigene11618_A11	1427	3.63	2.59	2.05	37.32	32.63	28.90	7.02	2.28	3.02	-4.86E-01	6.66E-02		-8.23E-01	2.70E-03		-1.94E-01	6.74E-03		-3.69E-01	1.36E-07		-1.62E+00	2.35E-19	Down	-1.22E+00	2.59E-13	Down	Unigene11618_A11//gi|297833894|ref|XP_002884829.1|//1.00E-164//steroid hormone receptor/ transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297330669|gb|EFH61088.1| steroid hormone receptor/ transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene11618_A11//0.00E+00//AT2G40320| unknown protein	Unigene11618_A11//0.00E+00//TC173302				nr -
Unigene11619_A11	1555	2.22	2.93	3.32	23.29	20.77	15.68	8.24	2.53	4.87	4.01E-01	1.65E-01		5.81E-01	3.56E-02		-1.65E-01	7.87E-02		-5.70E-01	3.54E-11		-1.71E+00	2.50E-26	Down	-7.59E-01	4.10E-08		Unigene11619_A11//gi|297833894|ref|XP_002884829.1|//1.00E-143//steroid hormone receptor/ transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297330669|gb|EFH61088.1| steroid hormone receptor/ transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene11619_A11//4.00E-149//AT2G40320| unknown protein	Unigene11619_A11//0.00E+00//TC135572				nr -
Unigene116197_A11	214	0.49	0.00	0.50	1.86	0.64	1.06	91.87	61.13	18.43	-8.93E+00	3.75E-01		2.54E-02	1.00E+00		-1.53E+00	2.06E-01		-8.20E-01	5.07E-01		-5.88E-01	1.11E-07		-2.32E+00	1.97E-61	Down	Unigene116197_A11//gi|211906506|gb|ACJ11746.1|//1.00E-11//luminal binding protein [Gossypium hirsutum]	Unigene116197_A11//5.00E-13//AT5G42020| BIP2; ATP binding	Unigene116197_A11//1.00E-42//TC165456		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr -
Unigene116211_A11	215	0.00	0.94	0.00	1.62	2.72	0.42	1.38	4.67	6.49	9.88E+00	1.37E-01		null	null		7.47E-01	4.81E-01		-1.95E+00	1.96E-01		1.76E+00	7.67E-03		2.24E+00	7.92E-05	Up			Unigene116211_A11//3.00E-105//CO103526				
Unigene116213_A11	215	0.00	0.00	0.00	0.00	0.00	0.00	117.01	294.90	122.67	null	null		null	null		null	null		null	null		1.33E+00	1.32E-88	Up	6.81E-02	5.52E-01				Unigene116213_A11//8.00E-29//TC159659				ESTscan -
Unigene116222_A11	216	0.73	1.41	0.49	0.00	0.00	4.60	1.17	3.68	0.00	9.54E-01	5.04E-01		-5.60E-01	7.76E-01		null	null		1.22E-01	6.15E-06	Up	1.65E+00	2.88E-02		-1.02E+01	3.01E-02								
Unigene116224_A11	216	0.00	0.00	0.00	0.00	0.00	0.00	4.89	0.77	0.18	null	null		null	null		null	null		null	null		-2.66E+00	2.25E-04	Down	-4.73E+00	8.85E-07	Down								
Unigene116226_A11	216	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.64	0.00	null	null		null	null		null	null		null	null		1.22E+01	3.93E-07	Up	null	null									
Unigene11624_A11	4341	5.60	12.94	9.54	5.34	7.64	7.84	12.56	17.83	19.04	1.21E+00	4.71E-55	Up	7.68E-01	6.55E-19		5.18E-01	2.08E-09		5.56E-01	5.00E-10		5.05E-01	2.56E-21		6.00E-01	1.86E-31		Unigene11624_A11//gi|186529839|ref|NP_001119383.1|//1.00E-110//NLI interacting factor (NIF) family protein [Arabidopsis thaliana]	Unigene11624_A11//1.00E-111//AT5G46410| NLI interacting factor (NIF) family protein	Unigene11624_A11//0.00E+00//TC167376				nr -
Unigene116240_A11	217	0.96	3.97	0.25	3.21	2.38	2.50	2.34	3.27	8.08	2.04E+00	1.59E-02		-1.97E+00	3.82E-01		-4.33E-01	6.06E-01		-3.64E-01	6.81E-01		4.86E-01	5.42E-01		1.79E+00	1.28E-04	Up			Unigene116240_A11//2.00E-20//AW186738				
Unigene116252_A11	217	0.48	7.01	1.23	1.61	0.79	0.62	1.95	3.08	1.29	3.86E+00	1.23E-06	Up	1.35E+00	4.09E-01		-1.02E+00	4.23E-01		-1.36E+00	3.37E-01		6.61E-01	4.02E-01		-6.00E-01	5.53E-01		Unigene116252_A11//gi|111038269|gb|ABH03531.1|//1.00E-11//class II knotted-like homeobox protein [Prunus persica] >gi|215983122|gb|ACJ71731.1| class II knotted-like homeobox transcription factor [Prunus persica]	Unigene116252_A11//5.00E-13//AT5G25220| KNAT3 (KNOTTED1-LIKE HOMEOBOX GENE 3); transcription activator/ transcription factor	Unigene116252_A11//4.00E-55//gi|11201779|gb|BF270784.1|BF270784	HB			nr +
Unigene116278_A11	220	0.00	2.30	0.00	0.45	0.00	0.21	0.96	4.75	0.91	1.12E+01	4.05E-03		null	null		-8.82E+00	3.15E-01		-1.14E+00	6.78E-01		2.31E+00	8.56E-04	Up	-8.58E-02	9.61E-01									
Unigene116279_A11	220	16.89	4.61	8.47	49.36	61.67	29.97	26.52	8.93	28.79	-1.87E+00	1.28E-07	Down	-9.95E-01	2.95E-03		3.21E-01	3.73E-02		-7.20E-01	1.94E-05		-1.57E+00	4.03E-11	Down	1.19E-01	6.04E-01				Unigene116279_A11//3.00E-65//TC129604				
Unigene116297_A11	220	0.00	0.00	0.00	0.00	0.00	0.00	0.38	6.84	4.71	null	null		null	null		null	null		null	null		4.15E+00	2.17E-08	Up	3.61E+00	1.38E-05	Up								
Unigene1163_A11	3626	2.40	0.88	1.60	4.40	3.41	3.18	8.12	3.82	4.38	-1.44E+00	7.73E-12	Down	-5.82E-01	4.37E-03		-3.67E-01	6.26E-03		-4.69E-01	6.29E-04		-1.09E+00	2.08E-30	Down	-8.89E-01	1.33E-22		Unigene1163_A11//gi|83423282|emb|CAI64810.1|//0.00E+00//nucleoporin [Lotus japonicus] >gi|83423284|emb|CAI64811.1| nucleoporin [Lotus japonicus]	Unigene1163_A11//0.00E+00//AT3G05120| LOCATED IN: chloroplast; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Nup133, N-terminal (InterPro:IPR014908); Has 103 Blast hits to 103 proteins in 31 species: Archae - 0; Bacteria - 0; Metazoa - 79; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene1163_A11//0.00E+00//TC168837		GO:0005506//GO:0016491		nr +
Unigene116313_A11	221	0.24	1.60	0.48	0.45	0.00	0.20	0.00	1.89	4.33	2.76E+00	9.60E-02		1.03E+00	7.04E-01		-8.82E+00	3.15E-01		-1.14E+00	6.78E-01		1.09E+01	3.65E-03		1.21E+01	5.69E-07	Up								
Unigene116319_A11	222	0.00	0.00	0.00	0.67	0.31	0.20	530.41	113.53	188.43	null	null		null	null		-1.12E+00	5.84E-01		-1.73E+00	5.02E-01		-2.22E+00	0.00E+00	Down	-1.49E+00	2.26E-200	Down	Unigene116319_A11//gi|87240949|gb|AB032807.1|//5.00E-36//Major intrinsic protein [Medicago truncatula]	Unigene116319_A11//2.00E-37//AT5G60660| PIP2;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;4); water channel	Unigene116319_A11//4.00E-120//gi|48792282|gb|CO093596.1|CO093596				nr -
Unigene11632_A11	2894	0.49	1.54	1.80	1.95	2.09	1.50	1.74	2.53	2.52	1.66E+00	1.15E-07	Up	1.89E+00	5.24E-10	Up	1.07E-01	7.30E-01		-3.77E-01	1.54E-01		5.40E-01	5.19E-03		5.35E-01	4.36E-03		Unigene11632_A11//gi|267631890|gb|ACY78680.1|//0.00E+00//calcium-dependent protein kinase 1 [Panax ginseng]	Unigene11632_A11//3.00E-179//AT4G04720| CPK21; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene11632_A11//0.00E+00//TC130026		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0016020//GO:0032559//GO:0046872	nr -
Unigene116324_A11	222	31.35	19.40	33.82	44.65	18.92	46.38	1.52	1.88	1.26	-6.92E-01	1.79E-03		1.10E-01	6.24E-01		-1.24E+00	7.32E-13	Down	5.49E-02	7.95E-01		3.05E-01	7.58E-01		-2.78E-01	7.81E-01				Unigene116324_A11//3.00E-47//CO099551				
Unigene116329_A11	222	0.00	0.00	0.00	0.00	0.16	0.00	0.57	21.46	0.36	null	null		null	null		7.28E+00	8.34E-01		null	null		5.23E+00	4.46E-29	Up	-6.71E-01	7.20E-01		Unigene116329_A11//gi|255543735|ref|XP_002512930.1|//5.00E-07//ribonuclease t2, putative [Ricinus communis] >gi|223547941|gb|EEF49433.1| ribonuclease t2, putative [Ricinus communis]	Unigene116329_A11//2.00E-06//AT1G14220| ribonuclease T2 family protein					nr -
Unigene11633_A11	1770	2.51	2.18	0.93	17.53	15.76	18.01	6.35	4.16	4.25	-2.08E-01	4.94E-01		-1.43E+00	5.11E-06	Down	-1.54E-01	1.44E-01		3.90E-02	7.32E-01		-6.13E-01	4.78E-05		-5.79E-01	8.08E-05		Unigene11633_A11//gi|224083155|ref|XP_002306955.1|//0.00E+00//calcium dependent protein kinase 27 [Populus trichocarpa] >gi|222856404|gb|EEE93951.1| calcium dependent protein kinase 27 [Populus trichocarpa]	Unigene11633_A11//0.00E+00//AT1G76040| CPK29; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene11633_A11//0.00E+00//ES824808		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0016020//GO:0032559//GO:0046872	nr -
Unigene11638_A11	1197	27.62	54.99	26.83	31.54	27.50	31.81	39.07	31.63	12.65	9.93E-01	4.34E-47		-4.24E-02	6.99E-01		-1.98E-01	2.46E-02		1.19E-02	9.30E-01		-3.04E-01	1.18E-05		-1.63E+00	1.11E-90	Down	Unigene11638_A11//gi|195608970|gb|ACG26315.1|//3.00E-75//calcyclin-binding protein [Zea mays]	Unigene11638_A11//3.00E-73//AT1G30070| SGS domain-containing protein	Unigene11638_A11//0.00E+00//gi|84149129|gb|DN780429.1|DN780429			GO:0016020	nr -
Unigene116384_A11	226	0.00	0.22	0.00	0.00	0.00	0.00	85.31	22.19	5.29	7.81E+00	6.19E-01		null	null		null	null		null	null		-1.94E+00	8.63E-47	Down	-4.01E+00	2.79E-103	Down	Unigene116384_A11//gi|48675345|dbj|BAD22820.1|//2.00E-27//nitrate transporter [Prunus persica]	Unigene116384_A11//4.00E-11//AT1G12110| NRT1.1; nitrate transmembrane transporter/ transporter	Unigene116384_A11//4.00E-77//TC165574				nr -
Unigene11639_A11	1506	11.95	8.34	12.09	15.94	17.67	13.02	16.56	5.02	9.13	-5.18E-01	6.77E-05		1.70E-02	9.19E-01		1.49E-01	2.09E-01		-2.93E-01	9.77E-03		-1.72E+00	3.25E-51	Down	-8.60E-01	2.66E-18		Unigene11639_A11//gi|222423637|dbj|BAH19787.1|//1.00E-168//AT2G34560 [Arabidopsis thaliana] >gi|222423638|dbj|BAH19806.1| AT2G34560 [Arabidopsis thaliana]	Unigene11639_A11//5.00E-169//AT2G34560| katanin, putative	Unigene11639_A11//0.00E+00//EX164211			GO:0032559//GO:0042623	nr +

Unigene116399_All	227	14827.08	6527.21	17871.35	3686.03	4388.91	3285.39	0.56	0.92	0.18	-1.18E+00	0.00E+00	Down	2.69E-01	7.59E-265		2.52E-01	3.71E-71		-1.66E-01	2.33E-24		7.20E-01	6.32E-01		-1.67E+00	4.78E-01		Unigene116399_All//gi|224072580|ref|XP_002303791.1//4.00E-25//light-harvesting complex I protein Lhca2 [Populus trichocarpa] >gi|222841223|gb|EEE78770.1| light-harvesting complex I protein Lhca2 [Populus trichocarpa]	Unigene116399_All//2.00E-09//AT3G61470| LHCA2; chlorophyll binding	Unigene116399_All//2.00E-125//TC131837		ko00196|Photosynthesis - antenna proteins		nr -
Unigene11640_All	2476	8.14	12.52	9.25	9.64	8.57	9.36	10.62	4.36	3.01	6.22E-01	1.58E-10		1.85E-01	1.47E-01		-1.70E-01	1.61E-01		-4.25E-02	7.48E-01		-1.29E+00	2.81E-35	Down	-1.82E+00	5.25E-60	Down	Unigene11640_All//gi|56201862|db|BAD73312.1|/1.00E-159//vacuolar protein sorting factor 4B-like [Oryza sativa Japonica Group] >gi|56201915|db|BAD73365.1| vacuolar protein sorting factor 4B-like [Oryza sativa Japonica Group]	Unigene11640_All//8.00E-159//AT2G34560| katanin, putative	Unigene11640_All//0.00E+00//gi|78333495|gb|DT553769.1|DT553769			GO:0032559//GO:0042623	nr +
Unigene11641_All	1428	3.22	3.16	3.10	125.27	106.34	96.84	102.15	262.36	60.04	-3.00E-02	9.30E-01		-5.90E-02	8.43E-01		-2.36E-01	9.50E-12		-3.71E-01	2.70E-24		1.36E+00	0.00E+00	Up	-7.67E-01	2.07E-84		Unigene11641_All//gi|224134154|ref|XP_002322769.1|//0.00E+00//coniferylaldehyde 5- hydroxylase [Populus trichocarpa] >gi|222836854|gb|EEE75247.1| coniferylaldehyde 5- hydroxylase [Populus trichocarpa]	Unigene11641_All//0.00E+00//AT4G36220| FAH1 (FERULIC ACID 5-HYDROXYLASE 1); ferulate 5-hydroxylase/ monooxygenase	Unigene11641_All//0.00E+00//DW225229		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016491	nr +
Unigene116417_All	228	0.00	0.44	0.00	0.00	0.00	0.00	0.74	4.03	4.19	8.80E+00	3.89E-01		null	null		null	null		null	null		2.44E+00	1.33E-03		2.50E+00	6.42E-04	Up	Unigene116417_All//gi|297737079|emb|CBI26280.3|//1.00E-10//unnamed protein product [Vitis vinifera]		Unigene116417_All//2.00E-26//gi|54121950|gb|CO497459.1|CO497459				nr +
Unigene116418_All	228	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10.27	0.17	null	null		null	null		null	null		null	null		1.33E+01	1.83E-16	Up	7.45E+00	6.46E-01								
Unigene11642_All	1863	3.43	4.13	2.77	79.95	70.44	63.35	6.29	1.97	27.71	2.71E-01	2.20E-01		-3.06E-01	2.39E-01		-1.83E-01	3.21E-06		-3.36E-01	6.26E-17		-1.67E+00	1.80E-23	Down	2.14E+00	3.89E-143	Up	Unigene11642_All//gi|47933890|gb|AAT38511.1|/0.00E+00//ferulate 5-hydroxylase [Camptotheca acuminata]	Unigene11642_All//0.00E+00//AT4G36220| FAH1 (FERULIC ACID 5-HYDROXYLASE 1); ferulate 5-hydroxylase/ monooxygenase	Unigene11642_All//0.00E+00//TC152108		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016491	nr -
Unigene116432_All	229	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.74	0.00	null	null		null	null		null	null		null	null		1.14E+01	1.47E-04	Up	null	null		Unigene116432_All//gi|114159828|gb|ABI53721.1|/2.00E-18//polyubiquitin [Porphyra yezoensis]	Unigene116432_All//2.00E-19//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene116432_All//1.00E-30//CD486028		ko03010|Ribosome		nr -
Unigene11644_All	2059	0.81	1.65	0.16	1.11	1.05	0.92	9.75	21.37	37.30	1.02E+00	2.66E-03		-2.39E+00	1.21E-04	Down	-7.90E-02	8.45E-01		-2.73E-01	5.68E-01		1.13E+00	7.16E-48	Up	1.94E+00	1.27E-186	Up	Unigene11644_All//gi|297818990|ref|XP_002877378.1|/0.00E+00//phosphatidate cytidylyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323216|gb|EFH53637.1| phosphatidate cytidylyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11644_All//0.00E+00//AT3G45040| phosphatidate cytidylyltransferase family protein	Unigene11644_All//0.00E+00//TC157004		ko00510|N-Glycan biosynthesis	GO:0016301//GO:0031224	nr -
Unigene116447_All	230	0.00	1.98	0.00	0.00	0.75	0.20	0.37	2.91	5.89	1.10E+01	7.44E-03		null	null		9.55E+00	2.27E-01		7.62E+00	6.99E-01		2.98E+00	2.86E-03		4.00E+00	1.31E-07	Up			Unigene116447_All//1.00E-104//CO108092				
Unigene116461_All	231	1.81	0.88	0.23	4.10	0.60	2.54	1.28	3.26	0.17	-1.05E+00	3.66E-01		-2.97E+00	6.46E-02		-2.78E+00	4.58E-04	Down	-6.89E-01	3.58E-01		1.35E+00	7.61E-02		-2.89E+00	6.77E-02		Unigene116461_All//gi|32362295|gb|AAP80175.1|/2.00E-12//At3g55350 [Arabidopsis thaliana]	Unigene116461_All//8.00E-14//AT3G55350| unknown protein					nr -
Unigene116463_All	231	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.52	0.00	null	null		null	null		null	null		null	null		1.21E+01	2.02E-07	Up	null	null								
Unigene116465_All	232	0.45	10.05	5.51	0.86	1.48	3.11	2.37	5.58	1.37	4.48E+00	7.48E-11	Up	3.61E+00	3.41E-05	Up	7.89E-01	5.96E-01		1.86E+00	4.71E-02		1.24E+00	2.18E-02		-7.86E-01	3.62E-01				Unigene116465_All//7.00E-91//TC144883				
Unigene116466_All	232	0.00	0.00	0.00	0.00	0.00	0.00	4.37	7.03	0.69	null	null		null	null		null	null		null	null		6.84E-01	1.42E-01		-2.67E+00	1.94E-01	Down								
Unigene116467_All	232	0.68	1.97	0.92	0.00	0.15	0.00	4.01	10.09	1.37	1.54E+00	1.96E-01		4.40E-01	7.76E-01		7.21E+00	8.34E-01		null	null		1.33E+00	5.14E-04	Up	-1.55E+00	1.68E-02				Unigene116467_All//5.00E-126//TC173535				
Unigene116472_All	232	0.00	0.87	0.23	1.50	0.30	0.19	8.75	18.38	24.56	9.77E+00	1.37E-01		7.84E+00	6.39E-01		-2.34E+00	1.01E-01		-2.95E+00	8.31E-02		1.07E+00	5.70E-05	Up	1.49E+00	2.31E-10	Up	Unigene116472_All//gi|224130846|ref|XP_002320939.1|/1.00E-13//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222861712|gb|EEE99254.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene116472_All//8.00E-08//AT3G62150| PGP21 (P-GLYCOPROTEIN 21); ATPase, coupled to transmembrane movement of substances	Unigene116472_All//4.00E-77//gi|73864444|gb|DT467183.1|DT467183		ko02010|ABC transporters		nr +
Unigene116477_All	232	0.00	0.00	0.00	0.00	0.00	0.00	3.83	2.70	0.52	null	null		null	null		null	null		null	null		-5.02E-01	4.60E-01		-2.89E+00	3.04E-04	Down	Unigene116477_All//gi|168068591|ref|XP_001786133.1|/4.00E-09//predicted protein [Physcomitrella patens subsp. patens] >gi|162662081|gb|EDQ49057.1| predicted protein [Physcomitrella patens subsp. patens]		Unigene116477_All//1.00E-15//gi|109830702|gb|DW229261.1|DW229261				nr -
Unigene116484_All	232	0.00	0.66	0.00	0.21	0.89	0.97	0.91	5.95	0.69	9.36E+00	2.36E-01		null	null		2.05E+00	3.95E-01		2.18E+00	3.23E-01		2.71E+00	1.42E-05	Up	-4.08E-01	7.56E-01				Unigene116484_All//2.00E-125//DW484004				ESTscan +
Unigene11649_All	536	0.00	0.38	2.19	0.84	0.58	0.76	1.34	0.86	0.22	8.56E+00	1.37E-01		1.11E+01	1.77E-06	Up	-5.33E-01	5.96E-01		-1.41E-01	9.00E-01		-6.45E-01	4.01E-01		-2.59E+00	2.81E-03		Unigene11649_All//gi|6739629|gb|AAF22340.1|AF186020|//3.00E-15//abscisic acid-activated protein kinase [Vicia faba]	Unigene11649_All//5.00E-16//AT5G66880| SNRK2.3 (SUCROSE NONFERMENTING 1(SNF1)-RELATED PROTEIN KINASE 2.3); kinase/ protein kinase	Unigene11649_All//7.00E-121//EX169027			GO:0004672//GO:0006464//GO:0006970//GO:0009738//GO:0009845//GO:0032559//GO:0043231//GO:0044444	nr +
Unigene116497_All	233	0.45	0.43	0.00	2.35	4.88	2.33	4.72	10.40	11.63	-4.64E-02	9.90E-01		-8.81E+00	3.96E-01		1.05E+00	1.10E-01		-1.59E-02	9.75E-01		1.14E+00	2.01E-03		1.30E+00	1.53E-04	Up			Unigene116497_All//1.00E-33//CO131853				
Unigene116500_All	233	1250.76	522.35	580.49	1552.79	1446.73	1499.50	351.67	142.79	206.72	-1.26E+00	8.13E-304	Down	-1.11E+00	3.62E-240	Down	-1.02E-01	5.64E-05		-5.04E-02	9.66E-02		-1.30E+00	3.85E-110	Down	-7.67E-01	8.58E-48		Unigene116500_All//gi|32401253|gb|AAP80800.1|/2.00E-17//class VII chitinase precursor [Gossypium hirsutum] >gi|32401255|gb|AAP80801.1| class VII chitinase precursor [Gossypium hirsutum]	Unigene116500_All//1.00E-09//AT1G05850| POM1 (POM-POM1); chitinase	Unigene116500_All//1.00E-126//gi|21100178|gb|BQ412491.1|BQ412491				nr +
Unigene116504_All	234	2.68	0.87	1.82	2.98	2.06	1.16	33.07	13.22	10.04	-1.63E+00	9.23E-02		-5.60E-01	5.54E-01		-5.33E-01	5.45E-01		-1.36E+00	1.31E-01		-1.32E+00	2.15E-11	Down	-1.72E+00	6.36E-17	Down			Unigene116504_All//3.00E-56//gi|21093336|gb|BQ405649.1|BQ405649				
Unigene11651_All	374	39.59	80.20	47.41	35.16	37.20	41.30	59.92	67.50	66.89	1.02E+00	9.48E-23	Up	2.60E-01	7.05E-02		8.11E-02	6.61E-01		2.32E-01	1.33E-01		1.72E-01	1.04E-01		1.59E-01	1.21E-01		Unigene11651_All//gi|186516051|ref|NP_001119111.1|/2.00E-61//OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase [Arabidopsis thaliana]	Unigene11651_All//8.00E-63//AT4G33950| OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase	Unigene11651_All//0.00E+00//TC142675			GO:0004674//GO:0005984//GO:0006464//GO:0006633//GO:0006641//GO:0006800//GO:0006952//GO:0006970//GO:0009738//GO:0009845//GO:0010118//GO:0032559//GO:0043231//GO:0044444//GO:0048827	nr +
Unigene116512_All	234	0.00	0.00	0.46	2.55	2.35	1.93	1.26	16.08	1.19	null	null		8.83E+00	4.01E-01		-1.18E-01	8.76E-01		-4.04E-01	6.73E-01		3.67E+00	1.56E-18	Up	-8.58E-02	9.52E-01								
Unigene116524_All	235	0.00	1.08	0.00	0.00	0.73	0.38	0.18	1.78	2.88	1.01E+01	7.88E-02		null	null		9.52E+00	2.27E-01		8.59E+00	4.79E-01		3.31E+00	2.00E-02		4.00E+00	4.30E-04	Up			Unigene116524_All//3.00E-07//TC148620				
Unigene116526_All	235	159.41	136.92	164.51	165.34	189.91	173.16	195.03	104.76	51.20	-2.20E-01	1.53E-02		4.54E-02	6.45E-01		2.00E-01	1.25E-02		6.66E-02	5.34E-01		-8.97E-01	3.16E-34		-1.93E+00	1.44E-112	Down	Unigene116526_All//gi|18403820|ref|NP_566732.1|/4.00E-24//dienelactone hydrolase family protein [Arabidopsis thaliana] >gi|17381241|gb|AAL36041.1| AT3g23600/MDB19_9 [Arabidopsis thaliana] >gi|20453365|gb|AAM19921.1| AT3g23600/MDB19_9 [Arabidopsis thaliana] >gi|21536848|gb|AAM61180.1| contains similarity to endo-1,3-1,4-beta-D-glucanase [Arabidopsis thaliana]	Unigene116526_All//1.00E-25//AT3G23600| dienelactone hydrolase family protein	Unigene116526_All//8.00E-128//TC162002			GO:0004091//GO:0005576//GO:0006970//GO:0016020//GO:0043231	nr -
Unigene11654_All	3138	33.75	15.84	27.00	15.48	17.28	16.12	10.25	9.36	8.43	-1.09E+00	3.72E-88	Down	-3.22E-01	3.24E-10		1.59E-01	3.18E-02		5.86E-02	5.45E-01		-1.31E-01	1.70E-01		-2.83E-01	7.33E-04		Unigene11654_All//gi|297796141|ref|XP_002865955.1|/0.00E+00//FTSH11 [Arabidopsis lyrata subsp. lyrata] >gi|297311790|gb|EFH42214.1| FTSH11 [Arabidopsis lyrata subsp. lyrata]	Unigene11654_All//0.00E+00//AT5G53170| FTSH11 (FtsH protease 11); ATP-dependent peptidase/ ATPase/ metallopeptidase	Unigene11654_All//0.00E+00//TC146914			GO:0004175//GO:0006950//GO:0009536//GO:0009642//GO:0032559//GO:0042623//GO:0044257	nr +
Unigene116545_All	237	0.00	0.00	0.00	0.00	0.00	0.00	0.36	4.06	0.00	null	null		null	null		null	null		null	null		3.51E+00	5.50E-05	Up	-8.48E+00	3.59E-01								
Unigene116547_All	237	0.00	0.00	0.00	0.00	0.00	0.00	0.18	3.53	0.50	null	null		null	null		null	null		null	null		4.31E+00	5.68E-05	Up	1.50E+00	5.58E-01								ESTscan -
Unigene116549_All	237	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.29	0.00	null	null		null	null		null	null		null	null		1.12E+01	5.37E-04	Up	null	null		Unigene116549_All//gi|145334857|ref|NP_001078774.1|/3.00E-09//AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase [Arabidopsis thaliana]	Unigene116549_All//1.00E-10//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase				GO:0005488//GO:0009725//GO:0032502//GO:0043231//GO:0070011	nr +
Unigene11655_All	1713	4.95	4.44	3.23	9.22	12.66	10.31	12.12	2.37	4.51	-1.57E-01	4.65E-01		-6.14E-01	2.97E-03		4.58E-01	3.43E-05		1.61E-01	2.94E-01		-2.36E+00	4.22E-64	Down	-1.43E+00	1.18E-33	Down	Unigene11655_All//gi|115480615|ref|NP_001063901.1|/2.00E-74//Os09g0556800 [Oryza sativa Japonica Group] >gi|113632134|dbj|BAF25815.1| Os09g0556800 [Oryza sativa Japonica Group]		Unigene11655_All//0.00E+00//TC135786				nr -
Unigene116552_All	237	0.00	0.00	0.00	0.00	0.00	0.00	2.85	1.94	0.00	null	null		null	null		null	null		null	null		-5.57E-01	4.89E-01		-1.15E+01	3.56E-05	Down							ESTscan -
Unigene116559_All	237	0.00	0.00	0.00	0.00	0.00	0.00	12.31	5.64	1.34	null	null		null	null		null	null		null	null		-1.13E+00	6.78E-04	Down	-3.19E+00	1.79E-13	Down	Unigene116559_All//gi|219118863|ref|XP_002180198.1|/2.00E-36//ubiquitin extension protein 4 [Phaeodactylum tricornutum CCAP 1055/1] >gi|217408455|gb|EEC48389.1| ubiquitin extension protein 4 [Phaeodactylum tricornutum CCAP 1055/1]	Unigene116559_All//3.00E-37//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene116559_All//2.00E-08//DW238310			GO:0044424	nr +
Unigene116656_All	323	1.94	12.08	3.13	2.62	2.45	5.87	3.27	6.34	3.33	2.64E+00	1.32E-11	Up	6.88E-01	3.42E-01		-9.66E-02	8.77E-01		1.16E+00	1.59E-02		9.54E-01	1.83E-02		2.52E-02	9.76E-01		Unigene116656_All//gi|195606966|gb|ACG25313.1|/6.00E-25//zinc finger, C3HC4 type family protein [Zea mays]	Unigene116656_All//5.00E-19//AT5G45290| zinc finger (C3HC4-type RING finger) family protein	Unigene116656_All//6.00E-120//DR455518			GO:0043231//GO:0046914	nr -
Unigene116657_All	3891	11.19	53.78	26.47	12.84	22.25	20.72	11.43	17.00	13.25	2.27E+00	0.00E+00	Up	1.24E+00	2.91E-102	Up	7.93E-01	2.58E-50		6.90E-01	1.94E-33		5.73E-01	7.83E-23		2.13E-01	1.18E-03		Unigene116657_All//gi|115480615|ref|NP_001063901.1|/4.00E-89//Os09g0556800 [Oryza sativa Japonica Group] >gi|113632134|dbj|BAF25815.1| Os09g0556800 [Oryza sativa Japonica Group]	Unigene116657_All//2.00E-29//AT5G45290| zinc finger (C3HC4-type RING finger) family protein	Unigene116657_All//0.00E+00//TC158702			GO:0046914	nr +
Unigene116580_All	238	14.95	18.73	14.10	32.65	17.80	25.81	30.73	23.88	10.38	3.26E-01	2.74E-01		-8.48E-02	8.01E-01		-8.76E-01	5.58E-06		-3.39E-01	1.26E-01		-3.64E-01	6.87E-02		-1.57E+00	3.77E-14	Down			Unigene116580_All//3.00E-50//TC168990				
Unigene116588_All	239	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.27	0.00	null	null		null	null		null	null		null	null		1.12E+01	5.37E-04	Up	null	null		Unigene116588_All//gi|299473653|emb|CBN78047.1|/1.00E-13//flagellar associated protein, quinone reductase-like protein [Ectocarpus siliculosus]	Unigene116588_All//1.00E-07//AT4G27270| quinone reductase family protein					nr +
Unigene116592_All	239	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.25	0.00	null	null		null	null		null	null		null	null		1.24E+01	7.17E-09	Up	null	null		Unigene116592_All//sp|Q9RAJ1|DHAR_MYCSX//2.00E-10//HTH-type transcriptional repressor dhaR OS=Mycobacterium sp. (strain GP1) GN=dhaR PE=4 SV=1						swissprot -
Unigene116593_All	239	0.22	0.00	0.00	0.00	0.29	0.38	2.30	16.79	1.83	-7.77E+00	6.16E-01		-7.77E+00	6.28E-01		8.17E+00	6.13E-01		8.56E+00	4.79E-01		2.87E+00	7.07E-16	Up	-3.27E-01	6.72E-01				Unigene116593_All//3.00E-07//CD809346				

Unigene11660_All	564	6.12	2.07	1.61	10.07	6.53	6.17	13.34	12.45	10.81	-1.57E+00	9.76E-06	Down	-1.93E+00	5.28E-07	Down	-6.24E-01	8.10E-03		-7.08E-01	4.04E-03		-1.00E-01	6.31E-01		-3.04E-01	1.11E-01		Unigene11660_All//gi|47497095|dbj|BAD19146.1|//2.00E-58//ankyrin repeat protein-like [Oryza sativa Japonica Group]	Unigene11660_All//5.00E-69//AT3G04470| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Ankyrin (InterPro:IPR002110); BEST Arabidopsis thaliana protein match is: ankyrin repeat family protein (TAIR:AT1G04780.1); Has 842 Blast hits to 642 proteins in 95 species: Archae - 0; Bacteria - 6; Metazoa - 523; Fungi - 26; Plants - 165; Viruses - 4; Other Eukaryotes - 118 (source: NCBI BLink).	Unigene11660_All//0.00E+00//C0113709			GO:0016020	nr -
Unigene11663_All	637	1.31	1.51	2.17	1.96	3.51	1.56	2.12	6.30	4.50	2.02E-01	7.54E-01		7.26E-01	2.28E-01		8.46E-01	4.73E-02		-3.26E-01	6.41E-01		1.57E+00	7.47E-08	Up	1.08E+00	8.63E-04	Up	Unigene11663_All//gi|163644184|dbj|BAF95742.1|//7.00E-41//ethylene receptor homolog [Physcomitrella patens]	Unigene11663_All//2.00E-30//AT1G66340| ETR1 (ETHYLENE RESPONSE 1); ethylene binding / protein histidine kinase/ two-component response regulator	Unigene11663_All//2.00E-103//gi|109853628|gb|DW482607.1|DW482607	Orphans		GO:0004871//GO:0005488//GO:0016020//GO:0016301//GO:0023060//GO:0044237	nr -
Unigene116630_All	242	0.00	0.00	0.00	0.00	0.00	0.00	198.65	28.84	1.98	null	null		null	null		null	null		null	null		-2.78E+00	2.04E-178	Down	-6.65E+00	0.00E+00	Down								
Unigene116642_All	243	0.00	0.00	0.00	0.00	0.00	0.00	2.78	2.58	0.00	null	null		null	null		null	null		null	null		-1.10E-01	8.90E-01		-1.14E+01	3.56E-05	Down			Unigene116642_All//7.00E-11//ES845934					
Unigene11665_All	4684	77.27	186.32	118.29	20.75	14.32	13.52	9.07	10.23	4.55	1.27E+00	0.00E+00	Up	6.14E-01	6.11E-167		-5.35E-01	4.78E-29		-6.18E-01	2.08E-33		1.73E-01	1.68E-02		-9.95E-01	8.41E-39		Unigene11665_All//gi|75755655|ref|YP_319761.1|//0.00E+00//photosystem II 44 kDa protein [Acorus calamus] >gi|74381705|emb|CAI53790.1| PSII 43 kDa protein [Acorus calamus]	Unigene11665_All//0.00E+00//ATCG00280| chloroplast gene encoding a CP43 subunit of the photosystem II reaction center, promoter contains a blue-light responsive element.	Unigene11665_All//0.00E+00//TC129711		ko00195|Photosynthesis	GO:0006464//GO:0009055//GO:0009521//GO:0009534//GO:0009767//GO:0031224//GO:0042716//GO:0043169//GO:0046906//GO:0051234	nr -
Unigene116653_All	244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.23	0.00	null	null		null	null		null	null		null	null		1.11E+01	5.36E-04	Up	null	null		Unigene116653_All//gi|295708597|emb|CBJ48460.1|//2.00E-32//Molecular chaperones GRP78/BiP/KAR2, HSP70 superfamily [Ectocarpus siliculosus]	Unigene116653_All//2.00E-24//AT5G28540| BIP1; ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03060|Protein export	GO:0032559//GO:0050896	nr -
Unigene116660_All	244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.45	1.31	null	null		null	null		null	null		null	null		1.21E+01	1.04E-07	Up	1.04E+01	1.34E-02									ESTscan -
Unigene116664_All	244	10.72	2.49	5.67	21.84	11.85	13.88	3.81	5.31	7.67	-2.11E+00	2.26E-06	Down	-9.18E-01	2.50E-02		-8.82E-01	2.40E-04		-6.54E-01	1.09E-02		4.78E-01	3.95E-01		1.01E+00	1.46E-02		Unigene116664_All//gi|119888002|gb|ABR05953.1|//2.00E-07//proline-rich protein [Gossypium hirsutum]		Unigene116664_All//2.00E-88//gi|109838020|gb|DW236581.1|DW236581				nr +
Unigene11667_All	2100	3.64	1.95	5.71	2.13	1.18	0.84	0.58	0.52	0.17	-8.96E-01	2.44E-05		6.49E-01	1.25E-04		-8.55E-01	1.33E-03		-1.35E+00	3.28E-06	Down	-1.74E-01	7.49E-01		-1.77E+00	1.72E-03		Unigene11667_All//gi|168012500|ref|XP_001758940.1|//6.00E-69//plastid sigma facor SIG2 [Physcomitrella patens subsp. patens] >gi|12697780|dbj|BAB21618.1| PpSIG2 [Physcomitrella patens] >gi|14669832|dbj|BAB62008.1| PpSIG2 [Physcomitrella patens] >gi|162690077|gb|EDQ76446.1| plastid sigma facor SIG2 [Physcomitrella patens subsp. patens]	Unigene11667_All//7.00E-59//AT2G36990| SIGP (RNA POLYMERASE SIGMA-SUBUNIT F); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor	Unigene11667_All//0.00E+00//DR452614	Sigma70-like		GO:0000996//GO:0001071//GO:0006351//GO:0009536//GO:0009639//GO:0009791//GO:0010557//GO:0034062	nr -
Unigene116672_All	245	0.00	0.62	1.30	0.81	0.00	0.74	176.02	156.78	1371.75	9.28E+00	2.36E-01		1.03E+01	4.53E-02		-9.67E+00	8.46E-02		-1.41E-01	9.35E-01		-1.67E-01	3.06E-02		2.96E+00	0.00E+00	Up	Unigene116672_All//gi|3970689|emb|CAA77191.1|//9.00E-39//(+)-delta-cadinene synthase [Gossypium arboreum]	Unigene116672_All//4.00E-16//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene116672_All//4.00E-136//TC145282		ko00904|Diterpenoid biosynthesis	GO:0010334//GO:0046872	nr -
Unigene116677_All	245	0.00	0.00	0.00	0.00	0.00	0.00	1.55	15.18	4.88	null	null		null	null		null	null		null	null		3.29E+00	9.25E-17	Up	1.65E+00	3.87E-03				Unigene116677_All//3.00E-07//TC144453				
Unigene116687_All	246	0.00	0.00	0.00	0.00	0.00	0.00	0.69	10.36	0.00	null	null		null	null		null	null		null	null		3.91E+00	2.40E-13	Up	-9.43E+00	1.08E-01		Unigene116687_All//gi|1545805|dbj|BAA10929.1|//3.00E-11//cytochrome P450 like TBP [Nicotiana tabacum]		Unigene116687_All//8.00E-20//gi|73861424|gb|DT464163.1|DT464163				nr -
Unigene116690_All	246	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.80	0.00	null	null		null	null		null	null		null	null		1.27E+01	8.76E-12	Up	null	null		Unigene116690_All//gi|168068200|ref|XP_001785975.1|//5.00E-11//predicted protein [Physcomitrella patens subsp. patens] >gi|162662338|gb|EDQ49215.1| predicted protein [Physcomitrella patens subsp. patens]		Unigene116690_All//2.00E-14//TC155558				nr -
Unigene116701_All	247	0.00	0.00	0.00	0.81	0.00	0.00	0.34	2.37	3.71	null	null		null	null		-9.66E+00	8.45E-02		-9.66E+00	1.34E-01		2.79E+00	8.26E-03		3.44E+00	7.53E-05	Up	Unigene116701_All//gi|255568217|ref|XP_002525084.1|//5.00E-06//ATP-binding cassette transporter, putative [Ricinus communis] >gi|223535665|gb|EEF37331.1| ATP-binding cassette transporter, putative [Ricinus communis]	Unigene116701_All//9.00E-05//AT3G55090| ATPase, coupled to transmembrane movement of substances	Unigene116701_All//5.00E-18//gi|78349095|gb|DT569369.1|DT569369			GO:0016787	nr +
Unigene116704_All	247	35.37	11.69	20.05	51.43	45.59	47.72	160.05	67.35	47.10	-1.60E+00	1.09E-13	Down	-8.19E-01	5.58E-05		-1.74E-01	3.19E-01		-1.08E-01	5.90E-01		-1.25E+00	2.67E-50	Down	-1.76E+00	4.36E-86	Down	Unigene116704_All//gi|195658145|gb|ACG48540.1|//6.00E-09//60S ribosomal protein L23 [Zea mays]	Unigene116704_All//2.00E-10//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene116704_All//5.00E-123//gi|132468858|gb|BE055726.2|BE055726		ko03010|Ribosome		nr +
Unigene116705_All	247	0.00	0.00	0.00	0.00	0.00	0.00	9.59	38.07	0.16	null	null		null	null		null	null		null	null		1.99E+00	7.31E-24	Up	-5.89E+00	5.63E-16	Down			Unigene116705_All//1.00E-09//TC146753				
Unigene116708_All	247	40.46	18.67	15.09	131.29	92.15	173.34	115.54	55.33	88.23	-1.12E+00	2.65E-09	Down	-1.42E+00	1.25E-12	Down	-5.11E-01	3.20E-09		4.01E-01	3.93E-07		-1.06E+00	2.21E-28	Down	-3.89E-01	1.05E-05		Unigene116708_All//gi|183393002|gb|ACC61674.1|//2.00E-30//mitochondrial cytochrome c [Vitis vinifera]	Unigene116708_All//4.00E-31//AT4G10040| CYTC-2 (cytochrome c-2); electron carrier/ heme binding / iron ion binding	Unigene116708_All//1.00E-108//gi|18099811|gb|BM359065.1|BM359065			GO:0005506//GO:0005743//GO:0006091//GO:0044425//GO:0051234	nr +
Unigene116714_All	247	136.84	90.47	137.54	124.43	120.59	162.00	284.83	84.10	158.06	-5.97E-01	1.14E-10		7.40E-03	9.64E-01		-4.52E-02	7.28E-01		3.81E-01	3.69E-06		-1.76E+00	1.09E-147	Down	-8.50E-01	5.75E-49				Unigene116714_All//2.00E-70//gi|109836664|gb|DW235225.1|DW235225				
Unigene116672_All	3206	4.70	1.53	3.95	15.54	9.60	8.95	8.39	2.65	3.27	-1.62E+00	1.82E-23	Down	-2.50E-01	1.17E-01		-6.94E-01	6.94E-24		-7.97E-01	7.31E-27		-1.66E+00	1.31E-52	Down	-1.36E+00	2.17E-40	Down	Unigene116672_All//gi|300143215|gb|EFJ09908.1|//0.00E+00//trehalose phosphate synthase [Selaginella moellendorffii]	Unigene116672_All//0.00E+00//AT4G17770| ATTPS5; protein binding / transferase, transferring glycosyl groups / trehalose-phosphatase	Unigene116672_All//0.00E+00//TC150954		ko00500|Starch and sucrose metabolism	GO:0005488//GO:0005991//GO:0019203//GO:0035251	nr -
Unigene116722_All	248	0.00	0.00	0.00	0.00	0.00	0.00	1.53	5.56	0.00	null	null		null	null		null	null		null	null		1.86E+00	7.81E-04	Up	-1.06E+01	4.20E-03		Unigene116722_All//gi|299470138|emb|CBN78167.1|//2.00E-18//ribosomal protein L34 [Ectocarpus siliculosus]	Unigene116722_All//3.00E-15//AT1G26880| 60S ribosomal protein L34 (RPL34A)			ko03010|Ribosome	GO:0043231	nr +
Unigene11674_All	944	1.72	2.04	2.31	2.16	1.61	1.58	1.75	2.97	3.88	2.48E-01	6.22E-01		4.29E-01	3.62E-01		-4.31E-01	3.48E-01		-4.55E-01	3.46E-01		7.64E-01	2.26E-02		1.15E+00	5.48E-05	Up	Unigene11674_All//gi|10177638|dbj|BAB10911.1|//1.00E-90//receptor protein kinase [Arabidopsis thaliana] >gi|224589711|gb|ACN59387.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene11674_All//3.00E-92//AT5G49660| leucine-rich repeat transmembrane protein kinase, putative	Unigene11674_All//0.00E+00//DW508005			GO:0004674//GO:0004871//GO:0006464//GO:0016491//GO:0031224//GO:0043410//GO:0032559	nr +
Unigene116745_All	251	0.00	0.00	0.00	0.00	0.00	0.00	2.53	2.33	0.00	null	null		null	null		null	null		null	null		-1.16E-01	8.88E-01		-1.13E+01	7.11E-05	Down	Unigene116745_All//gi|300261783|gb|EFJ45994.1|//1.00E-19//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene116745_All//7.00E-20//AT4G39200| 40S ribosomal protein S25 (RPS25E)			ko03010|Ribosome	GO:0010467//GO:0015935//GO:0016020	nr -
Unigene116747_All	252	0.00	0.00	0.00	0.00	0.00	0.00	2.35	1.82	0.00	null	null		null	null		null	null		null	null		-3.65E-01	6.49E-01		-1.12E+01	1.41E-04	Down								
Unigene11675_All	3370	1.75	1.56	2.35	20.19	11.98	9.82	56.68	26.55	11.30	-1.66E-01	5.31E-01		4.24E-01	5.22E-02		-7.54E-01	1.66E-37		-1.04E+00	6.43E-57	Down	-1.09E+00	1.11E-194	Down	-2.33E+00	0.00E+00	Down	Unigene11675_All//gi|10177638|dbj|BAB10911.1|//0.00E+00//receptor protein kinase [Arabidopsis thaliana] >gi|224589711|gb|ACN59387.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene11675_All//0.00E+00//AT5G49660| leucine-rich repeat transmembrane protein kinase, putative	Unigene11675_All//0.00E+00//TC142851			GO:0004702//GO:0006464//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene116765_All	253	0.00	0.00	0.00	0.00	0.00	0.00	2.17	1.49	0.00	null	null		null	null		null	null		null	null		-5.47E-01	5.52E-01		-1.11E+01	2.81E-04	Down								
Unigene11678_All	844	0.12	0.00	0.13	1.89	0.69	1.34	1.70	2.87	4.48	-6.95E+00	3.75E-01		2.54E-02	1.00E+00		-1.45E+00	4.07E-03		-4.98E-01	3.77E-01		7.54E-01	3.93E-02		1.40E+00	1.36E-06	Up	Unigene11678_All//gi|33350934|gb|AK39643.3|//1.00E-115//ATP-binding cassette transporter AtABC4 [Arabidopsis thaliana]	Unigene11678_All//3.00E-109//AT2G41700| ATPase, coupled to transmembrane movement of substances / amino acid transmembrane transporter				GO:0017111//GO:0032559	nr -
Unigene116792_All	255	0.00	0.00	0.00	0.00	0.00	0.00	0.66	3.93	4.69	null	null		null	null		null	null		null	null		2.57E+00	4.79E-04	Up	2.82E+00	3.02E-05	Up								
Unigene116794_All	255	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.13	0.00	null	null		null	null		null	null		null	null		1.11E+01	5.36E-04	Up	null	null		Unigene116794_All//gi|159477663|ref|XP_001696928.1|//1.00E-24//aldehyde dehydrogenase [Chlamydomonas reinhardtii] >gi|158274840|gb|EDP00620.1| aldehyde dehydrogenase [Chlamydomonas reinhardtii]	Unigene116794_All//2.00E-16//AT5G62530| ALDH12A1; 1-pyrroline-5-carboxylate dehydrogenase/ 3-chloroallyl aldehyde dehydrogenase			ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0004030//GO:0008152//GO:0043231	nr -
Unigene116804_All	256	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.45	0.31	null	null		null	null		null	null		null	null		1.13E+01	1.47E-04	Up	8.28E+00	4.05E-01		Unigene116804_All//gi|193878342|gb|ACF25911.1|//1.00E-20//MLO-like protein 6 [Vitis vinifera]	Unigene116804_All//5.00E-13//AT2G39200| MLO12 (MILDEW RESISTANCE LOCUS O 12); calmodulin binding				GO:0009987//GO:0031224	nr +
Unigene116807_All	257	0.00	0.00	0.00	0.19	0.27	0.18	3.62	1.95	0.47	null	null		null	null		4.68E-01	9.60E-01		-1.42E-01	9.55E-01		-8.91E-01	1.72E-01		-2.96E+00	1.72E-04	Down								
Unigene11681_All	2500	2.66	0.45	1.79	3.91	3.07	3.92	4.75	2.62	2.71	-2.58E+00	4.97E-19	Down	-5.71E-01	1.67E-02		-3.47E-01	5.84E-02		5.50E-03	9.78E-01		-8.56E-01	7.83E-09		-8.11E-01	2.14E-08		Unigene11681_All//gi|124360024|gb|ABN08040.1|//0.00E+00//Acyl-coA-binding protein, ACBP; Serine/threonine protein phosphatase, BSU1 [Medicago truncatula]	Unigene11681_All//0.00E+00//AT3G05420| ACBP4 (ACYL-COA BINDING PROTEIN 4); acyl-CoA binding	Unigene11681_All//0.00E+00//gi|161247899|gb|ES796003.1|ES796003		ko04712|Circadian rhythm - plant	GO:0005504//GO:0006810//GO:0009314//GO:0009725//GO:0043231//GO:0044444	nr +
Unigene116817_All	257	0.00	0.00	0.00	1.94	0.00	0.35	0.82	1.46	0.00	null	null		null	null		-1.09E+01	8.99E-04	Down	-2.46E+00	4.83E-02		8.31E-01	4.67E-01		-9.68E+00	5.80E-02		Unigene116817_All//gi|297596372|ref|NP_001042475.2|//3.00E-15//0s01g0228200 [Oryza sativa Japonica Group] >gi|255673021|dbj|BAF04389.2|0s01g0228200 [Oryza sativa Japonica Group]	Unigene116817_All//7.00E-12//AT1G17240| AtRLP2 (Receptor Like Protein 2); protein binding / protein kinase	Unigene116817_All//2.00E-08//ES834884		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016628//GO:0031224//GO:0032559	nr -
Unigene11682_All	2293	5.50	6.23	3.86	12.93	12.70	11.19	8.28	4.32	3.96	1.80E-01	2.62E-01		-5.12E-01	1.96E-03		-2.49E-02	8.29E-01		-2.08E-01	4.75E-02		-9.39E-01	9.31E-16		-1.06E+00	8.83E-20	Down	Unigene11682_All//gi|124360024|gb|ABN08040.1|//0.00E+00//Acyl-coA-binding protein, ACBP; Serine/threonine protein phosphatase, BSU1 [Medicago truncatula]	Unigene11682_All//0.00E+00//AT3G05420| ACBP4 (ACYL-COA BINDING PROTEIN 4); acyl-CoA binding	Unigene11682_All//0.00E+00//ES825853		ko04712|Circadian rhythm - plant	GO:0005504//GO:0006810//GO:0009314//GO:0009725//GO:0043231//GO:0044444	nr -
Unigene116824_All	258	0.00	0.00	0.00	0.00	0.00	0.00	0.66	3.56	5.25	null	null		null	null		null	null		null	null		2.44E+00	1.33E-03		3.00E+00	3.58E-06	Up								
Unigene116832_All	258	306.22	470.36	779.14	610.51	533.21	995.52	55.72	127.17	132.02	6.19E-01	1.38E-38		1.35E+00	3.04E-226	Up	-1.95E-01	2.24E-07		7.05E-01	1.26E-109		1.19E+00	7.74E-39	Up	1.24E+00	3.97E-44	Up	Unigene116832_All//gi|23506611|gb|AAN37904.1|//1.00E-19//histone H1D [Nicotiana tabacum]	Unigene116832_All//4.00E-12//AT2G18050| HIS1-3 (HISTONE H1-3); DNA binding / nucleosomal DNA binding	Unigene116832_All//5.00E-126//EV498964			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr -
Unigene116843_All	259	0.00	0.00	0.00	1.15	0.00	0.00	0.65	4.68	1.08	null	null		null	null		-1.02E+01	2.02E-02		-1.02E+01	4.00E-02		2.84E+00	3.39E-05	Up	7.22E-01	5.97E-01									ESTscan +

Unigene116849_All	260	0.00	0.97	0.00	0.00	0.00	0.00	57.08	31.35	302.93	9.93E+00	7.88E-02		null	null		null	null		null	null		-8.65E-01	5.42E-11		2.41E+00	8.71E-252	Up	Unigene116849_All//gi|11132838|sp|O64967.1|HDH2_GOSHI//9.00E-42//RecName: Full=3-hydroxy-3-methylglutaryl-coenzyme A reductase 2; Short=HMG-CoA reductase 2 >gi|2933200|gb|AAC05089.1| 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 [Gossypium hirsutum]	Unigene116849_All//1.00E-37//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene116849_All//1.00E-135//TC162385		ko00900|Terpenoid backbone biosynthesis	GO:0000166//GO:0005740//GO:0006720//GO:0006732//GO:0009526//GO:0016616//GO:0031090//GO:0031224//GO:0048037	nr +
Unigene116857_All	260	0.60	0.00	0.82	2.30	1.46	1.74	0.33	2.89	0.15	-9.24E+00	2.16E-01		4.40E-01	7.76E-01		-6.58E-01	4.78E-01		-4.04E-01	6.73E-01		3.15E+00	9.54E-04	Up	-1.09E+00	6.77E-01											
Unigene116858_All	260	0.20	1.36	0.00	0.00	0.00	0.00	1.14	5.30	1.38	2.76E+00	9.60E-02		-7.65E+00	6.28E-01		null	null		null	null		2.22E+00	1.31E-04	Up	2.77E-01	7.87E-01											
Unigene116886_All	968	1.84	3.87	4.29	4.89	5.48	4.01	3.32	7.82	4.16	1.08E+00	8.32E-04	Up	1.22E+00	1.23E-04	Up	1.64E-01	5.91E-01		-2.85E-01	3.57E-01		1.24E+00	4.29E-10	Up	3.25E-01	2.41E-01		|BAH80551.1|//8.00E-37//transcription factor squamosa promoter binding protein-like [Eucalyptus grandis]	Unigene11686_All//2.00E-35//AT5G43270| SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2); DNA binding / transcription factor	Unigene11686_All//0.00E+00//TC150184	SBP		GO:0050789	nr -
Unigene116868_All	261	0.00	0.00	0.00	0.00	0.00	0.00	1.46	5.93	0.00	null	null		null	null		null	null		null	null		2.02E+00	1.30E-04	Up	-1.05E+01	4.20E-03											
Unigene11687_All	1671	2.41	4.88	2.26	2.86	4.31	2.86	2.99	4.10	2.86	1.02E+00	9.45E-07	Up	-9.17E-02	7.74E-01		5.90E-01	5.07E-03		1.50E-03	9.98E-01		4.58E-01	2.36E-02		-6.16E-02	8.06E-01		Unigene11687_All//gi|242390089|dbj|BAH80551.1|//4.00E-53//transcription factor squamosa promoter binding protein-like [Eucalyptus grandis]	Unigene11687_All//3.00E-38//AT5G43270| SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2); DNA binding / transcription factor	Unigene11687_All//0.00E+00//TC167346	SBP		GO:0048506	nr -
Unigene116875_All	262	0.00	0.00	0.00	0.00	0.00	0.00	1.45	5.42	0.00	null	null		null	null		null	null		null	null		1.90E+00	5.03E-04	Up	-1.05E+01	4.20E-03		Unigene116875_All//gi|19908703|gb|AAM02974.1|AF421541_1//3.00E-25//Hsp90 [Crypthecodinium cohnii]	Unigene116875_All//3.00E-22//AT5G56010| HSP81-3; ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr -
Unigene11688_All	1783	0.65	1.68	1.25	1.20	1.47	1.29	1.14	1.97	0.98	1.38E+00	2.60E-04	Up	9.58E-01	3.31E-02		2.89E-01	5.28E-01		1.05E-01	8.18E-01		7.91E-01	7.01E-03		-2.11E-01	6.05E-01		Unigene11688_All//gi|242390089|dbj|BAH80551.1|//2.00E-92//transcription factor squamosa promoter binding protein-like [Eucalyptus grandis]	Unigene11688_All//8.00E-69//AT5G43270| SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2); DNA binding / transcription factor	Unigene11688_All//0.00E+00//TC167346	SBP		GO:0050789	nr +
Unigene116880_All	262	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.39	0.61	null	null		null	null		null	null		null	null		1.12E+01	1.47E-04	Up	9.25E+00	1.40E-01											
Unigene116898_All	264	0.00	0.00	0.00	0.00	0.00	0.00	0.64	4.75	0.00	null	null		null	null		null	null		null	null		2.89E+00	1.97E-05	Up	-9.32E+00	1.08E-01					Unigene116898_All//2.00E-17//FL576877						
Unigene116899_All	264	3.17	0.00	1.41	0.94	1.43	1.20	1.12	1.58	0.15	-1.16E+01	5.57E-05	Down	-1.17E+00	1.52E-01		6.05E-01	6.59E-01		3.44E-01	7.97E-01		4.98E-01	6.33E-01		-2.89E+00	6.77E-02											
Unigene116902_All	265	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.68	0.00	null	null		null	null		null	null		null	null		1.25E+01	1.29E-10	Up	null	null					Unigene116902_All//8.00E-11//TC167383						
Unigene116903_All	265	0.00	0.00	0.00	0.19	0.00	0.00	0.00	2.68	0.30	null	null		null	null		-7.55E+00	5.59E-01		-7.55E+00	6.40E-01		1.14E+01	3.98E-05	Up	8.23E+00	4.05E-01					Unigene116903_All//3.00E-07//gi|73863255|gb|DT465994.1|DT465994						
Unigene116912_All	266	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.20	0.00	null	null		null	null		null	null		null	null		1.11E+01	2.81E-04	Up	null	null		Unigene116912_All//gi|219120887|ref|XP_002185675.1|//6.00E-06//predicted protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|209582524|gb|AC165145.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1]						nr -
Unigene116918_All	266	21.44	6.86	10.41	42.89	46.86	34.47	50.55	9.90	22.02	-1.64E+00	1.49E-09	Down	-1.04E+00	7.12E-05	Down	1.28E-01	5.21E-01		-3.15E-01	7.26E-02		-2.35E+00	1.13E-41	Down	-1.20E+00	4.05E-17	Down	Unigene116918_All//gi|225463470|ref|XP_002276512.1|//2.00E-16//PREDICTED: similar to RPL18AA (60S RIBOSOMAL PROTEIN L18A-1); structural constituent of ribosome isoform 1 [Vitis vinifera]	Unigene116918_All//5.00E-15//AT2G34480| 60S ribosomal protein L18A (RPL18aB)	Unigene116918_All//2.00E-85//gi|164262579|gb|EV487043.1|EV487043		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene116692_All	270	5.04	1.13	4.73	3.32	1.79	2.68	5.95	2.79	2.07	-2.16E+00	9.05E-04	Down	-9.01E-02	8.77E-01		-8.95E-01	2.14E-01		-3.11E-01	6.88E-01		-1.09E+00	1.97E-02		-1.53E+00	1.16E-03		Unigene11692_All//gi|240255277|ref|NP_187084.6|//1.00E-42//emb2458 (embryo defective 2458); ATP binding / ATPase/ metalloendopeptidase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene11692_All//4.00E-44//AT3G04340| emb2458 (embryo defective 2458); ATP binding / ATPase/ metalloendopeptidase/ nucleoside-triphosphatase/ nucleotide binding	Unigene11692_All//2.00E-144//gi|48748088|gb|C0078607.1|C0078607			GO:0004175//GO:0019538//GO:0032559//GO:0042623	nr -
Unigene116920_All	267	0.00	0.00	0.00	0.00	0.00	0.00	3.48	5.64	0.15	null	null		null	null		null	null		null	null		6.94E-01	1.55E-01		-4.55E+00	6.41E-06	Down	Unigene116920_All//gi|4139170|gb|AD03711.1|//8.00E-35//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene116920_All//1.00E-31//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene116920_All//1.00E-25//CD809343			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene116921_All	267	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.35	1.04	null	null		null	null		null	null		null	null		1.12E+01	1.47E-04	Up	1.00E+01	2.44E-02											
Unigene116928_All	267	0.00	1.33	1.00	0.93	0.13	0.51	0.16	2.97	1.04	1.04E+01	2.46E-02		9.96E+00	8.03E-02		-2.85E+00	1.37E-01		-8.78E-01	6.16E-01		4.23E+00	1.05E-04	Up	2.72E+00	9.95E-02					Unigene116928_All//8.00E-11//C0114754						
Unigene116930_All	268	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.00	null	null		null	null		null	null		null	null		1.11E+01	2.81E-04	Up	null	null					Unigene116930_All//1.00E-21//ES790885						
Unigene116936_All	268	0.00	0.00	0.00	0.00	0.00	0.00	1.89	2.65	0.00	null	null		null	null		null	null		null	null		4.86E-01	5.42E-01		-1.09E+01	5.54E-04	Down	Unigene116936_All//gi|300264012|gb|EFJ48210.1|//2.00E-38//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene116936_All//8.00E-40//AT2G18020| EMB2296 (embryo defective 2296); structural constituent of ribosome	Unigene116936_All//9.00E-17//ES821617		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene116940_All	269	0.00	2.45	0.20	0.74	0.51	0.17	1.10	3.11	1.04	1.13E+01	6.26E-04	Up	7.63E+00	6.38E-01		-5.33E-01	7.49E-01		-2.14E+00	3.47E-01		1.50E+00	3.73E-02		-8.58E-02	9.52E-01											
Unigene116942_All	269	0.00	0.00	0.00	0.00	0.00	0.00	1.41	5.28	0.00	null	null		null	null		null	null		null	null		1.90E+00	5.03E-04	Up	-1.05E+01	4.20E-03											
Unigene116949_All	270	0.00	0.00	0.00	0.74	0.26	0.00	158.94	21.98	32.90	null	null		null	null		-1.53E+00	4.16E-01		-9.53E+00	1.34E-01		-2.85E+00	1.42E-163	Down	-2.27E+00	4.79E-130	Down				Unigene116949_All//9.00E-134//gi|13245508|gb|BE052503.2|BE052503						
Unigene11695_All	1295	1.82	0.63	1.40	4.92	3.94	2.79	2.12	1.10	2.31	-1.54E+00	4.45E-04	Down	-3.79E-01	3.92E-01		-3.23E-01	1.80E-01		-8.20E-01	3.47E-04		-9.52E-01	5.03E-03		1.21E-01	7.13E-01		Unigene11695_All//gi|195605628|gb|ACG24644.1|//3.00E-58//protein SYS1 [Zea mays]	Unigene11695_All//1.00E-57//AT1G79990| LOCATED IN: endomembrane system, COPI vesicle coat, Golgi membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SYS1 homologue (InterPro:IPR016972); Has 55556 Blast hits to 24059 proteins in 620 species: Archae - 38; Bacteria - 5697; Metazoa - 25539; Fungi - 10898; Plants - 5309; Viruses - 0; Other Eukaryotes - 8075 (source: NCBI BLink).	Unigene11695_All//0.00E+00//TC174885			GO:0015031//GO:0030120	nr -
Unigene116955_All	271	8.69	5.42	5.89	34.74	23.38	25.66	105.62	85.29	27.49	-6.80E-01	1.01E-01		-5.60E-01	2.06E-01		-5.71E-01	1.09E-03		-4.37E-01	2.10E-02		-3.09E-01	7.34E-04		-1.94E+00	3.41E-71	Down	Unigene116955_All//gi|15241844|ref|NP_198206.1|//7.00E-19//BIP1: ATP binding [Arabidopsis thaliana] >gi|18206379|sp|Q9LKR3.1|BIP1_ARATH RecName: Full=Luminal-binding protein 1; Short=BiP1; Short=AtBP1; Flags: Precursor >gi|9502169|gb|AAF88019.1| Hypothetical protein T2803.10 [Arabidopsis thaliana] >gi|23306406|gb|AAN17430.1| Unknown protein [Arabidopsis thaliana] >gi|24899769|gb|AAN65099.1| Unknown protein [Arabidopsis thaliana]	Unigene116955_All//3.00E-20//AT5G28540| BIP1; ATP binding	Unigene116955_All//7.00E-147//TC179555		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0000741//GO:0006950//GO:0009536//GO:0016020//GO:0016628//GO:0030312//GO:0031410//GO:0032559//GO:0043161//GO:0044432	nr +
Unigene116964_All	271	0.00	1.12	1.96	0.00	1.02	2.67	0.94	1.39	0.74	1.01E+01	4.44E-02		1.09E+01	4.05E-03		9.99E+00	7.02E-02		1.14E+01	2.31E-04	Up	5.68E-01	6.38E-01		-3.49E-01	7.67E-01					Unigene116964_All//6.00E-21//BG444481						
Unigene116968_All	272	21.93	38.75	13.12	41.57	27.98	41.84	21.61	31.19	10.11	8.21E-01	3.58E-06		-7.41E-01	3.34E-03		-5.71E-01	2.71E-04		9.30E-03	9.57E-01		5.30E-01	2.83E-03		-1.10E+00	4.95E-07	Down				Unigene116968_All//2.00E-57//gi|72280248|gb|DT052441.1|DT052441						
Unigene116973_All	272	1.54	1.86	1.37	3.30	1.65	0.33	1.55	5.53	1.46	2.76E-01	7.64E-01		-1.67E-01	8.79E-01		-1.00E+00	1.61E-01		-3.31E+00	5.80E-04	Down	1.83E+00	4.72E-04	Up	-8.58E-02	9.39E-01		Unigene116973_All//gi|297799832|ref|XP_002867800.1|//8.00E-17//PRH26 protein [Arabidopsis lyrata subsp. lyrata] >gi|297313636|gb|EFH44059.1| PRH26 protein [Arabidopsis lyrata subsp. lyrata]	Unigene116973_All//7.00E-18//AT4G21990| APK3 (APS REDUCTASE 3); adenylyl-sulfate reductase	Unigene116973_All//8.00E-79//TC149017			GO:0000097//GO:0009532//GO:0016671//GO:0019725//GO:0031976	nr -
Unigene116979_All	273	0.00	0.00	0.00	0.00	0.00	0.00	1.08	4.44	0.00	null	null		null	null		null	null		null	null		2.03E+00	8.61E-04	Up	-1.01E+01	1.58E-02		Unigene116979_All//gi|255076213|ref|XP_002501781.1|//2.00E-26//histone H2B [Micromonas sp. RCC299] >gi|226517045|gb|AC063039.1| histone H2B [Micromonas sp. RCC299]	Unigene116979_All//1.00E-27//AT3G09480| histone H2B, putative				GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr +
Unigene11698_All	600	1.05	1.35	1.69	2.74	2.47	2.86	5.64	6.06	11.69	3.69E-01	6.22E-01		6.88E-01	3.42E-01		-1.51E-01	8.02E-01		6.21E-02	9.25E-01		1.04E-01	7.34E-01		1.05E+00	1.11E-07	Up	Unigene11698_All//gi|297601401|ref|NP_001050782.2|//3.00E-24//Os03g0649000 [Oryza sativa Japonica Group] >gi|255674749|dbj|BAF12696.2| Os03g0649000 [Oryza sativa Japonica Group]	Unigene11698_All//1.00E-50//AT3G11760| unknown protein	Unigene11698_All//0.00E+00//TC166259			GO:0043231	nr -
Unigene116987_All	274	0.00	0.00	0.00	0.36	0.00	0.82	0.62	6.41	1.16	null	null		null	null		-8.51E+00	3.15E-01		1.18E+00	5.50E-01		3.38E+00	2.17E-08	Up	9.14E-01	4.53E-01					Unigene116987_All//2.00E-104//CO101692						
Unigene116998_All	275	0.00	0.18	0.58	0.72	0.75	0.16	0.00	4.56	0.87	7.53E+00	6.19E-01		9.18E+00	2.39E-01		5.22E-02	9.89E-01		-2.14E+00	3.47E-01		1.22E+01	7.17E-09	Up	9.76E+00	4.40E-02					Unigene116998_All//2.00E-11//TC142238						
Unigene1170_All	1751	18.23	14.93	12.47	1.48	4.72	4.85	2.54	21.08	127.27	-2.88E-01	2.99E-03		-5.48E-01	2.26E-08		1.67E+00	1.13E-15	Up	1.71E+00	2.17E-15	Up	3.06E+00	2.45E-150	Up	5.65E+00	0.00E+00	Up	Unigene1170_All//gi|297827611|ref|XP_002881688.1|//1.00E-166//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327527|gb|EFH57947.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1170_All//1.00E-160//AT2G39980| transferase family protein	Unigene1170_All//4.00E-94//DR461983		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene117002_All	276	0.00	2.57	0.00	0.72	0.12	0.65	2.30	3.94	1.59	1.13E+01	3.33E-04	Up	null	null		-2.53E+00	2.34E-01		-1.41E-01	9.35E-01		7.77E-01	1.94E-01		-5.33E-01	4.94E-01					Unigene117002_All//3.00E-07//ES842675						
Unigene117003_All	276	0.00	0.00	0.00	0.00	0.00	0.00	2.14	1.82	0.00	null	null		null	null		null	null		null	null		-2.39E-01	7.65E-01		-1.11E+01	1.41E-04	Down	Unigene117003_All//gi|254933823|gb|ACT87561.1|//1.00E-12//60S ribosomal protein L14 [Amoebophrya sp. ex Karlodinium veneficum]	Unigene117003_All//1.00E-07//AT4G27090| 60S ribosomal protein L14 (RPL14B)			ko03010|Ribosome	GO:0009536//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene117008_All	276	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.97	0.00	null	null		null	null		null	null		null	null		1.09E+01	5.36E-04	Up	null	null		Unigene117008_All//gi|298714497|emb|CBJ27519.1|//1.00E-06//eukaryotic elongation factor-1 B gamma [Ectocarpus siliculosus]	Unigene117008_All//1.00E-05//AT1G09640| elongation factor 1B-gamma, putative / eEF-1B gamma, putative					nr -
Unigene117010_All	277	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.26	0.00	null	null		null	null		null	null		null	null		1.11E+01	1.47E-04	Up	null	null		Unigene117010_All//gi|38325811|gb|AAR17078.1|//3.00E-43//heat shock protein 70-1 [Nicotiana tabacum]	Unigene117010_All//1.00E-34//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene117010_All//1.00E-12//TC166610		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr +
Unigene117011_All	277	0.00	0.00	0.00	0.36	0.37	0.00	0.00	2.41	0.29	null	null		null	null		5.20E-02	9.67E-01		-8.49E+00	4.03E-01		1.12E+01	7.64E-05	Up	8.17E+00	4.05E-01					Unigene117011_All//8.00E-153//ES809411						
Unigene117016_All	277	0.94	0.00	0.38	0.90	0.62	0.65	1.07	6.04	1.73	-9.88E+00	6.72E-02		-1.30E+00	4.37E-01		-5.33E-01	7.13E-01		-4.63E-01	7.45E-01		2.50E+00	3.97E-06	Up	6.92E-01	4.63E-01					Unigene117016_All//5.00E-40//TC154162						
Unigene117017_All	277	0.00	0.00	0.00	0.00	0.00	0.00	1.83	1.21	0.00	null	null		null	null		null	null		null	null		-6.02E-01	5.32E-01		-1.08E+01	5.54E-04	Down	Unigene117017_All//gi|32394540|gb|AAM93968.1|//1.00E-15//Gbp1 [Griffithsia japonica]	Unigene117017_All//1.00E-09//AT1G02840| SR1, RNA binding / nucleic acid binding / nucleotide binding			ko03040|Spliceosome	GO:0046872	nr -
Unigene117024_All	278	0.00	0.00	0.00	0.00	0.00	0.00	20.08	16.69	0.00	null	null		null	null		null	null		null	null		-2.67E-01	2.76E-01		-1.43E+01	4.80E-41	Down	Unigene117024_All//gi|168068200|ref|XP_001785975.1|//6.00E-14//predicted protein [Physcomitrella patens subsp. patens] >gi|162662338|gb|EDQ49215.1| predicted protein [Physcomitrella patens subsp. patens]		Unigene117024_All//1.00E-28//gi|78348172|gb|DT568446.1|DT568446				nr -
Unigene117026_All	278	0.38	0.00	0.00	0.36	0.00	0.00	1.37	5.41	3.01	-8.56E+00	3.75E-01		-8.56E+00	3.96E-01		-8.49E+00	3.15E-01		-8.49E+00	4.03E-01		1.98E+00	2.06E-04	Up	1.14E+00	9.20E-02					Unigene117026_All//3.00E-07//TC154702						
Unigene117027_All	278	0.00	0.73	0.00	0.00	0.00	0.00	0.30	6.92	0.72	9.51E+00	1.37E-01		null	null		null	null		null	null		4.51E+00	4.15E-11	Up	1.24E+00	4.69E-01		Unigene117027_All//gi|33411464|emb|CAA12387.1|//8.00E-19//Hsp20.1 protein [Solanum peruvianum]	Unigene117027_All//4.00E-17//AT2G29500| 17.6 kDa class I small heat shock protein (HSP17.6B-CI)	Unigene117027_All//1.00E-108//TC145915				nr +

Unigene117028_A11	278	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.56	0.00	null	null		null	null		null	null		null	null		1.13E+01	3.98E-05	Up	null	null		Unigene117028_A11//gi|38325811|gb|AAR17078.1|//1.00E-39//heat shock protein 70-1 [Nicotiana tabacum]	Unigene117028_A11//5.00E-32//AT3G09440| heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	Unigene117028_A11//5.00E-12//EX170481		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr +
Unigene117703_A11	1944	15.29	8.78	10.71	3.84	6.59	7.99	1.35	2.19	1.23	-7.99E-01	2.65E-15		-5.13E-01	4.73E-07		7.78E-01	1.50E-07		1.06E+00	1.39E-13	Up	7.02E-01	7.42E-03		-1.33E-01	6.99E-01		Unigene117703_A11//gi|297796055|ref|XP_002865912.1|//1.00E-132//hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311747|gb|EFH42171.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene117703_A11//5.00E-118//AT4G25620| hydroxyproline-rich glycoprotein family protein	Unigene117703_A11//0.00E+00//TC144318				nr +
Unigene117704_A11	2079	2.24	10.87	3.59	2.68	3.89	4.00	3.13	3.32	4.73	2.28E+00	1.92E-54	Up	6.79E-01	2.20E-03		5.37E-01	6.61E-03		5.75E-01	4.02E-03		8.29E-02	7.20E-01		5.96E-01	1.73E-04		Unigene117704_A11//gi|224067156|ref|XP_002302383.1|//1.00E-173//amino acid transporter [Populus trichocarpa] >gi|222844109|gb|EEE81656.1| amino acid transporter [Populus trichocarpa]	Unigene117704_A11//6.00E-132//AT3G30390| amino acid transporter family protein	Unigene117704_A11//0.00E+00//gi|109861836|gb|DW490813.1|DW490813			GO:0031224	nr -
Unigene117042_A11	280	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.22	0.00	null	null		null	null		null	null		null	null		1.24E+01	2.52E-10	Up	null	null		Unigene117042_A11//gi|42565109|ref|NP_188851.2|//4.00E-08//CWLP (CELL WALL-PLASMA MEMBRANE LINKER PROTEIN); lipid binding [Arabidopsis thaliana] >gi|124301006|gb|ABN04755.1| At3g22120 [Arabidopsis thaliana]						nr +
Unigene117045_A11	281	0.00	0.00	0.00	1.77	0.37	0.16	0.30	34.36	0.14	null	null		null	null		-2.27E+00	4.22E-02		-3.46E+00	1.61E-02		6.84E+00	2.12E-64	Up	-1.09E+00	6.77E-01		Unigene117045_A11//gi|224073330|ref|XP_002304078.1|//1.00E-12//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222841510|gb|EEE79057.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene117045_A11//8.00E-14//AT5G64530| XND1; transcription factor		NAC			nr +
Unigene117046_A11	281	0.00	0.00	0.00	0.53	0.37	0.00	1.20	5.50	0.14	null	null		null	null		-5.33E-01	7.85E-01		-9.05E+00	2.34E-01		2.19E+00	5.11E-05	Up	-3.09E+00	3.92E-02					Unigene117046_A11//4.00E-68//DW508129				
Unigene117051_A11	281	0.56	6.31	1.14	0.00	0.00	0.32	0.15	1.19	0.43	3.50E+00	3.83E-07	Up	1.03E+00	4.71E-01		null	null		8.33E+00	4.79E-01		2.98E+00	5.74E-02		1.50E+00	5.58E-01					Unigene117051_A11//3.00E-38//TC173468				
Unigene117053_A11	281	0.00	0.36	0.00	0.00	0.00	0.00	293.55	57.71	76.70	8.49E+00	3.89E-01		null	null		null	null		null	null		-2.35E+00	9.02E-252	Down	-1.94E+00	5.33E-203	Down	Unigene117053_A11//gi|255045895|gb|ACU00104.1|//2.00E-15//plasma membrane intrinsic protein PIP2.2 [Populus trichocarpa x Populus deltoides]	Unigene117053_A11//2.00E-13//AT3G54820| PIP2;5 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;5); water channel	Unigene117053_A11//2.00E-98//gi|31407371|gb|CD486406.1|CD486406				nr +
Unigene117060_A11	282	0.00	0.00	0.00	0.00	0.24	0.00	0.30	2.82	0.71	null	null		null	null		7.93E+00	6.13E-01		null	null		3.23E+00	5.44E-04	Up	1.24E+00	4.69E-01		Unigene117060_A11//gi|92886073|gb|ABE88083.1|//1.00E-07//Protein kinase [Medicago truncatula]	Unigene117060_A11//4.00E-08//AT4G05200| protein kinase family protein					nr -
Unigene117061_A11	283	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.07	0.00	null	null		null	null		null	null		null	null		1.10E+01	2.81E-04	Up	null	null		Unigene117061_A11//gi|38325811|gb|AAR17078.1|//7.00E-44//heat shock protein 70-1 [Nicotiana tabacum]	Unigene117061_A11//3.00E-34//AT1G09080| BIP3; ATP binding	Unigene117061_A11//1.00E-12//gi|78350754|gb|DT571028.1|DT571028		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03060|Protein export		nr -
Unigene117068_A11	284	4539.38	2046.05	4863.94	698.80	824.75	499.18	0.45	1.91	0.84	-1.15E+00	0.00E+00	Down	9.96E-02	1.44E-13		2.39E-01	2.07E-15		-4.85E-01	7.76E-44		2.10E+00	3.71E-02		9.14E-01	5.42E-01		Unigene117068_A11//gi|231610|sp|P29790.1|ATPG_TOBAC//3.00E-24//RecName: Full=ATP synthase gamma chain, chloroplastic; AltName: Full=F-ATPase gamma subunit; Flags: Precursor >gi|19785|emb|CAA45152.1| ATP synthase (gamma subunit) [Nicotiana tabacum]		Unigene117068_A11//2.00E-159//gi|164250171|gb|EX167616.1|EX167616		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr +
Unigene11707_A11	1201	14.72	34.55	17.56	28.04	30.48	42.87	35.87	57.91	72.78	1.23E+00	4.92E-42	Up	2.54E-01	5.05E-02		1.20E-01	2.34E-01		6.13E-01	1.48E-17		6.91E-01	4.12E-33		1.02E+00	1.35E-81	Up	Unigene11707_A11//gi|42570941|ref|NP_973544.1|//1.00E-120//OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|79602271|ref|NP_973546.2| OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|186503523|ref|NP_973545.2| OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|110735090|gb|ABG89115.1| OTU-containing protein 6 [synthetic construct]	Unigene11707_A11//3.00E-109//AT2G27350| OTU-like cysteine protease family protein	Unigene11707_A11//0.00E+00//TC136519			GO:0043231	nr -
Unigene117079_A11	286	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.34	0.00	null	null		null	null		null	null		null	null		1.12E+01	7.64E-05	Up	null	null		Unigene117079_A11//gi|50843988|gb|AAT84169.1|//1.00E-26//60S ribosomal protein L27 [Chara globularis]	Unigene117079_A11//5.00E-24//AT3G22230| 60S ribosomal protein L27 (RPL27B)			ko03010|Ribosome		nr -
Unigene11708_A11	2215	4.84	7.87	5.12	7.74	8.05	9.36	9.07	13.62	23.40	7.01E-01	1.52E-07		8.06E-02	6.63E-01		5.79E-02	7.49E-01		2.75E-01	2.86E-02		5.87E-01	2.48E-11		1.37E+00	5.01E-77	Up	Unigene11708_A11//gi|226494281|ref|NP_001151795.1|//1.00E-141//cysteine-type peptidase [Zea mays] >gi|195649739|gb|ACG44337.1| cysteine-type peptidase [Zea mays]	Unigene11708_A11//1.00E-111//AT2G27350| OTU-like cysteine protease family protein	Unigene11708_A11//0.00E+00//TC153990			GO:0043231	nr +
Unigene117083_A11	286	0.00	0.00	0.00	0.00	0.24	0.00	0.15	3.07	0.14	null	null		null	null		7.91E+00	6.12E-01		null	null		4.38E+00	3.08E-05	Up	-8.55E-02	9.73E-01					Unigene117083_A11//3.00E-66//DT467436				
Unigene117089_A11	287	0.18	0.00	0.00	0.00	0.00	0.16	1.18	1.60	5.27	-7.51E+00	6.16E-01		-7.51E+00	6.28E-01		null	null		7.30E+00	6.99E-01		4.43E-01	6.32E-01		2.16E+00	5.30E-05	Up	Unigene117089_A11//gi|164604966|dbj|BAF98279.1|//5.00E-31//hydroxymethylglutaryl-CoA synthase [Hevea brasiliensis]	Unigene117089_A11//7.00E-28//AT4G11820| MVA1; acetyl-CoA C-acetyltransferase/ hydroxymethylglutaryl-CoA synthase	Unigene117089_A11//3.00E-118//gi|13248420|gb|BF275790.2|BF275790		ko00280|Valine, leucine and isoleucine degradation//ko00650|Butanoate metabolism//ko00900|Terpenoid backbone biosynthesis//ko00072|Synthesis and degradation of ketone bodies		nr +
Unigene11709_A11	490	12.71	29.88	27.60	21.15	25.72	23.69	19.59	23.46	21.55	1.23E+00	2.30E-15	Up	1.12E+00	7.68E-12	Up	2.83E-01	8.61E-02		1.64E-01	4.00E-01		2.60E-01	1.02E-01		1.38E-01	4.23E-01		Unigene11709_A11//gi|89257511|gb|AB065001.1|//5.00E-41//Mo25 family protein [Brassica oleracea]	Unigene11709_A11//3.00E-40//AT5G47540| binding	Unigene11709_A11//0.00E+00//gi|78351728|gb|DT572002.1|DT572002			GO:0016020	nr +
Unigene117091_A11	287	77.84	31.60	48.24	41.83	31.20	22.66	1.47	2.33	0.69	-1.30E+00	4.49E-25	Down	-6.90E-01	8.24E-09		-4.23E-01	6.77E-03		-8.84E-01	3.54E-08		6.61E-01	4.02E-01		-1.09E+00	2.82E-01									ESTscan -
Unigene117096_A11	288	0.00	0.00	0.00	0.17	0.00	0.16	0.00	1.89	0.55	null	null		null	null		-7.43E+00	5.59E-01		-1.42E-01	9.55E-01		1.09E+01	5.36E-04	Up	9.11E+00	1.40E-01		Unigene117096_A11//gi|46931304|gb|AAT06456.1|//1.00E-26//At5g50410 [Arabidopsis thaliana]	Unigene117096_A11//2.00E-28//AT5G50410| unknown protein	Unigene117096_A11//2.00E-51//DR453384				nr -
Unigene117097_A11	288	0.18	2.29	0.00	0.35	0.84	0.31	0.15	2.61	0.42	3.65E+00	4.10E-03		-7.51E+00	6.28E-01		1.27E+00	5.32E-01		-1.41E-01	9.51E-01		4.15E+00	1.92E-04	Up	1.50E+00	5.58E-01					Unigene117097_A11//2.00E-110//TC147893				
Unigene117099_A11	288	881.82	376.15	293.80	799.97	847.37	509.81	329.14	134.97	200.99	-1.23E+00	8.52E-255	Down	-1.59E+00	0.00E+00	Down	8.31E-02	1.31E-02		-6.50E-01	7.69E-86		-1.29E+00	3.65E-125	Down	-7.12E-01	1.56E-48		Unigene117099_A11//gi|7387726|sp|O22582.3|H2B_GOSHI//2.00E-29//RecName: Full=Histone H2B >gi|2558962|gb|AAB97163.1| histone H2B1 [Gossypium hirsutum]		Unigene117099_A11//4.00E-142//TC144873				nr -
Unigene1171_A11	1560	2.52	3.96	3.14	3.54	7.90	25.94	8.10	8.63	35.04	6.56E-01	5.80E-03		3.20E-01	2.79E-01		1.16E+00	1.47E-13	Up	2.87E+00	4.99E-135	Up	9.03E-02	6.09E-01		2.11E+00	5.54E-149	Up	Unigene1171_A11//gi|297827611|ref|XP_002881688.1|//1.00E-178//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327527|gb|EFH57947.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1171_A11//4.00E-174//AT2G39980| transferase family protein	Unigene1171_A11//0.00E+00//TC162451		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016747	nr +
Unigene11710_A11	715	27.44	30.54	34.71	26.06	25.67	27.29	22.77	17.54	9.36	1.55E-01	2.31E-01		3.39E-01	3.22E-03		-2.16E-02	8.88E-01		6.66E-02	6.74E-01		-3.77E-01	2.46E-03		-1.28E+00	1.00E-22	Down	Unigene11710_A11//gi|240256410|ref|NP_199565.4|//5.00E-86//binding [Arabidopsis thaliana] >gi|15214076|sp|Q9FGK3.1|M025N_ARATH RecName: Full=Putative M025-like protein At5g47540 >gi|16226301|gb|AAL16128.1|AF428296_1 AT5g47540/MNJ7_13 [Arabidopsis thaliana] >gi|193211497|gb|ACF16168.1| At5g47540 [Arabidopsis thaliana]	Unigene11710_A11//3.00E-87//AT5G47540| binding	Unigene11710_A11//0.00E+00//TC136454			GO:0016020	nr +
Unigene117104_A11	289	0.00	0.00	0.00	0.00	0.00	0.00	0.15	2.89	0.14	null	null		null	null		null	null		null	null		4.31E+00	5.67E-05	Up	-8.64E-02	9.73E-01		Unigene117104_A11//COG0438//6.00E-12//Glycosyltransferase						cog +
Unigene117106_A11	289	0.00	0.00	0.00	0.00	0.00	0.00	2.78	7.38	0.00	null	null		null	null		null	null		null	null		1.41E+00	5.52E-04	Up	-1.14E+01	4.43E-06	Down									ESTscan +
Unigene117108_A11	290	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.31	0.00	null	null		null	null		null	null		null	null		1.12E+01	7.64E-05	Up	null	null		Unigene117108_A11//gi|3107919|dbj|BAA25911.1|//2.00E-09//actin [Nannochloris bacillaris]	Unigene117108_A11//2.00E-10//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene117108_A11//4.00E-13//TC129604		ko04145|Phagosome		nr +
Unigene117112_A11	290	0.00	0.00	0.00	0.00	0.00	0.00	2.33	2.74	0.14	null	null		null	null		null	null		null	null		2.31E-01	7.35E-01		-4.09E+00	3.10E-04	Down	Unigene117112_A11//gi|112253381|gb|ABI14278.1|//2.00E-29//translation elongation factor P [Fliesteria piscicida] >gi|112253383|gb|ABI14279.1| translation initiation factor 5A [Fliesteria piscicida]	Unigene117112_A11//4.00E-28//AT1G26630| FBR12 (FUMONISIN B1-RESISTANT12); translation initiation factor					nr +
Unigene117120_A11	291	0.00	0.00	0.00	0.00	0.00	0.00	1.89	4.60	0.00	null	null		null	null		null	null		null	null		1.28E+00	1.56E-02		-1.09E+01	2.81E-04	Down	Unigene117120_A11//gi|44917163|dbj|BAD12182.1|//1.00E-32//14-3-3 [-1 protein [Nicotiana tabacum]	Unigene117120_A11//2.00E-32//AT1G26480| GRF12 (GENERAL REGULATORY FACTOR 12); protein binding / protein phosphorylated amino acid binding	Unigene117120_A11//6.00E-21//gi|5046419|gb|AI727567.1|AI727567				nr -
Unigene117122_A11	291	221.87	201.98	223.80	341.51	392.87	388.00	74.54	118.92	160.45	-1.36E-01	5.28E-02		1.25E-02	8.78E-01		2.02E-01	8.66E-06		1.84E-01	1.43E-04		6.74E-01	3.29E-16		1.11E+00	4.96E-50	Up	Unigene117122_A11//gi|300510880|gb|ADK25058.1|//2.00E-10//AN1-like transcription factor [Glycine max]	Unigene117122_A11//1.00E-08//AT3G12630| zinc finger (AN1-like) family protein	Unigene117122_A11//1.00E-120//gi|164266342|gb|ES822249.1|ES822249				nr -
Unigene117124_A11	292	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.86	0.00	null	null		null	null		null	null		null	null		1.09E+01	5.36E-04	Up	null	null		Unigene117124_A11//gi|32401377|gb|AAP80858.1|//5.00E-39//ribosomal protein L19 [Triticum aestivum]	Unigene117124_A11//3.00E-22//AT1G02780| emb2386 (embryo defective 2386); structural constituent of ribosome	Unigene117124_A11//3.00E-07//gi|11200775|gb|BF269780.1|BF269780		ko03010|Ribosome		nr -
Unigene117126_A11	292	0.00	0.00	0.00	0.00	0.00	0.00	2.32	2.86	0.00	null	null		null	null		null	null		null	null		3.05E-01	6.47E-01		-1.12E+01	3.56E-05	Down	Unigene117126_A11//gi|195618310|gb|ACG30985.1|//2.00E-22//60S acidic ribosomal protein P1 [Zea mays] >gi|195625300|gb|ACG34480.1| 60S acidic ribosomal protein P1 [Zea mays]	Unigene117126_A11//1.00E-08//AT5G24510| 60s acidic ribosomal protein P1, putative			ko03010|Ribosome		nr +
Unigene11713_A11	425	23.76	17.41	7.52	46.88	32.90	37.83	40.59	35.90	21.47	-4.49E-01	1.33E-02		-1.66E+00	7.79E-16	Down	-5.11E-01	6.76E-06		-3.10E-01	1.38E-02		-1.77E-01	1.80E-01		-9.19E-01	2.29E-14					Unigene11713_A11//0.00E+00//TC139822				
Unigene117134_A11	293	0.00	0.00	0.00	0.00	0.00	0.00	1.44	5.42	0.00	null	null		null	null		null	null		null	null		1.91E+00	1.97E-04	Up	-1.05E+01	2.14E-03									ESTscan -
Unigene117142_A11	295	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.38	0.00	null	null		null	null		null	null		null	null		1.26E+01	3.04E-13	Up	null	null		Unigene117142_A11//sp|Q99334|MT1_COLGL//1.00E-06//Metallothionein-like protein CAP3 OS=Colletotrichum gloeosporioides GN=CAP3 PE=2 SV=1						swissprot +
Unigene117147_A11	296	0.00	0.00	0.00	0.17	0.00	0.00	0.00	1.84	0.27	null	null		null	null		-7.39E+00	5.59E-01		-7.39E+00	6.40E-01		1.08E+01	5.36E-04	Up	8.07E+00	4.05E-01		Unigene117147_A11//gi|21311555|gb|AAM46778.1|AF466103_1//1.00E-41//15.8 kDa oleosin [Theobroma cacao]	Unigene117147_A11//9.00E-18//AT2G25890| glycine-rich protein / oleosin	Unigene117147_A11//4.00E-164//TC144426				nr +
Unigene117715_A11	345	12.74	5.73	6.17	11.55	6.99	10.47	16.79	8.60	4.85	-1.15E+00	9.42E-05	Down	-1.05E+00	6.04E-04	Down	-7.25E-01	1.20E-02		-1.41E-01	6.92E-01		-9.65E-01	1.38E-05		-1.79E+00	1.35E-13	Down	Unigene11715_A11//gi|86611379|gb|AB014373.1|//2.00E-34//cyclin-dependent kinase type A [Prunus dulcis]	Unigene11715_A11//2.00E-34//AT3G48750| CDC2 (CELL DIVISION CONTROL 2); cyclin-dependent protein kinase/ kinase/ protein binding / protein kinase	Unigene11715_A11//2.00E-175//gi|164338395|gb|ES829952.1|ES829952			GO:0000087//GO:0004674//GO:0006464//GO:0032559	nr +

Unigene117157_All	297	0.00	0.00	0.00	0.00	0.00	0.00	0.57	3.52	0.00	null	null		null	null		null	null		null	null		2.63E+00	2.86E-04	Up	-9.15E+00	1.08E-01		Unigene117157_All//gi|18403247|ref|NP_566697.1|//9.00E-13//receptor protein kinase-related [Arabidopsis thaliana] >gi|75273758|sp|Q9LRJ9.1|CRR38_ARATH RecName: Full=Cysteine-rich repeat secretory protein 38; Flags: Precursor >gi|90186230|gb|ABD91491.1|At3g22060 [Arabidopsis thaliana]	Unigene117157_All//3.00E-14//AT3G22060| receptor protein kinase-related					nr -
Unigene117716_All	1617	8.61	6.77	7.74	16.97	15.35	15.67	17.36	10.68	7.86	-3.47E-01	2.39E-02		-1.53E-01	3.92E-01		-1.45E-01	2.09E-01		-1.16E-01	3.54E-01		-7.02E-01	3.12E-14		-1.14E+00	2.66E-32	Down	Unigene11716_All//gi|157683271|gb|ABV64386.1|//1.00E-161//cyclin-dependent kinase A [Gossypium hirsutum]	Unigene11716_All//2.00E-143//AT3G48750| CDC2 (CELL DIVISION CONTROL 2); cyclin-dependent protein kinase/ kinase/ protein binding / protein kinase	Unigene11716_All//0.00E+00//gi|164248123|gb|ES806283.1|ES806283				nr +
Unigene117162_All	299	0.00	0.34	0.18	0.50	0.23	0.00	0.00	1.96	0.67	8.40E+00	3.89E-01		7.48E+00	6.38E-01		-1.12E+00	5.84E-01		-8.97E+00	2.34E-01		1.09E+01	2.81E-04	Up	9.38E+00	7.90E-02								
Unigene117163_All	299	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.82	1.07	null	null		null	null		null	null		null	null		1.08E+01	5.36E-04	Up	1.01E+01	1.34E-02								
Unigene117166_All	300	0.00	0.00	0.00	0.00	0.00	0.00	2.11	1.53	0.00	null	null		null	null		null	null		null	null		-4.64E-01	5.94E-01		-1.10E+01	7.11E-05	Down	Unigene117166_All//gi|255087726|ref|XP_002505786.1|//1.00E-18//histone chaperone [Micromonas sp. RCC299] >gi|226521056|gb|ACO67044.1|histone chaperone [Micromonas sp. RCC299]	Unigene117166_All//5.00E-19//AT3G28730| ATHMG (ARABIDOPSIS THALIANA HIGH MOBILITY GROUP); transcription factor			ko03410|Base excision repair		nr -
Unigene117168_All	300	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.97	0.00	null	null		null	null		null	null		null	null		1.28E+01	1.05E-14	Up	null	null		Unigene117168_All//gi|1655699|emb|CAA60032.1|//4.00E-13//pherophorin-S [Volvox carteri f. nagariensis]						nr +
Unigene11717_All	1804	11.60	6.40	7.91	17.40	14.07	10.87	15.16	7.32	4.59	-8.57E-01	2.62E-12		-5.52E-01	8.15E-06		-3.06E-01	8.08E-04		-6.79E-01	4.13E-13		-1.05E+00	9.23E-27	Down	-1.72E+00	7.20E-58	Down	Unigene11717_All//gi|17224978|gb|AAL37195.1|AF321361_1|//1.00E-158//cyclin dependent kinase [Helianthus annuus]	Unigene11717_All//1.00E-145//AT3G48750| CDC2 (CELL DIVISION CONTROL 2); cyclin-dependent protein kinase/ kinase/ protein binding / protein kinase	Unigene11717_All//0.00E+00//TC151725				nr +
Unigene117171_All	301	0.00	0.00	0.00	0.00	0.11	0.15	0.00	2.22	0.00	null	null		null	null		6.84E+00	8.34E-01		7.23E+00	6.99E-01		1.11E+01	7.64E-05	Up	null	null								
Unigene117176_All	301	0.00	0.00	0.00	0.00	0.00	0.00	3.65	1.81	0.26	null	null		null	null		null	null		null	null		-1.02E+00	8.43E-02		-3.79E+00	3.27E-06	Down							ESTscan -
Unigene117180_All	302	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.80	0.00	null	null		null	null		null	null		null	null		1.08E+01	5.36E-04	Up	null	null		Unigene117180_All//gi|17367847|sp|Q9XF97.1|RL4_PRUAR//2.00E-25//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|9887131|gb|AAD32206.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene117180_All//4.00E-24//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)			ko03010|Ribosome		nr -
Unigene117719_All	1677	582.95	50.70	194.01	323.54	312.05	125.63	96.84	7.03	35.75	-3.52E+00	0.00E+00	Down	-1.59E+00	0.00E+00	Down	-5.22E-02	2.09E-02		-1.36E+00	0.00E+00	Down	-3.78E+00	0.00E+00	Down	-1.44E+00	6.93E-261	Down	Unigene11719_All//gi|23452315|gb|AAN32988.1|//0.00E+00//beta-tubulin 1 [Gossypium hirsutum]	Unigene11719_All//0.00E+00//AT5G12250| TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton	Unigene11719_All//0.00E+00//TC155561		ko04145|Phagosome	GO:0006970//GO:0007017//GO:0015630//GO:0016020//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene117190_All	304	0.00	0.00	0.00	0.00	0.00	0.00	0.28	3.02	0.00	null	null		null	null		null	null		null	null		3.44E+00	9.84E-05	Up	-8.12E+00	3.59E-01								ESTscan -
Unigene117195_All	305	0.00	0.00	0.00	0.82	0.79	0.30	8.87	2.33	2.87	null	null		null	null		-4.72E-02	9.52E-01		-1.46E+00	4.07E-01		-1.93E+00	3.86E-07	Down	-1.63E+00	4.80E-06	Down		Unigene117195_All//3.00E-07//DW509255					
Unigene117197_All	305	0.00	0.00	0.35	0.65	0.79	0.74	15.66	5.34	1.44	null	null		8.45E+00	4.01E-01		2.75E-01	8.95E-01		1.81E-01	9.35E-01		-1.55E+00	4.27E-09	Down	-3.45E+00	4.00E-23	Down		Unigene117197_All//3.00E-07//FL576500					
Unigene117198_All	306	0.00	0.83	0.00	1.63	0.00	0.00	1.38	2.32	7.03	9.69E+00	7.87E-02		null	null		-1.07E+01	8.98E-04	Down	-1.07E+01	2.98E-03		7.49E-01	3.41E-01		2.35E+00	2.10E-07	Up		Unigene117198_All//3.00E-66//DW485235					
Unigene11720_All	1754	42.48	14.82	29.60	322.43	241.30	150.99	20.25	16.92	8.18	-1.52E+00	1.15E-103	Down	-5.21E-01	4.20E-17		-4.18E-01	1.23E-106		-1.09E+00	0.00E+00	Down	-2.59E-01	1.57E-03		-1.31E+00	4.82E-50	Down	Unigene11720_All//gi|54036488|sp|Q6VAF5.1|TBB7_GOSHI//0.00E+00//RecName: Full=Tubulin beta-7 chain; AltName: Full=Beta-7-tubulin >gi|37529498|gb|AAQ92667.1| beta-tubulin 7 [Gossypium hirsutum]	Unigene11720_All//0.00E+00//AT5G12250| TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton	Unigene11720_All//0.00E+00//TC153064		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene117201_All	306	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.14	0.00	null	null		null	null		null	null		null	null		1.16E+01	7.61E-07	Up	null	null		Unigene117201_All//gi|38325813|gb|AAR17079.1|//4.00E-31//heat shock protein 70-2 [Nicotiana tabacum]	Unigene117201_All//6.00E-30//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene117201_All//1.00E-22//gi|84149718|gb|DN781018.1|DN781018		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -
Unigene117208_All	307	0.00	0.00	0.00	0.00	0.00	0.00	2.34	1.63	0.00	null	null		null	null		null	null		null	null		-5.19E-01	5.08E-01		-1.12E+01	1.78E-05	Down	Unigene117208_All//sp|Q9EER8|S28A3_MOUSE//8.00E-21//Solute carrier family 28 member 3 OS=Mus musculus GN=Slc28a3 PE=2 SV=1						swissprot +
Unigene117209_All	308	0.00	0.00	0.00	0.00	0.00	0.00	0.14	2.58	0.65	null	null		null	null		null	null		null	null		4.23E+00	1.05E-04	Up	2.24E+00	2.49E-01		Unigene117209_All//gi|255603215|ref|XP_002538008.1|//3.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223514214|gb|EEF24374.1|conserved hypothetical protein [Ricinus communis]						nr +
Unigene11721_All	743	2.46	11.66	4.37	4.96	4.96	4.26	2.90	2.81	1.45	2.24E+00	7.62E-21	Up	8.27E-01	2.17E-02		-6.00E-04	9.87E-01		-2.22E-01	5.48E-01		-4.52E-02	9.27E-01		-1.00E+00	7.92E-03		Unigene11721_All//gi|20141056|sp|Q9M2D2.2|YU88_ARATH//2.00E-74//RecName: Full=UPF0187 protein At3g61320, chloroplastic; Flags: Precursor >gi|16604549|gb|AAL24280.1|AT3g61320/T20K12_220 [Arabidopsis thaliana] >gi|23296291|gb|AAN12915.1|At3g61320/T20K12_220 [Arabidopsis thaliana]	Unigene11721_All//1.00E-75//AT3G61320| unknown protein	Unigene11721_All//0.00E+00//DW508764				nr -
Unigene117210_All	308	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.31	0.26	null	null		null	null		null	null		null	null		1.12E+01	3.98E-05	Up	8.02E+00	4.05E-01								
Unigene117213_All	309	0.00	0.98	3.45	1.45	0.22	0.88	1.23	1.89	0.52	9.94E+00	4.44E-02		1.18E+01	6.63E-06	Up	-2.70E+00	3.24E-02		-7.26E-01	5.32E-01		6.21E-01	4.78E-01		-1.26E+00	2.48E-01								
Unigene117216_All	310	0.00	1.96	0.00	0.96	0.67	0.44	0.00	2.02	0.26	1.09E+01	1.17E-03		null	null		-5.33E-01	6.79E-01		-1.14E+00	4.58E-01		1.10E+01	1.47E-04	Up	8.01E+00	4.05E-01			Unigene117216_All//4.00E-07//ES806034					
Unigene117218_All	310	0.17	0.00	0.00	0.32	0.00	0.00	2.32	27.91	1.29	-7.40E+00	6.16E-01		-7.40E+00	6.28E-01		-8.33E+00	3.15E-01		-8.33E+00	4.02E-01		3.59E+00	3.32E-41	Up	-8.51E-01	2.39E-01			Unigene117218_All//4.00E-07//DW507929					
Unigene117234_All	313	0.00	0.00	0.00	0.00	0.00	0.00	0.41	3.47	0.00	null	null		null	null		null	null		null	null		3.10E+00	4.52E-05	Up	-8.66E+00	2.00E-01		Unigene117234_All//sp|Q54LY1|Y6311_DICDI//9.00E-06//G8 domain-containing protein DDB_G0286311 OS=Dictyostelium discoideum GN=DDB_G0286311 PE=3 SV=1						swissprot +
Unigene117236_All	313	0.00	0.00	0.68	1.27	0.00	0.00	0.00	4.94	1.02	null	null		9.41E+00	1.41E-01		-1.03E+01	4.39E-03		-1.03E+01	1.11E-02		1.23E+01	6.59E-11	Up	9.99E+00	1.34E-02								
Unigene117237_All	314	0.50	0.00	0.00	0.00	0.00	0.00	0.54	3.86	0.76	-8.97E+00	2.16E-01		-8.97E+00	2.46E-01		null	null		null	null		2.84E+00	3.39E-05	Up	4.99E-01	7.08E-01			Unigene117237_All//4.00E-07//TC172964					
Unigene117238_All	314	0.00	0.00	0.00	0.00	0.00	0.00	2.02	6.92	1.14	null	null		null	null		null	null		null	null		1.78E+00	2.47E-05	Up	-8.23E-01	2.93E-01			Unigene117238_All//4.00E-07//DT046802					
Unigene11724_All	1171	13.99	2.77	3.09	23.06	18.76	29.00	26.14	7.32	12.35	-2.34E+00	4.00E-41	Down	-2.18E+00	2.80E-36	Down	-2.97E-01	3.10E-03		3.31E-01	2.86E-04		-1.84E+00	1.55E-68	Down	-1.08E+00	3.31E-32	Down	Unigene11724_All//gi|15229546|ref|NP_189036.1|//1.00E-159//dehydratase family [Arabidopsis thaliana] >gi|17953301|gb|AAL48233.1|AF446360_1 AT3g23940/F14O13_13 [Arabidopsis thaliana] >gi|9294662|dbj|BAB03011.1|dihydroxy-acid dehydratase [Arabidopsis thaliana]	Unigene11724_All//1.00E-157//AT3G23940| dehydratase family	Unigene11724_All//0.00E+00//TC143517		ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene117245_All	317	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.75	0.13	null	null		null	null		null	null		null	null		1.22E+01	1.29E-10	Up	6.97E+00	6.46E-01			Unigene117245_All//6.00E-12//ES807146					
Unigene117246_All	318	0.00	0.00	0.00	0.00	0.00	0.00	0.00	8.81	0.00	null	null		null	null		null	null		null	null		1.31E+01	1.07E-19	Up	null	null								
Unigene11725_All	2528	19.52	7.10	7.77	26.60	29.82	42.68	35.57	23.16	41.48	-1.46E+00	6.39E-65	Down	-1.33E+00	2.30E-54	Down	1.65E-01	6.14E-03		6.82E-01	1.15E-43		-6.19E-01	3.24E-35		2.22E-01	6.01E-07		Unigene11725_All//gi|255671803|gb|ACU26534.1|//0.00E+00//dihydroxyacid dehydratase [Glycine max]	Unigene11725_All//0.00E+00//AT3G23940| dehydratase family	Unigene11725_All//0.00E+00//TC136783		ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis	GO:0006549//GO:0006573//GO:0008652//GO:0009532//GO:0016836//GO:0016914//GO:0048229	nr -
Unigene117251_All	320	0.00	0.00	0.00	0.00	0.00	0.00	2.64	3.53	0.00	null	null		null	null		null	null		null	null		4.16E-01	4.92E-01		-1.14E+01	2.21E-06	Down	Unigene117251_All//gi|145343549|ref|XP_001416382.1|//6.00E-38//ribosomal protein L19 [Ostreococcus lucimarinus CCE9901] >gi|144576607|gb|ABO94675.1|ribosomal protein L19 [Ostreococcus lucimarinus CCE9901]	Unigene117251_All//2.00E-37//AT4G02230| 60S ribosomal protein L19 (RPL19C)			ko03010|Ribosome		nr +
Unigene117254_All	322	0.00	0.00	0.00	0.00	0.00	0.00	0.26	3.12	0.12	null	null		null	null		null	null		null	null		3.57E+00	3.08E-05	Up	-1.09E+00	6.77E-01								
Unigene117255_All	322	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.73	0.00	null	null		null	null		null	null		null	null		1.14E+01	2.86E-06	Up	null	null		Unigene117255_All//gi|32400971|gb|AAP80691.1|//3.00E-46//ubiquitin-conjugating enzyme [Griffithsia japonica]	Unigene117255_All//8.00E-46//AT3G08690| UBC11 (UBIQUITIN-CONJUGATING ENZYME 11); ubiquitin-protein ligase	Unigene117255_All//1.00E-10//EX170326		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene117256_All	322	0.00	0.00	0.00	0.00	0.00	0.00	0.39	3.76	0.00	null	null		null	null		null	null		null	null		3.26E+00	8.29E-06	Up	-8.62E+00	2.00E-01								ESTscan +
Unigene117259_All	323	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.07	0.00	null	null		null	null		null	null		null	null		1.10E+01	7.64E-05	Up	null	null								ESTscan +
Unigene11726_All	1506	14.87	5.79	7.85	9.20	6.63	4.89	4.46	1.42	1.35	-1.36E+00	6.53E-27	Down	-9.22E-01	4.32E-14		-4.72E-01	8.57E-04		-9.12E-01	8.65E-10		-1.66E+00	1.20E-13	Down	-1.73E+00	6.72E-15	Down	Unigene11726_All//gi|82569446|gb|ABB83365.1|//1.00E-174//enoyl-ACP reductase [Malus x domestica]	Unigene11726_All//2.00E-154//AT2G05990| MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ enoyl-[acyl-carrier-protein] reductase/ oxidoreductase	Unigene11726_All//0.00E+00//gi|109852131|gb|DW481110.1|DW481110		ko00061|Fatty acid biosynthesis	GO:0004312//GO:0006631	nr -
Unigene117262_All	323	4.70	5.65	6.59	6.48	2.35	3.22	2.23	5.82	1.48	2.66E-01	6.07E-01		4.89E-01	2.95E-01		-1.47E+00	6.01E-04	Down	-1.01E+00	2.37E-02		1.39E+00	1.52E-03		-5.88E-01	4.09E-01			Unigene117262_All//4.00E-07//TC143316					
Unigene117263_All	324	0.00	0.00	0.00	0.00	0.00	0.00	0.65	3.23	0.00	null	null		null	null		null	null		null	null		2.31E+00	8.56E-04	Up	-9.35E+00	5.80E-02								ESTscan +
Unigene117266_All	325	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.93	0.00	null	null		null	null		null	null		null	null		1.09E+01	1.47E-04	Up	null	null		Unigene117266_All//COG0778//2.00E-06//Nitroreductase						cog +
Unigene11727_All	1767	19.31	8.17	6.12	19.11	15.90	15.21	21.63	5.65	6.45	-1.24E+00	2.96E-35	Down	-1.66E+00	2.92E-52	Down	-2.65E-01	2.99E-03		-3.30E-01	3.03E-04		-1.94E+00	1.22E-91	Down	-1.75E+00	4.88E-82	Down	Unigene11727_All//gi|82569446|gb|ABB83365.1|//0.00E+00//enoyl-ACP reductase [Malus x domestica]	Unigene11727_All//6.00E-149//AT2G05990| MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH)/ enoyl-[acyl-carrier-protein] reductase/ oxidoreductase	Unigene11727_All//0.00E+00//TC155088		ko00061|Fatty acid biosynthesis	GO:0004312//GO:0006631	nr +
Unigene117279_All	329	0.00	0.00	0.00	0.00	0.21	0.55	0.00	1.65	1.09	null	null		null	null		7.71E+00	6.12E-01		9.10E+00	1.95E-01		1.07E+01	5.36E-04	Up	1.01E+01	7.30E-03		Unigene117279_All//gi|18405611|ref|NP_566829.1|//1.00E-28//nodulin MtN3 family protein [Arabidopsis thaliana] >gi|25090096|gb|AAN72227.1|At3g28008/At3g28008 [Arabidopsis thaliana]	Unigene117279_All//6.00E-30//AT3G28007| nodulin MtN3 family protein					nr -
Unigene11728_All	724	1.37	0.00	1.54	2.13	2.09	0.50	1.40	0.35	0.88	-1.04E+01	7.46E-06	Down	1.70E-01	7.78E-01		-2.74E-02	9.58E-01		-2.10E+00	3.41E-04	Down	-2.02E+00	2.83E-03		-6.71E-01	2.53E-01		Unigene11728_All//gi|15217667|ref|NP_174087.1|//6.00E-45//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|218563530|sp|Q95F23.2|BH110_ARATH RecName: Full=Transcription factor bHLH110; AltName: Full=Transcription factor EN 59; AltName: Full=bHLH transcription factor bHLH110; AltName: Full=Basic helix-loop-helix protein 110; Short=bHLH 110; Short=AtbHLH110	Unigene11728_All//6.00E-37//AT1G27660| ethylene-responsive protein -related	Unigene11728_All//3.00E-93//CO085880	bHLH		GO:0010468//GO:0043231	nr -
Unigene117286_All	331	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.90	0.00	null	null		null	null		null	null		null	null		1.15E+01	7.61E-07	Up	null	null		Unigene117286_All//sp|Q8KU07|AZOB_XENAZ//3.00E-06//NAD(P)H azoreductase OS=Xenophilus azovorans GN=azoB PE=1 SV=2						swissprot +

Unigene117289_All	332	0.00	0.00	0.00	0.00	0.00	0.00	1.91	3.15	0.00	null	null		null	null		null	null		null	null		7.20E-01	2.38E-01		-1.09E+01	7.11E-05	Down	Unigene117289_All//gi|13661265|gb|AAK37834.1|AF182558_1//2.00E-58//beta-tubulin [Euglena gracilis] >gi|13661269|gb|AAK37836.1|AF182554_1 beta-tubulin [Euglena gracilis] >gi|13661271|gb|AAK37837.1|AF182555_1 beta-tubulin [Euglena gracilis] >gi|13661273|gb|AAK37838.1|AF182759_1 beta-tubulin [Euglena gracilis]	Unigene117289_All//4.00E-57//AT1G20010| TUB8; structural constituent of cytoskeleton	Unigene117289_All//1.00E-22//TC129598		ko04145|Phagosome		nr -
Unigene11729_All	323	0.00	0.78	0.49	0.77	0.43	0.00	3.93	0.39	0.37	9.62E+00	7.87E-02		8.95E+00	2.39E-01		-8.55E-01	5.74E-01		-9.59E+00	7.35E-02		-3.34E+00	3.42E-06	Down	-3.41E+00	1.45E-06	Down	Unigene11729_All//gi|15217667|ref|NP_174087.1|//2.00E-21//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|218563530|sp|Q9SFZ3.2|BHI10_ARATH RecName: Full=Transcription factor bHLH110; AltName: Full=Transcription factor EN 59; AltName: Full=bHLH transcription factor bHLH110; AltName: Full=Basic helix-loop-helix protein 110; Short=bHLH 110; Short=AtbHLH110	Unigene11729_All//9.00E-23//AT1G27660| ethylene-responsive protein -related	Unigene11729_All//6.00E-83//DW507031	bHLH		GO:0001071//GO:0010468//GO:0043231	nr +
Unigene117292_All	333	0.00	0.00	0.64	0.00	0.00	0.00	0.13	2.26	0.24	null	null		9.32E+00	1.41E-01		null	null		null	null		4.15E+00	1.92E-04	Up	9.14E-01	7.50E-01		Unigene117292_All//gi|294514718|gb|ADE95828.1|//2.00E-31//4-coumarate:CoA ligase 1 [Corchorus capsularis]	Unigene117292_All//7.00E-30//AT1G51660| 4CL1 (4-COUMARATE:COA LIGASE 1); 4-coumarate-CoA ligase	Unigene117292_All//2.00E-95//gi|82756624|gb|DV850186.1|DV850186		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene11773_All	3567	3.55	16.05	3.58	8.60	8.83	9.08	10.69	8.25	11.07	2.18E+00	1.34E-129	Up	1.34E-02	9.57E-01		3.82E-02	7.84E-01		7.76E-02	5.11E-01		-3.74E-01	1.24E-06		4.99E-02	5.99E-01		Unigene11773_All//gi|115478695|ref|NP_001062941.1|//0.00E+00//Os09g0346700 [Oryza sativa Japonica Group] >gi|113631174|dbj|BAF24855.1|Os09g0346700 [Oryza sativa Japonica Group]	Unigene11773_All//0.00E+00//AT2G25800| INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Munc13 homology 1 (InterPro:IPR014770), Protein of unknown function DUF810 (InterPro:IPR008528), Munc13 homology 2 (InterPro:IPR014772); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G20010.2); Has 242 Blast hits to 156 proteins in 35 species: Archae - 0; Bacteria - 8; Metazoa - 36; Fungi - 18; Plants - 94; Viruses - 0; Other Eukaryotes - 86 (source: NCBI BLink).	Unigene11773_All//0.00E+00//TC162496				nr -
Unigene11730_All	2100	1.59	3.31	2.76	15.56	13.61	7.61	7.79	4.94	5.86	1.05E+00	3.80E-06	Up	7.94E-01	1.96E-03		-1.93E-01	4.54E-02		-1.03E+00	2.99E-27	Down	-6.59E-01	8.18E-08		-4.11E-01	6.10E-04		Unigene11730_All//gi|15217667|ref|NP_174087.1|//3.00E-46//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|218563530|sp|Q9SFZ3.2|BHI10_ARATH RecName: Full=Transcription factor bHLH110; AltName: Full=Transcription factor EN 59; AltName: Full=bHLH transcription factor bHLH110; AltName: Full=Basic helix-loop-helix protein 110; Short=bHLH 110; Short=AtbHLH110	Unigene11730_All//1.00E-35//AT1G27660| ethylene-responsive protein -related	Unigene11730_All//0.00E+00//TC162179	bHLH			nr -
Unigene117301_All	339	0.00	0.00	0.00	0.00	0.00	0.00	1.00	5.79	1.53	null	null		null	null		null	null		null	null		2.54E+00	3.39E-07	Up	6.15E-01	4.94E-01					Unigene117301_All//6.00E-145//CD125364					
Unigene117305_All	341	0.00	0.00	0.00	0.15	0.10	0.00	0.62	3.80	1.99	null	null		null	null		-5.33E-01	8.27E-01		-7.19E+00	6.40E-01		2.62E+00	4.08E-05	Up	1.68E+00	3.70E-02										
Unigene117308_All	343	0.00	0.00	0.00	0.00	0.00	0.00	0.74	4.02	0.00	null	null		null	null		null	null		null	null		2.44E+00	4.59E-05	Up	-9.53E+00	3.04E-02		Unigene117308_All//sp|Q02817|MUC2_HUMAN//7.00E-06//Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2							swissprot +
Unigene11731_All	1226	2.60	0.41	4.21	4.23	4.07	2.14	1.79	0.17	1.23	-2.66E+00	8.99E-10	Down	6.95E-01	1.14E-02		-5.32E-02	8.47E-01		-9.84E-01	1.49E-04		-3.39E+00	1.88E-10	Down	-5.38E-01	1.51E-01		Unigene11731_All//gi|15217667|ref|NP_174087.1|//4.00E-56//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|218563530|sp|Q9SFZ3.2|BHI10_ARATH RecName: Full=Transcription factor bHLH110; AltName: Full=Transcription factor EN 59; AltName: Full=bHLH transcription factor bHLH110; AltName: Full=Basic helix-loop-helix protein 110; Short=bHLH 110; Short=AtbHLH110	Unigene11731_All//4.00E-48//AT1G27660| ethylene-responsive protein -related	Unigene11731_All//0.00E+00//gi|78352935|gb|DT573209.1|DT573209	bHLH		GO:0010468//GO:0043231	nr +
Unigene117312_All	346	0.00	0.00	0.00	0.00	0.00	0.26	0.00	9.30	1.38	null	null		null	null		null	null		8.03E+00	4.79E-01		1.32E+01	1.23E-22	Up	1.04E+01	1.15E-03					Unigene117312_All//4.00E-38//TC137853					
Unigene117316_All	349	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.71	0.00	null	null		null	null		null	null		null	null		1.19E+01	3.67E-09	Up	null	null		Unigene117316_All//sp|O94564|YGD6_SCHPO//2.00E-06//Zinc-type alcohol dehydrogenase-like protein C1773.06c OS=Schizosaccharomyces pombe GN=SPBC1773.06c PE=2 SV=1							swissprot -
Unigene117318_All	349	0.00	0.00	0.00	0.00	0.00	0.00	2.06	2.40	0.00	null	null		null	null		null	null		null	null		2.18E-01	7.44E-01		-1.10E+01	1.78E-05	Down									ESTscan +
Unigene117326_All	354	0.00	0.00	0.00	0.00	0.00	0.00	2.39	5.90	0.00	null	null		null	null		null	null		null	null		1.31E+00	1.39E-03		-1.12E+01	2.21E-06	Down	Unigene117326_All//gi|161701447|gb|ABX75541.1|//3.00E-89//60S ribosomal protein L17-like protein [Panax ginseng]	Unigene117326_All//4.00E-48//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene117326_All//1.00E-10//TC153743		ko03010|Ribosome		nr +
Unigene117329_All	355	0.00	0.00	0.00	0.00	0.00	0.00	2.50	5.77	0.00	null	null		null	null		null	null		null	null		1.21E+00	3.25E-03		-1.13E+01	1.10E-06	Down	Unigene117329_All//gi|14423905|sp|Q9XGL4.1|RL31_CYAPA//7.00E-31//RecName: Full=60S ribosomal protein L31 >gi|5123727|emb|CAB45375.1|ribosomal protein L31 [Cyanophora paradoxa]	Unigene117329_All//1.00E-25//AT4G26230| 60S ribosomal protein L31 (RPL31B)			ko03010|Ribosome		nr +
Unigene11733_All	1591	2.66	3.09	5.72	3.79	4.11	4.43	0.58	0.53	0.30	2.14E-01	4.53E-01		1.10E+00	5.14E-08	Up	1.18E-01	6.68E-01		2.25E-01	3.81E-01		-1.54E-01	8.08E-01		-9.60E-01	1.20E-01		Unigene11733_All//gi|7767672|gb|AAF69169.1|AC007915_21//4.00E-67//F27F5.21 [Arabidopsis thaliana]	Unigene11733_All//7.00E-35//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene11733_All//5.00E-07//TC133829			GO:0003676//GO:0016722//GO:0043231//GO:0044238//GO:0044260	nr -
Unigene117335_All	362	0.43	0.28	0.59	0.00	0.00	0.25	0.00	8.89	0.00	-6.32E-01	7.28E-01		4.40E-01	7.76E-01		null	null		7.96E+00	4.79E-01		1.31E+01	1.22E-22	Up	null	null					Unigene117335_All//1.00E-50//CO118951					
Unigene11734_All	1920	3.27	4.35	7.16	4.64	5.47	5.57	2.49	1.72	1.56	4.13E-01	4.25E-02		1.13E+00	3.43E-12	Up	2.36E-01	2.23E-01		2.64E-01	1.66E-01		-5.33E-01	3.16E-02		-6.77E-01	4.26E-03		Unigene11734_All//gi|38344244|emb|CAD41337.2|//9.00E-26//OJ991113_30.21 [Oryza sativa (japonica cultivar-group)]	Unigene11734_All//7.00E-27//AT2G18410| unknown protein	Unigene11734_All//0.00E+00//TC178231			GO:0043231	nr -
Unigene117344_All	371	0.00	0.00	0.00	0.00	0.00	0.00	0.80	4.06	0.00	null	null		null	null		null	null		null	null		2.35E+00	3.01E-05	Up	-9.64E+00	1.58E-02		Unigene117344_All//gi|255078736|ref|XP_002502948.1|//7.00E-39//translation elongation factor EF-1alpha/Tu [Micromonas sp. RCC299] >gi|226518214|gb|ACO64206.1|translation elongation factor EF-1alpha/Tu [Micromonas sp. RCC299]	Unigene117344_All//6.00E-20//AT5G60390| elongation factor 1-alpha / EF-1-alpha					nr +
Unigene117345_All	371	0.00	0.00	0.00	0.54	0.00	0.00	0.34	5.07	0.21	null	null		null	null		-9.07E+00	8.45E-02		-9.07E+00	1.34E-01		3.89E+00	6.17E-10	Up	-6.71E-01	7.20E-01										
Unigene117354_All	379	0.28	0.00	0.00	0.39	0.18	0.00	0.11	3.97	0.63	-8.11E+00	3.74E-01		-8.11E+00	3.96E-01		-1.12E+00	5.84E-01		-8.62E+00	2.34E-01		5.15E+00	2.32E-09	Up	2.50E+00	1.59E-01										
Unigene117355_All	379	0.00	0.00	0.00	0.00	0.00	0.00	2.57	4.30	0.00	null	null		null	null		null	null		null	null		7.45E-01	1.10E-01		-1.13E+01	2.72E-07	Down	Unigene117355_All//gi|116056034|emb|CAL58567.1|//6.00E-11//Nucleolar GTPase/ATPase p130 (ISS) [Ostreococcus tauri]				ko03018|RNA degradation		nr -
Unigene117359_All	383	0.68	0.26	0.00	0.13	0.45	0.47	1.21	16.26	0.94	-1.37E+00	3.83E-01		-9.42E+00	8.59E-02		1.79E+00	5.21E-01		1.86E+00	4.59E-01		3.74E+00	8.12E-31	Up	-3.75E-01	6.65E-01		Unigene117359_All//gi|115469074|ref|NP_001058136.1|//8.00E-06//Os06g0634300 [Oryza sativa Japonica Group] >gi|51535777|dbj|BAD37816.1| MutT domain protein-like [Oryza sativa Japonica Group] >gi|51535894|dbj|BAD37977.1| MutT domain protein-like [Oryza sativa Japonica Group] >gi|113596176|dbj|BAF20050.1|Os06g0634300 [Oryza sativa Japonica Group]	Unigene117359_All//3.00E-06//AT4G25434| ATNUDT10 (Arabidopsis thaliana Nudix hydrolase homolog 10); ADP-ribose diphosphatase/ NAD or NADH binding / catalytic	Unigene117359_All//9.00E-135//DR458609				nr -
Unigene117362_All	390	0.00	0.00	0.00	0.00	0.00	0.00	0.43	3.11	0.20	null	null		null	null		null	null		null	null		2.84E+00	3.39E-05	Up	-1.09E+00	5.53E-01										
Unigene117365_All	392	0.13	0.26	0.00	0.89	1.32	0.92	0.54	99.26	1.52	9.53E-01	7.27E-01		-7.06E+00	6.28E-01		5.67E-01	6.04E-01		5.13E-02	9.69E-01		7.52E+00	2.68E-265	Up	1.50E+00	7.88E-02					Unigene117365_All//3.00E-08//TC148689					ESTscan -
Unigene117366_All	392	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.71	0.00	null	null		null	null		null	null		null	null		1.07E+01	7.64E-05	Up	null	null		Unigene117366_All//gi|1743354|emb|CAA71003.1|//5.00E-40//aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]	Unigene117366_All//1.00E-40//AT3G48000| ALDH2B4 (ALDEHYDE DEHYDROGENASE 2B4); 3-chloroallyl aldehyde dehydrogenase/ ATP binding / aldehyde dehydrogenase (NAD)			ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr -
Unigene117369_All	394	0.00	0.00	0.00	0.00	0.00	0.00	0.21	4.67	0.10	null	null		null	null		null	null		null	null		4.44E+00	1.47E-10	Up	-1.09E+00	6.77E-01										
Unigene11737_All	1646	29.02	17.12	25.91	11.92	12.24	10.59	7.55	4.88	3.27	-7.62E-01	2.95E-22		-1.63E-01	5.55E-02		3.76E-02	8.39E-01		-1.71E-01	2.26E-01		-6.31E-01	9.49E-06		-1.21E+00	4.38E-16	Down	Unigene11737_All//gi|58760232|gb|AAW82030.1|//9.00E-93//inositol monophosphatase [Chlamydomonas incerta]	Unigene11737_All//4.00E-82//AT1G31190| IMPL1 (MYO-INOSITOL MONOPHOSPHATASE LIKE 1); 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase/ inositol-1(or 4)-monophosphatase	Unigene11737_All//0.00E+00//CO132745		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0004437//GO:0008252//GO:0009532//GO:0044237	nr +
Unigene117371_All	394	0.27	0.00	0.00	0.00	0.17	0.46	0.64	8.27	1.21	-8.05E+00	3.74E-01		-8.05E+00	3.96E-01		7.45E+00	6.12E-01		8.84E+00	1.95E-01		3.68E+00	3.48E-16	Up	9.14E-01	3.38E-01										

Unigene117372_All	395	0.00	0.00	0.00	0.00	0.00	0.00	2.86	0.00	null	null		null	null		null	null		null	null		1.15E+01	5.32E-08	Up	null	null		Unigene117372_All//gi|145344436|ref|XP_001416738.1|//6.00E-56//Peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Ostreococcus lucimarinus CCE9901] >gi|144576964|gb|AB095031.1| Peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Ostreococcus lucimarinus CCE9901]	Unigene117372_All//2.00E-45//AT3G56070| ROC2 (ROTAMASE CYCLOPHILIN 2); cyclosporin A binding / peptidyl-prolyl cis-trans isomerase	Unigene117372_All//3.00E-11//gi|48796304|gb|C0097618.1|C0097618				nr +
Unigene117373_All	396	0.26	0.00	0.54	0.00	0.00	0.00	0.00	11.93	0.10	-8.05E+00	3.74E-01		1.03E+00	5.92E-01		null	null		null	null		1.35E+01	2.92E-33	Up	6.65E+00	6.46E-01				Unigene117373_All//5.00E-07//TC173397				
Unigene117374_All	398	0.00	0.00	0.00	0.00	0.00	0.00	2.10	0.00	null	null		null	null		null	null		null	null		1.10E+01	5.54E-06	Up	null	null		Unigene117374_All//gi|293336034|ref|NP_001168895.1|//4.00E-11//hypothetical protein LOC100382700 [Zea mays] >gi|223973529|gb|ACN30952.1| unknown [Zea mays]						nr -
Unigene117375_All	398	0.00	0.00	0.00	0.00	0.09	0.00	0.00	4.20	0.00	null	null		null	null		6.43E+00	8.34E-01		null	null		1.20E+01	8.75E-12	Up	null	null									
Unigene117376_All	402	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.22	0.00	null	null		null	null		null	null		null	null		1.17E+01	3.67E-09	Up	null	null									
Unigene117378_All	403	0.00	0.00	0.00	0.00	0.00	0.00	0.73	4.36	0.00	null	null		null	null		null	null		null	null		2.57E+00	1.41E-06	Up	-9.82E+00	1.58E-02				Unigene117378_All//2.00E-09//TC137772				ESTscan +
Unigene117379_All	403	0.00	0.00	0.00	0.00	0.00	0.00	0.21	5.70	0.00	null	null		null	null		null	null		null	null		4.76E+00	1.36E-13	Up	-7.71E+00	3.59E-01		Unigene117379_All//gi|226458329|gb|EEH55626.1|//8.00E-09//predicted protein [Micromonas pusilla CCMP1545]	Unigene117379_All//9.00E-05//AT2G02380| ATGSTZ2; catalytic/ glutathione transferase					nr -
Unigene11738_All	1911	1.51	2.23	2.73	21.22	18.07	16.61	13.41	3.15	5.23	5.65E-01	5.65E-02		8.59E-01	1.65E-03		-2.31E-01	4.68E-03		-3.53E-01	1.57E-05		-2.09E+00	4.25E-68	Down	-1.36E+00	1.99E-38	Down	Unigene11738_All//gi|297805050|ref|XP_002870409.1|//0.00E+00//glycosyl hydrolase family 79 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297316245|gb|EFH46668.1| glycosyl hydrolase family 79 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene11738_All//0.00E+00//AT5G34940| AtGUS3 (Arabidopsis thaliana glucuronidase 3); beta-glucuronidase	Unigene11738_All//0.00E+00//TC157182			GO:0005618//GO:0016787//GO:0031410//GO:0043167//GO:0044238	nr +
Unigene117381_All	408	0.00	0.00	0.00	0.00	0.00	0.00	2.07	4.92	0.10	null	null		null	null		null	null		null	null		1.25E+00	2.74E-03		-4.41E+00	2.37E-05	Down	Unigene117381_All//gi|55168340|gb|AAV44205.1|//1.00E-06//unknow protein [Oryza sativa Japonica Group]		Unigene117381_All//9.00E-21//TC139311				nr +
Unigene117384_All	413	0.00	0.00	0.00	0.00	0.00	0.00	1.52	0.00	null	null		null	null		null	null		null	null		1.06E+01	1.47E-04	Up	null	null		Unigene117384_All//gi|297242517|gb|ADI24922.1|//5.00E-39//pirin [Carica papaya]	Unigene117384_All//3.00E-37//AT2G43120| pirin, putative					nr +
Unigene117386_All	413	1.01	0.00	0.77	0.36	0.50	0.66	0.31	2.33	0.77	-9.99E+00	1.05E-02		-3.90E-01	7.17E-01		4.68E-01	8.25E-01		8.59E-01	6.31E-01		2.92E+00	2.38E-04	Up	1.33E+00	2.93E-01				Unigene117386_All//5.00E-07//TC177933				
Unigene11739_All	1948	8.70	6.74	9.35	25.83	22.04	32.44	29.04	13.50	15.75	-3.69E-01	6.79E-03		1.03E-01	5.02E-01		-2.29E-01	1.49E-03		3.29E-01	3.02E-07		-1.11E+00	3.85E-59	Down	-8.83E-01	3.61E-42		Unigene11739_All//gi|297805050|ref|XP_002870409.1|//0.00E+00//glycosyl hydrolase family 79 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297316245|gb|EFH46668.1| glycosyl hydrolase family 79 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene11739_All//0.00E+00//AT5G34940| AtGUS3 (Arabidopsis thaliana glucuronidase 3); beta-glucuronidase	Unigene11739_All//0.00E+00//TC141405			GO:0005618//GO:0016787//GO:0031410//GO:0043167//GO:0044238	nr +
Unigene117390_All	420	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.48	0.47	null	null		null	null		null	null		null	null		1.18E+01	2.52E-10	Up	8.89E+00	7.90E-02									
Unigene117391_All	421	0.00	0.00	0.00	0.00	0.00	0.00	1.51	1.69	0.00	null	null		null	null		null	null		null	null		1.64E-01	8.24E-01		-1.06E+01	7.11E-05	Down	Unigene117391_All//gi|8050572|gb|AAF71706.1|AF213663_1|9.00E-50//elongation factor 2 [Euglena gracilis]	Unigene117391_All//2.00E-48//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene117391_All//3.00E-08//ES844303				nr -
Unigene117392_All	422	0.00	0.00	0.00	0.00	0.00	0.00	1.30	7.43	0.00	null	null		null	null		null	null		null	null		2.51E+00	5.72E-11	Up	-1.03E+01	2.80E-04	Down	Unigene117392_All//gi|115435924|ref|NP_001042720.1|//5.00E-06//Os01g0274800 [Oryza sativa Japonica Group] >gi|113532225|dbj|BAF04634.1| Os01g0274800 [Oryza sativa Japonica Group]						nr -
Unigene117393_All	422	0.00	2.52	0.25	0.35	0.16	0.75	2.00	2.48	0.28	1.13E+01	3.82E-06	Up	7.98E+00	4.01E-01		-1.12E+00	5.84E-01		1.08E+00	4.76E-01		3.05E-01	6.58E-01		-2.82E+00	5.38E-04	Down							
Unigene117397_All	425	1115.60	789.61	1219.11	227.86	327.18	190.96	1.19	4.03	1.50	-4.99E-01	5.20E-101		1.28E-01	1.40E-08		5.22E-01	9.93E-39		-2.55E-01	6.45E-07		1.76E+00	2.64E-04	Up	3.29E-01	6.60E-01		Unigene117397_All//gi|62910995|gb|AAY21210.1|//1.00E-36//ultraviolet-B-repressible protein [Gossypium hirsutum]		Unigene117397_All//0.00E+00//gi|84148317|gb|DN779617.1|DN779617				nr -
Unigene117398_All	426	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.37	0.00	null	null		null	null		null	null		null	null		1.04E+01	2.81E-04	Up	null	null		Unigene117398_All//sp|P19752|HSP30_NEUCR//8.00E-16//30 kDa heat shock protein OS=Neurospora crassa GN=hsp30 PE=3 SV=1						swissprot +
Unigene1174_All	476	4.29	8.73	3.24	3.87	4.12	10.15	3.64	4.92	1.84	1.03E+00	6.93E-04	Up	-4.02E-01	3.83E-01		9.08E-02	8.64E-01		1.39E+00	8.19E-07	Up	4.33E-01	2.64E-01		-9.84E-01	2.16E-02		Unigene1174_All//gi|1839022|emb|CAA72006.1|//2.00E-34//amino acid carrier [Ricinus communis]	Unigene1174_All//3.00E-35//AT5G49630| AAP6 (AMINO ACID PERMEASE 6); acidic amino acid transmembrane transporter/ amino acid transmembrane transporter/ neutral amino acid transmembrane transporter	Unigene1174_All//6.00E-121//TC145723			GO:0015171//GO:0015711//GO:0015801//GO:0031224//GO:0051707	nr +
Unigene11740_All	577	12.42	5.71	6.00	22.19	20.53	18.86	18.76	8.62	10.77	-1.12E+00	5.92E-07	Down	-1.05E+00	5.32E-06	Down	-1.12E-01	5.50E-01		-2.34E-01	1.77E-01		-1.12E+00	3.10E-12	Down	-8.00E-01	1.41E-07		Unigene11740_All//gi|15234416|ref|NP_192948.1|//3.00E-80//SM01-1 (STEROL-4ALPHA-METHYL OXIDASE 1-1); 4,4-dimethyl-9beta,19-cyclopropylsterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase/ catalytic [Arabidopsis thaliana] >gi|21928127|gb|AAM78091.1| AT4g12110/F16J13_180 [Arabidopsis thaliana] >gi|23308291|gb|AAN18115.1| At4g12110/F16J13_180 [Arabidopsis thaliana]	Unigene11740_All//2.00E-69//AT4G12110| SM01-1 (STEROL-4ALPHA-METHYL OXIDASE 1-1); 4,4-dimethyl-9beta,19-cyclopropylsterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase/ catalytic	Unigene11740_All//0.00E+00//TC163490		ko00100|Steroid biosynthesis	GO:0000254//GO:0000631//GO:0006694//GO:0031224//GO:0043231//GO:0046914	nr +
Unigene117400_All	426	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.12	1.22	null	null		null	null		null	null		null	null		1.20E+01	2.29E-12	Up	1.02E+01	6.14E-04	Up			Unigene117400_All//1.00E-07//NP_129581110				
Unigene117401_All	428	0.00	0.00	0.00	0.00	0.00	0.00	1.09	3.71	0.19	null	null		null	null		null	null		null	null		1.77E+00	4.38E-04	Up	-2.54E+00	2.35E-02		Unigene117401_All//gi|192913002|gb|ACF06609.1|//1.00E-51//ribosomal protein L19 [Elaeis guineensis]	Unigene117401_All//4.00E-37//AT3G16780| 60S ribosomal protein L19 (RPL19B)	Unigene117401_All//1.00E-07//ES804152		ko03010|Ribosome		nr +
Unigene117402_All	431	0.00	0.00	0.00	0.00	0.00	0.00	2.26	3.01	0.00	null	null		null	null		null	null		null	null		4.14E-01	4.51E-01		-1.11E+01	2.72E-07	Down	Unigene117402_All//gi|109398329|gb|ABG33906.1|//3.00E-26//Ole e 2 allergen [Olea europaea]	Unigene117402_All//3.00E-18//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding					nr +
Unigene117405_All	434	0.00	0.00	0.00	0.00	0.00	0.00	0.29	5.01	0.00	null	null		null	null		null	null		null	null		4.10E+00	8.27E-12	Up	-8.19E+00	2.00E-01									ESTscan -
Unigene117406_All	435	0.00	0.00	0.00	0.00	0.00	0.00	0.10	2.21	0.00	null	null		null	null		null	null		null	null		4.51E+00	8.92E-06	Up	-6.60E+00	6.14E-01		Unigene117406_All//sp|P48060|GLIP1_HUMAN//3.00E-07//Glioma pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR1 PE=1 SV=3	Unigene117406_All//1.00E-05//AT2G14610| PR1 (PATHOGENESIS-RELATED GENE 1)			ko04626|Plant-pathogen interaction		swissprot +
Unigene117407_All	443	0.00	0.00	0.00	0.00	0.00	0.00	0.38	2.36	0.00	null	null		null	null		null	null		null	null		2.63E+00	2.86E-04	Up	-8.58E+00	1.08E-01									ESTscan -
Unigene117408_All	444	0.00	0.00	0.00	0.00	0.00	0.00	0.19	2.54	0.00	null	null		null	null		null	null		null	null		3.74E+00	5.20E-06	Up	-7.57E+00	3.59E-01		Unigene117408_All//gi|53801490|gb|AAU93947.1|//1.00E-19//thioredoxin H [Helicosporidium sp. ex Simulium jonesi]	Unigene117408_All//2.00E-17//AT1G19730| ATTRX4; oxidoreductase, acting on sulfur group of donors, disulfide as acceptor					nr +
Unigene11741_All	1452	20.58	8.41	11.52	13.52	11.12	12.47	12.26	6.22	8.42	-1.29E+00	6.56E-33	Down	-8.37E-01	6.73E-16		-2.81E-01	2.25E-02		-1.16E-01	4.43E-01		-9.79E-01	7.37E-16		-5.41E-01	2.12E-06		Unigene11741_All//gi|15234416|ref|NP_192948.1|//1.00E-140//SM01-1 (STEROL-4ALPHA-METHYL OXIDASE 1-1); 4,4-dimethyl-9beta,19-cyclopropylsterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase/ catalytic [Arabidopsis thaliana] >gi|21928127|gb|AAM78091.1| AT4g12110/F16J13_180 [Arabidopsis thaliana] >gi|23308291|gb|AAN18115.1| At4g12110/F16J13_180 [Arabidopsis thaliana]	Unigene11741_All//3.00E-134//AT4G12110| SM01-1 (STEROL-4ALPHA-METHYL OXIDASE 1-1); 4,4-dimethyl-9beta,19-cyclopropylsterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase/ catalytic	Unigene11741_All//0.00E+00//gi|164310790|gb|EX171182.1|EX171182		ko00100|Steroid biosynthesis		nr +
Unigene117412_All	449	0.00	0.00	0.00	0.00	0.00	0.00	1.70	4.19	0.00	null	null		null	null		null	null		null	null		1.31E+00	2.64E-03		-1.07E+01	8.87E-06	Down	Unigene117412_All//gi|224006369|ref|XP_002292145.1|//4.00E-41//sulfolipid biosynthesis protein [Thalassiosira pseudonana CCMP1335] >gi|220972664|gb|EED90996.1| sulfolipid biosynthesis protein [Thalassiosira pseudonana CCMP1335]	Unigene117412_All//1.00E-27//AT4G33030| SQD1; UDPsulfoquinovose synthase/ sulfotransferase			ko00520|Amino sugar and nucleotide sugar metabolism//ko00561|Glycerolipid metabolism		nr -
Unigene117413_All	450	0.00	0.00	0.00	0.00	0.00	0.00	555.84	214.27	797.22	null	null		null	null		null	null		null	null		-1.38E+00	0.00E+00	Down	5.20E-01	1.80E-103		Unigene117413_All//gi|124365601|gb|AAK50778.4|AF361893_1|7.00E-14//bacterial-induced lipoxygenase [Gossypium hirsutum]	Unigene117413_All//2.00E-11//AT3G22400| LOX5; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene117413_All//8.00E-43//TC147960		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr +
Unigene117414_All	456	0.00	0.00	0.00	0.00	0.00	0.00	2.32	3.21	0.00	null	null		null	null		null	null		null	null		4.69E-01	3.70E-01		-1.12E+01	6.72E-08	Down	Unigene117414_All//gi|298705540|emb|CBJ28807.1|//5.00E-06//conserved unknown protein [Ectocarpus siliculosus]						nr -
Unigene117415_All	457	0.00	0.00	0.00	0.00	0.00	0.00	0.65	3.48	0.00	null	null		null	null		null	null		null	null		2.42E+00	1.10E-05	Up	-9.34E+00	1.58E-02		Unigene117415_All//gi|18406066|ref|NP_565985.1|//9.00E-59//PP5.2 (PROTEIN PHOSPHATASE 5.2); phosphoprotein phosphatase/ protein binding / protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|16930441|gb|AAL31906.1|AF419574_1 At2g42810/F7D19.19 [Arabidopsis thaliana] >gi|33589766|gb|AAQ22649.1| At2g42810/F7D19.19 [Arabidopsis thaliana]	Unigene117415_All//6.00E-60//AT2G42810| PP5.2 (PROTEIN PHOSPHATASE 5.2); phosphoprotein phosphatase/ protein binding / protein serine/threonine phosphatase					nr -
Unigene117416_All	458	0.00	0.00	0.00	0.00	0.00	0.00	0.18	2.19	0.00	null	null		null	null		null	null		null	null		3.57E+00	3.08E-05	Up	-7.53E+00	3.59E-01									ESTscan +
Unigene117417_All	459	0.00	0.00	0.00	0.00	0.00	0.00	6.26	8.83	0.43	null	null		null	null		null	null		null	null		4.96E-01	7.25E-02		-3.85E+00	1.93E-15	Down								
Unigene117418_All	459	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.64	0.00	null	null		null	null		null	null		null	null		1.14E+01	1.40E-08	Up	null	null									ESTscan -
Unigene11742_All	728	3.45	29.44	8.19	4.93	21.29	33.81	22.07	46.33	69.12	3.09E+00	4.02E-72	Up	1.25E+00	1.62E-06	Up	2.11E+00	1.45E-39	Up	2.78E+00	1.99E-79	Up	1.07E+00	9.78E-34	Up	1.65E+00	3.65E-98	Up	Unigene11742_All//gi|20197500|gb|AAD03372.2|//2.00E-46//expressed protein [Arabidopsis thaliana]	Unigene11742_All//1.00E-47//AT2G24100| unknown protein	Unigene11742_All//0.00E+00//TC140257				nr -
Unigene117420_All	465	0.00	0.00	0.00	0.00	0.00	0.00	5.55	2.88	0.34	null	null		null	null		null	null		null	null		-9.47E-01	7.11E-03		-4.02E+00	2.52E-14	Down	Unigene117420_All//gi|226461892|gb|EEH59185.1|//7.00E-11//transcription elongation-nucleosome displacement protein Spt6 [Micromonas pusilla CCMP1545]						nr +

Unigene117421_All	468	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.95	0.00	null	null		null	null		null	null		null	null		1.15E+01	9.64E-10	Up	null	null		Unigene117421_All//gi|5002232|gb|AD37373.1|AF145234_1//3.00E-43//NADPH:quinone oxidoreductase [Arabidopsis thaliana]	Unigene117421_All//9.00E-38//AT3G27890| NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN reductase					nr +
Unigene117422_All	468	0.00	0.00	0.00	0.00	0.00	0.00	0.90	3.48	0.09	null	null		null	null		null	null		null	null		1.95E+00	1.26E-04	Up	-3.41E+00	1.24E-02		Unigene117422_All//gi|159483497|ref|XP_001699797.1|//1.00E-45//ribosomal protein S3, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158281739|gb|EDP07493.1| ribosomal protein S3, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii]	Unigene117422_All//8.00E-47//AT2G31610| 40S ribosomal protein S3 (RPS3A)			ko03010|Ribosome		nr +
Unigene117423_All	469	0.00	0.00	0.00	0.00	0.00	0.00	1.62	3.74	0.00	null	null		null	null		null	null		null	null		1.21E+00	7.16E-03		-1.07E+01	8.87E-06	Down									ESTscan +
Unigene117743_All	927	2.71	21.32	9.02	4.62	25.00	32.45	12.95	32.33	47.40	2.98E+00	4.72E-64	Up	1.74E+00	4.58E-14	Up	2.44E+00	3.63E-70	Up	2.81E+00	3.12E-98	Up	1.32E+00	1.32E-41	Up	1.87E+00	2.15E-102	Up	Unigene117743_All//gi|20197500|gb|AD03372.2|//5.00E-13//expressed protein [Arabidopsis thaliana]	Unigene117743_All//1.00E-14//AT4G30780| unknown protein	Unigene117743_All//4.00E-176//gi|73864036|gb|DT466775.1|DT466775				nr +
Unigene117431_All	477	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.24	0.00	null	null		null	null		null	null		null	null		1.17E+01	6.59E-11	Up	null	null		Unigene117431_All//gi|18408550|ref|NP_564878.1|//1.00E-55//60S ribosomal protein L10 (RPL10C) [Arabidopsis thaliana] >gi|297838747|ref|XP_002887255.1| 60S ribosomal protein L10 [Arabidopsis lyrata subsp. lyrata] >gi|75249285|sp|Q93W22.1|RL103_ARATH RecName: Full=60S ribosomal protein L10-3 >gi|14194141|gb|AAK56265.1|AF367276_1 At1g66580/T12I7_3 [Arabidopsis thaliana] >gi|15777885|gb|AAL05903.1| At1g66580/T12I7_3 [Arabidopsis thaliana] >gi|297333096|gb|EFH63514.1| 60S ribosomal protein L10 [Arabidopsis lyrata subsp. lyrata]	Unigene117431_All//9.00E-57//AT1G66580| 60S ribosomal protein L10 (RPL10C)	Unigene117431_All//4.00E-14//CD486423		ko03010|Ribosome		nr +
Unigene117432_All	479	0.00	0.00	0.00	0.00	0.00	0.00	1.15	1.92	0.00	null	null		null	null		null	null		null	null		7.42E-01	2.60E-01		-1.02E+01	2.80E-04	Down	Unigene117432_All//gi|145344432|ref|XP_001416736.1|//2.00E-47//Ribosomal protein L10, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901] >gi|144576962|gb|ABO95029.1| Ribosomal protein L10, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901]	Unigene117432_All//8.00E-48//AT1G26910| 60S ribosomal protein L10 (RPL10B)	Unigene117432_All//2.00E-15//CD485839		ko03010|Ribosome		nr +
Unigene117433_All	480	0.00	0.00	0.00	0.00	0.00	0.00	2.11	11.15	0.75	null	null		null	null		null	null		null	null		2.40E+00	2.50E-17	Up	-1.50E+00	1.41E-02										
Unigene117434_All	481	0.00	0.00	0.00	0.00	0.00	0.00	0.53	5.39	0.00	null	null		null	null		null	null		null	null		3.35E+00	4.80E-12	Up	-9.04E+00	3.04E-02										ESTscan +
Unigene117437_All	492	0.43	0.21	0.43	0.20	0.28	0.00	0.60	4.33	1.86	-1.05E+00	5.65E-01		2.52E-02	1.00E+00		4.68E-01	8.77E-01		-7.66E+00	4.02E-01		2.83E+00	1.12E-08	Up	1.63E+00	1.45E-02										
Unigene117438_All	493	0.00	0.21	0.00	0.10	0.14	0.00	0.51	2.80	0.00	7.68E+00	3.89E-01		null	null		4.68E-01	9.60E-01		-6.66E+00	6.40E-01		2.44E+00	4.59E-05	Up	-9.01E+00	3.04E-02		Unigene117438_All//gi|297720735|ref|NP_001172729.1|//5.00E-44//Os01g0935200 [Oryza sativa Japonica Group] >gi|148921414|dbj|BAF64446.1| HAP3 subunit of HAP complex [Oryza sativa Japonica Group] >gi|255674039|dbj|BAH91459.1| Os01g0935200 [Oryza sativa Japonica Group]	Unigene117438_All//3.00E-41//AT2G47810| NF-YB5 (NUCLEAR FACTOR Y, SUBUNIT B5); transcription factor		CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication		nr -
Unigene11744_All	1983	12.66	72.16	30.80	18.97	89.26	125.29	40.57	110.80	183.76	2.51E+00	0.00E+00	Up	1.28E+00	7.88E-64	Up	2.23E+00	0.00E+00	Up	2.72E+00	0.00E+00	Up	1.45E+00	0.00E+00	Up	2.18E+00	0.00E+00	Up	Unigene11744_All//gi|115466824|ref|NP_001057011.1|//1.00E-116//Os06g0186600 [Oryza sativa Japonica Group] >gi|113595051|dbj|BAF18925.1| Os06g0186600 [Oryza sativa Japonica Group]	Unigene11744_All//2.00E-110//AT2G24100| unknown protein	Unigene11744_All//0.00E+00//TC138776				nr -
Unigene117440_All	506	0.21	0.00	0.00	0.10	0.00	0.00	0.58	3.80	0.24	-7.69E+00	3.74E-01		-7.69E+00	3.96E-01		-6.62E+00	5.59E-01		-6.62E+00	6.40E-01		2.70E+00	1.69E-07	Up	-1.31E+00	3.13E-01		Unigene117440_All//gi|95117792|gb|ABF57084.1|//1.00E-60//GDHB glutamate dehydrogenase [Vitis vinifera] >gi|95117794|gb|ABF57085.1| GDHB glutamate dehydrogenase [Vitis vinifera]	Unigene117440_All//2.00E-58//AT5G18170| GDH1 (GLUTAMATE DEHYDROGENASE 1); ATP binding / glutamate dehydrogenase (NAD(P)+)/ oxidoreductase	Unigene117440_All//2.00E-80//TC143512		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr +
Unigene117441_All	516	0.00	0.00	0.00	0.00	0.00	0.00	0.90	3.00	0.00	null	null		null	null		null	null		null	null		1.73E+00	6.66E-04	Up	-9.82E+00	1.09E-03		Unigene117441_All//gi|192910906|gb|ACF06561.1|//2.00E-49//ribosomal protein L18a [Elaeis guineensis]	Unigene117441_All//1.00E-45//AT1G29970| RPL18AA (60S RIBOSOMAL PROTEIN L18A-1)			ko03010|Ribosome		nr -
Unigene117442_All	519	0.00	0.00	0.00	0.00	0.00	0.00	1.47	4.03	0.00	null	null		null	null		null	null		null	null		1.46E+00	4.39E-04	Up	-1.05E+01	8.87E-06	Down									ESTscan -
Unigene117443_All	521	0.00	0.00	0.00	0.00	0.00	0.00	0.73	3.05	0.00	null	null		null	null		null	null		null	null		2.06E+00	8.20E-05	Up	-9.51E+00	4.19E-03		Unigene117443_All//gi|300262824|gb|EFJ47028.1|//3.00E-10//transcription factor jumonji domain-containing protein [Volvox carteri f. nagariensis]					ko04144|Endocytosis		nr -
Unigene117444_All	530	0.00	0.57	0.00	0.38	0.26	0.09	0.32	3.39	1.20	9.16E+00	4.44E-02		null	null		-5.33E-01	7.49E-01		-2.14E+00	3.47E-01		3.41E+00	1.21E-08	Up	1.91E+00	2.60E-02										
Unigene117446_All	544	0.00	0.00	0.00	0.00	0.00	0.00	1.01	3.61	0.29	null	null		null	null		null	null		null	null		1.84E+00	4.40E-05	Up	-1.79E+00	5.07E-02										
Unigene117447_All	544	0.00	0.00	0.00	0.00	0.00	0.00	0.78	2.84	0.00	null	null		null	null		null	null		null	null		1.87E+00	3.06E-04	Up	-9.60E+00	2.14E-03		Unigene117447_All//gi|2500261|sp|P93099.1|RL13A_CYAPA//4.00E-52//RecName: Full=60S ribosomal protein L13a >gi|1743007|emb|CAA71090.1| ribosomal protein L13a [Cyanophora paradoxa]	Unigene117447_All//2.00E-46//AT5G48760| 60S ribosomal protein L13A (RPL13aD)			ko03010|Ribosome		nr +
Unigene117448_All	552	0.00	0.00	0.00	0.00	0.00	0.00	1.46	1.89	0.07	null	null		null	null		null	null		null	null		3.79E-01	5.56E-01		-4.33E+00	4.54E-05	Down	Unigene117448_All//gi|160339969|ref|XP_001712192.1|//6.00E-81//ef2 [Hemiselmis andersenii] >gi|159765639|gb|ABW97867.1| ef2 [Hemiselmis andersenii]	Unigene117448_All//5.00E-73//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene117448_All//7.00E-07//BP277406				nr -
Unigene117449_All	556	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.38	0.00	null	null		null	null		null	null		null	null		1.17E+01	3.04E-13	Up	null	null										ESTscan -
Unigene11745_All	2188	2.80	1.41	1.44	2.28	3.76	2.97	8.14	21.83	30.86	-9.86E-01	4.56E-05		-9.62E-01	1.24E-04		7.24E-01	1.56E-04		3.85E-01	1.15E-01		1.42E+00	6.48E-74	Up	1.92E+00	7.97E-163	Up	Unigene11745_All//gi|115469978|ref|NP_001658588.1|//1.00E-149//Os06g0716000 [Oryza sativa Japonica Group] >gi|53791786|dbj|BAD53580.1| receptor-like protein kinase-like [Oryza sativa Japonica Group] >gi|113596628|dbj|BAF20502.1| Os06g0716000 [Oryza sativa Japonica Group]	Unigene11745_All//6.00E-168//AT1G30755| unknown protein	Unigene11745_All//4.00E-178//DT047820				nr +
Unigene117450_All	557	0.00	0.00	0.00	0.00	0.00	0.00	1.06	4.13	0.79	null	null		null	null		null	null		null	null		1.96E+00	2.90E-06	Up	-4.34E-01	6.08E-01										
Unigene117451_All	558	0.00	0.00	0.00	0.00	0.00	0.00	0.30	3.22	0.00	null	null		null	null		null	null		null	null		3.41E+00	1.21E-08	Up	-8.24E+00	1.08E-01										
Unigene117452_All	559	0.19	0.00	0.00	0.00	0.00	0.16	1.29	4.64	2.28	-7.55E+00	3.74E-01		-7.55E+00	3.96E-01		null	null		7.34E+00	4.79E-01		1.85E+00	1.60E-06	Up	8.27E-01	1.08E-01				Unigene117452_All//1.00E-35//DN800918						
Unigene117453_All	564	0.00	0.00	0.00	0.00	0.00	0.00	0.22	2.82	0.35	null	null		null	null		null	null		null	null		3.65E+00	4.24E-08	Up	6.51E-01	6.66E-01		Unigene117453_All//gi|21593366|gb|AAM65315.1|//2.00E-28//ethylene-forming-enzyme-like dioxygenase-like protein [Arabidopsis thaliana]	Unigene117453_All//1.00E-29//AT5G20490| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene117453_All//0.00E+00//CO125364		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis		nr -
Unigene117455_All	569	0.00	0.00	0.00	0.00	0.00	0.00	0.07	2.79	0.14	null	null		null	null		null	null		null	null		5.23E+00	6.39E-10	Up	9.14E-01	7.50E-01		Unigene117455_All//gi|55168340|gb|AAV44205.1|//2.00E-07//unknow protein [Oryza sativa Japonica Group]		Unigene117455_All//7.00E-07//EX171356				nr +
Unigene117459_All	586	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.21	1.50	null	null		null	null		null	null		null	null		1.57E+00	5.46E-01		4.37E+00	2.26E-05	Up	Unigene117459_All//gi|75321780|sp|Q5W274.1|PDR3_TOBAC//4.00E-78//RecName: Full=Pleiotropic drug resistance protein 3; AltName: Full=NtPDR3 >gi|59356942|emb|CAH39853.1| PDR-like ABC transporter [Nicotiana tabacum]	Unigene117459_All//2.00E-76//AT3G53480| PDR9 (PLEIOTROPIC DRUG RESISTANCE 9); ATPase, coupled to transmembrane movement of substances			ko03040|Spliceosome//ko02010|ABC transporters		nr +
Unigene11746_All	2426	1.62	13.18	3.58	1.19	2.90	2.72	17.57	36.02	47.95	3.03E+00	4.19E-105	Up	1.15E+00	4.19E-08	Up	1.28E+00	3.41E-09	Up	1.19E+00	2.81E-07	Up	1.04E+00	8.89E-82	Up	1.45E+00	1.94E-187	Up	Unigene11746_All//gi|115469978|ref|NP_001658588.1|//1.00E-142//Os06g0716000 [Oryza sativa Japonica Group] >gi|53791786|dbj|BAD53580.1| receptor-like protein kinase-like [Oryza sativa Japonica Group] >gi|113596628|dbj|BAF20502.1| Os06g0716000 [Oryza sativa Japonica Group]	Unigene11746_All//2.00E-163//AT1G30755| unknown protein	Unigene11746_All//0.00E+00//DT464104				nr +
Unigene117460_All	591	0.27	0.34	0.45	0.76	0.00	0.84	0.64	2.62	0.81	3.69E-01	8.17E-01		7.62E-01	6.44E-01		-9.57E+00	2.00E-03		1.48E-01	9.06E-01		2.02E+00	1.30E-04	Up	3.29E-01	7.08E-01		Unigene117460_All//gi|223452528|gb|ACM89591.1|//2.00E-50//leucine-rich repeat family protein / protein kinase family protein [Glycine max]	Unigene117460_All//3.00E-44//AT4G08850| kinase	Unigene117460_All//6.00E-140//gi|48777745|gb|CO087111.1|CO087111		ko04626|Plant-pathogen interaction		nr -
Unigene117461_All	603	0.00	0.00	0.00	0.00	0.00	0.00	1.47	4.23	0.00	null	null		null	null		null	null		null	null		1.52E+00	4.46E-05	Up	-1.05E+01	1.10E-06	Down	Unigene117461_All//gi|6093872|sp|O65082.1|RL15B_PICMA//5.00E-80//RecName: Full=60S ribosomal protein L15-2 >gi|29823318|gb|AAC32144.1| probable 60S ribosomal protein L15 [Picea mariana]	Unigene117461_All//6.00E-68//AT4G17390| 60S ribosomal protein L15 (RPL15B)			ko03010|Ribosome		nr -
Unigene117462_All	613	0.09	0.00	0.17	0.16	0.45	0.07	2.76	6.00	51.54	-6.42E+00	6.16E-01		1.02E+00	7.04E-01		1.47E+00	4.20E-01		-1.14E+00	6.78E-01		1.12E+00	1.14E-04	Up	4.22E+00	1.30E-171	Up	Unigene117462_All//gi|297801996|ref|XP_002868882.1|//4.00E-46//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314718|gb|EFH45141.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene117462_All//3.00E-45//AT4G39070| zinc finger (B-box type) family protein		DBB	ko04712|Circadian rhythm - plant		nr +
Unigene117463_All	613	0.00	0.00	0.00	0.00	0.00	0.00	0.48	3.34	0.00	null	null		null	null		null	null		null	null		2.79E+00	3.35E-08	Up	-8.92E+00	1.58E-02		Unigene117463_All//gi|1208549|gb|AAC49455.1|//8.00E-44//Pseudotsain [Pseudotsuga menziesii]	Unigene117463_All//3.00E-42//AT4G36880| CP1 (CYSTEINE PROTEINASE1); cysteine-type endopeptidase/ cysteine-type peptidase					nr +

Unigene117464_All	625	0.00	0.00	0.00	0.00	0.00	0.00	0.27	2.81	0.00	null	null		null	null		null	null		null	null		3.38E+00	2.17E-08	Up	-8.08E+00	1.08E-01		Unigene117464_All//gi|224101487|ref|XP_002312301.1|//1.00E-26//1-cys peroxiredoxin [Populus trichocarpa] >gi|222852121|gb|EEE89668.1| 1-cys peroxiredoxin [Populus trichocarpa]	Unigene117464_All//4.00E-21//AT1G48130| ATPER1: antioxidant/ thioredoxin peroxidase			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene117465_All	641	0.00	0.00	0.00	0.00	0.21	0.14	483.62	201.81	1138.17	null	null		null	null		7.75E+00	3.19E-01		7.14E+00	4.79E-01		-1.26E+00	0.00E+00	Down	1.23E+00	0.00E+00	Up	Unigene117465_All//gi|124365601|gb|AAK50778.4|AF361893|1/9.00E-94//bacterial-induced lipoxygenase [Gossypium hirsutum]	Unigene117465_All//8.00E-82//AT3G22400| LOX5; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene117465_All//0.00E+00//gi|164249251|gb|ES810220.1|ES810220		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr -
Unigene117466_All	650	0.16	0.00	0.00	0.00	0.00	0.00	0.13	2.96	0.12	-7.33E+00	3.74E-01		-7.33E+00	3.96E-01		null	null		null	null		4.51E+00	4.15E-11	Up	-8.57E-02	9.73E-01		Unigene117466_All|gi|4887010|gb|AAD32141.1|AF123503_1/5.00E-96//Nt-gh3 deduced protein [Nicotiana tabacum]	Unigene117466_All//2.00E-93//AT2G14960| GH3.1	Unigene117466_All//0.00E+00//gi|78352188|gb|DT572462.1|DT572462				nr +
Unigene117467_All	652	0.00	0.00	0.00	0.00	0.00	0.00	0.71	3.27	0.00	null	null		null	null		null	null		null	null		2.20E+00	1.16E-06	Up	-9.48E+00	1.09E-03		Unigene117467_All//gi|70663909|emb|CAE01636.3|//1.00E-43//OSJNBa0029802.21 [Oryza sativa (japonica cultivar-group)]	Unigene117467_All//2.00E-38//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene117467_All//5.00E-08//DW519718		ko03010|Ribosome		nr +
Unigene117468_All	657	0.00	0.31	0.00	0.38	0.00	0.14	0.00	7.32	0.12	8.27E+00	1.37E-01		null	null		-8.57E+00	4.19E-02		-1.46E+00	4.07E-01		1.28E+01	7.48E-34	Up	6.92E+00	4.05E-01		Unigene117468_All|gi|125620180|gb|ABN46982.1|//1.00E-32//small molecular heat shock protein 19 [Nelumbo nucifera]	Unigene117468_All//1.00E-17//AT1G59860| 17.6 kDa class I heat shock protein (HSP17.6A-CI)					nr -
Unigene117469_All	699	0.00	0.00	0.00	0.00	0.00	0.00	0.73	2.51	0.23	null	null		null	null		null	null		null	null		1.79E+00	1.73E-04	Up	-1.67E+00	7.78E-02		Unigene117469_All|gi|18421592|ref|NP_568543.1|//7.00E-75//DegP10 (DegP protease 10); catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase [Arabidopsis thaliana] >gi|75262529|sp|Q9FIV6.1|DGP10_ARATH RecName: Full=Protease Do-like 10, mitochondrial; Flags: Precursor >gi|10178214|dbj|BAB11638.1| serine protease-like protein [Arabidopsis thaliana] >gi|17978951|gb|AAL47441.1| AT5g36950/MLF18_70 [Arabidopsis thaliana] >gi|50897262|gb|AAT85770.1| At5g36950 [Arabidopsis thaliana]	Unigene117469_All//3.00E-76//AT5G36950| DegP10 (DegP protease 10); catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase					nr +
Unigene117470_All	705	0.00	0.00	0.00	0.00	0.00	0.00	0.30	3.26	0.00	null	null		null	null		null	null		null	null		3.44E+00	5.53E-11	Up	-8.23E+00	5.80E-02		Unigene117470_All//gi|28558781|gb|AA045752.1|//6.00E-39//pol protein [Cucumis melo]		Unigene117470_All//6.00E-48//FL577265				nr -
Unigene117471_All	729	0.43	2.02	0.51	1.44	3.35	3.59	4.93	19.09	14.59	2.23E+00	4.29E-04	Up	2.48E-01	8.23E-01		1.22E+00	2.37E-03		1.32E+00	9.26E-04	Up	1.95E+00	3.84E-34	Up	1.57E+00	5.80E-20	Up	Unigene117471_All//gi|224082488|ref|XP_002306712.1|//3.00E-54//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222856616|gb|EEE93708.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene117471_All//5.00E-20//AT5G50080| DNA binding / transcription factor	Unigene117471_All//0.00E+00//ES831270	AP2-EREBP			nr -
Unigene117472_All	754	0.00	0.00	0.00	0.00	0.00	0.00	0.56	4.32	0.00	null	null		null	null		null	null		null	null		2.95E+00	2.30E-13	Up	-9.13E+00	2.14E-03		Unigene117472_All|gi|300268606|gb|EF152786.1|//5.00E-63//eukaryotic translation initiation factor 1 alpha 1 [Volvox carteri f. nagariensis]	Unigene117472_All//3.00E-22//AT5G60390| elongation factor 1-alpha / EF-1-alpha					nr -
Unigene117473_All	790	0.00	0.00	0.00	0.00	0.00	0.00	0.11	2.75	0.00	null	null		null	null		null	null		null	null		4.68E+00	9.19E-13	Up	-6.74E+00	3.59E-01		Unigene117473_All|gi|600118|emb|CAA84230.1|//2.00E-10//extensin-like protein [Zea mays] >gi|1096557|prf|2111476A extensin-like domain						nr -
Unigene117474_All	809	0.00	0.00	0.13	0.49	0.17	0.11	1.31	4.34	0.39	null	null		7.04E+00	4.01E-01		-1.53E+00	2.06E-01		-2.14E+00	1.26E-01		1.73E+00	6.71E-08	Up	-1.73E+00	4.76E-03		Unigene117474_All|gi|240256087|ref|NP_194459.4|//7.00E-77//ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene117474_All//4.00E-78//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding					nr -
Unigene117475_All	839	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9.51	0.00	null	null		null	null		null	null		null	null		1.32E+01	2.39E-56	Up	null	null		Unigene117475_All|gi|115468044|ref|NP_001057621.1|//3.00E-10//Os06g0472200 [Oryza sativa Japonica Group] >gi|113595661|dbj|BAF19535.1| Os06g0472200 [Oryza sativa Japonica Group]	Unigene117475_All//2.00E-11//AT1G75280| isoflavone reductase, putative			ko00640|Propanoate metabolism		nr +
Unigene117476_All	857	0.00	0.00	0.00	0.12	0.00	0.00	0.39	5.36	0.09	null	null		null	null		-6.86E+00	3.15E-01		-6.86E+00	4.02E-01		3.76E+00	5.49E-23	Up	-2.09E+00	1.07E-01										
Unigene117477_All	1186	0.00	0.00	0.00	0.00	0.17	0.00	453.39	146.71	1033.55	null	null		null	null		7.44E+00	1.57E-01		null	null		-1.63E+00	0.00E+00	Down	1.19E+00	0.00E+00	Up	Unigene117477_All|gi|124365601|gb|AAK50778.4|AF361893|1/1.00E-142//bacterial-induced lipoxygenase [Gossypium hirsutum]	Unigene117477_All//5.00E-125//AT1G55020| LOX1; lipoxygenase	Unigene117477_All//4.00E-167//DR463563		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr -
Unigene117478_All	892	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.61	18.53	null	null		null	null		null	null		null	null		5.14E-01	5.89E-01		5.44E+00	1.35E-103	Up	Unigene117478_All|gi|22218276|gb|AAM94617.1|//4.00E-14//PR10-like protein [Glycine max]		Unigene117478_All//4.00E-74//DR454610				nr -
Unigene117479_All	373	0.00	0.14	0.00	0.00	0.00	0.00	0.23	0.45	2.03	7.09E+00	6.19E-01		null	null		null	null		null	null		9.83E-01	6.34E-01		3.16E+00	6.83E-04	Up	Unigene117479_All|gi|115475257|ref|NP_001061225.1|//3.00E-14//Os08g0203700 [Oryza sativa Japonica Group] >gi|113623194|dbj|BAF23139.1| Os08g0203700 [Oryza sativa Japonica Group]	Unigene117479_All//2.00E-11//AT3G11080| ArRLP35 (Receptor Like Protein 35); kinase/ protein binding	Unigene117479_All//6.00E-108//gi|48789604|gb|CO090918.1|CO090918				nr -
Unigene117481_All	610	0.00	0.00	0.00	0.00	0.00	0.00	1.04	0.14	4.96	null	null		null	null		null	null		null	null		-2.92E+00	4.20E-03		2.26E+00	1.11E-09	Up	Unigene117481_All|gi|224057862|ref|XP_002299361.1|//2.00E-30//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene117481_All//4.00E-29//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene117481_All//2.00E-10//DT467060				nr +
Unigene117482_All	298	0.00	0.00	0.00	0.00	0.00	0.00	2.13	17.95	3.88	null	null		null	null		null	null		null	null		3.08E+00	1.95E-22	Up	8.65E-01	1.14E-01		Unigene117482_All|gi|33636090|emb|CAD91338.1|//5.00E-16//beta-fructofuranosidase [Glycine max]	Unigene117482_All//4.00E-16//AT3G52600| AtcwINV2 (Arabidopsis thaliana cell wall invertase 2); hydrolase, hydrolyzing O-glycosyl compounds	Unigene117482_All//5.00E-74//TC171440		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr +
Unigene117483_All	474	0.55	1.50	0.67	1.05	1.16	2.57	2.32	2.82	7.23	1.44E+00	1.06E-01		2.89E-01	8.10E-01		1.46E-01	9.05E-01		1.29E+00	4.33E-02		2.83E-01	6.34E-01		1.64E+00	2.03E-07	Up	Unigene117483_All|gi|224106844|ref|XP_002333623.1|//2.00E-33//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837867|gb|EEE76232.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene117483_All//2.00E-13//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene117483_All//7.00E-167//gi|109856029|gb|DW485008.1|DW485008		ko04626|Plant-pathogen interaction		nr -
Unigene117488_All	344	9.28	7.81	3.56	9.56	10.31	15.10	9.34	13.85	12.51	-2.49E-01	4.89E-01		-1.38E+00	2.46E-04	Down	1.09E-01	8.02E-01		6.60E-01	1.20E-02		5.68E-01	2.17E-02		4.21E-01	1.04E-01		Unigene117488_All|gi|115187640|gb|ABI84264.1|//5.00E-19//ubiquitin-conjugating enzyme [Arachis hypogaea]	Unigene117488_All//3.00E-19//AT3G46460| UBC13 (ubiquitin-conjugating enzyme 13); ubiquitin-protein ligase	Unigene117488_All//1.00E-56//TC161010		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene117489_All	581	1.08	0.00	0.46	1.11	1.66	2.18	1.31	1.94	3.09	-1.01E+01	7.92E-04	Down	-1.24E+00	2.13E-01		5.74E-01	4.52E-01		9.66E-01	1.22E-01		5.68E-01	3.44E-01		1.24E+00	4.17E-03				Unigene117489_All//3.00E-55//TC173528				
Unigene11749_All	2361	3.68	3.43	2.41	5.36	4.96	5.83	5.21	2.18	8.39	-9.94E-02	6.21E-01		-6.08E-01	2.84E-03		-1.12E-01	5.54E-01		1.23E-01	4.99E-01		-1.26E+00	2.11E-16	Down	6.86E-01	3.38E-10		Unigene11749_All|gi|12043533|emb|CAC19789.1|//1.00E-163//MYB-like DNA-binding protein [Catharanthus roseus]	Unigene11749_All//2.00E-139//AT5G13820| TBP1 (TELOMERIC DNA BINDING PROTEIN 1); DNA binding / double-stranded telomeric DNA binding	Unigene11749_All//0.00E+00//TC158069	MYB-related			nr +
Unigene117491_All	663	0.00	0.00	0.24	0.15	0.10	0.07	1.66	2.27	7.69	null	null		7.91E+00	2.39E-01		-5.33E-01	8.18E-01		-1.14E+00	6.78E-01		4.53E-01	3.78E-01		2.21E+00	1.94E-15	Up	Unigene117491_All|gi|133925821|gb|ABO43663.1|//5.00E-12//calcineurin B-like protein 4-1 [Populus trichocarpa]	Unigene117491_All//1.00E-10//AT5G24270| SOS3 (SALT OVERLY SENSITIVE 3); calcium ion binding / calcium-dependent protein serine/threonine phosphatase	Unigene117491_All//4.00E-64//gi|73851161|gb|DT460181.1|DT460181		ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene117493_All	1629	0.00	0.00	0.00	0.03	0.00	0.00	1.25	0.33	1.59	null	null		null	null		-4.94E+00	5.59E-01		-4.94E+00	6.40E-01		-1.90E+00	1.90E-05	Down	3.52E-01	3.26E-01		Unigene117493_All|gi|3152598|gb|AAC17079.1|//1.00E-160//Contains similarity to C2-HC type zinc finger protein C.e-MyT1 gb|U57079 from C. elegans and to hypersensitivity-related gene 201 isolog T28M21.14 from A. thaliana BAC gb|AF002109 [Arabidopsis thaliana]	Unigene117493_All//8.00E-153//AT1G78990| transferase family protein	Unigene117493_All//0.00E+00//DW488553		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene117496_All	871	0.00	0.00	0.00	0.00	0.00	0.00	2.48	0.53	12.21	null	null		null	null		null	null		null	null		-2.23E+00	7.33E-07	Down	2.30E+00	7.31E-33	Up	Unigene117496_All|gi|171452356|dbj|BAG15869.1|//8.00E-45//ankyrin repeat protein [Bruguiera gymnorhiza]	Unigene117496_All//2.00E-39//AT4G10720| ankyrin repeat family protein	Unigene117496_All//0.00E+00//TC175880				nr -
Unigene117498_All	255	21.54	36.56	43.44	26.96	50.10	39.50	7.30	4.75	9.37	7.63E-01	5.32E-05		1.01E+00	1.99E-08	Up	8.94E-01	2.15E-09		5.51E-01	2.04E-03		-6.18E-01	1.52E-01		3.62E-01	3.36E-01		Unigene117498_All|gi|124360233|gb|ABN08246.1|//3.00E-20//Solute carrier family 35 member B3, related [Medicago truncatula]	Unigene117498_All//5.00E-21//AT1G12600| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf whorl, petal, male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: UAA transporter (InterPro:IPR013657); BEST Arabidopsis thaliana protein match is: UDP-galactose transporter-related (TAIR:AT4G23010.1); Has 943 Blast hits to 943 proteins in 196 species: Archae - 2; Bacteria - 55; Metazoa - 506; Fungi - 148; Plants - 112; Viruses - 0; Other Eukaryotes - 120 (source: NCBI BLink).	Unigene117498_All//7.00E-73//BQ403172				nr -

Unigene117499_All	335	0.31	0.00	0.00	0.30	0.00	0.00	0.13	0.25	3.69	-8.29E+00	3.74E-01		-8.29E+00	3.96E-01		-8.22E+00	3.15E-01		-8.22E+00	4.02E-01		9.83E-01	7.33E-01		4.87E+00	9.59E-08	Up	Unigene117499_All//gi|115441637|ref|NP_001045098.1|//1.00E-26//0s01g0899000 [Oryza sativa Japonica Group] >gi|113534629|dbj|BAF07012.1|Os01g0899000 [Oryza sativa Japonica Group]	Unigene117499_All//1.00E-27//AT3G59350| serine/threonine protein kinase, putative	Unigene117499_All//5.00E-99//TC146290		ko04626|Plant-pathogen interaction		nr +
Unigene1175_All	1936	26.89	94.56	58.37	79.02	63.37	103.37	18.43	22.39	35.17	1.81E+00	0.00E+00	Up	1.12E+00	7.10E-95	Up	-3.18E-01	1.59E-17		3.88E-01	3.46E-29		2.81E-01	1.17E-04		9.32E-01	5.83E-55		Unigene1175_All//gi|15240523|ref|NP_199774.1|//0.00E+00//AAP6 (AMINO ACID PERMEASE 6); acidic amino acid transmembrane transporter/ amino acid transmembrane transporter/ neutral amino acid transmembrane transporter [Arabidopsis thaliana] >gi|75220393|sp|P92934.1|AAP6_ARATH RecName: Full=Amino acid permease 6; AltName: Full=Amino acid transporter AAP6 >gi|1769887|emb|CAA65051.1| amino acid permease 6 [Arabidopsis thaliana] >gi|8809686|dbj|BAA97227.1| amino acid permease 6 [Arabidopsis thaliana] >gi|110738094|dbj|BAF00980.1| amino acid permease 6 [Arabidopsis thaliana]	Unigene1175_All//0.00E+00//AT5G49630| AAP6 (AMINO ACID PERMEASE 6); acidic amino acid transmembrane transporter/ amino acid transmembrane transporter/ neutral amino acid transmembrane transporter	Unigene1175_All//0.00E+00//TC145723			GO:0015171//GO:0015711//GO:0015801//GO:0031224//GO:0051707	nr +
Unigene11750_All	1324	20.43	5.13	6.92	26.90	12.51	5.15	19.48	1.96	13.45	-1.99E+00	2.12E-55	Down	-1.56E+00	3.86E-38	Down	-1.10E+00	1.30E-37	Down	-2.38E+00	4.01E-99	Down	-3.32E+00	4.63E-114	Down	-5.34E-01	1.11E-08		Unigene11750_All//gi|260424374|gb|ACX37656.1|//1.00E-108//homeodomain associated leucine zipper protein [Gossypium arboreum]	Unigene11750_All//3.00E-73//AT4G16780| ATHB-2 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 2); DNA binding / protein homodimerization/ sequence-specific DNA binding / transcription factor	Unigene11750_All//0.00E+00//TC151568	HB		GO:0000902//GO:0001071//GO:0003677//GO:0006351//GO:0009639//GO:0009755//GO:0010468//GO:0030528//GO:0042802//GO:0043231//GO:0048513	nr +
Unigene117500_All	418	0.13	0.36	0.25	0.24	0.33	0.65	1.42	0.50	6.58	1.54E+00	5.32E-01		1.03E+00	7.04E-01		4.68E-01	8.77E-01		1.44E+00	4.09E-01		-1.50E+00	9.13E-02		2.22E+00	1.10E-08	Up	Unigene117500_All//gi|15919089|emb|CAC86996.1|//4.00E-15//ATP citrate lyase b-subunit [Lupinus albus]	Unigene117500_All//4.00E-15//AT1G10670| ACLA-1; ATP citrate synthase	Unigene117500_All//1.00E-60//BP274632		ko00020|Citrate cycle (TCA cycle)		nr +
Unigene117513_All	535	0.00	0.00	0.20	0.00	0.26	0.00	0.16	0.39	3.20	null	null		7.64E+00	4.01E-01		8.01E+00	3.19E-01		null	null		1.30E+00	4.48E-01		4.34E+00	5.93E-10	Up			Unigene117513_All//6.00E-07//DN817073				ESTscan +
Unigene117520_All	337	0.00	2.26	0.00	0.00	0.92	0.54	0.13	1.49	1.77	1.11E+01	1.77E-04	Up	null	null		9.84E+00	4.55E-02		9.07E+00	1.95E-01		3.57E+00	6.53E-03		3.82E+00	1.35E-03								
Unigene117526_All	276	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.17	null	null		null	null		null	null		null	null		null	null		1.11E+01	1.76E-04	Up	Unigene117526_All//gi|66271061|gb|AAY43808.1|//3.00E-09//Fb17 [Gossypium hirsutum]		Unigene117526_All//1.00E-49//gi|109890392|gb|DW519356.1|DW519356				nr +
Unigene117533_All	400	0.26	0.89	1.33	0.12	0.17	0.23	0.42	1.46	6.27	1.76E+00	2.18E-01		2.35E+00	5.88E-02		4.68E-01	9.60E-01		8.59E-01	7.95E-01		1.79E+00	5.30E-02		3.89E+00	2.29E-13	Up	Unigene117533_All//gi|297849964|ref|XP_002889863.1|//6.00E-24//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335705|gb|EFH66122.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene117533_All//1.00E-24//AT1G11300| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene117533_All//8.00E-160//gi|109861376|gb|DW490353.1|DW490353				nr -
Unigene117542_All	328	0.00	0.00	0.49	0.00	0.00	0.00	0.00	0.00	1.94	null	null		8.93E+00	2.39E-01		null	null		null	null		null	null		1.09E+01	9.35E-05	Up							
Unigene117544_All	304	0.00	0.00	0.00	0.00	0.00	0.00	0.42	5.36	0.79	null	null		null	null		null	null		null	null		3.68E+00	2.33E-08	Up	9.14E-01	5.42E-01								
Unigene117545_All	1458	0.00	0.00	0.00	0.07	0.02	0.12	0.17	0.20	8.69	null	null		null	null		-1.53E+00	5.87E-01		8.59E-01	6.96E-01		2.06E-01	8.68E-01		5.64E+00	1.18E-80	Up	Unigene117545_All//gi|12322008|gb|AAG51046.1|AC069473_8//2.00E-34//gypsy/Ty-3 retroelement polyprotein: 69905-74404 [Arabidopsis thaliana] >gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]						nr -
Unigene11756_All	595	4.48	1.36	3.58	9.29	6.54	4.63	0.92	0.98	0.47	-1.72E+00	3.82E-05	Down	-3.25E-01	4.20E-01		-5.07E-01	3.93E-02		-1.01E+00	5.86E-05	Down	9.02E-02	9.27E-01		-9.79E-01	2.50E-01		Unigene11756_All//gi|82880418|gb|AB892748.1|//2.00E-44//UDP-glucose glucosyltransferase [Fragaria x ananassa]	Unigene11756_All//2.00E-34//AT3G21790| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene11756_All//0.00E+00//gi|78337285|gb|DT557559.1|DT557559			GO:0016758	nr +
Unigene117560_All	371	0.00	0.27	0.00	0.00	0.00	0.00	0.34	0.45	5.91	8.09E+00	3.89E-01		null	null		null	null		null	null		3.98E-01	8.15E-01		4.11E+00	3.56E-12	Up							
Unigene117563_All	487	0.00	0.10	0.00	0.00	0.00	0.00	0.26	0.00	2.86	6.70E+00	6.19E-01		null	null		null	null		null	null		-8.03E+00	2.36E-01		3.46E+00	4.41E-07	Up	Unigene117563_All//gi|255560201|ref|XP_002521118.1|//4.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223539687|gb|EEF41269.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene117569_All	605	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.14	2.44	null	null		null	null		null	null		null	null		-1.66E-02	1.01E+00		4.12E+00	2.19E-08	Up							
Unigene11757_All	1766	28.59	18.99	20.96	19.04	19.13	15.34	5.70	6.22	1.62	-5.90E-01	3.11E-15		-4.48E-01	4.13E-09		6.70E-03	9.56E-01		-3.11E-01	7.20E-04		1.28E-01	4.81E-01		-1.81E+00	2.50E-23	Down	Unigene11757_All//gi|283362116|dbj|BA165911.1|//1.00E-120//UDP-sugar;glycosyltransferase [Forsythia x intermedia]	Unigene11757_All//8.00E-101//AT3G21780| UGT71B6 (UDP-glucosyl transferase 71B6); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring glycosyl groups	Unigene11757_All//0.00E+00//gi|109871404|gb|DW500380.1|DW500380			GO:0035251	nr +
Unigene117575_All	219	0.00	0.00	0.00	0.00	0.00	0.00	12.36	9.54	0.73	null	null		null	null		null	null		null	null		-3.73E-01	3.08E-01		-4.09E+00	3.55E-15	Down	Unigene117575_All//gi|242070905|ref|XP_002450729.1|//1.00E-10//hypothetical protein SORBIDRAFT_05g016460 [Sorghum bicolor] >gi|241936572|gb|EES09717.1| hypothetical protein SORBIDRAFT_05g016460 [Sorghum bicolor]		Unigene117575_All//2.00E-32//TC146753				nr +
Unigene11758_All	2012	3.41	2.42	1.48	10.67	5.77	3.28	1.37	0.62	0.53	-4.95E-01	2.79E-02		-1.20E+00	5.60E-07	Down	-8.88E-01	6.19E-16		-1.70E+00	1.34E-38	Down	-1.13E+00	9.60E-04	Down	-1.35E+00	7.11E-05	Down	Unigene11758_All//gi|283362116|dbj|BA165911.1|//1.00E-118//UDP-sugar;glycosyltransferase [Forsythia x intermedia]	Unigene11758_All//2.00E-99//AT3G21780| UGT71B6 (UDP-glucosyl transferase 71B6); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring glycosyl groups	Unigene11758_All//0.00E+00//TC170176			GO:0035251	nr -
Unigene117582_All	287	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.73	1.80	null	null		null	null		null	null		null	null		9.51E+00	7.86E-02		1.08E+01	6.14E-04	Up							
Unigene117584_All	279	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.14	null	null		null	null		null	null		null	null		null	null		1.16E+01	2.05E-06	Up							
Unigene117585_All	511	0.00	0.10	0.00	0.10	0.40	0.35	0.00	0.00	2.81	6.63E+00	6.19E-01		null	null		2.05E+00	3.95E-01		1.86E+00	4.58E-01		null	null		1.15E+01	2.48E-10	Up	Unigene117585_All//gi|15242647|ref|NP_198848.1|//1.00E-12//DC1 domain-containing protein [Arabidopsis thaliana] >gi|10178142|dbj|BAB11587.1| CHP-rich zinc finger protein-like [Arabidopsis thaliana]	Unigene117585_All//1.00E-14//AT1G38037| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular signaling cascade; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein kinase C, phorbol ester/diacylglycerol binding (InterPro:IPR002219), DC1 (InterPro:IPR004146), C1-like (InterPro:IPR011424); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT5G45730.1); Has 1201 Blast hits to 455 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 1193; Viruses - 0; Other Eukarryotes - 5 (source: NCBI BLink).	Unigene117585_All//7.00E-16//ES842244				nr -
Unigene117587_All	303	1.38	0.67	0.00	1.32	0.91	0.30	0.42	0.00	3.68	-1.05E+00	3.66E-01		-1.04E+01	1.56E-02		-5.33E-01	6.16E-01		-2.14E+00	1.26E-01		-8.71E+00	2.36E-01		3.14E+00	2.19E-05	Up							
Unigene117588_All	710	0.00	0.00	0.00	0.77	0.00	0.13	3.57	3.30	2.24	null	null		null	null		-9.59E+00	4.01E-04	Down	-2.60E+00	2.93E-02		-1.16E-01	7.57E-01		-6.71E-01	4.94E-02		Unigene117588_All//gi|224114718|ref|XP_002332307.1|//4.00E-08//predicted protein [Populus trichocarpa] >gi|222832306|gb|EEE70783.1| predicted protein [Populus trichocarpa]						nr +
Unigene117590_All	276	215.92	673.39	296.93	627.37	535.74	692.34	204.97	120.84	196.45	1.64E+00	7.74E-287	Up	4.60E-01	4.79E-15		-2.28E-01	1.20E-10		1.42E-01	1.16E-04		-7.62E-01	4.85E-32		-6.12E-02	4.03E-01		Unigene117590_All//gi|56121699|gb|AAV74186.1|//2.00E-13//metallothionein-like protein [Gossypium hirsutum]	Unigene117590_All//4.00E-05//AT3G09390| MT2A (METALLOTHIONEIN 2A); copper ion binding	Unigene117590_All//7.00E-67//TC156098			GO:0043169	nr +
Unigene117603_All	457	0.00	0.78	0.12	0.22	0.00	0.20	0.37	1.10	5.32	9.60E+00	2.46E-02		6.86E+00	6.38E-01		-7.77E+00	3.15E-01		-1.41E-01	9.51E-01		1.57E+00	1.18E-01		3.84E+00	7.47E-13	Up	Unigene117603_All//gi|18411945|ref|NP_565179.1|//4.00E-06//VQ motif-containing protein [Arabidopsis thaliana] >gi|17979514|gb|AAL50092.1| At1g78410/F3F9_27 [Arabidopsis thaliana] >gi|20857141|gb|AAM26702.1| At1g78410/F3F9_27 [Arabidopsis thaliana] >gi|85982672|gb|AAY69753.1| tobacco rattle virus-induced protein variant 1 [Arabidopsis thaliana]	Unigene117603_All//1.00E-07//AT1G78410| VQ motif-containing protein	Unigene117603_All//0.00E+00//TC165064			GO:0006950	nr -
Unigene117604_All	621	0.00	0.00	0.00	0.00	0.11	0.00	0.75	0.61	3.34	null	null		null	null		6.79E+00	6.12E-01		null	null		-3.06E-01	7.36E-01		2.16E+00	1.54E-06	Up	Unigene117604_All//gi|82568711|dbj|BAE48668.1|//3.00E-45//Alcohol acyl-transferase [Prunus mume]	Unigene117604_All//4.00E-37//AT5G48930| HCT (HYDROXYCINNAMOYL-COA SHIKIMATE/QUINATE HYDROXYCINNAMOYL TRANSFERASE); quinate O-hydroxycinnamoyltransferase/ shikimate O-hydroxycinnamoyltransferase/ transferase	Unigene117604_All//4.00E-150//TC146659		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016747	nr +
Unigene117608_All	375	0.00	0.41	0.00	0.13	0.00	0.12	0.00	1.23	2.44	8.66E+00	2.36E-01		null	null		-7.05E+00	5.59E-01		-1.41E-01	9.55E-01		1.03E+01	1.94E-03		1.13E+01	1.08E-06	Up							
Unigene11761_All	862	3.76	34.86	2.10	10.17	33.92	5.71	12.80	10.57	170.72	3.21E+00	1.28E-104	Up	-8.41E-01	1.97E-02		1.74E+00	8.49E-58	Up	-8.33E-01	1.27E-05		-2.76E-01	8.75E-02		3.74E+00	0.00E+00	Up	Unigene11761_All//gi|171452368|dbj|BAG15875.1|//4.00E-52//WRKY transcription factor [Bruguiera gymnorhiza]	Unigene11761_All//2.00E-31//AT4G22810| WRKY53; DNA binding / protein binding / transcription activator/ transcription factor	Unigene11761_All//0.00E+00//gi|73864993|gb|DT467732.1|DT467732	WRKY		GO:0001071//GO:0003677//GO:0010468//GO:0043231	nr -
Unigene117610_All	336	0.16	0.00	0.00	2.08	1.64	2.15	7.80	2.49	5.69	-7.28E+00	6.16E-01		-7.28E+00	6.28E-01		-3.40E-01	6.80E-01		5.12E-02	9.48E-01		-1.65E+00	9.48E-06	Down	-4.55E-01	1.85E-01		Unigene117610_All//gi|224113571|ref|XP_002332539.1|//4.00E-15//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222832683|gb|EEE71160.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene117610_All//8.00E-10//AT1G12220| RPS5 (RESISTANT TO P. SYRINGAE 5); nucleotide binding	Unigene117610_All//6.00E-74//DT463318		ko04626|Plant-pathogen interaction	GO:0005488	nr +

Unigene117614_All	252	0.00	0.20	0.00	0.79	1.09	0.36	1.17	1.00	8.06	7.65E+00	6.19E-01		null	null		4.67E-01	8.17E-01		-1.14E+00	5.69E-01		-2.39E-01	8.40E-01		2.78E+00	2.59E-08	Up	Unigene117614_All//gi|217070972|gb|ACJ83846.1|//5.00E-10//unknown [Medicago truncatula]		Unigene117614_All//7.00E-76//TC162083				nr -
Unigene117615_All	219	0.00	0.00	0.00	0.00	0.00	0.00	9.65	0.57	3.27	null	null		null	null		null	null		null	null		-4.08E+00	1.66E-11	Down	-1.56E+00	1.14E-04	Down			Unigene117615_All//4.00E-37//gi|73850352|gb|DT459372.1|DT459372				
Unigene117617_All	841	0.31	0.24	0.76	0.53	0.57	0.75	0.50	0.00	7.06	-3.68E-01	7.79E-01		1.29E+00	1.87E-01		1.05E-01	9.55E-01		4.96E-01	6.37E-01		-8.97E+00	3.25E-03		3.81E+00	2.30E-30	Up	Unigene117617_All//gi|56121882|gb|AAV74222.1|//9.00E-19//AtSg40700 [Arabidopsis thaliana] >gi|63003888|gb|AAY25473.1| AtSg40700 [Arabidopsis thaliana]	Unigene117617_All//3.00E-21//AT3G27350| unknown protein	Unigene117617_All//4.00E-86//DT462327			GO:0016020	nr +
Unigene11762_All	439	0.60	4.16	0.00	3.74	6.67	4.73	2.50	1.62	17.70	2.80E+00	4.13E-06	Up	-9.22E+00	8.58E-02		8.32E-01	2.07E-02		3.38E-01	4.92E-01		-6.30E-01	2.93E-01		2.82E+00	3.07E-30	Up	Unigene11762_All//gi|174523400|dbj|BAG15875.1|//6.00E-30//WRKY transcription factor [Bruguiera gymnorhiza]	Unigene11762_All//3.00E-26//AT4G11070| WRKY41; transcription factor	Unigene11762_All//2.00E-65//gi|73864993|gb|DT467732.1|DT467732	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0006351//GO:0009536//GO:0009743//GO:0010260//GO:0010468//GO:0010557//GO:0030528//GO:0042742	nr -
Unigene117620_All	237	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.19	null	null		null	null		null	null		null	null		null	null		1.11E+01	6.14E-04	Up								
Unigene117629_All	237	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.86	null	null		null	null		null	null		null	null		null	null		1.15E+01	4.97E-05	Up								
Unigene11763_All	1029	30.05	21.62	22.05	13.36	19.98	14.05	5.10	2.88	13.63	-4.75E-01	8.90E-07		-4.47E-01	7.79E-06		5.80E-01	2.74E-07		7.20E-02	7.01E-01		-8.21E-01	4.17E-04		1.42E+00	1.17E-22	Up	Unigene11763_All//gi|18700139|gb|AAL77681.1|//2.00E-52//AtIg64350/F15H21_2 [Arabidopsis thaliana] >gi|88193800|gb|ABD42989.1| AtIg64355 [Arabidopsis thaliana]	Unigene11763_All//1.00E-53//AT1G64355| unknown protein	Unigene11763_All//0.00E+00//TC140916			GO:0009536	nr -
Unigene117635_All	230	0.00	33.93	0.69	0.00	0.00	0.20	0.00	0.00	0.35	1.51E+01	1.26E-44	Up	9.44E+00	2.39E-01		null	null		7.62E+00	6.99E-01		null	null		8.44E+00	4.05E-01				Unigene117635_All//2.00E-29//DN800060					ESTscan +
Unigene117637_All	764	0.00	0.00	0.00	0.00	0.00	0.00	0.66	0.27	21.43	null	null		null	null		null	null		null	null		-1.28E+00	1.86E-01		5.01E+00	1.11E-98	Up			Unigene117637_All//2.00E-60//TC141760					
Unigene11764_All	3750	3.36	35.18	3.45	7.44	21.97	8.05	8.17	8.46	78.23	3.39E+00	0.00E+00	Up	3.73E-02	8.31E-01		1.56E+00	2.95E-140	Up	1.13E-01	3.40E-01		4.95E-02	6.21E-01		3.26E+00	0.00E+00	Up	Unigene11764_All//gi|259121389|gb|ACV92014.1|//1.00E-125//WRKY transcription factor 12 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene11764_All//3.00E-60//AT4G11070| WRKY41; transcription factor	Unigene11764_All//0.00E+00//TC150705	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0010467	nr +
Unigene117640_All	960	0.00	0.21	0.22	0.00	0.00	0.00	0.97	0.96	5.81	7.72E+00	1.37E-01		7.79E+00	1.41E-01		null	null		null	null		-1.66E-02	1.02E+00		2.58E+00	5.31E-20	Up								
Unigene117654_All	247	0.00	0.41	0.00	0.00	0.00	0.00	0.51	0.17	4.19	8.68E+00	3.89E-01		null	null		null	null		null	null		-1.60E+00	5.35E-01		3.03E+00	6.50E-05	Up			Unigene117654_All//5.00E-123//FL577603					
Unigene11767_All	2648	6.82	14.79	7.26	13.54	10.61	20.89	16.81	37.49	30.06	1.12E+00	3.60E-34	Up	9.08E-02	5.52E-01		-3.52E-01	2.32E-05		6.25E-01	1.66E-19		1.16E+00	8.73E-111	Up	8.38E-01	9.88E-54		Unigene11767_All//gi|15229641|ref|NP_188473.1|//0.00E+00//AtALMT9 (aluminum-activated malate transporter 9); anion channel [Arabidopsis thaliana]	Unigene11767_All//6.00E-178//AT3G18440| AtALMT9 (aluminum-activated malate transporter 9); anion channel	Unigene11767_All//0.00E+00//TC154916			GO:0000325//GO:0010038//GO:0015740	nr +
Unigene117671_All	512	32.90	43.15	36.82	10.90	14.19	24.43	11.40	9.80	3.19	3.91E-01	8.43E-04		1.62E-01	2.64E-01		3.81E-01	8.47E-02		1.17E+00	7.71E-13	Up	-2.18E-01	3.80E-01		-1.84E+00	3.90E-14	Down	Unigene117671_All//gi|161778780|gb|ABX79341.1|//1.00E-59//cysteine protease [Vitis vinifera]	Unigene117671_All//5.00E-54//AT4G39090| RD19 (RESPONSIVE TO DEHYDRATION 19); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene117671_All//1.00E-146//gi|164285445|gb|ES796421.1|ES796421			GO:0070011	nr -
Unigene117681_All	269	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	7.70	null	null		null	null		null	null		null	null		7.28E+00	6.37E-01		1.29E+01	7.51E-15	Up								
Unigene117687_All	245	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.00	2.93	null	null		null	null		null	null		null	null		-7.43E+00	6.61E-01		4.08E+00	2.41E-04	Up	Unigene117687_All//gi|242070905|ref|XP_002450729.1|//3.00E-08//hypothetical protein SORBIDRAFT_05g016460 [Sorghum bicolor] >gi|241936572|gb|EES09717.1| hypothetical protein SORBIDRAFT_05g016460 [Sorghum bicolor]		Unigene117687_All//3.00E-22//TC146753				nr +
Unigene11770_All	1286	6.47	6.90	11.43	16.19	16.39	21.35	21.63	9.07	12.73	9.21E-02	6.48E-01		8.21E-01	6.37E-08		1.74E-02	9.11E-01		3.99E-01	8.56E-05		-1.25E+00	7.02E-36	Down	-7.65E-01	9.19E-17		Unigene11770_All//gi|209978718|gb|ACJ04704.1|//1.00E-91//hexokinase 1 [Cucumis melo]	Unigene11770_All//1.00E-74//AT4G29130| HXK1 (HEXOKINASE 1); ATP binding / fructokinase/ glucokinase/ hexokinase	Unigene11770_All//0.00E+00//gi|78324449|gb|DT544723.1|DT544723		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism	GO:0004396//GO:0006007//GO:0008219//GO:0009527//GO:0009757//GO:0031224//GO:0032259//GO:0046914	nr -
Unigene117701_All	228	0.00	0.00	0.00	0.00	0.30	0.20	0.00	2.57	4.72	null	null		null	null		8.24E+00	6.12E-01		7.63E+00	6.99E-01		1.13E+01	2.81E-04	Up	1.22E+01	8.30E-08	Up								
Unigene11771_All	837	17.19	9.20	8.14	20.35	12.67	18.13	29.25	17.98	9.23	-9.02E-01	2.04E-09		-1.08E+00	7.98E-12	Down	-6.84E-01	2.86E-08		-1.67E-01	2.82E-01		-7.02E-01	1.56E-12		-1.66E+00	2.20E-49	Down	Unigene11771_All//gi|297828127|ref|XP_002881946.1|//6.00E-66//dihydrodipicolinate reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327785|gb|EFH58205.1| dihydrodipicolinate reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11771_All//3.00E-67//AT2G44040| dihydrodipicolinate reductase family protein	Unigene11771_All//0.00E+00//TC135930		ko00300|Lysine biosynthesis	GO:0009089//GO:0009536//GO:0016628	nr -
Unigene117718_All	256	0.00	0.00	0.83	0.19	0.40	0.18	1.49	3.92	6.69	null	null		9.70E+00	1.41E-01		1.05E+00	8.09E-01		-1.42E-01	9.55E-01		1.40E+00	2.82E-02		2.17E+00	1.39E-05	Up			Unigene117718_All//7.00E-42//gi|109849493|gb|DW478472.1|DW478472				
Unigene117719_All	676	0.00	0.15	0.00	0.15	0.00	0.00	0.38	0.06	5.07	7.23E+00	3.89E-01		null	null		-7.20E+00	3.15E-01		-7.20E+00	4.02E-01		-2.60E+00	1.44E-01		3.76E+00	1.41E-17	Up	Unigene117719_All//gi|224069196|ref|XP_002326298.1|//7.00E-45//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372128|gb|ABQ62995.1| RAP2-like protein [Populus trichocarpa] >gi|222833491|gb|EEE71968.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene117719_All//2.00E-36//AT1G19210| AP2 domain-containing transcription factor, putative	Unigene117719_All//6.00E-20//gi|78324292|gb|DT544566.1|DT544566	AP2-EREBP		GO:0001071//GO:0006351//GO:0006950//GO:0010468//GO:0043231	nr +
Unigene11773_All	1016	1.60	1.90	5.50	4.51	5.05	5.16	4.04	5.14	1.49	2.48E-01	6.22E-01		1.79E+00	5.79E-10	Up	1.63E-01	6.04E-01		1.93E-01	5.28E-01		3.49E-01	1.53E-01		-1.44E+00	1.99E-07	Down	Unigene11773_All//gi|124359162|gb|ABN05685.1|//5.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene11773_All//0.00E+00//gi|21095789|gb|BQ408102.1|BQ408102				nr -
Unigene117736_All	476	0.44	1.49	0.22	1.36	1.01	1.33	1.07	2.72	4.60	1.76E+00	5.61E-02		-9.75E-01	6.21E-01		-4.26E-01	6.09E-01		-3.46E-02	9.53E-01		1.35E+00	1.28E-02		2.11E+00	1.02E-06	Up	Unigene117736_All//gi|145335397|ref|NP_172597.2|//3.00E-33//ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene117736_All//1.00E-30//AT1G11300| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene117736_All//0.00E+00//C0081719		ko04626|Plant-pathogen interaction		nr +
Unigene117740_All	505	0.73	0.80	0.00	0.20	0.41	0.18	0.50	0.83	6.63	1.47E-01	8.98E-01		-9.50E+00	2.79E-02		1.05E+00	6.13E-01		-1.41E-01	9.51E-01		7.20E-01	5.07E-01		3.72E+00	4.55E-17	Up								
Unigene117745_All	1036	0.00	0.00	0.00	0.10	0.07	0.17	1.43	0.16	3.65	null	null		null	null		-5.33E-01	8.18E-01		8.58E-01	6.96E-01		-3.15E+00	8.54E-07	Down	1.35E+00	2.45E-06	Up	Unigene117745_All//gi|226507536|ref|NP_001148133.1|//1.00E-07//WAK53a - OsWAK receptor-like protein kinase [Zea mays] >gi|195616018|gb|ACG29839.1| WAK53a - OsWAK receptor-like protein kinase [Zea mays]	Unigene117745_All//1.00E-08//AT1G16090| WAKL7 (wall associated kinase-like 7); protein serine/threonine kinase	Unigene117745_All//7.00E-178//TC169886			GO:0016301	nr +
Unigene117749_All	1580	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	3.05	null	null		null	null		null	null		null	null		5.73E+00	4.03E-01		1.16E+01	1.69E-34	Up	Unigene117749_All//gi|38344889|emb|CAD41912.2|//1.00E-133//OSJNBa0033G05.13 [Oryza sativa (japonica cultivar-group)]	Unigene117749_All//2.00E-21//ATMG00300| hypothetical protein	Unigene117749_All//3.00E-48//FL576972				nr +
Unigene117750_All	238	11.21	1.70	2.01	10.47	10.85	6.07	0.18	1.05	0.67	-2.72E+00	1.79E-08	Down	-2.48E+00	2.65E-07	Down	5.23E-02	9.16E-01		-7.85E-01	5.15E-02		2.57E+00	1.53E-01		1.91E+00	3.78E-01		Unigene117750_All//gi|48310189|gb|AAT41771.1|//1.00E-09//At5g42680 [Arabidopsis thaliana] >gi|52218794|gb|AAU29467.1| At5g42680 [Arabidopsis thaliana]	Unigene117750_All//5.00E-11//AT5G42680| unknown protein	Unigene117750_All//8.00E-57//ES820721				nr +
Unigene117751_All	868	0.12	0.00	0.00	0.00	0.08	0.00	0.54	0.34	2.16	-6.91E+00	3.74E-01		-6.91E+00	3.96E-01		6.31E+00	6.12E-01		null	null		-6.69E-01	5.09E-01		2.01E+00	1.50E-05	Up	Unigene117751_All//gi|15236937|ref|NP_195254.1|//2.00E-46//zinc finger (C2H2 type) family protein [Arabidopsis thaliana] >gi|91806770|gb|ABE66112.1| zinc finger family protein [Arabidopsis thaliana]	Unigene117751_All//6.00E-42//AT4G35280| zinc finger (C2H2 type) family protein		C2H2		GO:0005488//GO:0010468	nr -
Unigene117758_All	708	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.06	0.90	null	null		null	null		null	null		null	null		-1.70E-02	1.01E+00		3.91E+00	7.66E-04	Up	Unigene117758_All//gi|224074401|ref|XP_002304364.1|//3.00E-81//4-coumarate-coa ligase [Populus trichocarpa] >gi|222841796|gb|EEE79343.1| 4-coumarate-coa ligase [Populus trichocarpa]	Unigene117758_All//1.00E-65//AT4G19010| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene117758_All//0.00E+00//BQ402740		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0008152//GO:0016405//GO:0016491//GO:0031410	nr -
Unigene11776_All	1450	4.19	1.71	1.98	3.26	3.75	5.79	1.98	0.81	1.48	-1.29E+00	2.76E-07	Down	-1.08E+00	2.21E-05	Down	2.01E-01	5.12E-01		8.28E-01	2.59E-05		-1.30E+00	1.31E-04	Down	-4.18E-01	1.98E-01		Unigene11776_All//gi|224059034|ref|XP_002299685.1|//8.00E-49//heavy metal ATPase [Populus trichocarpa] >gi|222846943|gb|EEE84490.1| heavy metal ATPase [Populus trichocarpa]	Unigene11776_All//1.00E-33//AT4G33520| PAA1 (P-TYPE ATPASE 1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / copper ion transmembrane transporter	Unigene11776_All//6.00E-176//gi|164350307|gb|ES831374.1|ES831374			GO:0000166//GO:0000502//GO:0005375//GO:0009526//GO:0009532//GO:0010038//GO:0015662//GO:0016020//GO:0019941//GO:0022900	nr +
Unigene117769_All	453	0.92	4.81	1.76	1.65	3.72	3.59	1.03	0.46	2.29	2.38E+00	4.02E-06	Up	9.32E-01	2.56E-01		1.18E+00	2.09E-02		1.12E+00	3.47E-02		-1.15E+00	2.53E-01		1.16E+00	5.12E-02				Unigene117769_All//1.00E-97//TC169302					
Unigene11779_All	3470	1.07	1.11	1.06	2.44	2.50	3.36	2.44	1.72	5.01	5.20E-02	8.75E-01		-1.57E-02	9.85E-01		3.52E-02	8.85E-01		4.60E-01	5.63E-03		-5.01E-01	4.93E-03		1.04E+00	2.18E-17	Up	Unigene11779_All//gi|108708012|gb|ABF95807.1|//1.00E-160//Lung seven transmembrane receptor family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene11779_All//5.00E-140//AT1G61670| FUNCTIONS IN: molecular_function unknown; LOCATED IN: endomembrane system, integral to membrane; CONTAINS InterPro DOMAIN/s: Transmembrane receptor, eukaryota (InterPro:IPR009637); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10980.1); Has 473 Blast hits to 471 proteins in 125 species: Archae - 0; Bacteria - 2; Metazoa - 242; Fungi - 99; Plants - 92; Viruses - 0; Other Eukaryotes - 38 (source: NCBI BLink).	Unigene11779_All//0.00E+00//DR454835				nr +
Unigene117794_All	282	0.00	0.18	0.76	0.18	0.00	0.00	0.15	0.59	3.25	7.49E+00	6.19E-01		9.56E+00	1.41E-01		-7.46E+00	5.59E-01		-7.46E+00	6.40E-01		1.98E+00	3.80E-01		4.44E+00	1.24E-05	Up			Unigene117794_All//8.00E-82//DW225774					
Unigene117796_All	251	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	2.54	null	null		null	null		null	null		null	null		7.38E+00	6.37E-01		1.13E+01	9.35E-05	Up			Unigene117796_All//3.00E-07//BE055792					
Unigene117808_All	601	0.52	0.00	0.00	0.08	0.00	0.00	0.63	0.14	4.97	-9.03E+00	3.66E-02		-9.03E+00	4.92E-02		-6.37E+00	5.59E-01		-6.37E+00	6.40E-01		-2.19E+00	8.76E-02		2.97E+00	1.11E-12	Up	Unigene117808_All//gi|224060299|ref|XP_002300130.1|//4.00E-82//glutaredoxin [Populus trichocarpa] >gi|222847388|gb|EEE84935.1| glutaredoxin [Populus trichocarpa]	Unigene117808_All//1.00E-18//AT5G14070| ROXY2; electron carrier/ protein disulfide oxidoreductase	Unigene117808_All//2.00E-164//DW503331			GO:0005488//GO:0006350//GO:0015036//GO:0019725//GO:0031410//GO:0043231//GO:0048449	nr +
Unigene117823_All	345	2.12	0.29	0.31	11.26	3.19	2.75	3.19	2.18	1.96	-2.85E+00	6.26E-03		-2.78E+00	1.05E-02		-1.82E+00	4.05E-09	Down	-2.03E+00	2.68E-09	Down	-5.47E-01	3.72E-01		-6.99E-01	2.11E-01				Unigene117823_All//4.00E-07//TC136732					
Unigene117824_All	395	0.00	0.00	0.00	0.25	0.17	0.23	0.43	0.74	4.54	null	null		null	null		-5.32E-01	8.18E-01		-1.41E-01	9.51E-01		7.91E-01	5.63E-01		3.41E+00	8.04E-09	Up	Unigene117824_All//gi|224055915|ref|XP_002298700.1|//3.00E-29//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222845958|gb|EEE83505.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene117824_All//2.00E-22//AT1G12210| RPL1 (RPS5-like 1); ATP binding / protein binding			ko04626|Plant-pathogen interaction	GO:0000166//GO:0006950//GO:0016787//GO:0051707	nr -

Unigene11783_All	1785	0.85	1.87	0.92	2.79	5.15	4.76	11.04	2.41	6.14	1.14E+00	9.68E-04	Up	1.22E-01	8.08E-01		8.84E-01	8.77E-07		7.69E-01	8.21E-05		-2.19E+00	7.77E-56	Down	-8.47E-01	2.75E-14		Unigene11783_All//gi|22330658|ref|NP_177758.2|//1.00E-150//CYCB2;4 (CYCLIN B2;4); cyclin-dependent protein kinase regulator [Arabidopsis thaliana] >gi|147636286|sp|Q9SFW6.2|CCB24_ARATH RecName: Full=Cyclin-B2-4; AltName: Full=G2/mitotic-specific cyclin-B2-4; Short=CycB2;4	Unigene11783_All//6.00E-145//AT1G20610| CYCB2;3 (Cyclin B2;3); cyclin-dependent protein kinase regulator	Unigene11783_All//0.00E+00//DW501540			GO:0009987//GO:0043231	nr -
Unigene117831_All	352	0.45	0.00	0.00	0.14	0.39	0.00	0.48	0.59	3.06	-8.80E+00	2.16E-01		-8.80E+00	2.45E-01		1.47E+00	6.19E-01		-7.14E+00	6.40E-01		3.05E-01	8.36E-01		2.67E+00	1.42E-04	Up	Unigene117831_All//gi|10177558|dbj|BAB10837.1|//1.00E-13//retroelement pol polyprotein-like [Arabidopsis thaliana]						GO:0003676//GO:0004518//GO:0006260//GO:0034061//GO:0042254//GO:0044424//GO:0046914	nr -
Unigene117838_All	604	0.00	0.00	0.09	0.00	0.00	0.00	0.28	1.11	7.65	null	null		6.46E+00	6.38E-01		null	null		null	null		1.98E+00	2.26E-02		4.77E+00	1.93E-27	Up	Unigene117838_All//gi|178601110|emb|CAN82922.1|//9.00E-08//hypothetical protein [Vitis vinifera]		Unigene117838_All//6.00E-60//gi|109849827|gb|DW478806.1|DW478806			GO:0005488//GO:0016020//GO:0044237//GO:0044424	nr +
Unigene11784_All	2101	5.08	4.90	2.84	14.25	14.75	12.25	16.52	5.57	10.20	-5.34E-02	7.73E-01		-8.40E-01	3.87E-06		4.99E-02	6.95E-01		-2.18E-01	3.62E-02		-1.57E+00	3.26E-62	Down	-6.96E-01	1.14E-17		Unigene11784_All//gi|22330658|ref|NP_177758.2|//1.00E-160//CYCB2;4 (CYCLIN B2;4); cyclin-dependent protein kinase regulator [Arabidopsis thaliana] >gi|147636286|sp|Q9SFW6.2|CCB24_ARATH RecName: Full=Cyclin-B2-4; AltName: Full=G2/mitotic-specific cyclin-B2-4; Short=CycB2;4	Unigene11784_All//1.00E-147//AT1G76310| CYCB2;4 (CYCLIN B2;4); cyclin-dependent protein kinase regulator	Unigene11784_All//0.00E+00//TC175569			GO:0009987//GO:0043231	nr +
Unigene11785_All	934	3.14	0.33	0.34	20.69	11.61	4.21	10.32	3.54	1.62	-3.27E+00	6.04E-11	Down	-3.20E+00	3.48E-10	Down	-8.33E-01	5.85E-13		-2.30E+00	1.38E-51	Down	-1.55E+00	1.79E-17	Down	-2.67E+00	7.63E-36	Down	Unigene11785_All//gi|75100616|sp|O82318.1|Y2579_ARATH//8.00E-53//RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase At2g25790; Flags: Precursor >gi|224589523|gb|ACN59295.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene11785_All//6.00E-54//AT2G25790| leucine-rich repeat transmembrane protein kinase, putative	Unigene11785_All//0.00E+00//CO1211142		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004871//GO:0008152//GO:0016020//GO:0016301//GO:0016491	nr -
Unigene117851_All	822	0.13	0.12	0.26	0.18	0.42	0.11	1.59	0.10	0.34	-4.61E-02	9.90E-01		1.03E+00	5.92E-01		1.20E+00	4.26E-01		-7.26E-01	7.16E-01		-3.97E+00	3.35E-07	Down	-2.23E+00	1.19E-04	Down	Unigene117851_All//gi|18076679|emb|CAC84774.1|//9.00E-35//P70 protein [Nicotiana tabacum]	Unigene117851_All//2.00E-20//AT5G60210| LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT2G37080.1); Has 77946 Blast hits to 39215 proteins in 1793 species: Archae - 845; Bacteria - 8877; Metazoa - 39997; Fungi - 6049; Plants - 2988; Viruses - 248; Other Eukaryotes - 18942 (source: NCBI BLink).	Unigene117851_All//0.00E+00//DW225237			GO:0005515	nr +
Unigene117852_All	241	14.33	4.84	14.36	12.61	11.72	5.81	0.35	0.35	1.32	-1.57E+00	9.76E-06	Down	3.40E-03	9.90E-01		-1.06E-01	8.10E-01		-1.12E+00	1.74E-03		-1.65E-02	1.01E+00		1.91E+00	1.54E-01					Unigene117852_All//4.00E-43//TC139629				
Unigene117857_All	353	0.00	0.00	0.45	0.00	0.10	0.00	0.12	0.47	1.92	null	null		8.82E+00	2.39E-01		6.61E+00	8.34E-01		null	null		1.98E+00	3.80E-01		4.00E+00	4.30E-04	Up			Unigene117857_All//4.00E-47//gi|164335631|gb|ES806224.1|ES806224				
Unigene11786_All	3146	1.31	0.18	0.14	4.09	3.61	1.88	7.12	3.96	1.80	-2.89E+00	1.41E-13	Down	-3.28E+00	1.62E-14	Down	-1.78E-01	3.07E-01		-1.12E+00	1.46E-12	Down	-8.47E-01	1.17E-15		-1.99E+00	1.40E-57	Down	Unigene11786_All//gi|75100616|sp|O82318.1|Y2579_ARATH//0.00E+00//RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase At2g25790; Flags: Precursor >gi|224589523|gb|ACN59295.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene11786_All//0.00E+00//AT2G25790| leucine-rich repeat transmembrane protein kinase, putative	Unigene11786_All//0.00E+00//CO1211141			GO:0003824//GO:0016020	nr -
Unigene11787_All	3239	3.18	1.56	2.15	21.07	18.69	19.84	28.63	49.72	10.54	-1.02E+00	1.97E-08	Down	-5.63E-01	2.33E-03		-1.73E-01	5.88E-03		-8.66E-02	2.46E-01		7.96E-01	1.22E-96		-1.44E+00	7.89E-150	Down	Unigene11787_All//gi|75100616|sp|O82318.1|Y2579_ARATH//0.00E+00//RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase At2g25790; Flags: Precursor >gi|224589523|gb|ACN59295.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene11787_All//0.00E+00//AT2G25790| leucine-rich repeat transmembrane protein kinase, putative	Unigene11787_All//0.00E+00//TC133977			GO:0004871//GO:0006464//GO:0007167//GO:0016301//GO:0016628//GO:0031224//GO:0032559	nr +
Unigene117872_All	505	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	1.42	null	null		null	null		null	null		null	null		-6.39E+00	6.61E-01		4.08E+00	2.41E-04	Up	Unigene117872_All//gi|76559894|tpe|CAI56334.1|//6.00E-13//TPA: isoflavone reductase-like protein 5 [Vitis vinifera]	Unigene117872_All//1.00E-09//AT4G39230| isoflavone reductase, putative			ko00640|Propanoate metabolism	GO:0043231	nr +
Unigene117873_All	575	0.18	0.00	0.00	1.21	0.84	0.16	0.44	0.73	2.98	-7.51E+00	3.74E-01		-7.51E+00	3.96E-01		-5.33E-01	5.45E-01		-2.95E+00	5.84E-03		7.20E-01	5.07E-01		2.76E+00	4.59E-07	Up	Unigene117873_All//gi|255584614|ref|XP_002533031.1|//3.00E-14//conserved hypothetical protein [Ricinus communis] >gi|223527193|gb|EEF29362.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene117881_All	979	0.00	0.00	0.00	0.20	0.04	0.00	0.60	1.15	1.79	null	null		null	null		-2.53E+00	2.34E-01		-7.67E+00	1.34E-01		9.31E-01	1.09E-01		1.57E+00	5.53E-04	Up	Unigene117881_All//gi|210063111|gb|ACJ06506.1|//9.00E-80//polygalacturonase [Diospyros kaki]	Unigene117881_All//3.00E-74//AT3G07970| QRT2 (QUARTET 2); polygalacturonase	Unigene117881_All//0.00E+00//gi|3325965|gb|AI054851.1|AI054851		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553//GO:0008152	nr -
Unigene117882_All	286	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.79	null	null		null	null		null	null		null	null		null	null		1.14E+01	7.36E-06	Up							
Unigene117898_All	236	0.00	0.00	0.00	0.00	0.00	0.00	0.36	0.35	4.73	null	null		null	null		null	null		null	null		-1.66E-02	1.01E+00		3.72E+00	4.35E-06	Up			Unigene117898_All//5.00E-18//gi|109859340|gb|DW488319.1|DW488319				ESTscan -
Unigene117903_All	223	0.00	0.00	0.00	0.00	0.00	0.00	1.14	0.75	5.36	null	null		null	null		null	null		null	null		-6.02E-01	6.48E-01		2.24E+00	3.02E-04	Up			Unigene117903_All//2.00E-14//TC134559				
Unigene117909_All	477	287.82	242.19	153.16	160.62	256.28	253.56	358.10	630.18	954.21	-2.49E-01	1.13E-08		-9.10E-01	5.87E-82		6.74E-01	1.27E-53		6.59E-01	5.24E-46		8.15E-01	3.32E-187		1.41E+00	0.00E+00	Up	Unigene117909_All//gi|298706692|emb|CBJ34222.1|//1.00E-18//conserved unknown protein [Ectocarpus siliculosus] >gi|298713886|emb|CBJ33762.1| conserved unknown protein [Ectocarpus siliculosus]		Unigene117909_All//3.00E-110//gi|133351010|gb|BG441370.1|BG441370				nr +
Unigene11791_All	2806	18.94	15.58	19.20	22.92	32.64	26.93	23.69	26.17	9.81	-2.82E-01	1.10E-04		1.97E-02	8.16E-01		5.10E-01	1.33E-24		2.33E-01	9.29E-05		1.44E-01	1.26E-02		-1.27E+00	6.33E-89	Down	Unigene11791_All//gi|18396647|ref|NP_564298.1|//0.00E+00//SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|42571671|ref|NP_973926.1| SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75331738|sp|Q93V09.1|SCP45_ARATH RecName: Full=Serine carboxypeptidase-like 45; Flags: Precursor >gi|31376397|gb|AAP49525.1| At1g28110 [Arabidopsis thaliana]	Unigene11791_All//0.00E+00//AT1G28110| SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase	Unigene11791_All//0.00E+00//TC171096			GO:0004180//GO:0005618//GO:0019538//GO:0031410	nr -
Unigene117917_All	442	0.36	0.46	0.48	0.90	0.23	0.20	0.29	0.00	2.16	3.69E-01	8.17E-01		4.41E-01	7.76E-01		-1.95E+00	1.19E-01		-2.14E+00	1.26E-01		-8.16E+00	2.36E-01		2.91E+00	1.88E-04	Up	Unigene117917_All//gi|115439195|ref|NP_001043877.1|//2.00E-09//Os01g0681000 [Oryza sativa Japonica Group] >gi|113533408|dbj|BAF05791.1| Os01g0681000 [Oryza sativa Japonica Group]	Unigene117917_All//2.00E-08//AT3G49190| condensation domain-containing protein	Unigene117917_All//6.00E-13//TC157940				nr +
Unigene117945_All	752	0.00	0.13	0.07	0.00	0.00	0.00	1.01	1.72	11.76	7.07E+00	3.89E-01		6.15E+00	6.38E-01		null	null		null	null		7.68E-01	1.50E-01		3.54E+00	2.24E-42	Up			Unigene117945_All//5.00E-76//TC147375				
Unigene117951_All	305	9.09	1.83	4.71	8.17	2.60	1.33	5.82	47.00	2.61	-2.31E+00	1.92E-07	Down	-9.48E-01	1.68E-02		-1.65E+00	2.41E-05	Down	-2.62E+00	3.98E-08	Down	3.01E+00	6.39E-58	Up	-1.16E+00	6.84E-03				Unigene117951_All//1.00E-96//BQ409813				
Unigene117958_All	821	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.00	2.86	null	null		null	null		null	null		null	null		-7.69E+00	1.35E-01		3.80E+00	2.43E-12	Up	Unigene117958_All//gi|224132258|ref|XP_002328224.1|//1.00E-33//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837739|gb|EEE76104.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene117958_All//5.00E-25//AT3G14470| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene117972_All	474	0.00	0.00	0.11	0.00	0.22	0.57	0.18	1.23	1.77	null	null		6.81E+00	6.38E-01		7.77E+00	4.57E-01		9.16E+00	7.04E-02		2.79E+00	8.26E-03		3.31E+00	2.30E-04	Up	Unigene117972_All//gi|188509950|gb|ACD56636.1|//6.00E-06//disease resistance related protein [Gossypium raimondii]		Unigene117972_All//4.00E-91//TC176729				nr -
Unigene117973_All	231	0.00	9.21	8.53	0.43	0.00	0.00	1.46	3.62	18.28	1.32E+01	4.10E-12	Up	1.31E+01	7.46E-11	Up	-8.75E+00	3.15E-01		-8.75E+00	4.02E-01		1.31E+00	6.56E-02		3.64E+00	4.95E-21	Up	Unigene117973_All//gi|145408581|ref|YP_001152305.1|//5.00E-08//O8F58e [Pinus koraiensis] >gi|145048830|gb|ABF35448.1| O8F58e [Pinus koraiensis]		Unigene117973_All//2.00E-48//gi|109859341|gb|DW488320.1|DW488320			GO:0009536	nr -
Unigene117980_All	698	0.00	0.15	0.00	0.36	0.10	0.00	0.48	1.08	1.94	7.18E+00	3.89E-01		null	null		-1.85E+00	2.75E-01		-8.48E+00	7.34E-02		1.15E+00	1.26E-01		2.00E+00	3.24E-04	Up	Unigene117980_All//gi|76339171|ref|NP_172362.3|//4.00E-30//BON3 (BONZAI 3); calcium-dependent phospholipid binding [Arabidopsis thaliana] >gi|53636240|gb|AAU89273.1| BON3 [Arabidopsis thaliana]	Unigene117980_All//9.00E-27//AT1G08860| BON3 (BONZAI 3); calcium-dependent phospholipid binding				GO:0006968//GO:0010941	nr +
Unigene117989_All	720	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.64	8.19	null	null		null	null		null	null		null	null		3.44E+00	1.16E-02		7.12E+00	2.30E-40	Up	Unigene117989_All//gi|301016726|dbj|BAJ11284.1|//2.00E-19//dehydration responsive protein [Corchorus olitorius]		Unigene117989_All//2.00E-13//TC152783				nr -
Unigene117994_All	242	0.00	0.42	0.00	0.00	0.00	0.56	0.17	0.86	2.96	8.71E+00	3.89E-01		null	null		null	null		9.13E+00	3.12E-01		2.31E+00	2.40E-01		4.08E+00	2.41E-04	Up							
Unigene117998_All	920	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	6.80	null	null		null	null		null	null		null	null		7.51E+00	1.39E-01		1.27E+01	8.68E-45	Up	Unigene117998_All//gi|225455127|ref|XP_002267039.1|//2.00E-12//PREDICTED: hypothetical protein [Vitis vinifera]					GO:0003676//GO:0006259//GO:0046914	nr -
Unigene118002_All	363	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.09	null	null		null	null		null	null		null	null		null	null		1.10E+01	1.39E-05	Up	Unigene118002_All//gi|124359276|gb|ABN05778.1|//7.00E-10//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene118002_All//7.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative				GO:0003824	nr -
Unigene118005_All	414	0.51	0.24	0.64	0.96	0.33	0.22	0.20	0.50	2.02	-1.05E+00	5.65E-01		3.47E-01	7.97E-01		-1.53E+00	2.06E-01		-2.14E+00	1.26E-01		1.31E+00	4.47E-01		3.31E+00	2.30E-04	Up							
Unigene11801_All	2412	9.72	28.91	21.37	18.13	21.69	27.49	16.35	26.77	28.82	1.57E+00	1.66E-101	Up	1.14E+00	1.19E-44	Up	2.58E-01	2.13E-04		6.00E-01	1.16E-21		7.11E-01	2.35E-32		8.18E-01	4.19E-45				Unigene11801_All//0.00E+00//TC174620				
Unigene118012_All	229	0.00	0.00	0.00	0.00	0.30	0.99	0.00	2.37	4.52	null	null		null	null		8.23E+00	6.12E-01		9.95E+00	1.19E-01		1.12E+01	5.36E-04	Up	1.21E+01	1.58E-07	Up	Unigene118012_All//gi|1769897|emb|CAA69271.1|//7.00E-12//lectin receptor kinase [Arabidopsis thaliana]	Unigene118012_All//2.00E-11//AT1G48720| unknown protein	Unigene118012_All//3.00E-16//TC178414			GO:0005488	nr -

Unigene11802_All	706	21.79	2.44	15.01	12.49	13.12	5.50	1.38	0.83	0.17	-3.16e+00	1.89E-53	Down	-5.38E-01	2.67E-04		7.12E-02	7.85E-01		-1.18E+00	1.44E-09	Down	-7.33E-01	2.48E-01		-3.02E+00	9.60E-05	Down	Unigene11802_All//gi|163889378|gb|ABY48148.1|//4.00E-18//lectin [Medicago truncatula]	Unigene11802_All//6.00E-07//AT5G10530| lectin protein kinase, putative	Unigene11802_All//9.00E-90//TC144439			GO:0004672//GO:0005488	nr +
Unigene118020_All	224	0.93	1.13	4.28	5.11	4.77	0.00	1.51	1.31	1.42	2.76E-01	8.43E-01		2.20E+00	9.10E-03		-1.02E-01	8.56E-01		-1.23E+01	3.58E-07	Down	-2.09E-01	8.50E-01		-8.58E-02	9.47E-01		Unigene118020_All//gi|297739057|emb|CBI28546.3|//7.00E-07//unnamed protein product [Vitis vinifera]	Unigene118020_All//3.00E-06//AT1G60460| unknown protein	Unigene118020_All//1.00E-40//BG445931				nr -
Unigene118023_All	294	0.00	0.00	0.36	0.00	0.00	0.00	6.62	0.43	1.22	null	null		8.50E+00	4.00E-01		null	null		null	null		-3.96E+00	2.04E-10	Down	-2.44E+00	3.73E-07	Down	Unigene118023_All//gi|253759874|ref|XP_002488951.1|//6.00E-11//hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor] >gi|241947058|gb|EES20203.1| hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor]		Unigene118023_All//3.00E-23//TC148521				nr -
Unigene118024_All	262	6.99	29.78	14.43	10.08	12.62	36.37	12.75	9.57	6.39	2.09E+00	2.53E-17	Up	1.05E+00	1.60E-03		3.24E-01	3.92E-01		1.85E+00	4.23E-19	Up	-4.14E-01	1.91E-01		-9.97E-01	7.10E-04		Unigene118024_All//gi|2764806|emb|CAA55294.1|//1.00E-27//epoxide hydrolase [Glycine max]	Unigene118024_All//4.00E-26//AT3G05600| epoxide hydrolase, putative	Unigene118024_All//3.00E-115//gi|48753192|gb|C0083711.1|C0083711			GO:0004713	nr -
Unigene118026_All	598	0.09	0.17	0.36	0.08	0.29	0.15	1.06	0.14	0.07	9.54E-01	7.27E-01		2.03E+00	3.62E-01		1.79E+00	5.21E-01		8.58E-01	7.95E-01		-2.92E+00	4.20E-03		-3.99E+00	5.82E-04	Down	Unigene118026_All//gi|15218183|ref|NP_175630.1|//2.00E-41//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|75186219|sp|Q96R17.1|PTR2X_ARATH RecName: Full=Probable peptide transporter At1g52190	Unigene118026_All//6.00E-36//AT1G52190| proton-dependent oligopeptide transport (POT) family protein				GO:0015833//GO:0044464	nr -
Unigene118028_All	323	0.00	0.00	0.00	0.31	0.11	0.14	0.26	0.00	2.84	null	null		null	null		-1.53E+00	5.87E-01		-1.14E+00	6.78E-01		-8.03E+00	4.05E-01		3.44E+00	7.53E-05	Up	Unigene118028_All//gi|3894393|gb|AAC78596.1|//4.00E-18//Hcr2-5D [Solanum lycopersicum var. cerasiforme]	Unigene118028_All//2.00E-13//AT2G01950| BRL2 (BRI1-LIKE 2); ATP binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase				GO:0003824	nr -
Unigene11803_All	497	13.48	2.85	5.57	8.12	6.65	3.27	0.94	4.29	0.56	-2.24E+00	2.32E-16	Down	-1.27E+00	1.97E-07	Down	-2.88E-01	3.81E-01		-1.31E+00	1.89E-05	Down	2.20E+00	1.16E-06	Up	-7.38E-01	4.26E-01		Unigene11803_All//gi|115440305|ref|NP_001044432.1|//3.00E-18//Os01g0779300 [Oryza sativa Japonica Group] >gi|113533963|dbj|BAF06346.1| Os01g0779300 [Oryza sativa Japonica Group]	Unigene11803_All//6.00E-11//AT5G42120| lectin protein kinase family protein	Unigene11803_All//0.00E+00//TC164982			GO:0004672//GO:0006464//GO:0031410//GO:0032559	nr +
Unigene118037_All	904	0.06	0.00	0.06	0.00	0.00	0.00	0.23	1.20	1.06	-5.86E+00	6.15E-01		2.47E-02	9.96E-01		null	null		null	null		2.36E+00	5.23E-04	Up	2.18E+00	1.83E-03						Unigene118037_All//1.00E-15//TC149689				
Unigene11804_All	2310	0.91	0.22	0.69	7.14	7.51	5.32	3.73	9.14	3.83	-2.05E+00	4.33E-05	Down	-3.90E-01	3.94E-01		7.39E-02	6.52E-01		-4.25E-01	1.74E-03		1.29E+00	1.38E-28	Up	3.62E-02	8.54E-01		Unigene11804_All//gi|115440305|ref|NP_001044432.1|//1.00E-127//Os01g0779300 [Oryza sativa Japonica Group] >gi|113533963|dbj|BAF06346.1| Os01g0779300 [Oryza sativa Japonica Group]	Unigene11804_All//2.00E-124//AT5G10530| lectin protein kinase, putative	Unigene11804_All//0.00E+00//DW242638		ko04626|Plant-pathogen interaction		nr -
Unigene118044_All	335	0.00	0.00	0.00	0.00	0.00	0.00	0.50	0.37	3.57	null	null		null	null		null	null		null	null		-4.32E-01	7.93E-01		2.82E+00	3.02E-05	Up	Unigene118044_All//gi|253721991|gb|ACT34060.1|//4.00E-19//Cf2/Cf5-like disease resistance protein [Aegilops tauschii]	Unigene118044_All//1.00E-13//AT2G34930| disease resistance family protein			ko04626|Plant-pathogen interaction	GO:0016491	nr -
Unigene118049_All	403	8.44	14.46	5.02	13.72	19.05	18.38	19.30	22.30	9.19	7.77E-01	1.60E-03		-7.49E-01	3.29E-02		4.74E-01	2.21E-02		4.22E-01	5.69E-02		2.08E-01	2.75E-01		-1.07E+00	1.04E-08	Down	Unigene118049_All//gi|18423628|ref|NP_568808.1|//2.00E-06//universal stress protein (USP) family protein [Arabidopsis thaliana]		Unigene118049_All//2.00E-101//gi|78351714|gb|DT571988.1|DT571988				nr -
Unigene11805_All	2393	4.72	1.74	4.87	6.87	7.18	4.17	4.06	6.13	1.95	-1.44E+00	3.56E-15	Down	4.53E-02	8.06E-01		6.39E-02	7.18E-01		-7.20E-01	7.03E-08		5.93E-01	5.08E-06		-1.06E+00	1.58E-10	Down	Unigene11805_All//gi|226498024|ref|NP_001147903.1|//1.00E-125//protein kinase [Zea mays] >gi|195614480|gb|ACG29070.1| protein kinase [Zea mays]	Unigene11805_All//1.00E-86//AT5G10530| lectin protein kinase, putative	Unigene11805_All//0.00E+00//ES817348		ko04626|Plant-pathogen interaction		nr -
Unigene118056_All	463	0.11	0.00	0.23	0.65	0.37	0.29	1.19	0.00	0.34	-6.82E+00	6.15E-01		1.03E+00	7.04E-01		-7.96E-01	5.57E-01		-1.14E+00	4.58E-01		-1.02E+01	4.61E-04	Down	-1.79E+00	5.07E-02		Unigene118056_All//gi|224056507|ref|XP_002298888.1|//2.00E-15//predicted protein [Populus trichocarpa] >gi|118485886|gb|ABK94789.1| unknown [Populus trichocarpa] >gi|222846146|gb|EEE83693.1| predicted protein [Populus trichocarpa]		Unigene118056_All//6.00E-47//TC168043				nr -
Unigene118059_All	617	0.00	0.00	0.00	0.00	0.00	0.00	0.69	0.27	5.04	null	null		null	null		null	null		null	null		-1.34E+00	2.24E-01		2.88E+00	9.23E-13	Up			Unigene118059_All//8.00E-84//gi|73859503|gb|DT462242.1|DT462242				
Unigene11806_All	981	0.11	0.10	0.43	1.12	1.79	2.35	7.93	3.11	60.43	-4.67E-02	9.90E-01		2.03E+00	1.40E-01		6.80E-01	1.82E-01		1.07E+00	1.20E-02		-1.35E+00	8.60E-12	Down	2.93E+00	2.49E-235	Up	Unigene11806_All//gi|124359440|gb|ABN05887.1|//1.00E-149//[2Fe-2S]-binding [Medicago truncatula]	Unigene11806_All//2.00E-142//AT3G62010| unknown protein	Unigene11806_All//2.00E-140//gi|54117136|gb|CO492645.1|CO492645				nr -
Unigene11807_All	1602	0.62	1.17	1.13	3.54	4.51	4.96	9.79	5.37	25.56	9.15E-01	5.49E-02		8.65E-01	8.81E-02		3.49E-01	1.23E-01		4.85E-01	2.00E-02		-8.65E-01	1.37E-11		1.38E+00	3.66E-62	Up	Unigene11807_All//gi|297817536|ref|XP_002876651.1|//0.00E+00//metal ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322489|gb|EFH52910.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene11807_All//0.00E+00//AT3G62010| unknown protein	Unigene11807_All//0.00E+00//gi|54117136|gb|CO492645.1|CO492645				nr +
Unigene118070_All	463	0.00	0.00	0.00	0.11	0.00	0.00	0.00	0.00	1.55	null	null		null	null		-6.75E+00	5.59E-01		-6.75E+00	6.40E-01		null	null		1.06E+01	2.63E-05	Up								
Unigene118076_All	384	0.00	0.00	0.00	0.00	0.00	0.00	0.77	0.22	3.53	null	null		null	null		null	null		null	null		-1.82E+00	2.11E-01		2.19E+00	1.27E-04	Up	Unigene118076_All//gi|55168340|gb|AAV44205.1|//1.00E-08//unknown protein [Oryza sativa Japonica Group]		Unigene118076_All//2.00E-12//TC139311				nr +
Unigene118079_All	407	0.00	0.00	0.00	0.00	0.00	0.00	0.62	1.13	5.68	null	null		null	null		null	null		null	null		8.58E-01	3.96E-01		3.19E+00	1.37E-10	Up	Unigene118079_All//gi|147860110|emb|CAN82922.1|//2.00E-07//hypothetical protein [Vitis vinifera]		Unigene118079_All//4.00E-38//gi|109849827|gb|DW478806.1|DW478806			GO:0005488//GO:0016020//GO:0044237//GO:0044424	nr +
Unigene11808_All	853	1.35	1.31	4.74	3.62	4.32	5.61	6.49	3.82	4.48	-4.63E-02	9.53E-01		1.81E+00	1.57E-07	Up	2.55E-01	4.94E-01		6.32E-01	2.25E-02		-7.65E-01	6.81E-04		-5.34E-01	1.46E-02		Unigene11808_All//gi|297817536|ref|XP_002876651.1|//1.00E-125//metal ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322489|gb|EFH52910.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene11808_All//3.00E-126//AT3G62010| unknown protein	Unigene11808_All//9.00E-177//gi|54117136|gb|CO492645.1|CO492645				nr -
Unigene118086_All	577	0.18	0.35	0.00	0.26	0.66	0.39	0.29	0.94	3.25	9.54E-01	6.22E-01		-7.50E+00	3.96E-01		1.34E+00	3.40E-01		5.96E-01	7.22E-01		1.68E+00	7.92E-02		3.47E+00	2.57E-09	Up								
Unigene11809_All	1369	2.14	34.20	6.07	11.03	19.80	20.95	13.03	29.31	47.67	4.00E+00	8.96E-196	Up	1.50E+00	1.73E-11	Up	8.44E-01	1.03E-17		9.26E-01	6.40E-20		1.17E+00	5.35E-46	Up	1.87E+00	1.30E-151	Up	Unigene11809_All//gi|206584341|gb|ACI15343.1|//0.00E+00//NAC domain protein NAC6 [Gossypium hirsutum] >gi|206584359|gb|ACI15352.1| NAC domain protein NAC6 [Gossypium hirsutum]	Unigene11809_All//4.00E-94//AT5G18270| ANAC087; transcription factor	Unigene11809_All//0.00E+00//TC145720	NAC		GO:0003676//GO:0010468	nr -
Unigene118095_All	229	0.00	0.00	0.23	0.22	0.45	0.00	0.00	0.00	4.70	null	null		7.86E+00	6.38E-01		1.05E+00	8.09E-01		-7.76E+00	6.40E-01		null	null		1.22E+01	8.30E-08	Up			Unigene118095_All//1.00E-46//gi|78346504|gb|DT566778.1|DT566778				
Unigene1181_All	1246	3.07	10.70	4.49	7.00	11.58	11.89	7.13	8.76	6.84	1.80E+00	4.96E-24	Up	5.50E-01	3.77E-02		7.27E-01	1.42E-07		7.65E-01	8.13E-08		2.97E-01	6.56E-02		-5.86E-02	7.49E-01		Unigene1181_All//gi|225442186|ref|XP_002276676.1|//1.00E-135//PREDICTED: similar to mitochondrial substrate carrier family protein isoform 1 [Vitis vinifera]	Unigene1181_All//9.00E-115//AT1G72820| mitochondrial substrate carrier family protein	Unigene1181_All//0.00E+00//gi|164250315|gb|ES810237.1|ES810237				nr -
Unigene11810_All	1577	2.39	4.88	3.61	8.78	4.98	8.31	45.52	134.77	184.95	1.03E+00	1.52E-06	Up	5.97E-01	2.21E-02		-8.19E-01	3.68E-09		-8.04E-02	6.64E-01		1.57E+00	0.00E+00	Up	2.02E+00	0.00E+00	Up	Unigene11810_All//gi|206584341|gb|ACI15343.1|//1.00E-126//NAC domain protein NAC6 [Gossypium hirsutum] >gi|206584359|gb|ACI15352.1| NAC domain protein NAC6 [Gossypium hirsutum]	Unigene11810_All//1.00E-97//AT5G18270| ANAC087; transcription factor	Unigene11810_All//0.00E+00//TC171573	NAC			nr +
Unigene118100_All	602	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.52	null	null		null	null		null	null		null	null		null	null		1.06E+01	1.08E-06	Up	Unigene118100_All//gi|224064413|ref|XP_002300467.1|//8.00E-06//predicted protein [Populus trichocarpa] >gi|222847725|gb|EEE85272.1| predicted protein [Populus trichocarpa]						nr +
Unigene118102_All	236	0.89	0.00	0.00	0.00	0.00	0.00	0.90	2.30	6.75	-9.79E+00	1.22E-01		-9.79E+00	1.46E-01		null	null		null	null		1.36E+00	1.44E-01		2.91E+00	5.82E-07	Up			Unigene118102_All//7.00E-14//TC157689				
Unigene118109_All	240	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.87	2.49	null	null		null	null		null	null		null	null		9.77E+00	7.86E-02		1.13E+01	1.76E-04	Up								
Unigene118119_All	500	0.10	0.00	0.21	0.20	0.00	0.18	0.00	0.17	2.71	-6.71E+00	6.15E-01		1.03E+00	7.04E-01		-7.64E+00	3.15E-01		-1.41E-01	9.51E-01		7.39E+00	4.03E-01		1.14E+01	9.04E-10	Up	Unigene118119_All//gi|171988286|gb|ACB59355.1|//7.00E-35//peroxisome biogenesis factor 13 [Nicotiana tabacum]	Unigene118119_All//3.00E-12//AT3G07560| PEX13 (PEROXIN 13); protein binding	Unigene118119_All//5.00E-32//gi|78334975|gb|DT555249.1|DT555249		ko03040|Spliceosome	GO:0006625//GO:0009062//GO:0044439	nr -
Unigene118139_All	477	0.00	0.00	0.00	0.00	0.07	0.00	0.44	0.88	4.18	null	null		null	null		6.17E+00	8.33E-01		null	null		9.83E-01	3.73E-01		3.24E+00	2.44E-09	Up			Unigene118139_All//5.00E-35//BQ407647				
Unigene118148_All	250	0.84	6.08	2.77	9.37	3.72	6.14	0.34	1.50	0.64	2.86E+00	2.69E-05	Up	1.73E+00	7.68E-02		-1.33E+00	7.69E-04	Down	-6.09E-01	1.55E-01		2.15E+00	9.45E-02		9.14E-01	6.25E-01				Unigene118148_All//9.00E-60//TC157852				
Unigene118163_All	238	10.77	5.54	2.68	7.33	12.01	9.87	35.35	10.71	13.39	-9.61E-01	1.52E-02		-2.00E+00	1.34E-05	Down	7.13E-01	5.38E-02		4.30E-01	3.46E-01		-1.72E+00	8.53E-18	Down	-1.40E+00	8.29E-14	Down	Unigene118163_All//gi|255581663|ref|XP_002531635.1|//3.00E-09//alpha-glucosidase, putative [Ricinus communis] >gi|223528753|gb|EEF30763.1| alpha-glucosidase, putative [Ricinus communis]	Unigene118163_All//3.00E-06//AT1G68560| XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Unigene118163_All//3.00E-84//BQ414225				nr -
Unigene118166_All	543	0.00	0.00	0.00	0.00	0.06	0.00	0.31	0.92	16.80	null	null		null	null		5.99E+00	8.33E-01		null	null		1.57E+00	1.18E-01		5.75E+00	1.32E-58	Up	Unigene118166_All//gi|145408582|ref|YP_001152206.1|//1.00E-07//O8F137 [Pinus koraiensis] >gi|145048831|gb|ABF35449.1| O8F137 [Pinus koraiensis]		Unigene118166_All//2.00E-44//gi|109823694|gb|DW008546.1|DW008546			GO:0009536	nr +
Unigene118167_All	733	0.14	0.00	0.00	0.14	0.09	0.00	0.46	0.40	2.28	-7.16E+00	3.74E-01		-7.16E+00	3.96E-01		-5.32E-01	8.17E-01		-7.09E+00	4.02E-01		-2.09E-01	8.50E-01		2.31E+00	8.00E-06	Up	Unigene118167_All//gi|224071947|ref|XP_002303599.1|//5.00E-80//tir-nbs resistance protein [Populus trichocarpa] >gi|222841031|gb|EEE78578.1| tir-nbs resistance protein [Populus trichocarpa]	Unigene118167_All//4.00E-67//AT4G23460| nucleoside-triphosphatase/ nucleotide binding / transmembrane receptor				GO:0004872//GO:0006952//GO:0012501//GO:0016462//GO:0023060//GO:0032559//GO:0043231//GO:0044425	nr -
Unigene118177_All	503	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.25	2.06	null	null		null	null		null	null		null	null		7.96E+00	2.41E-01		1.10E+01	1.58E-07	Up			Unigene118177_All//2.00E-161//CO112141					ESTscan +
Unigene11818_All	540	3.88	4.32	3.06	6.64	4.97	4.43	6.50	2.63	6.12	1.55E-01	7.01E-01		-3.42E-01	4.64E-01		-4.17E-01	2.08E-01		-5.83E-01	7.68E-02		-1.30E+00	1.72E-05	Down	-8.58E-02	7.71E-01		Unigene11818_All//gi|30695999|ref|NP_199921.2|//6.00E-26//RNase H domain-containing protein [Arabidopsis thaliana] >gi|79330542|ref|NP_001032053.1| RNase H domain-containing protein [Arabidopsis thaliana] >gi|29028872|gb|AAO64815.1| At5g51080 [Arabidopsis thaliana] >gi|222424417|dbj|BAH20164.1| AT5G51080 [Arabidopsis thaliana]	Unigene11818_All//1.00E-23//AT1G24090| RNase H domain-containing protein	Unigene11818_All//0.00E+00//TC177117			GO:0005488//GO:0016891	nr +
Unigene118181_All	310	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.00	2.06	null	null		null	null		null	null		null	null		-7.09E+00	6.60E-01		3.91E+00	7.66E-04	Up								ESTscan +
Unigene11820_All	706	5.85	2.30	3.85	4.73	5.95	4.67	1.44	1.95	1.86	-1.35E+00	1.53E-05	Down	-6.06E-01	5.38E-02		3.32E-01	3.12E-01		-1.77E-02	9.50E-01		4.43E-01	3.96E-01		3.74E-01	4.74E-01		Unigene11820_All//gi|9369399|gb|AAF87147.1|AC002423_12//1.00E-25//T23E23.24 [Arabidopsis thaliana]	Unigene11820_All//2.00E-23//AT1G24090| RNase H domain-containing protein	Unigene11820_All//0.00E+00//TC177117			GO:0005488//GO:0016891	nr +

Unigene118202_All	355	0.29	0.14	0.15	0.14	0.10	0.00	0.24	0.00	2.81	-1.05E+00	6.85E-01			-9.75E-01	7.21E-01			-5.33E-01	8.27E-01			-7.13E+00	6.39E-01			-7.90E+00	4.05E-01			3.56E+00	2.43E-05	Up							
Unigene118204_All	447	0.00	0.00	0.00	0.00	0.23	0.00	0.00	0.19	1.52	null	null			null	null			7.85E+00	4.57E-01			null	null			7.55E+00	4.03E-01			1.06E+01	4.97E-05	Up			Unigene118204_All//2.00E-34//TC177455				
Unigene118205_All	313	1.00	1.30	2.04	1.59	1.21	1.01	0.95	0.93	4.96	3.69E-01	7.24E-01			1.03E+00	2.81E-01			-3.95E-01	6.89E-01			-6.56E-01	5.50E-01			-1.67E-02	1.02E+00			2.39E+00	1.16E-05	Up			Unigene118205_All//4.00E-47//TC174278				
Unigene118208_All	392	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.00	2.74	null	null			null	null			null	null			null	null			-8.75E+00	1.35E-01			2.67E+00	1.42E-04	Up							
Unigene118215_All	239	0.00	0.00	0.22	0.00	0.43	0.38	0.00	0.70	2.17	null	null			7.80E+00	6.38E-01			8.76E+00	4.57E-01			8.56E+00	4.79E-01			9.45E+00	1.39E-01			1.11E+01	6.14E-04	Up							
Unigene118822_All	503	0.42	0.40	0.42	4.16	3.70	3.77	6.14	4.82	2.93	-4.65E-02	9.89E-01			2.54E-02	1.00E+00			-1.70E-01	7.32E-01			-1.41E-01	7.55E-01			-3.49E-01	3.05E-01			-1.07E+00	5.76E-04	Down	Unigene11822_All//gi|224064438|ref|XP_002301476.1|//6.00E-72//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222843202|gb|EEE80749.1|multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene11822_All//4.00E-30//AT2G47800| ATMRP4 (ARABIDOPSIS THALIANA MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 4): ATPase, coupled to transmembrane movement of substances / folic acid transporter	Unigene11822_All//0.00E+00//ES834598		ko02010|ABC transporters	GO:0005773//GO:0006950//GO:0008152//GO:0009987//GO:0015405//GO:0015893//GO:0016628//GO:0017111//GO:0031090//GO:0031224//GO:0032559//GO:0051183//GO:0051707	nr +
Unigene118223_All	978	21.93	13.57	16.72	6.11	6.27	2.72	0.43	0.64	0.65	-6.92E-01	5.96E-09			-3.92E-01	1.53E-03			3.62E-02	9.05E-01			-1.17E+00	1.48E-06	Down		5.68E-01	5.04E-01			5.92E-01	4.53E-01		Unigene118223_All//gi|240256095|ref|NP_194537.6|//3.00E-24//binding [Arabidopsis thaliana]	Unigene118223_All//3.00E-20//AT4G28080| binding	Unigene118223_All//4.00E-99//DN800287			GO:0005488	nr -
Unigene118226_All	431	0.00	0.24	0.12	0.00	0.16	0.21	0.69	0.39	4.44	7.88E+00	3.89E-01			6.95E+00	6.38E-01			7.32E+00	6.12E-01			7.71E+00	4.79E-01			-8.24E-01	5.40E-01			2.69E+00	1.24E-07	Up							
Unigene11823_All	295	1.42	0.34	2.53	4.39	1.05	2.76	5.30	5.24	2.97	-2.05E+00	1.21E-01			8.33E-01	3.39E-01			-2.06E+00	6.01E-04	Down		-6.72E-01	2.74E-01			-1.66E-02	1.01E+00			-8.36E-01	6.46E-02		Unigene11823_All//gi|297596742|ref|XP_001043000.2|//2.00E-37//Os01g0356000 [Oryza sativa Japonica Group] >gi|255673217|dbj|BAF04914.2|Os01g0356000 [Oryza sativa Japonica Group]	Unigene11823_All//5.00E-38//AT2G47800| ATMRP4 (ARABIDOPSIS THALIANA MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 4): ATPase, coupled to transmembrane movement of substances / folic acid transporter	Unigene11823_All//1.00E-71//CO127490		ko02010|ABC transporters	GO:0000166//GO:0005773//GO:0006950//GO:0009987//GO:0015405//GO:0015893//GO:0016491//GO:0017111//GO:0031090//GO:0031410//GO:0051183//GO:0051707	nr -
Unigene118235_All	227	0.00	0.00	3.05	0.44	0.46	0.20	0.93	0.00	1.05	null	null			1.16E+01	6.17E-04	Up		5.23E-02	9.67E-01			-1.14E+00	6.77E-01			-9.86E+00	7.45E-02			1.77E-01	9.09E-01								
Unigene11824_All	1315	7.60	4.55	6.36	26.74	21.63	25.62	9.32	19.29	12.97	-7.41E-01	4.30E-05			-2.57E-01	2.03E-01			-3.06E-01	3.39E-04			-6.19E-02	6.13E-01			1.05E+00	8.67E-25	Up		4.76E-01	4.84E-05		Unigene11824_All//gi|186478074|ref|NP_001117218.1|//1.00E-111//NLA (nitrogen limitation adaptation); ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene11824_All//5.00E-113//AT1G02860| NLA (nitrogen limitation adaptation); ubiquitin-protein ligase				GO:0046872	nr -
Unigene118243_All	295	0.18	0.00	0.00	0.00	0.00	0.00	1.58	0.71	6.89	-7.47E+00	6.15E-01			-7.47E+00	6.28E-01			null	null			null	null			-1.15E+00	2.53E-01			2.13E+00	2.44E-06	Up	Unigene118243_All//gi|224116168|ref|XP_002331978.1|//2.00E-17//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222832102|gb|EEE70579.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene118243_All//2.00E-15//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative				GO:0005488	nr +
Unigene118247_All	593	0.00	0.00	0.27	0.25	0.00	0.00	0.00	0.07	1.88	null	null			8.07E+00	2.39E-01			-7.98E+00	1.66E-01			-7.98E+00	2.34E-01			6.14E+00	6.37E-01			1.09E+01	4.36E-08	Up							
Unigene118252_All	381	0.27	0.00	0.00	0.00	0.00	0.24	0.33	0.99	12.02	-8.10E+00	3.74E-01			-8.10E+00	3.96E-01			null	null			7.89E+00	4.79E-01			1.57E+00	1.95E-01			5.17E+00	2.53E-28	Up	Unigene118252_All//gi|151301818|gb|ABN50365.2|//5.00E-31//ethylene responsive element binding protein 1 [Gossypium barbadense]	Unigene118252_All//1.00E-19//AT5G47220| ERF2 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 2): DNA binding / transcription activator/ transcription factor	Unigene118252_All//3.00E-45//gi|109825974|gb|DW224695.1|DW224695	AP2-EREBP		GO:0000160//GO:0001071//GO:0002218//GO:0003676//GO:0006351//GO:0009743//GO:0010468//GO:0010557//GO:0030528//GO:0043231	nr +
Unigene118256_All	354	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.80	null	null			null	null			null	null			null	null			null	null			1.08E+01	9.35E-05	Up							
Unigene11826_All	3420	12.50	5.38	9.26	17.77	14.05	12.41	58.05	134.27	99.68	-1.22E+00	1.04E-42	Down		-4.32E-01	2.34E-07			-3.39E-01	3.92E-08			-5.18E-01	1.79E-15			1.21E+00	0.00E+00	Up		7.80E-01	5.73E-201		Unigene11826_All//gi|30695748|ref|NP_199787.2|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|30102752|gb|AAP21294.1|At5g49760 [Arabidopsis thaliana] >gi|224589713|gb|ACN59388.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene11826_All//0.00E+00//AT5G49760| leucine-rich repeat family protein / protein kinase family protein	Unigene11826_All//0.00E+00//gi|109879548|gb|DW508518.1|DW508518			GO:0004674//GO:0004871//GO:0006464//GO:0007167//GO:0016020//GO:0016491//GO:0031410//GO:0032559//GO:0043231	nr -
Unigene118267_All	397	0.00	0.00	0.00	0.00	0.09	0.00	0.11	0.74	2.31	null	null			null	null			6.44E+00	8.33E-01			null	null			2.79E+00	9.48E-02			4.44E+00	1.24E-05	Up			Unigene118267_All//5.00E-07//DR455508				
Unigene118268_All	237	0.00	0.00	0.00	0.00	0.00	0.00	1.25	0.88	7.73	null	null			null	null			null	null			null	null			-5.02E-01	6.78E-01			2.63E+00	3.47E-07	Up			Unigene118268_All//9.00E-103//CO132424				
Unigene118269_All	525	0.00	0.00	0.00	0.00	0.00	0.17	0.48	0.72	2.81	null	null			null	null			null	null			7.43E+00	4.79E-01			5.68E-01	6.38E-01			2.54E+00	9.95E-06	Up			Unigene118269_All//6.00E-07//gi|164269365|gb|ES827929.1|ES827929				ESTscan -
Unigene11828_All	4184	2.01	0.46	0.52	4.74	8.55	8.32	3.63	7.31	5.47	-2.13E+00	3.31E-19	Down		-1.95E+00	2.00E-16	Down		8.52E-01	1.29E-23			8.13E-01	2.11E-19			1.01E+00	4.89E-28	Up		5.91E-01	3.86E-09		Unigene11828_All//gi|224122448|ref|XP_002318839.1|//0.00E+00//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222859512|gb|EEE97059.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene11828_All//2.00E-126//AT5G36930| disease resistance protein (TIR-NBS-LRR class), putative	Unigene11828_All//6.00E-166//TC167883		ko04626|Plant-pathogen interaction		nr -
Unigene118280_All	699	0.00	0.00	0.15	0.00	0.00	0.00	0.12	1.08	0.46	null	null			7.25E+00	4.00E-01			null	null			null	null			3.15E+00	9.54E-04	Up		1.91E+00	1.54E-01				Unigene118280_All//2.00E-16//gi|109878436|gb|DW507406.1|DW507406				
Unigene118284_All	233	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.54	5.47	null	null			null	null			null	null			null	null			9.07E+00	2.41E-01			1.24E+01	3.29E-09	Up							
Unigene118285_All	364	0.00	0.00	0.00	0.27	0.00	0.12	7.20	0.92	0.44	null	null			-8.10E+00	3.15E-01			-8.10E+00	3.15E-01			-1.14E+00	6.77E-01			-2.97E+00	5.45E-11	Down		-4.04E+00	1.31E-14	Down			Unigene118285_All//3.00E-122//DW510069				
Unigene118286_All	232	0.00	0.00	0.00	0.00	0.00	0.00	0.36	0.36	3.78	null	null			null	null			null	null			null	null			-1.67E-02	1.01E+00			3.37E+00	1.32E-04	Up							
Unigene11829_All	1463	1.50	2.42	1.78	3.10	2.85	2.41	18.61	23.63	91.74	6.91E-01	3.52E-02			2.48E-01	5.65E-01			-1.22E-01	7.14E-01			-3.64E-01	2.34E-01			3.44E-01	2.52E-05			2.30E+00	0.00E+00	Up	Unigene11829_All//gi|195618208|gb|ACG30934.1|//2.00E-34//60S ribosomal protein L19-3 [Zea mays] >gi|195635187|gb|ACG37062.1| 60S ribosomal protein L19-3 [Zea mays]	Unigene11829_All//2.00E-26//AT1G18270| ketose-bisphosphate aldolase class-II family protein	Unigene11829_All//0.00E+00//TC143184		ko03010|Ribosome	GO:0005622	nr -
Unigene118295_All	259	0.00	0.00	0.00	0.00	0.00	0.00	0.33	0.16	3.38	null	null			null	null			null	null			null	null			-1.02E+00	7.26E-01			3.37E+00	1.32E-04	Up			Unigene118295_All//2.00E-29//DT461892				
Unigene118296_All	240	0.44	0.00	0.00	0.00	0.00	0.19	0.18	2.79	1.00	-8.77E+00	3.74E-01			-8.77E+00	3.96E-01			null	null			7.56E+00	6.99E-01			3.98E+00	6.38E-04	Up		2.50E+00	1.59E-01				Unigene118296_All//2.00E-35//gi|73863313|gb|DT466052.1|DT466052				
Unigene118297_All	351	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.27	null	null			null	null			null	null			null	null			null	null			1.11E+01	7.36E-06	Up							
Unigene1183_All	742	2.26	3.48	4.31	4.16	5.43	5.23	29.35	78.97	85.69	6.26E-01	1.14E-01			9.32E-01	1.04E-02			3.84E-01	2.34E-01			3.31E-01	3.38E-01			1.43E+00	7.14E-91	Up		1.55E+00	4.39E-113	Up	Unigene1183_All//gi|4530126|gb|AAD21872.1|//8.00E-48//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene1183_All//7.00E-39//AT4G21410| protein kinase family protein	Unigene1183_All//0.00E+00//TC153623		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006464//GO:0032559	nr -
Unigene118304_All	582	0.09	0.00	0.27	0.09	0.36	0.39	0.29	0.07	1.64	-6.49E+00	6.15E-01			1.61E+00	5.11E-01			2.05E+00	3.95E-01			2.18E+00	3.23E-01			-2.02E+00	3.68E-01			2.50E+00	6.42E-04	Up	Unigene118304_All//gi|5237223|ref|NP_197702.1|//5.00E-31//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene118304_All//3.00E-32//AT5G23110| zinc finger (C3HC4-type RING finger) family protein				GO:0046872	nr -
Unigene118315_All	331	0.16	1.38	0.97	4.06	2.91	3.55	0.64	2.40	6.50	3.12E+00	3.58E-02			2.61E+00	1.46E-01			-4.80E-01	4.15E-01			-1.96E-01	7.30E-01			1.91E+00	1.37E-02			3.35E+00	2.59E-10	Up	Unigene118315_All//gi|24461861|gb|AAN62348.1|AF506028_15//7.00E-18//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene118315_All//1.00E-12//AT1G61310| ATP binding / protein binding	Unigene118315_All//5.00E-170//DR461626		ko04626|Plant-pathogen interaction		nr +
Unigene118325_All	233	0.00	1.74	0.00	0.64	0.30	1.55	0.00	0.90	2.74	1.08E+01	1.36E-02			null	null			-1.12E+00	5.84E-01			1.27E+00	3.82E-01			9.81E+00	7.86E-02			1.14E+01	9.34E-05	Up			Unigene118325_All//3.00E-07//DW478609				
Unigene118331_All	668	0.24	0.91	0.56	0.52	0.72	0.27	0.13	0.69	4.71	1.95E+00	6.04E-02			1.25E+00	3.66E-01			4.67E-01	7.04E-01			-9.49E-01	4.81E-01			2.44E+00	3.74E-02			5.22E+00	1.18E-19	Up			Unigene118331_All//9.00E-16//BF276866				
Unigene11834_All	1223	16.86	17.90	21.51	14.01	10.19	6.61	1.21	1.64	0.75	8.66E-02	5.25E-01			3.52E-01	1.51E-03			-4.59E-01	2.40E-04			-1.08E+00	9.61E-16	Down		4.39E-01	3.08E-01			-6.92E-01	1.40E-01		Unigene11834_All//gi|297829562|ref|XP_002882663.1|//1.00E-133//anion-transporting ATPase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328503|gb|EFH58922.1|anion-transporting ATPase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11834_All//9.00E-120//AT3G10350| anion-transporting ATPase family protein	Unigene11834_All//0.00E+00//CO081126				nr +
Unigene118341_All	475	4.74	4.16	5.94	9.02	10.80	7.13	10.41	5.10	6.79	-1.87E-01	6.44E-01			3.27E-01	4.00E-01			2.60E-01	3.85E-01			-3.39E-01	2.89E-01			-1.03E+00	2.41E-05	Down		-6.16E-01	8.02E-03		Unigene118341_All//gi|34481803|emb|CAC87837.1|//2.00E-74//cullin 1C [Nicotiana tabacum]	Unigene118341_All//2.00E-73//AT4G02570| ATCUL1 (ARABIDOPSIS THALIANA CULLIN 1): protein binding	Unigene118341_All//0.00E+00//gi|13355430|gb|BG445778.1|BG445778		ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair	GO:0000151//GO:0019899//GO:0019941	nr +
Unigene118347_All	246	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.34	2.11	null	null			null	null			null	null			null	null			8.41E+00	4.03E-01			1.10E+01	6.14E-04	Up							
Unigene118351_All	418	0.00	0.61	0.51	0.12	0.25	0.00	0.10	0.10	2.00	9.24E+00	7.87E-02			8.99E+00	1.41E-01			1.05E+00	8.09E-01			-6.90E+00	6.39E-01			-1.58E-02	1.01E+00			4.31E+00	4.11E-05	Up	Unigene118351_All//gi|15239544|ref|NP_200218.1|//7.00E-23//AT-HSFA9; DNA binding / transcription factor [Arabidopsis thaliana] >gi|75264295|sp|Q9LVW2.1|HSFA9_ARATH RecName: Full=Heat stress transcription factor A-9; Short=AtHsfA9; AltName: Full=AtHsf-21	Unigene118351_All//4.00E-24//AT5G54070| AT-HSFA9; DNA binding / transcription factor	Unigene118351_All//2.00E-25//TC158707	HSF		GO:0001071//GO:0003677//GO:0006350//GO:0009408//GO:0010557//GO:0030528//GO:0043231	nr -
Unigene11837_All	3115	0.10	0.49	0.27	0.37	0.45	0.67	0.45	0.50	0.77	2.28E+00	2.68E-04	Up		1.44E+00	8.23E-02			3.01E-01	6.16E-01			8.59E-01	6.02E-02			1.49E-01	7.61E-01			7.77E-01	2.89E-02		Unigene11837_All//gi|75336836|sp|Q9SZ16.1|RPK2_ARATH//0.00E+00//RecName: Full=LRR receptor-like serine/threonine-protein kinase RPK2; AltName: Full=Receptor-like protein kinase 2; AltName: Full=Protein TOADSTOOL 2; Flags: Precursor	Unigene11837_All//0.00E+00//AT3G02130| RPK2 (RECEPTOR-LIKE PROTEIN KINASE 2): ATP binding / kinase/ protein serine/threonine kinase	Unigene11837_All//0.00E+00//TC164113		ko04626|Plant-pathogen interaction	GO:0000578//GO:0003006//GO:0005488//GO:0006950//GO:0009555//GO:0009698//GO:0009856//GO:0016020//GO:0016772//GO:0043231//GO:0044444	nr -
Unigene118373_All	255	0.00	0.00	0.00	0.00	0.00	0.00	9.45	2.13	0.78	null	null			null	null			null	null			null	null			-2.15E+00	2.78E-07	Down		-3.60E+00	2.13E-12	Down	Unigene118373_All//gi|75858833|gb|ABA28993.1|//4.00E-37//polyubiquitin [Symbiodinium sp. C3]	Unigene118373_All//5.00E-37//AT5G03240| UBQ3 (POLYUBIQUITIN 3): protein binding	Unigene118373_All//2.00E-30//TC134297			GO:0043231	nr +
Unigene118374_All	341	1.07	1.19	0.78	0.00	0.61	0.00	0.25	0.25	2.80	1.46E-01	8.98E-01			-4.60E-01	6.97E-01			9.24E+00	1.57E-01			null	null			-1.70E-02	1.01E+00			3.50E+00	4.29E-05	Up			Unigene118374_All//1.00E-47//TC170579				
Unigene118378_All	249	0.21	1.42	0.00	0.20	0.69	0.00	0.00	0.17	2.56	2.76E+00	9.60E-02			-7.71E+00	6.28E-01			1.79E+00	5.21E-01			-7.64E+00	6.39E-01			7.39E+00	6.37E-01			1.13E+01	9.34E-05	Up							
Unigene118384_All	1391	0.00	0.07	0.00	0.07	0.10	0.13	0.52	0.18	4.87	6.19E+00	3.89E-01			null	null			4.68E-01	8.77E-01			8.59E-01	6.96E-01			-1.52E+00	5.42E-02			3.24E+00	3.56E-30	Up	Unigene118384_All//gi|115467526|ref|NP_001057362.1|//5.00E-122//Os06g0271600 [Oryza sativa Japonica Group] >gi|113595402|dbj|BAF19276.1|Os06g0271600 [Oryza sativa Japonica Group]	Unigene118384_All//4.00E-13//AT5G57750| zinc finger (C3HC4-type RING finger) family protein	Unigene118384_All//3.00E-60//TC152784			GO:0003006//GO:0031410//GO:0046872	nr +
Unigene118388_All	330	0.00	0.00	0.00	0.00	0.00	0.00	0.64	1.90	3.50	null	null			null	null			null	null			null	null			1.57E+00	7.10E-02			2.45E+00	1.69E-04	Up							ESTscan +
Unigene11839_All	1307	5.52	15.97	6.76	2.67	3.50	7.33	32.28	94.14	92.24	1.53E+00	1.07E-29	Up		2.92E-01	1.68E-01			3.93E-01	1.84E-01			1.46E+00	8.26E-14	Up		1.54E+00	1.96E-213	Up		1.51E+00	2.00E-207	Up	Unigene11839_All//gi|42572503|ref|NP_974347.1|//1.00E-170//NADK1 (NAD KINASE 1): NAD+ kinase/ NADH kinase/ calmodulin binding [Arabidopsis thaliana] >gi|94717660|sp|Q56YN3.2|NADK1_ARATH RecName: Full=NAD(H) kinase 1; Short=AtNADK-1 >gi|398433359|gb|AAR32133.1| NADK1 [Arabidopsis thaliana]	Unigene11839_All//1.00E-171//AT3G21070| NADK1 (NAD KINASE 1): NAD+ kinase/ NADH kinase/ calmodulin binding	Unigene11839_All//0.00E+00//gi|164361092|gb|ES819069.1|ES819069		ko00760|Nicotinate and nicotinamide metabolism	GO:0016301//GO:0043169//GO:0044424	nr +
Unigene118395_All	302	0.00	0.00	0.00	0.00	0.00	0.30	0.00	0.00	5.01	null	null			null	null			null	null			8.22E+00	4.79E-01			null	null			1.23E+01	6.77E-11	Up							
Unigene118396_All	241	0.00	0.00	0.00	0.00	0.00	0.00	6.84	2.60	0.99	null	null			null	null			null	null			null	null			-1.40E+00	3.12E-03			-2.79E+00	5.06E-07	Down	Unigene118396_All//gi|148524155|gb|ABQ81936.1|//8.00E-20//elongation factor 1-alpha [Chara australis]	Unigene118396_All//3.00E-18//AT5G60390| elongation factor 1-alpha / EF-1-alpha				GO:0004779//GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene1184_All	2369	1.59	3.57	2.74	3.45	4.59	9.21	24.08	50.76	73.22	1.17E+00	1.68E-08	Up		7.86E-01	1.06E-03			4.14E-01	1.49E-02			1.42E+00	1.46E-29	Up		1.08E+00	2.29E-119	Up		1.60E+00	0.00E+00	Up	Unigene1184_All//gi|4530126|gb|AAD21872.1|//0.00E+00//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene1184_All//1.00E-152//AT4G23180| CRK10 (CYSTEINE-RICH RLK10): ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene1184_All//0.00E+00//TC153623		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0004871	nr +

Unigene11840_A11	1851	0.88	0.96	1.32	1.05	1.15	0.68	5.09	2.73	1.64	1.29E-01	7.79E-01		5.95E-01	1.60E-01		1.36E-01	8.19E-01		-6.20E-01	1.97E-01		-8.99E-01	1.03E-07		-1.64E+00	3.75E-19	Down	Unigene11840_A11//gi|42572503|ref|NP_974347.1|//0.00E+00//NADK1 (NAD KINASE 1); NAD+ kinase/ NADH kinase/ calmodulin binding [Arabidopsis thaliana] >gi|94717660|sp|Q56YN3.2|NADK1_ARATH RecName: Full=NAD(H) kinase 1; Short=AtNADK-1 >gi|39843359|gb|AAR32133.1| NADK1 [Arabidopsis thaliana]	Unigene11840_A11//0.00E+00//AT3G21070| NADK1 (NAD KINASE 1); NAD+ kinase/ NADH kinase/ calmodulin binding	Unigene11840_A11//0.00E+00//gi|164361092|gb|ES819069.1|ES819069		ko00760|Nicotinate and nicotinamide metabolism	GO:0005515//GO:0006739//GO:0009108//GO:0016301//GO:0043169//GO:0044424	nr +
Unigene118405_A11	664	0.00	0.00	0.00	0.00	0.00	0.95	1.46	1.32	5.46	null	null		null	null		null	null		9.90E+00	7.60E-04	Up	-1.48E-01	8.13E-01		1.90E+00	2.37E-09	Up								
Unigene11841_A11	1466	2.75	3.97	1.63	3.13	6.93	10.01	3.20	3.48	3.37	5.32E-01	3.13E-02		-7.50E-01	1.82E-02		1.15E+00	4.06E-11	Up	1.68E+00	1.52E-25	Up	1.20E-01	6.40E-01		7.40E-02	7.68E-01		Unigene11841_A11//gi|124360132|gb|ABN08148.1|//3.00E-72//tRNA intron endonuclease, catalytic C-terminal [Medicago truncatula]	Unigene11841_A11//6.00E-71//AT3G45590| ATSEN1 (SPLICING ENDONUCLEASE 1); nuclease/ nucleic acid binding / tRNA-intron endonuclease	Unigene11841_A11//0.00E+00//TC170905			GO:0000394//GO:0004549//GO:0005488//GO:0043234	nr +
Unigene118412_A11	522	0.00	1.07	0.00	0.00	0.00	0.00	0.24	1.12	2.59	1.01E+01	2.19E-03		null	null		null	null		null	null		2.21E+00	2.34E-02		3.42E+00	7.76E-07	Up		Unigene118412_A11//5.00E-97//DW491233					
Unigene118421_A11	231	0.91	0.66	0.69	37.52	34.44	9.58	3.84	1.81	5.86	-4.61E-01	7.58E-01		-3.90E-01	8.08E-01		-1.24E-01	5.86E-01		-1.97E+00	2.82E-19	Down	-1.09E+00	1.07E-01		6.09E-01	2.25E-01		Unigene118421_A11//gi|40217878|gb|AAR82850.1|//8.00E-24//expansin-2 [Petunia x hybrida]	Unigene118421_A11//1.00E-22//AT2G39700| ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	Unigene118421_A11//4.00E-105//TC139820			GO:0007047//GO:0044464	nr +
Unigene118422_A11	360	0.15	0.99	0.00	0.28	0.67	0.75	1.41	0.12	8.08	2.76E+00	9.60E-02		-7.18E+00	6.28E-01		1.28E+00	5.32E-01		1.44E+00	4.09E-01		-3.60E+00	5.77E-03		2.52E+00	1.68E-10	Up	Unigene118422_A11//gi|225451968|ref|XP_002279750.1|//7.00E-15//PREDICTED: similar to mangrin [Vitis vinifera]	Unigene118422_A11//6.00E-09//AT3G25780| AOC3 (ALLENE OXIDE CYCLASE 3); allene-oxide cyclase	Unigene118422_A11//5.00E-176//gi|78325914|gb|DT546188.1|DT546188		ko00592|alpha-Linolenic acid metabolism	GO:0009536//GO:0009975	nr -
Unigene118432_A11	418	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.10	-7.97E+00	3.74E-01		-7.97E+00	3.96E-01		null	null		null	null		null	null		1.10E+01	2.05E-06	Up	Unigene118432_A11//gi|170660047|gb|ACE28472.1|//1.00E-46//polyprotein [Ananas comosus]		Unigene118432_A11//3.00E-11//CK640452			GO:0003676//GO:0006260//GO:0034061//GO:0043229	nr -
Unigene118434_A11	239	0.00	2.12	0.00	0.21	0.00	0.00	0.00	1.40	5.00	1.10E+01	4.05E-03		null	null		-7.70E+00	5.58E-01		-7.70E+00	6.39E-01		1.05E+01	1.27E-02		1.23E+01	1.20E-08	Up								
Unigene118435_A11	345	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.00	2.77	null	null		null	null		null	null		null	null		-6.94E+00	6.60E-01		4.50E+00	6.81E-06	Up			Unigene118435_A11//1.00E-37//TC178834					
Unigene118436_A11	622	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.73	null	null		null	null		null	null		null	null		null	null		1.08E+01	8.30E-08	Up	Unigene118436_A11//gi|115473321|ref|NP_001060259.1|//3.00E-09//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]						nr -
Unigene118443_A11	749	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.11	3.35	null	null		null	null		null	null		6.91E+00	4.79E-01		6.80E+00	4.03E-01		1.17E+01	5.71E-18	Up								
Unigene118447_A11	248	20.68	4.09	11.17	3.21	3.61	0.91	0.00	1.35	0.64	-2.34E+00	2.46E-13	Down	-8.89E-01	1.29E-03		1.68E-01	8.32E-01		-1.82E+00	3.32E-02		1.04E+01	1.27E-02		9.33E+00	1.40E-01		Unigene118447_A11//gi|255543699|ref|XP_002512912.1|//3.00E-18//conserved hypothetical protein [Ricinus communis] >gi|223547923|gb|EEF49415.1| conserved hypothetical protein [Ricinus communis]		Unigene118447_A11//3.00E-53//TC141372				nr +
Unigene11846_A11	728	1.80	5.78	4.54	1.03	3.31	2.42	0.81	0.98	2.24	1.68E+00	2.01E-07	Up	1.34E+00	2.75E-04	Up	1.69E+00	6.31E-05	Up	1.24E+00	1.46E-02		2.63E-01	7.21E-01		1.46E+00	1.69E-03		Unigene11846_A11//gi|6635256|dbj|BAA88627.1|//4.00E-22//tRNA intron endonuclease [Arabidopsis thaliana] >gi|6635258|dbj|BAA88628.1| tRNA intron endonuclease [Arabidopsis thaliana]	Unigene11846_A11//4.00E-23//AT3G45590| ATSEN1 (SPLICING ENDONUCLEASE 1); nuclease/ nucleic acid binding / tRNA-intron endonuclease	Unigene11846_A11//0.00E+00//gi|54115565|gb|CO491074.1|CO491074			GO:0000394//GO:0004549//GO:0005488//GO:0043234	nr -
Unigene118463_A11	917	0.00	0.00	0.00	0.11	0.23	0.20	0.37	0.18	14.34	null	null		null	null		1.05E+00	6.13E-01		8.59E-01	6.96E-01		-1.02E+00	4.00E-01		5.28E+00	2.49E-81	Up		Unigene118463_A11//2.00E-72//TC173686					
Unigene118465_A11	1427	0.00	0.00	0.00	0.00	0.00	0.00	0.39	0.00	5.81	null	null		null	null		null	null		null	null		-8.59E+00	4.61E-04	Down	3.91E+00	5.23E-43	Up	Unigene118465_A11//gi|224107585|ref|XP_002314526.1|//0.00E+00//flavine-containing monoxygenase [Populus trichocarpa] >gi|222863566|gb|EEF00697.1| flavine-containing monoxygenase [Populus trichocarpa]	Unigene118465_A11//2.00E-173//AT1G06610| flavin-containing monooxygenase / FMO (YUCCA3)	Unigene118465_A11//5.00E-13//gi|78348897|gb|DT569171.1|DT569171		ko00380|Tryptophan metabolism	GO:0008152//GO:0016709//GO:0030554	nr +
Unigene118467_A11	497	0.74	1.02	1.07	1.30	0.97	0.55	2.89	1.77	0.64	4.68E-01	6.11E-01		5.40E-01	6.10E-01		-4.26E-01	6.09E-01		-1.26E+00	1.83E-01		-7.12E-01	1.55E-01		-2.17E+00	6.89E-05	Down	Unigene118467_A11//gi|42567229|ref|NP_194611.2|//3.00E-10//zinc finger (HIT type) family protein [Arabidopsis thaliana] >gi|92856590|gb|ABE77404.1| At4g28820 [Arabidopsis thaliana]	Unigene118467_A11//2.00E-11//AT4G28820| zinc finger (HIT type) family protein	Unigene118467_A11//1.00E-85//TC148315				nr +
Unigene118472_A11	252	0.00	0.00	0.00	0.20	0.27	0.00	0.67	0.33	9.49	null	null		null	null		4.67E-01	9.59E-01		-7.63E+00	6.39E-01		-1.02E+00	6.15E-01		3.82E+00	1.35E-12	Up		Unigene118472_A11//6.00E-64//FL576842					
Unigene118486_A11	489	0.00	0.00	0.00	0.00	0.00	0.00	0.52	0.68	2.53	null	null		null	null		null	null		null	null		3.98E-01	7.24E-01		2.28E+00	1.88E-04	Up								
Unigene118488_A11	289	44.36	113.79	63.75	61.02	37.53	71.89	93.34	211.87	87.67	1.36E+00	6.63E-39	Up	5.23E-01	8.43E-05		-7.01E-01	6.63E-09		2.37E-01	6.64E-02		1.18E+00	4.75E-71	Up	-9.03E-02	3.95E-01		Unigene118488_A11//gi|4150974|emb|CAA11899.1|//3.00E-08//cystatin [Castanea sativa]	Unigene118488_A11//3.00E-07//AT5G12140| ATCYS1 (A. thaliana cystatin-1); cysteine-type endopeptidase inhibitor	Unigene118488_A11//2.00E-58//gi|13247918|gb|BF273082.2|BF273082			GO:0004866//GO:0016787	nr -
Unigene118849_A11	2156	16.67	14.22	17.83	19.29	23.02	22.58	18.45	9.73	7.65	-2.30E-01	1.29E-02		9.71E-02	3.56E-01		2.55E-01	4.13E-04		2.27E-01	3.25E-03		-9.23E-01	2.82E-31		-1.27E+00	1.71E-53	Down	Unigene11849_A11//gi|81074221|gb|AB855364.1|//0.00E+00//aspartate aminotransferase-like [Solanum tuberosum]	Unigene11849_A11//0.00E+00//AT4G31990| ASP5 (ASPARTATE AMINOTRANSFERASE 5); L-aspartate:2-oxoglutarate aminotransferase	Unigene11849_A11//0.00E+00//TC144385		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism//ko00350|Tyrosine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0005576//GO:0006950//GO:0008483//GO:0009064//GO:0009066//GO:0009526//GO:0010038//GO:0031980//GO:0043648//GO:0048037	nr -
Unigene118491_A11	232	0.00	0.00	0.00	0.21	0.15	0.19	2.55	3.60	13.57	null	null		null	null		-5.33E-01	8.27E-01		-1.41E-01	9.54E-01		4.98E-01	4.86E-01		2.41E+00	8.65E-11	Up			Unigene118491_A11//2.00E-69//gi|109868468|gb|DW497444.1|DW497444					
Unigene118493_A11	464	0.00	0.00	0.00	0.00	0.00	0.00	0.46	2.97	4.38	null	null		null	null		null	null		null	null		2.71E+00	1.42E-05	Up	3.26E+00	1.40E-09	Up			Unigene118493_A11//5.00E-07//C0074079					
Unigene118494_A11	445	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	2.60	null	null		null	null		null	null		null	null		7.55E+00	4.03E-01		1.13E+01	2.28E-08	Up								
Unigene1185_A11	6346	1.10	2.47	2.01	6.04	3.89	5.28	4.10	1.96	3.87	1.17E+00	4.05E-15	Up	8.71E-01	1.29E-07		-6.38E-01	6.19E-16		-1.95E-01	3.24E-02		-1.06E+00	6.43E-26	Down	-8.35E-02	4.45E-01		Unigene1185_A11//gi|124360779|gb|AB008751.1|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene1185_A11//0.00E+00//AT5G66890| protein kinase family protein	Unigene1185_A11//0.00E+00//TC177762		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016020//GO:0032559//GO:0043231	nr +
Unigene118509_A11	261	0.00	0.00	0.20	0.00	0.00	0.17	2.43	5.12	23.96	null	null		7.67E+00	6.38E-01		null	null		7.43E+00	6.99E-01		1.08E+00	4.02E-02		3.30E+00	2.02E-28	Up	Unigene118509_A11//gi|224127106|ref|XP_002329398.1|//1.00E-15//predicted protein [Populus trichocarpa] >gi|222867048|gb|EEF07579.1| predicted protein [Populus trichocarpa]	Unigene118509_A11//2.00E-15//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene118509_A11//5.00E-83//TC142413		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis	GO:0008152//GO:0016701//GO:0016706	nr -
Unigene11851_A11	3301	9.05	13.42	10.55	14.46	13.67	14.84	13.64	20.83	28.83	5.68E-01	1.37E-12		2.21E-01	2.49E-02		-8.12E-02	3.82E-01		3.82E-02	6.77E-01		6.11E-01	1.83E-26		1.08E+00	2.98E-97	Up	Unigene11851_A11//gi|42567457|ref|NP_568003.2|//0.00E+00//FAD linked oxidase family protein [Arabidopsis thaliana] >gi|42573191|ref|NP_974692.1| FAD linked oxidase family protein [Arabidopsis thaliana] >gi|294956519|sp|Q23240.3|D2HDH_ARATH RecName: Full=D-2-hydroxyglutarate dehydrogenase, mitochondrial; Short=AtD-2HGDH; Flags: Precursor	Unigene11851_A11//0.00E+00//AT4G36400| FAD linked oxidase family protein	Unigene11851_A11//0.00E+00//TC170837		ko04146|Peroxisome//ko00620|Pyruvate metabolism	GO:0004457//GO:0008152//GO:0030554//GO:0043231	nr -
Unigene118512_A11	275	0.00	0.00	0.97	0.00	0.13	0.16	0.00	0.00	2.32	null	null		9.92E+00	8.03E-02		6.97E+00	8.33E-01		7.36E+00	6.99E-01		null	null		1.12E+01	9.34E-05	Up								
Unigene118513_A11	245	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.28	null	null		null	null		null	null		null	null		null	null		1.12E+01	3.28E-04	Up								
Unigene11852_A11	505	6.94	11.34	11.39	10.26	16.23	14.49	4.35	9.44	6.31	7.08E-01	4.33E-03		7.14E-01	5.56E-03		6.62E-01	5.94E-04		4.98E-01	2.27E-02		1.12E+00	8.85E-06	Up	5.36E-01	7.73E-02		Unigene11852_A11//gi|297806241|ref|XP_002871004.1|//1.00E-16//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316841|gb|EFH47263.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11852_A11//7.00E-18//AT5G02970| hydrolase, alpha/beta fold family protein	Unigene11852_A11//0.00E+00//gi|78351500|gb|DT571774.1|DT571774				nr +
Unigene118529_A11	223	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.19	2.86	null	null		null	null		null	null		null	null		-1.68E-02	1.01E+00		3.91E+00	7.66E-04	Up								
Unigene118533_A11	458	0.00	0.00	0.00	0.00	0.00	0.20	0.18	0.37	2.17	null	null		null	null		null	null		7.62E+00	4.79E-01		9.84E-01	6.34E-01		3.56E+00	2.43E-05	Up	Unigene118533_A11//gi|297838715|ref|XP_002887239.1|//6.00E-34//oxygen binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297333080|gb|EFH63498.1| oxygen binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene118533_A11//6.00E-31//AT1G69500| electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0006091//GO:0016712//GO:0031410	nr +
Unigene118545_A11	243	28.42	11.68	20.16	7.99	5.38	9.48	0.00	0.00	0.00	-1.28E+00	3.99E-08	Down	-4.95E-01	3.54E-02		-5.70E-01	2.20E-01		2.46E-01	6.31E-01		null	null		null	null		Unigene118545_A11//gi|115485721|ref|NP_001068004.1|//4.00E-17//Os11g0528500 [Oryza sativa Japonica Group] >gi|77531234|gb|ABA94031.1| Rubredoxin family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113645226|dbj|BAF28367.1| Os11g0528500 [Oryza sativa Japonica Group]	Unigene118545_A11//6.00E-16//AT5G51010| rubredoxin family protein	Unigene118545_A11//6.00E-107//gi|109886952|gb|DW515921.1|DW515921			GO:0006810//GO:0043169//GO:0043231	nr +
Unigene11856_A11	1276	2.75	6.19	4.26	12.92	11.85	13.77	32.67	77.30	27.29	1.17E+00	4.78E-08	Up	6.32E-01	1.80E-02		-1.25E-01	4.37E-01		9.15E-02	5.93E-01		1.24E+00	3.26E-123	Up	-2.60E-01	3.60E-04		Unigene11856_A11//gi|297812691|ref|XP_002874229.1|//3.00E-34//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320066|gb|EFH50488.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11856_A11//7.00E-13//AT5G24870| zinc finger (C3HC4-type RING finger) family protein	Unigene11856_A11//0.00E+00//TC145984				nr +
Unigene118561_A11	722	0.00	0.84	0.00	0.00	0.00	0.13	0.29	0.41	6.73	9.72E+00	1.17E-03		null	null		null	null		6.97E+00	4.79E-01		4.69E-01	7.06E-01		4.52E+00	5.55E-28	Up	Unigene118561_A11//gi|224071451|ref|XP_002303466.1|//3.00E-10//predicted protein [Populus trichocarpa] >gi|222840898|gb|EEE78445.1| predicted protein [Populus trichocarpa]		Unigene118561_A11//0.00E+00//gi|109885675|gb|DW514645.1|DW514645				nr -
Unigene118562_A11	779	0.00	0.00	0.00	0.00	0.00	0.00	2.71	0.43	0.51	null	null		null	null		null	null		null	null		-2.66E+00	4.31E-08	Down	-2.41E+00	1.32E-07	Down	Unigene118562_A11//gi|224127106|ref|XP_002329398.1|//1.00E-15//predicted protein [Populus trichocarpa] >gi|222870448|gb|EEF07579.1| predicted protein [Populus trichocarpa]		Unigene118562_A11//6.00E-45//TC175720				nr +
Unigene118573_A11	490	0.21	0.21	0.43	0.00	0.00	0.00	0.09	0.51	1.79	-4.67E-02	9.90E-01		1.03E+00	5.92E-01		null	null		null	null		2.57E+00	1.53E-01		4.37E+00	2.26E-05	Up	Unigene118573_A11//gi|21553445|gb|AAM62538.1|//3.00E-18//bZIP transcription factor-like protein [Arabidopsis thaliana]	Unigene118573_A11//1.00E-13//AT4G37730| AthZIP7 (Arabidopsis thaliana basic leucine-zipper 7); DNA binding / transcription factor		bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0043231	nr +

Unigene118576_All	470	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.27	2.29	null	null		null	null		null	null		null	null		8.06E+00	2.41E-01		1.12E+01	8.30E-08	Up	Unigene118576_All//gi|302142601|emb|CBI19804.3|//6.00E-09//unnamed protein product [Vitis vinifera]	Unigene118576_All//7.00E-06//AT4G16310| LDL3 (LSD1-LIKE3); amine oxidase/ electron carrier/ oxidoreductase	Unigene118576_All//2.00E-16//TC165986			GO:0008152//GO:0016641//GO:0016741	nr +
Unigene118578_All	254	0.00	0.00	0.00	0.20	0.00	0.00	0.00	0.16	2.04	null	null		null	null		-7.62E+00	5.58E-01		-7.62E+00	6.39E-01		7.36E+00	6.37E-01		1.10E+01	6.14E-04	Up							
Unigene11858_All	2809	11.98	16.54	13.29	30.56	24.98	21.38	29.88	65.20	25.02	4.66E-01	1.98E-09		1.50E-01	1.36E-01		-2.90E-01	1.59E-08		-5.15E-01	2.06E-21		1.13E+00	3.23E-195	Up	-2.56E-01	2.65E-07		Unigene11858_All//gi|297812691|ref|XP_002874229.1|//5.00E-86//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320066|gb|EFH50488.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11858_All//1.00E-64//AT5G24870| zinc finger (C3HC4-type RING finger) family protein	Unigene11858_All//0.00E+00//TC145984		ko00190|Oxidative phosphorylation	GO:0005488	nr -
Unigene118584_All	349	0.00	0.00	0.57	0.10	0.52	4.36	0.72	3.88	null	null		null	null		-2.53E+00	2.34E-01		-1.41E-01	9.35E-01		-2.60E+00	6.96E-06	Down	-1.68E-01	7.13E-01			Unigene118584_All//5.00E-28//CO080430					ESTscan +
Unigene1186_All	2238	24.03	11.84	10.87	65.80	59.50	40.66	33.31	20.45	20.60	-1.02E+00	1.52E-40	Down	-1.14E+00	6.13E-47	Down	-1.45E-01	3.68E-04		-6.94E-01	8.83E-62		-7.04E-01	1.33E-36		-6.94E-01	1.06E-36		Unigene1186_All//gi|42571735|ref|NP_973958.1|//1.00E-74//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|14532532|gb|AAK63994.1| At1g33470/F10C21_14 [Arabidopsis thaliana] >gi|18655391|gb|AAL76151.1| At1g33470/F10C21_14 [Arabidopsis thaliana]	Unigene1186_All//5.00E-52//AT1G33470| RNA recognition motif (RRM)-containing protein	Unigene1186_All//0.00E+00//TC167468		ko03040|Spliceosome	GO:0003676	nr -
Unigene118605_All	438	0.12	0.00	0.24	0.00	0.00	0.10	0.10	0.29	1.91	-6.90E+00	6.15E-01		1.03E+00	7.04E-01		null	null		6.69E+00	6.99E-01		1.57E+00	5.46E-01		4.31E+00	4.11E-05	Up	Unigene118605_All//gi|226290819|gb|ACO40485.1|//3.00E-37//terpene synthase [Actinidia deliciosa]	Unigene118605_All//1.00E-19//AT1G79460| GA2 (GA REQUIRING 2); ent-kaurene synthase			ko00904|Diterpenoid biosynthesis	GO:0016838	nr +
Unigene118615_All	483	0.22	15.95	0.00	0.00	0.21	0.47	0.00	0.00	0.49	6.20E+00	1.33E-40	Up	-7.76E+00	3.96E-01		7.74E+00	4.57E-01		8.87E+00	1.19E-01		null	null		8.95E+00	4.40E-02		Unigene118615_All//gi|295393494|gb|ADG03603.1|//7.00E-28//galactinol synthase [Brassica napus]	Unigene118615_All//2.00E-28//AT2G47180| AtGolS1 (Arabidopsis thaliana galactinol synthase 1); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene118615_All//1.00E-109//TC156180			GO:0000302//GO:0005975//GO:0009642//GO:0035250	nr +
Unigene11862_All	3083	68.92	176.05	108.56	82.71	180.83	255.19	42.92	143.63	50.82	1.35E+00	0.00E+00	Up	6.56E-01	2.86E-113		1.13E+00	0.00E+00	Up	1.63E+00	0.00E+00	Up	1.74E+00	0.00E+00	Up	2.44E-01	9.73E-12		Unigene11862_All//gi|6682841|dbj|BAA88904.1|//0.00E+00//sucrose synthase [Citrus unshiu]	Unigene11862_All//0.00E+00//AT4G02280| SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups	Unigene11862_All//0.00E+00//TC147396		ko00500|Starch and sucrose metabolism	GO:0005985//GO:0006073//GO:0035251//GO:0048316	nr -
Unigene118863_All	1205	3.34	1.68	1.24	7.28	7.00	3.79	7.96	2.25	3.34	-9.91E-01	1.19E-03		-1.43E+00	1.53E-05	Down	-5.55E-02	8.33E-01		-9.43E-01	8.97E-07		-1.82E+00	9.61E-22	Down	-1.25E+00	2.54E-13	Down	Unigene11863_All//gi|54035683|sp|Q81221.1|ACT_GOSHI//0.00E+00//RecName: Full=Actin >gi|3420239|gb|AAC31886.1| actin [Gossypium hirsutum]	Unigene11863_All//0.00E+00//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene11863_All//0.00E+00//gi|48801570|gb|CO102884.1|CO102884		ko04145|Phagosome	GO:0006996//GO:0016020//GO:0030312//GO:0032559//GO:0043231//GO:0043232//GO:0048588	nr +
Unigene118634_All	399	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.52	6.49	null	null		null	null		null	null		null	null		9.03E+00	7.86E-02		1.27E+01	1.54E-18	Up							
Unigene11864_All	1227	2.09	1.69	1.30	6.74	6.88	3.13	8.20	1.60	2.11	-3.03E-01	4.47E-01		-6.82E-01	1.00E-01		2.89E-02	9.11E-01		-1.11E+00	3.60E-08	Down	-2.36E+00	1.96E-31	Down	-1.96E+00	7.61E-26	Down	Unigene11864_All//gi|54035683|sp|Q81221.1|ACT_GOSHI//0.00E+00//RecName: Full=Actin >gi|3420239|gb|AAC31886.1| actin [Gossypium hirsutum]	Unigene11864_All//0.00E+00//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene11864_All//0.00E+00//TC140956		ko04145|Phagosome	GO:0006996//GO:0016020//GO:0030312//GO:0032559//GO:0043231//GO:0043232//GO:0048588	nr +
Unigene118647_All	609	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.27	1.64	null	null		null	null		null	null		null	null		9.83E-01	6.34E-01		3.56E+00	2.43E-05	Up	Unigene118647_All//gi|53749404|gb|AAU90262.1|//5.00E-12//integrase core domain containing protein [Oryza sativa Japonica Group]		Unigene118647_All//4.00E-24//gi|195983411|gb|FL576905.1|FL576905			GO:0005488	nr -
Unigene11865_All	1442	5.77	4.50	2.84	19.03	17.00	12.84	15.98	5.88	6.66	-3.59E-01	7.97E-02		-1.02E+00	1.43E-06	Down	-1.63E-01	1.47E-01		-5.68E-01	1.46E-08		-1.44E+00	9.31E-37	Down	-1.26E+00	4.44E-31	Down	Unigene11865_All//gi|54035683|sp|Q81221.1|ACT_GOSHI//0.00E+00//RecName: Full=Actin >gi|3420239|gb|AAC31886.1| actin [Gossypium hirsutum]	Unigene11865_All//0.00E+00//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene11865_All//0.00E+00//TC165291		ko04145|Phagosome	GO:0007010//GO:0016020//GO:0030312//GO:0032559//GO:0043231//GO:0043232//GO:0048588	nr +
Unigene118659_All	246	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.34	2.11	null	null		null	null		null	null		null	null		8.41E+00	4.03E-01		1.10E+01	6.14E-04	Up							
Unigene118661_All	587	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.00	3.26	null	null		null	null		null	null		null	null		-7.76E+00	2.36E-01		3.91E+00	2.32E-10	Up	Unigene118661_All//gi|15214248|sp|Q9V068.1|RIC1_PHYIN//2.00E-10//RecName: Full=Protein Ric1 >gi|5531402|emb|CAB50926.1| RIC1 protein [Phytophthora infestans]	Unigene118661_All//2.00E-07//AT4G30660| hydrophobic protein, putative / low temperature and salt responsive protein, putative				GO:0016020//GO:0031410	nr -
Unigene11867_All	986	9.23	11.36	3.35	13.44	15.02	17.82	28.82	20.64	17.13	2.99E-01	9.02E-02		-1.46E+00	4.98E-12	Down	1.60E-01	3.33E-01		4.07E-01	2.00E-03		-4.81E-01	1.02E-07		-7.50E-01	1.43E-16		Unigene11867_All//gi|226497034|ref|NP_001149714.1|//7.00E-78//LOC100283341 [Zea mays] >gi|195629710|gb|ACG36496.1| adenylate kinase [Zea mays]	Unigene11867_All//2.00E-77//AT2G39270| adenylate kinase family protein	Unigene11867_All//0.00E+00//TC160571		ko00230|Purine metabolism	GO:0006520//GO:0009117//GO:0009532//GO:0016776//GO:0019205//GO:0032559//GO:0048513	nr +
Unigene118670_All	270	0.97	0.38	0.00	0.00	0.26	0.00	0.31	0.15	6.79	-1.37E+00	3.83E-01		-9.92E+00	8.58E-02		7.99E+00	6.12E-01		null	null		-1.02E+00	7.26E-01		4.44E+00	9.60E-11	Up			Unigene118670_All//5.00E-89//CA992796				
Unigene118673_All	342	363.95	527.44	666.40	416.28	467.59	859.42	257.64	317.50	529.67	5.35E-01	4.99E-44		8.73E-01	8.65E-127		1.68E-01	1.16E-05		1.05E+00	2.92E-244	Up	3.01E-01	7.97E-12		1.04E+00	1.92E-173	Up	Unigene118673_All//gi|115460714|ref|NP_001053957.1|//2.00E-37//Os04g0628100 [Oryza sativa Japonica Group] >gi|113565528|dbj|BAF15871.1| Os04g0628100 [Oryza sativa Japonica Group]	Unigene118673_All//6.00E-38//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene118673_All//3.00E-177//gi|13352460|gb|BG442808.1|BG442808			GO:0031410	nr -
Unigene118683_All	976	0.11	0.16	0.00	0.00	0.00	0.00	0.00	0.00	3.84	5.39E-01	7.79E-01		-6.74E+00	3.96E-01		null	null		null	null		null	null		1.19E+01	8.55E-27	Up							
Unigene118690_All	349	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.94	null	null		null	null		null	null		null	null		null	null		1.09E+01	4.97E-05	Up	Unigene118690_All//gi|113129056|gb|ABI30334.1|//1.00E-08//Cys-3-His zinc finger protein [Capsicum annuum]	Unigene118690_All//2.00E-06//AT2G40140| CZF1; transcription factor	Unigene118690_All//1.00E-07//DW226743	C3H		GO:0046872	nr +
Unigene118692_All	1753	0.00	0.00	0.00	0.00	0.00	0.00	0.34	0.00	0.23	null	null		null	null		null	null		null	null		-8.40E+00	2.39E-04	Down	-5.71E-01	4.78E-01		Unigene118692_All//gi|224139828|ref|XP_002323296.1|//1.00E-129//cytochrome P450 [Populus trichocarpa] >gi|222867926|gb|EEF05057.1| cytochrome P450 [Populus trichocarpa]	Unigene118692_All//1.00E-119//AT2G42250| CYP712A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene118697_All	236	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	3.38	null	null		null	null		null	null		null	null		7.47E+00	6.37E-01		1.17E+01	7.36E-06	Up	Unigene118697_All//gi|297830676|ref|XP_002883220.1|//1.00E-07//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297329060|gb|EFH59479.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene118697_All//6.00E-09//AT3G19990| unknown protein				GO:0009532	nr -
Unigene1187_All	1501	4.88	2.77	2.09	7.60	6.58	5.33	9.30	4.09	10.80	-8.18E-01	1.55E-04		-1.22E+00	1.35E-07	Down	-2.07E-01	2.62E-01		-5.13E-01	1.98E-03		-1.18E+00	7.59E-17	Down	2.17E-01	8.87E-02		Unigene1187_All//gi|115436734|ref|NP_001043123.1|//1.00E-168//Os01g0496900 [Oryza sativa Japonica Group] >gi|113532654|dbj|BAF05037.1| Os01g0496900 [Oryza sativa Japonica Group]	Unigene1187_All//0.00E+00//AT3G16200| unknown protein	Unigene1187_All//0.00E+00//gi|78330964|gb|DT551238.1|DT551238			GO:0043231	nr +
Unigene118700_All	477	0.00	0.42	0.00	0.00	0.00	0.00	0.00	0.18	1.42	8.73E+00	1.37E-01		null	null		null	null		null	null		7.45E+00	4.03E-01		1.05E+01	4.97E-05	Up	Unigene118700_All//gi|297725715|ref|NP_001175221.1|//1.00E-19//Os07g0513300 [Oryza sativa Japonica Group] >gi|255677803|dbj|BAH93949.1| Os07g0513300 [Oryza sativa Japonica Group]	Unigene118700_All//6.00E-19//AT1G48120| calcineurin-like phosphoesterase family protein	Unigene118700_All//6.00E-07//gi|78334205|gb|DT554479.1|DT554479				nr +
Unigene118706_All	1361	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	5.77	null	null		null	null		null	null		null	null		4.94E+00	6.37E-01		1.25E+01	3.11E-56	Up	Unigene118706_All//gi|297793719|ref|XP_002864744.1|//2.00E-45//myb family transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297310579|gb|EFH41003.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene118706_All//1.00E-46//AT5G61620| myb family transcription factor		MYB-related	ko04712|Circadian rhythm - plant	GO:0005488	nr +
Unigene118711_All	258	0.00	0.00	0.00	0.39	0.27	1.40	0.00	0.65	2.32	null	null		null	null		-5.33E-01	8.17E-01		1.86E+00	2.20E-01		9.34E+00	1.39E-01		1.12E+01	1.76E-04	Up							
Unigene118723_All	1147	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.15	2.54	null	null		null	null		null	null		null	null		1.98E+00	3.79E-01		6.10E+00	2.88E-19	Up							
Unigene118724_All	399	0.00	0.00	0.00	0.00	0.00	0.00	0.74	0.73	4.39	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		2.57E+00	9.62E-07	Up							
Unigene11873_All	810	7.30	6.82	5.19	9.84	4.76	4.85	5.17	4.64	2.85	-9.83E-02	6.91E-01		-4.91E-01	5.68E-02		-1.05E+00	4.49E-08	Down	-1.02E+00	5.35E-07	Down	-1.54E-01	6.33E-01		-8.57E-01	8.55E-04		Unigene11873_All//gi|145322873|ref|NP_001030648.2|//3.00E-22//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene11873_All//2.00E-17//AT3G06330| zinc finger (C3HC4-type RING finger) family protein	Unigene11873_All//5.00E-138//gi|73852414|gb|DT461434.1|DT461434			GO:0009536//GO:0019787//GO:0046914	nr -
Unigene118730_All	409	0.13	0.25	0.52	0.85	0.25	0.22	0.10	0.31	1.85	9.54E-01	7.27E-01		2.03E+00	3.62E-01		-1.76E+00	1.90E-01		-1.95E+00	1.96E-01		1.57E+00	5.46E-01		4.16E+00	1.34E-04	Up	Unigene118730_All//gi|224126033|ref|XP_002319739.1|//8.00E-19//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222858115|gb|EEE95662.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene118730_All//8.00E-20//AT3G54280| RGB3 (ROOT GROWTH DEFECTIVE 3); ATP binding / DNA binding / binding / helicase/ nucleic acid binding	Unigene118730_All//2.00E-105//DW484463			GO:0003676//GO:0010467//GO:0017111//GO:0032559//GO:0034062//GO:0043231	nr -
Unigene118733_All	683	0.08	0.45	0.55	0.36	0.96	0.20	0.87	1.53	2.68	2.54E+00	1.51E-01		2.83E+00	9.31E-02		1.39E+00	1.51E-01		-8.78E-01	6.16E-01		8.20E-01	1.79E-01		1.63E+00	2.55E-04	Up		Unigene118733_All//8.00E-44//CO110587				
Unigene118744_All	400	0.00	0.25	0.00	0.00	0.17	0.00	0.11	0.31	5.98	7.98E+00	3.89E-01		null	null		7.43E+00	6.12E-01		null	null		1.57E+00	5.46E-01		5.82E+00	1.17E-15	Up		Unigene118744_All//7.00E-40//TC162362				
Unigene118748_All	499	0.00	0.00	0.00	0.10	0.00	0.00	0.00	0.34	1.60	null	null		null	null		-6.64E+00	5.58E-01		-6.64E+00	6.39E-01		8.39E+00	1.39E-01		1.06E+01	7.36E-06	Up	Unigene118748_All//gi|115485947|ref|NP_001068117.1|//4.00E-28//Os11g0569500 [Oryza sativa Japonica Group] >gi|113645339|dbj|BAF28480.1| Os11g0569500 [Oryza sativa Japonica Group]	Unigene118748_All//3.00E-13//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488//GO:0044464	nr +
Unigene11875_All	341	0.31	0.89	0.00	0.58	1.72	0.00	0.99	3.80	0.93	1.54E+00	3.23E-01		-8.26E+00	3.96E-01		1.55E+00	1.41E-01		-9.19E+00	1.34E-01		1.94E+00	8.28E-04	Up	-8.58E-02	9.47E-01			Unigene11875_All//2.00E-65//AT5G09660| PMDH2 (peroxisomal NAD-malate dehydrogenase 2); malate dehydrogenase	Unigene11875_All//7.00E-12//TC164570				
Unigene118754_All	991	0.32	0.26	0.75	0.20	0.14	0.73	0.94	0.00	0.24	-3.10E-01	7.89E-01		1.25E+00	1.54E-01		-5.33E-01	7.49E-01		1.86E+00	4.71E-02		-9.87E+00	1.14E-06	Down	-1.96E+00	3.98E-03		Unigene118754_All//gi|30697152|ref|NP_851217.1|//5.00E-95//GIL1 (GRAVITROPIC IN THE LIGHT) [Arabidopsis thaliana]	Unigene118754_All//5.00E-93//AT5G58960| GIL1 (GRAVITROPIC IN THE LIGHT)	Unigene118754_All//0.00E+00//TC146888			GO:0009416//GO:0009630	nr +
Unigene118758_All	373	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.34	2.99	null	null		null	null		null	null		null	null		5.69E-01	7.83E-01		3.72E+00	4.35E-06	Up			Unigene118758_All//5.00E-25//gi|78330320|gb|DT550594.1|DT550594				
Unigene118767_All	491	0.00	0.00	0.00	0.00	0.14	1.47	0.00	0.85	6.00	null	null		null	null		7.13E+00	6.12E-01		1.05E+01	2.31E-04	Up	9.73E+00	3.65E-03		1.26E+01	4.24E-21	Up							
Unigene118772_All	680	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.37	2.23	null	null		null	null		null	null		null	null		8.53E+00	4.31E-02		1.11E+01	6.77E-11	Up	Unigene118772_All//gi|297843370|ref|XP_002889566.1|//1.00E-60//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335408|gb|EFH65825.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene118772_All//2.00E-61//AT1G05800| DGL (DONGLE); triacylglycerol lipase				GO:0004091//GO:0006641//GO:0006952//GO:0009532//GO:0009668//GO:0009694//GO:0010260//GO:0016049	nr -
Unigene118775_All	289	0.00	0.00	0.37	0.00	0.60	0.16	0.15	0.14	10.06	null	null		8.53E+00	4.00E-01		9.22E+00	2.27E-01		7.29E+00	6.99E-01		-1.69E-02	1.01E+00		6.10E+00	2.88E-19	Up		Unigene118775_All//7.00E-30//DR463937				
Unigene118790_All	274	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.61	2.04	null	null		null	null		null	null		null	null		9.25E+00	1.39E-01		1.10E+01	3.28E-04	Up							
Unigene118799_All	996	0.16	0.00	0.00	0.15	0.17	0.09	0.08	0.21	2.72	-7.30E+00	2.16E-01		-7.30E+00	2.45E-01		2.05E-01	9.50E-01		-7.26E-01	7.16E-01		1.31E+00	4.47E-01		5.00E+00	1.18E-16	Up	Unigene118799_All//gi|33465891|gb|AAQ19327.1|//4.00E-11//bZIP-like protein [Oryza sativa Japonica Group]	Unigene118799_All//4.00E-06//AT2G01050| nucleic acid binding / zinc ion binding				GO:0005488	nr -

Unigene1188_A11	1563	16.03	8.33	8.89	21.86	18.86	17.74	10.87	4.25	6.14	-9.45E-01	4.86E-17		-8.51E-01	8.77E-14		-2.13E-01	2.07E-02		-3.01E-01	9.88E-04		-1.35E+00	6.13E-25	Down	-8.24E-01	6.34E-12		Unigene1188_A11//gi|115436734|ref|NP_001043123.1|//1.00E-170//0s01g0496900 [Oryza sativa Japonica Group] >gi|113532654|dbj|BAF05037.1|0s01g0496900 [Oryza sativa Japonica Group]	Unigene1188_A11//0.00E+00//AT3G16200| unknown protein	Unigene1188_A11//0.00E+00//TC132326			GO:0043231	nr +
Unigene118804_A11	1392	0.04	0.11	0.00	0.07	0.02	0.00	0.21	0.27	11.33	1.54E+00	5.32E-01		-5.23E+00	6.27E-01		-1.54E+00	5.87E-01		-6.16E+00	4.02E-01		3.46E-01	7.38E-01		5.74E+00	4.83E-101	Up	Unigene118804_A11//gi|224079880|ref|XP_002305957.1|//5.00E-08//histone acetyltransferase [Populus trichocarpa] >gi|222848921|gb|EEE86468.1|histone acetyltransferase [Populus trichocarpa]						nr +
Unigene11882_A11	799	1.64	0.63	0.53	2.31	3.79	1.36	2.59	2.09	0.80	-1.37E+00	2.40E-02		-1.62E+00	1.33E-02		7.17E-01	4.36E-02		-7.66E-01	1.18E-01		-3.09E-01	4.71E-01		-1.70E+00	4.43E-05	Down	Unigene11882_A11//gi|22326882|ref|NP_197349.2|//1.00E-70//PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana]	Unigene11882_A11//4.00E-65//AT5G18480| PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene11882_A11//0.00E+00//EE593156			GO:0005622//GO:0016758//GO:0044238	nr -
Unigene11883_A11	1311	1.20	0.39	1.10	2.28	3.15	2.62	3.58	1.28	0.94	-1.63E+00	3.58E-03		-1.27E-01	8.07E-01		4.67E-01	1.30E-01		2.00E-01	6.28E-01		-1.49E+00	1.80E-08	Down	-1.93E+00	3.07E-12	Down	Unigene11883_A11//gi|22326882|ref|NP_197349.2|//1.00E-147//PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana]	Unigene11883_A11//3.00E-133//AT5G18480| PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene11883_A11//0.00E+00//EE593156			GO:0031410	nr -
Unigene118835_A11	519	0.00	0.00	0.00	0.00	0.00	0.00	0.73	0.89	4.45	null	null		null	null		null	null		null	null		2.73E-01	7.69E-01		2.60E+00	8.88E-09	Up	Unigene118835_A11//gi|15241735|ref|NP_198755.1|//1.00E-19//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana]	Unigene118835_A11//3.00E-21//AT5G39390| leucine-rich repeat family protein / protein kinase family protein	Unigene118835_A11//2.00E-44//TC151383		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016491//GO:0031224//GO:0032559	nr -
Unigene118837_A11	430	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.48	null	null		null	null		null	null		null	null		null	null		1.05E+01	9.34E-05	Up							
Unigene118841_A11	845	0.12	0.00	0.00	0.24	0.00	0.00	1.20	0.49	3.54	-6.95E+00	3.74E-01		-6.95E+00	3.96E-01		-7.88E+00	8.45E-02		-7.88E+00	1.34E-01		-1.28E+00	4.06E-02		1.56E+00	3.58E-06	Up			Unigene118841_A11//2.00E-76//gi|31072987|gb|CA993266.1|CA993266				
Unigene118847_A11	531	0.30	1.34	0.40	0.47	0.19	0.34	0.40	0.47	2.10	2.18E+00	2.50E-02		4.40E-01	7.76E-01		-1.27E+00	4.24E-01		-4.64E-01	7.45E-01		2.47E-01	8.53E-01		2.40E+00	2.76E-04	Up			Unigene118847_A11//3.00E-46//DT048530				
Unigene11885_A11	787	6.71	7.92	4.80	25.26	27.30	16.87	14.67	4.89	5.72	2.38E-01	3.55E-01		-4.83E-01	7.93E-02		1.13E-01	4.29E-01		-5.82E-01	1.20E-06		-1.59E+00	1.58E-21	Down	-1.36E+00	8.22E-18	Down	Unigene11885_A11//gi|16226792|gb|AAL16263.1|AF428333_1//1.00E-66//At1g35780/F14D7_9 [Arabidopsis thaliana]	Unigene11885_A11//4.00E-67//AT1G35780| unknown protein	Unigene11885_A11//0.00E+00//gi|78332729|gb|DT553003.1|DT553003			GO:0003676	nr +
Unigene11886_A11	1504	4.52	2.43	2.09	13.94	13.71	10.93	12.17	4.36	2.78	-8.99E-01	7.23E-05		-1.11E+00	3.12E-06	Down	-2.39E-02	8.67E-01		-3.51E-01	3.40E-03		-1.48E+00	1.61E-30	Down	-2.13E+00	1.30E-51	Down	Unigene11886_A11//gi|227202770|dbj|BAH56858.1|//3.00E-99//AT1G78150 [Arabidopsis thaliana]	Unigene11886_A11//6.00E-100//AT1G78150| unknown protein	Unigene11886_A11//0.00E+00//TC163710				nr -
Unigene118860_A11	1081	0.15	0.00	0.25	0.00	0.13	0.08	0.70	0.31	2.95	-7.18E+00	2.16E-01		7.62E-01	6.44E-01		6.99E+00	3.19E-01		6.39E+00	4.79E-01		-1.19E+00	1.12E-01		2.07E+00	3.44E-09	Up	Unigene118860_A11//gi|399213|sp|P31542.1|CLPXB_SOLLC//1.00E-117//RecName: Full=ATP-dependent Clp protease ATP-binding subunit clpA homolog CD4B, chloroplastic; Flags: Precursor >gi|170435|gb|AAA34161.1| ATP-dependent protease (CD4B) [Solanum lycopersicum]	Unigene118860_A11//5.00E-111//AT5G50920| CLPC1: ATP binding / ATP-dependent peptidase/ ATPase	Unigene118860_A11//3.00E-152//CK640493				nr +
Unigene118864_A11	377	0.14	0.13	0.00	0.66	0.18	0.12	0.34	1.00	2.32	-4.65E-02	9.86E-01		-7.12E+00	6.27E-01		-1.85E+00	2.75E-01		-2.46E+00	2.24E-01		1.57E+00	1.95E-01		2.79E+00	5.37E-04	Up							
Unigene11887_A11	1630	15.60	9.01	8.40	23.99	24.91	17.12	29.78	7.95	9.34	-7.91E-01	5.49E-13		-8.94E-01	3.81E-15		5.41E-02	5.98E-01		-4.87E-01	3.70E-09		-1.91E+00	9.25E-114	Down	-1.67E+00	6.29E-98	Down	Unigene11887_A11//gi|227202770|dbj|BAH56858.1|//2.00E-90//AT1G78150 [Arabidopsis thaliana]	Unigene11887_A11//1.00E-91//AT1G78150| unknown protein	Unigene11887_A11//0.00E+00//gi|78323239|gb|DT543513.1|DT543513				nr -
Unigene11888_A11	1277	1.27	4.48	2.67	4.02	4.37	4.49	3.71	2.52	2.28	1.82E+00	7.41E-11	Up	1.07E+00	2.37E-03		1.21E-01	6.96E-01		1.61E-01	6.01E-01		-5.57E-01	2.48E-02		-7.03E-01	3.17E-03		Unigene11888_A11//gi|9454542|gb|AAF87865.1|AC022520_9//1.00E-146//Unknown protein [Arabidopsis thaliana]	Unigene11888_A11//5.00E-141//AT1G53040| unknown protein	Unigene11888_A11//0.00E+00//ES797722				nr -
Unigene118886_A11	311	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	3.71	null	null		null	null		null	null		null	null		7.07E+00	6.37E-01		1.19E+01	2.28E-08	Up			Unigene118886_A11//4.00E-07//TC171906				
Unigene11889_A11	2064	0.94	1.74	2.01	5.16	5.14	5.91	5.98	4.66	4.19	8.94E-01	6.08E-03		1.10E+00	4.78E-04	Up	-7.30E-03	9.67E-01		1.94E-01	2.99E-01		-3.61E-01	1.37E-02		-5.14E-01	2.27E-04		Unigene11889_A11//gi|9454542|gb|AAF87865.1|AC022520_9//1.00E-179//Unknown protein [Arabidopsis thaliana]	Unigene11889_A11//1.00E-170//AT1G53040| unknown protein	Unigene11889_A11//0.00E+00//gi|78344783|gb|DT565057.1|DT565057				nr -
Unigene118894_A11	857	0.00	0.00	0.00	0.00	0.00	0.32	0.20	0.83	3.07	null	null		null	null		null	null		8.30E+00	7.04E-02		2.07E+00	1.45E-02		3.96E+00	3.85E-14	Up	Unigene118894_A11//gi|297722269|ref|NP_001173498.1|//3.00E-08//0s03g0565600 [Oryza sativa Japonica Group] >gi|255674640|dbj|BAH92226.1|0s03g0565600 [Oryza sativa Japonica Group]	Unigene118894_A11//2.00E-08//AT4G21790| TOM1 (TOBAMOVIRUS MULTIPLICATION 1); protein binding				GO:0044464	nr +
Unigene118896_A11	293	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.71	2.04	null	null		null	null		null	null		null	null		9.48E+00	7.86E-02		1.10E+01	1.76E-04	Up							
Unigene118898_A11	505	0.00	0.00	0.42	0.00	0.41	0.18	0.08	0.25	1.81	null	null		8.72E+00	1.41E-01		8.68E+00	1.57E-01		7.48E+00	4.79E-01		1.57E+00	5.46E-01		4.44E+00	1.24E-05	Up	Unigene118898_A11//gi|32492359|emb|CAE05990.1|//3.00E-28//OSJNBa0004L19.22 [Oryza sativa (japonica cultivar-group)]					GO:0003676//GO:0009987//GO:0043170//GO:0044238	nr +
Unigene118902_A11	385	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.66	null	null		null	null		null	null		null	null		null	null		1.07E+01	9.34E-05	Up	Unigene118902_A11//gi|15225286|ref|NP_180201.1|//7.00E-09//ER (ERECTA); transmembrane receptor protein kinase [Arabidopsis thaliana] >gi|75319658|sp|Q42371.1|ERECT_ARATH RecName: Full=LRR receptor-like serine/threonine-protein kinase ERECTA; AltName: Full=Protein QUANTITATIVE RESISTANCE TO PLECTOSPHAERELLA 1; AltName: Full=Protein QUANTITATIVE RESISTANCE TO RALSTONIA SOLANACEARUM 1; AltName: Full=Protein TRANSPIRATION EFFICIENCY 1; Flags: Precursor >gi|1345132|gb|AAC49302.1| ERECTA [Arabidopsis thaliana] >gi|1389566|dbj|BAA11869.1|receptor protein kinase [Arabidopsis thaliana] >gi|224589525|gb|ACN59296.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene118902_A11//4.00E-10//AT2G26330| ER (ERECTA); transmembrane receptor protein kinase			ko04626|Plant-pathogen interaction	GO:0004672//GO:0006952//GO:0009886//GO:0009887//GO:0016043//GO:0043231//GO:0050794	nr -
Unigene118904_A11	1164	0.00	0.00	0.00	0.00	0.00	0.00	0.29	0.25	3.46	null	null		null	null		null	null		null	null		-2.10E-01	8.50E-01		3.57E+00	9.17E-20	Up	Unigene118904_A11//gi|209970600|gb|ACJ03063.1|//6.00E-78//M18-6p [Malus floribunda]	Unigene118904_A11//1.00E-34//AT5G27060| ArRLP53 (Receptor Like Protein 53); kinase/ protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene118905_A11	318	0.00	0.00	0.00	0.00	0.00	0.85	0.13	1.45	3.38	null	null		null	null		null	null		9.73E+00	7.04E-02		3.44E+00	1.16E-02		4.67E+00	1.11E-06	Up							
Unigene118907_A11	468	0.00	0.00	0.00	0.11	0.00	0.00	0.36	0.09	4.43	null	null		null	null		-6.73E+00	5.58E-01		-6.73E+00	6.39E-01		-2.02E+00	3.68E-01		3.61E+00	1.45E-10	Up							
Unigene118910_A11	587	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.07	1.49	null	null		null	null		null	null		null	null		6.15E+00	6.37E-01		1.05E+01	2.05E-06	Up							
Unigene118914_A11	427	0.00	0.00	0.00	0.00	0.00	0.00	0.79	0.59	4.29	null	null		null	null		null	null		null	null		-4.32E-01	7.03E-01		2.44E+00	1.14E-06	Up							
Unigene11892_A11	1966	4.39	2.19	2.55	9.91	9.77	10.04	13.72	6.36	8.04	-1.00E+00	5.57E-07	Down	-7.86E-01	1.20E-04		-1.96E-02	8.97E-01		1.91E-02	9.16E-01		-1.11E+00	8.45E-29	Down	-7.70E-01	1.79E-16		Unigene11892_A11//gi|297820766|ref|XP_002878266.1|//0.00E+00//UDP-galactose transporter 6 [Arabidopsis lyrata subsp. lyrata] >gi|297324104|gb|EFH54525.1| UDP-galactose transporter 6 [Arabidopsis lyrata subsp. lyrata]	Unigene11892_A11//3.00E-180//AT2G43240| nucleotide-sugar transmembrane transporter/ sugar:hydrogen symporter	Unigene11892_A11//0.00E+00//TC154914			GO:0005402//GO:0008643//GO:0012505//GO:0015144//GO:0031224	nr -
Unigene118935_A11	426	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.06	null	null		null	null		null	null		null	null		null	null		1.10E+01	2.05E-06	Up	Unigene118935_A11//gi|4996363|dbj|BAA78424.1|//6.00E-19//polyprotein [Arabidopsis thaliana]	Unigene118935_A11//6.00E-11//AT4G23160| protein kinase family protein	Unigene118935_A11//3.00E-30//ES812448			GO:0003676	nr -
Unigene118936_A11	228	0.00	0.00	0.47	0.44	0.15	0.20	0.93	2.20	4.54	null	null		8.87E+00	4.00E-01		-1.53E+00	5.87E-01		-1.14E+00	6.77E-01		1.25E+00	2.04E-01		2.29E+00	7.17E-04	Up			Unigene118936_A11//1.00E-30//CO113944				
Unigene11894_A11	620	24.73	15.85	12.28	11.89	13.16	4.66	2.86	1.89	1.99	-6.41E-01	6.77E-06		-1.01E+00	2.39E-11	Down	1.47E-01	5.42E-01		-1.35E+00	7.94E-10	Down	-6.02E-01	1.78E-01		-5.24E-01	2.19E-01		Unigene11894_A11//gi|297852222|ref|XP_002893992.1|//6.00E-39//universal stress protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339834|gb|EFH70251.1|universal stress protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11894_A11//3.00E-38//AT1G44760| universal stress protein (USP) family protein	Unigene11894_A11//0.00E+00//TC176468				nr +
Unigene118940_A11	534	0.00	0.00	0.00	0.09	0.00	0.00	0.08	0.00	2.98	null	null		null	null		-6.54E+00	5.58E-01		-6.54E+00	6.39E-01		-6.31E+00	6.60E-01		5.24E+00	3.60E-10	Up							
Unigene118948_A11	403	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.93	2.67	null	null		null	null		null	null		null	null		2.15E+00	9.45E-02		3.67E+00	7.76E-06	Up	Unigene118948_A11//gi|297601110|ref|NP_001050390.2|//8.00E-25//0s03g0422800 [Oryza sativa Japonica Group] >gi|108708887|gb|ABF96682.1| D-mannose binding lectin family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255674599|dbj|BAF12304.2|0s03g0422800 [Oryza sativa Japonica Group]	Unigene118948_A11//1.00E-17//AT5G24080| protein kinase family protein	Unigene118948_A11//1.00E-10//CO079258			GO:0004672//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene11895_A11	461	11.58	8.46	5.20	3.35	7.84	1.37	3.76	1.45	4.06	-4.52E-01	8.33E-02		-1.16E+00	2.65E-05	Down	1.23E+00	1.09E-04	Up	-1.29E+00	1.75E-02		-1.37E+00	2.67E-03		1.11E-01	7.90E-01		Unigene11895_A11//gi|157849662|gb|ABV89614.1|//8.00E-16//universal stress protein family protein [Brassica rapa]	Unigene11895_A11//9.00E-11//AT1G44760| universal stress protein (USP) family protein	Unigene11895_A11//0.00E+00//ES792017			GO:0050896	nr -
Unigene118958_A11	977	0.00	0.00	0.00	0.00	0.00	0.05	0.82	0.94	2.69	null	null		null	null		null	null		5.53E+00	6.98E-01		1.95E-01	7.62E-01		1.71E+00	3.42E-06	Up			Unigene118958_A11//3.00E-72//ES836194				
Unigene118959_A11	277	0.00	0.00	0.00	0.00	0.00	0.00	0.46	3.17	0.86	null	null		null	null		null	null		null	null		2.79E+00	6.97E-04	Up	9.14E-01	5.42E-01		Unigene118959_A11//gi|229893769|gb|ACQ90242.1|//6.00E-20//cinnamyl alcohol dehydrogenase [Glycine max]	Unigene118959_A11//1.00E-18//AT4G37980| ELI3-1 (ELICITOR-ACTIVATED GENE 3-1); binding / catalytic/ oxidoreductase/ zinc ion binding	Unigene118959_A11//1.00E-31//TC179502		ko00940|Phenylpropanoid biosynthesis	GO:0008152//GO:0016616//GO:0046914	nr +
Unigene118896_A11	741	5.15	4.10	2.52	3.09	1.77	2.93	3.31	2.59	1.45	-3.29E-01	3.15E-01		-1.04E+00	1.71E-03		-8.08E-01	4.44E-02		-8.00E-02	8.60E-01		-3.51E-01	3.73E-01		-1.19E+00	8.55E-04	Down	Unigene11896_A11//gi|38603890|gb|AAR24690.1|//1.00E-23//At1g48200 [Arabidopsis thaliana] >gi|38603976|gb|AAR24731.1|At1g48200 [Arabidopsis thaliana]	Unigene11896_A11//1.00E-20//AT1G48200| unknown protein	Unigene11896_A11//0.00E+00//gi|109872156|gb|DW501132.1|DW501132				nr +
Unigene118960_A11	231	0.00	0.00	0.92	0.22	0.15	0.00	0.18	1.09	3.10	null	null		9.85E+00	1.41E-01		-5.32E-01	8.26E-01		-7.75E+00	6.39E-01		2.57E+00	1.53E-01		4.08E+00	2.41E-04	Up			Unigene118960_A11//1.00E-27//CO108330				
Unigene118961_A11	312	0.00	0.00	0.00	0.32	0.00	0.43	0.95	3.88	7.41	null	null		null	null		-8.32E+00	3.15E-01		4.44E-01	8.62E-01		2.03E+00	8.61E-04	Up	2.96E+00	6.16E-10	Up	Unigene118961_A11//gi|225452181|ref|XP_002265308.1|//4.00E-11//PREDICTED: similar to LHT1 (LYSINE HISTIDINE TRANSPORTER 1); amino acid transmembrane transporter [Vitis vinifera]	Unigene118961_A11//1.00E-12//AT5G40780| LHT1; amino acid transmembrane transporter	Unigene118961_A11//7.00E-55//gi|48778405|gb|CO087771.1|CO087771			GO:0006865//GO:0015171//GO:0031224//GO:0043231	nr -
Unigene118962_A11	225	0.00	0.00	1.42	2.21	3.21	1.81	4.70	0.74	5.49	null	null		1.05E+01	4.53E-02		5.38E-01	5.64E-01		-2.94E-01	7.57E-01		-2.66E+00	2.25E-04	Down	2.25E-01	6.66E-01				Unigene118962_A11//7.00E-91//CO094931				

Unigene11897_All	880	7.02	6.56	3.45	5.55	4.62	4.36	1.63	0.85	1.72	-9.60E-02	6.91E-01		-1.02E+00	4.34E-05	Down	-2.65E-01	3.69E-01		-3.47E-01	2.31E-01		-9.34E-01	6.12E-02		7.46E-02	8.85E-01		Unigene11897_All//gi|115464025|ref|NP_001055612.1|//5.00E-50//0s05g0428400 [Oryza sativa Japonica Group] >gi|113579163|dbj|BAF17526.1| Os05g0428400 [Oryza sativa Japonica Group]	Unigene11897_All//1.00E-46//AT1G44760| universal stress protein (USP) family protein	Unigene11897_All//0.00E+00//gi|164275001|gb|ES823111.1|ES823111			GO:0050896	nr -
Unigene118982_All	601	2.87	13.49	8.51	0.83	3.09	2.03	0.98	0.56	1.86	2.23E+00	1.97E-19	Up	1.57E+00	1.01E-07	Up	1.90E+00	1.74E-04	Up	1.29E+00	4.33E-02		-8.24E-01	3.48E-01		9.14E-01	1.03E-01									
Unigene118984_All	207	3.79	5.63	3.86	18.77	10.15	3.49	2.45	2.42	5.20	5.70E-01	3.77E-01		2.54E-02	9.94E-01		-8.87E-01	2.22E-03		-2.43E+00	2.00E-11	Down	-1.66E-02	1.02E+00		1.08E+00	5.98E-02					Unigene118984_All//2.00E-07//BP278120					
Unigene118985_All	348	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.49	null	null		null	null		null	null		null	null		null	null		1.05E+01	6.14E-04	Up									
Unigene118989_All	248	0.42	0.41	0.86	0.00	0.69	0.00	1.70	2.36	6.75	-4.62E-02	9.90E-01		1.03E+00	5.92E-01		9.44E+00	2.27E-01		null	null		4.69E-01	6.13E-01		1.98E+01	5.62E-05	Up				Unigene118989_All//2.00E-54//TC130711					
Unigene118996_All	397	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.95	6.32	null	null		null	null		null	null		null	null		9.89E+00	6.86E-03		1.26E+01	5.71E-18	Up				Unigene118996_All//5.00E-07//TC153841					
Unigene118999_All	361	0.00	0.28	1.03	0.28	0.00	0.00	0.00	0.81	4.64	8.13E+00	3.89E-01		1.00E+01	2.50E-02		-8.11E+00	3.15E-01		-8.11E+00	4.02E-01		9.66E+00	2.35E-02		1.22E+01	5.04E-12	Up									
Unigene119_All	519	0.40	1.86	0.00	4.22	2.26	2.09	4.81	1.53	1.23	2.20E+00	6.58E-03		-8.66E+00	1.46E-01		-9.05E-01	2.79E-02		-1.02E+00	1.93E-02		-1.65E+00	1.62E-05	Down	-1.97E+00	4.57E-07	Down	Unigene119_All//gi|60327635|gb|AAX19057.1|//3.00E-84//class III HD-Zip protein 8 [Populus trichocarpa]	Unigene119_All//1.00E-82//AT4G32880| ATHB-8 (HOMEOBOX GENE 8); DNA binding / transcription factor	Unigene119_All//0.00E+00//TC178623	HB			nr -
Unigene1190_All	3046	2.08	4.76	2.60	2.91	2.87	2.49	2.75	4.67	26.11	1.19E+00	1.69E-14	Up	3.26E-01	1.46E-01		-1.97E-02	9.32E-01		-2.25E-01	3.07E-01		7.63E-01	1.12E-08		3.25E+00	0.00E+00	Up	Unigene1190_All//gi|75170629|sp|Q9FHK4.1|Y5519_ARATH//1.00E-22//RecName: Full=Uncharacterized protein At5g05190 >gi|30725434|gb|AAP37739.1| At5g05190 [Arabidopsis thaliana]	Unigene1190_All//2.00E-17//AT5G05190| unknown protein	Unigene1190_All//0.00E+00//DT465398				nr +
Unigene11900_All	1916	11.80	9.18	7.87	1.35	1.91	2.62	14.85	20.00	47.39	-3.62E-01	1.78E-03		-5.85E-01	8.23E-07		4.95E-01	1.36E-01		9.53E-01	3.53E-04		4.30E-01	2.27E-08		1.67E+00	1.17E-180	Up	Unigene11900_All//gi|240256105|ref|NP_567845.4|//0.00E+00//ATDGK7 (Diacylglycerol kinase 7); diacylglycerol kinase [Arabidopsis thaliana]	Unigene11900_All//0.00E+00//AT4G30340| ATDGK7 (Diacylglycerol kinase 7); diacylglycerol kinase	Unigene11900_All//0.00E+00//TC155811		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0007186//GO:0016301	nr -
Unigene119002_All	236	0.00	0.00	0.00	0.00	0.00	0.00	10.75	1.42	11.31	null	null		null	null		null	null		null	null		-2.92E+00	1.70E-10	Down	7.34E-02	8.38E-01		Unigene119002_All//gi|1181331|emb|CAA54678.1|//7.00E-07//calnexin [Zea mays]		Unigene119002_All//1.00E-40//TC158845		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr -
Unigene119003_All	232	2.26	2.18	2.30	6.23	3.41	0.58	0.36	0.18	1.72	-4.63E-02	9.76E-01		2.54E-02	9.99E-01		-8.67E-01	1.04E-01		-3.41E+00	3.16E-06	Down	-1.02E+00	7.26E-01		2.24E+00	6.43E-02									
Unigene119005_All	428	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.86	null	null		null	null		null	null		null	null		null	null		1.09E+01	7.36E-06	Up	Unigene119005_All//gi|115473125|ref|NP_001060161.1|//4.00E-09//Os07g0592200 [Oryza sativa Japonica Group] >gi|113611697|dbj|BAF22075.1| Os07g0592200 [Oryza sativa Japonica Group]	Unigene119005_All//4.00E-09//AT5G43100| aspartyl protease family protein					nr -
Unigene119015_All	389	0.00	0.00	0.00	0.26	0.00	0.00	0.43	0.21	2.87	null	null		null	null		-8.00E+00	3.15E-01		-8.00E+00	4.02E-01		-1.02E+00	6.15E-01		2.72E+00	8.54E-05	Up				Unigene119015_All//3.00E-73//DW485235					
Unigene119027_All	328	1.28	6.49	1.62	0.00	0.00	0.00	0.00	0.00	0.00	2.35E+00	6.59E-06	Up	3.47E-01	7.06E-01		null	null		null	null		null	null		null	null		Unigene119027_All//gi|148608655|gb|ABQ95657.1|//2.00E-07//auxin hydrogen symporter [Malus x domestica]	Unigene119027_All//2.00E-08//AT5G65980| auxin efflux carrier family protein	Unigene119027_All//4.00E-149//C0124843				nr +
Unigene119030_All	339	0.00	0.60	0.16	0.15	0.20	0.00	1.12	0.99	4.11	9.22E+00	1.37E-01		7.30E+00	6.38E-01		4.68E-01	9.59E-01		-7.20E+00	6.39E-01		-1.87E-01	8.57E-01		1.87E+00	4.97E-04	Up									
Unigene119032_All	428	0.00	0.12	0.12	0.00	0.00	0.00	0.10	0.10	2.70	6.89E+00	6.19E-01		6.96E+00	6.38E-01		null	null		null	null		-1.62E-02	1.01E+00		4.77E+00	3.27E-07	Up				Unigene119032_All//3.00E-27//gi|109875078|gb|DW504052.1|DW504052					ESTscan +
Unigene119047_All	946	0.00	0.00	0.00	0.05	0.00	0.00	0.27	0.04	4.46	null	null		null	null		-5.72E+00	5.58E-01		-5.72E+00	6.39E-01		-2.60E+00	1.44E-01		4.06E+00	9.27E-23	Up	Unigene119047_All//gi|18025342|gb|AAK38482.1|//2.00E-63//beta-D-xylosidase [Hordeum vulgare]	Unigene119047_All//4.00E-59//AT3G19620| glycosyl hydrolase family 3 protein	Unigene119047_All//4.00E-80//gi|48751990|gb|C0082509.1|C0082509		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr +
Unigene119068_All	258	0.41	4.32	0.83	1.74	2.67	3.50	0.98	0.32	1.54	3.41E+00	1.24E-04	Up	1.03E+00	5.92E-01		6.19E-01	5.30E-01		1.01E+00	1.96E-01		-1.60E+00	3.11E-01		6.51E-01	5.45E-01									
Unigene119073_All	830	0.00	0.00	0.00	0.36	0.12	0.22	0.71	0.45	3.79	null	null		null	null		-1.53E+00	2.98E-01		-7.26E-01	6.39E-01		-6.54E-01	4.45E-01		2.41E+00	8.65E-11	Up	Unigene119073_All//gi|15239119|ref|NP_196723.1|//8.00E-07//SWIM zinc finger family protein / mitogen-activated protein kinase kinase kinase (MAPKKK)-related [Arabidopsis thaliana] >gi|66865892|gb|AAY57580.1| PHD family protein [Arabidopsis thaliana]	Unigene119073_All//4.00E-08//AT5G11620| SWIM zinc finger family protein / mitogen-activated protein kinase kinase kinase (MAPKKK)-related	Unigene119073_All//2.00E-29//TC135767				nr -
Unigene119078_All	468	0.22	0.87	0.00	0.43	1.62	0.00	1.26	1.61	3.92	1.95E+00	1.44E-01		-7.80E+00	3.96E-01		1.93E+00	3.36E-02		-8.73E+00	1.34E-01		3.46E-01	6.20E-01		1.63E+00	2.55E-04	Up	Unigene119078_All//gi|224121322|ref|XP_002330798.1|//1.00E-17//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222872600|gb|EEF09731.1| cc-nbs-lrr resistance protein [Populus trichocarpa]		Unigene119078_All//1.00E-66//TC177573				nr +
Unigene119086_All	231	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.41	null	null		null	null		null	null		null	null		null	null		1.12E+01	3.28E-04	Up									
Unigene11909_All	1407	0.82	0.40	0.42	1.88	1.71	0.77	2.61	0.83	1.67	-1.05E+00	1.01E-01		-9.75E-01	1.46E-01		-1.31E-01	7.77E-01		-1.28E+00	1.04E-03		-1.65E+00	8.80E-08	Down	-6.46E-01	1.89E-02		Unigene11909_All//gi|240255377|ref|NP_188747.5|//4.00E-48//RNA binding / nucleic acid binding / nucleotide binding [Arabidopsis thaliana]	Unigene11909_All//2.00E-48//AT3G21100| RNA binding / nucleic acid binding / nucleotide binding	Unigene11909_All//0.00E+00//gi|109891506|gb|DW520469.1|DW520469			GO:0003676//GO:0046914	nr -
Unigene119095_All	446	0.00	0.00	0.00	0.00	0.00	0.00	0.76	1.22	10.45	null	null		null	null		null	null		null	null		6.84E-01	4.49E-01		3.78E+00	7.66E-24	Up									
Unigene1191_All	603	10.50	10.34	5.48	13.30	15.42	24.79	25.87	18.99	12.29	-2.26E-02	9.42E-01		-9.39E-01	1.31E-04		2.13E-01	3.10E-01		8.98E-01	3.66E-10		-4.46E-01	4.05E-04		-1.07E+00	1.14E-16	Down	Unigene1191_All//gi|3914431|sp|O24362.1|PSA3_SPIOL//2.00E-97//RecName: Full=Proteasome subunit alpha type-3; AltName: Full=20S proteasome alpha subunit G; AltName: Full=20S proteasome subunit alpha-7; AltName: Full=Proteasome component C8 >gi|2285802|dbj|BAA21651.1| 26S proteasome alpha subunit [Spinacia oleracea]	Unigene1191_All//3.00E-89//AT2G27020| PAG1; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene1191_All//0.00E+00//gi|7958792|gb|AW587509.1|AW587509		ko03050|Proteasome	GO:0004175//GO:0005576//GO:0005839//GO:0006950//GO:0010038//GO:0016020//GO:0019941//GO:0043231	nr +
Unigene11910_All	2681	5.21	1.98	4.65	8.77	6.74	4.51	6.83	2.54	3.31	-1.39E+00	1.21E-17	Down	-1.65E-01	3.49E-01		-3.79E-01	3.35E-04		-9.58E-01	1.50E-17		-1.43E+00	6.58E-29	Down	-1.04E+00	1.54E-18	Down	Unigene11910_All//gi|240256278|ref|NP_568277.5|//1.00E-138//nucleic acid binding / nucleotide binding / zinc ion binding [Arabidopsis thaliana]	Unigene11910_All//7.00E-113//AT3G21100| RNA binding / nucleic acid binding / nucleotide binding	Unigene11910_All//0.00E+00//gi|109860677|gb|DW489656.1|DW489656				nr -
Unigene119100_All	207	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.00	5.97	null	null		null	null		null	null		null	null		-7.67E+00	6.60E-01		4.87E+00	9.59E-08	Up									
Unigene119112_All	337	0.00	0.00	0.63	0.00	0.00	0.13	0.00	0.62	2.48	null	null		9.30E+00	1.41E-01		null	null		7.07E+00	6.98E-01		9.28E+00	7.86E-02		1.13E+01	3.89E-06	Up	Unigene119112_All//gi|57168305|gb|AAW38936.1|//4.00E-56//3-phosphoinositide-dependent protein kinase-1 [Solanum lycopersicum]	Unigene119112_All//1.00E-56//AT5G04510| PDK1 (2'-PHOSPHOINOSITIDE-DEPENDENT PROTEIN KINASE 1); 3-phosphoinositide-dependent protein kinase/ kinase/ phosphoinositide binding / protein binding / protein kinase	Unigene119112_All//9.00E-110//TC154807				nr -
Unigene119113_All	510	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.03	null	null		null	null		null	null		null	null		null	null		1.10E+01	1.58E-07	Up	Unigene119113_All//gi|28558781|gb|AX045752.1|//9.00E-52//pol protein [Cucumis melo]		Unigene119113_All//4.00E-08//TC136589				nr -
Unigene11912_All	2964	9.81	26.21	6.27	7.80	20.32	15.22	45.39	80.22	113.72	1.42E+00	6.43E-97	Up	-6.47E-01	4.13E-10		1.38E+00	1.27E-85	Up	9.65E-01	3.36E-33		8.22E-01	3.82E-150		1.33E+00	0.00E+00	Up	Unigene11912_All//gi|224101393|ref|XP_002312260.1|//0.00E+00//phol-like protein [Populus trichocarpa] >gi|222852080|gb|EEE89627.1| phol-like protein [Populus trichocarpa]	Unigene11912_All//0.00E+00//AT1G14040| LOCATED IN: integral to membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03240.1); Has 732 Blast hits to 696 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 238; Fungi - 246; Plants - 151; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink).	Unigene11912_All//0.00E+00//TC166082			GO:0004871//GO:0031224	nr +
Unigene119132_All	255	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.50	null	null		null	null		null	null		null	null		null	null		1.13E+01	9.34E-05	Up									
Unigene11914_All	1718	3.38	4.84	2.29	9.37	9.94	6.62	5.37	9.12	2.62	5.17E-01	1.04E-02		-5.60E-01	3.04E-02		8.61E-02	6.10E-01		-5.00E-01	2.36E-04		7.66E-01	1.55E-09		-1.03E+00	1.20E-09	Down	Unigene11914_All//gi|297825919|ref|XP_002880842.1|//0.00E+00//phosphoesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326681|gb|EFH57101.1| phosphoesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11914_All//0.00E+00//AT2G26870| phosphoesterase family protein	Unigene11914_All//0.00E+00//TC174320		ko00564|Glycerophospholipid metabolism//ko00562|Inositol phosphate metabolism//ko00565|Ether lipid metabolism	GO:0016787	nr +
Unigene119141_All	487	0.21	0.00	0.98	0.20	0.57	0.28	1.39	3.18	18.24	-7.75E+00	3.74E-01		2.20E+00	9.15E-02		1.47E+00	4.20E-01		4.43E-01	8.62E-01		1.19E+00	1.35E-02		3.72E+00	2.85E-44	Up	Unigene119141_All//gi|89258498|gb|ABD65462.1|//6.00E-60//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene119141_All//7.00E-28//AT3G51680| short-chain dehydrogenase/reductase (SDR) family protein	Unigene119141_All//0.00E+00//gi|164249167|gb|ES803626.1|ES803626		ko00906|Carotenoid biosynthesis		nr +
Unigene119159_All	314	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.93	15.61	null	null		null	null		null	null		null	null		9.86E+00	2.35E-02		1.39E+01	4.53E-35	Up	Unigene119159_All//gi|122831047|gb|ABM66813.1|//1.00E-28//ACC synthase [Gossypium hirsutum]	Unigene119159_All//5.00E-18//AT5G28360| ACS3 (1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE LIKE PSEUDOGENE); 1-aminocyclopropane-1-carboxylate synthase/ catalytic/ pyridoxal phosphate binding / transferase, transferring nitrogenous groups	Unigene119159_All//1.00E-120//gi|73860861|gb|DT463600.1|DT463600		ko00270|Cysteine and methionine metabolism		nr -
Unigene119164_All	229	0.00	0.00	0.00	0.65	0.00	0.39	0.00	0.18	2.44	null	null		null	null		-9.35E+00	1.66E-01		-7.27E-01	7.16E-01		7.51E+00	6.36E-01		1.13E+01	3.28E-04	Up				Unigene119164_All//3.00E-07//C0078033					
Unigene119169_All	250	0.00	0.00	0.00	0.00	0.00	0.00	0.34	0.17	3.67	null	null		null	null		null	null		null	null		-1.02E+00	7.25E-01		3.44E+00	7.53E-05	Up									
Unigene119171_All	785	0.00	1.16	0.00	0.25	0.70	0.35	0.97	0.69	6.55	1.02E+01	2.62E-05	Up	null	null		1.47E+00	1.77E-01		4.44E-01	7.64E-01		-4.86E-01	5.25E-01		2.76E+00	9.06E-20	Up				Unigene119171_All//4.00E-43//ES831637					
Unigene119176_All	517	0.00	0.00	0.00	0.48	0.07	0.00	0.49	0.00	3.70	null	null		null	null		-2.85E+00	1.37E-01		-8.91E+00	7.34E-02		-8.94E+00	4.04E-02		2.91E+00	3.25E-08	Up	Unigene119176_All//gi|224089779|ref|XP_002308812.1|//3.00E-14//predicted protein [Populus trichocarpa] >gi|222854788|gb|EEE92335.1| predicted protein [Populus trichocarpa]						nr -
Unigene119177_All	585	0.00	0.00	0.00	0.00	0.12	0.00	0.07	0.29	3.54	null	null		null	null		6.88E+00	6.12E-01		null	null		1.98E+00	3.79E-01		5.61E+00	1.89E-13	Up	Unigene119177_All//gi|89202791|gb|AAL09044.3|AF418563_1|//2.00E-08//calcium-dependent protein kinase 2 [Solanum tuberosum] >gi|300390204|gb|ADK10905.1| calcium-dependent protein kinase 2 [Solanum tuberosum]		Unigene119177_All//9.00E-102//C0130555		ko04626|Plant-pathogen interaction		nr +
Unigene119186_All	279	0.00	0.18	0.76	0.00	0.74	1.13	0.00	0.00	1.86	7.50E+00	6.19E-01		9.58E+00	1.41E-01		9.53E+00	1.57E-01		1.01E+01	4.08E-02		null	null		1.09E+01	6.14E-04	Up	Unigene119186_All//gi|225445342|ref|XP_002281542.1|//7.00E-30//PREDICTED: similar to GRV2 (KATAMARI2); binding / heat shock protein binding [Vitis vinifera]	Unigene119186_All//2.00E-26//AT2G26890| GRV2 (GRAVITROPISM DEFECTIVE 2); binding / heat shock protein binding	Unigene119186_All//5.00E-74//C0101514				nr -

Unigene119188_All	243	0.00	0.00	0.88	0.82	0.00	0.19	1.39	1.55	7.71	null	null		9.78E+00	1.41E-01		-9.68E+00	8.45E-02		-2.14E+00	3.47E-01		1.53E-01	8.90E-01		2.47E+00	6.92E-07	Up	Unigene119188_All//gi|297849514|ref|XP_002892638.1|//2.00E-14//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338480|gb|EFH68897.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene119188_All//2.00E-15//AT1G11350| SD1-13 (S-DOMAIN-113); kinase/ protein kinase/ protein serine/threonine kinase	Unigene119188_All//9.00E-63//DT468630				nr +
Unigene119191_All	974	0.00	0.00	0.05	0.20	0.28	0.14	0.56	0.94	2.21	null	null		5.77E+00	6.38E-01		4.67E-01	8.17E-01		-5.57E-01	7.33E-01		7.43E-01	2.60E-01		1.97E+00	4.04E-06	Up	Unigene119191_All//gi|18378607|gb|AAL68641.1|AF458765_1//2.00E-40//polyprotein [Oryza sativa Japonica Group]		Unigene119191_All//4.00E-37//gi|13245062|gb|BE052163.2|BE052163				nr +
Unigene119194_All	324	0.00	0.00	0.49	0.00	0.00	0.00	2.09	0.65	6.39	null	null		8.95E+00	2.39E-01		null	null		null	null		-1.69E+00	4.19E-02		1.61E+00	1.01E-04	Up	Unigene119194_All//gi|224127726|ref|XP_002329162.1|//2.00E-14//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene119194_All//1.00E-07//AT4G12010| disease resistance protein (TIR-NBS-LRR class), putative	Unigene119194_All//2.00E-09//TC140957				nr +
Unigene1192_All	1152	3.50	4.84	2.59	5.66	4.01	7.06	10.61	5.59	4.63	4.68E-01	6.73E-02		-4.34E-01	1.81E-01		-5.00E-01	2.43E-02		3.17E-01	1.45E-01		-9.25E-01	3.36E-10		-1.19E+00	1.49E-15	Down	Unigene1192_All//gi|3914431|sp|O24362.1|PS43_SPIOL//1.00E-131//RecName: Full=Proteasome subunit alpha type-3; AltName: Full=20S proteasome alpha subunit G; AltName: Full=20S proteasome subunit alpha-7; AltName: Full=Proteasome component C8 >gi|2285802|dbj|BAA21651.1| 20S proteasome alpha subunit [Spinacia oleracea]	Unigene1192_All//9.00E-124//AT2G27020| PAG1; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene1192_All//0.00E+00//TC132572		ko03050|Proteasome		nr +
Unigene11920_All	1590	3.75	6.53	4.12	4.45	7.02	6.59	5.05	9.70	13.15	8.00E-01	7.23E-06		1.35E-01	6.23E-01		6.57E-01	4.18E-05		5.67E-01	1.14E-03		9.41E-01	5.39E-13		1.38E+00	4.96E-32	Up	Unigene11920_All//gi|15232597|ref|NP_190248.1|//1.00E-73//PCL1 (PHYTOCLOCK 1); DNA binding / transcription factor [Arabidopsis thaliana] >gi|79314533|ref|NP_001030823.1| PCL1 (PHYTOCLOCK 1); DNA binding / transcription factor [Arabidopsis thaliana] >gi|30162630|gb|AAP21233.1| At3g46640 [Arabidopsis thaliana] >gi|71067050|dbj|BAE16277.1| PHYTOCLOCK 1 [Arabidopsis thaliana]	Unigene11920_All//2.00E-59//AT3G46640| PCL1 (PHYTOCLOCK 1); DNA binding / transcription factor	Unigene11920_All//0.00E+00//TC164856	G2-like		GO:0010468//GO:0048511	nr +
Unigene11921_All	1671	0.31	0.33	0.45	1.58	1.67	2.43	7.01	9.40	17.26	9.15E-02	9.33E-01		5.11E-01	5.47E-01		7.92E-02	8.55E-01		6.23E-01	4.21E-02		4.24E-01	7.57E-04		1.30E+00	4.42E-40	Up	Unigene11921_All//gi|71067056|dbj|BAE16280.1|//6.00E-81//NbPCL1 [Nicotiana benthamiana]	Unigene11921_All//5.00E-63//AT3G46640| PCL1 (PHYTOCLOCK 1); DNA binding / transcription factor	Unigene11921_All//0.00E+00//TC151156	G2-like		GO:0010468//GO:0048511	nr +
Unigene119212_All	203	8.76	7.24	7.08	4.42	5.94	8.01	20.62	15.65	8.24	-2.76E-01	5.91E-01		-3.07E-01	5.62E-01		4.27E-01	5.52E-01		8.59E-01	1.08E-01		-3.98E-01	1.48E-01		-1.32E+00	9.06E-07	Down			Unigene119212_All//4.00E-89//gi|164259363|gb|ES810975.1|ES810975				
Unigene119216_All	424	0.00	0.00	0.00	0.12	0.24	0.00	0.10	0.20	1.69	null	null		null	null		1.05E+00	8.09E-01		-6.88E+00	6.39E-01		9.83E-01	7.32E-01		4.08E+00	2.41E-04	Up							
Unigene119225_All	238	0.00	0.00	0.00	0.00	0.00	0.00	0.89	0.18	12.05	null	null		null	null		null	null		null	null		-2.34E+00	2.37E-01		3.76E+00	7.85E-15	Up	Unigene119225_All//gi|28300303|gb|AAO37646.1|//2.00E-13//NBS-LRR resistance protein RGH2 [Manihot esculenta]		Unigene119225_All//4.00E-65//TC143926				nr -
Unigene119227_All	341	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.34	null	null		null	null		null	null		null	null		null	null		1.12E+01	7.36E-06	Up							
Unigene11924_All	873	5.21	12.83	2.68	5.59	6.51	8.28	9.54	12.54	8.58	1.30E+00	7.48E-13	Up	-9.58E-01	1.25E-03		2.19E-01	4.50E-01		5.66E-01	9.32E-03		3.95E-01	1.14E-02		-1.53E-01	4.29E-01		Unigene11924_All//gi|297799318|ref|XP_002867543.1|//1.00E-81//hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313379|gb|EFH43802.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene11924_All//2.00E-77//AT4G26750| hydroxyproline-rich glycoprotein family protein	Unigene11924_All//0.00E+00//gi|48799908|gb|CO101222.1|CO101222		ko04144|Endocytosis	GO:0005488	nr +
Unigene119242_All	420	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.42	null	null		null	null		null	null		null	null		null	null		1.05E+01	1.76E-04	Up	Unigene119242_All//gi|224116348|ref|XP_002331960.1|//3.00E-18//flavonoid o-methyltransferase related [Populus trichocarpa] >gi|222874737|gb|EEF11868.1| flavonoid o-methyltransferase related [Populus trichocarpa]						nr -
Unigene119251_All	316	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.89	null	null		null	null		null	null		null	null		null	null		1.09E+01	1.76E-04	Up							
Unigene119259_All	830	0.44	0.12	0.45	0.36	0.33	0.27	0.56	0.50	3.07	-1.85E+00	1.87E-01		2.53E-02	1.00E+00		-1.18E-01	9.01E-01		-4.04E-01	7.51E-01		-1.54E-01	8.70E-01		2.45E+00	4.71E-09	Up	Unigene119259_All//gi|209970625|gb|ACJ03073.1|//1.00E-26//HB09p [Malus floribunda]	Unigene119259_All//3.00E-27//AT1G74180| AtRLP14 (Receptor Like Protein 14); protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene119263_All	438	0.00	0.00	0.00	0.23	0.00	0.00	0.00	0.00	3.00	null	null		null	null		-7.83E+00	3.14E-01		-7.83E+00	4.02E-01		null	null		1.16E+01	1.73E-09	Up	Unigene119263_All//gi|20269055|emb|CAC84708.1|//2.00E-07//aux/IAA protein [Populus tremula x Populus tremuloides]		Unigene119263_All//1.00E-118//TC172305				nr -
Unigene119267_All	550	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	5.51	null	null		null	null		null	null		null	null		6.25E+00	6.36E-01		1.24E+01	1.14E-21	Up							
Unigene119269_All	629	0.00	0.00	0.00	0.16	0.00	0.43	0.61	0.73	5.76	null	null		null	null		-7.31E+00	3.14E-01		1.44E+00	4.09E-01		2.73E-01	7.69E-01		3.25E+00	1.58E-16	Up	Unigene119269_All//gi|19698452|gb|AAL93154.1|AF485268_1//2.00E-22//bacterial-induced class III peroxidase [Gossypium hirsutum]	Unigene119269_All//4.00E-17//AT5G64120| peroxidase, putative	Unigene119269_All//3.00E-74//TC147787		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene11927_All	2096	12.93	7.20	6.17	26.45	21.47	28.68	47.36	30.45	28.02	-8.44E-01	2.59E-15		-1.07E+00	2.19E-21	Down	-3.01E-01	4.59E-06		1.17E-01	1.29E-01		-6.37E-01	8.03E-41		-7.58E-01	1.51E-56		Unigene11927_All//gi|13623892|dbj|BAB41076.1|//0.00E+00//MAR-binding protein [Nicotiana tabacum]	Unigene11927_All//0.00E+00//AT3G05060| SAR DNA-binding protein, putative	Unigene11927_All//0.00E+00//TC145583		ko03040|Spliceosome	GO:0003676//GO:0043231	nr +
Unigene119270_All	245	0.00	0.00	0.00	0.00	0.00	0.00	0.35	0.68	3.09	null	null		null	null		null	null		null	null		9.84E-01	6.34E-01		3.16E+00	6.83E-04	Up	Unigene119270_All//gi|224083434|ref|XP_002307025.1|//2.00E-09//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222856474|gb|EEE94021.1| cc-nbs-lrr resistance protein [Populus trichocarpa]						nr -
Unigene11929_All	670	0.94	4.84	2.23	1.34	4.37	3.24	25.87	57.14	51.97	2.37E+00	9.96E-09	Up	1.25E+00	3.19E-02		1.71E+00	5.93E-06	Up	1.27E+00	4.37E-03		1.14E+00	2.13E-42	Up	1.01E+00	2.71E-32	Up	Unigene11929_All//gi|15230231|ref|NP_191273.1|//5.00E-80//patatin-related [Arabidopsis thaliana] >gi|42572707|ref|NP_974449.1| patatin-related [Arabidopsis thaliana] >gi|29029050|gb|AAO64904.1| At3g57140 [Arabidopsis thaliana]	Unigene11929_All//3.00E-81//AT3G57140| patatin-related	Unigene11929_All//0.00E+00//gi|54119744|gb|CO495253.1|CO495253			GO:0003824//GO:0005811//GO:0006641//GO:0032561	nr -
Unigene11930_All	3755	2.55	16.91	3.70	5.72	14.35	7.81	51.11	134.25	140.94	2.73E+00	3.69E-187	Up	5.38E-01	5.74E-04		1.33E+00	3.82E-72	Up	4.49E-01	3.92E-06		1.39E+00	0.00E+00	Up	1.46E+00	0.00E+00	Up	Unigene11930_All//gi|297806369|ref|XP_002871068.1|//0.00E+00//sugar-dependent1 [Arabidopsis lyrata subsp. lyrata] >gi|297316905|gb|EFH47327.1| sugar-dependent1 [Arabidopsis lyrata subsp. lyrata]	Unigene11930_All//0.00E+00//AT5G04040| SDP1 (SUGAR-DEPENDENT1); triacylglycerol lipase	Unigene11930_All//0.00E+00//TC160895			GO:0003824//GO:0005811//GO:0006641//GO:0032561	nr -
Unigene119306_All	473	0.33	0.32	0.00	0.53	0.00	0.48	0.18	0.18	1.77	-4.59E-02	9.89E-01		-8.37E+00	2.45E-01		-9.04E+00	4.19E-02		-1.42E-01	9.29E-01		-1.70E-02	1.01E+00		3.31E+00	2.30E-04	Up		Unigene119306_All//3.00E-05//AT4G29120| 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein	Unigene119306_All//1.00E-103//ES794126				
Unigene119314_All	522	0.00	0.00	0.00	0.00	0.00	0.09	0.00	0.00	1.07	null	null		null	null		null	null		6.43E+00	6.98E-01		null	null		1.01E+01	3.28E-04	Up	Unigene119314_All//gi|15239147|ref|NP_196170.1|//8.00E-32//protein kinase-related [Arabidopsis thaliana] >gi|50253522|gb|AAT71963.1| At5g05510 [Arabidopsis thaliana] >gi|56381969|gb|AAV85703.1| At5g05510 [Arabidopsis thaliana]	Unigene119314_All//2.00E-33//AT5G05510| protein kinase-related	Unigene119314_All//4.00E-76//CK640467				nr +
Unigene119318_All	477	0.00	1.06	0.00	0.00	0.00	0.00	0.62	0.61	3.51	1.01E+01	4.03E-03		null	null		null	null		null	null		-1.66E-02	1.02E+00		2.50E+00	2.63E-06	Up	Unigene119318_All//gi|269924823|gb|ACZ52698.1|//4.00E-42//hydroxycinnamoyl-CoA quinate hydroxycinnamoyltransferase [Lonicera japonica]	Unigene119318_All//3.00E-27//AT5G48930| HCT (HYDROXYCINNAMOYL-COA SHIKIMATE/QUINATE HYDROXYCINNAMOYL TRANSFERASE); quinate O-hydroxycinnamoyltransferase/ shikimate O-hydroxycinnamoyltransferase/ transferase	Unigene119318_All//0.00E+00//TC147324		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene119319_All	243	0.22	0.00	0.00	0.21	0.28	0.19	0.00	2.41	1.15	-7.75E+00	6.15E-01		-7.75E+00	6.27E-01		4.67E-01	9.59E-01		-1.41E-01	9.54E-01		1.12E+01	2.81E-04	Up	1.02E+01	2.44E-02				Unigene119319_All//2.00E-57//gi|78335925|gb|DT556199.1|DT556199				
Unigene119322_All	636	0.00	0.00	0.00	0.16	0.32	0.14	0.27	0.66	2.51	null	null		null	null		1.05E+00	6.12E-01		-1.41E-01	9.51E-01		1.31E+00	2.35E-01		3.24E+00	1.34E-07	Up	Unigene119322_All//gi|22655797|gb|AAM04214.1|//3.00E-06//Putative retroelement [Oryza sativa Japonica Group]						nr -
Unigene119326_All	432	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.06	null	null		null	null		null	null		null	null		null	null		1.20E+01	1.38E-12	Up							
Unigene119328_All	486	0.00	0.00	0.00	0.00	0.00	0.19	0.52	0.86	2.54	null	null		null	null		null	null		7.54E+00	4.78E-01		7.20E-01	5.07E-01		2.28E+00	1.88E-04	Up			Unigene119328_All//2.00E-16//gi|21096607|gb|BQ408920.1|BQ408920				
Unigene11933_All	500	0.00	0.00	0.00	0.00	0.00	0.00	3.13	6.77	2.55	null	null		null	null		null	null		null	null		1.11E+00	2.51E-04	Up	-2.95E-01	5.44E-01		Unigene11933_All//gi|34850945|dbj|BAC87845.1|//2.00E-29//leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	Unigene11933_All//4.00E-20//AT1G35710| leucine-rich repeat transmembrane protein kinase, putative			ko03410|Base excision repair	GO:0005488//GO:0016301	nr +
Unigene119331_All	295	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.19	null	null		null	null		null	null		null	null		null	null		1.20E+01	6.29E-09	Up			Unigene119331_All//9.00E-11//BF270107				
Unigene119341_All	872	0.12	0.00	0.37	0.17	0.28	0.62	1.07	1.87	5.03	-6.91E+00	3.74E-01		1.61E+00	3.05E-01		6.89E-01	7.32E-01		1.86E+00	1.03E-01		8.09E-01	8.07E-02		2.24E+00	1.56E-13	Up	Unigene119341_All//gi|293337813|gb|ADE43150.1|//2.00E-21//SFBBepsilon protein [Malus x domestica]	Unigene119341_All//4.00E-16//AT4G12560| F-box family protein	Unigene119341_All//1.00E-132//gi|78325190|gb|DT545464.1|DT545464				nr -
Unigene119347_All	768	0.00	0.00	0.00	0.06	0.00	0.00	1.87	1.96	6.85	null	null		null	null		-6.02E+00	5.58E-01		-6.02E+00	6.39E-01		6.58E-02	9.05E-01		1.87E+00	5.79E-13	Up	Unigene119347_All//gi|18402268|ref|NP_565695.1|//2.00E-56//ASL5; DNA binding / protein binding [Arabidopsis thaliana] >gi|29427828|sp|Q8LBW3.2|LBD12_ARATH RecName: Full=LOB domain-containing protein 12; AltName: Full=ASYMMETRIC LEAVES 2-like protein 5; Short=AS2-like protein 5 >gi|3150407|gb|AAC16959.1| expressed protein [Arabidopsis thaliana] >gi|45330813|dbj|BAD12425.1| ASYMMETRIC LEAVES2-like gene 5 protein [Arabidopsis thaliana] >gi|219807086|dbj|BAH10549.1| ASYMMETRIC LEAVES2-like 5 protein [Arabidopsis thaliana]	Unigene119347_All//8.00E-58//AT2G30130| ASL5; DNA binding / protein binding	Unigene119347_All//0.00E+00//gi|73861707|gb|DT464446.1|DT464446		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -

Unigene11935_All	3392	0.69	0.60	0.68	4.08	1.50	1.64	8.56	22.64	6.84	-2.16E-01	5.99E-01		-4.03E-02	9.38E-01		-1.44E+00	1.82E-22	Down	-1.32E+00	2.69E-17	Down	1.40E+00	1.23E-115	Up	-3.25E-01	2.18E-04		Unigene11935_All//gi|223452528|gb|ACM89591.1|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Glycine max]	Unigene11935_All//8.00E-172//AT4G08850| kinase	Unigene11935_All//0.00E+00//gi|3326428|gb|AI055314.1|AI055314		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0044464	nr +
Unigene119353_All	333	0.00	0.00	0.80	0.30	0.52	0.14	1.52	1.63	5.14	null	null		9.64E+00	8.03E-02		7.89E-01	7.71E-01		-1.14E+00	6.77E-01		9.89E-02	9.21E-01		1.76E+00	1.93E-04	Up	Unigene119353_All//gi|116317776|emb|CAH65754.1|//6.00E-06//OSIGBa0123D13.3 [Oryza sativa (indica cultivar-group)]	Unigene119353_All//1.00E-05//AT5G64460| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G58280.3); Has 385 Blast hits to 382 proteins in 84 species: Archae - 0; Bacteria - 19; Metazoa - 2; Fungi - 201; Plants - 67; Viruses - 0; Other Eukaryotes - 96 (source: NCBI BLink).				nr -
Unigene11936_All	1893	12.16	7.74	11.25	31.66	24.96	15.27	6.61	9.32	21.70	-6.53E-01	1.10E-08		-1.12E-01	3.87E-01		-3.43E-01	3.48E-08		-1.05E+00	3.65E-51	Down	4.95E-01	2.50E-05		1.71E+00	6.20E-85	Up	Unigene11936_All//gi|242390089|dbj|BAH80551.1|//3.00E-82//transcription factor squamosa promoter binding protein-like [Eucalyptus grandis]	Unigene11936_All//2.00E-63//AT5G43270| SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2); DNA binding / transcription factor	Unigene11936_All//0.00E+00//TC135638	SBP		GO:0010468//GO:0048506	nr +
Unigene119368_All	915	0.00	0.00	0.00	0.16	0.19	0.00	0.32	0.69	2.05	null	null		null	null		2.05E-01	9.50E-01		-7.35E+00	2.34E-01		1.08E+00	1.99E-01		2.66E+00	2.08E-07	Up							
Unigene11937_All	1060	0.79	1.15	0.65	2.16	1.92	1.92	0.44	0.55	1.58	5.39E-01	3.76E-01		-2.74E-01	7.05E-01		-1.74E-01	7.09E-01		-1.73E-01	6.82E-01		3.31E-01	6.89E-01		1.85E+00	1.32E-04	Up	Unigene11937_All//gi|295815792|gb|ADG36381.1|//2.00E-51//promoter-binding protein SPL10 [Vitis vinifera]	Unigene11937_All//5.00E-43//AT5G43270| SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2); DNA binding / transcription factor	Unigene11937_All//0.00E+00//gi|78351702|gb|DT571976.1|DT571976	SBP		GO:0048506	nr -
Unigene119373_All	1322	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.85	5.09	null	null		null	null		null	null		null	null		2.15E+00	8.74E-04	Up	4.73E+00	1.40E-39	Up	Unigene119373_All//gi|270048197|gb|ACZ58492.1|//2.00E-07//beta' subunit of RNA polymerase [Floydiella terrestris]						nr -
Unigene11938_All	1861	1.69	0.68	2.17	4.68	3.63	3.18	1.48	2.36	5.33	-1.31E+00	3.06E-04	Down	3.66E-01	2.58E-01		-3.69E-01	5.75E-02		-5.59E-01	3.81E-03		6.75E-01	8.85E-03		1.85E+00	2.05E-23	Up	Unigene11938_All//gi|242390089|dbj|BAH80551.1|//5.00E-69//transcription factor squamosa promoter binding protein-like [Eucalyptus grandis]	Unigene11938_All//6.00E-55//AT5G43270| SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2); DNA binding / transcription factor	Unigene11938_All//0.00E+00//TC135638	SBP		GO:0010468//GO:0048506	nr -
Unigene11939_All	2179	0.82	0.47	1.34	3.38	2.96	1.33	1.65	2.46	8.81	-8.12E-01	9.59E-02		7.19E-01	5.98E-02		-1.95E-01	4.19E-01		-1.35E+00	7.94E-10	Down	5.74E-01	1.29E-02		2.42E+00	3.53E-62	Up	Unigene11939_All//gi|242390089|dbj|BAH80551.1|//9.00E-74//transcription factor squamosa promoter binding protein-like [Eucalyptus grandis]	Unigene11939_All//1.00E-60//AT5G43270| SPL2 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 2); DNA binding / transcription factor	Unigene11939_All//0.00E+00//TC165754	SBP		GO:0010468//GO:0048506	nr +
Unigene119399_All	400	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.00	4.58	null	null		null	null		null	null		null	null		-6.72E+00	6.59E-01		5.44E+00	8.34E-12	Up	Unigene119399_All//gi|224137170|ref|XP_002327053.1|//8.00E-08//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222835368|gb|EEE73803.1| AP2/EBP domain-containing transcription factor [Populus trichocarpa]		Unigene119399_All//3.00E-36//BP275652				nr +
Unigene1194_All	1124	7.08	4.42	4.97	9.79	10.05	10.73	18.21	8.70	6.52	-6.80E-01	9.43E-04		-5.08E-01	1.88E-02		3.70E-02	8.58E-01		1.31E-01	4.98E-01		-1.07E+00	1.14E-20	Down	-1.48E+00	4.25E-35	Down	Unigene1194_All//gi|15225839|ref|NP_180270.1|//1.00E-132//PAG1; endopeptidase/ peptidase/ threonine-type endopeptidase [Arabidopsis thaliana] >gi|12644056|sp|O23715.2|PSA3_ARATH RecName: Full=Proteasome subunit alpha type-3; AltName: Full=Proteasome subunit alpha type-7; AltName: Full=20S proteasome alpha subunit G-1; AltName: Full=Proteasome component 8; AltName: Full= Di| 17A-2a >gi|14030729|gb|AAK53039.1|AF37545 5_1 At2g27020/T20P8.7 [Arabidopsis thaliana] >gi|3421096|gb|AAC32064.1| 20S proteasome subunit PAG1 [Arabidopsis thaliana] >gi|3885332|gb|AAC77860.1| 20S proteasome alpha subunit G (PAG1) [Arabidopsis thaliana] >gi|21617882|gb|AAM66932.1| 20S proteasome subunit C8 (PAG1/PRC8_ARATH) [Arabidopsis thaliana] >gi|21700783|gb|AAM70515.1| At2g27020/T20P8.7 [Arabidopsis thaliana]	Unigene1194_All//1.00E-125//AT2G27020| PAG1; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene1194_All//0.00E+00//TC132572		ko03050|Proteasome		nr -
Unigene119403_All	355	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.00	5.27	null	null		null	null		null	null		null	null		-7.90E+00	4.05E-01		4.47E+00	5.22E-11	Up							
Unigene119419_All	281	0.19	0.36	0.00	0.00	0.00	0.64	0.30	1.64	2.98	9.54E-01	7.27E-01		-7.54E+00	6.27E-01		null	null		9.33E+00	1.95E-01		2.44E+00	3.74E-02		3.31E+00	2.30E-04	Up			Unigene119419_All//4.00E-133//BP276244				
Unigene11942_All	767	6.82	58.73	18.54	6.75	18.90	19.43	3.69	6.65	7.06	3.11E+00	9.38E-152	Up	1.44E+00	3.96E-18	Up	1.48E+00	4.80E-23	Up	1.52E+00	1.25E-22	Up	8.48E-01	3.43E-04		9.36E-01	3.27E-05		Unigene11942_All//gi|3643082|gb|AAC36697.1|//3.00E-94//protein phosphatase-2C [Mesembryanthemum crystallinum]	Unigene11942_All//7.00E-63//AT4G26080| ABI1 (ABA INSENSITIVE 1); calcium ion binding / protein serine/threonine phosphatase	Unigene11942_All//0.00E+00//DW496976			GO:0004721//GO:0006464//GO:0006950//GO:0009738//GO:0009767//GO:0010118//GO:0043231//GO:0043234//GO:0046872	nr -
Unigene119420_All	712	0.15	0.00	0.00	0.00	0.19	0.00	0.36	0.12	1.79	-7.20E+00	3.74E-01		-7.20E+00	3.96E-01		7.60E+00	3.19E-01		null	null		-1.60E+00	3.11E-01		2.33E+00	1.17E-04	Up	Unigene119420_All//gi|261666931|gb|ACY71071.1|//8.00E-28//heat stress transcription factor A3 [Solanum lycopersicum]		Unigene119420_All//3.00E-176//DT464624				nr +
Unigene119422_All	335	0.00	0.00	0.00	0.00	0.51	0.54	0.13	0.37	2.02	null	null		null	null		9.01E+00	2.27E-01		9.07E+00	1.95E-01		1.57E+00	5.46E-01		4.00E+00	4.30E-04	Up			Unigene119422_All//1.00E-93//CO090244				
Unigene119426_All	454	0.00	0.00	0.00	0.22	0.00	0.00	0.00	0.00	1.32	null	null		null	null		-7.78E+00	3.14E-01		-7.78E+00	4.02E-01		null	null		1.04E+01	1.76E-04	Up							
Unigene119429_All	399	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	1.40	null	null		null	null		null	null		null	null		6.71E+00	6.36E-01		1.04E+01	3.28E-04	Up							
Unigene11943_All	1527	3.22	52.00	20.71	9.75	23.81	22.42	4.65	4.32	6.52	4.01E+00	0.00E+00	Up	2.69E+00	9.84E-90	Up	1.29E+00	1.67E-46	Up	1.20E+00	7.51E-36	Up	-1.05E-01	6.23E-01		4.88E-01	2.00E-03		Unigene11943_All//gi|3643082|gb|AAC36697.1|//1.00E-126//protein phosphatase-2C [Mesembryanthemum crystallinum]	Unigene11943_All//8.00E-72//AT4G26080| ABI1 (ABA INSENSITIVE 1); calcium ion binding / protein serine/threonine phosphatase	Unigene11943_All//0.00E+00//gi|78346494|gb|DT566768.1|DT566768			GO:0004721//GO:0006464//GO:0006950//GO:0009738//GO:0009767//GO:0010118//GO:0043231//GO:0043234//GO:0046872	nr +
Unigene119430_All	309	0.00	0.16	0.00	0.32	0.00	0.00	0.00	0.27	1.93	7.36E+00	6.18E-01		null	null		-8.33E+00	3.14E-01		-8.33E+00	4.02E-01		8.08E+00	4.03E-01		1.09E+01	1.76E-04	Up			Unigene119430_All//4.00E-19//DW507908				
Unigene119438_All	499	0.00	0.20	0.21	0.20	0.48	0.00	0.00	0.17	1.60	7.67E+00	3.88E-01		7.74E+00	4.00E-01		1.27E+00	5.32E-01		-7.64E+00	4.02E-01		7.39E+00	4.03E-01		1.06E+01	7.36E-06	Up	Unigene119438_All//gi|124360746|gb|ABN08723.1|//1.00E-11//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene119438_All//9.00E-08//AT4G04650| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cold; LOCATED IN: stromule; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43730.1); Has 608 Blast hits to 598 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 608; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).						nr -
Unigene11944_All	1522	8.56	20.97	10.85	2.98	9.64	11.19	2.78	5.63	7.90	1.29E+00	4.82E-35	Up	3.42E-01	1.90E-02		1.69E+00	4.42E-28	Up	1.91E+00	3.63E-35	Up	1.02E+00	1.56E-08	Up	1.51E+00	2.46E-21	Up	Unigene11944_All//gi|3643082|gb|AAC36697.1|//5.00E-89//protein phosphatase-2C [Mesembryanthemum crystallinum]	Unigene11944_All//2.00E-72//AT4G26080| ABI1 (ABA INSENSITIVE 1); calcium ion binding / protein serine/threonine phosphatase	Unigene11944_All//0.00E+00//TC151685			GO:0016787	nr -
Unigene119442_All	277	0.00	0.00	0.00	0.00	0.00	0.65	0.00	2.11	1.29	null	null		null	null		null	null		9.35E+00	1.95E-01		1.10E+01	2.81E-04	Up	1.03E+01	7.29E-03		Unigene119442_All//gi|225016149|gb|ACN78973.1|//2.00E-15//copia-type polyprotein [Glycine max] >gi|225016157|gb|ACN78980.1| copia-type polyprotein [Glycine max]	Unigene119442_All//8.00E-07//ATMG00300| hypothetical protein					nr -
Unigene119443_All	449	62.11	24.60	13.64	25.52	22.85	6.74	38.80	9.40	10.03	-1.34E+00	2.05E-32	Down	-2.19E+00	6.47E-62	Down	-1.59E-01	4.12E-01		-1.92E+00	1.68E-24	Down	-2.04E+00	2.96E-45	Down	-1.95E+00	5.95E-44	Down	Unigene119443_All//gi|195618226|gb|ACG30943.1|//2.00E-44//histone H3 [Zea mays]	Unigene119443_All//4.00E-41//AT4G40030| histone H3.2	Unigene119443_All//2.00E-160//TC155014				nr +
Unigene119446_All	461	1.59	1.43	0.92	4.54	5.68	16.26	6.33	8.61	17.72	-1.53E-01	8.35E-01		-7.82E-01	3.80E-01		3.23E-01	4.58E-01		1.84E+00	5.10E-15	Up	4.45E-01	1.16E-01		1.49E+00	1.96E-14	Up			Unigene119446_All//6.00E-53//gi|73859450|gb|DT462189.1|DT462189				
Unigene119447_All	459	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.46	6.94	null	null		null	null		null	null		null	null		1.31E+00	4.47E-01		5.24E+00	6.28E-20	Up	Unigene119447_All//gi|145408595|ref|YP_001152219.1|//1.00E-14//O8F58f [Pinus koraiensis] >gi|145048844|gb|ABP35460.1| O8F58f [Pinus koraiensis]		Unigene119447_All//1.00E-26//TC150009				nr -
Unigene11945_All	2406	22.09	15.71	19.68	20.58	35.74	75.23	46.37	10.23	80.47	-4.92E-01	9.94E-12		-1.67E-01	3.68E-02		7.96E-01	2.55E-50		1.87E+00	0.00E+00	Up	-2.18E+00	0.00E+00	Down	7.95E-01	2.43E-118		Unigene11945_All//gi|224085523|ref|XP_002307605.1|//0.00E+00//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222857054|gb|EEE94601.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene11945_All//0.00E+00//AT3G51895| SULTR3;1 (SULFATE TRANSPORTER 3;1); secondary active sulfate transmembrane transporter/ sulfate transmembrane transporter/ transporter	Unigene11945_All//0.00E+00//TC168996			GO:0015103//GO:0015291//GO:0015698//GO:0031224	nr +
Unigene119457_All	401	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.52	2.19	null	null		null	null		null	null		null	null		9.03E+00	7.85E-02		1.11E+01	2.05E-06	Up	Unigene119457_All//gi|133712623|gb|AB037118.1|//6.00E-17//cuticular water permeability [Solanum habrochaites]	Unigene119457_All//4.00E-07//AT4G38260| unknown protein					nr -
Unigene119459_All	234	6.48	33.13	11.38	8.94	24.43	12.74	0.54	0.89	5.79	2.35E+00	8.43E-20	Up	8.11E-01	4.43E-02		1.45E+00	5.31E-09	Up	5.11E-01	1.82E-01		7.20E-01	6.32E-01		3.42E+00	7.76E-07	Up			Unigene119459_All//3.00E-07//DW508052				
Unigene119462_All	313	0.33	0.16	0.00	0.00	0.00	0.00	0.00	0.00	2.29	-1.05E+00	6.85E-01		-8.39E+00	3.96E-01		null	null		null	null		null	null		1.12E+01	2.63E-05	Up							
Unigene11947_All	538	2.72	4.24	2.57	2.78	2.18	2.69	1.73	2.87	5.41	6.38E-01	1.33E-01		-8.15E-02	8.85E-01		-3.52E-01	5.50E-01		-4.83E-02	9.41E-01		7.33E-01	1.29E-01		1.64E+00	1.92E-06	Up			Unigene11947_All//5.00E-91//gi|21092657|gb|BQ404970.1|BQ404970				
Unigene119475_All	499	0.52	0.10	0.00	0.60	0.41	0.36	0.85	0.17	3.03	-2.37E+00	2.14E-01		-9.03E+00	8.58E-02		-5.33E-01	6.79E-01		-7.27E-01	6.39E-01		-2.34E+00	5.46E-02		1.84E+00	3.16E-04	Up	Unigene119475_All//gi|297596372|ref|NP_001042475.2|//6.00E-23//Os01g0228200 [Oryza sativa (japonica Group)] >gi|255673021|dbj|BAF04389.2| Os01g0228200 [Oryza sativa (japonica Group)]	Unigene119475_All//2.00E-14//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction		nr -

Unigene119477_All	253	0.00	0.40	0.00	0.00	0.00	0.00	0.00	0.33	2.20	8.65E+00	3.88E-01		null	null		null	null		null	null		8.37E+00	4.03E-01		1.11E+01	3.28E-04	Up			Unigene119477_All//3.00E-10//gi|78338048|gb|DT558322.1|DT558322				
Unigene119483_All	389	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.00	1.95	null	null		null	null		null	null		null	null		-6.76E+00	6.59E-01		4.16E+00	1.34E-04	Up	Unigene119483_All//gi|195957709|gb|ACG59769.1|//6.00E-24//lipoxygenase 1 [Prunus persica]	Unigene119483_All//2.00E-14//AT1G17420| LOX3; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene119483_All//3.00E-85//TC177785		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr +
Unigene119485_All	301	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.97	2.65	null	null		null	null		null	null		null	null		1.79E+00	2.24E-01		3.24E+00	3.96E-04	Up			Unigene119485_All//1.00E-77//TC129826				
Unigene119489_All	271	71.63	130.13	79.58	74.81	75.73	197.65	83.16	192.17	123.34	8.61E-01	2.68E-20		1.52E-01	2.61E-01		1.76E-02	9.11E-01		1.40E+00	8.64E-71	Up	1.21E+00	1.25E-62	Up	5.69E-01	3.93E-12		Unigene119489_All//gi|117607067|gb|ABK42077.1|//3.00E-08//ubiquitin extension protein [Capsicum annuum]	Unigene119489_All//1.00E-08//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene119489_All//7.00E-113//gi|78343300|gb|DT563574.1|DT563574		ko03010|Ribosome		nr +
Unigene119949_All	1059	3.36	2.25	3.07	11.52	6.15	6.74	4.47	2.96	2.18	-5.79E-01	7.72E-02		-1.31E-01	7.01E-01		-9.07E-01	1.34E-09		-7.74E-01	9.52E-07		-5.95E-01	1.63E-02		-1.04E+00	2.14E-05	Down	Unigene119949_All//gi|98960885|gb|AB558926.1|//1.00E-19//At1g68430 [Arabidopsis thaliana]	Unigene119949_All//1.00E-18//AT1G68430| unknown protein	Unigene119949_All//8.00E-85//gi|21092657|gb|BQ404970.1|BQ404970				nr +
Unigene119491_All	529	0.30	0.38	0.00	0.00	0.13	0.09	0.56	0.00	2.33	3.69E-01	8.17E-01		-8.21E+00	2.45E-01		7.02E+00	6.12E-01		6.42E+00	6.98E-01		-9.13E+00	2.18E-02		2.06E+00	5.00E-04	Up	Unigene119491_All//gi|224139116|ref|XP_002322984.1|//8.00E-21//predicted protein [Populus trichocarpa] >gi|222867614|gb|EEF04745.1| predicted protein [Populus trichocarpa]						nr +
Unigene119493_All	256	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.58	null	null		null	null		null	null		null	null		null	null		1.18E+01	1.08E-06	Up	Unigene119493_All//gi|12656894|gb|AAC28902.2|//5.00E-06//polygalacturonase 3 [Solanum lycopersicum]	Unigene119493_All//4.00E-08//AT2G43890| polygalacturonase, putative / pectinase, putative					nr +
Unigene119494_All	285	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.24	null	null		null	null		null	null		null	null		null	null		1.11E+01	9.34E-05	Up							
Unigene1195_All	1245	10.80	9.12	8.77	9.12	5.73	6.02	12.90	7.08	4.38	-2.45E-01	1.31E-01		-3.01E-01	7.10E-02		-6.72E-01	1.50E-05		-5.99E-01	2.76E-04		-8.65E-01	7.52E-12		-1.56E+00	8.08E-30	Down	Unigene1195_All//gi|164604966|dbj|BAF98279.1|//1.00E-148//hydroxymethylglutaryl-CoA synthase [Hevea brasiliensis]	Unigene1195_All//1.00E-133//AT4G11820| MVA1; acetyl-CoA C-acetyltransferase/ hydroxymethylglutaryl-CoA synthase	Unigene1195_All//0.00E+00//gi|11206540|gb|BF275470.1|BF275470		ko00280|Valine, leucine and isoleucine degradation//ko00650|Butanoate metabolism//ko00900|Terpenoid backbone biosynthesis//ko00072|Synthesis and degradation of ketone bodies		nr -
Unigene119516_All	584	0.00	0.00	0.00	0.00	0.00	0.00	0.58	0.93	6.48	null	null		null	null		null	null		null	null		6.84E-01	4.49E-01		3.48E+00	2.96E-18	Up			Unigene119516_All//2.00E-87//gi|78332089|gb|DT552363.1|DT552363				
Unigene119519_All	593	0.00	0.00	0.00	0.00	0.06	0.00	0.00	0.14	1.28	null	null		null	null		5.86E+00	8.33E-01		null	null		7.14E+00	4.03E-01		1.03E+01	1.39E-05	Up	Unigene119519_All//gi|124360070|gb|ABN08886.1|//5.00E-09//Putative non-LTR retroelement reverse transcriptase, related [Medicago truncatula]	Unigene119519_All//3.00E-10//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene119519_All//6.00E-69//BM358539				nr -
Unigene11952_All	1494	1.75	5.87	4.10	7.17	7.95	9.46	21.23	32.03	20.35	1.74E+00	2.29E-15	Up	1.23E+00	1.61E-06	Up	1.50E-01	4.45E-01		4.00E-01	7.70E-03		5.94E-01	8.37E-18		-6.10E-02	5.56E-01		Unigene11952_All//gi|30692911|ref|NP_174631.2|//1.00E-152//catalytic/ glucosylceramidase [Arabidopsis thaliana] >gi|79319136|ref|NP_001031135.1| catalytic/ glucosylceramidase [Arabidopsis thaliana]	Unigene11952_All//8.00E-146//AT4G10060| catalytic/ glucosylceramidase	Unigene11952_All//4.00E-23//TC156942				nr +
Unigene119526_All	426	0.00	0.00	0.00	0.00	0.00	0.00	0.30	0.49	4.21	null	null		null	null		null	null		null	null		7.21E-01	6.32E-01		3.82E+00	1.36E-09	Up	Unigene119526_All//gi|224082172|ref|XP_002306593.1|//2.00E-09//predicted protein [Populus trichocarpa] >gi|222856042|gb|EEE93589.1| predicted protein [Populus trichocarpa]						nr -
Unigene11953_All	2749	2.51	7.04	4.65	7.30	7.40	8.17	30.67	65.32	26.03	1.49E+00	1.98E-26	Up	8.88E-01	7.12E-08		1.97E-02	9.02E-01		1.61E-01	2.22E-01		1.09E+00	7.14E-182	Up	-2.37E-01	1.97E-06		Unigene11953_All//gi|30695777|ref|NP_199801.2|//0.00E+00//catalytic/ glucosylceramidase [Arabidopsis thaliana] >gi|34365725|gb|AAQ65174.1| At5g49900 [Arabidopsis thaliana]	Unigene11953_All//0.00E+00//AT5G49900| catalytic/ glucosylceramidase	Unigene11953_All//5.00E-36//TC177169			GO:0004553//GO:0006678//GO:0016020//GO:0043231	nr -
Unigene119530_All	502	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	3.41	null	null		null	null		null	null		null	null		8.96E+00	4.31E-02		1.17E+01	2.63E-12	Up	Unigene119530_All//gi|224127358|ref|XP_002320054.1|//3.00E-06//predicted protein [Populus trichocarpa] >gi|222860827|gb|EEE98369.1| predicted protein [Populus trichocarpa]						nr -
Unigene119539_All	761	0.00	0.00	0.00	0.00	0.00	0.18	0.11	0.33	4.45	null	null		null	null		null	null		7.48E+00	3.11E-01		1.57E+00	3.26E-01		5.32E+00	2.66E-21	Up	Unigene119539_All//gi|126143480|dbj|BAF47279.1|//4.00E-64//lectin-receptor like protein kinase 3 [Nicotiana tabacum]	Unigene119539_All//3.00E-63//AT4G04960| lectin protein kinase, putative				GO:0000166//GO:0004713//GO:0044238//GO:0044260	nr -
Unigene119540_All	473	0.00	0.11	0.00	0.00	0.00	0.00	0.09	0.18	1.68	6.74E+00	6.18E-01		null	null		null	null		null	null		9.83E-01	7.32E-01		4.24E+00	7.42E-05	Up							
Unigene119542_All	451	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.33	null	null		null	null		null	null		null	null		null	null		1.04E+01	1.76E-04	Up							
Unigene119544_All	309	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.93	null	null		null	null		null	null		null	null		null	null		1.09E+01	1.76E-04	Up	Unigene119544_All//gi|115473321|ref|NP_001060259.1|//3.00E-11//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]						nr -
Unigene119550_All	606	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.21	1.97	null	null		null	null		null	null		null	null		7.69E+00	2.41E-01		1.09E+01	1.20E-08	Up	Unigene119550_All//gi|224055679|ref|XP_002298599.1|//3.00E-53//lysine/histidine transporter [Populus trichocarpa] >gi|222845857|gb|EEE83404.1| lysine/histidine transporter [Populus trichocarpa]	Unigene119550_All//2.00E-48//AT5G40780| LHT1; amino acid transmembrane transporter	Unigene119550_All//5.00E-11//C0081946			GO:0006865//GO:0015171//GO:0031224	nr +
Unigene119558_All	377	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	3.59	null	null		null	null		7.51E+00	6.12E-01		null	null		null	null		1.18E+01	9.04E-10	Up							
Unigene11956_All	708	0.96	2.15	2.11	2.18	2.38	1.53	6.75	2.54	2.25	1.16E+00	3.43E-02		1.13E+00	4.89E-02		1.28E-01	8.26E-01		-5.11E-01	3.72E-01		-1.41E+00	5.29E-08	Down	-1.58E+00	1.10E-09	Down	Unigene11956_All//gi|18415647|ref|NP_568185.1|//4.00E-26//mitochondrial transcription termination factor family protein / mTERF family protein [Arabidopsis thaliana]	Unigene11956_All//8.00E-25//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene11956_All//0.00E+00//gi|109876454|gb|DW505428.1|DW505428				nr -
Unigene119564_All	332	0.00	0.00	0.00	0.30	0.00	0.14	0.25	1.01	3.48	null	null		null	null		-8.23E+00	3.14E-01		-1.14E+00	6.77E-01		1.98E+00	1.44E-01		3.77E+00	2.44E-06	Up							
Unigene119569_All	1483	0.00	0.00	0.00	0.40	0.09	0.00	5.67	1.41	4.11	null	null		null	null		-2.12E+00	3.06E-02		-8.66E+00	7.71E-04	Down	-2.01E+00	9.49E-22	Down	-4.65E-01	7.29E-03		Unigene119569_All//gi|224069338|ref|XP_002302959.1|//2.00E-12//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222844685|gb|EEE82232.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene119569_All//5.00E-06//AT1G69545| leucine-rich repeat family protein	Unigene119569_All//3.00E-85//ES828348			GO:0003824	nr -
Unigene11957_All	1110	9.24	4.75	9.45	12.88	11.32	11.88	6.09	2.03	2.80	-9.61E-01	1.25E-07		3.27E-02	8.70E-01		-1.86E-01	2.57E-01		-1.17E-01	5.15E-01		-1.58E+00	6.47E-13	Down	-1.12E+00	3.11E-08	Down	Unigene11957_All//gi|18415647|ref|NP_568185.1|//3.00E-43//mitochondrial transcription termination factor family protein / mTERF family protein [Arabidopsis thaliana]	Unigene11957_All//1.00E-44//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene11957_All//0.00E+00//TC175627				nr +
Unigene119573_All	390	0.00	0.00	0.00	0.26	0.00	0.23	0.00	0.00	3.47	null	null		null	null		-8.00E+00	3.14E-01		-1.42E-01	9.51E-01		null	null		1.18E+01	9.04E-10	Up	Unigene119573_All//gi|124359162|gb|ABN05885.1|//5.00E-06//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]						nr +
Unigene119576_All	457	0.00	0.00	0.00	0.00	0.00	0.30	0.09	0.18	3.40	null	null		null	null		null	null		8.21E+00	3.11E-01		9.84E-01	7.32E-01		5.20E+00	6.73E-10	Up			Unigene119576_All//2.00E-25//gi|45438778|gb|CF932197.1|CF932197				
Unigene119577_All	589	0.00	0.00	0.00	0.00	0.23	0.00	0.43	0.85	2.23	null	null		null	null		7.87E+00	3.19E-01		null	null		9.83E-01	3.11E-01		2.37E+00	7.20E-05	Up			Unigene119577_All//2.00E-10//DT468110				
Unigene11958_All	1527	3.15	1.89	2.23	5.81	4.85	3.28	5.65	2.63	2.90	-7.37E-01	7.10E-03		-4.98E-01	8.56E-02		-2.60E-01	2.06E-01		-8.23E-01	1.41E-05		-1.10E+00	1.11E-09	Down	-9.64E-01	3.45E-08		Unigene11958_All//gi|18415647|ref|NP_568185.1|//7.00E-57//mitochondrial transcription termination factor family protein / mTERF family protein [Arabidopsis thaliana]	Unigene11958_All//1.00E-55//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene11958_All//0.00E+00//TC175627				nr +
Unigene11959_All	1335	7.05	5.35	2.95	12.91	11.40	13.84	9.03	6.04	8.15	-3.99E-01	3.63E-02		-1.26E+00	5.51E-10	Down	-1.79E-01	2.23E-01		9.99E-02	5.32E-01		-5.79E-01	6.47E-05		-1.48E-01	3.59E-01		Unigene11959_All//gi|133778858|gb|AB033769.1|//1.00E-177//At5g50420 [Arabidopsis thaliana]	Unigene11959_All//5.00E-178//AT5G50420| unknown protein	Unigene11959_All//0.00E+00//TC166428			GO:0016740	nr -
Unigene1196_All	1828	13.17	10.67	11.30	34.69	26.73	22.01	143.03	93.77	638.90	-3.03E-01	7.41E-03		-2.20E-01	7.33E-02		-3.76E-01	3.72E-10		-6.56E-01	2.14E-24		-6.09E-01	4.93E-98		2.16E+00	0.00E+00	Up	Unigene1196_All//gi|164604966|dbj|BAF98279.1|//0.00E+00//hydroxymethylglutaryl-CoA synthase [Hevea brasiliensis]	Unigene1196_All//0.00E+00//AT4G11820| MVA1; acetyl-CoA C-acetyltransferase/ hydroxymethylglutaryl-CoA synthase	Unigene1196_All//0.00E+00//TC133596		ko00280|Valine, leucine and isoleucine degradation//ko00650|Butanoate metabolism//ko00900|Terpenoid backbone biosynthesis//ko00072|Synthesis and degradation of ketone bodies	GO:0006084//GO:0006720//GO:0016453//GO:0046912	nr +
Unigene119604_All	351	0.30	0.14	0.00	0.28	0.69	0.00	0.60	0.71	2.95	-1.05E+00	6.85E-01		-8.22E+00	3.96E-01		1.27E+00	5.32E-01		-8.15E+00	4.02E-01		2.47E-01	8.53E-01		2.29E+00	7.17E-04	Up							
Unigene119610_All	245	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.28	null	null		null	null		null	null		null	null		null	null		1.12E+01	3.28E-04	Up	Unigene119610_All//gi|224122320|ref|XP_002330594.1|//4.00E-09//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222872152|gb|EEF09283.1| cc-nbs-lrr resistance protein [Populus trichocarpa]					GO:0000166//GO:0016787	nr -
Unigene119612_All	459	0.23	0.00	0.00	0.00	0.00	0.00	0.00	0.27	2.69	-7.83E+00	3.74E-01		-7.83E+00	3.96E-01		null	null		null	null		8.09E+00	2.41E-01		1.14E+01	6.29E-09	Up		Unigene119612_All//3.00E-06//AT5G25190| ethylene-responsive element-binding protein, putative	Unigene119612_All//2.00E-19//EX168096	AP2-EREBP			
Unigene119617_All	430	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.22	null	null		null	null		null	null		null	null		null	null		1.11E+01	5.69E-07	Up							
Unigene119619_All	568	0.00	0.00	0.00	0.00	0.06	0.24	0.37	0.15	3.86	null	null		null	null		5.92E+00	8.32E-01		7.90E+00	3.11E-01		-1.34E+00	4.30E-01		3.37E+00	1.47E-10	Up	Unigene119619_All//gi|224120698|ref|XP_002318395.1|//4.00E-21//predicted protein [Populus trichocarpa] >gi|222859068|gb|EEE96615.1| predicted protein [Populus trichocarpa]					GO:0005488	nr -
Unigene119620_All	386	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.75	null	null		null	null		null	null		null	null		null	null		1.08E+01	4.97E-05	Up	Unigene119620_All//gi|21311559|gb|AAM46780.1|AF467803_1//5.00E-18//latex plastidic aldolase-like protein [Hevea brasiliensis]	Unigene119620_All//9.00E-19//AT3G21330| fructose-bisphosphate aldolase, putative	Unigene119620_All//8.00E-18//EX169626		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway	GO:0006007//GO:0016832	nr +
Unigene119626_All	509	0.00	0.00	0.00	0.00	0.00	0.00	0.91	1.64	10.02	null	null		null	null		null	null		null	null		8.46E-01	2.31E-01		3.45E+00	3.28E-24	Up	Unigene119626_All//gi|158828300|gb|AB981175.1|//7.00E-06//non-LTR retrotransposon transposase [Arabidopsis cebennensis]	Unigene119626_All//2.00E-06//AT5G42905| nucleic acid binding / ribonuclease H					nr -
Unigene11963_All	1805	5.65	6.46	4.31	6.84	6.60	7.51	4.94	5.90	10.24	1.92E-01	2.88E-01		-3.92E-01	4.01E-02		-5.22E-02	8.15E-01		1.33E-01	4.76E-01		2.57E-01	1.26E-01		1.05E+00	8.54E-19	Up	Unigene11963_All//gi|66271061|gb|AAY43808.1|//9.00E-43//Fb17 [Gossypium hirsutum]		Unigene11963_All//4.00E-156//gi|54123099|gb|CO498608.1|CO498608				nr -

Unigene119632_All	1004	0.00	0.00	0.00	0.00	0.00	0.18	0.08	0.17	2.14	null	null		null	null		null	null		7.49E+00	1.95E-01		9.84E-01	6.34E-01		4.67E+00	7.12E-13	Up	Unigene119632_All//gi|116308876|emb|CAH66011.1|//8.00E-07//OS10Gb0093M15.1 [Oryza sativa (indica cultivar-group)]						nr +
Unigene119633_All	401	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.19	null	null		null	null		null	null		null	null		null	null		1.11E+01	2.05E-06	Up							
Unigene119638_All	431	0.00	0.00	0.00	0.00	0.08	0.10	0.20	0.00	1.76	null	null		null	null		6.32E+00	8.32E-01		6.71E+00	6.98E-01		-7.62E+00	4.05E-01		3.16E+00	6.83E-04	Up							
Unigene11964_All	4095	12.65	7.46	8.24	10.52	11.85	9.43	7.59	1.41	4.85	-7.62E-01	4.68E-24		-6.18E-01	3.52E-16		1.71E-01	2.89E-02		-1.58E-01	7.32E-02		-2.43E+00	3.58E-99	Down	-6.45E-01	5.09E-14		Unigene11964_All//gi|9795593|gb|AAF98411.1|AC026238_3//0.00E+00//Unknown protein [Arabidopsis thaliana] >gi|20856609|gb|AAM26675.1|At1g18620/F25I16_13 [Arabidopsis thaliana] >gi|32306507|gb|AAPT8937.1|At1g18620 [Arabidopsis thaliana]	Unigene11964_All//0.00E+00//AT1G74160| unknown protein	Unigene11964_All//0.00E+00//TC153949				nr -
Unigene11965_All	2282	1.35	1.20	1.05	4.28	3.82	2.65	7.99	3.52	2.95	-1.74E-01	6.09E-01		-3.65E-01	3.48E-01		-1.64E-01	4.34E-01		-6.90E-01	1.17E-04		-1.18E+00	9.40E-22	Down	-1.44E+00	5.54E-30	Down	Unigene11965_All//gi|224092702|ref|XP_002309704.1|//1.00E-33//nbs-lrr resistance protein [Populus trichocarpa] >gi|222855680|gb|EEE93227.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene11965_All//1.00E-06//AT5G46260| disease resistance protein (TIR-NBS-LRR class), putative	Unigene11965_All//0.00E+00//TC167637				nr +
Unigene119651_All	615	0.17	0.58	0.95	3.32	3.02	1.91	1.72	0.34	0.19	1.76E+00	2.18E-01		2.49E+00	3.75E-02		-1.35E-01	8.02E-01		-7.99E-01	7.94E-02		-2.34E+00	6.78E-04	Down	-3.15E+00	2.96E-05	Down	Unigene119651_All//gi|15983378|gb|AAL11557.1|AF424563_1//3.00E-22//AT5g01890/T20L15_160 [Arabidopsis thaliana] >gi|28416471|gb|AA042766.1|At5g01890/T20L15_160 [Arabidopsis thaliana] >gi|224589655|gb|ACN59360.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene119651_All//2.00E-22//AT5G01890| leucine-rich repeat transmembrane protein kinase, putative	Unigene119651_All//9.00E-28//TC171867			GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016020//GO:0016491//GO:0032559	nr -
Unigene119656_All	733	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	2.99	null	null		null	null		null	null		null	null		6.83E+00	4.03E-01		1.15E+01	1.06E-15	Up	Unigene119656_All//gi|124360594|gb|ABN08593.1|//9.00E-49//TIR [Medicago truncatula]	Unigene119656_All//7.00E-54//AT1G52900| disease resistance protein (TIR class), putative				GO:0004872//GO:0006952//GO:0023060//GO:0031224//GO:0043231	nr -
Unigene119659_All	240	0.00	0.00	0.00	0.42	0.00	0.00	0.88	0.35	6.64	null	null		null	null		-8.70E+00	3.14E-01		-8.70E+00	4.02E-01		-1.34E+00	4.30E-01		2.91E+00	5.82E-07	Up			Unigene119659_All//3.00E-10//gi|109847720|gb|DW476700.1|DW476700					
Unigene11966_All	2146	1.56	1.09	1.59	5.69	3.79	2.46	10.21	6.10	3.23	-5.23E-01	1.24E-01		2.54E-02	9.59E-01		-5.87E-01	8.97E-05		-1.21E+00	1.99E-13	Down	-7.43E-01	2.12E-12		-1.66E+00	3.90E-44	Down			Unigene11966_All//0.00E+00//TC177532					
Unigene119663_All	276	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.45	null	null		null	null		null	null		null	null		null	null		1.13E+01	4.97E-05	Up							
Unigene119669_All	386	0.00	0.00	0.14	0.13	0.00	0.00	0.33	0.54	2.17	null	null		7.11E+00	6.38E-01		-7.01E+00	5.58E-01		-7.01E+00	6.38E-01		7.20E-01	6.32E-01		2.72E+00	8.98E-04	Up							
Unigene119671_All	260	0.00	0.00	0.00	0.00	0.00	0.00	20.00	9.48	28.96	null	null		null	null		null	null		null	null		-1.08E+00	6.13E-06	Down	5.34E-01	3.79E-03		Unigene119671_All//gi|297724399|ref|NP_001174563.1|//3.00E-09//Os06g0109100 [Oryza sativa Japonica Group] >gi|255676647|dbj|BAH93291.1|Os06g0109100 [Oryza sativa Japonica Group]						nr -
Unigene119672_All	228	0.23	0.00	1.17	0.00	0.30	0.00	0.56	0.92	5.77	-7.84E+00	6.15E-01		2.35E+00	2.40E-01		8.24E+00	6.12E-01		null	null		7.20E-01	6.32E-01		3.37E+00	1.37E-06	Up			Unigene119672_All//4.00E-52//DT462368					
Unigene119674_All	373	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.22	1.71	null	null		null	null		null	null		null	null		7.81E+00	4.03E-01		1.07E+01	9.34E-05	Up								
Unigene119688_All	258	0.00	0.00	0.00	0.00	0.27	0.00	0.00	0.65	2.32	null	null		null	null		8.06E+00	6.12E-01		null	null		9.34E+00	1.39E-01		1.12E+01	1.76E-04	Up			Unigene119688_All//3.00E-07//EX165412					
Unigene11969_All	450	1.98	4.17	1.18	2.99	7.88	6.52	1.97	0.00	0.53	1.08E+00	2.50E-02		-7.40E-01	3.48E-01		1.40E+00	1.72E-05	Up	1.13E+00	2.27E-03		-1.09E+01	2.24E-06	Down	-1.88E+00	6.34E-03				Unigene11969_All//7.00E-65//EX170517					
Unigene119691_All	254	0.00	0.00	0.21	0.00	0.00	0.00	1.00	5.10	6.43	null	null		7.71E+00	6.38E-01		null	null		null	null		2.35E+00	1.25E-04	Up	2.69E+00	1.30E-06	Up			Unigene119691_All//2.00E-63//ES848236					
Unigene119695_All	387	0.00	0.00	0.00	0.00	0.00	0.00	0.22	0.76	4.63	null	null		null	null		null	null		null	null		1.79E+00	2.24E-01		4.41E+00	1.76E-10	Up								
Unigene119699_All	529	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	8.13	null	null		null	null		null	null		null	null		7.30E+00	4.02E-01		1.30E+01	8.72E-31	Up								
Unigene1197_All	997	11.23	8.44	2.14	16.64	7.70	8.02	34.01	17.73	15.98	-4.13E-01	1.61E-02		-2.39E+00	6.12E-28	Down	-1.11E+00	7.03E-18	Down	-1.05E+00	1.39E-14	Down	-9.40E-01	1.48E-27		-1.09E+00	5.64E-36	Down	Unigene1197_All//gi|5669656|gb|AAD46413.1|AF096263_1//2.00E-24//ER33 protein [Solanum lycopersicum]	Unigene1197_All//2.00E-24//AT1G05710| ethylene-responsive protein, putative	Unigene1197_All//0.00E+00//TC179467	bHLH		GO:0001071//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene11970_All	1504	2.50	4.35	2.37	3.01	5.38	4.83	3.94	1.47	1.25	7.95E-01	5.73E-04		-7.84E-02	8.10E-01		8.36E-01	1.54E-05		6.82E-01	1.47E-03		-1.42E+00	8.42E-10	Down	-1.66E+00	1.47E-12	Down	Unigene11970_All//gi|297803220|ref|XP_002869494.1|//1.00E-156//RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315330|gb|EFH45753.1|RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene11970_All//5.00E-156//AT4G28550| RabGAP/TBC domain-containing protein	Unigene11970_All//0.00E+00//TC150082				nr -
Unigene119709_All	1370	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.76	null	null		null	null		null	null		null	null		null	null		1.14E+01	4.44E-27	Up	Unigene119709_All//gi|5690095|emb|CAB51950.1|//3.00E-12//transposase related protein [Zea mays]	Unigene119709_All//4.00E-05//AT1G64255| SWIM zinc finger family protein	Unigene119709_All//3.00E-66//TC148530				nr +
Unigene11971_All	1628	3.21	3.49	4.71	4.47	8.10	6.85	3.87	1.82	1.76	1.17E-01	6.43E-01		5.52E-01	1.21E-02		8.59E-01	4.40E-09		6.17E-01	2.25E-04		-1.09E+00	4.09E-07	Down	-1.14E+00	7.47E-08	Down	Unigene11971_All//gi|297803220|ref|XP_002869494.1|//1.00E-157//RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315330|gb|EFH45753.1|RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene11971_All//1.00E-158//AT4G28550| RabGAP/TBC domain-containing protein	Unigene11971_All//0.00E+00//TC150082				nr +
Unigene119713_All	228	0.00	0.00	0.00	0.00	0.00	0.00	1.67	1.28	6.47	null	null		null	null		null	null		null	null		-3.79E-01	7.23E-01		1.95E+00	2.09E-04	Up			Unigene119713_All//8.00E-23//C0091281					
Unigene119719_All	307	0.17	0.00	0.17	0.97	0.11	0.15	2.07	0.00	0.00	-7.41E+00	6.15E-01		2.60E-02	9.95E-01		-3.12E+00	7.56E-02		-2.73E+00	1.37E-01		-1.10E+01	1.23E-04	Down	-1.10E+01	7.11E-05	Down			Unigene119719_All//1.00E-77//TC154798					
Unigene11972_All	1270	2.10	2.83	1.64	3.45	0.98	1.49	11.65	15.20	11.20	4.31E-01	1.95E-01		-3.62E-01	3.99E-01		-1.82E+00	2.97E-10	Down	-1.21E+00	3.03E-05	Down	3.84E-01	6.54E-04		-5.72E-02	6.86E-01		Unigene11972_All//gi|162279926|ref|XP_006061.2|//1.00E-147//cytochrome c oxidase subunit 2 [Beta vulgaris subsp. vulgaris] >gi|87248025|gb|ABD36067.1|cytochrome oxidase subunit 2 [Beta vulgaris subsp. vulgaris] >gi|148491430|dbj|BAA99453.2|cytochrome c oxidase subunit 2 [Beta vulgaris subsp. vulgaris]	Unigene11972_All//3.00E-119//ATMG00160| cytochrome c oxidase subunit 2	Unigene11972_All//0.00E+00//TC166313		ko00190|Oxidative phosphorylation		nr +
Unigene119721_All	670	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.44	2.20	null	null		null	null		null	null		null	null		8.77E+00	2.35E-02		1.11E+01	1.30E-10	Up	Unigene119721_All//gi|224120764|ref|XP_002318411.1|//4.00E-15//predicted protein [Populus trichocarpa] >gi|222859084|gb|EEE96631.1|predicted protein [Populus trichocarpa]						nr -
Unigene119723_All	343	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.97	null	null		null	null		null	null		null	null		null	null		1.09E+01	4.97E-05	Up							ESTscan +
Unigene119725_All	373	2.10	0.00	0.57	4.81	5.35	3.51	3.63	3.03	2.35	-1.10E+01	1.09E-04	Down	-1.88E+00	4.13E-02		1.55E-01	7.98E-01		-4.53E-01	3.94E-01		-2.62E-01	6.63E-01		-6.26E-01	2.05E-01		Unigene119725_All//gi|224132268|ref|XP_002321297.1|//1.00E-54//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222862070|gb|EEE99612.1|multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene119725_All//1.00E-52//AT1G04120| ATMRP5; ATPase, coupled to transmembrane movement of substances / sulfonylurea receptor	Unigene119725_All//9.00E-172//gi|78347763|gb|DT568037.1|DT568037		ko02010|ABC transporters	GO:0004888//GO:0005773//GO:0006810//GO:0006875//GO:0006970//GO:0008152//GO:0015405//GO:0016628//GO:0017111//GO:0031090//GO:0031224//GO:0032559	nr -
Unigene119731_All	286	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.95	null	null		null	null		null	null		null	null		null	null		1.09E+01	3.28E-04	Up							ESTscan +
Unigene119733_All	241	0.43	0.21	0.00	0.00	0.43	0.00	0.70	0.87	10.91	-1.05E+00	6.85E-01		-8.76E+00	3.96E-01		8.74E+00	4.57E-01		null	null		3.05E-01	8.36E-01		3.96E+00	3.85E-14	Up	Unigene119733_All//gi|255552137|ref|XP_002517113.1|//7.00E-07//N-acetyltransferase, putative [Ricinus communis] >gi|223543748|gb|EEF45276.1| N-acetyltransferase, putative [Ricinus communis]		Unigene119733_All//9.00E-106//gi|73860697|gb|DT463436.1|DT463436				nr +
Unigene119735_All	417	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.20	2.68	null	null		null	null		null	null		null	null		-1.65E-02	1.01E+00		3.72E+00	4.35E-06	Up								
Unigene11974_All	1093	0.53	0.28	0.19	7.43	2.90	3.80	7.54	1.34	3.39	-9.21E-01	3.43E-01		-1.43E+00	1.76E-01		-1.36E+00	3.36E-12	Down	-9.67E-01	1.45E-06		-2.49E+00	1.29E-27	Down	-1.15E+00	2.99E-10	Down	Unigene11974_All//gi|192910708|gb|ACF06462.1|//4.00E-92//24 kDa seed maturation protein [Elaeis guineensis]	Unigene11974_All//3.00E-76//AT5G41600| BT13 (VIRB2-INTERACTING PROTEIN 3)	Unigene11974_All//0.00E+00//ES826057			GO:0031090//GO:0043231	nr -
Unigene119742_All	477	0.22	0.00	0.00	0.21	0.07	0.19	0.53	0.35	2.84	-7.78E+00	3.74E-01		-7.78E+00	3.96E-01		-1.53E+00	5.87E-01		-1.41E-01	9.51E-01		-6.02E-01	6.48E-01		2.42E+00	4.43E-05	Up	Unigene119742_All//gi|15241393|ref|NP_199929.1|//8.00E-14//ankyrin repeat family protein [Arabidopsis thaliana] >gi|45825143|gb|AAS77479.1|At5g51160 [Arabidopsis thaliana]	Unigene119742_All//5.00E-15//AT5G51160| ankyrin repeat family protein					nr +
Unigene119743_All	405	0.52	0.00	0.00	0.25	0.51	0.56	0.73	0.52	4.33	-9.01E+00	1.22E-01		-9.01E+00	1.46E-01		1.05E+00	6.12E-01		1.18E+00	5.50E-01		-5.02E-01	6.78E-01		2.57E+00	9.62E-07	Up			Unigene119743_All//2.00E-108//gi|21098019|gb|BQ410332.1|BQ410332					
Unigene119744_All	940	0.00	0.27	0.00	0.16	0.62	0.29	0.31	0.18	1.99	8.07E+00	7.87E-02		null	null		1.97E+00	7.04E-02		8.59E-01	6.31E-01		-8.24E-01	5.40E-01		2.66E+00	2.08E-07	Up			Unigene119744_All//4.00E-62//TC146349					
Unigene11975_All	1724	40.70	15.84	16.56	71.23	55.93	69.16	90.89	32.90	60.59	-1.36E+00	7.14E-83	Down	-1.30E+00	1.87E-74	Down	-3.49E-01	9.49E-17		-4.25E-02	4.72E-01		-1.47E+00	4.16E-252	Down	-5.85E-01	1.75E-56		Unigene11975_All//gi|192910708|gb|ACF06462.1|//1.00E-102//24 kDa seed maturation protein [Elaeis guineensis]	Unigene11975_All//2.00E-95//AT2G46170| reticulon family protein (RTNLB5)	Unigene11975_All//0.00E+00//TC129939			GO:0016020//GO:0043231	nr -
Unigene119754_All	267	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.31	2.09	null	null		null	null		null	null		null	null		8.29E+00	4.02E-01		1.10E+01	3.28E-04	Up			Unigene119754_All//2.00E-27//ES851169					
Unigene119760_All	380	4.68	20.40	20.32	4.85	2.99	1.31	0.33	0.55	0.73	2.12E+00	1.53E-17	Up	2.12E+00	7.79E-17	Up	-6.98E-01	1.37E-01		-1.89E+00	2.31E-04	Down	7.20E-01	6.32E-01		1.14E+00	3.99E-01		Unigene119760_All//gi|224081248|ref|XP_002306351.1|//2.00E-10//stress enhanced protein 2 [Populus trichocarpa] >gi|222858800|gb|EEE93347.1|stress enhanced protein 2 [Populus trichocarpa]	Unigene119760_All//4.00E-09//AT2G21970| SEP2 (STRESS ENHANCED PROTEIN 2); chlorophyll binding	Unigene119760_All//4.00E-115//TC153414				nr -

Unigene11977_A11	1124	2.84	0.45	1.04	3.81	3.95	2.69	1.77	0.97	1.95	-2.66E+00	8.99E-10	Down	-1.45E+00	1.39E-04	Down	5.23E-02	8.78E-01		-5.02E-01	9.59E-02		-8.71E-01	3.39E-02		1.41E-01	7.15E-01		Unigene11977_A11//gi|15235247|ref|NP_192122.1|//5.00E-59//GATL6; polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|30679061|ref|NP_849285.1|GATL6; polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|79324977|ref|NP_001031573.1|GATL6; polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|75317781|sp|Q94253.1|GATL6_ARATH RecName: Full=Probable galacturonosyltransferase-like 6; AltName: Full=Like glycosyl transferase 10 >gi|110738563|dbj|BAF01207.1|glycosyl transferase like protein [Arabidopsis thaliana]	Unigene11977_A11//2.00E-60//AT4G02130| GATL6; polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene11977_A11//5.00E-114//gi|73851572|gb|DT460592.1|DT460592			GO:0005975//GO:0008194//GO:0031410	nr -
Unigene119770_A11	339	0.15	0.75	0.16	0.15	0.30	0.67	1.00	2.10	3.88	2.28E+00	2.34E-01		2.59E-02	9.95E-01		1.05E+00	8.09E-01		2.18E+00	3.23E-01		1.07E+00	1.67E-01		1.96E+00	5.04E-04	Up						
Unigene119775_A11	263	0.00	0.00	0.00	0.00	0.00	49.03	63.25	6.82	null	null			null	null		null	null		null	null		3.67E-01	2.84E-03		-2.85E+00	4.83E-51	Down	Unigene119775_A11//gi|224075052|ref|XP_002304537.1|//9.00E-36//cation proton exchanger [Populus trichocarpa] >gi|222841969|gb|EEE79516.1|cation proton exchanger [Populus trichocarpa]	Unigene119775_A11//3.00E-25//AT5G41610| ATCHX18; monovalent cation:proton antiporter/ sodium:hydrogen antiporter				GO:0006811//GO:0015298//GO:0031224	nr -
Unigene119776_A11	285	0.00	0.18	0.00	0.00	0.48	0.00	0.00	0.44	2.10	7.47E+00	6.18E-01		null	null		8.92E+00	3.19E-01		null	null		8.78E+00	2.41E-01		1.10E+01	1.76E-04	Up						
Unigene119777_A11	270	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.31	5.46	null	null		null	null		null	null		null	null		8.27E+00	4.02E-01		1.24E+01	1.30E-10	Up						
Unigene11978_A11	1887	10.01	6.07	5.76	13.23	14.45	5.96	6.54	1.11	2.26	-7.22E-01	1.59E-08		-7.98E-01	1.59E-09		1.28E-01	2.94E-01		-1.15E+00	6.77E-25	Down	-2.56E+00	2.81E-42	Down	-1.53E+00	1.26E-22	Down	Unigene11978_A11//gi|22331906|ref|NP_191825.2|//1.00E-170//GATL7 (Galacturonosyltransferase-like 7); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|75161472|sp|Q8VYF4.1|GATL7_ARATH RecName: Full=Probable galacturonosyltransferase-like 7	Unigene11978_A11//3.00E-168//AT3G62660| GATL7 (Galacturonosyltransferase-like 7); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene11978_A11//0.00E+00//ES791852				nr -
Unigene119784_A11	257	0.00	0.20	0.00	0.00	0.00	1.97	0.00	1.40	7.62E+00	6.18E-01			null	null		null	null		null	null		-1.09E+01	8.89E-04	Down	-5.01E-01	5.83E-01		Unigene119784_A11//gi|297807667|ref|XP_002871717.1|//6.00E-13//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317554|gb|EFH47976.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene119784_A11//2.00E-10//AT5G16420| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene119786_A11	262	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.00	2.58	null	null		null	null		null	null		7.43E+00	6.98E-01		null	null		1.13E+01	4.97E-05	Up						
Unigene119787_A11	566	0.00	0.00	0.00	0.00	0.00	0.00	73.43	105.52	12.04	null	null		null	null		null	null		null	null		5.23E-01	1.11E-17		-2.61E+00	3.20E-148	Down	Unigene119787_A11//gi|298713887|emb|CBJ33763.1|//3.00E-08//conserved unknown protein [Ectocarpus siliculosus]		Unigene119787_A11//3.00E-15//TC133518				nr +
Unigene119795_A11	480	0.00	0.00	0.00	0.00	0.00	0.56	0.00	0.26	2.49	null	null		null	null		null	null		9.14E+00	7.04E-02		8.03E+00	2.41E-01		1.13E+01	1.20E-08	Up						
Unigene1198_A11	1939	1.19	1.07	0.00	2.44	1.19	0.79	3.92	1.57	0.92	-1.48E-01	7.16E-01		-1.02E+01	1.38E-12	Down	-1.04E+00	5.90E-05	Down	-1.62E+00	2.19E-08	Down	-1.32E+00	3.62E-11	Down	-2.09E+00	2.25E-21	Down	Unigene1198_A11//gi|5669656|gb|AAD46413.1|AF096263_1//5.00E-10//ER33 protein [Solanum lycopersicum]	Unigene1198_A11//1.00E-09//AT1G05710| ethylene-responsive protein, putative	Unigene1198_A11//0.00E+00//ES801173	bHLH		GO:0001071//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene119805_A11	269	0.00	0.00	0.00	0.00	0.00	0.00	0.47	1.09	3.26	null	null		null	null		null	null		null	null		1.21E+00	3.92E-01		2.79E+00	5.37E-04	Up	Unigene119805_A11//gi|10177638|dbj|BAB10911.1|//7.00E-18//receptor protein kinase [Arabidopsis thaliana] >gi|224589711|gb|ACN59387.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene119805_A11//3.00E-19//AT5G49660| leucine-rich repeat transmembrane protein kinase, putative	Unigene119805_A11//1.00E-18//TC156741			GO:0004702//GO:0006464//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene11981_A11	981	22.03	7.59	5.75	32.65	35.07	26.56	20.56	11.03	9.06	-1.54E+00	5.00E-31	Down	-1.94E+00	4.24E-41	Down	1.03E-01	3.38E-01		-2.98E-01	1.77E-03		-8.98E-01	1.51E-15		-1.18E+00	1.03E-24	Down	Unigene11981_A11//gi|124360746|gb|ABN08723.1|//4.00E-13//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene11981_A11//3.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene11981_A11//2.00E-128//BF274628			GO:0044464	nr +
Unigene119810_A11	222	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.75	2.51	null	null		null	null		null	null		null	null		9.56E+00	1.39E-01		1.13E+01	3.28E-04	Up		Unigene119810_A11//7.00E-91//DT464646					
Unigene119819_A11	345	0.00	0.00	0.00	0.00	0.00	0.00	5.27	0.61	4.27	null	null		null	null		null	null		null	null		-3.12E+00	3.72E-08	Down	-3.03E-01	4.88E-01		Unigene119819_A11//gi|30725324|gb|AAP37684.1|//7.00E-14//At3g01680 [Arabidopsis thaliana]	Unigene119819_A11//7.00E-15//AT3G01680| unknown protein	Unigene119819_A11//2.00E-89//gi|109857958|gb|DW486937.1|DW486937				nr +
Unigene11982_A11	989	3.39	0.67	1.67	6.80	5.64	3.01	0.60	0.68	0.40	-2.35E+00	5.69E-09	Down	-1.02E+00	4.12E-03		-2.70E-01	2.69E-01		-1.17E+00	2.28E-07	Down	1.76E-01	8.15E-01		-5.71E-01	4.78E-01		Unigene11982_A11//gi|124360746|gb|ABN08723.1|//5.00E-19//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene11982_A11//4.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene11982_A11//3.00E-127//BF274628				nr +
Unigene11983_A11	795	3.95	2.68	3.88	15.41	11.57	5.34	2.66	0.95	1.00	-5.61E-01	1.13E-01		-2.35E-02	9.68E-01		-4.15E-01	7.43E-03		-1.53E+00	4.15E-19	Down	-1.49E+00	3.03E-04	Down	-1.41E+00	3.88E-04	Down	Unigene11983_A11//gi|124359510|gb|ABB28627.2|//5.00E-11//RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H [Medicago truncatula]	Unigene11983_A11//2.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene11983_A11//8.00E-26//TC144919				nr +
Unigene119830_A11	313	0.00	0.32	0.34	0.16	0.44	0.00	0.41	1.20	9.04	8.34E+00	3.88E-01		8.41E+00	4.00E-01		1.47E+00	6.19E-01		-7.31E+00	6.38E-01		1.57E+00	1.95E-01		4.48E+00	2.14E-16	Up		Unigene119830_A11//4.00E-07//EX164316					
Unigene119836_A11	429	0.24	0.00	0.00	0.00	0.16	0.00	0.00	0.78	1.21	-7.93E+00	3.74E-01		-7.93E+00	3.96E-01		7.33E+00	6.12E-01		null	null		9.61E+00	1.27E-02		1.02E+01	6.14E-04	Up	Unigene119836_A11//gi|212717123|gb|ACJ37403.1|//1.00E-11//CC-NBS-LRR class disease resistance protein [Glycine max]	Unigene119836_A11//8.00E-08//AT5G43470| RPP8 (RECOGNITION OF PERONOSPORA PARASITICA 8); nucleotide binding				GO:0003824	nr +
Unigene11984_A11	465	3.38	2.18	0.11	10.61	8.74	4.08	2.82	0.72	1.37	-6.31E-01	2.31E-01		-4.88E+00	2.04E-07	Down	-2.79E-01	3.28E-01		-1.38E+00	5.63E-07	Down	-1.97E+00	6.34E-04	Down	-1.04E+00	3.96E-02							
Unigene119843_A11	642	0.00	0.00	0.00	0.00	0.00	0.00	0.07	0.07	1.92	null	null		null	null		null	null		null	null		-1.76E-02	1.00E+00		4.87E+00	9.59E-08	Up						
Unigene11985_A11	1027	3.67	1.33	0.78	7.71	8.78	3.39	1.65	0.81	1.36	-1.46E+00	1.16E-05	Down	-2.24E+00	5.18E-09	Down	1.88E-01	3.97E-01		-1.19E+00	1.03E-08	Down	-1.02E+00	2.47E-02		-2.78E-01	5.53E-01		Unigene11985_A11//gi|124359339|gb|ABB28498.2|//4.00E-11//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene11985_A11//9.00E-06//AT3G09510| nucleic acid binding	Unigene11985_A11//3.00E-118//TC144919				nr -
Unigene119850_A11	821	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.00	2.14	null	null		null	null		null	null		null	null		-7.69E+00	1.35E-01		3.37E+00	1.42E-08	Up	Unigene119850_A11//gi|297791785|ref|XP_002863777.1|//1.00E-06//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309612|gb|EFH00036.1|kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene119850_A11//7.00E-08//AT5G42490| kinesin motor family protein				GO:0000166//GO:0003774//GO:0015630	nr +
Unigene119853_A11	726	0.72	0.14	0.07	0.21	0.28	0.12	0.58	0.52	2.36	-2.37E+00	4.76E-02		-3.30E+00	2.40E-02		4.68E-01	8.25E-01		-7.26E-01	7.16E-01		-1.69E-01	8.65E-01		2.02E+00	3.60E-05	Up	Unigene119853_A11//gi|224071533|ref|XP_002303505.1|//2.00E-69//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222840937|gb|EEE78484.1|chromatin remodeling complex subunit [Populus trichocarpa]	Unigene119853_A11//3.00E-40//AT5G44800| CHR4 (CHROMATIN REMODELING 4); ATP binding / DNA binding / chromatin binding / helicase/ nucleic acid binding / protein binding / zinc ion binding			ko00310|Lysine degradation	GO:0003676//GO:0016740//GO:0043229//GO:0044238//GO:0044260//GO:0046872	nr +
Unigene119858_A11	1487	0.28	0.37	0.07	0.40	0.49	0.52	0.28	0.34	4.85	4.13E-01	6.37E-01		-1.98E+00	1.51E-01		2.75E-01	8.01E-01		3.61E-01	6.80E-01		2.47E-01	7.84E-01		4.09E+00	1.05E-38	Up	Unigene119858_A11//gi|8778615|gb|AAF79623.1|AC027665_24//5.00E-09//F5M15.9 [Arabidopsis thaliana]	Unigene119858_A11//1.00E-06//AT1G20580| small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative	Unigene119858_A11//2.00E-24//AJ513517		ko03040|Spliceosome		nr +
Unigene119862_A11	257	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13.18	null	null		null	null		null	null		null	null		null	null		1.37E+01	3.14E-24	Up						
Unigene119863_A11	495	0.00	0.00	0.00	0.00	0.00	0.18	0.17	0.34	3.06	null	null		null	null		null	null		7.51E+00	4.78E-01		9.83E-01	6.34E-01		4.16E+00	1.21E-08	Up						
Unigene119864_A11	440	0.00	0.00	0.24	0.23	0.00	0.00	0.96	0.95	3.53	null	null		7.92E+00	4.00E-01		-7.82E+00	3.14E-01		-7.82E+00	4.02E-01		-1.66E-02	1.02E+00		1.88E+00	2.07E-04	Up						
Unigene119868_A11	542	0.39	0.28	0.00	0.37	0.38	0.00	0.31	0.23	3.45	-4.61E-01	7.58E-01		-8.59E+00	1.46E-01		5.24E-02	9.89E-01		-8.52E+00	1.34E-01		-4.32E-01	7.93E-01		3.47E+00	2.57E-09	Up	Unigene119868_A11//gi|75334109|sp|Q9FN93.1|Y5596_ARATH//2.00E-16//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At5g59680; Flags: Precursor >gi|9758834|dbj|BAB09506.1|receptor-like protein kinase [Arabidopsis thaliana] >gi|224589735|gb|ACN59399.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene119868_A11//1.00E-17//AT5G59680| leucine-rich repeat protein kinase, putative				GO:0016301	nr -
Unigene11987_A11	726	5.19	0.28	1.03	8.44	8.82	2.99	2.15	0.69	0.66	-4.22E+00	7.09E-17	Down	-2.34E+00	1.84E-09	Down	6.40E-02	8.21E-01		-1.50E+00	1.44E-09	Down	-1.64E+00	1.02E-03		-1.71E+00	4.59E-04	Down	Unigene11987_A11//gi|124359510|gb|ABB28627.2|//2.00E-10//RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H [Medicago truncatula]	Unigene11987_A11//1.00E-07//AT2G02650| reverse transcriptase-related	Unigene11987_A11//3.00E-22//TC144919				nr -
Unigene119870_A11	476	0.00	0.11	0.00	0.00	0.14	0.00	1.07	1.05	3.60	6.73E+00	6.18E-01		null	null		7.18E+00	6.12E-01		null	null		-1.66E-02	1.02E+00		1.76E+00	1.93E-04	Up		Unigene119870_A11//3.00E-36//TC140792					
Unigene119873_A11	397	0.00	0.26	0.00	0.00	0.09	0.23	0.32	0.32	2.91	8.00E+00	3.88E-01		null	null		6.44E+00	8.32E-01		7.83E+00	4.78E-01		-1.68E-02	1.02E+00		3.19E+00	1.26E-05	Up		Unigene119873_A11//1.00E-78//ES802395					ESTscan +
Unigene11988_A11	454	0.23	2.46	0.70	0.88	2.50	1.19	3.17	3.68	6.23	3.41E+00	1.24E-04	Up	1.61E+00	3.05E-01		1.51E+00	2.36E-02		4.44E-01	6.78E-01		2.18E-01	6.32E-01		9.77E-01	2.66E-03		Unigene11988_A11//gi|44681378|gb|AS47629.1|//6.00E-08//At1g26580 [Arabidopsis thaliana] >gi|45773908|gb|AAS76758.1|At1g26580 [Arabidopsis thaliana]	Unigene11988_A11//4.00E-09//AT1G26580| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: myb family transcription factor / ELM2 domain-containing protein (TAIR:AT2G03470.1); Has 82 Blast hits to 82 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 78; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene11988_A11//1.00E-44//DR462874				nr +

Unigene119880_All	294	0.00	0.00	0.00	0.00	0.00	0.58	0.00	5.69	null	null		null	null		null	null		null	null		-9.17E+00	1.35E-01		3.31E+00	4.37E-08	Up	Unigene119880_All//gi|62548111|gb|AAX86687.1|//7.00E-12//non-symbiotic hemoglobin protein [Gossypium hirsutum]	Unigene119880_All//3.00E-10//AT2G16060| AHB1 (ARABIDOPSIS HEMOGLOBIN 1); oxygen binding / oxygen transporter	Unigene119880_All//3.00E-47//gi|31406938|gb|CD485973.1|CD485973			GO:0005506//GO:0015669//GO:0034399//GO:0050896	nr -
Unigene119890_All	354	0.00	0.00	0.00	0.00	0.00	0.13	0.72	0.00	5.96	null	null		null	null		null	null		7.00E+00	6.98E-01		-9.49E+00	4.04E-02		3.06E+00	2.16E-09	Up	Unigene119890_All//gi|3970689|emb|CAA77191.1|//1.00E-15//(+)-delta-cadinene synthase [Gossypium arboreum]		Unigene119890_All//7.00E-52//TC129577		ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0010334//GO:0046872	nr +
Unigene119895_All	384	0.00	0.00	0.00	0.00	0.09	0.12	0.11	0.98	2.18	null	null		null	null		6.49E+00	8.32E-01		6.88E+00	6.98E-01		3.15E+00	3.41E-02		4.31E+00	4.11E-05	Up	Unigene119895_All//gi|79507164|ref|NP_196165.3|//4.00E-13//hydrolase, acting on glycosyl bonds / mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase [Arabidopsis thaliana]	Unigene119895_All//2.00E-14//AT5G05460| hydrolase, acting on glycosyl bonds / mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase	Unigene119895_All//3.00E-45//AT3G10715			GO:0004553//GO:0044424	nr +
Unigene119897_All	571	0.00	2.04	0.00	0.26	0.90	0.79	0.37	1.90	7.67	1.10E+01	1.05E-06	Up	null	null		1.79E+00	1.26E-01		1.60E+00	2.05E-01		2.36E+00	5.23E-04	Up	4.37E+00	8.92E-25	Up	Unigene119897_All//gi|115443853|ref|NP_001045706.1|//4.00E-09//Os02g0120100 [Oryza sativa Japonica Group] >gi|113535237|dbj|BAF07620.1|Os02g0120100 [Oryza sativa Japonica Group]	Unigene119897_All//9.00E-10//AT4G38470| protein kinase family protein	Unigene119897_All//7.00E-41//TC130901			GO:0004672//GO:0006464//GO:0031406//GO:0032559	nr -
Unigene1199_All	958	12.12	7.67	3.22	18.72	11.65	9.71	40.03	16.75	11.69	-6.61E-01	6.94E-05		-1.91E+00	6.62E-22	Down	-6.85E-01	1.07E-08		-9.47E-01	2.83E-13		-1.26E+00	2.73E-49	Down	-1.78E+00	2.73E-84	Down	Unigene1199_All//gi|222424490|dbj|BAH20200.1|//5.00E-43//AT1G05710 [Arabidopsis thaliana]	Unigene1199_All//3.00E-44//AT1G05710| ethylene-responsive protein, putative	Unigene1199_All//0.00E+00//TC177923	bHLH		GO:0001071//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene119904_All	354	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.71	2.70	null	null		null	null		null	null		null	null		1.57E+00	3.26E-01		3.50E+00	4.29E-05	Up									ESTscan -
Unigene119905_All	397	0.00	0.00	0.00	0.13	0.17	0.00	0.11	0.84	1.91	null	null		null	null		4.67E-01	9.59E-01		-6.97E+00	6.38E-01		2.98E+00	5.74E-02		4.16E+00	1.34E-04	Up	Unigene119905_All//gi|24461866|gb|AAN62353.1|AF506028_20//1.00E-42//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene119905_All//6.00E-33//AT1G12280| disease resistance protein (CC-NBS-LRR class), putative	Unigene119905_All//3.00E-11//TC176855		ko04626|Plant-pathogen interaction	GO:0000166//GO:0016787	nr +
Unigene119909_All	332	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.56	null	null		null	null		null	null		null	null		null	null		1.06E+01	6.14E-04	Up	Unigene119909_All//gi|158828152|gb|ABW81031.1|//9.00E-23//LTRGag-pol-polymerase 3 [Arabidopsis lyrata subsp. lyrata]	Unigene119909_All//3.00E-20//ATMG00810| hypothetical protein				GO:0005488//GO:0009987	nr -
Unigene11991_All	1023	0.10	0.15	0.10	1.22	0.77	2.87	0.99	5.15	1.52	5.39E-01	7.79E-01		2.52E-02	1.00E+00		-6.53E-01	2.80E-01		1.24E+00	8.60E-04	Up	2.38E+00	6.93E-17	Up	6.15E-01	1.85E-01		Unigene11991_All//gi|253684301|gb|ACT33369.1|//6.00E-40//mago nashi [Lycoris radiata]	Unigene11991_All//3.00E-47//AT1G02140| MAGO (MAGO NASHI); protein binding	Unigene11991_All//6.00E-135//CO087742		ko03040|Spliceosome	GO:0003006//GO:0043231	nr +
Unigene119912_All	246	0.00	4.94	0.00	0.00	0.00	0.00	0.00	0.00	0.16	1.23E+01	5.48E-07	Up	null	null		null	null		null	null		null	null		7.34E+00	6.46E-01		Unigene119912_All//gi|167387|gb|AAA92730.1|//4.00E-25//storage protein [Gossypium hirsutum]		Unigene119912_All//1.00E-15//TC165354			GO:0007275	nr -
Unigene119916_All	472	0.00	0.00	0.00	0.00	0.00	0.00	1.25	0.53	4.64	null	null		null	null		null	null		null	null		-1.24E+00	1.54E-01		1.89E+00	6.22E-06	Up			Unigene119916_All//3.00E-141//DW513887					
Unigene119922_All	386	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.27	null	null		null	null		null	null		null	null		null	null		1.11E+01	2.05E-06	Up	Unigene119922_All//gi|227438239|gb|ACP30609.1|//6.00E-12//disease resistance protein [Brassica rapa subsp. pekinensis]					GO:0003676//GO:0004175//GO:0006260//GO:0006325//GO:0019538//GO:0034061//GO:0044464	nr +
Unigene119923_All	1005	0.00	0.00	0.05	0.00	0.14	0.31	0.08	0.08	8.48	null	null		5.73E+00	6.38E-01		7.10E+00	3.19E-01		8.30E+00	4.08E-02		-1.55E-02	1.01E+00		6.66E+00	2.22E-57	Up	Unigene119923_All//gi|224133962|ref|XP_002327722.1|//1.00E-12//predicted protein [Populus trichocarpa] >gi|222836807|gb|EEE75200.1|predicted protein [Populus trichocarpa]		Unigene119923_All//3.00E-10//DR454610				nr +
Unigene119926_All	327	0.00	0.00	0.00	0.46	0.21	1.52	1.55	6.26	9.99	null	null		null	null		-1.12E+00	5.84E-01		1.73E+00	1.43E-01		2.01E+00	7.69E-06	Up	2.69E+00	1.66E-12	Up	Unigene119926_All//gi|34419961|gb|AAQ67366.1|//3.00E-36//PO09 precursor [Gossypium hirsutum]	Unigene119926_All//1.00E-22//AT5G64100| peroxidase, putative	Unigene119926_All//1.00E-118//TC134559		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209	nr -
Unigene119929_All	465	0.00	0.00	0.00	0.00	0.00	0.00	0.55	0.99	5.65	null	null		null	null		null	null		null	null		8.58E-01	3.96E-01		3.37E+00	1.52E-12	Up	Unigene119929_All//gi|253760977|ref|XP_002489033.1|//3.00E-08//hypothetical protein SORBIDRAFT_03S1s002020 [Sorghum bicolor] >gi|241947330|gb|EES20475.1|hypothetical protein SORBIDRAFT_03S1s002020 [Sorghum bicolor]		Unigene119929_All//7.00E-25//TC148521				nr +
Unigene119937_All	457	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.39	null	null			null	null		null	null		null	null		null	null		1.04E+01	9.34E-05	Up	Unigene119937_All//gi|297804542|ref|XP_002870155.1|//1.00E-24//ATINT4 [Arabidopsis lyrata subsp. lyrata] >gi|297315991|gb|EFH46414.1|ATINT4 [Arabidopsis lyrata subsp. lyrata]	Unigene119937_All//1.00E-25//AT4G16480| INT4 (INOSITOL TRANSPORTER 4); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen symporter				GO:0005365//GO:0006810//GO:0031224	nr -
Unigene119942_All	306	0.00	0.00	0.00	0.00	0.00	0.30	0.00	0.00	2.08	null	null		null	null		null	null		8.21E+00	4.78E-01		null	null		1.10E+01	9.34E-05	Up									
Unigene119943_All	545	0.00	0.00	0.00	0.00	0.00	0.08	0.93	1.53	3.44	null	null		null	null		null	null		6.37E+00	6.98E-01		7.20E-01	3.10E-01		1.88E+00	3.59E-05	Up			Unigene119943_All//1.00E-23//TC162327					
Unigene119949_All	282	0.19	0.00	0.76	0.00	0.00	0.48	0.00	0.00	2.12	-7.54E+00	6.13E-01		2.03E+00	3.62E-01		null	null		8.91E+00	3.11E-01		null	null		1.10E+01	1.73E-04	Up			Unigene119949_All//4.00E-62//ES841268					
Unigene119954_All	669	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.00	2.02	null	null		null	null		null	null		null	null		-6.98E+00	4.05E-01		4.00E+00	1.31E-07	Up			Unigene119954_All//2.00E-10//DT468594					
Unigene119960_All	453	0.00	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.93	9.39E+00	4.44E-02		null	null		null	null		null	null		null	null		1.09E+01	2.05E-06	Up	Unigene119960_All//gi|46394306|tpg|DAA05091.1|//9.00E-17//TPA: TPA, inf: WRKY transcription factor 26 [Oryza sativa (japonica cultivar-group)]		Unigene119960_All//1.00E-07//TC174768		ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0010468//GO:0043231	nr -
Unigene119964_All	262	0.00	0.39	0.00	0.38	0.00	0.00	0.32	0.48	3.04	8.60E+00	3.88E-01		null	null		-8.57E+00	3.14E-01		-8.57E+00	4.02E-01		5.69E-01	7.83E-01		3.24E+00	3.96E-04	Up			Unigene119964_All//2.00E-66//ES834328					
Unigene11997_All	1769	3.14	4.18	0.99	2.34	2.69	1.89	3.87	2.53	3.42	4.16E-01	5.71E-02		-1.66E+00	6.02E-09	Down	2.01E-01	5.52E-01		-3.07E-01	3.55E-01		-6.15E-01	2.05E-03		-1.78E-01	4.00E-01		Unigene11997_All//gi|115456073|ref|NP_001051637.1|//1.00E-112//Os03g0806700 [Oryza sativa Japonica Group] >gi|108711652|gb|ABF99447.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550108|dbj|BAF13551.1|Os03g0806700 [Oryza sativa Japonica Group]	Unigene11997_All//2.00E-94//AT5G28150| unknown protein	Unigene11997_All//0.00E+00//gi|54120281|gb|CO495790.1|CO495790				nr +
Unigene119990_All	328	29.19	38.93	13.31	28.40	19.63	26.30	23.46	35.81	23.08	4.15E-01	9.17E-03		-1.13E+00	1.05E-08	Down	-5.33E-01	2.66E-03		-1.11E-01	6.08E-01		6.10E-01	3.39E-05		-2.37E-02	9.23E-01				Unigene119990_All//0.00E+00//TC167919					
Unigene120_All	645	3.73	2.36	2.89	4.02	5.45	10.78	8.46	11.21	13.77	-6.63E-01	1.06E-01		-3.69E-01	4.00E-01		4.39E-01	2.05E-01		1.43E+00	7.19E-10	Up	4.07E-01	4.02E-02		7.04E-01	2.98E-05		Unigene120_All//gi|60327635|gb|AAX19057.1|//3.00E-92//class III HD-Zip protein 8 [Populus trichocarpa]	Unigene120_All//1.00E-67//AT1G30490| PHV (PHAVOLUTA); DNA binding / protein binding / transcription factor	Unigene120_All//0.00E+00//TC178623	HB			nr +
Unigene120004_All	281	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.45	2.13	null	null		null	null		null	null		null	null		8.80E+00	2.41E-01		1.11E+01	1.75E-04	Up									ESTscan +
Unigene120006_All	547	0.19	0.19	0.39	0.36	0.38	0.66	0.08	0.23	1.46	-4.60E-02	9.90E-01		1.03E+00	5.92E-01		5.21E-02	9.89E-01		8.58E-01	5.42E-01		1.57E+00	5.45E-01		4.24E+00	7.42E-05	Up	Unigene120006_All//gi|30678519|ref|NP_188875.2|//2.00E-41//BIG (BIG); binding / ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana]	Unigene120006_All//2.00E-34//AT3G02260| BIG (BIG); binding / ubiquitin-protein ligase/ zinc ion binding	Unigene120006_All//0.00E+00//TC160407			GO:0003676//GO:0006260//GO:0019787//GO:0034061//GO:0046914	nr +
Unigene120024_All	399	0.00	0.00	0.00	0.00	0.00	0.00	0.74	1.05	3.69	null	null		null	null		null	null		null	null		4.98E-01	6.33E-01		2.32E+00	3.06E-05	Up	Unigene120024_All//gi|255586944|ref|XP_002534072.1|//2.00E-39//ER glycerol-phosphate acyltransferase [Ricinus communis] >gi|223525899|gb|EEF28316.1|ER glycerol-phosphate acyltransferase [Ricinus communis]	Unigene120024_All//2.00E-24//AT1G06520| GPAT1 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 1); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase			ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0003006//GO:0016411//GO:0043231	nr +
Unigene120044_All	321	0.33	0.00	0.00	0.16	0.43	0.84	0.26	0.13	2.36	-8.35E+00	3.74E-01		-8.35E+00	3.96E-01		1.47E+00	6.19E-01		2.44E+00	2.22E-01		-1.02E+00	7.25E-01		3.16E+00	6.83E-04	Up	Unigene120044_All//gi|10177699|dbj|BAB11025.1|//8.00E-35//pattern formation protein [Arabidopsis thaliana]	Unigene120044_All//3.00E-36//AT5G39500| pattern formation protein, putative	Unigene120044_All//1.00E-13//gi|78335598|gb|DT555872.1|DT555872				nr -
Unigene120047_All	484	0.76	0.00	0.44	0.72	1.07	0.75	0.17	0.52	2.39	-9.56E+00	1.97E-02		-7.82E-01	5.53E-01		5.67E-01	6.04E-01		5.11E-02	9.69E-01		1.57E+00	3.26E-01		3.77E+00	2.44E-06	Up	Unigene120047_All//gi|255568760|ref|XP_002525351.1|//9.00E-08//glutaredoxin, grx, putative [Ricinus communis] >gi|223535314|gb|EEF36989.1|glutaredoxin, grx, putative [Ricinus communis]	Unigene120047_All//2.00E-06//AT4G28730| glutaredoxin family protein	Unigene120047_All//1.00E-35//ES834524				nr +
Unigene120049_All	332	0.00	0.15	0.00	0.15	0.10	0.00	0.38	1.01	5.28	7.25E+00	6.18E-01		null	null		-5.33E-01	8.26E-01		-7.23E+00	6.38E-01		1.40E+00	2.76E-01		3.79E+00	2.44E-09	Up									
Unigene120050_All	1248	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.78	null	null		null	null		null	null		null	null		null	null		1.14E+01	8.44E-25	Up	Unigene120050_All//gi|15221080|ref|NP_175246.1|//2.00E-24//calcineurin-like phosphoesterase family protein [Arabidopsis thaliana]	Unigene120050_All//5.00E-25//AT1G48120| calcineurin-like phosphoesterase family protein	Unigene120050_All//2.00E-42//gi|78334205|gb|DT554479.1|DT554479				nr +
Unigene120052_All	559	3.28	0.36	0.76	5.53	3.02	4.36	0.76	0.22	0.14	-3.18E+00	6.73E-07	Down	-2.10E+00	2.07E-04	Down	-8.72E-01	8.98E-03		-3.41E-01	3.89E-01		-1.75E+00	1.24E-01		-2.41E+00	3.94E-02		Unigene120052_All//gi|116268422|gb|ABJ96379.1|//5.00E-71//expressed protein [Prunus persica]	Unigene120052_All//5.00E-70//AT4G24530| unknown protein	Unigene120052_All//4.00E-141//TC135004				nr -
Unigene120056_All	360	0.00	0.42	0.00	0.00	0.38	0.25	0.12	0.70	1.88	8.72E+00	2.36E-01		null	null		8.58E+00	3.19E-01		7.97E+00	4.78E-01		2.57E+00	1.53E-01		4.00E+00	4.30E-04	Up	Unigene120056_All//gi|224096333|ref|XP_002310605.1|//7.00E-17//cytochrome P450 [Populus trichocarpa] >gi|222853508|gb|EEE91055.1|cytochrome P450 [Populus trichocarpa]	Unigene120056_All//2.00E-14//AT1G34540| CYP94D1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene120056_All//9.00E-101//ES842907		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene120062_All	454	0.00	0.00	0.00	0.00	0.00	0.00	0.37	0.92	19.04	null	null		null	null		null	null		null	null		1.31E+00	2.35E-01		5.68E+00	2.92E-55	Up									
Unigene120063_All	626	0.33	0.65	0.17	0.00	0.00	0.07	0.68	0.27	6.55	9.54E-01	4.14E-01		-9.75E-01	6.21E-01		null	null		6.17E+00	6.98E-01		-1.34E+00	2.24E-01		3.28E+00	9.40E-19	Up									ESTscan -
Unigene120068_All	287	0.00	0.00	0.00	0.00	0.00	0.79	0.00	0.87	2.22	null	null		null	null		null	null		9.62E+00	1.19E-01		9.77E+00	4.31E-02		1.11E+01	9.34E-05	Up	Unigene120068_All//gi|283135872|gb|ADB11327.1|//4.00E-10//tau class glutathione transferase GSTU45 [Populus trichocarpa]						nr -
Unigene120072_All	302	0.00	0.00	0.00	0.00	0.00	0.75	0.14	0.55	6.46	null	null		null	null		null	null		9.55E+00	1.19E-01		1.98E+00	3.79E-01		5.53E+00	1.26E-12	Up	Unigene120072_All//gi|300793630|tpg|DAA33874.1|//8.00E-43//TPA: TPA, inf: aquaporin NIP1;1 [Gossypium hirsutum]	Unigene120072_All//3.00E-39//AT4G18910| NIP1;2 (NOD26-LIKE INTRINSIC PROTEIN 1;2); arsenite transmembrane transporter/ water channel	Unigene120072_All//8.00E-36//gi|164295610|gb|ES813875.1|ES813875				nr -
Unigene120088_All	1597	0.00	0.00	0.07	0.12	0.00	0.17	0.79	0.26	15.12	null	null		6.06E+00	4.00E-01		-6.96E+00	8.45E-02		4.43E-01	7.64E-01		-1.60E+00	4.42E-03		4.25E+00	8.48E-132	Up	Unigene120088_All//gi|224103053|ref|XP_002312905.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222849313|gb|EEE86860.1|cytochrome P450 [Populus trichocarpa]	Unigene120088_All//9.00E-171//AT2G27690| CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene120088_All//0.00E+00//gi|78347798|gb|DT568072.1|DT568072		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene120089_All	1201	0.44	1.43	0.71	0.87	0.72	0.64	0.46	0.59	3.65	1.72E+00	1.41E-03		7.04E-01	3.83E-01		-2.81E-01	6.74E-01		-4.46E-01	5.32E-01		3.70E-01	6.67E-01		2.99E+00	2.10E-18	Up	Unigene120089_All//gi|75323193|sp|Q6D7E4.1|Y1609_ARATH//8.00E-26//RecName: Full=Uncharacterized protein At1g26090, chloroplastic; Flags: Precursor	Unigene120089_All//1.00E-18//AT1G26090| unknown protein	Unigene120089_All//2.00E-110//gi|109858164|gb|DW487143.1|DW487143				nr -
Unigene12009_All	1126	19.10	9.27	11.78	77.38	62.57	52.94	39.54	35.26	37.01	-1.04E+00	3.26E-17	Down	-6.98E-01	1.19E-08		-3.06E-01	1.64E-09		-5.47E-01	3.23E-24		-1.65E-01	2.96E-02		-9.54E-02	2.27E-01		Unigene12009_All//gi|297850988|ref|XP_002893375.1|//1.00E-166//dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339217|gb|EFH69634.1|dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12009_All//3.00E-162//AT1G26850| dehydration-responsive family protein	Unigene12009_All//0.00E+00//TC141204				nr -

Unigene120090_All	649	0.00	0.00	0.00	0.00	0.00	0.00	0.59	0.64	3.99	null	null		null	null		null	null		null	null		1.35E-01	8.99E-01		2.77E+00	2.35E-10	Up		Unigene120090_All//2.00E-06//AT3G52990| pyruvate kinase, putative	Unigene120090_All//1.00E-30//gi|73863724|gb|DT466463.1|DT466463		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		kegg +
Unigene120096_All	299	8.05	6.78	7.48	14.49	13.01	5.44	1.41	0.70	1.60	-2.48E-01	5.63E-01		-1.06E-01	7.97E-01		-1.55E-01	6.16E-01		-1.41E+00	1.98E-06	Down	-1.02E+00	3.51E-01		1.77E-01	8.46E-01				Unigene120096_All//2.00E-70//ES794127				
Unigene120100_All	397	0.00	0.38	0.00	0.00	0.00	0.00	0.00	0.11	1.61	8.58E+00	2.36E-01		null	null		null	null		null	null		6.72E+00	6.36E-01		1.06E+01	9.34E-05	Up								
Unigene120105_All	449	0.12	0.23	0.36	0.11	0.08	0.00	0.09	1.30	2.13	9.54E-01	7.27E-01		1.61E+00	5.11E-01		-5.32E-01	8.26E-01		-6.79E+00	6.38E-01		3.79E+00	2.07E-03		4.50E+00	6.81E-06	Up			Unigene120105_All//3.00E-08//TC169966				
Unigene120113_All	290	0.18	0.00	0.00	0.34	0.36	0.62	0.44	0.43	5.36	-7.50E+00	6.13E-01		-7.50E+00	6.27E-01		5.24E-02	9.67E-01		8.59E-01	6.96E-01		-1.66E-02	1.02E+00		3.61E+00	4.47E-08	Up			Unigene120113_All//3.00E-07//ES847501				
Unigene120116_All	429	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.30	null	null		null	null		null	null		null	null		null	null		1.03E+01	3.28E-04	Up		Unigene120116_All//gi|18398467|ref|NP_565420.1|//4.00E-17//undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein [Arabidopsis thaliana] >gi|84029498|sp|Q8S2T1.2|DDPS6_ARATH RecName: Full=Dehydrodolichyl diphosphate synthase 6; Short=Dedol-PP synthase 6 >gi|20198261|gb|AAD32914.2| expressed protein [Arabidopsis thaliana]	Unigene120116_All//2.00E-18//AT2G17570| undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene120121_All	401	0.26	0.00	0.00	0.12	0.00	0.00	0.32	1.67	2.29	-8.03E+00	3.74E-01		-8.03E+00	3.96E-01		-6.96E+00	5.58E-01		-6.96E+00	6.38E-01		2.40E+00	9.04E-03		2.85E+00	3.18E-04	Up							
Unigene120127_All	322	0.00	7.08	0.33	0.93	0.64	0.14	0.13	1.17	3.84	1.28E+01	5.64E-13	Up	8.37E+00	4.00E-01		-5.33E-01	6.79E-01		-2.73E+00	1.37E-01		3.15E+00	3.41E-02		4.87E+00	9.59E-08	Up		Unigene120127_All//gi|15217543|ref|NP_177315.1|//3.00E-12//ATCK1 (CHOLINE KINASE 1); choline kinase [Arabidopsis thaliana] >gi|30725296|gb|AAP37670.1| At1g71697 [Arabidopsis thaliana] >gi|110739418|dbj|BAF01619.1| choline kinase like protein [Arabidopsis thaliana] >gi|110741310|dbj|BAF02205.1| choline kinase like protein [Arabidopsis thaliana]	Unigene120127_All//2.00E-13//AT1G71697| ATCK1 (CHOLINE KINASE 1); choline kinase	Unigene120127_All//6.00E-86//CO091031		ko00564|Glycerophospholipid metabolism		nr +
Unigene12013_All	3036	23.04	18.66	19.52	35.31	32.85	38.92	51.19	25.28	15.04	-3.04E-01	1.09E-06		-2.39E-01	2.66E-04		-1.04E-01	4.78E-02		1.40E-01	4.19E-03		-1.02E+00	5.16E-141	Down	-1.77E+00	0.00E+00	Down		Unigene12013_All//gi|15237538|ref|NP_201189.1|//0.00E+00//RSW3 (RADIAL SWELLING 3); glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|10177672|dbj|BAB11032.1| glucosidase II alpha subunit [Arabidopsis thaliana]	Unigene12013_All//2.00E-00//AT5G63810| RSW3 (RADIAL SWELLING 3); glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene12013_All//0.00E+00//TC174705		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0000902//GO:0004558//GO:0005488//GO:0006952//GO:0009250//GO:0009536//GO:0010038	nr -
Unigene120132_All	226	0.00	0.22	0.00	0.00	0.61	0.40	0.37	1.66	6.52	7.81E+00	6.18E-01		null	null		9.25E+00	3.19E-01		8.64E+00	4.78E-01		2.15E+00	9.45E-02		4.12E+00	2.19E-08	Up							
Unigene120134_All	523	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.72	2.36	null	null		null	null		null	null		null	null		1.57E+00	1.95E-01		3.28E+00	4.18E-06	Up								
Unigene120136_All	422	0.25	0.00	0.25	0.12	0.49	0.54	0.40	0.50	2.27	-7.95E+00	3.74E-01		2.54E-02	1.00E+00		2.05E+00	3.95E-01		2.18E+00	3.23E-01		3.05E-01	8.36E-01		2.50E+00	6.42E-04	Up		Unigene120136_All//gi|115453383|ref|NP_001050292.1|//2.00E-19//Os03g0395300 [Oryza sativa Japonica Group] >gi|14029007|gb|AAK52548.1|AC07985 3.1 Putative myosin heavy chain-like [Oryza sativa Japonica Group] >gi|113548763|dbj|BAF12206.1| Os03g0395300 [Oryza sativa Japonica Group]	Unigene120136_All//1.00E-28//AT3G26570| unknown protein	Unigene120136_All//0.00E+00//TC130798			nr +
Unigene12014_All	4096	3.51	2.21	1.83	10.23	10.48	9.26	10.92	2.91	3.84	-6.66E-01	6.51E-06		-9.38E-01	1.52E-09		3.45E-02	7.69E-01		-1.43E-01	1.19E-01		-1.91E+00	3.76E-105	Down	-1.51E+00	1.16E-77	Down		Unigene12014_All//gi|115448815|ref|NP_001048187.1|//0.00E+00//Os02g0760200 [Oryza sativa Japonica Group] >gi|113537718|dbj|BAF10101.1| Os02g0760200 [Oryza sativa Japonica Group]	Unigene12014_All//0.00E+00//AT4G24610| unknown protein	Unigene12014_All//0.00E+00//TC131435			GO:0005488//GO:0009987//GO:0016020	nr +
Unigene120143_All	278	0.00	0.55	0.00	0.00	0.00	0.00	0.15	0.00	3.01	9.09E+00	2.36E-01		null	null		null	null		null	null		-7.25E+00	6.59E-01		4.31E+00	4.11E-05	Up								
Unigene120149_All	574	0.00	0.00	0.00	0.17	0.06	0.00	0.00	0.07	2.92	null	null		null	null		-1.53E+00	5.87E-01		-7.44E+00	4.02E-01		6.19E+00	6.36E-01		1.15E+01	5.04E-12	Up		Unigene120149_All//gi|9759309|dbj|BAB09815.1|//1.00E-07//non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]						nr -
Unigene12015_All	2127	0.39	0.45	0.10	2.58	2.01	1.34	1.95	0.63	0.69	2.02E-01	7.54E-01		-1.98E+00	2.71E-02		-3.60E-01	1.64E-01		-9.46E-01	1.63E-04		-1.63E+00	1.57E-08	Down	-1.49E+00	7.29E-08	Down		Unigene12015_All//gi|115448815|ref|NP_001048187.1|//0.00E+00//Os02g0760200 [Oryza sativa Japonica Group] >gi|113537718|dbj|BAF10101.1| Os02g0760200 [Oryza sativa Japonica Group]	Unigene12015_All//0.00E+00//AT4G24610| unknown protein	Unigene12015_All//0.00E+00//TC161341			GO:0005488//GO:0009987//GO:0016020	nr -
Unigene120151_All	802	0.00	0.13	0.00	0.00	0.09	0.00	0.05	0.26	1.04	6.98E+00	3.88E-01		null	null		6.42E+00	6.12E-01		null	null		2.31E+00	2.40E-01		4.31E+00	4.11E-05	Up			Unigene120151_All//3.00E-102//DR456158				
Unigene120158_All	586	0.00	0.69	0.00	0.26	0.88	0.08	0.58	0.64	2.58	9.43E+00	1.38E-02		null	null		1.79E+00	1.26E-01		-1.73E+00	5.01E-01		1.53E-01	8.90E-01		2.16E+00	5.30E-05	Up			Unigene120158_All//3.00E-86//DR459948				
Unigene12016_All	1007	31.38	80.16	38.66	31.31	77.21	110.82	12.01	29.43	33.15	1.35E+00	6.82E-94	Up	3.01E-01	8.01E-04		1.30E+00	4.65E-101	Up	1.82E+00	7.09E-215	Up	1.29E+00	6.52E-40	Up	1.47E+00	2.88E-55	Up		Unigene12016_All//gi|6573770|gb|AAF17690.1|AC009243_17//1.00E-39//F28K19.28 [Arabidopsis thaliana]	Unigene12016_All//2.00E-32//AT1G78070| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: CUL4 RING ubiquitin ligase complex; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), WD40 repeat, region (InterPro:IPR017986), WD40/YVTN repeat-like (InterPro:IPR015943), WD40 repeat (InterPro:IPR001680); BEST Arabidopsis thaliana protein match is: WD-40 repeat family protein (TAIR:AT1G36070.1); Has 110 Blast hits to 110 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 28; Plants - 80; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene12016_All//0.00E+00//CO123858			GO:0031461	nr -
Unigene120161_All	781	0.00	0.00	0.20	0.06	0.22	0.17	0.27	0.80	4.28	null	null		7.68E+00	2.39E-01		1.79E+00	5.21E-01		1.44E+00	6.39E-01		1.57E+00	7.10E-02		3.98E+00	6.32E-18	Up		Unigene120161_All//gi|225467800|ref|XP_002267844.1|//9.00E-14//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene120161_All//4.00E-05//AT5G65020| ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding	Unigene120161_All//9.00E-07//DT047533				nr +
Unigene12017_All	1703	3.13	7.44	6.13	4.56	9.79	12.81	3.72	5.60	7.88	1.25E+00	1.32E-13	Up	9.68E-01	1.83E-07		1.10E+00	7.38E-17	Up	1.49E+00	8.54E-32	Up	5.88E-01	3.86E-04		1.08E+00	1.61E-14	Up		Unigene12017_All//gi|13937195|gb|AK50091.1|AF372951_1//2.00E-09//At1g78070/F28K19_28 [Arabidopsis thaliana] >gi|25090156|gb|ACN72242.1| At1g78070/F28K19_28 [Arabidopsis thaliana]	Unigene12017_All//2.00E-10//AT1G78070| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: CUL4 RING ubiquitin ligase complex; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), WD40 repeat, region (InterPro:IPR017986), WD40/YVTN repeat-like (InterPro:IPR015943), WD40 repeat (InterPro:IPR001680); BEST Arabidopsis thaliana protein match is: WD-40 repeat family protein (TAIR:AT1G36070.1); Has 110 Blast hits to 110 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 28; Plants - 80; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene12017_All//1.00E-103//TC158761			GO:0031461	nr -
Unigene120170_All	218	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.38	2.74	null	null		null	null		null	null		null	null		8.58E+00	4.02E-01		1.14E+01	1.75E-04	Up								
Unigene120185_All	295	0.00	0.69	0.00	0.00	0.00	0.31	2.29	1.84	6.35	9.42E+00	1.37E-01		null	null		null	null		8.26E+00	4.78E-01		-3.16E-01	6.74E-01		1.47E+00	6.61E-04	Up			Unigene120185_All//3.00E-38//ES791384				
Unigene120189_All	555	0.00	0.00	0.00	0.09	0.00	0.00	0.00	0.00	3.95	null	null		null	null		-6.49E+00	5.57E-01		-6.49E+00	6.38E-01		null	null		1.19E+01	1.06E-15	Up		Unigene120189_All//gi|224147195|ref|XP_002336426.1|//7.00E-30//cc-nbs resistance protein [Populus trichocarpa] >gi|222834979|gb|EEE73428.1| cc-nbs resistance protein [Populus trichocarpa]	Unigene120189_All//4.00E-08//AT4G26090| RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene120190_All	231	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	3.62	null	null		null	null		null	null		null	null		7.50E+00	6.36E-01		1.18E+01	3.89E-06	Up								
Unigene120195_All	368	0.00	0.14	0.00	0.00	0.00	0.49	0.92	0.91	4.44	7.11E+00	6.18E-01		null	null		null	null		8.94E+00	1.95E-01		-1.66E-02	1.02E+00		2.27E+00	1.29E-05	Up								
Unigene120198_All	260	0.20	0.00	0.00	0.19	0.26	0.00	0.00	0.00	2.76	-7.65E+00	6.14E-01		-7.65E+00	6.27E-01		4.67E-01	9.59E-01		-7.58E+00	6.38E-01		null	null		1.14E+01	2.63E-05	Up			Unigene120198_All//3.00E-07//ES795077				
Unigene120200_All	301	0.35	0.34	0.00	0.33	0.23	0.00	0.00	1.11	2.25	-4.60E-02	9.90E-01		-8.44E+00	3.96E-01		-5.33E-01	8.17E-01		-8.37E+00	4.02E-01		1.01E-01	1.27E-02		1.11E+01	4.97E-05	Up								
Unigene120201_All	468	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.09	2.30	null	null		null	null		null	null		null	null		6.48E+00	6.36E-01		1.12E+01	8.30E-08	Up		Unigene120201_All//gi|22550336|ref|NP_689386.1|//6.00E-29//cytochrome c oxidase subunit 1 [Chaetosphaeridium globosum] >gi|22417002|gb|AAM96601.1|AF494279_6 cytochrome c oxidase subunit 1 [Chaetosphaeridium globosum]	Unigene120201_All//5.00E-26//ATMG01360| cytochrome c oxidase subunit 1		ko00190|Oxidative phosphorylation		nr +
Unigene120208_All	378	0.00	0.00	0.00	0.53	0.18	0.96	0.56	0.22	4.64	null	null		null	null		-1.53E+00	4.16E-01		8.59E-01	5.42E-01		-1.34E+00	4.30E-01		3.05E+00	6.73E-08	Up								
Unigene120209_All	258	0.00	0.00	0.00	0.00	0.00	1.40	0.00	2.27	2.16	null	null		null	null		null	null		1.05E+01	2.37E-02		1.11E+01	2.81E-04	Up	1.11E+01	3.28E-04	Up		Unigene120209_All//gi|297826743|ref|XP_002881254.1|//3.00E-09//PAZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327093|gb|EFH57513.1| PAZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene120209_All//2.00E-10//AT2G32940| AGO6 (ARGONAUTE 6); nucleic acid binding	Unigene120209_All//7.00E-42//DN804161			nr +
Unigene12021_All	4935	1.27	2.58	1.40	3.19	2.81	2.91	8.09	5.60	6.42	1.02E+00	4.36E-10	Up	1.41E-01	5.91E-01		-1.82E-01	2.38E-01		-1.32E-01	4.29E-01		-5.31E-01	2.10E-12		-3.34E-01	6.20E-06			Unigene12021_All//gi|297601656|ref|NP_001051208.2|//0.00E+00//Os03g0738100 [Oryza sativa Japonica Group] >gi|255674880|dbj|BAF13122.2| Os03g0738100 [Oryza sativa Japonica Group]	Unigene12021_All//2.00E-05//AT2G35075| unknown protein	Unigene12021_All//0.00E+00//TC171678			GO:0004673//GO:0009987//GO:0023060//GO:0032559//GO:0044464	nr -
Unigene120212_All	249	0.00	0.00	2.99	0.00	0.14	0.00	0.34	0.17	1.12	null	null		1.15E+01	3.28E-04	Up	7.11E+00	8.32E-01		null	null		-1.02E+00	7.25E-01		1.72E+00	2.30E-01			Unigene120212_All//gi|124360022|gb|ABN08038.1|//1.00E-10//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene120212_All//1.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene120212_All//3.00E-07//TC169302				nr +

Unigene12022_All	4363	2.05	4.67	1.48	3.28	4.53	2.72	11.04	15.83	67.30	1.19E+00	7.11E-20	Up	-4.74E-01	1.96E-02		4.67E-01	6.16E-05		-2.67E-01	8.97E-02		5.20E-01	4.33E-20		2.61E+00	0.00E+00	Up	Unigene12022_All//gi|115482440|ref|NP_001064813.1|//0.00E+00//Os10g0468500 [Oryza sativa Japonica Group] >gi|78708798|gb|ABB47773.1| Leucine Rich Repeat family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639422|dbj|BAF26727.1| Os10g0468500 [Oryza sativa Japonica Group]	Unigene12022_All//0.00E+00//AT1G35710| leucine-rich repeat transmembrane protein kinase, putative	Unigene12022_All//0.00E+00//ES803124		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene120225_All	508	0.93	2.09	1.47	0.10	0.34	0.62	0.00	0.41	1.33	1.18E+00	8.18E-02		6.63E-01	4.19E-01		1.79E+00	5.21E-01		2.67E+00	1.44E-01		8.68E+00	7.85E-02		1.04E+01	4.97E-05	Up	Unigene120225_All//gi|302142925|emb|CBI20220.3|//8.00E-08//unnamed protein product [Vitis vinifera]							nr +
Unigene120228_All	435	3.37	0.35	2.20	0.92	1.03	1.45	1.26	0.19	1.47	-3.27E+00	8.97E-06	Down	-6.12E-01	2.90E-01		1.68E-01	9.04E-01		6.66E-01	4.92E-01		-2.72E+00	1.22E-02		2.14E-01	7.73E-01		Unigene120228_All//gi|195619190|gb|ACG31425.1|//3.00E-12//fructokinase-2 [Zea mays]	Unigene120228_All//3.00E-11//AT1G66430| pfkB-type carbohydrate kinase family protein	Unigene120228_All//2.00E-166//TC168961		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene120229_All	454	0.58	0.22	0.23	1.10	0.30	0.50	2.61	0.09	7.28	-1.37E+00	3.83E-01		-1.30E+00	4.37E-01		-1.85E+00	8.44E-02		-1.14E+00	3.07E-01		-4.82E+00	2.83E-07	Down	1.48E+00	2.50E-06	Up			Unigene120229_All//6.00E-87//C0083773				
Unigene12023_All	4399	8.03	23.22	16.10	14.70	12.98	13.04	9.32	12.59	8.43	1.53E+00	5.91E-143	Up	1.00E+00	4.94E-50	Up	-1.80E-01	5.33E-03		-1.73E-01	1.08E-02		4.33E-01	6.76E-12		-1.45E-01	6.22E-02		Unigene12023_All//gi|224086046|ref|XP_002307793.1|//0.00E+00//cholesterol transport protein [Populus trichocarpa] >gi|222857242|gb|EEE94789.1| cholesterol transport protein [Populus trichocarpa]	Unigene12023_All//0.00E+00//AT1G42470| patched family protein	Unigene12023_All//0.00E+00//TC157444			GO:0004888//GO:0015918//GO:0031224//GO:0043231	nr +
Unigene12024_All	940	26.05	47.38	27.13	27.03	29.31	37.43	27.80	50.73	63.36	8.63E-01	1.63E-25		5.89E-02	6.24E-01		1.17E-01	3.29E-01		4.70E-01	8.76E-08		8.68E-01	1.11E-33		1.19E+00	3.19E-71	Up	Unigene12024_All//gi|25992529|gb|AAN77145.1|//6.00E-60//fiber protein Fb2 [Gossypium barbadense]	Unigene12024_All//4.00E-39//AT3G05700| INVOLVED IN: response to water deprivation; CONTAINS InterPro DOMAIN/s: Drought induced 19 (InterPro:IPR006598); BEST Arabidopsis thaliana protein match is: drought-responsive family protein (TAIR:AT5G26990.1); Has 167 Blast hits to 167 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 38; Fungi - 0; Plants - 128; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene12024_All//0.00E+00//TC136486				nr +
Unigene120244_All	654	0.00	0.00	0.00	0.53	0.32	0.00	0.13	0.45	2.92	null	null		null	null		-7.55E-01	5.67E-01		-9.06E+00	2.13E-02		1.79E+00	2.24E-01		4.50E+00	2.83E-11	Up	Unigene120244_All//gi|115437018|ref|NP_001043191.1|//3.00E-27//Os01g0515300 [Oryza sativa Japonica Group] >gi|113532722|dbj|BAF05105.1| Os01g0515300 [Oryza sativa Japonica Group]	Unigene120244_All//1.00E-25//AT4G08850| kinase			ko04626|Plant-pathogen interaction		nr -
Unigene120245_All	954	0.05	0.11	0.00	0.16	0.00	0.24	0.22	0.61	4.05	9.55E-01	7.27E-01		-5.78E+00	6.27E-01		-7.29E+00	1.66E-01		5.96E-01	7.22E-01		1.47E+00	1.02E-01		4.19E+00	2.48E-21	Up							
Unigene120246_All	227	0.00	0.00	0.00	0.00	0.00	0.00	0.93	0.74	8.42	null	null		null	null		null	null		null	null		-3.39E-01	8.12E-01		3.18E+00	7.45E-09	Up			Unigene120246_All//2.00E-125//TC178738				
Unigene120248_All	588	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.44	-7.48E+00	3.74E-01		-7.48E+00	3.96E-01		null	null		null	null		null	null		1.13E+01	2.48E-10	Up	Unigene120248_All//gi|224092069|ref|XP_002309462.1|//2.00E-10//leucine-rich repeat protein kinase [Populus trichocarpa] >gi|222855438|gb|EEE92985.1| leucine-rich repeat protein kinase [Populus trichocarpa]	Unigene120248_All//9.00E-05//AT3G26330| ER (ERECTA); transmembrane receptor protein kinase	Unigene120248_All//5.00E-54//C0104679				nr +
Unigene120258_All	268	0.00	0.95	0.00	0.56	0.77	0.34	0.00	0.00	1.93	9.88E+00	7.87E-02		null	null		4.67E-01	8.25E-01		-7.27E-01	7.16E-01		null	null		1.09E+01	6.14E-04	Up	Unigene120258_All//gi|225460207|ref|XP_002277587.1|//3.00E-10//PREDICTED: similar to TNP2 [Vitis vinifera]		Unigene120258_All//5.00E-15//DW498310				nr -
Unigene12026_All	4393	5.40	3.59	4.61	12.35	9.67	8.51	16.40	7.85	10.64	-5.89E-01	1.48E-07		-2.28E-01	6.42E-02		-3.52E-01	8.02E-08		-5.37E-01	8.80E-15		-1.06E+00	1.62E-70	Down	-6.25E-01	1.21E-29		Unigene12026_All//gi|225430654|ref|XP_002268225.1|//0.00E+00//PREDICTED: similar to KLK/PIR/PIR121/PIRP (KLUNKER, PIROGI) [Vitis vinifera]	Unigene12026_All//0.00E+00//AT5G18410| PIR121: transcription activator	Unigene12026_All//0.00E+00//TC166719			GO:0000904//GO:0007015//GO:0030528//GO:0043234	nr +
Unigene120263_All	294	0.00	0.00	0.00	0.00	0.00	0.00	8.63	0.43	1.22	null	null		null	null		null	null		null	null		-4.34E+00	2.93E-14	Down	-2.82E+00	1.53E-10	Down							
Unigene12027_All	4409	0.28	0.44	0.36	0.72	0.73	0.48	1.69	0.38	1.18	6.17E-01	1.90E-01		3.47E-01	5.29E-01		2.20E-02	9.63E-01		-5.87E-01	9.87E-02		-2.15E+00	4.69E-21	Down	-5.12E-01	5.70E-03		Unigene12027_All//gi|225430654|ref|XP_002268225.1|//0.00E+00//PREDICTED: similar to KLK/PIR/PIR121/PIRP (KLUNKER, PIROGI) [Vitis vinifera]	Unigene12027_All//0.00E+00//AT5G18410| PIR121: transcription activator	Unigene12027_All//0.00E+00//TC166719			GO:0000904//GO:0007015//GO:0030528//GO:0043234	nr +
Unigene120272_All	696	0.45	0.95	0.23	0.14	0.00	0.26	0.61	1.32	5.67	1.07E+00	2.37E-01		-9.75E-01	5.06E-01		-7.16E+00	3.14E-01		8.59E-01	6.95E-01		1.12E+00	8.95E-02		3.22E+00	8.93E-18	Up			Unigene120272_All//1.00E-45//TC179279				
Unigene120273_All	302	0.00	0.00	0.00	0.00	0.00	0.00	0.42	0.28	4.35	null	null		null	null		null	null		null	null		-6.02E-01	7.67E-01		3.37E+00	1.37E-06	Up			Unigene120273_All//7.00E-21//BQ413522				
Unigene120278_All	1145	0.00	0.00	0.00	0.00	0.00	0.00	0.55	0.15	3.03	null	null		null	null		null	null		null	null		-1.92E+00	3.09E-02		2.45E+00	5.15E-12	Up	Unigene120278_All//gi|4559334|gb|AAD22996.1|//3.00E-99//expressed protein [Arabidopsis thaliana]	Unigene120278_All//2.00E-108//AT2G30900| unknown protein	Unigene120278_All//2.00E-107//TC144190				nr -
Unigene12028_All	1311	6.47	5.80	7.51	10.64	8.67	10.20	9.16	9.15	2.95	-1.57E-01	4.65E-01		2.17E-01	2.92E-01		-2.96E-01	5.00E-02		-6.12E-02	7.21E-01		-1.50E-03	1.01E+00		-1.64E+00	4.28E-24	Down	Unigene12028_All//gi|18421967|ref|NP_568580.1|//2.00E-26//metal-dependent phosphohydrolase HD domain-containing protein [Arabidopsis thaliana] >gi|14488069|gb|AAK63855.1|AF38928_2_1 AT5g40270/MSN9_170 [Arabidopsis thaliana] >gi|20968076|gb|AAM26721.1| AT5g40270/MSN9_170 [Arabidopsis thaliana]	Unigene12028_All//9.00E-28//AT5G40270| metal-dependent phosphohydrolase HD domain-containing protein	Unigene12028_All//0.00E+00//TC167683			GO:0008168//GO:0042254//GO:0044424//GO:0051540	nr +
Unigene120281_All	497	0.53	0.51	0.64	0.40	0.76	0.55	0.26	0.08	2.81	-4.62E-02	9.87E-01		2.88E-01	8.10E-01		9.27E-01	5.23E-01		4.44E-01	7.64E-01		-1.60E+00	5.35E-01		3.46E+00	4.41E-07	Up	Unigene120281_All//gi|297843542|ref|XP_002889652.1|//4.00E-21//FTSH10 [Arabidopsis lyrata subsp. lyrata] >gi|297335494|gb|EFH65911.1| FTSH10 [Arabidopsis lyrata subsp. lyrata]	Unigene120281_All//8.00E-19//AT1G07510| ftsh10 (FtsH protease 10); ATP binding / ATPase/ metalloendopeptidase/ nucleoside-triphosphatase/ nucleotide binding / zinc ion binding	Unigene120281_All//8.00E-31//gi|48800014|gb|CO101328.1|CO101328				nr -
Unigene120284_All	452	0.00	0.00	0.00	0.00	0.15	0.00	0.56	0.46	3.79	null	null		null	null		7.25E+00	6.12E-01		null	null		-2.80E-01	8.29E-01		2.76E+00	4.59E-07	Up	Unigene120284_All//gi|38346716|emb|CAE04866.2|//1.00E-11//OSJNBa0086006.14 [Oryza sativa (japonica cultivar-group)]		Unigene120284_All//5.00E-07//TC137106				nr -
Unigene12029_All	1730	11.83	9.08	14.37	17.36	20.90	23.99	15.13	12.59	5.90	-3.81E-01	1.84E-03		2.82E-01	1.59E-02		2.68E-01	2.01E-03		4.67E-01	5.86E-09		-2.65E-01	6.50E-03		-1.36E+00	2.50E-39	Down	Unigene12029_All//gi|18421967|ref|NP_568580.1|//0.00E+00//metal-dependent phosphohydrolase HD domain-containing protein [Arabidopsis thaliana] >gi|14488069|gb|AAK63855.1|AF38928_2_1 AT5g40270/MSN9_170 [Arabidopsis thaliana] >gi|20968076|gb|AAM26721.1| AT5g40270/MSN9_170 [Arabidopsis thaliana]	Unigene12029_All//0.00E+00//AT5G40270| metal-dependent phosphohydrolase HD domain-containing protein	Unigene12029_All//0.00E+00//TC133147			GO:0003824	nr +
Unigene120291_All	241	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	2.15	null	null		null	null		null	null		null	null		7.44E+00	6.36E-01		1.11E+01	6.14E-04	Up							
Unigene120295_All	229	0.69	1.33	0.23	1.52	2.11	0.20	0.00	0.00	2.61	9.54E-01	5.03E-01		-1.56E+00	5.34E-01		4.67E-01	7.04E-01		-2.95E+00	8.31E-02		null	null		1.13E+01	1.75E-04	Up			Unigene120295_All//3.00E-07//ES847883				
Unigene120296_All	332	0.00	0.00	0.00	0.00	0.00	0.00	4.97	3.02	1.56	null	null		null	null		null	null		null	null		-7.17E-01	1.22E-01		-1.67E+00	3.93E-04	Down	Unigene120296_All//gi|126566038|gb|AB020848.1|//3.00E-18//cytochrome P450-like TBP protein [Lilium longiflorum]		Unigene120296_All//2.00E-43//gi|45595417|gb|CK988266.1|CK988266				nr +
Unigene12030_All	3105	24.89	10.53	19.28	41.09	40.22	17.50	3.35	1.76	0.59	-1.24E+00	3.72E-79	Down	-3.69E-01	1.17E-09		-3.06E-02	6.13E-01		-1.23E+00	1.04E-139	Down	-9.26E-01	8.10E-09		-2.50E+00	5.75E-36	Down	Unigene12030_All//gi|297811331|ref|XP_002873549.1|//0.00E+00//mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319386|gb|EFH49808.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene12030_All//0.00E+00//AT5G12080| MSL10 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 10); mechanically-gated ion channel	Unigene12030_All//0.00E+00//gi|109884739|gb|DW513709.1|DW513709			GO:0005216//GO:0009612//GO:0016020//GO:0043231	nr -
Unigene120310_All	474	0.00	0.00	0.00	0.11	0.15	0.00	0.00	0.26	2.27	null	null		null	null		4.67E-01	9.59E-01		-6.72E+00	6.38E-01		8.05E+00	2.41E-01		1.11E+01	8.30E-08	Up	Unigene120310_All//gi|224128592|ref|XP_002329370.1|//1.00E-44//dehydroquinate dehydratase/ shikimate dehydrogenase [Populus trichocarpa] >gi|222861143|gb|EEE98685.1| dehydroquinate dehydratase/ shikimate dehydrogenase [Populus trichocarpa]	Unigene120310_All//1.00E-23//AT3G06350| MEE32 (MATERNAL EFFECT EMBRYO ARREST 32); 3-dehydroquinate dehydratase/ NADP or NADPH binding / binding / catalytic/ shikimate 5-dehydrogenase			ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene120312_All	395	0.26	0.00	0.00	0.50	0.00	0.11	0.21	1.06	2.82	-8.05E+00	3.74E-01		-8.05E+00	3.96E-01		-8.98E+00	8.44E-02		-2.14E+00	3.47E-01		2.31E+00	6.00E-02		3.72E+00	4.35E-06	Up			Unigene120312_All//3.00E-39//TC141043				
Unigene120314_All	489	0.00	0.00	0.00	0.00	0.00	0.09	0.26	0.34	2.44	null	null		null	null		null	null		6.53E+00	6.98E-01		3.98E-01	8.14E-01		3.24E+00	7.29E-06	Up	Unigene120314_All//gi|116309862|emb|CAH66897.1|//3.00E-14//OS1GRa0099L20.12 [Oryza sativa (indica cultivar-group)]		Unigene120314_All//1.00E-20//gi|78343242|gb|DT563516.1|DT563516				nr +
Unigene120320_All	453	0.00	0.45	0.24	0.00	0.15	0.00	1.96	0.92	0.35	8.81E+00	1.37E-01		7.88E+00	4.00E-01		7.25E+00	6.12E-01		null	null		-1.09E+00	1.07E-01		-2.48E+00	9.93E-04	Down			Unigene120320_All//1.00E-97//gi|72268947|gb|DT046941.1|DT046941				
Unigene120321_All	287	0.00	0.00	0.56	0.00	0.24	0.00	0.44	3.79	1.11	null	null		9.12E+00	2.39E-01		7.91E+00	6.12E-01		null	null		3.10E+00	4.52E-05	Up	1.33E+00	2.93E-01								
Unigene120322_All	456	0.00	0.00	0.00	0.11	0.45	0.50	0.28	1.10	3.93	null	null		null	null		2.05E+00	3.95E-01		2.18E+00	3.23E-01		1.98E+00	5.74E-02		3.82E+00	1.36E-09	Up			Unigene120322_All//6.00E-47//DW519316				
Unigene120323_All	603	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.00	2.64	null	null		null	null		7.42E+00	4.57E-01		null	null		null	null		1.14E+01	1.85E-11	Up	Unigene120323_All//gi|224057784|ref|XP_002299322.1|//4.00E-55//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222846580|gb|EEE84127.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene120323_All//2.00E-48//AT5G40740| ATPase, coupled to transmembrane movement of substances			ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene120333_All	485	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.79	null	null		null	null		null	null		null	null		null	null		1.14E+01	9.04E-10	Up							
Unigene120336_All	786	0.27	0.19	0.81	0.13	0.26	0.52	0.54	1.01	3.29	-4.62E-01	7.58E-01		1.61E+00	1.11E-01		1.05E+00	6.12E-01		2.03E+00	1.49E-01		9.09E-01	2.11E-01		2.61E+00	8.54E-10	Up	Unigene120336_All//gi|24461861|gb|AAN62348.1|AF506028_15//6.00E-24//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene120336_All//7.00E-21//AT1G61190| disease resistance protein (CC-NBS-LRR class), putative	Unigene120336_All//0.00E+00//TC155066		ko04626|Plant-pathogen interaction		nr -
Unigene120339_All	557	11.46	20.56	12.05	12.61	11.44	13.78	74.92	128.91	37.19	8.43E-01	6.67E-07		7.19E-02	7.68E-01		-1.41E-01	5.87E-01		1.28E-01	6.38E-01		7.83E-01	2.72E-42		-1.01E+00	4.72E-39	Down	Unigene120339_All//gi|192910686|gb|ACF06451.1|//8.00E-15//QM-like protein [Elaeis guineensis]	Unigene120339_All//1.00E-11//AT1G26910| 60S ribosomal protein L10 (RPL10B)	Unigene120339_All//0.00E+00//CO093073		ko03010|Ribosome		nr +
Unigene120342_All	410	0.89	1.48	0.91	3.04	1.76	0.44	1.24	1.02	0.78	7.31E-01	4.16E-01		2.53E-02	1.00E+00		-7.84E-01	1.82E-01		-2.79E+00	1.35E-04	Down	-2.80E-01	7.49E-01		-6.71E-01	4.48E-01				Unigene120342_All//5.00E-16//TC157312				
Unigene120347_All	509	0.00	0.00	0.00	0.00	0.00	0.00	1.74	0.08	1.33	null	null		null	null		null	null		null	null		-4.41E+00	2.44E-05	Down	-3.91E-01	5.53E-01				Unigene120347_All//2.00E-19//TC161176				ESTscan +
Unigene120348_All	240	1.74	2.11	2.44	0.00	4.73	1.69	0.70	0.35	1.49	2.76E-01	7.64E-01		4.85E-01	6.30E-01		1.22E+01	5.31E-07	Up	1.07E+01	1.36E-02		-1.02E+00	6.15E-01		1.08E+00	3.50E-01								
Unigene120349_All	392	0.00	0.00	0.00	0.00	0.00	0.46	0.11	0.64	7.22	null	null		null	null		null	null		8.85E+00	1.95E-01		2.57E+00	1.53E-01		6.06E+00	1.04E-18	Up							

Unigene120352_A11	1173	0.00	0.04	0.00	0.00	0.12	0.04	0.97	0.57	0.20	5.43E+00	6.18E-01		null	null		6.88E+00	3.19E-01			5.27E+00	6.98E-01		-7.72E-01	1.81E-01		-2.26E+00	3.40E-04	Down	Unigene120352_A11//gi|3287835|sp|Q43714.1|DCS3_GOSAR//7.00E-90//RecName: Full=(+)-delta-cadinene synthase isozyme A; Short=D-cadinene synthase A >gi|1002523|gb|AAB41259.1| (+)-delta-cadinene synthase isozyme A [Gossypium arboreum] >gi|1217956|emb|CAA65289.1| (+)-delta-cadinene synthase [Gossypium arboreum]	Unigene120352_A11//1.00E-51//AT3G14490| terpene synthase/cyclase family protein	Unigene120352_A11//0.00E+00//TC142314		ko00904|Diterpenoid biosynthesis		
Unigene120361_A11	270	0.00	0.75	0.00	0.18	0.00	0.00	0.00	0.31	1.92	9.55E+00	1.37E-01		null	null		-7.53E+00	5.57E-01		-7.53E+00	6.38E-01		8.27E+00	4.02E-01		1.09E+01	6.14E-04	Up								
Unigene120368_A11	539	0.19	0.00	0.00	0.00	0.26	0.00	0.00	0.93	2.00	-7.60E+00	3.74E-01		-7.60E+00	3.96E-01		8.00E+00	3.19E-01		null	null		9.86E+00	1.02E-03		1.10E+01	8.30E-08	Up	Unigene120368_A11//gi|415833|emb|CAA80273.1|//7.00E-26//5B protein [Solanum lycopersicum]	Unigene120368_A11//8.00E-24//AT3G07450| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein					nr +
Unigene12037_A11	2146	18.07	18.37	13.92	13.00	14.28	23.76	13.22	46.18	42.66	2.40E-02	8.02E-01		-3.76E-01	2.23E-05		1.36E-01	2.21E-01		8.70E-01	1.42E-31		1.80E+00	1.21E-214	Up	1.69E+00	1.15E-184	Up	Unigene12037_A11//gi|291245406|gb|ADB84880.1|//1.00E-137//mitochondrial AOX2 [Citrullus lanatus]	Unigene12037_A11//4.00E-120//AT5G64210| AOX2; alternative oxidase	Unigene12037_A11//0.00E+00//TC155891				nr +
Unigene120372_A11	588	0.00	0.52	0.00	0.59	0.53	0.84	0.72	0.36	3.12	9.01E+00	4.44E-02		null	null		-1.70E-01	8.58E-01		5.11E-01	6.41E-01		-1.02E+00	3.51E-01		2.12E+00	9.21E-06	Up	Unigene120372_A11//gi|115471637|ref|NP_001059417.1|//9.00E-07//Os07g0298100 [Oryza sativa Japonica Group] >gi|113610953|dbj|BAF21331.1| Os07g0298100 [Oryza sativa Japonica Group]	Unigene120372_A11//7.00E-05//AT1G74220| unknown protein					nr +
Unigene120374_A11	446	0.47	0.00	0.00	0.11	0.00	0.10	0.19	0.09	1.70	-8.87E+00	1.22E-01		-8.87E+00	1.46E-01		-6.80E+00	5.57E-01		-1.41E-01	9.54E-01		-1.02E+00	7.25E-01		3.16E+00	6.83E-04	Up	Unigene120374_A11//gi|255567632|ref|XP_002524795.1|//6.00E-59//conserved hypothetical protein [Ricinus communis] >gi|223535979|gb|EEF37638.1| conserved hypothetical protein [Ricinus communis]	Unigene120374_A11//1.00E-36//AT2G48060| unknown protein					nr -
Unigene120375_A11	659	0.32	0.15	0.48	0.45	0.37	0.14	0.13	0.13	2.96	-1.05E+00	5.65E-01		6.10E-01	6.25E-01		-3.10E-01	8.20E-01		-1.73E+00	2.89E-01		-1.70E-02	1.01E+00		4.53E+00	1.53E-11	Up	Unigene120375_A11//gi|297826949|ref|XP_002881357.1|//2.00E-45//EDA28/MEE23 [Arabidopsis lyrata subsp. lyrata] >gi|297327196|gb|EFH57616.1| EDA28/MEE23 [Arabidopsis lyrata subsp. lyrata]	Unigene120375_A11//3.00E-40//AT1G26390| FAD-binding domain-containing protein	Unigene120375_A11//3.00E-34//TC170571				nr -
Unigene120376_A11	252	1.25	0.00	1.27	3.56	2.19	0.36	0.34	0.00	0.32	-1.03E+01	3.66E-02		2.55E-02	1.00E+00		-7.03E-01	3.25E-01		-3.31E+00	5.80E-04	Down	-8.39E+00	4.05E-01		-8.59E-02	9.72E-01		Unigene120376_A11//gi|2500715|sp|Q40374.1|PR1_MEDTR//3.00E-33//RecName: Full=Pathogenesis-related protein PR-1; Flags: Precursor >gi|505553|emb|CAA56174.1| PR-1 [Medicago truncatula]	Unigene120376_A11//5.00E-29//AT4G30320| allergen V5/Tpx-1-related family protein	Unigene120376_A11//1.00E-92//TC139677	ko04626|Plant-pathogen interaction		nr -
Unigene12038_A11	2544	3.54	4.44	3.68	30.88	17.34	9.98	8.16	4.22	2.57	3.28E-01	5.93E-02		5.86E-02	7.74E-01		-8.33E-01	2.10E-51		-1.63E+00	1.22E-131	Down	-9.51E-01	1.64E-17		-1.67E+00	3.61E-42	Down	Unigene12038_A11//gi|22327681|ref|NP_199827.2|//0.00E+00//FRO8 (FERRIC REDUCTION OXIDASE 8); ferric-chelate reductase/ oxidoreductase [Arabidopsis thaliana]	Unigene12038_A11//3.00E-168//AT5G50160| FRO8 (FERRIC REDUCTION OXIDASE 8); ferric-chelate reductase/ oxidoreductase	Unigene12038_A11//0.00E+00//C0079075	ko04626|Plant-pathogen interaction	GO:0008152//GO:0016723//GO:0030554//GO:0031224//GO:0043231//GO:0046914	nr +
Unigene120381_A11	972	0.54	0.26	0.05	0.10	0.25	0.00	0.44	0.17	9.02	-1.05E+00	3.11E-01		-3.30E+00	2.40E-02		1.27E+00	5.32E-01		-6.68E+00	4.02E-01		-1.34E+00	2.24E-01		4.37E+00	4.78E-49	Up								
Unigene12039_A11	3258	1.70	3.31	2.86	68.27	65.19	59.90	17.78	6.38	4.98	9.61E-01	5.91E-08		7.49E-01	1.27E-04		-6.65E-02	7.37E-02		-1.89E-01	1.03E-08		-1.48E+00	7.51E-95	Down	-1.84E+00	6.34E-133	Down	Unigene12039_A11//gi|241740158|gb|ACS68199.1|//0.00E+00//cellulose synthase 8.2 catalytic subunit [Brassica napus]	Unigene12039_A11//0.00E+00//AT4G18780| IRX1 (IRREGULAR XYLEM 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene12039_A11//0.00E+00//TC173436			GO:0000160//GO:0006952//GO:0009250//GO:0009688//GO:0009832//GO:0016759//GO:0052333//GO:0030312//GO:0031224//GO:0042545//GO:0046914	nr -
Unigene120396_A11	449	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.22	null	null		null	null		null	null		null	null		null	null		1.11E+01	3.00E-07	Up			Unigene120396_A11//4.00E-103//TC158273				
Unigene1204_A11	2926	8.94	6.55	7.28	6.35	5.32	5.43	4.87	2.43	2.40	-4.50E-01	2.20E-05		-2.97E-01	8.61E-03		-2.56E-01	4.88E-02		-2.25E-01	1.04E-01		-1.00E+00	2.33E-13	Down	-1.02E+00	3.40E-14	Down	Unigene1204_A11//gi|162459980|ref|NP_001106061.1|//1.00E-160//CRM family member 3 [Zea mays] >gi|156789080|gb|ABL96081.1| CRM family member 3 [Zea mays]	Unigene1204_A11//8.00E-123//AT4G29750| RNA binding	Unigene1204_A11//0.00E+00//gi|78348748|gb|DT569022.1|DT569022				nr -
Unigene12041_A11	810	0.97	0.75	0.72	2.34	1.15	0.56	2.51	2.01	1.23	-3.68E-01	6.23E-01		-4.22E-01	6.21E-01		-1.03E+00	2.20E-02		-2.07E+00	6.30E-05	Down	-3.16E-01	4.65E-01		-1.03E+00	8.71E-03		Unigene12041_A11//gi|22327387|ref|NP_198442.2|//3.00E-40//AMP-dependent synthetase and ligase family protein [Arabidopsis thaliana]	Unigene12041_A11//2.00E-41//AT5G35930| AMP-dependent synthetase and ligase family protein				GO:0022892//GO:0043231//GO:0047661	nr -
Unigene120424_A11	2359	0.00	0.00	0.00	0.00	0.00	0.02	0.14	0.11	5.73	null	null		null	null		null	null		4.26E+00	6.98E-01		-4.32E-01	7.03E-01		5.32E+00	8.03E-84	Up	Unigene120424_A11//gi|9294121|dbj|BAB01972.1|//0.00E+00//copia-like retrotransposable element [Arabidopsis thaliana]	Unigene120424_A11//2.00E-82//AT4G23160| protein kinase family protein	Unigene120424_A11//2.00E-13//C0096412				nr +
Unigene120428_A11	1219	0.21	0.00	0.00	0.00	0.06	0.00	0.07	0.00	2.81	-7.75E+00	6.72E-02		-7.75E+00	8.58E-02		5.82E+00	6.12E-01		null	null		-6.12E+00	4.05E-01		5.34E+00	1.41E-21	Up	Unigene120428_A11//gi|224092069|ref|XP_002309462.1|//8.00E-38//leucine-rich repeat protein kinase [Populus trichocarpa] >gi|222855438|gb|EEE92985.1| leucine-rich repeat protein kinase [Populus trichocarpa]	Unigene120428_A11//2.00E-35//AT2G26330| ER (ERECTA); transmembrane receptor protein kinase	Unigene120428_A11//5.00E-31//C0092850				nr +
Unigene120437_A11	526	0.20	0.87	0.91	0.38	0.33	0.77	1.21	0.79	3.41	2.12E+00	9.60E-02		2.20E+00	9.15E-02		-2.11E-01	8.59E-01		1.03E+00	4.29E-01		-6.02E-01	4.67E-01		1.50E+00	7.33E-04	Up			Unigene120437_A11//5.00E-137//gi|109874626|gb|DW503600.1|DW503600				
Unigene120438_A11	330	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.89	2.17	null	null		null	null		null	null		null	null		9.79E+00	2.35E-02		1.11E+01	2.63E-05	Up	Unigene120438_A11//gi|87280657|gb|ABD36507.1|//2.00E-16//receptor kinase TRKa [Oryza sativa Indica Group]	Unigene120438_A11//2.00E-16//AT5G20480| EFR (EF-TU RECEPTOR); ATP binding / kinase/ protein serine/threonine kinase		ko04626|Plant-pathogen interaction		nr +
Unigene120442_A11	214	8.07	6.16	9.95	6.29	7.40	8.65	17.78	22.07	7.45	-3.90E-01	4.27E-01		3.03E-01	5.19E-01		2.36E-01	6.99E-01		4.61E-01	3.82E-01		3.12E-01	2.39E-01		-1.26E+00	8.09E-06	Down			Unigene120442_A11//5.00E-101//gi|164303528|gb|ES831560.1|ES831560				
Unigene120447_A11	659	0.32	0.38	0.00	0.15	0.26	0.07	0.13	0.70	2.24	2.75E-01	8.43E-01		-8.31E+00	1.46E-01		7.89E-01	7.71E-01		-1.14E+00	6.77E-01		2.44E+00	3.74E-02		4.12E+00	2.19E-08	Up								
Unigene12045_A11	2093	0.55	0.63	0.64	0.71	1.10	1.06	12.52	12.86	28.27	1.95E-01	7.26E-01		2.10E-01	7.07E-01		6.27E-01	1.48E-01		5.66E-01	2.14E-01		3.82E-02	7.30E-01		1.17E+00	2.04E-69	Up	Unigene12045_A11//gi|164604978|dbj|BAF98285.1|//1.00E-13//diphosphomevalonate decarboxylase [Hevea brasiliensis]	Unigene12045_A11//4.00E-13//AT3G54250| mevalonate diphosphate decarboxylase, putative	Unigene12045_A11//1.00E-79//TC165602	ko00900|Terpenoid backbone biosynthesis	GO:0006084//GO:0006720//GO:0006796//GO:0016772//GO:0016831//GO:0032559//GO:0042802	nr -
Unigene120455_A11	648	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.95	null	null		null	null		null	null		null	null		null	null		1.15E+01	1.02E-13	Up	Unigene120455_A11//gi|15239540|ref|NP_197965.1|//7.00E-06//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|5107831|gb|AAD10144.1|AF149413_25 contains similarity to protein kinase domains (Pfam F00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana] >gi|224589685|gb|ACN59374.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene120455_A11//1.00E-07//AT5G25930| leucine-rich repeat family protein / protein kinase family protein					nr +
Unigene120463_A11	719	0.51	0.63	0.30	0.14	0.19	0.13	0.12	0.06	1.88	3.16E-01	7.45E-01		-7.82E-01	5.53E-01		4.67E-01	8.77E-01		-1.42E-01	9.51E-01		-1.02E+00	7.25E-01		4.00E+00	1.31E-07	Up	Unigene120463_A11//gi|115455579|ref|NP_001051390.1|//3.00E-26//Os03g0767800 [Oryza sativa Japonica Group] >gi|10121845|gb|AAG13395.1|AF283006_1 cold acclimation protein WCOR413-like protein [Oryza sativa Japonica Group] >gi|40539079|gb|AAR87336.1| cold acclimation protein WCOR413-like protein [Oryza sativa Japonica Group] >gi|113549861|dbj|BAF13304.1| Os03g0767800 [Oryza sativa Japonica Group]	Unigene120463_A11//5.00E-20//AT3G50830| COR413-PM2 (COLD-REGULATED 413-PLASMA MEMBRANE 2)	Unigene120463_A11//2.00E-97//TC142774				nr +
Unigene120464_A11	561	0.00	0.00	0.00	0.00	0.00	0.48	0.38	0.22	3.83	null	null		null	null		null	null		8.92E+00	7.03E-02		-7.54E-01	6.32E-01		3.35E+00	2.59E-10	Up								
Unigene120465_A11	971	0.00	0.00	0.33	0.00	0.00	0.00	0.65	0.60	23.10	null	null		8.36E+00	4.53E-02		null	null		null	null		-1.16E-01	8.88E-01		5.14E+00	7.76E-137	Up	Unigene120465_A11//gi|55168340|gb|AAV44205.1|//5.00E-35//unknow protein [Oryza sativa Japonica Group]		Unigene120465_A11//2.00E-174//TC139311				nr +
Unigene120477_A11	219	0.00	0.46	0.00	0.23	0.00	0.00	0.19	0.19	3.46	8.85E+00	3.88E-01		null	null		-7.83E+00	5.57E-01		-7.83E+00	6.38E-01		-1.73E-02	1.00E+00		4.16E+00	1.34E-04	Up								
Unigene12048_A11	720	1.67	1.41	2.00	1.94	3.11	1.19	3.41	2.21	1.05	-2.48E-01	6.62E-01		2.57E-01	6.28E-01		6.82E-01	1.16E-01		-7.01E-01	2.32E-01		-6.27E-01	8.69E-02		-1.70E+00	7.66E-06	Down	Unigene12048_A11//gi|165994488|dbj|BAF99694.1|//4.00E-53//1-O-acylglucose:anthocyanin-O-acyltransferase [Clitoria ternatea]	Unigene12048_A11//3.00E-51//AT5G09640| SCPL19; serine-type carboxypeptidase/ sinapoyltransferase	Unigene12048_A11//7.00E-106//ES813131	ko00940|Phenylpropanoid biosynthesis	GO:0004180//GO:0016752//GO:0019538	nr +
Unigene120480_A11	357	0.00	0.57	0.00	0.00	0.00	0.00	0.24	0.00	2.34	9.15E+00	1.37E-01		null	null		null	null		null	null		-7.89E+00	4.05E-01		3.31E+00	2.30E-04	Up								
Unigene120490_A11	264	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.63	2.57	null	null		null	null		null	null		null	null		1.98E+00	3.79E-01		4.00E+00	4.29E-04	Up								
Unigene120495_A11	292	0.00	3.12	0.00	0.00	0.12	0.00	1.74	0.57	4.64	1.16E+01	2.62E-05	Up	null	null		6.88E+00	8.32E-01		null	null		-1.60E+00	1.07E-01		1.42E+00	6.15E-03		Unigene120495_A11//gi|261362484|gb|ACX71613.1|//8.00E-06//AM3 [Oryza sativa Japonica Group]		Unigene120495_A11//3.00E-07//DT047112				nr -
Unigene120497_A11	501	0.00	0.10	0.00	0.10	0.07	0.09	1.10	3.09	7.24	6.66E+00	6.18E-01		null	null		-5.33E-01	8.26E-01		-1.42E-01	9.54E-01		1.49E+00	2.61E-03		2.72E+00	5.57E-14	Up	Unigene120497_A11//gi|224080723|ref|XP_002306216.1|//1.00E-26//lysine/histidine transporter [Populus trichocarpa] >gi|222849180|gb|EEE86727.1| lysine/histidine transporter [Populus trichocarpa]	Unigene120497_A11//2.00E-09//AT1G47670| amino acid transporter family protein	Unigene120497_A11//2.00E-62//TC174042				nr -
Unigene120498_A11	294	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.28	4.07	null	null		null	null		null	null		null	null		8.15E+00	4.02E-01		1.20E+01	1.20E-08	Up			Unigene120498_A11//1.00E-120//TC141619				
Unigene120500_A11	295	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.14	2.97	null	null		null	null		null	null		null	null		7.15E+00	6.36E-01		1.15E+01	2.05E-06	Up								
Unigene120503_A11	1622	0.00	0.00	0.00	0.03	0.00	0.00	0.50	0.59	11.20	null	null		null	null		-4.94E+00	5.57E-01		-4.94E+00	6.38E-01		2.59E-01	6.78E-01		4.50E+00	5.58E-103	Up	Unigene120503_A11//gi|269924823|gb|ACZ52698.1|//1.00E-136//hydroxycinnamoyl-CoA quinate hydroxycinnamoyltransferase [Lonicera japonica]	Unigene120503_A11//4.00E-123//AT5G48930| HCT (HYDROXYCINNAMOYL-COA SHIKIMATE/QUINATE HYDROXYCINNAMOYL TRANSFERASE); quinate O-hydroxycinnamoyltransferase/ shikimate O-hydroxycinnamoyltransferase/ transferase	Unigene120503_A11//1.00E-10//gi|48826968|gb|C0125358.1|C0125358	ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene120504_A11	284	5.90	3.03	3.00	3.86	8.00	4.61	17.57	3.83	6.31	-9.59E-01	5.93E-02		-9.75E-01	6.91E-02		1.05E+00	1.23E-02		2.57E-01	6.93E-01		-2.20E+00	1.05E-14	Down	-1.48E+00	3.57E-09	Down	Unigene120504_A11//gi|242129044|gb|ACS83601.1|//3.00E-25//ATP synthase delta subunit 1 [Gossypium hirsutum]	Unigene120504_A11//3.00E-20//AT5G47030| ATP synthase delta' chain, mitochondrial	Unigene120504_A11//4.00E-96//gi|11207954|gb|BF276884.1|BF276884	ko00190|Oxidative phosphorylation		nr +
Unigene120507_A11	562	0.00	0.00	0.28	0.00	0.12	0.24	0.08	0.22	1.42	null	null		8.15E+00	2.39E-01		6.94E+00	6.11E-01		7.91E+00	3.11E-01		1.57E+00	5.45E-01		4.24E+00	7.42E-05	Up								

Unigene120511_All	697	0.15	1.24	0.00	0.43	0.20	0.65	0.61	0.90	2.06	3.04E+00	1.94E-03		-7.23E+00	3.95E-01		-1.12E+00	4.24E-01		5.96E-01	6.40E-01		5.68E-01	5.04E-01		1.76E+00	7.26E-04	Up	Unigene120511_All//gi|87162939|gb|ABD28734.1|//1.00E-53//UDP-N-acetylglucosamine transferase subunit ALG14, related [Medicago truncatula]	Unigene120511_All//2.00E-51//AT4G18230| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Oligosaccharide biosynthesis protein Alg14 like (InterPro:IPR013969); Has 453 Blast hits to 453 proteins in 176 species: Archae - 4; Bacteria - 199; Metazoa - 76; Fungi - 83; Plants - 28; Viruses - 0; Other Eukaryotes - 63 (source: NCBI BLink).	Unigene120511_All//6.00E-165//gi|13351693|gb|BG442041.1|BG442041		ko00510|N-Glycan biosynthesis		nr +
Unigene120512_All	535	0.59	0.28	0.70	0.28	0.39	0.00	0.63	0.63	13.03	-1.05E+00	4.44E-01		2.48E-01	8.23E-01		4.68E-01	8.25E-01		-8.13E+00	2.34E-01		-1.65E-02	1.02E+00		4.37E+00	4.53E-39	Up	Unigene120512_All//gi|115447489|ref|NP_001047524.1|//6.00E-15//Os02g0636600 [Oryza sativa Japonica Group] >gi|49387970|dbj|BAD25078.1| ABA-responsive protein-like [Oryza sativa Japonica Group] >gi|49388695|dbj|BAD25876.1| ABA-responsive protein-like [Oryza sativa Japonica Group] >gi|113537055|dbj|BAF09438.1| Os02g0636600 [Oryza sativa Japonica Group]	Unigene120512_All//7.00E-16//AT5G23350| GRAM domain-containing protein / ABA-responsive protein-related	Unigene120512_All//2.00E-87//gi|3326748|gb|AI055634.1|AI055634				nr -
Unigene120515_All	269	0.00	0.00	0.20	0.00	0.00	0.00	0.00	0.00	2.07	null	null		7.63E+00	6.37E-01		null	null		null	null		null	null		1.10E+01	3.28E-04	Up								
Unigene120516_All	329	0.00	0.00	0.00	0.00	0.10	0.00	5.65	0.64	9.69	null	null		null	null		6.71E+00	8.32E-01		null	null		-3.15E+00	2.08E-08	Down	7.77E-01	9.76E-03		Unigene120516_All//gi|314433494|gb|AAP54999.1|//2.00E-16//oxidoreductase, 2OG-Fe oxygenase family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene120516_All//5.00E-16//AT4G25310| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene120516_All//2.00E-169//BE054468		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene120520_All	360	5.96	0.84	1.78	2.49	1.43	1.38	0.70	0.23	1.00	-2.82E+00	3.52E-07	Down	-1.75E+00	4.05E-04	Down	-7.96E-01	2.75E-01		-8.52E-01	2.63E-01		-1.60E+00	3.11E-01		4.99E-01	6.27E-01		Unigene120520_All//gi|42567348|ref|NP_195046.3|//3.00E-06//XI-1; motor/ protein binding [Arabidopsis thaliana] >gi|110737839|dbj|BAF00858.1| myosin - like protein [Arabidopsis thaliana]	Unigene120520_All//1.00E-07//AT4G33200| XI-1; motor/ protein binding	Unigene120520_All//4.00E-47//TC150008				nr -
Unigene120525_All	423	5.44	5.51	1.76	0.59	0.33	1.07	0.10	0.00	0.09	1.79E-02	9.86E-01		-1.63E+00	5.02E-04	Down	-8.55E-01	5.74E-01		8.59E-01	4.70E-01		-6.64E+00	6.59E-01		-8.62E-02	9.72E-01		Unigene120525_All//gi|297810295|ref|XP_002873031.1|//4.00E-10//legume lectin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318868|gb|EFH49290.1| legume lectin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene120525_All//8.00E-07//AT3G09035| legume lectin family protein	Unigene120525_All//0.00E+00//gi|13245882|gb|BE054695.2|BE054695			GO:0005488//GO:0009648	nr +
Unigene120528_All	395	0.93	0.26	1.08	1.26	0.87	0.91	0.96	1.06	3.93	-1.85E+00	1.87E-01		2.18E-01	8.31E-01		-5.33E-01	5.94E-01		-4.63E-01	6.59E-01		1.35E-01	8.99E-01		2.03E+00	8.65E-05	Up	Unigene120528_All//gi|255560084|ref|XP_002521060.1|//2.00E-07//hypothetical protein RCOM_1393220 [Ricinus communis] >gi|223539763|gb|EEF41344.1| hypothetical protein RCOM_1393220 [Ricinus communis]	Unigene120528_All//2.00E-05//AT4G15090| FAR1 (FAR-RED IMPAIRED RESPONSE 1); transcription activator/ transcription factor	Unigene120528_All//3.00E-33//TC160812				nr +
Unigene120530_All	1726	0.00	0.00	0.00	0.00	0.00	0.00	0.37	0.63	14.17	null	null		null	null		null	null		null	null		7.77E-01	1.94E-01		5.27E+00	6.14E-151	Up	Unigene120530_All//gi|224134853|ref|XP_002321921.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222868917|gb|EEF06048.1| cytochrome P450 [Populus trichocarpa]	Unigene120530_All//1.00E-177//AT5G52400| CYP71SA1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene120530_All//3.00E-39//TC161990		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0008152//GO:0016491	nr -
Unigene120536_All	549	0.00	0.09	0.00	0.09	0.06	0.08	0.23	0.00	2.18	6.53E+00	6.18E-01		null	null		-5.33E-01	8.26E-01		-1.40E-01	9.54E-01		-7.85E+00	2.36E-01		3.24E+00	7.29E-06	Up			Unigene120536_All//8.00E-19//EY198072				
Unigene120537_All	632	0.00	0.00	0.00	0.00	0.00	0.00	0.40	1.32	5.48	null	null		null	null		null	null		null	null		1.72E+00	1.94E-02		3.77E+00	7.80E-18	Up	Unigene120537_All//gi|270048197|gb|ACZ58492.1|//7.00E-06//beta' subunit of RNA polymerase [Floydiella terrestris]						nr -
Unigene120542_All	311	3.53	5.87	7.02	10.57	13.51	6.53	14.68	29.43	29.72	7.31E-01	1.30E-01		9.91E-01	2.99E-02		3.54E-01	2.74E-01		-6.94E-01	4.28E-02		1.00E+00	7.49E-09	Up	1.02E+00	2.25E-09	Up								
Unigene120546_All	467	0.11	0.00	0.00	0.00	0.00	0.00	0.00	0.36	1.54	-6.81E+00	6.14E-01		-6.81E+00	6.27E-01		null	null		null	null		8.48E+00	1.39E-01		1.06E+01	2.63E-05	Up	Unigene120546_All//gi|224760941|gb|ACN62415.1|//2.00E-36//CONSTANS-like protein [Mangifera indica]	Unigene120546_All//5.00E-28//AT5G24930| zinc finger (B-box type) family protein		C2C2-CO-like	ko04712|Circadian rhythm - plant		nr -
Unigene120549_All	496	0.00	1.02	0.21	1.41	0.07	0.46	0.43	0.84	1.29	1.00E+01	4.05E-03		7.75E+00	4.00E-01		-4.34E+00	2.80E-04	Down	-1.63E+00	7.45E-02		9.84E-01	3.73E-01		1.59E+00	5.48E-02		Unigene120549_All//gi|18394685|ref|NP_564070.1|//3.00E-42//DNA cross-link repair protein-related [Arabidopsis thaliana]	Unigene120549_All//2.00E-43//AT1G19025| DNA cross-link repair protein-related				GO:0003824	nr -
Unigene12055_All	1172	8.53	12.71	11.72	8.59	11.17	10.17	2.53	1.14	1.67	5.76E-01	6.87E-05		4.59E-01	3.73E-03		3.79E-01	1.35E-02		2.45E-01	1.76E-01		-1.15E+00	4.94E-04	Down	-6.00E-01	5.54E-02		Unigene12055_All//gi|15225431|ref|NP_182045.1|//1.00E-109//GOS12 (GOLGI SNARE 12); SNARE binding [Arabidopsis thaliana] >gi|11132048|sp|Q22151.1|GOS12_ARATH RecName: Full=Golgi SNARE 12 protein; Short=AtGOS12; AltName: Full=Golgi SNAP receptor complex member 1-2 >gi|13898895|gb|AAK48905.1|AF357529_1 Golgi SNARE 12 protein [Arabidopsis thaliana] >gi|88196757|gb|ABD43021.1| At2g45200 [Arabidopsis thaliana]	Unigene12055_All//1.00E-101//AT2G45200| GOS12 (GOLGI SNARE 12); SNARE binding	Unigene12055_All//0.00E+00//TC142916		ko04130|SNARE interactions in vesicular transport		nr +
Unigene120552_All	478	0.11	0.00	0.00	0.21	0.07	0.00	0.44	0.17	2.17	-6.77E+00	6.14E-01		-6.77E+00	6.27E-01		-1.53E+00	5.87E-01		-7.70E+00	4.01E-01		-1.34E+00	4.30E-01		2.29E+00	7.17E-04	Up								
Unigene12056_All	2548	8.91	18.08	11.41	65.96	86.06	93.73	33.34	34.48	22.91	1.02E+00	1.22E-34	Up	3.57E-01	6.50E-04		3.84E-01	9.08E-35		5.07E-01	1.23E-56		4.87E-02	4.29E-01		-5.41E-01	4.16E-27		Unigene12056_All//gi|224068380|ref|XP_002302732.1|//0.00E+00//ethylene receptor 1 [Populus trichocarpa] >gi|222844458|gb|EEE82005.1| ethylene receptor 1 [Populus trichocarpa]	Unigene12056_All//0.00E+00//AT2G40940| ERS1 (ETHYLENE RESPONSE SENSOR 1); ethylene binding / protein histidine kinase/ receptor	Unigene12056_All//0.00E+00//TC174002		ko04712|Circadian rhythm - plant	GO:0004673//GO:0004871//GO:0006468//GO:0023060//GO:0032559//GO:0044464	nr +
Unigene120565_All	261	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.32	1.98	null	null		null	null		null	null		null	null		8.32E+00	4.02E-01		1.10E+01	6.14E-04	Up								
Unigene120566_All	284	0.00	0.00	0.00	0.00	0.00	0.00	0.30	0.00	4.07	null	null		null	null		null	null		null	null		-8.22E+00	4.05E-01		3.77E+00	2.44E-06	Up			Unigene120566_All//3.00E-07//TC140987				
Unigene12057_All	559	109.13	59.19	82.69	55.25	42.01	27.23	6.81	2.99	2.57	-8.83E-01	4.04E-36		-4.00E-01	5.96E-09		-3.95E-01	1.08E-05		-1.02E+00	2.29E-25	Down	-1.19E+00	3.42E-05	Down	-1.41E+00	9.17E-07	Down	Unigene12057_All//gi|13487787|gb|AAK27720.1|AF356004_1//4.00E-57//ADP-glucose pyrophosphorylase small subunit CagpS1 [Cicer arietinum]	Unigene12057_All//2.00E-54//AT5G48300| ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE 1); glucose-1-phosphate adenylyltransferase	Unigene12057_All//0.00E+00//gi|109889239|gb|DW518207.1|DW518207		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0032559//GO:0070566	nr +
Unigene120570_All	485	0.00	0.00	0.00	0.00	0.28	0.00	0.17	0.69	1.73	null	null		null	null		8.15E+00	3.19E-01		null	null		1.98E+00	1.44E-01		3.31E+00	2.30E-04	Up								
Unigene120577_All	281	12.66	70.68	22.74	4.43	4.53	16.39	0.00	0.30	0.14	2.48E+00	5.96E-53	Up	8.45E-01	5.03E-04		3.29E-02	9.69E-01		1.89E+00	1.00E-09	Up	8.22E+00	4.02E-01		7.15E+00	6.46E-01		Unigene120577_All//gi|225428877|ref|XP_002282482.1|//3.00E-11//PREDICTED: similar to leucine-rich repeat family protein [Vitis vinifera]		Unigene120577_All//3.00E-63//TC163057		ko03040|Spliceosome		nr -
Unigene120658_All	1524	155.80	75.34	132.60	76.19	69.19	63.12	33.76	19.47	18.74	-1.05E+00	1.71E-184	Down	-2.33E-01	3.37E-12		-1.39E-01	3.29E-03		-2.72E-01	4.04E-09		-7.94E-01	2.67E-31		-8.49E-01	5.08E-36		Unigene120658_All//gi|166863714|gb|AB201673.1|//0.00E+00//ADP-glucose pyrophosphorylase small subunit ADPGp-1 [Gossypium hirsutum]	Unigene120658_All//0.00E+00//AT5G48300| ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE 1); glucose-1-phosphate adenylyltransferase	Unigene120658_All//0.00E+00//TC137079		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0032559//GO:0070566	nr -
Unigene120583_All	693	0.00	0.07	0.77	0.00	0.10	0.26	0.18	0.12	2.59	6.19E+00	6.18E-01		9.59E+00	4.05E-03		6.64E+00	6.11E-01		8.03E+00	1.95E-01		-6.02E-01	7.67E-01		3.82E+00	1.36E-09	Up	Unigene120583_All//gi|297851452|ref|XP_002893607.1|//2.00E-57//ATINT2 [Arabidopsis lyrata subsp. lyrata] >gi|297339449|gb|EFH69866.1| ATINT2 [Arabidopsis lyrata subsp. lyrata]	Unigene120583_All//5.00E-45//AT1G30220| INT2 (INOSITOL TRANSPORTER 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene120583_All//9.00E-47//TC133276			GO:0005365//GO:0015791//GO:0016020	nr +
Unigene120584_All	845	0.12	0.06	0.00	0.06	0.00	0.00	0.00	0.00	3.49	-1.05E+00	6.85E-01		-6.95E+00	3.95E-01		-5.88E+00	5.57E-01		-5.88E+00	6.38E-01		null	null		1.18E+01	4.24E-21	Up	Unigene120584_All//gi|32483159|emb|CAE02147.1|//8.00E-07//OSJNBa0081G05.2 [Oryza sativa (japonica cultivar-group)] >gi|116309213|emb|CAH66305.1| OS1GBa0135K14.2 [Oryza sativa (indica cultivar-group)] >gi|116309230|emb|CAH66320.1| OS1GBa0150M16.3 [Oryza sativa (indica cultivar-group)]	Unigene120584_All//5.00E-06//AT3G31430| unknown protein				GO:0003676	nr +
Unigene120586_All	284	0.18	0.71	0.19	0.00	0.00	0.80	0.30	0.74	5.61	1.95E+00	3.75E-01		2.56E-02	9.95E-01		null	null		9.64E+00	1.19E-01		1.31E+00	4.47E-01		4.24E+00	3.63E-09	Up			Unigene120586_All//7.00E-67//TC179320				
Unigene120587_All	265	0.00	0.00	0.00	0.00	0.13	0.17	0.00	0.00	1.95	null	null		null	null		7.02E+00	8.32E-01		7.41E+00	6.98E-01		null	null		1.09E+01	6.14E-04	Up								
Unigene120589_All	263	0.99	0.39	1.21	1.70	2.49	2.92	1.45	3.02	5.30	-1.37E+00	3.83E-01		2.88E-01	8.10E-01		5.45E-01	5.86E-01		7.76E-01	3.78E-01		1.06E+00	1.41E-01		1.87E+00	4.97E-04	Up			Unigene120589_All//1.00E-65//DT527202				
Unigene120593_All	380	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.57	null	null		null	null		null	null		null	null		null	null		1.06E+01	1.75E-04	Up								
Unigene120599_All	341	0.15	0.00	0.00	0.29	0.00	0.00	0.00	0.61	2.10	-7.26E+00	6.14E-01		-7.26E+00	6.27E-01		-8.19E+00	3.14E-01		-8.19E+00	4.01E-01		9.26E+00	7.85E-02		1.10E+01	2.63E-05	Up								
Unigene1206_All	2850	2.11	4.05	5.03	10.75	12.37	10.19	3.19	1.95	2.12	9.41E-01	3.34E-08		1.25E+00	8.30E-15	Up	2.03E-01	2.82E-02		-7.72E-02	5.31E-01		-7.10E-01	3.01E-05		-5.86E-01	3.87E-04		Unigene1206_All//gi|23452226|gb|AAN32954.1|//0.00E+00//alkaline alpha-galactosidase seed imbibition protein [Solanum lycopersicum]	Unigene1206_All//0.00E+00//AT1G55740| AtSIP1 (Arabidopsis thaliana seed imbibition 1); hydrolase, hydrolyzing O-glycosyl compounds	Unigene1206_All//0.00E+00//gi|48794228|gb|CO095542.1|CO095542		ko00052|Galactose metabolism	GO:0008152//GO:0008378	nr +
Unigene12060_All	2246	44.77	19.67	22.14	219.93	204.40	152.64	33.64	17.99	11.94	-1.19E+00	9.98E-96	Down	-1.02E+00	4.04E-72	Down	-1.06E-01	5.44E-07		-5.27E-01	6.06E-126		-9.03E-01	1.64E-56		-1.49E+00	5.00E-129	Down	Unigene12060_All//gi|1255951|emb|CAA65634.1|//0.00E+00//PS60 [Nicotiana tabacum]	Unigene12060_All//0.00E+00//AT1G76160| sks3 (SKU5 Similar 5); copper ion binding / oxidoreductase	Unigene12060_All//0.00E+00//TC135178		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0004091//GO:0005576//GO:0005618//GO:0008152//GO:0016682//GO:0046914	nr +
Unigene120601_All	596	0.00	0.00	0.00	0.00	0.00	0.23	0.28	0.42	2.41	null	null		null	null		null	null		7.83E+00	3.11E-01		5.68E-01	6.74E-01		3.08E+00	1.21E-06	Up			Unigene120601_All//7.00E-02//DR455508				
Unigene120608_All	283	0.00	0.00	0.00	0.18	0.24	0.48	0.30	0.00	3.66	null	null		null	null		4.68E-01	9.59E-01		1.44E+00	6.39E-01		-8.22E+00	4.05E-01		3.61E+00	1.38E-05	Up			Unigene120608_All//3.00E-07//gi|21093286|gb|BQ405599.1|BQ405599				
Unigene12061_All	883	5.57	2.18	3.38	10.49	11.78	5.73	4.50	2.65	4.78	-1.35E+00	1.86E-06	Down	-7.22E-01	1.07E-02		1.67E-01	4.23E-01		-8.73E-01	2.42E-06		-7.64E-01	5.07E-03		8.75E-02	7.45E-01		Unigene12061_All//gi|108706009|gb|ABF93804.1|//1.00E-42//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene12061_All//2.00E-59//AT2G17550| unknown protein	Unigene12061_All//0.00E+00//DW241161				nr +
Unigene120610_All	1024	0.00	0.00	0.00	0.10	0.00	0.00	0.78	0.04	19.45	null	null		null	null		-6.60E+00	3.14E-01		-6.60E+00	4.01E-01		-4.27E+00	8.48E-05	Down	4.63E+00	7.15E-115	Up	Unigene120610_All//gi|2055230|dbj|BAA19769.1|//4.00E-30//SRC2 [Glycine max]	Unigene120610_All//6.00E-17//AT1G09070| SRC2 (SOYBEAN GENE REGULATED BY COLD-2); protein binding	Unigene120610_All//0.00E+00//TC164100				nr +
Unigene120611_All	536	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.57	null	null		null	null		null	null		null	null		null	null		1.18E+01	1.02E-13	Up	Unigene120611_All//gi|6642775|gb|AF20282.1|//6.00E-18//gag-pol polyprotein [Vitis vinifera]					GO:0005488	nr +
Unigene120614_All	564	0.19	0.18	0.00	0.18	0.31	0.64	0.75	2.67	1.77	-4.58E-02	9.90E-01		-7.54E+00	3.95E-01		7.90E-01	7.71E-01		1.86E+00	2.20E-01		1.83E+00	4.72E-04	Up	1.24E+00	4.26E-02									

Unigene120617_All	636	0.00	0.00	0.00	0.00	0.00	0.00	3.79	9.27	18.85	null	null		null	null		null	null		null	null		1.29E+00	1.53E-08	Up	2.31E+00	3.46E-37	Up	Unigene120617_All//gi|238014838|gb|ACR38454.1|//4.00E-18//unknown [Zea mays]		Unigene120617_All//2.00E-44//TC146753				nr +
Unigene120062_All	1160	1.53	0.44	2.39	1.85	2.11	1.75	1.09	0.86	1.03	-1.81E+00	6.59E-04	Down	6.38E-01	1.08E-01		1.91E-01	6.89E-01		-7.59E-02	8.77E-01		-3.39E-01	5.58E-01		-8.59E-02	8.72E-01		Unigene12062_All//gi|108706008|gb|ABF93803.1|//9.00E-11//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene12062_All//7.00E-23//AT2G17550| unknown protein	Unigene12062_All//6.00E-154//gi|84153927|gb|DN803282.1|DN803282			GO:0043231	nr -
Unigene120620_All	290	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.72	1.79	null	null		null	null		null	null		null	null		9.49E+00	7.85E-02		1.08E+01	6.14E-04	Up	Unigene120620_All//gi|77548855|gb|ABA91652.1|//2.00E-08//Leucine Rich Repeat family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene120620_All//1.00E-07//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0003824//GO:0031410	nr +
Unigene120622_All	439	0.00	0.23	0.49	0.34	0.39	0.72	0.00	0.10	1.82	7.85E+00	3.88E-01		8.92E+00	1.41E-01		2.04E-01	9.50E-01		1.08E+00	4.76E-01		6.57E+00	6.36E-01		1.08E+01	7.36E-06	Up	Unigene120622_All//gi|223452564|gb|ACM89609.1|//8.00E-50//protein kinase [Glycine max]	Unigene120622_All//1.00E-18//AT5G38250| serine/threonine protein kinase, putative	Unigene120622_All//4.00E-57//DW499534		ko00270|Cysteine and methionine metabolism	GO:0004672//GO:0006464//GO:0031410 //GO:0032559//GO:0043231	nr -
Unigene120628_All	1467	0.00	0.00	0.04	0.03	0.00	0.06	0.12	0.23	7.71	null	null		5.18E+00	6.37E-01		-5.09E+00	5.57E-01		8.57E-01	7.95E-01		9.83E-01	4.24E-01		6.06E+00	5.32E-74	Up	Unigene120628_All//gi|297738384|emb|CBI27585.3|//2.00E-10//unnamed protein product [Vitis vinifera]		Unigene120628_All//3.00E-45//TC161766				nr +
Unigene12063_All	3217	3.04	0.74	1.08	4.43	5.88	1.98	3.54	2.12	4.14	-2.04E+00	4.99E-21	Down	-1.50E+00	2.48E-13	Down	4.08E-01	7.62E-04		-1.16E+00	1.12E-14	Down	-7.39E-01	8.96E-07		2.26E-01	1.10E-01		Unigene12063_All//gi|115450511|ref|NP_001048856.1|//2.00E-98//Os03g0130700 [Oryza sativa (japonica Group)] >gi|113547327|dbj|BAF10770.1| Os03g0130700 [Oryza sativa (japonica Group)]	Unigene12063_All//8.00E-88//AT2G17550| unknown protein	Unigene12063_All//0.00E+00//DW241161				nr +
Unigene120634_All	386	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.17	null	null		null	null		null	null		null	null		null	null		1.11E+01	3.89E-06	Up	Unigene120634_All//gi|147805049|emb|CAN71438.1|//9.00E-08//hypothetical protein [Vitis vinifera]					GO:0003676	nr +
Unigene120642_All	272	0.00	0.56	0.00	0.00	0.00	0.00	0.00	0.00	3.52	9.13E+00	2.36E-01		null	null		null	null		null	null		null	null		1.18E+01	5.69E-07	Up							
Unigene120650_All	364	323.27	285.78	388.55	190.64	281.92	638.49	1109.39	457.34	550.30	-1.78E-01	2.33E-04		2.65E-01	1.63E-09		5.64E-01	5.95E-33		1.74E+00	0.00E+00	Up	-1.28E+00	0.00E+00	Down	-1.01E+00	0.00E+00	Down	Unigene120650_All//gi|292653525|gb|ADE34280.1|//7.00E-23//aquaporin PIP1;11 [Gossypium hirsutum]	Unigene120650_All//7.00E-23//AT2G45960| PIP1B (NAMED PLASMA MEMBRANE INTRINSIC PROTEIN 1B); water channel	Unigene120650_All//1.00E-75//TC165394				nr +
Unigene120651_All	266	0.00	0.00	0.00	0.00	0.00	0.17	0.00	0.00	1.95	null	null		null	null		null	null		7.41E+00	6.97E-01		null	null		1.09E+01	6.14E-04	Up							
Unigene120654_All	346	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.48	10.71	null	null		null	null		null	null		null	null		9.83E-01	6.34E-01		5.45E+00	1.67E-23	Up							
Unigene120656_All	328	11.96	49.59	23.54	18.38	13.23	23.96	15.73	52.63	11.66	2.05E+00	1.50E-34	Up	9.77E-01	8.76E-06		-4.74E-01	4.30E-02		3.83E-01	7.64E-02		1.74E+00	3.37E-36	Up	-4.32E-01	6.11E-02		Unigene120656_All//gi|224144535|ref|XP_002325324.1|//3.00E-06//cytochrome P450 [Populus trichocarpa] >gi|222862199|gb|EEE99705.1| cytochrome P450 [Populus trichocarpa]	Unigene120656_All//7.00E-07//AT2G46950| CYP70B2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene120656_All//4.00E-56//TC170894			GO:0005506//GO:0008152//GO:0016491 //GO:0031410//GO:0043231	nr -
Unigene12066_All	1620	6.81	14.61	9.57	20.20	22.96	21.19	19.65	31.81	34.85	1.10E+00	2.02E-20	Up	4.89E-01	8.86E-04		1.84E-01	4.24E-02		6.87E-02	5.65E-01		6.95E-01	5.46E-25		8.26E-01	1.83E-37		Unigene12066_All//gi|75174756|sp|Q9LME4.1|P2C09_ARATH//1.00E-124//RecName: Full=Probable protein phosphatase 2C 9; Short=AtPP2C09; AltName: Full=Phytochrome-associated protein phosphatase 2C; Short=PAPP2C >gi|9392686|gb|AAF87263.1|AC068562_10 Strong similarity to protein phosphatase type 2C (PP2C2) from Lotus japonicus gb|AF092432 and contains a protein phosphatase 2C PF|00481 domain. EST gb|T46258 comes from this gene [Arabidopsis thaliana]	Unigene12066_All//4.00E-118//AT1G22280| protein phosphatase 2C, putative / PP2C, putative	Unigene12066_All//0.00E+00//TC169274				nr +
Unigene120662_All	457	0.00	0.00	0.00	0.33	0.38	0.40	0.00	0.18	1.66	null	null		null	null		2.05E-01	9.50E-01		2.74E-01	9.05E-01		7.51E+00	4.02E-01		1.07E+01	1.39E-05	Up							
Unigene120668_All	358	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.78	null	null		null	null		null	null		null	null		null	null		1.08E+01	9.34E-05	Up	Unigene120668_All//gi|146233385|gb|ABQ14360.1|//8.00E-21//abscisic acid ABA receptor [Populus trichocarpa]	Unigene120668_All//1.00E-19//AT2G20770| GCL2 (GCR2-LIKE 2); catalytic	Unigene120668_All//8.00E-58//gi|13350600|gb|BG440948.1|BG440948			GO:0043231//GO:0044425	nr -
Unigene120669_All	266	0.00	1.14	0.00	0.00	0.00	0.00	0.00	0.16	2.25	1.02E+01	4.44E-02		null	null		null	null		null	null		7.30E+00	6.36E-01		1.11E+01	1.75E-04	Up							
Unigene12067_All	1704	6.54	6.90	6.41	17.54	14.91	13.70	10.25	11.43	25.76	7.70E-02	6.61E-01		-2.98E-02	8.80E-01		-2.34E-01	1.76E-02		-3.56E-01	2.51E-04		1.58E-01	2.12E-01		1.33E+00	1.13E-62	Up	Unigene12067_All//gi|75174756|sp|Q9LME4.1|P2C09_ARATH//1.00E-121//RecName: Full=Probable protein phosphatase 2C 9; Short=AtPP2C09; AltName: Full=Phytochrome-associated protein phosphatase 2C; Short=PAPP2C >gi|9392686|gb|AAF87263.1|AC068562_10 Strong similarity to protein phosphatase type 2C (PP2C2) from Lotus japonicus gb|AF092432 and contains a protein phosphatase 2C PF|00481 domain. EST gb|T46258 comes from this gene [Arabidopsis thaliana]	Unigene12067_All//3.00E-113//AT1G22280| protein phosphatase 2C, putative / PP2C, putative	Unigene12067_All//0.00E+00//gi|84172716|gb|DR461364.1|DR461364				nr +
Unigene120673_All	978	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.20	null	null		null	null		null	null		null	null		null	null		1.11E+01	2.03E-15	Up	Unigene120673_All//gi|297806821|ref|XP_002871294.1|//6.00E-18//mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317131|gb|EFH47553.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene120673_All//1.00E-19//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene120673_All//1.00E-09//BQ414570				nr -
Unigene12068_All	3115	5.01	2.55	5.06	9.55	8.81	7.21	8.74	4.58	2.95	-9.71E-01	2.29E-11		1.57E-02	9.35E-01		-1.16E-01	3.07E-01		-4.06E-01	2.66E-05		-9.34E-01	4.50E-22		-1.57E+00	2.83E-50	Down	Unigene12068_All//gi|18408845|ref|NP_564904.1|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|263430191|sp|C0LGI2.1|Y1677_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g67720; Flags: Precursor >gi|224589467|gb|ACN59267.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene12068_All//0.00E+00//AT1G67720| leucine-rich repeat family protein / protein kinase family protein	Unigene12068_All//0.00E+00//TC140029			GO:0004672//GO:0006464//GO:0016020 //GO:0031410//GO:0032559	nr -
Unigene120680_All	709	0.15	0.21	0.15	0.21	0.39	0.13	0.48	1.47	2.36	5.39E-01	7.79E-01		2.52E-02	1.00E+00		8.82E-01	5.95E-01		-7.27E-01	7.16E-01		1.63E+00	1.04E-02		2.31E+00	8.00E-06	Up							
Unigene120681_All	217	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	3.30	null	null		null	null		null	null		null	null		7.59E+00	6.36E-01		1.17E+01	2.63E-05	Up			Unigene120681_All//4.00E-09//gi|109873402|gb|DW502377.1|DW502377				
Unigene120685_All	300	0.00	0.00	0.00	0.00	0.00	0.00	0.70	0.70	4.38	null	null		null	null		null	null		null	null		-1.67E-02	1.02E+00		2.64E+00	2.27E-05	Up	Unigene120685_All//gi|15229833|ref|NP_187777.1|//2.00E-07//ATKRS-1 (ARABIDOPSIS THALIANA LYSYL-TRNA SYNTHETASE 1); ATP binding / aminoacyl-tRNA ligase/ lysine-tRNA ligase/ nucleic acid binding / nucleotide binding [Arabidopsis thaliana] >gi|55583786|sp|Q9ZP11.1|SYK_ARATH RecName: Full=Lysyl-tRNA synthetase; AltName: Full=Lysine--tRNA ligase; Short=LysRS >gi|6041823|gb|AAF02138.1|AC009918_10 lysyl-tRNA synthetase [Arabidopsis thaliana] >gi|4325324|gb|AAD17333.1| lysyl-tRNA synthetase [Arabidopsis thaliana] >gi|20466171|gb|AAM20403.1| lysyl-tRNA synthetase [Arabidopsis thaliana] >gi|25083918|gb|AAN72134.1| lysyl-tRNA synthetase [Arabidopsis thaliana]	Unigene120685_All//8.00E-09//AT3G11710| ATKRS-1 (ARABIDOPSIS THALIANA LYSYL-TRNA SYNTHETASE 1); ATP binding / aminoacyl-tRNA ligase/ lysine-tRNA ligase/ nucleic acid binding / nucleotide binding	Unigene120685_All//8.00E-39//TC166126		ko00970|Aminoacyl-tRNA biosynthesis	GO:0004812//GO:0005488//GO:0006412	nr +
Unigene120688_All	562	3.35	0.72	1.71	5.23	4.66	2.89	1.58	1.64	1.21	-2.22E+00	4.65E-05	Down	-9.75E-01	5.03E-02		-1.67E-01	6.73E-01		-8.54E-01	1.88E-02		5.04E-02	9.61E-01		-3.91E-01	5.53E-01		Unigene120688_All//gi|259130059|gb|ACV95482.1|//8.00E-23//SCL6 [Citrus trifoliata]		Unigene120688_All//3.00E-129//TC146886			GO:0010467	nr +
Unigene120689_All	502	0.00	0.20	0.74	0.30	0.21	0.18	0.59	0.25	2.38	7.66E+00	3.88E-01		9.54E+00	2.50E-02		-5.33E-01	7.85E-01		-7.27E-01	7.16E-01		-1.24E+00	3.73E-01		2.01E+00	7.79E-04	Up	Unigene120689_All//gi|108863072|gb|ABG22121.1|//7.00E-58//polyprotein [Solanum melongena]	Unigene120689_All//8.00E-12//AT4G23160| protein kinase family protein	Unigene120689_All//0.00E+00//TC142698			GO:0003676//GO:0004518//GO:0006259 //GO:0008233//GO:0016779//GO:00469 14	nr -
Unigene120692_All	575	0.00	0.00	0.00	0.00	0.12	0.00	0.81	0.87	3.81	null	null		null	null		6.90E+00	6.11E-01		null	null		1.09E-01	9.15E-01		2.24E+00	3.75E-07	Up	Unigene120692_All//gi|297600122|ref|NP_001048517.2|//3.00E-27//Os02g0816900 [Oryza sativa (japonica Group)] >gi|255671354|dbj|BAF10431.2| Os02g0816900 [Oryza sativa (japonica Group)]	Unigene120692_All//7.00E-26//AT5G43900| MYA2 (ARABIDOPSIS MYOSIN 2); GTP-dependent protein binding / Rab GTPase binding / motor				GO:0008092//GO:0015629//GO:0017111 //GO:0032559	nr +
Unigene120696_All	337	0.00	0.00	0.00	0.00	0.00	0.00	0.38	0.50	2.60	null	null		null	null		null	null		null	null		3.98E-01	8.14E-01		2.79E+00	5.37E-04	Up			Unigene120696_All//8.00E-64//DN801902				
Unigene120697_All	408	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.54	null	null		null	null		null	null		null	null		null	null		1.13E+01	1.58E-07	Up	Unigene120697_All//gi|255570568|ref|XP_002526241.1|//8.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223534435|gb|EEF36138.1| conserved hypothetical protein [Ricinus communis]		Unigene120697_All//2.00E-40//CO112141				nr -
Unigene1207_All	2803	0.69	1.50	1.03	2.86	3.44	3.03	0.71	0.19	0.23	1.12E+00	2.18E-04	Up	5.71E-01	1.42E-01		2.66E-01	1.79E-01		8.23E-02	7.11E-01		-1.87E+00	2.98E-05	Down	-1.64E+00	1.05E-04	Down	Unigene1207_All//gi|23452226|gb|AAN32954.1|//0.00E+00//alkaline alpha-galactosidase seed imbibition protein [Solanum lycopersicum]	Unigene1207_All//0.00E+00//AT1G5740| AtSIPI (Arabidopsis thaliana seed imbibition 1); hydrolase, hydrolyzing O-glycosyl compounds	Unigene1207_All//0.00E+00//gi|48794228|gb|CO095542.1|CO095542		ko00052|Galactose metabolism	GO:0008152//GO:0008378	nr +
Unigene120700_All	513	0.41	0.00	0.00	0.10	0.00	0.00	0.08	0.24	2.41	-8.67E+00	1.22E-01		-8.67E+00	1.46E-01		-6.60E+00	5.57E-01		-6.60E+00	6.38E-01		1.57E+00	5.45E-01		4.87E+00	9.59E-08	Up			Unigene120700_All//1.00E-35//CO087197				
Unigene120703_All	241	113.11	89.35	86.17	73.17	52.01	68.21	94.56	52.03	23.97	-3.40E-01	1.17E-03		-3.92E-01	2.80E-04		-4.93E-01	5.59E-05		-1.01E-01	5.36E-01		-8.62E-01	2.34E-16		-1.98E+00	2.56E-58	Down			Unigene120703_All//1.00E-117//gi|13355216|gb|BG445468.1|BG445468				
Unigene120707_All	240	0.00	0.00	0.67	0.00	0.00	0.00	0.00	0.35	4.32	null	null		9.38E+00	2.39E-01		null	null		null	null		8.44E+00	4.02E-01		1.21E+01	1.58E-07	Up	Unigene120707_All//gi|3157938|gb|AAC17621.1|//3.00E-11//Similar to seryl-tRNA synthetase gb|U10400 from S cerevisiae. EST gb|N96627 comes from this gene [Arabidopsis thaliana]	Unigene120707_All//2.00E-06//AT3G06895| unknown protein					nr +

Unigene120708_All	412	0.13	0.74	0.00	0.24	0.08	0.33	47.41	36.11	325.77	2.54E+00	1.51E-01		-6.99E+00	6.27E-01		-1.53E+00	5.87E-01		4.44E-01	8.62E-01		-3.93E-01	4.42E-04		2.78E+00	0.00E+00	Up	Unigene120708_All//gi|39706891|emb|CAA77191.1|//3.00E-18//(+)-delta-cadinene synthase [Gossypium arboreum]	Unigene120708_All//6.00E-05//AT1G70080| terpene synthase/cyclase family protein	Unigene120708_All//4.00E-69//TC145282		ko00904|Diterpenoid biosynthesis	GO:0010334//GO:0046872	nr +
Unigene120711_All	321	0.00	0.00	0.00	0.62	0.00	0.00	4.48	19.14	9.18	null	null		null	null		-9.28E+00	8.44E-02		-9.28E+00	1.34E-01		2.10E+00	6.87E-17	Up	1.04E+00	1.16E-03		Unigene120711_All//gi|74273639|gb|ABA01487.1|//6.00E-17//flavin-containing monooxygenase family protein FMO2 [Gossypium hirsutum]	Unigene120711_All//6.00E-11//AT1G12140| FMO GS-OXS (FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5); S-methylthiopropyl glucosinolate S-oxygenase/ flavin-containing monooxygenase/ monooxygenase	Unigene120711_All//1.00E-22//TC129641			GO:0005789//GO:0008152//GO:0016709//GO:0030554	nr -
Unigene120713_All	283	0.18	0.00	0.19	0.70	0.00	0.00	9.86	1.77	5.49	-7.53E+00	6.14E-01		2.55E-02	9.95E-01		-9.46E+00	8.44E-02		-9.46E+00	1.34E-01		-2.48E+00	1.01E-09	Down	-8.45E-01	8.91E-03				Unigene120713_All//2.00E-42//gi|164256764|gb|ES837017.1|ES837017				
Unigene120718_All	886	0.00	0.00	0.00	0.00	0.00	0.05	0.24	0.61	2.70	null	null		null	null		null	null		5.67E+00	6.97E-01		1.36E+00	1.44E-01		3.50E+00	8.45E-12	Up	Unigene120718_All//gi|124359343|gb|ABD28505.2|//1.00E-23//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene120718_All//5.00E-05//AT4G00310| hypothetical protein			ko00270|Cysteine and methionine metabolism	GO:0005488//GO:0016740	nr -
Unigene120723_All	869	0.18	0.58	0.00	0.34	0.28	0.21	0.88	0.29	3.39	1.69E+00	1.34E-01		-7.50E+00	2.45E-01		-3.10E-01	8.20E-01		-7.26E-01	6.39E-01		-1.60E+00	3.70E-02		1.95E+00	5.08E-08	Up	Unigene120723_All//gi|240256061|ref|XP_194242.6|//1.00E-112//ATP binding / ATP-dependent DNA helicase/ DNA binding / hydrolase [Arabidopsis thaliana]	Unigene120723_All//7.00E-114//AT4G25120| ATP binding / ATP-dependent DNA helicase/ DNA binding / hydrolase			ko03420|Nucleotide excision repair//ko03430|Mismatch repair	GO:0004386//GO:0005488	nr +
Unigene120724_All	431	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.00	2.22	null	null		null	null		-6.85E+00	5.57E-01		-6.85E+00	6.38E-01		null	null		1.11E+01	5.69E-07	Up	Unigene120724_All//gi|6002055|emb|CAB56692.1|//3.00E-28//lipoxygenase [Arabidopsis thaliana]	Unigene120724_All//2.00E-29//AT1G17420| LOX3; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene120724_All//5.00E-124//TC177785		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0006633//GO:0006950//GO:0009642//GO:0009694//GO:0009719//GO:0016702//GO:0042221//GO:0043231//GO:0051707	nr +
Unigene120725_All	544	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.56	null	null		null	null		null	null		null	null		null	null		1.13E+01	4.73E-10	Up							
Unigene120727_All	274	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.15	2.33	null	null		null	null		null	null		null	null		-1.69E-02	1.00E+00		3.91E+00	7.66E-04	Up							
Unigene120730_All	725	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.23	1.92	null	null		null	null		null	null		null	null		1.98E+00	3.79E-01		5.04E+00	8.10E-09	Up	Unigene120730_All//gi|297823307|ref|XP_002879536.1|//3.00E-49//NPSN11 [Arabidopsis lyrata subsp. lyrata] >gi|297325375|gb|EFH55795.1| NPSN11 [Arabidopsis lyrata subsp. lyrata]	Unigene120730_All//9.00E-50//AT2G35190| NPSN11 (NOVEL PLANT SNARE 11); SNAP receptor/ protein transporter	Unigene120730_All//8.00E-152//gi|84166780|gb|DR455428.1|DR455428			GO:0005515//GO:0016020//GO:0044444//GO:0051301	nr -
Unigene120731_All	449	0.00	0.00	0.00	0.00	0.00	0.00	2.73	8.84	0.00	null	null		null	null		null	null		null	null		1.70E+00	1.33E-08	Up	-1.14E+01	4.03E-09	Down							
Unigene120734_All	400	0.00	0.00	0.00	0.00	0.00	0.11	0.00	0.10	10.96	null	null		null	null		null	null		6.82E+00	6.97E-01		6.71E+00	6.36E-01		1.34E+01	2.35E-31	Up	Unigene120734_All//gi|297834288|ref|XP_002885026.1|//9.00E-10//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297330866|gb|EFH61285.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene120734_All//7.00E-10//AT3G14250| protein binding / zinc ion binding	Unigene120734_All//2.00E-64//TC164726				nr -
Unigene120740_All	257	0.20	0.99	0.21	0.00	0.00	0.53	0.66	4.72	5.43	2.28E+00	2.34E-01		2.53E-02	9.95E-01		null	null		9.04E+00	3.11E-01		2.84E+00	3.39E-05	Up	3.04E+00	2.09E-06	Up							
Unigene120744_All	295	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.78	null	null		null	null		null	null		null	null		null	null		1.19E+01	4.36E-08	Up			Unigene120744_All//6.00E-49//DR453511				
Unigene120749_All	488	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.34	2.20	null	null		null	null		null	null		null	null		-3.39E-01	8.12E-01		2.35E+00	4.46E-04	Up	Unigene120749_All//gi|297720181|ref|NP_001172452.1|//1.00E-20//Os01g0601675 [Oryza sativa Japonica Group] >gi|20161036|dbj|BAB89968.1| HcrVf1 protein-like [Oryza sativa Japonica Group] >gi|20521201|dbj|BAB91719.1| HcrVf1 protein-like [Oryza sativa Japonica Group] >gi|255673433|dbj|BAH91182.1| Os01g0601675 [Oryza sativa Japonica Group]	Unigene120749_All//4.00E-09//AT5G20480| EFR (EF-TU RECEPTOR); ATP binding / kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction	GO:0003824	nr -
Unigene120753_All	287	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.29	2.08	null	null		null	null		null	null		null	null		8.19E+00	4.02E-01		1.10E+01	1.75E-04	Up	Unigene120753_All//gi|116174033|emb|CAL59721.1|//3.00E-16//glutathione peroxidase [Medicago sativa]	Unigene120753_All//3.00E-15//AT2G31570| ATGPX2 (GLUTATHIONE PEROXIDASE 2); glutathione peroxidase			ko00480|Glutathione metabolism//ko00590|Arachidonic acid metabolism	GO:0004601//GO:0005488//GO:0044424	nr -
Unigene120757_All	333	0.00	0.00	0.00	0.00	0.00	0.00	0.63	1.38	5.02	null	null		null	null		null	null		null	null		1.12E+00	2.74E-01		2.98E+00	1.99E-07	Up	Unigene120757_All//gi|253759136|ref|XP_002488914.1|//1.00E-07//hypothetical protein SORBIDRAFT_1962s002010 [Sorghum bicolor] >gi|241947219|gb|EES20364.1| hypothetical protein SORBIDRAFT_1962s002010 [Sorghum bicolor]		Unigene120757_All//2.00E-08//TC137772				nr -
Unigene120758_All	1290	0.00	0.00	0.00	0.00	0.00	0.07	1.18	0.23	1.27	null	null		null	null		null	null		6.13E+00	4.78E-01		-2.38E+00	2.15E-05	Down	1.02E-01	8.22E-01		Unigene120758_All//gi|18402992|ref|NP_566685.1|//4.00E-56//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|29029088|gb|AAO64923.1| At3g21420 [Arabidopsis thaliana]	Unigene120758_All//4.00E-58//AT3G21420| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene120758_All//1.00E-44//gi|310735529|gb|CA993808.1|CA993808		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis	GO:0008152//GO:0016491	nr +
Unigene120760_All	307	0.51	0.00	0.00	0.32	0.22	0.00	0.00	0.54	3.76	-9.00E+00	2.16E-01		-9.00E+00	2.45E-01		-5.33E-01	8.17E-01		-8.34E+00	4.01E-01		9.09E+00	1.39E-01		1.19E+01	2.28E-08	Up			Unigene120760_All//2.00E-33//TC151793				
Unigene120766_All	455	0.23	0.00	0.00	0.00	0.00	0.00	0.19	0.37	1.93	-7.85E+00	3.74E-01		-7.85E+00	3.95E-01		null	null		null	null		9.84E-01	6.34E-01		3.37E+00	1.32E-04	Up							
Unigene120767_All	368	0.00	0.00	0.00	0.00	0.00	0.00	0.34	0.34	4.22	null	null		null	null		null	null		null	null		-1.68E-02	1.02E+00		3.61E+00	4.47E-08	Up							
Unigene120769_All	308	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.81	null	null		null	null		null	null		null	null		null	null		1.08E+01	3.28E-04	Up	Unigene120769_All//gi|2244915|emb|CAB10337.1|//3.00E-07//reverse transcriptase like protein [Arabidopsis thaliana] >gi|7268307|emb|CAB78601.1| reverse transcriptase like protein [Arabidopsis thaliana]	Unigene120769_All//2.00E-05//AT4G20520| RNA binding / RNA-directed DNA polymerase					nr +
Unigene120779_All	237	0.00	0.00	0.00	0.00	0.00	0.38	0.00	0.00	2.19	null	null		null	null		null	null		8.57E+00	4.78E-01		null	null		1.11E+01	6.14E-04	Up			Unigene120779_All//3.00E-99//TC179259				
Unigene12078_All	2118	18.08	8.25	9.00	26.53	22.55	29.06	42.92	20.82	19.02	-1.13E+00	3.15E-34	Down	-1.01E+00	2.47E-27	Down	-2.35E-01	4.76E-04		1.32E-01	7.30E-02		-1.04E+00	3.60E-86	Down	-1.17E+00	4.50E-107	Down	Unigene12078_All//gi|297826149|ref|XP_002880957.1|//0.00E+00//CPN60A [Arabidopsis lyrata subsp. lyrata] >gi|297326796|gb|EFH57216.1| CPN60A [Arabidopsis lyrata subsp. lyrata]	Unigene12078_All//0.00E+00//AT2G28000| CPN60A (CHAPERONIN-60ALPHA); ATP binding / protein binding	Unigene12078_All//0.00E+00//TC137712		ko03018|RNA degradation	GO:0005515//GO:0005576//GO:0005840//GO:0006457//GO:0007275//GO:0009526//GO:0009532//GO:0009657//GO:0032559	nr -
Unigene120783_All	715	0.15	0.07	0.30	0.35	0.10	0.06	0.47	0.41	4.07	-1.05E+00	6.85E-01		1.02E+00	5.92E-01		-1.86E+00	2.75E-01		-2.46E+00	2.24E-01		-2.09E-01	8.50E-01		3.10E+00	7.47E-13	Up							
Unigene120784_All	347	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.95	null	null		null	null		null	null		null	null		null	null		1.09E+01	4.97E-05	Up							
Unigene120785_All	408	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.03	null	null		null	null		null	null		null	null		null	null		1.16E+01	6.29E-09	Up	Unigene120785_All//gi|9294121|dbj|BAB01972.1|//9.00E-21//copia-like retrotransposable element [Arabidopsis thaliana]					GO:0005488//GO:0009987	nr -
Unigene120786_All	291	0.00	0.35	0.37	0.68	0.71	0.47	0.29	0.00	3.70	8.44E+00	3.88E-01		8.52E+00	4.00E-01		5.23E-02	9.89E-01		-5.56E-01	7.33E-01		-8.18E+00	4.05E-01		3.67E+00	7.76E-06	Up	Unigene120786_All//gi|224094531|ref|XP_002310176.1|//6.00E-15//predicted protein [Populus trichocarpa] >gi|222853079|gb|EEE90626.1| predicted protein [Populus trichocarpa]	Unigene120786_All//3.00E-08//AT3G50380| INVOLVED IN: protein localization; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Vacuolar protein sorting-associated protein (InterPro:IPR009543); Has 239 Blast hits to 235 proteins in 73 species: Archae - 0; Bacteria - 0; Metazoa - 130; Fungi - 71; Plants - 23; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink).					nr +
Unigene12079_All	1968	0.74	0.18	0.32	1.01	1.21	0.76	2.99	1.15	2.37	-2.05E+00	8.60E-04	Down	-1.20E+00	4.21E-02		2.54E-01	5.87E-01		-4.19E-01	3.88E-01		-1.38E+00	2.19E-09	Down	-3.34E-01	1.26E-01		Unigene12079_All//gi|297839631|ref|XP_002887697.1|//1.00E-105//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333538|gb|EFH63956.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12079_All//2.00E-106//AT1G77720| protein kinase family protein	Unigene12079_All//0.00E+00//gi|164320529|gb|ES845294.1|ES845294			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene120794_All	382	0.00	0.00	0.00	0.00	0.00	0.35	0.22	0.11	2.19	null	null		null	null		null	null		8.47E+00	3.11E-01		-1.02E+00	7.25E-01		3.31E+00	2.30E-04	Up							
Unigene12080_All	2736	1.93	1.50	0.66	2.97	1.80	1.72	6.92	5.24	3.77	-3.65E-01	1.72E-01		-1.55E+00	8.52E-08	Down	-7.22E-01	1.27E-04		-7.90E-01	7.30E-05		-4.02E-01	4.01E-04		-8.76E-01	1.51E-14		Unigene12080_All//gi|297839631|ref|XP_002887697.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333538|gb|EFH63956.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12080_All//0.00E+00//AT1G77720| protein kinase family protein	Unigene12080_All//0.00E+00//ES838706			GO:0000166//GO:0004672	nr +
Unigene120800_All	442	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.97	null	null		null	null		null	null		null	null		null	null		1.15E+01	1.73E-09	Up	Unigene120800_All//gi|75174963|sp|Q6LN65.1|PPP7L_ARATH//7.00E-13//RecName: Full=Serine/threonine-protein phosphatase 7 long form homolog >gi|6778513|gb|AAF79521.1|AC023673_9 F21D18.16 [Arabidopsis thaliana]	Unigene120800_All//3.00E-14//AT1G48120| calcineurin-like phosphoesterase family protein					nr -
Unigene120801_All	423	0.00	0.00	0.00	0.00	0.41	0.32	0.00	0.89	2.26	null	null		null	null		8.67E+00	2.27E-01		8.32E+00	3.11E-01		9.80E+00	6.86E-03		1.11E+01	5.69E-07	Up	Unigene120801_All//gi|15223122|ref|NP_172287.1|//4.00E-09//ACA7 (ALPHA CARBONIC ANHYDRASE 7); carbonate dehydratase/ zinc ion binding [Arabidopsis thaliana]	Unigene120801_All//3.00E-10//AT1G08080| ACA7 (ALPHA CARBONIC ANHYDRASE 7); carbonate dehydratase/ zinc ion binding	Unigene120801_All//0.00E+00//DT463453		ko00910|Nitrogen metabolism	GO:0016836//GO:0031410//GO:0044237//GO:0046914	nr -
Unigene120804_All	257	0.00	0.20	1.86	0.19	0.40	0.00	0.00	0.33	2.02	7.62E+00	6.18E-01		1.09E+01	7.49E-03		1.05E+00	8.08E-01		-7.60E+00	6.38E-01		8.35E+00	4.02E-01		1.10E+01	6.14E-04	Up							
Unigene120806_All	1798	0.12	0.11	0.12	0.00	0.04	0.00	0.00	0.05	7.82	-4.66E-02	9.89E-01		2.58E-02	1.00E+00		5.26E+00	6.11E-01		null	null		5.54E+00	4.02E-01		1.29E+01	5.66E-101	Up			Unigene120806_All//3.00E-95//DN801641				
Unigene120807_All	253	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	2.83	null	null		null	null		null	null		null	null		7.37E+00	6.36E-01		1.15E+01	2.63E-05	Up							
Unigene120808_All	781	0.00	0.00	0.00	0.00	0.00	0.46	0.11	0.27	2.75	null	null		null	null		null	null		8.85E+00	2.37E-02		1.31E+00	4.47E-01		4.67E+00	7.12E-13	Up	Unigene120808_All//gi|18265373|dbj|BAB84015.1|//9.00E-51//polyprotein [Arabidopsis thaliana]	Unigene120808_All//5.00E-34//ATMG00810| hypothetical protein				GO:0005488	nr +
Unigene12081_All	1624	3.06	2.00	3.15	13.62	11.17	8.79	16.48	10.55	4.71	-6.16E-01	2.20E-02		4.05E-02	8.91E-01		-2.85E-01	1.25E-02		-6.32E-01	2.23E-08		-6.43E-01	8.62E-12		-1.81E+00	1.81E-60	Down	Unigene12081_All//gi|124359631|gb|ABN06010.1|//7.00E-66//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene12081_All//2.00E-49//AT4G29100| ethylene-responsive family protein	Unigene12081_All//0.00E+00//gi|78350945|gb|DT571219.1|DT571219	b4LH			nr -
Unigene120818_All	1038	0.00	0.15	0.00	0.14	0.23	0.78	0.41	0.97	4.95	7.19E+00	2.36E-01		null	null		6.89E-01	7.32E-01		2.44E+00	8.58E-03		1.25E+00	4.78E-02		3.60E+00	3.00E-25	Up	Unigene120818_All//gi|18092335|gb|AAL59227.1|AF448416_5//1.00E-127//serine threonine kinase [Zea mays]	Unigene120818_All//3.00E-101//AT2G24370| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene120818_All//6.00E-18//TC150706		ko04626|Plant-pathogen interaction		nr +
Unigene12082_All	462	0.45	0.22	0.81	3.88	2.53	0.98	1.83	0.36	0.09	-1.05E+00	5.63E-01		8.33E-01	5.16E-01		-6.15E-01	2.02E-01		-1.99E+00	1.66E-04	Down	-2.34E+00	2.95E-03		-4.41E+00	2.37E-05	Down			Unigene12082_All//5.00E-07//gi|13350370|gb|BG440718.1|BG440718				
Unigene120823_All	267	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.09	null	null		null	null		null	null		null	null		null	null		1.10E+01	3.28E-04	Up							
Unigene120828_All	404	0.00	0.00	0.00	0.49	0.17	0.11	0.42	1.34	2.76	null	null		null	null		-1.53E+00	4.16E-01		-2.14E+00	3.47E-01		1.68E+00	7.92E-02		2.72E+00	8.54E-05	Up			Unigene120828_All//1.00E-47//CD485672				

Unigene120829_A11	345	0.00	0.00	0.00	0.00	0.00	0.00	1.23	0.73	4.73	null	null		null	null		null	null		null	null		-7.54E-01	4.77E-01		1.95E+00	8.71E-05	Up			Unigene120829_A11//3.00E-08//gi|164335934|gb|ES793141.1|ES793141				
Unigene12083_A11	1678	1.78	1.54	1.65	13.45	8.17	9.61	10.48	11.46	3.59	-2.07E-01	5.99E-01		-1.07E-01	7.74E-01		-7.19E-01	9.56E-12		-4.85E-01	1.50E-05		1.28E-01	3.30E-01		-1.55E+00	2.86E-32	Down	Unigene12083_A11//gi|124359631|gb|ABN06010.1|//3.00E-70//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene12083_A11//1.00E-41//AT4G29100| ethylene-responsive family protein	Unigene12083_A11//0.00E+00//ES825648	b6LH				nr -
Unigene120833_A11	330	0.00	0.00	0.00	0.30	0.10	0.00	1.03	1.39	4.10	null	null		null	null		-1.53E+00	5.87E-01		-8.24E+00	4.01E-01		4.43E-01	6.32E-01		2.00E+00	3.24E-04	Up								
Unigene120837_A11	416	0.00	0.00	0.00	0.00	0.25	0.76	0.00	0.80	3.64	null	null		null	null		7.96E+00	4.57E-01		9.57E+00	4.08E-02		9.65E+00	1.27E-02		1.18E+01	6.77E-11	Up			Unigene120837_A11//5.00E-07//TC165305				
Unigene12084_A11	1596	1.11	0.35	0.80	4.68	4.36	2.97	9.35	5.84	2.47	-1.67E+00	1.37E-03		-4.77E-01	3.67E-01		-1.03E-01	6.79E-01		-6.56E-01	1.76E-03		-6.79E-01	1.48E-07		-1.92E+00	5.79E-37	Down	Unigene12084_A11//gi|124359631|gb|ABN06010.1|//3.00E-83//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene12084_A11//5.00E-66//AT4G29100| ethylene-responsive family protein	Unigene12084_A11//0.00E+00//TC149208	b6LH				nr +
Unigene120841_A11	1137	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.40	4.10	null	null		null	null		null	null		null	null		1.86E+00	8.80E-02		5.20E+00	7.14E-29	Up	Unigene120841_A11//gi|89179421|gb|AB063156.1|//7.00E-35//Retrotransposon gag protein [Asparagus officinalis]		Unigene120841_A11//6.00E-55//FL577106					nr -
Unigene120843_A11	417	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.50	4.30	null	null		null	null		null	null		null	null		8.97E+00	7.85E-02		1.21E+01	7.17E-13	Up	Unigene120843_A11//gi|2501025|sp|Q43776.1|SYK_SOLLC//5.00E-13//RecName: Full=Lysyl-tRNA synthetase; AltName: Full=Lysine--tRNA ligase; Short=LysRS >gi|11475851|emb|CAA64223.1| Lysyl-tRNA synthetase [Solanum lycopersicum]	Unigene120843_A11//2.00E-13//AT3G11710| ATKRS-1 (ARABIDOPSIS THALIANA LYSYL-TRNA SYNTHETASE 1); ATP binding / aminoacyl-tRNA ligase/ lysine+tRNA ligase/ nucleic acid binding / nucleotide binding			ko00970|Aminoacyl-tRNA biosynthesis	GO:0000166//GO:0004812//GO:0006418	nr -
Unigene120845_A11	403	0.26	0.00	0.00	0.12	0.34	0.00	0.31	0.62	3.86	-8.02E+00	3.74E-01		-8.02E+00	3.95E-01		1.47E+00	6.19E-01		-6.95E+00	6.38E-01		9.84E-01	5.17E-01		3.61E+00	4.47E-08	Up			Unigene120845_A11//2.00E-18//TC162543				
Unigene12085_A11	2560	15.41	12.92	12.36	33.78	29.10	31.01	33.23	20.75	12.43	-2.54E-01	3.48E-03		-3.19E-01	3.26E-04		-2.15E-01	4.33E-05		-1.23E-01	4.11E-02		-6.79E-01	3.41E-39		-1.42E+00	3.22E-134	Down	Unigene12085_A11//gi|5733806|gb|AAD6742.1|AF170921_1//0.00E+00//G protein beta subunit [Pisum sativum]	Unigene12085_A11//1.00E-174//AT4G34460| AGB1 (GTP BINDING PROTEIN BETA 1); GTPase/ nucleotide binding / protein binding	Unigene12085_A11//0.00E+00//TC159862			GO:0004468//GO:0005488//GO:0023060//GO:0031090//GO:0043231//GO:0060089	nr +
Unigene120850_A11	568	0.37	0.00	0.00	0.00	0.00	0.00	0.45	0.00	2.95	-8.53E+00	1.22E-01		-8.53E+00	1.46E-01		null	null		null	null		-8.80E+00	4.04E-02		2.72E+00	7.72E-07	Up	Unigene120850_A11//gi|15241674|ref|NP_195827.1|//1.00E-42//protein kinase-related [Arabidopsis thaliana] >gi|75335716|sp|Q9LZM4.1|WAKL9_ARATH RecName: Full=Wall-associated receptor kinase-like 20; Flags: Precursor	Unigene120850_A11//5.00E-44//AT5G02070| protein kinase-related				GO:0000166//GO:0004674	nr +
Unigene120851_A11	274	0.00	0.00	0.00	0.00	0.00	0.00	0.31	2.91	null	null	null		null	null		null	null		null	null		8.25E+00	4.02E-01		1.15E+01	7.36E-06	Up	Unigene120851_A11//gi|226440555|gb|ACO57136.1|//6.00E-10//lipoxygenase 1 [Capsicum annuum]	Unigene120851_A11//2.00E-10//AT1G55020| LOX1; lipoxygenase	Unigene120851_A11//9.00E-17//TC166459		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0008152	nr -
Unigene120855_A11	523	0.00	0.00	0.00	0.19	0.00	0.35	0.16	0.00	2.82	null	null		null	null		-7.57E+00	3.14E-01		8.59E-01	6.95E-01		-7.34E+00	4.05E-01		4.12E+00	2.19E-08	Up							
Unigene120857_A11	876	0.00	0.00	0.00	0.00	0.00	0.00	450.99	1299.68	68.54	null	null		null	null		null	null		null	null		1.53E+00	0.00E+00	Up	-2.72E+00	0.00E+00	Down	Unigene120857_A11//gi|5734103|sp|Q6CQE5|TAR1_KLULA//4.00E-06//Protein TAR1 OS=Kluyveromyces lactis GN=TAR1-A PE=4 SV=2		Unigene120857_A11//4.00E-09//DW234221				swissprot +
Unigene12086_A11	675	21.32	14.49	15.46	22.36	28.31	20.14	25.56	12.14	13.69	-5.57E-01	1.55E-04		-4.63E-01	2.65E-03		3.41E-01	5.73E-03		-1.51E-01	3.80E-01		-1.07E+00	8.67E-18	Down	-9.00E-01	6.60E-14		Unigene12086_A11//gi|195625480|gb|ACG34570.1|//8.00E-72//translocase of chloroplast 34 [Zea mays]	Unigene12086_A11//8.00E-65//AT1G02280| TOC33 (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 33); GTP binding / GTPase/ protein binding	Unigene12086_A11//0.00E+00//gi|78348021|gb|DT568295.1|DT568295			GO:0006605//GO:0008320//GO:0009527//GO:0017111//GO:0032561//GO:0042802	nr +
Unigene120866_A11	326	0.32	0.16	0.33	0.15	0.21	0.55	0.13	0.64	1.96	-1.05E+00	6.85E-01		2.54E-02	1.00E+00		4.68E-01	9.59E-01		1.86E+00	4.58E-01		2.31E+00	2.40E-01		3.91E+00	7.66E-04	Up							
Unigene120879_A11	1458	0.00	0.00	0.04	0.00	0.00	0.00	0.15	0.03	5.27	null	null		5.19E+00	6.37E-01		null	null		null	null		-2.34E+00	2.37E-01		5.18E+00	2.60E-47	Up	Unigene120879_A11//gi|297794385|ref|XP_002865077.1|//1.00E-54//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310912|gb|EFH11336.1|kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene120879_A11//6.00E-55//AT5G66310| kinesin motor family protein	Unigene120879_A11//7.00E-09//CO132658			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr -
Unigene120888_A11	2253	64.12	32.88	41.39	110.13	94.20	48.47	54.16	53.04	59.06	-9.64E-01	6.48E-98		-6.32E-01	6.27E-46		-2.26E-01	9.05E-15		-1.18E+00	4.36E-255	Down	-3.02E-02	5.98E-01		1.25E-01	2.01E-03		Unigene12088_A11//gi|116744390|dbj|BAF35859.1|//0.00E+00//soluble acid invertase [Pyrus pyrifolia var. culta] >gi|186397269|dbj|BAG30920.1|soluble acid invertase [Pyrus pyrifolia]	Unigene12088_A11//0.00E+00//AT1G12240| ATBETAFRUCT4; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene12088_A11//0.00E+00//CO084404		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism	GO:0004553//GO:0005618//GO:0043231//GO:0044238	nr +
Unigene120885_A11	673	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	4.44	null	null		null	null		null	null		null	null		7.54E+00	2.41E-01		1.21E+01	2.20E-21	Up	Unigene120885_A11//gi|122219157|sp|Q49KT9.1|YCF68_ELCCG//2.00E-13//RecName: Full=Uncharacterized protein ycf68; AltName: Full=ORF113	Unigene120885_A11//3.00E-06//AT3G26220| CYP71B3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene120885_A11//4.00E-67//TC175763		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0009536//GO:0019113//GO:0042598//GO:0044425	nr +
Unigene120889_A11	1022	0.00	0.05	0.00	0.00	0.00	0.00	0.41	0.16	2.30	5.63E+00	6.18E-01		null	null		null	null		null	null		-1.34E+00	2.24E-01		2.47E+00	1.78E-08	Up	Unigene120889_A11//gi|161564730|dbj|BAF98212.1|//9.00E-26//CM0216.280.nc [Lotus japonicus]	Unigene120889_A11//8.00E-31//AT4G35690| unknown protein					nr +
Unigene12089_A11	2298	9.27	3.22	5.07	17.69	14.01	8.04	8.52	7.51	8.20	-1.53E+00	2.90E-30	Down	-8.69E-01	3.24E-12		-3.36E-01	1.52E-05		-1.14E+00	1.50E-39	Down	-1.82E-01	1.37E-01		-5.50E-02	6.57E-01		Unigene12089_A11//gi|115548293|dbj|BAF34362.1|//0.00E+00//beta-fructofuranosidase [Citrus sinensis]	Unigene12089_A11//0.00E+00//AT1G12240| ATBETAFRUCT4; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene12089_A11//0.00E+00//TC138551		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism	GO:0004553//GO:0005618//GO:0043231//GO:0044238	nr +
Unigene120891_A11	262	0.20	0.19	0.20	0.00	0.00	0.17	0.48	0.48	3.35	-4.62E-02	9.86E-01		2.51E-02	9.95E-01		null	null		7.43E+00	6.97E-01		-1.65E-02	1.02E+00		2.79E+00	5.37E-04	Up			Unigene120891_A11//4.00E-25//ES815055				
Unigene120892_A11	229	0.00	0.00	0.00	0.00	0.15	0.00	17.17	27.19	2.78	null	null		null	null		7.23E+00	8.32E-01		null	null		6.63E-01	1.64E-03		-2.63E+00	8.53E-15	Down							
Unigene120894_A11	433	0.24	0.47	0.00	0.00	0.08	0.00	0.00	0.00	3.59	9.54E-01	6.22E-01		-7.92E+00	3.95E-01		6.31E+00	8.32E-01		null	null		null	null		1.18E+01	3.54E-11	Up							
Unigene12090_A11	685	0.99	1.55	1.87	5.16	4.17	2.31	1.23	1.10	1.05	6.46E-01	3.37E-01		9.10E-01	1.46E-01		-3.07E-01	3.82E-01		-1.16E+00	3.83E-04	Down	-1.69E-01	7.99E-01		-2.38E-01	7.03E-01		Unigene12090_A11//gi|225446195|ref|XP_002262878.1|//1.00E-63//PREDICTED: similar to TIP1 (TIP GROWTH DEFECTIVE 1) [Vitis vinifera]	Unigene12090_A11//1.00E-56//AT5G20350| TIP1 (TIP GROWTH DEFECTIVE 1); S-acyltransferase/ acyl binding	Unigene12090_A11//2.00E-180//gi|78326647|gb|DT546921.1|DT546921			GO:0008152//GO:0008415//GO:0009826//GO:0016628//GO:0044464//GO:0046914	nr -
Unigene120907_A11	249	0.21	0.20	0.86	0.20	0.00	0.18	0.51	0.17	9.12	-4.60E-02	9.86E-01		2.03E+00	3.62E-01		-7.64E+00	5.57E-01		-1.42E-01	9.54E-01		-1.60E+00	5.34E-01		4.16E+00	1.07E-12	Up			Unigene120907_A11//6.00E-30//TC154678				
Unigene120909_A11	450	0.00	0.00	0.00	0.00	0.00	0.00	0.28	3.99	1.42	null	null		null	null		null	null		null	null		3.82E+00	2.08E-09	Up	2.33E+00	1.05E-02		Unigene120909_A11//gi|224138226|ref|XP_002322761.1|//5.00E-56//cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa] >gi|222867391|gb|EEF04522.1|cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa]	Unigene120909_A11//1.00E-174//AT4G37990| ELI3-2 (ELICITOR-ACTIVATED GENE 3-2); aryl-alcohol dehydrogenase/ mannitol dehydrogenase	Unigene120909_A11//3.00E-98//TC179502		ko00940|Phenylpropanoid biosynthesis	GO:0008152//GO:0016616//GO:0046914	nr -
Unigene120910_A11	285	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.80	null	null		null	null		null	null		null	null		null	null		1.14E+01	7.36E-06	Up							ESTscan +
Unigene120911_A11	550	0.10	0.18	0.29	0.18	0.00	0.16	0.00	0.00	1.45	9.55E-01	7.27E-01		1.61E+00	5.11E-01		-7.50E+00	3.14E-01		-1.41E-01	9.51E-01		null	null		1.05E+01	7.36E-06	Up	Unigene120911_A11//gi|297800842|ref|XP_002868305.1|//2.00E-09//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297314141|gb|EFH44564.1|binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene120911_A11//1.00E-10//AT4G14190| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT3G42630.1); Has 7409 Blast hits to 2639 proteins in 94 species: Archae - 1; Bacteria - 0; Metazoa - 60; Fungi - 16; Plants - 7130; Viruses - 0; Other Eukaryotes - 202 (source: NCBI BLink).	Unigene120911_A11//5.00E-94//TC134631				nr -
Unigene120912_A11	355	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.91	null	null		null	null		null	null		null	null		null	null		1.09E+01	4.97E-05	Up	Unigene120912_A11//gi|297796257|ref|XP_002866013.1|//4.00E-30//glycosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311848|gb|EFH42272.1|glycosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene120912_A11//3.00E-30//AT5G54010| glycosyltransferase family protein	Unigene120912_A11//4.00E-146//TC159247			GO:0016757	nr -
Unigene120914_A11	434	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	4.50	null	null		null	null		null	null		null	null		7.59E+00	4.02E-01		1.21E+01	5.31E-14	Up							
Unigene120915_A11	259	0.40	0.59	0.00	0.00	0.00	0.35	1.47	0.16	10.15	5.39E-01	7.79E-01		-8.66E+00	3.95E-01		null	null		8.45E+00	4.78E-01		-3.19E+00	3.12E-02		2.79E+00	1.39E-10	Up			Unigene120915_A11//5.00E-49//TC149929				
Unigene120918_A11	447	0.59	0.11	0.95	0.56	0.46	1.01	16.93	21.23	63.19	-2.37E+00	2.14E-01		7.04E-01	5.54E-01		-2.70E-01	8.23E-01		8.59E-01	4.70E-01		3.26E-01	5.95E-02		1.90E+00	1.99E-67	Up	Unigene120918_A11//gi|195623082|gb|ACG33371.1|//1.00E-09//lactoylglutathione lyase [Zea mays]	Unigene120918_A11//2.00E-10//AT1G08110| lactoylglutathione lyase, putative / glyoxalase I, putative	Unigene120918_A11//5.00E-44//gi|31407128|gb|CD486163.1|CD486163		ko00620|Pyruvate metabolism	GO:0016846//GO:0043169	nr -
Unigene120922_A11	262	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.98	null	null		null	null		null	null		null	null		null	null		1.09E+01	6.14E-04	Up							
Unigene120925_A11	354	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.03	null	null		null	null		null	null		null	null		null	null		1.10E+01	2.63E-05	Up							
Unigene120926_A11	460	0.00	0.11	0.00	0.00	0.30	0.00	0.09	0.36	1.82	6.78E+00	6.18E-01		null	null		8.23E+00	3.19E-01		null	null		1.98E+00	3.79E-01		4.31E+00	4.10E-05	Up							
Unigene12093_A11	1807	15.35	12.76	21.28	1.76	2.31	7.85	0.28	1.41	0.93	-2.66E-01	1.17E-02		4.71E-01	9.72E-08		3.86E-01	2.25E-01		2.15E+00	3.13E-34	Up	2.33E+00	2.37E-08	Up	1.72E+00	2.90E-04	Up	Unigene12093_A11//gi|224075238|ref|XP_002304580.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222842012|gb|EEE79559.1|cytochrome P450 [Populus trichocarpa]	Unigene12093_A11//0.00E+00//AT3G61880| CYP78A9 (CYTOCHROME P450 78A9); monooxygenase/ oxygen binding	Unigene12093_A11//0.00E+00//TC151338		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016709//GO:0048608	nr -
Unigene120930_A11	339	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.12	2.23	null	null		null	null		null	null		null	null		-1.02E+00	7.25E-01		3.16E+00	6.83E-04	Up	Unigene120930_A11//gi|225445146|ref|XP_002280643.1|//4.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]						nr +
Unigene120933_A11	437	0.00	0.00	0.00	0.00	0.00	0.00	0.39	1.24	2.37	null	null		null	null		null	null		null	null		1.68E+00	7.92E-02		2.61E+00	2.37E-04	Up			Unigene120933_A11//9.00E-12//TC171825				
Unigene120934_A11	340	0.00	0.00	0.00	0.15	0.00	0.00	0.00	0.86	3.28	null	null		null	null		-7.19E+00	5.57E-01		-7.19E+00	6.38E-01		9.75E+00	2.35E-02		1.17E+01	4.36E-08	Up			Unigene120934_A11//2.00E-15//TC168986				
Unigene120938_A11	355	0.15	0.14	0.00	0.14	0.00	0.00	0.12	0.47	1.80	-4.68E-02	9.85E-01		-7.20E+00	6.26E-01		-7.13E+00	5.57E-01		-7.13E+00	6.38E-01		1.98E+00	3.79E-01		3.91E+00	7.65E-04	Up							
Unigene12094_A11	1824	22.14	11.42	6.31	6.83	9.95	19.34	5.17	2.29	0.52	-9.56E-01	1.65E-27		-1.81E+00	5.45E-70	Down	5.43E-01	7.86E-06		1.50E+00	8.71E-52	Up	-1.17E+00	1.66E-11	Down	-3.30E+00	2.59E-43	Down	Unigene12094_A11//gi|224075238|ref|XP_002304580.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222842012|gb|EEE79559.1|cytochrome P450 [Populus trichocarpa]	Unigene12094_A11//0.00E+00//AT3G61880| CYP78A9 (CYTOCHROME P450 78A9); monooxygenase/ oxygen binding	Unigene12094_A11//0.00E+00//TC131541		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016709//GO:0048608	nr +
Unigene120940_A11	383	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	8.22	null	null		null	null		null	null		null	null		6.77E+00	6.36E-01		1.30E+01	1.60E-22	Up							
Unigene120945_A11	351	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.93	null	null		null	null		null	null		null	null		null	null		1.09E+01	4.97E-05	Up							
Unigene12095_A11	1385	20.29	18.77	17.11	29.06	25.41	26.94	22.16	12.80	10.79	-1.12E-01	3.37E-01		-2.46E-01	2.62E-02		-1.94E-01	2.25E-02		-1.10E-01	2.69E-01		-7.93E-01	6.04E-19		-1.04E+00	2.79E-30	Down	Unigene12095_A11//gi|297793621|ref|XP_002864695.1|//0.00E+00//phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310530|gb|EFH40954.1|phospholipid/glycerol acyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12095_A11//0.00E+00//AT5G60620| phospholipid/glycerol acyltransferase family protein	Unigene12095_A11//0.00E+00//TC167090		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0008374	nr -

Unigene120953_All	335	0.00	6.05	0.32	0.30	0.00	0.13	1.39	5.86	12.84	1.26E+01	1.54E-11	Up	8.31E+00	4.00E-01		-8.22E+00	3.14E-01		-1.14E+00	6.77E-01		2.08E+00	7.81E-06	Up	3.21E+00	2.88E-19	Up	Unigene120953_All//gi|18417474|ref|NP_567835.1|//3.00E-09//CFIM-25 [Arabidopsis thaliana] >gi|15081674|gb|AAK82492.1|AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|20147173|gb|AAM10303.1|AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|21554114|gb|AAM63194.1| mRNA cleavage factor subunit-like protein [Arabidopsis thaliana]		Unigene120953_All//2.00E-46//TC161737			GO:0003824	nr -
Unigene120956_All	258	0.00	1.57	0.62	1.16	1.87	2.45	4.10	0.32	2.78	1.06E+01	1.36E-02		9.27E+00	2.39E-01		6.90E-01	5.67E-01		1.08E+00	2.69E-01		-3.66E+00	1.31E-05	Down	-5.60E-01	3.39E-01					Unigene120956_All//2.00E-63//TC179592					
Unigene120957_All	424	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.07	null	null		null	null		null	null		null	null		null	null		1.10E+01	2.05E-06	Up									
Unigene12096_All	1333	5.22	6.88	4.31	2.62	2.79	2.71	2.76	1.22	0.99	3.98E-01	3.94E-02		-2.75E-01	2.58E-01		9.30E-02	8.33E-01		5.13E-02	9.04E-01		-1.17E+00	5.63E-05	Down	-1.48E+00	4.90E-07	Down	Unigene12096_All//gi|18424377|ref|NP_568925.1|//1.00E-105//phospholipid/glycerol acyltransferase family protein [Arabidopsis thaliana] >gi|253509573|gb|ACT32031.1|AtGPAT9 [Arabidopsis thaliana]	Unigene12096_All//5.00E-106//AT5G60620|phospholipid/glycerol acyltransferase family protein	Unigene12096_All//0.00E+00//TC167090		ko00564|Glycerophospholipid metabolism/ko00561|Glycerolipid metabolism	GO:0016747	nr +
Unigene120962_All	473	1.44	2.89	0.11	1.26	0.73	0.29	23.51	2.92	4.21	1.01E+00	7.95E-02		-3.67E+00	4.81E-03		-7.96E-01	3.88E-01		-2.14E+00	4.39E-02		-3.01E+00	3.47E-45	Down	-2.48E+00	5.53E-38	Down				Unigene120962_All//1.00E-69//DW492418					
Unigene120966_All	231	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.41	null	null		null	null		null	null		null	null		null	null		1.12E+01	3.28E-04	Up									
Unigene12097_All	1317	0.68	0.81	0.93	21.33	20.11	22.74	8.44	7.74	3.96	2.58E-01	6.75E-01		4.62E-01	4.60E-01		-8.54E-02	5.06E-01		9.19E-02	4.58E-01		-1.25E-01	4.90E-01		-1.09E+00	1.98E-12	Down	Unigene12097_All//gi|30725324|gb|AAP37684.1|//6.00E-77//At3g01680 [Arabidopsis thaliana]	Unigene12097_All//3.00E-73//AT3G01680| unknown protein	Unigene12097_All//0.00E+00//ES817637				nr -
Unigene120971_All	635	0.00	0.00	0.00	0.31	0.33	0.57	0.27	0.46	3.70	null	null		null	null		5.24E-02	9.89E-01		8.59E-01	5.42E-01		7.91E-01	5.63E-01		3.80E+00	2.43E-12	Up	Unigene120971_All//gi|116309781|emb|CAH66822.1|//3.00E-28//OS10Ga0093K19.9 [Oryza sativa (indica cultivar-group)]	Unigene120971_All//9.00E-20//AT1G49920| zinc finger protein-related					nr -
Unigene120972_All	591	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.30	null	null		null	null		null	null		null	null		null	null		1.17E+01	5.31E-14	Up									
Unigene120973_All	395	0.00	0.00	0.00	0.13	0.17	0.00	0.32	0.00	2.22	null	null		null	null		4.68E-01	9.59E-01		-6.98E+00	6.38E-01		-8.33E+00	2.36E-01		2.79E+00	5.37E-04	Up									
Unigene120975_All	883	0.00	0.00	0.00	0.11	0.00	0.00	0.81	0.00	0.63	null	null		null	null		-6.82E+00	3.14E-01		-6.82E+00	4.01E-01		-9.67E+00	3.26E-05	Down	-3.66E-01	6.05E-01		Unigene120975_All//gi|17979520|gb|AAL50095.1|//8.00E-63//At2g41800/T11A7.10 [Arabidopsis thaliana] >gi|20153311|gb|AAM19894.1|At2g41800/T11A7.10 [Arabidopsis thaliana]	Unigene120975_All//2.00E-65//AT2G41810| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41800.1); Has 161 Blast hits to 157 proteins in 12 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 159; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene120975_All//9.00E-143//gi|78342877|gb|DT563151.1|DT563151			GO:0005618//GO:0008202//GO:0016741	nr +
Unigene120978_All	305	3.60	0.50	0.35	1.47	1.24	1.78	2.36	1.64	1.31	-2.85E+00	4.77E-04	Down	-3.37E+00	2.67E-04	Down	-2.43E-01	8.22E-01		2.74E-01	7.83E-01		-5.19E-01	5.08E-01		-8.51E-01	2.39E-01		Unigene120978_All//gi|112419535|dbj|BAF02935.1|//7.00E-24//RAD51 homolog [Populus nigra]	Unigene120978_All//2.00E-20//AT5G20850| ATRAD51; ATP binding / DNA binding / DNA-dependent ATPase/ damaged DNA binding / nucleoside-triphosphatase/ nucleotide binding / protein binding / sequence-specific DNA binding	Unigene120978_All//8.00E-70//gi|109885422|gb|DW514392.1|DW514392		ko03440|Homologous recombination	GO:0003677//GO:0006259//GO:0032559//GO:0033554//GO:0042623//GO:0043231	nr -
Unigene120980_All	772	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15.33	null	null		null	null		null	null		null	null		null	null		1.39E+01	6.75E-85	Up	Unigene120980_All//gi|11994232|dbj|BAB01354.1|//1.00E-20//pectin methylesterase-like protein [Arabidopsis thaliana]	Unigene120980_All//1.00E-21//AT3G24130| pectinesterase family protein			ko00500|Starch and sucrose metabolism/ko00040|Pentose and glucuronate interconversions	GO:0005618//GO:0016788	nr -
Unigene120981_All	343	0.00	0.15	0.00	0.00	0.20	0.00	0.00	0.24	1.51	7.21E+00	6.18E-01		null	null		7.65E+00	6.11E-01		null	null		7.93E+00	4.02E-01		1.06E+01	6.14E-04	Up				Unigene120981_All//4.00E-07//TC173839					
Unigene120983_All	381	0.00	0.13	0.00	0.00	0.00	0.00	0.11	0.11	2.51	7.06E+00	6.18E-01		null	null		null	null		null	null		-1.70E-02	1.00E+00		4.50E+00	6.81E-06	Up									
Unigene120985_All	526	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	5.98	null	null		null	null		null	null		null	null		-6.33E+00	6.59E-01		6.22E+00	6.08E-21	Up	Unigene120985_All//gi|836954|gb|AAC23542.1|//1.00E-33//receptor protein kinase [Ipomoea trifida]	Unigene120985_All//2.00E-31//AT4G27300| S-locus protein kinase, putative	Unigene120985_All//3.00E-09//DT463474		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004871//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene120987_All	729	0.00	0.00	0.00	0.14	0.09	0.06	0.23	0.06	1.86	null	null		null	null		-5.33E-01	8.17E-01		-1.14E+00	6.77E-01		-2.02E+00	3.68E-01		3.00E+00	3.58E-06	Up	Unigene120987_All//gi|79513307|ref|NP_196944.3|//8.00E-48//CYP724A1: electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	Unigene120987_All//9.00E-50//AT5G14400| CYP724A1: electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00905|Brassinosteroid biosynthesis	GO:0005506//GO:0009646//GO:0016129//GO:0016491//GO:0031410//GO:0032501	nr +
Unigene12099_All	2600	192.92	131.18	144.98	52.13	87.48	70.77	49.09	86.15	99.35	-5.57E-01	2.57E-130		-4.12E-01	4.64E-73		7.47E-01	4.22E-119		4.41E-01	5.30E-34		8.11E-01	1.91E-138		1.02E+00	2.94E-238	Up	Unigene12099_All//gi|18407650|ref|NP_564801.1|//0.00E+00//SCO1 (SNOWY COTYLEDON 1): ATP binding / translation elongation factor/ translation factor, nucleic acid binding [Arabidopsis thaliana] >gi|6630460|gb|AAF19548.1|AC007190_16 F23N19.11 [Arabidopsis thaliana] >gi|90855593|tpg|DAA05753.1|TPA_exp: elongation factor G [Arabidopsis thaliana]	Unigene12099_All//0.00E+00//AT1G62750| SCO1 (SNOWY COTYLEDON 1): ATP binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene12099_All//0.00E+00//TC146979			GO:0005576//GO:0006412//GO:0007275//GO:0008135//GO:0009526//GO:0009532//GO:0009657//GO:0017111//GO:0032559	nr -
Unigene120992_All	404	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.41	4.83	null	null		null	null		null	null		null	null		8.69E+00	1.39E-01		1.22E+01	5.31E-14	Up	Unigene120992_All//gi|24414262|gb|AAN59765.1|//6.00E-06//Putative retroelement [Oryza sativa Japonica Group]		Unigene120992_All//4.00E-131//TC170228				nr -
Unigene120994_All	284	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.00	1.96	null	null		null	null		null	null		7.31E+00	6.97E-01		null	null		1.09E+01	3.28E-04	Up									
Unigene120999_All	1860	0.00	0.00	0.00	0.08	0.00	0.02	2.27	0.99	4.58	null	null		null	null		-6.33E+00	1.66E-01		-1.72E+00	5.01E-01		-1.20E+00	8.94E-06	Down	1.01E+00	1.21E-08	Up	Unigene120999_All//gi|223452302|gb|ACM89479.1|//1.00E-137//cysteine-rich protein [Glycine max]	Unigene120999_All//9.00E-133//AT4G23180| CRK10 (CYSTEINE-RICH RLK10): ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene120999_All//6.00E-158//DT469086		ko04626|Plant-pathogen interaction		nr -
Unigene121_All	457	0.46	1.88	0.35	9.05	5.80	4.35	4.44	1.65	3.92	2.04E+00	1.59E-02		-3.90E-01	8.08E-01		-6.41E-01	2.48E-02		-1.06E+00	3.71E-04	Down	-1.43E+00	6.46E-04	Down	-1.79E-01	6.47E-01		Unigene121_All//gi|109729909|tpg|DA005768.1|//2.00E-21//TPA: TPA_inf: class III HD-Zip protein CNA2 [Medicago truncatula]	Unigene121_All//9.00E-21//AT1G52150| ATHB-15; DNA binding / transcription factor	Unigene121_All//3.00E-67//TC178623	HB			nr -
Unigene1210_All	2261	6.09	11.94	6.57	4.58	6.03	6.99	3.80	3.44	28.54	9.73E-01	4.10E-19		1.11E-01	5.18E-01		3.96E-01	7.67E-03		6.09E-01	8.62E-06		-1.43E-01	4.89E-01		2.91E+00	1.87E-254	Up	Unigene1210_All//gi|223452426|gb|ACM89540.1|//0.00E+00//protein kinase family protein [Glycine max]	Unigene1210_All//0.00E+00//AT1G70520| protein kinase family protein	Unigene1210_All//0.00E+00//TC148709		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr -
Unigene12100_All	1566	23.32	15.73	16.36	29.58	23.09	23.76	66.96	34.16	27.45	-5.69E-01	1.44E-10		-5.12E-01	1.85E-08		-3.58E-01	6.17E-07		-3.16E-01	3.51E-05		-9.71E-01	3.55E-88		-1.29E+00	2.31E-142	Down	Unigene12100_All//gi|118196907|gb|ABK78670.1|//1.00E-156//plastid phosphoenolpyruvate/phosphate translocator [Brassica napus] >gi|187940348|gb|ACD39395.1|plastid phosphoenolpyruvate/phosphate translocator [Brassica napus]	Unigene12100_All//9.00E-131//AT5G33320| CUE1 (CAB UNDEREXPRESSED 1): antiporter/ triose-phosphate transmembrane transporter	Unigene12100_All//0.00E+00//TC138063				nr +
Unigene121003_All	277	0.00	0.00	0.00	1.08	0.25	0.16	0.00	0.00	2.16	null	null		null	null		-2.12E+00	1.66E-01		-2.73E+00	1.37E-01		null	null		1.11E+01	1.75E-04	Up									
Unigene121008_All	576	0.36	0.53	1.11	0.61	0.24	0.47	0.51	0.22	2.70	5.39E-01	6.72E-01		1.61E+00	1.11E-01		-1.34E+00	3.08E-01		-3.64E-01	7.55E-01		-1.24E+00	3.73E-01		2.39E+00	1.16E-05	Up	Unigene121008_All//gi|226529551|ref|NP_001147794.1|//2.00E-122//BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 [Zea mays] >gi|195613782|gb|ACG28721.1|BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor [Zea mays]	Unigene121008_All//1.00E-110//AT5G48380| leucine-rich repeat family protein / protein kinase family protein				GO:0000166//GO:0016301//GO:0031410	nr +
Unigene121009_All	224	1.40	0.90	0.00	0.00	0.00	0.81	0.38	1.31	5.16	-6.31E-01	6.22E-01		-1.05E+01	4.92E-02		null	null		9.66E+00	1.95E-01		1.79E+00	2.24E-01		3.77E+00	2.44E-06	Up		Unigene121009_All//3.00E-05//AT5G16600| MYB43 (myb domain protein 43): DNA binding / transcription factor	Unigene121009_All//7.00E-51//DT462062				
Unigene121011_All	444	0.12	0.23	0.00	0.79	0.70	0.20	0.76	2.26	4.04	9.54E-01	7.27E-01		-6.88E+00	6.26E-01		-1.70E-01	8.58E-01		-1.95E+00	1.96E-01		1.57E+00	1.54E-02		2.41E+00	1.87E-06	Up	Unigene121011_All//gi|224123354|ref|XP_002319058.1|//2.00E-28//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222857434|gb|EEE94981.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene121011_All//5.00E-22//AT5G36930| disease resistance protein (TIR-NBS-LRR class), putative	Unigene121011_All//3.00E-98//BG441725			GO:0005488	nr +
Unigene121014_All	282	0.00	0.18	0.76	0.00	0.00	0.16	0.15	1.33	3.25	7.49E+00	6.18E-01		9.56E+00	1.41E-01		null	null		7.32E+00	6.97E-01		3.15E+00	3.41E-02		4.44E+00	1.24E-05	Up			Unigene121014_All//9.00E-17//TC149710					
Unigene121019_All	605	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.28	1.84	null	null		null	null		null	null		null	null		8.11E+00	1.39E-01		1.08E+01	4.36E-08	Up	Unigene121019_All//gi|8778679|gb|AF79687.1|AC022314.28//3.00E-02//PSC16.9 [Arabidopsis thaliana]	Unigene121019_All//6.00E-05//AT1G64255| SWIM zinc finger family protein	Unigene121019_All//2.00E-19//TC173041				nr +
Unigene12102_All	419	0.75	0.97	0.38	10.22	18.16	21.56	3.33	8.38	12.46	3.69E-01	7.24E-01		-9.74E-01	5.06E-01		8.29E-01	3.54E-05		1.08E+00	2.19E-08	Up	1.33E+00	1.24E-05	Up	1.90E+00	3.79E-13	Up	Unigene12102_All//gi|226532148|ref|NP_001148091.1|//3.00E-43//cytokinin-O-glucosyltransferase 2 [Zea mays] >gi|195615732|gb|ACG29696.1|cytokinin-O-glucosyltransferase 2 [Zea mays]	Unigene12102_All//3.00E-41//AT1G22400| UGT85A1: UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucuronosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene12102_All//0.00E+00//DW479450		ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis	GO:0035251	nr -
Unigene121020_All	427	0.74	1.66	0.25	0.12	0.40	0.42	0.59	1.76	3.55	1.18E+00	1.75E-01		-1.56E+00	3.30E-01		1.79E+00	5.21E-01		1.86E+00	4.58E-01		1.57E+00	4.21E-02		2.58E+00	6.02E-06	Up	Unigene121020_All//gi|42565171|ref|NP_189132.2|//6.00E-19//DNA binding [Arabidopsis thaliana]	Unigene121020_All//4.00E-20//AT3G24880| DNA binding				GO:0043231	nr -
Unigene121023_All	268	0.00	0.19	0.00	0.93	0.39	0.51	0.32	0.00	3.72	7.56E+00	6.18E-01		null	null		-1.27E+00	4.24E-01		-8.78E-01	6.16E-01		-8.30E+00	4.05E-01		3.56E+00	2.43E-05	Up	Unigene121023_All//gi|42568534|ref|NP_200268.3|//3.00E-09//BGLU41 (BETA GLUCOSIDASE 41): catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|281312219|sp|Q9FIU7.2|BGL41_ARATH RecName: Full=Putative beta-glucosidase 41; Short=AtBGLU41; Flags: Precursor	Unigene121023_All//1.00E-110//AT5G54570| BGLU41 (BETA GLUCOSIDASE 41): catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene121023_All//3.00E-41//CO118920		ko00500|Starch and sucrose metabolism/ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0015926//GO:0043167//GO:0044238	nr -
Unigene121024_All	323	0.32	0.16	0.00	0.77	0.75	0.70	0.00	0.65	2.10	-1.05E+00	6.85E-01		-8.34E+00	3.95E-01		-4.72E-02	9.51E-01		-1.41E-01	9.29E-01		9.34E+00	7.85E-02		1.10E+01	4.97E-05	Up	Unigene121024_All//gi|300507127|gb|ADK23939.1|//6.00E-17//3FAD [Gossypium hirsutum]	Unigene121024_All//2.00E-17//AT5G05580| FAD8 (FATTY ACID DESATURASE 8): omega-3 fatty acid desaturase	Unigene121024_All//9.00E-150//gi|109847537|gb|DW476517.1|DW476517		ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene121028_All	289	0.72	0.53	0.18	0.69	0.36	0.47	1.46	1.59	5.79	-4.61E-01	7.58E-01		-1.97E+00	3.81E-01		-9.48E-01	5.88E-01		-5.57E-01	7.33E-01		1.21E-01	9.07E-01		1.98E+00	5.62E-05	Up			Unigene121028_All//1.00E-68//gi|21097416|gb|BQ409729.1|BQ409729					

Unigene12103_All	702	2.16	6.64	2.96	7.66	8.98	8.94	0.54	0.18	0.85	1.62E+00	9.62E-08	Up	4.53E-01	3.48E-01		2.28E-01	3.93E-01		2.23E-01	4.06E-01		-1.60E+00	1.81E-01		6.51E-01	4.23E-01		Unigene12103_All//gi|37993655|gb|AAR06913.1|//7.00E-30//UDP-glycosyltransferase 85A8 [Stevia rebaudiana]	Unigene12103_All//9.00E-29//AT1G78270| AtUGT85A4 (UDP-glucosyl transferase 85A4); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring hexosyl groups	Unigene12103_All//7.00E-134//gi|48803456|gb|CO104770.1|CO104770		ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0035251	nr -
Unigene121038_All	734	0.00	0.14	0.00	0.20	0.09	0.55	0.06	0.06	2.50	7.11E+00	3.88E-01		null	null		-1.12E+00	5.84E-01		1.44E+00	2.82E-01		-1.76E-02	1.00E+00		5.44E+00	8.34E-12	Up	Unigene121038_All//gi|14589309|emb|CAC43237.1|//5.00E-88//lipoxygenase [Sesbania rostrata]	Unigene121038_All//2.00E-87//AT1G17420| LOX3; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene121038_All//4.00E-95//CO106436		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr -
Unigene12104_All	524	5.49	2.90	5.49	10.17	16.10	17.32	4.76	6.06	27.22	-9.21E-01	1.28E-02		-1.10E-03	9.98E-01		6.63E-01	4.67E-04		7.68E-01	4.37E-05		3.49E-01	2.96E-01		2.52E+00	1.61E-48	Up	Unigene12104_All//gi|226532148|ref|NP_001148091.1|//8.00E-43//cytokinin-O-glucosyltransferase 2 [Zea mays] >gi|195615732|gb|ACG29696.1|cytokinin-O-glucosyltransferase 2 [Zea mays]	Unigene12104_All//1.00E-40//AT1G78270| AtUGT85A4 (UDP-glucosyl transferase 85A4); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring hexosyl groups	Unigene12104_All//3.00E-172//TC148955		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0035251	nr -
Unigene121042_All	326	0.00	0.00	0.00	0.15	0.11	0.00	0.00	1.28	4.77	null	null		null	null		-5.33E-01	8.26E-01		-7.26E+00	6.38E-01		1.03E+01	3.65E-03		1.22E+01	3.54E-11	Up			Unigene121042_All//6.00E-154//DV848639					
Unigene121049_All	511	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.33	1.87	null	null		null	null		null	null		null	null		9.83E-01	6.34E-01		3.50E+00	4.29E-05	Up	Unigene121049_All//gi|209970622|gb|ACJ03072.1|//1.00E-32//HB06p [Malus floribunda]	Unigene121049_All//3.00E-10//AT2G15080| AtRLP19 (Receptor Like Protein 19); kinase/ protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene12105_All	1058	0.40	0.77	0.96	12.57	14.78	22.54	7.75	15.37	23.72	9.54E-01	2.26E-01		1.27E+00	8.36E-02		2.33E-01	1.19E-01		8.42E-01	2.78E-14		9.87E-01	1.03E-14		1.61E+00	5.77E-48	Up	Unigene12105_All//gi|37993655|gb|AAR06913.1|//5.00E-92//UDP-glycosyltransferase 85A8 [Stevia rebaudiana]	Unigene12105_All//7.00E-81//AT1G22380| AtUGT85A3 (UDP-glucosyl transferase 85A3); glucuronosyltransferase/ transcription factor/ transferase, transferring glycosyl groups	Unigene12105_All//0.00E+00//TC148955		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis	GO:0016757	nr +
Unigene121050_All	414	0.00	0.24	0.00	0.24	0.08	0.00	0.20	0.71	1.92	7.94E+00	3.88E-01		null	null		-1.53E+00	5.87E-01		-7.91E+00	4.01E-01		1.79E+00	2.24E-01		3.24E+00	3.96E-04	Up								
Unigene121051_All	222	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.51	null	null		null	null		null	null		null	null		null	null		1.13E+01	3.28E-04	Up			Unigene121051_All//3.00E-81//gi|78333794|gb|DT554068.1|DT554068					
Unigene121052_All	568	0.18	0.62	0.00	0.00	0.06	0.00	0.30	1.18	1.96	1.76E+00	2.18E-01		-7.53E+00	3.95E-01		5.92E+00	8.32E-01		null	null		1.98E+00	2.26E-02		2.72E+00	8.54E-05	Up	Unigene121052_All//gi|145358598|ref|NP_198601.2|//6.00E-21//SOS4 (SALT OVERLY SENSITIVE 4); kinase/ pyridoxal kinase [Arabidopsis thaliana] >gi|15277979|gb|AAK94021.1|AF400125_2 pyridoxal kinase-like protein SOS4 [Arabidopsis thaliana]	Unigene121052_All//1.00E-22//AT5G37850| SOS4 (SALT OVERLY SENSITIVE 4); kinase/ pyridoxal kinase	Unigene121052_All//0.00E+00//TC152567		ko00750|Vitamin B6 metabolism		nr +
Unigene121058_All	268	0.00	0.38	0.00	0.00	0.26	1.69	0.00	0.47	2.38	8.56E+00	3.88E-01		null	null		8.01E+00	6.11E-01		1.07E+01	7.76E-03		8.87E+00	2.41E-01		1.12E+01	9.34E-05	Up								ESTscan +
Unigene121059_All	940	0.33	0.54	0.00	0.48	0.04	0.48	0.63	0.18	5.09	6.90E-01	4.99E-01		-8.38E+00	4.92E-02		-3.70E+00	1.07E-02		1.08E-02	1.00E+00		-1.82E+00	4.72E-02		3.01E+00	3.91E-20	Up								
Unigene12106_All	1463	7.15	10.49	8.81	10.39	13.44	16.27	10.43	14.26	46.59	5.53E-01	1.01E-04		3.00E-01	7.92E-02		3.72E-01	1.89E-03		6.48E-01	2.95E-09		4.50E-01	2.65E-05		2.16E+00	7.64E-191	Up	Unigene12106_All//gi|157734205|gb|ABV68925.1|//1.00E-140//mandelonitrile glucosyltransferase UGT85A19 [Prunus dulcis]	Unigene12106_All//9.00E-130//AT1G22400| UGT85A1; UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucuronosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene12106_All//0.00E+00//TC136452		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene121063_All	407	1.03	1.37	1.83	3.43	2.96	4.99	97.23	88.62	286.21	4.13E-01	6.37E-01		8.33E-01	3.39E-01		-2.11E-01	7.29E-01		5.43E-01	2.57E-01		-1.34E-01	1.13E-01		1.56E+00	7.63E-209	Up			Unigene121063_All//6.00E-65//TC150997					
Unigene121065_All	723	0.00	0.14	0.00	0.62	0.14	0.12	0.76	0.69	2.42	7.13E+00	3.88E-01		null	null		-2.12E+00	7.28E-02		-2.31E+00	7.81E-02		-1.32E-01	8.80E-01		1.67E+00	2.73E-04	Up			Unigene121065_All//9.00E-07//TC167286					
Unigene121068_All	635	0.00	0.00	0.00	0.08	0.11	0.00	0.13	0.33	4.20	null	null		null	null		4.69E-01	9.59E-01		-6.29E+00	6.37E-01		1.30E+00	4.47E-01		4.98E+00	2.21E-16	Up								
Unigene121069_All	1961	0.05	0.23	0.00	0.20	0.14	0.09	0.26	0.06	5.61	2.12E+00	9.60E-02		-5.74E+00	3.95E-01		-5.32E-01	6.16E-01		-1.14E+00	3.80E-01		-2.02E+00	5.20E-02		4.44E+00	5.71E-62	Up	Unigene121069_All//gi|10176937|dbj|BAB10136.1|//3.00E-86//serine/threonine-specific kinase like protein [Arabidopsis thaliana]	Unigene121069_All//1.00E-80//AT5G65600| legume lectin family protein / protein kinase family protein			ko04626|Plant-pathogen interaction		nr +
Unigene12107_All	283	1.11	0.00	0.00	10.21	4.62	2.39	3.14	7.53	3.80	-1.01E+01	3.66E-02		-1.01E+01	4.92E-02		-1.14E+00	9.74E-04	Down	-2.09E+00	2.67E-07	Down	1.26E+00	1.68E-03		2.77E-01	6.37E-01		Unigene12107_All//gi|15225054|ref|NP_181455.1|//6.00E-12//PLP6 (PATATIN-LIKE PROTEIN 6); nutrient reservoir [Arabidopsis thaliana] >gi|3402683|gb|AAC28986.1| similar to latex allergen from Hevea brasiliensis [Arabidopsis thaliana] >gi|31711904|gb|AAP68308.1|At2g39220 [Arabidopsis thaliana]	Unigene12107_All//2.00E-13//AT2G39220| PLP6 (PATATIN-LIKE PROTEIN 6); nutrient reservoir	Unigene12107_All//1.00E-59//TC151191			GO:0003824//GO:0044238	nr +
Unigene121072_All	275	0.00	0.00	0.00	0.00	0.00	0.00	0.31	0.15	2.75	null	null		null	null		null	null		null	null		-1.02E+00	7.25E-01		3.16E+00	6.83E-04	Up								
Unigene121073_All	442	0.00	0.00	0.00	0.00	0.00	0.00	0.38	1.23	3.97	null	null		null	null		null	null		null	null		1.68E+00	7.92E-02		3.37E+00	1.42E-08	Up	Unigene121073_All//gi|145408590|ref|YP_001152214.1|//2.00E-06//08F124 [Pinus koraiensis] >gi|145048839|gb|ABF35456.1|08F124 [Pinus koraiensis]		Unigene121073_All//4.00E-26//TC142576				nr -
Unigene121075_All	382	1.64	7.03	0.42	3.52	4.24	2.13	8.41	11.27	9.39	2.10E+00	1.94E-06	Up	-1.97E+00	6.50E-02		2.67E-01	6.37E-01		-7.26E-01	2.23E-01		4.22E-01	1.20E-01		1.58E-01	6.05E-01		Unigene121075_All//gi|14030723|gb|AAK53036.1|AF375452_1//4.00E-10//AT4g27450/F27G19_50 [Arabidopsis thaliana]		Unigene121075_All//7.00E-46//EV496019				nr -
Unigene121076_All	584	0.00	0.00	0.09	0.00	0.00	0.08	0.22	0.00	2.39	null	null		6.51E+00	6.37E-01		null	null		6.27E+00	6.97E-01		-7.76E+00	2.36E-01		3.46E+00	4.41E-07	Up	Unigene121076_All//gi|2160169|gb|AB60732.1|//5.00E-41//P21M12.17 gene product [Arabidopsis thaliana]	Unigene121076_All//2.00E-42//AT1G09790| COBL6 (COBRA-LIKE PROTEIN 6 PRECURSOR)					nr -
Unigene121077_All	849	0.00	0.42	0.06	0.12	0.16	0.00	0.25	0.59	1.74	8.71E+00	2.46E-02		5.97E+00	6.37E-01		4.68E-01	8.77E-01		-6.87E+00	4.01E-01		1.25E+00	2.04E-01		2.80E+00	2.86E-06	Up	Unigene121077_All//gi|2865437|gb|AAC02672.1|//8.00E-55//polyprotein [Arabidopsis arenosa]	Unigene121077_All//7.00E-46//AT4G23160| protein kinase family protein					nr +
Unigene121078_All	300	0.35	18.75	0.36	0.33	1.38	1.96	1.41	4.32	2.92	5.75E+00	6.36E-29	Up	2.54E-02	1.00E+00		2.05E+00	1.47E-01		2.56E+00	2.87E-02		1.62E+00	3.75E-03		1.05E+00	1.07E-01				Unigene121078_All//4.00E-05//AT4G02120| CTP synthase, putative / UTP--ammonia ligase, putative					
Unigene121080_All	370	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.23	null	null		null	null		null	null		null	null		null	null		1.17E+01	1.20E-08	Up								
Unigene121083_All	279	0.00	0.00	0.00	0.00	0.25	0.00	0.30	0.30	4.14	null	null		null	null		7.95E+00	6.11E-01		null	null		-1.68E-02	1.01E+00		3.77E+00	2.44E-06	Up								
Unigene121084_All	306	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.00	2.21	null	null		null	null		null	null		null	null		-7.11E+00	6.59E-01		4.00E+00	4.29E-04	Up								ESTscan +
Unigene121088_All	751	0.00	0.47	0.14	0.00	0.18	0.12	0.34	1.28	2.81	8.88E+00	2.46E-02		7.15E+00	4.00E-01		7.52E+00	3.19E-01		6.91E+00	4.78E-01		1.92E+00	5.42E-03		3.06E+00	2.16E-09	Up			Unigene121088_All//9.00E-07//gi|78324822|gb|DT545096.1|DT545096					
Unigene121091_All	827	0.63	0.18	0.39	0.36	0.12	0.11	0.46	0.45	2.46	-1.78E+00	1.08E-01		-7.12E-01	4.97E-01		-1.53E+00	2.98E-01		-1.73E+00	2.89E-01		-1.64E-02	1.02E+00		2.42E+00	3.00E-07	Up			Unigene121091_All//1.00E-06//TC138217					
Unigene121097_All	700	0.00	0.00	0.15	0.00	0.00	0.00	0.42	0.96	17.19	null	null		7.25E+00	4.00E-01		null	null		null	null		1.18E+00	1.44E-01		5.35E+00	7.19E-75	Up								
Unigene1211_All	2297	0.64	0.77	0.35	21.30	6.42	3.42	19.57	3.88	22.96	2.76E-01	5.96E-01		-8.75E-01	1.34E-01		-1.73E+00	4.25E-103	Down	-2.64E+00	5.49E-153	Down	-2.34E+00	1.26E-136	Down	2.31E-01	3.39E-04		Unigene1211_All//gi|15231450|ref|NP_187390.1|//1.00E-106//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75313804|sp|Q9SRT2.1|BH062_ARATH RecName: Full=Transcription factor bHLH62; AltName: Full=Transcription factor EN 85; AltName: Full=bHLH transcription factor bHLH062; AltName: Full=Basic helix-loop-helix protein 62; Short=bHLH 62; Short=AtbHLH62 >gi|11074462|gb|AB404604.1|At3g07340 [Arabidopsis thaliana]	Unigene1211_All//7.00E-108//AT3G07340| basic helix-loop-helix (bHLH) family protein	Unigene1211_All//0.00E+00//gi|3326739|gb|AI055625.1|AI055625	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr +
Unigene12110_All	1128	1.21	0.09	0.57	5.74	4.27	3.92	7.38	9.04	22.85	-3.75E+00	5.95E-06	Down	-1.09E+00	7.48E-02		-4.26E-01	6.22E-02		-5.49E-01	1.77E-02		2.92E-01	8.23E-02		1.63E+00	6.11E-50	Up	Unigene12110_All//gi|42565806|ref|NP_190631.2|//1.00E-106//nodulation protein-related [Arabidopsis thaliana] >gi|45773806|gb|AA576707.1|At3g50620 [Arabidopsis thaliana] >gi|11405071|gb|AB149485.1|At3g50620 [Arabidopsis thaliana]	Unigene12110_All//6.00E-102//AT3G50620| nodulation protein-related	Unigene12110_All//1.00E-133//C0070003			GO:0006787//GO:0016705//GO:0016782	nr -
Unigene121104_All	537	0.00	0.28	0.00	0.00	0.06	0.08	0.31	0.39	1.85	8.15E+00	2.36E-01		null	null		6.00E+00	8.32E-01		6.39E+00	6.97E-01		3.06E-01	8.36E-01		2.56E+00	3.91E-04	Up			Unigene121104_All//6.00E-07//gi|21098650|gb|BQ410963.1|BQ410963					
Unigene121105_All	431	0.00	0.00	0.00	0.00	0.00	0.31	0.00	0.19	1.76	null	null		null	null		null	null		8.30E+00	3.11E-01		7.60E+00	4.02E-01		1.08E+01	1.39E-05	Up	Unigene121105_All//gi|225426710|ref|XP_002275471.1|//2.00E-58//PREDICTED: similar to subtilase [Vitis vinifera]	Unigene121105_All//1.00E-37//AT5G67360| ARA12; serine-type endopeptidase					nr -
Unigene121109_All	280	0.00	0.00	0.00	0.00	0.00	0.00	44.85	98.82	2.70	null	null		null	null		null	null		null	null		1.14E+00	1.01E-30	Up	-4.05E+00	6.10E-68	Down								
Unigene12111_All	1363	2.38	1.52	0.86	2.81	3.21	2.72	4.00	0.49	1.58	-6.43E-01	6.20E-02		-1.47E+00	9.62E-05	Down	1.89E-01	5.85E-01		-5.07E-02	8.93E-01		-3.03E+00	1.35E-22	Down	-1.34E+00	9.90E-09	Down	Unigene12111_All//gi|42565806|ref|NP_190631.2|//1.00E-137//nodulation protein-related [Arabidopsis thaliana] >gi|45773806|gb|AA576707.1|At3g50620 [Arabidopsis thaliana] >gi|11405071|gb|AB149485.1|At3g50620 [Arabidopsis thaliana]	Unigene12111_All//3.00E-138//AT3G50620| nodulation protein-related	Unigene12111_All//0.00E+00//BE055090				nr +
Unigene12110_All	352	0.30	0.58	0.45	0.00	0.59	2.31	0.72	0.36	1.70	9.54E-01	6.22E-01		6.10E-01	7.48E-01		9.20E+00	1.57E-01		1.12E+01	6.95E-05	Up	-1.02E+00	4.95E-01		1.24E+00	1.39E-01									
Unigene121111_All	1238	0.17	0.00	0.04	0.00	0.03	0.00	1.20	2.53	3.57	-7.40E+00	1.22E-01		-1.97E+00	3.81E-01		4.80E+00	8.32E-01		null	null		1.08E+00	6.38E-04	Up	1.58E+00	6.84E-09	Up	Unigene121111_All//gi|18398327|ref|NP_566341.1|//2.00E-65//protein kinase family protein [Arabidopsis thaliana]	Unigene121111_All//9.00E-67//AT3G09010| protein kinase family protein	Unigene121111_All//0.00E+00//TC178777		ko04626|Plant-pathogen interaction		nr +
Unigene121112_All	289	0.36	2.10	0.37	0.00	0.24	2.66	0.15	0.00	1.10	2.54E+00	2.46E-02		2.53E-02	1.00E+00		7.90E+00	6.11E-01		1.14E+01	1.27E-04	Up	-7.19E+00	6.59E-01		2.91E+00	5.99E-02									
Unigene121115_All	456	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.49	null	null		null	null		null	null		null	null		null	null		1.05E+01	4.97E-05	Up	Unigene121115_All//gi|124359343|gb|ABR28505.2|//1.00E-22//RNA-directed DNA polymerase (Reverse transcriptase): Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene121115_All//9.00E-06//ATMG01250| hypothetical protein					nr +
Unigene121123_All	284	0.00	0.00	0.00	0.18	0.73	0.16	0.00	0.59	4.21	null	null		null	null		2.05E+00	3.95E-01		-1.42E-01	9.54E-01		9.20E+00	1.39E-01		1.20E+01	1.20E-08	Up								
Unigene121125_All	790	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.21	2.72	null	null		null	null		null	null		null	null		9.84E-01	6.34E-01		4.67E+00	7.12E-13	Up			Unigene121125_All//1.00E-27//TC159777					nr +
Unigene12113_All	2866	3.38	2.51	2.92	4.35	2.99	3.66	4.69	2.19	2.79	-4.28E-01	2.15E-02		-2.11E-01	3.13E-01		-5.38E-01	2.98E-04		-2.49E-01	1.51E-01		-1.10E+00	1.43E-14	Down	-7.48E-01	2.84E-08		Unigene12113_All//gi|297839813|ref|XP_002887788.1|//0.00E+00//EMB2217 [Arabidopsis lyrata subsp. lyrata] >gi|297333629|gb|EFH64047.1|EMB2217 [Arabidopsis lyrata subsp. lyrata]	Unigene12113_All//0.00E+00//AT1G79490| EMB2217 (embryo defective 2217)	Unigene12113_All//0.00E+00//TC162139			GO:0043231	nr +
Unigene121134_All	957	0.00	0.53	0.00	0.42	0.18	0.09	0.35	0.26	4.25	9.05E+00	4.05E-03		null	null		-1.21E+00	3.14E-01		-2.14E+00	1.26E-01		-4.32E-01	7.03E-01		3.59E+00	5.13E-20	Up	Unigene121134_All//gi|51471932|gb|AAU04436.1|//4.00E-55//MAPKK [Solanum lycopersicum]	Unigene121134_All//2.00E-54//AT1G73500| MKK9 (MAP KINASE KINASE 9); MAP kinase kinase/ kinase/ protein kinase activator	Unigene121134_All//0.00E+00//TC178080		ko04626|Plant-pathogen interaction		nr -
Unigene121136_All	346	0.15	0.29	0.15	0.29	0.20	0.00	0.12	0.48	1.84	9.54E-01	7.27E-01		2.55E-02	9.95E-01		-5.33E-01	8.17E-01		-8.17E+00	4.01E-01		1.98E+00	3.79E-01		3.91E+00	7.65E-04	Up								

Unigene121137_All	443	0.00	0.34	0.48	0.45	0.86	0.51	0.38	0.85	2.16	8.42E+00	2.36E-01		8.91E+00	1.41E-01		9.27E-01	5.23E-01		1.80E-01	9.35E-01		1.15E+00	3.27E-01		2.50E+00	6.42E-04	Up	Unigene121137_All//gi|124359892|gb|ABN07918.1|//4.00E-51//Zinc finger, ZZ-type; Zinc finger, C2H2-type [Medicago truncatula]	Unigene121137_All//2.00E-41//AT3G02260| BIG (BIG); binding / ubiquitin-protein ligase/ zinc ion binding	Unigene121137_All//0.00E+00//TC141392				nr -
Unigene121145_All	789	0.00	0.00	0.00	0.00	0.00	0.00	1.07	0.11	0.91	null	null		null	null		null	null		null	null		-3.34E+00	2.51E-04	Down	-2.38E-01	7.03E-01		Unigene121145_All//gi|288559172|sp|B9HBX2.1|U4978_POPTR//5.00E-61//RecName: Full=UPF0497 membrane protein 8	Unigene121145_All//2.00E-47//AT5G06200| integral membrane family protein					nr -
Unigene12115_All	3737	0.98	2.25	0.61	2.29	2.05	3.11	6.12	6.14	5.40	1.20E+00	8.66E-09	Up	-6.78E-01	4.48E-02		-1.65E-01	4.68E-01		4.38E-01	8.94E-03		4.60E-03	1.01E+00		-1.80E-01	9.20E-02		Unigene12115_All//gi|297835306|ref|XP_002885535.1|//0.00E+00//elongation factor Tu family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331375|gb|EFH61794.1| elongation factor Tu family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12115_All//0.00E+00//AT3G22980| elongation factor Tu family protein	Unigene12115_All//0.00E+00//TC154283			GO:0008135//GO:0017111//GO:0032561	nr +
Unigene121153_All	227	0.00	0.00	0.00	0.22	0.00	0.00	0.19	1.29	3.51	null	null		null	null		-7.78E+00	5.57E-01		-7.78E+00	6.37E-01		2.79E+00	9.48E-02		4.24E+00	7.42E-05	Up								
Unigene121160_All	278	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.15	2.01	null	null		null	null		null	null		null	null		7.23E+00	6.36E-01		1.10E+01	3.28E-04	Up								
Unigene121163_All	363	0.00	0.00	0.00	0.00	0.00	0.12	0.00	0.00	2.09	null	null		null	null		null	null		6.96E+00	6.97E-01		null	null		1.10E+01	1.39E-05	Up	Unigene121163_All//gi|226494135|ref|NP_001148004.1|//4.00E-25//serine carboxypeptidase [Zea mays] >gi|195615072|gb|ACG29366.1| serine carboxypeptidase [Zea mays]	Unigene121163_All//1.00E-24//AT5G23210| SCPL34; serine-type carboxypeptidase					nr +
Unigene121167_All	272	0.38	1.30	0.00	0.18	0.13	4.15	0.00	0.46	2.34	1.76E+00	2.18E-01		-8.59E+00	3.95E-01		-5.32E-01	8.26E-01		4.50E+00	1.14E-05	Up	8.85E+00	2.41E-01		1.12E+01	9.34E-05	Up		Unigene121167_All//2.00E-82//TC171084					
Unigene12117_All	2667	8.16	6.06	8.45	13.39	13.44	14.22	16.82	13.43	7.32	-4.29E-01	2.59E-04		4.95E-02	7.05E-01		5.30E-03	9.67E-01		8.70E-02	4.13E-01		-3.25E-01	4.64E-06		-1.20E+00	3.93E-55	Down	Unigene12117_All//gi|18407911|ref|NP_566873.1|//0.00E+00//2-phosphoglycerate kinase-related [Arabidopsis thaliana]	Unigene12117_All//0.00E+00//AT3G45090| 2-phosphoglycerate kinase-related	Unigene12117_All//0.00E+00//TC176167				nr -
Unigene121171_All	377	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.59	null	null		null	null		null	null		null	null		null	null		1.06E+01	1.75E-04	Up	Unigene121171_All//gi|1170239|sp|P42044.1|HEM1_CUCSA//4.00E-14//RecName: Full=Ferrochelatase-2, chloroplastic; AltName: Full=Ferrochelatase II; AltName: Full=Protoheme ferro-lyase 2; AltName: Full=Heme synthase 2; Flags: Precursor >gi|474968|dbj|BAA05102.1| ferrochelatase [Cucumis sativus]	Unigene121171_All//9.00E-14//AT5G26030| FC1 (ferrochelatase 1); ferrochelatase	Unigene121171_All//7.00E-09//EX168018		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene121173_All	1019	0.41	0.10	0.94	0.39	0.88	0.35	0.54	0.16	2.50	-2.05E+00	1.21E-01		1.20E+00	1.15E-01		1.17E+00	1.33E-01		-1.41E-01	9.04E-01		-1.72E+00	7.23E-02		2.21E+00	4.17E-08	Up	Unigene121173_All//gi|297847516|ref|XP_002891639.1|//1.00E-117//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337481|gb|EFH67898.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene121173_All//4.00E-119//AT1G51440| lipase class 3 family protein	Unigene121173_All//0.00E+00//C0080078				nr +
Unigene121174_All	751	0.00	0.00	0.20	0.28	0.90	0.28	0.50	4.46	null	null		null	null		4.67E-01	8.25E-01		2.18E+00	3.14E-02		8.31E-01	4.67E-01		3.98E+00	6.32E-18	Up	Unigene121174_All//gi|115468796|ref|NP_001057997.1|//4.00E-18//Os06g0598900 [Oryza sativa Japonica Group] >gi|113596037|dbj|BAF19911.1| Os06g0598900 [Oryza sativa Japonica Group]	Unigene121174_All//6.00E-18//AT1G52730| transducin family protein / WD-40 repeat family protein	Unigene121174_All//8.00E-38//ES836039				nr +
Unigene121176_All	323	0.00	0.78	0.16	0.46	0.00	0.00	0.26	0.39	3.70	9.62E+00	7.87E-02		7.37E+00	6.37E-01		-8.85E+00	1.66E-01		-8.85E+00	2.34E-01		5.68E-01	7.82E-01		3.82E+00	1.37E-06	Up	Unigene121176_All//gi|10120315|emb|CAC08184.1|//1.00E-09//beta-ketoacyl-acyl carrier protein synthase III [Pisum sativum]	Unigene121176_All//6.00E-11//AT1G62640| KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III); 3-oxoacyl-[acyl-carrier-protein] synthase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene121176_All//1.00E-50//TC156688		ko00061|Fatty acid biosynthesis		nr -
Unigene121180_All	453	0.00	0.00	0.00	0.11	0.00	0.00	0.00	0.00	2.55	null	null		null	null		-6.78E+00	5.57E-01		-6.78E+00	6.37E-01		null	null		1.13E+01	2.28E-08	Up		Unigene121180_All//4.00E-54//TC177763					
Unigene121182_All	325	0.00	0.00	0.00	0.00	0.00	0.14	0.00	0.26	4.17	null	null		null	null		null	null		7.12E+00	6.97E-01		8.01E+00	4.02E-01		1.20E+01	9.04E-10	Up	Unigene121182_All//gi|255571990|ref|XP_002526936.1|//4.00E-10//conserved hypothetical protein [Ricinus communis] >gi|223533688|gb|EEF35423.1| conserved hypothetical protein [Ricinus communis]		Unigene121182_All//4.00E-13//EX170406				nr +
Unigene121184_All	333	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	2.75	null	null		null	null		null	null		null	null		6.97E+00	6.36E-01		1.14E+01	1.08E-06	Up	Unigene121184_All//gi|301016726|dbj|BAJ11784.1|//9.00E-15//dehydration responsive protein [Corchorus olitorius]		Unigene121184_All//6.00E-111//TC171825				nr -
Unigene121187_All	719	0.22	0.28	0.89	1.25	1.34	2.01	29.34	117.95	35.24	3.69E-01	8.17E-01		2.03E+00	5.59E-02		1.05E-01	9.03E-01		6.89E-01	2.32E-01		2.01E+00	5.26E-212	Up	2.64E-01	6.10E-03		Unigene121187_All//gi|297610489|ref|NP_001064615.2|//2.00E-17//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene121187_All//1.00E-13//AT1G60690| aldo/keto reductase family protein	Unigene121187_All//0.00E+00//CD809346				nr +
Unigene121193_All	314	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.80	2.28	null	null		null	null		null	null		null	null		9.64E+00	4.31E-02		1.12E+01	2.63E-05	Up		Unigene121193_All//2.00E-15//TC150019					
Unigene121194_All	822	0.00	0.00	0.00	0.00	0.00	0.05	0.46	0.36	2.86	null	null		null	null		null	null		5.78E+00	6.97E-01		-3.79E-01	7.23E-01		2.63E+00	5.32E-09	Up	Unigene121194_All//gi|115466618|ref|NP_001056908.1|//4.00E-53//Os06g0165500 [Oryza sativa Japonica Group] >gi|113594948|dbj|BAF18822.1| Os06g0165500 [Oryza sativa Japonica Group]	Unigene121194_All//4.00E-11//AT1G11410| S-locus protein kinase, putative					nr +
Unigene121195_All	553	0.00	0.09	0.00	0.00	0.12	0.49	0.69	0.53	6.84	6.52E+00	6.18E-01		null	null		6.96E+00	6.11E-01		8.94E+00	7.03E-02		-3.79E-01	7.23E-01		3.31E+00	1.65E-17	Up								
Unigene121196_All	541	0.00	0.37	0.10	0.00	0.00	0.17	0.23	0.62	2.28	8.55E+00	1.37E-01		6.62E+00	6.37E-01		null	null		7.38E+00	4.78E-01		1.40E+00	2.76E-01		3.28E+00	4.18E-06	Up	Unigene121196_All//gi|30693380|ref|NP_190663.2|//5.00E-17//AAA-type ATPase family protein [Arabidopsis thaliana] >gi|109946623|gb|ABG48490.1| At3g50940 [Arabidopsis thaliana]	Unigene121196_All//4.00E-12//AT3G50940| AAA-type ATPase family protein					nr +
Unigene121199_All	814	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.20	null	null		null	null		null	null		null	null		null	null		1.11E+01	7.17E-13	Up	Unigene121199_All//gi|115469348|ref|NP_001058273.1|//2.00E-08//Os06g0661000 [Oryza sativa Japonica Group] >gi|113596313|dbj|BAF20187.1| Os06g0661000 [Oryza sativa Japonica Group]						nr +
Unigene1212_All	1920	1.85	0.79	2.41	8.74	5.20	1.55	13.26	4.44	13.28	-1.23E+00	2.50E-04	Down	3.81E-01	2.12E-01		-7.49E-01	1.71E-09		-2.49E+00	2.07E-49	Down	-1.58E+00	3.29E-46	Down	2.50E-03	9.79E-01		Unigene1212_All//gi|15231450|ref|NP_187390.1|//1.00E-101//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75313804|sp|Q9SRT2.1|BH062_ARATH RecName: Full=Transcription factor bHLH62; AltName: Full=Transcription factor EN 85; AltName: Full=bHLH transcription factor bHLH062; AltName: Full=Basic helix-loop-helix protein 62; Short=bHLH 62; Short=AtbHLH62 >gi|111074462|gb|ABH04604.1| At3g07340 [Arabidopsis thaliana]	Unigene1212_All//8.00E-87//AT5G48560| basic helix-loop-helix (bHLH) family protein	Unigene1212_All//0.00E+00//gi|11204357|gb|BF273287.1|BP273287	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr +
Unigene121202_All	315	0.00	0.16	0.00	0.16	0.55	0.29	2.55	0.27	0.25	7.33E+00	6.18E-01		null	null		1.79E+00	5.21E-01		8.59E-01	7.95E-01		-3.26E+00	4.48E-04	Down	-3.33E+00	2.47E-04	Down		Unigene121202_All//2.00E-42//TC132056					
Unigene121203_All	404	0.00	3.39	0.00	0.37	2.73	1.90	4.81	13.14	11.14	1.17E+01	7.80E-08	Up	null	null		2.88E+00	3.08E-04	Up	2.36E+00	1.34E-02		1.45E+00	4.10E-09	Up	1.21E+00	2.42E-06	Up	Unigene121203_All//gi|3132675|gb|AAC16325.1|//1.00E-28//asparagine synthetase [Eleaeagnus umbellata]	Unigene121203_All//6.00E-28//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene121203_All//3.00E-76//gi|164361517|gb|ES840729.1|ES840729		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene121208_All	297	0.00	0.00	0.00	0.17	0.00	0.00	28.90	29.55	2.82	null	null		null	null		-7.39E+00	5.57E-01		-7.39E+00	6.37E-01		3.23E-02	8.80E-01		-3.36E+00	4.24E-40	Down		Unigene121208_All//8.00E-42//TC146107					
Unigene121209_All	736	0.14	0.83	0.00	0.20	0.33	0.98	0.17	0.06	2.44	2.54E+00	2.46E-02		-7.15E+00	3.95E-01		6.90E-01	7.32E-01		2.27E+00	2.08E-02		-1.60E+00	5.34E-01		3.82E+00	1.36E-09	Up	Unigene121209_All//gi|9759599|dbj|BAB11387.1|//5.00E-14//DNA-directed RNA polymerase subunit [Arabidopsis thaliana]	Unigene121209_All//5.00E-15//AT5G45140| NRPC2; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding	Unigene121209_All//2.00E-75//C0079646		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene121210_All	303	0.69	1.34	0.53	0.66	1.93	0.89	3.07	4.00	7.49	9.54E-01	4.14E-01		-3.90E-01	8.08E-01		1.55E+00	1.41E-01		4.44E-01	7.64E-01		3.82E-01	5.17E-01		1.29E+00	6.77E-04	Up	Unigene121210_All//gi|224110996|ref|XP_002333000.1|//1.00E-11//nbs-lrr resistance protein [Populus trichocarpa] >gi|222834485|gb|EEE72962.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene121210_All//1.00E-07//AT5G11250| disease resistance protein (TIR-NBS-LRR class), putative	Unigene121210_All//7.00E-101//TC144827				nr +
Unigene121213_All	863	0.12	0.00	0.00	0.00	0.00	0.00	1.47	0.34	1.25	-6.92E+00	3.74E-01		-6.92E+00	3.95E-01		null	null		null	null		-2.12E+00	4.17E-04	Down	-2.38E-01	6.32E-01		Unigene121213_All//gi|224122896|ref|XP_002318943.1|//3.00E-34//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222857319|gb|EEE94866.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene121213_All//1.00E-21//AT1G12290| disease resistance protein (CC-NBS-LRR class), putative	Unigene121213_All//6.00E-73//TC162123		ko04626|Plant-pathogen interaction		nr +
Unigene121214_All	879	0.00	0.00	0.00	0.00	0.00	0.00	0.87	0.38	3.44	null	null		null	null		null	null		null	null		-1.19E+00	1.12E-01		1.99E+00	2.09E-08	Up	Unigene121214_All//gi|147862859|emb|CAN83204.1|//3.00E-09//hypothetical protein [Vitis vinifera]						nr +
Unigene121217_All	297	0.18	5.63	1.08	0.00	1.62	0.61	0.28	0.28	1.48	5.00E+00	2.47E-08	Up	2.61E+00	1.46E-01		1.07E+01	5.07E-03		9.25E+00	1.95E-01		-1.63E-02	1.01E+00		2.37E+00	4.05E-02				Unigene121217_All//3.00E-23//gi|5045766|gb|AI726914.1|AI726914					
Unigene121218_All	843	0.37	0.00	0.00	0.00	0.00	0.05	0.00	0.10	5.77	-8.54E+00	3.66E-02		-8.54E+00	4.92E-02		null	null		5.74E+00	6.97E-01		6.63E+00	4.02E-01		1.25E+01	8.75E-35	Up	Unigene121218_All//gi|115473321|ref|NP_001060259.1|//2.00E-08//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]						nr +
Unigene121220_All	1221	0.17	0.00	0.00	0.00	0.00	0.04	0.00	0.00	4.76	-7.42E+00	1.22E-01		-7.42E+00	1.46E-01		null	null		5.21E+00	6.97E-01		null	null		1.22E+01	1.21E-41	Up	Unigene121220_All//gi|147823314|emb|CAN77450.1|//1.00E-06//hypothetical protein [Vitis vinifera]						nr -
Unigene121225_All	1336	0.27	0.61	0.12	0.19	0.10	0.20	0.60	0.75	14.25	1.15E+00	1.48E-01		-1.20E+00	3.96E-01		-8.54E-01	5.74E-01		1.22E-01	9.44E-01		3.20E-01	6.45E-01		4.57E+00	6.48E-109	Up	Unigene121225_All//gi|224123006|ref|XP_002330418.1|//5.00E-24//predicted protein [Populus trichocarpa] >gi|222871803|gb|EEF08934.1| predicted protein [Populus trichocarpa]						nr +

Unigene121226_All	282	0.00	0.00	0.00	0.71	0.00	0.00	1.95	0.00	0.28	null	null		null	null		-9.46E+00	8.44E-02		-9.46E+00	1.34E-01		-1.09E+01	4.61E-04	Down	-2.79E+00	7.96E-03		Unigene121226_All//gi|240255605|ref|NP_001030839.5|//9.00E-19//ETO1 (ETHYLENE OVERPRODUCER 1); protein binding, bridging [Arabidopsis thaliana]	Unigene121226_All//4.00E-20//AT3G51770| ETO1 (ETHYLENE OVERPRODUCER 1); protein binding, bridging	Unigene121226_All//4.00E-93//C0105972				nr -
Unigene121229_All	294	0.00	0.00	0.72	1.02	0.00	0.31	0.00	0.00	1.90	null	null		9.50E+00	1.41E-01		-9.99E+00	2.02E-02		-1.73E+00	2.89E-01		null	null		1.09E+01	3.28E-04	Up				Unigene121229_All//3.00E-07//TC164247				
Unigene121231_All	413	0.00	0.74	0.00	0.00	0.67	0.33	0.82	0.40	3.86	9.52E+00	4.44E-02		null	null		9.38E+00	7.02E-02		8.36E+00	3.11E-01		-1.02E+00	4.00E-01		2.24E+00	2.08E-05	Up				Unigene121231_All//4.00E-174//EX164245				
Unigene121232_All	359	22.15	24.28	48.21	5.97	5.18	6.16	1.88	1.86	13.87	1.32E-01	5.48E-01		1.12E+00	4.97E-15	Up	-2.04E-01	6.56E-01		4.71E-02	9.34E-01		-1.66E-02	1.02E+00		2.88E+00	4.80E-20	Up				Unigene121232_All//3.00E-66//gi|48792990|gb|C0094304.1|C0094304				
Unigene121233_All	285	0.00	0.00	0.00	0.00	2.30	0.48	0.00	0.73	1.82	null	null		null	null		1.12E+01	4.92E-04	Up	8.89E+00	3.11E-01		9.52E+00	7.85E-02		1.08E+01	6.14E-04	Up				Unigene121233_All//9.00E-11//C0126445				
Unigene121238_All	955	0.00	0.00	0.00	0.26	0.07	0.00	0.09	0.74	3.59	null	null		null	null		-1.85E+00	2.75E-01		-8.03E+00	7.34E-02		3.07E+00	1.67E-03		5.34E+00	1.41E-21	Up	Unigene121238_All//gi|115435462|ref|NP_001042489.1|//3.00E-13//Os01g0229700 [Oryza sativa Japonica Group] >gi|113532020|dbj|BAF04403.1|Os01g0229700 [Oryza sativa Japonica Group]						nr -
Unigene121124_All	734	0.14	1.24	0.22	0.34	1.50	1.23	3.00	3.25	28.71	3.12E+00	1.14E-03		6.10E-01	7.48E-01		2.15E+00	3.06E-03		1.86E+00	2.18E-02		1.16E-01	7.64E-01		3.26E+00	3.48E-93	Up	Unigene121124_All//gi|225457283|ref|XP_002284415.1|//5.00E-81//PREDICTED: similar to EMB2733/ESP3 (EMBRYO DEFECTIVE 27333); ATP-dependent RNA helicase [Vitis vinifera]	Unigene121124_All//4.00E-71//AT1G32490| ESP3 (ENHANCED SILENCING PHENOTYPE 3); ATP binding / ATP-dependent RNA helicase/ ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene121124_All//0.00E+00//gi|73861548|gb|DT464287.1|DT464287		ko03040|Spliceosome	GO:0003006//GO:0003724//GO:0006396//GO:0016441//GO:0032559//GO:0042623//GO:0043231	nr +
Unigene121246_All	382	0.00	0.00	0.00	0.26	0.00	0.00	36.64	34.25	13.14	null	null		null	null		-8.03E+00	3.14E-01		-8.03E+00	4.01E-01		-9.73E-02	5.56E-01		-1.48E+00	3.11E-24	Down				Unigene121246_All//2.00E-34//FL577610				
Unigene121249_All	862	0.00	0.00	0.00	0.00	0.00	0.68	0.20	0.00	9.80	null	null		null	null		null	null		9.41E+00	1.37E-03		-7.62E+00	1.35E-01		5.64E+00	7.22E-54	Up	Unigene121249_All//gi|134038598|gb|AB048367.1|//6.00E-51//C-repeat binding facor 6 [Populus trichocarpa]	Unigene121249_All//2.00E-33//AT4G25490| CBF1 (C-REPEAT/DRE BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor		AP2-EREBP			nr -
Unigene121250_All	500	0.00	0.41	0.00	0.00	0.00	0.18	0.17	0.33	2.47	8.66E+00	1.37E-01		null	null		null	null		7.50E+00	4.78E-01		9.84E-01	6.34E-01		3.87E+00	7.61E-07	Up								
Unigene121252_All	287	0.55	0.00	0.00	0.52	0.00	0.00	0.00	0.00	2.22	-9.10E+00	2.16E-01		-9.10E+00	2.45E-01		-9.02E+00	1.66E-01		-9.02E+00	2.34E-01		null	null		1.11E+01	9.34E-05	Up								
Unigene121253_All	762	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.05	3.97	null	null		null	null		null	null		null	null		-1.60E+00	5.34E-01		4.58E+00	9.86E-18	Up	Unigene121253_All//sp|Q60LV4|MYO3_CAEBR//2.00E-06//Myosin-3 OS=Caenorhabditis briggsae GN=myo-3 PE=3 SV=1	Unigene121253_All//5.00E-05//AT5G41790| CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding	Unigene121253_All//4.00E-12//FL577611				swissprot -
Unigene121256_All	754	0.00	0.13	0.00	0.00	0.00	0.00	0.39	1.16	3.91	7.07E+00	3.88E-01		null	null		null	null		null	null		1.57E+00	2.54E-02		3.32E+00	8.67E-14	Up	Unigene121256_All//gi|301070456|gb|ADG55590.1|//9.00E-36//plastid NEP interaction protein [Nicotiana benthamiana]	Unigene121256_All//4.00E-36//AT4G35840| zinc finger (C3HC4-type RING finger) family protein					nr -
Unigene121257_All	420	0.00	0.00	0.00	0.00	0.08	0.00	0.30	0.40	2.75	null	null		null	null		6.36E+00	8.32E-01		null	null		3.99E-01	8.14E-01		3.19E+00	1.26E-05	Up								
Unigene121126_All	1210	10.55	12.81	11.18	8.73	10.19	7.84	2.38	1.59	0.86	2.80E-01	5.67E-02		8.33E-02	6.16E-01		2.23E-01	2.05E-01		-1.55E-01	4.57E-01		-5.81E-01	8.20E-02		-1.47E+00	1.25E-05	Down	Unigene121126_All//gi|15226607|ref|NP_182266.1|//1.00E-127//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]	Unigene121126_All//3.00E-108//AT2G47440| DNAJ heat shock N-terminal domain-containing protein	Unigene121126_All//0.00E+00//TC142421			GO:0005488//GO:0043231//GO:0044267	nr +
Unigene121262_All	673	0.78	0.00	0.00	0.22	0.15	0.00	0.00	0.00	1.24	-9.60E+00	2.93E-03		-9.60E+00	4.76E-03		-5.33E-01	7.85E-01		-7.80E+00	2.34E-01		null	null		1.03E+01	3.89E-06	Up	Unigene121262_All//gi|224135839|ref|XP_002322173.1|//8.00E-22//predicted protein [Populus trichocarpa] >gi|222869169|gb|EEF06300.1|predicted protein [Populus trichocarpa]	Unigene121262_All//5.00E-16//AT3G48200| unknown protein					nr +
Unigene121265_All	324	0.00	0.00	0.00	0.15	0.00	0.00	0.00	0.00	2.21	null	null		null	null		-7.26E+00	5.57E-01		-7.26E+00	6.37E-01		null	null		1.11E+01	2.63E-05	Up				Unigene121265_All//3.00E-14//DT465398				ESTscan -
Unigene121127_All	1979	11.90	1.49	2.10	31.19	17.64	9.22	12.33	1.61	4.41	-3.00E+00	1.28E-77	Down	-2.50E+00	1.75E-61	Down	-8.22E-01	1.53E-39		-1.76E+00	2.91E-115	Down	-2.94E+00	3.92E-96	Down	-1.48E+00	9.05E-42	Down	Unigene121127_All//gi|15226607|ref|NP_182266.1|//0.00E+00//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]	Unigene121127_All//0.00E+00//AT2G47440| DNAJ heat shock N-terminal domain-containing protein	Unigene121127_All//0.00E+00//ES807678			GO:0005515//GO:0043231//GO:0044267//GO:0050896	nr +
Unigene121278_All	527	0.40	0.00	0.00	0.38	0.65	0.00	0.80	0.63	3.70	-8.63E+00	1.22E-01		-8.63E+00	1.46E-01		7.89E-01	5.96E-01		-8.56E+00	1.34E-01		-3.39E-01	7.30E-01		2.21E+00	2.29E-06	Up	Unigene121278_All//gi|87240457|gb|ABD32315.1|//5.00E-35//CCT [Medicago truncatula]	Unigene121278_All//1.00E-31//AT5G59990| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot apex, stem, leaf whorl, flower; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: CCT domain (InterPro:IPR010402); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41380.1); Has 918 Blast hits to 918 proteins in 64 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 885; Viruses - 0; Other Eukaryotes - 32 (source: NCBI BLink).	Unigene121278_All//0.00E+00//gi|109886292|gb|DW515262.1|DW515262	Orphans			nr -
Unigene121128_All	581	11.62	24.77	11.46	8.49	11.14	7.70	18.41	29.57	34.56	1.09E+00	1.39E-12	Up	-2.00E-02	9.52E-01		3.93E-01	9.89E-02		-1.41E-01	6.48E-01		6.83E-01	1.19E-08		9.09E-01	3.60E-16		Unigene121128_All//gi|115477631|ref|NP_001062411.1|//5.00E-37//Os08g0545000 [Oryza sativa Japonica Group] >gi|113624380|dbj|BAF24325.1|Os08g0545000 [Oryza sativa Japonica Group]	Unigene121128_All//2.00E-29//AT5G51920| catalytic/ pyridoxal phosphate binding	Unigene121128_All//0.00E+00//C0083107				nr +
Unigene121280_All	282	0.37	0.00	0.00	0.53	0.24	0.32	0.15	0.44	2.83	-8.54E+00	3.74E-01		-8.54E+00	3.95E-01		-1.12E+00	5.84E-01		-7.26E-01	7.16E-01		1.57E+00	5.45E-01		4.24E+00	7.42E-05	Up				Unigene121280_All//2.00E-70//ES850612				
Unigene121282_All	230	0.00	0.00	0.00	0.00	0.00	0.00	11.58	0.55	5.02	null	null		null	null		null	null		null	null		-4.41E+00	4.29E-15	Down	-1.21E+00	4.07E-04	Down								
Unigene121284_All	294	0.00	0.00	0.91	0.00	0.00	0.00	0.00	0.00	2.44	null	null		9.82E+00	8.02E-02		null	null		null	null		null	null		1.13E+01	2.63E-05	Up	Unigene121284_All//gi|119720772|gb|ABL97956.1|//4.00E-16//zinc finger A20 and AN1 domains-containing protein [Brassica rapa]	Unigene121284_All//3.00E-17//AT4G22820| zinc finger (AN1-like) family protein					nr -
Unigene121285_All	488	0.00	0.00	0.00	0.00	0.00	0.00	0.78	0.00	2.94	null	null		null	null		null	null		null	null		-9.61E+00	6.18E-03		1.91E+00	3.23E-04	Up	Unigene121285_All//gi|300176984|emb|CBK25553.2|//4.00E-06//unnamed protein product [Blastocystis hominis]						nr +
Unigene121286_All	805	0.00	0.76	0.00	0.12	0.26	0.00	0.21	0.16	3.71	9.56E+00	1.17E-03		null	null		1.05E+00	6.12E-01		-6.95E+00	4.01E-01		-4.31E-01	7.93E-01		4.14E+00	1.73E-16	Up	Unigene121286_All//gi|9989046|gb|AG10809.1|AC018460.3|//2.00E-11//Similar to mutator transposase [Arabidopsis thaliana]	Unigene121286_All//2.00E-09//AT1G64260| zinc finger protein-related	Unigene121286_All//7.00E-94//TC148530				nr -
Unigene121129_All	1679	9.47	6.58	6.09	11.42	7.24	5.35	5.41	10.43	10.01	-5.26E-01	1.60E-04		-6.38E-01	1.00E-05		-6.58E-01	1.15E-08		-1.09E+00	8.50E-18	Down	9.46E-01	9.13E-15		8.87E-01	3.52E-13		Unigene121129_All//gi|15242219|ref|NP_200005.1|//1.00E-124//catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana]	Unigene121129_All//2.00E-118//AT5G51920| catalytic/ pyridoxal phosphate binding	Unigene121129_All//0.00E+00//DT466467				nr -
Unigene121293_All	477	0.00	0.00	0.00	0.94	0.29	0.28	1.24	0.00	6.10	null	null		null	null		-1.70E+00	1.35E-01		-1.73E+00	1.61E-01		-1.03E+01	2.39E-04	Down	2.30E+00	1.62E-09	Up	Unigene121293_All//gi|416642|sp|P32295.1|ARG7_PHAAU//5.00E-17//RecName: Full=Indole-3-acetic acid-induced protein ARG7	Unigene121293_All//5.00E-16//AT4G34770| auxin-responsive family protein	Unigene121293_All//2.00E-31//TC150846				nr +
Unigene121298_All	360	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.00	1.99	null	null		null	null		null	null		null	null		-6.88E+00	6.58E-01		4.08E+00	2.41E-04	Up				Unigene121298_All//3.00E-79//gi|78335915|gb|DT556189.1|DT556189				
Unigene121299_All	229	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.73	11.13	null	null		null	null		null	null		null	null		9.51E+00	1.39E-01		1.34E+01	2.96E-18	Up				Unigene121299_All//1.00E-15//gi|109859355|gb|DW488334.1|DW488334				
Unigene12130_All	669	27.29	187.53	53.25	40.58	51.99	92.96	111.04	135.45	108.08	2.78E+00	0.00E+00	Up	9.64E-01	8.56E-24		3.57E-01	2.99E-05		1.20E+00	2.44E-64	Up	2.87E-01	3.60E-09		-3.90E-02	5.63E-01		Unigene12130_All//gi|169807674|emb|CAQ16336.1|//5.00E-41//alkaline alpha galactosidase [Platanus x acerifolia]	Unigene12130_All//2.00E-47//AT3G57520| AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase, hydrolyzing O-glycosyl compounds	Unigene12130_All//0.00E+00//gi|72267972|gb|DT046532.1|DT046532			GO:0016757	nr +
Unigene121307_All	344	0.00	0.00	0.00	0.00	0.00	0.00	1.47	0.12	6.25	null	null		null	null		null	null		null	null		-3.60E+00	5.77E-03		2.08E+00	1.61E-06	Up	Unigene121307_All//gi|55168340|gb|AAV41205.1|//1.00E-15//unknow protein [Oryza sativa Japonica Group]		Unigene121307_All//4.00E-38//TC139311				nr -
Unigene12131_All	2267	35.06	221.36	93.75	79.70	92.46	164.00	107.03	123.84	111.17	2.66E+00	0.00E+00	Up	1.42E+00	7.49E-259	Up	2.14E-01	2.64E-11		1.04E+00	0.00E+00	Up	2.10E-01	4.05E-15		5.47E-02	7.93E-02		Unigene12131_All//gi|187941007|gb|ACD39775.1|//0.00E+00//seed imbibition protein 1 [Vitis vinifera]	Unigene12131_All//0.00E+00//AT3G57520| AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase, hydrolyzing O-glycosyl compounds	Unigene12131_All//0.00E+00//TC137657		ko00052|Galactose metabolism		nr +
Unigene121313_All	294	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.00	2.17	null	null		null	null		null	null		null	null		-7.17E+00	6.58E-01		3.91E+00	7.65E-04	Up								
Unigene121314_All	358	0.00	0.57	0.30	0.28	0.96	0.76	3.66	0.70	4.67	9.14E+00	1.37E-01		8.22E+00	4.00E-01		1.79E+00	2.58E-01		1.44E+00	4.09E-01		-2.39E+00	9.40E-05	Down	3.52E-01	4.39E-01					Unigene121314_All//1.00E-115//TC157450				
Unigene121315_All	304	0.00	0.00	0.18	0.00	0.00	0.00	0.14	0.14	2.62	null	null		7.45E+00	6.37E-01		null	null		null	null		-1.67E-02	1.00E+00		4.24E+00	7.42E-05	Up	Unigene121315_All//gi|297791785|ref|XP_002863777.1|//8.00E-21//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309612|gb|EFH40036.1|kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene121315_All//8.00E-20//AT5G42490| kinesin motor family protein					nr +
Unigene121318_All	309	0.00	0.00	0.64	0.00	0.00	0.00	0.00	0.00	3.09	null	null		null	null		-9.33E+00	8.44E-02		-9.33E+00	1.34E-01		null	null		1.16E+01	5.69E-07	Up				Unigene121318_All//1.00E-19//TC176534				
Unigene121325_All	570	0.37	0.36	0.84	0.35	0.18	0.32	7.64	41.06	18.24	-4.63E-02	9.89E-01		1.20E+00	3.03E-01		-9.48E-01	5.88E-01		-1.42E-01	9.35E-01		2.43E+00	1.68E-74	Up	1.26E+00	2.94E-14	Up	Unigene121325_All//gi|115438617|ref|NP_001043588.1|//7.00E-45//Os01g0618100 [Oryza sativa Japonica Group] >gi|113533119|dbj|BAF05502.1|Os01g0618100 [Oryza sativa Japonica Group]	Unigene121325_All//2.00E-24//AT1G60690| aldo/keto reductase family protein	Unigene121325_All//9.00E-108//TC169053		ko00053|Ascorbate and aldarate metabolism		nr +
Unigene121327_All	365	0.00	0.00	0.00	0.00	0.09	0.00	0.00	0.00	1.53	null	null		null	null		6.56E+00	8.32E-01		null	null		null	null		1.06E+01	3.28E-04	Up	Unigene121327_All//gi|79386570|ref|NP_186781.4|//1.00E-08//SNL1 (SIN3-LIKE 1) [Arabidopsis thaliana] >gi|296439818|sp|Q9SRH9.2|SNL1_ARATH RecName: Full=Paired amphipathic helix protein Sin3-like 1	Unigene121327_All//4.00E-10//AT3G01320| SNL1 (SIN3-LIKE 1)					nr +
Unigene121330_All	306	9.75	12.75	12.36	5.21	6.64	14.76	1.66	2.87	0.91	3.88E-01	2.23E-01		3.42E-01	3.21E-01		3.50E-01	4.98E-01		1.50E+00	4.15E-07	Up	7.91E-01	2.41E-01		-8.63E-01	3.39E-01					Unigene121330_All//6.00E-80//BF279097				
Unigene121334_All	462	0.00	0.00	0.00	0.00	0.00	0.00	0.27	0.00	2.24	null	null		null	null		null	null		null	null		-8.10E+00	2.36E-01		3.03E+00	6.50E-05	Up								
Unigene121337_All	308	0.00	0.16	0.00	0.32	0.00	0.00	1.24	0.27	12.93	7.36E+00	6.18E-01		null	null		-8.34E+00	3.14E-01		-8.34E+00	4.01E-01		-2.19E+00	8.76E-02		3.39E+00	9.61E-19	Up				Unigene121337_All//2.00E-30//gi|164352536|gb|EX166155.1|EX166155		ko00190|Oxidative phosphorylation		kegg +
Unigene121340_All	347	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.12	3.56	null	null		null	null		null	null		null	null		-1.02E+00	7.25E-01		3.87E+00	7.61E-07	Up	Unigene121340_All//gi|122831047|gb|ABM66813.1|//9.00E-31//ACC synthase [Gossypium hirsutum]	Unigene121340_All//1.00E-26//AT1G01480| ACS2; 1-aminocyclopropane-1-carboxylate synthase	Unigene121340_All//8.00E-104//gi|73860861|gb|DT463600.1|DT463600		ko00270|Cysteine and methionine metabolism		nr +
Unigene121346_All	718	0.00	0.00	0.00	0.00	0.00	0.00	0.29	1.16	2.27	null	null		null	null		null	null		null	null		1.98E+00	8.88E-03		2.95E+00	3.41E-07	Up				Unigene121346_All//2.00E-17//TC149074				
Unigene121348_All	310	0.00	0.00	0.34	0.00	0.11	0.00	0.00	0.81	4.50	null	null		8.42E+00	4.00E-01		6.80E+00	8.32E-01		null	null		9.66E+00	4.31E-02		1.21E+01	4.73E-10	Up	Unigene121348_All//gi|295913576|gb|ADG58034.1|//4.00E-07//transcription factor [Lycoris longituba]	Unigene121348_All//1.00E-07//AT2G35940| BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene121348_All//1.00E-22//TC162985	HB			nr -

Unigene12135_All	3102	20.98	12.82	12.33	39.89	51.10	33.33	19.40	8.73	14.40	-7.11E-01	1.08E-26		-7.68E-01	2.53E-29		3.57E-01	4.04E-22		-2.59E-01	6.39E-09		-1.15E+00	4.74E-67	Down	-4.30E-01	4.48E-13		Unigene12135_All//gi|15219271|ref|NP_175737.1|//0.00E+00//TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 1); binding [Arabidopsis thaliana] >gi|75336154|sp|Q9MAH1.1|TTL1_ARATH RecName: Full=TPR repeat-containing thioredoxin TTL1; AltName: Full=Tetratricopeptide repeat thioredoxin-like 1 >gi|7769858|gb|AAF69536.1|AC008007_11 F12M16.20 [Arabidopsis thaliana] >gi|30102668|gb|AAP21252.1|At1g53300 [Arabidopsis thaliana]	Unigene12135_All//0.00E+00//AT1G53300| TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 1); binding	Unigene12135_All//0.00E+00//TC148828			GO:0005488//GO:0006970//GO:0009738//GO:0010051//GO:0043401//GO:0065007	nr +
Unigene121350_All	296	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.99	2.02	-7.47E+00	6.14E-01		-7.47E+00	6.26E-01		null	null		null	null		9.95E+00	2.35E-02		1.10E+01	1.75E-04	Up								
Unigene121352_All	536	0.20	0.38	0.00	0.00	0.00	0.00	0.00	0.70	6.69	9.54E-01	6.22E-01		-7.61E+00	3.95E-01		null	null		null	null		9.45E+00	6.86E-03		1.27E+01	1.18E-25	Up	Unigene121352_All//gi|224073248|ref|XP_002304043.1|//2.00E-15//predicted protein [Populus trichocarpa] >gi|222841475|gb|EEE79022.1|predicted protein [Populus trichocarpa]						nr +
Unigene121353_All	289	0.00	0.00	0.00	0.00	0.00	0.00	7.75	0.29	1.24	null	null		null	null		null	null		null	null		-4.74E+00	2.70E-13	Down	-2.64E+00	8.10E-09	Down	Unigene121353_All//gi|7159750|gb|AAC36746.2|//6.00E-35//elongation factor-1 alpha [Blastocystis hominis]	Unigene121353_All//3.00E-34//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene121353_All//2.00E-14//TC173271				nr -
Unigene121355_All	749	0.00	0.00	0.00	0.00	0.00	0.00	0.06	0.28	4.15	null	null		null	null		null	null		null	null		2.31E+00	2.40E-01		6.20E+00	1.16E-20	Up	Unigene121355_All//gi|300123648|emb|CBK24920.2|//4.00E-07//unnamed protein product [Blastocystis hominis]		Unigene121355_All//7.00E-66//FL577672				nr -
Unigene121356_All	383	0.00	0.00	0.00	0.00	0.00	0.00	0.77	0.87	4.06	null	null		null	null		null	null		null	null		1.76E-01	8.80E-01		2.39E+00	1.16E-05	Up								
Unigene121359_All	522	0.00	0.29	1.02	0.19	0.20	0.00	0.00	0.00	0.99	8.19E+00	2.36E-01		9.99E+00	4.04E-03		5.20E-02	9.67E-01		-7.58E+00	4.01E-01		null	null		9.95E+00	6.13E-04	Up	Unigene121359_All//gi|225468901|ref|XP_002268759.1|//5.00E-08//PREDICTED: hypothetical protein, partial [Vitis vinifera]						nr +
Unigene121361_All	418	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.00	2.95	null	null		null	null		null	null		null	null		-7.66E+00	4.05E-01		3.87E+00	7.61E-07	Up	Unigene121361_All//gi|159360119|gb|ABL66788.1|//2.00E-08//At2g32100 [Arabidopsis thaliana]		Unigene121361_All//5.00E-10//TC156577				nr -
Unigene121365_All	395	0.26	0.64	2.56	0.63	0.78	1.03	0.32	0.32	4.54	1.28E+00	4.35E-01		3.27E+00	5.93E-04	Up	3.15E-01	8.38E-01		7.06E-01	5.97E-01		-1.67E-02	1.02E+00		3.82E+00	1.36E-09	Up	Unigene121365_All//gi|73761699|gb|AAZ83349.1|//9.00E-23//MAP kinase [Gossypium hirsutum]		Unigene121365_All//1.00E-78//ES823084				nr +
Unigene121366_All	400	0.00	0.00	0.00	0.00	0.00	0.00	0.74	0.63	3.29	null	null		null	null		null	null		null	null		-2.39E-01	8.40E-01		2.15E+00	2.01E-04	Up								
Unigene121367_All	341	0.15	0.59	0.00	0.44	0.20	0.00	0.00	0.25	2.10	1.95E+00	3.75E-01		-7.26E+00	6.26E-01		-1.12E+00	5.84E-01		-8.78E+00	2.34E-01		7.94E+00	4.02E-01		1.10E+01	2.63E-05	Up			Unigene121367_All//4.00E-07//TC152567				
Unigene121372_All	2752	0.00	0.00	0.00	0.09	0.00	0.07	0.31	0.35	5.27	null	null		null	null		-6.50E+00	4.19E-02		-4.64E-01	7.45E-01		1.85E-01	7.65E-01		4.10E+00	2.11E-77	Up	Unigene121372_All//gi|87280654|gb|ABD36512.1|//0.00E+00//bacterial blight resistance protein XA26 [Oryza sativa Indica Group] >gi|90018761|gb|ABD84046.1|bacterial blight resistance protein XA26 [Oryza sativa Indica Group] >gi|90018763|gb|ABD84047.1|bacterial blight resistance protein XA26 [Oryza sativa Japonica Group]	Unigene121372_All//4.00E-127//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative		ko04626|Plant-pathogen interaction		nr +
Unigene121373_All	305	2.74	0.50	0.17	1.14	1.02	0.30	0.97	0.00	0.65	-2.46E+00	6.70E-03		-3.97E+00	9.08E-04	Down	-1.70E-01	8.58E-01		-1.95E+00	1.96E-01		-9.92E+00	2.18E-02		-5.71E-01	6.28E-01		Unigene121373_All//gi|159025721|emb|CAN88861.1|//5.00E-17//D3-type cyclin [Populus trichocarpa]	Unigene121373_All//2.00E-06//AT4G34160| CYCD3;1 (CYCLIN D3;1); cyclin-dependent protein kinase regulator/ protein binding	Unigene121373_All//7.00E-21//TC170510				nr +
Unigene121138_All	1535	4.74	5.18	5.38	2.43	4.46	3.53	1.71	2.78	4.23	1.29E-01	5.81E-01		1.83E-01	4.09E-01		8.75E-01	4.12E-05		5.37E-01	4.00E-02		7.02E-01	7.42E-03		1.31E+00	8.82E-10	Up	Unigene121138_All//gi|224061655|ref|XP_002300588.1|//1.00E-172//actin related protein [Populus trichocarpa] >gi|222847846|gb|EEE85393.1| actin related protein [Populus trichocarpa]	Unigene121138_All//5.00E-155//AT5G56180| ATARP8 (ACTIN-RELATED PROTEIN 8); structural constituent of cytoskeleton	Unigene121138_All//0.00E+00//ES797408	ko04145|Phagosome		nr -
Unigene121384_All	653	0.00	0.16	0.00	0.31	0.21	0.14	1.04	1.22	4.70	7.28E+00	3.88E-01		null	null		-5.33E-01	7.49E-01		-1.14E+00	5.69E-01		2.31E-01	7.35E-01		2.18E+00	1.94E-09	Up			Unigene121384_All//8.00E-81//ES802684				
Unigene121386_All	415	0.13	0.37	0.26	0.00	0.17	0.11	0.00	0.30	2.11	1.54E+00	5.31E-01		1.03E+00	7.03E-01		7.38E+00	6.11E-01		6.77E+00	6.97E-01		8.24E+00	2.41E-01		1.10E+01	2.05E-06	Up			Unigene121386_All//1.00E-07//gi|48797028|gb|CO098342.1|CO098342				
Unigene121389_All	326	0.00	0.31	0.00	0.00	0.00	0.00	0.26	0.00	5.38	8.28E+00	3.88E-01		null	null		null	null		null	null		-8.02E+00	4.05E-01		4.37E+00	3.24E-10	Up			Unigene121389_All//1.00E-77//DR457075				
Unigene12139_All	368	57.15	114.83	90.15	8.93	24.05	14.36	3.10	7.61	2.49	1.01E+00	3.77E-31	Up	6.57E-01	8.86E-12		1.43E+00	1.98E-13	Up	6.85E-01	8.35E-03		1.29E+00	1.73E-04	Up	-3.17E-01	5.87E-01		Unigene12139_All//gi|218117601|dbj|BAH03208.1|//6.00E-48//peroxisomal monodehydroascorbate reductase [Glycine max]	Unigene12139_All//3.00E-49//AT3G27820| MDAR4 (MONODEHYDROASCORBATE REDUCTASE 4); monodehydroascorbate reductase (NADH)	Unigene12139_All//0.00E+00//CO090262	ko00360|Phenylalanine metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0006091//GO:0016655//GO:0016667//GO:0019725//GO:0030554//GO:0042743//GO:0044439	nr -
Unigene121395_All	500	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	2.87	null	null		null	null		null	null		7.50E+00	4.78E-01		null	null		1.15E+01	2.48E-10	Up								
Unigene121396_All	546	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.15	2.77	null	null		null	null		null	null		null	null		9.84E-01	7.32E-01		5.16E+00	1.25E-09	Up			Unigene121396_All//2.00E-40//FL577600				
Unigene1214_All	590	21.73	15.97	16.79	15.62	12.55	16.30	10.46	24.44	9.12	-4.44E-01	5.04E-03		-3.72E-01	2.62E-02		-3.16E-01	1.02E-01		6.19E-02	7.70E-01		1.22E+00	2.89E-18	Up	-1.99E-01	3.76E-01		Unigene1214_All//gi|115472689|ref|NP_001059943.1|//7.00E-31//Os07g0551400 [Oryza sativa Japonica Group] >gi|33146953|dbj|BAC80026.1| CHP-rich zinc finger protein-like [Oryza sativa Japonica Group] >gi|113611479|dbj|BAF21857.1|Os07g0551400 [Oryza sativa Japonica Group]	Unigene1214_All//2.00E-12//AT1G11360| universal stress protein (USP) family protein	Unigene1214_All//0.00E+00//DW507214		GO:0043231//GO:0050896	nr -
Unigene12140_All	1692	33.86	153.48	57.75	18.40	29.98	41.43	25.16	47.06	27.43	2.18E+00	0.00E+00	Up	7.70E-01	4.10E-44		7.04E-01	3.70E-24		1.17E+00	4.26E-70	Up	9.03E-01	1.69E-59		1.25E-01	9.34E-02		Unigene12140_All//gi|15232273|ref|NP_189420.1|//0.00E+00//MDAR4 (MONODEHYDROASCORBATE REDUCTASE 4); monodehydroascorbate reductase (NADH) [Arabidopsis thaliana] >gi|50401174|sp|Q9LK94.1|MDAR2_ARATH RecName: Full=Probable monodehydroascorbate reductase, cytoplasmic isoform 2; Short=MDAR 2 >gi|11994487|dbj|BAB02528.1|cytosolic monodehydroascorbate reductase [Arabidopsis thaliana]	Unigene12140_All//0.00E+00//AT3G27820| MDAR4 (MONODEHYDROASCORBATE REDUCTASE 4); monodehydroascorbate reductase (NADH)	Unigene12140_All//0.00E+00//TC133881	ko00360|Phenylalanine metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0006091//GO:0016655//GO:0016667//GO:0030554//GO:0042743//GO:0044439	nr -
Unigene121403_All	364	0.00	0.00	0.00	0.00	0.00	0.00	1.16	0.80	7.88	null	null		null	null		null	null		null	null		-5.31E-01	6.34E-01		2.76E+00	2.24E-11	Up	Unigene121403_All//gi|225456525|ref|XP_002284739.1|//3.00E-11//PREDICTED: similar to MtN19-like protein [Vitis vinifera]	Unigene121403_All//8.00E-12//AT5G61820| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Stress up-regulated Nod 19 (InterPro:IPR011692); Has 27 Blast hits to 27 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene121403_All//3.00E-82//TC142983				nr -
Unigene121408_All	252	0.00	0.00	0.00	0.00	0.00	0.00	1.01	8.29	3.95	null	null		null	null		null	null		null	null		3.04E+00	4.79E-09	Up	1.97E+00	2.91E-03									
Unigene121411_All	308	0.00	0.00	0.00	0.32	0.00	0.00	0.27	0.95	4.92	null	null		null	null		-8.34E+00	3.14E-01		-8.34E+00	4.01E-01		1.79E+00	2.24E-01		4.16E+00	1.20E-08	Up								
Unigene12142_All	3287	2.23	2.70	1.12	2.64	2.93	2.23	7.36	2.66	3.08	2.76E-01	1.75E-01		-9.95E-01	1.15E-05		1.54E-01	4.91E-01		-2.45E-01	2.61E-01		-1.47E+00	1.24E-39	Down	-1.26E+00	2.44E-32	Down	Unigene12142_All//gi|124360144|gb|ABN08160.1|//1.00E-147//Heat shock protein DnaJ [Medicago truncatula]	Unigene12142_All//4.00E-68//AT3G04980| DNAJ heat shock N-terminal domain-containing protein	Unigene12142_All//5.00E-24//gi|3326262|gb|AI055148.1|AI055148				nr -
Unigene121420_All	1603	0.07	0.00	0.03	0.12	0.04	0.25	0.24	0.21	8.57	-6.03E+00	3.74E-01		-9.76E-01	7.21E-01		-1.53E+00	4.16E-01		1.03E+00	4.29E-01		-1.87E-01	8.57E-01		5.17E+00	3.30E-84	Up	Unigene121420_All//gi|124359163|gb|ABN05886.1|//5.00E-13//Zinc finger, CCHC-type [Medicago truncatula]	Unigene121420_All//1.00E-05//AT5G25200| unknown protein	Unigene121420_All//9.00E-92//gi|164340167|gb|ES851746.1|ES851746				nr +
Unigene121421_All	787	0.00	0.00	0.00	0.00	0.00	0.00	0.70	0.74	3.14	null	null		null	null		null	null		null	null		9.03E-02	9.27E-01		2.17E+00	1.07E-07	Up								
Unigene121424_All	304	0.00	0.00	0.00	0.98	0.23	0.45	48.68	1.10	4.32	null	null		null	null		-2.12E+00	1.66E-01		-1.14E+00	4.58E-01		-5.47E+00	6.17E-92	Down	-3.49E+00	4.63E-71	Down								
Unigene121425_All	298	0.00	0.68	0.00	0.00	0.00	0.00	0.00	0.28	3.74	9.41E+00	1.37E-01		null	null		null	null		null	null		8.13E+00	4.02E-01		1.19E+01	4.36E-08	Up			Unigene121425_All//3.00E-07//DR462279				
Unigene121427_All	299	0.00	0.34	0.00	0.00	0.12	0.30	0.00	0.00	3.06	8.40E+00	3.88E-01		null	null		6.85E+00	8.31E-01		8.24E+00	4.78E-01		null	null		1.16E+01	1.08E-06	Up	Unigene121427_All//gi|224132846|ref|XP_002321424.1|//2.00E-09//predicted protein [Populus trichocarpa] >gi|222868420|gb|EEF05551.1|predicted protein [Populus trichocarpa]						nr -
Unigene12143_All	3273	11.64	9.49	17.12	12.33	24.48	39.30	0.05	0.63	1.29	-2.94E-01	7.73E-04		5.57E-01	1.34E-14		9.90E-01	1.88E-67		1.67E+00	1.35E-219	Up	3.60E+00	3.47E-10	Up	4.64E+00	9.68E-25	Up	Unigene12143_All//gi|225444541|ref|XP_002275549.1|//0.00E+00//PREDICTED: inward rectifying shaker-like K+ channel [Vitis vinifera]	Unigene12143_All//0.00E+00//AT5G46240| KAT1 (POTASSIUM CHANNEL IN ARABIDOPSIS THALIANA 1); cyclic nucleotide binding / inward rectifier potassium channel	Unigene12143_All//0.00E+00//TC163749	ko04626|Plant-pathogen interaction	GO:0000166//GO:0005249//GO:0005515//GO:0009642//GO:0009987//GO:0030001//GO:0031224//GO:0048511	nr -
Unigene121433_All	331	0.00	0.00	0.00	0.00	0.00	0.00	0.26	0.38	4.45	null	null		null	null		null	null		null	null		5.68E-01	7.82E-01		4.12E+00	2.19E-08	Up			Unigene121433_All//1.00E-16//TC149074				
Unigene121434_All	404	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	2.56	null	null		null	null		null	null		null	null		6.69E+00	6.36E-01		1.13E+01	1.58E-07	Up	Unigene121434_All//gi|145408590|ref|YP_001152214.1|//3.00E-07//O8F124 [Pinus koraiensis] >gi|145048839|gb|ABF35456.1|O8F124 [Pinus koraiensis]		Unigene121434_All//2.00E-12//TC135251				nr +
Unigene121439_All	298	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.70	2.94	null	null		null	null		null	null		null	null		1.31E+00	4.47E-01		3.37E+00	1.32E-04	Up	Unigene121439_All//gi|301016726|dbj|BAJ11784.1|//7.00E-07//dehydration responsive protein [Corchorus olitorius]		Unigene121439_All//6.00E-15//TC149487				nr -
Unigene12144_All	2323	11.55	13.07	17.65	31.09	30.57	82.69	66.05	66.55	50.09	1.77E-01	9.03E-02		6.11E-01	9.76E-13		-2.47E-02	7.83E-01		1.41E+00	1.18E-255	Up	1.09E-02	8.16E-01		-3.99E-01	6.81E-28		Unigene12144_All//gi|257815407|gb|ACY70032.1|//0.00E+00//3-ketoacyl-CoA thiolase 1 [Petunia x hybrida]	Unigene12144_All//9.00E-180//AT2G33150| PKT3 (PEROXISOMAL 3-KETOACYL-COA THIOLASE 3); acetyl-CoA C-acyltransferase	Unigene12144_All//0.00E+00//TC136889	ko04146|Peroxisome//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids	GO:0006950//GO:0009062//GO:0009536//GO:0009657//GO:0009694//GO:0016020//GO:0016408//GO:0031981//GO:0042579	nr +
Unigene121441_All	458	0.00	1.11	0.00	0.33	1.28	0.39	2.49	1.19	6.18	1.01E+01	4.05E-03		null	null		1.97E+00	7.04E-02		2.74E-01	9.05E-01		-1.07E+00	6.31E-02		1.31E+00	9.67E-05	Up			Unigene121441_All//2.00E-59//TC141376				
Unigene121442_All	945	0.11	0.27	0.23	0.37	0.07	0.00	0.76	0.35	5.14	1.28E+00	4.33E-01		1.03E+00	5.92E-01		-2.34E+00	1.01E-01		-8.53E+00	2.13E-02		-1.10E+00	1.49E-01		2.76E+00	9.52E-19	Up								
Unigene121443_All	1085	0.00	0.00	0.00	0.05	0.00	0.00	0.12	0.04	4.96	null	null		null	null		-5.52E+00	5.57E-01		-5.52E+00	6.37E-01		-1.60E+00	5.34E-01		5.41E+00	7.85E-34	Up			Unigene121443_All//4.00E-28//TC166260				
Unigene121450_All	281	1.12	8.11	6.44	0.71	0.37	1.29	0.15	0.00	0.99	2.86E+00	1.28E-07	Up	2.53E+00	2.82E-05	Up	-9.48E-01	5.88E-01		8.59E-01	5.42E-01		-7.23E+00	6.58E-01		2.72E+00	9.94E-02				Unigene121450_All//3.00E-07//TC140954				
Unigene121454_All	591	0.00	0.00	0.09	0.00	0.00	0.00	0.14	0.00	7.28	null	null		6.49E+00	6.37E-01		null	null		null	null		-7.16E+00	4.05E-01		5.67E+00	1.18E-27	Up								
Unigene121455_All	1464	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.09	5.71	null	null		null	null		null	null		null	null		6.42E+00	2.41E-01		1.25E+01	5.90E-60	Up	Unigene121455_All//gi|117622276|gb|ABK51384.1|//3.00E-06//IMP dehydrogenase/GMP reductase [Hevea brasiliensis]		Unigene121455_All//7.00E-12//FL576849				nr -
Unigene121456_All	326	6.42	243.09	7.68	36.06	113.13	204.48	86.51	450.65	306.86	5.24E+00	0.00E+00	Up	2.58E-01	5.55E-01		1.65E+00	8.27E-68	Up	2.50E+00	1.79E-191	Up	2.38E+00	0.00E+00	Up	1.83E+00	1.09E-224	Up	Unigene121456_All//gi|1778370|gb|AAC49613.1|//7.00E-17//asparagine synthetase 2 [Glycine max]	Unigene121456_All//6.00E-177//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene121456_All//3.00E-63//gi|164267576|gb|ES851998.1|ES851998	ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +

Unigene121459_All	308	0.17	0.00	0.00	0.00	0.00	0.15	0.69	1.63	3.88	-7.41E+00	6.14E-01		-7.41E+00	6.26E-01		null	null		7.20E+00	6.97E-01		1.25E+00	2.04E-01		2.50E+00	1.03E-04	Up	Unigene121459_All//gi|297843964|ref|XP_002889863.1|//4.00E-31//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335705|gb|EFH66122.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene121459_All//3.00E-32//AT1G11330| S-locus lectin protein kinase family protein	Unigene121459_All//4.00E-16//C0081719		ko04626|Plant-pathogen interaction		nr +
Unigene12146_All	1374	4.30	9.15	5.08	6.49	6.07	5.46	8.62	9.79	8.96	1.09E+00	5.13E-11	Up	2.39E-01	3.43E-01		-9.76E-02	6.65E-01		-2.50E-01	2.37E-01		1.85E-01	2.29E-01		5.64E-02	7.21E-01		Unigene12146_All//gi|15239276|ref|NP_201417.1|//9.00E-70//JR700; peptidase/ protein binding / zinc ion binding [Arabidopsis thaliana] >gi|6942147|gb|AAF32325.1|AF218807_1 ReMembR-H2 protein JR700 [Arabidopsis thaliana] >gi|10177131|dbj|BAB10421.1| ReMembR-H2 protein JR700 [Arabidopsis thaliana]	Unigene12146_All//8.00E-65//AT5G66160| JR700; peptidase/ protein binding / zinc ion binding	Unigene12146_All//3.00E-97//gi|78332644|gb|DT552918.1|DT552918			GO:0044464//GO:0046872	nr +
Unigene121464_All	445	0.24	0.00	0.00	0.45	0.31	0.41	1.05	0.19	6.18	-7.88E+00	3.74E-01		-7.88E+00	3.95E-01		-5.33E-01	7.49E-01		-1.41E-01	9.35E-01		-2.48E+00	3.38E-02		2.56E+00	3.79E-10	Up								
Unigene121467_All	406	0.00	0.25	0.00	0.00	0.00	0.00	0.10	1.54	15.11	7.96E+00	3.88E-01		null	null		null	null		null	null		3.89E+00	1.15E-03		7.18E+00	4.60E-42	Up			Unigene121467_All//1.00E-38//TC175163					
Unigene12147_All	1696	15.58	10.43	12.28	18.21	14.96	17.55	10.99	9.14	4.56	-5.79E-01	4.09E-08		-3.44E-01	1.94E-03		-2.83E-01	2.42E-03		-5.34E-02	6.66E-01		-2.66E-01	2.51E-02		-1.27E+00	1.51E-25	Down	Unigene12147_All//gi|15239276|ref|NP_201417.1|//2.00E-54//JR700; peptidase/ protein binding / zinc ion binding [Arabidopsis thaliana] >gi|6942147|gb|AAF32325.1|AF218807_1 ReMembR-H2 protein JR700 [Arabidopsis thaliana] >gi|10177131|dbj|BAB10421.1| ReMembR-H2 protein JR700 [Arabidopsis thaliana]	Unigene12147_All//1.00E-55//AT5G66160| JR700; peptidase/ protein binding / zinc ion binding	Unigene12147_All//0.00E+00//gi|78332644|gb|DT552918.1|DT552918			GO:0005488//GO:0044464	nr +
Unigene121470_All	1097	0.00	0.00	0.00	0.05	0.13	0.04	0.35	0.88	2.87	null	null		null	null		1.47E+00	6.19E-01		-1.40E-01	9.54E-01		1.34E+00	4.02E-02		3.05E+00	1.25E-13	Up	Unigene121470_All//gi|124359343|gb|ABD28505.2|//9.00E-27//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]							nr -
Unigene121471_All	877	0.12	0.00	0.00	0.23	0.00	0.21	0.29	0.43	3.54	-6.90E+00	3.74E-01		-6.90E+00	3.95E-01		-7.83E+00	8.44E-02		-1.41E-01	9.35E-01		5.68E-01	6.38E-01		3.61E+00	1.52E-15	Up	Unigene121471_All//gi|42570080|ref|NP_683294.2|//6.00E-70//phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis thaliana]	Unigene121471_All//3.00E-71//AT1G09935| phosphoglycerate/bisphosphoglycerate mutase family protein						nr +
Unigene121473_All	238	0.00	0.00	0.22	0.00	0.00	0.38	0.00	1.05	3.18	null	null		7.81E+00	6.37E-01		null	null		8.57E+00	4.78E-01		1.00E+01	4.31E-02		1.16E+01	1.39E-05	Up								ESTscan -
Unigene121479_All	378	19.52	10.59	12.82	35.05	31.98	33.10	60.51	459.86	132.06	-8.82E-01	4.52E-05		-6.06E-01	6.86E-03		-1.33E-01	4.64E-01		-8.29E-02	6.60E-01		2.93E+00	0.00E+00	Up	1.13E+00	6.06E-55	Up	Unigene121479_All//gi|297610489|ref|NP_001064615.2|//6.00E-30//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene121479_All//2.00E-24//AT1G60690| aldo/keto reductase family protein	Unigene121479_All//0.00E+00//TC140911		ko00053|Ascorbate and aldarate metabolism		nr +
Unigene121480_All	459	0.34	0.22	0.23	0.22	0.00	0.00	0.64	1.46	3.56	-6.31E-01	7.28E-01		-5.60E-01	7.76E-01		-7.76E+00	3.14E-01		-7.76E+00	4.01E-01		1.18E+00	1.44E-01		2.46E+00	4.32E-06	Up								
Unigene121481_All	348	12.33	17.33	12.09	20.18	17.61	15.83	6.68	2.16	5.04	4.91E-01	4.39E-02		-2.84E-02	9.42E-01		-1.97E-01	4.26E-01		-3.56E-01	1.32E-01		-1.63E+00	4.15E-05	Down	-4.08E-01	2.71E-01				Unigene121481_All//6.00E-148//TC158813					ESTscan +
Unigene121482_All	669	0.08	1.06	0.00	0.37	0.82	0.88	0.00	0.56	5.00	3.76E+00	2.36E-03		-6.29E+00	6.26E-01		1.15E+00	2.97E-01		1.24E+00	2.31E-01		9.14E+00	6.86E-03		1.23E+01	6.05E-24	Up			Unigene121482_All//8.00E-07//TC158843					
Unigene121485_All	474	0.00	0.86	1.12	1.47	2.98	2.29	0.80	0.35	4.79	9.74E+00	1.36E-02		1.01E+01	4.04E-03		1.02E+00	7.53E-02		6.36E-01	3.73E-01		-1.19E+00	3.09E-01		2.58E+00	1.48E-08	Up	Unigene121485_All//gi|226532590|ref|NP_001147292.1|//3.00E-06//glutamate carboxypeptidase 2 [Zea mays] >gi|195609594|gb|ACG26627.1| glutamate carboxypeptidase 2 [Zea mays]	Unigene121485_All//8.00E-07//AT5G19740| peptidase M28 family protein						nr -
Unigene121487_All	485	0.00	0.00	0.00	0.00	0.00	0.00	1.57	1.47	27.44	null	null		null	null		null	null		null	null		-9.91E-02	8.96E-01		4.13E+00	2.12E-71	Up			Unigene121487_All//2.00E-25//TC142983					
Unigene121488_All	600	8.28	6.42	12.43	5.06	1.89	1.73	1.06	0.49	1.13	-3.68E-01	1.84E-01		5.85E-01	8.64E-03		-1.42E+00	3.26E-05	Down	-1.55E+00	2.75E-05	Down	-1.12E+00	1.80E-01		9.48E-02	9.12E-01		Unigene121488_All//gi|125550682|gb|EAY86391.1|//1.00E-06//hypothetical protein Osl_18290 [Oryza sativa Indica Group]		Unigene121488_All//2.00E-105//TC163297					nr +
Unigene121149_All	1613	9.24	6.57	8.42	12.69	11.40	13.78	19.90	10.86	8.79	-4.94E-01	6.40E-04		-1.35E-01	4.08E-01		-1.55E-01	2.56E-01		1.18E-01	3.94E-01		-8.74E-01	3.30E-23		-1.18E+00	1.50E-38	Down	Unigene12149_All//gi|224122474|ref|XP_002330490.1|//1.00E-170//arginine methyltransferease [Populus trichocarpa] >gi|222872424|gb|EEF09555.1| arginine methyltransferease [Populus trichocarpa]	Unigene12149_All//1.00E-160//AT4G26910| PRMT11 (ARGININE METHYLTRANSFERASE 11); protein-arginine N-methyltransferase	Unigene12149_All//0.00E+00//TC133684				nr +
Unigene121492_All	376	0.00	0.00	0.00	0.00	0.00	0.00	2.36	0.56	6.89	null	null		null	null		null	null		null	null		-2.09E+00	4.71E-03		1.54E+00	2.12E-05	Up			Unigene121492_All//3.00E-60//BM455269					
Unigene121497_All	228	0.00	0.00	0.00	0.00	0.00	0.00	12.05	5.32	104.66	null	null		null	null		null	null		null	null		-1.18E+00	6.00E-04	Down	3.12E+00	4.23E-101	Up	Unigene121497_All//gi|3970689|emb|CAA77191.1|//7.00E-09//(+)-delta-cadinene synthase [Gossypium arboreum]		Unigene121497_All//3.00E-16//ES830782					nr -
Unigene121500_All	1022	0.00	0.00	0.00	0.24	0.13	0.00	0.62	0.25	2.26	null	null		null	null		-8.54E-01	5.74E-01		-7.93E+00	7.34E-02		-1.34E+00	1.13E-01		1.87E+00	3.98E-06	Up	Unigene121500_All//gi|54645911|gb|AAV36561.1|//4.00E-59//RD22-like protein [Vitis vinifera]	Unigene121500_All//1.00E-47//AT5G25610| RD22; nutrient reservoir						nr -
Unigene121504_All	541	0.00	0.00	0.00	0.00	0.00	0.00	74.01	41.80	18.78	null	null		null	null		null	null		null	null		-8.24E-01	4.09E-26		-1.98E+00	8.87E-102	Down	Unigene121504_All//gi|297836874|ref|XP_002886319.1|//1.00E-15//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332159|gb|EFH62578.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene121504_All//3.00E-46//TC160883					nr +
Unigene121506_All	1100	0.00	0.09	0.19	0.09	0.00	0.16	0.12	0.30	6.56	6.53E+00	3.88E-01		7.60E+00	1.41E-01		-6.50E+00	3.14E-01		8.58E-01	6.95E-01		1.40E+00	2.76E-01		5.83E+00	1.30E-46	Up								
Unigene121507_All	346	0.30	1.03	0.62	0.58	0.30	0.39	1.22	1.57	6.68	1.76E+00	2.18E-01		1.03E+00	5.92E-01		-9.48E-01	5.88E-01		-5.56E-01	7.33E-01		3.62E-01	6.73E-01		2.45E+00	2.94E-08	Up			Unigene121507_All//3.00E-85//TC166679					
Unigene12151_All	1577	8.26	2.99	5.07	11.15	6.27	12.37	17.88	7.79	5.13	-1.47E+00	8.70E-18	Down	-7.06E-01	1.27E-05		-8.31E-01	8.80E-12		1.50E-01	3.08E-01		-1.20E+00	6.79E-34	Down	-1.80E+00	1.95E-63	Down	Unigene12151_All//gi|224122474|ref|XP_002330490.1|//1.00E-174//arginine methyltransferease [Populus trichocarpa] >gi|222872424|gb|EEF09555.1| arginine methyltransferease [Populus trichocarpa]	Unigene12151_All//2.00E-162//AT4G26910| PRMT11 (ARGININE METHYLTRANSFERASE 11); protein-arginine N-methyltransferase	Unigene12151_All//0.00E+00//TC158956				nr +
Unigene121511_All	309	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.81	null	null		null	null		null	null		null	null		null	null		1.08E+01	3.28E-04	Up								
Unigene121514_All	1019	0.05	0.99	0.73	0.20	0.51	0.27	1.00	0.86	6.06	4.28E+00	7.16E-05	Up	3.83E+00	2.23E-03		1.37E+00	2.26E-01		4.44E-01	7.64E-01		-2.09E-01	7.31E-01		2.61E+00	2.91E-22	Up			Unigene121514_All//0.00E+00//gi|48804597|gb|C0105911.1|C0105911					
Unigene121519_All	356	0.00	0.00	0.45	0.14	0.19	0.00	0.24	0.00	2.57	null	null		8.81E+00	2.39E-01		4.68E-01	9.59E-01		-7.13E+00	6.37E-01		-7.89E+00	4.05E-01		3.44E+00	7.53E-05	Up	Unigene121519_All//gi|297792067|ref|XP_002863918.1|//2.00E-06//hypothetical protein ARALYDRAFT_357086 [Arabidopsis lyrata subsp. lyrata] >gi|297309753|gb|EFH40177.1| hypothetical protein ARALYDRAFT_357086 [Arabidopsis lyrata subsp. lyrata]							nr -
Unigene121520_All	497	0.00	0.51	0.11	0.00	0.76	0.00	0.00	0.50	1.04	8.99E+00	7.87E-02		6.74E+00	6.37E-01		9.57E+00	1.96E-02		null	null		8.98E+00	4.31E-02		1.00E+01	6.13E-04	Up			Unigene121520_All//6.00E-07//TC170856					
Unigene121521_All	353	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.58	null	null		null	null		null	null		null	null		null	null		1.06E+01	3.28E-04	Up								
Unigene121523_All	534	0.00	0.00	0.00	0.19	0.00	0.00	0.63	1.02	2.61	null	null		null	null		-7.54E+00	3.14E-01		-7.54E+00	4.01E-01		6.84E-01	4.49E-01		2.04E+00	2.08E-04	Up								
Unigene121524_All	345	0.00	0.59	0.31	2.02	0.10	0.00	1.96	1.21	3.12	9.20E+00	1.37E-01		8.27E+00	4.00E-01		-4.34E+00	2.80E-04	Down	-1.10E+01	1.96E-04	Down	-6.95E-01	3.94E-01		6.69E-01	2.44E-01		Unigene121524_All//gi|18418211|ref|NP_567920.1|//1.00E-12//BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE); kinase/ protein binding / protein heterodimerization/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|29427920|sp|Q94F62.2|BAK1_ARATH RecName: Full=BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1; Short=BRI1-associated receptor kinase 1; Short=AtBAK1; AltName: Full=Somatic embryogenesis receptor kinase 3; Short=AtSERK3; AltName: Full=Somatic embryogenesis receptor-like kinase 3; AltName: Full=Protein ELONGATED; Flags: Precursor >gi|224589645|gb|ACN59355.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene121524_All//5.00E-14//AT4G33430| BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE); kinase/ protein binding / protein heterodimerization/ protein serine/threonine kinase	Unigene121524_All//2.00E-79//DT466374		ko04626|Plant-pathogen interaction		nr +
Unigene121526_All	554	0.00	0.09	0.19	0.27	0.31	0.33	0.92	0.75	2.95	6.52E+00	6.18E-01		7.59E+00	4.00E-01		2.04E-01	9.50E-01		2.73E-01	9.05E-01		-2.80E-01	7.49E-01		1.69E+00	4.33E-04	Up	Unigene121526_All//gi|15239888|ref|NP_197388.1|//6.00E-44//inosine-uridine preferring nucleoside hydrolase-related [Arabidopsis thaliana]	Unigene121526_All//6.00E-35//AT5G18870| inosine-uridine preferring nucleoside hydrolase-related				GO:0003824//GO:0030312//GO:0031410	nr -
Unigene121527_All	727	1.08	0.00	0.15	0.00	0.00	0.00	0.12	0.06	0.82	-1.01E+01	1.09E-04	Down	-2.88E+00	6.35E-03		null	null		null	null		-1.02E+00	7.25E-01		2.82E+00	5.66E-03		Unigene121527_All//gi|115472647|ref|NP_001059922.1|//1.00E-27//Os07g0546400 [Oryza sativa Japonica Group] >gi|113611458|dbj|BAF21836.1| Os07g0546400 [Oryza sativa Japonica Group]	Unigene121527_All//8.00E-24//AT3G22104| phototropic-responsive NPH3 protein-related	Unigene121527_All//6.00E-20//TC163220				nr -
Unigene121529_All	305	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.00	3.13	null	null		null	null		null	null		null	null		-7.11E+00	6.58E-01		4.50E+00	6.81E-06	Up			Unigene121529_All//5.00E-31//DT462517					
Unigene121532_All	345	0.00	0.15	0.00	0.00	0.00	0.00	0.74	1.21	18.94	7.20E+00	6.18E-01		null	null		null	null		null	null		7.20E-01	5.07E-01		4.69E+00	3.15E-38	Up								
Unigene121535_All	406	0.00	0.00	0.00	0.25	0.00	0.00	0.21	0.41	1.86	null	null		null	null		-7.94E+00	3.14E-01		-7.94E+00	4.01E-01		9.83E-01	6.34E-01		3.16E+00	6.83E-04	Up			Unigene121535_All//5.00E-16//ES844511					
Unigene121537_All	471	0.00	0.00	0.11	0.63	0.00	0.10	0.36	0.27	3.55	null	null		6.82E+00	6.37E-01		-9.31E+00	2.02E-02		-2.73E+00	1.37E-01		-4.32E-01	7.93E-01		3.31E+00	4.37E-08	Up								
Unigene12154_All	1522	0.69	1.13	1.75	2.55	1.72	1.04	2.25	1.32	1.39	7.19E-01	1.48E-01		1.35E+00	1.20E-03		-5.70E-01	5.80E-02		-1.30E+00	3.36E-05	Down	-7.72E-01	9.48E-03		-6.98E-01	1.49E-02		Unigene12154_All//gi|28950829|gb|AAO63338.1|//1.00E-57//At1g68160 [Arabidopsis thaliana]	Unigene12154_All//1.00E-49//AT1G68160| unknown protein	Unigene12154_All//0.00E+00//gi|109838864|gb|DW237425.1|DW237425				nr -
Unigene121541_All	1038	0.00	0.20	0.00	0.10	0.00	0.00	0.29	0.93	1.84	7.61E+00	1.37E-01		null	null		-6.59E+00	3.14E-01		-6.59E+00	4.01E-01		1.70E+00	1.17E-02		2.69E+00	1.24E-07	Up	Unigene121541_All//gi|297827079|ref|XP_002881422.1|//5.00E-17//abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327261|gb|EFH57681.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene121541_All//3.00E-18//AT2G36020| HVA22J (HVA22-LIKE PROTEIN J)	Unigene121541_All//1.00E-46//ES833630			GO:0044464	nr -
Unigene121543_All	390	0.00	0.26	0.00	0.00	0.00	0.00	1.95	1.61	7.87	8.02E+00	3.88E-01		null	null		null	null		null	null		-2.80E-01	6.96E-01		2.01E+00	1.34E-08	Up			Unigene121543_All//5.00E-07//CD486178					
Unigene121545_All	747	0.00	0.00	0.00	0.13	0.28	0.24	0.11	1.06	2.29	null	null		null	null		1.05E+00	6.12E-01		8.58E-01	6.95E-01		3.23E+00	5.44E-04	Up	4.34E+00	5.93E-10	Up	Unigene121545_All//gi|109134221|gb|ABG25108.1|//1.00E-26//At5g63905 [Arabidopsis thaliana]	Unigene121545_All//5.00E-10//AT5G63905| unknown protein	Unigene121545_All//1.00E-144//DR460635				nr +
Unigene121548_All	553	4.45	7.24	9.92	6.13	6.23	8.09	5.05	5.22	6.05	7.03E-01	2.12E-02		1.16E+00	1.86E-05	Up	2.37E-02	9.57E-01		4.01E-01	1.94E-01		4.75E-02	9.04E-01		2.62E-01	4.05E-01		Unigene121548_All//gi|195638478|gb|ACG38707.1|//8.00E-10//DNA repair protein recA [Zea mays]	Unigene121548_All//4.00E-10//AT2G19490| recA family protein	Unigene121548_All//7.00E-90//TC153847		ko03440|Homologous recombination	GO:0006259//GO:0019829//GO:0031668//GO:0032559//GO:0033554//GO:0043231//GO:0043566	nr +

Unigene121549_All	313	0.00	0.00	0.00	0.48	0.11	0.43	0.68	0.93	5.85	null	null		null	null	-2.12E+00	3.87E-01		-1.42E-01	9.44E-01		4.69E-01	7.06E-01		3.12E+00	2.25E-08	Up	Unigene121549_All//gi|255671803|gb|ACU26534.1|//4.00E-08//dihydroxyacid dehydratase [Glycine max]	Unigene121549_All//2.00E-06//AT3G23940| dehydratase family	Unigene121549_All//4.00E-25//TC136783		ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene121550_All	2152	0.00	0.00	0.00	0.00	0.00	0.20	0.00	24.57	null	null			null	null	null	null		null	null		-7.62E+00	3.25E-03		6.97E+00	0.00E+00	Up	Unigene121550_All//gi|7671450|emb|CAB89390.1|//0.00E+00//lectin-like protein kinase-like [Arabidopsis thaliana] >gi|91806848|gb|ABE66151.1| lectin protein kinase [Arabidopsis thaliana]	Unigene121550_All//0.00E+00//AT5G10530| lectin protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004702//GO:0004713//GO:0006464//GO:0030246//GO:0032559	nr -
Unigene121551_All	648	0.73	0.00	0.00	0.23	0.00	0.14	0.39	0.06	3.20	-9.51E+00	5.56E-03		-9.51E+00	8.66E-03	-7.85E+00	1.66E-01		-7.26E-01	7.16E-01		-2.60E+00	1.44E-01		3.03E+00	3.73E-09	Up	Unigene121551_All//gi|15228447|ref|NP_186954.1|//2.00E-16//F-box family protein [Arabidopsis thaliana] >gi|75263775|sp|Q9LDJ9.1|FB133_ARATH RecName: Full=F-box protein At3g03040	Unigene121551_All//1.00E-17//AT3G03040| F-box family protein	Unigene121551_All//1.00E-122//C0123234				nr +
Unigene121556_All	1454	2.23	0.87	3.00	5.31	2.23	2.55	3.00	1.24	1.73	-1.36E+00	1.50E-04	Down	4.29E-01	1.64E-01	-1.25E+00	2.56E-10	Down	-1.06E+00	3.40E-07	Down	-1.28E+00	1.95E-06	Down	-7.95E-01	1.51E-03		Unigene12156_All//gi|28950829|gb|AA063338.1|//1.00E-57//At1g68160 [Arabidopsis thaliana]	Unigene12156_All//5.00E-51//AT1G10820| unknown protein	Unigene12156_All//0.00E+00//gi|109838864|gb|DW237425.1|DW237425				nr -
Unigene121568_All	963	0.00	0.00	0.00	0.31	0.00	0.00	2.28	1.04	4.76	null	null		null	null	-8.28E+00	2.02E-02		-8.28E+00	4.00E-02		-1.13E+00	3.71E-03		1.06E+00	2.27E-05	Up	Unigene121568_All//gi|73624747|gb|AAZ79231.1|//2.00E-79//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene121568_All//9.00E-74//AT4G23990| ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	Unigene121568_All//5.00E-12//TC160226			GO:0009987//GO:0016020//GO:0016757	nr -
Unigene121569_All	321	0.16	0.00	0.17	0.16	0.43	0.14	0.00	0.00	1.61	-7.35E+00	6.14E-01		2.54E-02	9.95E-01	1.47E+00	6.19E-01		-1.42E-01	9.54E-01		null	null		1.07E+01	6.13E-04	Up			Unigene121569_All//4.00E-07//TC131524				
Unigene121572_All	347	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.48	3.90	null	null		null	null	null	null		null	null		8.91E+00	1.39E-01		1.19E+01	9.04E-10	Up							
Unigene121575_All	310	0.17	0.00	0.00	0.00	0.33	0.29	0.41	0.27	2.83	-7.40E+00	6.14E-01		-7.40E+00	6.26E-01	8.38E+00	4.57E-01		8.19E+00	4.78E-01		-6.02E-01	7.67E-01		2.79E+00	5.33E-04	Up			Unigene121575_All//4.00E-07//AW187849				
Unigene121576_All	334	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.88	2.15	null	null		null	null	null	null		null	null		2.79E+00	9.48E-02		4.08E+00	2.41E-04	Up							
Unigene121577_All	384	0.14	1.32	1.11	0.52	0.00	0.47	0.00	0.00	2.28	3.28E+00	2.11E-02		3.02E+00	5.73E-02	-9.02E+00	8.44E-02		-1.41E-01	9.35E-01		null	null		1.12E+01	2.05E-06	Up							
Unigene121578_All	317	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.13	2.01	-7.37E+00	6.14E-01		-7.37E+00	6.26E-01	null	null		null	null		7.04E+00	6.36E-01		1.10E+01	9.34E-05	Up							
Unigene12158_All	3753	2.17	2.24	1.72	3.28	2.84	2.77	6.75	2.57	2.56	4.34E-02	8.39E-01		-3.41E-01	1.23E-01	-2.10E-01	2.29E-01		-2.44E-01	1.65E-01		-1.39E+00	2.89E-38	Down	-1.40E+00	9.32E-40	Down	Unigene12158_All//gi|224124794|ref|XP_002329950.1|//0.00E+00//tubulin gamma complex-associated protein [Populus trichocarpa] >gi|222871972|gb|EEF09103.1| tubulin gamma complex-associated protein [Populus trichocarpa]	Unigene12158_All//0.00E+00//AT1G80260| emb1427 (embryo defective 1427); tubulin binding	Unigene12158_All//0.00E+00//TC179590			GO:0003006//GO:0008092//GO:0015630//GO:0044430	nr -
Unigene121586_All	969	0.00	0.00	0.00	0.98	0.53	0.05	0.31	0.52	6.41	null	null		null	null	-8.74E-01	2.10E-01		-4.39E+00	5.96E-05	Down	7.61E-01	4.22E-01		4.39E+00	5.11E-35	Up	Unigene121586_All//gi|100853485|gb|ABE91953.2|//3.00E-70//Protein kinase-like [Medicago truncatula]	Unigene121586_All//4.00E-58//AT1G57700| protein kinase family protein	Unigene121586_All//3.00E-75//gi|48749613|gb|C0080132.1|C0080132			GO:0004674//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene121588_All	313	0.17	0.00	0.00	3.50	2.53	5.34	10.54	6.28	0.89	-7.39E+00	6.14E-01		-7.39E+00	6.26E-01	-4.69E-01	4.83E-01		6.09E-01	2.56E-01		-7.48E-01	1.39E-02		-3.56E+00	1.31E-16	Down							
Unigene121595_All	259	0.00	0.20	0.00	0.00	0.00	0.00	4.57	1.45	11.38	7.61E+00	6.18E-01		null	null	null	null		null	null		-1.65E+00	5.03E-03		1.32E+00	6.13E-05	Up			Unigene121595_All//8.00E-54//C0106719				
Unigene121598_All	778	0.00	0.00	0.00	0.26	0.09	0.23	0.11	1.07	6.88	null	null		null	null	-1.53E+00	4.16E-01		-1.41E-01	9.35E-01		3.31E+00	3.10E-04	Up	5.98E+00	6.78E-35	Up			Unigene121598_All//1.00E-30//FF403790				
Unigene121599_All	316	0.00	0.00	0.00	0.00	0.44	0.29	0.00	0.00	2.52	null	null		null	null	8.77E+00	3.19E-01		8.16E+00	4.78E-01		null	null		1.13E+01	7.36E-06	Up	Unigene121599_All//gi|55163138|emb|CAH05087.1|//2.00E-17//orcinol O-methyltransferase 4 [Rosa hybrid cultivar]	Unigene121599_All//5.00E-07//AT1G21130| O-methyltransferase, putative	Unigene121599_All//4.00E-07//TC177360		ko00402|Benzoxazinoid biosynthesis	GO:0008168	nr +
Unigene121600_All	1515	9.91	6.79	5.13	10.85	11.18	9.03	20.37	12.33	8.81	-5.46E-01	1.48E-04		-9.50E-01	4.03E-10	4.35E-02	8.22E-01		-2.65E-01	6.88E-02		-7.24E-01	2.09E-16		-1.21E+00	1.15E-38	Down	Unigene121600_All//gi|21536851|gb|AAM61183.1|//1.00E-107//protein kinase ADK1-like protein [Arabidopsis thaliana]	Unigene121600_All//6.00E-89//AT4G28540| CKL6 (CASEIN KINASE I-LIKE 6); kinase/ protein serine/threonine kinase	Unigene121600_All//0.00E+00//ES822774				nr +
Unigene121600_All	910	0.00	0.00	0.00	0.00	0.11	0.15	0.60	0.37	2.45	null	null		null	null	6.83E+00	4.57E-01		7.22E+00	3.11E-01		-7.17E-01	4.22E-01		2.02E+00	1.66E-06	Up	Unigene121600_All//gi|224092404|ref|XP_002309594.1|//1.00E-113//flavine-containing monooxygenase [Populus trichocarpa] >gi|222855570|gb|EEE93117.1| flavine-containing monooxygenase [Populus trichocarpa]	Unigene121600_All//6.00E-85//AT5G11320| YUC4 (YUCCA4); monooxygenase/ oxidoreductase	Unigene121600_All//6.00E-175//gi|78346609|gb|DT566883.1|DT566883		ko00380|Tryptophan metabolism	GO:0009653//GO:0009793//GO:0009850//GO:0009908//GO:0016709//GO:0030554//GO:0048366	nr +
Unigene121602_All	390	0.00	0.00	0.00	0.00	0.00	0.12	0.33	0.86	3.68	null	null		null	null	null	null		6.86E+00	6.97E-01		1.40E+00	2.76E-01		3.50E+00	2.50E-07	Up							ESTscan -
Unigene121609_All	571	1.65	0.62	1.40	0.17	1.03	0.63	2.52	0.37	0.63	-1.41E+00	5.70E-02		-2.38E-01	7.23E-01	2.55E+00	2.84E-02		1.86E+00	2.20E-01		-2.78E+00	5.95E-06	Down	-2.00E+00	1.70E-04	Down	Unigene121609_All//gi|93115321|gb|ABE98329.1|//5.00E-32//SRC2-like protein [Nicotiana benthamiana]	Unigene121609_All//4.00E-08//AT1G09070| SRC2 (SOYBEAN GENE REGULATED BY COLD-2); protein binding	Unigene121609_All//1.00E-180//TC138421		ko03040|Spliceosome		nr +
Unigene121613_All	549	0.00	0.00	0.00	0.00	0.19	0.00	0.00	0.15	1.52	null	null		null	null	7.56E+00	4.57E-01		null	null		7.25E+00	4.02E-01		1.06E+01	3.88E-06	Up	Unigene121613_All//gi|224092069|ref|XP_002309462.1|//4.00E-15//leucine-rich repeat protein kinase [Populus trichocarpa] >gi|222855538|gb|EEE92985.1| leucine-rich repeat protein kinase [Populus trichocarpa]	Unigene121613_All//1.00E-14//AT2G26330| ER (ERECTA); transmembrane receptor protein kinase				GO:0003006//GO:0006952//GO:0009886//GO:0009887//GO:0016043//GO:0016301//GO:0043231//GO:0048229//GO:0050794	nr -
Unigene121614_All	482	0.22	0.00	0.44	1.55	0.07	1.12	0.35	0.43	2.31	-7.76E+00	3.74E-01		1.03E+00	5.92E-01	-4.44E+00	1.31E-04	Down	-4.63E-01	6.06E-01		3.05E-01	8.36E-01		2.72E+00	8.54E-05	Up			Unigene121614_All//6.00E-07//TC172443				
Unigene12162_All	1412	1.26	0.29	2.60	2.26	1.54	2.33	3.32	1.92	2.29	-2.13E+00	1.23E-04	Down	1.05E+00	1.91E-03	-5.55E-01	1.04E-01		4.84E-02	9.14E-01		-7.89E-01	1.45E-03		-5.40E-01	2.46E-02		Unigene12162_All//gi|224120480|ref|XP_002331058.1|//1.00E-121//arogenate dehydrogenase [Populus trichocarpa] >gi|222872988|gb|EEF10119.1| arogenate dehydrogenase [Populus trichocarpa]	Unigene12162_All//9.00E-114//AT5G34930| arogenate dehydrogenase	Unigene12162_All//0.00E+00//gi|5049952|gb|AI731100.1|AI731100		ko00270|Cysteine and methionine metabolism	GO:0006570//GO:0009536//GO:0016628	nr +
Unigene121620_All	562	0.37	0.09	0.09	0.18	0.43	0.40	0.15	0.74	1.42	-2.05E+00	3.34E-01		-1.97E+00	3.81E-01	1.27E+00	5.32E-01		1.18E+00	5.50E-01		2.31E+00	6.00E-02		3.24E+00	3.96E-04	Up	Unigene121620_All//gi|115469358|ref|NP_001068278.1|//3.00E-14//Os06g0661800 [Oryza sativa Japonica Group] >gi|113596318|dbj|BAF20192.1| Os06g0661800 [Oryza sativa Japonica Group]	Unigene121620_All//2.00E-11//AT5G24830| CRY3 (cryptochrome 3); DNA binding / DNA photolyase/ FMN binding	Unigene121620_All//0.00E+00//gi|21095955|gb|BQ408268.1|BQ408268			GO:0000166//GO:0003676//GO:0003913//GO:0006259//GO:0009536	nr +
Unigene121621_All	592	0.00	0.17	0.00	0.17	0.41	0.23	0.71	0.78	2.69	7.42E+00	3.88E-01		null	null	1.27E+00	5.32E-01		4.44E-01	8.62E-01		1.21E-01	9.07E-01		1.91E+00	1.35E-04	Up							
Unigene121623_All	400	0.26	0.00	0.00	0.00	0.00	0.00	0.00	0.10	1.29	-8.03E+00	3.74E-01		-8.03E+00	3.95E-01	null	null		null	null		6.71E+00	6.36E-01		1.03E+01	6.13E-04	Up							
Unigene121624_All	503	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.61	null	null		null	null	null	null		null	null		null	null		1.14E+01	1.73E-09	Up							
Unigene121625_All	338	0.00	0.00	0.00	0.29	0.00	0.00	0.00	0.12	1.53	null	null		null	null	-8.20E+00	3.14E-01		-8.20E+00	4.01E-01		6.95E+00	6.36E-01		1.06E+01	6.13E-04	Up							
Unigene121627_All	747	0.00	0.00	0.00	0.27	0.18	0.00	0.11	0.17	4.96	null	null		null	null	-5.32E-01	7.49E-01		-8.06E+00	1.34E-01		5.69E-01	7.82E-01		5.45E+00	1.66E-23	Up			Unigene121627_All//7.00E-26//gi|73862584|gb|DT465323.1|DT465323				
Unigene12163_All	2920	2.51	1.02	1.20	2.81	1.58	2.77	2.62	1.86	1.61	-1.29E+00	1.16E-08	Down	-1.06E+00	3.42E-06	Down	-8.33E-01	8.03E-06		-2.39E-02	9.34E-01		-4.94E-01	8.89E-03		-7.03E-01	1.15E-04		Unigene12163_All//gi|224120480|ref|XP_002331058.1|//0.00E+00//arogenate dehydrogenase [Populus trichocarpa] >gi|222872988|gb|EEF10119.1| arogenate dehydrogenase [Populus trichocarpa]	Unigene12163_All//0.00E+00//AT5G34930| arogenate dehydrogenase	Unigene12163_All//0.00E+00//TC160753			GO:0006570//GO:0016628	nr -
Unigene121631_All	433	0.12	0.00	0.00	0.12	0.48	0.10	0.78	0.29	3.31	-6.92E+00	6.14E-01		-6.92E+00	6.26E-01	2.05E+00	3.95E-01		-1.41E-01	9.53E-01		-1.43E+00	2.59E-01		2.08E+00	1.33E-04	Up							
Unigene121634_All	329	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.70	null	null		null	null	null	null		null	null		null	null		1.07E+01	3.28E-04	Up	Unigene121634_All//gi|87241351|gb|ABD33209.1|//2.00E-06//Ribonuclease H [Medicago truncatula]	Unigene121634_All//3.00E-07//AT5G42905| nucleic acid binding / ribonuclease H				GO:0005488	nr -
Unigene121635_All	423	0.25	0.24	0.13	1.30	0.57	0.32	0.60	3.85	1.22	-4.62E-02	9.90E-01		-9.75E-01	7.21E-01	-1.18E+00	2.25E-01		-2.02E+00	7.05E-02		2.68E+00	2.03E-06	Up	1.03E+00	2.53E-01									
Unigene121636_All	550	0.10	0.00	0.00	0.09	0.19	0.00	0.15	0.00	3.04	-6.57E+00	6.14E-01		-6.57E+00	6.26E-01	1.05E+00	8.08E-01		-6.50E+00	6.37E-01		-7.26E+00	4.05E-01		4.31E+00	1.09E-09	Up	Unigene121636_All//gi|147781849|emb|CAN69946.1|//2.00E-07//hypothetical protein [Vitis vinifera]						nr +
Unigene121638_All	292	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.14	2.59	null	null		null	null	null	null		null	null		7.16E+00	6.36E-01		1.13E+01	1.39E-05	Up							
Unigene12164_All	2019	2.28	1.41	1.82	3.80	4.13	5.23	9.78	19.11	27.66	-6.98E-01	1.29E-02		-3.26E-01	2.89E-01	1.19E-01	6.10E-01		4.62E-01	8.73E-03		9.66E-01	1.18E-32		1.50E+00	3.65E-95	Up	Unigene12164_All//gi|224113069|ref|XP_002316381.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222865421|gb|EEF02552.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene12164_All//0.00E+00//AT5G60740| ATPase, coupled to transmembrane movement of substances	Unigene12164_All//0.00E+00//DW240599		ko03040|Spliceosome//ko02010|ABC transporters	GO:0032559//GO:0042626//GO:0044464	nr +
Unigene121640_All	1086	0.19	0.00	0.10	0.00	0.00	0.08	0.86	1.31	8.66	-7.59E+00	1.22E-01		-9.74E-01	6.21E-01	null	null		6.38E+00	4.78E-01		6.11E-01	2.36E-01		3.34E+00	8.37E-43	Up	Unigene121640_All//gi|224052970|ref|XP_002297642.1|//1.00E-137//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222844900|gb|EEE82447.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene121640_All//7.00E-128//AT3G13610| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene121640_All//0.00E+00//FL577006		ko00941|Flavonoid biosynthesis	GO:0016706	nr -
Unigene121641_All	492	0.00	0.00	0.00	0.00	0.14	0.37	0.52	0.85	5.34	null	null		null	null	7.13E+00	6.11E-01		8.52E+00	1.95E-01		7.20E-01	5.07E-01		3.37E+00	1.52E-12	Up	Unigene121641_All//gi|1769897|emb|CAA69271.1|//3.00E-17//lectin receptor kinase [Arabidopsis thaliana]	Unigene121641_All//3.00E-11//AT1G48720| unknown protein	Unigene121641_All//1.00E-26//DT468735			GO:0005488	nr +
Unigene121643_All	335	0.16	0.45	0.32	0.30	0.93	0.13	0.00	0.37	2.50	1.54E+00	5.31E-01		1.03E+00	7.03E-01	1.64E+00	3.21E-01		-1.14E+00	6.77E-01		8.55E+00	2.41E-01		1.13E+01	3.88E-06	Up	Unigene121643_All//gi|240256309|ref|NP_974804.4|//3.00E-10//ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene121643_All//9.00E-11//AT5G18525| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase				GO:0006464//GO:0016301//GO:0032559	nr +
Unigene121645_All	498	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	1.44	null	null		null	null	null	null		null	null		-6.41E+00	6.58E-01		4.08E+00	2.41E-04	Up							
Unigene121646_All	439	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.29	2.27	null	null		null	null	null	null		null	null		8.16E+00	2.41E-01		1.11E+01	3.00E-07	Up			Unigene121646_All//3.00E-11//ES808969				
Unigene121648_All	563	0.00	0.00	0.00	0.00	0.00	0.24	0.00	0.45	1.91	null	null		null	null	null	null		7.91E+00	3.11E-01		8.80E+00	4.31E-02		1.09E+01	8.30E-08	Up	Unigene121648_All//gi|224146420|ref|XP_002326001.1|//5.00E-76//GRAS family transcription factor [Populus trichocarpa] >gi|222862876|gb|EEF00383.1| GRAS family transcription factor [Populus trichocarpa]	Unigene121648_All//7.00E-11//AT5G66770| scarecrow transcription factor family protein		GRAS		GO:0010468//GO:0043231	nr -
Unigene121649_All	548	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.31	1.38	null	null		null	null	null	null		null	null		1.98E+00	3.79E-01		4.16E+00	1.34E-04	Up							ESTscan -
Unigene121665_All	4233	0.48	0.67	0.36	0.98	1.07	1.43	2.34	2.86	7.22	4.76E-01	2.13E-01		-4.02E-01	3.83E-01	1.26E-01	7.26E-01		5.50E-01	2.37E-02		2.93E-01	5.33E-02		1.63E+00	6.71E-59	Up	Unigene121665_All//gi|297847738|ref|XP_002891750.1|//0.00E+00//ATPase, coupled to transmembrane movement of substances [Arabidopsis lyrata subsp. lyrata] >gi|297337592|gb|EFH68009.1| ATPase, coupled to transmembrane movement of substances [Arabidopsis lyrata subsp. lyrata]	Unigene121665_All//0.00E+00//AT1G53390| ATPase, coupled to transmembrane movement of substances	Unigene121665_All//0.00E+00//DW240599		ko03040|Spliceosome//ko02010|ABC transporters	GO:0032559//GO:0042626//GO:0044464	nr -
Unigene121651_All	468	0.00	0.32	0.00	0.11	0.07	0.00	0.54	0.80	3.06	8.34E+00	2.36E-01		null	null	-5.32E-01	8.26E-01		-6.73E+00	6.37E-01		5.68E-01	6.38E-01		2.50E+00	1.65E-05	Up			Unigene121651_All//4.00E-08//gi|78331729|gb|DT552003.1|DT552003				
Unigene121652_All	409	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.75	null	null		null	null	null	null		null	null		null	null		1.08E+01	2.63E-05	Up							
Unigene121655_All	539	0.00	0.00	0.59	0.00	0.00	0.00	0.16	0.23	2.22	null	null		9.21E+00	4.53E-02	null	null		null	null		5.68E-01	7.82E-01		3.82E+00	1.37E-06	Up	Unigene121655_All//gi|29465762|gb|AAM14671.1|//4.00E-50//peptide/glutathione transporter OPT1 [Vitis vinifera]	Unigene121655_All//7.00E-50//AT4G27730| OPT6 (OLIGOPEPTIDE TRANSPORTER 1); oligopeptide transporter	Unigene121655_All//3.00E-21//TC152622			GO:0015197//GO:0015833//GO:0016020	nr -
Unigene121656_All	686	0.08	0.00	0.00	0.07	0.10	0.07	0.68	0.00	2.96	-6.25E+00	6.14E-01		-6.25E+00	6.26E-01	4.68E-01	9.59E-01		-1.42E-01	9.53E-01		-9.41E+00	1.71E-03		2.13E+00	2.44E-06	Up	Unigene121656_All//gi|18087533|gb|AAL58900.1|AF462806_1|1.00E-22//AT3g06940/F17A9_9 [Arabidopsis thaliana] >gi|20855902|gb|AAM26637.1| AT3g06940/F17A9_9 [Arabidopsis thaliana]	Unigene121656_All//7.00E-07//AT1G79570| protein kinase family protein	Unigene121656_All//0.00E+00//DR461029			GO:0046914	nr -

Unigene121657_All	312	0.17	0.00	0.68	0.32	0.22	0.00	0.14	1.07	2.55	-7.39E+00	6.14E-01		2.03E+00	3.61E-01		-5.33E-01	8.17E-01		-8.32E+00	4.01E-01		2.98E+00	5.74E-02		4.24E+00	7.42E-05	Up							
Unigene121658_All	555	0.00	0.00	0.00	0.00	0.00	0.00	5.64	1.28	32.80	null	null		null	null		null	null		null	null		-2.14E+00	3.41E-09	Down	2.54E+00	1.97E-62	Up	Unigene121658_All//gi|27372773|gb|AA003558.1|//5.00E-06//lipoxygenase 1 [Brassica napus]	Unigene121658_All//3.00E-07//AT1G55020| LOX1; lipoxygenase	Unigene121658_All//6.00E-32//ES824586		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr +
Unigene121660_All	529	0.00	0.00	0.00	0.00	0.00	0.00	0.48	0.55	3.84	null	null		null	null		null	null		null	null		2.06E-01	8.68E-01		3.00E+00	6.43E-09	Up							
Unigene121667_All	411	0.00	0.00	0.00	0.00	0.00	0.00	1.34	0.00	9.50	null	null		null	null		null	null		null	null		-1.04E+01	4.61E-04	Down	2.83E+00	1.37E-15	Up							
Unigene121673_All	310	0.00	0.00	0.00	0.00	0.00	0.00	8.46	0.54	2.18	null	null		null	null		null	null		null	null		-3.97E+00	6.69E-14	Down	-1.95E+00	2.58E-07	Down	Unigene121673_All//gi|300137035|gb|EFJ04209.1|//3.00E-11//hypothetical protein SELMODRAFT_139061 [Selaginella moellendorffii]		Unigene121673_All//1.00E-22//gi|78340871|gb|DT561145.1|DT561145				nr -
Unigene121680_All	458	0.00	0.44	0.23	0.22	0.00	0.20	0.09	0.00	1.91	8.79E+00	1.37E-01		7.86E+00	4.00E-01		-7.76E+00	3.14E-01		-1.41E-01	9.51E-01		-6.53E+00	6.58E-01		4.37E+00	2.26E-05	Up							
Unigene121683_All	991	0.37	0.41	0.32	0.55	0.80	0.91	0.73	0.25	4.02	1.46E-01	8.98E-01		-1.97E-01	8.66E-01		5.32E-01	5.40E-01		7.21E-01	3.62E-01		-1.52E+00	5.42E-02		2.47E+00	8.05E-14	Up	Unigene121683_All//gi|297719995|ref|NP_001172359.1|//1.00E-69//Os01g0388566 [Oryza sativa Japonica Group] >gi|255673262|dbj|BAH91089.1|Os01g0388566 [Oryza sativa Japonica Group]	Unigene121683_All//4.00E-69//AT2G48060| unknown protein				GO:0044464	nr -
Unigene121684_All	300	0.35	0.17	1.60	0.00	0.23	0.00	0.14	0.14	2.26	-1.05E+00	6.85E-01		2.20E+00	9.15E-02		7.84E+00	6.11E-01		null	null		-1.65E-02	1.00E+00		4.00E+00	4.29E-04	Up							
Unigene121685_All	484	0.00	0.00	0.00	0.00	0.00	0.19	0.09	1.21	3.37	null	null		null	null		null	null		7.54E+00	4.78E-01		3.79E+00	2.07E-03		5.27E+00	1.93E-10	Up	Unigene121685_All//gi|115485949|ref|NP_001068118.1|//5.00E-34//Os11g0569600 [Oryza sativa Japonica Group] >gi|113645340|dbj|BAF28481.1|Os11g0569600 [Oryza sativa Japonica Group]	Unigene121685_All//1.00E-30//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672//GO:0006952//GO:0016020//GO:0031410//GO:0032446//GO:0032559	nr -
Unigene121688_All	721	0.00	0.00	0.00	0.14	0.00	0.19	0.12	1.04	8.56	null	null		null	null		-7.11E+00	3.14E-01		4.43E-01	8.62E-01		3.15E+00	9.54E-04	Up	6.19E+00	9.00E-41	Up	Unigene121688_All//gi|224139556|ref|XP_002323167.1|//1.00E-09//ABC transporter family protein [Populus trichocarpa] >gi|222867797|gb|EEF04928.1| ABC transporter family protein [Populus trichocarpa]	Unigene121688_All//2.00E-08//AT4G18670| protein binding / structural constituent of cell wall					nr -
Unigene121689_All	516	0.91	1.57	1.34	0.00	0.07	0.18	0.00	0.00	2.70	7.84E-01	3.23E-01		5.56E-01	5.28E-01		6.06E+00	8.31E-01		7.45E+00	4.78E-01		null	null		1.14E+01	4.73E-10	Up	Unigene121689_All//gi|115445817|ref|NP_001046688.1|//4.00E-08//Os02g0321600 [Oryza sativa Japonica Group] >gi|113536219|dbj|BAF08602.1|Os02g0321600 [Oryza sativa Japonica Group]	Unigene121689_All//2.00E-26//AT3G14760| unknown protein					nr -
Unigene12169_All	209	55.83	21.33	22.93	26.69	15.32	16.86	20.43	39.60	33.17	-1.39E+00	8.80E-15	Down	-1.28E+00	1.32E-12	Down	-8.01E-01	6.27E-04		-6.63E-01	7.84E-03		9.55E-01	1.67E-07		6.99E-01	2.99E-04		Unigene12169_All//gi|90093298|gb|AB085162.1|//3.00E-26//At3g14150 [Arabidopsis thaliana]	Unigene12169_All//1.00E-27//AT3G14150| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene12169_All//4.00E-89//gi|109887304|gb|DW516273.1|DW516273		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0000166//GO:0003973//GO:0008152//GO:0042579	nr -
Unigene121690_All	819	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20	3.84	null	null		null	null		null	null		null	null		7.67E+00	1.39E-01		1.19E+01	1.60E-22	Up			Unigene121690_All//3.00E-16//TC159143					
Unigene121693_All	304	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.15	null	null		null	null		null	null		null	null		null	null		1.16E+01	5.69E-07	Up							
Unigene121697_All	446	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.19	1.25	null	null		null	null		null	null		null	null		7.55E+00	4.02E-01		1.03E+01	3.28E-04	Up	Unigene121697_All//gi|301016726|dbj|BAJ11784.1|//2.00E-07//dehydration responsive protein [Corchorus olitorius]		Unigene121697_All//8.00E-46//TC152783				nr +
Unigene121698_All	460	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	3.64	null	null		null	null		null	null		null	null		7.51E+00	4.02E-01		1.18E+01	5.04E-12	Up	Unigene121698_All//gi|20269055|emb|CAC84708.1|//2.00E-09//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene121698_All//4.00E-10//AT3G17600| IAA31 (INDOLE-3-ACETIC ACID INDUCIBLE 31); transcription factor	Unigene121698_All//2.00E-49//TC172305			GO:0009987//GO:0010467	nr -
Unigene121699_All	472	0.22	0.97	0.45	0.21	0.00	0.38	0.09	0.97	1.69	2.12E+00	9.60E-02		1.03E+00	5.92E-01		-7.72E+00	3.14E-01		8.58E-01	6.95E-01		3.44E+00	1.16E-02		4.24E+00	7.42E-05	Up			Unigene121699_All//2.00E-93//gi|48745467|gb|CO075986.1|CO075986					
Unigene12170_All	418	32.29	13.70	14.78	12.99	7.17	9.08	30.65	43.90	37.46	-1.24E+00	2.38E-14	Down	-1.13E+00	6.27E-12	Down	-8.58E-01	3.05E-04		-5.17E-01	4.58E-02		5.18E-01	6.44E-06		2.89E-01	2.15E-02		Unigene12170_All//gi|9294638|dbj|BAB02977.1|//1.00E-30//glycolate oxidase [Arabidopsis thaliana]	Unigene12170_All//5.00E-18//AT3G14130| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene12170_All//4.00E-174//DW516273		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0000166//GO:0003973//GO:0008152//GO:0042579	nr +
Unigene121700_All	553	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	3.10	null	null		null	null		-7.49E+00	3.14E-01		-7.49E+00	4.01E-01		null	null		1.16E+01	2.63E-12	Up							
Unigene121701_All	656	0.00	0.00	0.16	0.00	0.00	0.00	0.32	0.00	2.00	null	null		7.34E+00	4.00E-01		null	null		null	null		-8.33E+00	7.45E-02		2.64E+00	2.27E-05	Up			Unigene121701_All//9.00E-56//DT461883					
Unigene121705_All	370	0.00	0.41	0.00	0.67	0.19	0.24	1.14	1.36	4.95	8.68E+00	2.36E-01		null	null		-1.86E+00	2.75E-01		-1.46E+00	4.07E-01		2.46E-01	7.84E-01		2.12E+00	9.21E-06	Up			Unigene121705_All//4.00E-07//TC139058					
Unigene121707_All	491	0.00	0.00	0.33	1.01	0.14	0.00	0.00	0.00	6.17	null	null		8.35E+00	2.39E-01		-2.85E+00	1.78E-02		-9.99E+00	2.98E-03		null	null		1.26E+01	1.14E-21	Up			Unigene121707_All//6.00E-07//TC146861					
Unigene121708_All	364	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.53	null	null		null	null		null	null		null	null		null	null		1.06E+01	3.28E-04	Up	Unigene121708_All//gi|60327214|gb|AAX19030.1|//3.00E-18//Hcr2-p7.1 [Solanum pimpinellifolium]	Unigene121708_All//7.00E-19//AT5G56040| leucine-rich repeat protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0016772	nr +
Unigene12171_All	507	24.15	10.49	8.93	13.85	6.79	9.89	16.68	25.56	22.47	-1.20E+00	1.53E-12	Down	-1.44E+00	1.53E-15	Down	-1.03E+00	5.51E-07	Down	-4.87E-01	2.92E-02		6.16E-01	9.98E-06		4.30E-01	3.41E-03		Unigene12171_All//gi|90093298|gb|AB085162.1|//2.00E-32//At3g14150 [Arabidopsis thaliana]	Unigene12171_All//1.00E-33//AT3G14150| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene12171_All//2.00E-44//TC154385		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0000166//GO:0003973//GO:0008152//GO:0042579	nr -
Unigene121711_All	625	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.74	null	null		null	null		null	null		null	null		null	null		1.14E+01	2.63E-12	Up	Unigene121711_All//gi|198401802|gb|ACH87552.1|//9.00E-83//L-myo inositol-1 phosphate synthase 1 [Cicer arietinum]	Unigene121711_All//1.00E-30//AT2G22240| MIPS2 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 2); binding / catalytic/ inositol-3-phosphate synthase			ko00562|Inositol phosphate metabolism	GO:0016853//GO:0044237//GO:0044238	nr +
Unigene121712_All	300	0.00	0.51	0.00	1.00	0.00	0.90	0.00	0.70	2.92	8.99E+00	2.36E-01		null	null		-9.96E+00	2.02E-02		-1.41E-01	9.21E-01		9.44E+00	7.85E-02		1.15E+01	2.05E-06	Up							
Unigene121713_All	304	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.28	9.96	null	null		null	null		null	null		null	null		-1.67E-02	1.01E+00		5.16E+00	7.83E-19	Up			Unigene121713_All//2.00E-30//DW479423					
Unigene121715_All	511	0.00	0.59	0.00	0.00	0.00	0.00	0.00	0.33	2.57	9.22E+00	4.44E-02		null	null		null	null		null	null		8.35E+00	1.39E-01		1.13E+01	1.73E-09	Up	Unigene121715_All//gi|23821326|dbj|BAB97197.2|//1.00E-23//peroxidase 1 [Marchantia polymorpha]	Unigene121715_All//5.00E-20//AT3G17070| peroxidase, pstative			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0016209	nr +
Unigene121716_All	548	0.00	0.00	0.00	0.00	0.06	0.00	0.46	0.15	3.05	null	null		null	null		5.97E+00	8.31E-01		null	null		-1.60E+00	3.11E-01		2.72E+00	7.72E-07	Up							
Unigene121718_All	507	0.00	0.00	0.00	0.00	0.00	0.00	0.08	1.07	4.87	null	null		null	null		null	null		null	null		3.68E+00	3.69E-03		5.87E+00	3.27E-16	Up	Unigene121718_All//gi|7671451|emb|CAB88391.1|//2.00E-20//Pto kinase interactor-like protein [Arabidopsis thaliana]	Unigene121718_All//6.00E-14//AT5G10520| RBK1 (Rop Binding protein Kinases 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase				GO:0005488//GO:0016301//GO:0044444//GO:0051707	nr +
Unigene121172_All	1474	6.00	1.79	2.46	3.75	1.96	2.57	8.52	14.06	10.05	-1.75E+00	1.28E-15	Down	-1.29E+00	9.44E-10	Down	-9.35E-01	6.99E-05		-5.44E-01	3.32E-02		7.23E-01	2.95E-11		2.39E-01	7.08E-02		Unigene121172_All//gi|9294638|dbj|BAB02977.1|//3.00E-22//glycolate oxidase [Arabidopsis thaliana]	Unigene121172_All//5.00E-24//AT3G14130| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene121172_All//3.00E-119//DW516273		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0000166//GO:0003973//GO:0008152//GO:0042579	nr -
Unigene121722_All	383	0.00	0.00	0.00	0.00	0.00	0.00	3.42	0.44	1.66	null	null		null	null		null	null		null	null		-2.97E+00	8.34E-06	Down	-1.04E+00	3.96E-02		Unigene121722_All//gi|22326870|ref|NP_197272.2|//2.00E-21//MATE efflux family protein [Arabidopsis thaliana]	Unigene121722_All//7.00E-23//AT5G17700| MATE efflux family protein				GO:0015291//GO:0015893//GO:0044464	nr +
Unigene121725_All	1409	0.00	0.00	0.00	0.21	0.00	0.13	0.24	0.18	8.37	null	null		null	null		-7.73E+00	2.02E-02		-7.26E-01	6.39E-01		-4.32E-01	7.03E-01		5.12E+00	6.02E-72	Up	Unigene121725_All//gi|6650982|gb|AF22112.1|AF119414_1/0.00E+00/1-aminocyclopropane-1-carboxylate synthase 5 [Lupinus albus]	Unigene121725_All//1.00E-139//AT4G26200| ACS7; 1-aminocyclopropane-1-carboxylate synthase			ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016740//GO:0016846//GO:0048037	nr +
Unigene121728_All	505	0.00	0.00	0.00	0.00	0.00	0.00	2.34	0.00	2.76	null	null		null	null		null	null		null	null		-1.12E+01	1.97E-08	Down	2.36E-01	6.46E-01									
Unigene121732_All	557	0.00	0.55	0.00	0.00	0.00	0.00	0.00	0.00	1.72	9.09E+00	4.44E-02		null	null		null	null		null	null		null	null		1.07E+01	5.69E-07	Up	Unigene121732_All//gi|255543875|ref|XP_002513000.1|//2.00E-15//conserved hypothetical protein [Ricinus communis] >gi|223548011|gb|EEF49503.1|conserved hypothetical protein [Ricinus communis]						nr +
Unigene121734_All	757	0.00	0.00	0.00	0.00	0.00	0.06	0.22	0.22	2.53	null	null		null	null		null	null		5.90E+00	6.97E-01		-1.69E-02	1.02E+00		3.50E+00	1.45E-09	Up							
Unigene121737_All	738	0.14	0.00	0.14	2.16	0.79	0.43	0.46	0.28	1.35	-7.15E+00	3.74E-01		2.52E-02	1.00E+00		-1.45E+00	4.07E-03		-2.33E+00	8.02E-05	Down	-6.95E-01	5.78E-01		1.56E+00	1.33E-02				Unigene121737_All//0.00E+00//gi|11210487|gb|BF279417.1|BF279417					
Unigene121739_All	790	0.00	0.00	0.00	0.06	0.09	0.57	1.55	0.11	0.25	null	null		null	null		4.67E-01	9.59E-01		3.18E+00	3.79E-02		-3.87E+00	1.15E-06	Down	-2.62E+00	4.02E-05	Down	Unigene121739_All//gi|145335796|ref|NP_173134.2|//2.00E-73//sugar binding / transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|9802774|gb|AAF99843.1|AC051629_10 Hypothetical protein [Arabidopsis thaliana] >gi|30989911|gb|AAQ56838.1|At1g16900 [Arabidopsis thaliana]	Unigene121739_All//4.00E-73//AT1G16900| sugar binding / transferase, transferring glycosyl groups	Unigene121739_All//0.00E+00//TC169562		ko00510|N-Glycan biosynthesis	GO:0005789//GO:0006497//GO:0016740	nr +
Unigene121744_All	606	1.04	0.50	0.09	0.00	0.11	0.00	1.60	0.00	5.79	-1.05E+00	2.50E-01		-3.56E+00	8.32E-03		6.83E+00	6.11E-01		null	null		-1.06E+01	5.83E-07	Down	1.85E+00	8.62E-09	Up	Unigene121744_All//gi|297817132|ref|XP_002876449.1|//2.00E-16//VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297322287|gb|EFH52708.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene121744_All//6.00E-12//AT3G58000| VQ motif-containing protein				GO:0043231	nr +
Unigene121748_All	387	0.00	0.26	0.00	0.00	0.36	0.35	0.44	0.00	2.47	8.03E+00	3.88E-01		null	null		8.48E+00	3.19E-01		8.45E+00	3.11E-01		-8.77E+00	1.35E-01		2.50E+00	6.42E-04	Up							
Unigene121749_All	788	0.00	0.00	0.00	0.00	0.00	0.00	1.40	0.11	7.03	null	null		null	null		null	null		null	null		-3.72E+00	7.15E-06	Down	2.33E+00	9.68E-18	Up	Unigene121749_All//gi|11385439|gb|AAG34802.1|AF243367_1//5.00E-54//glutathione S-transferase GST 12 [Glycine max]	Unigene121749_All//8.00E-51//AT5G62480| ATGSTU9 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 9); glutathione transferase			ko00480|Glutathione metabolism	GO:0009404//GO:0016829//GO:0044424	nr -
Unigene12175_All	2765	2.25	3.30	2.56	7.62	6.21	6.88	7.97	4.69	3.89	5.51E-01	3.95E-03		1.86E-01	4.44E-01		-2.94E-01	1.20E-02		-1.48E-01	2.88E-01		-7.66E-01	4.46E-13		-1.03E+00	7.91E-22	Down	Unigene12175_All//gi|13605659|gb|AK32823.1|AF361810_1/1.00E-150//AT4g39690/T19P19_80 [Arabidopsis thaliana] >gi|21700889|gb|AAM70568.1|AT4g39690/T19P19_80 [Arabidopsis thaliana]	Unigene12175_All//1.00E-119//AT4G39690| unknown protein	Unigene12175_All//0.00E+00//TC174918		ko03440|Homologous recombination//ko03450|Non-homologous end-joining	GO:0043231	nr -
Unigene121750_All	513	0.10	0.79	0.00	0.00	0.07	0.44	0.33	0.08	2.80	2.95E+00	5.91E-02		-6.67E+00	6.26E-01		6.07E+00	8.31E-01		8.78E+00	1.19E-01		-2.02E+00	3.68E-01		3.08E+00	1.21E-06	Up	Unigene121750_All//gi|224126891|ref|XP_002319952.1|//2.00E-10//predicted protein [Populus trichocarpa] >gi|222858328|gb|EEE95875.1|predicted protein [Populus trichocarpa]		Unigene121750_All//2.00E-16//TC150819				nr +
Unigene121751_All	336	0.00	0.00	0.00	0.00	0.00	0.00	0.25	0.75	2.49	null	null		null	null		null	null		null	null		1.57E+00	3.26E-01		3.31E+00	2.30E-04	Up			Unigene121751_All//1.00E-37//DW497022					
Unigene121753_All	563	0.00	0.36	0.00	0.00	0.06	0.00	0.23	0.37	1.49	8.49E+00	1.37E-01		null	null		5.94E+00	8.31E-01		null	null		7.20E-01	6.32E-01		2.72E+00	8.98E-04	Up	Unigene121753_All//gi|114145388|dbj|BAF30983.1|//2.00E-09//basic helix-loop-helix protein [Nicotiana tabacum]		Unigene121753_All//1.00E-08//DT465287			GO:0010468//GO:0043231	nr +
Unigene121755_All	324	0.00	0.00	0.99	0.00	0.00	0.00	0.52	0.00	4.06	null	null		9.95E+00	4.53E-02		null	null		null	null		-9.03E+00	1.35E-01		2.96E+00	6.13E-06	Up	Unigene121755_All//gi|115469102|ref|NP_001058150.1|//3.00E-07//Os06g0638100 [Oryza sativa Japonica Group] >gi|113396190|dbj|BAF20064.1|Os06g0638100 [Oryza sativa Japonica Group]	Unigene121755_All//2.00E-06//AT2G15290| TIC21 (TRANSLOCON AT INNER MEMBRANE OF CHLOROPLASTS 21); copper uptake transmembrane transporter/ iron ion transmembrane transporter/ protein homodimerization	Unigene121755_All//4.00E-44//gi|21093935|gb|BQ406248.1|BQ406248				nr +

Unigene121756_All	717	0.15	0.78	0.00	0.56	0.14	0.50	0.18	0.93	4.33	2.41E+00	3.93E-02			-7.19E+00	3.95E-01			-1.95E+00	1.19E-01			-1.41E-01	9.04E-01			2.40E+00	9.04E-03			4.61E+00	2.87E-18	Up				Unigene121756_All//3.00E-99//TC172236				
Unigene121761_All	562	5.21	0.90	2.08	4.88	3.68	4.26	1.13	0.82	0.50	-2.53E+00	1.33E-08	Down		-1.32E+00	7.76E-04	Down		-4.07E-01	3.05E-01			-1.95E-01	6.39E-01			-4.64E-01	5.94E-01			-1.19E+00	1.33E-01			Unigene121761_All//gi|115441491|ref|NP_001045025.1|//8.00E-37//Os01g0885600 [Oryza sativa Japonica Group] >gi|56784309|dbj|BAD82235.1|hydrolase-like protein [Oryza sativa Japonica Group] >gi|113534556|dbj|BAF06939.1|Os01g0885600 [Oryza sativa Japonica Group]	Unigene121761_All//1.00E-33//AT4G10030| hydrolase, alpha/beta fold family protein	Unigene121761_All//4.00E-150//gi|78337034|gb|DT557308.1|DT557308			GO:0008152//GO:0016787//GO:0043231	nr +
Unigene121764_All	363	0.00	0.00	0.00	1.37	0.00	0.00	0.70	0.12	2.52	null	null			null	null			-1.04E+01	8.98E-04	Down		-1.04E+01	2.98E-03			-2.60E+00	1.44E-01			1.85E+00	6.88E-03			Unigene121764_All//gi|297719995|ref|NP_001172359.1|//9.00E-07//Os01g0388566 [Oryza sativa Japonica Group] >gi|255673262|dbj|BAH91089.1|Os01g0388566 [Oryza sativa Japonica Group]	Unigene121764_All//4.00E-09//AT2G48060| unknown protein	Unigene121764_All//5.00E-50//DT052676			GO:0044464	nr -
Unigene121765_All	389	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.00	2.87	null	null			null	null			null	null			null	null			-8.76E+00	1.35E-01			2.72E+00	8.54E-05	Up				Unigene121765_All//1.00E-13//TC163664				
Unigene121770_All	1529	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.00	4.66	null	null			null	null			null	null			null	null			-8.11E+00	3.25E-03			4.08E+00	3.53E-38	Up		Unigene121770_All//gi|224066581|ref|XP_002302147.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222843873|gb|EEE81420.1|cytochrome P450 [Populus trichocarpa]	Unigene121770_All//8.00E-126//AT2G42850| CYP718; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00906|Carotenoid biosynthesis	GO:0005506//GO:0008152//GO:0016491	nr +
Unigene121772_All	921	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	18.38	null	null			null	null			null	null			null	null			null	null			1.42E+01	1.20E-121	Up								
Unigene121775_All	389	0.81	0.00	0.00	0.00	0.18	0.00	0.54	0.21	2.66	-9.66E+00	3.66E-02			-9.66E+00	4.92E-02			7.47E+00	6.11E-01			null	null			-1.34E+00	4.30E-01			2.29E+00	7.17E-04	Up								
Unigene121777_All	743	0.00	0.00	0.00	0.09	0.00	0.11	0.00	3.43	null	null				null	null			6.53E+00	6.11E-01			null	null			-6.83E+00	4.04E-01			4.91E+00	1.44E-15	Up		Unigene121777_All//gi|22854880|gb|AAN09798.1|//1.00E-63//benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Nicotiana tabacum]	Unigene121777_All//3.00E-49//AT5G17540| transferase family protein			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016747	nr -
Unigene121780_All	560	0.00	0.90	0.00	0.53	0.06	0.16	0.15	0.22	3.34	9.82E+00	4.05E-03			null	null			-3.12E+00	7.56E-02			-1.73E+00	2.89E-01			5.68E-01	7.82E-01			4.47E+00	5.22E-11	Up				Unigene121780_All//1.00E-17//C0118839				
Unigene121781_All	366	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.11	3.16	null	null			null	null			null	null			null	null			-1.02E+00	7.25E-01			3.77E+00	2.44E-06	Up								
Unigene121782_All	418	0.00	0.00	0.51	0.00	0.00	0.00	0.30	1.40	3.24	null	null			8.99E+00	1.41E-01			null	null			null	null			2.21E+00	2.34E-02			3.42E+00	7.76E-07	Up								
Unigene121783_All	439	32.89	82.64	21.35	63.43	58.91	99.59	9.25	51.41	65.88	1.33E+00	1.99E-41	Up		-6.24E-01	4.30E-05			-1.07E-01	3.82E-01			6.51E-01	1.25E-16			2.48E+00	1.50E-73	Up		2.83E+00	3.50E-111	Up		Unigene121783_All//gi|559557|gb|AAA51649.1|//6.00E-20//arabinogalactan-protein [Pyrus communis]		Unigene121783_All//8.00E-46//TC174004		ko04141|Protein processing in endoplasmic reticulum//ko03420|Nucleotide excision repair		nr +
Unigene121784_All	401	0.00	0.00	0.00	0.00	0.00	0.00	0.63	0.00	2.78	null	null			null	null			null	null			null	null			-9.31E+00	4.04E-02			2.14E+00	7.62E-04	Up		Unigene121784_All//gi|18404687|ref|NP_564644.1|//1.00E-10//senescence-associated protein-related [Arabidopsis thaliana] >gi|28416881|gb|AA042971.1|At1g53885 [Arabidopsis thaliana]	Unigene121784_All//8.00E-09//AT1G53903| CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF581 (InterPro:IPR007650); BEST Arabidopsis thaliana protein match is: senescence-associated protein-related (TAIR:AT1G53885.1); Has 277 Blast hits to 277 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 277; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene121784_All//2.00E-157//DR453511				nr +
Unigene121787_All	693	0.00	0.00	0.00	0.00	0.00	0.00	0.31	0.06	8.85	null	null			null	null			null	null			null	null			-2.34E+00	2.37E-01			4.86E+00	1.24E-36	Up								
Unigene121791_All	591	0.00	0.00	0.00	0.00	0.00	0.00	1.93	0.28	9.44	null	null			null	null			null	null			null	null			-2.77E+00	7.62E-05	Down		2.29E+00	1.78E-17	Up				Unigene121791_All//2.00E-53//TC175880				
Unigene121794_All	790	0.00	0.00	0.00	0.00	0.00	0.23	0.75	0.48	2.92	null	null			null	null			null	null			7.84E-00	1.95E-01			-6.54E-01	4.45E-01			1.96E+00	1.69E-06	Up								
Unigene121796_All	407	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.13	null	null			null	null			null	null			null	null			null	null			1.16E+01	3.29E-09	Up			Unigene121796_All//7.00E-06//AT5G09380| DNA-directed RNA polymerase III RPC4 family protein	Unigene121796_All//2.00E-09//gi|78351087|gb|DT571361.1|DT571361		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		kegg +
Unigene121799_All	432	0.00	0.00	0.00	0.12	0.00	0.10	0.00	0.29	1.94	null	null			null	null			-6.85E+00	5.57E-01			-1.42E-01	9.53E-01			8.18E+00	2.41E-01			1.09E+01	3.88E-06	Up		Unigene121799_All//gi|15239225|ref|NP_196192.1|//2.00E-10//ASA1 (ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1); anthranilate synthase [Arabidopsis thaliana] >gi|418133|sp|P32068.1|TRPE_ARATH RecName: Full=Anthranilate synthase component I-1, chloroplastic; Flags: Precursor >gi|166604|gb|AAA32738.1|anthranilate synthase alpha subunit [Arabidopsis thaliana] >gi|9759098|dbj|BAB09667.1|anthranilate synthase component I-1 precursor [Arabidopsis thaliana]		Unigene121799_All//3.00E-48//TC159312		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene1218_All	1846	1.19	0.80	0.58	1.78	1.68	0.88	6.44	2.76	2.87	-5.81E-01	1.81E-01			-1.05E+00	2.24E-02			-8.52E-02	8.11E-01			-1.02E+00	2.77E-03			-1.22E+00	3.82E-15	Down		-1.16E+00	1.38E-14	Down		Unigene1218_All//gi|281333041|gb|AD60975.1|//1.00E-101//lateral root primordium 1 [Brassica rapa subsp. pekinensis]	Unigene1218_All//2.00E-59//AT5G12330| LRP1 (LATERAL ROOT PRIMORDIUM 1); protein homodimerization	Unigene1218_All//0.00E+00//gi|164255597|gb|ES817102.1|ES817102	SRS		GO:0009725//GO:0042802//GO:0048513	nr -
Unigene12180_All	583	6.82	10.43	9.59	10.85	16.54	23.63	13.42	17.99	22.69	6.13E-01	1.07E-02			4.92E-01	6.45E-02			6.08E-01	5.34E-04			1.12E+00	2.64E-13	Up		4.24E-01	7.69E-03			7.58E-01	2.80E-08			Unigene12180_All//gi|37202074|gb|AAQ89652.1|//2.00E-24//At3g54880 [Arabidopsis thaliana]	Unigene12180_All//9.00E-26//AT3G54880| unknown protein	Unigene12180_All//0.00E+00//gi|164348562|gb|EX170669.1|EX170669			GO:0043231	nr +
Unigene121800_All	380	0.00	0.00	0.00	0.00	0.00	0.00	0.67	0.11	13.21	null	null			null	null			null	null			null	null			-2.60E+00	1.44E-01			4.31E+00	4.95E-28	Up				Unigene121800_All//4.00E-07//DW513674				
Unigene121801_All	416	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.10	1.92	null	null			null	null			null	null			null	null			6.65E+00	6.35E-01			1.09E+01	7.36E-06	Up		Unigene121801_All//gi|31321894|gb|AAK84428.1|//6.00E-13//papillar cell-specific pectin methylesterase-like protein [Brassica napus]	Unigene121801_All//3.00E-12//AT2G47550| pectinesterase family protein			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0044464	nr -
Unigene121802_All	669	0.31	0.00	0.00	0.00	0.10	0.00	0.19	1.06	6.55	-8.29E+00	1.22E-01			-8.29E+00	1.46E-01			6.69E+00	6.11E-01			null	null			2.49E+00	5.53E-03			5.11E+00	5.92E-27	Up								
Unigene121803_All	411	0.00	0.00	0.00	0.12	0.00	0.00	0.21	0.20	2.13	null	null			null	null			-6.92E+00	5.57E-01			-6.92E+00	6.37E-01			-1.62E-02	1.01E+00			3.37E+00	1.32E-04	Up				Unigene121803_All//1.00E-13//AT127447				
Unigene121804_All	656	0.00	0.00	0.00	0.00	0.00	0.00	1.48	0.51	4.49	null	null			null	null			null	null			null	null			-1.54E+00	1.90E-02			1.60E+00	2.64E-06	Up				Unigene121804_All//2.00E-16//TC167637				
Unigene121805_All	757	0.00	0.00	0.00	0.00	0.00	0.12	0.11	0.00	3.42	null	null			null	null			null	null			6.90E+00	4.78E-01			-6.80E+00	4.04E-01			4.94E+00	7.71E-16	Up		Unigene121805_All//gi|15890547|gb|AB982529.1|//1.00E-131//class III peroxidase [Gossypium hirsutum]	Unigene121805_All//2.00E-65//AT1G49570| peroxidase, putative	Unigene121805_All//0.00E+00//NP12958150		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0016209//GO:0031410//GO:0046872	nr +
Unigene121808_All	752	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.76	null	null			null	null			null	null			null	null			null	null			1.19E+01	3.03E-20	Up								
Unigene121809_All	415	0.25	0.49	0.13	0.48	0.17	0.22	0.00	0.30	3.46	9.54E-01	6.22E-01			-9.75E-01	7.21E-01			-1.53E+00	4.16E-01			-1.14E+00	5.69E-01			8.24E+00	2.41E-01			1.18E+01	2.48E-10	Up								
Unigene12181_All	2465	0.93	2.82	4.06	4.28	6.79	6.93	6.67	7.07	8.24	1.59E+00	6.44E-11	Up		2.12E+00	1.03E-21	Up		6.64E-01	1.63E-07			6.93E-01	1.32E-07			8.36E-02	5.78E-01			3.05E-01	4.72E-03			Unigene12181_All//gi|37202074|gb|AAQ89652.1|//9.00E-15//At3g54880 [Arabidopsis thaliana]	Unigene12181_All//4.00E-16//AT3G54880| unknown protein	Unigene12181_All//0.00E+00//C0130354			GO:0043231	nr -
Unigene121810_All	447	0.00	0.00	0.00	0.45	1.16	0.61	0.00	0.00	1.78	null	null			null	null			1.37E+00	2.26E-01			4.43E-01	7.64E-01			null	null			1.08E+01	7.36E-06	Up		Unigene121810_All//gi|15236590|ref|NP_193496.1|//3.00E-20//tRNA/rRNA methyltransferase (SpoU) family protein [Arabidopsis thaliana]	Unigene121810_All//2.00E-21//AT4G17610| tRNA/rRNA methyltransferase (SpoU) family protein					nr +
Unigene121811_All	398	0.26	0.00	0.00	0.75	1.21	0.79	0.64	1.16	3.20	-8.04E+00	3.74E-01			-8.04E+00	3.95E-01			6.90E-01	5.67E-01			8.09E-02	9.50E-01			8.58E-01	3.96E-01			2.33E+00	1.17E-04	Up								
Unigene121813_All	456	0.00	0.67	1.63	0.11	0.30	0.40	1.21	0.37	1.14	9.38E+00	4.44E-02			1.07E+01	3.28E-04	Up		1.47E+00	6.19E-01			1.86E+00	4.58E-01			-1.72E+00	7.23E-02			-8.58E-02	9.27E-01			Unigene121813_All//gi|224120560|ref|XP_002318360.1|//3.00E-32//predicted protein [Populus trichocarpa] >gi|222859033|gb|EEE96580.1|predicted protein [Populus trichocarpa]	Unigene121813_All//6.00E-17//AT5G52950| unknown protein					nr -
Unigene121815_All	1342	0.00	0.00	0.00	0.00	0.00	0.07	0.44	0.25	1.93	null	null			null	null			null	null			6.07E+00	4.78E-01			-8.24E-01	3.48E-01			2.13E+00	7.12E-08	Up		Unigene121815_All//gi|224087611|ref|XP_002308196.1|//1.00E-138//laccase 110a [Populus trichocarpa] >gi|222854172|gb|EEE91719.1|laccase 110a [Populus trichocarpa]	Unigene121815_All//7.00E-118//AT3G09220| LAC7 (laccase 7); laccase	Unigene121815_All//9.00E-36//TC175599		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene121816_All	677	0.00	0.00	0.00	0.00	0.00	0.07	1.12	0.62	3.94	null	null			null	null			null	null			6.06E+00	6.97E-01			-8.65E-01	2.39E-01			1.81E+00	1.04E-06	Up		Unigene121816_All//gi|240255863|ref|NP_680697.4|//5.00E-17//ATRTL1 (ARABIDOPSIS THALIANA RNASEIII-LIKE 1); RNA binding / ribonuclease III [Arabidopsis thaliana]	Unigene121816_All//2.00E-18//AT4G15417| ATRTL1 (ARABIDOPSIS THALIANA RNASEIII-LIKE 1); RNA binding / ribonuclease III	Unigene121816_All//3.00E-09//AT729675			GO:0003676//GO:0010467//GO:0016891//GO:0044464	nr -
Unigene121819_All	429	0.00	0.00	0.00	0.23	0.16	0.53	0.00	0.00	1.86	null	null			null	null			-5.33E-01	8.17E-01			1.18E+00	5.50E-01			null	null			1.09E+01	7.36E-06	Up								
Unigene12182_All	1010	4.71	5.57	10.18	12.77	15.72	13.64	7.12	6.79	17.67	2.40E-01	3.62E-01			1.11E+00	4.85E-09	Up		2.99E-01	3.44E-02			9.45E-02	6.36E-01			-6.85E-02	7.56E-01			1.31E+00	1.78E-25	Up		Unigene12182_All//gi|297794533|ref|XP_002865151.1|//1.00E-120//low-level beta-amylase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297310986|gb|EFH41410.1|low-level beta-amylase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene12182_All//3.00E-105//AT5G47010| LBA1 (LOW-LEVEL BETA-AMYLASE 1); ATP binding / DNA binding / RNA helicase/ hydrolase	Unigene12182_All//0.00E+00//TC133127			GO:0000166//GO:0017111	nr -
Unigene121820_All	415	0.25	0.00	0.00	0.00	0.00	0.00	0.51	0.91	3.36	-7.98E+00	3.74E-01			-7.98E+00	3.95E-01			null	null			null	null			8.31E-01	4.67E-01			2.72E+00	8.11E-06	Up		Unigene121820_All//gi|30689839|ref|NP_195114.2|//9.00E-15//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75298259|sp|Q84WX0.1|BHH85_ARATH RecName: Full=Transcription factor bHLH85; AltName: Full=Transcription factor EN 115; AltName: Full=bHLH transcription factor bHLH085; AltName: Full=Basic helix-loop-helix protein 85; Short=bHLH 85; Short=AtbHLH85 >gi|27808578|gb|AAO24569.1|At4g33880 [Arabidopsis thaliana]	Unigene121820_All//3.00E-13//AT2G14760| basic helix-loop-helix protein / bHLH protein		bHLH			nr +
Unigene121822_All	408	0.00	0.00	0.00	0.00	0.00	0.00	0.41	1.13	3.42	null	null			null	null			null	null			null	null			1.44E+00	1.67E-01			3.04E+00	2.09E-06	Up		Unigene121822_All//gi|238018838|gb|ACR38454.1|//3.00E-16//unknown [Zea mays]		Unigene121822_All//2.00E-28//TC152959				nr -
Unigene121823_All	664	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.38	3.18	null	null			null	null			null	null			null	null			8.56E+00	4.31E-02			1.16E+01	3.90E-15	Up		Unigene121823_All//gi|297596172|ref|NP_001042123.2|//4.00E-23//Os01g0167800 [Oryza sativa Japonica Group] >gi|255672908|dbj|BAF04037.2|Os01g0167800 [Oryza sativa Japonica Group]	Unigene121823_All//5.00E-21//AT1G48120| calcineurin-like phosphoesterase family protein	Unigene121823_All//8.00E-07//DR463910				nr +
Unigene121825_All	895	0.00	0.11	0.00	0.00	0.38	0.30	0.14	0.61	17.94	6.82E+00	3.88E-01			null	null			8.59E+00	3.01E-02			8.24E+00	7.03E-02			2.10E+00	3.71E-02			6.98E+00	3.04E-109	Up		Unigene121825_All//gi|224137172|ref|XP_002327054.1|//1.00E-51//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222835369|gb|EEE73804.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene121825_All//7.00E-52//AT2G44840| ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	Unigene121825_All//1.00E-34//TC173432	AP2-EREBP		GO:0000160//GO:0001071//GO:0003676//GO:0006351//GO:0009743//GO:0010468//GO:0043231	nr -
Unigene121826_All	383	0.00	0.00	0.00	0.00	0.00	0.00	0.33	0.00	16.23	null	null			null	null			null	null			null	null			-8.37E+00	2.36E-01			5.61E+00	1.19E-39	Up		Unigene121826_All//gi|225444311|ref|XP_002263655.1|//6.00E-14//PREDICTED: similar to stigma-specific Stig1 family protein [Vitis vinifera]	Unigene121826_All//2.00E-11//AT1G11925| Encodes a Stigma-specific Stig1 family protein					nr +

Unigene121827_All	435	0.72	0.00	0.00	0.00	0.32	1.04	0.19	0.10	3.66	-9.50E+00	3.66E-02		-9.50E+00	4.92E-02		8.31E+00	3.19E-01		1.00E+01	7.76E-03		-1.02E+00	7.25E-01		4.24E+00	3.63E-09	Up	Unigene121827_All//gi|226510010|ref|NP_001148087.1|//2.00E-25//LOC100281695 [Zea mays]>gi|195615714|gb|ACG29687.1| peroxisomal fatty acid beta-oxidation multifunctional protein [Zea mays]	Unigene121827_All//3.00E-25//AT4G29010| AIM1 (ABNORMAL INFLORESCENCE MERISTEM); enoyl-CoA hydratase	Unigene121827_All//9.00E-18//TC178290		ko00592|alpha-Linolenic acid metabolism	GO:0009062//GO:0009536//GO:0009791//GO:0016836//GO:0016853//GO:0030312//GO:0042579//GO:0048037	nr +
Unigene121829_All	920	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.90	null	null		null	null		null	null		null	null		null	null		1.15E+01	4.17E-19	Up	Unigene121829_All//gi|297720061|ref|NP_001172392.1|//8.00E-09//Os01g0531200 [Oryza sativa Japonica Group]>gi|255673314|dbj|BAH91122.1| Os01g0531200 [Oryza sativa Japonica Group]	Unigene121829_All//3.00E-09//AT1G48120| calcineurin-like phosphoesterase family protein					nr -
Unigene121830_All	849	0.00	0.00	0.00	0.12	0.00	0.00	0.20	0.20	5.58	null	null		null	null		-6.87E+00	3.14E-01		-6.87E+00	4.01E-01		-1.68E-02	1.02E+00		4.81E+00	2.97E-28	Up	Unigene121830_All//gi|124361091|gb|ABN09063.1|//2.00E-86//Major facilitator superfamily [Medicago truncatula]	Unigene121830_All//9.00E-80//AT3G20660| AtOCT4 (Arabidopsis thaliana ORGANIC CATION/CARNITINE TRANSPORTER4); carbohydrate transmembrane transporter/ sugar:hydrogen symporter				GO:0006810//GO:0009534//GO:0022891//GO:0031224	nr -
Unigene121831_All	1097	0.00	0.00	0.00	0.00	0.03	0.00	0.00	0.15	9.62	null	null		null	null		4.97E+00	8.31E-01		null	null		7.25E+00	1.39E-01		1.32E+01	1.02E-75	Up			Unigene121831_All//6.00E-12//DW504421					
Unigene121834_All	470	60.34	47.33	40.33	2.86	13.70	18.16	0.27	0.36	0.42	-3.50E-01	6.14E-04		-5.81E-01	2.80E-08		2.26E+00	6.05E-18	Up	2.67E+00	1.50E-26	Up	3.98E-01	8.14E-01		6.51E-01	6.65E-01		Unigene121834_All//gi|15236529|ref|NP_192597.1|//6.00E-45//heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related [Arabidopsis thaliana]>gi|3377812|gb|AAC28185.1| contains similarity to heavy-metal-associated domain containing proteins (Pfam: HMA.hm, score: 12.02) [Arabidopsis thaliana]	Unigene121834_All//4.00E-46//AT4G08570| heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	Unigene121834_All//0.00E+00//TC161123			GO:0006812//GO:0043169	nr +
Unigene121835_All	446	0.70	0.91	0.36	1.45	1.24	1.01	2.65	5.62	6.61	3.69E-01	7.24E-01		-9.75E-01	5.06E-01		-2.33E-01	8.07E-01		-5.20E-01	5.88E-01		1.08E+00	2.69E-03		1.32E+00	6.13E-05	Up			Unigene121835_All//3.00E-70//gi|195982815|gb|FL577072.1|FL577072					
Unigene121836_All	421	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.30	8.80	null	null		null	null		null	null		null	null		5.68E-01	7.82E-01		5.45E+00	1.66E-23	Up								
Unigene121838_All	446	0.12	2.39	2.27	0.89	0.77	0.10	3.41	4.87	3.48	4.35E+00	3.95E-05	Up	4.27E+00	1.19E-04	Up	-2.11E-01	8.25E-01		-3.14E+00	4.88E-02		5.14E-01	2.02E-01		2.96E-02	9.69E-01		Unigene121838_All//gi|208964720|gb|ACI31550.1|//6.00E-12//SGT1-2 [Glycine max]	Unigene121838_All//2.00E-09//AT4G11260| SGT1B; protein binding	Unigene121838_All//5.00E-81//TC148581		ko04626|Plant-pathogen interaction		nr +
Unigene121839_All	488	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	4.00	null	null		null	null		null	null		null	null		7.42E+00	4.02E-01		1.20E+01	5.31E-14	Up								
Unigene12184_All	1107	0.09	0.55	0.38	0.54	0.59	0.33	1.99	0.45	1.62	2.54E+00	2.46E-02		2.03E+00	1.40E-01		1.30E-01	9.05E-01		-7.26E-01	4.60E-01		-2.13E+00	1.20E-06	Down	-2.94E-01	4.52E-01		Unigene12184_All//gi|297794533|ref|XP_002865151.1|//1.00E-136//low-level beta-amylase 1 [Arabidopsis lyrata subsp. lyrata]>gi|297310986|gb|EFH41410.1| low-level beta-amylase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene12184_All//2.00E-108//AT5G47010| LBA1 (LOW-LEVEL BETA-AMYLASE 1); ATP binding / DNA binding / RNA helicase/ hydrolase	Unigene12184_All//0.00E+00//TC133127			GO:0000956//GO:0003676//GO:0017111//GO:0032559//GO:0044424//GO:0046914	nr -
Unigene121840_All	422	0.12	0.00	0.00	0.00	0.00	0.21	0.10	0.59	3.78	-6.95E+00	6.14E-01		-6.95E+00	6.26E-01		null	null		7.74E+00	4.78E-01		2.57E+00	1.53E-01		5.24E+00	3.60E-10	Up								
Unigene121841_All	481	0.22	0.00	0.00	0.21	0.00	0.00	0.53	0.17	4.47	-7.77E+00	3.74E-01		-7.77E+00	3.95E-01		-7.69E+00	3.14E-01		-7.69E+00	4.01E-01		-1.60E+00	3.11E-01		3.08E+00	1.25E-09	Up								
Unigene121842_All	477	0.22	1.70	0.78	0.21	0.29	0.47	0.62	0.44	3.76	2.95E+00	3.29E-03		1.83E+00	2.13E-01		4.67E-01	8.77E-01		1.18E+00	5.50E-01		-5.02E-01	6.78E-01		2.60E+00	5.78E-07	Up								ESTscan -
Unigene121844_All	488	0.43	1.66	0.00	0.41	0.64	1.30	0.43	1.46	2.78	1.95E+00	2.43E-02		-8.74E+00	1.46E-01		6.37E-01	6.95E-01		1.67E+00	9.80E-02		1.75E+00	3.21E-02		2.68E+00	1.36E-05	Up								
Unigene121845_All	426	1.72	0.00	0.00	0.23	0.00	0.00	0.79	0.88	3.46	-1.07E+01	2.11E-04	Down	-1.07E+01	4.13E-04	Down	-7.87E+00	3.14E-01		-7.87E+00	4.01E-01		1.53E-01	8.90E-01		2.12E+00	8.39E-05	Up	Unigene121845_All//gi|224087124|ref|XP_002308075.1|//6.00E-20//equilibrative nucleoside transporter [Populus trichocarpa]>gi|222854051|gb|EEE91598.1| equilibrative nucleoside transporter [Populus trichocarpa]	Unigene121845_All//5.00E-15//AT1G02630| equilibrative nucleoside transporter, putative (ENT8)	Unigene121845_All//1.00E-07//TC176124			GO:0015932//GO:0044464//GO:0051234	nr +
Unigene121846_All	525	0.00	0.10	0.00	0.28	0.13	0.26	0.56	0.40	4.10	6.59E+00	6.18E-01		null	null		-1.12E+00	5.84E-01		-1.42E-01	9.44E-01		-5.02E-01	6.78E-01		2.86E+00	5.28E-09	Up			Unigene121846_All//6.00E-07//ES795421					
Unigene121848_All	455	0.00	0.00	0.00	0.44	0.08	0.10	5.48	0.92	2.28	null	null		null	null		-2.53E+00	2.34E-01		-2.14E+00	3.47E-01		-2.58E+00	3.91E-09	Down	-1.27E+00	3.68E-04	Down			Unigene121848_All//5.00E-35//CO080430					
Unigene121850_All	755	0.00	0.00	0.28	0.73	0.96	0.72	0.22	0.55	2.69	null	null		8.14E+00	1.41E-01		4.00E-01	6.64E-01		-1.60E-02	9.75E-01		1.31E+00	2.35E-01		3.59E+00	2.59E-10	Up	Unigene121850_All//gi|297797667|ref|XP_002866718.1|//1.00E-74//MAPKKK19 [Arabidopsis lyrata subsp. lyrata]>gi|297312553|gb|EFH42977.1| MAPKKK19 [Arabidopsis lyrata subsp. lyrata]	Unigene121850_All//5.00E-75//AT3G50310| MAPKKK20; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene121850_All//7.00E-131//gi|78333718|gb|DT553992.1|DT553992		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674	nr +
Unigene121851_All	500	0.00	0.00	0.00	0.00	0.00	0.18	0.17	1.67	3.27	null	null		null	null		null	null		7.50E+00	4.78E-01		3.31E+00	3.10E-04	Up	4.27E+00	1.99E-09	Up			Unigene121851_All//8.00E-28//TC140708					
Unigene121853_All	489	0.00	0.00	0.00	0.00	0.00	0.00	0.35	0.09	3.67	null	null		null	null		null	null		null	null		-2.02E+00	3.68E-01		3.41E+00	8.01E-09	Up								
Unigene121854_All	533	0.98	7.61	3.70	3.18	1.68	0.93	0.87	2.35	0.52	2.95E+00	1.79E-13	Up	1.91E+00	2.96E-04	Up	-9.20E-01	5.65E-02		-1.77E+00	9.00E-04	Down	1.43E+00	1.04E-02		-7.38E-01	4.26E-01		Unigene121854_All//gi|5360263|dbj|BAA81904.1|//1.00E-40//NtPRp27 [Nicotiana tabacum]	Unigene121854_All//2.00E-35//AT2G15220| secretory protein, putative	Unigene121854_All//3.00E-175//gi|78326892|gb|DT547166.1|DT547166				nr -
Unigene121855_All	1048	0.00	0.10	0.00	0.00	0.20	0.04	0.04	0.00	3.19	6.60E+00	3.88E-01		null	null		7.62E+00	1.57E-01		5.43E+00	6.97E-01		-5.33E+00	6.58E-01		6.31E+00	2.43E-22	Up	Unigene121855_All//gi|240256467|ref|NP_200882.4|//1.00E-144//ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana]>gi|75333734|sp|Q9FF46.1|AB28G_ARATH RecName: Full=ABC transporter G family member 28; Short=ABC transporter ABCG.28; Short=AtABCG28; AltName: Full=Putative white-brown complex homolog protein 29; Short=AtWBC29>gi|9759338|dbj|BAB09847.1| ABC transporter-like protein [Arabidopsis thaliana]	Unigene121855_All//1.00E-129//AT5G60740| ATPase, coupled to transmembrane movement of substances					nr -
Unigene121857_All	533	0.00	0.00	0.20	0.09	0.39	0.34	0.56	1.10	2.84	null	null		7.64E+00	4.00E-01		2.05E+00	3.95E-01		1.86E+00	4.58E-01		9.83E-01	2.59E-01		2.35E+00	1.89E-05	Up								
Unigene121858_All	1000	0.05	0.00	0.00	0.10	0.07	0.14	0.47	0.50	13.90	-5.71E+00	6.14E-01		-5.71E+00	6.26E-01		-5.32E-01	8.17E-01		4.44E-01	8.62E-01		1.09E-01	9.15E-01		4.90E+00	7.10E-83	Up	Unigene121858_All//gi|224064167|ref|XP_002301396.1|//3.00E-37//AP2/ERF domain-containing transcription factor [Populus trichocarpa]>gi|222843122|gb|EEE80669.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene121858_All//1.00E-27//AT3G61630| CRF6 (CYTOKININ RESPONSE FACTOR 6); DNA binding / transcription factor	Unigene121858_All//0.00E+00//DT464116	AP2-EREBP		GO:0006350//GO:0006606//GO:0009793//GO:0010468//GO:0048827	nr +
Unigene12186_All	610	7.46	5.57	5.67	6.53	2.94	2.96	4.23	2.74	1.89	-4.23E-01	1.39E-01		-3.95E-01	1.97E-01		-1.15E+00	5.65E-05	Down	-1.14E+00	1.80E-04	Down	-6.25E-01	7.82E-02		-1.16E+00	8.00E-04	Down	Unigene12186_All//gi|297797343|ref|XP_002866556.1|//7.00E-14//SAP domain-containing protein [Arabidopsis lyrata subsp. lyrata]>gi|297312391|gb|EFH42815.1| SAP domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene12186_All//6.00E-15//AT5G63460| SAP domain-containing protein	Unigene12186_All//3.00E-145//CO074829			GO:0003676//GO:0043231	nr +
Unigene121860_All	948	0.11	0.86	0.00	0.00	0.15	0.57	0.62	0.53	7.65	2.95E+00	3.29E-03		-6.79E+00	3.95E-01		7.18E+00	3.19E-01		9.16E+00	2.46E-03		-2.39E-01	7.65E-01		3.61E+00	1.84E-35	Up	Unigene121860_All//gi|157072492|gb|ABV08790.1|//8.00E-33//DREB2B [Thellungiella halophila]	Unigene121860_All//1.00E-18//AT5G05410| DREB2A; DNA binding / transcription activator/ transcription factor		AP2-EREBP		GO:0006350//GO:0010468	nr +
Unigene121861_All	599	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.93	null	null		null	null		null	null		null	null		null	null		1.09E+01	2.28E-08	Up	Unigene121861_All//gi|297724159|ref|NP_001174443.1|//4.00E-10//Os05g0134000 [Oryza sativa Japonica Group]>gi|255676397|dbj|BAH93171.1| Os05g0134000 [Oryza sativa Japonica Group]					GO:0003676//GO:0006260//GO:0034061//GO:0043231	nr +
Unigene121864_All	629	0.00	0.00	0.00	0.00	0.00	0.00	0.27	0.00	2.91	null	null		null	null		null	null		null	null		-8.07E+00	1.35E-01		3.44E+00	4.55E-09	Up	Unigene121864_All//gi|224111284|ref|XP_002332949.1|//5.00E-21//cc-nbs-lrr resistance protein [Populus trichocarpa]>gi|222834261|gb|EEE72738.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene121864_All//4.00E-06//AT1G12280| disease resistance protein (CC-NBS-LRR class), putative	Unigene121864_All//9.00E-19//FL576903		ko04626|Plant-pathogen interaction		nr +
Unigene121867_All	629	0.00	0.00	0.00	0.00	0.00	0.00	0.47	0.00	4.43	null	null		null	null		null	null		null	null		-8.88E+00	2.18E-02		3.24E+00	8.25E-13	Up								
Unigene121869_All	672	0.00	0.00	0.00	0.96	0.21	0.13	0.13	0.00	3.85	null	null		null	null		-2.23E+00	1.79E-02		-2.84E+00	1.02E-02		-6.98E+00	4.04E-01		4.94E+00	7.71E-16	Up	Unigene121869_All//gi|222822564|gb|ACM68431.1|//1.00E-58//xyloglucan-specific endoglucanase inhibitor protein [Capsicum annuum]	Unigene121869_All//5.00E-46//AT1G03220| extracellular dermal glycoprotein, putative / EDGP, putative	Unigene121869_All//0.00E+00//TC176754			GO:0031410	nr +
Unigene12187_All	802	1.96	2.08	4.45	5.22	5.93	3.10	7.28	3.75	1.19	9.13E-02	8.53E-01		1.18E+00	6.20E-04	Up	1.84E-01	5.76E-01		-7.52E-01	1.07E-02		-9.55E-01	1.53E-05		-2.61E+00	1.87E-21	Down	Unigene12187_All//gi|297797343|ref|XP_002866556.1|//2.00E-09//SAP domain-containing protein [Arabidopsis lyrata subsp. lyrata]>gi|297312391|gb|EFH42815.1| SAP domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene12187_All//1.00E-10//AT5G63460| SAP domain-containing protein	Unigene12187_All//6.00E-79//CO074829			GO:0003676//GO:0043231	nr +
Unigene121871_All	724	0.00	0.00	0.00	0.00	0.00	0.00	2.74	0.75	2.04	null	null		null	null		null	null		null	null		-1.87E+00	2.98E-05	Down	-4.31E-01	2.89E-01		Unigene121871_All//gi|297827389|ref|XP_002881577.1|//4.00E-12//DNA binding protein [Arabidopsis lyrata subsp. lyrata]>gi|297327416|gb|EFH57836.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene121871_All//2.00E-13//AT2G38300| DNA binding / transcription factor		G2-like		GO:0001071//GO:0003676//GO:0010468//GO:0043231	nr -
Unigene121874_All	744	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.16	null	null		null	null		null	null		null	null		null	null		1.16E+01	7.77E-17	Up	Unigene121874_All//gi|223452339|gb|ACM89497.1|//6.00E-61//receptor-like protein kinase like protein [Glycine max]	Unigene121874_All//9.00E-49//AT5G35370| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0044238//GO:0044260//GO:0044464	nr +
Unigene121876_All	813	0.00	0.00	0.00	0.00	0.08	0.00	0.83	0.10	3.04	null	null		null	null		6.40E+00	6.11E-01		null	null		-3.02E+00	2.43E-03		1.87E+00	1.66E-06	Up	Unigene121876_All//gi|158828300|gb|ABW81175.1|//2.00E-09//non-LTR retrotransposon transposase [Arabidopsis cebennensis]		Unigene121876_All//0.00E+00//gi|72277451|gb|DT051144.1|DT051144			GO:0003824//GO:0005488	nr +
Unigene121877_All	1346	0.00	0.00	0.00	0.00	0.00	0.00	1.04	1.09	20.19	null	null		null	null		null	null		null	null		6.82E-02	9.02E-01		4.28E+00	4.82E-149	Up	Unigene121877_All//gi|15234693|ref|NP_193934.1|//1.00E-86//F-box family protein [Arabidopsis thaliana]	Unigene121877_All//3.00E-75//AT4G04480| LOCATED IN: chloroplast; EXPRESSED IN: flower, pollen tube; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT4G22030.1); Has 51 Blast hits to 51 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr +
Unigene12188_All	924	0.91	3.56	1.61	2.05	4.25	4.06	3.11	1.31	0.95	1.98E+00	3.16E-07	Up	8.33E-01	1.43E-01		1.05E+00	4.34E-04	Up	9.86E-01	1.88E-03		-1.25E+00	2.22E-04	Down	-1.71E+00	8.59E-07	Down			Unigene12188_All//2.00E-17//TC134762					
Unigene121884_All	200	0.26	0.00	0.00	0.00	0.00	0.00	2.96	0.00	2.59	-8.03E+00	6.14E-01		-8.03E+00	6.26E-01		null	null		null	null		-1.15E+01	2.39E-04	Down	-1.93E-01	7.94E-01									
Unigene121887_All	200	0.00	0.00	0.00	0.25	0.00	0.00	47.57	140.85	8.37	null	null		null	null		-7.96E+00	5.57E-01		-7.96E+00	6.37E-01		1.57E+00	2.03E-50	Up	-2.51E+00	5.33E-33	Down			Unigene121887_All//7.00E-23//CD486256					
Unigene121895_All	200	1.31	26.60	48.19	0.25	0.00	0.68	0.63	0.21	5.98	4.35E+00	7.74E-24	Up	5.20E+00	2.37E-46	Up	-7.96E+00	5.57E-01		1.44E+00	6.39E-01		-1.60E+00	5.34E-01		3.24E+00	7.29E-06	Up			Unigene121895_All//2.00E-87//TC134552					

Unigene121896_All	200	0.00	0.51	0.00	0.00	0.00	0.23	0.42	0.63	17.93	8.99E+00	3.88E-01		null	null		null	null		7.82E+00	6.97E-01		5.68E-01	7.82E-01		5.41E+00	1.12E-22	Up	Unigene121896_All//gi|22331680|ref|NP_680110.1|//2.00E-09//CYP71A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|13878403|sp|Q9STL1.1|C71AM_ARATH RecName: Full=Cytochrome P450 71A22 >gi|4678357|emb|CAB41167.1| cytochrome P450-like protein [Arabidopsis thaliana]	Unigene121896_All//1.00E-08//AT3G26180| CYP71B20; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene121896_All//7.00E-29//gi|109855176|gb|DW484155.1|DW484155		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506//GO:0008152//GO:0043231//GO:0044425	nr +
Unigene1219_All	1954	1.47	0.99	0.98	3.42	2.89	1.83	2.75	3.49	5.69	-5.80E-01	1.19E-01		-5.86E-01	1.37E-01		-2.41E-01	3.21E-01		-9.04E-01	5.24E-05		3.43E-01	1.02E-01		1.05E+00	1.25E-11	Up	Unigene1219_All//gi|281333041|gb|ADA60975.1|//1.00E-105//lateral root primordium 1 [Brassica rapa subsp. pekinensis]	Unigene1219_All//2.00E-67//AT5G12330| LRP1 (LATERAL ROOT PRIMORDIUM 1); protein homodimerization	Unigene1219_All//0.00E+00//TC150000	SRS		GO:0009725//GO:0042802//GO:0048513	nr -
Unigene12191_All	1390	17.99	11.56	15.13	36.98	35.45	29.08	22.75	9.08	7.45	-6.39E-01	4.85E-09		-2.50E-01	3.48E-02		-6.11E-02	5.22E-01		-3.47E-01	1.26E-06		-1.33E+00	3.17E-44	Down	-1.61E+00	1.08E-60	Down	Unigene12191_All//gi|163955692|gb|ABY49844.1|//0.00E+00//24-sterol C-methyltransferase [Gossypium hirsutum]	Unigene12191_All//0.00E+00//AT1G20330| SMT2 (STEROL METHYLTRANSFERASE 2); S-adenosylmethionine-dependent methyltransferase	Unigene12191_All//0.00E+00//TC129914		ko00100|Steroid biosynthesis	GO:0003002//GO:0006694//GO:0008757//GO:0010948//GO:0016049//GO:0043231	nr -
Unigene12192_All	1427	81.54	32.28	37.28	89.16	65.23	44.85	92.86	15.58	13.88	-1.34E+00	2.41E-133	Down	-1.13E+00	4.81E-99	Down	-4.51E-01	8.84E-28		-9.91E-01	4.30E-98		-2.58E+00	0.00E+00	Down	-2.74E+00	0.00E+00	Down	Unigene12192_All//gi|163955690|gb|ABY49843.1|//0.00E+00//24-sterol C-methyltransferase [Gossypium hirsutum]	Unigene12192_All//0.00E+00//AT1G20330| SMT2 (STEROL METHYLTRANSFERASE 2); S-adenosylmethionine-dependent methyltransferase	Unigene12192_All//0.00E+00//TC141479		ko00100|Steroid biosynthesis	GO:0003002//GO:0006694//GO:0008169//GO:0008757//GO:0010948//GO:0016049//GO:0043231	nr -
Unigene121927_All	201	22.39	56.72	21.46	19.08	25.36	33.25	42.28	58.64	28.94	1.34E+00	1.07E-13	Up	-6.10E-02	8.39E-01		4.10E-01	1.37E-01		8.01E-01	3.60E-04		4.72E-01	1.40E-03		-5.47E-01	1.43E-03				Unigene121927_All//6.00E-85//gi|21100157|gb|BQ412470.1|BQ412470				
Unigene121929_All	201	0.00	0.00	0.00	0.00	0.00	0.45	1.26	2.70	15.06	null	null		null	null		null	null		8.81E+00	4.78E-01		1.10E+00	2.36E-01		3.58E+00	4.87E-15	Up	Unigene121929_All//gi|171452356|dbj|BAG15869.1|//3.00E-09//ankyrin repeat protein [Bruguiera gymnorhiza]	Unigene121929_All//2.00E-10//AT4G10720| ankyrin repeat family protein	Unigene121929_All//4.00E-55//TC136712			GO:0010033	nr +
Unigene12193_All	2391	13.61	33.86	22.34	15.13	24.44	29.22	20.23	25.12	27.29	1.32E+00	3.42E-90	Up	7.15E-01	1.96E-21		6.92E-01	5.62E-27		9.50E-01	7.56E-50		3.12E-01	2.47E-07		4.32E-01	3.54E-14		Unigene12193_All//gi|258546336|dbj|BAI39595.1|//1.00E-125//protein phosphatase 2C AB12 homolog [Solanum lycopersicum]	Unigene12193_All//3.00E-124//AT1G72770| HAB1 (HOMOLOGY TO ABI1); catalytic/ protein serine/threonine phosphatase	Unigene12193_All//0.00E+00//TC167002				nr -
Unigene12194_All	2809	10.34	26.37	17.91	11.28	17.93	18.86	10.60	15.91	11.81	1.35E+00	4.70E-86	Up	7.93E-01	3.94E-24		6.69E-01	5.55E-22		7.42E-01	4.71E-25		5.86E-01	2.63E-16		1.57E-01	7.17E-02		Unigene12194_All//gi|258546336|dbj|BAI39595.1|//1.00E-175//protein phosphatase 2C AB12 homolog [Solanum lycopersicum]	Unigene12194_All//8.00E-176//AT1G72770| HAB1 (HOMOLOGY TO ABI1); catalytic/ protein serine/threonine phosphatase	Unigene12194_All//0.00E+00//TC152208			GO:0004721//GO:0006464//GO:0043169//GO:0043234	nr +
Unigene121942_All	202	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.62	18.54	null	null		null	null		null	null		null	null		9.28E+00	2.41E-01		1.42E+01	8.55E-27	Up	Unigene121942_All//gi|269819290|gb|ACZ44835.1|//8.00E-16//glycosyltransferase [Malus x domestica]	Unigene121942_All//7.00E-15//AT5G21790| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene121942_All//2.00E-13//TC169837		ko00940|Phenylpropanoid biosynthesis	GO:0016758	nr +
Unigene121946_All	202	0.00	0.50	0.00	0.00	0.17	0.22	0.42	1.03	22.68	8.97E+00	3.88E-01		null	null		7.41E+00	8.31E-01		7.80E+00	6.97E-01		1.31E+00	4.47E-01		5.76E+00	1.34E-29	Up	Unigene121946_All//gi|9802753|gb|AAF99822.1|AC027134_4/1.00E-13//Unknown protein [Arabidopsis thaliana]	Unigene121946_All//2.00E-11//AT1G13520| unknown protein	Unigene121946_All//4.00E-80//gi|78325059|gb|DT545333.1|DT545333				nr +
Unigene121948_All	202	0.26	1.00	0.26	0.99	0.17	0.89	39.98	125.18	286.36	1.95E+00	3.75E-01		2.54E-02	9.95E-01		-2.53E+00	2.34E-01		-1.41E-01	9.35E-01		1.65E+00	1.10E-48	Up	2.84E+00	2.00E-222	Up	Unigene121948_All//gi|40218371|gb|AAR83118.1|//8.00E-14//secretory laccase [Gossypium arboreum]	Unigene121948_All//3.00E-96//AT5G09360| LAC14 (laccase 14); laccase	Unigene121948_All//3.00E-96//TC150997		ko00910|Nitrogen metabolism	GO:0008152//GO:0016682//GO:0046872	nr +
Unigene121959_All	203	0.00	0.00	0.00	0.25	0.00	0.22	0.62	0.21	7.07	null	null		null	null		-7.94E+00	5.57E-01		-1.41E-01	9.53E-01		-1.60E+00	5.34E-01		3.50E+00	2.50E-07	Up			Unigene121959_All//2.00E-07//gi|164281671|gb|ES814920.1|ES814920				
Unigene121963_All	203	0.00	0.00	0.00	0.00	0.00	0.45	0.00	2.68	0.98	null	null		null	null		null	null		8.80E+00	4.78E-01		1.14E+01	5.36E-04	Up	9.94E+00	7.89E-02									
Unigene121966_All	203	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.21	5.89	null	null		null	null		null	null		null	null		-1.67E-02	1.00E+00		4.82E+00	1.77E-07	Up			Unigene121966_All//1.00E-42//ES790450				
Unigene12197_All	3332	0.47	0.12	0.13	1.47	1.24	0.92	2.86	1.22	1.57	-1.95E+00	7.99E-04	Down	-1.88E+00	1.82E-03		-2.40E-01	4.22E-01		-6.69E-01	1.34E-02		-1.23E+00	1.93E-12	Down	-8.66E-01	1.29E-07		Unigene12197_All//gi|33235471|emb|CAE17327.1|//0.00E+00//lipoxygenase [Fragaria x ananassa]	Unigene12197_All//0.00E+00//AT1G55020| LOX1; lipoxygenase	Unigene12197_All//0.00E+00//TC166459		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0006633//GO:0016702//GO:0044424//GO:0046914//GO:0048527	nr -
Unigene121975_All	203	0.00	0.00	0.00	0.00	0.17	0.00	0.21	0.00	3.53	null	null		null	null		7.41E+00	8.31E-01		null	null		-7.70E+00	6.58E-01		4.08E+00	2.41E-04	Up							
Unigene121976_All	203	66.50	43.18	26.49	62.82	71.42	91.44	270.14	137.33	102.25	-6.23E-01	4.51E-05		-1.33E+00	3.13E-15	Down	1.85E-01	2.66E-01		5.42E-01	1.54E-05		-9.76E-01	6.69E-47		-1.40E+00	2.77E-85	Down	Unigene121976_All//gi|61807078|gb|AAX55706.1|//8.00E-27//cyc07 [Vitis vinifera]	Unigene121976_All//4.00E-26//AT4G34670| 40S ribosomal protein S3A (RPS3aB)	Unigene121976_All//3.00E-111//DW235906		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene12198_All	3760	7.68	4.58	5.34	14.89	14.05	7.07	20.31	5.61	11.91	-7.45E-01	2.77E-13		-5.25E-01	4.02E-07		-8.40E-02	3.07E-01		-1.07E+00	1.87E-49	Down	-1.86E+00	2.75E-172	Down	-7.70E-01	6.16E-45		Unigene12198_All//gi|223452530|gb|ACM89592.1|//0.00E+00//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene12198_All//0.00E+00//AT3G56270| leucine-rich repeat transmembrane protein kinase, putative	Unigene12198_All//0.00E+00//gi|78333021|gb|DT553295.1|DT553295		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004713//GO:0004871//GO:0006464//GO:0007167//GO:0016128//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene121981_All	204	132.08	121.95	116.94	1310.06	1572.38	2661.32	140.93	150.79	138.46	-1.15E-01	3.35E-01		-1.76E-01	1.41E-01		2.63E-01	4.00E-25		1.02E+00	0.00E+00	Up	9.75E-02	3.53E-01		-2.56E-02	8.05E-01		Unigene121981_All//gi|110816007|gb|ABG91751.1|//4.00E-20//HyPRP1 [Gossypium hirsutum]	Unigene121981_All//5.00E-107//gi|78350159|gb|DT570433.1|DT570433				nr +
Unigene121982_All	204	0.00	0.00	0.00	0.24	0.00	0.66	1.04	1.02	7.03	null	null		null	null		-7.93E+00	5.57E-01		1.44E+00	6.39E-01		-1.67E-02	1.02E+00		2.76E+00	4.81E-06	Up			Unigene121982_All//2.00E-07//TC132550				
Unigene121984_All	204	0.00	0.00	0.00	0.00	0.00	0.00	1.04	0.61	28.32	null	null		null	null		null	null		null	null		-7.54E-01	6.32E-01		4.77E+00	3.45E-34	Up	Unigene121984_All//gi|292668917|gb|ADE41113.1|//9.00E-10//AP2 domain class transcription factor [Malus x domestica]		Unigene121984_All//4.00E-98//DT464116				nr +
Unigene121988_All	204	0.00	0.00	0.00	0.24	0.34	0.00	0.41	1.23	3.71	null	null		null	null		4.67E-01	9.59E-01		-7.93E+00	6.37E-01		1.57E+00	3.26E-01		3.16E+00	6.83E-04	Up			Unigene121988_All//2.00E-109//ES820997				
Unigene121990_All	204	0.00	0.00	0.00	0.00	0.00	0.00	0.41	1.02	5.66	null	null		null	null		null	null		null	null		1.31E+00	4.47E-01		3.77E+00	2.44E-06	Up			Unigene121990_All//2.00E-07//TC143058				
Unigene122_All	3170	2.43	2.22	1.80	5.45	5.91	3.43	8.32	12.50	3.67	-1.27E-01	5.98E-01		-4.33E-01	5.18E-02		1.16E-01	4.59E-01		-6.67E-01	2.65E-07		5.87E-01	1.39E-14		-1.18E+00	5.41E-32	Down	Unigene122_All//gi|60327635|gb|AAX19057.1|//0.00E+00//class III HD-Zip protein 8 [Populus trichocarpa]	Unigene122_All//0.00E+00//AT4G32880| ATHB-8 (HOMEOBOX GENE 8); DNA binding / transcription factor	Unigene122_All//0.00E+00//TC178623	HB			nr +
Unigene12200_All	883	1.36	0.57	2.89	5.70	6.43	1.38	0.48	0.09	0.32	-1.25E+00	4.69E-02		1.09E+00	9.22E-03		1.75E-01	5.49E-01		-2.04E+00	5.94E-12	Down	-2.34E+00	5.46E-02		-6.00E-01	5.53E-01		Unigene12200_All//gi|3293031|emb|CAA07563.1|//5.00E-88//amino acid carrier [Ricinus communis]	Unigene12200_All//1.00E-82//AT5G09220| AAP2 (AMINO ACID PERMEASE 2); amino acid transmembrane transporter	Unigene12200_All//0.00E+00//TC134386			GO:0005275//GO:0006865//GO:0016021	nr +
Unigene122005_All	205	0.00	0.00	0.00	0.24	0.17	2.86	0.00	1.02	2.92	null	null		null	null		-5.33E-01	8.26E-01		3.56E+00	8.48E-03		9.99E+00	7.85E-02		1.15E+01	1.75E-04	Up							
Unigene122008_All	205	0.00	0.00	0.00	0.24	0.00	0.00	0.00	0.00	2.72	null	null		null	null		-7.92E+00	5.57E-01		-7.92E+00	6.37E-01		null	null		1.14E+01	3.28E-04	Up							
Unigene122009_All	205	94.43	39.55	12.21	41.80	32.08	26.88	195.31	45.26	41.59	-1.26E+00	1.05E-20	Down	-2.95E+00	1.90E-60	Down	-3.82E-01	5.06E-02		-6.37E-01	1.01E-03		-2.11E+00	2.58E-107	Down	-2.23E+00	1.04E-118	Down	Unigene122009_All//gi|224113151|ref|XP_002316408.1|//1.00E-27//histone H2 [Populus trichocarpa] >gi|222865448|gb|EEF02579.1| histone H2 [Populus trichocarpa]	Unigene122009_All//4.00E-29//AT5G02570| histone H2B, putative	Unigene122009_All//2.00E-112//gi|21099636|gb|BQ411949.1|BQ411949			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr +
Unigene12201_All	2064	9.86	3.54	6.35	93.55	59.68	39.26	78.89	24.02	70.07	-1.48E+00	1.01E-27	Down	-6.36E-01	4.36E-07		-6.49E-01	2.82E-81		-1.25E+00	4.00E-217	Down	-1.72E+00	0.00E+00	Down	-1.71E-01	1.31E-06		Unigene12201_All//gi|224093533|ref|XP_002334831.1|//0.00E+00//amino acid permease [Populus trichocarpa] >gi|222875165|gb|EEF12296.1| amino acid permease [Populus trichocarpa]	Unigene12201_All//0.00E+00//AT1G77380| AAP3; amino acid transmembrane transporter	Unigene12201_All//0.00E+00//TC160173			GO:0005275//GO:0006865//GO:0016021	nr -
Unigene122018_All	205	0.00	0.00	0.00	0.00	0.00	0.00	75.69	9.99	45.09	null	null		null	null		null	null		null	null		-2.92E+00	6.13E-61	Down	-7.48E-01	2.09E-09									
Unigene12202_All	1275	1.27	0.08	0.33	8.05	5.62	4.53	7.00	1.38	6.72	-4.00E+00	2.71E-07	Down	-1.93E+00	1.19E-03		-5.19E-01	1.99E-03		-8.28E-01	2.09E-06		-2.35E+00	8.70E-28	Down	-5.87E-02	7.47E-01		Unigene12202_All//gi|224093533|ref|XP_002334831.1|//2.00E-71//amino acid permease [Populus trichocarpa] >gi|222875165|gb|EEF12296.1| amino acid permease [Populus trichocarpa]	Unigene12202_All//6.00E-68//AT5G09220| AAP2 (AMINO ACID PERMEASE 2); amino acid transmembrane transporter	Unigene12202_All//0.00E+00//DW479705			GO:0005275//GO:0006865//GO:0016021	nr +
Unigene122022_All	206	0.51	0.98	2.84	0.73	0.67	0.00	3.28	7.91	9.48	9.54E-01	6.22E-01		2.48E+00	3.75E-02		-1.18E-01	9.11E-01		-9.50E+00	2.34E-01		1.27E+00	7.03E-03		1.53E+00	3.17E-04	Up			Unigene122022_All//3.00E-77//gi|109844447|gb|DW243005.1|DW243005				
Unigene122024_All	206	0.25	0.00	0.00	0.48	0.17	0.22	0.41	0.00	3.67	-7.99E+00	6.14E-01		-7.99E+00	6.26E-01		-1.53E+00	5.87E-01		-1.14E+00	6.77E-01		-8.68E+00	4.04E-01		3.16E+00	6.83E-04	Up			Unigene122024_All//2.00E-07//gi|109874218|gb|DW503192.1|DW503192				
Unigene122203_All	3213	1.79	3.39	2.78	10.99	12.88	16.84	8.94	15.04	19.45	9.21E-01	1.57E-07		6.36E-01	1.45E-03		2.29E-01	5.12E-03		6.15E-01	1.44E-18		7.51E-01	8.85E-27		1.12E+00	2.93E-68	Up	Unigene12203_All//gi|2160189|gb|AAB60752.1|//0.00E+00//Similar to A. thaliana receptor-like protein kinase (gb|RLK5_ARATH). ESTs gb|ATTS0475,gb|ATTS4362 come from this gene [Arabidopsis thaliana]	Unigene12203_All//0.00E+00//AT1G09970| LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene12203_All//0.00E+00//TC143993			GO:0003006//GO:0004713//GO:0004871//GO:0006464//GO:0008233//GO:0016128//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene122032_All	206	0.00	3.20	0.00	0.48	0.84	0.88	0.62	0.00	1.55	1.16E+01	6.26E-04	Up	null	null		7.89E-01	7.71E-01		8.59E-01	6.95E-01		-9.27E+00	2.36E-01		1.33E+00	2.93E-01				Unigene122032_All//9.00E-78//AI055392				
Unigene122052_All	207	0.00	0.00	0.00	0.00	0.00	0.00	790.25	1475.97	223.25	null	null		null	null		null	null		null	null		9.01E-01	1.59E-225		-1.82E+00	0.00E+00	Down	Unigene122052_All//gi|300137372|gb|EFJ04348.1|//5.00E-06//hypothetical protein SELMODRAFT_138833 [Selaginella moellendorffii]		Unigene122052_All//1.00E-12//TC148521				nr -
Unigene12206_All	2547	13.62	11.06	17.23	22.22	20.77	20.75	34.51	24.45	70.67	-3.00E-01	1.13E-03		3.39E-01	4.56E-05		-9.75E-02	2.25E-01		-9.89E-02	2.30E-01		-4.97E-01	1.88E-23		1.03E+00	8.73E-171	Up	Unigene12206_All//gi|1389768|gb|AAB02913.1|//1.00E-152//phosphoribosylanthranilate transferase [Arabidopsis thaliana] >gi|28394222|gb|AAO42464.1| phosphoribosyl anthranilate transferase 1 [Arabidopsis thaliana]	Unigene12206_All//4.00E-136//AT5G17990| TRP1 (tryptophan biosynthesis 1); anthranilate phosphoribosyltransferase	Unigene12206_All//0.00E+00//TC147379		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0016740	nr -
Unigene122060_All	207	1.01	1.22	0.00	0.96	1.33	2.18	32.27	3.84	4.04	2.76E-01	8.43E-01		-9.98E+00	1.46E-01		4.67E-01	8.17E-01		1.18E+00	3.38E-01		-3.07E+00	6.31E-28	Down	-3.00E+00	3.30E-28	Down			Unigene122060_All//7.00E-97//ES806765				
Unigene122061_All	207	0.00	0.24	0.00	1.20	0.33	0.00	2.86	4.24	10.20	7.94E+00	6.18E-01		null	null		-1.85E+00	2.75E-01		-1.02E-01	7.34E-02		5.68E-01	3.99E-01		1.83E+00	1.46E-05	Up			Unigene122061_All//2.00E-26//CO103625				
Unigene122063_All	207	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	26.75	null	null		null	null		null	null		null	null		null	null		1.47E+01	1.22E-39	Up	Unigene122063_All//gi|28912426|gb|AAO53311.1|//2.00E-16//pectin methylesterase [Lupinus angustifolius]	Unigene122063_All//8.00E-17//AT2G36710| pectinesterase family protein			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0030312//GO:0071555	nr +
Unigene122066_All	207	0.00	0.00	0.00	0.00	0.00	0.00	802.30	1810.74	160.32	null	null		null	null		null	null		null	null		1.17E+00	0.00E+00	Up	-2.32E+00	0.00E+00	Down			Unigene122066_All//9.00E-07//gi|82755128|gb|DV848690.1|DV848690				ESTscan +
Unigene12207_All	3029	8.74	4.06	4.89	50.08	43.23	42.41	31.20	11.29	13.34	-1.10E+00	5.34E-23	Down	-8.39E-01	3.40E-14		-2.12E-01	3.01E-08		-2.40E-01	2.20E-09		-1.47E+00	2.35E-152	Down	-1.23E+00	4.29E-119	Down	Unigene12207_All//gi|5042434|gb|AAD38273.1|AC006193_29/0.00E+00//Hypothetical protein [Arabidopsis thaliana]	Unigene12207_All//0.00E+00//AT5G16730| LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Spectrin/alpha-actinin (InterPro:IPR018159); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02930.1); Has 241703 Blast hits to 112530 proteins in 2711 species: Archae - 2642; Bacteria - 41887; Metazoa - 104467; Fungi - 18239; Plants - 8786; Viruses - 1373; Other Eukaryotes - 64309 (source: NCBI BLink).	Unigene12207_All//0.00E+00//TC153669				nr -
Unigene12209_All	1091	6.19	3.02	1.66	17.30	13.89	6.33	7.05	2.34	1.42	-1.04E+00	6.88E-06	Down	-1.90E+00	7.68E-13	Down	-3.17E-01	1.03E-02		-1.45E+00	5.66E-27	Down	-1.59E+00	1.04E-14	Down	-2.31E+00	2.06E-24	Down	Unigene12209_All//gi|9651945|gb|AAF91324.1|AF244890_1/1.00E-147//receptor-like protein kinase 3 [Glycine max]	Unigene12209_All//1.00E-134//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene12209_All//0.00E+00//gi|164275587|gb|ES806843.1|ES806843				nr +
Unigene122097_All	209	0.00	0.73	0.76	0.95	1.15	0.43	3.64	1.80	24.97	9.51E+00	2.36E-01		9.58E+00	2.39E-01		2.75E-01	8.95E-01		-1.14E+00	5.69E-01		-1.02E+00	1.69E-01		2.78E+00	3.15E-20	Up	Unigene122097_All//gi|62083994|emb|CAI29046.1|//2.00E-09//allene-oxide cyclase [Medicago truncatula]		Unigene122097_All//9.00E-115//TC166132		ko00592|alpha-Linolenic acid metabolism		nr +

Unigene12210_All	3170	1.95	0.94	0.97	16.91	17.52	7.92	2.75	1.65	0.67	-1.05E+00	1.53E-05	Down	-9.99E-01	6.43E-05		5.14E-02	5.79E-01		-1.09E+00	8.27E-49	Down	-7.37E-01	2.34E-05		-2.04E+00	9.65E-24	Down	Unigene12210_All//gi|15239123|ref|NP_201371.1|//0.00E+00//BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|2827715|emb|CAA16688.1| receptor protein kinase - like protein [Arabidopsis thaliana] >gi|10173328|dbj|BAB10677.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|20466696|gb|AAM20665.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|31711786|gb|AAP68249.1| At5g65700 [Arabidopsis thaliana] >gi|110741066|dbj|BAE98627.1| receptor protein kinase like protein [Arabidopsis thaliana] >gi|224589751|gb|ACN59407.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene12210_All//0.00E+00//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene12210_All//0.00E+00//TC141219			GO:0003006//GO:0004674//GO:0004871//GO:0005982//GO:0006464//GO:0006950//GO:0007167//GO:0009536//GO:0009933//GO:0010073//GO:0016020//GO:0016160//GO:0016491//GO:0031410//GO:0032559	nr -
Unigene122108_All	209	0.00	0.24	0.00	0.00	0.00	0.00	0.20	1.20	6.29	7.92E+00	6.18E-01		null	null		null	null		null	null		2.57E+00	1.53E-01		4.96E+00	2.80E-08	Up								
Unigene12211_All	2223	58.53	58.05	86.47	8.02	17.07	33.62	9.95	12.45	40.52	-1.19E-02	8.22E-01		5.63E-01	9.34E-50		1.09E+00	2.18E-37	Up	2.07E+00	4.71E-170	Up	3.23E-01	4.97E-04		2.03E+00	2.23E-232	Up	Unigene12211_All//gi|18700129|gb|AAL77676.1|//0.00E+00//At2g36630/F11011.26 [Arabidopsis thaliana] >gi|22137236|gb|AAM91463.1| At2g36630/F11011.26 [Arabidopsis thaliana]	Unigene12211_All//1.00E-157//AT2G36630| unknown protein	Unigene12211_All//0.00E+00//TC130953			GO:0031224	nr +
Unigene12212_All	2298	7.88	4.94	2.60	29.35	23.99	19.40	27.25	8.49	14.58	-6.74E-01	2.34E-07		-1.60E+00	1.31E-26	Down	-2.91E-01	7.71E-07		-5.98E-01	5.18E-22		-1.68E+00	2.23E-123	Down	-9.02E-01	2.82E-48		Unigene12212_All//gi|297800554|ref|XP_002868161.1|//0.00E+00//ATSEB1 [Arabidopsis lyrata subsp. lyrata] >gi|297313997|gb|EFH44420.1| ATSEB1 [Arabidopsis lyrata subsp. lyrata]	Unigene12212_All//0.00E+00//AT4G16120| COBL7 (COBRA-LIKE 7)	Unigene12212_All//0.00E+00//TC142317			GO:0031225//GO:0043231//GO:0048764	nr -
Unigene122124_All	209	0.00	0.97	0.51	0.00	1.15	0.22	0.40	2.40	4.38	9.92E+00	1.37E-01		8.99E+00	4.00E-01		1.02E+01	1.04E-01		7.76E+00	6.97E-01		2.57E+00	2.28E-02		3.44E+00	7.53E-05	Up			Unigene122124_All//5.00E-98//TC176818					
Unigene122126_All	209	0.25	0.24	0.00	0.72	0.66	0.65	0.00	0.20	5.91	-4.63E-02	9.85E-01		-7.97E+00	6.26E-01		-1.18E-01	9.11E-01		-1.41E-01	9.44E-01		7.64E+00	6.35E-01		1.25E+01	6.29E-09	Up			Unigene122126_All//2.00E-07//TC172510					
Unigene12213_All	3195	114.55	22.09	57.50	116.09	111.37	66.07	44.91	13.64	19.60	-2.37E+00	0.00E+00	Down	-9.94E-01	7.35E-253		-5.99E-02	3.04E-02		-8.13E-01	3.71E-204		-1.72E+00	6.43E-291	Down	-1.20E+00	1.40E-173	Down	Unigene12213_All//gi|18398958|ref|NP_565447.1|//0.00E+00//SLP3; serine-type peptidase [Arabidopsis thaliana] >gi|3176726|gb|AAD12040.1| subtilisin-like serine protease [Arabidopsis thaliana]	Unigene12213_All//0.00E+00//AT2G19170| SLP3; serine-type peptidase	Unigene12213_All//0.00E+00//TC135716			GO:0004175//GO:0005515//GO:0019538//GO:0030312//GO:0031410//GO:0044092	nr -
Unigene12214_All	542	4.63	37.30	3.14	12.22	26.24	55.16	12.25	32.39	47.48	3.01E+00	3.05E-66	Up	-5.60E-01	1.86E-01		1.10E+00	1.83E-14	Up	2.17E+00	1.23E-72	Up	1.40E+00	4.81E-27	Up	1.96E+00	7.41E-64	Up	Unigene12214_All//gi|71980112|gb|AJ257337.1|//3.00E-22//Trichoderma-induced protein kinase [Cucumis sativus] >gi|110748608|gb|ABG89857.1| NO3-stress-induced mitogen activated protein kinase [Cucumis sativus]	Unigene12214_All//2.00E-18//AT2G43790| ATMPK6 (ARABIDOPSIS THALIANA MAP KINASE 6); MAP kinase/ kinase	Unigene12214_All//2.00E-158//DT467539		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0005515//GO:0006464//GO:0032559	nr -
Unigene12215_All	1703	5.59	59.98	6.35	13.51	36.50	72.40	27.31	86.59	122.00	3.42E+00	0.00E+00	Up	1.83E-01	3.64E-01		1.43E+00	2.49E-93	Up	2.42E+00	0.00E+00	Up	1.66E+00	4.60E-285	Up	2.16E+00	0.00E+00	Up	Unigene12215_All//gi|122894104|gb|ABM67698.1|//0.00E+00//mitogen-activated protein kinase [Citrus sinensis]	Unigene12215_All//0.00E+00//AT3G45640| ATMPK3 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP kinase/ kinase/ protein binding / protein kinase	Unigene12215_All//0.00E+00//TC144621		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0032559	nr -
Unigene122161_All	211	12.65	6.24	5.80	16.29	10.44	16.70	111.41	53.09	41.54	-1.02E+00	8.74E-03		-1.12E+00	6.04E-03		-6.41E-01	4.48E-02		3.55E-02	9.38E-01		-1.07E+00	8.97E-24	Down	-1.42E+00	6.54E-38	Down			Unigene122161_All//8.00E-103//gi|109879589|gb|DW508559.1|DW508559					
Unigene122171_All	211	542.30	780.69	945.12	601.55	621.14	1142.14	230.04	517.59	325.51	5.26E-01	5.43E-39		8.01E-01	5.69E-96		4.62E-02	4.15E-01		9.25E-01	1.52E-163		1.17E+00	4.96E-124	Up	5.01E-01	3.18E-19		Unigene122171_All//gi|75171219|sp|Q9FKA5.1|Y5957_ARATH//2.00E-12//RecName: Full=Uncharacterized protein At5g39570 >gi|16604364|gb|AAL24188.1| AT5g39570/MIJ24_40 [Arabidopsis thaliana] >gi|23308191|gb|AAN18065.1| At5g39570/MIJ24_40 [Arabidopsis thaliana]	Unigene122171_All//1.00E-05//AT1G11440| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT3G29075.1); Has 22740 Blast hits to 8622 proteins in 417 species: Archae - 22; Bacteria - 573; Metazoa - 11353; Fungi - 2147; Plants - 905; Viruses - 631; Other Eukaryotes - 7109 (source: NCBI BLink).	Unigene122171_All//8.00E-109//gi|78335986|gb|DT556260.1|DT556260				nr -
Unigene122218_All	3165	0.88	0.83	0.71	2.52	2.26	2.64	5.26	3.94	2.47	-7.36E-02	8.43E-01		-3.10E-01	4.36E-01		-1.54E-01	5.31E-01		6.80E-02	7.63E-01		-4.20E-01	5.75E-04		-1.09E+00	3.17E-18	Down	Unigene12218_All//gi|115456529|ref|NP_001051865.1|//0.00E+00//Os03g0843600 [Oryza sativa Japonica Group] >gi|62286620|sp|Q75LD5.1|CASTO_ORYSJ RecName: Full=Probable ion channel CASTOR; Short=OsCASTOR; AltName: Full=Probable ion channel DMI1-like >gi|41469646|gb|AAS07369.1| expressed protein [Oryza sativa Japonica Group] >gi|113550336|dbj|BAF13779.1| Os03g0843600 [Oryza sativa Japonica Group]	Unigene12218_All//0.00E+00//AT5G49960| binding / catalytic	Unigene12218_All//1.00E-06//DN804145			GO:0005515//GO:0005635//GO:0006811//GO:0015075//GO:0031224//GO:0044003	nr -
Unigene122183_All	212	0.00	0.00	0.00	0.00	0.00	0.21	0.00	0.00	6.39	null	null		null	null		null	null		7.73E+00	6.97E-01		null	null		1.26E+01	9.04E-10	Up	Unigene122183_All//gi|416662|sp|P32765.1|ASP_THECC//1.00E-11//RecName: Full=21 kDa seed protein; Flags: Precursor >gi|99954|pir||S16252 trypsin inhibitor homolog - soybean >gi|21909|emb|CAA39860.1| 21 kDa seed protein [Theobroma cacao]		Unigene122183_All//3.00E-74//ES801549			GO:0061135	nr +
Unigene122185_All	212	0.00	0.00	0.75	0.00	0.00	0.00	5.38	1.18	0.94	null	null		9.56E+00	2.39E-01		null	null		null	null		-2.19E+00	6.84E-04	Down	-2.52E+00	1.20E-04	Down								
Unigene12219_All	2732	12.98	63.84	32.14	13.51	21.11	31.33	17.30	20.32	36.37	2.30E+00	0.00E+00	Up	1.31E+00	1.82E-94	Up	6.44E-01	1.69E-23		1.21E+00	1.96E-90	Up	2.32E-01	3.11E-04		1.07E+00	2.79E-100	Up	Unigene12219_All//gi|4206122|gb|AAD11430.1|//0.00E+00//protein phosphatase 2C homolog [Mesembryanthemum crystallinum]	Unigene12219_All//2.00E-159//AT3G51370| protein phosphatase 2C, putative / PP2C, putative	Unigene12219_All//0.00E+00//gi|78346365|gb|DT566639.1|DT566639		ko00190|Oxidative phosphorylation	GO:0004721//GO:0006464//GO:0043169//GO:0043234	nr +
Unigene122191_All	213	343.16	180.55	191.75	498.14	474.82	402.65	307.87	117.54	153.56	-9.26E-01	9.64E-47		-8.40E-01	2.84E-38		-6.92E-02	2.35E-01		-3.07E-01	1.99E-10		-1.39E+00	1.20E-97	Down	-1.00E+00	3.46E-60	Down	Unigene122191_All//gi|225459538|ref|XP_002284225.1|//7.00E-13//PREDICTED: similar to F28H19.26 [Vitis vinifera]	Unigene122191_All//7.00E-13//AT4G08685| SAM7	Unigene122191_All//8.00E-100//TC154716			GO:0044421	nr +
Unigene122192_All	213	822.40	774.08	1327.00	298.42	444.26	533.48	380.92	218.59	64.71	-8.74E-02	3.66E-02		6.90E-01	7.71E-105		5.74E-01	2.46E-31		8.38E-01	1.73E-65		-8.01E-01	1.24E-49		-2.56E+00	2.44E-282	Down	Unigene122192_All//gi|145049666|gb|ABP35525.1|//3.00E-14//S-adenosyl-L-methionine synthetase [Ipomoea batatas]	Unigene122192_All//5.00E-15//AT4G01850| SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase	Unigene122192_All//1.00E-116//gi|78347054|gb|DT567328.1|DT567328		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0016765//GO:0032559//GO:0044237//GO:0044424//GO:0046872	nr +
Unigene12220_All	1039	10.93	22.43	16.91	7.86	6.79	7.30	5.49	15.65	8.63	1.04E+00	2.24E-18	Up	6.30E-01	3.84E-06		-2.11E-01	3.42E-01		-1.07E-01	6.58E-01		1.51E+00	6.22E-28	Up	6.51E-01	9.95E-05		Unigene12220_All//gi|297814880|ref|XP_002875323.1|//3.00E-35//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297321161|gb|EFH51582.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene12220_All//2.00E-36//AT3G26580| INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Tetratricopeptide region (InterPro:IPR013026); Has 2147 Blast hits to 1154 proteins in 168 species: Archae - 2; Bacteria - 99; Metazoa - 1301; Fungi - 180; Plants - 105; Viruses - 57; Other Eukaryotes - 403 (source: NCBI BLink).	Unigene12220_All//0.00E+00//TC137556			GO:0009534//GO:0016787	nr +
Unigene122204_All	213	82.78	98.48	79.00	147.57	170.40	288.37	67.09	96.15	148.51	2.51E-01	4.42E-02		-6.74E-02	6.46E-01		2.08E-01	2.15E-02		9.67E-01	3.91E-45		5.19E-01	1.59E-06		1.15E+00	3.85E-36	Up	Unigene122204_All//gi|224112617|ref|XP_002316242.1|//8.00E-17//proline transporter [Populus trichocarpa] >gi|222865282|gb|EEF02413.1| proline transporter [Populus trichocarpa]	Unigene122204_All//2.00E-16//AT3G28890| PROT1 (PROLINE TRANSPORTER 1); L-proline transmembrane transporter/ amino acid transmembrane transporter	Unigene122204_All//4.00E-89//TC141717			GO:0015175//GO:0015804//GO:0031224//GO:0031410	nr -
Unigene122206_All	213	0.00	0.00	0.00	0.00	0.00	0.00	0.40	0.20	11.41	null	null		null	null		null	null		null	null		-1.02E+00	7.25E-01		4.84E+00	9.34E-15	Up								ESTscan -
Unigene122208_All	214	0.00	0.24	0.00	0.00	0.32	0.00	0.00	0.00	3.16	7.89E+00	6.17E-01		null	null		8.33E+00	6.11E-01		null	null		null	null		1.16E+01	4.97E-05	Up								
Unigene122217_All	214	0.00	0.00	0.00	0.23	0.00	0.00	1.38	0.00	13.78	null	null		null	null		-7.86E+00	5.56E-01		-7.86E+00	6.37E-01		-1.04E+01	2.18E-02		3.32E+00	8.67E-14	Up			Unigene122217_All//1.00E-15//EX169291					
Unigene122226_All	215	919.14	905.22	828.72	416.35	462.87	610.65	414.74	234.25	102.47	-2.20E-02	6.13E-01		-1.49E-01	8.76E-05		1.53E-01	2.97E-03		5.53E-01	1.37E-36		-8.24E-01	3.95E-57		-2.02E+00	1.32E-231	Down	Unigene122226_All//gi|223635320|sp|A4PU48.1|METK_MEDTR//7.00E-33//RecName: Full=S-adenosylmethionine synthase; Short=AdoMet synthase; AltName: Full=Methionine adenosyltransferase; Short=MAT >gi|140655593|gb|AB080948.1| S-adenosylmethionine synthetase [Medicago truncatula]	Unigene122226_All//1.00E-31//AT3G17390| MTO3 (METHIONINE OVER-ACCUMULATOR 3); methionine adenosyltransferase	Unigene122226_All//6.00E-116//BG440546		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0016765//GO:0032559//GO:0044237//GO:0044424//GO:0046872	nr +
Unigene122228_All	215	0.00	0.24	0.50	0.00	0.48	1.05	2.36	0.00	1.85	7.88E+00	6.17E-01		8.95E+00	4.00E-01		8.91E+00	4.56E-01		1.00E+01	1.19E-01		-1.12E+01	8.89E-04	Down	-3.49E-01	6.73E-01				Unigene122228_All//7.00E-88//CO096417					
Unigene122231_All	215	0.00	2.12	0.25	0.23	0.16	0.84	18.68	5.05	7.97	1.11E+01	7.44E-03		7.95E+00	6.37E-01		-5.32E-01	8.26E-01		1.86E+00	4.58E-01		-1.89E+00	5.78E-10	Down	-1.23E+00	6.35E-06	Down	Unigene122231_All//gi|5902372|gb|AAD55474.1|AC009322_14//8.00E-06//Unknown protein [Arabidopsis thaliana] >gi|14532496|gb|AAK63976.1| At1g80180/F18B13_26 [Arabidopsis thaliana] >gi|18653371|gb|AAL76141.1| At1g80180/F18B13_26 [Arabidopsis thaliana]	Unigene122231_All//3.00E-07//AT1G80180| unknown protein	Unigene122231_All//7.00E-57//DW504161			GO:0016020	nr +
Unigene122233_All	215	0.24	0.47	0.00	0.00	0.00	0.63	0.00	0.19	4.26	9.53E-01	7.26E-01		-7.93E+00	6.26E-01		null	null		9.30E+00	3.11E-01		7.60E+00	6.35E-01		1.21E+01	1.08E-06	Up	Unigene122233_All//gi|292653551|gb|ADE34293.1|//6.00E-24//aquaporin NIP1;3 [Gossypium hirsutum]	Unigene122233_All//2.00E-23//AT4G18910| NIP1;2 (NOD26-LIKE INTRINSIC PROTEIN 1;2); arsenite transmembrane transporter/ water channel	Unigene122233_All//2.00E-32//TC166706			GO:0005372//GO:0010035//GO:0015103//GO:0015698//GO:0031224	nr +
Unigene122238_All	215	40.40	37.71	31.45	49.35	31.39	26.89	181.12	78.93	57.81	-9.94E-02	6.21E-01		-3.61E-01	8.61E-02		-6.53E-01	5.42E-05		-8.76E-01	3.36E-07		-1.20E+00	1.73E-46	Down	-1.65E+00	5.34E-77	Down			Unigene122238_All//2.00E-118//gi|11205376|gb|BF274306.1|BF274306					

Unigene12224_All	2681	17.76	28.90	26.02	22.22	15.44	20.67	20.72	14.39	5.53	7.02E-01	6.25E-31		5.51E-01	1.03E-17		-5.26E-01	2.15E-17		-1.05E-01	1.87E-01		-5.26E-01	1.10E-16		-1.91E+00	4.14E-134	Down	Unigene12224_All//gi|211906458|gb|ACJ11722.1|//0.00E+00//2-nitropropane dioxygenase [Gossypium hirsutum]	Unigene12224_All//8.00E-133//AT5G64250| 2-nitropropane dioxygenase family / NPD family	Unigene12224_All//0.00E+00//TC149187		ko00061|Fatty acid biosynthesis	GO:0008152//GO:0016703	nr -
Unigene12249_All	216	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.40	null	null		null	null		null	null		null	null		null	null		1.12E+01	6.13E-04	Up			Unigene12249_All//2.00E-07//ES851112				
Unigene12225_All	2925	7.82	5.70	7.28	27.20	24.84	22.59	13.57	8.47	5.97	-4.56E-01	6.51E-05		-1.02E-01	4.42E-01		-1.31E-01	3.05E-02		-2.68E-01	2.57E-06		-6.80E-01	9.37E-19		-1.19E+00	5.51E-48	Down	Unigene12225_All//gi|47076396|dbj|BAD18102.1|//0.00E+00//leucine-rich repeat receptor-like kinase [Ipomoea batatas]	Unigene12225_All//0.00E+00//AT1G60800| NIK3 (NSP-INTERACTING KINASE 3); kinase	Unigene12225_All//0.00E+00//TC157453		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006464//GO:0016491//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene12252_All	216	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.39	3.14	null	null		null	null		null	null		null	null		8.60E+00	4.02E-01		1.16E+01	4.97E-05	Up									
Unigene12255_All	216	0.00	0.00	0.00	0.23	0.16	0.00	1.17	2.52	7.19	null	null		null	null		-5.33E-01	8.26E-01		-7.85E+00	6.57E-01		1.10E+00	2.36E-01		2.61E+00	3.62E-06	Up									
Unigene12257_All	216	0.00	0.00	0.00	0.00	0.00	0.00	0.98	0.97	27.85	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		4.83E+00	8.11E-36	Up			Unigene12257_All//6.00E-11//TC150009					ESTscan -
Unigene12226_All	3635	4.66	2.13	4.51	5.76	5.98	5.01	24.41	43.24	21.65	-1.13E+00	1.65E-15	Down	-4.76E-02	7.52E-01		5.46E-02	7.31E-01		-2.01E-01	1.27E-01		8.25E-01	3.83E-100		-1.74E-01	4.19E-04		Unigene12226_All//gi|115442373|ref|NP_001045466.1|//0.00E+00//Os01g0960400 [Oryza sativa Japonica Group] >gi|113534997|dbj|BAF07380.1|Os01g0960400 [Oryza sativa Japonica Group]	Unigene12226_All//0.00E+00//AT1G06840| leucine-rich repeat transmembrane protein kinase, putative	Unigene12226_All//0.00E+00//ES835146		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0007167//GO:0016491//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene12263_All	216	0.00	0.00	0.00	0.00	0.00	0.00	7.44	3.10	15.12	null	null		null	null		null	null		null	null		-1.26E+00	7.61E-03		1.02E+00	6.62E-04	Up			Unigene12263_All//3.00E-28//C0091281					
Unigene12283_All	217	0.00	0.00	1.47	0.46	0.00	0.42	0.00	0.19	2.39	null	null		1.05E+01	4.53E-02		-8.84E+00	3.14E-01		-1.41E-01	9.51E-01		7.59E+00	6.35E-01		1.12E+01	6.13E-04	Up	Unigene12283_All//gi|33149681|gb|AAP86920.1|//3.00E-28//pyruvate decarboxylase [Dianthus caryophyllus]	Unigene12283_All//8.00E-27//AT4G33070| pyruvate decarboxylase, putative	Unigene12283_All//3.00E-65//C0128657		ko00010|Glycolysis / Gluconeogenesis//ko00380|Tryptophan metabolism	GO:0016831//GO:0019842//GO:0044464//GO:0046872//GO:0050896	nr -
Unigene122287_All	217	0.00	4.44	0.00	0.23	2.06	1.67	21.04	91.68	51.96	1.21E+01	1.38E-05	Up	null	null		3.17E+00	3.95E-02		2.86E+00	9.45E-02		2.12E+00	5.74E-54	Up	1.30E+00	2.91E-16	Up	Unigene122287_All//gi|156767195|gb|ABU95104.1|//3.00E-09//asparagine synthetase [Phaseolus vulgaris]	Unigene122287_All//5.00E-10//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene122287_All//9.00E-35//C0128870		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0006528//GO:0016884	nr -
Unigene122288_All	217	122.00	123.05	133.98	152.43	129.81	145.90	59.62	34.48	28.09	1.24E-02	9.32E-01		1.35E-01	2.46E-01		-2.32E-01	1.24E-02		-6.32E-02	6.17E-01		-7.90E-01	2.01E-08		-1.09E+00	3.31E-14	Down	Unigene122288_All//gi|238478683|ref|NP_001154384.1|//5.00E-06//double-stranded DNA-binding family protein [Arabidopsis thaliana]	Unigene122288_All//2.00E-07//AT1G29850| double-stranded DNA-binding family protein	Unigene122288_All//3.00E-108//TC144408				nr +
Unigene12293_All	218	0.00	4.65	0.24	2.29	2.21	5.18	0.78	0.38	1.46	1.22E+01	7.26E-06	Up	7.93E+00	6.37E-01		-4.73E-02	9.49E-01		1.18E+00	7.75E-02		-1.02E+00	6.14E-01		9.14E-01	4.53E-01				Unigene12293_All//3.00E-34//TC175975					
Unigene122296_All	218	1.44	0.23	1.22	1.14	0.79	2.49	0.39	0.96	6.76	-2.63E+00	1.31E-01		-2.38E-01	8.50E-01		-5.33E-01	7.13E-01		1.12E+00	3.05E-01		1.31E+00	4.47E-01		4.12E+00	2.19E-08	Up		Unigene122296_All//3.00E-05//AT4G10970| unknown protein	Unigene122296_All//4.00E-120//TC137370				
Unigene1223_All	3832	0.56	0.29	0.58	0.79	0.75	0.44	0.99	0.41	0.82	-9.44E-01	3.15E-02		6.01E-02	8.94E-01		-8.83E-02	8.11E-01		-8.63E-01	1.54E-02		-1.26E+00	1.26E-05	Down	-2.74E-01	3.49E-01		Unigene1223_All//gi|113926887|emb|CAJ53855.1|//1.00E-149//luminidependens [Arabidopsis thaliana] >gi|113926889|emb|CAJ53856.1|luminidependens [Arabidopsis thaliana] >gi|113926891|emb|CAJ53857.1|luminidependens [Arabidopsis thaliana] >gi|113926893|emb|CAJ53858.1|luminidependens [Arabidopsis thaliana] >gi|113926895|emb|CAJ53859.1|luminidependens [Arabidopsis thaliana] >gi|113926897|emb|CAJ53860.1|luminidependens [Arabidopsis thaliana] >gi|113926899|emb|CAJ53861.1|luminidependens [Arabidopsis thaliana] >gi|113926901|emb|CAJ53862.1|luminidependens [Arabidopsis thaliana] >gi|113926903|emb|CAJ53863.1|luminidependens [Arabidopsis thaliana] >gi|113926905|emb|CAJ53864.1|luminidependens [Arabidopsis	Unigene1223_All//2.00E-138//AT4G02560| LD (luminidependens); transcription factor	Unigene1223_All//0.00E+00//gi|78354304|gb|DT574578.1|DT574578	HB		GO:0003677//GO:0006351//GO:0010468	nr +
Unigene122300_All	218	0.00	0.00	0.00	0.00	0.32	2.07	0.00	0.00	3.11	null	null		null	null		8.30E+00	6.11E-01		1.10E+01	7.76E-03		null	null		1.16E+01	4.97E-05	Up								
Unigene122305_All	218	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.96	2.38	null	null		null	null		null	null		null	null		9.90E+00	7.85E-02		1.12E+01	6.13E-04	Up	Unigene122305_All//gi|6522592|emb|CAB61957.1|//1.00E-16//receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene122305_All//5.00E-18//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene12231_All	2613	9.77	10.68	3.26	20.76	21.35	11.04	23.88	7.68	10.86	1.29E-01	2.56E-01		-1.58E+00	1.01E-36	Down	4.03E-02	6.57E-01		-9.11E-01	1.45E-36		-1.64E+00	2.32E-118	Down	-1.14E+00	3.90E-70	Down	Unigene12231_All//gi|75156391|sp|Q8L1Y0.1|CSLC1_ORYSJ//0.00E+00//Rec Name: Full=Probable xyloglucan glycosyltransferase 1; AltName: Full=Cellulose synthase-like protein C1; AltName: Full=OsCslC1 >gi|34119216|tpg|BAA01749.1|TPA_exp: cellulose synthase-like C1 [Oryza sativa (japonica cultivar-group)]	Unigene12231_All//0.00E+00//AT4G31590| ATCSLC5 (CELLULOSE-SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups	Unigene12231_All//0.00E+00//TC149633			GO:0016759//GO:0044464	nr +
Unigene12232_All	3203	5.54	3.84	5.42	5.01	6.76	5.03	10.19	18.41	34.15	-5.27E-01	5.92E-05		-3.10E-02	8.36E-01		4.33E-01	9.70E-05		7.40E-03	9.59E-01		8.53E-01	2.65E-40		1.74E+00	1.31E-230	Up	Unigene12232_All//gi|240255733|ref|NP_192232.4|//0.00E+00//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene12232_All//0.00E+00//AT4G03230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene12232_All//0.00E+00//DT468110		ko04626|Plant-pathogen interaction		nr -
Unigene122322_All	219	0.00	3.01	0.24	0.23	1.10	0.21	1.16	0.19	1.64	1.16E+01	6.26E-04	Up	7.93E+00	6.37E-01		2.27E+00	3.05E-01		-1.42E-01	9.53E-01		-2.60E+00	1.44E-01		4.99E-01	6.27E-01		Unigene122322_All//gi|115442353|ref|NP_001045456.1|//1.00E-09//Os01g0958800 [Oryza sativa Japonica Group] >gi|113534987|dbj|BAF07370.1|Os01g0958800 [Oryza sativa Japonica Group]	Unigene122322_All//9.00E-15//AT3G11620| unknown protein	Unigene122322_All//8.00E-69//TC173424			GO:0043231	nr +
Unigene122327_All	220	0.00	0.92	0.00	0.00	0.00	0.41	0.00	0.57	2.90	9.85E+00	1.37E-01		null	null		null	null		8.68E+00	4.78E-01		9.15E+00	2.40E-01		1.15E+01	9.34E-05	Up								
Unigene12233_All	3242	0.40	0.80	0.49	0.65	1.07	0.59	1.45	2.57	3.67	9.82E-01	1.33E-02		2.88E-01	6.16E-01		7.33E-01	2.43E-02		-1.41E-01	7.55E-01		8.26E-01	4.45E-06		1.34E+00	6.71E-18	Up	Unigene12233_All//gi|240255733|ref|NP_192232.4|//0.00E+00//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene12233_All//0.00E+00//AT4G03230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene12233_All//0.00E+00//gi|164286549|gb|ES806016.1|ES806016		ko04626|Plant-pathogen interaction		nr -
Unigene122331_All	220	335.57	423.55	352.18	651.21	405.08	426.59	178.54	180.67	68.27	3.36E-01	3.22E-10		6.97E-02	3.40E-01		-6.85E-01	1.70E-66		-6.10E-01	6.68E-48		1.71E-02	8.58E-01		-1.39E+00	2.31E-60	Down			Unigene122331_All//2.00E-57//gi|48812620|gb|C0113933.1|C0113933					
Unigene122338_All	220	0.00	0.00	0.00	0.00	0.00	0.00	0.19	0.76	3.62	null	null		null	null		null	null		null	null		1.98E+00	3.79E-01		4.24E+00	7.42E-05	Up								
Unigene12234_All	2165	160.10	155.54	220.01	81.20	90.93	65.82	153.07	66.24	45.29	-4.17E-02	1.83E-01		4.59E-01	1.58E-84		1.63E-01	1.59E-06		-3.03E-01	1.82E-16		-1.21E+00	0.00E+00	Down	-1.76E+00	0.00E+00	Down	Unigene12234_All//gi|73647513|gb|AAZ79355.1|//0.00E+00//aldehyde dehydrogenase [Vitis pseudoreticulata]	Unigene12234_All//0.00E+00//AT3G48000| ALDH2B4 (ALDEHYDE DEHYDROGENASE 2B4); 3-chloroallyl aldehyde dehydrogenase/ ATP binding / aldehyde dehydrogenase (NAD)	Unigene12234_All//0.00E+00//TC137271		ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0004030//GO:0008152//GO:0009536//GO:0010038//GO:0032559	nr -
Unigene122343_All	221	0.00	0.00	0.00	0.23	0.00	0.00	0.19	0.19	100.23	null	null		null	null		-7.82E+00	5.56E-01		-7.82E+00	6.37E-01		-1.67E-02	1.00E+00		9.03E+00	7.25E-157	Up								ESTscan -
Unigene122347_All	221	0.00	0.00	0.00	0.00	0.00	0.00	0.57	0.19	15.50	null	null		null	null		null	null		null	null		-1.60E+00	5.34E-01		4.76E+00	2.01E-20	Up			Unigene122347_All//5.00E-30//gi|109861800|gb|DW490777.1|DW490777					
Unigene122352_All	221	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.88	null	null		null	null		null	null		null	null		null	null		1.15E+01	9.34E-05	Up			Unigene122352_All//2.00E-07//DW508188					
Unigene122354_All	221	0.00	0.00	0.00	0.00	0.00	0.00	37.50	38.58	129.79	null	null		null	null		null	null		null	null		4.11E-02	8.42E-01		1.79E+00	3.02E-63	Up			Unigene122354_All//5.00E-67//DW519317					ESTscan -
Unigene122358_All	221	0.00	0.00	0.00	0.00	0.00	0.00	2.68	3.78	8.47	null	null		null	null		null	null		null	null		4.98E-01	4.86E-01		1.66E+00	1.72E-04	Up			Unigene122358_All//2.00E-32//gi|78339631|gb|DT559905.1|DT559905					
Unigene12236_All	1780	4.85	2.16	1.97	4.51	5.38	3.70	2.19	0.38	1.10	-1.16E+00	1.15E-08	Down	-1.30E+00	1.26E-09	Down	2.55E-01	2.05E-01		-2.83E-01	2.06E-01		-2.54E+00	1.19E-13	Down	-9.95E-01	2.37E-04		Unigene12236_All//gi|42568733|ref|NP_201147.2|//1.00E-155//emb2746 (embryo defective 2746); DNA binding / catalytic/ hydrolase [Arabidopsis thaliana]	Unigene12236_All//1.00E-156//AT5G63420| emb2746 (embryo defective 2746); DNA binding / catalytic/ hydrolase	Unigene12236_All//0.00E+00//TC171766	Trihelix		GO:0043231	nr +
Unigene122364_All	222	0.00	0.00	0.00	0.00	0.00	0.00	1.14	1.13	12.02	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		3.40E+00	8.62E-13	Up								
Unigene122365_All	222	0.00	1.14	0.48	0.22	0.47	0.20	0.57	1.13	8.25	1.02E+01	7.87E-02		8.91E+00	4.00E-01		1.05E+00	8.08E-01		-1.42E-01	9.53E-01		9.83E-01	5.17E-01		3.85E+00	7.54E-10	Up			Unigene122365_All//6.00E-110//TC170381					
Unigene122367_All	222	0.00	0.00	0.00	0.00	0.00	0.00	499.17	1317.13	19.20	null	null		null	null		null	null		null	null		1.40E+00	0.00E+00	Up	-4.70E+00	0.00E+00	Down								
Unigene122369_All	222	0.00	0.00	0.48	0.45	0.16	0.00	0.19	1.88	5.38	null	null		8.91E+00	4.00E-01		-1.53E+00	5.87E-01		-8.81E+00	4.01E-01		3.30E+00	2.00E-02		4.82E+00	1.77E-07	Up								
Unigene122375_All	223	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12	6.07	null	null		null	null		null	null		null	null		1.01E+01	4.31E-02		1.26E+01	9.04E-10	Up								
Unigene122383_All	223	0.00	0.00	0.00	0.00	0.00	0.00	30.53	40.30	8.04	null	null		null	null		null	null		null	null		4.01E-01	2.18E-02		-1.92E+00	2.28E-17	Down	Unigene122383_All//gi|224075052|ref|XP_002304537.1|//3.00E-22//cation proton exchanger [Populus trichocarpa] >gi|222841969|gb|EEE79516.1|cation proton exchanger [Populus trichocarpa]	Unigene122383_All//2.00E-22//AT5G41610| ATCHX18; monovalent cation:proton antiporter/ sodium:hydrogen antiporter	Unigene122383_All//3.00E-31//BG446460			GO:0006811//GO:0015298//GO:0031224	nr +
Unigene122395_All	224	0.00	0.00	0.00	0.00	0.00	0.00	371.27	568.53	174.47	null	null		null	null		null	null		null	null		6.15E-01	6.78E-49		-1.09E+00	5.93E-87	Down								
Unigene1224_All	4237	7.96	2.15	3.90	79.11	69.94	37.83	36.21	5.78	13.67	-1.89E+00	4.03E-64	Down	-1.03E+00	4.03E-25	Down	-1.78E-01	1.17E-12		-1.06E+00	4.80E-290	Down	-2.65E+00	0.00E+00	Down	-1.41E+00	3.12E-238	Down	Unigene1224_All//gi|15234126|ref|NP_194473.1|//0.00E+00//CIP7 (COP1-INTERACTING PROTEIN 7); transcription activator [Arabidopsis thaliana] >gi|186514102|ref|NP_001119068.1|CIP7 (COP1-INTERACTING PROTEIN 7); transcription activator [Arabidopsis thaliana] >gi|33273868|dbj|BAA31738.1| COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana] >gi|4972068|emb|CAB43875.1| COP1-interacting protein 7 (CIP7) [Arabidopsis thaliana] >gi|7269597|emb|CAB81393.1| COP1-interacting protein 7 (CIP7) [Arabidopsis thaliana]	Unigene1224_All//2.00E-112//AT4G27430| CIP7 (COP1-INTERACTING PROTEIN 7); transcription activator	Unigene1224_All//0.00E+00//ES798316			GO:0006779//GO:0009314//GO:0009813//GO:0030528//GO:0043231	nr +

Unigene12240_All	807	7.33	3.58	8.25	6.91	7.51	4.81	7.07	8.13	2.91	-1.03E+00	2.97E-05	Down	1.71E-01	5.09E-01		1.19E-01	6.81E-01		-5.23E-01	4.01E-02		2.01E-01	3.93E-01		-1.28E+00	1.62E-08	Down	Unigene12240_All//gi|297842751|ref|XP_002889257.1|//2.00E-26//ABC1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335098|gb|EFH65516.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12240_All//1.00E-27//AT1G79600| ABC1 family protein	Unigene12240_All//0.00E+00//gi|3326255|gb|AI055141.1|AI055141			GO:0006464//GO:0009570//GO:0016301//GO:0032559	nr -
Unigene122400_All	225	0.00	0.00	0.00	0.00	0.00	0.00	166.30	165.51	48.69	null	null		null	null		null	null		null	null		-6.90E-03	9.70E-01		-1.77E+00	5.45E-82	Down										
Unigene122409_All	225	0.00	0.00	0.00	0.00	0.00	0.00	0.38	2.04	10.80	null	null		null	null		null	null		null	null		2.44E+00	3.74E-02		4.85E+00	9.34E-15	Up			Unigene122409_All//5.00E-92//C0073397						
Unigene122412_All	225	0.23	0.23	0.00	0.66	0.31	0.60	0.75	1.49	4.43	-4.60E-02	9.83E-01		-7.86E+00	6.26E-01		-1.12E+00	5.84E-01		-1.41E-01	9.44E-01		9.84E-01	4.24E-01		2.56E+00	3.91E-04	Up			Unigene122412_All//3.00E-124//DW240192						
Unigene12242_All	528	0.40	0.00	0.10	0.09	0.85	1.71	8.25	14.57	23.69	-8.63E+00	1.22E-01		-1.97E+00	3.81E-01		3.17E+00	3.95E-02		4.18E+00	1.95E-04	Up	8.20E-01	1.25E-05		1.52E+00	1.97E-22	Up	Unigene12242_All//gi|115489036|ref|NP_001067005.1|//6.00E-33//Os12g0556600 [Oryza sativa Japonica Group] >gi|113649512|dbj|BAF30024.1|Os12g0556600 [Oryza sativa Japonica Group]	Unigene12242_All//5.00E-23//AT4G02120| CTP synthase, putative / UTP--ammonia ligase, putative	Unigene12242_All//5.00E-94//DW484682		ko00240|Pyrimidine metabolism	GO:0006220//GO:0016879//GO:0044464	nr +
Unigene122425_All	227	0.00	0.00	0.00	0.00	0.00	0.00	0.75	1.29	5.09	null	null		null	null		null	null		null	null		7.91E-01	5.63E-01		2.77E+00	5.09E-05	Up										
Unigene122426_All	227	0.00	0.45	0.00	0.00	0.00	0.00	0.19	0.18	3.16	8.80E+00	3.88E-01		null	null		null	null		null	null		-1.71E-02	1.00E+00		4.08E+00	2.41E-04	Up	Unigene122426_All//gi|23428804|gb|AAM23263.1|//2.00E-13//L-asparaginase [Glycine max]	Unigene122426_All//9.00E-15//AT3G16150| L-asparaginase, putative / L-asparagine amidohydrolase, putative	Unigene122426_All//2.00E-63//gi|21090062|gb|BQ402375.1|BQ402375			GO:0009057//GO:0016811	nr +
Unigene122243_All	785	0.00	0.32	0.00	0.38	0.83	1.50	3.12	7.61	10.20	8.33E+00	7.87E-02		null	null		1.13E+00	2.38E-01		1.97E+00	4.50E-03		1.29E+00	1.31E-08	Up	1.71E+00	3.95E-17	Up	Unigene12243_All//gi|15230562|ref|NP_187873.1|//2.00E-48//emb2742 (embryo defective 2742): CTP synthase/ catalytic [Arabidopsis thaliana] >gi|11994408|dbj|BAB02410.1| CTP synthase [Arabidopsis thaliana] >gi|30725394|gb|AAP37719.1|At3g12670 [Arabidopsis thaliana]	Unigene12243_All//4.00E-48//AT3G12670| emb2742 (embryo defective 2742): CTP synthase/ catalytic	Unigene12243_All//0.00E+00//TC162543		ko00240|Pyrimidine metabolism	GO:0003006//GO:0006220//GO:0009064//GO:0010038//GO:0016879//GO:0044464	nr +
Unigene122437_All	228	0.00	0.00	0.00	0.44	0.00	0.00	0.00	0.00	2.27	null	null		null	null		-8.77E+00	3.14E-01		-8.77E+00	4.01E-01		null	null		1.11E+01	6.13E-04	Up			Unigene122437_All//3.00E-13//TC145826						
Unigene12244_All	1646	1.65	0.65	0.49	5.05	6.30	10.67	13.41	21.33	33.11	-1.35E+00	6.14E-04	Down	-1.77E+00	4.22E-05	Down	3.17E-01	8.34E-02		1.08E+00	8.46E-16	Up	6.70E-01	2.95E-16		1.30E+00	2.66E-75	Up	Unigene12244_All//gi|297834070|ref|XP_002884917.1|//0.00E+00//EMB2742 [Arabidopsis lyrata subsp. lyrata] >gi|297330757|gb|EFH61176.1|EMB2742 [Arabidopsis lyrata subsp. lyrata]	Unigene12244_All//0.00E+00//AT3G12670| emb2742 (embryo defective 2742): CTP synthase/ catalytic	Unigene12244_All//0.00E+00//TC162543		ko00240|Pyrimidine metabolism	GO:0003006//GO:0006220//GO:0009064//GO:0010038//GO:0016879//GO:0044464	nr -
Unigene122445_All	228	0.23	0.00	0.00	0.00	0.00	0.00	0.37	2.38	7.69	-7.84E+00	6.14E-01		-7.84E+00	6.26E-01		null	null		null	null		2.68E+00	1.38E-02		4.37E+00	3.24E-10	Up			Unigene122445_All//7.00E-11//gi|73862812|gb|DT465551.1|DT465551						
Unigene122447_All	228	0.00	1.11	0.00	0.22	0.00	0.40	0.00	0.55	5.42	1.01E+01	7.87E-02		null	null		-7.77E+00	5.56E-01		8.59E-01	7.95E-01		9.10E+00	2.40E-01		1.24E+01	6.29E-09	Up			Unigene122447_All//3.00E-07//TC160727						
Unigene122449_All	229	0.46	0.00	0.00	0.00	0.00	0.20	0.37	0.37	6.78	-8.84E+00	3.73E-01		-8.84E+00	3.95E-01		null	null		7.62E+00	6.97E-01		-1.69E-02	1.01E+00		4.20E+00	6.62E-09	Up			Unigene122449_All//2.00E-88//DT465323						
Unigene12245_All	1119	2.38	1.63	0.71	4.99	9.88	11.99	28.07	50.20	77.36	-5.49E-01	1.54E-01		-1.74E+00	6.32E-05	Down	9.86E-01	1.50E-09		1.27E+00	1.50E-15	Up	8.39E-01	2.59E-37		1.46E+00	1.21E-141	Up	Unigene12245_All//gi|226507866|ref|NP_001152016.1|//1.00E-126//CTP synthase [Zea mays] >gi|195651853|gb|ACG45394.1| CTP synthase [Zea mays]	Unigene12245_All//3.00E-94//AT3G12670| emb2742 (embryo defective 2742): CTP synthase/ catalytic	Unigene12245_All//0.00E+00//ES818469		ko00240|Pyrimidine metabolism		nr -
Unigene122454_All	229	96.65	82.75	86.73	81.36	83.46	170.99	36.19	60.05	65.93	-2.24E-01	6.69E-02		-1.56E-01	2.44E-01		3.68E-02	8.17E-01		1.07E+00	3.32E-34	Up	7.31E-01	7.29E-08		8.66E-01	1.76E-11				Unigene122454_All//2.00E-69//gi|109857799|gb|DW486778.1|DW486778						
Unigene12246_All	1888	13.61	8.80	5.56	72.43	55.83	61.12	84.74	43.77	34.94	-6.28E-01	5.10E-09		-1.29E+00	2.37E-27	Down	-3.76E-01	2.61E-21		-2.45E-01	7.70E-09		-9.53E-01	3.69E-130		-1.28E+00	1.23E-214	Down	Unigene12246_All//gi|283488493|gb|ADB22768.1|//0.00E+00//UDP-D-glucose dehydrogenase [Gossypium hirsutum]	Unigene12246_All//0.00E+00//AT5G15490| UDP-glucose 6-dehydrogenase, putative	Unigene12246_All//0.00E+00//TC132310		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions	GO:0000166//GO:0008152//GO:0016616	nr +
Unigene122470_All	230	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.09	2.60	null	null		null	null		null	null		null	null		1.01E+01	4.31E-02		1.13E+01	1.75E-04	Up	Unigene122470_All//gi|297836874|ref|XP_002886319.1|//2.00E-06//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332159|gb|EFH62578.1|expressed protein [Arabidopsis lyrata subsp. lyrata]							nr -
Unigene122471_All	230	0.00	0.00	0.00	0.22	0.00	0.39	0.55	0.55	5.02	null	null		null	null		-7.76E+00	5.56E-01		8.58E-01	7.95E-01		-1.66E-02	1.02E+00		3.19E+00	1.26E-05	Up										
Unigene122475_All	231	0.23	0.00	0.00	0.00	0.00	0.00	0.55	0.36	6.73	-7.82E+00	6.14E-01		-7.82E+00	6.26E-01		null	null		null	null		-6.02E-01	7.67E-01		3.61E+00	4.47E-08	Up			Unigene122475_All//3.00E-07//TC138233						
Unigene12248_All	600	3.31	0.34	0.53	7.72	4.13	3.01	0.70	0.00	0.53	-3.29E+00	1.16E-07	Down	-2.64E+00	6.10E-06	Down	-9.02E-01	5.45E-04		-1.36E+00	1.83E-06	Down	-9.46E+00	3.25E-03		-4.08E-01	6.54E-01		Unigene12248_All//gi|240255713|ref|NP_192042.5|//2.00E-44//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene12248_All//3.00E-34//AT4G01330| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene12248_All//2.00E-142//TC156255		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism	GO:0004674//GO:0004871//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene122484_All	231	0.00	0.00	0.92	0.00	0.00	0.00	0.55	0.72	9.31	null	null		9.85E+00	1.41E-01		null	null		null	null		3.98E-01	8.14E-01		4.08E+00	6.49E-12	Up			Unigene122484_All//3.00E-07//DR457465						
Unigene12249_All	1773	4.87	0.69	1.71	13.35	9.85	8.05	0.98	0.24	0.45	-2.83E+00	4.28E-27	Down	-1.51E+00	6.26E-12	Down	-4.39E-01	2.44E-05		-7.29E-01	2.68E-11		-2.05E+00	3.55E-05	Down	-1.12E+00	9.40E-03		Unigene12249_All//gi|14194119|gb|AAK56254.1|AF367263_1//0.00E+00//At1g01540/F22L4_6 [Arabidopsis thaliana] >gi|20334728|gb|AAM16225.1|At1g01540/F22L4_6 [Arabidopsis thaliana]	Unigene12249_All//2.00E-176//AT1G01540| protein kinase family protein	Unigene12249_All//0.00E+00//TC156255		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene122490_All	232	0.00	0.00	0.00	0.00	0.00	0.00	241.29	407.69	115.91	null	null		null	null		null	null		null	null		7.57E-01	2.61E-52		-1.06E+00	4.36E-56	Down			Unigene122490_All//1.00E-09//DW234221						
Unigene122491_All	232	0.68	2.62	2.07	1.72	4.30	2.34	14.21	2.52	83.63	1.95E+00	6.04E-02		1.61E+00	1.82E-01		1.33E+00	6.66E-02		4.44E-01	6.78E-01		-2.49E+00	1.85E-11	Down	2.56E+00	6.02E-67	Up	Unigene122491_All//gi|296080964|emb|CB118596.3|//6.00E-07//unnamed protein product [Vitis vinifera]		Unigene122491_All//1.00E-52//DT464746				nr -
Unigene122492_All	232	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.36	3.78	null	null		null	null		null	null		null	null		9.84E-01	7.32E-01		4.37E+00	2.26E-05	Up			Unigene122492_All//4.00E-12//TC146753						
Unigene122498_All	233	0.00	0.22	0.00	0.00	0.00	0.00	0.00	0.18	2.91	7.76E+00	6.17E-01		null	null		null	null		null	null		7.49E+00	6.35E-01		1.15E+01	4.97E-05	Up			Unigene122498_All//3.00E-07//TC154790						
Unigene1225_All	2876	8.79	49.24	21.31	15.55	22.27	19.10	4.90	5.80	5.80	2.49E+00	0.00E+00	Up	1.28E+00	9.59E-64	Up	5.18E-01	9.05E-18		2.96E-01	2.27E-05		2.44E-01	5.72E-02		2.46E-01	4.61E-02		Unigene1225_All//gi|18402131|ref|NP_564524.1|//1.00E-118//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|8778962|gb|AAD49768.2|AC007932_16 F11A17.16 [Arabidopsis thaliana]	Unigene1225_All//6.00E-111//AT1G48280| hydroxyproline-rich glycoprotein family protein	Unigene1225_All//0.00E+00//TC179521				nr -
Unigene12250_All	1950	26.40	15.51	17.53	24.63	23.26	11.37	18.82	3.64	7.05	-7.67E-01	3.25E-24		-5.91E-01	6.63E-15		-8.25E-02	3.68E-01		-1.11E+00	4.02E-45	Down	-2.37E+00	1.51E-113	Down	-1.42E+00	2.71E-58	Down	Unigene12250_All//gi|240255713|ref|NP_192042.5|//0.00E+00//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene12250_All//0.00E+00//AT1G01540| protein kinase family protein	Unigene12250_All//0.00E+00//TC137221		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene122503_All	233	0.00	1.09	0.00	0.00	0.15	0.00	0.36	0.54	7.52	1.01E+01	7.87E-02		null	null		7.21E+00	8.31E-01		null	null		5.68E-01	7.82E-01		4.37E+00	3.24E-10	Up	Unigene122503_All//gi|14249015|gb|AAK57698.1|AF377316_1//2.00E-16//myb-like transcription factor Myb 5 [Gossypium hirsutum]	Unigene122503_All//2.00E-11//AT2G47190| MYB2 (MYB DOMAIN PROTEIN 2): DNA binding / calmodulin binding / transcription activator/ transcription factor	Unigene122503_All//5.00E-126//TC146739	MYB		GO:0001071//GO:0003676//GO:0005515//GO:0006970//GO:0009725//GO:0010038//GO:0010468//GO:0030528//GO:0043231	nr +
Unigene122512_All	233	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	24.11	null	null		null	null		null	null		null	null		7.49E+00	6.35E-01		1.46E+01	3.27E-40	Up	Unigene122512_All//gi|222142539|gb|ACM45956.1|//2.00E-14//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Glycine max]	Unigene122512_All//2.00E-14//AT1G07250| UGT71C4 (UDP-GLUCOSYL TRANSFERASE 71C4): quercetin 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene122512_All//5.00E-21//AT726414			GO:0035251	nr -
Unigene122526_All	234	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.36	22.81	null	null		null	null		null	null		null	null		8.48E+00	4.02E-01		1.45E+01	3.26E-38	Up			Unigene122526_All//2.00E-17//TC149487						
Unigene122542_All	236	568.21	166.61	243.46	871.12	668.42	926.61	297.39	141.86	132.85	-1.77E+00	8.36E-232	Down	-1.22E+00	1.79E-129	Down	-3.82E-01	6.57E-33		8.91E-02	1.51E-02		-1.07E+00	3.18E-69	Down	-1.16E+00	1.53E-81	Down	Unigene122542_All//gi|209967449|gb|ACJ02353.1|//6.00E-44//60S ribosomal protein L27A [Vernicia fordii]	Unigene122542_All//6.00E-45//AT1G70600| structural constituent of ribosome	Unigene122542_All//8.00E-131//EV487350		ko03010|Ribosome		nr -
Unigene122546_All	236	0.00	0.00	0.00	0.00	0.00	0.00	416.71	924.11	23.13	null	null		null	null		null	null		null	null		1.15E+00	4.40E-240	Up	-4.17E+00	0.00E+00	Down										
Unigene122547_All	236	0.00	0.21	0.00	0.00	0.29	0.19	0.18	0.18	6.92	7.75E+00	6.17E-01		null	null		8.19E+00	6.11E-01		7.58E+00	6.97E-01		-1.70E-02	1.00E+00		5.27E+00	1.93E-10	Up	Unigene122547_All//gi|149728050|gb|ABR28344.1|//1.00E-81//MYB transcription factor MYB70 [Medicago truncatula]	Unigene122547_All//5.00E-12//AT3G23250| MYB15 (MYB DOMAIN PROTEIN 15): DNA binding / transcription factor	Unigene122547_All//1.00E-67//TC147251	MYB			nr -
Unigene122551_All	237	0.00	0.00	0.00	0.00	0.00	0.38	1.96	3.00	51.61	null	null		null	null		null	null		8.57E+00	4.77E-01		6.11E-01	4.27E-01		4.72E+00	2.01E-71	Up	Unigene122551_All//gi|83853815|gb|ABC47848.1|//5.00E-27//N-hydroxycinnamoyl/benzoyltransferase 6 [Glycine max]	Unigene122551_All//9.00E-26//AT5G07850| transferase family protein					nr +
Unigene12256_All	1880	7.74	9.73	10.96	37.47	40.48	50.40	60.52	16.18	26.30	3.31E-01	1.21E-02		5.03E-01	5.83E-05		1.12E-01	8.39E-02		4.28E-01	7.52E-17		-1.90E+00	1.88E-265	Down	-1.20E+00	6.44E-139	Down	Unigene12256_All//gi|30692538|gb|AAP33475.1|//0.00E+00//polygalacturonase-like protein [Fragaria x ananassa]	Unigene12256_All//0.00E+00//AT3G61490| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene12256_All//0.00E+00//TC133994		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553//GO:0030312//GO:0044238//GO:0045229	nr -
Unigene122565_All	238	0.00	0.00	0.00	0.00	0.00	0.95	0.18	0.53	2.85	null	null		null	null		null	null		9.89E+00	1.19E-01		1.57E+00	5.45E-01		4.00E+00	4.29E-04	Up										
Unigene122568_All	238	0.00	0.00	0.00	0.00	0.00	0.00	1.60	0.18	94.41	null	null		null	null		null	null		null	null		-3.19E+00	3.12E-02		5.88E+00	3.22E-145	Up	Unigene122568_All//gi|114145388|dbj|BAF30983.1|//1.00E-07//basic helix-loop-helix protein [Nicotiana tabacum]	Unigene122568_All//3.00E-07//AT5G43650| basic helix-loop-helix (bHLH) family protein	Unigene122568_All//1.00E-129//DT465287	bHLH			nr +
Unigene122573_All	239	84.06	41.98	19.61	427.49	639.72	492.45	65.28	28.33	20.00	-1.00E+00	3.74E-15	Down	-2.10E+00	1.82E-42	Down	5.82E-01	1.19E-51		2.04E-01	1.28E-05		-1.20E+00	2.99E-19	Down	-1.71E+00	6.29E-33	Down	Unigene122573_All//gi|112350249|gb|ABI15167.1|//1.00E-43//GASA-like protein [Gossypium hirsutum]		Unigene122573_All//1.00E-132//TC161726		ko03040|Spliceosome		nr +
Unigene122575_All	239	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.83	null	null		null	null		null	null		null	null		null	null		1.15E+01	4.97E-05	Up	Unigene122575_All//gi|22330656|ref|NP_177742.2|//6.00E-08//macC-like dehydratase domain-containing protein [Arabidopsis thaliana] >gi|17929531|gb|AAL50100.1|At1g76150/T23E18_38 [Arabidopsis thaliana] >gi|20147215|gb|AAM10336.1|At1g76150/T23E18_38 [Arabidopsis thaliana]	Unigene122575_All//3.00E-09//AT1G76150| macC-like dehydratase domain-containing protein					nr -
Unigene122582_All	240	0.22	0.00	0.00	3.94	0.72	1.32	3.88	0.70	9.30	-7.77E+00	6.13E-01		-7.77E+00	6.26E-01		-2.46E+00	1.25E-03		-1.58E+00	3.51E-02		-2.48E+00	1.07E-03		1.26E+00	9.46E-04	Up			Unigene122582_All//2.00E-88//gi|78327349|gb|DT547823.1|DT547823						
Unigene122590_All	241	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.69	37.69	null	null		null	null		null	null		null	null		1.98E+00	3.79E-01		7.75E+00	4.49E-63	Up			Unigene122590_All//5.00E-61//DW479423						
Unigene122591_All	241	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.31	null	null		null	null		null	null		null	null		null	null		1.17E+01	7.36E-06	Up										
Unigene122592_All	241	0.00	0.00	0.00	0.00	0.00	0.00	0.53	1.39	7.27	null	null		null	null		null	null		null	null		1.40E+00	2.76E-01		3.79E+00	2.44E-09	Up	Unigene122592_All//gi|94807642|gb|ABF47118.1|//7.00E-23//At5g57123 [Arabidopsis thaliana]	Unigene122592_All//3.00E-24//AT5G57123| unknown protein					nr +
Unigene122595_All	241	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	7.60	null	null		null	null		null	null		null	null		-7.45E+00	6.58E-01		5.44E+00	8.34E-12	Up			Unigene122595_All//6.00E-36//gi|73859581|gb|DT462320.1|DT462320						
Unigene122597_All	242	0.00	0.00	0.00	0.00	0.00	0.00	0.52	0.35	4.61	null	null		null	null		null	null		null	null		-6.02E-01	7.67E-01		3.14E+00	2.19E-05	Up			Unigene122597_All//2.00E-32//TC152783						
Unigene122598_All	242	0.00	0.00	0.00	0.00	0.00	0.00	0.35	0.35	3.46	null	null		null	null		null	null		null	null		-1.66E-02	1.01E+00		3.31E+00	2.30E-04	Up			Unigene122598_All//3.00E-07//TC146132						
Unigene1226_All	3540	12.80	13.15	13.82	8.81	8.89	10.05	16.57	10.76	5.77	3.94E-02	6.50E-01		1.11E-01	2.13E-01		1.34E-02	9.18E-01		1.91E-01	4.68E-02		-6.23E-01	1.62E-23		-1.52E+00	6.50E-103	Down	Unigene1226_All//gi|224064996|ref|XP_002301626.1|//0.00E+00//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222843352|gb|EEES0899.1|glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene1226_All//0.00E+00//AT2G32400| GLR5 (GLUTAMATE RECEPTOR 5): intracellular ligand-gated ion channel	Unigene1226_All//0.00E+00//TC165928			GO:0005231//GO:0005488//GO:0006810//GO:0006875//GO:0007166//GO:0008066//GO:0009314//GO:0030313//GO:0031224//GO:0031410	nr -

Unigene12261_All	810	1.03	0.88	3.29	2.21	2.21	0.78	1.25	0.62	0.74	-2.39E-01	7.25E-01			1.67E+00	1.07E-04	Up	-2.20E-03	9.82E-01		-1.50E+00	2.75E-03		-1.02E+00	1.00E-01		-7.64E-01	1.95E-01		Unigene12261_All//gi|297597139|ref|NP_001043490.2|//4.00E-09//Os01g0600300 [Oryza sativa Japonica Group] >gi|255673428|dbj|BAF05404.2|Os01g0600300 [Oryza sativa Japonica Group]	Unigene12261_All//4.00E-11//AT5G11780| unknown protein					nr -
Unigene122611_All	243	0.00	0.00	0.00	0.00	0.14	0.00	0.17	0.34	2.79	null	null			null	null		7.15E+00	8.31E-01		null	null		9.83E-01	7.32E-01		4.00E+00	4.29E-04	Up							
Unigene122615_All	243	0.00	0.00	0.00	0.00	0.00	0.00	0.52	0.17	5.08	null	null			null	null		null	null		null	null		-1.60E+00	5.34E-01		3.28E+00	4.18E-06	Up							
Unigene122618_All	244	13.29	4.98	11.35	38.99	44.03	23.51	17.50	10.28	33.14	-1.42E+00	8.53E-05	Down	-2.28E-01	5.51E-01		1.75E-01	3.84E-01		-7.30E-01	5.87E-05		-7.68E-01	3.30E-03		9.21E-01	3.46E-07		Unigene122618_All//gi|18379261|ref|NP_565267.1|//3.00E-12//epsin N-terminal homology (ENTH) domain-containing protein [Arabidopsis thaliana] >gi|46395897|sp|Q8LBH2.2|CAP8_ARATH RecName: Full=Putative clathrin assembly protein At2g01600 >gi|159834338|gb|AAL11587.1|AF424593_1 At2g01600/F21B.22 [Arabidopsis thaliana] >gi|20197399|gb|AAM15059.1| expressed protein [Arabidopsis thaliana]	Unigene122618_All//1.00E-13//AT2G01600| epsin N-terminal homology (ENTH) domain-containing protein	Unigene122618_All//1.00E-55//ES809512				nr -
Unigene122624_All	244	0.00	0.00	0.00	0.00	0.00	0.00	0.69	1.03	5.71	null	null			null	null		null	null		null	null		5.68E-01	6.74E-01		3.04E+00	2.09E-06	Up							
Unigene12263_All	1098	2.33	1.02	1.21	2.00	2.32	2.84	3.12	0.65	4.43	-1.20E+00	2.87E-03		-9.46E-01	2.31E-02		2.17E-01	6.16E-01		5.08E-01	1.72E-01		-2.27E+00	1.07E-10	Down	5.05E-01	3.34E-02		Unigene12263_All//gi|297597139|ref|NP_001043490.2|//4.00E-16//Os01g0600300 [Oryza sativa Japonica Group] >gi|255673428|dbj|BAF05404.2|Os01g0600300 [Oryza sativa Japonica Group]	Unigene12263_All//1.00E-66//AT5G11780| unknown protein					nr +
Unigene122635_All	245	0.00	1.03	0.00	0.81	0.00	0.00	0.35	2.39	7.81	1.00E+01	7.87E-02		null	null		-9.67E+00	8.44E-02		-9.67E+00	1.34E-01		2.79E+00	8.26E-03		4.50E+00	2.83E-11	Up							
Unigene122636_All	245	0.00	0.00	0.00	0.41	0.00	0.00	0.00	0.17	2.44	null	null		null	null		-8.67E+00	3.14E-01		-8.67E+00	4.01E-01		7.41E+00	6.35E-01		1.13E+01	1.75E-04	Up	Unigene122636_All//gi|224071585|ref|XP_002303528.1|//2.00E-25//cytochrome P450 [Populus trichocarpa] >gi|222840960|gb|EEE78507.1| cytochrome P450 [Populus trichocarpa]	Unigene122636_All//3.00E-18//AT4G12300| CYP706A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene122638_All	245	0.00	0.00	0.00	0.41	0.28	0.37	0.52	1.71	3.74	null	null			null	null		-5.33E-01	8.17E-01		-1.41E-01	9.51E-01		1.72E+00	1.35E-01		2.85E+00	3.18E-04	Up			Unigene122638_All//3.00E-07//TC166857				
Unigene122640_All	245	0.43	0.00	0.87	2.64	0.00	0.00	0.35	0.17	0.49	-8.74E+00	3.73E-01		1.03E+00	5.92E-01		-1.14E+01	7.85E-05	Down	-1.14E+01	3.90E-04	Down	-1.02E+00	7.25E-01		4.99E-01	8.08E-01		Unigene122640_All//gi|42567571|ref|NP_195783.3|//1.00E-17//BRCA2B (BRCA2-LIKE B); protein binding / single-stranded DNA binding [Arabidopsis thaliana] >gi|31335362|emb|CAD32572.1| breast cancer susceptibility protein 2b [Arabidopsis thaliana]	Unigene122640_All//8.00E-16//AT5G01630| BRCA2B (BRCA2-LIKE B); protein binding / single-stranded DNA binding			ko03440|Homologous recombination		nr +
Unigene122642_All	246	0.85	0.41	0.65	0.41	0.98	2.57	1.03	5.61	5.67	-1.05E+00	5.65E-01		-3.90E-01	8.08E-01		1.27E+00	5.32E-01		2.67E+00	1.83E-02		2.44E+00	4.59E-05	Up	2.46E+00	2.70E-05	Up	Unigene122642_All//gi|297823145|ref|XP_002879455.1|//1.00E-11//hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325294|gb|EFH55714.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]		Unigene122642_All//4.00E-34//BM359039				nr -
Unigene122646_All	246	0.00	0.00	0.00	0.00	0.00	0.00	139.04	103.13	36.92	null	null		null	null		null	null		null	null		-4.31E-01	1.33E-07		-1.91E+00	3.09E-83	Down			Unigene122646_All//3.00E-13//TC146753				
Unigene122647_All	246	1.06	0.00	0.00	0.00	0.00	0.00	0.17	0.34	3.72	-1.01E+01	6.71E-02		-1.01E+01	8.58E-02		null	null		null	null		9.83E-01	7.32E-01		4.41E+00	1.24E-05	Up							
Unigene122657_All	246	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.51	2.11	null	null		null	null		null	null		null	null		8.99E+00	2.40E-01		1.10E+01	6.13E-01	Up							
Unigene122663_All	247	0.00	0.82	0.00	1.01	0.28	1.65	0.34	0.51	4.84	9.68E+00	1.37E-01		null	null		-1.85E+00	2.75E-01		7.07E-01	5.97E-01		5.68E-01	7.82E-01		3.82E+00	1.37E-06	Up			Unigene122663_All//3.00E-07//TC146460				
Unigene122668_All	248	0.00	0.00	0.00	0.20	0.00	0.36	0.00	0.00	5.94	null	null		null	null		-7.65E+00	5.56E-01		8.58E-01	7.95E-01		null	null		1.25E+01	1.30E-10	Up	Unigene122668_All//gi|115463071|ref|NP_001055135.1|//4.00E-06//Os05g0301600 [Oryza sativa Japonica Group] >gi|113578686|dbj|BAF17049.1| Os05g0301600 [Oryza sativa Japonica Group]	Unigene122668_All//3.00E-07//AT5G52200| unknown protein					nr -
Unigene122674_All	249	0.42	0.61	0.64	1.00	0.83	0.18	0.34	0.67	3.20	5.39E-01	7.79E-01		6.11E-01	7.48E-01		-2.70E-01	8.23E-01		-2.46E+00	2.24E-01		9.83E-01	6.34E-01		3.24E+00	3.96E-04	Up			Unigene122674_All//1.00E-09//CO103526				
Unigene122682_All	250	0.00	0.81	0.00	0.00	0.00	0.00	0.51	1.84	5.74	9.66E+00	1.37E-01		null	null		null	null		null	null		1.86E+00	8.80E-02		3.50E+00	2.50E-07	Up	Unigene122682_All//gi|4205113|gb|AAD10959.1|//3.00E-14//cell wall invertase [Fragaria x ananassa]	Unigene122682_All//1.00E-14//AT3G13784| AtcwINV5 (Arabidopsis thaliana cell wall invertase 5); hydrolase, hydrolyzing O-glycosyl compounds	Unigene122682_All//2.00E-30//TC147820		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene12269_All	897	5.19	5.37	6.47	13.00	12.25	8.86	7.02	3.03	3.29	4.78E-02	8.69E-01		3.18E-01	2.36E-01		-8.56E-02	6.64E-01		-5.52E-01	7.01E-04		-1.21E+00	2.44E-08	Down	-1.10E+00	1.82E-07	Down	Unigene12269_All//gi|18421489|ref|NP_568530.1|//3.00E-66//EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana]	Unigene12269_All//1.00E-67//AT5G35730| EXS family protein / ERD1/XPR1/SYG1 family protein				GO:0031224//GO:0031410	nr -
Unigene122690_All	251	7809.77	3715.02	7960.77	1930.65	2062.69	1165.79	0.67	2.33	1.11	-1.07E+00	0.00E+00	Down	2.76E-02	2.87E-02		9.54E-02	4.68E-06		-7.28E-01	6.42E-220		1.79E+00	5.30E-02		7.22E-01	5.97E-01		Unigene122690_All//gi|255560287|ref|XP_002521161.1|//1.00E-21//photosystem I reaction center subunit IV A, chloroplast precursor [Ricinus communis] >gi|223539730|gb|EEF41312.1| photosystem I reaction center subunit IV A, chloroplast precursor [Ricinus communis]		Unigene122690_All//8.00E-57//EX167214		ko00195|Photosynthesis		nr -
Unigene122697_All	251	0.21	0.00	0.00	0.00	0.41	0.54	0.84	4.33	7.62	-7.70E+00	6.13E-01		-7.70E+00	6.25E-01		8.69E+00	4.56E-01		9.08E+00	3.11E-01		2.36E+00	5.23E-04	Up	3.18E+00	7.45E-09	Up			Unigene122697_All//3.00E-07//ES831747				
Unigene122704_All	252	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.17	2.53	null	null		null	null		null	null		null	null		7.37E+00	6.35E-01		1.13E+01	9.34E-05	Up	Unigene122704_All//gi|15218456|ref|NP_177379.1|//1.00E-15//MADS-box protein (AGL60) [Arabidopsis thaliana] >gi|32402434|gb|AAN52799.1| MADS-box protein AGL60 [Arabidopsis thaliana] >gi|91806071|gb|ABE65764.1| MADS-box protein [Arabidopsis thaliana] >gi|105829930|gb|ABF74708.1| AtlgT2350 [Arabidopsis thaliana]	Unigene122704_All//4.00E-17//AT1G72350| MADS-box protein (AGL60)		MADS			nr -
Unigene12271_All	1945	4.95	4.35	4.71	9.25	7.65	7.34	12.54	8.34	6.00	-1.86E-01	3.66E-01		-7.19E-02	7.18E-01		-2.74E-01	3.67E-02		-3.34E-01	1.17E-02		-5.89E-01	2.27E-09		-1.06E+00	3.65E-25	Down	Unigene12271_All//gi|18421489|ref|NP_568530.1|//0.00E+00//EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana]	Unigene12271_All//0.00E+00//AT5G35730| EXS family protein / ERD1/XPR1/SYG1 family protein	Unigene12271_All//0.00E+00//gi|164299032|gb|EX164205.1|EX164205			GO:0031224//GO:0031410	nr -
Unigene122710_All	253	0.00	0.00	0.00	0.20	0.14	0.00	0.00	0.50	2.36	null	null		null	null		-5.33E-01	8.25E-01		-7.62E+00	6.36E-01		8.95E+00	2.40E-01		1.12E+01	1.75E-04	Up	Unigene122710_All//gi|115477581|ref|NP_001062386.1|//4.00E-10//Os08g0541300 [Oryza sativa Japonica Group] >gi|113624355|dbj|BAF24300.1| Os08g0541300 [Oryza sativa Japonica Group]	Unigene122710_All//2.00E-07//AT2G34930| disease resistance family protein					nr +
Unigene122713_All	253	0.00	0.00	0.42	0.20	0.27	0.00	8.52	2.97	102.98	null	null		8.72E+00	3.99E-01		4.67E-01	9.58E-01		-7.62E+00	6.36E-01		-1.52E+00	2.06E-04	Down	3.59E+00	2.40E-125	Up	Unigene122713_All//gi|297837039|ref|XP_002886401.1|//8.00E-09//F2K11.21 [Arabidopsis lyrata subsp. lyrata] >gi|297332242|gb|EFH62660.1| F2K11.21 [Arabidopsis lyrata subsp. lyrata]	Unigene122713_All//1.00E-07//AT1G63410| unknown protein	Unigene122713_All//1.00E-114//DW517934				nr -
Unigene122717_All	254	0.00	0.00	0.84	0.00	0.14	0.00	1.17	0.82	6.43	null	null		9.71E+00	1.41E-01		7.08E+00	8.31E-01		null	null		-5.02E-01	6.78E-01		2.46E+00	4.32E-06	Up			Unigene122717_All//1.00E-34//DT054260				
Unigene122728_All	254	0.00	0.00	0.00	0.00	0.00	0.00	0.17	0.82	4.23	null	null		null	null		null	null		null	null		2.31E+00	2.40E-01		4.67E+00	1.11E-06	Up							
Unigene122731_All	255	127.42	92.99	107.96	157.06	135.99	166.13	47.09	27.21	19.53	-4.54E-01	1.38E-06		-2.39E-01	1.91E-02		-2.08E-01	1.34E-02		8.10E-02	4.23E-01		-7.91E-01	6.84E-08		-1.27E+00	9.47E-17	Down	Unigene122731_All//gi|12585330|sp|Q9ZSQ4.1|PGMC_POPTN//4.00E-36//RecName: Full=Phosphoglucomutase, cytoplasmic; Short=PGM; AltName: Full=Glucose phosphomutase >gi|4234941|gb|AAD13031.1| cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]	Unigene122731_All//5.00E-35//AT1G23190| phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative	Unigene122731_All//2.00E-137//gi|5044798|gb|AI725946.1|AI725946		ko00500|Starch and sucrose metabolism//ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene122732_All	255	0.00	0.20	0.00	0.00	0.00	0.00	0.17	0.33	8.59	7.63E+00	6.17E-01		null	null		null	null		null	null		9.83E-01	7.32E-01		5.70E+00	2.82E-14	Up			Unigene122732_All//4.00E-77//DT466059				
Unigene122734_All	255	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	9.84	null	null		null	null		null	null		null	null		7.36E+00	6.35E-01		1.33E+01	5.71E-18	Up							
Unigene122742_All	256	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.65	1.05	null	null		null	null		null	null		null	null		9.35E+00	1.39E-01		1.20E+01	1.58E-07	Up							
Unigene122748_All	256	0.00	0.00	0.00	0.19	0.00	0.00	0.00	0.16	2.65	null	null		null	null		-7.60E+00	5.56E-01		-7.60E+00	6.36E-01		7.35E+00	6.35E-01		1.14E+01	4.96E-05	Up							
Unigene122750_All	257	1.02	0.00	0.62	0.39	2.28	1.05	5.43	1.46	6.51	-9.99E+00	6.71E-02		-7.12E-01	6.22E-01		2.55E+00	2.84E-02		1.44E+00	4.09E-01		-1.89E+00	5.91E-04	Down	2.62E-01	5.87E-01				Unigene122750_All//2.00E-39//TC164682				
Unigene122752_All	257	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.17	null	null		null	null		null	null		null	null		null	null		1.11E+01	3.28E-04	Up							
Unigene12276_All	956	12.70	12.67	8.13	46.38	32.27	23.43	11.23	7.87	4.54	-3.40E-03	9.81E-01		-6.43E-01	1.32E-04		-5.23E-01	5.95E-13		-9.85E-01	4.05E-34		-5.14E-01	9.27E-04		-1.31E+00	1.03E-15	Down	Unigene12276_All//gi|17511264|gb|AA068755.2|//5.00E-17//Unknown protein [Arabidopsis thaliana]	Unigene12276_All//2.00E-18//AT3G20420| RTL2 (RNASE THREE-LIKE PROTEIN 2); double-stranded RNA binding / ribonuclease III	Unigene12276_All//0.00E+00//TC145247			GO:0003676//GO:0016891//GO:0043231	nr -
Unigene122760_All	258	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.32	2.78	null	null		null	null		null	null		null	null		8.34E+00	4.02E-01		1.14E+01	2.63E-05	Up							
Unigene122777_All	260	0.00	0.00	0.00	0.00	0.00	0.00	0.33	1.29	2.91	null	null		null	null		null	null		null	null		1.98E+00	1.44E-01		3.16E+00	6.83E-04	Up							
Unigene12278_All	1315	5.65	11.48	6.60	11.18	11.84	13.50	9.90	13.95	24.90	1.02E+00	6.50E-12	Up	2.24E-01	3.10E-01		8.29E-02	6.22E-01		2.72E-01	4.83E-02		4.95E-01	1.67E-05		1.33E+00	5.51E-47	Up	Unigene12278_All//gi|115454833|ref|NP_001051017.1|//1.00E-106//Os03g0703400 [Oryza sativa Japonica Group] >gi|113549488|dbj|BAF12931.1| Os03g0703400 [Oryza sativa Japonica Group]	Unigene12278_All//8.00E-76//AT4G08500| MEKK1 (MAP KINASE KINASE KINASE 1); DNA binding / MAP kinase kinase kinase/ kinase/ kinase binding / protein binding	Unigene12278_All//0.00E+00//TC163348		ko04626|Plant-pathogen interaction		nr +
Unigene122780_All	261	0.00	0.00	0.00	0.19	0.13	0.00	0.16	0.48	2.90	null	null		null	null		-5.33E-01	8.25E-01		-7.58E+00	6.36E-01		1.57E+00	5.45E-01		4.16E+00	1.34E-04	Up	Unigene122780_All//gi|281486604|gb|ADA70805.1|//5.00E-24//cytochrome P450 CYP71D176 [Scoparia dulcis]	Unigene122780_All//4.00E-18//AT3G61040| CYP76C7; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene122780_All//3.00E-50//ES824538		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene122786_All	261	0.00	0.19	0.00	0.00	0.00	0.17	0.16	0.16	3.97	7.60E+00	6.17E-01		null	null		null	null		7.43E+00	6.97E-01		-1.70E-02	1.00E+00		4.61E+00	2.04E-06	Up	Unigene122786_All//gi|110739553|dbj|BAF01685.1|//3.00E-27//anthranilate phosphoribosyltransferase-like protein [Arabidopsis thaliana]	Unigene122786_All//1.00E-28//AT3G57880| C2 domain-containing protein	Unigene122786_All//2.00E-131//gi|78329612|gb|DT549886.1|DT549886				nr -
Unigene122788_All	262	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	2.28	null	null		null	null		null	null		null	null		7.32E+00	6.35E-01		1.12E+01	1.75E-04	Up			Unigene122788_All//6.00E-67//TC164002				
Unigene12279_All	1762	3.33	5.55	2.96	3.99	5.96	4.23	5.95	7.97	13.75	7.39E-01	5.74E-05		-1.67E-01	5.52E-01		5.80E-01	5.20E-04		8.54E-02	7.20E-01		4.22E-01	1.71E-03		1.21E+00	3.20E-30	Up	Unigene12279_All//gi|297813307|ref|XP_002874537.1|//3.00E-82//MAPKKK9 [Arabidopsis lyrata subsp. lyrata] >gi|297320374|gb|EFH50796.1| MAPKKK9 [Arabidopsis lyrata subsp. lyrata]	Unigene12279_All//2.00E-66//AT4G08480| MAPKKK9; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene12279_All//0.00E+00//TC163348		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0032559	nr -
Unigene122790_All	262	0.00	2.71	0.20	0.00	0.26	0.00	0.00	1.12	3.50	1.14E+01	3.33E-04	Up	7.67E+00	6.37E-01		8.04E+00	6.11E-01		null	null		1.01E+01	2.35E-02		1.18E+01	1.08E-06	Up			Unigene122790_All//2.00E-113//gi|78353304|gb|DT573578.1|DT573578				

Unigene122796_All	262	0.00	0.00	0.00	0.00	0.00	0.00	1.29	7.02	12.01	null	null		null	null		null	null		null	null		2.44E+00	1.59E-06	Up	3.22E+00	2.65E-14	Up	Unigene122796_All//gi|226528218|ref|NP_001149326.1|//6.00E-13//patatin class I [Zea mays] >gi|195626416|gb|ACG35038.1| patatin class I precursor [Zea mays]	Unigene122796_All//3.00E-13//AT4G37060| PLP5 (PATATIN-LIKE PROTEIN 5); nutrient reservoir					nr -
Unigene1228_All	2365	1.24	4.26	1.51	4.00	2.77	3.61	7.97	9.08	3.67	1.78E+00	4.35E-18	Up	2.84E-01	4.09E-01		-5.33E-01	2.42E-03		-1.49E-01	4.99E-01		1.88E-01	1.01E-01		-1.12E+00	2.95E-21	Down	Unigene1228_All//gi|14190431|gb|AAK55696.1|AF378893_1//3.00E-37//AT5g02770/F9G14_80 [Arabidopsis thaliana] >gi|15215889|gb|AAX91488.1| AT5g02770/F9G14_80 [Arabidopsis thaliana]	Unigene1228_All//2.00E-38//AT5G02770| unknown protein	Unigene1228_All//0.00E+00//TC165032				nr +
Unigene122800_All	263	0.00	0.00	0.00	0.00	0.00	0.17	0.64	1.43	4.39	null	null		null	null		null	null		7.42E+00	6.97E-01		1.15E+00	3.27E-01		2.77E+00	5.09E-05	Up		Unigene122800_All//8.00E-08//TC141655					
Unigene122801_All	263	0.40	0.00	0.20	0.38	1.44	0.17	0.32	0.00	2.88	-8.64E+00	3.73E-01		-9.75E-01	7.21E-01		1.93E+00	1.94E-01		-1.14E+00	6.77E-01		-8.33E+00	4.04E-01		3.16E+00	6.83E-04	Up	Unigene122801_All//gi|297838477|ref|XP_002887120.1|//1.00E-16//peptidase [Arabidopsis lyrata subsp. lyrata] >gi|297332961|gb|EFH63379.1| peptidase [Arabidopsis lyrata subsp. lyrata]	Unigene122801_All//2.00E-17//AT1G67420| peptidase	Unigene122801_All//7.00E-42//DR453250				nr +
Unigene122805_All	264	0.00	0.00	0.00	0.00	0.00	0.00	0.80	0.00	16.75	null	null		null	null		null	null		null	null		-9.65E+00	7.45E-02		4.39E+00	4.83E-25	Up		Unigene122805_All//4.00E-145//DT461758					
Unigene122809_All	264	0.79	1.15	0.00	0.19	1.04	3.42	1.76	0.32	1.66	5.39E-01	6.72E-01		-9.63E+00	1.46E-01		2.47E+00	2.23E-01		4.18E+00	1.95E-04	Up	-2.48E+00	3.38E-02		-8.59E-02	9.34E-01		Unigene122809_All//gi|225441874|ref|XP_002278603.1|//3.00E-12//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene122809_All//1.00E-05//AT3G10310| ATP binding / microtubule motor	Unigene122809_All//2.00E-36//CA994011				nr -
Unigene12281_All	1768	0.53	14.07	3.22	1.92	3.82	11.21	3.99	49.60	34.75	4.72E+00	4.12E-116	Up	2.60E+00	7.18E-16	Up	9.95E-01	4.24E-06		2.55E+00	2.82E-58	Up	3.63E+00	0.00E+00	Up	3.12E+00	1.15E-259	Up	Unigene12281_All//gi|9454571|gb|AAF87894.1|AC015447_4//1.00E-137//branched-chain alpha keto-acid dehydrogenase E1 - alpha subunit [Arabidopsis thaliana]	Unigene12281_All//8.00E-125//AT1G21400| 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative	Unigene12281_All//0.00E+00//TC150248		ko00280|Valine, leucine and isoleucine degradation		nr +
Unigene122812_All	264	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.57	null	null		null	null		null	null		null	null		null	null		1.13E+01	4.96E-05	Up		Unigene122812_All//3.00E-07//TC178646					
Unigene12282_All	1790	0.47	20.32	7.35	3.12	7.27	19.13	1.82	32.85	34.83	5.44E+00	1.95E-182	Up	3.97E+00	1.09E-53	Up	1.22E+00	1.52E-15	Up	2.62E+00	1.87E-103	Up	4.18E+00	0.00E+00	Up	4.26E+00	0.00E+00	Up	Unigene12282_All//gi|9454571|gb|AAF87894.1|AC015447_4//0.00E-00//branched-chain alpha keto-acid dehydrogenase E1 - alpha subunit [Arabidopsis thaliana]	Unigene12282_All//2.00E-165//AT1G21400| 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative	Unigene12282_All//0.00E+00//TC179203		ko00280|Valine, leucine and isoleucine degradation	GO:0016903	nr +
Unigene122822_All	265	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.32	2.41	null	null		null	null		null	null		null	null		9.84E-01	7.32E-01		3.91E+00	7.65E-04	Up	Unigene122822_All//gi|300793630|tpg|BAA33874.1|//8.00E-16//TPA: TPA_inf: aquaporin NIP1:1 [Gossypium hirsutum]	Unigene122822_All//7.00E-10//AT4G18910| NIP1;2 (NOD26-LIKE INTRINSIC PROTEIN 1;2); arsenite transmembrane transporter/ water channel	Unigene122822_All//2.00E-11//TC166706				nr +
Unigene122824_All	265	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.10	null	null		null	null		null	null		null	null		null	null		1.10E+01	3.28E-04	Up							
Unigene12283_All	319	1.97	1.43	3.84	5.47	5.29	8.92	4.24	13.36	3.50	-4.61E-01	6.19E-01		9.64E-01	1.38E-01		-4.72E-02	9.17E-01		7.07E-01	6.27E-02		1.66E+00	6.62E-09	Up	-2.79E-01	6.04E-01		Unigene12283_All//gi|187942421|gb|ACD40019.1|//1.00E-41//DNase 2 [Eucommia ulmoides] >gi|187942425|gb|ACD40021.1| DNase 2 [Eucommia ulmoides]	Unigene12283_All//1.00E-40//AT2G40410| Ca(2+)-dependent nuclease, putative	Unigene12283_All//9.00E-150//gi|164328432|gb|ES803489.1|ES803489			GO:0004518//GO:0006412//GO:0016876//GO:0032559//GO:0044424	nr -
Unigene122830_All	265	0.00	0.19	0.00	0.38	1.17	0.34	0.64	0.16	8.87	7.58E+00	6.17E-01		null	null		1.64E+00	3.21E-01		-1.41E-01	9.51E-01		-2.02E+00	3.67E-01		3.80E+00	2.43E-12	Up	Unigene122830_All//gi|110931846|gb|ABB02922.1|//3.00E-17//MYB transcription factor MYB122 [Glycine max]	Unigene122830_All//4.00E-12//AT3G01140| MYB106 (myb domain protein 106); DNA binding / transcription factor	Unigene122830_All//4.00E-59//DN817124	MYB			nr +
Unigene122831_All	266	0.00	0.00	0.00	0.00	0.00	0.00	4.29	0.94	10.03	null	null		null	null		null	null		null	null		-2.19E+00	6.84E-04	Down	1.23E+00	3.61E-04	Up	Unigene122831_All//gi|147781907|emb|CAN68929.1|//8.00E-06//hypothetical protein [Vitis vinifera]						nr -
Unigene122834_All	266	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.16	5.99	null	null		null	null		null	null		null	null		7.30E+00	6.35E-01		1.25E+01	1.85E-11	Up		Unigene122834_All//3.00E-07//TC173686					
Unigene122835_All	266	4520.05	20492.74	13382.56	5328.06	4068.54	5370.20	220.78	293.83	106.94	2.18E+00	0.00E+00	Up	1.57E+00	0.00E+00	Up	-3.89E-01	1.41E-233		1.14E-02	5.21E-01		4.12E-01	4.49E-15		-1.05E+00	9.83E-58	Down	Unigene122835_All//gi|56121699|gb|AAV74186.1|//6.00E-38//metallothionein-like protein [Gossypium hirsutum]	Unigene122835_All//1.00E-07//AT3G09390| MT2A (METALLOTHIONEIN 2A); copper ion binding	Unigene122835_All//2.00E-141//TC170238				nr +
Unigene122837_All	266	0.20	0.00	0.00	0.00	1.29	0.34	0.79	0.63	37.89	-7.62E+00	6.13E-01		-7.62E+00	6.25E-01		1.03E+01	3.01E-02		8.41E+00	4.77E-01		-3.39E-01	8.12E-01		5.58E+00	6.45E-64	Up							
Unigene122838_All	266	0.20	2.86	0.20	0.00	0.00	0.00	0.16	0.00	2.40	3.86E+00	1.33E-03		2.54E-02	9.95E-01		null	null		null	null		-7.31E+00	6.58E-01		3.91E+00	7.65E-04	Up		Unigene122838_All//3.00E-10//TC157063					
Unigene12284_All	644	0.57	1.73	2.56	2.94	1.82	2.17	3.22	5.45	1.18	1.61E+00	1.95E-02		2.17E+00	3.37E-04	Up	-6.93E-01	1.33E-01		-4.35E-01	4.01E-01		7.61E-01	9.51E-03		-1.45E+00	3.18E-04	Down	Unigene12284_All//gi|60476854|gb|AAX21543.1|//2.00E-48//Ca(2+)-dependent DNase [Populus tomentosa]	Unigene12284_All//2.00E-37//AT2G40410| Ca(2+)-dependent nuclease, putative	Unigene12284_All//0.00E+00//TC165075			GO:0000166//GO:0006412//GO:0016788	nr -
Unigene122841_All	267	0.00	0.00	0.00	0.00	0.00	0.34	0.16	0.94	2.69	null	null		null	null		null	null		8.40E+00	4.77E-01		2.57E+00	1.53E-01		4.08E+00	2.41E-04	Up	Unigene122841_All//gi|7523705|gb|AF63144.1|AC011001_14//6.00E-27//Similar to maize transposon mmdrA protein [Arabidopsis thaliana] >gi|46518483|gb|AAS99723.1| At1g06740 [Arabidopsis thaliana] >gi|62319905|dbj|BAD93972.1| mmdrA-like protein [Arabidopsis thaliana]	Unigene122841_All//4.00E-10//AT1G64260| zinc finger protein-related					nr +
Unigene122846_All	267	0.00	0.00	0.00	0.00	0.13	0.00	0.00	0.00	4.03	null	null		null	null		7.01E+00	8.31E-01		null	null		null	null		1.20E+01	8.30E-08	Up		Unigene122846_All//8.00E-08//ES816770					
Unigene122847_All	268	0.00	0.00	0.00	0.37	0.26	0.34	0.00	0.47	2.23	null	null		null	null		-5.32E-01	8.17E-01		-1.41E-01	9.51E-01		8.87E+00	2.40E-01		1.11E+01	1.75E-04	Up							
Unigene122848_All	268	0.00	0.00	0.00	0.00	0.00	0.00	97.34	97.47	23.93	null	null		null	null		null	null		null	null		2.00E-03	1.02E+00		-2.02E+00	1.41E-68	Down		Unigene122848_All//6.00E-24//ES790725					
Unigene12285_All	1315	2.63	2.50	3.32	5.42	4.11	3.19	5.24	12.65	1.88	-6.83E-02	8.37E-01		3.39E-01	2.81E-01		-3.98E-01	6.80E-02		-7.62E-01	3.89E-04		1.27E+00	3.54E-22	Up	-1.48E+00	2.19E-12	Down	Unigene12285_All//gi|2501231|sp|Q39635.1|X38K_CORSE//1.00E-106//RecName: Full=Uncharacterized 38.1 kDa protein >gi|444333|prf||1906382A pCSC71 protein	Unigene12285_All//8.00E-61//AT2G40410| Ca(2+)-dependent nuclease, putative	Unigene12285_All//0.00E+00//TC165075			GO:0000166//GO:0006412//GO:0016788	nr +
Unigene122850_All	268	65.01	69.58	60.80	37.55	41.76	36.57	22.40	48.03	27.50	9.79E-02	5.03E-01		-9.66E-02	5.46E-01		1.53E-01	4.49E-01		-3.81E-02	8.61E-01		1.10E+00	5.85E-14	Up	2.96E-01	1.29E-01		Unigene122850_All//gi|51980218|gb|AAU20773.1|//4.00E-35//late elongated hypocotyl [Castanea sativa]	Unigene122850_All//8.00E-06//AT1G01060| LHY (LATE ELONGATED HYPOCOTYL); DNA binding / transcription factor	Unigene122850_All//3.00E-140//gi|78341309|gb|DT561583.1|DT561583	MYB-related	ko04712|Circadian rhythm - plant		nr -
Unigene12853_All	268	0.00	0.00	0.00	0.00	0.00	0.00	0.16	0.16	2.38	null	null		null	null		null	null		null	null		-1.66E-02	1.00E+00		3.91E+00	7.65E-04	Up	Unigene12853_All//gi|77554179|gb|ABA96973.1|//5.00E-16//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene12853_All//8.00E-16//AT1G32120| unknown protein					nr -
Unigene12286_All	1417	3.73	1.79	2.22	3.97	4.06	7.49	6.86	15.63	3.68	-1.06E+00	5.92E-05	Down	-7.50E-01	5.62E-03		3.09E-02	9.25E-01		9.15E-01	1.31E-07		1.19E+00	2.20E-26	Up	-8.98E-01	3.38E-08		Unigene12286_All//gi|60476854|gb|AAX21543.1|//1.00E-130//Ca(2+)-dependent DNase [Populus tomentosa]	Unigene12286_All//2.00E-107//AT2G40410| Ca(2+)-dependent nuclease, putative	Unigene12286_All//0.00E+00//gi|48792302|gb|CO093616.1|CO093616				nr +
Unigene122866_All	270	0.00	0.00	0.00	0.37	0.00	0.00	0.47	2.63	19.92	null	null		null	null		-8.53E+00	3.14E-01		-8.53E+00	4.01E-01		2.49E+00	5.53E-03		5.41E+00	7.85E-34	Up		Unigene122866_All//6.00E-58//TC165754					
Unigene12287_All	2675	10.70	26.27	19.19	16.56	21.20	26.91	14.92	19.97	23.86	1.30E+00	1.21E-76	Up	8.43E-01	2.97E-27		3.57E-01	3.40E-08		7.01E-01	1.00E-30		4.20E-01	6.36E-11		6.77E-01	3.71E-30		Unigene12287_All//gi|18418600|ref|NP_567980.1|//0.00E+00//BSK1 (BR-SIGNALING KINASE 1); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|75331881|sp|Q944A7.1|Y4523_ARATH RecName: Full=Probable serine/threonine-protein kinase At4g35230 >gi|16612249|gb|AAL27496.1|AF439824_1 AT4g35230/F23E12_210 [Arabidopsis thaliana] >gi|22655470|gb|AAM98327.1| At4g35230/F23E12_210 [Arabidopsis thaliana]	Unigene12287_All//0.00E+00//AT4G35230| BSK1 (BR-SIGNALING KINASE 1); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase	Unigene12287_All//0.00E+00//TC151049			GO:0004672//GO:0004871//GO:0006464//GO:0016020//GO:0016787//GO:0032559//GO:0043231//GO:0043401//GO:0045229	nr +
Unigene122872_All	271	0.00	0.00	0.00	0.00	0.00	0.00	1.09	1.08	7.20	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		2.72E+00	7.37E-08	Up							
Unigene122873_All	271	0.00	0.00	0.00	0.00	0.00	0.00	0.47	0.00	3.23	null	null		null	null		null	null		null	null		-8.87E+00	2.36E-01		2.79E+00	5.37E-04	Up							ESTscan +
Unigene122874_All	271	0.00	0.00	0.00	0.00	0.00	0.00	425.30	1292.12	20.73	null	null		null	null		null	null		null	null		1.60E+00	0.00E+00	Up	-4.36E+00	0.00E+00	Down							
Unigene122876_All	271	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.35	null	null		null	null		null	null		null	null		null	null		1.12E+01	9.34E-05	Up							
Unigene122883_All	272	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.05	null	null		null	null		null	null		null	null		null	null		1.10E+01	3.28E-04	Up							
Unigene122886_All	272	0.00	0.37	0.00	0.37	0.25	0.17	0.00	0.15	2.20	8.54E+00	3.88E-01		null	null		-5.33E-01	8.17E-01		-1.14E+00	6.77E-01		7.26E+00	6.35E-01		1.11E+01	1.75E-04	Up		Unigene122886_All//4.00E-65//gi|82756621|gb|DV850183.1|DV850183					
Unigene122888_All	273	0.00	0.00	0.00	0.18	0.76	0.00	0.15	0.92	2.63	null	null		null	null		2.05E+00	3.95E-01		-7.51E+00	6.36E-01		2.57E+00	1.53E-01		4.08E+00	2.41E-04	Up							
Unigene122899_All	274	9.55	19.79	9.72	6.91	5.91	10.38	8.64	46.07	11.20	1.05E+00	5.58E-05	Up	2.54E-02	9.67E-01		-2.26E-01	6.37E-01		5.88E-01	1.29E-01		2.41E+00	2.93E-40	Up	3.74E-01	2.41E-01		Unigene122899_All//gi|15225601|ref|NP_179032.1|//2.00E-11//ALD06B2; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase [Arabidopsis thaliana] >gi|118582304|sp|Q0WM29.2|MMSA_ARATH RecName: Full=Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial; Short=Malonate-semialdehyde dehydrogenase [acylating]; Short=MMSDH; Short=MM-ALDH; AltName: Full=Aldehyde dehydrogenase family 6 member B2; Flags: Precursor	Unigene122899_All//9.00E-13//AT2G14170| ALD06B2; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase	Unigene122899_All//7.00E-73//TC175258		ko00562|Inositol phosphate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism		nr +
Unigene122900_All	274	0.00	0.00	0.00	0.36	0.00	0.00	0.00	0.61	6.69	null	null		null	null		-8.51E+00	3.14E-01		-8.51E+00	4.01E-01		9.25E+00	1.39E-01		1.27E+01	3.75E-13	Up							
Unigene122902_All	274	5.54	8.14	6.61	9.64	9.55	9.07	9.72	19.83	26.32	5.55E-01	2.02E-01		2.55E-01	6.40E-01		-1.27E-02	9.66E-01		-8.80E-02	8.32E-01		1.03E+00	8.89E-06	Up	1.44E+00	2.86E-12	Up	Unigene122902_All//gi|189163920|gb|ACD77110.1|//4.00E-19//protein kinase 1b [Solanum lycopersicum]	Unigene122902_All//2.00E-19//AT5G02290| NAK; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene122902_All//1.00E-55//DR462408		ko04626|Plant-pathogen interaction		nr +
Unigene122905_All	274	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.46	2.04	null	null		null	null		null	null		7.36E+00	6.97E-01		8.84E+00	2.40E-01		1.10E+01	3.28E-04	Up		Unigene122905_All//4.00E-139//gi|109884562|gb|DW513532.1|DW513532					
Unigene122906_All	274	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.31	2.33	null	null		null	null		null	null		null	null		8.25E+00	4.02E-01		1.12E+01	9.34E-05	Up	Unigene122906_All//gi|37651066|emb|CAE02593.1|//1.00E-28//SYM10 protein [Pisum sativum] >gi|376510068|emb|CAE02594.1| SYM10 protein [Pisum sativum]	Unigene122906_All//2.00E-19//AT2G25220| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase			ko04626|Plant-pathogen interaction		nr -
Unigene12291_All	1812	54.40	41.30	24.16	19.57	21.84	21.29	22.94	23.00	30.08	-3.97E-01	1.82E-14		-1.17E+00	5.64E-89	Down	1.58E-01	8.18E-02		1.21E-01	2.28E-01		3.80E-03	1.00E+00		3.91E-01	4.06E-10		Unigene12291_All//gi|22326830|ref|NP_197090.2|//1.00E-172//ATPCME (PRENYLCYSTEINE METHYLESTERASE); prenylcysteine methylesterase [Arabidopsis thaliana]	Unigene12291_All//6.00E-174//AT5G15860| ATPCME (PRENYLCYSTEINE METHYLESTERASE); prenylcysteine methylesterase	Unigene12291_All//0.00E+00//TC130299				nr -
Unigene122910_All	275	0.00	0.00	0.00	0.18	0.25	0.33	0.62	1.22	6.95	null	null		null	null		4.67E-01	9.58E-01		8.59E-01	7.95E-01		9.83E-01	4.24E-01		3.50E+00	1.45E-09	Up							
Unigene122915_All	276	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.03	null	null		null	null		null	null		null	null		null	null		1.16E+01	3.88E-06	Up	Unigene122915_All//gi|299471119|emb|CBN78977.1|//2.00E-06//beta strand repeat-containing protein [Ectocarpus siliculosus]						nr -

Unigene122916_All	276	0.00	0.00	0.00	0.00	0.00	0.33	0.00	1.06	2.02	null	null		null	null		null	null		8.35E+00	4.77E-01		1.00E+01	2.35E-02		1.10E+01	3.28E-04	Up							
Unigene122919_All	276	0.00	0.00	0.00	0.00	0.00	0.33	0.00	0.00	4.04	null	null		null	null		null	null		8.35E+00	4.77E-01		null	null		1.20E+01	4.36E-08	Up							
Unigene12292_All	1986	44.05	34.29	43.89	40.93	67.59	53.33	24.21	10.31	11.69	-3.61E-01	5.92E-11		-5.10E-03	9.57E-01		7.23E-01	1.50E-66		3.82E-01	2.76E-15		-1.23E+00	1.18E-59	Down	-1.05E+00	1.10E-47	Down	Unigene12292_All//gi|42569717|ref|NP_181337.2|//0.00E+00//ceramidase family protein [Arabidopsis thaliana] >gi|110810580|sp|Q304B9.1|NCASE_ARATH RecName: Full=Neutral ceramidase; Short=N-CDase; Short=NCDase; AltName: Full=Acylsphingosine deacylase; AltName: Full=N-acylsphingosine amidohydrolase; Flags: Precursor	Unigene12292_All//0.00E+00//AT2G38010| ceramidase family protein	Unigene12292_All//0.00E+00//TC148564			GO:0016020//GO:0016811	nr +
Unigene12922_All	276	0.00	0.00	0.00	0.00	0.00	0.16	0.46	0.30	3.03	null	null		null	null		null	null		7.35E+00	6.97E-01		-6.02E-01	7.67E-01		2.72E+00	8.98E-04	Up							
Unigene122926_All	277	0.19	0.00	0.00	0.00	0.00	0.00	0.15	0.15	2.88	-7.56E+00	6.13E-01		-7.56E+00	6.25E-01		null	null		null	null		-1.62E-02	1.00E+00		4.24E+00	7.42E-05	Up							
Unigene12293_All	2770	26.35	22.33	24.30	26.63	36.91	29.48	10.94	7.89	5.16	-2.39E-01	1.11E-04		-1.17E-01	9.33E-02		4.71E-01	9.98E-24		1.46E-01	1.59E-02		-4.72E-01	6.42E-08		-1.08E+00	5.38E-32	Down	Unigene12293_All//gi|42569717|ref|NP_181337.2|//0.00E+00//ceramidase family protein [Arabidopsis thaliana] >gi|110810580|sp|Q304B9.1|NCASE_ARATH RecName: Full=Neutral ceramidase; Short=N-CDase; Short=NCDase; AltName: Full=Acylsphingosine deacylase; AltName: Full=N-acylsphingosine amidohydrolase; Flags: Precursor	Unigene12293_All//0.00E+00//AT2G38010| ceramidase family protein	Unigene12293_All//0.00E+00//TC145645			GO:0016020//GO:0016811	nr -
Unigene12931_All	278	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.00	3.73	null	null		null	null		null	null		null	null		-7.25E+00	6.58E-01		4.61E+00	2.03E-06	Up	Unigene12931_All//gi|15236188|ref|NP_195203.1|//1.00E-21//auxin-responsive family protein [Arabidopsis thaliana]	Unigene12931_All//4.00E-23//AT4G34770| auxin-responsive family protein						nr +
Unigene12932_All	278	0.19	0.00	0.00	0.00	0.37	1.14	17.03	11.73	52.02	-7.56E+00	6.13E-01		-7.56E+00	6.25E-01		8.54E+00	4.56E-01		1.02E+01	4.08E-02		-5.39E-01	3.08E-02		1.61E+00	6.30E-28	Up			Unigene12932_All//1.00E-65//DT049252					
Unigene12937_All	278	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.35	2.01	null	null		null	null		null	null		null	null		1.04E+01	6.86E-03		1.10E+01	3.28E-04	Up			Unigene12937_All//8.00E-113//ES810677					ESTscan +
Unigene12294_All	1672	8.76	174.65	13.50	14.21	20.22	20.20	21.72	67.54	79.01	4.32E+00	0.00E+00	Up	6.24E-01	1.44E-07		5.09E-01	2.58E-09		5.08E-01	1.53E-08		1.64E+00	3.47E-213	Up	1.86E+00	1.43E-304	Up	Unigene12294_All//gi|225461088|ref|XP_002282119.1|//0.00E+00//PREDICTED: similar to polyubiquitin [Vitis vinifera]	Unigene12294_All//0.00E+00//AT4G05320| UBQ10 (POLYUBIQUITIN 10); protein binding	Unigene12294_All//0.00E+00//TC132757			GO:0010033//GO:0032502//GO:0043231//GO:0043412	nr +
Unigene122940_All	279	0.00	0.00	0.00	0.00	0.00	0.00	0.15	0.30	2.28	null	null		null	null		null	null		null	null		9.84E-01	7.32E-01		3.91E+00	7.65E-04	Up	Unigene122940_All//gi|115485953|ref|NP_001068120.1|//1.00E-12//Os11g0570000 [Oryza sativa Japonica Group] >gi|113645342|dbj|BAF28483.1|Os11g0570000 [Oryza sativa Japonica Group]	Unigene122940_All//6.00E-09//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction		nr +
Unigene122944_All	279	0.19	0.00	0.19	0.71	0.12	0.65	0.00	0.30	2.14	-7.55E+00	6.13E-01		2.59E-02	9.95E-01		-2.53E+00	2.34E-01		-1.41E-01	9.35E-01		8.23E+00	4.02E-01		1.11E+01	1.75E-04	Up							
Unigene122947_All	280	4956.46	2436.66	4304.12	6447.92	6599.40	5230.08	919.75	413.78	479.49	-1.02E+00	0.00E+00	Down	-2.04E-01	3.83E-53		3.35E-02	4.37E-03		-3.02E-01	3.38E-163		-1.15E+00	3.68E-285	Down	-9.40E-01	8.96E-210		Unigene122947_All//gi|167367|gb|AAA99868.1|//1.00E-48//peroxidase [Gossypium hirsutum]	Unigene122947_All//2.00E-42//AT4G21960| PRXR1; electron carrier/ heme binding / peroxidase	Unigene122947_All//8.00E-156//gi|13246718|gb|BE053818.2|BE053818		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene122951_All	280	0.56	0.36	0.19	0.00	0.49	0.97	0.60	1.49	3.41	-6.31E-01	7.28E-01		-1.56E+00	5.33E-01		8.94E+00	3.19E-01		9.92E+00	7.03E-02		1.31E+00	2.34E-01		2.50E+00	6.42E-04	Up							
Unigene122957_All	281	0.00	1.44	0.00	0.00	0.12	0.00	0.00	0.15	2.27	1.05E+01	1.36E-02		null	null		6.94E+00	8.31E-01		null	null		7.22E+00	6.35E-01		1.11E+01	9.34E-05	Up	Unigene122957_All//gi|255560351|ref|XP_002521191.1|//4.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223539605|gb|EEF41191.1| conserved hypothetical protein [Ricinus communis]		Unigene122957_All//4.00E-16//gi|78348151|gb|DT568425.1|DT568425				nr +
Unigene122959_All	281	0.00	0.00	0.00	0.00	0.00	0.00	0.75	0.60	9.36	null	null		null	null		null	null		null	null		-3.38E-01	8.12E-01		3.64E+00	2.63E-13	Up	Unigene122959_All//gi|225443192|ref|XP_002269242.1|//3.00E-08//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene122960_All	281	0.00	0.00	0.00	0.00	0.12	0.00	1.66	3.12	19.00	null	null		null	null		6.94E+00	8.31E-01		null	null		9.16E-01	1.77E-01		3.52E+00	1.02E-25	Up							
Unigene122963_All	281	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.41	null	null		null	null		null	null		null	null		null	null		1.12E+01	4.96E-05	Up							ESTscan -
Unigene122964_All	281	0.00	0.00	0.19	1.06	0.74	0.48	0.00	0.15	3.69	null	null		7.57E+00	6.37E-01		-5.33E-01	6.79E-01		-4.14E+00	4.58E-01		7.22E+00	6.35E-01		1.18E+01	1.58E-07	Up			Unigene122964_All//3.00E-07//ES804901					
Unigene122965_All	282	0.00	0.00	0.00	0.00	0.49	0.32	0.90	0.44	4.66	null	null		null	null		8.93E+00	3.19E-01		8.32E+00	4.77E-01		-1.02E+00	4.95E-01		2.37E+00	7.20E-05	Up							
Unigene122966_All	282	0.00	0.00	0.00	0.00	0.00	0.00	1.20	0.44	4.80	null	null		null	null		null	null		null	null		-1.43E+00	2.59E-01		2.00E+00	3.24E-04	Up			Unigene122966_All//3.00E-07//CD488231					
Unigene122967_All	282	507.44	129.19	102.72	56.00	30.89	23.54	62.67	26.09	53.68	-1.97E+00	7.33E-287	Down	-2.30E+00	0.00E+00	Down	-8.58E-01	3.37E-11		-1.25E+00	3.88E-18	Down	-1.26E+00	2.30E-23	Down	-2.23E-01	6.30E-02		Unigene122967_All//gi|3094012|gb|AAC15460.1|//6.00E-35//cold-regulated LTC0812 [Lavatera thuringiaca]	Unigene122967_All//1.00E-29//AT1G75750| GASA1 (GAST1 PROTEIN HOMOLOG 1)	Unigene122967_All//3.00E-155//TC168295				nr +
Unigene122969_All	282	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.89	1.98	null	null		null	null		null	null		null	null		9.80E+00	4.31E-02		1.09E+01	3.28E-04	Up	Unigene122969_All//gi|15237301|ref|NP_197728.1|//6.00E-32//GRAM domain-containing protein / ABA-responsive protein-related [Arabidopsis thaliana] >gi|75171743|sp|Q9FW84.1|GEML8_ARATH RecName: Full=Putative GEM-like protein 8	Unigene122969_All//3.00E-33//AT5G23370| GRAM domain-containing protein / ABA-responsive protein-related	Unigene122969_All//1.00E-83//ES832934				nr +
Unigene12297_All	1090	23.38	24.08	22.13	38.48	29.38	38.12	28.82	18.98	13.30	4.28E-02	7.18E-01		-7.90E-02	5.50E-01		-3.89E-01	2.47E-07		-1.36E-02	9.08E-01		-6.03E-01	2.79E-12		-1.12E+00	1.18E-34	Down	Unigene12297_All//gi|297833906|ref|XP_002884835.1|//1.00E-111//PHD finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330675|gb|EFH61094.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12297_All//1.00E-100//AT3G11200| AL2 (ALFIN-LIKE 2); DNA binding / methylated histone residue binding	Unigene12297_All//0.00E+00//TC135306	Alfin-like		GO:0046914	nr -
Unigene122982_All	284	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.96	null	null		null	null		null	null		null	null		null	null		1.09E+01	3.28E-04	Up							
Unigene122989_All	284	0.00	0.00	0.00	0.00	0.00	0.00	0.45	0.15	5.33	null	null		null	null		null	null		null	null		-1.60E+00	5.34E-01		3.58E+00	7.96E-08	Up	Unigene122989_All//gi|227204287|dbj|BAU56995.1|//4.00E-10//AT4G18950 [Arabidopsis thaliana]	Unigene122989_All//2.00E-11//AT4G18950| ankyrin protein kinase, putative	Unigene122989_All//6.00E-55//TC157027				nr +
Unigene122992_All	285	0.37	0.00	0.19	0.00	0.00	0.00	0.74	0.29	4.33	-8.52E+00	3.73E-01		-9.75E-01	7.21E-01		null	null		null	null		-1.34E+00	4.30E-01		2.55E+00	6.27E-05	Up	Unigene122992_All//gi|224054164|ref|XP_002298123.1|//4.00E-33//pleiotropic drug resistance, ABC transporter family protein [Populus trichocarpa] >gi|222845381|gb|EEE82928.1| pleiotropic drug resistance, ABC transporter family protein [Populus trichocarpa]	Unigene122992_All//4.00E-30//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances					nr +
Unigene122998_All	285	0.00	0.00	0.00	0.87	1.69	1.90	0.74	1.32	3.63	null	null		null	null		9.53E-01	4.24E-01		1.12E+00	3.05E-01		8.31E-01	4.67E-01		2.29E+00	7.17E-04	Up			Unigene122998_All//1.00E-105//TC155690					
Unigene122999_All	285	0.18	0.00	0.75	0.00	0.00	0.00	0.00	0.00	2.10	-7.52E+00	6.13E-01		2.03E+00	3.61E-01		null	null		null	null		null	null		1.10E+01	1.75E-04	Up							
Unigene123_All	3508	3.89	2.22	4.17	3.81	3.69	7.88	16.48	21.40	21.11	-8.07E-01	1.40E-07		1.01E-01	5.70E-01		-4.42E-02	8.39E-01		1.05E+00	1.62E-23	Up	3.77E-01	2.03E-12		3.58E-01	1.66E-11		Unigene123_All//gi|60327635|gb|AAX19057.1|//0.00E+00//class III HD-Zip protein 8 [Populus trichocarpa]	Unigene123_All//0.00E+00//AT4G32880| ATHB-8 (HOMEOBOX GENE 8); DNA binding / transcription factor	Unigene123_All//0.00E+00//TC178623	HB			nr -
Unigene123000_All	285	1.10	1.07	0.00	0.00	0.24	0.00	0.00	0.00	2.52	-4.63E-02	9.85E-01		-1.01E+01	4.92E-02		7.92E+00	6.11E-01		null	null		null	null		1.13E+01	2.63E-05	Up							
Unigene123004_All	286	0.00	0.00	0.00	0.00	0.24	0.47	1.63	0.73	12.54	null	null		null	null		7.91E+00	6.11E-01		8.89E+00	3.11E-01		-1.15E+00	2.53E-01		2.95E+00	5.95E-15	Up							
Unigene123006_All	286	2.38	7.44	1.49	2.26	6.14	7.42	0.00	1.61	5.15	1.65E+00	4.95E-04	Up	-6.75E-01	4.41E-01		1.44E+00	4.16E-03		1.71E+00	2.72E-04	Up	1.07E+01	1.94E-03		1.23E+01	1.30E-10	Up							
Unigene123008_All	286	0.73	0.35	0.19	0.17	0.24	1.42	0.30	1.17	4.88	-1.05E+00	5.65E-01		-1.97E+00	3.81E-01		4.67E-01	9.58E-01		3.03E+00	6.03E-02		1.98E+00	1.44E-01		4.04E+00	7.22E-08	Up	Unigene123008_All//gi|148562451|gb|ABQ88337.1|//3.00E-09//OAS-TL3 cysteine synthase [Glycine max] >gi|148562454|gb|ABQ88338.1| OAS-TL3 cysteine synthase [Glycine max]	Unigene123008_All//8.00E-09//AT3G61440| CYSC1 (CYSTEINE SYNTHASE C1); L-3-cyanoalanine synthase/ cysteine synthase	Unigene123008_All//8.00E-156//gi|13356009|gb|BG446357.1|BG446357		ko00270|Cysteine and methionine metabolism//ko00460|Cyanoamino acid metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr +
Unigene123009_All	286	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.23	null	null		null	null		null	null		null	null		null	null		1.11E+01	9.34E-05	Up							
Unigene123012_All	287	0.00	0.35	0.00	0.00	0.24	0.00	0.15	0.44	5.55	8.46E+00	3.88E-01		null	null		7.91E+00	6.11E-01		null	null		1.57E+00	5.45E-01		5.24E+00	3.60E-10	Up	Unigene123012_All//gi|297820588|ref|XP_002878177.1|//9.00E-20//C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297324015|gb|EFH54436.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene123012_All//7.00E-21//AT3G57850| C2 domain-containing protein	Unigene123012_All//6.00E-95//gi|78329612|gb|DT549886.1|DT549886				nr -
Unigene123013_All	287	0.55	0.00	0.00	0.00	0.12	0.00	0.00	0.44	3.05	-9.10E+00	2.16E-01		-9.10E+00	2.45E-01		6.91E+00	8.31E-01		null	null		8.77E+00	2.40E-01		1.16E+01	2.05E-06	Up			Unigene123013_All//3.00E-07//EX165270					
Unigene123014_All	287	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.94	null	null		null	null		null	null		null	null		null	null		1.09E+01	3.28E-04	Up							
Unigene12302_All	240	4.36	3.80	0.44	1.25	4.02	0.75	0.70	1.04	0.00	-1.98E-01	7.41E-01		-3.30E+00	4.59E-04	Down	1.69E+00	2.52E-02		-7.27E-01	6.39E-01		5.68E-01	6.74E-01		-9.46E+00	1.08E-01		Unigene12302_All//gi|15224445|ref|NP_181346.1|//1.00E-22//GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase [Arabidopsis thaliana] >gi|71159388|sp|Q80437.1|GPAT6_ARATH RecName: Full=Glycerol-3-phosphate acyltransferase 6; Short=AtGPAT6 >gi|17065290|gb|AAL32799.1| Unknown protein [Arabidopsis thaliana]	Unigene12302_All//5.00E-23//AT2G38110| GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase	Unigene12302_All//1.00E-89//gi|48744430|gb|CO074949.1|CO074949		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0006633//GO:0009791//GO:0016411//GO:0044464	nr -
Unigene123020_All	288	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.73	null	null		null	null		null	null		null	null		null	null		1.19E+01	8.30E-08	Up							
Unigene123022_All	288	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.29	2.07	null	null		null	null		null	null		null	null		8.18E+00	4.02E-01		1.10E+01	1.75E-04	Up							
Unigene123025_All	288	0.18	0.35	0.18	0.00	0.12	1.88	0.15	0.73	2.49	9.54E-01	7.26E-01		2.52E-02	9.95E-01		6.90E+00	8.31E-01		1.09E+01	2.46E-03		2.31E+00	2.40E-01		4.08E+00	2.41E-04	Up							
Unigene123029_All	289	0.91	0.35	0.00	0.00	0.00	0.00	0.15	0.00	8.13	-1.37E+00	3.83E-01		-9.82E+00	8.58E-02		null	null		null	null		-7.19E+00	6.58E-01		5.80E+00	2.21E-15	Up							
Unigene12303_All	1141	37.05	6.17	9.75	10.35	10.56	2.61	3.78	2.64	1.19	-2.59E+00	1.64E-118	Down	-1.93E+00	1.66E-79	Down	2.98E-02	8.84E-01		-1.99E+00	2.34E-26	Down	-5.19E-01	4.92E-02		-1.67E+00	1.87E-09	Down	Unigene12303_All//gi|226530011|ref|NP_001149307.1|//1.00E-134//LOC100282930 [Zea mays] >gi|195626246|gb|ACG34953.1| glycerol-3-phosphate acyltransferase 8 [Zea mays]	Unigene12303_All//8.00E-114//AT2G38110| GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase	Unigene12303_All//0.00E+00//TC177537		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr +
Unigene123030_All	289	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.00	2.48	null	null		null	null		null	null		7.29E+00	6.96E-01		null	null		1.13E+01	2.63E-05	Up			Unigene123030_All//6.00E-21//FL577227					
Unigene123033_All	289	0.00	0.00	0.00	0.00	0.00	0.16	0.15	0.43	3.03	null	null		null	null		null	null		7.29E+00	6.96E-01		1.57E+00	5.45E-01		4.37E+00	2.26E-05	Up							
Unigene123036_All	290	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.58	2.06	null	null		null	null		null	null		null	null		9.17E+00	1.39E-01		1.10E+01	1.75E-04	Up	Unigene123036_All//gi|56202191|dbj|BAD73674.1|//4.00E-08//S-receptor kinase-like [Oryza sativa Japonica Group] >gi|56202248|dbj|BAD73689.1| S-receptor kinase-like [Oryza sativa Japonica Group]					GO:0004672	nr -
Unigene123039_All	290	0.00	0.00	0.00	0.17	0.00	0.31	0.00	0.00	2.34	null	null		null	null		-7.42E+00	5.56E-01		8.59E-01	7.95E-01		null	null		1.12E+01	4.96E-05	Up	Unigene123039_All//gi|255558180|ref|XP_002520117.1|//2.00E-06//Protein kinase APK1A, chloroplast precursor, putative [Ricinus communis] >gi|223540609|gb|EEF42172.1| Protein kinase APK1A, chloroplast precursor, putative [Ricinus communis]	Unigene123039_All//7.00E-07//AT1G14370| APK2A (PROTEIN KINASE 2A); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase				GO:0004672	nr +

Unigene12304_All	1766	176.31	197.48	151.49	27.64	42.08	47.57	18.60	17.16	5.91	1.64E-01	1.10E-09		-2.19E-01	3.94E-14		6.06E-01	3.78E-27		7.83E-01	3.01E-43		-1.17E-01	2.31E-01		-1.65E+00	1.82E-65	Down	Unigene12304_All//gi|297827363|ref|XP_002881564.1|//0.00E+00//glycerol-3-phosphate acyltransferase 6 [Arabidopsis lyrata subsp. lyrata] >gi|297327403|gb|EFH57823.1| glycerol-3-phosphate acyltransferase 6 [Arabidopsis lyrata subsp. lyrata]	Unigene12304_All//0.00E+00//AT2G38110| GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase	Unigene12304_All//0.00E+00//TC151567		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0006633//GO:0009791//GO:0016411//GO:0044464	nr -
Unigene12043_All	290	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.79	null	null		null	null		null	null		null	null		null	null		1.08E+01	6.13E-04	Up								
Unigene12305_All	1609	21.20	13.29	11.12	15.39	12.63	13.02	12.82	3.87	3.89	-6.74E-01	3.71E-13		-9.31E-01	1.67E-21		-2.85E-01	7.55E-03		-2.41E-01	3.61E-02		-1.73E+00	1.00E-42	Down	-1.72E+00	8.04E-44	Down	Unigene12305_All//gi|294992380|gb|ADF57328.1|//1.00E-117//1,2-diacyl-sn-glycerol:acyl-CoA acyltransferase 2 [Euonymus alatus]	Unigene12305_All//7.00E-101//AT3G51520| diacylglycerol acyltransferase family	Unigene12305_All//0.00E+00//TC156146				nr -
Unigene123050_All	291	0.72	6.09	0.18	1.71	1.54	0.93	0.73	0.72	1.51	3.08E+00	1.81E-06	Up	-1.97E+00	3.81E-01		-1.54E-01	8.50E-01		-8.78E-01	4.20E-01		-1.68E-02	1.02E+00		1.05E+00	2.98E-01			Unigene123050_All//2.00E-11//DR453337					
Unigene123051_All	291	0.00	0.52	0.00	0.00	0.00	0.00	0.87	1.87	4.38	9.03E+00	2.36E-01		null	null		null	null		null	null		1.10E+00	2.36E-01		2.33E+00	1.17E-04	Up								ESTscan -
Unigene123052_All	292	0.00	0.00	0.00	0.00	0.00	0.00	0.29	1.15	2.59	null	null		null	null		null	null		null	null		1.98E+00	1.44E-01		3.16E+00	6.83E-04	Up								
Unigene123054_All	293	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13.60	null	null		null	null		null	null		null	null		null	null		1.37E+01	1.67E-28	Up								
Unigene123059_All	294	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.50	null	null		null	null		null	null		null	null		null	null		1.27E+01	1.02E-13	Up								ESTscan -
Unigene12306_All	1384	7.18	2.05	4.31	10.47	8.06	5.65	17.69	4.68	18.45	-1.81E+00	2.65E-18	Down	-7.37E-01	9.17E-05		-3.78E-01	7.66E-03		-8.92E-01	7.26E-10		-1.92E+00	3.21E-58	Down	6.10E-02	6.11E-01		Unigene12306_All//gi|294992380|gb|ADF57328.1|//1.00E-124//1,2-diacyl-sn-glycerol:acyl-CoA acyltransferase 2 [Euonymus alatus]	Unigene12306_All//5.00E-114//AT3G51520| diacylglycerol acyltransferase family	Unigene12306_All//0.00E+00//TC156364				nr +
Unigene123060_All	294	0.00	0.00	0.00	0.00	0.00	0.15	0.72	0.71	59.35	null	null		null	null		null	null		7.26E+00	6.96E-01		-1.67E-02	1.02E+00		6.37E+00	7.79E-116	Up	Unigene123060_All//gi|18404687|ref|NP_564644.1|//2.00E-11//senescence-associated protein-related [Arabidopsis thaliana] >gi|28416881|gb|AA042971.1| At1g53885 [Arabidopsis thaliana]	Unigene123060_All//7.00E-13//AT1G53903| CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF581 (InterPro:IPR007650); BEST Arabidopsis thaliana protein match is: senescence-associated protein-related (TAIR:AT1G53885.1); Has 277 Blast hits to 277 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 277; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene123060_All//6.00E-163//DW514274				nr -
Unigene123061_All	294	0.36	10.51	3.62	1.52	3.28	1.08	3.16	1.56	3.39	4.88E+00	6.17E-15	Up	3.35E+00	3.36E-04	Up	1.10E+00	1.35E-01		-5.04E-01	6.49E-01		-1.02E+00	1.21E-01		9.86E-02	8.78E-01									
Unigene123062_All	294	0.53	1.55	0.36	0.51	0.23	1.54	0.43	1.00	2.98	1.54E+00	1.96E-01		-5.60E-01	7.76E-01		-1.12E+00	5.84E-01		1.60E+00	2.03E-01		1.21E+00	3.92E-01		2.79E+00	5.37E-04	Up								
Unigene123068_All	296	0.00	0.34	0.00	0.00	0.12	0.00	0.14	0.28	3.77	8.42E+00	3.88E-01		null	null		6.86E+00	8.31E-01		null	null		9.84E-01	7.32E-01		4.72E+00	6.01E-07	Up								
Unigene123071_All	297	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.09	null	null		null	null		null	null		null	null		null	null		1.16E+01	1.08E-06	Up								
Unigene123075_All	298	0.18	0.00	0.00	0.00	0.35	0.00	0.00	0.70	2.94	-7.46E+00	6.13E-01		-7.46E+00	6.25E-01		8.44E+00	4.56E-01		null	null		9.45E+00	7.85E-02		1.15E+01	2.05E-06	Up								
Unigene12308_All	2090	6.83	7.76	5.89	7.79	7.88	11.11	8.31	9.80	20.83	1.83E-01	2.22E-01		-2.16E-01	1.97E-01		1.50E-02	9.42E-01		5.11E-01	3.78E-06		2.37E-01	3.79E-02		1.33E+00	7.94E-62	Up	Unigene12308_All//gi|15233141|ref|NP_191713.1|//0.00E+00//peptidase family protein [Arabidopsis thaliana] >gi|6858845|emb|CAB71084.1| prolyl aminopeptidase-like protein [Arabidopsis thaliana] >gi|15450667|gb|AAK96605.1| AT3g61540/F2A19_140 [Arabidopsis thaliana] >gi|17380608|gb|AAL36067.1| AT3g61540/F2A19_140 [Arabidopsis thaliana]	Unigene12308_All//0.00E+00//AT3G61540| peptidase family protein	Unigene12308_All//0.00E+00//gi|109850728|gb|DW479707.1|DW479707			GO:0008238//GO:0019538//GO:0043231	nr -
Unigene123083_All	299	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.73	null	null		null	null		null	null		null	null		null	null		1.08E+01	6.13E-04	Up								
Unigene123085_All	299	0.53	0.00	0.18	0.00	0.35	0.30	0.99	1.12	4.00	-9.04E+00	2.16E-01		-1.56E+00	5.33E-01		8.43E+00	4.56E-01		8.24E+00	4.77E-01		1.76E-01	8.80E-01		2.01E+00	7.79E-04	Up	Unigene123085_All//gi|224101393|ref|XP_002312260.1|//2.00E-17//phol-like protein [Populus trichocarpa] >gi|222852080|gb|EEE89627.1| phol-like protein [Populus trichocarpa]	Unigene123085_All//9.00E-18//AT1G10400| LOCATED IN: integral to membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03240.1); Has 732 Blast hits to 696 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 238; Fungi - 246; Plants - 151; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink).	Unigene123085_All//1.00E-16//gi|78325773|gb|DT546047.1|DT546047			GO:0031224	nr -
Unigene123086_All	299	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.00	3.06	null	null		null	null		null	null		null	null		-8.14E+00	4.04E-01		3.44E+00	7.53E-05	Up	Unigene123086_All//gi|115438929|ref|NP_001043744.1|//1.00E-13//0s01g0653800 [Oryza sativa Japonica Group] >gi|55296497|dbj|BAD68693.1| WD-40 repeat family protein-like [Oryza sativa Japonica Group] >gi|113533275|dbj|BAF05658.1| Os01g0653800 [Oryza sativa Japonica Group]	Unigene123086_All//5.00E-14//AT5G24710| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), WD40 repeat, region (InterPro:IPR017986), WD40 repeat (InterPro:IPR001680), WD40/YVTN repeat-like (InterPro:IPR015943); Has 46946 Blast hits to 23834 proteins in 1336 species: Archae - 160; Bacteria - 9572; Metazoa - 15324; Fungi - 6794; Plants - 1938; Viruses - 1106; Other Eukaryotes - 12052 (source: NCBI BLink).	Unigene123086_All//1.00E-25//TC136007				nr +
Unigene123087_All	299	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.14	3.73	null	null		null	null		null	null		null	null		7.13E+00	6.35E-01		1.19E+01	4.36E-08	Up		Unigene123087_All//1.00E-111//TC134388					ESTscan +
Unigene123088_All	299	0.00	0.00	0.18	0.67	0.00	0.76	0.14	0.00	7.19	null	null		7.48E+00	6.37E-01		-9.38E+00	8.44E-02		1.81E-01	9.35E-01		-7.14E+00	6.58E-01		5.67E+00	5.32E-14	Up		Unigene123088_All//3.00E-07//ES842223					
Unigene12309_All	852	8.17	9.81	9.69	8.42	10.31	6.57	4.76	2.35	4.16	2.65E-01	2.14E-01		2.46E-01	2.70E-01		2.92E-01	1.59E-01		-3.57E-01	1.21E-01		-1.02E+00	1.87E-04	Down	-1.95E-01	4.98E-01		Unigene12309_All//gi|21165527|dbj|BAB93531.1|//2.00E-65//mitogen-activated protein kinase [Solanum tuberosum]	Unigene12309_All//1.00E-65//AT4G01370| ATMPK4 (ARABIDOPSIS THALIANA MAP KINASE 4); MAP kinase/ kinase	Unigene12309_All//0.00E+00//gi|5047135|gb|AI728283.1|AI728283		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0032559	nr -
Unigene123091_All	300	0.00	0.00	0.00	0.00	0.00	0.00	0.85	0.28	25.90	null	null		null	null		null	null		null	null		-1.60E+00	3.11E-01		4.94E+00	1.17E-16	Up		Unigene123091_All//1.00E-56//FL577761					
Unigene123093_All	300	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.42	3.72	null	null		null	null		null	null		null	null		5.68E-01	7.82E-01		3.72E+00	4.35E-06	Up								
Unigene123097_All	300	0.17	0.00	0.00	0.00	0.46	0.15	0.00	0.70	1.86	-7.45E+00	6.13E-01		-7.45E+00	6.25E-01		8.84E+00	3.19E-01		7.23E+00	6.96E-01		9.44E+00	7.85E-02		1.09E+01	3.28E-04	Up		Unigene123097_All//3.00E-07//TC133452					
Unigene123098_All	300	105.86	69.25	97.98	81.53	48.90	43.36	371.78	131.24	149.53	-6.12E-01	1.67E-10		-1.12E-01	3.30E-01		-7.38E-01	3.05E-13		-9.11E-01	8.34E-17		-1.50E+00	3.15E-186	Down	-1.31E+00	1.94E-156	Down		Unigene123098_All//2.00E-159//gi|21102438|gb|BQ414751.1|BQ414751					
Unigene12310_All	3624	6.06	5.79	5.17	21.35	17.19	17.43	16.37	6.67	9.18	-6.70E-02	6.10E-01		-2.29E-01	7.56E-02		-3.13E-01	8.19E-09		-2.92E-01	3.84E-07		-1.30E+00	1.60E-79	Down	-8.35E-01	3.34E-40		Unigene12310_All//gi|30692538|gb|AAP33475.1|//0.00E+00//polygalacturonase-like protein [Fragaria x ananassa]	Unigene12310_All//0.00E+00//AT4G23500| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene12310_All//0.00E+00//TC151355		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004553//GO:0004702//GO:0006464//GO:0030312//GO:0032559//GO:0045229	nr +
Unigene123100_All	300	0.00	0.00	0.00	0.00	0.00	0.15	0.14	0.28	3.19	null	null		null	null		null	null		7.23E+00	6.96E-01		9.84E-01	7.32E-01		4.50E+00	6.81E-06	Up		Unigene123100_All//4.00E-13//FL576748					
Unigene123103_All	301	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.85	null	null		null	null		null	null		null	null		null	null		1.09E+01	3.28E-04	Up								ESTscan -
Unigene123105_All	301	0.00	0.00	0.18	0.66	0.00	0.15	0.00	0.14	2.25	null	null		7.47E+00	6.37E-01		-9.37E+00	8.44E-02		-2.14E+00	3.47E-01		7.12E+00	6.35E-01		1.11E+01	4.96E-05	Up		Unigene123105_All//3.00E-75//TC164875					
Unigene123106_All	301	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.28	2.38	null	null		null	null		null	null		null	null		8.12E+00	4.02E-01		1.12E+01	2.63E-05	Up		Unigene123106_All//1.00E-77//ES801247					
Unigene123109_All	302	0.00	0.00	0.00	0.33	0.23	0.00	0.28	0.83	3.56	null	null		null	null		-5.33E-01	8.17E-01		-8.37E+00	4.01E-01		1.57E+00	3.26E-01		3.67E+00	7.76E-06	Up		Unigene123109_All//3.00E-41//C0123662					
Unigene12311_All	1159	22.53	9.44	13.97	16.68	17.68	12.63	13.35	4.44	3.61	-1.25E+00	1.29E-27	Down	-6.90E-01	3.64E-10		8.42E-02	5.88E-01		-4.02E-01	1.22E-03		-1.59E+00	1.07E-28	Down	-1.89E+00	1.95E-37	Down	Unigene12311_All//gi|238481516|ref|NP_001154770.1|//1.00E-75//XRI1 (X-RAY INDUCED TRANSCRIPT 1) [Arabidopsis thaliana] >gi|239977726|sp|Q6NLW5.2|XRI1_ARATH RecName: Full=Protein XRI1; AltName: Full=Protein X-RAY INDUCED 1	Unigene12311_All//5.00E-77//AT5G48720| XRI1 (X-RAY INDUCED TRANSCRIPT 1)	Unigene12311_All//0.00E+00//TC168177			GO:0005488//GO:0006259//GO:0007126//GO:0010212//GO:0043231//GO:0048229	nr -
Unigene123113_All	302	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.00	22.69	null	null		null	null		null	null		null	null		-8.13E+00	4.04E-01		6.34E+00	1.51E-45	Up								
Unigene123114_All	302	0.00	0.34	0.18	0.00	0.23	0.15	0.14	0.83	3.56	8.39E+00	3.88E-01		7.46E+00	6.37E-01		7.83E+00	6.11E-01		7.22E+00	6.96E-01		2.57E+00	1.53E-01		4.67E+00	1.11E-06	Up	Unigene123114_All//gi|33149681|gb|AAP96920.1|//3.00E-45//pyruvate decarboxylase [Dianthus caryophyllus]	Unigene123114_All//1.00E-44//AT5G01320| pyruvate decarboxylase, putative	Unigene123114_All//2.00E-85//C0110104		ko00380|Tryptophan metabolism	GO:0016831//GO:0019842//GO:0046872//GO:0050896	nr -
Unigene123116_All	302	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.28	1.98	null	null		null	null		null	null		null	null		8.11E+00	4.02E-01		1.10E+01	1.75E-04	Up								
Unigene12312_All	1408	5.46	3.60	5.22	2.69	3.86	2.60	3.42	1.51	1.36	-6.02E-01	4.03E-03		-6.58E-02	7.74E-01		5.23E-01	3.99E-02		-4.94E-02	8.98E-01		-1.18E+00	2.70E-06	Down	-1.33E+00	9.48E-08	Down	Unigene12312_All//gi|238481516|ref|NP_001154770.1|//6.00E-72//XRI1 (X-RAY INDUCED TRANSCRIPT 1) [Arabidopsis thaliana] >gi|239977726|sp|Q6NLW5.2|XRI1_ARATH RecName: Full=Protein XRI1; AltName: Full=Protein X-RAY INDUCED 1	Unigene12312_All//5.00E-73//AT5G48720| XRI1 (X-RAY INDUCED TRANSCRIPT 1)	Unigene12312_All//0.00E+00//TC168177			GO:0005488//GO:0006259//GO:0007126//GO:0010212//GO:0043231//GO:0048229	nr +
Unigene123120_All	303	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.00	2.89	null	null		null	null		null	null		null	null		-8.12E+00	4.04E-01		3.37E+00	1.32E-04	Up								
Unigene123126_All	304	0.00	0.00	0.00	0.00	0.00	0.00	0.42	0.00	7.21	null	null		null	null		null	null		null	null		-8.70E+00	2.36E-01		4.11E+00	3.56E-12	Up								
Unigene12313_All	1520	13.36	7.10	8.37	11.67	13.39	8.59	3.59	1.24	1.68	-9.12E-01	3.48E-13		-6.74E-01	9.27E-08		1.99E-01	1.31E-01		-4.42E-01	6.37E-04		-1.54E+00	3.89E-10	Down	-1.10E+00	1.35E-06	Down	Unigene12313_All//gi|238481516|ref|NP_001154770.1|//4.00E-73//XRI1 (X-RAY INDUCED TRANSCRIPT 1) [Arabidopsis thaliana] >gi|239977726|sp|Q6NLW5.2|XRI1_ARATH RecName: Full=Protein XRI1; AltName: Full=Protein X-RAY INDUCED 1	Unigene12313_All//2.00E-74//AT5G48720| XRI1 (X-RAY INDUCED TRANSCRIPT 1)	Unigene12313_All//0.00E+00//TC150708			GO:0005488//GO:0006259//GO:0007126//GO:0010212//GO:0043231//GO:0048229	nr +
Unigene123131_All	305	0.17	0.00	0.17	0.00	0.00	0.00	0.14	0.00	2.48	-7.42E+00	6.13E-01		2.58E-02	9.95E-01		null	null		null	null		-7.11E+00	6.58E-01		4.16E+00	1.34E-04	Up	Unigene123131_All//gi|110294166|gb|ABG66535.1|//2.00E-08//reverse transcriptase [Phytophthora ramorum]		Unigene123131_All//9.00E-08//BG440230			GO:0003676//GO:0006260//GO:0034061	nr +
Unigene123137_All	306	0.00	0.00	0.00	0.00	0.23	0.59	0.14	0.27	2.86	null	null		null	null		7.81E+00	6.11E-01		9.21E+00	1.95E-01		9.83E-01	7.32E-01		4.37E+00	2.26E-05	Up			Unigene123137_All//2.00E-08//gi|3326854|gb|AI055740.1|AI055740					
Unigene123139_All	306	0.00	0.17	0.52	1.47	0.23	1.48	0.14	1.09	2.60	7.37E+00	6.17E-01		9.03E+00	2.39E-01		-2.70E+00	3.24E-02		1.06E-02	1.00E+00		2.98E+00	5.73E-02		4.24E+00	7.42E-05	Up		Unigene123139_All//3.00E-106//DR226140					
Unigene123145_All	307	0.17	0.50	0.00	0.49	0.00	0.15	1.51	0.54	8.43	1.54E+00	5.31E-01		-7.41E+00	6.25E-01		-8.93E+00	1.66E-01		-1.73E+00	5.01E-01		-1.48E+00	1.53E-01		2.48E+00	2.85E-09	Up		Unigene123145_All//4.00E-07//TC175300					
Unigene123146_All	307	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.00	2.60	null	null		null	null		null	null		null	null		-7.11E+00	6.58E-01		4.24E+00	7.42E-05	Up								
Unigene123149_All	308	0.00	0.66	0.00	0.00	0.00	0.44	0.00	0.00	1.81	9.36E+00	1.37E-01		null	null		null	null		8.78E+00	3.11E-01		null	null		1.08E+01	3.28E-04	Up	Unigene123149_All//gi|224128396|ref|XP_002329319.1|//1.00E-07//predicted protein [Populus trichocarpa] >gi|222861092|gb|EEE98634.1| predicted protein [Populus trichocarpa]						nr -

Unigene123151_All	308	1077.33	956.47	1174.96	458.84	576.23	712.94	481.83	342.64	152.76	-1.72E-01	4.38E-10		1.25E-01	5.66E-06		3.29E-01	3.38E-21		6.36E-01	3.98E-78		-4.92E-01	2.87E-38		-1.66E+00	6.82E-294	Down	Unigene123151_All//gi|224130888|ref|XP_002320949.1|//6.00E-56//s-adenosylmethionine synthetase 4 [Populus trichocarpa] >gi|223635313|sp|A9P822.1|METK1_POPTR RecName: Full=S-adenosylmethionine synthase 1; Short=AdoMet synthase 1; AltName: Full=Methionine adenosyltransferase 1; Short=MAT 1 >gi|222861722|gb|EEE99264.1| s-adenosylmethionine synthetase 4 [Populus trichocarpa]	Unigene123151_All//3.00E-56//AT4G01850| SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase	Unigene123151_All//6.00E-157//TC132629		ko00270|Cysteine and methionine metabolism/ko00450|Selenoamino acid metabolism	GO:0016765//GO:0032559//GO:0044237//GO:0044424//GO:0046872	nr +
Unigene123153_All	308	0.00	0.66	0.00	0.16	0.22	0.59	0.82	2.31	4.01	9.36E+00	1.37E-01		null	null		4.68E-01	9.58E-01		1.86E+00	4.58E-01		1.49E+00	6.15E-02		2.28E+00	1.88E-04	Up			Unigene123153_All//1.00E-53//DR457778					
Unigene123154_All	309	0.00	0.33	0.00	0.00	0.22	0.00	0.00	1.76	1.68	8.36E+00	3.88E-01		null	null		7.80E+00	6.10E-01		null	null		1.08E+01	5.36E-04	Up	1.07E+01	6.13E-04	Up								
Unigene123155_All	309	125.13	111.01	141.14	62.07	59.84	55.54	258.88	306.37	108.94	-1.73E-01	5.90E-02		1.74E-01	5.11E-02		-5.26E-02	7.56E-01		-1.60E-01	2.69E-01		2.43E-01	3.47E-07		-1.25E+00	7.09E-104	Down			Unigene123155_All//1.00E-120//gi|13244840|gb|BE054188.2|BE054188					kegg +
Unigene123156_All	309	0.00	0.00	0.00	0.00	0.00	0.15	0.00	0.00	1.81	null	null		null	null		null	null		7.19E+00	6.96E-01		null	null		1.08E+01	3.28E-04	Up								
Unigene123160_All	310	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	1.93	null	null		null	null		null	null		null	null		7.07E+00	6.35E-01		1.09E+01	1.75E-04	Up								ESTscan +
Unigene123162_All	310	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.83	null	null		null	null		null	null		null	null		null	null		1.15E+01	2.05E-06	Up	Unigene123162_All//gi|297808613|ref|XP_002872190.1|//4.00E-06//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318027|gb|EFH48449.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]		Unigene123162_All//2.00E-30//TC162436			GO:0005488//GO:0016301	nr -
Unigene123164_All	310	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	1.80	null	null		null	null		null	null		null	null		7.07E+00	6.35E-01		1.08E+01	3.28E-04	Up			Unigene123164_All//7.00E-24//TC159777					
Unigene123165_All	311	0.00	0.16	0.17	0.00	0.22	0.00	0.27	0.40	5.76	7.35E+00	6.17E-01		7.42E+00	6.37E-01		7.79E+00	6.10E-01		null	null		5.68E-01	7.82E-01		4.41E+00	1.76E-10	Up			Unigene123165_All//2.00E-86//DR458571					
Unigene123169_All	311	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.18	null	null		null	null		null	null		null	null		null	null		1.11E+01	4.96E-05	Up	Unigene123169_All//gi|758250|emb|CAA59799.1|//1.00E-10//H(+)-transporting ATPase [Phaseolus vulgaris]	Unigene123169_All//9.00E-10//AT4G30190| AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	Unigene123169_All//8.00E-33//TC141856		ko00190|Oxidative phosphorylation	GO:0006811//GO:0009206//GO:0015662//GO:0031224//GO:0032559	nr +
Unigene123173_All	312	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.17	null	null		null	null		null	null		null	null		null	null		1.11E+01	4.96E-05	Up								ESTscan -
Unigene123174_All	312	0.00	0.00	0.00	0.00	0.00	0.29	0.00	0.13	3.83	null	null		null	null		null	null		8.18E+00	4.77E-01		7.07E+00	6.35E-01		1.19E+01	1.20E-08	Up								
Unigene123177_All	313	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.04	null	null		null	null		null	null		null	null		null	null		1.10E+01	9.34E-05	Up			Unigene123177_All//1.00E-09//TC148050					
Unigene123178_All	313	0.00	0.00	0.00	0.00	0.00	0.00	0.41	0.00	2.67	null	null		null	null		null	null		null	null		-8.66E+00	2.36E-01		2.72E+00	8.98E-04	Up	Unigene123178_All//gi|224053248|ref|XP_002297736.1|//3.00E-30//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222844994|gb|EEE82541.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene123178_All//1.00E-26//AT3G14470| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction	GO:0006950//GO:0012501//GO:0016791//GO:0032559	nr -
Unigene12319_All	4040	1.57	1.12	0.61	3.91	4.32	4.77	8.67	3.67	3.40	-4.89E-01	3.81E-02		-1.37E+00	8.22E-08	Down	1.45E-01	3.44E-01		2.88E-01	2.67E-02		-1.24E+00	4.59E-44	Down	-1.35E+00	1.10E-51	Down	Unigene12319_All//gi|297812057|ref|XP_002873912.1|//0.00E+00//EMB3013 [Arabidopsis lyrata subsp. lyrata] >gi|297319749|gb|EFH50171.1| EMB3013 [Arabidopsis lyrata subsp. lyrata]	Unigene12319_All//0.00E+00//AT5G18700| EMB3013 (embryo defective 3013); ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene12319_All//0.00E+00//TC136478			GO:0004674//GO:0006464//GO:0032559	nr +
Unigene123191_All	314	0.00	0.00	0.17	0.16	0.66	0.29	0.67	0.00	3.30	null	null		7.41E+00	6.37E-01		2.05E+00	3.95E-01		8.59E-01	7.95E-01		-9.40E+00	7.45E-02		2.29E+00	7.17E-04	Up								
Unigene123192_All	314	0.00	0.00	0.00	0.00	0.00	0.14	0.94	1.33	46.44	null	null		null	null		null	null		7.17E+00	6.96E-01		4.98E-01	6.33E-01		5.62E+00	1.16E-92	Up	Unigene123192_All//gi|224121846|ref|XP_002318687.1|//7.00E-31//cytochrome P450 [Populus trichocarpa] >gi|222859360|gb|EEE96907.1| cytochrome P450 [Populus trichocarpa]	Unigene123192_All//1.00E-27//AT3G48280| CYP71A25; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene123192_All//4.00E-158//gi|109855176|gb|DW484155.1|DW484155		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism	GO:0005506//GO:0009607//GO:0016709//GO:0042598//GO:0043231//GO:0044425	nr +
Unigene123194_All	315	0.00	0.32	0.51	0.16	0.00	0.14	0.27	0.80	3.41	8.33E+00	3.88E-01		8.99E+00	2.39E-01		-7.30E+00	5.56E-01		-1.41E-01	9.53E-01		1.57E+00	3.26E-01		3.67E+00	7.75E-06	Up								
Unigene123199_All	316	0.00	0.00	0.00	0.00	0.22	0.29	45.89	41.80	17.27	null	null		null	null		7.77E+00	6.10E-01		8.16E+00	4.77E-01		-1.35E-01	3.87E-01		-1.41E+00	2.14E-23	Down	Unigene123199_All//gi|224057942|ref|XP_002299401.1|//1.00E-08//predicted protein [Populus trichocarpa] >gi|118482175|gb|ABK93017.1| unknown [Populus trichocarpa] >gi|118483037|gb|ABK93429.1| unknown [Populus trichocarpa] >gi|118483600|gb|ABK93696.1| unknown [Populus trichocarpa] >gi|222846659|gb|EEE84206.1| predicted protein [Populus trichocarpa]		Unigene123199_All//7.00E-169//DW501483				nr -
Unigene123201_All	316	0.00	0.00	0.00	0.00	0.22	0.00	2.41	0.26	3.28	null	null		null	null		7.77E+00	6.10E-01		null	null		-3.19E+00	7.93E-04	Down	4.45E-01	4.58E-01		Unigene123201_All//gi|227438151|gb|ACP30565.1|//8.00E-19//disease resistance protein [Brassica rapa subsp. pekinensis]	Unigene123201_All//2.00E-18//AT1G12280| disease resistance protein (CC-NBS-LRR class), putative	Unigene123201_All//9.00E-08//TC158982		ko04626|Plant-pathogen interaction	GO:0000166	nr -
Unigene123204_All	316	0.00	0.00	0.00	0.00	0.00	0.00	0.94	0.66	57.36	null	null		null	null		null	null		null	null		-5.02E-01	6.78E-01		5.94E+00	1.45E-117	Up			Unigene123204_All//3.00E-32//TC134836					
Unigene123206_All	317	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.13	2.89	null	null		null	null		null	null		null	null		7.04E+00	6.35E-01		1.15E+01	1.08E-06	Up								ESTscan -
Unigene123208_All	318	0.00	0.00	0.00	0.16	0.00	0.00	0.66	1.31	7.27	null	null		null	null		-7.29E+00	5.56E-01		-7.29E+00	6.36E-01		9.83E-01	3.73E-01		3.45E+00	2.66E-11	Up								
Unigene123210_All	319	0.49	1.75	0.67	0.31	0.97	0.85	0.40	0.39	5.62	1.83E+00	9.02E-02		4.41E-01	7.76E-01		1.64E+00	3.21E-01		1.44E+00	4.09E-01		-1.64E-02	1.02E+00		3.82E+00	1.36E-09	Up			Unigene123210_All//9.00E-08//gi|84170083|gb|DR458731.1|DR458731					
Unigene123213_All	319	0.00	0.64	0.00	0.16	0.11	0.28	0.13	0.92	3.00	9.31E+00	1.37E-01		null	null		-5.34E-01	8.25E-01		8.58E-01	7.95E-01		2.79E+00	9.48E-02		4.50E+00	6.81E-06	Up	Unigene123213_All//gi|255564037|ref|XP_002523017.1|//2.00E-06//mandelonitrile lyase, putative [Ricinus communis] >gi|223537739|gb|EEF39359.1| mandelonitrile lyase, putative [Ricinus communis]				ko00460|Cyanoamino acid metabolism		nr -
Unigene123217_All	320	0.33	0.00	0.33	0.16	0.11	1.41	273.37	115.33	111.55	-8.35E+00	3.73E-01		2.54E-02	1.00E+00		-5.33E-01	8.25E-01		3.18E+00	3.79E-02		-1.25E+00	7.04E-110	Down	-1.29E+00	7.32E-120	Down	Unigene123217_All//gi|292653537|gb|ADE34286.1|//2.00E-53//aquaporin TIP1;11 [Gossypium hirsutum]	Unigene123217_All//4.00E-45//AT2G36830| GAMMA-TIP (GAMMA TONOPLAST INTRINSIC PROTEIN); water channel	Unigene123217_All//1.00E-167//TC161862			GO:0006810//GO:0031224	nr -
Unigene12322_All	228	1.61	0.00	0.00	3.71	5.59	1.39	5.38	1.28	7.34	-1.06E+01	1.97E-02		-1.06E+01	2.78E-02		5.89E-01	3.55E-01		-1.42E+00	7.34E-02		-2.07E+00	6.67E-04	Down	4.49E-01	3.23E-01									
Unigene123221_All	321	0.00	0.00	0.00	0.00	0.00	0.42	0.13	0.00	2.73	null	null		null	null		null	null		8.72E+00	3.11E-01		-7.04E+00	6.58E-01		4.37E+00	2.26E-05	Up	Unigene123221_All//gi|15485720|emb|CAC67501.1|//4.00E-26//selenium binding protein [Medicago sativa]	Unigene123221_All//1.00E-24//AT4G14040| SBP2 (SELENIUM-BINDING PROTEIN 2); selenium binding	Unigene123221_All//8.00E-33//EV491675			GO:0000741//GO:0005488//GO:0006810//GO:0044464	nr +
Unigene123224_All	322	0.00	0.31	0.33	0.00	0.00	0.00	0.26	0.00	11.88	8.30E+00	3.88E-01		8.37E+00	3.99E-01		null	null		null	null		-8.04E+00	4.04E-01		5.50E+00	2.47E-24	Up								
Unigene123227_All	323	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.52	1.85	null	null		null	null		null	null		null	null		9.02E+00	1.39E-01		1.09E+01	1.75E-04	Up								
Unigene123229_All	323	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.56	null	null		null	null		null	null		null	null		null	null		1.22E+01	1.30E-10	Up								
Unigene123231_All	323	0.00	0.16	0.66	0.62	0.21	0.00	0.26	0.78	2.59	7.29E+00	6.17E-01		9.37E+00	1.41E-01		-1.53E+00	4.16E-01		-9.27E+00	1.34E-01		1.57E+00	3.26E-01		3.31E+00	2.30E-04	Up								
Unigene123236_All	325	0.00	0.00	0.00	0.00	0.21	0.00	2.21	0.00	1.35	null	null		null	null		7.73E+00	6.10E-01		null	null		-1.11E+01	3.26E-05	Down	-7.14E-01	3.27E-01		Unigene123236_All//gi|33942041|gb|AAQ55273.1|//2.00E-30//At1g11000 [Arabidopsis thaliana] >gi|110736290|dbj|BAF00115.1| membrane protein MLO4 [Arabidopsis thaliana]	Unigene123236_All//1.00E-22//AT1G11000| MLO4 (MILDEW RESISTANCE LOCUS O 4); calmodulin binding	Unigene123236_All//1.00E-155//gi|78342090|gb|DT562364.1|DT562364			GO:0006950//GO:0009987//GO:0031224	nr +
Unigene12324_All	1026	0.41	0.49	1.35	4.37	4.56	1.67	35.73	22.12	42.63	2.76E-01	7.64E-01		1.73E+00	6.71E-03		6.29E-02	8.45E-01		-1.39E+00	1.91E-06	Down	-6.92E-01	6.73E-18		2.55E-01	3.34E-04		Unigene12324_All//gi|188573187|gb|ACD65511.1|//9.00E-73//beta-glucosidase D7 [Lotus japonicus]	Unigene12324_All//1.00E-61//AT2G44480| BGLU17 (BETA GLUCOSIDASE 17); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene12324_All//1.00E-58//gi|164247168|gb|ES814462.1|ES814462		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0004553//GO:0043167//GO:0044238	nr -
Unigene123240_All	326	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.57	null	null		null	null		null	null		null	null		null	null		1.13E+01	3.88E-06	Up	Unigene123240_All//gi|297799226|ref|XP_002867497.1|//4.00E-35//glycosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313333|gb|EFH43756.1| glycosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene123240_All//2.00E-36//AT4G27570| glycosyltransferase family protein	Unigene123240_All//0.00E+00//ES827205		ko00908|Zeatin biosynthesis//ko00942|Anthocyanin biosynthesis	GO:0035251	nr +
Unigene123242_All	326	94.85	114.55	140.15	214.69	177.46	129.26	274.95	83.59	102.53	2.72E-01	2.25E-03		5.63E-01	2.82E-12		-2.75E-01	2.11E-06		-7.32E-01	1.81E-32		-1.72E+00	9.96E-182	Down	-1.42E+00	3.98E-142	Down			Unigene123242_All//8.00E-107//gi|31407649|gb|CD486684.1|CD486684					
Unigene123247_All	328	0.00	0.00	0.32	0.00	0.00	0.00	0.39	0.25	2.67	null	null		8.34E+00	3.99E-01		null	null		null	null		-6.01E-01	7.67E-01		2.79E+00	5.37E-04	Up								
Unigene123251_All	329	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.63	null	null		null	null		null	null		null	null		null	null		1.18E+01	1.20E-08	Up								
Unigene123256_All	330	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.51	1.69	null	null		null	null		null	null		null	null		8.98E+00	1.39E-01		1.07E+01	3.28E-04	Up								ESTscan +
Unigene123257_All	330	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.25	2.54	null	null		null	null		null	null		null	null		7.98E+00	4.02E-01		1.13E+01	3.88E-06	Up								
Unigene123259_All	331	0.00	0.00	0.00	0.90	0.00	0.00	0.38	0.25	3.97	null	null		null	null		-9.82E+00	2.02E-02		-9.82E+00	4.00E-02		-6.02E-01	7.67E-01		3.37E+00	1.37E-06	Up	Unigene123259_All//gi|19911211|dbj|BAB86932.1|//6.00E-16//glucosyltransferase-14 [Vigna angularis]	Unigene123259_All//9.00E-13//AT2G36760| UGT73C2 (UDP-glucosyl transferase 73C2); UDP-glycosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups			ko00908|Zeatin biosynthesis	GO:0016757	nr -
Unigene12326_All	4371	3.10	2.77	2.75	7.07	8.16	8.78	9.49	6.47	4.71	-1.62E-01	3.41E-01		-1.71E-01	3.35E-01		2.08E-01	2.25E-02		3.14E-01	2.38E-04		-5.52E-01	9.92E-14		-1.01E+00	8.58E-39	Down	Unigene12326_All//gi|15221490|ref|NP_177039.1|//1.00E-178//TADA (TRNA ARGININE ADENOSINE DEAMINASE); catalytic/ hydrolase/ zinc ion binding [Arabidopsis thaliana] >gi|75338834|sp|Q9SZ10.1|Y1872_ARATH RecName: Full=Uncharacterized protein At1g68720 >gi|5734706|gb|AAD49971.1|AC008075_4 Contains similarity to gi|3329316 cytosine deaminase from Chlamydia trachomatis genome gb|AE001357 and contains a PFF00383 cytidine deaminase zinc-binding region. EST gb|W43306 comes from this gene [Arabidopsis thaliana]	Unigene12326_All//8.00E-151//AT1G68720| TADA (TRNA ARGININE ADENOSINE DEAMINASE); catalytic/ hydrolase/ zinc ion binding	Unigene12326_All//0.00E+00//TC162080				nr -
Unigene123261_All	332	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.68	null	null		null	null		null	null		null	null		null	null		1.07E+01	3.28E-04	Up								
Unigene123263_All	333	0.00	0.00	0.00	0.15	0.10	0.00	0.00	0.25	1.56	null	null		null	null		-5.33E-01	8.25E-01		-7.23E+00	6.36E-01		7.97E+00	4.02E-01		1.06E+01	6.13E-04	Up								
Unigene123267_All	334	0.00	1.97	0.00	0.60	0.00	0.27	0.25	0.25	6.80	1.09E+01	6.26E-04	Up	null	null		-9.22E+00	8.44E-02		-1.14E+00	5.69E-01		-1.66E-02	1.01E+00		4.73E+00	1.12E-13	Up								
Unigene123268_All	334	0.00	0.00	0.32	0.15	0.00	0.00	0.76	0.25	6.32	null	null		8.32E+00	3.99E-01		-7.22E+00	5.56E-01		-7.22E+00	6.36E-01		-1.60E+00	3.11E-01		3.06E+00	2.16E-09	Up	Unigene123268_All//gi|74038611|dbj|BAE43839.1|//2.00E-11//tobamovirus multiplication 1 homolog 2 [Solanum lycopersicum]	Unigene123268_All//7.00E-10//AT4G21790| TOM1 (TOBAMOVIRUS MULTIPLICATION 1); protein binding	Unigene123268_All//6.00E-09//TC142126				nr +
Unigene123270_All	335	0.47	1.51	0.16	0.89	0.10	0.40	0.38	0.50	6.07	1.69E+00	1.34E-01		-1.56E+00	5.33E-01		-3.12E+00	7.56E-02		-1.14E+00	4.58E-01		3.99E-01	8.14E-01		4.00E+00	3.90E-11	Up	Unigene123270_All//gi|30698866|ref|NP_565040.2|//9.00E-07//ALAAT2 (ALANINE AMINOTRANSFERASE 2); ATP binding / L-alanine:2-oxoglutarate aminotransferase [Arabidopsis thaliana] >gi|9082268|gb|AAF82781.1|AF275371_1 alanine aminotransferase [Arabidopsis thaliana]	Unigene123270_All//4.00E-08//AT1G72330| ALAAT2 (ALANINE AMINOTRANSFERASE 2); ATP binding / L-alanine:2-oxoglutarate aminotransferase	Unigene123270_All//1.00E-40//TC170913		ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism	GO:0008152//GO:0008483//GO:0016846//GO:0032559//GO:0043231//GO:0044464	nr -
Unigene123272_All	336	0.00	0.30	0.00	0.00	0.00	0.00	232.04	770.86	202.04	8.24E+00	3.88E-01		null	null		null	null		null	null		1.73E+00	0.00E+00	Up	-2.00E-01	1.37E-04				Unigene123272_All//2.00E-45//TC159659					ESTscan -

Unigene123273_All	336	0.78	0.45	0.63	0.00	0.00	0.00	0.00	0.12	1.90	-7.83E-01	6.20E-01			-2.97E-01	8.32E-01		null	null		null	null		6.96E+00	6.35E-01		1.09E+01	9.34E-05	Up	Unigene123273_All//gi|255541450|ref|XP_002511789.1|//8.00E-08//dimethyladenosine transferase, putative [Ricinus communis] >gi|223548969|gb|EEF50458.1| dimethyladenosine transferase, putative [Ricinus communis]	Unigene123273_All//9.00E-07//AT1G01860| PPF1 (PALEFACE 1); mRNA (2'-O-methyladenosine-N6-)-methyltransferase	Unigene123273_All//4.00E-07//C0084775			GO:0008168	nr -
Unigene123275_All	336	0.00	0.60	0.00	0.00	0.00	0.00	0.00	0.00	2.25	9.24E+00	1.37E-01			null	null		null	null		null	null		null	null		1.11E+01	1.39E-05	Up							
Unigene123276_All	337	0.00	0.00	0.00	0.30	0.20	0.13	0.38	0.87	4.02	null	null			null	null		-5.32E-01	8.17E-01		-1.14E+00	6.77E-01		1.21E+00	3.92E-01		3.42E+00	7.76E-07	Up							
Unigene123277_All	337	0.00	0.00	0.00	0.00	0.20	0.00	0.13	0.25	6.27	null	null			null	null		7.68E+00	6.10E-01		null	null		9.83E-01	7.32E-01		5.61E+00	1.00E-13	Up							
Unigene123278_All	337	0.00	1.95	0.00	0.15	0.00	0.00	0.38	0.99	3.66	1.09E+01	6.26E-04	Up		null	null		-7.21E+00	5.56E-01		-7.21E+00	6.36E-01		1.40E+00	2.76E-01		3.28E+00	4.18E-06	Up							
Unigene123279_All	338	0.00	0.00	0.00	0.00	0.20	0.00	0.75	0.00	6.25	null	null			null	null		7.67E+00	6.10E-01		null	null		-9.55E+00	4.04E-02		3.06E+00	2.16E-09	Up		Unigene123279_All//4.00E-07//EX166371					
Unigene123285_All	338	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.12	null	null			null	null		null	null		null	null		null	null		1.11E+01	2.63E-05	Up							
Unigene123287_All	339	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.12	2.12	null	null			null	null		null	null		null	null		-1.63E-02	1.00E-00		4.08E+00	2.41E-04	Up							
Unigene123294_All	341	7.83	7.73	5.00	25.42	16.97	9.01	66.58	30.03	18.23	-1.83E-02	9.80E-01			-6.47E-01	1.12E-01		-5.83E-01	1.48E-03		-1.50E+00	2.87E-13	Down	-1.15E+00	1.03E-25	Down	-1.87E+00	7.78E-54	Down		Unigene123294_All//5.00E-136//TC146988					
Unigene123295_All	341	0.15	0.00	0.00	0.29	0.20	0.79	0.25	0.86	2.22	-7.26E+00	6.13E-01			-7.26E+00	6.25E-01		-5.33E-01	8.17E-01		1.44E+00	4.09E-01		1.79E+00	2.24E-01		3.16E+00	6.83E-04	Up							
Unigene123297_All	342	0.00	0.00	0.00	0.00	0.00	0.00	2.23	1.10	6.64	null	null			null	null		null	null		null	null		-1.02E+00	1.69E-01		1.58E+00	5.86E-05	Up	Unigene123297_All//gi|145357869|ref|NP_196633.2|//2.00E-10//AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase [Arabidopsis thaliana] >gi|7405848|gb|AAZ98829.1| cytokinin independent 2 [Arabidopsis thaliana]	Unigene123297_All//3.00E-11//AT5G10720| AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase		Orphans		GO:0002237//GO:0004672//GO:0009738//GO:0009873//GO:0010119//GO:0016020//GO:0034614//GO:0043231//GO:0048513//GO:0071241	nr +
Unigene123299_All	343	0.00	0.30	0.00	1.45	0.40	0.79	0.00	0.37	3.48	8.21E+00	3.88E-01			null	null		-1.85E+00	8.43E-02		-8.78E-01	4.20E-01		8.51E+00	2.40E-01		1.18E+01	1.20E-08	Up							
Unigene1233_All	1794	0.55	4.07	3.12	1.58	1.00	1.23	2.17	2.45	1.29	2.88E+00	3.59E-23	Up		2.49E+00	6.81E-15	Up	-6.65E-01	6.39E-02		-3.60E-01	3.82E-01		1.74E-01	5.63E-01		-7.51E-01	4.81E-03		Unigene1233_All//gi|13161397|dbj|BAB33033.1|//1.00E-124//CPRD2 [Vigna unguiculata]	Unigene1233_All//2.00E-100//AT5G44380| FAD-binding domain-containing protein	Unigene1233_All//0.00E+00//gi|109883384|gb|DW512354.1|DW512354				nr +
Unigene123300_All	343	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.12	2.21	null	null			null	null		null	null		null	null		6.93E+00	6.35E-01		1.11E+01	1.39E-05	Up							
Unigene123301_All	343	0.00	0.00	0.00	0.00	0.20	0.00	1.11	0.00	4.41	null	null			null	null		7.65E+00	6.10E-01		null	null		-1.01E+01	6.18E-03		1.99E+00	1.35E-04	Up	Unigene123301_All//gi|224089458|ref|XP_002308724.1|//6.00E-14//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222854700|gb|EEE92247.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]					GO:0004871	nr +
Unigene123305_All	344	0.00	1.18	0.31	0.00	0.00	0.39	0.00	0.73	1.62	1.02E+01	1.36E-02			8.27E+00	3.99E-01		null	null		8.62E+00	3.11E-01		9.51E+00	4.31E-02		1.07E+01	3.28E-04	Up		Unigene123305_All//3.00E-05//AT5G63510| GAMMA CAL1 (GAMMA CARBONIC ANHYDRASE LIKE 1); carbonate dehydratase						
Unigene123306_All	344	0.00	0.00	0.00	0.00	0.00	0.39	0.37	1.22	95.08	null	null			null	null		null	null		8.62E+00	3.11E-01		1.72E+00	1.35E-01		8.01E+00	1.65E-228	Up		Unigene123306_All//5.00E-130//DT465287					
Unigene123307_All	344	0.00	0.00	0.00	0.00	0.00	0.00	0.49	0.36	3.01	null	null			null	null		null	null		null	null		-4.32E-01	7.93E-01		2.61E+00	2.37E-04	Up	Unigene123307_All//gi|295799979|emb|CAX68207.1|//2.00E-06//Copia-like retrotransposon [Helianthus annuus]					GO:0005488	nr +
Unigene123311_All	345	0.00	0.29	0.15	0.29	0.50	0.26	0.12	0.24	2.43	8.20E+00	3.88E-01			7.27E+00	6.37E-01		7.89E-01	7.71E-01		-1.42E-01	9.51E-01		9.83E-01	7.32E-01		4.31E+00	4.10E-05	Up	Unigene123311_All//gi|7940287|gb|AAF70846.1|AC003113_13//2.00E-15//F2401.16 [Arabidopsis thaliana]	Unigene123311_All//4.00E-30//AT3G07350| unknown protein	Unigene123311_All//5.00E-102//TC138160				nr +
Unigene123313_All	345	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.36	3.46	null	null			null	null		null	null		null	null		8.51E+00	2.40E-01		1.18E+01	1.20E-08	Up							
Unigene123315_All	346	0.00	0.00	0.00	0.00	0.00	0.78	0.12	0.48	7.94	null	null			null	null		null	null		9.61E+00	7.03E-02		1.98E+00	3.79E-01		6.02E+00	3.74E-18	Up	Unigene123315_All//gi|151301818|gb|ABN50365.2|//3.00E-14//ethylene responsive element binding protein 1 [Gossypium barbadense]		Unigene123315_All//3.00E-08//gi|109863259|gb|DW492236.1|DW492236			GO:0006350//GO:0010468	nr -
Unigene123316_All	346	0.00	0.29	0.00	0.00	0.20	0.00	0.00	0.36	2.19	8.19E+00	3.88E-01			null	null		7.64E+00	6.10E-01		null	null		8.50E+00	2.40E-01		1.11E+01	1.39E-05	Up	Unigene123316_All//gi|4996369|dbj|BAA78427.1|//7.00E-12//polyprotein [Arabidopsis thaliana]	Unigene123316_All//4.00E-06//ATMG00820| hypothetical protein				GO:0005488//GO:0008152	nr -
Unigene12332_All	686	2.29	1.63	3.03	9.15	4.42	9.41	3.08	3.35	0.99	-4.94E-01	3.61E-01			4.04E-01	3.93E-01		-1.05E+00	1.65E-06	Down	4.12E-02	8.91E-01		1.21E-01	7.61E-01		-1.64E+00	5.85E-05	Down		Unigene12332_All//2.00E-29//TC140699					ESTscan +
Unigene123320_All	347	0.00	1.17	2.15	0.00	0.00	0.00	0.00	0.12	1.84	1.02E+01	1.36E-02			1.11E+01	3.28E-04	Up	null	null		null	null		6.91E+00	6.35E-01		1.08E+01	9.33E-05	Up	Unigene123320_All//gi|46404797|gb|AAS82266.1|//3.00E-17//alpha-farnesene synthase [Pyrus pyrifolia]	Unigene123320_All//7.00E-10//AT4G16740| ATTPS03; (E)-beta-ocimene synthase/ myrcene synthase			ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis		nr +
Unigene123322_All	347	0.30	1.61	0.15	0.43	0.40	0.26	4.26	10.72	18.60	2.41E+00	3.93E-02			-9.74E-01	7.21E-01		-1.18E-01	9.11E-01		-7.27E-01	7.16E-01		1.33E+00	6.52E-06	Up	2.12E+00	2.07E-18	Up		Unigene123322_All//3.00E-48//gi|48800402|gb|CO101716.1|CO101716					
Unigene123324_All	348	0.00	0.00	0.00	0.57	0.59	0.26	0.36	1.20	3.89	null	null			null	null		5.22E-02	9.89E-01		-1.14E+00	5.69E-01		1.72E+00	1.35E-01		3.42E+00	7.76E-07	Up	Unigene123324_All//gi|42567298|ref|NP_194851.2|//2.00E-25//protein kinase family protein [Arabidopsis thaliana] >gi|91806758|gb|ABE66106.1| protein kinase family protein [Arabidopsis thaliana]	Unigene123324_All//3.00E-22//AT4G31230| protein kinase family protein	Unigene123324_All//3.00E-11//TC150706			GO:0004672//GO:0006464//GO:0032559//GO:0050896	nr +
Unigene123326_All	348	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.86	null	null			null	null		null	null		null	null		null	null		1.15E+01	3.00E-07	Up	Unigene123326_All//gi|147767925|emb|CAN73401.1|//8.00E-06//hypothetical protein [Vitis vinifera]					GO:0003676	nr -
Unigene123327_All	348	0.00	0.00	0.31	0.00	0.00	0.26	0.49	0.60	3.89	null	null			8.26E+00	3.99E-01		null	null		8.02E+00	4.77E-01		3.05E-01	8.36E-01		3.00E+00	3.58E-06	Up		Unigene123327_All//1.00E-164//CO131740					
Unigene123329_All	348	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.78	null	null			null	null		null	null		null	null		null	null		1.19E+01	1.73E-09	Up		Unigene123329_All//2.00E-05//AT1G48120| calcineurin-like phosphoesterase family protein	Unigene123329_All//7.00E-18//FL577166				ESTscan -
Unigene123331_All	349	0.15	13.36	1.68	0.86	0.59	1.68	0.85	0.00	0.68	6.48E+00	6.45E-25	Up		3.49E+00	1.21E-02		-5.33E-01	6.79E-01		9.74E-01	3.46E-01		-9.73E+00	2.18E-02		-3.08E-01	7.75E-01		Unigene123331_All//gi|17221648|dbj|BAB78478.1|//4.00E-31//prepro MP73 [Cucurbita maxima]				ko03040|Spliceosome		nr -
Unigene123333_All	349	0.00	0.15	0.00	0.00	0.99	0.00	0.00	0.48	1.48	7.18E+00	6.17E-01			null	null		9.95E+00	3.01E-02		null	null		8.90E+00	1.39E-01		1.05E+01	6.13E-04	Up	Unigene123333_All//gi|15724182|gb|AAL06483.1|AF411790_1//3.00E-09//At2g20670/F23N11.1 [Arabidopsis thaliana] >gi|20147393|gb|AAM10406.1| At2g20670/F23N11.1 [Arabidopsis thaliana]		Unigene123333_AI1//2.00E-15//TC149668				nr +
Unigene123335_All	350	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.36	4.55	null	null			null	null		null	null		null	null		5.68E-01	7.82E-01		4.24E+00	3.63E-09	Up							
Unigene123336_All	350	0.45	0.29	0.00	0.00	0.00	0.52	0.24	0.36	2.50	-6.32E-01	7.28E-01			-8.81E+00	2.45E-01		null	null		9.01E+00	1.94E-01		5.68E-01	7.82E-01		3.37E+00	1.32E-04	Up	Unigene123336_AI1//gi|15221448|ref|NP_172118.1|//1.00E-23//LBD2 (LOB DOMAIN-CONTAINING PROTEIN 2) [Arabidopsis thaliana] >gi|259016262|sp|Q9LNB9.2|LBD2_ARATH RecName: Full=LOB domain-containing protein 2; AltName: Full=ASYMMETRIC LEAVES 2-like protein 32; Short=AS2-like protein 32 >gi|219807140|dbj|BAH10576.1| ASYMMETRIC LEAVES2-like 32 protein [Arabidopsis thaliana]	Unigene123336_AI1//6.00E-25//AT1G06280| LBD2 (LOB DOMAIN-CONTAINING PROTEIN 2)			ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0009536	nr -
Unigene123337_All	351	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.59	null	null			null	null		null	null		null	null		null	null		1.06E+01	3.28E-04	Up							
Unigene123338_All	352	0.00	0.00	0.00	1.70	0.10	0.13	0.00	0.59	2.26	null	null			null	null		-4.12E+00	1.25E-03		-3.73E+00	4.96E-03		9.21E+00	7.85E-02		1.11E+01	7.36E-06	Up	Unigene123338_AI1//gi|102139738|gb|ABF69945.1|//8.00E-35//AMP-dependent synthetase and ligase family protein, 5' partial [Musa acuminata]					GO:0003824	nr -
Unigene123339_All	352	0.00	0.58	0.00	0.00	0.00	0.13	0.00	0.59	98.01	9.17E+00	1.37E-01			null	null		null	null		7.00E+00	6.96E-01		9.21E+00	7.85E-02		1.66E+01	1.79E-248	Up							
Unigene12334_All	2103	3.91	3.06	3.75	29.09	11.43	17.91	4.38	5.76	2.24	-3.52E-01	8.95E-02			-5.98E-02	7.84E-01		-1.35E+00	1.48E-88	Down	-7.00E-01	2.58E-26		3.95E-01	7.15E-03		-9.71E-01	8.60E-09				Unigene12334_AI1//0.00E+00//gi|164295958|gb|EX170447.1|EX170447					ESTscan -
Unigene123340_All	352	0.00	0.00	0.30	0.42	0.10	0.13	0.00	0.12	2.26	null	null			8.24E+00	3.99E-01		-2.12E+00	3.86E-01		-1.73E+00	5.01E-01		6.89E+00	6.35E-01		1.11E+01	7.36E-06	Up	Unigene123340_AI1//gi|255577753|ref|XP_002529751.1|//1.00E-10//conserved hypothetical protein [Ricinus communis] >gi|223530749|gb|EEF32617.1| conserved hypothetical protein [Ricinus communis]	Unigene123340_AI1//1.00E-07//AT2G31600| unknown protein	Unigene123340_AI1//5.00E-28//gi|78333737|gb|DT554011.1|DT554011				nr +
Unigene123341_All	353	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.47	null	null			null	null		null	null		null	null		null	null		1.05E+01	6.13E-04	Up		Unigene123341_AI1//1.00E-37//FL577241					
Unigene123342_All	353	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.60	null	null			null	null		null	null		null	null		null	null		1.13E+01	1.08E-06	Up	Unigene123342_AI1//gi|145408590|ref|YP_001152214.1|//5.00E-08//O8F124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| O8F124 [Pinus koraiensis]		Unigene123342_AI1//1.00E-13//TC135460				nr +
Unigene123343_All	353	0.00	0.72	0.00	0.14	0.10	0.26	0.00	0.36	1.69	9.49E+00	7.87E-02			null	null		-5.32E-01	8.25E-01		8.59E-01	7.95E-01		8.47E+00	2.40E-01		1.07E+01	1.75E-04	Up							ESTscan +
Unigene123344_All	353	0.00	0.00	0.00	0.14	0.49	0.00	0.00	0.00	1.69	null	null			null	null		1.79E+00	5.21E-01		-7.14E+00	6.36E-01		null	null		1.07E+01	1.75E-04	Up	Unigene123344_AI1//gi|15228190|ref|NP_191137.1|//6.00E-28//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|7263566|emb|CAB81603.1| beta-1, 3-glucanase-like protein [Arabidopsis thaliana]	Unigene123344_AI1//4.00E-24//AT3G55780| glycosyl hydrolase family 17 protein	Unigene123344_AI1//7.00E-09//ES803342		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0008152	nr -
Unigene123346_All	354	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.36	null	null			null	null		null	null		null	null		null	null		1.12E+01	3.88E-06	Up	Unigene123346_AI1//gi|4544460|gb|AAD22368.1|//5.00E-06//putative non-LTR retroelement reverse transcriptase [Arabidopsis thaliana]	Unigene123346_AI1//3.00E-05//AT5G42905| nucleic acid binding / ribonuclease H					nr +
Unigene123348_All	355	0.59	0.57	0.30	0.00	0.29	0.13	0.24	0.47	3.59	-4.63E-02	9.89E-01			-9.75E-01	6.21E-01		8.18E+00	4.56E-01		6.99E+00	6.96E-01		9.83E-01	6.34E-01		3.91E+00	4.24E-07	Up	Unigene123348_AI1//gi|297851452|ref|XP_002893607.1|//5.00E-40//ATINT2 [Arabidopsis lyrata subsp. lyrata] >gi|297339449|gb|EFH69866.1| ATINT2 [Arabidopsis lyrata subsp. lyrata]	Unigene123348_AI1//4.00E-41//AT1G30220| INT2 (INOSITOL TRANSPORTER 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene123348_AI1//1.00E-170//TC178854			GO:0005365//GO:0008152//GO:0015791//GO:0016628//GO:0031224	nr -
Unigene123350_AI1	356	0.00	0.00	0.00	0.14	0.00	0.00	0.00	0.00	1.45	null	null			null	null		-7.13E+00	5.56E-01		-7.13E+00	6.36E-01		null	null		1.05E+01	6.13E-04	Up							
Unigene123351_All	357	0.44	0.28	0.60	0.70	0.48	1.27	1.66	1.05	5.02	-6.31E-01	7.28E-01			4.40E-01	7.76E-01		-5.33E-01	7.13E-01		8.59E-01	4.69E-01		-6.54E-01	4.45E-01		1.60E+00	3.75E-04	Up		Unigene123351_AI1//8.00E-61//TC177693					
Unigene123352_All	357	0.00	0.43	0.00	0.28	0.00	0.00	0.71	0.70	4.46	8.73E+00	2.36E-01			null	null		-8.12E+00	3.14E-01		-8.12E+00	4.01E-01		-1.67E-02	1.02E+00		2.65E+00	2.17E-06	Up	Unigene123352_AI1//gi|258642469|gb|ACV88819.1|//8.00E-35//NBS-LRR resistance protein [Hevea benthamiana]	Unigene123352_AI1//9.00E-13//AT3G07040| RPM1 (RESISTANCE TO P. SYRINGAE PV MACULICOLA 1); nucleotide binding / protein binding			ko04626|Plant-pathogen interaction	GO:0000166	nr +
Unigene123353_All	358	0.00	0.00	0.30	0.00	0.00	0.25	0.12	1.05	2.00	null	null			8.22E+00	3.99E-01		null	null		7.98E+00	4.77E-01		3.15E+00	3.41E-02		4.08E+00	2.41E-04	Up	Unigene123353_AI1//gi|90265102|emb|CAH67715.1|//5.00E-26//H0512B01.10 [Oryza sativa (indica cultivar-group)]	Unigene123353_AI1//8.00E-20//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene123353_AI1//5.00E-170//DT462365			GO:0004702//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr -
Unigene123355_AI1	358	0.00	0.00	0.00	0.00	0.00	0.00	0.35	0.58	3.78	null	null			null	null		null	null		null	null		7.20E-01	6.32E-01		3.42E+00	7.76E-07	Up							

Unigene123356_All	359	0.00	0.28	0.00	0.00	0.38	0.63	0.24	0.00	3.55	8.14E+00	3.88E-01		null	null		8.58E+00	3.19E-01		9.30E+00	1.19E-01		-7.88E+00	4.04E-01		3.91E+00	4.24E-07	Up	Unigene123356_All//gi|195957709|gb|ACG59769.1|//1.00E-42//lipoxygenase 1 [Prunus persica]	Unigene123356_All//1.00E-34//AT1G17420| LOX3; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene123356_All//0.00E+00//ES820694		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0006633//GO:0006950//GO:0009536//GO:0009642//GO:0009694//GO:0009719//GO:0016702//GO:0042221//GO:0046914//GO:0051707	nr -
Unigene123357_All	360	1.16	5.49	1.18	5.53	4.50	2.51	26.31	4.88	32.20	2.24E+00	2.78E-05	Up	2.53E-02	1.00E+00		-3.00E-01	5.56E-01		-1.14E+00	1.33E-02		-2.43E+00	1.03E-30	Down	2.92E-01	5.13E-02		Unigene123357_All//gi|195619594|gb|ACG31627.1|//2.00E-19//glycerophosphodiester phosphodiesterase [Zea mays]	Unigene123357_All//2.00E-20//AT3G02040| SAG3 (senescence-related gene 3); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase	Unigene123357_All//2.00E-49//TC141623			GO:0008081//GO:0019400	nr -
Unigene123358_All	361	0.14	0.28	1.48	0.00	0.00	0.50	0.94	0.23	5.85	9.54E-01	7.26E-01		3.35E+00	2.06E-02		null	null		8.97E+00	1.94E-01		-2.02E+00	1.36E-01		2.64E+00	3.33E-08	Up	Unigene123358_All//gi|259121419|gb|ACV92029.1|//9.00E-23//WRKY transcription factor 27 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene123358_All//1.00E-13//AT4G23810| WRKY53; DNA binding / protein binding / transcription activator/ transcription factor	Unigene123358_All//0.00E+00//gi|73864117|gb|DT466856.1|DT466856	WRKY			nr -
Unigene123359_All	361	0.00	0.56	0.00	0.00	0.38	0.38	0.70	0.69	7.50	9.13E+00	1.37E-01		null	null		8.58E+00	3.19E-01		8.55E+00	3.11E-01		-1.65E-02	1.02E+00		3.42E+00	4.88E-13	Up									
Unigene123360_All	361	0.00	1.12	1.62	0.55	0.76	0.38	0.23	0.23	2.54	1.01E+01	1.36E-02		1.07E+01	2.17E-03		4.67E-01	8.17E-01		-5.57E-01	7.33E-01		-1.61E-02	1.01E+00		3.44E+00	7.53E-05	Up	Unigene123360_All//gi|145323958|ref|NP_001007568.1|//3.00E-07//AAE1 (ACYL ACTIVATING ENZYME 1): AMP binding [Arabidopsis thaliana]	Unigene123360_All//1.00E-08//AT1G20560| AAE1 (ACYL ACTIVATING ENZYME 1); AMP binding				GO:0042579	nr +
Unigene123363_All	361	0.00	0.56	0.00	0.00	0.00	0.25	0.70	0.81	4.97	9.13E+00	1.37E-01		null	null		null	null		7.97E+00	4.77E-01		2.06E-01	8.68E-01		2.82E+00	1.60E-07	Up									
Unigene123364_All	362	0.00	0.00	0.00	0.00	0.00	0.50	0.47	1.27	3.52	null	null		null	null		null	null		8.96E+00	1.94E-01		1.44E+00	1.67E-01		2.91E+00	1.05E-05	Up	Unigene123364_All//gi|15219130|ref|NP_173062.1|//5.00E-08//WAKL6 (wall associated kinase-like 6); kinase [Arabidopsis thaliana]	Unigene123364_All//2.00E-09//AT1G16110| WAKL6 (wall associated kinase-like 6); kinase					nr +
Unigene123366_All	362	0.00	0.00	0.00	0.00	0.00	0.00	0.47	0.12	5.61	null	null		null	null		null	null		null	null		-2.02E+00	3.67E-01		3.59E+00	2.59E-10	Up	Unigene123366_All//gi|224133962|ref|XP_002327722.1|//8.00E-09//predicted protein [Populus trichocarpa] >gi|222836807|gb|EEE75200.1| predicted protein [Populus trichocarpa]						nr -
Unigene123367_All	362	0.00	0.00	0.00	0.00	0.00	0.00	1.52	1.04	7.37	null	null		null	null		null	null		null	null		-5.47E-01	5.52E-01		2.28E+00	9.98E-09	Up									
Unigene123368_All	363	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.54	null	null		null	null		null	null		null	null		null	null		1.06E+01	3.28E-04	Up									
Unigene123373_All	365	0.14	0.69	0.29	0.14	0.00	0.12	0.00	0.69	2.40	2.28E+00	2.34E-01		1.03E+00	7.03E-01		-7.09E+00	5.56E-01		-1.42E-01	9.53E-01		9.42E+00	4.31E-02		1.12E+01	2.05E-06	Up									ESTscan +
Unigene123375_All	365	0.29	1.25	0.58	0.27	0.00	0.00	0.12	0.00	5.89	2.12E+00	9.59E-02		1.03E+00	5.92E-01		-8.09E+00	3.14E-01		-8.09E+00	4.01E-01		-6.86E+00	6.58E-01		5.67E+00	5.32E-14	Up	Unigene123375_All//gi|14517476|gb|AAK62628.1|//3.00E-24//At2g43320/T1024.6 [Arabidopsis thaliana] >gi|20196858|gb|AAB64311.2| expressed protein [Arabidopsis thaliana] >gi|20197145|gb|AAM14937.1| expressed protein [Arabidopsis thaliana] >gi|22136568|gb|AAM91070.1| At2g43320/T1024.6 [Arabidopsis thaliana]	Unigene123375_All//5.00E-20//AT2G43320| unknown protein	Unigene123375_All//2.00E-18//DW228030			GO:0043231	nr +
Unigene123376_All	366	0.00	1.25	0.00	0.00	0.19	0.00	316.41	971.01	227.39	1.03E+01	7.44E-03		null	null		7.56E+00	6.10E-01		null	null		1.62E+00	0.00E+00	Up	-4.77E-01	3.23E-29		Unigene123376_All//gi|71534908|gb|AAZ32858.1|//1.00E-22//BURP domain-containing protein [Medicago sativa]	Unigene123376_All//1.00E-23//AT1G49320| BURP domain-containing protein	Unigene123376_All//5.00E-96//ES840078				nr -
Unigene123380_All	368	0.00	0.28	0.00	0.00	0.00	0.00	0.00	0.00	1.62	8.11E+00	3.88E-01		null	null		null	null		null	null		null	null		1.07E+01	1.75E-04	Up	Unigene123380_All//gi|124359162|gb|ABN05685.1|//8.00E-09//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]						nr +
Unigene123381_All	369	0.00	0.00	0.29	0.00	0.00	0.00	0.00	0.00	9.61	null	null		8.17E+00	3.99E-01		null	null		null	null		null	null		1.32E+01	2.27E-25	Up			Unigene123381_All//2.00E-18//TC175987						
Unigene123383_All	370	3280.94	1836.56	2415.10	5494.37	4344.52	4796.84	1152.42	587.06	485.71	-8.37E-01	0.00E+00		-4.42E-01	7.93E-201		-3.39E-01	3.78E-258		-1.96E-01	2.46E-80		-9.73E-01	0.00E+00		-1.25E+00	0.00E+00	Down	Unigene123383_All//gi|167367|gb|AAA99868.1|//3.00E-15//peroxidase [Gossypium hirsutum]	Unigene123383_All//9.00E-14//AT4G21960| PRX8I; electron carrier/ heme binding / peroxidase	Unigene123383_All//0.00E+00//TC159024		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209//GO:0044464	nr +
Unigene123385_All	371	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.83	null	null		null	null		null	null		null	null		null	null		1.08E+01	4.96E-05	Up	Unigene123385_All//gi|115488632|ref|NP_001066803.1|//2.00E-10//Os12g0493900 [Oryza sativa Japonica Group] >gi|77555831|gb|ABA98627.1| Pumilio-family RNA binding repeat containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113649310|dbj|BAF29822.1| Os12g0493900 [Oryza sativa Japonica Group]	Unigene123385_All//3.00E-11//AT1G22240| APUM8 (Arabidopsis Pumilio 8); RNA binding / binding					nr +
Unigene123386_All	371	0.00	0.00	0.00	0.00	0.09	0.00	0.34	0.00	3.01	null	null		null	null		6.54E+00	8.31E-01		null	null		-8.42E+00	2.36E-01		3.14E+00	2.19E-05	Up	Unigene123386_All//gi|18379010|ref|NP_563662.1|//2.00E-33//pectinesterase family protein [Arabidopsis thaliana] >gi|75313808|sp|Q9SRX4.1|PME7_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 7; Includes: RecName: Full=Pectinesterase inhibitor 7; AltName: Full=Pectin methylesterase inhibitor 7; Includes: RecName: Full=Pectinesterase 7; Short=PE 7; AltName: Full=Pectin methylesterase 7; AltName: Full=Pectin methylesterase 1; Short=AtPME1; Flags: Precursor >gi|6056422|gb|AAF02886.1|AC009525_20 Similar to pectinesterases [Arabidopsis thaliana] >gi|133778888|gb|AB038784.1| At1g02810 [Arabidopsis thaliana]	Unigene123386_All//7.00E-35//AT1G02810| pectinesterase family protein	Unigene123386_All//3.00E-08//TC151219		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618	nr -
Unigene123388_All	371	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.56	3.01	null	null		null	null		null	null		null	null		2.30E+00	2.40E-01		4.72E+00	6.01E-07	Up	Unigene123388_All//gi|224054164|ref|XP_002298123.1|//4.00E-50//pleiotropic drug resistance, ABC transporter family protein [Populus trichocarpa] >gi|222845381|gb|EEE82928.1| pleiotropic drug resistance, ABC transporter family protein [Populus trichocarpa]	Unigene123388_All//3.00E-47//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene123388_All//4.00E-72//gi|73862561|gb|DT465300.1|DT465300		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015604//GO:0032559//GO:0042626//GO:0044464	nr +
Unigene123389_All	371	0.42	0.27	0.57	0.54	0.84	1.34	0.00	0.23	2.47	-6.31E-01	7.28E-01		4.40E-01	7.75E-01		6.37E-01	6.95E-01		1.32E+00	2.52E-01		7.82E+00	4.02E-01		1.13E+01	1.08E-06	Up	Unigene123389_All//gi|22327146|ref|NP_198205.2|//5.00E-11//FRS10 (FAR1-related sequence 10); zinc ion binding [Arabidopsis thaliana] >gi|257051024|sp|Q9LKR4.2|FRS10_ARATH RecName: Full=Putative protein FAR1-RELATED SEQUENCE 10	Unigene123389_All//2.00E-12//AT5G28530| FRS10 (FAR1-related sequence 10); zinc ion binding				GO:0046914	nr -
Unigene123392_All	374	0.00	0.00	0.00	0.27	0.00	0.00	0.45	0.45	11.93	null	null		null	null		-8.06E+00	3.14E-01		-8.06E+00	4.01E-01		-1.67E-02	1.02E+00		4.72E+00	2.33E-26	Up									
Unigene123393_All	375	0.00	0.14	0.00	0.13	0.00	0.00	0.00	0.67	20.18	7.08E+00	6.17E-01		null	null		-7.05E+00	5.56E-01		-7.05E+00	6.36E-01		9.39E+00	4.31E-02		1.43E+01	3.14E-54	Up									
Unigene123394_All	375	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.37	null	null		null	null		null	null		null	null		null	null		1.26E+01	4.04E-17	Up									
Unigene123395_All	375	0.00	0.00	0.00	0.00	0.00	0.12	0.23	0.00	5.84	null	null		null	null		null	null		6.91E+00	6.96E-01		-7.82E+00	4.04E-01		4.70E+00	3.84E-13	Up									
Unigene123396_All	376	0.00	0.00	0.00	0.27	0.27	0.24	0.00	0.00	1.48	null	null		null	null		5.19E-02	9.67E-01		-1.42E-01	9.51E-01		null	null		1.05E+01	3.28E-04	Up	Unigene123396_All//gi|224154489|ref|XP_002337484.1|//3.00E-06//predicted protein [Populus trichocarpa] >gi|222839453|gb|EEE77790.1| predicted protein [Populus trichocarpa]						nr -
Unigene123397_All	376	0.00	0.00	0.00	0.00	0.00	0.00	876.19	2718.06	62.72	null	null		null	null		null	null		null	null		1.63E+00	0.00E+00	Up	-3.80E+00	0.00E+00	Down									
Unigene1234_All	1806	14.20	16.30	8.43	19.36	19.89	19.36	0.35	0.23	0.02	2.00E-01	5.83E-02		-7.51E-01	1.67E-11		3.85E-02	7.65E-01		-5.00E-04	9.95E-01		-6.02E-01	4.67E-01		-3.99E+00	5.82E-04	Down	Unigene1234_All//gi|13161397|dbj|BAB33033.1|//1.00E-169//CPRD2 [Yigna unguiculata]	Unigene1234_All//2.00E-134//AT1G30700| FAD-binding domain-containing protein	Unigene1234_All//0.00E+00//ES808271		ko00620|Pyruvate metabolism//ko00908|Zeatin biosynthesis		nr -
Unigene123400_All	377	0.00	0.00	0.99	1.72	0.18	0.00	0.00	0.00	1.80	null	null		9.95E+00	2.50E-02		-3.23E+00	2.48E-03		-1.07E+01	3.90E-04	Down	null	null		1.08E+01	4.96E-05	Up	Unigene123400_All//gi|297803538|ref|XP_002869653.1|//8.00E-09//predicted protein [Arabidopsis lyrata subsp. lyrata] >gi|297315489|gb|EFH45912.1| predicted protein [Arabidopsis lyrata subsp. lyrata]						nr -
Unigene123401_All	379	0.14	0.00	0.00	0.00	0.00	0.24	0.11	0.66	2.21	-7.11E+00	6.13E-01		-7.11E+00	6.25E-01		null	null		7.90E+00	4.77E-01		2.57E+00	1.53E-01		4.31E+00	4.10E-05	Up			Unigene123401_All//4.00E-07//BQ411269						
Unigene123403_All	380	0.28	0.80	0.70	0.52	0.18	0.48	0.00	0.77	2.52	1.54E+00	3.23E-01		1.35E+00	4.09E-01		-1.53E+00	4.16E-01		-1.42E-01	9.35E-01		9.59E+00	2.35E-02		1.13E+01	5.69E-07	Up	Unigene123403_All//gi|5080805|gb|AAD39314.1|AC007258_3/2.00E-41//Hypothetical protein [Arabidopsis thaliana]	Unigene123403_All//1.00E-42//AT1G59720| CRR28 (CHLORORESPIRATORY REDUCTION28); endonuclease	Unigene123403_All//3.00E-36//gi|48813189|gb|CO114502.1|CO114502			GO:0009451//GO:0009536	nr -
Unigene123404_All	380	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.99	null	null		null	null		null	null		null	null		null	null		1.10E+01	1.39E-05	Up									
Unigene123405_All	380	0.00	3.87	0.00	0.52	0.09	1.43	0.67	0.11	1.99	1.19E+01	2.11E-08	Up	null	null		-2.53E+00	2.34E-01		1.44E+00	1.93E-01		-2.60E+00	1.44E-01		1.58E+00	3.40E-02										
Unigene123406_All	380	1.38	0.00	0.00	0.26	0.27	0.00	0.11	1.10	6.71	-1.04E+01	2.93E-03		-1.04E+01	4.76E-03		5.24E-02	9.67E-01		-8.03E+00	4.01E-01		3.30E+00	2.00E-02		5.91E+00	9.13E-17	Up									
Unigene123408_All	381	0.27	0.00	0.00	0.26	0.09	0.12	0.11	0.22	1.67	-8.10E+00	3.73E-01		-8.10E+00	3.95E-01		-1.53E+00	5.86E-01		-1.14E+00	6.77E-01		9.83E-01	7.32E-01		3.91E+00	7.65E-04	Up	Unigene123408_All//gi|15239524|ref|NP_200211.1|//1.00E-13//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|10177262|dbj|BAB10730.1| ethylene-forming-enzyme-like dioxygenase [Arabidopsis thaliana] >gi|67633882|gb|AAT28865.1| oxidoreductase [Arabidopsis thaliana]	Unigene123408_All//5.00E-15//AT5G54000| oxidoreductase, 2OG-Fe(II) oxygenase family protein				GO:0016706	nr +
Unigene12341_All	1844	1.62	1.95	2.86	2.94	2.89	2.28	5.30	2.11	1.94	2.71E-01	4.14E-01		8.22E-01	2.41E-03		-2.47E-02	9.32E-01		-3.70E-01	1.73E-01		-1.33E+00	2.87E-14	Down	-1.45E+00	1.26E-16	Down	Unigene12341_All//gi|2500521|sp|Q40468.1|IF415_TOBAC//1.00E-111//RecName: Full=Eukaryotic initiation factor 4A-15; Short=eIF-4A-15; AltName: Full=ATP-dependent RNA helicase eIF4A-15	Unigene12341_All//7.00E-103//AT3G13920| EIF4A1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 4A1); ATP-dependent helicase/ translation initiation factor	Unigene12341_All//0.00E+00//gi|73849035|gb|DT458055.1|DT458055				nr -
Unigene123412_All	385	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	42.84	null	null		null	null		null	null		null	null		null	null		1.54E+01	1.74E-118	Up		Unigene123412_All//4.00E-05//AT5G28770| unknown protein						
Unigene123413_All	385	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.48	null	null		null	null		null	null		null	null		null	null		1.13E+01	5.69E-07	Up			Unigene123413_All//4.00E-07//FL577601						

Unigene123414_All	386	0.14	0.39	0.55	0.13	0.00	0.47	5.04	10.61	56.25	1.54E+00	5.31E-01		2.03E+00	3.61E-01		-7.01E+00	5.56E-01		1.86E+00	4.58E-01		1.07E+00	7.89E-05	Up	3.48E+00	9.93E-102	Up	Unigene123414_All//gi|104295003|gb|ABF72018.1|//7.00E-28//protein kinase family protein [Musa acuminata]	Unigene123414_All//3.00E-25//AT4G18950| ankyrin protein kinase, putative	Unigene123414_All//3.00E-131//DW506519			GO:0004713//GO:0006464//GO:0007165//GO:0032559//GO:0043231	nr +
Unigene123417_All	389	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.54	null	null		null	null		null	null		null	null		null	null		1.06E+01	1.75E-04	Up	Unigene123417_All//gi|28301674|emb|CAB63264.3|//2.00E-11//calcium-binding protein [Lotus japonicus]	Unigene123417_All//8.00E-11//AT2G43290| MSS3 (multicopy suppressors of snf4 deficiency in yeast 3); calcium ion binding			ko04626|Plant-pathogen interaction	GO:0005976//GO:0016628//GO:0044464//GO:0046872	nr -
Unigene123418_All	389	0.00	0.00	0.00	0.00	0.18	0.00	0.87	0.64	3.99	null	null		null	null		7.47E+00	6.10E-01		null	null		-4.32E-01	7.03E-01		2.20E+00	3.33E-05	Up			Unigene123418_All//5.00E-07//FL577082					
Unigene123419_All	391	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.21	2.34	null	null		null	null		null	null		null	null		9.84E-01	7.32E-01		4.44E+00	1.24E-05	Up	Unigene123419_All//gi|98960881|gb|ABF58924.1|//3.00E-10//At5g49410 [Arabidopsis thaliana]	Unigene123419_All//6.00E-11//AT5G49410| unknown protein	Unigene123419_All//1.00E-118//TC141695				nr +
Unigene12342_All	869	10.42	6.71	4.72	1.15	0.87	1.97	2.24	0.53	0.69	-6.35E-01	8.74E-04		-1.14E+00	2.28E-08	Down	-3.95E-01	5.73E-01		7.85E-01	1.31E-01		-2.08E+00	8.32E-06	Down	-1.70E+00	7.95E-05	Down	Unigene12342_All//gi|56544480|gb|AAY92905.1|//4.00E-72//Avr9/Cf-9 rapidly elicited protein 256 [Nicotiana tabacum]	Unigene12342_All//2.00E-56//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene12342_All//0.00E+00//gi|54123100|gb|CO498609.1|CO498609		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene123421_All	392	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.53	7.22	null	null		null	null		null	null		null	null		9.06E+00	7.85E-02		1.28E+01	3.03E-20	Up								ESTscan +
Unigene123422_All	392	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.11	2.74	null	null		null	null		7.46E+00	6.10E-01		null	null		6.74E+00	6.35E-01		1.14E+01	8.30E-08	Up	Unigene123422_All//gi|38194915|gb|AAR13303.1|//4.00E-38//phytochelatin synthetase-like protein [Phaseolus vulgaris]	Unigene123422_All//1.00E-38//AT5G60920| COB (COBRA)				GO:0005618//GO:0005746//GO:0006970//GO:0009986//GO:0015078//GO:0016049//GO:0030198//GO:0031225//GO:0031410//GO:0045333	nr -
Unigene123423_All	392	0.53	0.00	0.00	0.00	0.00	0.00	0.00	0.21	15.14	-9.06E+00	1.22E-01		-9.06E+00	1.46E-01		null	null		null	null		7.74E+00	4.02E-01		1.39E+01	1.68E-42	Up			Unigene123423_All//4.00E-75//CA993703					
Unigene123424_All	393	0.00	0.77	0.14	0.00	0.09	0.00	1.08	0.74	4.16	9.60E+00	4.44E-02		7.08E+00	6.37E-01		6.45E+00	8.30E-01		null	null		-5.31E-01	6.34E-01		1.93E+00	8.71E-05	Up								
Unigene123426_All	394	0.00	0.13	0.54	0.25	0.44	0.23	0.64	1.70	4.04	7.01E+00	6.17E-01		9.08E+00	1.41E-01		7.89E-01	7.71E-01		-1.41E-01	9.51E-01		1.40E+00	8.81E-02		2.65E+00	2.17E-06	Up			Unigene123426_All//5.00E-07//TC178915					
Unigene123427_All	394	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.21	8.49	null	null		null	null		null	null		null	null		7.73E+00	4.02E-01		1.31E+01	6.05E-24	Up								
Unigene123428_All	395	0.00	0.00	0.00	0.00	0.00	0.00	27.08	0.95	9.38	null	null		null	null		null	null		null	null		-4.83E+00	1.33E-62	Down	-1.50E+00	4.42E-19	Down								
Unigene123429_All	395	0.00	0.00	0.00	0.00	0.00	0.00	0.43	0.74	2.42	null	null		null	null		null	null		null	null		7.91E-01	5.63E-01		2.50E+00	6.42E-04	Up			Unigene123429_All//1.00E-53//CO122813					
Unigene12343_All	2168	23.05	10.61	17.27	9.56	9.32	6.69	0.92	0.56	0.46	-1.12E+00	1.14E-43	Down	-4.17E-01	5.65E-08		-3.59E-02	8.36E-01		-5.15E-01	1.12E-05		-7.13E-01	8.37E-02		-9.97E-01	1.18E-02		Unigene12343_All//gi|297726167|ref|NP_001175447.1|//1.00E-127//Os08g0230800 [Oryza sativa Japonica Group] >gi|255678252|dbj|BAH94175.1|Os08g0230800 [Oryza sativa Japonica Group]	Unigene12343_All//8.00E-77//AT1G34300| lectin protein kinase family protein	Unigene12343_All//0.00E+00//gi|54123100|gb|CO498609.1|CO498609		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene123430_All	395	0.00	0.00	0.27	0.00	0.00	0.00	0.32	0.00	3.43	null	null		8.07E+00	3.99E-01		null	null		null	null		-8.33E+00	2.36E-01		3.42E+00	7.76E-07	Up			Unigene123430_All//1.00E-93//TC166764					
Unigene123431_All	396	0.00	0.26	0.00	0.25	0.26	0.57	1.28	0.42	5.73	8.00E+00	3.88E-01		null	null		5.24E-02	9.67E-01		1.18E+00	5.49E-01		-1.60E+00	1.07E-01		2.16E+00	4.04E-07	Up			Unigene123431_All//9.00E-138//TC134074					
Unigene123432_All	400	0.00	0.25	0.00	0.12	0.00	0.00	0.00	0.94	5.08	7.98E+00	3.88E-01		null	null		-6.96E+00	5.56E-01		-6.96E+00	6.36E-01		9.88E+00	6.88E-03		1.23E+01	1.44E-14	Up			Unigene123432_All//9.00E-172//TC162553					
Unigene123433_All	400	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.99	null	null		null	null		null	null		null	null		null	null		1.15E+01	1.20E-08	Up								
Unigene123434_All	400	0.00	0.38	0.00	0.00	0.09	0.68	0.21	0.21	2.29	8.57E+00	2.36E-01		null	null		6.43E+00	8.30E-01		9.40E+00	7.03E-02		-1.65E-02	1.01E+00		3.44E+00	7.53E-05	Up	Unigene123434_All//gi|225428388|ref|XP_002283561.1|//4.00E-13//PREDICTED: similar to JAB [Vitis vinifera]	Unigene123434_All//6.00E-12//AT1G22920| CSN5A (COP9 SIGNALOSOME 5A)	Unigene123434_All//3.00E-110//gi|78350859|gb|DT571133.1|DT571133			GO:0000338//GO:0003006//GO:0005488//GO:0009640//GO:0009725//GO:0043234//GO:0043623//GO:0051319	nr +
Unigene123437_All	401	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.29	null	null		null	null		null	null		null	null		null	null		1.03E+01	6.13E-04	Up								
Unigene123438_All	402	0.00	0.00	0.00	0.12	0.09	0.22	0.21	1.56	2.77	null	null		null	null		-5.32E-01	8.25E-01		8.59E-01	7.95E-01		2.89E+00	4.88E-03		3.72E+00	4.35E-06	Up	Unigene123438_All//gi|209970600|gb|ACJ03063.1|//2.00E-21//M18-6p [Malus floribunda]	Unigene123438_All//1.00E-16//AT2G34930| disease resistance family protein			ko04626|Plant-pathogen interaction		nr +
Unigene123439_All	403	0.00	0.00	0.00	0.00	0.17	0.00	0.00	0.21	3.26	null	null		null	null		7.42E+00	6.10E-01		null	null		7.70E+00	4.02E-01		1.17E+01	1.73E-09	Up								
Unigene12344_All	1489	7.52	8.64	4.22	12.18	10.87	19.78	16.84	25.18	46.10	2.01E-01	2.31E-01		-8.33E-01	2.49E-06		-1.64E-01	2.59E-01		7.00E-01	7.34E-13		5.81E-01	1.35E-13		1.45E+00	2.15E-111	Up	Unigene12344_All//gi|79315417|ref|NP_001030877.1|//6.00E-82//AGK2 (GUANYLATE KINASE); guanylate kinase [Arabidopsis thaliana]	Unigene12344_All//3.00E-88//AT3G57550| AGK2 (GUANYLATE KINASE); guanylate kinase	Unigene12344_All//0.00E+00//TC135074		ko00230|Purine metabolism	GO:0009117//GO:0016776	nr -
Unigene123441_All	405	65.37	140.37	86.91	158.42	141.74	111.51	134.77	153.56	65.22	1.10E+00	3.08E-48	Up	4.11E-01	1.04E-05		-1.61E-01	1.52E-02		-5.07E-01	1.07E-15		1.88E-01	2.18E-03		-1.05E+00	7.77E-54	Down			Unigene123441_All//5.00E-81//gi|164280913|gb|ES814905.1|ES814905					
Unigene123443_All	406	0.00	0.50	0.00	0.00	0.00	0.00	0.10	0.21	2.45	8.96E+00	1.37E-01		null	null		null	null		null	null		9.84E-01	7.32E-01		4.56E+00	3.72E-06	Up	Unigene123443_All//gi|124359343|gb|ABD28505.2|//4.00E-07//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene123443_All//2.00E-05//AT5G42905| nucleic acid binding / ribonuclease H	Unigene123443_All//3.00E-14//DT464644			GO:0043231	nr -
Unigene123444_All	408	0.00	0.00	0.00	0.00	0.00	0.00	1.87	1.02	10.35	null	null		null	null		null	null		null	null		-8.65E-01	2.39E-01		2.47E+00	1.29E-14	Up								
Unigene123445_All	409	0.00	0.00	0.00	0.00	0.00	0.00	0.21	1.12	11.40	null	null		null	null		null	null		null	null		2.44E+00	3.74E-02		5.78E+00	3.73E-30	Up	Unigene123445_All//gi|38346480|emb|CAE03719.2|//2.00E-21//OSJNBa0021F22.13 [Oryza sativa (japonica cultivar-group)]	Unigene123445_All//9.00E-16//AT3G47580| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152//GO:0016020//GO:0016491	nr +
Unigene123447_All	410	0.00	0.00	0.00	0.00	0.17	0.22	0.10	0.31	3.21	null	null		null	null		7.39E+00	6.10E-01		7.78E+00	4.77E-01		1.57E+00	5.45E-01		4.96E+00	2.80E-08	Up								
Unigene123449_All	411	0.00	0.25	0.00	0.00	0.00	0.00	0.10	0.61	1.94	7.95E+00	3.88E-01		null	null		null	null		null	null		2.57E+00	1.53E-01		4.24E+00	7.42E-05	Up								
Unigene12345_All	2252	10.66	10.10	5.72	12.50	10.63	25.17	22.17	47.60	67.29	-7.81E-02	5.52E-01		-8.98E-01	1.89E-14		-2.34E-01	2.19E-02		1.01E+00	8.59E-45	Up	1.10E+00	1.02E-110	Up	1.60E+00	9.80E-283	Up	Unigene12345_All//gi|124360196|gb|ABN08209.1|//1.00E-152//Guanylate kinase/L-type calcium channel region; Galactose oxidase, central [Medicago truncatula]	Unigene12345_All//2.00E-151//AT3G57550| AGK2 (GUANYLATE KINASE); guanylate kinase	Unigene12345_All//0.00E+00//TC149182		ko00230|Purine metabolism		nr -
Unigene123450_All	411	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.81	3.78	null	null		null	null		null	null		null	null		9.67E+00	1.27E-02		1.19E+01	3.54E-11	Up	Unigene123450_All//gi|299473100|emb|CBN77493.1|//9.00E-28//Inositol-3-phosphate synthase [Ectocarpus siliculosus]	Unigene123450_All//3.00E-25//AT4G39800| MIPS1 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 1); inositol-3-phosphate synthase			ko00562|Inositol phosphate metabolism	GO:0003824//GO:0008152	nr +
Unigene123451_All	413	0.51	0.49	0.00	0.24	0.00	0.22	0.31	0.20	2.32	-4.63E-02	9.89E-01		-8.99E+00	1.46E-01		-7.91E+00	3.14E-01		-1.41E-01	9.51E-01		-6.02E-01	7.67E-01		2.91E+00	1.88E-04	Up			Unigene123451_All//5.00E-07//TC151576					
Unigene123452_All	414	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20	1.35	null	null		null	null		null	null		null	null		7.66E+00	4.02E-01		1.04E+01	3.28E-04	Up								
Unigene123453_All	414	0.00	0.12	0.00	0.24	0.08	0.11	0.20	0.61	19.34	6.94E+00	6.17E-01		null	null		-1.53E+00	5.86E-01		-1.14E+00	6.77E-01		1.57E+00	3.26E-01		6.56E+00	1.03E-53	Up								
Unigene123455_All	415	42.99	44.20	29.51	31.93	26.05	31.12	172.38	101.72	38.01	3.99E-02	7.78E-01		-5.43E-01	6.20E-05		-2.93E-01	6.01E-02		-3.68E-02	8.46E-01		-7.61E-01	3.44E-40		-2.18E+00	1.36E-205	Down			Unigene123455_All//1.00E-121//gi|13354448|gb|BG444796.1|BG444796					
Unigene123456_All	415	0.00	0.00	0.00	0.12	0.25	0.87	0.41	1.71	4.03	null	null		null	null		1.05E+00	8.08E-01		2.86E+00	9.45E-02		2.07E+00	1.45E-02		3.31E+00	4.37E-08	Up			Unigene123456_All//4.00E-165//gi|109889849|gb|DW518817.1|DW518817					
Unigene123457_All	415	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.02	null	null		null	null		null	null		null	null		null	null		1.10E+01	3.88E-06	Up	Unigene123457_All//gi|75174963|sp|Q9LN65.1|PP97L_ARATH//3.00E-22//RecName: Full=Serine/threonine-protein phosphatase 7 long form homolog >gi|8778513|gb|AAF79521.1|AC023673_9 F21D18.16 [Arabidopsis thaliana]	Unigene123457_All//7.00E-20//AT1G48120| calcineurin-like phosphoesterase family protein					nr +
Unigene123458_All	417	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.10	3.63	6.92E+00	6.17E-01		null	null		null	null		null	null		6.65E+00	6.35E-01		1.18E+01	6.77E-11	Up			Unigene123458_All//8.00E-12//ES836490					
Unigene12346_All	1745	4.11	3.54	4.49	3.91	5.25	5.46	2.91	0.84	2.15	-2.14E-01	3.73E-01		1.27E-01	6.11E-01		4.25E-01	2.42E-02		4.82E-01	9.95E-03		-1.79E+00	1.25E-11	Down	-4.38E-01	5.95E-02		Unigene12346_All//gi|297809407|ref|XP_002872587.1|//1.00E-110//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297318424|gb|EFH48846.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene12346_All//9.00E-105//AT4G11440| binding	Unigene12346_All//0.00E+00//DW508867			GO:0006810//GO:0016020	nr +
Unigene123461_All	419	0.00	0.00	0.00	0.36	0.25	0.86	0.50	0.40	4.37	null	null		null	null		-5.33E-01	7.85E-01		1.27E+00	3.82E-01		-3.39E-01	8.12E-01		3.12E+00	2.25E-08	Up			Unigene123461_All//5.00E-07//ES820730					
Unigene123462_All	419	0.00	0.12	0.25	0.36	2.14	0.32	1.41	1.80	13.50	6.92E+00	6.17E-01		7.99E+00	3.99E-01		2.58E+00	3.22E-03		-1.41E-01	9.43E-01		3.46E-01	6.20E-01		3.26E+00	1.86E-25	Up	Unigene123462_All//gi|259121399|gb|ACV92019.1|//1.00E-31//WRKY transcription factor 17 ([Populus tomentosa x P. bolleana] x P. tomentosa]	Unigene123462_All//1.00E-27//AT2G38470| WRKY33; transcription factor	Unigene123462_All//0.00E+00//TC133205	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0010468//GO:0043231	nr +
Unigene123463_All	422	0.00	0.00	0.00	0.00	0.00	0.00	0.20	1.39	3.21	null	null		null	null		null	null		null	null		2.79E+00	8.26E-03		4.00E+00	1.31E-07	Up			Unigene123463_All//0.00E+00//TC178436					
Unigene123464_All	422	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.70	null	null		null	null		null	null		null	null		null	null		1.07E+01	2.63E-05	Up								ESTscan +
Unigene123468_All	426	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.06	null	null		null	null		null	null		null	null		null	null		1.10E+01	2.05E-06	Up								
Unigene123469_All	428	0.00	0.00	0.00	0.00	0.00	0.00	0.49	0.29	44.77	null	null		null	null		null	null		null	null		-7.53E-01	6.32E-01		6.50E+00	5.50E-128	Up			Unigene123469_All//2.00E-31//DW479423					
Unigene12347_All	1974	2.92	3.31	3.64	4.26	5.23	3.04	1.16	0.34	0.77	1.84E-01	4.55E-01		3.21E-01	1.76E-01		2.95E-01	1.12E-01		-4.87E-01	1.48E-02		-1.77E+00	1.47E-05	Down	-5.93E-01	1.05E-01		Unigene12347_All//gi|145340110|ref|NP_192883.2|//1.00E-75//binding [Arabidopsis thaliana]	Unigene12347_All//7.00E-69//AT4G11440| binding	Unigene12347_All//0.00E+00//DW508867			GO:0006810//GO:0016020	nr +
Unigene123472_All	432	0.00	0.12	0.00	0.00	0.00	0.21	0.69	0.10	3.97	6.87E+00	6.17E-01		null	null		null	null		7.71E+00	4.77E-01		-2.82E+00	8.85E-02		2.53E+00	1.59E-06	Up								
Unigene123473_All	433	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.04	null	null		null	null		null	null		null	null		null	null		1.16E+01	1.73E-09	Up	Unigene123473_All//gi|33413768|gb|AAN28293.1|//4.00E-10//cellulose synthase 2 [Gossypium barbadense]		Unigene123473_All//7.00E-28//ES803124			GO:0009987//GO:0016020//GO:0016757//GO:0046872	nr -
Unigene123474_All	435	0.00	0.47	0.00	0.00	0.00	0.31	0.49	0.67	33.34	8.86E+00	1.37E-01		null	null		null	null		8.28E+00	3.11E-01		4.69E-01	7.06E-01		6.10E+00	5.54E-95	Up			Unigene123474_All//1.00E-07//EX170439					
Unigene123475_All	436	0.00	0.00	0.00	1.14	0.00	0.10	0.19	0.10	2.01	null	null		null	null		-1.02E+01	8.98E-04	Down	-3.46E+00	1.61E-02		-1.02E+00	7.25E-01		3.37E+00	1.32E-04	Up	Unigene123475_All//gi|102139738|gb|ABF69945.1|//4.00E-11//AMP-dependent synthetase and ligase family protein, 5' partial [Musa acuminata]					GO:0003824	nr +
Unigene123476_All	438	0.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.64	-7.90E+00	3.73E-01		-7.90E+00	3.95E-01		null	null		null	null		null	null		1.25E+01	1.09E-17	Up			Unigene123476_All//9.00E-15//DR463937					
Unigene123477_All	439	0.48	0.00	0.49	0.23	0.31	0.10	0.00	0.19	3.36	-8.90E+00	1.22E-01		2.55E-02	1.00E+00		4.68E-01	8.77E-01		-1.14E+00	6.77E-01		7.57E+00	4.02E-01		1.17E+01	1.30E-10	Up	Unigene123477_All//gi|224069172|ref|XP_002326292.1|//1.00E-32//actin 8 [Populus trichocarpa] >gi|222833485|gb|EEE71962.1| actin 8 [Populus trichocarpa]	Unigene123477_All//4.00E-19//AT2G42100| actin, putative				GO:0000166//GO:0044424	nr -
Unigene123478_All	440	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.27	null	null		null	null		null	null		null	null		null	null		1.03E+01	3.28E-04	Up	Unigene123478_All//gi|145336181|ref|NP_174096.3|//4.00E-38//nucleic acid binding [Arabidopsis thaliana]	Unigene123478_All//2.00E-39//AT1G27750| nucleic acid binding	Unigene123478_All//0.00E+00//TC131700			GO:0005488//GO:0043231	nr +
Unigene12348_All	2574	1.42	0.67	1.84	2.23	2.27	1.81	0.59	0.16	0.51	-1.09E+00	8.27E-04	Down	3.72E-01	2.18E-01		3.12E-02	9.24E-01		-3.00E-01	2.69E-01		-1.86E+00	3.50E-04	Down	-2.11E-01	6.41E-01		Unigene12348_All//gi|145340110|ref|NP_192883.2|//5.00E-96//binding [Arabidopsis thaliana]	Unigene12348_All//3.00E-89//AT4G11440| binding	Unigene12348_All//0.00E+00//gi|164266211|gb|ES807988.1|ES807988			GO:0006810//GO:0016020	nr +
Unigene123480_All	443	0.00	0.00	0.00	0.00	0.00	0.00	0.10	0.19	3.24	null	null		null	null		null	null		null	null		9.84E-01	7.32E-01		5.08E+00	4.35E-09	Up	Unigene123480_All//gi|169142753|ref|YP_001687180.1|//1.00E-06//ycf2 [Oenothera argillicola] >gi|169142770|ref|YP_001687197.1|ycf2 [Oenothera argillicola] >gi|205413133|sp|B0Z4R9.1|YCF2_OENAR RecName: Full=Protein ycf2 >gi|159792991|gb|ABW98747.1| ycf2 [Oenothera argillicola] >gi|159793008|gb|ABW98764.1| ycf2 [Oenothera argillicola]		Unigene123480_All//0.00E+00//CO132424				nr -
Unigene123481_All	444	0.00	0.00	0.00	0.00	0.00	0.00	7.24	1.04	5.83	null	null		null	null		null	null		null	null		-2.81E+00	1.30E-12	Down	-3.11E-01	3.26E-01		Unigene123481_All//gi|145408591|ref|YP_001152215.1|//6.00E-12//O8F441 [Pinus koraiensis] >gi|145048840|gb|ABF35457.1|O8F441 [Pinus koraiensis]		Unigene123481_All//3.00E-36//gi|11208621|gb|BF277551.1|BF277551			GO:0009536	nr +
Unigene123482_All	444	0.00	0.00	0.00	0.22	0.00	0.00	0.00	0.00	6.82	null	null		null	null		-7.81E+00	3.14E-01		-7.81E+00	4.01E-01		null	null		1.27E+01	1.14E-21	Up			Unigene123482_All//2.00E-22//gi|11201362|gb|BF270367.1|BF270367					
Unigene123483_All	446	0.00	1.59	0.00	0.11	0.46	0.41	0.19	0.37	7.06	1.06E+01	3.33E-04	Up	null	null		2.05E+00	3.95E-01		1.86E+00	4.58E-01		9.83E-01	6.34E-01		5.22E+00	1.18E-19	Up			Unigene123483_All//1.00E-10//TC176796					
Unigene123484_All	447	0.00	0.00	0.00	0.00	0.00	0.00	0.66	0.19	4.90	null	null		null	null		null	null		null	null		-1.82E+00	2.11E-01		2.89E+00	3.09E-09	Up								
Unigene123485_All	448	0.00	0.00	0.00	0.00	0.61	0.00	0.28	0.28	3.29	null	null		null	null		9.26E+00	7.02E-02		null	null		-1.64E-02	1.02E+00		3.54E+00	1.41E-07	Up	Unigene123485_All//gi|299470938|emb|CBN79922.1|//3.00E-26//Hypothetical leucine rich repeat protein [Ectocarpus siliculosus]	Unigene123485_All//5.00E-22//AT2G26330| ER (ERECTA); transmembrane receptor protein kinase	Unigene123485_All//1.00E-13//DR460799		ko04626|Plant-pathogen interaction	GO:0016301	nr +
Unigene123486_All	448	0.00	0.00	0.00	0.00	0.00	0.00	0.28	0.65	8.36	null	null		null	null		null	null		null	null		1.21E+00	3.92E-01		4.88E+00	1.37E-22	Up	Unigene123486_All//gi|7523686|gb|AAF63125.1|AC009526_10//6.00E-09//Similar to Athila ORF 1 [Arabidopsis thaliana]		Unigene123486_All//5.00E-38//gi|164282946|gb|ES796927.1|ES796927				nr -
Unigene123487_All	449	0.00	0.00	0.00	0.00	0.00	0.00	0.09	0.00	2.31	null	null		null	null		null	null		null	null		-6.56E+00	6.58E-01		4.61E+00	2.03E-06	Up	Unigene123487_All//gi|34452085|gb|AAQ72499.1|//9.00E-32//MADS-box protein 14 [Petunia x hybrida]	Unigene123487_All//1.00E-27//AT3G57230| AGL16 (AGAMOUS-LIKE 16); transcription factor		MADS		GO:0003677//GO:0006350//GO:0010468//GO:0016491	nr -

Unigene123489_All	450	0.00	0.00	0.00	0.00	0.00	0.00	0.66	0.56	3.28	null	null		null	null		null	null		null	null		-2.39E-01	8.40E-01		2.32E+00	3.06E-05	Up							
Unigene12349_All	1897	9.41	19.37	17.60	8.88	17.64	26.86	13.89	20.12	40.34	1.04E+00	1.02E-28	Up	9.04E-01	4.14E-20		9.91E-01	2.31E-28		1.60E+00	1.37E-81	Up	5.35E-01	4.87E-12		1.54E+00	4.95E-135	Up	Unigene12349_All//gi|156752165|gb|AB439833.1|//1.00E-149//inositol phosphate kinase [Glycine max]	Unigene12349_All//1.00E-129//AT4G08170| inositol 1,3,4-trisphosphate 5/6-kinase family protein	Unigene12349_All//0.00E+00//TC142634		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene123490_All	451	0.12	0.00	0.00	0.44	0.15	0.60	0.38	0.93	3.36	-6.86E+00	6.13E-01		-6.86E+00	6.25E-01		-1.53E+00	4.16E-01		4.44E-01	7.64E-01		1.31E+00	2.34E-01		3.16E+00	4.04E-07	Up			Unigene123490_All//7.00E-28//FL576974				
Unigene123491_All	465	0.00	0.00	0.00	0.96	0.22	0.10	0.55	1.26	2.66	null	null		null	null		-2.12E+00	7.28E-02		-3.31E+00	2.84E-02		1.21E+00	1.71E-01		2.28E+00	1.88E-04	Up	Unigene123491_All//gi|124359343|gb|AB028505.2|//4.00E-15//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene123491_All//5.00E-06//AT3G25720| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10613.1); Has 363 Blast hits to 328 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 363; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene123492_All	465	0.00	0.00	0.00	0.00	0.00	0.00	623.29	1845.66	28.10	null	null		null	null		null	null		null	null		1.57E+00	0.00E+00	Up	-4.47E+00	0.00E+00	Down							
Unigene123493_All	468	0.45	0.65	0.00	0.21	1.69	0.68	0.72	0.63	3.75	5.39E-01	6.72E-01		-8.80E+00	1.46E-01		2.99E+00	2.96E-03		1.67E+00	3.09E-01		-2.09E-01	8.50E-01		2.37E+00	3.01E-06	Up							
Unigene123494_All	468	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.18	38.22	null	null		null	null		null	null		null	null		-1.69E-02	1.01E+00		7.72E+00	3.53E-124	Up	Unigene123494_All//gi|15229583|ref|NP_189055.1|//3.00E-35//pectinesterase family protein [Arabidopsis thaliana] >gi|75339286|sp|Q4PSN0.1|PME29_ARATH RecName: Full=Probable pectinesterase 29; Short=PE 29; AltName: Full=Pectin methylesterase 29; Short=AtPME29; Flags: Precursor >gi|67633660|gb|AAY78754.1| pectinesterase family protein [Arabidopsis thaliana]	Unigene123494_All//6.00E-32//AT3G24130| pectinesterase family protein			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0005618//GO:0016788//GO:0031410	nr +
Unigene123495_All	471	0.00	0.00	0.00	0.00	0.22	0.00	0.18	0.00	3.64	null	null		null	null		7.78E+00	4.56E-01		null	null		-7.49E+00	4.04E-01		4.34E+00	5.93E-10	Up	Unigene123495_All//gi|224150180|ref|XP_002336919.1|//2.00E-30//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837129|gb|EEE75508.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene123495_All//1.00E-14//AT1G58400| disease resistance protein (CC-NBS-LRR class), putative	Unigene123495_All//2.00E-157//gi|84154596|gb|DN803951.1|DN803951		ko04626|Plant-pathogen interaction	GO:0016787	nr -
Unigene123496_All	472	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.52	null	null		null	null		null	null		null	null		null	null		1.06E+01	2.63E-05	Up	Unigene123496_All//sp|Q98864|HSS_RHILO//3.00E-40//Homospermidine synthase OS=Rhizobium loti GN=hss PE=3 SV=1						swissprot +
Unigene123498_All	475	0.00	0.00	0.00	0.00	0.00	0.00	0.27	0.44	2.26	null	null		null	null		null	null		null	null		7.21E-01	6.32E-01		3.08E+00	3.77E-05	Up	Unigene123498_All//gi|124359343|gb|AB028505.2|//4.00E-06//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]						nr -
Unigene123499_All	476	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.84	null	null		null	null		null	null		null	null		null	null		1.08E+01	2.05E-06	Up	Unigene123499_All//gi|54606709|dbj|BAD66732.1|//2.00E-10//orf147a [Beta vulgaris subsp. vulgaris] >gi|54606753|dbj|BAD66776.1| orf147a [Beta vulgaris subsp. vulgaris]	Unigene123499_All//1.00E-09//AT4G04650| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cold; LOCATED IN: stromule; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43730.1); Has 608 Blast hits to 598 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 608; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					GO:0043231//GO:0044444	nr -
Unigene1235_All	3944	2.51	2.18	1.17	5.14	3.97	4.34	5.94	4.71	4.94	-1.99E-01	3.17E-01		-1.09E+00	1.63E-08	Down	-3.72E-01	1.31E-03		-2.44E-01	5.89E-02		-3.36E-01	9.64E-04		-2.66E-01	8.12E-03		Unigene1235_All//gi|9954728|gb|AAG09081.1|AC026237.2|/0.00E+00//Similar to tRNA-splicing endonuclease positive effector SEN1 [Arabidopsis thaliana]	Unigene1235_All//0.00E+00//AT1G16800| tRNA-splicing endonuclease positive effector-related	Unigene1235_All//0.00E+00//TC175445		ko03030|DNA replication	GO:0008187//GO:0016787	nr +
Unigene12350_All	618	5.08	9.84	5.51	5.72	5.01	5.33	6.16	16.23	7.48	9.54E-01	8.56E-05		1.19E-01	7.27E-01		-1.91E-01	5.98E-01		-1.01E-01	7.69E-01		1.40E+00	1.02E-15	Up	2.80E-01	2.79E-01		Unigene12350_All//gi|224127758|ref|XP_002329170.1|//4.00E-72//acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa] >gi|222870951|gb|EEF08082.1| acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]	Unigene12350_All//8.00E-66//AT5G16370| AAE5 (ACYL ACTIVATING ENZYME 5); catalytic	Unigene12350_All//0.00E+00//gi|109842412|gb|DW240972.1|DW240972		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0016405//GO:0042579	nr -
Unigene123500_All	476	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	3.43	null	null		null	null		null	null		null	null		7.46E+00	4.02E-01		1.17E+01	9.65E-12	Up							
Unigene123502_All	481	0.00	0.00	0.00	0.00	0.00	0.00	0.35	0.09	2.65	null	null		null	null		null	null		null	null		-2.02E+00	3.67E-01		2.91E+00	1.05E-05	Up	Unigene123502_All//gi|124359343|gb|AB028505.2|//3.00E-06//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]						nr +
Unigene123503_All	483	0.11	0.00	0.00	0.72	0.14	0.19	0.88	0.43	6.10	-6.76E+00	6.13E-01		-6.76E+00	6.25E-01		-2.34E+00	1.01E-01		-1.95E+00	1.96E-01		-1.02E+00	3.51E-01		2.80E+00	7.78E-12	Up							
Unigene123504_All	486	0.11	0.00	0.11	0.62	0.14	0.19	2.00	0.26	1.64	-6.75E+00	6.13E-01		2.52E-02	9.95E-01		-2.12E+00	1.65E-01		-1.73E+00	2.89E-01		-2.96E+00	1.89E-04	Down	-2.88E-01	6.35E-01		Unigene123504_All//gi|83853818|gb|ABC47851.1|//7.00E-43//heat shock transcription factor [Glycine max]	Unigene123504_All//7.00E-28//AT1G46264| AT-HSFB4; DNA binding / transcription factor	Unigene123504_All//1.00E-51//gi|78340237|gb|DT560511.1|DT560511	HSF		GO:0051301	nr -
Unigene123505_All	489	0.11	0.00	0.00	0.20	0.28	0.00	0.35	1.45	4.24	-6.74E+00	6.13E-01		-6.74E+00	6.25E-01		4.68E-01	8.77E-01		-7.67E+00	4.01E-01		2.07E+00	1.45E-02		3.61E+00	1.45E-10	Up			Unigene123505_All//6.00E-07//TC144954				
Unigene123506_All	490	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68	2.93	null	null		null	null		null	null		null	null		9.41E+00	1.27E-02		1.15E+01	2.48E-10	Up	Unigene123506_All//gi|224118358|ref|XP_002317799.1|//1.00E-26//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222858472|gb|EEE96019.1| oligopeptide transporter OPT family [Populus trichocarpa]	Unigene123506_All//2.00E-13//AT4G27730| OPT6 (OLIGOPEPTIDE TRANSPORTER 1); oligopeptide transporter	Unigene123506_All//6.00E-10//gi|109891415|gb|DW520378.1|DW520378			GO:0015197//GO:0015833//GO:0016020	nr +
Unigene123508_All	494	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.98	null	null		null	null		null	null		null	null		null	null		1.15E+01	1.30E-10	Up	Unigene123508_All//gi|15239540|ref|NP_197965.1|//5.00E-13//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|5107831|gb|AAD40144.1|AF149413_23 contains similarity to protein kinase domains (Pfam PF00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana] >gi|224589685|gb|ACN59374.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene123508_All//7.00E-09//AT5G25930| leucine-rich repeat family protein / protein kinase family protein	Unigene123508_All//8.00E-31//gi|48780226|gb|CO089592.1|CO089592			GO:0016020//GO:0016301	nr +
Unigene123509_All	496	0.00	0.00	0.00	0.00	0.14	0.09	0.00	0.00	1.45	null	null		null	null		7.12E+00	6.10E-01		6.51E+00	6.96E-01		null	null		1.05E+01	2.63E-05	Up							
Unigene123512_All	499	0.00	0.00	0.00	0.10	0.00	0.00	0.08	0.08	2.63	null	null		null	null		-6.64E+00	5.56E-01		-6.64E+00	6.36E-01		-1.54E-02	1.00E+00		4.96E+00	2.80E-08	Up			Unigene123512_All//1.00E-32//gi|48778760|gb|CO088126.1|CO088126				
Unigene123513_All	502	0.63	0.81	0.00	0.20	0.00	0.18	0.17	0.25	2.94	3.69E-01	7.24E-01		-9.29E+00	4.92E-02		-7.63E+00	3.14E-01		-1.42E-01	9.51E-01		5.69E-01	7.82E-01		4.12E+00	2.19E-08	Up							
Unigene123514_All	503	0.00	0.20	0.00	0.69	0.14	0.45	0.34	0.83	3.41	7.65E+00	3.87E-01		null	null		-2.34E+00	1.01E-01		-6.27E-01	6.21E-01		1.31E+00	2.34E-01		3.34E+00	2.49E-08	Up	Unigene123514_All//gi|4587572|gb|AA025803.1|AC006550.11|/7.00E-36//Similar to gb|U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF|00400 WD40, G-beta repeats. ESTs gb|T43386 and gb|AA395236 come from this gene [Arabidopsis thaliana]	Unigene123514_All//2.00E-30//AT1G03060| WD-40 repeat family protein / beige-related	Unigene123514_All//0.00E+00//TC176911				nr +
Unigene123515_All	508	0.00	0.00	0.00	0.00	0.07	0.00	0.17	0.00	4.39	null	null		null	null		6.08E+00	8.30E-01		null	null		-7.38E+00	4.04E-01		4.72E+00	2.07E-13	Up	Unigene123515_All//gi|18025342|gb|AAK38482.1|//3.00E-49//beta-D-xylosidase [Hordeum vulgare]	Unigene123515_All//5.00E-49//AT1G78060| glycosyl hydrolase family 3 protein	Unigene123515_All//2.00E-53//TC147850		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0005576//GO:0005618//GO:0009536//GO:0015926//GO:0016020//GO:0044238	nr -
Unigene123516_All	508	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.92	null	null		null	null		null	null		null	null		null	null		1.19E+01	2.77E-14	Up	Unigene123516_All//gi|297835022|ref|XP_002885393.1|//2.00E-51//carbohydrate transporter/ sugar porter [Arabidopsis lyrata subsp. lyrata] >gi|297331233|gb|EFH61652.1| carbohydrate transporter/ sugar porter [Arabidopsis lyrata subsp. lyrata]	Unigene123516_All//2.00E-43//AT3G20660| At0CT4 (Arabidopsis thaliana ORGANIC CATION/CARNITINE TRANSPORTER4); carbohydrate transmembrane transporter/ sugar:hydrogen symporter				GO:0006810//GO:0009534//GO:0022891//GO:0031224	nr +
Unigene123517_All	511	0.00	0.00	0.00	0.00	0.00	0.00	406.09	818.49	21.99	null	null		null	null		null	null		null	null		1.01E+00	0.00E+00	Up	-4.21E+00	0.00E+00	Down							
Unigene123518_All	512	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.18	null	null		null	null		null	null		null	null		null	null		1.11E+01	4.36E-08	Up	Unigene123518_All//gi|224081403|ref|XP_002306397.1|//3.00E-59//GRAS family transcription factor [Populus trichocarpa] >gi|222855846|gb|EEE93393.1| GRAS family transcription factor [Populus trichocarpa]	Unigene123518_All//7.00E-19//AT5G41920| scarecrow transcription factor family protein		GRAS		GO:0010468	nr -
Unigene123519_All	515	0.20	0.00	0.41	0.29	0.00	0.00	0.49	0.89	4.41	-7.67E+00	3.73E-01		1.03E+00	5.92E-01		-8.18E+00	1.66E-01		-8.18E+00	2.33E-01		8.58E-01	3.96E-01		3.16E+00	2.39E-10	Up							
Unigene123520_All	522	0.00	0.00	0.00	0.00	0.13	0.09	0.00	0.40	3.97	null	null		null	null		7.04E+00	6.10E-01		6.43E+00	6.96E-01		8.64E+00	7.85E-02		1.20E+01	7.51E-15	Up	Unigene123520_All//gi|10998537|gb|AAG25966.1|AF302082.1|/7.00E-57//cytokinin-regulated kinase 1 [Nicotiana tabacum]	Unigene123520_All//6.00E-49//AT5G47850| CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase				GO:0004713//GO:0006464//GO:0031410//GO:0032559//GO:0042802	nr -
Unigene123521_All	522	0.00	0.19	0.00	0.00	0.79	0.17	0.32	0.00	2.59	7.60E+00	3.87E-01		null	null		9.63E+00	1.25E-02		7.43E+00	4.77E-01		-8.34E+00	1.35E-01		3.00E+00	3.58E-06	Up	Unigene123521_All//gi|83728524|gb|ABC41950.1|//3.00E-42//FAD-linked oxidoreductase 1 [Glycine max]	Unigene123521_All//5.00E-38//AT5G44400| FAD-binding domain-containing protein	Unigene123521_All//4.00E-14//TC170571			GO:0003824	nr -

Unigene123522_All	523	0.00	0.19	0.00	0.00	0.00	0.00	0.32	0.64	6.63	7.60E+00	3.87E-01		null	null		null	null		null	null		9.83E-01	4.24E-01		4.36E+00	1.18E-19	Up	Unigene123522_All//gi|30680158|ref|NP_172229.2|//3.00E-22//RTFL3 (ROTUNDIFOLIA LIKE 3) [Arabidopsis thaliana] >gi|42822051|tpg|DAA02280.1| TPA_exp: DVL9 [Arabidopsis thaliana] >gi|88900362|gb|ABD57493.1| At1g07490 [Arabidopsis thaliana]	Unigene123522_All//7.00E-11//AT2G29125| RTFL2 (ROTUNDIFOLIA LIKE 2)	Unigene123522_All//8.00E-28//DR462210			GO:0048513	nr +
Unigene123523_All	523	0.00	0.00	0.00	0.00	0.00	0.00	0.24	0.48	1.90	null	null		null	null		null	null		null	null		9.84E-01	5.17E-01		2.97E+00	1.11E-04	Up	Unigene123523_All//gi|75174963|sp|Q6L9G5.1|PPP7L_ARATH//7.00E-22//RecName: Full=Serine/threonine-protein phosphatase 7 long form homolog >gi|8778513|gb|AAF79521.1|AC023673_9 F21D18.16 [Arabidopsis thaliana]	Unigene123523_All//4.00E-23//AT1G48120| calcineurin-like phosphoesterase family protein	Unigene123523_All//8.00E-102//FL577665				nr +
Unigene123524_All	528	0.20	0.00	0.20	0.19	0.52	0.17	0.40	0.24	2.11	-7.63E+00	3.73E-01		2.53E-02	1.00E+00		1.47E+00	4.20E-01		-1.41E-01	9.51E-01		-7.54E-01	6.32E-01		2.40E+00	2.76E-04	Up	Unigene123524_All//gi|297727483|ref|NP_001176105.1|//2.00E-15//Os10g0357350 [Oryza sativa Japonica Group] >gi|255678530|dbj|BAH94833.1| Os10g0357350 [Oryza sativa Japonica Group]		Unigene123524_All//0.00E+00//TC177897			GO:0003676//GO:0006259//GO:0008233	nr -
Unigene123525_All	529	0.00	0.38	0.00	0.57	0.13	0.09	0.16	0.16	2.33	8.58E+00	1.37E-01		null	null		-2.12E+00	1.65E-01		-2.73E+00	1.37E-01		-1.63E-02	1.01E+00		3.87E+00	7.61E-07	Up	Unigene123525_All//gi|224088497|ref|XP_002335092.1|//3.00E-06//predicted protein [Populus trichocarpa] >gi|222832803|gb|EEE71280.1| predicted protein [Populus trichocarpa]						nr +
Unigene123526_All	529	0.00	0.10	0.00	0.09	0.13	0.00	0.00	0.00	1.73	6.58E+00	6.17E-01		null	null		4.67E-01	9.58E-01		-6.56E+00	6.36E-01		null	null		1.08E+01	1.08E-06	Up			Unigene123526_All//4.00E-08//DR463958				
Unigene123528_All	533	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.87	null	null		null	null		null	null		null	null		null	null		1.09E+01	3.00E-07	Up	Unigene123528_All//gi|121501700|gb|ABM55241.1|//3.00E-09//retrotransposon protein [Beta vulgaris]						nr +
Unigene123529_All	535	0.20	0.00	0.00	0.00	0.13	0.00	0.32	0.00	1.94	-7.61E+00	3.73E-01		-7.61E+00	3.95E-01		7.01E+00	6.10E-01		null	null		-8.30E+00	1.35E-01		2.61E+00	2.37E-04	Up	Unigene123529_All//gi|23491567|dbj|BAC16756.1|//2.00E-33//cis-prenyltransferase [Periploca sepium]	Unigene123529_All//2.00E-27//AT2G17570| undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein	Unigene123529_All//3.00E-12//TC138206		ko00900|Terpenoid backbone biosynthesis		nr +
Unigene12353_All	711	14.20	8.20	5.02	21.51	15.89	33.09	15.52	6.94	11.32	-7.93E-01	1.13E-05		-1.50E+00	9.20E-14	Down	-4.37E-01	1.14E-03		6.22E-01	1.45E-08		-1.16E+00	3.94E-13	Down	-4.56E-01	2.19E-03				Unigene12353_All//0.00E+00//gi|21094019|gb|BQ406344.1|BQ406344				
Unigene123531_All	543	0.00	1.12	0.00	0.00	0.19	0.33	0.47	0.46	3.01	1.01E+01	1.17E-03		null	null		7.57E+00	4.56E-01		8.38E+00	1.94E-01		-1.68E-02	1.02E+00		2.69E+00	1.30E-06	Up	Unigene123531_All//gi|297793123|ref|XP_002864446.1|//9.00E-29//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297310281|gb|EFH40705.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene123531_All//6.00E-30//AT5G36310| pentatricopeptide (PPR) repeat-containing protein				GO:0031410	nr +
Unigene123532_All	544	0.00	0.09	0.20	0.73	0.06	0.00	0.31	0.77	2.12	6.54E+00	6.17E-01		7.61E+00	3.99E-01		-3.53E+00	2.10E-02		-9.52E+00	1.11E-02		1.31E+00	2.34E-01		2.77E+00	5.09E-05	Up	Unigene123532_All//gi|4587540|gb|AAD25771.1|AC006577_7//4.00E-26//Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family [Arabidopsis thaliana]	Unigene123532_All//5.00E-26//AT5G40990| GLIP1 (GDSL LIPASE1); carboxylesterase/ lipase	Unigene123532_All//3.00E-120//TC138489				nr -
Unigene123534_All	548	0.00	0.00	0.00	0.00	0.00	0.00	0.23	0.46	28.35	null	null		null	null		null	null		null	null		9.83E-01	5.17E-01		6.94E+00	1.48E-105	Up	Unigene123534_All//gi|116518570|gb|ABJ99502.1|//7.00E-74//1-aminocyclopropane-1-carboxylate synthase [Gossypium hirsutum]	Unigene123534_All//1.00E-64//AT4G11280| ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase	Unigene123534_All//5.00E-94//TC129594		ko00270|Cysteine and methionine metabolism	GO:0005515//GO:0006555//GO:0006950//GO:0008629//GO:0009605//GO:0009725//GO:0016740//GO:0016846//GO:0048037	nr +
Unigene123535_All	563	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	2.12	null	null		null	null		null	null		null	null		-6.23E+00	6.58E-01		4.82E+00	1.77E-07	Up	Unigene123535_All//sp|Q6DFL0|C102A_XENLA//5.00E-06//Coiled-coil domain-containing protein 102A OS=Xenopus laevis GN=ccdc102a PE=2 SV=1	Unigene123535_All//6.00E-06//AT5G60210| LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT2G37080.1); Has 77946 Blast hits to 39215 proteins in 1793 species: Archae - 845; Bacteria - 8877; Metazoa - 39997; Fungi - 6049; Plants - 2988; Viruses - 248; Other Eukaryotes - 18942 (source: NCBI BLink).						swissprot -
Unigene123536_All	568	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	19.43	null	null		null	null		null	null		null	null		null	null		1.42E+01	3.69E-79	Up							
Unigene123538_All	569	0.18	0.18	0.09	0.00	0.24	0.00	0.82	2.28	4.48	-4.62E-02	9.90E-01		-9.74E-01	7.21E-01		7.92E+00	3.19E-01		null	null		1.48E+00	7.16E-03		2.45E+00	4.71E-09	Up			Unigene123538_All//3.00E-61//ES817646				
Unigene123539_All	570	0.00	0.00	0.00	0.09	0.24	0.48	0.00	0.44	2.80	null	null		null	null		1.47E+00	6.19E-01		2.44E+00	2.22E-01		8.78E+00	4.31E-02		1.14E+01	1.85E-11	Up							
Unigene12354_All	672	1.64	1.21	3.33	3.11	3.89	3.49	2.64	0.56	1.25	-4.39E-01	4.95E-01		1.03E+00	2.31E-02		3.23E-01	4.58E-01		1.67E-01	7.02E-01		-2.24E+00	8.44E-06	Down	-1.09E+00	1.06E-02				Unigene12354_All//3.00E-68//BQ406344				
Unigene123540_All	571	0.09	0.18	0.00	0.00	0.00	0.00	0.30	0.22	1.74	9.54E-01	7.26E-01		-6.52E+00	6.25E-01		null	null		null	null		-4.32E-01	7.93E-01		2.56E+00	3.91E-04	Up			Unigene123540_All//2.00E-41//TC161176				ESTscan -
Unigene123541_All	573	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.64	null	null		null	null		null	null		null	null		null	null		1.14E+01	6.77E-11	Up	Unigene123541_All//gi|224119836|ref|XP_002331173.1|//1.00E-10//predicted protein [Populus trichocarpa] >gi|222873256|gb|EEF10387.1| predicted protein [Populus trichocarpa]		Unigene123541_All//3.00E-49//FL577203				nr +
Unigene123542_All	574	0.00	0.44	0.00	0.00	0.00	0.00	0.00	0.00	2.15	8.79E+00	7.87E-02		null	null		null	null		null	null		null	null		1.11E+01	6.29E-09	Up			Unigene123542_All//2.00E-13//DW235752				
Unigene123543_All	577	0.00	0.18	0.00	0.00	1.07	0.47	0.51	0.65	3.18	7.46E+00	3.87E-01		null	null		1.01E+01	7.90E-04	Up	8.88E+00	7.03E-02		3.46E-01	7.38E-01		2.63E+00	3.47E-07	Up							ESTscan -
Unigene123544_All	580	0.54	0.00	0.00	0.17	0.00	0.00	0.51	0.86	3.09	-9.08E+00	3.66E-02		-9.08E+00	4.92E-02		-7.42E+00	3.14E-01		-7.42E+00	4.01E-01		7.61E-01	4.22E-01		2.60E+00	5.78E-07	Up	Unigene123544_All//gi|5882740|gb|AAD55293.1|AC008263_24//5.00E-48//P2544.20 [Arabidopsis thaliana]	Unigene123544_All//3.00E-36//AT1G74830| unknown protein	Unigene123544_All//1.00E-08//TC146989				nr +
Unigene123545_All	580	0.00	0.17	0.64	0.34	0.00	0.00	0.58	0.29	20.47	7.45E+00	3.87E-01		9.33E+00	2.50E-02		-8.42E+00	8.44E-02		-8.42E+00	1.34E-01		-1.02E+00	4.00E-01		5.13E+00	1.69E-72	Up							
Unigene123546_All	586	0.00	0.00	0.00	0.00	0.00	0.00	0.14	0.36	2.86	null	null		null	null		null	null		null	null		1.31E+00	4.47E-01		4.31E+00	1.09E-09	Up	Unigene123546_All//sp|Q03185|TS11_GIALA//1.00E-08//Major surface trophozoite antigen 11 OS=Giardia lamblia GN=TSP11 PE=3 SV=1						swissprot -
Unigene123547_All	590	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.24	null	null		null	null		null	null		null	null		null	null		1.17E+01	1.02E-13	Up			Unigene123547_All//7.00E-07//gi|109875045|gb|DW504019.1|DW504019				
Unigene123548_All	602	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.18	null	null		null	null		null	null		null	null		null	null		1.11E+01	1.73E-09	Up	Unigene123548_All//gi|116310096|emb|CAH67116.1|//9.00E-24//HO502605.7 [Oryza sativa (indica cultivar-group)]					GO:0003676//GO:0003824//GO:0009987//GO:0043170//GO:0044238//GO:0044464	nr -
Unigene123549_All	603	0.00	0.00	0.00	0.50	0.29	0.30	1.47	1.04	17.31	null	null		null	null		-7.96E-01	5.57E-01		-7.26E-01	6.39E-01		-5.02E-01	4.60E-01		3.56E+00	4.28E-50	Up			Unigene123549_All//7.00E-10//DR457626				
Unigene123550_All	616	0.17	0.00	0.00	0.00	0.00	0.00	0.14	0.34	2.20	-7.41E+00	3.73E-01		-7.41E+00	3.95E-01		null	null		null	null		1.31E+00	4.47E-01		4.00E+00	1.31E-07	Up							
Unigene123551_All	618	0.59	0.00	0.17	0.16	0.50	0.66	0.68	1.08	4.00	-9.21E+00	1.97E-02		-1.78E+00	2.34E-01		1.64E+00	3.21E-01		2.03E+00	1.49E-01		6.62E-01	4.02E-01		2.55E+00	3.94E-09	Up	Unigene123551_All//gi|297798788|ref|XP_002867278.1|//8.00E-19//enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313114|gb|EFH43537.1| enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene123551_All//3.00E-19//AT4G31810| enoyl-CoA hydratase/isomerase family protein	Unigene123551_All//1.00E-150//TC176597			GO:0009062//GO:0016289//GO:0016836//GO:0043231	nr +
Unigene123552_All	621	0.00	0.65	0.00	0.00	0.00	0.00	0.00	0.13	3.72	9.35E+00	1.36E-02		null	null		null	null		null	null		7.07E+00	4.02E-01		1.19E+01	1.49E-16	Up							
Unigene123553_All	629	0.00	0.32	0.17	0.00	0.22	0.00	0.20	0.27	2.28	8.33E+00	1.37E-01		7.40E+00	3.99E-01		7.77E+00	3.19E-01		null	null		3.98E-01	8.14E-01		3.50E+00	2.50E-07	Up	Unigene123553_All//gi|115463309|ref|NP_001055254.1|//9.00E-07//Os05g0344400 [Oryza sativa Japonica Group] >gi|75110699|sp|Q5W6M3.1|U497J_ORYSJ RecName: Full=UPF0497 membrane protein Os05g0344400 >gi|113578805|dbj|BAF17168.1| Os05g0344400 [Oryza sativa Japonica Group]	Unigene123553_All//2.00E-11//AT2G38480| integral membrane protein, putative	Unigene123553_All//8.00E-87//DT052356				nr -
Unigene123555_All	640	0.00	0.00	0.00	0.00	0.00	0.00	0.86	0.78	62.12	null	null		null	null		null	null		null	null		-1.32E-01	8.80E-01		6.18E+00	2.39E-261	Up	Unigene123555_All//gi|4530126|gb|AAD21872.1|//2.00E-29//receptor-like protein kinase homolog RKD20-1 [Phaseolus vulgaris]	Unigene123555_All//1.00E-22//AT4G38830| protein kinase family protein				GO:0000166//GO:0004672	nr +
Unigene123556_All	645	0.00	0.00	0.00	0.31	0.00	0.00	1.18	0.97	3.21	null	null		null	null		-8.27E+00	8.44E-02		-8.27E+00	1.34E-01		-2.80E-01	6.96E-01		1.44E+00	3.77E-04	Up							
Unigene123558_All	668	0.16	0.68	0.32	0.15	0.00	0.14	0.13	0.94	3.82	2.12E+00	9.59E-02		1.03E+00	5.92E-01		-7.22E+00	3.13E-01		-1.41E-01	9.51E-01		2.89E+00	4.88E-03		4.91E+00	1.44E-15	Up							
Unigene123559_All	670	0.00	0.00	0.00	0.00	0.00	0.00	1.14	0.12	14.03	null	null		null	null		null	null		null	null		-3.19E+00	7.93E-04	Down	3.63E+00	6.28E-46	Up							
Unigene123560_All	681	0.00	0.00	0.00	0.37	0.35	0.13	0.06	0.61	14.98	null	null		null	null		-4.69E-02	9.51E-01		-1.46E+00	4.07E-01		3.30E+00	2.00E-02		7.91E+00	4.75E-71	Up	Unigene123560_All//gi|297741057|emb|CBI31788.3|//1.00E-07//unnamed protein product [Vitis vinifera]						nr -
Unigene123561_All	690	0.00	0.15	0.31	0.43	0.20	0.59	1.10	1.15	9.12	7.20E+00	3.87E-01		8.27E+00	1.41E-01		-1.12E+00	4.24E-01		4.44E-01	7.01E-01		6.13E-02	9.50E-01		3.05E+00	1.40E-26	Up	Unigene123561_All//gi|297791015|ref|XP_002863392.1|//1.00E-11//ubiquitin-specific protease 21 [Arabidopsis lyrata subsp. lyrata] >gi|297309227|gb|EFH39651.1| ubiquitin-specific protease 21 [Arabidopsis lyrata subsp. lyrata]	Unigene123561_All//2.00E-11//AT4G17895| UBP20 (UBIQUITIN-SPECIFIC PROTEASE 20); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene123561_All//0.00E+00//C0073398		ko04144|Endocytosis	GO:0008234	nr -
Unigene123562_All	691	0.00	0.00	0.00	0.00	0.00	0.00	0.61	1.21	7.38	null	null		null	null		null	null		null	null		9.83E-01	1.58E-01		3.59E+00	5.37E-25	Up							
Unigene123564_All	746	0.00	0.54	0.00	0.13	0.00	0.00	0.45	0.73	35.41	9.09E+00	1.36E-02		null	null		-7.06E+00	3.13E-01		-7.06E+00	4.01E-01		6.84E-01	4.49E-01		6.29E+00	1.28E-174	Up			Unigene123564_All//1.00E-58//DT463919				
Unigene123565_All	751	0.28	0.07	0.00	0.00	0.09	0.00	0.00	0.33	3.61	-2.05E+00	3.34E-01		-8.12E+00	1.46E-01		6.52E+00	6.10E-01		null	null		8.38E+00	4.31E-02		1.18E+01	2.17E-19	Up	Unigene123565_All//gi|75142699|sp|Q7XIZ1.1|GRX39_ORYSJ//1.00E-28//RecName: Full=Glutaredoxin-C9 >gi|33146704|dbj|BAC79508.1| glutaredoxin-like protein [Oryza sativa Japonica Group] >gi|50509780|dbj|BAD31906.1| glutaredoxin-like protein [Oryza sativa Japonica Group]	Unigene123565_All//2.00E-23//AT3G02000| ROXY1; disulfide oxidoreductase	Unigene123565_All//9.00E-07//TC174810			GO:0005488//GO:0006350//GO:0015036//GO:0019725//GO:0043231//GO:0048449	nr +
Unigene123566_All	769	0.27	0.66	0.00	0.13	0.00	0.47	0.27	0.33	9.17	1.28E+00	2.31E-01		-8.09E+00	1.46E-01		-7.02E+00	3.13E-01		1.86E+00	2.20E-01		2.46E-01	8.53E-01		5.06E+00	6.44E-43	Up			Unigene123566_All//0.00E+00//TC140720				
Unigene123567_All	773	0.41	0.39	0.14	0.13	0.00	0.00	0.44	0.97	38.55	-4.62E-02	9.85E-01		-1.56E+00	3.30E-01		-7.01E+00	3.13E-01		-7.01E+00	4.01E-01		1.15E+00	1.26E-01		6.46E+00	1.20E-198	Up			Unigene123567_All//0.00E+00//gi|73860822|gb|DT463561.1|DT463561				
Unigene123568_All	778	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.36	null	null		null	null		null	null		null	null		null	null		1.12E+01	3.75E-13	Up			Unigene123568_All//2.00E-07//DW507908				ESTscan +
Unigene123570_All	816	0.00	0.68	0.00	0.00	0.17	0.11	0.16	0.67	2.25	9.42E+00	2.18E-03		null	null		7.40E+00	3.19E-01		6.79E+00	4.77E-01		2.10E+00	3.71E-02		3.85E+00	7.54E-10	Up	Unigene123570_All//gi|224103967|ref|XP_002313265.1|//1.00E-141//calcium dependent protein kinase 25 [Populus trichocarpa] >gi|222849673|gb|EEE87220.1| calcium dependent protein kinase 25 [Populus trichocarpa]	Unigene123570_All//1.00E-141//AT5G12180| CPK17; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene123570_All//2.00E-78//DR454622		ko04626|Plant-pathogen interaction		nr -
Unigene123571_All	817	0.06	0.12	0.46	0.06	0.21	0.06	0.05	0.26	2.83	9.54E-01	7.26E-01		2.83E+00	9.31E-02		1.79E+00	5.21E-01		-1.42E-01	9.53E-01		2.30E+00	2.40E-01		5.77E+00	4.18E-15	Up							

Unigene123572_All	845	0.00	0.00	0.00	0.24	0.00	0.11	0.10	0.25	4.20	null	null		null	null		-7.88E+00	8.44E-02		-1.14E+00	5.69E-01		1.30E+00	4.47E-01		5.39E+00	2.11E-22	Up	Unigene123572_All//gi|115451173|ref|NP_001049187.1|//3.00E-13//Os03g0184100 [Oryza sativa Japonica Group] >gi|108706546|gb|ABF94341.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108706547|gb|ABF94342.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108706548|gb|ABF94343.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547658|dbj|BAF11101.1| Os03g0184100 [Oryza sativa Japonica Group]	Unigene123572_All//8.00E-23//AT5G42900| unknown protein	Unigene123572_All//0.00E+00//DR454451				nr +
Unigene123573_All	912	0.57	0.22	0.06	0.33	0.53	0.50	1.30	0.87	5.46	-1.37E+00	1.97E-01		-3.30E+00	2.40E-02		6.90E-01	5.67E-01		5.96E-01	6.40E-01		-5.76E-01	3.18E-01		2.07E+00	5.78E-14	Up							
Unigene123574_All	924	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.01	null	null		null	null		null	null		null	null		null	null		1.20E+01	1.65E-26	Up	Unigene123574_All//gi|15218202|ref|NP_177929.1|//2.00E-80//glycosyl hydrolase family 3 protein [Arabidopsis thaliana] >gi|259585708|sp|Q8GZZ5.2|BXL7_ARATH RecName: Full=Probable beta-D-xylosidase 7; Short=AtBXL7; Flags: Precursor >gi|18086336|gb|AAL57631.1| At1g78060/F28K19_32 [Arabidopsis thaliana]	Unigene123574_All//8.00E-82//AT1G78060| glycosyl hydrolase family 3 protein	Unigene123574_All//0.00E+00//TC155221		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0005576//GO:0005618//GO:0009536//GO:0015926//GO:0031410//GO:0044238	nr +
Unigene123575_All	1022	0.00	0.00	0.00	0.00	0.00	0.00	0.66	0.16	14.03	null	null		null	null		null	null		null	null		-2.02E+00	1.98E-02		4.41E+00	2.51E-80	Up	Unigene123575_All//gi|4530126|gb|AAD21872.1|//3.00E-65//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene123575_All//7.00E-62//AT4G38830| protein kinase family protein	Unigene123575_All//3.00E-16//TC174638		ko04626|Plant-pathogen interaction	GO:0004672	nr -
Unigene123576_All	1046	0.00	0.39	0.00	0.00	0.00	0.00	0.61	1.00	3.77	8.60E+00	1.36E-02		null	null		null	null		null	null		7.20E-01	2.38E-01		2.64E+00	1.16E-14	Up	Unigene123576_All//gi|226505988|ref|NP_001149183.1|//2.00E-56//LOC100282805 [Zea mays] >gi|195625298|gb|ACG34479.1| ubiquitin fusion degradation protein 1 [Zea mays]	Unigene123576_All//5.00E-54//AT4G38930| ubiquitin fusion degradation UFD1 family protein					nr -
Unigene123577_All	1076	0.00	0.00	0.00	0.00	0.06	0.25	0.55	0.51	34.69	null	null		null	null		6.00E+00	6.10E-01		7.98E+00	7.03E-02		-1.23E-01	8.84E-01		5.98E+00	1.26E-242	Up	Unigene123577_All//gi|74273615|gb|AB401475.1|//1.00E-156//1-aminocyclopropane-1-carboxylate synthase ACS6 [Gossypium hirsutum]	Unigene123577_All//3.00E-110//AT4G11280| ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase	Unigene123577_All//2.00E-94//TC129594		ko00270|Cysteine and methionine metabolism		nr +
Unigene123578_All	1092	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	3.25	null	null		null	null		null	null		null	null		6.84E+00	2.40E-01		1.17E+01	2.27E-25	Up	Unigene123578_All//gi|297843370|ref|XP_002889566.1|//1.00E-147//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335408|gb|EFH65825.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene123578_All//8.00E-149//AT1G05800| DGL (DONGLE); triacylglycerol lipase	Unigene123578_All//2.00E-36//gi|193219615|gb|EY198077.1|EY198077				nr -
Unigene123579_All	1561	0.00	0.00	0.00	0.06	0.00	0.12	0.73	0.94	6.58	null	null		null	null		-6.00E+00	3.13E-01		8.59E-01	6.95E-01		3.58E-01	4.96E-01		3.17E+00	1.32E-44	Up	Unigene123579_All//gi|30693378|ref|NP_190662.2|//1.00E-127//BCS1 (CYTOCHROME BC1 SYNTHESIS); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana] >gi|18086343|gb|AAL57634.1| AT3g50930/F18B3_210 [Arabidopsis thaliana] >gi|27363216|gb|AAO11527.1| At3g50930/F18B3_210 [Arabidopsis thaliana]	Unigene123579_All//1.00E-108//AT3G50930| BCS1 (CYTOCHROME BC1 SYNTHESIS); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene123579_All//1.00E-10//ES820227				nr -
Unigene12359_All	1774	0.94	1.54	1.44	2.16	2.68	2.29	1.17	0.54	3.03	7.09E-01	6.30E-02		6.10E-01	1.42E-01		3.09E-01	3.14E-01		8.37E-02	7.99E-01		-1.11E+00	6.05E-03		1.38E+00	7.77E-09	Up	Unigene12359_All//gi|124484391|dbj|BAF46306.1|//1.00E-111//ataxin-2 related protein [Ipomoea nil]	Unigene12359_All//7.00E-80//AT1G54170| CID3 (CTC-Interacting Domain 3)	Unigene12359_All//0.00E+00//gi|78342019|gb|DT562293.1|DT562293		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene12360_All	401	2.22	1.90	1.33	0.75	1.80	3.49	9.70	5.84	6.86	-2.27E-01	7.27E-01		-7.40E-01	3.48E-01		1.27E+00	1.56E-01		2.23E+00	5.33E-04	Up	-7.33E-01	7.92E-03		-5.01E-01	6.27E-02		Unigene12360_All//gi|22330644|ref|NP_177657.2|//2.00E-22//5' nucleotidase family protein [Arabidopsis thaliana]	Unigene12360_All//8.00E-22//AT1G75210| 5' nucleotidase family protein					nr +
Unigene12364_All	765	15.05	14.70	11.97	23.12	18.46	18.42	33.99	25.90	15.15	-3.32E-02	8.55E-01		-3.30E-01	6.78E-02		-3.25E-01	1.13E-02		-3.28E-01	1.45E-02		-3.92E-01	3.75E-05		-1.17E+00	6.96E-31	Down	Unigene12364_All//gi|224993590|gb|ACN76474.1|//4.00E-11//CBL-interacting protein kinase 24 [Populus euphratica]	Unigene12364_All//2.00E-11//AT1G30270| CIPK23 (CBL-INTERACTING PROTEIN KINASE 23); kinase/ protein binding / protein serine/threonine kinase	Unigene12364_All//1.00E-132//gi|164331686|gb|EX166727.1|EX166727		ko00020|Citrate cycle (TCA cycle)//ko00640|Propanoate metabolism	GO:0004674//GO:0006464//GO:0006950//GO:0016020//GO:0023060//GO:0031667//GO:0032559//GO:0043231//GO:0044444//GO:0071805	nr -
Unigene12365_All	2725	52.70	18.26	43.24	5.58	6.67	5.15	35.70	11.09	11.65	-1.53E+00	2.65E-201	Down	-2.85E-01	5.58E-11		2.59E-01	5.17E-02		-1.13E-01	5.13E-01		-1.69E+00	3.36E-192	Down	-1.62E+00	6.49E-186	Down	Unigene12365_All//gi|300680945|sp|B5W8Z9.1|FAO2_LOTJA//0.00E+00//RecName: Full=Long-chain-alcohol oxidase FAO2; AltName: Full=Long-chain fatty alcohol oxidase 2 >gi|209570222|emb|CAP15763.1| long chain fatty alcohol oxidase FAO2 [Lotus japonicus]	Unigene12365_All//0.00E+00//AT4G28570| alcohol oxidase-related	Unigene12365_All//0.00E+00//TC153280			GO:0006950//GO:0016020//GO:0016899//GO:0030554//GO:0043231//GO:0044481	nr +
Unigene12369_All	577	1.63	1.23	1.11	2.76	2.03	2.04	4.47	1.45	3.80	-4.09E-01	5.67E-01		-5.60E-01	4.39E-01		-4.45E-01	4.08E-01		-4.41E-01	4.28E-01		-1.63E+00	1.43E-05	Down	-2.35E-01	5.25E-01		Unigene12369_All//gi|297791271|ref|XP_002863520.1|//6.00E-70//cyclin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309355|gb|EFH39779.1| cyclin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12369_All//1.00E-68//AT5G45190| cyclin family protein	Unigene12369_All//0.00E+00//CO074284			GO:0000904//GO:0007049//GO:0009791//GO:0043231//GO:0048827//GO:0050789//GO:0051707	nr +
Unigene12374_All	440	4.76	5.07	13.80	7.70	6.34	5.34	0.77	0.76	1.36	9.12E-02	8.27E-01		1.54E+00	8.08E-09	Up	-2.80E-01	4.41E-01		-5.28E-01	1.28E-01		-1.66E-02	1.02E+00		8.21E-01	3.20E-01		Unigene12374_All//gi|15450996|gb|AB96769.1|//4.00E-25//Unknown protein [Arabidopsis thaliana] >gi|53828651|gb|AU194435.1| At4g16100 [Arabidopsis thaliana]	Unigene12374_All//2.00E-26//AT4G16100| unknown protein	Unigene12374_All//2.00E-133//gi|164269237|gb|ES809201.1|ES809201				nr +
Unigene12375_All	2252	31.09	37.84	69.05	20.66	22.20	20.38	11.34	9.84	9.64	2.84E-01	4.51E-07		1.15E+00	9.82E-137	Up	1.04E-01	2.26E-01		-2.00E-02	8.43E-01		-2.05E-01	4.43E-02		-2.34E-01	1.55E-02		Unigene12375_All//gi|30725294|gb|AAP37669.1|//1.00E-105//At2g01260 [Arabidopsis thaliana]	Unigene12375_All//3.00E-97//AT2G01260| unknown protein	Unigene12375_All//0.00E+00//TC134826				nr +
Unigene1238_All	2275	6.55	2.14	9.99	15.68	3.28	1.15	104.04	40.80	17.18	-1.62E+00	3.17E-23	Down	6.09E-01	2.57E-07		-2.25E+00	1.18E-107	Down	-3.77E+00	1.25E-157	Down	-1.35E+00	0.00E+00	Down	-2.60E+00	0.00E+00	Down	Unigene1238_All//gi|297851686|ref|XP_002893724.1|//0.00E+00//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339566|gb|EFH69983.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1238_All//0.00E+00//AT1G32450| NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	Unigene1238_All//0.00E+00//TC160811			GO:0004871//GO:0015833//GO:0044464	nr +
Unigene12385_All	941	40.14	16.80	26.26	35.42	34.47	37.20	14.11	12.66	13.08	-1.26E+00	9.08E-40	Down	-6.13E-01	8.32E-12		-3.89E-02	7.67E-01		7.08E-02	5.44E-01		-1.56E-01	3.26E-01		-1.09E-01	4.82E-01		Unigene12385_All//gi|115446295|ref|NP_001046927.1|//2.00E-22//Os02g0509500 [Oryza sativa Japonica Group] >gi|113536458|dbj|BAF08841.1| Os02g0509500 [Oryza sativa Japonica Group]	Unigene12385_All//9.00E-13//AT3G27030| unknown protein	Unigene12385_All//0.00E+00//TC153353			GO:0031224//GO:0031410	nr -
Unigene12386_All	1771	4.96	3.63	4.84	6.22	4.74	5.58	14.37	6.37	5.98	-4.50E-01	2.18E-02		-3.60E-02	8.70E-01		-3.90E-01	1.95E-02		-1.55E-01	4.49E-01		-1.17E+00	1.11E-29	Down	-1.26E+00	2.77E-34	Down	Unigene12386_All//gi|44681324|gb|AAS47602.1|//2.00E-26//At5g40980 [Arabidopsis thaliana] >gi|45773828|gb|AAS76718.1| At5g40980 [Arabidopsis thaliana]	Unigene12386_All//2.00E-21//AT5G40980| unknown protein	Unigene12386_All//0.00E+00//DW502398			GO:0031224//GO:0031410	nr -
Unigene12388_All	1391	4.97	28.81	11.10	30.65	40.35	46.66	75.08	78.33	66.59	2.54E+00	4.46E-109	Up	1.16E+00	3.32E-14	Up	3.97E-01	9.30E-10		6.06E-01	1.42E-21		6.13E-02	2.42E-01		-1.73E-01	1.20E-04		Unigene12388_All//gi|211906524|gb|ACJ11755.1|//1.00E-167//UDP-D-xylose 4-epimerase [Gossypium hirsutum]	Unigene12388_All//2.00E-165//AT1G30620| MUR4 (MURUS 4); UDP-arabinose 4-epimerase/ catalytic	Unigene12388_All//0.00E+00//TC138656		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene1239_All	2373	0.09	0.11	0.29	0.29	0.01	0.04	4.37	1.36	0.60	2.76E-01	8.43E-01		1.73E+00	7.68E-02		-4.34E+00	2.80E-04	Down	-2.95E+00	5.84E-03		-1.69E+00	4.08E-21	Down	-2.85E+00	3.12E-41	Down	Unigene1239_All//gi|297851686|ref|XP_002893724.1|//0.00E+00//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339566|gb|EFH69983.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1239_All//0.00E+00//AT1G32450| NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	Unigene1239_All//0.00E+00//TC160811			GO:0004871//GO:0015833//GO:0044464	nr +
Unigene12390_All	391	3.21	0.26	2.18	0.76	3.35	1.85	1.08	1.07	0.92	-3.63E+00	2.00E-05	Down	-5.60E-01	3.87E-01		2.13E+00	1.00E-03		1.27E+00	1.56E-01		-1.66E-02	1.02E+00		-2.38E-01	7.88E-01					Unigene12390_All//3.00E-70//gi|132466971|gb|BE053548.2|BE053548				
Unigene12392_All	2537	9.78	8.53	8.69	10.37	11.25	10.72	4.28	2.37	1.60	-1.97E-01	8.99E-02		-1.70E-01	1.70E-01		1.18E-01	3.16E-01		4.78E-02	6.98E-01		-8.52E-01	4.36E-08		-1.42E+00	6.51E-18	Down	Unigene12392_All//gi|195606206|gb|ACG24933.1|//3.00E-43//60S ribosomal protein L13a [Zea mays]	Unigene12392_All//1.00E-43//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene12392_All//0.00E+00//TC135203		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr +
Unigene12394_All	1752	2.09	6.16	3.34	4.29	2.81	3.48	11.17	12.74	8.75	1.56E+00	4.29E-16	Up	6.78E-01	7.90E-03		-6.11E-01	2.14E-03		-3.03E-01	1.90E-01		1.89E-01	9.12E-02		-3.52E-01	1.25E-03		Unigene12394_All//gi|15220265|ref|NP_172571.1|//4.00E-59//DNAJ chaperone C-terminal domain-containing protein [Arabidopsis thaliana] >gi|1931643|gb|AAB65478.1| DnaJ isolog; 47062-48761 [Arabidopsis thaliana] >gi|67633364|gb|AAY78607.1| DNAJ chaperone C-terminal domain-containing protein [Arabidopsis thaliana]	Unigene12394_All//3.00E-61//AT1G11040| DNAJ chaperone C-terminal domain-containing protein	Unigene12394_All//0.00E+00//TC150939			GO:0005515//GO:0044267	nr -
Unigene12397_All	3136	29.71	20.65	26.79	30.16	28.99	30.37	22.61	13.01	11.23	-5.25E-01	2.20E-22		-1.49E-01	1.09E-02		-5.74E-02	3.84E-01		9.90E-03	9.00E-01		-7.98E-01	3.86E-43		-1.01E+00	1.22E-65	Down	Unigene12397_All//gi|15222192|ref|NP_177667.1|//1.00E-148//OTC (ORNITHINE CARBAMOYLTRANSFERASE); amino acid binding / carboxyl- or carbamoyltransferase/ ornithine carbamoyltransferase [Arabidopsis thaliana] >gi|4917022|sp|O50039.2|OTC_ARATH RecName: Full=Ornithine carbamoyltransferase, chloroplastic; AltName: Full=Ornithine transcarbamylase; Short=OTCase; Flags: Precursor >gi|10120450|gb|AAG13075.1|AC022375_13 Ornithine carbamoyltransferase [Arabidopsis thaliana]	Unigene12397_All//7.00E-149//AT1G19600| pfkB-type carbohydrate kinase family protein	Unigene12397_All//0.00E+00//gi|78329081|gb|DT549355.1|DT549355		ko00330|Arginine and proline metabolism		nr -

Unigene12399_All	576	5.18	3.69	5.18	11.16	8.31	8.70	5.29	2.83	2.56	-4.87E-01	1.84E-01		-1.00E-04	1.00E+00		-4.25E-01	6.42E-02		-3.58E-01	1.44E-01		-9.01E-01	4.73E-03		-1.05E+00	7.86E-04	Down	Unigene12399_All//gi|45752648|gb|AAS76222.1|//1.00E-61//At4g36660 [Arabidopsis thaliana] >gi|45773768|gb|AAS76688.1| At4g36660 [Arabidopsis thaliana]	Unigene12399_All//2.00E-45//AT4G36660| unknown protein	Unigene12399_All//0.00E+00//TC159498			GO:0006810//GO:0008152//GO:0016628//GO:0031224	nr -
Unigene124_All	1003	2.71	3.08	2.97	2.63	3.23	5.72	11.00	12.13	22.52	1.84E-01	6.10E-01		1.32E-01	7.19E-01		2.94E-01	4.54E-01		1.12E+00	7.00E-06	Up	1.40E-01	4.04E-01		1.03E+00	3.53E-22	Up	Unigene124_All||gi|224121336|ref|XP_002318557.1|//1.00E-157//aminophospholipid ATPase [Populus trichocarpa] >gi|222859230|gb|EEE96777.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene124_All//1.00E-144//AT1G68710| haloacid dehalogenase-like hydrolase family protein	Unigene124_All//2.00E-08//TC173667				nr +
Unigene1240_All	952	1.32	1.38	1.40	3.35	0.25	0.19	17.45	15.85	4.52	6.92E-02	9.12E-01		8.43E-02	8.85E-01		-3.73E+00	1.55E-16	Down	-4.14E+00	2.61E-15	Down	-1.39E-01	3.26E-01		-1.95E+00	6.96E-42	Down	Unigene1240_All||gi|297851686|ref|XP_002890724.1|//4.00E-09//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309566|gb|EFH69983.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1240_All//2.00E-10//AT1G32450| NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter				GO:0015833//GO:0044464	nr -
Unigene12400_All	991	3.06	3.12	4.57	5.58	4.86	5.61	5.16	2.74	2.37	2.65E-02	9.60E-01		5.77E-01	5.28E-02		-1.98E-01	4.95E-01		6.70E-03	9.81E-01		-9.13E-01	1.17E-04		-1.12E+00	1.94E-06	Down	Unigene12400_All||gi|45752648|gb|AAS76222.1|//5.00E-65//At4g36660 [Arabidopsis thaliana] >gi|45773768|gb|AAS76688.1| At4g36660 [Arabidopsis thaliana]	Unigene12400_All//3.00E-56//AT4G36660| unknown protein	Unigene12400_All//2.00E-101//gi|109885651|gb|DW514621.1|DW514621			GO:0006810//GO:0008152//GO:0016628//GO:0031224	nr +
Unigene12401_All	904	7.58	3.81	6.48	13.34	12.53	15.14	11.41	8.18	5.46	-9.92E-01	1.27E-05		-2.27E-01	3.79E-01		-8.96E-02	6.34E-01		1.83E-01	2.98E-01		-4.80E-01	2.58E-03		-1.06E+00	3.87E-11	Down	Unigene12401_All||gi|45752648|gb|AAS76222.1|//4.00E-63//At4g36660 [Arabidopsis thaliana] >gi|45773768|gb|AAS76688.1| At4g36660 [Arabidopsis thaliana]	Unigene12401_All//9.00E-49//AT4G36660| unknown protein	Unigene12401_All//0.00E+00//TC159498			GO:0006810//GO:0008152//GO:0016628//GO:0031224	nr -
Unigene12402_All	3528	2.17	1.59	2.42	5.96	4.88	3.70	17.58	13.22	6.80	-4.42E-01	3.81E-02		1.58E-01	4.84E-01		-2.88E-01	1.45E-02		-6.88E-01	3.55E-09		-4.11E-01	4.40E-12		-1.37E+00	3.56E-93	Down	Unigene12402_All||gi|59976864|gb|AY68281.1|//0.00E+00//maturase [Pavonia spinifex]	Unigene12402_All//0.00E+00//ATMG00520| hypothetical protein	Unigene12402_All//0.00E+00//EE593145			GO:0003676//GO:0006260//GO:0006396//GO:0034061//GO:0043231	nr +
Unigene12403_All	503	19.45	3.22	3.18	73.78	24.92	14.73	9.83	1.99	1.11	-2.59E+00	6.21E-28	Down	-2.61E+00	5.10E-27	Down	-1.57E+00	1.39E-67	Down	-2.33E+00	3.80E-100	Down	-2.30E+00	2.19E-15	Down	-3.15E+00	4.43E-22	Down	Unigene12403_All||gi|297836448|ref|XP_002886106.1|//6.00E-87//phosphate-responsive 1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331946|gb|EFH62365.1| phosphate-responsive 1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12403_All//5.00E-67//AT2G17230| EXL5 (EXORDIUM LIKE 5)	Unigene12403_All//0.00E+00//TC143870			GO:0031410	nr +
Unigene12404_All	1518	9.38	2.17	2.03	42.43	20.89	8.51	10.47	0.94	0.79	-2.11E+00	1.19E-31	Down	-2.20E+00	4.63E-32	Down	-1.02E+00	1.10E-59	Down	-2.32E+00	4.96E-173	Down	-3.48E+00	1.15E-73	Down	-3.73E+00	1.16E-80	Down	Unigene12404_All||gi|18398352|ref|NP_565409.1|//1.00E-146//EXL5 (EXORDIUM LIKE 5) [Arabidopsis thaliana] >gi|4584346|gb|AAD25141.1| expressed protein [Arabidopsis thaliana] >gi|16604330|gb|AAL24171.1| At2g17230/T23A1.9 [Arabidopsis thaliana] >gi|19699196|gb|AAL90964.1| At2g17230/T23A1.9 [Arabidopsis thaliana]	Unigene12404_All//2.00E-126//AT2G17230| EXL5 (EXORDIUM LIKE 5)	Unigene12404_All//0.00E+00//TC153429		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr -
Unigene12405_All	1251	12.34	1.42	1.79	60.05	26.34	12.17	8.31	0.94	0.70	-3.12E+00	4.97E-53	Down	-2.79E+00	1.84E-45	Down	-1.19E+00	4.26E-89	Down	-2.30E+00	3.37E-200	Down	-3.15E+00	3.30E-44	Down	-3.57E+00	4.60E-51	Down	Unigene12405_All||gi|18398352|ref|NP_565409.1|//1.00E-151//EXL5 (EXORDIUM LIKE 5) [Arabidopsis thaliana] >gi|4584346|gb|AAD25141.1| expressed protein [Arabidopsis thaliana] >gi|16604330|gb|AAL24171.1| At2g17230/T23A1.9 [Arabidopsis thaliana] >gi|19699196|gb|AAL90964.1| At2g17230/T23A1.9 [Arabidopsis thaliana]	Unigene12405_All//6.00E-124//AT2G17230| EXL5 (EXORDIUM LIKE 5)	Unigene12405_All//0.00E+00//TC133629				nr +
Unigene12409_All	4017	10.56	30.63	18.09	16.10	19.15	17.27	16.47	24.40	15.16	1.54E+00	1.20E-172	Up	7.77E-01	2.16E-33		2.51E-01	7.11E-06		1.02E-01	1.60E-01		5.67E-01	8.40E-33		-1.19E-01	4.85E-02		Unigene12409_All||gi|15233015|ref|NP_186939.1|//2.00E-68//PHD finger protein-related [Arabidopsis thaliana]	Unigene12409_All//5.00E-44//AT3G02890| PHD finger protein-related	Unigene12409_All//0.00E+00//TC169773				nr +
Unigene1241_All	2204	1.26	1.06	5.17	6.83	2.11	0.55	11.28	3.00	2.22	-2.51E-01	5.25E-01		2.04E+00	1.83E-23	Up	-1.69E+00	6.89E-31	Down	-3.62E+00	1.81E-64	Down	-1.91E+00	6.81E-59	Down	-2.34E+00	1.68E-78	Down	Unigene1241_All||gi|30692706|ref|NP_174523.2|//0.00E+00//NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter [Arabidopsis thaliana]	Unigene1241_All//0.00E+00//AT1G32450| NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	Unigene1241_All//0.00E+00//TC160811			GO:0004871//GO:0015833//GO:0044464	nr -
Unigene12412_All	450	2.21	0.34	0.00	5.87	5.13	1.00	8.17	14.86	18.59	-2.71E+00	1.41E-03		-1.11E+01	1.77E-05	Down	-1.95E-01	6.28E-01		-2.55E+00	2.37E-08	Down	8.62E-01	2.26E-05		1.19E+00	1.03E-10	Up	Unigene12412_All||gi|297733653|emb|CBI14900.3|//7.00E-11//unnamed protein product [Vitis vinifera]		Unigene12412_All//5.00E-106//TC142103			GO:0004468//GO:0006351//GO:0008134//GO:0043231//GO:0046914	nr -
Unigene12413_All	1450	5.16	17.30	1.95	42.77	37.67	11.77	44.20	118.73	115.94	1.75E+00	1.03E-42	Up	-1.41E+00	1.87E-09	Down	-1.83E-01	5.33E-03		-1.86E+00	2.59E-125	Down	1.43E+00	5.11E-265	Up	1.39E+00	1.24E-254	Up	Unigene12413_All||gi|283123373|dbj|BAI63592.1|//1.00E-119//BTB/POZ domain-containing protein [Lotus japonicus]	Unigene12413_All//2.00E-102//AT5G63160| BT1 (BTB AND TAZ DOMAIN PROTEIN 1); protein binding / transcription regulator	Unigene12413_All//0.00E+00//TC150080		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005488	nr +
Unigene12416_All	1011	13.71	572.65	110.56	10.99	79.43	160.69	25.22	120.14	333.45	5.38E+00	0.00E+00	Up	3.01E+00	0.00E+00	Up	2.85E+00	3.27E-289	Up	3.87E+00	0.00E+00	Up	2.25E+00	0.00E+00	Up	3.73E+00	0.00E+00	Up	Unigene12416_All||gi|206584355|gb|AC115345.1|//1.00E-169//NAC domain protein NAC4 [Gossypium hirsutum] >gi|206584355|gb|AC115350.1| NAC domain protein NAC4 [Gossypium hirsutum]	Unigene12416_All//1.00E-99//AT4G27410| RD26 (RESPONSIVE TO DESICCATION 26); transcription activator/ transcription factor	Unigene12416_All//0.00E+00//TC137134	NAC			nr -
Unigene12417_All	1318	2.30	171.23	12.12	3.89	12.46	63.19	14.56	48.36	221.23	6.22E+00	0.00E+00	Up	2.40E+00	6.41E-40	Up	1.68E+00	5.05E-31	Up	4.02E+00	0.00E+00	Up	1.73E+00	1.49E-130	Up	3.93E+00	0.00E+00	Up	Unigene12417_All||gi|206584355|gb|AC115345.1|//1.00E-169//NAC domain protein NAC4 [Gossypium hirsutum] >gi|206584355|gb|AC115350.1| NAC domain protein NAC4 [Gossypium hirsutum]	Unigene12417_All//1.00E-106//AT4G27410| RD26 (RESPONSIVE TO DESICCATION 26); transcription activator/ transcription factor	Unigene12417_All//0.00E+00//TC143201	NAC			nr +
Unigene12419_All	4516	0.17	0.77	0.68	3.97	3.19	3.21	8.63	7.02	6.07	2.16E+00	1.99E-08	Up	1.98E+00	1.58E-06	Up	-3.17E-01	1.30E-02		-3.07E-01	2.22E-02		-2.99E-01	1.01E-04		-5.08E-01	1.25E-11		Unigene12419_All||gi|15231885|ref|NP_188075.1|//0.00E+00//ATGSL04 (glucan synthase-like 4); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene12419_All//0.00E+00//AT3G14570| ATGSL04 (glucan synthase-like 4); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups	Unigene12419_All//4.00E-22//CO128550			GO:0006074//GO:0035251//GO:0043234//GO:0044464	nr -
Unigene12420_All	1470	0.46	0.86	1.34	2.17	1.36	2.21	6.16	2.19	2.44	8.97E-01	1.36E-01		1.53E+00	2.38E-03		-6.75E-01	4.26E-02		2.85E-02	9.47E-01		-1.49E+00	1.21E-15	Down	-1.34E+00	8.27E-14	Down	Unigene12420_All||gi|227270347|emb|CAX94844.1|//1.00E-116//inositol monophosphatase [Phaseolus vulgaris] >gi|227284273|emb|CAY10404.1| 3.1.2 inositol monophosphatase [Phaseolus vulgaris]	Unigene12420_All//5.00E-112//AT3G02870| VTC4; 3'(2'),5'-bisphosphate nucleotidase/ L-galactose-1-phosphate phosphatase/ inositol or phosphatidylinositol phosphatase/ inositol-1(or 4)-monophosphatase	Unigene12420_All//0.00E+00//gi|48751155|gb|CO081674.1|CO081674		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene12421_All	1347	22.72	10.34	16.13	20.78	23.29	25.52	17.70	7.85	9.61	-1.14E+00	1.23E-27	Down	-4.95E-01	8.29E-07		1.64E-01	1.14E-01		2.96E-01	1.25E-03		-1.17E+00	7.54E-28	Down	-8.81E-01	3.10E-18		Unigene12421_All||gi|55275406|gb|AAV49506.1|//1.00E-130//L-galactose-1-phosphate phosphatase [Actinidia deliciosa]	Unigene12421_All//9.00E-123//AT3G02870| VTC4; 3'(2'),5'-bisphosphate nucleotidase/ L-galactose-1-phosphate phosphatase/ inositol or phosphatidylinositol phosphatase/ inositol-1(or 4)-monophosphatase	Unigene12421_All//0.00E+00//TC139799		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene12422_All	2845	3.59	3.62	2.66	7.76	7.01	6.05	6.96	3.31	3.43	1.17E-02	9.72E-01		-4.32E-01	2.25E-02		-1.46E-01	2.68E-01		-3.59E-01	1.99E-03		-1.07E+00	2.99E-20	Down	-1.02E+00	2.91E-19	Down	Unigene12422_All||gi|297799572|ref|XP_002867670.1|//0.00E+00//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297313506|gb|EFH43929.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene12422_All//0.00E+00//AT4G24270| RNA recognition motif (RRM)-containing protein	Unigene12422_All//0.00E+00//TC173971			GO:0005488	nr -
Unigene12423_All	1317	1.39	29.62	2.14	6.54	6.93	3.33	10.08	7.84	13.43	4.41E+00	1.12E-174	Up	6.24E-01	1.13E-01		8.25E-02	7.45E-01		-9.76E-01	4.99E-07		-3.63E-01	9.71E-03		4.14E-01	3.17E-04		Unigene12423_All||gi|15235152|ref|NP_195118.1|//2.00E-92//protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|75279001|sp|Q81760.1|P2C63_ARATH RecName: Full=Probable protein phosphatase 2C 63; Short=AtPP2C63 >gi|13937198|gb|AAK50092.1|AF372953_1 AT4g33920/F17I5_110 [Arabidopsis thaliana] >gi|19548015|gb|AAL87371.1| AT4g33920/F17I5_110 [Arabidopsis thaliana]	Unigene12423_All//1.00E-93//AT4G33920| protein phosphatase 2C family protein / PP2C family protein	Unigene12423_All//0.00E+00//gi|78323635|gb|DT543909.1|DT543909			GO:0004721//GO:0006464//GO:0043231//GO:0043234//GO:0046914	nr -
Unigene12424_All	1618	4.62	70.43	3.65	16.35	21.07	10.75	11.65	10.67	21.47	3.93E+00	0.00E+00	Up	-3.40E-01	1.40E-01		3.66E-01	2.28E-05		-6.05E-01	3.34E-09		-1.28E-01	3.41E-01		8.82E-01	5.15E-26		Unigene12424_All||gi|15235152|ref|NP_195118.1|//1.00E-162//protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|75279001|sp|Q81760.1|P2C63_ARATH RecName: Full=Probable protein phosphatase 2C 63; Short=AtPP2C63 >gi|13937198|gb|AAK50092.1|AF372953_1 AT4g33920/F17I5_110 [Arabidopsis thaliana] >gi|19548015|gb|AAL87371.1| AT4g33920/F17I5_110 [Arabidopsis thaliana]	Unigene12424_All//3.00E-163//AT4G33920| protein phosphatase 2C family protein / PP2C family protein	Unigene12424_All//0.00E+00//TC145047			GO:0004721//GO:0006464//GO:0043169//GO:0043234	nr -
Unigene12426_All	803	8.86	17.04	14.39	22.83	19.68	22.16	9.48	6.35	3.77	9.43E-01	1.34E-09		7.00E-01	5.14E-05		-2.14E-01	1.14E-01		-4.29E-02	7.78E-01		-5.78E-01	2.13E-03		-1.33E+00	1.10E-11	Down			Unigene12426_All//4.00E-114//BF276374				
Unigene12428_All	580	7.40	5.59	7.90	6.36	7.30	1.40	0.15	0.00	0.00	-4.04E-01	1.77E-01		9.41E-02	7.47E-01		2.00E-01	5.62E-01		-2.18E+00	1.29E-09	Down	-7.19E+00	4.04E-01		-7.19E+00	3.59E-01		Unigene12428_All||gi|18416592|ref|NP_567725.1|//1.00E-36//ACD1-LIKE (ACD1-LIKE); 2 iron, 2 sulfur cluster binding / electron carrier/ oxidoreductase [Arabidopsis thaliana] >gi|15983402|gb|AAL11569.1|AF424575_1 AT4g25650/L7K19_30 [Arabidopsis thaliana] >gi|37962888|gb|AAR05798.1| LLS1-like protein [Arabidopsis thaliana]	Unigene12428_All//8.00E-38//AT4G25650| ACD1-LIKE (ACD1-LIKE); 2 iron, 2 sulfur cluster binding / electron carrier/ oxidoreductase	Unigene12428_All//0.00E+00//gi|109860678|gb|DW489657.1|DW489657		ko00860|Porphyrin and chlorophyll metabolism	GO:0008152//GO:0009526//GO:0016703//GO:0043169//GO:0051536	nr -

Unigene12429_All	1284	89.73	81.06	88.96	12.76	14.05	15.16	1.15	0.81	0.34	-1.47E-01	3.25E-03		-1.24E-02	8.30E-01		1.39E-01	3.62E-01		2.48E-01	6.16E-02		-5.02E-01	3.26E-01		-1.76E+00	5.33E-04	Down	Unigene12429_All//gi|18416592|ref|NP_567725.1|//1.00E-176//ACD1-LIKE (ACD1-LIKE); 2 iron, 2 sulfur cluster binding / electron carrier/ oxidoreductase [Arabidopsis thaliana] >gi|15983402|gb|AAL11569.1|AF424575_1 AT4g25650/L73G19_30 [Arabidopsis thaliana] >gi|37962888|gb|AAR05798.1| LLS1-like protein [Arabidopsis thaliana]	Unigene12429_All//4.00E-177//AT4G25650| ACD1-LIKE (ACD1-LIKE); 2 iron, 2 sulfur cluster binding / electron carrier/ oxidoreductase	Unigene12429_All//0.00E+00//gi|48743480|gb|C0073999.1|C0073999		ko00860|Porphyrin and chlorophyll metabolism	GO:0008152//GO:0016703//GO:0043169//GO:0051536	nr +
Unigene12431_All	2842	4.33	7.26	3.99	13.65	17.51	31.35	46.46	58.34	77.69	7.46E-01	1.06E-09		-1.16E-01	5.41E-01		3.59E-01	2.54E-07		1.20E+00	1.90E-92	Up	3.29E-01	1.43E-20		7.42E-01	1.29E-119		Unigene12431_All//gi|224144210|ref|XP_002325221.1|//0.00E+00//f-box family protein [Populus trichocarpa] >gi|222866655|gb|EEF03786.1| f-box family protein [Populus trichocarpa]	Unigene12431_All//0.00E+00//AT2G25490| EBF1 (E3N3-BINDING F BOX PROTEIN 1); protein binding / ubiquitin-protein ligase	Unigene12431_All//0.00E+00//TC137292		ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0009873//GO:0019941//GO:0031461//GO:0043231	nr +
Unigene12433_All	2333	8.77	6.34	10.91	4.85	5.59	8.32	0.60	0.86	1.49	-4.68E-01	1.17E-04		3.15E-01	5.71E-03		2.07E-01	2.29E-01		7.80E-01	2.24E-10		5.24E-01	2.15E-01		1.31E+00	1.22E-05	Up	Unigene12433_All//gi|4176420|dbj|BAA37167.1|//1.00E-175//cytochrome P450 [Arabidopsis thaliana]	Unigene12433_All//2.00E-171//AT4G36380| ROT3 (ROTUNDIFOLIA 3); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding / steroid hydroxylase	Unigene12433_All//0.00E+00//TC169211		ko00905|Brassinosteroid biosynthesis		nr +
Unigene12434_All	2568	1.85	1.32	0.68	2.81	2.21	2.15	3.75	2.70	2.27	-4.88E-01	7.83E-02		-1.44E+00	1.91E-06	Down	-3.46E-01	1.16E-01		-3.91E-01	8.29E-02		-4.75E-01	4.16E-03		-7.29E-01	5.89E-06		Unigene12434_All//gi|224132088|ref|XP_002328182.1|//0.00E+00//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222837697|gb|EEE76062.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene12434_All//0.00E+00//AT5G22750| RAD5; ATP binding / ATP-dependent helicase/ DNA binding / helicase/ hydrolase, acting on acid anhydrides, in phosphorus-containing anhydrides / nucleic acid binding / protein binding / zinc ion binding	Unigene12434_All//0.00E+00//TC143914			GO:0003676//GO:0009292//GO:0032559//GO:0042623//GO:0046914	nr +
Unigene12435_All	2627	24.56	11.46	16.50	19.38	22.78	8.85	14.90	3.53	4.67	-1.10E+00	1.17E-54	Down	-5.74E-01	1.33E-17		2.33E-01	3.46E-04		-1.13E+00	7.16E-49	Down	-2.08E+00	6.80E-103	Down	-1.67E+00	3.51E-79	Down	Unigene12435_All//gi|225457626|ref|XP_002274415.1|//0.00E+00//PREDICTED: hexose transporter-like [Vitis vinifera]	Unigene12435_All//0.00E+00//AT4G35300| TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter	Unigene12435_All//0.00E+00//TC155371			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr +
Unigene12436_All	3074	3.27	2.29	2.39	3.00	3.90	0.90	3.91	0.46	1.44	-5.12E-01	4.56E-03		-4.51E-01	1.77E-02		3.79E-01	1.96E-02		-1.74E+00	2.20E-17	Down	-3.08E+00	8.13E-50	Down	-1.44E+00	3.79E-20	Down	Unigene12436_All//gi|225457626|ref|XP_002274415.1|//0.00E+00//PREDICTED: hexose transporter-like [Vitis vinifera]	Unigene12436_All//0.00E+00//AT4G35300| TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter	Unigene12436_All//0.00E+00//TC155371			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr -
Unigene1244_All	3101	3.46	1.57	2.06	6.12	5.66	3.58	7.65	2.29	3.44	-1.14E+00	2.95E-10	Down	-7.47E-01	3.51E-05		-1.12E-01	4.55E-01		-7.73E-01	4.36E-10		-1.74E+00	1.97E-49	Down	-1.15E+00	9.82E-28	Down	Unigene1244_All//gi|115445391|ref|NP_001046475.1|//1.00E-131//Os02g0258300 [Oryza sativa Japonica Group] >gi|47497873|dbj|BAD20057.1| extra-large G-protein-like [Oryza sativa Japonica Group] >gi|113536006|dbj|BAF08389.1| Os02g0258300 [Oryza sativa Japonica Group]	Unigene1244_All//5.00E-162//AT3G61670| unknown protein	Unigene1244_All//0.00E+00//ES798670				nr -
Unigene12442_All	1523	12.57	28.05	13.60	17.43	19.04	20.02	14.38	13.61	12.97	1.16E+00	2.61E-39	Up	1.13E-01	4.12E-01		1.27E-01	2.77E-01		1.99E-01	5.70E-02		-7.92E-02	5.46E-01		-1.48E-01	1.86E-01		Unigene12442_All//gi|42567717|ref|NP_196344.2|//1.00E-164//ankyrin repeat family protein [Arabidopsis thaliana] >gi|122239678|sp|Q4FE45.1|XB33_ARATH RecName: Full=E3 ubiquitin-protein ligase XBAT33; AltName: Full=Ankyrin repeat domain and RING finger-containing protein XBAT33; AltName: Full=Protein XB3 homolog 3 >gi|70905089|gb|AAZ14070.1| At5g07270 [Arabidopsis thaliana] >gi|117168057|gb|ABK32111.1| At5g07270 [Arabidopsis thaliana]	Unigene12442_All//3.00E-151//AT5G07270| ankyrin repeat family protein	Unigene12442_All//0.00E+00//gi|78322997|gb|DT543271.1|DT543271				nr +
Unigene12444_All	1578	1.36	3.56	2.09	2.46	7.24	5.21	10.24	11.12	20.63	1.39E+00	1.67E-07	Up	6.22E-01	8.22E-02		1.56E+00	1.66E-19	Up	1.08E+00	9.74E-08	Up	1.20E-01	3.99E-01		1.01E+00	1.79E-30	Up	Unigene12444_All//gi|15225220|ref|NP_180164.1|//9.00E-28//ELF3 (EARLY FLOWERING 3); protein C-terminus binding / transcription factor [Arabidopsis thaliana] >gi|28201800|sp|082804.1|ELF3_ARATH RecName: Full=Protein EARLY FLOWERING 3; AltName: Full=Nematode-responsive protein	Unigene12444_All//7.00E-27//AT2G25930| ELF3 (EARLY FLOWERING 3); protein C-terminus binding / transcription factor	Unigene12444_All//0.00E+00//TC165519		ko04712|Circadian rhythm - plant	GO:0050896	nr -
Unigene12445_All	2611	3.03	11.16	4.53	5.59	14.16	9.63	15.89	16.39	23.18	1.88E+00	6.84E-55	Up	5.81E-01	6.59E-04		1.34E+00	2.57E-50	Up	7.85E-01	2.10E-13		4.53E-02	6.54E-01		5.45E-01	1.00E-19		Unigene12445_All//gi|118767203|gb|ABL11477.1|//2.00E-47//ELF3 protein [Triticum aestivum]	Unigene12445_All//1.00E-35//AT3G21320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: ELF3 (EARLY FLOWERING 3); protein C-terminus binding / transcription factor (TAIR:AT2G25930.1); Has 39 Blast hits to 37 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene12445_All//0.00E+00//TC160344		ko04712|Circadian rhythm - plant		nr +
Unigene12446_All	2549	0.27	0.38	0.08	0.14	0.54	0.48	0.95	1.28	2.39	5.02E-01	4.72E-01		-1.67E+00	8.71E-02		1.98E+00	1.29E-03		1.81E+00	6.71E-03		4.36E-01	1.70E-01		1.34E+00	1.58E-09	Up	Unigene12446_All//gi|118767203|gb|ABL11477.1|//1.00E-59//ELF3 protein [Triticum aestivum]	Unigene12446_All//2.00E-43//AT2G25930| ELF3 (EARLY FLOWERING 3); protein C-terminus binding / transcription factor	Unigene12446_All//0.00E+00//TC160344		ko04712|Circadian rhythm - plant		nr +
Unigene12449_All	3705	3.30	9.35	3.15	4.32	6.23	5.99	11.31	18.00	20.37	1.50E+00	1.84E-47	Up	-7.02E-02	6.99E-01		5.29E-01	5.95E-07		4.72E-01	3.37E-05		6.71E-01	3.15E-30		8.49E-01	4.76E-52		Unigene12449_All//gi|297597467|ref|NP_001044016.2|//1.00E-103//Os01g0706400 [Oryza sativa Japonica Group] >gi|56784921|dbj|BAD82253.1| MAPK activating protein-like [Oryza sativa Japonica Group] >gi|255673607|dbj|BAF05930.2| Os01g0706400 [Oryza sativa Japonica Group]	Unigene12449_All//2.00E-71//AT2G19710| unknown protein	Unigene12449_All//0.00E+00//TC133234				nr -
Unigene12452_All	2746	3.93	6.42	3.20	8.38	9.97	7.45	5.60	6.68	12.46	7.10E-01	8.72E-08		-2.95E-01	1.22E-01		2.50E-01	1.60E-02		-1.70E-01	1.88E-01		2.54E-01	3.57E-02		1.15E+00	2.22E-39	Up	Unigene12452_All//gi|151303119|gb|ABR92762.1|//1.00E-127//transcription factor TF3 [Gossypium hirsutum]	Unigene12452_All//3.00E-31//AT5G40080| bZIP transcription factor family protein	Unigene12452_All//0.00E+00//gi|109871529|gb|DW500505.1|DW500505	bZIP		GO:0003677//GO:0043231	nr -
Unigene12455_All	536	2.34	6.24	4.77	7.62	4.56	6.07	10.02	10.76	9.37	1.41E+00	6.99E-05	Up	1.03E+00	1.37E-02		-7.41E-01	9.16E-03		-3.29E-01	3.18E-01		1.03E-01	6.75E-01		-9.72E-02	6.80E-01		Unigene12455_All//gi|140055579|gb|AB080934.1|//4.00E-21//Heat shock protein DnaJ, N-terminal [Medicago truncatula]	Unigene12455_All//2.00E-08//AT3G62190| DNAJ heat shock N-terminal domain-containing protein	Unigene12455_All//7.00E-167//ES827972			GO:0005515//GO:0044267//GO:0050896	nr -
Unigene12458_All	627	0.92	2.18	1.78	1.27	2.20	3.82	4.59	5.33	3.37	1.25E+00	3.35E-02		9.58E-01	1.54E-01		7.89E-01	1.80E-01		1.59E+00	2.41E-04	Up	2.18E-01	5.27E-01		-4.45E-01	1.70E-01		Unigene12458_All//gi|15229049|ref|NP_188371.1|//2.00E-09//hAT dimerisation domain-containing protein [Arabidopsis thaliana]	Unigene12458_All//1.00E-10//AT3G17450| hAT dimerisation domain-containing protein	Unigene12458_All//3.00E-145//ES833858			GO:0005488	nr -
Unigene12460_All	1198	0.39	1.44	0.71	1.58	2.73	2.87	3.14	1.81	4.59	1.87E+00	6.55E-04	Up	8.55E-01	2.80E-01		7.89E-01	1.92E-02		8.59E-01	1.02E-02		-7.92E-01	4.88E-03		5.47E-01	1.31E-02		Unigene12460_All//gi|15239132|ref|NP_199109.1|//9.00E-99//GYF domain-containing protein [Arabidopsis thaliana]	Unigene12460_All//2.00E-93//AT5G42950| GYF domain-containing protein	Unigene12460_All//0.00E+00//TC144417				nr +
Unigene12464_All	2577	18.13	6.08	5.00	21.77	17.91	7.36	5.02	1.99	2.84	-1.58E+00	6.68E-69	Down	-1.86E+00	9.78E-84	Down	-2.82E-01	1.79E-05		-1.56E+00	1.28E-88	Down	-1.33E+00	1.08E-18	Down	-8.20E-01	3.24E-09		Unigene12464_All//gi|15236625|ref|NP_194113.1|//0.00E+00//glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	Unigene12464_All//0.00E+00//AT4G23820| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene12464_All//0.00E+00//TC135646		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553//GO:0044238//GO:0044464//GO:0045229	nr -
Unigene12465_All	553	11.92	2.75	11.46	61.88	49.50	37.81	8.18	4.46	2.38	-2.12E+00	4.54E-15	Down	-5.71E-02	8.16E-01		-3.22E-01	1.90E-04		-7.11E-01	2.22E-15		-8.76E-01	5.55E-04		-1.78E+00	9.79E-11	Down	Unigene12465_All//gi|115455947|ref|NP_001051574.1|//2.00E-34//Os03g0799100 [Oryza sativa Japonica Group] >gi|108711573|gb|ABF99368.1| Targeting protein for Xklp2 containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550045|dbj|BAF13488.1| Os03g0799100 [Oryza sativa Japonica Group]	Unigene12465_All//2.00E-33//AT3G23090| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: inflorescence meristem, leaf apex, hypocotyl, flower, root; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: WDL1 (TAIR:AT3G01630.3); Has 483 Blast hits to 450 proteins in 87 species: Archae - 2; Bacteria - 15; Metazoa - 188; Fungi - 17; Plants - 148; Viruses - 0; Other Eukaryotes - 113 (source: NCBI BLink).	Unigene12465_All//4.00E-144//TC176862			GO:0043231	nr -

Unigene12466_All	564	7.14	2.79	6.80	29.50	22.41	23.54	8.17	3.26	3.11	-1.36E+00	1.82E-05	Down	-7.15E-02	8.22E-01		-3.97E-01	2.15E-03		-3.25E-01	1.95E-02		-1.33E+00	4.05E-07	Down	-1.39E+00	6.58E-08	Down	Unigene12466_All//gi|255551931|ref|XP_002517010.1|//2.00E-20//conserved hypothetical protein [Ricinus communis] >gi|223543645|gb|EEF45173.1| conserved hypothetical protein [Ricinus communis]	Unigene12466_All//2.00E-05//AT3G23090| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: inflorescence meristem, leaf apex, hypocotyl, flower, root; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: WDL1 (TAIR:AT3G04630.3); Has 483 Blast hits to 450 proteins in 87 species: Archae - 2; Bacteria - 15; Metazoa - 188; Fungi - 17; Plants - 148; Viruses - 0; Other Eukaryotes - 113 (source: NCBI BLink).	Unigene12466_All//0.00E+00//DR456174				nr -
Unigene12467_All	1821	9.77	3.26	6.75	46.83	40.39	24.75	13.47	5.67	4.29	-1.59E+00	7.87E-27	Down	-5.32E-01	8.92E-05		-2.13E-01	5.95E-05		-9.20E-01	3.42E-58		-1.25E+00	1.77E-31	Down	-1.65E+00	5.93E-49	Down	Unigene12467_All//gi|27765054|gb|AO23648.1|//7.00E-67//At3g23090 [Arabidopsis thaliana]	Unigene12467_All//9.00E-68//AT3G23090| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: inflorescence meristem, leaf apex, hypocotyl, flower, root; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: WDL1 (TAIR:AT3G04630.3); Has 483 Blast hits to 450 proteins in 87 species: Archae - 2; Bacteria - 15; Metazoa - 188; Fungi - 17; Plants - 148; Viruses - 0; Other Eukaryotes - 113 (source: NCBI BLink).	Unigene12467_All//0.00E+00//TC176862				nr +
Unigene12469_All	2879	1.31	1.80	1.17	2.60	2.73	3.00	5.14	8.00	17.68	4.56E-01	8.72E-02		-1.67E-01	6.31E-01		7.14E-02	8.05E-01		2.07E-01	3.66E-01		6.38E-01	4.07E-10		1.78E+00	6.34E-111	Up	Unigene12469_All//gi|19920098|gb|AA008530.1|AC079035.2|1.00E-158//Putative calmodulin-binding protein similar to ER66 [Oryza sativa Japonica Group] >gi|19920231|gb|AAM09663.1|AC113338_19 Putative calmodulin binding protein similar to ER66 [Oryza sativa Japonica Group]	Unigene12469_All//3.00E-149//AT5G61220| calmodulin-binding protein	Unigene12469_All//0.00E+00//TC168183	CAMTA			nr +
Unigene12470_All	3431	0.41	0.99	0.47	1.80	0.99	1.54	3.40	5.80	9.67	1.27E+00	2.63E-04	Up	1.78E-01	7.24E-01		-8.58E-01	9.91E-05		-2.25E-01	4.01E-01		7.70E-01	5.59E-12		1.51E+00	2.69E-57	Up	Unigene12470_All//gi|297806971|ref|XP_002871369.1|//0.00E+00//calmodulin-binding transcription activator 1 [Arabidopsis lyrata subsp. lyrata] >gi|297317206|gb|EFH47628.1| calmodulin-binding transcription activator 1 [Arabidopsis lyrata subsp. lyrata]	Unigene12470_All//2.00E-122//AT5G61220| calmodulin-binding protein	Unigene12470_All//0.00E+00//TC168183	CAMTA			nr +
Unigene12471_All	2786	6.76	6.15	6.67	9.48	9.41	9.65	7.69	4.50	3.78	-1.37E-01	3.39E-01		-1.94E-02	9.02E-01		-1.08E-02	9.41E-01		2.55E-02	8.52E-01		-7.74E-01	5.78E-13		-1.03E+00	4.82E-21	Down	Unigene12471_All//gi|297809595|ref|XP_002872681.1|//1.00E-138//AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318518|gb|EFH48940.1| AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12471_All//1.00E-138//AT4G04180| AAA-type ATPase family protein	Unigene12471_All//0.00E+00//TC153875		ko04141|Protein processing in endoplasmic reticulum	GO:0032559//GO:0042623//GO:0043231	nr +
Unigene12473_All	2757	0.68	0.85	0.93	1.52	1.15	1.65	1.09	0.27	0.77	3.07E-01	4.72E-01		4.40E-01	2.98E-01		-4.01E-01	1.83E-01		1.25E-01	6.80E-01		-2.00E+00	3.62E-08	Down	-5.08E-01	1.06E-01		Unigene12473_All//gi|297834580|ref|XP_002885172.1|//0.00E+00//DEAD-box ATP-dependent RNA helicase 13 [Arabidopsis lyrata subsp. lyrata] >gi|297331012|gb|EFH61431.1| DEAD-box ATP-dependent RNA helicase 13 [Arabidopsis lyrata subsp. lyrata]	Unigene12473_All//0.00E+00//AT3G16840| ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene12473_All//0.00E+00//gi|78329556|gb|DT549830.1|DT549830			GO:0032559//GO:0042623//GO:0043231	nr -
Unigene12475_All	2692	6.41	3.65	3.20	6.29	5.08	4.66	4.51	2.59	3.11	-8.13E-01	1.82E-09		-1.00E+00	1.55E-12	Down	-3.09E-01	2.01E-02		-4.32E-01	1.19E-03		-7.98E-01	4.55E-08		-5.37E-01	1.39E-04		Unigene12475_All//gi|152319863|ref|NP_190938.1|//0.00E+00//MEE40 (maternal effect embryo arrest 40) [Arabidopsis thaliana] >gi|75174107|sp|Q9LFF1.1|PP281_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g53700, chloroplastic; AltName: Full=Protein MATERNAL EFFECT EMBRYO ARREST 40; Flags: Precursor >gi|15982931|gb|AAL09812.1| AT3g53700/F4P12_400 [Arabidopsis thaliana]	Unigene12475_All//0.00E+00//AT3G53700| MEE40 (maternal effect embryo arrest 40)	Unigene12475_All//0.00E+00//TC171112			GO:0009536	nr +
Unigene12476_All	664	52.71	44.18	53.25	14.85	12.24	14.01	20.44	38.40	8.64	-2.55E-01	6.10E-03		1.46E-02	8.97E-01		-2.79E-01	1.41E-01		-8.43E-02	6.72E-01		9.10E-01	7.78E-20		-1.24E+00	3.26E-18	Down	Unigene12476_All//gi|224090769|ref|XP_002309074.1|//3.00E-20//HLIP/One helix protein [Populus trichocarpa] >gi|222855050|gb|EEE92597.1| HLIP/One helix protein [Populus trichocarpa]	Unigene12476_All//1.00E-11//AT5G02120| OHP (ONE HELIX PROTEIN)	Unigene12476_All//2.00E-180//TC176164			GO:0009534//GO:0009642//GO:0016701//GO:0019758	nr -
Unigene12477_All	1822	13.96	6.20	8.15	23.98	23.66	29.08	19.05	11.56	10.01	-1.17E+00	3.37E-24	Down	-7.75E-01	5.13E-12		-1.91E-02	8.44E-01		2.78E-01	1.05E-04		-7.21E-01	3.40E-18		-9.28E-01	1.95E-28		Unigene12477_All//gi|15241687|ref|NP_195833.1|//1.00E-125//NDP1 (RANDOM POTATO CDNA CLONE); binding [Arabidopsis thaliana] >gi|989611125|gb|ABF59046.1| At5g02130 [Arabidopsis thaliana]	Unigene12477_All//2.00E-126//AT5G02130| NDP1 (RANDOM POTATO CDNA CLONE); binding	Unigene12477_All//0.00E+00//TC159196				nr +
Unigene12481_All	1788	2.43	1.45	0.48	3.84	5.20	4.88	4.82	1.24	2.21	-7.49E-01	9.91E-03		-2.35E+00	6.82E-11	Down	4.36E-01	1.94E-02		3.43E-01	9.72E-02		-1.96E+00	1.34E-21	Down	-1.13E+00	2.41E-10	Down	Unigene12481_All//gi|857395|dbj|BAA09465.1|//1.00E-146//mitotic cyclin a2-type [Glycine max]	Unigene12481_All//3.00E-133//AT5G11300| CYC3B (MITOTIC-LIKE CYCLIN 3B FROM ARABIDOPSIS); cyclin-dependent protein kinase regulator	Unigene12481_All//0.00E+00//ES836633				nr +
Unigene12482_All	1945	2.07	1.12	0.30	2.84	3.31	1.67	3.93	0.69	2.19	-8.87E-01	3.59E-03		-2.78E+00	3.91E-12	Down	2.20E-01	4.12E-01		-7.66E-01	2.12E-03		-2.52E+00	6.22E-26	Down	-8.44E-01	4.51E-06		Unigene12482_All//gi|5420276|emb|CAB46642.1|//1.00E-128//cyclin A2 [Solanum lycopersicum]	Unigene12482_All//3.00E-112//AT5G11300| CYC3B (MITOTIC-LIKE CYCLIN 3B FROM ARABIDOPSIS); cyclin-dependent protein kinase regulator	Unigene12482_All//0.00E+00//gi|109860574|gb|DW489553.1|DW489553				nr -
Unigene12483_All	2994	1.92	1.42	1.81	4.34	4.69	2.87	4.22	1.31	2.13	-4.35E-01	8.19E-02		-8.36E-02	7.49E-01		1.12E-01	5.65E-01		-5.99E-01	8.34E-05		-1.69E+00	1.37E-25	Down	-9.88E-01	4.92E-12		Unigene12483_All//gi|21928151|gb|AAM78103.1|//1.00E-85//AT3g53540/F4P12_240 [Arabidopsis thaliana] >gi|23308447|gb|AAN18193.1| At3g53540/F4P12_240 [Arabidopsis thaliana]	Unigene12483_All//6.00E-75//AT3G53540| unknown protein	Unigene12483_All//0.00E+00//TC161210				nr -
Unigene12484_All	1059	5.88	3.35	7.89	7.34	10.50	6.31	6.63	5.60	3.24	-8.12E-01	6.10E-04		4.25E-01	4.50E-02		5.17E-01	1.51E-03		-2.17E-01	3.65E-01		-2.42E-01	2.61E-01		-1.03E+00	1.45E-07	Down	Unigene12484_All//gi|90399096|emb|CAJ86156.1|//2.00E-14//H0413E07.9 [Oryza sativa (indica cultivar-group)]		Unigene12484_All//0.00E+00//gi|164273404|gb|ES817737.1|ES817737				nr -
Unigene12485_All	2281	10.12	8.55	12.65	14.44	14.21	13.23	10.05	8.54	3.39	-2.42E-01	4.09E-02		3.23E-01	2.27E-03		-2.31E-02	8.34E-01		-1.26E-01	2.43E-01		-2.35E-01	2.83E-02		-1.57E+00	1.44E-42	Down	Unigene12485_All//gi|38344894|emb|CAD41917.2|//4.00E-46//OSJNBa0033G05.18 [Oryza sativa (japonica cultivar-group)]	Unigene12485_All//4.00E-23//AT5G11430| zinc ion binding	Unigene12485_All//0.00E+00//gi|164273404|gb|ES817737.1|ES817737				nr +
Unigene12486_All	3174	2.06	2.44	0.96	3.17	2.41	2.28	3.72	3.56	4.37	2.45E-01	2.69E-01		-1.11E+00	5.73E-06	Down	-3.97E-01	2.41E-02		-4.78E-01	7.90E-03		-6.39E-02	7.15E-01		2.33E-01	9.22E-02		Unigene12486_All//gi|297817502|ref|XP_002876634.1|//1.00E-122//nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297322472|gb|EFH52893.1| nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene12486_All//1.00E-100//AT3G61690| unknown protein	Unigene12486_All//0.00E+00//TC146298				nr +
Unigene12487_All	2823	4.26	13.68	8.04	4.78	4.83	7.12	2.85	3.51	1.88	1.68E+00	3.84E-62	Up	9.15E-01	4.06E-14		1.46E-02	9.53E-01		5.74E-01	1.61E-06		3.02E-01	7.61E-02		-6.00E-01	6.90E-04		Unigene12487_All//gi|115459352|ref|NP_001053276.1|//0.00E+00//Os04g0509100 [Oryza sativa Japonica Group] >gi|32488294|emb|CAE03360.1| OSJNBb0065L13.3 [Oryza sativa (japonica cultivar-group)] >gi|113568847|dbj|BAF15190.1| Os04g0509100 [Oryza sativa Japonica Group]	Unigene12487_All//0.00E+00//AT4G13550| triacylglycerol lipase	Unigene12487_All//0.00E+00//gi|73861394|gb|DT464133.1|DT464133		ko04626|Plant-pathogen interaction	GO:0004091//GO:0043231//GO:0044238	nr +
Unigene12488_All	3257	2.97	1.79	1.05	10.54	8.66	6.59	27.44	19.25	43.77	-7.32E-01	7.10E-05		-1.51E+00	2.79E-13	Down	-2.83E-01	1.22E-03		-6.78E-01	3.05E-14		-5.12E-01	4.58E-25		6.73E-01	1.39E-65		Unigene12488_All//gi|18402176|ref|NP_029567.1|//0.00E+00//VLN1 (VILLIN-LIKE 1); actin binding / actin filament binding [Arabidopsis thaliana] >gi|147744599|sp|081643.2|VIL11_ARATH RecName: Full=Villin-1	Unigene12488_All//0.00E+00//AT2G29890| VLN1 (VILLIN-LIKE 1); actin binding / actin filament binding	Unigene12488_All//0.00E+00//TC138468			GO:0003779//GO:0005856//GO:0006810//GO:0016020//GO:0051693	nr +
Unigene12492_All	2200	3.83	4.17	3.41	7.52	7.89	9.32	13.99	7.16	29.59	1.23E-01	5.70E-01		-1.66E-01	4.58E-01		6.96E-02	6.79E-01		3.10E-01	1.24E-02		-9.66E-01	3.08E-26		1.08E+00	7.28E-67	Up	Unigene12492_All//gi|158827646|gb|ABR81000.1|//0.00E+00//PI-phospholipase C PLC4 [Solanum lycopersicum]	Unigene12492_All//0.00E+00//AT5G58700| phosphoinositide-specific phospholipase C family protein	Unigene12492_All//0.00E+00//TC164966		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0004629//GO:0023060//GO:0044238//GO:0046872//GO:0060089	nr +
Unigene12494_All	2817	3.12	7.70	5.01	13.65	10.15	9.25	12.65	15.15	11.48	1.30E+00	2.61E-24	Up	6.83E-01	9.64E-06		-4.28E-01	5.60E-08		-5.61E-01	1.63E-11		2.60E-01	4.37E-04		-1.40E-01	9.99E-02		Unigene12494_All//gi|224144210|ref|XP_002325221.1|//0.00E+00//f-box family protein [Populus trichocarpa] >gi|222866655|gb|EEF03786.1| f-box family protein [Populus trichocarpa]	Unigene12494_All//4.00E-174//AT2G25490| EBF1 (EIN3-BINDING F BOX PROTEIN 1); protein binding / ubiquitin-protein ligase	Unigene12494_All//0.00E+00//ES838765		ko04626|Plant-pathogen interaction//ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0009873//GO:0019941//GO:0031461//GO:0043231	nr +
Unigene12496_All	3162	2.60	5.30	4.38	8.29	8.37	7.31	6.58	8.71	9.30	1.03E+00	2.79E-13	Up	7.53E-01	1.46E-06		1.53E-02	9.12E-01		-1.80E-01	1.24E-01		4.05E-01	1.10E-05		4.99E-01	1.06E-08		Unigene12496_All//gi|297816576|ref|XP_002876171.1|//1.00E-175//kcbp-interacting protein kinase [Arabidopsis lyrata subsp. lyrata] >gi|297322009|gb|EFH52430.1| kcbp-interacting protein kinase [Arabidopsis lyrata subsp. lyrata]	Unigene12496_All//2.00E-159//AT2G36350| protein kinase, putative	Unigene12496_All//0.00E+00//ES804239			GO:0004672//GO:0006464//GO:0032559	nr +

Unigene12497_All	1903	16.44	45.08	14.02	13.19	23.20	20.08	29.71	50.69	123.31	1.46E+00	2.61E-111	Up	-2.30E-01	2.78E-02		8.14E-01	5.93E-27		6.06E-01	6.17E-13		7.71E-01	4.53E-55		2.05E+00	0.00E+00	Up	Unigene12497_All//gi|15217736|ref|NP_176653.1|//1.00E-140//CP5 [Arabidopsis thaliana] >gi|5042409|gb|AAD38248.1|AC006193_4 Putative membrane related protein [Arabidopsis thaliana]	Unigene12497_All//1.00E-139//AT1G64720| CP5	Unigene12497_All//0.00E+00//TC159497				nr -
Unigene12498_All	2290	6.40	13.90	9.95	11.72	11.34	17.41	8.66	8.38	10.19	1.12E+00	6.01E-28	Up	6.38E-01	6.65E-08		-4.84E-02	7.28E-01		5.71E-01	3.60E-12		-4.77E-02	7.25E-01		2.36E-01	2.10E-02		Unigene12498_All//gi|42571665|ref|NP_973923.1|//4.00E-80//interferon-related developmental regulator family protein / IFRD protein family [Arabidopsis thaliana]	Unigene12498_All//2.00E-81//AT1G27760| interferon-related developmental regulator family protein / IFRD protein family	Unigene12498_All//0.00E+00//ES794517			GO:0006970//GO:0043231	nr +
Unigene12499_All	3299	0.46	1.75	0.48	2.30	3.00	3.52	4.10	3.74	4.02	1.93E+00	8.96E-12	Up	7.43E-02	8.89E-01		3.84E-01	3.53E-02		6.16E-01	1.63E-04		-1.34E-01	3.99E-01		-2.83E-02	8.57E-01		Unigene12499_All//gi|56609044|gb|AAW03152.1|//0.00E+00//kinesin [Gossypium hirsutum]	Unigene12499_All//0.00E+00//AT2G47500| ATP binding / microtubule motor	Unigene12499_All//0.00E+00//TC155731			GO:0000166//GO:0003774//GO:0015630//GO:0015631	nr +
Unigene125_All	919	3.25	1.76	2.90	6.83	6.93	9.93	9.43	4.55	22.02	-8.79E-01	1.49E-02		-1.64E-01	6.56E-01		2.14E-02	9.55E-01		5.40E-01	4.48E-03		-1.05E+00	4.67E-09	Down	1.22E+00	6.83E-26	Up	Unigene125_All//gi|224121336|ref|XP_002318557.1|//3.00E-90//aminophospholipid ATPase [Populus trichocarpa] >gi|222859230|gb|EEE96777.1|aminophospholipid ATPase [Populus trichocarpa]	Unigene125_All//1.00E-76//AT3G25610| haloacid dehalogenase-like hydrolase family protein					nr -
Unigene12502_All	1304	13.76	11.19	15.11	10.93	10.70	5.30	2.43	1.99	1.89	-2.98E-01	2.59E-02		1.35E-01	3.62E-01		-3.08E-02	8.58E-01		-1.04E+00	1.94E-12	Down	-2.91E-01	4.01E-01		-3.60E-01	2.48E-01		Unigene12502_All//gi|22330801|ref|NP_566156.2|//1.00E-113//yrdC family protein [Arabidopsis thaliana] >gi|19310491|gb|AAL84979.1|At3g1920/F28J7.25 [Arabidopsis thaliana] >gi|23505865|gb|AAN28792.1|At3g1920/F28J7.25 [Arabidopsis thaliana]	Unigene12502_All//3.00E-114//AT3G01920| yrdC family protein	Unigene12502_All//0.00E+00//CO098595			GO:0043231	nr +
Unigene12505_All	2640	9.45	7.97	11.19	38.62	29.64	27.65	37.52	16.99	17.35	-2.47E-01	2.86E-02		2.44E-01	2.33E-02		-3.82E-01	1.59E-16		-4.83E-01	1.49E-22		-1.14E+00	1.10E-108	Down	-1.11E+00	5.76E-107	Down	Unigene12505_All//gi|20799733|gb|AAM28629.1|AF503771_1/0.00E+00//acyl-CoA synthetase-like protein [Arabidopsis thaliana]	Unigene12505_All//0.00E+00//AT3G23790| AMP-binding protein, putative	Unigene12505_All//0.00E+00//TC160877		ko04146|Peroxisome//ko00071|Fatty acid metabolism	GO:0006633//GO:0009526//GO:0015645	nr +
Unigene12509_All	2589	16.61	11.82	13.76	33.73	30.10	36.14	23.58	21.62	10.65	-4.91E-01	1.31E-09		-2.72E-01	1.48E-03		-1.64E-01	2.61E-03		9.98E-02	9.77E-02		-1.26E-01	5.57E-02		-1.15E+00	1.52E-69	Down	Unigene12509_All//gi|15450411|gb|AAK96499.1|//1.00E-146//At1g52320/F19K6_7 [Arabidopsis thaliana] >gi|23308427|gb|AAN18183.1|At1g52320/F19K6_7 [Arabidopsis thaliana] >gi|62320232|dbj|BAD94485.1| bZIP protein [Arabidopsis thaliana]	Unigene12509_All//6.00E-161//AT1G52320| unknown protein	Unigene12509_All//0.00E+00//ES848847		ko03040|Spliceosome	GO:0016020	nr -
Unigene12510_All	1750	11.24	34.89	17.98	13.55	19.62	35.95	30.71	28.18	42.75	1.63E+00	5.48E-94	Up	6.78E-01	8.59E-12		5.34E-01	2.97E-10		1.41E+00	1.27E-83	Up	-1.24E-01	8.10E-02		4.77E-01	3.44E-19		Unigene12510_All//gi|126153733|emb|CAM35498.1|//1.00E-178//spermine synthase [Lotus japonicus]	Unigene12510_All//3.00E-163//AT5G53120| SPDS3 (SPERMIDINE SYNTHASE 3); spermidine synthase/ spermine synthase	Unigene12510_All//0.00E+00//TC138252		ko00270|Cysteine and methionine metabolism//ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism//ko00410|beta-Alanine metabolism		nr -
Unigene12513_All	1891	13.97	6.27	17.74	18.28	19.98	84.45	45.61	42.39	23.72	-1.16E+00	1.20E-24	Down	3.45E-01	3.66E-04		1.28E-01	1.91E-01		2.21E+00	0.00E+00	Up	-1.06E-01	5.47E-02		-9.43E-01	3.19E-71		Unigene12513_All//gi|20196920|gb|AC31831.2|//2.00E-45//expressed protein [Arabidopsis thaliana]	Unigene12513_All//2.00E-49//AT2G28580| unknown protein	Unigene12513_All//0.00E+00//DT053821				nr -
Unigene12516_All	452	6.71	14.57	7.07	6.61	7.24	7.49	27.50	21.45	22.12	1.12E+00	2.13E-06	Up	7.43E-02	8.34E-01		1.30E-01	7.71E-01		1.81E-01	6.32E-01		-3.58E-01	1.40E-02		-3.14E-01	2.73E-02		Unigene12516_All//gi|74038607|dbj|BAE43837.1|//2.00E-57//tobamovirus multiplication 3 [Nicotiana tabacum]	Unigene12516_All//4.00E-46//AT2G02180| TOM3; protein binding	Unigene12516_All//0.00E+00//gi|78343497|gb|DT563771.1|DT563771			GO:0005488//GO:0022415	nr -
Unigene12518_All	1237	0.85	1.80	0.52	1.17	1.48	0.66	3.35	2.16	0.84	1.09E+00	1.21E-02		-7.11E-01	3.15E-01		3.37E-01	5.52E-01		-8.29E-01	1.41E-01		-6.31E-01	1.82E-02		-2.00E+00	2.04E-11	Down	Unigene12518_All//gi|2462732|gb|AAB71951.1|//5.00E-41//Hypothetical Protein [Arabidopsis thaliana]	Unigene12518_All//3.00E-42//AT1G60560| SWIM zinc finger family protein	Unigene12518_All//0.00E+00//CO075071			GO:0046914	nr +
Unigene1252_All	1369	2.18	5.11	4.90	7.17	8.60	8.97	17.51	18.81	18.57	1.23E+00	1.06E-07	Up	1.17E+00	1.30E-06	Up	2.63E-01	1.34E-01		3.24E-01	5.43E-02		1.03E-01	3.74E-01		8.44E-02	4.47E-01		Unigene1252_All//gi|23328895|ref|NP_194141.2|//1.00E-27//protein kinase family protein [Arabidopsis thaliana]	Unigene1252_All//6.00E-29//AT4G24100| protein kinase family protein	Unigene1252_All//0.00E+00//TC171303			GO:0004672//GO:0006464//GO:0016020//GO:0031410//GO:0032559	nr -
Unigene12520_All	2572	5.21	1.73	1.43	20.24	16.95	7.66	7.40	3.75	2.52	-1.59E+00	2.08E-20	Down	-1.87E+00	2.08E-24	Down	-2.56E-01	2.25E-04		-1.40E+00	6.03E-70	Down	-9.79E-01	7.10E-17		-1.55E+00	6.18E-35	Down	Unigene12520_All//gi|15220579|ref|NP_176957.1|//0.00E+00//phototropic-responsive NPH3 family protein [Arabidopsis thaliana] >gi|42572025|ref|NP_974103.1|phototropic-responsive NPH3 family protein [Arabidopsis thaliana] >gi|31711740|gb|AAP68226.1|At1g67900 [Arabidopsis thaliana]	Unigene12520_All//0.00E+00//AT1G67900| phototropic-responsive NPH3 family protein	Unigene12520_All//0.00E+00//TC158206			GO:0005488//GO:0009314//GO:0060089	nr -
Unigene12521_All	2206	5.05	5.37	2.53	9.44	4.53	4.77	10.98	6.14	3.99	8.94E-02	6.22E-01		-9.95E-01	3.01E-08		-1.06E+00	1.04E-20	Down	-9.85E-01	2.61E-16		-8.39E-01	1.34E-16		-1.46E+00	1.53E-40	Down	Unigene12521_All//gi|3192399|gb|AAC19283.1|//0.00E+00//T14P8.19 [Arabidopsis thaliana] >gi|7268999|emb|CAB80732.1| NAD+ ADP-ribosyltransferase [Arabidopsis thaliana]	Unigene12521_All//0.00E+00//AT4G02390| APP (ARABIDOPSIS POLY(ADP-RIBOSE) POLYMERASE); NAD+ ADP-ribosyltransferase/ nucleic acid binding	Unigene12521_All//0.00E+00//gi|84172323|gb|DR460971.1|DR460971		ko03410|Base excision repair	GO:0003676//GO:0006464//GO:0016763//GO:0043231	nr +
Unigene12524_All	1272	9.71	4.22	8.41	17.86	19.00	18.53	11.93	6.70	9.83	-1.20E+00	1.27E-12	Down	-2.06E-01	2.51E-01		8.98E-02	5.29E-01		5.36E-02	6.81E-01		-8.32E-01	1.45E-10		-2.79E-01	2.96E-02		Unigene12524_All//gi|22328982|ref|NP_194494.2|//1.00E-156//importin beta-2 subunit family protein [Arabidopsis thaliana] >gi|38564254|gb|AAR23706.1|At4g27640 [Arabidopsis thaliana]	Unigene12524_All//6.00E-142//AT4G27640| importin beta-2 subunit family protein	Unigene12524_All//0.00E+00//TC146369				nr +
Unigene12525_All	3638	3.35	2.33	2.68	5.63	5.64	6.48	7.67	3.50	5.94	-5.27E-01	1.14E-03		-3.23E-01	6.45E-02		3.50E-03	9.85E-01		2.04E-01	9.59E-02		-1.13E+00	1.28E-30	Down	-3.70E-01	3.57E-05		Unigene12525_All//gi|297799210|ref|XP_002867489.1|//0.00E+00//import in beta-2 subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313325|gb|EFH43748.1|importin beta-2 subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12525_All//0.00E+00//AT4G27640| importin beta-2 subunit family protein	Unigene12525_All//0.00E+00//TC146369			GO:0005635//GO:0006606//GO:0022892	nr -
Unigene12527_All	2369	5.21	101.72	27.78	9.19	23.81	51.76	37.41	96.58	129.42	4.29E+00	0.00E+00	Up	2.41E+00	2.94E-165	Up	1.37E+00	1.75E-79	Up	2.49E+00	0.00E+00	Up	1.37E+00	0.00E+00	Up	1.79E+00	0.00E+00	Up	Unigene12527_All//gi|14225723|emb|CAM84258.1|//1.00E-133//abscisic insensitive 1B [Populus tremula] >gi|14225725|emb|CAM84259.1|abscisic insensitive 1B [Populus tremula] >gi|14225735|emb|CAM84264.1|abscisic insensitive 1B [Populus tremula] >gi|14225747|emb|CAM84270.1|abscisic insensitive 1B [Populus tremula] >gi|14225751|emb|CAM84272.1|abscisic insensitive 1B [Populus tremula] >gi|14225759|emb|CAM84276.1|abscisic insensitive 1B [Populus tremula] >gi|14225761|emb|CAM84277.1|abscisic insensitive 1B [Populus tremula] >gi|14225763|emb|CAM84278.1|abscisic insensitive 1B [Populus tremula] >gi|14225765|emb|CAM84279.1|abscisic insensitive 1B [Populus tremula] >gi|14225773|emb|CAM84283.1|abscisic insensitive 1B [Populus tremula]	Unigene12527_All//2.00E-111//AT5G57050| ABI2 (ABA INSENSITIVE 2); protein serine/threonine phosphatase	Unigene12527_All//0.00E+00//TC171505				nr -
Unigene12528_All	2901	2.18	0.91	1.60	4.53	5.29	6.96	3.85	5.14	5.29	-1.26E+00	2.30E-07	Down	-4.51E-01	7.11E-02		2.24E-01	1.45E-01		6.18E-01	2.23E-07		4.19E-01	1.26E-03		4.59E-01	2.22E-04		Unigene12528_All//gi|240254179|ref|NP_174268.7|//0.00E+00//RKF1 (RECEPTOR-LIKE KINASE IN FLOWERS 1); ATP binding / kinase/ protein serine/threonine kinase/ receptor signaling protein serine/threonine kinase [Arabidopsis thaliana] >gi|75334468|sp|Q9FXF2.1|RKF1_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase RFK1; AltName: Full=Receptor-like kinase in flowers 1; Flags: Precursor >gi|9972369|gb|AAG10619.1|AC008030_19 Receptor-like serine/threonine kinase (RFK1) [Arabidopsis thaliana]	Unigene12528_All//0.00E+00//AT1G29750| RKF1 (RECEPTOR-LIKE KINASE IN FLOWERS 1); ATP binding / kinase/ protein serine/threonine kinase/ receptor signaling protein serine/threonine kinase	Unigene12528_All//0.00E+00//TC145805		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0007167//GO:0016491//GO:0032559	nr -
Unigene12529_All	3334	1.91	3.05	2.44	4.27	4.26	3.81	5.01	4.69	10.06	6.74E-01	1.69E-04		3.52E-01	1.09E-01		-6.10E-03	9.64E-01		-1.67E-01	3.35E-01		-9.55E-02	5.25E-01		1.01E+00	3.85E-31	Up	Unigene12529_All//gi|224097301|ref|XP_002310900.1|//0.00E+00//histone acetyltransferase [Populus trichocarpa] >gi|222853803|gb|EEE91350.1|histone acetyltransferase [Populus trichocarpa]	Unigene12529_All//0.00E+00//AT1G79000| HAC1 (HISTONE ACETYLTRANSFERASE OF THE CBP FAMILY 1); H3/H4 histone acetyltransferase/ histone acetyltransferase/ transcription cofactor	Unigene12529_All//2.00E-39//TC135240	TAZ		GO:0004468//GO:0005488//GO:0009791//GO:0043543	nr +
Unigene12534_All	603	81.47	48.82	38.15	143.25	108.27	164.40	154.26	68.20	49.29	-7.39E-01	1.00E-21		-1.09E+00	5.46E-40	Down	-4.04E-01	1.53E-15		1.99E-01	1.23E-04		-1.18E+00	5.72E-107	Down	-1.65E+00	1.17E-182	Down	Unigene12534_All//gi|6094040|sp|O65743.1|RL24_CICAR//1.00E-51//RecName: Full=60S ribosomal protein L24 >gi|2961300|emb|CAA12358.1|ribosomal protein L24 [Cicer arietinum]	Unigene12534_All//2.00E-27//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome	Unigene12534_All//2.00E-164//gi|164261124|gb|ES798699.1|ES798699		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr -
Unigene12535_All	954	2.52	3.56	3.57	4.91	4.80	4.36	1.11	1.23	3.05	4.96E-01	1.41E-01		5.02E-01	1.53E-01		-3.20E-02	9.12E-01		-1.72E-01	6.14E-01		1.47E-01	7.92E-01		1.46E+00	1.46E-05	Up			Unigene12535_All//0.00E+00//TC133592				ESTscan -
Unigene12536_All	648	2.99	4.85	0.74	5.30	2.29	3.48	4.76	3.55	7.50	6.99E-01	4.63E-02		-2.01E+00	2.05E-04	Down	-1.21E+00	1.07E-04	Down	-6.06E-01	7.32E-02		-4.25E-01	1.99E-01		6.55E-01	5.47E-03		Unigene12536_All//gi|62287245|sp|Q6EMB7.1|RR7_HYDMC//2.00E-122//RecName: Full=30S ribosomal protein S7, chloroplastic >gi|34333520|gb|AAO64554.1|ribosomal protein S7 [Hydrangea macrophylla]	Unigene12536_All//4.00E-13//ATCG00900| encodes a chloroplast ribosomal protein S7, a constituent of the small subunit of the ribosomal complex	Unigene12536_All//0.00E+00//gi|78322936|gb|DT543210.1|DT543210		ko03010|Ribosome	GO:0030529//GO:0043231//GO:0044444	nr -

Unigene12540_All	2049	10.57	7.07	8.24	27.11	26.20	26.98	29.45	10.83	9.06	-5.80E-01	8.23E-07		-3.60E-01	3.70E-03		-4.91E-02	5.81E-01		-6.80E-03	9.53E-01		-1.44E+00	3.73E-95	Down	-1.70E+00	2.45E-124	Down	Unigene12540_All//gi|75163671|sp|Q93YW6.1|2A5I_ARATH//1.00E-176//RecName: Full=Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' iota isoform; Short=PP2A, B' subunit, iota isoform; Short=AtB' iota	Unigene12540_All//1.00E-153//AT5G25510| serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative	Unigene12540_All//0.00E+00//TC144457			GO:0008287//GO:0019888//GO:0023060	nr -
Unigene12544_All	1739	1.29	0.93	1.53	0.72	0.83	0.36	5.71	2.09	9.46	-4.73E-01	2.72E-01		2.43E-01	5.70E-01		2.16E-01	7.52E-01		-9.78E-01	1.14E-01		-1.45E+00	1.95E-16	Down	7.28E-01	1.87E-09		Unigene12544_All//gi|284026888|gb|AB866335.1|//1.00E-80//CC-NBS-LRR protein [Quercus suber]	Unigene12544_All//2.00E-28//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene12544_All//5.00E-78//TC168228				nr +
Unigene12546_All	1784	36.37	64.98	70.53	47.80	65.99	70.63	28.82	31.25	11.25	8.38E-01	4.70E-62		9.56E-01	1.09E-81		4.65E-01	1.07E-26		5.63E-01	2.38E-36		1.17E-01	9.48E-02		-1.36E+00	3.82E-76	Down	Unigene12546_All//gi|27597231|dbj|BAC53156.1|//0.00E+00//purple acid phosphatase [Nicotiana tabacum]	Unigene12546_All//0.00E+00//AT2G16430| PAP10 (PURPLE ACID PHOSPHATASE 10); acid phosphatase/ protein serine/threonine phosphatase	Unigene12546_All//0.00E+00//TC142786			GO:0016791//GO:0044421//GO:0046914	nr -
Unigene12547_All	1569	5.97	14.27	4.11	22.32	18.72	33.85	41.42	45.37	87.29	1.26E+00	8.71E-24	Up	-5.40E-01	5.91E-03		-2.54E-01	3.99E-03		6.01E-01	1.68E-17		1.31E-01	2.74E-02		1.08E+00	9.50E-139	Up	Unigene12547_All//gi|297800784|ref|XP_002868276.1|//1.00E-132//cbl-interacting protein kinase 4 [Arabidopsis lyrata subsp. lyrata] >gi|297314112|gb|EFH44535.1| cbl-interacting protein kinase 4 [Arabidopsis lyrata subsp. lyrata]	Unigene12547_All//5.00E-108//AT4G14580| CIPK4 (CBL-interacting protein kinase 4); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene12547_All//0.00E+00//gi|78345746|gb|DT566020.1|DT566020		ko04140|Regulation of autophagy	GO:0000166//GO:0004672//GO:0009987//GO:0043231	nr +
Unigene12548_All	235	16.92	3.88	3.63	6.78	1.76	5.00	0.36	0.71	0.68	-2.12E+00	2.10E-09	Down	-2.22E+00	2.09E-09	Down	-1.95E+00	2.04E-04	Down	-4.41E-01	4.28E-01		9.84E-01	6.34E-01		9.14E-01	6.24E-01				Unigene12548_All//5.00E-27//TC156880				
Unigene12549_All	821	19.76	4.32	4.15	17.23	10.57	10.29	3.19	1.02	1.84	-2.19E+00	9.85E-38	Down	-2.25E+00	1.96E-37	Down	-7.05E-01	2.52E-07		-7.44E-01	3.02E-07		-1.65E+00	9.48E-06	Down	-7.92E-01	1.79E-02		Unigene12549_All//gi|225465284|ref|XP_002270616.1|//6.00E-68//PREDICTED: pectin methylesterase PME1 [Vitis vinifera] >gi|150815598|gb|AAK81875.1| pectin methylesterase PME1 [Vitis vinifera]	Unigene12549_All//2.00E-64//AT3G43270| pectinesterase family protein	Unigene12549_All//0.00E+00//gi|78334991|gb|DT555265.1|DT555265		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0030234//GO:0071555	nr +
Unigene12550_All	2285	38.81	9.45	8.81	25.48	17.77	17.00	5.20	2.49	1.90	-2.04E+00	1.12E-185	Down	-2.14E+00	3.65E-191	Down	-5.20E-01	1.01E-16		-5.84E-01	2.36E-18		-1.06E+00	2.58E-12	Down	-1.45E+00	3.67E-20	Down	Unigene12550_All//gi|6093744|sp|Q43062.1|PME_PRUPE//0.00E+00//RecName: Full=Pectinesterase/pectinesterase inhibitor PPE8B; Includes: RecName: Full=Pectinesterase inhibitor PPE8B; AltName: Full=Pectin methylesterase inhibitor PPE8B; Includes: RecName: Full=Pectinesterase PPE8B; Short=PE PPE8B; AltName: Full=Pectin methylesterase PPE8B; Flags: Precursor >gi|1213629|emb|CAA65237.1| pectinesterase [Prunus persica]	Unigene12550_All//0.00E+00//AT4G33220| enzyme inhibitor/ pectinesterase	Unigene12550_All//0.00E+00//TC154918		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0030234//GO:0045229//GO:0071555	nr +
Unigene12552_All	2981	14.60	4.11	3.55	21.04	16.31	10.44	16.25	1.95	4.18	-1.83E+00	5.03E-79	Down	-2.04E+00	3.12E-88	Down	-3.67E-01	1.23E-09		-1.01E+00	3.54E-50	Down	-3.06E+00	3.22E-198	Down	-1.96E+00	2.53E-121	Down	Unigene12552_All//gi|166078960|gb|ABY81650.1|//0.00E+00//minichromosome maintenance 4 protein [Pisum sativum]	Unigene12552_All//0.00E+00//AT2G16440| DNA replication licensing factor, putative	Unigene12552_All//0.00E+00//TC175193		ko03030|DNA replication	GO:0003676//GO:0006259//GO:0016462//GO:0032559//GO:0043231	nr +
Unigene12553_All	1795	19.62	21.76	7.12	25.73	24.42	29.34	67.58	90.88	47.74	1.50E-01	1.06E-01		-1.46E+00	5.95E-45	Down	-7.51E-02	4.31E-01		1.90E-01	1.23E-02		4.27E-01	1.36E-32		-5.01E-01	1.96E-33		Unigene12553_All//gi|33391721|gb|AAU17461.1|//0.00E+00//beta-D glucosidase [Gossypium hirsutum]	Unigene12553_All//0.00E+00//AT5G20950| glycosyl hydrolase family 3 protein	Unigene12553_All//0.00E+00//TC132101		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0005618//GO:0008422//GO:0044238	nr +
Unigene12556_All	947	2.54	0.86	1.91	4.47	2.73	3.15	3.44	3.22	3.58	-1.57E+00	3.01E-04	Down	-4.11E-01	3.61E-01		-7.13E-01	1.04E-02		-5.06E-01	9.46E-02		-9.36E-02	7.78E-01		5.68E-02	8.62E-01		Unigene12556_All//gi|87241357|gb|AB033215.1|//3.00E-61//D111/G-patch; Zinc finger, C2H2-type [Medicago truncatula]	Unigene12556_All//7.00E-25//AT5G26610| D111/G-patch domain-containing protein	Unigene12556_All//0.00E+00//gi|164325036|gb|ES841875.1|ES841875	C2H2		GO:0031410//GO:0046914	nr +
Unigene12557_All	756	2.70	0.13	0.42	0.72	0.96	0.48	0.00	0.00	0.00	-4.33E+00	1.70E-09	Down	-2.68E+00	3.63E-06	Down	4.00E-01	6.64E-01		-6.01E-01	5.66E-01		null	null		null	null		Unigene12557_All//gi|34850945|dbj|BAC87845.1|//2.00E-66//leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	Unigene12557_All//4.00E-51//AT4G08850| kinase			ko04626|Plant-pathogen interaction		nr -
Unigene12558_All	656	4.39	0.15	0.81	2.05	0.89	0.48	0.13	0.13	0.00	-4.83E+00	4.99E-14	Down	-2.43E+00	1.09E-07	Down	-1.20E+00	3.02E-02		-2.09E+00	1.00E-03		-1.69E-02	1.01E+00		-7.01E+00	3.59E-01		Unigene12558_All//gi|34850945|dbj|BAC87845.1|//7.00E-46//leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	Unigene12558_All//1.00E-29//AT4G08850| kinase			ko04626|Plant-pathogen interaction//ko03410|Base excision repair	GO:0000166//GO:0004672//GO:0016020	nr -
Unigene12256_All	3905	1.84	1.44	1.02	4.09	3.37	3.37	6.40	14.89	10.94	-3.50E-01	1.22E-01		-8.44E-01	2.11E-04		-2.82E-01	4.38E-02		-2.83E-01	5.18E-02		1.22E+00	1.04E-70	Up	7.73E-01	1.40E-25		Unigene1256_All//gi|75219581|sp|O49318.1|Y2317_ARATH//0.00E+00//RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At2g33170; Flags: Precursor >gi|224589539|gb|ACN59303.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene1256_All//0.00E+00//AT2G33170| leucine-rich repeat transmembrane protein kinase, putative	Unigene1256_All//0.00E+00//TC163302		ko04626|Plant-pathogen interaction	GO:0004672//GO:0016020	nr -
Unigene12562_All	366	1.43	2.49	0.00	1.91	0.94	3.33	4.85	9.71	9.80	8.02E-01	2.71E-01		-1.05E+01	4.76E-03		-1.02E+00	2.25E-01		8.06E-01	2.11E-01		1.00E+00	6.52E-04	Up	1.01E+00	3.78E-04	Up	Unigene12562_All//gi|297823651|ref|XP_002879708.1|//9.00E-15//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297325547|gb|EFH55967.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene12562_All//5.00E-16//AT2G37770| aldo/keto reductase family protein	Unigene12562_All//3.00E-119//TC165004		ko00010|Glycolysis / Gluconeogenesis//ko00561|Glycerolipid metabolism	GO:0004033//GO:0006970//GO:0008152	nr -
Unigene12563_All	1958	2.30	4.63	1.50	5.55	7.69	9.02	25.93	37.61	66.35	1.01E+00	2.40E-07	Up	-6.20E-01	3.86E-02		4.71E-01	5.94E-04		7.01E-01	5.33E-08		5.36E-01	1.43E-22		1.36E+00	2.99E-189	Up	Unigene12563_All//gi|30687261|ref|NP_181315.2|//1.00E-68//aldo/keto reductase family protein [Arabidopsis thaliana] >gi|29028836|gb|AAO64797.1| At2g37790 [Arabidopsis thaliana] >gi|111182167|gb|ABH07516.1| aldo-keto reductase [Arabidopsis thaliana]	Unigene12563_All//2.00E-67//AT2G37790| aldo/keto reductase family protein	Unigene12563_All//0.00E+00//TC165004		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism	GO:0006970//GO:0008152//GO:0016616//GO:0043231//GO:0044444	nr -
Unigene12565_All	1787	5.91	9.02	9.21	10.54	12.60	11.58	27.19	71.78	93.61	6.08E-01	1.15E-05		6.39E-01	6.42E-06		2.58E-01	2.70E-02		1.36E-01	3.45E-01		1.40E+00	1.85E-192	Up	1.78E+00	0.00E+00	Up	Unigene12565_All//gi|224145557|ref|XP_002325685.1|//0.00E+00//equilibrative nucleoside transporter [Populus trichocarpa] >gi|222862560|gb|EEF00067.1| equilibrative nucleoside transporter [Populus trichocarpa]	Unigene12565_All//9.00E-159//AT4G05120| FUR1 (FUDR RESISTANT 1); nucleoside transmembrane transporter	Unigene12565_All//0.00E+00//gi|48816860|gb|CO118173.1|CO118173			GO:0015932//GO:0044464//GO:0051234	nr +
Unigene12566_All	1369	0.84	2.48	2.02	2.44	2.29	3.63	13.43	9.40	4.39	1.56E+00	1.38E-05	Up	1.27E+00	1.71E-03		-9.09E-02	8.26E-01		5.74E-01	3.59E-02		-5.15E-01	7.17E-06		-1.61E+00	1.02E-35	Down	Unigene12566_All//gi|4958922|dbj|BAA78050.1|//7.00E-48//NADPH oxidoreductase homolog [Cicer arietinum]	Unigene12566_All//2.00E-47//AT1G49670| NQR; binding / catalytic/ oxidoreductase/ zinc ion binding	Unigene12566_All//0.00E+00//TC145969			GO:0006952//GO:0006970//GO:0008152//GO:0009532//GO:0016020//GO:0016616//GO:0016646//GO:0016655//GO:0042579//GO:0046914	nr +
Unigene12568_All	2157	41.50	43.67	27.28	40.09	51.57	68.74	80.13	132.15	205.88	7.34E-02	2.30E-01		-6.05E-01	1.33E-26		3.63E-01	4.19E-16		7.78E-01	4.01E-75		7.22E-01	7.97E-144		1.36E+00	0.00E+00	Up	Unigene12568_All//gi|224114762|ref|XP_002316850.1|//0.00E+00//Sec61 transport protein [Populus trichocarpa] >gi|222859915|gb|EEE97462.1| Sec61 transport protein [Populus trichocarpa]	Unigene12568_All//0.00E+00//AT2G34250| protein transport protein sec61, putative	Unigene12568_All//0.00E+00//TC135106		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export	GO:0006810//GO:0008320//GO:0016020//GO:0043231	nr +
Unigene12569_All	667	0.08	3.42	0.40	1.42	3.05	1.02	0.51	0.13	0.36	5.45E+00	1.23E-11	Up	2.35E+00	2.39E-01		1.10E+00	1.46E-02		-4.82E-01	5.19E-01		-2.02E+00	1.36E-01		-5.01E-01	6.49E-01		Unigene12569_All//gi|170131|gb|AAA34039.1|//5.00E-13//ribosomal protein 30S submit [Spinacia oleracea]	Unigene12569_All//3.00E-12//AT5G24490| 30S ribosomal protein, putative	Unigene12569_All//6.00E-57//TC139727			GO:0003723//GO:0009532//GO:0010467//GO:0030529	nr -
Unigene12574_All	640	1.88	0.95	6.41	3.35	3.12	3.53	1.65	2.09	1.25	-9.85E-01	1.13E-01		1.77E+00	2.20E-07	Up	-1.01E-01	8.20E-01		7.62E-02	8.80E-01		3.40E-01	5.46E-01		-4.08E-01	4.85E-01		Unigene12574_All//gi|240256481|ref|NP_201353.4|//3.00E-10//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene12574_All//2.00E-06//AT5G65500| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ ubiquitin-protein ligase	Unigene12574_All//1.00E-14//TC146809				nr +
Unigene12575_All	2807	0.80	1.12	1.12	4.72	2.27	2.94	10.26	21.65	9.78	4.82E-01	1.76E-01		4.82E-01	1.98E-01		-1.06E+00	2.90E-13	Down	-6.81E-01	6.03E-06		1.08E+00	7.67E-61	Up	-6.90E-02	5.19E-01		Unigene12575_All//gi|240256481|ref|NP_201353.4|//0.00E+00//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene12575_All//0.00E+00//AT5G65500| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ ubiquitin-protein ligase				GO:0000166//GO:0006464//GO:0016301	nr +
Unigene12576_All	2737	0.19	0.33	0.04	0.95	0.42	0.68	2.89	6.78	3.17	8.01E-01	2.71E-01		-2.30E+00	6.77E-02		-1.19E+00	1.33E-03		-4.84E-01	2.37E-01		1.23E+00	1.79E-23	Up	1.36E-01	4.84E-01		Unigene12576_All//gi|240256481|ref|NP_201353.4|//0.00E+00//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene12576_All//0.00E+00//AT5G65500| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ ubiquitin-protein ligase				GO:0016301	nr +
Unigene12577_All	2582	18.10	7.12	8.39	44.01	36.36	54.17	71.00	45.87	47.55	-1.35E+00	2.13E-54	Down	-1.11E+00	8.28E-39	Down	-2.76E-01	4.25E-10		3.00E-01	6.29E-13		-6.30E-01	3.28E-73		-5.78E-01	1.35E-64		Unigene12577_All//gi|7211427|gb|AAF40306.1|AP156667_1|//0.00E+00//RNA helicase [Vigna radiata]	Unigene12577_All//0.00E+00//AT5G62190| PRH75; ATP-dependent helicase/ DEAD/H-box RNA helicase binding	Unigene12577_All//0.00E+00//TC140240		ko03040|Spliceosome	GO:0003676//GO:0019899//GO:0031981//GO:0032559//GO:0042623//GO:0044464	nr -
Unigene12578_All	2427	1.94	13.26	5.38	1.68	1.25	11.35	29.42	150.01	135.98	2.77E+00	1.18E-96	Up	1.47E+00	3.76E-17	Up	-4.31E-01	1.56E-01		2.75E+00	5.08E-88	Up	2.35E+00	0.00E+00	Up	2.21E+00	0.00E+00	Up	Unigene12578_All//gi|75297894|sp|Q84MB3.1|ACCH1_ARATH//1.00E-124//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene12578_All//8.00E-118//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene12578_All//2.00E-13//TC174072		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene12579_All	1374	1.98	77.96	26.43	1.78	23.66	45.06	4.49	7.67	23.57	5.30E+00	0.00E+00	Up	3.74E+00	2.13E-141	Up	3.74E+00	5.89E-149	Up	4.66E+00	0.00E+00	Up	7.71E-01	9.71E-07		2.39E+00	4.55E-103	Up	Unigene12579_All//gi|18394031|ref|NP_563933.1|//2.00E-71//AFP2 (ABI FIVE BINDING PROTEIN 2) [Arabidopsis thaliana] >gi|75174856|sp|Q9LMX5.1|AFP2_ARATH RecName: Full=Ninja-family protein AFP2; AltName: Full=ABI five-binding protein 2; Short=ABI5-binding protein 2 >gi|90093290|gb|ABD85158.1| At1g13740 [Arabidopsis thaliana]	Unigene12579_All//6.00E-56//AT1G13740| AFP2 (ABI FIVE BINDING PROTEIN 2)	Unigene12579_All//0.00E+00//TC171467			GO:0005488//GO:0009725//GO:0009987	nr +
Unigene12580_All	1953	14.41	6.49	6.76	30.23	17.10	26.94	49.10	27.22	32.41	-1.15E+00	4.62E-26	Down	-1.09E+00	4.97E-23	Down	-8.22E-01	8.27E-38		-1.66E-01	2.13E-02		-8.51E-01	8.74E-65		-5.99E-01	2.07E-36		Unigene12580_All//gi|289065767|gb|ADC80921.1|//0.00E+00//delta-8 sphingolipid desaturase [Vernicia fordii]	Unigene12580_All//0.00E+00//AT2G46210| delta-8 sphingolipid desaturase, putative	Unigene12580_All//0.00E+00//TC151630		ko00910|Nitrogen metabolism	GO:0005506//GO:0006631//GO:0016705	nr +

Unigene12581_All	923	2.49	0.66	3.00	10.63	7.83	5.97	6.05	1.86	1.12	-1.92E+00	3.76E-05	Down	2.66E-01	5.14E-01		-4.41E-01	1.22E-02		-8.33E-01	3.27E-06		-1.70E+00	6.91E-12	Down	-2.43E+00	5.31E-19	Down	Unigene12581_All//gi|126217792|gb|ABN81349.1|//1.00E-127//auxin influx transport protein [Casuarina glauca] >gi|126217794|gb|ABN81350.1| auxin influx transport protein [Casuarina glauca]	Unigene12581_All//4.00E-122//AT5G01240| amino acid permease, putative	Unigene12581_All//5.00E-46//gi|48811000|gb|CO112313.1|CO112313				nr -
Unigene12583_All	1869	1.37	2.01	1.88	14.87	13.78	8.17	6.97	2.48	1.39	5.49E-01	8.47E-02		4.55E-01	1.96E-01		-1.10E-01	3.60E-01		-8.65E-01	1.86E-17		-1.49E+00	4.01E-22	Down	-2.33E+00	3.18E-41	Down	Unigene12583_All//gi|224098529|ref|XP_002311208.1|//0.00E+00//auxin influx carrier component [Populus trichocarpa] >gi|222851028|gb|EEE88575.1| auxin influx carrier component [Populus trichocarpa]	Unigene12583_All//0.00E+00//AT2G38120| AUX1 (AUXIN RESISTANT 1); amino acid transmembrane transporter/ auxin binding / auxin influx transmembrane transporter/ transporter	Unigene12583_All//6.00E-47//gi|48741175|gb|CO071694.1|CO071694			GO:0009755//GO:0015291//GO:0015837//GO:0031224	nr -
Unigene12588_All	751	2.79	5.80	2.48	5.90	5.59	5.53	9.57	13.41	11.56	1.06E+00	3.36E-04	Up	-1.67E-01	7.06E-01		-7.77E-02	8.32E-01		-9.36E-02	7.60E-01		4.87E-01	2.55E-03		2.73E-01	1.26E-01				Unigene12588_All//0.00E+00//DW503074					
Unigene12259_All	4371	0.48	0.52	0.69	0.91	0.91	0.74	1.10	1.17	2.51	1.24E-01	7.62E-01		5.36E-01	1.53E-01		-9.00E-03	9.65E-01		-2.94E-01	3.98E-01		8.13E-02	7.58E-01		1.18E+00	9.58E-14	Up	Unigene12259_All//gi|22328167|ref|NP_191917.2|//0.00E+00//MEE44 (maternal effect embryo arrest 44); nucleotidyltransferase [Arabidopsis thaliana] >gi|19699089|gb|AAL90911.1| AT4g00060/F6N15_10 [Arabidopsis thaliana] >gi|25090419|gb|AAN72296.1| At4g00060/F6N15_10 [Arabidopsis thaliana]	Unigene12259_All//0.00E+00//AT4G00060| MEE44 (maternal effect embryo arrest 44); nucleotidyltransferase	Unigene12259_All//0.00E+00//gi|78330670|gb|DT550944.1|DT550944		ko03018|RNA degradation	GO:0003006//GO:0016779//GO:0043231	nr +
Unigene12591_All	1777	16.84	9.75	9.56	19.43	15.44	22.04	25.93	15.64	12.31	-7.88E-01	4.68E-15		-8.17E-01	2.70E-15		-3.31E-01	1.11E-04		1.82E-01	4.63E-02		-7.30E-01	2.20E-24		-1.08E+00	1.44E-47	Down	Unigene12591_All//gi|186522075|ref|NP_568244.2|//0.00E+00//ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana] >gi|108861899|sp|Q9LFN6.2|RH56_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 56 >gi|14190381|gb|AAK55671.1|AF378868_1 AT5g11200/F2111_90 [Arabidopsis thaliana] >gi|15450405|gb|AAK96496.1| AT5g11170/F2111_60 [Arabidopsis thaliana] >gi|16323360|gb|AAL15393.1| AT5g11200/F2111_90 [Arabidopsis thaliana] >gi|24111365|gb|AAN46806.1| At5g11170/F2111_60 [Arabidopsis thaliana] >gi|110740954|dbj|BAE98572.1| DEAD BOX RNA helicase RH15 - like protein [Arabidopsis thaliana]	Unigene12591_All//0.00E+00//AT5G11170| ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene12591_All//0.00E+00//TC157575		ko03040|Spliceosome	GO:0010038//GO:0030312//GO:0031981//GO:0032559//GO:0042623	nr +
Unigene12596_All	1354	2.16	1.91	2.36	6.70	4.17	3.54	6.28	10.12	2.80	-1.81E-01	6.03E-01		1.25E-01	7.21E-01		-6.83E-01	1.13E-04		-9.21E-01	9.60E-07		6.90E-01	3.60E-07		-1.17E+00	1.03E-10	Down	Unigene12596_All//gi|162459484|ref|NP_001105726.1|//5.00E-82//eukaryotic translation initiation factor 3 subunit A [Zea mays] >gi|6685541|sp|Q9XHR2.1|EIF3A_MAIZE RecName: Full=Eukaryotic translation initiation factor 3 subunit A; Short=eIF3a; AltName: Full=eIF-3-theta; AltName: Full=Eukaryotic translation initiation factor 3 large subunit >gi|5106764|gb|AAD39834.1|AF073329_1 eukaryotic translation initiation factor 3 large subunit [Zea mays]	Unigene12596_All//7.00E-79//AT4G11420| EIF3A (EUKARYOTIC TRANSLATION INITIATION FACTOR 3A); translation initiation factor	Unigene12596_All//0.00E+00//DW236232			GO:0006412//GO:0016020//GO:0044424	nr +
Unigene12597_All	2282	10.84	5.91	7.21	44.53	63.27	27.00	9.43	1.96	5.73	-8.77E-01	6.11E-15		-5.89E-01	1.78E-07		5.07E-01	3.97E-38		-7.22E-01	8.14E-46		-2.27E+00	2.12E-63	Down	-7.20E-01	6.07E-12		Unigene12597_All//gi|297814259|ref|XP_002875013.1|//1.00E-153//IQ-domain 17 [Arabidopsis lyrata subsp. lyrata] >gi|297320850|gb|EFH51272.1| IQ-domain 17 [Arabidopsis lyrata subsp. lyrata]	Unigene12597_All//7.00E-135//AT4G00820| iqd17 (IQ-domain 17); calmodulin binding	Unigene12597_All//0.00E+00//gi|78352224|gb|DT572498.1|DT572498				nr -
Unigene12598_All	2874	4.92	2.84	4.30	7.19	9.55	5.58	3.65	2.11	1.64	-7.92E-01	1.38E-07		-1.93E-01	2.47E-01		4.09E-01	2.61E-05		-3.67E-01	2.32E-03		-7.91E-01	5.48E-07		-1.16E+00	7.49E-13	Down	Unigene12598_All//gi|75150503|sp|Q8GTR4.1|PULA1_ARATH//0.00E+00//RecName: Full=Pullulanase 1, chloroplastic; Short=AtPU1; AltName: Full=Protein LIMIT DEXTRINASE; Short=AtLDA; Flags: Precursor >gi|27311611|gb|AAO00771.1| pullulanase-like protein (starch debranching enzyme) [Arabidopsis thaliana]	Unigene12598_All//0.00E+00//AT5G04360| ATLDA (LIMIT DEXTRINASE); alpha-amylase/ limit dextrinase/ pullulanase	Unigene12598_All//0.00E+00//CO128344			GO:0016160//GO:0043167//GO:0044238	nr -
Unigene126_All	3982	4.43	3.32	3.52	6.46	8.09	8.65	22.15	21.96	44.57	-4.15E-01	1.74E-03		-3.32E-01	1.81E-02		3.25E-01	3.27E-04		4.23E-01	2.04E-06		-1.25E-02	8.45E-01		1.01E+00	9.00E-162	Up	Unigene126_All//gi|224121336|ref|XP_002318557.1|//0.00E+00//aminophospholipid ATPase [Populus trichocarpa] >gi|222859230|gb|EEE96777.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene126_All//0.00E+00//AT1G68710| haloacid dehalogenase-like hydrolase family protein	Unigene126_All//0.00E+00//DT465302				nr +
Unigene12601_All	1257	11.82	8.59	11.95	10.86	10.44	8.91	18.16	9.94	8.56	-4.61E-01	1.50E-03		1.52E-02	9.40E-01		-5.71E-02	7.84E-01		-2.85E-01	7.44E-02		-8.69E-01	1.29E-16		-1.09E+00	2.17E-24	Down	Unigene12601_All//gi|30697915|ref|NP_568981.2|//1.00E-131//ATHDM (HISTIDINOL DEHYDROGENASE); histidinol dehydrogenase [Arabidopsis thaliana] >gi|29427983|sp|Q9C5U8.1|HISX_ARATH RecName: Full=Histidinol dehydrogenase, chloroplastic; Short=HDH; Flags: Precursor >gi|13516461|dbj|BAB40445.1| histidinol dehydrogenase [Arabidopsis thaliana] >gi|14532514|gb|AAK63985.1| AT5g63890/MG119_9 [Arabidopsis thaliana] >gi|23565959|gb|AAN28839.1| At5g63890/MG119_9 [Arabidopsis thaliana]	Unigene12601_All//3.00E-132//AT5G63890| ATHDM (HISTIDINOL DEHYDROGENASE); histidinol dehydrogenase	Unigene12601_All//0.00E+00//TC136402		ko00340|Histidine metabolism		nr -
Unigene12605_All	1182	49.97	52.77	50.73	60.27	65.05	61.44	39.81	28.85	19.08	7.85E-02	3.10E-01		2.16E-02	7.88E-01		1.10E-01	8.67E-02		2.78E-02	7.15E-01		-4.64E-01	1.59E-11		-1.06E+00	1.49E-47	Down	Unigene12605_All//gi|5360953|emb|CAB46439.1|//1.00E-117//v-ATPase subunit D [Arabidopsis thaliana]	Unigene12605_All//3.00E-118//AT3G58730| vacuolar ATP synthase subunit D (VATD) / V-ATPase D subunit / vacuolar proton pump D subunit (VATPD)	Unigene12605_All//0.00E+00//TC135989		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0006754//GO:0016469//GO:0019829	nr -
Unigene12608_All	3557	3.62	1.74	1.71	8.37	5.85	8.81	10.84	4.01	5.62	-1.06E+00	7.51E-11	Down	-1.08E+00	9.64E-11	Down	-5.18E-01	9.79E-09		7.34E-02	5.53E-01		-1.44E+00	1.21E-60	Down	-9.47E-01	1.46E-32		Unigene12608_All//gi|160334208|gb|ABX24524.1|//0.00E+00//slow walker 2 [Arabidopsis thaliana]	Unigene12608_All//0.00E+00//AT1G72440| EDA25 (embryo sac development arrest 25)	Unigene12608_All//0.00E+00//TC160416				nr -
Unigene12610_All	3573	4.06	1.13	1.80	16.60	20.56	25.70	22.60	28.44	34.31	-1.84E+00	6.26E-27	Down	-1.17E+00	1.74E-13	Down	3.08E-01	4.60E-08		6.30E-01	1.97E-32		3.31E-01	3.93E-13		6.02E-01	1.65E-46		Unigene12610_All//gi|10177918|dbj|BAB11329.1|//0.00E+00//kinesin-like protein [Arabidopsis thaliana]	Unigene12610_All//0.00E+00//AT5G47820| FRA1 (FRAGILE FIBER 1); microtubule motor	Unigene12610_All//0.00E+00//TC161512			GO:0003774//GO:0007017//GO:0009536//GO:0015630//GO:0030198//GO:0032559	nr -
Unigene12612_All	1376	48.21	8.03	23.41	148.86	81.73	38.89	18.65	41.04	47.83	-2.59E+00	7.66E-186	Down	-1.04E+00	9.62E-50	Down	-8.65E-01	6.27E-143		-1.94E+00	0.00E+00	Down	1.14E+00	1.09E-61	Up	1.36E+00	1.32E-96	Up	Unigene12612_All//gi|4835787|gb|AAD30253.1|AC007296_14//3.00E-46//ESTs gb|R65381 and gb|T14635 come from this gene [Arabidopsis thaliana] >gi|27808534|gb|AAO24547.1| AtTgl1700 [Arabidopsis thaliana]	Unigene12612_All//2.00E-42//AT1G61930| unknown protein	Unigene12612_All//0.00E+00//TC138458			GO:0009536	nr +
Unigene12614_All	2619	3.50	5.55	3.60	21.44	24.63	16.45	11.51	4.63	6.81	6.68E-01	5.65E-06		4.18E-02	8.39E-01		2.00E-01	1.71E-03		-3.82E-01	1.89E-08		-1.31E+00	1.11E-41	Down	-7.56E-01	9.33E-18		Unigene12614_All//gi|15225633|ref|NP_181541.1|//1.00E-166//protein kinase family protein [Arabidopsis thaliana]	Unigene12614_All//1.00E-157//AT2G40120| protein kinase family protein	Unigene12614_All//0.00E+00//TC138375			GO:0004672	nr -
Unigene12616_All	1442	2.76	2.67	2.47	12.92	9.36	6.26	10.97	5.33	6.30	-4.63E-02	8.87E-01		-1.56E-01	6.16E-01		-4.65E-01	9.24E-05		-1.04E+00	4.26E-16	Down	-1.04E+00	1.44E-15	Down	-8.00E-01	1.21E-10		Unigene12616_All//gi|15221582|ref|NP_177064.1|//8.00E-79//BIM2 (BES1-interacting Myc-like protein 2); DNA binding / transcription factor [Arabidopsis thaliana] >gi|61211674|sp|Q9CAA4.1|BIM2_ARATH RecName: Full=Transcription factor BIM2; AltName: Full=BES1-interacting Myc-like protein 2; AltName: Full=Transcription factor EN 125; AltName: Full=bHLH transcription factor bHLH102; AltName: Full=Basic helix-loop-helix protein 102; Short=bHLH 102; Short=AtbHLH102	Unigene12616_All//3.00E-78//AT1G69010| BIM2 (BES1-interacting Myc-like protein 2); DNA binding / transcription factor	Unigene12616_All//0.00E+00//ES832737	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr -
Unigene12617_All	407	2.70	1.99	0.26	1.96	2.71	1.33	0.73	1.44	1.57	-4.39E-01	4.95E-01		-3.37E+00	2.67E-04	Down	4.67E-01	5.30E-01		-5.56E-01	4.98E-01		9.83E-01	2.59E-01		1.11E+00	1.64E-01		Unigene12617_All//gi|3540190|gb|AAC34340.1|//5.00E-35//Hypothetical protein [Arabidopsis thaliana]	Unigene12617_All//7.00E-26//AT1G58520| hydrolase, acting on ester bonds / lipase	Unigene12617_All//1.00E-44//CO106878			GO:0031410	nr +
Unigene12619_All	2944	4.19	10.14	6.17	7.65	10.35	9.60	5.62	7.62	9.85	1.27E+00	4.78E-32	Up	5.56E-01	3.29E-05		4.37E-01	1.62E-06		3.28E-01	1.23E-03		4.41E-01	1.83E-05		8.11E-01	4.33E-19		Unigene12619_All//gi|115489730|ref|NP_001067352.1|//0.00E+00//Os12g0633600 [Oryza sativa Japonica Group] >gi|113649859|dbj|BAF30371.1| Os12g0633600 [Oryza sativa Japonica Group]	Unigene12619_All//0.00E+00//AT1G58520| hydrolase, acting on ester bonds / lipase	Unigene12619_All//0.00E+00//TC172450			GO:0031410	nr +
Unigene1262_All	805	3.51	6.61	7.94	5.14	4.41	2.86	8.82	9.97	8.36	9.13E-01	4.65E-04		1.18E+00	2.17E-06	Up	-2.21E-01	5.19E-01		-8.44E-01	4.34E-03		1.76E-01	3.97E-01		-7.73E-02	7.10E-01		Unigene1262_All//gi|18481628|gb|AAL73489.1|AF464906_1//2.00E-30//repressor protein [Glycine max]	Unigene1262_All//2.00E-10//AT5G23090| NF-YB13 (NUCLEAR FACTOR Y, SUBUNIT B13); transcription factor	Unigene1262_All//0.00E+00//TC145868	CCAAT			nr +
Unigene12620_All	363	0.00	0.14	2.35	1.10	0.95	1.49	0.00	0.58	0.11	7.13E+00	6.17E-01		1.12E+01	9.03E-05	Up	-2.11E-01	8.25E-01		4.44E-01	6.78E-01		9.17E+00	7.85E-02		6.78E+00	6.45E-01		Unigene12620_All//gi|13324449|gb|AK187511.1|//1.00E-38//patatin-like protein [Vigna unguiculata] >gi|13489049|gb|AAK27797.1| patatin-like protein [Vigna unguiculata]	Unigene12620_All//4.00E-39//AT2G26560| PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	Unigene12620_All//3.00E-97//TC133986			GO:0003824//GO:0044238	nr -

Unigene12621_All	2140	53.37	23.54	42.58	51.72	46.79	79.90	14.50	64.92	30.90	-1.18E+00	6.84E-108	Down	-3.26E-01	3.21E-11		-1.45E-01	2.83E-03		6.27E-01	1.60E-59		2.16E+00	0.00E+00	Up	1.09E+00	5.13E-69	Up	Unigene12621_All//gi|62766606|gb|AX99411.1|//1.00E-157//patatin-like protein [Gossypium hirsutum]	Unigene12621_All//2.00E-134//AT2G26560| PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	Unigene12621_All//0.00E+00//TC133986				nr -
Unigene12622_All	2537	4.91	4.35	5.23	1.98	4.00	2.46	5.83	3.26	2.45	-1.73E-01	3.29E-01		9.06E-02	6.42E-01		1.01E+00	3.42E-09	Up	3.09E-01	2.35E-01		-8.39E-01	1.90E-10		-1.25E+00	5.30E-20	Down	Unigene12622_All//gi|33468530|emb|CAE30324.1|//1.00E-179//NIN-like protein 1 [Lotus japonicus]	Unigene12622_All//4.00E-137//AT1G20640| RWP-RK domain-containing protein	Unigene12622_All//0.00E+00//TC171490	RWP-RK			nr +
Unigene12624_All	1744	1.47	2.91	4.09	4.66	4.42	6.42	1.82	2.32	1.71	9.83E-01	2.65E-04		1.48E+00	1.04E-09	Up	-7.40E-02	7.82E-01		4.64E-01	6.34E-03		3.55E-01	2.18E-01		-8.58E-02	7.83E-01		Unigene12624_All//gi|45476565|gb|AAS65948.1|//6.00E-44//At5g11600 [Arabidopsis thaliana] >gi|46339849|gb|AAS88788.1| At5g11600 [Arabidopsis thaliana]	Unigene12624_All//7.00E-36//AT5G11600| unknown protein	Unigene12624_All//3.00E-135//C0073541			GO:0043231	nr +
Unigene12625_All	2440	12.74	12.81	14.73	20.13	22.31	15.66	21.40	11.82	9.01	8.50E-03	9.57E-01		2.10E-01	3.15E-02		1.49E-01	4.76E-02		-3.62E-01	7.62E-07		-8.57E-01	4.94E-36		-1.25E+00	5.35E-68	Down	Unigene12625_All//gi|227206122|dbj|BAH57116.1|//4.00E-77//AT5G67610 [Arabidopsis thaliana]	Unigene12625_All//4.00E-103//AT5G67610| unknown protein	Unigene12625_All//0.00E+00//TC162267			GO:0031410	nr +
Unigene12627_All	961	6.53	6.54	7.31	11.20	9.57	6.81	14.74	13.53	7.13	1.00E-03	9.97E-01		1.63E-01	5.16E-01		-2.27E-01	2.27E-01		-7.16E-01	2.34E-05		-1.24E-01	4.24E-01		-1.05E+00	1.22E-14	Down	Unigene12627_All//gi|23327858|ref|NP_200371.2|//1.00E-91//agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein [Arabidopsis thaliana] >gi|186532338|ref|NP_001119443.1| agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein [Arabidopsis thaliana] >gi|18087548|gb|AAL58906.1|AF46281 S_1 AT5g55600/MDF20_4 [Arabidopsis thaliana] >gi|24111271|gb|AAN46759.1| At5g55600/MDF20_4 [Arabidopsis thaliana]	Unigene12627_All//3.00E-88//AT5G55600| agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein	Unigene12627_All//0.00E+00//TC170556			GO:0003676	nr -
Unigene12630_All	1694	13.59	21.75	11.88	16.53	16.38	20.10	19.19	10.36	8.40	6.78E-01	2.95E-14		-1.94E-01	1.33E-01		-1.25E-02	9.24E-01		2.83E-01	2.30E-03		-8.89E-01	3.47E-24		-1.19E+00	8.16E-40	Down	Unigene12630_All//gi|211906520|gb|ACJ11753.1|//0.00E+00//UDP-D-apiose/UPD-D-xylose synthetase [Gossypium hirsutum]	Unigene12630_All//0.00E+00//AT1G08200| AXS2 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 2); UDP-glucuronate decarboxylase	Unigene12630_All//0.00E+00//ES811961		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0000166//GO:0005576//GO:0009225//GO:0016831//GO:0016836//GO:0044424//GO:0048037	nr +
Unigene12634_All	1338	31.83	15.79	15.28	55.77	43.88	53.60	38.49	27.24	28.11	-1.01E+00	9.64E-32	Down	-1.06E+00	6.59E-33	Down	-3.46E-01	3.28E-10		-5.72E-02	4.58E-01		-4.99E-01	3.68E-14		-4.54E-01	2.12E-12		Unigene12634_All//gi|297790396|ref|XP_002863091.1|//1.00E-115//nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308909|gb|EFH39350.1| nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12634_All//4.00E-87//AT3G25150| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene12634_All//0.00E+00//TC139227		ko03040|Spliceosome	GO:0005622	nr -
Unigene12635_All	1374	0.08	0.22	0.54	1.23	0.60	1.12	19.14	36.47	46.13	1.54E+00	3.23E-01		2.83E+00	8.52E-03		-1.04E+00	3.10E-02		-1.41E-01	7.81E-01		9.30E-01	1.25E-39		1.27E+00	7.28E-84	Up	Unigene12635_All//gi|18401743|ref|NP_564507.1|//1.00E-114//hydrolase [Arabidopsis thaliana] >gi|5668813|gb|AAD46039.1|AC007519_24 Similar to gb|X77136 HSR203J protein from Nicotiana tabacum and is a member of the PF|00135 Carboxylesterase family. ESTs gb|Z25688 and gb|F14025 come from this gene [Arabidopsis thaliana]	Unigene12635_All//2.00E-115//AT1G47480| hydrolase	Unigene12635_All//0.00E+00//TC172020				nr +
Unigene12636_All	1465	0.79	29.05	8.43	5.98	4.91	7.80	48.57	71.52	100.92	5.21E+00	3.82E-209	Up	3.42E+00	1.04E-44	Up	-2.85E-01	1.61E-01		3.82E-01	2.62E-02		5.58E-01	4.31E-34		1.06E+00	4.51E-145	Up	Unigene12636_All//gi|18401743|ref|NP_564507.1|//1.00E-114//hydrolase [Arabidopsis thaliana] >gi|5668813|gb|AAD46039.1|AC007519_24 Similar to gb|X77136 HSR203J protein from Nicotiana tabacum and is a member of the PF|00135 Carboxylesterase family. ESTs gb|Z25688 and gb|F14025 come from this gene [Arabidopsis thaliana]	Unigene12636_All//7.00E-116//AT1G47480| hydrolase	Unigene12636_All//0.00E+00//TC149967				nr -
Unigene12639_All	1716	1.65	1.74	1.68	0.64	1.06	2.32	2.69	2.68	2.21	8.14E-02	8.19E-01		2.54E-02	9.65E-01		7.36E-01	1.37E-01		1.86E+00	2.62E-08	Up	-3.40E-03	1.02E+00		-2.84E-01	2.68E-01		Unigene12639_All//gi|115489538|ref|NP_001067256.1|//5.00E-64//Os12g0612100 [Oryza sativa Japonica Group] >gi|113649763|dbj|BAF30275.1| Os12g0612100 [Oryza sativa Japonica Group]	Unigene12639_All//9.00E-39//AT4G26850| VTC2 (vitamin c defective 2); GDP-D-glucose phosphorylase/ GDP-galactose:glucose-1-phosphate guanyltransferase/ GDP-galactose:mannose-1-phosphate guanyltransferase/ GDP-galactose:myoinositol-1-phosphate guanyltransferase/ galactose-1-phosphate guanylyltra	Unigene12639_All//0.00E+00//ES812694				nr -
Unigene1264_All	3720	5.43	3.42	4.27	21.29	20.56	12.53	17.86	8.35	8.32	-6.67E-01	5.45E-08		-3.48E-01	7.20E-03		-5.05E-02	5.08E-01		-7.65E-01	1.45E-39		-1.10E+00	1.96E-68	Down	-1.10E+00	7.42E-71	Down	Unigene1264_All//gi|115482822|ref|NP_001065004.1|//1.00E-151//Os10g0504600 [Oryza sativa Japonica Group] >gi|110289363|gb|AAP54507.2| Chorion family 2 protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639613|dbj|BAF26918.1| Os10g0504600 [Oryza sativa Japonica Group]	Unigene1264_All//0.00E+00//AT1G63300| unknown protein	Unigene1264_All//0.00E+00//gi|164239392|gb|ES792343.1|ES792343				nr -
Unigene12641_All	1704	5.53	6.27	4.94	8.04	3.80	9.94	32.01	68.85	64.97	1.83E-01	3.43E-01		-1.63E-01	4.36E-01		-1.08E+00	3.24E-14	Down	3.06E-01	2.84E-02		1.11E+00	1.40E-121	Up	1.02E+00	2.88E-103	Up	Unigene12641_All//gi|133778900|gb|AB038790.1|//1.00E-141//At1g76360 [Arabidopsis thaliana]	Unigene12641_All//8.00E-136//AT1G76360| protein kinase, putative	Unigene12641_All//0.00E+00//TC139317		ko04626|Plant-pathogen interaction		nr +
Unigene12643_All	1041	5.48	8.03	5.78	6.84	9.06	6.94	5.56	9.23	11.40	5.52E-01	5.94E-03		7.74E-02	7.63E-01		4.06E-01	2.96E-02		2.06E-02	9.50E-01		7.31E-01	9.58E-06		1.04E+00	4.16E-12	Up	Unigene12643_All//gi|42565288|ref|NP_566850.3|//4.00E-96//R1K (RS2-Interacting KH protein); RNA binding [Arabidopsis thaliana] >gi|156633616|sp|Q9LIA4.2|R1K_ARATH RecName: Full=Protein R1K; AltName: Full=Rough sheath 2-interacting KH domain protein; Short=RS2-interacting KH domain protein >gi|62997489|gb|AAY24687.1| KH-domain protein [Arabidopsis thaliana]	Unigene12643_All//4.00E-85//AT3G29390| R1K (RS2-Interacting KH protein); RNA binding	Unigene12643_All//6.00E-172//TC148068			GO:0003676//GO:0043231	nr -
Unigene12645_All	1851	20.32	10.87	14.90	15.47	12.99	10.44	11.70	4.22	6.18	-9.03E-01	2.05E-23		-4.48E-01	5.89E-07		-2.53E-01	1.11E-02		-5.67E-01	6.80E-09		-1.47E+00	1.41E-35	Down	-9.21E-01	7.39E-18		Unigene12645_All//gi|124360683|gb|ABN08672.1|//0.00E+00//Isocitrate lyase and phosphoenylmutase [Medicago truncatula]	Unigene12645_All//1.00E-170//AT2G43180| catalytic	Unigene12645_All//0.00E+00//gi|164278638|gb|ES812603.1|ES812603		ko00630|Glyoxylate and dicarboxylate metabolism	GO:0003824	nr +
Unigene12647_All	1642	55.95	53.14	65.74	126.57	119.60	145.28	117.62	106.60	45.90	-7.45E-02	2.29E-01		2.32E-01	6.28E-06		-8.17E-02	2.72E-02		1.99E-01	3.35E-10		-1.42E-01	2.05E-05		-1.36E+00	2.83E-284	Down	Unigene12647_All//gi|18390896|ref|NP_563816.1|//0.00E+00//CRT3 (CALRETICULIN 3); calcium ion binding / unfolded protein binding [Arabidopsis thaliana] >gi|166998136|sp|O04153.2|CALR3_ARATH RecName: Full=Calreticulin-3; Flags: Precursor	Unigene12647_All//0.00E+00//AT1G08450| CRT3 (CALRETICULIN 3); calcium ion binding / unfolded protein binding	Unigene12647_All//0.00E+00//TC138930		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	GO:0002218//GO:0005515//GO:0009812//GO:0031090//GO:0031410//GO:0033554//GO:0043231//GO:0044267//GO:0046872//GO:0055065	nr +
Unigene1265_All	3079	2.79	13.49	5.69	1.18	1.64	1.10	16.93	19.32	13.29	2.28E+00	1.80E-99	Up	1.03E+00	2.57E-13	Up	4.77E-01	7.69E-02		-1.02E-01	7.63E-01		1.90E-01	2.54E-03		-3.50E-01	4.49E-08		Unigene1265_All//gi|30690286|ref|NP_849563.1|//0.00E+00//TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|20453189|gb|AAM19835.1| AT4g35300/F23E12_140 [Arabidopsis thaliana]	Unigene1265_All//0.00E+00//AT4G35300| TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter	Unigene1265_All//0.00E+00//TC173221				nr +
Unigene12650_All	2743	1.60	0.92	1.40	2.16	2.77	2.91	1.87	3.99	2.15	-7.95E-01	5.88E-03		-1.97E-01	5.44E-01		3.60E-01	9.78E-02		4.31E-01	4.04E-02		1.10E+00	5.88E-12	Up	2.05E-01	3.76E-01		Unigene12650_All//gi|15230921|ref|NP_188604.1|//1.00E-146//IKU2 (HAIKU2); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|75273596|sp|Q9LJM4.1|IKU2_ARATH RecName: Full=Receptor-like protein kinase HAIKU2; Flags: Precursor >gi|9294437|dbj|BAB02557.1| receptor-like protein kinase [Arabidopsis thaliana]	Unigene12650_All//5.00E-139//AT3G19700| IKU2 (HAIKU2); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene12650_All//2.00E-124//TC156612				nr +
Unigene12652_All	889	1.41	1.14	0.96	1.79	2.40	3.51	3.19	4.94	8.11	-3.09E-01	6.21E-01		-5.60E-01	3.87E-01		4.22E-01	3.82E-01		9.67E-01	6.30E-03		6.32E-01	1.45E-02		1.35E+00	3.18E-11	Up	Unigene12652_All//gi|18401703|ref|NP_564504.1|//5.00E-98//protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] >gi|75172944|sp|Q9FX08.1|P2C12_ARATH RecName: Full=Probable protein phosphatase 2C 12; Short=AtPP2C12 >gi|9993354|gb|AAG11427.1|AC015449_9 Unknown protein [Arabidopsis thaliana]	Unigene12652_All//2.00E-99//AT1G47380| protein phosphatase 2C-related / PP2C-related	Unigene12652_All//0.00E+00//gi|78347146|gb|DT567420.1|DT567420			GO:0004721	nr +
Unigene12653_All	2196	7.43	3.60	3.39	4.47	4.22	2.92	13.30	12.28	35.87	-1.05E+00	2.55E-13	Down	-1.13E+00	2.36E-14	Down	-8.33E-02	7.13E-01		-6.14E-01	6.18E-04		-1.16E-01	2.60E-01		1.43E+00	8.42E-125	Up	Unigene12653_All//gi|18401703|ref|NP_564504.1|//0.00E+00//protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] >gi|75172944|sp|Q9FX08.1|P2C12_ARATH RecName: Full=Probable protein phosphatase 2C 12; Short=AtPP2C12 >gi|9993354|gb|AAG11427.1|AC015449_9 Unknown protein [Arabidopsis thaliana]	Unigene12653_All//0.00E+00//AT1G47380| protein phosphatase 2C-related / PP2C-related	Unigene12653_All//0.00E+00//TC176076			GO:0004721	nr -
Unigene12657_All	630	6.06	1.85	4.90	8.14	5.63	3.58	7.32	0.80	1.90	-1.71E+00	5.39E-07	Down	-3.06E-01	3.81E-01		-5.33E-01	3.72E-02		-1.18E+00	7.48E-06	Down	-3.20E+00	3.36E-20	Down	-1.95E+00	3.38E-12	Down	Unigene12657_All//gi|3860321|emb|CAA10128.1|//1.00E-82//beta-galactosidase [Cicer arietinum]	Unigene12657_All//3.00E-75//AT1G45130| BGAL5 (beta-galactosidase 5); beta-galactosidase/ catalytic/ cation binding	Unigene12657_All//3.00E-126//gi|78325228|gb|DT545502.1|DT545502		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series	GO:0015925//GO:0030246//GO:0031410//GO:0043167//GO:0043234//GO:0044238	nr +

Unigene12658_All	2693	25.74	7.15	14.83	35.35	25.89	14.74	20.77	3.21	5.73	-1.85E+00	2.00E-127	Down	-7.96E-01	3.66E-33		-4.49E-01	9.90E-21		-1.26E+00	2.08E-108	Down	-2.69E+00	3.54E-200	Down	-1.86E+00	1.60E-130	Down	Unigene12658_All//gi|3860321|emb|CAA10128.1|//0.00E+00//beta-galactosidase [Cicer arietinum]	Unigene12658_All//0.00E+00//AT1G45130| BGAL5 (beta-galactosidase 5); beta-galactosidase/ catalytic/ cation binding	Unigene12658_All//0.00E+00//TC168823		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series	GO:0015925//GO:0030246//GO:0043167//GO:0043234//GO:0044238//GO:0044464	nr +
Unigene12659_All	666	0.94	2.97	1.28	1.20	1.60	3.32	1.78	0.31	1.02	1.65E+00	8.01E-04	Up	4.41E-01	5.83E-01		4.22E-01	5.72E-01		1.47E+00	1.00E-03		-2.50E+00	1.47E-04	Down	-8.06E-01	1.31E-01		Unigene12659_All//gi|134142079|gb|AB061383.1|//2.00E-79//plastid serine hydroxymethyltransferase [Populus tremuloides]	Unigene12659_All//4.00E-75//AT4G32520| SHM3 (SERINE HYDROXYMETHYLTRANSFERASE 3); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene12659_All//0.00E+00//CO119838		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate	GO:0009069//GO:0009536//GO:0016742//GO:0048037	nr +
Unigene1266_All	227	6.45	8.04	14.78	8.34	18.05	18.90	4.66	4.23	2.11	3.16E-01	5.24E-01		1.20E+00	8.71E-04	Up	1.11E+00	1.37E-04	Up	1.18E+00	6.57E-05	Up	-1.37E-01	8.15E-01		-1.14E+00	4.77E-02								
Unigene12660_All	1389	50.32	21.38	30.98	53.90	38.67	60.87	74.45	37.91	33.64	-1.24E+00	4.37E-71	Down	-7.00E-01	7.18E-27		-4.79E-01	2.05E-18		1.75E-01	2.39E-03		-9.74E-01	2.16E-87		-1.15E+00	4.62E-117	Down	Unigene12660_All//gi|225429452|ref|XP_002277146.1|//0.00E+00//PREDICTED: similar to plastid serine hydroxymethyltransferase [Vitis vinifera]	Unigene12660_All//0.00E+00//AT4G32520| SHM3 (SERINE HYDROXYMETHYLTRANSFERASE 3); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene12660_All//0.00E+00//TC167034		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate	GO:0009069//GO:0009536//GO:0016742//GO:0048037	nr +
Unigene12662_All	1621	6.23	19.72	14.32	19.11	18.57	21.90	13.20	10.08	10.89	1.66E+00	9.65E-51	Up	1.20E+00	3.35E-22	Up	-4.20E-02	7.52E-01		1.96E-01	4.01E-02		-3.89E-01	2.53E-04		-2.78E-01	8.35E-03		Unigene12662_All//gi|15234225|ref|NP_192064.1|//1.00E-31//anac069 (Arabidopsis NAC domain containing protein 69); transcription factor [Arabidopsis thaliana] >gi|75181714|sp|Q9M126.1|NAC69_ARATH RecName: Full=NAC domain-containing protein 69; Short=ANAC069; AltName: Full=Protein NAC WITH TRANSMEMBRANE MOTIF 2	Unigene12662_All//1.00E-27//AT4G01550| anac069 (Arabidopsis NAC domain containing protein 69); transcription factor	Unigene12662_All//0.00E+00//TC179237	NAC			nr -
Unigene12664_All	1657	11.08	5.14	11.70	17.95	13.70	15.75	10.28	7.14	8.13	-1.11E+00	2.69E-16	Down	7.79E-02	6.21E-01		-3.90E-01	2.19E-05		-1.88E-01	7.83E-02		-5.27E-01	1.07E-05		-3.40E-01	4.06E-03		Unigene12664_All//gi|15230073|ref|NP_189058.1|//4.00E-87//PMP (PUTATIVE TYPE 1 MEMBRANE PROTEIN) [Arabidopsis thaliana] >gi|15450743|gb|AAX96643.1|AT3g24160/MUJ8_16 [Arabidopsis thaliana] >gi|22137144|gb|AAM91417.1|AT3g24160/MUJ8_16 [Arabidopsis thaliana]	Unigene12664_All//6.00E-87//AT3G24160| PMP (PUTATIVE TYPE 1 MEMBRANE PROTEIN)	Unigene12664_All//0.00E+00//TC135257			GO:0016020//GO:0043231//GO:0044444	nr +
Unigene12665_All	1378	0.15	2.35	1.43	5.17	4.37	19.63	0.06	0.06	0.00	3.95E+00	8.18E-14	Up	3.23E+00	4.12E-07	Up	-2.41E-01	3.18E-01		1.93E+00	2.99E-56	Up	-1.65E-02	1.01E+00		-5.94E+00	3.59E-01		Unigene12665_All//gi|2564237|emb|CAA71199.1|//0.00E+00//omega-6 desaturase [Gossypium hirsutum]	Unigene12665_All//7.00E-174//AT3G12120| FAD2 (FATTY ACID DESATURASE 2); delta12-fatty acid dehydrogenase/ omega-6 fatty acid desaturase	Unigene12665_All//0.00E+00//gi|109879276|gb|DW508246.1|DW508246		ko01040|Biosynthesis of unsaturated fatty acids	GO:0003824//GO:0044238	nr +
Unigene12666_All	1425	3.41	2.52	3.48	4.93	3.94	2.25	6.08	0.97	2.49	-4.36E-01	1.17E-01		2.54E-02	9.44E-01		-3.24E-01	1.56E-01		-1.13E+00	2.90E-07	Down	-2.65E+00	5.14E-31	Down	-1.29E+00	1.30E-12	Down	Unigene12666_All//gi|2564237|emb|CAA71199.1|//0.00E+00//omega-6 desaturase [Gossypium hirsutum]	Unigene12666_All//8.00E-179//AT3G12120| FAD2 (FATTY ACID DESATURASE 2); delta12-fatty acid dehydrogenase/ omega-6 fatty acid desaturase	Unigene12666_All//0.00E+00//NP385892		ko01040|Biosynthesis of unsaturated fatty acids	GO:0016705//GO:0044238	nr +
Unigene12669_All	307	0.51	5.94	1.39	2.43	4.04	3.38	0.69	0.82	0.65	3.54E+00	2.15E-07	Up	1.44E+00	2.53E-01		7.30E-01	2.54E-01		4.75E-01	5.13E-01		2.47E-01	8.53E-01		-8.59E-02	9.61E-01			Unigene12669_All//4.00E-07//TC152609				
Unigene1267_All	3718	8.40	18.98	11.89	15.98	21.69	21.46	17.91	20.88	25.78	1.18E+00	3.57E-66	Up	5.01E-01	9.74E-10		4.41E-01	1.10E-16		4.25E-01	3.87E-14		2.21E-01	3.56E-05		5.26E-01	8.35E-29		Unigene1267_All//gi|297841455|ref|XP_002888609.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334450|gb|EFH64868.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1267_All//0.00E+00//AT1G67580| protein kinase family protein	Unigene1267_All//0.00E+00//gi|48746937|gb|CO077456.1|CO077456				nr +
Unigene12673_All	1565	11.03	3.46	3.47	18.65	14.02	9.21	15.72	2.56	5.47	-1.67E+00	4.63E-28	Down	-1.67E+00	6.76E-27	Down	-4.12E-01	8.24E-06		-1.02E+00	6.37E-24	Down	-2.62E+00	1.36E-85	Down	-1.52E+00	9.55E-44	Down	Unigene12673_All//gi|225639908|gb|ACD87452.2|//1.00E-171//minichromosome maintenance 5 protein [Pisum sativum]	Unigene12673_All//2.00E-166//AT2G07690| minichromosome maintenance family protein / MCM family protein	Unigene12673_All//0.00E+00//TC131475		ko03030|DNA replication		nr +
Unigene12674_All	2606	2.71	0.88	0.65	5.49	4.81	2.62	6.88	1.33	2.63	-1.63E+00	1.57E-11	Down	-2.05E+00	8.68E-15	Down	-1.90E-01	2.42E-01		-1.07E+00	6.26E-13	Down	-2.37E+00	8.18E-56	Down	-1.39E+00	4.81E-28	Down	Unigene12674_All//gi|225639908|gb|ACD87452.2|//0.00E+00//minichromosome maintenance 5 protein [Pisum sativum]	Unigene12674_All//0.00E+00//AT2G07690| minichromosome maintenance family protein / MCM family protein	Unigene12674_All//0.00E+00//TC161204		ko03030|DNA replication	GO:0003676//GO:0006259//GO:0015698//GO:0032559//GO:0043231	nr -
Unigene12675_All	1234	6.06	3.70	4.70	13.28	10.97	12.15	16.48	4.81	10.10	-7.14E-01	7.88E-04		-3.66E-01	1.12E-01		-2.76E-01	4.53E-02		-1.28E-01	4.37E-01		-1.78E+00	9.33E-44	Down	-7.06E-01	5.57E-11		Unigene12675_All//gi|115479367|ref|NP_001063277.1|//1.00E-148//Os09g0439700 [Oryza sativa Japonica Group] >gi|51091402|dbj|BAD36145.1|membrane protein PTM1-like [Oryza sativa Japonica Group] >gi|113631510|dbj|BAF25191.1|Os09g0439700 [Oryza sativa Japonica Group]	Unigene12675_All//4.00E-159//AT1G72480| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: Golgi apparatus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Transmembrane receptor, eukaryota (InterPro:IPR009637); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G01070.1); Has 422 Blast hits to 420 proteins in 121 species: Archae - 0; Bacteria - 0; Metazoa - 208; Fungi - 101; Plants - 83; Viruses - 0; Other Eukaryotes - 30 (source: NCBI BLink).	Unigene12675_All//0.00E+00//TC136433				nr +
Unigene1268_All	3441	0.56	1.56	1.21	6.41	4.34	3.83	2.85	4.64	1.52	1.47E+00	9.05E-08	Up	1.10E+00	4.78E-04	Up	-5.62E-01	1.37E-07		-7.43E-01	6.70E-11		7.03E-01	1.83E-08		-9.10E-01	1.95E-08		Unigene1268_All//gi|24461849|gb|AAN62336.1|AF506028_3//0.00E+00//CTV.2 [Citrus trifoliata]	Unigene1268_All//0.00E+00//AT1G80490| TPR1 (TOPLESS-RELATED 1)	Unigene1268_All//0.00E+00//TC145070		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene12680_All	419	0.50	2.90	1.02	3.09	1.07	2.37	2.02	2.00	2.19	2.54E+00	5.98E-04	Up	1.03E+00	3.97E-01		-1.53E+00	7.65E-03		-3.82E-01	5.50E-01		-1.66E-02	1.02E+00		1.16E-01	8.57E-01		Unigene12680_All//gi|22325409|ref|NP_671763.1|//8.00E-19//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|79316317|ref|NP_001030936.1|zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|46931308|gb|AAT06458.1|At2g01275 [Arabidopsis thaliana]	Unigene12680_All//5.00E-20//AT2G01275| zinc finger (C3HC4-type RING finger) family protein	Unigene12680_All//3.00E-42//TC157689			GO:0046914	nr -
Unigene12682_All	1502	1.29	4.52	2.27	2.49	2.54	2.17	2.31	2.64	3.08	1.81E+00	1.18E-12	Up	8.16E-01	1.97E-02		3.29E-02	9.44E-01		-2.00E-01	5.95E-01		1.96E-01	5.32E-01		4.15E-01	9.52E-02		Unigene12682_All//gi|297817714|ref|XP_002876740.1|//2.00E-69//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322578|gb|EFH52999.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12682_All//2.00E-66//AT2G01275| zinc finger (C3HC4-type RING finger) family protein	Unigene12682_All//3.00E-128//DW512441		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene12683_All	783	18.64	9.25	15.71	12.47	11.52	7.50	13.55	7.85	8.24	-1.01E+00	2.26E-11	Down	-2.47E-01	1.30E-01		-1.14E-01	5.99E-01		-7.34E-01	4.16E-05		-7.89E-01	4.97E-07		-7.18E-01	2.57E-06		Unigene12683_All//gi|11320956|gb|AAG33975.1|AF250961_1//2.00E-42//methionine aminopeptidase-like protein [Arabidopsis thaliana]	Unigene12683_All//9.00E-44//AT1G13270| MAP1C (METHIONINE AMINOPEPTIDASE 1B); aminopeptidase/ metalloexopeptidase	Unigene12683_All//0.00E+00//DW225988			GO:0008237//GO:0008238//GO:0009536//GO:0018193//GO:0043169	nr +
Unigene12684_All	829	3.16	2.69	1.48	2.82	1.95	0.87	3.01	2.27	3.08	-2.31E-01	5.78E-01		-1.09E+00	8.04E-03		-5.33E-01	2.00E-01		-1.70E+00	1.02E-04	Down	-4.07E-01	2.79E-01		3.15E-02	9.51E-01		Unigene12684_All//gi|11320956|gb|AAG33975.1|AF250961_1//4.00E-17//methionine aminopeptidase-like protein [Arabidopsis thaliana]	Unigene12684_All//2.00E-18//AT1G13270| MAP1C (METHIONINE AMINOPEPTIDASE 1B); aminopeptidase/ metalloexopeptidase	Unigene12684_All//0.00E+00//CA993980			GO:0008237//GO:0008238//GO:0009536//GO:0018193//GO:0043169	nr +
Unigene12688_All	2385	2.39	1.19	1.90	5.89	4.92	5.04	5.34	3.43	2.72	-1.01E+00	6.41E-05	Down	-3.33E-01	2.25E-01		-2.59E-01	9.31E-02		-2.26E-01	1.71E-01		-6.36E-01	6.32E-06		-9.71E-01	8.69E-12		Unigene12688_All//gi|35187466|gb|AQ84324.1|//2.00E-47//fiber protein FbS2 [Gossypium barbadense]	Unigene12688_All//5.00E-14//AT2G31130| unknown protein	Unigene12688_All//4.00E-33//TC171920				nr -
Unigene12689_All	3079	4.42	3.13	2.58	11.73	9.76	6.51	10.52	2.86	2.91	-4.99E-01	1.06E-03		-7.78E-01	8.91E-07		-2.65E-01	2.06E-03		-8.49E-01	7.88E-22		-1.88E+00	1.35E-74	Down	-1.85E+00	1.46E-75	Down	Unigene12689_All//gi|115440183|ref|NP_001044371.1|//0.00E+00//Os01g0769200 [Oryza sativa Japonica Group] >gi|113533902|dbj|BAF06285.1|Os01g0769200 [Oryza sativa Japonica Group]	Unigene12689_All//0.00E+00//AT4G20430| subtilase family protein	Unigene12689_All//0.00E+00//TC158596			GO:0004175//GO:0005515//GO:0005618//GO:0019538//GO:0031410//GO:0044492	nr -
Unigene12691_All	1427	4.84	31.46	14.59	29.32	27.41	33.71	17.45	22.79	27.53	2.70E+00	6.29E-131	Up	1.59E+00	2.31E-30	Up	-9.72E-02	3.08E-01		2.01E-01	1.11E-02		3.85E-01	4.83E-06		6.58E-01	5.39E-18		Unigene12691_All//gi|115441063|ref|NP_001044811.1|//3.00E-18//Os01g0850000 [Oryza sativa Japonica Group] >gi|113534342|dbj|BAF06725.1|Os01g0850000 [Oryza sativa Japonica Group]	Unigene12691_All//2.00E-26//AT5G59050| unknown protein	Unigene12691_All//0.00E+00//TC178720				nr -
Unigene12692_All	2142	88.37	309.34	79.65	133.47	388.32	381.55	133.95	299.20	532.37	1.81E+00	0.00E+00	Up	-1.50E-01	1.21E-04		1.54E+00	0.00E+00	Up	1.52E+00	0.00E+00	Up	1.16E+00	0.00E+00	Up	1.99E+00	0.00E+00	Up	Unigene12692_All//gi|59668410|emb|CAI39245.1|//0.00E+00//beta-amylase [Glycine max]	Unigene12692_All//7.00E-172//AT5G18670| BMY3; beta-amylase/ catalytic/ cation binding	Unigene12692_All//0.00E+00//TC139018		ko00500|Starch and sucrose metabolism	GO:0005976//GO:0016160//GO:0043167	nr +
Unigene12695_All	877	1.73	1.04	1.52	0.91	1.14	1.13	3.37	10.63	7.22	-7.34E-01	1.70E-01		-1.89E-01	7.21E-01		3.25E-01	6.73E-01		3.18E-01	6.73E-01		1.66E+00	1.49E-18	Up	1.10E+00	1.83E-07	Up	Unigene12695_All//gi|115475281|ref|NP_001061237.1|//3.00E-17//Os08g0205900 [Oryza sativa Japonica Group] >gi|113623206|dbj|BAF23151.1|Os08g0205900 [Oryza sativa Japonica Group]	Unigene12695_All//2.00E-16//AT3G22200| POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase/ 4-aminobutyrate:pyruvate transaminase	Unigene12695_All//0.00E+00//TC169629				nr +
Unigene12696_All	1504	76.57	100.83	123.78	99.89	105.71	120.69	93.30	194.75	137.82	3.97E-01	8.98E-22		6.93E-01	1.25E-69		8.16E-02	6.29E-02		2.73E-01	5.67E-14		1.06E+00	1.25E-283	Up	5.63E-01	3.37E-69		Unigene12696_All//gi|29837286|gb|AA062257.1|//0.00E+00//gamma-aminobutyrate transaminase subunit precursor isozyme 3 [Solanum lycopersicum] >gi|171854587|dbj|BAG16484.1|gamma aminobutyrate transaminase isoform3 [Solanum lycopersicum]	Unigene12696_All//0.00E+00//AT3G22200| POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase/ 4-aminobutyrate:pyruvate transaminase	Unigene12696_All//0.00E+00//TC136659		ko00330|Arginine and proline metabolism	GO:0008483//GO:0043231//GO:0048037	nr -
Unigene12701_All	488	0.96	6.02	1.42	0.41	1.41	2.22	2.08	7.54	3.27	2.64E+00	6.36E-09	Up	5.56E-01	5.28E-01		1.79E+00	6.10E-02		2.44E+00	1.61E-03		1.86E+00	5.37E-09	Up	6.51E-01	1.51E-01		Unigene12701_All//gi|77994685|gb|ABB13620.1|//2.00E-38//USP-like protein [Astragalus sinicus]	Unigene12701_All//3.00E-19//AT3G62550| universal stress protein (USP) family protein	Unigene12701_All//0.00E+00//TC161003			GO:0050896	nr +
Unigene12702_All	816	7.44	84.08	15.99	6.65	13.88	23.85	8.65	24.18	10.69	3.50E+00	1.07E-257	Up	1.10E+00	3.29E-11	Up	1.06E+00	6.04E-11	Up	1.84E+00	2.85E-38	Up	1.48E+00	7.81E-33	Up	3.05E-01	8.23E-02		Unigene12702_All//gi|77994685|gb|ABB13620.1|//2.00E-49//USP-like protein [Astragalus sinicus]	Unigene12702_All//2.00E-35//AT3G62550| universal stress protein (USP) family protein	Unigene12702_All//0.00E+00//gi|84166793|gb|DR455441.1|DR455441			GO:0050896	nr +
Unigene12703_All	975	5.37	29.36	9.34	6.39	23.20	23.62	8.80	24.31	12.50	2.45E+00	4.60E-75	Up	7.99E-01	5.49E-05		1.86E+00	4.31E-49	Up	1.89E+00	1.06E-46	Up	1.47E+00	1.25E-38	Up	5.06E-01	3.25E-04		Unigene12703_All//gi|77994685|gb|ABB13620.1|//6.00E-57//USP-like protein [Astragalus sinicus]	Unigene12703_All//8.00E-38//AT3G62550| universal stress protein (USP) family protein	Unigene12703_All//0.00E+00//TC146015			GO:0050896	nr -
Unigene12704_All	559	2.06	2.90	0.57	5.70	4.25	3.07	5.60	3.81	2.71	4.94E-01	3.53E-01		-1.85E+00	1.07E-02		-4.24E-01	2.31E-01		-8.94E-01	9.76E-03		-5.54E-01	8.20E-02		-1.05E+00	6.42E-04	Down	Unigene12704_All//gi|195613152|gb|ACG28406.1|//1.00E-35//cytochrome c-type biogenesis protein cycL precursor [Zea mays]	Unigene12704_All//2.00E-28//AT1G15220| CCMH; oxidoreductase	Unigene12704_All//3.00E-101//gi|164298229|gb|ES813017.1|ES813017			GO:0003824//GO:0005488//GO:0007275//GO:0019866//GO:0032991//GO:0043231	nr +

Unigene12705_A11	1000	8.89	10.39	9.96	13.15	16.94	14.36	7.70	4.93	3.67	2.24E-01	2.33E-01		1.63E-01	4.18E-01		3.65E-01	5.41E-03		1.27E-01	4.69E-01		-6.42E-01	5.79E-04		-1.07E+00	1.26E-08	Down	Unigene12705_A11//gi|115445519|ref|NP_001046539.1|//3.00E-36//Os02g0275100 [Oryza sativa Japonica Group] >gi|47848023|dbj|BAD21809.1| cytochrome c biogenesis protein-like [Oryza sativa Japonica Group] >gi|47848060|dbj|BAD21845.1| cytochrome c biogenesis protein-like [Oryza sativa Japonica Group] >gi|113536020|dbj|BAF08453.1| Os02g0275100 [Oryza sativa Japonica Group]	Unigene12705_A11//3.00E-31//ATIG15220| CCMH; oxidoreductase	Unigene12705_A11//5.00E-151//gi|164273141|gb|ES792489.1|ES792489			GO:0003824//GO:0005488//GO:0007275//GO:0019866//GO:0032991//GO:0043231	nr +
Unigene12706_A11	1731	36.63	83.10	60.39	36.55	38.18	43.13	133.07	125.00	92.29	1.18E+00	3.04E-135	Up	7.21E-01	4.36E-42		6.29E-02	4.35E-01		2.39E-01	6.39E-05		-9.02E-02	4.39E-03		-5.28E-01	9.22E-69		Unigene12706_A11//gi|30698009|ref|NP_201242.2|//0.00E+00//BETA-UP (beta-ureidopropionase); beta-ureidopropionase [Arabidopsis thaliana] >gi|28193999|gb|AAO33358.1|AF465754_1 N-carbamyl-beta-alanine amidohydrolase [Arabidopsis thaliana] >gi|23306402|gb|AAN17428.1| beta-ureidopropionase [Arabidopsis thaliana] >gi|30725680|gb|AAP37862.1| At5g64370 [Arabidopsis thaliana]	Unigene12706_A11//0.00E+00//AT5G64370| BETA-UP (beta-ureidopropionase); beta-ureidopropionase	Unigene12706_A11//0.00E+00//TC145988		ko00240|Pyrimidine metabolism//ko00380|Tryptophan metabolism//ko00910|Nitrogen metabolism//ko00460|Cyanoamino acid metabolism//ko00410|beta-Alanine metabolism//ko00770|Pantothenate and CoA biosynthesis	GO:0006208//GO:0016811//GO:0031669//GO:0044444	nr -
Unigene12707_A11	1904	0.36	0.75	0.31	7.98	3.94	5.86	1.82	2.20	1.86	1.06E+00	6.14E-02		-2.16E-01	7.88E-01		-1.02E+00	3.03E-14	Down	-4.46E-01	1.65E-03		2.70E-01	3.64E-01		3.24E-02	9.35E-01		Unigene12707_A11//gi|59668410|emb|CAI39245.1|//1.00E-177//beta-amylase [Glycine max]	Unigene12707_A11//2.00E-145//AT5G18670| BMY3; beta-amylase/ catalytic/ cation binding	Unigene12707_A11//0.00E+00//TC146463		ko00500|Starch and sucrose metabolism	GO:0043231	nr +
Unigene12712_A11	3016	6.77	6.08	6.32	4.48	6.75	7.67	6.06	1.54	4.06	-1.54E-01	2.46E-01		-9.81E-02	4.99E-01		5.92E-01	1.82E-07		7.77E-01	3.86E-12		-1.98E+00	2.14E-45	Down	-5.79E-01	2.91E-07		Unigene12712_A11//gi|18422366|ref|NP_568628.1|//0.00E+00//phosphotransferase-related [Arabidopsis thaliana] >gi|15450498|gb|AAK96542.1|AT5g02940/F9G14_250 [Arabidopsis thaliana] >gi|16974323|gb|AAL31146.1|AT5g02940/F9G14_250 [Arabidopsis thaliana]	Unigene12712_A11//0.00E+00//AT5G43745| phosphotransferase-related	Unigene12712_A11//0.00E+00//TC160296			GO:0009536	nr +
Unigene12718_A11	1204	3.82	3.75	1.46	7.28	9.75	5.25	9.55	8.68	9.13	-3.00E-02	9.30E-01		-1.39E+00	5.62E-06	Down	4.22E-01	9.11E-03		-4.72E-01	1.60E-02		-1.38E-01	4.22E-01		-6.48E-02	6.88E-01		Unigene12718_A11//gi|73624747|gb|AZ79231.1|//1.00E-156//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene12718_A11//8.00E-150//AT4G23990| ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	Unigene12718_A11//0.00E+00//ES847571				nr -
Unigene12720_A11	2151	1.90	1.72	0.69	2.39	3.14	3.17	2.12	1.96	2.94	-1.42E-01	6.32E-01		-1.45E+00	1.07E-05	Down	3.96E-01	8.59E-02		4.11E-01	7.85E-02		-1.13E-01	6.82E-01		4.72E-01	2.10E-02		Unigene12720_A11//gi|124359597|gb|ABD28747.2|//3.00E-27//Putative non-LTR retroelement reverse transcriptase, related [Medicago truncatula]	Unigene12720_A11//2.00E-16//AT3G24255| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G23910.1); Has 2302 Blast hits to 2235 proteins in 74 species: Archae - 4; Bacteria - 15; Metazoa - 871; Fungi - 12; Plants - 1295; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).			ko00270|Cysteine and methionine metabolism		nr -
Unigene12722_A11	1940	6.66	5.75	5.76	5.16	5.27	3.49	4.51	2.26	1.89	-2.13E-01	2.07E-01		-2.09E-01	2.37E-01		3.06E-02	8.94E-01		-5.64E-01	1.53E-03		-9.96E-01	2.04E-08		-1.26E+00	3.01E-12	Down	Unigene12722_A11//gi|224082190|ref|XP_002306596.1|//1.00E-138//f-box family protein [Populus trichocarpa] >gi|222856045|gb|EEE93592.1| f-box family protein [Populus trichocarpa]	Unigene12722_A11//2.00E-134//AT1G22040| kelch repeat-containing F-box family protein	Unigene12722_A11//0.00E+00//TC164799				nr -
Unigene12725_A11	585	9.39	6.06	17.02	2.90	3.53	1.85	3.47	3.14	7.22	-6.31E-01	1.29E-02		8.58E-01	5.63E-06		2.87E-01	5.78E-01		-6.44E-01	2.19E-01		-1.42E-01	7.30E-01		1.06E+00	5.28E-05	Up	Unigene12725_A11//gi|255537553|ref|XP_002509843.1|//1.00E-29//bell homeotic protein, putative [Ricinus communis] >gi|223549742|gb|EEF51230.1| bell homeotic protein, putative [Ricinus communis]		Unigene12725_A11//4.00E-30//TC164821			GO:0003677//GO:0006350//GO:0010468	nr +
Unigene12726_A11	2776	37.36	22.36	31.88	7.30	4.73	5.52	8.10	13.91	16.68	-7.40E-01	3.38E-45		-2.29E-01	1.43E-05		-6.28E-01	1.93E-08		-4.05E-01	7.77E-04		7.80E-01	5.71E-23		1.04E+00	4.65E-45	Up	Unigene12726_A11//gi|31323443|gb|AAP47023.1|AF375964_1//1.00E-161//bel1-like homeodomain protein 3 [Solanum lycopersicum]	Unigene12726_A11//2.00E-118//AT5G41410| BEL1 (BELL 1); DNA binding / protein binding / transcription factor	Unigene12726_A11//0.00E+00//TC146909	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene12728_A11	2420	24.21	17.27	24.86	16.04	5.71	2.65	3.90	2.73	3.19	-4.87E-01	1.22E-12		3.82E-02	6.24E-01		-1.49E+00	1.25E-65	Down	-2.60E+00	2.81E-119	Down	-5.14E-01	2.10E-03		-2.87E-01	8.92E-02		Unigene12728_A11//gi|297797663|ref|XP_002866716.1|//0.00E+00//phospholipase C [Arabidopsis lyrata subsp. lyrata] >gi|297312551|gb|EFH42975.1| phospholipase C [Arabidopsis lyrata subsp. lyrata]	Unigene12728_A11//3.00E-177//AT5G67130| phospholipase C/ phosphoric diester hydrolase	Unigene12728_A11//0.00E+00//TC143170		ko04120|Ubiquitin mediated proteolysis	GO:0004620//GO:0042578//GO:0044238	nr +
Unigene12729_A11	2108	21.57	25.36	19.30	27.36	27.39	30.55	27.28	14.55	12.49	2.34E-01	1.52E-03		-1.60E-01	6.89E-02		1.60E-03	9.89E-01		1.59E-01	2.14E-02		-9.06E-01	1.67E-43		-1.13E+00	1.03E-63	Down	Unigene12729_A11//gi|218963693|gb|ACL13550.1|//0.00E+00//delta-1-pyrroline-5-carboxylate dehydrogenase 1 protein [Malus x domestica]	Unigene12729_A11//0.00E+00//AT5G62530| ALDH12A1; 1-pyrroline-5-carboxylate dehydrogenase/ 3-chloroallyl aldehyde dehydrogenase	Unigene12729_A11//0.00E+00//TC161914		ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0004030//GO:0006536//GO:0006970//GO:0009536//GO:0016646//GO:0046914	nr -
Unigene1273_A11	3958	2.37	5.04	6.67	7.16	5.72	8.22	26.80	23.21	26.40	1.09E+00	3.72E-17	Up	1.50E+00	4.52E-35	Up	-3.25E-01	7.42E-04		1.98E-01	4.86E-02		-2.08E-01	4.29E-06		-2.17E-02	6.79E-01		Unigene1273_A11//gi|87240970|gb|AB032828.1|//1.00E-162//|, related [Medicago truncatula]	Unigene1273_A11//4.00E-120//AT4G00440| unknown protein	Unigene1273_A11//0.00E+00//C0092519				nr +
Unigene12730_A11	2274	9.76	12.12	7.00	15.99	12.66	12.45	6.97	3.14	2.03	3.13E-01	2.79E-03		-4.79E-01	6.90E-05		-3.37E-01	4.78E-05		-3.61E-01	3.23E-05		-1.15E+00	3.25E-18	Down	-1.78E+00	2.11E-35	Down	Unigene12730_A11//gi|218963693|gb|ACL13550.1|//0.00E+00//delta-1-pyrroline-5-carboxylate dehydrogenase 1 protein [Malus x domestica]	Unigene12730_A11//0.00E+00//AT5G62530| ALDH12A1; 1-pyrroline-5-carboxylate dehydrogenase/ 3-chloroallyl aldehyde dehydrogenase	Unigene12730_A11//0.00E+00//TC137874		ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0004030//GO:0006536//GO:0006970//GO:0009536//GO:0016646//GO:0046914	nr +
Unigene12731_A11	1623	10.64	8.09	5.74	67.83	76.87	46.30	68.36	17.25	57.00	-3.96E-01	3.24E-03		-8.90E-01	2.06E-10		1.81E-01	3.77E-05		-5.51E-01	8.64E-31		-1.99E+00	4.22E-274	Down	-2.62E-01	9.45E-10		Unigene12731_A11//gi|297833520|ref|XP_002884642.1|//0.00E+00//glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] >gi|297330482|gb|EFH60901.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	Unigene12731_A11//0.00E+00//AT3G07320| glycosyl hydrolase family 17 protein	Unigene12731_A11//0.00E+00//gi|78351977|gb|DT572251.1|DT572251		ko00500|Starch and sucrose metabolism	GO:0005618//GO:0016798//GO:0043167//GO:0044238	nr +
Unigene12732_A11	1718	29.24	34.71	32.82	24.65	28.20	49.47	44.77	46.08	49.69	2.48E-01	3.27E-04		1.67E-01	3.06E-02		1.94E-01	1.10E-02		1.01E+00	1.90E-66	Up	4.17E-02	5.43E-01		1.51E-01	3.11E-03		Unigene12732_A11//gi|18417554|ref|NP_567842.1|//9.00E-66//protein binding [Arabidopsis thaliana] >gi|16226657|gb|AAL16225.1|AF428456_1 AT4g30240/F9N11_90 [Arabidopsis thaliana] >gi|221371126|gb|AAM91408.1| At4g30240/F9N11_90 [Arabidopsis thaliana]	Unigene12732_A11//4.00E-63//AT4G30240| protein binding	Unigene12732_A11//0.00E+00//TC142300			GO:0005488//GO:0016192//GO:0043231	nr +
Unigene12734_A11	2662	4.58	1.69	3.14	11.96	8.15	5.70	15.01	7.47	7.30	-1.43E+00	3.63E-16	Down	-5.44E-01	1.22E-03		-5.53E-01	2.12E-10		-1.07E+00	3.98E-28	Down	-1.01E+00	4.10E-36	Down	-1.04E+00	3.63E-39	Down	Unigene12734_A11//gi|224074675|ref|XP_002304419.1|//1.00E-179//GRAS family transcription factor [Populus trichocarpa] >gi|222841851|gb|EEE79398.1| GRAS family transcription factor [Populus trichocarpa]	Unigene12734_A11//1.00E-86//AT4G00150| scarecrow-like transcription factor 6 (SCL6)	Unigene12734_A11//0.00E+00//TC144419	GRAS			nr +
Unigene12737_A11	2361	5.56	2.79	2.98	91.04	64.51	26.49	26.09	4.55	3.71	-9.96E-01	4.47E-10		-9.02E-01	3.00E-08		-4.97E-01	6.96E-56		-1.78E+00	0.00E+00	Down	-2.52E+00	1.47E-204	Down	-2.81E+00	2.46E-238	Down	Unigene12737_A11//gi|224589543|gb|ACN59305.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene12737_A11//0.00E+00//AT2G36570| leucine-rich repeat transmembrane protein kinase, putative	Unigene12737_A11//0.00E+00//TC137495		ko04626|Plant-pathogen interaction	GO:0004871//GO:0006464//GO:0007167//GO:0016301//GO:0031224//GO:0032559	nr +
Unigene12743_A11	1357	1.66	2.50	4.28	3.19	3.55	2.80	3.15	4.53	5.37	5.94E-01	7.88E-02		1.37E+00	3.21E-07	Up	1.54E-01	6.19E-01		-1.92E-01	5.74E-01		5.25E-01	1.42E-02		7.72E-01	4.34E-05					Unigene12743_A11//1.00E-124//gi|21095094|gb|BQ407407.1|BQ407407				
Unigene12748_A11	2187	8.92	3.45	9.37	9.36	7.23	10.04	2.71	2.64	2.55	-1.37E+00	9.02E-24	Down	7.11E-02	6.24E-01		-3.73E-01	1.17E-03		1.00E-01	4.81E-01		-3.74E-02	8.86E-01		-8.58E-02	7.08E-01		Unigene12748_A11//gi|224589537|gb|ACN59302.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene12748_A11//0.00E+00//AT2G31880| leucine-rich repeat transmembrane protein kinase, putative	Unigene12748_A11//0.00E+00//TC167706			GO:0004674//GO:0004871//GO:0006464//GO:0032559	nr +
Unigene12749_A11	621	1.26	0.08	0.94	4.57	4.33	2.62	2.04	4.31	4.75	-3.95E+00	8.54E-04	Down	-4.22E-01	6.21E-01		-8.02E-02	8.22E-01		-8.04E-01	3.06E-02		1.08E+00	1.94E-03		1.22E+00	1.78E-04	Up	Unigene12749_A11//gi|227438217|gb|ACF30598.1|//3.00E-27//disease resistance protein [Brassica rapa subsp. pekinensis]	Unigene12749_A11//1.00E-23//AT1G63870| disease resistance protein (TIR-NBS-LRR class), putative	Unigene12749_A11//2.00E-75//DT047949			GO:0005488//GO:0009987	nr +
Unigene12751_A11	2906	5.38	4.90	3.54	5.83	6.67	7.41	5.82	2.40	2.77	-1.36E-01	3.85E-01		-6.06E-01	3.19E-05		1.95E-01	1.54E-01		3.47E-01	3.45E-03		-1.28E+00	1.02E-22	Down	-1.07E+00	6.34E-18	Down	Unigene12751_A11//gi|15220191|ref|NP_172540.1|//1.00E-159//ribose-phosphate pyrophosphokinase 3 / phosphoribosyl diphosphate synthetase 3 (PRS3) [Arabidopsis thaliana] >gi|62286943|sp|Q93266.1|KPRS3_ARATH RecName: Full=Ribose-phosphate pyrophosphokinase 3; AltName: Full=Phosphoribosyl pyrophosphate synthase 3 >gi|16604386|gb|AAL24199.1|At1g10700/F20B24.13 [Arabidopsis thaliana] >gi|19699210|gb|AAL90971.1|At1g10700/F20B24.13 [Arabidopsis thaliana]	Unigene12751_A11//2.00E-153//AT1G10700| ribose-phosphate pyrophosphokinase 3 / phosphoribosyl diphosphate synthetase 3 (PRS3)	Unigene12751_A11//0.00E+00//TC146600		ko00230|Purine metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene12753_A11	2261	15.02	14.93	11.71	27.56	27.35	29.82	52.30	30.32	21.48	-9.00E-03	9.49E-01		-3.60E-01	1.74E-04		-1.10E-02	8.99E-01		1.14E-01	1.14E-01		-7.87E-01	8.92E-70		-1.28E+00	5.47E-160	Down	Unigene12753_A11//gi|79321519|ref|NP_001031305.1|//0.00E+00//HSP91; ATP binding [Arabidopsis thaliana]	Unigene12753_A11//0.00E+00//AT1G79920| ATP binding	Unigene12753_A11//0.00E+00//TC160091		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0006950//GO:0008152//GO:0010038//GO:0016020//GO:0016628//GO:0032559//GO:0043231	nr +
Unigene12754_A11	1840	6.26	2.81	4.20	3.03	2.43	1.96	3.54	2.04	2.14	-1.16E+00	3.71E-11	Down	-5.76E-01	9.05E-04		-3.18E-01	2.26E-01		-6.27E-01	1.23E-02		-7.92E-01	1.18E-04		-7.23E-01	2.89E-04		Unigene12754_A11//gi|42571865|ref|NP_974023.1|//0.00E+00//RNA binding [Arabidopsis thaliana]	Unigene12754_A11//0.00E+00//AT1G54310| RNA binding				GO:0016020	nr +
Unigene12756_A11	2855	14.35	27.35	22.33	18.48	32.38	30.75	11.63	23.85	21.53	9.31E-01	4.45E-50		6.38E-01	6.26E-21		8.10E-01	1.20E-55		7.35E-01	1.55E-40		1.04E+00	6.22E-64	Up	8.89E-01	5.37E-46		Unigene12756_A11//gi|229020999|gb|AAM54141.2|AF515632_1//0.00E+00//Na/H antiporter [Gossypium hirsutum]	Unigene12756_A11//0.00E+00//AT3G05030| NHX2 (SODIUM HYDROGEN EXCHANGER 2); sodium ion transmembrane transporter/ sodium:hydrogen antiporter	Unigene12756_A11//0.00E+00//TC135827			GO:0005451//GO:0030001//GO:0031224//GO:0055067	nr +

Unigene12757_All	1135	31.30	2.99	3.10	50.34	9.59	8.87	48.39	31.01	28.96	-3.39E+00	3.87E-131	Down	-3.34E+00	9.09E-125	Down	-2.39E+00	9.14E-186	Down	-2.50E+00	2.44E-168	Down	-6.42E-01	3.00E-23		-7.41E-01	1.62E-30		Unigene12757_All//gi|75099990|sp|Q80920.1|PYL4_ARATH//3.00E-71//RecName: Full=Abscisic acid receptor PYL4; AltName: Full=PYR1-like protein 4; AltName: Full=ABI1-binding protein 2; AltName: Full=Regulatory components of ABA receptor 10 >gi|3395441|gb|AAC28773.1| expressed protein [Arabidopsis thaliana] >gi|14517502|gb|AAK62641.1| At2g38310/T19C21.20 [Arabidopsis thaliana] >gi|15809748|gb|AAL06802.1| At2g38310/T19C21.20 [Arabidopsis thaliana]	Unigene12757_All//7.00E-66//AT2G38310| unknown protein	Unigene12757_All//0.00E+00//gi|78350201|gb|DT570475.1|DT570475			GO:0004871//GO:0009755//GO:0019840//GO:0043231	nr +
Unigene12758_All	1780	13.99	0.57	1.82	29.05	5.09	4.16	20.90	8.59	11.10	-4.62E+00	4.18E-116	Down	-2.94E+00	2.17E-77	Down	-2.51E+00	1.93E-178	Down	-2.80E+00	6.86E-173	Down	-1.28E+00	2.36E-49	Down	-9.13E-01	1.27E-29		Unigene12758_All//gi|75099990|sp|Q80920.1|PYL4_ARATH//1.00E-70//RecName: Full=Abscisic acid receptor PYL4; AltName: Full=PYR1-like protein 4; AltName: Full=ABI1-binding protein 2; AltName: Full=Regulatory components of ABA receptor 10 >gi|3395441|gb|AAC28773.1| expressed protein [Arabidopsis thaliana] >gi|14517502|gb|AAK62641.1| At2g38310/T19C21.20 [Arabidopsis thaliana] >gi|15809748|gb|AAL06802.1| At2g38310/T19C21.20 [Arabidopsis thaliana]	Unigene12758_All//2.00E-65//AT2G38310| unknown protein	Unigene12758_All//0.00E+00//gi|78350201|gb|DT570475.1|DT570475			GO:0004871//GO:0009755//GO:0019840//GO:0043231	nr -
Unigene12761_All	2277	7.10	2.67	5.66	25.03	17.51	14.74	14.52	7.62	8.56	-1.41E+00	1.10E-20	Down	-3.27E-01	2.71E-02		-5.15E-01	4.44E-16		-7.64E-01	1.48E-28		-9.31E-01	1.77E-26		-7.63E-01	1.11E-19		Unigene12761_All|gi|115479513|ref|NP_001063350.1|//1.00E-74//Os05g0454200 [Oryza sativa Japonica Group] >gi|51535214|dbj|BAD38263.1| hydroxyproline-rich glycoprotein-like protein [Oryza sativa Japonica Group] >gi|51535954|dbj|BAD38036.1| hydroxyproline-rich glycoprotein-like protein [Oryza sativa Japonica Group] >gi|113631583|dbj|BAF25264.1| Os09g0454200 [Oryza sativa Japonica Group]	Unigene12761_All//3.00E-52//AT1G10790| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT3G56590.2); Has 40 Blast hits to 40 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene12761_All//0.00E+00//TC134262		ko03040|Spliceosome//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr -
Unigene12763_All	1436	1.93	1.62	1.11	2.39	3.57	2.48	3.80	1.66	1.53	-2.51E-01	5.25E-01		-7.96E-01	4.51E-02		5.78E-01	2.66E-02		5.38E-02	8.97E-01		-1.20E+00	3.62E-07	Down	-1.32E+00	1.71E-08	Down	Unigene12763_All|gi|238481234|ref|NP_001154704.1|//1.00E-65//ALF4 (ABERRANT LATERAL ROOT FORMATION 4) [Arabidopsis thaliana]	Unigene12763_All//4.00E-61//AT5G11030| ALF4 (ABERRANT LATERAL ROOT FORMATION 4)	Unigene12763_All//8.00E-163//TC167045			GO:0044424	nr -
Unigene12764_All	2063	3.55	3.56	2.94	4.52	4.01	4.77	5.35	2.01	1.39	4.40E-03	9.82E-01		-2.71E-01	2.51E-01		-1.73E-01	4.22E-01		7.99E-02	6.99E-01		-1.42E+00	1.52E-17	Down	-1.94E+00	5.43E-28	Down	Unigene12764_All|gi|238481234|ref|NP_001154704.1|//2.00E-80//ALF4 (ABERRANT LATERAL ROOT FORMATION 4) [Arabidopsis thaliana]	Unigene12764_All//3.00E-100//AT5G11030| ALF4 (ABERRANT LATERAL ROOT FORMATION 4)	Unigene12764_All//1.00E-177//gi|21096022|gb|BQ408335.1|BQ408335				nr +
Unigene12767_All	1296	2.95	2.35	2.67	6.03	10.15	8.40	3.46	1.03	1.51	-3.29E-01	3.15E-01		-1.42E-01	6.60E-01		7.50E-01	2.63E-07		4.77E-01	5.75E-03		-1.74E+00	5.38E-10	Down	-1.20E+00	2.72E-06	Down	Unigene12767_All|gi|1621463|gb|AAB17192.1|//1.00E-167//laccase [Liriodendron tulipifera]	Unigene12767_All//2.00E-152//AT5G60020| LAC17 (laccase 17); laccase	Unigene12767_All//8.00E-141//DR452622		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene12768_All	2068	1.37	1.86	2.29	5.47	8.64	7.93	9.02	3.33	4.43	4.47E-01	1.57E-01		7.46E-01	9.59E-03		6.60E-01	6.52E-08		5.36E-01	6.82E-05		-1.43E+00	1.07E-29	Down	-1.03E+00	2.36E-18	Down	Unigene12768_All|gi|1621463|gb|AAB17192.1|//0.00E+00//laccase [Liriodendron tulipifera]	Unigene12768_All//0.00E+00//AT5G60020| LAC17 (laccase 17); laccase	Unigene12768_All//1.00E-146//DR452622		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr -
Unigene12771_All	2010	12.05	14.39	13.01	42.83	42.09	35.37	115.78	84.40	46.46	2.56E-01	1.35E-02		1.10E-01	3.96E-01		-2.49E-02	7.56E-01		-2.76E-01	3.87E-07		-4.56E-01	6.36E-52		-1.32E+00	0.00E+00	Down	Unigene12771_All|gi|5731259|gb|AAD48837.1|AF166351_1|/0.00E+00//alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis thaliana]	Unigene12771_All//0.00E+00//AT4G39660| AGT2 (ALANINE:GLYOXYLATE AMINOTRANSFERASE 2); alanine-glyoxylate transaminase/ catalytic/ pyridoxal phosphate binding / transaminase	Unigene12771_All//0.00E+00//TC133027		ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism	GO:0006527//GO:0008483//GO:0010038//GO:0016020//GO:0043231//GO:0046914//GO:0048037	nr -
Unigene12772_All	1372	5.91	5.91	7.68	9.51	11.12	8.46	9.71	9.50	4.09	-5.00E-04	9.97E-01		3.79E-01	4.40E-02		2.25E-01	1.44E-01		-1.69E-01	3.53E-01		-3.04E-02	8.54E-01		-1.25E+00	5.88E-18	Down	Unigene12772_All|gi|115459706|ref|NP_001053453.1|//9.00E-37//Os04g0543200 [Oryza sativa Japonica Group] >gi|38345947|emb|CAE04271.2| OSJNB0103108.18 [Oryza sativa (japonica cultivar-group)] >gi|38345949|emb|CAE04337.2| OSJNB0038F03.1 [Oryza sativa (japonica cultivar-group)] >gi|113565024|dbj|BAF15367.1| Os04g0543200 [Oryza sativa Japonica Group]	Unigene12772_All//1.00E-29//AT2G44710| RNA recognition motif (RRM)-containing protein	Unigene12772_All//0.00E+00//TC152008		ko03040|Spliceosome	GO:0005488//GO:0031410	nr +
Unigene12775_All	2133	6.16	7.55	3.40	9.90	10.30	10.31	15.28	17.99	60.22	2.95E-01	3.92E-02		-8.59E-01	1.19E-07		5.68E-02	7.14E-01		5.85E-02	6.98E-01		2.35E-01	2.99E-03		1.98E+00	0.00E+00	Up	Unigene12775_All|gi|2495155|sp|P93111.1|HEM11_CUCSA//0.00E+00//RecName: Full=Glutamyl-tRNA reductase 1, chloroplastic; Short=GluTR; Flags: Precursor >gi|1694926|dbj|BAA08910.1| glutamyl-tRNA reductase [Cucumis sativus]	Unigene12775_All//0.00E+00//AT1G58290| HEMA1; glutamyl-tRNA reductase	Unigene12775_All//0.00E+00//TC157546		ko00860|Porphyrin and chlorophyll metabolism	GO:0000166//GO:0006779//GO:0006950//GO:0009314//GO:0009536//GO:0016616//GO:0016620	nr -
Unigene12776_All	2434	0.86	1.10	0.61	1.00	1.16	2.21	2.62	2.09	8.61	3.60E-01	3.75E-01		-4.89E-01	3.03E-01		2.10E-01	6.10E-01		1.14E+00	1.09E-05	Up	-3.24E-01	1.38E-01		1.71E+00	9.69E-44	Up	Unigene12776_All|gi|2495155|sp|P93111.1|HEM11_CUCSA//0.00E+00//RecName: Full=Glutamyl-tRNA reductase 1, chloroplastic; Short=GluTR; Flags: Precursor >gi|1694926|dbj|BAA08910.1| glutamyl-tRNA reductase [Cucumis sativus]	Unigene12776_All//0.00E+00//AT1G58290| HEMA1; glutamyl-tRNA reductase	Unigene12776_All//0.00E+00//TC157546		ko00860|Porphyrin and chlorophyll metabolism	GO:0000166//GO:0006779//GO:0006950//GO:0009314//GO:0009536//GO:0016616//GO:0016620	nr -
Unigene12784_All	352	0.45	3.89	0.15	1.98	1.86	1.67	0.48	1.31	1.70	3.12E+00	3.45E-05	Up	-1.56E+00	5.33E-01		-9.21E-02	8.95E-01		-2.48E-01	7.56E-01		1.44E+00	1.67E-01		1.82E+00	3.94E-02		Unigene12784_All|gi|297810923|ref|XP_002873345.1|//9.00E-15//EMB1873 [Arabidopsis lyrata subsp. lyrata] >gi|297319182|gb|EFH49604.1| EMB1873 [Arabidopsis lyrata subsp. lyrata]	Unigene12784_All//6.00E-16//AT5G08170| EMB1873 (EMBRYO DEFECTIVE 1873); agmatine deiminase	Unigene12784_All//7.00E-86//ES847041		ko00330|Arginine and proline metabolism	GO:0003006//GO:0006596//GO:0016813	nr +
Unigene12789_All	838	5.56	2.60	4.13	17.48	11.71	4.37	2.52	0.75	0.76	-1.10E+00	1.17E-04	Down	-4.28E-01	1.49E-01		-5.78E-01	1.84E-05		-2.00E+00	6.43E-33	Down	-1.75E+00	3.84E-05	Down	-1.73E+00	2.86E-05	Down	Unigene12789_All|gi|297822685|ref|XP_002879225.1|//2.00E-19//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325064|gb|EFH55484.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12789_All//2.00E-20//AT2G29660| zinc finger (C2H2 type) family protein	Unigene12789_All//0.00E+00//TC168436	C2H2		GO:0001071//GO:0010468//GO:0031224//GO:0043231//GO:0046914	nr +
Unigene12790_All	2091	24.17	8.26	12.66	59.49	52.20	19.14	4.29	1.44	1.71	-1.55E+00	1.63E-72	Down	-9.33E-01	9.75E-32		-1.88E-01	1.40E-05		-1.64E+00	1.78E-209	Down	-1.57E+00	1.00E-16	Down	-1.32E+00	1.73E-13	Down	Unigene12790_All|gi|297822685|ref|XP_002879225.1|//1.00E-105//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325064|gb|EFH55484.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12790_All//3.00E-93//AT2G29660| zinc finger (C2H2 type) family protein	Unigene12790_All//0.00E+00//TC168436	C2H2			nr +
Unigene12791_All	4056	4.48	3.61	2.13	16.27	16.17	11.96	17.96	4.97	6.18	-3.10E-01	1.97E-02		-1.07E+00	1.14E-14	Down	-8.90E-03	9.15E-01		-4.44E-01	8.18E-13		-1.85E+00	2.57E-164	Down	-1.54E+00	5.56E-130	Down	Unigene12791_All|gi|27462172|gb|AA015358.1|AF242356_1|/0.00E+00//kinesin related protein [Solanum lycopersicum]	Unigene12791_All//4.00E-98//AT3G20150| kinesin motor family protein	Unigene12791_All//0.00E+00//ES820941			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr +
Unigene12792_All	2511	3.02	2.26	2.61	4.88	5.84	5.23	4.66	2.16	2.08	-4.19E-01	5.06E-02		-2.12E-01	3.86E-01		2.60E-01	8.82E-02		1.01E-01	6.21E-01		-1.11E+00	6.29E-13	Down	-1.17E+00	2.06E-14	Down	Unigene12792_All|gi|30690461|ref|NP_195299.2|//0.00E+00//RecQ13; ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana] >gi|75334307|sp|Q9FT72.1|RQL3_ARATH RecName: Full=ATP-dependent DNA helicase Q-like 3; AltName: Full=RecQ-like protein 3; Short=AtRecQ13; Short=AtRecQ3 >gi|11121447|emb|CAC14867.1| DNA Helicase [Arabidopsis thaliana]	Unigene12792_All//0.00E+00//AT4G35740| RecQ13; ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene12792_All//0.00E+00//gi|164260658|gb|ES843119.1|ES843119		ko03440|Homologous recombination	GO:0003678//GO:0003690//GO:0006259//GO:0032559//GO:0042623	nr -
Unigene12793_All	1714	39.19	26.55	43.31	13.02	18.50	13.75	4.81	1.39	4.25	-5.62E-01	2.09E-18		1.44E-01	3.20E-02		5.07E-01	1.04E-08		7.91E-02	5.90E-01		-1.79E+00	2.20E-18	Down	-1.77E-01	3.55E-01		Unigene12793_All|gi|297789349|ref|XP_002862652.1|//1.00E-155//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308299|gb|EFH38910.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12793_All//1.00E-155//AT3G07360| PUB9 (PLANT U-BOX 9); ubiquitin-protein ligase	Unigene12793_All//0.00E+00//TC160186			GO:0019787//GO:0032446//GO:0043234	nr +
Unigene12794_All	1662	8.00	3.81	7.18	3.39	4.89	3.18	3.31	2.64	8.03	-1.07E+00	2.35E-11	Down	-1.56E-01	3.96E-01		5.30E-01	7.28E-03		-9.12E-02	7.38E-01		-3.25E-01	1.77E-01		1.28E+00	1.43E-18	Up	Unigene12794_All|gi|297789349|ref|XP_002862652.1|//1.00E-161//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308299|gb|EFH38910.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12794_All//5.00E-162//AT3G07360| PUB9 (PLANT U-BOX 9); ubiquitin-protein ligase	Unigene12794_All//0.00E+00//TC160186			GO:0019787//GO:0032446//GO:0043234	nr -
Unigene12797_All	1531	0.14	0.03	0.03	0.00	0.09	0.06	1.16	0.30	0.47	-2.05E+00	3.34E-01		-1.97E+00	3.81E-01		6.49E+00	3.19E-01		5.88E+00	4.77E-01		-1.95E+00	5.37E-05	Down	-1.31E+00	2.53E-03		Unigene12797_All|gi|297793377|ref|XP_002864573.1|//1.00E-127//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297310408|gb|EFH40832.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene12797_All//1.00E-118//AT5G58410| binding / protein binding / zinc ion binding	Unigene12797_All//0.00E+00//CO109318			GO:0046872	nr -
Unigene12799_All	1161	12.03	15.97	16.88	7.85	9.46	8.48	1.02	1.87	2.44	4.09E-01	1.53E-03		4.88E-01	1.51E-04		2.69E-01	1.41E-01		1.11E-01	6.38E-01		8.76E-01	2.43E-02		1.26E+00	1.67E-04	Up	Unigene12799_All|gi|226528427|ref|NP_001151619.1|//7.00E-55//LOC100285253 [Zea mays] >gi|195648134|gb|ACG43535.1| protein phosphatase 2C [Zea mays]	Unigene12799_All//1.00E-26//AT4G33500| protein phosphatase 2C-related / PP2C-related	Unigene12799_All//0.00E+00//TC135249			GO:0016791	nr -
Unigene128_All	2927	2.90	6.08	6.53	7.96	14.95	22.11	9.66	2.66	5.21	1.07E+00	7.10E-15	Up	1.17E+00	9.95E-18	Up	9.09E-01	4.28E-32		1.47E+00	4.98E-92	Up	-1.86E+00	1.29E-64	Down	-8.91E-01	7.74E-22		Unigene128_All//gi|186478314|ref|NP_172981.3|//0.00E+00//binding [Arabidopsis thaliana]	Unigene128_All//0.00E+00//AT1G15290| binding	Unigene128_All//0.00E+00//gi|164240850|gb|ES821071.1|ES821071				nr +

Unigene12802_All	839	1.68	1.69	2.86	4.51	5.13	6.19	3.68	3.64	8.78	6.20E-03	9.91E-01		7.62E-01	7.76E-02		1.85E-01	5.85E-01		4.56E-01	9.47E-02		-1.66E-02	9.94E-01		1.26E+00	2.33E-10	Up	Unigene12802_All//gi|9955545|emb|CAC05430.1|//3.00E-90//ankyrin-repeat containing protein [Arabidopsis thaliana]	Unigene12802_All//1.00E-69//AT5G13530| KEG (KEEP ON GOING); protein binding / protein kinase/ ubiquitin-protein ligase				GO:0006950//GO:0009755//GO:0016301//GO:0016787//GO:0019787//GO:0032446//GO:0040007//GO:0046872	nr +
Unigene12804_All	2800	4.19	0.74	1.96	12.08	10.93	8.77	6.81	2.28	2.89	-2.50E+00	5.95E-32	Down	-1.10E+00	5.43E-10	Down	-1.44E-01	1.57E-01		-4.61E-01	2.51E-07		-1.58E+00	9.25E-35	Down	-1.24E+00	4.39E-25	Down	Unigene12804_All//gi|224097178|ref|XP_002310865.1|//1.00E-155//nucleobase ascorbate transporter [Populus trichocarpa]>gi|22285376 8|gb|EEE91315.1|nucleobase ascorbate transporter [Populus trichocarpa]	Unigene12804_All//9.00E-134//AT4G38050| transmembrane transporter	Unigene12804_All//0.00E+00//TC175919			GO:0006810//GO:0044464	nr +
Unigene12805_All	2464	0.98	0.19	0.30	3.13	2.85	2.11	1.56	0.54	0.82	-2.40E+00	8.36E-07	Down	-1.69E+00	2.30E-04	Down	-1.36E-01	5.82E-01		-5.72E-01	5.81E-03		-1.52E+00	2.66E-07	Down	-9.21E-01	6.62E-04		Unigene12805_All//gi|79499196|ref|NP_195518.2|//0.00E+00//transmembrane transporter [Arabidopsis thaliana]>gi|75128428|sp|Q6S287.1|NAT11_ARATH RecName: Full=Nucleobase-ascorbate transporter 11; Short=AtNAT11>gi|38350521|gb|AAR18373.1|nucleobase-ascorbate transporter 11 [Arabidopsis thaliana]	Unigene12805_All//0.00E+00//AT4G38050| transmembrane transporter	Unigene12805_All//0.00E+00//TC175919			GO:0005215//GO:0006810//GO:0016020	nr -
Unigene12806_All	1827	2.21	15.61	4.02	19.52	16.66	18.32	95.21	192.74	73.51	2.82E+00	2.00E-87	Up	8.67E-01	1.12E-04		-2.29E-01	9.94E-03		-9.19E-02	3.99E-01		1.02E+00	0.00E+00	Up	-3.73E-01	6.45E-28		Unigene12806_All//gi|30680102|ref|NP_849967.1|//1.00E-170//aspartyl protease family protein [Arabidopsis thaliana]>gi|22655368|gb|AAM88276.1|At2g17760/At2g17760 [Arabidopsis thaliana]	Unigene12806_All//2.00E-171//AT2G17760| aspartyl protease family protein	Unigene12806_All//0.00E+00//TC150237			GO:0004175//GO:0019538	nr +
Unigene12808_All	853	2.15	2.79	2.87	1.23	1.66	2.01	2.23	5.98	3.46	3.79E-01	3.64E-01		4.20E-01	3.39E-01		4.33E-01	4.94E-01		7.14E-01	1.72E-01		1.42E+00	1.43E-08	Up	6.32E-01	4.47E-02		Unigene12808_All//gi|15224916|ref|NP_181989.1|//1.00E-07//RAB6A; GTP binding / protein binding [Arabidopsis thaliana]>gi|75318653|sp|O80501.1|RBH1B_ARATH RecName: Full=Ras-related protein RABH1B>gi|107738267|gb|ABF83670.1|At2g44610 [Arabidopsis thaliana]>gi|741994|prf||2008312A GTP-binding protein	Unigene12808_All//3.00E-05//AT5G64990| AtRABH1a (Arabidopsis Rab GTPase homolog H1a); GTP binding	Unigene12808_All//5.00E-141//TC136240			GO:0006810//GO:0032561//GO:0035556//GO:0043231	nr -
Unigene1281_All	561	2.80	1.72	3.70	1.42	4.79	4.51	1.36	1.94	6.32	-7.05E-01	1.80E-01		4.04E-01	3.93E-01		1.75E+00	1.10E-05	Up	1.67E+00	7.87E-05	Up	5.14E-01	3.96E-01		2.22E+00	5.24E-11	Up	Unigene1281_All//gi|79325165|ref|NP_001031667.1|//1.00E-36//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene1281_All//6.00E-38//AT4G18975| pentatricopeptide (PPR) repeat-containing protein	Unigene1281_All//4.00E-45//TC179262				nr -
Unigene12811_All	316	3.15	0.32	1.35	17.97	8.61	3.00	3.61	1.32	1.01	-3.29E+00	3.81E-04	Down	-1.22E+00	1.00E-01		-1.06E+00	4.87E-06	Down	-2.58E+00	1.16E-17	Down	-1.45E+00	1.40E-02		-1.84E+00	1.97E-03				Unigene12811_All//1.00E-90//BG442430				
Unigene12812_All	908	11.24	5.25	5.75	58.10	33.56	12.19	9.55	2.12	0.92	-1.10E+00	2.86E-09	Down	-9.67E-01	2.72E-07		-7.92E-01	9.81E-32		-2.25E+00	7.21E-137	Down	-2.17E+00	1.17E-24	Down	-3.37E+00	1.22E-40	Down	Unigene12812_All//gi|53370641|gb|AE89136.1|//1.00E-12//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene12812_All//8.00E-08//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene12812_All//0.00E+00//TC146292				nr -
Unigene12813_All	652	7.38	2.25	3.59	34.30	17.69	6.58	6.10	0.77	0.73	-1.71E+00	1.29E-08	Down	-1.04E+00	3.28E-04	Down	-9.55E-01	9.92E-19		-2.38E+00	2.84E-62	Down	-2.99E+00	2.04E-16	Down	-3.06E+00	2.20E-17	Down	Unigene12813_All//gi|53370641|gb|AE89136.1|//4.00E-17//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene12813_All//2.00E-13//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene12813_All//0.00E+00//TC146292				nr -
Unigene12814_All	1145	4.48	3.72	1.91	14.84	10.29	7.34	1.59	0.80	0.52	-2.69E-01	3.41E-01		-1.23E+00	1.37E-05	Down	-5.28E-01	2.13E-05		-1.02E+00	4.25E-14	Down	-9.83E-01	2.32E-02		-1.61E+00	2.86E-04	Down	Unigene12814_All//gi|53370641|gb|AE89136.1|//2.00E-12//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene12814_All//1.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene12814_All//0.00E+00//TC146292				nr -
Unigene12817_All	2930	4.21	1.87	3.42	6.99	7.87	6.37	3.16	2.45	3.79	-1.17E+00	3.35E-12	Down	-3.03E-01	8.31E-02		1.72E-01	1.65E-01		-1.34E-01	3.52E-01		-3.65E-01	3.51E-02		2.64E-01	8.96E-02		Unigene12817_All//gi|299149726|gb|ADJ17363.1|//0.00E+00//receptor kinase [Gossypium hirsutum]	Unigene12817_All//0.00E+00//AT5G65710| HSL2 (HAESA-Like 2); ATP binding / kinase/ protein serine/threonine kinase	Unigene12817_All//0.00E+00//TC151274			GO:0008152//GO:0009791//GO:0016301//GO:0050789	nr +
Unigene12818_All	330	0.00	0.00	0.00	1.21	1.88	0.27	0.38	3.42	11.23	null	null		null	null		6.37E-01	5.49E-01		-2.14E+00	1.26E-01		3.15E+00	2.58E-05	Up	4.87E+00	2.55E-22	Up			Unigene12818_All//3.00E-20//gi|73860410|gb|DT463149.1|DT463149				
Unigene12819_All	2095	2.42	6.46	5.87	5.11	5.61	4.05	8.31	17.48	46.09	1.41E+00	2.09E-17	Up	1.28E+00	3.38E-13	Up	1.33E-01	5.20E-01		-3.35E-01	6.53E-02		1.07E+00	1.21E-36	Up	2.47E+00	0.00E+00	Up	Unigene12819_All//gi|260513718|gb|ACX42571.1|//9.00E-93//CONSTANS-like zinc finger protein [Glycine max]	Unigene12819_All//8.00E-79//AT2G47890| zinc finger (B-box type) family protein	Unigene12819_All//0.00E+00//TC144764	C2C2-CO-like		ko04712|Circadian rhythm - plant	GO:0001071//GO:0010468//GO:0044464//GO:0046914	nr +
Unigene12820_All	989	11.32	0.72	0.70	16.42	16.61	5.25	9.83	1.52	2.18	-3.98E+00	2.03E-47	Down	-4.02E+00	8.72E-46	Down	1.64E-02	9.33E-01		-1.64E+00	6.57E-28	Down	-2.69E+00	2.73E-35	Down	-2.18E+00	1.52E-28	Down	Unigene12820_All//gi|27261142|gb|AAN87547.1|AF118784_1/1.00E-167//ribonucleotide reductase large subunit A [Glycine max]	Unigene12820_All//2.00E-148//AT2G21790| RNR1 (RIBONUCLEOTIDE REDUCTASE 1); ATP binding / protein binding / ribonucleoside-diphosphate reductase	Unigene12820_All//0.00E+00//TC156270		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism		nr -
Unigene12821_All	2218	18.38	4.07	4.51	20.68	15.21	10.79	23.90	9.14	5.35	-2.18E+00	4.98E-93	Down	-2.03E+00	5.98E-82	Down	-4.43E-01	5.43E-10		-9.39E-01	1.32E-32		-1.39E+00	6.60E-79	Down	-2.16E+00	1.35E-150	Down	Unigene12821_All//gi|27261142|gb|AAN87547.1|AF118784_1/0.00E+00//ribonucleotide reductase large subunit A [Glycine max]	Unigene12821_All//0.00E+00//AT2G21790| RNR1 (RIBONUCLEOTIDE REDUCTASE 1); ATP binding / protein binding / ribonucleoside-diphosphate reductase	Unigene12821_All//0.00E+00//TC132313		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism	GO:0006259//GO:0009142//GO:0010038//GO:0016728//GO:0032559//GO:0043234	nr +
Unigene12823_All	2923	9.09	2.63	2.51	23.48	23.47	13.89	7.28	3.26	4.23	-1.79E+00	5.15E-47	Down	-1.85E+00	1.23E-47	Down	-1.00E-03	9.88E-01		-7.58E-01	8.62E-34		-1.16E+00	1.97E-24	Down	-7.84E-01	1.45E-13		Unigene12823_All//gi|225439035|ref|XP_002264349.1|//0.00E+00//PREDICTED: similar to SCARECROW [Vitis vinifera]	Unigene12823_All//8.00E-178//AT3G54220| SCR (SCARECROW); protein binding / protein homodimerization/ sequence-specific DNA binding / transcription factor	Unigene12823_All//0.00E+00//TC156432	GRAS			GO:0003002//GO:0003677//GO:0009606//GO:0010167//GO:0032507//GO:0042802//GO:0043231//GO:0051301	nr +
Unigene12824_All	1690	2.72	3.27	5.58	6.34	7.50	5.48	2.35	2.87	2.64	2.63E-01	3.34E-01		1.03E+00	1.65E-07	Up	2.43E-01	1.56E-01		-2.10E-01	2.88E-01		2.87E-01	2.76E-01		1.67E-01	5.55E-01		Unigene12824_All//gi|22331831|ref|NP_191271.2|//1.00E-107//protein kinase family protein [Arabidopsis thaliana]	Unigene12824_All//1.00E-94//AT3G57120| protein kinase family protein	Unigene12824_All//0.00E+00//TC166604		ko04626|Plant-pathogen interaction		nr -
Unigene12825_All	2722	13.55	7.99	11.64	6.20	5.97	4.33	4.04	1.81	1.57	-7.63E-01	2.08E-17		-2.19E-01	2.20E-02		-5.52E-02	7.62E-01		-5.19E-01	8.35E-05		-1.16E+00	5.44E-13	Down	-1.37E+00	3.71E-17	Down	Unigene12825_All//gi|297811553|ref|XP_002873660.1|//1.00E-180//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]>gi|297319497|gb|EFH49919.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene12825_All//2.00E-180//AT3G46610| pentatricopeptide (PPR) repeat-containing protein	Unigene12825_All//0.00E+00//TC151961				nr -
Unigene12826_All	2649	22.06	15.53	20.32	10.08	11.22	7.37	10.10	2.19	4.62	-5.06E-01	1.82E-13		-1.19E-01	1.39E-01		1.55E-01	1.57E-01		-4.53E-01	9.40E-06		-2.20E+00	5.28E-76	Down	-1.13E+00	2.91E-30	Down	Unigene12826_All//gi|15232175|ref|NP_186824.1|//1.00E-164//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene12826_All//4.00E-158//AT3G01750| ankyrin repeat family protein	Unigene12826_All//0.00E+00//TC150039				nr -
Unigene12827_All	493	27.06	10.89	24.30	9.50	11.39	7.97	3.86	1.61	2.10	-1.31E+00	1.73E-15	Down	-1.55E-01	3.98E-01		2.62E-01	3.47E-01		-2.53E-01	4.16E-01		-1.26E+00	3.27E-03		-8.77E-01	2.99E-02		Unigene12827_All//gi|297847246|ref|XP_002891504.1|//1.00E-62//long-chain acyl-CoA synthetase 2 [Arabidopsis lyrata subsp. lyrata]>gi|297337346|gb|EFH67763.1| long-chain acyl-CoA synthetase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene12827_All//2.00E-63//AT1G49430| LACS2 (LONG-CHAIN ACYL-COA SYNTHETASE 2); long-chain-fatty-acid-CoA ligase	Unigene12827_All//0.00E+00//TC171883		ko04146|Peroxisome//ko00071|Fatty acid metabolism		GO:0006633//GO:0006952//GO:0010102//GO:0015645//GO:0043231	nr -
Unigene12828_All	2419	42.50	29.03	43.89	16.25	18.78	14.25	5.17	2.57	1.35	-5.50E-01	1.07E-26		4.65E-02	4.47E-01		2.09E-01	7.91E-03		-1.90E-01	3.55E-02		-1.01E+00	6.87E-12	Down	-1.94E+00	1.67E-31	Down	Unigene12828_All//gi|170576820|gb|ACB30545.1|//0.00E+00//long-chain acyl-CoA synthetase 4 [Ricinus communis]	Unigene12828_All//0.00E+00//AT1G64400| long-chain-fatty-acid—CoA ligase, putative / long-chain acyl-CoA synthetase, putative	Unigene12828_All//0.00E+00//gi|164296863|gb|ES809281.1|ES809281		ko04146|Peroxisome//ko00071|Fatty acid metabolism	GO:0006631//GO:0016020	nr +
Unigene12829_All	970	4.42	1.72	5.11	12.07	11.36	9.31	7.28	2.07	3.78	-1.36E+00	8.99E-06	Down	2.07E-01	4.89E-01		-8.73E-02	6.54E-01		-3.74E-01	2.69E-02		-1.82E+00	3.92E-16	Down	-9.46E-01	1.11E-06		Unigene12829_All//gi|195627520|gb|ACG35590.1|//1.00E-89//uncharacterized ACR, COG1565 family protein [Zea mays]	Unigene12829_All//4.00E-93//AT1G04900| unknown protein	Unigene12829_All//0.00E+00//TC179498				nr +
Unigene1283_All	3527	6.22	20.30	8.91	9.43	17.29	22.91	15.64	55.72	70.56	1.71E+00	3.43E-117	Up	5.19E-01	1.46E-07		8.74E-01	8.02E-42		1.28E+00	8.43E-93	Up	1.83E+00	0.00E+00	Up	2.17E+00	0.00E+00	Up	Unigene1283_All//gi|15239540|ref|NP_197965.1|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana]>gi|5107831|gb|AAD40144.1|AF149413_25 contains similarity to protein kinase domains (Pfam PF00069, Score=162.6, E=6.8e-45, N=1) and leucien rich repeats (Pfam PF00560, Score=210.7, E=2.2e-59, N=10) [Arabidopsis thaliana]>gi|224589685|gb|ACN59374.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene1283_All//0.00E+00//AT5G25930| leucine-rich repeat family protein / protein kinase family protein	Unigene1283_All//0.00E+00//ES828646				nr -
Unigene12830_All	1031	5.07	3.93	4.18	13.87	9.49	6.92	7.09	3.32	4.68	-3.68E-01	1.70E-01		-2.79E-01	3.42E-01		-5.48E-01	6.47E-05		-1.00E+00	1.03E-11	Down	-1.09E+00	3.22E-08	Down	-6.02E-01	1.25E-03		Unigene12830_All//gi|7211976|gb|AAF40447.1|AC004809_5//8.00E-87//F13M7.11 [Arabidopsis thaliana]	Unigene12830_All//4.00E-88//AT1G04900| unknown protein	Unigene12830_All//0.00E+00//TC179498				nr -
Unigene12831_All	1720	1.86	0.15	0.93	4.05	3.48	2.47	3.34	1.29	1.34	-3.66E+00	5.38E-13	Down	-9.98E-01	6.35E-03		-2.19E-01	3.72E-01		-7.16E-01	1.00E-03		-1.38E+00	3.70E-09	Down	-1.32E+00	6.64E-09	Down	Unigene12831_All//gi|7211976|gb|AAF40447.1|AC004809_5//1.00E-180//F13M7.11 [Arabidopsis thaliana]	Unigene12831_All//0.00E+00//AT1G04900| unknown protein	Unigene12831_All//0.00E+00//TC179498				nr -
Unigene12832_All	1906	45.60	155.84	91.75	29.19	26.09	38.03	6.61	7.46	3.83	1.77E+00	0.00E+00	Up	1.01E+00	4.79E-124	Up	-1.62E-01	2.44E-02		3.82E-01	1.18E-10		1.74E-01	2.40E-01		-7.89E-01	1.72E-08		Unigene12832_All//gi|15240707|ref|NP_196884.1|//0.00E+00//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]>gi|30684593|ref|NP_850815.1|hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]>gi|15912217|gb|AAL08242.1|AT5g13800/MAC12_25 [Arabidopsis thaliana]>gi|17979481|gb|AAL50077.1|AT5g13800/MAC12_25 [Arabidopsis thaliana]>gi|23506153|gb|AAN31088.1|At5g13800/MAC12_25 [Arabidopsis thaliana]>gi|222423623|dbj|BAH19780.1|AT5G13800 [Arabidopsis thaliana]	Unigene12832_All//1.00E-179//AT5G13800| hydrolase, alpha/beta fold family protein	Unigene12832_All//0.00E+00//TC143780				nr -
Unigene12833_All	1027	2.04	1.13	2.49	4.41	4.66	3.03	3.05	1.10	1.44	-8.45E-01	5.73E-02		2.88E-01	4.98E-01		7.85E-02	8.43E-01		-5.41E-01	6.09E-02		-1.47E+00	8.19E-06	Down	-1.09E+00	4.22E-04	Down	Unigene12833_All//gi|195536980|dbj|BAG68210.1|//1.00E-103//lectin receptor kinase-like protein [Nicotiana benthamiana]	Unigene12833_All//2.00E-86//AT5G03140| lectin protein kinase family protein	Unigene12833_All//0.00E+00//CO118585			GO:0000166//GO:0004672//GO:0030246//GO:0031410	nr -
Unigene12834_All	2237	3.16	1.45	3.78	4.45	5.82	3.27	3.21	0.80	3.08	-1.12E+00	7.12E-07	Down	2.62E-01	2.33E-01		3.86E-01	1.20E-02		-4.45E-01	1.45E-02		-2.00E+00	1.41E-18	Down	-6.06E-02	7.67E-01		Unigene12834_All//gi|195536980|dbj|BAG68210.1|//0.00E+00//lectin receptor kinase-like protein [Nicotiana benthamiana]	Unigene12834_All//0.00E+00//AT3G53380| lectin protein kinase family protein	Unigene12834_All//0.00E+00//TC144851		ko04626|Plant-pathogen interaction	GO:0004672//GO:0000871//GO:0006464//GO:0016020//GO:0030246//GO:0032559	nr -

Unigene12835_All	1869	12.23	12.34	9.63	60.88	35.54	32.72	8.82	4.94	4.39	1.20E-02	9.42E-01			-3.45E-01	4.13E-03		-7.76E-01	7.24E-66		-8.96E-01	4.31E-74		-8.36E-01	1.70E-11		-1.01E+00	6.95E-16	Down	Unigene12835_All//gi|297839389|ref|XP_002887576.1|//1.00E-124//SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333417|gb|EFH63835.1| SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12835_All//1.00E-123//AT1G75170| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene12835_All//0.00E+00//TC163367				nr +
Unigene12836_All	2419	2.08	0.82	1.03	8.83	4.56	4.57	2.87	1.11	1.12	-1.35E+00	1.57E-06	Down	-1.01E+00	3.53E-04	Down	-9.56E-01	6.37E-18		-9.50E-01	8.82E-16		-1.37E+00	7.36E-11	Down	-1.36E+00	5.08E-11	Down	Unigene12836_All//gi|297839389|ref|XP_002887576.1|//1.00E-122//SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333417|gb|EFH63835.1| SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12836_All//1.00E-123//AT1G75170| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene12836_All//0.00E+00//TC163367			GO:0051234	nr +
Unigene12838_All	1454	31.70	30.53	31.24	39.78	32.87	26.84	25.68	42.95	9.43	-5.45E-02	5.64E-01			-2.12E-02	8.18E-01		-2.75E-01	2.12E-05		-5.68E-01	2.45E-17		7.42E-01	1.12E-33		-1.45E+00	4.28E-61	Down	Unigene12838_All//gi|2829926|gb|AAC00634.1|//7.00E-37//Hypothetical protein [Arabidopsis thaliana] >gi|38454134|gb|AAR20761.1| At1g76980 [Arabidopsis thaliana] >gi|38604022|gb|AAR24754.1| At1g76980 [Arabidopsis thaliana]	Unigene12838_All//8.00E-22//AT1G76980| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: emb2170 (embryo defective 2170) (TAIR:AT1G21390.1); Has 33 Blast hits to 33 proteins in 14 species: Archae - 0; Bacteria - 4; Metazoa - 2; Fungi - 7; Plants - 14; Viruses - 2; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene12838_All//0.00E+00//gi|109879930|gb|DW508900.1|DW508900				nr +
Unigene12843_All	1881	6.29	14.03	7.28	8.40	11.55	31.05	49.16	62.04	265.15	1.16E+00	1.32E-24	Up	2.11E-01	2.22E-01		4.61E-01	3.07E-05		1.89E+00	7.43E-118	Up	3.36E-01	2.62E-15		2.43E+00	0.00E+00	Up	Unigene12843_All//gi|297804078|ref|XP_002869923.1|//0.00E+00//FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315759|gb|EFH46182.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene12843_All//3.00E-178//AT1G11770| FAD binding / catalytic/ electron carrier/ oxidoreductase	Unigene12843_All//0.00E+00//TC163182		ko00620|Pyruvate metabolism//ko00908|Zeatin biosynthesis	GO:0008152//GO:0030554//GO:0046993	nr -
Unigene12844_All	430	0.00	0.12	0.00	0.70	0.48	0.63	2.95	2.04	0.46	6.88E+00	6.17E-01		null	null		-5.33E-01	6.79E-01		-1.41E-01	9.21E-01		-5.31E-01	3.43E-01		-2.67E+00	2.31E-05	Down	Unigene12844_All//gi|18404931|ref|NP_566792.1|//3.00E-46//methyltransferase/ nucleic acid binding [Arabidopsis thaliana]	Unigene12844_All//2.00E-47//AT3G26410| methyltransferase/ nucleic acid binding	Unigene12844_All//5.00E-158//gi|11199260|gb|BF268229.1|BF268229			GO:0005488//GO:0006730//GO:0016741//GO:0044464	nr -
Unigene12846_All	1562	3.55	0.68	0.65	6.41	4.30	6.16	4.11	1.55	1.61	-2.38E+00	1.14E-14	Down	-2.45E+00	1.83E-14	Down	-5.76E-01	6.25E-04		-5.78E-02	7.80E-01		-1.41E+00	1.86E-10	Down	-1.36E+00	2.77E-10	Down	Unigene12846_All//gi|18404931|ref|NP_566792.1|//0.00E+00//methyltransferase/ nucleic acid binding [Arabidopsis thaliana]	Unigene12846_All//0.00E+00//AT3G26410| methyltransferase/ nucleic acid binding	Unigene12846_All//0.00E+00//TC167168			GO:0005488//GO:0006730//GO:0016741//GO:0044464	nr +
Unigene12848_All	245	0.00	2.07	4.56	0.81	1.69	1.47	1.55	1.19	0.16	1.10E+01	4.05E-03		1.22E+01	3.43E-06	Up	1.05E+00	4.26E-01		8.59E-01	5.42E-01		-3.79E-01	7.23E-01		-3.26E+00	2.22E-02											
Unigene1285_All	239	7.66	8.06	7.80	21.05	13.11	7.37	5.84	2.10	0.67	7.24E-02	8.79E-01		2.54E-02	9.77E-01		-6.83E-01	6.64E-03		-1.51E+00	4.44E-08	Down	-1.48E+00	4.92E-03		-3.13E+00	1.09E-06	Down			Unigene1285_All//6.00E-101//TC148688						
Unigene12852_All	2064	63.27	33.02	33.44	94.73	76.45	110.59	109.20	57.98	46.00	-9.38E-01	9.12E-85		-9.20E-01	1.97E-79		-3.09E-01	3.87E-21		2.23E-01	4.52E-12		-9.14E-01	1.53E-170		-1.25E+00	6.80E-291	Down	Unigene12852_All//gi|115462083|ref|NP_001054641.1|//0.00E+00//Os05g0147400 [Oryza sativa Japonica Group] >gi|113578192|dbj|BAF16555.1| Os05g0147400 [Oryza sativa Japonica Group]	Unigene12852_All//0.00E+00//AT3G02530| chaperonin, putative	Unigene12852_All//0.00E+00//TC133219			GO:0005515//GO:0010038//GO:0032559//GO:0041267//GO:0044424	nr -
Unigene12855_All	2414	2.12	1.05	1.81	3.26	2.87	2.97	4.19	2.61	3.48	-1.02E+00	1.44E-04	Down	-2.32E-01	4.15E-01		-1.85E-01	4.26E-01		-1.32E-01	6.13E-01		-6.79E-01	2.23E-05		-2.66E-01	1.05E-01		Unigene12855_All//gi|9857539|gb|AAG00894.1|AC064879_12//0.00E+00//Hypothetical protein [Arabidopsis thaliana]	Unigene12855_All//0.00E+00//AT1G02420| pentatricopeptide (PPR) repeat-containing protein	Unigene12855_All//0.00E+00//ES810421		ko00190|Oxidative phosphorylation	GO:0044464	nr -
Unigene12856_All	2001	231.82	154.54	229.31	54.82	71.71	92.49	18.97	38.87	55.51	-5.85E-01	7.22E-132		-1.57E-02	6.23E-01		3.88E-01	2.79E-23		7.55E-01	6.35E-89		1.03E+00	1.05E-72	Up	1.55E+00	1.68E-197	Up	Unigene12856_All//gi|156900672|gb|ABU96742.1|//0.00E+00//chloroplast omega-6 fatty acid desaturase [Jatropha curcas]	Unigene12856_All//0.00E+00//AT4G30950| FAD6 (FATTY ACID DESATURASE 6); omega-6 fatty acid desaturase	Unigene12856_All//0.00E+00//TC130778		ko01040|Biosynthesis of unsaturated fatty acids	GO:0006631//GO:0009767//GO:0009941//GO:0016705	nr -
Unigene12857_All	3185	4.58	2.48	2.42	8.79	6.25	9.53	12.00	5.50	5.65	-8.85E-01	2.86E-09		-9.19E-01	2.31E-09		-4.92E-01	1.50E-07		1.17E-01	3.20E-01		-1.13E+00	2.12E-41	Down	-1.09E+00	3.17E-40	Down	Unigene12857_All//gi|297824993|ref|XP_002880379.1|//0.00E+00//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297326218|gb|EFH56638.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene12857_All//5.00E-171//AT2G21440| RNA recognition motif (RRM)-containing protein	Unigene12857_All//0.00E+00//TC169406		ko03040|Spliceosome	GO:0003676	nr -
Unigene1286_All	728	4.31	2.44	2.05	6.57	5.25	1.61	7.09	4.02	1.70	-8.24E-01	1.88E-02		-1.07E+00	3.80E-03		-3.23E-01	2.67E-01		-2.03E+00	2.94E-11	Down	-8.18E-01	4.93E-04		-2.06E+00	1.51E-14	Down	Unigene1286_All//gi|124359162|gb|ABN05685.1|//3.00E-13//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene1286_All//1.00E-07//AT3G09510| nucleic acid binding	Unigene1286_All//0.00E+00//gi|164329780|gb|EX163942.1|EX163942				nr -
Unigene12860_All	1068	0.00	0.05	0.00	0.37	0.19	0.17	4.12	9.24	8.54	5.57E+00	6.17E-01		null	null		-9.47E-01	4.21E-01		-1.14E+00	3.79E-01		1.17E+00	7.36E-12	Up	1.05E+00	9.52E-10	Up	Unigene12860_All//gi|34485239|gb|AAQ73103.1|//6.00E-14//resistance protein RGC2 [Lactuca sativa]								nr +
Unigene12862_All	5409	0.00	0.04	0.00	0.02	0.00	0.03	2.45	9.69	8.34	5.23E+00	1.37E-01		null	null		-4.20E+00	3.13E-01		8.60E-01	6.95E-01		1.99E+00	2.12E-129	Up	1.77E+00	2.72E-97	Up	Unigene12862_All//gi|224117086|ref|XP_002331783.1|//1.00E-141//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222832242|gb|EEE70719.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene12862_All//2.00E-58//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene12862_All//0.00E+00//DT465090		ko04626|Plant-pathogen interaction		nr -
Unigene12864_All	1790	5.67	2.55	3.63	9.32	7.73	5.95	5.36	3.29	3.45	-1.15E+00	6.42E-10	Down	-6.44E-01	5.46E-04		-2.70E-01	4.95E-02		-6.47E-01	9.90E-07		-7.04E-01	1.99E-05		-6.36E-01	7.35E-05		Unigene12864_All//gi|297812025|ref|XP_002873896.1|//1.00E-110//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319733|gb|EFH50155.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene12864_All//3.00E-104//AT5G18475| pentatricopeptide (PPR) repeat-containing protein	Unigene12864_All//0.00E+00//gi|13246555|gb|BE054454.2|BE054454			GO:0044464	nr +
Unigene12866_All	324	21.96	19.55	16.93	35.67	29.44	39.45	74.51	46.57	36.15	-1.68E-01	4.79E-01		-3.76E-01	1.13E-01		-2.77E-01	1.06E-01		1.45E-01	4.43E-01		-6.78E-01	1.10E-11		-1.04E+00	3.54E-24	Down	Unigene12866_All//gi|5230728|gb|AAD40979.1|AF088851_1//2.00E-54//peroxisomal copper-containing amine oxidase [Glycine max]	Unigene12866_All//6.00E-54//AT2G42490| copper amine oxidase, putative	Unigene12866_All//0.00E+00//ES824806		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0006807//GO:0016641//GO:0042579//GO:0046914//GO:0048037	nr -
Unigene1287_All	2431	4.71	5.23	3.86	12.58	8.29	4.55	7.29	3.80	1.10	1.51E-01	3.89E-01		-2.90E-01	1.15E-01		-6.03E-01	1.32E-11		-1.47E+00	3.87E-44	Down	-9.40E-01	8.71E-15		-2.73E+00	7.87E-67	Down	Unigene1287_All//gi|124360022|gb|ABN08038.1|//3.00E-93//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene1287_All//4.00E-36//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene1287_All//0.00E+00//gi|13353921|gb|BG444269.1|BG444269				nr +
Unigene12873_All	3181	0.49	0.25	0.33	1.10	0.95	0.67	2.66	1.13	3.18	-9.53E-01	7.08E-02		-5.60E-01	3.18E-01		-2.03E-01	5.86E-01		-7.16E-01	3.01E-02		-1.23E+00	3.39E-11	Down	2.59E-01	1.14E-01		Unigene12873_All//gi|22330543|ref|NP_177187.2|//0.00E+00//KUP6; potassium ion transmembrane transporter [Arabidopsis thaliana] >gi|38503100|sp|Q8W414.1|PO76_ARATH RecName: Full=Potassium transporter 6; Short=AtPOT6; Short=AtHAK6 >gi|17064932|gb|AAL32620.1| Similar to high affinity potassium transporter [Arabidopsis thaliana] >gi|20239960|gb|AAM13327.1| similar to high affinity potassium transporter [Arabidopsis thaliana]	Unigene12873_All//0.00E+00//AT1G70300| KUP6; potassium ion transmembrane transporter	Unigene12873_All//0.00E+00//TC171906			GO:0016020//GO:0030001//GO:0046873	nr +
Unigene12874_All	2930	38.41	53.26	78.46	12.11	31.50	23.85	0.27	0.16	0.39	4.72E-01	1.82E-30		1.03E+00	8.18E-169	Up	1.38E+00	6.05E-131	Up	9.78E-01	2.71E-52		-8.05E-01	2.58E-01		5.24E-01	3.53E-01		Unigene12874_All//gi|60999458|dbj|BAD89968.1|//0.00E+00//phototropin [Phaseolus vulgaris]	Unigene12874_All//0.00E+00//AT5G58140| PHOT2 (PHOTOTROPIN 2); FMN binding / blue light photoreceptor/ kinase/ protein serine/threonine kinase	Unigene12874_All//0.00E+00//CO099385			GO:0004673//GO:0004674//GO:0005515//GO:0006351//GO:0006468//GO:0007017//GO:0009416//GO:0009606//GO:0009658//GO:0009881//GO:0010360//GO:0015630//GO:0016020//GO:0023060//GO:0032559//GO:0043231	nr -
Unigene12875_All	1694	72.74	34.52	59.73	33.88	33.18	28.29	39.76	19.99	21.50	-1.08E+00	4.40E-100	Down	-2.84E-01	1.88E-09		-3.02E-02	7.60E-01		-2.60E-01	1.55E-04		-9.92E-01	5.33E-59		-8.87E-01	1.92E-50		Unigene12875_All//gi|297798634|ref|XP_002867201.1|//1.00E-165//coclaurine N-methyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297310037|gb|EFH43460.1| coclaurine N-methyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene12875_All//9.00E-153//AT4G33110| coclaurine N-methyltransferase, putative	Unigene12875_All//0.00E+00//TC131887		ko00564|Glycerophospholipid metabolism	GO:0006629//GO:0008757	nr -
Unigene12877_All	1736	3.29	0.99	1.90	18.48	14.02	17.17	16.83	22.78	23.66	-1.73E+00	3.50E-10	Down	-7.89E-01	2.33E-03		-3.98E-01	5.82E-06		-1.06E-01	3.58E-01		4.37E-01	7.70E-09		4.92E-01	1.71E-11		Unigene12877_All//gi|224144860|ref|XP_002325441.1|//1.00E-163//f-box family protein [Populus trichocarpa] >gi|222862316|gb|EEE99822.1| f-box family protein [Populus trichocarpa]	Unigene12877_All//6.00E-56//AT5G39660| CDF2 (CYCLING DOF FACTOR 2); DNA binding / protein binding / transcription factor	Unigene12877_All//0.00E+00//gi|164357697|gb|ES828833.1|ES828833	C2C2-Dof			nr +
Unigene12878_All	1027	0.87	43.76	0.78	6.40	9.76	8.44	14.99	148.34	55.74	5.66E+00	3.60E-229	Up	-1.55E-01	8.24E-01		6.08E-01	3.96E-04		3.99E-01	4.82E-02		3.31E+00	0.00E+00	Up	1.90E+00	1.96E-135	Up	Unigene12878_All//gi|126770|sp|P17432.1|MASY_GOSHI//1.00E-119//RecName: Full=Malate synthase, glyoxysomal	Unigene12878_All//2.00E-96//AT5G03860| MLS (MALATE SYNTHASE); malate synthase	Unigene12878_All//0.00E+00//TC135600		ko00620|Pyruvate metabolism//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005777//GO:0009060//GO:0044262//GO:0046912	nr -
Unigene12879_All	1956	0.70	49.53	2.45	15.05	18.68	25.26	13.19	108.29	51.16	6.15E+00	0.00E+00	Up	1.82E+00	8.09E-09	Up	3.12E-01	2.20E-04		7.47E-01	1.10E-23		3.04E+00	0.00E+00	Up	1.96E+00	1.87E-246	Up	Unigene12879_All//gi|126770|sp|P17432.1|MASY_GOSHI//0.00E+00//RecName: Full=Malate synthase, glyoxysomal	Unigene12879_All//0.00E+00//AT5G03860| MLS (MALATE SYNTHASE); malate synthase	Unigene12879_All//0.00E+00//TC135600		ko00620|Pyruvate metabolism//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005777//GO:0009060//GO:0016747//GO:0044262//GO:0046912	nr +
Unigene12881_All	1826	5.10	3.91	2.01	5.57	3.56	4.06	25.93	64.25	43.57	-3.83E-01	4.56E-02		-1.34E+00	7.32E-11	Down	-6.43E-01	1.07E-04		-4.56E-01	1.11E-02		1.31E+00	9.26E-159	Up	7.49E-01	2.36E-44				Unigene12881_All//0.00E+00//TC168002						
Unigene12883_All	2970	6.29	6.84	4.45	11.66	11.61	11.75	12.51	18.21	27.50	1.21E-01	3.73E-01		-5.00E-01	1.58E-04		-6.30E-03	9.50E-01		1.20E-02	9.33E-01		5.41E-01	4.58E-17		1.14E+00	1.29E-90	Up	Unigene12883_All//gi|297611443|ref|NP_001067461.2|//0.00E+00//Os11g0206700 [Oryza sativa Japonica Group] >gi|255679896|dbj|BAF27824.2| Os11g0206700 [Oryza sativa Japonica Group]	Unigene12883_All//0.00E+00//AT1G31930| XLG3 (extra-large GTP-binding protein 3); guanyl nucleotide binding / signal transducer	Unigene12883_All//0.00E+00//TC137909			GO:0007166//GO:0009606//GO:0009612//GO:0009725//GO:0009746//GO:0023060//GO:0032561//GO:0034285//GO:0043231//GO:0048513//GO:0060089	nr +
Unigene12884_All	2697	2.19	0.96	1.32	31.12	25.47	18.34	50.01	15.88	10.64	-1.19E+00	2.09E-06	Down	-7.29E-01	4.06E-03		-2.89E-01	2.83E-08		-7.63E-01	9.95E-42		-1.65E+00	4.79E-259	Down	-2.23E+00	0.00E+00	Down	Unigene12884_All//gi|297834254|ref|XP_002885009.1|//0.00E+00//subtilase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330849|gb|EFH61268.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12884_All//0.00E+00//AT3G14067| subtilase family protein	Unigene12884_All//0.00E+00//TC151496			GO:0003006//GO:0004175//GO:0005515//GO:0005576//GO:0005618//GO:0009845//GO:0010191//GO:0016020//GO:0019538//GO:0031410//GO:0043231//GO:0044092	nr +

Unigene12886_All	992	1.11	0.82	1.40	4.87	5.10	3.92	2.73	1.31	0.72	-4.39E-01	4.95E-01		3.34E-01	5.87E-01		6.71E-02	8.21E-01		-3.15E-01	2.95E-01		-1.06E+00	2.03E-03		-1.92E+00	2.33E-07	Down	Unigene12886_All|gi|110931714|gb|ABH02856.1|/6.00E-54//MYB transcription factor WYB128 [Glycine max]	Unigene12886_All//4.00E-48//AT5G56840| DNA-binding family protein	Unigene12886_All//0.00E+00//TC135626	MYB-related		GO:0003676//GO:0010468//GO:0043231//GO:0046914	nr +
Unigene1289_All	2546	4.52	2.87	2.45	8.30	6.28	6.63	14.27	3.60	6.63	-6.58E-01	8.16E-05		-8.86E-01	4.07E-07		-4.03E-01	3.21E-04		-3.22E-01	7.57E-03		-1.99E+00	3.08E-90	Down	-1.10E+00	2.59E-39	Down	Unigene1289_All//gi|15238197|ref|NP_196618.1|//0.00E+00//glycosyl hydrolase family 3 protein [Arabidopsis thaliana] >gi|75264319|sp|Q9LXA8.1|BXL6_ARATH RecName: Full=Probable beta-D-xylosidase 6; Short=AtBXL6; Flags: Precursor >gi|7671447|emb|CAB89387.1| beta-xylosidase-like protein [Arabidopsis thaliana] >gi|15982753|gb|AAL09717.1|AT5g10560/F12B17_90 [Arabidopsis thaliana]	Unigene1289_All//0.00E+00//AT5G10560| glycosyl hydrolase family 3 protein	Unigene1289_All//0.00E+00//ES810089		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	nr +
Unigene12890_All	1296	0.08	0.04	0.04	1.50	1.81	2.13	2.64	1.94	15.77	-1.05E+00	6.85E-01		-9.73E-01	7.21E-01		2.69E-01	5.74E-01		5.04E-01	2.10E-01		-4.50E-01	1.43E-01		2.58E+00	4.08E-71	Up	Unigene12890_All//gi|42567989|ref|NP_197549.3|//1.00E-121//XIK: motor/ protein binding [Arabidopsis thaliana]	Unigene12890_All//5.00E-150//AT1G17580| MYA1 (MYOSIN 1); motor/ protein binding	Unigene12890_All//3.00E-26//CA992611				nr -
Unigene12893_All	1844	5.19	3.79	4.48	8.81	8.16	8.65	4.29	1.99	2.53	-4.53E-01	1.51E-02		-2.14E-01	3.08E-01		-1.10E-01	5.18E-01		-2.66E-02	8.83E-01		-1.10E+00	6.08E-09	Down	-7.62E-01	2.21E-05		Unigene12893_All|gi|297807715|ref|XP_002871741.1|//0.00E+00//exostosin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317578|gb|EFH48000.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12893_All//0.00E+00//AT5G16890| exostosin family protein	Unigene12893_All//0.00E+00//TC172963			GO:0009536	nr -
Unigene12899_All	2954	1.93	2.37	1.57	2.72	2.90	6.80	49.62	204.21	283.98	2.94E-01	2.09E-01		-3.00E-01	2.70E-01		9.64E-02	6.96E-01		1.33E+00	1.07E-24	Up	2.04E+00	0.00E+00	Up	2.52E+00	0.00E+00	Up	Unigene12899_All//gi|169160467|gb|ACA49724.1|//0.00E+00//phosphoinositide D gamma [Citrus sinensis]	Unigene12899_All//0.00E+00//AT2G42010| PLDBETA1 (PHOSPHOLIPASE D BETA 1); phospholipase D	Unigene12899_All//0.00E+00//TC177981		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism	GO:0003006//GO:0006620//GO:0006650//GO:0016020//GO:0035091//GO:0042742//GO:0046872	nr +
Unigene129_All	3266	0.67	0.87	1.55	0.87	1.98	2.46	2.01	0.45	1.24	3.69E-01	3.43E-01		1.20E+00	2.31E-05	Up	1.19E+00	1.24E-07	Up	1.50E+00	3.49E-12	Up	-2.16E+00	9.98E-19	Down	-6.90E-01	5.16E-04		Unigene129_All//gi|240256095|ref|NP_194537.6|//0.00E+00//binding [Arabidopsis thaliana]	Unigene129_All//0.00E+00//AT4G28080| binding	Unigene129_All//0.00E+00//gi|164240850|gb|ES821071.1|ES821071				nr +
Unigene1290_All	2544	1.83	1.00	2.64	6.46	5.54	6.27	1.75	0.54	1.46	-8.78E-01	1.71E-03		5.27E-01	2.68E-02		-2.23E-01	1.21E-01		-4.42E-02	7.85E-01		-1.69E+00	1.74E-09	Down	-2.61E-01	3.29E-01		Unigene1290_All|gi|163889365|gb|ABY48135.1|/0.00E+00//beta-D-xylosidase [Medicago truncatula]	Unigene1290_All//0.00E+00//AT5G10560| glycosyl hydrolase family 3 protein	Unigene1290_All//0.00E+00//gi|21099455|gb|BQ411768.1|BQ411768		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr -
Unigene12900_All	1515	11.71	8.96	10.69	10.23	14.52	23.79	12.92	32.33	29.06	-3.85E-01	3.68E-03		-1.32E-01	3.89E-01		5.06E-01	3.44E-06		1.22E+00	1.44E-38	Up	1.32E+00	8.21E-68	Up	1.17E+00	1.60E-51	Up	Unigene12900_All//gi|297843352|ref|XP_002889557.1|//1.00E-86//inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335399|gb|EFH65816.1| inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12900_All//9.00E-87//AT1G05620| URH2 (URIDINE-RIBOHYDROLASE 2); hydrolase	Unigene12900_All//0.00E+00//TC131226		ko00230|Purine metabolism//ko00760|Nicotinate and nicotinamide metabolism	GO:0008194	nr -
Unigene12904_All	1250	49.18	18.36	19.17	63.88	52.23	86.86	102.99	46.11	45.13	-1.42E+00	1.37E-77	Down	-1.36E+00	4.32E-70	Down	-2.91E-01	5.67E-08		4.43E-01	1.74E-20		-1.16E+00	3.08E-144	Down	-1.19E+00	1.29E-154	Down	Unigene12904_All//gi|55976189|sp|Q6UNT2.1|RL5_CUCSA//1.00E-143//RecName: Full=60S ribosomal protein L5 >gi|34484312|gb|AAQ72789.1| 60S ribosomal protein L5 [Cucumis sativus]	Unigene12904_All//7.00E-128//AT5G39740| 60S ribosomal protein L5 (RPL5B)	Unigene12904_All//0.00E+00//TC161592		ko03010|Ribosome	GO:0043231	nr +
Unigene12905_All	1827	38.57	3.63	15.86	21.76	15.00	12.95	37.61	15.08	19.41	-3.41E+00	2.48E-261	Down	-1.28E+00	1.84E-73	Down	-5.36E-01	3.45E-12		-7.48E-01	2.17E-19		-1.32E+00	1.76E-94	Down	-9.54E-01	4.92E-58		Unigene12905_All|gi|15231450|ref|NP_187390.1|//2.00E-79//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75313804|sp|Q9SRT2.1|BHH62_ARATH RecName: Full=Transcription factor bHLH62; AltName: Full=Transcription factor EN 85; AltName: Full=bHLH transcription factor bHLH062; AltName: Full=Basic helix-loop-helix protein 62; Short=bHLH 62; Short=AtbHLH62 >gi|111074462|gb|ABH04604.1|At3g07340 [Arabidopsis thaliana]	Unigene12905_All//2.00E-79//AT3G07340| basic helix-loop-helix (bHLH) family protein	Unigene12905_All//0.00E+00//TC143990	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0043231	nr -
Unigene12906_All	2028	11.15	7.35	11.19	18.77	23.74	17.50	11.65	4.51	5.83	-6.02E-01	1.70E-07		5.20E-03	9.91E-01		3.39E-01	1.91E-06		-1.00E-01	3.38E-01		-1.37E+00	6.78E-35	Down	-9.98E-01	4.41E-22		Unigene12906_All|gi|11538252|emb|CAC17794.1|//0.00E+00//microtubule-associated protein MAP65-1a [Nicotiana tabacum]	Unigene12906_All//0.00E+00//AT5G55230| ATMAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1); microtubule binding	Unigene12906_All//0.00E+00//TC164521			GO:0015631//GO:0022403//GO:0030865//GO:0031112//GO:0051301//GO:0055028	nr -
Unigene12909_All	1622	9.16	11.56	8.73	12.10	21.10	61.65	15.85	20.25	37.65	3.35E-01	9.81E-03		-6.91E-02	6.69E-01		8.02E-01	1.82E-20		2.35E+00	1.64E-266	Up	3.54E-01	2.49E-05		1.25E+00	8.34E-79	Up	Unigene12909_All|gi|21593333|gb|AAM65282.1|/3.00E-65//phytochrome-associated protein 1 (PAP1) [Arabidopsis thaliana]	Unigene12909_All//2.00E-65//AT3G16500| PAP1 (PHYTOCHROME-ASSOCIATED PROTEIN 1); transcription factor	Unigene12909_All//0.00E+00//TC148266			GO:0001071//GO:0005515//GO:0006350//GO:0006801//GO:0006970//GO:0009718//GO:0009725//GO:0010182//GO:0010468//GO:0016021//GO:0016791//GO:0043231	nr +
Unigene12910_All	273	6.71	2.04	5.66	1.28	1.51	3.14	0.46	0.31	0.58	-1.72E+00	9.01E-04	Down	-2.46E-01	6.28E-01		2.45E-01	8.53E-01		1.30E+00	1.07E-01		-6.02E-01	7.67E-01		3.29E-01	8.51E-01		Unigene12910_All|gi|225380880|gb|ACN88681.1|//2.00E-18//VTC2-like protein [Malus x domestica]	Unigene12910_All//1.00E-16//AT4G26850| VTC2 (vitamin c defective 2); GDP-D-glucose phosphorylase/ GDP-galactose:glucose-1-phosphate guanyltransferase/ GDP-galactose:mannose-1-phosphate guanyltransferase/ GDP-galactose:myoinositol-1-phosphate guanyltransferase/ galactose-1-phosphate guanylyltra	Unigene12910_All//3.00E-53//TC134604			GO:0004645//GO:0008905//GO:0009719//GO:0019852//GO:0035251//GO:0052482	nr +
Unigene12913_All	1181	10.85	22.44	10.10	52.85	70.50	48.41	20.23	7.54	3.51	1.05E+00	4.15E-21	Up	-1.04E-01	5.90E-01		4.16E-01	1.63E-15		-1.27E-01	8.43E-02		-1.42E+00	2.10E-37	Down	-2.53E+00	1.83E-82	Down	Unigene12913_All|gi|194708826|gb|ACF88497.1|//3.00E-49//At5g41050 [Arabidopsis thaliana]	Unigene12913_All//8.00E-41//AT5G41050| unknown protein	Unigene12913_All//0.00E+00//TC133721				nr +
Unigene12914_All	1287	36.10	28.98	62.27	17.22	19.24	25.23	4.57	3.09	1.49	-3.17E-01	4.83E-05		7.87E-01	1.40E-37		1.60E-01	1.89E-01		5.51E-01	1.92E-09		-5.66E-01	9.71E-03		-1.62E+00	4.52E-12	Down	Unigene12914_All|gi|194708826|gb|ACF88492.1|//4.00E-44//At5g41050 [Arabidopsis thaliana]	Unigene12914_All//3.00E-43//AT5G41050| unknown protein	Unigene12914_All//0.00E+00//TC141502				nr +
Unigene12915_All	497	2.84	9.38	3.86	4.61	7.76	5.54	4.25	3.70	5.21	1.72E+00	2.24E-08	Up	4.40E-01	3.86E-01		7.51E-01	1.36E-02		2.66E-01	5.40E-01		-2.01E-01	6.37E-01		2.93E-01	4.11E-01		Unigene12915_All|gi|227206384|dbj|BAH57247.1|//8.00E-47//AT4G08540 [Arabidopsis thaliana]	Unigene12915_All//1.00E-42//AT4G08540| unknown protein				GO:0034062	nr +
Unigene12916_All	1746	4.76	12.01	4.48	7.33	5.74	6.54	3.78	4.96	5.43	1.33E+00	2.16E-24	Up	-8.78E-02	6.89E-01		-3.53E-01	2.19E-02		-1.64E-01	3.81E-01		3.92E-01	2.90E-02		5.24E-01	1.22E-03		Unigene12916_All|gi|109946637|gb|ABG48497.1|//1.00E-123//At1g77890 [Arabidopsis thaliana]	Unigene12916_All//0.00E+00//AT4G08540| unknown protein	Unigene12916_All//0.00E+00//CO103520			GO:0034062	nr +
Unigene1292_All	2195	2.10	0.81	2.38	5.08	6.28	4.94	2.77	1.73	3.58	-1.38E+00	3.10E-06	Down	1.81E-01	5.41E-01		3.04E-01	4.83E-02		-4.19E-02	8.37E-01		-6.79E-01	1.45E-03		3.66E-01	4.61E-02		Unigene1292_All|gi|18412472|ref|NP_565218.1|//0.00E+00//atnudt3 (Arabidopsis thaliana Nudix hydrolase homolog 3); hydrolase >gi|68565909|sp|Q8LS31.1|NUDT3_ARATH RecName: Full=Nudix hydrolase 3; Short=AtNUDT3	Unigene1292_All//0.00E+00//AT1G79690| atnudt3 (Arabidopsis thaliana Nudix hydrolase homolog 3); hydrolase	Unigene1292_All//0.00E+00//TC136657				nr -
Unigene12920_All	575	3.82	1.85	3.52	4.50	2.87	4.79	5.37	2.47	2.84	-1.05E+00	1.61E-02		-1.19E-01	7.81E-01		-6.48E-01	8.79E-02		8.89E-02	8.34E-01		-1.12E+00	4.79E-04	Down	-9.18E-01	2.72E-03		Unigene12920_All|gi|15219169|ref|NP_175713.1|//5.00E-93//protein kinase family protein [Arabidopsis thaliana] >gi|9454540|gb|AAF87863.1|AC022520_7 similar to cdc2 protein kinase [Arabidopsis thaliana]	Unigene12920_All//2.00E-93//AT1G53050| protein kinase family protein	Unigene12920_All//0.00E+00//gi|164276692|gb|ES844087.1|ES844087			GO:0003676//GO:0004674//GO:0005515//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene12922_All	2701	13.71	7.11	8.81	19.25	14.38	13.73	11.82	4.95	5.93	-9.48E-01	5.92E-25		-6.38E-01	2.03E-12		-4.21E-01	2.77E-10		-4.88E-01	4.90E-12		-1.26E+00	4.40E-41	Down	-9.95E-01	2.33E-29		Unigene12922_All|gi|15219169|ref|NP_175713.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|9454540|gb|AAF87863.1|AC022520_7 similar to cdc2 protein kinase [Arabidopsis thaliana]	Unigene12922_All//0.00E+00//AT1G53050| protein kinase family protein	Unigene12922_All//0.00E+00//TC138042			GO:0004674//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene12924_All	2454	0.77	1.05	0.54	1.34	1.94	7.32	1.72	3.82	6.20	4.56E-01	2.50E-01		-5.01E-01	3.23E-01		5.32E-01	5.45E-02		2.45E+00	1.50E-50	Up	1.15E+00	4.97E-11	Up	1.85E+00	2.22E-35	Up	Unigene12924_All|gi|297844244|ref|XP_002890003.1|//1.00E-145//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297335845|gb|EFH66262.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene12924_All//2.00E-120//AT1G13410| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 8 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT4G02750.1); Has 13539 Blast hits to 4793 proteins in 111 species: Archae - 0; Bacteria - 0; Metazoa - 25; Fungi - 35; Plants - 13298; Viruses - 0; Other Eukaryotes - 181 (source: NCBI BLink).	Unigene12924_All//2.00E-29//TC152220				nr +
Unigene12925_All	2164	16.88	7.42	9.20	32.76	32.03	40.49	19.09	3.98	7.20	-1.19E+00	4.00E-35	Down	-8.75E-01	9.57E-21		-3.23E-02	6.96E-01		3.06E-01	1.26E-08		-2.26E+00	8.01E-121	Down	-1.41E+00	8.05E-65	Down	Unigene12925_All|gi|115476754|ref|NP_001061973.1|//5.00E-64//Os08g0459300 [Oryza sativa Japonica Group] >gi|113623942|dbj|BAF23887.1|Os08g0459300 [Oryza sativa Japonica Group]	Unigene12925_All//3.00E-33//AT1G02180| ferredoxin-related	Unigene12925_All//0.00E+00//TC138721			GO:0031410	nr +
Unigene12927_All	1373	3.09	2.95	1.71	8.82	8.58	11.55	9.02	14.16	23.39	-6.42E-02	8.29E-01		-8.55E-01	5.55E-03		-3.96E-02	8.22E-01		3.89E-01	5.71E-03		6.50E-01	6.37E-09		1.37E+00	2.25E-48	Up	Unigene12927_All|gi|14718995|gb|AAK73021.1|AF367245_1|/3.00E-94//ceramide glucosyltransferase [Gossypium arboreum]	Unigene12927_All//2.00E-72//AT2G19880| ceramide glucosyltransferase, putative	Unigene12927_All//0.00E+00//TC131629			GO:0016740//GO:0044464	nr -
Unigene12930_All	2388	1.10	1.42	1.94	2.96	2.45	2.55	3.68	2.56	1.84	3.76E-01	2.76E-01		8.25E-01	4.76E-03		-2.73E-01	2.42E-01		-2.14E-01	3.87E-01		-5.27E-01	2.40E-03		-1.00E+00	7.27E-09	Down	Unigene12930_All|gi|297803560|ref|XP_002869664.1|//1.00E-103//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315500|gb|EFH45923.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene12930_All//2.00E-88//AT4G25610| zinc finger (C2H2 type) family protein	Unigene12930_All//0.00E+00//gi|78334615|gb|DT554889.1|DT554889	C2H2			nr +

Unigene12931_All	2748	2.57	2.10	0.74	3.26	3.63	2.84	4.83	2.62	3.77	-2.90E-01	2.12E-01			-1.80E+00	1.50E-12	Down	1.55E-01	4.71E-01			-1.99E-01	3.77E-01			-8.85E-01	2.76E-10			-3.58E-01	8.22E-03		Unigene12931_All//gi|225440123|ref|XP_002277489.1|//0.00E+00//PREDICTED: similar to SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein [Vitis vinifera]	Unigene12931_All//0.00E+00//AT5G05130| SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein	Unigene12931_All//0.00E+00//TC175272			GO:0003676//GO:0017111//GO:0032559//GO:0046914	nr -
Unigene12932_All	1145	41.45	17.61	24.51	57.21	58.95	49.46	66.69	50.19	58.52	-1.23E+00	1.96E-48	Down	-7.58E-01	4.54E-21		4.31E-02	6.06E-01			-2.10E-01	1.31E-03			-4.10E-01	1.32E-14			-1.88E-01	3.95E-04		Unigene12932_All//gi|95020537|gb|AB530792.1|//1.00E-108//leucine-rich repeat transmembrane protein kinase [Isatis tinctoria]	Unigene12932_All//1.00E-73//AT3G14350| SRF7 (STRUBBELIG-RECEPTOR FAMILY 7); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene12932_All//0.00E+00//TC148661			GO:0004672//GO:0006464//GO:0007167//GO:0016020//GO:0031410//GO:0032559//GO:0043231	nr -
Unigene12935_All	561	4.10	6.05	3.61	4.17	3.87	3.22	1.51	2.46	4.62	5.60E-01	9.65E-02		-1.86E-01	6.58E-01		-1.10E-01	8.22E-01			-3.74E-01	4.05E-01			7.06E-01	1.71E-01			1.61E+00	1.06E-05	Up			Unigene12935_All//2.00E-99//TC155829				
Unigene12936_All	1261	45.06	106.36	57.81	23.78	26.32	30.69	12.51	32.61	35.42	1.24E+00	6.80E-136	Up	3.60E-01	9.04E-09		1.47E-01	1.57E-01			3.68E-01	1.16E-05		Up	1.38E+00	5.53E-61	Up	1.50E+00	2.31E-76	Up	Unigene12936_All//gi|18423084|ref|NP_568715.1|//5.00E-77//NFU2 (NIFU-LIKE PROTEIN 2); structural molecule [Arabidopsis thaliana] >gi|75163219|sp|Q93W20.1|NIFU2_ARATH RecName: Full=NifU-like protein 2, chloroplastic; Short=AtCnfu2; Short=AtCnfU-V; Flags: Precursor >gi|16226434|gb|AAL16167.1|AF428399_1 AT5g49940/K9P8_8 [Arabidopsis thaliana] >gi|28207818|emb|CAD55559.1| NFU2 protein [Arabidopsis thaliana]	Unigene12936_All//9.00E-78//AT5G49940| NFU2 (NIFU-LIKE PROTEIN 2); structural molecule	Unigene12936_All//0.00E+00//TC171352			GO:0009536//GO:0009657//GO:0031163//GO:0046914//GO:0051540	nr -
Unigene12938_All	1280	3.15	2.49	1.58	2.37	2.02	2.54	5.19	2.87	2.21	-3.36E-01	2.85E-01		-9.93E-01	1.86E-03		-2.35E-01	5.44E-01			9.77E-02	7.89E-01			-8.52E-01	2.99E-05		-1.23E+00	3.10E-09	Down	Unigene12938_All//gi|75164334|sp|Q945M6.1|U497L_ARATH//5.00E-60//RecName: Full=UPF0497 membrane protein At3g53850 >gi|15724236|gb|AAL06511.1|AF412058_1 AT4g31460/F3L17_30 [Arabidopsis thaliana] >gi|21464571|gb|AAM52240.1|AT4g31460/F3L17_30 [Arabidopsis thaliana]	Unigene12938_All//5.00E-47//AT3G53850| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0497, trans-membrane plant (InterPro:IPR006702); BEST Arabidopsis thaliana protein match is: integral membrane protein, putative (TAIR:AT5G02060.1); Has 100 Blast hits to 100 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 100; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene12938_All//7.00E-132//TC162042		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0032559//GO:0043231	nr +
Unigene1294_All	480	4.03	1.48	2.22	70.88	42.11	27.47	7.31	5.83	2.82	-1.45E+00	2.85E-03		-8.62E-01	7.98E-02		-7.51E-01	7.88E-19			-1.37E+00	3.91E-44	Down		-3.26E-01	3.05E-01			-1.37E+00	4.17E-06	Down	Unigene1294_All//gi|224067288|ref|XP_002302449.1|//2.00E-14//f-box family protein [Populus trichocarpa] >gi|222844175|gb|EEE81722.1| f-box family protein [Populus trichocarpa]		Unigene1294_All//5.00E-109//gi|109843226|gb|DW241784.1|DW241784		ko03040|Spliceosome		nr +
Unigene12940_All	2360	31.88	105.98	57.20	23.83	30.98	45.43	28.29	50.05	82.36	1.73E+00	0.00E+00	Up	8.43E-01	5.53E-71		3.78E-01	1.49E-11			9.31E-01	9.99E-74			8.23E-01	3.55E-75		1.54E+00	0.00E+00	Up	Unigene12940_All//gi|14596217|gb|AK68836.1|//1.00E-139//Unknown protein [Arabidopsis thaliana] >gi|15809913|gb|AL068884.1|At2g24100/F27D4.1 [Arabidopsis thaliana] >gi|31376399|gb|AAP49526.1|At2g24100 [Arabidopsis thaliana]	Unigene12940_All//8.00E-150//AT4G30780| unknown protein	Unigene12940_All//0.00E+00//TC146047				nr -
Unigene12945_All	331	4.43	0.00	2.25	1.20	2.29	1.36	0.38	0.13	0.12	-1.21E+01	1.65E-08	Down	-9.75E-01	9.25E-02		9.27E-01	2.97E-01			1.81E-01	8.84E-01			-1.60E+00	5.34E-01		-1.67E+00	4.77E-01		Unigene12945_All//gi|3819099|emb|CAA08855.1|//1.00E-21//copper amine oxidase [Cicer arietinum]	Unigene12945_All//4.00E-23//AT1G31710| copper amine oxidase, putative	Unigene12945_All//2.00E-82//gi|78343452|gb|DT563726.1|DT563726			GO:0006807//GO:0016641//GO:0046914//GO:0048037	nr +
Unigene12946_All	2173	4.53	1.07	2.13	6.42	3.96	4.24	7.14	6.77	2.70	-2.08E+00	1.22E-21	Down	-1.09E+00	2.19E-08	Down	-6.96E-01	4.43E-07			-5.98E-01	4.36E-05			-7.68E-02	6.46E-01		-1.41E+00	7.25E-25	Down	Unigene12946_All//gi|186479101|ref|NP_174450.2|//0.00E+00//amine oxidase/ copper ion binding / quinone binding [Arabidopsis thaliana]	Unigene12946_All//0.00E+00//AT1G31710| copper amine oxidase, putative	Unigene12946_All//0.00E+00//gi|78343452|gb|DT563726.1|DT563726		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0006807//GO:0016641//GO:0046914//GO:0048037	nr -
Unigene12947_All	2205	78.09	20.64	41.39	83.11	66.23	86.03	14.17	3.47	5.38	-1.92E+00	0.00E+00	Down	-9.16E-01	8.51E-104		-3.28E-01	4.55E-22			4.97E-02	2.74E-01			-2.03E+00	7.19E-80	Down	-1.40E+00	1.13E-48	Down	Unigene12947_All//gi|20196847|gb|AB80674.2|//0.00E+00//expressed protein [Arabidopsis thaliana] >gi|22655220|gb|AAM88200.1| expressed protein [Arabidopsis thaliana] >gi|31711902|gb|AAP68307.1|At2g33570 [Arabidopsis thaliana]	Unigene12947_All//0.00E+00//AT2G33570| unknown protein	Unigene12947_All//0.00E+00//TC145983				nr -
Unigene12949_All	3118	1.41	0.85	0.61	2.97	1.73	2.84	6.70	3.73	4.40	-7.38E-01	1.05E-02		-1.20E+00	1.03E-04	Down	-7.77E-01	8.06E-06			-6.59E-02	7.57E-01			-8.46E-01	1.29E-14		-6.08E-01	7.54E-09		Unigene12949_All//gi|240255294|ref|NP_187305.4|//0.00E+00//binding [Arabidopsis thaliana]	Unigene12949_All//0.00E+00//AT3G06530| binding	Unigene12949_All//0.00E+00//CO130046				nr +
Unigene1295_All	1271	2.72	1.04	0.54	12.50	8.99	6.64	1.70	1.78	1.22	-1.39E+00	6.07E-05	Down	-2.32E+00	1.21E-08	Down	-4.75E-01	2.66E-04			-9.12E-01	3.79E-11			6.58E-02	8.76E-01		-4.73E-01	2.16E-01		Unigene1295_All//gi|224067288|ref|XP_002302449.1|//4.00E-57//f-box family protein [Populus trichocarpa] >gi|222844175|gb|EEE81722.1| f-box family protein [Populus trichocarpa]	Unigene1295_All//8.00E-23//AT1G47655| Dof-type zinc finger domain-containing protein	Unigene1295_All//0.00E+00//TC162221	C2C2-Dof			nr +
Unigene12950_All	494	28.17	17.23	29.97	8.97	14.29	3.02	1.97	1.10	1.21	-7.09E-01	2.51E-06		8.91E-02	6.23E-01		6.71E-01	1.45E-03			-1.57E+00	1.44E-07	Down		-8.40E-01	1.87E-01		-7.02E-01	2.43E-01		Unigene12950_All//gi|266742|sp|Q01289.1|POR_PEA//2.00E-09//RecName: Full=Protochlorophyllide reductase, chloroplastic; Short=PCR; AltName: Full=NADPH-protochlorophyllide oxidoreductase; Short=POR; Flags: Precursor >gi|20830|emb|CAA44786.1|protochlorophyllide reductase [Pisum sativum]	Unigene12950_All//2.00E-06//AT5G54190| PORA; oxidoreductase/ protochlorophyllide reductase	Unigene12950_All//7.00E-93//gi|109847150|gb|DW476130.1|DW476130			GO:0009536//GO:0016491//GO:0044237	nr +
Unigene12951_All	1790	218.08	105.27	160.88	43.08	71.72	30.30	2.48	0.56	1.78	-1.05E+00	2.72E-304	Down	-4.39E-01	6.38E-64		7.35E-01	1.78E-65			-5.08E-01	8.17E-19			-2.15E+00	8.54E-13	Down	-4.78E-01	5.62E-02		Unigene12951_All//gi|10720220|sp|Q41249.1|PORA_CUCSA//0.00E+00//RecName: Full=Protochlorophyllide reductase, chloroplastic; Short=PCR; AltName: Full=NADPH-protochlorophyllide oxidoreductase; Short=POR; Flags: Precursor >gi|2244614|dbj|BAA21089.1| NADPH-protochlorophyllide oxidoreductase [Cucumis sativus]	Unigene12951_All//3.00E-165//AT5G54190| PORA; oxidoreductase/ protochlorophyllide reductase	Unigene12951_All//0.00E+00//TC136438		ko00860|Porphyrin and chlorophyll metabolism	GO:0006779//GO:0009536//GO:0009725//GO:0016628	nr -
Unigene12959_All	3916	0.77	0.22	0.03	1.65	1.92	1.59	5.14	0.90	5.05	-1.82E+00	3.90E-06	Down	-4.83E+00	4.90E-14	Down	2.13E-01	3.83E-01			-5.52E-02	8.36E-01			-2.52E+00	3.45E-67	Down	-2.64E-02	8.34E-01		Unigene12959_All//gi|42567496|ref|NP_195520.2|//0.00E+00//bHLH family protein [Arabidopsis thaliana]	Unigene12959_All//6.00E-159//AT4G38070| bHLH family protein	Unigene12959_All//0.00E+00//TC170437	bHLH			nr +
Unigene1296_All	1237	4.82	2.79	3.31	58.11	42.40	25.92	10.83	5.95	3.74	-7.92E-01	1.10E-03		-5.41E-01	3.42E-02		-4.55E-01	4.03E-16			-1.16E+00	3.31E-72	Down		-8.66E-01	5.06E-10		-1.54E+00	1.56E-24	Down	Unigene1296_All//gi|224067288|ref|XP_002302449.1|//3.00E-56//f-box family protein [Populus trichocarpa] >gi|222844175|gb|EEE81722.1| f-box family protein [Populus trichocarpa]	Unigene1296_All//3.00E-23//AT3G50410| OBP1 (OBF BINDING PROTEIN 1); DNA binding / protein binding / transcription factor	Unigene1296_All//0.00E+00//TC138819	C2C2-Dof	ko03040|Spliceosome		nr +
Unigene12961_All	1117	8.38	5.76	2.91	9.41	8.02	7.20	10.18	8.46	8.63	-5.41E-01	3.96E-03		-1.53E+00	3.95E-13	Down	-2.31E-01	2.23E-01			-3.87E-01	3.13E-02			-2.68E-01	9.24E-02		-2.38E-01	1.21E-01		Unigene12961_All//gi|15242483|ref|NP_199387.1|//1.00E-107//AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding [Arabidopsis thaliana] >gi|75171186|sp|Q9FK68.1|RA41C_ARATH RecName: Full=Ras-related protein RABA1c >gi|9758678|dbj|BAB09217.1| Rab-type small GTP-binding protein-like [Arabidopsis thaliana]	Unigene12961_All//2.00E-108//AT5G45750| AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding	Unigene12961_All//0.00E+00//TC149476				nr +
Unigene12962_All	1258	3.24	1.33	2.24	9.66	7.34	9.33	11.56	7.84	6.56	-1.29E+00	3.74E-05	Down	-5.32E-01	9.47E-02		-3.97E-01	1.11E-02			-4.98E-02	7.95E-01			-5.60E-01	1.77E-05		-8.19E-01	3.15E-10		Unigene12962_All//gi|15242483|ref|NP_199387.1|//1.00E-105//AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding [Arabidopsis thaliana] >gi|75171186|sp|Q9FK68.1|RA41C_ARATH RecName: Full=Ras-related protein RABA1c >gi|9758678|dbj|BAB09217.1| Rab-type small GTP-binding protein-like [Arabidopsis thaliana]	Unigene12962_All//4.00E-102//AT5G45750| AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding	Unigene12962_All//0.00E+00//TC161532				nr -
Unigene12963_All	2537	6.58	9.07	5.35	3.97	6.49	6.25	19.32	38.85	64.65	4.63E-01	4.83E-05		-2.98E-01	4.33E-02		7.10E-01	3.05E-08			6.56E-01	1.63E-06			1.01E+00	4.26E-88	Up	1.74E+00	0.00E+00	Up	Unigene12963_All//gi|42741727|gb|AS45124.1|//0.00E+00//WAK-like kinase [Solanum lycopersicum]	Unigene12963_All//0.00E+00//AT2G23450| protein kinase family protein	Unigene12963_All//0.00E+00//TC163946		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152//GO:0016491//GO:0043231	nr -
Unigene12964_All	2779	4.48	1.64	2.53	7.76	4.81	5.88	4.58	4.51	3.47	-1.45E+00	9.74E-17	Down	-8.25E-01	7.44E-07		-6.91E-01	1.65E-10			-4.00E-01	5.97E-04			-2.14E-02	9.09E-01		-4.01E-01	3.73E-03		Unigene12964_All//gi|224106455|ref|XP_002314172.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222850580|gb|EEE88127.1| GRAS family transcription factor [Populus trichocarpa]	Unigene12964_All//0.00E+00//AT1G07530| SCL14 (SCARECROW-LIKE 14); transcription factor	Unigene12964_All//0.00E+00//TC178547	GRAS		GO:0032583//GO:0042221//GO:0043231//GO:0044444	nr -
Unigene12965_All	3396	5.45	2.39	3.25	22.37	16.25	14.96	37.96	46.95	37.45	-1.19E+00	2.44E-18	Down	-7.49E-01	1.90E-08		-4.61E-01	2.06E-17			-5.80E-01	1.76E-23			3.07E-01	1.64E-17		-1.97E-02	6.79E-01		Unigene12965_All//gi|2160756|gb|AAB58829.1|//0.00E+00//CLV1 receptor kinase [Arabidopsis thaliana]	Unigene12965_All//0.00E+00//AT1G75820| CLV1 (CLAVATA 1); ATP binding / kinase/ protein serine/threonine kinase/ receptor signaling protein serine/threonine kinase	Unigene12965_All//0.00E+00//TC158291			GO:0004702//GO:0005515//GO:0006464//GO:0007169//GO:0009909//GO:0009933//GO:0016628//GO:0031224//GO:0032559//GO:0048869	nr -
Unigene12968_All	3014	3.80	16.56	7.16	1.95	1.79	2.82	11.04	33.84	20.90	2.12E+00	1.65E-109	Up	9.12E-01	2.11E-13		-1.21E-01	6.63E-01			5.31E-01	7.51E-03			1.62E+00	4.68E-189	Up	9.21E-01	6.87E-50		Unigene12968_All//gi|109676362|gb|AB637663.1|//0.00E+00//CCHC-type integrase [Populus trichocarpa]	Unigene12968_All//3.00E-102//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene12968_All//3.00E-148//TC169127		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674//GO:0004871//GO:0044238//GO:0044260	nr +

Unigene12969_All	1060	15.45	10.85	8.99	50.43	54.19	44.44	13.12	5.72	6.77	-5.10E-01	2.01E-04		-7.81E-01	4.56E-08		1.04E-01	1.87E-01		-1.82E-01	1.55E-02		-1.20E+00	3.96E-17	Down	-9.56E-01	1.69E-12		Unigene12969_All//gi|115468724|ref|NP_001057961.1|//3.00E-41//0s06g0589500 [Oryza sativa Japonica Group] >gi|113596001|dbj|BAF19875.1|Os06g0589500 [Oryza sativa Japonica Group]	Unigene12969_All//2.00E-36//AT5G62550| unknown protein	Unigene12969_All//0.00E+00//TC145582			GO:0016020//GO:0043231	nr -
Unigene12971_All	2361	1.77	1.80	0.95	3.50	2.23	2.09	5.19	1.93	2.83	2.41E-02	9.55E-01		-9.04E-01	3.67E-03		-6.50E-01	5.13E-04		-7.48E-01	1.45E-04		-1.43E+00	1.14E-19	Down	-8.73E-01	1.10E-09		Unigene12971_All|gi|12006360|gb|AAG44842.1|AF281154_1|/1.00E-46//cohesion family protein SYN2 [Arabidopsis thaliana]	Unigene12971_All//3.00E-45//AT5G40840| SYN2	Unigene12971_All//0.00E+00//gi|78323377|gb|DT543651.1|DT543651				nr -
Unigene12972_All	2767	2.69	1.50	2.16	28.39	22.38	14.25	11.29	4.89	5.07	-8.39E-01	9.40E-05		-3.17E-01	1.74E-01		-3.44E-01	1.39E-10		-9.95E-01	4.74E-61		-1.21E+00	7.69E-38	Down	-1.16E+00	1.85E-36	Down	Unigene12972_All|gi|8493576|gb|AAF75799.1|AC011000.2|/0.00E+00//Contains weak similarity to T-type calcium channel isoform from Rattus norvegicus gb|AF125161. EST gb|H30034 comes from this gene [Arabidopsis thaliana]	Unigene12972_All//0.00E+00//AT1G12380| unknown protein	Unigene12972_All//0.00E+00//TC141989			GO:0005488	nr -
Unigene12973_All	1682	29.83	14.85	21.84	87.10	62.83	55.58	19.15	11.26	7.96	-1.01E+00	5.68E-37	Down	-4.50E-01	4.16E-09		-4.71E-01	1.25E-34		-6.48E-01	1.82E-54		-7.67E-01	8.57E-19		-1.27E+00	2.57E-43	Down	Unigene12973_All|gi|15219544|ref|NP_177517.1|//3.00E-89//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene12973_All//3.00E-80//AT1G73760| zinc finger (C3HC4-type RING finger) family protein	Unigene12973_All//0.00E+00//TC134312			GO:0046914	nr -
Unigene12974_All	3044	5.24	3.31	5.28	2.31	2.09	1.81	1.33	0.25	0.52	-6.62E-01	2.04E-06		1.11E-02	9.62E-01		-1.41E-01	5.87E-01		-3.50E-01	1.32E-01		-2.43E+00	1.47E-13	Down	-1.35E+00	9.19E-07	Down	Unigene12974_All|gi|49388598|dbj|BAD25713.1|/0.00E+00//transducin-like [Oryza sativa Japonica Group]	Unigene12974_All//3.00E-09//AT3G06880| nucleotide binding	Unigene12974_All//0.00E+00//gi|109886256|gb|DW515226.1|DW515226			GO:0043231	nr +
Unigene12975_All	2364	6.86	1.69	3.31	5.37	2.33	1.38	10.64	3.94	2.07	-2.02E+00	5.41E-34	Down	-1.05E+00	9.58E-13	Down	-1.21E+00	1.13E-15	Down	-1.97E+00	5.92E-28	Down	-1.43E+00	1.08E-39	Down	-2.36E+00	4.03E-80	Down	Unigene12975_All|gi|115455585|ref|NP_001051393.1|//1.00E-147//0s03g0769000 [Oryza sativa Japonica Group] >gi|113549864|dbj|BAF13307.1|Os03g0769000 [Oryza sativa Japonica Group]	Unigene12975_All//1.00E-162//AT5G66600| unknown protein	Unigene12975_All//0.00E+00//TC169939				nr +
Unigene12977_All	2351	16.11	12.80	15.29	6.06	9.68	6.40	2.10	0.41	1.42	-3.32E-01	1.42E-04		-7.57E-02	4.68E-01		6.76E-01	2.50E-10		7.81E-02	6.62E-01		-2.36E+00	7.41E-16	Down	-5.61E-01	1.55E-02		Unigene12977_All|gi|17667009|gb|ACB73218.1|/0.00E+00//homeodomain protein GL2-like 1 [Gossypium hirsutum]	Unigene12977_All//0.00E+00//AT4G00730| ANL2 (ANTHOCYANINLESS 2); transcription factor/ transcription regulator	Unigene12977_All//0.00E+00//TC134187	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231//GO:0043479//GO:0048513	nr +
Unigene12979_All	1081	2.90	2.11	3.35	3.09	3.34	1.04	3.99	2.98	2.10	-4.61E-01	1.96E-01		2.06E-01	5.72E-01		1.16E-01	7.89E-01		-1.56E+00	8.21E-06	Down	-4.22E-01	1.18E-01		-9.25E-01	2.70E-04		Unigene12979_All|gi|222424960|dbj|BAH20431.1|//2.00E-11//AT4G10360 [Arabidopsis thaliana]	Unigene12979_All//8.00E-13//AT4G10360| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TRAM, LAG1 and CLN8 homology (InterPro:IPR006634); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G31300.2); Has 453 Blast hits to 451 proteins in 101 species: Archae - 0; Bacteria - 0; Metazoa - 225; Fungi - 97; Plants - 91; Viruses - 3; Other Eukaryotes - 37 (source: NCBI BLink).	Unigene12979_All//2.00E-129//gi|109880812|gb|DW509782.1|DW509782			GO:0031224	nr +
Unigene12982_All	2294	0.64	4.04	4.16	2.21	2.57	3.41	21.64	73.94	82.02	2.66E+00	4.95E-27	Up	2.70E+00	2.03E-27	Up	2.13E-01	4.57E-01		6.21E-01	2.62E-03		1.77E+00	0.00E+00	Up	1.92E+00	0.00E+00	Up	Unigene12982_All|gi|15225053|ref|NP_181454.1|//0.00E+00//nodulin family protein [Arabidopsis thaliana] >gi|16930479|gb|AAL31925.1|AF419593_1 At2g39210/T16B24.15 [Arabidopsis thaliana] >gi|3402684|gb|AAC28987.1| nodulin-like protein [Arabidopsis thaliana]	Unigene12982_All//0.00E+00//AT2G39210| nodulin family protein	Unigene12982_All//1.00E-17//DW498332			GO:0006810	nr +
Unigene12983_All	1192	9.17	4.80	5.09	13.12	15.69	11.59	14.19	9.64	5.55	-9.33E-01	9.62E-08		-8.49E-01	2.24E-06		2.58E-01	4.93E-02		-1.79E-01	2.66E-01		-5.57E-01	3.50E-06		-1.35E+00	1.38E-25	Down	Unigene12983_All|gi|79324927|ref|NP_001031548.1|//7.00E-48//ARF11 (AUXIN RESPONSE FACTOR 11); transcription factor [Arabidopsis thaliana] >gi|238054388|sp|Q9ZPY6.3|ARFK_ARATH RecName: Full=Auxin response factor 11 >gi|49616357|gb|AAT67075.1| ARF11 [Arabidopsis thaliana]	Unigene12983_All//7.00E-49//AT2G46530| ARF11 (AUXIN RESPONSE FACTOR 11); transcription factor	Unigene12983_All//0.00E+00//TC179252	ARF		GO:0009987	nr -
Unigene12984_All	2490	3.21	2.91	2.65	6.96	8.38	6.38	6.28	3.34	1.58	-1.44E-01	5.28E-01		-2.78E-01	2.25E-01		2.68E-01	2.79E-02		-1.25E-01	4.35E-01		-9.11E-01	1.53E-12		-1.99E+00	1.69E-40	Down	Unigene12984_All|gi|15233647|ref|NP_194129.1|//0.00E+00//ARF9 (AUXIN RESPONSE FACTOR 9); transcription factor [Arabidopsis thaliana] >gi|46576670|sp|Q9XED8.1|ARF1_ARATH RecName: Full=Auxin response factor 9 >gi|4580575|gb|AAD24427.1|AF082176_1 auxin response factor 9 [Arabidopsis thaliana] >gi|12744967|gb|AAK06863.1|AF344312_1 auxin response factor 9 [Arabidopsis thaliana] >gi|4972102|emb|CAB43898.1| auxin response factor 9 (ARF9) [Arabidopsis thaliana] >gi|7269247|emb|CAB81316.1| auxin response factor 9 (ARF9) [Arabidopsis thaliana]	Unigene12984_All//0.00E+00//AT4G23980| ARF9 (AUXIN RESPONSE FACTOR 9); transcription factor	Unigene12984_All//0.00E+00//TC170774	ARF		GO:0006351	nr +
Unigene12985_All	2550	1.19	0.79	0.86	2.01	2.61	1.38	1.34	0.79	0.62	-5.82E-01	1.05E-01		-4.75E-01	2.18E-01		3.73E-01	1.13E-01		-5.43E-01	4.19E-02		-7.72E-01	9.48E-03		-1.10E+00	1.68E-04	Down	Unigene12985_All|gi|15233647|ref|NP_194129.1|//0.00E+00//ARF9 (AUXIN RESPONSE FACTOR 9); transcription factor [Arabidopsis thaliana] >gi|46576670|sp|Q9XED8.1|ARF1_ARATH RecName: Full=Auxin response factor 9 >gi|4580575|gb|AAD24427.1|AF082176_1 auxin response factor 9 [Arabidopsis thaliana] >gi|12744967|gb|AAK06863.1|AF344312_1 auxin response factor 9 [Arabidopsis thaliana] >gi|4972102|emb|CAB43898.1| auxin response factor 9 (ARF9) [Arabidopsis thaliana] >gi|7269247|emb|CAB81316.1| auxin response factor 9 (ARF9) [Arabidopsis thaliana]	Unigene12985_All//0.00E+00//AT4G23980| ARF9 (AUXIN RESPONSE FACTOR 9); transcription factor	Unigene12985_All//0.00E+00//TC179252	ARF		GO:0001071//GO:0005488//GO:0006351//GO:0009725//GO:0010468//GO:0044464	nr -
Unigene12986_All	2457	0.02	0.00	0.00	0.28	0.31	0.17	0.98	0.56	0.08	-4.41E+00	6.13E-01		-4.41E+00	6.25E-01		1.20E-01	9.05E-01		-7.79E-01	3.93E-01		-8.05E-01	2.78E-02		-3.60E+00	2.13E-12	Down	Unigene12986_All|gi|79325241|ref|NP_001031706.1|//1.00E-175//ARF9 (AUXIN RESPONSE FACTOR 9); transcription factor [Arabidopsis thaliana]	Unigene12986_All//7.00E-175//AT4G23980| ARF9 (AUXIN RESPONSE FACTOR 9); transcription factor	Unigene12986_All//0.00E+00//TC170774	ARF		GO:0006350	nr +
Unigene12988_All	2233	5.65	12.05	5.51	10.82	8.07	7.67	20.92	52.86	86.55	1.09E+00	6.66E-23	Up	-3.57E-02	8.42E-01		-4.24E-01	3.84E-05		-4.97E-01	3.91E-06		1.34E+00	4.99E-165	Up	2.05E+00	0.00E+00	Up	Unigene12988_All|gi|226530423|ref|NP_001149013.1|//7.00E-30//abhydrolase domain-containing protein 5 [Zea mays] >gi|195623984|gb|ACG33822.1| abhydrolase domain-containing protein 5 [Zea mays]	Unigene12988_All//9.00E-29//AT4G24160| hydrolase, alpha/beta fold family protein	Unigene12988_All//0.00E+00//gi|21089645|gb|BQ401970.1|BQ401970			GO:0004091//GO:0031410//GO:0071617	nr +
Unigene12989_All	850	12.19	4.53	8.46	28.13	21.76	19.07	21.49	14.51	10.17	-1.43E+00	9.38E-14	Down	-5.27E-01	4.37E-03		-3.71E-01	4.11E-04		-5.61E-01	2.19E-07		-5.67E-01	8.55E-07		-1.08E+00	1.67E-19	Down	Unigene12989_All|gi|18396647|ref|NP_564298.1|//3.00E-61//SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|42571671|ref|NP_973926.1|SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75331738|sp|Q93Y09.1|SCP45_ARATH RecName: Full=Serine carboxypeptidase-like 45; Flags: Precursor >gi|31376397|gb|AAP49525.1|At1g28110 [Arabidopsis thaliana]	Unigene12989_All//1.00E-62//AT1G28110| SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase	Unigene12989_All//0.00E+00//gi|48821556|gb|CO122869.1|CO122869			GO:0005618//GO:0016787	nr -
Unigene12990_All	1687	18.98	5.29	16.19	51.26	34.11	26.93	28.32	16.43	12.75	-1.84E+00	5.39E-59	Down	-2.29E-01	2.65E-02		-5.88E-01	1.18E-30		-9.29E-01	6.34E-60		-7.86E-01	1.28E-28		-1.15E+00	6.40E-55	Down	Unigene12990_All|gi|18396647|ref|NP_564298.1|//1.00E-154//SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|42571671|ref|NP_973926.1|SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75331738|sp|Q93Y09.1|SCP45_ARATH RecName: Full=Serine carboxypeptidase-like 45; Flags: Precursor >gi|31376397|gb|AAP49525.1|At1g28110 [Arabidopsis thaliana]	Unigene12990_All//2.00E-155//AT1G28110| SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase	Unigene12990_All//0.00E+00//TC137912				nr +
Unigene12992_All	2473	14.81	7.52	9.54	6.18	5.36	5.79	8.94	7.01	4.19	-9.78E-01	5.89E-26		-6.35E-01	3.55E-12		-2.06E-01	1.77E-01		-9.52E-02	6.07E-01		-3.50E-01	8.36E-04		-1.09E+00	6.20E-24	Down	Unigene12992_All|gi|223452516|gb|ACM89585.1|//0.00E+00//receptor-like protein kinase [Glycine max]	Unigene12992_All//0.00E+00//AT5G56040| leucine-rich repeat protein kinase, putative	Unigene12992_All//0.00E+00//TC172264			GO:0005488//GO:0016020//GO:0016301	nr +

Unigene12994_All	1313	13.39	15.32	14.56	15.18	24.73	32.02	65.66	68.98	89.87	1.94E-01	1.36E-01		1.21E-01	3.99E-01		7.05E-01	1.30E-15		1.08E+00	5.18E-37	Up	7.12E-02	2.18E-01		4.53E-01	4.43E-27		Unigene12994_All//gi|74476783|gb|AB08442.1|//0.00//neutral/alkaline invertase [Manihot esculenta]	Unigene12994_All//0.00E+00//AT4G09510| beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative	Unigene12994_All//0.00E+00//TC152907			GO:0004553	nr -
Unigene12995_All	1370	5.27	10.61	8.82	9.53	10.23	15.40	8.92	8.66	14.63	1.01E+00	2.80E-11	Up	7.43E-01	1.04E-05		1.03E-01	5.85E-01		6.93E-01	3.12E-09		-4.18E-02	8.05E-01		7.14E-01	5.66E-11		Unigene12995_All//gi|8778818|gb|AAF26770.2|AC007396_19//7.00E-19//T4012.10 [Arabidopsis thaliana]	Unigene12995_All//3.00E-17//AT1G75860| unknown protein	Unigene12995_All//0.00E+00//TC144751				nr -
Unigene12996_All	1236	3.56	4.96	1.77	5.20	6.30	8.22	4.31	4.16	10.67	4.80E-01	4.59E-02		-1.01E+00	8.93E-04	Down	2.76E-01	2.23E-01		6.61E-01	1.76E-04		-5.14E-02	8.44E-01		1.31E+00	5.97E-19	Up	Unigene12996_All//gi|8778818|gb|AAF26770.2|AC007396_19//2.00E-23//T4012.10 [Arabidopsis thaliana]	Unigene12996_All//2.00E-21//AT1G75860| unknown protein	Unigene12996_All//0.00E+00//TC144751				nr +
Unigene130_All	4835	33.23	18.80	33.41	16.63	24.83	17.41	3.74	1.69	3.42	-8.22E-01	2.69E-83		7.90E-03	8.78E-01		5.79E-01	2.98E-40		6.64E-02	3.45E-01		-1.15E+00	1.05E-20	Down	-1.30E-01	3.12E-01		Unigene130_All//gi|186478514|ref|NP_172981.3|//0.00E+00//binding [Arabidopsis thaliana]	Unigene130_All//0.00E+00//AT1G15290| binding	Unigene130_All//0.00E+00//TC142957				nr -
Unigene13000_All	734	2.71	0.83	3.19	10.72	10.79	5.41	2.65	0.91	1.36	-1.71E+00	5.22E-04	Down	2.37E-01	6.13E-01		9.00E-03	9.73E-01		-9.86E-01	1.42E-06		-1.54E+00	4.03E-04	Down	-9.66E-01	1.58E-02		Unigene13000_All//gi|40823013|gb|AB82253.1|//1.00E-110//At2g15730 [Arabidopsis thaliana] >gi|45752690|gb|AAS76243.1| At2g15730 [Arabidopsis thaliana]	Unigene13000_All//6.00E-112//AT2G15730| unknown protein	Unigene13000_All//0.00E+00//CO121055			GO:0006787//GO:0016705//GO:0016782	nr +
Unigene13002_All	502	0.63	0.81	0.64	2.68	1.23	0.99	14.32	8.08	2.54	3.69E-01	7.24E-01		2.56E-02	1.00E+00		-1.12E+00	4.30E-02		-1.44E+00	1.59E-02		-8.26E-01	2.25E-05		-2.50E+00	5.47E-25	Down	Unigene13002_All//gi|18406012|ref|NP_565978.1|//6.00E-34//LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|30689086|ref|NP_850374.1| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|6691165|gb|AAF24517.1|AF218765_1 177 protein [Arabidopsis thaliana] >gi|4559331|gb|AAD22993.1| expressed protein [Arabidopsis thaliana] >gi|28372972|gb|AAO39968.1| At2g42610 [Arabidopsis thaliana]	Unigene13002_All//1.00E-31//AT2G42610| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10)	Unigene13002_All//0.00E+00//TC137828				nr -
Unigene13003_All	1091	0.48	0.46	0.24	8.22	3.19	3.15	11.24	6.32	2.04	-4.65E-02	9.76E-01		-9.75E-01	3.76E-01		-1.37E+00	1.50E-13	Down	-1.39E+00	2.91E-12	Down	-8.30E-01	1.16E-08		-2.46E+00	2.28E-41	Down	Unigene13003_All//gi|18406012|ref|NP_565978.1|//6.00E-67//LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|30689086|ref|NP_850374.1| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|6691165|gb|AAF24517.1|AF218765_1 177 protein [Arabidopsis thaliana] >gi|4559331|gb|AAD22993.1| expressed protein [Arabidopsis thaliana] >gi|28372972|gb|AAO39968.1| At2g42610 [Arabidopsis thaliana]	Unigene13003_All//9.00E-65//AT2G42610| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10)	Unigene13003_All//0.00E+00//TC134661				nr +
Unigene13004_All	975	0.91	2.65	1.09	22.58	16.88	16.54	5.90	4.07	2.29	1.54E+00	2.26E-04	Up	2.60E-01	6.82E-01		-4.20E-01	1.14E-04		-4.50E-01	8.11E-05		-5.34E-01	1.62E-02		-1.37E+00	2.20E-09	Down	Unigene13004_All//gi|18406012|ref|NP_565978.1|//4.00E-71//LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|30689086|ref|NP_850374.1| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|6691165|gb|AAF24517.1|AF218765_1 177 protein [Arabidopsis thaliana] >gi|4559331|gb|AAD22993.1| expressed protein [Arabidopsis thaliana] >gi|28372972|gb|AAO39968.1| At2g42610 [Arabidopsis thaliana]	Unigene13004_All//1.00E-67//AT2G42610| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10)	Unigene13004_All//2.00E-107//TC132248				nr +
Unigene13011_All	885	24.95	24.28	20.82	70.58	40.00	18.52	7.41	5.43	2.97	-3.95E-02	7.57E-01		-2.61E-01	3.93E-02		-8.19E-01	8.13E-40		-1.93E+00	1.40E-132	Down	-4.47E-01	3.20E-02		-1.32E+00	4.74E-10	Down	Unigene13011_All//gi|124359162|gb|ABN05685.1|//6.00E-08//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene13011_All//6.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene13011_All//2.00E-171//gi|13351086|gb|BG441434.1|BG441434				nr +
Unigene13012_All	1423	13.20	10.90	9.80	32.73	21.95	11.77	4.19	3.50	1.46	-2.77E-01	3.58E-02		-4.29E-01	1.23E-03		-5.77E-01	3.92E-16		-1.47E+00	1.53E-67	Down	-2.61E-01	2.66E-01		-1.52E+00	2.82E-11	Down	Unigene13012_All//gi|124359339|gb|ABD28498.2|//8.00E-23//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene13012_All//2.00E-14//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene13012_All//0.00E+00//gi|78332267|gb|DT552541.1|DT552541				nr +
Unigene13015_All	1395	2.44	10.13	6.22	4.71	9.97	20.56	30.40	56.60	47.04	2.06E+00	3.50E-30	Up	1.35E+00	2.65E-10	Up	1.08E+00	9.61E-14	Up	2.12E+00	1.02E-67	Up	8.97E-01	2.63E-58		6.30E-01	2.39E-27		Unigene13015_All//gi|15230127|ref|NP_180995.1|//3.00E-84//AT-HSFC1; DNA binding / transcription factor [Arabidopsis thaliana] >gi|75311616|sp|Q9LV52.1|HSFC1_ARATH RecName: Full=Heat stress transcription factor C-1; Short=AtHsfC1; AltName: Full=AtHsf-08 >gi|15810194|gb|AAL06998.1| AT3g24520/MOB24_5 [Arabidopsis thaliana] >gi|18252249|gb|AAL62005.1| AT3g24520/MOB24_5 [Arabidopsis thaliana]	Unigene13015_All//3.00E-67//AT3G24520| AT-HSFC1; DNA binding / transcription factor	Unigene13015_All//0.00E+00//TC139160	HSF		GO:0001071//GO:0003677//GO:0006351//GO:0031410//GO:0043231	nr +
Unigene13018_All	2917	0.68	1.79	1.13	0.99	1.30	1.47	2.88	3.12	3.00	1.39E+00	4.97E-07	Up	7.32E-01	4.06E-02		3.91E-01	2.44E-01		5.71E-01	5.67E-02		1.15E-01	5.84E-01		5.89E-02	7.52E-01		Unigene13018_All//gi|297844222|ref|XP_002889992.1|//1.00E-162//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335834|gb|EFH66251.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13018_All//1.00E-79//AT1G13190| RNA recognition motif (RRM)-containing protein	Unigene13018_All//0.00E+00//ES839444		ko03040|Spliceosome	GO:0005488	nr +
Unigene13019_All	849	4.19	9.31	9.53	11.56	20.24	20.85	56.92	65.43	70.90	1.15E+00	7.75E-08	Up	1.19E+00	5.39E-08	Up	8.08E-01	1.35E-10		8.51E-01	6.09E-11		2.01E-01	2.03E-03		3.17E-01	9.14E-08		Unigene13019_All//gi|297804388|ref|XP_002870078.1|//2.00E-76//zinc-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315914|gb|EFH46337.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13019_All//3.00E-71//AT4G17900| zinc-binding family protein	Unigene13019_All//0.00E+00//gi|48806138|gb|CO107452.1|CO107452	PLATZ			nr -
Unigene13020_All	1287	14.23	43.50	29.17	47.18	73.45	66.36	131.83	148.51	183.81	1.61E+00	1.29E-84	Up	1.04E+00	3.95E-28	Up	6.38E-01	9.56E-38		4.92E-01	1.52E-19		1.72E-01	2.08E-07		4.80E-01	3.71E-59		Unigene13020_All//gi|297804388|ref|XP_002870078.1|//7.00E-92//zinc-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315914|gb|EFH46337.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13020_All//2.00E-83//AT4G17900| zinc-binding family protein	Unigene13020_All//0.00E+00//TC139926	PLATZ			nr +
Unigene13021_All	1764	32.18	79.59	21.16	36.03	43.14	75.27	140.05	126.41	225.12	1.31E+00	1.96E-154	Up	-6.05E-01	4.73E-17		2.60E-01	3.47E-06		1.06E+00	2.01E-113	Up	-1.48E-01	3.52E-07		6.85E-01	1.17E-186		Unigene13021_All//gi|224132448|ref|XP_002328275.1|//0.00E+00//aromatic and neutral amino acid transporter [Populus trichocarpa] >gi|222837790|gb|EEE76155.1| aromatic and neutral amino acid transporter [Populus trichocarpa]	Unigene13021_All//4.00E-158//AT4G38250| amino acid transporter family protein	Unigene13021_All//0.00E+00//TC165286			GO:0031224	nr -
Unigene13026_All	2476	21.85	3.56	6.30	46.78	21.56	13.43	19.98	13.23	5.79	-2.62E+00	1.17E-153	Down	-1.79E+00	2.34E-92	Down	-1.12E+00	2.91E-124	Down	-1.80E+00	1.92E-223	Down	-5.94E-01	2.05E-18		-1.79E+00	2.41E-109	Down	Unigene13026_All//gi|170649924|gb|AAL32616.1|//1.00E-157//SCARECROW gene regulator [Arabidopsis thaliana] >gi|27311949|gb|AAO00940.1| SCARECROW gene regulator [Arabidopsis thaliana]	Unigene13026_All//1.00E-141//AT5G66770| scarecrow transcription factor family protein	Unigene13026_All//0.00E+00//TC148361	GRAS			nr -
Unigene13029_All	1791	12.94	48.15	27.38	20.08	34.69	29.93	9.68	19.91	44.24	1.90E+00	6.96E-163	Up	1.08E+00	3.17E-39	Up	7.89E-01	8.13E-36		5.76E-01	2.10E-16		1.04E+00	4.72E-34	Up	2.19E+00	4.33E-226	Up	Unigene13029_All//gi|289466351|gb|ADC94861.1|//1.00E-106//HSP transcription factor [Vitis pseudoreticulata]	Unigene13029_All//1.00E-75//AT4G11660| AT-HSFB2B; transcription factor/ transcription repressor	Unigene13029_All//0.00E+00//gi|78341159|gb|DT561433.1|DT561433	HSF		GO:0001071//GO:0009743//GO:0030528	nr -
Unigene13030_All	492	9.89	17.92	20.13	18.83	21.91	20.47	9.02	10.79	7.13	8.58E-01	1.22E-05		1.03E+00	9.19E-08	Up	2.18E-01	2.59E-01		1.20E-01	6.00E-01		2.58E-01	3.12E-01		-3.41E-01	1.88E-01		Unigene13030_All//gi|30696612|ref|NP_200364.2|//1.00E-33//C2 domain-containing protein [Arabidopsis thaliana] >gi|42573678|ref|NP_974935.1| C2 domain-containing protein [Arabidopsis thaliana] >gi|42573680|ref|NP_974936.1| C2 domain-containing protein [Arabidopsis thaliana] >gi|57222230|gb|AAW39022.1| At5g55530 [Arabidopsis thaliana] >gi|59958302|gb|AAX12861.1| At5g55530 [Arabidopsis thaliana]	Unigene13030_All//8.00E-35//AT5G55530| C2 domain-containing protein	Unigene13030_All//0.00E+00//CO127042			GO:0005506//GO:0008152//GO:0016491	nr +
Unigene13031_All	1562	16.31	37.01	17.83	28.73	36.90	28.77	24.25	24.72	17.32	1.18E+00	9.44E-55	Up	1.28E-01	2.84E-01		3.61E-01	1.72E-08		1.80E-03	9.84E-01		2.78E-02	7.68E-01		-4.86E-01	1.66E-10		Unigene13031_All//gi|30696612|ref|NP_200364.2|//1.00E-116//C2 domain-containing protein [Arabidopsis thaliana] >gi|42573678|ref|NP_974935.1| C2 domain-containing protein [Arabidopsis thaliana] >gi|42573680|ref|NP_974936.1| C2 domain-containing protein [Arabidopsis thaliana] >gi|57222230|gb|AAW39022.1| At5g55530 [Arabidopsis thaliana] >gi|59958302|gb|AAX12861.1| At5g55530 [Arabidopsis thaliana]	Unigene13031_All//4.00E-102//AT5G55530| C2 domain-containing protein	Unigene13031_All//0.00E+00//TC171360				nr -
Unigene13037_All	590	6.12	5.58	9.48	7.94	8.05	5.21	7.74	4.04	2.70	-1.32E-01	6.81E-01		6.31E-01	1.62E-02		2.13E-02	9.51E-01		-6.09E-01	2.93E-02		-9.39E-01	2.09E-04		-1.52E+00	8.61E-09	Down			Unigene13037_All//3.00E-120//gi|21098285|gb|BQ410598.1|BQ410598				
Unigene13038_All	916	5.20	7.69	5.12	5.06	5.79	3.06	3.28	3.19	1.57	5.65E-01	1.06E-02		-2.30E-02	9.55E-01		1.95E-01	5.34E-01		-7.26E-01	8.91E-03		-3.71E-02	9.30E-01		-1.07E+00	7.05E-04	Down			Unigene13038_All//0.00E+00//gi|13247628|gb|BF271411.2|BF271411				
Unigene13039_All	2490	88.74	54.52	87.57	37.21	44.02	47.10	12.24	32.50	10.30	-7.03E-01	2.96E-87		-1.90E-02	6.43E-01		2.42E-01	1.15E-07		3.40E-01	1.02E-13		1.41E+00	1.26E-122	Up	-2.49E-01	4.22E-03		Unigene13039_All//gi|195536980|dbj|BAG68210.1|//3.00E-80//lectin receptor kinase-like protein [Nicotiana benthamiana]	Unigene13039_All//1.00E-75//AT5G03140| lectin protein kinase family protein	Unigene13039_All//0.00E+00//TC136605		ko04626|Plant-pathogen interaction	GO:0006464//GO:0016301//GO:0030246//GO:0032559//GO:0044464	nr +

Unigene13042_All	1617	11.03	7.80	8.73	2.28	3.39	5.25	0.29	0.49	0.34	-5.00E-01	1.32E-04		-3.38E-01	1.51E-02		5.71E-01	2.25E-02		1.20E+00	2.42E-09	Up	7.72E-01	2.88E-01		2.62E-01	7.46E-01		Unigene13042_All//gi|125863280|gb|ABN58427.1|//1.00E-169//inducer of CBF expression 1 [Populus trichocarpa]	Unigene13042_All//7.00E-67//AT3G26744| ICE1 (INDUCER OF CBF EXPRESSION 1); DNA binding / transcription activator/ transcription factor	Unigene13042_All//0.00E+00//TC154950	bHLH	ko04626|Plant-pathogen interaction	GO:0009409//GO:0010556//GO:0030528	nr -
Unigene13043_All	1216	5.72	13.42	9.63	1.02	3.12	1.56	0.00	0.00	0.00	1.23E+00	6.07E-17	Up	7.52E-01	1.20E-05		1.60E+00	5.37E-07	Up	6.07E-01	2.23E-01		null	null		null	null		Unigene13043_All//gi|125863280|gb|ABN58427.1|//1.00E-146//inducer of CBF expression 1 [Populus trichocarpa]	Unigene13043_All//5.00E-54//AT3G26744| ICE1 (INDUCER OF CBF EXPRESSION 1); DNA binding / transcription activator/ transcription factor	Unigene13043_All//0.00E+00//TC154950	bHLH	ko04626|Plant-pathogen interaction	GO:0003676//GO:0009409//GO:0010374//GO:0010468//GO:0010557//GO:0030528//GO:0043231	nr +
Unigene13045_All	2447	3.83	8.78	5.79	7.29	4.24	12.70	21.49	20.45	180.16	1.20E+00	3.24E-21	Up	5.97E-01	1.07E-04		-7.83E-01	8.24E-11		8.01E-01	5.76E-17		-7.22E-02	3.70E-01		3.07E+00	0.00E+00	Up	Unigene13045_All//gi|5732076|gb|AAD48975.1|AF162444_7//0.00E+00//contains similarity to Pfam family PF00070 - Pyridine nucleotide-disulphide oxidoreductase class-I; score=26.1, E=0.0008, N=1 [Arabidopsis thaliana] >gi|7267261|emb|CAB81044.1|AT4g05020 [Arabidopsis thaliana]	Unigene13045_All//0.00E+00//AT4G05020| NDB2 (NAD(P)H dehydrogenase B2); FAD binding / disulfide oxidoreductase/ oxidoreductase	Unigene13045_All//0.00E+00//TC138233		ko00190|Oxidative phosphorylation	GO:0005743//GO:0008152//GO:0030554//GO:0046872//GO:0050136	nr -
Unigene13046_All	946	1.77	0.05	0.00	3.79	2.77	1.05	0.58	1.15	3.71	-5.05E+00	1.72E-08	Down	-1.08E+01	3.83E-09	Down	-4.55E-01	1.64E-01		-1.85E+00	1.10E-07	Down	9.83E-01	9.75E-02		2.67E+00	2.67E-13	Up			Unigene13046_All//0.00E+00//TC175977				
Unigene13048_All	1152	1.54	1.54	0.60	8.43	9.57	3.61	2.42	4.54	3.42	-4.50E-03	9.89E-01		-1.36E+00	1.01E-02		1.82E-01	3.51E-01		-1.23E+00	4.80E-11	Down	9.05E-01	1.13E-04		4.99E-01	6.29E-02		Unigene13048_All//gi|18406605|ref|NP_566024.1|//1.00E-89//ARAC9; GTP binding [Arabidopsis thaliana] >gi|51701867|sp|Q9XGU0.1|RAC9_ARATH RecName: Full=Rac-like GTP-binding protein ARAC9; AltName: Full=GTPase protein ROP8; Flags: Precursor >gi|5381420|gb|AAD42972.1|AF156896_1 rac-like protein ARAC9 [Arabidopsis thaliana] >gi|105829866|gb|ABF74706.1|At2g44690 [Arabidopsis thaliana]	Unigene13048_All//2.00E-85//AT2G44690| ARAC9; GTP binding	Unigene13048_All//0.00E+00//TC147928		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity	GO:0004620//GO:0006810//GO:0016020//GO:0032561//GO:0035556//GO:0044424	nr -
Unigene13049_All	788	0.80	0.64	0.14	4.80	4.24	1.95	0.16	0.48	0.30	-3.09E-01	7.01E-01		-2.56E+00	2.72E-02		-1.81E-01	6.08E-01		-1.30E+00	4.17E-05	Down	1.57E+00	1.95E-01		9.14E-01	5.42E-01				Unigene13049_All//0.00E+00//TC175977				
Unigene13050_All	1430	0.88	0.25	0.63	1.74	1.81	1.26	0.59	1.26	1.50	-1.82E+00	5.22E-03		-4.72E-01	4.42E-01		5.22E-02	9.16E-01		-4.63E-01	2.77E-01		1.09E+00	1.32E-02		1.35E+00	6.13E-04	Up	Unigene13050_All//gi|18406605|ref|NP_566024.1|//2.00E-83//ARAC9; GTP binding [Arabidopsis thaliana] >gi|51701867|sp|Q9XGU0.1|RAC9_ARATH RecName: Full=Rac-like GTP-binding protein ARAC9; AltName: Full=GTPase protein ROP8; Flags: Precursor >gi|5381420|gb|AAD42972.1|AF156896_1 rac-like protein ARAC9 [Arabidopsis thaliana] >gi|105829866|gb|ABF74706.1|At2g44690 [Arabidopsis thaliana]	Unigene13050_All//2.00E-82//AT2G44690| ARAC9; GTP binding	Unigene13050_All//0.00E+00//gi|109881824|gb|DW510794.1|DW510794		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity	GO:0004620//GO:0006810//GO:0016020//GO:0032561//GO:0035556//GO:0044424	nr +
Unigene13052_All	877	11.51	8.03	10.14	13.52	12.37	11.28	10.70	7.86	3.77	-5.20E-01	3.93E-03		-1.83E-01	3.83E-01		-1.28E-01	5.21E-01		-2.61E-01	1.40E-01		-4.45E-01	8.44E-03		-1.51E+00	6.00E-17	Down	Unigene13052_All//gi|42567425|ref|NP_195289.3|//1.00E-54//ATSERAT3;2 (Serine acetyltransferase 3;2); acetyltransferase/ serine O-acetyltransferase [Arabidopsis thaliana] >gi|75162049|sp|Q8W288.1|SAT4_ARATH RecName: Full=Serine acetyltransferase 4; Short=AtSAT-4; Short=AtSERAT3;2 >gi|17225592|gb|AAL37489.1|AF331847_1 serine acetyltransferase [Arabidopsis thaliana]	Unigene13052_All//6.00E-56//AT4G35640| ATSERAT3;2 (Serine acetyltransferase 3;2); acetyltransferase/ serine O-acetyltransferase	Unigene13052_All//0.00E+00//DT048231		ko00270|Cysteine and methionine metabolism//ko00920|Sulfur metabolism	GO:0006563//GO:0006790//GO:0016412//GO:0044444	nr +
Unigene13053_All	1635	3.30	3.87	4.01	3.38	3.73	4.14	3.78	3.07	1.68	2.33E-01	3.63E-01		2.81E-01	2.63E-01		1.41E-01	6.10E-01		2.93E-01	2.32E-01		-3.00E-01	1.87E-01		-1.17E+00	5.05E-08	Down	Unigene13053_All//gi|42567425|ref|NP_195289.3|//1.00E-128//ATSERAT3;2 (Serine acetyltransferase 3;2); acetyltransferase/ serine O-acetyltransferase [Arabidopsis thaliana] >gi|75162049|sp|Q8W288.1|SAT4_ARATH RecName: Full=Serine acetyltransferase 4; Short=AtSAT-4; Short=AtSERAT3;2 >gi|17225592|gb|AAL37489.1|AF331847_1 serine acetyltransferase [Arabidopsis thaliana]	Unigene13053_All//5.00E-124//AT4G35640| ATSERAT3;2 (Serine acetyltransferase 3;2); acetyltransferase/ serine O-acetyltransferase	Unigene13053_All//0.00E+00//TC146387		ko00270|Cysteine and methionine metabolism//ko00920|Sulfur metabolism	GO:0006563//GO:0016412//GO:0044424	nr +
Unigene13054_All	1725	35.64	15.74	33.03	68.99	66.30	59.56	52.04	8.21	20.16	-1.18E+00	3.65E-58	Down	-1.10E-01	1.55E-01		-5.75E-02	3.07E-01		-2.12E-01	4.60E-06		-2.66E+00	0.00E+00	Down	-1.37E+00	4.84E-134	Down	Unigene13054_All//gi|226505252|ref|NP_001149360.1|//1.00E-100//LOC100282984 [Zea mays] >gi|195626644|gb|ACG35152.1|harpin-induced protein [Zea mays]	Unigene13054_All//2.00E-43//AT1G45688| unknown protein	Unigene13054_All//0.00E+00//TC148859				nr +
Unigene13055_All	1802	7.46	3.80	2.07	8.90	4.38	7.47	25.06	26.95	23.10	-9.75E-01	5.60E-10		-1.85E+00	3.09E-24	Down	-1.02E+00	3.49E-15	Down	-2.53E-01	8.73E-02		1.05E-01	1.76E-01		-1.17E-01	1.21E-01		Unigene13055_All//gi|223452436|gb|ACM89545.1|//1.00E-149//calmodulin-binding receptor-like cytoplasmic kinase [Glycine max]	Unigene13055_All//1.00E-135//AT2G11520| CRCK3; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene13055_All//0.00E+00//TC158519		ko04626|Plant-pathogen interaction		nr +
Unigene13057_All	1370	3.74	1.74	1.24	28.83	30.36	10.02	7.50	3.42	7.33	-1.11E+00	4.12E-05	Down	-1.59E+00	7.17E-08	Down	7.46E-02	4.70E-01		-1.52E+00	3.17E-60	Down	-1.13E+00	7.60E-12	Down	-3.33E-02	8.53E-01		Unigene13057_All//gi|15222452|ref|NP_177136.1|//8.00E-85//ATHB13; DNA binding / sequence-specific DNA binding / transcription factor [Arabidopsis thaliana] >gi|118573191|sp|Q8LC03.2|ATB13_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-13; AltName: Full=Homeodomain transcription factor ATHB-13; AltName: Full=HD-ZIP protein ATHB-13 >gi|6614295|gb|AAF20996.1|AF208044_1 homeodomain leucine-zipper protein ATHB13 [Arabidopsis thaliana] >gi|12325190|gb|AAG52541.1|AC013289_8 homeobox gene 13 protein; 11736-10437 [Arabidopsis thaliana] >gi|15982929|gb|AAL09811.1|At1g69780/T6C23_2 [Arabidopsis thaliana] >gi|22137260|gb|AAM91475.1|At1g69780/T6C23_2 [Arabidopsis thaliana]	Unigene13057_All//8.00E-76//AT1G69780| ATHB13; DNA binding / sequence-specific DNA binding / transcription factor	Unigene13057_All//0.00E+00//TC153217	HB		GO:0001071//GO:0003006//GO:0003677//GO:0006351//GO:0009887//GO:0010068//GO:0034285//GO:0043231	nr -
Unigene13058_All	1355	3.75	1.83	1.96	30.29	29.15	12.03	5.02	0.71	3.35	-1.03E+00	1.29E-04	Down	-9.31E-01	8.31E-04		-5.55E-02	5.97E-01		-1.33E+00	4.48E-51	Down	-2.82E+00	3.61E-26	Down	-5.84E-01	2.63E-03		Unigene13058_All//gi|15222452|ref|NP_177136.1|//3.00E-92//ATHB13; DNA binding / sequence-specific DNA binding / transcription factor [Arabidopsis thaliana] >gi|118573191|sp|Q8LC03.2|ATB13_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-13; AltName: Full=Homeodomain transcription factor ATHB-13; AltName: Full=HD-ZIP protein ATHB-13 >gi|6614295|gb|AAF20996.1|AF208044_1 homeodomain leucine-zipper protein ATHB13 [Arabidopsis thaliana] >gi|12325190|gb|AAG52541.1|AC013289_8 homeobox gene 13 protein; 11736-10437 [Arabidopsis thaliana] >gi|15982929|gb|AAL09811.1|At1g69780/T6C23_2 [Arabidopsis thaliana] >gi|22137260|gb|AAM91475.1|At1g69780/T6C23_2 [Arabidopsis thaliana]	Unigene13058_All//1.00E-90//AT1G69780| ATHB13; DNA binding / sequence-specific DNA binding / transcription factor	Unigene13058_All//0.00E+00//TC153217	HB		GO:0001071//GO:0003006//GO:0003677//GO:0006351//GO:0009887//GO:0010068//GO:0034285//GO:0043231	nr +
Unigene13061_All	2146	20.16	8.64	14.59	43.11	46.00	41.88	26.14	16.69	19.86	-1.22E+00	1.54E-43	Down	-4.67E-01	1.82E-08		9.39E-02	1.01E-01		-4.16E-02	5.63E-01		-6.47E-01	4.56E-24		-3.96E-01	1.15E-10		Unigene13061_All//gi|7671528|emb|CAB89490.1|//0.00E+00//CRK1 protein [Beta vulgaris subsp. vulgaris] >gi|7688002|emb|CAB88665.1| CRK1 protein [Beta vulgaris subsp. vulgaris]	Unigene13061_All//0.00E+00//AT1G54610| protein kinase family protein	Unigene13061_All//0.00E+00//TC148568			GO:0004674//GO:0006464//GO:0016020//GO:0032559//GO:0043231	nr +
Unigene13064_All	1192	9.61	6.12	4.96	51.11	50.38	50.43	73.99	28.58	30.21	-6.51E-01	9.94E-05		-9.55E-01	5.99E-08		-2.07E-02	8.41E-01		-1.93E-02	8.20E-01		-1.37E+00	1.03E-128	Down	-1.29E+00	1.08E-120	Down	Unigene13064_All//gi|15223288|ref|NP_171613.1|//1.00E-104//AtPPa1 (Arabidopsis thaliana pyrophosphorylase 1); inorganic diphosphatase >gi|15450699|gb|AAK96621.1|At1g01050/T25K16_5 [Arabidopsis thaliana] >gi|16323129|gb|AAL15299.1|At1g01050/T25K16_5 [Arabidopsis thaliana] >gi|24797046|gb|AAN64535.1|At1g01050/T25K16_5 [Arabidopsis thaliana]	Unigene13064_All//9.00E-106//AT1G01050| AtPPa1 (Arabidopsis thaliana pyrophosphorylase 1); inorganic diphosphatase	Unigene13064_All//0.00E+00//TC148742		ko00190|Oxidative phosphorylation		nr +
Unigene13065_All	1520	2.51	1.23	2.52	19.07	12.98	13.10	7.51	2.25	2.49	-1.03E+00	1.16E-03		5.50E-03	1.00E+00		-5.55E-01	1.40E-09		-5.42E-01	2.52E-08		-1.74E+00	4.03E-24	Down	-1.59E+00	4.05E-22	Down	Unigene13065_All//gi|224102121|ref|XP_002312555.1|//0.00E+00//argonaute protein group [Populus trichocarpa] >gi|222852375|gb|EEE89922.1|argonaute protein group [Populus trichocarpa]	Unigene13065_All//0.00E+00//AT5G43810| ZLL (ZWILLE); translation initiation factor	Unigene13065_All//0.00E+00//gi|78334019|gb|DT554293.1|DT554293			GO:0008135//GO:0019827//GO:0034660//GO:0044424	nr -
Unigene13067_All	447	2.11	1.59	2.38	3.57	5.08	4.04	2.08	5.24	3.03	-4.09E-01	5.67E-01		1.77E-01	7.74E-01		5.12E-01	2.55E-01		1.81E-01	7.19E-01		1.33E+00	5.14E-04	Up	5.42E-01	2.85E-01		Unigene13067_All//gi|224103131|ref|XP_002312937.1|//3.00E-14//f-box family protein [Populus trichocarpa] >gi|222849345|gb|EEE86892.1| f-box family protein [Populus trichocarpa]	Unigene13067_All//9.00E-14//AT2G17020| F-box family protein (FBL10)				GO:0003824//GO:0019941//GO:0043231	nr -

Unigene13069_All	509	18.91	15.53	8.26	23.10	19.55	26.26	32.98	23.07	18.94	-2.84E-01	1.38E-01		-1.19E+00	1.86E-09	Down	-2.40E-01	1.66E-01		1.85E-01	2.97E-01		-5.15E-01	1.94E-05		-8.00E-01	3.01E-11		Unigene13069_All//gi|50198801|gb|AAT70434.1|/5.00E-21//At2g17990 [Arabidopsis thaliana] >gi|56121928|gb|AAV74245.1| At2g17990 [Arabidopsis thaliana]	Unigene13069_All//3.00E-22//AT2G17990| LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is; kinectin-related (TAIR:AT5G66250.3); Has 6110 Blast hits to 4860 proteins in 486 species: Archae - 160; Bacteria - 541; Metazoa - 3188; Fungi - 404; Plants - 270; Viruses - 41; Other Eukaryotes - 1506 (source: NCBI BLink).	Unigene13069_All//0.00E+00//gi|164271715|gb|ES800016.1|ES800016			GO:0016772//GO:0043231	nr -
Unigene13074_All	594	5.28	2.39	6.63	2.77	6.72	2.66	0.93	0.84	1.01	-1.15E+00	1.33E-03		3.28E-01	3.33E-01		1.28E+00	1.99E-05	Up	-5.66E-02	9.28E-01		-1.32E-01	8.80E-01		1.21E-01	8.88E-01		Unigene13074_All//gi|195626524|gb|ACG35092.1|/2.00E-10//2-cys peroxiredoxin BAS1 [Zea mays]	Unigene13074_All//9.00E-10//AT5G06290| 2-Cys Prx B (2-Cysteine peroxiredoxin B); antioxidant/ peroxiredoxin	Unigene13074_All//6.00E-35//TC139561			GO:0016491//GO:0043231	nr +
Unigene13079_All	341	61.68	21.40	87.29	7.74	13.43	11.26	0.00	0.00	0.00	-1.53E+00	5.84E-30	Down	5.01E-01	8.57E-07		7.95E-01	3.55E-03		5.40E-01	9.43E-02		null	null		null	null		Unigene13079_All//gi|54645911|gb|AAV36561.1|/4.00E-08//RD22-like protein [Vitis vinifera]	Unigene13079_All//2.00E-135//ES815964				nr +
Unigene1308_All	2338	1.41	1.60	1.98	1.60	2.67	2.63	0.94	0.89	2.08	1.86E-01	5.95E-01		4.91E-01	9.78E-02		7.38E-01	1.10E-03		7.17E-01	2.43E-03		-7.33E-02	8.60E-01		1.14E+00	2.81E-06	Up	Unigene1308_All//gi|297792239|ref|XP_002864004.1|//1.00E-177//xylulose kinase [Arabidopsis lyrata subsp. lyrata] >gi|297309839|gb|EFH60263.1| xylulose kinase [Arabidopsis lyrata subsp. lyrata]	Unigene1308_All//6.00E-179//AT5G49650| xylulose kinase, putative	Unigene1308_All//0.00E+00//TC131804		ko00040|Pentose and glucuronate interconversions		nr +
Unigene13081_All	3045	11.60	6.06	11.47	4.38	5.04	3.53	0.96	0.84	6.14	-9.37E-01	2.14E-23		-1.58E-02	8.88E-01		2.02E-01	1.96E-01		-3.13E-01	5.05E-02		-1.94E-01	6.12E-01		2.68E+00	6.57E-68	Up	Unigene13081_All//gi|130582|sp|P10978.1|POLX_TOBAC//1.00E-130//RecName: Full=Retrovirus-related Pol polyprotein from transposon TNT 1-94; Includes: RecName: Full=Protease; Includes: RecName: Full=Reverse transcriptase; Includes: RecName: Full=Endonuclease	Unigene13081_All//3.00E-39//AT4G23160| protein kinase family protein	Unigene13081_All//0.00E+00//TC173567				nr -
Unigene13084_All	1576	24.90	8.39	6.89	43.78	38.98	49.35	81.77	30.02	39.28	-1.57E+00	1.56E-57	Down	-1.85E+00	4.27E-70	Down	-1.67E-01	7.67E-03		1.73E-01	4.49E-03		-1.45E+00	4.09E-203	Down	-1.06E+00	5.37E-128	Down	Unigene13084_All//gi|17367847|sp|Q9XF97.1|RL4_PRUAR//0.00E+00//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32206.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene13084_All//3.00E-178//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)	Unigene13084_All//0.00E+00//TC150210		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0030312//GO:0031981	nr -
Unigene13086_All	2171	16.15	15.75	17.81	10.05	7.39	20.45	75.10	77.33	51.64	-3.55E-02	7.23E-01		1.41E-01	1.47E-01		-4.43E-01	4.65E-05		1.02E+00	4.88E-36	Up	4.24E-02	3.37E-01		-5.40E-01	5.35E-51		Unigene13086_All//gi|224127866|ref|XP_002320183.1|/0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222860956|gb|EEE98498.1| GH3 family protein [Populus trichocarpa]	Unigene13086_All//0.00E+00//AT2G46370| JAR1 (JASMONATE RESISTANT 1); ATP binding / adenylyltransferase/ catalytic/ jasmonate-amino synthetase	Unigene13086_All//0.00E+00//TC152052			GO:0002218//GO:0006800//GO:0007602//GO:0009611//GO:0009639//GO:0009725//GO:0009814//GO:0010118//GO:0016779//GO:0016881//GO:0031407//GO:0032559//GO:0043231	nr +
Unigene13087_All	2705	7.00	7.29	5.24	15.78	14.25	15.58	25.59	15.73	11.06	5.75E-02	6.71E-01		-4.19E-01	1.54E-03		-1.48E-01	8.72E-02		-1.88E-02	8.58E-01		-7.02E-01	6.73E-34		-1.21E+00	1.17E-85	Down	Unigene13087_All//gi|297606074|ref|NP_001057949.2|//0.00E+00//Os06g0585200 [Oryza sativa Japonica Group] >gi|255677176|dbj|BAF19863.2| Os06g0585200 [Oryza sativa Japonica Group]	Unigene13087_All//3.00E-120//AT3G28720| unknown protein	Unigene13087_All//0.00E+00//TC171662			GO:0031410	nr +
Unigene1309_All	476	6.16	7.45	6.94	5.02	7.23	7.97	2.49	2.20	0.25	2.76E-01	4.08E-01		1.72E-01	6.15E-01		5.26E-01	1.22E-01		6.66E-01	3.68E-02		-1.80E-01	7.44E-01		-3.31E+00	4.89E-06	Down			Unigene1309_All//2.00E-133//gi|21100098|gb|BQ412411.1|BQ412411				
Unigene13091_All	2014	2.78	2.84	3.33	5.61	6.10	4.24	1.95	1.29	0.89	3.24E-02	9.12E-01		2.61E-01	3.02E-01		1.21E-01	5.61E-01		-4.06E-01	1.75E-02		-6.02E-01	2.95E-02		-1.13E+00	3.23E-05	Down	Unigene13091_All//gi|297811507|ref|XP_002873637.1|/6.00E-11//zinc knuckle (CCHC-type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319474|gb|EFH49896.1| zinc knuckle (CCHC-type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13091_All//3.00E-12//AT5G13920| zinc knuckle (CCHC-type) family protein	Unigene13091_All//0.00E+00//gi|13350924|gb|BG441272.1|BG441272		ko03410|Base excision repair		nr -
Unigene13092_All	1193	5.70	4.42	3.35	0.75	3.18	2.08	96.43	84.47	53.36	-3.68E-01	1.12E-01		-7.68E-01	1.04E-03		2.08E+00	1.13E-09	Up	1.47E+00	4.35E-04	Up	-1.91E-01	1.07E-05		-8.54E-01	3.81E-80		Unigene13092_All//gi|224129714|ref|XP_002320653.1|/1.00E-118//flavine-containing monoxygenase [Populus trichocarpa] >gi|222861426|gb|EEE98968.1| flavine-containing monoxygenase [Populus trichocarpa]	Unigene13092_All//3.00E-88//AT1G48910| YUCCA; FAD binding / monooxygenase/ oxidoreductase	Unigene13092_All//0.00E+00//TC150206		ko00380|Tryptophan metabolism	GO:0000166//GO:0004497//GO:0009653//GO:0031410	nr +
Unigene13093_All	1648	2.13	2.09	0.65	0.76	1.40	0.71	71.58	59.57	30.60	-2.49E-02	9.58E-01		-1.72E+00	3.68E-06	Down	8.90E-01	3.33E-02		-8.49E-02	9.00E-01		-2.65E-01	3.57E-10		-1.23E+00	1.99E-148	Down	Unigene13093_All//gi|224129714|ref|XP_002320653.1|/1.00E-164//flavine-containing monoxygenase [Populus trichocarpa] >gi|222861426|gb|EEE98968.1| flavine-containing monoxygenase [Populus trichocarpa]	Unigene13093_All//9.00E-115//AT1G48910| YUCCA; FAD binding / monooxygenase/ oxidoreductase	Unigene13093_All//0.00E+00//TC150206		ko00380|Tryptophan metabolism		nr -
Unigene13096_All	1721	34.48	12.75	23.42	87.73	66.83	59.47	48.08	23.70	16.69	-1.44E+00	5.31E-76	Down	-5.58E-01	1.84E-15		-3.93E-01	1.66E-25		-5.61E-01	1.94E-43		-1.02E+00	1.17E-75	Down	-1.53E+00	1.13E-145	Down	Unigene13096_All//gi|297820184|ref|XP_002877975.1|/1.00E-92//transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297323813|gb|EFH54234.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene13096_All//1.00E-80//AT3G54390| transcription factor	Unigene13096_All//0.00E+00//gi|78333873|gb|DT554147.1|DT554147	Trihelix			nr +
Unigene13097_All	1289	23.70	87.50	43.29	20.13	33.13	34.83	11.58	23.77	31.62	1.88E+00	3.69E-211	Up	8.69E-01	3.92E-31		7.18E-01	4.29E-21		7.91E-01	9.81E-24		1.04E+00	3.00E-29	Up	1.45E+00	3.28E-66	Up	Unigene13097_All//gi|18414270|ref|NP_568123.1|//4.00E-78//nucleobase:cation symporter [Arabidopsis thaliana] >gi|14326525|gb|AAK60307.1|AF38571_1 AT5g03560/F12E4 [Arabidopsis thaliana] >gi|19548041|gb|AAL87384.1| AT5g03560/F12E4 [Arabidopsis thaliana]	Unigene13097_All//2.00E-75//AT5G03560| nucleobase:cation symporter	Unigene13097_All//0.00E+00//TC162360			GO:0015205	nr -
Unigene13103_All	1317	8.98	8.23	13.22	20.31	17.20	15.71	9.76	10.06	24.50	-1.25E-01	4.96E-01		5.58E-01	4.69E-05		-2.40E-01	2.23E-02		-3.71E-01	3.34E-04		4.38E-02	7.86E-01		1.33E+00	3.45E-46	Up	Unigene13103_All//gi|224141963|ref|XP_002324330.1|/1.00E-87//chorismate mutase [Populus trichocarpa] >gi|222865764|gb|EEF02895.1| chorismate mutase [Populus trichocarpa]	Unigene13103_All//1.00E-81//AT5G10870| ATCM2 (chorismate mutase 2); chorismate mutase	Unigene13103_All//0.00E+00//TC147930		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0004601//GO:0008652//GO:0016866//GO:0043231//GO:0043648//GO:0044444	nr -
Unigene13106_All	1990	53.61	8.58	29.92	178.98	153.83	273.61	46.83	68.68	66.38	-2.64E+00	2.73E-306	Down	-8.42E-01	7.06E-56		-2.18E-01	8.53E-20		6.12E-01	9.76E-181		5.53E-01	2.07E-43		5.04E-01	1.76E-36		Unigene13106_All//gi|283488495|gb|ADB24769.1|/0.00E+00//UDP-D-glucuronic acid 4-epimerase [Gossypium hirsutum]	Unigene13106_All//0.00E+00//AT3G23820| GAE6 (UDP-D-GLUCURONATE 4-EPIMERASE 6); UDP-glucuronate 4-epimerase/ catalytic	Unigene13106_All//0.00E+00//TC148574		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0006139//GO:0016857//GO:0048037	nr -
Unigene13107_All	3582	2.85	5.79	3.61	10.56	11.65	6.73	15.64	17.50	10.01	1.02E+00	4.78E-16	Up	3.43E-01	4.14E-02		1.43E-01	1.11E-01		-6.49E-01	1.71E-14		1.62E-01	9.11E-03		-6.44E-01	1.69E-24		Unigene13107_All//gi|24461849|gb|AN62336.1|AF506028_3/0.00E+00//CTV.2 [Citrus trifoliata]	Unigene13107_All//0.00E+00//AT1G15750| TPL (TOPLESS); protein binding / protein homodimerization/ transcription repressor	Unigene13107_All//0.00E+00//TC173967		ko03040|Spliceosome	GO:0003002//GO:0003006//GO:0009725//GO:0023033//GO:0030528//GO:0042802//GO:0043231//GO:0044444	nr +
Unigene13112_All	2697	3.26	2.93	1.07	5.54	5.87	4.15	6.74	1.84	2.70	-1.53E-01	4.70E-01		-1.61E+00	2.60E-13	Down	8.40E-02	6.17E-01		-4.16E-01	3.87E-03		-1.87E+00	5.40E-42	Down	-1.32E+00	2.38E-26	Down	Unigene13112_All//gi|238481396|ref|NP_198107.2|/0.00E+00//ATP binding / microtubule motor [Arabidopsis thaliana]	Unigene13112_All//0.00E+00//AT5G27550| ATP binding / microtubule motor	Unigene13112_All//0.00E+00//TC162003			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr -
Unigene13115_All	1174	1.07	2.76	0.95	2.29	3.08	2.42	7.82	119.30	6.35	1.37E+00	1.42E-04	Up	-1.67E-01	7.75E-01		4.27E-01	2.13E-01		8.10E-02	8.51E-01		3.93E+00	0.00E+00	Up	-3.01E-01	7.78E-02		Unigene13115_All//gi|269838632|gb|ACZ48681.1|/3.00E-44//Bcl-2-associated athanogene-like protein [Vitis vinifera]	Unigene13115_All//7.00E-18//AT1G12060| ATBAG5 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 5); protein binding	Unigene13115_All//0.00E+00//TC152126			GO:0005488//GO:0006915	nr -
Unigene13116_All	1226	0.81	0.91	0.56	1.99	1.66	1.58	1.07	19.19	1.56	1.65E-01	7.79E-01		-5.22E-01	4.60E-01		-2.65E-01	5.39E-01		-3.30E-01	4.62E-01		4.17E+00	1.10E-124	Up	5.45E-01	1.86E-01		Unigene13116_All//gi|269838632|gb|ACZ48681.1|/4.00E-43//Bcl-2-associated athanogene-like protein [Vitis vinifera]	Unigene13116_All//3.00E-18//AT1G12060| ATBAG5 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 5); protein binding	Unigene13116_All//0.00E+00//TC152126			GO:0005488	nr -
Unigene13117_All	1137	19.47	9.63	11.76	32.38	26.53	32.29	39.90	21.17	18.75	-1.02E+00	5.52E-17	Down	-7.28E-01	1.64E-09		-2.87E-01	6.13E-04		-3.70E-03	9.67E-01		-9.14E-01	5.55E-35		-1.09E+00	7.36E-48	Down	Unigene13117_All//gi|15221298|ref|NP_177596.1|//1.00E-110//NRP1 (NAP1-RELATED PROTEIN 1); DNA binding / chromatin binding / histone binding [Arabidopsis thaliana] >gi|14326533|gb|AAK60311.1|AF38572_1 At1g74560/F1M20_24 [Arabidopsis thaliana] >gi|19548045|gb|AAL87386.1| At1g74560/F1M20_24 [Arabidopsis thaliana]	Unigene13117_All//2.00E-99//AT1G74560| NRP1 (NAP1-RELATED PROTEIN 1); DNA binding / chromatin binding / histone binding	Unigene13117_All//0.00E+00//TC130464			GO:0034728//GO:0043231	nr -
Unigene13118_All	1263	5.34	2.61	4.51	10.29	9.92	9.26	12.92	6.29	6.78	-1.04E+00	6.88E-06	Down	-2.44E-01	3.40E-01		-5.28E-02	8.03E-01		-1.53E-01	4.05E-01		-1.04E+00	5.04E-16	Down	-9.30E-01	6.72E-14		Unigene13118_All//gi|15221298|ref|NP_177596.1|//1.00E-111//NRP1 (NAP1-RELATED PROTEIN 1); DNA binding / chromatin binding / histone binding [Arabidopsis thaliana] >gi|14326533|gb|AAK60311.1|AF38572_1 At1g74560/F1M20_24 [Arabidopsis thaliana] >gi|19548045|gb|AAL87386.1| At1g74560/F1M20_24 [Arabidopsis thaliana]	Unigene13118_All//1.00E-88//AT1G74560| NRP1 (NAP1-RELATED PROTEIN 1); DNA binding / chromatin binding / histone binding	Unigene13118_All//0.00E+00//TC137415			GO:0034728//GO:0043231	nr +
Unigene13119_All	2211	0.19	0.50	2.10	6.20	6.15	14.83	73.37	216.86	147.16	1.41E+00	3.61E-02		3.47E+00	3.97E-17	Up	-1.03E-02	9.50E-01		1.26E+00	5.63E-37	Up	1.56E+00	0.00E+00	Up	1.00E+00	1.14E-293	Up	Unigene13119_All//gi|115481730|ref|NP_001064458.1|//0.00E+00//Os10g0370500 [Oryza sativa Japonica Group] >gi|19920182|gb|AAN08614.1|AC10731_5 Putative Glucan 1,3-beta-glucosidase precursor [Oryza sativa Japonica Group] >gi|20043013|gb|AAN08821.1|AC11333_5_1 Putative Glucan 1,3-beta-glucosidase precursor [Oryza sativa Japonica Group] >gi|31431628|gb|AAP53379.1| Cellulase containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639067|dbj|BAF26372.1| Os10g0370500 [Oryza sativa Japonica Group]	Unigene13119_All//3.00E-09//BF272991			ko00500|Starch and sucrose metabolism	GO:0016798//GO:0043167//GO:0044238	nr -

Unigene1312_All	828	6.57	5.81	7.72	9.20	8.48	8.51	3.06	1.26	2.79	-1.77E-01	5.24E-01			2.32E-01	3.85E-01		-1.18E-01	6.20E-01			-1.13E-01	6.47E-01			-1.28E+00	4.33E-04	Down	-1.35E-01	7.01E-01				Unigene1312_All//8.00E-29//TC145334				
Unigene13123_All	1699	5.45	6.98	6.58	19.94	21.52	19.30	7.76	3.89	3.78	3.57E-01	3.42E-02			2.72E-01	1.45E-01		1.11E-01	2.91E-01			-4.70E-02	6.96E-01			-9.98E-01	2.53E-12		-1.04E+00	1.49E-13	Down	Unigene13123_All//gi|297797663|ref|XP_002866716.1|//0.00E+00//phospholipase C [Arabidopsis lyrata subsp. lyrata] >gi|297312251|gb|EFH42975.1|phospholipase C [Arabidopsis lyrata subsp. lyrata]	Unigene13123_All//1.00E-179//AT5G67130| phospholipase C/ phosphoric diester hydrolase	Unigene13123_All//0.00E+00//TC143170			GO:0004620//GO:0042578//GO:0044238	nr -
Unigene13125_All	2613	3.58	1.36	2.32	19.73	14.67	18.08	11.76	1.87	4.18	-1.40E+00	3.57E-12	Down	-6.26E-01	1.33E-03		-4.28E-01	1.71E-10			-1.26E-01	1.28E-01			-2.65E+00	2.18E-108	Down	-1.49E+00	6.30E-53	Down	Unigene13125_All//gi|115444741|ref|NP_001046150.1|//0.00E+00//Os02g0190500 [Oryza sativa Japonica Group] >gi|113535681|dbj|BAF08064.1|Os02g0190500 [Oryza sativa Japonica Group]	Unigene13125_All//0.00E+00//AT4G22130| SRF8 (STRUBBELIG-RECEPTOR FAMILY 8); ATP binding / kinase/ protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene13125_All//0.00E+00//TC157440		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene13126_All	1617	3.27	1.07	1.55	4.81	3.41	4.61	63.54	77.96	49.92	-1.62E+00	1.03E-08	Down	-1.08E+00	8.74E-05	Down	-4.96E-01	1.29E-02			-6.05E-02	7.92E-01			2.95E-01	4.37E-13		-3.48E-01	6.44E-15		Unigene13126_All//gi|3892714|emb|CAA22164.1|//1.00E-156//trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana] >gi|7269105|emb|CAB79214.1|trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana] >gi|62321206|dbj|BAD94370.1|trehalose-6-phosphate phosphatase - like protein [Arabidopsis thaliana] >gi|222422885|dbj|BAH19429.1|AT4G22590 [Arabidopsis thaliana]	Unigene13126_All//2.00E-160//AT4G12430| trehalose-6-phosphate phosphatase, putative	Unigene13126_All//4.00E-174//gi|18099857|gb|BM359111.1|BM359111		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0019203	nr +
Unigene13127_All	1928	1.79	36.53	2.90	9.64	14.29	15.18	18.77	21.61	122.55	4.35E+00	0.00E+00	Up	6.95E-01	7.94E-03		5.68E-01	3.00E-09			6.55E-01	1.82E-11			2.03E-01	8.03E-03		2.71E+00	0.00E+00	Up	Unigene13127_All//gi|85720766|gb|AB075833.1|//0.00E+00//1-aminocyclopropane-1-carboxylate synthase [Gossypium hirsutum]	Unigene13127_All//4.00E-180//AT4G11280| ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase	Unigene13127_All//0.00E+00//TC129594		ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016740//GO:0016846//GO:0048037	nr -
Unigene13128_All	3243	1.98	0.33	0.26	3.52	2.92	4.36	8.70	3.16	6.87	-2.60E+00	1.30E-18	Down	-2.92E+00	4.66E-20	Down	-2.69E-01	1.23E-01			3.09E-01	4.66E-02			-1.46E+00	9.77E-46	Down	-3.41E-01	1.35E-04		Unigene13128_All//gi|297835130|ref|XP_002885447.1|//0.00E+00//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331287|gb|EFH61706.1|transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13128_All//0.00E+00//AT3G21540| transducin family protein / WD-40 repeat family protein	Unigene13128_All//0.00E+00//TC172797		ko03040|Spliceosome	GO:0016740//GO:0019897//GO:0031981	nr +
Unigene1313_All	883	5.81	1.49	2.89	5.19	3.24	6.60	2.68	2.04	0.86	-1.96E+00	7.99E-11	Down	-1.00E+00	3.06E-04	Down	-6.81E-01	1.06E-02			3.46E-01	1.95E-01			-3.98E-01	3.10E-01		-1.65E+00	1.81E-05	Down			Unigene1313_All//0.00E+00//TC157247				
Unigene13130_All	2236	45.32	21.48	39.77	3.14	3.11	4.40	2.25	0.60	1.10	-1.08E+00	1.17E-82	Down	-1.89E-01	5.17E-04		-1.40E-02	9.62E-01			4.87E-01	7.75E-03			-1.91E+00	1.67E-12	Down	-1.03E+00	1.30E-05	Down	Unigene13130_All//gi|224108317|ref|XP_002314803.1|//0.00E+00//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222863843|gb|EEF00974.1|sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene13130_All//0.00E+00//AT1G23090| AST91 (SULFATE TRANSPORTER 91); sulfate transmembrane transporter	Unigene13130_All//0.00E+00//TC175397			GO:0015103//GO:0015291//GO:0015698//GO:0031224	nr +
Unigene13133_All	1525	14.55	36.08	18.19	27.96	37.51	36.84	29.61	46.10	55.09	1.31E+00	3.49E-61	Up	3.23E-01	2.90E-03		4.24E-01	3.66E-11			3.98E-01	4.92E-09			6.39E-01	3.18E-29		8.96E-01	2.54E-63		Unigene13133_All//gi|157955933|gb|AB906390.1|//1.00E-124//CBL3 [Gossypium hirsutum] >gi|157955939|gb|AB906393.1| CBL3 [Gossypium hirsutum]	Unigene13133_All//6.00E-116//AT4G26570| ATCBL3 (ARABIDOPSIS THALIANA CALCINEURIN B-LIKE 3); calcium ion binding	Unigene13133_All//0.00E+00//TC129653		ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene13134_All	1847	3.54	1.56	2.97	4.23	3.36	3.30	5.52	2.44	2.52	-1.18E+00	7.06E-07	Down	-2.54E-01	3.27E-01		-3.35E-01	1.12E-01			-3.59E-01	9.92E-02			-1.17E+00	2.19E-12	Down	-1.13E+00	4.74E-12	Down	Unigene13134_All//gi|79328173|ref|NP_001031908.1|//1.00E-170//transferase [Arabidopsis thaliana]	Unigene13134_All//8.00E-151//AT5G19485| transferase	Unigene13134_All//0.00E+00//TC132587			GO:0008135//GO:0008152//GO:0016772	nr +
Unigene13136_All	2585	1.98	2.08	0.84	4.43	4.94	5.35	10.16	20.18	10.50	6.69E-02	7.99E-01		-1.23E+00	1.37E-05	Down	1.57E-01	3.95E-01			2.71E-01	9.39E-02			9.90E-01	1.16E-45		4.72E-02	6.54E-01		Unigene13136_All//gi|193237591|dbj|BAG50072.1|//3.00E-84//transcription factor CPP [Lotus japonicus]	Unigene13136_All//4.00E-57//AT3G22760| SOL1; transcription factor	Unigene13136_All//0.00E+00//DT468558	CPP		GO:0009933//GO:0043231	nr +
Unigene13139_All	1597	0.07	258.61	20.84	3.43	23.91	89.11	20.17	88.15	111.88	1.19E+01	0.00E+00	Up	8.31E+00	3.96E-184	Up	2.80E+00	8.40E-135	Up	4.70E+00	0.00E+00	Up	2.13E+00	0.00E+00	Up	2.47E+00	0.00E+00	Up	Unigene13139_All//gi|296278600|gb|ADB04264.1|//4.00E-70//HB1 [Nicotiana benthamiana]	Unigene13139_All//2.00E-55//AT2G46680| ATHB-7 (ARABIDOPSIS THALIANA HOMEOBOX 7); transcription activator/ transcription factor	Unigene13139_All//0.00E+00//TC150407	HB		GO:0001071//GO:0003677//GO:0006351//GO:0006970//GO:0009755//GO:0010468//GO:0010557//GO:0030528//GO:0043231	nr -
Unigene13140_All	1804	4.90	2.67	2.45	31.01	24.20	10.11	9.35	4.70	5.48	-8.77E-01	7.23E-06		-1.00E+00	9.72E-07	Down	-3.58E-01	2.97E-08			-1.62E+00	1.05E-92	Down	-9.92E-01	2.30E-15		-7.72E-01	1.12E-10		Unigene13140_All//gi|240254664|ref|NP_182201.4|//2.00E-54//RNA binding / nucleic acid binding / nucleotide binding [Arabidopsis thaliana] >gi|63003880|gb|AAY25469.1|At2g46780 [Arabidopsis thaliana]	Unigene13140_All//8.00E-56//AT2G46780| RNA binding / nucleic acid binding / nucleotide binding	Unigene13140_All//0.00E+00//TC166825		ko03040|Spliceosome	GO:0003676	nr +
Unigene13144_All	1229	5.58	4.04	5.16	3.85	6.00	6.84	4.51	5.24	10.08	-4.65E-01	3.96E-02		-1.13E-01	6.31E-01		6.39E-01	1.93E-03			8.28E-01	2.59E-05			2.17E-01	3.58E-01		1.16E+00	5.53E-15	Up	Unigene13144_All//gi|157399678|gb|ABV53463.1|//2.00E-37//pseudo-response regulator 7 [Castanea sativa]	Unigene13144_All//31/AT5G02810| PRR7 (PSEUDO-RESPONSE REGULATOR 7); transcription regulator/ two-component response regulator	Unigene13144_All//0.00E+00//gi|78348771|gb|DT569045.1|DT569045		ko04712|Circadian rhythm - plant	GO:0003676//GO:0004871//GO:0006351//GO:0009628//GO:0023033//GO:0023060//GO:0030528//GO:0043231//GO:0048511	nr +
Unigene13148_All	1450	22.59	92.01	4.26	37.31	47.00	63.26	68.06	46.96	56.13	2.03E+00	5.48E-275	Up	-2.41E+00	1.23E-81	Down	3.33E-01	1.26E-08			7.62E-01	5.22E-45			-5.35E-01	6.81E-30		-2.78E-01	1.07E-09		Unigene13148_All//gi|3759184|dbj|BAA33810.1|//1.00E-132//phi-1 [Nicotiana tabacum]	Unigene13148_All//7.00E-122//AT4G08950| EXO (EXORDIUM)	Unigene13148_All//0.00E+00//TC133141				nr -
Unigene13149_All	1962	26.05	7.05	15.01	34.71	24.62	15.38	53.36	40.67	18.11	-1.89E+00	1.07E-96	Down	-7.96E-01	1.37E-24		-4.95E-01	8.06E-18			-1.17E+00	2.36E-69	Down	-3.92E-01	3.44E-18		-1.56E+00	7.12E-190	Down	Unigene13149_All//gi|87240487|gb|ABD32345.1|//1.00E-119//Octicosapeptide/Phox/BemIp [Medicago truncatula]	Unigene13149_All//5.00E-86//AT4G05150| octicosapeptide/Phox/BemIp (PB1) domain-containing protein	Unigene13149_All//0.00E+00//gi|78337274|gb|DT557548.1|DT557548				nr +
Unigene1315_All	3066	39.90	24.44	38.57	43.88	50.81	30.08	7.01	4.12	3.18	-7.07E-01	4.23E-49		-4.87E-02	3.98E-01		2.11E-01	2.47E-08			-5.45E-01	8.42E-37			-7.67E-01	8.34E-13		-1.14E+00	9.76E-25	Down	Unigene1315_All//gi|9945082|gb|AAG03119.1|AC004133_13//1.00E-128//F5A9.24 [Arabidopsis thaliana]	Unigene1315_All//8.00E-31//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene1315_All//0.00E+00//TC137636				nr +
Unigene13150_All	1996	23.46	38.97	30.71	17.40	19.70	29.78	39.10	42.03	224.02	7.32E-01	2.52E-33		3.88E-01	1.55E-08		1.80E-01	4.18E-02			7.76E-01	3.00E-30			1.04E-01	6.38E-02		2.52E+00	0.00E+00	Up	Unigene13150_All//gi|291245406|gb|ADD84880.1|//1.00E-147//mitochondrial AOX2 [Citrullus lanatus]	Unigene13150_All//2.00E-130//AT5G64210| AOX2; alternative oxidase	Unigene13150_All//0.00E+00//TC140135				nr +
Unigene13151_All	707	3.33	8.24	4.07	2.04	4.58	3.77	1.08	1.06	2.20	1.31E+00	4.01E-07	Up	2.88E-01	4.63E-01		1.16E+00	5.71E-04	Up	8.83E-01	2.37E-02		-1.66E-02	1.02E+00		1.03E+00	2.56E-02		Unigene13151_All//gi|14190357|gb|AK555659.1|AF378856_1//1.00E-50//AT4g19390/T5K18_170 [Arabidopsis thaliana]	Unigene13151_All//8.00E-52//AT4G19390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP022348 (InterPro:IPR016804), Uncharacterised protein family UPF0114 (InterPro:IPR005134); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13720.1); Has 553 Blast hits to 553 proteins in 219 species: Archae - 18; Bacteria - 407; Metazoa - 0; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 74 (source: NCBI BLink).	Unigene13151_All//2.00E-128//TC178069			GO:0009536	nr -
Unigene13152_All	1307	31.50	47.68	50.52	22.87	49.85	45.82	2.52	2.14	1.65	5.98E-01	5.20E-19		6.81E-01	2.80E-24		1.12E+00	2.35E-67	Up	1.00E+00	9.60E-47	Up	-2.36E-01	4.86E-01		-6.16E-01	3.59E-02		Unigene13152_All//gi|14190357|gb|AK555659.1|AF378856_1//6.00E-69//AT4g19390/T5K18_170 [Arabidopsis thaliana]	Unigene13152_All//3.00E-70//AT4G19390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP022348 (InterPro:IPR016804), Uncharacterised protein family UPF0114 (InterPro:IPR005134); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13720.1); Has 553 Blast hits to 553 proteins in 219 species: Archae - 18; Bacteria - 407; Metazoa - 0; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 74 (source: NCBI BLink).	Unigene13152_All//0.00E+00//TC178069			GO:0009536	nr -
Unigene13153_All	1913	16.00	14.28	8.82	15.08	17.44	19.83	26.32	62.68	128.01	-1.64E-01	1.20E-01		-8.59E-01	5.90E-17		2.10E-01	2.68E-02			3.95E-01	2.95E-06			1.25E+00	2.13E-151	Up	2.28E+00	0.00E+00	Up	Unigene13153_All//gi|60459371|gb|AX320031.1|//1.00E-168//RING-finger protein [Capsicum annuum]	Unigene13153_All//3.00E-170//AT5G14420| RGLG2 (RING domain Ligase2); ubiquitin-protein ligase	Unigene13153_All//0.00E+00//TC146141				nr -
Unigene13154_All	1530	5.47	8.38	6.20	8.73	11.28	15.53	39.13	80.23	87.96	6.15E-01	9.32E-05		1.79E-01	3.97E-01		3.70E-01	4.38E-03			8.31E-01	6.22E-14			1.04E+00	1.53E-114	Up	1.17E+00	1.15E-155	Up	Unigene13154_All//gi|15241400|ref|NP_196946.1|//1.00E-142//RGLG2 (RING domain Ligase2); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|30684895|ref|NP_850818.1|RGLG2 (RING domain Ligase2); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|42573365|ref|NP_974779.1|RGLG2 (RING domain Ligase2); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|42573367|ref|NP_974780.1|RGLG2 (RING domain Ligase2); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75181029|sp|Q9LX87.1|RGLG2_ARATH RecName: Full=E3 ubiquitin-protein ligase RGLG2; AltName: Full=RING domain ligase 2 >gi|70905105|gb|AAZ14078.1|At5g14420 [Arabidopsis thaliana]	Unigene13154_All//2.00E-140//AT3G01650| RGLG1 (RING domain Ligase1); protein binding / zinc ion binding	Unigene13154_All//0.00E+00//gi|78340190|gb|DT560464.1|DT560464				nr +

Unigene1316_All	2123	79.78	56.28	78.96	61.78	65.84	66.59	45.69	30.28	19.46	-5.03E-01	3.74E-37		-1.48E-02	7.55E-01		9.17E-02	4.72E-02		1.08E-01	1.89E-02		-5.93E-01	3.20E-35		-1.23E+00	4.89E-123	Down	Unigene1316_All//gi|15226633|ref|NP_182281.1|//1.00E-174//PHR2 (photolyase/blue-light receptor 2); DNA photolyase [Arabidopsis thaliana] >gi|116248577|sp|Q8LB72.2|PHR2_ARATH RecName: Full=Blue-light photoreceptor PHR2 >gi|2529668|gb|AAC62851.1| photolyase/blue-light receptor (PHR2) [Arabidopsis thaliana] >gi|3319288|gb|AAC26199.1| photolyase/blue light photoreceptor PHR2 [Arabidopsis thaliana] >gi|115646759|gb|ABJ17108.1| At2g47590 [Arabidopsis thaliana]	Unigene1316_All//4.00E-158//AT2G47590| PHR2 (photolyase/blue-light receptor 2); DNA photolyase	Unigene1316_All//0.00E+00//TC160664				nr -
Unigene13161_All	2615	25.03	3.33	10.59	74.27	53.90	48.38	11.14	10.72	7.40	-2.91E+00	2.94E-208	Down	-1.24E+00	7.73E-65	Down	-4.63E-01	2.75E-44		-6.19E-01	2.40E-66		-5.48E-02	6.56E-01		-5.89E-01	2.19E-11		Unigene13161_All//gi|152182002|ref|NP_177929.1|//0.00E+00//glycosyl hydrolase family 3 protein [Arabidopsis thaliana] >gi|259585708|sp|Q8GZZ5.2|BXL7_ARATH RecName: Full=Probable beta-D-xylosidase 7; Short=AtBXL7; Flags: Precursor >gi|180866336|gb|AAL57631.1| At1g78060/F28K19_32 [Arabidopsis thaliana]	Unigene13161_All//0.00E+00//AT1G78060| glycosyl hydrolase family 3 protein	Unigene13161_All//0.00E+00//TC154195		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0005576//GO:0005618//GO:0009536//GO:0015926//GO:0031410//GO:0044238	nr -
Unigene13162_All	1798	4.80	33.11	9.71	6.32	11.97	22.71	2.45	9.86	7.89	2.79E+00	1.90E-179	Up	1.02E+00	5.17E-13	Up	9.22E-01	2.48E-16		1.85E+00	4.37E-80	Up	2.01E+00	6.22E-45	Up	1.69E+00	2.84E-29	Up	Unigene13162_All//gi|115465387|ref|NP_001056293.1|//1.00E-127//Os05g0557900 [Oryza sativa Japonica Group] >gi|113578644|dbj|BAF18207.1| Os05g0557900 [Oryza sativa Japonica Group]	Unigene13162_All//1.00E-117//AT2G44970| lipase-related	Unigene13162_All//0.00E+00//TC138519				nr +
Unigene13164_All	2729	1.94	2.82	5.66	8.51	11.09	6.72	1.77	0.86	1.85	5.43E-01	9.80E-03		1.55E+00	9.75E-22	Up	3.83E-01	3.35E-05		-3.40E-01	2.69E-03		-1.04E+00	2.55E-05	Down	7.00E-02	7.79E-01		Unigene13164_All//gi|224111296|ref|XP_002332952.1|//1.00E-157//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834264|gb|EEE72741.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene13164_All//2.00E-31//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene13164_All//0.00E+00//DR463399		ko04626|Plant-pathogen interaction		nr -
Unigene13169_All	3723	1.10	2.84	1.26	2.13	1.86	2.63	17.70	23.22	54.40	1.38E+00	3.00E-13	Up	1.99E-01	5.20E-01		-1.95E-01	4.03E-01		3.07E-01	1.18E-01		3.91E-01	4.26E-15		1.62E+00	0.00E+00	Up	Unigene13169_All//gi|297817842|ref|XP_002876804.1|//0.00E+00//ATPSKR1 [Arabidopsis lyrata subsp. lyrata] >gi|297322642|gb|EFH53063.1| ATPSKR1 [Arabidopsis lyrata subsp. lyrata]	Unigene13169_All//0.00E+00//AT2G02220| PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase	Unigene13169_All//0.00E+00//TC141849			GO:0004672//GO:0004872//GO:0006464//GO:0006950//GO:0007167//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene13171_All	1715	0.27	0.71	0.75	0.84	0.72	0.05	0.59	0.39	0.79	1.37E+00	3.15E-02		1.44E+00	2.61E-02		-2.21E-01	7.05E-01		-4.00E+00	5.84E-07	Down	-6.02E-01	3.45E-01		4.17E-01	4.10E-01		Unigene13171_All//gi|71905561|gb|AAZ52758.1|//1.00E-144//expressed protein [Arabidopsis thaliana] >gi|71905563|gb|AAZ52759.1| expressed protein [Arabidopsis thaliana]	Unigene13171_All//7.00E-145//AT5G19160| unknown protein	Unigene13171_All//0.00E+00//TC145827				nr +
Unigene13172_All	2137	57.07	17.45	25.49	89.91	80.65	61.27	61.29	11.83	36.07	-1.71E+00	8.08E-201	Down	-1.16E+00	9.15E-109	Down	-1.57E-01	5.52E-06		-5.53E-01	8.69E-54		-2.37E+00	0.00E+00	Down	-7.65E-01	1.47E-75		Unigene13172_All//gi|157273662|gb|ABV27485.1|//0.00E+00//fasciclin-like arabinogalactan protein 14 [Gossypium hirsutum]	Unigene13172_All//5.00E-166//AT5G06390| FLA17 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 17 PRECURSOR)	Unigene13172_All//0.00E+00//TC174392			GO:0009987//GO:0043231	nr +
Unigene13175_All	1642	26.96	12.00	21.73	8.59	8.20	5.12	2.11	2.16	2.01	-1.17E+00	2.00E-41	Down	-3.11E-01	1.86E-04		-6.63E-02	7.31E-01		-7.47E-01	2.90E-07		3.52E-02	9.27E-01		-6.83E-02	8.19E-01		Unigene13175_All//gi|297807259|ref|XP_002871513.1|//1.00E-124//PDE149 [Arabidopsis lyrata subsp. lyrata] >gi|297317350|gb|EFH47772.1| PDE149 [Arabidopsis lyrata subsp. lyrata]	Unigene13175_All//5.00E-102//AT5G12130| PDE149 (PIGMENT DEFECTIVE 149)	Unigene13175_All//0.00E+00//TC154808			GO:0030684//GO:0031224	nr -
Unigene13179_All	1164	20.95	25.90	18.85	8.43	4.79	6.48	1.89	4.38	5.96	3.06E-01	2.15E-03		-1.52E-01	2.38E-01		-8.15E-01	1.32E-06		-3.80E-01	4.28E-02		1.21E+00	6.88E-07	Up	1.66E+00	2.36E-14	Up	Unigene13179_All//gi|15240623|ref|NP_196845.1|//2.00E-67//immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana] >gi|75335665|sp|Q9LYR5.1|FKBP7_ARATH RecName: Full=Probable FKBP-type peptidyl-prolyl cis-trans isomerase 7, chloroplastic; Short=PPIase; AltName: Full=Rotamase; Flags: Precursor >gi|46931302|gb|AAT06455.1| At5g13410 [Arabidopsis thaliana] >gi|222423171|dbj|BAH19563.1| AT5G13410 [Arabidopsis thaliana]	Unigene13179_All//1.00E-66//AT5G13410| immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	Unigene13179_All//0.00E+00//TC137831			GO:0009534//GO:0016853//GO:0044436	nr -
Unigene13180_All	1767	13.00	17.18	12.84	5.05	3.55	4.40	1.48	4.21	4.80	4.02E-01	4.08E-05		-1.80E-02	8.98E-01		-5.09E-01	5.41E-03		-1.99E-01	3.78E-01		1.50E+00	3.85E-13	Up	1.69E+00	6.36E-18	Up	Unigene13180_All//gi|15240623|ref|NP_196845.1|//9.00E-86//immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana] >gi|75335665|sp|Q9LYR5.1|FKBP7_ARATH RecName: Full=Probable FKBP-type peptidyl-prolyl cis-trans isomerase 7, chloroplastic; Short=PPIase; AltName: Full=Rotamase; Flags: Precursor >gi|46931302|gb|AAT06455.1| At5g13410 [Arabidopsis thaliana] >gi|222423171|dbj|BAH19563.1| AT5G13410 [Arabidopsis thaliana]	Unigene13180_All//1.00E-83//AT5G13410| immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	Unigene13180_All//0.00E+00//TC137831			GO:0005527//GO:0009534//GO:0016859//GO:0044267//GO:0044436	nr +
Unigene13182_All	782	13.05	3.50	12.46	56.95	26.73	18.60	9.30	9.94	3.72	-1.90E+00	5.38E-20	Down	-6.62E-02	7.34E-01		-1.09E+00	4.90E-46	Down	-1.61E+00	9.22E-74	Down	9.63E-02	6.41E-01		-1.32E+00	4.10E-11	Down			Unigene13182_All//3.00E-59//DR462334				
Unigene13183_All	1302	4.50	1.75	4.34	22.57	11.53	7.25	6.88	4.62	2.17	-1.36E+00	1.31E-07	Down	-5.40E-02	8.37E-01		-9.69E-01	4.42E-25		-1.64E+00	7.28E-50	Down	-5.75E-01	7.95E-04		-1.66E+00	1.24E-18	Down	Unigene13183_All//gi|53370641|gb|AU89136.1|//6.00E-17//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene13183_All//2.00E-09//AT3G25270| nucleic acid binding	Unigene13183_All//2.00E-70//DR462334				nr +
Unigene13184_All	2432	6.45	3.04	3.17	11.27	9.66	12.18	11.04	4.43	8.08	-1.09E+00	1.41E-13	Down	-1.02E+00	7.46E-12	Down	-2.22E-01	3.41E-02		1.13E-01	3.45E-01		-1.32E+00	2.84E-37	Down	-4.51E-01	7.71E-07		Unigene13184_All//gi|13605559|gb|AK32773.1|AF361605_1//6.00E-87//AT3g03250/T17B22_6 [Arabidopsis thaliana]	Unigene13184_All//3.00E-88//AT3G03250| UGP (UDP-glucose pyrophosphorylase); UTP:glucose-1-phosphate uridylyltransferase/ nucleotidyltransferase	Unigene13184_All//0.00E+00//TC149755		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00040|Pentose and glucuronate interconversions//ko00052|Galactose metabolism	GO:0000314//GO:0005198//GO:0005488//GO:0006952//GO:0009532//GO:0009581//GO:0010467//GO:0016020//GO:0033554	nr +
Unigene13185_All	2408	5.71	2.38	2.41	10.01	6.99	9.77	6.60	3.89	2.08	-1.27E+00	4.22E-15	Down	-1.25E+00	4.16E-14	Down	-5.18E-01	3.62E-07		-3.51E-02	7.96E-01		-7.64E-01	1.25E-09		-1.66E+00	2.30E-32	Down	Unigene13185_All//gi|192338746|gb|ACF04278.1|//1.00E-109//UTP-glucose 1 phosphate uridylyltransferase [Eucalyptus grandis]	Unigene13185_All//2.00E-105//AT3G03250| UGP (UDP-glucose pyrophosphorylase); UTP:glucose-1-phosphate uridylyltransferase/ nucleotidyltransferase	Unigene13185_All//0.00E+00//TC149755		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00040|Pentose and glucuronate interconversions//ko00052|Galactose metabolism	GO:0005622//GO:0016740	nr -
Unigene13186_All	2101	52.22	158.59	103.38	69.59	84.74	119.91	51.03	62.07	45.75	1.60E+00	0.00E+00	Up	9.85E-01	3.92E-148		2.84E-01	3.00E-16		7.85E-01	2.10E-129		2.82E-01	1.71E-12		-1.58E-01	4.19E-04		Unigene13186_All//gi|116265960|gb|ABJ91228.1|//0.00E+00//CBL-interacting protein kinase 22 [Populus trichocarpa]	Unigene13186_All//1.00E-160//AT5G58380| SIP1 (SOS3-INTERACTING PROTEIN 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene13186_All//0.00E+00//TC141658		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0023060//GO:0032559	nr +
Unigene13188_All	2160	54.57	38.71	33.33	193.35	195.47	128.86	43.08	15.83	19.62	-4.96E-01	2.22E-25		-7.11E-01	3.10E-46		1.57E-02	6.18E-01		-5.85E-01	7.41E-129		-1.44E+00	1.11E-146	Down	-1.13E+00	9.98E-104	Down	Unigene13188_All//gi|15239643|ref|NP_197410.1|//1.00E-146//heavy-metal-associated domain-containing protein [Arabidopsis thaliana]	Unigene13188_All//8.00E-34//AT3G06130| heavy-metal-associated domain-containing protein	Unigene13188_All//0.00E+00//TC174545		ko03040|Spliceosome		nr -
Unigene13189_All	2013	11.70	9.59	9.89	47.61	45.28	25.04	11.32	2.95	4.31	-2.86E-01	1.30E-02		-2.42E-01	4.86E-02		-7.24E-02	2.39E-01		-9.27E-01	3.32E-66		-1.94E+00	4.10E-55	Down	-1.39E+00	1.42E-35	Down	Unigene13189_All//gi|15239643|ref|NP_197410.1|//1.00E-139//heavy-metal-associated domain-containing protein [Arabidopsis thaliana]	Unigene13189_All//8.00E-34//AT3G06130| heavy-metal-associated domain-containing protein	Unigene13189_All//0.00E+00//TC174545		ko03040|Spliceosome//ko03018|RNA degradation		nr +
Unigene1319_All	1384	1.21	0.40	1.96	1.51	1.72	1.27	3.27	2.48	1.18	-1.59E+00	3.09E-03		6.98E-01	8.11E-02		1.84E-01	7.12E-01		-2.48E-01	6.39E-01		-4.01E-01	1.30E-01		-1.47E+00	2.40E-08	Down	Unigene1319_All//gi|42572087|ref|NP_974134.1|//1.00E-42//NF-YA3 (NUCLEAR FACTOR Y, SUBUNIT A3); transcription factor [Arabidopsis thaliana]	Unigene1319_All//1.00E-48//AT1G72830| NF-YA3 (NUCLEAR FACTOR Y, SUBUNIT A3); transcription factor	Unigene1319_All//0.00E+00//TC169987	CCAAT			nr +
Unigene13190_All	579	5.42	2.10	4.32	8.78	6.84	7.25	1.10	1.01	0.28	-1.37E+00	1.77E-04	Down	-3.27E-01	3.87E-01		-3.60E-01	1.88E-01		-2.75E-01	3.57E-01		-1.16E-01	8.88E-01		-1.99E+00	2.04E-02		Unigene13190_All//gi|210061121|gb|ACJ05633.1|//1.00E-56//squalene epoxidase 1 [Nigella sativa]	Unigene13190_All//1.00E-42//AT1G58440| XF1; squalene monooxygenase	Unigene13190_All//4.00E-147//TC132552		ko00100|Steroid biosynthesis	GO:0004497//GO:0008152//GO:0030554//GO:0031224//GO:0031410//GO:0043231	nr -
Unigene13191_All	677	4.25	0.75	0.47	11.63	6.71	6.34	1.56	1.42	0.24	-2.51E+00	2.27E-08	Down	-3.17E+00	6.12E-10	Down	-7.92E-01	3.48E-05		-8.75E-01	1.63E-05		-1.37E-01	8.15E-01		-2.73E+00	1.12E-04	Down	Unigene13191_All//gi|62945915|gb|AY22200.1|//6.00E-72//squalene monooxygenase [Datura inoxia]	Unigene13191_All//6.00E-67//AT1G58440| XF1; squalene monooxygenase	Unigene13191_All//0.00E+00//TC143054		ko00100|Steroid biosynthesis	GO:0004497//GO:0008152//GO:0016020//GO:0031410	nr +
Unigene13198_All	737	2.84	10.31	7.30	2.70	4.44	7.48	1.03	0.62	0.86	1.86E+00	1.37E-14	Up	1.36E+00	1.06E-06	Up	7.15E-01	3.51E-02		1.47E+00	2.87E-08	Up	-7.27E-01	3.32E-01		-2.56E-01	6.97E-01		Unigene13198_All//gi|53370754|gb|AU89249.1|//3.00E-18//C1-like domain containing protein [Oryza sativa Japonica Group]	Unigene13198_All//5.00E-12//AT1G60120| DC1 domain-containing protein	Unigene13198_All//0.00E+00//CO130617			GO:0003824	nr +
Unigene13199_All	1503	3.79	21.74	13.32	4.01	9.00	15.23	4.92	5.39	3.07	2.52E+00	2.64E-88	Up	1.81E+00	5.57E-35	Up	1.17E+00	4.77E-15	Up	1.93E+00	1.11E-47	Up	1.32E-01	5.44E-01		-6.79E-01	2.53E-04		Unigene13199_All//gi|115440447|ref|NP_001044503.1|//1.00E-103//Os01g0794400 [Oryza sativa Japonica Group] >gi|122222435|sp|Q0JIL1.1|NRX2_ORYSJ RecName: Full=Probable nucleoredoxin 2; Short=OsNrx2 >gi|113534034|dbj|BAF06417.1| Os01g0794400 [Oryza sativa Japonica Group]	Unigene13199_All//2.00E-55//AT1G60120| DC1 domain-containing protein	Unigene13199_All//0.00E+00//TC135053			GO:0003824	nr +
Unigene13200_All	2835	2.81	1.41	1.41	4.87	3.24	2.79	7.10	3.73	2.81	-9.90E-01	2.24E-06		-9.94E-01	4.52E-06		-5.86E-01	2.68E-05		-8.04E-01	5.30E-08		-9.29E-01	2.24E-16		-1.34E+00	1.10E-29	Down	Unigene13200_All//gi|9758730|dbj|BAB09168.1|//0.00E+00//replication protein A1-like [Arabidopsis thaliana]	Unigene13200_All//0.00E+00//AT5G45400| replication protein, putative	Unigene13200_All//0.00E+00//gi|109869723|gb|DW498699.1|DW498699		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair	GO:0003676//GO:0046872	nr -
Unigene13201_All	2704	1.34	1.27	0.89	3.21	2.55	2.20	4.30	1.96	2.22	-6.74E-02	8.35E-01		-5.91E-01	8.29E-02		-3.32E-01	9.46E-02		-5.40E-01	5.52E-03		-1.13E+00	3.01E-13	Down	-9.51E-01	1.66E-10		Unigene13201_All//gi|297809977|ref|XP_002872872.1|//0.00E+00//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318709|gb|EFH49131.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13201_All//8.00E-176//AT4G01860| transducin family protein / WD-40 repeat family protein	Unigene13201_All//0.00E+00//gi|78343229|gb|DT563503.1|DT563503				nr -

Unigene13204_All	2530	10.22	7.91	13.95	30.62	24.31	41.70	17.18	10.79	6.58	-3.69E-01	5.96E-04		4.50E-01	1.24E-06		-3.33E-01	7.12E-10		4.46E-01	4.04E-20		-6.71E-01	5.00E-20		-1.38E+00	1.69E-66	Down	Unigene13204_All//gi|48310551|gb|AAT41837.1|//1.00E-178//At5g23850 [Arabidopsis thaliana]	Unigene13204_All//3.00E-179//AT5G23850| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Lipopolysaccharide-modifying protein (InterPro:IPR006598), Protein of unknown function DUF821, CAP10-like (InterPro:IPR008539); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48980.1); Has 588 Blast hits to 567 proteins in 103 species: Archae - 2; Bacteria - 34; Metazoa - 301; Fungi - 69; Plants - 115; Viruses - 3; Other Eukaryotes - 64 (source: NCBI BLink).	Unigene13204_All//2.00E-146//DW508042				nr +
Unigene13208_All	1619	4.69	5.04	4.67	13.75	19.19	14.62	9.24	4.23	4.58	1.05E-01	6.14E-01		-4.70E-03	1.00E+00		4.80E-01	8.66E-08		8.79E-02	5.34E-01		-1.13E+00	1.02E-16	Down	-1.01E+00	1.14E-14	Down	Unigene13208_All//gi|150036249|gb|ABR67412.1|//1.00E-107//microtubule binding protein [Cucumis melo]	Unigene13208_All//5.00E-91//AT3G05330| ATN (TANGLED)	Unigene13208_All//0.00E+00//TC170765			GO:0000911//GO:0015630//GO:0032506	nr +
Unigene13209_All	1677	33.94	17.52	29.15	15.77	14.44	8.97	5.04	2.34	2.61	-9.54E-01	2.36E-38		-2.20E-01	3.13E-03		-1.28E-01	2.97E-01		-8.15E-01	4.41E-15		-1.11E+00	1.57E-09	Down	-9.48E-01	7.44E-08		Unigene13209_All//gi|109895092|gb|ABG47411.1|//1.00E-150//maltose transporter [Malus x domestica]	Unigene13209_All//9.00E-112//AT5G17520| RCP1 (ROOT CAP 1); maltose transmembrane transporter	Unigene13209_All//0.00E+00//TC133302				nr +
Unigene13210_All	1511	43.87	237.65	90.04	59.21	125.94	107.96	48.16	139.49	123.73	2.44E+00	0.00E+00	Up	1.04E+00	4.27E-101	Up	1.09E+00	5.99E-187	Up	8.67E-01	2.60E-99		1.53E+00	0.00E+00	Up	1.36E+00	5.60E-274	Up	Unigene13210_All//gi|224091544|ref|XP_002309282.1|//1.00E-133//f-box family protein [Populus trichocarpa] >gi|222855258|gb|EEE92805.1| f-box family protein [Populus trichocarpa]	Unigene13210_All//6.00E-49//AT1G15670| kelch repeat-containing F-box family protein	Unigene13210_All//0.00E+00//ES809389				nr -
Unigene13211_All	2116	1.34	1.36	1.56	4.00	4.87	2.52	4.72	1.84	3.24	3.17E-02	9.49E-01		2.25E-01	5.53E-01		2.82E-01	1.35E-01		-6.68E-01	6.02E-04		-1.36E+00	4.72E-15	Down	-5.42E-01	5.48E-04		Unigene13211_All//gi|224053985|ref|XP_002298071.1|//0.00E+00//RNA polymerase IV subunit [Populus trichocarpa] >gi|222845329|gb|EEE82876.1| RNA polymerase IV subunit [Populus trichocarpa]	Unigene13211_All//1.00E-156//AT1G63020| NRPD1A (NUCLEAR RNA POLYMERASE D 1A); DNA binding / DNA-directed RNA polymerase	Unigene13211_All//0.00E+00//TC179217			GO:0005488//GO:0006807//GO:0016779	nr +
Unigene13212_All	1612	76.05	46.68	71.02	78.34	56.93	44.88	14.24	8.71	6.94	-7.04E-01	7.14E-49		-9.86E-02	6.20E-02		-4.61E-01	1.15E-28		-8.04E-01	2.53E-68		-7.09E-01	5.35E-12		-1.04E+00	8.78E-23	Down	Unigene13212_All//gi|62286954|sp|Q9XJ98.1|KPRS1_SP10L//1.00E-176//RecName: Full=Ribose-phosphate pyrophokinase 1; AltName: Full=Phosphoribosyl pyrophosphate synthase 1 >gi|4902849|emb|CAB43599.1| phosphoribosyl pyrophosphate synthase [Spinacia oleracea]	Unigene13212_All//6.00E-177//AT2G45530| ribose-phosphate pyrophosphokinase, putative / phosphoribosyl diphosphate synthetase, putative	Unigene13212_All//0.00E+00//TC130690		ko00230|Purine metabolism//ko00030|Pentose phosphate pathway	GO:0009124//GO:0016778//GO:0046872	nr -
Unigene13213_All	2474	19.44	7.25	9.69	25.53	23.17	10.68	0.24	0.24	0.13	-1.42E+00	6.69E-61	Down	-1.00E+00	4.36E-34	Down	-1.40E-01	4.18E-02		-1.26E+00	1.14E-71	Down	-1.70E-02	1.02E+00		-8.94E-01	2.72E-01		Unigene13213_All//gi|297791157|ref|XP_002863463.1|//0.00E+00//subtilase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309298|gb|EFH39722.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13213_All//0.00E+00//AT5G45650| subtilase family protein	Unigene13213_All//0.00E+00//TC174218			GO:0004175//GO:0016491//GO:0019538//GO:0031410	nr -
Unigene13216_All	1792	49.08	70.52	87.45	78.81	196.70	260.80	9.67	10.94	9.76	5.23E-01	8.49E-30		8.33E-01	1.04E-80		1.32E+00	0.00E+00	Up	1.73E+00	0.00E+00	Up	1.77E-01	1.46E-01		1.28E-02	9.45E-01		Unigene13216_All//gi|157313310|gb|ABV32548.1|//0.00E+00//endo-1,4-beta-mannosidase protein 2 [Prunus persica]	Unigene13216_All//9.00E-159//AT5G66460| (1-4)-beta-mannan endohydrolase, putative	Unigene13216_All//0.00E+00//gi|164343572|gb|ES830972.1|ES830972			GO:0016798//GO:0043167//GO:0044238	nr +
Unigene13217_All	1448	18.32	10.95	13.57	15.79	12.70	14.53	17.78	9.29	8.69	-7.42E-01	3.54E-12		-4.33E-01	7.26E-05		-3.14E-01	4.38E-03		-1.20E-01	3.94E-01		-9.36E-01	5.39E-21		-1.03E+00	2.72E-25	Down	Unigene13217_All//gi|28416651|gb|AAO42856.1|//3.00E-13//At4g18070 [Arabidopsis thaliana] >gi|222423345|dbj|BAH19647.1| AT4G18070 [Arabidopsis thaliana]	Unigene13217_All//3.00E-08//AT4G18070| unknown protein	Unigene13217_All//0.00E+00//gi|78330746|gb|DT551020.1|DT551020				nr +
Unigene13218_All	1732	15.47	11.00	15.93	17.17	11.95	13.30	10.62	4.66	5.41	-4.92E-01	2.57E-06		4.22E-02	7.17E-01		-5.23E-01	7.35E-09		-3.69E-01	1.51E-04		-1.19E+00	4.09E-22	Down	-9.74E-01	9.95E-17		Unigene13218_All//gi|46518395|gb|AAS98679.1|//2.00E-15//At1g29530 [Arabidopsis thaliana] >gi|48310441|gb|AAT41821.1| At1g29530 [Arabidopsis thaliana]	Unigene13218_All//4.00E-08//AT4G18070| unknown protein	Unigene13218_All//0.00E+00//gi|78330746|gb|DT551020.1|DT551020		ko03040|Spliceosome		nr -
Unigene13219_All	2210	3.05	2.84	3.78	9.76	5.92	4.33	7.33	4.54	7.81	-1.03E-01	6.55E-01		3.09E-01	1.54E-01		-7.21E-01	2.71E-11		-1.17E+00	3.14E-22	Down	-6.91E-01	2.36E-08		9.12E-02	5.09E-01		Unigene13219_All//gi|18414996|ref|NP_567546.1|//2.00E-79//DNA-binding family protein [Arabidopsis thaliana] >gi|119657370|tpd|FAA00284.1| TPA: AT-hook motif nuclear localized protein 13 [Arabidopsis thaliana]	Unigene13219_All//8.00E-62//AT4G17950| DNA-binding family protein	Unigene13219_All//0.00E+00//TC171654				nr +
Unigene13223_All	1972	2.18	0.85	2.24	5.38	3.65	2.91	4.97	1.44	1.74	-1.36E+00	8.99E-06	Down	4.29E-02	8.93E-01		-5.60E-01	5.99E-04		-8.87E-01	2.42E-07		-1.79E+00	1.16E-21	Down	-1.52E+00	7.08E-18	Down	Unigene13223_All//gi|62857020|dbj|BAD95895.1|//1.00E-138//Ser/Thr protein kinase [Lotus japonicus]	Unigene13223_All//7.00E-121//AT5G38260| serine/threonine protein kinase, putative	Unigene13223_All//0.00E+00//TC161773		ko04626|Plant-pathogen interaction		nr +
Unigene13225_All	981	1.92	1.65	1.19	1.27	0.77	0.83	3.49	0.55	2.23	-2.16E-01	6.26E-01		-6.85E-01	1.66E-01		-7.17E-01	2.26E-01		-6.15E-01	3.33E-01		-2.66E+00	1.11E-12	Down	-6.44E-01	2.47E-02		Unigene13225_All//gi|18415647|ref|NP_568185.1|//1.00E-56//mitochondrial transcription termination factor family protein / mTERF family protein [Arabidopsis thaliana]	Unigene13225_All//5.00E-56//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene13225_All//0.00E+00//TC142429				nr +
Unigene13227_All	2491	2.67	1.32	2.80	7.10	5.49	3.99	10.96	3.05	3.89	-1.01E+00	1.24E-05	Down	7.01E-02	7.69E-01		-3.71E-01	3.15E-03		-8.32E-01	1.22E-10		-1.84E+00	1.48E-61	Down	-1.50E+00	2.95E-47	Down	Unigene13227_All//gi|297828123|ref|XP_002881944.1|//1.00E-140//inositol 1,3,4-trisphosphate 5/6-kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327783|gb|EFH58203.1| inositol 1,3,4-trisphosphate 5/6-kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13227_All//5.00E-133//AT2G43980| AtITPK4 (inositol 1,3,4-trisphosphate 5/6-kinase 4); ATP binding / catalytic/ inositol tetrakisphosphate 1-kinase/ inositol-1,3,4-trisphosphate 5/6-kinase/ magnesium ion binding	Unigene13227_All//0.00E+00//TC143619		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0032559//GO:0043647//GO:0044464//GO:0046872//GO:0051765//GO:0051766	nr -
Unigene13228_All	2227	0.87	0.39	0.31	1.39	0.79	0.91	1.92	0.92	0.57	-1.17E+00	1.36E-02		-1.48E+00	3.61E-03		-8.14E-01	1.50E-02		-6.04E-01	9.44E-02		-1.06E+00	6.43E-05	Down	-1.74E+00	6.71E-10	Down	Unigene13228_All//gi|297828123|ref|XP_002881944.1|//1.00E-140//inositol 1,3,4-trisphosphate 5/6-kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327783|gb|EFH58203.1| inositol 1,3,4-trisphosphate 5/6-kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13228_All//5.00E-133//AT2G43980| AtITPK4 (inositol 1,3,4-trisphosphate 5/6-kinase 4); ATP binding / catalytic/ inositol tetrakisphosphate 1-kinase/ inositol-1,3,4-trisphosphate 5/6-kinase/ magnesium ion binding	Unigene13228_All//0.00E+00//TC143619		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0032559//GO:0043647//GO:0044464//GO:0046872//GO:0051765//GO:0051766	nr +
Unigene13229_All	2169	3.11	6.26	7.14	4.20	7.56	9.87	2.22	5.74	5.80	1.01E+00	1.46E-10	Up	1.20E+00	5.70E-15	Up	8.46E-01	6.43E-11		1.23E+00	1.66E-23	Up	1.37E+00	9.43E-19	Up	1.39E+00	1.02E-19	Up	Unigene13229_All//gi|115434188|ref|NP_001041852.1|//1.00E-116//Os01g0117500 [Oryza sativa Japonica Group] >gi|113531383|dbj|BAF03766.1| Os01g0117500 [Oryza sativa Japonica Group]	Unigene13229_All//2.00E-94//AT1G66920| serine/threonine protein kinase, putative	Unigene13229_All//0.00E+00//gi|189092617|gb|FG548152.1|FG548152		ko04626|Plant-pathogen interaction		nr -
Unigene13233_All	1362	33.34	6.36	17.55	35.77	30.69	15.09	12.48	4.57	3.54	-2.39E+00	3.48E-116	Down	-9.26E-01	3.52E-28		-2.21E-01	2.78E-03		-1.25E+00	1.51E-54	Down	-1.45E+00	1.63E-27	Down	-1.82E+00	4.95E-39	Down	Unigene13233_All//gi|225455352|ref|XP_002277097.1|//1.00E-131//PREDICTED: similar to ABIL3 (ABL INTERACTOR-LIKE PROTEIN 3) [Vitis vinifera]	Unigene13233_All//3.00E-92//AT5G24310| ABIL3 (ABL INTERACTOR-LIKE PROTEIN 3)	Unigene13233_All//0.00E+00//gi|78346964|gb|DT567238.1|DT567238			GO:0000904//GO:0005856//GO:0048513	nr +
Unigene13237_All	1362	29.73	58.33	35.03	35.77	33.02	26.93	16.27	12.67	7.20	9.72E-01	9.16E-55		2.37E-01	3.79E-03		-1.15E-01	1.69E-01		-4.10E-01	2.26E-08		-3.60E-01	5.73E-04		-1.18E+00	7.61E-27	Down	Unigene13237_All//gi|166407425|gb|ABY87519.1|//1.00E-163//Hsp70-interacting protein 1 [Vitis labrusca]	Unigene13237_All//8.00E-88//AT4G22670| AtHip1 (Arabidopsis thaliana Hsp70-interacting protein 1); binding	Unigene13237_All//0.00E+00//TC172168			GO:0031072//GO:0032269//GO:0032558//GO:0032991//GO:0042026//GO:0044464//GO:0051259	nr +
Unigene13238_All	2567	2.77	1.03	0.44	5.80	3.35	3.24	4.51	2.49	2.31	-1.43E+00	9.76E-10	Down	-2.67E+00	3.34E-20	Down	-7.91E-01	2.86E-09		-8.42E-01	3.09E-09		-8.57E-01	1.20E-08		-9.65E-01	1.04E-10		Unigene13238_All//gi|49615724|gb|AAT67044.1|//0.00E+00//DNA mismatch repair protein [Petunia x hybrida]	Unigene13238_All//0.00E+00//AT3G18524| MSH2 (MUTS HOMOLOG 2); ATP binding / damaged DNA binding / mismatched DNA binding / protein binding	Unigene13238_All//0.00E+00//TC158087		ko03430|Mismatch repair	GO:0003690//GO:0006281//GO:0010520//GO:0016020//GO:0032300//GO:0032559//GO:0043231	nr -
Unigene1324_All	660	3.41	12.97	4.36	9.51	5.79	7.25	4.36	3.10	2.96	1.93E+00	4.05E-17	Up	3.54E-01	3.85E-01		-7.16E-01	1.11E-03		-3.91E-01	1.14E-01		-4.89E-01	1.47E-01		-5.59E-01	8.00E-02				Unigene1324_All//0.00E+00//DW504659				
Unigene13240_All	1505	7.40	45.18	7.85	14.00	18.56	17.50	24.36	51.90	59.19	2.61E+00	9.56E-191	Up	8.51E-02	6.33E-01		4.06E-01	2.43E-05		3.21E-01	2.50E-03		1.09E+00	1.32E-79	Up	1.28E+00	3.04E-119	Up	Unigene13240_All//gi|3643085|gb|AAC36698.1|//1.00E-146//protein phosphatase-2C [Mesembryanthemum crystallinum]	Unigene13240_All//2.00E-131//AT3G62260| protein phosphatase 2C, putative / PP2C, putative	Unigene13240_All//0.00E+00//gi|78346536|gb|DT566810.1|DT566810	D6P			nr -
Unigene13243_All	2806	3.32	0.81	0.59	4.90	3.66	2.70	8.77	1.74	2.87	-2.03E+00	6.06E-20	Down	-2.50E+00	1.94E-24	Down	-4.22E-01	3.38E-03		-8.58E-01	7.85E-09		-2.33E+00	6.85E-75	Down	-1.61E+00	1.67E-47	Down	Unigene13243_All//gi|15220980|ref|NP_176725.1|//0.00E+00//FAS1 (FASCIATA 1); histone binding [Arabidopsis thaliana] >gi|8887626|dbj|BAA72811.1| FAS1 [Arabidopsis thaliana] >gi|22022526|gb|AAM83221.1| At1g65470/F5I14_33 [Arabidopsis thaliana]	Unigene13243_All//1.00E-175//AT1G65470| FAS1 (FASCIATA 1); histone binding	Unigene13243_All//0.00E+00//ES848513		ko03040|Spliceosome	GO:0000725//GO:0006338//GO:0009933//GO:0034728//GO:0035315//GO:0043234//GO:0048229//GO:0048827//GO:0051726	nr -
Unigene13244_All	902	2.03	1.97	2.54	7.68	6.60	6.01	3.19	7.55	2.65	-4.63E-02	9.33E-01		3.22E-01	4.69E-01		-2.17E-01	3.82E-01		-3.54E-01	1.32E-01		1.24E+00	2.87E-09	Up	-2.66E-01	4.27E-01		Unigene13244_All//gi|18404020|ref|NP_565832.1|//5.00E-59//HVA22J (HVA22-LIKE PROTEIN J) [Arabidopsis thaliana] >gi|57012598|sp|Q8GXE9.2|HA22J_ARATH RecName: Full=HVA22-like protein j; Short=AtHVA22j >gi|20197992|gb|AAD21455.2| expressed protein [Arabidopsis thaliana] >gi|91806321|gb|ABE65888.1| abscisic acid-responsive HVA22 family protein [Arabidopsis thaliana]	Unigene13244_All//4.00E-60//AT2G36020| HVA22J (HVA22-LIKE PROTEIN J)	Unigene13244_All//0.00E+00//DR456804				nr +

Unigene13247_All	3369	0.78	0.74	0.70	2.26	1.80	1.57	3.46	1.53	2.07	-7.53E-02	8.43E-01			-1.59E-01	6.90E-01			-3.31E-01	1.25E-01			-5.28E-01	1.20E-02			-1.18E+00	3.29E-14	Down	-7.43E-01	3.12E-07		Unigene13247_All//gi|15220892|ref|NP_178208.1|//0.00E+00//MIF4G domain-containing protein / MA3 domain-containing protein [Arabidopsis thaliana] >gi|6503305|gb|AAF14681.1|AC011713_29 Contains similarity to gb|U19615 LET 858 gene from Caenorhabditis elegans. ESTs gb|AI995150, gb|H76674 and gb|R84035 come from this gene [Arabidopsis thaliana] >gi|22654971|gb|AAM98078.1|At1g80930/F23A5_23 [Arabidopsis thaliana] >gi|28416525|gb|AAO42793.1|At1g80930/F23A5_23 [Arabidopsis thaliana]	Unigene13247_All//0.00E+00//AT1G80930| MIF4G domain-containing protein / MA3 domain-containing protein	Unigene13247_All//0.00E+00//DW504769			GO:0005488//GO:0010467//GO:0043231//GO:0044260//GO:0044444	nr -
Unigene13248_All	1487	1.48	6.27	6.12	6.57	8.45	44.50	67.16	189.16	186.57	2.09E+00	1.73E-20	Up	2.05E+00	5.51E-19	Up	3.64E-01	2.12E-02		2.76E+00	8.52E-212	Up	1.49E+00	0.00E+00	Up	1.47E+00	0.00E+00	Up	Unigene13248_All//gi|30693380|ref|NP_190663.2|//1.00E-100//AAA-type ATPase family protein [Arabidopsis thaliana] >gi|109946623|gb|ABG48490.1|At3g50940 [Arabidopsis thaliana]	Unigene13248_All//1.00E-101//AT3G50940| AAA-type ATPase family protein	Unigene13248_All//0.00E+00//TC139401				nr +
Unigene13249_All	1799	9.42	21.94	8.23	51.23	27.26	66.85	46.49	68.23	46.08	1.22E+00	1.88E-39	Up	-1.96E-01	2.02E-01		-9.10E-01	3.39E-70		3.84E-01	1.73E-17		5.54E-01	3.24E-39		-1.26E-02	8.41E-01		Unigene13249_All//gi|9958056|gb|AAG05645.1|AC011810_4//3.00E-82//Unknown protein [Arabidopsis thaliana]	Unigene13249_All//4.00E-68//AT1G13340| unknown protein	Unigene13249_All//0.00E+00//gi|78333956|gb|DT554230.1|DT554230			GO:0043231	nr -
Unigene13251_All	1194	8.46	2.80	4.68	2.38	3.92	3.74	0.60	1.30	1.67	-1.59E+00	1.14E-15	Down	-8.53E-01	5.53E-06		7.22E-01	7.59E-03		6.55E-01	2.30E-02		1.11E+00	2.15E-02		1.47E+00	4.17E-04	Up	Unigene13251_All//gi|297829768|ref|XP_002882766.1|//1.00E-104//EMB2738 [Arabidopsis lyrata subsp. lyrata] >gi|297326606|gb|EFH59025.1|EMB2738 [Arabidopsis lyrata subsp. lyrata]	Unigene13251_All//1.00E-105//AT3G12080| emb2738 (embryo defective 2738); GTP binding	Unigene13251_All//3.00E-17//DW507429			GO:0032561//GO:0043231	nr +
Unigene13254_All	2161	5.67	3.47	4.12	6.06	6.20	5.31	7.94	2.86	6.45	-7.07E-01	1.22E-05		-4.61E-01	6.44E-03		3.21E-02	8.67E-01		-1.92E-01	2.80E-01		-1.47E+00	1.89E-28	Down	-3.00E-01	1.15E-02		Unigene13254_All//gi|224121846|ref|XP_002318887.1|//1.00E-169//cytochrome P450 [Populus trichocarpa] >gi|222859360|gb|EEE96907.1|cytochrome P450 [Populus trichocarpa]	Unigene13254_All//2.00E-101//AT3G48310| CYP71A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene13254_All//0.00E+00//TC155220		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene13255_All	1972	1.11	1.52	1.24	0.93	1.43	1.47	5.12	9.45	35.60	4.44E-01	2.28E-01		1.57E-01	6.98E-01		6.16E-01	1.04E-01		6.49E-01	8.54E-02		8.83E-01	4.72E-14		2.80E+00	2.18E-265	Up	Unigene13255_All//gi|225457283|ref|XP_002284415.1|//0.00E+00//PREDICTED: similar to EMB2733/ESP3 (EMBRYO DEFECTIVE 2733); ATP-dependent RNA helicase [Vitis vinifera]	Unigene13255_All//0.00E+00//AT1G32490| ESP3 (ENHANCED SILENCING PHENOTYPE 3); ATP binding / ATP-dependent RNA helicase/ ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene13255_All//0.00E+00//TC148325		ko03040|Spliceosome	GO:0003006//GO:0003724//GO:0006396//GO:0016441//GO:0032559//GO:0042623//GO:0043231	nr -
Unigene13262_All	1349	0.74	2.10	0.87	8.20	5.23	4.72	8.09	11.53	5.14	1.51E+00	1.25E-04	Up	2.37E-01	6.97E-01		-6.48E-01	4.10E-05		-7.96E-01	1.88E-06		5.11E-01	4.90E-05		-6.54E-01	1.25E-05		Unigene13262_All//gi|124359163|gb|ABN05686.1|//8.00E-22//Zinc finger, CCHC-type [Medicago truncatula]	Unigene13262_All//9.00E-09//AT3G31430| unknown protein	Unigene13262_All//1.00E-50//gi|21102186|gb|BQ414499.1|BQ414499				nr +
Unigene13263_All	1486	0.63	2.01	0.43	6.17	4.12	3.25	3.87	4.61	1.64	1.67E+00	1.99E-05	Up	-5.60E-01	4.39E-01		-5.81E-01	1.08E-03		-9.24E-01	7.77E-07		2.54E-01	2.41E-01		-1.24E+00	3.17E-08	Down	Unigene13263_All//gi|115473321|ref|NP_001060259.1|//7.00E-36//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene13263_All//2.00E-14//ATMG00310| hypothetical protein	Unigene13263_All//1.00E-75//gi|21102186|gb|BQ414499.1|BQ414499				nr +
Unigene13264_All	1612	2.14	0.97	1.02	2.75	3.23	2.72	3.51	2.13	2.52	-1.14E+00	7.70E-04	Down	-1.06E+00	2.37E-03		2.30E-01	4.48E-01		-1.73E-02	9.46E-01		-7.25E-01	1.09E-03		-4.80E-01	2.71E-02		Unigene13264_All//gi|14030731|gb|AAK53040.1|AF375456_1//1.00E-149//AT5g65380/MNA5_11 [Arabidopsis thaliana] >gi|23506079|gb|AAN28899.1|At5g65380/MNA5_11 [Arabidopsis thaliana]	Unigene13264_All//4.00E-141//AT5G65380| ripening-responsive protein, putative	Unigene13264_All//0.00E+00//TC167248			GO:0015291//GO:0015893//GO:0044464	nr -
Unigene13266_All	2670	1.49	21.50	1.95	5.07	10.52	8.00	4.39	12.85	16.53	3.85E+00	2.43E-233	Up	3.92E-01	1.60E-01		1.05E+00	2.95E-26	Up	6.57E-01	1.43E-08		1.55E+00	2.17E-60	Up	1.91E+00	5.44E-106	Up	Unigene13266_All//gi|18378994|ref|NP_563660.1|//0.00E+00//lipase class 3 family protein [Arabidopsis thaliana]	Unigene13266_All//1.00E-174//AT1G02660| lipase class 3 family protein	Unigene13266_All//0.00E+00//ES820313			GO:0004091//GO:0044238	nr +
Unigene13267_All	1187	24.64	16.31	17.50	42.72	33.83	38.31	22.55	15.85	8.99	-5.96E-01	2.65E-09		-4.94E-01	1.58E-06		-3.37E-01	8.53E-07		-1.57E-01	4.88E-02		-5.09E-01	5.11E-08		-1.33E+00	1.06E-38	Down	Unigene13267_All//gi|1381676|gb|AAB97114.1|//1.00E-110//small GTP-binding protein [Glycine max]	Unigene13267_All//4.00E-103//AT5G65270| AtRAB4a (Arabidopsis Rab GTPase homolog A4a); GTP binding	Unigene13267_All//0.00E+00//TC134192			GO:0016020//GO:0016197//GO:0019899//GO:0032561	nr +
Unigene13268_All	345	4.25	51.84	11.88	1.16	6.59	32.33	1.59	5.94	27.94	3.61E+00	3.23E-69	Up	1.48E+00	6.60E-06	Up	2.51E+00	2.56E-07	Up	4.81E+00	3.95E-56	Up	1.90E+00	1.83E-05	Up	4.13E+00	6.42E-52	Up	Unigene13268_All//gi|78359315|gb|AY98512.2|//4.00E-49//9-cis-epoxycarotenoid dioxygenase [Stylosanthes guianensis]	Unigene13268_All//4.00E-48//AT3G14440| NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	Unigene13268_All//4.00E-38//gi|78348871|gb|DT569145.1|DT569145		ko00906|Carotenoid biosynthesis	GO:0006972//GO:0008152//GO:0009532//GO:0009534//GO:0010436	nr -
Unigene13269_All	2366	2.85	95.36	19.54	1.45	10.19	32.91	5.34	14.04	58.56	5.06E+00	0.00E+00	Up	2.78E+00	6.93E-136	Up	2.81E+00	2.79E-85	Up	4.50E+00	0.00E+00	Up	1.39E+00	5.04E-50	Up	3.45E+00	0.00E+00	Up	Unigene13269_All//gi|83628266|gb|AB226013.1|//0.00E+00//9-cis-epoxycarotenoid dioxygenase 3 [Citrus clementina]	Unigene13269_All//0.00E+00//AT3G14440| NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	Unigene13269_All//0.00E+00//TC175846		ko00906|Carotenoid biosynthesis	GO:0008152//GO:0016702	nr +
Unigene13270_All	2077	33.98	32.91	37.43	37.53	46.34	39.14	24.26	10.79	10.72	-4.63E-02	5.40E-01		1.40E-01	3.38E-02		3.04E-01	3.70E-10		6.04E-02	4.02E-01		-1.17E+00	1.06E-57	Down	-1.18E+00	4.71E-60	Down	Unigene13270_All//gi|3695059|gb|AAC62624.1|//1.00E-157//rac GTPase activating protein I [Lotus japonicus]	Unigene13270_All//1.00E-125//AT5G22400| rac GTPase activating protein, putative	Unigene13270_All//0.00E+00//TC145108				nr -
Unigene13272_All	651	5.47	33.62	10.31	9.95	11.11	15.33	1.49	2.89	1.41	2.62E+00	5.05E-62	Up	9.15E-01	1.12E-04		1.59E-01	5.60E-01		6.24E-01	4.69E-04		9.52E-01	2.51E-02		-8.59E-02	8.91E-01		Unigene13272_All//gi|255546477|ref|XP_002514298.1|//6.00E-14//short-chain dehydrogenase, putative [Ricinus communis] >gi|223546754|gb|EEF48252.1|short-chain dehydrogenase, putative [Ricinus communis]		Unigene13272_All//0.00E+00//TC137993				nr +
Unigene13273_All	1969	11.51	107.90	19.01	19.05	19.36	23.79	4.77	8.43	4.01	3.23E+00	0.00E+00	Up	7.25E-01	1.48E-15		2.33E-02	8.23E-01		3.20E-01	2.52E-05		8.22E-01	3.06E-11		-2.51E-01	1.43E-01		Unigene13273_All//gi|297790540|ref|XP_002863155.1|//0.00E+00//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308989|gb|EFH39414.1|short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13273_All//0.00E+00//AT4G13250| short-chain dehydrogenase/reductase (SDR) family protein	Unigene13273_All//0.00E+00//TC137993		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0006787//GO:0009526//GO:0016616//GO:0044257	nr +
Unigene13274_All	656	5.26	16.84	16.88	20.50	19.53	6.82	0.58	1.02	0.06	1.68E+00	3.41E-18	Up	1.68E+00	1.12E-17	Up	-7.03E-02	7.16E-01		-1.59E+00	4.26E-22	Down	8.13E-01	3.15E-01		-3.26E+00	2.22E-02				Unigene13274_All//0.00E+00//TC150013				
Unigene13275_All	2012	31.73	22.01	29.35	41.62	38.18	41.44	38.29	108.04	14.28	-5.27E-01	1.05E-15		-1.12E-01	1.39E-01		-1.24E-01	3.60E-02		-6.30E-03	9.43E-01		1.50E+00	0.00E+00	Up	-1.42E+00	2.84E-122	Down	Unigene13275_All//gi|145333011|ref|NP_001078371.1|//2.00E-64//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene13275_All//7.00E-61//AT4G10720| ankyrin repeat family protein	Unigene13275_All//0.00E+00//TC130834			GO:0010033	nr +
Unigene13276_All	3252	1.54	1.18	2.26	5.84	5.98	2.78	5.01	3.10	3.01	-3.83E-01	1.60E-01		5.49E-01	1.47E-02		3.58E-02	8.21E-01		-1.07E+00	4.70E-17	Down	-6.93E-01	2.02E-08		-7.32E-01	1.67E-09		Unigene13276_All//gi|76393760|ref|NP_187155.2|//0.00E+00//HST (HASTY); nucleocytoplasmic transporter [Arabidopsis thaliana]	Unigene13276_All//0.00E+00//AT3G05040| HST (HASTY); nucleocytoplasmic transporter	Unigene13276_All//0.00E+00//TC178027			GO:0005215//GO:0006405//GO:0009526//GO:0009887//GO:0009908//GO:0009943//GO:0010354//GO:0012505//GO:0016109//GO:0045426	nr -
Unigene13277_All	1206	30.33	32.52	38.59	62.25	48.26	36.77	9.33	5.79	3.63	1.01E-01	3.01E-01		3.48E-01	1.49E-05		-3.67E-01	1.96E-11		-7.59E-01	4.78E-37		-6.88E-01	5.15E-06		-1.36E+00	2.10E-17	Down	Unigene13277_All//gi|115473321|ref|NP_001060259.1|//3.00E-08//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]		Unigene13277_All//0.00E+00//gi|21093543|gb|BQ405856.1|BQ405856			GO:0044464	nr +
Unigene13278_All	1152	38.51	11.22	9.38	39.26	30.94	24.42	56.48	23.22	21.79	-1.78E+00	1.21E-77	Down	-2.04E+00	7.40E-90	Down	-3.44E-01	2.42E-06		-6.85E-01	6.63E-19		-1.28E+00	9.28E-86	Down	-1.37E+00	4.31E-98	Down	Unigene13278_All//gi|10946427|gb|AG24908.1|AF305075_1//1.00E-138//proliferating cell nuclear antigen [Nicotiana benthamiana]	Unigene13278_All//9.00E-134//AT2G29570| PCNA2 (PROLIFERATING CELL NUCLEAR ANTIGEN 2); DNA binding / DNA polymerase processivity factor	Unigene13278_All//0.00E+00//gi|78343386|gb|DT563660.1|DT563660		ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03430|Mismatch repair		nr +
Unigene13279_All	3315	5.76	11.57	8.71	12.64	13.24	15.40	19.36	22.42	22.86	1.01E+00	2.55E-28	Up	5.96E-01	8.81E-09		6.76E-02	5.18E-01		2.85E-01	9.82E-05		2.12E-01	1.19E-04		2.40E-01	5.61E-06		Unigene13279_All//gi|30680527|ref|NP_196066.2|//1.00E-178//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene13279_All//8.00E-142//AT5G04160| protein binding / zinc ion binding	Unigene13279_All//0.00E+00//gi|164314099|gb|ES817851.1|ES817851			GO:0005488	nr +
Unigene13282_All	1089	5.14	16.70	3.23	8.14	9.52	13.98	45.39	87.31	57.98	1.70E+00	4.69E-30	Up	-6.72E-01	1.05E-02		2.25E-01	2.52E-01		7.80E-01	2.96E-08		9.44E-01	2.61E-76		3.53E-01	9.65E-10		Unigene13282_All//gi|119935815|gb|ABM06001.1|//1.00E-73//At5g64300 [Arabidopsis thaliana]	Unigene13282_All//7.00E-75//AT5G64300| ATGCH; 3,4-dihydroxy-2-butanone-4-phosphate synthase/ GTP cyclohydrolase II	Unigene13282_All//0.00E+00//gi|48808419|gb|CO109733.1|CO109733		ko00740|Riboflavin metabolism	GO:0003933//GO:0006771//GO:0016830//GO:0043231//GO:0046914	nr +
Unigene13283_All	2100	9.72	20.27	8.29	14.87	14.48	21.98	35.86	58.59	41.53	1.06E+00	4.07E-34	Up	-2.29E-01	8.80E-02		-3.87E-02	7.77E-01		5.64E-01	1.10E-13		7.09E-01	1.56E-60		2.12E-01	1.64E-05		Unigene13283_All//gi|298561264|dbj|BAJ09646.1|//0.00E+00//GTP cyclohydrolase II/3,4-dihydroxy-2-butanone 4-phosphate synthase [Nicotiana benthamiana]	Unigene13283_All//0.00E+00//AT5G64300| ATGCH; 3,4-dihydroxy-2-butanone-4-phosphate synthase/ GTP cyclohydrolase II	Unigene13283_All//0.00E+00//TC135576		ko00740|Riboflavin metabolism	GO:0003933//GO:0006771//GO:0016830//GO:0043231//GO:0046914	nr -
Unigene13292_All	1016	3.55	3.64	3.20	7.94	9.80	29.12	30.30	88.69	75.72	3.50E-02	9.28E-01		-1.52E-01	6.45E-01		3.02E-01	1.10E-01		1.87E+00	2.57E-59	Up	1.55E+00	2.68E-157	Up	1.32E+00	3.92E-108	Up	Unigene13292_All//gi|224112939|ref|XP_002332682.1|//1.00E-111//cytochrome P450 [Populus trichocarpa] >gi|222838808|gb|EEE77159.1|cytochrome P450 [Populus trichocarpa]	Unigene13292_All//5.00E-83//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene13292_All//0.00E+00//TC176121		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0016491	nr -
Unigene13294_All	485	3.56	2.93	4.83	11.91	8.73	13.41	3.05	3.62	7.47	-2.83E-01	5.86E-01		4.40E-01	3.25E-01		-4.48E-01	6.56E-02		1.71E-01	5.34E-01		2.46E-01	6.30E-01		1.29E+00	9.57E-06	Up	Unigene13294_All//gi|27463527|gb|AA015846.1|//8.00E-33//resistance protein KR4 [Glycine max]	Unigene13294_All//2.00E-14//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene13294_All//1.00E-140//ES801884				nr -
Unigene13296_All	2853	2.82	3.57	2.45	7.25	5.67	3.61	3.66	2.09	4.25	3.38E-01	6.64E-02		-2.08E-01	3.80E-01		-3.53E-01	2.18E-03		-1.01E+00	9.44E-17	Down	-8.05E-01	3.73E-07		2.14E-01	1.58E-01		Unigene13296_All//gi|115455633|ref|NP_001051417.1|//0.00E+00//Os03g0773600 [Oryza sativa Japonica Group] >gi|108711311|gb|ABF99106.1|Kinesin motor domain containing protein, expressed [Oryza sativa (Japonica cultivar-group)] >gi|113549888|dbj|BAF13331.1|Os03g0773600 [Oryza sativa Japonica Group]	Unigene13296_All//6.00E-166//AT3G49650| kinesin motor protein-related	Unigene13296_All//0.00E+00//TC168718			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr +
Unigene13297_All	540	0.87	0.00	0.89	0.46	1.98	2.17	2.98	0.46	1.33	-9.77E+00	5.56E-03		2.54E-02	1.00E+00		2.10E+00	4.32E-03		2.24E+00	1.82E-03		-2.68E+00	2.38E-06	Down	-1.16E+00	1.02E-02					Unigene13297_All//0.00E+00//gi|78345830|gb|DT566104.1|DT566104				
Unigene13303_All	2312	2.35	1.82	1.15	2.67	2.26	2.68	5.03	2.71	4.10	-3.72E-01	1.54E-01		-1.03E+00	1.29E-04	Down	-2.39E-01	3.55E-01		2.40E-03	9.94E-01		-8.91E-01	3.31E-09		-2.94E-01	4.79E-02		Unigene13303_All//gi|8778846|gb|AAF79845.1|AC026875_25//1.00E-177//T6D22.6 [Arabidopsis thaliana]	Unigene13303_All//7.00E-158//AT1G07970| unknown protein	Unigene13303_All//0.00E+00//TC178480				nr -
Unigene13305_All	470	0.78	1.19	1.13	2.12	0.95	0.86	2.88	1.33	0.76	6.06E-01	5.31E-01		5.40E-01	6.10E-01		-1.15E+00	8.41E-02		-1.29E+00	7.06E-02		-1.11E+00	3.31E-02		-1.92E+00	4.37E-04	Down				Unigene13305_All//9.00E-09//TC148815				
Unigene13306_All	723	4.20	8.55	8.18	4.55	5.48	4.19	3.51	2.31	1.65	1.03E+00	2.23E-05	Up	9.62E-01	1.66E-04		2.68E-01	4.42E-01		-1.20E-01	7.39E-01		-6.02E-01	9.38E-02		-1.09E+00	1.73E-03					Unigene13306_All//3.00E-19//TC148815				

Unigene13308_All	1174	9.49	4.23	10.07	27.41	26.13	13.54	7.74	3.42	1.46	-1.17E+00	5.57E-11	Down	8.51E-02	6.33E-01		-6.88E-02	5.63E-01		-1.02E+00	2.93E-26	Down	-1.18E+00	3.29E-11	Down	-2.41E+00	3.83E-30	Down	Unigene13308_All//gi|15230827|ref|NP_189164.1|//3.00E-10//nucleic acid binding [Arabidopsis thaliana] >gi|9294184|dbj|BAB02086.1| reverse transcriptase-like protein [Arabidopsis thaliana]	Unigene13308_All//1.00E-10//AT3G25270| nucleic acid binding	Unigene13308_All//2.00E-15//DW237182				nr +
Unigene13309_All	1287	1.38	0.91	2.11	4.61	3.85	2.11	0.99	0.49	0.50	-6.10E-01	2.16E-01		6.10E-01	1.32E-01		-2.58E-01	3.19E-01		-1.13E+00	3.19E-06	Down	-1.02E+00	5.93E-02		-9.93E-01	5.40E-02		Unigene13309_All//gi|15230827|ref|NP_189164.1|//2.00E-11//nucleic acid binding [Arabidopsis thaliana] >gi|9294184|dbj|BAB02086.1| reverse transcriptase-like protein [Arabidopsis thaliana]	Unigene13309_All//1.00E-11//AT3G25270| nucleic acid binding	Unigene13309_All//2.00E-15//gi|78347908|gb|DT568182.1|DT568182			GO:0044464	nr +
Unigene13312_All	1677	6.18	7.07	7.21	15.83	14.44	14.97	6.38	2.87	3.80	1.95E-01	2.74E-01		2.23E-01	2.28E-01		-1.33E-01	2.68E-01		-8.04E-02	5.49E-01		-1.15E+00	1.26E-12	Down	-7.47E-01	9.37E-07		Unigene13312_All//gi|209863160|gb|AC188738.1|//1.00E-156//At5g14550 [Arabidopsis thaliana]	Unigene13312_All//5.00E-153//AT5G14550| unknown protein	Unigene13312_All//0.00E+00//TC158153			GO:0044464	nr -
Unigene13313_All	2795	10.54	5.89	6.46	12.35	18.71	13.52	5.69	3.95	1.45	-8.39E-01	2.03E-16		-7.06E-01	7.55E-12		6.00E-01	7.54E-19		1.31E-01	1.92E-01		-5.27E-01	2.25E-05		-1.97E+00	1.31E-40	Down	Unigene13313_All//gi|6224712|gb|AAF05914.1|AF180390_1//0.00E+00//non-phototropic hypocotyl 3 [Arabidopsis thaliana]	Unigene13313_All//0.00E+00//AT5G64330| NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3); protein binding / signal transducer	Unigene13313_All//0.00E+00//ES806814			GO:0005488//GO:0009314//GO:0009606//GO:0016020//GO:0030522//GO:0060089	nr +
Unigene13314_All	1962	3.79	12.24	5.65	4.29	2.93	7.48	19.57	68.49	22.76	1.69E+00	3.06E-39	Up	5.76E-01	1.15E-03		-5.50E-01	3.42E-03		8.02E-01	2.36E-08		1.81E+00	1.48E-291	Up	2.18E-01	2.13E-03		Unigene13314_All//gi|224077380|ref|XP_002305237.1|//0.00E+00//acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa] >gi|222848201|gb|EEE85748.1| acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]	Unigene13314_All//0.00E+00//AT1G66120| acyl-activating enzyme 11 (AAE11)	Unigene13314_All//0.00E+00//TC159592	ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0016405//GO:0019758	nr -
Unigene13315_All	800	14.58	29.26	20.57	35.06	58.02	50.75	32.71	31.09	33.51	1.00E+00	1.54E-17	Up	4.96E-01	4.85E-04		7.27E-01	2.24E-23		5.34E-01	4.82E-11		-7.37E-02	5.37E-01		3.49E-02	7.47E-01		Unigene13315_All//gi|183584854|gb|ACC63895.1|//7.00E-72//MAP kinase [Gossypium raimondii]	Unigene13315_All//3.00E-68//AT1G53510| ATMPK18; MAP kinase	Unigene13315_All//0.00E+00//gi|78347149|gb|DT567423.1|DT567423	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0032559	nr -
Unigene13316_All	2407	4.85	2.80	1.57	10.12	9.04	6.55	6.97	2.69	4.47	-7.92E-01	2.07E-06		-1.63E+00	1.09E-17	Down	-1.63E-01	1.75E-01		-6.28E-01	4.61E-09		-1.37E+00	3.83E-25	Down	-6.42E-01	6.12E-08		Unigene13316_All//gi|79339424|ref|NP_172370.3|//0.00E+00//CAX11: calcium:sodium antiporter/ cation:cation antiporter [Arabidopsis thaliana] >gi|45773954|gb|AAS76781.1| At1g08960 [Arabidopsis thaliana]	Unigene13316_All//2.00E-163//AT1G08960| CAX11: calcium:sodium antiporter/ cation:cation antiporter	Unigene13316_All//0.00E+00//TC176723			GO:0006811//GO:0015298//GO:0031224	nr -
Unigene13318_All	1748	3.14	4.35	6.34	153.35	171.19	150.14	159.32	26.66	25.14	4.68E-01	2.80E-02		1.01E+00	1.99E-08	Up	1.59E-01	3.74E-09		-3.05E-02	4.53E-01		-2.58E+00	0.00E+00	Down	-2.66E+00	0.00E+00	Down	Unigene13318_All//gi|240256390|ref|NP_199107.5|//1.00E-120//triacylglycerol lipase [Arabidopsis thaliana]	Unigene13318_All//4.00E-121//AT5G42930| triacylglycerol lipase	Unigene13318_All//0.00E+00//TC151789				nr +
Unigene1332_All	1307	2.20	23.38	12.63	15.02	22.03	27.51	6.92	35.98	17.16	3.41E+00	2.61E-112	Up	2.52E+00	1.01E-43	Up	5.53E-01	3.35E-09		8.73E-01	1.51E-22		2.38E+00	1.44E-145	Up	1.31E+00	1.06E-31	Up	Unigene1332_All//gi|222423130|dbj|BAH19544.1|//4.00E-12//AT4G21215 [Arabidopsis thaliana]	Unigene1332_All//3.00E-08//AT4G21215| unknown protein	Unigene1332_All//0.00E+00//gi|109837813|gb|DW236374.1|DW236374				nr +
Unigene13320_All	2115	10.24	7.07	8.48	13.80	9.23	6.56	4.06	1.94	0.77	-5.35E-01	5.23E-06		-2.72E-01	3.31E-02		-5.80E-01	2.11E-10		-1.07E+00	4.81E-26	Down	-1.07E+00	3.63E-09	Down	-2.39E+00	2.60E-28	Down	Unigene13320_All//gi|124359162|gb|ABN06683.1|//1.00E-103//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene13320_All//6.00E-34//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene13320_All//1.00E-66//TC141427				nr -
Unigene13324_All	1962	8.99	5.86	9.04	4.11	4.42	2.67	3.28	2.83	1.36	-6.16E-01	2.91E-06		8.20E-03	9.78E-01		1.05E-01	6.56E-01		-6.23E-01	1.92E-03		-2.09E-01	3.77E-01		-1.27E+00	2.37E-09	Down	Unigene13324_All//gi|15238440|ref|NP_198372.1|//0.00E+00//EGY1 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN 1); metalloendopeptidase [Arabidopsis thaliana]	Unigene13324_All//0.00E+00//AT5G35220| EGY1 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN 1); metalloendopeptidase	Unigene13324_All//0.00E+00//TC146545			GO:0004175//GO:0009314//GO:0009536//GO:0009630//GO:0009668//GO:0009725//GO:0019538//GO:0019684//GO:0043623	nr -
Unigene13328_All	1213	8.93	23.52	11.37	6.82	9.57	11.73	8.47	11.13	18.43	1.40E+00	2.91E-35	Up	3.49E-01	3.06E-02		4.89E-01	2.22E-03		7.83E-01	8.23E-08		3.94E-01	4.32E-03		1.12E+00	6.26E-25	Up	Unigene13328_All//gi|294612078|gb|ADF27783.1|//2.00E-98//neutral/alkaline invertase 2 [Phelipanche ramosa]	Unigene13328_All//3.00E-92//AT3G05820| beta-fructofuranosidase/ catalytic	Unigene13328_All//4.00E-44//CO113640			GO:0004553	nr +
Unigene13331_All	917	2.74	1.38	7.26	18.69	13.97	11.92	0.51	2.96	1.04	-9.87E-01	1.38E-02		1.41E+00	1.66E-08	Up	-4.20E-01	8.78E-04		-6.49E-01	6.29E-07		2.55E+00	9.86E-10	Up	1.04E+00	9.27E-02					Unigene13331_All//1.00E-77//DW227571				
Unigene13332_All	478	1.09	1.48	0.67	1.25	3.67	4.06	0.71	0.44	0.75	4.39E-01	6.16E-01		-7.12E-01	4.97E-01		1.55E+00	2.14E-03		1.70E+00	6.03E-04	Up	-6.95E-01	5.78E-01		8.41E-02	9.57E-01		Unigene13332_All//gi|225437451|ref|XP_002268905.1|//4.00E-16//PREDICTED: similar to helicase domain-containing protein [Vitis vinifera]	Unigene13332_All//2.00E-05//AT1G33390| helicase domain-containing protein	Unigene13332_All//1.00E-174//DW227571			GO:0005488//GO:0017111	nr -
Unigene13333_All	1119	1.36	0.68	1.24	6.81	5.85	4.52	0.38	2.05	0.25	-9.97E-01	6.49E-02		-1.32E-01	8.01E-01		-2.20E-01	3.37E-01		-5.91E-01	4.57E-03		2.44E+00	5.47E-08	Up	-6.00E-01	5.53E-01									
Unigene13334_All	1929	0.46	0.26	0.83	2.53	1.96	1.55	0.64	2.45	0.68	-8.12E-01	2.68E-01		8.45E-01	1.25E-01		-3.66E-01	1.90E-01		-7.12E-01	8.23E-03		1.95E+00	5.16E-12	Up	1.01E-01	8.49E-01		Unigene13334_All//gi|225437451|ref|XP_002268905.1|//4.00E-14//PREDICTED: similar to helicase domain-containing protein [Vitis vinifera]		Unigene13334_All//8.00E-176//DW227571				nr +
Unigene13335_All	2451	3.44	2.13	2.61	15.89	14.13	13.41	9.16	4.35	5.04	-6.91E-01	5.17E-04		-3.99E-01	6.08E-02		-1.69E-01	5.76E-02		-2.45E-01	4.93E-03		-1.07E+00	6.40E-23	Down	-8.62E-01	1.23E-16		Unigene13335_All//gi|18397574|ref|NP_566284.1|//0.00E+00//galactosyltransferase family protein [Arabidopsis thaliana] >gi|75167739|sp|Q94SW1.1|B3GTG_ARATH RecName: Full=Probable beta-1,3-galactosyltransferase 16 >gi|13605629|gb|AAK32808.1|AF36164 0_1 AT3g06440/F24P17_7 [Arabidopsis thaliana] >gi|25090104|gb|AAN72229.1| At3g06440/F24P17_7 [Arabidopsis thaliana]	Unigene13335_All//0.00E+00//AT3G06440| galactosyltransferase family protein				GO:0004721//GO:0006464//GO:0016758//GO:0030246//GO:0031224//GO:0043469//GO:0043231//GO:0043234	nr +
Unigene13336_All	707	8.07	6.31	5.20	13.11	8.23	5.56	2.21	1.83	2.59	-3.55E-01	1.65E-01		-6.34E-01	1.46E-02		-6.71E-01	1.23E-04		-1.24E+00	1.01E-10	Down	-2.72E-01	6.13E-01		2.28E-01	6.00E-01		Unigene13336_All//gi|110288963|gb|AAP53315.2|//2.00E-08//retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]		Unigene13336_All//1.00E-156//DN779890				nr +
Unigene13337_All	1374	1.22	1.29	1.28	1.96	1.28	0.76	2.74	0.94	2.12	8.30E-02	8.64E-01		6.98E-02	8.91E-01		-6.15E-01	1.01E-01		-1.37E+00	4.31E-04	Down	-1.54E+00	3.04E-07	Down	-3.72E-01	1.88E-01		Unigene13337_All//gi|115442463|ref|NP_001045511.1|//8.00E-16//Os01g0967700 [Oryza sativa (japonica Group)] >gi|113535042|dbj|BAF07425.1| Os01g0967700 [Oryza sativa (japonica Group)]	Unigene13337_All//9.00E-11//AT3G25270| nucleic acid binding	Unigene13337_All//0.00E+00//DN779890			GO:0005488	nr -
Unigene13339_All	869	20.71	7.81	11.46	10.66	6.74	7.54	5.60	5.58	4.49	-1.41E+00	7.66E-23	Down	-8.54E-01	3.82E-10		-6.62E-01	1.52E-04		-5.01E-01	7.77E-03		-4.10E-03	1.02E+00		-3.17E-01	2.00E-01		Unigene13339_All//gi|8810469|gb|AAF80130.1|AC024174_12//1.00E-63//Contains similarity to a b-Zip binding protein from Arabidopsis thaliana gb|Z86093 and contains a b-Zip transcription factor PF|00170 domain. ESTs gb|AV551499, gb|T04752, gb|AV550784, gb|AV550336, gb|AV545846, gb|AV538486, gb|AV542369, gb|AV538179 come from this gene >gi|17065886|emb|CAD12037.1 AthZIP transcription factor [Arabidopsis thaliana] >gi|110739188|dbj|BAF01510.1| bZip transcription factor AtbZip69 [Arabidopsis thaliana] >gi|114213515|gb|ABI54340.1| At1g06070 [Arabidopsis thaliana]	Unigene13339_All//3.00E-37//AT1G06070| bZIP transcription factor, putative (bZIP69)	Unigene13339_All//0.00E+00//TC177684	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0043231	nr +
Unigene13341_All	2586	1.56	1.02	1.13	7.90	5.13	3.37	4.33	3.25	13.83	-6.13E-01	4.41E-02		-4.60E-01	1.52E-01		-6.23E-01	2.13E-08		-1.23E+00	1.12E-22	Down	-4.15E-01	6.65E-03		1.67E+00	1.07E-71	Up	Unigene13341_All//gi|30696817|ref|NP_200517.2|//1.00E-106//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	Unigene13341_All//7.00E-16//AT5G57070| hydroxyproline-rich glycoprotein family protein	Unigene13341_All//4.00E-24//ES797216			GO:0044464	nr -
Unigene13344_All	2704	3.37	3.17	1.81	4.22	2.87	3.77	14.54	3.90	4.95	-8.84E-02	6.57E-01		-8.94E-01	7.33E-06		-5.58E-01	3.57E-04		-1.60E-01	4.12E-01		-1.90E+00	5.85E-92	Down	-1.55E+00	1.59E-71	Down	Unigene13344_All//gi|224103837|ref|XP_002313213.1|//0.00E+00//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222849621|gb|EEE87168.1| oligopeptide transporter OPT family [Populus trichocarpa]	Unigene13344_All//0.00E+00//AT5G64410| OPT4 (OLIGOPEPTIDE TRANSPORTER 4); oligopeptide transporter	Unigene13344_All//0.00E+00//gi|54122982|gb|CO498491.1|CO498491			GO:0015197//GO:0015833//GO:0044464	nr +
Unigene13345_All	1900	4.35	1.44	2.30	3.36	3.12	2.42	2.07	0.95	1.01	-1.60E+00	5.72E-13	Down	-9.21E-01	1.26E-05		-1.06E-01	7.00E-01		-4.69E-01	4.81E-02		-1.13E+00	5.35E-05	Down	-1.04E+00	1.18E-04	Down	Unigene13345_All//gi|297835104|ref|XP_002885434.1|//0.00E+00//RNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331274|gb|EFH61693.1| RNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13345_All//0.00E+00//AT3G21300| RNA methyltransferase family protein		ko00350|Tyrosine metabolism//ko00450|Selenoamino acid metabolism//ko00340|Histidine metabolism	GO:0003676//GO:0008168//GO:0010467//GO:0043231	nr -
Unigene13346_All	657	4.06	9.49	9.97	3.11	5.56	1.92	9.07	6.87	6.91	1.22E+00	6.60E-07	Up	1.30E+00	1.78E-07	Up	8.38E-01	7.51E-03		-6.92E-01	1.32E-01		-4.01E-01	7.26E-02		-3.93E-01	6.58E-02		Unigene13346_All//gi|224054176|ref|XP_002298129.1|//7.00E-38//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene13346_All//2.00E-33//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene13346_All//0.00E+00//DW498803		ko00904|Diterpenoid biosynthesis	GO:0016491//GO:0044464	nr +
Unigene13347_All	1193	9.21	25.82	24.01	7.31	18.62	10.22	21.48	12.72	20.14	1.49E+00	1.07E-41	Up	1.38E+00	8.17E-34	Up	1.35E+00	1.46E-30	Up	4.84E-01	2.65E-03		-7.56E-01	9.19E-15		-9.30E-02	3.93E-01		Unigene13347_All//gi|224054176|ref|XP_002298129.1|//1.00E-107//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene13347_All//1.00E-103//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene13347_All//0.00E+00//DW498803		ko00904|Diterpenoid biosynthesis	GO:0008152//GO:0016491//GO:0044464	nr -
Unigene13348_All	1779	17.71	63.12	40.17	13.89	13.57	29.80	11.60	9.49	8.87	1.83E+00	1.25E-202	Up	1.18E+00	1.10E-65	Up	-3.36E-02	8.31E-01		1.10E+00	3.12E-48	Up	-2.89E-01	9.16E-03		-3.87E-01	2.44E-04		Unigene13348_All//gi|124360437|gb|ABN08447.1|//1.00E-129//Patatin [Medicago truncatula]	Unigene13348_All//4.00E-112//AT1G53270| patatin-related	Unigene13348_All//0.00E+00//TC173010				nr +
Unigene13354_All	1598	6.19	5.96	5.00	8.20	9.03	4.47	3.97	2.22	1.77	-5.39E-02	7.79E-01		-3.08E-01	1.23E-01		1.39E-01	4.26E-01		-8.77E-01	9.64E-09		-8.36E-01	6.37E-05		-1.16E+00	3.39E-08	Down				Unigene13354_All//0.00E+00//DT050265				
Unigene13355_All	2395	2.16	13.56	1.20	2.18	5.16	2.09	4.61	9.07	17.27	2.65E+00	7.54E-93	Up	-8.49E-01	1.98E-03		1.24E+00	4.00E-15	Up	-6.12E-02	8.37E-01		9.78E-01	4.12E-19		1.91E+00	9.14E-99	Up	Unigene13355_All//gi|10998537|gb|AAG25966.1|AF302082_1//0.00E+00//cytokinin-regulated kinase 1 [Nicotiana tabacum]	Unigene13355_All//0.00E+00//AT5G47850| CCR4 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 4); kinase	Unigene13355_All//0.00E+00//gi|78341544|gb|DT561818.1|DT561818		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0042802	nr +
Unigene13356_All	2289	12.14	35.93	14.26	19.89	30.49	28.02	42.43	66.52	130.97	1.57E+00	7.51E-119	Up	2.33E-01	2.27E-02		6.16E-01	2.79E-26		4.94E-01	6.17E-15		6.49E-01	4.43E-64		1.63E+00	0.00E+00	Up	Unigene13356_All//gi|42567655|ref|NP_196133.3|//1.00E-101//transcription elongation factor-related [Arabidopsis thaliana]	Unigene13356_All//3.00E-90//AT5G05140| transcription elongation factor-related	Unigene13356_All//0.00E+00//gi|164314812|gb|ES842982.1|ES842982				nr -

Unigene13359_A11	1847	7.00	4.25	4.84	28.56	27.78	63.01	4.83	2.96	4.38	-7.19E-01	4.73E-06		-5.31E-01	1.13E-03		-4.01E-02	6.66E-01		1.14E+00	1.40E-111	Up	-7.04E-01	4.13E-05		-1.42E-01	4.54E-01		Unigene13359_A11//gi|18420859|ref|NP_568463.1|//1.00E-172//CYP714A1: electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|16604324|gb|AAL24168.1|At5g24910/F6A4_120 [Arabidopsis thaliana] >gi|27363368|gb|AAO11603.1|At5g24910/F6A4_120 [Arabidopsis thaliana]	Unigene13359_A11//2.00E-165//AT5G24910| CYP714A1: electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene13359_A11//0.00E+00//TC145839		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids	GO:0005506//GO:0008152//GO:0016634	nr -
Unigene13360_A11	1044	19.39	8.40	8.21	28.39	24.31	33.22	64.11	23.70	30.26	-1.21E+00	2.19E-20	Down	-1.24E+00	2.39E-20	Down	-2.24E-01	2.48E-02		2.27E-01	1.65E-02		-1.44E+00	1.08E-104	Down	-1.08E+00	1.75E-69	Down	Unigene13360_A11//gi|1173256|sp|P46299.1|RS4_GOSHI//1.00E-145//RecName: Full=40S ribosomal protein S4 >gi|488739|emb|CAA55882.1|ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene13360_A11//3.00E-125//AT5G58420| 40S ribosomal protein S4 (RPS4D)	Unigene13360_A11//0.00E+00//TC152261		ko03010|Ribosome		nr +
Unigene13365_A11	1942	12.96	3.52	5.13	11.54	11.51	14.54	16.11	14.14	40.13	-1.88E+00	1.08E-47	Down	-1.34E+00	3.02E-28	Down	-4.40E-03	9.68E-01		3.33E-01	1.06E-03		-1.88E-01	4.03E-02		1.32E+00	6.93E-109	Up	Unigene13365_A11//gi|116518570|gb|ABJ99502.1|//0.00E+00//1-aminocyclopropane-1-carboxylate synthase [Gossypium hirsutum]	Unigene13365_A11//0.00E+00//AT4G11280| ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase	Unigene13365_A11//0.00E+00//TC165150		ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016740//GO:0016846//GO:0048037	nr -
Unigene13366_A11	3602	0.87	1.06	1.27	10.11	9.84	6.70	4.65	2.00	1.45	2.76E-01	3.86E-01		5.45E-01	6.70E-02		-3.94E-02	7.48E-01		-5.94E-01	4.72E-12		-1.22E+00	5.30E-21	Down	-1.68E+00	1.42E-34	Down	Unigene13366_A11//gi|297824981|ref|XP_002880373.1|//0.00E+00//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326212|gb|EFH56632.1|kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13366_A11//gi|297824981|ref|XP_002880373.1|//0.00E+00//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326212|gb|EFH56632.1|kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13366_A11//0.00E+00//AT2G21300| kinesin motor family protein	Unigene13366_A11//0.00E+00//TC177250			GO:0000166//GO:0003774//GO:0016020	nr +
Unigene13367_A11	1265	64.89	232.84	111.93	56.82	90.19	97.40	23.33	55.94	25.67	1.84E+00	0.00E+00	Up	7.86E-01	4.64E-66		6.66E-01	4.64E-49		7.77E-01	1.98E-62		1.26E+00	1.02E-90	Up	1.38E-01	1.25E-01		Unigene13367_A11//gi|15237703|ref|NP_201248.1|//1.00E-103//octicosapeptide/Phox/BemIp (PB1) domain-containing protein [Arabidopsis thaliana] >gi|17064916|gb|AAL32612.1|Unknown protein [Arabidopsis thaliana] >gi|31711922|gb|AAP68317.1|At5g64430 [Arabidopsis thaliana]	Unigene13367_A11//4.00E-85//AT5G64430| octicosapeptide/Phox/BemIp (PB1) domain-containing protein	Unigene13367_A11//0.00E+00//TC147781				nr -
Unigene13368_A11	1820	16.99	8.44	9.36	33.86	21.19	21.76	27.95	16.72	29.68	-1.01E+00	3.30E-23	Down	-8.60E-01	3.69E-17		-6.76E-01	4.16E-28		-6.38E-01	1.43E-22		-7.41E-01	1.47E-27		8.69E-02	2.25E-01		Unigene13368_A11//gi|297848386|ref|XP_002892074.1|//0.00E+00//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337916|gb|EFH68333.1|aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13368_A11//7.00E-169//AT1G01300| aspartyl protease family protein	Unigene13368_A11//0.00E+00//TC131447			GO:0004175//GO:0005618//GO:0019538	nr +
Unigene13369_A11	4339	0.47	0.47	0.12	3.19	2.67	2.31	6.28	1.70	3.64	-9.80E-03	9.87E-01		-1.94E+00	1.99E-04	Down	-2.55E-01	1.02E-01		-4.66E-01	1.77E-03		-1.89E+00	2.44E-63	Down	-7.87E-01	3.14E-17		Unigene13369_A11//gi|297613448|ref|NP_001067167.2|//0.00E+00//Os12g0590500 [Oryza sativa Japonica Group] >gi|255670442|dbj|BAF30186.2|Os12g0590500 [Oryza sativa Japonica Group]	Unigene13369_A11//2.00E-170//AT3G19050| P0K2 (PHRAGMOPLASTORIENTING KINESIN 2); ATP binding / microtubule motor				GO:0000166//GO:0003774//GO:0043229	nr -
Unigene13370_A11	1895	54.03	38.32	26.27	132.12	119.46	141.59	53.15	13.83	15.98	-4.96E-01	3.62E-22		-1.04E+00	2.41E-76	Down	-1.45E-01	1.18E-06		9.99E-02	1.68E-03		-1.94E+00	1.38E-241	Down	-1.73E+00	7.37E-213	Down	Unigene13370_A11//gi|297848386|ref|XP_002892074.1|//0.00E+00//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337916|gb|EFH68333.1|aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13370_A11//2.00E-173//AT1G01300| aspartyl protease family protein	Unigene13370_A11//0.00E+00//TC168995			GO:0004175//GO:0005618//GO:0019538	nr +
Unigene13373_A11	680	0.46	0.45	0.08	0.88	1.16	2.46	2.11	1.91	5.10	-4.64E-02	9.85E-01		-2.56E+00	1.59E-01		4.06E-01	6.32E-01		1.48E+00	5.30E-03		-1.50E-01	7.64E-01		1.27E+00	2.11E-05	Up	Unigene13373_A11//gi|152248869|ref|NP_181965.1|//2.00E-15//DC1 domain-containing protein [Arabidopsis thaliana] >gi|40822978|gb|AAM92250.1|At2g44370 [Arabidopsis thaliana] >gi|45752684|gb|AAS76240.1|At2g44370 [Arabidopsis thaliana]	Unigene13373_A11//1.00E-16//AT2G44370| DC1 domain-containing protein	Unigene13373_A11//4.00E-166//gi|48793188|gb|CO094502.1|CO094502				nr -
Unigene13374_A11	1584	5.75	1.54	1.85	10.00	4.33	10.04	6.01	2.43	2.69	-1.90E+00	5.50E-18	Down	-1.64E+00	4.75E-14	Down	-1.21E+00	1.54E-19	Down	5.10E-03	9.72E-01		-1.31E+00	1.40E-13	Down	-1.16E+00	9.39E-12	Down	Unigene13374_A11//gi|15229101|ref|NP_190487.1|//1.00E-129//RID3 (ROOT INITIATION DEFECTIVE 3); nucleotide binding [Arabidopsis thaliana] >gi|28416679|gb|AAO42870.1|At3g49180 [Arabidopsis thaliana]	Unigene13374_A11//1.00E-130//AT3G49180| RID3 (ROOT INITIATION DEFECTIVE 3); nucleotide binding	Unigene13374_A11//0.00E+00//TC133715		ko03040|Spliceosome//ko03022|Basal transcription factors	GO:0043231	nr +
Unigene13375_A11	1992	7.51	18.54	7.75	6.78	7.87	12.13	6.16	7.15	9.32	1.30E+00	5.94E-41	Up	4.54E-02	7.74E-01		2.15E-01	1.59E-01		8.40E-01	2.15E-14		2.17E-01	1.33E-01		5.99E-01	9.80E-08		Unigene13375_A11//gi|18086417|gb|AAL57636.1|//0.00E+00//At1g34630/F12K21.3 [Arabidopsis thaliana] >gi|22655322|gb|AAM98253.1|At1g34630/F12K21.3 [Arabidopsis thaliana]	Unigene13375_A11//0.00E+00//AT1G34630| unknown protein	Unigene13375_A11//0.00E+00//TC148227				nr +
Unigene13379_A11	523	0.40	0.78	0.81	3.24	2.37	7.51	1.46	2.48	4.11	9.54E-01	4.14E-01		1.03E+00	3.97E-01		-4.50E-01	3.87E-01		1.21E+00	1.00E-04	Up	7.68E-01	1.50E-01		1.50E+00	1.81E-04	Up			Unigene13379_A11//3.00E-141//TC131816				
Unigene13381_A11	1357	17.23	26.73	20.80	27.05	30.88	28.06	41.10	27.38	20.02	6.33E-01	1.53E-12		2.71E-01	1.31E-02		1.91E-01	2.28E-02		5.25E-02	6.29E-01		-5.86E-01	3.74E-20		-1.04E+00	3.73E-54	Down	Unigene13381_A11//gi|115483130|ref|NP_001065158.1|//5.00E-91//Os10g0533900 [Oryza sativa Japonica Group] >gi|31433255|gb|AAP54793.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113639767|dbj|BAF27072.1|Os10g0533900 [Oryza sativa Japonica Group]	Unigene13381_A11//8.00E-85//AT4G25680| unknown protein	Unigene13381_A11//0.00E+00//TC143172				nr +
Unigene13382_A11	1138	3.31	22.13	3.42	27.45	31.17	24.05	78.73	102.58	125.01	2.74E+00	7.85E-75	Up	4.53E-02	8.94E-01		1.83E-01	5.06E-02		-1.91E-01	6.67E-02		3.82E-01	2.90E-19		6.67E-01	2.10E-64		Unigene13382_A11//gi|239056193|emb|CAQ58630.1|//9.00E-64//Unknown gene [Vitis vinifera]	Unigene13382_A11//4.00E-50//AT2G38640| unknown protein	Unigene13382_A11//0.00E+00//TC158452			GO:0043231	nr +
Unigene13383_A11	2002	3.74	2.86	3.17	2.46	2.68	2.12	3.08	10.98	2.01	-3.86E-01	7.65E-02		-2.40E-01	3.19E-01		1.23E-01	6.95E-01		-2.16E-01	4.77E-01		1.83E+00	3.75E-49	Up	-6.18E-01	2.60E-03		Unigene13383_A11//gi|79362513|ref|NP_175422.2|//1.00E-102//methyltransferase [Arabidopsis thaliana]	Unigene13383_A11//2.00E-97//AT1G50000| methyltransferase	Unigene13383_A11//0.00E+00//gi|84156076|gb|DN817302.1|DN817302			GO:0009536//GO:0016741//GO:0042254	nr +
Unigene13384_A11	1718	1.16	0.80	0.65	3.13	3.59	5.78	4.75	1.73	2.57	-5.39E-01	2.35E-01		-8.30E-01	8.49E-02		1.96E-01	4.84E-01		8.85E-01	8.17E-07		-1.46E+00	9.24E-14	Down	-8.84E-01	7.30E-07		Unigene13384_A11//gi|289065767|gb|ADC80921.1|//1.00E-120//delta-8 sphingolipid desaturase [Vernicia fordii]	Unigene13384_A11//7.00E-113//AT2G46210| delta-8 sphingolipid desaturase, putative	Unigene13384_A11//0.00E+00//TC151044		ko00910|Nitrogen metabolism		nr -
Unigene13388_A11	1735	86.10	86.91	135.81	171.58	172.95	55.55	11.14	7.95	4.16	1.36E-02	7.77E-01		6.58E-01	2.70E-80		1.15E-02	8.04E-01		-1.63E+00	0.00E+00	Down	-4.86E-01	1.32E-05		-1.42E+00	2.86E-31	Down	Unigene13388_A11//gi|15228863|ref|NP_188920.1|//0.00E+00//phosphoinositide binding [Arabidopsis thaliana]	Unigene13388_A11//8.00E-128//AT3G22810| phosphoinositide binding	Unigene13388_A11//0.00E+00//TC147551			GO:0005543//GO:0023060	nr -
Unigene13389_A11	1985	10.70	11.36	9.63	15.13	15.51	18.95	46.92	104.50	122.55	8.60E-02	5.20E-01		-1.52E-01	2.65E-01		3.54E-02	8.03E-01		3.25E-01	1.63E-04		1.16E+00	2.58E-230	Up	1.38E+00	0.00E+00	Up	Unigene13389_A11//gi|15450862|gb|AAK96702.1|//1.00E-135//Unknown protein [Arabidopsis thaliana] >gi|31711882|gb|AAP68297.1|At5g44250 [Arabidopsis thaliana]	Unigene13389_A11//2.00E-135//AT5G44250| unknown protein	Unigene13389_A11//0.00E+00//TC135200				nr -
Unigene1339_A11	2650	23.91	17.53	29.22	13.16	22.78	15.85	21.97	8.64	22.75	-4.48E-01	9.55E-12		2.89E-01	2.18E-06		7.92E-01	4.66E-35		2.69E-01	1.12E-03		-1.35E+00	1.05E-82	Down	5.01E-02	4.90E-01		Unigene1339_A11//gi|224060241|ref|XP_002300101.1|//0.00E+00//Cl-channel clc-7 [Populus trichocarpa] >gi|222847359|gb|EEE84906.1| Cl-channel clc-7 [Populus trichocarpa]	Unigene1339_A11//0.00E+00//AT5G40890| ATCLC-A (CHLORIDE CHANNEL A); anion channel/ nitrate transmembrane transporter/ voltage-gated chloride channel	Unigene1339_A11//0.00E+00//C0074460				nr -
Unigene13390_A11	1973	6.10	3.18	3.62	13.48	9.44	7.65	6.00	2.73	2.42	-9.38E-01	1.70E-08		-7.54E-01	8.42E-06		-5.14E-01	9.46E-08		-8.18E-01	2.78E-15		-1.13E+00	1.55E-13	Down	-1.31E+00	2.87E-17	Down	Unigene13390_A11//gi|31711716|gb|AAP68214.1|//0.00E+00//At4g24530 [Arabidopsis thaliana] >gi|110743919|dbj|BAE99793.1|PsRT17-1 like protein [Arabidopsis thaliana]	Unigene13390_A11//0.00E+00//AT4G24530| unknown protein	Unigene13390_A11//0.00E+00//TC135004				nr +
Unigene13393_A11	2197	1.24	2.51	2.69	14.40	13.73	11.06	0.92	0.74	0.60	1.02E+00	7.32E-05	Up	1.12E+00	1.46E-05	Up	-6.85E-02	5.71E-01		-3.81E-01	4.86E-05		-3.16E-01	4.65E-01		-6.26E-01	1.09E-01		Unigene13393_A11//gi|15230158|ref|NP_188497.1|//5.00E-39//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene13393_A11//3.00E-27//AT3G18670| ankyrin repeat family protein	Unigene13393_A11//7.00E-07//DN758589				nr +
Unigene13394_A11	1675	6.12	13.67	7.63	7.73	6.41	9.17	1.77	5.17	4.28	1.16E+00	1.84E-21	Up	3.18E-01	6.19E-02		-2.70E-01	9.33E-02		2.46E-01	1.12E-01		1.55E+00	9.37E-16	Up	1.28E+00	2.41E-10	Up	Unigene13394_A11//gi|297604224|ref|NP_001055130.2|//1.00E-127//Os05g0299500 [Oryza sativa Japonica Group] >gi|255676221|dbj|BAF17044.2|Os05g0299500 [Oryza sativa Japonica Group]	Unigene13394_A11//7.00E-110//AT3G59340| unknown protein	Unigene13394_A11//0.00E+00//TC158356				nr -
Unigene13396_A11	3663	11.14	10.07	10.34	12.51	9.19	8.63	28.94	21.68	10.48	-1.46E-01	1.07E-01		-1.08E-01	2.69E-01		-4.45E-01	4.90E-10		-5.36E-01	1.53E-12		-4.17E-01	1.59E-20		-1.46E+00	2.36E-175	Down	Unigene13396_A11//gi|225452676|ref|XP_002282227.1|//0.00E+00//PREDICTED: similar to Histidine acid phosphatase [Vitis vinifera]	Unigene13396_A11//0.00E+00//AT3G01310| acid phosphatase/ oxidoreductase/ transition metal ion binding	Unigene13396_A11//0.00E+00//TC176861			GO:0016020//GO:0016791//GO:0032559//GO:0046872	nr +
Unigene13398_A11	1360	4.08	2.31	3.41	4.07	2.63	3.19	9.95	2.15	2.37	-8.20E-01	1.18E-03		-2.60E-01	3.64E-01		-6.27E-01	8.90E-03		-3.51E-01	1.94E-01		-2.21E+00	6.92E-39	Down	-2.07E+00	5.87E-37	Down	Unigene13398_A11//gi|115464161|ref|NP_001055680.1|//1.00E-103//Os05g0444300 [Oryza sativa Japonica Group] >gi|113579231|dbj|BAF17594.1|Os05g0444300 [Oryza sativa Japonica Group]	Unigene13398_A11//3.00E-67//AT3G59310| unknown protein	Unigene13398_A11//0.00E+00//TC149024			GO:0043231	nr +
Unigene13399_A11	366	1.72	3.32	1.45	0.82	2.26	2.22	2.31	0.91	0.22	9.54E-01	1.22E-01		-2.38E-01	7.75E-01		1.47E+00	7.56E-02		1.44E+00	8.45E-02		-1.34E+00	5.68E-02		-3.41E+00	1.35E-04	Down	Unigene13399_A11//gi|224109590|ref|XP_002315247.1|//8.00E-16//metal tolerance protein [Populus trichocarpa] >gi|145453064|gb|ABF68858.1| Mn-specific cation diffusion facilitator transporter [Populus trichocarpa] >gi|222864287|gb|EEF01418.1| metal tolerance protein [Populus trichocarpa]	Unigene13399_A11//9.00E-16//AT2G39450| MTP11; cation transmembrane transporter/ manganese ion transmembrane transporter/ manganese:hydrogen antiporter	Unigene13399_A11//9.00E-138//DR453942			GO:0005768//GO:0006810//GO:0010038//GO:0015082//GO:0030005//GO:0051139	nr -
Unigene1340_A11	3555	2.83	2.15	0.90	4.74	4.29	4.59	5.57	2.36	4.38	-3.93E-01	3.22E-02		-1.65E+00	1.17E-15	Down	-1.42E-01	3.57E-01		-4.64E-02	7.67E-01		-1.24E+00	3.58E-25	Down	-3.45E-01	1.47E-03		Unigene1340_A11//gi|240255799|ref|NP_193011.4|//0.00E+00//sequence-specific DNA binding / transcription factor [Arabidopsis thaliana]	Unigene1340_A11//0.00E+00//AT4G12750| sequence-specific DNA binding / transcription factor	Unigene1340_A11//0.00E+00//gi|109874760|gb|DN503734.1|DN503734				nr +

Unigene13400_All	1791	7.57	8.91	8.86	16.80	14.46	8.47	9.61	6.70	4.69	2.36E-01	1.10E-01		2.28E-01	1.42E-01		-2.17E-01	2.98E-02		-9.88E-01	1.98E-23		-5.21E-01	1.21E-05		-1.03E+00	3.11E-17	Down	Unigene13400_All//gi|224109590|ref|XP_002315247.1|//0.00E+00//metal tolerance protein [Populus trichocarpa] >gi|145453064|gb|ABF68858.1| Mn-specific cation diffusion facilitator transporter [Populus trichocarpa] >gi|222864287|gb|EEF01418.1| metal tolerance protein [Populus trichocarpa]	Unigene13400_All//0.00E+00//AT2G39450| MTP11; cation transmembrane transporter/ manganese ion transmembrane transporter/ manganese:hydrogen antiporter	Unigene13400_All//0.00E+00//TC150406			GO:0005768//GO:0006811//GO:0010038//GO:0015082//GO:0030005//GO:0051139	nr -
Unigene13403_All	605	0.78	1.17	0.53	0.41	0.51	1.12	6.36	18.03	8.30	5.91E-01	4.78E-01		-5.60E-01	6.28E-01		3.15E-01	8.38E-01		1.44E+00	1.28E-01		1.50E+00	7.02E-19	Up	3.84E-01	1.07E-01		Unigene13403_All//gi|15215650|gb|AAK91370.1|//9.00E-13//At2g21620/F2G1.11 [Arabidopsis thaliana] >gi|20334876|gb|AAM16194.1| At2g21620/F2G1.11 [Arabidopsis thaliana]	Unigene13403_All//5.00E-14//AT2G21620| RD2	Unigene13403_All//0.00E+00//TC174061			GO:0005488//GO:0009414	nr -
Unigene13404_All	743	0.77	9.00	1.00	0.94	2.32	6.63	1.71	12.04	8.79	3.54E+00	1.02E-25	Up	3.73E-01	6.23E-01		1.30E+00	9.73E-03		2.82E+00	2.18E-16	Up	2.82E+00	5.33E-34	Up	2.36E+00	4.01E-21	Up	Unigene13404_All//gi|15215650|gb|AAK91370.1|//2.00E-07//At2g21620/F2G1.11 [Arabidopsis thaliana] >gi|20334876|gb|AAM16194.1| At2g21620/F2G1.11 [Arabidopsis thaliana]	Unigene13404_All//4.00E-08//AT2G21620| RD2	Unigene13404_All//4.00E-135//TC142685				nr -
Unigene13405_All	961	17.48	21.46	18.90	18.45	24.33	94.60	28.99	129.65	83.41	2.96E-01	1.70E-02		1.13E-01	4.54E-01		3.99E-01	1.93E-04		2.36E+00	1.93E-243	Up	2.16E+00	0.00E+00	Up	1.52E+00	1.76E-139	Up	Unigene13405_All//gi|30681471|ref|NP_850015.1|//1.00E-83//RD2 [Arabidopsis thaliana] >gi|20198098|gb|AAD23643.2| expressed protein [Arabidopsis thaliana] >gi|21592708|gb|AAM64657.1| RD2 protein [Arabidopsis thaliana]	Unigene13405_All//1.00E-77//AT2G21620| RD2	Unigene13405_All//0.00E+00//TC142685			GO:0005488//GO:0009414	nr -
Unigene13407_All	1236	19.60	10.29	7.54	34.90	41.85	80.94	16.83	1.15	5.71	-9.30E-01	4.42E-16		-1.38E+00	1.86E-28	Down	2.62E-01	1.87E-04		1.21E+00	1.11E-105	Up	-3.87E+00	6.42E-105	Down	-1.56E+00	1.84E-38	Down	Unigene13407_All//gi|15232373|ref|NP_188718.1|//1.00E-153//leucine-rich repeat family protein [Arabidopsis thaliana] >gi|9294409|dbj|BAB02490.1| polygalacturonase inhibitor-like protein [Arabidopsis thaliana]	Unigene13407_All//5.00E-144//AT3G20820| leucine-rich repeat family protein	Unigene13407_All//0.00E+00//TC144428		ko04626|Plant-pathogen interaction		nr +
Unigene13408_All	2717	4.95	2.26	2.20	3.81	3.69	3.13	8.70	8.17	6.35	-1.13E+00	1.56E-12	Down	-1.17E+00	1.30E-12	Down	-4.82E-02	8.13E-01		-2.87E-01	1.32E-01		-9.08E-02	4.49E-01		-4.54E-01	3.36E-06		Unigene13408_All//gi|115442229|ref|NP_001045394.1|//0.00E+00//Os01g0948500 [Oryza sativa Japonica Group] >gi|22830929|dbj|BAC15794.1| armadillo repeat-containing protein-like [Oryza sativa Japonica Group] >gi|113534925|dbj|BAF07308.1| Os01g0948500 [Oryza sativa Japonica Group]	Unigene13408_All//3.00E-42//AT1G20780| SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein ligase	Unigene13408_All//0.00E+00//gi|11204983|gb|BF273925.1|BF273925				nr +
Unigene13409_All	1848	9.48	13.16	16.25	66.99	67.01	59.29	29.90	14.70	7.57	4.73E-01	1.86E-05		7.77E-01	3.78E-14		5.00E-04	9.95E-01		-1.76E-01	1.33E-04		-1.02E+00	4.06E-51	Down	-1.98E+00	1.52E-140	Down	Unigene13409_All//gi|158634904|gb|ABR76289.1|//0.00E+00//beta-glucosidase G4 [Medicago truncatula]	Unigene13409_All//0.00E+00//AT5G36890| BGLU42 (BETA GLUCOSIDASE 42); beta-glucosidase/ catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene13409_All//0.00E+00//TC146388		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0009251//GO:0015926//GO:0043167	nr -
Unigene1341_All	1901	37.84	17.57	21.79	101.17	74.21	217.10	85.72	111.07	105.35	-1.11E+00	1.55E-61	Down	-7.96E-01	1.95E-34		-4.47E-01	3.48E-41		1.10E+00	0.00E+00	Up	3.74E-01	7.01E-33		2.98E-01	3.73E-21		Unigene1341_All//gi|66792614|gb|AAY56409.1|//1.00E-180//At2g17630 [Arabidopsis thaliana] >gi|109134145|gb|ABG25070.1| At2g17630 [Arabidopsis thaliana]	Unigene1341_All//2.00E-170//AT2G17630| phosphoserine aminotransferase, putative	Unigene1341_All//0.00E+00//TC135477		ko00260|Glycine, serine and threonine metabolism//ko00750|Vitamin B6 metabolism		nr -
Unigene13413_All	1642	4.21	3.86	3.53	3.88	2.96	3.41	4.53	4.15	1.92	-1.25E-01	5.95E-01		-2.51E-01	3.16E-01		-3.93E-01	9.17E-02		-1.87E-01	4.83E-01		-1.27E-01	5.85E-01		-1.24E+00	2.25E-10	Down	Unigene13413_All//gi|42562591|ref|NP_175188.3|//2.00E-95//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|40832234|gb|AAR92268.1| At1g47570 [Arabidopsis thaliana] >gi|46518399|gb|AAS99681.1| At1g47570 [Arabidopsis thaliana]	Unigene13413_All//9.00E-86//AT1G47570| zinc finger (C3HC4-type RING finger) family protein	Unigene13413_All//0.00E+00//TC159581			GO:0046914	nr +
Unigene13416_All	1478	26.27	65.58	90.76	60.57	98.79	113.67	18.97	17.79	16.36	1.32E+00	1.71E-108	Up	1.79E+00	1.09E-228	Up	7.06E-01	2.41E-69		9.08E-01	1.10E-110		-9.26E-02	3.97E-01		-2.13E-01	2.14E-02		Unigene13416_All//gi|296046563|gb|ADG86423.1|//4.00E-85//TCP1 [Passiflora morifolia]	Unigene13416_All//6.00E-51//AT2G45680| TCP family transcription factor, putative	Unigene13416_All//0.00E+00//TC166155	TCP		GO:0043231	nr +
Unigene13417_All	1018	7.14	16.77	8.16	21.09	24.69	40.90	107.57	155.24	333.85	1.23E+00	9.68E-18	Up	1.92E-01	3.97E-01		2.28E-01	4.15E-02		9.56E-01	3.36E-30		5.29E-01	2.33E-46		1.63E+00	0.00E+00	Up	Unigene13417_All//gi|297381026|gb|AD139634.1|//6.00E-64//plastid jasmonates ZIM-domain protein [Hevea brasiliensis]	Unigene13417_All//5.00E-41//AT1G19180| JAZ1 (JASMONATE-ZIM-DOMAIN PROTEIN 1); protein binding	Unigene13417_All//0.00E+00//TC167469	Tify	ko04626|Plant-pathogen interaction	GO:0005488//GO:0006952//GO:0009719//GO:0009791//GO:0023033//GO:0043231//GO:0048229	nr +
Unigene1342_All	907	2.65	3.80	5.17	4.50	5.96	4.63	3.59	7.88	19.41	5.18E-01	1.23E-01		9.61E-01	9.79E-04		4.04E-01	1.28E-01		4.02E-02	9.21E-01		1.13E+00	1.79E-08	Up	2.44E+00	1.46E-57	Up	Unigene1342_All//gi|21592886|gb|AAM64836.1|//3.00E-21//F1F0-ATPase inhibitor protein [Arabidopsis thaliana]	Unigene1342_All//2.00E-22//AT2G27730| unknown protein	Unigene1342_All//0.00E+00//TC140291				nr +
Unigene13420_All	1239	20.61	20.20	15.21	35.74	40.11	32.44	54.05	33.26	20.55	-2.86E-02	8.11E-01		-4.38E-01	8.60E-05		1.66E-01	3.24E-02		-1.40E-01	1.18E-01		-7.01E-01	1.03E-32		-1.40E+00	2.70E-103	Down	Unigene13420_All//gi|219879372|gb|ACL51018.1|//1.00E-169//transport inhibitor response protein [Citrus trifoliata]	Unigene13420_All//3.00E-165//AT3G26810| AFB2 (AUXIN SIGNALING F-BOX 2); auxin binding / ubiquitin-protein ligase	Unigene13420_All//0.00E+00//TC172087		ko04626|Plant-pathogen interaction		nr +
Unigene13421_All	452	11.11	21.64	20.97	9.26	10.06	6.99	5.80	1.66	0.71	9.61E-01	2.72E-07		9.16E-01	2.63E-06		1.19E-01	7.43E-01		-4.04E-01	1.99E-01		-1.80E+00	2.14E-06	Down	-3.04E+00	1.19E-11	Down	Unigene13421_All//gi|30681129|ref|NP_850003.1|//6.00E-29//GCL2 (GCR2-LIKE 2); catalytic [Arabidopsis thaliana]	Unigene13421_All//2.00E-30//AT2G20770| GCL2 (GCR2-LIKE 2); catalytic	Unigene13421_All//2.00E-96//gi|78334583|gb|DT554857.1|DT554857			GO:0005488//GO:0043231//GO:0044425	nr -
Unigene13422_All	1658	20.26	49.23	31.28	17.76	18.84	17.57	20.81	5.02	2.40	1.28E+00	2.48E-87	Up	6.27E-01	1.22E-16		8.53E-02	4.79E-01		-1.53E-02	9.16E-01		-2.05E+00	2.30E-89	Down	-3.11E+00	2.47E-148	Down	Unigene13422_All//gi|30681129|ref|NP_850003.1|//1.00E-171//GCL2 (GCR2-LIKE 2); catalytic [Arabidopsis thaliana]	Unigene13422_All//6.00E-173//AT2G20770| GCL2 (GCR2-LIKE 2); catalytic	Unigene13422_All//0.00E+00//gi|78334583|gb|DT554857.1|DT554857				nr -
Unigene13423_All	1809	1.65	0.81	1.15	3.22	1.71	3.22	5.84	2.01	3.22	-1.02E+00	5.06E-03		-5.22E-01	1.72E-01		-9.11E-01	6.38E-05		-5.00E-04	9.96E-01		-1.54E+00	5.61E-19	Down	-8.62E-01	2.67E-08		Unigene13423_All//gi|240255886|ref|NP_193320.6|//0.00E+00//ATRH1; ATP-dependent helicase/ DEAD/H-box RNA helicase binding [Arabidopsis thaliana]	Unigene13423_All//0.00E+00//AT4G15850| ATRH1; ATP-dependent helicase/ DEAD/H-box RNA helicase binding	Unigene13423_All//0.00E+00//CO112896			GO:0032559//GO:0042623	nr -
Unigene13424_All	297	3.70	25.42	8.43	18.79	19.94	9.43	3.42	1.13	2.01	2.78E+00	3.76E-23	Up	1.19E+00	5.25E-03		8.62E-02	8.01E-01		-9.95E-01	6.36E-05		-1.60E+00	1.27E-02		-7.64E-01	1.95E-01		Unigene13424_All//gi|224101035|ref|XP_002312114.1|//8.00E-13//predicted protein [Populus trichocarpa] >gi|222851934|gb|EEE89481.1| predicted protein [Populus trichocarpa]	Unigene13424_All//9.00E-07//AT3G11420| fringe-related protein	Unigene13424_All//1.00E-157//TC163333				nr -
Unigene13425_All	1889	4.13	11.53	6.68	12.34	17.35	15.11	2.62	1.26	1.83	1.48E+00	1.51E-29	Up	6.95E-01	2.37E-05		4.92E-01	1.57E-08		2.92E-01	4.39E-03		-1.05E+00	1.59E-05	Down	-5.13E-01	2.82E-02		Unigene13425_All//gi|15229746|ref|NP_187749.1|//1.00E-159//fringe-related protein [Arabidopsis thaliana] >gi|34098873|gb|AAQ56819.1| At3g11420 [Arabidopsis thaliana]	Unigene13425_All//1.00E-160//AT3G11420| fringe-related protein	Unigene13425_All//0.00E+00//TC160631				nr +
Unigene13428_All	1654	73.51	25.09	22.57	145.32	133.04	68.24	221.27	21.48	79.03	-1.55E+00	4.52E-174	Down	-1.70E+00	5.40E-193	Down	-1.27E-01	4.34E-05		-1.09E+00	1.88E-216	Down	-3.36E+00	0.00E+00	Down	-1.49E+00	0.00E+00	Down	Unigene13428_All//gi|219810208|gb|ACL36352.1|//1.00E-158//fasciclin-like arabinogalactan protein [Gossypium hirsutum]	Unigene13428_All//4.00E-112//AT4G12730| FLA2 (FASCICLIN-LIKE ARABINOGALACTAN 2)	Unigene13428_All//0.00E+00//TC150464		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene13430_All	1118	60.09	236.35	113.98	84.35	120.22	106.85	179.79	209.02	131.17	1.98E+00	0.00E+00	Up	9.24E-01	3.86E-78		5.11E-01	4.44E-36		3.41E-01	4.88E-14		2.17E-01	1.71E-13		-4.55E-01	5.56E-46		Unigene13430_All//gi|297822777|ref|XP_002879271.1|//1.00E-146//BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325110|gb|EFH55530.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13430_All//2.00E-144//AT2G30600| BTB/POZ domain-containing protein	Unigene13430_All//0.00E+00//TC148036				nr +
Unigene13432_All	1962	4.72	10.43	7.52	13.86	17.20	25.44	23.17	12.80	6.44	1.14E+00	6.93E-19	Up	6.72E-01	8.12E-06		3.11E-01	4.31E-04		8.76E-01	3.06E-31		-8.56E-01	2.06E-31		-1.85E+00	2.70E-105	Down	Unigene13432_All//gi|18397936|ref|NP_565381.1|//1.00E-171//SQN (SQUINT); peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi|75333353|sp|Q9C566.1|CYP40_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase CYP40; Short=PPIase CYP40; AltName: Full=Cyclophilin of 40 kDa; Short=Cyclophilin-40; AltName: Full=Rotamase CYP40; AltName: Full=Protein SQUINT >gi|13442983|gb|AAK02067.1| cyclophilin-40 [Arabidopsis thaliana] >gi|20197802|gb|AAD41985.2| expressed protein [Arabidopsis thaliana] >gi|115311455|gb|ABI93908.1| At2g15790 [Arabidopsis thaliana]	Unigene13432_All//7.00E-139//AT2G15790| SQN (SQUINT); peptidyl-prolyl cis-trans isomerase	Unigene13432_All//0.00E+00//gi|164346027|gb|ES822679.1|ES822679			GO:0016859//GO:0044267	nr +
Unigene13433_All	835	2.38	0.97	2.49	1.67	3.55	4.38	0.71	0.10	0.38	-1.29E+00	5.96E-03		6.28E-02	8.93E-01		1.09E+00	2.27E-03		1.39E+00	2.57E-05	Up	-2.82E+00	7.17E-03		-8.93E-01	2.72E-01		Unigene13433_All//gi|15227701|ref|NP_180588.1|//8.00E-79//ATKT1 (POTASSIUM TRANSPORTER 1); potassium ion transmembrane transporter [Arabidopsis thaliana] >gi|38502834|sp|O22397.2|POT1_ARATH RecName: Full=Potassium transporter 1; Short=AtPOT1; Short=AtKUP1; Short=AtKT1 >gi|2654088|gb|AAB87687.1| potassium transporter [Arabidopsis thaliana] >gi|26889079|gb|AAB88901.1| high-affinity potassium transporter [Arabidopsis thaliana] >gi|3150413|gb|AAC16965.1| high affinity K+ transporter (AtKUP1/AtKT1p) [Arabidopsis thaliana] >gi|20197230|gb|AAM14984.1| high affinity K+ transporter (AtKUP1 AtKT1p) [Arabidopsis thaliana] >gi|62320122|dbj|BAD94310.1| high affinity K+ transporter [Arabidopsis thaliana]	Unigene13433_All//4.00E-80//AT2G30070| ATKT1 (POTASSIUM TRANSPORTER 1); potassium ion transmembrane transporter				GO:0030001//GO:0044464//GO:0046873//GO:0050896	nr -

Unigene13434_All	2574	12.20	2.72	5.17	16.26	14.58	14.51	1.54	0.42	0.67	-2.17E+00	2.18E-71	Down	-1.24E+00	3.51E-31	Down	-1.57E-01	7.05E-02		-1.64E-01	6.67E-02		-1.87E+00	9.07E-10	Down	-1.21E+00	8.95E-06	Down	Unigene13434_All//gi|15227701|ref|NP_180568.1|//0.00E+00//ATKT1 (POTASSIUM TRANSPORTER 1); potassium ion transmembrane transporter [Arabidopsis thaliana] >gi|38502834|sp|Q22397.2|POT1_ARATH RecName: Full=Potassium transporter 1; Short=AtPOT1; Short=AtKUP1; Short=AtKT1 >gi|2654088|gb|AAB87687.1| potassium transporter [Arabidopsis thaliana] >gi|2688979|gb|AAB88901.1| high-affinity potassium transporter [Arabidopsis thaliana] >gi|3150413|gb|AAC16965.1| high affinity K+ transporter (AtKUP1/AtKT1p) [Arabidopsis thaliana] >gi|20197230|gb|AAM14984.1| high affinity K+ transporter (AtKUP1 AtKT1p) [Arabidopsis thaliana] >gi|62320122|dbj|BAD94310.1| high affinity K+ transporter [Arabidopsis thaliana]	Unigene13434_All//0.00E+00//AT2G30070| ATKT1 (POTASSIUM TRANSPORTER 1); potassium ion transmembrane transporter	Unigene13434_All//8.00E-10//EX170389			GO:0030001//GO:0044464//GO:0046873	nr +
Unigene13438_All	2679	10.25	8.72	7.27	7.12	12.65	8.77	23.03	74.40	48.72	-2.34E-01	2.96E-02		-4.95E-01	3.39E-06		8.29E-01	2.21E-21		3.00E-01	9.04E-03		1.69E+00	0.00E+00	Up	1.08E+00	2.42E-133	Up	Unigene13438_All//gi|15238657|ref|NP_200125.1|//0.00E+00//CNGC1 (CYCLIC NUCLEOTIDE GATED CHANNEL 1); calmodulin binding / cation channel/ cyclic nucleotide binding / intracellular cyclic nucleotide activated cation channel/ inward rectifier potassium channel [Arabidopsis thaliana] >gi|38502855|sp|O65717.1|CNGC1_ARATH RecName: Full=Cyclic nucleotide-gated ion channel 1; Short=AtCNGC1; AltName: Full=Cyclic nucleotide- and calmodulin-regulated ion channel 1 >gi|9757994|dbj|BAB08416.1| cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]	Unigene13438_All//0.00E+00//AT4G01010| ATCNGC13; calmodulin binding / cyclic nucleotide binding / ion channel	Unigene13438_All//0.00E+00//TC149706		ko04626|Plant-pathogen interaction	GO:0000166//GO:0005217//GO:0005249//GO:0005515//GO:0016020//GO:0070838	nr +
Unigene13439_All	2009	6.95	8.00	7.08	13.24	13.03	11.17	11.76	15.50	26.61	2.01E-01	1.77E-01		2.54E-02	8.85E-01		-2.35E-02	8.51E-01		-2.45E-01	2.50E-02		3.98E-01	3.89E-06		1.18E+00	4.28E-63	Up	Unigene13439_All//gi|124361203|gb|ABN09175.1|//2.00E-96//Homeodomain-related [Medicago truncatula]	Unigene13439_All//5.00E-60//AT3G10760| myb family transcription factor	Unigene13439_All//0.00E+00//TC147914	G2-like		GO:0010468	nr -
Unigene1344_All	2326	26.43	13.31	30.43	7.09	8.41	14.70	5.63	5.37	3.37	-9.90E-01	6.11E-44		2.03E-01	2.15E-03		2.46E-01	5.55E-02		1.05E+00	4.62E-29	Up	-6.87E-02	6.69E-01		-7.40E-01	5.88E-08		Unigene1344_All//gi|115459830|ref|NP_001053515.1|//0.00E+00//Os04g0555300 [Oryza sativa Japonica Group] >gi|38345584|emb|CAD41637.2|OSJNBa0012E24.2 [Oryza sativa (japonica cultivar-group)] >gi|113565086|dbj|BAF15429.1|Os04g0555300 [Oryza sativa Japonica Group]	Unigene1344_All//2.00E-150//AT3G47420| glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative	Unigene1344_All//0.00E+00//DW497419				nr +
Unigene13440_All	2001	8.52	5.98	9.98	98.01	80.19	48.35	68.08	385.92	75.74	-5.12E-01	1.32E-04		2.27E-01	9.40E-02		-2.89E-01	1.00E-18		-1.02E+00	3.36E-158	Down	2.50E+00	0.00E+00	Up	1.54E-01	3.28E-05		Unigene13440_All//gi|297791393|ref|XP_002863581.1|//0.00E+00//FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297309416|gb|EFH39840.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13440_All//2.00E-790| MEE23 (MATERNAL EFFECT EMBRYO ARREST 23); FAD binding / catalytic/ electron carrier/ oxidoreductase	Unigene13440_All//0.00E+00//TC166708			GO:0008152//GO:0030554//GO:0046993	nr -
Unigene13442_All	2512	2.85	7.04	1.44	8.53	10.38	10.52	3.30	8.67	9.25	1.30E+00	5.89E-20	Up	-9.85E-01	1.77E-05		2.83E-01	6.90E-03		3.03E-01	4.62E-03		1.39E+00	4.88E-33	Up	1.49E+00	1.51E-39	Up	Unigene13442_All//gi|209529755|gb|ACI49772.1|//0.00E+00//At5g01100 [Arabidopsis thaliana]	Unigene13442_All//0.00E+00//AT2G37980| unknown protein	Unigene13442_All//0.00E+00//TC151928				nr -
Unigene13445_All	1445	0.76	2.84	1.95	1.79	2.26	1.88	3.57	2.89	3.03	1.90E+00	2.00E-08	Up	1.36E+00	7.25E-04	Up	3.37E-01	3.74E-01		6.51E-02	8.90E-01		-3.04E-01	2.33E-01		-2.35E-01	3.44E-01		Unigene13445_All//gi|11072024|gb|AC28903.1|AC008113_19//1.00E-104//F12A21.19 [Arabidopsis thaliana]	Unigene13445_All//2.00E-105//AT1G67660| DNA binding / nuclease	Unigene13445_All//0.00E+00//TC165073			GO:0004518	nr +
Unigene13446_All	2419	10.04	9.76	8.50	15.88	16.23	13.85	15.92	6.81	9.24	-4.01E-02	7.39E-01		-2.40E-01	4.65E-02		3.16E-02	8.09E-01		-1.97E-01	3.03E-02		-1.23E+00	1.20E-47	Down	-7.85E-01	6.86E-24		Unigene13446_All//gi|297838621|ref|XP_002887192.1|//1.00E-180//F24J5.16 [Arabidopsis lyrata subsp. lyrata] >gi|297333033|gb|EFH63451.1|F24J5.16 [Arabidopsis lyrata subsp. lyrata]	Unigene13446_All//4.00E-177//AT1G25480| unknown protein	Unigene13446_All//0.00E+00//TC141505			GO:0010038	nr -
Unigene13449_All	1535	2.66	5.45	3.54	4.67	6.57	3.88	9.64	10.56	11.29	1.03E+00	4.59E-07	Up	4.12E-01	1.36E-01		4.92E-01	4.68E-03		-2.67E-01	2.69E-01		1.32E-01	3.67E-01		2.28E-01	6.07E-02		Unigene13449_All//gi|193848598|gb|ACF22782.1|//2.00E-95//pH/EDR2 [Brachypodium distachyon]	Unigene13449_All//2.00E-101//AT1G06050| unknown protein	Unigene13449_All//0.00E+00//TC140445				nr +
Unigene13450_All	559	129.91	105.24	184.52	22.90	31.85	18.02	5.14	2.09	3.92	-3.04E-01	6.79E-07		5.06E-01	2.68E-22		4.76E-01	1.23E-04		-3.46E-01	3.24E-02		-1.30E+00	1.31E-04	Down	-3.92E-01	2.33E-01		Unigene13450_All//gi|15225249|ref|NP_180178.1|//3.00E-99//AtGLDP2 (Arabidopsis thaliana glycine decarboxylase P-protein 2); ATP binding / glycine dehydrogenase (decarboxylating) >gi|12229797|sp|O80988.1|GCSP1_ARATH RecName: Full=Glycine dehydrogenase [decarboxylating] 1, mitochondrial; AltName: Full=Glycine decarboxylase 1; AltName: Full=Glycine cleavage system P protein 1; Flags: Precursor	Unigene13450_All//2.00E-100//AT2G26080| AtGLDP2 (Arabidopsis thaliana glycine decarboxylase P-protein 2); ATP binding / glycine dehydrogenase (decarboxylating)	Unigene13450_All//0.00E+00//TC137790		ko00260|Glycine, serine and threonine metabolism	GO:0005576//GO:0006546//GO:0009526//GO:0010038//GO:0016628//GO:0016642//GO:0032559//GO:0043234//GO:0048037	nr +
Unigene13451_All	1072	69.99	70.95	104.86	29.41	33.86	31.81	29.46	9.40	15.01	1.96E-02	7.77E-01		5.83E-01	3.42E-31		2.03E-01	2.53E-02		1.13E-01	3.07E-01		-1.65E+00	7.51E-61	Down	-9.73E-01	5.24E-28		Unigene13451_All//gi|224088838|ref|XP_002308562.1|//1.00E-133//precursor of carboxylase p-protein 1, glycine decarboxylase complex [Populus trichocarpa] >gi|222854538|gb|EEE92085.1| precursor of carboxylase p-protein 1, glycine decarboxylase complex [Populus trichocarpa]	Unigene13451_All//1.00E-121//AT2G26080| AtGLDP2 (Arabidopsis thaliana glycine decarboxylase P-protein 2); ATP binding / glycine dehydrogenase (decarboxylating)	Unigene13451_All//0.00E+00//TC146943		ko00260|Glycine, serine and threonine metabolism		nr -
Unigene13452_All	2386	5.20	4.42	6.29	7.56	8.56	7.86	6.93	3.15	3.47	-2.35E-01	1.67E-01		2.76E-01	8.05E-02		1.79E-01	1.78E-01		5.57E-02	7.12E-01		-1.14E+00	1.31E-18	Down	-9.96E-01	1.14E-15		Unigene13452_All//gi|55819802|gb|AAV66096.1|//6.00E-64//At5g59830 [Arabidopsis thaliana]	Unigene13452_All//3.00E-68//AT5G13060| unknown protein	Unigene13452_All//0.00E+00//TC149189				nr +
Unigene13453_All	2274	2.76	2.72	3.86	3.53	3.73	3.71	2.86	1.38	1.49	-2.24E-02	9.43E-01		4.85E-01	1.77E-02		7.89E-02	7.71E-01		7.46E-02	7.42E-01		-1.05E+00	5.05E-07	Down	-9.43E-01	3.32E-06		Unigene13453_All//gi|55819802|gb|AAV66096.1|//2.00E-65//At5g59830 [Arabidopsis thaliana]	Unigene13453_All//7.00E-67//AT5G59830| unknown protein	Unigene13453_All//0.00E+00//TC149189				nr +
Unigene13454_All	331	51.06	9.49	30.89	12.64	11.55	3.68	0.00	0.00	0.00	-2.43E+00	2.25E-44	Down	-7.25E-01	2.20E-07		-1.31E-01	7.02E-01		-1.78E+00	2.00E-08	Down	null	null		null	null		Unigene13454_All//gi|222424140|dbj|BAH20029.1|//2.00E-20//AT3G52720 [Arabidopsis thaliana]	Unigene13454_All//8.00E-22//AT3G52720| ACA1 (ALPHA CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding		ko00910|Nitrogen metabolism	GO:0005261//GO:0005515//GO:0009206//GO:0009528//GO:0009532//GO:0016836//GO:0019829//GO:0031410//GO:0046914//GO:0070838	nr +
Unigene13455_All	1161	49.12	30.38	49.12	12.31	19.37	27.97	30.59	35.64	8.37	-6.93E-01	1.55E-22		0.00E+00	1.00E+00		6.53E-01	1.20E-09		1.18E+00	2.82E-33	Up	2.20E-01	3.87E-03		-1.87E+00	9.26E-84	Down	Unigene13455_All//gi|297819992|ref|XP_002877879.1|//4.00E-67//carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323717|gb|EFH54138.1| carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13455_All//1.00E-66//AT3G52720| ACA1 (ALPHA CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	Unigene13455_All//1.00E-164//TC149389		ko00910|Nitrogen metabolism	GO:0005261//GO:0005515//GO:0009528//GO:0009532//GO:0016829//GO:0019829//GO:0031410//GO:0044237//GO:0046872	nr -
Unigene13457_All	2216	9.75	7.29	5.65	51.23	46.42	44.80	66.49	31.89	35.09	-4.19E-01	3.90E-04		-7.88E-01	1.38E-10		-1.42E-01	2.89E-03		-1.94E-01	5.35E-05		-1.06E+00	8.77E-143	Down	-9.22E-01	1.40E-116		Unigene13457_All//gi|15223914|ref|NP_172936.1|//0.00E+00//ADL1C (ARABIDOPSIS DYNAMIN-LIKE PROTEIN 1C); GTP binding / GTPase [Arabidopsis thaliana] >gi|60392231|sp|Q8LF21.2|DRP1C_ARATH RecName: Full=Dynamin-related protein 1C; AltName: Full=Dynamin-like protein C; AltName: Full=Dynamin-like protein 5; AltName: Full=Dynamin-like protein DLP1 >gi|11991506|emb|CAC19656.1| dynamin-like protein DLP1 [Arabidopsis thaliana]	Unigene13457_All//0.00E+00//AT1G14830| ADL1C (ARABIDOPSIS DYNAMIN-LIKE PROTEIN 1C); GTP binding / GTPase	Unigene13457_All//0.00E+00//TC146362		ko04144|Endocytosis	GO:0007005//GO:0009555//GO:0016020//GO:0017111//GO:0032561//GO:0044464	nr -
Unigene13458_All	1586	2.71	3.87	4.70	5.31	6.23	5.64	2.51	2.35	5.33	5.15E-01	3.22E-02		7.97E-01	3.29E-04		2.31E-01	2.51E-01		8.71E-02	6.85E-01		-9.55E-02	7.47E-01		1.09E+00	1.57E-09	Up	Unigene13458_All//gi|28558780|gb|AA045751.1|//6.00E-27//gag-protease polyprotein [Cucumis melo]		Unigene13458_All//3.00E-30//DT462826				nr +
Unigene13465_All	2224	1.08	0.87	0.62	1.19	1.27	1.77	2.36	1.11	1.11	-3.22E-01	4.35E-01		-7.98E-01	6.37E-02		9.69E-02	8.25E-01		5.74E-01	7.04E-02		-1.09E+00	4.51E-06	Down	-1.09E+00	2.77E-06	Down	Unigene13465_All//gi|297840529|ref|XP_002888146.1|//1.00E-119//cysteine-type peptidase [Arabidopsis lyrata subsp. lyrata] >gi|297333987|gb|EFH64405.1| cysteine-type peptidase [Arabidopsis lyrata subsp. lyrata]	Unigene13465_All//2.00E-108//AT1G60220| ULP1D (UB-LIKE PROTEASE 1D); SUMO-specific protease/ cysteine-type peptidase	Unigene13465_All//0.00E+00//gi|21096490|gb|BQ408803.1|BQ408803			GO:0003006//GO:0006970//GO:0019783//GO:0043231//GO:0070646	nr +
Unigene13466_All	270	4.26	3.94	2.37	12.91	7.14	9.70	13.31	5.42	7.23	-1.13E-01	8.45E-01		-8.49E-01	2.06E-01		-8.55E-01	5.84E-03		-4.13E-01	2.35E-01		-1.30E+00	1.46E-05	Down	-8.81E-01	1.69E-03		Unigene13466_All//gi|53828547|gb|AAU94383.1|//3.00E-17//At3g57420 [Arabidopsis thaliana] >gi|59958348|gb|AAX12884.1| At3g57420 [Arabidopsis thaliana]	Unigene13466_All//1.00E-18//AT3G57420| unknown protein	Unigene13466_All//9.00E-131//gi|109866727|gb|DW495703.1|DW495703			GO:0030312	nr +
Unigene13467_All	545	11.62	5.86	8.31	38.48	38.92	39.78	11.79	2.30	7.68	-9.88E-01	3.15E-05		-4.84E-01	5.03E-02		1.64E-02	9.18E-01		4.78E-02	7.33E-01		-2.36E+00	2.46E-20	Down	-6.20E-01	2.01E-03		Unigene13467_All//gi|2335100|gb|AAC02770.1|//6.00E-39//expressed protein [Arabidopsis thaliana]	Unigene13467_All//3.00E-40//AT2G41770| unknown protein	Unigene13467_All//0.00E+00//gi|109864999|gb|DW493975.1|DW493975			GO:0030312	nr +
Unigene13468_All	2931	8.28	7.47	6.38	29.22	22.45	24.53	24.91	10.62	15.43	-1.49E-01	2.18E-01		-3.77E-01	1.11E-03		-3.80E-01	8.47E-14		-2.52E-01	4.36E-06		-1.23E+00	4.68E-90	Down	-6.91E-01	8.70E-36		Unigene13468_All//gi|2335100|gb|AAC02770.1|//0.00E+00//expressed protein [Arabidopsis thaliana]	Unigene13468_All//0.00E+00//AT2G41770| unknown protein	Unigene13468_All//0.00E+00//TC140577			GO:0030312	nr +
Unigene13469_All	242	1.73	0.63	0.66	0.82	1.42	0.19	17.65	1.04	1.81	-1.46E+00	2.34E-01		-1.39E+00	2.80E-01		7.89E-01	5.96E-01		-2.14E+00	3.47E-01		-4.09E+00	8.53E-23	Down	-3.28E+00	6.79E-20	Down			Unigene13469_All//2.00E-134//gi|21098996|gb|BQ411309.1|BQ411309				
Unigene1347_All	4605	0.75	2.34	1.48	0.56	1.07	1.10	0.00	0.05	0.00	1.64E+00	2.60E-17	Up	9.81E-01	3.17E-05		9.27E-01	3.64E-04		9.66E-01	2.73E-04		5.77E+00	4.31E-02		null	null		Unigene1347_All//gi|297838415|ref|XP_002887089.1|//0.00E+00//ATPDR11/PDR11 [Arabidopsis lyrata subsp. lyrata] >gi|297332930|gb|EFH63348.1|ATPDR11/PDR11 [Arabidopsis lyrata subsp. lyrata]	Unigene1347_All//0.00E+00//AT1G66950| PDR11 (PLEIOTROPIC DRUG RESISTANCE 11); ATPase, coupled to transmembrane movement of substances	Unigene1347_All//0.00E+00//gi|78338248|gb|DT558522.1|DT558522		ko03040|Spliceosome//ko02010|ABC transporters		nr -

Unigene13470_All	2252	6.02	6.52	17.33	12.98	16.61	15.58	40.97	5.38	12.61	1.17E-01	4.75E-01		1.53E+00	3.43E-53	Up	3.55E-01	1.54E-05		2.63E-01	4.19E-03		-2.93E+00	0.00E+00	Down	-1.70E+00	1.35E-189	Down	Unigene13470_All//gi|294516938|gb|ADE96997.1|//0.00E+00//p-coumarate:CoA-ligase 3 [Sorbus aucuparia]	Unigene13470_All//0.00E+00//TC131151		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0006575//GO:0006952//GO:0009416//GO:0010208//GO:0016405//GO:0016703//GO:0032559	nr +
Unigene13471_All	1360	11.77	23.96	10.34	26.52	24.08	36.93	32.74	69.58	72.53	1.03E+00	6.79E-25	Up	-1.88E-01	2.34E-01		-1.39E-01	1.57E-01		4.78E-01	3.74E-11		1.09E+00	9.74E-96	Up	1.15E+00	4.32E-111	Up	Unigene13471_All//gi|192913012|gb|ACF06614.1|//2.00E-61//holocarboxylase synthetase [Elaeis guineensis]	Unigene13471_All//9.00E-62//AT4G08830| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP009193 (InterPro:IPR016549); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41780.1); Has 56 Blast hits to 56 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene13471_All//0.00E+00//TC142617				nr +
Unigene13473_All	1631	21.94	47.97	20.44	34.12	32.26	38.77	21.49	23.37	27.70	1.13E+00	1.28E-68	Up	-1.02E-01	3.45E-01		-8.07E-02	3.31E-01		1.84E-01	6.77E-03		1.21E-01	1.67E-01		3.66E-01	1.16E-07		Unigene13473_All//gi|15229847|ref|NP_187144.1|//4.00E-86//transcription regulator [Arabidopsis thaliana]	Unigene13473_All//4.00E-51//AT5G28040| transcription regulator	Unigene13473_All//0.00E+00//gi|109847523|gb|DW476503.1|DW476503	GeBP			nr -
Unigene13475_All	2372	3.93	0.34	1.89	3.70	1.83	5.83	18.73	6.61	14.34	-3.52E+00	7.10E-36	Down	-1.06E+00	1.14E-07	Down	-1.01E+00	2.10E-08	Down	6.57E-01	8.86E-06		-1.50E+00	1.13E-74	Down	-3.85E-01	3.09E-08		Unigene13475_All//gi|186514864|ref|NP_194754.2|//0.00E+00//ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene13475_All//0.00E+00//AT4G30250| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene13475_All//0.00E+00//gi|164317346|gb|ES820227.1|ES820227			GO:0009725//GO:0016462//GO:0032559//GO:0043231	nr -
Unigene13476_All	1436	20.15	14.08	13.50	35.21	30.67	20.44	6.01	2.91	4.16	-5.17E-01	2.52E-07		-5.78E-01	2.32E-08		-1.99E-01	6.72E-03		-7.84E-01	1.49E-26		-1.05E+00	6.30E-09	Down	-5.29E-01	1.87E-03		Unigene13476_All//gi|297816764|ref|XP_002876265.1|//1.00E-143//sugar isomerase domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297322103|gb|EFH52524.1| sugar isomerase domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13476_All//2.00E-140//AT3G54690| sugar isomerase (SIS) domain-containing protein / CBS domain-containing protein	Unigene13476_All//0.00E+00//TC167905			GO:0003824//GO:0030246//GO:0044238	nr -
Unigene13478_All	1888	5.99	4.11	5.81	7.84	6.80	12.97	6.83	5.14	2.64	-5.44E-01	1.26E-03		-4.30E-02	8.18E-01		-2.04E-01	1.93E-01		7.26E-01	1.74E-11		-4.11E-01	3.59E-03		-1.37E+00	4.20E-20	Down	Unigene13478_All//gi|224110750|ref|XP_002315623.1|//1.00E-176//acyl:coa ligase [Populus trichocarpa] >gi|222864963|gb|EEF01794.1| acyl:coa ligase [Populus trichocarpa]	Unigene13478_All//2.00E-136//AT5G63380| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene13478_All//0.00E+00//TC150663		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene13482_All	2237	2.92	12.32	3.95	6.81	5.22	5.98	7.75	15.43	4.74	2.08E+00	5.24E-59	Up	4.35E-01	3.44E-02		-3.85E-01	4.94E-03		-1.89E-01	2.36E-01		9.94E-01	1.14E-30		-7.10E-01	1.38E-09		Unigene13482_All//gi|297829424|ref|XP_002882394.1|//0.00E+00//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328434|gb|EFH58853.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13482_All//3.00E-124//AT3G08970| ATERDJ3A; oxidoreductase	Unigene13482_All//0.00E+00//TC178503			GO:0000904//GO:0003824//GO:0005515//GO:0009408//GO:0044267//GO:0044432	nr +
Unigene13483_All	1876	2.18	2.84	4.14	3.05	4.57	2.36	9.06	1.00	4.93	3.83E-01	1.48E-01		9.30E-01	2.02E-05		5.82E-01	2.10E-03		-3.72E-01	1.56E-01		-3.18E+00	2.15E-72	Down	-8.79E-01	3.32E-13		Unigene13483_All//gi|30678198|ref|NP_563639.2|//1.00E-178//SBTI1.1; serine-type endopeptidase [Arabidopsis thaliana]	Unigene13483_All//3.00E-170//AT1G01900| SBTI1.1; serine-type endopeptidase	Unigene13483_All//0.00E+00//TC178965			GO:0008152//GO:0016787	nr -
Unigene13484_All	2324	1.58	0.70	0.37	13.61	9.44	4.84	24.69	2.41	13.32	-1.18E+00	3.36E-04	Down	-2.10E+00	3.53E-08	Down	-5.28E-01	1.51E-09		-1.49E+00	8.47E-47	Down	-3.36E+00	3.41E-256	Down	-8.90E-01	2.42E-43		Unigene13484_All//gi|224065140|ref|XP_002301687.1|//0.00E+00//leucine-rich repeat transmembrane protein [Populus trichocarpa] >gi|222843413|gb|EEE80960.1| leucine-rich repeat transmembrane protein [Populus trichocarpa]	Unigene13484_All//2.00E-176//AT3G17840| RLK902; ATP binding / kinase/ protein serine/threonine kinase	Unigene13484_All//0.00E+00//gi|164274897|gb|ES815972.1|ES815972			GO:0004672//GO:0005618//GO:0006464//GO:0007167//GO:0009408//GO:0016628//GO:0031225//GO:0032559	nr +
Unigene13486_All	1192	1.67	2.13	2.10	25.12	22.65	33.87	107.44	186.47	226.23	3.50E-01	3.92E-01		3.32E-01	4.26E-01		-1.49E-01	1.64E-01		4.32E-01	1.18E-07		7.95E-01	8.01E-133		1.07E+00	5.87E-272	Up	Unigene13486_All//gi|297823825|ref|XP_002879795.1|//1.00E-129//esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325634|gb|EFH56054.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13486_All//3.00E-128//AT2G39420| esterase/lipase/thioesterase family protein	Unigene13486_All//0.00E+00//TC134023		ko00561|Glycerolipid metabolism		nr -
Unigene13489_All	2051	4.72	31.08	9.50	4.23	5.74	20.17	15.91	37.21	25.54	2.72E+00	3.66E-187	Up	1.01E+00	2.72E-14	Up	4.42E-01	5.77E-03		2.25E+00	4.94E-105	Up	1.23E+00	1.91E-93	Up	6.83E-01	2.96E-25		Unigene13489_All//gi|224098499|ref|XP_002311196.1|//0.00E+00//proline transporter [Populus trichocarpa] >gi|222851016|gb|EEE88563.1| proline transporter [Populus trichocarpa]	Unigene13489_All//4.00E-175//AT2G38890| PROT1 (PROLINE TRANSPORTER 1); L-proline transmembrane transporter/ amino acid transmembrane transporter	Unigene13489_All//0.00E+00//TC141038			GO:0015175//GO:0015804//GO:0031224	nr +
Unigene13492_All	1717	57.38	43.65	41.25	61.10	64.30	53.05	25.12	56.64	15.34	-3.95E-01	2.76E-14		-4.76E-01	4.13E-19		7.36E-02	1.94E-01		-2.04E-01	4.41E-05		1.17E+00	5.04E-111	Up	-7.12E-01	1.38E-22		Unigene13492_All//gi|189163920|gb|ACD77110.1|//1.00E-179//protein kinase 1b [Solanum lycopersicum]	Unigene13492_All//3.00E-158//AT2G28930| APK1B; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene13492_All//0.00E+00//TC149840		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene13500_All	1834	9.47	8.51	7.84	8.42	10.46	10.10	19.32	12.49	6.78	-1.55E-01	2.93E-01		-2.73E-01	5.90E-02		3.13E-01	1.22E-02		2.62E-01	5.30E-02		-6.29E-01	8.69E-15		-1.51E+00	6.27E-62	Down	Unigene13500_All//gi|115467162|ref|NP_001057180.1|//4.00E-85//Os06g0222800 [Oryza sativa Japonica Group] >gi|113595220|dbj|BAF19094.1| Os06g0222800 [Oryza sativa Japonica Group]	Unigene13500_All//6.00E-07//AT1G53710| hydrolase/ protein serine/threonine phosphatase	Unigene13500_All//1.00E-146//DR463108				nr -
Unigene13501_All	465	0.45	4.14	0.92	0.32	0.44	0.00	0.55	4.22	3.00	3.20E+00	3.42E-07	Up	1.03E+00	3.97E-01		4.67E-01	8.25E-01		-8.33E+00	2.33E-01		2.95E+00	2.58E-08	Up	2.46E+00	2.70E-05	Up			Unigene13501_All//7.00E-31//BF268565				
Unigene13502_All	1361	0.50	0.11	0.43	0.37	0.25	0.53	3.26	2.06	0.88	-2.16E+00	2.84E-02		-2.16E-01	7.88E-01		-5.33E-01	5.94E-01		5.37E-01	5.60E-01		-6.65E-01	9.44E-03		-1.89E+00	2.23E-11	Down	Unigene13502_All//gi|115467162|ref|NP_001057180.1|//1.00E-89//Os06g0222800 [Oryza sativa Japonica Group] >gi|113595220|dbj|BAF19094.1| Os06g0222800 [Oryza sativa Japonica Group]	Unigene13502_All//2.00E-07//AT1G53710| hydrolase/ protein serine/threonine phosphatase	Unigene13502_All//9.00E-147//DR463108				nr -
Unigene13505_All	1842	5.23	2.34	4.68	6.00	5.89	2.70	2.59	0.43	0.80	-1.16E+00	1.60E-09	Down	-1.58E-01	4.46E-01		-2.79E-02	8.87E-01		-1.15E+00	2.03E-11	Down	-2.59E+00	5.87E-17	Down	-1.70E+00	1.36E-10	Down	Unigene13505_All//gi|2911040|emb|CAA17550.1|//1.00E-166//receptor protein kinase-like protein [Arabidopsis thaliana] >gi|7270372|emb|CAB80139.1| receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene13505_All//7.00E-143//AT4G34220| leucine-rich repeat transmembrane protein kinase, putative	Unigene13505_All//0.00E+00//ES816524		ko04626|Plant-pathogen interaction	GO:0005488//GO:0008152//GO:0016020//GO:0016301//GO:0016491	nr -
Unigene13509_All	1308	12.48	14.41	14.53	10.78	9.74	8.29	10.09	2.49	4.02	2.08E-01	1.26E-01		2.20E-01	1.20E-01		-1.46E-01	3.98E-01		-3.79E-01	1.18E-02		-2.02E+00	7.70E-34	Down	-1.33E+00	1.52E-19	Down	Unigene13509_All//gi|224660889|gb|ACQ83560.1|//2.00E-97//calcineurin B-like protein 06 [Vitis vinifera]	Unigene13509_All//2.00E-87//AT4G33000| CBL10 (CALCINEURIN B-LIKE 10); calcium ion binding	Unigene13509_All//0.00E+00//TC165098		ko04650|Natural killer cell mediated cytotoxicity	GO:0000325//GO:0006972//GO:0016020//GO:0032844//GO:0046872	nr +
Unigene13510_All	473	0.66	0.21	0.90	3.37	3.06	3.15	10.10	6.01	2.95	-1.63E+00	2.77E-01		4.40E-01	6.77E-01		-1.40E-01	8.18E-01		-9.70E-02	8.59E-01		-7.49E-01	2.22E-03		-1.78E+00	3.06E-11	Down			Unigene13510_All//1.00E-128//EE593039				
Unigene13512_All	1401	77.16	37.90	47.78	36.41	35.34	34.85	11.35	1.34	1.48	-1.03E+00	2.37E-81	Down	-6.92E-01	2.15E-40		-4.28E-02	6.42E-01		-6.33E-02	4.99E-01		-3.08E+00	8.95E-66	Down	-2.94E+00	7.16E-65	Down	Unigene13512_All//gi|74273629|gb|AB001482.1|//1.00E-176//gibberellin 20-oxidase 1 [Gossypium hirsutum]	Unigene13512_All//5.00E-156//AT3G51240| F3H (FLAVANONE 3-HYDROXYLASE); naringenin 3-dioxygenase	Unigene13512_All//0.00E+00//TC130194		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr -
Unigene13513_All	1753	8.48	10.90	12.24	11.00	12.96	10.41	9.09	4.43	3.43	3.62E-01	4.53E-03		5.30E-01	1.39E-05		2.38E-01	4.35E-02		-7.94E-02	6.40E-01		-1.04E+00	1.37E-15	Down	-1.41E+00	1.60E-25	Down	Unigene13513_All//gi|224077516|ref|XP_002305282.1|//1.00E-165//4-coumarate-coa ligase [Populus trichocarpa] >gi|222848246|gb|EEE85793.1| 4-coumarate-coa ligase [Populus trichocarpa]	Unigene13513_All//8.00E-160//AT4G05160| 4-coumarate--CoA ligase, putative / 4-coumaroyl-CoA synthase, putative	Unigene13513_All//6.00E-87//DR459736		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene13514_All	1185	6.62	8.00	6.25	6.22	6.51	3.09	8.35	7.05	2.96	2.72E-01	1.65E-01		-8.45E-02	7.05E-01		6.52E-02	8.23E-01		-1.01E+00	1.95E-06	Down	-2.43E-01	1.66E-01		-1.50E+00	1.12E-17	Down	Unigene13514_All//gi|224127622|ref|XP_002329323.1|//1.00E-155//4-coumarate-coa ligase [Populus trichocarpa] >gi|224127626|ref|XP_002329324.1| acyl:coa ligase [Populus trichocarpa] >gi|222870777|gb|EEF07908.1| 4-coumarate-coa ligase [Populus trichocarpa] >gi|222870778|gb|EEF07909.1| acyl:coa ligase [Populus trichocarpa]	Unigene13514_All//7.00E-151//AT4G05160| 4-coumarate--CoA ligase, putative / 4-coumaroyl-CoA synthase, putative	Unigene13514_All//0.00E+00//ES850570		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene13515_All	1220	50.95	41.16	24.18	38.54	29.95	21.88	116.31	120.87	79.29	-3.08E-01	3.77E-06		-1.08E+00	4.80E-49	Down	-3.64E-01	2.95E-07		-8.17E-01	1.69E-26		5.55E-02	2.20E-01		-5.53E-01	2.39E-46		Unigene13515_All//gi|115500890|dbj|BAF34116.1|//4.00E-91//glycerophosphodiesterase-like protein [Nicotiana tabacum]	Unigene13515_All//3.00E-84//AT4G26690| SHV3 (SHAVEN 3); glycerophosphodiester phosphodiesterase/ kinase	Unigene13515_All//0.00E+00//TC169204		ko00564|Glycerophospholipid metabolism	GO:0000904//GO:0005576//GO:0005618//GO:0008081//GO:0009536//GO:0009526//GO:0010383//GO:0016772//GO:0019409400//GO:0031225//GO:0031410//GO:0035315//GO:0048764	nr +
Unigene13517_All	1358	26.55	11.57	11.88	44.20	35.78	46.79	68.21	55.95	57.26	-1.20E+00	2.69E-35	Down	-1.16E+00	2.74E-32	Down	-3.05E-01	1.13E-06		8.22E-02	3.07E-01		-2.86E-01	2.56E-09		-2.52E-01	8.93E-08		Unigene13517_All//gi|281485191|gb|ADA70361.1|//0.00E+00//actin [Persea americana]	Unigene13517_All//0.00E+00//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene13517_All//0.00E+00//TC171105		ko04145|Phagosome	GO:0032559//GO:0043232	nr -
Unigene13518_All	1751	3.59	4.51	3.38	10.47	8.08	7.07	9.71	3.46	5.39	3.32E-01	1.23E-01		-8.71E-02	7.26E-01		-3.73E-01	2.40E-03		-5.67E-01	6.21E-06		-1.49E+00	1.34E-28	Down	-8.48E-01	1.76E-12		Unigene13518_All//gi|18402672|ref|NP_566664.1|//0.00E+00//ATPDIL5-3 (PDI-LIKE 5-3); protein disulfide isomerase [Arabidopsis thaliana] >gi|15215847|gb|AAK91468.1| AT3g20560/K10D20_9 [Arabidopsis thaliana]	Unigene13518_All//0.00E+00//AT3G20560| ATPDIL5-3 (PDI-LIKE 5-3); protein disulfide isomerase	Unigene13518_All//0.00E+00//TC178942		ko04141|Protein processing in endoplasmic reticulum	GO:0016862//GO:0019725	nr +

Unigene1352_All	1278	17.19	23.87	12.08	24.87	25.44	26.82	17.14	11.02	6.39	4.73E-01	1.23E-06		-5.09E-01	2.46E-05		3.26E-02	8.19E-01		1.09E-01	3.22E-01		-6.37E-01	1.22E-09		-1.42E+00	2.27E-35	Down	Unigene1352_All//gi|15237641|ref|NP_201225.1|//3.00E-88//ATSC35; RNA binding / nucleic acid binding / nucleotide binding [Arabidopsis thaliana] >gi|30697964|ref|NP_851261.1| ATSC35; RNA binding / nucleic acid binding / nucleotide binding [Arabidopsis thaliana] >gi|20022546|gb|AAM83231.1| AT5g64200/MSJ1_4 [Arabidopsis thaliana] >gi|23505861|gb|AAN28790.1| At5g64200/MSJ1_4 [Arabidopsis thaliana]	Unigene1352_All//2.00E-53//AT5G64200| ATSC35; RNA binding / nucleic acid binding / nucleotide binding	Unigene1352_All//0.00E+00//gi|78329013|gb|DT549287.1|DT549287		ko03040|Spliceosome		nr +
Unigene13520_All	2604	0.62	2.43	0.57	1.82	2.04	1.80	3.47	4.22	2.86	1.97E+00	3.79E-13	Up	-1.22E-01	8.10E-01		1.64E-01	5.91E-01		-1.08E-02	9.64E-01		2.81E-01	8.22E-02		-2.80E-01	1.06E-01		Unigene13520_All//gi|6635380|gb|AAF19803.1|//5.00E-44//RPS2 protein [Brassica oleracea]	Unigene13520_All//9.00E-45//AT1G15890| disease resistance protein (CC-NBS-LRR class), putative			ko04626|Plant-pathogen interaction		nr -
Unigene13522_All	1803	2.03	1.49	1.92	1.93	1.32	1.58	3.92	2.46	1.22	-4.48E-01	1.69E-01		-8.15E-02	8.07E-01		-5.54E-01	8.51E-02		-2.93E-01	4.20E-01		-6.72E-01	5.95E-04		-1.69E+00	3.78E-15	Down	Unigene13522_All//gi|94421574|gb|ABF18894.1|//6.00E-80//SNI1 [Solanum tuberosum]	Unigene13522_All//1.00E-57//AT4G18470| SNI1; transcription repressor	Unigene13522_All//0.00E+00//TC178556			GO:0002832//GO:0006310//GO:0006464//GO:0030528//GO:0043231	nr -
Unigene13524_All	2052	16.93	7.46	11.99	14.54	8.04	8.10	5.91	3.69	4.23	-1.18E+00	2.36E-33	Down	-4.98E-01	1.01E-07		-8.55E-01	1.19E-20		-8.44E-01	5.66E-18		-6.82E-01	2.49E-06		-4.83E-01	6.14E-04		Unigene13524_All//gi|186511411|ref|NP_001118908.1|//0.00E+00//ubiquitin thiolesterase [Arabidopsis thaliana]	Unigene13524_All//1.00E-155//AT4G01037| ubiquitin thiolesterase	Unigene13524_All//0.00E+00//CO115018				nr -
Unigene13525_All	1414	6.36	4.84	6.67	11.94	9.52	7.12	6.58	4.67	3.21	-3.96E-01	4.28E-02		6.68E-02	7.44E-01		-3.27E-01	1.32E-02		-7.46E-01	1.51E-08		-4.94E-01	3.37E-03		-1.03E+00	9.81E-10	Down	Unigene13525_All//gi|25052804|gb|AN65180.1|//0.00E+00//mitogen-activated protein kinase 4 [Petroselinum crispum]	Unigene13525_All//0.00E+00//AT4G01370| ATMPK4 (ARABIDOPSIS THALIANA MAP KINASE 4); MAP kinase/ kinase	Unigene13525_All//0.00E+00//gi|78329322|gb|DT549596.1|DT549596		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0032559	nr +
Unigene13526_All	2373	45.64	18.04	33.93	13.18	12.23	9.00	13.51	41.02	7.00	-1.34E+00	2.10E-124	Down	-4.28E-01	2.66E-17		-1.08E-01	3.31E-01		-5.50E-01	3.59E-09		1.60E+00	2.18E-178	Up	-9.48E-01	2.95E-27		Unigene13526_All//gi|224124122|ref|XP_002330110.1|//0.00E+00//ABC transporter family protein [Populus trichocarpa] >gi|222871244|gb|EEF08375.1| ABC transporter family protein [Populus trichocarpa]	Unigene13526_All//0.00E+00//AT5G39040| ATTAP2; ATPase, coupled to transmembrane movement of substances / transporter	Unigene13526_All//0.00E+00//TC156819		ko02010|ABC transporters	GO:0006810//GO:0031224//GO:0032559//GO:0042626//GO:0043234	nr +
Unigene13528_All	2174	2.33	1.98	3.31	1.70	3.26	4.99	13.38	20.26	7.68	-2.37E-01	3.84E-01		5.02E-01	2.82E-02		9.44E-01	6.59E-06		1.56E+00	4.42E-17	Up	5.99E-01	1.09E-16		-8.01E-01	7.05E-19		Unigene13528_All//gi|62857020|dbj|BAD95895.1|//2.00E-96//Ser/Thr protein kinase [Lotus japonicus]	Unigene13528_All//2.00E-91//AT5G38260| serine/threonine protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672	nr +
Unigene13530_All	1927	17.38	26.29	21.80	10.13	10.35	9.75	0.13	0.89	0.33	5.98E-01	1.38E-15		3.27E-01	1.27E-04		3.00E-02	8.40E-01		-5.57E-02	7.01E-01		2.76E+00	6.93E-07	Up	1.33E+00	1.00E-01		Unigene13530_All//gi|19911205|dbj|BAB86929.1|//1.00E-118//glucosyltransferase-11 [Vigna angularis]	Unigene13530_All//3.00E-80//AT1G22360| AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups	Unigene13530_All//0.00E+00//TC173969		ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0016740	nr +
Unigene13531_All	1574	3.19	7.47	3.65	6.23	5.89	5.28	2.90	2.04	1.49	1.23E+00	2.23E-12	Up	1.95E-01	4.77E-01		-8.33E-02	7.13E-01		-2.40E-01	2.31E-01		-5.05E-01	4.83E-02		-9.58E-01	1.03E-04		Unigene13531_All//gi|297853312|ref|XP_002894537.1|//1.00E-173//pyridoxal-5'-phosphate-dependent enzyme, beta family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340379|gb|EFH70796.1| pyridoxal-5'-phosphate-dependent enzyme, beta family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13531_All//2.00E-162//AT1G55880| pyridoxal-5'-phosphate-dependent enzyme, beta family protein	Unigene13531_All//0.00E+00//TC159072		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr -
Unigene13532_All	1660	127.34	105.22	112.50	67.10	65.70	53.90	65.18	46.53	30.72	-2.75E-01	1.80E-15		-1.79E-01	7.40E-07		-3.05E-02	6.17E-01		-3.16E-01	1.69E-11		-4.86E-01	1.46E-27		-1.09E+00	3.60E-112	Down	Unigene13532_All//gi|226498180|ref|NP_001146927.1|//1.00E-180//YLS5 [Zea mays] >gi|195605312|gb|ACG24486.1| YLS5 [Zea mays]	Unigene13532_All//1.00E-172//AT3G02720| DJ-1 family protein / protease-related	Unigene13532_All//0.00E+00//TC131965			GO:0016787	nr -
Unigene13535_All	2373	4.01	3.01	3.14	4.72	5.83	5.20	8.86	4.46	3.69	-4.15E-01	2.75E-02		-3.53E-01	7.93E-02		3.05E-01	4.69E-02		1.38E-01	4.69E-01		-9.91E-01	6.44E-19		-1.26E+00	2.28E-28	Down	Unigene13535_All//gi|51971395|dbj|BAD44362.1|//4.00E-29//At1g70950 [Arabidopsis thaliana]	Unigene13535_All//2.00E-30//AT1G70950| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23060.1); Has 875 Blast hits to 771 proteins in 143 species: Archae - 0; Bacteria - 102; Metazoa - 281; Fungi - 65; Plants - 205; Viruses - 3; Other Eukaryotes - 219 (source: NCBI BLink).	Unigene13535_All//0.00E+00//TC154288			GO:0009536	nr -
Unigene13536_All	1126	4.88	5.89	5.53	1.55	1.93	1.32	1.50	1.19	3.86	2.73E-01	2.54E-01		1.82E-01	4.96E-01		3.15E-01	5.34E-01		-2.26E-01	6.76E-01		-3.39E-01	4.82E-01		1.36E+00	3.47E-07	Up	Unigene13536_All//gi|7767678|gb|AAF69175.1|AC007915_27//5.00E-42//F27F5.3 [Arabidopsis thaliana]	Unigene13536_All//8.00E-48//AT1G44920| unknown protein	Unigene13536_All//0.00E+00//TC134324			GO:0009536	nr -
Unigene13538_All	4550	0.25	0.46	0.25	4.34	1.39	0.98	25.91	16.62	7.93	8.52E-01	5.74E-02		-4.17E-02	9.65E-01		-1.64E+00	1.68E-38	Down	-2.14E+00	3.28E-48	Down	-6.41E-01	9.35E-49		-1.71E+00	1.08E-243	Down	Unigene13538_All//gi|224131694|ref|XP_002328085.1|//0.00E+00//aldehyde oxidase 2 [Populus trichocarpa] >gi|222837600|gb|EEE75965.1| aldehyde oxidase 2 [Populus trichocarpa]	Unigene13538_All//0.00E+00//AT3G43600| AAO2 (ALDEHYDE OXIDASE 2); aldehyde oxidase	Unigene13538_All//0.00E+00//DW488506		ko00230|Purine metabolism//ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00906|Carotenoid biosynthesis//ko00232|Caffeine metabolism	GO:0009850//GO:0016623//GO:0030554//GO:0046914//GO:0051536	nr +
Unigene13539_All	351	2.09	6.06	3.94	1.56	3.04	1.93	2.05	1.31	1.48	1.54E+00	9.72E-04	Up	9.18E-01	1.27E-01		9.62E-01	1.64E-01		3.06E-01	7.22E-01		-6.45E-01	4.01E-01		-4.73E-01	5.20E-01		Unigene13539_All//gi|18402863|ref|NP_564560.1|//2.00E-27//CLPR1; serine-type endopeptidase [Arabidopsis thaliana] >gi|75315328|sp|Q9XJ35.1|CLPR1_ARATH RecName: Full=ATP-dependent Clp protease proteolytic subunit-related protein 1, chloroplastic; Short=ClpR1; AltName: Full=nClpP5; Flags: Precursor >gi|8569101|gb|AAF76446.1|AC015445_13 Identical to nClpP5 from Arabidopsis thaliana gb|AB022330 and contains prenyltransferase PF|00432 and CLP protease PF|00574 domains. ESTs gb|H76908, gb|AA665567, gb|T21932, gb|T22976 come from this gene >gi|5360595|dbj|BAA82069.1| nClpP5 [Arabidopsis thaliana] >gi|15010752|gb|AAK74035.1| At1g49970/F2J10_5 [Arabidopsis thaliana] >gi|23308343|gb|AAN18141.1| At1g49970/F2J10_5 [Arabidopsis thaliana]	Unigene13539_All//2.00E-21//AT1G49970| CLPR1; serine-type endopeptidase	Unigene13539_All//4.00E-180//CO126324			GO:0004175//GO:0009368//GO:0009532//GO:0019538//GO:0031976	nr -
Unigene13544_All	1922	12.09	7.72	7.56	21.69	19.17	25.43	16.48	6.72	10.70	-6.46E-01	1.31E-08		-6.76E-01	7.82E-09		-1.78E-01	3.49E-02		2.29E-01	2.92E-03		-1.29E+00	1.03E-42	Down	-6.23E-01	1.68E-13		Unigene13544_All//gi|186494992|ref|NP_001117592.1|//1.00E-119//eukaryotic translation initiation factor-related [Arabidopsis thaliana]	Unigene13544_All//2.00E-120//AT1G73180| eukaryotic translation initiation factor-related	Unigene13544_All//0.00E+00//TC138687			GO:0008135	nr -
Unigene13545_All	1449	41.71	26.51	29.29	82.27	95.20	93.82	88.30	25.67	52.16	-6.54E-01	1.46E-21		-5.10E-01	1.79E-13		2.11E-01	2.14E-07		1.90E-01	1.27E-05		-1.78E+00	7.20E-273	Down	-7.60E-01	6.03E-73		Unigene13545_All//gi|224089205|ref|XP_002308657.1|//0.00E+00//cellulose synthase [Populus trichocarpa] >gi|222854633|gb|EEE92180.1| cellulose synthase [Populus trichocarpa]	Unigene13545_All//2.00E-410| CESA1 (CELLULOSE SYNTHASE 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene13545_All//0.00E+00//TC145932			GO:0006972//GO:0009250//GO:0009832//GO:0016759//GO:0031224//GO:0043231//GO:0045229//GO:0046914	nr -
Unigene13546_All	2203	6.55	2.69	4.25	6.74	6.96	4.20	13.11	13.19	9.26	-1.28E+00	3.59E-16	Down	-6.24E-01	4.30E-05		4.58E-02	8.22E-01		-6.81E-01	1.41E-06		8.50E-03	9.63E-01		-5.02E-01	1.16E-08		Unigene13546_All//gi|224143880|ref|XP_002325107.1|//1.00E-162//serine/threonine protein kinase [Populus trichocarpa] >gi|222866541|gb|EEF03672.1| serine/threonine protein kinase [Populus trichocarpa]	Unigene13546_All//7.00E-140//AT4G30520| leucine-rich repeat family protein / protein kinase family protein	Unigene13546_All//0.00E+00//ES847909				nr +
Unigene1355_All	2078	0.71	1.17	1.67	2.97	2.12	2.11	2.52	2.66	2.26	7.31E-01	7.31E-02		1.24E+00	4.59E-04	Up	-4.87E-01	3.47E-02		-4.96E-01	4.00E-02		7.36E-02	7.70E-01		-1.57E-01	5.43E-01		Unigene1355_All//gi|224056879|ref|XP_002299069.1|//1.00E-171//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222846327|gb|EEE83874.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene1355_All//1.00E-162//AT1G55730| ATCAX5; calcium:cation antiporter/ cation:cation antiporter	Unigene1355_All//0.00E+00//TC139689				nr -
Unigene13550_All	1616	1.85	1.32	2.41	5.12	4.01	4.14	2.93	2.04	1.08	-4.87E-01	1.84E-01		3.82E-01	2.47E-01		-3.53E-01	8.16E-02		-3.07E-01	1.54E-01		-5.20E-01	3.73E-02		-1.43E+00	2.06E-08	Down	Unigene13550_All//gi|15227690|ref|NP_178463.1|//2.00E-54//CDC48B; ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana] >gi|28201774|sp|Q9ZPR1.1|CD48B_ARATH RecName: Full=Cell division control protein 48 homolog B; Short=AtCDC48b >gi|30725416|gb|AAP37730.1| At2g03670 [Arabidopsis thaliana]	Unigene13550_All//5.00E-51//AT2G03670| CDC48B; ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene13550_All//0.00E+00//gi|78354217|gb|DT574491.1|DT574491		ko04141|Protein processing in endoplasmic reticulum	GO:0000166//GO:0042623	nr +
Unigene13553_All	2483	6.68	3.02	5.30	11.70	11.14	13.79	13.64	9.53	10.96	-1.15E+00	1.57E-15	Down	-3.35E-01	2.17E-02		-7.08E-02	5.75E-01		2.37E-01	1.22E-02		-5.18E-01	3.26E-10		-3.16E-01	9.51E-05		Unigene13553_All//gi|123720792|dbj|BAF45348.1|//0.00E+00//nucleoporin [Lotus japonicus]	Unigene13553_All//0.00E+00//AT4G32910| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nucleoporin, Nup85-like (InterPro:IPR011502); Has 161 Blast hits to 158 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 128; Fungi - 10; Plants - 21; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene13553_All//0.00E+00//TC162727				nr +

Unigene13554_All	1628	2.06	1.00	0.69	2.75	2.01	3.36	21.89	30.68	56.06	-1.05E+00	2.17E-03		-1.58E+00	2.43E-05	Down	-4.55E-01	1.09E-01		2.86E-01	3.15E-01		4.87E-01	3.43E-13		1.36E+00	2.30E-133	Up	Unigene13554_All//gi|115435302|ref|NP_001042409.1|//4.00E-31//Os01g0218100 [Oryza sativa Japonica Group] >gi|108000070|dbj|BAB16490.1| DNA binding protein-like [Oryza sativa Japonica Group] >gi|21327944|dbj|BAC00537.1| DNA binding protein-like [Oryza sativa Japonica Group] >gi|113531940|dbj|BAF04323.1| Os01g0218100 [Oryza sativa Japonica Group]	Unigene13554_All//1.00E-20//AT1G68810| basic helix-loop-helix (bHLH) family protein	Unigene13554_All//0.00E+00//TC152411	bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene13557_All	1207	7.41	4.41	3.26	29.30	33.67	26.49	11.28	40.96	20.76	-7.50E-01	9.94E-05		-1.18E+00	1.03E-08	Down	2.00E-01	1.83E-02		-1.46E-01	1.50E-01		1.86E+00	5.80E-112	Up	8.80E-01	5.73E-19		Unigene13557_All//gi|115476370|ref|NP_001061781.1|//3.00E-21//Os08g0409500 [Oryza sativa Japonica Group] >gi|113623750|dbj|BAF23695.1| Os08g0409500 [Oryza sativa Japonica Group]	Unigene13557_All//7.00E-19//AT1G35830| VQ motif-containing protein	Unigene13557_All//0.00E+00//TC153007				nr -
Unigene13558_All	1540	2.92	1.35	1.56	15.14	14.78	11.58	3.60	9.31	5.28	-1.12E+00	1.23E-04	Down	-9.09E-01	2.29E-03		-3.45E-02	8.31E-01		-3.86E-01	5.44E-04		1.37E+00	1.62E-21	Up	5.53E-01	1.72E-03		Unigene13558_All//gi|115476370|ref|NP_001061781.1|//2.00E-27//Os08g0409500 [Oryza sativa Japonica Group] >gi|113623750|dbj|BAF23695.1| Os08g0409500 [Oryza sativa Japonica Group]	Unigene13558_All//9.00E-19//AT1G35830| VQ motif-containing protein	Unigene13558_All//0.00E+00//TC153007				nr +
Unigene13559_All	1672	12.36	19.00	12.01	12.16	11.29	13.75	16.29	37.72	22.33	6.20E-01	1.04E-10		-4.19E-02	7.61E-01		-1.07E-01	4.62E-01		1.78E-01	1.63E-01		1.21E+00	5.14E-76	Up	4.55E-01	2.89E-09		Unigene13559_All//gi|207999344|emb|CAQ53097.1|//2.00E-48//basic-leucine zipper [Humulus lupulus]	Unigene13559_All//2.00E-28//AT5G40080| bZIP transcription factor family protein	Unigene13559_All//0.00E+00//gi|78322894|gb|DT543168.1|DT543168	bZIP		GO:0003677//GO:0043231	nr +
Unigene13560_All	1596	3.57	5.49	1.23	13.48	25.14	27.48	29.64	62.01	34.07	6.20E-01	1.46E-03		-1.53E+00	2.82E-08	Down	8.99E-01	6.74E-29		1.03E+00	1.00E-35	Up	1.06E+00	1.02E-96	Up	2.01E-01	1.70E-03		Unigene13560_All//gi|297832776|ref|XP_002884270.1|//1.00E-165//GHMP kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330110|gb|EFH60529.1| GHMP kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13560_All//3.00E-166//AT3G01640| GHMP kinase family protein	Unigene13560_All//0.00E+00//TC143718				nr -
Unigene13562_All	1781	4.96	1.54	2.66	25.56	21.42	23.05	1.26	2.79	1.28	-1.69E+00	5.67E-15	Down	-9.00E-01	9.10E-06		-2.55E-01	6.90E-04		-1.49E-01	8.29E-02		1.15E+00	2.95E-06	Up	1.91E-02	9.69E-01		Unigene13562_All//gi|468562|emb|CAA83436.1|//0.00E+00//sucrose carrier [Ricinus communis]	Unigene13562_All//3.00E-159//AT1G22710| SUC2 (SUCROSE-PROTON SYMPORTER 2); carbohydrate transmembrane transporter/ sucrose transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter	Unigene13562_All//0.00E+00//TC150853			GO:0015154//GO:0015766//GO:0016021	nr +
Unigene13563_All	1591	66.43	38.28	25.77	19.76	16.67	12.18	33.01	9.38	3.88	-7.95E-01	5.03E-52		-1.37E+00	3.29E-121	Down	-2.46E-01	9.43E-03		-6.98E-01	9.38E-14		-1.82E+00	3.34E-115	Down	-3.09E+00	1.20E-223	Down	Unigene13563_All//gi|87240487|gb|AB032345.1|//1.00E-110//Octicosapeptide/Phox/BemIp [Medicago truncatula]	Unigene13563_All//2.00E-83//AT4G05150| octicosapeptide/Phox/BemIp (PB1) domain-containing protein	Unigene13563_All//0.00E+00//ES819665			GO:0043231	nr +
Unigene13564_All	2208	2.82	5.19	2.46	5.37	6.96	7.18	7.51	14.69	36.37	8.79E-01	2.39E-07		-1.97E-01	4.50E-01		3.73E-01	7.34E-03		4.19E-01	2.69E-03		9.69E-01	1.10E-27		2.28E+00	4.70E-240	Up	Unigene13564_All//gi|15232315|ref|NP_188700.1|//4.00E-63//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|75299591|sp|Q8GXT3.1|BH123_ARATH RecName: Full=Transcription factor bHLH123; AltName: Full=Transcription factor EN 63; AltName: Full=bHLH transcription factor bHLH123; AltName: Full=Basic helix-loop-helix protein 123; Short=bHLH 123; Short=AtbHLH123	Unigene13564_All//2.00E-64//AT3G20640| ethylene-responsive protein -related	Unigene13564_All//0.00E+00//TC158064	bHLH			nr +
Unigene13565_All	1598	3.11	0.25	0.47	11.04	7.95	8.08	5.90	3.40	2.87	-3.62E+00	8.62E-20	Down	-2.74E+00	1.28E-14	Down	-4.73E-01	1.15E-04		-4.49E-01	5.37E-04		-7.95E-01	2.04E-06		-1.04E+00	5.92E-10	Down	Unigene13565_All//gi|42567636|ref|NP_196051.2|//0.00E+00//pectate lyase family protein [Arabidopsis thaliana]	Unigene13565_All//2.00E-158//AT5G04310| pectate lyase family protein	Unigene13565_All//0.00E+00//CO112892		ko00040|Pentose and glucuronate interconversions	GO:0016837	nr -
Unigene13566_All	1391	11.21	5.86	8.04	12.78	25.62	13.64	2.67	3.28	4.07	-9.35E-01	1.02E-10		-4.80E-01	1.10E-03		1.00E+00	9.14E-31	Up	9.31E-02	5.64E-01		2.92E-01	2.86E-01		6.05E-01	5.20E-03		Unigene13566_All//gi|226504718|ref|NP_001150409.1|//1.00E-34//LOC100284039 [Zea mays] >gi|195639036|gb|ACG38986.1| protein SPATULA [Zea mays]	Unigene13566_All//6.00E-35//AT4G34530| CIB1 (CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1); DNA binding / transcription factor	Unigene13566_All//0.00E+00//TC133135	bHLH	ko04712|Circadian rhythm - plant	GO:0010468//GO:0043231	nr -
Unigene13567_All	1557	8.17	1.86	2.80	31.83	23.93	12.01	13.96	4.05	3.30	-2.14E+00	8.55E-29	Down	-1.54E+00	7.57E-18	Down	-4.12E-01	1.90E-09		-1.41E+00	6.69E-67	Down	-1.78E+00	5.80E-47	Down	-2.08E+00	2.58E-59	Down	Unigene13567_All//gi|188509929|gb|ACD56618.1|//0.00E+00//peptidoglycan-binding LysM domain-containing related protein [Gossypioides kirkii]	Unigene13567_All//8.00E-158//AT1G21880| LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR)	Unigene13567_All//0.00E+00//TC131356		ko04626|Plant-pathogen interaction	GO:0009056	nr +
Unigene13570_All	2247	42.96	14.86	8.56	60.90	72.52	53.69	135.20	32.59	33.95	-1.53E+00	9.34E-136	Down	-2.33E+00	4.36E-231	Down	2.52E-01	5.95E-12		-1.82E-01	2.73E-05		-2.05E+00	0.00E+00	Down	-1.99E+00	0.00E+00	Down	Unigene13570_All//gi|134035508|gb|AB047742.1|//0.00E+00//alpha-tubulin [Gossypium hirsutum]	Unigene13570_All//0.00E+00//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene13570_All//0.00E+00//TC130341		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene13572_All	2711	1.10	2.39	1.57	19.26	12.19	16.01	10.50	8.08	4.76	1.12E+00	2.48E-06	Up	5.14E-01	9.77E-02		-6.59E-01	7.70E-23		-2.66E-01	2.35E-04		-3.78E-01	3.10E-05		-1.14E+00	1.36E-32	Down	Unigene13572_All//gi|297842639|ref|XP_002889201.1|//0.00E+00//mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335042|gb|EFH65460.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13572_All//7.00E-168//AT1G78610| MSL6 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 6)	Unigene13572_All//9.00E-13//TC178511			GO:0016020	nr +
Unigene13574_All	1808	22.20	10.06	15.11	7.55	13.96	10.57	0.44	0.35	0.75	-1.14E+00	2.48E-36	Down	-5.55E-01	1.41E-10		8.87E-01	6.48E-18		4.85E-01	8.90E-05		-3.57E-01	6.49E-01		7.54E-01	1.30E-01		Unigene13574_All//gi|297832360|ref|XP_002884062.1|//1.00E-152//auxin efflux carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329902|gb|EFH60321.1| auxin efflux carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13574_All//3.00E-145//AT2G17500| auxin efflux carrier family protein	Unigene13574_All//0.00E+00//TC141730				nr +
Unigene13575_All	1849	0.88	163.22	34.50	5.58	42.05	54.25	1.42	6.42	26.39	7.54E+00	0.00E+00	Up	5.30E+00	0.00E+00	Up	2.91E+00	4.57E-286	Up	3.28E+00	0.00E+00	Up	2.18E+00	1.54E-33	Up	4.22E+00	9.88E-265	Up	Unigene13575_All//gi|7768151|emb|CAB90633.1|//1.00E-133//protein phpsphatase 2C (PP2C) [Fagus sylvatica]	Unigene13575_All//6.00E-121//AT1G07430| protein phosphatase 2C, putative / PP2C, putative	Unigene13575_All//0.00E+00//gi|48879355|gb|CO130377.1|CO130377				nr +
Unigene13576_All	1861	2.59	25.57	3.38	4.42	9.46	18.81	6.18	14.94	34.59	3.31E+00	5.79E-170	Up	3.85E-01	1.32E-01		1.10E+00	1.03E-17	Up	2.09E+00	6.96E-81	Up	1.27E+00	1.33E-36	Up	2.48E+00	1.36E-213	Up	Unigene13576_All//gi|224075800|ref|XP_002304773.1|//0.00E+00//cytokinin oxidase [Populus trichocarpa] >gi|222842205|gb|EEE79752.1| cytokinin oxidase [Populus trichocarpa]	Unigene13576_All//0.00E+00//AT3G63440| CKX6 (CYTOKININ OXIDASE/DEHYDROGENASE 6); cytokinin dehydrogenase	Unigene13576_All//0.00E+00//D8461372		ko00908|Zeatin biosynthesis	GO:0009690//GO:0009888//GO:0016645//GO:0030554//GO:0043231	nr +
Unigene13579_All	1069	2.45	0.76	1.10	8.48	6.86	3.80	4.11	1.76	2.35	-1.69E+00	5.80E-05	Down	-1.16E+00	5.19E-03		-3.06E-01	1.19E-01		-1.16E+00	1.65E-09	Down	-1.23E+00	3.87E-06	Down	-8.09E-01	1.17E-03		Unigene13579_All//gi|75213510|sp|Q9SYZ7.1|U4964_ARATH//8.00E-74//RecName: Full=UPF0496 protein At4g34320	Unigene13579_All//3.00E-64//AT2G18630| unknown protein	Unigene13579_All//0.00E+00//gi|164306438|gb|ES838811.1|ES838811			GO:0043231	nr -
Unigene13580_All	1820	2.16	1.98	2.57	5.17	3.77	3.50	3.46	1.10	3.15	-1.25E-01	6.85E-01		2.56E-01	3.85E-01		-4.58E-01	1.06E-02		-5.64E-01	2.24E-03		-1.65E+00	8.96E-13	Down	-1.35E-01	5.67E-01		Unigene13580_All//gi|158706508|sp|Q56XQ0.2|U4961_ARATH//1.00E-101//RecName: Full=UPF0496 protein At2g18630	Unigene13580_All//2.00E-82//AT2G18630| unknown protein	Unigene13580_All//0.00E+00//gi|164306438|gb|ES838811.1|ES838811				nr -
Unigene13582_All	1441	20.30	2.81	6.28	32.36	16.87	40.24	18.78	4.58	7.33	-2.85E+00	2.42E-91	Down	-1.69E+00	3.71E-46	Down	-9.40E-01	1.37E-37		3.15E-01	3.09E-06		-2.03E+00	1.86E-69	Down	-1.36E+00	1.49E-40	Down	Unigene13582_All//gi|18401521|ref|NP_566579.1|//1.00E-126//RPL3P (RIBOSOMAL PROTEIN L3 PLASTID; structural constituent of ribosome [Arabidopsis thaliana] >gi|42559534|sp|Q9LKN8.1|RK3B_ARATH RecName: Full=50S ribosomal protein L3-2, chloroplastic; Flags: Precursor >gi|11994685|dbj|BAB02923.1| 50S ribosomal protein L3 [Arabidopsis thaliana]	Unigene13582_All//5.00E-121//AT3G17465| RPL3P (RIBOSOMAL PROTEIN L3 PLASTID); structural constituent of ribosome	Unigene13582_All//0.00E+00//gi|78334368|gb|DT554642.1|DT554642		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene13584_All	751	45.42	33.46	46.09	62.55	54.15	53.04	22.41	14.92	9.87	-4.41E-01	1.52E-06		2.10E-02	8.45E-01		-2.08E-01	6.37E-03		-2.38E-01	2.33E-03		-5.87E-01	1.11E-06		-1.18E+00	8.85E-21	Down			Unigene13584_All//0.00E+00//TC143423				
Unigene13587_All	1698	2.96	1.67	1.47	13.55	10.34	8.59	8.47	1.62	1.74	-8.24E-01	2.09E-03		-1.01E+00	3.53E-04	Down	-3.90E-01	2.58E-04		-6.58E-01	2.79E-09		-2.38E+00	3.67E-45	Down	-2.29E+00	2.17E-44	Down	Unigene13587_All//gi|297826769|ref|XP_002881267.1|//1.00E-136//TMS membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327106|gb|EFH57526.1| TMS membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13587_All//3.00E-146//AT2G33205| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: TMS membrane protein/tumour differentially expressed protein (InterPro:IPR005016); BEST Arabidopsis thaliana protein match is: MEE55 (maternal effect embryo arrest 55) (TAIR:AT4G13345.1); Has 602 Blast hits to 593 proteins in 136 species: Archae - 0; Bacteria - 0; Metazoa - 389; Fungi - 90; Plants - 84; Viruses - 0; Other Eukaryotes - 48 (source: NCBI BLink).	Unigene13587_All//0.00E+00//TC144118				nr -
Unigene13588_All	1778	19.19	5.19	4.40	9.97	8.08	10.69	8.37	3.76	4.26	-1.89E+00	8.57E-65	Down	-2.12E+00	6.21E-73	Down	-3.05E-01	1.88E-02		1.01E-01	5.19E-01		-1.15E+00	2.99E-17	Down	-9.75E-01	9.82E-14		Unigene13588_All//gi|20197029|gb|AC27466.2|//1.00E-153//expressed protein [Arabidopsis thaliana]	Unigene13588_All//2.00E-148//AT2G44640| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, chloroplast, plasma membrane, plastid, chloroplast envelope; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: PDE320 (PIGMENT DEFECTIVE 320) (TAIR:AT3G06960.1); Has 25 Blast hits to 24 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene13588_All//0.00E+00//TC150783			GO:0043231//GO:0044444	nr -
Unigene13589_All	1205	53.15	47.43	48.74	79.08	69.84	75.18	31.23	21.16	10.84	-1.64E-01	1.69E-02		-1.25E-01	9.39E-02		-1.79E-01	4.44E-04		-7.29E-02	2.49E-01		-5.62E-01	6.44E-13		-1.53E+00	1.17E-66	Down	Unigene13589_All//gi|253721463|gb|ACT33948.1|//1.00E-83//biotin carboxyl carrier protein subunit [Jatropha curcas]	Unigene13589_All//7.00E-39//AT5G15530| BCCP2 (BIOTIN CARBOXYL CARRIER PROTEIN 2); biotin binding	Unigene13589_All//0.00E+00//TC139535		ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis	GO:0009536//GO:0016874//GO:0019842	nr -
Unigene13594_All	2285	0.00	0.00	0.00	0.00	0.00	0.00	45.07	12.88	25.94	null	null		null	null		null	null		null	null		-1.81E+00	4.37E-224	Down	-7.97E-01	6.11E-64		Unigene13594_All//gi|1334480|emb|CAA87600.1|//2.00E-06//putative orf79.1 [Chondrus crispus]		Unigene13594_All//3.00E-18//ES846329				nr -

Unigene13595_All	2565	0.00	0.00	0.00	0.00	0.00	0.00	50.93	24.90	6.57	null	null		null	null		null	null		null	null		-1.03E+00	2.16E-121	Down	-2.95E+00	0.00E+00	Down	Unigene13595_All//gi|145408595|ref|XP_001152219.1|//9.00E-07//O8F58f [Pinus koraiensis] >gi|145048844|gb|ABF35460.1|O8F58f [Pinus koraiensis]		Unigene13595_All//3.00E-12//TC172353			GO:0043231//GO:0044444	nr +
Unigene136_All	602	7.82	1.52	6.10	1.82	2.35	1.50	0.56	0.14	0.26	-2.37E+00	1.79E-12	Down	-3.58E-01	2.33E-01		3.65E-01	5.62E-01		-2.79E-01	6.89E-01		-2.02E+00	1.36E-01		-1.09E+00	3.55E-01		Unigene136_All//gi|224111296|ref|XP_002332862.1|//3.00E-17//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834264|gb|EEE72741.1| cc-nbs-lrr resistance protein [Populus trichocarpa]		Unigene136_All//8.00E-16//ES823904				nr -
Unigene1360_All	5071	0.51	1.93	0.79	2.86	2.48	6.99	10.99	58.11	7.71	1.93E+00	1.73E-19	Up	6.40E-01	4.52E-02		-2.06E-01	1.94E-01		1.29E+00	1.82E-41	Up	2.40E+00	0.00E+00	Up	-5.12E-01	1.97E-16		Unigene1360_All//gi|224116838|ref|XP_002331826.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222875064|gb|EEF12195.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene1360_All//0.00E+00//AT3G59140| ATMRP14: ATPase, coupled to transmembrane movement of substances	Unigene1360_All//0.00E+00//TC139924		ko02010|ABC transporters		nr -
Unigene13602_All	1388	6.56	5.18	10.51	72.96	67.21	53.43	31.34	15.75	13.03	-3.40E-01	8.27E-02		6.81E-01	7.01E-06		-1.19E-01	2.59E-02		-4.50E-01	9.66E-20		-9.93E-01	1.96E-38		-1.27E+00	4.02E-58	Down	Unigene13602_All//gi|115451567|ref|NP_001049384.1|//1.00E-61//Os03g0216500 [Oryza sativa Japonica Group] >gi|108706852|gb|ABF94647.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547855|dbj|BAF11298.1| Os03g0216500 [Oryza sativa Japonica Group]	Unigene13602_All//2.00E-55//AT3G08490| unknown protein	Unigene13602_All//0.00E+00//CO094728				nr +
Unigene13605_All	457	18.66	33.48	27.38	46.87	58.32	73.53	18.78	53.59	8.37	8.43E-01	5.91E-09		5.53E-01	8.29E-04		3.15E-01	1.95E-03		6.50E-01	7.03E-13		1.51E+00	8.52E-42	Up	-1.17E+00	8.45E-11	Down	Unigene13605_All//gi|9665122|gb|AAF97306.1|AC007843_9//2.00E-35//Hypothetical protein [Arabidopsis thaliana]	Unigene13605_All//6.00E-30//AT1G17330| metal-dependent phosphohydrolase HD domain-containing protein-related	Unigene13605_All//0.00E+00//TC160190			GO:0003824	nr +
Unigene13606_All	1455	8.16	14.52	9.81	14.41	23.97	27.63	9.65	22.46	7.31	8.31E-01	8.82E-12		2.65E-01	1.03E-01		7.34E-01	6.04E-18		9.39E-01	2.54E-28		1.22E+00	3.74E-40	Up	-4.00E-01	2.18E-03		Unigene13606_All//gi|15220978|ref|NP_173176.1|//1.00E-81//metal-dependent phosphohydrolase HD domain-containing protein-related [Arabidopsis thaliana] >gi|32362289|gb|AAP80172.1| At1g17330 [Arabidopsis thaliana]	Unigene13606_All//5.00E-66//AT1G17330| metal-dependent phosphohydrolase HD domain-containing protein-related	Unigene13606_All//0.00E+00//TC154899			GO:0003824	nr +
Unigene13608_All	2527	4.89	2.31	3.54	9.01	6.57	7.43	7.73	2.58	2.85	-1.08E+00	8.04E-11	Down	-4.65E-01	5.74E-03		-4.56E-01	1.69E-05		-2.77E-01	1.88E-02		-1.58E+00	8.33E-36	Down	-1.44E+00	4.07E-32	Down	Unigene13608_All//gi|145338120|ref|NP_187133.3|//0.00E+00//pseudouridine synthase [Arabidopsis thaliana]	Unigene13608_All//0.00E+00//AT3G04820| pseudouridine synthase	Unigene13608_All//0.00E+00//TC169965			GO:0001522//GO:0006399//GO:0016866	nr -
Unigene13609_All	2152	8.00	4.64	5.25	19.51	16.21	11.86	22.83	16.78	8.29	-7.86E-01	5.81E-09		-6.09E-01	1.05E-05		-2.68E-01	6.31E-04		-7.19E-01	4.24E-19		-4.44E-01	4.11E-11		-1.46E+00	2.26E-81	Down	Unigene13609_All//gi|297811357|ref|XP_002873562.1|//1.00E-108//C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319399|gb|EFH49821.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13609_All//2.00E-102//AT5G12300| C2 domain-containing protein	Unigene13609_All//0.00E+00//gi|11206272|gb|BF275202.1|BF275202				nr -
Unigene1361_All	2632	23.10	7.66	29.90	91.66	38.48	61.09	48.79	5.43	20.07	-1.59E+00	1.12E-90	Down	3.72E-01	5.21E-10		-1.25E+00	0.00E+00	Down	-5.85E-01	1.34E-74		-3.17E+00	0.00E+00	Down	-1.28E+00	4.14E-173	Down	Unigene1361_All//gi|8570441|gb|AAF76468.1|AC020622_2//0.00E+00//Contains similarity to p69d gene from Lycopersicon esculentum gb|Y17278 and contains a Peptidase S8 PF|00082 domain [Arabidopsis thaliana]	Unigene1361_All//0.00E+00//AT1G01900| SBT11.1; serine-type endopeptidase	Unigene1361_All//0.00E+00//TC138789				nr +
Unigene13615_All	2258	4.03	2.47	2.22	10.55	9.91	6.52	6.10	1.31	1.34	-7.08E-01	2.02E-04		-8.63E-01	1.45E-05		-8.93E-02	5.27E-01		-6.94E-01	1.86E-10		-2.22E+00	9.66E-40	Down	-2.19E+00	2.35E-40	Down	Unigene13615_All//gi|2829868|gb|AAC00576.1|//5.00E-24//Unknown protein [Arabidopsis thaliana]	Unigene13615_All//3.00E-29//AT3G26050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xk1p2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27350.1); Has 5651 Blast hits to 1894 proteins in 233 species: Archae - 0; Bacteria - 757; Metazoa - 997; Fungi - 564; Plants - 231; Viruses - 18; Other Eukaryotes - 3084 (source: NCBI BLink).	Unigene13615_All//0.00E+00//gi|48803578|gb|CO104892.1|CO104892				nr -
Unigene13618_All	200	0.78	3.55	0.00	7.47	2.07	1.13	4.02	2.72	0.00	2.18E+00	2.50E-02		-9.62E+00	2.45E-01		-1.85E+00	5.94E-04	Down	-2.73E+00	2.67E-05	Down	-5.64E-01	4.30E-01		-1.20E+01	4.43E-06	Down							
Unigene13619_All	1439	3.89	1.87	3.15	10.90	6.25	2.67	4.99	2.00	1.44	-1.06E+00	3.43E-05	Down	-3.07E-01	2.62E-01		-8.04E-01	5.28E-10		-2.03E+00	6.29E-36	Down	-1.32E+00	1.41E-10	Down	-1.79E+00	1.04E-16	Down	Unigene13619_All//gi|254789790|sp|B9SVG9.1|RBR_RICCO//1.00E-142//RecName: Full=Retinoblastoma-related protein	Unigene13619_All//1.00E-127//AT3G12280| RBR1 (RETINOBLASTOMA-RELATED 1); transcription factor binding	Unigene13619_All//0.00E+00//ES795927				nr -
Unigene1362_All	1123	11.23	6.54	3.56	13.84	25.42	19.30	27.79	6.25	13.91	-7.79E-01	1.08E-06		-1.66E+00	1.30E-19	Down	8.77E-01	7.50E-20		4.80E-01	3.06E-05		-2.15E+00	6.66E-86	Down	-9.99E-01	7.02E-29		Unigene1362_All//gi|6562280|emb|CAB62650.1|//1.00E-95//MS5-like protein [Arabidopsis thaliana] >gi|30102656|gb|AAP21246.1| At3g51280 [Arabidopsis thaliana] >gi|110735963|dbj|BAE99956.1| MS5 like protein [Arabidopsis thaliana]	Unigene1362_All//1.00E-96//AT3G51280| male sterility MS5, putative	Unigene1362_All//0.00E+00//TC164387				nr -
Unigene13621_All	1041	14.68	6.81	8.80	29.67	29.51	27.51	42.56	26.26	26.44	-1.11E+00	1.22E-13	Down	-7.38E-01	6.19E-07		-7.90E-03	9.57E-01		-1.09E-01	3.51E-01		-6.97E-01	9.86E-22		-6.87E-01	7.96E-22		Unigene13621_All//gi|79320606|ref|NP_001031225.1|//1.00E-36//D111/G-patch domain-containing protein [Arabidopsis thaliana]	Unigene13621_All//3.00E-22//AT1G63980| D111/G-patch domain-containing protein	Unigene13621_All//0.00E+00//TC156062			GO:0005488//GO:0044464	nr -
Unigene13624_All	1312	1.32	6.72	3.45	2.81	4.70	5.40	26.65	16.98	37.80	2.35E+00	2.01E-22	Up	1.39E+00	6.56E-06	Up	7.42E-01	1.13E-03		9.44E-01	1.49E-05		-6.50E-01	1.98E-15		5.04E-01	2.62E-14		Unigene13624_All//gi|114384143|gb|ABI73973.1|//3.00E-83//transcription factor MYBJ7 [Glycine max]	Unigene13624_All//2.00E-62//AT5G37620| MYB36 (myb domain protein 36); DNA binding / transcription factor	Unigene13624_All//2.00E-101//gi|098890159|gb|DW519123.1|DW519123	MYB		GO:0003676//GO:0009725//GO:0010468//GO:0030522//GO:0043231	nr -
Unigene13626_All	3319	0.93	1.07	1.04	3.35	2.54	2.59	2.87	2.22	6.95	2.00E-01	5.71E-01		1.65E-01	6.21E-01		-3.97E-01	1.64E-02		-3.73E-01	3.30E-02		-3.71E-01	2.94E-02		1.28E+00	2.16E-31	Up	Unigene13626_All//gi|297849670|ref|XP_002892666.1|//1.00E-114//transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297338508|gb|EFH68925.1| transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13626_All//4.00E-113//AT1G11950| transcription factor	Unigene13626_All//0.00E+00//TC160627			GO:0005488	nr +
Unigene1363_All	1231	9.05	7.57	3.59	15.17	25.20	15.74	16.97	3.36	9.61	-2.57E-01	1.48E-01		-1.33E+00	8.99E-13	Down	7.32E-01	6.30E-16		5.27E-02	7.21E-01		-2.34E+00	8.15E-64	Down	-8.20E-01	2.49E-14		Unigene1363_All//gi|6562280|emb|CAB62650.1|//1.00E-149//MS5-like protein [Arabidopsis thaliana] >gi|30102656|gb|AAP21246.1| At3g51280 [Arabidopsis thaliana] >gi|110735963|dbj|BAE99956.1| MS5 like protein [Arabidopsis thaliana]	Unigene1363_All//4.00E-143//AT3G51280| male sterility MS5, putative	Unigene1363_All//0.00E+00//TC164387				nr -
Unigene13631_All	942	9.61	8.93	15.21	15.81	19.30	8.58	26.08	12.47	24.87	-1.06E-01	6.07E-01		6.62E-01	1.50E-05		2.88E-01	2.79E-02		-8.82E-01	6.14E-10		-1.06E+00	1.26E-24	Down	-6.85E-02	5.59E-01		Unigene1363_All//gi|224111880|ref|XP_002316010.1|//1.00E-103//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene13631_All//4.00E-56//AT3G14630| CYP72A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene13631_All//0.00E+00//gi|54118029|gb|CO493538.1|CO493538		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0016491	nr +
Unigene13632_All	1007	2.75	8.05	3.97	5.89	6.91	6.32	60.42	38.10	47.47	1.55E+00	3.80E-12	Up	5.26E-01	1.03E-01		2.31E-01	3.54E-01		1.03E-01	6.86E-01		-6.65E-01	2.91E-27		-3.48E-01	3.40E-09		Unigene13632_All//gi|224111880|ref|XP_002316010.1|//3.00E-85//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene13632_All//1.00E-57//AT3G14630| CYP72A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene13632_All//0.00E+00//TC174988		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids	GO:0005506//GO:0008152//GO:0016491	nr +
Unigene13633_All	2334	1.41	0.09	0.73	4.16	2.80	4.68	4.20	2.40	3.87	-4.02E+00	2.27E-14	Down	-9.52E-01	7.85E-03		-5.70E-01	9.00E-04		1.70E-01	3.95E-01		-8.09E-01	8.20E-07		-1.17E-01	5.29E-01		Unigene13633_All//gi|21425669|emb|CAC95022.1|//0.00E+00//mitochondrial RNA polymerase [Nicotiana tabacum]	Unigene13633_All//0.00E+00//AT1G68990| DNA-directed RNA polymerase, mitochondrial (RPOMT)	Unigene13633_All//0.00E+00//gi|164368537|gb|ES827263.1|ES827263			GO:0003676//GO:0009536//GO:0010467//GO:0034062	nr -
Unigene13634_All	1837	25.78	5.08	11.57	16.16	10.18	6.22	10.38	4.98	9.50	-2.34E+00	2.31E-118	Down	-1.16E+00	4.65E-42	Down	-6.67E-01	1.91E-13		-1.38E+00	5.12E-39	Down	-1.06E+00	3.87E-19	Down	-1.28E-01	3.06E-01		Unigene13634_All//gi|75099142|sp|O64647.1|TCP9_ARATH//4.00E-67//RecName: Full=Transcription factor TCP9	Unigene13634_All//1.00E-63//AT2G45660| TCP family transcription factor, putative	Unigene13634_All//0.00E+00//gi|78338050|gb|DT558324.1|DT558324	TCP		GO:0010468//GO:0043231	nr +
Unigene13635_All	1251	29.28	16.97	11.58	46.83	39.94	53.18	60.50	32.04	36.02	-7.87E-01	3.44E-18		-1.34E+00	6.28E-41	Down	-2.30E-01	4.74E-04		1.84E-01	5.55E-03		-9.17E-01	4.09E-58		-7.48E-01	2.02E-42		Unigene13635_All//gi|224104989|ref|XP_002313645.1|//2.00E-72//histone deacetylase [Populus trichocarpa] >gi|222850053|gb|EEE87600.1| histone deacetylase [Populus trichocarpa]	Unigene13635_All//4.00E-27//AT5G03740| HD2C (HISTONE DEACETYLASE 2C); histone deacetylase/ nucleic acid binding / transcription repressor/ zinc ion binding	Unigene13635_All//0.00E+00//TC150722	C2H2	ko00270|Cysteine and methionine metabolism	GO:0005488//GO:0005622//GO:0009987	nr +
Unigene13636_All	1574	4.39	8.92	3.62	6.23	7.39	5.14	1.50	2.07	0.89	1.02E+00	3.96E-11	Up	-2.78E-01	2.55E-01		2.46E-01	1.65E-01		-2.80E-01	1.56E-01		4.61E-01	1.44E-01		-7.64E-01	3.12E-02		Unigene13636_All//gi|295881692|gb|ADG56590.1|//8.00E-47//ALCATRAZ/SPATULA-like protein [Prunus persica]	Unigene13636_All//2.00E-32//AT4G36930| SPT (SPATULA); DNA binding / transcription factor	Unigene13636_All//0.00E+00//ES808517	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0001071//GO:0006950//GO:0009639//GO:0010029//GO:0010468//GO:0043231//GO:0048437	nr -
Unigene13638_All	1899	8.51	8.97	8.52	22.87	18.77	27.99	21.95	26.32	47.56	7.46E-02	6.22E-01		1.90E-03	9.88E-01		-2.85E-01	1.76E-04		2.91E-01	4.36E-05		2.62E-01	1.05E-04		1.12E+00	2.99E-97	Up	Unigene13638_All//gi|18424516|ref|NP_568941.1|//0.00E+00//GUT1; catalytic/ glucuronoxylan glucuronosyltransferase [Arabidopsis thaliana] >gi|15809826|gb|AAL06841.1| AT5g61840/mac9_140 [Arabidopsis thaliana] >gi|17978869|gb|AAL47406.1| AT5g61840/mac9_140 [Arabidopsis thaliana]	Unigene13638_All//0.00E+00//AT5G61840| GUT1; catalytic/ glucuronoxylan glucuronosyltransferase	Unigene13638_All//0.00E+00//TC140005			GO:0009832//GO:0010413//GO:0015020//GO:0031410//GO:0043231	nr +

Unigene13640_All	1273	20.80	35.78	18.95	24.10	18.66	29.80	43.48	91.47	153.63	7.83E-01	3.45E-22		-1.34E-01	2.73E-01		-3.69E-01	4.73E-05		3.06E-01	3.85E-04		1.07E+00	4.23E-115	Up	1.82E+00	0.00E+00	Up	Unigene13640_All//gi|297803700|ref|XP_002869734.1|//1.00E-138//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315570|gb|EFH45993.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13640_All//3.00E-139//AT4G24160| hydrolase, alpha/beta fold family protein	Unigene13640_All//0.00E+00//TC146381				nr +
Unigene13641_All	1501	14.12	19.38	17.49	19.35	18.24	32.65	5.97	7.74	15.47	4.57E-01	5.02E-06		3.09E-01	5.90E-03		-8.52E-02	4.96E-01		7.55E-01	6.57E-24		3.74E-01	1.33E-02		1.37E+00	3.26E-35	Up	Unigene13641_All//gi|186509740|ref|NP_001118567.1|//1.00E-114//myb family transcription factor [Arabidopsis thaliana] >gi|6223653|gb|AAF05867.1|AC011698_18 transfactor-like [Arabidopsis thaliana]	Unigene13641_All//5.00E-112//AT3G04030| myb family transcription factor	Unigene13641_All//0.00E+00//C0123196	G2-like		GO:0043231	nr +
Unigene13642_All	1642	4.11	3.76	7.30	5.64	4.19	7.26	0.59	1.78	1.41	-1.27E-01	5.93E-01		8.28E-01	1.14E-06		-4.28E-01	1.94E-02		3.64E-01	3.10E-02		1.59E+00	4.96E-06	Up	1.25E+00	8.33E-04	Up	Unigene13642_All//gi|186509740|ref|NP_001118567.1|//1.00E-115//myb family transcription factor [Arabidopsis thaliana] >gi|6223653|gb|AAF05867.1|AC011698_18 transfactor-like [Arabidopsis thaliana]	Unigene13642_All//2.00E-113//AT3G04030| myb family transcription factor	Unigene13642_All//0.00E+00//C0123196	G2-like		GO:0043231	nr +
Unigene13646_All	3051	10.65	6.71	7.42	17.16	10.44	14.67	37.46	27.26	12.48	-6.67E-01	2.42E-12		-5.22E-01	7.51E-08		-7.17E-01	1.60E-26		-2.26E-01	2.16E-03		-4.58E-01	3.60E-26		-1.59E+00	2.12E-212	Down	Unigene13646_All//gi|9838393|ref|NP_064005.1|//7.00E-23//orf152 [Beta vulgaris subsp. vulgaris] >gi|9049307|dbj|BAA99317.1| orf152 [Beta vulgaris subsp. vulgaris] >gi|54606701|dbj|BAD66724.1| orf152 [Beta vulgaris subsp. vulgaris] >gi|54606745|dbj|BAD66768.1| orf152 [Beta vulgaris subsp. vulgaris]		Unigene13646_All//0.00E+00//TC149864				nr +
Unigene1365_All	2579	7.89	4.38	3.53	7.59	9.76	6.55	2.89	1.04	2.38	-8.49E-01	8.29E-12		-1.16E+00	1.80E-18	Down	3.63E-01	4.55E-04		-2.13E-01	1.18E-01		-1.48E+00	8.03E-13	Down	-2.78E-01	1.52E-01		Unigene1365_All//gi|297720017|ref|NP_001172370.1|//1.00E-154//Os01g0500550 [Oryza sativa Japonica Group] >gi|56201797|dbj|BAD73247.1| bZIP protein-like [Oryza sativa Japonica Group] >gi|255673275|dbj|BAH91100.1| Os01g0500550 [Oryza sativa Japonica Group]	Unigene1365_All//0.00E+00//AT5G25590| INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF630 (InterPro:IPR006868), Protein of unknown function DUF632 (InterPro:IPR006867), Actin-binding FH2 (InterPro:IPR015425); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52320.4); Has 31848 Blast hits to 18905 proteins in 762 species: Archae - 79; Bacteria - 761; Metazoa - 13943; Fungi - 3494; Plants - 1748; Viruses - 431; Other Eukaryotes - 9392 (source: NCBI BLink).	Unigene1365_All//0.00E+00//TC155946		ko03040|Spliceosome		nr +
Unigene13651_All	1880	79.71	38.51	75.14	7.92	11.56	5.17	0.05	0.00	0.00	-1.05E+00	7.90E-117	Down	-8.50E-02	7.82E-02		5.45E-01	6.58E-07		-6.17E-01	1.18E-05		-5.49E+00	4.04E-01		-5.49E+00	3.59E-01		Unigene13651_All//gi|13487783|gb|AK27718.1|AF356002_1//0.00E+00//ADP-glucose pyrophosphorylase [Cicer arietinum]	Unigene13651_All//0.00E+00//AT5G19220| APL1 (ADP GLUCOSE PYROPHOSPHORYLASE LARGE SUBUNIT 1); glucose-1-phosphate adenylyltransferase	Unigene13651_All//0.00E+00//TC142060		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene13652_All	2432	3.44	2.08	1.36	2.48	3.44	3.70	6.69	1.62	3.00	-7.24E-01	2.89E-04		-1.34E+00	7.86E-10	Down	4.73E-01	1.60E-02		5.76E-01	2.50E-03		-2.05E+00	1.73E-42	Down	-1.16E+00	1.69E-19	Down	Unigene13652_All//gi|240255315|ref|NP_187642.4|//0.00E+00//ATP binding / microtubule motor [Arabidopsis thaliana]	Unigene13652_All//0.00E+00//AT3G10310| ATP binding / microtubule motor	Unigene13652_All//0.00E+00//ES813050				nr -
Unigene13653_All	959	35.41	23.25	21.43	54.80	74.58	49.78	22.44	13.73	7.81	-6.07E-01	5.17E-11		-7.24E-01	3.90E-14		4.45E-01	4.33E-15		-1.39E-01	8.27E-02		-7.09E-01	2.71E-11		-1.52E+00	2.24E-38	Down	Unigene13653_All//gi|62125392|gb|AX63768.1|//5.00E-76//auxin-responsive protein IAA [Populus tomentosa]	Unigene13653_All//3.00E-68//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene13653_All//0.00E+00//TC170355				nr +
Unigene13655_All	1818	23.05	15.80	15.35	40.17	34.04	41.24	45.54	23.50	21.26	-5.45E-01	3.57E-11		-5.87E-01	4.07E-12		-2.39E-01	3.14E-05		3.79E-02	6.21E-01		-9.55E-01	7.22E-68		-1.10E+00	8.49E-88	Down	Unigene13655_All//gi|15240939|ref|NP_198099.1|//0.00E+00//seryl-tRNA synthetase / serine--tRNA ligase [Arabidopsis thaliana] >gi|2501056|sp|Q39230.1|SYS_ARATH RecName: Full=Seryl-tRNA synthetase; AltName: Full=Seryl-tRNA(Ser/Sec) synthetase; AltName: Full=Serine--tRNA ligase; Short=SerRS >gi|1359497|emb|CAA94388.1| seryl-tRNA Synthetase [Arabidopsis thaliana]	Unigene13655_All//0.00E+00//AT5G27470| seryl-tRNA synthetase / serine--tRNA ligase	Unigene13655_All//0.00E+00//TC143069		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene13656_All	2330	2.34	0.83	1.21	4.55	4.73	4.32	8.17	3.10	3.69	-1.50E+00	4.25E-08	Down	-9.47E-01	4.06E-04		5.46E-02	8.21E-01		-7.52E-02	7.03E-01		-1.40E+00	4.45E-29	Down	-1.14E+00	3.21E-22	Down	Unigene13656_All//gi|224089995|ref|XP_002308898.1|//0.00E+00//condensin complex components subunit [Populus trichocarpa] >gi|222854874|gb|EEE92421.1| condensin complex components subunit [Populus trichocarpa]	Unigene13656_All//0.00E+00//AT3G57060| binding	Unigene13656_All//0.00E+00//DR463756				nr -
Unigene13657_All	2108	12.36	5.19	8.77	19.80	16.69	12.96	13.54	4.78	12.64	-1.25E+00	1.83E-27	Down	-4.96E-01	6.24E-06		-2.46E-01	1.98E-03		-6.11E-01	2.10E-14		-1.50E+00	3.46E-48	Down	-9.87E-02	3.38E-01		Unigene13657_All//gi|115452803|ref|NP_001050002.1|//1.00E-105//Os03g0328900 [Oryza sativa Japonica Group] >gi|108707942|gb|ABF95737.1| Zinc finger C-x8-C-x5-C-x3-H type family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548473|dbj|BAF11916.1| Os03g0328900 [Oryza sativa Japonica Group]	Unigene13657_All//6.00E-95//AT3G51950| zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein	Unigene13657_All//0.00E+00//gi|48806951|gb|C0108265.1|C0108265	C3H			nr +
Unigene13658_All	1402	4.52	2.31	2.54	17.66	22.84	13.98	8.59	4.41	3.58	-9.65E-01	4.63E-05		-8.27E-01	7.05E-04		3.71E-01	3.36E-05		-3.37E-01	2.04E-03		-9.62E-01	1.06E-10		-1.26E+00	1.11E-16	Down	Unigene13658_All//gi|284504570|gb|ADB90475.1|//0.00E+00//pectate lyase [Gossypium herbaceum]	Unigene13658_All//0.00E+00//AT4G24780| pectate lyase family protein	Unigene13658_All//0.00E+00//ES828007		ko00040|Pentose and glucuronate interconversions		nr -
Unigene13660_All	2067	11.92	5.69	8.71	76.16	68.49	71.10	69.51	24.08	27.12	-1.07E+00	2.33E-20	Down	-4.53E-01	6.52E-05		-1.53E-01	8.15E-05		-9.91E-02	2.36E-02		-1.53E+00	4.37E-246	Down	-1.36E+00	9.99E-212	Down	Unigene13660_All//gi|134142069|gb|AB061378.1|//0.00E+00//mitochondrial serine hydroxymethyltransferase [Populus tremuloides]	Unigene13660_All//0.00E+00//AT5G26780| SHM2 (SERINE HYDROXYMETHYLTRANSFERASE 2); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene13660_All//0.00E+00//TC179195		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr -
Unigene13662_All	2450	1.35	0.50	1.43	4.33	3.06	2.49	7.39	8.94	9.45	-1.44E+00	5.81E-05	Down	9.25E-02	7.81E-01		-4.99E-01	2.48E-03		-7.99E-01	2.96E-06		2.75E-01	1.07E-02		3.55E-01	3.60E-04		Unigene13662_All//gi|66271061|gb|AY43808.1|//2.00E-30//Fb17 [Gossypium hirsutum]	Unigene13662_All//0.00E+00//gi|11209398|gb|BF278328.1|BF278328				nr +
Unigene13667_All	1436	0.87	0.28	1.78	3.61	3.05	2.45	4.18	1.78	2.50	-1.63E+00	1.05E-02		1.03E+00	1.37E-02		-2.44E-01	3.96E-01		-5.56E-01	3.58E-02		-1.24E+00	3.43E-08	Down	-7.44E-01	3.70E-04		Unigene13667_All//gi|75183398|sp|Q9M2Y6.1|Y3972_ARATH//1.00E-105//RecName: Full=Uncharacterized protein At3g49720 >gi|222424727|dbj|BAH20317.1| AT3G49720 [Arabidopsis thaliana]	Unigene13667_All//1.00E-98//AT3G49720| unknown protein	Unigene13667_All//5.00E-96//DT049245				nr +
Unigene13668_All	212	1.97	2.39	0.00	3.76	0.00	0.85	9.57	58.75	6.01	2.76E-01	7.64E-01		-1.09E+01	1.56E-02		-1.19E+01	6.49E-06	Down	-2.14E+00	1.54E-02		2.62E+00	1.59E-43	Up	-6.71E-01	8.49E-02					Unigene13668_All//3.00E-90//gi|31072401|gb|CA992680.1|CA992680				
Unigene13669_All	1360	3.96	3.91	3.48	25.75	19.34	10.76	89.57	237.81	145.24	-1.85E-02	9.63E-01		-1.85E-01	5.22E-01		-4.13E-01	7.28E-07		-1.26E+00	5.17E-40	Down	1.41E+00	0.00E+00	Up	6.97E-01	2.98E-96		Unigene13669_All//gi|113367218|gb|AB134666.1|//1.00E-42//bZIP transcription factor bZIP124 [Glycine max]	Unigene13669_All//3.00E-20//AT1G75390| AthZIP44 (Arabidopsis thaliana basic leucine-zipper 44); DNA binding / protein heterodimerization/ transcription factor	Unigene13669_All//0.00E+00//TC139631	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene13671_All	1956	2.43	3.19	1.93	3.13	2.52	4.48	14.44	29.94	16.21	3.89E-01	1.10E-01		-3.33E-01	2.65E-01		-3.15E-01	2.06E-01		5.16E-01	8.22E-03		1.05E+00	2.05E-56	Up	1.67E-01	5.98E-02		Unigene13671_All//gi|10798894|gb|AC231130.1|//0.00E+00//diacylglycerol kinase variant A [Solanum lycopersicum]	Unigene13671_All//0.00E+00//AT2G20900| diacylglycerol kinase, putative	Unigene13671_All//0.00E+00//gi|48814361|gb|C0115674.1|C0115674		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr +
Unigene13673_All	2306	5.06	2.75	4.53	5.27	5.54	3.41	5.30	0.87	3.87	-8.81E-01	1.58E-07		-1.61E-01	3.99E-01		7.19E-02	7.33E-01		-6.29E-01	6.96E-05		-2.61E+00	1.20E-42	Down	-4.53E-01	1.25E-03		Unigene13673_All//gi|21950739|gb|AM78582.1|//0.00E+00//RanGAP1 interacting protein [Arabidopsis thaliana]	Unigene13673_All//0.00E+00//AT5G18590| kelch repeat-containing protein	Unigene13673_All//0.00E+00//gi|73847973|gb|DT456993.1|DT456993		ko04712|Circadian rhythm - plant		nr -
Unigene13676_All	1406	1.23	3.60	1.40	9.60	11.24	10.09	7.13	5.89	3.60	1.55E+00	6.56E-08	Up	1.91E-01	6.77E-01		2.28E-01	1.29E-01		7.11E-02	6.71E-01		-2.76E-01	1.07E-01		-9.86E-01	1.08E-09		Unigene13676_All//gi|15222980|ref|NP_172845.1|//3.00E-39//remorin family protein [Arabidopsis thaliana] >gi|5080768|gb|AAD39278.1|AC007576_1 Hypothetical protein [Arabidopsis thaliana]	Unigene13676_All//1.00E-22//AT1G13920| remorin family protein	Unigene13676_All//3.00E-79//DW512129				nr -
Unigene13677_All	1163	33.02	18.21	37.32	127.30	106.44	56.70	14.83	4.56	4.18	-8.59E-01	5.48E-22		1.76E-01	4.82E-02		-2.58E-01	1.57E-11		-1.17E+00	8.77E-149	Down	-1.70E+00	4.72E-35	Down	-1.83E+00	7.01E-40	Down	Unigene13677_All//gi|15224801|ref|NP_179547.1|//1.00E-101//CDA1 (CYTIDINE DEAMINASE 1); cytidine deaminase [Arabidopsis thaliana] >gi|6090835|gb|AAF03358.1|AF134487_1 cytidine deaminase 1 [Arabidopsis thaliana] >gi|3046700|emb|CAA06460.1| cytidine deaminase [Arabidopsis thaliana] >gi|3093276|emb|CAA06671.1| cytidine deaminase [Arabidopsis thaliana] >gi|30984516|gb|AAP42721.1| At2g19570 [Arabidopsis thaliana]	Unigene13677_All//6.00E-99//AT2G19570| CDA1 (CYTIDINE DEAMINASE 1); cytidine deaminase	Unigene13677_All//0.00E+00//TC153423		ko00240|Pyrimidine metabolism		nr +
Unigene13679_All	2352	9.28	14.93	10.19	34.12	24.76	25.52	15.08	24.56	5.98	6.87E-01	6.62E-14		1.35E-01	3.00E-01		-4.63E-01	1.61E-18		-4.19E-01	6.47E-14		7.03E-01	1.69E-28		-1.33E+00	1.54E-51	Down	Unigene13679_All//gi|119507463|dbj|BAF42039.1|//0.00E+00//pectin methylesterase 2 [Pyrus communis]	Unigene13679_All//0.00E+00//AT5G09760| pectinesterase family protein	Unigene13679_All//0.00E+00//TC145513		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene1368_All	2398	35.63	10.52	27.91	28.36	23.28	10.90	13.44	9.52	29.56	-1.76E+00	1.17E-146	Down	-3.52E-01	8.62E-10		-2.85E-01	1.24E-06		-1.38E+00	6.81E-89	Down	-4.98E-01	3.90E-09		1.14E+00	6.55E-79	Up	Unigene1368_All//gi|87162706|gb|ABD28501.1|//1.00E-122//Zinc finger, C2H2-type [Medicago truncatula]	Unigene1368_All//1.00E-101//AT3G13810| AtIDD11 (Arabidopsis thaliana Indeterminate(ID)-Domain 11); nucleic acid binding / transcription factor/ zinc ion binding	Unigene1368_All//0.00E+00//TC140948	C2H2			nr -

Unigene13680_All	2048	6.46	5.69	7.07	8.44	8.73	8.67	7.47	4.41	3.31	-1.84E-01	2.74E-01			1.30E-01	4.38E-01		4.81E-02	8.03E-01			3.82E-02	8.07E-01		-7.62E-01	2.93E-09		-1.18E+00	8.28E-19	Down	Unigene13680_All//gi|18406426|ref|NP_566005.1|//0.00E+00//mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana] >gi|3212859|gb|AAC23410.1| expressed protein [Arabidopsis thaliana]	Unigene13680_All//0.00E+00//AT2G44020| mitochondrial transcription termination factor-related / mTERF-related	Unigene13680_All//0.00E+00//TC178578				nr +
Unigene13683_All	2367	7.65	11.00	12.82	30.52	18.01	20.19	4.89	1.87	1.85	5.25E-01	8.09E-07			7.46E-01	2.36E-13		-7.61E-01	1.91E-40			-5.96E-01	1.95E-23		-1.39E+00	7.57E-18	Down	-1.40E+00	1.01E-18	Down	Unigene13683_All//gi|9294427|dbj|BAB02547.1|//0.00E+00//beta-1,4-xylosidase [Arabidopsis thaliana]	Unigene13683_All//0.00E+00//AT3G19620| glycosyl hydrolase family 3 protein	Unigene13683_All//0.00E+00//gi|164248931|gb|ES793662.1|ES793662		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00660|Cyanoamino acid metabolism		nr -
Unigene13684_All	1540	39.68	111.74	247.89	62.33	58.99	58.77	38.33	24.89	24.65	1.49E+00	1.42E-231	Up	2.64E+00	0.00E+00	Up	-7.96E-02	1.86E-01			-8.49E-02	1.66E-01		-6.23E-01	1.18E-23		-6.37E-01	2.88E-25		Unigene13684_All//gi|159895667|gb|ABX10444.1|//0.00E+00//phosphoethanolamine N-methyltransferase [Gossypium hirsutum]	Unigene13684_All//0.00E+00//AT1G48600| phosphoethanolamine N-methyltransferase 2, putative (NMT2)	Unigene13684_All//0.00E+00//TC147333		ko00564|Glycerophospholipid metabolism/ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00100|Steroid biosynthesis		nr -
Unigene13688_All	2460	1.45	1.30	1.54	6.28	4.28	3.75	8.63	3.04	4.32	-1.57E-01	6.22E-01			8.77E-02	7.86E-01		-5.51E-01	2.59E-05			-7.45E-01	7.30E-08		-1.50E+00	4.24E-36	Down	-9.97E-01	7.15E-20		Unigene13688_All//gi|224589517|gb|ACN59292.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene13688_All//0.00E+00//AT2G23300| leucine-rich repeat transmembrane protein kinase, putative	Unigene13688_All//0.00E+00//TC162283		ko04626|Plant-pathogen interaction		nr +
Unigene13689_All	2684	14.50	8.61	10.22	24.20	18.72	26.50	38.00	19.54	17.02	-7.53E-01	6.48E-18			-5.05E-01	8.78E-09		-3.71E-01	3.99E-10			1.31E-01	5.16E-02		-9.59E-01	4.41E-84		-1.16E+00	2.12E-117	Down	Unigene13689_All//gi|240255269|ref|NP_186925.4|//0.00E+00//ATP binding / aminoacyl-tRNA ligase/ histidine-tRNA ligase/ nucleotide binding [Arabidopsis thaliana]	Unigene13689_All//0.00E+00//AT3G02760| ATP binding / aminoacyl-tRNA ligase/ histidine-tRNA ligase/ nucleotide binding	Unigene13689_All//0.00E+00//TC160823		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene1369_All	2502	5.25	11.48	16.71	6.95	3.12	4.03	3.87	5.88	3.39	1.13E+00	1.14E-25	Up	1.67E+00	7.41E-65	Up	-1.15E+00	7.29E-20	Down	-7.88E-01	1.38E-09		6.04E-01	3.37E-06				-1.90E-01	2.76E-01		Unigene1369_All//gi|115465379|ref|NP_001056289.1|//4.00E-79//Os05g0557500 [Oryza sativa Japonica Group] >gi|113579840|dbj|BAF18203.1| Os05g0557500 [Oryza sativa Japonica Group]	Unigene1369_All//4.00E-118//AT4G21700| unknown protein	Unigene1369_All//0.00E+00//TC139543				nr -
Unigene13690_All	361	0.58	1.12	0.00	15.87	8.39	3.88	11.24	1.97	2.32	9.54E-01	4.14E-01			-9.18E+00	1.46E-01		-9.19E-01	6.58E-05			-2.03E+00	1.95E-13	Down	-2.51E+00	4.64E-14	Down	-2.28E+00	4.69E-13	Down	Unigene13690_All//gi|297839191|ref|XP_002887477.1|//2.00E-09//sugar transporter family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333318|gb|EFH63736.1| sugar transporter family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13690_All//6.00E-10//AT1G73220| AtOCT1 (Arabidopsis thaliana ORGANIC CATION/CARNITINE TRANSPORTER1); carbohydrate transmembrane transporter/ carnitine transporter/ transporter					nr -
Unigene13691_All	1709	2.36	0.71	1.46	61.85	36.25	11.55	28.87	6.60	8.16	-1.73E+00	2.02E-07	Down	-6.87E-01	3.07E-02		-7.71E-01	1.81E-60			-2.42E+00	3.32E-299	Down	-2.13E+00	1.25E-133	Down	-1.82E+00	3.51E-112	Down	Unigene13691_All//gi|297839191|ref|XP_002887477.1|//1.00E-167//sugar transporter family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333318|gb|EFH63736.1| sugar transporter family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13691_All//3.00E-149//AT1G73220| AtOCT1 (Arabidopsis thaliana ORGANIC CATION/CARNITINE TRANSPORTER1); carbohydrate transmembrane transporter/ carnitine transporter/ transporter					nr -
Unigene13692_All	1920	14.12	7.52	7.63	34.12	29.40	27.87	26.80	17.50	12.70	-9.08E-01	3.03E-17			-8.88E-01	6.15E-16		-2.15E-01	5.31E-04			-2.92E-01	3.88E-06		-6.15E-01	2.91E-20		-1.08E+00	3.47E-53	Down	Unigene13692_All//gi|32487791|emb|CAE05414.1|//1.00E-172//OSJNBa0035104.2 [Oryza sativa (japonica cultivar-group)] >gi|38669918|emb|CAE05953.3| OSJNBb0088C09.12 [Oryza sativa (japonica cultivar-group)] >gi|116309409|emb|CAH66485.1| OSIGBa0076114.6 [Oryza sativa (indica cultivar-group)]	Unigene13692_All//2.00E-166//AT1G43580| unknown protein	Unigene13692_All//0.00E+00//TC147095				nr -
Unigene13693_All	417	14.93	6.80	11.75	12.18	6.77	5.20	3.65	1.70	2.20	-1.13E+00	3.09E-06	Down	-3.46E-01	1.78E-01		-8.48E-01	6.06E-04			-1.23E+00	4.12E-06	Down	-1.10E+00	2.32E-02		-7.32E-01	1.11E-01		Unigene13693_All//gi|30682484|ref|NP_849647.1|//1.00E-09//SRS (SERYL-TRNA SYNTHETASE); serine-tRNA ligase [Arabidopsis thaliana]	Unigene13693_All//7.00E-51//AT1G11870| SRS (SERYL-TRNA SYNTHETASE); serine-tRNA ligase	Unigene13693_All//0.00E+00//TC169864		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene13694_All	2054	11.06	4.54	7.34	4.78	3.96	3.98	3.17	2.36	2.13	-1.28E+00	5.40E-25	Down	-5.92E-01	5.74E-07		-2.72E-01	1.57E-01			-2.64E-01	1.90E-01		-4.26E-01	4.29E-02		-5.71E-01	4.13E-03		Unigene13694_All//gi|30682484|ref|NP_849647.1|//0.00E-00//SRS (SERYL-TRNA SYNTHETASE); serine-tRNA ligase [Arabidopsis thaliana]	Unigene13694_All//0.00E+00//AT1G11870| SRS (SERYL-TRNA SYNTHETASE); serine-tRNA ligase	Unigene13694_All//0.00E+00//TC169864		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene13696_All	1217	5.98	5.00	7.83	121.28	114.57	101.79	22.69	4.46	5.11	-2.58E-01	2.56E-01			3.90E-01	4.89E-02		-8.22E-02	7.24E-02			-2.53E-01	4.90E-10		-2.35E+00	1.49E-84	Down	-2.15E+00	2.04E-78	Down	Unigene13696_All//gi|38454180|gb|AK20784.1|//1.00E-119//At1g09610 [Arabidopsis thaliana] >gi|44681448|gb|AAS47664.1| At1g09610 [Arabidopsis thaliana]	Unigene13696_All//1.00E-113//AT1G09610| unknown protein	Unigene13696_All//0.00E+00//TC152973				nr -
Unigene13697_All	3661	1.26	0.62	0.58	7.13	7.20	5.66	13.78	9.93	5.92	-1.01E+00	3.60E-04	Down	-1.11E+00	1.90E-04	Down	1.32E-02	9.30E-01			-3.33E-01	1.72E-03		-4.72E-01	1.21E-12		-1.22E+00	2.30E-63	Down	Unigene13697_All//gi|30685832|ref|NP_850218.1|//0.00E+00//PHO2 (PHOSPHATE 2); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75331117|sp|Q8VY10.1|UBC24_ARATH RecName: Full=Probable ubiquitin-conjugating enzyme E2 24; AltName: Full=Ubiquitin-protein ligase 24; AltName: Full=Ubiquitin carrier protein 24; AltName: Full=AtPHO2 >gi|663544556|gb|AAY44863.1| ubiquitinating enzyme [Arabidopsis thaliana]	Unigene13697_All//0.00E+00//AT2G33770| PHO2 (PHOSPHATE 2); ubiquitin-protein ligase	Unigene13697_All//0.00E+00//ES842734		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene13699_All	2310	33.97	21.15	30.84	41.23	46.96	37.62	23.34	11.38	10.54	-6.84E-01	5.11E-30			-1.40E-01	3.28E-02		1.88E-01	7.27E-05			-1.32E-01	1.85E-02		-1.04E+00	8.37E-51	Down	-1.15E+00	1.64E-61	Down	Unigene13699_All//gi|226935214|gb|ACO92659.1|//0.00E+00//mitochondrial L-galactono-1,4-lactone dehydrogenase [Citrus unshiu]	Unigene13699_All//0.00E+00//AT3G47930| ATGLDH (L-GALACTONO-1,4-LACTONE DEHYDOROGENASE); L-gulono-1,4-lactone dehydrogenase/ galactonolactone dehydrogenase	Unigene13699_All//0.00E+00//TC151735		ko00053|Ascorbate and aldarate metabolism//ko00908|Zeatin biosynthesis		nr +
Unigene13700_All	934	6.50	8.14	3.25	10.72	9.18	7.45	11.45	16.60	54.47	3.25E-01	1.35E-01			-1.00E+00	7.54E-05		-2.24E-01	2.56E-01			-5.26E-01	3.29E-03		5.36E-01	2.15E-05		2.25E+00	4.61E-150	Up	Unigene13700_All//gi|61845107|emb|CAI70375.1|//3.00E-91//beta 1,2 xylosyltransferase [Populus alba x Populus tremula]	Unigene13700_All//4.00E-76//AT5G55500| XYLT (ARABIDOPSIS THALIANA BETA-1,2-XYLOSYLTRANSFERASE); xylosyltransferase	Unigene13700_All//0.00E+00//TC165267		ko00510|N-Glycan biosynthesis		nr +
Unigene13701_All	2081	3.34	3.85	3.38	6.22	6.16	5.49	5.67	7.99	28.07	2.02E-01	3.73E-01			1.45E-02	9.71E-01		-1.59E-02	9.36E-01			-1.81E-01	3.15E-01		4.96E-01	4.37E-05		2.31E+00	1.31E-177	Up	Unigene13701_All//gi|156103422|gb|ABI48859.1|//0.00E+00//xylosyltransferase 2 [Nicotiana benthamiana]	Unigene13701_All//0.00E+00//AT5G55500| XYLT (ARABIDOPSIS THALIANA BETA-1,2-XYLOSYLTRANSFERASE); xylosyltransferase	Unigene13701_All//0.00E+00//TC165267		ko00510|N-Glycan biosynthesis		nr +
Unigene13704_All	2125	41.91	66.45	54.93	27.43	22.74	31.37	3.84	9.85	3.79	6.65E-01	9.11E-51			3.90E-01	8.31E-16		-2.71E-01	2.72E-05			1.94E-01	3.09E-03		1.36E+00	1.20E-30	Up	-2.01E-02	9.37E-01		Unigene13704_All//gi|2764524|emb|CAA04157.1|//0.00E+00//Rieske iron-sulfur protein Tic55 [Pisum sativum]	Unigene13704_All//0.00E+00//AT2G24820| TIC55 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 55); 2 iron, 2 sulfur cluster binding / electron carrier/ oxidoreductase	Unigene13704_All//0.00E+00//TC137397		ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene13707_All	1534	6.89	28.37	10.90	162.66	305.47	293.50	20.64	34.85	27.37	2.04E+00	6.20E-91	Up	6.62E-01	2.40E-06		9.09E-01	0.00E+00			8.52E-01	1.47E-265		7.55E-01	7.90E-30		4.07E-01	1.49E-08		Unigene13707_All//gi|18420811|ref|NP_568449.1|//1.00E-111//copper-binding family protein [Arabidopsis thaliana]	Unigene13707_All//1.00E-67//AT5G24580| copper-binding family protein	Unigene13707_All//0.00E+00//gi|78322895|gb|DT543169.1|DT543169				nr +
Unigene13708_All	1987	7.61	4.74	8.33	17.72	14.90	12.84	5.94	2.40	4.57	-6.82E-01	2.09E-06		1.31E-01	3.94E-01		-2.50E-01	4.48E-03			-4.65E-01	1.06E-07		-1.31E+00	1.14E-16	Down	-3.77E-01	9.07E-03		Unigene13708_All//gi|15222611|ref|NP_173922.1|//1.00E-178//aspartyl protease family protein [Arabidopsis thaliana]	Unigene13708_All//1.00E-163//AT1G25510| aspartyl protease family protein	Unigene13708_All//0.00E+00//TC172187				nr -
Unigene13709_All	1462	0.43	0.14	0.44	2.62	4.40	11.52	3.30	13.06	9.35	-1.63E+00	9.23E-02			2.56E-02	9.97E-01		7.47E-01	7.51E-04			2.13E+00	3.67E-40	Up	1.99E+00	1.28E-47	Up	1.50E+00	5.40E-24	Up	Unigene13709_All//gi|119360031|gb|ABL66744.1|//1.00E-51//At1g54200 [Arabidopsis thaliana]	Unigene13709_All//8.00E-27//AT1G54200| unknown protein	Unigene13709_All//3.00E-20//TC140234				nr +
Unigene1371_All	1028	3.77	13.55	7.20	18.70	13.37	13.62	59.51	78.31	80.34	1.85E+00	6.32E-26	Up	9.35E-01	3.08E-05		-4.85E-01	3.09E-05			-4.58E-01	2.03E-04		3.96E-01	1.97E-14		4.33E-01	9.29E-18		Unigene1371_All//gi|224071055|ref|XP_002303349.1|//4.00E-76//heavy metal ATPase [Populus trichocarpa] >gi|222840781|gb|EEE78328.1| heavy metal ATPase [Populus trichocarpa]	Unigene1371_All//4.00E-66//AT5G44790| RAN1 (RESPONSIVE-TO-ANTAGONIST 1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / copper ion transmembrane transporter	Unigene1371_All//0.00E+00//gi|73861455|gb|DT464194.1|DT464194				nr +
Unigene13710_All	1533	2.35	1.88	1.88	0.68	0.54	0.50	0.86	0.95	2.13	-3.22E-01	3.45E-01			-3.28E-01	3.60E-01		-3.40E-01	5.96E-01			-4.46E-01	5.32E-01		1.58E-01	7.51E-01		1.32E+00	2.17E-05	Up	Unigene13710_All//gi|119360031|gb|ABL66744.1|//6.00E-53//At1g54200 [Arabidopsis thaliana]	Unigene13710_All//5.00E-32//AT1G54200| unknown protein	Unigene13710_All//1.00E-69//DR462548				nr +
Unigene13712_All	1515	8.84	13.38	13.95	60.96	61.87	56.70	137.47	143.60	56.75	5.98E-01	1.02E-06		6.58E-01	9.01E-08		2.14E-02	7.93E-01			-1.05E-01	8.10E-02		6.29E-02	7.08E-02		-1.28E+00	1.02E-278	Down	Unigene13712_All//gi|294514718|gb|ADE95828.1|//0.00E+00//4-coumarate:CoA ligase 1 [Corchorus capsularis]	Unigene13712_All//1.00E-155//AT1G51680| 4CL1 (4-COUMARATE:COA LIGASE 1); 4-coumarate-CoA ligase	Unigene13712_All//0.00E+00//TC144604		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene13714_All	1467	3.64	2.14	4.50	9.71	9.48	7.76	4.96	2.45	3.29	-7.65E-01	3.05E-03		3.07E-01	2.25E-01		-3.43E-02	8.37E-01			-3.24E-01	3.44E-02		-1.02E+00	2.40E-07	Down	-5.93E-01	1.52E-03		Unigene13714_All//gi|115448281|ref|NP_001047920.1|//1.00E-139//Os02g0714500 [Oryza sativa Japonica Group] >gi|113537451|dbj|BAF09834.1| Os02g0714500 [Oryza sativa Japonica Group]	Unigene13714_All//1.00E-83//AT5G65950| unknown protein	Unigene13714_All//0.00E+00//TC170527				nr +
Unigene13721_All	1959	2.67	8.51	8.81	4.45	7.44	7.91	2.89	1.64	3.60	1.67E+00	5.73E-27	Up	1.72E+00	3.66E-28	Up	7.41E-01	7.13E-08			8.29E-01	2.92E-09		-8.16E-01	2.47E-04		3.16E-01	1.11E-01		Unigene13721_All//gi|224063973|ref|XP_002301328.1|//4.00E-30//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222843054|gb|EEE80601.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene13721_All//1.00E-29//AT5G24590| TIP (TCV-INTERACTING PROTEIN); transcription coactivator/ transcription factor	Unigene13721_All//0.00E+00//TC171761	NAC			nr -
Unigene13722_All	1189	17.21	17.17	15.05	40.97	43.53	51.39	28.16	67.53	114.69	-2.70E-03	9.81E-01		-1.93E-01	1.54E-01		8.73E-02	3.15E-01			3.27E-01	5.75E-07		1.26E+00	7.72E-103	Up	2.03E+00	0.00E+00	Up	Unigene13722_All//gi|171854669|dbj|BAG16524.1|//2.00E-96//C2 domain-containing protein [Capsicum chinense]	Unigene13722_All//4.00E-51//AT4G34150| C2 domain-containing protein	Unigene13722_All//0.00E+00//gi|78353961|gb|DT574235.1|DT574235		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism/ko00565|Ether lipid metabolism		nr +
Unigene13724_All	1306	3.73	3.14	3.26	4.23	3.98	8.30	6.12	11.81	14.70	-2.46E-01	3.77E-01		-1.92E-01	5.33E-01		-8.87E-02	7.86E-01			9.71E-01	1.69E-08		9.49E-01	3.69E-13		1.26E+00	7.02E-26	Up	Unigene13724_All//gi|15238957|ref|NP_199057.1|//1.00E-133//transporter-related [Arabidopsis thaliana] >gi|94442449|gb|ABF19012.1| At5g42420 [Arabidopsis thaliana]	Unigene13724_All//1.00E-120//AT5G42420| transporter-related	Unigene13724_All//1.00E-158//gi|164360328|gb|EX168561.1|EX168561				nr +

Unigene13726_A11	730	1.65	0.28	1.68	2.59	2.03	2.41	1.80	2.46	1.20	-2.57E+00	5.35E-04	Down	2.53E-02	9.87E-01		-3.54E-01	4.76E-01		-1.04E-01	8.32E-01		4.55E-01	3.20E-01		-5.81E-01	2.51E-01		Unigene13726_A11//gi|193806495|sp|Q9LQ14.2|PPR96_ARATH//3.00E-53//RecName: Full=Pentatricopeptide repeat-containing protein At1g62930, chloroplastic; Flags: Precursor	Unigene13726_A11//3.00E-54//AT1G62930| INVOLVED IN: biological_process unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT1G63130.1); Has 29147 Blast hits to 6292 proteins in 192 species: Archae - 8; Bacteria - 22; Metazoa - 1258; Fungi - 858; Plants - 25291; Viruses - 0; Other Eukaryotes - 1710 (source: NCBI BLink).	Unigene13726_A11//0.00E+00//gi|48743365|gb|C0073884.1|C0073884				nr +
Unigene13728_A11	1164	1.30	2.00	0.73	3.94	2.87	3.07	5.59	3.27	1.92	6.19E-01	1.37E-01		-8.33E-01	1.40E-01		-4.56E-01	1.03E-01		-3.61E-01	2.35E-01		-7.76E-01	1.60E-04		-1.55E+00	1.85E-12	Down	Unigene13728_A11//gi|297829404|ref|XP_002882584.1|//9.00E-70//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297328424|gb|EFH58843.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene13728_A11//2.00E-58//AT3G08800| binding	Unigene13728_A11//1.00E-164//TC154599				nr -
Unigene13732_A11	1830	3.83	2.16	2.82	6.10	4.29	3.01	4.27	0.43	1.18	-8.27E-01	1.90E-04		-4.41E-01	6.05E-02		-5.07E-01	1.50E-03		-1.02E+00	1.68E-09	Down	-3.30E+00	7.82E-35	Down	-1.86E+00	5.28E-19	Down	Unigene13732_A11//gi|15239475|ref|NP_198516.1|//1.00E-152//exostosin family protein [Arabidopsis thaliana]	Unigene13732_A11//6.00E-145//AT5G37000| exostosin family protein					nr +
Unigene13733_A11	1404	8.79	28.44	9.06	11.03	26.95	7.33	22.92	18.37	37.57	1.69E+00	7.64E-65	Up	4.36E-02	8.04E-01		1.29E+00	1.93E-48	Up	-5.89E-01	1.92E-05		-3.19E-01	1.83E-04		7.13E-01	2.23E-27		Unigene13733_A11//gi|224074873|ref|XP_002304470.1|//1.00E-124//f-box family protein [Populus trichocarpa] >gi|222841902|gb|EEE79449.1| f-box family protein [Populus trichocarpa]	Unigene13733_A11//2.00E-109//AT1G12710| AtPP2-A12 (Phloem protein 2-A12); carbohydrate binding	Unigene13733_A11//0.00E+00//DW518165				nr +
Unigene13734_A11	1226	96.32	23.81	31.45	104.71	91.68	127.86	174.19	58.57	79.81	-2.02E+00	1.37E-243	Down	-1.61E+00	1.22E-173	Down	-1.92E-01	6.40E-06		2.88E-01	2.00E-13		-1.57E+00	0.00E+00	Down	-1.13E+00	3.01E-234	Down	Unigene13734_A11//gi|55976189|sp|Q6UNT2.1|RL5_CUCSA//1.00E-144//RecName: Full=60S ribosomal protein L5 >gi|34484312|gb|AAQ72789.1| 60S ribosomal protein L5 [Cucumis sativus]	Unigene13734_A11//3.00E-132//AT3G25520| ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); 5S rRNA binding / structural constituent of ribosome	Unigene13734_A11//0.00E+00//TC163796		ko03010|Ribosome		nr +
Unigene13737_A11	1141	1.47	1.69	3.22	1.96	2.41	1.27	5.26	4.29	2.55	2.02E-01	6.50E-01		1.13E+00	8.24E-04	Up	2.97E-01	4.95E-01		-6.33E-01	1.48E-01		-2.96E-01	2.02E-01		-1.05E+00	1.06E-06	Down	Unigene13737_A11//gi|9759135|dbj|BAB08620.1|//4.00E-65//amylogenin: reversibly glycosylatable polypeptide [Arabidopsis thaliana] >gi|21594813|gb|AAM66046.1| amylogenin [Arabidopsis thaliana]	Unigene13737_A11//2.00E-66//AT5G16510| reversibly glycosylated polypeptide, putative	Unigene13737_A11//0.00E+00//gi|11200657|gb|BF269662.1|BF269662				nr -
Unigene13739_A11	1361	7.65	4.02	5.52	23.86	22.75	36.54	69.71	766.82	184.65	-9.28E-01	2.40E-07		-4.72E-01	1.11E-02		-6.92E-02	5.56E-01		6.15E-01	4.58E-17		3.46E+00	0.00E+00	Up	1.41E+00	0.00E+00	Up	Unigene13739_A11//gi|115456551|ref|NP_001051876.1|//1.00E-126//0s03g0845000 [Oryza sativa Japonica Group] >gi|113550347|dbj|BAF13790.1| Os03g0845000 [Oryza sativa Japonica Group]	Unigene13739_A11//1.00E-123//AT2G43120| pirin, putative	Unigene13739_A11//0.00E+00//TC143102				nr +
Unigene13740_A11	1714	5.46	4.46	3.48	7.12	8.94	6.22	10.58	28.02	20.87	-2.92E-01	1.36E-01		-6.51E-01	8.34E-04		3.28E-01	2.09E-02		-1.95E-01	2.90E-01		1.40E+00	8.93E-73	Up	9.80E-01	8.91E-32		Unigene13740_A11//gi|79313852|ref|NP_001030781.1|//1.00E-154//hydrolase [Arabidopsis thaliana]	Unigene13740_A11//2.00E-151//AT3G27320| hydrolase	Unigene13740_A11//0.00E+00//gi|164290907|gb|ES802601.1|ES802601				nr -
Unigene13741_A11	775	61.64	58.12	78.81	38.82	45.54	27.56	4.64	3.18	1.39	-8.47E-02	3.44E-01		3.55E-01	2.72E-07		2.30E-01	1.06E-02		-4.94E-01	2.17E-07		-5.43E-01	6.42E-02		-1.74E+00	1.92E-08	Down	Unigene13741_A11//gi|53370641|gb|AU89136.1|//9.00E-10//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene13741_A11//1.00E-06//AT2G02650| reverse transcriptase-related	Unigene13741_A11//0.00E+00//EX171425				nr +
Unigene13743_A11	1140	5.28	9.07	9.72	9.53	6.28	2.22	27.15	10.08	12.37	7.81E-01	1.24E-05		8.80E-01	7.97E-07		-6.00E-01	1.78E-04		-2.10E+00	4.01E-26	Down	-1.43E+00	1.76E-48	Down	-1.13E+00	4.67E-35	Down	Unigene13743_A11//gi|224055785|ref|XP_002298652.1|//2.00E-61//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222845910|gb|EEE83457.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene13743_A11//2.00E-42//AT5G13180| ANAC083 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 83); transcription factor	Unigene13743_A11//0.00E+00//DW505736	NAC			nr +
Unigene13744_A11	1429	75.53	55.67	71.62	54.00	48.46	48.10	47.46	17.29	16.23	-4.40E-01	6.73E-19		-7.67E-02	1.95E-01		-1.56E-01	8.63E-03		-1.67E-01	6.50E-03		-1.46E+00	1.90E-108	Down	-1.55E+00	4.53E-122	Down	Unigene13744_A11//gi|255547878|ref|XP_002514996.1|//1.00E-142//Ketoacyl-ACP Reductase (KAR) [Ricinus communis] >gi|223546047|gb|EEF47550.1| Ketoacyl-ACP Reductase (KAR) [Ricinus communis]	Unigene13744_A11//4.00E-102//AT1G24360| 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase	Unigene13744_A11//0.00E+00//TC146867		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis		nr +
Unigene13745_A11	1900	8.45	7.41	7.40	25.22	13.63	12.46	7.08	8.27	8.16	-1.89E-01	2.11E-01		-1.92E-01	2.28E-01		-8.88E-01	4.05E-35		-1.02E+00	7.04E-39	Down	2.25E-01	9.45E-02		2.05E-01	1.18E-01		Unigene13745_A11//gi|102139855|gb|ABF70013.1|//8.00E-66//myb DNA-binding domain-containing protein [Musa acuminata]	Unigene13745_A11//4.00E-42//AT2G03500| myb family transcription factor	Unigene13745_A11//0.00E+00//gi|78342907|gb|DT563181.1|DT563181	G2-like			nr +
Unigene13746_A11	1177	31.52	39.05	43.52	6.69	13.78	11.01	3.05	2.34	2.98	3.09E-01	8.58E-05		4.66E-01	7.19E-10		1.04E+00	4.35E-15	Up	7.20E-01	2.69E-06		-3.82E-01	2.13E-01		-3.58E-02	9.20E-01		Unigene13746_A11//gi|224065699|ref|XP_002301927.1|//0.00E+00//precursor of protein cell division protease ftsh-like protein [Populus trichocarpa] >gi|222843653|gb|EEE81200.1| precursor of protein cell division protease ftsh-like protein [Populus trichocarpa]	Unigene13746_A11//3.00E-168//AT5G42270| VAR1 (VARIEGATED 1); ATP-dependent peptidase/ ATPase/ metallopeptidase	Unigene13746_A11//0.00E+00//ES800611				nr -
Unigene13747_A11	1365	29.97	54.86	32.30	71.09	94.00	78.12	80.38	193.15	273.53	8.72E-01	3.69E-43		1.08E-01	2.46E-01		4.03E-01	2.14E-22		1.36E-01	9.40E-03		1.26E+00	0.00E+00	Up	1.77E+00	0.00E+00	Up	Unigene13747_A11//gi|16648773|gb|AAL25577.1|//2.00E-55//At1g68440/T2E12_1 [Arabidopsis thaliana] >gi|21700823|gb|AAM70535.1| At1g68440/T2E12_1 [Arabidopsis thaliana]	Unigene13747_A11//1.00E-45//AT1G68440| unknown protein	Unigene13747_A11//0.00E+00//TC134197				nr -
Unigene13748_A11	1438	55.05	31.89	43.21	94.71	80.20	59.17	59.39	19.91	17.92	-7.88E-01	1.61E-38		-3.49E-01	5.43E-09		-2.40E-01	2.51E-09		-6.79E-01	6.16E-55		-1.58E+00	3.15E-153	Down	-1.73E+00	8.52E-180	Down	Unigene13748_A11//gi|115480295|ref|NP_001063741.1|//1.00E-106//0s09g0529100 [Oryza sativa Japonica Group] >gi|113631974|dbj|BAF25655.1| Os09g0529100 [Oryza sativa Japonica Group]	Unigene13748_A11//7.00E-105//AT5G24400| emb2024 (embryo defective 2024); 6-phosphoglutconolactonase/ catalytic	Unigene13748_A11//0.00E+00//TC137918		ko00030|Pentose phosphate pathway		nr -
Unigene13749_A11	1204	44.67	29.12	41.80	10.47	8.87	9.53	4.46	1.74	1.52	-6.17E-01	1.79E-17		-9.61E-02	2.56E-01		-2.40E-01	1.56E-01		-1.36E-01	4.66E-01		-1.36E+00	1.78E-08	Down	-1.55E+00	1.78E-10	Down	Unigene13749_A11//gi|297823235|ref|XP_002879500.1|//7.00E-88//At2g34460/T31E10.20 [Arabidopsis lyrata subsp. lyrata] >gi|297325339|gb|EFH55759.1| At2g34460/T31E10.20 [Arabidopsis lyrata subsp. lyrata]	Unigene13749_A11//3.00E-81//AT2G34460| flavin reductase-related	Unigene13749_A11//0.00E+00//ES851602				nr -
Unigene13751_A11	604	1.73	2.18	1.59	6.43	2.51	3.96	4.34	4.22	3.36	3.32E-01	5.83E-01		-1.27E-01	8.44E-01		-1.36E+00	4.01E-06	Down	-6.99E-01	2.39E-02		-4.01E-02	9.29E-01		-3.68E-01	2.94E-01		Unigene13751_A11//gi|8886954|gb|AAF80640.1|AC069251_33//3.00E-54//F2D10.6 [Arabidopsis thaliana] >gi|29028862|gb|AA064810.1| At1g20575 [Arabidopsis thaliana]	Unigene13751_A11//6.00E-55//AT1G20575| dolichyl-phosphate beta-D-mannosyltransferase, putative / dolichol-phosphate mannosyltransferase, putative / mannose-P-dolichol synthase, putative	Unigene13751_A11//6.00E-174//gi|109870497|gb|DW499473.1|DW499473		ko00510|N-Glycan biosynthesis		nr -
Unigene13753_A11	1613	35.78	37.00	39.19	23.01	12.79	9.80	16.67	27.47	13.14	4.86E-02	5.59E-01		1.31E-01	8.02E-02		-8.47E-01	3.42E-25		-1.23E+00	6.21E-41	Down	7.20E-01	5.91E-23		-3.43E-01	1.76E-04		Unigene13753_A11//gi|21553600|gb|AAM62693.1|//1.00E-154//lysophospholipase-like protein [Arabidopsis thaliana]	Unigene13753_A11//1.00E-144//AT5G11650| hydrolase, alpha/beta fold family protein	Unigene13753_A11//0.00E+00//TC133099		ko00561|Glycerolipid metabolism		nr -
Unigene13758_A11	1833	21.75	5.45	9.12	36.53	24.25	32.01	21.98	6.09	10.76	-2.00E+00	1.43E-81	Down	-1.25E+00	2.89E-40	Down	-5.91E-01	4.97E-24		-1.91E-01	3.54E-03		-1.85E+00	5.19E-91	Down	-1.03E+00	5.58E-39	Down	Unigene13758_A11//gi|15239488|ref|NP_200904.1|//1.00E-172//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75262710|sp|Q9FM24.1|PP438_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g60960, mitochondrial; Flags: Precursor	Unigene13758_A11//2.00E-169//AT5G60960| pentatricopeptide (PPR) repeat-containing protein	Unigene13758_A11//0.00E+00//TC145256				nr +
Unigene13759_A11	1196	43.44	47.79	46.84	44.69	44.45	40.29	60.42	32.85	28.31	1.38E-01	6.72E-02		1.09E-01	1.86E-01		-7.60E-03	9.41E-01		-1.50E-01	5.56E-02		-8.79E-01	9.44E-52		-1.09E+00	4.23E-76	Down	Unigene13759_A11//gi|211906482|gb|ACJ11734.1|//1.00E-166//S-formylglutathione hydrolase [Gossypium hirsutum]	Unigene13759_A11//6.00E-140//AT2G41530| SFGH (S-FORMYLGLUTATHIONE HYDROLASE); S-formylglutathione hydrolase/ hydrolase, acting on ester bonds	Unigene13759_A11//0.00E+00//TC130037				nr +
Unigene13762_A11	1216	11.01	35.29	22.51	19.21	21.38	32.02	48.02	51.97	44.10	1.68E+00	6.77E-69	Up	1.03E+00	1.68E-20	Up	1.54E-01	1.94E-01		7.37E-01	2.39E-18		1.14E-01	8.05E-02		-1.23E-01	5.79E-02		Unigene13762_A11//gi|62321517|dbj|BAD94991.1|//6.00E-32//cytoplasmic aconitate hydratase [Arabidopsis thaliana]	Unigene13762_A11//3.00E-33//AT2G05710| aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative	Unigene13762_A11//1.00E-176//ES822744		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene13763_A11	1914	10.69	6.72	7.34	17.83	14.64	15.93	12.61	7.66	5.99	-6.69E-01	4.12E-08		-5.41E-01	1.60E-05		-2.84E-01	1.25E-03		-1.63E-01	1.09E-01		-7.19E-01	7.51E-13		-1.07E+00	2.84E-25	Down	Unigene13763_A11//gi|18401824|ref|NP_566605.1|//1.00E-113//CYP77A5P; catalytic [Arabidopsis thaliana]	Unigene13763_A11//1.00E-151//AT3G18270| CYP77A5P; catalytic	Unigene13763_A11//0.00E+00//TC138075				nr +
Unigene13764_A11	1692	9.83	6.38	6.42	22.58	21.31	10.76	8.07	1.80	1.44	-6.24E-01	4.45E-06		-6.15E-01	1.25E-05		-8.37E-02	4.24E-01		-1.07E+00	1.04E-33	Down	-2.16E+00	3.22E-38	Down	-2.49E+00	1.12E-46	Down	Unigene13764_A11//gi|256561133|gb|ACU86966.1|//1.00E-114//expansin B1 [Raphanus sativus] >gi|256561135|gb|ACU86967.1| expansin B1 [Raphanus sativus]	Unigene13764_A11//2.00E-102//AT4G28250| ATEXPB3 (ARABIDOPSIS THALIANA EXPANSIN B3)	Unigene13764_A11//0.00E+00//TC164155				nr -
Unigene13767_A11	1171	5.00	1.99	4.41	6.81	4.53	4.82	4.55	4.85	5.34	-1.33E+00	2.28E-07	Down	-1.82E-01	5.08E-01		-5.88E-01	2.31E-03		-4.98E-01	1.58E-02		9.36E-02	7.12E-01		2.32E-01	2.98E-01		Unigene13767_A11//gi|297723421|ref|NP_001174074.1|//2.00E-28//0s04g0590366 [Oryza sativa Japonica Group] >gi|255675737|dbj|BAH92802.1| Os04g0590366 [Oryza sativa Japonica Group]	Unigene13767_A11//4.00E-12//AT5G27260| unknown protein	Unigene13767_A11//0.00E+00//TC162222				nr -

Unigene13769_All	1090	21.36	11.48	17.98	22.12	23.44	14.34	21.76	12.46	8.19	-8.96E-01	1.36E-14		-2.49E-01	4.43E-02		8.37E-02	5.52E-01		-6.26E-01	6.39E-09		-8.04E-01	3.50E-15		-1.41E+00	1.00E-37	Down	Unigene13769_All//gi|30686594|ref|NP_564098.2|//4.00E-85//AVA-P2; ATPase/ proton-transporting ATPase, rotational mechanism [Arabidopsis thaliana] >gi|27923953|sp|P59228.1|VATL2_ARATH RecName: Full=V-type proton ATPase 16 kDa proteolipid subunit c2; Short=V-ATPase 16 kDa proteolipid subunit c2; AltName: Full=Vacuolar proton pump 16 kDa proteolipid subunit c2; AltName: Full=Vacuolar H(+)-ATPase subunit c isoform 2 >gi|10086482|gb|AAG12542.1|AC00779 7_2 vacuolar H+-pumping ATPase [Arabidopsis thaliana] >gi|926937|gb|AAS99937.1| vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana] >gi|89274155|gb|ABD65598.1| At1g19910 [Arabidopsis thaliana]	Unigene13769_All//2.00E-58//AT1G19910| AVA-P2; ATPase/ proton-transporting ATPase, rotational mechanism	Unigene13769_All//0.00E+00//TC152540		ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene1377_All	898	0.76	0.45	0.00	1.05	1.42	0.75	3.81	1.07	3.28	-7.47E-01	3.80E-01		-9.56E+00	7.65E-04	Down	4.29E-01	5.32E-01		-4.83E-01	5.19E-01		-1.83E+00	2.62E-08	Down	-2.16E-01	4.89E-01		Unigene1377_All//gi|186510760|ref|NP_190372.3|//9.00E-78//ubiquitin thiolesterase/ zinc ion binding [Arabidopsis thaliana]	Unigene1377_All//2.00E-78//AT3G47890| ubiquitin thiolesterase/ zinc ion binding					nr +
Unigene13776_All	2777	1.00	0.49	1.27	1.69	0.82	0.63	2.80	5.98	3.54	-1.02E+00	7.32E-03		3.42E-01	3.45E-01		-1.04E+00	5.92E-05	Down	-1.41E+00	7.19E-07	Down	1.09E+00	1.42E-17	Up	3.39E-01	3.66E-02		Unigene13776_All//gi|124359162|gb|ABN05685.1|//3.00E-66//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene13776_All//2.00E-41//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene13776_All//0.00E+00//DW508167				nr +
Unigene13777_All	1462	6.01	2.98	7.32	41.26	40.56	22.46	12.64	3.34	10.33	-1.01E+00	3.47E-07	Down	2.84E-01	1.41E-01		-2.48E-02	8.10E-01		-8.78E-01	3.54E-38		-1.92E+00	4.08E-44	Down	-2.91E-01	1.07E-02		Unigene13777_All//gi|115452547|ref|NP_001049874.1|//1.00E-50//Os03g0303100 [Oryza sativa Japonica Group] >gi|108707708|gb|ABF95503.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548345|dbj|BAF11788.1| Os03g0303100 [Oryza sativa Japonica Group]	Unigene13777_All//2.00E-35//AT3G62630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1645 (InterPro:IPR012442); BEST Arabidopsis thaliana protein match is: calmodulin-binding protein (TAIR:AT2G15760.1); Has 207 Blast hits to 197 proteins in 50 species: Archae - 3; Bacteria - 4; Metazoa - 52; Fungi - 9; Plants - 91; Viruses - 0; Other Eukaryotes - 48 (source: NCBI BLink).	Unigene13777_All//0.00E+00//TC143734				nr -
Unigene13778_All	1386	26.05	23.98	24.36	38.49	37.69	46.47	74.37	42.85	33.60	-1.19E-01	2.32E-01		-9.67E-02	3.77E-01		-3.04E-02	7.72E-01		2.72E-01	2.36E-05		-7.95E-01	4.61E-62		-1.15E+00	1.03E-116	Down	Unigene13778_All//gi|21264030|sp|Q82662.1|SUCB_ARATH//0.00E+00//RecName: Full=Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial; AltName: Full=Succinyl-CoA synthetase beta chain; Short=SCS-beta; Flags: Precursor >gi|3660469|emb|CAA05024.1| succinyl-CoA-ligase beta subunit [Arabidopsis thaliana] >gi|20197853|gb|AAM15283.1| succinyl-CoA ligase beta subunit [Arabidopsis thaliana] >gi|20166482|gb|AAM20558.1| succinyl-CoA ligase beta subunit [Arabidopsis thaliana] >gi|22136422|gb|AAM91289.1| succinyl-CoA ligase beta subunit [Arabidopsis thaliana]	Unigene13778_All//0.00E+00//AT2G20420| succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative	Unigene13778_All//0.00E+00//TC131525		ko00020|Citrate cycle (TCA cycle)//ko00640|Propanoate metabolism		nr +
Unigene13779_All	2323	1.26	2.62	1.47	8.51	10.05	11.14	11.50	12.00	11.47	1.05E+00	1.70E-05	Up	2.18E-01	5.58E-01		2.40E-01	3.88E-02		3.88E-01	2.31E-04		6.11E-02	6.13E-01		-3.70E-03	9.66E-01		Unigene13779_All//gi|22328976|ref|NP_194480.2|//1.00E-144//PP11 (PROTON PUMP INTERACTOR 1); protein binding [Arabidopsis thaliana] >gi|13992437|emb|CAA05145.2| proton pump interactor [Arabidopsis thaliana] >gi|15215674|gb|AAK91382.1| AT4g27500/F27G19_100 [Arabidopsis thaliana] >gi|23505987|gb|AAN28853.1| At4g27500/F27G19_100 [Arabidopsis thaliana]	Unigene13779_All//6.00E-112//AT4G27500| PP11 (PROTON PUMP INTERACTOR 1); protein binding	Unigene13779_All//0.00E+00//ES824016				nr +
Unigene13784_All	886	3.96	1.83	1.98	6.41	6.34	6.42	5.06	4.29	3.51	-1.11E+00	8.77E-04	Down	-9.96E-01	4.03E-03		-1.68E-02	9.58E-01		3.00E-03	9.92E-01		-2.37E-01	4.01E-01		-5.28E-01	3.25E-02		Unigene13784_All//gi|28950775|gb|AA063311.1|//4.00E-07//At3g02220 [Arabidopsis thaliana]		Unigene13784_All//2.00E-94//DT466150				nr -
Unigene13785_All	1169	7.21	4.55	4.24	8.86	8.78	12.36	10.38	6.15	5.18	-6.63E-01	8.55E-04		-7.66E-01	2.17E-04		-1.39E-02	9.53E-01		4.80E-01	9.85E-04		-7.55E-01	2.06E-07		-1.00E+00	7.42E-12	Down	Unigene13785_All//gi|28950775|gb|AA063311.1|//4.00E-71//At3g02220 [Arabidopsis thaliana]	Unigene13785_All//8.00E-64//AT3G02220| unknown protein	Unigene13785_All//0.00E+00//gi|78344515|gb|DT564789.1|DT564789				nr -
Unigene13786_All	1992	33.54	10.51	19.59	27.28	23.23	16.19	8.47	5.43	3.34	-1.67E+00	4.29E-107	Down	-7.76E-01	1.28E-30		-2.32E-01	7.23E-04		-7.53E-01	1.36E-26		-6.40E-01	1.13E-07		-1.34E+00	3.50E-25	Down	Unigene13786_All//gi|149789412|gb|ABR29877.1|//0.00E+00//phosphoenol pyruvate carboxylase [Ricinus communis]	Unigene13786_All//0.00E+00//AT1G68750| ATPPC4; phosphoenolpyruvate carboxylase	Unigene13786_All//0.00E+00//TC177195		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene13787_All	430	1.83	4.48	7.06	7.41	4.97	7.35	1.97	1.65	1.39	1.29E+00	7.23E-03		1.95E+00	2.48E-06	Up	-5.79E-01	8.72E-02		-1.21E-02	9.66E-01		-2.51E-01	7.13E-01		-5.01E-01	4.47E-01				Unigene13787_All//4.00E-91//TC138464				
Unigene13790_All	2386	32.04	21.47	20.98	68.85	62.45	63.90	37.34	23.11	17.70	-5.77E-01	7.89E-22		-6.11E-01	3.77E-23		-1.41E-01	2.40E-04		-1.08E-01	1.04E-02		-6.92E-01	2.22E-42		-1.08E+00	2.31E-91	Down	Unigene13790_All//gi|15236611|ref|NP_192621.1|//0.00E+00//SUB1; calcium ion binding [Arabidopsis thaliana] >gi|15912229|gb|AAL08248.1| AT4g08810/T32A17_120 [Arabidopsis thaliana] >gi|27363304|gb|AAO11571.1| At4g08810/T32A17_120 [Arabidopsis thaliana]	Unigene13790_All//0.00E+00//AT4G08810| SUB1; calcium ion binding	Unigene13790_All//0.00E+00//TC167027				nr +
Unigene13793_All	3156	9.35	4.42	5.85	9.88	8.58	6.27	17.28	13.95	9.34	-1.08E+00	9.36E-25	Down	-6.75E-01	5.13E-11		-2.04E-01	3.83E-02		-6.57E-01	2.59E-12		-3.10E-01	1.23E-06		-8.88E-01	4.84E-41		Unigene13793_All//gi|297791069|ref|XP_002863419.1|//0.00E+00//KH domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297309254|gb|EFH39678.1| KH domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13793_All//3.00E-164//AT5G46190| KH domain-containing protein	Unigene13793_All//0.00E+00//gi|164340427|gb|ES827526.1|ES827526				nr -
Unigene13795_All	1868	1.71	0.41	1.23	0.91	0.77	0.24	0.93	1.23	2.82	-2.07E+00	1.81E-07	Down	-4.79E-01	1.98E-01		-2.28E-01	6.59E-01		-1.91E+00	4.25E-04	Down	4.07E-01	3.09E-01		1.60E+00	1.32E-10	Up	Unigene13795_All//gi|18403860|ref|NP_565805.1|//1.00E-22//shikimate kinase-related [Arabidopsis thaliana] >gi|15724242|gb|AAL06514.1|AF412061_1 At2g35500/T32F12.12 [Arabidopsis thaliana] >gi|18377827|gb|AAL67100.1| At2g35500/T32F12.12 [Arabidopsis thaliana] >gi|20197350|gb|AAC36171.2| expressed protein [Arabidopsis thaliana]	Unigene13795_All//4.00E-24//AT2G35500| shikimate kinase-related	Unigene13795_All//2.00E-117//gi|21099519|gb|BQ411832.1|BQ411832				nr +
Unigene13796_All	1440	17.91	13.86	20.75	9.06	8.49	6.21	2.41	0.61	0.55	-3.70E-01	5.89E-04		2.12E-01	5.04E-02		-9.44E-02	5.96E-01		-5.46E-01	3.53E-04		-1.98E+00	3.06E-09	Down	-2.12E+00	2.21E-10	Down	Unigene13796_All//gi|224071393|ref|XP_002303438.1|//1.00E-147//shikimate kinase-like protein [Populus trichocarpa] >gi|222840870|gb|EEE78417.1| shikimate kinase-like protein [Populus trichocarpa]	Unigene13796_All//4.00E-139//AT2G35500| shikimate kinase-related	Unigene13796_All//0.00E+00//TC136998		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr +
Unigene13797_All	2342	3.42	2.47	2.11	8.00	9.44	7.19	7.15	3.53	6.53	-4.71E-01	2.27E-02		-6.93E-01	1.16E-03		2.39E-01	4.52E-02		-1.53E-01	3.07E-01		-1.02E+00	7.27E-16	Down	-1.30E-01	3.35E-01		Unigene13797_All//gi|115488294|ref|NP_001066634.1|//0.00E+00//Os12g0407500 [Oryza sativa Japonica Group] >gi|113649141|dbj|BAF29653.1| Os12g0407500 [Oryza sativa Japonica Group]	Unigene13797_All//0.00E+00//AT3G19420| ATPEN2 (ARABIDOPSIS THALIANA PTEN 2); phosphatase/ protein tyrosine phosphatase	Unigene13797_All//0.00E+00//TC141243		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene13798_All	209	0.00	3.64	1.78	2.62	1.65	1.08	1.21	1.40	0.95	1.18E+01	1.77E-04	Up	1.08E+01	2.50E-02		-6.70E-01	4.97E-01		-1.28E+00	2.24E-01		2.06E-01	8.68E-01		-3.49E-01	7.66E-01				Unigene13798_All//2.00E-07//TC152669				
Unigene13799_All	1416	3.33	13.88	3.23	6.68	7.54	9.66	7.41	13.46	9.85	2.06E+00	6.68E-42	Up	-4.02E-02	8.98E-01		1.74E-01	3.93E-01		5.32E-01	3.74E-04		8.62E-01	8.43E-14		4.11E-01	1.74E-03		Unigene13799_All//gi|297852370|ref|XP_002894066.1|//7.00E-50//organellar single-stranded [Arabidopsis lyrata subsp. lyrata] >gi|297339908|gb|EFH70325.1| organellar single-stranded [Arabidopsis lyrata subsp. lyrata]	Unigene13799_All//1.00E-48//AT1G47720| OSB1 (Organellar Single-stranded); single-stranded DNA binding	Unigene13799_All//0.00E+00//gi|18100009|gb|BM359263.1|BM359263				nr +
Unigene1380_All	666	0.31	0.76	0.24	13.84	9.77	6.04	3.75	6.34	1.44	1.28E+00	2.31E-01		-3.89E-01	8.08E-01		-5.02E-01	5.21E-03		-1.20E+00	3.76E-10	Down	7.59E-01	3.95E-03		-1.38E+00	1.26E-04	Down			Unigene1380_All//9.00E-19//CO132539				ESTscan -

Unigene13801_A11	2022	10.53	8.37	12.04	8.67	6.88	4.96	12.59	5.68	3.90	-3.31E-01	6.02E-03		1.93E-01	1.22E-01		-3.34E-01	9.35E-03		-8.06E-01	4.86E-10		-1.15E+00	1.20E-28	Down	-1.69E+00	1.79E-52	Down	Unigene13801_A11//gi|115489142|ref|NP_001067058.1|//1.00E-128//Os12g0566900 [Oryza sativa Japonica Group] >gi|113649565|dbj|BAF30077.1|Os12g0566900 [Oryza sativa Japonica Group]	Unigene13801_A11//1.00E-78//AT3G09470| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF895, eukaryotic (InterPro:IPR010291), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); Has 638 Blast hits to 624 proteins in 112 species: Archae - 2; Bacteria - 10; Metazoa - 433; Fungi - 116; Plants - 40; Viruses - 0; Other Eukaryotes - 37 (source: NCBI BLink).	Unigene13801_A11//0.00E+00//TC151960				nr -
Unigene13802_A11	2414	3.53	0.94	1.15	7.80	4.24	7.02	8.37	2.79	5.07	-1.90E+00	6.98E-17	Down	-1.62E+00	4.72E-13	Down	-8.81E-01	7.54E-14		-1.53E-01	3.05E-01		-1.59E+00	3.86E-37	Down	-7.25E-01	2.16E-11		Unigene13802_A11//gi|297832492|ref|XP_002884128.1|//0.00E+00//AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329968|gb|EFH60387.1| AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13802_A11//0.00E+00//AT2G18330| AAA-type ATPase family protein	Unigene13802_A11//0.00E+00//TC167255		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene13803_A11	1288	17.87	108.93	62.26	11.56	62.13	73.43	17.40	48.06	47.45	2.61E+00	0.00E+00	Up	1.80E+00	5.60E-138	Up	2.43E+00	1.26E-241	Up	2.67E+00	1.44E-291	Up	1.47E+00	9.55E-100	Up	1.45E+00	1.07E-98	Up	Unigene13803_A11//gi|32364482|gb|AA061674.1|//1.00E-121//AKIN gamma [Medicago truncatula]	Unigene13803_A11//2.00E-95//AT3G48530| KING1 (SNF1-RELATED PROTEIN KINASE REGULATORY SUBUNIT GAMMA 1)	Unigene13803_A11//0.00E+00//TC139147				nr +
Unigene13804_A11	1484	22.46	15.91	13.10	24.77	20.79	16.10	12.54	2.87	3.30	-4.97E-01	8.53E-08		-7.78E-01	1.21E-15		-2.53E-01	3.14E-03		-6.22E-01	3.95E-13		-2.13E+00	1.05E-50	Down	-1.92E+00	5.14E-46	Down	Unigene13804_A11//gi|115440019|ref|NP_001044289.1|//1.00E-136//Os01g0756600 [Oryza sativa Japonica Group] >gi|113533820|dbj|BAF06203.1|Os01g0756600 [Oryza sativa Japonica Group]	Unigene13804_A11//1.00E-150//AT1G29980| INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, anchored to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34510.1); Has 174 Blast hits to 163 proteins in 15 species: Archae - 0; Bacteria - 10; Metazoa - 0; Fungi - 0; Plants - 164; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene13804_A11//0.00E+00//TC135941				nr -
Unigene1381_A11	1947	5.21	2.37	3.61	15.35	9.14	8.47	30.66	29.90	16.02	-1.14E+00	1.02E-09	Down	-5.30E-01	4.62E-03		-7.48E-01	1.89E-16		-8.59E-01	1.66E-18		-3.62E-02	6.19E-01		-9.37E-01	5.38E-49		Unigene1381_A11//gi|37780214|gb|AAP55487.1|//9.00E-22//resistance protein RGC2 [Lactuca sativa]	Unigene1381_A11//4.00E-07//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene1381_A11//0.00E+00//ES810366		ko04626|Plant-pathogen interaction		nr -
Unigene13811_A11	1157	111.97	148.55	152.89	30.96	39.67	34.31	6.03	5.13	2.10	4.08E-01	8.96E-26		4.49E-01	1.54E-30		3.58E-01	9.04E-07		1.49E-01	1.17E-01		-2.33E-01	2.86E-01		-1.52E+00	5.23E-13	Down	Unigene13811_A11//gi|53062688|gb|AAD42000.1|//1.00E-58//expressed protein [Arabidopsis thaliana] >gi|88193802|gb|ABD42990.1|At2g27290 [Arabidopsis thaliana]	Unigene13811_A11//2.00E-43//AT2G27290| unknown protein	Unigene13811_A11//0.00E+00//TC163850				nr +
Unigene13817_A11	1408	6.61	13.89	6.43	7.01	7.48	10.94	7.33	10.57	19.41	1.07E+00	2.60E-16	Up	-4.09E-02	8.45E-01		9.54E-02	6.53E-01		6.43E-01	3.73E-06		5.28E-01	4.21E-05		1.41E+00	1.04E-42	Up	Unigene13817_A11//gi|94442479|gb|ABF19027.1|//2.00E-24//At4g17440 [Arabidopsis thaliana]	Unigene13817_A11//1.00E-14//AT4G17440| unknown protein	Unigene13817_A11//0.00E+00//TC163556				nr -
Unigene13818_A11	1317	21.69	21.35	10.67	50.91	56.37	40.19	19.45	23.36	28.95	-2.27E-02	8.42E-01		-1.02E+00	4.62E-21	Down	1.47E-01	1.79E-02		-3.41E-01	3.43E-08		2.64E-01	3.01E-03		5.73E-01	6.71E-14		Unigene13818_A11//gi|37572449|dbj|BAC98494.1|//7.00E-63//AG-motif binding protein-4 [Nicotiana tabacum]	Unigene13818_A11//1.00E-38//AT5G66320| zinc finger (GATA type) family protein	Unigene13818_A11//0.00E+00//TC145165	C2C2-GATA			nr -
Unigene13821_A11	1331	13.09	162.90	6.28	38.92	34.75	34.54	29.07	30.37	74.50	3.64E+00	0.00E+00	Up	-1.06E+00	8.23E-14	Down	-1.64E-01	2.96E-02		-1.72E-01	2.63E-02		6.31E-02	5.05E-01		1.36E+00	4.82E-145	Up	Unigene13821_A11//gi|68131790|gb|AAY85179.1|//1.00E-135//Fiber expressed protein [Gossypium hirsutum]	Unigene13821_A11//1.00E-74//AT1G61260| unknown protein	Unigene13821_A11//0.00E+00//gi|78351963|gb|DT572237.1|DT572237				nr +
Unigene13822_A11	1605	4.14	4.04	3.95	3.35	2.36	1.60	1.26	0.57	1.49	-3.50E-02	8.90E-01		-6.85E-02	7.76E-01		-5.06E-01	4.22E-02		-1.06E+00	3.03E-05	Down	-1.14E+00	5.27E-03		2.36E-01	5.49E-01		Unigene13822_A11//gi|297821369|ref|XP_002878567.1|//1.00E-157//EMB2219 [Arabidopsis lyrata subsp. lyrata] >gi|297324406|gb|EFH54826.1|EMB2219 [Arabidopsis lyrata subsp. lyrata]	Unigene13822_A11//9.00E-156//AT2G21710| EMB2219 (embryo defective 2219)	Unigene13822_A11//0.00E+00//D8455388				nr -
Unigene13824_A11	1090	6.38	2.98	3.96	10.24	9.70	7.38	7.02	8.32	6.03	-1.10E+00	1.33E-06	Down	-6.90E-01	2.82E-03		-7.79E-02	7.12E-01		-4.73E-01	5.19E-03		2.45E-01	1.86E-01		-2.19E-01	2.64E-01		Unigene13824_A11//gi|115473321|ref|NP_001060259.1|//7.00E-19//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene13824_A11//9.00E-21//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene13824_A11//0.00E+00//TC174842				nr +
Unigene13825_A11	1098	28.64	11.81	30.55	34.80	36.76	35.91	14.09	25.73	18.65	-1.28E+00	4.61E-34	Down	9.34E-02	4.00E-01		7.90E-02	4.52E-01		4.53E-02	6.86E-01		8.69E-01	2.61E-20		4.04E-01	1.40E-04		Unigene13825_A11//gi|115473321|ref|NP_001060259.1|//1.00E-12//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene13825_A11//4.00E-11//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene13825_A11//2.00E-82//TC174842				nr +
Unigene13827_A11	2501	4.69	7.52	1.98	10.34	10.09	9.70	19.54	16.63	40.86	6.82E-01	9.90E-08		-1.24E+00	4.54E-12	Down	-3.46E-02	8.16E-01		-9.22E-02	4.79E-01		-2.33E-01	7.33E-04		1.06E+00	6.45E-102	Up	Unigene13827_A11//gi|297800554|ref|XP_002868161.1|//0.00E+00//ATSEB1 [Arabidopsis lyrata subsp. lyrata] >gi|297313997|gb|EFH44420.1|ATSEB1 [Arabidopsis lyrata subsp. lyrata]	Unigene13827_A11//0.00E+00//AT4G16120| COBL7 (COBRA-LIKE 7)	Unigene13827_A11//0.00E+00//TC152514				nr -
Unigene13828_A11	955	19.72	46.90	25.93	44.39	48.39	50.89	20.28	20.70	44.14	1.25E+00	2.05E-46	Up	3.95E-01	5.33E-04		1.25E-01	1.53E-01		1.97E-01	1.25E-02		2.99E-02	8.23E-01		1.12E+00	2.75E-46	Up			Unigene13828_A11//1.00E-145//gi|21092375|gb|BQ404688.1|BQ404688				
Unigene13830_A11	1919	17.86	18.69	19.15	19.99	29.16	19.75	30.47	9.87	16.53	6.60E-02	5.33E-01		1.01E-01	3.48E-01		5.45E-01	4.95E-17		-1.76E-02	8.80E-01		-1.63E+00	6.09E-110	Down	-8.83E-01	1.53E-43		Unigene13830_A11//gi|15228881|ref|NP_188308.1|//1.00E-175//glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	Unigene13830_A11//4.00E-170//AT3G16850| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene13830_A11//0.00E+00//TC171853		ko00500|Starch and sucrose metabolism/ko00040|Pentose and glucuronate interconversions		nr +
Unigene13831_A11	2736	17.25	10.63	10.16	57.92	45.95	27.63	0.46	1.63	0.16	-6.98E-01	5.21E-19		-7.64E-01	3.16E-21		-3.34E-01	8.10E-20		-1.07E+00	6.62E-138	Down	1.82E+00	1.73E-10	Up	-1.53E+00	4.40E-03		Unigene13831_A11//gi|15226313|ref|NP_180366.1|//2.00E-77//BLH8 (BEL1-LIKE HOMEODOMAIN 8); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75265949|sp|Q9SJJ3.1|BLH8_ARATH RecName: Full=BEL1-like homeodomain protein 8; Short=BEL1-like protein 8; AltName: Full=Protein FOUND-FOOLISH >gi|29028954|gb|AAO64856.1|At2g27990 [Arabidopsis thaliana]	Unigene13831_A11//2.00E-75//AT2G27990| BLH8 (BEL1-LIKE HOMEODOMAIN 8); DNA binding / transcription factor	Unigene13831_A11//0.00E+00//TC158655	HB			nr -
Unigene13838_A11	1170	9.53	31.01	47.38	9.75	10.15	9.84	17.96	15.29	8.96	1.70E+00	1.90E-59	Up	2.31E+00	2.63E-132	Up	5.86E-02	8.07E-01		1.37E-02	9.51E-01		-2.32E-01	3.95E-02		-1.00E+00	6.52E-20	Down	Unigene13838_A11//gi|71000457|dbj|BAE07178.1|//2.00E-19//phosphoethanolamine N-methyltransferase [Beta vulgaris]	Unigene13838_A11//7.00E-20//AT3G18000| XPL1 (XIPOTL 1); methyltransferase/ phosphoethanolamine N-methyltransferase	Unigene13838_A11//0.00E+00//DW008670		ko00564|Glycerophospholipid metabolism		nr +
Unigene1384_A11	2502	5.83	13.81	8.94	3.76	3.58	3.81	5.75	6.58	11.66	1.24E+00	1.12E-35	Up	6.16E-01	2.44E-07		-7.25E-02	7.69E-01		1.75E-02	9.52E-01		1.96E-01	1.42E-01		1.02E+00	8.27E-28	Up	Unigene1384_A11//gi|8778748|gb|AAF79756.1|AC009317_15 T30E16.22 [Arabidopsis thaliana] >gi|6520233|dbj|BAA87958.1| CW14 [Arabidopsis thaliana]	Unigene1384_A11//6.00E-162//AT1G59650| CW14	Unigene1384_A11//0.00E+00//ES819929				nr -
Unigene13840_A11	1725	7.13	78.10	49.64	6.32	56.11	96.77	5.15	27.28	22.82	3.45E+00	0.00E+00	Up	2.80E+00	3.68E-254	Up	3.15E+00	0.00E+00	Up	3.94E+00	0.00E+00	Up	2.41E+00	9.04E-148	Up	2.15E+00	8.51E-110	Up	Unigene13840_A11//gi|46931316|gb|AAT06462.1|//7.00E-42//At3g27250 [Arabidopsis thaliana]	Unigene13840_A11//7.00E-38//AT3G27250| unknown protein	Unigene13840_A11//0.00E+00//TC163008				nr +
Unigene13841_A11	1613	6.10	4.68	7.03	6.89	8.50	8.20	6.21	13.71	16.30	-3.82E-01	4.01E-02		2.06E-01	2.80E-01		3.03E-01	4.98E-02		2.53E-01	1.31E-01		1.14E+00	8.89E-25	Up	1.39E+00	1.57E-40	Up	Unigene13841_A11//gi|145358598|ref|NP_198601.2|//1.00E-137//SOS4 (SALT OVERLY SENSITIVE 4); kinase/ pyridoxal kinase [Arabidopsis thaliana] >gi|15277979|gb|AAK94021.1|AF400125_2 pyridoxal kinase-like protein SOS4 [Arabidopsis thaliana]	Unigene13841_A11//2.00E-138//AT5G37850| SOS4 (SALT OVERLY SENSITIVE 4); kinase/ pyridoxal kinase	Unigene13841_A11//0.00E+00//TC152567		ko00750|Vitamin B6 metabolism		nr +
Unigene13844_A11	2405	3.50	3.60	1.77	6.79	9.01	5.88	11.11	2.68	3.38	4.07E-02	8.46E-01		-9.84E-01	2.71E-06		4.07E-01	2.74E-04		-2.09E-01	1.70E-01		-2.05E+00	2.04E-69	Down	-1.72E+00	2.79E-56	Down	Unigene13844_A11//gi|42540755|gb|AAS19278.1|//0.00E+00//mitogen-activated protein kinase kinase kinase [Vitis vinifera]	Unigene13844_A11//0.00E+00//AT3G06030| ANP3 (ARABIDOPSIS NPK1-RELATED PROTEIN KINASE 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene13844_A11//0.00E+00//TC162055		ko04626|Plant-pathogen interaction		nr -
Unigene13848_A11	1328	0.28	0.72	0.32	1.61	0.36	0.44	1.50	1.48	0.78	1.39E+00	5.77E-02		2.18E-01	8.31E-01		-2.15E+00	1.86E-06	Down	-1.87E+00	6.85E-05	Down	-1.67E-02	1.00E+00		-9.40E-01	1.71E-02		Unigene13848_A11//gi|124360403|gb|ABN08416.1|//4.00E-84//Protein kinase PKN/PRK1, effector [Medicago truncatula]	Unigene13848_A11//3.00E-69//AT1G55170| unknown protein	Unigene13848_A11//0.00E+00//TC130823				nr +
Unigene13849_A11	1942	10.05	17.87	17.66	20.78	20.80	21.35	59.61	28.82	56.33	8.31E-01	7.75E-19		8.13E-01	2.46E-17		1.50E-03	9.90E-01		3.92E-02	6.92E-01		-1.05E+00	2.25E-110	Down	-8.16E-02	7.71E-02		Unigene13849_A11//gi|297833742|ref|XP_002884753.1|//1.00E-122//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330593|gb|EFH61012.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13849_A11//3.00E-114//AT3G09760| zinc finger (C3HC4-type RING finger) family protein	Unigene13849_A11//0.00E+00//gi|78351491|gb|DT571765.1|DT571765		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene13854_A11	2060	10.31	9.59	12.10	4.35	4.61	3.03	1.21	0.28	0.58	-1.04E-01	4.32E-01		2.30E-01	5.33E-02		8.40E-02	7.31E-01		-5.25E-01	5.99E-03		-2.09E+00	2.75E-07	Down	-1.06E+00	2.35E-03		Unigene13854_A11//gi|18416350|ref|NP_568233.1|//0.00E+00//pentatricopeptide (PPR) repeat-containing protein / CBS domain-containing protein [Arabidopsis thaliana] >gi|75161461|sp|Q8YVD6.1|PP374_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g10690	Unigene13854_A11//0.00E+00//AT5G10690| pentatricopeptide (PPR) repeat-containing protein / CBS domain-containing protein	Unigene13854_A11//0.00E+00//gi|78325989|gb|DT546263.1|DT546263				nr -

Unigene1386_All	2849	11.50	3.73	2.21	20.96	13.32	9.94	21.10	3.83	7.27	-1.62E+00	1.82E-50	Down	-2.38E+00	1.20E-80	Down	-6.54E-01	9.73E-26		-1.08E+00	5.85E-53	Down	-2.46E+00	2.12E-194	Down	-1.54E+00	3.69E-107	Down	Unigene1386_All//gi|68236762|gb|AAN73052.2|//0.00E+00//mini-chromosome maintenance protein MCM6 [Pisum sativum]	Unigene1386_All//0.00E+00//AT5G4635| minichromosome maintenance family protein / MCM family protein	Unigene1386_All//0.00E+00//TC136222		ko03030|DNA replication		nr -
Unigene13860_All	1780	3.29	6.01	7.09	3.92	5.77	11.34	5.56	5.21	6.27	8.68E-01	8.89E-07		1.11E+00	6.63E-11	Up	5.57E-01	1.06E-03		1.53E+00	9.74E-31	Up	-9.26E-02	6.67E-01		1.73E-01	2.92E-01		Unigene13860_All|gi|56236086|gb|AAY84499.1|//0.00E+00//At5g45275 [Arabidopsis thaliana] >gi|56790236|gb|AAW30035.1| At5g45275 [Arabidopsis thaliana]	Unigene13860_All//0.00E+00//AT5G45275| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Nodulin-like (InterPro:IPR010658), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: nodulin-related (TAIR:AT4G19450.1); Has 697 Blast hits to 659 proteins in 149 species: Archae - 19; Bacteria - 126; Metazoa - 5; Fungi - 146; Plants - 324; Viruses - 0; Other Eukaryotes - 77 (source: NCBI BLink).	Unigene13860_All//0.00E+00//gi|109855193|gb|DW484172.1|DW484172				nr +
Unigene13863_All	3812	0.30	1.83	0.78	0.14	0.10	0.04	0.26	0.39	1.06	2.60E+00	4.80E-20	Up	1.37E+00	4.39E-04	Up	-5.32E-01	5.85E-01		-2.02E+00	7.05E-02		6.30E-01	2.04E-01		2.05E+00	2.79E-11	Up	Unigene13863_All|gi|297802890|ref|XP_002869329.1|//0.00E+00//ABC1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315165|gb|EFH45588.1| ABC1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13863_All//0.00E+00//AT4G31390| ABC1 family protein	Unigene13863_All//0.00E+00//CO084746				nr +
Unigene13864_All	540	4.36	7.41	4.73	5.72	6.70	14.64	11.20	46.13	123.28	7.66E-01	1.21E-02		1.19E-01	7.66E-01		2.27E-01	5.67E-01		1.36E+00	2.24E-10	Up	2.04E+00	3.72E-64	Up	3.46E+00	0.00E+00	Up	Unigene13864_All|gi|115478897|ref|NP_001063042.1|//4.00E-06//Os09g0376300 [Oryza sativa Japonica Group] >gi|113631275|dbj|BAF24956.1| Os09g0376300 [Oryza sativa Japonica Group]		Unigene13864_All//0.00E+00//TC149440				nr -
Unigene13865_All	1313	4.94	7.02	3.41	7.82	10.94	15.96	18.93	64.21	138.75	5.07E-01	7.59E-03		-5.37E-01	2.71E-02		4.85E-01	5.65E-04		1.03E+00	1.98E-17	Up	1.76E+00	1.03E-176	Up	2.87E+00	0.00E+00	Up	Unigene13865_All|gi|115476412|ref|NP_001061802.1|//7.00E-20//Os08g0414300 [Oryza sativa Japonica Group] >gi|113623771|dbj|BAF23716.1| Os08g0414300 [Oryza sativa Japonica Group]	Unigene13865_All//9.00E-17//AT4G38060| unknown protein	Unigene13865_All//0.00E+00//TC149440				nr +
Unigene13867_All	2194	19.36	20.21	19.93	9.56	6.28	6.65	14.47	38.46	21.81	6.15E-02	5.16E-01		4.13E-02	6.58E-01		-6.07E-01	3.22E-08		-5.24E-01	6.94E-06		1.41E+00	4.27E-128	Up	5.92E-01	3.77E-18		Unigene13867_All|gi|17064754|gb|AAL32531.1|//0.00E+00//nitrate transporter (NTL1) [Arabidopsis thaliana] >gi|27311911|gb|AAO00921.1| nitrate transporter (NTL1) [Arabidopsis thaliana]	Unigene13867_All//0.00E+00//AT1G69850| ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter	Unigene13867_All//0.00E+00//DT526894				nr +
Unigene13868_All	1595	0.82	2.95	0.83	2.37	1.12	0.91	48.62	71.93	59.05	1.85E+00	3.03E-09	Up	2.53E-02	9.85E-01		-1.08E+00	2.44E-04	Down	-1.39E+00	1.44E-05	Down	5.65E-01	4.59E-38		2.80E-01	2.02E-09		Unigene13868_All|gi|15235200|ref|NP_193716.1|//1.00E-141//glycosyl hydrolase family 18 protein [Arabidopsis thaliana] >gi|119360133|gb|ABL66795.1| At4g19810 [Arabidopsis thaliana]	Unigene13868_All//3.00E-133//AT4G19810| glycosyl hydrolase family 18 protein	Unigene13868_All//0.00E+00//CO106445				nr -
Unigene13869_All	2793	0.52	0.60	0.27	2.94	3.08	1.44	3.71	3.29	6.12	1.91E-01	6.91E-01		-9.75E-01	9.25E-02		6.68E-02	8.11E-01		-1.03E+00	2.56E-07	Down	-1.72E-01	3.48E-01		7.22E-01	1.13E-09		Unigene13869_All|gi|115473321|ref|NP_001060259.1|//7.00E-66//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene13869_All//4.00E-16//AT1G43760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706), Endonuclease/exonuclease/phosphatase (InterPro:IPR005135); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40390.1); Has 2614 Blast hits to 2551 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 1517; Fungi - 2; Plants - 1086; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene13869_All//7.00E-29//TC145821				nr +
Unigene13870_All	1469	33.27	27.84	28.46	53.24	51.85	48.51	84.85	42.62	41.82	-2.57E-01	8.15E-04		-2.25E-01	5.37E-03		-3.81E-02	6.02E-01		-1.34E-01	3.40E-02		-9.93E-01	1.03E-108		-1.02E+00	7.72E-117	Down	Unigene13870_All|gi|18394761|ref|NP_564091.1|//1.00E-133//GAMMA CA1 (GAMMA CARBONIC ANHYDRASE 1); carbonate dehydratase [Arabidopsis thaliana] >gi|9795586|gb|AAP98404.1|AC024609_5 Unknown protein [Arabidopsis thaliana]	Unigene13870_All//1.00E-134//AT1G19580| GAMMA CA1 (GAMMA CARBONIC ANHYDRASE 1); carbonate dehydratase	Unigene13870_All//0.00E+00//gi|78341105|gb|DT561379.1|DT561379				nr +
Unigene13871_All	1429	9.92	25.85	9.02	13.07	17.74	15.52	15.09	27.23	58.27	1.38E+00	1.09E-44	Up	-1.38E-01	4.11E-01		4.40E-01	1.39E-05		2.47E-01	4.31E-02		8.52E-01	8.89E-27		1.95E+00	3.60E-204	Up	Unigene13871_All|gi|297814934|ref|XP_002875350.1|//1.00E-32//ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321188|gb|EFH51609.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13871_All//6.00E-25//AT3G26980| MUB4 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 4 PRECURSOR)	Unigene13871_All//0.00E+00//TC167119				nr +
Unigene13872_All	1941	4.45	4.52	3.95	6.36	6.24	5.91	7.97	20.39	34.99	2.20E-02	9.31E-01		-1.71E-01	4.35E-01		-2.74E-02	8.81E-01		-1.07E-01	6.03E-01		1.35E+00	6.10E-57	Up	2.13E+00	2.04E-187	Up	Unigene13872_All|gi|223452488|gb|ACM89571.1|//1.00E-169//protein kinase [Glycine max]	Unigene13872_All//2.00E-155//AT3G09830| protein kinase, putative	Unigene13872_All//0.00E+00//TC173966				nr -
Unigene13873_All	1379	7.40	3.20	9.31	6.14	8.79	8.81	7.45	3.27	4.04	-1.21E+00	1.09E-10	Down	3.31E-01	4.97E-02		5.17E-01	8.33E-04		5.21E-01	1.18E-03		-1.19E+00	1.14E-12	Down	-8.81E-01	2.26E-08		Unigene13873_All|gi|117958621|gb|ABK59675.1|//1.00E-36//At4g30993 [Arabidopsis thaliana]	Unigene13873_All//9.00E-52//AT4G30993| unknown protein	Unigene13873_All//0.00E+00//gi|13350732|gb|BG441080.1|BG441080				nr +
Unigene13874_All	1122	95.46	61.69	40.48	173.20	118.68	144.67	281.19	161.71	111.14	-6.30E-01	2.99E-35		-1.24E+00	1.98E-105	Down	-5.45E-01	7.37E-60		-2.60E-01	1.13E-13		-7.98E-01	1.39E-189		-1.34E+00	0.00E+00	Down	Unigene13874_All|gi|239056191|emb|CAQ58628.1|//1.00E-143//Putative 2-3 biphosphoglycerate independant phosphoglycerate mutase [Vitis vinifera]	Unigene13874_All//3.00E-138//AT1G09780| 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative	Unigene13874_All//0.00E+00//TC140966		ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene13875_All	2158	10.13	3.12	4.66	25.83	16.55	16.62	23.94	17.02	12.72	-1.70E+00	3.57E-36	Down	-1.12E+00	9.69E-19	Down	-6.43E-01	2.77E-23		-6.36E-01	2.09E-20		-4.92E-01	7.13E-14		-9.13E-01	9.55E-41		Unigene13875_All|gi|15223556|ref|NP_173376.1|//0.00E+00//KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups [Arabidopsis thaliana] >gi|75311386|sp|Q9LVK9.1|KCS4_ARATH RecName: Full=3-ketoacyl-CoA synthase 4; Short=KCS-4; AltName: Full=Very long-chain fatty acid condensing enzyme 4; Short=VLCFA condensing enzyme 4 >gi|8778420|gb|AAF79428.1|AC025808_10 F18014.21 [Arabidopsis thaliana] >gi|190610070|gb|ACE79746.1| At1g19440 [Arabidopsis thaliana]	Unigene13875_All//0.00E+00//AT1G19440| KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene13875_All//0.00E+00//gi|164269281|gb|ES813610.1|ES813610		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr +
Unigene13877_All	1317	2.66	2.35	2.43	1.70	1.28	1.58	1.77	0.79	0.64	-1.82E-01	6.20E-01		-1.34E-01	6.97E-01		-4.10E-01	3.48E-01		-1.10E-01	8.00E-01		-1.15E+00	2.28E-03		-1.48E+00	1.01E-04	Down	Unigene13877_All|gi|2462735|gb|AAB71954.1|//9.00E-78//Hypothetical protein [Arabidopsis thaliana]	Unigene13877_All//9.00E-75//AT1G60160| unknown protein	Unigene13877_All//0.00E+00//DW224202				nr +
Unigene1388_All	3515	7.16	3.34	7.65	13.86	11.64	9.82	7.27	1.26	1.79	-1.10E+00	1.05E-21	Down	9.56E-02	4.33E-01		-2.52E-01	4.90E-04		-4.98E-01	1.06E-11		-2.53E+00	2.15E-85	Down	-2.02E+00	5.39E-67	Down	Unigene1388_All|gi|224589557|gb|ACN59312.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene1388_All//0.00E+00//AT3G03770| leucine-rich repeat transmembrane protein kinase, putative	Unigene1388_All//0.00E+00//TC155186				nr -
Unigene13882_All	1888	4.30	3.52	3.69	3.93	2.86	5.02	4.01	1.77	3.00	-2.89E-01	1.74E-01		-2.17E-01	3.53E-01		-4.57E-01	2.78E-02		3.54E-01	7.05E-02		-1.18E+00	1.89E-09	Down	-4.20E-01	2.34E-02		Unigene13882_All|gi|59800202|sp|P69242.1|RPOT3_NICSY//0.00E+00//RecName: Full=DNA-directed RNA polymerase 3, chloroplastic; AltName: Full=T7 bacteriophage-type single subunit RNA polymerase 3; AltName: Full=NsRpoT-C; Flags: Precursor >gi|59800203|sp|P69243.1|RPO3A_TOBAC RecName: Full=DNA-directed RNA polymerase 3A, chloroplastic; AltName: Full=T7 bacteriophage-type single subunit RNA polymerase 3A; AltName: Full=NictaRpoT3-syl; Flags: Precursor >gi|21425641|emb|CAC82576.3| phage-type RNA polymerase [Nicotiana sylvestris] >gi|21425679|emb|CAC95027.2| plastid RNA polymerase [Nicotiana tabacum] >gi|24475541|dbj|BAC22693.1| T7 bacteriophage-type single subunit RNA polymerase [Nicotiana sylvestris] >gi|24475543|dbj|BAC22694.1| T7 bacteriophage-type single subunit RNA polymerase [Nicotiana sylvestris]	Unigene13882_All//0.00E+00//AT2G24120| SCA3 (SCABRA 3); DNA binding / DNA-directed RNA polymerase	Unigene13882_All//0.00E+00//gi|73862624|gb|DT465363.1|DT465363				nr +
Unigene13883_All	414	1.64	2.94	3.09	2.05	2.33	2.62	1.53	4.85	3.46	8.38E-01	1.73E-01		9.10E-01	1.46E-01		1.87E-01	8.11E-01		3.56E-01	6.40E-01		1.66E+00	1.31E-04	Up	1.18E+00	1.59E-02					Unigene13883_All//9.00E-61//CO109867				
Unigene13885_All	1318	10.08	6.92	5.41	7.94	9.48	24.43	29.90	57.24	87.42	-5.43E-01	4.20E-04		-8.97E-01	2.82E-08		2.57E-01	1.30E-01		1.62E+00	7.34E-53	Up	9.37E-01	5.77E-60		1.55E+00	1.08E-204	Up	Unigene13885_All|gi|297839443|ref|XP_002887603.1|//4.00E-79//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333444|gb|EFH63862.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13885_All//7.00E-73//AT1G75540| STH2 (SALT TOLERANCE HOMOLOG2); transcription factor/ zinc ion binding	Unigene13885_All//2.00E-42//DR457994	DEB	ko04712|Circadian rhythm - plant		nr -

Unigene13886_All	1933	3.06	1.65	2.23	5.41	4.52	4.18	4.51	1.45	1.57	-8.89E-01	2.81E-04		-4.55E-01	7.87E-02		-2.58E-01	1.64E-01		-3.72E-01	3.99E-02		-1.64E+00	3.62E-17	Down	-1.52E+00	4.52E-16	Down	Unigene13886_All//gi|226529489|ref|NP_001148892.1|//0.00E+00//ATP binding protein [Zea mays] >gi|195622982|gb|ACG33321.1| ATP binding protein [Zea mays]	Unigene13886_All//0.00E+00//AT5G46570| BSK2 (BR-SIGNALING KINASE 2); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase	Unigene13886_All//0.00E+00//ES835318		ko04626|Plant-pathogen interaction		nr -
Unigene13887_All	1330	5.39	11.66	5.81	4.68	3.62	4.28	5.69	7.45	11.29	1.11E+00	6.84E-14	Up	1.07E-01	6.27E-01		-3.69E-01	1.23E-01		-1.30E-01	6.32E-01		3.88E-01	1.91E-02		9.89E-01	4.76E-14		Unigene13887_All//gi|18402362|ref|NP_566645.1|//1.00E-85//VPS9A| Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana]	Unigene13887_All//1.00E-81//AT3G19770| VPS9A; Rho guanyl-nucleotide exchange factor	Unigene13887_All//0.00E+00//TC167003				nr +
Unigene13890_All	556	0.38	0.18	0.00	0.90	0.99	1.30	1.90	1.20	0.14	-1.05E+00	5.65E-01		-8.56E+00	1.46E-01		1.45E-01	9.05E-01		5.37E-01	5.60E-01		-6.60E-01	2.78E-01		-3.73E+00	6.13E-06	Down	Unigene13890_All//gi|297830862|ref|NP_002883313.1|//5.00E-68//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329153|gb|EFH59572.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13890_All//2.00E-57//AT3G21690| MATE efflux family protein	Unigene13890_All//2.00E-111//TC165171				nr -
Unigene13891_All	1887	1.44	1.34	1.19	8.55	5.24	4.19	4.82	3.10	0.93	-1.03E-01	7.77E-01		-2.83E-01	4.93E-01		-7.08E-01	2.53E-08		-1.03E+00	1.01E-13	Down	-6.36E-01	1.81E-04		-2.37E+00	1.16E-29	Down	Unigene13891_All//gi|126363776|dbj|BAF47752.1|//0.00E+00//multi antimicrobial extrusion family protein [Nicotiana tabacum]	Unigene13891_All//1.00E-44//AT3G21690| MATE efflux family protein	Unigene13891_All//0.00E+00//TC165171				nr -
Unigene13892_All	1608	2.25	1.39	1.72	7.53	4.37	4.47	4.63	2.42	2.30	-6.95E-01	3.13E-02		-3.83E-01	2.71E-01		-7.85E-01	1.50E-07		-7.53E-01	2.03E-06		-9.37E-01	1.18E-06		-1.01E+00	1.19E-07	Down	Unigene13892_All//gi|13877549|gb|AK43852.1|AF370475_1//4.00E-73//Unknown protein [Arabidopsis thaliana]	Unigene13892_All//1.00E-44//AT3G07510| unknown protein	Unigene13892_All//0.00E+00//TC141021				nr -
Unigene13893_All	976	3.91	1.66	3.00	9.75	7.09	7.73	2.73	1.46	1.02	-1.24E+00	1.25E-04	Down	-3.83E-01	2.52E-01		-4.59E-01	9.94E-03		-3.35E-01	8.52E-02		-9.07E-01	8.59E-03		-1.42E+00	4.85E-05	Down	Unigene13893_All//gi|13877549|gb|AK43852.1|AF370475_1//2.00E-73//Unknown protein [Arabidopsis thaliana]	Unigene13893_All//5.00E-45//AT3G07510| unknown protein	Unigene13893_All//0.00E+00//TC141021				nr -
Unigene13894_All	359	3.64	0.71	2.82	14.43	14.48	12.08	5.42	2.10	2.77	-2.37E+00	5.60E-04	Down	-3.71E-01	5.53E-01		5.30E-03	9.92E-01		-2.57E-01	3.94E-01		-1.37E+00	1.35E-03		-9.66E-01	1.58E-02		Unigene13894_All//gi|226501020|ref|NP_001150271.1|//2.00E-58//ras-related protein Rab-6A [Zea mays] >gi|195637990|gb|ACG38463.1| ras-related protein Rab-6A [Zea mays]	Unigene13894_All//2.00E-59//AT2G44610| RAB6A; GTP binding / protein binding	Unigene13894_All//0.00E+00//gi|164365599|gb|EV486130.1|EV486130				nr +
Unigene13897_All	244	31.95	85.56	56.31	34.91	50.52	28.32	0.00	0.17	0.00	1.42E+00	1.22E-26	Up	8.18E-01	2.12E-07		5.33E-01	4.86E-04		-3.02E-01	1.55E-01		7.42E+00	6.35E-01		null	null				Unigene13897_All//2.00E-05//AT3G62730| unknown protein	Unigene13897_All//7.00E-79//gi|48745212|gb|C0075731.1|C0075731				
Unigene13898_All	438	31.77	96.25	61.64	18.20	26.18	21.86	0.00	0.00	0.00	1.60E+00	4.26E-63	Up	9.56E-01	6.42E-18		5.25E-01	1.03E-03		2.65E-01	1.93E-01		null	null		null	null					Unigene13898_All//5.00E-109//gi|164347041|gb|EX169190.1|EX169190				
Unigene13899_All	1124	7.59	4.37	3.03	35.23	28.86	32.06	0.00	0.07	0.00	-7.95E-01	6.10E-05		-1.32E+00	8.42E-10	Down	-2.88E-01	3.35E-04		-1.36E-01	1.55E-01		6.22E+00	4.02E-01		null	null		Unigene13899_All//gi|15294284|gb|AK95319.1|AF410333_1//5.00E-48//AT3g62730/F26B9_160 [Arabidopsis thaliana] >gi|20147275|gb|AAM10351.1| AT3g62730/F26K9_160 [Arabidopsis thaliana]	Unigene13899_All//4.00E-47//AT3G62730| unknown protein	Unigene13899_All//3.00E-26//TC156087				nr -
Unigene13900_All	1755	81.03	56.30	83.83	29.80	50.23	36.03	0.65	1.31	1.77	-5.25E-01	8.62E-34		4.91E-02	3.58E-01		7.53E-01	6.70E-47		2.74E-01	2.47E-05		1.01E+00	7.55E-03		1.44E+00	8.29E-06	Up	Unigene13900_All//gi|11387206|sp|Q9THX6.1|APX4_SOLLC//1.00E-89//RecName: Full=Putative L-ascorbate peroxidase, chloroplastic; AltName: Full=Thylakoid lumenal 29 kDa protein; Short=TL29; AltName: Full=P29; AltName: Full=LeAPx09; Flags: Precursor	Unigene13900_All//3.00E-85//AT4G09010| APX4 (ASCORBATE PEROXIDASE 4); heme binding / peroxidase	Unigene13900_All//0.00E+00//TC156832		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene13904_All	2309	3.06	3.23	1.41	4.77	6.03	6.49	7.89	6.93	6.61	7.66E-02	7.29E-01		-1.12E+00	1.70E-06	Down	3.38E-01	2.47E-02		4.46E-01	1.89E-03		-1.87E-01	1.39E-01		-2.56E-01	2.77E-02		Unigene13904_All//gi|22329715|ref|NP_173580.2|//1.00E-60//wound-responsive family protein [Arabidopsis thaliana] >gi|19699100|gb|AAL90916.1| At1g21610/F24J8_11 [Arabidopsis thaliana] >gi|21928029|gb|AAMT8043.1| At1g21610/F24J8_11 [Arabidopsis thaliana]	Unigene13904_All//3.00E-63//AT1G21610| wound-responsive family protein	Unigene13904_All//2.00E-62//gi|21091136|gb|BQ403449.1|BQ403449				nr -
Unigene13906_All	1930	1.41	4.52	0.86	1.52	2.37	2.18	3.42	6.54	27.35	1.68E+00	1.57E-14	Up	-7.21E-01	7.25E-02		6.40E-01	2.07E-02		5.15E-01	9.32E-02		9.36E-01	1.06E-10		3.00E+00	1.04E-214	Up	Unigene13906_All//gi|15231963|ref|NP_187488.1|//1.00E-174//ATSIK; ATP binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|194294570|gb|ACF40324.1| At3g08760 [Arabidopsis thaliana] >gi|222424853|dbj|BAH20378.1| AT3G08760 [Arabidopsis thaliana]	Unigene13906_All//1.00E-164//AT3G08760| ATSIK; ATP binding / kinase/ protein kinase/ protein tyrosine kinase	Unigene13906_All//0.00E+00//TC178915		ko04626|Plant-pathogen interaction		nr +
Unigene13907_All	1425	16.23	12.16	13.83	10.00	5.56	11.54	17.74	81.95	165.31	-4.16E-01	2.51E-04		-2.31E-01	6.41E-02		-8.47E-01	6.04E-10		2.07E-01	1.77E-01		2.21E+00	0.00E+00	Up	3.22E+00	0.00E+00	Up	Unigene13907_All//gi|15237530|ref|NP_198915.1|//1.00E-108//GLIP1 (GDSL LIPASE1); carboxylesterase/ lipase [Arabidopsis thaliana] >gi|75171498|sp|Q9FLN0.1|GLIP1_ARATH RecName: Full=GDSL esterase/lipase 1; AltName: Full=Extracellular lipase 1; Flags: Precursor >gi|9759145|dbj|BAB09701.1| GDSL-motif lipase/hydrolase-like protein [Arabidopsis thaliana]	Unigene13907_All//2.00E-109//AT5G40990| GLIP1 (GDSL LIPASE1); carboxylesterase/ lipase	Unigene13907_All//0.00E+00//TC138489				nr +
Unigene1391_All	892	0.23	1.53	1.01	2.46	2.63	2.43	4.12	7.87	10.27	2.71E+00	1.29E-04	Up	2.11E+00	1.42E-02		9.54E-02	8.37E-01		-1.59E-02	9.62E-01		9.33E-01	2.83E-06		1.32E+00	1.45E-13	Up	Unigene1391_All//gi|30387531|gb|AAP31931.1|//3.00E-41//At3g26670 [Arabidopsis thaliana]	Unigene1391_All//2.00E-42//AT3G26670| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF803 (InterPro:IPR008521); BEST Arabidopsis thaliana protein match is: permease-related (TAIR:AT3G23870.1); Has 715 Blast hits to 711 proteins in 119 species: Archae - 0; Bacteria - 0; Metazoa - 298; Fungi - 244; Plants - 119; Viruses - 2; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene1391_All//0.00E+00//gi|78353890|gb|DT574164.1|DT574164				nr -
Unigene13910_All	1609	6.41	5.64	3.28	19.20	21.70	14.74	16.08	3.74	5.65	-1.85E-01	3.48E-01		-9.67E-01	2.33E-07		1.77E-01	6.41E-02		-3.81E-01	5.92E-05		-2.10E+00	2.33E-69	Down	-1.51E+00	2.01E-45	Down	Unigene13910_All//gi|15218562|ref|NP_177411.1|//1.00E-77//iq68 (IQ-domain 8); calmodulin binding [Arabidopsis thaliana] >gi|38016019|gb|AAR07516.1| At1g72670 [Arabidopsis thaliana]	Unigene13910_All//4.00E-66//AT1G72670| iq68 (IQ-domain 8); calmodulin binding	Unigene13910_All//0.00E+00//gi|78335607|gb|DT555881.1|DT555881				nr +
Unigene13916_All	895	12.86	14.89	13.86	29.05	34.05	32.30	39.78	32.36	19.59	2.11E-01	2.04E-01		1.08E-01	5.77E-01		2.29E-01	2.04E-02		1.53E-01	1.83E-01		-2.98E-01	2.39E-04		-1.02E+00	4.46E-34	Down	Unigene13916_All//gi|18404934|ref|NP_565899.1|//5.00E-29//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|15724197|gb|AAL06490.1|AF411180_1_1 At2g39050/T7F6.22 [Arabidopsis thaliana] >gi|20147403|gb|AAM10411.1| At2g39050/T7F6.22 [Arabidopsis thaliana] >gi|20197446|gb|AAC79615.2| expressed protein [Arabidopsis thaliana]	Unigene13916_All//2.00E-30//AT2G39050| hydroxyproline-rich glycoprotein family protein	Unigene13916_All//0.00E+00//gi|84165402|gb|DR454050.1|DR454050				nr +
Unigene1392_All	878	0.54	0.35	0.30	1.70	2.31	1.34	2.41	3.05	4.90	-6.31E-01	5.54E-01		-8.23E-01	4.57E-01		4.43E-01	3.67E-01		-3.48E-01	5.60E-01		3.40E-01	3.69E-01		1.03E+00	7.08E-05	Up	Unigene1392_All//gi|30387531|gb|AAP31931.1|//5.00E-58//At3g26670 [Arabidopsis thaliana]	Unigene1392_All//2.00E-59//AT3G26670| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF803 (InterPro:IPR008521); BEST Arabidopsis thaliana protein match is: permease-related (TAIR:AT3G23870.1); Has 715 Blast hits to 711 proteins in 119 species: Archae - 0; Bacteria - 0; Metazoa - 298; Fungi - 244; Plants - 119; Viruses - 2; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene1392_All//0.00E+00//gi|78353890|gb|DT574164.1|DT574164				nr +
Unigene13920_All	1730	6.93	3.19	3.20	15.09	13.81	11.67	10.88	3.94	4.12	-1.12E+00	5.10E-11	Down	-1.11E+00	1.87E-10	Down	-1.27E-01	3.03E-01		-3.71E-01	4.09E-04		-1.47E+00	6.79E-31	Down	-1.40E+00	9.03E-30	Down	Unigene13920_All//gi|297806471|ref|XP_002871119.1|//0.00E+00//glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata] >gi|297316956|gb|EFH47378.1| glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata]	Unigene13920_All//7.00E-180//AT5G04885| glycosyl hydrolase family 3 protein	Unigene13920_All//0.00E+00//TC131066		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr -
Unigene13921_All	2440	2.53	0.56	1.48	5.51	4.88	4.76	3.93	0.82	2.29	-2.17E+00	1.28E-14	Down	-7.70E-01	1.88E-03		-1.75E-01	3.15E-01		-2.13E-01	2.15E-01		-2.26E+00	1.56E-28	Down	-7.83E-01	1.33E-06		Unigene13921_All//gi|297806471|ref|XP_002871119.1|//0.00E+00//glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata] >gi|297316956|gb|EFH47378.1| glycosyl hydrolase family 3 protein [Arabidopsis lyrata subsp. lyrata]	Unigene13921_All//0.00E+00//AT5G04885| glycosyl hydrolase family 3 protein	Unigene13921_All//0.00E+00//TC131066		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00460|Cyanoamino acid metabolism		nr -
Unigene13922_All	1513	1.83	4.02	3.27	42.37	52.76	38.45	11.68	7.18	4.11	1.13E+00	4.48E-06	Up	8.37E-01	2.92E-03		3.16E-01	3.96E-09		-1.40E-01	4.71E-02		-7.02E-01	2.88E-09		-1.51E+00	3.19E-31	Down	Unigene13922_All//gi|167858185|gb|ACA04033.1|//1.00E-171//galactinol synthase 4 [Populus trichocarpa x Populus deltoides]	Unigene13922_All//2.00E-165//AT2G47180| AtGolS1 (Arabidopsis thaliana galactinol synthase 1); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene13922_All//0.00E+00//ES818894				nr +

Unigene13925_All	967	3.79	1.94	3.69	8.96	9.40	4.06	2.40	1.12	1.44	-9.66E-01	2.76E-03		-3.78E-02	9.21E-01		6.88E-02	8.01E-01		-1.14E+00	6.24E-09	Down	-1.10E+00	3.58E-03		-7.38E-01	3.95E-02		Unigene13925_All//gi|115445171|ref|NP_001046365.1|//7.00E-58//0s02g0230200 [Oryza sativa Japonica Group] >gi|113535896|dbj|BAF08279.1|Os02g0230200 [Oryza sativa Japonica Group]	Unigene13925_All//7.00E-87//AT3G58800| unknown protein	Unigene13925_All//0.00E+00//ES828671				nr +
Unigene13929_All	1489	8.85	2.52	7.44	8.70	10.31	10.62	4.46	8.53	4.60	-1.81E+00	3.87E-24	Down	-2.51E-01	1.42E-01		2.46E-01	1.01E-01		2.88E-01	5.02E-02		9.37E-01	9.00E-11		4.58E-02	8.35E-01		Unigene13929_All//gi|18411876|ref|NP_567110.1|//3.00E-58//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene13929_All//2.00E-91//AT3G61180| zinc finger (C3HC4-type RING finger) family protein	Unigene13929_All//0.00E+00//gi|78344708|gb|DT564982.1|DT564982				nr +
Unigene1393_All	1539	3.77	7.61	2.87	8.67	9.35	6.69	22.69	41.23	44.91	1.01E+00	3.02E-09	Up	-3.94E-01	1.41E-01		1.09E-01	5.46E-01		-3.75E-01	1.63E-02		8.61E-01	5.70E-44		9.85E-01	4.57E-61		Unigene1393_All//gi|30387531|gb|AAP31931.1|//1.00E-171//At3g26670 [Arabidopsis thaliana]	Unigene1393_All//2.00E-163//AT3G26670| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF803 (InterPro:IPR008521); BEST Arabidopsis thaliana protein match is: permease-related (TAIR:AT3G23870.1); Has 715 Blast hits to 711 proteins in 119 species: Archae - 0; Bacteria - 0; Metazoa - 298; Fungi - 244; Plants - 119; Viruses - 2; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene1393_All//0.00E+00//TC140150				nr -
Unigene13930_All	1117	25.95	61.42	25.55	40.45	42.82	57.82	113.59	118.28	57.28	1.24E+00	3.75E-70	Up	-2.23E-02	8.50E-01		8.22E-02	3.80E-01		5.15E-01	3.47E-16		5.83E-02	2.24E-01		-9.88E-01	1.12E-112		Unigene13930_All//gi|28380080|sp|Q9CSF1.1|IF5Y_ARATH//1.00E-75//RecName: Full=Probable eukaryotic translation initiation factor 5-1; Short=eIF-5 1	Unigene13930_All//2.00E-58//AT1G36730| eukaryotic translation initiation factor 5, putative / eIF-5, putative	Unigene13930_All//0.00E+00//TC173090				nr -
Unigene13931_All	1351	44.11	55.66	66.81	15.01	12.46	17.35	2.35	0.59	1.12	3.36E-01	2.19E-08		5.99E-01	2.39E-26		-2.68E-01	2.82E-02		2.09E-01	8.57E-02		-2.00E+00	1.36E-08	Down	-1.07E+00	4.72E-04	Down	Unigene13931_All//gi|21593371|gb|AM65320.1|//1.00E-113//mutT domain protein-like [Arabidopsis thaliana]	Unigene13931_All//7.00E-115//AT5G47240| atmudt8 (Arabidopsis thaliana Nudix hydrolase homolog 8); hydrolase	Unigene13931_All//0.00E+00//TC139415				nr +
Unigene13932_All	1168	22.89	16.92	20.61	29.13	44.78	63.11	12.05	51.96	41.92	-4.36E-01	3.15E-05		-1.52E-01	2.13E-01		6.21E-01	5.19E-20		1.12E+00	3.25E-68	Up	2.11E+00	8.57E-162	Up	1.80E+00	5.73E-108	Up	Unigene13932_All//gi|30697354|ref|NP_176821.2|//8.00E-44//PMI2 (plastid movement impaired 2) [Arabidopsis thaliana] >gi|75126954|sp|Q6NLC8.1|Y1648_ARATH RecName: Full=Uncharacterized protein At1g66480 >gi|45476561|gb|AAS65946.1|At1g66480 [Arabidopsis thaliana] >gi|46402440|gb|AAS92322.1|At1g66480 [Arabidopsis thaliana]	Unigene13932_All//5.00E-40//AT5G37840| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: PMI2 (plastid movement impaired 2) (TAIR:AT1G66480.1); Has 49 Blast hits to 49 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene13932_All//0.00E+00//TC147524				nr +
Unigene13937_All	1114	44.48	40.34	46.89	41.54	40.31	36.61	25.35	18.57	11.23	-1.41E-01	8.19E-02		7.63E-02	3.87E-01		-4.35E-02	6.58E-01		-1.82E-01	2.65E-02		-4.49E-01	7.35E-07		-1.17E+00	6.78E-34	Down	Unigene13937_All//gi|226490896|ref|NP_001149300.1|//8.00E-27//nucleolin [Zea mays] >gi|195626178|gb|ACG34919.1|nucleolin [Zea mays]		Unigene13937_All//0.00E+00//CO087702				nr -
Unigene13938_All	1094	7.94	6.21	6.28	4.05	3.02	3.01	2.94	1.15	2.00	-3.55E-01	7.77E-02		-3.38E-01	1.11E-01		-4.24E-01	1.45E-01		-4.27E-01	1.56E-01		-1.36E+00	2.29E-05	Down	-5.52E-01	6.49E-02		Unigene13938_All//gi|297822235|ref|XP_002879000.1|//1.00E-116//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324839|gb|EFH55259.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13938_All//2.00E-109//AT2G26700| PID2 (PINOID2); ATP binding / kinase/ protein kinase	Unigene13938_All//8.00E-150//gi|78336874|gb|DT557148.1|DT557148				nr -
Unigene13939_All	1581	3.11	1.99	1.28	0.72	1.29	1.31	1.28	0.42	1.18	-6.47E-01	1.67E-02		-1.28E+00	1.10E-05	Down	8.26E-01	6.99E-02		8.59E-01	6.02E-02		-1.60E+00	1.82E-04	Down	-1.16E-01	7.65E-01		Unigene13939_All//gi|115434816|ref|NP_001042166.1|//1.00E-152//Os01g0174700 [Oryza sativa Japonica Group] >gi|113531697|dbj|BAF04080.1|Os01g0174700 [Oryza sativa Japonica Group]	Unigene13939_All//6.00E-111//AT2G26700| PID2 (PINOID2); ATP binding / kinase/ protein kinase	Unigene13939_All//0.00E+00//gi|78336874|gb|DT557148.1|DT557148				nr +
Unigene13943_All	1583	11.17	11.56	11.34	28.20	22.45	20.60	29.54	18.93	9.51	4.87E-02	7.27E-01		2.11E-02	8.93E-01		-3.29E-01	8.34E-06		-4.53E-01	3.65E-09		-6.42E-01	6.55E-20		-1.63E+00	2.72E-91	Down	Unigene13943_All//gi|56550679|gb|AAV37793.1|//1.00E-129//At5g10750 [Arabidopsis thaliana] >gi|57222152|gb|AAW38983.1|At5g10750 [Arabidopsis thaliana]	Unigene13943_All//3.00E-129//AT5G10750| unknown protein	Unigene13943_All//0.00E+00//TC174397				nr -
Unigene13944_All	1072	12.49	14.75	13.51	20.63	18.70	23.80	10.25	7.17	3.75	2.39E-01	1.06E-01		1.13E-01	5.14E-01		-1.42E-01	2.87E-01		2.06E-01	7.47E-02		-5.15E-01	7.53E-04		-1.45E+00	1.11E-18	Down			Unigene13944_All//0.00E+00//TC156895				
Unigene13947_All	1685	1.68	0.81	1.74	3.31	2.70	2.41	3.66	2.53	1.75	-1.05E+00	5.46E-03		5.18E-02	8.95E-01		-2.96E-01	2.73E-01		-4.57E-01	7.71E-02		-5.34E-01	1.22E-02		-1.07E+00	4.68E-07	Down	Unigene13947_All//gi|224074267|ref|XP_002304329.1|//2.00E-63//predicted protein [Populus trichocarpa] >gi|222841761|gb|EEE79308.1|predicted protein [Populus trichocarpa]	Unigene13947_All//1.00E-26//AT4G10890| unknown protein	Unigene13947_All//0.00E+00//ES824860				nr +
Unigene13949_All	2042	4.28	1.71	2.76	8.95	10.49	6.83	2.44	2.05	1.52	-1.32E+00	1.67E-10	Down	-6.30E-01	1.90E-03		2.29E-01	6.40E-02		-3.90E-01	2.46E-03		-2.55E-01	3.37E-01		-6.83E-01	3.15E-03		Unigene13949_All//gi|238821222|gb|ACR58456.1|//1.00E-160//GAI/RGA-like protein [Gossypium hirsutum] >gi|257219877|gb|ACV52016.1|GAI/RGA-like 4-b [Gossypium hirsutum] >gi|296398837|gb|ADH10266.1| GAI4b [Gossypium hirsutum]	Unigene13949_All//2.00E-111//AT1G14920| GAI (GIBBERELLIC ACID INSENSITIVE); transcription factor	Unigene13949_All//0.00E+00//TC152264	GRAS			nr -
Unigene13950_All	602	2.26	5.89	3.98	4.80	6.12	6.98	2.88	3.12	5.49	1.38E+00	5.43E-05	Up	8.17E-01	5.74E-02		3.51E-01	3.08E-01		5.40E-01	7.62E-02		1.18E-01	7.88E-01		9.32E-01	1.68E-03				Unigene13950_All//5.00E-128//BE055188				
Unigene13951_All	1367	11.87	28.65	16.75	26.97	36.43	49.89	21.71	32.26	40.68	1.27E+00	8.79E-42	Up	4.98E-01	2.45E-05		4.34E-01	3.41E-10		8.88E-01	1.80E-43		5.71E-01	2.07E-15		9.06E-01	5.24E-43		Unigene13951_All//gi|115459094|ref|NP_001053147.1|//5.00E-18//Os04g0488000 [Oryza sativa Japonica Group] >gi|75233131|sp|Q7XUF4.2|CDKG2_ORYSJ RecName: Full=Cyclin-dependent kinase G-2; Short=CDKG;2 >gi|158512881|sp|A2XUW1.1|CDKG2_ORYSI RecName: Full=Cyclin-dependent kinase G-2; Short=CDKG;2 >gi|38344237|emb|CAD41330.2|OJ991113_30.14 [Oryza sativa (japonica cultivar-group)] >gi|113564718|dbj|BAF15061.1|Os04g0488000 [Oryza sativa Japonica Group]		Unigene13951_All//0.00E+00//TC150917				nr -
Unigene13953_All	1082	11.75	7.59	11.17	16.48	17.63	15.61	17.97	9.27	6.66	-6.31E-01	6.35E-05		-7.29E-02	6.78E-01		9.73E-02	5.53E-01		-7.83E-02	6.18E-01		-9.55E-01	1.39E-16		-1.43E+00	8.88E-32	Down	Unigene13953_All//gi|46931230|gb|AAT06419.1|//1.00E-52//At1g55340 [Arabidopsis thaliana] >gi|48310451|gb|AAT41823.1|At1g55340 [Arabidopsis thaliana]	Unigene13953_All//9.00E-54//AT1G55340| unknown protein	Unigene13953_All//0.00E+00//TC172895				nr +
Unigene13959_All	1660	57.40	23.17	23.35	60.68	46.76	44.73	16.00	10.30	10.01	-1.31E+00	9.35E-106	Down	-1.30E+00	5.66E-101	Down	-3.76E-01	7.62E-16		-4.40E-01	6.80E-19		-6.35E-01	1.81E-11		-6.77E-01	4.07E-13		Unigene13959_All//gi|224108539|ref|XP_002314884.1|//1.00E-157//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222863924|gb|EEF01055.1|glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene13959_All//2.00E-153//AT1G13250| GATL3 (Galacturonosyltransferase-like 3); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene13959_All//0.00E+00//TC143745				nr +
Unigene13960_All	1442	19.19	13.60	29.51	26.88	44.66	72.44	24.95	9.45	13.51	-4.97E-01	1.29E-06		6.20E-01	1.59E-13		7.33E-01	9.77E-33		1.43E+00	5.09E-142	Up	-1.40E+00	1.35E-54	Down	-8.85E-01	2.91E-27		Unigene13960_All//gi|297807233|ref|XP_002871500.1|//1.00E-158//ndr family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317337|gb|EFH47759.1| ndr family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13960_All//1.00E-152//AT5G11790| Ndr family protein	Unigene13960_All//0.00E+00//TC163978				nr -
Unigene13962_All	2261	17.75	9.59	13.33	14.50	9.55	10.97	12.62	46.05	35.75	-8.88E-01	3.04E-24		-4.13E-01	1.88E-06		-6.02E-01	2.12E-12		-4.03E-01	1.07E-05		1.87E+00	2.89E-236	Up	1.50E+00	1.26E-137	Up	Unigene13962_All//gi|297827267|ref|XP_002881516.1|//0.00E+00//sodium-and lithium-tolerant 1 [Arabidopsis lyrata subsp. lyrata] >gi|297327355|gb|EFH57775.1|sodium-and lithium-tolerant 1 [Arabidopsis lyrata subsp. lyrata]	Unigene13962_All//0.00E+00//AT2G37570| SLT1 (sodium- and lithium-tolerant 1)	Unigene13962_All//0.00E+00//TC160248				nr +
Unigene13967_All	1498	6.15	7.04	19.69	2.66	1.15	2.86	5.19	3.54	1.52	1.95E-01	3.12E-01		1.68E+00	3.11E-46	Up	-1.21E+00	2.54E-05	Down	1.07E-01	7.40E-01		-5.52E-01	3.03E-03		-1.78E+00	8.99E-18	Down	Unigene13967_All//gi|15235633|ref|NP_195474.1|//1.00E-170//HLS1 (HOOKLESS 1); N-acetyltransferase [Arabidopsis thaliana] >gi|4468983|emb|CAB38297.1|probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|7270740|emb|CAB80423.1|probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|51969462|dbj|BAD43423.1|probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|51970376|dbj|BAD43880.1|probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|111074338|gb|AB004542.1|At4g37580 [Arabidopsis thaliana]	Unigene13967_All//2.00E-171//AT4G37580| HLS1 (HOOKLESS 1); N-acetyltransferase					nr +
Unigene13969_All	2616	1.64	2.25	1.79	13.39	10.03	13.17	9.65	4.63	1.93	4.54E-01	6.68E-02		1.27E-01	6.61E-01		-4.16E-01	5.66E-07		-2.32E-02	8.41E-01		-1.06E+00	4.77E-25	Down	-2.32E+00	1.06E-78	Down	Unigene13969_All//gi|297849032|ref|XP_002892397.1|//0.00E+00//ceramidase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338239|gb|EFH68656.1|ceramidase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13969_All//0.00E+00//AT1G07380| ceramidase family protein	Unigene13969_All//0.00E+00//TC160755				nr +

Unigene1397_All	1427	11.84	9.80	12.35	18.82	13.13	7.98	6.04	6.09	3.63	-2.73E-01	5.08E-02		6.07E-02	6.84E-01		-5.19E-01	5.86E-08		-1.24E+00	5.13E-30	Down	1.14E-02	9.86E-01		-7.36E-01	1.69E-05		Unigene1397_All//gi|15233901|ref|NP_192687.1|//7.00E-06//RNase H domain-containing protein [Arabidopsis thaliana]	Unigene1397_All//3.00E-07//AT4G09490| RNase H domain-containing protein	Unigene1397_All//0.00E+00//ES794334				nr -
Unigene13971_All	1914	7.16	2.57	3.26	11.32	8.01	11.44	11.95	5.31	6.54	-1.48E+00	6.59E-19	Down	-1.14E+00	2.88E-12	Down	-5.00E-01	3.96E-06		1.56E-02	9.31E-01		-1.17E+00	1.11E-26	Down	-8.71E-01	3.37E-17		Unigene13971_All//gi|145340466|ref|NP_193845.2|//1.00E-86//EMB2271 (EMBRYO DEFECTIVE 2271); nucleotide binding [Arabidopsis thaliana] >gi|62910985|gb|AAY21208.1| U3-SSK-like protein 2 [Arabidopsis thaliana]	Unigene13971_All//2.00E-83//AT4G21130| EMB2271 (EMBRYO DEFECTIVE 2271); nucleotide binding	Unigene13971_All//2.00E-164//DW515799				nr -
Unigene13973_All	1388	3.81	3.36	3.68	12.45	10.77	13.50	10.91	6.08	4.19	-1.81E-01	5.19E-01		-4.78E-02	8.66E-01		-2.10E-01	1.39E-01		1.17E-01	4.58E-01		-8.42E-01	9.64E-11		-1.38E+00	1.27E-23	Down	Unigene13973_All//gi|115439491|ref|NP_001044025.1|//7.00E-63//Os01g0708300 [Oryza sativa Japonica Group] >gi|113533556|dbj|BAF05939.1| Os01g0708300 [Oryza sativa Japonica Group]	Unigene13973_All//8.00E-120//AT5G11960| unknown protein	Unigene13973_All//0.00E+00//TC159972				nr +
Unigene13975_All	1630	11.23	5.16	9.74	5.81	5.83	4.65	5.27	3.03	2.15	-1.12E+00	1.50E-16	Down	-2.07E-01	1.50E-01		6.00E-03	9.83E-01		-3.19E-01	1.07E-01		-7.99E-01	5.83E-06		-1.29E+00	1.57E-12	Down	Unigene13975_All//gi|42562445|ref|NP_174435.2|//1.00E-128//endonuclease/exonuclease/phosphatase family protein [Arabidopsis thaliana]	Unigene13975_All//2.00E-126//AT1G31500| endonuclease/exonuclease/phosphatase family protein	Unigene13975_All//0.00E+00//TC173802		ko03018|RNA degradation		nr +
Unigene13977_All	1718	3.90	5.52	3.91	11.92	12.55	14.38	6.03	2.82	3.52	5.01E-01	7.48E-03		2.70E-03	9.89E-01		7.44E-02	6.01E-01		2.71E-01	1.65E-02		-1.10E+00	2.49E-11	Down	-7.75E-01	6.12E-07		Unigene13977_All//gi|297844282|ref|XP_002890022.1|//1.00E-143//XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335864|gb|EFH66281.1| XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13977_All//2.00E-100//AT1G13790| XH/XS domain-containing protein / XS zinc finger domain-containing protein	Unigene13977_All//0.00E+00//TC155456				nr -
Unigene13978_All	1812	1.07	3.02	1.50	3.22	3.65	4.16	2.10	1.31	1.28	1.50E+00	4.28E-08	Up	4.88E-01	2.35E-01		1.82E-01	5.11E-01		3.72E-01	9.53E-02		-6.76E-01	1.59E-02		-7.20E-01	7.67E-03		Unigene13978_All//gi|297844282|ref|XP_002890022.1|//1.00E-151//XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335864|gb|EFH66281.1| XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene13978_All//5.00E-120//AT1G13790| XH/XS domain-containing protein / XS zinc finger domain-containing protein	Unigene13978_All//0.00E+00//TC155456				nr -
Unigene13979_All	249	1.05	1.42	1.28	3.40	1.38	1.81	4.25	0.67	1.28	4.39E-01	7.01E-01		2.88E-01	8.10E-01		-1.30E+00	8.01E-02		-9.07E-01	2.47E-01		-2.66E+00	2.25E-04	Down	-1.73E+00	4.76E-03		Unigene13979_All//gi|37781556|gb|AAP42567.1|//2.00E-35//UDP-glucose 4-epimerase [Solanum tuberosum]	Unigene13979_All//7.00E-36//AT4G10960| UGE5 (UDP-D-glucose/UDP-D-galactose 4-epimerase 5); UDP-glucose 4-epimerase/ protein dimerization	Unigene13979_All//2.00E-32//FL577529		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism		nr +
Unigene1398_All	2631	3.34	2.85	2.04	24.18	18.83	17.82	9.88	3.32	3.91	-2.29E-01	2.69E-01		-7.09E-01	4.53E-04		-3.60E-01	1.91E-09		-4.40E-01	3.57E-12		-1.57E+00	5.15E-47	Down	-1.34E+00	3.40E-38	Down	Unigene1398_All//gi|15227816|ref|NP_179917.1|//1.00E-104//transport protein-related [Arabidopsis thaliana] >gi|75206690|sp|Q9SLN1.1|FPP7_ARATH RecName: Full=Filament-like plant protein 7; Short=AtFPP7	Unigene1398_All//1.00E-88//AT2G23360| transport protein-related	Unigene1398_All//0.00E+00//TC134907				nr +
Unigene13980_All	1258	3.70	4.47	3.22	6.85	5.89	3.99	4.97	1.93	2.06	2.72E-01	3.08E-01		-2.02E-01	5.16E-01		-2.19E-01	3.16E-01		-7.82E-01	4.85E-05		-1.37E+00	8.16E-10	Down	-1.27E+00	3.51E-09	Down	Unigene13980_All//gi|37781556|gb|AAP42567.1|//1.00E-172//UDP-glucose 4-epimerase [Solanum tuberosum]	Unigene13980_All//2.00E-154//AT4G10960| UGE5 (UDP-D-glucose/UDP-D-galactose 4-epimerase 5); UDP-glucose 4-epimerase/ protein dimerization	Unigene13980_All//0.00E+00//AI730444		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism		nr +
Unigene13981_All	1436	9.07	44.99	15.35	36.35	33.57	39.91	39.51	65.20	32.82	2.31E+00	2.89E-157	Up	7.59E-01	3.65E-10		-1.15E-01	1.56E-01		1.35E-01	7.79E-02		7.23E-01	7.71E-48		-2.68E-01	1.29E-05		Unigene13981_All//gi|225426282|ref|XP_002266388.1|//1.00E-119//PREDICTED: similar to B2 protein [Vitis vinifera]	Unigene13981_All//5.00E-95//AT5G42050| FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27090.1); Has 5084 Blast hits to 2870 proteins in 85 species: Archae - 0; Bacteria - 24; Metazoa - 270; Fungi - 58; Plants - 157; Viruses - 8; Other Eukaryotes - 4567 (source: NCBI BLink).	Unigene13981_All//0.00E+00//TC146652				nr +
Unigene13985_All	2970	0.44	0.34	0.32	7.35	4.77	2.13	6.05	2.74	2.24	-3.68E-01	5.31E-01		-4.49E-01	4.58E-01		-6.25E-01	5.85E-09		-1.79E+00	6.32E-42	Down	-1.14E+00	2.73E-20	Down	-1.43E+00	1.74E-29	Down	Unigene13985_All//gi|7329636|emb|CAB82701.1|//1.00E-117//centromere protein-like [Arabidopsis thaliana]	Unigene13985_All//4.00E-157//AT2G39300| unknown protein	Unigene13985_All//0.00E+00//ES826521		ko03440|Homologous recombination//ko03450|Non-homologous end-joining		nr +
Unigene13986_All	1266	7.19	4.76	7.36	6.26	6.83	3.35	9.85	2.77	3.52	-5.94E-01	1.80E-03		3.37E-02	8.75E-01		1.26E-01	5.96E-01		-9.00E-01	8.99E-06		-1.83E+00	3.39E-28	Down	-1.48E+00	8.97E-22	Down	Unigene13986_All//gi|297802006|ref|XP_002868887.1|//1.00E-128//inositol monophosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314723|gb|EFH45146.1| inositol monophosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene13986_All//1.00E-128//AT4G39120| IMPL2 (MYO-INOSITOL MONOPHOSPHATASE LIKE 2); 3'(2'),5'-bisphosphate nucleotidase/ L-galactose-1-phosphate phosphatase/ inositol or phosphatidylinositol phosphatase/ inositol-1(or 4)-monophosphatase	Unigene13986_All//0.00E+00//TC151998		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene13987_All	2132	4.34	3.54	3.40	7.27	8.27	7.03	1.33	1.06	0.52	-2.95E-01	1.34E-01		-3.55E-01	8.10E-02		1.87E-01	2.01E-01		-4.71E-02	7.75E-01		-3.28E-01	3.67E-01		-1.34E+00	5.86E-05	Down	Unigene13987_All//gi|224103771|ref|XP_002313187.1|//0.00E+00//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222849595|gb|EEE87142.1| nucleobase ascorbate transporter [Populus trichocarpa]	Unigene13987_All//0.00E+00//AT1G49960| xanthine/uracil permease family protein	Unigene13987_All//0.00E+00//gi|164293563|gb|ES812396.1|ES812396				nr +
Unigene1399_All	3649	1.42	1.07	0.98	8.10	5.61	6.83	4.92	1.83	1.33	-4.09E-01	1.27E-01		-5.38E-01	5.17E-02		-5.30E-01	5.16E-09		-2.45E-01	1.72E-02		-1.43E+00	2.19E-28	Down	-1.89E+00	2.62E-43	Down	Unigene1399_All//gi|15227816|ref|NP_179917.1|//4.00E-69//transport protein-related [Arabidopsis thaliana] >gi|75206690|sp|Q9SLN1.1|FPP7_ARATH RecName: Full=Filament-like plant protein 7; Short=AtFPP7	Unigene1399_All//5.00E-30//AT2G23360| transport protein-related	Unigene1399_All//0.00E+00//gi|164344693|gb|ES790545.1|ES790545				nr +
Unigene13993_All	1744	1.71	59.07	5.77	27.22	20.91	14.48	81.38	201.69	50.16	5.11E+00	0.00E+00	Up	1.75E+00	4.48E-17	Up	-3.81E-01	6.62E-08		-9.11E-01	4.31E-32		1.31E+00	0.00E+00	Up	-6.98E-01	7.28E-70		Unigene13993_All//gi|75313797|sp|Q9SR86.1|AGT23_ARATH//0.00E+00//Rec Name: Full=Alanine--glyoxylate aminotransferase 2 homolog 3, mitochondrial; AltName: Full=Beta-alanine-pyruvate aminotransferase 3; Flags: Precursor >gi|110740902|dbj|BAE98547.1| aminotransferase like protein [Arabidopsis thaliana]	Unigene13993_All//0.00E+00//AT3G08860| alanine--glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putative	Unigene13993_All//0.00E+00//TC134911		ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism		nr -
Unigene13994_All	750	5.02	3.18	2.63	42.38	19.88	39.98	140.82	49.93	455.59	-6.62E-01	3.62E-02		-9.35E-01	4.73E-03		-1.09E+00	5.71E-33	Down	-8.38E-02	4.74E-01		-1.50E+00	2.94E-175	Down	1.69E+00	0.00E+00	Up	Unigene13994_All//gi|291264192|gb|ADD85331.1|//1.00E-46//codeine O-demethylase [Papaver somniferum]	Unigene13994_All//2.00E-43//AT1G17020| SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc	Unigene13994_All//0.00E+00//gi|163360666|gb|EX167980.1|EX167980		ko00941|Flavonoid biosynthesis		nr -
Unigene13995_All	1179	0.93	2.45	1.40	17.32	8.18	13.22	200.32	71.89	605.28	1.39E+00	2.96E-04	Up	5.87E-01	2.72E-01		-1.08E+00	4.96E-21	Down	-3.90E-01	1.19E-03		-1.48E+00	0.00E+00	Down	1.60E+00	0.00E+00	Up	Unigene13995_All//gi|297842633|ref|XP_002889198.1|//2.00E-74//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297335039|gb|EFH65457.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene13995_All//1.00E-74//AT1G78550| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene13995_All//0.00E+00//TC166096		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene13996_All	1626	4.83	2.49	2.29	5.88	4.26	5.11	5.43	3.26	3.92	-9.53E-01	5.77E-06		-1.07E+00	1.02E-06	Down	-4.67E-01	8.48E-03		-2.03E-01	3.42E-01		-7.35E-01	2.11E-05		-4.71E-01	5.13E-03		Unigene13996_All//gi|46093880|gb|AAS79793.1|//1.00E-160//sucrose phosphate phosphatase [Malus x domestica]	Unigene13996_All//8.00E-150//AT2G35840| sucrose-phosphatase 1 (SPP1)	Unigene13996_All//0.00E+00//CO095362		ko00500|Starch and sucrose metabolism		nr -
Unigene140_All	1408	1.78	0.65	1.78	1.66	2.59	2.25	1.62	1.90	2.52	-1.46E+00	4.80E-04	Down	-5.00E-03	9.89E-01		6.41E-01	4.48E-02		4.33E-01	2.45E-01		2.29E-01	5.57E-01		6.35E-01	2.47E-02		Unigene140_All//gi|224110992|ref|XP_002332999.1|//3.00E-55//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834484|gb|EEE72961.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene140_All//3.00E-09//AT4G26090| RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding	Unigene140_All//3.00E-48//ES820741		ko04626|Plant-pathogen interaction		nr +
Unigene14000_All	2835	0.83	1.02	0.62	1.44	1.43	2.28	11.86	16.22	44.98	2.95E-01	4.32E-01		-4.22E-01	3.51E-01		-7.50E-03	9.69E-01		6.61E-01	4.12E-03		4.52E-01	9.36E-11		1.92E+00	0.00E+00	Up	Unigene14000_All//gi|224144210|ref|XP_002325221.1|//0.00E+00//f-box family protein [Populus trichocarpa] >gi|222866655|gb|EEF03786.1| f-box family protein [Populus trichocarpa]	Unigene14000_All//0.00E+00//AT2G25490| EBF1 (EIN3-BINDING F BOX PROTEIN 1); protein binding / ubiquitin-protein ligase	Unigene14000_All//0.00E+00//TC170108		ko04626|Plant-pathogen interaction//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene14002_All	800	5.30	4.50	6.12	6.54	19.84	28.23	8.93	16.56	16.18	-2.36E-01	4.38E-01		2.09E-01	4.86E-01		1.60E+00	4.34E-28	Up	2.11E+00	6.33E-53	Up	8.91E-01	2.33E-10		8.58E-01	7.88E-10		Unigene14002_All//gi|297599775|ref|NP_001047802.2|//1.00E-72//Os02g0693500 [Oryza sativa Japonica Group] >gi|255671179|dbj|BAF09716.2| Os02g0693500 [Oryza sativa Japonica Group]	Unigene14002_All//3.00E-71//AT4G17790| INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (InterPro:IPR015414); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G71940.1); Has 2258 Blast hits to 2258 proteins in 517 species: Archae - 4; Bacteria - 1129; Metazoa - 188; Fungi - 22; Plants - 104; Viruses - 0; Other Eukaryotes - 811 (source: NCBI BLink).	Unigene14002_All//0.00E+00//TC143707				nr -

Unigene14003_All	1513	0.76	3.08	1.41	2.24	6.58	6.27	5.03	13.56	10.95	2.02E+00	3.52E-10	Up	8.88E-01	5.42E-02		1.55E+00	5.50E-17	Up	1.49E+00	4.61E-14	Up	1.43E+00	2.04E-32	Up	1.12E+00	9.46E-19	Up	Unigene14003_All//gi|51997111|emb|CAH03736.1|//1.00E-71//Gtk16 protein [Gerbera hybrid cultivar]	Unigene14003_All//8.00E-67//AT4G17790| INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (InterPro:IPR015414); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G71940.1); Has 2258 Blast hits to 2258 proteins in 517 species: Archae - 4; Bacteria - 1129; Metazoa - 188; Fungi - 22; Plants - 104; Viruses - 0; Other Eukaryotes - 811 (source: NCBI BLink).	Unigene14003_All//0.00E+00//TC143707				nr -
Unigene14005_All	1494	2.17	4.54	1.53	4.07	4.98	3.75	6.88	2.18	4.51	1.07E+00	3.85E-06	Up	-5.03E-01	1.67E-01		2.92E-01	2.06E-01		-1.18E-01	6.79E-01		-1.66E+00	1.96E-20	Down	-6.10E-01	7.88E-05		Unigene14005_All//gi|15231088|ref|NP_190761.1|//1.00E-147//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|30725344|gb|AAP37694.1| At3g51930 [Arabidopsis thaliana]	Unigene14005_All//6.00E-146//AT3G51930| transducin family protein / WD-40 repeat family protein			ko03022|Basal transcription factors		nr -
Unigene14006_All	1782	17.76	9.10	11.89	11.77	10.26	9.28	7.92	6.87	3.60	-9.65E-01	4.54E-22		-5.79E-01	4.22E-09		-1.98E-01	1.19E-01		-3.43E-01	4.31E-03		-2.06E-01	1.56E-01		-1.14E+00	1.39E-16	Down	Unigene14006_All//gi|297842783|ref|XP_002889273.1|//1.00E-155//PDE318 [Arabidopsis lyrata subsp. lyrata] >gi|297335114|gb|EFH65532.1| PDE318 [Arabidopsis lyrata subsp. lyrata]	Unigene14006_All//3.00E-155//AT1G80770| PDE318 (pigment defective 318); GTP binding	Unigene14006_All//0.00E+00//gi|164323457|gb|ES801515.1|ES801515				nr -
Unigene14008_All	775	132.39	79.63	106.50	33.10	37.23	27.91	15.22	8.47	5.40	-7.33E-01	5.43E-44		-3.14E-01	1.72E-09		1.70E-01	1.18E-01		-2.46E-01	2.78E-02		-8.46E-01	1.30E-08		-1.50E+00	6.86E-21	Down	Unigene14008_All//gi|186886514|gb|ACX30639.1|//3.00E-89//extracellular Cu/Zn superoxide dismutase [Gossypium hirsutum]	Unigene14008_All//7.00E-66//AT5G18100| CSD3 (copper/zinc superoxide dismutase 3); superoxide dismutase	Unigene14008_All//0.00E+00//ES828180		ko04146|Peroxisome		nr +
Unigene14009_All	1926	11.17	8.31	11.67	2.95	5.88	2.04	2.41	0.61	0.81	-4.26E-01	3.25E-04		6.35E-02	6.21E-01		9.96E-01	6.25E-10		-5.31E-01	3.48E-02		-1.99E+00	3.27E-12	Down	-1.58E+00	1.97E-09	Down	Unigene14009_All//gi|186886514|gb|ACX30639.1|//1.00E-88//extracellular Cu/Zn superoxide dismutase [Gossypium hirsutum]	Unigene14009_All//2.00E-65//AT5G18100| CSD3 (copper/zinc superoxide dismutase 3); superoxide dismutase	Unigene14009_All//0.00E+00//gi|164315784|gb|ES828180.1|ES828180		ko04146|Peroxisome		nr -
Unigene14010_All	1807	12.94	8.52	8.13	4.49	6.61	4.00	3.81	1.73	2.65	-6.03E-01	9.54E-08		-6.70E-01	9.24E-09		5.57E-01	3.30E-04		-1.68E-01	4.74E-01		-1.14E+00	3.11E-08	Down	-5.28E-01	6.33E-03		Unigene14010_All//gi|297794363|ref|XP_002865066.1|//1.00E-156//GTP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297310901|gb|EFH41325.1| GTP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14010_All//4.00E-141//AT5G66470| GTP binding / RNA binding	Unigene14010_All//0.00E+00//TC166638				nr +
Unigene14016_All	1212	20.68	6.90	13.88	12.25	11.05	3.91	4.88	3.14	8.32	-1.58E+00	1.78E-37	Down	-5.75E-01	2.86E-07		-1.48E-01	3.75E-01		-1.65E+00	1.36E-25	Down	-6.38E-01	3.26E-03		7.68E-01	1.19E-06		Unigene14016_All//gi|225439143|ref|XP_002271738.1|//3.00E-99//PREDICTED: R2R3 MYB60 transcription factor [Vitis vinifera] >gi|195376735|gb|ACF21938.1| R2R3 MYB60 transcription factor [Vitis vinifera]	Unigene14016_All//4.00E-78//AT1G08810| MYB60 (myb domain protein 60); DNA binding / transcription factor	Unigene14016_All//4.00E-118//gi|48803680|gb|CO104994.1|CO104994	MYB			nr +
Unigene14018_All	1583	2.97	3.04	2.42	5.38	3.87	2.14	4.67	3.09	2.49	3.17E-02	9.24E-01		-2.97E-01	3.38E-01		-4.75E-01	1.24E-02		-1.33E+00	5.15E-11	Down	-5.98E-01	1.76E-03		-9.08E-01	1.49E-06		Unigene14018_All//gi|30679518|ref|NP_187199.2|//1.00E-169//RAD9 [Arabidopsis thaliana] >gi|115646872|gb|ABJ17148.1| At3g05180 [Arabidopsis thaliana]	Unigene14018_All//4.00E-163//AT3G05480| RAD9	Unigene14018_All//0.00E+00//TC154549				nr -
Unigene14019_All	1452	17.30	82.95	38.10	11.36	15.70	21.62	13.22	32.04	15.97	2.26E+00	2.11E-285	Up	1.14E+00	4.58E-48	Up	4.67E-01	1.33E-05		9.29E-01	7.41E-22		1.28E+00	5.03E-61	Up	2.73E-01	7.01E-03		Unigene14019_All//gi|30697614|ref|NP_201008.2|//3.00E-83//AT-HSFB2A; DNA binding / transcription factor [Arabidopsis thaliana] >gi|11386851|sp|Q9SCW4.1|HFB2A_ARATH RecName: Full=Heat stress transcription factor B-2a; Short=AtHsfB2a; AltName: Full=Heat shock factor protein 6; Short=HSF 6; AltName: Full=Heat shock transcription factor 6; Short=HSTF 6; AltName: Full=AtHsf-22 >gi|6624616|emb|CAB63802.1| heat shock factor 6 [Arabidopsis thaliana] >gi|10176919|dbj|BAB10163.1| heat shock factor 6 [Arabidopsis thaliana] >gi|110739232|dbj|BAF01530.1| heat shock factor 6 [Arabidopsis thaliana]	Unigene14019_All//2.00E-77//AT5G62020| AT-HSFB2A; DNA binding / transcription factor	Unigene14019_All//0.00E+00//TC175677	HSF			nr -
Unigene14021_All	938	48.25	47.37	53.36	60.17	48.68	46.17	43.90	27.49	21.45	-2.64E-02	7.67E-01		1.45E-01	8.49E-02		-3.06E-01	2.46E-06		-3.82E-01	1.69E-08		-6.75E-01	3.29E-19		-1.03E+00	5.58E-40	Down	Unigene14021_All//gi|78191476|gb|AB029959.1|//2.00E-86//ubiquitin fusion-degradation protein-like [Solanum tuberosum]	Unigene14021_All//3.00E-65//AT2G21270| ubiquitin fusion degradation UFD1 family protein	Unigene14021_All//0.00E+00//TC136082				nr -
Unigene14023_All	2319	5.44	2.16	2.32	9.95	9.77	6.97	8.42	1.77	3.90	-1.33E+00	5.86E-15	Down	-1.23E+00	9.90E-13	Down	-2.56E-02	8.48E-01		-5.13E-01	3.50E-06		-2.25E+00	3.32E-57	Down	-1.11E+00	9.27E-22	Down	Unigene14023_All//gi|297790440|ref|XP_002863111.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308933|gb|EFH39370.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14023_All//0.00E+00//AT1G69910| protein kinase family protein	Unigene14023_All//0.00E+00//TC170209		ko04626|Plant-pathogen interaction		nr +
Unigene14025_All	1032	3.40	2.50	4.08	18.92	16.15	12.91	2.87	1.30	0.77	-4.40E-01	1.90E-01		2.63E-01	4.03E-01		-2.29E-01	7.60E-02		-5.52E-01	5.28E-06		-1.15E+00	4.94E-04	Down	-1.89E+00	7.36E-08	Down	Unigene14025_All//gi|115476754|ref|NP_001061973.1|//2.00E-27//Os08g0459300 [Oryza sativa Japonica Group] >gi|113623942|dbj|BAF23887.1| Os08g0459300 [Oryza sativa Japonica Group]	Unigene14025_All//3.00E-19//AT1G02180| ferredoxin-related	Unigene14025_All//0.00E+00//CO093199				nr -
Unigene14026_All	1064	9.54	7.14	6.31	35.39	28.77	21.01	10.45	2.91	2.88	-4.17E-01	2.14E-02		-5.97E-01	1.35E-03		-2.99E-01	2.82E-04		-7.52E-01	1.43E-18		-1.85E+00	1.56E-25	Down	-1.86E+00	1.39E-26	Down	Unigene14026_All//gi|115476754|ref|NP_001061973.1|//5.00E-60//Os08g0459300 [Oryza sativa Japonica Group] >gi|113623942|dbj|BAF23887.1| Os08g0459300 [Oryza sativa Japonica Group]	Unigene14026_All//1.00E-36//AT1G02180| ferredoxin-related	Unigene14026_All//0.00E+00//TC159721				nr +
Unigene14027_All	1170	23.03	55.30	40.19	23.97	31.85	40.26	44.88	87.09	91.36	1.26E+00	6.27E-68	Up	8.03E-01	4.58E-23		4.10E-01	4.84E-07		7.48E-01	1.15E-22		9.56E-01	1.64E-83		1.03E+00	2.32E-100	Up	Unigene14027_All//gi|18394229|ref|NP_563971.1|//1.00E-33//MBD10; DNA binding / methyl-CpG binding [Arabidopsis thaliana] >gi|5103831|gb|AAD39661.1|AC007591_26 ESTs gb|H37032, gb|R6425, gb|Z34651, gb|N37268, gb|AA713172 and gb|Z34241 come from this gene [Arabidopsis thaliana] >gi|20453139|gb|AAM19811.1| At1g15340/F9L1_28 [Arabidopsis thaliana] >gi|56382007|gb|AAV85722.1| At1g15340 [Arabidopsis thaliana]	Unigene14027_All//5.00E-35//AT1G15340| MBD10; DNA binding / methyl-CpG binding	Unigene14027_All//0.00E+00//TC140377				nr +
Unigene14028_All	1702	2.09	1.43	3.66	11.44	12.02	9.02	5.32	1.84	3.02	-5.49E-01	9.40E-02		8.08E-01	1.03E-03		7.06E-02	6.32E-01		-3.43E-01	6.33E-03		-1.53E+00	3.33E-16	Down	-8.16E-01	1.14E-06		Unigene14028_All//gi|240254583|ref|NP_181015.6|//1.00E-147//AIR9; protein binding [Arabidopsis thaliana]	Unigene14028_All//1.00E-110//AT2G34680| AIR9; protein binding					nr -
Unigene14029_All	1006	3.28	2.22	1.38	6.14	5.72	3.55	6.09	6.81	5.43	-5.64E-01	9.92E-02		-1.25E+00	6.16E-04	Down	-1.03E-01	7.18E-01		-7.92E-01	6.94E-04		1.61E-01	4.87E-01		-1.68E-01	4.68E-01		Unigene14029_All//gi|240255958|ref|NP_567522.5|//5.00E-57//peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi|15912321|gb|AAL08294.1| AT4g17070/d14565c [Arabidopsis thaliana] >gi|23505941|gb|AAN28830.1| At4g17070/d14565c [Arabidopsis thaliana]	Unigene14029_All//3.00E-58//AT4G17070| peptidyl-prolyl cis-trans isomerase	Unigene14029_All//0.00E+00//ES801988				nr -
Unigene14032_All	1869	22.79	26.19	30.09	54.61	49.45	85.86	41.35	32.78	17.22	2.01E-01	1.05E-02		4.01E-01	2.48E-08		-1.43E-01	4.92E-03		6.53E-01	6.45E-60		-3.35E-01	2.17E-10		-1.26E+00	2.87E-102	Down	Unigene14032_All//gi|18402794|ref|NP_564555.1|//0.00E+00//ATMTK (ARABIDOPSIS THALIANA S-METHYL-5-THIORIBOSE KINASE); S-methyl-5-thioribose kinase [Arabidopsis thaliana] >gi|165760998|pdb|2PYW|A Chain A, Structure Of A. Thaliana 5-Methylthioribose Kinase In Complex With Adp And Mtr >gi|165760999|pdb|2PYW|B Chain B, Structure Of A. Thaliana 5-Methylthioribose Kinase In Complex With Adp And Mtr >gi|15982811|gb|AAL09753.1| At1g98820/F10F5_1 [Arabidopsis thaliana] >gi|19699220|gb|AAL90976.1| At1g98820/F10F5_1 [Arabidopsis thaliana]	Unigene14032_All//0.00E+00//AT1G49820| ATMTK (ARABIDOPSIS THALIANA S-METHYL-5-THIORIBOSE KINASE); S-methyl-5-thioribose kinase	Unigene14032_All//0.00E+00//TC143991				nr -
Unigene14035_All	2189	1.96	1.53	2.26	5.48	4.36	3.82	9.27	3.95	3.79	-3.59E-01	2.35E-01		2.07E-01	4.89E-01		-3.32E-01	4.11E-02		-5.23E-01	1.14E-03		-1.23E+00	1.31E-25	Down	-1.29E+00	1.92E-28	Down	Unigene14035_All//gi|17065078|gb|AAL32693.1|//1.00E-157//Unknown protein [Arabidopsis thaliana]	Unigene14035_All//2.00E-158//AT5G27970| binding	Unigene14035_All//0.00E+00//TC175646				nr -
Unigene14036_All	2032	0.44	0.50	0.05	0.56	0.68	0.36	1.08	0.41	0.67	1.88E-01	7.64E-01		-3.06E+00	2.25E-03		2.66E-01	6.81E-01		-6.65E-01	3.16E-01		-1.40E+00	4.75E-04	Down	-6.99E-01	5.93E-02		Unigene14036_All//gi|15241106|ref|NP_198149.1|//0.00E+00//binding [Arabidopsis thaliana]	Unigene14036_All//0.00E+00//AT5G27970| binding	Unigene14036_All//0.00E+00//TC175646				nr -

Unigene14037_All	1496	61.06	13.48	29.76	51.98	25.04	32.42	44.71	11.45	24.53	-2.18E+00	2.40E-208	Down	-1.04E+00	8.19E-68	Down	-1.05E+00	1.04E-75	Down	-6.81E-01	9.02E-32		-1.96E+00	4.40E-163	Down	-8.66E-01	3.88E-48		Unigene14037_All//gi|115440019|ref|NP_001044289.1|//1.00E-143//Os01g0756600 [Oryza sativa Japonica Group] >gi|113533820|dbj|BAF06203.1|Os01g0756600 [Oryza sativa Japonica Group]	Unigene14037_All//0.00E+00//TC131341				nr +
Unigene14039_All	1965	39.89	83.21	57.10	30.52	25.32	27.97	12.76	18.89	18.51	1.06E+00	3.10E-129	Up	5.18E-01	3.53E-25		-2.69E-01	2.18E-05		-1.26E-01	9.45E-02		5.66E-01	6.61E-13		5.37E-01	6.53E-12		Unigene14039_All//gi|15234236|ref|NP_192894.1|//1.00E-134//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|30681816|ref|NP_849359.1| haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|166488789|gb|AAL25585.1| AT4g11570/F25E4_190 [Arabidopsis thaliana] >gi|20466125|gb|AAM19984.1| AT4g11570/F25E4_190 [Arabidopsis thaliana]	Unigene14039_All//2.00E-129//AT4G11570| haloacid dehalogenase-like hydrolase family protein	Unigene14039_All//0.00E+00//TC136455		ko00740|Riboflavin metabolism		nr -
Unigene14043_All	1662	4.97	3.96	2.72	44.78	27.20	21.06	7.61	3.62	2.21	-3.28E-01	1.17E-01		-8.69E-01	3.58E-05		-7.19E-01	9.40E-38		-1.09E+00	4.91E-67	Down	-1.07E+00	3.48E-13	Down	-1.79E+00	1.46E-28	Down	Unigene14043_All//gi|237682426|gb|ACR10262.1|//1.00E-140//UDP-glucosyl transferase 74b1 [Brassica rapa subsp. pekinensis]	Unigene14043_All//2.00E-116//AT2G43820| UGT74F2 (UDP-GLUCOSYLTRANSFERASE 74F2); UDP-glucose:4-aminobenzoate acylglucosyltransferase/ UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene14043_All//0.00E+00//TC155323		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr +
Unigene14045_All	2064	0.46	0.17	0.39	0.29	0.38	0.09	1.78	0.45	0.48	-1.41E+00	5.70E-02		-2.38E-01	7.23E-01		4.06E-01	6.32E-01		-1.73E+00	9.04E-02		-2.00E+00	7.23E-10	Down	-1.89E+00	1.62E-09	Down	Unigene14045_All//gi|15235211|ref|NP_195130.1|//7.00E-85//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|51536502|gb|AAU05489.1| At4g34040 [Arabidopsis thaliana] >gi|56381955|gb|AAV85696.1| At4g34040 [Arabidopsis thaliana]	Unigene14045_All//2.00E-68//AT4G34040| zinc finger (C3HC4-type RING finger) family protein	Unigene14045_All//0.00E+00//CO124550				nr +
Unigene14055_All	2425	21.94	55.98	43.41	18.92	31.79	30.51	16.56	19.51	17.73	1.35E+00	3.17E-157	Up	9.84E-01	7.75E-72		7.49E-01	1.17E-40		6.89E-01	1.18E-30		2.36E-01	7.68E-04		9.79E-02	2.23E-01		Unigene14055_All//gi|297792717|ref|XP_002861243.1|//0.00E+00//OBP3-responsive gene 1 [Arabidopsis lyrata subsp. lyrata] >gi|297310078|gb|EFH40502.1| OBP3-responsive gene 1 [Arabidopsis lyrata subsp. lyrata]	Unigene14055_All//0.00E+00//AT5G53450| OBG1 (OBP3-responsive gene 1); ATP binding / kinase/ protein kinase	Unigene14055_All//0.00E+00//TC139281				nr +
Unigene14056_All	2424	1.14	2.61	1.98	1.56	2.61	2.05	1.81	1.45	1.23	1.19E+00	9.47E-07	Up	7.89E-01	5.84E-03		7.43E-01	9.08E-04		3.92E-01	1.73E-01		-3.25E-01	2.36E-01		-5.58E-01	2.53E-02		Unigene14056_All//gi|297792717|ref|XP_002861243.1|//0.00E+00//OBP3-responsive gene 1 [Arabidopsis lyrata subsp. lyrata] >gi|297310078|gb|EFH40502.1| OBP3-responsive gene 1 [Arabidopsis lyrata subsp. lyrata]	Unigene14056_All//0.00E+00//AT5G53450| OBG1 (OBP3-responsive gene 1); ATP binding / kinase/ protein kinase	Unigene14056_All//0.00E+00//TC139281				nr -
Unigene14058_All	2350	1.80	1.92	2.36	18.21	11.93	9.11	7.11	3.95	2.90	8.96E-02	7.55E-01		3.86E-01	1.52E-01		-6.10E-01	2.03E-16		-9.99E-01	9.78E-34		-8.48E-01	6.78E-12		-1.29E+00	1.33E-23	Down	Unigene14058_All//gi|297792079|ref|XP_002863924.1|//0.00E+00//phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309759|gb|EFH40183.1| phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14058_All//0.00E+00//AT5G48800| phototropic-responsive NPH3 family protein	Unigene14058_All//0.00E+00//TC150737				nr +
Unigene14059_All	545	0.19	1.67	0.10	1.01	1.39	0.66	3.80	1.38	1.54	3.12E+00	1.14E-03		-9.75E-01	7.21E-01		4.67E-01	6.07E-01		-6.01E-01	5.66E-01		-1.46E+00	4.45E-04	Down	-1.31E+00	9.85E-04	Down	Unigene14059_All//gi|297848940|ref|XP_002892351.1|//4.00E-41//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297338193|gb|EFH68610.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14059_All//5.00E-42//AT1G06590| unknown protein	Unigene14059_All//0.00E+00//TC164425				nr -
Unigene1406_All	2746	12.10	1.94	3.63	53.61	39.25	33.12	67.52	7.88	21.57	-2.64E+00	1.52E-95	Down	-1.74E+00	2.12E-54	Down	-4.50E-01	6.22E-32		-6.95E-01	8.55E-62		-3.10E+00	0.00E+00	Down	-1.65E+00	0.00E+00	Down	Unigene1406_All//gi|292630923|sp|A5JTQ3.1|XYL2_MEDVA//0.00E+00//RecName: Full=Beta-xylosidase/alpha-L-arabinofuranosidase 2; AltName: Full=Xylan 1,4-beta-xylosidase/Alpha-N-arabinofuranosidase 2; Short=MsXyl2; Includes: RecName: Full=Beta-xylosidase; AltName: Full=1,4-beta-D-xylan xylohydrolase; AltName: Full=Xylan 1,4-beta-xylosidase; Includes: RecName: Full=Alpha-N-arabinofuranosidase; AltName: Full=Alpha-L-arabinofuranosidase; Short=Arabinosidase; Flags: Precursor >gi|146762263|gb|ABQ45228.1| beta-xylosidase/alpha-L-arabinosidase [Medicago sativa subsp. x varia]	Unigene1406_All//0.00E+00//AT5G64570| XYL4; hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Unigene1406_All//0.00E+00//TC144576		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr +
Unigene14062_All	476	14.84	4.47	7.72	22.29	20.62	9.96	10.21	1.05	2.18	-1.73E+00	1.80E-12	Down	-9.43E-01	4.42E-05		-1.13E-01	5.82E-01		-1.16E+00	4.36E-11	Down	-3.28E+00	9.74E-22	Down	-2.23E+00	4.16E-15	Down	Unigene14062_All//gi|110737096|dbj|BAF00500.1|//6.00E-25//thaumatin-like protein [Arabidopsis thaliana]	Unigene14062_All//2.00E-11//AT4G38660| thaumatin, putative	Unigene14062_All//0.00E+00//TC166743				nr -
Unigene14063_All	1466	39.51	9.37	15.58	62.11	51.79	21.63	13.30	1.40	1.55	-2.08E+00	2.37E-124	Down	-1.34E+00	8.62E-65	Down	-2.62E-01	1.65E-07		-1.52E+00	5.18E-138	Down	-3.25E+00	9.04E-85	Down	-3.10E+00	9.91E-84	Down	Unigene14063_All//gi|110737096|dbj|BAF00500.1|//1.00E-117//thaumatin-like protein [Arabidopsis thaliana]	Unigene14063_All//9.00E-103//AT4G38660| thaumatin, putative	Unigene14063_All//0.00E+00//gi|164327512|gb|ES828314.1|ES828314				nr -
Unigene14064_All	3171	0.68	0.53	0.13	8.23	10.53	7.76	50.73	18.73	26.09	-3.60E-01	4.08E-01		-2.33E+00	1.26E-05	Down	3.56E-01	4.96E-05		-8.47E-02	5.23E-01		-1.44E+00	2.41E-251	Down	-9.59E-01	7.01E-136		Unigene14064_All//gi|259019463|gb|ACV90014.1|//1.00E-30//rubber elongation factor [Morus alba]	Unigene14064_All//4.00E-28//AT3G05500| rubber elongation factor (REF) family protein	Unigene14064_All//0.00E+00//TC176139				nr +
Unigene14065_All	1575	4.29	2.67	5.68	15.59	10.08	10.64	3.70	1.83	1.39	-6.82E-01	2.47E-03		4.07E-01	4.71E-02		-6.30E-01	3.76E-10		-5.52E-01	2.27E-07		-1.02E+00	4.71E-06	Down	-1.41E+00	5.81E-10	Down	Unigene14065_All//gi|90093310|gb|AB085168.1|//7.00E-95//At3g22970 [Arabidopsis thaliana]	Unigene14065_All//3.00E-85//AT2G38820| unknown protein	Unigene14065_All//0.00E+00//DW488686				nr +
Unigene14066_All	1292	101.16	49.06	55.48	160.20	175.77	157.69	122.00	96.60	69.44	-1.04E+00	3.90E-101	Down	-8.67E-01	7.07E-72		1.34E-01	3.09E-05		-2.28E-02	6.18E-01		-3.37E-01	1.63E-20		-8.13E-01	8.92E-101		Unigene14066_All//gi|211906440|gb|ACJ11713.1|//1.00E-174//UDP-L-rhamnose synthase [Gossypium hirsutum]	Unigene14066_All//6.00E-151//AT1G63000| NRS/ER (NUCLEOTIDE-RHAMNOSE SYNTHASE/EPIMERASE-REDUCTASE); UDP-4-keto-6-deoxy-glucose-3,5-epimerase/ UDP-4-keto-rhamnose-4-keto-reductase/ dTDP-4-dehydrorhamnose 3,5-epimerase/ dTDP-4-dehydrorhamnose reductase	Unigene14066_All//0.00E+00//TC131118		ko00520|Amino sugar and nucleotide sugar metabolism//ko00523|Polyketide sugar unit biosynthesis		nr +
Unigene14067_All	886	9.74	25.11	24.46	35.76	46.95	55.00	83.80	53.92	98.25	1.37E+00	1.02E-26	Up	1.33E+00	3.43E-24	Up	3.93E-01	2.98E-07		6.21E-01	4.72E-17		-6.36E-01	1.25E-30		2.30E-01	2.83E-06		Unigene14067_All//gi|225346675|gb|ACN86359.1|//1.00E-103//GID1-4 [Gossypium hirsutum]	Unigene14067_All//3.00E-85//AT3G05120| GID1A (GA INSENSITIVE DWARF1A); hydrolase	Unigene14067_All//0.00E+00//TC173019				nr +
Unigene14068_All	953	2.75	3.78	1.51	3.76	3.32	3.03	12.82	10.26	6.40	4.60E-01	1.62E-01		-8.64E-01	3.52E-02		-1.79E-01	6.03E-01		-3.11E-01	3.95E-01		-3.21E-01	3.13E-02		-1.00E+00	6.08E-12	Down			Unigene14068_All//0.00E+00//TC159093				
Unigene1407_All	1448	13.84	65.05	23.94	21.64	16.00	25.36	22.31	29.33	52.25	2.23E+00	9.05E-220	Up	7.91E-01	1.02E-16		-4.35E-01	8.67E-07		2.29E-01	1.22E-02		3.95E-01	5.80E-08		1.23E+00	6.15E-95	Up	Unigene1407_All//gi|15240452|ref|NP_200316.1|//1.00E-102//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75170788|sp|Q9FIA1.1|GDLS7_ARATH RecName: Full=GDSL esterase/lipase At5g55050; AltName: Full=Extracellular lipase At5g55050; Flags: Precursor >gi|10177380|dbj|BAB10579.1| GDSL-motif lipase/hydrolase-like protein [Arabidopsis thaliana]	Unigene1407_All//2.00E-94//AT5G55050| GDSL-motif lipase/hydrolase family protein	Unigene1407_All//0.00E+00//TC158324				nr -
Unigene14071_All	2078	5.01	6.36	3.92	12.15	9.21	8.00	6.90	2.55	3.51	3.45E-01	2.91E-02		-3.54E-01	6.25E-02		-4.00E-01	7.43E-05		-6.04E-01	8.85E-09		-1.43E+00	5.77E-23	Down	-9.75E-01	2.94E-13		Unigene14071_All//gi|36950063|gb|AAC62626.1|//1.00E-129//rac GTPase activating protein 3 [Lotus japonicus]	Unigene14071_All//1.00E-124//AT4G03100| rac GTPase activating protein, putative	Unigene14071_All//0.00E+00//gi|78328469|gb|DT548743.1|DT548743				nr +
Unigene14072_All	1001	35.96	26.42	30.43	47.18	62.92	53.65	4.82	1.25	2.59	-4.45E-01	5.87E-07		-2.41E-01	1.21E-02		4.15E-01	7.98E-12		1.85E-01	1.36E-02		-1.94E+00	2.97E-12	Down	-8.96E-01	1.69E-04		Unigene14072_All//gi|226500126|ref|NP_001149571.1|//1.00E-44//lactoylglutathione lyase [Zea mays] >gi|195628124|gb|ACG35892.1| lactoylglutathione lyase [Zea mays]	Unigene14072_All//2.00E-38//AT1G80160| lactoylglutathione lyase family protein / glyoxalase I family protein					nr +
Unigene14075_All	571	0.00	0.00	0.00	0.09	0.00	0.00	4.07	27.89	7.05	null	null		null	null		-6.45E+00	5.56E-01		-6.45E+00	6.36E-01		2.78E+00	4.28E-59	Up	7.91E-01	2.66E-03		Unigene14075_All//gi|4127662|emb|CAA72062.1|//6.00E-64//fructosidase [Cichorium intybus]	Unigene14075_All//5.00E-61//AT5G11920| AtcwINV6 (6-&1-fructan exohydrolase); hydrolase, hydrolyzing O-glycosyl compounds / inulinase/ levanase	Unigene14075_All//0.00E+00//gi|164317843|gb|ES818324.1|ES818324		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene14076_All	2026	1.99	0.80	0.92	14.70	14.14	8.98	116.84	157.05	118.57	-1.31E+00	3.13E-05	Down	-1.11E+00	5.49E-04	Down	-5.62E-02	6.41E-01		-7.11E-01	1.81E-13		4.27E-01	1.37E-62		2.12E-02	5.75E-01		Unigene14076_All//gi|53127612|emb|CAD49079.1|//0.00E+00//fructan 1-exohydrolase [Campanula rapunculoides]	Unigene14076_All//2.00E-179//AT3G13790| ATBFRUCT1; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene14076_All//0.00E+00//TC152854		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -

Unigene14078_All	1789	7.25	1.30	2.77	23.14	18.05	12.98	11.91	4.56	4.70	-2.48E+00	5.22E-35	Down	-1.39E+00	1.12E-15	Down	-3.58E-01	2.86E-06		-8.35E-01	3.08E-24		-1.39E+00	3.70E-32	Down	-1.34E+00	1.46E-31	Down	Unigene14078_All//gi|75150628|sp|Q8GU14.1|UGP16_ARATH//1.00E-159//RecName: Full=Uncharacterized GPI-anchored protein At1g61900; Flags: Precursor >gi|27311769|gb|AA000850.1| Unknown protein [Arabidopsis thaliana] >gi|30387511|gb|AAF31921.1| At1g61900 [Arabidopsis thaliana]	Unigene14078_All//4.00E-151//AT1G61900| unknown protein	Unigene14078_All//0.00E+00//TC153912				nr -
Unigene14079_All	1830	5.49	3.77	3.23	8.44	8.26	6.64	10.03	4.59	5.33	-5.44E-01	2.58E-03		-7.65E-01	4.50E-05		-3.07E-02	8.51E-01		-3.46E-01	1.65E-02		-1.13E+00	2.52E-20	Down	-9.11E-01	5.22E-15		Unigene14079_All//gi|297842389|ref|XP_002889076.1|//1.00E-135//integral membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334917|gb|EFH65335.1| integral membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14079_All//3.00E-108//AT1G76340| integral membrane family protein	Unigene14079_All//0.00E+00//TC129672				nr +
Unigene14081_All	1195	31.83	209.00	93.84	25.14	36.51	51.74	22.25	17.24	12.74	2.72E+00	0.00E+00	Up	1.56E+00	2.89E-157	Up	5.39E-01	4.22E-13		1.04E+00	2.55E-51	Up	-3.68E-01	9.36E-05		-8.05E-01	1.76E-17		Unigene14081_All//gi|224071850|ref|XP_002303583.1|//4.00E-92//glutathione peroxidase [Populus trichocarpa] >gi|222841015|gb|EEE78562.1| glutathione peroxidase [Populus trichocarpa]	Unigene14081_All//4.00E-75//AT4G11600| ATGPX6 (GLUTATHIONE PEROXIDASE 6); glutathione peroxidase	Unigene14081_All//0.00E+00//TC140215		ko00480|Glutathione metabolism//ko00590|Arachidonic acid metabolism		nr -
Unigene14084_All	1329	43.90	64.47	65.63	58.36	82.42	99.88	13.74	34.59	17.06	5.55E-01	1.15E-22		5.80E-01	4.22E-24		4.98E-01	4.17E-28		7.75E-01	6.72E-67		1.33E+00	2.57E-64	Up	3.12E-01	2.12E-03		Unigene14084_All//gi|15237269|ref|NP_200093.1|//1.00E-120//ornithine cyclodeaminase/mu-crystallin family protein [Arabidopsis thaliana] >gi|57610643|gb|AAW52557.1| At5g52810 [Arabidopsis thaliana] >gi|630003756|gb|AAY25407.1| At5g52810 [Arabidopsis thaliana]	Unigene14084_All//1.00E-102//AT5G52810| ornithine cyclodeaminase/mu-crystallin family protein	Unigene14084_All//0.00E+00//TC154038		ko00330|Arginine and proline metabolism		nr +
Unigene14086_All	1610	1.75	1.48	1.62	1.86	1.65	2.41	3.05	1.77	1.46	-2.47E-01	5.29E-01		-1.15E-01	7.63E-01		-1.73E-01	6.55E-01		3.78E-01	2.60E-01		-7.87E-01	1.11E-03		-1.06E+00	9.46E-06	Down	Unigene14086_All//gi|297851930|ref|XP_002893846.1|//0.00E+00//RECQL2 [Arabidopsis lyrata subsp. lyrata] >gi|297339688|gb|EFH70105.1| RECQL2 [Arabidopsis lyrata subsp. lyrata]	Unigene14086_All//0.00E+00//AT1G31360| RECQL2 (ARABIDOPSIS RECQ HELICASE L2); 3'-5' DNA helicase/ ATP-dependent helicase/ four-way junction helicase/ protein binding	Unigene14086_All//1.00E-47//CO080049		ko03440|Homologous recombination		nr +
Unigene14087_All	1926	11.08	4.31	6.03	21.98	14.57	9.29	15.30	2.82	3.91	-1.36E+00	1.11E-25	Down	-8.79E-01	1.79E-12		-5.93E-01	1.82E-15		-1.24E+00	2.39E-47	Down	-2.44E+00	1.64E-94	Down	-1.97E+00	1.32E-74	Down	Unigene14087_All//gi|115479367|ref|NP_001063277.1|//0.00E+00//Os09g0439700 [Oryza sativa Japonica Group] >gi|51091402|dbj|BAD36145.1| membrane protein PTM1-like [Oryza sativa Japonica Group] >gi|113631510|dbj|BAF25191.1| Os09g0439700 [Oryza sativa Japonica Group]	Unigene14087_All//0.00E+00//AT1G72480| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: Golgi apparatus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Transmembrane receptor, eukaryota (InterPro:IPR009637); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G01070.1); Has 422 Blast hits to 420 proteins in 121 species: Archae - 0; Bacteria - 0; Metazoa - 208; Fungi - 101; Plants - 83; Viruses - 0; Other Eukaryotes - 30 (source: NCBI BLink)…	Unigene14087_All//0.00E+00//TC166325				nr -
Unigene14088_All	1753	4.48	3.47	4.80	1.71	2.85	1.49	10.08	4.17	3.27	-3.68E-01	8.19E-02		1.00E-01	6.37E-01		7.40E-01	4.32E-03		-1.90E-01	6.29E-01		-1.27E+00	1.36E-23	Down	-1.62E+00	1.10E-34	Down	Unigene14088_All//gi|32815816|gb|AAP88291.1|//1.00E-157//protein kinase [Cucumis sativus]	Unigene14088_All//9.00E-159//AT5G50180| protein kinase, putative	Unigene14088_All//0.00E+00//TC147234				nr -
Unigene14089_All	1943	12.52	2.56	3.37	15.59	9.07	15.81	16.08	10.00	18.88	-2.29E+00	1.88E-59	Down	-1.89E+00	7.41E-45	Down	-7.81E-01	6.05E-18		2.01E-02	8.79E-01		-6.85E-01	3.97E-15		2.32E-01	3.32E-03		Unigene14089_All//gi|201440867|sp|Q9MT28.1|THRC_SOLTU//0.00E+00//RecName: Full=Threonine synthase, chloroplastic; Short=TS; Flags: Precursor >gi|8439547|gb|AAF74984.1|AF082894_1 threonine synthase [Solanum tuberosum]	Unigene14089_All//0.00E+00//AT4G29840| MTO2 (METHIONINE OVER-ACCUMULATOR 2); threonine synthase	Unigene14089_All//0.00E+00//TC133423		ko00260|Glycine, serine and threonine metabolism//ko00750|Vitamin B6 metabolism		nr +
Unigene1409_All	946	1.71	3.43	1.86	1.74	1.64	1.96	3.17	2.47	1.47	1.00E+00	4.04E-03		1.16E-01	8.09E-01		-8.52E-02	8.59E-01		1.72E-01	7.30E-01		-3.59E-01	2.95E-01		-1.11E+00	4.59E-04	Down			Unigene1409_All//0.00E+00//gi|164283125|gb|ES821618.1|ES821618				
Unigene14090_All	1940	0.65	0.05	0.30	0.80	0.78	0.79	0.54	0.67	0.43	-3.63E+00	2.00E-05	Down	-1.10E+00	8.60E-02		-2.74E-02	9.58E-01		-8.20E-03	9.81E-01		2.94E-01	6.23E-01		-3.37E-01	5.77E-01		Unigene14090_All//gi|201440867|sp|Q9MT28.1|THRC_SOLTU//0.00E+00//RecName: Full=Threonine synthase, chloroplastic; Short=TS; Flags: Precursor >gi|8439547|gb|AAF74984.1|AF082894_1 threonine synthase [Solanum tuberosum]	Unigene14090_All//0.00E+00//AT4G29840| MTO2 (METHIONINE OVER-ACCUMULATOR 2); threonine synthase	Unigene14090_All//0.00E+00//TC133423		ko00260|Glycine, serine and threonine metabolism//ko00750|Vitamin B6 metabolism		nr +
Unigene14091_All	664	0.87	1.91	0.80	3.15	1.92	1.09	1.21	2.64	0.90	1.14E+00	6.20E-02		-1.12E-01	9.07E-01		-7.16E-01	9.63E-02		-1.53E+00	8.31E-04	Down	1.13E+00	1.16E-02		-4.27E-01	5.42E-01		Unigene14091_All//gi|53370641|gb|AA589136.1|//1.00E-08//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene14091_All//1.00E-30//TC160503				nr -
Unigene14093_All	898	1.05	0.90	0.24	1.33	1.34	2.36	2.97	1.30	0.75	-2.16E-01	7.32E-01		-2.14E+00	1.16E-02		1.17E-02	9.99E-01		8.28E-01	6.69E-02		-1.19E+00	7.13E-04	Down	-1.98E+00	1.60E-07	Down	Unigene14093_All//gi|53370641|gb|AA589136.1|//4.00E-11//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene14093_All//2.00E-08//AT2G13980| nucleic acid binding	Unigene14093_All//7.00E-45//DW499472				nr +
Unigene14094_All	413	0.00	0.00	0.52	8.20	6.17	3.72	0.61	0.91	1.25	null	null		9.01E+00	1.41E-01		-4.11E-01	2.31E-01		-1.14E+00	6.61E-04	Down	5.68E-01	6.37E-01		1.03E+00	2.53E-01		Unigene14094_All//gi|9759561|dbj|BAB11163.1|//2.00E-42//MtN21 nodulin protein-like [Arabidopsis thaliana]	Unigene14094_All//7.00E-43//AT5G07050| LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF6, transmembrane (InterPro:IPR000620); BEST Arabidopsis thaliana protein match is: nodulin MtN21 family protein (TAIR:AT2G40900.1); Has 2288 Blast hits to 2270 proteins in 280 species: Archae - 23; Bacteria - 774; Metazoa - 5; Fungi - 0; Plants - 641; Viruses - 0; Other Eukaryotes - 845 (source: NCBI BLink)…	Unigene14094_All//6.00E-170//gi|109882304|gb|DW511274.1|DW511274				nr +
Unigene14095_All	1502	1.74	4.72	3.40	143.64	89.30	16.57	14.64	39.12	11.27	1.44E+00	1.04E-09	Up	9.67E-01	4.96E-04		-6.86E-01	2.66E-100		-3.12E+00	0.00E+00	Down	1.42E+00	3.41E-90	Up	-3.77E-01	2.20E-04		Unigene14095_All//gi|2598575|emb|CAA75575.1|//1.00E-144//MtN21 [Medicago truncatula]	Unigene14095_All//7.00E-140//AT5G07050| LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF6, transmembrane (InterPro:IPR000620); BEST Arabidopsis thaliana protein match is: nodulin MtN21 family protein (TAIR:AT2G40900.1); Has 2288 Blast hits to 2270 proteins in 280 species: Archae - 23; Bacteria - 774; Metazoa - 5; Fungi - 0; Plants - 641; Viruses - 0; Other Eukaryotes - 845 (source: NCBI BLink)…	Unigene14095_All//0.00E+00//TC159804				nr +
Unigene14100_All	1477	16.72	44.32	21.31	24.69	22.17	31.40	22.50	23.88	29.75	1.41E+00	7.05E-81	Up	3.50E-01	4.79E-04		-1.55E-01	1.01E-01		3.47E-01	5.02E-06		8.61E-02	3.84E-01		4.03E-01	9.17E-09		Unigene14100_All//gi|15235150|ref|NP_193705.1|//4.00E-70//RING; protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene14100_All//3.00E-54//AT5G45100| protein binding / zinc ion binding	Unigene14100_All//0.00E+00//TC142928				nr -
Unigene14101_All	869	2.41	4.31	5.82	8.43	2.69	2.86	100.13	659.79	159.86	8.41E-01	8.02E-03		1.27E+00	8.54E-06	Up	-1.64E+00	1.34E-14	Down	-1.56E+00	5.75E-12	Down	2.72E+00	0.00E+00	Up	6.75E-01	3.39E-64		Unigene14101_All//gi|195973264|gb|ABW69659.2|//9.00E-78//glutathione S-transferase [Gossypium hirsutum]	Unigene14101_All//7.00E-58//AT3G09270| ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	Unigene14101_All//0.00E+00//DW511031		ko00480|Glutathione metabolism		nr -
Unigene14103_All	2137	6.41	2.39	3.96	6.90	4.22	2.32	2.77	1.35	1.73	-1.42E+00	7.57E-18	Down	-6.95E-01	9.61E-06		-7.09E-01	1.13E-07		-1.57E+00	9.39E-24	Down	-1.04E+00	2.62E-06	Down	-6.76E-01	1.29E-03		Unigene14103_All//gi|75119312|sp|Q69VD5.1|PNH1_ORYSJ//0.00E+00//RecName: Full=Protein argonaute PNH1; AltName: Full=Protein PINHEAD homolog 1; Short=OsPNH1 >gi|50725578|dbj|BAD33046.1| ZLL/PNH homologous protein [Oryza sativa Japonica Group]	Unigene14103_All//0.00E+00//AT5G43810| ZLL (ZWILLE); translation initiation factor	Unigene14103_All//0.00E+00//TC130173				nr -
Unigene14106_All	2102	2.91	3.18	2.51	37.06	34.37	28.47	9.94	2.80	3.13	1.28E-01	5.94E-01		-2.16E-01	4.05E-01		-1.09E-01	8.68E-02		-3.81E-01	2.06E-11		-1.83E+00	1.34E-46	Down	-1.67E+00	2.02E-42	Down	Unigene14106_All//gi|115443731|ref|NP_001045645.1|//0.00E+00//Os02g0109800 [Oryza sativa Japonica Group] >gi|41052919|dbj|BAD07830.1| kinesin light chain-like protein [Oryza sativa Japonica Group] >gi|50252012|dbj|BAD27945.1| kinesin light chain-like protein [Oryza sativa Japonica Group] >gi|113535176|dbj|BAF07559.1| Os02g0109800 [Oryza sativa Japonica Group]	Unigene14106_All//0.00E+00//AT4G10840| kinesin light chain-related	Unigene14106_All//0.00E+00//TC139410				nr -
Unigene14110_All	1449	14.48	10.18	17.09	11.93	15.57	9.26	0.29	0.38	1.90	-5.09E-01	2.08E-05		2.39E-01	4.48E-02		3.84E-01	4.70E-04		-3.66E-01	6.28E-03		3.62E-01	6.73E-01		2.70E+00	1.08E-10	Up	Unigene14110_All//gi|222422849|dbj|BAH19411.1|//1.00E-151//AT3G45780 [Arabidopsis thaliana]	Unigene14110_All//2.00E-139//AT3G45780| PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase	Unigene14110_All//0.00E+00//gi|164351783|gb|ES826633.1|ES826633		ko04712|Circadian rhythm - plant		nr +
Unigene14112_All	1588	3.43	2.84	2.75	4.27	3.75	3.58	6.66	3.37	3.31	-2.71E-01	3.20E-01		-3.18E-01	2.51E-01		-1.86E-01	4.68E-01		-2.52E-01	3.20E-01		-9.82E-01	8.56E-10		-1.01E+00	1.64E-10	Down	Unigene14112_All//gi|115435792|ref|NP_001042654.1|//1.00E-73//Os01g0262700 [Oryza sativa Japonica Group] >gi|113532185|dbj|BAF04568.1| Os01g0262700 [Oryza sativa Japonica Group]	Unigene14112_All//2.00E-122//AT4G36440| unknown protein	Unigene14112_All//0.00E+00//ES812087				nr -
Unigene14113_All	1272	58.37	29.16	42.41	71.98	72.77	87.81	37.66	19.91	10.21	-1.00E+00	6.15E-54	Down	-4.61E-01	9.65E-14		1.57E-02	8.24E-01		2.87E-01	1.18E-09		-9.19E-01	3.05E-37		-1.88E+00	7.91E-114	Down	Unigene14113_All//gi|255566360|ref|XP_002524166.1|//5.00E-85//hydroxyacyl-ACP Dehydrase [Ricinus communis] >gi|223536584|gb|EEF38229.1| hydroxyacyl-ACP Dehydrase [Ricinus communis]	Unigene14113_All//2.00E-79//AT2G22230| beta-hydroxyacyl-ACP dehydratase, putative	Unigene14113_All//0.00E+00//gi|78351536|gb|DT571810.1|DT571810		ko00061|Fatty acid biosynthesis		nr -

Unigene14116_All	1262	8.25	6.26	3.97	13.18	9.82	18.75	20.07	29.01	49.09	-3.98E-01	2.65E-02		-1.06E+00	1.76E-08	Down	-4.25E-01	9.31E-04		5.08E-01	3.35E-06		5.32E-01	1.78E-11		1.29E+00	4.08E-84	Up	Unigene14116_All//gi|18379026|ref|NP_563689.1|//1.00E-100//TPK1 (THIAMIN PYROPHOSPHOKINASE1); thiamin diphosphokinase [Arabidopsis thaliana] >gi|6056414|gb|AAF02878.1|AC009525_12 Unknown protein [Arabidopsis thaliana]	Unigene14116_All//2.00E-101//AT1G02880| TPK1 (THIAMIN PYROPHOSPHOKINASE1); thiamin diphosphokinase	Unigene14116_All//0.00E+00//gi|164262524|gb|ES839860.1|ES839860		ko00730|Thiamine metabolism		nr -
Unigene14118_All	1768	5.77	2.26	2.08	5.33	4.54	3.30	3.13	1.02	1.69	-1.35E+00	1.63E-12	Down	-1.47E+00	1.54E-13	Down	-2.31E-01	2.56E-01		-6.92E-01	1.53E-04		-1.62E+00	4.45E-11	Down	-8.90E-01	5.42E-05		Unigene14118_All//gi|30682143|ref|NP_196406.2|//2.00E-75//myosin heavy chain-related [Arabidopsis thaliana] >gi|79327239|ref|NP_001031851.1|myosin heavy chain-related [Arabidopsis thaliana] >gi|222423567|dbj|BAH19753.1|AT5G07890 [Arabidopsis thaliana]	Unigene14118_All//8.00E-72//AT5G07890| myosin heavy chain-related	Unigene14118_All//0.00E+00//TC168941				nr +
Unigene14119_All	1789	1.73	0.59	1.43	1.75	2.02	1.19	1.28	0.56	0.96	-1.54E+00	4.33E-05	Down	-2.72E-01	4.75E-01		2.04E-01	5.81E-01		-5.64E-01	1.18E-01		-1.19E+00	1.96E-03		-4.14E-01	2.67E-01		Unigene14119_All//gi|30682143|ref|NP_196406.2|//3.00E-94//myosin heavy chain-related [Arabidopsis thaliana] >gi|79327239|ref|NP_001031851.1|myosin heavy chain-related [Arabidopsis thaliana] >gi|222423567|dbj|BAH19753.1|AT5G07890 [Arabidopsis thaliana]	Unigene14119_All//2.00E-88//AT5G07890| myosin heavy chain-related	Unigene14119_All//0.00E+00//TC168941				nr -
Unigene14120_All	808	8.61	23.14	6.59	8.75	12.27	18.50	7.12	20.74	12.08	1.43E+00	4.69E-24	Up	-3.86E-01	1.06E-01		4.88E-01	5.61E-03		1.08E+00	1.51E-13	Up	1.54E+00	1.11E-29	Up	7.63E-01	2.07E-06			Unigene14120_All//0.00E+00//TC172773					
Unigene14125_All	2993	4.39	2.62	3.67	3.81	4.92	3.14	1.38	0.49	1.86	-7.42E-01	1.95E-06		-2.60E-01	1.33E-01		3.70E-01	9.72E-03		-2.80E-01	1.20E-01		-1.50E+00	1.18E-07	Down	4.29E-01	5.31E-02		Unigene14125_All//gi|15238978|ref|NP_199063.1|//0.00E+00//ARC6 (ACCUMULATION AND REPLICATION OF CHLOROPLASTS 6); protein binding [Arabidopsis thaliana]	Unigene14125_All//0.00E+00//AT5G42480| ARC6 (ACCUMULATION AND REPLICATION OF CHLOROPLASTS 6); protein binding	Unigene14125_All//0.00E+00//TC137978				nr -
Unigene14126_All	1296	35.53	93.13	45.53	26.52	30.90	26.31	10.24	21.35	12.63	1.39E+00	4.60E-146	Up	3.58E-01	3.57E-07		2.21E-01	8.70E-03		-1.15E-02	9.35E-01		1.06E+00	2.18E-27	Up	3.03E-01	1.33E-02		Unigene14126_All//gi|37572449|dbj|BAC98494.1|//4.00E-61//AG-motif binding protein-4 [Nicotiana tabacum]	Unigene14126_All//6.00E-52//AT5G66320| zinc finger (GATA type) family protein	Unigene14126_All//0.00E+00//TC141896	C2C2-GATA			nr +
Unigene14127_All	1111	8.90	31.33	9.49	10.94	13.02	11.87	19.67	40.67	22.81	1.82E+00	2.44E-62	Up	9.25E-02	6.24E-01		2.51E-01	1.05E-01		1.18E-01	5.38E-01		1.05E+00	2.04E-43	Up	2.13E-01	3.04E-02		Unigene14127_All//gi|18422940|ref|NP_568701.1|//7.00E-52//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|30695512|ref|NP_851156.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|42573624|ref|NP_974908.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene14127_All//1.00E-41//AT5G48655| zinc finger (C3HC4-type RING finger) family protein	Unigene14127_All//0.00E+00//TC161691		ko04120|Ubiquitin mediated proteolysis//ko04146|Peroxisome		nr +
Unigene1413_All	1381	16.71	151.05	46.27	19.26	44.04	70.61	78.50	76.36	63.23	3.18E+00	0.00E+00	Up	1.47E+00	3.77E-82	Up	1.19E+00	4.97E-69	Up	1.87E+00	7.05E-195	Up	-3.99E-02	4.82E-01		-3.12E-01	6.29E-13		Unigene1413_All//gi|13937195|gb|AAK50091.1|AF372951_1//1.00E-165//At1g78070/F28K19_28 [Arabidopsis thaliana] >gi|25090156|gb|AAN72242.1|At1g78070/F28K19_28 [Arabidopsis thaliana]	Unigene1413_All//3.00E-166//AT1G78070| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: CUL4 RING ubiquitin ligase complex; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), WD40 repeat, region (InterPro:IPR017986), WD40/YVTN repeat-like (InterPro:IPR015943), WD40 repeat (InterPro:IPR001680); BEST Arabidopsis thaliana protein match is: WD-40 repeat family protein (TAIR:AT1G36070.1); Has 110 Blast hits to 110 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 28; Plants - 80; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene1413_All//0.00E+00//TC153989		ko03040|Spliceosome//ko03018|RNA degradation		nr -
Unigene14130_All	1631	63.93	55.48	63.27	3.24	5.13	6.42	0.16	0.97	0.81	-2.05E-01	6.40E-05		-1.50E-02	8.07E-01		6.64E-01	4.82E-04		9.89E-01	1.83E-08		2.65E+00	3.44E-06	Up	2.37E+00	7.20E-05	Up	Unigene14130_All//gi|289065765|gb|ADC80920.1|//1.00E-152//delta-9 fatty acid desaturase [Vernicia fordii]	Unigene14130_All//2.00E-139//AT3G15850| FAD5 (FATTY ACID DESATURASE 5); 16:0 monogalactosyldiacylglycerol desaturase/ oxidoreductase	Unigene14130_All//0.00E+00//TC131677		ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene14132_All	2287	5.10	13.69	7.38	5.86	6.64	7.90	6.47	8.35	9.79	1.42E+00	9.35E-40	Up	5.33E-01	1.38E-04		1.81E-01	2.67E-01		4.31E-01	8.25E-04		3.68E-01	1.19E-03		5.97E-01	4.05E-09		Unigene14132_All//gi|30678079|ref|NP_178475.2|//4.00E-21//18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|42570677|ref|NP_973412.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|79316683|ref|NP_001030966.1|18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|186499149|ref|NP_001118260.1|18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana]	Unigene14132_All//1.00E-19//AT2G03810| 18S pre-ribosomal assembly protein gar2-related	Unigene14132_All//0.00E+00//TC174080				nr +
Unigene14133_All	1157	4.48	5.87	6.67	5.47	5.30	6.71	5.04	3.68	2.38	3.91E-01	9.00E-02		5.76E-01	8.34E-03		-4.56E-02	8.57E-01		2.96E-01	1.96E-01		-4.53E-01	4.22E-02		-1.09E+00	6.79E-07	Down	Unigene14133_All//gi|297850954|ref|XP_002893358.1|//2.00E-78//regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339200|gb|EFH69617.1|regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14133_All//2.00E-69//AT1G27060| regulator of chromosome condensation (RCC1) family protein	Unigene14133_All//0.00E+00//gi|78335142|gb|DT555416.1|DT555416		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene14135_All	1571	1.63	0.39	0.75	4.50	4.23	2.90	9.04	12.48	4.95	-2.08E+00	3.67E-06	Down	-1.13E+00	7.05E-03		-9.00E-02	7.44E-01		-6.33E-01	3.54E-03		4.65E-01	2.80E-05		-8.71E-01	5.03E-11		Unigene14135_All//gi|11072030|gb|AC28909.1|AC008113_25//1.00E-41//F12A21.9 [Arabidopsis thaliana]	Unigene14135_All//1.00E-52//AT5G38690| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: DDT superfamily (InterPro:IPR018501), DDT subgroup (InterPro:IPR018500), Cell division cycle-associated protein (InterPro:IPR018866); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67780.1); Has 492 Blast hits to 468 proteins in 97 species: Archae - 9; Bacteria - 41; Metazoa - 179; Fungi - 19; Plants - 99; Viruses - 2; Other Eukaryotes - 143 (source: NCBI BLink).	Unigene14135_All//0.00E+00//TC169898				nr -
Unigene14136_All	2338	1.72	0.74	1.12	5.48	3.87	3.71	5.79	8.88	3.54	-1.23E+00	8.77E-05	Down	-6.27E-01	4.87E-02		-4.99E-01	7.05E-04		-5.62E-01	2.66E-04		6.19E-01	9.34E-09		-7.07E-01	1.24E-07		Unigene14136_All//gi|20147346|gb|AAM10386.1|//1.00E-106//AT5G38690/MEB18_24 [Arabidopsis thaliana] >gi|23463059|gb|AAN33199.1|At5g38690/MEB18_24 [Arabidopsis thaliana]	Unigene14136_All//2.00E-104//AT5G38690| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: DDT superfamily (InterPro:IPR018501), DDT subgroup (InterPro:IPR018500), Cell division cycle-associated protein (InterPro:IPR018866); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67780.1); Has 492 Blast hits to 468 proteins in 97 species: Archae - 9; Bacteria - 41; Metazoa - 179; Fungi - 19; Plants - 99; Viruses - 2; Other Eukaryotes - 143 (source: NCBI BLink).	Unigene14136_All//0.00E+00//TC160339				nr +
Unigene14139_All	980	39.93	30.25	24.89	79.14	80.99	84.24	39.78	19.62	24.63	-4.01E-01	2.49E-06		-6.82E-01	1.19E-14		3.33E-02	6.62E-01		9.01E-02	1.78E-01		-1.02E+00	4.90E-36	Down	-6.91E-01	1.59E-19		Unigene14139_All//gi|255957396|emb|CBA13552.1|//1.00E-131//cytosolic chaperonin, delta subunit [Glycine max]	Unigene14139_All//6.00E-131//AT3G18190| chaperonin, putative	Unigene14139_All//0.00E+00//gi|78323788|gb|DT544062.1|DT544062				nr -
Unigene14141_All	1269	64.77	252.31	114.18	75.41	73.24	68.94	55.87	101.51	55.63	1.96E+00	0.00E+00	Up	8.18E-01	2.73E-72		-4.21E-02	5.58E-01		-1.29E-01	2.14E-02		8.61E-01	1.84E-88		-6.30E-03	9.45E-01		Unigene14141_All//gi|115456071|ref|NP_001051636.1|//3.00E-19//Os03g0806600 [Oryza sativa Japonica Group] >gi|108711649|gb|ABF99444.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550107|dbj|BAF13550.1|Os03g0806600 [Oryza sativa Japonica Group]	Unigene14141_All//1.00E-28//AT3G03870| unknown protein	Unigene14141_All//0.00E+00//TC152436				nr -
Unigene14143_All	714	12.97	43.50	14.24	14.58	20.93	18.72	57.62	136.80	170.23	1.75E+00	8.88E-53	Up	1.35E-01	5.14E-01		5.22E-01	1.33E-04		3.61E-01	2.20E-02		1.25E+00	8.67E-123	Up	1.56E+00	5.46E-219	Up	Unigene14143_All//gi|297797531|ref|XP_002866650.1|//3.00E-15//acyl-CoA oxidase [Arabidopsis lyrata subsp. lyrata] >gi|297312485|gb|EFH42909.1| acyl-CoA oxidase [Arabidopsis lyrata subsp. lyrata]	Unigene14143_All//1.00E-16//AT5G65110| ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase	Unigene14143_All//0.00E+00//gi|164278527|gb|ES797323.1|ES797323		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids	GO:0005777//GO:0009062//GO:0015002//GO:0016634//GO:0030554	nr +

Unigene14144_All	1232	7.47	13.28	11.67	6.15	7.57	7.33	8.03	11.43	17.82	8.30E-01	2.80E-09		6.43E-01	2.54E-05		3.02E-01	1.28E-01		2.55E-01	2.33E-01		5.10E-01	1.29E-04		1.15E+00	1.81E-25	Up	Unigene14144_All//gi|75164899|sp|Q94A20.1|BI1L_ARATH//2.00E-97//RecName: Full=BI1-like protein >gi|15215827|gb|AAK91458.1| AT4g15470/d13775w [Arabidopsis thaliana] >gi|20453267|gb|AAM19872.1| AT4g15470/d13775w [Arabidopsis thaliana]	Unigene14144_All//4.00E-89//AT4G15470| EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0005 (InterPro:IPR006214); BEST Arabidopsis thaliana protein match is: glutamate binding (TAIR:AT1G03070.1); Has 4000 Blast hits to 3999 proteins in 955 species: Archae - 0; Bacteria - 1775; Metazoa - 750; Fungi - 92; Plants - 143; Viruses - 77; Other Eukaryotes - 1163 (source: NCBI BLink).	Unigene14144_All//0.00E+00//TC153196			GO:0031224	nr +
Unigene14146_All	1589	13.07	8.42	6.27	12.04	10.23	8.33	531.04	76.78	37.83	-6.35E-01	1.42E-07		-1.06E+00	2.20E-16	Down	-2.35E-01	7.01E-02		-5.32E-01	1.46E-05		-2.79E+00	0.00E+00	Down	-3.81E+00	0.00E+00	Down	Unigene14146_All//gi|18398038|ref|NP_566316.1|//1.00E-141//kelch repeat-containing protein [Arabidopsis thaliana] >gi|11692832|gb|AAG40019.1|AF32466 8_1 MLP3.17 [Arabidopsis thaliana] >gi|14517448|gb|AAK62614.1| AT3g07720/F17A17_6 [Arabidopsis thaliana] >gi|23507767|gb|AAN38687.1| At3g07720/F17A17_6 [Arabidopsis thaliana]	Unigene14146_All//3.00E-142//AT3G07720| kelch repeat-containing protein	Unigene14146_All//0.00E+00//TC134383		ko04712|Circadian rhythm - plant	GO:0019759//GO:0044271//GO:0051707	nr -
Unigene14147_All	983	2.13	6.29	7.42	17.43	13.10	9.83	19.61	50.60	22.61	1.56E+00	1.47E-09	Up	1.80E+00	5.65E-13	Up	-4.12E-01	1.12E-03		-8.26E-01	3.22E-10		1.37E+00	2.43E-72	Up	2.05E-01	5.40E-02		Unigene14147_All//gi|117168087|gb|ABK32126.1|//6.00E-14//At1g52565 [Arabidopsis thaliana]	Unigene14147_All//3.00E-05//AT3G15760| unknown protein	Unigene14147_All//1.00E-126//TC171639				nr +
Unigene14148_All	2197	0.69	0.74	0.63	1.75	2.18	1.62	3.75	3.73	7.62	9.58E-02	8.47E-01		-1.32E-01	8.01E-01		3.20E-01	2.93E-01		-1.04E-01	7.54E-01		-9.30E-03	9.98E-01		1.02E+00	2.39E-16	Up	Unigene14148_All//gi|297719995|ref|NP_001172359.1|/8.00E-94//Os01g0388566 [Oryza sativa Japonica Group] >gi|255673262|dbj|BAH91089.1| Os01g0388566 [Oryza sativa Japonica Group]	Unigene14148_All//0.00E+00//AT2G48060| unknown protein	Unigene14148_All//9.00E-176//TC160317			GO:0031410	nr -
Unigene14152_All	2023	1.91	2.78	1.50	2.14	2.89	2.95	6.35	10.66	16.60	5.39E-01	3.28E-02		-3.51E-01	3.00E-01		4.34E-01	8.22E-02		4.60E-01	6.68E-02		7.47E-01	2.69E-12		1.39E+00	3.41E-51	Up	Unigene14152_All//gi|115445193|ref|NP_001046376.1|//1.00E-164//Os02g0233100 [Oryza sativa Japonica Group] >gi|50251785|dbj|BAD27717.1| LAs17 Binding protein; Ls03p-like [Oryza sativa Japonica Group] >gi|113535907|dbj|BAF08290.1| Os02g0233100 [Oryza sativa Japonica Group]	Unigene14152_All//1.00E-133//AT1G29800| phosphoinositide binding / zinc ion binding	Unigene14152_All//0.00E+00//TC136785		ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0046914	nr -
Unigene14154_All	2107	4.30	2.72	2.22	15.13	19.55	14.64	12.38	9.07	5.22	-6.61E-01	5.41E-04		-9.50E-01	2.26E-06		3.69E-01	1.81E-06		-4.76E-02	7.03E-01		-4.50E-01	2.05E-06		-1.25E+00	2.29E-34	Down	Unigene14154_All//gi|124360876|gb|ABN08848.1|//1.00E-169//Zinc finger, RING-type [Medicago truncatula]	Unigene14154_All//1.00E-18//AT2G38970| zinc finger (C3HC4-type RING finger) family protein	Unigene14154_All//0.00E+00//ES819045			GO:0046914	nr -
Unigene14156_All	2200	1.17	2.07	1.48	1.86	0.92	1.58	3.50	2.49	2.39	8.31E-01	3.41E-03		3.42E-01	3.69E-01		-1.01E+00	3.37E-04	Down	-2.32E-01	4.93E-01		-4.91E-01	9.14E-03		-5.49E-01	2.45E-03		Unigene14156_All//gi|124359772|gb|ABN06098.1|//0.00E+00//Pre-mRNA processing ribonucleoprotein, binding region; NOSIC [Medicago truncatula]	Unigene14156_All//4.00E-173//AT1G60170| emb1220 (embryo defective 1220)	Unigene14156_All//0.00E+00//TC141055		ko03040|Spliceosome	GO:0003006//GO:0005688//GO:0032991	nr -
Unigene14159_All	893	13.07	9.08	8.59	16.73	17.24	11.43	5.07	2.81	1.96	-5.25E-01	1.54E-03		-6.06E-01	4.33E-04		4.26E-02	8.42E-01		-5.50E-01	9.67E-05		-8.51E-01	7.80E-04		-1.37E+00	1.40E-07	Down	Unigene14159_All//gi|4544453|gb|AAD22361.1|//4.00E-97//expressed protein [Arabidopsis thaliana] >gi|117168219|gb|ABK32192.1| At2g22370 [Arabidopsis thaliana]	Unigene14159_All//2.00E-94//AT2G22370| unknown protein	Unigene14159_All//0.00E+00//TC151715			GO:0006355//GO:0016251//GO:0016787//GO:0043234	nr +
Unigene14160_All	893	2.75	2.04	2.21	4.63	3.32	2.23	0.80	0.61	0.00	-4.31E-01	2.96E-01		-3.20E-01	4.54E-01		-4.81E-01	1.04E-01		-1.06E+00	3.71E-04	Down	-4.04E-01	6.23E-01		-9.65E+00	1.78E-05	Down	Unigene14160_All//gi|4544453|gb|AAD22361.1|//1.00E-84//expressed protein [Arabidopsis thaliana] >gi|117168219|gb|ABK32192.1| At2g22370 [Arabidopsis thaliana]	Unigene14160_All//7.00E-86//AT2G22370| unknown protein	Unigene14160_All//0.00E+00//TC151715			GO:0006355//GO:0008233//GO:0016251//GO:0043234	nr +
Unigene14161_All	2509	11.66	5.33	7.07	4.86	4.36	2.83	8.34	7.65	8.86	-1.13E+00	3.37E-26	Down	-7.22E-01	3.35E-12		-1.56E-01	4.01E-01		-7.83E-01	7.14E-07		-1.26E-01	3.17E-01		8.70E-02	4.69E-01		Unigene14161_All//gi|195648250|gb|ACG43593.1|//1.00E-119//ASC1-like protein 1 [Zea mays]	Unigene14161_All//9.00E-101//AT1G13580| LAG13 (LAG1 LONGEVITY ASSURANCE HOMOLOG 3)	Unigene14161_All//0.00E+00//TC157230				nr +
Unigene14162_All	966	8.23	11.96	7.50	20.78	14.12	11.08	2.54	5.88	2.76	5.39E-01	1.25E-03		-1.35E-01	5.81E-01		-5.58E-01	7.28E-07		-9.07E-01	8.30E-14		1.21E+00	1.40E-07	Up	1.22E-01	7.25E-01				Unigene14162_All//0.00E+00//gi|13245224|gb|BE052172.2|BE052172				
Unigene14164_All	1127	43.50	84.21	50.37	105.82	92.55	98.74	38.30	803.76	47.26	9.53E-01	3.64E-63		2.12E-01	4.66E-03		-1.93E-01	1.28E-05		-9.98E-02	5.37E-02		4.39E+00	0.00E+00	Up	3.03E-01	1.72E-06		Unigene14164_All//gi|297342387|gb|AD133725.1|//2.00E-90//glycosyltransferase [Solanum lycopersicum]	Unigene14164_All//3.00E-83//AT4G01070| GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene14164_All//0.00E+00//TC142764			GO:0035251	nr +
Unigene14166_All	1217	0.99	2.04	2.19	2.99	2.24	3.86	2.15	6.18	2.59	1.04E+00	1.03E-02		1.15E+00	5.09E-03		-4.19E-01	2.02E-01		3.69E-01	2.21E-01		1.52E+00	1.78E-13	Up	2.64E-01	4.11E-01		Unigene14166_All//gi|18400820|ref|NP_565593.1|//3.00E-35//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene14166_All//1.00E-32//AT2G25410| protein binding / zinc ion binding	Unigene14166_All//0.00E+00//TC154738			GO:0005488	nr +
Unigene14167_All	1826	2.58	3.83	2.33	11.40	11.50	6.33	13.24	6.27	8.38	5.70E-01	1.02E-02		-1.45E-01	6.12E-01		1.26E-02	9.47E-01		-8.49E-01	7.81E-13		-1.08E+00	9.30E-25	Down	-6.61E-01	1.42E-11		Unigene14167_All//gi|30697215|ref|NP_176737.2|//0.00E+00//HEXO3 (BETA-HEXOSAMINIDASE 3); beta-N-acetylhexosaminidase/ hexosaminidase [Arabidopsis thaliana] >gi|2135811|gb|AAM91092.1| At1g65600/F5I14_13 [Arabidopsis thaliana] >gi|23463073|gb|AAX33206.1| At1g65600/F5I14_13 [Arabidopsis thaliana]	Unigene14167_All//0.00E+00//AT1G65590| HEXO3 (BETA-HEXOSAMINIDASE 3); beta-N-acetylhexosaminidase/ hexosaminidase	Unigene14167_All//0.00E+00//gi|78328882|gb|DT549156.1|DT549156		ko00520|Amino sugar and nucleotide sugar metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series//ko00603|Glycosphingolipid biosynthesis - globo series	GO:0005618//GO:0015929//GO:0016020//GO:0031410//GO:0043167//GO:0044238	nr -
Unigene14169_All	1417	6.68	17.49	11.57	12.59	13.00	19.03	19.39	23.77	45.80	1.39E+00	2.13E-30	Up	7.92E-01	2.79E-08		4.69E-02	8.06E-01		5.96E-01	4.52E-09		2.94E-01	4.46E-04		1.24E+00	8.77E-83	Up	Unigene14169_All//gi|297721647|ref|NP_001173186.1|//1.00E-47//Os02g0802800 [Oryza sativa Japonica Group] >gi|255671323|dbj|BAH91915.1| Os02g0802800 [Oryza sativa Japonica Group]		Unigene14169_All//0.00E+00//TC133908				nr -
Unigene1417_All	1962	6.37	13.56	7.33	13.46	14.80	16.32	28.21	44.67	39.60	1.09E+00	1.64E-22	Up	2.01E-01	2.34E-01		1.37E-01	2.28E-01		2.78E-01	3.85E-03		6.63E-01	1.10E-38		4.89E-01	9.31E-21		Unigene1417_All//gi|3334195|sp|Q40224.1|GPA1_LUPLU//0.00E+00//RecName: Full=Guanine nucleotide-binding protein alpha-1 subunit; Short=GP-alpha-1 >gi|1480298|emb|CAA67845.1| G protein [Lupinus luteus]	Unigene1417_All//1.00E-179//AT2G26300| GP ALPHA 1 (G PROTEIN ALPHA SUBUNIT 1); GTP binding / GTPase/ channel regulator/ signal transducer	Unigene1417_All//0.00E+00//TC143624				nr +
Unigene14170_All	1079	21.29	19.82	13.23	50.83	42.16	36.67	32.99	13.48	26.07	-1.03E-01	4.14E-01		-6.87E-01	5.84E-09		-2.70E-01	5.42E-05		-4.71E-01	6.59E-12		-1.29E+00	9.02E-48	Down	-3.40E-01	1.50E-05		Unigene14170_All//gi|145359142|ref|NP_200019.2|//8.00E-78//ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1); protein binding [Arabidopsis thaliana]	Unigene14170_All//1.00E-70//AT5G62060| ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1); protein binding	Unigene14170_All//0.00E+00//TC131566			GO:0005488//GO:0006915//GO:0043231//GO:0043412	nr -
Unigene14172_All	979	0.64	0.52	1.31	10.38	4.85	2.63	2.20	1.20	1.99	-3.09E-01	7.01E-01		1.03E+00	1.03E-01		-1.10E+00	6.65E-11	Down	-1.98E+00	1.11E-22	Down	-8.82E-01	2.39E-02		-1.44E-01	7.07E-01		Unigene14172_All//gi|157863708|gb|ABV90875.1|//1.00E-71//inositol-1,4,5-triphosphate-5-phosphatase [Solanum lycopersicum]	Unigene14172_All//3.00E-62//AT4G18010| ATSPTASE2 (MYO-INOSITOL POLYPHOSPHATE 5-PHOSPHATASE 2); inositol-polyphosphate 5-phosphatase	Unigene14172_All//3.00E-155//ES829939			GO:0009725//GO:0032501//GO:0043647//GO:0046030	nr -
Unigene14174_All	2501	0.21	0.32	0.72	15.56	7.28	2.89	2.30	0.87	1.70	6.32E-01	4.02E-01		1.79E+00	1.06E-03		-1.09E+00	1.84E-40	Down	-2.43E+00	1.24E-110	Down	-1.40E+00	2.06E-09	Down	-4.32E-01	4.60E-02		Unigene14174_All//gi|157863708|gb|ABV90875.1|//0.00E+00//inositol-1,4,5-triphosphate-5-phosphatase [Solanum lycopersicum]	Unigene14174_All//1.00E-108//AT4G18010| ATSPTASE2 (MYO-INOSITOL POLYPHOSPHATE 5-PHOSPHATASE 2); inositol-polyphosphate 5-phosphatase	Unigene14174_All//0.00E+00//ES829939			GO:0016491//GO:0043231	nr +
Unigene14175_All	1327	2.96	7.64	3.21	4.13	2.23	3.27	3.89	3.75	4.02	1.37E+00	1.28E-12	Up	1.19E-01	7.03E-01		-8.88E-01	1.71E-04		-3.38E-01	2.20E-01		-5.25E-02	8.43E-01		4.95E-02	8.46E-01		Unigene14175_All//gi|301069164|dbj|BAJ11961.1|//3.00E-45//MdFBX13 [Malus x domestica]	Unigene14175_All//1.00E-18//AT3G07870| F-box family protein	Unigene14175_All//0.00E+00//TC145887				nr +
Unigene14176_All	1731	2.45	5.80	2.71	1.99	2.98	2.56	2.34	1.81	1.06	1.24E+00	6.92E-11	Up	1.45E-01	6.11E-01		5.88E-01	2.32E-02		3.65E-01	2.38E-01		-3.73E-01	1.90E-01		-1.15E+00	1.90E-05	Down	Unigene14176_All//gi|301069164|dbj|BAJ11961.1|//3.00E-44//MdFBX13 [Malus x domestica]	Unigene14176_All//2.00E-17//AT3G07870| F-box family protein	Unigene14176_All//0.00E+00//TC145887				nr +
Unigene14177_All	2060	0.00	21.28	0.16	3.72	2.69	2.78	2.16	4.99	0.77	1.44E+01	4.47E-253	Up	7.28E+00	4.53E-02		-4.69E-01	2.07E-02		-4.20E-01	5.10E-02		1.21E+00	4.68E-13	Up	-1.48E+00	2.87E-08	Down	Unigene14177_All//gi|113029|sp|P17069.1|ACLA_GOSHI//0.00E+00//RecName: Full=Isocitrate lyase; Short=ICL; Short=Isocitratase; Short=Isocitrase	Unigene14177_All//0.00E+00//AT3G21720| ICL (ISOCITRATE LYASE); catalytic/ isocitrate lyase	Unigene14177_All//0.00E+00//TC146124		ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005488//GO:0005777//GO:0009060//GO:0016833//GO:0043436//GO:0044262	nr -
Unigene14178_All	1800	8.60	13.46	5.89	4.12	3.75	5.44	1.15	3.18	2.19	6.45E-01	6.69E-09		-5.47E-01	1.92E-04		-1.37E-01	5.87E-01		4.01E-01	3.27E-02		1.47E+00	6.15E-10	Up	9.29E-01	5.42E-04		Unigene14178_All//gi|22329651|ref|NP_173272.2|//1.00E-116//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|17979489|gb|AAL50081.1| At1g18360/F15H18_2 [Arabidopsis thaliana] >gi|20147303|gb|AAM10365.1| At1g18360/F15H18_2 [Arabidopsis thaliana]	Unigene14178_All//1.00E-114//AT1G18360| hydrolase, alpha/beta fold family protein	Unigene14178_All//0.00E+00//TC149242				nr +
Unigene14179_All	1931	4.52	7.01	6.34	13.03	9.15	7.58	22.16	55.43	106.62	6.31E-01	3.66E-05		4.87E-01	3.86E-03		-5.10E-01	2.90E-07		-7.82E-01	1.99E-13		1.32E+00	2.75E-147	Up	2.27E+00	0.00E+00	Up	Unigene14179_All//gi|16612314|gb|AL27516.1|AF439848_1//1.00E-109//AT5g40470/K21I16_20 [Arabidopsis thaliana]	Unigene14179_All//7.00E-85//AT5G40470| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: F-box family protein (FBL4) (TAIR:AT4G15475.1); Has 1784 Blast hits to 1176 proteins in 130 species: Archae - 0; Bacteria - 16; Metazoa - 963; Fungi - 149; Plants - 477; Viruses - 0; Other Eukaryotes - 179 (source: NCBI BLink).	Unigene14179_All//0.00E+00//TC134367			GO:0044464	nr +
Unigene1418_All	2067	301.47	252.59	206.69	85.12	97.51	97.10	46.11	31.50	20.66	-2.55E-01	2.86E-38		-5.45E-01	5.34E-151		1.96E-01	2.96E-09		1.90E-01	5.28E-08		-5.49E-01	3.08E-30		-1.16E+00	9.76E-110	Down	Unigene1418_All//gi|297826149|ref|XP_002880957.1|//0.00E+00//CPN60A [Arabidopsis lyrata subsp. lyrata] >gi|297326796|gb|EFH57216.1| CPN60A [Arabidopsis lyrata subsp. lyrata]	Unigene1418_All//0.00E+00//AT2G28000| CPN60A (CHAPERONIN-60ALPHA); ATP binding / protein binding	Unigene1418_All//0.00E+00//TC130123		ko03018|RNA degradation		nr -

Unigene14181_All	569	0.18	1.78	0.00	1.93	2.06	1.98	1.19	0.81	0.49	3.28E+00	3.79E-04	Up	-7.52E+00	3.95E-01			9.54E-02	9.01E-01			4.30E-02	9.43E-01		-5.57E-01	4.89E-01		-1.28E+00	9.49E-02		Unigene14181_All//gi|52353612|gb|AAU44178.1|//5.00E-12//ptative chromosome condensation factor [Oryza sativa (japonica Group)]	Unigene14181_All//1.00E-12//AT1G76950| PRAF1; Ran GTPase binding / chromatin binding / zinc ion binding	Unigene14181_All//4.00E-119//ES831983			GO:0017016//GO:0031410//GO:0043231//GO:0046914	nr +
Unigene14184_All	1331	84.71	83.87	92.94	58.27	60.93	42.14	15.03	14.07	6.44	-1.45E-02	7.97E-01		1.34E-01	7.96E-03			6.43E-02	3.62E-01			-4.68E-01	2.36E-16		-9.50E-02	4.75E-01		-1.22E+00	8.27E-26	Down	Unigene14184_All//gi|124359163|gb|ABN06686.1|//9.00E-21//Zinc finger, CCHC-type [Medicago truncatula]	Unigene14184_All//4.00E-08//AT2G01050| nucleic acid binding / zinc ion binding	Unigene14184_All//0.00E+00//TC167533				nr -
Unigene14185_All	2084	5.52	1.07	3.12	11.88	9.47	13.02	12.64	8.18	6.04	-2.37E+00	1.51E-29	Down	-8.25E-01	2.16E-06			-3.27E-01	1.72E-03			1.33E-01	2.77E-01		-6.27E-01	3.80E-11		-1.07E+00	3.64E-27	Down	Unigene14185_All//gi|297822571|ref|XP_002879168.1|//1.00E-130//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297325007|gb|EFH55427.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14185_All//2.00E-118//AT2G28600| ATP binding / ATP-dependent helicase/ nucleic acid binding	Unigene14185_All//0.00E+00//TC163332	ko03040|Spliceosome	GO:0005488	nr +
Unigene14187_All	286	7.68	5.67	9.68	14.98	13.97	18.63	3.10	0.58	0.28	-4.39E-01	3.23E-01		3.34E-01	3.94E-01			-1.01E-01	7.85E-01			3.15E-01	2.68E-01		-2.41E+00	1.79E-03		-3.48E+00	7.34E-05	Down	Unigene14187_All//gi|115444905|ref|NP_00104623 2.1|//4.00E-23//Os02g0202600 [Oryza sativa (japonica Group)] >gi|113535763|dbj|BAF08146.1| Os02g0202600 [Oryza sativa (japonica Group)]	Unigene14187_All//2.00E-22//AT2G25570| binding	Unigene14187_All//2.00E-82//DW517756		GO:0043231	nr +
Unigene14188_All	1317	5.36	3.35	5.86	7.49	7.63	5.73	5.75	5.17	2.36	-6.80E-01	1.98E-03		1.29E-01	6.09E-01			2.78E-02	9.05E-01			-3.87E-01	3.85E-02		-1.52E-01	4.92E-01		-1.28E+00	4.64E-11	Down	Unigene14188_All//gi|297825607|ref|XP_002880686.1|//1.00E-116//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297326525|gb|EFH56945.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14188_All//6.00E-112//AT2G25570| binding	Unigene14188_All//0.00E+00//TC133229	ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene14189_All	1270	1.57	2.03	3.52	2.63	2.87	1.53	1.27	0.53	0.56	3.78E-01	3.59E-01		1.17E+00	1.19E-04	Up	1.29E-01	7.55E-01			-7.81E-01	2.08E-02		-1.26E+00	7.61E-03		-1.16E+00	1.02E-02		Unigene14189_All//gi|297825607|ref|XP_002880686.1|//1.00E-116//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297326525|gb|EFH56945.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14189_All//4.00E-117//AT2G25570| binding	Unigene14189_All//0.00E+00//TC133229	ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene1419_All	2843	3.07	2.50	3.35	12.79	9.54	6.39	12.72	5.65	3.97	-3.01E-01	1.36E-01		1.26E-01	5.70E-01			-4.22E-01	2.12E-07		-1.00E+00	6.94E-29	Down	-1.17E+00	1.04E-41	Down	-1.68E+00	1.31E-73	Down	Unigene1419_All//gi|30681908|ref|NP_850165.1|//0.00E+00//PARP2 (POLY(ADP-RIBOSE) POLYMERASE 2); DNA binding / NAD or NADH binding / NAD+ ADP-ribosyltransferase/ zinc ion binding [Arabidopsis thaliana] >gi|73921622|sp|Q9ZP54.2|PARP1_ARATH RecName: Full=Poly [ADP-ribose] polymerase 1; Short=PARP-1; AltName: Full=NAD(+) ADP-ribosyltransferase 1; Short=ADPRT-1; AltName: Full=Poly[ADP-ribose] synthase 1 >gi|4038491|emb|CAA10482.1| poly(ADP-ribose) polymerase [Arabidopsis thaliana]	Unigene1419_All//0.00E+00//AT2G31320| PARP2 (POLY(ADP-RIBOSE) POLYMERASE 2); DNA binding / NAD or NADH binding / NAD+ ADP-ribosyltransferase/ zinc ion binding	Unigene1419_All//0.00E+00//TC147600	ko03410|Base excision repair		nr -
Unigene14192_All	1970	4.28	4.50	3.89	113.33	75.78	39.02	19.94	28.15	13.14	7.40E-02	7.19E-01		-1.36E-01	5.63E-01			-5.81E-01	4.63E-77		-1.54E+00	0.00E+00	Down	4.98E-01	3.98E-15		-6.01E-01	1.54E-15		Unigene14192_All//gi|115465946|ref|NP_00105657 2.1|//4.00E-23//Os06g0108900 [Oryza sativa (japonica Group)] >gi|113594612|dbj|BAF18486.1| Os06g0108900 [Oryza sativa (japonica Group)]	Unigene14192_All//2.00E-22//AT5G02030| RPL (REPLUMLESS); DNA binding / sequence-specific DNA binding / transcription factor	Unigene14192_All//0.00E+00//gi|109826149|gb|DR224870.1|DR224870	HB		GO:0003677//GO:0006350//GO:0010468	nr +
Unigene14193_All	1232	6.50	27.39	8.39	49.09	38.43	48.06	55.42	69.61	48.99	2.08E+00	3.99E-72	Up	3.68E-01	5.24E-02			-3.53E-01	1.10E-08		-3.05E-02	7.13E-01		3.29E-01	4.54E-11		-1.78E-01	1.74E-03		Unigene14193_All//gi|87162905|gb|AB028700.1|//3.00E-93//ATP binding , related [Medicago truncatula] >gi|124360477|gb|ABN08487.1| ATP binding , related [Medicago truncatula]	Unigene14193_All//1.00E-77//AT4G00300| fringe-related protein	Unigene14193_All//0.00E+00//TC156775		GO:0004672//GO:0016020	nr -
Unigene14194_All	1079	5.38	10.80	7.30	11.36	12.61	15.24	2.70	4.14	4.32	1.00E+00	4.00E-09	Up	4.40E-01	4.41E-02			1.51E-01	4.03E-01		4.24E-01	1.90E-03		6.16E-01	1.60E-02		6.76E-01	5.11E-03		Unigene14194_All//gi|297810359|ref|XP_002873063.1|//1.00E-44//heavy-metal-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297318900|gb|EFH49322.1| heavy-metal-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene14194_All//5.00E-39//AT2G37390| heavy-metal-associated domain-containing protein	Unigene14194_All//0.00E+00//ES816695			nr -
Unigene14196_All	1029	1.17	1.87	2.12	3.15	2.24	1.32	2.59	2.40	3.45	6.78E-01	1.45E-01		8.59E-01	5.86E-02			-4.89E-01	1.56E-01		-1.26E+00	2.89E-04	Down	-1.11E-01	7.62E-01		4.13E-01	1.55E-01		Unigene14196_All//gi|31431841|gb|AAP53560.1|//3.00E-06//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene14196_All//5.00E-08//AT1G72390| unknown protein	Unigene14196_All//0.00E+00//TC176535			nr +
Unigene14199_All	1605	46.94	18.72	25.78	97.21	81.98	74.34	65.94	31.33	51.36	-1.33E+00	1.78E-85	Down	-8.65E-01	1.95E-41			-2.46E-01	4.36E-11		-3.87E-01	6.52E-23		-1.07E+00	6.67E-105	Down	-3.61E-01	2.56E-16		Unigene14199_All//gi|30697941|ref|NP_201208.2|//1.00E-148//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75245766|sp|Q8LTV3.1|PMTQ_ARATH RecName: Full=Probable methyltransferase PMT26 >gi|21928175|gb|AAM78114.1| AT5g64030/MBM17_13 [Arabidopsis thaliana] >gi|27764914|gb|AAO23578.1| At5g64030/MBM17_13 [Arabidopsis thaliana]	Unigene14199_All//3.00E-114//AT5G64030| dehydration-responsive protein-related	Unigene14199_All//0.00E+00//TC177186			nr -
Unigene1420_All	2326	1.21	1.81	1.79	36.92	34.46	40.72	76.89	239.90	116.96	5.74E-01	5.39E-02		5.56E-01	7.83E-02			-9.93E-02	1.05E-01		1.41E-01	1.15E-02		1.64E+00	0.00E+00	Up	6.05E-01	4.60E-103		Unigene1420_All//gi|224119712|ref|XP_002331142.1|//0.00E+00//sulfate /bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222873225|gb|EEF10356.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene1420_All//0.00E+00//AT5G19600| SULTR3;5 (SULFATE TRANSPORTER 3;5); sulfate transmembrane transporter	Unigene1420_All//0.00E+00//TC165200			nr -
Unigene14201_All	1320	0.75	2.57	3.07	4.26	2.09	2.87	6.02	6.49	5.01	1.77E+00	1.59E-06	Up	2.03E+00	1.29E-08	Up	-1.03E+00	9.87E-06	Down	-5.69E-01	2.34E-02		1.08E-01	6.29E-01		-2.65E-01	1.58E-01		Unigene14201_All//gi|297813231|ref|XP_002874499.1|//1.00E-105//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320336|gb|EFH50758.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14201_All//7.00E-94//AT4G08980| F-box family protein (FBW2)	Unigene14201_All//0.00E+00//TC141739			nr -
Unigene14202_All	1484	1.06	3.89	0.57	3.32	2.09	3.20	2.65	3.21	2.07	1.88E+00	2.11E-11	Up	-8.82E-01	1.13E-01			-6.70E-01	8.65E-03		-5.65E-02	8.60E-01		2.77E-01	3.05E-01		-3.58E-01	1.94E-01		Unigene14202_All//gi|297813231|ref|XP_002874499.1|//1.00E-105//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320336|gb|EFH50758.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14202_All//5.00E-96//AT4G08980| F-box family protein (FBW2)	Unigene14202_All//0.00E+00//gi|78334500|gb|DT554774.1|DT554774			nr +
Unigene14203_All	1302	10.61	4.36	4.54	7.58	5.69	5.17	4.90	1.83	1.90	-1.28E+00	1.76E-15	Down	-1.22E+00	8.32E-14	Down	-4.14E-01	1.94E-02		-5.52E-01	2.15E-03		-1.42E+00	1.49E-10	Down	-1.37E+00	2.30E-10	Down	Unigene14203_All//gi|297793507|ref|XP_002864638.1|//1.00E-149//protein-s-isoprenylcysteine O-methyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297310473|gb|EFH10897.1| protein-s-isoprenylcysteine O-methyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene14203_All//6.00E-137//AT5G59500| unknown protein	Unigene14203_All//0.00E+00//DW241851			nr +
Unigene14205_All	1857	1.27	3.71	2.47	3.27	3.30	2.80	5.60	4.05	3.35	1.55E+00	1.89E-10	Up	9.60E-01	1.15E-03		1.23E-02	9.67E-01		-2.27E-01	4.02E-01		-4.67E-01	3.23E-03		-7.43E-01	1.54E-06		Unigene14205_All//gi|30678946|ref|NP_187031.2|//1.00E-159//EDA30 (embryo sac development arrest 30) [Arabidopsis thaliana]	Unigene14205_All//8.00E-150//AT3G03810| EDA30 (embryo sac development arrest 30)	Unigene14205_All//0.00E+00//TC168314			nr +
Unigene14206_All	2205	5.79	1.45	2.73	6.39	5.64	7.70	10.57	3.13	5.37	-2.00E+00	1.44E-26	Down	-1.09E+00	1.13E-10	Down	-1.82E-01	2.77E-01		2.69E-01	5.95E-02		-1.76E+00	3.17E-49	Down	-9.77E-01	4.62E-21		Unigene14206_All//gi|145338411|ref|NP_187835.2|//0.00E+00//PRMT3 (PROTEIN ARGININE METHYLTRANSFERASE 3); methyltransferase/ zinc ion binding [Arabidopsis thaliana] >gi|122230175|sp|Q9WYD6.1|ANM3_ARATH RecName: Full=Probable protein arginine N-methyltransferase 3	Unigene14206_All//0.00E+00//AT3G12270| PRMT3 (PROTEIN ARGININE METHYLTRANSFERASE 3); methyltransferase/ zinc ion binding	Unigene14206_All//0.00E+00//ES815103		GO:0016274//GO:0044464//GO:0046914	nr -
Unigene14207_All	1281	34.19	44.97	51.13	21.00	31.37	31.03	6.73	1.57	2.86	3.96E-01	1.03E-08		5.81E-01	2.87E-18		5.79E-01	1.00E-13		5.63E-01	7.40E-12		-2.10E+00	1.35E-23	Down	-1.23E+00	8.62E-12	Down	Unigene14207_All//gi|124359191|gb|ABD32189.2|//3.00E-09//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene14207_All//4.00E-07//AT3G09510| nucleic acid binding	Unigene14207_All//0.00E+00//BF271539		GO:0003824//GO:0005488	nr +
Unigene14211_All	1568	5.84	6.14	6.55	5.59	4.63	4.84	2.64	0.75	2.21	7.24E-02	7.12E-01		1.67E-01	3.97E-01		-2.71E-01	1.86E-01		-2.09E-01	3.51E-01		-1.82E+00	7.76E-10	Down	-2.58E-01	3.58E-01		Unigene14211_All//gi|18396510|ref|NP_566201.1|//1.00E-165//lecithin:cholesterol acyltransferase family protein / LACT family protein [Arabidopsis thaliana] >gi|33312308|gb|AAQ04051.1|AF421148.1 phospholipase A1 [Arabidopsis thaliana] >gi|15809942|gb|AAL06898.1| AT3g03310/T21P5_27 [Arabidopsis thaliana] >gi|15912273|gb|AAL08270.1| AT3g03310/T21P5_27 [Arabidopsis thaliana] >gi|21360561|gb|AAM47477.1| AT3g03310/T21P5_27 [Arabidopsis thaliana]	Unigene14211_All//7.00E-167//AT3G03310| lecithin:cholesterol acyltransferase family protein / LACT family protein	Unigene14211_All//0.00E+00//ES848792		GO:0008374//GO:0044238	nr -
Unigene14212_All	2559	1.80	2.10	0.71	9.30	11.37	12.37	11.05	6.78	8.62	2.22E-01	4.06E-01		-1.35E+00	9.83E-06	Down	2.89E-01	3.07E-03		4.11E-01	1.11E-05		-7.06E-01	1.83E-14		-3.58E-01	5.71E-05		Unigene14212_All//gi|115488128|ref|NP_001066551.1|//1.00E-179//Os12g0271600 [Oryza sativa (japonica Group)] >gi|113649058|dbj|BAF29570.1| Os12g0271600 [Oryza sativa (japonica Group)]	Unigene14212_All//2.00E-82//AT5G55860| unknown protein	Unigene14212_All//0.00E+00//TC165327			nr -

Unigene14213_All	356	1.62	2.28	3.59	7.28	6.58	5.07	13.30	6.34	5.93	4.94E-01	5.26E-01		1.15E+00	6.95E-02		-1.46E-01	7.47E-01		-5.20E-01	2.05E-01		-1.07E+00	1.99E-05	Down	-1.17E+00	2.40E-06	Down	Unigene14213_All//gi|98960881|gb|AB558924.1|//2.00E-07//At5g49110 [Arabidopsis thaliana]	Unigene14213_All//1.00E-08//AT5G49410| unknown protein	Unigene14213_All//8.00E-135//TC167333				nr +
Unigene14215_All	741	2.97	0.89	1.29	4.84	1.95	2.07	2.85	1.64	1.94	-1.74E+00	1.97E-04	Down	-1.20E+00	9.38E-03		-1.31E+00	2.05E-05	Down	-1.22E+00	1.72E-04	Down	-8.03E-01	4.24E-02		-5.60E-01	1.43E-01			Unigene14215_All//2.00E-94//DR456919				
Unigene14216_All	1306	106.32	90.75	66.18	132.85	109.55	128.09	289.97	161.61	88.31	-2.29E-01	1.47E-07		-6.84E-01	8.26E-51		-2.78E-01	1.98E-15		-5.27E-02	2.65E-01		-8.43E-01	5.90E-250		-1.72E+00	0.00E+00	Down	Unigene14216_All//gi|211906450|gb|ACJ11718.1|//0.00E+00//phosphoglycerate kinase [Gossypium hirsutum]	Unigene14216_All//4.00E-167//AT1G79550| PGK (PHOSPHOGLYCERATE KINASE); phosphoglycerate kinase	Unigene14216_All//0.00E+00//TC129980		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms	GO:0006007//GO:0016301//GO:0044424	nr +
Unigene14219_All	1915	4.95	11.48	5.78	10.72	11.65	13.75	14.99	20.34	20.72	1.22E+00	3.47E-22	Up	2.26E-01	2.37E-01		1.21E-01	3.85E-01		3.60E-01	6.22E-04		4.40E-01	7.57E-09		4.67E-01	3.23E-10		Unigene14219_All//gi|115470227|ref|NP_001058712.1|//3.00E-24//Os07g0107900 [Oryza sativa Japonica Group] >gi|113610248|dbj|BAF20626.1|Os07g0107900 [Oryza sativa Japonica Group]	Unigene14219_All//1.00E-26//AT5G53930| unknown protein	Unigene14219_All//0.00E+00//TC158708				nr +
Unigene1422_All	1219	1.76	4.82	2.93	5.76	6.21	11.41	16.79	20.54	35.49	1.45E+00	2.72E-08	Up	7.34E-01	3.11E-02		1.09E-01	6.70E-01		9.86E-01	5.49E-11		2.91E-01	3.34E-03		1.08E+00	1.05E-44	Up	Unigene1422_All//gi|18650616|gb|AAL75907.1|//8.00E-84//AT4g03420/F9H3_4 [Arabidopsis thaliana] >gi|20453247|gb|AAM19862.1|AT4g03420/F9H3_4 [Arabidopsis thaliana]	Unigene1422_All//6.00E-79//AT4G03420| unknown protein	Unigene1422_All//0.00E+00//gi|11203685|gb|BF272615.1|BF272615				nr -
Unigene14221_All	227	2.30	5.36	3.28	8.78	2.43	1.99	3.17	2.03	1.93	1.22E+00	5.24E-02		5.11E-01	5.47E-01		-1.85E+00	4.61E-05	Down	-2.14E+00	2.33E-05	Down	-6.45E-01	4.01E-01		-7.14E-01	3.27E-01			Unigene14221_All//4.00E-108//TC137767				
Unigene14223_All	1378	22.25	10.30	22.72	31.81	32.76	25.43	6.50	1.61	3.01	-1.11E+00	8.64E-27	Down	3.03E-02	7.84E-01		4.24E-02	6.82E-01		-3.23E-01	4.08E-05		-2.02E+00	3.16E-23	Down	-1.11E+00	1.70E-10	Down	Unigene14223_All//gi|15226087|ref|NP_179134.1|//1.00E-147//leucine-rich repeat family protein [Arabidopsis thaliana]	Unigene14223_All//2.00E-123//AT2G15320| leucine-rich repeat family protein	Unigene14223_All//0.00E+00//TC135980		ko04626|Plant-pathogen interaction		nr +
Unigene14224_All	1465	18.96	17.26	17.30	13.84	12.43	12.36	9.73	5.34	2.94	-1.36E-01	2.33E-01		-1.32E-01	2.66E-01		-1.54E-01	2.61E-01		-1.63E-01	2.39E-01		-8.66E-01	1.28E-10		-1.73E+00	1.17E-30	Down	Unigene14224_All//gi|115438526|ref|NP_001043561.1|//3.00E-53//Os01g0613300 [Oryza sativa Japonica Group] >gi|113533092|dbj|BAF05475.1|Os01g0613300 [Oryza sativa Japonica Group]	Unigene14224_All//4.00E-59//AT1G29040| unknown protein	Unigene14224_All//0.00E+00//TC144009			GO:0009536//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene14225_All	1310	46.01	202.52	109.83	28.67	61.41	51.75	28.72	37.74	42.30	2.14E+00	0.00E+00	Up	1.26E+00	4.16E-145	Up	1.10E+00	3.58E-80	Up	8.52E-01	2.36E-40		3.94E-01	4.13E-09		5.58E-01	6.50E-19		Unigene14225_All//gi|15237049|ref|NP_194461.1|//7.00E-41//zinc finger (B-box type) family protein [Arabidopsis thaliana]	Unigene14225_All//1.00E-25//AT4G27310| zinc finger (B-box type) family protein	Unigene14225_All//0.00E+00//TC172216	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene14226_All	1046	42.67	22.23	48.16	31.81	37.63	46.50	78.13	28.77	39.61	-9.40E-01	1.59E-29		1.75E-01	3.33E-02		2.42E-01	3.75E-03		5.48E-01	1.06E-13		-1.44E+00	1.82E-128	Down	-9.80E-01	6.07E-72		Unigene14226_All//gi|224123262|ref|XP_002319035.1|//1.00E-65//histidine phosphotransfer protein [Populus trichocarpa] >gi|222857411|gb|EEE94958.1|histidine phosphotransfer protein [Populus trichocarpa]	Unigene14226_All//9.00E-49//AT3G21510| AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 1); histidine phosphotransfer kinase	Unigene14226_All//0.00E+00//TC176768			GO:0008152//GO:0016628//GO:0023060//GO:0060089	nr +
Unigene14227_All	1779	6.18	11.05	4.67	10.30	9.66	11.22	14.31	31.48	31.46	8.39E-01	3.42E-11		-4.04E-01	2.66E-02		-9.33E-02	5.51E-01		1.23E-01	4.05E-01		1.14E+00	3.34E-61	Up	1.14E+00	1.85E-62	Up	Unigene14227_All//gi|30697711|ref|NP_177025.2|//2.00E-72//agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein [Arabidopsis thaliana] >gi|30725466|gb|AAP37755.1|At1g68580 [Arabidopsis thaliana]	Unigene14227_All//2.00E-78//AT1G68580| agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein	Unigene14227_All//0.00E+00//ES792785				nr -
Unigene14229_All	1279	0.70	1.90	1.50	28.32	20.62	21.26	6.71	10.56	14.61	1.45E+00	6.88E-04	Up	1.11E+00	2.53E-02		-4.57E-01	1.88E-08		-4.14E-01	1.69E-06		6.53E-01	1.67E-06		1.12E+00	5.13E-21	Up	Unigene14229_All//gi|219560132|gb|ACL27274.1|//2.00E-74//homeodomain leucine-zipper 1 [Nicotiana benthamiana]	Unigene14229_All//9.00E-62//AT4G37790| HAT22; transcription factor	Unigene14229_All//0.00E+00//TC168379	HB		GO:0001071//GO:0003677//GO:0006351//GO:0009725//GO:0010468//GO:0043231	nr +
Unigene14230_All	1607	4.69	2.68	3.28	1.61	1.48	0.98	0.95	1.20	8.75	-8.07E-01	1.49E-04		-5.15E-01	2.10E-02		-1.25E-01	7.92E-01		-7.13E-01	7.29E-02		3.37E-01	4.47E-01		3.21E+00	1.89E-61	Up	Unigene14230_All//gi|15220982|ref|NP_171690.1|//1.00E-08//PFC1 (PALEFACE 1); mRNA (2'-O-methyladenosine-N6-)-methyltransferase [Arabidopsis thaliana] >gi|3005590|gb|AAC09322.1|dimethyladenosine transferase [Arabidopsis thaliana]	Unigene14230_All//5.00E-10//AT1G01860| PFC1 (PALEFACE 1); mRNA (2'-O-methyladenosine-N6-)-methyltransferase	Unigene14230_All//3.00E-14//CO084775			GO:0006364//GO:0006950//GO:0008170//GO:0008174//GO:0008649//GO:0043231	nr +
Unigene14231_All	1476	7.41	3.67	4.40	1.28	1.47	2.51	1.35	0.79	0.89	-1.01E+00	9.70E-09	Down	-7.51E-01	2.60E-05		1.97E-01	7.04E-01		9.68E-01	2.42E-03		-7.64E-01	6.34E-02		-5.96E-01	1.32E-01		Unigene14231_All//gi|15220982|ref|NP_171690.1|//1.00E-123//PFC1 (PALEFACE 1); mRNA (2'-O-methyladenosine-N6-)-methyltransferase [Arabidopsis thaliana] >gi|3005590|gb|AAC09322.1|dimethyladenosine transferase [Arabidopsis thaliana]	Unigene14231_All//3.00E-124//AT1G01860| PFC1 (PALEFACE 1); mRNA (2'-O-methyladenosine-N6-)-methyltransferase	Unigene14231_All//2.00E-95//CO084775			GO:0006364//GO:0008170//GO:0008649//GO:0043231	nr -
Unigene14233_All	1626	1.61	2.84	2.00	4.07	3.03	1.36	5.82	5.37	13.11	8.18E-01	3.73E-03		3.12E-01	3.83E-01		-4.28E-01	5.70E-02		-1.58E+00	4.25E-11	Down	-1.17E-01	5.65E-01		1.17E+00	1.95E-25	Up	Unigene14233_All//gi|193788742|gb|ACF20470.1|//1.00E-132//At4g12840 [Arabidopsis thaliana]	Unigene14233_All//2.00E-151//AT4G18530| unknown protein	Unigene14233_All//0.00E+00//TC135103				nr -
Unigene14234_All	1910	1.70	2.94	3.26	4.36	3.59	2.10	5.62	5.27	5.03	7.94E-01	1.58E-03		9.42E-01	1.42E-04		-2.80E-01	1.83E-01		-1.05E+00	1.38E-07	Down	-9.24E-02	6.47E-01		-1.62E-01	3.41E-01		Unigene14234_All//gi|240254425|ref|NP_178255.4|//0.00E+00//ATP binding / kinase [Arabidopsis thaliana]	Unigene14234_All//1.00E-152//AT2G01460| ATP binding / kinase	Unigene14234_All//0.00E+00//ES813947			GO:0008152//GO:0016772//GO:0016787//GO:0032559	nr +
Unigene14235_All	1909	17.71	7.01	10.80	38.46	41.54	63.47	0.00	0.00	0.00	-1.34E+00	3.41E-39	Down	-7.14E-01	9.77E-14		1.11E-01	7.94E-02		7.23E-01	3.67E-54		null	null		null	null		Unigene14235_All//gi|115440537|ref|NP_001044548.1|//2.00E-81//Os01g0802700 [Oryza sativa Japonica Group] >gi|75110110|sp|Q5VQY3.1|PIN5_ORYSJ RecName: Full=Probable auxin efflux carrier component 5; AltName: Full=OsPIN5 >gi|113534079|dbj|BAF06162.1|Os01g0802700 [Oryza sativa Japonica Group] >gi|294831580|tpd|FAA00687.1| TPA: auxin efflux carrier [Oryza sativa Japonica Group]	Unigene14235_All//8.00E-65//AT1G23080| PIN7 (PIN-FORMED 7); auxin efflux transmembrane transporter/ auxin:hydrogen symporter/ transporter				GO:0006810//GO:0031224	nr +
Unigene14236_All	2080	7.92	6.85	4.05	17.82	14.07	25.21	22.54	13.36	11.09	-2.11E-01	1.45E-01		-9.70E-01	2.03E-11		-3.41E-01	3.23E-05		5.01E-01	1.34E-12		-7.55E-01	3.06E-26		-1.02E+00	1.09E-44	Down	Unigene14236_All//gi|14488063|gb|AK63852.1|AF389279_1//9.00E-98//AT5g66540/K1F13_21 [Arabidopsis thaliana] >gi|23506141|gb|AAN31082.1|At5g66540/K1F13_21 [Arabidopsis thaliana]	Unigene14236_All//4.00E-88//AT5G66540| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: rRNA processing; LOCATED IN: cytosol, nucleolus, nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: U3 small nucleolar ribonucleoprotein complex, subunit Mpp10p (InterPro:IPR012173), Mpp10 protein (InterPro:IPR007151); Has 76240 Blast hits to 38667 proteins in 1479 species: Archae - 252; Bacteria - 6537; Metazoa - 31185; Fungi - 9935; Plants - 3937; Viruses - 750; Other Eukaryotes - 23644 (source: NCBI BLink).	Unigene14236_All//0.00E+00//ES828552			GO:0031981//GO:0032991//GO:0042254//GO:0044444	nr +
Unigene14237_All	2004	4.44	19.49	11.48	3.01	2.04	2.79	2.41	3.17	3.82	2.13E+00	1.91E-86	Up	1.37E+00	6.59E-27	Up	-5.57E-01	1.55E-02		-1.06E-01	6.80E-01		3.98E-01	6.40E-02		6.66E-01	2.68E-04		Unigene14237_All//gi|8403838|ref|NP_561600.1|//5.00E-85//AR791; actin binding [Arabidopsis thaliana] >gi|13605851|gb|AAK32911.1|AF367324_1 At1g52080/F5F19_14 [Arabidopsis thaliana] >gi|4220455|gb|AAD12682.1|Identical to gene gb|D88746 AR791 from Arabidopsis thaliana >gi|22137184|gb|AAM91437.1|At1g52080/F5F19_14 [Arabidopsis thaliana]	Unigene14237_All//2.00E-86//AT1G52080| AR791; actin binding	Unigene14237_All//0.00E+00//TC160584			GO:0009527//GO:0009658	nr +
Unigene14239_All	671	1.64	1.51	1.19	0.74	0.00	0.81	7.62	10.71	7.60	-1.17E-01	8.44E-01		-4.60E-01	4.97E-01		-9.54E+00	8.98E-04	Down	1.22E-01	9.21E-01		4.91E-01	1.23E-02		-4.70E-03	9.80E-01		Unigene14239_All//gi|209970603|gb|ACJ03064.1|//5.00E-48//AM19-5p [Malus floribunda]	Unigene14239_All//4.00E-21//AT2G34930| disease resistance family protein	Unigene14239_All//0.00E+00//TC136096		ko04626|Plant-pathogen interaction	GO:0003824	nr -
Unigene1424_All	1955	3.85	8.50	3.62	5.96	9.16	11.32	20.91	21.42	51.90	1.14E+00	2.06E-15	Up	-8.93E-02	7.01E-01		6.19E-01	3.91E-07		9.25E-01	1.81E-15		3.47E-02	7.05E-01		1.31E+00	1.03E-140	Up	Unigene1424_All//gi|18650616|gb|AAL75907.1|//1.00E-116//AT4g03420/F9H3_4 [Arabidopsis thaliana] >gi|20453247|gb|AAM19862.1|AT4g03420/F9H3_4 [Arabidopsis thaliana]	Unigene1424_All//1.00E-111//AT4G03420| unknown protein	Unigene1424_All//0.00E+00//TC177570				nr +
Unigene14240_All	619	0.34	1.64	0.69	4.10	5.12	1.61	1.91	3.04	13.58	2.28E+00	4.10E-03		1.03E+00	3.97E-01		3.19E-01	4.15E-01		-1.35E+00	7.72E-04	Down	6.68E-01	1.21E-01		2.83E+00	9.62E-33	Up	Unigene14240_All//gi|209970620|gb|ACJ03071.1|//1.00E-39//M18S-3Cp [Malus floribunda]	Unigene14240_All//6.00E-31//AT3G11080| AtRLP35 (Receptor Like Protein 35); kinase/ protein binding	Unigene14240_All//1.00E-39//ES811464		ko04626|Plant-pathogen interaction		nr +
Unigene14245_All	1221	10.20	48.64	14.74	16.93	19.91	19.57	0.45	0.92	4.11	2.25E+00	2.66E-140	Up	5.32E-01	8.09E-05		2.34E-01	3.94E-02		2.09E-01	8.28E-02		1.04E+00	7.39E-02		3.19E+00	2.96E-22	Up	Unigene14245_All//gi|164562231|gb|ABV61030.1|//2.00E-66//zinc finger-homeodomain protein 1 [Cucumis sativus]	Unigene14245_All//4.00E-42//AT1G49600| ZFHD1 (ZINC FINGER HOMEODOMAIN 1); DNA binding / transcription activator/ transcription factor	Unigene14245_All//0.00E+00//TC179093	zf-HD			nr -
Unigene14249_All	2021	112.74	228.05	94.70	14.39	14.59	10.79	0.04	0.00	0.00	1.02E+00	0.00E+00	Up	-2.52E-01	1.52E-13		1.90E-02	8.82E-01		-4.15E-01	2.13E-05		-5.39E+00	4.04E-01		-5.39E+00	3.59E-01		Unigene14249_All//gi|30678265|ref|NP_171723.2|//0.00E+00//CER1 (ECERIFERUM 1); octadecanal decarbonylase [Arabidopsis thaliana]	Unigene14249_All//0.00E+00//AT1G02205| CER1 (ECERIFERUM 1); octadecanal decarbonylase	Unigene14249_All//0.00E+00//TC148723		ko00100|Steroid biosynthesis	GO:0003006//GO:0003824//GO:0006633//GO:0031224//GO:0043231//GO:0043667//GO:0046914	nr +
Unigene1425_All	2499	4.69	1.99	3.62	3.33	3.14	2.17	3.54	1.12	1.82	-1.24E+00	1.39E-12	Down	-3.73E-01	3.50E-02		-8.35E-02	7.41E-01		-6.18E-01	1.74E-03		-1.66E+00	1.04E-17	Down	-9.60E-01	2.53E-08		Unigene1425_All//gi|297834714|ref|XP_002885239.1|//0.00E+00//EMB1270 [Arabidopsis lyrata subsp. lyrata] >gi|297331079|gb|EFH61498.1|EMB1270 [Arabidopsis lyrata subsp. lyrata]	Unigene1425_All//0.00E+00//AT3G18110| EMB1270 (embryo defective 1270)	Unigene1425_All//0.00E+00//ES796531				nr +
Unigene14250_All	2365	1.19	0.60	0.81	4.68	2.37	5.88	9.06	3.92	5.14	-9.94E-01	8.04E-03		-5.60E-01	1.52E-01		-9.78E-01	7.18E-10		3.31E-01	3.35E-02		-1.21E+00	2.84E-26	Down	-8.19E-01	1.17E-14		Unigene14250_All//gi|145338044|ref|NP_186956.2|//0.00E+00//ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene14250_All//0.00E+00//AT3G03060| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene14250_All//0.00E+00//TC158583		ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03050|Proteasome	GO:0005618//GO:0032559//GO:0042623//GO:0043234//GO:0046914	nr +
Unigene14254_All	2045	85.35	16.77	42.26	112.51	101.40	131.10	70.23	21.28	25.73	-2.35E+00	0.00E+00	Down	-1.01E+00	1.28E-124	Down	-1.50E-01	1.61E-06		2.21E-01	9.57E-14		-1.72E+00	3.87E-292	Down	-1.45E+00	1.95E-233	Down	Unigene14254_All//gi|21553837|gb|AAM62930.1|//0.00E+00//phytochelatin synthetase-like protein [Arabidopsis thaliana]	Unigene14254_All//0.00E+00//AT5G60920| COB (COBRA)	Unigene14254_All//0.00E+00//TC136204			GO:0005618//GO:0005746//GO:0006970//GO:0009986//GO:0015078//GO:0016049//GO:0030198//GO:0031225//GO:0031410//GO:0045333	nr -

Unigene14255_All	1242	3.62	1.63	2.96	4.57	4.94	4.15	3.23	2.69	2.34	-1.15E+00	7.88E-05	Down	-2.92E-01	3.59E-01		1.10E-01	7.13E-01		-1.41E-01	6.13E-01		-2.65E-01	3.82E-01		-4.66E-01	7.90E-02		Unigene14255_All//gi|297803194|ref|XP_002869481.1|//1.00E-150//pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315317|gb|EFH45740.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14255_All//2.00E-141//AT4G28706| pfkB-type carbohydrate kinase family protein	Unigene14255_All//0.00E+00//TC165976		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene14256_All	2892	5.55	2.65	2.84	14.14	9.24	11.31	28.60	7.79	8.25	-1.07E+00	1.41E-13	Down	-9.70E-01	3.84E-11		-6.14E-01	7.02E-16		-3.23E-01	8.07E-05		-1.88E+00	1.93E-189	Down	-1.79E+00	2.73E-183	Down	Unigene14256_All//gi|145338243|ref|NP_187434.2|//0.00E+00//ATP binding [Arabidopsis thaliana]	Unigene14256_All//0.00E+00//AT3G07770| ATP binding	Unigene14256_All//0.00E+00//gi|78351641|gb|DT571915.1|DT571915		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0003006//GO:0005515//GO:0006970//GO:0009416//GO:0009526//GO:0009532//GO:0010035//GO:0016020//GO:0032559//GO:0044267	nr +
Unigene14257_All	367	1.14	5.52	4.06	0.95	0.75	1.23	2.30	3.99	3.80	2.28E+00	1.73E-05	Up	1.83E+00	2.94E-03		-3.40E-01	7.86E-01		3.73E-01	7.32E-01		7.91E-01	1.12E-01		7.22E-01	1.40E-01		Unigene14257_All//gi|42565106|ref|NP_188849.3|//7.00E-18//phototropic-responsive NPH3 protein-related [Arabidopsis thaliana]	Unigene14257_All//3.00E-19//AT3G22104| phototropic-responsive NPH3 protein-related			GO:0005488	nr -
Unigene14258_All	2125	1.70	5.34	4.08	2.93	3.92	2.06	10.66	10.33	17.32	1.65E+00	2.68E-18	Up	1.27E+00	2.27E-09	Up	4.20E-01	3.60E-02		-5.07E-01	3.39E-02		-4.65E-02	7.10E-01		7.00E-01	8.83E-19		Unigene14258_All//gi|42565106|ref|NP_188849.3|//1.00E-111//phototropic-responsive NPH3 protein-related [Arabidopsis thaliana]	Unigene14258_All//8.00E-101//AT3G22104| phototropic-responsive NPH3 protein-related	Unigene14258_All//1.00E-125//CO072894				nr +
Unigene14259_All	2495	3.59	10.52	3.74	10.30	13.69	11.19	14.10	12.82	13.19	1.55E+00	6.66E-38	Up	5.88E-02	7.74E-01		4.10E-01	1.63E-06		1.19E-01	3.34E-01		-1.38E-01	1.27E-01		-9.62E-02	2.89E-01		Unigene14259_All//gi|15241733|ref|NP_198754.1|//8.00E-37//calmodulin-binding protein-related [Arabidopsis thaliana]	Unigene14259_All//1.00E-22//AT5G39380| calmodulin-binding protein-related	Unigene14259_All//0.00E+00//TC157324				nr -
Unigene14260_All	1810	1.27	0.45	0.71	3.19	2.38	2.32	2.94	3.14	2.99	-1.51E+00	6.57E-04	Down	-8.49E-01	5.44E-02		-4.25E-01	8.34E-02		-4.60E-01	7.00E-02		9.36E-02	7.12E-01		2.44E-02	9.42E-01		Unigene14260_All//gi|115473321|ref|NP_001060259.1|//7.00E-16//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene14260_All//3.00E-06//AT2G41590| unknown protein	Unigene14260_All//2.00E-87//DW230999				nr +
Unigene14264_All	2727	7.62	2.82	4.80	20.44	19.60	12.72	36.03	7.51	14.62	-1.43E+00	6.24E-27	Down	-6.65E-01	9.21E-08		-6.08E-02	5.02E-01		-6.84E-01	3.87E-23		-2.26E+00	9.53E-287	Down	-1.30E+00	8.52E-136	Down	Unigene14264_All//gi|75191439|sp|Q9MS64.1|Y1143_ARATH//0.00E+00//Rec Name: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g14390; Flags: Precursor >gi|7262681|gb|AAF43939.1|AC012188_16 Contains similarity to a Receptor-like Protein Kinase 5 Precursor from Arabidopsis thaliana gi|1350783 and contains an Eukaryotic Protein Kinase PF|00069 domain and Leucine Rich PF|00560 repeats >gi|224588392|gb|ACN59230.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene14264_All//0.00E+00//AT1G14390| leucine-rich repeat transmembrane protein kinase, putative	Unigene14264_All//0.00E+00//TC155538		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0007167//GO:0032559	nr +
Unigene14265_All	2534	2.99	1.48	1.07	8.81	8.78	9.11	6.19	3.83	3.71	-1.02E+00	2.35E-06	Down	-1.48E+00	2.63E-10	Down	-4.60E-03	9.66E-01		4.84E-02	7.19E-01		-6.94E-01	3.58E-08		-7.39E-01	2.56E-09		Unigene14265_All//gi|15227266|ref|NP_179556.1|//6.00E-70//DC1 domain-containing protein [Arabidopsis thaliana] >gi|49917427|gb|AAS49038.1|At2g19660 [Arabidopsis thaliana]	Unigene14265_All//9.00E-77//AT5G37620| DC1 domain-containing protein	Unigene14265_All//0.00E+00//gi|109878350|gb|DW507321.1|DW507321				nr +
Unigene14267_All	1401	3.14	8.54	4.49	2.56	6.44	3.19	6.46	10.47	27.58	1.44E+00	6.20E-16	Up	5.16E-01	3.76E-02		1.33E+00	2.38E-12	Up	3.18E-01	3.15E-01		6.97E-01	9.60E-08		2.09E+00	2.04E-104	Up	Unigene14267_All//gi|42569943|ref|NP_182100.2|//2.00E-25//BAP2 (BON ASSOCIATION PROTEIN 2) [Arabidopsis thaliana] >gi|94442457|gb|ABF19016.1|At2g45760 [Arabidopsis thaliana]	Unigene14267_All//1.00E-26//AT2G45760| BAP2 (BON ASSOCIATION PROTEIN 2)	Unigene14267_All//0.00E+00//TC145416			GO:0006952//GO:0008289//GO:0009628//GO:0009987//GO:0010033//GO:0044464	nr -
Unigene14269_All	1307	32.47	13.80	17.68	59.38	40.55	49.66	47.23	16.76	24.72	-1.23E+00	2.38E-43	Down	-8.77E-01	4.26E-24		-5.50E-01	1.71E-24		-2.58E-01	8.37E-06		-1.50E+00	1.33E-102	Down	-9.34E-01	2.06E-50		Unigene14269_All//gi|12802327|gb|AK07827.1|AF297643_1//1.00E-170//mitochondrial processing peptidase beta subunit [Cucumis melo]	Unigene14269_All//7.00E-147//AT3G02090| mitochondrial processing peptidase beta subunit, putative	Unigene14269_All//0.00E+00//TC148340				nr -
Unigene14273_All	942	12.39	13.23	10.23	18.40	21.46	12.47	37.07	83.77	32.31	9.53E-02	6.19E-01		-2.76E-01	1.34E-01		2.22E-01	8.35E-02		-5.62E-01	1.43E-05		1.18E+00	1.51E-90	Up	-1.98E-01	1.59E-02		Unigene14273_All//gi|4206122|gb|AAD11430.1|//1.00E-32//protein phosphatase 2C homolog [Mesembryanthemum crystallinum]	Unigene14273_All//2.00E-31//AT4G38520| protein phosphatase 2C family protein / PP2C family protein	Unigene14273_All//0.00E+00//TC138580			GO:0004721//GO:0006464//GO:0043169//GO:0043234	nr +
Unigene14279_All	1748	7.78	5.94	6.31	6.01	5.10	4.39	6.99	5.79	3.44	-3.89E-01	1.16E-02		-3.04E-01	6.60E-02		-2.37E-01	2.09E-01		-4.53E-01	1.01E-02		-2.73E-01	7.42E-02		-1.02E+00	2.74E-12	Down	Unigene14279_All//gi|89000983|gb|AB359081.1|//3.00E-92//At5g63040 [Arabidopsis thaliana]	Unigene14279_All//9.00E-94//AT5G63040| unknown protein	Unigene14279_All//0.00E+00//TC172805			GO:0009526	nr +
Unigene14281_All	1099	16.52	43.43	37.65	27.74	25.38	34.11	13.93	23.54	19.68	1.39E+00	2.19E-58	Up	1.19E+00	1.59E-38	Up	-1.28E-01	2.45E-01		2.98E-01	6.15E-04		7.57E-01	6.31E-15		4.99E-01	1.22E-06					Unigene14281_All//8.00E-36//DW232422				
Unigene14283_All	2198	2.88	0.85	2.28	3.49	2.43	3.60	10.10	4.39	6.49	-1.76E+00	1.82E-11	Down	-3.39E-01	1.83E-01		-5.23E-01	8.88E-03		4.30E-02	8.66E-01		-1.20E+00	6.19E-27	Down	-6.38E-01	4.12E-10		Unigene14283_All//gi|75150653|sp|Q8GNL1.1|Y3739_ARATH//0.00E+00//Rec Name: Full=Uncharacterized membrane protein At3g27390 >gi|27311557|gb|AA000744.1|Unknown protein [Arabidopsis thaliana]	Unigene14283_All//4.00E-180//AT5G40640| unknown protein	Unigene14283_All//0.00E+00//DW497310				nr +
Unigene14284_All	1601	5.82	6.71	3.83	14.19	13.16	12.69	15.66	31.07	37.25	2.06E-01	2.72E-01		-6.05E-01	2.02E-03		-1.08E-01	4.26E-01		-1.61E-01	2.21E-01		9.88E-01	2.00E-43		1.25E+00	3.85E-77	Up	Unigene14284_All//gi|18491247|gb|AAL69448.1|//6.00E-54//At2g44600/F16B22.9 [Arabidopsis thaliana]	Unigene14284_All//2.00E-42//AT2G44600| unknown protein	Unigene14284_All//0.00E+00//TC156262			GO:0016020	nr -
Unigene14286_All	1643	4.01	11.26	5.09	2.55	2.03	2.45	33.84	16.79	20.00	1.49E+00	2.54E-25	Up	3.43E-01	1.14E-01		-3.25E-01	3.06E-01		-5.80E-02	8.65E-01		-1.01E+00	2.36E-50	Down	-7.58E-01	3.89E-32		Unigene14286_All//gi|115468176|ref|NP_001057687.1|//1.00E-151//Os06g0494400 [Oryza sativa Japonica Group] >gi|113595727|dbj|BAF19601.1|Os06g0494400 [Oryza sativa Japonica Group]	Unigene14286_All//1.00E-139//AT5G52450| MATE efflux protein-related	Unigene14286_All//8.00E-12//TC160792			GO:0015291//GO:0015893//GO:0044464	nr -
Unigene14287_All	1555	35.50	10.52	18.63	56.67	74.41	67.29	24.55	30.99	27.16	-1.75E+00	1.67E-94	Down	-9.30E-01	2.04E-34		3.93E-01	2.58E-19		2.48E-01	4.75E-07		3.36E-01	8.10E-07		1.46E-01	5.81E-02		Unigene14287_All//gi|27311805|gb|AA000868.1|//1.00E-123//Unknown protein [Arabidopsis thaliana] >gi|30984572|gb|AAP42749.1|At3g52060 [Arabidopsis thaliana]	Unigene14287_All//2.00E-119//AT3G52060| unknown protein	Unigene14287_All//0.00E+00//TC171198			GO:0031410	nr +
Unigene14288_All	1690	2.41	2.07	0.60	2.71	2.55	2.08	3.55	1.90	5.35	-2.23E-01	4.82E-01		-2.01E+00	1.41E-08	Down	-9.05E-02	8.05E-01		-3.80E-01	2.07E-01		-9.00E-01	3.25E-05		5.91E-01	3.77E-04		Unigene14288_All//gi|224143888|ref|XP_002325110.1|//0.00E+00//SET domain protein [Populus trichocarpa] >gi|222866544|gb|EEF03675.1| SET domain protein [Populus trichocarpa]	Unigene14288_All//3.00E-171//AT4G30860| SDG4 (SET DOMAIN GROUP 4); histone methyltransferase	Unigene14288_All//3.00E-138//DN818176		ko00310|Lysine degradation	GO:0016279//GO:0043231//GO:0046914	nr -
Unigene14290_All	1902	7.95	6.77	3.89	13.33	10.90	12.42	6.29	4.29	4.61	-2.33E-01	1.26E-01		-1.03E+00	1.45E-11	Down	-2.91E-01	5.56E-03		-1.02E-01	4.40E-01		-5.54E-01	1.41E-04		-4.49E-01	1.59E-03		Unigene14290_All//gi|297825719|ref|XP_002880742.1|//1.00E-155//galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326581|gb|EFH57001.1|galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14290_All//4.00E-129//AT2G26100| galactosyltransferase family protein	Unigene14290_All//0.00E+00//TC175795				nr +
Unigene14295_All	759	2.07	3.60	1.75	1.58	2.09	2.74	4.12	6.77	11.23	8.02E-01	3.56E-02		-2.38E-01	6.42E-01		4.06E-01	4.93E-01		7.97E-01	8.12E-02		7.16E-01	2.31E-03		1.45E+00	1.75E-14	Up	Unigene14295_All//gi|66271061|gb|AY43808.1|//3.00E-11//Fb17 [Gossypium hirsutum]		Unigene14295_All//2.00E-165//gi|164338764|gb|ES834975.1|ES834975				nr +
Unigene14296_All	1307	4.76	8.02	6.07	2.55	6.27	5.63	2.88	4.76	14.11	7.52E-01	2.09E-05		3.50E-01	1.18E-01		1.30E+00	7.93E-11	Up	1.14E+00	1.42E-07	Up	7.27E-01	5.57E-04		2.29E+00	3.75E-56	Up	Unigene14296_All//gi|66271061|gb|AY43808.1|//6.00E-11//Fb17 [Gossypium hirsutum]		Unigene14296_All//0.00E+00//gi|164338764|gb|ES834975.1|ES834975				nr +
Unigene14297_All	1201	0.44	1.52	0.98	1.16	1.15	0.68	0.88	1.25	4.68	1.80E+00	6.20E-04	Up	1.16E+00	8.16E-02		-1.81E-02	9.59E-01		-7.79E-01	1.82E-01		5.09E-01	3.12E-01		2.41E+00	1.17E-18	Up	Unigene14297_All//gi|66271061|gb|AY43808.1|//5.00E-11//Fb17 [Gossypium hirsutum]		Unigene14297_All//0.00E+00//TC130605				nr +
Unigene14299_All	1505	8.52	6.40	6.55	19.66	18.46	18.67	11.57	10.69	4.92	-4.13E-01	9.32E-03		-3.80E-01	2.33E-02		-9.06E-02	4.58E-01		-7.50E-02	5.56E-01		-1.14E-01	4.07E-01		-1.23E+00	7.18E-23	Down	Unigene14299_All//gi|124359459|gb|ABB32253.2|//0.00E+00//Esterase/lipase/thioesterase [Medicago truncatula]	Unigene14299_All//9.00E-135//AT3G01690| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Alpha/beta hydrolase fold-1 (InterPro:IPR000073); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G14390.1); Has 2954 Blast hits to 2948 proteins in 496 species: Archae - 2; Bacteria - 741; Metazoa - 618; Fungi - 134; Plants - 170; Viruses - 6; Other Eukaryotes - 1283 (source: NCBI BLink).	Unigene14299_All//0.00E+00//DW511312				nr -
Unigene14302_All	1423	1.91	3.81	1.72	5.60	3.94	5.84	10.43	15.10	26.43	9.95E-01	1.27E-04		-1.51E-01	7.00E-01		-5.06E-01	9.84E-03		6.02E-02	7.90E-01		5.34E-01	4.11E-07		1.34E+00	1.65E-54	Up	Unigene14302_All//gi|77550744|gb|AB93541.1|//1.00E-96//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene14302_All//4.00E-109//AT1G52155| unknown protein	Unigene14302_All//2.00E-77//gi|164353438|gb|ES805219.1|ES805219			GO:0044464	nr +
Unigene14305_All	1243	14.31	14.10	13.45	20.84	21.08	19.87	29.66	25.62	13.53	-2.10E-02	8.92E-01		-8.94E-02	5.82E-01		1.67E-02	9.05E-01		-6.84E-02	6.40E-01		-2.11E-01	1.01E-02		-1.13E+00	1.57E-41	Down	Unigene14305_All//gi|115453353|ref|NP_001050277.1|//2.00E-50//Os03g0390700 [Oryza sativa Japonica Group] >gi|108708565|gb|ABF96360.1|Transthyretin precursor family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548748|dbj|BAF12191.1|Os03g0390700 [Oryza sativa Japonica Group]	Unigene14305_All//4.00E-50//AT5G58220| TTL (Transthyretin-Like protein); steroid binding	Unigene14305_All//0.00E+00//TC132247		ko00230|Purine metabolism	GO:0000255//GO:0001558//GO:0005488//GO:0009898//GO:0016812//GO:0042579//GO:0043401//GO:0051234//GO:0051260	nr -
Unigene14309_All	1252	0.92	2.31	0.68	1.75	1.57	1.62	1.99	2.67	2.77	1.33E+00	5.21E-04	Up	-4.34E-01	5.10E-01		-1.59E-01	7.48E-01		-1.09E-01	8.04E-01		4.23E-01	1.80E-01		4.75E-01	1.03E-01		Unigene14309_All//gi|4056427|gb|AAC98001.1|//2.00E-86//Contains similarity to gb|AJ006354 zinc finger protein (ZAC) from Homo sapiens [Arabidopsis thaliana] >gi|28416647|gb|AAO42854.1|At1g05060 [Arabidopsis thaliana]	Unigene14309_All//1.00E-87//AT1G05060| unknown protein	Unigene14309_All//0.00E+00//TC164503			GO:0043231	nr -
Unigene14310_All	2079	4.13	2.75	3.59	7.38	10.60	7.43	7.54	4.50	3.41	-5.84E-01	3.05E-03		-2.03E-01	3.75E-01		5.23E-01	1.57E-06		9.70E-03	9.48E-01		-7.45E-01	3.89E-09		-1.15E+00	1.73E-18	Down	Unigene14310_All//gi|102139987|gb|ABF70122.1|//2.00E-29//transcriptional factor B3 family protein / AT hook motif-containing protein [Musa balbisiana]	Unigene14310_All//1.00E-15//AT4G33280| DNA binding / transcription factor	Unigene14310_All//0.00E+00//TC166691	ABI3VP1			nr +

Unigene14311_All	2035	0.93	0.87	0.42	0.91	1.25	0.55	0.91	0.18	0.65	-8.69E-02	8.47E-01			-1.14E+00	2.33E-02		4.67E-01	2.72E-01			-7.07E-01	1.48E-01		-2.31E+00	3.11E-06	Down	-5.01E-01	2.29E-01		Unigene14311_All//gi|115454147|ref|NP_001050674.1|//2.00E-18//0s03g0619600 [Oryza sativa Japonica Group] >gi|75120137|sp|Q6AV22.1|Y3196_ORYSJ RecName: Full=B3 domain-containing protein Os03g0619600 >gi|108709864|gb|ABF97659.1| B3 DNA binding domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549145|dbj|BAF12588.1| Os03g0619600 [Oryza sativa Japonica Group]	Unigene14311_All//3.00E-14//AT4G34400| DNA binding / transcription factor	Unigene14311_All//0.00E+00//TC166691	ABI3VP1			nr -
Unigene14312_All	1474	1.70	3.20	0.72	2.60	5.79	5.42	11.99	30.91	65.27	9.08E-01	1.16E-03			-1.24E+00	3.81E-03		1.15E+00	1.70E-09	Up	1.06E+00	2.54E-07	Up	1.37E+00	3.02E-66	Up	2.44E+00	0.00E+00	Up	Unigene14312_All//gi|15225326|ref|NP_180221.1|//7.00E-70//AR781 [Arabidopsis thaliana] >gi|27390378|gb|AM145601.1| AR781, similar to yeast pheromone receptor [Arabidopsis thaliana] >gi|23297321|gb|AAN12941.1| AR781 [Arabidopsis thaliana]	Unigene14312_All//3.00E-42//AT2G26530| AR781	Unigene14312_All//0.00E+00//TC141741			GO:0016020	nr -
Unigene14313_All	1111	3.30	1.46	1.87	2.82	2.79	2.93	4.11	1.62	1.40	-1.18E+00	3.36E-04	Down	-8.18E-01	1.47E-02		-1.81E-02	9.49E-01		5.13E-02	9.08E-01		-1.35E+00	3.32E-07	Down	-1.56E+00	4.52E-09	Down	Unigene14313_All//gi|108707128|gb|ABF94923.1|//8.00E-89//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene14313_All//3.00E-105//AT4G35987| unknown protein	Unigene14313_All//0.00E+00//ES808624			GO:0043231	nr +
Unigene14314_All	1601	15.07	6.17	8.61	34.51	23.44	34.58	0.55	1.75	0.80	-1.29E+00	1.32E-26	Down	-8.06E-01	3.45E-12		-5.58E-01	5.86E-18		3.30E-03	9.66E-01		1.66E+00	4.10E-06	Up	5.22E-01	3.24E-01		Unigene14314_All//gi|225456461|ref|XP_002284464.1|//1.00E-101//PREDICTED: similar to bHLH transcription factor Upa20 [Vitis vinifera]	Unigene14314_All//3.00E-50//AT5G59915| basic helix-loop-helix (bHLH) family protein	Unigene14314_All//0.00E+00//TC159484	bHLH	ko04712|Circadian rhythm - plant	GO:0009725//GO:0010468//GO:0043231	nr -
Unigene14315_All	1512	3.74	2.38	2.15	6.16	4.05	4.18	3.66	1.49	1.98	-6.51E-01	9.07E-03		-7.99E-01	2.17E-03		-6.04E-01	5.72E-04		-5.59E-01	2.63E-03		-1.30E+00	3.90E-08	Down	-8.90E-01	5.42E-05		Unigene14315_All//gi|297821058|ref|XP_002878412.1|//0.00E+00//EMB1703 [Arabidopsis lyrata subsp. lyrata] >gi|297324250|gb|EFH54671.1| EMB1703 [Arabidopsis lyrata subsp. lyrata]	Unigene14315_All//1.00E-157//AT3G61780| emb1703 (embryo defective 1703)	Unigene14315_All//0.00E+00//CO106656			GO:0003006//GO:0009536//GO:0019787//GO:0019941//GO:0032446//GO:0032501//GO:0046914	nr +
Unigene14318_All	1976	1.83	1.49	0.92	3.40	3.57	3.47	5.20	1.59	2.70	-2.97E-01	3.73E-01		-9.96E-01	3.45E-03		7.00E-02	8.16E-01		2.97E-02	9.27E-01		-1.71E+00	2.16E-21	Down	-9.45E-01	2.69E-09		Unigene14318_All//gi|42573726|ref|NP_974959.1|//1.00E-133//GTP binding [Arabidopsis thaliana] >gi|222423373|dbj|BAH19659.1| AT5G58370 [Arabidopsis thaliana]	Unigene14318_All//1.00E-124//AT5G58370| GTP binding	Unigene14318_All//0.00E+00//ES831214			GO:0032506//GO:0032561//GO:0044464	nr -
Unigene14319_All	1847	17.17	13.41	17.15	36.79	29.07	26.43	56.15	34.03	19.46	-3.56E-01	2.09E-04		-1.00E-03	9.91E-01		-3.40E-01	4.67E-09		-4.77E-01	6.48E-15		-7.22E-01	6.09E-53		-1.53E+00	6.54E-183	Down	Unigene14319_All//gi|224145672|ref|XP_002325726.1|//0.00E+00//calcium dependent protein kinase 12 [Populus trichocarpa] >gi|222862601|gb|EEF00108.1| calcium dependent protein kinase 12 [Populus trichocarpa]	Unigene14319_All//0.00E+00//AT1G35670| ATCDPK2 (CALCIUM-DEPENDENT PROTEIN KINASE 2); calmodulin-dependent protein kinase/ kinase	Unigene14319_All//0.00E+00//TC138640		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0009738//GO:0016020//GO:0032559//GO:0046872	nr +
Unigene14320_All	3985	2.98	2.34	2.83	4.64	3.78	3.14	5.70	4.33	2.73	-3.49E-01	3.74E-02		-7.32E-02	6.90E-01		-2.97E-01	1.95E-02		-5.63E-01	6.57E-06		-3.95E-01	1.17E-04		-1.06E+00	2.00E-23	Down	Unigene14320_All//gi|297829256|ref|XP_002882510.1|//1.00E-154//membrane protein [Arabidopsis lyrata subsp. lyrata] >gi|297328350|gb|EFH58769.1| membrane protein [Arabidopsis lyrata subsp. lyrata]	Unigene14320_All//5.00E-142//AT3G07080| membrane protein	Unigene14320_All//0.00E+00//CO094483				nr -
Unigene14325_All	818	24.43	18.52	26.95	18.57	16.46	17.23	11.68	7.26	5.50	-4.00E-01	1.22E-03		1.42E-01	2.99E-01		-1.74E-01	2.78E-01		-1.09E-01	5.39E-01		-6.87E-01	3.21E-05		-1.09E+00	1.00E-10	Down	Unigene14325_All//gi|164605014|dbj|BAF98303.1|//2.00E-97//geranylgeranyl-diphosphate synthase [Hevea brasiliensis]	Unigene14325_All//9.00E-74//AT4G38460| GGR (geranylgeranyl reductase); farnesyltranstransferase	Unigene14325_All//0.00E+00//TC140109		ko00900|Terpenoid backbone biosynthesis	GO:0004659//GO:0009536//GO:0016101//GO:0016628	nr -
Unigene14326_All	1503	6.30	6.68	2.98	6.23	5.22	4.18	5.32	4.25	3.23	8.32E-02	6.62E-01		-1.08E+00	4.70E-08	Down	-2.54E-01	2.02E-01		-5.77E-01	1.80E-03		-3.22E-01	9.40E-02		-7.17E-01	5.67E-05		Unigene14326_All//gi|115468966|ref|NP_001058082.1|//9.00E-81//Os06g0618000 [Oryza sativa Japonica Group] >gi|113596122|dbj|BAF19996.1| Os06g0618000 [Oryza sativa Japonica Group]	Unigene14326_All//2.00E-109//AT1G51130| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Nse4 (InterPro:IPR014854); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G20760.1); Has 200 Blast hits to 198 proteins in 89 species: Archae - 0; Bacteria - 0; Metazoa - 63; Fungi - 88; Plants - 37; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink).	Unigene14326_All//0.00E+00//gi|164355808|gb|ES834599.1|ES834599				nr -
Unigene14327_All	1609	5.92	9.45	4.24	9.16	8.15	7.97	7.17	6.08	16.74	6.75E-01	2.60E-06		-4.82E-01	1.37E-02		-1.69E-01	3.09E-01		-2.01E-01	2.20E-01		-2.39E-01	1.36E-01		1.22E+00	4.06E-34	Up	Unigene14327_All//gi|224137588|ref|XP_002327163.1|//2.00E-74//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222835478|gb|EEE73913.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene14327_All//6.00E-122//AT1G54330| ANAC020 (Arabidopsis NAC domain containing protein 20); transcription factor	Unigene14327_All//7.00E-145//DR456198	NAC			nr +
Unigene14328_All	1807	5.85	2.16	2.48	12.60	7.45	12.97	6.32	2.54	5.86	-1.44E+00	3.72E-14	Down	-1.24E+00	6.48E-11	Down	-7.58E-01	6.20E-13		4.21E-02	7.55E-01		-1.31E+00	3.11E-16	Down	-1.07E-01	5.35E-01		Unigene14328_All//gi|15227184|ref|NP_182320.1|//0.00E+00//SWA1 (SLOW WALKER1); nucleotide binding [Arabidopsis thaliana]	Unigene14328_All//2.00E-170//AT2G47990| SWA1 (SLOW WALKER1); nucleotide binding	Unigene14328_All//0.00E+00//TC173298		ko03018|RNA degradation	GO:0009553//GO:0031461//GO:0031981//GO:0042254	nr +
Unigene14329_All	970	74.06	86.14	80.53	53.05	55.03	78.17	26.85	35.68	88.47	2.18E-01	1.55E-04		1.21E-01	7.04E-02		5.28E-02	5.75E-01		5.59E-01	7.90E-22		4.10E-01	4.52E-07		1.72E+00	1.80E-177	Up	Unigene14329_All//gi|13877691|gb|AK43923.1|AF370604_1|/5.00E-06//Unknown protein [Arabidopsis thaliana] >gi|10773818|gb|ABF83640.1| At2g43340 [Arabidopsis thaliana]	Unigene14329_All//3.00E-07//AT2G43340| unknown protein	Unigene14329_All//0.00E+00//gi|48804668|gb|CO105982.1|CO105982				nr +
Unigene14330_All	2060	4.98	1.82	5.82	5.30	3.29	12.63	34.97	50.22	39.05	-1.45E+00	6.03E-14	Down	2.25E-01	2.26E-01		-6.85E-01	1.59E-05		1.25E+00	3.05E-29	Up	5.22E-01	6.91E-30		1.59E-01	2.44E-03		Unigene14330_All//gi|297826137|ref|XP_002880951.1|//0.00E+00//nodulin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326790|gb|EFH57210.1| nodulin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14330_All//0.00E+00//AT2G28120| nodulin family protein	Unigene14330_All//0.00E+00//TC175845			GO:0006810	nr +
Unigene14331_All	995	21.35	27.80	21.57	41.15	29.69	23.92	14.32	31.38	6.17	3.81E-01	2.26E-04		1.47E-02	9.26E-01		-4.71E-01	5.57E-10		-7.83E-01	1.55E-21		1.13E+00	3.49E-34	Up	-1.22E+00	1.82E-18	Down	Unigene14331_All//gi|288558967|sp|B9SA89.1|U497E_RICCO|/5.00E-84//RecName: Full=UPF0497 membrane protein 14	Unigene14331_All//3.00E-62//AT2G35760| integral membrane family protein	Unigene14331_All//0.00E+00//TC168315			GO:0031224	nr +
Unigene14332_All	722	2.68	4.49	6.42	2.97	2.48	2.63	3.92	1.79	1.66	7.44E-01	3.09E-02		1.26E+00	2.75E-05	Up	-2.59E-01	5.87E-01		-1.75E-01	6.91E-01		-1.13E+00	8.07E-04	Down	-1.25E+00	1.68E-04	Down				Unigene14332_All//4.00E-120//ES839918				
Unigene14333_All	920	7.85	9.47	6.19	5.20	3.89	2.95	1.01	2.63	1.13	2.72E-01	1.89E-01		-3.42E-01	1.44E-01		-4.17E-01	1.33E-01		-8.20E-01	2.53E-03		1.38E+00	2.52E-04	Up	1.85E-01	7.86E-01					Unigene14333_All//2.00E-131//ES839918				
Unigene14334_All	1041	2.11	5.26	6.34	3.16	3.01	3.30	1.83	1.32	1.07	1.32E+00	8.45E-07	Up	1.59E+00	5.71E-10	Up	-6.92E-02	8.38E-01		6.21E-02	8.78E-01		-4.64E-01	2.90E-01		-7.70E-01	5.65E-02					Unigene14334_All//9.00E-125//ES839918				
Unigene14335_All	1746	11.87	6.91	11.74	15.09	13.73	6.39	5.09	3.45	2.88	-7.81E-01	1.66E-10		-1.53E-02	9.24E-01		-1.37E-01	2.52E-01		-1.24E+00	1.54E-29	Down	-5.61E-01	1.13E-03		-8.23E-01	1.21E-06		Unigene14335_All//gi|30687001|ref|NP_850275.1|//4.00E-57//TRFL8 (TRF-LIKE 8); DNA binding [Arabidopsis thaliana] >gi|79324500|ref|NP_001031497.1| TRFL8 (TRF-LIKE 8); DNA binding [Arabidopsis thaliana]	Unigene14335_All//9.00E-42//AT2G37025| TRFL8 (TRF-LIKE 8); DNA binding	Unigene14335_All//0.00E+00//TC131994			GO:0003676//GO:0010468//GO:0043231	nr -
Unigene14336_All	1367	16.73	4.78	10.56	8.45	5.14	5.85	25.61	11.19	5.86	-1.81E+00	3.88E-41	Down	-6.64E-01	1.89E-08		-7.18E-01	2.86E-06		-5.32E-01	1.20E-03		-1.19E+00	1.16E-41	Down	-2.13E+00	6.87E-98	Down	Unigene14336_All//gi|22329014|ref|NP_194662.2|//2.00E-82//DER1 (DERLIN-1) [Arabidopsis thaliana] >gi|75161705|sp|Q8VZU9.1|DERL1_ARATH RecName: Full=Derlin-1; AltName: Full=AtDerlinl-1	Unigene14336_All//5.00E-79//AT4G29330| DER1 (DERLIN-1)	Unigene14336_All//3.00E-82//TC140227			GO:0019538//GO:0043231//GO:0044425	nr +
Unigene14337_All	398	1.05	0.00	0.00	0.63	0.52	0.00	5.31	0.63	2.20	-1.00E+01	1.05E-02		-1.00E+01	1.56E-02		-2.70E-01	8.23E-01		-9.29E+00	7.34E-02		-3.08E+00	2.88E-09	Down	-1.27E+00	1.15E-03									
Unigene14338_All	1429	0.04	0.14	0.00	0.35	0.24	0.06	2.16	0.79	0.36	1.95E+00	3.75E-01		-5.19E+00	6.25E-01		-5.33E-01	5.94E-01		-2.46E+00	4.83E-02		-1.45E+00	1.20E-05	Down	-2.58E+00	1.52E-11	Down	Unigene14338_All//gi|22329014|ref|NP_194662.2|//2.00E-82//DER1 (DERLIN-1) [Arabidopsis thaliana] >gi|75161705|sp|Q8VZU9.1|DERL1_ARATH RecName: Full=Derlin-1; AltName: Full=AtDerlinl-1	Unigene14338_All//5.00E-79//AT4G29330| DER1 (DERLIN-1)	Unigene14338_All//7.00E-83//TC140227			GO:0019538//GO:0043231//GO:0044425	nr +
Unigene14339_All	1872	33.40	19.22	21.31	147.90	126.69	151.56	66.15	21.50	28.60	-7.97E-01	3.28E-31		-6.49E-01	4.05E-21		-2.23E-01	3.84E-16		3.53E-02	3.58E-01		-1.62E+00	4.39E-231	Down	-1.21E+00	1.42E-152	Down	Unigene14339_All//gi|115468496|ref|NP_001057847.1|//3.00E-29//Os06g0554300 [Oryza sativa Japonica Group] >gi|537926271|dbj|BAD53684.1| dentin sialophosphoprotein-like [Oryza sativa Japonica Group] >gi|113595887|dbj|BAF19761.1| Os06g0554300 [Oryza sativa Japonica Group]	Unigene14339_All//2.00E-29//AT4G37820| unknown protein	Unigene14339_All//0.00E+00//TC148905		ko03040|Spliceosome		nr +
Unigene14340_All	2122	3.82	2.39	1.43	8.85	14.54	10.60	10.34	2.54	4.90	-6.79E-01	8.38E-04		-1.42E+00	2.59E-10	Down	7.16E-01	2.86E-15		2.60E-01	3.07E-02		-2.03E+00	4.16E-56	Down	-1.08E+00	3.38E-23	Down	Unigene14340_All//gi|115455609|ref|NP_001051405.1|//1.00E-39//Os03g0770900 [Oryza sativa Japonica Group] >gi|50872452|gb|AAT85052.1| expressed protein [Oryza sativa Japonica Group] >gi|108711293|gb|ABF99088.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549876|dbj|BAF13319.1| Os03g0770900 [Oryza sativa Japonica Group]	Unigene14340_All//8.00E-63//AT4G17000| unknown protein	Unigene14340_All//0.00E+00//ES832212				nr +
Unigene14344_All	1673	4.47	4.76	2.80	7.83	4.36	6.69	12.56	9.39	4.21	8.85E-02	6.82E-01		-6.75E-01	2.31E-03		-8.44E-01	3.95E-09		-2.26E-01	1.91E-01		-4.19E-01	8.84E-05		-1.58E+00	2.30E-39	Down	Unigene14344_All//gi|18411962|ref|NP_567241.1|//0.00E+00//XT2 (UDP-XYLOSYLTRANSFERASE 2); UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups / xyloglucan 6-xylosyltransferase [Arabidopsis thaliana] >gi|46576207|sp|Q22775.1|GT2_ARATH RecName: Full=Putative glycosyltransferase 2; Short=AtGT2 >gi|31932287|gb|AAC19271.1| T14P8.23 [Arabidopsis thaliana] >gi|16209669|gb|AAL14393.1| AT4g02500/T10P11_20 [Arabidopsis thaliana] >gi|30387559|gb|AAP31945.1| At4g02500 [Arabidopsis thaliana]	Unigene14344_All//0.00E+00//AT4G02500| XT2 (UDP-XYLOSYLTRANSFERASE 2); UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups / xyloglucan 6-xylosyltransferase	Unigene14344_All//0.00E+00//DR454344			GO:0008194//GO:0009250//GO:0031224//GO:0042285//GO:0043231//GO:0048488	nr -

Unigene14345_All	300	2.96	3.55	2.13	2.16	4.94	1.35	5.78	17.00	10.62	2.59E-01	6.75E-01			-4.77E-01	5.33E-01		1.19E+00	3.13E-02		-6.72E-01	4.78E-01		1.56E+00	1.12E-09	Up	8.79E-01	3.62E-03				Unigene14345_All//5.00E-68//TC177715				
Unigene14346_All	1772	11.93	16.87	10.94	14.67	17.68	19.83	17.94	41.47	33.12	5.00E-01	3.96E-07			-1.25E-01	3.85E-01		2.69E-01	4.38E-03		4.34E-01	8.01E-07		1.21E+00	4.66E-88	Up	8.84E-01	1.53E-43		Unigene14346_All//gi|223452496|gb|ACN09573.1|//1.00E-180//protein kinase-like protein [Glycine max]	Unigene14346_All//1.00E-162//AT5G02800| protein kinase family protein	Unigene14346_All//0.00E+00//TC133011	ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr -
Unigene14347_All	2369	10.05	11.76	15.55	25.46	27.14	44.21	15.92	17.38	7.92	2.27E-01	3.40E-02			6.30E-01	4.03E-12		9.19E-02	2.26E-01		7.96E-01	2.55E-55		1.26E-01	1.30E-01		-1.01E+00	3.36E-35	Down	Unigene14347_All//gi|15242504|ref|NP_199392.1|//0.00E+00//MEE62 (maternal effect embryo arrest 62); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|9758684|dbj|BAB09223.1| receptor kinase-like protein [Arabidopsis thaliana] >gi|224589699|gb|ACN59381.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene14347_All//0.00E+00//AT5G45800| MEE62 (maternal effect embryo arrest 62); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene14347_All//0.00E+00//TC162714		GO:0003006//GO:0004672//GO:0006464//GO:0007167//GO:0032559	nr -
Unigene14349_All	1375	21.80	17.91	21.61	8.84	9.82	6.86	6.73	3.31	3.30	-2.84E-01	4.72E-03			-1.29E-02	9.22E-01		1.51E-01	4.02E-01		-3.65E-01	2.78E-02		-1.02E+00	3.16E-09	Down	-1.03E+00	1.33E-09	Down	Unigene14349_All//gi|119391879|emb|CAF04055.2|//1.00E-145//S-adenosylmethionine transporter [Nicotiana benthamiana]	Unigene14349_All//6.00E-125//AT4G39460| SAMC1 (S-ADENOSYLMETHIONINE CARRIER 1); S-adenosylmethionine transmembrane transporter/ binding	Unigene14349_All//0.00E+00//CO095168			nr -
Unigene14351_All	317	8.58	22.70	10.08	29.07	24.33	20.66	68.56	65.00	43.86	1.40E+00	1.69E-09	Up		2.32E-01	5.45E-01		-2.57E-01	2.02E-01		-4.93E-01	9.12E-03		-7.68E-02	5.63E-01		-6.44E-01	4.48E-10		Unigene14351_All//gi|34581773|gb|AAQ76042.1|//8.00E-51//signal recognition particle receptor protein [Cucumis sativus]	Unigene14351_All//5.00E-43//AT4G30600| signal recognition particle receptor alpha subunit family protein	Unigene14351_All//3.00E-174//TC135947	ko03060|Protein export	GO:0000270//GO:0003723//GO:0004871//GO:0006613//GO:0017111//GO:0030867//GO:0031224//GO:0032561//GO:0043021//GO:0048500	nr -
Unigene14352_All	1623	3.51	7.27	3.74	11.23	15.70	12.02	4.69	8.34	6.65	1.05E+00	7.40E-10	Up		9.01E-02	7.20E-01		4.83E-01	1.51E-06		9.78E-02	5.29E-01		8.31E-01	1.72E-09		5.05E-01	8.15E-04		Unigene14352_All//gi|15237299|ref|NP_197124.1|//6.00E-22//50S ribosomal protein-related [Arabidopsis thaliana] >gi|502534720|gb|AAT71937.1| At5g16200 [Arabidopsis thaliana] >gi|51972088|gb|AAU15148.1| At5g16200 [Arabidopsis thaliana]		Unigene14352_All//0.00E+00//TC152986			nr +
Unigene14357_All	818	9.72	3.72	9.11	8.95	10.86	9.17	3.05	2.09	1.22	-1.39E+00	2.60E-10	Down		-9.32E-02	6.76E-01		2.79E-01	1.76E-01		3.40E-02	9.04E-01		-5.42E-01	1.39E-01		-1.32E+00	2.18E-04	Down			Unigene14357_All//1.00E-49//DW517062			
Unigene14360_All	653	14.26	12.57	15.00	20.90	17.88	19.57	57.11	26.56	33.25	-1.82E-01	3.69E-01			7.32E-02	7.15E-01		-2.26E-01	1.63E-01		-9.48E-02	6.38E-01		-1.10E+00	3.47E-39	Down	-7.80E-01	6.44E-23		Unigene14360_All//gi|125620176|gb|ABV46980.1|//2.00E-41//small molecular heat shock protein 10 [Nelumbo nucifera]	Unigene14360_All//9.00E-42//AT1G14980| CPN10 (CHAPERONIN 10); chaperone binding	Unigene14360_All//0.00E+00//TC157921		GO:0006950//GO:0032559//GO:0043231//GO:0044267//GO:0046914	nr +
Unigene14361_All	2142	1.56	0.69	0.65	1.86	2.22	1.39	2.05	2.40	2.75	-1.19E+00	5.85E-04	Down		-1.27E+00	4.44E-04	Down	2.54E-01	4.20E-01		-4.19E-01	1.94E-01		2.25E-01	4.02E-01		4.23E-01	4.87E-02		Unigene14361_All//gi|42569848|ref|NP_181714.3|//1.00E-143//cyclin-related [Arabidopsis thaliana]	Unigene14361_All//5.00E-137//AT2G41830| cyclin-related	Unigene14361_All//1.00E-171//BG443377			nr -
Unigene14362_All	608	11.45	16.33	5.96	22.61	80.88	48.13	17.32	19.18	36.56	5.13E-01	4.85E-03			-9.42E-01	5.14E-05		1.84E+00	5.86E-105	Up	1.09E+00	2.15E-26	Up	1.48E-01	4.02E-01		1.08E+00	2.43E-23	Up	Unigene14362_All//gi|15529234|gb|AAK97711.1|//5.00E-19//AT3g15630/MSJ11_3 [Arabidopsis thaliana] >gi|16974391|gb|AAL31121.1| AT3g15630/MSJ11_3 [Arabidopsis thaliana]	Unigene14362_All//3.00E-20//AT3G15630| unknown protein	Unigene14362_All//5.00E-162//TC152367			nr +
Unigene14363_All	1015	4.28	5.94	3.36	8.10	36.81	18.55	16.83	14.00	22.10	4.74E-01	5.18E-02			-3.50E-01	2.65E-01		2.18E+00	1.67E-99	Up	1.20E+00	7.75E-20	Up	-2.66E-01	3.41E-02		3.93E-01	9.96E-05		Unigene14363_All//gi|15529234|gb|AAK97711.1|//1.00E-23//AT3g15630/MSJ11_3 [Arabidopsis thaliana] >gi|16974391|gb|AAL31121.1| AT3g15630/MSJ11_3 [Arabidopsis thaliana]	Unigene14363_All//8.00E-25//AT3G15630| unknown protein	Unigene14363_All//0.00E+00//gi|109883548|gb|DW512518.1|DW512518		GO:0043231	nr -
Unigene14364_All	1810	0.52	6.75	2.24	5.04	2.42	3.34	1.94	2.61	3.06	3.70E+00	2.70E-48	Up		2.10E+00	5.19E-09	Up	-1.06E+00	2.52E-09	Down	-5.91E-01	1.62E-03		4.29E-01	9.24E-02		6.58E-01	2.65E-03		Unigene14364_All//gi|30693481|ref|NP_851107.1|//1.00E-82//structural constituent of ribosome [Arabidopsis thaliana]	Unigene14364_All//2.00E-80//AT5G39785| structural constituent of ribosome	Unigene14364_All//8.00E-142//DW490979			nr +
Unigene14367_All	1833	606.64	432.61	398.58	53.67	90.27	220.96	3.74	8.66	5.91	-4.88E-01	7.68E-227			-6.06E-01	0.00E+00		7.50E-01	2.67E-87		2.04E+00	0.00E+00	Up	1.21E+00	8.93E-20	Up	6.62E-01	1.15E-05		Unigene14367_All//gi|224090994|ref|XP_002309138.1|//0.00E+00//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222855114|gb|EEE92661.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene14367_All//2.00E-149//AT3G51860| CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	Unigene14367_All//0.00E+00//TC133989		GO:0006811//GO:0015075//GO:0031224	nr -
Unigene14369_All	1595	0.92	5.72	0.33	5.00	4.66	9.97	5.30	19.23	33.24	2.64E+00	2.42E-26	Up		-1.46E+00	1.49E-02		-9.97E-02	6.80E-01		9.96E-01	1.12E-12		1.86E+00	1.20E-69	Up	2.65E+00	3.73E-189	Up	Unigene14369_All//gi|15242769|ref|NP_195969.1|//1.00E-143//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|7378633|emb|CAB83309.1| UDPG glucosyltransferase-like protein [Arabidopsis thaliana] >gi|111074184|gb|ABH04465.1| At5g03490 [Arabidopsis thaliana]	Unigene14369_All//1.00E-129//AT5G03490| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene14369_All//0.00E+00//gi|78353754|gb|DT574028.1|DT574028	ko00908|Zeatin biosynthesis		nr -
Unigene14370_All	537	1.85	0.94	1.78	10.58	4.81	4.46	12.20	3.35	3.26	-9.72E-01	1.58E-01			-5.26E-02	9.54E-01		-1.14E+00	1.10E-06	Down	-1.25E+00	6.90E-07	Down	-1.87E+00	1.41E-15	Down	-1.90E+00	1.67E-16	Down			Unigene14370_All//0.00E+00//gi|21089843|gb|BQ402156.1|BQ402156				
Unigene14371_All	1158	5.11	2.36	4.32	19.31	10.91	14.82	7.19	1.99	2.55	-1.11E+00	8.34E-06	Down		-2.40E-01	3.90E-01		-8.24E-01	1.25E-14		-3.82E-01	8.41E-04		-1.86E+00	1.80E-19	Down	-1.50E+00	4.84E-15	Down			Unigene14371_All//0.00E+00//gi|21089842|gb|BQ492155.1|BQ492155				
Unigene14372_All	599	1.40	0.93	0.27	1.66	2.82	2.56	0.71	1.12	3.06	-5.87E-01	4.26E-01			-2.39E+00	1.14E-02		7.60E-01	1.44E-01		6.24E-01	2.70E-01		6.62E-01	4.02E-01		2.12E+00	9.21E-06	Up	Unigene14372_All//gi|7406426|emb|CAB85535.1|//1.00E-67//ubiquitin-protein ligase E3-alpha-like protein [Arabidopsis thaliana]	Unigene14372_All//1.00E-62//AT5G02310| PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase	Unigene14372_All//9.00E-139//TC171763		GO:0019787//GO:0046914	nr -
Unigene14373_All	2437	0.88	0.48	1.09	1.21	1.99	1.95	3.30	1.56	5.20	-8.80E-01	4.38E-02			3.12E-01	4.42E-01		7.24E-01	6.11E-03		6.90E-01	1.27E-02		-1.08E+00	9.09E-09	Down	6.57E-01	2.08E-06		Unigene14373_All//gi|30679594|ref|NP_195851.2|//0.00E+00//PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene14373_All//5.00E-168//AT5G02310| PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase	Unigene14373_All//5.00E-162//TC148735		GO:0016874	nr -
Unigene14375_All	1925	38.32	24.37	25.23	11.26	9.21	15.46	4.02	10.31	13.91	-6.53E-01	4.45E-26			-6.03E-01	7.06E-22		-2.89E-01	1.23E-02		4.58E-01	2.05E-06		1.36E+00	4.28E-29	Up	1.79E+00	4.61E-59	Up	Unigene14375_All//gi|145326102|ref|NP_001077760.1|//4.00E-82//translation release factor [Arabidopsis thaliana] >gi|145326104|ref|NP_001077761.1| translation release factor [Arabidopsis thaliana]	Unigene14375_All//5.00E-78//AT1G62850| translation release factor	Unigene14375_All//0.00E+00//TC172957		GO:0006412//GO:0008079//GO:0043231	nr -
Unigene14378_All	1608	8.23	9.55	7.75	9.91	7.02	6.97	0.84	2.18	1.44	2.14E-01	1.58E-01			-8.72E-02	6.33E-01		-4.97E-01	1.25E-04		-5.09E-01	1.90E-04		1.38E+00	7.04E-06	Up	7.72E-01	3.30E-02		Unigene14378_All//gi|21553596|gb|AAM62689.1|//2.00E-66//zinc finger protein [Arabidopsis thaliana]	Unigene14378_All//1.00E-54//AT5G20220| zinc knuckle (CCHC-type) family protein			GO:0005515//GO:0043231//GO:0046914	nr +
Unigene14379_All	1596	9.24	4.51	7.67	9.21	9.06	6.28	9.09	6.08	8.89	-1.04E+00	6.21E-12	Down		-2.69E-01	9.14E-02		-2.30E-02	8.95E-01		-5.52E-01	1.08E-04		-5.81E-01	8.97E-06		-3.21E-02	8.27E-01		Unigene14379_All//gi|297849756|ref|XP_002892759.1|//1.00E-149//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338601|gb|EFH69018.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14379_All//6.00E-148//AT1G13570| F-box family protein	Unigene14379_All//0.00E+00//gi|164307645|gb|ES841549.1|ES841549		GO:0003824	nr +
Unigene14380_All	1577	1.82	1.54	1.82	1.58	2.62	1.00	2.09	0.95	1.69	-2.43E-01	5.32E-01			-1.10E-03	9.98E-01		7.30E-01	1.24E-02		-6.56E-01	1.10E-01		-1.13E+00	2.47E-04	Down	-3.05E-01	3.30E-01		Unigene14380_All//gi|297849756|ref|XP_002892759.1|//1.00E-154//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338601|gb|EFH69018.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14380_All//2.00E-151//AT1G13570| F-box family protein	Unigene14380_All//0.00E+00//TC140694		GO:0003824	nr +
Unigene14384_All	584	0.72	0.17	0.91	2.81	2.00	0.31	6.37	2.58	1.50	-2.05E+00	1.21E-01			3.47E-01	7.06E-01		-4.90E-01	3.41E-01		-3.19E+00	1.23E-06	Down	-1.31E+00	8.71E-06	Down	-2.09E+00	7.28E-11	Down	Unigene14384_All//gi|224122896|ref|XP_002318943.1|//5.00E-35//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222857319|gb|EEE94866.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene14384_All//1.00E-30//AT1G12220| RPS5 (RESISTANT TO P. SYRINGAE 5); nucleotide binding	Unigene14384_All//0.00E+00//gi|21089801|gb|BQ402114.1|BQ402114	ko04626|Plant-pathogen interaction	GO:0005488//GO:0016787	nr +
Unigene14385_All	775	0.34	0.78	0.21	2.06	2.04	1.11	3.55	2.59	1.65	1.22E+00	2.07E-01			-7.12E-01	6.22E-01		-9.10E-03	9.69E-01		-8.94E-01	9.15E-02		-4.54E-01	1.98E-01		-1.11E+00	8.40E-04	Down	Unigene14385_AllAN62348.1|AF506028_15|//1.00E-40//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene14385_All//8.00E-27//AT1G12280| disease resistance protein (CC-NBS-LRR class), putative	Unigene14385_All//6.00E-85//gi|21089801|gb|BQ402114.1|BQ402114	ko04626|Plant-pathogen interaction		nr +
Unigene14387_All	1241	56.92	10.90	30.64	44.36	68.51	22.27	102.82	233.13	280.48	-2.38E+00	5.68E-180	Down		-8.94E-01	4.48E-41		6.27E-01	6.12E-33		-9.94E-01	7.15E-43		1.18E+00	0.00E+00	Up	1.45E+00	0.00E+00	Up	Unigene14387_All//gi|15082058|gb|AAK84008.1|AF393847_1|//1.00E-140//beta-amylase PCT-BMY1 [Solanum tuberosum]	Unigene14387_All//5.00E-139//AT4G17090| CT-BMY (CHLOROPLAST BETA-AMYLASE); beta-amylase	Unigene14387_All//0.00E+00//TC159642	ko00500|Starch and sucrose metabolism		nr +
Unigene14389_All	1059	7.31	15.65	6.94	11.57	10.63	11.77	30.74	32.76	27.31	1.10E+00	1.78E-14	Up		-7.55E-02	7.37E-01		-1.22E-01	5.38E-01		2.46E-02	9.13E-01		9.16E-02	3.54E-01		-1.71E-01	5.01E-02		Unigene14389_All//gi|18391087|ref|NP_563857.1|//2.00E-75//TRAF-type zinc finger-related [Arabidopsis thaliana] >gi|22531082|gb|AAM97045.1| expressed protein [Arabidopsis thaliana] >gi|23197978|gb|AAN15516.1| expressed protein [Arabidopsis thaliana]	Unigene14389_All//1.00E-76//AT1G09920| TRAF-type zinc finger-related	Unigene14389_All//0.00E+00//TC169254		GO:0046914	nr -
Unigene14393_All	674	0.00	0.00	0.00	0.00	0.51	0.00	2.95	15.81	20.33	null	null			null	null		9.00E+00	3.01E-02		null	null		2.42E+00	3.05E-34	Up	2.79E+00	4.06E-52	Up	Unigene14393_All//gi|5734440|emb|CAB52689.1|//1.00E-16//hexose transporter [Solanum lycopersicum]	Unigene14393_All//2.00E-17//AT5G26340| MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter	Unigene14393_All//5.00E-119//CO090629		GO:0005356//GO:0006810//GO:0008152//GO:0016628//GO:0031224	nr +
Unigene14394_All	1836	2.02	7.04	6.18	4.78	19.37	54.26	115.46	422.83	910.73	1.80E+00	3.04E-23	Up		1.61E+00	4.82E-17	Up	2.02E+00	6.65E-86	Up	3.51E+00	0.00E+00	Up	1.87E+00	0.00E+00	Up	2.98E+00	0.00E+00	Up	Unigene14394_All//gi|5734440|emb|CAB52689.1|//0.00E+00//hexose transporter [Solanum lycopersicum]	Unigene14394_All//0.00E+00//AT5G26340| MSS1; carbohydrate transmembrane transporter/ hexose:hydrogen symporter/ high-affinity hydrogen:glucose symporter/ sugar:hydrogen symporter	Unigene14394_All//0.00E+00//TC144992		GO:0005356//GO:0006810//GO:0008152//GO:0016628//GO:0031224	nr +
Unigene14395_All	1880	0.14	15.39	0.17	0.98	4.73	5.04	1.17	3.05	26.40	6.79E+00	1.26E-156	Up		2.88E-01	8.10E-01		2.27E+00	8.15E-25	Up	2.36E+00	9.62E-26	Up	1.38E+00	3.78E-09	Up	4.50E+00	9.83E-281	Up	Unigene14395_All//gi|224075800|ref|XP_002304773.1|//0.00E+00//cytokinin oxidase [Populus trichocarpa] >gi|222842205|gb|EEE79752.1| cytokinin oxidase [Populus trichocarpa]	Unigene14395_All//0.00E+00//AT3G63440| CKX6 (CYTOKININ OXIDASE/DEHYDROGENASE 6); cytokinin dehydrogenase	Unigene14395_All//0.00E+00//ES837714	ko00908|Zeatin biosynthesis	GO:0009690//GO:0009888//GO:0016645//GO:0030554//GO:0043231	nr +
Unigene14396_All	427	2.33	1.07	1.12	1.52	1.13	0.63	2.67	2.35	0.19	-1.12E+00	1.09E-01			-1.05E+00	1.48E-01		-4.26E-01	6.09E-01		-1.26E+00	1.83E-01		-1.87E-01	7.39E-01		-3.84E+00	1.74E-06	Down	Unigene14396_All//gi|225439619|ref|XP_002266325.1|//4.00E-26//PREDICTED: similar to curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein [Vitis vinifera]	Unigene14396_All//3.00E-11//AT3G51710| curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein	Unigene14396_All//3.00E-141//AT730971			nr -

Unigene14397_All	1505	2.89	1.52	1.42	1.59	2.40	1.08	2.50	5.86	1.09	-9.30E-01	1.47E-03		-1.03E+00	7.90E-04	Down	5.97E-01	6.62E-02		-5.57E-01	1.96E-01		1.23E+00	1.51E-11	Up	-1.20E+00	1.88E-05	Down	Unigene14397_All//gi|225439619|ref|XP_002266325.1|//1.00E-154//PREDICTED: similar to curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein [Vitis vinifera]	Unigene14397_All//2.00E-114//AT3G54710| curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein	Unigene14397_All//0.00E+00//AI730971			GO:0009987//GO:0030246	nr +
Unigene14398_All	1632	12.47	36.73	19.09	26.83	33.06	37.19	13.70	13.52	12.38	1.56E+00	3.33E-86	Up	6.14E-01	6.57E-10		3.01E-01	7.58E-06		4.71E-01	4.90E-13		-1.94E-02	8.85E-01		-1.47E-01	1.86E-01		Unigene14398_All//gi|71905561|gb|AA252758.1|//0.00E+00//expressed protein [Arabidopsis thaliana] >gi|71905563|gb|AA252759.1| expressed protein [Arabidopsis thaliana]	Unigene14398_All//0.00E+00//AT5G19160| unknown protein	Unigene14398_All//0.00E+00//TC172110				nr +
Unigene14399_All	1203	41.32	23.33	23.77	36.15	33.49	30.45	61.61	13.13	27.29	-8.24E-01	2.19E-26		-7.98E-01	5.04E-24		-1.10E-01	2.28E-01		-2.48E-01	2.32E-03		-2.23E+00	1.45E-212	Down	-1.17E+00	1.62E-87	Down	Unigene14399_All//gi|294862567|gb|ADF45668.1|//1.00E-108//nucleoside diphosphate kinase 1 [Solanum tuberosum]	Unigene14399_All//2.00E-94//AT4G11010| NDPK3 (NUCLEOSIDE DIPHOSPHATE KINASE 3); ATP binding / nucleoside diphosphate kinase	Unigene14399_All//0.00E+00//TC130345		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism	GO:0009206//GO:0009209//GO:0016776//GO:0032559//GO:0044424	nr -
Unigene144_All	662	9.80	2.60	5.63	7.98	5.51	5.73	8.05	7.01	4.15	-1.91E+00	4.27E-13	Down	-8.00E-01	8.94E-04		-5.33E-01	3.37E-02		-4.77E-01	7.25E-02		-2.00E-01	4.38E-01		-9.55E-01	2.52E-05		Unigene144_All//gi|9838413|ref|NP_064026.1|//2.00E-54//orf145 [Beta vulgaris subsp. vulgaris] >gi|9049327|dbj|BAA99337.1| orf145 [Beta vulgaris subsp. vulgaris]	Unigene144_All//2.00E-31//ATMG00660| hypothetical protein	Unigene144_All//0.00E+00//ES808132				nr -
Unigene14404_All	623	1.68	0.81	0.51	1.60	1.55	1.16	1.43	0.00	1.73	-1.05E+00	1.20E-01		-1.71E+00	2.35E-02		-4.72E-02	9.36E-01		-4.63E-01	5.26E-01		-1.05E+01	2.24E-06	Down	2.77E-01	6.37E-01		Unigene14404_All//gi|297849756|ref|XP_002892759.1|//5.00E-26//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338601|gb|EFH69018.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14404_All//2.00E-26//AT1G13570| F-box family protein	Unigene14404_All//9.00E-133//TC139405			GO:0003824	nr +
Unigene14405_All	1702	3.38	1.13	2.66	5.47	5.20	4.06	3.50	1.82	1.97	-1.58E+00	3.88E-09	Down	-3.47E-01	2.00E-01		-7.39E-02	7.64E-01		-4.31E-01	2.37E-02		-9.47E-01	1.42E-05		-8.33E-01	7.80E-05		Unigene14405_All//gi|297849756|ref|XP_002892759.1|//5.00E-77//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338601|gb|EFH69018.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14405_All//2.00E-76//AT1G13570| F-box family protein	Unigene14405_All//0.00E+00//ES793336			GO:0003824	nr -
Unigene14406_All	1285	23.29	20.03	21.22	36.01	24.98	22.35	19.61	9.47	10.73	-2.18E-01	3.53E-02		-1.35E-01	2.40E-01		-5.28E-01	9.90E-14		-6.88E-01	1.75E-19		-1.05E+00	9.87E-25	Down	-8.70E-01	7.66E-19		Unigene14406_All//gi|3413511|emb|CAA03982.1|//4.00E-58//glucose-6-phosphate isomerase [Spinacia oleracea]	Unigene14406_All//2.00E-57//AT4G24620| PGI1 (PHOSPHOGLUCOSE ISOMERASE 1); glucose-6-phosphate isomerase	Unigene14406_All//0.00E+00//gi|164334705|gb|ES793094.1|ES793094		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway	GO:0002376//GO:0003676//GO:0006007//GO:0006073//GO:0009526//GO:0009532//GO:0009908//GO:0016861//GO:0032559	nr +
Unigene14408_All	1890	3.35	3.11	3.69	5.38	4.76	5.95	9.46	5.17	4.47	-1.07E-01	6.53E-01		1.40E-01	5.92E-01		-1.77E-01	3.86E-01		1.46E-01	4.78E-01		-8.71E-01	3.15E-13		-1.08E+00	3.33E-19	Down	Unigene14408_All//gi|297795501|ref|XP_002865635.1|//1.00E-158//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297311470|gb|EFH41894.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene14408_All//7.00E-153//AT5G48440| oxidoreductase	Unigene14408_All//0.00E+00//TC135826				nr +
Unigene14412_All	1173	3.52	7.17	3.27	4.08	5.96	6.28	2.34	4.06	2.58	1.03E+00	5.24E-07	Up	-1.09E-01	7.25E-01		5.48E-01	1.12E-02		6.22E-01	3.58E-03		7.94E-01	1.24E-03		1.40E-01	6.66E-01		Unigene14412_All//gi|5103822|gb|AAD39652.1|AC007591_17//3.00E-26//ESTs gb|R30529, gb|Z48463, gb|Z48467, gb|AA597369 and gb|AA394772 come from this gene [Arabidopsis thaliana] >gi|16209680|gb|AAL14398.1| At1g15230/F9L1_18 [Arabidopsis thaliana] >gi|21360405|gb|AAM47318.1| At1g15230/F9L1_18 [Arabidopsis thaliana]	Unigene14412_All//1.00E-17//AT1G15230| unknown protein	Unigene14412_All//0.00E+00//TC163883				nr -
Unigene14415_All	1362	23.43	10.16	16.89	4.10	4.35	4.61	5.43	1.96	3.04	-1.21E+00	1.23E-31	Down	-4.72E-01	1.47E-06		8.63E-02	8.01E-01		1.70E-01	5.47E-01		-1.47E+00	1.18E-12	Down	-8.37E-01	8.01E-06		Unigene14415_All//gi|18406816|ref|NP_566045.1|//9.00E-77//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|2975645|gb|AAC06154.1| expressed protein [Arabidopsis thaliana] >gi|27311551|gb|AAO00741.1| Unknown protein [Arabidopsis thaliana] >gi|30023706|gb|AAP13386.1| At2g45530 [Arabidopsis thaliana]	Unigene14415_All//2.00E-61//AT2G45530| zinc finger (C3HC4-type RING finger) family protein	Unigene14415_All//0.00E+00//TC147162		ko04141|Protein processing in endoplasmic reticulum	GO:0046914	nr -
Unigene14416_All	2853	0.18	0.32	0.30	5.60	2.93	2.69	2.39	1.04	13.70	8.02E-01	2.71E-01		7.03E-01	3.83E-01		-9.34E-01	4.91E-13		-1.06E+00	3.42E-14	Down	-1.20E+00	8.80E-09	Down	2.52E+00	4.45E-132	Up	Unigene14416_All//gi|297812077|ref|XP_002873922.1|//0.00E+00//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297319759|gb|EFH50181.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14416_All//0.00E+00//AT5G18980| binding	Unigene14416_All//0.00E+00//TC139297				nr -
Unigene14417_All	1619	0.00	0.19	0.00	0.58	0.51	0.36	0.37	0.10	1.18	7.55E+00	4.44E-02		null	null		-1.96E-01	8.04E-01		-6.89E-01	3.58E-01		-1.82E+00	4.72E-02		1.69E+00	1.15E-04	Up	Unigene14417_All//gi|297812077|ref|XP_002873922.1|//1.00E-179//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297319759|gb|EFH50181.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14417_All//4.00E-180//AT5G18980| binding	Unigene14417_All//0.00E+00//TC139297				nr +
Unigene14418_All	1813	41.18	23.45	34.19	44.37	43.84	43.07	28.17	8.58	13.62	-8.13E-01	2.49E-38		-2.69E-01	1.81E-05		-1.76E-02	8.13E-01		-4.30E-02	5.82E-01		-1.72E+00	1.20E-103	Down	-1.05E+00	1.68E-50	Down	Unigene14418_All//gi|57222232|gb|AAW39023.1|//1.00E-180//At3g27230 [Arabidopsis thaliana] >gi|63003758|gb|AAY25408.1| At3g27230 [Arabidopsis thaliana]	Unigene14418_All//3.00E-171//AT3G27230| LOCATED IN: Golgi apparatus; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: methyltransferase (TAIR:AT5G40830.2); Has 184 Blast hits to 183 proteins in 14 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 182; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene14418_All//0.00E+00//TC135146				nr +
Unigene14420_All	1711	9.08	9.36	10.11	2.47	4.23	2.53	0.05	0.51	0.40	4.32E-02	7.76E-01		1.55E-01	3.17E-01		7.72E-01	1.86E-04		3.42E-02	9.34E-01		3.38E+00	1.75E-04	Up	3.00E+00	2.00E-03		Unigene14420_All//gi|224114037|ref|XP_002332458.1|//1.00E-153//cytochrome P450 [Populus trichocarpa] >gi|222832529|gb|EEE71006.1| cytochrome P450 [Populus trichocarpa]	Unigene14420_All//7.00E-95//AT5G25120| CYP71B11; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene14420_All//0.00E+00//TC167076		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene14421_All	880	3.09	76.46	10.23	15.11	32.95	36.23	12.16	37.57	51.20	4.63E+00	0.00E+00	Up	1.73E+00	5.47E-15	Up	1.12E+00	4.38E-30	Up	1.26E+00	4.50E-36	Up	1.63E+00	2.13E-62	Up	2.07E+00	3.77E-120	Up	Unigene14421_All//gi|18415709|ref|NP_567629.1|//1.00E-33//F-box family protein [Arabidopsis thaliana] >gi|142989915|sp|Q65416.2|SK12_ARATH RecName: Full=F-box protein SK12P2; AltName: Full=SKP1-interacting partner 27 >gi|117168229|gb|ABK32197.1| At4g21510 [Arabidopsis thaliana]	Unigene14421_All//7.00E-35//AT4G21510| F-box family protein	Unigene14421_All//0.00E+00//TC167279				nr -
Unigene14423_All	1754	23.36	14.50	30.21	7.16	4.71	3.09	0.05	0.00	0.00	-6.88E-01	3.54E-16		3.71E-01	6.32E-07		-6.03E-01	4.16E-05		-1.21E+00	7.24E-14	Down	-5.59E+00	4.04E-01		-5.59E+00	3.59E-01		Unigene14423_All//gi|51849627|dbj|BAD42345.1|//0.00E+00//sorbitol transporter [Malus x domestica]	Unigene14423_All//1.00E-165//AT3G18830| ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann	Unigene14423_All//0.00E+00//ES816133			GO:0006810//GO:0008152//GO:0016020//GO:0022857//GO:0031224	nr +
Unigene1443_All	1978	43.62	59.25	35.83	29.92	32.68	67.01	8.38	2.81	7.55	4.42E-01	1.49E-20		-2.84E-01	8.38E-07		1.27E-01	6.89E-02		1.16E+00	6.38E-131	Up	-1.58E+00	2.63E-30	Down	-1.50E-01	2.54E-01		Unigene1443_All//gi|224068414|ref|XP_002302739.1|//1.00E-175//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222844465|gb|EEE32012.1| glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene1443_All//2.00E-158//AT3G62660| GATL7 (Galacturonosyltransferase-like 7); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene1443_All//0.00E+00//TC153136				nr +
Unigene14432_All	1826	17.91	21.84	18.11	13.15	16.31	31.11	47.42	49.62	171.20	2.86E-01	8.19E-04		1.61E-02	8.89E-01		3.11E-01	1.10E-03		1.24E+00	1.89E-62	Up	6.55E-02	2.58E-01		1.85E+00	0.00E+00	Up	Unigene14432_All//gi|269980527|gb|ACZ56438.1|//0.00E+00//IAA-amino acid hydrolase [Populus tomentosa]	Unigene14432_All//2.00E-175//AT1G51760| IAR3 (IAA-ALANINE RESISTANT 3); IAA-Ala conjugate hydrolase/ metallopeptidase	Unigene14432_All//0.00E+00//TC177148		ko00330|Arginine and proline metabolism	GO:0003824//GO:0005488	nr -
Unigene14433_All	1267	13.21	16.28	12.86	14.59	27.86	80.92	12.68	7.72	38.71	3.01E-01	1.52E-02		-3.91E-02	7.98E-01		9.34E-01	4.19E-27		2.47E+00	3.72E-290	Up	-7.16E-01	8.87E-09		1.61E+00	1.19E-92	Up	Unigene14433_All//gi|68131790|gb|AAY85179.1|//5.00E-63//fiber expressed protein [Gossypium hirsutum]	Unigene14433_All//1.00E-49//AT1G61260| unknown protein	Unigene14433_All//2.00E-21//DW509563				nr -
Unigene14434_All	585	4.74	1.21	3.28	7.15	6.48	6.25	2.39	0.86	1.09	-1.97E+00	3.25E-06	Down	-5.33E-01	1.82E-01		-1.44E-01	6.61E-01		-1.94E-01	5.79E-01		-1.48E+00	4.92E-03		-1.13E+00	2.13E-02		Unigene14434_All//gi|76880190|dbj|BAE45866.1|//3.00E-25//UDP-N-acetylmuramate-alanine ligase [Physcomitrella patens]		Unigene14434_All//7.00E-155//TC153508				nr -
Unigene14435_All	1523	1.48	1.56	1.15	2.68	3.35	2.55	1.78	0.71	0.97	8.21E-02	8.41E-01		-3.57E-01	4.20E-01		3.19E-01	2.72E-01		-7.27E-02	8.26E-01		-1.32E+00	1.83E-04	Down	-8.76E-01	7.81E-03		Unigene14435_All//gi|76880190|dbj|BAE45866.1|//3.00E-96//UDP-N-acetylmuramate-alanine ligase [Physcomitrella patens]		Unigene14435_All//0.00E+00//TC153508				nr +
Unigene1444_All	2023	35.54	7.79	28.93	23.49	19.25	12.37	6.00	8.82	2.42	-2.19E+00	5.11E-165	Down	-2.97E-01	3.04E-06		-2.87E-01	6.92E-05		-9.26E-01	5.60E-33		5.57E-01	1.85E-06		-1.31E+00	1.12E-17	Down	Unigene1444_All//gi|9758280|dbj|BAB08804.1|//0.00E+00//auxin-independent growth promoter-like protein [Arabidopsis thaliana]	Unigene1444_All//8.00E-175//AT5G63390| unknown protein	Unigene1444_All//2.00E-10//gi|164335612|gb|ES801045.1|ES801045				nr +
Unigene14441_All	2247	4.96	3.29	1.68	9.71	11.37	9.55	11.95	3.33	4.65	-5.91E-01	5.02E-04		-1.56E+00	5.72E-16	Down	2.28E-01	3.95E-02		-2.44E-02	8.73E-01		-1.84E+00	1.74E-60	Down	-1.36E+00	1.80E-40	Down	Unigene14441_All//gi|115434848|ref|NP_001042182.1|//1.00E-166//0s01g0176500 [Oryza sativa Japonica Group] >gi|113531713|dbj|BAF04096.1| Os01g0176500 [Oryza sativa Japonica Group]	Unigene14441_All//2.00E-172//AT3G15550| unknown protein	Unigene14441_All//0.00E+00//TC150514				nr +

Unigene14444_All	1794	0.23	0.68	0.95	1.50	1.06	0.98	2.38	2.03	2.73	1.54E+00	1.75E-02		2.03E+00	5.20E-04	Up	-5.06E-01	1.87E-01		-6.11E-01	1.21E-01		-2.32E-01	4.20E-01		1.99E-01	4.41E-01		Unigene14444_All//gi|2194136|gb|AAB61111.1|/3.00E-54//Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb|U12626) [Arabidopsis thaliana]	Unigene14444_All//1.00E-16//AT1G21280| unknown protein					nr +
Unigene14445_All	1908	1.15	0.61	0.28	1.88	1.61	1.63	4.12	1.18	2.32	-9.15E-01	3.46E-02		-2.04E+00	5.31E-05	Down	-2.27E-01	5.42E-01		-2.03E-01	6.00E-01		-1.80E+00	1.07E-17	Down	-8.31E-01	4.54E-06		Unigene14445_All//gi|225451615|ref|XP_002275754.1|//0.00E+00//PREDICTED: similar to SUVH4 (SU(VAR)3-9 HOMOLOG 4) [Vitis vinifera]	Unigene14445_All//4.00E-163//AT5G13960| SUVH4 (SU(VAR)3-9 HOMOLOG 4); double-stranded methylated DNA binding / histone methyltransferase(H3-K9 specific) / methyl-CpG binding / methyl-CpNpG binding / methyl-CpNpN binding	Unigene14445_All//0.00E+00//TC151717		ko00310|Lysine degradation		nr +
Unigene14447_All	968	0.65	0.00	0.33	1.80	1.25	0.56	0.79	0.78	1.32	-9.34E+00	7.92E-04	Down	-9.74E-01	3.16E-01		-5.33E-01	2.92E-01		-1.69E+00	1.17E-03		-1.66E-02	1.02E+00		7.44E-01	1.50E-01		Unigene14447_All//gi|225451615|ref|XP_002275754.1|//1.00E-100//PREDICTED: similar to SUVH4 (SU(VAR)3-9 HOMOLOG 4) [Vitis vinifera]	Unigene14447_All//5.00E-183//AT5G13960| SUVH4 (SU(VAR)3-9 HOMOLOG 4); double-stranded methylated DNA binding / histone methyltransferase(H3-K9 specific) / methyl-CpG binding / methyl-CpNpG binding / methyl-CpNpN binding	Unigene14447_All//5.00E-166//TC151717		ko00310|Lysine degradation	GO:0000166//GO:0003690//GO:0006259//GO:0018024//GO:0034968//GO:0043231//GO:0046914	nr -
Unigene14448_All	1657	1.96	10.31	1.61	6.10	5.40	15.43	18.58	40.21	48.59	2.40E+00	8.40E-44	Up	-2.85E-01	4.36E-01		-1.76E-01	3.90E-01		1.34E+00	1.01E-31	Up	1.11E+00	2.95E-70	Up	1.39E+00	8.70E-122	Up	Unigene14448_All//gi|28416693|gb|AA042877.1|//1.00E-160//At2g39110 [Arabidopsis thaliana]	Unigene14448_All//7.00E-152//AT2G39110| protein kinase, putative	Unigene14448_All//0.00E+00//TC141524		ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0032559	nr -
Unigene1445_All	950	7.71	20.11	15.86	4.67	5.84	10.60	5.03	76.55	11.03	1.38E+00	1.75E-23	Up	1.04E+00	9.88E-12	Up	3.23E-01	2.34E-01		1.18E+00	1.06E-10	Up	3.93E+00	0.00E+00	Up	1.13E+00	2.43E-12	Up	Unigene1445_All//gi|13492676|gb|AAK28304.1|AF346432|//4.00E-60//phenylpropanoid:glucosyltransferase 2 [Nicotiana tabacum]	Unigene1445_All//2.00E-55//AT4G34131| UGT73B3 (UDP-glucosyl transferase 73B3); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring hexosyl groups	Unigene1445_All//0.00E+00//TC169312		ko00908|Zeatin biosynthesis		nr -
Unigene14450_All	713	0.15	0.07	0.90	0.70	0.29	0.13	2.55	1.82	0.89	-1.05E+00	6.85E-01		2.61E+00	2.33E-02		-1.27E+00	2.22E-01		-2.46E+00	4.83E-02		-4.89E-01	2.74E-01		-1.51E+00	5.47E-04	Down	Unigene14450_All//gi|225440318|ref|XP_002269811.1|//3.00E-18//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene14450_All//2.00E-09//AT3G09450| unknown protein	Unigene14450_All//0.00E+00//DT049676				nr +
Unigene14451_All	728	4.46	2.51	4.68	3.42	1.04	2.36	2.67	1.38	1.42	-8.31E-01	1.57E-02		7.12E-02	8.36E-01		-1.72E+00	1.30E-05	Down	-5.37E-01	1.99E-01		-9.55E-01	2.18E-02		-9.09E-01	2.28E-02		Unigene14451_All//gi|297727859|ref|NP_001176293.1|//1.00E-33//Os11g0100300 [Oryza sativa Japonica Group] >gi|77548278|gb|ABA91075.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255679678|dbj|BAH95021.1| Os11g0100300 [Oryza sativa Japonica Group]	Unigene14451_All//2.00E-50//AT3G09450| unknown protein	Unigene14451_All//3.00E-74//DT049676			GO:0044464	nr -
Unigene14452_All	1357	2.27	1.19	2.67	0.29	0.94	0.83	1.31	0.62	0.38	-9.29E-01	8.94E-03		2.30E-01	5.16E-01		1.68E+00	7.61E-03		1.50E+00	2.74E-02		-1.09E+00	1.38E-02		-1.78E+00	1.06E-04	Down	Unigene14452_All//gi|297727859|ref|NP_001176293.1|//4.00E-40//Os11g0100300 [Oryza sativa Japonica Group] >gi|77548278|gb|ABA91075.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255679678|dbj|BAH95021.1| Os11g0100300 [Oryza sativa Japonica Group]	Unigene14452_All//2.00E-70//AT3G09450| unknown protein	Unigene14452_All//0.00E+00//DT049676				nr +
Unigene14453_All	969	27.86	16.47	14.45	36.40	37.63	43.16	20.42	8.76	10.48	-7.58E-01	8.01E-13		-9.47E-01	1.30E-17		4.82E-02	6.74E-01		2.46E-01	3.25E-03		-1.22E+00	9.88E-25	Down	-9.62E-01	1.43E-17				Unigene14453_All//5.00E-09//BQ405485				
Unigene14454_All	1490	8.36	5.68	9.76	6.85	3.61	2.67	2.89	3.31	1.44	-5.57E-01	4.82E-04		2.23E-01	1.71E-01		-9.27E-01	2.10E-08		-1.36E+00	1.55E-13	Down	1.94E-01	4.79E-01		-1.00E+00	8.71E-05	Down	Unigene14454_All//gi|297804448|ref|XP_002870108.1|//1.00E-160//oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315944|gb|EFH46367.1| oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14454_All//2.00E-161//AT4G17370| oxidoreductase family protein	Unigene14454_All//0.00E+00//TC133591		ko00562|Inositol phosphate metabolism	GO:0004033//GO:0008152	nr +
Unigene14455_All	1146	2.42	2.56	5.02	6.52	6.01	7.09	2.51	2.81	2.82	8.38E-02	8.15E-01		1.05E+00	5.48E-05	Up	-1.18E-01	6.18E-01		1.22E-01	6.42E-01		1.63E-01	6.34E-01		1.67E-01	6.06E-01		Unigene14455_All//gi|297609753|ref|NP_001063588.2|//1.00E-09//Os09g0502600 [Oryza sativa Japonica Group] >gi|255679035|dbj|BAF25502.2| Os09g0502600 [Oryza sativa Japonica Group]	Unigene14455_All//7.00E-05//AT1G61330| F-box family protein	Unigene14455_All//1.00E-148//DW477126				nr -
Unigene14456_All	1147	105.51	53.32	41.41	193.18	191.54	123.80	40.99	15.49	17.96	-9.85E-01	3.98E-85		-1.35E+00	3.66E-136	Down	-1.23E-02	8.18E-01		-6.42E-01	8.92E-81		-1.40E+00	2.34E-71	Down	-1.19E+00	5.14E-57	Down	Unigene14456_All//gi|15241485|ref|NP_196417.1|//3.00E-57//E13L3 (GLUCAN ENDO-1,3-BETA-GLUCOSIDASE-LIKE PROTEIN 3); callose binding / polysaccharide binding [Arabidopsis thaliana] >gi|75203196|sp|Q9SD84.1|E13L3_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase-like protein 3; Flags: Precursor >gi|26452180|dbj|BAC43178.1| GPI-anchored protein [Arabidopsis thaliana] >gi|28372924|gb|AAO39944.1| At5g08000 [Arabidopsis thaliana]	Unigene14456_All//8.00E-40//AT5G08000| E13L3 (GLUCAN ENDO-1,3-BETA-GLUCOSIDASE-LIKE PROTEIN 3); callose binding / polysaccharide binding	Unigene14456_All//0.00E+00//TC139365			GO:0005618//GO:0005911//GO:0030247//GO:0031225//GO:0031410//GO:0052386	nr -
Unigene14457_All	1136	33.35	69.05	52.31	42.84	45.89	66.12	29.25	19.50	14.80	1.05E+00	2.68E-61	Up	6.50E-01	3.45E-20		9.93E-02	2.40E-01		6.26E-01	2.51E-26		-5.85E-01	2.52E-12		-9.83E-01	6.15E-30		Unigene14457_All//gi|15242619|ref|NP_195928.1|//4.00E-94//phosphatidic acid phosphatase-related / PAP2-related [Arabidopsis thaliana] >gi|38564298|gb|AAR23728.1| At5g03080 [Arabidopsis thaliana] >gi|46402486|gb|AAS92345.1| At5g03080 [Arabidopsis thaliana]	Unigene14457_All//1.00E-86//AT5G03080| phosphatidic acid phosphatase-related / PAP2-related	Unigene14457_All//0.00E+00//TC142710		ko00510|N-Glycan biosynthesis	GO:0016462//GO:0044464	nr -
Unigene1446_All	1461	59.48	204.48	59.81	23.56	18.79	88.35	15.08	401.48	62.91	1.78E+00	0.00E+00	Up	7.90E-03	9.16E-01		-3.27E-01	1.42E-04		1.91E+00	5.25E-264	Up	4.73E+00	0.00E+00	Up	2.06E+00	2.41E-242	Up	Unigene1446_All//gi|204022238|dbj|BAG71127.1|//1.00E-151//glucosyltransferase [Phytolacca americana] >gi|219566998|dbj|BAH05017.1| glucosyltransferase [Phytolacca americana]	Unigene1446_All//5.00E-134//AT4G34135| UGT73B2 (UDP-GLUCOSYLTRANSFERASE 73B2); UDP-glucosyltransferase/ UDP-glycosyltransferase/ flavonol 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase	Unigene1446_All//0.00E+00//TC169312		ko00908|Zeatin biosynthesis		nr +
Unigene14460_All	1067	2.01	6.13	2.50	2.71	18.75	18.71	4.79	3.45	13.59	1.61E+00	1.88E-10	Up	3.12E-01	4.42E-01		2.79E+00	2.84E-70	Up	2.79E+00	1.08E-64	Up	-4.76E-01	4.73E-02		1.50E+00	2.10E-25	Up	Unigene14460_All//gi|30685840|ref|NP_173276.2|//3.00E-50//BEE1 (BR Enhanced Expression 1); transcription factor [Arabidopsis thaliana] >gi|75299631|sp|Q8GZI3.1|BEE1_ARATH RecName: Full=Transcription factor BEE 1; AltName: Full=Protein Brassinosteroid enhanced expression 1; AltName: Full=Transcription factor EN 77; AltName: Full=bHLH transcription factor bHLH044; AltName: Full=Basic helix-loop-helix protein 44; Short=bHLH 44; Short=AtbHLH44 >gi|28950817|gb|AAO63332.1| At1g18400 [Arabidopsis thaliana]	Unigene14460_All//1.00E-51//AT1G18400| BEE1 (BR Enhanced Expression 1); transcription factor	Unigene14460_All//0.00E+00//TC141393	bHLH	ko04712|Circadian rhythm - plant	GO:0010468//GO:0043231	nr -
Unigene14463_All	1687	13.77	6.79	8.71	18.99	16.31	22.73	22.61	14.07	11.31	-1.02E+00	6.48E-18	Down	-6.61E-01	1.67E-08		-2.19E-01	2.15E-02		2.60E-01	2.97E-03		-6.84E-01	3.10E-18		-9.99E-01	4.06E-35		Unigene14463_All//gi|297828964|ref|XP_002882364.1|//0.00E+00//tRNA synthetase class I family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328204|gb|EFH58623.1| tRNA synthetase class I family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14463_All//0.00E+00//AT3G04600| tRNA synthetase class I (W and Y) family protein	Unigene14463_All//0.00E+00//TC145738		ko00380|Tryptophan metabolism//ko00970|Aminoacyl-tRNA biosynthesis	GO:0004812//GO:0006418//GO:0032559//GO:0044444	nr -
Unigene14465_All	1407	2.49	43.58	4.88	3.61	5.73	5.94	3.40	4.46	23.16	4.13E+00	2.45E-262	Up	9.71E-01	3.50E-05		6.65E-01	6.30E-04		7.18E-01	2.75E-04		3.92E-01	7.17E-02		2.77E+00	2.94E-122	Up	Unigene14465_All//gi|34761724|gb|AAQ82035.1|//1.00E-58//gag/pol polyprotein [Pisum sativum]		Unigene14465_All//4.00E-69//TC175180			GO:0003676//GO:0003824//GO:0009987//GO:0043170//GO:0044238	nr +
Unigene14467_All	1754	5.10	3.35	3.76	28.94	32.85	68.62	25.99	120.55	45.02	-6.06E-01	1.61E-03		-4.38E-01	3.16E-02		1.83E-01	8.64E-03		1.25E+00	2.19E-132	Up	2.21E+00	0.00E+00	Up	7.93E-01	1.56E-48		Unigene14467_All//gi|15240694|ref|NP_196325.1|//1.00E-104//transferase family protein [Arabidopsis thaliana] >gi|9759564|dbj|BAB11166.1| hypersensitivity related protein-like [Arabidopsis thaliana]	Unigene14467_All//1.00E-105//AT5G07080| transferase family protein	Unigene14467_All//0.00E+00//TC138309		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016410	nr +
Unigene14468_All	1409	0.37	0.58	0.08	31.15	8.75	13.98	9.75	1.66	1.70	6.32E-01	4.02E-01		-2.30E+00	6.77E-02		-1.83E+00	2.84E-100	Down	-1.16E+00	9.38E-44	Down	-2.55E+00	8.53E-47	Down	-2.52E+00	1.15E-47	Down	Unigene14468_All//gi|14289169|dbj|BAB59066.1|//0.00E+00//pectate lyase [Salix gilgiana]	Unigene14468_All//0.00E+00//AT1G67750| pectate lyase family protein	Unigene14468_All//0.00E+00//TC153962		ko00040|Pentose and glucuronate interconversions	GO:0016837//GO:0044464	nr -
Unigene14476_All	931	4.61	2.78	3.78	3.37	2.63	1.26	0.36	0.36	0.86	-7.31E-01	1.24E-02		-2.88E-01	3.82E-01		-3.60E-01	3.17E-01		-1.42E+00	7.40E-05	Down	-1.68E-02	1.02E+00		1.24E+00	7.69E-02				Unigene14476_All//5.00E-18//ES841009				
Unigene14477_All	1131	1.30	1.84	1.08	1.10	1.71	3.31	2.17	2.73	1.94	5.04E-01	2.63E-01		-2.58E-01	6.23E-01		6.31E-01	1.93E-01		1.59E+00	1.84E-06	Up	3.35E-01	3.27E-01		-1.63E-01	6.47E-01		Unigene14477_All//gi|297606541|ref|NP_001058631.2|//6.00E-17//Os06g0726600 [Oryza sativa Japonica Group] >gi|54291134|dbj|BAD61807.1| MAP kinase activating protein-like [Oryza sativa Japonica Group] >gi|255677415|dbj|BAF20545.2| Os06g0726600 [Oryza sativa Japonica Group]	Unigene14477_All//3.00E-17//AT4G38360| unknown protein	Unigene14477_All//2.00E-54//TC170835			GO:0031410//GO:0043231	nr +
Unigene14479_All	840	43.60	25.27	31.13	62.09	50.83	64.52	37.05	18.51	17.79	-7.87E-01	3.44E-18		-4.86E-01	8.66E-08		-2.89E-01	2.40E-05		5.54E-02	5.56E-01		-1.00E+00	4.41E-28	Down	-1.06E+00	1.28E-31	Down	Unigene14479_All//gi|297811075|ref|XP_002873421.1|//7.00E-77//ribosomal protein L17 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319258|gb|EFH49680.1| ribosomal protein L17 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14479_All//9.00E-61//AT5G64650| ribosomal protein L17 family protein	Unigene14479_All//0.00E+00//TC130223		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr -

Unigene14480_All	942	5.22	4.73	6.05	10.95	10.09	7.96	3.37	1.60	1.86	-1.41E-01	6.17E-01		2.12E-01	4.34E-01		-1.18E-01	5.83E-01		-4.60E-01	9.77E-03		-1.08E+00	6.26E-04	Down	-8.55E-01	4.42E-03		Unigene14480_All//gi|297811075|ref|XP_002873421.1|//2.00E-72//ribosomal protein L17 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319258|gb|EFH49680.1| ribosomal protein L17 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14480_All//1.00E-56//AT5G64650| ribosomal protein L17 family protein	Unigene14480_All//0.00E+00//TC130223		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr -
Unigene14481_All	2055	1.32	3.80	2.23	2.01	6.10	5.27	9.18	8.16	5.37	1.52E+00	1.96E-11	Up	7.51E-01	1.06E-02		1.60E+00	3.36E-22	Up	1.39E+00	1.52E-14	Up	-1.70E-01	1.78E-01		-7.73E-01	7.43E-12		Unigene14481_All//gi|59024061|gb|AAD55508.1|AC008148_18//1.00E-31//Hypothetical protein [Arabidopsis thaliana] >gi|46518435|gb|AAS99699.1| At1g70950 [Arabidopsis thaliana]	Unigene14481_All//2.00E-32//AT1G70950| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Targeting for Xk1p2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23060.1); Has 875 Blast hits to 771 proteins in 143 species: Archae - 0; Bacteria - 102; Metazoa - 281; Fungi - 65; Plants - 205; Viruses - 3; Other Eukaryotes - 219 (source: NCBI BLink).	Unigene14481_All//0.00E+00//TC159301				nr -
Unigene14485_All	1482	10.80	20.07	12.43	7.87	5.32	8.93	14.06	44.25	19.46	8.94E-01	2.70E-18		2.03E-01	1.57E-01		-5.64E-01	2.57E-04		1.83E-01	3.08E-01		1.65E+00	7.36E-126	Up	4.69E-01	1.02E-07		Unigene14485_All//gi|115474397|ref|NP_001060795.1|//6.00E-76//Os08g0107100 [Oryza sativa Japonica Group] >gi|113622764|dbj|BAF22709.1| Os08g0107100 [Oryza sativa Japonica Group]	Unigene14485_All//2.00E-43//AT4G19950| unknown protein	Unigene14485_All//0.00E+00//TC141921				nr +
Unigene14486_All	988	4.98	15.74	7.28	16.59	21.23	15.77	10.23	18.83	22.02	1.66E+00	5.41E-25	Up	5.48E-01	1.63E-02		3.56E-01	2.13E-03		-7.29E-02	6.70E-01		8.80E-01	6.10E-14		1.11E+00	8.86E-24	Up	Unigene14486_All//gi|297819638|ref|XP_002877702.1|//8.00E-31//bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323340|gb|EFH53961.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14486_All//2.00E-22//AT4G37730| AtbZIP7 (Arabidopsis thaliana basic leucine-zipper 7); DNA binding / transcription factor	Unigene14486_All//4.00E-71//ES838565	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0003677//GO:0043231	nr +
Unigene14489_All	1388	13.68	800.42	76.73	3.09	10.74	26.84	34.91	46.88	44.26	5.87E+00	0.00E+00	Up	2.49E+00	5.40E-277	Up	1.80E+00	5.72E-31	Up	3.12E+00	4.26E-135	Up	4.26E-01	2.10E-13		3.42E-01	5.25E-09		Unigene14489_All//gi|256542214|dbj|BAB98060.1|//1.00E-156//galactinol synthase [Solanum lycopersicum]	Unigene14489_All//1.00E-144//AT1G56600| AtGolS2 (Arabidopsis thaliana galactinol synthase 2); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene14489_All//0.00E+00//TC143077				nr -
Unigene1449_All	2269	0.92	0.71	0.87	1.65	1.31	0.86	2.31	0.96	2.00	-3.68E-01	4.01E-01		-8.72E-02	8.46E-01		-3.35E-01	3.10E-01		-9.44E-01	2.66E-03		-1.27E+00	1.55E-07	Down	-2.07E-01	4.00E-01		Unigene1449_All//gi|225432364|ref|XP_002275431.1|//0.00E+00//PREDICTED: similar to protein kinase family protein [Vitis vinifera]	Unigene1449_All//0.00E+00//AT5G18610| protein kinase family protein	Unigene1449_All//0.00E+00//TC149578		ko04626|Plant-pathogen interaction		nr +
Unigene14490_All	1286	43.37	33.85	21.32	70.11	67.08	70.13	36.36	41.86	34.85	-3.58E-01	3.65E-07		-1.02E+00	1.02E-40	Down	-6.38E-02	3.24E-01		4.00E-04	9.95E-01		2.03E-01	2.15E-03		-6.12E-02	4.52E-01		Unigene14490_All//gi|18399468|ref|NP_565484.1|//1.00E-86//protein binding / structural molecule [Arabidopsis thaliana] >gi|4454472|gb|AAD20919.1| expressed protein [Arabidopsis thaliana] >gi|15982817|gb|AAL09756.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|16323101|gb|AAL15285.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|108385429|gb|ABF85787.1| At2g20760 [Arabidopsis thaliana]	Unigene14490_All//1.00E-52//AT2G20760| protein binding / structural molecule	Unigene14490_All//0.00E+00//TC175916			GO:0006810//GO:0012505//GO:0044425//GO:0044444	nr +
Unigene14493_All	1157	4.97	3.20	3.41	6.72	12.62	12.92	1.10	2.75	1.62	-6.38E-01	9.87E-03		-5.47E-01	3.60E-02		9.10E-01	5.68E-11		9.44E-01	5.49E-11		1.32E+00	3.89E-05	Up	5.62E-01	1.76E-01		Unigene14493_All//gi|115473321|ref|NP_001060259.1|//2.00E-19//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene14493_All//1.00E-16//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene14493_All//3.00E-20//gi|109834139|gb|DW232704.1|DW232704				nr +
Unigene14494_All	870	3.73	0.70	2.20	1.95	2.77	2.28	1.02	1.15	1.92	-2.42E+00	5.43E-09	Down	-7.59E-01	3.56E-02		5.09E-01	2.36E-01		2.31E-01	6.49E-01		1.76E-01	7.73E-01		9.14E-01	3.75E-02		Unigene14494_All//gi|115455891|ref|NP_001051546.1|//1.00E-113//Os03g0795200 [Oryza sativa Japonica Group] >gi|113550017|dbj|BAF13460.1| Os03g0795200 [Oryza sativa Japonica Group]	Unigene14494_All//2.00E-113//AT2G02980| pentatricopeptide (PPR) repeat-containing protein	Unigene14494_All//2.00E-45//CO111412				nr -
Unigene14495_All	1279	1.06	1.55	1.29	0.55	0.83	0.71	0.26	1.34	1.31	5.39E-01	2.41E-01		2.79E-01	6.20E-01		6.14E-01	3.94E-01		3.73E-01	6.26E-01		2.34E+00	7.21E-06	Up	2.31E+00	8.00E-06	Up	Unigene14495_All//gi|297814598|ref|XP_002875182.1|//1.00E-172//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297321020|gb|EFH51441.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene14495_All//2.00E-172//AT2G02980| pentatricopeptide (PPR) repeat-containing protein	Unigene14495_All//0.00E+00//CO111412				nr -
Unigene14496_All	1045	26.14	27.20	21.20	31.99	37.50	28.31	46.89	40.00	23.45	5.77E-02	6.20E-01		-3.02E-01	6.04E-03		2.29E-01	6.65E-03		-1.76E-01	8.02E-02		-2.30E-01	8.82E-04		-1.00E+00	6.02E-45	Down	Unigene14496_All//gi|15450824|gb|AAK96683.1|//8.00E-48//Unknown protein [Arabidopsis thaliana]	Unigene14496_All//3.00E-37//AT5G58990| unknown protein	Unigene14496_All//0.00E+00//TC174794			GO:0043231	nr +
Unigene14497_All	1671	34.85	48.79	24.47	39.02	32.93	54.06	31.70	65.56	41.65	4.85E-01	3.94E-17		-5.10E-01	5.23E-13		-2.45E-01	6.17E-05		4.70E-01	4.95E-19		1.05E+00	2.91E-104	Up	3.94E-01	8.07E-13		Unigene14497_All//gi|115460446|ref|NP_001053823.1|//1.00E-127//Os04g0609600 [Oryza sativa Japonica Group] >gi|122240832|sp|Q0JAA0.1|P2C44_ORYSJ RecName: Full=Probable protein phosphatase 2C 44; Short=OsPP2C44 >gi|113565394|dbj|BAF15737.1| Os04g0609600 [Oryza sativa Japonica Group]	Unigene14497_All//8.00E-87//AT4G28400| protein phosphatase 2C, putative / PP2C, putative	Unigene14497_All//0.00E+00//gi|78333381|gb|DT553655.1|DT553655			GO:0004721	nr -
Unigene14499_All	1305	21.89	11.07	18.36	62.60	63.99	92.37	137.92	80.97	63.28	-9.84E-01	1.26E-20		-2.54E-01	2.03E-02		3.16E-02	6.75E-01		5.61E-01	1.41E-34		-7.69E-01	1.34E-101		-1.12E+00	6.35E-197	Down	Unigene14499_All//gi|1843527|gb|AA867994.1|//1.00E-174//annexin [Gossypium hirsutum]	Unigene14499_All//3.00E-130//AT5G65020| ANNAT2 (Annexin Arabidopsis 2); calcium ion binding / calcium-dependent phospholipid binding	Unigene14499_All//0.00E+00//TC131765				nr +
Unigene145_All	978	15.62	6.89	15.19	4.02	7.64	2.68	1.08	0.68	4.68	-1.18E+00	4.79E-15	Down	-4.03E-02	8.02E-01		9.25E-01	5.26E-06		-5.87E-01	6.00E-02		-6.61E-01	2.78E-01		2.12E+00	3.13E-13	Up	Unigene145_All//gi|224365683|ref|YP_002608410.1|//4.00E-23//orf145 [Vitis vinifera] >gi|209954207|emb|CAQ77680.1| orf145 [Vitis vinifera] >gi|239764742|gb|ACS15213.1| ORF145 [Vitis vinifera]	Unigene145_All//3.00E-10//AtMG00660| hypothetical protein	Unigene145_All//3.00E-106//ES810379				nr -
Unigene14501_All	897	4.72	2.99	4.81	19.99	14.43	13.04	19.89	15.00	9.37	-6.58E-01	2.51E-02		2.54E-02	9.50E-01		-4.70E-01	1.09E-04		-6.16E-01	1.19E-06		-4.07E-01	5.29E-04		-1.09E+00	2.96E-19	Down	Unigene14501_All//gi|192910878|gb|ACF06547.1|//1.00E-112//Mob1 [Eleusis guineensis]	Unigene14501_All//1.00E-111//AT5G45550| mob1/phocein family protein	Unigene14501_All//0.00E+00//TC137846				nr +
Unigene14502_All	1439	16.11	14.58	10.55	20.49	16.82	23.35	7.05	12.05	2.96	-1.44E-01	2.46E-01		-6.11E-01	1.77E-07		-2.85E-01	3.01E-03		1.88E-01	5.91E-02		7.74E-01	1.25E-10		-1.25E+00	5.50E-14	Down	Unigene14502_All//gi|15233273|ref|NP_188226.1|//1.00E-122//A37; protein heterodimerization [Arabidopsis thaliana] >gi|45477214|sp|Q9ZN86.1|PDX12_ARATH RecName: Full=Probable pyridoxal biosynthesis protein PDX1.2; Short=AtPDX1.2; Short=AtPDX1;3 >gi|4103952|gb|AAD01897.1| A37 [Arabidopsis thaliana] >gi|4103954|gb|AAD01898.1| A37 [Arabidopsis thaliana] >gi|9294451|dbj|BAB02670.1| A37 protein; ethylene-inducible protein-like [Arabidopsis thaliana] >gi|27808576|gb|AAO24568.1| At3g16050 [Arabidopsis thaliana]	Unigene14502_All//5.00E-124//AT3G16050| A37; protein heterodimerization	Unigene14502_All//0.00E+00//TC161877		ko00750|Vitamin B6 metabolism		nr -
Unigene14506_All	879	5.36	46.46	19.99	6.06	14.02	18.09	10.20	17.93	38.71	3.12E+00	4.58E-138	Up	1.90E+00	8.85E-33	Up	1.21E+00	1.63E-14	Up	1.58E+00	2.75E-25	Up	8.14E-01	1.50E-10		1.92E+00	1.94E-82	Up	Unigene14506_All//gi|60317458|gb|AAX18706.1|//2.00E-40//cold-related protein Cor413 [Gossypium barbadense] >gi|115432869|gb|ABI97481.1| COR413-like protein [Gossypium barbadense]	Unigene14506_All//1.00E-38//AT3G50830| COR413-PM2 (COLD-REGULATED 413-PLASMA MEMBRANE 2)	Unigene14506_All//0.00E+00//TC163659			GO:0016020//GO:0050896	nr +
Unigene14507_All	2119	12.99	7.80	13.62	8.89	9.36	6.65	7.50	5.66	3.27	-7.37E-01	1.89E-12		6.86E-02	5.91E-01		7.50E-02	6.16E-01		-4.18E-01	8.65E-04		-4.06E-01	1.19E-03		-1.20E+00	4.88E-20	Down	Unigene14507_All//gi|225464788|ref|XP_002266883.1|//0.00E+00//PREDICTED: similar to Cytochrome P450 97B2 [Vitis vinifera]	Unigene14507_All//0.00E+00//AT4G15110| CYP97B3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene14507_All//0.00E+00//TC152972		ko04146|Peroxisome//ko00592|alpha-linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00906|Carotenoid biosynthesis//ko00590|Arachidonic acid metabolism	GO:0005506//GO:0008152//GO:0009532//GO:0016712	nr +
Unigene14508_All	1156	18.24	12.89	13.13	34.60	33.96	20.12	12.91	4.63	7.41	-5.01E-01	2.62E-05		-4.74E-01	1.27E-04		-2.71E-02	8.23E-01		-7.82E-01	4.99E-21		-1.48E+00	5.04E-25	Down	-8.01E-01	4.00E-10		Unigene14508_All//gi|4191776|gb|AAD10145.1|//5.00E-16//expressed protein [Arabidopsis thaliana] >gi|20197011|gb|AAM14873.1| expressed protein [Arabidopsis thaliana] >gi|50253564|gb|AAT71984.1| At2g19160 [Arabidopsis thaliana]	Unigene14508_All//1.00E-19//AT5G11970| unknown protein	Unigene14508_All//0.00E+00//D9516108			GO:0016020	nr +
Unigene14509_All	931	23.88	11.05	19.16	27.61	23.23	23.92	26.52	25.01	20.84	-1.11E+00	1.19E-19	Down	-3.18E-01	9.94E-03		-2.49E-01	1.97E-02		-2.07E-01	7.19E-02		-8.49E-02	4.78E-01		-3.48E-01	2.88E-04		Unigene14509_All//gi|27447974|gb|AAO13749.1|AF268257_1//4.00E-98//PTEN-like protein [Arabidopsis thaliana]	Unigene14509_All//6.00E-99//AT3G19420| ATPEN2 (ARABIDOPSIS THALIANA PTEN 2); phosphatase/ protein tyrosine phosphatase	Unigene14509_All//0.00E+00//gi|78333233|gb|DT553507.1|DT553507		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0004721//GO:0006464//GO:0006796//GO:0008033//GO:0016104//GO:0035159	nr -

Unigene14513_A11	1238	22.36	16.08	11.74	29.21	29.68	31.74	30.67	21.20	14.80	-4.75E-01	3.76E-06		-9.29E-01	1.72E-17		2.29E-02	8.32E-01		1.20E-01	2.29E-01		-5.33E-01	6.56E-12		-1.05E+00	6.19E-38	Down	Unigene14513_A11//gi|224109756|ref|XP_002315301.1|//1.00E-167//chorismate synthase [Populus trichocarpa] >gi|222864341|gb|EEF01472.1| chorismate synthase [Populus trichocarpa]	Unigene14513_A11//1.00E-167//AT1G48850| EMB1144 (embryo defective 1144); chorismate synthase	Unigene14513_A11//0.00E+00//TC131212		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr +
Unigene14515_A11	396	1.32	1.02	0.00	4.15	1.22	0.46	5.12	0.63	2.01	-3.68E-01	6.83E-01		-1.04E+01	4.76E-03		-1.77E+00	4.68E-04	Down	-3.19E+00	1.23E-06	Down	-3.02E+00	9.07E-09	Down	-1.35E+00	8.26E-04	Down				Unigene14515_A11//1.00E-50//BQ404065				
Unigene14516_A11	3112	0.62	0.55	0.38	8.84	6.59	2.71	5.16	0.97	2.16	-1.68E-01	7.03E-01		-7.25E-01	1.38E-01		-4.22E-01	1.00E-05		-1.70E+00	2.64E-49	Down	-2.42E+00	2.94E-51	Down	-1.25E+00	1.00E-21	Down	Unigene14516_A11//gi|8493576|gb|AAF75799.1|AC011000_2//0.00E+00//Contains weak similarity to T-type calcium channel isoform from Rattus norvegicus gb|AF125161. EST gb|R30034 comes from this gene [Arabidopsis thaliana]	Unigene14516_A11//0.00E+00//AT1G62870| unknown protein	Unigene14516_A11//0.00E+00//gi|48812434|gb|CO113747.1|CO113747			GO:0005488	nr +
Unigene14517_A11	748	1.54	0.81	1.21	1.07	1.70	0.72	2.49	0.67	1.65	-9.21E-01	1.43E-01		-3.47E-01	6.16E-01		6.77E-01	2.91E-01		-5.57E-01	4.98E-01		-1.89E+00	5.01E-05	Down	-5.91E-01	1.51E-01		Unigene14517_A11//gi|18399401|ref|NP_565478.1|//4.00E-18//NFD6 (NUCLEAR FUSION DEFECTIVE 6) [Arabidopsis thaliana] >gi|20198036|gb|AAM15363.1| Expressed protein [Arabidopsis thaliana] >gi|21655277|gb|AAM65350.1| At2g20587/At2g20587 [Arabidopsis thaliana]	Unigene14517_A11//3.00E-16//AT2G20585| NFD6 (NUCLEAR FUSION DEFECTIVE 6)	Unigene14517_A11//8.00E-180//TC148284			GO:0009536	nr +
Unigene14518_A11	901	3.60	2.42	4.49	2.49	2.22	3.41	6.48	2.69	1.59	-5.74E-01	9.59E-02		3.19E-01	3.41E-01		-1.67E-01	7.29E-01		4.54E-01	2.33E-01		-1.27E+00	2.85E-08	Down	-2.02E+00	5.58E-16	Down	Unigene14518_A11//gi|18399401|ref|NP_565478.1|//1.00E-18//NFD6 (NUCLEAR FUSION DEFECTIVE 6) [Arabidopsis thaliana] >gi|20198036|gb|AAM15363.1| Expressed protein [Arabidopsis thaliana] >gi|21655277|gb|AAM65350.1| At2g20587/At2g20587 [Arabidopsis thaliana]	Unigene14518_A11//5.00E-16//AT2G20585| NFD6 (NUCLEAR FUSION DEFECTIVE 6)	Unigene14518_A11//0.00E+00//TC148284				nr +
Unigene1452_A11	1768	3.26	6.91	4.94	10.88	13.09	14.36	16.76	14.54	18.00	1.09E+00	1.08E-10	Up	6.02E-01	3.04E-03		2.67E-01	1.93E-02		4.01E-01	1.65E-04		-2.06E-01	2.80E-02		1.03E-01	2.80E-01		Unigene1452_A11//gi|18417554|ref|NP_567842.1|//4.00E-68//protein binding [Arabidopsis thaliana] >gi|16226657|gb|AAL16225.1|AF428456_1 AT4g30240/F9N11_90 [Arabidopsis thaliana] >gi|22137126|gb|AAM91408.1| At4g30240/F9N11_90 [Arabidopsis thaliana]	Unigene1452_A11//4.00E-68//AT4G30240| protein binding	Unigene1452_A11//0.00E+00//TC164106		ko04130|SNARE interactions in vesicular transport		nr -
Unigene14521_A11	1030	1.37	0.79	1.96	2.32	2.24	1.49	3.37	1.54	3.44	-8.01E-01	1.49E-01		5.19E-01	2.78E-01		-5.15E-02	8.99E-01		-6.39E-01	1.31E-01		-1.13E+00	1.75E-04	Down	3.24E-02	9.35E-01		Unigene14521_A11//gi|264664532|sp|COLGU1.1|Y5374_ARATH//2.00E-85//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At5g37450; Flags: Precursor >gi|224589689|gb|ACN59376.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene14521_A11//2.00E-80//AT1G06840| leucine-rich repeat transmembrane protein kinase, putative	Unigene14521_A11//4.00E-25//TC150008		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152//GO:0016020//GO:0031410	nr +
Unigene14525_A11	1121	17.04	3.84	5.61	6.35	6.36	4.11	8.22	6.26	3.98	-2.15E+00	3.32E-43	Down	-1.60E+00	4.32E-28	Down	1.00E-03	9.97E-01		-6.29E-01	3.63E-03		-3.93E-01	2.28E-02		-1.05E+00	7.94E-10	Down	Unigene14525_A11//gi|297816246|ref|XP_002876006.1|//7.00E-55//LOB domain protein 38 [Arabidopsis lyrata subsp. lyrata] >gi|297321844|gb|EFH52265.1| LOB domain protein 38 [Arabidopsis lyrata subsp. lyrata]	Unigene14525_A11//2.00E-54//AT3G49940| LBD38 (LOB DOMAIN-CONTAINING PROTEIN 38)	Unigene14525_A11//0.00E+00//ES807748				nr -
Unigene14526_A11	1455	13.74	26.05	12.48	7.53	9.11	10.40	6.04	14.28	13.28	9.23E-01	2.32E-24		-1.38E-01	3.43E-01		2.75E-01	8.68E-02		4.65E-01	1.06E-03		1.24E+00	1.77E-26	Up	1.14E+00	4.23E-22	Up	Unigene14526_A11//gi|224143892|ref|XP_002325111.1|//1.00E-130//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222866545|gb|EEF03676.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene14526_A11//1.00E-100//AT1G16060| ovule development protein, putative	Unigene14526_A11//0.00E+00//CO116658	AP2-EREBP			nr +
Unigene14529_A11	462	4.64	2.52	3.34	3.56	2.61	2.54	4.03	1.00	2.41	-8.80E-01	4.38E-02		-4.74E-01	3.12E-01		-4.48E-01	3.94E-01		-4.85E-01	3.82E-01		-2.02E+00	2.13E-05	Down	-7.38E-01	7.07E-02					Unigene14529_A11//3.00E-73//TC149763				
Unigene14530_A11	1798	9.78	7.05	13.03	8.42	9.75	9.62	12.51	4.67	7.31	-4.73E-01	3.41E-04		4.14E-01	4.07E-04		2.11E-01	1.39E-01		1.92E-01	2.01E-01		-1.42E+00	3.78E-35	Down	-7.75E-01	5.10E-14		Unigene14530_A11//gi|15240941|ref|NP_188689.1|//0.00E+00//tryptophan synthase-related [Arabidopsis thaliana] >gi|10176821|dbj|BAB10143.1| tryptophan synthase beta chain [Arabidopsis thaliana] >gi|19699005|gb|AAL91238.1| tryptophan synthase beta chain [Arabidopsis thaliana] >gi|23198094|gb|AAN15574.1| tryptophan synthase beta chain [Arabidopsis thaliana]	Unigene14530_A11//0.00E+00//AT5G38530| tryptophan synthase-related	Unigene14530_A11//0.00E+00//TC149763		ko00260|Glycine, serine and threonine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0006568//GO:0016836//GO:0043231//GO:0048037	nr -
Unigene14531_A11	1220	23.42	24.63	27.50	27.72	26.96	27.21	17.15	11.55	6.92	7.29E-02	5.32E-01		2.32E-01	2.10E-02		-4.06E-02	7.48E-01		-2.71E-02	8.09E-01		-5.71E-01	9.26E-08		-1.31E+00	6.93E-30	Down	Unigene14531_A11//gi|6119844|gb|AAF04253.1|AF097651_1//4.00E-79//short-chain alcohol dehydrogenase SAD-C [Pisum sativum]	Unigene14531_A11//1.00E-67//AT2G47140| short-chain dehydrogenase/reductase (SDR) family protein	Unigene14531_A11//0.00E+00//TC156245		ko00906|Carotenoid biosynthesis	GO:0008152//GO:0016616	nr +
Unigene14534_A11	808	4.66	4.70	7.05	7.15	6.82	9.67	3.98	3.67	8.43	1.26E-02	9.88E-01		5.97E-01	2.21E-02		-6.87E-02	8.30E-01		4.35E-01	4.10E-02		-1.15E-01	7.31E-01		1.08E+00	8.06E-08	Up	Unigene14534_A11//gi|224127726|ref|XP_002329162.1|//8.00E-54//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene14534_A11//5.00E-42//AT4G12020| WRKY19; transcription factor	Unigene14534_A11//0.00E+00//TC135081				nr +
Unigene14535_A11	1890	15.42	10.72	15.33	32.92	31.12	37.04	19.80	42.04	27.74	-5.24E-01	1.57E-07		-8.70E-03	9.59E-01		-8.11E-02	3.08E-01		1.70E-01	8.80E-03		1.09E+00	2.43E-80	Up	4.87E-01	3.57E-14		Unigene14535_A11//gi|155242084|gb|ABT18094.1|//2.00E-94//FERONIA receptor-like kinase [Brassica oleracea]	Unigene14535_A11//2.00E-86//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene14535_A11//0.00E+00//gi|54120320|gb|CO495829.1|CO495829			GO:0016301	nr +
Unigene14539_A11	1221	33.25	67.48	39.34	58.38	63.57	77.34	64.68	61.41	50.05	1.02E+00	1.75E-61	Up	2.43E-01	2.80E-03		1.23E-01	4.99E-02		4.06E-01	2.77E-15		-7.49E-02	2.28E-01		-3.70E-01	5.54E-13		Unigene14539_A11//gi|297810739|ref|XP_002873253.1|//1.00E-115//NC domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319090|gb|EFH49512.1| NC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene14539_A11//1.00E-116//AT5G06370| NC domain-containing protein	Unigene14539_A11//0.00E+00//TC152880				nr -
Unigene14540_A11	1036	14.24	24.41	22.31	20.87	19.61	31.30	61.13	53.33	30.15	7.77E-01	1.65E-12		6.47E-01	3.32E-08		-8.97E-02	5.52E-01		5.85E-01	1.96E-10		-1.97E-01	1.13E-03		-1.02E+00	1.03E-59	Down	Unigene14540_A11//gi|4958922|dbj|BAA78050.1|//4.00E-97//NADPH oxidoreductase homolog [Cicer arietinum]	Unigene14540_A11//9.00E-96//AT1G19670| NQR; binding / catalytic/ oxidoreductase/ zinc ion binding	Unigene14540_A11//0.00E+00//TC145969			GO:0006952//GO:0006970//GO:0008152//GO:0009532//GO:0016020//GO:0016166//GO:0016646//GO:0016655//GO:0042579//GO:0046914	nr -
Unigene14542_A11	1884	4.08	2.45	5.48	6.37	5.78	4.72	2.72	0.95	1.67	-7.38E-01	4.28E-04		4.26E-01	2.35E-02		-1.42E-01	4.52E-01		-4.32E-01	8.20E-03		-1.51E+00	2.47E-09	Down	-7.01E-01	2.13E-03		Unigene14542_A11//gi|62177683|gb|AAX71115.1|//0.00E+00//phytase [Medicago truncatula]	Unigene14542_A11//0.00E+00//AT3G07130| PAP15 (PURPLE ACID PHOSPHATASE 15); acid phosphatase/ protein serine/threonine phosphatase	Unigene14542_A11//0.00E+00//TC173108			GO:0009856//GO:0016791//GO:0032501//GO:0043169	nr -
Unigene14544_A11	1918	32.22	49.06	45.09	4.78	6.84	4.54	0.40	0.00	0.46	6.07E-01	4.99E-29		4.85E-01	2.04E-17		5.17E-01	4.56E-04		-7.25E-02	7.32E-01		-8.63E+00	1.68E-05	Down	2.04E-01	7.47E-01		Unigene14544_A11//gi|15221439|ref|NP_177024.1|//0.00E+00//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|5734721|gb|AAD49986.1|AC008075_19 Similar to gb|AF023472 peptide transporter from Hordeum vulgare and is a member of the PF|00854 Peptide transporter family. ESTs gb|T41927 and gb|AA395024 come from this gene [Arabidopsis thaliana] >gi|20147231|gb|AAM10330.1| At1g68570/F24J5_7 [Arabidopsis thaliana] >gi|25090385|gb|AAN72289.1| At1g68570/F24J5_7 [Arabidopsis thaliana] >gi|110742209|dbj|BAE99031.1| peptide transporter like [Arabidopsis thaliana]	Unigene14544_A11//0.00E+00//AT1G68570| proton-dependent oligopeptide transport (POT) family protein	Unigene14544_A11//0.00E+00//gi|78351962|gb|DT572236.1|DT572236			GO:0015833//GO:0016020	nr -
Unigene14548_A11	1150	7.01	6.34	9.45	8.49	15.99	10.76	1.07	0.87	0.14	-1.43E-01	5.28E-01		4.31E-01	1.79E-02		9.13E-01	8.53E-14		3.42E-01	3.97E-02		-2.90E-01	6.39E-01		-2.94E+00	1.14E-05	Down				Unigene14548_A11//3.00E-07//DB462582				
Unigene14549_A11	1480	0.74	1.13	2.12	3.30	4.10	2.84	0.46	0.37	0.05	6.06E-01	2.36E-01		1.52E+00	8.23E-05	Up	3.12E-01	2.26E-01		-2.17E-01	4.78E-01		-3.16E-01	6.74E-01		-3.09E+00	1.45E-03					Unigene14549_A11//5.00E-59//CO092801				
Unigene14555_A11	1208	19.49	19.38	12.61	14.31	13.83	15.22	30.98	16.37	13.85	-8.30E-03	9.68E-01		-6.29E-01	6.09E-08		-4.96E-02	7.86E-01		8.87E-02	5.98E-01		-9.21E-01	2.53E-29		-1.16E+00	8.46E-44	Down	Unigene14555_A11//gi|253721463|gb|ACT33948.1|//5.00E-79//biotin carboxyl carrier protein subunit [Jatropha curcas]	Unigene14555_A11//3.00E-44//AT5G15530| BCCP2 (BIOTIN CARBOXYL CARRIER PROTEIN 2); biotin binding	Unigene14555_A11//0.00E+00//gi|78322880|gb|DT543154.1|DT543154		ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis	GO:0006631//GO:0009536//GO:0016421//GO:0019842//GO:0043234	nr +
Unigene14558_A11	745	16.50	22.85	13.72	36.84	25.14	41.22	35.24	100.03	23.85	4.70E-01	4.89E-04		-2.66E-01	1.38E-01		-5.51E-01	5.47E-09		1.62E-01	1.34E-01		1.51E+00	1.02E-124	Up	-5.63E-01	1.29E-09		Unigene14558_A11//gi|227345480|gb|ACP28172.1|//1.00E-46//roothairless1/slippery [Lotus japonicus]	Unigene14558_A11//9.00E-36//AT2G24260| basic helix-loop-helix (bHLH) family protein	Unigene14558_A11//0.00E+00//TC179230	bHLH		GO:0010468//GO:0043231	nr +
Unigene1456_A11	2634	1.11	3.06	1.92	3.73	4.51	3.15	8.22	9.25	5.23	1.46E+00	3.88E-11	Up	7.88E-01	4.50E-03		2.76E-01	1.09E-01		-2.40E-01	2.31E-01		1.71E-01	1.15E-01		-6.51E-01	3.27E-10		Unigene1456_A11//gi|57283536|emb|CAG27608.1|//0.00E+00//monosaccharide transporter [Populus tremula x Populus tremuloides]	Unigene1456_A11//0.00E+00//AT5G26250| sugar transporter, putative	Unigene1456_A11//0.00E+00//DW227554				nr +
Unigene14562_A11	1714	1.10	0.38	0.06	1.02	1.19	1.34	2.57	1.71	1.60	-1.52E+00	2.28E-03		-4.15E+00	4.26E-08	Down	2.21E-01	6.69E-01		4.02E-01	3.93E-01		-5.88E-01	2.31E-02		-6.78E-01	6.40E-03		Unigene14562_A11//gi|297820766|ref|XP_002878266.1|//1.00E-167//UDP-galactose transporter 6 [Arabidopsis lyrata subsp. lyrata] >gi|297324104|gb|EFH54525.1| UDP-galactose transporter 6 [Arabidopsis lyrata subsp. lyrata]	Unigene14562_A11//5.00E-159//AT2G43240| nucleotide-sugar transmembrane transporter/ sugar:hydrogen symporter	Unigene14562_A11//0.00E+00//DW500048				nr -
Unigene14564_A11	1403	6.45	20.87	13.32	15.05	18.58	22.89	18.11	26.10	45.74	1.69E+00	9.24E-48	Up	1.05E+00	1.62E-14	Up	3.04E-01	3.42E-03		6.04E-01	6.32E-11		5.27E-01	2.66E-11		1.34E+00	6.24E-92	Up	Unigene14564_A11//gi|115458304|ref|NP_001052752.1|//8.00E-47//Os04g0414100 [Oryza sativa Japonica Group] >gi|38346330|emb|CAD40585.2|OJ000126_13.12 [Oryza sativa (japonica cultivar-group)] >gi|113564323|dbj|BAF14666.1| Os04g0414100 [Oryza sativa Japonica Group]	Unigene14564_A11//1.00E-09//AT2G27350| OTU-like cysteine protease family protein	Unigene14564_A11//0.00E+00//TC146655			GO:0043231	nr +

Unigene14565_A11	1300	7.08	10.13	8.77	9.77	9.69	8.93	5.69	8.13	11.89	5.17E-01	8.70E-04		3.07E-01	9.17E-02		-1.13E-02	9.60E-01		-1.30E-01	4.89E-01		5.15E-01	9.95E-04		1.06E+00	3.88E-16	Up	Unigene14565_A11//gi|115459632|ref|NP_001053416.1|//4.00E-59//Os04g0534400 [Oryza sativa Japonica Group] >gi|113564987|dbj|BAF15330.1|Os04g0534400 [Oryza sativa Japonica Group] >gi|116310461|emb|CAH67465.1|OS1GBa0159110.10 [Oryza sativa (indica cultivar-group)]	Unigene14565_A11//4.00E-29//AT2G45140| PVA12 (PLANT VAP HOMOLOG 12); structural molecule	Unigene14565_A11//2.00E-52//gi|48803132|gb|CO104446.1|CO104446			GO:0000322//GO:0005488//GO:0031224	nr -
Unigene14569_A11	939	82.47	140.08	46.50	63.29	51.19	80.90	28.86	61.65	76.50	7.64E-01	3.40E-60		-8.27E-01	1.88E-39		-3.06E-01	1.19E-06		3.54E-01	8.99E-10		1.09E+00	1.76E-59	Up	1.41E+00	5.67E-111	Up	Unigene14569_A11//gi|124109193|gb|ABM91072.1|//1.00E-103//xyloglucan endotransglycosylase/hydrolase precursor XTH-39 [Populus tremula]	Unigene14569_A11//1.00E-89//AT1G14720| XTR2 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE RELATED 2); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene14569_A11//0.00E+00//TC166305			GO:0005576//GO:0009888//GO:0016758//GO:0016798//GO:0030312//GO:0044042	nr -
Unigene14570_A11	1442	2.79	13.99	6.17	3.01	6.81	10.43	9.44	65.62	10.91	2.32E+00	8.67E-50	Up	1.14E+00	2.97E-08	Up	1.18E+00	3.41E-11	Up	1.80E+00	1.18E-28	Up	2.80E+00	0.00E+00	Up	2.09E-01	1.09E-01		Unigene14570_A11//gi|112819971|gb|ABI22959.1|//1.00E-109//WRKY transcription factor 2 [Gossypium hirsutum]	Unigene14570_A11//2.00E-63//AT4G31800| WRKY18; transcription factor	Unigene14570_A11//0.00E+00//TC170183	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0010467	nr -
Unigene14571_A11	1170	593.60	519.04	948.53	358.49	344.24	357.49	71.48	70.41	34.12	-1.94E-01	2.46E-25		6.76E-01	0.00E+00		-5.85E-02	2.32E-02		-4.10E-03	9.16E-01		-2.17E-02	7.28E-01		-1.07E+00	1.54E-84	Down	Unigene14571_A11//gi|297824439|ref|XP_002880102.1|//5.00E-59//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325941|gb|EFH56361.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14571_A11//6.00E-54//AT2G44310| calcium-binding EF hand family protein	Unigene14571_A11//0.00E+00//TC153739			GO:0046872	nr +
Unigene14572_A11	1299	3.14	2.85	1.52	7.13	5.59	5.91	6.61	4.96	4.75	-1.42E-01	6.32E-01		-1.05E+00	9.53E-04	Down	-3.51E-01	6.33E-02		-2.71E-01	1.91E-01		-4.15E-01	2.04E-02		-4.75E-01	5.52E-03		Unigene14572_A11//gi|297802336|ref|XP_002869052.1|//1.00E-45//La domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297314888|gb|EFH45311.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene14572_A11//6.00E-20//AT4G35890| La domain-containing protein	Unigene14572_A11//0.00E+00//TC151584				nr +
Unigene14574_A11	991	64.25	63.81	87.48	41.57	36.24	38.97	29.57	17.71	10.41	-1.00E-02	9.07E-01		4.45E-01	5.22E-15		-1.98E-01	1.78E-02		-9.34E-02	3.58E-01		-7.39E-01	3.77E-16		-1.51E+00	4.30E-51	Down	Unigene14574_A11//gi|90588094|gb|AB094072.1|//2.00E-59//At5g47870 [Arabidopsis thaliana]	Unigene14574_A11//1.00E-60//AT5G47870| unknown protein	Unigene14574_A11//0.00E+00//TC141602			GO:0009536	nr -
Unigene14576_A11	1332	15.36	6.81	13.51	11.52	11.01	7.09	1.52	0.75	1.56	-1.17E+00	1.06E-19	Down	-1.85E-01	1.79E-01		-6.47E-02	7.23E-01		-7.01E-01	4.32E-07		-1.02E+00	1.24E-02		2.97E-02	9.62E-01		Unigene14576_A11//gi|159885612|dbj|BAF93184.1|//1.00E-157//nitric oxide associated 1 [Nicotiana benthamiana]	Unigene14576_A11//1.00E-146//AT3G47450| NOA1 (NO ASSOCIATED 1); GTPase/ nitric-oxide synthase	Unigene14576_A11//0.00E+00//TC155401		ko04626|Plant-pathogen interaction//ko00330|Arginine and proline metabolism		nr +
Unigene14577_A11	3086	2.36	3.94	2.78	0.74	0.42	0.76	17.67	30.53	62.96	7.42E-01	5.28E-06		2.37E-01	2.80E-01		-8.08E-01	4.44E-02		3.55E-02	9.44E-01		7.89E-01	6.82E-56		1.83E+00	0.00E+00	Up	Unigene14577_A11//gi|5545339|emb|jB|AA82556.1|//0.00E+00//lectin-like protein kinase [Populus nigra]	Unigene14577_A11//1.00E-108//AT5G06740| lectin protein kinase family protein	Unigene14577_A11//7.00E-51//gi|109871230|gb|DW500206.1|DW500206		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr -
Unigene14578_A11	1488	48.10	41.85	55.97	7.73	7.75	5.52	1.51	1.35	0.56	-2.01E-01	1.49E-03		2.19E-01	2.61E-04		3.60E-03	9.89E-01		-4.85E-01	3.41E-03		-1.60E-01	6.91E-01		-1.42E+00	2.20E-04	Down	Unigene14578_A11//gi|116310848|emb|CAH67790.1|//0.00E+00//OS1GBa0132E09-OS1GBa0108L24.4 [Oryza sativa (indica cultivar-group)]	Unigene14578_A11//0.00E+00//AT1G73110| ribulose bisphosphate carboxylase/oxygenase activase, putative / RuBisCO activase, putative	Unigene14578_A11//0.00E+00//TC179219			GO:0009534//GO:0017111//GO:0032559	nr -
Unigene1458_A11	2328	2.14	4.81	3.20	3.98	5.62	4.15	2.80	4.04	3.35	1.17E+00	4.68E-11	Up	5.85E-01	8.64E-03		4.98E-01	7.87E-04		6.09E-02	7.74E-01		5.30E-01	1.52E-03		2.62E-01	1.70E-01		Unigene1458_A11//gi|57283536|emb|CAG27608.1|//0.00E+00//monosaccharide transporter [Populus tremula x Populus tremuloides]	Unigene1458_A11//0.00E+00//AT5G26250| sugar transporter, putative	Unigene1458_A11//0.00E+00//DW227554				nr +
Unigene14580_A11	1881	43.34	9.67	46.99	11.52	6.94	2.62	0.00	0.00	0.00	-2.16E+00	2.72E-184	Down	1.17E-01	6.08E-02		-7.32E-01	1.28E-11		-2.14E+00	8.10E-53	Down	null	null		null	null		Unigene14580_A11//gi|260513722|gb|ACX42573.1|//9.00E-86//CONSTANS-like zinc finger protein [Glycine max]	Unigene14580_A11//3.00E-77//AT1G25440| zinc finger (B-box type) family protein	Unigene14580_A11//0.00E+00//gi|48775242|gb|CO084608.1|CO084608	C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0044464	nr +
Unigene14582_A11	1771	32.11	15.59	16.09	11.73	7.02	6.35	31.06	125.95	147.36	-1.04E+00	2.86E-44	Down	-9.97E-01	9.40E-40		-7.41E-01	2.13E-11		-8.85E-01	1.04E-13		2.02E+00	0.00E+00	Up	2.25E+00	0.00E+00	Up	Unigene14582_A11//gi|15221382|ref|NP_177616.1|//0.00E+00//nodulin family protein [Arabidopsis thaliana] >gi|5882744|gb|AAD55297.1|AC008263_28 Strong similarity to gb|AF031243 nodule-specific protein (Nlj70) from Lotus japonicus and is a member of the PF|00083 Sugar (and other) transporter family. EST gb|Z37715 comes from this gene [Arabidopsis thaliana]	Unigene14582_A11//0.00E+00//AT1G74780| nodulin family protein	Unigene14582_A11//0.00E+00//TC154702				nr +
Unigene14585_A11	447	1.76	0.00	0.48	4.79	3.08	2.02	0.47	0.65	0.62	-1.08E+01	1.09E-04	Down	-1.88E+00	4.13E-02		-6.37E-01	1.39E-01		-1.25E+00	4.94E-03		4.69E-01	7.06E-01		4.00E-01	7.43E-01					Unigene14585_A11//0.00E+00//DT461120				
Unigene14586_A11	1325	2.45	1.68	1.89	6.62	4.78	2.69	1.24	1.61	0.93	-5.41E-01	1.20E-01		-3.74E-01	3.18E-01		-4.69E-01	1.21E-02		-1.30E+00	6.61E-11	Down	3.70E-01	3.84E-01		-4.17E-01	3.52E-01		Unigene14586_A11//gi|124359982|gb|ABN07998.1|//2.00E-08//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene14586_A11//1.00E-09//AT2G13980| nucleic acid binding	Unigene14586_A11//0.00E+00//DT461120				nr -
Unigene14587_A11	1342	52.98	195.13	103.68	11.69	10.65	13.93	1.86	3.21	1.25	1.88E+00	0.00E+00	Up	9.69E-01	2.49E-92		-1.35E-01	4.15E-01		2.53E-01	6.24E-02		7.87E-01	2.52E-03		-5.76E-01	9.73E-02		Unigene14587_A11//gi|297823673|ref|XP_002879719.1|//2.00E-75//soul heme-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325558|gb|EFH55978.1| soul heme-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14587_A11//6.00E-71//AT2G37970| SOUL-1; binding	Unigene14587_A11//0.00E+00//gi|31072447|gb|CA992726.1|CA992726				nr -
Unigene1459_A11	1856	1.35	8.35	5.97	7.49	9.96	35.94	43.08	126.76	90.20	2.63E+00	3.55E-44	Up	2.14E+00	2.93E-24	Up	4.12E-01	7.89E-04		2.26E+00	5.45E-170	Up	1.56E+00	0.00E+00	Up	1.07E+00	5.37E-167	Up	Unigene1459_A11//gi|148612415|gb|AB096123.1|//0.00E+00//gibberellic acid receptor-b [Gossypium hirsutum]	Unigene1459_A11//4.00E-159//AT3G63010| GID1B (GA INSENSITIVE DWARF1B); hydrolase	Unigene1459_A11//0.00E+00//TC159388				nr +
Unigene14591_A11	523	14.41	4.26	13.95	10.19	9.68	7.25	2.10	1.52	0.91	-1.76E+00	1.62E-13	Down	-4.65E-02	8.41E-01		-7.45E-02	8.20E-01		-4.91E-01	6.35E-02		-4.69E-01	4.31E-01		-1.20E+00	3.41E-02		Unigene14591_A11//gi|211906456|gb|ACJ11721.1|//2.00E-56//quinone oxidoreductase [Gossypium hirsutum]	Unigene14591_A11//5.00E-30//AT1G23740| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene14591_A11//0.00E+00//TC177055			GO:0008152//GO:0016655//GO:0046914	nr +
Unigene14592_A11	1145	136.40	43.81	91.85	120.95	93.26	66.90	9.23	9.31	4.91	-1.64E+00	5.77E-242	Down	-5.71E-01	2.01E-41		-3.75E-01	1.58E-21		-8.54E-01	3.74E-83		1.19E-02	9.76E-01		-9.12E-01	4.79E-09		Unigene14592_A11//gi|211906456|gb|ACJ11721.1|//1.00E-179//quinone oxidoreductase [Gossypium hirsutum]	Unigene14592_A11//1.00E-98//AT1G23740| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene14592_A11//0.00E+00//TC142488				nr +
Unigene14593_A11	1286	16.52	17.93	12.22	19.14	25.14	16.47	2.43	1.14	2.14	1.18E-01	3.71E-01		-4.35E-01	4.33E-04		3.94E-01	8.72E-06		-2.16E-01	6.56E-02		-1.10E+00	5.48E-04	Down	-1.87E-01	5.86E-01		Unigene14593_A11//gi|297806597|ref|XP_002871182.1|//9.00E-55//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317019|gb|EFH47441.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14593_A11//1.00E-51//AT5G08830| zinc finger (C3HC4-type RING finger) family protein	Unigene14593_A11//0.00E+00//DR460602			GO:0046914	nr +
Unigene14595_A11	390	3.76	0.52	0.00	3.45	1.68	2.43	0.43	2.14	1.74	-2.85E+00	3.60E-05	Down	-1.19E+01	5.25E-08	Down	-1.04E+00	6.04E-02		-5.04E-01	4.05E-01		2.31E+00	3.54E-03		2.00E+00	1.69E-02		Unigene14595_A11//gi|18398123|ref|NP_565388.1|//3.00E-51//metal ion binding [Arabidopsis thaliana] >gi|20198032|gb|AAD22294.2| expressed protein [Arabidopsis thaliana]	Unigene14595_A11//1.00E-52//AT2G16460| metal ion binding	Unigene14595_A11//2.00E-105//TC155639			GO:0016020//GO:0043169//GO:0043231	nr +
Unigene14597_A11	1161	13.34	43.64	20.73	32.18	30.58	42.17	15.26	15.66	19.70	1.71E+00	2.76E-83	Up	6.36E-01	2.83E-08		-7.36E-02	5.09E-01		3.90E-01	1.09E-07		3.74E-02	7.85E-01		3.68E-01	2.34E-04		Unigene14597_A11//gi|297851272|ref|XP_002890517.1|//2.00E-77//VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297339359|gb|EFH69776.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene14597_A11//7.00E-60//AT1G28280| VQ motif-containing protein	Unigene14597_A11//0.00E+00//TC171787				nr +
Unigene1460_A11	2919	5.32	11.23	6.31	9.88	10.30	11.77	11.33	11.15	15.42	1.08E+00	4.34E-27	Up	2.46E-01	8.21E-02		5.97E-02	6.17E-01		2.53E-01	6.86E-03		-2.22E-02	8.30E-01		4.45E-01	1.38E-10		Unigene1460_A11//gi|19699093|gb|AAL90913.1|//0.00E+00//At4g35870/F4B14_140 [Arabidopsis thaliana]	Unigene1460_A11//0.00E+00//AT4G35870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: protein targeting to vacuole; LOCATED IN: membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF221 (InterPro:IPR003864); BEST Arabidopsis thaliana protein match is: early-responsive to dehydration protein-related / ERD protein-related (TAIR:AT3G21620.1); Has 615 Blast hits to 495 proteins in 120 species: Archae - 0; Bacteria - 0; Metazoa - 267; Fungi - 110; Plants - 180; Viruses - 0; Other Eukaryotes - 58 (source: NCBI BLink).	Unigene1460_A11//0.00E+00//gi|164256700|gb|ES830249.1|ES830249				nr +
Unigene14600_A11	983	110.60	38.76	39.17	130.74	103.83	78.01	10.37	17.56	2.23	-1.51E+00	4.47E-150	Down	-1.50E+00	3.53E-143	Down	-3.33E-01	4.95E-16		-7.45E-01	5.07E-61		7.61E-01	2.66E-10		-2.22E+00	1.47E-30	Down	Unigene14600_A11//gi|37730469|gb|AA059439.1|//3.00E-55//ethylene-responsive element binding factor [Gossypium hirsutum]	Unigene14600_A11//8.00E-35//AT5G07580| DNA binding / transcription factor	Unigene14600_A11//0.00E+00//TC145306	AP2-EREBP		GO:0006350//GO:0006950	nr +
Unigene14602_A11	1996	1.21	0.38	0.43	1.72	1.78	2.06	4.17	3.43	2.73	-1.66E+00	1.53E-04	Down	-1.50E+00	8.47E-04	Down	4.54E-02	9.10E-01		2.58E-01	4.56E-01		-2.81E-01	1.39E-01		-6.10E-01	4.37E-04		Unigene14602_A11//gi|297842515|ref|XP_002889139.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297334980|gb|EFH65398.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene14602_A11//0.00E+00//AT1G77360| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene14603_A11	1425	5.21	12.84	6.76	6.08	11.94	8.11	44.86	85.82	101.96	1.30E+00	1.51E-20	Up	3.76E-01	5.73E-02		9.73E-01	3.76E-14		4.16E-01	1.38E-02		9.36E-01	1.54E-96		1.18E+00	1.21E-171	Up	Unigene14603_A11//gi|289976573|gb|AD021635.1|//1.00E-121//matrix metalloprotease 1 [Nicotiana benthamiana]	Unigene14603_A11//0.00E+00//gi|78353667|gb|DT573941.1|DT573941	Unigene14603_A11//0.00E+00//gi|78353667|gb|DT573941.1|DT573941			GO:0008233//GO:0031410	nr +
Unigene14606_A11	882	18.75	7.01	8.88	52.47	28.66	32.57	27.32	28.43	15.27	-1.42E+00	2.53E-21	Down	-1.08E+00	1.64E-13	Down	-8.73E-01	6.21E-33		-6.88E-01	1.75E-19		5.74E-02	6.31E-01		-8.40E-01	4.79E-17		Unigene14606_A11//gi|87240507|gb|ABD32365.1|//7.00E-36//DNA-binding WRKY, VQ [Medicago truncatula]	Unigene14606_A11//6.00E-31//AT1G28280| VQ motif-containing protein	Unigene14606_A11//0.00E+00//TC157384				nr +
Unigene14609_A11	1291	15.48	6.75	9.82	10.42	7.31	6.68	2.16	0.78	2.13	-1.20E+00	7.22E-20	Down	-6.57E-01	2.36E-07		-5.12E-01	3.42E-04		-6.41E-01	1.75E-05		-1.48E+00	2.73E-05	Down	-2.17E-02	9.65E-01		Unigene14609_A11//gi|53828627|gb|AAL94423.1|//8.00E-83//At4g24090 [Arabidopsis thaliana]	Unigene14609_A11//1.00E-67//AT4G24090| unknown protein	Unigene14609_A11//0.00E+00//gi|48741165|gb|CO071684.1|CO071684			GO:0009536	nr -

Unigene1461_All	745	2.39	3.33	2.72	21.80	10.26	5.21	3.46	2.58	3.69	4.81E-01	2.34E-01		1.86E-01	6.80E-01		-1.09E+00	6.56E-17	Down	-2.06E+00	6.13E-38	Down	-4.24E-01	2.45E-01		9.20E-02	7.88E-01		Unigene1461_All//gi|224087124|ref|XP_002308075.1|//9.00E-94//equilibrative nucleoside transporter [Populus trichocarpa] >gi|222854051|gb|EEE91598.1| equilibrative nucleoside transporter [Populus trichocarpa]	Unigene1461_All//7.00E-70//AT1G02630| equilibrative nucleoside transporter, putative (ENT8)	Unigene1461_All//0.00E+00//gi|109883932|gb|DW512902.1|DW512902				nr -
Unigene14610_All	906	62.31	45.92	46.73	173.20	148.27	205.68	86.99	56.14	41.11	-4.41E-01	2.82E-10		-4.15E-01	7.19E-09		-2.24E-01	2.01E-09		2.48E-01	4.78E-12		-6.32E-01	4.46E-32		-1.08E+00	1.96E-81	Down	Unigene14610_All//gi|192910870|gb|ACF06543.1|//9.00E-89//uridylate kinase [Elaeis guineensis]	Unigene14610_All//2.00E-89//AT5G26667| PYR6; cytidylate kinase/ uridylate kinase	Unigene14610_All//0.00E+00//TC139508		ko00240|Pyrimidine metabolism	GO:0009129//GO:0016776//GO:0019201//GO:0019206//GO:0032559//GO:0044424	nr -
Unigene14613_All	1008	1.92	12.22	0.95	4.84	15.37	22.04	32.26	74.76	43.40	2.67E+00	8.11E-36	Up	-1.01E+00	3.97E-02		1.67E+00	5.56E-29	Up	2.19E+00	1.91E-54	Up	1.21E+00	8.70E-91	Up	4.28E-01	1.19E-09		Unigene14613_All//gi|224066255|ref|XP_002302049.1|//8.00E-60//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222843775|gb|EEE81322.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene14613_All//4.00E-31//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene14613_All//2.00E-17//EX167849	AP2-EREBP		GO:0006350//GO:0010468	nr -
Unigene14614_All	673	15.24	9.49	9.26	4.00	7.32	7.11	16.02	5.78	14.86	-6.84E-01	1.24E-04		-7.19E-01	1.03E-04		8.72E-01	7.95E-04		8.32E-01	2.37E-03		-1.47E+00	3.77E-18	Down	-1.09E-01	5.44E-01		Unigene14614_All//gi|260513716|gb|ACX42570.1|//4.00E-30//CONSTANS-like zinc finger protein [Glycine max]	Unigene14614_All//5.00E-11//AT5G24930| zinc finger (B-box type) family protein	Unigene14614_All//0.00E+00//gi|783333366|gb|DT553640.1|DT553640	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene14615_All	1311	32.81	21.57	23.72	11.59	14.45	19.09	16.45	6.31	9.91	-6.05E-01	1.15E-13		-4.68E-01	1.88E-08		3.18E-01	1.12E-02		7.20E-01	1.51E-11		-1.38E+00	2.33E-32	Down	-7.31E-01	2.80E-12		Unigene14615_All//gi|260513716|gb|ACX42570.1|//3.00E-59//CONSTANS-like zinc finger protein [Glycine max]	Unigene14615_All//1.00E-23//AT5G24930| zinc finger (B-box type) family protein	Unigene14615_All//0.00E+00//gi|783333366|gb|DT553640.1|DT553640	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene14617_All	1258	18.13	26.95	17.19	1.43	0.77	12.85	1.01	14.25	44.56	5.71E-01	6.33E-10		-7.75E-02	5.90E-01		-8.95E-01	5.47E-02		3.17E+00	1.23E-59	Up	3.82E+00	3.10E-89	Up	5.47E+00	0.00E+00	Up	Unigene14617_All//gi|297842165|ref|XP_002888964.1|//3.00E-88//sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334805|gb|EFH65223.1| sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14617_All//2.00E-88//AT1G74100| SOT16 (SULFOTRANSFERASE 16); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene14617_All//0.00E+00//TC170250		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism	GO:0008146//GO:0009753//GO:0019758	nr -
Unigene14618_All	1173	18.78	7.95	4.63	36.35	34.49	25.07	27.14	6.38	7.68	-1.24E+00	5.03E-23	Down	-2.02E+00	2.92E-44	Down	-7.57E-02	4.55E-01		-5.36E-01	9.74E-12		-2.09E+00	2.02E-84	Down	-1.82E+00	1.33E-72	Down	Unigene14618_All//gi|13124019|sp|Q41596.1|CHI1_THECC//1.00E-103//RecName: Full=Endochitinase 1; Flags: Precursor >gi|92495|gb|AAA80656.1| class I chitinase [Theobroma cacao]	Unigene14618_All//2.00E-87//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene14618_All//0.00E+00//TC131054		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0000272//GO:0016798	nr +
Unigene14619_All	977	0.32	1.66	0.00	8.16	5.71	3.37	2.47	2.91	1.92	2.37E+00	1.02E-04	Up	-8.33E+00	4.92E-02		-5.15E-01	8.54E-03		-1.27E+00	1.05E-09	Down	2.38E-01	5.25E-01		-3.64E-01	3.24E-01		Unigene14619_All//gi|225463464|ref|XP_002272948.1|//3.00E-74//PREDICTED: similar to cytochrome B561-related [Vitis vinifera]	Unigene14619_All//8.00E-67//AT4G18260| cytochrome B561-related	Unigene14619_All//0.00E+00//gi|54118119|gb|CO493628.1|CO493628			GO:0043231	nr +
Unigene1462_All	2479	1.29	1.94	1.12	11.13	4.57	2.00	3.62	2.21	4.00	5.93E-01	3.11E-02		-2.05E-01	6.06E-01		-1.28E+00	3.63E-37	Down	-2.47E+00	2.85E-80	Down	-7.11E-01	3.33E-05		1.46E-01	4.05E-01		Unigene1462_All//gi|224087124|ref|XP_002308075.1|//9.00E-83//equilibrative nucleoside transporter [Populus trichocarpa] >gi|222854051|gb|EEE91598.1| equilibrative nucleoside transporter [Populus trichocarpa]	Unigene1462_All//3.00E-69//AT1G02630| equilibrative nucleoside transporter, putative (ENT8)	Unigene1462_All//0.00E+00//TC176124				nr +
Unigene14623_All	625	2.43	4.13	3.58	6.70	4.85	1.95	0.41	0.13	0.38	7.68E-01	5.07E-02		5.60E-01	2.20E-01		-4.66E-01	1.14E-01		-1.78E+00	2.00E-08	Down	-1.60E+00	3.11E-01		-8.57E-02	9.57E-01		Unigene14623_All//gi|115480315|ref|NP_001063751.1|//6.00E-36//Os09g0530800 [Oryza sativa Japonica Group] >gi|113631984|dbj|BAF25665.1| Os09g0530800 [Oryza sativa Japonica Group]	Unigene14623_All//5.00E-36//AT4G10540| subtilase family protein				GO:0008152//GO:0070011	nr +
Unigene14625_All	1650	4.19	2.95	3.26	3.59	3.97	1.67	0.54	0.33	0.10	-5.06E-01	2.42E-02		-3.61E-01	1.39E-01		1.42E-01	6.08E-01		-1.11E+00	4.92E-06	Down	-7.09E-01	2.97E-01		-2.48E+00	9.93E-04	Down	Unigene14625_All//gi|18398655|ref|NP_564412.1|//1.00E-120//SBT3.5; identical protein binding / serine-type endopeptidase [Arabidopsis thaliana] >[Arabidopsis thaliana]	Unigene14625_All//2.00E-112//AT1G32940| SBT3.5; identical protein binding / serine-type endopeptidase	Unigene14625_All//6.00E-53//DN803119				nr -
Unigene14627_All	1335	1.10	5.47	1.91	1.31	1.08	4.47	38.76	68.94	45.69	2.32E+00	2.44E-18	Up	8.03E-01	5.20E-02		-2.70E-01	6.05E-01		1.77E+00	1.78E-11	Up	8.31E-01	1.18E-59		2.37E-01	6.65E-05		Unigene14627_All//gi|259121391|gb|ACV92015.1|//1.00E-99//WRKY transcription factor 13 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene14627_All//2.00E-53//AT2G47260| WRKY23; transcription factor	Unigene14627_All//0.00E+00//gi|109877840|gb|DW506813.1|DW506813	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0006350//GO:0009725//GO:0010468//GO:0051707	nr +
Unigene14628_All	646	16.36	48.87	62.15	27.14	39.34	118.15	35.34	30.86	52.79	1.58E+00	1.52E-46	Up	1.93E+00	8.41E-76	Up	5.35E-01	9.21E-08		2.12E+00	1.61E-179	Up	-1.96E-01	7.54E-02		5.79E-01	9.97E-13		Unigene14628_All//gi|114329246|gb|AB164152.1|//5.00E-79//hydroxymethylbutenyl diphosphate reductase [Camptotheca acuminata]	Unigene14628_All//5.00E-73//AT4G34350| HDR (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE REDUCTASE); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase/ 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Unigene14628_All//0.00E+00//gi|164369255|gb|ES850705.1|ES850705		ko00900|Terpenoid backbone biosynthesis	GO:0006090//GO:0006721//GO:0009532//GO:0016726//GO:0042221//GO:0052592	nr -
Unigene1463_All	2526	33.72	10.71	11.68	45.06	34.12	44.98	41.98	155.07	30.64	-1.65E+00	4.98E-134	Down	-1.53E+00	8.99E-116	Down	-4.01E-01	4.14E-20		-2.50E-03	9.62E-01		1.89E+00	0.00E+00	Up	-4.54E-01	1.28E-24		Unigene1463_All//gi|3721540|dbj|BAA33531.1|//0.00E+00//sulfite reductase [Nicotiana tabacum] >gi|3738234|dbj|BAA33796.1| sulfite reductase [Nicotiana tabacum]	Unigene1463_All//0.00E+00//AT5G04590| SIR; sulfite reductase (ferredoxin)/ sulfite reductase	Unigene1463_All//0.00E+00//TC144979		ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr -
Unigene14630_All	1599	3.70	4.06	3.26	3.86	4.31	2.97	1.59	0.65	0.62	1.34E-01	6.18E-01		-1.80E-01	5.12E-01		1.57E-01	5.56E-01		-3.81E-01	1.28E-01		-1.28E+00	4.33E-04	Down	-1.35E+00	1.51E-04	Down			Unigene14630_All//1.00E-16//TC175016				
Unigene14631_All	889	3.30	1.82	2.28	2.69	3.56	2.08	1.43	5.78	5.11	-8.54E-01	1.94E-02		-5.34E-01	1.65E-01		4.06E-01	2.83E-01		-3.69E-01	4.06E-01		2.02E+00	1.28E-13	Up	1.84E+00	4.49E-11	Up	Unigene14631_All//gi|42567430|ref|NP_195309.2|//5.00E-32//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565196|sp|Q8GT75.2|ATL4M_ARATH RecName: Full=RING-H2 finger protein ATL4M; AltName: Full=NEP1-interacting protein 1 >gi|30017273|gb|AAP12870.1| At4g35840 [Arabidopsis thaliana]	Unigene14631_All//2.00E-33//AT4G35840| zinc finger (C3HC4-type RING finger) family protein					nr -
Unigene14632_All	773	0.47	2.16	2.00	1.03	3.39	0.99	0.16	0.54	1.13	2.19E+00	1.76E-04	Up	2.08E+00	8.49E-04	Up	1.72E+00	2.10E-05	Up	-5.40E-02	9.53E-01		1.72E+00	1.35E-01		2.79E+00	5.37E-04	Up	Unigene14632_All//gi|42567430|ref|NP_195309.2|//2.00E-16//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565196|sp|Q8GT75.2|ATL4M_ARATH RecName: Full=RING-H2 finger protein ATL4M; AltName: Full=NEP1-interacting protein 1 >gi|30017273|gb|AAP12870.1| At4g35840 [Arabidopsis thaliana]	Unigene14632_All//3.00E-17//AT4G35840| zinc finger (C3HC4-type RING finger) family protein				GO:0009743//GO:0046872	nr -
Unigene14633_All	1677	13.17	25.53	15.02	16.49	21.50	24.08	19.26	26.02	45.18	9.55E-01	5.34E-29		1.90E-01	1.20E-01		3.83E-01	4.30E-06		5.46E-01	1.98E-11		4.34E-01	1.43E-09		1.23E+00	2.31E-95	Up	Unigene14633_All//gi|297793703|ref|XP_002864736.1|//1.00E-159//small G protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310571|gb|EFH40995.1| small G protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14633_All//7.00E-160//AT5G61530| small G protein family protein / RhoGAP family protein	Unigene14633_All//0.00E+00//gi|109837165|gb|DW235726.1|DW235726				nr +
Unigene14635_All	1670	32.71	8.98	14.83	31.41	21.28	17.34	10.18	9.34	5.32	-1.86E+00	9.72E-102	Down	-1.14E+00	1.77E-47	Down	-5.62E-01	2.66E-17		-8.58E-01	5.36E-32		-1.25E-01	3.85E-01		-9.36E-01	1.39E-14		Unigene14635_All//gi|224128217|ref|XP_002329110.1|//1.00E-150//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222869779|gb|EEF06910.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene14635_All//1.00E-111//AT3G15510| ATNAC2 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 2); transcription factor	Unigene14635_All//0.00E+00//TC154308	NAC		GO:0001071//GO:0003676//GO:0010468	nr -
Unigene14638_All	1079	3.05	3.33	3.06	2.45	3.38	3.47	2.94	1.43	2.70	1.26E-01	6.95E-01		2.30E-03	9.93E-01		4.67E-01	1.62E-01		5.06E-01	1.27E-01		-1.04E+00	9.55E-04	Down	-1.25E-01	6.87E-01		Unigene14638_All//gi|117168235|gb|ABK32200.1|//1.00E-101//At1g67060 [Arabidopsis thaliana] >gi|222424301|dbj|BAH20107.1| AT1G67060 [Arabidopsis thaliana]	Unigene14638_All//2.00E-95//AT1G67060| unknown protein	Unigene14638_All//2.00E-08//gi|48820882|gb|CO122195.1|CO122195			GO:0044464	nr -
Unigene1464_All	399	17.31	35.56	19.75	20.35	20.63	26.37	57.22	56.98	32.95	1.04E+00	1.68E-11	Up	1.91E-01	4.00E-01		1.95E-02	9.51E-01		3.74E-01	3.96E-02		-6.00E-03	9.95E-01		-7.96E-01	7.31E-15		Unigene1464_All//gi|115394656|gb|AB197244.1|//6.00E-33//PHD5 [Glycine max]	Unigene1464_All//4.00E-32//AT2G02470| AL6 (ALFIN-LIKE 6); DNA binding / methylated histone residue binding	Unigene1464_All//0.00E+00//TC166243	Alfin-like			nr -
Unigene14640_All	1534	2.97	1.35	1.70	4.03	4.94	6.04	4.02	3.08	1.92	-1.13E+00	9.07E-05	Down	-8.03E-01	6.64E-03		2.95E-01	1.94E-01		5.84E-01	1.81E-03		-3.86E-01	7.85E-02		-1.07E+00	4.68E-07	Down	Unigene14640_All//gi|87241485|gb|AB033343.1|//1.00E-155//Tetratricopeptide-like helical [Medicago truncatula]	Unigene14640_All//1.00E-152//AT3G46790| CRR2 (CHLORORESPIRATORY REDUCTION 2)	Unigene14640_All//0.00E+00//DR456512			GO:0009888//GO:0010051//GO:0048827	nr +
Unigene14641_All	1540	19.23	12.47	16.77	34.84	31.75	27.89	26.99	10.42	9.16	-6.25E-01	3.51E-10		-1.97E-01	7.38E-02		-1.34E-01	8.20E-02		-3.21E-01	4.85E-06		-1.37E+00	4.76E-61	Down	-1.56E+00	6.96E-76	Down	Unigene14641_All//gi|18138083|gb|AAL60068.1|AF216835_1/1.00E-168//forever young oxidoreductase [Solanum lycopersicum]	Unigene14641_All//3.00E-151//AT4G27760| FEY (FOREVER YOUNG); binding / catalytic/ oxidoreductase	Unigene14641_All//0.00E+00//TC174961		ko00051|Fructose and mannose metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism//ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene14645_All	1811	75.49	43.23	57.93	117.67	116.46	107.78	78.49	52.14	31.48	-8.04E-01	1.98E-68		-3.82E-01	1.09E-17		-1.49E-02	7.76E-01		-1.27E-01	3.10E-04		-5.90E-01	9.49E-51		-1.32E+00	3.94E-200	Down	Unigene14645_All//gi|24212904|gb|ACS83603.1|//1.00E-104//ATP synthase delta subunit 2 [Gossypium hirsutum]	Unigene14645_All//9.00E-82//AT5G47030| ATP synthase delta' chain, mitochondrial	Unigene14645_All//0.00E+00//gi|109829887|gb|DW228446.1|DW228446		ko00190|Oxidative phosphorylation	GO:0000275//GO:0006970//GO:0015078//GO:0015986//GO:0019829//GO:0032559//GO:0046914	nr +
Unigene14647_All	2059	1.25	0.91	1.97	4.48	3.85	4.32	4.21	1.06	2.61	-4.52E-01	2.56E-01		6.59E-01	3.80E-02		-2.19E-01	2.98E-01		-5.07E-02	8.15E-01		-2.00E+00	3.44E-22	Down	-6.88E-01	5.19E-05		Unigene14647_All//gi|297843916|ref|XP_002889839.1|//0.00E+00//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297335681|gb|EFH66098.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14647_All//0.00E+00//AT1G10850| ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene14647_All//0.00E+00//TC174612			GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016628//GO:0003124//GO:0032559	nr -
Unigene14648_All	1259	11.93	8.09	7.91	35.77	33.23	38.28	35.40	22.18	14.18	-5.60E-01	9.81E-05		-5.93E-01	7.11E-05		-1.06E-01	2.39E-01		9.78E-02	2.86E-01		-6.75E-01	1.11E-20		-1.32E+00	1.95E-63	Down	Unigene14648_All//gi|297798522|ref|XP_002867145.1|//1.00E-117//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297312981|gb|EFH43404.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene14648_All//8.00E-111//AT4G33910| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene14648_All//0.00E+00//TC173687		ko00330|Arginine and proline metabolism	GO:0005488//GO:0016491//GO:0031410	nr -

Unigene14650_All	2191	2.84	5.83	3.04	4.14	4.02	4.12	14.51	7.88	10.46	1.04E+00	2.15E-10	Up	9.64E-02	6.96E-01		-4.04E-02	8.48E-01		-5.30E-03	9.75E-01		-8.81E-01	2.53E-23		-4.73E-01	1.41E-08		Unigene14650_All//gi|30678079|ref|NP_178475.2|//3.00E-50//18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|42570677|ref|NP_973412.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|79316683|ref|NP_001030966.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|186499149|ref|NP_001118260.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana]	Unigene14650_All//5.00E-43//AT2G03810| 18S pre-ribosomal assembly protein gar2-related	Unigene14650_All//0.00E+00//TC169145				nr +
Unigene14655_All	902	14.27	21.80	19.48	9.06	11.57	8.41	5.30	4.31	2.43	6.11E-01	8.92E-07		4.49E-01	1.10E-03		3.53E-01	4.80E-02		-1.07E-01	6.58E-01		-2.98E-01	2.58E-01		-1.12E+00	4.32E-06	Down	Unigene14655_All//gi|168054193|ref|XP_001776517.1|//3.00E-74//Rab5/RabF-family small GTPase [Physcomitrella patens subsp. patens] >gi|162669099|gb|EDQ55693.1| Rab5/RabF-family small GTPase [Physcomitrella patens subsp. patens]	Unigene14655_All//5.00E-68//AT4G19640| ARA7; GTP binding	Unigene14655_All//0.00E+00//TC167497		ko04145|Phagosome//ko04144|Endocytosis	GO:0003824//GO:0006810//GO:0032561//GO:0035556	nr -
Unigene14656_All	1684	4.54	1.65	2.56	3.90	4.85	3.92	1.61	0.15	0.80	-1.45E+00	1.30E-10	Down	-8.25E-01	1.71E-04		3.12E-01	1.47E-01		4.00E-03	9.87E-01		-3.43E+00	7.61E-13	Down	-9.98E-01	2.61E-03		Unigene14656_All//gi|115483923|ref|NP_001065623.1|//1.00E-145//Os11g0126100 [Oryza sativa Japonica Group] >gi|77548508|gb|ABA91305.1| MATE efflux family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113644327|dbj|BAF27468.1| Os11g0126100 [Oryza sativa Japonica Group]	Unigene14656_All//3.00E-132//AT5G17700| MATE efflux family protein	Unigene14656_All//0.00E+00//TC152974			GO:0015291//GO:0015893//GO:0044464	nr -
Unigene14658_All	1071	53.10	26.54	28.69	52.05	49.80	35.34	30.71	17.83	16.63	-1.00E+00	1.97E-41	Down	-8.88E-01	7.67E-33		-6.35E-02	4.71E-01		-5.59E-01	2.88E-16		-7.84E-01	6.81E-20		-8.85E-01	5.21E-25		Unigene14658_All//gi|124359162|gb|ABN05685.1|//5.00E-22//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene14658_All//8.00E-07//AT3G09510| nucleic acid binding	Unigene14658_All//0.00E+00//gi|11206634|gb|BF275564.1|BF275564				nr +
Unigene1466_All	2096	19.02	73.30	8.87	12.72	16.76	15.84	28.74	106.32	203.07	1.95E+00	3.19E-300	Up	-1.10E+00	7.57E-33	Down	3.98E-01	2.36E-06		3.17E-01	6.48E-04		1.89E+00	0.00E+00	Up	2.82E+00	0.00E+00	Up	Unigene1466_All//gi|259121421|gb|ACV92030.1|//1.00E-175//WRKY transcription factor 28 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene1466_All//4.00E-106//AT1G62300| WRKY6; transcription factor	Unigene1466_All//0.00E+00//TC164018	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene14660_All	845	11.39	6.24	10.46	9.20	6.28	3.90	4.75	4.85	1.56	-8.69E-01	3.15E-06		-1.23E-01	5.78E-01		-5.51E-01	5.16E-03		-1.24E+00	4.38E-09	Down	2.82E-02	9.43E-01		-1.61E+00	1.84E-08	Down	Unigene14660_All//gi|30688336|ref|NP_030605.2|//1.00E-51//appr-1-p processing enzyme family protein [Arabidopsis thaliana]	Unigene14660_All//7.00E-53//AT2G40600| appr-1-p processing enzyme family protein	Unigene14660_All//0.00E+00//gi|21090459|gb|BQ402772.1|BQ402772			GO:0016740//GO:0044464	nr -
Unigene14661_All	2458	9.54	18.57	10.44	18.87	20.97	20.71	50.88	73.41	175.14	9.62E-01	3.32E-31		1.31E-01	2.99E-01		1.53E-01	4.79E-02		1.34E-01	1.04E-01		5.29E-01	9.67E-53		1.78E+00	0.00E+00	Up	Unigene14661_All//gi|297816784|ref|XP_002876275.1|//0.00E+00//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322113|gb|EFH52534.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14661_All//0.00E+00//AT3G54850| PUB14; ubiquitin-protein ligase	Unigene14661_All//0.00E+00//TC138312		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0019787//GO:0032446//GO:0043231//GO:0043244	nr -
Unigene14664_All	1314	18.40	10.57	7.82	29.95	22.67	23.82	18.89	3.09	5.79	-8.00E-01	1.31E-12		-1.23E+00	5.22E-24	Down	-4.02E-01	2.65E-07		-3.30E-01	7.67E-05		-2.61E+00	3.15E-86	Down	-1.71E+00	7.60E-52	Down	Unigene14664_All//gi|124300986|gb|ABN04745.1|//9.00E-60//At2g26110 [Arabidopsis thaliana]	Unigene14664_All//6.00E-47//AT2G26110| unknown protein	Unigene14664_All//0.00E+00//TC168063				nr +
Unigene14665_All	1863	3.06	2.04	3.20	12.59	17.50	14.55	8.33	1.97	3.74	-5.86E-01	1.86E-02		6.46E-02	8.02E-01		4.75E-01	5.32E-08		2.08E-01	6.31E-02		-2.08E+00	3.40E-41	Down	-1.15E+00	1.63E-18	Down	Unigene14665_All//gi|224087694|ref|XP_002308208.1|//0.00E+00//laccase lc [Populus trichocarpa] >gi|222854184|gb|EEE91731.1| laccase lc [Populus trichocarpa]	Unigene14665_All//0.00E+00//AT2G38080| IRX12 (IRREGULAR XYLEM 12); laccase	Unigene14665_All//0.00E+00//TC130781		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0009832//GO:0016682//GO:0046914	nr -
Unigene14666_All	1851	23.26	13.19	20.25	34.26	32.35	29.72	35.09	19.69	13.45	-8.18E-01	1.12E-22		-2.00E-01	2.39E-02		-8.26E-02	2.93E-01		-2.05E-01	2.13E-03		-8.33E-01	1.27E-42		-1.38E+00	7.69E-99	Down	Unigene14666_All//gi|297843736|ref|XP_002889749.1|//0.00E+00//ATP-citrate lyase A-3 [Arabidopsis lyrata subsp. lyrata] >gi|297335591|gb|EFH66008.1| ATP-citrate lyase A-3 [Arabidopsis lyrata subsp. lyrata]	Unigene14666_All//0.00E+00//AT1G09430| ACLA-3; ATP citrate synthase	Unigene14666_All//0.00E+00//gi|164335136|gb|ES797466.1|ES797466		ko00020|Citrate cycle (TCA cycle)	GO:0004774//GO:0006084//GO:0032559//GO:0043234	nr -
Unigene14667_All	1416	7.80	3.76	2.33	17.84	10.21	7.85	12.48	3.31	3.01	-1.05E+00	2.36E-09	Down	-1.74E+00	2.02E-18	Down	-8.04E-01	8.11E-16		-1.18E+00	2.18E-26	Down	-1.92E+00	3.37E-42	Down	-2.05E+00	1.52E-47	Down	Unigene14667_All//gi|116311987|emb|CAJ86345.1|//4.00E-93//H0814G11.12 [Oryza sativa (indica cultivar-group)]	Unigene14667_All//3.00E-76//AT1G45688| unknown protein	Unigene14667_All//0.00E+00//TC165179			GO:0004672//GO:0006464//GO:0016020//GO:0031410//GO:0032559//GO:0043231	nr -
Unigene14668_All	2474	1.27	1.19	1.66	5.58	4.79	4.18	5.83	1.89	2.83	-9.52E-02	7.78E-01		3.85E-01	2.32E-01		-2.20E-01	1.69E-01		-4.16E-01	5.86E-03		-1.62E+00	1.41E-27	Down	-1.04E+00	1.01E-14	Down	Unigene14668_All//gi|224077882|ref|XP_566511.1|//0.00E+00//choline transporter-related [Arabidopsis thaliana]	Unigene14668_All//0.00E+00//AT4G15380| choline transporter-related	Unigene14668_All//0.00E+00//C0132030			GO:0031224	nr +
Unigene14669_All	1719	9.41	6.37	3.97	8.95	8.07	10.59	10.48	9.26	6.79	-5.63E-01	4.57E-05		-1.25E+00	1.74E-16	Down	-1.50E-01	3.55E-01		2.42E-01	8.12E-02		-1.78E-01	1.67E-01		-6.26E-01	4.06E-08		Unigene14669_All//gi|226506980|ref|NP_001152183.1|//1.00E-170//LOC100285821 [Zea mays] >gi|195653617|gb|ACG46276.1| RNA-binding post-transcriptional regulator csxl [Zea mays]	Unigene14669_All//6.00E-133//AT5G19350| RNA-binding protein 45 (RBP45), putative	Unigene14669_All//0.00E+00//TC139750		ko03040|Spliceosome		nr +
Unigene14670_All	932	8.87	2.66	4.91	58.90	20.28	29.03	27.72	6.41	8.85	-1.74E+00	1.59E-14	Down	-8.52E-01	4.97E-05		-1.54E+00	2.87E-97	Down	-1.02E+00	1.12E-44	Down	-2.11E+00	1.44E-69	Down	-1.65E+00	2.31E-51	Down			Unigene14670_All//0.00E+00//gi|109862849|gb|DW491826.1|DW491826				
Unigene14671_All	657	31.93	29.23	27.56	58.84	49.43	58.29	39.38	27.04	18.31	-1.28E-01	3.50E-01		-2.13E-01	1.12E-01		-2.52E-01	2.47E-03		-1.34E-02	9.15E-01		-5.43E-01	1.21E-08		-1.10E+00	2.79E-28	Down	Unigene14671_All//gi|2493130|sp|Q43433.1|VATB2_GOSHI//8.00E-50//RecName: Full=V-type proton ATPase subunit B 2; Short=V-ATPase subunit B 2; AltName: Full=Vacuolar proton pump subunit B 2 >gi|459200|gb|AAA57550.1| vacuolar H+-ATPase subunit B [Gossypium hirsutum]	Unigene14671_All//1.00E-48//AT4G38510| vacuolar ATP synthase subunit B, putative / V-ATPase B subunit, putative / vacuolar proton pump B subunit, putative / V-ATPase 57 kDa subunit, putative	Unigene14671_All//0.00E+00//gi|109891266|gb|DW520229.1|DW520229		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0015078//GO:0015986//GO:0019829//GO:0032559//GO:0033176	nr -
Unigene14672_All	1063	18.70	35.61	21.39	20.81	43.54	40.02	34.84	138.13	149.09	9.29E-01	1.43E-24		1.94E-01	1.36E-01		1.07E+00	6.08E-44	Up	9.44E-01	3.23E-30		1.99E+00	0.00E+00	Up	2.10E+00	0.00E+00	Up	Unigene14672_All//gi|149727987|gb|ABR28340.1|//4.00E-90//MYB transcription factor MYB52 [Medicago truncatula]	Unigene14672_All//1.00E-65//AT3G16350| myb family transcription factor	Unigene14672_All//2.00E-14//TC143218	MYB-related		GO:0003676//GO:0006970//GO:0009725//GO:0010038//GO:0010468//GO:0046872	nr +
Unigene14675_All	885	26.66	33.84	23.71	61.47	65.72	67.97	84.46	52.80	36.06	3.44E-01	5.42E-04		-1.70E-01	1.85E-01		9.65E-02	2.27E-01		1.45E-01	4.71E-02		-6.78E-01	2.06E-34		-1.23E+00	1.27E-94	Down	Unigene14675_All//gi|15450427|gb|AA96507.1|//2.00E-51//At1g08480/T27G7_10 [Arabidopsis thaliana] >gi|16974435|gb|AAL31221.1| At1g08480/T27G7_10 [Arabidopsis thaliana]	Unigene14675_All//8.00E-53//AT1G08480| unknown protein	Unigene14675_All//0.00E+00//gi|109828139|gb|DW226773.1|DW226773			GO:0009451//GO:0016020//GO:0043231	nr -
Unigene14676_All	1339	1.60	2.95	1.15	4.61	4.76	4.92	35.90	68.86	103.72	8.82E-01	4.23E-03		-4.74E-01	3.12E-01		4.45E-02	8.78E-01		9.42E-02	7.15E-01		9.40E-01	1.90E-73		1.53E+00	1.37E-242	Up	Unigene14676_All//gi|259121421|gb|ACV92030.1|//1.00E-112//WRKY transcription factor 28 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene14676_All//2.00E-88//AT1G62300| WRKY6; transcription factor	Unigene14676_All//0.00E+00//C0071372	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0006350//GO:0009267//GO:0009743//GO:0010468//GO:0043565	nr -
Unigene14678_All	2091	3.50	0.53	0.28	2.98	1.45	4.97	27.40	20.45	50.76	-2.72E+00	3.87E-22	Down	-3.64E+00	7.22E-28	Down	-1.04E+00	2.35E-06	Down	7.38E-01	2.18E-05		-4.22E-01	9.58E-12		8.90E-01	8.14E-79		Unigene14678_All//gi|15227274|ref|NP_179257.1|//0.00E+00//nodulin family protein [Arabidopsis thaliana] >gi|4581109|gb|AAD24599.1| nodulin-like protein [Arabidopsis thaliana] >gi|20465250|gb|AAM19945.1| At2g16660/T24I21.7 [Arabidopsis thaliana] >gi|23463081|gb|AAN33210.1| At2g16660/T24I21.7 [Arabidopsis thaliana]	Unigene14678_All//0.00E+00//AT2G16660| nodulin family protein	Unigene14678_All//0.00E+00//TC176182			GO:0043231	nr +
Unigene14679_All	1740	0.99	0.96	0.49	2.40	1.58	1.19	2.53	0.98	1.53	-4.62E-02	9.36E-01		-1.02E+00	5.27E-02		-6.03E-01	3.46E-02		-1.01E+00	5.97E-04	Down	-1.36E+00	4.56E-07	Down	-7.20E-01	3.78E-03		Unigene14679_All//gi|297796945|ref|XP_002866357.1|//1.00E-179//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297312192|gb|EFH42616.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene14679_All//1.00E-179//AT5G59900| pentatricopeptide (PPR) repeat-containing protein	Unigene14679_All//0.00E+00//TC166999				nr -
Unigene14680_All	1643	1.94	1.76	2.04	8.67	3.21	5.72	2.62	3.82	6.13	-1.44E-01	6.73E-01		7.19E-02	8.35E-01		-1.44E+00	6.22E-23	Down	-6.01E-01	3.24E-05		5.40E-01	1.07E-02		1.22E+00	2.36E-13	Up	Unigene14680_All//gi|2501494|sp|Q40287.1|UFGS_MANES//1.00E-141//RecName: Full=Anthocyanidin 3-O-glucosyltransferase 5; AltName: Full=Flavonol 3-O-glucosyltransferase 5; AltName: Full=UDP-glucose flavonoid 3-O-glucosyltransferase 5 >gi|453249|emb|CAA54612.1| UTP-glucose glucosyltransferase [Manihot esculenta]	Unigene14680_All//1.00E-120//AT2G18570| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene14680_All//0.00E+00//TC133743		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene14681_All	1110	12.96	27.57	19.09	18.80	20.51	17.50	12.11	22.86	17.55	1.09E+00	8.91E-26	Up	5.59E-01	5.43E-06		1.25E-01	3.50E-01		-1.04E-01	4.72E-01		9.16E-01	5.74E-20		5.35E-01	9.20E-07		Unigene14681_All//gi|224077882|ref|XP_002305450.1|//1.00E-111//ebs-bah-phd domain-containing protein [Populus trichocarpa] >gi|222848414|gb|EEE85961.1| ebs-bah-phd domain-containing protein [Populus trichocarpa]	Unigene14681_All//8.00E-90//AT4G22140| DNA binding / protein binding / zinc ion binding	Unigene14681_All//0.00E+00//TC132695			GO:0001071//GO:0003676//GO:0007275//GO:0009639//GO:0016563//GO:0043231//GO:0046914	nr +
Unigene14683_All	1276	5.54	14.65	4.63	7.73	9.88	9.03	8.02	8.75	12.80	1.40E+00	1.58E-23	Up	-2.57E-01	2.95E-01		3.54E-01	2.59E-02		2.24E-01	2.34E-01		1.25E-01	4.88E-01		6.75E-01	2.42E-08		Unigene14683_All//gi|46518377|gb|AAS99670.1|//4.00E-29//At1g15800 [Arabidopsis thaliana] >gi|48310380|gb|AAT41809.1| At1g15800 [Arabidopsis thaliana]	Unigene14683_All//6.00E-12//AT1G15800| unknown protein	Unigene14683_All//0.00E+00//TC174115				nr +

Unigene14684_All	1022	3.12	15.67	2.19	8.09	4.85	10.47	23.00	11.86	76.56	2.33E+00	1.03E-39	Up	-5.13E-01	1.61E-01		-7.38E-01	7.42E-05		3.72E-01	3.85E-02		-9.56E-01	6.86E-20		1.73E+00	8.56E-164	Up	Unigene14684_All//gi|18416997|ref|NP_568287.1|//4.00E-38//JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10) [Arabidopsis thaliana] >gi|75163798|sp|Q93ZM9.1|TIF9_ARATH RecName: Full=Protein TIFY 9; AltName: Full=Protein JASMONATE-ASSOCIATED 1; AltName: Full=Jasmonate ZIM domain-containing protein 10 >gi|15912333|gb|AAL08300.1|AT5g13220/T31B5_40 [Arabidopsis thaliana] >gi|19548009|gb|AAL87368.1|AT5g13220/T31B5_40 [Arabidopsis thaliana]	Unigene14684_All//1.00E-37//AT5G13220| JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10)	Unigene14684_All//0.00E+00//DT468590	Tify			GO:0002831//GO:0005488//GO:0006950//GO:0009725//GO:0043231	nr -
Unigene14685_All	1372	358.09	322.67	491.36	62.63	92.04	70.31	1.17	1.10	2.38	-1.50E-01	2.09E-11		4.57E-01	1.62E-118		5.55E-01	2.51E-39		1.67E-01	1.91E-03		-9.46E-02	8.44E-01		1.02E+00	6.62E-04	Up	Unigene14685_All//gi|15222235|ref|NP_177679.1|//1.00E-108//ATP-dependent protease La (LON) domain-containing protein [Arabidopsis thaliana] >gi|10120444|gb|AAG13069.1|AC02375 4_7 Unknown protein [Arabidopsis thaliana]	Unigene14685_All//6.00E-93//AT1G75460| ATP-dependent protease La (LON) domain-containing protein	Unigene14685_All//0.00E+00//TC145867			GO:0019538//GO:0042623//GO:0043231	nr +
Unigene14686_All	722	3.12	2.39	1.62	4.48	3.39	4.19	4.68	2.37	1.71	-3.85E-01	3.69E-01		-9.41E-01	3.61E-02		-4.05E-01	2.53E-01		-9.77E-02	7.92E-01		-9.81E-01	1.12E-03		-1.45E+00	2.30E-06	Down	Unigene14686_All//gi|149391425|gb|ABR25730.1|//5.00E-14//ubiquitin fusion protein [Oryza sativa Indica Group]	Unigene14686_All//3.00E-15//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene14686_All//7.00E-177//TC156156		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0031981//GO:0032446	nr -
Unigene14687_All	680	37.55	24.66	24.43	37.21	29.37	43.10	55.34	25.51	14.53	-6.06E-01	1.81E-08		-6.20E-01	2.31E-08		-3.41E-01	8.67E-04		2.12E-01	4.53E-02		-1.12E+00	2.83E-40	Down	-1.93E+00	1.53E-92	Down	Unigene14687_All//gi|225440831|ref|XP_002282071.1|//7.00E-68//PREDICTED: similar to ubiquitin fusion protein [Vitis vinifera] >gi|71040673|gb|AAZ20285.1|ubiquitin fusion protein [Arachis hypogaea] >gi|192910738|gb|ACF06477.1|ubiquitin fusion protein [Elaeis guineensis] >gi|284433784|gb|AD885098.1|ubiquitin C variant [Jatropha curcas]	Unigene14687_All//2.00E-68//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene14687_All//0.00E+00//TC156156		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0031981//GO:0032446	nr +
Unigene14689_All	688	0.23	2.65	0.62	0.36	2.90	1.51	5.78	8.08	6.43	3.54E+00	2.15E-07	Up	1.44E+00	2.53E-01		3.00E+00	1.12E-07	Up	2.06E+00	6.55E-03		4.84E-01	3.41E-02		1.54E-01	5.97E-01		Unigene14689_All//gi|42572029|ref|NP_974105.1|//4.00E-18//ATTPS6; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase [Arabidopsis thaliana] >gi|172045841|sp|Q94A88.2|TPS6_ARATH RecName: Full=Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 6; AltName: Full=Trehalose-6-phosphate synthase 6; Short=AtTPS6	Unigene14689_All//2.00E-19//AT1G68020| ATTPS6; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase	Unigene14689_All//0.00E+00//gi|164261427|gb|ES824909.1|ES824909		ko00500|Starch and sucrose metabolism	GO:0005488//GO:0005991//GO:0019203//GO:0035251//GO:0044464	nr +
Unigene14690_All	726	42.95	108.74	39.39	76.03	126.74	115.40	296.43	324.81	245.67	1.34E+00	1.60E-90	Up	-1.25E-01	2.65E-01		7.37E-01	3.41E-47		6.02E-01	2.25E-27		1.32E-01	1.11E-05		-2.71E-01	3.71E-19		Unigene14690_All//gi|42572029|ref|NP_974105.1|//2.00E-85//ATTPS6; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase [Arabidopsis thaliana] >gi|172045841|sp|Q94A88.2|TPS6_ARATH RecName: Full=Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 6; AltName: Full=Trehalose-6-phosphate synthase 6; Short=AtTPS6	Unigene14690_All//1.00E-86//AT1G68020| ATTPS6; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase	Unigene14690_All//0.00E+00//TC140776		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0019203//GO:0035251//GO:0043231	nr -
Unigene14692_All	1303	61.88	21.89	44.67	8.41	7.29	4.51	1.33	0.64	0.89	-1.50E+00	6.18E-110	Down	-4.70E-01	2.11E-15		-2.06E-01	2.80E-01		-9.00E-01	9.83E-08		-1.05E+00	1.87E-02		-5.85E-01	1.73E-01		Unigene14692_All//gi|115463807|ref|NP_001055503.1|//4.00E-69//Os05g0104400 [Oryza sativa Japonica Group] >gi|113579054|dbj|BAF17417.1|Os05g0104400 [Oryza sativa Japonica Group]	Unigene14692_All//3.00E-69//AT2G48070| RPH1 (RESISTANCE TO PHYTOPHTHORA 1)	Unigene14692_All//0.00E+00//TC135666			GO:0002239//GO:0009536//GO:0010726//GO:0046914	nr -
Unigene14695_All	570	2.66	0.18	3.08	0.87	1.63	3.01	3.34	2.20	4.89	-3.90E+00	9.44E-07	Down	2.12E-01	6.61E-01		9.00E-01	2.35E-01		1.78E+00	9.22E-04	Up	-6.02E-01	1.58E-01		5.52E-01	9.26E-02		Unigene14695_All//gi|297799384|ref|XP_002867576.1|//5.00E-45//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313412|gb|EFH43835.1|mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14695_All//6.00E-46//AT4G26180| mitochondrial substrate carrier family protein	Unigene14695_All//1.00E-73//TC149482			GO:0006810//GO:0016020//GO:0043231	nr -
Unigene14697_All	937	0.78	0.11	0.23	0.32	0.15	0.34	0.81	1.12	2.34	-2.85E+00	6.26E-03		-1.78E+00	6.00E-02		-1.12E+00	4.24E-01		8.09E-02	9.50E-01		4.57E-01	4.63E-01		1.53E+00	1.25E-04	Up	Unigene14697_All//gi|297799384|ref|XP_002867576.1|//5.00E-40//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313412|gb|EFH43835.1|mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14697_All//5.00E-40//AT4G26180| mitochondrial substrate carrier family protein	Unigene14697_All//0.00E+00//BF276697			GO:0043231	nr -
Unigene14698_All	1033	2.68	8.19	5.36	14.27	8.67	51.07	39.66	98.56	76.32	1.61E+00	2.44E-13	Up	9.98E-01	1.71E-04		-7.20E-01	7.16E-08		1.84E+00	7.30E-103	Up	1.31E+00	1.41E-138	Up	9.44E-01	6.72E-65		Unigene14698_All//gi|283131283|dbj|BA163297.1|//1.00E-113//thaumatin-like protein [Citrus jambhiri]	Unigene14698_All//9.00E-107//AT2G28790| osmotin-like protein, putative	Unigene14698_All//3.00E-87//TC131406			GO:0031410	nr +
Unigene14700_All	984	3.88	2.27	1.79	9.37	5.56	8.67	7.09	4.50	5.67	-7.77E-01	1.30E-02		-1.12E+00	7.38E-04	Down	-7.51E-01	1.72E-05		-1.11E-01	6.13E-01		-6.55E-01	8.95E-04		-3.23E-01	1.05E-01		Unigene14700_All//gi|87116610|gb|ABD19669.1|//1.00E-76//At4g10090 [Arabidopsis thaliana]	Unigene14700_All//6.00E-78//AT4G10090| unknown protein	Unigene14700_All//0.00E+00//AW187193				nr +
Unigene14701_All	1017	144.31	13.15	23.51	56.03	24.31	73.27	7.94	1.64	3.84	-3.46E+00	0.00E+00	Down	-2.62E+00	0.00E+00	Down	-1.20E+00	4.41E-69	Down	3.87E-01	3.26E-11		-2.27E+00	2.70E-24	Down	-1.05E+00	9.64E-09	Down	Unigene14701_All//gi|217384812|gb|ACK43222.1|//1.00E-136//expansin 2 [Ziziphus jujuba]	Unigene14701_All//6.00E-106//AT2G40610| ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	Unigene14701_All//0.00E+00//TC156518				nr -
Unigene14703_All	1258	1.58	1.17	0.25	4.44	2.96	1.72	4.07	0.90	1.17	-4.36E-01	3.56E-01		-2.64E+00	6.10E-06	Down	-5.85E-01	1.47E-02		-1.36E+00	1.09E-07	Down	-2.18E+00	6.48E-15	Down	-1.80E+00	3.87E-12	Down	Unigene14703_All//gi|115464839|ref|NP_001056019.1|//4.00E-73//Os05g0512000 [Oryza sativa Japonica Group] >gi|113579570|dbj|BAF17933.1|Os05g0512000 [Oryza sativa Japonica Group]	Unigene14703_All//8.00E-68//AT4G21070| ATBRCA1; ubiquitin-protein ligase	Unigene14703_All//0.00E+00//TC168294			GO:0005488	nr -
Unigene14704_All	928	3.89	1.75	3.44	2.68	3.30	3.07	4.69	1.85	2.96	-1.15E+00	4.66E-04	Down	-1.76E-01	6.43E-01		2.99E-01	4.51E-01		1.92E-01	6.46E-01		-1.35E+00	6.54E-07	Down	-6.64E-01	7.90E-03		Unigene14704_All//gi|22143566|dbj|BAH19312.1|//1.00E-109//urease accessory protein ureD [Morus alba]	Unigene14704_All//5.00E-92//AT2G35035| URED (urease accessory protein D); nickel ion binding	Unigene14704_All//0.00E+00//TC168458			GO:0008152//GO:0044424//GO:0046914	nr +
Unigene14705_All	419	2.00	0.60	0.89	5.35	2.30	3.88	2.12	0.20	0.19	-1.72E+00	3.63E-02		-1.17E+00	1.52E-01		-1.22E+00	2.63E-03		-4.63E-01	3.12E-01		-3.41E+00	1.40E-04	Down	-3.48E+00	7.34E-05	Down	Unigene14705_All//gi|224068959|ref|XP_002302866.1|//1.00E-06//predicted protein [Populus trichocarpa] >gi|222844592|gb|EEE82139.1|predicted protein [Populus trichocarpa]						nr +
Unigene14706_All	1279	6.10	3.21	5.50	18.58	15.00	17.76	26.81	12.61	17.85	-9.26E-01	1.09E-05		-1.49E-01	5.32E-01		-3.09E-01	4.24E-03		-6.48E-02	6.39E-01		-1.09E+00	3.05E-35	Down	-5.87E-01	3.77E-13		Unigene14706_All//gi|14486705|gb|AAK63247.1|AF367433_1//1.00E-116//phosphatidylinositol transfer-like protein III [Lotus japonicus]	Unigene14706_All//2.00E-101//AT4G39170| SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative	Unigene14706_All//0.00E+00//gi|78351623|gb|DT571897.1|DT571897			GO:0016020//GO:0051234	nr -
Unigene14707_All	1084	29.54	73.81	82.23	17.28	5.31	6.87	259.38	645.56	263.29	1.32E+00	9.18E-90	Up	1.48E+00	2.27E-115	Up	-1.70E+00	1.10E-38	Down	-1.33E+00	1.62E-23	Down	1.32E+00	0.00E+00	Up	2.16E-02	5.24E-01		Unigene14707_All//gi|20981684|sp|P23472.2|CHLY_HEVBR//1.00E-140//RecName: Full=Hevamine-A; Includes: RecName: Full=Chitinase; Includes: RecName: Full=Lysozyme; Flags: Precursor >gi|3452147|emb|CAA07608.1|chitinase [Hevea brasiliensis]	Unigene14707_All//8.00E-116//AT5G24090| acidic endochitinase (CHIB1)	Unigene14707_All//0.00E+00//TC163812		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene14709_All	967	6.82	8.91	7.93	4.79	10.08	5.74	1.05	2.68	2.43	3.86E-01	5.49E-02		2.18E-01	3.65E-01		1.07E+00	1.23E-09	Up	2.62E-01	3.63E-01		1.35E+00	1.90E-04	Up	1.21E+00	1.01E-03		Unigene14709_All//gi|6227005|gb|AAF06041.1|AC009360_6//4.00E-69//Contains similarity to gb|D90908 DNA mismatch repair protein MutS2 from Synechocystis sp. and is a member of PF|00488 Muts family of mismatch repair proteins [Arabidopsis thaliana]	Unigene14709_All//2.00E-72//AT1G65070| DNA mismatch repair MutS family protein			ko03430|Mismatch repair	GO:0003677//GO:0006281//GO:0032559//GO:0043231	nr +
Unigene14711_All	1007	5.04	10.67	5.87	5.34	7.25	7.00	19.31	54.79	198.48	1.08E+00	1.88E-09	Up	2.20E-01	4.04E-01		4.40E-01	4.18E-02		3.89E-01	9.20E-02		1.50E+00	1.96E-92	Up	3.36E+00	0.00E+00	Up	Unigene14711_All//gi|4056453|gb|AAC98026.1|//4.00E-68//EST gb|AA597511 comes from this gene [Arabidopsis thaliana] >gi|29028842|gb|AAO64800.1|At1g23710 [Arabidopsis thaliana]	Unigene14711_All//2.00E-54//AT1G23710| unknown protein	Unigene14711_All//0.00E+00//gi|78323305|gb|DT543579.1|DT543579				nr -
Unigene14712_All	1319	20.07	45.14	28.78	40.83	48.77	63.89	17.92	12.14	8.37	1.17E+00	2.10E-55	Up	5.20E-01	5.08E-09		2.57E-01	3.34E-05		6.46E-01	3.73E-31		-5.62E-01	1.96E-08		-1.10E+00	1.09E-25	Down	Unigene14712_All//gi|297812999|ref|XP_002874383.1|//1.00E-138//ATGID1C/GID1C [Arabidopsis lyrata subsp. lyrata] >gi|297320220|gb|EFH50642.1|ATGID1C/GID1C [Arabidopsis lyrata subsp. lyrata]	Unigene14712_All//2.00E-138//AT5G27320| GID1C (GA INSENSITIVE DWARF1C); hydrolase	Unigene14712_All//0.00E+00//TC150874			GO:0003824	nr -
Unigene14716_All	1216	11.06	7.96	8.36	4.22	3.99	3.34	1.84	1.00	0.46	-4.75E-01	2.02E-03		-4.03E-01	1.29E-02		-7.96E-02	8.17E-01		-3.36E-01	2.34E-01		-8.87E-01	2.04E-02		-2.01E+00	1.43E-06	Down	Unigene14716_All//gi|115445849|ref|NP_001046704.1|//8.00E-73//Os02g0326000 [Oryza sativa Japonica Group] >gi|113536235|dbj|BAF08618.1|Os02g0326000 [Oryza sativa Japonica Group]	Unigene14716_All//4.00E-75//AT1G26180| unknown protein	Unigene14716_All//0.00E+00//TC145127			GO:0044464	nr +

Unigene14717_All	1681	5.20	2.71	2.69	5.93	5.49	3.68	6.87	2.04	2.18	-9.38E-01	2.12E-06		-9.49E-01	3.61E-06		-1.10E-01	6.10E-01		-6.87E-01	1.04E-04		-1.75E+00	1.10E-24	Down	-1.66E+00	1.42E-23	Down	Unigene14717_All//gi|15010754|gb|AAK74036.1|//7.00E-85//AT3g08600/F17O14_7 [Arabidopsis thaliana] >gi|15810099|gb|AAL06975.1| AT3g08600/F17O14_7 [Arabidopsis thaliana]	Unigene14717_All//9.00E-78//AT3G08600| unknown protein	Unigene14717_All//0.00E+00//TC160767			GO:0016020//GO:0031410	nr +
Unigene14720_All	996	3.47	1.22	2.03	3.55	2.66	3.08	3.01	2.01	2.36	-1.51E+00	1.85E-05	Down	-7.71E-01	2.64E-02		-4.16E-01	2.16E-01		-2.04E-01	6.01E-01		-5.81E-01	7.49E-02		-3.53E-01	2.75E-01		Unigene14720_All//gi|92893902|gb|ABE91952.1|//6.00E-26//Zinc finger, CCHC-type [Medicago truncatula]	Unigene14720_All//6.00E-17//AT2G01050| nucleic acid binding / zinc ion binding	Unigene14720_All//4.00E-142//BM456626				nr -
Unigene14722_All	830	56.29	32.78	44.72	36.31	30.49	16.05	0.51	0.50	0.24	-7.80E-01	1.15E-22		-3.32E-01	3.61E-05		-2.52E-01	9.20E-03		-1.18E+00	4.31E-31	Down	-1.65E-02	1.02E+00		-1.09E+00	2.82E-01		Unigene14722_All//gi|62087115|dbj|BAD91878.1|//1.00E-102//transcription factor lim1 [Eucalyptus globulus] >gi|62087117|dbj|BAD91879.1| transcription factor lim1 [Eucalyptus globulus] >gi|62087119|dbj|BAD91880.1| transcription factor lim1 [Eucalyptus camaldulensis] >gi|62087121|dbj|BAD91881.1| transcription factor lim1 [Eucalyptus camaldulensis]	Unigene14722_All//2.00E-96//AT1G10200| WLIM1; transcription factor/ zinc ion binding	Unigene14722_All//0.00E+00//TC137502	LIM		GO:0016020//GO:0046914	nr +
Unigene14723_All	855	19.21	19.91	20.99	10.37	5.40	3.54	0.15	0.15	0.00	5.14E-02	7.23E-01		1.27E-01	3.87E-01		-9.42E-01	1.44E-07		-1.55E+00	2.93E-14	Down	-1.66E-02	1.02E+00		-7.21E+00	2.00E-01		Unigene14723_All//gi|117950167|gb|ABK58467.1|//5.00E-29//LIM domain protein WLIM1a [Populus tremula x Populus alba]	Unigene14723_All//4.00E-27//AT1G10200| WLIM1; transcription factor/ zinc ion binding	Unigene14723_All//0.00E+00//CO095729	LIM		GO:0046914	nr -
Unigene14724_All	1505	2.36	1.35	2.12	13.67	12.08	9.21	5.48	2.39	2.36	-8.12E-01	1.28E-02		-1.55E-01	6.41E-01		-1.78E-01	1.72E-01		-5.69E-01	1.29E-06		-1.20E+00	1.82E-10	Down	-1.22E+00	4.42E-11	Down	Unigene14724_All//gi|145324006|ref|NP_001077592.1|//1.00E-161//protein kinase family protein [Arabidopsis thaliana]	Unigene14724_All//3.00E-162//AT1G24030| protein kinase family protein	Unigene14724_All//0.00E+00//gi|109885558|gb|DW514558.1|DW514558		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene14725_All	1754	8.02	11.04	7.68	20.11	25.05	18.90	29.19	6.36	8.97	4.60E-01	2.46E-04		-6.31E-02	7.04E-01		3.17E-01	2.68E-05		-8.94E-02	4.18E-01		-2.20E+00	2.25E-144	Down	-1.70E+00	8.84E-106	Down	Unigene14725_All//gi|224106023|ref|XP_002314016.1|//1.00E-139//cyclin [Populus trichocarpa] >gi|222850424|gb|EEE87971.1| cyclin [Populus trichocarpa]	Unigene14725_All//7.00E-114//AT2G26760| CYCB1;4 (Cyclin B1;4); cyclin-dependent protein kinase regulator	Unigene14725_All//0.00E+00//TC178876				nr -
Unigene14727_All	1728	6.39	10.00	4.53	10.29	11.78	6.87	7.59	4.93	3.62	6.46E-01	1.33E-06		-4.96E-01	5.56E-03		1.95E-01	1.41E-01		-5.82E-01	5.01E-06		-6.20E-01	7.40E-06		-1.07E+00	5.22E-14	Down	Unigene14727_All//gi|3540181|gb|AAC34331.1|//7.00E-90//Unknown protein [Arabidopsis thaliana] >gi|40823449|gb|AAR92283.1| At1g10020 [Arabidopsis thaliana] >gi|46518421|gb|AAS99692.1| At1g10020 [Arabidopsis thaliana]	Unigene14727_All//3.00E-91//AT1G10020| unknown protein	Unigene14727_All//0.00E+00//TC149135				nr +
Unigene14729_All	643	33.93	35.85	38.76	40.21	44.66	42.71	141.64	103.22	47.96	7.95E-02	5.54E-01		1.92E-01	1.17E-01		1.52E-01	1.73E-01		8.69E-02	4.99E-01		-4.56E-01	7.25E-21		-1.56E+00	7.57E-166	Down	Unigene14729_All//gi|283135882|gb|ADB11332.1|//1.00E-17//phi class glutathione transferase GSTF4 [Populus trichocarpa]	Unigene14729_All//8.00E-13//AT2G47730| ATGSTF8 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE PHI 8); glutathione binding / glutathione transferase	Unigene14729_All//2.00E-109//TC136579		ko00480|Glutathione metabolism	GO:0003824//GO:0005488	nr -
Unigene1473_All	3662	6.13	5.12	5.58	11.92	10.48	10.17	16.44	6.30	8.04	-2.60E-01	2.96E-02		-1.35E-01	3.24E-01		-1.85E-01	2.36E-02		-2.28E-01	5.53E-03		-1.38E+00	3.47E-89	Down	-1.03E+00	6.51E-58	Down	Unigene1473_All//gi|145335200|ref|NP_172173.2|//0.00E+00//catalytic/ metal ion binding / metalloendopeptidase/ zinc ion binding [Arabidopsis thaliana]	Unigene1473_All//0.00E+00//AT1G06900| catalytic/ metal ion binding / metalloendopeptidase/ zinc ion binding	Unigene1473_All//0.00E+00//TC177733				nr -
Unigene14734_All	2508	1.42	0.59	0.93	8.48	6.37	2.34	4.84	6.75	5.37	-1.28E+00	1.51E-04	Down	-6.03E-01	7.90E-02		-4.13E-01	2.05E-04		-1.86E+00	4.28E-43	Down	4.80E-01	6.48E-05		1.50E-01	3.16E-01		Unigene14734_All//gi|30687725|ref|NP_850306.1|//0.00E+00//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene14734_All//0.00E+00//AT2G38970| zinc finger (C3HC4-type RING finger) family protein	Unigene14734_All//0.00E+00//TC175229			GO:0000166//GO:0004672//GO:0046914	nr +
Unigene14736_All	1093	16.32	49.37	25.19	14.31	16.51	16.24	36.86	43.52	139.02	1.60E+00	1.92E-80	Up	6.26E-01	4.09E-09		2.06E-01	1.44E-01		1.82E-01	2.22E-01		2.39E-01	6.21E-04		1.91E+00	0.00E+00	Up	Unigene14736_All//gi|20146110|dbj|BAB88944.1|//3.00E-13//protein phosphatase 2C [Mesembryanthemum crystallinum]	Unigene14736_All//8.00E-13//AT4G31750| WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase	Unigene14736_All//0.00E+00//TC160328			GO:0004721//GO:0006464//GO:0006952//GO:0016020//GO:0031410//GO:0043169//GO:0043231//GO:0043234	nr -
Unigene14737_All	1610	0.88	1.54	1.49	41.43	27.29	24.43	7.22	0.75	1.68	8.14E-01	4.40E-02		7.63E-01	7.76E-02		-6.02E-01	8.91E-25		-7.62E-01	3.65E-33		-3.26E+00	5.91E-51	Down	-2.10E+00	1.57E-32	Down	Unigene14737_All//gi|15233202|ref|NP_191734.1|//1.00E-123//auxin-responsive protein -related [Arabidopsis thaliana]	Unigene14737_All//4.00E-120//AT3G61750| auxin-responsive protein -related	Unigene14737_All//0.00E+00//TC148845			GO:0031410	nr +
Unigene14739_All	1472	11.84	3.20	6.22	1.76	1.57	0.98	8.39	1.76	3.27	-1.89E+00	2.22E-33	Down	-9.28E-01	3.23E-11		-1.67E-01	6.99E-01		-8.42E-01	3.22E-02		-2.25E+00	2.19E-36	Down	-1.36E+00	5.87E-19	Down	Unigene14739_All//gi|224064862|ref|XP_002301588.1|//1.00E-56//f-box family protein [Populus trichocarpa] >gi|222843314|gb|EEE80861.1| f-box family protein [Populus trichocarpa]	Unigene14739_All//3.00E-48//AT3G07870| F-box family protein					nr -
Unigene1474_All	4683	14.85	8.06	4.10	23.87	30.69	25.52	33.49	10.70	16.06	-8.81E-01	5.82E-41		-1.85E+00	3.31E-124	Down	3.62E-01	1.29E-20		9.63E-02	6.55E-02		-1.65E+00	7.49E-299	Down	-1.06E+00	3.89E-156	Down	Unigene1474_All//gi|26984133|gb|AAN85208.1|//0.00E+00//DNA topoisomerase II [Nicotiana tabacum] >gi|26984168|gb|AAN85208.1| DNA topoisomerase II [Nicotiana tabacum]	Unigene1474_All//0.00E+00//AT3G23890| TOP11 (TOPOISOMERASE II); ATP binding / DNA binding / DNA topoisomerase (ATP-hydrolyzing)/ DNA topoisomerase/ DNA-dependent ATPase	Unigene1474_All//0.00E+00//ES824064				nr -
Unigene14741_All	1455	5.68	2.26	2.93	3.97	4.35	2.79	2.96	0.32	1.26	-1.33E+00	4.79E-10	Down	-9.57E-01	6.08E-06		1.33E-01	6.20E-01		-5.08E-01	4.21E-02		-3.23E+00	4.23E-19	Down	-1.23E+00	2.47E-06	Down	Unigene14741_All//gi|29374148|gb|AAO72990.1|//1.00E-106//cyclin D [Populus alba]	Unigene14741_All//4.00E-85//AT5G67260| CYCD3;2 (CYCLIN D3;2); cyclin-dependent protein kinase	Unigene14741_All//0.00E+00//TC144106			GO:0009987//GO:0043231	nr -
Unigene14743_All	1361	10.34	29.37	18.12	8.45	9.36	8.73	1.96	1.11	0.64	1.51E+00	6.48E-55	Up	8.09E-01	1.59E-12		1.47E-01	4.31E-01		4.58E-02	8.13E-01		-8.24E-01	1.69E-02		-1.60E+00	7.34E-06	Down	Unigene14743_All//gi|56550681|gb|AAV97794.1|//3.00E-39//At5g67350 [Arabidopsis thaliana] >gi|59958292|gb|AAX12856.1| At5g67350 [Arabidopsis thaliana]	Unigene14743_All//2.00E-21//AT5G67350| unknown protein	Unigene14743_All//0.00E+00//gi|78352959|gb|DT573233.1|DT573233				nr -
Unigene14744_All	1344	9.50	7.43	7.09	12.82	12.61	8.74	26.65	13.22	11.50	-3.55E-01	2.72E-02		-4.22E-01	1.13E-02		-2.48E-02	8.77E-01		-5.54E-01	2.05E-05		-1.01E+00	9.66E-33	Down	-1.21E+00	7.24E-45	Down	Unigene14744_All//gi|18414049|ref|NP_567408.1|//1.00E-108//UNE16 (unfertilized embryo sac 16); transcription factor [Arabidopsis thaliana]	Unigene14744_All//2.00E-98//AT4G13640| UNE16 (unfertilized embryo sac 16); transcription factor	Unigene14744_All//0.00E+00//TC130277	G2-like			nr -
Unigene14747_All	926	12.37	10.12	9.60	21.03	15.58	24.34	31.05	33.17	13.68	-2.90E-01	9.59E-02		-3.66E-01	4.18E-02		-4.33E-01	2.04E-04		2.11E-01	9.17E-02		9.56E-02	3.68E-01		-1.18E+00	7.92E-35	Down	Unigene14747_All//gi|299855523|gb|ADJ57303.1|//2.00E-56//defender against cell death 1 [Gossypium hirsutum]	Unigene14747_All//8.00E-51//AT1G32210| ATDAD1 (DEFENDER AGAINST APOPTOTIC DEATH 1)	Unigene14747_All//0.00E+00//TC146877		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0031224//GO:0043066//GO:0043231	nr +
Unigene14751_All	1318	3.61	10.23	8.36	7.79	10.82	6.54	0.58	0.51	1.06	1.50E+00	6.98E-19	Up	1.21E+00	5.46E-11	Up	4.74E-01	8.02E-04		-2.51E-01	2.01E-01		-1.86E-01	7.91E-01		8.74E-01	7.41E-02		Unigene14751_All//gi|211906534|gb|ACJ11760.1|//0.00E+00//class III peroxidase [Gossypium hirsutum]	Unigene14751_All//3.00E-102//AT2G24800| peroxidase, putative	Unigene14751_All//0.00E+00//TC146932		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209	nr -
Unigene14754_All	1191	1.54	2.17	1.83	2.93	3.73	3.00	4.01	2.56	1.91	4.97E-01	2.16E-01		2.54E-01	5.98E-01		3.49E-01	2.61E-01		3.31E-02	9.41E-01		-6.47E-01	8.39E-03		-1.07E+00	1.04E-05	Down	Unigene14754_All//gi|15230767|ref|NP_187320.1|//8.00E-34//AGL91; transcription factor [Arabidopsis thaliana] >gi|12321914|gb|AAG50993.1|AC03610 6_6 SRF-type transcription factor; 29224-29760 [Arabidopsis thaliana] >gi|67633716|gb|AAY78782.1| MADS-box family protein [Arabidopsis thaliana]	Unigene14754_All//4.00E-32//AT3G66656| AGL91; transcription factor	Unigene14754_All//0.00E+00//TC159195	MADS		GO:0003677//GO:0006350//GO:0009561//GO:0010468//GO:0043231	nr +
Unigene14756_All	1493	3.08	1.56	1.14	5.54	3.69	3.27	4.84	2.88	1.63	-9.82E-01	5.34E-04		-1.43E+00	3.14E-06	Down	-5.86E-01	1.92E-03		-7.62E-01	1.11E-04		-7.48E-01	1.11E-04		-1.57E+00	4.45E-14	Down	Unigene14756_All//gi|297793893|ref|XP_002864831.1|//1.00E-124//WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310666|gb|EFH41090.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14756_All//4.00E-124//AT5G63010| WD-40 repeat family protein	Unigene14756_All//0.00E+00//TC155311		ko04120|Ubiquitin mediated proteolysis//ko04146|Peroxisome		nr +
Unigene14758_All	1301	13.03	9.74	10.36	21.56	43.81	45.20	42.12	49.18	103.35	-4.20E-01	1.91E-03		-3.32E-01	2.14E-02		1.02E+00	1.17E-50	Up	1.07E+00	7.36E-51	Up	2.24E-01	1.69E-04		1.30E+00	1.17E-182	Up	Unigene14758_All//gi|15450691|gb|AAB96617.1|//1.00E-113//AT3g04350/T6K12_3 [Arabidopsis thaliana] >gi|21360521|gb|AAM47376.1| AT3g04350/T6K12_3 [Arabidopsis thaliana]	Unigene14758_All//7.00E-107//AT3G04350| unknown protein	Unigene14758_All//0.00E+00//TC163629				nr -
Unigene14759_All	905	44.28	31.19	23.59	97.92	120.96	95.62	24.25	7.94	6.03	-5.06E-01	1.78E-09		-9.08E-01	3.63E-24		3.05E-01	1.53E-11		-3.44E-02	6.25E-01		-1.61E+00	4.17E-41	Down	-2.01E+00	3.38E-57	Down	Unigene14759_All//gi|435039|gb|AAA79360.1|//2.00E-26//proline-rich cell wall protein [Gossypium hirsutum]		Unigene14759_All//0.00E+00//TC147126		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00270|Cysteine and methionine metabolism//ko03020|RNA polymerase		nr +
Unigene1476_All	1178	1.78	4.00	3.48	5.20	5.29	5.90	9.87	11.96	8.79	1.17E+00	4.12E-05	Up	9.70E-01	2.08E-03		2.47E-02	9.46E-01		1.83E-01	4.76E-01		2.77E-01	4.75E-02		-1.67E-01	2.99E-01				Unigene1476_All//0.00E+00//TC170999				
Unigene14761_All	1392	26.27	13.07	26.05	68.32	53.85	73.78	5.98	2.52	2.09	-1.01E+00	3.36E-27	Down	-1.22E-02	9.17E-01		-3.43E-01	1.09E-12		1.11E-01	4.57E-02		-1.25E+00	3.38E-11	Down	-1.52E+00	2.57E-15	Down	Unigene14761_All//gi|53370641|gb|AU89136.1|//9.00E-23//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene14761_All//1.00E-19//AT3G09510| nucleic acid binding	Unigene14761_All//0.00E+00//gi|13352063|gb|BG442495.1|BG442495				nr +
Unigene14763_All	1346	4.28	11.41	2.85	7.51	14.22	30.60	19.92	45.15	77.78	1.42E+00	1.13E-19	Up	-5.86E-01	2.40E-02		9.21E-01	1.54E-14		2.03E+00	2.12E-91	Up	1.18E+00	2.36E-70	Up	1.97E+00	1.84E-259	Up	Unigene14763_All//gi|297792499|ref|XP_002864134.1|//1.00E-145//pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309969|gb|EFH40393.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14763_All//5.00E-145//AT5G51830| pfkB-type carbohydrate kinase family protein	Unigene14763_All//0.00E+00//gi|78334572|gb|DT554846.1|DT554846		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr +
Unigene14764_All	1224	11.50	21.28	16.31	2.12	2.42	3.03	2.21	0.14	2.31	8.88E-01	5.96E-16		5.05E-01	7.36E-05		1.93E-01	6.34E-01		5.16E-01	1.21E-01		-4.02E+00	1.90E-14	Down	6.40E-02	8.57E-01		Unigene14764_All//gi|115434716|ref|NP_001042116.1|//6.00E-16//Os01g0166500 [Oryza sativa Japonica Group] >gi|13486661|dbj|BAB39898.1| P0028E10.1 [Oryza sativa Japonica Group] >gi|113531647|dbj|BAF04030.1| Os01g0166500 [Oryza sativa Japonica Group]	Unigene14764_All//4.00E-09//AT5G01790| unknown protein	Unigene14764_All//0.00E+00//gi|21101384|gb|BQ413697.1|BQ413697				nr -
Unigene14765_All	2269	8.92	18.87	8.87	30.85	23.33	34.57	63.71	43.27	30.83	1.08E+00	2.45E-35	Up	-8.50E-03	9.72E-01		-4.03E-01	1.21E-12		1.65E-01	6.91E-03		-5.58E-01	9.85E-47		-1.05E+00	3.83E-141	Down	Unigene14765_All//gi|62546341|gb|AAX86047.1|//0.00E+00//tubulin A [Glycine max]	Unigene14765_All//1.00E-165//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene14765_All//0.00E+00//TC165463		ko04145|Phagosome	GO:0007017//GO:0009629//GO:0010038//GO:0015630//GO:0016020//GO:0017111//GO:0030312//GO:0032561//GO:0043234//GO:0043623//GO:0044444	nr +
Unigene14767_All	885	2.84	2.29	1.50	5.46	5.41	3.67	4.11	1.51	1.40	-3.09E-01	4.43E-01		-9.16E-01	2.91E-02		-1.36E-02	9.55E-01		-5.71E-01	3.85E-02		-1.44E+00	1.83E-06	Down	-1.56E+00	2.06E-07	Down	Unigene14767_All//gi|297837511|ref|XP_002886637.1|//7.00E-83//clathrin binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297332478|gb|EFH62896.1| clathrin binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14767_All//5.00E-70//AT1G60070| binding / clathrin binding / protein binding / protein transporter	Unigene14767_All//0.00E+00//BF271170			GO:0005488//GO:0015031//GO:0022892//GO:0030119//GO:0043231	nr -

Unigene14771_All	1212	0.39	1.88	0.48	1.23	1.56	1.30	2.76	1.93	2.66	2.28E+00	4.37E-06	Up	3.15E-01	7.19E-01		3.42E-01	5.30E-01		8.10E-02	9.00E-01		-5.13E-01	9.54E-02		-4.97E-02	8.82E-01		Unigene14771_All//gi|115452451|ref|NP_001049826.1|//5.00E-98//0s03g0295700 [Oryza sativa Japonica Group] >gi|108707640|gb|ABF95435.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548297|dbj|BAF11740.1| Os03g0295700 [Oryza sativa Japonica Group]	Unigene14771_All//1.00E-119//AT5G58510| unknown protein	Unigene14771_All//0.00E+00//AI727984				nr -
Unigene14772_All	1363	5.18	100.00	42.04	28.07	14.88	13.82	14.70	62.52	9.62	4.27E+00	0.00E+00	Up	3.02E+00	6.37E-184	Up	-9.16E-01	1.38E-29		-1.02E+00	2.27E-31	Down	2.09E+00	2.61E-224	Up	-6.13E-01	1.24E-08		Unigene14772_All//gi|162135178|gb|AB382698.1|//1.00E-103//stay green protein [Capsicum annuum] >gi|170947249|emb|CAN88917.2| chlorophyll retainer (stay green) [Capsicum annuum] >gi|171903868|gb|ACB56586.1| chlorophyll retainer [Capsicum annuum]	Unigene14772_All//6.00E-96//AT4G22920| NYE1 (NON-YELLOWING 1)	Unigene14772_All//1.00E-149//TC149223				nr -
Unigene14773_All	1629	3.34	7.03	2.06	7.40	4.84	13.81	20.06	28.12	61.29	1.07E+00	6.54E-10	Up	-6.98E-01	8.78E-03		-6.12E-01	4.74E-05		9.00E-01	5.00E-15		4.87E-01	3.51E-12		1.61E+00	4.93E-188	Up	Unigene14773_All//gi|16604352|gb|AAL24182.1|//0.00E-00//AT5g12010/F14F18_180 [Arabidopsis thaliana] >gi|25141199|gb|AAN73294.1| At5g12010/F14F18_180 [Arabidopsis thaliana]	Unigene14773_All//1.00E-177//AT5G12010| unknown protein	Unigene14773_All//0.00E+00//gi|78345767|gb|DT566041.1|DT566041			GO:0009536	nr +
Unigene14775_All	1528	0.92	1.89	1.57	6.26	8.81	15.28	38.96	15.37	17.13	1.03E+00	5.63E-03		7.62E-01	7.76E-02		4.93E-01	7.21E-04		1.29E+00	2.18E-27	Up	-1.34E+00	3.85E-84	Down	-1.19E+00	1.85E-71	Down	Unigene14775_All//gi|115453339|ref|NP_001050270.1|//1.00E-60//0s03g0389400 [Oryza sativa Japonica Group] >gi|113548741|dbj|BAF12184.1| Os03g0389400 [Oryza sativa Japonica Group]	Unigene14775_All//2.00E-55//AT1G02170| AMC1 (METACASPASE 1); cysteine-type endopeptidase	Unigene14775_All//0.00E+00//TC178900				nr +
Unigene14777_All	1313	0.48	2.01	1.30	1.02	4.07	1.55	6.60	5.09	3.13	2.07E+00	3.06E-06	Up	1.44E+00	8.28E-03		1.99E+00	8.68E-13	Up	5.96E-01	2.13E-01		-3.74E-01	3.74E-02		-1.08E+00	1.02E-09	Down			Unigene14777_All//6.00E-114//gi|189098330|gb|FG551482.1|FG551482				
Unigene14780_All	1506	2.95	3.40	4.03	1.82	2.77	2.91	5.53	633.43	9.58	2.03E-01	4.72E-01		4.49E-01	7.99E-02		6.05E-01	4.10E-02		6.77E-01	2.01E-02		6.84E+00	0.00E+00	Up	7.92E-01	1.39E-09		Unigene14780_All//gi|40645459|dbj|BAD06575.1|//1.00E-167//LEDI-5c protein [Lithospermum erythrorhizon]	Unigene14780_All//1.00E-163//AT1G76690| OPX2	Unigene14780_All//0.00E+00//TC173397		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene14782_All	1638	12.52	6.47	4.06	14.99	11.98	4.88	7.61	3.22	3.11	-9.54E-01	2.68E-14		-1.62E+00	1.16E-30	Down	-3.23E-01	2.11E-03		-1.62E+00	4.89E-41	Down	-1.24E+00	2.55E-16	Down	-1.29E+00	8.78E-18	Down	Unigene14782_All//gi|159025715|emb|CAN88858.1|//1.00E-110//D3-type cyclin [Populus trichocarpa]	Unigene14782_All//3.00E-87//AT4G34160| CYCD3;1 (CYCLIN D3;1); cyclin-dependent protein kinase regulator/ protein binding	Unigene14782_All//0.00E+00//TC142223			GO:0009987	nr -
Unigene14783_All	2783	28.52	59.65	26.31	14.14	14.09	18.13	9.65	16.87	21.21	1.06E+00	6.65E-132	Up	-1.16E-01	7.98E-02		-4.80E-03	9.61E-01		3.58E-01	7.56E-07		8.06E-01	2.62E-29		1.14E+00	7.80E-66	Up	Unigene14783_All//gi|116268423|gb|AB196380.1|//0.00E+00//expressed protein [Prunus persica]	Unigene14783_All//0.00E+00//AT1G58200| MSL3 (MscS-LIKE 3); ion channel	Unigene14783_All//0.00E+00//TC150410			GO:0006810//GO:0006950//GO:0006996//GO:0015075//GO:0031967	nr +
Unigene14784_All	2053	1.38	0.54	0.10	4.42	2.90	1.47	7.39	4.15	1.55	-1.34E+00	5.15E-04	Down	-3.73E+00	3.90E-11	Down	-6.06E-01	6.70E-04		-1.58E+00	5.42E-15	Down	-8.32E-01	1.45E-10		-2.25E+00	5.54E-46	Down	Unigene14784_All//gi|3540181|gb|AAC34331.1|//1.00E-147//Unknown protein [Arabidopsis thaliana] >gi|40823449|gb|AAR92283.1| At1g10020 [Arabidopsis thaliana] >gi|46518421|gb|AAS99692.1| At1g10020 [Arabidopsis thaliana]	Unigene14784_All//1.00E-126//AT1G10020| unknown protein	Unigene14784_All//0.00E+00//gi|78338680|gb|DT558954.1|DT558954				nr -
Unigene14786_All	1813	8.37	6.20	5.93	12.28	10.50	14.70	15.37	10.77	7.32	-4.32E-01	2.71E-03		-4.96E-01	8.63E-04		-2.26E-01	5.79E-02		2.59E-01	1.72E-02		-5.14E-01	1.94E-08		-1.07E+00	6.50E-29	Down	Unigene14786_All//gi|32489532|emb|CAE04735.1|//1.00E-173//OSJNBa0043L24.23 [Oryza sativa (japonica cultivar-group)] >gi|116310777|emb|CAH67570.1| OSIGBa0101P20.13 [Oryza sativa (indica cultivar-group)]	Unigene14786_All//2.00E-163//AT1G65055| GTF2H2 (GENERAL TRANSCRIPTION FACTOR IIH 2); general RNA polymerase II transcription factor	Unigene14786_All//0.00E+00//ES828922		ko03420|Nucleotide excision repair//ko03022|Basal transcription factors		nr -
Unigene14787_All	1711	3.67	2.19	1.31	5.88	5.64	4.78	5.93	2.88	4.00	-7.44E-01	1.56E-03		-1.49E+00	1.08E-08	Down	-6.16E-02	8.04E-01		-3.00E-01	1.19E-01		-1.04E+00	2.70E-10	Down	-5.66E-01	2.68E-04		Unigene14787_All//gi|20453219|gb|AAM19848.1|//1.00E-152//AT3g56750/T8M16_80 [Arabidopsis thaliana]	Unigene14787_All//6.00E-150//AT3G56750| unknown protein	Unigene14787_All//0.00E+00//TC148643				nr +
Unigene1479_All	1117	2.15	3.58	4.62	5.53	5.61	6.83	7.91	6.59	12.73	7.34E-01	1.60E-02		1.10E+00	7.59E-05	Up	2.09E-02	9.58E-01		3.05E-01	1.84E-01		-2.65E-01	1.53E-01		6.87E-01	1.40E-07		Unigene1479_All//2.00E-63//AT2G39340| SAC3/GANP family protein [Arabidopsis thaliana]	Unigene1479_All//0.00E+00//DW478050				nr +
Unigene14790_All	1677	20.00	14.35	14.70	25.66	18.60	25.61	33.33	17.55	16.30	-4.79E-01	2.29E-07		-4.44E-01	3.41E-06		-4.64E-01	3.32E-10		-3.00E-03	9.71E-01		-9.26E-01	8.25E-44		-1.03E+00	7.70E-54	Down	Unigene14790_All//gi|37983566|gb|AAR06290.1|//1.00E-165//5''-aminoimidazole ribonucleotide synthetase [Solanum tuberosum]	Unigene14790_All//3.00E-149//AT3G55010| PUR5; ATP binding / phosphoribosylformylglycinamidine cyclo-ligase	Unigene14790_All//0.00E+00//TC144370		ko00230|Purine metabolism		nr +
Unigene14791_All	1678	2.68	9.30	4.57	3.77	3.80	4.31	5.44	10.31	8.50	1.79E+00	7.60E-28	Up	7.69E-01	4.27E-04		1.00E-02	9.75E-01		1.92E-01	4.55E-01		9.22E-01	5.10E-14		6.43E-01	7.21E-07		Unigene14791_All//gi|223452470|gb|ACN89562.1|//1.00E-159//calmodulin-binding receptor-like cytoplasmic kinase [Glycine max]	Unigene14791_All//6.00E-131//AT4G00330| CRCK2; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene14791_All//0.00E+00//TC164647			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene14793_All	1665	16.81	12.51	10.91	27.50	32.90	27.40	2.49	2.03	5.41	-4.27E-01	2.98E-05		-6.24E-01	3.29E-09		2.59E-01	1.33E-04		-5.20E-03	9.50E-01		-2.92E-01	3.16E-01		1.12E+00	1.52E-10	Up	Unigene14793_All//gi|297800470|ref|XP_002868119.1|//1.00E-177//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313955|gb|EFH44378.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14793_All//4.00E-155//AT4G16563| aspartyl protease family protein	Unigene14793_All//0.00E+00//gi|78344115|gb|DT564389.1|DT564389			GO:0004175//GO:0019538	nr -
Unigene14794_All	1069	29.56	16.16	17.68	40.63	68.90	43.22	0.91	0.39	0.19	-8.71E-01	1.15E-18		-7.41E-01	1.01E-13		7.62E-01	5.19E-40		8.90E-02	3.52E-01		-1.22E+00	5.68E-02		-2.29E+00	9.84E-04	Down	Unigene14794_All//gi|297823869|ref|XP_002880817.1|//1.00E-158//nitrate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326656|gb|EFH57076.1| nitrate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene14794_All//6.00E-146//AT2G26690| nitrate transporter (NTP2)	Unigene14794_All//6.00E-169//TC140606				nr -
Unigene14795_All	942	0.22	0.86	0.90	1.59	2.49	0.96	3.82	2.22	1.35	1.95E+00	2.43E-02		2.03E+00	2.24E-02		6.48E-01	1.28E-01		-7.26E-01	1.93E-01		-7.82E-01	6.80E-03		-1.50E+00	5.84E-07	Down	Unigene14795_All//gi|224141919|ref|XP_002324308.1|//1.00E-103//plant synaptotagmin [Populus trichocarpa] >gi|222865742|gb|EEF02873.1| plant synaptotagmin [Populus trichocarpa]	Unigene14795_All//2.00E-98//AT5G11100| SYTD	Unigene14795_All//3.00E-13//DW501748			GO:0016020	nr +
Unigene148_All	4775	0.93	0.48	0.75	2.20	1.15	1.00	7.41	4.62	4.15	-9.64E-01	8.46E-04		-3.18E-01	3.14E-01		-9.32E-01	1.04E-08		-1.13E+00	1.34E-10	Down	-6.81E-01	7.13E-17		-8.38E-01	1.64E-24		Unigene148_All//gi|295311698|ref|YP_003587363.1|//1.00E-157//ribosomal protein L2 [Cucurbita pepo] >gi|259156826|gb|ACV96687.1| ribosomal protein L2 [Cucurbita pepo]	Unigene148_All//3.00E-81//ATMG00210| encodes a mitochondrial ribosomal protein L5, a constituent of the large subunit of the ribosomal complex	Unigene148_All//0.00E+00//TC133368		ko03010|Ribosome//ko00190|Oxidative phosphorylation		nr -
Unigene14801_All	1667	1.38	13.43	0.26	4.03	15.53	6.91	10.12	14.24	83.21	3.28E+00	1.12E-79	Up	-2.43E+00	2.90E-06	Down	1.95E+00	1.54E-59	Up	7.76E-01	2.29E-06		4.93E-01	7.73E-07		3.04E+00	0.00E+00	Up	Unigene14801_All//gi|259121407|gb|ACV92023.1|//1.00E-117//WRKY transcription factor 21 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene14801_All//6.00E-58//AT4G23810| WRKY53; DNA binding / protein binding / transcription activator/ transcription factor	Unigene14801_All//0.00E+00//gi|78345496|gb|DT565770.1|DT565770	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene14803_All	1872	2.66	0.92	2.56	12.19	9.77	7.82	8.29	9.15	5.51	-1.53E+00	1.17E-07	Down	-5.26E-02	8.56E-01		-3.19E-01	3.75E-03		-6.41E-01	8.10E-09		1.43E-01	3.01E-01		-5.89E-01	1.79E-06		Unigene14803_All//gi|15148922|gb|AAK84888.1|AF402607_1/1.00E-137//TGA-type basic leucine zipper protein TGA1.1 [Phaseolus vulgaris]	Unigene14803_All//5.00E-126//AT5G65210| TGA1; DNA binding / calmodulin binding / transcription factor	Unigene14803_All//0.00E+00//TC152655	bZIP			nr -
Unigene14805_All	1686	32.43	20.20	28.68	16.19	14.54	14.52	11.13	7.39	5.48	-6.83E-01	4.24E-21		-1.77E-01	2.33E-02		-1.55E-01	1.69E-01		-1.57E-01	1.81E-01		-5.92E-01	1.88E-07		-1.02E+00	2.14E-18	Down	Unigene14805_All//gi|115488878|ref|NP_001066926.1|//0.00E+00//Os12g0533700 [Oryza sativa Japonica Group] >gi|113649433|dbj|BAF29945.1| Os12g0533700 [Oryza sativa Japonica Group]	Unigene14805_All//0.00E+00//AT3G58140| phenylalanyl-tRNA synthetase class IIc family protein	Unigene14805_All//0.00E+00//TC147423		ko00970|Aminoacyl-tRNA biosynthesis	GO:0003723//GO:0004812//GO:0006418//GO:0009536//GO:0032559//GO:0016872	nr -
Unigene14806_All	1464	9.58	6.06	6.00	14.87	11.74	16.75	16.84	8.76	8.41	-6.61E-01	1.00E-05		-6.74E-01	1.35E-05		-3.41E-01	2.36E-03		1.72E-01	1.63E-01		-9.42E-01	2.46E-20		-1.00E+00	4.04E-23	Down	Unigene14806_All//gi|18407449|ref|NP_566111.1|//1.00E-157//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|15983390|gb|AAL11563.1|AF424569_1 At2g47790/F17A22.18 [Arabidopsis thaliana] >gi|20197308|gb|AAC63654.2| expressed protein [Arabidopsis thaliana] >gi|23308341|gb|AAN18140.1| At2g47790/F17A22.18 [Arabidopsis thaliana]	Unigene14806_All//3.00E-153//AT2G47790| transducin family protein / WD-40 repeat family protein	Unigene14806_All//0.00E+00//TC138517		ko03040|Spliceosome//ko04146|Peroxisome		nr -
Unigene14807_All	369	0.14	0.55	0.87	2.30	3.27	0.49	6.87	1.93	7.02	1.95E+00	3.75E-01		2.61E+00	1.46E-01		5.09E-01	4.57E-01		-2.23E+00	9.53E-03		-1.84E+00	2.33E-06	Down	2.97E-02	9.56E-01				Unigene14807_All//2.00E-12//ES840215				ESTscan +
Unigene14808_All	3328	0.64	0.27	0.51	1.12	1.42	0.86	6.16	1.44	5.16	-1.23E+00	5.86E-03		-3.32E-01	4.73E-01		3.37E-01	2.64E-01		-3.93E-01	2.42E-01		-2.09E+00	9.59E-55	Down	-2.56E-01	1.84E-02		Unigene14808_All//gi|15234126|ref|NP_194473.1|//1.00E-102//CIP7 (COP1-INTERACTING PROTEIN 7); transcription activator [Arabidopsis thaliana] >gi|186514102|ref|NP_001119068.1| CIP7 (COP1-INTERACTING PROTEIN 7); transcription activator [Arabidopsis thaliana] >gi|3327868|dbj|BAA31738.1| COP1-Interacting Protein 7 (CIP7) [Arabidopsis thaliana] >gi|4972068|emb|CAB43875.1| COP1-interacting protein 7 (CIP7) [Arabidopsis thaliana] >gi|7269597|emb|CAB81393.1| COP1-interacting protein 7 (CIP7) [Arabidopsis thaliana]	Unigene14808_All//2.00E-74//AT4G27430| CIP7 (COP1-INTERACTING PROTEIN 7); transcription activator	Unigene14808_All//4.00E-37//DR454091				nr +
Unigene14810_All	1287	0.33	0.16	0.37	5.15	3.37	3.58	8.05	3.41	3.37	-1.05E+00	3.66E-01		1.96E-01	8.39E-01		-6.11E-01	4.49E-03		-5.24E-01	2.22E-02		-1.24E+00	1.31E-13	Down	-1.25E+00	2.61E-14	Down	Unigene14810_All//gi|224127726|ref|XP_002329162.1|//9.00E-84//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene14810_All//2.00E-64//AT5G36930| disease resistance protein (TIR-NBS-LRR class), putative	Unigene14810_All//0.00E+00//TC145918		ko04626|Plant-pathogen interaction	GO:0000166//GO:0006952//GO:0009987	nr +

Unigene14811_All	2476	3.13	8.21	1.68	6.60	9.12	5.80	9.31	19.01	53.63	1.39E+00	3.62E-25	Up	-8.99E-01	3.92E-05		4.67E-01	1.48E-05		-1.86E-01	2.32E-01		1.03E+00	5.33E-44	Up	2.53E+00	0.00E+00	Up	Unigene14811_All//gi|16323145|gb|AAL15307.1|//1.00E-108//AT5g11000/T30N20_270 [Arabidopsis thaliana] >gi|21436003|gb|AAM51579.1| AT5g11000/T30N20_270 [Arabidopsis thaliana]	Unigene14811_All//3.00E-83//AT5G11000| unknown protein	Unigene14811_All//0.00E+00//ES818529				nr -
Unigene14812_All	1403	12.60	7.11	6.15	19.67	12.59	15.39	21.37	21.15	49.15	-8.25E-01	6.58E-10		-1.04E+00	1.59E-13	Down	-6.44E-01	8.78E-12		-3.54E-01	5.12E-04		-1.46E-02	9.03E-01		1.20E+00	8.83E-84	Up	Unigene14812_All//gi|18401444|ref|NP_565652.1|//1.00E-153//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|75216237|sp|Q9ZQG9.2|E1314_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 14; AltName: Full=(1->3)-beta-glucan endohydrolase 14; Short=(1->3)-beta-glucanase 14; AltName: Full=Beta-1,3-endoglucanase 14; Short=Beta-1,3-glucanase 14; Flags: Precursor	Unigene14812_All//5.00E-152//AT2G27500| glycosyl hydrolase family 17 protein	Unigene14812_All//0.00E+00//TC139594		ko00500|Starch and sucrose metabolism		nr +
Unigene14815_All	1667	1.35	1.37	1.47	1.88	3.74	3.47	1.52	3.36	3.82	1.93E-02	9.84E-01		1.23E-01	7.63E-01		9.90E-01	1.24E-05		8.81E-01	3.17E-04		1.14E+00	7.03E-07	Up	1.33E+00	7.92E-10	Up	Unigene14815_All//gi|297850850|ref|XP_002883306.1|//3.00E-52//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339148|gb|EFH69565.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14815_All//5.00E-42//AT1G23780| F-box family protein	Unigene14815_All//0.00E+00//TC166628				nr +
Unigene14816_All	223	0.00	0.00	0.00	0.45	0.00	0.20	0.19	4.87	8.04	null	null		null	null		-8.80E+00	3.13E-01		-1.14E+00	6.77E-01		4.68E+00	1.37E-06	Up	5.41E+00	1.56E-11	Up	Unigene14816_All//gi|15227042|ref|NP_178383.1|//2.00E-13//APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|42570659|ref|NP_973403.1| APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|75318425|sp|Q98940.1|APK2B_ARATH RecName: Full=Protein kinase 2B, chloroplastic; Flags: Precursor >gi|16226563|gb|AAL16201.1|AF428432_1 At2g02800/T20F6.6 [Arabidopsis thaliana] >gi|2852449|dbj|BAA24695.1| protein kinase [Arabidopsis thaliana] >gi|21928081|gb|AAM78069.1| At2g02800/T20F6.6 [Arabidopsis thaliana]	Unigene14816_All//2.00E-12//AT1G26970| protein kinase, putative	Unigene14816_All//5.00E-21//TC174934			GO:0004672//GO:0006464//GO:0016020//GO:0032559//GO:0043231	nr -
Unigene14817_All	1630	1.00	2.86	0.82	1.31	0.74	1.36	6.80	25.39	65.84	1.52E+00	3.73E-07	Up	-2.85E-01	6.21E-01		-8.30E-01	4.74E-02		4.71E-02	9.34E-01		1.90E+00	1.46E-96	Up	3.28E+00	0.00E+00	Up	Unigene14817_All//gi|15227042|ref|NP_178383.1|//1.00E-126//APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|42570659|ref|NP_973403.1| APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|75318425|sp|Q98940.1|APK2B_ARATH RecName: Full=Protein kinase 2B, chloroplastic; Flags: Precursor >gi|16226563|gb|AAL16201.1|AF428432_1 At2g02800/T20F6.6 [Arabidopsis thaliana] >gi|2852449|dbj|BAA24695.1| protein kinase [Arabidopsis thaliana] >gi|21928081|gb|AAM78069.1| At2g02800/T20F6.6 [Arabidopsis thaliana]	Unigene14817_All//3.00E-115//AT1G14370| APK2A (PROTEIN KINASE 2A); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene14817_All//0.00E+00//ES804901		ko04626|Plant-pathogen interaction		nr +
Unigene14824_All	1510	5.99	6.68	7.26	8.54	11.81	8.34	12.21	10.46	5.73	1.56E-01	4.22E-01		2.77E-01	1.40E-01		4.67E-01	1.62E-04		-3.41E-02	8.59E-01		-2.23E-01	7.00E-02		-1.09E+00	4.72E-20	Down	Unigene14824_All//gi|30684470|ref|NP_180571.2|//1.00E-132//ubiquitin family protein [Arabidopsis thaliana]	Unigene14824_All//4.00E-134//AT2G30100| ubiquitin family protein	Unigene14824_All//0.00E+00//TC144256		ko04626|Plant-pathogen interaction		nr +
Unigene14825_All	881	58.50	197.67	109.76	82.16	153.53	165.84	51.21	28.80	29.89	1.76E+00	5.87E-296	Up	9.08E-01	1.04E-57		9.02E-01	1.21E-97		1.01E+00	1.92E-115	Up	-8.30E-01	1.12E-29		-7.77E-01	2.57E-27		Unigene14825_All//gi|30984590|gb|AAP42758.1|//2.00E-82//At5g25770 [Arabidopsis thaliana]	Unigene14825_All//4.00E-78//AT5G25770| unknown protein	Unigene14825_All//0.00E+00//TC151453			GO:0043231	nr -
Unigene14826_All	997	88.90	36.08	43.80	113.17	106.62	123.26	83.88	50.05	44.11	-1.30E+00	1.71E-97	Down	-1.02E+00	3.52E-64	Down	-8.60E-02	1.07E-01		1.23E-01	1.17E-02		-7.45E-01	3.68E-45		-9.27E-01	3.80E-67		Unigene14826_All//gi|15237095|ref|NP_193777.1|//1.00E-114//smB (small nuclear ribonucleoprotein associated protein B) [Arabidopsis thaliana] >gi|30685110|ref|NP_849414.1| smB (small nuclear ribonucleoprotein associated protein B) [Arabidopsis thaliana] >gi|79325195|ref|NP_001031682.1| smB (small nuclear ribonucleoprotein associated protein B) [Arabidopsis thaliana] >gi|238480869|ref|NP_001154258.1| smB (small nuclear ribonucleoprotein associated protein B) [Arabidopsis thaliana] >gi|222423490|dbj|BAH19715.1| AT4G20140 [Arabidopsis thaliana]	Unigene14826_All//5.00E-52//AT4G20140| smB (small nuclear ribonucleoprotein associated protein B)	Unigene14826_All//0.00E+00//gi|78338765|gb|DT559039.1|DT559039		ko03040|Spliceosome		nr +
Unigene14827_All	1494	253.72	1182.97	486.49	87.02	96.78	179.23	20.12	42.02	20.48	2.22E+00	0.00E+00	Up	9.39E-01	0.00E+00		1.53E-01	1.88E-04		1.04E+00	2.40E-221	Up	1.06E+00	2.16E-61	Up	2.54E-02	8.00E-01		Unigene14827_All//gi|62900641|sp|Q9ZWQ8.1|PAP_CITUN//1.00E-126//RecName: Full=Plastid-lipid-associated protein, chloroplastic; AltName: Full=CitPAP; Flags: Precursor >gi|3928760|dbj|BAA34702.1| homolog to plastid-lipid-associated protein [Citrus unshiu]	Unigene14827_All//4.00E-101//AT4G04020| FIB (FIBRILLIN); structural molecule	Unigene14827_All//0.00E+00//TC133698				nr +
Unigene14828_All	1791	1.43	1.44	0.42	27.79	17.05	14.60	15.60	5.32	5.18	1.14E-02	9.83E-01		-1.78E+00	6.83E-05	Down	-7.04E-01	1.85E-24		-9.28E-01	1.10E-34		-1.55E+00	1.74E-49	Down	-1.59E+00	8.99E-53	Down	Unigene14828_All//gi|110737096|dbj|BAF00500.1|//1.00E-134//thaumatin-like protein [Arabidopsis thaliana]	Unigene14828_All//2.00E-126//AT4G38660| thaumatin, putative	Unigene14828_All//0.00E+00//TC151784				nr +
Unigene14829_All	2344	0.83	0.84	1.11	7.25	6.21	8.05	6.87	15.96	5.69	2.96E-02	9.68E-01		4.31E-01	3.05E-01		-2.22E-01	1.16E-01		1.52E-01	3.08E-01		1.22E+00	1.29E-45	Up	-2.71E-01	2.89E-02		Unigene14829_All//gi|2827550|emb|CAA16558.1|//0.00E+00//leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] >gi|7269119|emb|CAB79228.1| leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] >gi|38564276|gb|AAR23717.1| At4g22730 [Arabidopsis thaliana] >gi|51971929|dbj|BAD44629.1| leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] >gi|224589626|gb|ACN59346.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene14829_All//0.00E+00//AT4G22730| leucine-rich repeat transmembrane protein kinase, putative	Unigene14829_All//0.00E+00//TC129741			GO:0004672//GO:0005488//GO:0008152//GO:0016020	nr -
Unigene14830_All	278	3.39	1.46	1.15	15.77	10.65	2.27	5.63	2.71	8.03	-1.22E+00	9.43E-02		-1.56E+00	4.90E-02		-5.66E-01	4.23E-02		-2.79E+00	6.31E-15	Down	-1.06E+00	2.63E-02		5.12E-01	1.73E-01				Unigene14830_All//2.00E-91//gi|11206232|gb|BF275162.1|BF275162				
Unigene14834_All	912	19.96	9.00	7.30	27.15	19.52	32.93	54.70	16.73	16.73	-1.15E+00	4.53E-17	Down	-1.45E+00	3.20E-23	Down	-4.76E-01	2.29E-06		2.79E-01	5.36E-03		-1.71E+00	9.98E-101	Down	-1.71E+00	1.07E-103	Down	Unigene14834_All//gi|192913000|gb|ACF06608.1|//1.00E-105//ribosomal protein [Elaeis guineensis]	Unigene14834_All//7.00E-95//AT5G39850| 40S ribosomal protein S9 (RPS9C)	Unigene14834_All//0.00E+00//TC140798		ko03010|Ribosome		nr +
Unigene14835_All	1496	44.03	42.00	57.52	21.54	19.04	18.36	7.38	4.86	3.06	-6.82E-02	3.77E-01		3.86E-01	1.46E-11		-1.79E-01	7.21E-02		-2.31E-01	1.88E-02		-6.02E-01	7.75E-05		-1.27E+00	1.95E-15	Down	Unigene14835_All//gi|30687988|ref|NP_850950.1|//3.00E-98//tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana] >gi|222424443|dbj|BAH20177.1| AT1G22700 [Arabidopsis thaliana]	Unigene14835_All//2.00E-88//AT1G22700| tetratricopeptide repeat (TPR)-containing protein	Unigene14835_All//0.00E+00//gi|164245998|gb|ES804276.1|ES804276			GO:0009534//GO:0043623	nr -
Unigene14836_All	1693	1.30	1.11	0.82	5.68	1.46	0.64	30.09	147.38	58.73	-2.29E-01	6.22E-01		-6.67E-01	1.42E-01		-1.96E+00	3.28E-24	Down	-3.15E+00	2.14E-36	Down	2.29E+00	0.00E+00	Up	9.65E-01	1.48E-84		Unigene14836_All//gi|180000070|gb|AAL54886.1|AF092915_1/0.00E+00//cytochrome P450-dependent fatty acid hydroxylase [Nicotiana tabacum]	Unigene14836_All//1.00E-126//AT5G63450| CYP94B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene14836_All//2.00E-169//TC134800		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016712	nr +
Unigene14838_All	1083	12.75	7.86	13.42	9.20	8.49	7.76	29.05	25.28	12.54	-6.98E-01	3.85E-06		7.38E-02	6.49E-01		-1.16E-01	5.84E-01		-2.46E-01	2.21E-01		-2.00E-01	2.69E-02		-1.21E+00	1.76E-39	Down	Unigene14838_All//gi|297845214|ref|XP_002890488.1|//4.00E-43//ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336330|gb|EFH66747.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14838_All//1.00E-43//AT1G22050| MUB6 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 6 PRECURSOR)	Unigene14838_All//3.00E-41//ES811604			GO:0043412	nr -
Unigene14843_All	1228	1.79	3.92	2.95	4.38	3.48	5.63	30.57	55.24	51.49	1.13E+00	5.66E-05	Up	7.21E-01	3.30E-02		-3.33E-01	2.14E-01		3.61E-01	1.28E-01		8.53E-01	3.09E-46		7.52E-01	1.06E-35		Unigene14843_All//gi|226532198|ref|NP_001150776.1|//2.00E-81//syntaxin 121 [Zea mays] >gi|195641740|gb|ACG40338.1| syntaxin 121 [Zea mays]	Unigene14843_All//3.00E-56//AT3G11820| SYP121 (SYNTAXIN OF PLANTS 121); SNAP receptor/ protein anchor	Unigene14843_All//0.00E+00//TC173176		ko04130|SNARE interactions in vesicular transport	GO:0005515//GO:0015031//GO:0044464	nr +
Unigene14845_All	1110	16.69	11.73	7.92	41.51	55.50	69.41	18.05	4.18	10.48	-5.08E-01	7.23E-05		-1.08E+00	5.31E-15	Down	4.19E-01	9.47E-12		7.42E-01	3.37E-36		-2.11E+00	4.23E-54	Down	-7.85E-01	7.51E-13		Unigene14845_All//gi|123965225|gb|AAW02943.2|//1.00E-123//aquaporin [Vitis vinifera]	Unigene14845_All//7.00E-116//AT4G01470| TIP1;3 (TONOPLAST INTRINSIC PROTEIN 1;3); urea transmembrane transporter/ water channel	Unigene14845_All//0.00E+00//TC132412				nr +

Unigene14846_All	2406	0.74	0.80	0.58	2.24	2.30	1.33	5.29	2.26	5.32	1.14E-01	7.98E-01		-3.62E-01	4.82E-01		4.34E-02	8.90E-01		-7.47E-01	3.24E-03		-1.23E+00	2.57E-16	Down	7.00E-03	9.74E-01		Unigene14846_All//gi|18402188|ref|NP_566630.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|53828541|gb|AAU94380.1|At3g19300 [Arabidopsis thaliana] >gi|55733747|gb|AAV59270.1|At3g19300 [Arabidopsis thaliana]	Unigene14816_All//0.00E+00//AT3G19300| protein kinase family protein	Unigene14846_All//0.00E+00//gi|109850151|gb|DW479130.1|DW479130		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016020//GO:0031410//GO:0032559	nr +
Unigene14847_All	1630	1.32	0.44	0.23	1.83	2.28	2.05	3.03	1.13	2.47	-1.60E+00	6.02E-04	Down	-2.52E+00	4.25E-06	Down	3.15E-01	3.71E-01		1.61E-01	6.84E-01		-1.43E+00	2.14E-08	Down	-2.98E-01	2.24E-01		Unigene14847_All//gi|18405190|ref|NP_564674.1|//1.00E-140//zinc finger (Ran-binding) family protein [Arabidopsis thaliana]	Unigene14847_All//6.00E-90//AT1G55040| zinc finger (Ran-binding) family protein	Unigene14847_All//0.00E+00//CO079323			GO:0044464//GO:0046914	nr +
Unigene14848_All	949	55.63	43.84	58.58	80.05	94.78	74.05	6.33	1.63	1.05	-3.44E-01	2.14E-06		7.46E-02	4.01E-01		2.44E-01	1.90E-06		-1.12E-01	9.17E-02		-1.96E+00	3.22E-15	Down	-2.59E+00	6.82E-22	Down	Unigene14848_All//gi|2500717|sp|Q41495.1|ST14_SOLTU//1.00E-47//RecName: Full=STS14 protein; Flags: Precursor >gi|11177146|gb|AAG32153.1|U17111_1 pistil-specific; similar to PR-1 proteins, Swiss-Prot Accession Number P11670 [Solanum tuberosum] >gi|1236785|emb|CAA57976.1| sts14 [Solanum tuberosum] >gi|1589691|prf||2211417A sts14 gene	Unigene14848_All//2.00E-44//AT5G66590| allergen V5/Tpx-1-related family protein	Unigene14848_All//0.00E+00//gi|21098687|gb|BQ411000.1|BQ411000		ko04626|Plant-pathogen interaction	GO:0043231	nr -
Unigene14849_All	847	9.57	4.01	1.13	53.46	33.99	32.10	56.11	90.94	54.09	-1.26E+00	3.98E-09	Down	-3.08E+00	1.42E-26	Down	-6.53E-01	1.47E-19		-7.36E-01	2.14E-21		6.97E-01	3.99E-37		-5.28E-02	5.27E-01		Unigene14849_All//gi|15222875|ref|NP_177708.1|//7.00E-38//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|6721098|gb|AAF26752.1|AC007396_1 T4012.3 [Arabidopsis thaliana] >gi|18377860|gb|AAL67116.1|At1g75800/T4012_2 [Arabidopsis thaliana] >gi|20334826|gb|AAM16169.1|At1g75800/T4012_2 [Arabidopsis thaliana]	Unigene14849_All//6.00E-36//AT1G75800| pathogenesis-related thaumatin family protein	Unigene14849_All//0.00E+00//TC176010			GO:0009607//GO:0031224	nr -
Unigene14852_All	2180	11.66	21.64	5.35	9.60	8.48	13.20	7.23	16.01	16.12	8.92E-01	1.83E-28		-1.12E+00	7.57E-22	Down	-1.78E-01	1.67E-01		4.60E-01	2.92E-06		1.15E+00	7.13E-39	Up	1.16E+00	1.44E-40	Up	Unigene14852_All//gi|171906260|gb|ACB56927.1|//1.00E-142//glycosyltransferase UGT95A1 [Hieracium pilosella]	Unigene14852_All//4.00E-39//AT4G34138| UGT73B1 (UDP-glucosyl transferase 73B1); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase	Unigene14852_All//0.00E+00//TC131191		ko00908|Zeatin biosynthesis	GO:0016757	nr +
Unigene14853_All	1150	2.18	2.03	2.18	5.41	2.64	2.75	75.04	14.68	3.12	-1.08E-01	7.80E-01		-5.00E-03	9.89E-01		-1.04E+00	2.35E-06	Down	-9.78E-01	2.76E-05		-2.35E+00	2.81E-264	Down	-4.59E+00	0.00E+00	Down	Unigene14853_All//gi|48431269|gb|AAT44124.1|//3.00E-92//F3H-like protein [Saussurea medusa]	Unigene14853_All//2.00E-68//AT5G24530| DMR6 (DOWNY MILDEW RESISTANT 6); oxidoreductase/ oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene14853_All//0.00E+00//TC177628		ko00941|Flavonoid biosynthesis	GO:0016491	nr -
Unigene14854_All	1121	5.18	6.92	2.57	11.33	9.77	8.94	9.84	5.82	2.74	4.17E-01	4.93E-02		-1.01E+00	9.08E-05	Down	-2.14E-01	2.11E-01		-3.41E-01	3.64E-02		-7.59E-01	7.22E-07		-1.85E+00	3.51E-26	Down	Unigene14854_All//gi|224141325|ref|XP_002324024.1|//1.00E-131//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Populus trichocarpa] >gi|222867026|gb|EEF04157.1|oxidoreductase, 2OG-Fe(II) oxygenase family protein [Populus trichocarpa]	Unigene14854_All//8.00E-125//AT3G28480| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene14854_All//0.00E+00//TC160650		ko00330|Arginine and proline metabolism		nr -
Unigene14855_All	1556	6.19	1.56	2.36	30.83	16.75	10.65	9.46	2.95	2.74	-1.98E+00	5.15E-20	Down	-1.39E+00	8.75E-12	Down	-8.80E-01	1.29E-34		-1.53E+00	1.19E-73	Down	-1.68E+00	1.81E-29	Down	-1.79E+00	3.93E-33	Down	Unigene14855_All//gi|224105011|ref|XP_002313654.1|//8.00E-82//predicted protein [Populus trichocarpa] >gi|222850062|gb|EEE87609.1|predicted protein [Populus trichocarpa]	Unigene14855_All//1.00E-13//AT3G44716| unknown protein	Unigene14855_All//0.00E+00//TC134434				nr +
Unigene14856_All	878	16.45	157.38	4.91	55.49	45.38	41.67	40.45	24.66	35.98	3.26E+00	0.00E+00	Up	-1.74E+00	5.64E-24	Down	-2.90E-01	4.41E-05		-4.13E-01	1.69E-08		-7.14E-01	2.57E-18		-1.69E-01	4.16E-02		Unigene14856_All//gi|18401317|ref|NP_565634.1|//2.00E-81//harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana] >gi|42570933|ref|NP_973540.1|harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana] >gi|13877665|gb|AAK43910.1|AF37059_1 [Unknown protein [Arabidopsis thaliana] >gi|3885338|gb|AAC77866.1|expressed protein [Arabidopsis thaliana] >gi|15450381|gb|AAK96484.1|At2g27080/T20P8.13 [Arabidopsis thaliana] >gi|16974489|gb|AAL31248.1|At2g27080/T20P8.13 [Arabidopsis thaliana]	Unigene14856_All//5.00E-71//AT2G27080| harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	Unigene14856_All//0.00E+00//gi|31072575|gb|CA992854.1|CA992854		ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport		nr +
Unigene14858_All	1884	1.25	1.61	0.82	1.30	1.72	1.92	7.16	60.63	30.92	3.69E-01	3.22E-01		-6.08E-01	1.61E-01		4.07E-01	2.75E-01		5.66E-01	8.96E-02		3.08E+00	0.00E+00	Up	2.11E+00	1.51E-158	Up	Unigene14858_All//gi|209867508|gb|ACI90292.1|//1.00E-112//WRKY transcription factor [Picrorhiza kurrooa]	Unigene14858_All//1.00E-68//AT1G62300| WRKY6; transcription factor	Unigene14858_All//0.00E+00//CO075151	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene14860_All	827	2.72	1.16	2.64	4.28	4.46	2.46	3.68	1.62	1.49	-1.22E+00	4.90E-03		-4.33E-02	9.33E-01		5.91E-02	8.75E-01		-7.99E-01	1.40E-02		-1.19E+00	2.59E-04	Down	-1.30E+00	4.73E-05	Down	Unigene14860_All//gi|92893902|gb|ABE91952.1|//9.00E-12//Zinc finger, CCHC-type [Medicago truncatula]	Unigene14860_All//4.00E-69//AT2G01050| nucleic acid binding / zinc ion binding	Unigene14860_All//0.00E+00//ES819539				nr -
Unigene14863_All	773	24.71	25.17	23.35	24.23	25.04	32.19	48.68	26.49	23.45	2.69E-02	8.47E-01		-8.12E-02	6.08E-01		4.72E-02	7.97E-01		4.10E-01	1.34E-04		-8.78E-01	2.86E-27		-1.05E+00	9.07E-38	Down	Unigene14863_All//gi|75336159|sp|Q9MA39.1|PS10B_ARATH//1.00E-105//RecName: Full=26S protease regulatory subunit S10B homolog B; AltName: Full=26S proteasome subunit S10B homolog B; AltName: Full=26S proteasome AAA-ATPase subunit RPT4b; AltName: Full=Regulatory particle triple-A ATPase subunit 4b >gi|7767657|gb|AAF69154.1|AC007915_6 F27F5.8 [Arabidopsis thaliana] >gi|17065266|gb|AAL32767.1|similar to 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] >gi|21387177|gb|AAM47992.1| 26S proteasome AAA-ATPase subunit RPT4a-like protein [Arabidopsis thaliana]	Unigene14863_All//1.00E-106//AT1G45000| 26S proteasome regulatory complex subunit p42D, putative	Unigene14863_All//0.00E+00//TC150226		ko03050|Proteasome		nr -
Unigene14864_All	1974	3.82	18.40	7.69	6.28	7.97	11.65	11.87	15.82	14.57	2.27E+00	9.19E-87	Up	1.01E+00	2.80E-11	Up	3.43E-01	1.34E-02		8.90E-01	4.41E-15		4.15E-01	1.41E-06		2.96E-01	8.69E-04		Unigene14864_All//gi|224110308|ref|XP_002315479.1|//1.00E-168//f-box family protein [Populus trichocarpa] >gi|222864519|gb|EEF01650.1| f-box family protein [Populus trichocarpa]	Unigene14864_All//3.00E-161//AT1G16250| kelch repeat-containing F-box family protein	Unigene14864_All//0.00E+00//gi|78344757|gb|DT565031.1|DT565031				nr +
Unigene14866_All	1076	7.29	18.74	10.00	21.20	24.07	23.00	14.11	44.94	23.25	1.36E+00	3.43E-24	Up	4.55E-01	1.28E-02		1.83E-01	1.10E-01		1.17E-01	3.82E-01		1.67E+00	1.96E-94	Up	7.21E-01	1.06E-13		Unigene14866_All//gi|38016521|gb|AAR07596.1|//2.00E-64//fiber protein Fb34 [Gossypium barbadense]	Unigene14866_All//4.00E-55//AT1G61065| unknown protein	Unigene14866_All//0.00E+00//TC160548			GO:0044464	nr -
Unigene14868_All	2161	1.38	0.75	0.96	2.42	2.02	2.07	6.98	3.40	2.25	-8.79E-01	1.49E-02		-5.22E-01	1.72E-01		-2.58E-01	3.61E-01		-2.26E-01	4.51E-01		-1.04E+00	7.86E-15	Down	-1.63E+00	4.79E-30	Down	Unigene14868_All//gi|145323800|ref|NP_001077489.1|//0.00E+00//endomembrane protein 70 family protein [Arabidopsis thaliana]	Unigene14868_All//0.00E+00//AT1G08350| endomembrane protein 70 family protein	Unigene14868_All//0.00E+00//TC162326			GO:0003676//GO:0005198//GO:0005515//GO:0005618//GO:0010467//GO:0016044//GO:0030529//GO:0031224//GO:0031410//GO:0043231	nr +
Unigene14869_All	811	11.10	23.49	13.20	22.79	19.91	25.00	33.73	39.32	33.31	1.08E+00	3.56E-16	Up	2.50E-01	1.98E-01		-1.95E-01	1.59E-01		1.34E-01	3.61E-01		2.21E-01	1.26E-02		-1.83E-02	8.73E-01		Unigene14869_All//gi|15809982|gb|AAL06918.1|//5.00E-13//AT3g10250/F14P13_15 [Arabidopsis thaliana] >gi|18958054|gb|AAL79600.1|AT3g10250/F14P13_15 [Arabidopsis thaliana] >gi|222423631|dbj|BAH19784.1|AT3G10250 [Arabidopsis thaliana]	Unigene14869_All//3.00E-14//AT3G10250| unknown protein	Unigene14869_All//0.00E+00//TC178136				nr -
Unigene14875_All	265	3.95	0.76	4.82	13.35	7.15	11.25	2.55	7.41	2.41	-2.37E+00	2.49E-03		2.88E-01	6.09E-01		-9.01E-01	3.32E-03		-2.47E-01	5.02E-01		1.54E+00	3.87E-04	Up	-8.58E-02	9.15E-01		Unigene14875_All//gi|18404466|ref|NP_565865.1|//5.00E-22//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565090|sp|Q80927.2|ATL2J_ARATH RecName: Full=RING-H2 finger protein ATL2J >gi|20197250|gb|AAC23649.2|Expressed protein [Arabidopsis thaliana] >gi|89111920|gb|ABD60732.1|At2g37580 [Arabidopsis thaliana]	Unigene14875_All//2.00E-23//AT2G37580| zinc finger (C3HC4-type RING finger) family protein	Unigene14875_All//1.00E-145//TC142120			GO:0016740//GO:0046914	nr +
Unigene14876_All	1268	3.59	1.28	2.81	11.28	12.57	9.08	3.07	7.61	3.64	-1.49E+00	7.63E-07	Down	-3.51E-01	2.47E-01		1.57E-01	3.20E-01		-3.12E-01	4.19E-02		1.31E+00	8.08E-14	Up	2.49E-01	3.49E-01		Unigene14876_All//gi|18404466|ref|NP_565865.1|//2.00E-39//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565090|sp|Q80927.2|ATL2J_ARATH RecName: Full=RING-H2 finger protein ATL2J >gi|20197250|gb|AAC23649.2|Expressed protein [Arabidopsis thaliana] >gi|89111920|gb|ABD60732.1|At2g37580 [Arabidopsis thaliana]	Unigene14876_All//8.00E-40//AT2G37580| zinc finger (C3HC4-type RING finger) family protein	Unigene14876_All//0.00E+00//TC142120			GO:0005488	nr +

Unigene14880_All	1498	3.60	6.87	1.17	8.48	8.51	8.05	13.60	6.39	11.89	9.33E-01	2.71E-07		-1.62E+00	1.99E-08	Down	4.40E-03	9.87E-01		-7.51E-02	6.77E-01		-1.09E+00	2.37E-21	Down	-1.95E-01	8.38E-02		Unigene14880_All//gi|87241270|gb|AB033128.1|//4.00E-80//Zinc finger, RING-type; Thioredoxin-related [Medicago truncatula]	Unigene14880_All//1.00E-61//AT2G39720| RHC2A; protein binding / zinc ion binding	Unigene14880_All//0.00E+00//gi|13352102|gb|BG442354.1|BG442354			GO:0005488	nr -
Unigene14883_All	805	8.51	2.96	3.97	4.83	5.99	6.40	0.95	1.04	1.63	-1.53E+00	3.07E-10	Down	-1.10E+00	3.59E-06	Down	3.11E-01	3.06E-01		4.06E-01	1.45E-01		1.35E-01	8.42E-01		7.89E-01	1.19E-01		Unigene14883_All//gi|109255188|gb|ABG27019.1|//6.00E-49//SKP1-like a [Medicago truncatula]	Unigene14883_All//9.00E-47//AT1G75950| SKP1 (S PHASE KINASE-ASSOCIATED PROTEIN 1); protein binding / ubiquitin-protein ligase	Unigene14883_All//0.00E+00//gi|109876603|gb|DW505577.1|DW505577		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0019941	nr -
Unigene14884_All	1278	10.23	9.20	4.13	8.11	7.49	4.59	60.44	50.69	52.99	-1.54E-01	3.64E-01		-1.31E+00	1.66E-14	Down	-1.14E-01	5.81E-01		-8.20E-01	2.31E-06		-2.54E-01	1.80E-06		-1.90E-01	3.27E-04		Unigene14884_All//gi|115500890|dbj|BAF34116.1|//1.00E-135//glycerophosphodiesterase-like protein [Nicotiana tabacum]	Unigene14884_All//9.00E-131//AT1G66970| SVL2 (SHV3-LIKE 2); glycerophosphodiester phosphodiesterase/ kinase	Unigene14884_All//0.00E+00//TC169204		ko00564|Glycerophospholipid metabolism		nr +
Unigene14885_All	1444	3.66	8.21	4.54	3.66	1.88	3.97	2.37	5.18	5.08	1.17E+00	1.42E-11	Up	3.10E-01	2.24E-01		-9.57E-01	7.46E-05		1.19E-01	6.92E-01		1.13E+00	9.41E-09	Up	1.10E+00	1.67E-08	Up	Unigene14885_All//gi|4530126|gb|AA021872.1|//1.00E-135//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene14885_All//6.00E-116//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene14885_All//2.00E-126//TC172433		ko04626|Plant-pathogen interaction		nr +
Unigene14889_All	1935	19.09	10.47	17.45	13.85	10.46	9.06	8.94	9.87	70.64	-8.66E-01	1.77E-21		-1.30E-01	2.07E-01		-4.05E-01	3.25E-05		-6.13E-01	1.63E-09		1.44E-01	2.64E-01		2.98E+00	0.00E+00	Up	Unigene14889_All//gi|283136102|gb|ADB11370.1|//5.00E-81//tau class glutathione transferase GSTU44 [Populus trichocarpa]	Unigene14889_All//1.00E-49//AT3G09270| ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	Unigene14889_All//0.00E+00//ES834524		ko00480|Glutathione metabolism		nr -
Unigene14890_All	1140	16.11	5.07	7.61	22.15	20.15	13.07	4.86	1.58	1.68	-1.67E+00	9.62E-30	Down	-1.08E+00	5.40E-15	Down	-1.37E-01	2.67E-01		-7.61E-01	6.84E-13		-1.62E+00	4.45E-11	Down	-1.53E+00	1.26E-10	Down	Unigene14890_All//gi|115440817|ref|NP_001044688.1|//1.00E-48//Os01g0829400 [Oryza sativa Japonica Group] >gi|15624060|dbj|BAB68113.1| glutaredoxin-like [Oryza sativa Japonica Group] >gi|20160636|dbj|BAB89581.1| glutaredoxin-like [Oryza sativa Japonica Group] >gi|113534219|dbj|BAF06602.1| Os01g0829400 [Oryza sativa Japonica Group]	Unigene14890_All//1.00E-33//AT5G58530| glutaredoxin family protein	Unigene14890_All//0.00E+00//TC169545			GO:0015036//GO:0019725//GO:0043231	nr -
Unigene14891_All	1649	0.89	4.61	2.97	13.38	9.29	8.98	6.74	6.03	5.82	2.38E+00	1.24E-19	Up	1.74E+00	1.58E-08	Up	-5.26E-01	8.68E-07		-5.75E-01	3.66E-07		-1.61E-01	3.68E-01		-2.12E-01	1.83E-01		Unigene14891_All//gi|224079161|ref|XP_002305774.1|//1.00E-128//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222848738|gb|EEE86285.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene14891_All//3.00E-96//AT4G28500| ANAC073 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 73); transcription activator/ transcription factor	Unigene14891_All//0.00E+00//gi|164302197|gb|ES806146.1|ES806146	NAC		GO:0001071//GO:0030528//GO:0043231	nr -
Unigene14892_All	1191	3.03	6.42	5.72	3.35	3.24	3.00	3.98	4.84	4.62	1.08E+00	5.56E-07	Up	9.17E-01	9.42E-05		-4.72E-02	8.80E-01		-1.60E-01	6.42E-01		2.85E-01	2.37E-01		2.15E-01	3.69E-01		Unigene14892_All//gi|297795919|ref|XP_002868844.1|//2.00E-78//pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311679|gb|EFH42103.1| pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14892_All//4.00E-78//AT5G31140| pseudouridine synthase family protein	Unigene14892_All//0.00E+00//TC146904		ko00240|Pyrimidine metabolism	GO:0003676//GO:0004553//GO:0009451//GO:0016866//GO:0043231	nr +
Unigene14894_All	1027	3.36	5.43	2.96	7.03	9.69	15.26	8.93	12.01	4.93	6.91E-01	6.17E-03		-1.86E-01	6.29E-01		4.62E-01	8.98E-03		1.12E+00	5.94E-15	Up	4.26E-01	3.22E-03		-8.59E-01	2.77E-07		Unigene14894_All//gi|238055374|sp|B9SR15.1|U4973_RICCO//1.00E-78//RecName: Full=UPF0497 membrane protein 3	Unigene14894_All//1.00E-63//AT3G55390| integral membrane family protein	Unigene14894_All//0.00E+00//ES840083			GO:0031224//GO:0043231	nr +
Unigene14895_All	475	9.14	25.92	9.08	12.27	16.09	11.79	7.57	8.98	5.79	1.50E+00	2.38E-17	Up	-9.80E-03	9.98E-01		3.91E-01	6.79E-02		-5.76E-02	8.38E-01		2.46E-01	4.09E-01		-3.87E-01	1.81E-01					Unigene14895_All//4.00E-85//gi|73850747|gb|DT459767.1|DT459767				
Unigene14896_All	890	3.59	10.70	3.65	6.44	4.95	4.31	2.95	3.57	2.69	1.58E+00	1.60E-14	Up	2.54E-02	9.60E-01		-3.78E-01	1.34E-01		-5.78E-01	2.00E-02		2.77E-01	4.06E-01		-1.33E-01	6.99E-01					Unigene14896_All//1.00E-95//gi|73850747|gb|DT459767.1|DT459767				
Unigene14898_All	1901	16.65	8.40	7.17	23.92	20.47	16.49	58.00	29.33	24.67	-9.88E-01	6.56E-23		-1.22E+00	1.44E-30	Down	-2.25E-01	3.35E-03		-5.37E-01	1.66E-12		-9.84E-01	9.60E-95		-1.23E+00	3.41E-140	Down	Unigene14898_All//gi|193348591|gb|ACF22775.1|//1.00E-161//monodehydroascorbate reductase [Brachypodium distachyon]	Unigene14898_All//5.00E-120//AT1G63940| monodehydroascorbate reductase, putative	Unigene14898_All//0.00E+00//TC142563		ko00053|Ascorbate and aldarate metabolism		nr -
Unigene14899_All	1770	11.68	10.16	8.27	23.47	19.07	26.15	25.37	11.90	10.80	-2.00E-01	1.23E-01		-4.97E-01	7.01E-05		-3.00E-01	1.13E-04		1.56E-01	6.64E-02		-1.09E+00	3.49E-46	Down	-1.23E+00	1.99E-57	Down	Unigene14899_All//gi|108707354|gb|ABF96149.1|//1.00E-171//Enolase, C-terminal TIM barrel domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene14899_All//0.00E+00//AT2G29560| enolase, putative	Unigene14899_All//0.00E+00//TC137340		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation	GO:0006007//GO:0016836//GO:0043234//GO:0044424//GO:0046872	nr +
Unigene14900_All	361	52.18	28.49	24.49	94.38	86.71	122.23	151.32	78.15	65.33	-8.73E-01	1.77E-11		-1.09E+00	1.37E-15	Down	-1.22E-01	2.39E-01		3.73E-01	1.71E-06		-9.53E-01	5.94E-45		-1.21E+00	6.13E-68	Down	Unigene1490_All//gi|192910712|gb|ACF06464.1|//9.00E-52//ribosomal protein L32 [Elaeis guineensis]	Unigene1490_All//3.00E-43//AT4G18100| 60S ribosomal protein L32 (RPL32A)	Unigene1490_All//0.00E+00//gi|13245034|gb|BE052199.2|BE052199		ko03010|Ribosome		nr -
Unigene14900_All	1570	2.93	0.45	1.63	7.42	8.23	5.70	8.64	1.73	2.26	-2.70E+00	4.76E-14	Down	-8.49E-01	3.88E-03		1.48E-01	4.24E-01		-3.82E-01	2.36E-02		-2.32E+00	2.16E-41	Down	-1.94E+00	4.55E-34	Down	Unigene14900_All//gi|225427213|ref|XP_002280380.1|//1.00E-140//PREDICTED: similar to mitochondrial carrier protein isoform 1 [Vitis vinifera] >gi|225427215|ref|XP_002280391.1| PREDICTED: similar to mitochondrial carrier protein isoform 2 [Vitis vinifera]	Unigene14900_All//7.00E-122//AT5G46800| BOU (A BOUT DE SOUFFLE); binding / transporter	Unigene14900_All//0.00E+00//TC157025				nr +
Unigene14902_All	1251	5.52	4.58	5.66	5.73	5.64	3.94	5.64	2.14	1.46	-2.71E-01	2.45E-01		3.63E-02	8.84E-01		-2.31E-02	9.26E-01		-5.43E-01	1.26E-02		-1.40E+00	2.43E-11	Down	-1.95E+00	3.11E-18	Down	Unigene14902_All//gi|42566148|ref|NP_191821.2|//4.00E-20//sucrose-phosphatase-related [Arabidopsis thaliana] >gi|89000973|gb|ABD59076.1| At3g62620 [Arabidopsis thaliana]	Unigene14902_All//2.00E-21//AT3G62620| sucrose-phosphatase-related	Unigene14902_All//0.00E+00//DW499984				nr +
Unigene14903_All	1509	3.43	6.78	4.02	7.06	11.66	12.03	26.65	76.42	212.90	9.83E-01	7.62E-08		2.29E-01	3.90E-01		7.23E-01	4.84E-09		7.68E-01	1.69E-09		1.52E+00	1.68E-195	Up	3.00E+00	0.00E+00	Up	Unigene14903_All//gi|297836190|ref|XP_002885977.1|//3.00E-77//calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297331817|gb|EFH62236.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene14903_All//1.00E-61//AT2G15760| calmodulin-binding protein	Unigene14903_All//0.00E+00//TC174896			GO:0005515//GO:0016020	nr -
Unigene14905_All	842	36.54	30.75	33.27	44.08	35.46	37.01	17.93	17.72	8.52	-2.49E-01	1.31E-02		-1.35E-01	2.37E-01		-3.14E-01	1.43E-04		-2.52E-01	4.70E-03		-1.66E-02	9.29E-01		-1.07E+00	3.79E-16	Down	Unigene14905_All//gi|13899123|gb|AAK48983.1|AF370556_1//2.00E-43//Unknown protein [Arabidopsis thaliana] >gi|30102854|gb|AAP21345.1| At5g55640 [Arabidopsis thaliana]	Unigene14905_All//1.00E-44//AT5G55640| unknown protein	Unigene14905_All//0.00E+00//TC151083				nr +
Unigene14906_All	1047	0.75	3.15	2.54	3.43	3.26	3.11	2.06	2.16	1.26	2.07E+00	1.28E-07	Up	1.76E+00	5.21E-05	Up	-7.32E-02	8.17E-01		-1.41E-01	6.71E-01		6.59E-02	8.76E-01		-7.14E-01	5.74E-02		Unigene14906_All//gi|30696733|ref|NP_568840.3|//1.00E-36//calmodulin-binding protein [Arabidopsis thaliana]	Unigene14906_All//7.00E-38//AT5G56360| calmodulin-binding protein	Unigene14906_All//2.00E-17//TC147702		ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0031410	nr -
Unigene14908_All	2032	9.91	2.34	4.61	17.01	16.07	9.87	8.05	3.29	3.57	-2.08E+00	1.01E-43	Down	-1.10E+00	6.27E-17	Down	-8.27E-02	4.55E-01		-7.86E-01	2.16E-18		-1.29E+00	2.26E-22	Down	-1.17E+00	5.40E-20	Down	Unigene14908_All//gi|144962158|gb|ABP06278.1|//1.00E-147//ubiquitin ligase [Mirabilis jalapa]	Unigene14908_All//9.00E-130//AT2G28840| ankyrin repeat family protein	Unigene14908_All//0.00E+00//TC163483				nr +
Unigene14909_All	914	60.45	35.04	38.74	91.40	97.01	94.72	122.35	59.77	72.22	-7.87E-01	4.68E-27		-6.42E-01	2.15E-18		8.60E-02	1.66E-01		5.16E-02	4.80E-01		-1.03E+00	3.51E-104	Down	-7.61E-01	5.12E-64		Unigene14909_All//gi|7673355|gb|AAF66823.1|AF190655_1//1.00E-121//poly(A)-binding protein [Nicotiana tabacum]	Unigene14909_All//3.00E-117//AT4G34110| PAB2 (POLY(A) BINDING 2); RNA binding / translation initiation factor	Unigene14909_All//0.00E+00//TC137131		ko03040|Spliceosome		nr -
Unigene1491_All	517	27.63	16.07	15.14	32.28	27.24	37.21	95.68	30.40	32.13	-7.82E-01	1.66E-07		-8.68E-01	2.15E-08		-2.45E-01	8.11E-02		2.05E-01	1.37E-01		-1.65E+00	2.30E-95	Down	-1.57E+00	2.00E-91	Down	Unigene1491_All//gi|148270944|gb|AB925342.1|//8.00E-53//60S ribosomal protein L32A [Cucumis melo]	Unigene1491_All//3.00E-50//AT4G18100| 60S ribosomal protein L32 (RPL32A)	Unigene1491_All//0.00E+00//gi|13352874|gb|BG443222.1|BG443222		ko03010|Ribosome		nr +
Unigene14912_All	917	40.45	23.82	18.52	72.85	74.58	77.13	46.57	19.64	15.64	-7.64E-01	1.47E-17		-1.13E+00	9.77E-32	Down	3.39E-02	6.89E-01		8.24E-02	2.70E-01		-1.25E+00	4.95E-54	Down	-1.57E+00	5.05E-79	Down	Unigene14912_All//gi|77999277|gb|AB816985.1|//1.00E-63//profilin-like protein [Solanum tuberosum]	Unigene14912_All//2.00E-47//AT4G29340| PRF4 (PROFILIN 4); actin binding	Unigene14912_All//0.00E+00//TC167386			GO:0005856//GO:0007010//GO:0008092	nr -
Unigene14913_All	1132	3.37	0.72	1.88	2.77	1.61	1.76	5.19	6.57	2.04	-2.24E+00	1.31E-09	Down	-8.43E-01	1.01E-02		-7.82E-01	1.88E-02		-6.59E-01	6.34E-02		3.40E-01	8.77E-02		-1.35E+00	2.19E-09	Down	Unigene14913_All//gi|92893902|gb|ABE91952.1|//7.00E-24//Zinc finger, CCHC-type [Medicago truncatula]	Unigene14913_All//3.00E-22//AT2G01050| nucleic acid binding / zinc ion binding					nr -
Unigene14914_All	2222	5.35	11.47	6.97	7.49	8.20	9.51	10.58	11.34	10.92	1.10E+00	5.47E-22	Up	3.84E-01	1.03E-02		1.31E-01	3.95E-01		3.45E-01	4.05E-03		1.00E-01	3.95E-01		4.55E-02	6.81E-01		Unigene14914_All//gi|224115768|ref|XP_002322062.1|//0.00E+00//magnesium transporter [Populus trichocarpa] >gi|222831938|gb|EEE70415.1| magnesium transporter [Populus trichocarpa]	Unigene14914_All//0.00E+00//AT1G16010| magnesium transporter CorA-like family protein (MRS2-1)	Unigene14914_All//0.00E+00//gi|21090040|gb|BQ402353.1|BQ402353			GO:0006812//GO:0008324//GO:0044464	nr +
Unigene14916_All	1019	1.54	5.07	2.04	3.18	4.19	4.21	30.41	58.61	63.73	1.72E+00	3.48E-09	Up	4.04E-01	3.93E-01		3.99E-01	1.98E-01		4.06E-01	1.94E-01		9.47E-01	1.93E-48		1.07E+00	2.22E-65	Up	Unigene14916_All//gi|18406390|ref|NP_564747.1|//3.00E-33//ZCF37 [Arabidopsis thaliana] >gi|8778744|gb|AAF79752.1|AC009317_11 T30E16.15 [Arabidopsis thaliana] >gi|6520221|dbj|BAA87954.1| ZCF37 [Arabidopsis thaliana] >gi|89111900|gb|ABD60722.1| At1g59590 [Arabidopsis thaliana]	Unigene14916_All//2.00E-29//AT1G59590| ZCF37					nr +
Unigene14917_All	1800	11.16	34.15	23.49	14.58	16.11	17.11	22.08	17.83	13.50	1.61E+00	6.88E-93	Up	1.07E+00	1.74E-33	Up	1.43E-01	2.04E-01		2.31E-01	2.30E-02		-3.08E-01	4.98E-05		-7.10E-01	8.69E-21		Unigene14917_All//gi|7572929|emb|CAB87430.1|//0.00E+00//alpha-galactosidase-like protein [Arabidopsis thaliana]	Unigene14917_All//0.00E+00//AT3G56310| alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative	Unigene14917_All//0.00E+00//TC139892		ko00561|Glycerolipid metabolism//ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00603|Glycosphingolipid biosynthesis - globo series	GO:0015925//GO:0043167//GO:0043231//GO:0044238	nr +
Unigene14918_All	330	0.16	3.07	0.16	0.91	0.00	0.82	2.31	1.39	1.33	4.28E+00	7.16E-05	Up	2.62E-02	9.95E-01		-9.82E+00	2.02E-02		-1.41E-01	9.21E-01		-7.27E-01	3.32E-01		-7.96E-01	2.52E-01					Unigene14918_All//2.00E-42//CO120387				
Unigene1492_All	904	20.08	15.41	9.07	44.91	38.28	42.92	65.57	36.76	34.24	-3.82E-01	3.56E-03		-1.15E+00	3.06E-16	Down	-2.30E-01	4.88E-03		-6.55E-02	5.42E-01		-8.35E-01	4.16E-39		-9.37E-01	9.98E-49		Unigene1492_All//gi|13877126|gb|AAK43709.1|AF358665_1//6.00E-61//ribosomal protein L32 [Mercurialis annua] >gi|13899053|gb|AAK48948.1|AF370436_1 ribosomal protein L32 [Mercurialis annua] >gi|13899055|gb|AAK48949.1|AF370437_1 ribosomal protein L32 [Mercurialis annua] >gi|13899057|gb|AAK48950.1|AF370438_1 ribosomal protein L32 [Mercurialis annua]	Unigene1492_All//1.00E-55//AT4G18100| 60S ribosomal protein L32 (RPL32A)	Unigene1492_All//0.00E+00//TC156785		ko03010|Ribosome		nr -
Unigene14920_All	864	24.04	73.37	30.20	17.76	25.75	24.83	8.96	15.19	26.84	1.61E+00	1.77E-95	Up	3.29E-01	3.32E-03		5.36E-01	7.20E-07		4.84E-01	2.97E-05		7.62E-01	4.67E-08		1.58E+00	3.30E-43	Up	Unigene14920_All//gi|30023666|gb|AAP13366.1|//6.00E-37//At1g21820 [Arabidopsis thaliana]	Unigene14920_All//3.00E-32//AT1G21830| unknown protein	Unigene14920_All//0.00E+00//gi|164266385|gb|ES830392.1|ES830392				nr -

Unigene14922_All	1003	2.03	1.36	2.18	2.68	2.51	3.87	0.59	1.00	1.71	-5.77E-01	2.05E-01		9.75E-02	8.21E-01		-9.77E-02	8.36E-01		5.30E-01	9.91E-02		7.61E-01	2.28E-01		1.53E+00	8.06E-04	Up	Unigene14922_All//gi|22331742|ref|NP_190771.2|//8.00E-79//F-box family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|160332332|sp|Q8SV01.2|FBW4_ARATH RecName: Full=F-box/WD-40 repeat-containing protein At3g52030	Unigene14922_All//6.00E-70//AT3G52030| F-box family protein / WD-40 repeat family protein	Unigene14922_All//2.00E-125//gi|78325899|gb|DT546173.1|DT546173		ko03022|Basal transcription factors		nr +
Unigene14924_All	1701	3.01	1.55	2.41	6.62	6.11	5.18	12.88	24.67	3.02	-9.61E-01	3.13E-04		-3.23E-01	2.60E-01		-1.15E-01	5.73E-01		-3.54E-01	4.19E-02		9.38E-01	8.84E-34		-2.09E+00	3.52E-60	Down					Unigene14924_All//0.00E+00//C0097114				
Unigene14925_All	1318	4.21	2.38	3.07	16.82	15.78	14.15	8.69	0.32	2.42	-8.20E-01	1.18E-03		-4.55E-01	9.08E-02		-9.19E-02	5.31E-01		-2.49E-01	4.07E-02		-4.78E+00	1.28E-66	Down	-1.85E+00	3.91E-27	Down	Unigene14925_All//gi|134035510|gb|AB047743.1|//1.00E-157//homeobox protein [Gossypium hirsutum]	Unigene14925_All//4.00E-75//AT5G15150| ATHB-3 (ARABIDOPSIS THALIANA HOMEOBOX 3); DNA binding / sequence-specific DNA binding / transcription factor	Unigene14925_All//0.00E+00//TC164378	HB		GO:0003677//GO:0006350//GO:0010468	nr +
Unigene14926_All	452	2.32	4.48	5.30	9.37	4.34	7.59	6.73	7.49	5.64	9.54E-01	3.64E-02		1.20E+00	6.24E-03		-1.11E+00	5.88E-05	Down	-3.03E-01	3.56E-01		1.53E-01	6.26E-01		-2.56E-01	4.34E-01		Unigene14926_All//gi|63147384|gb|AA34165.1|//1.00E-65//At3g14910 [Arabidopsis thaliana] >gi|115646783|gb|ABJ17116.1| At3g14910 [Arabidopsis thaliana]	Unigene14926_All//7.00E-67//AT3G14910| unknown protein	Unigene14926_All//6.00E-161//ES813485				nr -
Unigene14929_All	1036	67.83	93.37	82.86	28.08	31.84	32.30	18.16	36.39	25.65	4.61E-01	1.98E-18		2.89E-01	5.48E-07		1.81E-01	6.60E-02		2.02E-01	4.03E-02		1.00E+00	6.75E-34	Up	4.98E-01	6.38E-08		Unigene14929_All//gi|146424720|dbj|BAF62127.1|//4.00E-58//DnaJ-like protein [Glycine max]	Unigene14929_All//1.00E-50//AT4G13830| J20 (DNAJ-LIKE 20); heat shock protein binding	Unigene14929_All//0.00E+00//TC165429			GO:0005515//GO:0043231//GO:0050896	nr -
Unigene14933_All	1591	1.02	0.70	0.10	5.20	6.06	4.20	4.38	3.36	5.71	-5.41E-01	2.98E-01		-3.34E+00	4.62E-06	Down	2.22E-01	2.88E-01		-3.07E-01	1.54E-01		-3.83E-01	6.04E-02		3.81E-01	2.37E-02		Unigene14933_All//gi|4097587|gb|AAD00119.1|//3.00E-40//NTGP5 [Nicotiana tabacum]	Unigene14933_All//2.00E-40//AT1G22050| MUB6 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 6 PRECURSOR)	Unigene14933_All//4.00E-180//ES811604			GO:0043412	nr -
Unigene14935_All	1057	84.69	38.88	72.95	82.33	71.25	25.42	0.84	1.98	0.41	-1.12E+00	3.44E-78	Down	-2.15E-01	1.82E-04		-2.09E-01	7.54E-05		-1.70E+00	2.90E-154	Down	1.23E+00	2.34E-03		-1.02E+00	1.09E-01		Unigene14935_All//gi|223452302|gb|ACN89479.1|//1.00E-109//cysteine-rich protein [Glycine max]	Unigene14935_All//2.00E-105//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene14935_All//0.00E+00//TC164246		ko04626|Plant-pathogen interaction		nr +
Unigene14936_All	2241	7.63	20.89	18.91	5.65	7.61	13.34	14.62	17.27	12.00	1.45E+00	7.43E-61	Up	1.31E+00	7.64E-46	Up	4.30E-01	8.06E-04		1.24E+00	5.35E-33	Up	2.40E-01	2.26E-03		-2.85E-01	5.72E-04		Unigene14936_All//gi|297793615|ref|XP_002864692.1|//1.00E-102//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310527|gb|EFH40951.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14936_All//1.00E-122//AT5G60580| zinc finger (C3HC4-type RING finger) family protein	Unigene14936_All//0.00E+00//TC145643		ko04141|Protein processing in endoplasmic reticulum	GO:0044464	nr +
Unigene14937_All	2070	0.20	0.83	0.57	0.17	0.32	0.20	0.90	0.93	0.67	2.04E+00	2.81E-04	Up	1.48E+00	3.04E-02		9.08E-01	3.42E-01		2.21E-01	8.63E-01		4.75E-02	9.29E-01		-4.16E-01	3.28E-01		Unigene14937_All//gi|18424371|ref|NP_568923.1|//1.00E-130//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|30697386|ref|NP_851231.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene14937_All//8.00E-108//AT5G60580| zinc finger (C3HC4-type RING finger) family protein	Unigene14937_All//0.00E+00//TC145643		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene14938_All	1114	184.86	106.71	156.12	60.10	67.20	70.66	55.34	22.21	26.68	-7.93E-01	3.23E-100		-2.44E-01	1.29E-11		1.61E-01	7.86E-03		2.34E-01	5.76E-05		-1.32E+00	1.15E-84	Down	-1.05E+00	3.48E-61	Down	Unigene14938_All//gi|1707878|sp|P54260.1|GCST_SOLTU//1.00E-140//RecName: Full=Aminomethyltransferase, mitochondrial; AltName: Full=Glycine cleavage system T protein; Short=GCVT; Flags: Precursor >gi|438254|emb|CAA81081.1| T-protein [Solanum tuberosum]	Unigene14938_All//2.00E-140//AT1G11860| aminomethyltransferase, putative	Unigene14938_All//0.00E+00//gi|164280064|gb|ES809523.1|ES809523		ko00910|Nitrogen metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr -
Unigene14940_All	603	51.54	76.80	57.49	22.97	55.51	34.83	28.61	56.00	70.69	5.76E-01	1.99E-13		1.58E-01	1.30E-01		1.27E+00	4.40E-42	Up	6.01E-01	2.69E-07		9.69E-01	8.01E-29		1.31E+00	3.73E-59	Up	Unigene14940_All//gi|75297894|sp|Q84MB3.1|ACCH1_ARATH//8.00E-78//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene14940_All//5.00E-79//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene14940_All//0.00E+00//gi|109890210|gb|DW519174.1|DW519174		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0008152//GO:0016706//GO:0046914	nr -
Unigene14941_All	1979	6.05	1.46	2.64	7.75	3.79	3.20	11.17	8.17	3.80	-2.05E+00	8.09E-26	Down	-1.20E+00	1.10E-11	Down	-1.03E+00	1.06E-14	Down	-1.28E+00	2.93E-18	Down	-4.51E-01	1.37E-05		-1.55E+00	1.38E-40	Down	Unigene14941_All//gi|15809986|gb|AAL06920.1|//0.00E+00//AT3g19540/T31J18_4 [Arabidopsis thaliana] >gi|22137022|gb|AAM91356.1| At3g19540/T31J18_4 [Arabidopsis thaliana]	Unigene14941_All//0.00E+00//AT3G19540| unknown protein	Unigene14941_All//0.00E+00//TC161168			GO:0009536//GO:0016020	nr -
Unigene14943_All	1246	2.69	2.32	1.15	2.96	3.73	2.94	1.76	3.66	1.28	-2.13E-01	5.55E-01		-1.22E+00	7.26E-04	Down	3.35E-01	2.74E-01		-1.10E-02	9.67E-01		1.05E+00	4.00E-05	Up	-4.64E-01	2.20E-01		Unigene14943_All//gi|124365591|gb|ABN08823.1|//5.00E-71//Thioredoxin domain 2; Thioredoxin fold [Medicago truncatula]	Unigene14943_All//3.00E-71//AT1G08570| ACHT4 (ATYPICAL CYS HIS RICH THIOREDOXIN 4); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	Unigene14943_All//0.00E+00//TC137575			GO:0005488//GO:0009532//GO:0009941//GO:0016667//GO:0019725	nr +
Unigene14944_All	1603	3.30	6.35	2.33	4.51	4.75	4.90	6.67	5.40	15.04	9.47E-01	2.16E-07		-5.04E-01	6.73E-02		7.53E-02	8.02E-01		1.22E-01	6.11E-01		-3.06E-01	5.92E-02		1.17E+00	1.03E-28	Up	Unigene14944_All//gi|30984566|gb|AAP42746.1|//2.00E-54//At4g33890 [Arabidopsis thaliana]	Unigene14944_All//9.00E-56//AT4G33890| unknown protein	Unigene14944_All//0.00E+00//DN800866				nr -
Unigene14945_All	1478	0.46	6.96	0.86	1.25	1.07	1.13	3.18	6.87	27.92	3.92E+00	1.31E-42	Up	9.10E-01	1.46E-01		-2.19E-01	6.59E-01		-1.41E-01	7.68E-01		1.11E+00	2.17E-11	Up	3.14E+00	1.93E-175	Up	Unigene14945_All//gi|259121423|gb|ACV92031.1|//5.00E-96//WRKY transcription factor 29 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene14945_All//5.00E-50//AT4G18170| WRKY28; transcription factor	Unigene14945_All//1.00E-90//AI054555	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0006350//GO:0010468	nr +
Unigene14948_All	1172	2.59	2.77	3.45	4.80	3.85	3.62	4.76	3.67	2.11	9.57E-02	7.79E-01		4.15E-01	2.04E-01		-3.19E-01	2.25E-01		-4.07E-01	1.21E-01		-3.75E-01	1.10E-01		-1.18E+00	2.04E-07	Down	Unigene14948_All//gi|30690667|ref|NP_198101.2|//1.00E-137//integral membrane Yip1 family protein [Arabidopsis thaliana]	Unigene14948_All//2.00E-130//AT5G27490| integral membrane Yip1 family protein	Unigene14948_All//0.00E+00//TC142955				nr -
Unigene14495_All	1098	3.29	3.32	2.52	6.26	4.42	1.52	3.35	2.82	2.18	1.51E-02	9.84E-01		-3.83E-01	2.71E-01		-5.02E-01	1.97E-02		-2.04E+00	4.24E-16	Down	-2.50E-01	4.21E-01		-6.22E-01	2.40E-02		Unigene1495_All//gi|196166341|gb|ACG70793.1|//2.00E-76//SMA9 [Malus x domestica]	Unigene1495_All//2.00E-65//AT5G67200| leucine-rich repeat transmembrane protein kinase, putative	Unigene1495_All//0.00E+00//TC171884				nr +
Unigene14952_All	1031	6.70	5.26	4.24	6.52	9.52	36.88	32.93	58.05	46.72	-3.49E-01	1.29E-01		-6.62E-01	4.38E-03		5.45E-01	1.86E-03		2.50E+00	4.31E-109	Up	8.18E-01	4.37E-38		5.05E-01	6.29E-14		Unigene14952_All//gi|91771911|gb|AB560812.1|//1.00E-128//caffeoyl coenzyme A 3-O-methyltransferase 2 [Leucaena leucocephala] >gi|105671456|gb|ABF74684.1| caffeoyl-CoA-O-methyltransferase [Leucaena leucocephala]	Unigene14952_All//1.00E-125//AT4G34050| caffeoyl-CoA 3-O-methyltransferase, putative	Unigene14952_All//0.00E+00//TC160494		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism//ko00965|Betalain biosynthesis		nr +
Unigene14953_All	1674	0.91	0.09	0.38	1.16	1.69	2.02	2.17	6.29	2.07	-3.32E+00	5.00E-06	Down	-1.25E+00	3.05E-02		5.40E-01	1.62E-01		8.02E-01	1.76E-02		1.53E+00	8.71E-19	Up	-6.91E-02	8.11E-01		Unigene14953_All//gi|21742317|emb|CAD40774.1|//1.00E-118//OSJNBa0039H02.5 [Oryza sativa (japonica cultivar-group)] >gi|38347155|emb|CAE05145.2| OSJNBa0039C07.1 [Oryza sativa (japonica cultivar-group)]	Unigene14953_All//1.00E-26//AT1G28080| unknown protein	Unigene14953_All//6.00E-16//gi|3326717|gb|AI055603.1|AI055603				nr -
Unigene14954_All	1116	2.67	2.77	1.72	15.13	15.64	13.72	5.72	2.58	3.07	5.16E-02	8.93E-01		-6.38E-01	9.30E-02		4.80E-02	8.07E-01		-1.41E-01	3.85E-01		-1.15E+00	8.80E-08	Down	-8.98E-01	1.09E-05		Unigene14954_All//gi|2224892|gb|AAB64346.1|//1.00E-94//gibberellin 7-oxidase [Cucurbita maxima]	Unigene14954_All//3.00E-27//AT3G19010| oxidoreductase, 20G-Fe(II) oxygenase family protein	Unigene14954_All//0.00E+00//gi|109877027|gb|DW506001.1|DW506001		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr +
Unigene14955_All	1170	20.17	3.33	13.15	8.39	4.12	3.28	2.75	2.29	0.48	-2.60E+00	1.10E-66	Down	-6.17E-01	1.02E-07		-1.03E+00	1.70E-09	Down	-1.35E+00	6.28E-13	Down	-2.65E-01	4.30E-01		-2.53E+00	9.47E-12	Down	Unigene14955_All//gi|1770305|emb|CAA92278.1|//1.00E-132//1,3-beta-glucanase [Gossypium hirsutum]	Unigene14955_All//1.00E-96//AT3G57240| BG3 (BETA-1,3-GLUCANASE 3); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene14955_All//0.00E+00//TC170841		ko00500|Starch and sucrose metabolism		nr -
Unigene14956_All	2094	9.09	2.15	2.01	14.75	10.36	14.95	20.37	5.23	8.16	-2.08E+00	2.55E-41	Down	-2.18E+00	3.58E-42	Down	-5.10E-01	8.89E-09		1.92E-02	8.85E-01		-1.96E+00	4.95E-104	Down	-1.32E+00	9.74E-61	Down	Unigene14956_All//gi|18400195|ref|NP_566466.1|//0.00E+00//HSP60-3A (HEAT SHOCK PROTEIN 60-3A); ATP binding / protein binding [Arabidopsis thaliana] >gi|85718628|sp|Q9SZW7.2|CH60C_ARATH RecName: Full=Chaperonin CPN60-like 2, mitochondrial; AltName: Full=HSP60-like 2; Flags: Precursor >gi|9294610|dbj|BAB02911.1| chaperonin; similar to GroEL protein [Arabidopsis thaliana] >gi|20453166|gb|AAM19824.1| AT3g13860/MCP4_7 [Arabidopsis thaliana] >gi|53850565|gb|AAL95459.1| At3g13860 [Arabidopsis thaliana]	Unigene14956_All//0.00E+00//AT3G13860| HSP60-3A (HEAT SHOCK PROTEIN 60-3A); ATP binding / protein binding	Unigene14956_All//0.00E+00//TC130528		ko03018|RNA degradation	GO:0005515//GO:0006457//GO:0010038//GO:0016020//GO:0032559//GO:0043231	nr +
Unigene14957_All	949	146.54	52.70	99.09	149.50	163.14	222.82	384.75	147.28	233.57	-1.48E+00	7.08E-185	Down	-5.65E-01	3.02E-36		1.26E-01	1.98E-03		5.76E-01	4.20E-63		-1.39E+00	0.00E+00	Down	-7.20E-01	2.35E-188		Unigene14957_All//gi|2098711|gb|AAB57670.1|//1.00E-105//pectinesterase [Citrus sinensis]	Unigene14957_All//5.00E-79//AT1G53830| ATPME2; pectinesterase	Unigene14957_All//0.00E+00//gi|164313237|gb|ES846876.1|ES846876		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005576//GO:0005618//GO:0030234//GO:0044424//GO:0045229//GO:0051707//GO:0071555	nr +
Unigene14958_All	1075	17.38	7.16	5.45	1.48	1.03	0.50	0.00	0.00	0.00	-1.28E+00	1.52E-20	Down	-1.67E+00	3.60E-29	Down	-5.33E-01	3.18E-01		-1.56E+00	4.07E-03		null	null		null	null		Unigene14958_All//gi|45861623|gb|AAS78640.1|//7.00E-90//MAP3Ka [Solanum lycopersicum]	Unigene14958_All//4.00E-88//AT1G53570| MAP3KA; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene14958_All//0.00E+00//TC142063		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0016628//GO:0032559	nr -
Unigene14959_All	1952	8.23	2.75	5.27	1.28	0.41	0.32	0.00	0.00	0.04	-1.58E+00	3.42E-24	Down	-6.44E-01	7.20E-06		-1.65E+00	2.41E-05	Down	-1.98E+00	5.65E-06	Down	null	null		5.35E+00	4.05E-01		Unigene14959_All//gi|45861623|gb|AAS78640.1|//1.00E-138//MAP3Ka [Solanum lycopersicum]	Unigene14959_All//3.00E-116//AT1G53570| MAP3KA; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene14959_All//0.00E+00//TC142063		ko04626|Plant-pathogen interaction		nr +
Unigene1496_All	1991	7.54	3.72	4.15	17.34	12.21	7.67	4.82	2.16	2.78	-1.02E+00	7.23E-12	Down	-8.63E-01	1.01E-08		-5.06E-01	1.27E-09		-1.18E+00	1.59E-35	Down	-1.16E+00	1.89E-11	Down	-7.93E-01	9.87E-07		Unigene1496_All//gi|75163506|sp|Q93106.1|Y5720_ARATH//0.00E+00//RecName: Full=Probable inactive receptor kinase At5g67200; Flags: Precursor >gi|166490055|gb|AAL24379.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|28059128|gb|AAO30018.1| receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene1496_All//0.00E+00//AT5G67200| leucine-rich repeat transmembrane protein kinase, putative	Unigene1496_All//0.00E+00//TC171884		ko04626|Plant-pathogen interaction		nr +
Unigene14960_All	1759	2.89	0.35	1.54	0.20	0.33	0.00	0.00	0.00	0.00	-3.06E+00	1.79E-17	Down	-9.02E-01	1.18E-03		7.48E-01	4.81E-01		-7.63E+00	2.13E-02		null	null		null	null		Unigene14960_All//gi|45861623|gb|AAS78640.1|//1.00E-140//MAP3Ka [Solanum lycopersicum]	Unigene14960_All//2.00E-117//AT1G53570| MAP3KA; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene14960_All//0.00E+00//TC142063		ko04626|Plant-pathogen interaction		nr -

Unigene14962_All	2200	1.52	0.74	0.51	3.40	3.80	2.94	4.09	0.72	1.52	-1.05E+00	2.17E-03		-1.58E+00	2.43E-05	Down	1.63E-01	5.00E-01		-2.10E-01	4.00E-01		-2.50E+00	3.21E-30	Down	-1.43E+00	3.91E-15	Down	Unigene14962_All//gi|115452545|ref|NP_001049873.1|//2.00E-88//0s03g0302900 [Oryza sativa Japonica Group] >gi|108707707|gb|ABF95502.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548344|dbj|BAF11787.1| Os03g0302900 [Oryza sativa Japonica Group]	Unigene14962_All//1.00E-29//AT5G26910| unknown protein	Unigene14962_All//0.00E+00//D8454754				nr +
Unigene14963_All	987	39.23	36.81	26.76	60.87	43.79	48.23	175.33	118.87	81.37	-9.18E-02	3.62E-01		-5.52E-01	3.92E-10		-4.75E-01	1.18E-14		-3.36E-01	3.27E-07		-5.61E-01	3.03E-56		-1.11E+00	6.42E-185	Down	Unigene14963_All//gi|17297979|dbj|BAB78487.1|//1.00E-108//26S proteasome regulatory particle non-ATPase subunit8 [Oryza sativa Japonica Group]	Unigene14963_All//9.00E-109//AT5G05780| RPN8A (RP NON-ATPASE SUBUNIT 8A)	Unigene14963_All//0.00E+00//TC152606		ko03050|Proteasome	GO:0043234	nr -
Unigene14964_All	945	15.67	20.59	26.37	52.71	37.71	16.34	52.79	24.15	8.31	3.94E-01	1.74E-03		7.51E-01	3.27E-11		-4.83E-01	1.37E-12		-1.69E+00	5.50E-88	Down	-1.13E+00	5.59E-54	Down	-2.67E+00	2.45E-182	Down	Unigene14964_All//gi|223452524|gb|ACM89589.1|//4.00E-74//leucine-rich repeat protein [Glycine max]	Unigene14964_All//1.00E-60//AT5G21090| leucine-rich repeat protein, putative	Unigene14964_All//0.00E+00//TC135179		ko04626|Plant-pathogen interaction	GO:0005488//GO:0008152//GO:0009987//GO:0016628//GO:0016772//GO:0023060//GO:0044464	nr -
Unigene14966_All	1229	3.28	75.78	2.51	5.31	3.67	13.12	46.55	92.84	143.67	4.53E+00	0.00E+00	Up	-3.83E-01	2.42E-01		-5.33E-01	1.56E-02		1.31E+00	1.85E-19	Up	9.96E-01	6.59E-100		1.63E+00	0.00E+00	Up	Unigene14966_All//gi|222139394|gb|ACM45716.1|//1.00E-124//class IV chitinase [Pyrus pyrifolia]	Unigene14966_All//4.00E-111//AT3G54420| ATEP3; chitinase	Unigene14966_All//0.00E+00//TC131593		ko00520|Amino sugars and nucleotide sugar metabolism		nr -
Unigene14967_All	670	21.16	10.44	19.63	33.31	31.40	43.07	43.79	23.71	29.49	-1.02E+00	3.17E-11	Down	-1.08E-01	5.40E-01		-8.50E-02	5.47E-01		3.71E-01	1.88E-04		-8.86E-01	9.22E-22		-5.70E-01	7.38E-11		Unigene14967_All//gi|587562|emb|CAA56520.1|//3.00E-56//mitochondrial processing peptidase [Solanum tuberosum]	Unigene14967_All//4.00E-44//AT1G51980| mitochondrial processing peptidase alpha subunit, putative	Unigene14967_All//0.00E+00//gi|109847819|gb|DW476799.1|DW476799			GO:0004175//GO:0005746//GO:0006970//GO:0009536//GO:0019538//GO:0032559//GO:0046914	nr -
Unigene14970_All	695	3.76	9.04	6.97	3.58	12.93	6.11	14.78	35.00	63.57	1.26E+00	2.84E-07	Up	8.89E-01	1.81E-03		1.85E+00	1.79E-19	Up	7.69E-01	9.03E-03		1.24E+00	5.34E-31	Up	2.10E+00	5.44E-120	Up	Unigene14970_All//gi|283132359|dbj|BAI63585.1|//8.00E-31//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene14970_All//4.00E-31//AT4G38470| protein kinase family protein	Unigene14970_All//8.00E-112//TC176323			GO:0004713//GO:0006464//GO:0031406//GO:0032559//GO:0043231//GO:0044464	nr -
Unigene14976_All	960	5.61	1.53	2.44	15.93	7.86	9.17	160.53	142.63	57.85	-1.87E+00	1.00E-10	Down	-1.20E+00	1.21E-05	Down	-1.02E+00	2.13E-14	Down	-7.96E-01	1.16E-08		-1.71E-01	4.59E-06		-1.47E+00	1.09E-256	Down	Unigene14976_All//gi|15232856|ref|NP_189427.1|//3.00E-86//NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN reductase [Arabidopsis thaliana] >gi|75273736|sp|Q9LK88.1|NQR_ARATH RecName: Full=NADPH:quinone oxidoreductase >gi|11994494|dbj|BAB02535.1| NADPH:quinone oxidoreductase [Arabidopsis thaliana] >gi|88193780|gb|ABD42979.1| At3g27890 [Arabidopsis thaliana]	Unigene14976_All//1.00E-87//AT3G27890| NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN reductase	Unigene14976_All//0.00E+00//TC138053			GO:0006952//GO:0006970//GO:0008152//GO:0009532//GO:0016020//GO:0016646//GO:0016655//GO:0042579//GO:0046914	nr -
Unigene14977_All	974	1.56	1.56	1.48	4.04	4.21	3.01	5.86	2.15	4.46	2.70E-03	9.97E-01		-7.77E-02	8.89E-01		5.84E-02	8.71E-01		-4.23E-01	1.93E-01		-1.45E+00	9.03E-10	Down	-3.95E-01	7.14E-02		Unigene14977_All//gi|3785977|gb|AAC67324.1|//2.00E-65//similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana] >gi|20260420|gb|AAM13108.1| similar to axi 1 protein [Arabidopsis thaliana] >gi|22136280|gb|AAM91218.1| similar to axi 1 protein [Arabidopsis thaliana] >gi|110742513|dbj|BAE99174.1| similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana]	Unigene14977_All//2.00E-66//AT2G01480| unknown protein	Unigene14977_All//0.00E+00//TC162164				nr +
Unigene14979_All	523	1.50	4.75	1.12	2.38	2.37	3.54	6.06	3.68	3.58	1.66E+00	1.26E-04	Up	-4.22E-01	6.21E-01		-6.60E-03	9.73E-01		5.72E-01	2.58E-01		-7.22E-01	2.05E-02		-7.60E-01	1.12E-02		Unigene14979_All//gi|63025168|gb|AAY27057.1|//9.00E-60//At5g40550 [Arabidopsis thaliana] >gi|87116622|gb|ABD19675.1| At5g40550 [Arabidopsis thaliana]	Unigene14979_All//2.00E-41//AT5G40550| unknown protein	Unigene14979_All//1.00E-149//ES826441			GO:0043231	nr +
Unigene14982_All	1049	30.52	126.07	80.66	26.88	32.04	46.02	10.80	18.41	21.95	2.05E+00	4.34E-276	Up	1.40E+00	2.87E-101	Up	2.53E-01	5.51E-03		7.76E-01	1.07E-24		7.69E-01	1.23E-11		1.02E+00	3.11E-22	Up	Unigene14982_All//gi|18397715|ref|NP_566293.1|//1.00E-84//glycine-rich protein [Arabidopsis thaliana]	Unigene14982_All//2.00E-22//AT3G06780| glycine-rich protein	Unigene14982_All//0.00E+00//TC147608				nr +
Unigene14985_All	526	11.54	114.83	38.98	60.61	62.65	243.59	3.86	25.51	4.01	3.31E+00	2.96E-216	Up	1.76E+00	2.61E-34	Up	4.78E-02	7.00E-01		2.01E+00	2.14E-280	Up	2.72E+00	6.41E-49	Up	5.71E-02	9.00E-01		Unigene14985_All//gi|15228790|ref|NP_191814.1|//1.00E-114//universal stress protein (USP) family protein [Arabidopsis thaliana]	Unigene14985_All//3.00E-15//AT3G62550| universal stress protein (USP) family protein	Unigene14985_All//2.00E-121//TC150561			GO:0043231//GO:0050896	nr +
Unigene14986_All	809	36.93	231.43	108.61	191.31	239.09	459.34	12.07	62.05	20.73	2.65E+00	0.00E+00	Up	1.56E+00	7.81E-123	Up	3.22E-01	3.64E-22		1.26E+00	0.00E+00	Up	2.36E+00	4.02E-154	Up	7.80E-01	9.70E-11		Unigene14986_All//gi|15228790|ref|NP_191814.1|//1.00E-65//universal stress protein (USP) family protein [Arabidopsis thaliana]	Unigene14986_All//7.00E-47//AT3G62550| universal stress protein (USP) family protein	Unigene14986_All//0.00E+00//TC150561			GO:0043231//GO:0050896	nr -
Unigene1499_All	1086	8.14	7.47	9.46	11.01	10.18	6.15	33.29	25.59	13.32	-1.25E-01	5.67E-01		2.17E-01	2.78E-01		-1.13E-01	5.64E-01		-8.39E-01	1.67E-07		-3.79E-01	1.81E-06		-1.32E+00	9.99E-52	Down	Unigene1499_All//gi|195624638|gb|ACG34149.1|//6.00E-70//catalytic/ protein phosphatase type 2C [Zea mays]	Unigene1499_All//5.00E-71//AT5G06750| protein phosphatase 2C family protein / PP2C family protein	Unigene1499_All//0.00E+00//ES807349				nr +
Unigene14990_All	1844	4.91	11.54	4.01	5.75	7.02	5.39	9.45	13.17	60.45	1.23E+00	5.61E-22	Up	-2.90E-01	1.64E-01		2.87E-01	7.63E-02		-9.47E-02	6.50E-01		4.79E-01	1.14E-06		2.68E+00	0.00E+00	Up	Unigene14990_All//gi|253760736|ref|XP_002489002.1|//9.00E-08//hypothetical protein SORBIDRAFT_0531s002010 [Sorghum bicolor] >gi|241947361|gb|EES20506.1| hypothetical protein SORBIDRAFT_0531s002010 [Sorghum bicolor]		Unigene14990_All//1.00E-103//TC148938				nr -
Unigene14991_All	965	30.25	83.38	41.33	109.13	99.74	84.29	71.33	58.25	72.54	1.46E+00	3.05E-105	Up	4.50E-01	2.08E-07		-1.30E-01	1.08E-02		-3.73E-01	1.24E-14		-2.92E-01	2.13E-07		2.42E-02	7.14E-01		Unigene14991_All//gi|297807405|ref|XP_002871586.1|//3.00E-54//glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317423|gb|EFH47845.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene14991_All//1.00E-43//AT5G13810| glutaredoxin family protein	Unigene14991_All//0.00E+00//TC139136			GO:0015036//GO:0019725	nr -
Unigene14993_All	845	99.19	50.85	53.00	152.92	126.49	363.66	165.72	80.08	91.70	-9.64E-01	3.83E-57		-9.04E-01	1.20E-49		-2.74E-01	2.83E-11		1.25E+00	0.00E+00	Up	-1.05E+00	1.65E-133	Down	-8.54E-01	2.20E-97		Unigene14993_All//gi|14699030|gb|AAB05224.1|//2.00E-63//fiber-specific acyl carrier protein [Gossypium hirsutum]	Unigene14993_All//5.00E-33//AT1G54580| ACP2 (ACYL CARRIER PROTEIN 2); acyl carrier	Unigene14993_All//0.00E+00//TC150445		ko00190|Oxidative phosphorylation	GO:0006631//GO:0009536//GO:0016597//GO:0022892	nr +
Unigene14994_All	1292	33.49	14.71	16.57	29.23	32.49	26.43	15.74	7.76	10.48	-1.19E+00	1.31E-41	Down	-1.02E+00	2.99E-31	Down	1.53E-01	8.25E-02		-1.45E-01	1.34E-01		-1.02E+00	3.47E-19	Down	-5.86E-01	3.74E-08		Unigene14994_All//gi|297840125|ref|XP_002887944.1|//2.00E-84//protease-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333785|gb|EFH64203.1| protease-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene14994_All//1.00E-84//AT1G63690| protease-associated (PA) domain-containing protein	Unigene14994_All//0.00E+00//gi|73851916|gb|DT460936.1|DT460936			GO:0004175//GO:0031224	nr -
Unigene14995_All	918	8.09	3.26	3.42	27.89	17.56	19.83	19.21	6.92	3.82	-1.31E+00	5.68E-09	Down	-1.24E+00	7.06E-08	Down	-6.68E-01	1.10E-11		-4.92E-01	2.34E-06		-1.47E+00	3.34E-29	Down	-2.33E+00	1.55E-55	Down	Unigene14995_All//gi|1381676|gb|AAB97114.1|//1.00E-100//small GTP-binding protein [Glycine max]	Unigene14995_All//7.00E-97//AT5G65270| ArRABA4a (Arabidopsis Rab GTPase homolog A4a); GTP binding	Unigene14995_All//0.00E+00//EV490755			GO:0003824//GO:0006810//GO:0016020//GO:0032561//GO:0035556	nr -
Unigene14997_All	918	76.94	18.38	22.16	62.95	33.05	21.70	22.25	2.73	5.16	-2.07E+00	1.59E-150	Down	-1.80E+00	1.05E-120	Down	-9.30E-01	1.08E-45		-1.54E+00	6.12E-89	Down	-3.03E+00	7.01E-83	Down	-2.11E+00	1.07E-56	Down	Unigene14997_All//gi|4335763|gb|AAD17440.1|//5.00E-80//expressed protein [Arabidopsis thaliana] >gi|29028804|gb|AAO64781.1| At2g03350 [Arabidopsis thaliana]	Unigene14997_All//2.00E-81//AT2G03350| unknown protein	Unigene14997_All//0.00E+00//TC140962				nr +
Unigene14999_All	1939	1.62	0.68	1.07	3.31	3.73	2.52	3.21	0.26	0.78	-1.25E+00	5.13E-04	Down	-5.96E-01	1.08E-01		1.70E-01	5.19E-01		-3.98E-01	1.01E-01		-3.63E+00	3.81E-30	Down	-2.04E+00	4.18E-17	Down	Unigene14999_All//gi|15222383|ref|NP_177119.1|//1.00E-91//structural constituent of ribosome [Arabidopsis thaliana]	Unigene14999_All//2.00E-92//AT1G69610| structural constituent of ribosome	Unigene14999_All//4.00E-51//DW490979			GO:0005622	nr -
Unigene15000_All	963	3.64	1.53	2.93	14.23	9.76	7.32	14.27	7.68	11.09	-1.25E+00	2.13E-04	Down	-3.13E-01	3.97E-01		-5.43E-01	1.13E-04		-9.59E-01	1.69E-10		-8.93E-01	8.97E-11		-3.64E-01	6.17E-03		Unigene15000_All//gi|30017251|gb|AAP12859.1|//8.00E-39//At3g16330 [Arabidopsis thaliana]	Unigene15000_All//4.00E-40//AT3G16330| unknown protein	Unigene15000_All//0.00E+00//TC137524				nr -
Unigene15002_All	1194	0.92	1.19	0.54	1.63	0.40	1.06	1.84	2.66	1.20	3.69E-01	5.15E-01		-7.82E-01	2.47E-01		-2.01E+00	1.88E-05	Down	-6.20E-01	1.97E-01		5.31E-01	9.39E-02		-6.16E-01	9.86E-02		Unigene15002_All//gi|18415785|ref|NP_568191.1|//2.00E-78//ATSTE14B; protein-S-isoprenylcysteine O-methyltransferase [Arabidopsis thaliana] >gi|75163228|sp|Q93W54.1|ICMTB_ARATH RecName: Full=Protein-S-isoprenylcysteine O-methyltransferase B; Short=AtICMTB; AltName: Full=Isoprenylcysteine carboxylmethyltransferase B; AltName: Full=Prenylcysteine carboxyl methyltransferase B; AltName: Full=Prenylated protein carboxyl methyltransferase B	Unigene15002_All//9.00E-80//AT5G08335| ATSTE14B; protein-S-isoprenylcysteine O-methyltransferase	Unigene15002_All//0.00E+00//ES835293			GO:0003880//GO:0006479//GO:0009738//GO:0009791//GO:0031224//GO:0031410//GO:0043231//GO:0048513	nr -
Unigene15007_All	828	22.50	169.51	79.42	21.78	98.90	92.02	23.18	41.09	57.59	2.91E+00	0.00E+00	Up	1.82E+00	7.11E-115	Up	2.18E+00	4.40E-218	Up	2.08E+00	1.37E-174	Up	8.26E-01	2.39E-22		1.31E+00	1.14E-66	Up	Unigene15007_All//gi|297843644|ref|XP_002889703.1|//3.00E-32//thioredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335545|gb|EFH65962.1| thioredoxin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15007_All//1.00E-31//AT1G08570| ACHT4 (ATYPICAL CYS HIS RICH THIOREDOXIN 4); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	Unigene15007_All//0.00E+00//TC158664			GO:0009532//GO:0009941//GO:0016667	nr +
Unigene15008_All	832	2.58	1.89	1.28	3.47	2.52	1.63	4.68	1.36	1.92	-4.50E-01	3.16E-01		-1.01E+00	2.88E-02		-4.60E-01	2.19E-01		-1.09E+00	2.96E-03		-1.79E+00	4.92E-09	Down	-1.29E+00	3.97E-06	Down	Unigene15008_All//gi|42562387|ref|NP_174198.2|//1.00E-59//apoptosis inhibitory 5 (AP15) family protein [Arabidopsis thaliana]	Unigene15008_All//8.00E-61//AT1G29030| apoptosis inhibitory 5 (AP15) family protein	Unigene15008_All//0.00E+00//ES812012			GO:0043066	nr +
Unigene1501_All	1464	0.57	1.52	2.00	0.54	1.36	0.93	2.80	3.00	2.18	1.41E+00	1.60E-03		1.81E+00	1.32E-05	Up	1.33E+00	3.95E-03		7.66E-01	2.05E-01		9.77E-02	7.32E-01		-3.64E-01	1.75E-01		Unigene1501_All//gi|195624638|gb|ACG34149.1|//6.00E-61//catalytic/ protein phosphatase type 2C [Zea mays]	Unigene1501_All//6.00E-62//AT5G06750| protein phosphatase 2C family protein / PP2C family protein	Unigene1501_All//0.00E+00//gi|164360009|gb|ES807349.1|ES807349				nr +
Unigene15013_All	1116	0.98	4.09	1.34	8.35	9.69	10.00	8.03	13.56	21.85	2.05E+00	3.50E-10	Up	4.41E-01	4.26E-01		2.15E-01	2.68E-01		2.60E-01	1.61E-01		7.55E-01	4.93E-09		1.44E+00	9.95E-40	Up	Unigene15013_All//gi|30686351|ref|NP_850622.1|//5.00E-91//SGP2; GTP binding [Arabidopsis thaliana] >gi|22316556|emb|CAD44270.1| monomeric G-protein [Arabidopsis thaliana]	Unigene15013_All//7.00E-81//AT3G21700| SGP2; GTP binding	Unigene15013_All//0.00E+00//TC129900			GO:0032561//GO:0035556//GO:0044464	nr +

Unigene15015_All	1289	3.17	0.98	1.40	3.21	2.11	3.85	3.67	1.43	2.57	-1.69E+00	2.74E-07	Down	-1.17E+00	2.59E-04	Down	-6.04E-01	3.58E-02		2.65E-01	3.95E-01		-1.36E+00	1.37E-07	Down	-5.18E-01	3.05E-02		Unigene15015_All//gi|15217597|ref|NP_177330.1|//3.00E-92//ubiquitin thiolesterase [Arabidopsis thaliana] >gi|7239512|gb|AAF43238.1|AC012654_22 Strong similarity to the higher plant tyrosine-specific protein phosphatases (PTPs) from A. thaliana gi|3413424 expressed during embryogenesis [Arabidopsis thaliana]	Unigene15015_All//9.00E-83//AT1G71850| ubiquitin thiolesterase	Unigene15015_All//0.00E+00//gi|84170841|gb|DR459489.1|DR459489			GO:0043231	nr +
Unigene15016_All	647	1.78	5.87	2.06	4.16	2.71	3.84	7.97	12.40	11.58	1.72E+00	5.68E-07	Up	2.10E-01	7.07E-01		-6.15E-01	1.01E-01		-1.15E-01	7.73E-01		6.38E-01	4.68E-04		5.38E-01	3.63E-03		Unigene15016_All//gi|115472189|ref|NP_001059693.1|//3.00E-17//Os07g0495100 [Oryza sativa Japonica Group] >gi|113611229|dbj|BAF21607.1|Os07g0495100 [Oryza sativa Japonica Group]	Unigene15016_All//3.00E-18//AT5G47080| CKB1; protein kinase regulator	Unigene15016_All//0.00E+00//TC179417		ko04712|Circadian rhythm - plant	GO:0005488//GO:0006464//GO:0016772//GO:0019207//GO:0043234	nr +
Unigene15018_All	925	21.44	5.70	16.46	31.07	21.37	6.59	5.71	5.42	3.10	-1.91E+00	1.39E-38	Down	-3.81E-01	3.36E-03		-5.40E-01	4.55E-09		-2.24E+00	4.89E-74	Down	-7.55E-02	7.68E-01		-8.82E-01	9.70E-05		Unigene15018_All//gi|150036253|gb|AB867416.1|//5.00E-53//cyclin-dependent kinase [Cucumis melo]	Unigene15018_All//5.00E-40//AT3G05327| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Negative regulatory factor PREG (InterPro:IPR012389), Cyclin-like (InterPro:IPR011028), Cyclin-related 2 (InterPro:IPR013922); BEST Arabidopsis thaliana protein match is: CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase (TAIR:AT2G41740.1); Has 846 Blast hits to 846 proteins in 152 species: Archae - 0; Bacteria - 16; Metazoa - 172; Fungi - 322; Plants - 130; Viruses - 0; Other Eukaryotes - 206 (source: NCBI BLink).	Unigene15018_All//0.00E+00//TC159198			GO:0016772	nr +
Unigene15019_All	915	13.90	7.97	13.73	5.99	6.77	2.12	0.55	0.23	0.04	-8.01E-01	4.96E-07		-1.68E-02	9.40E-01		1.78E-01	5.40E-01		-1.50E+00	1.33E-08	Down	-1.28E+00	1.86E-01		-3.67E+00	3.75E-03		Unigene15019_All//gi|116310078|emb|CAM67099.1|//6.00E-77//H0818E04.16 [Oryza sativa (indica cultivar-group)]	Unigene15019_All//2.00E-76//AT5G65400| unknown protein	Unigene15019_All//0.00E+00//TC1319917			GO:0016638//GO:0042579//GO:0042816	nr -
Unigene15024_All	1082	1.16	4.40	3.45	1.89	2.01	1.88	1.17	1.00	1.03	1.92E+00	8.44E-10	Up	1.57E+00	7.86E-06	Up	8.70E-02	8.62E-01		-7.10E-03	9.82E-01		-2.23E-01	6.77E-01		-1.85E-01	7.13E-01		Unigene15024_All//gi|115448041|ref|NP_001047800.1|//7.00E-27//Os02g0693200 [Oryza sativa Japonica Group] >gi|41052991|dbj|BAD07900.1| DnaJ protein-like [Oryza sativa Japonica Group] >gi|41053274|dbj|BAD07700.1| DnaJ protein-like [Oryza sativa Japonica Group] >gi|113537331|dbj|BAF09714.1|Os02g0693200 [Oryza sativa Japonica Group]	Unigene15024_All//3.00E-18//AT5G16650| DNAJ heat shock N-terminal domain-containing protein	Unigene15024_All//9.00E-48//gi|164358799|gb|ES850295.1|ES850295			GO:0005515//GO:0044267	nr -
Unigene15025_All	964	94.55	41.00	68.50	26.82	28.97	21.32	9.78	3.25	4.63	-1.21E+00	5.05E-89	Down	-4.65E-01	5.38E-17		1.11E-01	3.59E-01		-3.31E-01	1.90E-03		-1.59E+00	8.98E-18	Down	-1.08E+00	1.68E-10	Down	Unigene15025_All//gi|297811059|ref|XP_002873413.1|//1.00E-128//inorganic pyrophosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319250|gb|EFH49672.1|inorganic pyrophosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15025_All//2.00E-127//AT5G09650| AtPPa6 (Arabidopsis thaliana pyrophosphorylase 6); inorganic diphosphatase/ pyrophosphatase	Unigene15025_All//0.00E+00//CO091152		ko00190|Oxidative phosphorylation	GO:0006793//GO:0016462//GO:0044424	nr -
Unigene15027_All	963	3.86	1.21	3.87	10.24	9.65	11.30	8.78	5.21	4.67	-1.67E+00	1.25E-06	Down	4.90E-03	1.00E+00		-8.52E-02	7.02E-01		1.42E-01	4.88E-01		-7.54E-01	2.14E-05		-9.10E-01	2.20E-07		Unigene15027_All//gi|42566947|ref|NP_193639.2|//1.00E-122//EDR2; lipid binding [Arabidopsis thaliana]	Unigene15027_All//5.00E-123//AT4G19040| EDR2; lipid binding	Unigene15027_All//1.00E-145//ES849920				nr +
Unigene15029_All	2586	1.76	1.84	0.62	1.46	1.45	0.98	8.53	11.36	14.20	6.54E-02	8.13E-01		-1.51E+00	1.33E-06	Down	-1.25E-02	9.62E-01		-5.82E-01	6.95E-02		4.13E-01	3.39E-06		7.35E-01	2.47E-20		Unigene15029_All//gi|15239497|ref|NP_200989.1|//1.00E-157//ATEXO70E2 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN E2); protein binding [Arabidopsis thaliana] >gi|79331752|ref|NP_001032116.1|ATEXO70E2 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN E2); protein binding [Arabidopsis thaliana] >gi|9759448|dbj|BAB10364.1|leucine zipper protein-like [Arabidopsis thaliana] >gi|15215764|gb|AAK91427.1|AT5g61010/maf19_10 [Arabidopsis thaliana] >gi|16974329|gb|AAL31149.1|AT5g61010/maf19_10 [Arabidopsis thaliana] >gi|222424078|dbj|BAH19999.1|AT5G61010 [Arabidopsis thaliana]	Unigene15029_All//1.00E-152//AT5G61010| ATEXO70E2 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN E2); protein binding	Unigene15029_All//0.00E+00//TC139608				nr -
Unigene1503_All	3041	2.48	6.30	4.41	3.69	4.46	7.68	6.77	11.12	23.45	1.35E+00	1.26E-22	Up	8.33E-01	1.87E-07		2.76E-01	8.24E-02		1.06E+00	3.21E-20	Up	7.16E-01	1.60E-17		1.79E+00	3.26E-156	Up	Unigene1503_All//gi|115441287|ref|NP_001044923.1|//0.00E+00//Os01g0869000 [Oryza sativa Japonica Group] >gi|113534454|dbj|BAF06837.1|Os01g0869000 [Oryza sativa Japonica Group]	Unigene1503_All//0.00E+00//AT1G71240| unknown protein	Unigene1503_All//0.00E+00//TC141353				nr +
Unigene15032_All	620	13.50	12.99	10.91	43.15	29.21	30.81	7.50	1.96	1.67	-5.53E-02	7.89E-01		-3.08E-01	1.55E-01		-5.63E-01	4.38E-09		-4.86E-01	1.84E-06		-1.94E+00	7.87E-12	Down	-2.17E+00	5.36E-14	Down	Unigene15032_All//gi|50253462|gb|AAT71933.1|//2.00E-08//At4g24265 [Arabidopsis thaliana] >gi|51972102|gb|AAU15155.1|At4g24265 [Arabidopsis thaliana]	Unigene15032_All//3.00E-05//AT4G24265| unknown protein	Unigene15032_All//0.00E+00//gi|109887559|gb|DW516528.1|DW516528				nr -
Unigene15033_All	944	9.09	6.01	5.64	21.95	15.69	16.17	3.85	2.57	0.63	-5.97E-01	2.45E-03		-6.88E-01	7.76E-04		-4.85E-01	1.35E-05		-4.41E-01	1.93E-04		-5.85E-01	4.33E-02		-2.61E+00	1.25E-13	Down	Unigene15033_All//gi|50253462|gb|AAT71933.1|//2.00E-16//At4g24265 [Arabidopsis thaliana] >gi|51972102|gb|AAU15155.1|At4g24265 [Arabidopsis thaliana]	Unigene15033_All//2.00E-06//AT4G24265| unknown protein	Unigene15033_All//0.00E+00//gi|109887559|gb|DW516528.1|DW516528				nr -
Unigene15034_All	1273	37.61	22.65	13.59	59.91	45.82	42.04	67.72	43.57	17.65	-7.32E-01	7.68E-21		-1.47E+00	2.41E-61	Down	-3.87E-01	9.66E-13		-5.11E-01	7.77E-19		-6.36E-01	1.86E-35		-1.94E+00	1.18E-212	Down	Unigene15034_All//gi|6119723|gb|AAF04193.1|AF053438|//4.00E-77//short-chain alcohol dehydrogenase [Pisum sativum]	Unigene15034_All//2.00E-65//AT3G29250| copper ion binding / oxidoreductase	Unigene15034_All//0.00E+00//TC139086		ko00906|Carotenoid biosynthesis	GO:0008152//GO:0016616	nr +
Unigene15035_All	1485	3.98	2.63	3.62	8.72	6.45	4.08	2.14	1.75	0.38	-6.00E-01	1.36E-02		-1.37E-01	6.43E-01		-4.36E-01	3.35E-03		-1.10E+00	2.79E-12	Down	-2.91E-01	4.01E-01		-2.51E+00	1.63E-11	Down	Unigene15035_All//gi|224121164|ref|XP_002330759.1|//6.00E-28//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222872561|gb|EEF09692.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene15035_All//4.00E-06//AT4G19050| ATP binding / protein binding	Unigene15035_All//9.00E-21//gi|164360520|gb|ES850138.1|ES850138		ko04626|Plant-pathogen interaction		nr +
Unigene15036_All	1453	9.11	6.84	11.51	5.97	13.86	6.19	0.44	1.38	0.69	-4.15E-01	7.80E-03		3.37E-01	1.99E-02		1.22E+00	1.01E-23	Up	5.23E-02	8.15E-01		1.66E+00	1.31E-04	Up	6.51E-01	2.81E-01		Unigene15036_All//gi|92893902|gb|AB391952.1|//9.00E-17//Zinc finger, CCHC-type [Medicago truncatula]	Unigene15036_All//2.00E-17//AT2G01050| nucleic acid binding / zinc ion binding	Unigene15036_All//4.00E-07//gi|3325777|gb|AI054663.1|AI054663				nr -
Unigene15038_All	1046	35.16	24.90	28.66	60.86	59.03	47.88	51.42	28.09	23.73	-4.98E-01	1.54E-08		-2.95E-01	1.48E-03		-4.42E-02	6.02E-01		-3.46E-01	5.24E-08		-8.72E-01	3.19E-38		-1.12E+00	1.02E-58	Down	Unigene15038_All//gi|297836856|ref|XP_002886310.1|//1.00E-109//secretory carrier membrane protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332150|gb|EFH62569.1|secretory carrier membrane protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15038_All//8.00E-97//AT2G20840| secretory carrier membrane protein (SCAMP) family protein	Unigene15038_All//0.00E+00//TC149639				nr +
Unigene15042_All	1499	0.87	2.70	3.23	1.99	4.20	3.10	0.00	0.00	0.21	1.63E+00	6.72E-07	Up	1.89E+00	2.32E-09	Up	1.08E+00	1.97E-06	Up	6.38E-01	2.35E-02		null	null		7.73E+00	1.34E-02		Unigene15042_All//gi|219879368|gb|AL511016.1|//1.00E-105//squamosa promoter-binding protein [Citrus trifoliata]	Unigene15042_All//3.00E-48//AT5G50570| squamosa promoter-binding protein, putative	Unigene15042_All//0.00E+00//gi|78333042|gb|DT553316.1|DT553316	SBP			nr +
Unigene15044_All	2053	10.02	7.65	6.64	12.98	11.62	19.73	25.68	11.24	14.24	-3.89E-01	1.43E-03		-5.93E-01	2.11E-06		-1.59E-01	1.64E-01		6.04E-01	1.29E-13		-1.19E+00	3.56E-62	Down	-8.50E-01	5.54E-37		Unigene15044_All//gi|17978590|gb|AL48316.1|//0.00E+00//adenylosuccinate-AMP lyase [Vigna unguiculata]	Unigene15044_All//0.00E+00//AT1G36280| adenylosuccinate lyase, putative / adenylosuccinase, putative	Unigene15044_All//0.00E+00//TC155316		ko00230|Purine metabolism/ko00250|Alanine, aspartate and glutamate metabolism	GO:0009168//GO:0009532//GO:0016842	nr -
Unigene15045_All	1157	4.02	2.72	2.58	5.21	3.57	3.83	2.27	0.25	1.38	-5.68E-01	4.28E-02		-6.43E-01	2.77E-02		-5.45E-01	1.83E-02		-4.46E-01	7.24E-02		-3.16E+00	1.24E-11	Down	-7.18E-01	3.17E-02		Unigene15045_All//gi|297811917|ref|XP_002873842.1|//1.00E-107//methyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297319679|gb|EFH59101.1|methyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene15045_All//2.00E-108//AT5G17660| tRNA (guanine-N7-)-methyltransferase	Unigene15045_All//3.00E-109//TC174600			GO:0008033//GO:0016423	nr +
Unigene15046_All	1808	8.25	14.26	10.84	11.79	13.87	13.71	26.89	23.05	54.32	7.90E-01	4.22E-13		3.94E-01	2.47E-03		2.34E-01	3.58E-02		2.18E-01	6.29E-02		-2.23E-01	1.37E-03		1.01E+00	1.24E-90	Up	Unigene15046_All//gi|297600810|ref|NP_001049892.2|//5.00E-83//Os03g0307000 [Oryza sativa Japonica Group] >gi|108707740|gb|ABF95535.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255674449|dbj|BAF11806.2|Os03g0307000 [Oryza sativa Japonica Group]	Unigene15046_All//4.00E-75//AT1G56423| unknown protein	Unigene15046_All//0.00E+00//TC163366			GO:0031410	nr -
Unigene15047_All	729	55.41	51.43	69.90	43.94	36.04	24.29	6.09	2.98	1.75	-1.07E-01	2.52E-01		3.35E-01	1.17E-05		-2.86E-01	1.73E-03		-8.55E-01	1.13E-19		-1.03E+00	6.89E-05	Down	-1.80E+00	1.11E-10	Down	Unigene15047_All//gi|18397831|ref|NP_564375.1|//2.00E-45//SRX (SULFIREDOXIN); DNA binding / oxidoreductase, acting on sulfur group of donors [Arabidopsis thaliana] >gi|145324096|ref|NP_001077637.1|SRX (SULFIREDOXIN); DNA binding / oxidoreductase, acting on sulfur group of donors [Arabidopsis thaliana] >gi|28416893|gb|AAO42977.1|At1g31170 [Arabidopsis thaliana]	Unigene15047_All//1.00E-38//AT1G31170| SRX (SULFIREDOXIN); DNA binding / oxidoreductase, acting on sulfur group of donors	Unigene15047_All//0.00E+00//gi|109888794|gb|DW517763.1|DW517763			GO:0003676//GO:0006950//GO:0008152//GO:0009536//GO:0016667	nr -

Unigene15048_All	1632	2.15	2.30	1.01	0.46	0.57	6.67	2.25	8.68	40.79	9.71E-02	7.57E-01			-1.09E+00	1.80E-03			3.15E-01	7.04E-01			3.86E+00	1.60E-47	Up	1.95E+00	1.45E-34	Up	4.18E+00	0.00E+00	Up	Unigene15048_All//gi|124301028|gb|ABN04766.1|//5.00E-25//At5g01370 [Arabidopsis thaliana]	Unigene15048_All//3.00E-16//AT5G01370| unknown protein	Unigene15048_All//0.00E+00//TC179320				nr -
Unigene15049_All	1020	40.42	19.92	42.91	396.32	372.81	503.97	23.25	109.98	31.21	-1.02E+00	3.19E-31	Down	8.63E-02	3.84E-01			-8.82E-02	2.82E-04			3.47E-01	2.56E-60		2.24E+00	0.00E+00	Up	4.24E-01	3.60E-07		Unigene15049_All//gi|118406886|gb|ABK81651.1|//9.00E-83//glutathione S-transferase [Vitis vinifera]	Unigene15049_All//9.00E-72//AT2G47730| ATGSTF8 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE PHI 8); glutathione binding / glutathione transferase	Unigene15049_All//0.00E+00//TC130563		ko00480|Glutathione metabolism	GO:0005488//GO:0016765	nr +
Unigene15050_All	965	27.60	43.16	27.48	6.04	9.35	12.54	35.40	138.34	169.10	6.45E-01	9.87E-15		-6.10E-03	9.82E-01			6.30E-01	5.45E-04			1.05E+00	1.10E-10	Up	1.97E+00	0.00E+00	Up	2.26E+00	0.00E+00	Up	Unigene15050_All//gi|89257480|gb|ABD64971.1|//6.00E-10//sodium-dependent transporter family protein [Brassica oleracea]	Unigene15050_All//1.00E-10//AT5G47560| TDT (TONOPLAST DICARBOXYLATE TRANSPORTER); malate transmembrane transporter/ sodium:dicarboxylate symporter	Unigene15050_All//9.00E-131//TC161261			GO:0015556//GO:0015740//GO:0030001//GO:0030641//GO:0043231	nr +
Unigene15051_All	1332	6.76	8.37	9.27	8.00	10.96	15.26	5.05	10.57	9.00	3.09E-01	7.87E-02		4.57E-01	6.64E-03			4.54E-01	1.20E-03			9.31E-01	2.12E-14		1.07E+00	1.69E-14	Up	8.35E-01	8.42E-09		Unigene15051_All//gi|116668552|gb|ABK15530.1|//7.00E-95//guanylyl cyclase [Glycine max]	Unigene15051_All//1.00E-83//AT5G05930| guanylyl cyclase-related (GC1)	Unigene15051_All//1.00E-115//TC157416				nr -
Unigene15052_All	1479	4.39	3.01	3.53	7.61	6.50	7.91	16.38	10.09	8.08	-5.41E-01	1.96E-02		-3.14E-01	2.19E-01			-2.29E-01	2.09E-01			5.52E-02	7.75E-01		-6.99E-01	2.50E-12		-1.02E+00	2.22E-23	Down	Unigene15052_All//gi|297829390|ref|XP_002882577.1|//1.00E-115//alphavirus core protein family [Arabidopsis lyrata subsp. lyrata] >gi|297328417|gb|EFH58836.1| alphavirus core protein family [Arabidopsis lyrata subsp. lyrata]	Unigene15052_All//2.00E-87//AT3G08640| alphavirus core protein family	Unigene15052_All//0.00E+00//TC132872			GO:0043231	nr -
Unigene15053_All	1028	1.02	3.65	0.83	4.70	3.22	4.44	20.93	22.40	14.84	1.84E+00	1.81E-07	Up	-2.97E-01	6.42E-01			-5.48E-01	3.84E-02			-8.31E-02	7.81E-01		9.78E-02	4.17E-01		-4.96E-01	1.43E-06		Unigene15053_All//gi|4760710|dbj|BAA77395.1|//9.00E-54//SLL2-59-protein [Brassica rapa]	Unigene15053_All//2.00E-52//AT1G66680| AR401	Unigene15053_All//0.00E+00//TC171494			GO:0016741//GO:0044444	nr -
Unigene15059_All	682	16.49	1.78	3.67	30.82	17.77	36.75	40.92	18.20	21.96	-3.21E+00	8.25E-40	Down	-2.17E+00	6.41E-25	Down	-7.94E-01	5.72E-13			2.54E-01	2.48E-02		-1.17E+00	2.93E-32	Down	-8.98E-01	7.80E-22		Unigene15059_All//gi|115486013|ref|NP_001068150.1|//7.00E-69//Os11g0579800 [Oryza sativa Japonica Group] >gi|113645372|dbj|BAF28513.1| Os11g0579800 [Oryza sativa Japonica Group]	Unigene15059_All//1.00E-42//AT3G03920| Gar1 RNA-binding region family protein	Unigene15059_All//3.00E-145//DW224058			GO:0003723//GO:0005732//GO:0009534//GO:0016866//GO:0031981//GO:0042454	nr -
Unigene1506_All	3229	3.66	2.09	2.94	8.07	5.46	4.34	10.48	3.71	5.79	-8.11E-01	1.01E-06		-3.19E-01	7.42E-02			-5.63E-01	6.94E-09			-8.96E-01	2.21E-17		-1.50E+00	1.39E-56	Down	-8.56E-01	2.53E-24		Unigene1506_All//gi|224074675|ref|XP_002304419.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222841851|gb|EEE79398.1| GRAS family transcription factor [Populus trichocarpa]	Unigene1506_All//1.00E-76//AT4G00150| scarecrow-like transcription factor 6 (SCL6)	Unigene1506_All//0.00E+00//TC140654	GRAS			nr +
Unigene15063_All	1536	22.11	12.24	18.20	3.83	2.38	4.35	1.76	0.73	1.87	-8.53E-01	2.50E-19		-2.81E-01	4.05E-03			-6.87E-01	2.67E-03			1.85E-01	4.81E-01		-1.26E+00	3.10E-04	Down	8.41E-02	8.03E-01		Unigene15063_All//gi|297841963|ref|XP_002888863.1|//1.00E-36//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334704|gb|EFH65122.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15063_All//4.00E-34//AT5G10380| RING1; protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene15063_All//0.00E+00//gi|78342570|gb|DT562844.1|DT562844			GO:0046914	nr +
Unigene15064_All	1762	4.34	4.54	1.51	5.51	4.01	3.90	7.25	4.77	2.71	6.77E-02	7.51E-01		-1.52E+00	9.48E-11	Down	-4.61E-01	8.85E-03			-5.01E-01	6.13E-03		-6.04E-01	1.69E-05		-1.42E+00	7.31E-21	Down	Unigene15064_All//gi|297844196|ref|XP_002889979.1|//0.00E+00//glycosyl transferase family 17 protein [Arabidopsis lyrata subsp. lyrata] >gi|297335821|gb|EFH66238.1| glycosyl transferase family 17 protein [Arabidopsis lyrata subsp. lyrata]	Unigene15064_All//0.00E+00//AT1G12990| glycosyl transferase family 17 protein	Unigene15064_All//0.00E+00//TC141726				nr -
Unigene15066_All	1521	3.10	2.57	1.96	2.33	2.35	1.96	3.56	1.54	1.68	-2.71E-01	3.64E-01		-6.59E-01	2.34E-02			1.80E-02	9.65E-01			-2.47E-01	5.02E-01		-1.21E+00	3.08E-07	Down	-1.09E+00	1.86E-06	Down	Unigene15066_All//gi|297830178|ref|XP_002882971.1|//1.00E-176//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328811|gb|EFH59230.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene15066_All//6.00E-175//AT3G16010| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene1507_All	2610	10.28	29.99	8.65	12.86	16.60	12.25	25.59	38.66	68.46	1.54E+00	6.17E-111	Up	-2.50E-01	2.77E-02			3.68E-01	1.02E-06			-7.04E-02	5.55E-01		5.95E-01	9.88E-37		1.42E+00	6.75E-279	Up	Unigene1507_All//gi|166043552|gb|AAL24182.1|//1.00E-167//AT5g12010/F14F18_180 [Arabidopsis thaliana] >gi|25141199|gb|AAN73294.1| At5g12010/F14F18_180 [Arabidopsis thaliana]	Unigene1507_All//1.00E-153//AT5G12010| unknown protein	Unigene1507_All//0.00E+00//TC174702		ko00620|Pyruvate metabolism/ko00640|Propanoate metabolism/ko00061|Fatty acid biosynthesis		nr -
Unigene15070_All	1725	15.04	8.37	11.73	18.34	22.86	17.04	8.01	2.52	5.33	-8.46E-01	9.56E-15		-3.59E-01	1.30E-03			3.18E-01	7.77E-05			-1.06E-01	3.67E-01		-1.67E+00	1.55E-27	Down	-5.87E-01	7.60E-06		Unigene15070_All//gi|115452547|ref|NP_001049874.1|//9.00E-58//Os03g0303100 [Oryza sativa Japonica Group] >gi|108707708|gb|ABF95503.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548345|dbj|BAF11788.1| Os03g0303100 [Oryza sativa Japonica Group]	Unigene15070_All//2.00E-94//AT3G62630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1645 (InterPro:IPR012442); BEST Arabidopsis thaliana protein match is: calmodulin-binding protein (TAIR:AT2G15760.1); Has 207 Blast hits to 197 proteins in 50 species: Archae - 3; Bacteria - 4; Metazoa - 52; Fungi - 9; Plants - 91; Viruses - 0; Other Eukaryotes - 48 (source: NCBI BLink).	Unigene15070_All//0.00E+00//TC148510				nr +
Unigene15071_All	1579	7.99	17.39	11.10	10.28	10.47	11.30	35.35	36.53	38.00	1.12E+00	2.35E-24	Up	4.75E-01	5.57E-04			2.55E-02	8.82E-01			1.36E-01	3.97E-01		4.75E-02	5.56E-01		1.04E-01	1.09E-01		Unigene15071_All//gi|297820116|ref|XP_002877941.1|//1.00E-139//rhomboid family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323779|gb|EFH54290.1| rhomboid family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15071_All//1.00E-124//AT3G53780| rhomboid family protein	Unigene15071_All//0.00E+00//TC155166				nr -
Unigene15073_All	2741	6.64	22.70	9.36	7.98	9.51	18.75	31.05	42.01	29.90	1.77E+00	2.14E-107	Up	4.95E-01	7.45E-06			2.53E-01	1.79E-02			1.23E+00	7.72E-56	Up	4.36E-01	4.24E-24		-5.46E-02	3.61E-01		Unigene15073_All//gi|15236837|ref|NP_194400.1|//0.00E+00//ATFIM1; actin binding [Arabidopsis thaliana] >gi|79325277|ref|NP_001031726.1| ATFIM1; actin binding [Arabidopsis thaliana] >gi|59797940|sp|Q7G188.2|FIMB1_ARATH RecName: Full=Fimbrin-1; Short=AtFIM1 >gi|4455193|emb|CAB36516.1| fimbrin-like protein (ATFIM1) [Arabidopsis thaliana] >gi|7269522|emb|CAB79525.1| fimbrin-like protein (ATFIM1) [Arabidopsis thaliana]	Unigene15073_All//0.00E+00//AT4G26700| ATFIM1; actin binding	Unigene15073_All//0.00E+00//gi|48795075|gb|CO096389.1|CO096389			GO:0008092//GO:0043231//GO:0046914	nr +
Unigene15075_All	1412	2.11	12.42	3.66	4.09	4.88	5.50	3.77	6.19	3.95	2.56E+00	2.15E-48	Up	7.92E-01	3.87E-03			2.53E-01	3.15E-01			4.27E-01	4.65E-02		7.13E-01	4.12E-05		6.62E-02	7.80E-01		Unigene15075_All//gi|30685384|ref|NP_567623.2|//1.00E-133//HSA32 (HEAT-STRESS-ASSOCIATED 32); catalytic [Arabidopsis thaliana]	Unigene15075_All//5.00E-120//AT4G21320| HSA32 (HEAT-STRESS-ASSOCIATED 32); catalytic	Unigene15075_All//0.00E+00//DR454290			GO:0009108	nr -
Unigene15077_All	1407	12.09	4.83	7.08	28.85	18.58	18.01	56.88	48.54	17.13	-1.32E+00	8.61E-20	Down	-7.72E-01	3.34E-08			-6.35E-01	9.70E-17			-6.80E-01	7.88E-17		-2.29E-01	1.27E-05		-1.73E+00	5.81E-169	Down	Unigene15077_All//gi|297849840|ref|XP_002892801.1|//1.00E-180//UDP-galactose transporter 3 [Arabidopsis lyrata subsp. lyrata] >gi|297338643|gb|EFH69060.1| UDP-galactose transporter 3 [Arabidopsis lyrata subsp. lyrata]	Unigene15077_All//0.00E+00//AT1G14360| UTR3 (UDP-GALACTOSE TRANSPORTER 3); pyrimidine nucleotide sugar transmembrane transporter	Unigene15077_All//0.00E+00//gi|78341972|gb|DT562246.1|DT562246				nr -
Unigene15079_All	1161	5.68	12.66	9.04	10.38	10.71	15.13	13.95	20.27	39.46	1.16E+00	5.47E-14	Up	6.70E-01	2.40E-04			4.43E-02	8.24E-01			5.43E-01	2.62E-05		5.39E-01	7.66E-08		1.50E+00	3.24E-78	Up	Unigene15079_All//gi|14190455|gb|AAK55708.1|AF380627_1//1.00E-49//AT5g53330/K19E1_13 [Arabidopsis thaliana] >gi|15809720|gb|AAL06788.1| AT5g53330/K19E1_13 [Arabidopsis thaliana]	Unigene15079_All//4.00E-43//AT5G53330| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote (InterPro:IPR015940); Has 28 Blast hits to 28 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 11; Fungi - 2; Plants - 15; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene15079_All//2.00E-119//ES833183			GO:0043231	nr +
Unigene1508_All	3315	29.03	16.84	28.40	16.73	16.01	13.72	17.15	2.45	8.04	-7.85E-01	2.11E-46		-3.14E-02	6.10E-01			-6.33E-02	4.76E-01			-2.86E-01	3.93E-05		-2.81E+00	4.27E-213	Down	-1.09E+00	4.53E-60	Down	Unigene1508_All//gi|75335370|sp|Q9LKT1.1|YSH04_ARATH//0.00E+00//RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase At3g28040; Flags: Precursor >gi|11994124|dbj|BAB01126.1| receptor protein kinase [Arabidopsis thaliana] >gi|224589581|gb|ACN59324.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene1508_All//0.00E+00//AT3G28040| leucine-rich repeat transmembrane protein kinase, putative	Unigene1508_All//0.00E+00//TC144266				nr -
Unigene15081_All	877	28.28	14.33	21.37	16.98	19.79	21.78	18.56	6.43	6.77	-9.81E-01	6.53E-18		-4.04E-01	3.83E-04			2.21E-01	1.19E-01			3.59E-01	4.70E-03		-1.53E+00	1.65E-28	Down	-1.46E+00	2.16E-27	Down	Unigene15081_All//gi|238069187|gb|ACR40091.1|//1.00E-121//S-nitrosoglutathione reductase [Brassica juncea]	Unigene15081_All//2.00E-121//AT5G43940| HOT5 (sensitive to hot temperatures 5); S-(hydroxymethyl)glutathione dehydrogenase/ S-nitrosoglutathione reductase	Unigene15081_All//0.00E+00//EX165062		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism/ko00350|Tyrosine metabolism		nr -
Unigene15083_All	989	4.39	10.35	6.46	7.45	7.31	6.94	19.58	23.07	14.86	1.24E+00	5.24E-11	Up	5.57E-01	2.27E-02			-2.79E-02	9.07E-01			-1.03E-01	6.94E-01		2.37E-01	2.69E-02		-3.98E-01	2.74E-04		Unigene15083_All//gi|209529767|gb|ACI49778.1|//4.00E-46//At2g39950 [Arabidopsis thaliana]	Unigene15083_All//4.00E-41//AT2G39950| unknown protein	Unigene15083_All//0.00E+00//gi|164354918|gb|ES834569.1|ES834569				nr +

Unigene15087_All	1709	2.57	0.36	0.90	15.33	13.26	9.80	12.10	1.93	4.66	-2.85E+00	3.23E-14	Down	-1.51E+00	2.17E-06	Down	-2.10E-01	5.47E-02		-6.45E-01	3.85E-10		-2.65E+00	6.29E-73	Down	-1.38E+00	8.40E-32	Down	Unigene15087_All//gi|297603622|ref|NP_001054349.2|//7.00E-88//Os04g0690100 [Oryza sativa Japonica Group] >gi|255675912|dbj|BAF16263.2|Os04g0690100 [Oryza sativa Japonica Group]	Unigene15087_All//3.00E-67//AT1G75710| zinc finger (C2H2 type) family protein	Unigene15087_All//0.00E+00//CO112378	C2H2		GO:0043231	nr -
Unigene15090_All	1237	17.55	19.05	8.61	22.99	22.47	23.73	15.93	22.30	18.94	1.18E-01	3.65E-01		-1.03E+00	2.88E-16	Down	-3.36E-02	8.11E-01		4.55E-02	7.01E-01		4.86E-01	1.27E-07		2.50E-01	1.36E-02		Unigene15090_All//gi|115440841|ref|NP_001044700.1|//4.00E-66//Os01g0831200 [Oryza sativa Japonica Group] >gi|56785178|dbj|BAD81854.1| BAG domain containing protein-like [Oryza sativa Japonica Group] >gi|113534231|dbj|BAF06614.1|Os01g0831200 [Oryza sativa Japonica Group]	Unigene15090_All//4.00E-66//AT3G51780| ATBAG4 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 4); protein binding	Unigene15090_All//0.00E+00//TC141949			GO:0003006//GO:0006915//GO:0006970//GO:0043231	nr -
Unigene15091_All	1289	5.20	5.98	4.87	3.48	2.32	3.12	5.71	11.48	13.82	2.02E-01	3.68E-01		-9.20E-02	7.05E-01		-5.82E-01	3.42E-02		-1.58E-01	6.20E-01		1.01E+00	6.55E-14	Up	1.28E+00	2.30E-24	Up	Unigene15091_All//gi|1418127|dbj|BAA06642.1|//1.00E-123//CTP:phosphocholine cytidylyltransferase [Brassica napus]	Unigene15091_All//7.00E-115//AT2G32260| cholinephosphate cytidylyltransferase, putative / phosphorylcholine transferase, putative / CTP:phosphocholine cytidylyltransferase, putative	Unigene15091_All//0.00E+00//gi|78325848|gb|DT546122.1|DT546122		ko00564|Glycerophospholipid metabolism		nr +
Unigene15094_All	2775	0.04	0.02	0.13	3.46	2.10	0.99	8.27	4.70	6.13	-1.04E+00	6.85E-01		1.83E+00	2.13E-01		-7.24E-01	2.19E-05		-1.80E+00	5.61E-19	Down	-8.16E-01	4.48E-15		-4.33E-01	1.33E-05		Unigene15094_All//gi|28300299|gb|AA037645.1|//1.00E-137//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene15094_All//7.00E-71//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene15094_All//2.00E-164//TC177573		ko04626|Plant-pathogen interaction		nr -
Unigene15096_All	665	35.48	25.91	29.39	31.16	38.37	33.82	44.89	25.08	19.29	-4.54E-01	5.19E-05		-2.72E-01	2.49E-02		3.00E-01	4.35E-03		1.18E-01	3.90E-01		-8.40E-01	2.72E-20		-1.22E+00	7.55E-38	Down	Unigene15096_All//gi|18400858|ref|NP_566522.1|//4.00E-58//GRX4 (GLUTAREDOXIN 4); metal ion binding [Arabidopsis thaliana] >gi|79313249|ref|NP_001030704.1|GRX4 (GLUTAREDOXIN 4); metal ion binding [Arabidopsis thaliana] >gi|119370633|sp|Q8LBK6.2|GRS15_ARATH RecName: Full=Monothiol glutaredoxin-S15; Short=AtGrxS15 >gi|30102572|gb|AAP21204.1|At3g15660 [Arabidopsis thaliana] >gi|222424054|dbj|BAH19988.1|AT3G15660 [Arabidopsis thaliana]	Unigene15096_All//2.00E-59//AT3G15660| GRX4 (GLUTAREDOXIN 4); metal ion binding	Unigene15096_All//0.00E+00//gi|109884820|gb|DW513790.1|DW513790			GO:0015036//GO:0019725//GO:0043231//GO:0046914	nr -
Unigene15097_All	794	31.70	31.01	26.49	18.38	12.36	35.61	18.85	21.27	6.52	-3.13E-02	7.92E-01		-2.59E-01	2.72E-02		-5.73E-01	2.27E-05		9.54E-01	1.30E-20		1.74E-01	1.97E-01		-1.53E+00	3.64E-27	Down	Unigene15097_All//gi|18400858|ref|NP_566522.1|//5.00E-58//GRX4 (GLUTAREDOXIN 4); metal ion binding [Arabidopsis thaliana] >gi|79313249|ref|NP_001030704.1|GRX4 (GLUTAREDOXIN 4); metal ion binding [Arabidopsis thaliana] >gi|119370633|sp|Q8LBK6.2|GRS15_ARATH RecName: Full=Monothiol glutaredoxin-S15; Short=AtGrxS15 >gi|30102572|gb|AAP21204.1|At3g15660 [Arabidopsis thaliana] >gi|222424054|dbj|BAH19988.1|AT3G15660 [Arabidopsis thaliana]	Unigene15097_All//3.00E-59//AT3G15660| GRX4 (GLUTAREDOXIN 4); metal ion binding	Unigene15097_All//0.00E+00//TC159869			GO:0015036//GO:0019725//GO:0043231//GO:0046914	nr +
Unigene15099_All	2144	1.88	0.28	0.89	1.67	0.84	0.63	10.94	4.43	5.28	-2.73E+00	1.65E-12	Down	-1.07E+00	8.34E-04	Down	-1.00E+00	9.69E-04	Down	-1.40E+00	2.19E-05	Down	-1.31E+00	2.56E-32	Down	-1.05E+00	7.65E-24	Down	Unigene15099_All//gi|297795829|ref|XP_002865799.1|//0.00E+00//ATPAP27/PAP27 [Arabidopsis lyrata subsp. lyrata] >gi|297311634|gb|EFH42058.1|ATPAP27/PAP27 [Arabidopsis lyrata subsp. lyrata]	Unigene15099_All//0.00E+00//AT5G50400| PAP27 (PURPLE ACID PHOSPHATASE 27); acid phosphatase/ protein serine/threonine phosphatase	Unigene15099_All//0.00E+00//BG445914			GO:0016791//GO:0030312//GO:0043169	nr -
Unigene1510_All	1232	0.72	1.32	0.61	1.54	1.84	1.17	8.27	10.75	3.95	8.66E-01	9.50E-02		-2.55E-01	7.17E-01		2.64E-01	5.84E-01		-3.89E-01	4.48E-01		3.79E-01	6.81E-03		-1.07E+00	4.23E-11	Down	Unigene1510_All//gi|223452286|gb|ACM89471.1|//6.00E-75//FERONIA receptor-like kinase [Glycine max]	Unigene1510_All//8.00E-67//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene1510_All//0.00E+00//TC135914		ko04626|Plant-pathogen interaction		nr -
Unigene15100_All	1529	12.52	6.56	11.35	18.24	15.95	13.06	9.32	4.46	6.85	-9.33E-01	6.11E-13		-1.42E-01	3.43E-01		-1.94E-01	6.90E-02		-4.83E-01	1.21E-06		-1.06E+00	1.26E-14	Down	-4.44E-01	5.90E-04		Unigene15100_All//gi|18424178|ref|NP_568894.1|//1.00E-137//ATUCP2 (UNCOUPLING PROTEIN 2); oxidative phosphorylation uncoupler [Arabidopsis thaliana] >gi|40630007|dbj|BA536222.1|uncoupling protein [Arabidopsis thaliana] >gi|9759228|dbj|BAB09640.1|uncoupling protein [Arabidopsis thaliana] >gi|21593775|gb|AAM65742.1|uncoupling protein AtUCP2 [Arabidopsis thaliana]	Unigene15100_All//3.00E-120//AT5G58970| ATUCP2 (UNCOUPLING PROTEIN 2); oxidative phosphorylation uncoupler	Unigene15100_All//0.00E+00//gi|109851635|gb|DW480614.1|DW480614				nr +
Unigene15101_All	2728	1.29	1.17	1.23	0.99	0.59	1.52	2.63	5.75	9.20	-1.35E-01	6.79E-01		-6.35E-02	8.55E-01		-7.33E-01	4.55E-02		6.27E-01	3.85E-02		1.12E+00	2.14E-17	Up	1.80E+00	5.62E-56	Up	Unigene15101_All//gi|87162753|gb|AB028548.1|//0.00E+00//Protein kinase; Type I EGF [Medicago truncatula]	Unigene15101_All//3.00E-179//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase	Unigene15101_All//0.00E+00//TC166725		ko04626|Plant-pathogen interaction	GO:0000902//GO:0004672//GO:0005488//GO:0005975//GO:0006884//GO:0010033//GO:0016020	nr -
Unigene15105_All	1291	2.84	0.94	1.15	3.24	2.67	3.67	3.60	2.04	2.04	-1.59E+00	3.79E-06	Down	-1.30E+00	1.73E-04	Down	-2.81E-01	3.83E-01		1.81E-01	5.91E-01		-8.21E-01	9.85E-04		-8.23E-01	6.68E-04		Unigene15105_All//gi|18400953|ref|NP_565610.1|//1.00E-121//YebC-related [Arabidopsis thaliana] >gi|22096384|sp|Q82314.2|U082_ARATH RecName: Full=UPF0082 protein At2g25830 >gi|20197365|gb|AAC42247.2|expressed protein [Arabidopsis thaliana]	Unigene15105_All//2.00E-109//AT2G25830| YebC-related	Unigene15105_All//0.00E+00//CO095060				nr +
Unigene15106_All	1289	17.66	7.70	8.59	28.17	21.48	24.21	24.11	11.67	13.69	-1.20E+00	1.72E-22	Down	-1.04E+00	2.55E-17	Down	-3.91E-01	1.75E-06		-2.19E-01	1.79E-02		-1.05E+00	4.20E-30	Down	-8.16E-01	9.94E-21		Unigene15106_All//gi|9757942|dbj|BAB08430.1|//1.00E-161//GAMMA protein-like [Arabidopsis thaliana]	Unigene15106_All//2.00E-160//AT5G41970| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Metal-dependent protein hydrolase (InterPro:IPR003226); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G49320.1); Has 464 Blast hits to 461 proteins in 209 species: Archae - 0; Bacteria - 122; Metazoa - 131; Fungi - 87; Plants - 29; Viruses - 0; Other Eukaryotes - 95 (source: NCBI BLink).	Unigene15106_All//0.00E+00//TC169481				nr -
Unigene15107_All	659	17.07	11.38	14.14	17.99	14.06	18.85	14.69	9.07	6.35	-5.85E-01	5.37E-04		-2.72E-01	1.45E-01		-3.56E-01	2.77E-02		6.71E-02	7.15E-01		-6.96E-01	2.22E-05		-1.21E+00	9.34E-13	Down	Unigene15107_All//gi|297817268|ref|XP_002876517.1|//1.00E-55//mitochondrial ribosomal protein L51/S25/CI-B8 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322355|gb|EFH52776.1|mitochondrial ribosomal protein L51/S25/CI-B8 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15107_All//1.00E-56//AT3G59650| mitochondrial ribosomal protein L51/S25/CI-B8 family protein	Unigene15107_All//0.00E+00//TC165625			GO:0030529//GO:0043231	nr -
Unigene15109_All	643	48.01	38.22	56.07	33.31	34.54	29.99	3.81	7.67	5.14	-3.29E-01	7.71E-04		2.24E-01	2.06E-02		5.23E-02	7.44E-01		-1.52E-01	2.68E-01		1.01E+00	3.58E-05	Up	4.31E-01	1.53E-01		Unigene15109_All//gi|224097084|ref|XP_002310830.1|//2.00E-29//thioredoxin h [Populus trichocarpa] >gi|222853733|gb|EEE91280.1|thioredoxin h [Populus trichocarpa]	Unigene15109_All//2.00E-28//AT3G51030| ATTRX1; oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	Unigene15109_All//0.00E+00//TC170481			GO:0006091//GO:0015036//GO:0018904//GO:0019725//GO:0030234//GO:0044093//GO:0044444//GO:0051234	nr +
Unigene1511_All	1024	4.14	4.70	2.29	6.23	3.97	3.88	7.14	12.04	2.45	1.84E-01	5.36E-01		-8.55E-01	5.55E-03		-6.50E-01	2.99E-03		-6.82E-01	3.02E-03		7.53E-01	1.76E-07		-1.54E+00	7.26E-14	Down	Unigene1511_All//gi|223452315|gb|ACM89485.1|//7.00E-72//receptor-like kinase [Glycine max]	Unigene1511_All//1.00E-67//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene1511_All//0.00E+00//gi|78333985|gb|DT554259.1|DT554259		ko04626|Plant-pathogen interaction		nr -
Unigene15113_All	1936	7.62	8.48	3.00	11.24	15.55	17.73	28.59	50.17	181.25	1.54E-01	3.15E-01		-1.35E+00	6.18E-17	Down	4.67E-01	3.19E-07		6.57E-01	2.14E-13		8.12E-01	1.72E-60		2.66E+00	0.00E+00	Up	Unigene15113_All//gi|15222875|ref|NP_177708.1|//1.00E-121//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|6721098|gb|AAF26752.1|AC007396_1 T4012.3 [Arabidopsis thaliana] >gi|18377860|gb|AAL67116.1|At1g75800/T4012_2 [Arabidopsis thaliana] >gi|20334826|gb|AAM16169.1|At1g75800/T4012_2 [Arabidopsis thaliana]	Unigene15113_All//9.00E-104//AT1G75800| pathogenesis-related thaumatin family protein	Unigene15113_All//0.00E+00//gi|78340809|gb|DT561083.1|DT561083				nr +
Unigene15114_All	1608	3.87	2.33	4.07	4.52	4.30	2.13	7.49	13.41	26.11	-7.32E-01	1.96E-03		7.31E-02	7.67E-01		-7.14E-02	8.07E-01		-1.08E+00	4.89E-07	Down	8.40E-01	7.22E-15		1.80E+00	6.58E-93	Up	Unigene15114_All//gi|10178227|dbj|BAB11607.1|//6.00E-59//ZW10-like protein [Arabidopsis thaliana] >gi|222423885|dbj|BAH19906.1|AT5G64460 [Arabidopsis thaliana]	Unigene15114_All//3.00E-60//AT5G64460| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G58280.3); Has 385 Blast hits to 382 proteins in 84 species: Archae - 0; Bacteria - 19; Metazoa - 2; Fungi - 201; Plants - 67; Viruses - 0; Other Eukaryotes - 96 (source: NCBI BLink).	Unigene15114_All//4.00E-143//DW512355				nr +

Unigene15115_All	306	7.52	4.31	5.22	2.28	2.93	7.08	2.21	3.28	3.25	-8.05E-01	5.50E-02		-5.27E-01	2.36E-01		3.60E-01	6.55E-01		1.64E+00	3.84E-04	Up	5.68E-01	3.79E-01		5.58E-01	3.54E-01		Unigene15115_All//gi|297806221|ref|XP_002870994.1|//2.00E-40//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297316831|gb|EFH47253.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene15115_All//2.00E-41//AT5G02860| pentatricopeptide (PPR) repeat-containing protein				nr +
Unigene15117_All	1243	9.51	6.48	8.35	16.27	14.46	15.26	12.79	7.97	6.25	-5.54E-01	7.60E-04		-1.88E-01	3.23E-01		-1.70E-01	2.05E-01		-9.25E-02	5.48E-01		-6.83E-01	4.68E-08		-1.03E+00	5.63E-16	Down	Unigene15117_All//gi|115452225|ref|NP_001049713.1|//8.00E-82//Os03g0276600 [Oryza sativa Japonica Group] >gi|108707464|gb|ABF95259.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548184|dbj|BAF11627.1| Os03g0276600 [Oryza sativa Japonica Group]	Unigene15117_All//1.00E-88//AT3G04020| unknown protein	Unigene15117_All//0.00E+00//TC160090			GO:0000166	nr +
Unigene1512_All	1529	0.55	1.09	0.45	1.30	1.33	1.21	3.21	7.27	1.80	9.98E-01	5.09E-02		-2.74E-01	7.05E-01		2.81E-02	9.66E-01		-1.06E-01	8.23E-01		1.18E+00	1.61E-13	Up	-8.35E-01	3.78E-04		Unigene1512_All//gi|223452286|gb|ACM89471.1|//3.00E-89//FEROXIA receptor-like kinase [Glycine max]	Unigene1512_All//1.00E-79//AT3G51550| FER (FEROXIA); kinase/ protein kinase	Unigene1512_All//0.00E+00//TC161443		ko04626|Plant-pathogen interaction		nr +
Unigene15120_All	1268	1.57	1.40	2.23	2.12	1.68	3.06	7.00	4.25	2.86	-1.65E-01	7.05E-01		5.05E-01	2.05E-01		-3.33E-01	4.13E-01		5.30E-01	9.91E-02		-7.20E-01	2.97E-05		-1.29E+00	6.12E-13	Down	Unigene15120_All//gi|15221559|ref|NP_174376.1|//1.00E-123//molybdenum cofactor sulfurase family protein [Arabidopsis thaliana] >gi|9755390|gb|AAF98197.1|AC000107_20 F17F8.22 [Arabidopsis thaliana]	Unigene15120_All//4.00E-122//AT1G30910| molybdenum cofactor sulfurase family protein	Unigene15120_All//0.00E+00//TC131058			GO:0003824//GO:0046914//GO:0048037	nr +
Unigene15121_All	1331	14.62	12.37	11.64	24.70	19.48	16.93	19.85	10.68	8.17	-2.41E-01	6.56E-02		-3.29E-01	1.35E-02		-3.43E-01	9.55E-05		-5.45E-01	1.92E-09		-8.95E-01	5.08E-20		-1.28E+00	2.83E-36	Down	Unigene15121_All//gi|224081865|ref|XP_002306507.1|//1.00E-126//porin/voltage-dependent anion-selective channel protein [Populus trichocarpa] >gi|222855956|gb|EEE93503.1| porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	Unigene15121_All//2.00E-111//AT5G67500| VDAC2 (VOLTAGE DEPENDENT ANION CHANNEL 2); voltage-gated anion channel	Unigene15121_All//0.00E+00//TC179409			GO:0006810	nr +
Unigene15126_All	1117	5.71	2.77	2.72	5.75	2.68	4.73	2.12	1.87	2.71	-1.05E+00	1.06E-05	Down	-1.07E+00	1.38E-05	Down	-1.10E+00	3.88E-07	Down	-2.82E-01	2.70E-01		-1.80E-01	6.34E-01		3.55E-01	2.73E-01		Unigene15126_All//gi|4666360|gb|AAD26942.1|AF119050_1|/5.00E-42//zinc-finger protein 1 [Datisca glomerata]	Unigene15126_All//3.00E-32//AT1G27730| STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding	Unigene15126_All//0.00E+00//D#520490	C2H2		GO:0005488//GO:0010468	nr -
Unigene15128_All	1225	3.84	10.80	20.39	51.73	87.96	88.56	0.79	1.13	0.62	1.49E+00	2.43E-18	Up	2.41E+00	1.41E-62	Up	7.66E-01	5.54E-59		7.76E-01	7.97E-55		5.04E-01	3.48E-01		-3.61E-01	5.65E-01		Unigene15128_All//gi|211906484|gb|ACJ11735.1|//0.00E+00//granule bound starch synthase [Gossypium hirsutum]	Unigene15128_All//1.00E-140//AT1G32900| starch synthase, putative	Unigene15128_All//0.00E+00//gi|78343758|gb|DT564032.1|DT564032		ko00500|Starch and sucrose metabolism	GO:0005977//GO:0046527	nr -
Unigene15130_All	1633	0.48	153.03	8.64	0.40	23.43	43.45	7.64	42.08	76.36	8.31E+00	0.00E+00	Up	4.17E+00	1.30E-59	Up	5.88E+00	1.57E-226	Up	6.78E+00	0.00E+00	Up	2.46E+00	2.09E-221	Up	3.32E+00	0.00E+00	Up	Unigene15130_All//gi|14210079|gb|AAK56924.1|AF368237_1|/1.00E-105//circadian clock coupling factor ZGT [Nicotiana tabacum]	Unigene15130_All//2.00E-89//AT3G63060| EDL3 (EID1-like 3)	Unigene15130_All//0.00E+00//CO114825				nr -
Unigene15131_All	1285	13.03	4.42	6.67	12.64	11.09	12.58	11.55	7.19	6.85	-1.56E+00	9.58E-25	Down	-9.66E-01	1.66E-11		-1.88E-01	2.14E-01		-6.30E-03	9.62E-01		-6.84E-01	1.33E-07		-7.53E-01	3.82E-09		Unigene15131_All//gi|6647900|sp|P93394.1|UPP_TOBAC//1.00E-105//RecName: Full=Uracil phosphoribosyltransferase; Short=UPRTase; AltName: Full=UMP pyrophosphorylase >gi|1848214|emb|CAA72093.1| uracil phosphoribosyltransferase [Nicotiana tabacum]	Unigene15131_All//1.00E-99//AT3G53900| uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative	Unigene15131_All//0.00E+00//TC175983		ko00240|Pyrimidine metabolism	GO:0016763//GO:0019860//GO:0043231	nr -
Unigene15135_All	1416	15.67	12.70	13.43	121.26	141.78	94.70	40.49	26.00	17.70	-3.03E-01	1.08E-02		-2.23E-01	8.27E-02		2.26E-01	6.48E-12		-3.57E-01	1.06E-21		-6.39E-01	5.15E-24		-1.19E+00	1.24E-69	Down	Unigene15135_All//gi|224114113|ref|XP_002316671.1|//4.00E-28//NBS resistance protein [Populus trichocarpa] >gi|222859736|gb|EEE97283.1| NBS resistance protein [Populus trichocarpa]	Unigene15135_All//2.00E-24//AT4G19060| disease resistance protein-related	Unigene15135_All//0.00E+00//TC173569		ko04626|Plant-pathogen interaction		nr +
Unigene15136_All	1468	1.35	2.21	0.65	4.07	4.60	3.69	22.84	1.57	5.07	7.06E-01	4.07E-02		-1.05E+00	2.99E-02		1.75E-01	5.24E-01		-1.41E-01	6.40E-01		-3.87E+00	1.00E-168	Down	-2.17E+00	4.07E-96	Down	Unigene15136_All//gi|54035683|sp|Q81221.1|ACT_GOSHI//0.00E+00//RecName: Full=Actin >gi|3420239|gb|AAC31886.1| actin [Gossypium hirsutum]	Unigene15136_All//0.00E+00//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene15136_All//0.00E+00//TC130048		ko04145|Phagosome	GO:0006996//GO:0016020//GO:0030312//GO:0032559//GO:0043231//GO:0043232//GO:0048588	nr +
Unigene15137_All	1088	17.94	2.70	8.61	9.80	7.85	2.70	0.08	0.00	0.07	-2.73E+00	2.14E-58	Down	-1.06E+00	2.27E-15	Down	-3.20E-01	6.97E-02		-1.86E+00	6.89E-22	Down	-6.28E+00	4.04E-01		-8.61E-02	9.72E-01		Unigene15137_All//gi|297819734|ref|XP_002877750.1|//4.00E-97//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323388|gb|EFH54009.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15137_All//5.00E-97//AT3G50560| short-chain dehydrogenase/reductase (SDR) family protein	Unigene15137_All//0.00E+00//TC159571		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis//ko00860|Porphyrin and chlorophyll metabolism	GO:0003824//GO:0008152	nr +
Unigene15139_All	681	2.23	8.33	5.47	4.68	3.69	4.51	3.23	1.47	3.57	1.90E+00	2.17E-11	Up	1.30E+00	1.44E-04	Up	-3.43E-01	3.44E-01		-5.39E-02	8.98E-01		-1.13E+00	3.71E-03		1.45E-01	6.89E-01		Unigene15139_All//gi|224105833|ref|XP_002313948.1|//2.00E-74//sugar transporter/spinster transmembrane protein [Populus trichocarpa] >gi|222850356|gb|EEE87903.1| sugar transporter/spinster transmembrane protein [Populus trichocarpa]	Unigene15139_All//2.00E-60//AT5G64500| membrane protein-related	Unigene15139_All//0.00E+00//gi|5046646|gb|AI727794.1|AI727794			GO:0006810//GO:0022891//GO:0031224	nr +
Unigene15140_All	1479	9.98	7.06	5.22	7.78	7.66	6.66	7.26	6.25	2.69	-4.99E-01	6.01E-04		-9.34E-01	1.05E-09		-2.25E-02	9.08E-01		-2.25E-01	2.27E-01		-2.17E-01	2.04E-01		-1.43E+00	6.37E-18	Down	Unigene15140_All//gi|157673578|gb|ABV60088.1|//0.00E+00//trans-2-enoyl-CoA reductase [Gossypium hirsutum]	Unigene15140_All//2.00E-155//AT3G55360| CER10; 3-oxo-5-alpha-steroid 4-dehydrogenase/ fatty-acid elongase/ trans-2-enoyl-CoA reductase (NADPH)	Unigene15140_All//0.00E+00//TC156109		ko01040|Biosynthesis of unsaturated fatty acids	GO:0016491//GO:0031224//GO:0044238//GO:0044424	nr +
Unigene15141_All	1400	18.57	12.09	13.31	28.54	25.41	19.68	23.74	10.63	12.18	-6.20E-01	6.42E-09		-4.81E-01	1.24E-05		-1.68E-01	5.68E-02		-5.36E-01	4.93E-11		-1.16E+00	8.69E-38	Down	-9.63E-01	6.07E-29		Unigene15141_All//gi|18407012|ref|NP_566067.1|//1.00E-107//ABIL1 (Abi-1-like 1) [Arabidopsis thaliana] >gi|75160480|sp|Q8S8M5.1|ABIL1_ARATH RecName: Full=Protein ABIL1; AltName: Full=Abl interactor-like protein 1; Short=AtABIL1 >gi|20197375|gb|AAM15048.1| expressed protein [Arabidopsis thaliana] >gi|57240092|gb|AAW49256.1| Abl interactor-like protein-1 [Arabidopsis thaliana] >gi|108385243|gb|ABF85765.1| At2g46225 [Arabidopsis thaliana]	Unigene15141_All//3.00E-108//AT2G46225| ABIL1 (Abi-1-like 1)	Unigene15141_All//0.00E+00//TC136559				nr +
Unigene15142_All	695	20.70	19.39	16.70	38.78	33.49	31.00	44.29	17.26	10.03	-9.43E-02	5.86E-01		-3.10E-01	5.14E-02		-2.11E-01	4.80E-02		-3.23E-01	1.98E-03		-1.36E+00	9.22E-45	Down	-2.14E+00	7.04E-87	Down	Unigene15142_All//gi|15239564|ref|NP_197381.1|//6.00E-44//NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein [Arabidopsis thaliana] >gi|30687007|ref|NP_850849.1| NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein [Arabidopsis thaliana] >gi|297807915|ref|XP_002871841.1| NADH-ubiquinone oxidoreductase 19 kDa subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|21536569|gb|AAM60901.1| NADH:ubiquinone oxidoreductase-like protein [Arabidopsis thaliana] >gi|28466879|gb|AAO44048.1| At5g18800 [Arabidopsis thaliana] >gi|110735767|dbj|BAE99861.1| NADH:ubiquinone oxidoreductase like protein [Arabidopsis thaliana] >gi|297317678|gb|EFH48100.1| NADH-ubiquinone oxidoreductase 19 kDa subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15142_All//3.00E-45//AT5G18800| NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein	Unigene15142_All//0.00E+00//gi|164339361|gb|ES823264.1|ES823264		ko00190|Oxidative phosphorylation	GO:0005746//GO:0050136	nr +
Unigene15144_All	1711	9.69	3.35	6.32	14.67	9.50	13.88	1.93	0.37	0.42	-1.53E+00	6.22E-24	Down	-6.18E-01	1.19E-05		-6.27E-01	2.64E-10		-7.98E-02	5.67E-01		-2.40E+00	5.78E-11	Down	-2.20E+00	2.41E-10	Down	Unigene15144_All//gi|169972256|dbj|BAF99027.1|//1.00E-116//UDP-glucose:sesaminol 2"-O-glucoside-O-glucosyltransferase [Sesamum indicum]	Unigene15144_All//2.00E-55//AT5G49690| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene15144_All//0.00E+00//TC178592		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis	GO:0016740	nr -
Unigene15148_All	1551	86.12	265.24	172.52	113.89	150.33	253.39	26.20	33.58	29.38	1.62E+00	0.00E+00	Up	1.00E+00	9.69E-188	Up	4.01E-01	5.54E-40		1.15E+00	0.00E+00	Up	3.58E-01	3.99E-08		1.66E-01	2.16E-02		Unigene15148_All//gi|297799074|ref|XP_002867421.1|//1.00E-121//zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313257|gb|EFH43680.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15148_All//9.00E-112//AT4G29190| zinc finger (CCCH-type) family protein	Unigene15148_All//0.00E+00//TC162237	C3H		GO:0010260//GO:0023033//GO:0043231//GO:0046872	nr -
Unigene15149_All	1723	2.19	1.56	1.05	9.74	5.38	5.29	10.28	7.57	25.55	-4.88E-01	1.26E-01		-1.06E+00	1.50E-03		-8.58E-01	7.18E-12		-8.80E-01	4.36E-11		-4.42E-01	1.67E-04		1.31E+00	1.23E-61	Up	Unigene15149_All//gi|166574816|gb|ABQ42347.1|//5.00E-77//Dof6 transcription factor [Glycine max]	Unigene15149_All//1.00E-29//AT1G28310| Dof-type zinc finger domain-containing protein	Unigene15149_All//0.00E+00//TC139532	C2C2-Dof		GO:0003676//GO:0010468//GO:0046914	nr -
Unigene1515_All	1841	4.29	4.18	1.39	8.25	8.34	16.19	56.91	121.87	108.18	-3.67E-02	8.69E-01		-1.63E+00	3.47E-12	Down	1.56E-02	9.43E-01		9.72E-01	2.20E-22		1.10E+00	8.87E-230	Up	9.27E-01	1.26E-157		Unigene1515_All//gi|297834070|ref|XP_002884917.1|//1.00E-117//EMB2742 [Arabidopsis lyrata subsp. lyrata] >gi|297320757|gb|EFH61176.1| EMB2742 [Arabidopsis lyrata subsp. lyrata]	Unigene1515_All//1.00E-118//AT3G12670| emb2742 (embryo defective 2742); CTP synthase/ catalytic	Unigene1515_All//0.00E+00//TC151251		ko00240|Pyrimidine metabolism		nr -
Unigene15151_All	1538	1.94	1.35	1.73	14.58	14.13	10.25	11.13	4.43	3.19	-5.22E-01	1.50E-01		-1.64E-01	6.56E-01		-4.49E-02	7.81E-01		-5.08E-01	6.05E-06		-1.33E+00	1.97E-24	Down	-1.81E+00	6.12E-39	Down	Unigene15151_All//gi|297826871|ref|XP_002881318.1|//1.00E-50//IQ-domain 9 [Arabidopsis lyrata subsp. lyrata] >gi|297327157|gb|EFH57577.1| IQ-domain 9 [Arabidopsis lyrata subsp. lyrata]	Unigene15151_All//2.00E-39//AT2G33990| iqd9 (IQ-domain 9); calmodulin binding	Unigene15151_All//0.00E+00//TC162346			GO:0016020	nr -

Unigene15152_All	1955	6.26	29.08	12.09	6.98	9.78	5.31	0.00	0.81	1.08	2.22E+00	1.65E-131	Up	9.50E-01	1.34E-15		4.86E-01	4.27E-05		-3.94E-01	1.00E-02		9.67E+00	3.36E-11	Up	1.01E+01	3.90E-15	Up	Unigene15152_All//gi|18378959|ref|NP_563651.1|//1.00E-145//GPAT2 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 2); acyltransferase [Arabidopsis thaliana] >gi|83288232|sp|Q9FZ22.1|GPAT2_ARATH RecName: Full=Probable glycerol-3-phosphate acyltransferase 2; Short=AtGPAT2 >gi|9857535|gb|AAG00890.1|AC064879_8 Unknown protein [Arabidopsis thaliana] >gi|16930413|gb|AAL31892.1|AF419560_1 At1g02390/T6A9_17 [Arabidopsis thaliana] >gi|20453233|gb|AAM19855.1|At1g02390/T6A9_17 [Arabidopsis thaliana]	Unigene15152_All//3.00E-146//AT1G02390| GPAT2 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 2); acyltransferase			ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr -
Unigene15153_All	1475	1.10	1.34	2.02	7.60	21.10	23.33	28.15	39.47	27.66	2.85E-01	5.53E-01		8.79E-01	2.04E-02		1.47E+00	1.01E-48	Up	1.62E+00	2.76E-56	Up	4.88E-01	2.73E-15		-2.54E-02	7.65E-01		Unigene15153_All//gi|113203757|gb|ABI33979.1|//0.00E+00//phenylalanine ammonia lyase [Jatropha curcas]	Unigene15153_All//0.00E+00//AT2G37040| pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase	Unigene15153_All//0.00E+00//gi|164345296|gb|ES826680.1|ES826680		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00910|Nitrogen metabolism	GO:0006558//GO:0006575//GO:0016840//GO:0044424	nr -
Unigene15154_All	483	31.63	18.46	27.56	50.85	54.40	58.16	65.04	33.58	26.56	-7.77E-01	6.80E-08		-1.99E-01	2.24E-01		9.74E-02	4.47E-01		1.94E-01	7.90E-02		-9.54E-01	3.18E-26		-1.29E+00	1.54E-43	Down	Unigene15154_All//gi|15235985|ref|NP_194304.1|//1.00E-30//40S ribosomal protein S10 (RPS10A) [Arabidopsis thaliana] >gi|20139845|sp|Q9SK09.1|RS10I_ARATH RecName: Full=40S ribosomal protein S10-1		Unigene15154_All//0.00E+00//gi|109824545|gb|DW009370.1|DW009370		ko03010|Ribosome	GO:0010467//GO:0015935	nr +
Unigene15155_All	740	1.41	0.21	1.44	2.22	2.19	2.99	3.54	1.75	1.29	-2.78E+00	8.21E-04	Down	2.54E-02	9.89E-01		-2.25E-02	9.50E-01		4.29E-01	3.66E-01		-1.02E+00	3.65E-03		-1.46E+00	3.95E-05	Down			Unigene15155_All//3.00E-148//TC171831				
Unigene15156_All	1702	1.54	1.01	1.47	7.96	6.80	3.69	8.25	1.69	3.60	-6.03E-01	1.22E-01		-6.38E-02	8.77E-01		-2.28E-01	1.60E-01		-1.11E+00	4.83E-13	Down	-2.28E+00	5.85E-42	Down	-1.19E+00	1.01E-17	Down	Unigene15156_All//gi|18400732|ref|NP_566511.1|//0.00E+00//choline transporter-related [Arabidopsis thaliana]	Unigene15156_All//0.00E+00//AT3G15380| choline transporter-related	Unigene15156_All//0.00E+00//TC157543			GO:0016020	nr +
Unigene15157_All	1318	5.60	76.58	6.22	14.78	18.65	17.85	4.81	26.76	10.52	3.77E+00	0.00E+00	Up	1.53E-01	5.08E-01		3.36E-01	1.50E-03		2.73E-01	1.90E-02		2.48E+00	1.20E-114	Up	1.13E+00	6.00E-16	Up	Unigene15157_All//gi|4666360|gb|AAD26942.1|AF119050|//9.00E-52//zinc-finger protein 1 [Datisca glomerata]	Unigene15157_All//3.00E-29//AT3G49930| zinc finger (C2H2 type) family protein	Unigene15157_All//0.00E+00//TC152067	C2H2			nr +
Unigene15158_All	963	15.65	5.58	5.58	17.02	12.12	21.67	21.16	7.77	8.48	-1.49E+00	7.02E-21	Down	-1.49E+00	5.63E-20	Down	-4.90E-01	1.25E-04		3.48E-01	3.96E-03		-1.45E+00	9.66E-33	Down	-1.32E+00	1.85E-29	Down	Unigene15158_All//gi|297804652|ref|XP_002870210.1|//2.00E-85//At4g15770 [Arabidopsis lyrata subsp. lyrata] >gi|297316046|gb|EFH46469.1|At4g15770 [Arabidopsis lyrata subsp. lyrata]	Unigene15158_All//9.00E-87//AT4G15770| RNA binding / protein binding	Unigene15158_All//0.00E+00//TC135045			GO:0003676//GO:0042254//GO:0043231	nr -
Unigene15159_All	1714	8.79	8.48	7.83	9.15	18.52	11.86	7.35	10.44	16.85	-5.13E-02	7.37E-01		-1.67E-01	3.16E-01		1.02E+00	4.80E-28	Up	3.73E-01	2.20E-03		5.06E-01	1.42E-05		1.20E+00	2.30E-35	Up	Unigene15159_All//gi|224055321|ref|XP_002298479.1|//1.00E-165//cytochrome P450 [Populus trichocarpa] >gi|222845737|gb|EEE83284.1|cytochrome P450 [Populus trichocarpa]	Unigene15159_All//2.00E-114//AT3G56630| CYP94D2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506	nr -
Unigene1516_All	1613	4.93	17.31	4.26	6.24	6.47	11.12	22.78	81.49	76.84	1.81E+00	5.74E-50	Up	-2.11E-01	3.75E-01		5.23E-02	8.42E-01		8.33E-01	1.06E-10		1.84E+00	4.44E-292	Up	1.75E+00	4.01E-263	Up	Unigene1516_All//gi|115472185|ref|NP_001059691.1|//3.00E-44//Os07g0494900 [Oryza sativa Japonica Group] >gi|113611227|dbj|BAF21605.1|Os07g0494900 [Oryza sativa Japonica Group]	Unigene1516_All//1.00E-169//AT5G51150| unknown protein	Unigene1516_All//0.00E+00//TC147325				nr +
Unigene15162_All	1255	4.88	8.48	5.86	10.84	12.10	10.83	15.16	4.30	4.63	7.98E-01	5.83E-06		2.64E-01	2.66E-01		1.59E-01	3.28E-01		-5.00E-04	9.96E-01		-1.82E+00	2.56E-42	Down	-1.71E+00	4.43E-40	Down	Unigene15162_All//gi|15233958|ref|NP_195009.1|//1.00E-156//AtAUR1 (ATAURORA1); histone kinase(H3-S10 specific) / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|75335736|sp|Q9M077.1|AUR1_ARATH RecName: Full=Serine/threonine-protein kinase Aurora-1; Short=AtAur1; AltName: Full=Aurora-like kinase 1 >gi|55467118|emb|CAH69532.1|aurora-like kinase 1 [Arabidopsis thaliana] >gi|67858859|dbj|BAE00019.1|Aurora kinase [Arabidopsis thaliana]	Unigene15162_All//2.00E-157//AT4G32830| AtAUR1 (ATAURORA1); histone kinase(H3-S10 specific) / kinase/ protein serine/threonine kinase	Unigene15162_All//0.00E+00//TC155278				nr +
Unigene15163_All	1792	0.73	2.01	1.25	1.28	0.63	5.12	43.77	109.43	136.97	1.46E+00	2.10E-05	Up	7.74E-01	8.44E-02		-1.01E+00	1.11E-02		2.00E+00	2.53E-20	Up	1.32E+00	3.67E-269	Up	1.65E+00	0.00E+00	Up	Unigene15163_All//gi|15231757|ref|NP_190883.1|//1.00E-175//UGT73D1 (UDP-glucosyl transferase 73D1); UDP-glycosyltransferase/ transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|6630735|emb|CAB64218.1|glucosyltransferase-like protein [Arabidopsis thaliana]	Unigene15163_All//1.00E-176//AT3G53150| UGT73D1 (UDP-glucosyl transferase 73D1); UDP-glycosyltransferase/ transferase, transferring hexosyl groups			ko00908|Zeatin biosynthesis	GO:0035251	nr +
Unigene15166_All	784	29.96	9.63	8.35	44.10	23.19	37.91	94.38	27.51	31.61	-1.64E+00	7.04E-37	Down	-1.84E+00	8.92E-42	Down	-9.27E-01	2.46E-27		-2.18E-01	2.17E-02		-1.78E+00	1.42E-157	Down	-1.58E+00	7.31E-137	Down	Unigene15166_All//gi|125620176|gb|ABV46980.1|//7.00E-42//small molecular heat shock protein 10 [Nelumbo nucifera]	Unigene15166_All//7.00E-41//AT1G14980| CPN10 (CHAPERONIN 10); chaperone binding	Unigene15166_All//0.00E+00//TC156484			GO:0006950//GO:0032559//GO:0043231//GO:0044267//GO:0046914	nr -
Unigene15167_All	1800	6.66	3.77	3.20	11.01	6.87	11.44	20.11	7.41	7.92	-8.19E-01	6.64E-07		-1.06E+00	1.09E-09	Down	-6.82E-01	1.76E-09		5.49E-02	6.99E-01		-1.44E+00	3.02E-57	Down	-1.34E+00	4.43E-53	Down	Unigene15167_All//gi|297831116|ref|XP_002883440.1|//1.00E-136//brix domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329280|gb|EFH59699.1|brix domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene15167_All//2.00E-124//AT3G23620| brix domain-containing protein	Unigene15167_All//0.00E+00//ES806564				nr +
Unigene15168_All	1826	10.20	6.33	6.56	16.40	14.16	13.65	20.05	5.59	5.87	-6.89E-01	8.01E-08		-6.37E-01	1.47E-06		-2.11E-01	3.53E-02		-2.64E-01	8.72E-03		-1.84E+00	2.85E-82	Down	-1.77E+00	2.80E-80	Down	Unigene15168_All//gi|20197242|gb|AC28772.2|//1.00E-111//expressed protein [Arabidopsis thaliana]	Unigene15168_All//0.00E+00//AT5G01620| unknown protein	Unigene15168_All//0.00E+00//gi|78349286|gb|DT569560.1|DT569560				nr +
Unigene15169_All	1282	34.61	30.24	18.03	12.47	11.76	37.80	0.23	1.92	2.70	-1.95E-01	1.93E-02		-9.41E-01	2.68E-28		-8.43E-02	6.03E-01		1.60E+00	8.59E-78	Up	3.06E+00	1.29E-10	Up	3.55E+00	5.04E-17	Up	Unigene15169_All//gi|115476924|ref|NP_001062058.1|//3.00E-83//Os08g0480200 [Oryza sativa Japonica Group] >gi|113624027|dbj|BAF23972.1|Os08g0480200 [Oryza sativa Japonica Group]	Unigene15169_All//1.00E-62//AT2G36690| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene15169_All//0.00E+00//gi|78328739|gb|DT549013.1|DT549013		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr +
Unigene1517_All	2885	3.17	1.26	1.13	8.72	6.67	2.94	6.54	1.49	2.13	-1.33E+00	4.83E-11	Down	-1.50E+00	1.83E-12	Down	-3.86E-01	1.40E-04		-1.57E+00	4.37E-40	Down	-2.13E+00	1.49E-51	Down	-1.62E+00	7.63E-37	Down	Unigene1517_All//gi|297848532|ref|XP_002892147.1|//1.00E-123//kinase interacting family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337989|gb|EFH68406.1|kinase interacting family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1517_All//4.00E-109//AT1G03080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053), KIP1-like (InterPro:IPR011684); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT3G22790.1); Has 169162 Blast hits to 69460 proteins in 2232 species: Archae - 2114; Bacteria - 2494; Metazoa - 82448; Fungi - 11850; Plants - 6375; Viruses - 760; Other Eukaryotes - 40701 (source: NCBI BLink).	Unigene1517_All//0.00E+00//ES791078				nr +
Unigene15170_All	426	0.12	2.74	0.25	1.05	1.94	0.64	0.40	1.77	1.40	4.48E+00	1.19E-05	Up	1.03E+00	7.03E-01		8.82E-01	2.93E-01		-7.26E-01	5.32E-01		2.15E+00	9.17E-03		1.82E+00	3.94E-02		Unigene15170_All//gi|18398148|ref|NP_565389.1|//4.00E-42//3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein [Arabidopsis thaliana] >gi|20198183|gb|AAD26491.2|expressed protein [Arabidopsis thaliana]	Unigene15170_All//3.00E-35//AT2G16530| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein				GO:0016491//GO:0031224//GO:0043231//GO:0044238	nr +
Unigene15171_All	1063	0.49	1.72	1.10	0.94	1.78	1.61	2.19	1.42	3.22	1.80E+00	6.20E-04	Up	1.16E+00	8.16E-02		9.27E-01	5.02E-02		7.85E-01	1.31E-01		-6.28E-01	9.58E-02		5.59E-01	5.40E-02		Unigene15171_All//gi|297836348|ref|XP_002886056.1|//7.00E-41//3-oxo-5-alpha-steroid 4-dehydrogenase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331896|gb|EFH62315.1| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15171_All//1.00E-41//AT2G16530| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein	Unigene15171_All//0.00E+00//gi|109855207|gb|DW484186.1|DW484186			GO:0016491//GO:0031224//GO:0043231//GO:0044238	nr -
Unigene15172_All	623	31.91	42.37	36.58	41.50	39.80	46.32	26.54	26.50	11.96	4.09E-01	1.11E-04		1.97E-01	1.27E-01		-6.04E-02	6.40E-01		1.59E-01	1.61E-01		-1.90E-03	1.02E+00		-1.15E+00	1.48E-19	Down			Unigene15172_All//0.00E+00//gi|21096817|gb|BQ409130.1|BQ409130				
Unigene15173_All	241	0.00	0.00	0.00	0.00	0.00	0.19	2.98	0.52	0.17	null	null		null	null		null	null		7.55E+00	6.96E-01		-2.52E+00	4.69E-03		-4.17E+00	1.64E-04	Down	Unigene15173_All//gi|15232579|ref|NP_191037.1|//4.00E-09//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|7258381|emb|CAB77597.1| RNA binding protein-like [Arabidopsis thaliana]	Unigene15173_All//2.00E-09//AT3G54770| RNA recognition motif (RRM)-containing protein	Unigene15173_All//5.00E-55//TC136308			GO:0003676	nr -
Unigene15174_All	1210	4.54	2.68	0.70	8.77	4.67	3.06	22.54	12.75	11.82	-7.61E-01	2.73E-03		-2.69E+00	8.13E-16	Down	-9.10E-01	1.85E-08		-1.52E+00	1.89E-16	Down	-8.22E-01	5.61E-18		-9.31E-01	1.15E-22		Unigene15174_All//gi|21536939|gb|AAM61280.1|//3.00E-66//RNA binding protein-like [Arabidopsis thaliana]	Unigene15174_All//3.00E-60//AT3G54770| RNA recognition motif (RRM)-containing protein	Unigene15174_All//0.00E+00//TC132634		ko03040|Spliceosome	GO:0003676	nr +
Unigene15177_All	1275	0.25	0.40	0.08	0.43	0.51	0.57	1.62	1.44	3.41	6.91E-01	4.99E-01		-1.56E+00	3.30E-01		2.56E-01	8.22E-01		3.99E-01	6.52E-01		-1.72E-01	6.78E-01		1.07E+00	3.44E-05	Up	Unigene15177_All//gi|297817250|ref|XP_002876508.1|//1.00E-128//rhomboid family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322346|gb|EFH52767.1|rhomboid family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15177_All//2.00E-122//AT3G59520| ATRBL13 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 13)	Unigene15177_All//0.00E+00//ES823034			GO:0031224	nr -

Unigene15178_All	1100	53.75	47.08	40.42	43.52	42.86	34.41	10.84	6.04	4.64	-1.91E-01	6.96E-03		-4.11E-01	4.27E-09		-2.22E-02	8.20E-01		-3.39E-01	5.52E-06		-8.43E-01	1.19E-08		-1.23E+00	8.77E-16	Down	Unigene15178_All//gi|71089837|gb|AI23775.1|/7.00E-74//plastid division regulator MinE [Glycine max]	Unigene15178_All//2.00E-72//AT1G69390| ATMINE1 (Arabidopsis homologue of bacterial MinE 1); protein binding	Unigene15178_All//0.00E+00//TC146257			GO:0000917//GO:0005515//GO:0009658//GO:0043231	nr +
Unigene15179_All	1026	1.33	1.53	2.80	4.61	5.91	4.31	7.75	2.40	2.83	2.07E-01	6.79E-01		1.08E+00	5.58E-03		3.57E-01	1.58E-01		-9.65E-02	7.46E-01		-1.69E+00	2.08E-16	Down	-1.45E+00	9.34E-14	Down	Unigene15179_All//gi|224064501|ref|XP_002301506.1|/2.00E-56//multidrug resistance protein ABC transporter family protein [Populus trichocarpa] >gi|222843232|gb|EEE80779.1| multidrug resistance protein ABC transporter family protein [Populus trichocarpa]	Unigene15179_All//8.00E-18//AT4G02090| unknown protein					nr +
Unigene1518_All	2346	12.80	3.28	5.92	80.88	48.88	38.39	86.31	3.24	21.28	-1.96E+00	3.41E-60	Down	-1.11E+00	3.07E-25	Down	-7.27E-01	1.02E-97		-1.08E+00	5.24E-167	Down	-4.73E+00	0.00E+00	Down	-2.02E+00	0.00E+00	Down	Unigene1518_All//gi|2493321|sp|Q40588.1|ASO_TOBAC//0.00E+00//RecName: Full=L-ascorbate oxidase; Short=Ascorbase; Short=ASO; Flags: Precursor >gi|599594|dbj|BAA07734.1| ascorbate oxidase precursor [Nicotiana tabacum]	Unigene1518_All//0.00E+00//AT5G21100| L-ascorbate oxidase, putative	Unigene1518_All//0.00E+00//TC132158		ko00053|Ascorbate and aldarate metabolism		nr +
Unigene15180_All	1215	3.01	2.63	1.75	30.67	8.73	4.68	2.02	0.34	0.82	-1.98E-01	5.65E-01		-7.82E-01	2.00E-02		-1.81E+00	6.70E-84	Down	-2.71E+00	3.62E-120	Down	-2.55E+00	6.67E-09	Down	-1.30E+00	3.13E-04	Down	Unigene15180_All//gi|297825631|ref|XP_002880698.1|/1.00E-154//sulfate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326537|gb|EFH56957.1| sulfate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene15180_All//6.00E-139//AT2G25680| MOT1 (molybdate transporter 1); molybdate ion transmembrane transporter/ sulfate transmembrane transporter	Unigene15180_All//0.00E+00//TC165538				nr +
Unigene15182_All	628	5.83	7.02	12.72	17.45	15.30	13.52	9.22	4.86	5.39	2.67E-01	3.74E-01		1.12E+00	2.55E-07	Up	-1.90E-01	3.18E-01		-3.68E-01	3.71E-02		-9.25E-01	2.92E-05		-7.74E-01	2.85E-04		Unigene15182_All//gi|297298819|gb|ACI23561.1|/7.00E-66//agamous-like protein 2 [Gossypium barbadense]	Unigene15182_All//9.00E-33//AT3G58780| SHP1 (SHATTERPROOF 1); DNA binding / protein binding / transcription factor	Unigene15182_All//3.00E-157//TC157397	MADS		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene15185_All	1418	2.07	1.11	1.24	7.03	5.39	2.80	0.95	1.50	3.93	-9.00E-01	1.37E-02		-7.38E-01	5.40E-02		-3.82E-01	3.17E-02		-1.33E+00	1.02E-12	Down	6.56E-01	9.89E-02		2.04E+00	2.79E-15	Up	Unigene15185_All//gi|116309014|emb|CAH66131.1|/2.00E-25//OSIGBa0133L04.5 [Oryza sativa (indica cultivar-group)]	Unigene15185_All//7.00E-19//AT3G09510| nucleic acid binding	Unigene15185_All//3.00E-26//gi|72268834|gb|DT046903.1|DT046903				nr -
Unigene15187_All	1428	5.35	3.83	4.89	13.92	9.94	8.76	4.94	1.96	1.93	-4.81E-01	2.33E-02		-1.31E-01	6.03E-01		-4.86E-01	2.02E-05		-6.68E-01	2.61E-08		-1.33E+00	1.36E-10	Down	-1.36E+00	2.89E-11	Down	Unigene15187_All//gi|297805474|ref|XP_002870621.1|/1.00E-160//nucleotide-sugar transporter family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316457|gb|EFH46880.1| nucleotide-sugar transporter family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15187_All//2.00E-160//AT5G41760| nucleotide-sugar transporter family protein	Unigene15187_All//0.00E+00//CO132145			GO:0044464	nr +
Unigene15191_All	534	54.38	82.17	28.22	34.14	31.53	16.58	19.79	19.10	7.31	5.96E-01	1.58E-13		-9.46E-01	7.05E-19		-1.15E-01	4.52E-01		-1.04E+00	1.02E-15	Down	-5.17E-02	7.76E-01		-1.44E+00	9.16E-18	Down	Unigene15191_All//gi|23329532|ref|NP_683303.1|/4.00E-13//RTFL17 (ROOTUNDIFOLIA LIKE 17) [Arabidopsis thaliana] >gi|4850407|gb|AAD31077.1|AC007357_26 EST gb|T21221 comes from this gene [Arabidopsis thaliana] >gi|37955428|gb|AAP13819.1| DVL4 [Arabidopsis thaliana] >gi|91807634|gb|ABF47114.1| At1g13245 [Arabidopsis thaliana]	Unigene15191_All//2.00E-14//AT1G13245| RTFL17 (ROOTUNDIFOLIA LIKE 17)	Unigene15191_All//0.00E+00//TC170929			GO:0043231//GO:0048513	nr +
Unigene15193_All	687	0.00	0.00	0.08	0.00	0.05	1.64	6.65	0.49	1.04	null	null		6.28E+00	6.36E-01		5.65E+00	8.30E-01		1.07E+01	9.83E-07	Up	-3.77E+00	5.88E-23	Down	-2.67E+00	2.25E-17	Down	Unigene15193_All//gi|1052747|emb|CAA49471.1|/2.00E-19//18,9 KDa ABA-induced protein [Hordeum vulgare subsp. vulgare] >gi|11558300|emb|CAC17774.1| stress responsive protein [Hordeum vulgare subsp. vulgare]						nr +
Unigene15194_All	1068	47.57	35.68	109.54	67.07	49.23	67.11	0.24	0.12	0.15	-4.15E-01	1.93E-08		1.20E+00	1.89E-110	Up	-4.46E-01	1.64E-15		8.00E-04	9.90E-01		-1.02E+00	4.95E-01		-6.71E-01	6.05E-01		Unigene15194_All//gi|1052747|emb|CAA49471.1|/1.00E-17//18,9 KDa ABA-induced protein [Hordeum vulgare subsp. vulgare] >gi|11558300|emb|CAC17774.1| stress responsive protein [Hordeum vulgare subsp. vulgare]						nr -
Unigene15195_All	1343	4.48	8.98	0.59	7.01	18.18	19.30	12.18	12.57	121.62	1.00E+00	2.18E-09	Up	-2.91E+00	9.39E-19	Down	1.37E+00	1.58E-34	Up	1.46E+00	1.13E-36	Up	4.54E-02	7.50E-01		3.32E+00	0.00E+00	Up	Unigene15195_All//gi|4666360|gb|AAD26942.1|AF119050_1//1.00E-63//zinc-finger protein 1 [Datisca glomerata]	Unigene15195_All//4.00E-54//AT1G27730| STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding	Unigene15195_All//0.00E+00//TC144138	C2H2		GO:0005488	nr +
Unigene15197_All	671	0.16	3.02	3.10	5.35	7.34	6.93	3.02	3.86	2.61	4.28E+00	3.01E-09	Up	4.31E+00	3.63E-09	Up	4.57E-01	9.78E-02		3.75E-01	2.15E-01		3.53E-01	3.54E-01		-2.11E-01	6.05E-01		Unigene15197_All//gi|297810811|ref|XP_002873289.1|/1.00E-50//sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319126|gb|EFH49548.1| sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15197_All//7.00E-52//AT5G07010| ST2A (SULFOTRANSFERASE 2A); hydroxyjasmonate sulfotransferase/ sulfotransferase	Unigene15197_All//0.00E+00//gi|48805592|gb|CO106906.1|CO106906		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0008146//GO:0009719//GO:0031407	nr +
Unigene15198_All	1182	4.29	12.30	9.42	8.81	14.95	14.94	7.58	15.81	9.37	1.52E+00	1.19E-20	Up	1.13E+00	4.89E-10	Up	7.63E-01	6.64E-10		7.62E-01	3.84E-09		1.06E+00	9.23E-19	Up	3.05E-01	4.58E-02		Unigene15198_All//gi|297810811|ref|XP_002873289.1|/7.00E-89//sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319126|gb|EFH49548.1| sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15198_All//1.00E-89//AT5G07010| ST2A (SULFOTRANSFERASE 2A); hydroxyjasmonate sulfotransferase/ sulfotransferase	Unigene15198_All//0.00E+00//TC133486		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0008146//GO:0009719//GO:0031407	nr -
Unigene15199_All	1990	1.21	2.01	0.86	4.33	3.67	5.31	12.85	5.44	11.23	7.34E-01	1.60E-02		-4.98E-01	2.46E-01		-2.39E-01	2.62E-01		2.94E-01	1.18E-01		-1.24E+00	1.69E-32	Down	-1.95E-01	4.82E-02		Unigene15199_All//gi|300507129|gb|ADK23940.1|/0.00E+00//KAS II [Gossypium hirsutum]	Unigene15199_All//0.00E+00//AT1G74960| FAB1 (FATTY ACID BIOSYNTHESIS 1); 3-oxoacyl-[acyl-carrier-protein] synthase/ fatty-acid synthase	Unigene15199_All//0.00E+00//TC137705		ko00061|Fatty acid biosynthesis	GO:0004312//GO:0006633//GO:0009536	nr +
Unigene152_All	1203	0.83	0.72	0.93	2.86	1.98	1.20	3.13	2.88	3.78	-2.07E-01	7.37E-01		1.70E-01	7.78E-01		-5.33E-01	1.04E-01		-1.25E+00	1.88E-04	Down	-1.17E-01	7.06E-01		2.71E-01	3.04E-01		Unigene152_All//gi|224095220|ref|XP_002310362.1|/4.00E-53//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222853265|gb|EEE90812.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene152_All//5.00E-28//AT1G50410| SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein					nr -
Unigene1520_All	2681	2.77	0.15	2.09	3.07	2.43	0.62	3.60	3.73	11.74	-4.20E+00	8.89E-33	Down	-4.10E-01	7.35E-02		-3.37E-01	1.01E-01		-2.30E+00	3.52E-22	Down	5.14E-02	7.82E-01		1.71E+00	7.23E-65	Up	Unigene1520_All//gi|222060082|emb|CAX28549.1|/5.00E-91//NBS-LLR resistance protein [Gossypium arboreum]	Unigene1520_All//7.00E-47//AT3G46530| RPP13 (RECOGNITION OF PERONOSPORA PARASITICA 13); ATP binding	Unigene1520_All//0.00E+00//TC136447		ko04626|Plant-pathogen interaction		nr +
Unigene15200_All	944	6.37	21.15	5.13	21.37	23.93	12.39	28.62	53.00	23.34	1.73E+00	9.87E-34	Up	-3.12E-01	2.36E-01		1.63E-01	2.04E-01		-7.86E-01	5.35E-11		8.89E-01	1.03E-36		-2.94E-01	1.38E-03		Unigene15200_All//gi|124359162|gb|ABR05685.1|/2.00E-23//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene15200_All//1.00E-06//AT3G09510| nucleic acid binding	Unigene15200_All//0.00E+00//gi|13352000|gb|BG442432.1|BG442432				nr +
Unigene15201_All	987	90.54	137.38	103.10	96.15	78.40	65.66	95.36	60.17	42.50	6.02E-01	6.84E-41		1.87E-01	5.47E-04		-2.95E-01	1.34E-09		-5.50E-01	1.46E-26		-6.64E-01	1.27E-41		-1.17E+00	1.53E-109	Down	Unigene15201_All//gi|21901929|emb|CAC86383.1|/1.00E-133//carboxypeptidase type III [Theobroma cacao]	Unigene15201_All//6.00E-105//AT3G10410| scp149 (serine carboxypeptidase-like 49); serine-type carboxypeptidase	Unigene15201_All//0.00E+00//TC135113		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene15202_All	760	1.38	5.67	1.75	12.72	20.12	12.72	103.53	148.76	130.37	2.04E+00	1.37E-09	Up	3.47E-01	5.78E-01		6.62E-01	7.24E-07		2.00E-04	9.99E-01		5.23E-01	1.05E-32		3.33E-01	2.87E-13		Unigene15202_All//gi|18402886|ref|NP_565738.1|/1.00E-08//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|15982856|gb|AAL09775.1| At2g32150/F22D22.10 [Arabidopsis thaliana] >gi|20334756|gb|AAM16239.1| At2g32150/F22D22.10 [Arabidopsis thaliana]	Unigene15202_All//5.00E-10//AT3G32150| haloacid dehalogenase-like hydrolase family protein	Unigene15202_All//0.00E+00//BE052211				nr +
Unigene15206_All	1915	3.03	9.53	4.06	4.11	4.10	3.56	7.18	8.97	1.48	1.65E+00	6.07E-29	Up	4.21E-01	5.76E-02		-3.50E-03	9.80E-01		-2.07E-01	3.94E-01		3.22E-01	8.36E-03		-2.28E+00	2.40E-42	Down	Unigene15206_All//gi|15228865|ref|NP_188922.1|/1.00E-101//AT-HSFA6B; DNA binding / transcription factor [Arabidopsis thaliana] >gi|75311595|sp|Q9LUH8.1|HFA6B_ARATH RecName: Full=Heat stress transcription factor A-6b; Short=AtHsfA6b; AltName: Full=AtHsf-07 >gi|9279701|dbj|BAB01258.1| heat shock transcription factor-like protein [Arabidopsis thaliana]	Unigene15206_All//1.00E-99//AT3G22830| AT-HSFA6B; DNA binding / transcription factor	Unigene15206_All//0.00E+00//gi|78341176|gb|DT561450.1|DT561450	HSF			nr +
Unigene15207_All	2160	0.92	3.07	0.89	1.34	1.08	0.96	1.08	2.07	0.33	1.74E+00	9.19E-12	Up	-5.27E-02	9.19E-01		-3.03E-01	4.44E-01		-4.76E-01	2.21E-01		9.43E-01	2.35E-04		-1.70E+00	1.38E-05	Down	Unigene15207_All//gi|15228865|ref|NP_188922.1|/1.00E-101//AT-HSFA6B; DNA binding / transcription factor [Arabidopsis thaliana] >gi|75311595|sp|Q9LUH8.1|HFA6B_ARATH RecName: Full=Heat stress transcription factor A-6b; Short=AtHsfA6b; AltName: Full=AtHsf-07 >gi|9279701|dbj|BAB01258.1| heat shock transcription factor-like protein [Arabidopsis thaliana]	Unigene15207_All//7.00E-99//AT3G22830| AT-HSFA6B; DNA binding / transcription factor	Unigene15207_All//0.00E+00//gi|78341176|gb|DT561450.1|DT561450	HSF			nr +
Unigene15209_All	1078	6.16	14.20	9.83	34.15	51.59	42.27	14.71	21.21	7.61	1.20E+00	1.95E-15	Up	6.73E-01	2.06E-04		5.95E-01	9.11E-20		3.08E-01	7.09E-05		5.28E-01	2.18E-07		-9.50E-01	5.50E-14		Unigene15209_All//gi|166203244|gb|ABY84662.1|/1.00E-48//transcription factor [Glycine max]	Unigene15209_All//6.00E-31//AT3G56400| WRKY70; transcription factor/ transcription repressor	Unigene15209_All//0.00E+00//TC143644	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0002218//GO:0005488//GO:0009627//GO:0009719//GO:0009743//GO:0009987//GO:0030528	nr +
Unigene15215_All	1061	44.09	56.54	35.88	142.12	181.17	261.40	236.31	485.40	325.92	3.59E-01	1.12E-07		-2.97E-01	2.45E-04		3.50E-01	8.77E-26		8.79E-01	8.68E-173		1.04E+00	0.00E+00	Up	4.64E-01	4.90E-81						Unigene15215_All//0.00E+00//TC173689				
Unigene15221_All	1014	2.53	4.85	2.99	2.06	1.63	2.18	3.71	2.68	1.65	9.39E-01	5.95E-04		2.44E-01	5.33E-01		-3.40E-01	4.68E-01		8.10E-02	8.72E-01		-4.70E-01	1.04E-01		-1.17E+00	3.04E-05	Down	Unigene15221_All//gi|22331889|ref|NP_191650.2|/1.00E-108//catalytic/ methyltransferase [Arabidopsis thaliana]	Unigene15221_All//4.00E-109//AT3G60910| catalytic/ methyltransferase	Unigene15221_All//0.00E+00//gi|109875303|gb|DW504277.1|DW504277			GO:0008168	nr -
Unigene15222_All	878	2.56	2.89	6.31	2.89	5.80	4.58	9.82	9.28	20.19	1.71E-01	6.58E-01		1.30E+00	1.87E-06	Up	1.00E+00	8.35E-05	Up	6.62E-01	3.13E-02		-8.17E-02	6.83E-01		1.04E+00	9.40E-18	Up			Unigene15222_All//6.00E-67//gi|84164032|gb|DR452680.1|DR452680				

Unigene15223_All	1296	2.95	44.57	2.84	5.38	9.01	19.06	4.11	11.09	20.38	3.92E+00	6.68E-238	Up	-5.59E-02	8.68E-01		7.43E-01	1.90E-06		1.82E+00	7.57E-48	Up	1.43E+00	5.65E-23	Up	2.31E+00	8.96E-81	Up	Unigene15223_All//gi|27476089|gb|AA017020.1|//6.00E-16//Hypothetical protein [Oryza sativa Japonica Group] >gi|108705833|gb|ABF93628.1| expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene15223_All//4.00E-46//AT4G24110| unknown protein	Unigene15223_All//0.00E+00//TC161998				nr -
Unigene15224_All	730	10.18	12.63	7.95	20.06	13.11	21.28	11.41	6.01	5.24	3.12E-01	1.14E-01		-3.56E-01	1.27E-01		-6.13E-01	5.06E-06		8.52E-02	6.14E-01		-9.24E-01	3.32E-07		-1.12E+00	6.09E-10	Down	Unigene15224_All//gi|28416791|gb|AA042926.1|//9.00E-18//At4g39300 [Arabidopsis thaliana]	Unigene15224_All//2.00E-13//AT4G39300| unknown protein	Unigene15224_All//0.00E+00//TC173142			GO:0009536	nr +
Unigene15226_All	1101	3.47	7.50	5.56	6.20	6.07	6.40	7.60	4.86	6.59	1.11E+00	9.24E-08	Up	6.81E-01	6.16E-03		-3.08E-02	9.01E-01		4.60E-02	8.65E-01		-6.46E-01	2.81E-04		-2.07E-01	2.70E-01		Unigene15226_All//gi|18397049|ref|NP_564326.1|//1.00E-100//ERD2 (ENDOPLASMIC RETICULUM RETENTION DEFECTIVE 2); KDEL sequence binding / receptor [Arabidopsis thaliana] >gi|544250|sp|P35402.1|ERD2_ARATH RecName: Full=ER lumen protein retaining receptor; AltName: Full=HDEL receptor >gi|9502409|gb|AAF88108.1|AC021043_1 endoplasmic reticulum retention receptor Erd2 [Arabidopsis thaliana] >gi|12323512|gb|AAG51724.1|AC006867_3 ER lumen protein retaining receptor; 3333-1007 [Arabidopsis thaliana] >gi|20260682|gb|AAM13239.1| ER lumen protein retaining receptor; 3333-1007 [Arabidopsis thaliana] >gi|32189301|gb|AAP75805.1| At1g29330 [Arabidopsis thaliana]	Unigene15226_All//1.00E-99//AT1G29330| ERD2 (ENDOPLASMIC RETICULUM RETENTION DEFECTIVE 2); KDEL sequence binding / receptor	Unigene15226_All//0.00E+00//TC178135			GO:0004871//GO:0005048//GO:0006810//GO:0031090//GO:0031224//GO:0003537//GO:0043231	nr -
Unigene15227_All	2151	0.63	0.38	0.45	2.36	1.83	1.07	20.07	3.87	7.43	-7.47E-01	1.93E-01		-5.05E-01	3.82E-01		-3.72E-01	1.67E-01		-1.14E+00	1.63E-05	Down	-2.38E+00	6.11E-134	Down	-1.43E+00	1.17E-69	Down	Unigene15227_All//gi|117940083|sp|Q0WUD6.1|PLT4_ARATH//0.00E+00//RecName: Full=Probable polyol transporter 4	Unigene15227_All//7.00E-179//AT2G20780| mannitol transporter, putative	Unigene15227_All//0.00E+00//TC171633			GO:0006810//GO:0008152//GO:0016628//GO:0022891//GO:0031224	nr -
Unigene15228_All	739	2.76	0.82	2.95	19.75	21.76	21.76	6.64	4.58	6.52	-1.75E+00	3.40E-04	Down	9.75E-02	8.21E-01		1.40E-01	3.93E-01		1.40E-01	3.94E-01		-5.35E-01	2.85E-02		-2.49E-02	9.40E-01		Unigene15228_All//gi|63115354|gb|AA533856.1|//1.00E-105//class III HD-zip protein [Gossypium barbadense]	Unigene15228_All//7.00E-88//AT5G60690| REV (REVOLUTA); DNA binding / lipid binding / transcription factor	Unigene15228_All//0.00E+00//TC136782	HB		GO:0001071//GO:0003006//GO:0003677//GO:0006351//GO:0009799//GO:0009933//GO:0009943//GO:0010468//GO:0043231//GO:0048829	nr +
Unigene15229_All	1174	11.90	40.87	26.94	19.65	29.39	35.24	3.67	3.77	2.07	1.78E+00	1.98E-83	Up	1.18E+00	3.32E-29	Up	5.81E-01	6.47E-12		8.43E-01	2.15E-24		3.89E-02	9.01E-01		-8.28E-01	1.05E-03		Unigene15229_All//gi|30689631|ref|NP_195044.2|//1.00E-98//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|208879516|gb|ACI31303.1| At4g33180 [Arabidopsis thaliana]	Unigene15229_All//2.00E-94//AT4G33180| hydrolase, alpha/beta fold family protein	Unigene15229_All//0.00E+00//TC134850			GO:0003824	nr +
Unigene15230_All	1162	0.86	6.19	2.06	1.89	1.60	2.02	0.47	0.47	0.41	2.86E+00	1.07E-22	Up	1.27E+00	3.90E-03		-2.37E-01	6.11E-01		9.96E-02	8.28E-01		-1.66E-02	1.02E+00		-2.01E-01	7.93E-01		Unigene15230_All//gi|30689631|ref|NP_195044.2|//1.00E-101//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|208879516|gb|ACI31303.1| At4g33180 [Arabidopsis thaliana]	Unigene15230_All//2.00E-96//AT4G33180| hydrolase, alpha/beta fold family protein	Unigene15230_All//0.00E+00//gi|78333936|gb|DT554210.1|DT554210			GO:0003824	nr -
Unigene15231_All	1128	6.54	2.43	3.30	10.07	7.48	11.29	27.55	7.63	9.08	-1.43E+00	4.82E-10	Down	-9.85E-01	1.29E-05		-4.29E-01	7.89E-03		1.65E-01	3.82E-01		-1.85E+00	2.54E-70	Down	-1.60E+00	3.36E-59	Down	Unigene15231_All//gi|297792663|ref|XP_002864216.1|//4.00E-69//ribosomal protein L9 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310051|gb|EFH40475.1| ribosomal protein L9 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15231_All//1.00E-69//AT5G53070| ribosomal protein L9 family protein	Unigene15231_All//0.00E+00//TC144996		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0022613//GO:0030529//GO:0043231	nr +
Unigene15232_All	1517	9.55	1.67	7.97	18.36	6.06	3.07	5.04	0.74	0.76	-2.52E+00	9.71E-40	Down	-2.62E-01	1.05E-01		-1.60E+00	2.45E-52	Down	-2.58E+00	4.48E-85	Down	-2.76E+00	1.14E-28	Down	-2.73E+00	2.93E-29	Down	Unigene15232_All//gi|15223991|ref|NP_172953.1|//1.00E-131//scp150 (serine carboxypeptidase-like 50); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75336113|sp|Q9M9Q6.1|SCP50_ARATH RecName: Full=Serine carboxypeptidase-like 50; Flags: Precursor >gi|6899645|gb|AAF31022.1|AC012189_4 Contains similarity to serine-type carboxypeptidase like protein from Arabidopsis thaliana gi|4678929 and contains two Serine carboxypeptidase domains PF|00450 >gi|19715607|gb|AAL91626.1| At1g15000/T15D22_7 [Arabidopsis thaliana] >gi|27362234|gb|AAO11536.1| At1g15000/T15D22_7 [Arabidopsis thaliana]	Unigene15232_All//2.00E-127//AT1G15000| scp150 (serine carboxypeptidase-like 50); serine-type carboxypeptidase	Unigene15232_All//1.00E-44//TC142344		ko00940|Phenylpropanoid biosynthesis	GO:0031410	nr -
Unigene15235_All	309	0.00	3.28	0.52	0.64	0.00	2.34	1.09	4.46	0.52	1.17E+01	7.26E-06	Up	9.01E+00	2.39E-01		-9.33E+00	8.44E-02		1.86E+00	4.71E-02		2.03E+00	3.35E-04	Up	-1.09E+00	3.55E-01			Unigene15235_All//8.00E-141//TC174279				
Unigene15237_All	2462	2.53	2.43	2.79	5.50	4.70	4.27	4.19	2.55	1.68	-5.84E-02	8.10E-01		1.42E-01	5.90E-01		-2.28E-01	1.60E-01		-3.65E-01	1.88E-02		-7.19E-01	5.86E-06		-1.32E+00	2.70E-15	Down	Unigene15237_All//gi|124301072|gb|AB004788.1|//4.00E-79//At5g11640 [Arabidopsis thaliana]	Unigene15237_All//1.00E-64//AT5G11640| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Thioredoxin fold (InterPro:IPR012335), Thioredoxin-like fold (InterPro:IPR012336); Has 154 Blast hits to 154 proteins in 61 species: Archae - 0; Bacteria - 0; Metazoa - 125; Fungi - 0; Plants - 20; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene15237_All//0.00E+00//TC146956				nr -
Unigene15238_All	1171	2.41	5.32	7.32	3.74	4.76	3.70	7.80	6.92	8.85	1.14E+00	2.85E-06	Up	1.60E+00	6.36E-13	Up	3.48E-01	1.93E-01		-1.59E-02	9.49E-01		-1.72E-01	3.85E-01		1.82E-01	2.86E-01			Unigene15238_All//1.00E-77//DW495271				
Unigene15239_All	2193	1.48	1.04	1.31	7.11	5.65	2.45	9.35	3.91	4.34	-5.09E-01	1.40E-01		-1.74E-01	6.16E-01		-3.31E-01	1.68E-02		-1.54E+00	2.46E-24	Down	-1.26E+00	8.43E-27	Down	-1.11E+00	1.16E-22	Down	Unigene15239_All//gi|13877707|gb|AAK43931.1|AF370612_1//3.00E-54//similar to squamosa-promoter binding protein 1 isoloq gi|1707009 [Arabidopsis thaliana]	Unigene15239_All//8.00E-51//AT1G69170| squamosa promoter-binding protein-like 6 (SPL6)	Unigene15239_All//0.00E+00//TC172287	SBP			nr -
Unigene1524_All	1800	71.48	52.58	68.49	51.25	53.49	45.21	68.05	29.47	32.03	-4.43E-01	1.31E-22		-6.17E-02	2.56E-01		6.16E-02	3.30E-01		-1.81E-01	9.01E-04		-1.21E+00	2.22E-146	Down	-1.09E+00	2.86E-127	Down	Unigene1524_All//gi|18390900|ref|NP_563818.1|//1.00E-168//strictosidine synthase family protein [Arabidopsis thaliana] >gi|16930481|gb|AAL31926.1|AF419594_1 At1g08470/T27G7_9 [Arabidopsis thaliana]	Unigene1524_All//2.00E-167//AT1G08470| strictosidine synthase family protein	Unigene1524_All//0.00E+00//TC154122		ko00901|Indole alkaloid biosynthesis		nr +
Unigene15240_All	583	1.79	3.82	0.18	4.19	4.78	10.15	1.52	1.72	2.46	1.09E+00	1.21E-02		-3.30E+00	4.59E-04	Down	1.93E-01	6.52E-01		1.28E+00	2.77E-07	Up	1.76E-01	7.73E-01		6.92E-01	1.51E-01		Unigene15240_All//gi|224104873|ref|XP_002313601.1|//3.00E-42//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222850009|gb|EEE87556.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene15240_All//1.00E-18//AT2G27300| NTL8 (NTM1-LIKE 8); transcription factor	Unigene15240_All//6.00E-26//CO111117	NAC		GO:0005488	nr -
Unigene15241_All	1356	0.89	1.53	1.34	1.65	2.56	3.16	1.84	0.68	2.06	7.88E-01	7.73E-02		5.89E-01	2.42E-01		6.34E-01	5.49E-02		9.37E-01	1.35E-03		-1.44E+00	1.15E-04	Down	1.61E-01	6.28E-01		Unigene15241_All//gi|224104873|ref|XP_002313601.1|//1.00E-112//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222850009|gb|EEE87556.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene15241_All//1.00E-79//AT5G22290| anac089 (Arabidopsis NAC domain containing protein 89); transcription factor	Unigene15241_All//2.00E-157//CO111117	NAC		GO:0001071//GO:0005488//GO:0006970//GO:0016020//GO:0032501	nr +
Unigene15244_All	1658	16.95	9.02	12.40	17.07	12.94	14.36	20.99	8.02	8.39	-9.11E-01	6.43E-18		-4.51E-01	1.90E-05		-3.99E-01	2.34E-05		-2.50E-01	1.76E-02		-1.39E+00	4.00E-52	Down	-1.32E+00	6.38E-50	Down	Unigene15244_All//gi|50345543|gb|AAT14744.1|//1.00E-141//4-amino-4-deoxychorismate lyase [Solanum lycopersicum]	Unigene15244_All//6.00E-119//AT5G57850| aminotransferase class IV family protein	Unigene15244_All//0.00E+00//TC135743		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis	GO:0008483	nr +
Unigene15245_All	1643	22.83	12.61	11.38	499.48	338.00	166.69	160.78	63.60	52.86	-8.56E-01	2.13E-21		-1.01E+00	1.00E-26	Down	-5.63E-01	6.54E-268		-1.58E+00	0.00E+00	Down	-1.34E+00	0.00E+00	Down	-1.60E+00	0.00E+00	Down	Unigene15245_All//gi|224085766|ref|XP_002307691.1|//0.00E+00//mtn21-like protein [Populus trichocarpa] >gi|222857140|gb|EEE94687.1| mtn21-like protein [Populus trichocarpa]	Unigene15245_All//2.00E-155//AT1G75500| nodulin MtN21 family protein	Unigene15245_All//0.00E+00//TC143852			GO:0044464	nr -
Unigene15248_All	616	33.04	48.78	43.83	28.22	46.06	37.69	26.63	56.79	35.89	5.62E-01	1.18E-08		4.08E-01	1.68E-04		7.07E-01	9.15E-14		4.17E-01	1.87E-04		1.09E+00	3.87E-36	Up	4.31E-01	2.26E-05		Unigene15248_All//gi|21593125|gb|AAM65074.1|//7.00E-64//Bax inhibitor-1 like [Arabidopsis thaliana]	Unigene15248_All//5.00E-52//AT5G47120| ATBI1 (BAX INHIBITOR 1)	Unigene15248_All//0.00E+00//ES834508			GO:0005488//GO:0006631//GO:0006950//GO:0006984//GO:0012505//GO:0031224//GO:0043066//GO:0043231	nr +
Unigene1525_All	206	53.59	41.81	30.76	548.20	578.21	410.64	86.61	35.51	37.52	-3.58E-01	4.06E-02		-8.01E-01	6.82E-06		7.69E-02	1.52E-01		-4.17E-01	3.72E-19		-1.29E+00	3.37E-24	Down	-1.21E+00	1.18E-22	Down	Unigene1525_All//gi|295389384|dbj|BAJ06362.1|//2.00E-31//alpha-tubulin [Alopecurus aequalis]	Unigene1525_All//6.00E-32//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene1525_All//5.00E-113//EX170352		ko04145|Phagosome		nr -
Unigene15252_All	933	20.64	15.10	20.20	13.29	14.58	9.05	3.90	1.34	2.14	-4.51E-01	3.31E-04		-3.06E-02	8.31E-01		1.33E-01	4.67E-01		-5.55E-01	4.15E-04		-1.54E+00	5.18E-07	Down	-8.68E-01	1.82E-03		Unigene15252_All//gi|6554182|gb|AAF16628.1|AC011661_6//1.00E-85//T23J18.10 [Arabidopsis thaliana]	Unigene15252_All//3.00E-76//AT1G11430| plastid developmental protein DAG, putative	Unigene15252_All//0.00E+00//gi|109869635|gb|DW498611.1|DW498611			GO:0009532	nr -
Unigene15253_All	418	29.41	137.10	75.80	43.02	47.70	78.12	53.00	91.39	81.87	2.22E+00	5.87E-133	Up	1.37E+00	1.16E-36	Up	1.49E-01	2.99E-01		8.61E-01	4.81E-20		7.86E-01	4.98E-23		6.27E-01	1.33E-14		Unigene15253_All//gi|186531506|ref|NP_001119419.1|//8.00E-06//CPu0RF14 (Conserved peptide upstream open reading frame 14) [Arabidopsis thaliana]	Unigene15253_All//5.00E-07//AT5G52552| CPu0RF14 (Conserved peptide upstream open reading frame 14)	Unigene15253_All//2.00E-170//gi|164294105|gb|ES818245.1|ES818245				nr -

Unigene15255_All	510	30.67	26.92	30.70	28.42	27.75	40.03	61.68	36.96	28.51	-1.88E-01	2.16E-01		1.10E-03	9.93E-01		-3.45E-02	8.34E-01		4.94E-01	3.34E-05		-7.39E-01	2.88E-17		-1.11E+00	1.34E-34	Down	Unigene15255_All//gi|297726827|ref|NP_001175777.1|//3.00E-27//0s09g0326850 [Oryza sativa Japonica Group] >gi|255678784|dbj|BAH94505.1|Os09g0326850 [Oryza sativa Japonica Group]	Unigene15255_All//6.00E-12//AT2G37975| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Yos1-like (InterPro:IPR013880); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54085.2); Has 146 Blast hits to 146 proteins in 66 species: Archae - 0; Bacteria - 0; Metazoa - 89; Fungi - 25; Plants - 26; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink).	Unigene15255_All//0.00E+00//gi|21094561|gb|BQ406874.1|BQ406874			GO:0031410	nr -
Unigene15256_All	668	14.73	14.64	14.75	23.71	21.03	25.29	31.90	17.71	14.49	-8.40E-03	9.84E-01		2.20E-03	9.89E-01		-1.73E-01	2.70E-01		9.26E-02	5.98E-01		-8.49E-01	5.51E-15		-1.14E+00	1.46E-24	Down	Unigene15256_All//gi|115453913|ref|NP_001050557.1|//9.00E-23//Os03g0581800 [Oryza sativa Japonica Group] >gi|41469325|gb|AAS07181.1|expressed protein [Oryza sativa Japonica Group] >gi|113549028|dbj|BAF12471.1|Os03g0581800 [Oryza sativa Japonica Group]	Unigene15256_All//4.00E-21//AT2G20820| unknown protein	Unigene15256_All//0.00E+00//gi|109891718|gb|DW520681.1|DW520681				nr -
Unigene15258_All	861	4.38	22.66	8.10	13.19	48.51	35.83	10.80	13.54	46.32	2.37E+00	2.20E-49	Up	8.89E-01	1.23E-04		1.88E+00	9.30E-92	Up	1.44E+00	1.10E-42	Up	3.26E-01	3.33E-02		2.10E+00	4.34E-108	Up	Unigene15258_All//gi|18390998|ref|NP_563839.1|//2.00E-36//transcription factor [Arabidopsis thaliana] >gi|75278846|sp|Q60482.1|BH149_ARATH RecName: Full=Transcription factor bHLH149; AltName: Full=Transcription factor EN 144; AltName: Full=bHLH transcription factor bHLH149; AltName: Full=Basic helix-loop-helix protein 149; Short=bHLH 149; Short=AtbHLH149 >gi|3249098|gb|AAC24081.1| ESTs gb|T04610, gb|N38459, gb|T45174, gb|R30481 and gb|N64971 come from this gene [Arabidopsis thaliana] >gi|27764992|gb|AAO23617.1|At1g09250 [Arabidopsis thaliana]	Unigene15258_All//4.00E-29//AT1G09250| transcription factor	Unigene15258_All//0.00E+00//gi|109890157|gb|DW519121.1|DW519121				nr -
Unigene15259_All	1165	16.30	6.31	14.76	6.11	6.65	7.71	2.18	1.22	0.68	-1.37E+00	3.73E-23	Down	-1.43E-01	3.39E-01		1.21E-01	6.19E-01		3.35E-01	9.93E-02		-8.36E-01	1.85E-02		-1.67E+00	6.58E-06	Down	Unigene15259_All//gi|18400310|ref|NP_566481.1|//3.00E-87//phosphoinositide phosphatase family protein [Arabidopsis thaliana] >gi|15215806|gb|AAK91448.1|At3g14201 [Arabidopsis thaliana] >gi|20334798|gb|AAM16260.1|at3g14201/at3g14201 [Arabidopsis thaliana] >gi|31415721|gb|AAP49835.1| SAC domain protein 2 [Arabidopsis thaliana]	Unigene15259_All//4.00E-81//AT3G14205| phosphoinositide phosphatase family protein	Unigene15259_All//0.00E+00//DW232172				nr -
Unigene1526_All	1687	187.70	72.72	76.61	143.18	142.23	93.43	52.56	30.30	20.71	-1.37E+00	0.00E+00	Down	-1.29E+00	0.00E+00	Down	-9.60E-03	8.25E-01		-6.16E-01	9.16E-82		-7.95E-01	2.15E-53		-1.34E+00	8.01E-129	Down	Unigene1526_All//gi|134035498|gb|AB047737.1|//0.00E+00//alpha-tubulin [Gossypium hirsutum]	Unigene1526_All//0.00E+00//AT1G50010| TUA2; structural constituent of cytoskeleton	Unigene1526_All//0.00E+00//TC166734		ko04145|Phagosome		nr +
Unigene15262_All	978	15.67	13.83	10.40	25.42	20.63	19.21	32.99	22.52	16.17	-1.80E-01	2.39E-01		-5.92E-01	5.94E-05		-3.01E-01	4.38E-03		-4.04E-01	1.64E-04		-5.51E-01	7.97E-11		-1.03E+00	2.90E-31	Down	Unigene15262_All//gi|297599905|ref|NP_001048085.2|//3.00E-61//Os02g0741900 [Oryza sativa Japonica Group] >gi|255671242|dbj|BAF09999.2|Os02g0741900 [Oryza sativa Japonica Group]	Unigene15262_All//2.00E-45//AT1G24050| unknown protein	Unigene15262_All//0.00E+00//gi|109883354|gb|DW512324.1|DW512324				nr +
Unigene15270_All	872	57.60	365.73	138.50	66.84	58.37	70.70	130.82	131.19	97.86	2.67E+00	0.00E+00	Up	1.27E+00	2.02E-123	Up	-1.96E-01	3.84E-03		8.10E-02	3.21E-01		4.10E-03	9.67E-01		-4.19E-01	7.24E-23		Unigene15270_All//gi|197131748|gb|ACH47392.1|//8.00E-82//ribosomal protein L23 [Erodium chrysanthum]	Unigene15270_All//1.00E-70//ATCG01310| encodes a chloroplast ribosomal protein L2, a constituent of the large subunit of the ribosomal complex	Unigene15270_All//0.00E+00//gi|109856184|gb|DW485163.1|DW485163		ko03010|Ribosome	GO:0003723//GO:0003824//GO:0005198//GO:0009536//GO:0010467//GO:0033279	nr -
Unigene15273_All	824	2.60	1.97	0.39	2.06	3.22	1.48	1.33	1.17	1.06	-4.04E-01	3.76E-01		-2.75E+00	1.29E-06	Down	6.47E-01	9.95E-02		-4.74E-01	3.86E-01		-1.94E-01	7.34E-01		-3.27E-01	5.82E-01				Unigene15273_All//6.00E-113//DW517995				
Unigene15274_All	1143	35.75	16.22	35.41	4.62	7.38	2.92	0.33	0.00	0.00	-1.14E+00	6.83E-37	Down	-1.39E-02	8.94E-01		6.76E-01	3.51E-04		-6.60E-01	1.06E-02		-8.38E+00	6.18E-03		-8.38E+00	4.19E-03		Unigene15274_All//gi|18402284|ref|NP_565696.1|//1.00E-96//catalytic [Arabidopsis thaliana] >gi|75099170|sp|Q64730.2|P2C26_ARATH RecName: Full=Probable protein phosphatase 2C 26; Short=AtPP2C26 >gi|20197099|gb|AAC16955.2|expressed protein [Arabidopsis thaliana]	Unigene15274_All//4.00E-98//AT2G30170| catalytic	Unigene15274_All//0.00E+00//TC171603			GO:0009536//GO:0016791	nr +
Unigene15277_All	839	10.54	12.98	21.33	8.79	8.95	8.18	11.14	8.82	11.44	3.01E-01	9.26E-02		1.02E+00	2.55E-13	Up	2.60E-02	9.28E-01		-1.03E-01	6.94E-01		-3.37E-01	5.28E-02		3.92E-02	8.32E-01				Unigene15277_All//4.00E-71//gi|48810464|gb|CO111777.1|CO111777				
Unigene1528_All	224	0.47	2.49	0.95	1.11	2.61	1.01	3.21	0.56	0.36	2.41E+00	3.93E-02		1.03E+00	5.92E-01		1.23E+00	2.33E-01		-1.41E-01	9.29E-01		-2.52E+00	4.69E-03		-3.17E+00	8.09E-04	Down	Unigene1528_All//gi|22331291|ref|NP_189009.2|//2.00E-31//KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor [Arabidopsis thaliana] >gi|21703149|gb|AAM74514.1|AT3g23670/MDB19_16 [Arabidopsis thaliana] >gi|23268687|gb|AAN16470.1|phragmoplast-associated kinesin-related protein 1-like protein [Arabidopsis thaliana] >gi|23268689|gb|AAN16471.1|phragmoplast-associated kinesin-related protein 1-like protein [Arabidopsis thaliana]	Unigene1528_All//1.00E-32//AT3G23670| KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor	Unigene1528_All//3.00E-121//ES836817				nr +
Unigene15280_All	3732	1.30	1.36	0.61	7.49	5.24	8.07	17.74	9.50	19.57	5.84E-02	8.32E-01		-1.09E+00	1.62E-04	Down	-5.15E-01	3.91E-08		1.08E-01	3.69E-01		-9.02E-01	1.57E-49		1.41E-01	1.17E-02		Unigene15280_All//gi|89357137|gb|ABD72304.1|//4.00E-22//apple fruit acidity-related protein [Malus x domestica]	Unigene15280_All//6.00E-17//AT3G22795| unknown protein	Unigene15280_All//0.00E+00//TC146646				nr -
Unigene15281_All	2560	0.20	1.88	0.10	0.97	1.79	1.94	4.10	4.60	6.02	3.20E+00	3.97E-17	Up	-9.75E-01	3.76E-01		8.79E-01	1.22E-03		9.96E-01	2.07E-04		1.69E-01	3.17E-01		5.56E-01	7.09E-06		Unigene15281_All//gi|186492938|ref|NP_001117544.1|//0.00E+00//AAA-type ATPase family protein [Arabidopsis thaliana]	Unigene15281_All//0.00E+00//AT1G64110| AAA-type ATPase family protein	Unigene15281_All//2.00E-103//ES819383			GO:0032559//GO:0042623//GO:0044464	nr +
Unigene15282_All	808	19.23	22.95	27.28	61.71	52.89	42.48	19.78	19.24	8.14	2.55E-01	5.68E-02		5.05E-01	2.77E-05		-2.23E-01	2.19E-03		-5.39E-01	9.95E-14		-3.97E-02	7.87E-01		-1.28E+00	2.58E-22	Down	Unigene15282_All//gi|22328609|ref|NP_193143.2|//3.00E-19//AAE15 (acyl-activating enzyme 15); long-chain-fatty-acid-[acyl-carrier-protein] ligase [Arabidopsis thaliana] >gi|17065456|gb|AAL32882.1| A6 anther-specific protein [Arabidopsis thaliana] >gi|340987885|gb|AAQ56775.1|At4g14070 [Arabidopsis thaliana] >gi|118420017|gb|ABK88270.1|chloroplast acyl ACP synthetase [Arabidopsis thaliana]	Unigene15282_All//2.00E-20//AT4G14070| AAE15 (acyl-activating enzyme 15); long-chain-fatty-acid-[acyl-carrier-protein] ligase	Unigene15282_All//0.00E+00//TC150654		ko04146|Peroxisome//ko00071|Fatty acid metabolism	GO:0006633//GO:0009526//GO:0015645	nr +
Unigene1529_All	3395	1.36	0.64	0.75	4.23	4.52	3.86	7.78	1.95	2.95	-1.08E+00	1.59E-04	Down	-8.49E-01	3.88E-03		9.83E-02	5.84E-01		-1.31E-01	4.61E-01		-2.00E+00	2.27E-66	Down	-1.40E+00	1.46E-41	Down	Unigene1529_All//gi|22331291|ref|NP_189009.2|//1.00E-141//KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor [Arabidopsis thaliana] >gi|21703149|gb|AAM74514.1|AT3g23670/MDB19_16 [Arabidopsis thaliana] >gi|23268687|gb|AAN16470.1|phragmoplast-associated kinesin-related protein 1-like protein [Arabidopsis thaliana] >gi|23268689|gb|AAN16471.1|phragmoplast-associated kinesin-related protein 1-like protein [Arabidopsis thaliana]	Unigene1529_All//1.00E-129//AT3G23670| KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor	Unigene1529_All//0.00E+00//ES836817				nr +
Unigene15291_All	780	27.70	11.43	17.95	34.68	22.87	18.07	10.41	3.43	3.22	-1.28E+00	1.30E-23	Down	-6.26E-01	2.70E-07		-6.01E-01	2.86E-10		-9.41E-01	1.60E-19		-1.60E+00	1.40E-15	Down	-1.69E+00	2.30E-17	Down	Unigene15291_All//gi|225435311|ref|XP_002285132.1|//2.00E-27//PREDICTED: similar to hydroxyproline-rich glycoprotein family protein [Vitis vinifera]		Unigene15291_All//0.00E+00//TC144905				nr +
Unigene15292_All	2727	0.46	2.45	1.46	1.10	0.37	0.60	7.29	8.80	7.76	2.41E+00	1.14E-17	Up	1.67E+00	1.06E-06	Up	-1.58E+00	6.09E-06	Down	-8.78E-01	1.45E-02		2.72E-01	7.90E-03		9.02E-02	4.62E-01		Unigene15292_All//gi|264664459|sp|C0LGJ1.1|Y1743_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g74360; Flags: Precursor >gi|224589485|gb|ACN59276.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene15292_All//0.00E+00//AT1G74360| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0016301//GO:0043231	nr -
Unigene15293_All	1635	158.21	707.39	422.35	75.74	95.89	184.63	25.11	55.52	36.23	2.16E+00	0.00E+00	Up	1.42E+00	0.00E+00	Up	3.40E-01	5.16E-20		1.29E+00	0.00E+00	Up	1.14E+00	1.02E-99	Up	5.29E-01	2.31E-18		Unigene15293_All//gi|17064820|gb|AAL32564.1|//1.00E-146//Unknown protein [Arabidopsis thaliana]	Unigene15293_All//2.00E-133//AT3G17800| mRNA level of the MEB5.2 gene (At3g17800) remains unchanged after cutting the inflorescence stem	Unigene15293_All//0.00E+00//TC140136				nr +
Unigene15294_All	1014	16.61	9.54	7.09	13.46	13.86	11.76	15.97	10.92	9.39	-8.00E-01	5.02E-09		-1.23E+00	8.51E-17	Down	4.17E-02	8.23E-01		-1.95E-01	2.54E-01		-5.48E-01	8.41E-06		-7.66E-01	3.64E-10		Unigene15294_All//gi|2673910|gb|AAB88644.1|//3.00E-30//expressed protein [Arabidopsis thaliana]	Unigene15294_All//4.00E-20//AT3G57930| unknown protein	Unigene15294_All//0.00E+00//TC172596				nr -

Unigene15298_All	1605	5.25	1.52	2.22	11.27	5.34	8.92	9.85	4.66	4.87	-1.79E+00	1.98E-15	Down	-1.24E+00	8.10E-09	Down	-1.08E+00	1.72E-18	Down	-3.37E-01	1.06E-02		-1.08E+00	1.69E-16	Down	-1.02E+00	1.55E-15	Down	Unigene15298_All//gi|297840495|ref|XP_002888129.1|//1.00E-152//ATRPAC43 [Arabidopsis lyrata subsp. lyrata] >gi|297333970|gb|EFH64388.1|ATRPAC43 [Arabidopsis lyrata subsp. lyrata]	Unigene15298_All//1.00E-144//AT1G60620| ATRPAC43; DNA binding / DNA-directed RNA polymerase/ protein dimerization	Unigene15298_All//0.00E+00//TC173156		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003676//GO:0000515//GO:0010467//GO:0031981//GO:0034062	nr +
Unigene15299_All	829	3.79	4.10	3.79	14.24	15.29	11.44	15.81	19.11	6.92	1.13E-01	7.29E-01		1.10E-03	9.96E-01		1.02E-01	6.01E-01		-3.16E-01	6.77E-02		2.73E-01	3.63E-02		-1.19E+00	1.45E-16	Down	Unigene15299_All//gi|224098854|ref|XP_002311292.1|//2.00E-111//predicted protein [Populus trichocarpa] >gi|222851112|gb|EEE88659.1|predicted protein [Populus trichocarpa]		Unigene15299_All//0.00E+00//CO076151				nr +
Unigene1530_All	2206	9.44	2.43	5.75	43.63	37.84	21.48	5.31	6.54	2.40	-1.96E+00	1.09E-41	Down	-7.16E-01	9.08E-09		-2.05E-01	3.71E-05		-1.02E+00	3.49E-78	Down	3.00E-01	2.78E-02		-1.14E+00	5.22E-14	Down	Unigene1530_All//gi|15218183|ref|NP_175630.1|//0.00E+00//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|75186219|sp|Q9M817.1|PTR2X_ARATH RecName: Full=Probable peptide transporter At1g52190	Unigene1530_All//0.00E+00//AT1G52190| proton-dependent oligopeptide transport (POT) family protein	Unigene1530_All//0.00E+00//TC143284				nr +
Unigene15300_All	1738	8.91	1.66	5.91	0.69	0.97	0.62	11.04	5.15	3.51	-2.42E+00	1.27E-40	Down	-5.92E-01	5.43E-05		4.97E-01	3.60E-01		-1.41E-01	8.16E-01		-1.10E+00	1.73E-20	Down	-1.66E+00	1.23E-38	Down	Unigene15300_All//gi|297828519|ref|XP_002882142.1|//1.00E-129//endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327981|gb|EFH58401.1|endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15300_All//3.00E-123//AT2G48030| endonuclease/exonuclease/phosphatase family protein	Unigene15300_All//0.00E+00//gi|78346975|gb|DT567249.1|DT567249				nr -
Unigene15302_All	698	23.24	91.03	78.88	41.32	55.16	143.77	50.15	58.92	67.41	1.97E+00	1.96E-126	Up	1.76E+00	4.27E-92	Up	4.17E-01	1.82E-07		1.80E+00	1.11E-189	Up	2.32E-01	2.29E-03		4.27E-01	2.99E-10		Unigene15302_All//gi|10716963|gb|AAG21984.1|AF270978_1//3.00E-57//LYTB-like protein precursor [Adonis aestivalis var. palaestina]	Unigene15302_All//5.00E-49//AT4G34350| HDR (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE REDUCTASE); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase/ 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Unigene15302_All//0.00E+00//gi|109878875|gb|DW507845.1|DW507845		ko00900|Terpenoid backbone biosynthesis	GO:0006090//GO:0006721//GO:0016726	nr -
Unigene15303_All	1597	11.17	6.92	11.17	13.16	12.12	13.63	26.05	13.69	11.28	-6.92E-01	1.43E-07		-2.00E-04	9.99E-01		-1.19E-01	3.96E-01		5.04E-02	7.15E-01		-9.29E-01	5.61E-33		-1.21E+00	1.03E-51	Down	Unigene15303_All//gi|297803826|ref|XP_002869797.1|//1.00E-170//mitochondrial dihydroorotase [Arabidopsis lyrata subsp. lyrata] >gi|297315633|gb|EFH46056.1|mitochondrial dihydroorotase [Arabidopsis lyrata subsp. lyrata]	Unigene15303_All//3.00E-170//AT4G22930| PYR4 (PYRIMIDIN 4); dihydroorotase/ hydrolase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides	Unigene15303_All//0.00E+00//gi|164367461|gb|ES827223.1|ES827223		ko00240|Pyrimidine metabolism	GO:0006206//GO:0006220//GO:0016812//GO:0046914	nr +
Unigene15304_All	1611	5.03	3.08	6.41	5.78	6.05	5.13	6.43	2.65	2.28	-7.08E-01	4.99E-04		3.49E-01	6.75E-02		6.51E-02	8.07E-01		-1.73E-01	4.32E-01		-1.28E+00	2.73E-14	Down	-1.50E+00	1.67E-18	Down	Unigene15304_All//gi|297803826|ref|XP_002869797.1|//1.00E-171//mitochondrial dihydroorotase [Arabidopsis lyrata subsp. lyrata] >gi|297315633|gb|EFH46056.1|mitochondrial dihydroorotase [Arabidopsis lyrata subsp. lyrata]	Unigene15304_All//8.00E-172//AT4G22930| PYR4 (PYRIMIDIN 4); dihydroorotase/ hydrolase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in cyclic amides	Unigene15304_All//0.00E+00//gi|164367461|gb|ES827223.1|ES827223		ko00240|Pyrimidine metabolism	GO:0006206//GO:0006220//GO:0016812//GO:0046914	nr +
Unigene15306_All	1780	1.32	0.77	0.81	4.59	3.37	1.50	1.21	0.80	0.38	-7.83E-01	5.88E-02		-7.12E-01	1.03E-01		-4.47E-01	2.26E-02		-1.62E+00	5.81E-14	Down	-6.02E-01	1.32E-01		-1.67E+00	3.81E-05	Down	Unigene15306_All//gi|38346596|emb|CAE04660.2|//8.00E-39//OSJNBa0061G20.16 [Oryza sativa (japonica cultivar-group)]	Unigene15306_All//5.00E-05//AT1G40390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Endonuclease/exonuclease/phosphatase (InterPro:IPR005135), RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43760.1); Has 480 Blast hits to 479 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 480; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene15306_All//1.00E-41//TC145821			GO:0005488	nr +
Unigene15307_All	1530	12.14	3.64	10.58	4.75	6.41	5.73	28.66	22.35	7.39	-1.74E+00	8.84E-32	Down	-1.98E-01	1.67E-01		4.32E-01	1.64E-02		2.69E-01	2.12E-01		-3.59E-01	5.33E-07		-1.95E+00	1.46E-109	Down	Unigene15307_All//gi|7527728|gb|AAF63177.1|AC010657_13//1.00E-114//T5E21.9 [Arabidopsis thaliana]	Unigene15307_All//1.00E-104//AT1G14590| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid lumen; CONTAINS InterPro DOMAIN/s: Nucleotide-diphospho-sugar transferase, predicted (InterPro:IPR005069); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G02061.1); Has 179 Blast hits to 175 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 172; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	Unigene15307_All//0.00E+00//CO101027				nr +
Unigene15308_All	2012	5.23	5.62	3.89	10.13	8.20	9.52	16.37	16.14	7.48	1.04E-01	6.02E-01		-4.26E-01	2.22E-02		-3.05E-01	1.03E-02		-8.94E-02	5.63E-01		-2.03E-02	8.46E-01		-1.13E+00	5.33E-37	Down	Unigene15308_All//gi|15240920|ref|NP_198662.1|//0.00E+00//ALG6, ALG8 glycosyltransferase family protein [Arabidopsis thaliana] >gi|21263376|sp|Q9FF17.1|ALG6_ARATH RecName: Full=Probable dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glucosyltransferase; AltName: Full=Dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase; AltName: Full=Asparagine-linked glycosylation protein 6 homolog >gi|9758824|dbj|BAB09358.1|glucosyltransferase-like protein [Arabidopsis thaliana]	Unigene15308_All//1.00E-95//AT5G38460| ALG6, ALG8 glycosyltransferase family protein	Unigene15308_All//0.00E+00//gi|78339260|gb|DT559534.1|DT559534		ko00510|N-Glycan biosynthesis	GO:0016757//GO:0031090	nr -
Unigene15309_All	1411	0.78	0.61	0.68	2.75	2.29	1.89	1.38	2.10	3.30	-3.51E-01	6.00E-01		-1.97E-01	7.50E-01		-2.63E-01	4.35E-01		-5.44E-01	8.53E-02		6.10E-01	6.23E-02		1.26E+00	6.59E-07	Up	Unigene15309_All//gi|297806423|ref|XP_002871095.1|//1.00E-114//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297316932|gb|EFH47354.1|protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene15309_All//3.00E-92//AT5G04460| protein binding / zinc ion binding	Unigene15309_All//8.00E-95//DW492735			GO:0005488	nr +
Unigene1531_All	3407	1.24	1.73	1.95	17.52	17.92	19.38	7.62	3.21	3.25	4.72E-01	5.67E-02		6.51E-01	6.01E-03		3.29E-02	7.25E-01		1.46E-01	3.49E-02		-1.25E+00	3.68E-33	Down	-1.23E+00	1.80E-33	Down	Unigene1531_All//gi|224065557|ref|XP_002301856.1|//0.00E+00//cellulose synthase [Populus trichocarpa] >gi|222843582|gb|EEE81129.1|cellulose synthase [Populus trichocarpa]	Unigene1531_All//0.00E+00//AT5G44030| CESA4 (CELLULOSE SYNTHASE A4); cellulose synthase/ transferase, transferring glycosyl groups	Unigene1531_All//0.00E+00//TC129590				nr -
Unigene15310_All	1912	2.05	4.61	3.37	7.89	9.53	6.64	12.32	12.88	7.31	1.17E+00	7.92E-09	Up	7.16E-01	3.01E-03		2.71E-01	4.03E-02		-2.50E-01	1.06E-01		6.40E-02	6.23E-01		-7.52E-01	6.08E-14		Unigene15310_All//gi|297851458|ref|XP_002893610.1|//4.00E-88//heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297339452|gb|EFH69869.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene15310_All//2.00E-71//AT1G30280| heat shock protein binding	Unigene15310_All//0.00E+00//TC131114			GO:0005515	nr +
Unigene15313_All	1553	1.92	1.99	0.96	4.68	3.68	3.00	13.23	6.32	20.96	5.16E-02	8.93E-01		-1.00E+00	8.59E-03		-3.47E-01	1.14E-01		-6.45E-01	2.51E-03		-1.06E+00	9.59E-21	Down	6.64E-01	2.69E-15		Unigene15313_All//gi|259121377|gb|ACV92008.1|//3.00E-99//WRKY transcription factor 6 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene15313_All//4.00E-40//AT2G46400| WRKY46; transcription factor	Unigene15313_All//0.00E+00//TC142216	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene15314_All	453	1.50	2.24	5.29	2.86	2.58	4.59	6.35	8.58	5.80	5.75E-01	3.83E-01		1.82E+00	9.66E-05	Up	-1.46E-01	8.22E-01		6.82E-01	1.40E-01		4.35E-01	1.31E-01		-1.29E-01	6.94E-01				Unigene15314_All//0.00E+00//DT054165				
Unigene15317_All	1415	1.70	4.33	3.27	6.58	6.16	4.25	4.45	4.19	4.50	1.35E+00	8.81E-08	Up	9.45E-01	1.27E-03		-9.66E-02	6.59E-01		-6.33E-01	6.04E-04		-8.61E-02	7.23E-01		1.69E-02	9.60E-01		Unigene15317_All//gi|240255501|ref|NP_190068.4|//1.00E-109//protein binding / signal transducer [Arabidopsis thaliana]	Unigene15317_All//2.00E-102//AT3G44820| protein binding / signal transducer	Unigene15317_All//0.00E+00//TC176596				nr +
Unigene1532_All	3009	29.42	14.13	19.68	24.17	21.40	24.24	17.92	29.34	18.07	-1.06E+00	3.03E-70	Down	-5.80E-01	2.05E-24		-1.76E-01	3.56E-03		4.20E-03	9.49E-01		7.12E-01	5.63E-44		1.26E-02	8.79E-01		Unigene1532_All//gi|155242084|gb|AB718094.1|//0.00E+00//FERONIA receptor-like kinase [Brassica oleracea]	Unigene1532_All//0.00E+00//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene1532_All//0.00E+00//TC144586		ko04626|Plant-pathogen interaction		nr +
Unigene15321_All	758	57.50	61.63	79.95	119.67	118.34	104.63	59.63	41.63	24.33	1.00E-01	2.50E-01		4.76E-01	5.56E-12		-1.61E-02	8.19E-01		-1.94E-01	3.80E-04		-5.18E-01	2.20E-13		-1.29E+00	2.57E-62	Down	Unigene15321_All//gi|15221266|ref|NP_177592.1|//5.00E-72//ATHVA22A [Arabidopsis thaliana] >gi|57012625|sp|Q8S7V4.1|HA22A_ARATH RecName: Full=HVA22-like protein a; Short=AtHVA22a >gi|4884944|gb|AAD31885.1|AF141977_1 AtHVA22a [Arabidopsis thaliana] >gi|12324799|gb|AAG52361.1|AC011765_13 AtHVA22a; 65476-64429 [Arabidopsis thaliana] >gi|4884922|gb|AAD31879.1|AtHVA22a [Arabidopsis thaliana]	Unigene15321_All//2.00E-73//AT1G74520| ATHVA22A	Unigene15321_All//0.00E+00//gi|164315355|gb|ES845856.1|ES845856			GO:0006972//GO:0009725//GO:0031410	nr -
Unigene15327_All	1574	5.29	3.22	5.21	7.75	7.83	9.24	7.58	25.33	58.24	-7.15E-01	3.58E-04		-2.07E-02	9.40E-01		1.45E-02	9.57E-01		2.53E-01	1.11E-01		1.74E+00	1.38E-82	Up	2.94E+00	0.00E+00	Up	Unigene15327_All//gi|18399375|ref|NP_566402.1|//1.00E-97//PUB24 (PLANT U-BOX 24); binding / ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene15327_All//7.00E-99//AT3G11840| PUB24 (PLANT U-BOX 24); binding / ubiquitin-protein ligase	Unigene15327_All//6.00E-59//gi|73860673|gb|DT463412.1|DT463412		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0002252//GO:0006950//GO:0009743//GO:0016567//GO:0019787	nr -
Unigene15329_All	666	8.09	14.38	10.31	14.51	17.01	18.38	36.69	114.91	69.99	8.30E-01	9.06E-06		3.50E-01	1.45E-01		2.29E-01	2.16E-01		3.41E-01	4.16E-02		1.65E+00	6.20E-146	Up	9.32E-01	7.02E-38		Unigene15329_All//gi|75272473|sp|Q8L8B8.1|LOG3_ARATH//9.00E-26//RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG3; AltName: Full=Protein LONELY GUY 3	Unigene15329_All//5.00E-27//AT2G37210| Encodes a protein of unknown function. It has been crystallized and shown to be structurally almost identical to the protein encoded by At5g11950.	Unigene15329_All//0.00E+00//TC178682			GO:0003824	nr +

Unigene15330_All	1517	7.79	12.36	8.28	17.60	16.39	19.53	11.87	14.46	5.86	6.65E-01	2.04E-07		8.79E-02	6.09E-01		-1.03E-01	4.16E-01		1.50E-01	1.86E-01		2.85E-01	7.89E-03		-1.02E+00	1.29E-17	Down	Unigene15330_All//gi|18394613|ref|NP_564053.1|//1.00E-151//calcineurin-like phosphoesterase family protein [Arabidopsis thaliana] >gi|75249570|sp|Q944L7.1|Y1480_ARATH RecName: Full=Uncharacterized protein At1g18480 >gi|16226290|gb|AAL16125.1|AF428293_1 At1g18480/F15H18_1 [Arabidopsis thaliana] >gi|23308175|gb|AAN18057.1|At1g18480/F15H18_1 [Arabidopsis thaliana]	Unigene15330_All//1.00E-147//AT1G18480| calcineurin-like phosphoesterase family protein	Unigene15330_All//0.00E+00//gi|78345234|gb|DT565508.1|DT565508				nr -
Unigene15332_All	1527	0.93	2.26	3.31	15.37	11.68	9.41	17.72	12.54	7.75	1.29E+00	1.88E-04	Up	1.84E+00	1.99E-09	Up	-3.95E-01	1.75E-04		-7.08E-01	1.13E-10		-4.99E-01	7.52E-08		-1.19E+00	2.61E-33	Down	Unigene15332_All//gi|15236514|ref|NP_194081.1|//0.00E+00//glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	Unigene15332_All//5.00E-179//AT4G23500| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene15332_All//0.00E+00//TC151355		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553//GO:0030312//GO:0044238//GO:0045229	nr -
Unigene15333_All	2385	1.67	1.19	0.96	0.88	1.07	1.93	1.19	0.89	5.26	-4.87E-01	1.17E-01		-7.96E-01	1.29E-02		2.85E-01	5.45E-01		1.14E+00	5.71E-05	Up	-4.10E-01	2.38E-01		2.15E+00	1.64E-35	Up	Unigene15333_All//gi|56561617|emb|CAG28412.1|//1.00E-124//S-receptor kinase-like protein 1 [Senecio squalidus]	Unigene15333_All//1.00E-114//AT3G16030| CESI01 (CALLUS EXPRESSION OF RBCS 101); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene15333_All//0.00E+00//gi|78350521|gb|DT570795.1|DT570795		ko04626|Plant-pathogen interaction		nr +
Unigene15334_All	983	8.57	164.79	52.49	11.81	40.22	53.89	1.20	18.88	2.23	4.27E+00	0.00E+00	Up	2.61E+00	4.67E-142	Up	1.77E+00	5.05E-80	Up	2.19E+00	1.03E-129	Up	3.97E+00	4.61E-95	Up	8.88E-01	1.77E-02		Unigene15334_All//gi|15148884|gb|AA84869.1|AF399821_1//2.00E-50//small heat stress protein class CIII [Solanum peruvianum]	Unigene15334_All//1.00E-27//AT1G54050| 17.4 kDa class III heat shock protein (HSP17.4-CIII)	Unigene15334_All//0.00E+00//TC160343			GO:0000302//GO:0009642	nr -
Unigene15337_All	827	17.59	6.43	9.40	31.86	21.61	37.03	45.25	20.06	18.69	-1.45E+00	1.86E-19	Down	-9.04E-01	4.29E-09		-5.60E-01	6.77E-09		2.17E-01	3.54E-02		-1.17E+00	3.03E-43	Down	-1.28E+00	1.14E-50	Down	Unigene15337_All//gi|115448443|ref|NP_001048001.1|//2.00E-60//Os02g0728600 (Oryza sativa Japonica Group) >gi|113537532|dbj|BAF09915.1|Os02g0728600 [Oryza sativa Japonica Group]	Unigene15337_All//3.00E-53//AT5G08180| ribosomal protein L7Ae/L30e/S12e/Gad45 family protein	Unigene15337_All//0.00E+00//TC170436			GO:0005488//GO:0032991	nr -
Unigene15338_All	1177	58.86	63.15	60.31	61.62	58.54	64.16	113.08	95.13	262.62	1.02E-01	1.30E-01		3.52E-02	6.24E-01		-7.40E-02	3.18E-01		5.82E-02	4.49E-01		-2.49E-01	3.16E-10		1.22E+00	0.00E+00	Up	Unigene15338_All//gi|30698866|ref|NP_565040.2|//5.00E-89//ALANT2 (ALANINE AMINOTRANSFERASE 2); ATP binding / L-alanine:2-oxoglutarate aminotransferase [Arabidopsis thaliana] >gi|9082268|gb|AAF82781.1|AF275371_1 alanine aminotransferase [Arabidopsis thaliana]	Unigene15338_All//3.00E-84//AT1G72330| ALANT2 (ALANINE AMINOTRANSFERASE 2); ATP binding / L-alanine:2-oxoglutarate aminotransferase	Unigene15338_All//0.00E+00//TC138039		ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism	GO:0008152//GO:0016769//GO:0016846//GO:0032559//GO:0043231//GO:0046914//GO:0048037	nr -
Unigene15339_All	1536	6.47	13.62	11.82	10.96	11.84	19.32	10.29	4.27	16.03	1.07E+00	1.74E-17	Up	8.69E-01	1.53E-10		1.11E-01	4.90E-01		8.18E-01	8.82E-17		-1.27E+00	4.24E-21	Down	6.39E-01	4.42E-11		Unigene15339_All//gi|224140995|ref|XP_002323861.1|//1.00E-159//amino acid transporter [Populus trichocarpa] >gi|222866863|gb|EEF03994.1| amino acid transporter [Populus trichocarpa]	Unigene15339_All//6.00E-137//AT3G28960| amino acid transporter family protein	Unigene15339_All//0.00E+00//TC155837				nr +
Unigene15340_All	2430	2.78	10.55	3.22	4.92	8.01	7.73	10.89	10.92	15.54	1.93E+00	7.77E-50	Up	2.14E-01	3.71E-01		7.03E-01	1.74E-09		6.52E-01	1.57E-07		4.00E-03	1.01E+00		5.13E-01	1.99E-11		Unigene15340_All//gi|224133944|ref|XP_002321698.1|//0.00E+00//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222868694|gb|EEF05825.1|chromatin remodeling complex subunit [Populus trichocarpa]	Unigene15340_All//1.00E-149//AT5G14170| CHC1	Unigene15340_All//0.00E+00//TC136585				nr +
Unigene15341_All	1442	5.19	4.11	0.78	6.08	2.22	21.20	7.95	4.49	6.41	-3.36E-01	1.27E-01		-2.74E+00	7.83E-22	Down	-1.45E+00	1.58E-14	Down	1.80E+00	3.88E-58	Up	-8.23E-01	4.93E-08		-3.10E-01	3.79E-02		Unigene15341_All//gi|150035050|gb|ABR87048.1|//1.00E-119//isopentenyltransferase [Gossypium hirsutum]	Unigene15341_All//1.00E-98//AT3G63110| ATIPT3 (ARABIDOPSIS THALIANA ISOPENTENYLTRANSFERASE 3); ATP binding / tRNA isopentenyltransferase/ transferase, transferring alkyl or aryl (other than methyl) groups	Unigene15341_All//0.00E+00//TC133714		ko00908|Zeatin biosynthesis	GO:0006399//GO:0016765//GO:0032559//GO:0043231	nr +
Unigene15342_All	651	45.41	28.33	26.91	27.62	32.43	36.91	27.02	50.53	80.53	-6.81E-01	1.08E-11		-7.55E-01	2.89E-13		2.31E-01	6.25E-02		4.18E-01	1.33E-04		9.03E-01	4.67E-25		1.58E+00	5.51E-96	Up	Unigene15342_All//gi|229609839|gb|ACQ83535.1|//7.00E-49//CBL-interacting protein kinase 19 [Vitis vinifera]	Unigene15342_All//2.00E-38//AT3G17510| CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding	Unigene15342_All//7.00E-180//gi|48779304|gb|CO088670.1|CO088670			GO:0004674//GO:0006464//GO:0006970//GO:0009725//GO:0016020//GO:0020360//GO:0032559//GO:0043231	nr -
Unigene15343_All	963	0.22	0.00	1.55	0.52	1.22	4.97	11.85	25.74	103.84	-7.76E+00	1.22E-01		2.83E+00	6.17E-05	Up	1.23E+00	5.68E-02		3.26E+00	2.52E-18	Up	1.12E+00	8.41E-27	Up	3.13E+00	0.00E+00	Up	Unigene15343_All//gi|13161397|dbj|BAB33033.1|//2.00E-90//CPRD2 [Vigna unguiculata]	Unigene15343_All//1.00E-77//AT4G20820| FAD-binding domain-containing protein	Unigene15343_All//2.00E-128//gi|3326694|gb|AI055580.1|AI055580		ko00620|Pyruvate metabolism//ko00908|Zeatin biosynthesis	GO:0003824	nr +
Unigene15344_All	1759	0.00	0.12	0.12	0.06	0.22	5.65	16.87	41.51	147.17	6.85E+00	1.37E-01		6.92E+00	1.41E-01		1.93E+00	1.94E-01		6.64E+00	7.57E-57	Up	1.30E+00	7.21E-98	Up	3.12E+00	0.00E+00	Up	Unigene15344_All//gi|13161397|dbj|BAB33033.1|//1.00E-162//CPRD2 [Vigna unguiculata]	Unigene15344_All//2.00E-135//AT5G44440| FAD-binding domain-containing protein	Unigene15344_All//0.00E+00//gi|3326535|gb|AI055421.1|AI055421		ko00620|Pyruvate metabolism//ko00908|Zeatin biosynthesis	GO:0003824	nr -
Unigene15346_All	1567	8.28	24.96	13.66	10.62	16.46	9.97	4.53	8.75	3.92	1.59E+00	3.14E-58	Up	7.22E-01	3.98E-09		6.32E-01	2.08E-10		-9.05E-02	6.12E-01		9.49E-01	8.65E-12		-2.11E-01	3.11E-01		Unigene15346_All//gi|94442455|gb|ABF19015.1|//3.00E-35//At4g02715 [Arabidopsis thaliana]	Unigene15346_All//1.00E-21//AT4G02715| unknown protein	Unigene15346_All//0.00E+00//TC130581				nr +
Unigene15347_All	1403	4.77	3.54	2.35	9.16	9.74	9.08	3.89	5.81	4.54	-4.32E-01	6.10E-02		-1.02E+00	1.98E-05	Down	8.91E-02	6.20E-01		-1.31E-02	9.47E-01		5.80E-01	1.37E-03		2.25E-01	3.10E-01		Unigene15347_All//gi|116734642|gb|ABK20308.1|//1.00E-120//Myb transcription factor [Malus x domestica]	Unigene15347_All//2.00E-85//AT3G55730| MYB109 (myb domain protein 109); DNA binding / transcription factor	Unigene15347_All//0.00E+00//DR455255	MYB		GO:0006970//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene1535_All	3298	1.89	0.97	0.79	3.84	3.31	3.85	15.70	7.31	13.23	-9.64E-01	5.53E-05		-1.25E+00	8.32E-07	Down	-2.13E-01	2.16E-01		4.40E-03	9.80E-01		-1.10E+00	5.40E-54	Down	-2.48E-01	1.32E-04		Unigene1535_All//gi|222423343|dbj|BAH19646.1|//0.00E+00//AT2G38280 [Arabidopsis thaliana]	Unigene1535_All//0.00E+00//AT2G38280| FAC1 (EMBRYONIC FACTOR1); AMP deaminase	Unigene1535_All//0.00E+00//TC143091		ko00230|Purine metabolism		nr +
Unigene15354_All	2357	4.68	1.98	3.89	10.93	8.06	12.26	15.19	6.53	6.93	-1.24E+00	5.77E-12	Down	-2.69E-01	1.50E-01		-4.38E-01	9.51E-06		1.67E-01	1.36E-01		-1.22E+00	5.52E-44	Down	-1.13E+00	2.40E-40	Down	Unigene15354_All//gi|15463019|ref|NP_001055109.1|//1.00E-177//Os05g0295100 [Oryza sativa Japonica Group] >gi|113578660|dbj|BAF17023.1|Os05g0295100 [Oryza sativa Japonica Group]	Unigene15354_All//0.00E+00//AT1G17690| unknown protein	Unigene15354_All//0.00E+00//TC162917				nr +
Unigene15355_All	976	0.91	0.83	1.42	1.63	3.49	1.94	1.21	0.98	1.39	-1.34E-01	8.41E-01		6.38E-01	2.82E-01		1.10E+00	7.80E-04	Up	2.51E-01	6.21E-01		-3.01E-01	6.31E-01		1.94E-01	6.94E-01		Unigene15355_All//gi|297802662|ref|XP_002869215.1|//6.00E-37//signal peptide peptidase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315051|gb|EFH45474.1|signal peptide peptidase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15355_All//3.00E-38//AT4G33410| signal peptide peptidase family protein	Unigene15355_All//7.00E-79//TC166079			GO:0004175//GO:0031224	nr +
Unigene15358_All	1558	12.49	16.94	34.38	2.37	8.89	51.51	8.82	25.75	8.23	4.40E-01	3.14E-05		1.46E+00	2.71E-68	Up	1.91E+00	4.18E-31	Up	4.44E+00	0.00E+00	Up	1.55E+00	3.66E-70	Up	-9.92E-02	5.26E-01		Unigene15358_All//gi|15227703|ref|NP_180570.1|//1.00E-105//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|3150411|gb|AAC16963.1|hookless1-like protein [Arabidopsis thaliana]	Unigene15358_All//1.00E-106//AT2G30090| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene15358_All//5.00E-53//ES827081			GO:0000902//GO:0009639//GO:0009755	nr -
Unigene15359_All	820	5.49	17.36	14.48	9.29	18.98	32.44	14.23	35.99	24.53	1.66E+00	5.98E-23	Up	1.40E+00	1.35E-14	Up	1.03E+00	3.26E-14	Up	1.80E+00	1.12E-50	Up	1.34E+00	7.19E-42	Up	7.86E-01	7.48E-13					Unigene15359_All//2.00E-153//gi|48823275|gb|CO124588.1|CO124588				
Unigene15360_All	737	20.87	8.53	13.94	50.56	28.69	30.33	12.68	5.33	3.46	-1.29E+00	2.53E-17	Down	-5.82E-01	7.74E-05		-8.18E-01	8.55E-24		-7.37E-01	9.41E-18		-1.25E+00	1.62E-12	Down	-1.87E+00	1.01E-22	Down				Unigene15360_All//5.00E-42//ES797721				
Unigene15363_All	346	3.33	2.93	1.85	3.60	3.98	2.61	12.22	7.61	2.42	-1.84E-01	7.48E-01		-8.49E-01	2.06E-01		1.45E-01	8.22E-01		-4.63E-01	4.78E-01		-6.83E-01	9.48E-03		-2.34E+00	5.77E-14	Down	Unigene15363_All//gi|297819918|ref|XP_002877842.1|//5.00E-08//ATRPB13.6 [Arabidopsis lyrata subsp. lyrata] >gi|297323680|gb|EFH54101.1|ATRPB13.6 [Arabidopsis lyrata subsp. lyrata]	Unigene15363_All//2.00E-09//AT3G52090| NRPB11; DNA binding / DNA-directed RNA polymerase	Unigene15363_All//1.00E-176//TC158653		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003676//GO:0005515//GO:0010467//GO:0016591//GO:0034062//GO:0055029	nr -
Unigene15364_All	753	47.87	34.25	49.15	51.93	39.15	45.34	19.76	15.32	9.63	-4.83E-01	5.63E-08		3.79E-02	7.11E-01		-4.08E-01	1.90E-07		-1.96E-01	2.94E-02		-3.68E-01	5.07E-03		-1.04E+00	4.12E-15	Down	Unigene15364_All//gi|297819918|ref|XP_002877842.1|//3.00E-53//ATRPB13.6 [Arabidopsis lyrata subsp. lyrata] >gi|297323680|gb|EFH54101.1|ATRPB13.6 [Arabidopsis lyrata subsp. lyrata]	Unigene15364_All//6.00E-54//AT3G52090| NRPB11; DNA binding / DNA-directed RNA polymerase	Unigene15364_All//0.00E+00//TC158653		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003676//GO:0005515//GO:0010467//GO:0016591//GO:0034062//GO:0055029	nr +
Unigene15365_All	1151	19.14	13.29	14.16	50.64	40.15	47.99	59.80	39.94	26.17	-5.26E-01	6.35E-06		-4.35E-01	3.32E-04		-3.35E-01	1.20E-07		-7.75E-02	3.66E-01		-5.82E-01	2.06E-24		-1.19E+00	2.93E-83	Down	Unigene15365_All//gi|164652934|gb|ABV65000.1|//4.00E-17//14-3-3a protein [Gossypium hirsutum]	Unigene15365_All//2.00E-13//AT1G22300| GBP10 (GENERAL REGULATORY FACTOR 10); ATP binding / protein binding / protein phosphorylated amino acid binding	Unigene15365_All//2.00E-178//gi|21090224|gb|BQ402537.1|BQ402537			GO:0009532//GO:0016020//GO:0019899//GO:0031406//GO:0032559//GO:0043401//GO:0051219	nr -
Unigene15366_All	1355	4.87	3.74	4.91	8.24	11.44	11.50	17.75	8.79	10.20	-3.80E-01	1.06E-01		1.39E-02	9.75E-01		4.74E-01	4.31E-04		4.82E-01	5.51E-04		-1.01E+00	2.37E-22	Down	-7.99E-01	1.04E-15		Unigene15366_All//gi|297609759|ref|NP_001063593.2|//1.00E-172//Os09g0503400 [Oryza sativa Japonica Group] >gi|255679038|dbj|BAF25507.2|Os09g0503400 [Oryza sativa Japonica Group]	Unigene15366_All//2.00E-152//AT1G69620| ATP binding / aminoacyl-tRNA ligase/ leucine-tRNA ligase/ nucleotide binding	Unigene15366_All//0.00E+00//TC150643		ko00970|Aminoacyl-tRNA biosynthesis//ko00290|Valine, leucine and isoleucine biosynthesis	GO:0004812//GO:0006418//GO:0032559//GO:0044424	nr -
Unigene15369_All	1876	1.65	1.62	0.51	17.68	9.43	5.27	8.38	1.14	1.53	-2.20E-02	9.69E-01		-1.69E+00	2.20E-05	Down	-9.06E-01	2.81E-25		-1.75E+00	1.62E-61	Down	-2.88E+00	6.18E-61	Down	-2.46E+00	9.17E-53	Down	Unigene15369_All//gi|21537059|gb|AAM61400.1|//0.00E+00//pectate lyase-like protein [Arabidopsis thaliana]	Unigene15369_All//0.00E+00//AT3G53190| pectate lyase family protein	Unigene15369_All//1.00E-14//TC153962		ko00040|Pentose and glucuronate interconversions	GO:0016837//GO:0031224	nr +
Unigene15370_All	474	22.30	11.01	16.06	33.21	23.83	39.83	44.78	28.22	24.37	-1.02E+00	1.51E-08	Down	-4.73E-01	1.02E-02		-4.79E-01	2.54E-04		2.62E-01	4.98E-02		-6.66E-01	4.44E-10		-8.78E-01	3.18E-16		Unigene15370_All//gi|18402264|ref|NP_565693.1|//8.00E-75//ATUBA1; ubiquitin activating enzyme/ ubiquitin-protein ligase [Arabidopsis thaliana] >gi|1750376|gb|AAB39246.1|ubiquitin activating enzyme [Arabidopsis thaliana] >gi|3150409|gb|AAC16961.1|ubiquitin activating enzyme 1 (UBA1) [Arabidopsis thaliana]	Unigene15370_All//1.00E-72//AT2G30110| ATUBA1; ubiquitin activating enzyme/ ubiquitin-protein ligase	Unigene15370_All//0.00E+00//gi|13353058|gb|BG443406.1|BG443406		ko04120|Ubiquitin mediated proteolysis	GO:0008641//GO:0009607//GO:0010038//GO:0016020//GO:0019787//GO:0019941//GO:0032446//GO:0032559	nr -
Unigene15372_All	1455	4.14	10.13	5.49	8.87	11.05	7.05	17.26	6.92	2.68	1.29E+00	1.40E-16	Up	4.09E-01	6.16E-02		3.18E-01	2.19E-02		-3.32E-01	4.06E-02		-1.32E+00	5.34E-35	Down	-2.69E+00	9.42E-93	Down	Unigene15372_All//gi|159025715|emb|CAN88858.1|//1.00E-101//D3-type cyclin [Populus trichocarpa]	Unigene15372_All//5.00E-85//AT4G34160| CYCD3;1 (CYCLIN D3;1); cyclin-dependent protein kinase regulator/ protein binding	Unigene15372_All//0.00E+00//TC174982			GO:0005488//GO:0008283//GO:0009725//GO:0019887//GO:0022402//GO:0034285//GO:0043231	nr -
Unigene15373_All	1448	20.49	9.48	11.66	47.54	40.93	67.34	60.44	45.37	38.77	-1.11E+00	6.25E-26	Down	-8.14E-01	4.66E-15		-2.16E-01	3.28E-04		5.02E-01	4.70E-23		-4.14E-01	6.98E-17		-6.41E-01	1.90E-37		Unigene15373_All//gi|21537157|gb|AAM61498.1|//0.00E+00//NAD+ dependent isocitrate dehydrogenase subunit 1 [Arabidopsis thaliana]	Unigene15373_All//2.00E-167//AT4G35260| IDH1 (ISOCITRATE DEHYDROGENASE 1); isocitrate dehydrogenase (NAD+)/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	Unigene15373_All//0.00E+00//TC138446		ko00020|Citrate cycle (TCA cycle)	GO:0000166//GO:0004448//GO:0009060//GO:0019752//GO:0043231//GO:0046914	nr +

Unigene15374_All	619	16.99	15.14	16.43	7.16	8.46	6.86	8.40	26.40	20.02	-1.66E-01	3.87E-01		-4.82E-02	8.04E-01		2.40E-01	4.22E-01		-6.26E-02	8.50E-01		1.65E+00	7.19E-32	Up	1.25E+00	9.24E-17	Up	Unigene15374_All//gi|15223919|ref|NP_172939.1|//7.00E-08//atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase >gi|68565943|sp|Q9LQU5.1|NUD18_ARATH RecName: Full=Nudix hydrolase 18, mitochondrial; Short=AtNUDT18; Flags: Precursor >gi|8778216|gb|AAF79225.1|AC006917_10 F10B6.26 [Arabidopsis thaliana]	Unigene15374_All//4.00E-69//AT2G01670| atnudt17 (Arabidopsis thaliana Nudix hydrolase homolog 17); hydrolase	Unigene15374_All//4.00E-175//TC147782			GO:0016462	nr +
Unigene15378_All	837	28.13	12.95	8.40	36.36	25.59	18.56	29.95	17.48	12.76	-1.12E+00	6.01E-21	Down	-1.74E+00	7.79E-39	Down	-5.07E-01	1.40E-08		-9.70E-01	5.06E-23		-7.77E-01	3.89E-15		-1.23E+00	1.83E-32	Down	Unigene15378_All//gi|15225884|ref|NP_180316.1|//2.00E-47//NF-YB11 (NUCLEAR FACTOR Y, SUBUNIT B11); transcription factor [Arabidopsis thaliana]	Unigene15378_All//5.00E-35//AT2G27470| NF-YB11 (NUCLEAR FACTOR Y, SUBUNIT B11); transcription factor	Unigene15378_All//0.00E+00//gi|164342770|gb|ES843181.1|ES843181	CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication	GO:0001071//GO:0003677//GO:0010468//GO:0043231	nr -
Unigene1538_All	407	1.03	3.36	4.06	3.30	5.67	4.99	3.12	2.16	2.06	1.71E+00	5.54E-03		1.98E+00	8.06E-04	Up	7.79E-01	6.50E-02		5.96E-01	2.13E-01		-5.31E-01	3.43E-01		-6.00E-01	2.45E-01		Unigene1538_All//gi|4850395|gb|AAD31065.1|AC007357_14//3.00E-22//ESTgb|N37870 comes from this gene [Arabidopsis thaliana]	Unigene1538_All//2.00E-23//AT1G13120| emb1745 (embryo defective 1745)	Unigene1538_All//9.00E-129//gi|164327866|gb|ES830814.1|ES830814				nr -
Unigene15380_All	1319	1.27	9.99	5.09	10.20	9.66	7.57	10.13	9.06	9.12	2.98E+00	7.37E-43	Up	2.00E+00	1.03E-13	Up	-7.81E-02	6.73E-01		-4.30E-01	4.87E-03		-1.61E-01	3.09E-01		-1.51E-01	3.12E-01		Unigene15380_All//gi|297799074|ref|XP_002867421.1|//1.00E-105//zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312257|gb|EFH43680.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15380_All//2.00E-92//AT2G19810| zinc finger (CCCH-type) family protein	Unigene15380_All//0.00E+00//TC173218	C3H		GO:0003676//GO:0010260//GO:0010468//GO:0023033//GO:0043231//GO:0046914	nr +
Unigene15383_All	1500	0.00	1.05	0.14	1.93	1.65	1.60	49.50	37.06	30.20	1.00E+01	5.71E-09	Up	7.15E+00	1.41E-01		-2.21E-01	5.88E-01		-2.71E-01	5.03E-01		-4.18E-01	1.10E-14		-7.13E-01	2.47E-38		Unigene15383_All//gi|224612177|gb|ACN60160.1|//1.00E-113//peroxidase [Tamarix hispida]	Unigene15383_All//4.00E-94//AT4G37530| peroxidase, putative	Unigene15383_All//1.00E-96//DW495286		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene15384_All	1060	66.54	28.25	61.19	17.76	16.37	14.74	10.21	3.51	3.65	-1.24E+00	8.90E-72	Down	-1.21E-01	8.72E-02		-1.18E-01	4.34E-01		-2.69E-01	4.27E-02		-1.54E+00	1.94E-19	Down	-1.49E+00	4.65E-19	Down	Unigene15384_All//gi|82621160|gb|AB886268.1|//1.00E-110//Tic20-like protein [Solanum tuberosum]	Unigene15384_All//7.00E-104//AT1G64940| TIC20 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 20)	Unigene15384_All//0.00E+00//TC155565				nr -
Unigene15386_All	1556	4.74	4.07	4.28	8.77	9.27	5.92	3.48	2.82	1.38	-2.20E-01	3.47E-01		-1.48E-01	5.53E-01		8.01E-02	6.59E-01		-5.67E-01	1.34E-04		-3.02E-01	2.21E-01		-1.33E+00	1.43E-08	Down	Unigene15386_All//gi|37625025|gb|AAQ96336.1|//1.00E-148//ribosomal protein L3B [Nicotiana tabacum]	Unigene15386_All//4.00E-122//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene15386_All//0.00E+00//CB066521		ko03010|Ribosome		nr +
Unigene15396_All	794	4.94	15.19	7.78	15.06	22.86	22.52	14.16	32.79	11.84	1.62E+00	7.20E-19	Up	6.55E-01	8.18E-03		6.02E-01	6.76E-07		5.81E-01	5.44E-06		1.21E+00	8.10E-32	Up	-2.59E-01	9.35E-02		Unigene15396_All//gi|18424977|ref|NP_569016.1|//1.00E-43//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|75180277|sp|Q9SLS8.1|Y5566_ARATH RecName: Full=Uncharacterized protein At5g65660 >gi|30102568|gb|AAP21202.1|At5g65660 [Arabidopsis thaliana]	Unigene15396_All//1.00E-36//AT5G65660| hydroxyproline-rich glycoprotein family protein	Unigene15396_All//0.00E+00//EX166296			GO:0016020	nr -
Unigene15397_All	1079	84.18	83.40	100.04	41.37	43.69	38.05	42.87	27.97	20.42	-1.34E-02	8.34E-01		2.49E-01	1.17E-06		7.89E-02	4.07E-01		-1.21E-01	1.89E-01		-6.16E-01	2.25E-18		-1.07E+00	2.26E-47	Down	Unigene15397_All//gi|18391391|ref|NP_563907.1|//1.00E-124//CLP2 (CLP PROTEASE PROTEOLYTIC SUBUNIT 2); serine-type endopeptidase [Arabidopsis thaliana] >gi|75315329|sp|Q9XJ36.1|CLPR2_ARATH RecName: Full=ATP-dependent Clp protease proteolytic subunit-related protein 2, chloroplastic; Short=ClpR2; Short=nClpP2; Flags: Precursor >gi|8778627|gb|AAF79635.1|AC025416_9 F5O11.13 [Arabidopsis thaliana] >gi|5360589|dbj|BAA82066.1| nClpP2 [Arabidopsis thaliana] >gi|17065388|gb|AAL32848.1| similar to nClpP2 [Arabidopsis thaliana] >gi|20148625|gb|AAM10203.1| similar to nClpP2 dbj|BAA82066.1 [Arabidopsis thaliana]	Unigene15397_All//3.00E-125//AT1G12410| CLP2 (CLP PROTEASE PROTEOLYTIC SUBUNIT 2); serine-type endopeptidase	Unigene15397_All//0.00E+00//TC143653			GO:0004175//GO:0019538	nr +
Unigene15398_All	1053	5.76	4.67	10.42	12.63	8.83	19.86	4.90	23.85	9.00	-3.04E-01	2.24E-01		8.54E-01	1.83E-06		-5.17E-01	3.23E-04		6.53E-01	2.56E-08		2.28E+00	2.30E-74	Up	8.78E-01	1.05E-07		Unigene15398_All//gi|15230110|ref|NP_189085.1|//1.00E-84//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|11994705|dbj|BAB02943.1| hydrolase-like protein [Arabidopsis thaliana] >gi|51536428|gb|AAU05452.1| At3g24420 [Arabidopsis thaliana] >gi|53828585|gb|AAU94402.1| At3g24420 [Arabidopsis thaliana]	Unigene15398_All//5.00E-86//AT3G24420| hydrolase, alpha/beta fold family protein	Unigene15398_All//0.00E+00//CO071741			GO:0003824	nr +
Unigene15399_All	1252	4.05	4.90	5.36	2.71	1.93	3.07	2.94	3.61	1.37	2.73E-01	2.78E-01		4.03E-01	9.64E-02		-4.91E-01	1.44E-01		1.81E-01	6.39E-01		2.95E-01	2.82E-01		-1.10E+00	9.20E-05	Down	Unigene15399_All//gi|15982773|gb|AAL09734.1|//2.00E-89//At1g36320/F7F23_4 [Arabidopsis thaliana] >gi|21655273|gb|AAM65348.1| At1g36320/F7F23_4 [Arabidopsis thaliana]	Unigene15399_All//6.00E-78//AT1G36320| unknown protein	Unigene15399_All//0.00E+00//gi|164319518|gb|ES848258.1|ES848258			GO:0043231	nr +
Unigene15400_All	700	68.02	101.19	163.86	82.05	120.28	125.55	74.35	37.26	23.22	5.73E-01	5.56E-20		1.27E+00	1.25E-117	Up	5.52E-01	5.12E-26		6.14E-01	1.14E-29		-9.97E-01	4.12E-46		-1.68E+00	1.85E-105	Down	Unigene15400_All//gi|297823659|ref|XP_002879712.1|//3.00E-38//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325551|gb|EFH55971.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15400_All//3.00E-29//AT2G37870| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene15400_All//2.00E-53//gi|164243185|gb|ES842373.1|ES842373			GO:0005488//GO:0006810//GO:0031410	nr -
Unigene15402_All	1264	3.77	43.53	7.16	28.30	17.84	20.90	12.48	29.69	10.24	3.53E+00	2.33E-208	Up	9.27E-01	3.66E-06		-6.65E-01	5.01E-16		-4.37E-01	4.84E-07		1.25E+00	7.63E-48	Up	-2.85E-01	2.30E-02		Unigene15402_All//gi|3426060|emb|CAA07573.1|//6.00E-69//src2-like protein [Arabidopsis thaliana]	Unigene15402_All//2.00E-41//AT1G09070| SRC2 (SOYBEAN GENE REGULATED BY COLD-2); protein binding	Unigene15402_All//0.00E+00//gi|78350876|gb|DT571150.1|DT571150		ko04626|Plant-pathogen interaction//ko03040|Spliceosome	GO:0005488//GO:0043231	nr -
Unigene15403_All	1968	28.74	11.56	17.07	61.31	45.62	58.01	60.28	37.10	33.97	-1.31E+00	2.09E-63	Down	-7.51E-01	1.24E-24		-4.27E-01	8.18E-24		-7.96E-02	1.38E-01		-7.00E-01	2.80E-57		-8.28E-01	2.17E-78		Unigene15403_All//gi|297793179|ref|XP_002864474.1|//0.00E+00//EMB2755 [Arabidopsis lyrata subsp. lyrata] >gi|297310309|gb|EFH40733.1| EMB2755 [Arabidopsis lyrata subsp. lyrata]	Unigene15403_All//0.00E+00//AT5G56680| SYNC1; ATP binding / aminoacyl-tRNA ligase/ asparagine-tRNA ligase/ aspartate-tRNA ligase/ nucleic acid binding / nucleotide binding	Unigene15403_All//0.00E+00//TC155310		ko00970|Aminoacyl-tRNA biosynthesis	GO:0003006//GO:0004812//GO:0006418//GO:0009536//GO:0010038//GO:0032559	nr +
Unigene15404_All	870	8.78	8.91	6.49	18.61	7.60	11.06	5.69	0.29	1.65	2.13E-02	9.40E-01		-4.37E-01	5.05E-02		-1.29E+00	3.80E-22	Down	-7.51E-01	2.58E-08		-4.30E+00	3.13E-27	Down	-1.79E+00	1.09E-11	Down			Unigene15404_All//0.00E+00//TC168641				
Unigene15406_All	1101	97.99	67.05	85.80	18.73	20.58	8.25	1.31	0.68	0.58	-5.47E-01	9.54E-28		-1.92E-01	2.51E-04		1.36E-01	3.15E-01		-1.18E+00	1.27E-21	Down	-9.34E-01	6.12E-02		-1.17E+00	1.53E-02		Unigene15406_All//gi|224126625|ref|XP_002329601.1|//6.00E-93//light harvesting-like protein 3 [Populus trichocarpa] >gi|222870310|gb|EEF07441.1| light harvesting-like protein 3 [Populus trichocarpa]	Unigene15406_All//4.00E-74//AT4G17600| LIL3;1; transcription factor	Unigene15406_All//0.00E+00//EX166943			GO:0006091//GO:0009534//GO:0010468	nr +
Unigene15407_All	1208	1.78	1.38	2.25	20.33	17.27	15.74	6.27	2.84	2.70	-3.59E-01	4.08E-01		3.40E-01	3.89E-01		-2.35E-01	3.44E-02		-3.69E-01	6.86E-04		-1.14E+00	4.88E-09	Down	-1.21E+00	3.52E-10	Down	Unigene15407_All//gi|30685673|ref|NP_850208.1|//4.00E-92//arpc2b (actin-related protein C2B); structural molecule [Arabidopsis thaliana]	Unigene15407_All//3.00E-88//AT2G33885| arpc2b (actin-related protein C2B); structural molecule	Unigene15407_All//0.00E+00//CO101332			GO:0015629//GO:0030036	nr -
Unigene15408_All	1281	0.57	3.96	1.00	2.29	3.33	4.87	3.30	13.25	12.63	2.79E+00	8.66E-16	Up	8.03E-01	2.01E-01		5.39E-01	6.87E-02		1.08E+00	4.71E-06	Up	2.00E+00	6.87E-43	Up	1.94E+00	6.45E-40	Up	Unigene15408_All//gi|222424048|dbj|BAH19985.1|//1.00E-62//AT2G45380 [Arabidopsis thaliana]	Unigene15408_All//4.00E-49//AT2G45380| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: inflorescence meristem, flower, cultured cell; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: calcium ion binding (TAIR:AT4G34070.1); Has 72 Blast hits to 71 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 15; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).					nr -
Unigene15410_All	1202	2.92	4.59	4.08	4.89	5.62	6.99	0.53	2.23	1.13	6.56E-01	9.72E-03		4.83E-01	9.29E-02		1.99E-01	4.51E-01		5.15E-01	1.01E-02		2.08E+00	1.12E-07	Up	1.09E+00	2.95E-02		Unigene15410_All//gi|223452302|gb|ACM89479.1|//1.00E-108//cysteine-rich protein [Glycine max]	Unigene15410_All//4.00E-97//AT4G11530| kinase	Unigene15410_All//0.00E+00//DR455101		ko04626|Plant-pathogen interaction		nr -
Unigene15411_All	1152	44.28	96.94	52.05	71.31	123.75	120.67	12.33	23.55	24.55	1.13E+00	5.90E-98	Up	2.33E-01	1.16E-03		7.95E-01	3.33E-83		7.59E-01	1.50E-67		9.33E-01	6.19E-22		9.94E-01	7.09E-26		Unigene15411_All//gi|224118954|ref|XP_002317948.1|//3.00E-77//f-box family protein [Populus trichocarpa] >gi|222858621|gb|EEE96168.1| f-box family protein [Populus trichocarpa]	Unigene15411_All//3.00E-50//AT5G60850| OBP4; DNA binding / transcription factor	Unigene15411_All//0.00E+00//TC168734	C2C2-Dof		GO:0005488	nr -
Unigene15412_All	1223	6.80	22.50	3.27	6.39	23.34	7.20	9.37	4.61	32.93	1.73E+00	4.48E-46	Up	-1.06E+00	6.24E-07	Down	1.87E+00	3.18E-62	Up	1.71E-01	4.57E-01		-1.02E+00	3.33E-11	Down	1.81E+00	5.35E-90	Up	Unigene15412_All//gi|15227225|ref|NP_179836.1|//1.00E-120//UCP5 (UNCOUPLING PROTEIN 5); binding [Arabidopsis thaliana] >gi|90567689|emb|CAJ86454.1| mitochondrial dicarboxylate carrier [Arabidopsis thaliana]	Unigene15412_All//4.00E-107//AT2G22500| UCP5 (UNCOUPLING PROTEIN 5); binding	Unigene15412_All//0.00E+00//gi|78345992|gb|DT566266.1|DT566266				nr +
Unigene15413_All	524	25.76	61.98	31.30	29.38	32.33	73.43	81.90	66.84	49.57	1.27E+00	1.51E-34	Up	2.81E-01	5.90E-02		1.38E-01	3.84E-01		1.32E+00	1.18E-46	Up	-2.93E-01	5.94E-05		-7.24E-01	3.70E-23			Unigene15413_All//3.00E-05//AT1G36730| eukaryotic translation initiation factor 5, putative / eIF-5, putative	Unigene15413_All//0.00E+00//TC138951				kegg -
Unigene15416_All	836	5.38	18.06	11.59	7.57	2.68	20.10	116.02	100.09	301.36	1.75E+00	5.29E-26	Up	1.11E+00	1.59E-08	Up	-1.50E+00	4.22E-11	Down	1.41E+00	1.07E-22	Up	-2.13E-01	6.84E-06		1.38E+00	0.00E+00	Up	Unigene15416_All//gi|89258498|gb|AB065462.1|//1.00E-108//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene15416_All//1.00E-49//AT1G52340| ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase	Unigene15416_All//0.00E+00//TC158778		ko00906|Carotenoid biosynthesis	GO:0008152//GO:0016616	nr +

Unigene15417_All	764	12.81	9.88	7.60	48.25	41.38	21.87	29.00	45.79	21.85	-3.74E-01	4.46E-02		-7.53E-01	7.53E-05		-2.22E-01	1.12E-02		-1.14E+00	4.32E-36	Down	6.59E-01	9.06E-16		-4.08E-01	5.60E-05		Unigene15417_All//gi|28628203|gb|AAO27366.1|//1.0E-35//rapid alkalinization factor 1 precursor [Populus trichocarpa x Populus deltoides]	Unigene15417_All//2.0E-24//AT4G15800| RALFL33 (ralf-like 33); signal transducer	Unigene15417_All//0.00E+00//DW225716			GO:0005618//GO:0060089	nr -
Unigene1542_All	1895	31.81	12.89	17.73	96.84	95.49	63.32	36.64	12.24	15.85	-1.30E+00	1.06E-66	Down	-8.43E-01	7.32E-32		-2.03E-02	6.93E-01		-6.13E-01	1.08E-61		-1.58E+00	3.32E-125	Down	-1.21E+00	9.14E-86	Down	Unigene1542_All//gi|145359142|ref|NP_200019.2|//7.0E-96//ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1); protein binding [Arabidopsis thaliana]	Unigene1542_All//1.0E-88//AT5G52060| ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1); protein binding	Unigene1542_All//0.00E+00//TC131673				nr +
Unigene15420_All	749	6.71	21.78	7.68	7.32	13.98	8.98	19.70	19.75	18.62	1.70E+00	5.11E-27	Up	1.95E-01	4.77E-01		9.34E-01	2.48E-08		2.96E-01	2.28E-01		3.90E-03	1.02E+00		-8.17E-02	6.01E-01		Unigene15420_All//gi|6730631|gb|AAF27052.1|AC008262|1/1.0E-28//F4N2.2 [Arabidopsis thaliana]	Unigene15420_All//3.0E-28//AT1G69040| ACR4 (ACT REPEAT 4); amino acid binding	Unigene15420_All//0.00E+00//ES837607				nr +
Unigene15423_All	561	193.15	134.94	202.56	56.74	89.49	66.34	1.43	6.71	3.20	-5.17E-01	3.08E-25		6.86E-02	2.36E-01		6.57E-01	3.01E-21		2.25E-01	1.30E-02		2.23E+00	2.11E-11	Up	1.16E+00	6.88E-03		Unigene15423_All//gi|8131595|dbj|BAA96362.1|//1.0E-38//oxygen evolving enhancer protein 3 [Bruguiera gymnorhiza]	Unigene15423_All//5.0E-27//AT4G21280| oxygen-evolving enhancer protein 3, chloroplast, putative (PSBQ) (PSBQ)	Unigene15423_All//3.0E-151//gi|73849058|gb|DT458078.1|DT458078		ko00195|Photosynthesis	GO:0009523//GO:0009532//GO:0009534//GO:0044237//GO:0046872	nr +
Unigene15424_All	735	296.70	193.37	327.76	79.36	129.59	104.95	2.42	8.36	5.47	-6.18E-01	1.24E-68		1.44E-01	2.63E-05		7.07E-01	1.78E-45		4.03E-01	1.88E-12		1.79E+00	7.45E-14	Up	1.18E+00	1.45E-05	Up	Unigene15424_All//gi|56122682|gb|AAV74404.1|//5.0E-78//chloroplast oxygen-evolving enhancer protein [Manihot esculenta]	Unigene15424_All//0.00E+00//gi|73849059|gb|DT458079.1|DT458079	Unigene15424_All//0.00E+00//gi|73849059|gb|DT458079.1|DT458079		ko00195|Photosynthesis	GO:0005576//GO:0009523//GO:0009532//GO:0009534//GO:0044237//GO:0046872	nr -
Unigene15426_All	1551	10.93	6.57	7.07	11.76	21.76	22.60	4.01	0.94	1.85	-7.35E-01	5.92E-08		-6.28E-01	6.56E-06		8.88E-01	6.71E-24		9.43E-01	6.08E-25		-2.09E+00	4.89E-17	Down	-1.12E+00	1.43E-07	Down	Unigene15426_All//gi|110430663|gb|ABG73453.1|//1.0E-164//glycosyl hydrolase family 29 [Oryza brachyantha]	Unigene15426_All//2.0E-133//AT2G28100| ATFUC1 (alpha-L-fucosidase 1); alpha-L-fucosidase	Unigene15426_All//0.00E+00//TC136356		ko00511|Other glycan degradation	GO:0009987//GO:0015928//GO:0043167//GO:0044238	nr +
Unigene15428_All	1296	0.97	15.91	0.86	1.65	6.00	9.44	18.24	48.89	68.76	4.04E+00	5.56E-87	Up	-1.67E-01	7.75E-01		1.86E+00	5.13E-17	Up	2.51E+00	1.50E-35	Up	1.42E+00	1.22E-97	Up	1.91E+00	2.16E-213	Up	Unigene15428_All//gi|75225360|sp|Q6Z4H0.1|6PGL2_ORYSJ//6.0E-65//RecName: Full=Probable 6-phosphogluconolactonase 2; Short=6PGL 2 >gi|158513646|sp|A2IYNH4.1|6PGL2_ORYSJ RecName: Full=Probable 6-phosphogluconolactonase 2; Short=6PGL 2	Unigene15428_All//3.0E-54//AT1G13700| glucosamine/galactosamine-6-phosphate isomerase family protein	Unigene15428_All//2.0E-150//gi|189098523|gb|FG551675.1|FG551675		ko00030|Pentose phosphate pathway	GO:0005975//GO:0016787	nr -
Unigene15429_All	965	2.01	0.84	0.28	4.39	2.21	3.14	3.07	2.43	1.86	-1.26E+00	8.35E-03		-2.86E+00	2.95E-06	Down	-9.88E-01	3.29E-04		-4.85E-01	1.13E-01		-3.39E-01	3.34E-01		-7.23E-01	2.04E-02		Unigene15429_All//gi|15228881|ref|NP_188308.1|//1.0E-108//glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	Unigene15429_All//8.0E-109//AT3G16850| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene15429_All//0.00E+00//DW501410		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0008152//GO:0016798//GO:0031410	nr -
Unigene1543_All	1482	4.48	6.56	9.74	5.82	8.27	5.24	0.40	1.30	9.03	5.50E-01	2.81E-03		1.12E+00	1.38E-12	Up	5.08E-01	9.61E-04		-1.50E-01	5.19E-01		1.70E+00	1.45E-04	Up	4.50E+00	5.52E-76	Up	Unigene1543_All//gi|15485720|emb|CAC67501.1|//1.0E-167//selenium binding protein [Medicago sativa]	Unigene1543_All//3.0E-156//AT4G14030| SBP1 (selenium-binding protein 1); selenium binding	Unigene1543_All//9.0E-169//DR454378				nr +
Unigene15430_All	1169	3.40	6.02	13.98	16.92	7.72	5.10	8.75	2.93	3.27	8.25E-01	1.97E-04		2.04E+00	1.74E-33	Up	-1.13E+00	6.81E-22	Down	-1.73E+00	2.22E-36	Down	-1.58E+00	4.85E-19	Down	-1.42E+00	6.24E-17	Down	Unigene15430_All//gi|89257606|gb|AB065094.1|//7.0E-38//myb family transcription factor [Brassica oleracea]	Unigene15430_All//9.0E-29//AT1G70000| DNA-binding family protein	Unigene15430_All//0.00E+00//TC131288	MYB-related		GO:0005488	nr +
Unigene15431_All	1027	3.72	9.23	2.28	10.62	11.80	13.24	22.77	57.30	78.82	1.31E+00	3.87E-11	Up	-7.05E-01	3.16E-02		1.52E-01	4.26E-01		3.17E-01	4.53E-02		1.33E+00	4.18E-82	Up	1.79E+00	3.40E-177	Up	Unigene15431_All//gi|23476279|gb|AAN28270.1|//1.0E-106//myb-like transcription factor 1 [Gossypium hirsutum]	Unigene15431_All//5.0E-76//AT1G22640| MYB3 (MYB DOMAIN PROTEIN 3); DNA binding / transcription factor	Unigene15431_All//0.00E+00//TC136894	MYB			nr -
Unigene15432_All	2825	1.82	0.47	0.62	5.70	5.51	2.99	0.91	0.43	0.55	-1.96E+00	7.99E-11	Down	-1.55E+00	1.40E-07	Down	-4.79E-02	8.09E-01		-9.30E-01	1.24E-11		-1.09E+00	2.12E-03		-7.31E-01	3.05E-02		Unigene15432_All//gi|30694120|ref|NP_191039.2|//0.0E+00//armadillo/beta-catenin repeat family protein / U-box domain-containing protein [Arabidopsis thaliana] >gi|17204574 2|sp|Q8GRV5.2|PUB3_ARATH RecName: Full=U-box domain-containing protein 3; AltName: Full=Plant U-box protein 3	Unigene15432_All//0.0E+00//AT3G54790| armadillo/beta-catenin repeat family protein / U-box domain-containing protein	Unigene15432_All//0.00E+00//AI725616		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0016874	nr -
Unigene15435_All	1230	5.15	18.87	8.75	0.49	0.64	1.14	3.88	3.13	1.91	1.87E+00	1.42E-43	Up	7.65E-01	2.20E-05		4.06E-01	6.32E-01		1.23E+00	3.60E-02		-3.13E-01	2.37E-01		-1.02E+00	2.37E-05	Down	Unigene15435_All//gi|224117652|ref|XP_002317634.1|//2.0E-83//auxin efflux carrier family protein [Populus trichocarpa] >gi|222860699|gb|EEE98246.1| auxin efflux carrier family protein [Populus trichocarpa]	Unigene15435_All//4.0E-84//AT1G76520| auxin efflux carrier family protein	Unigene15435_All//0.00E+00//gi|48741350|gb|C0071869.1|C0071869			GO:0031224//GO:0031410//GO:0060918	nr +
Unigene15436_All	1468	1.89	8.59	4.28	0.31	0.14	0.40	1.30	1.54	0.79	2.19E+00	3.82E-29	Up	1.18E+00	2.58E-06	Up	-1.12E+00	3.15E-01		3.89E-01	6.77E-01		2.46E-01	5.63E-01		-7.20E-01	7.44E-02		Unigene15436_All//gi|224117652|ref|XP_002317634.1|//1.0E-108//auxin efflux carrier family protein [Populus trichocarpa] >gi|222860699|gb|EEE98246.1| auxin efflux carrier family protein [Populus trichocarpa]	Unigene15436_All//6.0E-99//AT1G20925| auxin efflux carrier family protein	Unigene15436_All//0.00E+00//gi|78335064|gb|DT555338.1|DT555338				nr +
Unigene15439_All	593	37.67	65.71	51.36	40.24	39.89	66.79	56.47	214.19	49.98	8.03E-01	6.92E-20		4.47E-01	9.04E-06		-1.24E-02	9.32E-01		7.31E-01	2.02E-18		1.92E+00	6.40E-300	Up	-1.76E-01	3.92E-02		Unigene15439_All//gi|224057577|ref|XP_002299276.1|//9.0E-45//glutathione reductase [Populus trichocarpa] >gi|222846534|gb|EEE84081.1| glutathione reductase [Populus trichocarpa]	Unigene15439_All//7.0E-43//AT3G24170| ATGR1 (glutathione-disulfide reductase); FAD binding / NADP or NADPH binding / glutathione-disulfide reductase/ oxidoreductase	Unigene15439_All//0.00E+00//TC153927		ko00480|Glutathione metabolism	GO:0000729//GO:0006790//GO:0009314//GO:0009536//GO:0015038//GO:0019725//GO:0019953//GO:0030534//GO:0042579	nr -
Unigene1544_All	629	30.28	114.87	74.41	21.38	83.82	163.21	18.89	74.82	45.73	1.92E+00	2.95E-139	Up	1.30E+00	6.74E-50	Up	1.97E+00	2.36E-123	Up	2.93E+00	0.00E+00	Up	1.99E+00	2.86E-116	Up	1.28E+00	7.90E-39	Up	Unigene1544_All//gi|15485720|emb|CAC67501.1|//8.0E-98//selenium binding protein [Medicago sativa]	Unigene1544_All//3.0E-93//AT4G14040| SBP2 (SELENIUM-BINDING PROTEIN 2); selenium binding	Unigene1544_All//0.00E+00//TC137745				nr +
Unigene15440_All	868	5.49	0.82	1.41	4.71	2.78	3.28	7.70	2.46	2.52	-2.75E+00	8.98E-15	Down	-1.96E+00	1.37E-09	Down	-7.61E-01	7.29E-03		-5.22E-01	9.08E-02		-1.65E+00	1.82E-13	Down	-1.61E+00	1.79E-13	Down	Unigene15440_All//gi|115441385|ref|NP_001044972.1|//6.0E-59//Os01g0876900 [Oryza sativa Japonica Group] >gi|113534503|dbj|BAF06886.1| Os01g0876900 [Oryza sativa Japonica Group]	Unigene15440_All//2.0E-62//AT1G71310| unknown protein	Unigene15440_All//0.00E+00//TC131874			GO:0043231	nr -
Unigene15441_All	1520	0.90	0.37	0.42	2.69	3.51	2.44	3.25	2.28	1.28	-1.29E+00	2.82E-02		-1.09E+00	7.48E-02		3.86E-01	1.55E-01		-1.41E-01	6.87E-01		-5.12E-01	3.56E-02		-1.34E+00	5.41E-08	Down	Unigene15441_All//gi|224108581|ref|XP_002314898.1|//0.00E+00//pho1-like protein [Populus trichocarpa] >gi|222863938|gb|EEF01069.1| pho1-like protein [Populus trichocarpa]	Unigene15441_All//0.0E+00//AT1G68740| EXS family protein / ERD1/XPR1/SYG1 family protein	Unigene15441_All//2.0E-120//DW240668			GO:0004871//GO:0031224	nr +
Unigene15442_All	955	4.93	1.43	3.96	2.56	3.57	2.41	2.08	1.09	1.71	-1.78E+00	6.84E-09	Down	-3.17E-01	2.99E-01		4.82E-01	1.66E-01		-8.37E-02	8.51E-01		-9.27E-01	2.37E-02		-2.83E-01	4.99E-01		Unigene15442_All//gi|79380731|ref|NP_177638.2|//5.0E-53//ARC3 (ACCUMULATION AND REPLICATION OF CHLOROPLASTS 3) [Arabidopsis thaliana]	Unigene15442_All//3.0E-54//AT1G75010| ARC3 (ACCUMULATION AND REPLICATION OF CHLOROPLASTS 3)	Unigene15442_All//0.00E+00//gi|21095009|gb|BQ407322.1|BQ407322			GO:0005488	nr +
Unigene15443_All	978	30.98	976.97	453.60	24.60	87.99	244.61	7.82	38.21	63.83	4.98E+00	0.00E+00	Up	3.87E+00	0.00E+00	Up	1.84E+00	8.55E-184	Up	3.31E+00	0.00E+00	Up	2.29E+00	1.54E-110	Up	3.03E+00	3.58E-256	Up	Unigene15443_All//gi|296278600|gb|ADB04264.1|//9.0E-64//HB1 [Nicotiana benthamiana]	Unigene15443_All//2.0E-52//AT2G46680| ATHB-7 (ARABIDOPSIS THALIANA HOMEOBOX 7); transcription activator/ transcription factor	Unigene15443_All//4.0E-133//gi|84151834|gb|DN801189.1|DN801189	HB		GO:0001071//GO:0003677//GO:0006351//GO:0006970//GO:0009755//GO:0010468//GO:0010557//GO:0030528//GO:0043231	nr +
Unigene15444_All	619	54.10	22.67	21.33	82.08	69.15	108.93	149.45	79.81	71.37	-1.25E+00	3.11E-35	Down	-1.34E+00	1.26E-37	Down	-2.47E-01	4.66E-04		4.08E-01	3.30E-11		-9.05E-01	2.52E-69		-1.07E+00	2.60E-93	Down	Unigene15444_All//gi|229891614|sp|A5BUU4.1|RSSA_VITVI//1.0E-31//RecName: Full=40S ribosomal protein SA	Unigene15444_All//7.0E-17//AT1G72370| P40; structural constituent of ribosome	Unigene15444_All//0.00E+00//TC131519		ko03010|Ribosome	GO:0006970//GO:0009536//GO:0015935//GO:0016020	nr +
Unigene15445_All	1237	9.98	19.13	16.10	22.79	17.57	22.82	30.32	21.83	9.57	9.38E-01	6.62E-16		6.90E-01	6.26E-08		-3.76E-01	7.78E-05		1.70E-03	9.88E-01		-4.74E-01	1.12E-09		-1.66E+00	2.90E-75	Down	Unigene15445_All//gi|46931230|gb|AAT06419.1|//7.0E-07//At1g55340 [Arabidopsis thaliana] >gi|8831045 1|gb|AAT41823.1| At1g55340 [Arabidopsis thaliana]	Unigene15445_All//2.0E-08//AT1G55340| unknown protein	Unigene15445_All//9.0E-110//gi|57901483|gb|CB066543.1|CB066543				nr +
Unigene15446_All	1268	1.49	5.63	2.39	2.55	2.36	3.06	3.90	5.67	4.43	1.92E+00	2.39E-14	Up	6.88E-01	6.65E-02		-1.12E-01	7.90E-01		2.63E-01	4.58E-01		5.39E-01	5.71E-03		1.83E-01	4.46E-01		Unigene15446_All//gi|18409246|ref|NP_564959.1|//8.0E-77//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|196890230|gb|AAL91275.1| At1g69330/F10D13.3 [Arabidopsis thaliana] >gi|23505825|gb|AAN28772.1| At1g69330/F10D13.3 [Arabidopsis thaliana]	Unigene15446_All//4.0E-78//AT1G69330| zinc finger (C3HC4-type RING finger) family protein	Unigene15446_All//0.00E+00//TC162142			GO:0046914	nr +
Unigene15448_All	2088	3.28	0.49	0.05	9.02	4.54	1.77	11.32	2.54	3.84	-2.76E+00	4.37E-21	Down	-6.01E+00	1.15E-34	Down	-9.92E-01	7.79E-17		-2.35E+00	1.56E-51	Down	-2.15E+00	2.43E-65	Down	-1.56E+00	1.30E-43	Down	Unigene15448_All//gi|297796731|ref|XP_002866250.1|//0.00E+00//glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] >gi|297312085|gb|EFH42509.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	Unigene15448_All//0.0E+00//AT5G58090| glycosyl hydrolase family 17 protein	Unigene15448_All//0.00E+00//gi|78351923|gb|DT572197.1|DT572197		ko00500|Starch and sucrose metabolism	GO:0008422//GO:0031225//GO:0043167//GO:0044238	nr +
Unigene1545_All	1612	17.98	23.76	29.40	15.54	27.64	16.95	0.05	0.13	0.49	4.02E-01	3.09E-06		7.09E-01	7.71E-19		8.31E-01	4.00E-28		1.25E-01	3.08E-01		1.30E+00	4.47E-01		3.24E+00	3.96E-04	Up	Unigene1545_All//gi|15485720|emb|CAC67501.1|//0.00E+00//selenium binding protein [Medicago sativa]	Unigene1545_All//0.0E+00//AT4G14030| SBP1 (selenium-binding protein 1); selenium binding	Unigene1545_All//0.00E+00//gi|48828014|gb|C0126404.1|C0126404				nr +
Unigene15451_All	965	25.32	31.24	28.53	30.46	18.95	8.19	20.33	12.56	14.20	3.03E-01	2.37E-03		1.72E-01	1.39E-01		-6.85E-01	6.31E-14		-1.89E+00	5.02E-61	Down	-6.95E-01	4.94E-10		-5.18E-01	1.75E-06		Unigene15451_All//gi|217793704|gb|ACX56108.1|//3.0E-45//ELF4-like protein [Beta vulgaris]	Unigene15451_All//2.0E-30//AT1G17455| ELF4-L4 (ELF4-Like 4)	Unigene15451_All//0.00E+00//TC175686				nr +
Unigene15453_All	1230	2.68	2.06	1.00	5.35	3.58	3.56	3.30	1.16	3.04	-3.80E-01	2.76E-01		-1.43E+00	1.22E-04	Down	-5.77E-01	7.93E-03		-5.86E-01	1.02E-02		-1.51E+00	1.36E-07	Down	-1.16E-01	6.75E-01		Unigene15453_All//gi|20197616|gb|AAD24665.2|//3.0E-61//expressed protein [Arabidopsis thaliana]	Unigene15453_All//2.0E-79//AT2G05590| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TLDc (InterPro:IPR006571); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G39870.1); Has 522 Blast hits to 522 proteins in 113 species: Archae - 0; Bacteria - 0; Metazoa - 307; Fungi - 48; Plants - 62; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).	Unigene15453_All//0.00E+00//CO121782			GO:0009536	nr +
Unigene15455_All	1166	11.17	10.21	13.34	15.08	11.28	26.65	5.69	5.99	2.19	-1.30E-01	4.49E-01		2.55E-01	1.00E-01		-4.19E-01	7.52E-04		8.21E-01	1.10E-17		7.25E-02	7.44E-01		-1.38E+00	7.41E-11	Down			Unigene15455_All//0.00E+00//TC164952				

Unigene15457_All	1025	19.40	36.09	36.16	32.56	20.39	45.91	84.02	237.40	109.18	8.96E-01	1.20E-22		8.99E-01	4.92E-22		-6.75E-01	2.25E-15		4.96E-01	3.51E-11		1.50E+00	0.00E+00	Up	3.78E-01	1.22E-18		Unigene15457_All//gi|15226103|ref|NP_180896.1|//2.00E-86//RD20 (RESPONSIVE TO DESSICATION 20); calcium ion binding [Arabidopsis thaliana] >gi|2459421|gb|AAB80656.1| RD20 protein [Arabidopsis thaliana] >gi|10862968|dbj|BAB16823.1| RD20 protein [Arabidopsis thaliana]	Unigene15457_All//9.00E-88//AT2G33380| RD20 (RESPONSIVE TO DESSICATION 20); calcium ion binding	Unigene15457_All//0.00E+00//TC146695			GO:0003006//GO:0004497//GO:0006633//GO:0006970//GO:0006996//GO:0008374//GO:0009414//GO:0009532//GO:0009725//GO:0009941//GO:0016702//GO:0016705//GO:0031224//GO:0042398//GO:0046471//GO:0046872//GO:0051707	nr +
Unigene15459_All	687	0.61	22.72	1.55	4.35	3.81	37.93	3.08	62.91	27.54	5.22E+00	8.18E-77	Up	1.35E+00	6.01E-02		-1.92E-01	6.11E-01		3.12E+00	1.26E-94	Up	4.35E+00	9.94E-236	Up	3.16E+00	2.29E-81	Up	Unigene15459_All//gi|5031277|gb|AAD38144.1|AF139497_1/1.00E-42//homeobox leucine zipper protein [Prunus armeniaca]	Unigene15459_All//2.00E-34//AT3G61890| ATHB-12 (ARABIDOPSIS THALIANA HOMEOBOX 12); transcription activator/ transcription factor	Unigene15459_All//0.00E+00//TC176718	HB		GO:0001071//GO:0003677//GO:0006351//GO:0006970//GO:0009755//GO:0010468//GO:0010557//GO:0030528//GO:0043231	nr +
Unigene1546_All	2117	4.89	3.93	3.45	7.81	9.95	8.02	5.59	1.95	2.31	-3.18E-01	8.14E-02		-5.06E-01	6.39E-03		3.50E-01	2.51E-03		3.82E-02	8.13E-01		-1.52E+00	1.03E-20	Down	-1.27E+00	1.40E-16	Down	Unigene1546_All//gi|544184|sp|Q06801.1|DPEP_SOLTU//0.00E+00//RecName: Full=4-alpha-glucanotransferase, chloroplastic/amyloplastic; AltName: Full=Amylomaltase; AltName: Full=Disproportionating enzyme; Short=D-enzyme; Flags: Precursor >gi|296692|emb|CAA48630.1| 4-alpha-glucanotransferase precursor [Solanum tuberosum]	Unigene1546_All//0.00E+00//AT5G64860| DPE1 (DISPROPORTIONATING ENZYME); 4-alpha-glucanotransferase/ catalytic/ cation binding	Unigene1546_All//0.00E+00//TC136028		ko00500|Starch and sucrose metabolism		nr -
Unigene15461_All	979	113.57	46.37	62.66	52.10	57.90	46.82	2.94	5.00	2.44	-1.29E+00	6.81E-121	Down	-8.58E-01	3.77E-60		1.52E-01	3.71E-02		-1.54E-01	5.35E-02		7.66E-01	1.55E-03		-2.66E-01	4.27E-01		Unigene15461_All//gi|224118954|ref|XP_002317948.1|//1.00E-65//f-box family protein [Populus trichocarpa] >gi|222858621|gb|EEE96168.1| f-box family protein [Populus trichocarpa]	Unigene15461_All//3.00E-31//AT5G60850| OBP4; DNA binding / transcription factor	Unigene15461_All//0.00E+00//TC166653	C2C2-Dof			nr +
Unigene15462_All	1000	29.77	56.45	36.21	31.03	58.40	64.27	71.33	172.53	265.09	9.23E-01	6.51E-36		2.83E-01	2.65E-03		9.12E-01	5.18E-43		1.05E+00	4.75E-54	Up	1.27E+00	9.65E-224	Up	1.89E+00	0.00E+00	Up	Unigene15462_All//gi|3044212|gb|AAC13497.1|//1.00E-177//acyl-CoA oxidase [Arabidopsis thaliana]	Unigene15462_All//3.00E-178//AT5G65110| ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase	Unigene15462_All//0.00E+00//TC179376		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene15466_All	1004	8.08	2.47	4.83	16.77	16.84	15.61	16.93	2.96	4.96	-1.71E+00	5.83E-14	Down	-7.43E-01	4.47E-04		6.00E-03	9.72E-01		-1.04E-01	5.37E-01		-2.52E+00	8.18E-57	Down	-1.77E+00	1.13E-37	Down	Unigene15466_All//gi|7363244|dbj|BAA93004.1|//1.00E-73//nonclathrin coat protein zeta2-COP [Glycine max]	Unigene15466_All//4.00E-60//AT1G60970| clathrin adaptor complex small chain family protein	Unigene15466_All//0.00E+00//TC136334			GO:0051234	nr -
Unigene15467_All	547	0.96	1.39	2.63	1.64	0.88	7.51	0.93	7.87	2.26	5.39E-01	5.02E-01		1.46E+00	1.58E-02		-8.95E-01	2.14E-01		2.20E+00	1.74E-10	Up	3.09E+00	3.20E-18	Up	1.28E+00	1.71E-02		Unigene15467_All//gi|124360471|gb|ABN08481.1|//4.00E-36//Homeodomain-related [Medicago truncatula]	Unigene15467_All//2.00E-33//AT1G26780| myb family transcription factor (MYB117)	Unigene15467_All//1.00E-20//TC160467	MYB		GO:0003676//GO:0010160//GO:0010468//GO:0043231	nr +
Unigene15468_All	1362	0.85	1.82	1.09	3.15	1.69	10.74	2.39	6.97	4.27	1.11E+00	6.72E-03		3.73E-01	5.11E-01		-8.93E-01	1.09E-03		1.77E+00	2.05E-27	Up	1.54E+00	3.90E-17	Up	8.37E-01	9.71E-05		Unigene15468_All//gi|124360471|gb|ABN08481.1|//1.00E-69//Homeodomain-related [Medicago truncatula]	Unigene15468_All//1.00E-53//AT1G26780| myb family transcription factor (MYB117)	Unigene15468_All//1.00E-84//gi|78339014|gb|DT559288.1|DT559288	MYB		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene15469_All	1234	0.59	0.90	2.03	4.48	5.08	6.37	3.63	5.35	3.65	6.06E-01	3.59E-01		1.77E+00	8.83E-05	Up	1.81E-01	5.30E-01		5.07E-01	1.52E-02		5.59E-01	6.25E-03		6.50E-03	9.78E-01		Unigene15469_All//gi|115452617|ref|NP_001049909.1|//1.00E-112//0s03g0309000 [Oryza sativa Japonica Group] >gi|108707761|gb|ABF95556.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548380|dbj|BAF11823.1| Os03g0309000 [Oryza sativa Japonica Group]	Unigene15469_All//6.00E-126//AT3G62370| unknown protein	Unigene15469_All//0.00E+00//gi|78354277|gb|DT574551.1|DT574551			GO:0031410	nr +
Unigene15471_All	1078	31.74	68.06	45.54	12.29	13.07	22.16	19.02	46.68	31.52	1.10E+00	7.19E-62	Up	5.21E-01	1.71E-11		8.80E-02	6.18E-01		8.50E-01	1.56E-14		1.30E+00	2.15E-67	Up	7.29E-01	1.29E-18		Unigene15471_All//gi|5917664|gb|AAD55979.1|AF159296_1//6.00E-37//extensin-like protein [Solanum lycopersicum]		Unigene15471_All//0.00E+00//gi|78344744|gb|DT565018.1|DT565018		ko03040|Spliceosome		nr -
Unigene15473_All	1040	6.74	10.72	5.73	3.35	3.84	21.11	2.44	12.18	1.15	6.69E-01	8.59E-05		-2.33E-01	3.57E-01		1.96E-01	5.89E-01		2.65E+00	1.93E-67	Up	2.32E+00	1.54E-38	Up	-1.09E+00	1.73E-03		Unigene15473_All//gi|166203234|gb|ABY84657.1|//5.00E-39//transcription factor [Glycine max]	Unigene15473_All//2.00E-26//AT4G31800| WRKY18; transcription factor	Unigene15473_All//0.00E+00//TC161234	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene15474_All	1872	0.89	0.62	0.80	1.76	2.19	1.76	9.89	1.56	4.98	-5.23E-01	3.08E-01		-1.67E-01	7.36E-01		3.18E-01	3.29E-01		4.00E-03	9.93E-01		-2.66E+00	8.22E-66	Down	-9.90E-01	2.81E-17		Unigene15474_All//gi|11066213|gb|AAG28503.1|AF196968_1/0.00E+00//hexokinase [Citrus sinensis]	Unigene15474_All//2.00E-172//AT2G19860| HXK2 (HEXOKINASE 2); ATP binding / fructokinase/ glucokinase/ hexokinase	Unigene15474_All//0.00E+00//ES833381		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism	GO:0004396//GO:0006007//GO:0032559	nr +
Unigene15475_All	1010	2.90	1.00	1.48	9.37	7.67	4.52	2.47	0.74	0.91	-1.53E+00	7.46E-05	Down	-9.75E-01	1.12E-02		-2.89E-01	1.36E-01		-1.05E+00	1.38E-08	Down	-1.73E+00	7.81E-06	Down	-1.44E+00	7.03E-05	Down	Unigene15475_All//gi|27805752|sp|O23429.2|VAT24_ARATH//1.00E-105//RecName: Full=Vesicle-associated membrane protein 724; Short=AtVAMP724; AltName: Full=SYBL1-like protein >gi|8310135|gb|AAT41760.1| At4g15780 [Arabidopsis thaliana] >gi|50198886|gb|AAT70463.1| At4g15780 [Arabidopsis thaliana]	Unigene15475_All//2.00E-96//AT4G15780| ATVAMP724	Unigene15475_All//0.00E+00//TC163824		ko04130|SNARE interactions in vesicular transport	GO:0006810//GO:0031224	nr -
Unigene15476_All	1291	15.12	15.97	4.04	19.87	9.50	15.43	22.99	7.41	5.99	7.96E-02	5.80E-01		-1.90E+00	2.68E-36	Down	-1.07E+00	1.25E-25	Down	-3.65E-01	5.79E-04		-1.63E+00	1.90E-56	Down	-1.94E+00	9.30E-74	Down	Unigene15476_All//gi|15226223|ref|NP_178238.1|//1.00E-103//ribose-5-phosphate isomerase [Arabidopsis thaliana] >gi|6226027|sp|Q9ZU38.1|RPIA_ARATH RecName: Full=Probable ribose-5-phosphate isomerase; AltName: Full=Phosphoriboisomerase >gi|15809810|gb|AAL06833.1| At2g01290/F10A8.17 [Arabidopsis thaliana] >gi|17978867|gb|AAL47405.1| At2g01290/F10A8.17 [Arabidopsis thaliana]	Unigene15476_All//1.00E-104//AT2G01290| ribose-5-phosphate isomerase	Unigene15476_All//0.00E+00//TC149250		ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway	GO:0006098//GO:0009250//GO:0016861//GO:0043231//GO:0046108	nr -
Unigene15478_All	1194	26.25	11.84	22.52	25.49	22.44	25.08	22.88	13.79	9.38	-1.15E+00	8.38E-29	Down	-2.21E-01	3.58E-02		-1.84E-01	7.17E-02		-2.36E-02	8.53E-01		-7.30E-01	8.36E-15		-1.29E+00	9.86E-38	Down	Unigene15478_All//gi|2495230|sp|Q43072.1|HIS7_PEA//1.00E-103//RecName: Full=Imidazoleglycerol-phosphate dehydratase; Short=IGPD >gi|1381086|gb|AAB67738.1| imidazoleglycerol-phosphate dehydratase [Pisum sativum]	Unigene15478_All//2.00E-99//AT3G22425| IGPD; imidazoleglycerol-phosphate dehydratase	Unigene15478_All//0.00E+00//TC138358		ko00340|Histidine metabolism	GO:0006547//GO:0016836//GO:0043231	nr +
Unigene15479_All	1246	11.25	8.26	10.86	5.16	4.95	5.58	3.77	1.54	1.66	-4.47E-01	2.94E-03		-5.20E-02	7.55E-01		-6.01E-02	8.17E-01		1.14E-01	6.69E-01		-1.29E+00	5.91E-07	Down	-1.18E+00	2.10E-06	Down	Unigene15479_All//gi|297821515|ref|XP_002878640.1|//1.00E-121//EMB2001 [Arabidopsis lyrata subsp. lyrata] >gi|297324479|gb|EFH54899.1| EMB2001 [Arabidopsis lyrata subsp. lyrata]	Unigene15479_All//9.00E-120//AT2G22870| EMB2001 (embryo defective 2001); GTP binding	Unigene15479_All//0.00E+00//TC163437			GO:0043231	nr -
Unigene15480_All	1891	0.36	1.45	0.51	1.00	2.75	1.12	6.39	6.63	28.15	2.01E+00	3.07E-06	Up	4.95E-01	4.97E-01		1.46E+00	2.75E-08	Up	1.65E-01	7.20E-01		5.23E-02	7.53E-01		2.14E+00	2.46E-147	Up	Unigene15480_All//gi|115338597|gb|ABI94388.1|//6.00E-10//isopentyl diphosphate isomerase [Gossypium barbadense]	Unigene15480_All//4.00E-06//AT5G16440| IPP1 (ISOPENTENYL DIPHOSPHATE ISOMERASE 1); isopentenyl-diphosphate delta-isomerase	Unigene15480_All//0.00E+00//D8461288		ko00900|Terpenoid backbone biosynthesis	GO:0006720//GO:0006779//GO:0009536//GO:0016863	nr +
Unigene15481_All	1094	20.85	23.30	13.39	31.24	41.39	34.76	5.91	9.63	23.85	1.60E-01	1.73E-01		-6.40E-01	6.18E-08		4.06E-01	2.61E-08		1.54E-01	1.09E-01		7.03E-01	7.25E-06		2.01E+00	3.29E-67	Up	Unigene15481_All//gi|2829881|gb|AAC00589.1|//2.00E-33//Hypothetical protein [Arabidopsis thaliana]	Unigene15481_All//6.00E-37//AT5G13090| unknown protein	Unigene15481_All//0.00E+00//TC160581				nr +
Unigene15487_All	1111	19.97	41.64	25.59	31.57	36.70	42.81	81.06	155.30	134.00	1.06E+00	5.32E-37	Up	3.58E-01	7.20E-04		2.17E-01	9.11E-03		4.40E-01	3.52E-09		9.38E-01	1.98E-136		7.25E-01	7.43E-78		Unigene15487_All//gi|167962162|dbj|BAG09370.1|//1.00E-170//peroxisomal fatty acid beta-oxidation multifunctional protein [Glycine max]	Unigene15487_All//7.00E-158//AT3G06860| MFP2 (MULTIFUNCTIONAL PROTEIN 2); 3-hydroxyacyl-CoA dehydrogenase/ enoyl-CoA hydratase	Unigene15487_All//0.00E+00//TC139991		ko00592|alpha-Linolenic acid metabolism		nr -
Unigene15492_All	2656	1.04	1.35	1.00	5.16	6.00	5.54	8.93	7.95	18.10	3.76E-01	2.58E-01		-5.88E-02	8.85E-01		2.19E-01	1.46E-01		1.04E-01	5.70E-01		-1.68E-01	1.28E-01		1.02E+00	3.29E-45	Up	Unigene15492_All//gi|21928151|gb|AAM78103.1|//5.00E-34//AT3g53540/F4P12_240 [Arabidopsis thaliana] >gi|23308447|gb|AAN18193.1| At3g53540/F4P12_240 [Arabidopsis thaliana]	Unigene15492_All//1.00E-31//AT2G39435| unknown protein	Unigene15492_All//0.00E+00//TC130676				nr -
Unigene15493_All	1215	30.01	26.65	28.84	26.77	33.07	31.63	63.44	32.85	30.66	-1.72E-01	6.94E-02		-5.77E-02	6.15E-01		3.05E-01	1.35E-04		2.41E-01	6.29E-03		-9.49E-01	1.14E-62		-1.05E+00	7.10E-76	Down	Unigene15493_All//gi|40850676|gb|AAR23816.2|//0.00E+00//betaine-aldehyde dehydrogenase [Gossypium hirsutum]	Unigene15493_All//0.00E+00//AT1G74920| ALDH10A8; 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Unigene15493_All//0.00E+00//TC130371		ko00260|Glycine, serine and threonine metabolism	GO:0008152//GO:0009536//GO:0016620//GO:0030312//GO:0042579	nr -
Unigene15496_All	1674	199.47	92.29	195.15	18.15	13.70	6.96	0.00	0.00	0.05	-1.11E+00	2.26E-285	Down	-3.15E-02	3.74E-01		-4.06E-01	7.18E-06		-1.38E+00	3.73E-40	Down	null	null		5.57E+00	4.05E-01		Unigene15496_All//gi|260513722|gb|ACX42573.1|//1.00E-84//CONSTANS-like zinc finger protein [Glycine max]	Unigene15496_All//4.00E-79//AT1G25440| zinc finger (B-box type) family protein	Unigene15496_All//0.00E+00//TC167203	C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0044464	nr +
Unigene15498_All	923	3.23	1.65	3.40	4.26	4.22	3.43	3.30	1.31	2.07	-9.72E-01	7.36E-03		7.51E-02	8.33E-01		-1.63E-02	9.50E-01		-3.16E-01	3.53E-01		-1.33E+00	5.51E-05	Down	-6.71E-01	2.89E-02		Unigene15498_All//gi|15450478|gb|AAK96532.1|//7.00E-90//At2g34050/T14G11.17 [Arabidopsis thaliana] >gi|20196905|gb|AAB67623.2| expressed protein [Arabidopsis thaliana] >gi|24370040|gb|AAN64532.1| At2g34050/T14G11.17 [Arabidopsis thaliana]	Unigene15498_All//6.00E-91//AT2G34050| INVOLVED IN: protein complex assembly; LOCATED IN: mitochondrion, chloroplast; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: ATP11 (InterPro:IPR010591); Has 224 Blast hits to 224 proteins in 121 species: Archae - 0; Bacteria - 0; Metazoa - 87; Fungi - 80; Plants - 18; Viruses - 0; Other Eukaryotes - 39 (source: NCBI BLink).	Unigene15498_All//0.00E+00//TC160145			GO:0009536//GO:0016740//GO:0065003	nr -
Unigene15499_All	1488	0.00	0.07	0.04	6.13	2.29	3.31	1.62	3.76	0.94	6.09E+00	3.87E-01		5.16E+00	6.36E-01		-1.42E+00	1.44E-14	Down	-8.89E-01	2.02E-06		1.22E+00	1.63E-07	Up	-7.89E-01	2.45E-02		Unigene15499_All//gi|78213510|sp|Q9SZ77.1|4996A_ARATH//1.00E-155//RecName: Full=UPF0496 protein At4g34320	Unigene15499_All//2.00E-134//AT4G34320| unknown protein	Unigene15499_All//5.00E-56//TC139739				nr +
Unigene15500_All	1078	21.40	30.79	15.61	15.94	18.75	23.21	6.12	1.94	5.73	5.24E-01	1.87E-08		-4.56E-01	1.11E-04		2.34E-01	6.62E-02		5.42E-01	3.12E-07		-1.66E+00	2.04E-13	Down	-9.51E-02	6.58E-01		Unigene15500_All//gi|11131103|sp|O24542.1|AX22D_PHAAU//4.00E-67//RecName: Full=Auxin-induced protein 22D; AltName: Full=Indole-3-acetic acid-induced protein ARG13 >gi|2224731|dbj|BAA20848.1| Aux22d [Vigna radiata]	Unigene15500_All//4.00E-58//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene15500_All//0.00E+00//TC131211			GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr -

Unigene15501_All	769	5.85	5.14	6.16	13.67	17.06	11.45	5.28	1.47	4.51	-1.87E-01	5.43E-01		7.49E-02	7.97E-01		3.20E-01	4.18E-02		-2.55E-01	1.87E-01		-1.85E+00	8.42E-10	Down	-2.28E-01	4.14E-01		Unigene15501_All//gi|48766856|gb|AR00325.2|//5.00E-24//rapid alkalinization factor 1 [Solanum chacoense]	Unigene15501_All//5.00E-21//AT4G13950| RALFL31 (ralf-like 31); signal transducer	Unigene15501_All//0.00E+00//TC159610			GO:0005576//GO:0060089	nr -
Unigene15503_All	2430	0.75	2.75	2.78	5.76	8.59	6.36	0.02	0.14	0.00	1.87E+00	5.39E-13	Up	1.88E+00	8.52E-13	Up	5.76E-01	2.67E-07		1.42E-01	3.96E-01		2.98E+00	5.73E-02		-4.12E+00	6.13E-01		Unigene15503_All//gi|297806429|ref|XP_002871098.1|//0.00E+00//glycosyltransferase family protein 47 [Arabidopsis lyrata subsp. lyrata] >gi|297316935|gb|EFH47357.1| glycosyltransferase family protein 47 [Arabidopsis lyrata subsp. lyrata]	Unigene15503_All//0.00E+00//AT5G04500| glycosyltransferase family protein 47	Unigene15503_All//0.00E+00//TC166140			GO:0005789//GO:0008375	nr +
Unigene15504_All	851	0.06	1.01	1.94	18.32	15.50	33.33	85.36	126.47	49.01	4.04E+00	4.20E-04	Up	4.98E+00	6.48E-08	Up	-2.42E-01	9.95E-02		8.63E-01	1.43E-17		5.67E-01	5.52E-36		-8.00E-01	1.10E-45		Unigene15504_All//gi|28950703|gb|AO63275.1|//2.00E-59//At5g43180 [Arabidopsis thaliana]	Unigene15504_All//2.00E-47//AT5G43180| unknown protein					nr +
Unigene15505_All	1961	1.17	2.35	0.68	1.55	1.55	1.47	3.95	6.05	4.79	1.00E+00	4.30E-04	Up	-7.90E-01	7.45E-02		-3.90E-03	9.80E-01		-7.21E-02	8.59E-01		6.17E-01	2.44E-05		2.81E-01	9.85E-02		Unigene15505_All//gi|61845103|emb|CAI70373.1|//0.00E+00//alpha 1,3 fucosyltransferase [Populus alba x Populus tremula]	Unigene15505_All//2.00E-159//AT3G19280| FUT11 (FUCOSYLTRANSFERASE 11); 4-galactosyl-N-acetylglucosaminide 3-alpha-L-fucosyltransferase/ fucosyltransferase/ transferase, transferring glycosyl groups	Unigene15505_All//0.00E+00//TC156119		ko00510|N-Glycan biosynthesis	GO:0005794//GO:0008417//GO:0016020	nr -
Unigene15506_All	1396	1.27	0.62	0.69	7.21	3.63	2.04	30.04	27.45	5.02	-1.05E+00	3.39E-02		-8.92E-01	8.34E-02		-9.91E-01	3.24E-09		-1.82E+00	4.02E-20	Down	-1.30E-01	1.12E-01		-2.58E+00	9.81E-148	Down	Unigene15506_All//gi|297728361|ref|NP_001176544.1|//1.00E-101//Os11g0487100 [Oryza sativa Japonica Group] >gi|255680101|dbj|BAH95272.1| Os11g0487100 [Oryza sativa Japonica Group]	Unigene15506_All//3.00E-18//AT2G23520| catalytic/ pyridoxal phosphate binding	Unigene15506_All//0.00E+00//TC139122			GO:0043231	nr +
Unigene15507_All	674	5.51	4.29	6.56	13.23	12.36	14.61	9.10	5.08	4.20	-3.63E-01	2.66E-01		2.51E-01	4.14E-01		-9.76E-02	6.65E-01		1.43E-01	5.10E-01		-8.39E-01	8.27E-05		-1.12E+00	1.75E-07	Down	Unigene15507_All//gi|145357905|ref|NP_196717.3|//2.00E-61//catalytic [Arabidopsis thaliana]	Unigene15507_All//1.00E-58//AT5G11560| catalytic	Unigene15507_All//0.00E+00//TC138034			GO:0031410	nr +
Unigene15510_All	825	3.42	1.84	1.68	5.86	3.80	7.17	11.53	3.50	6.57	-8.94E-01	1.65E-02		-1.03E+00	8.85E-03		-6.25E-01	1.64E-02		2.92E-01	2.81E-01		-1.72E+00	5.20E-20	Down	-8.12E-01	6.42E-07		Unigene15510_All//gi|297725961|ref|NP_001175344.1|//2.00E-95//Os07g0689300 [Oryza sativa Japonica Group] >gi|255678077|dbj|BAH94072.1| Os07g0689300 [Oryza sativa Japonica Group]	Unigene15510_All//8.00E-94//AT5G26860| LON1 (LON PROTEASE 1); ATP binding / ATP-dependent peptidase/ serine-type peptidase	Unigene15510_All//0.00E+00//gi|164307594|gb|ES832678.1|ES832678			GO:0004175//GO:0005739//GO:0009536//GO:0019538//GO:0032559//GO:0042623	nr -
Unigene15513_All	833	189.44	126.03	212.55	20.45	18.73	9.00	0.86	0.50	0.91	-5.88E-01	1.08E-45		1.66E-01	3.41E-05		-1.27E-01	4.21E-01		-1.18E+00	5.75E-18	Down	-7.82E-01	3.10E-01		7.46E-02	9.33E-01		Unigene15513_All//gi|297808183|ref|XP_002871975.1|//6.00E-63//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317812|gb|EFH48234.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene15513_All//2.00E-49//AT5G21430| DNAJ heat shock N-terminal domain-containing protein	Unigene15513_All//0.00E+00//TC133048			GO:0005515//GO:0009534	nr +
Unigene15514_All	1106	10.88	5.36	12.28	1.98	2.55	1.23	0.15	0.04	0.22	-1.02E+00	1.14E-09	Down	1.74E-01	3.23E-01		3.65E-01	3.73E-01		-6.94E-01	1.18E-01		-2.02E+00	3.67E-01		4.99E-01	7.07E-01		Unigene15514_All//gi|30688196|ref|NP_850862.1|//3.00E-47//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|29294046|gb|AAO73883.1| DnaJ domain family [Arabidopsis thaliana]	Unigene15514_All//6.00E-38//AT5G21430| DNAJ heat shock N-terminal domain-containing protein	Unigene15514_All//0.00E+00//ES821748			GO:0009534	nr -
Unigene15515_All	1246	4.87	2.07	3.46	3.56	1.49	1.96	2.85	13.18	14.90	-1.23E+00	7.69E-07	Down	-4.93E-01	5.17E-02		-1.25E+00	3.72E-06	Down	-8.62E-01	2.37E-03		2.21E+00	6.15E-47	Up	2.39E+00	3.17E-59	Up	Unigene15515_All//gi|259121423|gb|ACV92031.1|//3.00E-77//WRKY transcription factor 29 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene15515_All//2.00E-49//AT1G29860| WRKY71; transcription factor	Unigene15515_All//0.00E+00//TC179071	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0010468	nr -
Unigene15516_All	1281	3.72	2.45	5.53	1.56	2.31	2.57	0.92	3.23	1.77	-6.00E-01	2.96E-02		5.73E-01	1.27E-02		5.72E-01	1.23E-01		7.27E-01	3.55E-02		1.81E+00	1.13E-09	Up	9.40E-01	1.07E-02		Unigene15516_All//gi|164457637|dbj|BAF96543.1|//6.00E-80//oxysterol-binding protein [Glycine max]	Unigene15516_All//5.00E-71//AT4G08180| OSP1C (OSBP(OXYSTEROL BINDING PROTEIN)-RELATED PROTEIN 1C); oxysterol binding / phosphoinositide binding	Unigene15516_All//2.00E-70//CO071443			GO:0005543//GO:0006629//GO:0023060//GO:0032934//GO:0043231	nr +
Unigene15517_All	1997	2.75	2.99	0.93	2.49	2.10	2.37	3.07	2.24	4.61	1.22E-01	6.16E-01		-1.56E+00	3.52E-08	Down	-2.46E-01	4.06E-01		-7.11E-02	8.08E-01		-4.55E-01	3.56E-02		5.86E-01	3.70E-04		Unigene15517_All//gi|87162841|gb|AB028636.1|//0.00E+00//Tetratricopeptide-like helical [Medicago truncatula]	Unigene15517_All//8.00E-140//AT5G57250| EXPRESSED IN: 9 plant structures; EXPRESSED DURING: F mature embryo stage, 4 leaf senescence stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT1G62910.1); Has 30133 Blast hits to 5951 proteins in 186 species: Archae - 6; Bacteria - 22; Metazoa - 601; Fungi - 543; Plants - 27743; Viruses - 0; Other Eukaryotes - 1218 (source: NCBI BLink).					nr +
Unigene15518_All	1007	11.12	3.77	4.28	24.98	17.88	15.74	16.08	11.54	20.30	-1.56E+00	9.21E-17	Down	-1.38E+00	2.02E-13	Down	-4.82E-01	1.32E-06		-6.66E-01	2.67E-10		-4.79E-01	1.01E-04		3.36E-01	1.70E-03		Unigene15518_All//gi|122894114|gb|ABM67703.1|//6.00E-60//histone 2b [Nicotiana benthamiana]	Unigene15518_All//3.00E-42//AT5G59910| HTB4; DNA binding	Unigene15518_All//0.00E+00//gi|13352234|gb|BG442582.1|BG442582			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr +
Unigene15521_All	1349	8.73	2.78	1.18	10.41	7.66	6.23	4.98	3.16	4.19	-1.65E+00	4.91E-19	Down	-2.88E+00	5.81E-36	Down	-4.43E-01	1.69E-03		-7.42E-01	3.65E-07		-6.57E-01	1.11E-03		-2.49E-01	2.35E-01		Unigene15521_All//gi|18409862|ref|NP_566986.1|//1.00E-103//chloroplast lumen common family protein [Arabidopsis thaliana]	Unigene15521_All//5.00E-81//AT3G53560| chloroplast lumen common family protein	Unigene15521_All//0.00E+00//TC151004			GO:0044434	nr +
Unigene15522_All	1374	1.18	1.25	0.74	4.86	1.88	2.04	6.31	1.37	4.78	8.69E-02	8.59E-01		-6.81E-01	2.14E-01		-1.37E+00	3.01E-10	Down	-1.25E+00	4.81E-08	Down	-2.20E+00	4.27E-25	Down	-3.99E-01	2.03E-02		Unigene15522_All//gi|1710401|sp|P49730.1|RIR2_TOBAC//1.00E-131//RecName: Full=Ribonucleoside-diphosphate reductase small chain; AltName: Full=Ribonucleotide reductase small subunit; AltName: Full=Ribonucleoside-diphosphate reductase R2 subunit >gi|1044912|emb|CAA63194.1| ribonucleotide reductase R2 [Nicotiana tabacum]	Unigene15522_All//6.00E-127//AT3G27060| TSO2 (TSO meaning 'ugly' in Chinese); oxidoreductase/ ribonucleoside-diphosphate reductase/ transition metal ion binding	Unigene15522_All//0.00E+00//DR461858		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism		nr +
Unigene15524_All	700	39.69	22.44	19.09	48.53	41.91	61.55	132.28	43.89	47.35	-8.23E-01	4.81E-15		-1.06E+00	1.49E-21	Down	-2.12E-01	2.24E-02		3.43E-01	1.56E-05		-1.59E+00	2.32E-168	Down	-1.48E+00	5.49E-156	Down	Unigene15524_All//gi|195606082|gb|ACG24871.1|//4.00E-75//40S ribosomal protein S23 [Zea mays] >gi|195618728|gb|ACG31194.1| 40S ribosomal protein S23 [Zea mays] >gi|195619636|gb|ACG31648.1| 40S ribosomal protein S23 [Zea mays] >gi|195625318|gb|ACG34489.1| 40S ribosomal protein S23 [Zea mays] >gi|195628702|gb|ACG36181.1| 40S ribosomal protein S23 [Zea mays] >gi|195657679|gb|ACG48307.1| 40S ribosomal protein S23 [Zea mays]	Unigene15524_All//2.00E-73//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene15524_All//0.00E+00//gi|109866745|gb|DW495721.1|DW495721		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene15525_All	621	0.76	0.82	0.51	0.16	0.22	0.15	3.20	16.42	10.65	1.06E-01	9.23E-01		-5.60E-01	6.28E-01		4.68E-01	8.77E-01		-1.41E-01	9.51E-01		2.36E+00	8.48E-32	Up	1.73E+00	1.36E-14	Up	Unigene15525_All//gi|226532506|ref|NP_001152411.1|//8.00E-15//ATFP4 [Zea mays] >gi|195656017|gb|ACG47476.1| ATFP4 [Zea mays]	Unigene15525_All//2.00E-09//AT5G48290| heavy-metal-associated domain-containing protein	Unigene15525_All//2.00E-41//TC164033				nr +
Unigene15526_All	723	11.07	3.08	17.16	5.17	2.86	2.06	65.96	196.84	13.50	-1.84E+00	2.94E-15	Down	6.32E-01	1.39E-04		-8.55E-01	4.07E-03		-1.33E+00	3.58E-05	Down	1.58E+00	1.42E-254	Up	-2.29E+00	9.72E-146	Down	Unigene15526_All//gi|115446969|ref|NP_001047264.1|//1.00E-19//Os02g0585100 [Oryza sativa Japonica Group] >gi|113536795|dbj|BAF09178.1| Os02g0585100 [Oryza sativa Japonica Group]	Unigene15526_All//4.00E-09//AT5G48290| heavy-metal-associated domain-containing protein	Unigene15526_All//1.00E-52//TC164033				nr -
Unigene15533_All	1208	46.95	86.99	57.22	35.83	71.64	53.61	50.72	105.18	94.06	8.90E-01	2.41E-62		2.85E-01	1.17E-05		9.99E-01	5.53E-74		5.81E-01	5.07E-20		1.05E+00	1.26E-121	Up	8.91E-01	1.42E-84		Unigene15533_All//gi|14596187|gb|AA68821.1|//4.00E-82//Unknown protein [Arabidopsis thaliana]	Unigene15533_All//2.00E-83//AT3G07310| unknown protein	Unigene15533_All//0.00E+00//TC144343			GO:0043231//GO:0044444	nr -
Unigene15534_All	999	1.57	2.94	3.20	1.75	2.86	3.62	0.89	1.80	2.19	9.05E-01	1.34E-02		1.03E+00	4.96E-03		7.13E-01	5.38E-02		1.05E+00	1.21E-03		1.02E+00	2.02E-02		1.30E+00	7.66E-04	Up	Unigene15534_All//gi|260513724|gb|ACX42574.1|//3.00E-53//CONSTANS-like zinc finger protein [Glycine max]	Unigene15534_All//1.00E-35//AT3G21880| zinc finger (B-box type) family protein		C2C2-CO-like		GO:0001071//GO:0010468//GO:0044464//GO:0046914	nr +
Unigene15535_All	1269	5.69	4.95	2.94	10.25	10.07	16.26	96.75	119.26	406.39	-2.01E-01	3.91E-01		-9.54E-01	2.89E-05		-2.53E-02	8.90E-01		6.67E-01	1.65E-08		3.02E-01	3.55E-16		2.07E+00	0.00E+00	Up	Unigene15535_All//gi|224092400|ref|XP_002306592.1|//9.00E-60//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222855568|gb|EEE93115.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene15535_All//2.00E-49//AT1G52800| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene15535_All//0.00E+00//gi|48812137|gb|CO113450.1|CO113450		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis	GO:0016706	nr +
Unigene15536_All	1398	1.80	0.87	0.65	4.53	3.37	3.07	1.24	1.61	1.08	-1.05E+00	9.42E-03		-1.47E+00	7.51E-04	Down	-4.23E-01	6.85E-02		-5.60E-01	1.68E-02		3.81E-01	3.53E-01		-1.95E-01	6.45E-01		Unigene15536_All//gi|224112391|ref|XP_002332782.1|//8.00E-83//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222833191|gb|EEE71668.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene15536_All//6.00E-56//AT5G63020| disease resistance protein (CC-NBS-LRR class), putative	Unigene15536_All//3.00E-76//TC176185		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene15537_All	1442	16.26	10.96	12.26	28.29	21.85	25.15	19.79	11.59	9.45	-5.68E-01	4.53E-07		-4.07E-01	5.30E-04		-3.73E-01	1.24E-06		-1.70E-01	5.92E-02		-7.72E-01	6.60E-17		-1.07E+00	2.00E-29	Down	Unigene15537_All//gi|297832328|ref|XP_002884046.1|//1.00E-150//homoserine kinase [Arabidopsis lyrata subsp. lyrata] >gi|297329886|gb|EFH60305.1| homoserine kinase [Arabidopsis lyrata subsp. lyrata]	Unigene15537_All//5.00E-133//AT2G17265| HSK (HOMOSERINE KINASE); homoserine kinase	Unigene15537_All//0.00E+00//TC132375		ko00260|Glycine, serine and threonine metabolism	GO:0043231	nr -
Unigene15539_All	1287	43.46	23.54	23.00	538.32	260.39	256.35	685.62	515.61	372.82	-8.84E-01	2.83E-33		-9.18E-01	4.26E-34		-1.05E+00	0.00E+00	Down	-1.07E+00	0.00E+00	Down	-4.11E-01	6.35E-161		-8.79E-01	0.00E+00		Unigene15539_All//gi|224056721|ref|XP_002298990.1|//1.00E-150//aquaporin, MIP family, NIP subfamily [Populus trichocarpa] >gi|222846248|gb|EEE83795.1| aquaporin, MIP family, NIP subfamily [Populus trichocarpa]	Unigene15539_All//2.00E-123//AT4G10380| NIP5;1; arsenite transmembrane transporter/ boron transporter/ water channel	Unigene15539_All//0.00E+00//TC134694				nr -

Unigene15540_All	1188	0.57	4.65	1.88	10.65	7.57	10.30	1.99	2.18	1.71	3.02E+00	1.51E-18	Up	1.72E+00	3.36E-04	Up	-4.94E-01	8.99E-04		-4.79E-02	7.89E-01		1.30E-01	7.27E-01		-2.21E-01	5.75E-01		Unigene15540_All//gi|38566676|gb|AR242228.1|/1.00E-144//At1g30300 [Arabidopsis thaliana] >gi|40824143|gb|AAR92355.1| At1g30300 [Arabidopsis thaliana]	Unigene15540_All//9.00E-146//AT1G30300| unknown protein	Unigene15540_All//0.00E+00//gi|78325440|gb|DT545714.1|DT545714				nr +
Unigene15541_All	1023	1.48	0.45	0.62	2.63	2.05	1.28	3.47	2.41	15.58	-1.73E+00	2.69E-03		-1.25E+00	3.05E-02		-3.57E-01	3.78E-01		-1.04E+00	6.71E-03		-5.26E-01	7.58E-02		2.17E+00	2.34E-45	Up	Unigene15541_All//gi|224094238|ref|XP_002310103.1|/6.00E-90//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222853006|gb|EEE90553.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene15541_All//1.00E-65//AT3G12910| transcription factor	Unigene15541_All//0.00E+00//TC146737				nr +
Unigene15542_All	836	137.06	140.86	118.22	50.41	46.09	69.26	34.29	21.70	13.20	3.94E-02	4.90E-01		-2.13E-01	2.07E-05		-1.29E-01	1.54E-01		4.58E-01	7.14E-12		-6.60E-01	4.00E-13		-1.38E+00	7.88E-44	Down	Unigene15542_All//gi|297828179|ref|XP_002881972.1|/1.00E-44//CHL-CPN10 [Arabidopsis lyrata subsp. lyrata] >gi|297327811|gb|EFH58234.1| CHL-CPN10 [Arabidopsis lyrata subsp. lyrata]	Unigene15542_All//8.00E-46//AT3G60210| chloroplast chaperonin 10, putative	Unigene15542_All//0.00E+00//gi|109891246|gb|DW520209.1|DW520209			GO:0009532//GO:0032559//GO:0044267	nr +
Unigene15543_All	1196	5.25	44.57	28.76	5.91	6.91	14.77	0.21	0.45	0.37	3.09E+00	2.16E-178	Up	2.45E+00	4.26E-88	Up	2.25E-01	3.18E-01		1.32E+00	1.25E-21	Up	1.10E+00	2.36E-01		7.89E-01	4.23E-01		Unigene15543_All//gi|9743343|gb|AAF97967.1|AC000103_17//6.00E-39//F21J9.24 [Arabidopsis thaliana]	Unigene15543_All//5.00E-37//AT1G67856| protein binding / zinc ion binding	Unigene15543_All//0.00E+00//TC138605			GO:0005488	nr +
Unigene15544_All	765	46.64	56.30	28.05	57.30	95.61	119.20	88.71	90.31	210.03	2.71E-01	9.66E-04		-7.34E-01	3.82E-15		7.39E-01	1.14E-37		1.06E+00	2.83E-77	Up	2.59E-02	7.20E-01		1.24E+00	8.42E-205	Up	Unigene15544_All//gi|71041082|gb|AAZ20429.1|/5.00E-92//MYB6 [Malus x domestica]	Unigene15544_All//1.00E-66//AT4G37260| MYB73 (MYB DOMAIN PROTEIN 73); DNA binding / transcription factor	Unigene15544_All//0.00E+00//TC133943	MYB		GO:0001071//GO:0000376//GO:0006351//GO:0006970//GO:0009725//GO:0009743//GO:0010038//GO:0010468//GO:0043231	nr +
Unigene15545_All	860	2.74	4.60	2.17	5.04	2.12	3.47	1.13	4.13	3.94	7.47E-01	1.49E-02		-3.37E-01	4.37E-01		-1.25E+00	5.47E-06	Down	-5.40E-01	6.94E-02		1.87E+00	8.84E-09	Up	1.80E+00	3.08E-08	Up	Unigene15545_All//gi|92893902|gb|BE931952.1|/7.00E-20//Zinc finger, CCHC-type [Medicago truncatula]	Unigene15545_All//7.00E-20//AT2G01050| nucleic acid binding / zinc ion binding	Unigene15545_All//3.00E-167//DW506021				nr +
Unigene15546_All	1212	0.43	0.46	0.70	9.25	6.53	4.21	2.37	2.38	3.02	9.13E-02	9.33E-01		7.04E-01	3.83E-01		-5.01E-01	1.69E-03		-1.14E+00	2.86E-11	Down	4.40E-03	1.02E+00		3.50E-01	2.26E-01		Unigene15546_All//gi|269924823|gb|ACZ52698.1|/1.00E-127//hydroxycinnamoyl-CoA quinate hydroxycinnamoyltransferase [Lonicera japonica]	Unigene15546_All//0.00E+00//TC130878	Unigene15546_All//0.00E+00//TC138559		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene15547_All	814	11.70	8.15	7.65	19.22	16.24	24.80	10.54	4.98	4.36	-5.21E-01	5.17E-03		-6.12E-01	1.53E-03		-2.42E-01	9.71E-02		3.68E-01	2.67E-03		-1.08E+00	2.35E-09	Down	-1.28E+00	2.65E-12	Down	Unigene15547_All//0.00E+00//TC152616						nr -
Unigene15548_All	1168	4.66	0.87	1.69	6.57	4.07	8.62	11.33	2.08	3.85	-2.42E+00	1.07E-14	Down	-1.47E+00	1.85E-07	Down	-6.91E-01	3.97E-04		3.93E-01	3.39E-02		-2.45E+00	5.41E-43	Down	-1.56E+00	1.14E-24	Down	Unigene15548_All//gi|42563413|ref|NP_186829.3|//3.00E-89//ribosome recycling factor family protein / ribosome releasing factor family protein [Arabidopsis thaliana] >gi|34146850|gb|AAQ62433.1| At3g01800 [Arabidopsis thaliana]	Unigene15548_All//2.00E-81//AT3G01800| ribosome recycling factor family protein / ribosome releasing factor family protein	Unigene15548_All//0.00E+00//TC138559			GO:0001071//GO:0006351//GO:0006412//GO:0043231	nr -
Unigene1555_All	2007	13.48	7.52	9.05	28.54	21.31	35.87	41.82	141.76	33.82	-8.41E-01	3.32E-15		-5.75E-01	8.52E-08		-4.22E-01	2.65E-11		3.30E-01	3.32E-08		1.76E+00	0.00E+00	Up	-3.06E-01	6.97E-10		Unigene1555_All//gi|1708191|sp|Q07423.1|HEX6_RICCO//0.00E+00//RecName: Full=Hexose carrier protein HEX6 >gi|467319|gb|AAA78857.1| hexose carrier protein [Ricinus communis]	Unigene1555_All//2.00E-145//AT3G19930| STP4 (SUGAR TRANSPORTER 4); carbohydrate transmembrane transporter/ monosaccharide transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter	Unigene1555_All//0.00E+00//TC145028				nr -
Unigene15550_All	754	31.02	46.97	35.45	7.47	11.46	10.42	4.93	1.44	1.22	5.99E-01	3.61E-11		1.93E-01	9.95E-02		6.19E-01	9.58E-04		4.81E-01	2.19E-02		-1.78E+00	1.29E-08	Down	-2.02E+00	1.81E-10	Down	Unigene15550_All//gi|260766533|gb|ACX50288.1|//1.00E-61//R2R3 MYB C2 repressor-like 2 protein [Vitis vinifera]	Unigene15550_All//7.00E-54//AT4G09460| ATMYB6; DNA binding / transcription factor	Unigene15550_All//0.00E+00//gi|13248777|gb|BF278419.2|BF278419	MYB		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene15552_All	1071	69.42	8.61	6.91	88.65	53.21	16.83	29.88	1.95	4.95	-3.01E+00	5.20E-245	Down	-3.33E+00	1.29E-260	Down	-7.36E-01	3.76E-50		-2.40E+00	1.29E-265	Down	-3.94E+00	2.57E-163	Down	-2.59E+00	1.37E-113	Down	Unigene15552_All//gi|224097317|ref|XP_002310906.1|/2.00E-65//high mobility group family [Populus trichocarpa] >gi|222853809|gb|EEE91356.1| high mobility group family [Populus trichocarpa]	Unigene15552_All//5.00E-17//AT5G23420| HMGB6; transcription factor	Unigene15552_All//0.00E+00//gi|164320321|gb|ES807798.1|ES807798		ko03410|Base excision repair	GO:0003676//GO:0043231	nr +
Unigene15554_All	759	1.59	1.94	2.81	1.84	1.50	1.73	4.79	2.64	1.89	2.88E-01	6.23E-01		8.24E-01	7.51E-02		-2.96E-01	6.17E-01		-9.08E-02	8.82E-01		-8.58E-01	2.84E-03		-1.34E+00	4.14E-06	Down	Unigene15554_All//gi|48958477|gb|AT4T791.1|/1.00E-54//At5g24170 [Arabidopsis thaliana] >gi|51972054|gb|AAU15131.1| At5g24170 [Arabidopsis thaliana]	Unigene15554_All//3.00E-36//AT5G24170| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SFT2-like (InterPro:IPR011691); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23550.1); Has 462 Blast hits to 462 proteins in 127 species: Archae - 0; Bacteria - 0; Metazoa - 206; Fungi - 92; Plants - 65; Viruses - 0; Other Eukaryotes - 99 (source: NCBI BLink).	Unigene15554_All//0.00E+00//DW501940			GO:0006810//GO:0044464	nr +
Unigene15555_All	561	9.61	14.45	8.45	7.64	7.49	5.47	7.31	3.95	3.48	5.89E-01	3.88E-03		-1.85E-01	5.22E-01		-2.82E-02	9.29E-01		-4.80E-01	1.14E-01		-8.89E-01	9.30E-04		-1.07E+00	5.19E-05	Down			Unigene15555_All//4.00E-33//gi|164265309|gb|ES815452.1|ES815452				
Unigene15559_All	954	3.35	2.66	6.59	21.20	11.48	13.21	5.41	7.97	1.59	-3.33E-01	3.65E-01		9.77E-01	7.53E-05		-8.85E-01	5.75E-15		-6.83E-01	9.46E-09		5.60E-01	2.95E-03		-1.77E+00	5.34E-12	Down	Unigene15559_All//gi|156066385|gb|ABU43058.1|/3.00E-78//NDR1/HIN1-like protein [Vitis vinifera]	Unigene15559_All//3.00E-69//AT3G33730| harpin-induced family protein / HIN1 family protein / harpin-responsive family protein	Unigene15559_All//0.00E+00//TC135625				nr +
Unigene1556_All	908	1.56	1.79	3.75	5.16	4.82	3.23	2.61	2.12	1.84	1.99E-01	6.82E-01		1.27E+00	3.90E-04	Up	-9.86E-02	7.79E-01		-6.74E-01	1.51E-02		-3.00E-01	4.48E-01		-5.01E-01	1.65E-01		Unigene1556_All//gi|8671880|gb|AAF78443.1|AC018748_22//1.00E-31//Contains similarity to H+-ATPase F0-part b-subunit from Lactococcus lactis subsp. cremoris gb|AF059739 [Arabidopsis thaliana] >gi|17386132|gb|AAL38612.1|AF446879_1 At1g53460/T3F20_21 [Arabidopsis thaliana] >gi|15450677|gb|AAK96610.1| At1g53460/T3F20_21 [Arabidopsis thaliana]	Unigene1556_All//7.00E-33//AT1G53460| unknown protein	Unigene1556_All//0.00E+00//BF270475				nr -
Unigene15562_All	1346	0.82	0.60	1.03	1.59	2.15	3.05	1.82	1.24	4.20	-4.39E-01	4.95E-01		3.34E-01	5.87E-01		4.33E-01	2.75E-01		9.40E-01	1.71E-03		-5.53E-01	1.34E-01		1.21E+00	1.05E-07	Up	Unigene15562_All//gi|15241481|ref|NP_196415.1|//3.00E-79//dentin sialophosphoprotein-related [Arabidopsis thaliana]	Unigene15562_All//2.00E-58//AT5G07980| dentin sialophosphoprotein-related	Unigene15562_All//2.00E-73//TC143292				nr -
Unigene15563_All	1267	7.89	262.43	118.56	33.97	153.18	227.56	0.33	0.49	3.21	5.06E+00	0.00E+00	Up	3.91E+00	0.00E+00	Up	2.17E+00	0.00E+00	Up	2.74E+00	0.00E+00	Up	5.68E-01	5.04E-01		3.26E+00	1.65E-18	Up	Unigene15563_All//gi|108385250|gb|ABF85766.1|//5.00E-63//At3g48510 [Arabidopsis thaliana]	Unigene15563_All//6.00E-64//AT5G63350| unknown protein	Unigene15563_All//0.00E+00//CO090001				nr -
Unigene15564_All	661	102.98	32.96	33.92	89.76	78.46	95.79	197.07	58.74	69.73	-1.64E+00	3.35E-106	Down	-1.60E+00	4.93E-99	Down	-1.94E-01	3.75E-03		9.39E-02	2.28E-01		-1.75E+00	4.67E-270	Down	-1.50E+00	7.22E-223	Down	Unigene15564_All//gi|39149035|sp|O65751.1|RSSA_CICAR//2.00E-30//RecName: Full=40S ribosomal protein SA; AltName: Full=p40 >gi|3204099|emb|CAA07226.1| ribosome-associated protein p40 [Cicer arietinum]	Unigene15564_All//4.00E-18//AT1G72370| P40; structural constituent of ribosome	Unigene15564_All//0.00E+00//gi|109830404|gb|DW228963.1|DW228963		ko03010|Ribosome	GO:0005737//GO:0030529	nr +
Unigene15565_All	648	17.12	21.66	15.37	31.13	20.78	22.93	66.55	32.96	63.45	3.40E-01	2.64E-02		-1.56E-01	4.13E-01		-5.83E-01	1.97E-07		-4.41E-01	2.39E-04		-1.01E+00	2.09E-39	Down	-6.89E-02	4.05E-01		Unigene15565_All//gi|211906526|gb|ACJ11756.1|//2.00E-20//rhamnose synthase [Gossypium hirsutum]	Unigene15565_All//7.00E-18//AT1G63000| NRS/ER (NUCLEOTIDE-RHAMNOSE SYNTHASE/EPIMERASE-REDUCTASE); UDP-4-keto-6-deoxy-glucose-3,5-epimerase/ UDP-4-keto-rhamnose-4-keto-reductase/ dTDP-4-dehydrorhamnose 3,5-epimerase/ dTDP-4-dehydrorhamnose reductase	Unigene15565_All//0.00E+00//TC159982		ko00520|Amino sugar and nucleotide sugar metabolism//ko00523|Polyketide sugar unit biosynthesis	GO:0016616//GO:0016836//GO:0033692//GO:0048037	nr -
Unigene15568_All	877	7.93	6.24	4.86	16.93	14.57	47.84	2.46	101.22	10.95	-3.47E-01	1.30E-01		-7.08E-01	2.17E-03		-2.17E-01	1.61E-01		1.50E+00	2.42E-61	Up	5.36E+00	0.00E+00	Up	2.15E+00	1.81E-27	Up	Unigene15568_All//gi|15228972|ref|NP_188338.1|//2.00E-31//invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana]	Unigene15568_All//3.00E-30//AT3G17130| invertase/pectin methylesterase inhibitor family protein	Unigene15568_All//0.00E+00//gi|109878692|gb|DW507662.1|DW507662			GO:0004857	nr +
Unigene15571_All	976	0.38	0.10	1.20	1.58	1.73	1.20	1.21	0.13	1.84	-1.85E+00	1.87E-01		1.68E+00	1.64E-02		1.28E-01	8.26E-01		-3.95E-01	4.84E-01		-3.24E+00	1.10E-05	Down	5.99E-01	1.59E-01		Unigene15571_All//gi|12323763|gb|AAG51843.1|AC010926_6//2.00E-07//DAG-like protein; 97518-96580 [Arabidopsis thaliana] >gi|124301130|gb|ABN04817.1| At1g72530 [Arabidopsis thaliana]	Unigene15571_All//9.00E-10//AT1G72530| plastid developmental protein DAG, putative	Unigene15571_All//2.00E-122//TC132433				nr +
Unigene15573_All	1459	1.33	0.00	0.15	8.84	5.31	4.43	2.03	1.92	2.18	-1.04E+01	3.38E-11	Down	-3.18E+00	7.30E-07	Down	-7.36E-01	3.30E-07		-9.98E-01	1.46E-10		-7.98E-02	8.17E-01		1.07E-01	7.39E-01		Unigene15573_All//gi|124359162|gb|ABN05685.1|//6.00E-94//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene15573_All//1.00E-17//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene15573_All//2.00E-80//DT469103				nr -
Unigene15574_All	1738	1.02	0.61	0.12	3.38	2.20	3.53	6.59	0.82	2.15	-7.41E-01	1.29E-01		-3.06E+00	3.81E-06	Down	-6.21E-01	7.18E-03		6.34E-02	8.16E-01		-3.01E+00	1.52E-46	Down	-1.61E+00	1.34E-22	Down	Unigene15574_All//gi|297842397|ref|XP_002889080.1|//0.00E+00//ribophorin I family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334921|gb|EFH65339.1| ribophorin I family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15574_All//0.00E+00//AT1G76400| ribophorin I family protein	Unigene15574_All//0.00E+00//gi|11203101|gb|BF272106.1|BF272106		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0006464//GO:0031224//GO:0043231	nr -
Unigene15576_All	785	2.80	0.90	3.46	2.79	2.32	2.65	1.99	1.17	1.27	-1.63E+00	4.00E-04	Down	3.06E-01	4.48E-01		-2.64E-01	5.72E-01		-7.73E-02	8.71E-01		-7.67E-01	1.07E-01		-6.51E-01	1.52E-01				Unigene15576_All//3.00E-71//TC167688				
Unigene15577_All	1193	5.00	4.46	6.03	125.52	59.23	29.45	26.19	16.82	3.47	-1.65E-01	5.31E-01		2.69E-01	2.60E-01		-1.08E+00	1.15E-152	Down	-2.09E+00	0.00E+00	Down	-6.39E-01	1.76E-13		-2.91E+00	9.50E-126	Down	Unigene15577_All//gi|225430575|ref|XP_002263122.1|//3.00E-37//PREDICTED: similar to GDU1 [Vitis vinifera]	Unigene15577_All//6.00E-15//AT5G57685| AtGDU3 (Arabidopsis thaliana GLUTAMINE DUMPER 3)	Unigene15577_All//0.00E+00//gi|164356774|gb|ES849465.1|ES849465			GO:0006868//GO:0032973//GO:0043231	nr -
Unigene15578_All	995	2.42	2.85	3.37	9.66	8.72	10.26	1.83	0.46	2.88	2.38E-01	5.47E-01		4.79E-01	1.81E-01		-1.48E-01	5.01E-01		8.63E-02	6.99E-01		-1.98E+00	3.39E-05	Down	6.58E-01	3.95E-02		Unigene15578_All//gi|4467126|emb|CAB37560.1|//1.00E-99//guanine nucleotide-exchange protein-like [Arabidopsis thaliana] >gi|7270804|emb|CAB50485.1| guanine nucleotide-exchange protein-like [Arabidopsis thaliana]	Unigene15578_All//2.00E-78//AT4G38200| guanine nucleotide exchange family protein			ko04626|Plant-pathogen interaction	GO:0009536	nr +
Unigene15579_All	568	13.36	8.65	15.94	21.66	16.13	18.61	14.44	4.78	9.96	-6.26E-01	3.01E-03		2.55E-01	2.37E-01		-4.26E-01	5.62E-03		-2.19E-01	2.23E-01		-1.59E+00	1.24E-15	Down	-5.36E-01	2.19E-03		Unigene15579_All//gi|124359308|gb|ABR28456.2|//1.00E-34//Ribosomal protein S21e [Medicago truncatula]	Unigene15579_All//3.00E-34//AT5G27700| structural constituent of ribosome	Unigene15579_All//3.00E-86//DN828231		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0031410	nr -

Unigene1558_All	3255	3.92	1.65	3.42	9.46	5.90	1.67	9.81	1.66	3.45	-1.25E+00	8.35E-14	Down	-1.98E-01	2.65E-01		-6.80E-01	2.14E-14		-2.51E+00	7.19E-91	Down	-2.57E+00	1.88E-108	Down	-1.51E+00	1.24E-55	Down	Unigene1558_All//gi|15229135|ref|NP_189853.1|//0.00E+00//CHR38 (CHROMATIN REMODELING 38); ATP binding / DNA binding / helicase/ nucleic acid binding [Arabidopsis thaliana]	Unigene1558_All//0.00E+00//AT3G42670| CHR38 (CHROMATIN REMODELING 38); ATP binding / DNA binding / helicase/ nucleic acid binding	Unigene1558_All//0.00E+00//gi|109859518|gb|DW488497.1|DW488497		ko03420|Nucleotide excision repair//ko03440|Homologous recombination		nr +
Unigene15580_All	708	0.59	0.43	0.15	1.34	0.58	0.70	3.05	3.84	0.96	-4.61E-01	6.50E-01		-1.97E+00	1.51E-01		-1.20E+00	8.32E-02		-9.30E-01	2.07E-01		3.33E-01	3.72E-01		-1.67E+00	3.81E-05	Down	Unigene15580_All//gi|115485835|ref|NP_001068061.1|//6.00E-09//Os11g0545800 [Oryza sativa Japonica Group] >gi|113645283|dbj|BAF28424.1|Os11g0545800 [Oryza sativa Japonica Group]	Unigene15580_All//1.00E-09//AT5G08710| regulator of chromosome condensation (RCC1) family protein / UVB-resistance protein-related	Unigene15580_All//0.00E+00//gi|5050174|gb|AI731322.1|AI731322			GO:0017016//GO:0043231	nr -
Unigene15581_All	628	3.58	2.66	3.65	2.78	3.78	2.88	4.24	1.00	1.59	-4.28E-01	3.28E-01		2.54E-02	9.72E-01		4.47E-01	3.09E-01		5.12E-02	9.37E-01		-2.09E+00	1.03E-07	Down	-1.42E+00	4.85E-05	Down	Unigene15581_All//gi|30682540|ref|NP_680156.2|//3.00E-58//regulator of chromosome condensation (RCC1) family protein / UVB-resistance protein-related [Arabidopsis thaliana]	Unigene15581_All//3.00E-50//AT5G08710| regulator of chromosome condensation (RCC1) family protein / UVB-resistance protein-related	Unigene15581_All//0.00E+00//TC159378		ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0043231	nr -
Unigene15582_All	850	26.10	109.98	42.60	35.75	46.75	80.55	46.46	94.70	92.99	2.08E+00	7.16E-199	Up	7.07E-01	1.86E-14		3.87E-01	8.85E-07		1.17E+00	1.37E-68	Up	1.03E+00	2.26E-74	Up	1.00E+00	1.39E-71	Up	Unigene15582_All//gi|27261731|gb|AAN86062.1|//1.00E-90//sugar transporter [Citrus unshiu]	Unigene15582_All//9.00E-75//AT1G67300| hexose transporter, putative	Unigene15582_All//0.00E+00//gi|48814447|gb|CO115760.1|CO115760			GO:0006810//GO:0008152//GO:0016628//GO:0022891//GO:0031224	nr +
Unigene15583_All	773	16.92	84.56	40.37	8.51	7.44	30.79	51.09	124.47	129.67	2.32E+00	4.91E-160	Up	1.25E+00	1.00E-31	Up	-1.93E-01	4.50E-01		1.86E+00	3.54E-47	Up	1.28E+00	1.29E-126	Up	1.34E+00	2.66E-144	Up	Unigene15583_All//gi|172045782|sp|Q9XI29.2|Y1540_ARATH//1.00E-16//RecName: Full=Uncharacterized protein At1g15400	Unigene15583_All//1.00E-12//AT5G20100| unknown protein	Unigene15583_All//0.00E+00//gi|109875187|gb|DW504161.1|DW504161				nr +
Unigene15585_All	1393	4.70	1.24	2.71	1.57	1.53	1.30	2.09	0.87	1.77	-1.92E+00	2.69E-13	Down	-7.91E-01	9.68E-04		-3.79E-02	9.29E-01		-2.79E-01	5.68E-01		-1.27E+00	1.57E-04	Down	-2.40E-01	4.77E-01		Unigene15585_All//gi|15450996|gb|AAK96769.1|//1.00E-67//Unknown protein [Arabidopsis thaliana] >gi|53828651|gb|AAU94435.1|At4g16100 [Arabidopsis thaliana]	Unigene15585_All//8.00E-65//AT4G16100| unknown protein	Unigene15585_All//0.00E+00//gi|78325812|gb|DT546086.1|DT546086			GO:0043231	nr -
Unigene15588_All	1316	150.96	102.65	40.34	633.20	896.49	1257.51	198.10	50.78	65.96	-5.57E-01	5.31E-52		-1.90E+00	0.00E+00	Down	5.02E-01	2.50E-305		9.90E-01	0.00E+00		-1.96E+00	0.00E+00	Down	-1.59E+00	0.00E+00	Down	Unigene15588_All//gi|254554080|gb|ACT67416.1|//1.00E-162//xyloglucan endotransglycosylase [Shorea parvifolia subsp. parvifolia]	Unigene15588_All//5.00E-145//AT5G13870| EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase	Unigene15588_All//0.00E+00//TC137123				nr +
Unigene15596_All	630	20.93	9.73	18.68	39.85	27.71	22.15	7.92	4.84	3.79	-1.10E+00	7.67E-12	Down	-1.64E-01	3.69E-01		-5.24E-01	1.35E-07		-8.47E-01	2.65E-15		-7.09E-01	2.99E-03		-1.06E+00	7.75E-06	Down	Unigene15596_All//gi|297843504|ref|XP_002889633.1|//1.00E-33//OB-fold nucleic acid binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335475|gb|EFH65892.1| OB-fold nucleic acid binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene15596_All//1.00E-34//AT1G07130| STN1; nucleic acid binding	Unigene15596_All//0.00E+00//TC157413		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair	GO:0000723//GO:0000781//GO:0005488	nr -
Unigene15597_All	893	12.71	64.91	23.85	13.44	16.89	12.64	22.96	43.48	27.04	2.35E+00	3.03E-144	Up	9.08E-01	3.90E-13		3.29E-01	2.17E-02		-8.85E-02	6.53E-01		9.21E-01	2.16E-30		2.36E-01	1.85E-02					Unigene15597_All//0.00E+00//gi|48746217|gb|CO076736.1|CO076736				
Unigene1560_All	2046	6.80	2.95	4.19	3.43	1.85	3.44	1.96	1.63	3.17	-1.21E+00	3.14E-14	Down	-6.99E-01	7.18E-06		-8.91E-01	1.31E-05		4.40E-03	9.85E-01		-2.65E-01	3.82E-01		6.93E-01	5.45E-04		Unigene1560_All//gi|15242850|ref|NP_200579.1|//1.00E-135//heat shock protein-related [Arabidopsis thaliana] >gi|9759268|dbj|BAB09589.1| 101 kDa heat shock protein; HSP101-like protein [Arabidopsis thaliana]	Unigene1560_All//3.00E-131//AT5G57710| heat shock protein-related	Unigene1560_All//0.00E+00//TC158972				nr -
Unigene15601_All	853	29.32	14.32	8.05	17.64	14.49	11.54	68.05	19.70	20.78	-1.03E+00	1.23E-19	Down	-1.86E+00	3.71E-45	Down	-2.83E-01	5.10E-02		-6.12E-01	1.27E-05		-1.79E+00	9.94E-125	Down	-1.71E+00	9.75E-121	Down	Unigene15601_All//gi|291067126|gb|ADD74180.1|//2.00E-69//high mobility group box 3 protein [Gossypium hirsutum]	Unigene15601_All//4.00E-24//AT1G20696| HMGB3 (HIGH MOBILITY GROUP B 3); DNA binding / chromatin binding / structural constituent of chromatin / transcription factor	Unigene15601_All//0.00E+00//gi|164287255|gb|ES845898.1|ES845898		ko03410|Base excision repair	GO:0003676//GO:0043231	nr +
Unigene15602_All	272	1.92	14.34	5.09	3.11	11.90	16.60	3.89	16.29	11.28	2.90E+00	9.29E-13	Up	1.40E+00	2.28E-02		1.93E+00	1.22E-07	Up	2.42E+00	8.63E-13	Up	2.07E+00	3.49E-12	Up	1.54E+00	3.29E-06	Up	Unigene15602_All//gi|15485716|emb|CAC67491.1|//3.00E-22//selenium binding protein [Lotus japonicus] >gi|15485718|emb|CAC67492.1| selenium binding protein [Lotus japonicus]	Unigene15602_All//2.00E-23//AT3G23800| SBP3 (selenium-binding protein 3); selenium binding	Unigene15602_All//1.00E-83//EX169369			GO:0000302//GO:0000741//GO:0006790//GO:0010269//GO:0046914	nr +
Unigene15603_All	829	45.19	196.87	94.10	29.98	123.41	245.38	31.42	119.84	62.57	2.12E+00	0.00E+00	Up	1.06E+00	5.03E-60	Up	2.04E+00	1.47E-250	Up	3.03E+00	0.00E+00	Up	1.93E+00	5.28E-236	Up	9.94E-01	9.84E-47		Unigene15603_All//gi|15485720|emb|CAC67501.1|//1.00E-144//selenium binding protein [Medicago sativa]	Unigene15603_All//1.00E-134//AT4G14030| SBP1 (selenium-binding protein 1); selenium binding	Unigene15603_All//0.00E+00//TC152015				nr +
Unigene15604_All	970	96.55	175.78	140.76	25.06	31.67	38.97	6.02	3.83	2.51	8.64E-01	6.01E-96		5.44E-01	2.39E-33		3.38E-01	2.68E-04		6.37E-01	6.08E-14		-6.49E-01	2.97E-03		-1.26E+00	1.57E-08	Down	Unigene15604_All//gi|46397070|sp|Q92UU2.2|U308_ARATH//1.00E-81//RecName: Full=UPF0308 protein At2g37240, chloroplastic; Flags: Precursor >gi|15215634|gb|AAK91362.1| At2g37240/F3G5.3 [Arabidopsis thaliana] >gi|20197473|gb|AAC98045.2| expressed protein [Arabidopsis thaliana] >gi|30102454|gb|AAP21145.1| At2g37240/F3G5.3 [Arabidopsis thaliana]	Unigene15604_All//2.00E-77//AT2G37240| INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Thioredoxin fold (InterPro:IPR012335), Thioredoxin-like fold (InterPro:IPR012336); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G65840.1); Has 252 Blast hits to 252 proteins in 46 species: Archae - 0; Bacteria - 20; Metazoa - 145; Fungi - 10; Plants - 66; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene15604_All//0.00E+00//TC177287			GO:0003824//GO:0009536	nr -
Unigene15605_All	871	38.38	11.29	29.41	65.60	46.49	17.22	8.93	3.12	1.65	-1.77E+00	4.98E-58	Down	-3.84E-01	6.54E-05		-4.97E-01	4.21E-15		-1.93E+00	2.64E-121	Down	-1.52E+00	6.77E-14	Down	-2.44E+00	2.66E-26	Down	Unigene15605_All//gi|115489196|ref|NP_001067085.1|//2.00E-23//Os12g0571300 [Oryza sativa Japonica Group] >gi|77556867|gb|ABA99663.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649592|dbj|BAF30104.1| Os12g0571300 [Oryza sativa Japonica Group]	Unigene15605_All//6.00E-69//AT3G55420| unknown protein	Unigene15605_All//0.00E+00//TC153464				nr -
Unigene15606_All	1006	133.09	34.75	227.72	240.70	297.77	193.31	210.81	55.17	98.53	-1.94E+00	8.06E-262	Down	7.75E-01	5.53E-104		3.07E-01	2.73E-31		-3.16E-01	2.57E-24		-1.93E+00	0.00E+00	Down	-1.10E+00	3.94E-223	Down	Unigene15606_All//gi|50313460|gb|AAT74600.1|//1.00E-131//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene15606_All//3.00E-68//AT3G23530| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene15606_All//0.00E+00//TC129559		ko00860|Porphyrin and chlorophyll metabolism	GO:0006629//GO:0008757	nr -
Unigene15607_All	1047	1.65	2.13	0.97	2.19	4.37	3.41	0.89	2.51	2.25	3.69E-01	3.84E-01		-7.71E-01	1.40E-01		9.99E-01	2.40E-04		6.39E-01	5.41E-02		1.50E+00	3.94E-05	Up	1.34E+00	3.44E-04	Up	Unigene15607_All//gi|30685543|ref|NP_173224.2|//1.00E-53//phosphoinositide binding [Arabidopsis thaliana] >gi|34098829|gb|AAQ56797.1|At1g17820 [Arabidopsis thaliana]	Unigene15607_All//5.00E-52//AT1G17820| phosphoinositide binding	Unigene15607_All//0.00E+00//DT455943			GO:0043231//GO:0044444	nr +
Unigene15608_All	576	4.00	6.33	4.81	7.70	4.54	4.86	5.95	16.25	7.54	6.64E-01	3.93E-02		2.66E-01	5.14E-01		-7.61E-01	4.81E-03		-6.63E-01	2.09E-02		1.45E+00	1.63E-15	Up	3.43E-01	1.94E-01		Unigene15608_All//gi|62857016|dbj|BAD85893.1|//2.00E-14//Ser/Thr protein kinase [Lotus japonicus]		Unigene15608_All//3.00E-98//gi|84149431|gb|DN780731.1|DN780731			GO:0004672//GO:0006464//GO:0016020//GO:0032559//GO:0043231//GO:0004444	nr +
Unigene15610_All	553	55.54	39.86	24.94	111.43	91.16	142.51	117.05	106.72	64.40	-4.79E-01	8.15E-07		-1.16E+00	2.09E-27	Down	-2.90E-01	3.00E-06		3.55E-01	3.73E-10		-1.33E-01	3.38E-02		-8.62E-01	3.17E-46		Unigene15610_All//gi|240254409|ref|NP_850984.4|//1.00E-70//ATP binding [Arabidopsis thaliana]	Unigene15610_All//5.00E-61//AT1G79930| HSP91; ATP binding	Unigene15610_All//0.00E+00//gi|164287762|gb|ES840795.1|ES840795		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0006950//GO:0008152//GO:0010038//GO:0016020//GO:0016628//GO:0032559//GO:0043231	nr +
Unigene15612_All	750	37.67	26.75	17.40	56.06	49.31	56.18	86.76	49.88	37.02	-4.94E-01	1.16E-06		-1.11E+00	6.98E-24	Down	-1.85E-01	2.68E-02		3.20E-03	9.71E-01		-7.99E-01	9.46E-40		-1.23E+00	1.58E-82	Down	Unigene15612_All//gi|124484511|dbj|BAF46352.1|//6.00E-75//alpha chain of nascent polypeptide associated complex [Nicotiana benthamiana]	Unigene15612_All//3.00E-61//AT3G12390| nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative	Unigene15612_All//0.00E+00//TC136540			GO:0005840//GO:0006810//GO:0006970	nr +
Unigene15613_All	803	9.90	4.80	6.37	22.33	21.78	16.59	30.59	14.47	17.61	-1.05E+00	6.73E-07	Down	-6.38E-01	2.92E-03		-3.58E-02	8.20E-01		-4.29E-01	8.84E-04		-1.08E+00	3.41E-25	Down	-7.97E-01	6.26E-16		Unigene15613_All//gi|17933310|gb|AL48237.1|AF446365_1//9.00E-93//At1g10950/T19D16_13 [Arabidopsis thaliana] >gi|15451172|gb|AAK96857.1| endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana] >gi|20148415|gb|AAM10098.1| endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]	Unigene15613_All//4.00E-82//AT1G10950| endomembrane protein 70, putative	Unigene15613_All//0.00E+00//TC147189			GO:0031224//GO:0031410//GO:0043231	nr -
Unigene15614_All	1204	55.10	37.29	46.48	2.81	4.58	2.21	3.48	4.96	0.46	-5.63E-01	2.93E-18		-2.45E-01	2.74E-04		7.02E-01	4.15E-03		-3.46E-01	3.45E-01		5.14E-01	1.84E-02		-2.91E+00	2.01E-17	Down	Unigene15614_All//gi|15241967|ref|NP_200497.1|//9.00E-46//GNC (GATA, nitrate-inducible, carbon metabolism-involved); transcription factor [Arabidopsis thaliana] >gi|71660831|sp|Q8H236.2|GAT21_ARATH RecName: Full=GATA transcription factor 21 >gi|109134121|gb|ABG25059.1| At5g56860 [Arabidopsis thaliana]	Unigene15614_All//6.00E-33//AT5G56860| GNC (GATA, nitrate-inducible, carbon metabolism-involved); transcription factor	Unigene15614_All//0.00E+00//CO092513	C2C2-GATA		GO:0005488//GO:0009314//GO:0009725//GO:0009987//GO:0019222//GO:0048511	nr +
Unigene15617_All	1210	4.50	8.25	5.06	3.75	3.79	1.75	1.08	1.66	1.22	8.75E-01	1.81E-06		1.70E-01	5.31E-01		1.48E-02	9.67E-01		-1.09E+00	1.03E-04	Down	6.14E-01	1.38E-01		1.70E-01	7.19E-01		Unigene15617_All//gi|284028888|gb|ADB66335.1|//1.00E-60//CC-NBS-LRR protein [Quercus suber]	Unigene15617_All//7.00E-27//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene15617_All//3.00E-112//TC176306				nr +
Unigene15618_All	865	14.09	33.33	13.67	21.83	16.92	14.93	40.42	46.97	46.29	1.24E+00	7.98E-30	Up	-4.44E-02	8.06E-01		-3.67E-01	2.41E-03		-5.48E-01	9.23E-06		2.16E-01	5.12E-03		1.95E-01	1.04E-02		Unigene15618_All//gi|14596001|gb|AA68728.1|//8.00E-58//Unknown protein [Arabidopsis thaliana]	Unigene15618_All//4.00E-36//AT4G11740| SAY1	Unigene15618_All//0.00E+00//gi|73864430|gb|DT467169.1|DT467169			GO:0044444	nr -
Unigene1562_All	2177	36.60	38.82	37.64	63.54	32.43	29.87	17.63	15.21	12.54	8.49E-02	1.84E-01		4.05E-02	5.91E-01		-9.71E-01	2.02E-117		-1.09E+00	2.22E-124	Down	-2.14E-01	7.49E-03		-4.92E-01	7.11E-11		Unigene1562_All//gi|15222993|ref|NP_172250.1|//0.00E+00//ankyrin repeat family protein [Arabidopsis thaliana] >gi|84398897|gb|AAF75083.1|AC007583_19 It contains Ank repeat PF|00023, EST gb|AI996003 comes from this gene [Arabidopsis thaliana]	Unigene1562_All//2.00E-168//AT1G07710| ankyrin repeat family protein	Unigene1562_All//0.00E+00//gi|164311358|gb|ES848504.1|ES848504				nr +

Unigene15620_All	683	11.26	27.15	29.63	13.57	25.51	33.19	22.04	26.37	29.16	1.27E+00	4.17E-20	Up	1.40E+00	2.31E-24	Up	9.11E-01	4.83E-13		1.29E+00	1.03E-26	Up	2.59E-01	3.34E-02		4.04E-01	1.75E-04		Unigene15620_All//gi|3913996|sp|O04979.1|LONM_SPIOL//1.0E-73//RecName: Full=Lon protease homolog, mitochondrial; Flags: Precursor >gi|2208927|dbj|BAA20482.1| ATP-dependent protease Lon [Spinacia oleracea]	Unigene15620_All//6.00E-74//AT5G47040| LON2 (LON PROTEASE 2); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase	Unigene15620_All//0.00E+00//DW479800			GO:0003676//GO:0004175//GO:0016558//GO:0019538//GO:0031980//GO:0032559//GO:0042623//GO:0044439//GO:0048528	nr +
Unigene15622_All	570	7.34	10.13	12.24	8.56	15.77	25.28	16.91	12.98	24.25	4.65E-01	6.36E-02		7.37E-01	1.38E-03		8.81E-01	1.34E-06		1.56E+00	1.20E-22	Up	-3.82E-01	2.33E-02		5.20E-01	7.53E-05		Unigene15622_All//gi|75334257|sp|Q9FRL3.1|ERDL6_ARATH//2.00E-66//RecName: Full=Sugar transporter ERD6-like 6 >gi|15724240|gb|AAL06513.1|AF412060_1 At1g75220/F22H5_6 [Arabidopsis thaliana] >gi|21700861|gb|AAM70554.1| At1g75220/F22H5_6 [Arabidopsis thaliana]	Unigene15622_All//1.00E-60//AT1G75220| integral membrane protein, putative	Unigene15622_All//1.00E-137//C0125766			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr +
Unigene15623_All	614	10.31	16.17	17.26	12.82	24.85	28.25	12.39	11.91	31.27	6.50E-01	3.46E-04		7.43E-01	4.28E-05		9.55E-01	2.34E-12		1.14E+00	5.35E-17	Up	-5.73E-02	7.89E-01		1.34E+00	4.64E-28	Up	Unigene15623_All//gi|75334257|sp|Q9FRL3.1|ERDL6_ARATH//1.00E-75//RecName: Full=Sugar transporter ERD6-like 6 >gi|15724240|gb|AAL06513.1|AF412060_1 At1g75220/F22H5_6 [Arabidopsis thaliana] >gi|21700861|gb|AAM70554.1| At1g75220/F22H5_6 [Arabidopsis thaliana]	Unigene15623_All//2.00E-70//AT1G75220| integral membrane protein, putative	Unigene15623_All//2.00E-152//C0125766			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr +
Unigene15625_All	547	21.90	49.00	29.50	25.50	30.97	33.69	13.53	8.94	10.20	1.16E+00	4.52E-25	Up	4.29E-01	3.03E-03		2.81E-01	4.11E-02		4.02E-01	1.73E-03		-5.98E-01	1.76E-03		-4.08E-01	3.02E-02					Unigene15625_All//2.00E-130//BF268653					
Unigene15626_All	840	18.00	11.04	21.68	14.65	14.10	14.14	24.56	12.54	7.73	-7.06E-01	9.62E-07		2.68E-01	5.68E-02		-5.48E-02	8.09E-01		-5.09E-02	7.86E-01		-9.70E-01	5.58E-18		-1.67E+00	6.46E-42	Down	Unigene15626_All//gi|195628060|gb|ACG35860.1|//3.00E-72//peroxisomal membrane protein PMP22 [Zea mays]	Unigene15626_All//0.00E+00//gi|109855169|gb|DW484148.1|DW484148		ko04146|Peroxisome	GO:0031224//GO:0044439	nr -
Unigene15629_All	1018	1.44	9.56	1.57	2.10	3.99	2.22	7.81	35.60	28.14	2.73E+00	4.06E-29	Up	1.25E-01	8.06E-01		9.24E-01	1.57E-03		7.62E-02	8.80E-01		2.19E+00	1.55E-101	Up	1.85E+00	6.00E-66	Up	Unigene15629_All//gi|21552998|gb|AM62421.1|AF515795_1//5.00E-38//Drm3 [Pisum sativum]	Unigene15629_All//5.00E-35//AT1G56220| dormancy/auxin associated family protein	Unigene15629_All//5.00E-86//ES837410				nr +
Unigene1563_All	4553	5.22	2.39	2.94	20.58	19.20	18.22	20.41	21.06	15.58	-1.12E+00	2.64E-21	Down	-8.30E-01	1.41E-12		-9.99E-02	8.34E-02		-1.76E-01	1.20E-03		4.50E-02	4.47E-01		-3.89E-01	1.56E-16		Unigene1563_All//gi|116309878|emb|CAH66915.1|//1.00E-141//OSIGBa0126B18.8 [Oryza sativa (indica cultivar-group)]	Unigene1563_All//0.00E+00//AT2G32240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cadmium ion; LOCATED IN: plasma membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G05320.3); Has 221693 Blast hits to 95553 proteins in 2574 species: Archae - 2848; Bacteria - 44259; Metazoa - 97474; Fungi - 15490; Plants - 8386; Viruses - 1229; Other Eukaryotes - 52007 (source: NCBI BLink).	Unigene1563_All//0.00E+00//TC139262				nr -
Unigene15630_All	1515	4.70	2.61	2.99	13.68	10.66	3.94	1.93	0.61	0.32	-8.48E-01	1.16E-04		-6.53E-01	4.23E-03		-3.60E-01	1.72E-03		-1.80E+00	3.60E-40	Down	-1.67E+00	2.16E-06	Down	-2.61E+00	4.19E-11	Down	Unigene15630_All//gi|124359162|gb|ABN06683.1|//9.00E-40//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene15630_All//2.00E-32//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene15630_All//0.00E+00//ES836566			GO:0044464	nr -
Unigene15636_All	729	7.03	8.97	5.99	14.90	7.13	16.91	46.17	56.82	28.14	3.50E-01	1.38E-01		-2.32E-01	4.15E-01		-1.06E+00	4.71E-11	Down	1.83E-01	3.26E-01		3.00E-01	5.66E-05		-7.14E-01	6.37E-18		Unigene15636_All//gi|1351856|sp|P49608.1|ACOC_CUCMA//1.00E-59//RecName: Full=Aconitate hydratase, cytoplasmic; Short=Aconitase; AltName: Full=Citrate hydro-lyase >gi|7437043|pir||T10101 aconitate hydratase (EC 4.2.1.3) - cucurbit >gi|868003|dbj|BAA06108.1| aconitase [Cucurbita cv. Kurokawa Amakuri]	Unigene15636_All//4.00E-60//AT2G05710| aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative	Unigene15636_All//0.00E+00//gi|48815016|gb|C0116329.1|C0116329		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0016836//GO:0043169//GO:0043231//GO:0044262//GO:0051536	nr +
Unigene15637_All	902	76.45	37.64	40.38	142.65	97.12	83.17	114.61	88.18	47.17	-1.02E+00	6.98E-52	Down	-9.21E-01	3.55E-42		-5.55E-01	6.03E-41		-7.78E-01	6.54E-66		-3.78E-01	7.11E-17		-1.28E+00	2.13E-139	Down	Unigene15637_All//gi|166343825|gb|ABV38653.1|//2.00E-85//beta-tubulin 4 [Gossypium hirsutum]	Unigene15637_All//4.00E-75//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene15637_All//0.00E+00//gi|13351281|gb|BG441629.1|BG441629	ko04145|Phagosome	GO:0006970//GO:0007017//GO:0010038//GO:0015630//GO:0016020//GO:0017111//GO:0030312//GO:0031981//GO:0032561//GO:0043234//GO:0043623	nr -
Unigene15638_All	1430	1.21	0.89	0.26	7.59	8.55	3.85	4.05	1.29	5.10	-4.47E-01	3.67E-01		-2.21E+00	2.05E-04	Down	1.71E-01	3.58E-01		-9.79E-01	1.01E-08		-1.66E+00	7.53E-12	Down	3.32E-01	8.69E-02		Unigene15638_All//gi|157273660|gb|ABV27484.1|//1.00E-151//fasciclin-like arabinogalactan protein 13 [Gossypium hirsutum]	Unigene15638_All//2.00E-77//AT3G60900| FLA10	Unigene15638_All//0.00E+00//TC129785			GO:0005576//GO:0005618//GO:0031225	nr +
Unigene15639_All	1670	12.12	4.88	10.65	9.99	7.69	2.79	0.48	0.00	0.31	-1.31E+00	4.39E-23	Down	-1.87E-01	1.75E-01		-3.78E-01	3.66E-03		-1.84E+00	1.47E-33	Down	-8.91E+00	8.58E-06	Down	-6.33E-01	3.56E-01		Unigene15639_All//gi|222875434|gb|ACM68923.1|//0.00E+00//gibberellin 20-oxidase [Gossypium hirsutum]	Unigene15639_All//6.00E-142//AT5G51810| GA20OX2 (GIBBERELLIN 20 OXIDASE 2); gibberellin 20-oxidase	Unigene15639_All//0.00E+00//gi|109856831|gb|DW485810.1|DW485810	ko00904|Diterpenoid biosynthesis	GO:0003824//GO:0008152//GO:0046914	nr +
Unigene15640_All	578	11.95	99.85	19.16	27.15	20.91	20.94	4.24	9.76	14.27	3.06E+00	1.05E-191	Up	6.81E-01	1.18E-04		-3.77E-01	5.26E-03		-3.75E-01	8.15E-03		1.20E+00	1.94E-07	Up	1.75E+00	3.37E-18	Up				Unigene15640_All//1.00E-82//ES835054				
Unigene15645_All	2260	11.44	3.25	7.19	0.75	1.25	5.90	0.73	0.46	0.69	-1.81E+00	1.05E-46	Down	-6.70E-01	1.30E-09		7.37E-01	4.68E-02		2.98E+00	3.11E-46	Up	-6.58E-01	1.54E-01		-8.57E-02	8.50E-01		Unigene15645_All//gi|62318763|dbj|BAD93796.1|//4.00E-65//glutamic acid-rich protein [Arabidopsis thaliana]	Unigene15645_All//2.00E-77//AT5G27330| LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G05130.1); Has 110457 Blast hits to 56483 proteins in 2051 species: Archae - 1653; Bacteria - 15111; Metazoa - 52441; Fungi - 7858; Plants - 4309; Viruses - 584; Other Eukaryotes - 28501 (source: NCBI BLink).	Unigene15645_All//1.00E-91//TC138257				nr +
Unigene15648_All	734	34.50	35.83	39.83	37.19	31.25	35.50	49.94	28.87	20.46	5.45E-02	6.36E-01		2.07E-01	5.98E-02		-2.51E-01	1.44E-02		-6.70E-02	6.36E-01		-7.91E-01	2.25E-22		-1.29E+00	2.29E-50	Down	Unigene15648_All//gi|15228322|ref|NP_190386.1|//7.00E-33//hypoxia-responsive family protein / zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565188|sp|Q7X843.2|ATL31_ARATH RecName: Full=RING-H2 finger protein ATL31; AltName: Full=YGHL1-C3HC4 RING fusion protein >gi|30038524|dbj|BAC75820.1| YGHL1-C3HC4 RING fusion protein [Arabidopsis thaliana]	Unigene15648_All//4.00E-34//AT3G48030| hypoxia-responsive family protein / zinc finger (C3HC4-type RING finger) family protein	Unigene15648_All//0.00E+00//TC156841				nr -
Unigene1565_All	1458	62.01	62.45	108.40	19.34	15.23	14.34	10.85	2.64	6.75	1.02E-02	8.79E-01		8.06E-01	7.66E-77		-3.44E-01	3.37E-04		-4.31E-01	1.40E-05		-2.04E+00	5.08E-41	Down	-6.84E-01	2.51E-08		Unigene1565_All//gi|15217873|ref|NP_174144.1|//1.00E-123//PUP1 (PURINE PERMEASE 1); purine nucleoside transmembrane transporter/ purine transmembrane transporter [Arabidopsis thaliana] >gi|75173386|sp|Q9FZ96.1|PUP1_ARATH RecName: Full=Purine permease 1; Short=AtPUP1 >gi|9795614|gb|AAF98432.1|AC021044_11 purine permease [Arabidopsis thaliana]	Unigene1565_All//1.00E-116//AT1G28230| PUP1 (PURINE PERMEASE 1); purine nucleoside transmembrane transporter/ purine transmembrane transporter	Unigene1565_All//0.00E+00//TC177508				nr +
Unigene15650_All	783	0.00	0.06	0.95	7.19	8.36	5.71	11.12	10.36	3.10	6.02E+00	6.17E-01		9.90E+00	3.28E-04	Up	2.17E-01	4.15E-01		-3.32E-01	2.21E-01		-1.03E-01	6.45E-01		-1.84E+00	9.23E-21	Down	Unigene15650_All//gi|224113569|ref|XP_002332538.1|//1.00E-11//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222832682|gb|EEE71159.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene15650_All//2.00E-38//ES850138				nr +
Unigene15654_All	1221	10.93	17.01	11.34	14.08	8.60	9.88	9.45	24.37	10.25	6.39E-01	1.25E-07		5.34E-02	7.49E-01		-7.11E-01	6.92E-09		-5.11E-01	9.09E-05		1.37E+00	1.50E-43	Up	1.16E-01	4.70E-01		Unigene15654_All//gi|2921340|gb|AAC04720.1|//1.00E-131//MYB-like DNA-binding domain protein [Gossypium hirsutum] >gi|23476309|gb|AAN28285.1| myb-like transcription factor 5 [Gossypium hirsutum]	Unigene15654_All//2.00E-62//AT4G09460| ATMYB6; DNA binding / transcription factor	Unigene15654_All//0.00E+00//TC147083	MYB			nr -
Unigene15656_All	1882	0.11	0.05	0.00	2.96	8.11	9.91	5.41	27.38	15.28	-1.05E+00	5.65E-01		-6.80E+00	1.46E-01		1.45E+00	1.89E-23	Up	1.74E+00	5.38E-34	Up	2.34E+00	2.36E-156	Up	1.50E+00	2.90E-49	Up	Unigene15656_All//gi|118573109|sp|Q8GXR2.2|PLT6_ARATH//0.00E+00//RecName: Full=Probable polyol transporter 6 >gi|2464913|emb|CAB16808.1| sugar transporter like protein [Arabidopsis thaliana] >gi|7270615|emb|CAB80333.1| sugar transporter like protein [Arabidopsis thaliana] >gi|145651782|gb|ABP98116.1| At4g36670 [Arabidopsis thaliana]	Unigene15656_All//0.00E+00//AT4G36670| mannitol transporter, putative					nr +
Unigene15657_All	1228	287.38	291.18	340.14	233.29	285.35	301.06	72.17	34.95	28.45	1.90E-02	5.78E-01		2.43E-01	8.24E-23		2.91E-01	5.36E-33		3.68E-01	1.36E-48		-1.05E+00	2.68E-84	Down	-1.34E+00	1.16E-128	Down	Unigene15657_All//gi|15234016|ref|NP_195581.1|//1.00E-148//1-phosphatidylinositol phosphodiesterase-related [Arabidopsis thaliana] >gi|179979229|gb|AAL49931.1| AT4g38690/F20M13_250 [Arabidopsis thaliana] >gi|20147101|gb|AAM10267.1| AT4g38690/F20M13_250 [Arabidopsis thaliana]	Unigene15657_All//4.00E-149//AT4G38690| 1-phosphatidylinositol phosphodiesterase-related	Unigene15657_All//0.00E+00//TC133382				nr +

Unigene15658_All	1041	551.35	335.85	563.04	105.90	103.44	70.41	3.94	1.97	0.92	-7.15E-01	1.04E-232		3.03E-02	2.39E-01		-3.39E-02	5.96E-01		-5.89E-01	1.05E-34		-1.00E+00	2.09E-04	Down	-2.10E+00	5.40E-12	Down	Unigene15658_All//gi|18405061|ref|NP_564667.1|//1.00E-104//thylakoid lumen 18.3 kDa protein [Arabidopsis thaliana] >gi|75217000|sp|Q9ZVL6.1|U603_ARATH RecName: Full=UPF0603 protein At1g54780, chloroplastic; AltName: Full=Thylakoid lumen 18.3 kDa protein; Flags: Precursor >gi|14030683|gb|AAK53016.1|AF375432_1 At1g54780/T22H22_19 [Arabidopsis thaliana] >gi|3776572|gb|AAC64889.1| ESTs gb|R65052, gb|AA712146, gb|H76533, gb|H76282, gb|AA650771, gb|H76287, gb|AA650887, gb|N37383, gb|Z29721 and gb|Z29722 come from this gene [Arabidopsis thaliana] >gi|17064782|gb|AAL32545.1| Unknown protein [Arabidopsis thaliana] >gi|23505937|gb|AAN28828.1| At1g54780/T22H22_19 [Arabidopsis thaliana] >gi|47825426|emb|CAD90763.1| lumenal protein subunit of photosystem II [Arabidopsis thaliana]	Unigene15658_All//4.00E-104//AT1G54780| thylakoid lumen 18.3 kDa protein	Unigene15658_All//0.00E+00//TC138484				nr -
Unigene1566_All	1454	4.39	15.05	3.44	4.63	8.27	10.56	5.96	19.81	11.40	1.78E+00	2.55E-38	Up	-3.51E-01	1.62E-01		8.38E-01	5.31E-08		1.19E+00	3.60E-16	Up	1.73E+00	2.12E-59	Up	9.35E-01	3.98E-14		Unigene1566_All//gi|259121377|gb|ACY92008.1|//1.00E-32//WRKY transcription factor 6 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene1566_All//5.00E-19//AT2G46400| WRKY46; transcription factor	Unigene1566_All//5.00E-22//TC142216	WRKY			nr +
Unigene15662_All	977	10.23	7.11	4.91	7.09	7.19	9.85	9.56	6.42	6.69	-5.26E-01	3.72E-03		-1.06E+00	3.29E-08	Down	2.08E-02	9.53E-01		4.74E-01	1.08E-02		-5.76E-01	5.77E-04		-5.16E-01	1.52E-03		Unigene15662_All//gi|222423299|dbj|BAH19625.1|//3.00E-76//AT4G32605 [Arabidopsis thaliana]	Unigene15662_All//5.00E-62//AT4G32605| LOCATED IN: mitochondrion; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Mitochondrial glycoprotein (InterPro:IPR003428); BEST Arabidopsis thaliana protein match is: mitochondrial glycoprotein family protein / MAM33 family protein (TAIR:AT3G55605.1); Has 195 Blast hits to 195 proteins in 67 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 64; Plants - 99; Viruses - 0; Other Eukaryotes - 32 (source: NCBI BLink).	Unigene15662_All//0.00E+00//gi|164355593|gb|ES795125.1|ES795125				nr +
Unigene15663_All	706	0.96	0.00	0.15	1.76	0.49	1.79	3.11	5.15	1.81	-9.91E+00	4.10E-04	Down	-2.68E+00	1.69E-02		-1.85E+00	2.11E-03		2.21E-02	9.71E-01		7.26E-01	1.17E-02		-7.86E-01	3.38E-02		Unigene15663_All//gi|224056246|ref|XP_002298773.1|//2.00E-23//porin/voltage-dependent anion-selective channel protein [Populus trichocarpa] >gi|222846031|gb|EEE83578.1| porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	Unigene15663_All//2.00E-19//AT5G67500| VDAC2 (VOLTAGE DEPENDENT ANION CHANNEL 2); voltage-gated anion channel	Unigene15663_All//2.00E-140//gi|73859655|gb|DT462394.1|DT462394				nr -
Unigene15664_All	1337	0.63	0.23	0.60	1.45	0.85	0.54	5.25	6.19	1.88	-1.46E+00	6.69E-02		-6.77E-02	9.40E-01		-7.74E-01	8.43E-02		-1.43E+00	2.70E-03		2.38E-01	2.30E-01		-1.48E+00	1.23E-12	Down	Unigene15664_All//gi|224056246|ref|XP_002298773.1|//6.00E-65//porin/voltage-dependent anion-selective channel protein [Populus trichocarpa] >gi|222846031|gb|EEE83578.1| porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	Unigene15664_All//7.00E-60//AT5G67500| VDAC2 (VOLTAGE DEPENDENT ANION CHANNEL 2); voltage-gated anion channel	Unigene15664_All//0.00E+00//gi|73859656|gb|DT462395.1|DT462395				nr +
Unigene15665_All	1730	11.64	9.23	13.85	11.95	12.68	8.12	2.96	0.46	0.32	-3.36E-01	7.00E-03		2.51E-01	3.88E-02		8.55E-02	5.59E-01		-5.58E-01	2.00E-06		-2.69E+00	7.62E-19	Down	-3.20E+00	3.92E-23	Down	Unigene15665_All//gi|30686958|ref|NP_194294.2|//0.00E+00//MATE efflux family protein [Arabidopsis thaliana]	Unigene15665_All//0.00E+00//AT4G25640| MATE efflux family protein	Unigene15665_All//0.00E+00//TC134382				nr +
Unigene15667_All	1638	16.77	11.26	12.26	12.65	11.79	8.41	10.89	3.88	3.11	-5.75E-01	2.71E-08		-4.52E-01	2.29E-05		-1.01E-01	4.94E-01		-5.89E-01	4.87E-07		-1.49E+00	4.81E-30	Down	-1.81E+00	1.36E-40	Down	Unigene15667_All//gi|15226866|ref|NP_178316.1|//3.00E-81//At1DD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding >gi|41059987|emb|CAF18564.1| ID1-like zinc finger protein 2 [Arabidopsis thaliana]	Unigene15667_All//2.00E-64//AT2G02070| AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding	Unigene15667_All//0.00E+00//TC174385	C2H2			nr -
Unigene1567_All	1962	7.89	21.87	6.79	7.29	15.08	18.25	10.30	35.60	21.60	1.47E+00	7.14E-57	Up	-2.18E-01	1.66E-01		1.05E+00	1.74E-27	Up	1.32E+00	1.32E-43	Up	1.79E+00	1.20E-149	Up	1.07E+00	4.45E-43	Up	Unigene1567_All//gi|259121377|gb|ACY92008.1|//8.00E-99//WRKY transcription factor 6 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene1567_All//4.00E-47//AT2G46400| WRKY46; transcription factor	Unigene1567_All//0.00E+00//gi|73863685|gb|DT466424.1|DT466424	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene15670_All	1391	3.61	3.97	2.87	15.29	11.14	6.85	2.43	0.12	0.06	1.37E-01	6.07E-01		-3.31E-01	2.52E-01		-4.57E-01	3.38E-05		-1.16E+00	1.53E-21	Down	-4.34E+00	7.30E-19	Down	-5.41E+00	6.05E-22	Down	Unigene15670_All//gi|297725701|ref|NP_001175214.1|//3.00E-14//0s07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1| Os07g0501200 [Oryza sativa Japonica Group]	Unigene15670_All//gi|AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene15670_All//6.00E-71//BF274864				nr +
Unigene15671_All	915	5.66	4.76	5.47	10.56	12.49	8.59	8.87	4.11	5.27	-2.49E-01	3.64E-01		-4.94E-02	8.63E-01		2.43E-01	1.80E-01		-2.98E-01	1.31E-01		-1.11E+00	3.14E-09	Down	-7.52E-01	2.15E-05		Unigene15671_All//gi|46518373|gb|AS99668.1|//3.00E-54//At1g20890 [Arabidopsis thaliana]	Unigene15671_All//2.00E-53//AT1G20890| unknown protein	Unigene15671_All//0.00E+00//TC140709				nr -
Unigene15672_All	856	8.80	8.11	5.23	13.79	9.86	10.92	50.43	16.36	23.64	-1.18E-01	6.00E-01		-7.52E-01	6.52E-04		-4.85E-01	1.79E-03		-3.37E-01	4.82E-02		-1.62E+00	3.64E-81	Down	-1.09E+00	8.69E-46	Down	Unigene15672_All//gi|227202846|dbj|BAH56896.1|//7.00E-09//AT1G18080 [Arabidopsis thaliana]	Unigene15672_All//3.00E-10//AT1G18080| ATARCA; nucleotide binding	Unigene15672_All//1.00E-166//DN817596				nr +
Unigene15673_All	825	4.12	1.72	4.78	9.00	5.63	6.41	5.89	4.91	11.54	-1.26E+00	2.55E-04	Down	2.13E-01	5.32E-01		-6.75E-01	7.02E-04		-4.90E-01	2.30E-02		-2.62E-01	3.29E-01		9.70E-01	5.79E-09		Unigene15673_All//gi|224092698|ref|XP_002309702.1|//2.00E-42//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222855678|gb|EEE93225.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene15673_All//2.00E-08//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene15673_All//0.00E+00//ES816551				nr +
Unigene15674_All	593	3.09	6.75	2.60	10.42	12.66	13.63	6.13	6.63	11.96	1.13E+00	2.94E-04	Up	-2.46E-01	6.28E-01		2.81E-01	2.24E-01		3.88E-01	6.82E-02		1.12E-01	7.16E-01		9.64E-01	7.70E-07		Unigene15674_All//gi|224092698|ref|XP_002309702.1|//9.00E-30//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222855678|gb|EEE93225.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene15674_All//5.00E-11//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene15674_All//3.00E-132//ES801940				nr -
Unigene15675_All	896	57.11	23.30	21.81	103.96	95.35	49.45	28.41	8.77	11.60	-1.29E+00	4.54E-56	Down	-1.39E+00	2.58E-60	Down	-1.25E-01	2.42E-02		-1.07E+00	8.75E-82	Down	-1.70E+00	3.69E-51	Down	-1.29E+00	2.03E-35	Down	Unigene15675_All//gi|218855173|gb|ACL12053.1|//1.00E-94//blue copper-like protein [Gossypium hirsutum]	Unigene15675_All//3.00E-24//AT5G15350| plastocyanin-like domain-containing protein	Unigene15675_All//0.00E+00//TC150979				nr +
Unigene15676_All	817	87.74	59.23	69.54	88.29	61.33	101.88	37.26	28.70	16.68	-5.67E-01	7.16E-20		-3.35E-01	1.19E-07		-5.26E-01	5.43E-21		2.07E-01	2.90E-04		-3.77E-01	1.61E-05		-1.16E+00	9.76E-36	Down	Unigene15676_All//gi|20197682|gb|AD20904.2|//9.00E-69//expressed protein [Arabidopsis thaliana] >gi|98961081|gb|ABF59024.1| At2g20930 [Arabidopsis thaliana] >gi|222424371|dbj|BAH20141.1| AT2G20930 [Arabidopsis thaliana]	Unigene15676_All//5.00E-70//AT2G20930| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: transport, ER to Golgi vesicle-mediated transport; LOCATED IN: intracellular; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Sedlin (InterPro:IPR006722), Longin-like (InterPro:IPR011012); Has 370 Blast hits to 370 proteins in 116 species: Archae - 0; Bacteria - 0; Metazoa - 216; Fungi - 55; Plants - 47; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene15676_All//0.00E+00//gi|109838572|gb|DW237133.1|DW237133				nr -
Unigene15677_All	1731	36.24	14.46	23.81	7.89	7.34	7.02	0.88	0.97	0.74	-1.33E+00	3.24E-71	Down	-6.06E-01	7.63E-19		-1.03E-01	5.76E-01		-1.68E-01	3.45E-01		1.35E-01	7.71E-01		-2.56E-01	6.16E-01		Unigene15677_All//gi|115463939|ref|NP_001055569.1|//1.00E-127//0s05g0419000 [Oryza sativa Japonica Group] >gi|113579120|dbj|BAF17483.1| Os05g0419000 [Oryza sativa Japonica Group]	Unigene15677_All//5.00E-116//AT5G38520| hydrolase, alpha/beta fold family protein	Unigene15677_All//0.00E+00//TC133314				nr +
Unigene15678_All	1341	6.44	7.97	9.65	8.17	5.80	6.53	18.73	16.49	9.33	3.09E-01	8.72E-02		5.84E-01	3.21E-04		-4.94E-01	2.30E-03		-3.23E-01	7.30E-02		-1.84E-01	7.95E-02		-1.01E+00	1.11E-23	Down	Unigene15678_All//gi|115480163|ref|NP_001063675.1|//4.00E-29//Os09g0516800 [Oryza sativa Japonica Group] >gi|113631908|dbj|BAF25589.1| Os09g0516800 [Oryza sativa Japonica Group]	Unigene15678_All//3.00E-27//AT4G25315| Expressed protein	Unigene15678_All//0.00E+00//TC171238				nr -
Unigene1568_All	2810	46.53	13.13	20.31	22.57	17.99	12.76	1.94	0.58	0.55	-1.83E+00	6.53E-236	Down	-1.20E+00	7.27E-122	Down	-3.27E-01	6.19E-08		-8.22E-01	5.99E-36		-1.74E+00	5.53E-12	Down	-1.81E+00	4.90E-13	Down	Unigene1568_All//gi|224101393|ref|XP_002312260.1|//0.00E+00//phol-like protein [Populus trichocarpa] >gi|222852080|gb|EEE89627.1| phol-like protein [Populus trichocarpa]	Unigene1568_All//0.00E+00//AT1G14040| LOCATED IN: integral to membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03240.1); Has 732 Blast hits to 696 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 238; Fungi - 246; Plants - 151; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink).	Unigene1568_All//0.00E+00//TC139137				nr +

Unigene15680_All	1263	0.62	0.32	0.72	4.54	3.16	7.97	25.71	27.73	56.49	-9.53E-01	2.33E-01		2.06E-01	7.64E-01		-5.20E-01	2.99E-02		8.14E-01	4.47E-06		1.09E-01	2.41E-01		1.14E+00	2.94E-79	Up	Unigene15680_All//gi|62956022|gb|AY23356.1|//1.00E-131//3-ketoacyl-CoA reductase 3 [Gossypium hirsutum]	Unigene15680_All//1.00E-93//AT4G11410| short-chain dehydrogenase/reductase (SDR) family protein	Unigene15680_All//0.00E+00//gi|109869626|gb|DW498602.1|DW498602		ko00051|Fructose and mannose metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism//ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene15682_All	1046	4.90	27.42	10.13	5.95	7.18	8.89	15.93	19.46	13.29	2.48E+00	2.55E-76	Up	1.05E+00	1.60E-08	Up	2.70E-01	2.45E-01		5.79E-01	1.91E-03		2.89E-01	9.79E-03		-2.61E-01	3.29E-02		Unigene15682_All//gi|21537123|gb|AM61464.1|//1.00E-117//electron transfer flavoprotein beta-subunit-like [Arabidopsis thaliana]	Unigene15682_All//1.00E-110//AT5G43430| ETFBETA; electron carrier	Unigene15682_All//0.00E+00//TC156981				nr -
Unigene15684_All	868	0.72	2.22	3.19	1.84	1.35	2.29	2.14	2.22	1.24	1.62E+00	1.18E-03		2.14E+00	1.76E-06	Up	-4.45E-01	4.08E-01		3.18E-01	5.38E-01		4.75E-02	9.29E-01		-7.90E-01	5.33E-02		Unigene15684_All//gi|302142541|emb|CBI19744.3|//4.00E-07//unnamed protein product [Vitis vinifera]	Unigene15684_All//4.00E-06//AT1G27630| CYCT1;3 (CYCLIN T 1;3); cyclin-dependent protein kinase	Unigene15684_All//2.00E-171//DW510802				nr +
Unigene15685_All	1376	6.08	9.21	13.27	26.64	31.96	28.10	25.07	11.82	7.24	5.98E-01	1.62E-04		1.13E+00	6.51E-16	Up	2.62E-01	6.76E-04		7.65E-02	4.71E-01		-1.09E+00	2.46E-35	Down	-1.79E+00	7.33E-77	Down	Unigene15685_All//gi|16323147|gb|AAL15308.1|//1.00E-109//At1g10380/F14N23_32 [Arabidopsis thaliana] >gi|21436013|gb|AAM51584.1| At1g10380/F14N23_32 [Arabidopsis thaliana]	Unigene15685_All//2.00E-105//AT1G10380| unknown protein	Unigene15685_All//0.00E+00//TC138608				nr +
Unigene15686_All	1484	16.32	15.77	19.45	19.10	26.17	20.21	3.16	1.46	1.93	-4.94E-02	6.81E-01		2.53E-01	1.99E-02		4.55E-01	9.63E-09		8.14E-02	5.06E-01		-1.11E+00	1.12E-05	Down	-7.10E-01	3.02E-03		Unigene15686_All//gi|297614182|gb|ADI48429.1|//3.00E-47//trichome birefringence [Arabidopsis thaliana]	Unigene15686_All//1.00E-80//AT3G12060| unknown protein	Unigene15686_All//1.00E-102//gi|5047044|gb|AIT28192.1|AI728192				nr +
Unigene15687_All	905	137.36	73.74	89.08	5.45	3.65	4.19	1.17	2.91	1.67	-8.98E-01	5.90E-75		-6.25E-01	7.77E-39		-5.77E-01	2.60E-02		-3.78E-01	1.91E-01		1.32E+00	2.33E-04	Up	5.18E-01	2.74E-01		Unigene15687_All//gi|115440763|ref|NP_001044661.1|//3.00E-55//Os01g0823600 [Oryza sativa Japonica Group] >gi|113534192|dbj|BAF06575.1| Os01g0823600 [Oryza sativa Japonica Group]	Unigene15687_All//2.00E-45//AT3G56290| unknown protein	Unigene15687_All//0.00E+00//DW477703				nr -
Unigene15688_All	1885	0.64	0.32	0.40	10.65	7.73	3.52	15.21	14.35	30.18	-9.85E-01	1.13E-01		-6.91E-01	2.86E-01		-4.63E-01	4.81E-05		-1.60E+00	5.91E-33	Down	-8.41E-02	4.38E-01		9.89E-01	9.57E-51		Unigene15688_All//gi|224130624|ref|XP_002320887.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222861660|gb|EEE99202.1| cytochrome P450 [Populus trichocarpa]	Unigene15688_All//0.00E+00//AT3G61880| CYP78A9 (CYTOCHROME P450 78A9); monooxygenase/ oxygen binding	Unigene15688_All//0.00E+00//TC152202		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene15689_All	1228	9.29	8.33	12.01	18.09	20.30	18.76	7.09	3.06	5.68	-1.56E-01	3.82E-01		3.71E-01	1.61E-02		1.66E-01	1.66E-01		5.21E-02	6.98E-01		-1.21E+00	3.39E-11	Down	-3.21E-01	6.52E-02		Unigene15689_All//gi|9294523|dbj|BAB02785.1|//1.00E-153//protein transport protein Sec23 [Arabidopsis thaliana]	Unigene15689_All//1.00E-154//AT3G23660| transport protein, putative	Unigene15689_All//0.00E+00//gi|109860744|gb|DW489723.1|DW489723				nr -
Unigene15693_All	1400	5.90	2.68	4.68	7.33	7.87	7.23	6.25	2.18	4.75	-1.14E+00	4.37E-08	Down	-3.36E-01	1.27E-01		1.03E-01	6.12E-01		-2.06E-02	9.33E-01		-1.52E+00	1.43E-15	Down	-3.96E-01	2.07E-02		Unigene15693_All//gi|18401324|ref|NP_565636.1|//3.00E-93//FRS3 (FAR1-related sequence 3); zinc ion binding [Arabidopsis thaliana] >gi|30683396|ref|NP_850098.1| FRS3 (FAR1-related sequence 3); zinc ion binding [Arabidopsis thaliana] >gi|75216958|sp|Q9ZVC9.2|FRS3_ARATH RecName: Full=Protein FAR1-RELATED SEQUENCE 3 >gi|15982769|gb|AAL09732.1| At2g27110/T20P8.16 [Arabidopsis thaliana] >gi|20197414|gb|AAC77869.2| Mutator-like transposase [Arabidopsis thaliana] >gi|27363374|gb|AAO14606.1| At2g27110/T20P8.16 [Arabidopsis thaliana]	Unigene15693_All//2.00E-94//AT3G27110| FRS3 (FAR1-related sequence 3); zinc ion binding	Unigene15693_All//0.00E+00//gi|109865530|gb|DW494506.1|DW494506				nr +
Unigene15699_All	525	7.18	18.53	10.45	13.00	10.36	14.02	22.07	28.26	17.60	1.37E+00	3.83E-12	Up	5.42E-01	4.35E-02		-3.27E-01	1.58E-01		1.09E-01	6.76E-01		3.57E-01	6.73E-03		-3.26E-01	2.73E-02					Unigene15699_All//0.00E+00//TC141932				ESTscan -
Unigene15700_All	1257	0.37	0.89	1.44	1.55	1.18	1.08	1.51	1.53	1.33	1.24E+00	6.10E-02		1.94E+00	4.89E-04	Up	-3.92E-01	4.20E-01		-5.20E-01	2.89E-01		1.51E-02	1.01E+00		-1.85E-01	6.46E-01		Unigene15700_All//gi|297599214|ref|NP_001046831.2|//1.00E-18//Os02g0470400 [Oryza sativa Japonica Group] >gi|255670894|dbj|BAF08745.2| Os02g0470400 [Oryza sativa Japonica Group]	Unigene15700_All//1.00E-59//AT4G17140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pleckstrin homology (InterPro:IPR001849); BEST Arabidopsis thaliana protein match is: phosphoinositide binding (TAIR:AT1G48090.2); Has 1924 Blast hits to 1182 proteins in 161 species: Archae - 0; Bacteria - 16; Metazoa - 911; Fungi - 304; Plants - 271; Viruses - 0; Other Eukaryotes - 422 (source: NCBI BLink).					nr -
Unigene15701_All	848	6.29	12.07	6.53	4.17	6.01	4.90	6.23	6.01	2.07	9.40E-01	2.42E-07		5.34E-02	8.43E-01		5.27E-01	4.59E-02		2.32E-01	4.94E-01		-5.17E-02	8.44E-01		-1.59E+00	1.08E-10	Down								
Unigene15702_All	972	15.83	13.40	17.70	9.33	7.83	104.96	6.13	30.79	13.89	-2.40E-01	1.10E-01		1.61E-01	2.97E-01		-2.53E-01	2.17E-01		3.49E+00	0.00E+00	Up	2.33E+00	1.59E-90	Up	1.18E+00	1.22E-16	Up	Unigene15702_All//gi|18423944|ref|NP_568850.1|//2.00E-57//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana]	Unigene15702_All//1.00E-46//AT5G57150| basic helix-loop-helix (bHLH) family protein	Unigene15702_All//0.00E+00//gi|73865788|gb|DT468526.1|DT468526	bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene15703_All	919	137.38	233.94	112.64	39.08	32.71	179.52	738.41	2173.29	697.33	7.68E-01	9.49E-99		-2.86E-01	8.59E-10		-2.57E-01	3.04E-03		2.20E+00	0.00E+00	Up	1.56E+00	0.00E+00	Up	-8.26E-02	1.29E-06		Unigene15703_All//gi|8515096|gb|AAF75824.1|AF101788_1//9.00E-36//phytocyanin homolog [Pinus taeda]	Unigene15703_All//5.00E-24//AT5G20230| ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier	Unigene15703_All//0.00E+00//gi|109850078|gb|DW479057.1|DW479057				nr -
Unigene15704_All	1188	2.86	1.75	2.33	2.68	3.16	3.73	3.24	2.15	1.51	-7.11E-01	3.36E-02		-2.97E-01	4.00E-01		2.36E-01	5.30E-01		4.73E-01	1.17E-01		-5.94E-01	3.41E-02		-1.10E+00	6.17E-05	Down	Unigene15704_All//gi|297803426|ref|XP_002869597.1|//1.00E-145//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315433|gb|EFH45856.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene15704_All//2.00E-145//AT4G26680| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene15706_All	729	21.17	19.39	8.55	26.65	19.32	26.45	134.73	113.00	44.81	-1.27E-01	4.13E-01		-1.31E+00	5.71E-17	Down	-4.64E-01	6.35E-05		-1.06E-02	9.47E-01		-2.54E-01	5.38E-08		-1.59E+00	4.16E-183	Down	Unigene15706_All//gi|288310312|gb|ADC45395.1|//1.00E-125//HSP90-1 [Glycine max]	Unigene15706_All//1.00E-114//AT5G56000| heat shock protein 81-4 (HSP81-4)	Unigene15706_All//0.00E+00//gi|78334981|gb|DT555255.1|DT555255		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene15707_All	1530	2.12	5.43	1.29	14.85	8.80	3.48	5.64	4.04	30.46	1.36E+00	2.33E-10	Up	-7.19E-01	4.60E-02		-7.55E-01	8.14E-13		-2.09E+00	8.11E-54	Down	-4.80E-01	6.56E-03		2.43E+00	3.96E-151	Up	Unigene15707_All//gi|224088629|ref|XP_002308504.1|//1.00E-166//f-box family protein [Populus trichocarpa] >gi|222854480|gb|EEE92027.1| f-box family protein [Populus trichocarpa]	Unigene15707_All//2.00E-113//AT4G33160| ubiquitin-protein ligase	Unigene15707_All//0.00E+00//TC132463				nr +
Unigene15708_All	1618	5.24	8.14	5.13	7.51	9.58	10.66	15.08	21.13	91.00	6.36E-01	4.09E-05		-2.90E-02	9.01E-01		3.50E-01	1.22E-02		5.05E-01	1.15E-04		4.87E-01	2.69E-09		2.59E+00	0.00E+00	Up	Unigene15708_All//gi|6560770|gb|AAF16770.1|AC010155_23//1.00E-55//F3M18.5 [Arabidopsis thaliana] >gi|15724222|gb|AAL06504.1|AF412051_1 At1g28510/F3M18_5 [Arabidopsis thaliana] >gi|18252247|gb|AAL62004.1| At1g28510/F3M18_5 [Arabidopsis thaliana]	Unigene15708_All//3.00E-49//AT1G28510| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Optic atrophy 3-like (InterPro:IPR010754); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G58150.1); Has 279 Blast hits to 279 proteins in 116 species: Archae - 0; Bacteria - 0; Metazoa - 133; Fungi - 74; Plants - 40; Viruses - 0; Other Eukaryotes - 32 (source: NCBI BLink).	Unigene15708_All//0.00E+00//TC144954				nr +
Unigene15709_All	1238	6.34	1.96	2.06	0.89	1.64	1.57	1.61	9.66	4.67	-1.69E+00	2.39E-13	Down	-1.62E+00	5.18E-12	Down	8.91E-01	4.93E-02		8.26E-01	8.28E-02		2.59E+00	2.71E-41	Up	1.54E+00	5.62E-11	Up	Unigene15709_All//gi|224075092|ref|XP_002304554.1|//1.00E-92//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222841986|gb|EEE79533.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene15709_All//3.00E-35//AT1G64380| AP2 domain-containing transcription factor, putative	Unigene15709_All//0.00E+00//gi|78338627|gb|DT558901.1|DT558901	AP2-EREBP			nr -
Unigene15710_All	2658	0.61	1.47	0.50	0.19	0.21	0.37	1.85	6.89	15.59	1.27E+00	7.80E-05	Up	-2.85E-01	6.21E-01		1.46E-01	9.05E-01		9.96E-01	1.72E-01		1.90E+00	4.37E-43	Up	3.08E+00	5.81E-173	Up	Unigene15710_All//gi|62857020|dbj|BAD95895.1|//1.00E-139//Ser/Thr protein kinase [Lotus japonicus]	Unigene15710_All//4.00E-144//AT4G18250| receptor serine/threonine kinase, putative	Unigene15710_All//0.00E+00//CO108759		ko04626|Plant-pathogen interaction		nr -
Unigene15713_All	1452	0.00	0.35	0.00	8.95	3.04	2.33	54.34	58.98	49.63	8.45E+00	4.05E-03		null	null		-1.56E+00	9.75E-24	Down	-1.94E+00	4.07E-28	Down	1.18E-01	2.92E-02		-1.31E-01	1.58E-02		Unigene15713_All//gi|18414224|ref|NP_567432.1|//3.00E-99//DNA-binding protein-related [Arabidopsis thaliana] >gi|30102626|gb|AAP21231.1| At4g14465 [Arabidopsis thaliana] >gi|119657384|tpd|FAA00291.1| TPA: AT-hook motif nuclear localized protein 20 [Arabidopsis thaliana]	Unigene15713_All//4.00E-68//AT4G14465| DNA-binding protein-related	Unigene15713_All//0.00E+00//DW502620				nr -
Unigene15715_All	707	17.98	71.31	39.99	20.64	32.29	34.94	38.09	85.37	76.97	1.99E+00	1.33E-101	Up	1.15E+00	2.89E-25	Up	6.45E-01	1.36E-09		7.59E-01	1.84E-12		1.16E+00	2.54E-68	Up	1.01E+00	1.16E-50	Up	Unigene15715_All//gi|295486062|gb|ADG21959.1|//5.00E-22//MYB3 [Morella rubra]		Unigene15715_All//0.00E+00//TC166957				nr +

Unigene15716_All	1246	5.92	1.34	4.49	15.91	22.41	20.88	4.55	0.74	2.27	-2.14E+00	5.05E-17	Down	-4.00E-01	8.20E-02		4.94E-01	2.08E-07		3.92E-01	1.90E-04		-2.62E+00	2.86E-20	Down	-1.00E+00	5.28E-06	Down	Unigene15716_All//gi|115452547|ref|NP_001049874.1|/1.00E-49//Os03g0303100 [Oryza sativa Japonica Group] >gi|108707708|gb|ABF95503.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548345|dbj|BAF11788.1| Os03g0303100 [Oryza sativa Japonica Group]	Unigene15716_All//9.00E-45//AT3G62630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1645 (InterPro:IPR012442); BEST Arabidopsis thaliana protein match is: calmodulin-binding protein (TAIR:AT2G15760.1); Has 207 Blast hits to 197 proteins in 50 species: Archae - 3; Bacteria - 4; Metazoa - 52; Fungi - 9; Plants - 91; Viruses - 0; Other Eukaryotes - 48 (source: NCBI BLink).	Unigene15716_All//0.00E+00//TC163137				nr +
Unigene15718_All	1463	1.00	1.04	0.91	7.15	5.20	3.49	8.70	3.74	4.74	5.32E-02	9.33E-01		-1.38E-01	7.97E-01		-4.59E-01	6.33E-03		-1.04E+00	3.49E-09	Down	-1.22E+00	4.26E-16	Down	-8.77E-01	4.52E-10		Unigene15718_All//gi|40806799|gb|AB92199.1|/6.00E-61//reduced vernalization response 1 [Brassica rapa]	Unigene15718_All//3.00E-35//AT3G18890| VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor	Unigene15718_All//0.00E+00//TC179365	ABI3VP1			nr -
Unigene1572_All	3817	0.22	0.32	0.38	0.74	0.56	0.43	1.65	0.68	0.49	5.39E-01	3.76E-01		7.81E-01	1.80E-01		-4.12E-01	2.88E-01		-8.04E-01	3.06E-02		-1.28E+00	5.19E-09	Down	-1.75E+00	2.84E-14	Down	Unigene1572_All//gi|73697836|gb|AAZ81522.1|/0.00E+00//auxin response factor 2 [Gossypium arboreum]	Unigene1572_All//2.00E-172//AT1G19220| ARF19 (AUXIN RESPONSE FACTOR 19); DNA binding / transcription factor	Unigene1572_All//0.00E+00//TC129554	ARF	ko03022|Basal transcription factors		nr +
Unigene15720_All	1482	8.01	6.09	7.62	12.10	8.39	9.93	20.80	8.40	9.76	-3.97E-01	1.69E-02		-7.32E-02	6.90E-01		-5.29E-01	1.14E-05		-2.85E-01	3.63E-02		-1.31E+00	3.04E-42	Down	-1.09E+00	6.80E-33	Down	Unigene15720_All//gi|21553676|gb|AAM62769.1|/1.00E-126//50S ribosomal protein L4 [Arabidopsis thaliana]	Unigene15720_All//9.00E-127//AT2G20060| ribosomal protein L4 family protein	Unigene15720_All//0.00E+00//TC141289		ko03010|Ribosome		nr -
Unigene15721_All	1684	4.35	0.81	1.20	3.58	4.72	3.62	10.87	1.81	5.96	-2.42E+00	1.61E-19	Down	-1.86E+00	1.72E-13	Down	4.00E-01	5.41E-02		1.66E-02	9.45E-01		-2.59E+00	5.51E-63	Down	-8.67E-01	7.61E-14		Unigene15721_All//gi|15239172|ref|NP_199122.1|/1.00E-126//CYCA3;1 (Cyclin A3;1); cyclin-dependent protein kinase regulator [Arabidopsis thaliana] >gi|75309211|sp|Q9FMH5.1|CCA31_ARATH RecName: Full=Putative cyclin-A3-1; AltName: Full=G2/mitotic-specific cyclin-A3-1; Short=CycA3;1 >gi|9757835|dbj|BAB08272.1| cyclin A-type [Arabidopsis thaliana]	Unigene15721_All//8.00E-113//AT5G43080| CYCA3;1 (Cyclin A3;1); cyclin-dependent protein kinase regulator	Unigene15721_All//0.00E+00//gi|78340919|gb|DT561193.1|DT561193				nr -
Unigene15724_All	1032	3.70	4.08	8.20	7.63	6.44	5.95	8.32	5.43	4.83	1.39E-01	6.37E-01		1.15E+00	5.94E-08	Up	-2.44E-01	2.80E-01		-3.58E-01	9.95E-02		-6.16E-01	4.46E-04		-7.85E-01	5.03E-06		Unigene15724_All//gi|18329230|ref|NP_563700.1|/3.00E-06//PRP39; binding [Arabidopsis thaliana]	Unigene15724_All//2.00E-07//AT1G04080| PRP39; binding	Unigene15724_All//5.00E-74//gi|109853680|gb|DW482659.1|DW482659				nr +
Unigene15725_All	941	20.35	14.75	12.73	21.86	14.42	17.95	26.51	12.93	16.98	-4.64E-01	2.29E-04		-6.77E-01	2.07E-07		-6.01E-01	6.06E-08		-2.85E-01	2.27E-02		-1.04E+00	5.91E-24	Down	-6.43E-01	2.18E-11		Unigene15725_All//gi|184094467|ref|NP_564986.1|/3.00E-68//ribosomal protein L12 family protein [Arabidopsis thaliana] >gi|21941123|gb|AAM61098.1| Similar to Secale chloroplast ribosomal protein L12 (gb|SCL121A). EST gb|H36579 comes from this gene [Arabidopsis thaliana]	Unigene15725_All//1.00E-50//AT1G70190| ribosomal protein L12 family protein	Unigene15725_All//0.00E+00//TC147728		ko03010|Ribosome		nr +
Unigene15726_All	382	3.29	14.72	8.92	4.56	8.65	9.34	0.44	3.72	5.21	2.16E+00	3.40E-13	Up	1.44E+00	7.73E-05	Up	9.23E-01	5.44E-03		1.03E+00	1.58E-03		3.07E+00	2.15E-06	Up	3.56E+00	4.60E-10	Up	Unigene15726_All//gi|269314023|gb|ACZ36914.1|/3.00E-19//MADS-box transcription factor 1 [Hevea brasiliensis]						nr +
Unigene15727_All	1033	13.47	86.23	30.72	10.56	20.67	44.11	2.50	7.57	12.50	2.68E+00	4.24E-257	Up	1.19E+00	1.06E-29	Up	9.69E-01	1.52E-17		2.06E+00	1.94E-103	Up	1.60E+00	5.70E-15	Up	2.32E+00	3.86E-40	Up	Unigene15727_All//gi|269314023|gb|ACZ36914.1|/4.00E-19//MADS-box transcription factor 1 [Hevea brasiliensis]						nr -
Unigene15728_All	1534	12.65	8.03	8.40	21.92	20.72	8.74	3.17	0.16	0.21	-6.57E-01	1.60E-07		-5.91E-01	4.72E-06		-8.12E-02	4.78E-01		-1.33E+00	1.26E-41	Down	-4.28E+00	1.13E-26	Down	-3.93E+00	4.33E-26	Down	Unigene15728_All//gi|15237350|ref|NP_199407.1|//2.00E-99//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75170952|sp|Q9FJ41.1|GDL85_ARATH RecName: Full=GDSL esterase/lipase At5g45950; AltName: Full=Extracellular lipase At5g45950; Flags: Precursor >gi|9758942|dbj|BAB09323.1| GDSL-motif lipase/hydrolase-like protein [Arabidopsis thaliana]	Unigene15728_All//7.00E-89//AT5G45950| GDSL-motif lipase/hydrolase family protein	Unigene15728_All//0.00E+00//gi|164242889|gb|ES809047.1|ES809047				nr -
Unigene15729_All	1057	15.34	5.90	9.57	14.52	12.87	15.51	17.48	8.26	7.43	-1.38E+00	4.34E-20	Down	-6.81E-01	1.90E-06		-1.74E-01	2.77E-01		9.56E-02	5.88E-01		-1.08E+00	3.58E-19	Down	-1.24E+00	2.88E-24	Down	Unigene15729_All//gi|90962982|gb|AB602415.1|/8.00E-96//At4g13720 [Arabidopsis thaliana]	Unigene15729_All//9.00E-94//AT4G13720| inosine triphosphate pyrophosphatase, putative / HAM1 family protein	Unigene15729_All//0.00E+00//TC134141		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism		nr -
Unigene1573_All	1850	1.56	6.14	5.18	5.01	4.52	24.39	102.62	201.32	769.04	1.98E+00	3.12E-23	Up	1.74E+00	4.71E-16	Up	-1.47E-01	5.17E-01		2.28E+00	2.55E-116	Up	9.72E-01	0.00E+00		2.91E+00	0.00E+00	Up	Unigene1573_All//gi|47078691|gb|AAT09980.1|/0.00E+00//cell wall apoplastic invertase [Vitis vinifera]	Unigene1573_All//0.00E+00//AT3G13790| ATBFRUCT1; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene1573_All//0.00E+00//gi|109871998|gb|DW500974.1|DW500974		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene15731_All	1331	1.97	5.25	1.32	5.13	3.13	3.09	4.80	5.53	5.48	1.42E+00	2.16E-09	Up	-5.74E-01	1.61E-01		-7.12E-01	6.51E-04		-7.32E-01	9.01E-04		2.04E-01	3.50E-01		1.92E-01	3.62E-01		Unigene15731_All//gi|115479867|ref|NP_001063527.1|/2.00E-46//Os09g0487700 [Oryza sativa Japonica Group] >gi|113631760|dbj|BAF25441.1| Os09g0487700 [Oryza sativa Japonica Group]	Unigene15731_All//7.00E-46//AT3G57810| OTU-like cysteine protease family protein	Unigene15731_All//0.00E+00//TC133959				nr -
Unigene15734_All	946	2.54	12.53	5.80	26.91	21.19	22.53	12.16	17.05	27.75	2.30E+00	3.64E-29	Up	1.19E+00	1.17E-05	Up	-3.45E-01	7.20E-04		-2.56E-01	2.18E-02		4.88E-01	7.63E-05		1.19E+00	5.63E-32	Up	Unigene15734_All//gi|12002863|gb|AG43410.1|/2.00E-08//self-pruning interacting protein 1 [Solanum lycopersicum]	Unigene15734_All//2.00E-08//AT3G10525| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: SIM (SIAMESE); cyclin-dependent protein kinase inhibitor (TAIR:AT5G04470.1); Has 23 Blast hits to 23 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene15734_All//0.00E+00//TC174820				nr +
Unigene15735_All	1341	223.49	38.77	58.33	50.89	34.72	12.43	0.35	0.06	0.06	-2.53E+00	0.00E+00	Down	-1.94E+00	0.00E+00	Down	-5.52E-01	1.11E-21		-2.03E+00	2.73E-155	Down	-2.48E+00	3.38E-02		-2.55E+00	2.35E-02		Unigene15735_All//gi|297833112|ref|XP_002884438.1|/1.00E-157//Li-tolerant lipase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297330278|gb|EFH60697.1| Li-tolerant lipase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene15735_All//4.00E-158//AT3G04290| LTL1 (LI-TOLERANT LIPASE 1); carboxylesterase/ hydrolase, acting on ester bonds	Unigene15735_All//0.00E+00//gi|164317662|gb|ES792252.1|ES792252				nr -
Unigene15736_All	1670	1.44	0.88	0.35	5.01	4.10	5.49	4.51	0.53	2.81	-7.12E-01	8.05E-02		-2.04E+00	2.15E-05	Down	-2.88E-01	1.64E-01		1.32E-01	5.75E-01		-3.10E+00	1.18E-31	Down	-6.79E-01	2.21E-04		Unigene15736_All//gi|124360970|gb|ABN08942.1|/1.00E-160//Quinoprotein alcohol dehydrogenase-like [Medicago truncatula]		Unigene15736_All//0.00E+00//CO071277				nr +
Unigene15737_All	1736	3.41	3.56	1.53	1.64	1.79	2.86	7.94	6.19	6.01	6.43E-02	7.92E-01		-1.15E+00	9.11E-06	Down	1.26E-01	7.87E-01		8.07E-01	2.58E-03		-3.60E-01	8.82E-03		-4.01E-01	2.36E-03		Unigene15737_All//gi|159895659|gb|ABX10440.1|/0.00E+00//3-ketoacyl-CoA synthase 10 [Gossypium hirsutum]	Unigene15737_All//0.00E+00//AT1G01120| KCS1 (3-KETOACYL-COA SYNTHASE 1); acyltransferase/ fatty acid elongase	Unigene15737_All//0.00E+00//TC129947				nr -
Unigene1574_All	2311	83.04	35.39	40.88	74.62	71.76	110.89	267.13	103.99	112.67	-1.23E+00	5.16E-193	Down	-1.02E+00	6.73E-139	Down	-5.64E-02	2.16E-01		5.71E-01	2.44E-75		-1.36E+00	0.00E+00	Down	-1.25E+00	0.00E+00	Down	Unigene1574_All//gi|6689892|gb|AAF23892.1|AF152172_1|/1.00E-116//pectin methyl esterase [Solanum tuberosum]	Unigene1574_All//1.00E-112//AT3G14310| ATPME3; pectinesterase	Unigene1574_All//0.00E+00//TC139206		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene15740_All	1389	8.17	8.50	7.71	10.47	11.30	16.42	21.03	11.86	10.38	5.64E-02	7.47E-01		-8.51E-02	6.42E-01		1.10E-01	5.35E-01		6.49E-01	6.30E-09		-8.27E-01	2.19E-19		-1.02E+00	5.73E-28	Down	Unigene15740_All//gi|18253965|gb|AAL66714.1|AF420435_1|/1.00E-132//ABC transporter-like protein [Glycine max]	Unigene15740_All//2.00E-108//AT1G64550| ATGCN3; transporter	Unigene15740_All//0.00E+00//TC140244				nr +
Unigene15741_All	917	3.48	1.60	2.61	6.68	6.91	3.64	3.92	1.00	2.30	-1.12E+00	1.52E-03		-4.14E-01	2.64E-01		4.84E-02	8.63E-01		-8.75E-01	1.94E-04		-1.97E+00	1.83E-09	Down	-7.67E-01	5.98E-03		Unigene15741_All//gi|297727877|ref|NP_001176302.1|/4.00E-08//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1| Os11g0106066 [Oryza sativa Japonica Group]	Unigene15741_All//4.00E-05//AT3G09510| nucleic acid binding	Unigene15741_All//0.00E+00//TC163602				nr -
Unigene15745_All	953	2.36	5.26	3.63	1.10	1.05	0.57	2.04	6.23	2.38	1.16E+00	2.65E-05	Up	6.22E-01	7.52E-02		-6.70E-02	9.06E-01		-9.49E-01	1.69E-01		1.61E+00	1.18E-11	Up	2.24E-01	5.86E-01		Unigene15745_All//gi|4218187|emb|CAA09028.1|/3.00E-36//cysteine-rich polycomb-like protein [Glycine max]	Unigene15745_All//5.00E-35//AT4G14770| TCX2 (TESMIN/TSO1-LIKE CXC 2); transcription factor	Unigene15745_All//3.00E-41//ES829328	CPP			nr +
Unigene15746_All	1217	8.86	33.56	12.69	15.10	12.62	16.81	24.25	19.54	19.28	1.92E+00	7.65E-79	Up	5.19E-01	4.21E-04		-2.59E-01	4.63E-02		1.55E-01	2.73E-01		-3.11E-01	5.20E-04		-3.31E-01	1.46E-04		Unigene15746_All//gi|15228108|ref|NP_178507.1|//2.00E-47//XERICO; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|42570685|ref|NP_973416.1| XERICO; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|116928778|gb|AAG40042.1|AF324691_1 T23O15.13 [Arabidopsis thaliana]	Unigene15746_All//1.00E-48//AT2G04240| XERICO; protein binding / zinc ion binding	Unigene15746_All//0.00E+00//TC147168				nr -
Unigene15748_All	850	6.03	1.07	6.20	33.23	25.60	8.82	1.19	1.48	1.78	-2.49E+00	2.65E-14	Down	4.00E-02	8.90E-01		-3.76E-01	7.55E-05		-1.91E+00	1.91E-59	Down	3.05E-01	6.11E-01		5.77E-01	2.20E-01		Unigene15748_All//gi|37542675|gb|AAL47207.1|/6.00E-53//HAP3-like transcriptional-activator [Oryza sativa Indica Group]	Unigene15748_All//9.00E-48//AT4G14540| NF-YB3 (NUCLEAR FACTOR Y, SUBUNIT B3); transcription factor	Unigene15748_All//5.00E-30//TC168815	CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication		nr +
Unigene15752_All	1536	0.41	1.72	1.63	1.23	1.12	2.03	2.67	1.71	4.85	2.07E+00	3.06E-06	Up	1.99E+00	1.79E-05	Up	-1.37E-01	8.10E-01		7.19E-01	4.40E-02		-6.39E-01	1.74E-02		8.61E-01	4.55E-06		Unigene15752_All//gi|124359647|gb|ABN06020.1|/1.00E-137//Cytochrome cd1-nitrite reductase-like, C-terminal haem d1 [Medicago truncatula]	Unigene15752_All//2.00E-131//AT5G49430| transducin family protein / WD-40 repeat family protein	Unigene15752_All//0.00E+00//gi|164265359|gb|ES823542.1|ES823542		ko03022|Basal transcription factors		nr -

Unigene15753_All	1890	1.14	1.42	0.51	1.85	0.84	0.96	21.83	31.14	71.81	3.24E-01	4.00E-01		-1.16E+00	1.29E-02		-1.14E+00	2.38E-04	Down	-9.49E-01	3.75E-03		5.12E-01	8.40E-17		1.72E+00	8.78E-280	Up	Unigene15753_All//gi|15242845|ref|NP_195990.1|//1.00E-150//PAN domain-containing protein [Arabidopsis thaliana] >gi|75181333|sp|Q9LZ88.1|Y5370_ARATH RecName: Full=PAN domain-containing protein At5g03700; Flags: Precursor >gi|7340655|emb|CAB82935.1| S-receptor kinase-like protein [Arabidopsis thaliana]	Unigene15753_All//2.00E-136//AT5G03700| PAN domain-containing protein					nr +
Unigene15754_All	2088	8.17	9.44	8.11	14.31	16.77	13.02	14.15	5.10	4.24	2.09E-01	1.16E-01		-1.05E-02	9.65E-01		2.29E-01	1.17E-02		-1.37E-01	2.31E-01		-1.47E+00	2.26E-48	Down	-1.74E+00	2.45E-63	Down	Unigene15754_All//gi|115452921|ref|NP_001050061.1|//1.00E-116//0s03g0339700 [Oryza sativa Japonica Group] >gi|108708050|gb|ABF95845.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548532|dbj|BAF11975.1| Os03g0339700 [Oryza sativa Japonica Group]	Unigene15754_All//7.00E-94//AT2G38370| unknown protein	Unigene15754_All//0.00E+00//gi|164353658|gb|ES849359.1|ES849359				nr +
Unigene15756_All	1479	2.09	4.56	5.15	3.37	4.35	3.94	2.06	2.35	3.15	1.13E+00	1.36E-06	Up	1.30E+00	1.19E-08	Up	3.70E-01	1.24E-01		2.26E-01	4.21E-01		1.88E-01	5.87E-01		6.15E-01	1.10E-02		Unigene15756_All//gi|18416875|ref|NP_568282.1|//5.00E-70//NF-YA1 (NUCLEAR FACTOR Y, SUBUNIT A1); transcription factor [Arabidopsis thaliana] >gi|42573353|ref|NP_974773.1| NF-YA1 (NUCLEAR FACTOR Y, SUBUNIT A1); transcription factor [Arabidopsis thaliana] >gi|75180950|sp|Q9LXV5.1|NFYA1_ARATH RecName: Full=Nuclear transcription factor Y subunit A-1; Short=AtNF-YA-1; AltName: Full=Transcriptional activator HAP2A; AltName: Full=Protein EMBRYO DEFECTIVE 2220 >gi|7630040|emb|CAB88248.1| CCAAT box binding factor/ transcription factor Hap2a [Arabidopsis thaliana] >gi|107738403|gb|ABF83691.1| At5g12840 [Arabidopsis thaliana]	Unigene15756_All//1.00E-65//AT5G12840| NF-YA1 (NUCLEAR FACTOR Y, SUBUNIT A1); transcription factor	Unigene15756_All//0.00E+00//TC156176	CCAAT			nr +
Unigene15759_All	901	6.62	8.21	5.73	4.59	3.29	2.86	5.21	7.51	15.74	3.11E-01	1.63E-01		-2.08E-01	4.34E-01		-4.82E-01	1.04E-01		-6.84E-01	2.20E-02		5.29E-01	8.91E-03		1.60E+00	4.79E-27	Up	Unigene15759_All//gi|6692110|gb|AAF24575.1|AC007764_17//4.00E-26//F22C12.17 [Arabidopsis thaliana]	Unigene15759_All//3.00E-27//AT1G64065| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G44000.1); Has 69 Blast hits to 69 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene15759_All//0.00E+00//TC154307				nr +
Unigene15760_All	680	14.31	4.69	8.61	24.10	15.09	12.62	19.83	7.99	8.26	-1.61E+00	2.63E-15	Down	-7.32E-01	1.23E-04		-6.75E-01	8.04E-08		-9.34E-01	6.51E-12		-1.31E+00	5.00E-19	Down	-1.26E+00	1.43E-18	Down	Unigene15760_All//gi|124359162|gb|ABN05685.1|//2.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene15760_All//7.00E-05//AT4G26090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene15760_All//0.00E+00//TC161132				nr +
Unigene15761_All	1876	7.00	49.62	7.95	13.33	13.55	12.86	12.60	16.71	18.31	2.83E+00	1.42E-284	Up	1.83E-01	2.63E-01		2.33E-02	8.64E-01		-5.22E-02	6.76E-01		4.07E-01	2.05E-06		5.39E-01	2.24E-11		Unigene15761_All//gi|224134993|ref|XP_002321956.1|//1.00E-90//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222868952|gb|EEF06083.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene15761_All//5.00E-74//AT5G24590| TIP (TCV-INTERACTING PROTEIN); transcription coactivator/ transcription factor	Unigene15761_All//0.00E+00//gi|78351862|gb|DT572136.1|DT572136	NAC			nr -
Unigene15762_All	1200	23.28	25.97	20.50	9.71	12.97	11.29	5.74	13.37	5.98	1.58E-01	1.33E-01		-1.84E-01	1.11E-01		4.17E-01	2.17E-03		2.17E-01	2.03E-01		1.22E+00	3.95E-20	Up	5.73E-02	7.84E-01		Unigene15762_All//gi|158323778|gb|ABW34393.1|//3.00E-85//R2R3 MYB C2 repressor motif-likel protein [Vitis vinifera]	Unigene15762_All//2.00E-66//AT4G38620| MYB4; DNA binding / transcription factor	Unigene15762_All//0.00E+00//TC134776	MYB			nr -
Unigene15763_All	1210	2.59	28.14	3.04	21.00	33.44	19.97	18.59	13.23	54.39	3.44E+00	4.04E-126	Up	2.27E-01	5.19E-01		6.71E-01	7.96E-18		-7.24E-02	6.15E-01		-4.91E-01	1.76E-06		1.55E+00	2.41E-117	Up	Unigene15763_All//gi|151301818|gb|ABN50365.2|//1.00E-144//ethylene responsive element binding protein 1 [Gossypium barbadense]	Unigene15763_All//2.00E-59//AT4G17500| ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene15763_All//0.00E+00//TC129756	AP2-EREBP			nr +
Unigene15764_All	1214	3.32	2.80	2.41	5.05	4.54	2.34	2.47	0.76	2.86	-2.47E-01	4.30E-01		-4.60E-01	1.52E-01		-1.53E-01	5.82E-01		-1.11E+00	3.18E-06	Down	-1.71E+00	9.31E-07	Down	2.07E-01	5.13E-01		Unigene15764_All//gi|15219271|ref|NP_175737.1|//1.00E-122//TTL1 (TETRATRICOPEPTIDE-REPEAT THIOREDOXIN-LIKE 1); binding [Arabidopsis thaliana] >gi|75336154|sp|Q9MAH1.1|TTL1_ARATH RecName: Full=TPR repeat-containing thioredoxin TTL1; AltName: Full=Tetratricopeptide repeat thioredoxin-like 1 >gi|7769858|gb|AAF69536.1|AC008007_11 F12M16.20 [Arabidopsis thaliana] >gi|30102668|gb|AAP21252.1| At1g53300 [Arabidopsis thaliana]	Unigene15764_All//2.00E-117//AT1G53300| TTL1 (TETRATRICOPEPTIDE-REPEAT THIOREDOXIN-LIKE 1); binding	Unigene15764_All//0.00E+00//TC167678				nr +
Unigene15766_All	1690	1.92	0.78	0.13	4.66	4.52	6.23	27.89	45.13	74.70	-1.30E+00	2.56E-04	Down	-3.93E+00	3.19E-13	Down	-4.20E-02	8.53E-01		4.19E-01	1.90E-02		6.94E-01	1.54E-36		1.42E+00	1.28E-197	Up	Unigene15766_All//gi|297804354|ref|XP_002870061.1|//1.00E-102//ATPUP10 [Arabidopsis lyrata subsp. lyrata] >gi|297315897|gb|EFH46320.1| ATPUP10 [Arabidopsis lyrata subsp. lyrata]	Unigene15766_All//8.00E-88//AT4G18210| ATPUP10; purine transmembrane transporter	Unigene15766_All//0.00E+00//gi|73862986|gb|DT465725.1|DT465725				nr +
Unigene15767_All	1442	1.31	0.42	1.18	6.84	6.45	6.77	4.08	0.81	2.68	-1.63E+00	1.19E-03		-1.45E-01	7.57E-01		-8.52E-02	7.02E-01		-1.59E-02	9.44E-01		-2.33E+00	2.17E-18	Down	-6.05E-01	4.14E-03		Unigene15767_All//gi|3435279|gb|AAC78477.1|//0.00E+00//protein kinase homolog [Arabidopsis thaliana]	Unigene15767_All//6.00E-152//AT1G53700| WAG1 (WAG 1); kinase/ protein serine/threonine kinase					nr +
Unigene15773_All	1002	25.90	36.51	16.26	53.84	46.98	48.32	95.83	125.26	223.61	4.95E-01	2.09E-08		-6.71E-01	1.13E-09		-1.97E-01	5.44E-03		-1.56E-01	4.23E-02		3.87E-01	4.23E-21		1.22E+00	7.89E-278	Up	Unigene15773_All//gi|164521171|gb|ABY60447.1|//1.00E-134//serine/threonine protein kinase [Adonis aestivalis var. palaestina]	Unigene15773_All//1.00E-128//AT5G20675| AtSK11; protein kinase/ protein serine/threonine kinase	Unigene15773_All//0.00E+00//TC139919				nr -
Unigene15776_All	902	6.09	9.49	11.75	8.01	3.21	2.40	16.55	43.56	230.55	6.40E-01	1.17E-03		9.48E-01	2.46E-07		-1.32E+00	1.86E-10	Down	-1.74E+00	1.11E-13	Down	1.40E+00	3.80E-59	Up	3.80E+00	0.00E+00	Up	Unigene15776_All//gi|255545600|ref|XP_002513860.1|//2.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223546946|gb|EEF48443.1| conserved hypothetical protein [Ricinus communis]		Unigene15776_All//6.00E-141//TC153190				nr -
Unigene15778_All	995	42.44	105.62	54.48	43.46	48.35	54.42	47.63	71.33	83.60	1.32E+00	6.01E-117	Up	3.61E-01	9.80E-07		1.54E-01	5.61E-02		3.25E-01	3.49E-06		5.82E-01	3.85E-25		8.12E-01	3.90E-53		Unigene15778_All//gi|151368154|gb|ABS10812.1|//3.00E-24//DNA binding protein-like protein [Gossypium arboreum]	Unigene15778_All//5.00E-08//AT3G15790| WBD11; DNA binding / methyl-CpG binding	Unigene15778_All//0.00E+00//TC163614				nr +
Unigene15782_All	1754	8.08	4.94	5.92	16.84	17.08	12.90	12.46	5.48	5.52	-7.11E-01	1.91E-06		-4.49E-01	3.93E-03		2.03E-02	8.73E-01		-3.85E-01	7.79E-05		-1.19E+00	5.34E-26	Down	-1.18E+00	1.93E-26	Down	Unigene15782_All//gi|74058450|gb|AA298830.1|//1.00E-155//homoserine dehydrogenase [Glycine max] >gi|110617765|gb|ABG78600.1| homoserine dehydrogenase [Glycine max]	Unigene15782_All//2.00E-145//AT5G21060| homoserine dehydrogenase family protein	Unigene15782_All//0.00E+00//ES800157		ko00270|Cysteine and methionine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00300|Lysine biosynthesis		nr -
Unigene15783_All	1354	12.87	9.77	9.95	13.61	11.57	10.07	4.97	5.99	2.27	-3.98E-01	2.92E-03		-3.71E-01	8.11E-03		-2.34E-01	7.79E-02		-4.34E-01	6.12E-04		2.70E-01	1.65E-01		-1.13E+00	2.74E-08	Down	Unigene15783_All//gi|15229025|ref|NP_190449.1|//3.00E-16//sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	Unigene15783_All//1.00E-17//AT3G48800| sterile alpha motif (SAM) domain-containing protein	Unigene15783_All//0.00E+00//TC166567				nr +
Unigene15785_All	590	1.06	5.07	1.26	1.52	1.40	5.28	2.87	10.77	3.85	2.25E+00	1.14E-07	Up	2.48E-01	7.45E-01		-1.18E-01	8.51E-01		1.80E+00	2.25E-06	Up	1.91E+00	1.57E-15	Up	4.25E-01	2.58E-01		Unigene15785_All//gi|195634795|gb|ACG36866.1|//3.00E-29//BSD domain containing protein [Zea mays]	Unigene15785_All//2.00E-26//AT1G69030| INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: BSD (InterPro:IPR005607); BEST Arabidopsis thaliana protein match is: BSD domain-containing protein (TAIR:AT1G26300.1); Has 173 Blast hits to 173 proteins in 34 species: Archae - 4; Bacteria - 4; Metazoa - 52; Fungi - 10; Plants - 92; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene15785_All//0.00E+00//TC169807				nr +
Unigene15786_All	1221	0.64	2.61	0.96	1.18	3.27	2.48	1.49	9.04	6.04	2.02E+00	3.18E-07	Up	5.78E-01	3.90E-01		1.47E+00	1.58E-06	Up	1.07E+00	3.16E-03		2.60E+00	2.24E-38	Up	2.02E+00	1.21E-19	Up	Unigene15786_All//gi|195634795|gb|ACG36866.1|//9.00E-67//BSD domain containing protein [Zea mays]	Unigene15786_All//2.00E-43//AT1G69030| INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: BSD (InterPro:IPR005607); BEST Arabidopsis thaliana protein match is: BSD domain-containing protein (TAIR:AT1G26300.1); Has 173 Blast hits to 173 proteins in 34 species: Archae - 4; Bacteria - 4; Metazoa - 52; Fungi - 10; Plants - 92; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene15786_All//0.00E+00//gi|78330383|gb|DT550657.1|DT550657				nr -

Unigene15787_All	1662	5.32	2.68	3.52	9.29	8.83	8.34	3.89	0.70	1.70	-9.88E-01	5.71E-07		-5.94E-01	3.25E-03		-7.41E-02	6.65E-01		-1.55E-01	3.52E-01		-2.47E+00	1.53E-21	Down	-1.19E+00	1.23E-08	Down	Unigene15787_All//gi|255586395|ref|XP_002533844.1|//8.00E-39//conserved hypothetical protein [Ricinus communis] >gi|223526211|gb|EEF28535.1| conserved hypothetical protein [Ricinus communis]		Unigene15787_All//0.00E+00//gi|78351007|gb|DT571281.1|DT571281				nr +
Unigene1579_All	1360	3.92	4.92	1.96	4.83	4.86	4.95	4.45	2.61	5.77	3.26E-01	1.67E-01		-1.00E+00	2.23E-04	Down	7.90E-03	9.82E-01		3.34E-02	9.14E-01		-7.67E-01	3.41E-04		3.76E-01	4.00E-02		Unigene1579_All//gi|42569807|ref|NP_181589.3|//1.00E-158//initiator tRNA phosphoribosyl transferase family protein [Arabidopsis thaliana] >gi|30725316|gb|AAP37680.1| At2g40570 [Arabidopsis thaliana]	Unigene1579_All//2.00E-159//AT2G40570| initiator tRNA phosphoribosyl transferase family protein	Unigene1579_All//0.00E+00//TC145329				nr -
Unigene15790_All	709	255.85	70.39	51.07	210.29	423.33	242.76	87.18	133.17	214.36	-1.86E+00	0.00E+00	Down	-2.32E+00	0.00E+00	Down	1.01E+00	6.66E-261	Up	2.07E-01	4.19E-08		6.11E-01	4.37E-36		1.30E+00	4.26E-207	Up	Unigene15790_All//gi|297734182|emb|CBI15429.3|//6.00E-07//unnamed protein product [Vitis vinifera]		Unigene15790_All//2.00E-106//gi|109870551|gb|DW499527.1|DW499527				nr -
Unigene15797_All	782	2.68	3.56	2.11	28.73	24.31	15.36	15.03	5.18	3.06	4.13E-01	2.83E-01		-3.42E-01	4.64E-01		-2.41E-01	3.93E-02		-9.03E-01	2.88E-15		-1.54E+00	6.09E-21	Down	-2.30E+00	1.14E-36	Down	Unigene15797_All//gi|170293723|gb|ACB12931.1|//9.00E-95//pectate lyase 1-27 [Populus tremula x Populus tremuloides]	Unigene15797_All//8.00E-91//AT1G04680| pectate lyase family protein	Unigene15797_All//0.00E+00//ES804114		ko00040|Pentose and glucuronate interconversions		nr -
Unigene158_All	1257	3.83	3.63	3.13	7.33	5.73	7.44	7.06	2.89	7.13	-7.80E-02	7.78E-01		-2.89E-01	3.47E-01		-3.57E-01	5.87E-02		2.07E-02	9.41E-01		-1.29E+00	1.83E-12	Down	1.37E-02	9.63E-01		Unigene158_All//gi|224111284|ref|XP_002332949.1|//1.00E-24//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834261|gb|EEE72738.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene158_All//3.00E-08//AT4G26090| RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding	Unigene158_All//0.00E+00//ES820741		ko04626|Plant-pathogen interaction		nr +
Unigene15801_All	1782	24.28	28.49	29.14	21.44	24.14	23.57	17.68	11.96	8.20	2.31E-01	2.37E-03		2.63E-01	6.36E-04		1.71E-01	4.28E-02		1.37E-01	1.38E-01		-5.63E-01	5.26E-11		-1.11E+00	2.36E-34	Down	Unigene15801_All//gi|22327548|ref|NP_199173.2|//0.00E+00//UAH (UREIDOGLYCOLATE AMIDOHYDROLASE); allantoate deiminase/ metallopeptidase [Arabidopsis thaliana] >gi|110741173|dbj|BAF02137.1| N-carbamyl-L-amino acid amidohydrolase-like protein [Arabidopsis thaliana]	Unigene15801_All//4.00E-178//AT5G43600| UAH (UREIDOGLYCOLATE AMIDOHYDROLASE); allantoate deiminase/ metallopeptidase	Unigene15801_All//0.00E+00//TC136882				nr +
Unigene15804_All	1525	4.15	8.64	6.36	6.60	8.11	5.66	7.98	7.76	8.36	1.06E+00	4.99E-11	Up	6.14E-01	1.30E-03		2.97E-01	7.34E-02		-2.22E-01	2.73E-01		-4.19E-02	8.05E-01		6.62E-02	6.70E-01		Unigene15804_All//gi|18398471|ref|NP_566348.1|//1.00E-102//zinc finger (DHHC type) family protein [Arabidopsis thaliana] >gi|75249276|sp|Q93VV0.1|ZDHC6_ARATH RecName: Full=Probable S-acyltransferase At3g09320; AltName: Full=Probable palmitoyltransferase At3g09320; AltName: Full=Zinc finger DHHC domain-containing protein At3g09320 >gi|14517366|gb|AAK62574.1| AT3g09320/F3L24_19 [Arabidopsis thaliana] >gi|16323274|gb|AAL15371.1| AT3g09320/F3L24_19 [Arabidopsis thaliana]	Unigene15804_All//1.00E-90//AT3G09320| zinc finger (DHHC type) family protein	Unigene15804_All//0.00E+00//gi|109849805|gb|DW478784.1|DW478784				nr +
Unigene15805_All	710	10.10	21.84	21.53	7.51	12.27	15.58	32.10	28.49	9.59	1.11E+00	6.84E-14	Up	1.09E+00	8.23E-13	Up	7.09E-01	1.30E-04		1.05E+00	8.19E-10	Up	-1.72E-01	1.28E-01		-1.74E+00	4.28E-49	Down	Unigene15805_All//gi|224062041|ref|XP_002300725.1|//5.00E-75//cytochrome P450 [Populus trichocarpa] >gi|222842451|gb|EEE79998.1| cytochrome P450 [Populus trichocarpa]	Unigene15805_All//9.00E-54//AT5G25140| CYP71B13; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene15805_All//0.00E+00//ES805212		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr -
Unigene15806_All	789	10.48	9.95	4.99	18.37	13.62	12.31	6.81	5.67	5.86	-7.39E-02	7.22E-01		-1.07E+00	5.44E-07	Down	-4.32E-01	1.89E-03		-5.78E-01	5.49E-05		-2.64E-01	2.95E-01		-2.17E-01	3.70E-01		Unigene15806_All//gi|6691216|gb|AAF24554.1|AC007508_17//1.00E-27//F1K23.22 [Arabidopsis thaliana] >gi|98961029|gb|ABF58998.1| At1g28540 [Arabidopsis thaliana]	Unigene15806_All//1.00E-27//AT1G28540| unknown protein	Unigene15806_All//2.00E-146//DN801811				nr -
Unigene15809_All	1859	0.06	0.05	0.00	0.72	0.00	0.00	5.09	2.25	2.57	-4.69E-02	9.89E-01		-5.82E+00	3.95E-01		-9.50E+00	5.66E-10	Down	-9.50E+00	2.08E-08	Down	-1.18E+00	1.19E-11	Down	-9.86E-01	3.23E-09		Unigene15809_All//gi|115439341|ref|NP_001043950.1|//1.00E-137//Os01g0694100 [Oryza sativa Japonica Group] >gi|113533481|dbj|BAF05864.1| Os01g0694100 [Oryza sativa Japonica Group]	Unigene15809_All//2.00E-91//AT3G47580| leucine-rich repeat transmembrane protein kinase, putative	Unigene15809_All//1.00E-07//DR460632		ko04626|Plant-pathogen interaction		nr -
Unigene15812_All	867	6.10	33.02	7.98	9.08	8.62	4.53	2.97	9.59	0.41	2.44E+00	1.48E-74	Up	3.90E-01	1.03E-01		-7.49E-02	7.84E-01		-1.00E+00	9.76E-07	Down	1.69E+00	4.17E-17	Up	-2.85E+00	8.60E-11	Down	Unigene15812_All//gi|87241090|gb|AB032948.1|//2.00E-95//Pathogen-related protein, related [Medicago truncatula]	Unigene15812_All//1.00E-92//AT1G78780| pathogenesis-related family protein	Unigene15812_All//0.00E+00//TC157473				nr +
Unigene15815_All	1221	9.34	12.66	5.84	8.36	25.18	8.06	8.00	6.06	46.82	4.38E-01	2.13E-03		-6.77E-01	1.03E-04		1.59E+00	1.02E-53	Up	-5.27E-02	7.93E-01		-4.01E-01	1.60E-02		2.55E+00	2.33E-195	Up	Unigene15815_All//gi|292668893|gb|ADE41101.1|//2.00E-67//AP2 domain class transcription factor [Malus x domestica]	Unigene15815_All//9.00E-51//AT5G47230| ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5); DNA binding / transcription activator/ transcription factor	Unigene15815_All//0.00E+00//TC151512	AP2-EREBP			nr -
Unigene15816_All	953	18.28	2.76	3.30	15.84	8.06	7.58	5.99	3.03	0.63	-2.73E+00	4.61E-52	Down	-2.47E+00	6.65E-45	Down	-9.75E-01	3.25E-13		-1.06E+00	1.64E-13	Down	-9.85E-01	1.12E-05		-3.26E+00	3.71E-26	Down	Unigene15816_All//gi|224123518|ref|XP_002319099.1|//2.00E-70//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222857475|gb|EEE95022.1| AP2/EBP domain-containing transcription factor [Populus trichocarpa]	Unigene15816_All//2.00E-42//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene15816_All//0.00E+00//gi|48789747|gb|C0091061.1|C0091061	AP2-EREBP			nr -
Unigene1582_All	3301	4.26	2.98	1.79	5.30	4.01	3.42	6.15	3.34	5.42	-5.18E-01	5.22E-04		-1.25E+00	1.59E-14	Down	-4.03E-01	1.29E-03		-6.31E-01	9.56E-07		-8.79E-01	3.99E-15		-1.82E-01	1.08E-01		Unigene1582_All//gi|297598416|ref|NP_001045553.2|//1.00E-125//Os01g0974300 [Oryza sativa Japonica Group] >gi|255674124|dbj|BAF07467.2| Os01g0974300 [Oryza sativa Japonica Group]	Unigene1582_All//0.00E+00//AT3G12590| unknown protein	Unigene1582_All//0.00E+00//TC170594				nr -
Unigene15820_All	1045	22.63	20.12	5.25	3.10	4.75	7.56	0.28	0.24	10.29	-1.70E-01	1.62E-01		-2.11E+00	3.55E-50	Down	6.15E-01	2.01E-02		1.29E+00	1.24E-09	Up	-2.39E-01	8.40E-01		5.18E+00	4.98E-66	Up	Unigene15820_All//gi|115434122|ref|NP_001041819.1|//8.00E-26//Os01g0113300 [Oryza sativa Japonica Group] >gi|113531350|dbj|BAF03733.1| Os01g0113300 [Oryza sativa Japonica Group]	Unigene15820_All//9.00E-06//AT2G46495| zinc finger (C3HC4-type RING finger) family protein	Unigene15820_All//0.00E+00//gi|78346865|gb|DT567139.1|DT567139				nr +
Unigene15822_All	1588	24.41	10.15	10.83	17.82	18.17	5.66	5.09	1.63	3.99	-1.27E+00	2.69E-41	Down	-1.17E+00	2.73E-35	Down	2.84E-02	8.24E-01		-1.65E+00	1.10E-48	Down	-1.64E+00	5.20E-16	Down	-3.50E-01	5.29E-02		Unigene15822_All//gi|227206194|dbj|BAH57152.1|//9.00E-76//AT3G15095 [Arabidopsis thaliana]	Unigene15822_All//3.00E-34//AT3G15095| unknown protein	Unigene15822_All//0.00E+00//TC152304				nr -
Unigene15825_All	918	0.68	0.55	0.64	3.09	4.28	4.43	9.99	31.32	21.22	-3.09E-01	7.01E-01		-1.00E-01	9.15E-01		4.67E-01	1.44E-01		5.18E-01	9.84E-02		1.65E+00	2.52E-55	Up	1.09E+00	8.43E-21	Up	Unigene15825_All//gi|14423842|sp|O50001.1|PRU1_PRUAR//7.00E-41//RecName: Full=Major allergen Pru ar 1; AltName: Allergen=Pru ar 1 >gi|2677826|gb|AAB97141.1| major allergen protein homolog [Prunus armeniaca]		Unigene15825_All//0.00E+00//CD486122				nr -
Unigene15827_All	2936	0.12	0.24	0.13	0.27	0.14	0.52	15.51	21.41	36.03	9.54E-01	2.62E-01		2.64E-02	1.00E+00		-9.48E-01	2.21E-01		9.46E-01	8.51E-02		4.65E-01	3.85E-15		1.22E+00	2.04E-130	Up	Unigene15827_All//gi|79525859|ref|NP_198387.2|//0.00E+00//ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene15827_All//0.00E+00//AT5G35370| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding			ko04626|Plant-pathogen interaction		nr +
Unigene15830_All	823	1.65	1.48	1.81	3.63	4.06	3.24	2.72	1.07	1.55	-1.62E-01	7.58E-01		1.32E-01	8.01E-01		1.60E-01	6.91E-01		-1.66E-01	6.88E-01		-1.35E+00	5.83E-04	Down	-8.14E-01	2.64E-02				Unigene15830_All//1.00E-49//DN501637				
Unigene15831_All	1122	0.19	2.80	1.23	0.18	0.37	2.25	31.35	77.71	95.58	3.91E+00	2.75E-13	Up	2.73E+00	1.78E-04	Up	1.05E+00	4.26E-01		3.67E+00	8.46E-11	Up	1.31E+00	3.25E-118	Up	1.61E+00	1.96E-201	Up	Unigene15831_All//gi|75181359|sp|Q9LZX1.1|Y5175_ARATH//7.00E-76//RecName: Full=UPF0706 protein At5g01750 >gi|13926237|gb|AAK49593.1|AF37287_1 AT5g01750/T20L15_20 [Arabidopsis thaliana] >gi|22655412|gb|AAM88298.1| At5g01750/T20L15_20 [Arabidopsis thaliana]	Unigene15831_All//4.00E-77//AT5G01750| unknown protein	Unigene15831_All//7.00E-24//TC133649				nr -
Unigene15836_All	428	25.30	53.51	28.24	25.02	59.94	41.26	36.06	74.51	90.75	1.08E+00	3.02E-19	Up	1.59E-01	3.97E-01		1.26E+00	8.35E-32	Up	7.21E-01	2.28E-08		1.05E+00	7.28E-31	Up	1.33E+00	1.19E-55	Up	Unigene15836_All//gi|4512647|gb|AAD21702.1|//8.00E-29//expressed protein [Arabidopsis thaliana] >gi|20197684|gb|AAM15201.1| expressed protein [Arabidopsis thaliana]	Unigene15836_All//3.00E-29//AT2G20670| unknown protein	Unigene15836_All//8.00E-117//gi|48809010|gb|C0110324.1|C0110324				nr +
Unigene15837_All	600	94.26	165.86	149.01	76.05	206.21	174.86	14.45	22.43	24.04	8.15E-01	5.57E-51		6.61E-01	5.47E-31		1.44E+00	5.76E-187	Up	1.20E+00	4.61E-109	Up	6.35E-01	3.34E-06		7.35E-01	1.60E-08		Unigene15837_All//gi|15450373|gb|AA96480.1|//1.00E-24//AT4g32480/FSB4_180 [Arabidopsis thaliana] >gi|16974485|gb|AAL31246.1| AT4g32480/FSB4_180 [Arabidopsis thaliana]	Unigene15837_All//6.00E-18//AT4G32480| unknown protein	Unigene15837_All//8.00E-167//C0131853				nr -
Unigene15838_All	2144	0.05	0.00	0.10	0.33	0.48	2.59	9.33	16.51	13.66	-5.61E+00	3.73E-01		1.02E+00	5.92E-01		5.67E-01	4.45E-01		2.99E+00	1.42E-19	Up	8.24E-01	3.89E-23		5.50E-01	3.63E-10		Unigene15838_All//gi|30686226|ref|NP_173345.2|//0.00E+00//inter-alpha-trypsin inhibitor heavy chain-related [Arabidopsis thaliana]	Unigene15838_All//0.00E+00//AT1G19110| inter-alpha-trypsin inhibitor heavy chain-related	Unigene15838_All//2.00E-84//TC144235				nr -
Unigene15839_All	2543	0.00	0.04	0.00	0.08	0.14	0.50	5.05	10.45	5.94	5.32E+00	3.87E-01		null	null		7.88E-01	5.96E-01		2.67E+00	2.42E-04	Up	1.05E+00	6.59E-26	Up	2.32E-01	7.74E-02		Unigene15839_All//gi|15218501|ref|NP_177394.1|//0.00E+00//inter-alpha-trypsin inhibitor heavy chain-related [Arabidopsis thaliana]	Unigene15839_All//4.00E-160//AT1G72500| inter-alpha-trypsin inhibitor heavy chain-related	Unigene15839_All//2.00E-81//C0119106				nr -
Unigene15842_All	1393	7.02	7.49	7.11	3.79	3.76	2.14	2.19	1.86	0.89	9.33E-02	6.09E-01		1.77E-02	9.45E-01		-1.27E-02	9.57E-01		-8.25E-01	1.26E-03		-2.32E-01	5.17E-01		-1.30E+00	4.73E-05	Down	Unigene15842_All//gi|114050645|gb|AB149472.1|//3.00E-89//At1g77122 [Arabidopsis thaliana]	Unigene15842_All//2.00E-72//AT1G77122| unknown protein	Unigene15842_All//0.00E+00//TC147190				nr +
Unigene15843_All	1273	5.18	11.03	6.27	5.09	6.68	6.67	8.64	11.79	7.26	1.09E+00	2.95E-12	Up	2.77E-01	2.27E-01		3.93E-01	4.86E-02		3.91E-01	5.76E-02		4.49E-01	5.00E-04		-2.50E-01	1.09E-01		Unigene15843_All//gi|297852682|ref|XP_002894222.1|//1.00E-50//ring-H2 finger protein RHY1a [Arabidopsis lyrata subsp. lyrata] >gi|297340064|gb|EFH70481.1| ring-H2 finger protein RHY1a [Arabidopsis lyrata subsp. lyrata]	Unigene15843_All//8.00E-34//AT1G49850| zinc finger (C3HC4-type RING finger) family protein	Unigene15843_All//0.00E+00//TC145787				nr -

Unigene15844_All	1649	1.33	0.80	0.81	2.21	1.25	4.08	3.62	7.65	11.06	-7.38E-01	8.62E-02		-7.23E-01	1.12E-01		-8.16E-01	7.13E-03		8.88E-01	7.41E-05		1.08E+00	2.32E-13	Up	1.61E+00	4.11E-35	Up	Unigene15844_All//gi|124359759|gb|ABD32403.2|//1.00E-108//DNA-binding WRKY [Medicago truncatula]	Unigene15844_All//4.00E-83//AT1G62300| WRKY6; transcription factor	Unigene15844_All//2.00E-43//gi|13355622|gb|BG445970.1|BG445970	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene15846_All	2687	1.23	0.55	0.32	1.30	1.32	1.19	3.26	2.66	4.77	-1.17E+00	8.03E-04	Down	-1.95E+00	8.53E-07	Down	2.46E-02	9.53E-01		-1.21E-01	7.28E-01		-2.92E-01	1.13E-01		5.52E-01	5.63E-05		Unigene15846_All//gi|4966374|gb|AAD34705.1|AC006341_33//0.00E+00//>F309.28 [Arabidopsis thaliana]	Unigene15846_All//0.00E+00//AT1G16480| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot apex; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT4G13650.1).	Unigene15846_All//0.00E+00//TC143684				nr +
Unigene15847_All	1402	1.83	2.46	2.70	91.35	50.35	35.89	38.33	12.61	4.69	4.27E-01	2.14E-01		5.61E-01	9.11E-02		-8.59E-01	2.21E-88		-1.35E+00	1.73E-161	Down	-1.60E+00	4.75E-99	Down	-3.03E+00	1.15E-224	Down	Unigene15847_All//gi|75173087|sp|Q9FXJ1.1|GDL6_ARATH//1.00E-104//RecName: Full=GDSL esterase/lipase At1g28570; AltName: Full=Extracellular lipase At1g28570; Flags: Precursor >gi|10764860|gb|AAG22837.1|AC00750 8_14 F1K23.19 [Arabidopsis thaliana]	Unigene15847_All//7.00E-95//AT1G28570| GDSL-motif lipase, putative	Unigene15847_All//0.00E+00//TC159178				nr +
Unigene15848_All	1345	7.12	58.17	5.11	8.00	10.88	9.07	9.21	11.03	11.70	3.03E+00	4.77E-257	Up	-4.79E-01	1.38E-02		4.44E-01	1.55E-03		1.81E-01	3.39E-01		2.60E-01	5.65E-02		3.45E-01	5.28E-03		Unigene15848_All//gi|18396691|ref|NP_566214.1|//1.00E-79//ATAPRL5 (APR-like 5) [Arabidopsis thaliana]	Unigene15848_All//2.00E-74//AT3G03860| ATAPRL5 (APR-like 5)	Unigene15848_All//0.00E+00//gi|78333677|gb|DT553951.1|DT553951				nr +
Unigene1585_All	1513	47.34	27.96	41.46	45.14	37.35	52.60	69.30	26.55	21.72	-7.60E-01	7.84E-33		-1.91E-01	3.83E-03		-2.73E-01	3.32E-06		2.21E-01	1.45E-04		-1.38E+00	6.35E-155	Down	-1.67E+00	8.97E-211	Down	Unigene1585_All//gi|192910782|gb|ACF06499.1|//1.00E-115//ribosomal protein [Elaeis guineensis]	Unigene1585_All//1.00E-109//AT5G35530| 40S ribosomal protein S3 (RPS3C)	Unigene1585_All//0.00E+00//TC130484		ko03010|Ribosome		nr -
Unigene15851_All	1313	10.88	15.82	13.91	8.01	2.54	9.70	29.37	50.74	25.85	5.40E-01	7.18E-06		3.55E-01	9.47E-03		-1.65E+00	6.03E-21	Down	2.77E-01	1.02E-01		7.89E-01	8.39E-40		-1.84E-01	1.88E-02		Unigene15851_All//gi|75169434|sp|Q9C827.1|COB22_ARATH//1.00E-122//RecName: Full=Coatomer subunit beta'-2; AltName: Full=Beta'-coat protein 2; Short=Beta'-COP 2	Unigene15851_All//8.00E-124//AT1G52360| coatomer protein complex, subunit beta 2 (beta prime), putative	Unigene15851_All//0.00E+00//TC143821				nr +
Unigene15852_All	1343	4.95	2.41	2.82	22.11	19.41	5.52	22.04	3.17	3.20	-1.04E+00	8.22E-06	Down	-8.14E-01	6.10E-04		-1.88E-01	7.00E-02		-2.00E+00	2.22E-66	Down	-2.80E+00	1.65E-110	Down	-2.78E+00	1.88E-113	Down	Unigene15852_All//gi|297818028|ref|XP_002876897.1|//2.00E-76//sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322735|gb|EFH53156.1|sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15852_All//1.00E-75//AT3G45070| sulfotransferase family protein	Unigene15852_All//0.00E+00//TC131748		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism		nr -
Unigene15853_All	1230	3.49	1.48	2.73	8.46	7.20	7.27	12.72	3.57	4.31	-1.23E+00	4.36E-05	Down	-3.55E-01	2.60E-01		-2.34E-01	2.19E-01		-2.19E-01	2.70E-01		-1.83E+00	2.65E-35	Down	-1.56E+00	3.60E-29	Down	Unigene15853_All//gi|115456585|ref|NP_001051893.1|//6.00E-70//Os03g0848400 [Oryza sativa Japonica Group] >gi|108712100|gb|ABF99895.1| B-cell receptor-associated protein 31-like containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550364|dbj|BAF13807.1|Os03g0848400 [Oryza sativa Japonica Group]	Unigene15853_All//5.00E-53//AT5G48860| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular protein transport; LOCATED IN: endomembrane system, integral to membrane, endoplasmic reticulum; CONTAINS InterPro DOMAIN/s: B-cell receptor-associated 31-like (InterPro:IPR008417); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G07190.1); Has 2128 Blast hits to 1846 proteins in 298 species: Archae - 50; Bacteria - 292; Metazoa - 902; Fungi - 143; Plants - 114; Viruses - 11; Other Eukaryotes - 616 (source: NCBI BLink).	Unigene15853_All//0.00E+00//TC171847				nr -
Unigene15855_All	2969	5.27	3.48	4.59	13.19	15.24	10.91	13.63	5.03	7.58	-5.98E-01	2.14E-05		-1.99E-01	2.17E-01		2.09E-01	8.02E-03		-2.74E-01	1.34E-03		-1.44E+00	8.12E-64	Down	-8.46E-01	2.37E-28		Unigene15855_All//gi|222143560|dbj|BAH19309.1|//0.00E+00//urease [Morus alba]	Unigene15855_All//0.00E+00//AT1G67550| URE (UREASE); urease	Unigene15855_All//0.00E+00//gi|109855094|gb|DW484073.1|DW484073		ko00230|Purine metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene15856_All	2962	0.49	0.38	1.11	1.03	0.93	1.65	0.80	0.18	0.31	-3.94E-01	4.70E-01		1.17E+00	1.19E-03		-1.41E-01	7.31E-01		6.83E-01	1.22E-02		-2.12E+00	4.52E-07	Down	-1.37E+00	2.21E-04	Down	Unigene15856_All//gi|222143560|dbj|BAH19309.1|//0.00E+00//urease [Morus alba]	Unigene15856_All//0.00E+00//AT1G67550| URE (UREASE); urease	Unigene15856_All//0.00E+00//TC139131		ko00230|Purine metabolism//ko00330|Arginine and proline metabolism		nr +
Unigene15857_All	725	5.34	6.01	3.16	6.94	5.03	8.16	4.49	4.09	1.81	1.71E-01	5.99E-01		-7.58E-01	1.98E-02		-4.63E-01	7.94E-02		2.34E-01	3.96E-01		-1.34E-01	6.85E-01		-1.31E+00	2.23E-05	Down			Unigene15857_All//6.00E-08//ES816175				
Unigene15859_All	1125	1.72	2.39	1.47	7.53	7.25	5.06	6.73	1.45	3.33	4.72E-01	2.27E-01		-2.30E-01	6.13E-01		-5.33E-02	8.13E-01		-5.74E-01	3.48E-03		-2.22E+00	3.91E-22	Down	-1.02E+00	7.24E-08	Down	Unigene15859_All//gi|86371770|gb|ABC94943.1|//1.00E-123//squalene epoxidase [Medicago sativa]	Unigene15859_All//2.00E-105//AT1G58440| XF1; squalene monooxygenase	Unigene15859_All//0.00E+00//TC173870		ko00100|Steroid biosynthesis		nr +
Unigene1586_All	894	4.39	3.17	3.28	7.41	6.32	3.18	4.59	3.18	7.93	-4.68E-01	1.34E-01		-4.22E-01	2.05E-01		-2.30E-01	3.55E-01		-1.22E+00	1.11E-07	Down	-5.29E-01	5.16E-02		7.90E-01	3.84E-05		Unigene1586_All//gi|297822435|ref|XP_002879100.1|//9.00E-31//dsRNA-binding protein 2 [Arabidopsis lyrata subsp. lyrata] >gi|297324939|gb|EFH55359.1|dsRNA-binding protein 2 [Arabidopsis lyrata subsp. lyrata]	Unigene1586_All//5.00E-32//AT2G28380| DRB2 (DSRNA-BINDING PROTEIN 2); double-stranded RNA binding	Unigene1586_All//0.00E+00//gi|78328872|gb|DT549146.1|DT549146				nr +
Unigene15860_All	780	47.42	30.34	26.22	37.74	29.80	41.81	21.36	13.72	9.81	-6.45E-01	3.49E-13		-8.55E-01	3.10E-20		-3.41E-01	2.74E-04		1.47E-01	1.67E-01		-6.39E-01	1.46E-07		-1.12E+00	5.40E-19	Down	Unigene15860_All//gi|8698730|gb|AAF78488.1|AC012187_8//7.00E-29//ESTs gb|Z18526, gb|AI994480, gb|T44186, gb|Z30806 come from this gene [Arabidopsis thaliana]	Unigene15860_All//2.00E-08//AT1G12830| unknown protein	Unigene15860_All//0.00E+00//ES799680				nr +
Unigene15861_All	805	17.35	28.51	34.86	30.57	28.40	28.44	52.78	18.48	15.24	7.16E-01	4.98E-10		1.01E+00	3.30E-20	Up	-1.06E-01	4.20E-01		-1.04E-01	4.39E-01		-1.51E+00	3.64E-72	Down	-1.79E+00	1.88E-94	Down	Unigene15861_All//gi|302142726|emb|CBI19929.3|//2.00E-07//unnamed protein product [Vitis vinifera]	Unigene15861_All//2.00E-06//AT1G76990| ACR3; amino acid binding	Unigene15861_All//0.00E+00//DW486618				nr -
Unigene15862_All	1240	1.10	3.31	0.82	0.16	0.97	2.04	5.08	12.44	14.94	1.59E+00	9.12E-07	Up	-4.27E-01	4.72E-01		2.60E+00	3.41E-04	Up	3.67E+00	8.46E-11	Up	1.29E+00	4.07E-21	Up	1.56E+00	7.53E-34	Up	Unigene15862_All//gi|281485189|gb|ADA70360.1|//2.00E-58//fruit weight 2.2-like protein [Persea americana]	Unigene15862_All//4.00E-40//AT1G14870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: plasma membrane; EXPRESSED IN: callus; CONTAINS InterPro DOMAIN/s: EGF-type aspartate/asparagine hydroxylation conserved site (InterPro:IPR000152), Protein of unknown function Cys-rich (InterPro:IPR006461); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35525.1); Has 492 Blast hits to 491 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 93; Fungi - 76; Plants - 297; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink).	Unigene15862_All//1.00E-47//gi|109881215|gb|DW510185.1|DW510185		ko04626|Plant-pathogen interaction		nr +
Unigene15864_All	722	1.38	7.09	1.99	2.07	2.53	4.25	1.87	3.70	2.98	2.36E+00	2.33E-13	Up	5.32E-01	3.71E-01		2.88E-01	5.96E-01		1.04E+00	3.68E-03		9.83E-01	4.42E-03		6.69E-01	7.75E-02				Unigene15864_All//2.00E-140//gi|21101399|gb|BQ413712.1|BQ413712				
Unigene15865_All	884	46.76	41.50	39.88	133.44	107.90	58.91	29.13	24.02	16.36	-1.72E-01	4.99E-02		-2.30E-01	9.90E-03		-3.07E-01	1.05E-12		-1.18E+00	1.05E-120	Down	-2.78E-01	4.50E-03		-8.32E-01	6.90E-18		Unigene15865_All//gi|124359981|gb|ABN07997.1|//1.00E-11//contains similarity to reverse trancriptase , related [Medicago truncatula]	Unigene15865_All//3.00E-10//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene15865_All//0.00E+00//BG444828				nr -
Unigene15866_All	787	199.71	55.18	59.20	122.79	108.82	121.55	47.28	377.91	129.74	-1.86E+00	5.94E-290	Down	-1.75E+00	7.00E-260	Down	-1.74E-01	6.04E-04		-1.48E-02	8.29E-01		3.00E+00	0.00E+00	Up	1.46E+00	6.36E-166	Up	Unigene15866_All//gi|18252504|gb|AAL66290.1|AF452450_1//1.00E-135//adenosine 5'-phosphosulfate reductase [Glycine max]	Unigene15866_All//2.00E-135//AT4G21990| APR3 (APS REDUCTASE 3); adenylyl-sulfate reductase	Unigene15866_All//0.00E+00//TC164687				nr -
Unigene15868_All	1740	0.69	1.66	0.67	11.62	2.83	1.45	4.86	8.36	41.33	1.26E+00	8.87E-04	Up	-3.87E-02	9.68E-01		-2.04E+00	1.52E-53	Down	-3.00E+00	1.13E-72	Down	7.83E-01	3.26E-09		3.09E+00	9.19E-301	Up	Unigene15868_All//gi|269996964|gb|ACZ57767.1|//0.00E+00//phospholipase A1 [Nicotiana attenuata]	Unigene15868_All//6.00E-163//AT4G16820| lipase class 3 family protein	Unigene15868_All//0.00E+00//gi|78333729|gb|DT554003.1|DT554003				nr +
Unigene15870_All	1400	3.44	3.91	5.48	9.11	6.81	6.55	7.25	5.02	1.71	1.85E-01	5.00E-01		6.72E-01	2.10E-03		-4.19E-01	5.46E-03		-4.76E-01	2.31E-03		-5.31E-01	8.96E-04		-2.09E+00	3.17E-28	Down	Unigene15870_All//gi|145323858|ref|NP_001077518.1|//1.00E-63//LEW1 (LEAF WILTING 1); dehydrodolichyl diphosphate synthase [Arabidopsis thaliana] >gi|25083010|gb|AAN72032.1|Unknown protein [Arabidopsis thaliana]	Unigene15870_All//6.00E-65//AT1G11755| LEW1 (LEAF WILTING 1); dehydrodolichyl diphosphate synthase	Unigene15870_All//0.00E+00//TC170702				nr +
Unigene15871_All	1331	5.23	6.66	2.84	8.50	8.54	3.19	0.22	0.31	0.00	3.50E-01	7.78E-02		-8.80E-01	1.49E-04		7.10E-03	9.74E-01		-1.41E+00	9.01E-16	Down	4.98E-01	6.33E-01		-7.80E+00	1.58E-02		Unigene15871_All//gi|15230370|ref|NP_191326.1|//1.00E-111//NTT (NO TRANSMITTING TRACT); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|18027012|gb|AAL55722.1|AF254447_1 WIP2 protein [Arabidopsis thaliana] >gi|4678280|emb|CAB41188.1| zinc finger-like protein [Arabidopsis thaliana] >gi|59958298|gb|AAX12859.1|At3g57670 [Arabidopsis thaliana]	Unigene15871_All//4.00E-108//AT3G57670| NTT (NO TRANSMITTING TRACT); nucleic acid binding / transcription factor/ zinc ion binding	Unigene15871_All//2.00E-61//TC163517	C2H2			nr -
Unigene15872_All	683	9.73	25.97	8.11	16.92	20.37	22.48	36.34	56.60	53.14	1.42E+00	1.25E-22	Up	-2.63E-01	3.02E-01		2.68E-01	8.71E-02		4.10E-01	4.04E-03		6.40E-01	1.76E-16		5.48E-01	2.57E-12		Unigene15872_All//gi|255555610|ref|XP_002518841.1|//4.00E-06//G-box-binding factor, putative [Ricinus communis] >gi|223542014|gb|EEF43559.1| G-box-binding factor, putative [Ricinus communis]		Unigene15872_All//0.00E+00//gi|13244752|gb|BE054911.2|BE054911				nr +
Unigene15873_All	1672	0.00	0.06	0.00	0.15	0.04	0.14	4.35	16.77	8.39	5.92E+00	3.87E-01		null	null		-1.85E+00	2.75E-01		-1.41E-01	9.29E-01		1.95E+00	8.76E-68	Up	9.47E-01	2.46E-12		Unigene15873_All//gi|15241393|ref|NP_199929.1|//9.00E-42//ankyrin repeat family protein [Arabidopsis thaliana] >gi|45825143|gb|AAS77479.1|At5g51160 [Arabidopsis thaliana]	Unigene15873_All//4.00E-43//AT5G51160| ankyrin repeat family protein	Unigene15873_All//3.00E-24//gi|3325947|gb|AI054833.1|AI054833				nr -
Unigene15874_All	970	0.27	5.85	0.11	0.92	1.70	6.01	0.52	2.41	5.50	4.44E+00	9.82E-26	Up	-1.30E+00	4.36E-01		8.82E-01	8.83E-02		2.70E+00	1.74E-18	Up	2.21E+00	2.81E-07	Up	3.40E+00	5.99E-25	Up	Unigene15874_All//gi|15241393|ref|NP_199929.1|//7.00E-24//ankyrin repeat family protein [Arabidopsis thaliana] >gi|45825143|gb|AAS77479.1|At5g51160 [Arabidopsis thaliana]	Unigene15874_All//3.00E-25//AT5G51160| ankyrin repeat family protein	Unigene15874_All//0.00E+00//gi|3325947|gb|AI054833.1|AI054833				nr +

Unigene15875_All	898	9.21	11.06	16.01	45.04	43.37	51.15	52.54	28.25	24.22	2.65E-01	1.66E-01		7.98E-01	1.96E-07		-5.46E-02	6.10E-01		1.83E-01	2.66E-02		-8.95E-01	4.05E-35		-1.12E+00	9.63E-52	Down	Unigene15875_All//gi|297833762|ref|XP_002884763.1|//1.00E-101//PIP5K9 [Arabidopsis lyrata subsp. lyrata] >gi|297330603|gb|EFH61022.1|PIP5K9 [Arabidopsis lyrata subsp. lyrata]	Unigene15875_All//4.00E-93//AT3G09920| PIP5K9 (PHOSPHATIDYL INOSITOL MONOPHOSPHATE 5 KINASE); 1-phosphatidylinositol-4-phosphate 5-kinase/ ATP binding / phosphatidylinositol phosphate kinase	Unigene15875_All//0.00E+00//gi|109856959|gb|DW485938.1|DW485938		ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene15876_All	856	2.26	1.01	1.24	7.57	6.44	3.11	0.00	0.20	0.00	-1.17E+00	1.36E-02		-8.62E-01	7.98E-02		-2.33E-01	3.55E-01		-1.28E+00	4.49E-08	Down	7.61E+00	1.39E-01		null	null		Unigene15876_All//gi|223452286|gb|ACM89471.1|//2.00E-74//FERONIA receptor-like kinase [Glycine max]	Unigene15876_All//2.00E-53//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene15876_All//1.00E-73//TC163657				nr -
Unigene15878_All	492	0.00	0.51	5.30	0.00	0.21	18.82	6.96	1.53	49.39	9.01E+00	7.86E-02		1.24E+01	2.12E-14	Up	7.71E+00	4.56E-01		1.42E+01	2.11E-56	Up	-2.19E+00	2.97E-10	Down	2.83E+00	2.61E-93	Up	Unigene15878_All//gi|281376745|gb|ADA67882.1|//5.00E-15//S-like RNase [Citrus reticulata]	Unigene15878_All//9.00E-15//AT2G39780| RNS2 (RIBONUCLEASE 2); RNA binding / endoribonuclease/ ribonuclease T2	Unigene15878_All//0.00E+00//TC138648				nr +
Unigene15879_All	856	1.41	93.05	93.87	2.97	9.86	463.14	161.02	152.63	1427.21	6.05E+00	0.00E+00	Up	6.06E+00	0.00E+00	Up	1.73E+00	9.63E-17	Up	7.29E+00	0.00E+00	Up	-7.72E-02	7.87E-02		3.15E+00	0.00E+00	Up	Unigene15879_All//gi|113374061|dbj|BAF03591.1|//2.00E-18//S-like RNase [Fagopyrum esculentum]	Unigene15879_All//1.00E-17//AT2G02990| RNS1 (RIBONUCLEASE 1); endoribonuclease/ ribonuclease	Unigene15879_All//0.00E+00//TC138648				nr -
Unigene15882_All	1675	0.16	1.21	0.35	0.21	2.32	12.92	86.20	42.15	125.51	2.95E+00	4.86E-07	Up	1.16E+00	2.47E-01		3.48E+00	8.97E-17	Up	5.96E+00	5.08E-120	Up	-1.03E+00	4.84E-134	Down	5.42E-01	1.27E-65		Unigene15882_All//gi|56785668|gb|AW28999.1|//0.00E+00//1-deoxy-D-xylulose-5-phosphate synthase [Antirrhinum majus]	Unigene15882_All//0.00E+00//AT4G15560| CLA1 (CLOROPLASTOS ALTERADOS 1); 1-deoxy-D-xylulose-5-phosphate synthase	Unigene15882_All//0.00E+00//TC140384		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene15885_All	1790	5.20	6.37	1.10	5.43	8.70	3.61	7.23	12.66	12.13	2.92E-01	9.55E-02		-2.24E+00	1.49E-21	Down	6.80E-01	2.68E-07		-5.89E-01	1.12E-03		8.08E-01	1.23E-14		7.47E-01	1.03E-12		Unigene15885_All//gi|18412854|ref|NP_565238.1|//1.00E-100//kelch repeat-containing F-box family protein [Arabidopsis thaliana] >gi|75186440|sp|Q9SEL2.1|FBK30_ARATH RecName: Full=F-box/kelch-repeat protein At1g80440	Unigene15885_All//4.00E-101//AT1G80440| kelch repeat-containing F-box family protein	Unigene15885_All//0.00E+00//TC178819				nr -
Unigene15886_All	1335	5.57	4.86	4.79	11.64	12.72	5.89	2.38	0.88	0.57	-1.96E-01	3.79E-01		-2.18E-01	3.78E-01		1.27E-01	4.27E-01		-9.84E-01	2.60E-12		-1.44E+00	1.03E-05	Down	-2.07E+00	2.80E-09	Down	Unigene15886_All//gi|79495605|ref|NP_195054.2|//3.00E-59//DNA binding / transcription factor [Arabidopsis thaliana] >gi|75159005|sp|Q8RYD1.1|REM16_ARATH RecName: Full=B3 domain-containing protein REM16; AltName: Full=Protein REPRODUCTIVE MERISTEM 16; AltName: Full=Auxin response factor 36 >gi|20145851|emb|CAD29616.1| auxin response factor 36 [Arabidopsis thaliana]	Unigene15886_All//7.00E-57//AT4G33280| DNA binding / transcription factor	Unigene15886_All//0.00E+00//TC138603	ABI3VP1			nr +
Unigene15888_All	1097	7.49	9.01	11.16	1.68	4.52	12.56	0.81	4.84	2.91	2.67E-01	1.63E-01		5.76E-01	5.79E-04		1.43E+00	1.05E-07	Up	2.90E+00	1.34E-46	Up	2.58E+00	1.23E-18	Up	1.84E+00	4.95E-08	Up	Unigene15888_All//gi|87162753|gb|ABD28548.1|//1.00E-74//Protein kinase; Type I EGF [Medicago truncatula]	Unigene15888_All//6.00E-56//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase					nr -
Unigene15889_All	738	5.67	2.20	2.45	11.47	10.55	7.10	5.56	6.97	3.89	-1.37E+00	1.07E-05	Down	-1.21E+00	1.39E-04	Down	-1.22E-01	6.01E-01		-6.93E-01	3.69E-04		3.26E-01	1.95E-01		-5.16E-01	4.78E-02						Unigene15889_All//9.00E-07//ES839918				
Unigene1589_All	3251	5.83	2.67	3.69	13.27	10.32	8.85	5.44	1.85	2.29	-1.13E+00	3.14E-17	Down	-6.61E-01	4.61E-07		-3.63E-01	1.13E-06		-5.85E-01	9.28E-14		-1.55E+00	1.25E-31	Down	-1.25E+00	1.45E-23	Down	Unigene1589_All//gi|15234061|ref|NP_192018.1|//1.00E-104//extra-large G-protein-related [Arabidopsis thaliana] >gi|17979014|gb|AAL47466.1|AT4g01090/F2N1_13 [Arabidopsis thaliana] >gi|20334762|gb|AAM16242.1|AT4g01090/F2N1_13 [Arabidopsis thaliana] >gi|222424660|dbj|BAH20284.1|AT4G01090 [Arabidopsis thaliana]	Unigene1589_All//2.00E-88//AT3G61670| unknown protein	Unigene1589_All//0.00E+00//TC149631				nr +
Unigene15892_All	1103	13.52	5.05	10.86	284.12	218.44	153.55	28.06	17.28	12.89	-1.42E+00	2.59E-19	Down	-3.16E-01	4.35E-02		-3.79E-01	2.60E-49		-8.88E-01	2.01E-200		-6.99E-01	1.60E-15		-1.12E+00	1.82E-34	Down	Unigene15892_All//gi|225446451|ref|XP_002275180.1|//3.00E-53//PREDICTED: similar to arabinogalactan-protein; AGP [Vitis vinifera]		Unigene15892_All//0.00E+00//DW224035				nr +
Unigene15893_All	1552	0.94	1.63	0.51	2.63	2.97	2.74	3.92	0.75	0.90	7.90E-01	4.67E-02		-8.75E-01	1.34E-01		1.76E-01	5.94E-01		5.56E-02	8.78E-01		-2.38E+00	1.66E-19	Down	-2.13E+00	1.13E-17	Down	Unigene15893_All//gi|15232012|ref|NP_187519.1|//8.00E-37//glycine-rich protein [Arabidopsis thaliana] >gi|75207465|sp|Q9SS80.1|U503A_ARATH RecName: Full=UPF0503 protein At3g09070, chloroplastic; Flags: Precursor	Unigene15893_All//7.00E-53//AT5G58930| unknown protein	Unigene15893_All//0.00E+00//gi|78351912|gb|DT572186.1|DT572186				nr -
Unigene15896_All	648	7.11	8.21	5.18	18.76	21.10	20.07	31.78	15.42	21.58	2.09E-01	4.43E-01		-4.57E-01	1.31E-01		1.70E-01	3.22E-01		9.78E-02	6.39E-01		-1.04E+00	3.89E-20	Down	-5.58E-01	1.27E-07		Unigene15896_All//gi|297805262|ref|XP_002870515.1|//4.00E-75//transporter [Arabidopsis lyrata subsp. lyrata] >gi|297316351|gb|EFH46774.1|transporter [Arabidopsis lyrata subsp. lyrata]	Unigene15896_All//2.00E-76//AT5G37310| LOCATED IN: integral to membrane, Golgi apparatus, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nonaspanin (TM9SF) (InterPro:IPR004240); BEST Arabidopsis thaliana protein match is: endomembrane protein 70, putative (TAIR:AT1G14670.1); Has 1019 Blast hits to 986 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 444; Fungi - 148; Plants - 242; Viruses - 0; Other Eukaryotes - 185 (source: NCBI BLink).	Unigene15896_All//0.00E+00//gi|48814563|gb|CO115876.1|CO115876				nr -
Unigene15897_All	1484	0.85	1.13	2.12	2.01	2.58	2.56	2.99	2.45	4.48	4.13E-01	4.09E-01		1.32E+00	4.53E-04	Up	3.55E-01	3.03E-01		3.44E-01	3.22E-01		-2.88E-01	3.03E-01		5.84E-01	3.12E-03		Unigene15897_All//gi|15234617|ref|NP_194739.1|//1.00E-178//tRNA-splicing endonuclease positive effector-related [Arabidopsis thaliana]	Unigene15897_All//3.00E-173//AT4G30100| tRNA-splicing endonuclease positive effector-related	Unigene15897_All//9.00E-27//ES793794				nr -
Unigene15900_All	477	148.96	114.30	77.70	109.03	87.35	102.26	82.34	46.88	37.75	-3.82E-01	5.89E-10		-9.39E-01	7.25E-45		-3.20E-01	2.35E-06		-9.25E-02	2.94E-01		-8.13E-01	4.89E-25		-1.13E+00	1.03E-43	Down	Unigene15900_All//gi|21780187|gb|AAM77651.1|AF522274_1//3.00E-81//cp10-like protein [Gossypium hirsutum]	Unigene15900_All//8.00E-58//AT5G20720| CPN20 (CHAPERONIN 20); calmodulin binding	Unigene15900_All//0.00E+00//gi|164259395|gb|ES813452.1|ES813452				nr +
Unigene15901_All	1159	20.31	15.61	15.58	24.20	22.40	29.58	13.61	7.21	6.74	-3.80E-01	7.66E-04		-3.83E-01	1.12E-03		-1.11E-01	3.48E-01		2.90E-01	1.65E-03		-9.16E-01	9.85E-13		-1.01E+00	2.09E-15	Down	Unigene15901_All//gi|226533056|ref|NP_001152375.1|//6.00E-71//DAG protein [Zea mays] >gi|195655685|gb|ACG47310.1| DAG protein [Zea mays]	Unigene15901_All//1.00E-66//AT3G06790| plastid developmental protein DAG, putative	Unigene15901_All//0.00E+00//gi|78353596|gb|DT573870.1|DT573870				nr +
Unigene15902_All	840	9.22	10.19	6.09	11.68	10.41	15.16	10.17	11.99	61.75	1.45E-01	5.05E-01		-5.99E-01	5.98E-03		-1.66E-01	4.25E-01		3.76E-01	1.98E-02		2.38E-01	1.72E-01		2.60E+00	1.78E-181	Up	Unigene15902_All//gi|226530657|ref|NP_001146964.1|//3.00E-44//mitochondrial import inner membrane translocase subunit TIM14 [Zea mays] >gi|195604188|gb|ACG23924.1|mitochondrial import inner membrane translocase subunit TIM14 [Zea mays] >gi|195605908|gb|ACG24784.1|mitochondrial import inner membrane translocase subunit TIM14 [Zea mays]	Unigene15902_All//2.00E-35//AT5G03030| DNAJ heat shock N-terminal domain-containing protein	Unigene15902_All//0.00E+00//TC149025				nr +
Unigene15904_All	866	0.66	3.80	1.78	11.96	8.51	4.59	50.24	140.16	89.89	2.52E+00	1.94E-09	Up	1.42E+00	1.36E-02		-4.92E-01	3.37E-03		-1.38E+00	4.87E-14	Down	1.48E+00	7.92E-198	Up	8.39E-01	1.09E-52		Unigene15904_All//gi|18407534|ref|NP_566126.1|//1.00E-36//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|84778472|dbj|BAE73263.1|xylogen like protein 7 [Arabidopsis thaliana]	Unigene15904_All//1.00E-32//AT2G48130| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene15904_All//0.00E+00//gi|109875410|gb|DW504384.1|DW504384				nr +
Unigene15905_All	995	4.05	3.06	4.82	3.40	1.35	0.14	1.02	0.13	0.16	-4.06E-01	1.92E-01		2.51E-01	3.92E-01		-1.33E+00	2.79E-05	Down	-4.64E+00	1.92E-17	Down	-3.02E+00	1.08E-04	Down	-2.67E+00	1.94E-04	Down	Unigene15905_All//gi|115434594|ref|NP_001042055.1|//2.00E-26//Os01g0153500 [Oryza sativa Japonica Group] >gi|113531586|dbj|BAF03969.1|Os01g0153500 [Oryza sativa Japonica Group]						nr -
Unigene15906_All	834	3.32	5.22	2.49	3.29	4.79	3.14	1.06	3.21	1.58	6.52E-01	2.46E-02		-4.17E-01	3.03E-01		5.44E-01	7.75E-02		-6.48E-02	8.82E-01		1.59E+00	1.38E-05	Up	5.66E-01	2.69E-01		Unigene15906_All//gi|15241574|ref|NP_196446.1|//2.00E-55//YLS8; catalytic [Arabidopsis thaliana] >gi|116928866|gb|AAG40036.1|AF324685_1 AT5g08290 [Arabidopsis thaliana] >gi|40530633|gb|AAK52991.1|AF375407_1 AT5g08290/F8L15_20 [Arabidopsis thaliana] >gi|13122294|dbj|BAB32888.1| Diml homolog [Arabidopsis thaliana] >gi|17978897|gb|AAL47418.1|AT5g08290/F8L15_20 [Arabidopsis thaliana]	Unigene15906_All//1.00E-56//AT5G08290| YLS8; catalytic	Unigene15906_All//3.00E-127//gi|3326171|gb|AI055057.1|AI055057		ko03040|Spliceosome		nr -
Unigene15908_All	671	8.03	3.62	5.87	6.01	5.39	3.30	2.65	2.18	1.25	-1.15E+00	1.33E-05	Down	-4.52E-01	9.87E-02		-1.58E-01	6.25E-01		-8.67E-01	3.88E-03		-2.80E-01	5.63E-01		-1.09E+00	1.06E-02		Unigene15908_All//gi|18410169|ref|NP_567011.1|//3.00E-25//catalytic [Arabidopsis thaliana]	Unigene15908_All//2.00E-26//AT3G54970| catalytic					nr +
Unigene15910_All	801	2.68	4.87	2.99	5.29	3.65	4.34	4.06	2.09	1.84	8.63E-01	5.48E-03		1.60E-01	7.03E-01		-5.33E-01	6.42E-02		-2.84E-01	3.98E-01		-9.62E-01	1.77E-03		-1.14E+00	1.61E-04	Down	Unigene15910_All//gi|145326686|ref|NP_001077790.1|//2.00E-53//iron ion binding / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors [Arabidopsis thaliana] >gi|71905463|gb|AAZ52709.1|expressed protein [Arabidopsis thaliana]	Unigene15910_All//1.00E-54//AT1G68050| iron ion binding / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene15910_All//1.00E-175//CO119968				nr -
Unigene15911_All	1067	0.34	0.24	1.05	2.52	3.13	3.22	3.92	1.88	4.74	-5.32E-01	6.27E-01		1.61E+00	2.44E-02		3.12E-01	4.12E-01		3.52E-01	3.41E-01		-1.06E+00	7.66E-05	Down	2.74E-01	2.64E-01		Unigene15911_All//gi|9743334|gb|AAF97958.1|AC000103_8//1.00E-07//F21J9.12 [Arabidopsis thaliana]	Unigene15911_All//5.00E-65//AT4G31570| unknown protein					nr +

Unigene15912_All	1261	10.79	1.77	5.15	28.88	17.23	16.69	10.63	3.75	2.50	-2.61E+00	6.99E-39	Down	-1.07E+00	4.98E-11	Down	-7.45E-01	7.79E-20		-7.91E-01	1.49E-19		-1.50E+00	4.32E-23	Down	-2.09E+00	4.01E-37	Down	Unigene15912_All//gi|83853831|gb|ABC47863.1|//1.00E-131//Heat shock transcription factor (HSF) [Glycine max]	Unigene15912_All//1.00E-88//AT1G46264| AT-HSFB4; DNA binding / transcription factor	Unigene15912_All//0.00E+00//TC156804	HSF			nr -
Unigene15913_All	1166	3.41	10.17	3.01	2.48	3.28	2.09	0.65	0.29	0.58	1.58E+00	7.07E-18	Up	-1.78E-01	6.19E-01		4.04E-01	2.26E-01		-2.45E-01	5.61E-01		-1.19E+00	1.12E-01		-1.68E-01	7.94E-01		Unigene15913_All//gi|18491247|gb|AAL69448.1|//3.00E-44//At2g44600|F16B22.9 [Arabidopsis thaliana]	Unigene15913_All//1.00E-36//AT2G44600| unknown protein	Unigene15913_All//0.00E+00//TC155161				nr -
Unigene15916_All	1417	24.33	24.21	22.25	36.00	35.21	31.59	25.45	15.34	10.77	-7.40E-03	9.63E-01		-1.29E-01	2.30E-01		-3.18E-02	7.62E-01		-1.89E-01	1.43E-02		-7.31E-01	2.58E-19		-1.24E+00	7.42E-47	Down	Unigene15916_All//gi|115483711|ref|NP_001065227.1|//1.00E-101//Os11g0102600 (Oryza sativa Japonica Group) >gi|115488856|ref|NP_001065234.1|Os12g0102200 (Oryza sativa Japonica Group) >gi|113644221|dbj|BAF27362.1|Os11g0102600 (Oryza sativa Japonica Group) >gi|113648422|dbj|BAF28934.1|Os12g0102200 (Oryza sativa Japonica Group)	Unigene15916_All//6.00E-94//AT3G55000| TONIA (TONNEAU 1)	Unigene15916_All//0.00E+00//TC173174				nr +
Unigene15917_All	2217	1.06	0.09	0.43	9.19	6.71	2.20	10.07	2.68	2.93	-3.54E+00	1.72E-09	Down	-1.30E+00	3.68E-03		-4.54E-01	5.99E-05		-2.06E+00	1.91E-47	Down	-1.91E+00	6.52E-53	Down	-1.78E+00	1.30E-49	Down	Unigene15917_All//gi|224118654|ref|XP_002317874.1|//0.00E+00//auxin efflux carrier component [Populus trichocarpa] >gi|222858547|gb|EEE96094.1| auxin efflux carrier component [Populus trichocarpa]	Unigene15917_All//0.00E+00//AT1G73590| PIN1 (PIN-FORMED 1); transporter	Unigene15917_All//0.00E+00//TC142535				nr +
Unigene15918_All	699	37.72	97.42	60.41	29.58	28.23	27.72	12.64	3.71	4.62	1.37E+00	9.84E-81	Up	6.79E-01	1.15E-15		-6.72E-02	6.42E-01		-9.35E-02	5.35E-01		-1.77E+00	2.44E-19	Down	-1.45E+00	3.09E-15	Down	Unigene15918_All//gi|225461183|ref|XP_002283133.1|//5.00E-11//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene15918_All//8.00E-07//AT5G54585| unknown protein	Unigene15918_All//0.00E+00//TC158636				nr -
Unigene15919_All	804	15.75	21.11	13.51	23.85	17.17	22.24	12.88	10.14	5.00	4.23E-01	1.80E-03		-2.21E-01	2.19E-01		-4.74E-01	4.89E-05		-1.01E-01	5.12E-01		-3.46E-01	3.40E-02		-1.36E+00	3.56E-16	Down			Unigene15919_All//4.00E-37//TC178925				
Unigene15921_All	1069	6.46	1.23	2.69	1.91	1.45	2.11	3.32	1.21	1.53	-2.39E+00	3.54E-18	Down	-1.26E+00	1.47E-07	Down	-3.98E-01	3.95E-01		1.45E-01	7.46E-01		-1.45E+00	2.12E-06	Down	-1.12E+00	9.97E-05	Down	Unigene15921_All//gi|6715637|gb|AAF26464.1|AC007323_5//2.00E-77//T25K16.17 [Arabidopsis thaliana]	Unigene15921_All//3.00E-99//AT1G01180| unknown protein					nr +
Unigene15923_All	1638	1.76	1.70	0.94	4.71	3.83	1.99	5.24	2.55	2.09	-4.62E-02	9.09E-01		-8.98E-01	2.06E-02		-3.01E-01	1.63E-01		-1.25E+00	3.82E-09	Down	-1.04E+00	8.49E-09	Down	-1.32E+00	5.38E-13	Down	Unigene15923_All//gi|195536980|dbj|BAG68210.1|//0.00E+00//lectin receptor kinase-like protein [Nicotiana benthamiana]	Unigene15923_All//3.00E-157//AT3G53380| lectin protein kinase family protein	Unigene15923_All//0.00E+00//gi|164365651|gb|ES850433.1|ES850433		ko04626|Plant-pathogen interaction		nr -
Unigene15928_All	894	16.56	12.70	20.43	14.04	7.01	9.55	0.95	1.36	1.29	-3.84E-01	9.06E-03		3.03E-01	2.91E-02		-1.00E+00	1.44E-11	Down	-5.56E-01	3.61E-04		5.19E-01	3.72E-01		4.50E-01	4.17E-01		Unigene15928_All//gi|225454743|ref|XP_002273566.1|//4.00E-34//PREDICTED: similar to S-norcoclaurine synthase 2 [Vitis vinifera]	Unigene15928_All//6.00E-05//AT5G45860| Bet v I allergen family protein	Unigene15928_All//0.00E+00//TC153994				nr +
Unigene15929_All	682	3.53	8.47	2.89	1.61	1.06	3.24	34.28	12.01	7.30	1.26E+00	9.64E-07	Up	-2.89E-01	5.12E-01		-6.00E-01	3.53E-01		1.01E+00	2.05E-02		-1.51E+00	5.06E-40	Down	-2.23E+00	1.30E-69	Down	Unigene15929_All//gi|21617992|gb|AAM67042.1|//5.00E-34//structural protein-like protein [Arabidopsis thaliana]		Unigene15929_All//2.00E-146//DW504066		ko03040|Spliceosome		nr -
Unigene15930_All	565	50.84	19.91	23.00	73.27	71.80	93.60	90.47	40.46	39.49	-1.35E+00	5.48E-34	Down	-1.14E+00	2.68E-25	Down	-2.93E-02	8.09E-01		3.53E-01	5.56E-07		-1.16E+00	8.15E-58	Down	-1.20E+00	2.37E-62	Down	Unigene15930_All//gi|209967437|gb|ACJ02347.1|//4.00E-39//60S ribosomal protein L17 [Vernicia fordii]	Unigene15930_All//2.00E-27//AT1G27400| 60S ribosomal protein L17 (RPL17A)	Unigene15930_All//0.00E+00//gi|21095604|gb|BQ407917.1|BQ407917		ko03010|Ribosome		nr +
Unigene15934_All	583	25.85	18.77	18.54	53.66	52.80	48.11	39.60	27.31	14.90	-4.61E-01	1.37E-03		-4.79E-01	1.37E-03		-2.32E-02	8.38E-01		-1.58E-01	1.41E-01		-5.36E-01	1.23E-07		-1.41E+00	9.64E-37	Down	Unigene15934_All//gi|115475611|ref|NP_001061402.1|//3.00E-25//Os08g0266200 (Oryza sativa Japonica Group) >gi|113623371|dbj|BAF23316.1|Os08g0266200 (Oryza sativa Japonica Group)	Unigene15934_All//2.00E-17//AT1G79660| unknown protein	Unigene15934_All//0.00E+00//gi|164309460|gb|ES798504.1|ES798504				nr -
Unigene15935_All	1153	0.95	0.97	0.32	0.56	1.73	2.43	1.17	0.94	2.21	2.09E-02	9.87E-01		-1.56E+00	3.05E-02		1.62E+00	5.51E-04	Up	2.11E+00	5.37E-07	Up	-3.16E-01	5.76E-01		9.14E-01	7.82E-03		Unigene15935_All//gi|18412730|ref|NP_567145.1|//1.00E-107//protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] >gi|229904900|sp|Q93YS2.2|PC51_ARATH RecName: Full=Probable protein phosphatase 2C 51; Short=AtPP2C51	Unigene15935_All//3.00E-102//AT3G63340| protein phosphatase 2C-related / PP2C-related	Unigene15935_All//0.00E+00//C0083918				nr +
Unigene15936_All	507	27.55	153.71	81.40	50.99	66.77	132.73	80.06	69.25	79.83	2.48E+00	2.98E-206	Up	1.56E+00	3.43E-58	Up	3.89E-01	6.71E-06		1.38E+00	8.59E-87	Up	-2.09E-01	7.01E-03		-4.00E-03	9.71E-01		Unigene15936_All//gi|29838631|gb|AAM75140.1|//2.00E-71//alkaline alpha galactosidase II [Cucumis melo]	Unigene15936_All//5.00E-61//AT3G57520| AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase, hydrolyzing O-glycosyl compounds	Unigene15936_All//0.00E+00//gi|78353262|gb|DT573536.1|DT573536		ko00052|Galactose metabolism		nr -
Unigene15938_All	513	24.07	50.18	30.41	20.20	15.24	25.62	61.32	84.98	69.27	1.06E+00	6.78E-21	Up	3.38E-01	2.48E-02		-4.07E-01	1.82E-02		3.43E-01	3.23E-02		4.71E-01	5.61E-11		1.76E-01	3.32E-02		Unigene15938_All//gi|192910838|gb|ACF06527.1|//7.00E-23//secretory carrier membrane protein [Elaeis guineensis]	Unigene15938_All//4.00E-14//AT1G61250| SC3 (SECRETORY CARRIER 3); transmembrane transporter	Unigene15938_All//1.00E-143//gi|78343519|gb|DT563793.1|DT563793				nr -
Unigene15939_All	779	5.24	8.00	6.90	50.07	45.84	47.95	57.04	93.36	23.42	6.11E-01	9.93E-03		3.98E-01	1.45E-01		-1.27E-01	1.78E-01		-6.25E-02	5.76E-01		7.11E-01	2.63E-36		-1.28E+00	1.22E-60	Down	Unigene15939_All//gi|48310594|gb|AAT41845.1|//2.00E-14//At1g72240 [Arabidopsis thaliana]		Unigene15939_All//3.00E-124//gi|13352806|gb|BG443154.1|BG443154				nr +
Unigene1594_All	2368	4.93	6.61	8.05	8.88	9.15	7.59	13.21	12.20	6.36	4.24E-01	2.77E-03		7.08E-01	5.94E-08		4.31E-02	8.07E-01		-2.26E-01	7.73E-02		-1.16E-01	2.42E-01		-1.06E+00	1.31E-31	Down	Unigene1594_All//gi|224112407|ref|XP_002316177.1|//0.00E+00//tubulin gamma complex-associated protein [Populus trichocarpa] >gi|222865217|gb|EEF02348.1|tubulin gamma complex-associated protein [Populus trichocarpa]	Unigene1594_All//0.00E+00//AT5G17410| tubulin family protein	Unigene1594_All//0.00E+00//TC160669				nr -
Unigene15940_All	1449	2.60	4.27	0.81	8.90	9.32	7.42	7.94	1.33	2.25	7.15E-01	2.65E-03		-1.69E+00	2.07E-06	Down	6.52E-02	7.54E-01		-2.63E-01	1.19E-01		-2.58E+00	9.81E-40	Down	-1.82E+00	1.22E-26	Down	Unigene15940_All//gi|150036249|gb|ABR67412.1|//1.00E-121//microtubule binding protein [Cucumis melo]	Unigene15940_All//1.00E-96//AT3G05330| ATN (TANGLED)	Unigene15940_All//0.00E+00//DR461156				nr +
Unigene15941_All	849	10.48	13.25	8.47	20.13	17.56	17.71	56.87	31.56	27.87	3.39E-01	5.12E-02		-3.07E-01	1.45E-01		-1.97E-01	1.71E-01		-1.84E-01	2.24E-01		-8.50E-01	5.99E-33		-1.03E+00	2.20E-46	Down	Unigene15941_All//gi|17933310|gb|AAL48237.1|AF446365_1//3.00E-84//At1g10950/T19D16_13 [Arabidopsis thaliana] >gi|15451172|gb|AAK96857.1|endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana] >gi|20148415|gb|AAM10098.1|endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]	Unigene15941_All//1.00E-63//AT1G10950| endomembrane protein 70, putative	Unigene15941_All//0.00E+00//TC151158				nr +
Unigene15948_All	807	2.46	2.13	2.24	7.35	3.84	1.85	4.82	6.11	8.59	-2.07E-01	6.31E-01		-1.35E-01	7.68E-01		-9.36E-01	3.40E-05		-1.99E+00	1.55E-13	Down	3.43E-01	1.80E-01		8.34E-01	1.90E-05		Unigene15948_All//gi|87240982|gb|ABD32840.1|//1.00E-111//Peptidase C1A, papain; Somatotropin hormone; Peptidase C1, propeptide [Medicago truncatula]	Unigene15948_All//6.00E-107//AT1G02305| cathepsin B-like cysteine protease, putative	Unigene15948_All//0.00E+00//TC134626				nr -
Unigene15949_All	1372	10.03	8.20	9.35	15.29	15.91	14.71	14.08	8.10	6.85	-2.91E-01	6.39E-02		-1.01E-01	5.88E-01		5.80E-02	7.07E-01		-5.50E-02	6.92E-01		-7.97E-01	2.36E-12		-1.04E+00	2.10E-19	Down	Unigene15949_All//gi|297852898|ref|XP_002884330.1|//1.00E-109//RWD domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297340172|gb|EFH70589.1| RWD domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene15949_All//2.00E-73//AT1G51730| RWD domain-containing protein	Unigene15949_All//0.00E+00//TC137356				nr -
Unigene1595_All	1104	9.48	7.71	7.96	10.74	11.35	9.98	15.66	9.73	6.53	-2.98E-01	1.05E-01		-2.52E-01	2.01E-01		8.03E-02	6.90E-01		-1.06E-01	6.21E-01		-6.87E-01	8.77E-09		-1.26E+00	1.63E-23	Down	Unigene1595_All//gi|22331623|ref|NP_190206.2|//2.00E-77//atNUDT9 (Arabidopsis thaliana Nudix hydrolase homolog 9); hydrolase >gi|68565917|sp|Q8YYK2.1|NUDT9_ARATH RecName: Full=Nudix hydrolase 9; Short=AtNUDT9	Unigene1595_All//1.00E-78//AT3G46200| atNUDT9 (Arabidopsis thaliana Nudix hydrolase homolog 9); hydrolase	Unigene1595_All//0.00E+00//TC151693				nr +
Unigene15950_All	1107	2.22	0.46	1.83	4.32	3.76	1.80	1.26	0.38	0.07	-2.28E+00	1.43E-06	Down	-2.81E-01	5.20E-01		-1.99E-01	5.31E-01		-1.27E+00	4.84E-06	Down	-1.74E+00	1.29E-03		-4.13E+00	3.70E-08	Down	Unigene15950_All//gi|124359162|gb|ABN05685.1|//3.00E-09//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene15950_All//2.00E-08//AT2G13980| nucleic acid binding	Unigene15950_All//3.00E-115//gi|78323420|gb|DT543694.1|DT543694				nr +
Unigene15952_All	1352	1.59	2.17	1.22	15.77	14.70	22.82	5.25	16.23	13.91	4.54E-01	2.21E-01		-3.78E-01	4.04E-01		-1.02E-01	4.81E-01		5.33E-01	1.61E-08		1.63E+00	1.21E-41	Up	1.40E+00	1.26E-29	Up	Unigene15952_All//gi|3435279|gb|AAC78477.1|//1.00E-148//protein kinase homolog [Arabidopsis thaliana]	Unigene15952_All//2.00E-138//AT1G53700| WAG1 (WAG 1); kinase/ protein serine/threonine kinase					nr +
Unigene15953_All	1580	7.75	21.20	20.39	15.61	24.56	30.21	15.01	21.16	18.48	1.45E+00	1.08E-43	Up	1.40E+00	1.61E-38	Up	6.54E-01	2.27E-16		9.53E-01	2.15E-34		4.95E-01	2.24E-09		3.00E-01	6.66E-04		Unigene15953_All//gi|57282619|emb|CAE53307.1|//1.00E-164//cysteine proteinase [Gossypium hirsutum]	Unigene15953_All//1.00E-128//AT5G43060| cysteine proteinase, putative / thiol protease, putative	Unigene15953_All//0.00E+00//TC151085				nr +
Unigene15954_All	832	15.53	44.52	23.62	17.18	17.05	25.13	29.68	44.81	36.25	1.52E+00	1.46E-51	Up	6.05E-01	2.39E-06		-1.11E-02	9.58E-01		5.49E-01	2.80E-06		5.94E-01	4.44E-14		2.89E-01	8.89E-04		Unigene15954_All//gi|15231750|ref|NP_190880.1|//3.00E-39//VPS37-1 [Arabidopsis thaliana] >gi|75202732|sp|Q9SCP9.1|VPS71_ARATH RecName: Full=Vacuolar protein-sorting-associated protein 37 homolog 1; Short=AtVPS37-1; AltName: Full=ESCRT-I complex subunit VPS37 homolog 1	Unigene15954_All//1.00E-40//AT3G53120| VPS37-1	Unigene15954_All//0.00E+00//gi|21097987|gb|BQ410300.1|BQ410300		ko04144|Endocytosis		nr -
Unigene15955_All	814	6.30	25.40	8.64	10.71	8.84	11.54	20.78	36.82	18.65	2.01E+00	1.17E-42	Up	4.55E-01	5.11E-02		-2.77E-01	1.75E-01		1.08E-01	6.25E-01		8.25E-01	9.01E-20		-1.56E-01	2.28E-01		Unigene15955_All//gi|18410249|ref|NP_565053.1|//8.00E-25//VPS46.2 [Arabidopsis thaliana] >gi|297839171|ref|XP_002887467.1|SNF7 family protein [Arabidopsis lyrata subsp. lyrata] >gi|50030962|gb|AAD55650.1|AC008017_23 Highly similar to developmental protein DG1118 [Arabidopsis thaliana] >gi|166489863|gb|AAL24333.1| Highly similar to developmental protein DG1118 [Arabidopsis thaliana] >gi|20148889|gb|AAM10235.1|similar to developmental protein DG1118 [Arabidopsis thaliana] >gi|297333308|gb|EFH63726.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15955_All//4.00E-26//AT1G73030| VPS46.2	Unigene15955_All//0.00E+00//TC175541		ko04144|Endocytosis		nr -
Unigene15956_All	670	150.87	418.59	110.47	35.69	28.32	118.91	50.99	684.95	254.55	1.47E+00	0.00E+00	Up	-4.50E-01	1.09E-17		-3.34E-01	1.71E-03		1.74E+00	2.03E-143	Up	3.75E+00	0.00E+00	Up	2.32E+00	0.00E+00	Up	Unigene15956_All//gi|89276793|gb|ABB66595.1|//2.00E-74//iron-binding protein [Pyrus pyrifolia]	Unigene15956_All//7.00E-58//AT5G01600| ATFER1; ferric iron binding / iron ion binding	Unigene15956_All//0.00E+00//gi|109848332|gb|DW477312.1|DW477312		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene15958_All	471	3.11	2.15	5.20	2.43	2.34	2.68	17.33	12.51	4.99	-5.32E-01	3.39E-01		7.42E-01	8.07E-02		-5.62E-02	9.17E-01		1.42E-01	8.21E-01		-4.70E-01	1.02E-02		-1.80E+00	7.26E-19	Down			Unigene15958_All//1.00E-162//gi|13246852|gb|BE055715.2|BE055715				

Unigene15960_All	1392	7.78	2.48	3.29	10.52	8.19	9.70	31.95	15.61	13.39	-1.65E+00	1.35E-17	Down	-1.24E+00	3.46E-11	Down	-3.62E-01	1.06E-02		-1.17E-01	5.04E-01		-1.03E+00	7.06E-42	Down	-1.25E+00	1.53E-58	Down	Unigene15960_All//gi|224125966|ref|XP_002329628.1|//1.00E-119//porin/voltage-dependent anion-selective channel protein [Populus trichocarpa] >gi|222870509|gb|EEF07640.1|porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	Unigene15960_All//6.00E-102//AT4G57490| VDAC4 (VOLTAGE DEPENDENT ANION CHANNEL 4); voltage-gated anion channel	Unigene15960_All//0.00E+00//TC150815				nr -
Unigene15964_All	563	47.67	19.80	19.39	69.10	64.41	75.81	98.60	29.92	44.65	-1.27E+00	7.74E-29	Down	-1.30E+00	9.43E-29	Down	-1.02E-01	3.16E-01		1.34E-01	1.45E-01		-1.72E+00	4.88E-113	Down	-1.14E+00	5.86E-63	Down	Unigene15964_All//gi|46397044|sp|Q96GL0.1|RL35_EUPES//1.00E-39//RecName: Full=60S ribosomal protein L35 >gi|6981224|gb|AAF34800.1|AF227980_1 60S ribosomal protein L35 [Euphorbia esula]	Unigene15964_All//6.00E-40//AT5G02610| 60S ribosomal protein L35 (RPL35D)	Unigene15964_All//0.00E+00//gi|11202107|gb|BF271112.1|BF271112		ko03010|Ribosome		nr -
Unigene15965_All	1446	3.08	2.52	1.36	3.65	5.57	5.40	6.40	1.85	4.41	-2.86E-01	3.50E-01		-1.17E+00	1.21E-04	Down	6.10E-01	1.84E-03		5.65E-01	6.44E-03		-1.79E+00	1.48E-20	Down	-5.39E-01	9.91E-04		Unigene15965_All//gi|15233463|ref|NP_193185.1|//1.00E-60//forkhead-associated domain-containing protein / FHA domain-containing protein [Arabidopsis thaliana] >gi|73921130|sp|Q23305.1|Y4419_ARATH RecName: Full=FHA domain-containing protein At4g14490	Unigene15965_All//7.00E-28//AT4G14490| forkhead-associated domain-containing protein / FHA domain-containing protein	Unigene15965_All//0.00E+00//gi|21089510|gb|BQ401823.1|BQ401823				nr +
Unigene15968_All	1303	4.06	13.69	8.91	6.77	8.32	10.12	12.69	15.36	18.31	1.75E+00	8.60E-31	Up	1.14E+00	1.77E-10	Up	2.99E-01	9.63E-02		5.81E-01	1.34E-04		2.76E-01	1.49E-02		5.30E-01	5.98E-08		Unigene15968_All//gi|9757978|dbj|BAB08314.1|//6.00E-80//ADP-ribosylation factor-like protein [Arabidopsis thaliana]	Unigene15968_All//1.00E-68//AT5G37680| ATARLA1A (ADP-ribosylation factor-like A1A); GTP binding	Unigene15968_All//0.00E+00//TC167925				nr -
Unigene15969_All	622	4.12	3.83	3.34	7.21	5.54	6.32	4.42	1.68	1.35	-1.06E-01	7.76E-01		-3.04E-01	4.70E-01		-3.81E-01	1.93E-01		-1.90E-01	5.69E-01		-1.40E+00	7.24E-05	Down	-1.72E+00	1.54E-06	Down	Unigene15969_All//gi|297795907|ref|XP_002865838.1|//3.00E-53//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311673|gb|EFH42097.1|short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15969_All//9.00E-54//AT5G31030| short-chain dehydrogenase/reductase (SDR) family protein	Unigene15969_All//0.00E+00//TC177651				nr -
Unigene15972_All	775	18.23	13.01	15.25	30.15	32.17	29.72	53.14	28.42	14.34	-4.87E-01	1.12E-03		-2.57E-01	1.20E-01		9.37E-02	4.94E-01		-2.05E-02	8.94E-01		-9.03E-01	3.51E-31		-1.89E+00	2.05E-98	Down	Unigene15972_All//gi|224144252|ref|XP_002325236.1|//6.00E-46//glutaredoxin C4 [Populus trichocarpa] >gi|222866670|gb|EEF03801.1|glutaredoxin C4 [Populus trichocarpa]	Unigene15972_All//1.00E-45//AT5G20500| glutaredoxin, putative	Unigene15972_All//0.00E+00//gi|109857910|gb|DW486889.1|DW486889				nr +
Unigene15973_All	889	149.84	78.65	111.53	224.47	246.74	190.26	98.59	174.66	201.16	-9.30E-01	3.70E-85		-4.26E-01	5.55E-21		1.37E-01	2.99E-05		-2.39E-01	5.07E-12		8.25E-01	5.62E-99		1.03E+00	2.53E-168	Up	Unigene15973_All//gi|115488050|ref|NP_001066512.1|//9.00E-18//Os12g0257500 [Oryza sativa Japonica Group] >gi|77554187|gb|ABA96983.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649019|dbj|BAF29531.1|Os12g0257500 [Oryza sativa Japonica Group]	Unigene15973_All//1.00E-44//AT3G11810| unknown protein	Unigene15973_All//0.00E+00//gi|48829453|gb|CO127843.1|CO127843				nr -
Unigene15974_All	1641	2.36	1.61	2.66	6.89	10.32	12.33	6.21	6.42	13.89	-5.55E-01	7.54E-02		1.74E-01	6.06E-01		5.83E-01	3.77E-06		8.39E-01	3.86E-12		4.78E-02	7.94E-01		1.16E+00	8.22E-27	Up	Unigene15974_All//gi|15810000|gb|AL06927.1|//4.00E-23//AT5g23340/MKD15_20 [Arabidopsis thaliana] >gi|22137014|gb|AAM91352.1|At5g23340/MKD15_20 [Arabidopsis thaliana]	Unigene15974_All//5.00E-20//AT5G23340| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Leucine-rich repeat, cysteine-containing subtype (InterPro:IPR006553); BEST Arabidopsis thaliana protein match is: F-box family protein (FBL4) (TAIR:AT4G15475.1); Has 9095 Blast hits to 3545 proteins in 210 species: Archae - 0; Bacteria - 454; Metazoa - 4575; Fungi - 774; Plants - 2118; Viruses - 15; Other Eukaryotes - 1159 (source: NCBI BLink).	Unigene15974_All//0.00E+00//TC170258		ko04626|Plant-pathogen interaction//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene15975_All	644	3.01	2.36	6.37	8.04	10.75	9.89	1.51	0.19	1.24	-3.49E-01	4.53E-01		1.08E+00	6.38E-04	Up	4.18E-01	6.39E-02		2.98E-01	2.43E-01		-2.96E+00	1.89E-04	Down	-2.88E-01	6.35E-01		Unigene15975_All//gi|297803408|ref|XP_002869588.1|//2.00E-39//AT-HF [Arabidopsis lyrata subsp. lyrata] >gi|297315424|gb|EFH45847.1| AT-HF [Arabidopsis lyrata subsp. lyrata]	Unigene15975_All//6.00E-34//AT4G26900| AT-HF (HIS HF); imidazoleglycerol-phosphate synthase	Unigene15975_All//7.00E-115//gi|78345861|gb|DT566135.1|DT566135		ko00340|Histidine metabolism		nr -
Unigene15977_All	226	0.00	0.00	0.00	0.00	0.00	0.40	2.25	0.00	0.18	null	null		null	null		null	null		8.64E+00	4.77E-01		-1.11E+01	8.89E-04	Down	-3.67E+00	3.75E-03		Unigene15977_All//gi|15220307|ref|NP_172585.1|//2.00E-32//BFN1 (BIFUNCTIONAL NUCLEASE I); T/G mismatch-specific endonuclease/ endoribonuclease, producing 5'-phosphomonoesters / nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease [Arabidopsis thaliana] >gi|5734731|gb|AAD49996.1|AC007259_9 bifunctional nuclease bfn1 [Arabidopsis thaliana] >gi|21594013|gb|AAM65931.1|bifunctional nuclease bfn1 [Arabidopsis thaliana]	Unigene15977_All//3.00E-33//AT1G11190| BFN1 (BIFUNCTIONAL NUCLEASE I); T/G mismatch-specific endonuclease/ endoribonuclease, producing 5'-phosphomonoesters / nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease	Unigene15977_All//4.00E-111//DW495821				nr -
Unigene15978_All	1276	1.15	3.53	3.17	55.01	31.52	21.84	20.94	11.86	11.68	1.62E+00	1.56E-07	Up	1.47E+00	9.64E-06	Up	-8.03E-01	3.37E-43		-1.33E+00	4.17E-87	Down	-8.21E-01	1.43E-17		-8.43E-01	6.59E-19		Unigene15978_All//gi|50657596|gb|AAT79582.1|//1.00E-135//endonuclease [Solanum tuberosum]	Unigene15978_All//4.00E-133//AT1G11190| BFN1 (BIFUNCTIONAL NUCLEASE I); T/G mismatch-specific endonuclease/ endoribonuclease, producing 5'-phosphomonoesters / nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease	Unigene15978_All//0.00E+00//DW495821				nr -
Unigene15980_All	811	6.00	3.81	3.74	10.75	9.64	7.91	2.50	1.55	0.79	-6.55E-01	1.60E-02		-6.81E-01	1.67E-02		-1.57E-01	4.93E-01		-4.43E-01	2.51E-02		-6.95E-01	8.83E-02		-1.67E+00	6.85E-05	Down	Unigene15980_All//gi|70663492|emb|CAJ15145.1|//2.00E-60//sialyltransferase-like protein [Gossypium raimondii]	Unigene15980_All//5.00E-14//AT1G08280| glycosyl transferase family 29 protein / sialyltransferase family protein	Unigene15980_All//0.00E+00//TC129588				nr +
Unigene15981_All	733	4.43	9.33	6.39	10.13	7.09	8.38	5.48	2.91	1.79	1.08E+00	2.88E-06	Up	5.31E-01	7.12E-02		-5.13E-01	1.20E-02		-2.73E-01	2.42E-01		-9.14E-01	7.76E-04		-1.61E+00	1.84E-08	Down	Unigene15981_All//gi|66968188|gb|AAV59532.1|//5.00E-18//expansin [Gossypium hirsutum]	Unigene15981_All//8.00E-18//AT2G39700| ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	Unigene15981_All//0.00E+00//gi|13355875|gb|BG446307.1|BG446307				nr +
Unigene15982_All	1074	2.78	1.37	1.98	1.58	2.40	2.61	5.08	2.22	4.45	-1.02E+00	5.06E-03		-4.86E-01	2.11E-01		6.09E-01	1.31E-01		7.25E-01	5.78E-02		-1.20E+00	3.62E-07	Down	-1.90E-01	4.29E-01		Unigene15982_All//gi|115444011|ref|NP_001045785.1|//2.00E-55//Os02g0130600 [Oryza sativa Japonica Group] >gi|113535316|dbj|BAF07699.1|Os02g0130600 [Oryza sativa Japonica Group]	Unigene15982_All//8.00E-91//AT2G47115| unknown protein	Unigene15982_All//0.00E+00//TC147947				nr -
Unigene15985_All	831	1.70	13.35	4.23	2.46	1.57	2.45	6.00	12.83	5.37	2.97E+00	3.76E-36	Up	1.31E+00	1.99E-04	Up	-6.42E-01	1.48E-01		-7.10E-03	9.81E-01		1.10E+00	1.30E-11	Up	-1.61E-01	5.44E-01		Unigene15985_All//gi|164605515|dbj|BAF98581.1|//5.00E-22//CM0216.450.nc [Lotus japonicus]	Unigene15985_All//4.00E-11//AT4G34630| unknown protein	Unigene15985_All//4.00E-09//TC133690				nr +
Unigene15986_All	1204	9.04	14.01	4.29	9.89	9.44	9.83	9.17	10.00	6.88	6.33E-01	2.93E-06		-1.08E+00	4.56E-09	Down	-6.72E-02	7.53E-01		-8.90E-03	9.54E-01		1.25E-01	4.64E-01		-4.13E-01	5.66E-03		Unigene15986_All//gi|186531328|ref|NP_568767.2|//3.00E-84//iron ion binding / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors [Arabidopsis thaliana]	Unigene15986_All//3.00E-76//AT5G51880| iron ion binding / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene15986_All//0.00E+00//gi|164353429|gb|EX169948.1|EX169948				nr +
Unigene15991_All	1225	4.23	4.80	3.87	4.92	6.92	5.71	14.25	4.95	5.95	1.82E-01	4.88E-01		-1.28E-01	6.39E-01		4.91E-01	1.14E-02		2.16E-01	3.91E-01		-1.53E+00	1.78E-30	Down	-1.26E+00	1.10E-23	Down	Unigene15991_All//gi|102139845|gb|ABF70003.1|//1.00E-142//ankyrin repeat family protein / methyltransferase-related [Musa acuminata]	Unigene15991_All//7.00E-140//AT5G65860| ankyrin repeat family protein	Unigene15991_All//0.00E+00//TC133539		ko00350|Tyrosine metabolism//ko00450|Selenoamino acid metabolism//ko00340|Histidine metabolism		nr -
Unigene15992_All	1620	0.48	0.19	0.07	7.10	10.29	2.59	4.15	6.40	1.99	-1.37E+00	9.60E-02		-2.88E+00	6.35E-03		5.35E-01	2.92E-05		-1.45E+00	1.03E-16	Down	6.25E-01	7.52E-05		-1.06E+00	1.57E-07	Down	Unigene15992_All//gi|224082844|ref|XP_002306863.1|//1.00E-166//GRAS family transcription factor [Populus trichocarpa] >gi|222856312|gb|EEE93859.1| GRAS family transcription factor [Populus trichocarpa]	Unigene15992_All//2.00E-107//AT3G54220| SCR (SCARECROW); protein binding / protein homodimerization/ sequence-specific DNA binding / transcription factor		GRAS			nr +
Unigene15993_All	664	16.31	54.94	54.21	18.68	8.09	26.39	2.80	5.16	3.48	1.75E+00	3.43E-62	Up	1.73E+00	7.41E-59	Up	-1.21E+00	2.35E-15	Down	4.99E-01	1.25E-04		8.82E-01	3.09E-03		3.13E-01	4.08E-01		Unigene15993_All//gi|79325121|ref|NP_001031645.1|//2.00E-22//zinc ion binding [Arabidopsis thaliana]	Unigene15993_All//1.00E-21//AT4G15248| zinc ion binding	Unigene15993_All//0.00E+00//TC167796	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr -
Unigene15994_All	766	63.11	74.42	47.55	50.92	43.70	59.55	39.91	145.68	16.75	2.38E-01	8.02E-04		-4.09E-01	1.73E-07		-2.21E-01	9.04E-03		2.26E-01	4.92E-03		1.87E+00	2.14E-253	Up	-1.25E+00	1.98E-40	Down	Unigene15994_All//gi|20466362|gb|AAM20498.1|//3.00E-50//calmodulin-like protein [Arabidopsis thaliana] >gi|22136314|gb|AAM91235.1|calmodulin-like protein [Arabidopsis thaliana]	Unigene15994_All//5.00E-44//AT3G50770| calmodulin-related protein, putative	Unigene15994_All//0.00E+00//TC135423		ko04626|Plant-pathogen interaction		nr -
Unigene15995_All	718	276.40	200.07	200.91	340.24	209.35	317.02	37.16	150.65	66.53	-4.66E-01	7.99E-38		-4.60E-01	1.17E-35		-7.01E-01	5.57E-118		-1.02E-01	2.32E-03		2.02E+00	1.69E-272	Up	8.40E-01	9.74E-33		Unigene15995_All//gi|39841350|gb|AAR31185.1|//9.00E-41//serine O-acetyltransferase 1 [Glycine max]	Unigene15995_All//3.00E-28//AT3G13110| ATSERAT2;2 (SERINE ACETYLTRANSFERASE 2;2); serine O-acetyltransferase	Unigene15995_All//0.00E+00//TC165199		ko00270|Cysteine and methionine metabolism//ko00920|Sulfur metabolism		nr -
Unigene15997_All	2279	0.39	0.02	0.35	2.40	2.24	6.66	2.02	4.81	3.79	-4.14E+00	2.52E-04	Down	-1.55E-01	8.24E-01		-1.05E-01	7.35E-01		1.47E+00	7.57E-22	Up	1.25E+00	1.75E-14	Up	9.08E-01	1.87E-07		Unigene15997_All//gi|297792837|ref|XP_002864303.1|//0.00E+00//calcium ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297310138|gb|EFH40562.1|calcium ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene15997_All//0.00E+00//AT5G54130| calcium-binding EF hand family protein	Unigene15997_All//8.00E-13//TC173904		ko03018|RNA degradation		nr +

Unigene15998_All	1205	16.93	3.15	4.64	22.36	10.75	25.04	35.23	7.32	7.70	-2.42E+00	2.15E-53	Down	-1.87E+00	5.30E-37	Down	-1.06E+00	1.38E-26	Down	1.63E-01	1.36E-01		-2.27E+00	1.83E-124	Down	-2.19E+00	4.02E-123	Down	Unigene15998_All//gi|297810699|ref|XP_002873233.1|//1.00E-58//mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319070|gb|EFH49492.1| mitochondrial glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene15998_All//2.00E-55//AT5G05990| mitochondrial glycoprotein family protein / MAM33 family protein	Unigene15998_All//0.00E+00//TC170771				nr +
Unigene15999_All	844	70.67	74.98	91.04	26.26	19.71	22.85	14.13	9.06	4.39	8.55E-02	2.52E-01		3.65E-01	1.80E-09		-4.15E-01	1.33E-04		-2.01E-01	1.14E-01		-6.41E-01	1.14E-05		-1.69E+00	5.87E-25	Down	Unigene15999_All//gi|15294156|gb|AK95255.1|AF410269_1//9.00E-32//At1g52220/F9I5_10 [Arabidopsis thaliana] >gi|20453285|gb|AAM19881.1| At1g52220/F9I5_10 [Arabidopsis thaliana]	Unigene15999_All//2.00E-24//AT1G52220| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: PSI-P (PHOTOSYSTEM I P SUBUNIT); DNA binding (TAIR:AT2G46820.2); Has 203 Blast hits to 203 proteins in 35 species: Archae - 0; Bacteria - 66; Metazoa - 0; Fungi - 0; Plants - 136; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene15999_All//0.00E+00//TC151585				nr +
Unigene16_All	774	3.58	5.50	3.51	7.21	5.96	5.66	6.77	18.36	14.51	6.18E-01	3.65E-02		-3.01E-02	9.55E-01		-2.74E-01	3.18E-01		-3.49E-01	1.95E-01		1.44E+00	7.37E-23	Up	1.10E+00	1.36E-12	Up	Unigene16_All//gi|240256140|ref|NP_001078484.4|//8.00E-53//1-phosphatidylinositol-4-phosphate 5-kinase/ ATP binding / phosphatidylinositol phosphate kinase/ protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene16_All//6.00E-48//AT4G33240| 1-phosphatidylinositol-4-phosphate 5-kinase/ ATP binding / phosphatidylinositol phosphate kinase/ protein binding / zinc ion binding	Unigene16_All//7.00E-137//TC156998		ko04145|Phagosome//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene16003_All	980	2.35	0.41	3.31	7.88	8.47	5.71	4.01	1.41	3.70	-2.51E+00	7.85E-07	Down	4.97E-01	1.72E-01		1.04E-01	6.70E-01		-4.63E-01	2.87E-02		-1.51E+00	2.31E-07	Down	-1.17E-01	6.78E-01		Unigene16003_All//gi|297831152|ref|XP_002883458.1|//3.00E-71//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329298|gb|EFH59717.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16003_All//1.00E-62//AT3G23750| leucine-rich repeat family protein / protein kinase family protein					nr +
Unigene16004_All	747	4.41	8.28	14.19	9.27	5.30	3.02	90.62	95.17	68.74	9.07E-01	1.54E-04		1.68E+00	5.52E-17	Up	-8.06E-01	9.23E-05		-1.62E+00	6.39E-12	Down	7.08E-02	2.87E-01		-3.99E-01	8.49E-13		Unigene16004_All//gi|224112855|ref|XP_002332708.1|//1.00E-20//predicted protein [Populus trichocarpa] >gi|222832962|gb|EEE71439.1| predicted protein [Populus trichocarpa]		Unigene16004_All//0.00E+00//gi|109870167|gb|DW499143.1|DW499143				nr +
Unigene16005_All	1775	2.24	1.43	0.75	10.33	14.74	5.32	4.60	0.85	4.40	-6.50E-01	3.35E-02		-1.58E+00	3.41E-06	Down	5.14E-01	1.93E-07		-9.58E-01	8.36E-14		-2.44E+00	1.19E-26	Down	-6.35E-02	7.45E-01		Unigene16005_All//gi|44681394|gb|AS47637.1|//1.00E-50//At5g51850 [Arabidopsis thaliana] >gi|53828599|gb|AAU94409.1| At5g51850 [Arabidopsis thaliana]	Unigene16005_All//9.00E-64//AT5G62170| unknown protein	Unigene16005_All//4.00E-134//ES848682				nr -
Unigene16007_All	1772	0.06	0.00	0.00	1.57	1.38	1.68	8.02	2.97	2.81	-5.89E+00	3.73E-01		-5.89E+00	3.95E-01		-1.90E-01	6.26E-01		9.56E-02	8.07E-01		-1.43E+00	9.78E-23	Down	-1.51E+00	2.22E-25	Down	Unigene16007_All//gi|297815710|ref|XP_002875738.1|//1.00E-175//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321576|gb|EFH51997.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16007_All//9.00E-168//AT3G45650| NAXT1 (NITRATE EXCRETION TRANSPORTER1); nitrate efflux transmembrane transporter/ transporter	Unigene16007_All//0.00E+00//gi|13354265|gb|BG444613.1|BG444613				nr -
Unigene16008_All	1109	19.72	26.64	34.00	25.24	20.96	21.83	27.07	2.49	5.32	4.34E-01	1.26E-05		7.86E-01	6.23E-18		-2.68E-01	7.32E-03		-2.10E-01	5.40E-02		-3.44E+00	2.57E-137	Down	-2.35E+00	6.93E-95	Down	Unigene16008_All//gi|297607826|ref|NP_001060690.2|//8.00E-91//Os07g0687100 [Oryza sativa Japonica Group] >gi|255678073|dbj|BAF22604.2| Os07g0687100 [Oryza sativa Japonica Group]	Unigene16008_All//1.00E-51//AT4G24380| unknown protein	Unigene16008_All//0.00E+00//TC134194				nr +
Unigene16009_All	1639	22.31	24.30	35.35	8.81	10.78	10.28	0.39	1.17	0.97	1.23E-01	1.91E-01		6.64E-01	1.96E-20		2.90E-01	2.92E-02		2.22E-01	1.33E-01		1.60E+00	2.94E-04	Up	1.33E+00	4.32E-03		Unigene16009_All//gi|33329886|gb|AAQ10316.1|//1.00E-164//lecithine cholesterol acyltransferase-like protein [Medicago truncatula]	Unigene16009_All//3.00E-135//AT1G27480| lecithin:cholesterol acyltransferase family protein / LACT family protein	Unigene16009_All//0.00E+00//CO077523				nr +
Unigene16012_All	900	1.80	3.38	1.83	5.70	4.36	5.72	3.62	2.83	1.42	9.06E-01	1.16E-02		2.54E-02	9.80E-01		-3.86E-01	1.52E-01		5.00E-03	9.87E-01		-3.53E-01	2.79E-01		-1.35E+00	1.29E-05	Down		Unigene16012_All//5.00E-15//TC160880				
Unigene16013_All	1340	5.51	2.68	4.33	14.28	11.41	6.17	8.33	1.00	6.09	-1.04E+00	2.27E-06	Down	-3.46E-01	1.42E-01		-3.23E-01	8.29E-03		-1.21E+00	8.37E-21	Down	-3.06E+00	4.32E-46	Down	-4.51E-01	2.30E-03		Unigene16013_All//gi|33339703|gb|AAQ14331.1|AF283506_1//6.00E-73//MYC1 [Catharanthus roseus]	Unigene16013_All//1.00E-67//AT1G59640| ZCW32; DNA binding / transcription factor	Unigene16013_All//0.00E+00//TC134401	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr +
Unigene16014_All	1240	24.30	10.42	17.74	11.45	9.61	7.65	8.39	5.09	5.91	-1.22E+00	1.63E-30	Down	-4.55E-01	7.30E-06		-2.53E-01	1.01E-01		-5.82E-01	5.97E-05		-7.21E-01	4.99E-06		-5.05E-01	1.00E-03		Unigene16014_All//gi|15236037|ref|NP_193462.1|//1.00E-177//NS1; asparagine-tRNA ligase [Arabidopsis thaliana] >gi|55584148|sp|O48593.3|SYNO_ARATH RecName: Full=Asparaginyl-tRNA synthetase, chloroplastic/mitochondrial; AltName: Full=Asparagine--tRNA ligase; Short=AsnRS; Flags: Precursor >gi|19310458|gb|AAL84964.1| AT4g17300/d14685w [Arabidopsis thaliana]	Unigene16014_All//1.00E-178//AT4G17300| NS1; asparagine-tRNA ligase	Unigene16014_All//0.00E+00//TC138615		ko00970|Aminoacyl-tRNA biosynthesis		nr +
Unigene16015_All	791	1.39	2.43	2.89	11.71	11.58	10.91	5.40	15.90	5.49	8.09E-01	8.28E-02		1.06E+00	1.72E-02		-1.65E-02	9.46E-01		-1.03E-01	6.45E-01		1.56E+00	8.68E-23	Up	2.42E-02	9.51E-01		Unigene16015_All//gi|38566628|gb|AK224204.1|//3.00E-31//At1g32690 [Arabidopsis thaliana] >gi|40824115|gb|AAR92349.1| At1g32690 [Arabidopsis thaliana]	Unigene16015_All//1.00E-25//AT1G32690| unknown protein	Unigene16015_All//0.00E+00//TC173583				nr +
Unigene16016_All	1644	16.39	4.65	7.87	16.09	13.32	10.85	17.00	12.74	10.64	-1.82E+00	1.01E-48	Down	-1.06E+00	5.33E-21	Down	-2.72E-01	8.38E-03		-5.68E-01	2.75E-08		-4.17E-01	5.07E-06		-6.76E-01	9.50E-14		Unigene16016_All//gi|75203068|sp|Q9SD53.1|Y3720_ARATH//6.00E-36//RecName: Full=UPF0481 protein At3g17200	Unigene16016_All//2.00E-43//AT2G36430| unknown protein	Unigene16016_All//0.00E+00//TC135029				nr -
Unigene16017_All	758	2.42	5.15	3.58	2.76	2.50	1.97	1.78	1.82	0.42	1.09E+00	5.36E-04	Up	5.69E-01	1.54E-01		-1.44E-01	7.85E-01		-4.89E-01	3.03E-01		2.78E-02	9.89E-01		-2.09E+00	1.85E-04	Down	Unigene16017_All//gi|42570301|ref|NP_850027.2|//1.00E-85//FAD-dependent oxidoreductase family protein [Arabidopsis thaliana]	Unigene16017_All//6.00E-79//AT2G22630| FAD-dependent oxidoreductase family protein	Unigene16017_All//7.00E-57//gi|78351689|gb|DT571963.1|DT571963				nr -
Unigene16018_All	1385	13.11	13.24	8.00	12.23	12.95	9.29	7.54	3.23	6.79	1.48E-02	9.33E-01		-7.13E-01	1.13E-07		8.31E-02	6.17E-01		-3.96E-01	3.21E-03		-1.22E+00	1.83E-13	Down	-1.52E-01	3.76E-01		Unigene16018_All//gi|15240411|ref|NP_198046.1|//4.00E-69//exonuclease family protein [Arabidopsis thaliana] >gi|30690464|ref|NP_851082.1| exonuclease family protein [Arabidopsis thaliana] >gi|30690468|ref|NP_851083.1| exonuclease family protein [Arabidopsis thaliana] >gi|42573491|ref|NP_974842.1| exonuclease family protein [Arabidopsis thaliana] >gi|108385373|gb|ABF85778.1| At5g26940 [Arabidopsis thaliana]	Unigene16018_All//2.00E-70//AT5G26940| exonuclease family protein	Unigene16018_All//0.00E+00//TC153309				nr +
Unigene1602_All	2812	47.97	94.58	84.02	128.34	111.69	97.01	6.33	13.45	12.01	9.80E-01	3.89E-184		8.09E-01	1.94E-115		-2.01E-01	4.73E-17		-4.04E-01	1.31E-56		1.09E+00	1.01E-38	Up	9.24E-01	2.33E-27		Unigene1602_All//gi|84453182|dbj|BAE71188.1|//1.00E-170//BEL1-like homeodomain transcription factor [Trifolium pratense]	Unigene1602_All//5.00E-112//AT2G35940| BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene1602_All//0.00E+00//TC152778	HB			nr -
Unigene16020_All	1591	2.57	1.31	1.91	6.48	2.75	0.85	23.44	16.94	0.78	-9.74E-01	1.33E-03		-4.27E-01	1.86E-01		-1.24E+00	2.43E-13	Down	-2.93E+00	2.64E-36	Down	-4.68E-01	1.99E-09		-4.92E+00	3.29E-227	Down	Unigene16020_All//gi|79407941|ref|NP_188636.2|//0.00E+00//aspartic-type endopeptidase [Arabidopsis thaliana] >gi|11994777|dbj|BAB03167.1| nucleoid chloroplast DNA-binding protein-like [Arabidopsis thaliana]	Unigene16020_All//2.00E-168//AT3G20015| aspartic-type endopeptidase	Unigene16020_All//0.00E+00//TC137848				nr +
Unigene16021_All	1889	0.78	0.59	0.06	1.56	1.48	1.98	2.39	1.73	2.51	-3.94E-01	4.70E-01		-3.78E+00	5.00E-06	Down	-7.55E-02	8.32E-01		3.51E-01	3.12E-01		-4.73E-01	6.81E-02		6.75E-02	7.94E-01		Unigene16021_All//gi|224059584|ref|XP_002299919.1|//1.00E-118//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222847177|gb|EEE84724.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene16021_All//5.00E-36//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene16021_All//0.00E+00//CO126534				nr +
Unigene16022_All	985	43.08	58.59	35.09	136.09	115.26	96.15	29.96	9.55	12.70	4.44E-01	1.34E-10		-2.96E-01	5.42E-04		-2.40E-01	3.60E-09		-5.01E-01	1.46E-31		-1.65E+00	5.74E-57	Down	-1.24E+00	2.26E-38	Down	Unigene16022_All//gi|38016521|gb|AA007596.1|//2.00E-91//fiber protein Fb34 [Gossypium barbadense]	Unigene16022_All//2.00E-70//AT4G27435| unknown protein	Unigene16022_All//0.00E+00//TC133088				nr +
Unigene16023_All	1097	24.47	17.23	19.32	38.23	34.40	33.55	25.28	10.02	8.32	-5.06E-01	1.27E-06		-3.41E-01	1.95E-03		-1.52E-01	8.08E-02		-1.88E-01	2.98E-02		-1.34E+00	2.48E-39	Down	-1.60E+00	4.84E-53	Down	Unigene16023_All//gi|1370186|emb|CAA98170.1|//1.00E-107//RABTC [Lotus japonicus]	Unigene16023_All//5.00E-108//AT3G18820| ATRAB7B (ARABIDOPSIS RAB GTPASE HOMOLOG G3F); GTP binding	Unigene16023_All//0.00E+00//TC155445		ko04145|Phagosome//ko04144|Endocytosis		nr +
Unigene16027_All	780	4.16	2.99	2.46	2.68	2.30	1.68	3.79	2.89	1.28	-4.77E-01	1.70E-01		-7.59E-01	3.56E-02		-2.25E-01	6.16E-01		-6.76E-01	1.36E-01		-3.91E-01	2.49E-01		-1.57E+00	2.94E-06	Down	Unigene16027_All//gi|2499488|sp|Q41140.1|PFPA_RICCO//4.00E-09//RecName: Full=Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha; Short=PFP; AltName: Full=6-phosphofructokinase, pyrophosphate dependent; AltName: Full=Pyrophosphate-dependent 6-phosphofructose-1-kinase; AltName: Full=PPi-PFK >gi|483347|emb|CAA83682.1| pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]	Unigene16027_All//3.00E-69//AT1G76550| pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative	Unigene16027_All//0.00E+00//TC136604		ko00051|Fructose and mannose metabolism		nr +

Unigene16029_All	1195	11.95	7.17	7.66	6.00	5.62	5.14	6.72	3.22	6.60	-7.38E-01	7.07E-07		-6.41E-01	2.91E-05		-9.53E-02	7.20E-01		-2.24E-01	3.74E-01		-1.06E+00	1.40E-08	Down	-2.63E-02	9.08E-01		Unigene16029_All//gi|15224901|ref|NP_181390.1|//1.00E-104//TFIIS (TRANSCRIPT ELONGATION FACTOR IIS); DNA binding / RNA polymerase II transcription elongation factor/ transcription factor [Arabidopsis thaliana]	Unigene16029_All//1.00E-94//AT2G38560| TFIIS (TRANSCRIPT ELONGATION FACTOR IIS); DNA binding / RNA polymerase II transcription elongation factor/ transcription factor	Unigene16029_All//0.00E+00//ES803895				nr -
Unigene16031_All	945	0.33	1.55	0.56	6.75	7.40	4.87	4.70	1.42	2.02	2.23E+00	4.29E-04	Up	7.62E-01	4.53E-01		1.33E-01	6.03E-01		-4.69E-01	4.81E-02		-1.73E+00	8.27E-10	Down	-1.22E+00	2.36E-06	Down	Unigene16031_All//gi|297745672|emb|CBI40926.3|//7.00E-32//unnamed protein product [Vitis vinifera]						nr -
Unigene16032_All	814	6.56	3.98	2.36	19.03	14.47	7.32	10.34	2.36	2.59	-7.19E-01	5.32E-03		-1.48E+00	2.09E-07	Down	-3.96E-01	3.40E-03		-1.38E+00	1.30E-20	Down	-2.13E+00	2.21E-23	Down	-1.99E+00	2.93E-22	Down	Unigene16032_All//gi|74027078|gb|AZ94630.1|//2.00E-70//zinc finger protein-like protein [Gossypium hirsutum]	Unigene16032_All//2.00E-51//AT3G15680| zinc finger (Ran-binding) family protein	Unigene16032_All//0.00E+00//TC134027				nr -
Unigene16035_All	593	12.62	19.74	25.59	17.56	21.43	21.10	11.19	29.81	19.82	6.46E-01	9.69E-05		1.02E+00	1.88E-11	Up	2.87E-01	7.99E-02		2.65E-01	1.26E-01		1.41E+00	1.59E-27	Up	8.24E-01	1.79E-08		Unigene16035_All//gi|224097704|ref|XP_002334590.1|//4.00E-14//predicted protein [Populus trichocarpa] >gi|224098800|ref|XP_002311271.1| predicted protein [Populus trichocarpa] >gi|222851091|gb|EEE88638.1| predicted protein [Populus trichocarpa] >gi|222873351|gb|EEF10482.1| predicted protein [Populus trichocarpa]	Unigene16035_All//7.00E-05//AT2G43290| MSS3 (multicopy suppressors of snf4 deficiency in yeast 3); calcium ion binding	Unigene16035_All//0.00E+00//DW511933				nr -
Unigene16037_All	1698	4.16	4.60	2.73	5.49	8.54	9.20	18.15	6.35	6.97	1.44E-01	5.33E-01		-6.09E-01	8.08E-03		6.38E-01	3.62E-06		7.46E-01	6.78E-08		-1.52E+00	1.28E-52	Down	-1.38E+00	2.88E-47	Down	Unigene16037_All//gi|193734712|gb|ACF19982.1|//1.00E-107//MYC2 [Hevea brasiliensis]	Unigene16037_All//3.00E-41//AT4G00870| basic helix-loop-helix (bHLH) family protein	Unigene16037_All//0.00E+00//TC165847	bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene16039_All	1270	33.66	21.19	37.48	13.92	14.40	22.94	5.46	4.77	2.48	-6.68E-01	4.82E-16		1.55E-01	7.17E-02		4.82E-02	8.00E-01		7.20E-01	2.34E-13		-1.94E-01	3.97E-01		-1.14E+00	1.32E-08	Down	Unigene16039_All//gi|222423823|dbj|BAH19877.1|//1.00E-121//AT5G08400 [Arabidopsis thaliana]	Unigene16039_All//2.00E-107//AT5G08400| unknown protein	Unigene16039_All//0.00E+00//TC137434				nr +
Unigene16040_All	1533	8.87	3.97	4.65	11.44	9.32	11.11	22.26	14.01	12.40	-1.16E+00	3.72E-13	Down	-9.31E-01	5.98E-09		-2.95E-01	2.44E-02		-4.24E-02	7.88E-01		-6.67E-01	9.58E-16		-8.44E-01	5.67E-24		Unigene16040_All//gi|94807665|gb|AB747129.1|//1.00E-128//At4g15640 [Arabidopsis thaliana]	Unigene16040_All//8.00E-126//AT4G15640| unknown protein	Unigene16040_All//0.00E+00//TC145834				nr +
Unigene16042_All	806	9.61	11.38	8.52	10.57	11.28	12.89	11.33	7.05	4.99	2.44E-01	2.27E-01		-1.73E-01	4.60E-01		9.39E-02	6.94E-01		2.86E-01	1.32E-01		-6.84E-01	5.40E-05		-1.18E+00	1.14E-11	Down	Unigene16042_All//gi|30688121|ref|NP_194612.2|//1.00E-68//methyltransferase/ nucleic acid binding [Arabidopsis thaliana] >gi|29028816|gb|AAO64787.1| At4g28830 [Arabidopsis thaliana]	Unigene16042_All//1.00E-45//AT4G28830| methyltransferase/ nucleic acid binding	Unigene16042_All//0.00E+00//TC148953				nr +
Unigene16044_All	824	223.00	164.80	212.74	37.42	41.29	32.28	0.87	0.66	2.76	-4.36E-01	4.06E-31		-6.79E-02	1.27E-01		1.42E-01	1.65E-01		-2.13E-01	3.78E-02		-4.04E-01	6.23E-01		1.66E+00	2.88E-05	Up	Unigene16044_All//gi|224082390|ref|XP_002306676.1|//2.00E-64//thioredoxin m [Populus trichocarpa] >gi|222856125|gb|EEE93672.1| thioredoxin m [Populus trichocarpa]	Unigene16044_All//2.00E-37//AT4G03520| ATHM2; enzyme activator	Unigene16044_All//0.00E+00//gi|109874658|gb|DW503632.1|DW503632				nr +
Unigene16045_All	887	10.91	8.80	8.52	12.97	13.94	11.15	13.39	6.17	7.14	-3.11E-01	1.04E-01		-3.56E-01	7.29E-02		1.03E-01	6.01E-01		-2.18E-01	2.38E-01		-1.12E+00	2.83E-13	Down	-9.07E-01	5.61E-10		Unigene16045_All//gi|195622834|gb|AC633247.1|//2.00E-74//calcineurin subunit B [Zea mays]	Unigene16045_All//1.00E-68//AT3G18430| calcium-binding EF hand family protein	Unigene16045_All//0.00E+00//TC147227		ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene16047_All	948	2.21	2.24	3.31	3.89	2.54	4.19	9.37	7.27	86.28	2.41E-02	9.77E-01		5.86E-01	1.14E-01		-6.13E-01	4.61E-02		1.09E-01	7.44E-01		-3.65E-01	4.04E-02		3.20E+00	0.00E+00	Up	Unigene16047_All//gi|297825169|ref|XP_002880467.1|//1.00E-13//VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297326306|gb|EFH56726.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]		Unigene16047_All//0.00E+00//DW506377				nr +
Unigene16049_All	973	0.91	8.28	1.59	2.66	3.15	2.88	23.94	45.28	27.02	3.18E+00	4.06E-28	Up	7.96E-01	1.50E-01		2.43E-01	5.52E-01		1.12E-01	7.83E-01		9.19E-01	2.96E-34		1.75E-01	7.65E-02		Unigene16049_All//gi|6730712|gb|AAF27107.1|AC011809_16//4.00E-78//unknown protein [Arabidopsis thaliana] >gi|15809884|gb|AAL06870.1| At1g18720/F6A14_17 [Arabidopsis thaliana] >gi|17978859|gb|AAL47401.1| At1g18720/F6A14_17 [Arabidopsis thaliana]	Unigene16049_All//1.00E-71//AT1G18720| unknown protein	Unigene16049_All//0.00E+00//DR452806				nr +
Unigene16050_All	799	23.12	34.12	28.72	25.62	23.49	31.09	23.28	26.57	7.88	5.62E-01	6.43E-08		3.13E-01	9.67E-03		-1.26E-01	3.77E-01		2.79E-01	1.29E-02		1.91E-01	9.81E-02		-1.56E+00	1.42E-34	Down	Unigene16050_All//gi|48958469|gb|AAT47787.1|//3.00E-24//At1g09645 [Arabidopsis thaliana] >gi|50897232|gb|AAT85755.1| At1g09645 [Arabidopsis thaliana]	Unigene16050_All//7.00E-08//AT1G09645| unknown protein	Unigene16050_All//0.00E+00//gi|164326695|gb|ES838510.1|ES838510				nr +
Unigene16051_All	753	1.32	0.67	1.20	2.12	0.96	2.40	2.64	4.44	1.01	-9.72E-01	1.58E-01		-1.35E-01	8.38E-01		-1.14E+00	2.19E-02		1.81E-01	7.19E-01		7.51E-01	1.28E-02		-1.39E+00	6.85E-04	Down	Unigene16051_All//gi|225453303|ref|XP_002268524.1|//4.00E-62//PREDICTED: similar to LOL3 (LSD ONE LIKE 3); caspase/ cysteine-type endopeptidase [Vitis vinifera]	Unigene16051_All//3.00E-63//AT1G02170| AMC1 (METACASPASE 1); cysteine-type endopeptidase	Unigene16051_All//4.00E-09//TC178900				nr +
Unigene16052_All	895	2.63	0.68	2.26	1.56	1.58	1.97	1.04	0.70	1.11	-1.95E+00	2.39E-05	Down	-2.19E-01	6.22E-01		1.76E-02	9.88E-01		3.37E-01	5.42E-01		-5.69E-01	4.02E-01		9.86E-02	8.78E-01		Unigene16052_All//gi|3258570|gb|AAC24380.1|//2.00E-49//Unknown protein [Arabidopsis thaliana]	Unigene16052_All//4.00E-49//AT1G02170| AMC1 (METACASPASE 1); cysteine-type endopeptidase	Unigene16052_All//4.00E-09//TC178900				nr -
Unigene16054_All	1078	1.12	0.94	0.64	3.19	2.87	1.22	13.18	9.73	9.09	-2.48E-01	6.62E-01		-7.98E-01	2.25E-01		-1.49E-01	6.88E-01		-1.39E+00	3.95E-05	Down	-4.37E-01	1.02E-03		-5.36E-01	3.34E-05		Unigene16054_All//gi|15221679|ref|NP_174417.1|//2.00E-69//LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4) [Arabidopsis thaliana] >gi|29428037|sp|Q9SHE9.1|LBD4_ARATH RecName: Full=LOB domain-containing protein 4; AltName: Full=ASYMMETRIC LEAVES 2-like protein 6; Short=AS2-like protein 6 >gi|6692123|gb|AAF24588.1|AC007654_4 T19E23.11 [Arabidopsis thaliana] >gi|50253474|gb|AAT71939.1| At1g31320 [Arabidopsis thaliana] >gi|51972120|gb|AAU15164.1| At1g31320 [Arabidopsis thaliana] >gi|219807088|dbj|BAH10550.1| ASYMMETRIC LEAVES2-like 6 protein [Arabidopsis thaliana]	Unigene16054_All//3.00E-53//AT1G31320| LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4)	Unigene16054_All//4.00E-102//TC144603		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene16056_All	700	38.12	9.34	9.36	19.85	10.77	5.16	49.29	17.73	27.49	-2.03E+00	6.47E-56	Down	-2.03E+00	9.03E-54	Down	-8.82E-01	2.25E-10		-1.94E+00	4.36E-30	Down	-1.47E+00	1.60E-56	Down	-8.42E-01	3.91E-24		Unigene16056_All//gi|3172242|gb|AAK14060.1|AF239177_1//3.00E-27//major latex-like protein [Prunus persica]	Unigene16056_All//5.00E-70//AT5G28000| Bet v I allergen family protein	Unigene16056_All//5.00E-70//DW505476				nr +
Unigene16057_All	989	3.02	1.23	0.00	7.30	0.42	1.42	29.03	5.41	14.22	-1.29E+00	5.17E-04	Down	-1.16E+01	2.42E-16	Down	-4.13E+00	2.06E-40	Down	-2.37E+00	3.07E-20	Down	-2.42E+00	2.10E-91	Down	-1.03E+00	5.64E-28	Down	Unigene16057_All//gi|15231803|ref|NP_188036.1|//3.00E-06//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]		Unigene16057_All//0.00E+00//DW509717				nr +
Unigene16058_All	1634	0.70	0.31	0.07	2.01	0.30	0.39	9.76	1.28	4.90	-1.18E+00	6.62E-02		-3.43E+00	1.54E-04	Down	-2.77E+00	6.86E-13	Down	-2.38E+00	1.57E-09	Down	-2.93E+00	8.58E-63	Down	-9.93E-01	4.58E-15		Unigene16058_All//gi|15231803|ref|NP_188036.1|//6.00E-46//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]	Unigene16058_All//1.00E-30//AT3G14200| DNAJ heat shock N-terminal domain-containing protein	Unigene16058_All//0.00E+00//DW509717		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene16059_All	884	13.73	9.92	12.89	14.65	14.22	11.39	11.81	4.30	5.23	-4.70E-01	3.95E-03		-9.11E-02	6.33E-01		-4.33E-02	8.13E-01		-3.63E-01	2.30E-02		-1.46E+00	2.34E-17	Down	-1.18E+00	4.10E-13	Down	Unigene16059_All//gi|15221835|ref|NP_173303.1|//9.00E-71//HNH endonuclease domain-containing protein [Arabidopsis thaliana] >gi|6730716|gb|AAF27111.1|AC011809_20 Unknown protein [Arabidopsis thaliana]	Unigene16059_All//6.00E-67//AT1G18680| HNH endonuclease domain-containing protein	Unigene16059_All//0.00E+00//TC155010				nr -
Unigene16060_All	1061	3.30	1.67	3.01	5.31	4.67	5.19	11.40	7.37	3.79	-9.83E-01	3.00E-03		-1.34E-01	6.97E-01		-1.83E-01	5.31E-01		-3.08E-02	9.28E-01		-6.30E-01	1.36E-05		-1.59E+00	2.86E-23	Down	Unigene16060_All//gi|108862647|gb|AB498345.2|//3.00E-38//Plastocyanin-like domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene16060_All//3.00E-21//AT1G08500| plastocyanin-like domain-containing protein	Unigene16060_All//0.00E+00//gi|109868503|gb|DW497479.1|DW497479				nr -
Unigene16065_All	1000	31.44	36.68	30.83	33.92	34.09	40.33	53.87	49.57	25.97	2.22E-01	1.52E-02		-2.84E-02	7.99E-01		7.10E-03	9.51E-01		2.50E-01	3.39E-03		-1.20E-01	9.24E-02		-1.05E+00	1.50E-53	Down	Unigene16065_All//gi|192911938|gb|ACF06577.1|//1.00E-81//G10 protein [Elaeis guineensis]	Unigene16065_All//7.00E-80//AT4G21110| G10 family protein	Unigene16065_All//0.00E+00//gi|48791123|gb|CO092437.1|CO092437		ko03040|Spliceosome		nr +
Unigene16066_All	894	5.33	6.29	1.97	22.79	30.70	27.53	10.26	19.87	14.04	2.40E-01	3.62E-01		-1.44E+00	1.91E-06	Down	4.30E-01	9.07E-06		2.73E-01	1.60E-02		9.53E-01	3.83E-15		4.52E-01	1.14E-03		Unigene16066_All//gi|115469758|ref|NP_001058478.1|//2.00E-13//Os06g0700300 [Oryza sativa Japonica Group] >gi|113596518|dbj|BAF20392.1| Os06g0700300 [Oryza sativa Japonica Group]	Unigene16066_All//9.00E-06//AT1G06980| unknown protein	Unigene16066_All//0.00E+00//TC140344				nr +
Unigene16067_All	1060	1.83	0.29	0.80	3.85	3.44	4.30	2.07	1.77	2.97	-2.67E+00	3.17E-06	Down	-1.18E+00	1.70E-02		-1.62E-01	6.16E-01		1.59E-01	6.18E-01		-2.25E-01	6.13E-01		5.18E-01	9.14E-02		Unigene16067_All//gi|18391032|ref|NP_563845.1|//5.00E-41//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|3482927|gb|AAC33212.1| Unknown protein [Arabidopsis thaliana] >gi|15529272|gb|AAK97730.1| At1g09520/F14J9_18 [Arabidopsis thaliana] >gi|25141213|gb|AAN73301.1| At1g09520/F14J9_18 [Arabidopsis thaliana]	Unigene16067_All//7.00E-25//AT1G09520| protein binding / zinc ion binding	Unigene16067_All//0.00E+00//TC157226				nr +
Unigene16068_All	858	3.48	4.55	9.37	15.73	18.18	15.11	11.09	4.38	5.20	3.88E-01	2.23E-01		1.43E+00	2.14E-10	Up	2.09E-01	1.72E-01		-5.86E-02	7.39E-01		-1.34E+00	4.63E-14	Down	-1.09E+00	8.91E-11	Down	Unigene16068_All//gi|15242552|ref|NP_198818.1|//3.00E-92//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|10176994|dbj|BAB10226.1| thaumatin-like protein [Arabidopsis thaliana] >gi|38603816|gb|AAR24653.1| At5g40020 [Arabidopsis thaliana] >gi|110736116|dbj|BAF00030.1| thaumatin-like protein [Arabidopsis thaliana]	Unigene16068_All//5.00E-93//AT5G40020| pathogenesis-related thaumatin family protein	Unigene16068_All//0.00E+00//DR459831				nr +
Unigene16069_All	1119	6.97	7.25	7.80	9.62	10.22	8.60	18.10	10.12	8.15	5.65E-02	7.89E-01		1.64E-01	4.55E-01		8.75E-02	6.74E-01		-1.62E-01	4.27E-01		-8.38E-01	5.45E-14		-1.15E+00	8.90E-24	Down	Unigene16069_All//gi|194708816|gb|ACF88492.1|//2.00E-64//At1g34350 [Arabidopsis thaliana]	Unigene16069_All//7.00E-60//AT1G34350| unknown protein	Unigene16069_All//0.00E+00//TC143813				nr -

Unigene1607_All	2237	122.32	78.96	102.69	32.44	33.33	21.30	9.30	3.40	15.40	-6.32E-01	2.14E-89		-2.52E-01	3.22E-16		3.87E-02	6.12E-01		-6.07E-01	2.58E-24		-1.45E+00	1.35E-33	Down	7.28E-01	7.63E-19		Unigene1607_All//gi|225434642|ref|XP_002279786.1|//0.00E+00//PREDICTED: similar to binding [Vitis vinifera]	Unigene1607_All//4.00E-131//AT2G29670| binding	Unigene1607_All//0.00E+00//TC170050				nr -
Unigene16072_All	1007	0.99	0.20	0.00	5.44	4.31	3.72	12.85	8.84	5.58	-2.29E+00	4.05E-03		-9.95E+00	1.77E-05	Down	-3.37E-01	2.02E-01		-5.48E-01	3.26E-02		-5.39E-01	1.09E-04		-1.20E+00	1.33E-16	Down	Unigene16072_All//gi|224109236|ref|XP_002315131.1|//1.00E-151//laccase 90c [Populus trichocarpa] >gi|222864171|gb|EEF01302.1| laccase 90c [Populus trichocarpa]	Unigene16072_All//2.00E-139//AT5G05390| LAC12 (laccase 12); laccase	Unigene16072_All//0.00E+00//DW241123		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene16073_All	1958	0.05	0.10	0.05	17.05	11.59	9.27	15.59	14.28	7.28	9.55E-01	6.22E-01		2.68E-02	1.00E+00		-5.57E-01	5.33E-11		-8.78E-01	2.13E-21		-1.27E-01	2.05E-01		-1.10E+00	7.11E-33	Down	Unigene16073_All//gi|224109236|ref|XP_002315131.1|//0.00E+00//laccase 90c [Populus trichocarpa] >gi|222864171|gb|EEF01302.1| laccase 90c [Populus trichocarpa]	Unigene16073_All//0.00E+00//AT2G40370| LAC5 (laccase 5); laccase	Unigene16073_All//0.00E+00//gi|109884864|gb|DW513834.1|DW513834		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene16074_All	1194	1.23	2.46	2.72	4.67	3.49	4.50	1.91	2.70	3.87	1.00E+00	6.41E-03		1.15E+00	1.62E-03		-4.21E-01	9.27E-02		-5.39E-02	8.57E-01		4.95E-01	1.19E-01		1.02E+00	4.03E-05	Up	Unigene16074_All//gi|115436188|ref|NP_001042852.1|//5.00E-42//Os01g0309800 [Oryza sativa Japonica Group] >gi|21328110|dbj|BAC00691.1| Oj1116_C07.8 [Oryza sativa Japonica Group] >gi|113532383|dbj|BAF04766.1| Os01g0309800 [Oryza sativa Japonica Group]	Unigene16074_All//2.00E-09//AT4G08570| heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	Unigene16074_All//0.00E+00//TC149718		ko00500|Starch and sucrose metabolism//ko04144|Endocytosis//ko00040|Pentose and glucuronate interconversions		nr +
Unigene16076_All	1034	1.87	3.72	1.03	4.34	7.39	9.70	2.45	3.03	5.97	9.92E-01	1.64E-03		-8.62E-01	7.98E-02		7.70E-01	1.18E-04		1.16E+00	2.36E-10	Up	3.05E-01	3.78E-01		1.28E+00	4.30E-09	Up	Unigene16076_All//gi|7267223|emb|CAB80830.1|//3.00E-06//AT4g04650 [Arabidopsis thaliana]	Unigene16076_All//2.00E-07//AT4G04650| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cold; LOCATED IN: stromule; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G45720.1); Has 608 Blast hits to 598 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 608; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene16077_All	515	17.98	15.15	7.13	37.14	24.07	26.75	67.98	96.01	45.41	-2.47E-01	2.16E-01		-1.33E+00	1.04E-10	Down	-6.26E-01	5.94E-08		-4.74E-01	1.22E-04		4.98E-01	1.36E-13		-5.82E-01	3.21E-13		Unigene16077_All//gi|7801679|emb|CAB91599.1|//1.00E-07//epsin-like protein [Arabidopsis thaliana]		Unigene16077_All//0.00E+00//TC170657				nr +
Unigene16079_All	874	4.07	20.52	5.24	31.97	25.89	29.87	7.16	4.02	19.51	2.33E+00	1.40E-44	Up	3.64E-01	2.38E-01		-3.05E-01	1.90E-03		-9.83E-02	4.32E-01		-8.34E-01	7.56E-05		1.45E+00	4.10E-28	Up	Unigene16079_All//gi|15215582|gb|AAK91336.1|//2.00E-36//AT5g13880/MAC12_16 [Arabidopsis thaliana] >gi|20334870|gb|AAM16191.1| AT5g13880/MAC12_16 [Arabidopsis thaliana]	Unigene16079_All//8.00E-37//AT5G47920| unknown protein					nr -
Unigene1608_All	3777	30.54	12.03	23.66	9.87	9.85	6.76	23.63	31.21	22.11	-1.34E+00	3.06E-133	Down	-3.69E-01	4.27E-14		-2.70E-03	9.75E-01		-5.46E-01	1.16E-10		4.01E-01	3.11E-21		-9.61E-02	6.64E-02		Unigene1608_All//gi|224081501|ref|XP_002306436.1|//0.00E+00//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222855885|gb|EEE93432.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene1608_All//0.00E+00//AT3G51480| ATGLR3.6 (GLUTAMATE RECEPTOR 3.6); intracellular ligand-gated ion channel	Unigene1608_All//0.00E+00//TC152197				nr +
Unigene16083_All	1152	0.82	2.33	1.25	2.51	2.57	2.63	5.58	4.32	3.11	1.51E+00	2.03E-04	Up	6.10E-01	2.96E-01		3.56E-02	9.50E-01		6.67E-02	8.77E-01		-3.70E-01	8.59E-02		-8.42E-01	3.22E-05		Unigene16083_All//gi|115480279|ref|NP_001063733.1|//8.00E-69//Os09g0527900 (Oryza sativa Japonica Group) >gi|113631966|dbj|BAF25647.1| Os09g0527900 [Oryza sativa Japonica Group]	Unigene16083_All//3.00E-55//AT4G38960| zinc finger (B-box type) family protein	Unigene16083_All//0.00E+00//TC137101	DBB	ko04712|Circadian rhythm - plant		nr +
Unigene16087_All	1590	1.94	3.22	1.24	2.76	4.11	4.86	0.96	0.11	1.35	7.29E-01	5.89E-03		-6.48E-01	8.21E-02		5.78E-01	9.76E-03		8.17E-01	7.61E-05		-3.19E+00	4.80E-07	Down	4.99E-01	1.96E-01		Unigene16087_All//gi|30696940|ref|NP_200588.2|//0.00E+00//CER3 (ECERIFERUM 3); binding / catalytic/ iron ion binding / oxidoreductase [Arabidopsis thaliana] >gi|75151993|sp|Q8HIZ0.1|WAX2_ARATH RecName: Full=Protein WAX2; AltName: Full=Protein YORE-YORE; AltName: Full=Protein FACELESS POLLEN 1 >gi|22900949|gb|AAN06975.1| cuticle protein [Arabidopsis thaliana] >gi|37051339|dbj|BAC81644.1| YORE-YORE protein [Arabidopsis thaliana] >gi|40714041|dbj|BAD06945.1| faceless pollen-1 [Arabidopsis thaliana]	Unigene16087_All//0.00E+00//AT5G57800| CER3 (ECERIFERUM 3); binding / catalytic/ iron ion binding / oxidoreductase	Unigene16087_All//0.00E+00//TC146919		ko00100|Steroid biosynthesis		nr +
Unigene16089_All	848	45.53	20.44	33.53	25.61	18.19	26.31	12.02	7.25	5.17	-1.16E+00	1.11E-35	Down	-4.41E-01	5.88E-07		-4.94E-01	5.19E-06		3.88E-02	7.82E-01		-7.30E-01	4.91E-06		-1.22E+00	1.74E-13	Down	Unigene16089_All//gi|60543361|gb|AAX22278.1|//3.00E-48//At5g20130 [Arabidopsis thaliana]	Unigene16089_All//6.00E-36//AT5G20130| unknown protein	Unigene16089_All//0.00E+00//TC146280				nr +
Unigene1609_All	3343	1.30	0.62	1.50	0.39	0.43	0.38	3.30	1.30	1.28	-1.06E+00	3.11E-04	Down	2.05E-01	4.91E-01		1.59E-01	8.26E-01		-3.43E-02	9.56E-01		-1.34E+00	2.78E-16	Down	-1.37E+00	2.54E-17	Down	Unigene1609_All//gi|224081501|ref|XP_002306436.1|//0.00E+00//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222855885|gb|EEE93432.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene1609_All//0.00E+00//AT3G51480| ATGLR3.6 (GLUTAMATE RECEPTOR 3.6); intracellular ligand-gated ion channel	Unigene1609_All//0.00E+00//TC152197				nr +
Unigene16091_All	790	1.99	39.45	4.04	6.81	10.07	13.09	5.83	5.71	35.00	4.31E+00	2.01E-137	Up	1.03E+00	4.96E-03		5.64E-01	4.49E-03		9.43E-01	8.81E-08		-2.99E-02	9.30E-01		2.58E+00	2.75E-96	Up	Unigene16091_All//gi|18397376|ref|NP_564349.1|//1.00E-23//JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8) [Arabidopsis thaliana] >gi|75155014|sp|Q8LBM2.1|TIF5A_ARATH RecName: Full=Protein TIFY 5A; AltName: Full=Jasmonate ZIM domain-containing protein 8 >gi|109946551|gb|ABG48454.1| Attig00135 [Arabidopsis thaliana]	Unigene16091_All//6.00E-25//AT1G30135| JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8)	Unigene16091_All//0.00E+00//TC142834	Tify			nr -
Unigene16092_All	462	1.13	6.36	3.11	1.73	2.09	2.25	2.20	1.45	1.12	2.49E+00	2.11E-08	Up	1.46E+00	1.58E-02		2.75E-01	7.47E-01		3.82E-01	6.27E-01		-6.02E-01	3.45E-01		-9.70E-01	9.93E-02		Unigene16092_All//gi|297813771|ref|XP_002874769.1|//1.00E-09//auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320606|gb|EFH51028.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16092_All//7.00E-09//AT4G12410| auxin-responsive family protein	Unigene16092_All//1.00E-20//gi|109870016|gb|DW498992.1|DW498992				nr -
Unigene16093_All	821	1.66	6.05	1.43	1.70	2.64	3.69	1.85	1.78	1.55	1.87E+00	7.98E-10	Up	-2.16E-01	7.04E-01		6.37E-01	1.55E-01		1.12E+00	2.03E-03		-5.72E-02	9.20E-01		-2.56E-01	6.16E-01		Unigene16093_All//gi|224071573|ref|XP_002303522.1|//6.00E-49//SAUR family protein [Populus trichocarpa] >gi|222840954|gb|EEE78501.1| SAUR family protein [Populus trichocarpa]	Unigene16093_All//2.00E-44//AT4G12410| auxin-responsive family protein	Unigene16093_All//3.00E-62//gi|48780243|gb|CO089609.1|CO089609				nr +
Unigene16095_All	965	17.08	11.97	14.29	40.63	18.84	28.41	37.29	13.64	26.88	-5.13E-01	1.75E-04		-2.57E-01	8.62E-02		-1.11E+00	1.31E-41	Down	-5.16E-01	3.76E-10		-1.45E+00	1.73E-57	Down	-4.72E-01	1.46E-09		Unigene16095_All//gi|300793639|tpg|DAA33877.1|//1.00E-126//TPA: TPA_inf: aquaporin SIP1;3 [Gossypium hirsutum]	Unigene16095_All//3.00E-44//AT3G04090| SIP1A (SMALL AND BASIC INTRINSIC PROTEIN 1A); water channel	Unigene16095_All//0.00E+00//TC138895				nr -
Unigene16096_All	2091	0.50	0.97	1.15	1.64	0.68	0.35	17.55	11.25	28.54	9.54E-01	3.64E-02		1.20E+00	6.24E-03		-1.28E+00	4.55E-05	Down	-2.25E+00	2.47E-09	Down	-6.41E-01	9.01E-16		7.02E-01	5.28E-30		Unigene16096_All//gi|224082802|ref|XP_002306845.1|//0.00E+00//high affinity inorganic phosphate transporter [Populus trichocarpa] >gi|222856294|gb|EEE93841.1| high affinity inorganic phosphate transporter [Populus trichocarpa]	Unigene16096_All//0.00E+00//AT2G38940| ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter	Unigene16096_All//0.00E+00//TC151311				nr -
Unigene16099_All	911	69.09	32.43	27.53	375.00	284.44	210.20	61.68	26.24	23.92	-1.09E+00	1.12E-52	Down	-1.33E+00	3.34E-69	Down	-3.99E-01	5.03E-59		-8.35E-01	7.78E-197		-1.23E+00	9.20E-70	Down	-1.37E+00	4.39E-84	Down	Unigene16099_All//gi|15241485|ref|NP_196417.1|//2.00E-46//E13L3 (GLUCAN ENDO-1,3-BETA-GLUCOSIDASE-LIKE PROTEIN 3); callose binding / polysaccharide binding [Arabidopsis thaliana] >gi|75200196|sp|Q9SS84.1|E13L3_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase-like protein 3; Flags: Precursor >gi|26452180|dbj|BAC43178.1| GPI-anchored protein [Arabidopsis thaliana] >gi|28372924|gb|AAO39944.1| At5g08000 [Arabidopsis thaliana]	Unigene16099_All//6.00E-34//AT1G18650| PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding	Unigene16099_All//0.00E+00//gi|78334988|gb|DT555262.1|DT555262				nr -
Unigene161_All	2805	0.95	0.63	1.50	4.64	4.26	3.91	4.18	1.16	3.14	-5.90E-01	1.27E-01		6.57E-01	3.43E-02		-1.22E-01	5.24E-01		-2.45E-01	1.49E-01		-1.85E+00	7.84E-27	Down	-4.12E-01	4.36E-03		Unigene161_All//gi|224083434|ref|XP_002307025.1|//1.00E-134//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222856474|gb|EEE94021.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene161_All//3.00E-43//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene161_All//0.00E+00//ES820741		ko04626|Plant-pathogen interaction		nr +
Unigene1610_All	1559	5.07	2.41	2.02	2.88	3.69	3.62	3.36	1.15	2.40	-1.08E+00	3.92E-07	Down	-1.33E+00	3.39E-09	Down	3.59E-01	1.65E-01		3.33E-01	2.23E-01		-1.54E+00	7.58E-10	Down	-4.85E-01	3.22E-02		Unigene1610_All//gi|291622145|emb|CBJ23782.1|//1.00E-105//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene1610_All//4.00E-106//AT3G22470| pentatricopeptide (PPR) repeat-containing protein	Unigene1610_All//0.00E+00//TC161851				nr +

Unigene16100_All	768	36.79	131.95	57.76	36.00	24.44	24.29	87.64	91.54	67.33	1.84E+00	3.89E-184	Up	6.51E-01	2.88E-15		-5.59E-01	2.88E-09		-5.68E-01	1.28E-08		6.27E-02	3.66E-01		-3.80E-01	9.56E-12		Unigene16100_All//gi|75121194|sp|Q6ENS0.1|YCF72_SACOF//6.00E-11//RecName: Full=Uncharacterized protein ycf72; AltName: Full=ORF137 >gi|75126316|sp|Q6L3B8.1|YCF72_SACHY RecName: Full=Uncharacterized protein ycf72; AltName: Full=ORF137		Unigene16100_All//0.00E+00//TC147440				nr +
Unigene16104_All	1591	0.36	0.00	0.07	1.53	0.41	2.04	9.57	82.70	68.41	-8.50E+00	1.52E-03		-2.43E+00	4.40E-02		-1.90E+00	2.93E-06	Down	4.14E-01	2.64E-01		3.11E+00	0.00E+00	Up	2.84E+00	0.00E+00	Up	Unigene16104_All//gi|223452333|gb|ACM89494.1|//1.00E-178//kinase-like protein [Glycine max]	Unigene16104_All//8.00E-169//AT2G05940| protein kinase, putative	Unigene16104_All//0.00E+00//DW512206		ko04626|Plant-pathogen interaction		nr +
Unigene16105_All	992	5.70	4.39	1.99	23.95	13.92	13.79	47.99	8.51	10.20	-3.75E-01	1.41E-01		-1.52E+00	4.13E-08	Down	-7.83E-01	2.98E-14		-7.96E-01	4.18E-13		-2.50E+00	1.97E-156	Down	-2.23E+00	3.23E-141	Down	Unigene16105_All//gi|331119959|emb|CAE12163.1|//1.00E-115//expansin-like protein [Quercus robur]	Unigene16105_All//1.00E-81//AT4G38400| ATEXLA2 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A2)	Unigene16105_All//0.00E+00//TC178614				nr -
Unigene16109_All	1276	0.86	1.59	2.04	5.54	3.13	2.48	1.59	1.02	1.22	8.83E-01	5.19E-02		1.25E+00	2.79E-03		-8.24E-01	5.12E-05		-1.16E+00	1.33E-07	Down	-6.47E-01	1.15E-01		-3.85E-01	3.45E-01		Unigene16109_All//gi|97052021|sp|Q2MER4.1|HT1_ARATH//1.00E-173//RecName: Full=Serine/threonine-protein kinase HT1; AltName: Full=High leaf temperature protein 1 >gi|84875482|dbj|BAE75921.1| HT1 protein kinase [Arabidopsis thaliana]	Unigene16109_All//1.00E-170//AT1G62400| HT1 (high leaf temperature 1); kinase/ protein serine/threonine/tyrosine kinase	Unigene16109_All//0.00E+00//DW237670				nr +
Unigene16112_All	2931	0.77	0.07	0.00	1.63	1.13	0.60	2.42	1.20	10.74	-3.47E+00	5.79E-09	Down	-9.58E+00	2.68E-12	Down	-5.33E-01	4.55E-02		-1.44E+00	3.30E-07	Down	-1.02E+00	3.40E-07	Down	2.15E+00	6.73E-88	Up	Unigene16112_All//gi|215598266|tpg|DAA06351.1|//0.00E+00//TPA_inf: ARO1-like protein 2 [Vitis vinifera]	Unigene16112_All//0.00E+00//AT5G66200| ARO2 (ARMADILLO REPEAT ONLY 2); binding	Unigene16112_All//0.00E+00//gi|78323196|gb|DT543470.1|DT543470				nr +
Unigene16113_All	925	2.32	2.90	5.24	10.29	10.46	11.03	31.08	26.30	20.24	3.24E-01	4.00E-01		1.18E+00	5.17E-05	Up	2.43E-02	9.21E-01		1.01E-01	6.35E-01		-2.41E-01	9.78E-03		-6.19E-01	3.45E-12		Unigene16113_All//gi|15450826|gb|AK96684.1|//7.00E-63//Unknown protein [Arabidopsis thaliana] >gi|88196723|gb|ABD43004.1| At5g42570 [Arabidopsis thaliana]	Unigene16113_All//1.00E-60//AT1G11905| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular protein transport; LOCATED IN: endomembrane system, integral to membrane, endoplasmic reticulum; CONTAINS InterPro DOMAIN/s: B-cell receptor-associated 31-like (InterPro:IPR008417); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G42570.1); Has 65 Blast hits to 65 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 65; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene16113_All//0.00E+00//TC158958				nr -
Unigene16114_All	1097	13.07	35.70	42.62	24.98	32.30	34.46	13.18	30.52	90.64	1.45E+00	6.83E-51	Up	1.71E+00	1.14E-74	Up	3.71E-01	1.10E-05		4.64E-01	3.72E-08		1.21E+00	1.10E-40	Up	2.78E+00	0.00E+00	Up	Unigene16114_All//gi|42570959|ref|NP_973553.1|//3.00E-71//RAP2.7 (RELATED TO AP2.7); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene16114_All//6.00E-53//AT2G28550| RAP2.7 (RELATED TO AP2.7); DNA binding / transcription factor	Unigene16114_All//0.00E+00//gi|164334348|gb|ES799806.1|ES799806	AP2-EREBP			nr -
Unigene16116_All	1001	4.18	3.49	2.02	8.11	8.63	4.69	7.77	5.34	5.77	-2.60E-01	3.89E-01		-1.05E+00	8.14E-04	Down	9.01E-02	7.22E-01		-7.90E-01	7.30E-05		-5.40E-01	3.70E-03		-4.30E-01	1.82E-02		Unigene16116_All//gi|79313852|ref|NP_001030781.1|//3.00E-82//hydrolase [Arabidopsis thaliana]	Unigene16116_All//2.00E-83//AT3G27320| hydrolase	Unigene16116_All//0.00E+00//DR455667				nr +
Unigene16117_All	877	8.77	7.97	8.99	33.17	33.81	28.32	38.71	17.01	10.04	-1.37E-01	5.59E-01		3.52E-02	8.81E-01		2.74E-02	8.29E-01		-2.28E-01	2.96E-02		-1.19E+00	5.44E-40	Down	-1.95E+00	1.34E-84	Down	Unigene16117_All//gi|18203448|sp|Q9SR72.1|GL32_ARATH//3.00E-81//RecName: Full=Germin-like protein subfamily 3 member 2; Flags: Precursor >gi|6143869|gb|AAF04416.1|AC010927_9 germin-like protein [Arabidopsis thaliana] >gi|21554012|gb|AAM63093.1| germin-like protein [Arabidopsis thaliana] >gi|126352262|gb|AB009876.1| At3g10080 [Arabidopsis thaliana]	Unigene16117_All//2.00E-82//AT3G10080| germin-like protein, putative	Unigene16117_All//0.00E+00//gi|109877413|gb|DW506386.1|DW506386				nr -
Unigene16118_All	1037	26.54	3.13	4.01	69.13	85.27	35.54	0.33	0.00	0.23	-3.09E+00	3.90E-93	Down	-2.73E+00	4.40E-79	Down	3.03E-01	2.58E-09		-9.60E-01	1.43E-52		-8.35E+00	1.17E-02		-5.01E-01	6.49E-01		Unigene16118_All//gi|115489104|ref|NP_001067039.1|//1.00E-46//Os12g0563700 [Oryza sativa Japonica Group] >gi|77556168|gb|ABA98964.1| Pectinesterase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113649546|dbj|BAF30058.1| Os12g0563700 [Oryza sativa Japonica Group]	Unigene16118_All//3.00E-37//AT5G47500| pectinesterase family protein			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene16119_All	1209	39.55	6.50	7.49	85.83	104.30	45.65	0.91	0.07	0.46	-2.61E+00	3.24E-135	Down	-2.40E+00	8.47E-119	Down	2.81E-01	2.00E-11		-9.11E-01	1.55E-69		-3.72E+00	7.15E-06	Down	-9.79E-01	8.01E-02		Unigene16119_All//gi|193848549|gb|ACF22736.1|//2.00E-92//pectinesterase family protein [Brachypodium distachyon]	Unigene16119_All//1.00E-86//AT5G19730| pectinesterase family protein	Unigene16119_All//0.00E+00//DW507252		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene1612_All	2244	4.29	203.67	36.83	5.24	36.25	83.54	10.89	43.34	119.20	5.57E+00	0.00E+00	Up	3.10E+00	1.85E-272	Up	2.79E+00	2.94E-286	Up	4.00E+00	0.00E+00	Up	1.99E+00	8.35E-241	Up	3.45E+00	0.00E+00	Up	Unigene1612_All//gi|297840531|ref|XP_002888147.1|//1.00E-137//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333988|gb|EFH64406.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1612_All//7.00E-132//AT1G10560| PUB18 (PLANT U-BOX 18); ubiquitin-protein ligase			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene16120_All	1393	18.29	80.31	44.69	10.16	23.56	20.72	20.18	26.46	256.65	2.13E+00	1.24E-246	Up	1.29E+00	1.47E-65	Up	1.21E+00	2.39E-38	Up	1.03E+00	9.70E-24	Up	3.91E-01	6.56E-07		3.67E+00	0.00E+00	Up			Unigene16120_All//0.00E+00//TC135337				ESTscan +
Unigene16125_All	816	3.85	2.98	3.26	5.01	3.25	4.04	5.65	2.51	1.76	-3.68E-01	3.11E-01		-2.38E-01	5.38E-01		-6.23E-01	3.07E-02		-3.09E-01	3.55E-01		-1.17E+00	5.27E-06	Down	-1.68E+00	3.77E-10	Down	Unigene16125_All//gi|20330749|gb|AAM19112.1|AC104427_10//3.00E-39//Unknown protein [Oryza sativa Japonica Group]	Unigene16125_All//6.00E-22//AT1G30845| unknown protein	Unigene16125_All//0.00E+00//TC160837				nr +
Unigene16127_All	940	110.93	223.75	167.00	21.94	71.84	63.95	0.00	1.07	1.31	1.01E+00	7.81E-154	Up	5.90E-01	2.77E-44		1.71E+00	9.29E-131	Up	1.54E+00	1.47E-91	Up	1.01E+01	3.93E-07	Up	1.04E+01	6.29E-09	Up	Unigene16127_All//gi|16323184|gb|AAL15326.1|//4.00E-13//At1g30260/F12P21_9 [Arabidopsis thaliana] >gi|21436007|gb|AAM51581.1| At1g30260/F12P21_9 [Arabidopsis thaliana]	Unigene16127_All//7.00E-10//AT1G30260| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cytokinin stimulus; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: galactosyltransferase family protein (TAIR:AT4G21060.1); Has 16 Blast hits to 16 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene16127_All//0.00E+00//TC161131				nr +
Unigene16128_All	704	28.09	10.08	9.83	49.89	36.93	44.59	88.04	38.77	40.69	-1.48E+00	6.16E-27	Down	-1.51E+00	8.80E-27	Down	-4.34E-01	1.68E-07		-1.62E-01	1.04E-01		-1.18E+00	4.29E-72	Down	-1.11E+00	2.39E-67	Down	Unigene16128_All//gi|161377377|gb|ABX71676.1|//3.00E-70//60S ribosomal protein L6-like protein [Panax quinquefolius]	Unigene16128_All//5.00E-46//AT1G18540| 60S ribosomal protein L6 (RPL6A)	Unigene16128_All//0.00E+00//TC151055		ko03010|Ribosome		nr -
Unigene16129_All	1165	2.29	1.13	1.42	4.36	4.79	6.82	0.62	0.79	2.29	-1.02E+00	8.74E-03		-6.93E-01	8.66E-02		1.35E-01	6.46E-01		6.46E-01	1.53E-03		3.55E-01	6.21E-01		1.89E+00	4.51E-07	Up	Unigene16129_All//gi|74418996|gb|AB403223.1|//3.00E-62//S-adenosylmethionine decarboxylase 3 [Populus maximowiczii x Populus nigra]	Unigene16129_All//3.00E-110//AT5G18930| BUD2 (BUSHY AND DWARF 2); adenosylmethionine decarboxylase	Unigene16129_All//0.00E+00//gi|78345756|gb|DT566030.1|DT566030		ko00270|Cysteine and methionine metabolism//ko00330|Arginine and proline metabolism		nr +
Unigene16130_All	1526	6.75	8.33	3.25	0.65	1.62	1.27	0.11	0.00	0.00	3.03E-01	6.43E-02		-1.06E+00	2.06E-08	Down	1.32E+00	1.05E-03		9.63E-01	4.20E-02		-6.79E+00	1.35E-01		-6.79E+00	1.08E-01		Unigene16130_All//gi|164562219|gb|ABV61024.1|//7.00E-99//zinc finger-homeodomain protein 2 [Sarruma henryi]	Unigene16130_All//2.00E-65//AT1G14440| AtHB31 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 31); DNA binding / transcription factor	Unigene16130_All//0.00E+00//ES831341	zf-HD			nr -
Unigene16131_All	1065	1.67	3.28	5.05	19.04	14.36	15.14	23.66	9.89	9.54	9.75E-01	3.40E-03		1.60E+00	2.68E-08	Up	-4.07E-01	3.78E-04		-3.31E-01	7.35E-03		-1.26E+00	9.79E-33	Down	-1.31E+00	7.30E-36	Down	Unigene16131_All//gi|40549303|gb|AA887711.1|//8.00E-96//salicylic acid-binding protein 2 [Nicotiana tabacum]	Unigene16131_All//2.00E-90//AT2G23620| MES1 (METHYL ESTERASE 1); hydrolase, acting on ester bonds / methyl indole-3-acetate esterase/ methyl jasmonate esterase/ methyl salicylate esterase	Unigene16131_All//0.00E+00//gi|78344431|gb|DT564705.1|DT564705		ko00901|Indole alkaloid biosynthesis		nr +
Unigene16132_All	553	8.61	81.00	14.16	16.84	15.82	27.85	49.85	110.88	107.99	3.23E+00	8.00E-157	Up	7.17E-01	8.78E-04		-9.09E-02	6.87E-01		7.25E-01	1.91E-07		1.15E+00	2.20E-68	Up	1.12E+00	1.40E-64	Up			Unigene16132_All//1.00E-125//gi|78341670|gb|DT561944.1|DT561944				
Unigene16133_All	599	26.90	15.82	12.45	47.40	45.01	41.09	63.31	26.10	27.93	-7.66E-01	4.14E-08		-1.11E+00	8.08E-14	Down	-7.46E-02	5.53E-01		-2.06E-01	5.72E-02		-1.28E+00	4.47E-50	Down	-1.18E+00	1.51E-45	Down	Unigene16133_All//gi|3193222|gb|AAC19244.1|//1.00E-34//malate dehydrogenase [Glycine max]	Unigene16133_All//9.00E-35//AT1G53240| malate dehydrogenase (NAD), mitochondrial	Unigene16133_All//0.00E+00//gi|21103451|gb|BQ415764.1|BQ415764		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene16134_All	1323	3.12	20.11	6.16	15.59	16.81	20.93	14.70	19.05	34.51	2.69E+00	2.56E-77	Up	9.79E-01	4.40E-06		1.09E-01	4.38E-01		4.25E-01	2.47E-05		3.74E-01	1.17E-04		1.23E+00	7.25E-58	Up			Unigene16134_All//0.00E+00//TC177053				
Unigene16140_All	1115	10.46	5.86	5.73	14.74	14.05	8.26	2.54	1.16	1.46	-8.36E-01	5.95E-07		-8.69E-01	5.38E-07		-6.93E-02	6.81E-01		-8.35E-01	5.31E-10		-1.13E+00	8.07E-04	Down	-7.94E-01	1.31E-02		Unigene16140_All//gi|297810749|ref|XP_002873258.1|//4.00E-50//glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319095|gb|EFH49517.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16140_All//4.00E-47//AT5G06470| glutaredoxin family protein	Unigene16140_All//3.00E-140//TC159796				nr +
Unigene16143_All	802	48.93	25.71	21.71	40.87	32.76	53.50	90.41	43.62	38.35	-9.28E-01	1.67E-25		-1.17E+00	1.07E-35	Down	-3.19E-01	3.18E-04		3.88E-01	8.86E-07		-1.05E+00	9.99E-70	Down	-1.24E+00	6.71E-93	Down	Unigene16143_All//gi|15229149|ref|NP_190516.1|//3.00E-73//NAC2 (NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX SUBUNIT ALPHA-LIKE PROTEIN 2) [Arabidopsis thaliana] >gi|71151985|sp|Q94JX9.2|NAC2_ARATH RecName: Full=Nascent polypeptide-associated complex subunit alpha-like protein 2; Short=NAC-alpha-like protein 2; AltName: Full=Alpha-NAC-like protein 2 >gi|6561948|emb|CAB62452.1| alpha NAC-like protein [Arabidopsis thaliana]	Unigene16143_All//5.00E-41//AT3G49470| NAC2 (NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX SUBUNIT ALPHA-LIKE PROTEIN 2)	Unigene16143_All//0.00E+00//TC151167				nr -
Unigene16148_All	541	13.06	14.14	10.24	30.85	19.22	27.05	47.36	140.61	70.99	1.15E-01	6.09E-01		-3.51E-01	1.40E-01		-6.82E-01	4.38E-08		-1.90E-01	2.17E-01		1.57E+00	2.09E-135	Up	5.84E-01	1.99E-14		Unigene16148_All//gi|479090|emb|CAA55655.1|//2.00E-21//sulfate adenylyltransferase [Solanum tuberosum]	Unigene16148_All//2.00E-20//AT3G22890| APS1 (ATP SULFURYLASE 1); sulfate adenylyltransferase (ATP)	Unigene16148_All//0.00E+00//gi|109834207|gb|DW232772.1|DW232772		ko00230|Purine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr -

Unigene1615_All	2066	33.71	31.05	19.92	11.43	30.19	19.52	2.66	2.25	2.04	-1.19E-01	8.11E-02		-7.59E-01	1.02E-30		1.40E+00	1.57E-90	Up	7.72E-01	1.46E-20		-2.45E-01	3.32E-01		-3.80E-01	9.10E-02		Unigene1615_All//gi|224113419|ref|XP_002316491.1|//0.00E+00//cationic amino acid transporter [Populus trichocarpa] >gi|222865531|gb|EEF02662.1| cationic amino acid transporter [Populus trichocarpa]	Unigene1615_All//0.00E+00//AT3G10600| CAT7 (CATIONIC AMINO ACID TRANSPORTER 7); cationic amino acid transmembrane transporter	Unigene1615_All//0.00E+00//ES794141				nr +
Unigene16150_All	2005	0.21	0.25	0.29	6.46	4.62	2.55	3.31	0.88	0.56	2.75E-01	7.64E-01		4.84E-01	6.30E-01		-4.84E-01	9.92E-04		-1.34E+00	1.10E-16	Down	-1.92E+00	2.45E-16	Down	-2.57E+00	6.19E-24	Down	Unigene16150_All//gi|15218674|ref|NP_171800.1|//0.00E+00//phototropic-responsive NPH3 family protein [Arabidopsis thaliana] >gi|4587577|gb|AAD25808.1|AC006550_16 F1003.17 [Arabidopsis thaliana]	Unigene16150_All//0.00E+00//AT1G03010| phototropic-responsive NPH3 family protein	Unigene16150_All//0.00E+00//TC149150				nr +
Unigene16154_All	1236	2.07	1.56	1.03	4.23	2.84	4.60	7.49	4.77	3.51	-4.13E-01	3.08E-01		-1.00E+00	1.57E-02		-5.75E-01	2.14E-02		1.22E-01	6.86E-01		-6.52E-01	1.05E-04		-1.09E+00	1.63E-10	Down	Unigene16154_All//gi|194466195|gb|ACF74328.1|//1.00E-73//hypoxanthine phosphoribosyltransferase [Arachis hypogaea]	Unigene16154_All//6.00E-68//AT1G71750| phosphoribosyltransferase family protein	Unigene16154_All//0.00E+00//gi|164331431|gb|EV487218.1|EV487218		ko00230|Purine metabolism		nr -
Unigene16155_All	1803	13.12	9.81	11.73	20.31	15.62	17.08	17.92	10.92	8.22	-4.19E-01	1.87E-04		-1.62E-01	2.12E-01		-3.78E-01	3.64E-06		-2.49E-01	5.61E-03		-7.15E-01	9.49E-17		-1.12E+00	4.72E-36	Down	Unigene16155_All//gi|297726799|ref|NP_001175763.1|//1.00E-143//0s09g0314333 [Oryza sativa Japonica Group] >gi|50726385|dbj|BAD33996.1| integral membrane protein-like [Oryza sativa Japonica Group] >gi|255678762|dbj|BAH94491.1| Os09g0314333 [Oryza sativa Japonica Group]	Unigene16155_All//1.00E-141//AT5G19980| integral membrane family protein	Unigene16155_All//0.00E+00//TC160699				nr +
Unigene16156_All	814	58.23	16.68	28.91	29.56	20.39	21.31	4.00	1.54	2.64	-1.80E+00	1.94E-84	Down	-1.01E+00	6.71E-34	Down	-5.36E-01	1.41E-07		-4.72E-01	1.26E-05		-1.38E+00	1.60E-05	Down	-5.98E-01	4.35E-02		Unigene16156_All//gi|15230779|ref|NP_187329.1|//1.00E-66//thioredoxin family protein [Arabidopsis thaliana] >gi|75186129|sp|Q9M7X9.1|CITRX_ARATH RecName: Full=Thioredoxin-like protein CITRX, chloroplastic; AltName: Full=CF-9-interacting thioredoxin; Short=AtCITrx; AltName: Full=Thioredoxin TRXP; Flags: Precursor	Unigene16156_All//1.00E-66//AT3G06730| thioredoxin family protein	Unigene16156_All//0.00E+00//gi|164277284|gb|ES828444.1|ES828444				nr -
Unigene16159_All	872	2.28	4.36	1.04	3.71	4.86	5.23	5.53	3.69	2.60	9.35E-01	3.14E-03		-1.14E+00	1.99E-02		3.88E-01	2.18E-01		4.95E-01	9.13E-02		-5.83E-01	1.76E-02		-1.09E+00	7.57E-06	Down	Unigene16159_All//gi|115458604|ref|NP_001052902.1|//5.00E-37//Os04g0445400 [Oryza sativa Japonica Group] >gi|383445444|emb|CAD40966.2| OSJNBa0027P08.12 [Oryza sativa (japonica cultivar-group)] >gi|113564173|dbj|BAF14816.1| Os04g0445400 [Oryza sativa Japonica Group] >gi|116310229|emb|CAH67238.1| OSIGBa0140007.6 [Oryza sativa (indica cultivar-group)]	Unigene16159_All//1.00E-36//AT3G08880| unknown protein	Unigene16159_All//4.00E-154//TC154117				nr -
Unigene1616_All	452	7.52	5.16	8.25	13.67	11.43	7.39	1.96	1.48	0.26	-5.45E-01	1.06E-01		1.32E-01	6.89E-01		-2.58E-01	3.10E-01		-8.86E-01	1.48E-04		-4.09E-01	5.62E-01		-2.89E+00	3.04E-04	Down	Unigene1616_All//gi|261866472|gb|ACX94235.2|//2.00E-33//peptide N-glycanase [Solanum lycopersicum]	Unigene1616_All//4.00E-25//AT3G14920| unknown protein					nr +
Unigene16160_All	754	22.48	25.81	9.18	42.28	36.81	36.00	68.97	29.05	28.58	1.99E-01	1.37E-01		-1.29E+00	3.17E-18	Down	-2.00E-01	4.06E-02		-2.32E-01	1.89E-02		-1.25E+00	7.88E-66	Down	-1.27E+00	1.10E-69	Down	Unigene16160_All//gi|1762945|gb|AAC49975.1|//3.00E-19//ORF; able to induce HR-like lesions [Nicotiana tabacum]	Unigene16160_All//5.00E-10//AT4G14420| lesion inducing protein-related	Unigene16160_All//0.00E+00//gi|21090346|gb|BQ402659.1|BQ402659				nr +
Unigene16163_All	1856	16.35	19.00	18.22	1.45	2.28	3.21	9.18	11.12	16.38	2.17E-01	2.10E-02		1.56E-01	1.42E-01		6.55E-01	2.40E-02		1.15E+00	2.61E-06	Up	2.77E-01	1.28E-02		8.35E-01	6.01E-21		Unigene16163_All//gi|292630778|sp|Q9FFN2.2|GLYT3_ARATH//0.00E+00//RecName: Full=Probable glycosyltransferase At5g03795	Unigene16163_All//0.00E+00//AT5G03795| LOCATED IN: membrane; EXPRESSED IN: embryo, sepal, flower; EXPRESSED DURING: C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Exostosin-like (InterPro:IPR004263); BEST Arabidopsis thaliana protein match is: exostosin family protein (TAIR:AT3G07620.1); Has 866 Blast hits to 860 proteins in 87 species: Archae - 0; Bacteria - 9; Metazoa - 265; Fungi - 4; Plants - 504; Viruses - 0; Other Eukaryotes - 84 (source: NCBI BLink).	Unigene16163_All//0.00E+00//TC143482				nr +
Unigene16164_All	1105	2.94	3.39	0.24	2.61	3.96	2.08	0.23	0.00	0.07	2.09E-01	5.37E-01		-3.61E+00	2.06E-12	Down	5.98E-01	3.75E-02		-3.27E-01	4.15E-01		-7.84E+00	4.04E-02		-1.67E+00	2.56E-01		Unigene16164_All//gi|161610920|gb|ABX75139.1|//1.00E-143//lipase [Gossypium hirsutum]	Unigene16164_All//5.00E-117//AT5G18430| GDSL-motif lipase/hydrolase family protein	Unigene16164_All//0.00E+00//gi|78333131|gb|DT553405.1|DT553405				nr +
Unigene16165_All	805	90.21	74.34	65.82	162.07	136.63	148.62	50.63	13.29	13.31	-2.79E-01	5.35E-06		-4.55E-01	3.75E-13		-2.46E-01	2.16E-09		-1.25E-01	7.82E-03		-1.93E+00	2.99E-97	Down	-1.93E+00	4.94E-100	Down	Unigene16165_All//gi|21703131|gb|AAM74506.1|//5.00E-62//AT5g16250/T21H19_170 [Arabidopsis thaliana] >gi|23505791|gb|AAN28755.1| At5g16250/T21H19_170 [Arabidopsis thaliana]	Unigene16165_All//7.00E-58//AT5G16250| unknown protein	Unigene16165_All//0.00E+00//TC143704				nr +
Unigene16166_All	1017	21.14	32.98	40.74	2.01	2.95	2.58	0.67	3.04	3.21	6.41E-01	6.70E-12		9.46E-01	9.61E-27		5.53E-01	1.37E-01		3.59E-01	4.01E-01		2.19E+00	2.47E-09	Up	2.27E+00	1.81E-10	Up	Unigene16166_All//gi|15229333|ref|NP_191841.1|//2.00E-44//invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana]	Unigene16166_All//1.00E-44//AT3G62820| invertase/pectin methylesterase inhibitor family protein	Unigene16166_All//0.00E+00//TC178216		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene16168_All	1435	0.88	16.24	5.68	1.04	1.27	2.49	0.21	0.38	0.14	4.21E+00	2.83E-101	Up	2.70E+00	1.89E-23	Up	2.88E-01	5.96E-01		1.26E+00	1.51E-04	Up	8.77E-01	3.46E-01		-5.71E-01	6.28E-01		Unigene16168_All//gi|66954652|dbj|BAD99306.1|//0.00E+00//FtsH protease [Solanum lycopersicum]	Unigene16168_All//0.00E+00//AT5G15250| FTSH6 (FTSH PROTEASE 6); ATP-dependent peptidase/ ATPase/ metallopeptidase/ peptidase/ zinc ion binding	Unigene16168_All//0.00E+00//gi|31072598|gb|CA992877.1|CA992877				nr +
Unigene1617_All	2087	4.59	2.57	3.57	6.61	5.10	3.79	2.82	3.60	1.24	-8.34E-01	7.76E-06		-3.61E-01	7.03E-02		-3.75E-01	1.02E-02		-8.04E-01	5.30E-08		3.56E-01	7.09E-02		-1.18E+00	8.02E-08	Down	Unigene1617_All//gi|261866472|gb|ACX94235.2|//0.00E+00//peptide N-glycanase [Solanum lycopersicum]	Unigene1617_All//6.00E-174//AT3G14920| unknown protein	Unigene1617_All//1.00E-69//TC173554				nr +
Unigene16172_All	537	2.05	1.60	3.57	14.38	11.41	3.45	10.24	5.29	2.89	-3.51E-01	6.00E-01		8.03E-01	1.02E-01		-3.33E-01	1.18E-01		-2.06E+00	3.07E-18	Down	-9.52E-01	3.08E-05		-1.82E+00	3.11E-13	Down				Unigene16172_All//0.00E+00//TC146668			
Unigene16173_All	2602	0.02	0.00	0.00	0.42	0.19	0.43	3.57	2.14	14.36	-4.33E+00	6.13E-01		-4.33E+00	6.25E-01		-1.18E+00	5.94E-02		4.29E-02	9.43E-01		-7.43E-01	9.98E-06		2.01E+00	1.47E-95	Up	Unigene16173_All//gi|297811519|ref|XP_002873643.1|//1.00E-161//ATEX070C2 [Arabidopsis lyrata subsp. lyrata] >gi|297319480|gb|EFH49902.1| ATEX070C2 [Arabidopsis lyrata subsp. lyrata]	Unigene16173_All//4.00E-152//AT5G13990| ATEX070C2 (exocyst subunit EX070 family protein C2); protein binding	Unigene16173_All//2.00E-41//TC141553				nr +
Unigene16174_All	444	9.78	8.22	5.88	10.66	10.94	9.97	107.03	41.70	29.97	-2.51E-01	3.97E-01		-7.35E-01	1.56E-02		3.70E-02	9.15E-01		-9.65E-02	7.46E-01		-1.36E+00	1.02E-68	Down	-1.84E+00	3.68E-109	Down	Unigene16174_All//gi|195606206|gb|ACG24953.1|//2.00E-13//60S ribosomal protein L13a [Zea mays]	Unigene16174_All//1.00E-13//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene16174_All//0.00E+00//gi|21098265|gb|BQ410578.1|BQ410578		ko03010|Ribosome		nr -
Unigene16178_All	1452	1.77	0.21	0.66	1.99	1.78	1.93	4.43	0.72	1.43	-3.08E+00	3.71E-09	Down	-1.42E+00	9.46E-04	Down	-1.62E-01	6.90E-01		-4.51E-02	9.22E-01		-2.62E+00	7.07E-23	Down	-1.63E+00	2.88E-13	Down	Unigene16178_All//gi|79514788|ref|NP_197171.2|//1.00E-114//ORC3 (ORIGIN RECOGNITION COMPLEX SUBUNIT 3); protein binding [Arabidopsis thaliana] >gi|47681285|gb|AAT37463.1| origin recognition complex protein 3 [Arabidopsis thaliana]	Unigene16178_All//1.00E-115//AT5G16690| ORC3 (ORIGIN RECOGNITION COMPLEX SUBUNIT 3); protein binding	Unigene16178_All//0.00E+00//DW513603				nr -
Unigene16182_All	554	18.13	8.05	12.98	30.66	26.17	33.67	43.73	20.07	23.51	-1.17E+00	4.81E-10	Down	-4.83E-01	1.08E-02		-2.29E-01	1.04E-01		1.35E-01	3.85E-01		-1.12E+00	1.89E-26	Down	-8.95E-01	5.47E-19		Unigene16182_All//gi|297820930|ref|XP_002878348.1|//2.00E-23//40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata] >gi|297324186|gb|EFH54607.1| 40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata]	Unigene16182_All//9.00E-25//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene16182_All//0.00E+00//TC171211		ko03010|Ribosome		nr +
Unigene16183_All	624	2.18	26.63	6.83	8.22	8.50	13.75	4.47	14.47	25.47	3.61E+00	2.37E-64	Up	1.65E+00	5.53E-07	Up	4.76E-02	8.78E-01		7.42E-01	1.33E-04		1.69E+00	1.43E-18	Up	2.51E+00	7.36E-54	Up	Unigene16183_All//gi|224133384|ref|XP_002321554.1|//8.00E-25//predicted protein [Populus trichocarpa] >gi|222868550|gb|EEF05681.1| predicted protein [Populus trichocarpa]		Unigene16183_All//0.00E+00//DW496875				nr -
Unigene16184_All	1092	8.29	2.27	5.90	1.64	0.09	1.61	8.67	16.00	13.64	-1.87E+00	2.00E-17	Down	-4.90E-01	1.46E-02		-4.12E+00	3.96E-10	Down	-2.59E-02	9.47E-01		8.83E-01	3.19E-13		6.54E-01	2.56E-07		Unigene16184_All//gi|15240379|ref|NP_200995.1|//3.00E-41//AP2 domain-containing transcription factor family protein [Arabidopsis thaliana] >gi|75262469|sp|Q9FH54.1|EF114_ARATH RecName: Full=Ethylene-responsive transcription factor ERF114 >gi|9758388|dbj|BAB08875.1| AP2 domain transcription factor-like [Arabidopsis thaliana] >gi|182623784|gb|ACB88827.1| At5g61890 [Arabidopsis thaliana]	Unigene16184_All//9.00E-29//AT5G61890| AP2 domain-containing transcription factor family protein	Unigene16184_All//2.00E-166//TC168532	AP2-EREBP			nr -
Unigene16185_All	1558	9.84	7.81	8.44	7.51	7.65	5.13	19.95	11.48	4.96	-3.34E-01	2.16E-02		-2.21E-01	1.62E-01		2.54E-02	9.05E-01		-5.50E-01	7.13E-04		-7.97E-01	2.44E-19		-2.01E+00	1.12E-80	Down	Unigene16185_All//gi|306847798|ref|NP_173081.2|//1.00E-159//cation efflux family protein [Arabidopsis thaliana]	Unigene16185_All//3.00E-143//AT1G16310| cation efflux family protein	Unigene16185_All//2.00E-12//TC150406				nr +
Unigene16187_All	678	1.31	1.20	4.24	1.10	1.78	1.73	3.87	4.38	4.88	-1.34E-01	8.41E-01		1.69E+00	4.22E-05	Up	6.90E-01	2.98E-01		6.52E-01	3.31E-01		1.79E-01	6.48E-01		3.35E-01	2.79E-01									
Unigene1619_All	790	0.60	0.13	0.47	9.77	4.23	5.95	4.01	2.59	1.87	-2.22E+00	7.77E-02		-3.37E-01	7.34E-01		-1.21E+00	9.26E-10	Down	-7.17E-01	4.72E-04		-6.31E-01	4.37E-02		-1.11E+00	3.07E-04	Down	Unigene1619_All//gi|297720125|ref|NP_001172424.1|//1.00E-09//Os01g0564600 [Oryza sativa Japonica Group] >gi|255673372|dbj|BAH91154.1| Os01g0564600 [Oryza sativa Japonica Group]	Unigene1619_All//9.00E-10//AT3G47210| unknown protein	Unigene1619_All//2.00E-51//gi|11201961|gb|BF273903.1|BF273903				nr +

Unigene16191_All	944	129.97	89.58	140.80	56.99	72.77	68.99	13.12	7.88	4.73	-5.37E-01	2.13E-30		1.15E-01	1.93E-02		3.53E-01	1.30E-09		2.76E-01	1.54E-05		-7.36E-01	3.00E-07		-1.47E+00	1.99E-21	Down	Unigene16191_All//gi|266607|sp|Q01402.1|NDK2_SPIOL//2.00E-85//RecName: Full=Nucleoside diphosphate kinase 2, chloroplastic; AltName: Full=Nucleoside diphosphate kinase II; Short=NDP kinase II; Short=NDPK II; Short=NDK II; Contains: RecName: Full=Nucleoside diphosphate kinase 2 high molecular weight; Contains: RecName: Full=Nucleoside diphosphate kinase 2 low molecular weight; Flags: Precursor >gi|218273|dbj|BAA02018.1| nucleoside diphosphate kinase II [Spinacia oleracea]	Unigene16191_All//1.00E-74//AT5G63310| NDPK2 (NUCLEOSIDE DIPHOSPHATE KINASE 2); ATP binding / nucleoside diphosphate kinase/ protein binding	Unigene16191_All//0.00E+00//TC131048		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism		nr +
Unigene16192_All	669	65.07	75.74	71.24	60.83	82.15	95.52	21.93	52.35	15.72	2.19E-01	4.08E-03		1.31E-01	1.37E-01		4.33E-01	3.51E-11		6.51E-01	4.61E-24		1.26E+00	6.04E-45	Up	-4.80E-01	1.53E-04		Unigene16192_All//gi|119888002|gb|ABM05953.1|//6.00E-24//proline-rich protein [Gossypium hirsutum]		Unigene16192_All//0.00E+00//TC162767				nr -
Unigene16193_All	1316	41.23	111.54	61.42	15.44	38.60	46.81	0.55	6.61	8.42	1.44E+00	2.27E-186	Up	5.75E-01	4.94E-22		1.32E+00	1.64E-67	Up	1.60E+00	8.07E-99	Up	3.60E+00	1.82E-41	Up	3.95E+00	1.25E-57	Up	Unigene16193_All//gi|89258498|gb|AB065462.1|//6.00E-96//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene16193_All//2.00E-65//AT3G51880| short-chain dehydrogenase/reductase (SDR) family protein	Unigene16193_All//0.00E+00//TC152313		ko00906|Carotenoid biosynthesis		nr +
Unigene16194_All	396	7.27	2.56	1.88	12.20	9.39	9.47	0.00	0.00	0.00	-1.51E+00	1.10E-04	Down	-1.95E+00	5.30E-06	Down	-3.78E-01	1.74E-01		-3.66E-01	2.12E-01		null	null		null	null		Unigene16194_All//gi|92886081|gb|AB588091.1|//4.00E-13//Transferase family [Medicago truncatula]	Unigene16194_All//2.00E-13//AT3G50300| transferase family protein	Unigene16194_All//8.00E-49//TC140818				nr -
Unigene16195_All	1807	7.41	3.65	4.21	8.63	6.27	4.92	0.00	0.05	0.04	-1.02E+00	1.03E-10	Down	-8.15E-01	3.52E-07		-4.61E-01	4.89E-04		-8.09E-01	4.72E-09		5.53E+00	4.02E-01		5.46E+00	4.05E-01		Unigene16195_All//gi|115474463|ref|NP_001068828.1|//1.00E-86//Os08g0112200 [Oryza sativa Japonica Group] >gi|113622797|dbj|BAF22742.1| Os08g0112200 [Oryza sativa Japonica Group]	Unigene16195_All//3.00E-83//AT5G67150| transferase family protein	Unigene16195_All//1.00E-125//TC140818		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene16196_All	2373	5.71	0.81	1.93	12.49	8.24	11.51	19.56	8.91	11.13	-2.82E+00	4.96E-42	Down	-1.57E+00	2.15E-19	Down	-6.00E-01	3.59E-11		-1.17E-01	3.21E-01		-1.13E+00	1.08E-50	Down	-8.14E-01	2.37E-30		Unigene16196_All//gi|297826537|ref|XP_002881151.1|//0.00E+00//GTP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297326990|gb|EFH57410.1| GTP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene16196_All//0.00E+00//AT2G31060| elongation factor family protein	Unigene16196_All//0.00E+00//TC171464				nr +
Unigene1620_All	1700	1.14	1.19	1.66	11.98	7.11	6.99	6.72	4.72	2.53	6.62E-02	8.88E-01		5.44E-01	1.66E-01		-7.53E-01	1.65E-11		-7.78E-01	6.43E-11		-5.09E-01	6.86E-04		-1.41E+00	1.47E-18	Down	Unigene1620_All//gi|115485799|ref|NP_001068043.1|//1.00E-28//Os11g0543300 [Oryza sativa Japonica Group] >gi|113645265|dbj|BAF28406.1| Os11g0543300 [Oryza sativa Japonica Group]	Unigene1620_All//4.00E-24//AT3G50130| unknown protein	Unigene1620_All//7.00E-65//gi|11204961|gb|BF273903.1|BF273903				nr -
Unigene16200_All	598	0.09	0.00	0.18	3.75	3.17	2.42	2.19	0.28	0.40	-6.45E+00	6.13E-01		1.03E+00	7.03E-01		-2.43E-01	5.93E-01		-6.33E-01	1.48E-01		-2.97E+00	8.34E-06	Down	-2.46E+00	4.22E-05	Down	Unigene16200_All//gi|124488476|gb|ABN12322.1|//2.00E-24//phenylcoumaran benzylic ether reductase-like protein [Gossypium hirsutum]	Unigene16200_All//1.00E-16//AT4G39230| isoflavone reductase, putative	Unigene16200_All//7.00E-121//TC139438		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism		nr +
Unigene16201_All	805	54.01	43.12	55.83	871.16	907.29	683.40	323.06	89.46	113.58	-3.25E-01	5.80E-05		4.78E-02	6.24E-01		5.86E-02	1.45E-03		-3.50E-01	4.95E-84		-1.85E+00	0.00E+00	Down	-1.51E+00	0.00E+00	Down	Unigene16201_All//gi|124488476|gb|ABN12322.1|//1.00E-133//phenylcoumaran benzylic ether reductase-like protein [Gossypium hirsutum]	Unigene16201_All//3.00E-98//AT4G39230| isoflavone reductase, putative	Unigene16201_All//0.00E+00//TC144649		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism		nr -
Unigene16203_All	868	15.73	8.17	30.31	74.49	44.39	55.62	2.73	5.97	0.73	-9.45E-01	1.20E-09		9.46E-01	3.52E-17		-7.47E-01	4.34E-35		-4.21E-01	1.90E-11		1.13E+00	2.50E-06	Up	-1.89E+00	1.88E-06	Down	Unigene16203_All//gi|124359694|gb|ABD32361.2|//1.00E-27//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene16203_All//5.00E-27//AT4G20970| basic helix-loop-helix (bHLH) family protein	Unigene16203_All//0.00E+00//TC143732	bHLH			nr -
Unigene16204_All	548	2.39	7.67	2.92	7.54	11.50	24.72	6.94	4.65	7.34	1.68E+00	2.01E-07	Up	2.88E-01	6.16E-01		6.08E-01	7.64E-03		1.71E+00	2.94E-24	Up	-5.78E-01	4.04E-02		8.05E-02	7.73E-01		Unigene16204_All//gi|40218371|gb|AB83118.1|//1.00E-12//secretory laccase [Gossypium arboreum]	Unigene16204_All//3.00E-09//AT3G09220| LAC7 (laccase 7); laccase	Unigene16204_All//2.00E-170//C0112879		ko00910|Nitrogen metabolism		nr -
Unigene16205_All	482	11.72	38.69	21.21	35.24	46.29	69.90	1.93	2.17	2.48	1.72E+00	2.38E-31	Up	8.56E-01	4.34E-06		3.94E-01	3.53E-04		9.88E-01	6.76E-26		1.68E-01	7.81E-01		3.62E-01	5.21E-01		Unigene16205_All//gi|40218371|gb|AB83118.1|//5.00E-13//secretory laccase [Gossypium arboreum]	Unigene16205_All//8.00E-11//AT5G09360| LAC14 (laccase 14); laccase	Unigene16205_All//3.00E-172//C0112879		ko00910|Nitrogen metabolism		nr -
Unigene16206_All	777	14.14	35.41	6.78	17.95	60.27	52.60	0.00	0.11	0.26	1.32E+00	2.07E-31	Up	-1.06E+00	6.01E-09	Down	1.75E+00	2.67E-93	Up	1.55E+00	8.12E-63	Up	6.75E+00	4.02E-01		8.00E+00	7.89E-02		Unigene16206_All//gi|224140209|ref|XP_002329477.1|//8.00E-27//SAUR family protein [Populus trichocarpa] >gi|222868107|gb|EEF05238.1| SAUR family protein [Populus trichocarpa]	Unigene16206_All//4.00E-19//AT3G09870| auxin-responsive family protein	Unigene16206_All//0.00E+00//TC138921				nr +
Unigene16207_All	1477	42.33	20.58	24.88	16.16	13.06	6.91	0.00	0.11	0.03	-1.04E+00	1.91E-48	Down	-7.67E-01	3.74E-28		-3.07E-01	4.36E-03		-1.23E+00	2.70E-26	Down	6.82E+00	1.39E-01		4.75E+00	6.45E-01		Unigene16207_All//gi|20563|emb|CAA78386.1|//1.00E-127//protein 1 [Petunia x hybrida]	Unigene16207_All//9.00E-98//AT5G15310| ATMYB16 (MYB DOMAIN PROTEIN 16); DNA binding / transcription factor	Unigene16207_All//0.00E+00//TC139493	MYB			nr +
Unigene1621_All	1909	42.89	15.47	24.18	40.39	28.99	29.19	22.68	18.89	15.09	-1.47E+00	1.49E-108	Down	-8.27E-01	1.05E-41		-4.79E-01	6.19E-19		-4.69E-01	2.54E-16		-2.63E-01	3.17E-04		-5.88E-01	2.07E-16		Unigene1621_All//gi|18399836|ref|NP_566442.1|//1.00E-102//myb family transcription factor [Arabidopsis thaliana] >gi|42572405|ref|NP_974298.1| myb family transcription factor [Arabidopsis thaliana]	Unigene1621_All//3.00E-71//AT3G13040| myb family transcription factor	Unigene1621_All//0.00E+00//TC131916	G2-like			nr +
Unigene16212_All	1568	14.85	15.90	13.96	8.77	12.58	7.06	0.00	0.21	0.38	9.86E-02	4.18E-01		-8.93E-02	5.11E-01		5.21E-01	7.01E-06		-3.13E-01	4.61E-02		7.74E+00	1.27E-02		8.57E+00	1.75E-04	Up	Unigene16212_All//gi|124359372|gb|ABN05838.1|//1.00E-142//Protein kinase [Medicago truncatula]	Unigene16212_All//4.00E-72//AT5G24080| protein kinase family protein	Unigene16212_All//1.00E-66//DW499534		ko04626|Plant-pathogen interaction		nr -
Unigene16213_All	1690	0.00	0.00	0.06	5.92	2.18	2.03	5.33	6.97	5.75	null	null		5.98E+00	3.99E-01		-1.44E+00	2.38E-16	Down	-1.54E+00	6.18E-16	Down	3.88E-01	9.46E-03		1.10E-01	5.59E-01		Unigene16213_All//gi|224126161|ref|XP_002319770.1|//1.00E-170//cytochrome P450 [Populus trichocarpa] >gi|222858146|gb|EEE95693.1| cytochrome P450 [Populus trichocarpa]	Unigene16213_All//1.00E-145//AT5G24900| CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene16213_All//7.00E-68//TC171887		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene16214_All	583	8.44	35.89	14.07	16.23	33.37	40.83	32.20	40.00	47.63	2.09E+00	2.58E-45	Up	7.38E-01	4.45E-04		1.04E+00	6.28E-18	Up	1.33E+00	2.54E-29	Up	3.13E-01	2.29E-03		5.65E-01	4.08E-10		Unigene16214_All//gi|728626|emb|CAA88492.1|//3.00E-07//TAF-2 [Nicotiana tabacum]		Unigene16214_All//0.00E+00//gi|48747599|gb|C0078118.1|C0078118				nr +
Unigene16216_All	715	54.37	55.63	57.12	68.97	68.29	66.32	90.41	45.65	31.48	3.31E-02	7.26E-01		7.13E-02	4.80E-01		-1.43E-02	8.77E-01		-5.65E-02	5.69E-01		-9.86E-01	4.74E-56		-1.52E+00	1.64E-113	Down	Unigene16216_All//gi|28416547|gb|AA042804.1|//2.00E-48//At4g16450 [Arabidopsis thaliana]	Unigene16216_All//1.00E-49//AT4G16450| unknown protein	Unigene16216_All//0.00E+00//BG446707				nr -
Unigene16217_All	1208	4.81	3.78	1.94	8.70	11.32	8.67	6.62	9.27	26.32	-3.49E-01	1.69E-01		-1.31E+00	8.75E-07	Down	3.79E-01	1.10E-02		-4.50E-03	9.77E-01		4.87E-01	1.33E-03		1.99E+00	1.15E-80	Up	Unigene16217_All//gi|29029104|gb|AA064931.1|//1.00E-80//At5g47310 [Arabidopsis thaliana]	Unigene16217_All//2.00E-80//AT5G47310| unknown protein	Unigene16217_All//0.00E+00//ES808128				nr -
Unigene16218_All	1416	10.05	4.83	8.50	13.26	12.04	7.05	8.21	2.42	0.76	-1.06E+00	6.81E-12	Down	-2.42E-01	1.41E-01		-1.40E-01	3.31E-01		-9.12E-01	4.61E-13		-1.76E+00	4.62E-25	Down	-3.43E+00	3.71E-55	Down	Unigene16218_All//gi|5926718|dbj|BAB48640.1|//3.00E-94//PRA2 [Pisum sativum]	Unigene16218_All//7.00E-82//AT1G01200| ATRABA3 (ARABIDOPSIS RAB GTPASE HOMOLOG A3); GTP binding	Unigene16218_All//0.00E+00//TC135338				nr +
Unigene16219_All	1135	6.08	2.46	7.84	12.16	9.74	6.21	0.67	0.66	0.77	-1.31E+00	2.33E-08	Down	3.65E-01	7.83E-02		-3.20E-01	3.27E-02		-9.70E-01	9.40E-11		-1.67E-02	1.02E+00		2.04E-01	7.47E-01		Unigene16219_All//gi|124359162|gb|ABN05685.1|//2.00E-09//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene16219_All//4.00E-06//AT3G25270| nucleic acid binding	Unigene16219_All//1.00E-179//gi|18099344|gb|BM358598.1|BM358598				nr -
Unigene1622_All	1817	4.43	1.67	3.31	3.84	2.79	3.28	3.07	2.55	1.18	-1.41E+00	1.23E-10	Down	-4.21E-01	5.23E-02		-4.62E-01	3.18E-02		-2.26E-01	3.77E-01		-2.67E-01	2.76E-01		-1.38E+00	3.21E-09	Down	Unigene1622_All//gi|18399836|ref|NP_566442.1|//1.00E-107//myb family transcription factor [Arabidopsis thaliana] >gi|42572405|ref|NP_974298.1| myb family transcription factor [Arabidopsis thaliana]	Unigene1622_All//3.00E-76//AT3G13040| myb family transcription factor	Unigene1622_All//0.00E+00//TC131916	G2-like			nr +
Unigene16221_All	887	33.27	55.47	51.03	12.13	24.61	16.80	20.07	3.39	13.61	7.38E-01	1.26E-21		6.17E-01	3.19E-14		1.02E+00	1.67E-19	Up	4.70E-01	1.04E-03		-2.56E+00	1.04E-60	Down	-5.60E-01	9.43E-07		Unigene16221_All//gi|20198088|gb|AAM15393.1|//2.00E-38//Expressed protein [Arabidopsis thaliana] >gi|56236118|gb|AAV84515.1| At2g20515 [Arabidopsis thaliana] >gi|89001021|gb|ABD59100.1| At2g20515 [Arabidopsis thaliana]	Unigene16221_All//9.00E-38//AT2G20515| unknown protein	Unigene16221_All//0.00E+00//TC135548				nr +
Unigene16226_All	1001	341.78	137.23	125.17	1316.12	1354.23	800.13	24.79	8.68	3.94	-1.32E+00	0.00E+00	Down	-1.45E+00	0.00E+00	Down	4.12E-02	2.45E-03		-7.18E-01	0.00E+00		-1.51E+00	1.90E-42	Down	-2.65E+00	1.79E-90	Down	Unigene16226_All//gi|144925053|gb|ABP03851.1|//5.00E-67//Plant lipid transfer/seed storage/trypsin-alpha amylase inhibitor [Medicago truncatula]	Unigene16226_All//1.00E-33//AT2G10940| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene16226_All//0.00E+00//gi|109873350|gb|DW502325.1|DW502325				nr +
Unigene16228_All	1670	1.13	0.00	0.35	0.00	0.00	0.00	2.71	9.21	1.48	-1.01E+01	6.73E-11	Down	-1.69E+00	1.44E-03		null	null		null	null		1.77E+00	6.48E-33	Up	-8.73E-01	3.94E-04		Unigene16228_All//gi|42566408|ref|NP_192810.2|//6.00E-59//ankyrin repeat family protein [Arabidopsis thaliana] >gi|66792696|gb|AAY56450.1| At4g10720 [Arabidopsis thaliana]	Unigene16228_All//1.00E-54//AT4G10720| ankyrin repeat family protein	Unigene16228_All//7.00E-68//TC148785				nr -
Unigene16230_All	777	3.57	3.06	6.03	8.14	13.65	9.88	14.37	9.47	5.33	-2.20E-01	5.88E-01		7.57E-01	9.03E-03		7.45E-01	6.22E-06		2.79E-01	2.28E-01		-6.02E-01	6.97E-05		-1.43E+00	1.41E-18	Down	Unigene16230_All//gi|226713187|sp|A7P0P3.1|U497G_VITVI//4.00E-68//RecName: Full=UPF0497 membrane protein 16	Unigene16230_All//1.00E-41//AT5G54980| integral membrane family protein	Unigene16230_All//0.00E+00//gi|109891402|gb|DW520365.1|DW520365				nr +
Unigene16232_All	738	16.73	119.46	47.04	15.73	31.36	46.33	41.31	151.10	120.76	2.84E+00	1.24E-270	Up	1.49E+00	8.84E-46	Up	9.96E-01	7.71E-20		1.56E+00	5.63E-53	Up	1.87E+00	9.64E-254	Up	1.55E+00	1.86E-158	Up	Unigene16232_All//gi|8131905|gb|AAF73132.1|AF149017_1//5.00E-73//homogentisate 1,2-dioxygenase [Solanum lycopersicum]	Unigene16232_All//2.00E-69//AT5G54080| HGO (HOMOGENTISATE 1,2-DIOXYGENASE); homogentisate 1,2-dioxygenase	Unigene16232_All//0.00E+00//TC148620		ko00350|Tyrosine metabolism		nr -
Unigene16233_All	637	18.32	20.12	17.14	21.66	21.08	22.62	45.86	21.98	18.82	1.36E-01	4.30E-01		-9.60E-02	6.19E-01		-3.91E-02	8.25E-01		6.23E-02	7.15E-01		-1.06E+00	5.48E-29	Down	-1.28E+00	3.35E-40	Down	Unigene16233_All//gi|297850248|ref|XP_002893005.1|//7.00E-35//3-phosphoserine phosphatase [Arabidopsis lyrata subsp. lyrata] >gi|297338847|gb|EFH69264.1| 3-phosphoserine phosphatase [Arabidopsis lyrata subsp. lyrata]	Unigene16233_All//4.00E-36//AT1G18640| PSP (3-PHOSPHOSERINE PHOSPHATASE); phosphoserine phosphatase	Unigene16233_All//0.00E+00//BF275353		ko00260|Glycine, serine and threonine metabolism		nr -
Unigene16234_All	1003	0.63	5.56	1.17	18.48	18.23	22.78	3.08	5.50	23.16	3.15E+00	1.88E-19	Up	9.00E-01	1.70E-01		-1.93E-02	9.02E-01		3.02E-01	9.50E-03		8.38E-01	2.15E-04		2.91E+00	5.78E-92	Up	Unigene16234_All//gi|209954711|dbj|BAG80546.1|//1.00E-94//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene16234_All//2.00E-81//AT1G24100| UGT74B1 (UDP-glucosyl transferase 74B1); UDP-glycosyltransferase/ thiohydroximate beta-D-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene16234_All//0.00E+00//TC144828		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr -
Unigene16235_All	490	8.54	7.86	5.43	42.60	36.68	39.73	97.85	98.26	44.15	-1.20E-01	6.82E-01		-6.53E-01	3.64E-02		-2.16E-01	8.47E-02		-1.01E-01	4.92E-01		6.10E-03	9.70E-01		-1.15E+00	6.81E-55	Down	Unigene16235_All//gi|211906506|gb|ACJ11746.1|//3.00E-61//luminal binding protein [Gossypium hirsutum]	Unigene16235_All//8.00E-46//AT5G42020| BIP2; ATP binding	Unigene16235_All//0.00E+00//TC140343		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr +

Unigene16236_All	616	13.00	8.88	4.50	1.94	1.23	7.63	0.89	29.11	1.55	-5.49E-01	7.44E-03		-1.53E+00	2.39E-11	Down	-6.58E-01	2.90E-01		1.97E+00	1.77E-10	Up	5.03E+00	1.61E-106	Up	7.99E-01	1.95E-01		Unigene16236_All//gi|15220033|ref|NP_173153.1|//2.00E-26//SOUL heme-binding family protein [Arabidopsis thaliana] >gi|5734756|gb|AAD50021.1|AC007651_16 Similar to SOUL Protein [Arabidopsis thaliana] >gi|21592576|gb|AAM64525.1| SOUL-like protein [Arabidopsis thaliana] >gi|88196741|gb|ABD43013.1|At1g17100 [Arabidopsis thaliana]	Unigene16236_All//1.00E-27//AT1G17100| SOUL heme-binding family protein	Unigene16236_All//5.00E-153//CA993140				nr +
Unigene16237_All	997	38.05	35.07	32.47	12.09	5.56	21.88	1.36	31.32	1.20	-1.18E-01	2.24E-01		-2.29E-01	1.46E-02		-1.12E+00	2.72E-13	Down	8.56E-01	1.88E-13		4.53E+00	1.13E-174	Up	-1.79E-01	7.13E-01		Unigene16237_All//gi|115435220|ref|NP_001042368.1|//1.00E-30//Os01g0210500 [Oryza sativa Japonica Group] >gi|113531899|dbj|BAF04282.1|Os01g0210500 [Oryza sativa Japonica Group]	Unigene16237_All//2.00E-31//AT1G17100| SOUL heme-binding family protein	Unigene16237_All//3.00E-177//gi|31072861|gb|CA993140.1|CA993140				nr -
Unigene16240_All	685	4.05	3.03	5.75	3.42	5.33	3.56	4.20	2.99	1.05	-4.17E-01	2.77E-01		5.07E-01	1.22E-01		6.41E-01	4.47E-02		5.89E-02	9.09E-01		-4.89E-01	1.47E-01		-2.00E+00	3.47E-08	Down	Unigene16240_All//gi|115450509|ref|NP_001048855.1|//5.00E-08//Os03g0130500 [Oryza sativa Japonica Group] >gi|108706005|gb|ABF93800.1| EF hand family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547326|dbj|BAF10769.1|Os03g0130500 [Oryza sativa Japonica Group]		Unigene16240_All//4.00E-21//EX164083				nr +
Unigene16241_All	850	5.79	34.87	11.21	4.22	4.13	4.73	4.78	20.11	4.59	2.59E+00	9.29E-83	Up	9.55E-01	9.71E-07		-3.02E-02	9.30E-01		1.64E-01	6.34E-01		2.07E+00	3.99E-45	Up	-5.61E-02	8.45E-01					Unigene16241_All//2.00E-91//gi|189092583|gb|FG548118.1|FG548118				
Unigene16246_All	645	9.49	36.29	43.34	35.45	8.12	9.10	3.61	2.53	1.67	1.94E+00	7.43E-46	Up	2.19E+00	1.82E-62	Up	-2.13E+00	5.04E-64	Down	-1.96E+00	8.20E-50	Down	-5.13E-01	1.82E-01		-1.11E+00	2.29E-03		Unigene16246_All//gi|295792206|gb|ADG29118.1|//3.00E-34//gamma-expansin natriuretic peptide [Alnus glutinosa]	Unigene16246_All//1.00E-28//AT2G18660| EXLB3 (EXPANSIN-LIKE B3 PRECURSOR)	Unigene16246_All//0.00E+00//TC165572				nr +
Unigene16247_All	854	1.78	4.92	4.99	2.80	4.15	4.13	2.13	1.81	3.55	1.47E+00	3.03E-06	Up	1.49E+00	3.94E-06	Up	5.69E-01	8.35E-02		5.59E-01	9.96E-02		-2.34E-01	6.42E-01		7.36E-01	1.74E-02					Unigene16247_All//3.00E-07//EX169027				
Unigene16249_All	392	2.40	9.69	13.04	5.97	4.57	6.45	6.36	2.77	1.32	2.01E+00	2.10E-08	Up	2.44E+00	2.39E-13	Up	-3.87E-01	3.73E-01		1.11E-01	7.90E-01		-1.20E+00	1.00E-03		-2.27E+00	2.76E-08	Down	Unigene16249_All//gi|15237967|ref|NP_197247.1|//5.00E-30//heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related [Arabidopsis thaliana] >gi|9755769|emb|CAC01889.1|farnesylated protein ATFP6-like protein [Arabidopsis thaliana] >gi|117168109|gb|ABX32137.1|At5g17450 [Arabidopsis thaliana]	Unigene16249_All//2.00E-31//AT5G17450| heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	Unigene16249_All//6.00E-136//TC175069				nr -
Unigene1625_All	1609	1.72	14.77	1.65	4.27	10.77	5.59	11.06	36.26	123.87	3.10E+00	4.51E-80	Up	-5.86E-02	8.85E-01		1.33E+00	1.82E-23	Up	3.87E-01	5.15E-02		1.71E+00	9.27E-118	Up	3.49E+00	0.00E+00	Up	Unigene1625_All//gi|259121399|gb|ACY92019.1|//1.00E-61//WRKY transcription factor 17 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene1625_All//4.00E-59//AT2G38470| WRKY33; transcription factor	Unigene1625_All//0.00E+00//TC141199	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene16250_All	592	7.95	17.63	20.87	8.75	7.68	7.32	11.57	5.93	3.23	1.15E+00	4.69E-10	Up	1.39E+00	5.00E-15	Up	-1.89E-01	5.39E-01		-2.57E-01	3.94E-01		-9.64E-01	1.89E-06		-1.84E+00	1.70E-16	Down	Unigene16250_All//gi|15237967|ref|NP_197247.1|//7.00E-60//heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related [Arabidopsis thaliana] >gi|9755769|emb|CAC01889.1|farnesylated protein ATFP6-like protein [Arabidopsis thaliana] >gi|117168109|gb|ABX32137.1|At5g17450 [Arabidopsis thaliana]	Unigene16250_All//4.00E-61//AT5G17450| heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	Unigene16250_All//0.00E+00//gi|109869216|gb|DW498192.1|DW498192				nr +
Unigene16251_All	687	0.84	1.18	1.63	0.29	0.40	0.53	1.91	0.24	0.87	4.94E-01	5.26E-01		9.58E-01	1.54E-01		4.68E-01	8.17E-01		8.59E-01	5.42E-01		-2.97E+00	8.34E-06	Down	-1.13E+00	2.59E-02		Unigene16251_All//gi|15237967|ref|NP_197247.1|//9.00E-61//heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related [Arabidopsis thaliana] >gi|9755769|emb|CAC01889.1|farnesylated protein ATFP6-like protein [Arabidopsis thaliana] >gi|117168109|gb|ABX32137.1|At5g17450 [Arabidopsis thaliana]	Unigene16251_All//5.00E-62//AT5G17450| heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	Unigene16251_All//0.00E+00//gi|109869216|gb|DW498192.1|DW498192				nr +
Unigene16252_All	520	18.31	16.66	11.57	19.64	18.54	23.62	80.98	51.44	33.71	-1.36E-01	5.08E-01		-6.62E-01	6.06E-04		-8.29E-02	7.06E-01		2.67E-01	1.27E-01		-6.55E-01	1.27E-18		-1.26E+00	3.68E-56	Down	Unigene16252_All//gi|115439995|ref|NP_001044277.1|//4.00E-11//Os01g0754100 [Oryza sativa Japonica Group] >gi|57899617|dbj|BAD87196.1| DNA-binding protein-related-like [Oryza sativa Japonica Group] >gi|57900332|dbj|BAD87285.1| DNA-binding protein-related-like [Oryza sativa Japonica Group] >gi|113533808|dbj|BAF06191.1|Os01g0754100 [Oryza sativa Japonica Group]	Unigene16252_All//6.00E-07//AT1G23750| DNA-binding protein-related	Unigene16252_All//0.00E+00//gi|21090214|gb|BQ402527.1|BQ402527		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +
Unigene16253_All	1410	0.59	0.00	0.08	3.64	2.86	3.84	12.86	1.01	5.09	-9.21E+00	5.57E-05	Down	-2.98E+00	3.83E-03		-3.49E-01	2.02E-01		7.90E-02	7.85E-01		-3.67E+00	8.05E-88	Down	-1.34E+00	6.66E-27	Down	Unigene16253_All//gi|15239360|ref|NP_200861.1|//1.00E-134//late embryogenesis abundant protein-related / LEA protein-related [Arabidopsis thaliana] >gi|23308395|gb|AAN18167.1|At5g60530/mif9_180 [Arabidopsis thaliana]	Unigene16253_All//1.00E-128//AT5G60530| late embryogenesis abundant protein-related / LEA protein-related	Unigene16253_All//3.00E-45//TC177555				nr +
Unigene16256_All	753	0.56	7.00	3.39	4.17	3.20	3.96	3.59	4.38	2.01	3.65E+00	6.74E-21	Up	2.61E+00	1.93E-07	Up	-3.81E-01	3.03E-01		-7.43E-02	8.50E-01		2.87E-01	3.97E-01		-8.38E-01	1.09E-02					Unigene16256_All//0.00E+00//TC161489				
Unigene16257_All	868	1.51	0.82	3.80	7.35	4.36	3.38	6.28	5.92	4.31	-8.83E-01	1.32E-01		1.34E+00	2.75E-04	Up	-7.51E-01	5.30E-04		-1.12E+00	1.49E-06	Down	-8.53E-02	7.31E-01		-5.43E-01	1.39E-02		Unigene16257_All//gi|15226168|ref|NP_178215.1|//4.00E-06//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene16257_All//1.00E-07//AT2G01050| nucleic acid binding / zinc ion binding	Unigene16257_All//4.00E-142//TC173113				nr -
Unigene1626_All	1677	3.93	23.66	2.86	7.25	22.34	15.86	17.14	43.64	206.18	2.59E+00	1.67E-110	Up	-4.60E-01	5.81E-02		1.62E+00	2.12E-67	Up	1.13E+00	1.91E-25	Up	1.35E+00	7.66E-104	Up	3.59E+00	0.00E+00	Up	Unigene1626_All//gi|259121399|gb|ACY92019.1|//1.00E-139//WRKY transcription factor 17 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene1626_All//6.00E-111//AT2G38470| WRKY33; transcription factor	Unigene1626_All//0.00E+00//gi|78323865|gb|DT544139.1|DT544139	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene16263_All	614	45.25	33.59	24.37	64.34	54.57	73.92	113.69	63.99	46.78	-4.30E-01	2.78E-05		-8.93E-01	1.84E-16		-2.38E-01	4.12E-03		2.00E-01	1.46E-02		-8.29E-01	2.28E-45		-1.28E+00	1.99E-94	Down	Unigene16263_All//gi|106879137|gb|ABF82598.1|//3.00E-16//At3g01130 [Arabidopsis thaliana]	Unigene16263_All//2.00E-17//AT3G01130| unknown protein	Unigene16263_All//0.00E+00//TC163106				nr -
Unigene16265_All	1410	16.14	3.77	3.89	9.47	9.35	5.93	0.21	0.47	0.71	-2.10E+00	8.05E-50	Down	-2.05E+00	1.09E-46	Down	-1.76E-02	9.25E-01		-6.76E-01	6.41E-06		1.18E+00	1.44E-01		1.75E+00	6.57E-03		Unigene16265_All//gi|15224182|ref|NP_179437.1|//1.00E-165//protein kinase family protein [Arabidopsis thaliana]	Unigene16265_All//4.00E-160//AT2G18470| protein kinase family protein	Unigene16265_All//0.00E+00//TC165138		ko00270|Cysteine and methionine metabolism		nr +
Unigene16266_All	762	18.74	15.43	18.31	10.07	13.33	16.00	17.98	6.31	11.87	-2.81E-01	6.75E-02		-3.39E-02	8.39E-01		4.05E-01	2.26E-02		6.69E-01	2.50E-05		-1.51E+00	1.01E-23	Down	-5.99E-01	5.58E-06		Unigene16266_All//gi|295646606|gb|ADE55749.1|//2.00E-31//secretory phospholipase A2 alpha [Citrus sinensis]	Unigene16266_All//3.00E-30//AT2G06925| PLA2-ALPHA; phospholipase A2	Unigene16266_All//0.00E+00//TC152737		ko00592|alpha-Linolenic acid metabolism//ko00564|Glycerophospholipid metabolism//ko00591|Linoleic acid metabolism//ko00565|Ether lipid metabolism//ko00590|Arachidonic acid metabolism		nr -
Unigene16268_All	692	20.34	22.41	12.54	26.71	22.49	25.91	36.48	24.52	18.19	1.40E-01	3.72E-01		-6.97E-01	6.59E-06		-2.48E-01	5.87E-02		-4.37E-02	7.71E-01		-5.73E-01	3.11E-09		-1.00E+00	1.00E-23	Down	Unigene16268_All//gi|30841446|gb|AAP43361.1|//2.00E-41//fiber protein Fb14 [Gossypium barbadense] >gi|66271051|gb|AAY43803.1| Fb14 [Gossypium hirsutum]	Unigene16268_All//2.00E-36//AT2G47690| NADH-ubiquinone oxidoreductase-related	Unigene16268_All//0.00E+00//TC160357		ko00190|Oxidative phosphorylation		nr +
Unigene16269_All	530	43.34	34.90	27.73	53.57	41.06	40.39	249.13	77.83	68.03	-3.13E-01	7.12E-03		-6.44E-01	4.43E-08		-3.84E-01	4.93E-05		-4.08E-01	3.99E-05		-1.68E+00	7.52E-259	Down	-1.87E+00	0.00E+00	Down			Unigene16269_All//0.00E+00//gi|164352574|gb|EX171513.1|EX171513		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		kegg +
Unigene1627_All	2344	59.87	9.88	16.49	91.68	93.57	63.89	29.38	8.13	7.92	-2.60E+00	0.00E+00	Down	-1.86E+00	1.52E-251	Down	2.94E-02	5.28E-01		-5.21E-01	6.34E-54		-1.85E+00	2.82E-155	Down	-1.89E+00	2.49E-164	Down	Unigene1627_All//gi|297834078|ref|XP_002884921.1|//1.00E-107//methyladenine glycosylase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330761|gb|EFH61180.1|methyladenine glycosylase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1627_All//1.00E-100//AT3G12710| methyladenine glycosylase family protein	Unigene1627_All//0.00E+00//TC146169		ko03410|Base excision repair		nr +
Unigene16271_All	517	12.95	25.97	16.07	36.61	29.71	28.39	50.70	84.64	127.45	1.00E+00	2.26E-10	Up	3.11E-01	1.52E-01		-3.02E-01	1.55E-02		-3.67E-01	3.82E-03		7.39E-01	1.07E-23		1.33E+00	1.27E-93	Up	Unigene16271_All//gi|259121417|gb|ACY92028.1|//1.00E-62//WRKY transcription factor 26 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene16271_All//1.00E-19//AT4G24240| WRKY7; calmodulin binding / transcription factor	Unigene16271_All//3.00E-46//DV849051	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene16272_All	614	4.60	6.02	2.34	9.49	9.42	8.09	6.40	2.79	3.89	3.89E-01	2.31E-01		-9.75E-01	1.32E-02		-1.07E-02	9.62E-01		-2.30E-01	4.06E-01		-1.20E+00	2.08E-05	Down	-7.18E-01	6.74E-03		Unigene16272_All//gi|94807638|gb|AB4F47116.1|//2.00E-09//At5g10745 [Arabidopsis thaliana]	Unigene16272_All//9.00E-11//AT5G10745| unknown protein					nr +
Unigene16273_All	2109	10.69	2.91	6.51	0.14	0.13	0.00	10.52	1.61	3.68	-1.88E+00	8.69E-43	Down	-7.15E-01	2.10E-09		-1.18E-01	9.01E-01		-7.15E+00	4.00E-02		-2.71E+00	2.12E-80	Down	-1.51E+00	2.98E-39	Down	Unigene16273_All//gi|22329258|ref|NP_195674.2|//0.00E+00//GGT1 (GAMMA-GLUTAMYL TRANSPEPTIDASE 1); gamma-glutamyltransferase/ glutathione gamma-glutamylcysteinyltransferase [Arabidopsis thaliana] >gi|42573241|ref|NP_974717.1| GGT1 (GAMMA-GLUTAMYL TRANSPEPTIDASE 1); gamma-glutamyltransferase/ glutathione gamma-glutamylcysteinyltransferase [Arabidopsis thaliana] >gi|17978922|gb|AAL47428.1|AT4g39640/T19F19_30 [Arabidopsis thaliana] >gi|23308189|gb|AAN18064.1|At4g39640/T19F19_30 [Arabidopsis thaliana]	Unigene16273_All//0.00E+00//AT4G39640| GGT1 (GAMMA-GLUTAMYL TRANSPEPTIDASE 1); gamma-glutamyltransferase/ glutathione gamma-glutamylcysteinyltransferase	Unigene16273_All//0.00E+00//TC130431		ko00480|Glutathione metabolism//ko00460|Cyanoamino acid metabolism//ko00450|Selenoamino acid metabolism//ko00590|Arachidonic acid metabolism//ko00430|Taurine and hypotaurine metabolism		nr +

Unigene16274_All	520	9.16	12.28	17.51	9.77	13.11	8.95	8.29	4.50	3.06	4.23E-01	7.51E-02		9.36E-01	2.82E-06		4.24E-01	6.16E-02		-1.27E-01	6.85E-01		-8.82E-01	7.19E-04		-1.44E+00	9.36E-08	Down	Unigene16274_All//gi|297603161|ref|NP_001053544.2|//1.00E-52//Os04g0560200 [Oryza sativa Japonica Group] >gi|75144354|sp|Q7XSQ7.2|TRL33_ORYSJ RecName: Full=Thioredoxin-like 3-3; AltName: Full=Thioredoxin-like 1 >gi|38345841|emb|CAE01844.2|OSJNBa0084K11.5 [Oryza sativa (Japonica cultivar-group)] >gi|116311129|emb|CAH68055.1|B0103C08-B0602B01.12 [Oryza sativa (indica cultivar-group)] >gi|255675680|dbj|BAF15458.2|Os04g0560200 [Oryza sativa Japonica Group]	Unigene16274_All//8.00E-47//AT3G53220| thioredoxin family protein	Unigene16274_All//0.00E+00//DW496619				nr -
Unigene16276_All	926	0.00	38.08	2.82	0.43	0.48	13.41	0.09	0.72	5.81	1.52E+01	1.84E-203	Up	1.15E+01	2.12E-14	Up	1.68E-01	9.04E-01		4.96E+00	1.47E-63	Up	2.98E+00	2.86E-03		5.99E+00	3.56E-35	Up			Unigene16276_All//3.00E-13//TC134564				
Unigene16277_All	1009	0.00	20.04	1.00	0.30	0.27	6.89	0.00	0.08	1.86	1.43E+01	2.55E-116	Up	9.97E+00	1.27E-05	Up	-1.18E-01	9.01E-01		4.54E+00	6.79E-34	Up	6.37E+00	4.02E-01		1.09E+01	1.95E-13	Up			Unigene16277_All//7.00E-36//TC134564				
Unigene16278_All	931	1.63	1.85	0.00	5.62	4.99	3.06	3.59	3.37	7.23	1.83E-01	6.99E-01		-1.07E+01	2.73E-08	Down	-1.70E-01	5.70E-01		-8.78E-01	6.42E-04		-9.16E-02	7.80E-01		1.01E+00	5.26E-07	Up	Unigene16278_All//gi|19911573|dbj|BAB86890.1|//1.00E-131//syringolide-induced protein 19-1-5 [Glycine max]	Unigene16278_All//8.00E-117//AT5G57560| TCH4 (Touch 4); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene16278_All//0.00E+00//TC136482				nr -
Unigene1628_All	534	1.86	0.76	0.40	2.99	0.90	3.13	1.50	0.78	2.61	-1.29E+00	6.74E-02		-2.22E+00	7.49E-03		-1.73E+00	7.76E-04	Down	6.81E-02	9.17E-01		-9.43E-01	1.88E-01		7.96E-01	1.05E-01		Unigene1628_All//gi|16604322|gb|AAL24167.1|//2.00E-30//At2g37940/T8P21.15 [Arabidopsis thaliana] >gi|19699184|gb|AAL90958.1|At2g37940/T8P21.15 [Arabidopsis thaliana]	Unigene1628_All//1.00E-31//AT2G37940| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: phosphatidic acid phosphatase-related / PAP2-related (TAIR:AT3G54020.1); Has 316 Blast hits to 316 proteins in 75 species: Archae - 0; Bacteria - 0; Metazoa - 213; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 55 (source: NCBI BLink).	Unigene1628_All//7.00E-161//gi|109868591|gb|DW497567.1|DW497567				nr -
Unigene16281_All	758	1.24	2.61	2.18	4.01	2.77	1.37	1.12	3.47	1.89	1.07E+00	2.17E-02		8.10E-01	1.35E-01		-5.33E-01	1.33E-01		-1.55E+00	2.75E-05	Down	1.64E+00	1.03E-05	Up	7.62E-01	1.12E-01		Unigene16281_All//gi|15231700|ref|NP_190855.1|//2.00E-65//calmodulin-binding family protein [Arabidopsis thaliana] >gi|24111367|gb|AAN46807.1|At3g52870/F8J2_40 [Arabidopsis thaliana]	Unigene16281_All//1.00E-66//AT3G52870| calmodulin-binding family protein	Unigene16281_All//2.00E-50//TC164920				nr -
Unigene16282_All	1237	4.48	3.73	0.86	6.97	2.81	2.77	18.70	7.91	12.14	-2.66E-01	3.23E-01		-2.38E+00	5.64E-14	Down	-1.31E+00	3.15E-12	Down	-1.33E+00	4.16E-11	Down	-1.24E+00	1.70E-29	Down	-6.23E-01	4.33E-10		Unigene16282_All//gi|47934119|gb|AAT39542.1|//1.00E-116//transcription factor DRE-binding factor 2 [Gossypium hirsutum] >gi|71800653|gb|AAZ41376.1|dehydration responsive element-binding protein 2 [Gossypium hirsutum]	Unigene16282_All//1.00E-57//AT1G78080| RAP2.4 (related to AP2 4); DNA binding / transcription factor	Unigene16282_All//0.00E+00//TC151416	AP2-EREBP			nr +
Unigene16285_All	786	28.56	263.27	71.81	23.77	26.42	19.36	1.67	1.54	1.06	3.20E+00	0.00E+00	Up	1.33E+00	1.81E-62	Up	1.53E-01	2.70E-01		-2.96E-01	2.47E-02		-1.13E-01	8.32E-01		-6.48E-01	1.98E-01		Unigene16285_All//gi|226713609|sp|A7NW78.1|U974_VITV1//2.00E-46//RecName: Full=UPF0497 membrane protein 4	Unigene16285_All//9.00E-23//AT4G15630| integral membrane family protein	Unigene16285_All//0.00E+00//gi|21093371|gb|BQ405684.1|BQ405684				nr +
Unigene16286_All	1761	0.30	0.29	0.12	1.10	1.25	0.67	20.50	16.12	133.88	-4.64E-02	9.76E-01		-1.30E+00	2.42E-01		1.82E-01	7.32E-01		-7.26E-01	1.27E-01		-3.48E-01	1.30E-05		2.71E+00	0.00E+00	Up	Unigene16286_All//gi|25991925|gb|AAN76990.1|AF461148_1/2.00E-55//MAP55-like protein [Arabidopsis thaliana] >gi|14517464|gb|AAK62622.1|At1g65820/F1E22_4 [Arabidopsis thaliana] >gi|17978909|gb|AAL47424.1|At1g65820/F1E22_4 [Arabidopsis thaliana]	Unigene16286_All//8.00E-54//AT1G65820| microsomal glutathione s-transferase, putative	Unigene16286_All//0.00E+00//TC154408		ko00480|Glutathione metabolism		nr +
Unigene16287_All	544	21.06	77.96	61.77	16.48	31.40	48.82	39.33	126.92	182.57	1.89E+00	6.17E-80	Up	1.55E+00	5.61E-47	Up	9.30E-01	3.27E-13		1.57E+00	1.52E-41	Up	1.69E+00	1.08E-136	Up	2.21E+00	7.83E-287	Up	Unigene16287_All//gi|7768151|emb|CAB90633.1|//2.00E-51//protein phpsphatase 2C (PP2C) [Fagus sylvatica]	Unigene16287_All//5.00E-38//AT3G11410| PP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA); protein binding / protein serine/threonine phosphatase	Unigene16287_All//0.00E+00//TC160722				nr -
Unigene16289_All	733	2.50	2.70	4.79	22.02	18.23	2.96	2.42	0.51	0.22	1.10E-01	8.04E-01		9.41E-01	6.30E-03		-2.73E-01	5.13E-02		-2.90E+00	5.26E-56	Down	-2.24E+00	8.44E-06	Down	-3.48E+00	4.53E-09	Down	Unigene16289_All//gi|115481460|ref|NP_001064323.1|//4.00E-48//Os10g0210500 [Oryza sativa Japonica Group] >gi|113638932|dbj|BAF26237.1|Os10g0210500 [Oryza sativa Japonica Group]	Unigene16289_All//1.00E-30//AT2G39510| nodulin MtN21 family protein	Unigene16289_All//0.00E+00//gi|48880177|gb|CO131199.1|CO131199				nr -
Unigene16290_All	812	3.93	3.18	3.87	7.48	7.46	6.79	16.51	11.68	5.45	-3.05E-01	3.81E-01		-2.27E-02	9.70E-01		-4.00E-03	9.80E-01		-1.41E-01	6.38E-01		-4.98E-01	2.71E-04		-1.60E+00	5.61E-26	Down	Unigene16290_All//gi|15223516|ref|NP_176029.1|//1.00E-87//ATSAR1B (SECRETION-ASSOCIATED RAS 1 B); GTP binding [Arabidopsis thaliana] >gi|266989|sp|Q01474.1|SAR1B_ARATH RecName: Full=GTP-binding protein SAR1B >gi|12321751|gb|AAG50911.1|AC06915_9_12 GTP-binding protein (SAR1B) [Arabidopsis thaliana] >gi|166734|gb|AAA32807.1| GTP-binding protein [Arabidopsis thaliana] >gi|21553950|gb|AAM63031.1| GTP-binding protein SAR1B [Arabidopsis thaliana]	Unigene16290_All//3.00E-79//AT1G56330| ATSAR1B (SECRETION-ASSOCIATED RAS 1 B); GTP binding	Unigene16290_All//0.00E+00//gi|5044982|gb|AI726130.1|AI726130		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene16292_All	738	4.89	2.13	1.30	5.60	4.71	3.24	2.23	1.02	2.21	-1.20E+00	2.92E-04	Down	-1.91E+00	3.28E-07	Down	-2.50E-01	4.50E-01		-7.89E-01	7.79E-03		-1.13E+00	1.43E-02		-1.36E-02	9.67E-01		Unigene16292_All//gi|22331750|ref|NP_680125.1|//2.00E-17//OFP6 (OVATE FAMILY PROTEIN 6) [Arabidopsis thaliana]	Unigene16292_All//7.00E-19//AT2G36026| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF623, plant (InterPro:IPR006458); BEST Arabidopsis thaliana protein match is: OFP6 (OVATE FAMILY PROTEIN 6) (TAIR:AT3G52525.1); Has 230 Blast hits to 230 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 228; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene16292_All//9.00E-10//DR461432				nr +
Unigene16293_All	653	11.46	20.95	7.50	12.74	10.49	14.80	11.78	6.72	4.27	8.71E-01	1.71E-08		-6.11E-01	5.97E-03		-2.80E-01	1.83E-01		2.16E-01	3.07E-01		-8.10E-01	1.55E-05		-1.46E+00	1.60E-13	Down	Unigene16293_All//gi|224131422|ref|XP_002328535.1|//6.00E-66//histone 2 [Populus trichocarpa] >gi|222838250|gb|EEE76615.1|histone 2 [Populus trichocarpa]	Unigene16293_All//4.00E-52//AT1G54690| GAMMA-H2AX (GAMMA HISTONE VARIANT H2AX); DNA binding	Unigene16293_All//0.00E+00//gi|109870449|gb|DW499425.1|DW499425				nr -
Unigene16294_All	622	16.40	83.58	53.85	22.18	44.23	32.53	39.43	28.89	41.70	2.35E+00	3.24E-129	Up	1.72E+00	5.36E-54	Up	9.96E-01	1.55E-23		5.52E-01	3.66E-06		-4.48E-01	4.74E-06		8.08E-02	4.66E-01		Unigene16294_All//gi|28416873|gb|AA042967.1|//4.00E-39//At5g19875 [Arabidopsis thaliana]	Unigene16294_All//5.00E-36//AT5G19875| unknown protein	Unigene16294_All//0.00E+00//DW515025				nr -
Unigene16295_All	1382	0.72	0.22	0.27	5.91	4.49	3.79	2.17	0.76	1.12	-1.71E+00	2.09E-02		-1.42E+00	6.08E-02		-3.98E-01	4.56E-02		-6.41E-01	1.29E-03		-1.52E+00	7.39E-06	Down	-9.50E-01	2.30E-03		Unigene16295_All//gi|20372915|emb|CAD30015.1|//1.00E-129//beta 1,3-glycosyltransferase-like protein 1 [Solanum lycopersicum]	Unigene16295_All//1.00E-122//AT5G53340| galactosyltransferase family protein	Unigene16295_All//0.00E+00//ES829663				nr -
Unigene16296_All	455	44.62	75.50	30.66	90.76	73.18	97.37	122.94	146.79	35.20	7.59E-01	4.43E-16		-5.41E-01	1.75E-05		-3.11E-01	6.34E-05		1.02E-01	2.88E-01		2.56E-01	8.85E-06		-1.80E+00	2.81E-125	Down	Unigene16296_All//gi|31324052|gb|AP47158.1|AF512999_1/3.00E-72//TPR1 [Medicago sativa]	Unigene16296_All//2.00E-75//AT4G12400| stress-inducible protein, putative	Unigene16296_All//0.00E+00//TC140580				nr -
Unigene16297_All	597	36.55	33.78	26.76	26.87	30.40	23.98	67.92	46.77	30.36	-1.14E-01	3.91E-01		-4.50E-01	2.19E-04		1.78E-01	2.21E-01		-1.64E-01	3.12E-01		-5.38E-01	6.81E-13		-1.16E+00	2.07E-47	Down	Unigene16297_All//gi|295687233|gb|ADG27842.1|//3.00E-65//transaldolase [Gossypium hirsutum]	Unigene16297_All//7.00E-53//AT1G12230| transaldolase, putative	Unigene16297_All//0.00E+00//gi|21098572|gb|BQ410885.1|BQ410885		ko00030|Pentose phosphate pathway		nr -
Unigene16298_All	651	6.91	5.84	9.16	8.80	3.44	1.39	1.82	1.28	0.92	-2.44E-01	4.04E-01		4.07E-01	1.19E-01		-1.36E+00	9.74E-09	Down	-2.67E+00	1.95E-18	Down	-5.02E-01	3.95E-01		-9.86E-01	6.53E-02		Unigene16298_All//gi|255543353|ref|XP_002512739.1|//1.00E-05//Anthranilate N-benzoyltransferase protein, putative [Ricinus communis] >gi|223547750|gb|EEF49242.1|Anthranilate N-benzoyltransferase protein, putative [Ricinus communis]		Unigene16298_All//5.00E-39//TC146659				nr +
Unigene16299_All	850	4.49	3.28	3.76	5.16	2.96	3.77	5.27	6.49	2.44	-4.55E-01	1.50E-01		-2.58E-01	4.43E-01		-8.02E-01	3.05E-03		-4.51E-01	1.32E-01		3.00E-01	2.20E-01		-1.11E+00	1.09E-05	Down			Unigene16299_All//2.00E-180//DN849543				
Unigene163_All	217	0.72	1.17	0.25	1.61	0.48	0.42	4.29	3.08	26.80	6.91E-01	6.27E-01		-1.56E+00	5.33E-01		-1.75E+00	1.90E-01		-1.95E+00	1.96E-01		-4.76E-01	4.76E-01		2.64E+00	2.39E-21	Up			Unigene163_All//1.00E-73//DT048127				

Unigene1630_A11	655	4.95	1.39	2.28	7.30	4.94	7.52	0.97	0.51	1.34	-1.83E+00	1.46E-06	Down	-1.12E+00	2.13E-03		-5.63E-01	3.35E-02		4.18E-02	9.06E-01		-9.23E-01	2.63E-01		4.67E-01	4.76E-01		Unigene1630_A11//gi|87240852|gb|AB D32710.1|//1.00E-55//Tetratricopeptide-like helical [Medicago truncatula]	Unigene1630_A11//1.00E-32//AT4G01400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: COG4 transport (InterPro:IPR013167), Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT5G46100.1); Has 11639 Blast hits to 3936 proteins in 180 species: Archae - 0; Bacteria - 2; Metazoa - 206; Fungi - 141; Plants - 11004; Viruses - 0; Other Eukaryotes - 286 (source: NCBI BLink).	Unigene1630_A11//0.00E+00//ES825559				nr +
Unigene16300_A11	584	138.06	112.53	105.04	272.10	175.77	173.85	152.90	107.50	38.75	-2.95E-01	3.42E-07		-3.94E-01	2.63E-11		-6.30E-01	1.28E-63		-6.46E-01	9.40E-59		-5.08E-01	9.27E-25		-1.98E+00	2.11E-226	Down	Unigene16300_A11//gi|269315890|gb|AC237071.1|//1.00E-33//thioredoxin h7 [Medicago truncatula]	Unigene16300_A11//1.00E-32//AT5G39950| ATTRX2 (THIOREDOXIN 2); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	Unigene16300_A11//0.00E+00//TC160209				nr -
Unigene16301_A11	527	2.28	4.04	1.62	2.36	4.97	2.49	31.85	19.83	14.67	8.23E-01	6.26E-02		-4.98E-01	4.26E-01		1.07E+00	5.31E-03		7.27E-02	9.24E-01		-6.84E-01	1.73E-08		-1.12E+00	5.00E-19	Down			Unigene16301_A11//0.00E+00//gi|73858851|gb|DT461590.1|DT461590				
Unigene16302_A11	713	92.68	85.42	102.47	63.44	74.91	72.59	9.84	8.62	3.30	-1.18E-01	9.42E-02		1.45E-01	3.25E-02		2.40E-01	5.67E-04		1.94E-01	1.07E-02		-1.92E-01	4.01E-01		-1.58E+00	9.36E-14	Down	Unigene16302_A11//gi|15218053|ref|NP_172962.1|//2.00E-14//RHA2A; protein binding / ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana] >gi|50401214|sp|Q9ZT50.1|RHA2A_ARATH RecName: Full=E3 ubiquitin-protein ligase RHA2A; AltName: Full=RING-H2 zinc finger protein RHA2a >gi|5103808|gb|AAD39638.1|AC007591_3 Identical to gb|AF078822 RING-H2 finger RHA2a protein from Arabidopsis thaliana, ESTs gb|N37587, gb|T04684, gb|AA394318, gb|Z35014 and gb|AA713343 come from this gene >gi|37969569|gb|AAC68671.1| RING-H2 finger protein RHA2a [Arabidopsis thaliana] >gi|19715570|gb|AAL91611.1|At1g15100/F9L1_3 [Arabidopsis thaliana] >gi|20334914|gb|AAM16213.1|At1g15100/F9L1_3 [Arabidopsis thaliana] >gi|66865898|gb|AAY57583.1| RING finger family protein [Arabidopsis thaliana]	Unigene16302_A11//9.00E-16//AT1G15100| RHA2A; protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene16302_A11//0.00E+00//TC162195		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene16303_A11	740	58.97	19.17	34.61	288.05	240.77	214.89	129.75	67.27	48.45	-1.62E+00	5.84E-67	Down	-7.69E-01	6.96E-20		-2.59E-01	1.82E-16		-4.23E-01	1.40E-36		-9.48E-01	1.16E-77		-1.42E+00	7.09E-152	Down	Unigene16303_A11//gi|284192456|gb|ADB82906.1|//7.00E-59//caffeic O-methyltransferase1 [Eucalyptus camaldulensis]	Unigene16303_A11//4.00E-54//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene16303_A11//0.00E+00//TC137886		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene16307_A11	805	2.40	7.05	3.90	2.48	3.89	3.53	1.68	1.56	1.44	1.55E+00	9.32E-09	Up	6.99E-01	5.72E-02		6.53E-01	6.35E-02		5.14E-01	1.94E-01		-1.10E-01	8.35E-01		-2.28E-01	6.35E-01		Unigene16307_A11//gi|296083882|emb|CBI24270.3|//2.00E-09//unnamed protein product [Vitis vinifera]		Unigene16307_A11//0.00E+00//gi|164241674|gb|ES799583.1|ES799583				nr -
Unigene16309_A11	4840	0.00	0.00	0.00	0.18	0.26	1.38	2.32	16.04	7.79	null	null		null	null		5.49E-01	4.06E-01		2.98E+00	2.20E-23	Up	2.79E+00	1.73E-287	Up	1.75E+00	4.46E-80	Up	Unigene16309_A11//gi|9755445|gb|AAF98206.1|AC007152_2//0.00E+00//Putative ABC transporter [Arabidopsis thaliana]	Unigene16309_A11//0.00E+00//AT1G66950| PDR11 (PLEIOTROPIC DRUG RESISTANCE 11); ATPase, coupled to transmembrane movement of substances	Unigene16309_A11//2.00E-98//gi|78338248|gb|DT558522.1|DT558522		ko02010|ABC transporters		nr +
Unigene16310_A11	1051	0.20	0.19	0.46	0.47	0.29	0.39	6.36	5.53	14.93	-4.64E-02	9.89E-01		1.20E+00	3.03E-01		-6.85E-01	5.15E-01		-2.94E-01	7.57E-01		-2.02E-01	3.86E-01		1.23E+00	1.67E-20	Up	Unigene16310_A11//gi|2346978|dbj|BAA21923.1|//1.00E-49//ZPT2-14 [Petunia x hybrida]	Unigene16310_A11//4.00E-25//AT2G28710| zinc finger (C2H2 type) family protein	Unigene16310_A11//4.00E-62//gi|48742683|gb|CO073202.1|CO073202	C2H2			nr -
Unigene16311_A11	690	1.44	10.72	2.78	1.66	4.59	3.40	31.01	101.58	146.94	2.90E+00	1.20E-23	Up	9.47E-01	5.40E-02		1.47E+00	2.82E-05	Up	1.04E+00	1.40E-02		1.71E+00	2.90E-141	Up	2.24E+00	1.11E-297	Up	Unigene16311_A11//gi|2346978|dbj|BAA21923.1|//1.00E-47//ZPT2-14 [Petunia x hybrida]	Unigene16311_A11//2.00E-24//AT2G28710| zinc finger (C2H2 type) family protein	Unigene16311_A11//4.00E-55//DW501288	C2H2			nr +
Unigene16314_A11	1363	1.88	2.12	1.48	1.97	2.27	2.15	3.04	1.75	1.02	1.72E-01	6.29E-01		-3.41E-01	4.07E-01		2.04E-01	6.02E-01		1.26E-01	7.47E-01		-7.98E-01	2.70E-03		-1.57E+00	2.02E-08	Down	Unigene16314_A11//gi|115446021|ref|NP_001046790.1|//1.00E-09//Os02g0461200 [Oryza sativa Japonica Group] >gi|113536321|dbj|BAF08704.1|Os02g0461200 [Oryza sativa Japonica Group]	Unigene16314_A11//6.00E-59//AT4G27510| unknown protein					nr +
Unigene16316_A11	873	3.30	36.39	9.15	2.00	6.04	8.90	2.03	6.99	10.68	3.46E+00	1.87E-118	Up	1.47E+00	9.26E-11	Up	1.60E+00	1.73E-09	Up	2.16E+00	5.73E-19	Up	1.78E+00	1.15E-13	Up	2.39E+00	3.29E-30	Up	Unigene16316_A11//gi|156567559|gb|ABU82739.1|//3.00E-33//cold acclimation WCOR413-like protein [Citrus trifoliata]	Unigene16316_A11//3.00E-14//AT2G15970| COR413-PM1	Unigene16316_A11//0.00E+00//gi|109874533|gb|DW503507.1|DW503507				nr -
Unigene16317_A11	1487	5.98	12.98	8.24	5.70	8.89	11.72	8.02	10.06	9.24	1.12E+00	3.15E-17	Up	4.62E-01	6.34E-03		6.43E-01	9.72E-06		1.04E+00	7.49E-15	Up	3.28E-01	1.31E-02		2.05E-01	1.46E-01		Unigene16317_A11//gi|50201959|gb|AAT70495.1|//1.00E-109//At5g19070 [Arabidopsis thaliana] >gi|58331785|gb|AAW70390.1|At5g19070 [Arabidopsis thaliana]	Unigene16317_A11//8.00E-89//AT5G19070| LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (InterPro:IPR015414); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G03260.1); Has 3029 Blast hits to 3029 proteins in 693 species: Archae - 10; Bacteria - 1724; Metazoa - 229; Fungi - 74; Plants - 161; Viruses - 0; Other Eukaryotes - 831 (source: NCBI BLink).	Unigene16317_A11//0.00E+00//CO089534				nr +
Unigene16318_A11	2258	1.32	1.44	1.44	2.23	1.54	2.54	9.27	9.53	19.35	1.21E-01	7.27E-01		1.23E-01	7.22E-01		-5.33E-01	3.97E-02		1.89E-01	5.11E-01		4.05E-02	7.47E-01		1.06E+00	5.76E-44	Up	Unigene16318_A11//gi|84104899|gb|ABC54558.1|//0.00E+00//nonexpresser of pathogenesis-related 1 [Gossypium hirsutum] >gi|157703518|gb|ABV68572.1|nonexpresser of PR protein [Gossypium hirsutum]	Unigene16318_A11//6.00E-174//AT1G64280| NPR1 (NONEXPRESSER OF PR GENES 1); protein binding / transcription activator	Unigene16318_A11//0.00E+00//TC134415				nr -
Unigene16319_A11	918	8.09	4.19	5.16	5.81	5.96	4.62	3.09	1.37	2.86	-9.48E-01	1.20E-05		-6.49E-01	3.61E-03		3.88E-02	9.04E-01		-3.28E-01	2.36E-01		-1.18E+00	5.06E-04	Down	-1.08E-01	7.48E-01		Unigene16319_A11//gi|297812521|ref|XP_002874144.1|//1.00E-45//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297319981|gb|EFH50403.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene16319_A11//1.00E-45//AT5G23710| DNA binding / DNA-directed RNA polymerase	Unigene16319_A11//0.00E+00//TC163324		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene16320_A11	683	3.60	27.08	13.18	9.70	23.70	61.23	43.46	74.35	89.01	2.91E+00	1.19E-58	Up	1.87E+00	1.08E-16	Up	1.29E+00	7.48E-21	Up	2.66E+00	1.56E-128	Up	7.75E-01	1.28E-29		1.03E+00	2.88E-58	Up	Unigene16320_A11//gi|32364482|gb|AA061674.1|//4.00E-18//AKIN gamma [Medicago truncatula]	Unigene16320_A11//5.00E-18//AT3G48530| KING1 (SNF1-RELATED PROTEIN KINASE REGULATORY SUBUNIT GAMMA 1)	Unigene16320_A11//3.00E-157//gi|84166568|gb|DR455216.1|DR455216				nr +
Unigene16321_A11	1125	3.44	2.12	1.18	2.57	3.55	3.77	1.01	0.22	0.85	-7.01E-01	2.39E-02		-1.54E+00	7.25E-06	Down	4.67E-01	1.39E-01		5.55E-01	6.68E-02		-2.19E+00	6.83E-04	Down	-2.56E-01	6.49E-01		Unigene16321_A11//gi|213959107|gb|ACJ54888.1|//1.00E-125//heat shock protein 40 [Oryza sativa Japonica Group]	Unigene16321_A11//1.00E-110//AT5G25530| DNAJ heat shock protein, putative	Unigene16321_A11//0.00E+00//gi|164312645|gb|ES840412.1|ES840412				nr -
Unigene16323_A11	1010	2.02	2.11	2.32	5.03	4.43	3.35	1.51	0.21	0.20	6.06E-02	8.97E-01		1.99E-01	6.25E-01		-1.83E-01	5.66E-01		-5.85E-01	2.83E-02		-2.86E+00	1.98E-06	Down	-2.93E+00	7.58E-07	Down	Unigene16323_A11//gi|107738065|gb|ABF83626.1|//7.00E-19//At4g33800 [Arabidopsis thaliana]	Unigene16323_A11//9.00E-14//AT4G33800| unknown protein	Unigene16323_A11//0.00E+00//ES806495				nr -
Unigene16324_A11	1451	1.44	0.80	0.37	2.61	0.95	2.12	5.25	2.28	2.94	-8.45E-01	5.73E-02		-1.97E+00	1.29E-04	Down	-1.46E+00	1.33E-06	Down	-3.02E-01	3.97E-01		-1.20E+00	8.34E-10	Down	-8.36E-01	5.84E-06		Unigene16324_A11//gi|145338580|ref|NP_188247.2|//1.00E-166//TRZ4 (TRNASE Z 4); 3'-tRNA processing endoribonuclease/ catalytic [Arabidopsis thaliana]	Unigene16324_A11//4.00E-154//AT3G16260| TRZ4 (TRNASE Z 4); 3'-tRNA processing endoribonuclease/ catalytic	Unigene16324_A11//0.00E+00//TC173806				nr -
Unigene16325_A11	1483	0.35	0.65	0.50	3.33	3.32	3.29	2.34	1.18	0.89	8.80E-01	2.13E-01		5.11E-01	5.47E-01		-2.10E-03	9.87E-01		-1.59E-02	9.47E-01		-9.82E-01	9.45E-04		-1.40E+00	3.45E-06	Down	Unigene16325_A11//gi|15230020|ref|NP_187213.1|//1.00E-163//pectinesterase family protein [Arabidopsis thaliana] >gi|75336123|sp|Q9M9W7.1|PME22_ARATH RecName: Full=Putative pectinesterase/pectinesterase inhibitor 22; Includes: RecName: Full=Pectinesterase inhibitor 22; AltName: Full=Pectin methylesterase inhibitor 22; Includes: RecName: Full=Pectinesterase 22; Short=PE 22; AltName: Full=Pectin methylesterase 22; Short=AtPME22; Flags: Precursor	Unigene16325_A11//3.00E-164//AT3G05620| pectinesterase family protein	Unigene16325_A11//0.00E+00//DW518240		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene16328_A11	831	4.16	4.88	4.87	9.95	8.16	6.14	0.92	1.71	2.40	2.31E-01	4.66E-01		2.29E-01	4.92E-01		-2.86E-01	1.72E-01		-6.96E-01	4.14E-04		9.01E-01	7.45E-02		1.39E+00	7.70E-04	Up	Unigene16328_A11//gi|297851670|ref|XP_002893716.1|//1.00E-31//ATHSFA1D [Arabidopsis lyrata subsp. lyrata] >gi|297336538|gb|EFH69975.1|ATHSFA1D [Arabidopsis lyrata subsp. lyrata]	Unigene16328_A11//7.00E-27//AT4G17750| HSF1 (HEAT SHOCK FACTOR 1); DNA binding / protein binding / transcription factor	Unigene16328_A11//0.00E+00//DT465984	HSF			nr +
Unigene16329_A11	511	61.74	31.63	31.57	127.90	82.95	166.78	241.68	170.21	86.62	-9.65E-01	5.46E-22		-9.67E-01	3.29E-21		-6.25E-01	6.61E-26		3.83E-01	1.69E-12		-5.06E-01	1.26E-33		-1.48E+00	1.78E-207	Down	Unigene16329_A11//gi|297797139|ref|XP_002866454.1|//6.00E-54//calnexin 1 [Arabidopsis lyrata subsp. lyrata] >gi|297312289|gb|EFH42713.1|calnexin 1 [Arabidopsis lyrata subsp. lyrata]	Unigene16329_A11//4.00E-50//AT5G61790| calnexin 1 (CNX1)	Unigene16329_A11//0.00E+00//gi|78323293|gb|DT543567.1|DT543567		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr +

Unigene16332_All	1045	3.96	8.63	3.06	9.15	13.18	6.74	139.22	350.84	667.61	1.13E+00	1.52E-08	Up	-3.72E-01	2.45E-01		5.26E-01	2.38E-04		-4.41E-01	1.84E-02		1.33E+00	0.00E+00	Up	2.26E+00	0.00E+00	Up	Unigene16332_All//gi|40457261|gb|AB586686.1|//1.00E-134//proline dehydrogenase [Glycine max]	Unigene16332_All//5.00E-118//AT5G38710| proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative	Unigene16332_All//0.00E+00//TC137432				nr -
Unigene16334_All	591	2.83	0.94	3.15	8.09	2.45	2.06	2.43	1.63	0.94	-1.59E+00	3.09E-03		1.55E-01	7.41E-01		-1.73E+00	2.38E-10	Down	-1.97E+00	6.96E-11	Down	-5.81E-01	2.52E-01		-1.37E+00	5.50E-03		Unigene16334_All//gi|297835186|ref|XP_002885475.1|//2.00E-20//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297835188|ref|XP_002885476.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331315|gb|EFH61734.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331316|gb|EFH61735.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16334_All//7.00E-21//AT3G21890| zinc finger (B-box type) family protein	Unigene16334_All//0.00E+00//gi|109884738|gb|DW513708.1|DW513708	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr -
Unigene16335_All	983	1.06	6.34	3.47	1.37	3.71	3.81	5.38	15.69	19.37	2.57E+00	1.01E-17	Up	1.70E+00	5.79E-06	Up	1.44E+00	7.36E-06	Up	1.48E+00	6.97E-06	Up	1.55E+00	2.04E-27	Up	1.85E+00	4.11E-44	Up	Unigene16335_All//gi|228480908|gb|ACQ42220.1|//3.00E-88//RZ83 transcription factor MYB108-like protein 1 [Vitis vinifera]	Unigene16335_All//2.00E-60//AT3G06490| MYB108 (myb domain protein 108); DNA binding / transcription factor	Unigene16335_All//3.00E-90//gi|78345617|gb|DT565891.1|DT565891	MYB			nr -
Unigene16336_All	1011	0.88	0.80	0.95	1.33	1.43	1.61	2.09	0.58	1.14	-1.34E-01	8.41E-01		1.08E-01	8.75E-01		1.05E-01	8.70E-01		2.74E-01	6.20E-01		-1.85E+00	1.76E-05	Down	-8.72E-01	2.17E-02		Unigene16336_All//gi|87240722|gb|AB032580.1|//2.00E-09//SAM (and some other nucleotide) binding motif; WW/Rsp5/WWP [Medicago truncatula]	Unigene16336_All//3.00E-09//AT1G45231| WW domain-containing protein	Unigene16336_All//0.00E+00//DW229822				nr -
Unigene16340_All	1345	0.19	0.23	0.71	4.15	2.15	0.91	4.24	1.06	1.66	2.17E-01	8.65E-01		1.87E+00	2.06E-02		-9.48E-01	5.08E-05		-2.19E+00	2.19E-14	Down	-2.01E+00	5.85E-15	Down	-1.36E+00	3.21E-09	Down	Unigene16340_All//gi|147886439|gb|AB452428.1|//1.00E-163//boron transporter [Citrus macrophylla]	Unigene16340_All//2.00E-129//AT2G47160| BOR1 (REQUIRES HIGH BORON 1); anion exchanger/ boron transporter	Unigene16340_All//0.00E+00//TC163485				nr +
Unigene16341_All	753	4.72	6.26	2.69	15.35	10.79	9.00	11.57	2.61	3.07	4.05E-01	1.51E-01		-8.14E-01	1.70E-02		-5.08E-01	1.17E-03		-7.71E-01	2.23E-06		-2.15E+00	1.93E-24	Down	-1.91E+00	7.77E-22	Down	Unigene16341_All//gi|225580061|gb|ACN94268.1|//2.00E-13//stress induced protein [Vitis vinifera]	Unigene16341_All//4.00E-13//AT5G25240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: NHL repeat-containing protein (TAIR:AT5G14890.1); Has 23 Blast hits to 23 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene16341_All//0.00E+00//TC144708				nr +
Unigene16342_All	753	1.88	65.68	7.00	1.26	2.15	3.12	31.33	82.37	99.52	5.13E+00	3.44E-241	Up	1.90E+00	3.34E-10	Up	7.74E-01	1.47E-01		1.31E+00	2.12E-03		1.39E+00	9.14E-93	Up	1.67E+00	2.15E-148	Up	Unigene16342_All//gi|224116396|ref|XP_002317287.1|//3.00E-07//predicted protein [Populus trichocarpa] >gi|222860352|gb|EEE97899.1| predicted protein [Populus trichocarpa]		Unigene16342_All//0.00E+00//TC159773				nr -
Unigene16343_All	885	13.72	13.00	8.54	19.81	15.25	19.70	2.63	0.94	6.39	-7.77E-02	6.50E-01		-6.83E-01	4.89E-05		-3.77E-01	2.77E-03		-8.40E-03	9.49E-01		-1.48E+00	1.54E-04	Down	1.28E+00	2.15E-08	Up	Unigene16343_All//gi|206584972|gb|ACI15395.1|//1.00E-93//UDP-glucose: flavonoid 3-O-glucosyltransferase [Vitis amurensis]	Unigene16343_All//3.00E-75//AT5G17030| UGT78D3 (UDP-GLUCOSYL TRANSFERASE 78D3); UDP-glycosyltransferase/ flavonol 3-O-arabinosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene16343_All//0.00E+00//TC140063		ko00944|Flavone and flavonol biosynthesis//ko00942|Anthocyanin biosynthesis		nr -
Unigene16344_All	484	0.76	20.10	1.54	5.76	2.28	19.69	2.97	46.63	24.45	4.73E+00	1.41E-45	Up	1.03E+00	2.37E-01		-1.34E+00	1.75E-04	Down	1.77E+00	5.07E-18	Up	3.97E+00	1.39E-115	Up	3.04E+00	2.98E-49	Up			Unigene16344_All//6.00E-155//TC176718				
Unigene16347_All	1144	0.50	4.12	2.93	0.61	0.90	1.42	26.57	58.13	106.21	3.03E+00	5.75E-16	Up	2.54E+00	2.43E-09	Up	5.67E-01	4.45E-01		1.22E+00	2.17E-02		1.13E+00	1.16E-71	Up	2.00E+00	0.00E+00	Up	Unigene16347_All//gi|18408342|ref|NP_564862.1|//4.00E-76//harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana]	Unigene16347_All//2.00E-47//AT1G65690| harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	Unigene16347_All//3.00E-23//DN827962		ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport		nr +
Unigene1635_All	2936	6.45	4.63	4.99	7.74	8.70	5.31	4.95	4.80	2.06	-4.80E-01	1.50E-04		-3.71E-01	5.42E-03		1.70E-01	1.51E-01		-5.44E-01	1.03E-06		-4.63E-02	7.67E-01		-1.26E+00	5.71E-20	Down	Unigene1635_All//gi|115468174|ref|NP_001057686.1|//1.00E-121//0s06g0494100 [Oryza sativa Japonica Group] >gi|113595726|dbj|BAF19600.1| Os06g0494100 [Oryza sativa Japonica Group]	Unigene1635_All//0.00E+00//AT4G32300| SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase	Unigene1635_All//0.00E+00//ES806913				nr +
Unigene16351_All	1140	15.38	2.22	2.10	1.31	0.63	0.32	25.81	2.42	1.78	-2.79E+00	1.03E-53	Down	-2.87E+00	3.22E-53	Down	-1.05E+00	4.31E-02		-2.05E+00	5.54E-04	Down	-3.42E+00	1.27E-133	Down	-3.86E+00	9.91E-153	Down	Unigene16351_All//gi|224054172|ref|XP_002298127.1|//5.00E-88//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845385|gb|EEE82932.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene16351_All//5.00E-79//AT1G52800| oxidoreductase, 2OG-Fe(II) oxygenase family protein			ko00904|Diterpenoid biosynthesis		nr +
Unigene16352_All	801	29.59	43.14	32.04	46.21	42.47	51.14	29.72	33.50	13.63	5.44E-01	2.58E-09		1.15E-01	3.76E-01		-1.22E-01	2.23E-01		1.46E-01	1.16E-01		1.73E-01	8.93E-02		-1.12E+00	7.89E-27	Down	Unigene16352_All//gi|25991925|gb|AAN76990.1|AF461148_1/9.00E-61//MAPEG-like protein [Arabidopsis thaliana] >gi|14517464|gb|AAK62622.1| At1g65820/F1E22_4 [Arabidopsis thaliana] >gi|17978909|gb|AAL47424.1| At1g65820/F1E22_4 [Arabidopsis thaliana]	Unigene16352_All//5.00E-62//AT1G65820| microsomal glutathione s-transferase, putative	Unigene16352_All//0.00E+00//TC141095		ko00480|Glutathione metabolism		nr -
Unigene16353_All	1225	0.77	2.03	0.65	3.42	2.92	3.83	6.45	4.61	9.04	1.40E+00	8.73E-04	Up	-2.38E-01	7.23E-01		-2.25E-01	5.06E-01		1.67E-01	6.35E-01		-4.87E-01	8.69E-03		4.86E-01	1.08E-03		Unigene16353_All//gi|297811301|ref|XP_002873534.1|//5.00E-43//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319371|gb|EFH49793.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16353_All//3.00E-44//AT5G11850| protein kinase family protein	Unigene16353_All//5.00E-74//ES795656				nr -
Unigene16354_All	916	11.99	20.69	17.38	5.28	6.69	5.87	1.48	6.11	7.09	7.86E-01	9.32E-10		5.35E-01	2.12E-04		3.43E-01	1.71E-01		1.54E-01	6.36E-01		2.05E+00	4.80E-15	Up	2.26E+00	5.88E-20	Up	Unigene16354_All//gi|18415285|ref|NP_568172.1|//6.00E-56//WCRKC1 (WCRKC THIOREDOXIN 1) [Arabidopsis thaliana] >gi|298286899|sp|Q9FG36.3|TRL31_ARATH RecName: Full=Thioredoxin-like 3-1, chloroplastic; AltName: Full=Thioredoxin WCRKC-1; Flags: Precursor >gi|117968721|gb|ABK59676.1| At5g06690 [Arabidopsis thaliana]	Unigene16354_All//4.00E-57//AT5G06690| WCRKC1 (WCRKC THIOREDOXIN 1)	Unigene16354_All//0.00E+00//TC175888				nr -
Unigene16356_All	1062	27.54	18.80	27.83	29.27	32.26	21.09	13.30	10.19	6.64	-5.51E-01	3.41E-08		1.50E-02	9.05E-01		1.41E-01	1.65E-01		-4.73E-01	4.54E-07		-3.84E-01	4.42E-03		-1.00E+00	1.24E-13	Down	Unigene16356_All//gi|13926235|gb|AAK49592.1|AF372876.1//2.00E-94//AT3g15820/MSJ11_22 [Arabidopsis thaliana] >gi|28416535|gb|AAO42798.1| At3g15820/MSJ11_22 [Arabidopsis thaliana]	Unigene16356_All//9.00E-96//AT3G15820| phosphatidic acid phosphatase-related / PAP2-related	Unigene16356_All//0.00E+00//gi|164286065|gb|ES810761.1|ES810761				nr -
Unigene16357_All	954	139.19	42.17	105.33	16.13	11.37	7.81	0.00	0.00	0.00	-1.72E+00	5.15E-221	Down	-4.02E-01	7.30E-19		-5.05E-01	1.32E-04		-1.05E+00	1.92E-13	Down	null	null		null	null		Unigene16357_All//gi|292653565|gb|ADE34299.1|//1.00E-151//aquaporin XIP1;1 [Gossypium hirsutum]	Unigene16357_All//3.00E-21//AT3G61430| PIP1A (PLASMA MEMBRANE INTRINSIC PROTEIN 1A); water channel	Unigene16357_All//0.00E+00//TC143730				nr +
Unigene16358_All	810	38.89	28.96	84.94	25.83	37.84	31.73	15.71	12.28	13.28	-4.25E-01	9.12E-06		1.13E+00	1.19E-58	Up	5.51E-01	1.05E-09		2.97E-01	6.45E-03		-3.55E-01	1.36E-02		-2.43E-01	9.29E-02		Unigene16358_All//gi|15218445|ref|NP_175036.1|//2.00E-45//emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana] >gi|7523682|gb|AAF63121.1|AC009526_6 Putative histidine decarboxylase [Arabidopsis thaliana] >gi|15011302|gb|AAK77493.1|AF389349_1 serine decarboxylase [Arabidopsis thaliana] >gi|17907848|dbj|BAB79456.1| histidine decarboxylase [Arabidopsis thaliana] >gi|17907853|dbj|BAB79457.1| histidine decarboxylase [Arabidopsis thaliana]	Unigene16358_All//3.00E-46//AT1G43710| emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding	Unigene16358_All//0.00E+00//gi|78325615|gb|DT545889.1|DT545889		ko00340|Histidine metabolism		nr +
Unigene1636_All	1273	38.51	20.66	33.34	12.29	11.31	8.48	10.03	4.04	3.57	-8.99E-01	4.90E-30		-2.08E-01	1.08E-02		-1.20E-01	4.76E-01		-5.35E-01	1.00E-04		-1.31E+00	4.50E-18	Down	-1.49E+00	1.90E-22	Down	Unigene1636_All//gi|228535374|gb|ACQ44244.1|//1.00E-105//chlorophyll synthase [Nicotiana tabacum]	Unigene1636_All//2.00E-96//AT3G51820| G4; chlorophyll synthetase	Unigene1636_All//0.00E+00//TC137897		ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene16361_All	1143	1.10	1.33	0.84	1.96	1.27	1.98	4.36	1.21	3.10	2.76E-01	5.98E-01		-3.90E-01	5.38E-01		-6.32E-01	1.31E-01		1.06E-02	9.82E-01		-1.85E+00	6.05E-12	Down	-4.93E-01	3.46E-02		Unigene16361_All//gi|297742414|emb|CBI34563.3|//6.00E-60//unnamed protein product [Vitis vinifera]						nr -
Unigene16362_All	1174	9.14	11.61	11.52	15.06	14.26	12.70	21.21	14.31	10.45	3.46E-01	2.60E-02		3.35E-01	4.17E-02		-7.95E-02	6.07E-01		-2.47E-01	7.80E-02		-5.68E-01	5.50E-09		-1.02E+00	4.51E-24	Down	Unigene16362_All//gi|119360057|gb|ABL66757.1|//3.00E-42//At1g69980 [Arabidopsis thaliana]	Unigene16362_All//9.00E-34//AT1G69980| unknown protein	Unigene16362_All//0.00E+00//TC135852				nr +
Unigene16364_All	611	6.94	2.40	5.58	9.38	8.06	6.21	6.16	13.68	6.98	-1.53E+00	1.21E-06	Down	-3.15E-01	3.36E-01		-2.18E-01	4.26E-01		-5.95E-01	1.63E-02		1.15E+00	5.43E-10	Up	1.80E-01	5.32E-01				Unigene16364_All//3.00E-34//TC150693				
Unigene16365_All	403	1.17	0.00	0.40	0.00	0.09	0.00	0.00	1.56	0.79	-1.02E+01	5.56E-03		-1.56E+00	2.04E-01		6.42E+00	8.30E-01		null	null		1.06E+01	1.47E-04	Up	9.63E+00	1.34E-02		Unigene16365_All//gi|19699178|gb|AAL90955.1|//2.00E-19//At2g04039/At2g04039 [Arabidopsis thaliana]	Unigene16365_All//4.00E-20//AT2G04039| unknown protein	Unigene16365_All//9.00E-61//TC152397				nr +
Unigene16366_All	519	12.00	5.08	7.39	1.54	3.12	0.87	0.00	0.56	0.61	-1.24E+00	4.57E-07	Down	-7.00E-01	4.52E-03		1.02E+00	5.05E-02		-8.20E-01	3.20E-01		9.14E+00	2.35E-02		9.26E+00	1.34E-02		Unigene16366_All//gi|19699178|gb|AAL90955.1|//5.00E-26//At2g04039/At2g04039 [Arabidopsis thaliana]	Unigene16366_All//3.00E-27//AT2G04039| unknown protein	Unigene16366_All//0.00E+00//TC152397				nr +
Unigene16368_All	752	2.23	3.64	2.34	1.52	3.66	3.42	3.26	1.50	4.82	7.09E-01	6.30E-02		6.98E-02	8.91E-01		1.27E+00	7.38E-04	Up	1.17E+00	3.51E-03		-1.12E+00	2.21E-03		5.64E-01	4.39E-02		Unigene16368_All//gi|171854980|dbj|BAG16714.1|//2.00E-50//protein disulfide isomerase [Glycine max]	Unigene16368_All//3.00E-47//AT1G21750| ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase	Unigene16368_All//1.00E-49//TC134091		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene16369_All	462	9.63	17.55	9.11	6.47	8.12	7.92	6.50	6.42	2.93	8.66E-01	2.50E-05		-8.02E-02	7.89E-01		3.29E-01	3.39E-01		2.92E-01	4.16E-01		-1.66E-02	9.94E-01		-1.15E+00	2.93E-04	Down			Unigene16369_All//0.00E+00//gi|78334105|gb|DT554379.1|DT554379				
Unigene1637_All	492	3.30	4.84	4.65	3.04	1.40	2.94	4.73	1.61	1.13	5.54E-01	1.84E-01		4.98E-01	2.62E-01		-1.12E+00	3.10E-02		-4.83E-02	9.41E-01		-1.55E+00	8.14E-05	Down	-2.06E+00	5.41E-07	Down			Unigene1637_All//0.00E+00//CA993982		ko00860|Porphyrin and chlorophyll metabolism		kegg +

Unigene16371_All	1329	1.34	1.22	0.92	2.66	1.58	2.55	2.42	2.14	4.89	-1.34E-01	7.71E-01		-5.38E-01	3.00E-01		-7.52E-01	1.53E-02		-6.24E-02	8.66E-01		-1.77E-01	6.32E-01		1.02E+00	7.99E-07	Up	Unigene16371_All//gi|240254548|ref|NP_180365.5|//6.00E-32//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene16371_All//2.00E-32//AT2G27980| protein binding / zinc ion binding	Unigene16371_All//4.00E-44//DW518371				nr +
Unigene16372_All	1197	2.71	1.44	0.80	3.00	3.19	1.55	1.27	1.47	2.63	-9.13E-01	8.10E-03		-1.76E+00	6.50E-06	Down	9.18E-02	8.32E-01		-9.54E-01	3.04E-03		2.06E-01	6.46E-01		1.05E+00	6.60E-04	Up	Unigene16372_All//gi|15230368|ref|NP_191325.1|//3.00E-73//NRPA1; DNA binding / DNA-directed RNA polymerase/ zinc ion binding [Arabidopsis thaliana] >gi|4678281|emb|CAB41189.1| DNA-directed RNA polymerase I 190K chain-like protein [Arabidopsis thaliana]	Unigene16372_All//3.00E-69//AT3G57660| NRPA1; DNA binding / DNA-directed RNA polymerase/ zinc ion binding	Unigene16372_All//5.00E-68//TC178084		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene16375_All	690	7.89	8.74	9.80	4.26	4.94	22.65	37.93	48.16	72.63	1.48E-01	5.85E-01		3.14E-01	2.07E-01		2.14E-01	5.87E-01		2.41E+00	3.75E-43	Up	3.44E-01	3.72E-05		9.37E-01	4.52E-41		Unigene16375_All//gi|83316226|gb|AB032397.1|//2.00E-61//1-aminocyclopropane-1-carboxylate oxidase [Gossypium hirsutum]	Unigene16375_All//1.00E-47//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene16375_All//0.00E+00//TC141735		ko00270|Cysteine and methionine metabolism		nr +
Unigene16376_All	665	13.69	7.85	8.01	7.27	7.61	4.82	1.34	0.13	0.24	-8.03E-01	2.73E-05		-7.74E-01	9.53E-05		6.71E-02	8.21E-01		-5.92E-01	3.13E-02		-3.41E+00	1.40E-04	Down	-2.48E+00	9.93E-04	Down	Unigene16376_All//gi|297725595|ref|NP_001175161.1|//2.00E-07//Os07g0417700 [Oryza sativa Japonica Group] >gi|255677700|dbj|BAH93889.1| Os07g0417700 [Oryza sativa Japonica Group]		Unigene16376_All//0.00E+00//gi|164313037|gb|ES817825.1|ES817825				nr -
Unigene16377_All	931	5.84	10.34	6.52	5.99	6.92	5.14	9.26	15.49	19.86	8.23E-01	9.91E-06		1.58E-01	5.71E-01		2.07E-01	4.43E-01		-2.21E-01	4.45E-01		7.41E-01	2.12E-08		1.10E+00	3.69E-20	Up	Unigene16377_All//gi|297815442|ref|XP_002875604.1|//1.00E-53//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321442|gb|EFH51863.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16377_All//3.00E-53//AT3G43230| zinc finger (FYVE type) family protein	Unigene16377_All//0.00E+00//TC140710		ko04145|Phagosome//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene16379_All	1390	48.33	7.87	50.11	733.49	1060.14	528.74	7.79	26.43	0.66	-2.62E+00	9.40E-191	Down	5.21E-02	5.05E-01		5.31E-01	0.00E+00		-4.72E-01	1.53E-212		1.76E+00	1.89E-77	Up	-3.56E+00	4.97E-53	Down	Unigene16379_All//gi|133902299|gb|AB041830.1|//0.00E+00//alcohol dehydrogenase A [Gossypium raimondii] >gi|133902312|gb|AB041841.1| alcohol dehydrogenase A [Gossypium hirsutum] >gi|133902321|gb|AB041849.1| alcohol dehydrogenase A [Gossypium hirsutum]	Unigene16379_All//2.00E-171//AT1G77120| ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase	Unigene16379_All//0.00E+00//TC138201		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr -
Unigene1638_All	1457	16.45	8.14	16.74	7.42	7.21	3.97	3.71	2.07	2.35	-1.02E+00	2.66E-18	Down	2.54E-02	8.43E-01		-4.15E-02	8.24E-01		-9.03E-01	1.14E-07		-8.47E-01	2.15E-04		-6.60E-01	2.82E-03		Unigene1638_All//gi|228535376|gb|ACQ44245.1|//0.00E+00//chlorophyll synthase [Nicotiana tabacum]	Unigene1638_All//3.00E-167//AT3G51820| G4; chlorophyll synthetase	Unigene1638_All//0.00E+00//TC137897		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene16380_All	1703	0.40	0.65	0.38	21.85	10.76	11.38	6.53	13.28	6.78	7.13E-01	2.69E-01		-9.02E-02	9.22E-01		-1.02E+00	1.32E-34	Down	-9.42E-01	1.11E-26		1.02E+00	2.37E-21	Up	5.52E-02	7.40E-01		Unigene16380_All//gi|15223175|ref|NP_172306.1|//3.00E-94//zinc finger (C2H2 type) protein (WIP3) [Arabidopsis thaliana] >gi|6579204|gb|AAF18247.1|AC011438_9 T23G18.15 [Arabidopsis thaliana] >gi|18027014|gb|AAL55723.1|AF254448_1 WIP3 protein [Arabidopsis thaliana]	Unigene16380_All//4.00E-89//AT1G08290| zinc finger (C2H2 type) protein (WIP3)	Unigene16380_All//7.00E-102//gi|109878785|gb|DW507755.1|DW507755	C2H2			nr -
Unigene16381_All	619	31.87	20.30	15.48	37.50	37.50	40.42	115.43	91.29	57.34	-6.51E-01	1.62E-07		-1.04E+00	3.86E-15	Down	-3.00E-04	9.95E-01		1.08E-01	4.09E-01		-3.39E-01	7.62E-10		-1.01E+00	4.05E-66	Down	Unigene16381_All//gi|7528270|gb|AAF63202.1|AF240679_1//8.00E-50//poly(A)-binding protein [Cucumis sativus]	Unigene16381_All//2.00E-38//AT1G49760| PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor	Unigene16381_All//0.00E+00//TC130955				nr +
Unigene16382_All	832	15.91	75.58	24.13	33.65	93.25	97.11	70.03	224.05	190.81	2.25E+00	4.40E-148	Up	6.01E-01	2.08E-06		1.47E+00	5.32E-121	Up	1.53E+00	2.63E-121	Up	1.68E+00	0.00E+00	Up	1.45E+00	6.30E-255	Up	Unigene16382_All//gi|224073168|ref|XP_002304005.1|//6.00E-66//f-box family protein [Populus trichocarpa] >gi|222841437|gb|EEE78984.1| f-box family protein [Populus trichocarpa]	Unigene16382_All//6.00E-18//AT3G59940| kelch repeat-containing F-box family protein	Unigene16382_All//0.00E+00//TC162725				nr -
Unigene16385_All	532	0.79	0.38	0.50	1.03	1.36	0.68	2.62	0.47	1.27	-1.05E+00	3.66E-01		-6.53E-01	5.94E-01		4.00E-01	6.64E-01		-6.01E-01	5.66E-01		-2.48E+00	3.36E-05	Down	-1.04E+00	3.24E-02		Unigene16385_All//gi|240255330|ref|NP_187840.7|//1.00E-06//FK506 binding / peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]		Unigene16385_All//0.00E+00//TC178451				nr +
Unigene16386_All	1427	1.25	0.60	0.22	1.61	1.16	0.79	2.87	1.46	2.35	-1.05E+00	3.39E-02		-2.48E+00	4.58E-05	Down	-4.71E-01	2.74E-01		-1.02E+00	1.56E-02		-9.73E-01	3.09E-04		-2.93E-01	2.86E-01		Unigene16386_All//gi|18416534|ref|NP_567717.1|//9.00E-29//immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related [Arabidopsis thaliana] >gi|15982872|gb|AAL09783.1| AT4g25340/T30C3_20 [Arabidopsis thaliana] >gi|23506115|gb|AAN28917.1| At4g25340/T30C3_20 [Arabidopsis thaliana]	Unigene16386_All//1.00E-29//AT3G12340| FK506 binding / peptidyl-prolyl cis-trans isomerase	Unigene16386_All//0.00E+00//TC178451				nr +
Unigene16389_All	662	5.53	26.48	7.08	2.78	2.44	1.43	3.00	13.57	13.60	2.26E+00	6.43E-42	Up	3.56E-01	2.37E-01		-1.88E-01	7.20E-01		-9.59E-01	4.69E-02		2.18E+00	1.56E-25	Up	2.18E+00	3.57E-26	Up	Unigene16389_All//gi|300268586|gb|EFJ52766.1|//3.00E-11//pathogenesis-related protein 1-like protein [Volvox carteri f. nagariensis]		Unigene16389_All//1.00E-94//DN827716		ko03040|Spliceosome		nr -
Unigene16390_All	799	2.23	6.15	4.33	19.58	24.01	24.19	14.50	7.11	10.67	1.47E+00	3.88E-07	Up	9.60E-01	5.72E-03		2.94E-01	1.96E-02		3.05E-01	1.78E-02		-1.03E+00	2.08E-11	Down	-4.42E-01	2.26E-03		Unigene16390_All//gi|15209179|gb|AAB91897.1|AC091627_10//2.00E-16//Hsp20/alpha crystallin family protein [Solanum demissum]	Unigene16390_All//5.00E-14//AT2G27140| heat shock family protein	Unigene16390_All//0.00E+00//gi|164278153|gb|ES841625.1|ES841625				nr -
Unigene16391_All	954	76.01	65.75	184.48	138.32	179.00	164.94	46.09	20.55	11.28	-2.09E-01	8.22E-04		1.28E+00	8.65E-183	Up	3.72E-01	1.25E-25		2.54E-01	1.03E-10		-1.17E+00	3.66E-50	Down	-2.03E+00	1.30E-115	Down	Unigene16391_All//gi|18410735|ref|NP_565095.1|//2.00E-33//senescence-associated protein-related [Arabidopsis thaliana] >gi|23306420|gb|AAN17437.1| expressed protein [Arabidopsis thaliana] >gi|27311889|gb|AA000910.1| expressed protein [Arabidopsis thaliana]	Unigene16391_All//1.00E-34//AT1G74940| senescence-associated protein-related	Unigene16391_All//0.00E+00//TC135324				nr -
Unigene16393_All	745	7.30	1.90	3.00	5.15	3.19	2.91	10.10	0.95	3.26	-1.94E+00	2.74E-11	Down	-1.28E+00	3.20E-06	Down	-6.91E-01	2.00E-02		-8.23E-01	7.84E-03		-3.40E+00	1.78E-34	Down	-1.63E+00	2.33E-15	Down	Unigene16393_All//gi|48310238|gb|AAT41781.1|//2.00E-38//At3g22540 [Arabidopsis thaliana] >gi|52218802|gb|AAU29471.1| At3g22540 [Arabidopsis thaliana]	Unigene16393_All//5.00E-38//AT3G22540| unknown protein	Unigene16393_All//0.00E+00//TC148016				nr +
Unigene16395_All	1258	2.99	2.34	3.26	7.37	6.71	5.17	12.94	1.73	4.12	-3.58E-01	2.70E-01		1.22E-01	6.99E-01		-1.35E-01	5.64E-01		-5.11E-01	6.52E-03		-2.90E+00	1.58E-63	Down	-1.65E+00	8.17E-33	Down	Unigene16395_All//gi|48310199|gb|AAT41773.1|//9.00E-62//At5g24600 [Arabidopsis thaliana] >gi|50198891|gb|AAT70465.1| At5g24600 [Arabidopsis thaliana]	Unigene16395_All//6.00E-68//AT3G18215| unknown protein	Unigene16395_All//0.00E+00//TC141563				nr +
Unigene16396_All	681	69.30	49.18	45.27	49.01	49.81	30.31	2.42	2.39	0.59	-4.95E-01	1.32E-10		-6.14E-01	1.16E-14		2.33E-02	8.37E-01		-6.93E-01	2.12E-14		-1.66E-02	1.01E+00		-2.05E+00	3.66E-05	Down			Unigene16396_All//0.00E+00//gi|31074043|gb|CA994322.1|CA994322				
Unigene16397_All	1472	1.39	0.48	0.36	1.39	1.94	0.77	3.62	5.76	0.87	-1.52E+00	1.32E-03		-1.94E+00	1.99E-04	Down	4.85E-01	2.15E-01		-8.55E-01	6.02E-02		6.71E-01	1.44E-04		-2.06E+00	5.27E-15	Down	Unigene16397_All//gi|297827539|ref|XP_002881652.1|//1.00E-140//ATEXO70H2 [Arabidopsis lyrata subsp. lyrata] >gi|297327491|gb|EFH57911.1| ATEXO70H2 [Arabidopsis lyrata subsp. lyrata]	Unigene16397_All//8.00E-137//AT2G39380| ATEXO70H2 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H2); protein binding					nr +
Unigene16398_All	884	61.02	85.75	65.60	87.85	78.06	111.84	73.03	167.42	105.41	4.91E-01	2.73E-16		1.04E-01	2.00E-01		-1.70E-01	3.42E-03		3.48E-01	3.71E-12		1.20E+00	5.16E-174	Up	5.29E-01	2.15E-28		Unigene16398_All//gi|34484310|gb|AAQ72788.1|//2.00E-88//hypersensitive-induced response protein [Cucumis sativus]	Unigene16398_All//1.00E-86//AT5G62740| band 7 family protein	Unigene16398_All//0.00E+00//TC173121				nr +
Unigene164_All	2759	3.77	7.31	2.53	3.77	3.88	8.66	9.73	11.09	34.76	9.54E-01	5.05E-14		-5.78E-01	1.67E-03		4.07E-02	8.44E-01		1.20E+00	4.28E-25	Up	1.89E-01	4.24E-02		1.84E+00	5.36E-217	Up	Unigene164_All//gi|76800640|gb|ABA55727.1|//0.00E+00//digalactosyldiacylglycerol synthase 1 [Vigna unguiculata]	Unigene164_All//0.00E+00//AT3G11670| DGD1 (DIGALACTOSYL DIACYLGLYCEROL DEFICIENT 1); UDP-galactosyltransferase/ galactolipid galactosyltransferase/ transferase, transferring glycosyl groups	Unigene164_All//0.00E+00//DR459322		ko00561|Glycerolipid metabolism		nr -
Unigene16400_All	597	7.36	11.12	17.04	21.86	25.84	31.09	26.06	56.01	55.59	5.95E-01	9.23E-03		1.21E+00	3.50E-10	Up	2.41E-01	1.07E-01		5.08E-01	5.19E-05		1.10E+00	3.90E-35	Up	1.09E+00	3.87E-35	Up			Unigene16400_All//0.00E+00//gi|109890675|gb|DW519639.1|DW519639				
Unigene16402_All	1644	0.32	1.05	0.06	0.45	1.74	1.62	3.32	4.96	6.42	1.72E+00	1.41E-03		-2.30E+00	6.77E-02		1.94E+00	8.54E-07	Up	1.83E+00	1.12E-05	Up	5.80E-01	1.37E-03		9.53E-01	1.38E-09		Unigene16402_All//gi|15230097|ref|NP_189076.1|//0.00E+00//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|119946695|dbj|BAB02933.1| beta-1,3-glucanase-like protein [Arabidopsis thaliana] >gi|67633662|gb|AAT78755.1| glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Unigene16402_All//0.00E+00//AT3G24330| glycosyl hydrolase family 17 protein	Unigene16402_All//8.00E-09//TC161334		ko00500|Starch and sucrose metabolism		nr +
Unigene16403_All	935	10.97	1.19	2.22	1.17	0.66	0.29	2.49	1.92	1.32	-3.20E+00	2.98E-36	Down	-2.30E+00	1.74E-24	Down	-8.22E-01	1.96E-01		-2.02E+00	4.74E-03		-3.72E-01	3.57E-01		-9.13E-01	1.12E-02		Unigene16403_All//gi|115466790|ref|NP_001056994.1|//1.00E-42//Os06g0184500 [Oryza sativa Japonica Group] >gi|55773915|dbj|BAD72520.1| non-phototropic hypocotyl 3-like [Oryza sativa Japonica Group] >gi|113595034|dbj|BAF18908.1| Os06g0184500 [Oryza sativa Japonica Group]	Unigene16403_All//2.00E-26//AT4G31820| ENP (ENHANCER OF PINOID); protein binding / signal transducer	Unigene16403_All//3.00E-72//gi|164344805|gb|ES807910.1|ES807910				nr -

Unigene16404_All	549	12.20	4.52	6.98	101.44	108.95	49.11	6.78	0.91	0.58	-1.43E+00	3.40E-09	Down	-8.05E-01	6.62E-04		1.03E-01	1.79E-01		-1.05E+00	3.45E-47	Down	-2.89E+00	6.16E-15	Down	-3.55E+00	1.41E-18	Down	Unigene16404_All//gi|15222452|ref|NP_177136.1|//2.00E-35//ATHB13; DNA binding / sequence-specific DNA binding / transcription factor [Arabidopsis thaliana] >gi|118573191|sp|Q8LC03.2|ATB13_ARATH RecName: Full=Homeobox-leucine zipper protein ATHB-13; AltName: Full=Homeodomain transcription factor ATHB-13; AltName: Full=HD-ZIP protein ATHB-13 >gi|6644295|gb|AAF20996.1|AF208044_1 homeodomain leucine-zipper protein ATHB13 [Arabidopsis thaliana] >gi|12325190|gb|AAG52541.1|AC013289_8 homeobox gene 13 protein; 11736-10437 [Arabidopsis thaliana] >gi|15982929|gb|AAL09811.1|At1g69780/T6C23_2 [Arabidopsis thaliana] >gi|22137260|gb|AAM91475.1|At1g69780/T6C23_2 [Arabidopsis thaliana]	Unigene16404_All//1.00E-36//AT1G69780| ATHB13; DNA binding / sequence-specific DNA binding / transcription factor	Unigene16404_All//0.00E+00//gi|164317272|gb|ES807719.1|ES807719	HB			nr +
Unigene16406_All	1040	3.62	11.11	5.58	5.94	16.56	18.02	6.75	11.98	14.98	1.62E+00	4.64E-18	Up	6.24E-01	1.52E-02		1.48E+00	3.62E-27	Up	1.60E+00	2.16E-30	Up	8.28E-01	9.88E-09		1.15E+00	2.45E-18	Up			Unigene16406_All//3.00E-07//TC149849				
Unigene16409_All	577	19.22	50.41	26.21	12.09	17.31	23.09	40.89	41.87	19.26	1.39E+00	1.09E-35	Up	4.47E-01	2.86E-03		5.18E-01	2.95E-03		9.34E-01	1.07E-09		3.42E-02	7.76E-01		-1.09E+00	3.57E-25	Down	Unigene16409_All//gi|79320849|ref|NP_001031246.1|//8.00E-11//MIR414 (MICRORNA 414) [Arabidopsis thaliana] >gi|186493663|ref|NP_001117563.1|MIR414 (MICRORNA 414) [Arabidopsis thaliana]	Unigene16409_All//3.00E-16//AT1G67195| MIR414 (MICRORNA 414)	Unigene16409_All//3.00E-169//TC174052				nr -
Unigene1641_All	551	6.84	5.43	8.70	5.88	8.37	9.67	10.74	4.55	7.88	-3.34E-01	3.12E-01		3.47E-01	2.44E-01		5.11E-01	7.13E-02		7.19E-01	5.26E-03		-1.24E+00	4.06E-08	Down	-4.47E-01	3.55E-02		Unigene1641_All//gi|160966277|gb|ABX55778.1|//3.00E-69//3-hydroxy-3-methylglutaryl coenzyme A synthase [Solanum lycopersicum]	Unigene1641_All//3.00E-69//AT4G11820| MVA1; acetyl-CoA C-acetyltransferase/ hydroxymethylglutaryl-CoA synthase	Unigene1641_All//0.00E+00//gi|13354351|gb|BG444699.1|BG444699		ko00280|Valine, leucine and isoleucine degradation//ko00650|Butanoate metabolism//ko00900|Terpenoid backbone biosynthesis//ko00072|Synthesis and degradation of ketone bodies		nr -
Unigene16411_All	1213	0.82	0.58	1.32	28.83	26.74	18.17	18.40	5.48	7.29	-4.87E-01	4.72E-01		6.84E-01	2.15E-01		-1.08E-01	3.10E-01		-6.66E-01	4.55E-14		-1.75E+00	6.64E-47	Down	-1.34E+00	8.52E-33	Down	Unigene16411_All//gi|117950161|gb|ABK58464.1|//9.00E-94//LIM domain protein GLIM1a [Populus tremula x Populus alba]	Unigene16411_All//4.00E-86//AT1G10200| WLIM1; transcription factor/ zinc ion binding	Unigene16411_All//0.00E+00//DW513212	LIM			nr -
Unigene16412_All	627	11.01	2.10	2.29	16.21	12.41	23.48	22.59	10.40	10.80	-2.39E+00	3.54E-18	Down	-2.26E+00	2.65E-16	Down	-3.85E-01	2.84E-02		5.35E-01	1.88E-04		-1.12E+00	1.06E-15	Down	-1.06E+00	5.26E-15	Down	Unigene16412_All//gi|15219330|ref|NP_173118.1|//4.00E-58//ribosomal protein L20 family protein [Arabidopsis thaliana] >gi|88011169|gb|ABD38912.1|At1g16740 [Arabidopsis thaliana]	Unigene16412_All//2.00E-59//AT1G16740| ribosomal protein L20 family protein	Unigene16412_All//0.00E+00//gi|109870142|gb|DW499118.1|DW499118		ko03010|Ribosome		nr -
Unigene16413_All	884	0.83	1.60	0.60	4.11	2.65	1.18	1.72	2.22	1.35	9.54E-01	9.02E-02		-4.60E-01	6.02E-01		-6.35E-01	4.04E-02		-1.81E+00	1.49E-07	Down	3.68E-01	4.00E-01		-3.49E-01	4.68E-01		Unigene16413_All//gi|11994595|dbj|BAB02650.1|//5.00E-58//receptor-like serine/threonine kinase [Arabidopsis thaliana]	Unigene16413_All//8.00E-59//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene16413_All//6.00E-175//TC133547		ko04626|Plant-pathogen interaction		nr +
Unigene16414_All	558	1.31	5.63	3.53	5.09	5.00	7.53	0.61	2.47	0.93	2.10E+00	1.99E-07	Up	1.43E+00	4.28E-03		-2.57E-02	9.51E-01		5.65E-01	6.31E-02		2.03E+00	3.35E-04	Up	6.15E-01	4.94E-01		Unigene16414_All//gi|50251780|dbj|BAD27712.1|//2.00E-41//disease resistance protein CF-2.1-like [Oryza sativa Japonica Group]	Unigene16414_All//3.00E-44//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene16414_All//7.00E-47//TC133547		ko04626|Plant-pathogen interaction		nr +
Unigene16418_All	690	3.72	0.88	0.93	3.10	3.09	4.71	1.90	2.00	1.67	-2.08E+00	3.67E-06	Down	-2.00E+00	1.34E-05	Down	-4.70E-03	9.78E-01		6.02E-01	8.84E-02		7.36E-02	8.96E-01		-1.82E-01	7.13E-01		Unigene16418_All//gi|18391414|ref|NP_563911.1|//1.00E-18//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75167758|sp|Q9SZ28.1|PPR37_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g12620 >gi|13605805|gb|AAK32746.1|AF361578_1 At1g12620/T12C24_25 [Arabidopsis thaliana] >gi|21111307|gb|AAN16777.1|At1g12620/T12C24_25 [Arabidopsis thaliana]	Unigene16418_All//8.00E-20//AT1G12620| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene16421_All	512	9.61	12.57	4.47	13.23	10.63	6.44	12.88	13.88	10.12	3.88E-01	1.03E-01		-1.10E+00	1.20E-04	Down	-3.16E-01	1.73E-01		-1.04E+00	3.26E-06	Down	1.07E-01	6.38E-01		-3.49E-01	8.69E-02				Unigene16421_All//0.00E+00//gi|109870396|gb|DW499372.1|DW499372				
Unigene16423_All	1207	6.59	7.18	5.47	9.00	6.36	7.37	5.92	3.46	2.21	1.24E-01	5.81E-01		-2.68E-01	2.38E-01		-5.00E-01	2.12E-03		-2.88E-01	1.20E-01		-7.74E-01	7.25E-05		-1.42E+00	4.26E-12	Down	Unigene16423_All//gi|75217928|sp|Q56XJ7.1|Y4276_ARATH//4.00E-41//RecName: Full=Uncharacterized protein At4g22760	Unigene16423_All//1.00E-38//AT4G22760| pentatricopeptide (PPR) repeat-containing protein	Unigene16423_All//0.00E+00//ES831368				nr -
Unigene16425_All	1116	8.39	8.35	6.20	13.52	9.84	11.66	10.42	5.88	3.36	-6.50E-03	9.90E-01		-4.36E-01	2.79E-02		-4.58E-01	6.71E-04		-2.15E-01	1.78E-01		-8.25E-01	3.52E-08		-1.63E+00	2.45E-23	Down	Unigene16425_All//gi|27808566|gb|AA024563.1|//2.00E-91//At5g14140 [Arabidopsis thaliana]	Unigene16425_All//8.00E-85//AT5G14140| zinc finger (C2H2 type) family protein	Unigene16425_All//0.00E+00//TC139339				nr -
Unigene16426_All	713	43.37	8.03	27.56	51.56	27.77	21.28	7.47	3.46	12.52	-2.43E+00	5.81E-81	Down	-6.54E-01	6.45E-11		-8.93E-01	2.93E-27		-1.28E+00	6.84E-43	Down	-1.11E+00	2.43E-06	Down	7.44E-01	1.01E-05		Unigene16426_All//gi|115455233|ref|NP_001051217.1|//2.00E-10//Os03g0740200 [Oryza sativa Japonica Group] >gi|113549688|dbj|BAF13131.1|Os03g0740200 [Oryza sativa Japonica Group]	Unigene16426_All//9.00E-14//AT2G23690| unknown protein					nr +
Unigene16428_All	923	47.39	37.22	44.60	53.38	43.80	49.86	25.42	11.95	10.83	-3.49E-01	1.45E-05		-8.76E-02	3.77E-01		-2.85E-01	5.47E-05		-9.83E-02	2.72E-01		-1.09E+00	2.12E-24	Down	-1.23E+00	2.11E-30	Down	Unigene16428_All//gi|15228345|ref|NP_187673.1|//1.00E-78//ATNUDX26 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 26); bis(5'-adenosyl)-pentaphosphatase/ bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) [Arabidopsis thaliana] >gi|75308944|sp|Q9CAF2.1|NUD26_ARATH RecName: Full=Nudix hydrolase 26, chloroplastic; Short=AtNUDT26; AltName: Full=Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical); Flags: Precursor	Unigene16428_All//4.00E-78//AT3G10620| ATNUDX26 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 26); bis(5'-adenosyl)-pentaphosphatase/ bis(5'-nucleosyl)-tetraphosphatase (asymmetrical)	Unigene16428_All//0.00E+00//TC161047		ko03018|RNA degradation		nr -
Unigene16429_All	539	6.60	14.48	8.10	10.07	10.99	10.05	21.26	40.56	27.13	1.13E+00	1.44E-07	Up	2.96E-01	3.61E-01		1.25E-01	6.65E-01		-2.70E-03	9.88E-01		9.32E-01	8.47E-18		3.52E-01	6.38E-03		Unigene16429_All//gi|225436962|ref|XP_002276508.1|//4.00E-11//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296086718|emb|CB132353.3|unnamed protein product [Vitis vinifera]		Unigene16429_All//0.00E+00//gi|21097749|gb|BQ410062.1|BQ410062				nr +
Unigene1643_All	2105	5.32	2.58	4.10	32.04	22.89	19.82	17.86	14.10	14.84	-1.05E+00	2.20E-09	Down	-3.76E-01	3.81E-02		-4.86E-01	4.84E-17		-6.93E-01	1.83E-28		-3.41E-01	1.23E-05		-2.67E-01	5.23E-04		Unigene1643_All//gi|224115800|ref|XP_002332060.1|//0.00E+00//nramp transporter [Populus trichocarpa] >gi|222831946|gb|EEE70423.1| nramp transporter [Populus trichocarpa]	Unigene1643_All//2.00E-177//AT1G80830| NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter	Unigene1643_All//0.00E+00//TC163670				nr +
Unigene16432_All	758	1.24	15.04	3.23	1.84	2.77	3.69	2.29	7.44	15.56	3.60E+00	3.92E-44	Up	1.38E+00	1.64E-03		5.91E-01	2.02E-01		1.01E+00	7.85E-03		1.70E+00	5.65E-12	Up	2.77E+00	1.30E-44	Up	Unigene16432_All//gi|115451009|ref|NP_001049105.1|//3.00E-14//Os03g0170100 [Oryza sativa Japonica Group] >gi|108706404|gb|ABF94199.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547576|dbj|BAF11019.1|Os03g0170100 [Oryza sativa Japonica Group]	Unigene16432_All//4.00E-15//AT2G35290| unknown protein	Unigene16432_All//0.00E+00//TC136603				nr -
Unigene16433_All	2293	0.46	0.55	0.98	0.87	1.22	0.81	1.64	1.20	5.51	2.75E-01	6.17E-01		1.10E+00	1.53E-02		4.85E-01	2.22E-01		-1.06E-01	8.23E-01		-4.48E-01	1.25E-01		1.75E+00	2.27E-27	Up	Unigene16433_All//gi|29427830|sp|Q8LPB4.1|PSKR1_DAUCA//1.00E-160//RecName: Full=Phytosulfokine receptor 1; Short=DcPSKR1; AltName: Full=Phytosulfokine LRR receptor kinase 1; Flags: Precursor >gi|21623969|dbj|BAC00995.1|phytosulfokine receptor [Daucus carota]	Unigene16433_All//7.00E-151//AT2G02220| PSKR1 (PHYTOSULFOKIN RECEPTOR 1); ATP binding / peptide receptor/ protein serine/threonine kinase	Unigene16433_All//0.00E+00//ES825855		ko04626|Plant-pathogen interaction		nr -
Unigene16434_All	729	4.52	8.76	5.19	3.42	5.34	4.27	5.34	3.44	2.51	9.54E-01	5.38E-05		1.98E-01	5.82E-01		6.44E-01	3.61E-02		3.23E-01	4.06E-01		-6.33E-01	2.23E-02		-1.09E+00	6.94E-05	Down	Unigene16434_All//gi|224105377|ref|XP_002313789.1|//5.00E-86//phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa] >gi|222850197|gb|EEE87744.1|phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa]	Unigene16434_All//3.00E-73//AT4G34540| isoflavone reductase family protein	Unigene16434_All//0.00E+00//TC144170		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism		nr +
Unigene16435_All	631	15.75	39.91	32.66	20.37	28.21	26.84	30.49	34.97	33.65	1.34E+00	2.36E-29	Up	1.05E+00	4.44E-16	Up	4.70E-01	1.50E-04		3.98E-01	3.17E-03		1.98E-01	7.75E-02		1.43E-01	2.15E-01		Unigene16435_All//gi|222423852|dbj|BAH19891.1|//2.00E-29//AT5G64170 [Arabidopsis thaliana]	Unigene16435_All//7.00E-30//AT5G64170| dentin sialophosphoprotein-related	Unigene16435_All//1.00E-60//gi|48827491|gb|CO125881.1|CO125881				nr -
Unigene16436_All	1224	0.73	0.62	1.22	1.26	0.62	0.89	12.50	43.95	34.89	-2.27E-01	7.27E-01		7.45E-01	1.91E-01		-1.03E+00	4.29E-02		-5.11E-01	3.72E-01		1.81E+00	1.50E-117	Up	1.48E+00	1.51E-71	Up	Unigene16436_All//gi|30686233|ref|NP_194086.3|//3.00E-41//WRKY29: transcription factor [Arabidopsis thaliana] >gi|29839684|sp|Q9SUS1.1|WRK29_ARATH RecName: Full=Probable WRKY transcription factor 29; AltName: Full=WRKY DNA-binding protein 29 >gi|17064160|gb|AAL35287.1|AF442394_1 WRKY transcription factor 29 [Arabidopsis thaliana] >gi|109946497|gb|ABG48427.1|At4g23550 [Arabidopsis thaliana]	Unigene16436_All//6.00E-43//AT4G23550| WRKY29; transcription factor	Unigene16436_All//2.00E-09//gi|78326580|gb|DT546854.1|DT546854	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene16438_All	1037	0.00	0.83	0.56	4.04	2.52	1.57	2.45	2.10	1.88	9.70E+00	4.95E-05	Up	9.14E+00	2.17E-03		-6.77E-01	1.64E-02		-1.36E+00	6.21E-06	Down	-2.23E-01	5.83E-01		-3.78E-01	2.88E-01		Unigene16438_All//gi|297833018|ref|XP_002885406.1|//9.00E-92//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331246|gb|EFH61665.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16438_All//9.00E-90//AT3G20830| protein kinase family protein	Unigene16438_All//4.00E-34//TC175904				nr -

Unigene1644_All	2130	1.20	1.14	1.48	6.57	3.67	6.47	3.75	1.33	1.22	-7.60E-02	8.43E-01			2.93E-01	4.27E-01		-8.41E-01	1.17E-09		-2.31E-02	9.09E-01		-1.49E+00	6.58E-14	Down	-1.63E+00	3.47E-16	Down	Unigene1644_All//gi|224115800|ref|XP_002332060.1|//0.00E+00//nramp transporter [Populus trichocarpa] >gi|222831946|gb|EEE70423.1| nramp transporter [Populus trichocarpa]	Unigene1644_All//0.00E+00//AT1G80830| NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter	Unigene1644_All//0.00E+00//TC163670				nr +
Unigene16440_All	734	17.75	14.70	13.28	15.54	13.14	16.43	14.69	30.81	16.66	-2.72E-01	9.55E-02			-4.19E-01	1.08E-02		-2.43E-01	1.70E-01		8.01E-02	6.94E-01		1.07E+00	7.83E-23	Up	1.82E-01	2.38E-01					Unigene16440_All//8.00E-149//BP278236				
Unigene16441_All	1237	7.70	11.55	11.28	10.55	8.80	7.92	4.07	4.29	1.74	5.86E-01	7.71E-05			5.51E-01	3.98E-04		-2.62E-01	1.03E-01		-4.13E-01	8.18E-03		7.72E-02	7.67E-01		-1.23E+00	3.59E-07	Down								
Unigene16444_All	1142	0.78	0.13	0.42	1.09	1.54	3.52	2.96	1.32	2.27	-2.55E+00	4.05E-03			-8.92E-01	2.47E-01		4.96E-01	3.46E-01		1.69E+00	1.89E-07	Up	-1.17E+00	1.31E-04	Down	-3.85E-01	1.99E-01		Unigene16444_All//gi|240256049|ref|NP_194085.4|//3.00E-88//binding [Arabidopsis thaliana]	Unigene16444_All//6.00E-83//AT4G23540| binding					nr -
Unigene16446_All	986	1.06	1.75	1.03	1.47	1.33	0.73	2.23	1.44	0.53	7.19E-01	1.48E-01			-4.87E-02	9.58E-01		-1.43E-01	8.15E-01		-9.99E-01	7.45E-02		-6.30E-01	1.07E-01		-2.09E+00	9.49E-07	Down	Unigene16446_All//gi|224055915|ref|XP_002298700.1|//7.00E-45//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222845958|gb|EEE83505.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene16446_All//9.00E-35//AT1G12280| disease resistance protein (CC-NBS-LRR class), putative	Unigene16446_All//1.00E-102//ES816451		ko04626|Plant-pathogen interaction		nr -
Unigene16447_All	1477	2.09	1.37	1.51	1.75	1.52	1.35	6.33	16.21	9.09	-6.07E-01	8.64E-02			-4.65E-01	2.25E-01		-2.11E-01	6.04E-01		-3.82E-01	3.76E-01		1.36E+00	7.09E-35	Up	5.23E-01	8.99E-05		Unigene16447_All//gi|226498222|ref|NP_001150116.1|//1.00E-111//nodulin-like protein 5NG4 [Zea mays] >gi|195636848|gb|ACG37892.1| nodulin-like protein 5NG4 [Zea mays]	Unigene16447_All//2.00E-69//AT1G75500| nodulin MtN21 family protein	Unigene16447_All//0.00E+00//TC139475				nr +
Unigene16450_All	656	22.17	9.50	21.51	2.51	2.52	0.90	2.58	3.06	3.64	-1.22E+00	3.93E-15	Down		-4.37E-02	7.90E-01		7.90E-03	9.98E-01		-1.49E+00	4.95E-03		2.46E-01	5.97E-01		4.99E-01	1.68E-01		Unigene16450_All//gi|21553353|gb|AAM62446.1|//1.00E-59//sorbitol dehydrogenase-like protein [Arabidopsis thaliana]	Unigene16450_All//8.00E-58//AT5G51970| sorbitol dehydrogenase, putative / L-iditol 2-dehydrogenase, putative	Unigene16450_All//4.00E-175//gi|73858960|gb|DT461699.1|DT461699		ko00051|Fructose and mannose metabolism		nr -
Unigene16451_All	440	3.09	0.69	5.08	0.91	0.00	0.00	0.29	0.10	0.18	-2.16E+00	9.05E-04	Down		7.17E-01	1.11E-01		-9.82E+00	4.39E-03		-9.82E+00	1.11E-02		-1.60E+00	5.34E-01		-6.71E-01	7.20E-01		Unigene16451_All//gi|115447305|ref|NP_001047432.1|//5.00E-17//Os02g0615800 [Oryza sativa Japonica Group] >gi|113536963|dbj|BAF09346.1| Os02g0615800 [Oryza sativa Japonica Group]	Unigene16451_All//9.00E-18//AT5G20480| EFR (EF-TU RECEPTOR); ATP binding / kinase/ protein serine/threonine kinase	Unigene16451_All//1.00E-168//C0121590		ko04626|Plant-pathogen interaction		nr +
Unigene16452_All	2536	0.21	0.00	0.06	0.00	0.00	0.00	15.34	10.88	3.24	-7.69E+00	2.93E-03			-1.71E+00	1.40E-01		null	null		null	null		-4.96E-01	8.57E-11		-2.24E+00	3.42E-116	Down	Unigene16452_All//gi|3894385|gb|AAC78592.1|//1.00E-146//Hcr2-0A [Solanum lycopersicum]	Unigene16452_All//9.00E-104//AT1G71390| AtRLP11 (Receptor Like Protein 11); protein binding	Unigene16452_All//0.00E+00//C0121590		ko04626|Plant-pathogen interaction		nr -
Unigene16454_All	569	3.40	2.76	2.81	3.59	1.94	2.06	5.05	1.54	2.17	-3.02E-01	5.29E-01			-2.77E-01	5.92E-01		-8.90E-01	3.87E-02		-7.99E-01	7.94E-02		-1.71E+00	1.59E-06	Down	-1.22E+00	1.94E-04	Down				Unigene16454_All//0.00E+00//ES826037				
Unigene16456_All	838	112.13	50.43	119.53	84.71	57.45	43.60	6.86	6.63	3.66	-1.15E+00	1.61E-85	Down		9.21E-02	1.28E-01		-5.60E-01	3.66E-23		-9.58E-01	6.50E-52		-4.88E-02	8.47E-01		-9.07E-01	2.79E-05					Unigene16456_All//3.00E-99//gi|164364813|gb|EX164038.1|EX164038				
Unigene16457_All	927	2.37	3.01	2.18	6.77	8.36	8.48	8.76	4.64	2.23	3.43E-01	3.72E-01			-1.19E-01	7.81E-01		3.04E-01	1.68E-01		3.24E-01	1.44E-01		-9.15E-01	6.14E-07		-1.97E+00	3.56E-21	Down	Unigene16457_All//gi|8671843|gb|AAF78406.1|AC009273_12//4.00E-24//ESTs gb|Z27282, gb|T44732, gb|Z29911, gb|AI997176 and gb|AI395420 come from this gene [Arabidopsis thaliana]	Unigene16457_All//4.00E-24//AT1G01730| unknown protein	Unigene16457_All//0.00E+00//ES801898				nr -
Unigene16458_All	1198	9.04	11.42	11.16	2.12	6.18	3.02	0.49	0.21	0.00	3.37E-01	3.01E-02			3.04E-01	6.88E-02		1.54E+00	1.38E-12	Up	5.08E-01	1.31E-01		-1.24E+00	1.54E-01		-8.95E+00	1.41E-04	Down	Unigene16458_All//gi|28140231|gb|AAO26314.1|//2.00E-67//protein disulphide isomerase [Elaeis guineensis]	Unigene16458_All//6.00E-63//AT3G54960| ATPDIL1-3 (PDI-LIKE 1-3); protein disulfide isomerase	Unigene16458_All//4.00E-90//TC135410		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene16459_All	929	1.69	1.47	1.95	2.63	1.15	1.02	2.46	0.94	0.56	-1.98E-01	6.85E-01			2.06E-01	6.64E-01		-1.19E+00	1.90E-03		-1.36E+00	9.53E-04	Down	-1.38E+00	4.07E-04	Down	-2.14E+00	3.51E-07	Down				Unigene16459_All//6.00E-61//FL576707				
Unigene16460_All	511	7.06	29.75	4.38	17.55	29.25	31.20	20.27	69.77	36.25	2.07E+00	8.83E-33	Up		-6.91E-01	4.23E-02		7.37E-01	5.32E-08		8.30E-01	1.58E-09		1.78E+00	2.33E-76	Up	8.39E-01	3.34E-13		Unigene16460_All//gi|44021989|gb|AAS46633.1|//2.00E-06//At2g04195 [Arabidopsis thaliana] >gi|45773862|gb|AAS76735.1| At2g04195 [Arabidopsis thaliana]		Unigene16460_All//2.00E-28//D8456350				nr -
Unigene16461_All	1204	1.61	0.97	0.27	4.63	4.86	4.61	7.30	3.58	4.27	-7.32E-01	1.17E-01			-2.60E+00	1.01E-05	Down	6.94E-02	8.12E-01		-6.20E-03	9.76E-01		-1.03E+00	6.74E-09	Down	-7.75E-01	4.94E-06		Unigene16461_All//gi|224140989|ref|XP_002323859.1|//1.00E-179//condensin complex components subunit [Populus trichocarpa] >gi|222866861|gb|EEF03992.1| condensin complex components subunit [Populus trichocarpa]	Unigene16461_All//2.00E-140//AT5G48600| ATSMC3 (ARABIDOPSIS THALIANA STRUCTURAL MAINTENANCE OF CHROMOSOME 3); ATP binding / transporter	Unigene16461_All//5.00E-65//gi|78353388|gb|DT573662.1|DT573662				nr -
Unigene16462_All	1777	0.65	0.31	0.00	2.83	0.91	1.37	22.41	9.57	10.29	-1.05E+00	1.01E-01			-9.34E+00	2.60E-06	Down	-1.64E+00	4.23E-10	Down	-1.04E+00	7.90E-05	Down	-1.23E+00	2.50E-49	Down	-1.12E+00	3.52E-44	Down	Unigene16462_All//gi|224131024|ref|XP_002328434.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222838149|gb|EEE76514.1| cytochrome P450 [Populus trichocarpa]	Unigene16462_All//3.00E-142//AT1G75130| CYP721A1: electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene16462_All//0.00E+00//gi|164341467|gb|ES827576.1|ES827576		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +
Unigene16463_All	605	28.02	85.76	46.74	21.16	27.72	22.54	29.84	50.15	57.16	1.61E+00	1.46E-78	Up		7.38E-01	2.81E-12		3.90E-01	2.99E-03		9.14E-02	6.13E-01		7.49E-01	4.70E-17		9.38E-01	1.24E-28		Unigene16463_All//gi|116265944|gb|ABJ91220.1|//3.00E-20//CBL-interacting protein kinase 13 [Populus trichocarpa]	Unigene16463_All//4.00E-17//AT1G01140| CIPK9 (CBL-INTERACTING PROTEIN KINASE 9); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene16463_All//3.00E-166//gi|78354381|gb|DT574655.1|DT574655		ko04140|Regulation of autophagy		nr -
Unigene16464_All	959	4.20	4.44	3.00	8.93	6.50	2.92	17.50	7.28	8.23	7.93E-02	7.88E-01			-4.87E-01	1.36E-01		-4.59E-01	1.57E-02		-1.61E+00	1.40E-14	Down	-1.27E+00	2.88E-22	Down	-1.09E+00	2.92E-18	Down				Unigene16464_All//3.00E-152//C0076644				
Unigene16468_All	774	26.70	19.57	22.98	26.00	29.36	34.37	71.34	34.99	15.65	-4.48E-01	2.08E-04			-2.17E-01	1.07E-01		1.75E-01	1.63E-01		4.03E-01	9.97E-05		-1.03E+00	2.39E-51	Down	-2.19E+00	1.49E-159	Down	Unigene16468_All//gi|15224918|ref|NP_181990.1|//2.00E-47//MTACP-1 (MITOCHONDRIAL ACYL CARRIER PROTEIN 1): acyl carrier/ cofactor binding / phosphopantetheine binding [Arabidopsis thaliana] >gi|1703091|sp|P53665.1|ACPM_ARATH RecName: Full=Acyl carrier protein, mitochondrial; AltName: Full=MtACP-1; Short=ACP; AltName: Full=NADH-ubiquinone oxidoreductase 9.6 kDa subunit; Flags: Precursor >gi|903689|gb|AAB96840.1| acyl carrier protein precursor [Arabidopsis thaliana] >gi|3341682|gb|AAC27464.1| acyl carrier protein [Arabidopsis thaliana]	Unigene16468_All//1.00E-48//AT2G44620| MTACP-1 (MITOCHONDRIAL ACYL CARRIER PROTEIN 1); acyl carrier/ cofactor binding / phosphopantetheine binding	Unigene16468_All//0.00E+00//TC145381		ko00190|Oxidative phosphorylation		nr +
Unigene16469_All	2028	4.21	4.07	2.57	9.09	9.75	7.24	7.38	3.44	3.22	-4.63E-02	8.24E-01			-7.09E-01	5.69E-04		1.01E-01	5.21E-01		-3.29E-01	1.19E-02		-1.10E+00	3.98E-16	Down	-1.20E+00	7.04E-19	Down	Unigene16469_All//gi|42567480|ref|NP_195428.3|//4.00E-79//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene16469_All//3.00E-80//AT2G23530| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Cell division cycle-associated protein (InterPro:IPR018860); BEST Arabidopsis thaliana protein match is: protein binding / zinc ion binding (TAIR:AT4G37710.1); Has 305 Blast hits to 301 proteins in 74 species: Archae - 0; Bacteria - 2; Metazoa - 117; Fungi - 39; Plants - 120; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink).	Unigene16469_All//0.00E+00//gi|78340036|gb|DT560310.1|DT560310				nr -
Unigene16471_All	972	7.75	3.44	5.20	9.33	8.93	12.41	11.74	14.15	7.75	-1.17E+00	9.88E-08	Down		-5.75E-01	9.54E-03		-6.32E-02	8.03E-01		4.12E-01	1.25E-02		2.69E-01	5.90E-02		-6.00E-01	3.79E-05		Unigene16471_All//gi|42568179|ref|NP_198638.2|//6.00E-94//hydrolase [Arabidopsis thaliana] >gi|79329126|ref|NP_001031978.1| hydrolase [Arabidopsis thaliana]	Unigene16471_All//5.00E-88//AT5G38220| hydrolase	Unigene16471_All//0.00E+00//gi|78333758|gb|DT554032.1|DT554032				nr +
Unigene16474_All	973	1.67	1.46	0.49	5.27	6.12	1.72	6.04	0.86	1.47	-1.93E-01	6.88E-01			-1.76E+00	2.55E-03		2.16E-01	4.43E-01		-1.62E+00	5.32E-09	Down	-2.81E+00	1.35E-22	Down	-2.03E+00	3.43E-16	Down	Unigene16474_All//gi|225459852|ref|XP_002284837.1|//2.00E-81//PREDICTED: similar to T23E18.17 [Vitis vinifera]	Unigene16474_All//4.00E-71//AT1G76240| unknown protein	Unigene16474_All//0.00E+00//TC148978				nr +
Unigene16475_All	1324	0.95	3.83	0.36	3.16	1.53	2.49	4.95	6.09	5.81	2.01E+00	5.70E-11	Up		-1.39E+00	3.39E-02		-1.04E+00	1.71E-04	Down	-3.44E-01	2.89E-01		3.00E-01	1.22E-01		2.31E-01	2.41E-01		Unigene16475_All//gi|6691218|gb|AAF24556.1|AC007508_19//7.00E-76//F1K23.6 [Arabidopsis thaliana]	Unigene16475_All//9.00E-61//AT1G28760| unknown protein	Unigene16475_All//0.00E+00//TC157437				nr +
Unigene16476_All	1164	9.39	10.19	11.16	12.50	11.48	8.96	1.96	3.88	0.82	1.17E-01	5.29E-01			2.49E-01	1.46E-01		-1.23E-01	4.86E-01		-4.80E-01	9.03E-04		9.83E-01	1.21E-04		-1.26E+00	7.78E-04	Down	Unigene16476_All//gi|53370641|gb|AAU89136.1|//8.00E-13//P-box domain containing protein [Oryza sativa Japonica Group]	Unigene16476_All//5.00E-05//AT3G09510| nucleic acid binding	Unigene16476_All//9.00E-159//TC165368				nr +
Unigene1648_All	354	5.76	1.29	6.62	7.60	7.10	5.61	3.58	3.90	5.63	-2.16E+00	2.79E-05	Down		1.99E-01	6.25E-01		-9.77E-02	8.36E-01		-4.37E-01	2.88E-01		1.21E-01	8.13E-01		6.51E-01	1.01E-01		Unigene1648_All//gi|108706673|gb|ABF94468.1|//2.00E-40//Zinc finger, C2H2 type family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene1648_All//2.00E-28//AT3G50700| AtIDD2 (Arabidopsis thaliana Indeterminate(ID)-Domain 2); nucleic acid binding / transcription factor/ zinc ion binding	Unigene1648_All//2.00E-74//C0103956	C2H2			nr -
Unigene16481_All	870	14.91	14.56	11.20	25.59	20.78	22.95	17.11	15.57	6.91	-3.47E-02	8.39E-01			-4.13E-01	1.23E-02		-3.01E-01	7.76E-03		-1.58E-01	2.29E-01		-1.36E-01	3.74E-01		-1.31E+00	1.88E-21	Down	Unigene16481_All//gi|168988200|gb|ACA35270.1|//2.00E-63//GCN5-related N-acetyltransferase [Cucumis sativus]	Unigene16481_All//4.00E-56//AT5G15770| AtGNA1 (Arabidopsis thaliana glucose-6-phosphate acetyltransferase 1); N-acetyltransferase/ glucosamine 6-phosphate N-acetyltransferase	Unigene16481_All//0.00E+00//TC163064		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene16482_All	1260	5.73	2.09	5.92	2.93	2.84	3.23	1.61	0.80	1.01	-1.45E+00	4.55E-10	Down		4.62E-02	8.43E-01		-4.17E-02	9.00E-01		1.41E-01	6.93E-01		-1.02E+00	1.24E-02		-6.71E-01	8.49E-02		Unigene16482_All//gi|297827997|ref|XP_002881881.1|//5.00E-82//DNA-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327720|gb|EFH58140.1| DNA-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16482_All//3.00E-61//AT2G42940| DNA-binding family protein					nr -
Unigene16483_All	621	16.85	6.85	8.92	26.87	17.97	15.13	20.36	4.11	6.16	-1.30E+00	4.16E-12	Down		-9.18E-01	6.77E-07		-5.81E-01	3.36E-06		-8.29E-01	5.08E-10		-2.31E+00	2.18E-38	Down	-1.72E+00	3.05E-27	Down	Unigene16483_All//gi|98961077|gb|ABF59022.1|//4.00E-17//At5g63150 [Arabidopsis thaliana]	Unigene16483_All//4.00E-06//AT5G63150| unknown protein	Unigene16483_All//0.00E+00//TC149234				nr -
Unigene16484_All	788	5.71	12.60	7.23	9.42	6.77	9.86	8.53	7.90	6.62	1.14E+00	1.57E-09	Up		3.41E-01	2.12E-01		-4.76E-01	2.11E-02		6.57E-02	7.85E-01		-1.10E-01	6.38E-01		-3.65E-01	6.78E-02		Unigene16484_All//gi|18411677|ref|NP_567214.1|//3.00E-29//serine protease inhibitor, Kazal-type family protein [Arabidopsis thaliana]	Unigene16484_All//6.00E-20//AT4G01575| serine protease inhibitor, Kazal-type family protein	Unigene16484_All//0.00E+00//TC153170				nr -

Unigene16486_All	1453	20.16	31.45	25.03	48.61	51.83	58.50	1.05	0.12	0.30	6.41E-01	6.24E-16		3.12E-01	7.95E-04		9.24E-02	1.73E-01		2.67E-01	1.21E-06		-3.19E+00	4.80E-07	Down	-1.80E+00	3.39E-04	Down	Unigene16486_All//gi|148611499|gb|AB429989.1|//2.00E-88//phospholipase A1 [Capsicum annuum]	Unigene16486_All//3.00E-85//AT2G31100| triacylglycerol lipase	Unigene16486_All//0.00E+00//TC144076				nr +
Unigene16487_All	1058	0.84	0.81	0.10	5.79	3.87	1.75	3.72	2.13	3.16	-4.62E-02	9.62E-01		-3.06E+00	2.25E-03		-5.80E-01	1.04E-02		-1.73E+00	1.34E-11	Down	-8.01E-01	3.50E-03		-2.33E-01	4.12E-01		Unigene16487_All//gi|4538901|emb|CAB39638.1|//4.00E-29//RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] >gi|7267666|emb|CAB78094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]	Unigene16487_All//1.00E-07//ATMG01250| hypothetical protein				nr +
Unigene16488_All	974	23.42	24.45	23.02	1344.68	1104.37	364.04	42.93	42.74	19.35	6.21E-02	6.04E-01		-2.51E-02	8.50E-01		-2.84E-01	4.88E-119		-1.89E+00	0.00E+00	Down	-6.40E-03	9.71E-01		-1.15E+00	4.20E-48	Down	Unigene16488_All//gi|297793807|ref|XP_002864788.1|//1.00E-49//invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310623|gb|EFH41047.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16488_All//6.00E-51//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene16488_All//0.00E+00//TC134796		ko00500|Starch and sucrose metabolism|ko00040|Pentose and glucuronate interconversions		nr -
Unigene16489_All	1276	0.62	0.28	0.08	0.82	0.65	0.71	2.45	4.13	5.59	-1.15E+00	1.53E-01		-2.88E+00	6.35E-03		-3.40E-01	5.96E-01		-2.12E-01	7.44E-01		7.51E-01	1.19E-03		1.19E+00	2.70E-09	Up	Unigene16489_All//gi|24661885|gb|AA62352.1|AF506028_19//2.00E-61//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene16489_All//4.00E-47//AT1G12210| RFL1 (RPS5-like 1); ATP binding / protein binding	Unigene16489_All//7.00E-92//ES832793		ko04626|Plant-pathogen interaction		nr -
Unigene16491_All	657	8.44	5.09	5.03	5.46	5.35	2.41	1.48	0.76	0.91	-7.30E-01	3.85E-03		-7.48E-01	4.48E-03		-3.02E-02	9.30E-01		-1.18E+00	2.74E-04	Down	-9.55E-01	1.35E-01		-7.02E-01	2.43E-01		Unigene16491_All//gi|18422509|ref|NP_568640.1|//2.00E-49//cytochrome c6 (ATC6) [Arabidopsis thaliana] >gi|27805454|sp|Q93VA3.1|CYC6_ARATH RecName: Full=Cytochrome c6, chloroplastic; AltName: Full=Soluble cytochrome f; AltName: Full=Cytochrome c-553; AltName: Full=Cytochrome c553; AltName: Full=Cytochrome c-552; Short=Atc6; Flags: Precursor >gi|13926305|gb|AAK49619.1|AF372903_1 AT5g45040/K21C13_23 [Arabidopsis thaliana] >gi|16323250|gb|AAL15359.1| AT5g45040/K21C13_23 [Arabidopsis thaliana] >gi|19571824|emb|CAD27418.1| c6 type cytochrome [Arabidopsis thaliana]	Unigene16491_All//3.00E-50//AT5G45040| cytochrome c6 (ATC6)	Unigene16491_All//0.00E+00//gi|48810837|gb|CO112150.1|CO112150		ko00195|Photosynthesis		nr -
Unigene16493_All	781	15.88	14.34	13.77	10.78	12.43	16.13	23.82	15.52	8.88	-1.47E-01	3.91E-01		-2.05E-01	2.52E-01		2.06E-01	3.19E-01		5.82E-01	1.95E-04		-6.18E-01	6.36E-08		-1.42E+00	3.29E-30	Down	Unigene16493_All//gi|34365673|gb|AQ65148.1|//5.00E-26//At5g12240 [Arabidopsis thaliana]	Unigene16493_All//1.00E-11//AT5G12240| unknown protein	Unigene16493_All//0.00E+00//gi|21098304|gb|BQ410617.1|BQ410617				nr -
Unigene16495_All	752	97.20	156.46	112.02	69.89	70.56	79.52	196.39	186.69	92.76	6.87E-01	7.93E-45		2.05E-01	6.13E-04		1.40E-02	8.83E-01		1.86E-01	8.08E-03		-7.31E-02	8.63E-02		-1.08E+00	4.19E-152	Down	Unigene16495_All//gi|146432261|gb|BQ411114.1|//1.00E-82//monodehydroascorbate reductase [Vitis vinifera]	Unigene16495_All//2.00E-76//AT5G03630| ATMDAR2; monodehydroascorbate reductase (NADH)	Unigene16495_All//0.00E+00//TC145676		ko00053|Ascorbate and aldarate metabolism		nr -
Unigene16496_All	1035	2.33	2.01	2.98	8.95	6.32	4.97	7.52	3.84	3.58	-2.12E-01	6.02E-01		3.60E-01	3.57E-01		-5.02E-01	5.06E-03		-8.48E-01	4.59E-06		-9.70E-01	2.76E-07		-1.07E+00	1.04E-08	Down	Unigene16496_All//gi|15218953|ref|NP_174245.1|//2.00E-58//AWPM-19-like membrane family protein [Arabidopsis thaliana]	Unigene16496_All//8.00E-53//AT1G29520| AWPM-19-like membrane family protein	Unigene16496_All//1.00E-74//DW510650				nr -
Unigene16497_All	726	3.24	8.44	8.88	2.33	0.71	1.62	3.14	1.78	1.70	1.38E+00	4.96E-08	Up	1.45E+00	1.24E-08	Up	-1.71E+00	5.29E-04	Down	-5.28E-01	3.21E-01		-8.17E-01	3.07E-02		-8.87E-01	1.47E-02		Unigene16497_All//gi|124361039|gb|ABN09011.1|//4.00E-80//General substrate transporter; Sugar transporter superfamily [Medicago truncatula]	Unigene16497_All//4.00E-78//AT1G54730| sugar transporter, putative	Unigene16497_All//0.00E+00//TC177438				nr +
Unigene16498_All	959	1.69	2.06	3.05	4.31	3.55	2.87	2.47	0.92	2.66	2.85E-01	5.53E-01		8.53E-01	2.56E-02		-2.78E-01	3.90E-01		-5.86E-01	5.25E-02		-1.43E+00	1.95E-04	Down	1.07E-01	7.62E-01		Unigene16498_All//gi|1708025|sp|P52425.1|GPDA_CUPLA//1.00E-131//RecName: Full=Glycerol-3-phosphate dehydrogenase [NAD+] >gi|840723|emb|CAA56125.1| glycerol-3-phosphate dehydrogenase (NAD+) [Cuphea lanceolata]	Unigene16498_All//3.00E-131//AT5G10610| glycerol-3-phosphate dehydrogenase (NAD+) / GPDH	Unigene16498_All//0.00E+00//TC142846		ko00564|Glycerophospholipid metabolism		nr +
Unigene16499_All	1108	10.67	20.30	29.32	24.59	9.88	13.37	7.10	23.58	2.48	9.28E-01	6.79E-15		1.46E+00	1.95E-41	Up	-1.32E+00	4.42E-38	Down	-8.79E-01	1.33E-17		1.73E+00	6.15E-54	Up	-1.52E+00	1.73E-14	Down	Unigene16499_All//gi|1729760|emb|CAA92277.1|//1.00E-132//chitinase [Gossypium hirsutum]	Unigene16499_All//2.00E-95//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene16499_All//0.00E+00//gi|164294490|gb|ES799404.1|ES799404		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene16500_All	1114	10.43	9.42	11.42	14.62	8.50	14.60	11.80	5.48	5.83	-1.47E-01	4.12E-01		1.32E-01	4.68E-01		-7.83E-01	6.50E-10		-2.70E-03	9.83E-01		-1.11E+00	2.10E-14	Down	-1.02E+00	4.56E-13	Down	Unigene16500_All//gi|30694398|ref|NP_191180.2|//8.00E-59//binding [Arabidopsis thaliana] >gi|145332873|ref|NP_001078302.1| binding [Arabidopsis thaliana] >gi|145332875|ref|NP_001078303.1| binding [Arabidopsis thaliana] >gi|38566594|gb|AAR24187.1| At3g56210 [Arabidopsis thaliana] >gi|40824082|gb|AAR92342.1| At3g56210 [Arabidopsis thaliana] >gi|222423263|dbj|BAH19608.1| AT3G56210 [Arabidopsis thaliana]	Unigene16500_All//4.00E-60//AT3G56210| binding	Unigene16500_All//0.00E+00//TC147381				nr -
Unigene16504_All	822	1.40	1.05	0.19	1.52	1.09	2.31	0.77	0.61	0.78	-4.18E-01	5.05E-01		-2.85E+00	6.02E-04	Down	-4.76E-01	4.40E-01		6.07E-01	2.23E-01		-3.38E-01	6.63E-01		7.30E-03	9.95E-01					Unigene16504_All//5.00E-24//DN800900				
Unigene16506_All	434	4.70	9.57	7.36	8.72	4.60	6.56	16.27	13.00	10.19	1.03E+00	6.93E-04	Up	6.47E-01	7.70E-02		-9.23E-01	1.72E-03		-4.12E-01	2.20E-01		-3.24E-01	1.19E-01		-6.75E-01	3.91E-04					Unigene16506_All//1.00E-127//TC130766				
Unigene16508_All	819	32.77	38.98	40.96	11.01	18.33	11.41	5.42	8.78	11.87	2.50E-01	1.08E-02		3.22E-01	9.25E-04		7.36E-01	5.19E-08		5.22E-02	8.10E-01		6.95E-01	3.39E-04		1.13E+00	1.76E-11	Up	Unigene16508_All//gi|224072971|ref|XP_002303944.1|//2.00E-14//predicted protein [Populus trichocarpa] >gi|222841376|gb|EEE78923.1| predicted protein [Populus trichocarpa]	Unigene16508_All//1.00E-05//AT5G06980| unknown protein	Unigene16508_All//0.00E+00//gi|109859284|gb|DW488263.1|DW488263				nr +
Unigene16509_All	1016	3.24	8.03	6.18	8.34	6.20	4.62	7.41	12.42	4.27	1.31E+00	1.16E-09	Up	9.31E-01	1.57E-04		-4.26E-01	2.76E-02		-8.50E-01	1.25E-05		7.46E-01	1.59E-07		-7.93E-01	1.80E-05					Unigene16509_All//4.00E-19//gi|164329168|gb|ES824267.1|ES824267				
Unigene16516_All	620	6.41	4.58	5.93	9.96	6.78	8.52	160.73	47.66	77.62	-4.87E-01	1.17E-01		-1.14E-01	7.21E-01		-5.56E-01	1.41E-02		-2.25E-01	4.01E-01		-1.75E+00	6.06E-208	Down	-1.05E+00	5.12E-98	Down	Unigene16516_All//gi|300608164|emb|CAZ86692.1|//1.00E-59//epoxide hydrolase 1 [Prunus persica]	Unigene16516_All//3.00E-59//AT2G26740| ATSEH (Arabidopsis thaliana soluble epoxide hydrolase); epoxide hydrolase	Unigene16516_All//0.00E+00//TC149045				nr +
Unigene16518_All	1136	11.51	13.65	16.27	13.77	12.94	16.58	14.14	9.23	6.00	2.45E-01	9.96E-02		4.98E-01	1.79E-04		-8.92E-02	6.03E-01		2.68E-01	4.46E-02		-6.15E-01	6.72E-07		-1.24E+00	2.77E-21	Down	Unigene16518_All//gi|297796487|ref|XP_002866128.1|//1.00E-159//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311963|gb|EFH42387.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16518_All//2.00E-159//AT5G56130| transducin family protein / WD-40 repeat family protein	Unigene16518_All//0.00E+00//TC139264		ko03040|Spliceosome		nr +
Unigene16519_All	619	14.37	16.13	4.65	9.01	13.74	15.91	16.67	10.60	12.23	1.66E-01	3.86E-01		-1.63E+00	1.17E-13	Down	6.08E-01	1.31E-03		8.19E-01	5.14E-06		-6.53E-01	3.68E-05		-4.47E-01	3.88E-03					Unigene16519_All//8.00E-10//DW234863				
Unigene1652_All	1169	8.95	10.45	7.65	6.86	8.81	3.86	8.86	1.89	3.03	2.23E-01	2.00E-01		-2.26E-01	2.47E-01		3.60E-01	4.45E-02		-8.29E-01	3.64E-05		-2.23E+00	3.36E-30	Down	-1.55E+00	2.43E-19	Down	Unigene1652_All//gi|297843532|ref|XP_002889647.1|//6.00E-84//sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297335489|gb|EFH65906.1| sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene1652_All//3.00E-85//AT1G07420| SMO2-1 (STEROL 4-ALPHA-METHYL-OXIDASE 2-1); 4-alpha-methyl-delta7-sterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase	Unigene1652_All//0.00E+00//TC148053		ko00100|Steroid biosynthesis		nr -
Unigene16522_All	1256	6.33	2.26	2.88	9.08	7.70	9.67	6.16	3.79	3.93	-1.49E+00	2.35E-11	Down	-1.14E+00	2.30E-07	Down	-2.37E-01	1.83E-01		9.08E-02	6.44E-01		-6.99E-01	1.70E-04		-6.47E-01	3.42E-04		Unigene16522_All//gi|5454194|gb|AAD43609.1|AC005698_8//1.00E-85//T3P18.8 [Arabidopsis thaliana]	Unigene16522_All//1.00E-67//AT1G62520| unknown protein	Unigene16522_All//0.00E+00//gi|78330480|gb|DT550754.1|DT550754				nr +
Unigene16525_All	1166	2.83	2.22	2.74	8.33	3.78	1.36	9.94	17.03	13.29	-3.51E-01	3.23E-01		-4.50E-02	9.07E-01		-1.14E+00	4.28E-11	Down	-2.62E+00	2.16E-30	Down	7.77E-01	3.84E-12		4.20E-01	6.88E-04		Unigene16525_All//gi|145361022|ref|NP_566042.2|//1.00E-11//ZPR1 (LITTLE ZIPPER 1); protein binding [Arabidopsis thaliana]	Unigene16525_All//1.00E-10//AT2G45450| ZPR1 (LITTLE ZIPPER 1); protein binding	Unigene16525_All//0.00E+00//DW501389				nr +
Unigene16526_All	499	11.85	11.88	16.33	39.73	28.91	16.20	8.81	8.38	3.51	3.90E-03	9.86E-01		4.63E-01	3.08E-02		-4.59E-01	6.48E-05		-1.29E+00	7.32E-24	Down	-7.32E-02	7.94E-01		-1.33E+00	4.27E-07	Down	Unigene16526_All//gi|242043568|ref|XP_002459655.1|//3.00E-06//hypothetical protein SORBIDRAFT_02g008050 [Sorghum bicolor] >gi|241923032|gb|EER96176.1| hypothetical protein SORBIDRAFT_02g008050 [Sorghum bicolor]		Unigene16526_All//8.00E-28//DT455851				nr -
Unigene16527_All	696	7.74	3.28	12.32	12.60	13.75	12.91	6.20	3.84	3.72	-1.24E+00	3.16E-06	Down	6.70E-01	1.07E-03		1.27E-01	5.77E-01		3.58E-02	8.86E-01		-6.89E-01	8.08E-03		-7.36E-01	3.43E-03		Unigene16527_All//gi|18481965|gb|AAL73563.1|AC079632_7//3.00E-44//Putative serine carboxypeptidase [Oryza sativa Japonica Group] >gi|19920203|gb|AAM08635.1|AC108883_8 Putative serine carboxypeptidase [Oryza sativa Japonica Group]	Unigene16527_All//2.00E-40//AT3G12203| scpl17 (serine carboxypeptidase-like 17); serine-type carboxypeptidase	Unigene16527_All//8.00E-44//TC162267		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene16528_All	1241	1.73	1.31	0.77	1.89	2.11	1.71	1.67	8.76	3.21	-4.04E-01	3.76E-01		-1.16E+00	1.29E-02		1.61E-01	7.42E-01		-1.41E-01	7.41E-01		2.39E+00	2.29E-34	Up	9.43E-01	4.16E-04		Unigene16528_All//gi|21742317|emb|CAD40774.1|//1.00E-18//OSJNBa0039F02.5 [Oryza sativa (japonica cultivar-group)] >gi|38347155|emb|CAE05145.2| OSJNBa0009C07.1 [Oryza sativa (japonica cultivar-group)]	Unigene16528_All//8.00E-28//AT1G28080| unknown protein	Unigene16528_All//2.00E-138//gi|3326717|gb|AI055603.1|AI055603				nr +
Unigene1653_All	1191	11.86	4.42	5.59	27.73	24.06	13.31	15.19	2.91	5.82	-1.42E+00	2.17E-18	Down	-1.09E+00	9.50E-12	Down	-2.05E-01	3.07E-02		-1.06E+00	9.86E-29	Down	-2.38E+00	1.03E-56	Down	-1.38E+00	3.32E-28	Down	Unigene1653_All//gi|297843532|ref|XP_002889647.1|//1.00E-120//sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297335489|gb|EFH65906.1| sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene1653_All//2.00E-121//AT1G07420| SMO2-1 (STEROL 4-ALPHA-METHYL-OXIDASE 2-1); 4-alpha-methyl-delta7-sterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase	Unigene1653_All//0.00E+00//TC138014		ko00100|Steroid biosynthesis		nr +
Unigene16530_All	269	5.45	0.75	7.13	3.15	4.35	2.52	0.47	0.31	0.30	-2.85E+00	3.60E-05	Down	3.88E-01	4.19E-01		4.67E-01	5.14E-01		-3.22E-01	6.87E-01		-6.02E-01	7.67E-01		-6.71E-01	7.20E-01									
Unigene16532_All	779	1.01	0.39	0.27	34.98	25.29	30.55	17.21	2.41	3.94	-1.37E+00	9.60E-02		-1.88E+00	4.13E-02		-4.68E-01	9.17E-07		-1.95E-01	8.16E-02		-2.83E+00	4.43E-51	Down	-2.13E+00	5.99E-38	Down	Unigene16532_All//gi|224144104|ref|XP_002325187.1|//1.00E-111//vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa] >gi|222866621|gb|EEF03752.1| vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa]	Unigene16532_All//3.00E-99//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene16532_All//0.00E+00//TC130017		ko00190|Oxidative phosphorylation		nr -

Unigene16535_All	876	1.31	0.64	1.22	3.92	3.22	0.77	2.08	1.05	0.91	-1.05E+00	1.01E-01		-1.12E-01	8.56E-01		-2.84E-01	4.27E-01		-2.34E+00	8.96E-10	Down	-9.83E-01	2.32E-02		-1.19E+00	4.84E-03		Unigene16535_All//gi|21554414|gb|AAM63519.1|/1.00E-12//glycoprotein homolog [Arabidopsis thaliana]	Unigene16535_All//5.00E-22//AT3G60380| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT4G16790.1); Has 5716 Blast hits to 3635 proteins in 329 species: Archae - 2; Bacteria - 249; Metazoa - 2628; Fungi - 569; Plants - 209; Viruses - 24; Other Eukaryotes - 2035 (source: NCBI BLink).	Unigene16535_All//0.00E+00//gi|161247375|gb|ES833921.1|ES833921				nr +
Unigene16538_All	392	19.62	8.27	13.18	23.89	16.69	13.02	37.53	52.88	38.01	-1.25E+00	1.35E-08	Down	-5.74E-01	8.70E-03		-5.17E-01	3.52E-03		-8.76E-01	1.97E-06		4.95E-01	4.14E-06		1.81E-02	9.19E-01				Unigene16538_All//5.00E-84//gi|164339249|gb|ES792685.1|ES792685				
Unigene16539_All	313	21.06	16.19	10.38	42.81	41.59	40.55	33.50	36.86	30.17	-3.80E-01	1.06E-01		-1.02E+00	2.32E-05	Down	-4.19E-02	8.17E-01		-7.84E-02	6.81E-01		1.38E-01	4.24E-01		-1.51E-01	3.76E-01		Unigene16539_All//gi|18400827|ref|NP_565595.1|/7.00E-47//epsin N-terminal homology (ENTH) domain-containing protein [Arabidopsis thaliana] >gi|46395898|sp|Q8LF20.2|CAP2_ARATH RecName: Full=Putative clathrin assembly protein At2g25430 >gi|4432855|gb|AAD20703.1| expressed protein [Arabidopsis thaliana] >gi|22654977|gb|AAM88081.1| At2g25430/F13B15.9 [Arabidopsis thaliana] >gi|30725272|gb|AAP37658.1| At2g25430/F13B15.9 [Arabidopsis thaliana]	Unigene16539_All//3.00E-48//AT2G25430| epsin N-terminal homology (ENTH) domain-containing protein	Unigene16539_All//1.00E-102//TC132918				nr -
Unigene16542_All	301	42.24	34.00	16.81	31.28	23.57	18.76	78.94	83.45	79.02	-3.13E-01	5.49E-02		-1.33E+00	2.07E-14	Down	-4.08E-01	2.51E-02		-7.38E-01	5.44E-05		8.02E-02	5.06E-01		1.30E-03	9.89E-01		Unigene16542_All//gi|297799324|ref|XP_002867546.1|/5.00E-31//MRH5/SHV3 [Arabidopsis lyrata subsp. lyrata] >gi|297313382|gb|EFH43805.1| MRH5/SHV3 [Arabidopsis lyrata subsp. lyrata]	Unigene16542_All//9.00E-31//AT5G55480| SVL1 (SHV3-LIKE 1); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase	Unigene16542_All//5.00E-148//TC169204		ko00564|Glycerophospholipid metabolism	nr +
Unigene16546_All	219	0.72	6.25	0.97	3.64	2.04	2.89	2.51	3.24	3.82	3.12E+00	3.45E-05	Up	4.41E-01	7.75E-01		-8.32E-01	2.88E-01		-3.34E-01	6.86E-01		3.70E-01	6.67E-01		6.06E-01	3.65E-01		Unigene16546_All//gi|22326767|ref|NP_196828.2|/1.00E-07//transcription regulator [Arabidopsis thaliana]	Unigene16546_All//6.00E-09//AT5G13240| transcription regulator	Unigene16546_All//1.00E-24//CO108395			nr -
Unigene16547_All	374	1.82	2.98	5.55	4.26	5.62	5.80	3.96	4.47	0.96	7.13E-01	2.69E-01		1.61E+00	1.12E-03		3.98E-01	4.17E-01		4.44E-01	3.51E-01		1.76E-01	7.12E-01		-2.05E+00	1.05E-04	Down			Unigene16547_All//3.00E-08//DT049763				
Unigene16548_All	283	64.15	45.30	40.45	84.14	90.16	134.05	174.95	69.12	89.39	-5.02E-01	1.06E-04		-6.65E-01	7.12E-07		9.98E-02	4.53E-01		6.72E-01	2.55E-15		-1.34E+00	5.88E-70	Down	-9.69E-01	4.11E-43		Unigene16548_All//gi|266743|sp|P29828.1|PDI_MEDSA//1.00E-33//RecName: Full=Protein disulfide-isomerase; Short=PDI; Flags: Precursor >gi|19654|emb|CAA77575.1| protein disulfide isomerase [Medicago sativa]	Unigene16548_All//5.00E-31//AT1G21750| ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase	Unigene16548_All//2.00E-156//gi|164349679|gb|EV490174.1|EV490174		ko04141|Protein processing in endoplasmic reticulum	nr -
Unigene16554_All	866	7.49	3.04	7.07	11.33	10.22	3.60	1.86	1.30	0.97	-1.30E+00	8.02E-08	Down	-8.33E-02	7.35E-01		-1.49E-01	4.89E-01		-1.65E+00	3.23E-17	Down	-5.10E-01	2.90E-01		-9.41E-01	3.51E-02				Unigene16554_All//0.00E+00//ES850612				
Unigene16557_All	672	13.47	10.03	3.09	24.02	7.58	28.23	20.26	5.29	4.92	-4.26E-01	2.77E-02		-2.12E+00	1.24E-19	Down	-1.66E+00	3.05E-32	Down	2.33E-01	8.70E-02		-1.94E+00	3.72E-33	Down	-2.04E+00	1.38E-36	Down	Unigene16557_All//gi|14625943|emb|CAC44011.1|/1.00E-12//snakin2 [Solanum tuberosum] >gi|194475635|gb|ACF74550.1| snakin-2 [Solanum tuberosum] >gi|194475637|gb|ACF74551.1| snakin-2 [Solanum tuberosum] >gi|194475639|gb|ACF74552.1| snakin-2 [Solanum tuberosum]	Unigene16557_All//7.00E-12//AT1G22690| gibberellin-responsive protein, putative	Unigene16557_All//0.00E+00//TC159306			nr +
Unigene16558_All	1613	2.43	0.75	0.50	3.92	3.12	2.32	4.53	0.21	0.91	-1.69E+00	4.76E-07	Down	-2.30E+00	1.21E-09	Down	-3.32E-01	1.67E-01		-7.55E-01	1.04E-03		-4.45E+00	6.22E-41	Down	-2.31E+00	2.81E-23	Down	Unigene16558_All//gi|224069605|ref|XP_002303010.1|/2.00E-35//predicted protein [Populus trichocarpa] >gi|222844736|gb|EEE82283.1| predicted protein [Populus trichocarpa]	Unigene16558_All//7.00E-12//AT3G23740| unknown protein	Unigene16558_All//0.00E+00//TC130687			nr +
Unigene16561_All	253	24.20	26.04	37.89	32.68	30.08	47.48	41.11	83.43	27.24	1.06E-01	6.53E-01		6.47E-01	7.59E-04		-1.20E-01	6.18E-01		5.39E-01	8.28E-04		1.02E+00	6.76E-20	Up	-5.94E-01	1.08E-04		Unigene16561_All//gi|233142300|gb|ACQ91103.1|/4.00E-17//vacuolar processing enzyme a [Populus tomentosa]	Unigene16561_All//3.00E-13//AT4G32940| GAMMA-VPE (GAMMA VACUOLAR PROCESSING ENZYME); cysteine-type endopeptidase	Unigene16561_All//5.00E-132//gi|78327399|gb|DT547673.1|DT547673			nr +
Unigene16562_All	1736	0.72	0.79	0.21	1.66	0.61	0.99	5.31	3.59	1.24	1.24E-01	8.17E-01		-1.75E+00	9.85E-03		-1.44E+00	4.54E-05	Down	-7.52E-01	4.17E-02		-5.66E-01	7.97E-04		-2.10E+00	6.41E-26	Down							
Unigene16563_All	827	127.35	89.39	93.62	224.92	197.33	215.93	123.82	93.80	55.98	-5.11E-01	5.46E-24		-4.44E-01	5.45E-18		-1.89E-01	4.27E-08		-5.88E-02	1.86E-01		-4.01E-01	1.58E-18		-1.15E+00	8.06E-116	Down	Unigene16563_All//gi|189046708|sp|A5YVF1.1|SGS3_SOLLC//1.00E-44//RecName: Full=Protein SUPPRESSOR OF GENE SILENCING 3; AltName: Full=S1SGS3 >gi|148613844|gb|ABQ96272.1| SGS3-like protein [Solanum lycopersicum]	Unigene16563_All//1.00E-37//AT5G23570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene16563_All//0.00E+00//gi|21098113|gb|BQ410426.1|BQ410426			nr -
Unigene16564_All	474	3.53	3.31	5.62	3.99	2.62	1.05	2.59	2.12	0.08	-9.21E-02	8.47E-01		6.69E-01	9.83E-02		-6.11E-01	1.90E-01		-1.93E+00	1.45E-04	Down	-2.90E-01	6.39E-01		-4.94E+00	6.14E-08	Down	Unigene16564_All//gi|42568915|ref|NP_178474.2|/3.00E-36//GEK1 (GEK01); D-aminoacyl-tRNA deacylase [Arabidopsis thaliana] >gi|83302950|sp|Q9ZFQ3.2|GEK1_ARATH RecName: Full=D-aminoacyl-tRNA deacylase; AltName: Full=Ethanol tolerance protein GEK01 >gi|28812213|dbj|BAC65101.1| GEK01 [Arabidopsis thaliana] >gi|63025186|gb|AAY27066.1| At2g03800 [Arabidopsis thaliana]	Unigene16564_All//2.00E-37//AT2G03800| GEK1 (GEK01); D-aminoacyl-tRNA deacylase	Unigene16564_All//0.00E+00//DW513606			nr -
Unigene16566_All	581	28.19	63.84	42.25	45.44	48.54	49.83	35.08	38.70	37.51	1.18E+00	3.02E-35	Up	5.84E-01	2.47E-07		9.52E-02	4.49E-01		1.33E-01	2.54E-01		1.42E-01	2.29E-01		9.67E-02	4.12E-01		Unigene16566_All//gi|186478335|ref|NP_001117260.1|/6.00E-51//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene16566_All//3.00E-52//AT1G10650| protein binding / zinc ion binding	Unigene16566_All//0.00E+00//gi|109887577|gb|DW516546.1|DW516546			nr +
Unigene1657_All	1110	45.63	17.76	42.74	5.79	4.03	3.46	1.64	0.75	1.58	-1.36E+00	5.14E-60	Down	-9.42E-02	2.87E-01		-5.22E-01	1.95E-02		-7.43E-01	1.13E-03		-1.12E+00	1.02E-02		-5.27E-02	9.14E-01		Unigene1657_All//gi|30684516|ref|NP_193609.2|/7.00E-21//transcription termination factor [Arabidopsis thaliana]	Unigene1657_All//2.00E-11//AT4G18740| transcription termination factor	Unigene1657_All//4.00E-164//CO071852			nr -
Unigene16570_All	537	4.97	3.21	10.31	5.84	5.58	6.90	2.60	2.72	3.19	-6.31E-01	1.02E-01		1.05E+00	7.79E-05	Up	-6.70E-02	8.48E-01		2.39E-01	5.08E-01		6.83E-02	9.02E-01		2.96E-01	5.24E-01				Unigene16570_All//1.00E-109//FL577561				
Unigene16571_All	758	1.24	0.80	0.84	1.25	1.77	2.09	2.23	2.76	41.10	-6.31E-01	3.66E-01		-5.60E-01	4.39E-01		5.05E-01	4.23E-01		7.40E-01	1.79E-01		3.05E-01	4.77E-01		4.20E+00	1.11E-168	Up	Unigene16571_All//gi|7940288|gb|AAF70847.1|AC003113.14//2.00E-31//F2401.15 [Arabidopsis thaliana]	Unigene16571_All//3.00E-27//AT1G62422| unknown protein	Unigene16571_All//0.00E+00//CO074155			nr +
Unigene16575_All	649	1.61	4.06	1.97	8.29	8.44	6.96	9.71	9.27	9.94	1.33E+00	9.56E-04	Up	2.88E-01	6.09E-01		2.53E-02	9.49E-01		-2.52E-01	3.93E-01		-6.59E-02	7.82E-01		3.49E-02	8.87E-01		Unigene16575_All//gi|224117962|ref|XP_002317699.1|/9.00E-07//predicted protein [Populus trichocarpa] >gi|222858372|gb|EEE95919.1| predicted protein [Populus trichocarpa]		Unigene16575_All//5.00E-156//TC171548			nr -
Unigene16578_All	311	21.37	14.34	15.41	46.61	44.73	51.12	71.51	34.81	32.67	-5.76E-01	1.16E-02		-4.71E-01	5.03E-02		-5.93E-02	7.64E-01		1.33E-01	4.26E-01		-1.04E+00	1.59E-21	Down	-1.13E+00	2.55E-25	Down	Unigene16578_All//gi|9294075|dbj|BAB02032.1|/1.00E-50//cytosolic chaperonin, delta-subunit [Arabidopsis thaliana]	Unigene16578_All//4.00E-52//AT3G18190| chaperonin, putative	Unigene16578_All//4.00E-161//TC142327			nr -
Unigene16579_All	606	13.73	12.71	8.26	17.43	13.30	16.62	34.81	25.17	9.20	-1.11E-01	6.04E-01		-7.33E-01	4.41E-04		-3.90E-01	2.24E-02		-6.84E-02	7.31E-01		-4.68E-01	1.10E-05		-1.92E+00	6.90E-52	Down	Unigene16579_All//gi|197312877|gb|ACH63219.1|/5.00E-44//ribosomal protein S27-like protein [Rheum australe]	Unigene16579_All//2.00E-38//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome	Unigene16579_All//0.00E+00//TC161675		ko03010|Ribosome	nr -
Unigene1658_All	2308	13.51	4.17	3.51	14.27	11.23	14.62	24.44	8.86	10.12	-1.70E+00	3.48E-51	Down	-1.95E+00	1.55E-59	Down	-3.45E-01	8.39E-05		3.51E-02	7.55E-01		-1.46E+00	5.45E-91	Down	-1.27E+00	1.13E-75	Down	Unigene1658_All//gi|195619614|gb|ACG31637.1|/2.00E-47//60S ribosomal protein L11-1 [Zea mays]	Unigene1658_All//1.00E-37//AT5G45775| 60S ribosomal protein L11 (RPL11D)	Unigene1658_All//0.00E+00//gi|21101061|gb|BQ413374.1|BQ413374		ko03010|Ribosome	nr -
Unigene16582_All	265	36.33	35.56	50.44	86.66	58.73	33.92	44.67	40.06	22.10	-3.07E-02	8.83E-01		4.73E-01	3.18E-03		-5.61E-01	7.56E-08		-1.35E+00	1.71E-29	Down	-1.57E-01	3.61E-01		-1.02E+00	8.22E-12	Down	Unigene16582_All//gi|186531506|ref|NP_001119419.1|/9.00E-10//CPuORF14 (Conserved peptide upstream open reading frame 14) [Arabidopsis thaliana]	Unigene16582_All//4.00E-11//AT5G52552| CPuORF14 (Conserved peptide upstream open reading frame 14)	Unigene16582_All//6.00E-129//TC158934			nr -
Unigene16584_All	290	157.32	77.75	41.50	121.62	115.18	84.25	118.97	40.79	62.92	-1.02E+00	2.95E-34	Down	-1.92E+00	1.31E-85	Down	-7.84E-02	4.85E-01		-5.30E-01	1.31E-09		-1.54E+00	1.82E-60	Down	-9.19E-01	7.82E-28		Unigene16584_All//gi|7387726|sp|O02582.3|H2B_GOSHI//6.00E-28//RecName: Full=Histone H2B >gi|2558962|gb|AAB97163.1| histone H2B1 [Gossypium hirsutum]		Unigene16584_All//7.00E-141//gi|109829292|gb|DW227880.1|DW227880			nr +
Unigene16585_All	678	1.54	6.95	5.89	8.89	3.61	5.66	27.44	9.74	8.17	2.17E+00	3.27E-11	Up	1.93E+00	4.86E-08	Up	-1.30E+00	1.23E-08	Down	-6.51E-01	6.32E-03		-1.49E+00	1.99E-31	Down	-1.75E+00	1.99E-40	Down	Unigene16585_All//gi|15811629|gb|AAL09033.1|AF416652_1//8.00E-65//ribonuclease-like PR-10 [Gossypium arboreum]	Unigene16585_All//2.00E-07//AT1G24020| MLP423 (MLP-LIKE PROTEIN 423)	Unigene16585_All//6.00E-94//TC173675			nr +
Unigene16586_All	280	31.77	12.31	14.64	59.78	46.24	60.00	80.79	29.41	35.71	-1.37E+00	3.21E-11	Down	-1.12E+00	5.70E-08	Down	-3.70E-01	4.39E-03		5.40E-03	9.70E-01		-1.46E+00	1.04E-36	Down	-1.18E+00	2.01E-27	Down	Unigene16586_All//gi|192910792|gb|ACF06504.1|/3.00E-24//60S ribosomal protein L28 [Elaeis guineensis]	Unigene16586_All//2.00E-24//AT2G19730| 60S ribosomal protein L28 (RPL28A)	Unigene16586_All//4.00E-105//TC143302		ko03010|Ribosome	nr -
Unigene16587_All	232	39.69	12.67	12.85	73.22	60.26	80.01	143.24	53.87	50.31	-1.65E+00	5.19E-15	Down	-1.63E+00	4.31E-14	Down	-2.81E-01	3.75E-02		1.28E-01	4.03E-01		-1.41E+00	5.02E-51	Down	-1.51E+00	4.85E-58	Down	Unigene16587_All//gi|192908658|gb|ACF06437.1|/5.00E-30//ribosomal L28-like protein [Elaeis guineensis]	Unigene16587_All//5.00E-28//AT2G19730| 60S ribosomal protein L28 (RPL28A)	Unigene16587_All//2.00E-128//TC143302		ko03010|Ribosome	nr -
Unigene16588_All	782	45.43	116.24	77.08	71.22	80.67	68.67	128.14	153.82	151.36	1.36E+00	5.70E-106	Up	7.63E-01	5.93E-27		1.80E-01	6.38E-03		-5.26E-02	5.72E-01		2.64E-01	2.89E-10		2.40E-01	7.14E-09		Unigene16588_All//gi|226504394|ref|NP_001152681.1|/6.00E-17//protein translation factor SUI1 [Zea mays] >gi|195610300|gb|ACG26980.1| protein translation factor SUI1 [Zea mays] >gi|195621196|gb|ACG32428.1| protein translation factor SUI1 [Zea mays] >gi|195655637|gb|ACG47286.1| protein translation factor SUI1 [Zea mays] >gi|195658863|gb|ACG48899.1| protein translation factor SUI1 [Zea mays]	Unigene16588_All//2.00E-16//AT1G54290| eukaryotic translation initiation factor SUI1, putative	Unigene16588_All//0.00E+00//TC162058			nr -

Unigene16589_All	349	2.70	11.61	9.77	11.85	4.93	8.93	47.97	41.92	21.12	2.11E+00	2.11E-09	Up	1.86E+00	1.28E-06	Up	-1.26E+00	7.59E-06	Down	-4.08E-01	1.98E-01		-1.95E-01	1.41E-01		-1.18E+00	1.08E-20	Down		Unigene1659_All//2.00E-138//gi|211906486|gb|ACJ11736.1|/1.00E-138//phosphoglycerate dehydrogenase [Gossypium hirsutum]	Unigene16589_All//2.00E-61//gi|72269693|gb|DT047283.1|DT047283				
Unigene1659_All	2144	6.34	4.04	5.94	2.90	3.45	3.83	0.91	2.59	13.47	-6.51E-01	1.89E-05		-9.61E-02	6.10E-01		2.50E-01	3.00E-01		4.01E-01	5.54E-02		1.52E+00	4.17E-10	Up	3.89E+00	5.66E-148	Up	Unigene1659_All//1.00E-134//AT3G19480| D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative	Unigene1659_All//0.00E+00//TC131014		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene16590_All	240	16.35	8.66	12.87	36.12	41.32	28.79	19.03	8.88	12.28	-9.18E-01	3.02E-03		-3.46E-01	3.04E-01		1.94E-01	3.44E-01		-3.27E-01	1.17E-01		-1.10E+00	1.82E-05	Down	-6.31E-01	9.44E-03				Unigene16590_All//7.00E-125//TC142812				
Unigene16595_All	596	2.46	2.04	2.86	12.45	12.42	5.00	1.14	0.14	0.07	-2.69E-01	6.13E-01		2.18E-01	6.56E-01		-3.70E-03	9.80E-01		-1.32E+00	1.59E-09	Down	-3.02E+00	2.43E-03		-4.09E+00	3.10E-04	Down	Unigene16595_All//1.00E-06//AT2G42200| SPL9 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9); transcription factor	Unigene16595_All//0.00E+00//TC139864	SBP			nr +
Unigene16597_All	350	7.62	5.94	5.17	11.24	7.08	9.16	37.81	28.78	15.37	-3.61E-01	3.75E-01		-5.60E-01	1.68E-01		-6.67E-01	2.29E-02		-2.95E-01	3.97E-01		-3.94E-01	4.79E-03		-1.30E+00	5.31E-19	Down	Unigene16597_All//8.00E-08//AT1G26570| UGD1 (UDP-GLUCOSE DEHYDROGENASE 1); NAD or NADH binding / UDP-glucose 6-dehydrogenase/ binding / catalytic/ coenzyme binding / oxidoreductase/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	Unigene16597_All//4.00E-155//gi|164319235|gb|ES794307.1|ES794307		ko00500|Starch and sucrose metabolism/ko00520|Amino sugar and nucleotide sugar metabolism/ko00053|Ascorbate and aldarate metabolism/ko00040|Pentose and glucuronate interconversions		nr -
Unigene16598_All	525	4.48	0.97	5.17	9.20	4.46	8.43	2.90	3.26	2.05	-2.22E+00	3.85E-06	Down	2.06E-01	6.40E-01		-1.05E+00	4.16E-05	Down	-1.27E-01	6.93E-01		1.71E-01	7.18E-01		-5.01E-01	2.87E-01				Unigene16598_All//0.00E+00//gi|54119286|gb|CO494795.1|CO494795				
Unigene16599_All	770	0.41	6.84	2.28	1.04	1.16	5.57	0.49	2.17	0.98	4.07E+00	1.28E-22	Up	2.48E+00	4.72E-05	Up	1.68E-01	8.32E-01		2.43E+00	3.01E-12	Up	2.14E+00	3.22E-05	Up	9.92E-01	1.63E-01				Unigene16599_All//1.00E-12//DW233256				
Unigene1660_All	1458	15.25	10.53	12.16	8.92	8.90	5.92	20.85	13.36	9.26	-5.34E-01	3.92E-06		-3.27E-01	7.93E-03		-2.20E-03	9.86E-01		-5.92E-01	1.03E-04		-6.42E-01	3.02E-13		-1.17E+00	3.34E-36	Down	Unigene1660_All//gi|11177137|dbj|BAB17836.1|/1.00E-116//nuclear coiled-coil protein AT4g30200 [Arabidopsis thaliana] >gi|118566356|gb|ABL01539.1| VIN3-like 2 protein [Arabidopsis thaliana]	Unigene1660_All//2.00E-116//AT4G30200| Encodes a protein with similarity to VRN5 and VIN3. Contains both a fibronectin III and PHD finger domain. VEL1 is a part of a polycomb repressive complex (PRC2) that is involved in epigenetic silencing of the FLC flowering locus.	Unigene1660_All//0.00E+00//TC132819				nr +
Unigene16601_All	755	3.67	3.29	6.21	7.85	8.89	7.42	2.91	1.66	1.21	-1.60E-01	6.64E-01		7.57E-01	9.03E-03		1.80E-01	5.13E-01		-8.20E-02	7.57E-01		-8.10E-01	3.61E-02		-1.26E+00	9.51E-04	Down			Unigene16601_All//3.00E-22//TC175491				
Unigene16603_All	1086	5.44	2.99	5.59	2.75	2.89	1.37	1.36	0.85	0.33	-8.67E-01	3.93E-04		3.81E-02	8.88E-01		6.82E-02	8.70E-01		-1.00E+00	5.22E-03		-6.86E-01	1.64E-01		-2.05E+00	1.05E-04	Down	Unigene16603_All//gi|124360549|gb|ABD33126.2|/1.00E-46//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene16603_All//1.00E-08//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene16603_All//4.00E-50//TC160935				nr +
Unigene16605_All	411	35.90	81.49	68.54	65.45	81.77	56.81	23.35	30.10	36.35	1.18E+00	4.99E-32	Up	9.33E-01	5.98E-18		3.21E-01	2.73E-04		-2.04E-01	6.96E-02		3.66E-01	1.22E-02		6.38E-01	4.53E-07		Unigene16605_All//gi|102139981|gb|ABF70116.1|/9.00E-15//dual specificity protein phosphatase family protein [Musa balbisiana]	Unigene16605_All//1.00E-13//AT5G56610| dual specificity protein phosphatase family protein	Unigene16605_All//0.00E+00//gi|109847878|gb|DW476838.1|DW476838				nr +
Unigene16606_All	1186	1.01	1.37	0.72	1.18	0.81	1.03	2.17	0.35	2.15	4.30E-01	3.96E-01		-4.98E-01	4.26E-01		-5.33E-01	3.45E-01		-1.94E-01	7.27E-01		-2.63E+00	1.34E-09	Down	-1.65E-02	9.68E-01		Unigene16606_All//gi|193103993|gb|AL849306.1|/3.00E-37//At2g43990/F6E13.12 [Arabidopsis thaliana]	Unigene16606_All//2.00E-34//AT2G43990| unknown protein	Unigene16606_All//1.00E-167//ES803868				nr +
Unigene16607_All	500	2.41	2.33	2.13	44.83	20.04	27.19	828.27	152.39	406.04	-4.63E-02	9.51E-01		-1.76E-01	7.68E-01		-1.16E+00	8.48E-26	Down	-7.22E-01	1.51E-10		-2.44E+00	0.00E+00	Down	-1.03E+00	0.00E+00	Down	Unigene16607_All//gi|559237|gb|AAA98492.1|/3.00E-62//tyrosine-rich hydroxyproline-rich glycoprotein [Petroselinum crispum]	Unigene16607_All//2.00E-06//AT3G09925| pollen Ole e 1 allergen and extensin family protein					nr -
Unigene16608_All	916	1.37	2.77	3.49	0.76	1.77	1.08	0.32	1.28	0.57	1.01E+00	1.17E-02		1.35E+00	3.24E-04	Up	1.21E+00	2.02E-02		5.11E-01	4.92E-01		1.98E+00	1.36E-03		8.07E-01	3.66E-01		Unigene16608_All//gi|212717149|gb|ACJ37146.1|/8.00E-35//stress-induced receptor-like kinase [Glycine max]	Unigene16608_All//2.00E-18//AT1G66910| protein kinase, putative	Unigene16608_All//8.00E-23//DT462619		ko04626|Plant-pathogen interaction		nr +
Unigene16609_All	1288	0.12	0.00	0.99	0.08	0.13	1.19	1.71	2.30	33.59	-6.93E+00	2.16E-01		3.02E+00	1.48E-04	Up	7.89E-01	7.71E-01		3.95E+00	4.90E-07	Up	4.33E-01	2.02E-01		4.30E+00	1.03E-237	Up	Unigene16609_All//gi|86212377|gb|ABC87761.1|/1.00E-139//JAR1-like protein [Nicotiana attenuata]	Unigene16609_All//4.00E-111//AT2G46370| JAR1 (JASMONATE RESISTANT 1); ATP binding / adenylyltransferase/ catalytic/ jasmonate-amino synthetase	Unigene16609_All//0.00E+00//TC152052				nr -
Unigene1661_All	1628	22.50	13.10	17.99	21.05	17.09	10.93	24.23	13.99	10.79	-7.80E-01	6.29E-18		-3.23E-01	4.86E-04		-3.01E-01	5.45E-04		-9.46E-01	8.59E-25		-7.92E-01	4.29E-24		-1.17E+00	1.73E-46	Down	Unigene1661_All//gi|11177137|dbj|BAB17836.1|/1.00E-156//nuclear coiled-coil protein AT4g30200 [Arabidopsis thaliana] >gi|118566356|gb|ABL01539.1| VIN3-like 2 protein [Arabidopsis thaliana]	Unigene1661_All//7.00E-157//AT4G30200| Encodes a protein with similarity to VRN5 and VIN3. Contains both a fibronectin III and PHD finger domain. VEL1 is a part of a polycomb repressive complex (PRC2) that is involved in epigenetic silencing of the FLC flowering locus.	Unigene1661_All//0.00E+00//TC132819				nr -
Unigene16620_All	688	14.75	31.67	25.46	7.67	4.40	11.23	3.13	6.74	2.20	1.10E+00	6.41E-19	Up	7.87E-01	1.03E-08		-8.01E-01	9.31E-04		5.49E-01	8.86E-03		1.11E+00	1.42E-05	Up	-5.10E-01	1.81E-01		Unigene16620_All//gi|115436714|ref|NP_001043115.1|/6.00E-15//Os01g0392100 [Oryza sativa Japonica Group] >gi|113532646|dbj|BAF05029.1|Os01g0392100 [Oryza sativa Japonica Group]		Unigene16620_All//0.00E+00//DW508106				nr -
Unigene16624_All	1365	0.15	0.00	0.00	2.01	0.15	0.40	13.07	1.81	5.66	-7.26E+00	1.22E-01		-7.26E+00	1.46E-01		-3.73E+00	2.97E-14	Down	-2.34E+00	6.98E-08	Down	-2.86E+00	2.40E-68	Down	-1.21E+00	1.18E-22	Down	Unigene16624_All//gi|115435584|ref|NP_001042550.1|/2.00E-15//Os01g0241000 [Oryza sativa Japonica Group] >gi|113532081|dbj|BAF04464.1|Os01g0241000 [Oryza sativa Japonica Group]	Unigene16624_All//1.00E-11//AT2G42760| unknown protein	Unigene16624_All//0.00E+00//gi|48814117|gb|CO115430.1|CO115430				nr +
Unigene16627_All	1889	0.00	0.80	0.37	0.26	0.22	0.81	1.50	9.25	67.64	9.65E+00	1.10E-08	Up	8.52E+00	6.17E-04	Up	-2.69E-01	8.02E-01		1.62E+00	4.20E-03		2.62E+00	5.67E-61	Up	5.50E+00	0.00E+00	Up	Unigene16627_All//gi|15235536|ref|NP_195453.1|/1.00E-167//CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|4468803|emb|CAB38204.1| cytochrome P450-like protein [Arabidopsis thaliana] >gi|7270719|emb|CAB80402.1| cytochrome P450-like protein [Arabidopsis thaliana] >gi|17473898|gb|AAL38368.1| cytochrome P450-like protein [Arabidopsis thaliana] >gi|23197764|gb|AAN15409.1| cytochrome P450-like protein [Arabidopsis thaliana]	Unigene16627_All//5.00E-162//AT4G37370| CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene16627_All//0.00E+00//TC134956		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene16628_All	610	14.75	42.45	15.28	23.52	29.98	30.80	2.77	6.37	50.22	1.52E+00	1.97E-36	Up	5.03E-02	8.07E-01		3.50E-01	5.53E-03		3.89E-01	2.21E-03		1.20E+00	2.32E-05	Up	4.18E+00	3.18E-165	Up			Unigene16628_All//0.00E+00//TC172510				
Unigene16629_All	448	3.62	6.11	5.11	5.89	8.07	16.73	57.38	41.42	36.55	7.54E-01	4.70E-02		4.98E-01	2.62E-01		4.54E-01	1.77E-01		1.51E+00	1.91E-11	Up	-4.70E-01	8.41E-07		-6.51E-01	6.08E-12		Unigene16629_All//gi|20386366|gb|AAK21638.1|AF492022_1//1.00E-24//geranylgeranyl pyrophosphate synthase [Cistus creticus]	Unigene16629_All//5.00E-22//AT4G36810| GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltranstransferase	Unigene16629_All//0.00E+00//gi|109891503|gb|DW520466.1|DW520466		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene1663_All	3836	5.35	4.27	4.86	10.92	11.17	9.05	15.42	7.62	6.22	-3.26E-01	8.32E-03		-1.38E-01	3.36E-01		3.21E-02	7.88E-01		-2.71E-01	9.99E-04		-1.02E+00	4.42E-54	Down	-1.31E+00	6.69E-83	Down	Unigene1663_All//gi|297814241|ref|XP_002875004.1|//0.00E+00//transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297320841|gb|EFH51263.1| transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene1663_All//0.00E+00//AT4G00990| transcription factor jumonji (jmjC) domain-containing protein	Unigene1663_All//0.00E+00//TC161654				nr -
Unigene16633_All	513	21.21	12.84	53.77	36.90	83.91	63.30	7.83	28.19	19.80	-7.24E-01	2.71E-05		1.34E+00	3.84E-31	Up	1.19E+00	2.09E-48	Up	7.79E-01	6.91E-17		1.85E+00	5.88E-33	Up	1.34E+00	2.62E-15	Up							
Unigene16635_All	688	2.97	78.29	8.20	1.45	5.51	9.85	0.25	0.91	0.23	4.72E+00	2.95E-251	Up	1.47E+00	9.38E-08	Up	1.93E+00	7.94E-09	Up	2.77E+00	5.61E-22	Up	1.89E+00	3.49E-02		-8.58E-02	9.66E-01		Unigene16635_All//gi|15240946|ref|NP_195750.1|/3.00E-56//phosphatidylethanolamine-binding family protein [Arabidopsis thaliana]	Unigene16635_All//2.00E-57//AT5G01300| phosphatidylethanolamine-binding family protein					nr -
Unigene16636_All	1179	0.84	26.43	3.03	0.55	1.90	2.18	0.18	0.71	0.34	4.97E+00	1.49E-149	Up	1.84E+00	7.60E-07	Up	1.79E+00	6.16E-05	Up	1.99E+00	4.68E-06	Up	1.98E+00	8.88E-03		9.14E-01	3.86E-01		Unigene16636_All//gi|15240946|ref|NP_195750.1|/3.00E-64//phosphatidylethanolamine-binding family protein [Arabidopsis thaliana]	Unigene16636_All//8.00E-65//AT5G01300| phosphatidylethanolamine-binding family protein					nr -
Unigene16637_All	837	3.25	1.45	1.40	4.11	3.37	1.62	1.92	1.80	2.62	-1.16E+00	2.76E-03		-1.22E+00	2.83E-03		-2.84E-01	4.27E-01		-1.34E+00	6.79E-05	Down	-9.46E-02	8.44E-01		4.48E-01	2.43E-01		Unigene16637_All//gi|115473321|ref|NP_001060259.1|/1.00E-08//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene16637_All//8.00E-10//AT3G25270| nucleic acid binding					nr -
Unigene16638_All	636	1.56	2.87	4.69	5.80	2.82	4.62	2.93	3.81	0.63	8.76E-01	7.03E-02		1.58E+00	7.34E-05	Up	-1.04E+00	4.93E-04	Down	-3.29E-01	3.51E-01		3.82E-01	3.27E-01		-2.22E+00	3.02E-06	Down							
Unigene16639_All	523	83.53	42.92	67.61	68.29	55.90	53.45	36.38	18.22	18.13	-9.61E-01	5.99E-30		-3.05E-01	2.80E-04		-2.89E-01	7.11E-04		-3.53E-01	5.73E-05		-9.98E-01	2.16E-17		-1.00E+00	3.90E-18	Down			Unigene16639_All//2.00E-161//TC133544				
Unigene16640_All	623	5.71	5.69	4.36	22.55	19.07	14.72	37.67	44.81	18.29	-4.50E-03	9.86E-01		-3.90E-01	2.65E-01		-2.42E-01	1.22E-01		-6.16E-01	2.38E-05		2.51E-01	7.97E-03		-1.04E+00	1.75E-23	Down	Unigene16640_All//gi|8778315|gb|AAF79324.1|AC002304_17//1.00E-13//F14J16.29 [Arabidopsis thaliana]		Unigene16640_All//0.00E+00//TC164240		ko03040|Spliceosome		nr +
Unigene16641_All	1095	1.29	3.47	2.72	1.64	2.14	1.44	0.50	0.69	0.51	1.43E+00	1.65E-05	Up	1.08E+00	4.70E-03		3.85E-01	4.03E-01		-1.82E-01	7.11E-01		4.53E-01	5.59E-01		2.11E-02	9.79E-01		Unigene16641_All//gi|109676376|gb|ABG37670.1|/2.00E-32//integrase [Populus trichocarpa]						nr -
Unigene16643_All	505	14.71	15.95	5.69	27.03	25.84	27.81	14.07	12.50	20.75	1.17E-01	5.91E-01		-1.37E+00	4.75E-09	Down	-6.46E-02	7.45E-01		4.13E-02	8.17E-01		-1.71E-01	4.42E-01		5.61E-01	2.51E-04		Unigene16643_All//gi|289541359|gb|ADD08803.1|/7.00E-33//ectoapyrase 1 [Gossypium hirsutum]	Unigene16643_All//2.00E-20//AT5G18280| ATAPY2 (ARABIDOPSIS THALIANA APYRASE 2); ATPase/ nucleotide diphosphatase	Unigene16643_All//0.00E+00//gi|13354997|gb|BG445345.1|BG445345		ko00230|Purine metabolism/ko00730|Thiamine metabolism		nr +
Unigene16654_All	422	21.08	19.57	16.15	22.78	12.81	17.34	28.45	27.63	11.80	-1.07E-01	6.06E-01		-3.84E-01	6.34E-02		-8.31E-01	1.11E-06		-3.94E-01	3.77E-02		-4.23E-02	8.05E-01		-1.27E+00	9.47E-17	Down			Unigene16654_All//0.00E+00//TC138544				
Unigene16656_All	654	4.88	1.55	2.44	5.94	3.53	5.32	9.89	5.75	4.39	-1.66E+00	9.88E-06	Down	-9.98E-01	6.35E-03		-7.52E-01	1.01E-02		-1.60E-01	6.47E-01		-7.82E-01	1.49E-04		-1.17E+00	1.98E-08	Down	Unigene16656_All//gi|98961015|gb|AB058991.1|/3.00E-23//At1g28395 [Arabidopsis thaliana]	Unigene16656_All//3.00E-22//AT1G28395| unknown protein	Unigene16656_All//3.00E-176//TC158912				nr -
Unigene16659_All	480	52.76	35.68	44.04	62.68	55.67	47.89	55.93	23.51	24.98	-5.64E-01	1.73E-07		-2.61E-01	2.55E-02		-1.71E-01	1.01E-01		-3.88E-01	5.50E-05		-1.25E+00	1.75E-34	Down	-1.16E+00	9.47E-32	Down	Unigene16659_All//gi|3334115|sp|O22342.1|ADT1_GOSHI//6.00E-44//RecName: Full=ADP,ATP carrier protein 1, mitochondrial; AltName: Full=ADP/ATP translocase 1; AltName: Full=Adenine nucleotide translocator 1; Short=ANT 1; Flags: Precursor >gi|2463664|gb|AAB72047.1| adenine nucleotide translocator 1 [Gossypium hirsutum]	Unigene16659_All//5.00E-34//AT5G13490| AAC2 (ADP/ATP carrier 2); ATP:ADP antiporter/ binding	Unigene16659_All//0.00E+00//ES839924				nr -
Unigene16660_All	595	49.24	282.22	69.72	97.54	137.16	148.47	41.85	87.24	92.87	2.52E+00	0.00E+00	Up	5.02E-01	3.31E-09		4.92E-01	1.44E-20		6.06E-01	3.51E-29		1.06E+00	1.07E-50	Up	1.15E+00	8.90E-63	Up	Unigene16660_All//gi|224124306|ref|XP_002329990.1|/1.00E-08//stress-induced hydrophobic peptide [Populus trichocarpa] >gi|222871415|gb|EEF08546.1| stress-induced hydrophobic peptide [Populus trichocarpa]		Unigene16660_All//2.00E-105//TC168849				nr +

Unigene16662_All	1325	0.12	0.88	0.40	2.26	2.24	0.92	1.21	1.14	2.07	2.89E+00	2.98E-04	Up	1.76E+00	1.29E-01		-1.33E-02	9.63E-01		-1.29E+00	3.86E-04	Down	-9.46E-02	8.44E-01		7.75E-01	1.79E-02		Unigene16662_All//gi|116310986|emb|CAH67921.1|/6.00E-98//OSIGBa0138E08-OSIGBa0161L23.2 [Oryza sativa (indica cultivar-group)]	Unigene16662_All//1.00E-122//AT1G68390| unknown protein	Unigene16662_All//0.00E+00//CO116661				nr +
Unigene16663_All	822	3.06	0.43	1.23	2.55	3.35	1.76	4.17	1.32	2.18	-2.82E+00	2.62E-08	Down	-1.31E+00	2.27E-03		3.97E-01	3.26E-01		-5.34E-01	2.49E-01		-1.66E+00	2.56E-07	Down	-9.34E-01	1.23E-03		Unigene16663_All//gi|297598191|ref|NP_001045200.2|//5.00E-28//Os01g0917300 [Oryza sativa Japonica Group] >gi|255674000|dbj|BAF07114.2| Os01g0917300 [Oryza sativa Japonica Group]	Unigene16663_All//9.00E-37//AT1G65295| unknown protein	Unigene16663_All//3.00E-47//gi|109887958|gb|DW516927.1|DW516927				nr -
Unigene16664_All	458	48.55	40.49	47.32	94.84	57.89	52.07	121.86	58.59	60.11	-2.62E-01	2.90E-02		-3.70E-02	7.77E-01		-7.12E-01	8.08E-22		-8.65E-01	5.46E-27		-1.06E+00	2.92E-54	Down	-1.02E+00	1.07E-52	Down			Unigene16664_All//0.00E+00//gi|164317038|gb|EV498722.1|EV498722				
Unigene16665_All	522	3.01	0.00	0.20	6.01	3.36	1.30	1.54	1.44	0.00	-1.16E+01	4.20E-09	Down	-3.88E+00	1.55E-06	Down	-8.38E-01	1.14E-02		-2.21E+00	2.10E-08	Down	-9.46E-02	8.99E-01		-1.06E+01	4.43E-06	Down	Unigene16665_All//gi|224105261|ref|XP_002313745.1|//5.00E-29//SAUR family protein [Populus trichocarpa] >gi|222850153|gb|EEE87700.1| SAUR family protein [Populus trichocarpa]	Unigene16665_All//5.00E-24//AT4G34810| auxin-responsive family protein	Unigene16665_All//3.00E-141//gi|109870953|gb|DW499929.1|DW499929				nr +
Unigene16666_All	1095	0.81	0.42	0.15	6.19	1.95	0.37	2.70	1.11	1.13	-9.64E-01	1.95E-01		-2.48E+00	7.18E-03		-1.67E+00	8.72E-14	Down	-4.06E+00	8.18E-32	Down	-1.29E+00	1.12E-04	Down	-1.26E+00	9.67E-05	Down	Unigene16666_All//gi|224105265|ref|XP_002313747.1|//3.00E-31//SAUR family protein [Populus trichocarpa] >gi|222850155|gb|EEE87702.1| SAUR family protein [Populus trichocarpa]	Unigene16666_All//3.00E-24//AT4G38860| auxin-responsive protein, putative	Unigene16666_All//0.00E+00//TC166039				nr -
Unigene16668_All	656	21.61	32.13	64.61	32.12	28.08	45.85	152.49	25.49	33.70	5.72E-01	1.71E-06		1.58E+00	1.04E-60	Up	-1.94E-01	1.28E-01		5.14E-01	7.97E-08		-2.58E+00	0.00E+00	Down	-2.18E+00	9.99E-287	Down	Unigene16668_All//gi|4204575|gb|AAD10774.1|//7.00E-33//cytochrome b5 DIF-F [Petunia x hybrida] >gi|40737984|gb|AAR89457.1| cytochrome B5 [Petunia x hybrida] >gi|85700983|gb|ABC74800.1| cytochrome B5 [Petunia x hybrida]	Unigene16668_All//3.00E-16//AT2G32720| CB5-B (CYTOCHROME B5 ISOFORM B); heme binding	Unigene16668_All//0.00E+00//TC157018		ko00910|Nitrogen metabolism		nr +
Unigene16670_All	603	8.24	36.13	6.27	2.31	5.60	5.54	3.86	8.73	8.79	2.13E+00	2.23E-48	Up	-3.95E-01	1.72E-01		1.27E+00	1.22E-04	Up	1.26E+00	2.51E-04	Up	1.18E+00	8.24E-07	Up	1.19E+00	4.00E-07	Up	Unigene16670_All//gi|225453230|ref|XP_002265692.1|//1.00E-11//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene16670_All//4.00E-65//AT1G32160| unknown protein					nr +
Unigene16672_All	495	13.00	7.37	6.02	16.00	11.41	16.06	37.58	23.81	23.26	-8.19E-01	4.27E-04		-1.11E+00	6.63E-06	Down	-4.88E-01	1.36E-02		5.10E-03	9.82E-01		-6.58E-01	9.05E-09		-6.92E-01	8.15E-10		Unigene16672_All//gi|124360846|gb|ABN08818.1|//2.00E-34//Mtx34-1 [Medicago truncatula]	Unigene16672_All//5.00E-34//AT1G10840| TIF2H1; translation initiation factor	Unigene16672_All//0.00E+00//TC175237				nr -
Unigene16679_All	538	35.20	37.39	29.30	52.31	60.36	57.17	142.72	124.77	52.50	8.69E-02	5.43E-01		-2.65E-01	5.46E-02		2.06E-01	3.33E-02		1.28E-01	2.59E-01		-1.94E-01	3.58E-04		-1.44E+00	2.21E-124	Down	Unigene16679_All//gi|166209291|gb|ABY85195.1|//4.00E-62//p-coumaryl-CoA 3"-hydroxylase [Populus alba x Populus grandidentata]	Unigene16679_All//2.00E-49//AT2G40890| CYP98A3 (cytochrome P450, family 98, subfamily A, polypeptide 3); monooxygenase/ p-coumarate 3-hydroxylase	Unigene16679_All//0.00E+00//TC154279		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene16680_All	1719	566.00	254.50	358.75	338.50	432.41	220.48	2.09	5.30	0.74	-1.15E+00	0.00E+00	Down	-6.58E-01	0.00E+00		3.53E-01	1.20E-100		-6.19E-01	5.65E-198		1.34E+00	1.58E-13	Up	-1.50E+00	5.84E-07	Down	Unigene16680_All//gi|79323495|ref|NP_001031446.1|//0.00E+00//RPT2 (ROOT PHOTOTROPISM 2); protein binding [Arabidopsis thaliana] >gi|145329993|ref|NP_001077982.1| RPT2 (ROOT PHOTOTROPISM 2); protein binding [Arabidopsis thaliana]	Unigene16680_All//0.00E+00//AT2G30520| RPT2 (ROOT PHOTOTROPISM 2); protein binding	Unigene16680_All//0.00E+00//TC137563				nr -
Unigene16682_All	461	3.40	6.27	4.50	7.56	5.38	7.45	27.70	12.87	8.99	8.80E-01	1.73E-02		4.04E-01	3.93E-01		-4.92E-01	1.35E-01		-2.28E-02	9.52E-01		-1.11E+00	5.75E-14	Down	-1.62E+00	2.61E-25	Down		Unigene16682_All//7.00E-06//AT1G79210| 20S proteasome alpha subunit B, putative	Unigene16682_All//3.00E-175//gi|164303063|gb|ES824112.1|ES824112		ko03050|Proteasome		kegg -
Unigene16684_All	2259	0.93	0.79	1.56	0.44	0.03	0.22	0.80	2.20	5.52	-2.39E-01	6.19E-01		7.48E-01	2.93E-02		-3.85E+00	1.61E-05	Down	-1.00E+00	1.57E-01		1.45E+00	1.29E-08	Up	2.78E+00	2.41E-47	Up	Unigene16684_All//gi|224127917|ref|XP_002329209.1|//1.00E-130//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870990|gb|EEF08121.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene16684_All//3.00E-106//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene16684_All//6.00E-69//DW486835		ko04626|Plant-pathogen interaction		nr +
Unigene16686_All	547	1.72	7.60	2.14	11.75	21.34	19.98	0.39	3.97	5.90	2.14E+00	8.24E-10	Up	3.15E-01	6.23E-01		8.61E-01	3.92E-08		7.66E-01	5.86E-06		3.36E+00	3.23E-10	Up	3.93E+00	3.78E-17	Up	Unigene16686_All//gi|224105265|ref|XP_002313747.1|//7.00E-22//SAUR family protein [Populus trichocarpa] >gi|222850155|gb|EEE87702.1| SAUR family protein [Populus trichocarpa]	Unigene16686_All//6.00E-19//AT4G34810| auxin-responsive family protein	Unigene16686_All//5.00E-20//DW503615				nr +
Unigene16689_All	1129	1.71	1.30	1.37	0.97	2.35	2.40	1.09	0.63	0.67	-3.98E-01	3.82E-01		-3.26E-01	5.10E-01		1.27E+00	9.04E-04	Up	1.31E+00	8.44E-04	Up	-7.87E-01	1.52E-01		-6.96E-01	1.86E-01		Unigene16689_All//gi|15242550|ref|NP_196557.1|//1.00E-06//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75170796|sp|Q9FIB2.1|PP373_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At5g59950 >gi|9758973|dbj|BAB09416.1| selenium-binding protein-like [Arabidopsis thaliana]	Unigene16689_All//6.00E-08//AT5G59950| pentatricopeptide (PPR) repeat-containing protein	Unigene16689_All//0.00E+00//TC148523				nr -
Unigene1669_All	4072	3.39	3.91	5.61	0.34	0.29	0.47	26.00	14.30	10.90	2.04E-01	1.73E-01		7.26E-01	8.99E-10		-2.53E-01	6.57E-01		4.44E-01	3.98E-01		-8.63E-01	4.16E-73		-1.25E+00	3.52E-138	Down	Unigene1669_All//gi|115460468|ref|NP_001053834.1|//0.00E+00//Os04g0610900 [Oryza sativa Japonica Group] >gi|38345798|emb|CAE03570.2| OSJNBa0085I10.15 [Oryza sativa (japonica cultivar-group)] >gi|113565405|dbj|BAF15748.1| Os04g0610900 [Oryza sativa Japonica Group]	Unigene1669_All//0.00E+00//AT4G24480| serine/threonine protein kinase, putative	Unigene1669_All//0.00E+00//CO071570				nr -
Unigene16690_All	539	7.57	3.76	7.51	9.70	9.07	12.40	2.82	2.25	5.84	-1.01E+00	9.03E-04	Down	-1.21E-02	9.93E-01		-9.72E-02	7.69E-01		3.54E-01	1.43E-01		-3.29E-01	5.30E-01		1.05E+00	6.60E-04	Up	Unigene16690_All//gi|7019678|emb|CAB75803.1|//3.00E-28//allyl alcohol dehydrogenase-like protein [Arabidopsis thaliana]	Unigene16690_All//2.00E-29//AT3G59840| unknown protein	Unigene16690_All//0.00E+00//TC157887				nr -
Unigene16691_All	559	10.95	8.16	15.53	498.86	250.16	298.85	17.77	14.80	4.92	-4.25E-01	7.88E-02		5.04E-01	1.41E-02		-9.96E-01	4.48E-247		-7.39E-01	3.75E-130		-2.64E-01	1.30E-01		-1.85E+00	9.00E-24	Down	Unigene16691_All//gi|195622626|gb|ACG33143.1|//5.00E-20//EF hand family protein [Zea mays]	Unigene16691_All//7.00E-07//AT5G42380| CML37 (CALMODULIN LIKE 37); calcium ion binding	Unigene16691_All//0.00E+00//DW508964		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr +
Unigene16694_All	781	3.35	0.13	0.82	3.57	3.04	2.95	3.09	0.86	1.12	-4.69E+00	1.34E-12	Down	-2.03E+00	8.61E-06	Down	-2.32E-01	5.74E-01		-2.76E-01	5.03E-01		-1.85E+00	3.94E-06	Down	-1.46E+00	8.41E-05	Down	Unigene16694_All//gi|18400647|ref|NP_566502.1|//1.00E-107//exonuclease family protein [Arabidopsis thaliana] >gi|75331425|sp|Q8W566.1|Y3514_ARATH RecName: Full=Uncharacterized exonuclease domain-containing protein At3g15140 >gi|16930517|gb|AAL31944.1|AF419612_1 AT3g15140/F4B12_5 [Arabidopsis thaliana] >gi|19310525|gb|AAL84996.1| AT3g15140/F4B12_5 [Arabidopsis thaliana]	Unigene16694_All//1.00E-108//AT3G15140| exonuclease family protein	Unigene16694_All//0.00E+00//TC143702				nr +
Unigene16696_All	597	8.24	40.06	22.83	3.92	14.07	47.66	3.40	2.45	1.80	2.28E+00	1.13E-57	Up	1.47E+00	6.63E-18	Up	1.84E+00	4.05E-18	Up	3.60E+00	2.23E-117	Up	-4.72E-01	2.59E-01		-9.16E-01	1.86E-02		Unigene16696_All//gi|224110588|ref|XP_002315567.1|//6.00E-36//glutaredoxin [Populus trichocarpa] >gi|222864607|gb|EEF01738.1| glutaredoxin [Populus trichocarpa]	Unigene16696_All//3.00E-36//AT5G18600| glutaredoxin family protein	Unigene16696_All//0.00E+00//gi|109866735|gb|DW495711.1|DW495711				nr -
Unigene16697_All	510	0.00	2.98	1.46	1.07	1.01	2.48	48.17	58.84	97.88	1.15E+01	1.10E-08	Up	1.05E+01	3.28E-04	Up	-8.52E-02	9.07E-01		1.21E+00	5.27E-02		2.89E-01	1.24E-03		1.02E+00	3.76E-47	Up	Unigene16697_All//gi|255553125|ref|XP_002517605.1|//2.00E-13//conserved hypothetical protein [Ricinus communis] >gi|223543237|gb|EEF44769.1| conserved hypothetical protein [Ricinus communis]	Unigene16697_All//7.00E-10//AT1G15385| unknown protein	Unigene16697_All//0.00E+00//TC168303				nr +
Unigene16698_All	654	3.60	5.42	6.19	8.38	7.69	5.39	0.00	0.13	5.18	5.91E-01	7.20E-02		7.82E-01	1.36E-02		-1.24E-01	6.66E-01		-6.37E-01	1.17E-02		7.00E+00	4.02E-01		1.23E+01	3.14E-24	Up	Unigene16698_All//gi|116311046|emb|CAH67977.1|//3.00E-23//OSIGBa0142I02-OSIGBa0101B20.20 [Oryza sativa (indica cultivar-group)]		Unigene16698_All//1.00E-116//TC168841				nr -
Unigene16699_All	572	1.65	7.35	3.72	1.92	3.31	7.82	3.18	3.87	9.05	2.16E+00	5.15E-10	Up	1.18E+00	1.19E-02		7.89E-01	9.95E-02		2.03E+00	2.45E-10	Up	2.85E-01	4.98E-01		1.51E+00	1.12E-09	Up	Unigene16699_All//gi|15233117|ref|NP_191705.1|//5.00E-37//BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|297820998|ref|XP_002878382.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata] >gi|4689366|gb|AAD27870.1|AF134155_1 BRH1 RING finger protein [Arabidopsis thaliana] >gi|6850837|emb|CAB71076.1| RING finger protein [Arabidopsis thaliana] >gi|21554590|gb|AAM63625.1| RING finger protein [Arabidopsis thaliana] >gi|297324220|gb|EFH54641.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata]	Unigene16699_All//5.00E-34//AT3G61460| BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding	Unigene16699_All//0.00E+00//gi|109829314|gb|DW227901.1|DW227901				nr +
Unigene16701_All	615	26.37	8.82	12.81	53.05	38.47	28.49	12.37	3.33	6.61	-1.58E+00	1.97E-24	Down	-1.04E+00	1.46E-12	Down	-4.64E-01	7.31E-08		-8.97E-01	1.16E-21		-1.89E+00	2.61E-18	Down	-9.05E-01	1.09E-06				Unigene16701_All//5.00E-48//TC177838				

Unigene16702_All	1026	0.41	0.00	0.52	7.43	4.09	2.07	0.95	0.37	4.70	-8.67E+00	1.05E-02		3.47E-01	7.06E-01		-8.59E-01	1.04E-05		-1.84E+00	1.30E-15	Down	-1.37E+00	3.41E-02		2.31E+00	2.29E-15	Up	Unigene16702_All//gi|18399468|ref|NP_565484.1|//2.00E-71//protein binding / structural molecule [Arabidopsis thaliana] >gi|4454472|gb|AAD20919.1| expressed protein [Arabidopsis thaliana] >gi|15982817|gb|AAL09756.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|16322101|gb|AAL15285.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|108385429|gb|ABF85787.1| At2g20760 [Arabidopsis thaliana]	Unigene16702_All//2.00E-55//AT2G20760| protein binding / structural molecule	Unigene16702_All//3.00E-13//DW227572				nr +
Unigene16703_All	646	0.89	0.16	0.00	4.09	3.52	0.63	0.72	0.19	0.62	-2.51E+00	2.94E-02		-9.80E+00	2.60E-03		-2.16E-01	6.10E-01		-2.70E+00	7.28E-09	Down	-1.89E+00	8.00E-02		-2.23E-01	7.90E-01		Unigene16703_All//gi|18399468|ref|NP_565484.1|//8.00E-11//protein binding / structural molecule [Arabidopsis thaliana] >gi|4454472|gb|AAD20919.1| expressed protein [Arabidopsis thaliana] >gi|15982817|gb|AAL09756.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|16322101|gb|AAL15285.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|108385429|gb|ABF85787.1| At2g20760 [Arabidopsis thaliana]	Unigene16703_All//7.00E-07//AT2G20760| protein binding / structural molecule					nr -
Unigene16704_All	1321	0.08	0.00	0.00	0.68	0.29	0.07	0.19	0.06	0.57	-6.31E+00	3.73E-01		-6.31E+00	3.95E-01		-1.24E+00	8.18E-02		-3.31E+00	5.80E-04	Down	-1.60E+00	3.11E-01		1.58E+00	3.40E-02		Unigene16704_All//gi|18399468|ref|NP_565484.1|//5.00E-79//protein binding / structural molecule [Arabidopsis thaliana] >gi|4454472|gb|AAD20919.1| expressed protein [Arabidopsis thaliana] >gi|15982817|gb|AAL09756.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|16322101|gb|AAL15285.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|108385429|gb|ABF85787.1| At2g20760 [Arabidopsis thaliana]	Unigene16704_All//4.00E-63//AT2G20760| protein binding / structural molecule	Unigene16704_All//4.00E-13//DW227572				nr -
Unigene16705_All	585	263.66	119.27	126.98	625.27	516.76	260.09	142.09	73.16	54.75	-1.14E+00	2.37E-138	Down	-1.05E+00	2.29E-117	Down	-2.75E-01	2.06E-31		-1.27E+00	0.00E+00	Down	-9.58E-01	1.67E-68		-1.38E+00	2.77E-125	Down	Unigene16705_All//gi|20269063|emb|CAC84712.1|//9.00E-60//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene16705_All//2.00E-49//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene16705_All//0.00E+00//gi|164272058|gb|ES831191.1|ES831191				nr +
Unigene16706_All	458	28.45	35.84	25.58	19.14	31.65	27.32	23.26	25.28	10.79	3.34E-01	1.72E-02		-1.53E-01	3.94E-01		7.26E-01	1.39E-07		5.13E-01	1.16E-03		1.20E-01	5.02E-01		-1.11E+00	3.08E-12	Down	Unigene16706_All//gi|88900354|gb|AB057489.1|//4.00E-08//At5g56520 [Arabidopsis thaliana]	Unigene16706_All//7.00E-06//AT5G56520| unknown protein	Unigene16706_All//5.00E-146//BF270971				nr +
Unigene16708_All	899	6.93	2.48	1.72	5.49	4.29	4.12	2.59	1.02	1.11	-1.48E+00	5.18E-09	Down	-2.01E+00	8.75E-13	Down	-3.55E-01	2.05E-01		-4.13E-01	1.44E-01		-1.34E+00	4.97E-04	Down	-1.22E+00	9.07E-04	Down	Unigene16708_All//gi|159025719|emb|CAN88860.1|//1.00E-108//D3-type cyclin [Populus trichocarpa]	Unigene16708_All//3.00E-84//AT5G67260| CYCD3;2 (CYCLIN D3;2); cyclin-dependent protein kinase	Unigene16708_All//0.00E+00//TC170510				nr +
Unigene16710_All	422	7.56	12.97	17.92	24.20	11.91	13.16	11.72	13.87	10.86	7.78E-01	2.29E-03		1.24E+00	4.72E-08	Up	-1.02E+00	8.21E-10	Down	-8.78E-01	5.55E-07		2.42E-01	3.19E-01		-1.11E-01	6.56E-01				Unigene16710_All//7.00E-31//gi|73846667|gb|DT455687.1|DT455687				
Unigene16711_All	685	12.45	12.35	10.57	28.80	25.69	17.74	25.43	23.98	9.77	-1.13E-02	9.77E-01		-2.36E-01	2.87E-01		-1.65E-01	2.28E-01		-6.99E-01	6.82E-09		-8.47E-02	5.70E-01		-1.38E+00	4.65E-27	Down	Unigene16711_All//gi|75099212|sp|Q64818.1|Y2309_ARATH//4.00E-15//RecName: Full=Uncharacterized protein At2g23090 >gi|31691182|gb|AAC17825.1| Expressed protein [Arabidopsis thaliana] >gi|15450484|gb|AAK96535.1| At2g23090/F21P24.15 [Arabidopsis thaliana] >gi|159121199|gb|AAL08233.1| At2g23090/F21P24.15 [Arabidopsis thaliana] >gi|23505759|gb|AAN28739.1| At2g23090/F21P24.15 [Arabidopsis thaliana]	Unigene16711_All//3.00E-13//AT2G23090| unknown protein	Unigene16711_All//0.00E+00//TC173781				nr +
Unigene16712_All	1034	2.63	3.63	4.27	9.01	4.36	5.50	3.19	2.14	2.35	4.63E-01	1.48E-01		7.00E-01	2.00E-02		-1.05E+00	2.51E-09	Down	-7.11E-01	1.11E-04		-5.74E-01	6.21E-02		-4.41E-01	1.41E-01								
Unigene16714_All	474	23.95	55.91	34.60	42.14	51.14	56.88	57.27	62.87	53.71	1.22E+00	7.86E-27	Up	5.31E-01	1.88E-04		2.79E-01	1.10E-02		4.33E-01	2.29E-05		1.35E-01	1.77E-01		-9.26E-02	3.79E-01		Unigene16714_All//gi|222424195|dbj|BAH20056.1|//1.00E-38//AT2G25670 [Arabidopsis thaliana]	Unigene16714_All//4.00E-22//AT4G32610| unknown protein	Unigene16714_All//0.00E+00//gi|78333764|gb|DT554038.1|DT554038				nr -
Unigene16715_All	753	179.27	182.89	223.89	305.83	270.82	279.50	57.95	180.73	72.91	2.89E-02	6.08E-01		3.21E-01	8.80E-16		-1.75E-01	1.19E-08		-1.30E-01	1.03E-04		1.64E+00	8.75E-258	Up	3.31E-01	1.04E-07		Unigene16715_All//gi|224125504|ref|XP_002319603.1|//8.00E-21//predicted protein [Populus trichocarpa] >gi|222857979|gb|EEE95526.1| predicted protein [Populus trichocarpa]	Unigene16715_All//0.00E+00//gi|109825433|gb|DW224166.1|DW224166				nr -
Unigene16717_All	659	5.16	2.31	6.63	11.72	10.56	7.40	1.35	0.76	1.75	-1.16E+00	6.70E-04	Down	3.61E-01	2.44E-01		-1.51E-01	5.53E-01		-6.63E-01	1.27E-03		-8.24E-01	2.24E-01		3.80E-01	5.04E-01								
Unigene16719_All	495	27.16	46.57	27.00	23.75	22.96	41.97	40.32	28.20	19.07	7.78E-01	1.71E-11		-8.70E-03	9.82E-01		-4.90E-02	8.27E-01		8.21E-01	5.08E-12		-5.16E-01	2.57E-06		-1.08E+00	3.03E-21	Down	Unigene16719_All//gi|297844954|ref|XP_002890358.1|//2.00E-31//vacuolar-H+-pumping ATPase 16 kDa proteolipid subunit 2 [Arabidopsis lyrata subsp. lyrata] >gi|297336200|gb|EFH66617.1| vacuolar-H+-pumping ATPase 16 kDa proteolipid subunit 2 [Arabidopsis lyrata subsp. lyrata]	Unigene16719_All//7.00E-15//AT4G34720| AVA-P1: ATPase/ proton-transporting ATPase, rotational mechanism	Unigene16719_All//0.00E+00//gi|72276612|gb|DT050722.1|DT050722		ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene1672_All	1847	2.61	1.98	1.27	4.21	4.72	2.67	3.32	0.68	1.68	-4.00E-01	1.51E-01		-1.04E+00	3.28E-04	Down	1.65E-01	4.79E-01		-6.59E-01	1.31E-03		-2.29E+00	8.74E-19	Down	-9.80E-01	3.17E-06		Unigene1672_All//gi|66792640|gb|AAY56422.1|//1.00E-111//At4g22860 [Arabidopsis thaliana]	Unigene1672_All//1.00E-97//AT4G22860| unknown protein	Unigene1672_All//0.00E+00//ES825890				nr -
Unigene16720_All	590	14.10	8.42	7.40	18.83	19.32	18.98	18.06	10.27	7.02	-7.44E-01	2.06E-04		-9.30E-01	9.74E-06		3.71E-02	8.57E-01		1.19E-02	9.46E-01		-8.14E-01	2.10E-07		-1.36E+00	1.39E-16	Down	Unigene16720_All//gi|297607456|ref|XP_001059993.2|//7.00E-15//Os07g0562900 [Oryza sativa Japonica Group] >gi|255677886|dbj|BAF21907.2| Os07g0562900 [Oryza sativa Japonica Group]	Unigene16720_All//2.00E-08//AT4G27380| unknown protein	Unigene16720_All//0.00E+00//gi|164336093|gb|ES816957.1|ES816957				nr +
Unigene16721_All	602	9.13	88.88	12.03	9.93	38.73	36.39	35.12	40.62	121.57	3.28E+00	5.74E-190	Up	3.99E-01	8.51E-02		1.96E+00	2.94E-54	Up	1.87E+00	5.32E-44	Up	2.10E-01	4.44E-02		1.79E+00	3.19E-160	Up	Unigene16721_All//gi|5903034|gb|AAD55593.1|AC008016_3//3.00E-17//F6DB.3 [Arabidopsis thaliana] >gi|28466819|gb|AAO44018.1| At1g32720 [Arabidopsis thaliana]	Unigene16721_All//2.00E-18//AT3G15630| unknown protein	Unigene16721_All//0.00E+00//TC167427				nr -
Unigene16722_All	571	24.47	25.47	11.75	19.11	24.79	35.75	19.62	16.98	25.88	5.79E-02	7.17E-01		-1.06E+00	3.55E-11	Down	3.76E-01	1.02E-02		9.04E-01	8.49E-14		-2.09E-01	2.15E-01		4.00E-01	1.69E-03		Unigene16722_All//gi|3293261|gb|AAC25687.1|//1.00E-31//cystathionine gamma-synthase precursor [Arabidopsis thaliana]	Unigene16722_All//1.00E-24//AT3G01120| MTO1 (METHIONINE OVERACCUMULATION 1); cystathionine gamma-synthase	Unigene16722_All//0.00E+00//gi|13352239|gb|BG442587.1|BG442587		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr -
Unigene16723_All	518	0.00	0.00	0.00	0.00	0.20	0.61	10.69	90.53	6.38	null	null		null	null		7.64E+00	4.56E-01		9.25E+00	4.08E-02		3.08E+00	1.52E-192	Up	-7.44E-01	6.59E-04		Unigene16723_All//gi|18397934|ref|NP_565380.1|//2.00E-31//glycine-rich protein [Arabidopsis thaliana] >gi|15294186|gb|AAK95270.1|AF410284_1 At2g15780/F19G14.22 [Arabidopsis thaliana] >gi|5306253|gb|AAD41986.1| expressed protein [Arabidopsis thaliana] >gi|20147265|gb|AAM10346.1| At2g15780/F19G14.22 [Arabidopsis thaliana]	Unigene16723_All//1.00E-32//AT2G15780| glycine-rich protein					nr -
Unigene16724_All	833	0.00	0.00	0.00	0.00	0.58	2.87	18.42	286.15	12.58	null	null		null	null		9.18E+00	5.07E-03		1.15E+01	2.54E-14	Up	3.96E+00	0.00E+00	Up	-5.51E-01	8.62E-06		Unigene16724_All//gi|18397934|ref|NP_565380.1|//3.00E-42//glycine-rich protein [Arabidopsis thaliana] >gi|15294186|gb|AAK95270.1|AF410284_1 At2g15780/F19G14.22 [Arabidopsis thaliana] >gi|5306253|gb|AAD41986.1| expressed protein [Arabidopsis thaliana] >gi|20147265|gb|AAM10346.1| At2g15780/F19G14.22 [Arabidopsis thaliana]	Unigene16724_All//7.00E-40//AT2G15780| glycine-rich protein					nr +
Unigene16729_All	733	12.13	7.05	10.17	9.38	7.47	8.63	27.51	15.74	10.60	-7.83E-01	5.22E-05		-2.55E-01	2.34E-01		-3.28E-01	1.56E-01		-1.21E-01	6.42E-01		-8.06E-01	4.43E-13		-1.38E+00	4.58E-31	Down	Unigene16729_All//gi|226531966|ref|NP_001152503.1|//8.00E-15//60S ribosomal protein L37 [Zea mays] >gi|195620270|gb|ACG31965.1| 60S ribosomal protein L37 [Zea mays] >gi|195651369|gb|ACG45152.1| 60S ribosomal protein L37 [Zea mays] >gi|195655801|gb|ACG47368.1| 60S ribosomal protein L37 [Zea mays] >gi|195656955|gb|ACG47945.1| 60S ribosomal protein L37 [Zea mays]	Unigene16729_All//4.00E-08//AT3G16080| 60S ribosomal protein L37 (RPL37C)	Unigene16729_All//5.00E-178//TC161175		ko03010|Ribosome		nr -
Unigene16731_All	361	40.58	61.76	67.26	98.94	126.77	117.35	67.46	95.75	324.23	6.06E-01	1.80E-07		7.29E-01	2.02E-10		3.58E-01	9.67E-07		2.46E-01	2.97E-03		5.05E-01	5.52E-10		2.26E+00	0.00E+00	Up	Unigene16731_All//gi|224551852|gb|ACN54324.1|//2.00E-23//NADPH:cytochrome P450 reductase [Gossypium hirsutum]		Unigene16731_All//0.00E+00//gi|13351588|gb|BG441936.1|BG441936				nr +
Unigene16733_All	493	114.72	236.39	215.27	95.59	240.56	202.27	37.65	55.19	132.85	1.04E+00	9.09E-90	Up	9.08E-01	2.67E-63		1.33E+00	1.69E-159	Up	1.08E+00	1.07E-87	Up	5.52E-01	2.74E-09		1.82E+00	1.72E-146	Up	Unigene16733_All//gi|212292507|gb|ACJ24185.1|//2.00E-38//CAPRICE [Gossypium hirsutum] >gi|212292511|gb|ACJ24187.1| CAPRICE [Gossypium hirsutum] >gi|212292515|gb|ACJ24189.1| CAPRICE [Gossypium hirsutum] >gi|212292519|gb|ACJ24191.1| CAPRICE [Gossypium hirsutum]	Unigene16733_All//1.00E-10//AT1G01380| ETC1 (ENHANCER OF TRY AND CPC 1); DNA binding / transcription factor	Unigene16733_All//4.00E-156//DW508052	MYB-related			nr +

Unigene16736_All	678	8.72	3.59	2.36	34.61	29.51	21.92	3.99	5.42	4.82	-1.28E+00	4.67E-07	Down	-1.89E+00	3.08E-11	Down	-2.30E-01	4.48E-02		-6.59E-01	1.77E-09		4.43E-01	1.34E-01		2.72E-01	3.91E-01		Unigene16736_All//gi|124359510|gb|ABB28627.2|//3.00E-08//RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H [Medicago truncatula]	Unigene16736_All//6.00E-06//AT3G26855| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: reverse transcriptase-related (TAIR:AT2G02650.1); Has 97 Blast hits to 97 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 97; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene16736_All//8.00E-149//TC162673				nr +
Unigene16738_All	1677	0.53	0.24	0.95	1.19	1.58	1.02	1.59	0.97	0.64	-1.13E+00	1.30E-01		8.45E-01	1.25E-01		4.12E-01	3.15E-01		-2.15E-01	6.67E-01		-7.09E-01	4.01E-02		-1.31E+00	1.48E-04	Down	Unigene16738_All//gi|297806669|ref|XP_002871218.1|//1.00E-158//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317055|gb|EFH47477.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene16738_All//5.00E-134//AT5G06400| pentatricopeptide (PPR) repeat-containing protein				nr -
Unigene16740_All	1023	0.72	0.30	0.42	3.17	4.81	3.62	3.80	1.18	1.48	-1.27E+00	1.36E-01		-7.82E-01	3.80E-01		6.05E-01	2.29E-02		1.94E-01	6.23E-01		-1.68E+00	2.23E-08	Down	-1.36E+00	1.34E-06	Down	Unigene16740_All//gi|297848532|ref|XP_002892147.1|//5.00E-57//kinase interacting family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337989|gb|EFH68406.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16740_All//1.00E-48//AT1G03080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053), KIP1-like (InterPro:IPR011684); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT3G22790.1); Has 169162 Blast hits to 69460 proteins in 2232 species: Archae - 2114; Bacteria - 24914; Metazoa - 82448; Fungi - 11850; Plants - 6375; Viruses - 760; Other Eukaryotes - 40701 (source: NCBI BLink).				nr -
Unigene16741_All	697	8.63	12.94	6.42	10.65	4.69	4.02	5.46	4.98	0.57	5.84E-01	2.34E-03		-4.28E-01	9.64E-02		-1.18E+00	4.35E-09	Down	-1.41E+00	1.78E-10	Down	-1.33E-01	6.55E-01		-3.26E+00	1.15E-17	Down	Unigene16741_All//gi|261876231|emb|CAZ15549.1|//9.00E-32//phloem protein 2 [Malus x domestica]	Unigene16741_All//1.00E-20//AT1G31200| ATPP2-A9 (Phloem protein 2-A9); carbohydrate binding	Unigene16741_All//2.00E-161//DW507919				nr +
Unigene16742_All	657	7.80	13.65	11.51	6.60	4.04	3.44	0.51	2.04	0.30	8.07E-01	3.05E-05		5.60E-01	1.14E-02		-7.09E-01	9.87E-03		-9.41E-01	1.07E-03		1.98E+00	5.28E-04	Up	-7.64E-01	5.01E-01		Unigene16742_All//gi|261876231|emb|CAZ15549.1|//3.00E-35//phloem protein 2 [Malus x domestica]	Unigene16742_All//2.00E-22//AT1G10155| ATPP2-A10 (PHLOEM PROTEIN 2-A10)	Unigene16742_All//0.00E+00//DW507919				nr +
Unigene16744_All	805	1.49	1.64	1.39	6.62	4.62	3.20	7.25	13.29	3.27	1.31E-01	8.13E-01		-1.06E-01	8.62E-01		-5.19E-01	3.83E-02		-1.05E+00	4.13E-05	Down	8.75E-01	2.73E-08		-1.15E+00	1.79E-07	Down	Unigene16744_All//gi|297724175|ref|NP_001174451.1|//6.00E-18//Os05g0442000 [Oryza sativa Japonica Group] >gi|255676407|dbj|BAH93179.1| Os05g0442000 [Oryza sativa Japonica Group]	Unigene16744_All//5.00E-22//AT5G06270| unknown protein	Unigene16744_All//0.00E+00//gi|164315325|gb|ES841086.1|ES841086				nr +
Unigene16745_All	384	14.85	32.46	23.44	4.93	5.65	4.47	13.76	16.00	7.16	1.13E+00	1.52E-11	Up	6.58E-01	9.53E-04		1.97E-01	7.04E-01		-1.41E-01	7.64E-01		2.17E-01	3.70E-01		-9.43E-01	3.36E-05		Unigene16745_All//gi|106879575|emb|CAJ38371.1|//9.00E-26//HMG-protein [Plantago major]	Unigene16745_All//2.00E-14//AT3G51880| HMGB1 (HIGH MOBILITY GROUP B 1); DNA binding / chromatin binding / structural constituent of chromatin / transcription factor	Unigene16745_All//1.00E-28//CK640533		ko03410|Base excision repair		nr -
Unigene16746_All	690	2.05	3.08	5.63	8.59	6.84	6.15	1.78	2.18	1.04	5.91E-01	1.83E-01		1.46E+00	1.62E-05	Up	-3.29E-01	1.91E-01		-4.82E-01	5.16E-02		2.95E-01	5.82E-01		-7.74E-01	1.40E-01		Unigene16746_All//gi|56269839|gb|AY85474.1|//7.00E-52//myb family transcription factor-related protein [Populus tomentosa]	Unigene16746_All//2.00E-09//AT1G79430| APL (ALTERED PHLOEM DEVELOPMENT); transcription factor/ transcription regulator	Unigene16746_All//0.00E+00//TC132408	G2-like			nr +
Unigene16748_All	363	12.11	35.04	15.40	12.49	13.94	11.70	6.99	7.02	6.58	1.53E+00	2.15E-18	Up	3.47E-01	2.06E-01		1.59E-01	5.96E-01		-9.46E-02	7.57E-01		7.20E-03	1.02E+00		-8.58E-02	8.08E-01					Unigene16748_All//5.00E-164//TC151799				
Unigene1675_All	2378	35.09	105.81	74.70	53.44	78.05	307.31	76.01	281.50	181.87	1.59E+00	0.00E+00	Up	1.09E+00	5.32E-143	Up	5.47E-01	4.40E-56		2.52E+00	0.00E+00	Up	1.89E+00	0.00E+00	Up	1.26E+00	0.00E+00	Up	Unigene1675_All//gi|211970690|emb|CAR98204.1|//0.00E+00//formate dehydrogenase [Lotus japonicus]	Unigene1675_All//0.00E+00//AT5G14780| FDH (FORMATE DEHYDROGENASE); NAD or NADH binding / binding / catalytic/ cofactor binding / oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	Unigene1675_All//0.00E+00//TC166102		ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene16751_All	1703	1.14	1.01	1.13	1.70	2.26	1.51	3.92	2.36	1.22	-1.68E-01	7.03E-01		-1.40E-02	9.99E-01		4.17E-01	2.05E-01		-1.67E-01	6.93E-01		-7.35E-01	2.77E-04		-1.69E+00	2.17E-14	Down	Unigene16751_All//gi|297829916|ref|XP_002882840.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328680|gb|EFH59099.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16751_All//3.00E-162//AT3G13690| protein kinase family protein	Unigene16751_All//0.00E+00//gi|132487383|gb|BF278246.2|BF278246		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism		nr -
Unigene16752_All	873	2.34	1.86	3.42	4.28	0.87	1.50	0.24	0.00	0.00	-3.32E-01	4.66E-01		5.47E-01	1.48E-01		-2.30E+00	7.89E-12	Down	-1.51E+00	3.73E-06	Down	-7.92E+00	7.45E-02		-7.92E+00	5.80E-02		Unigene16752_All//gi|15234659|ref|NP_192429.1|//3.00E-55//protein kinase family protein [Arabidopsis thaliana] >gi|75335771|sp|Q9M0X5.1|CRK25_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 25; Short=Cysteine-rich RLK25; Flags: Precursor >gi|7267280|emb|CAB81062.1| receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene16752_All//1.00E-51//AT4G05200| protein kinase family protein				nr -
Unigene16754_All	453	2.54	1.57	7.05	3.19	3.72	4.19	2.43	2.03	2.20	-6.98E-01	2.66E-01		1.47E+00	1.04E-04	Up	2.24E-01	7.06E-01		3.93E-01	4.53E-01		-2.58E-01	6.52E-01		-1.42E-01	7.90E-01		Unigene16754_All//gi|255570799|ref|XP_002526352.1|//2.00E-24//conserved hypothetical protein [Ricinus communis] >gi|223534311|gb|EEF36023.1| conserved hypothetical protein [Ricinus communis]	Unigene16754_All//5.00E-16//AT5G60370| unknown protein	Unigene16754_All//4.00E-11//CO116013				nr -
Unigene16755_All	899	9.25	6.31	12.26	2.99	4.21	1.81	0.00	0.19	0.62	-5.52E-01	5.98E-03		4.06E-01	2.50E-02		4.94E-01	1.27E-01		-7.26E-01	6.08E-02		7.54E+00	1.39E-01		9.28E+00	3.28E-04	Up	Unigene16755_All//gi|115435338|ref|NP_001042427.1|//4.00E-24//Os01g0220500 [Oryza sativa Japonica Group] >gi|113531958|dbj|BAF04341.1| Os01g0220500 [Oryza sativa Japonica Group]		Unigene16755_All//0.00E+00//ES846305				nr +
Unigene16756_All	691	4.39	2.49	3.31	1.30	1.84	1.05	0.00	0.30	0.86	-8.17E-01	2.23E-02		-4.06E-01	2.91E-01		5.07E-01	4.38E-01		-3.11E-01	6.88E-01		8.24E+00	7.85E-02		9.76E+00	1.75E-04	Up	Unigene16756_All//gi|115435338|ref|NP_001042427.1|//4.00E-21//Os01g0220500 [Oryza sativa Japonica Group] >gi|113531958|dbj|BAF04341.1| Os01g0220500 [Oryza sativa Japonica Group]	Unigene16756_All//1.00E-05//AT2G19170| SLP3; serine-type peptidase	Unigene16756_All//0.00E+00//CA994065				nr +
Unigene16758_All	392	19.75	20.04	8.56	14.74	17.92	13.60	78.52	29.96	20.94	2.04E-02	9.43E-01		-1.21E+00	7.45E-08	Down	2.82E-01	2.39E-01		-1.17E-01	6.93E-01		-1.39E+00	2.84E-46	Down	-1.91E+00	1.12E-74	Down	Unigene16758_All//gi|224113151|ref|XP_002316408.1|//2.00E-23//histone H2 [Populus trichocarpa] >gi|222865448|gb|EEF02579.1| histone H2 [Populus trichocarpa]	Unigene16758_All//1.00E-24//AT5G02570| histone H2B, putative	Unigene16758_All//0.00E+00//gi|13350468|gb|BG440816.1|BG440816				nr +
Unigene1676_All	2409	5.13	21.60	22.26	14.00	23.30	55.19	22.45	4.35	16.65	2.08E+00	6.66E-111	Up	2.12E+00	1.24E-114	Up	7.35E-01	9.83E-29		1.98E+00	9.98E-286	Up	-2.37E+00	8.05E-167	Down	-4.31E-01	6.98E-12		Unigene1676_All//gi|67003905|gb|AAN04196.2|//0.00E+00//endo-1,4-beta-glucanase [Gossypium hirsutum]	Unigene1676_All//0.00E+00//AT1G64390| AtGH9C2 (Arabidopsis thaliana glycosyl hydrolase 9C2); carbohydrate binding / catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene1676_All//0.00E+00//TC176131		ko00500|Starch and sucrose metabolism		nr +
Unigene16761_All	736	5.40	3.58	6.73	6.57	7.11	9.70	18.78	9.71	6.33	-5.94E-01	5.24E-02		3.17E-01	2.81E-01		1.15E-01	7.29E-01		5.63E-01	1.03E-02		-9.52E-01	5.80E-12		-1.57E+00	4.87E-26	Down	Unigene16761_All//gi|79319356|ref|NP_001031149.1|//2.00E-71//YbaK/prolyl-tRNA synthetase family protein [Arabidopsis thaliana]	Unigene16761_All//1.00E-72//AT1G44835| YbaK/prolyl-tRNA synthetase family protein	Unigene16761_All//0.00E+00//gi|13356658|gb|BG446910.1|BG446910		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene16763_All	848	11.72	2.21	9.92	1.53	1.95	1.28	0.00	0.79	0.00	-2.41E+00	4.39E-26	Down	-2.41E-01	2.33E-01		3.52E-01	5.61E-01		-2.57E-01	6.87E-01		9.62E+00	7.64E-05	Up	null	null									
Unigene16764_All	404	3.11	5.02	6.85	2.84	2.73	3.13	8.37	11.17	3.85	6.91E-01	1.29E-01		1.14E+00	4.31E-03		-5.63E-02	9.17E-01		1.42E-01	8.21E-01		4.16E-01	1.14E-01		-1.12E+00	1.49E-04	Down				Unigene16764_All//2.00E-139//gi|164270101|gb|ES802007.1|ES802007				
Unigene16765_All	591	4.78	10.12	7.30	4.72	5.07	6.50	12.52	16.05	10.45	1.08E+00	1.29E-05	Up	6.10E-01	4.59E-02		1.03E-01	8.36E-01		4.61E-01	1.62E-01		3.59E-01	3.63E-02		-2.61E-01	1.86E-01		Unigene16765_All//gi|240256410|ref|NP_199565.4|//5.00E-22//binding [Arabidopsis thaliana] >gi|152140076|sp|Q8VCA3.1|M025N_ARATH RecName: Full=Putative M025-like protein At5g47540 >gi|162263001|gb|AAL161128.1|AF42829 6_1 AT5g47540/MNJ7_13 [Arabidopsis thaliana] >gi|193211497|gb|ACF16168.1| At5g47540 [Arabidopsis thaliana]	Unigene16765_All//3.00E-23//AT5G47540| binding	Unigene16765_All//0.00E+00//gi|164270101|gb|ES802007.1|ES802007				nr +
Unigene16766_All	647	106.02	100.01	135.55	11.39	17.72	15.50	11.96	7.95	5.54	-8.42E-02	2.36E-01		3.55E-01	3.66E-10		6.37E-01	5.52E-05		4.44E-01	1.52E-02		-5.90E-01	1.54E-03		-1.11E+00	3.87E-09	Down	Unigene16766_All//gi|297823141|ref|XP_002879453.1|//6.00E-46//50S ribosomal protein L28, chloroplast [Arabidopsis lyrata subsp. lyrata] >gi|297325292|gb|EFH55712.1| 50S ribosomal protein L28, chloroplast [Arabidopsis lyrata subsp. lyrata]	Unigene16766_All//1.00E-46//AT2G33450| 50S ribosomal protein L28, chloroplast (CL28)	Unigene16766_All//0.00E+00//TC156305				nr -
Unigene16768_All	550	5.42	8.84	9.88	10.05	4.45	4.43	1.85	1.14	1.09	7.06E-01	9.66E-03		8.65E-01	1.17E-03		-1.18E+00	7.18E-07	Down	-1.18E+00	3.13E-06	Down	-6.95E-01	2.63E-01		-7.64E-01	1.95E-01					Unigene16768_All//3.00E-15//gi|189092673|gb|FG548208.1|FG548208				
Unigene16769_All	634	15.68	7.43	3.95	1.41	3.53	1.99	0.67	0.26	1.82	-1.08E+00	8.68E-09	Down	-1.99E+00	7.98E-20	Down	1.32E+00	2.04E-03		4.96E-01	4.48E-01		-1.34E+00	2.24E-01		1.45E+00	1.09E-02		Unigene16769_All//gi|255567469|ref|XP_002524714.1|//9.00E-09//ubiquitin-protein ligase, putative [Ricinus communis] >gi|223536075|gb|EEF37733.1| ubiquitin-protein ligase, putative [Ricinus communis]						nr -

Unigene16677_All	1840	33.92	14.32	22.75	19.76	23.39	25.09	12.73	17.49	15.50	-1.24E+00	2.83E-64	Down	-5.77E-01	3.34E-17		2.43E-01	2.09E-03		3.44E-01	6.53E-06		4.58E-01	5.82E-08		2.84E-01	1.51E-03		Unigene1677_All//gi|53749148|gb|AAU90059.1|//1.00E-166//At1g29120 [Arabidopsis thaliana]	Unigene1677_All//9.00E-154//AT1G29120| unknown protein	Unigene1677_All//0.00E+00//TC176899				nr -
Unigene16771_All	584	0.90	1.48	0.36	0.85	0.88	2.47	1.01	1.72	0.00	7.19E-01	3.48E-01		-1.30E+00	2.42E-01		5.23E-02	9.80E-01		1.54E+00	8.56E-03		7.61E-01	2.28E-01		-9.99E+00	1.41E-04	Down	Unigene16771_All//gi|115470755|ref|NP_001058976.1|//1.00E-17//Os07g0167200 [Oryza sativa Japonica Group] >gi|113610512|dbj|BAF20890.1| Os07g0167200 [Oryza sativa Japonica Group]	Unigene16771_All//9.00E-14//AT3G03740| ATBPM4 (BTB-POZ and MATH domain 4); protein binding	Unigene16771_All//1.00E-128//TC179240				nr -
Unigene16772_All	622	2.78	1.71	1.97	3.12	3.32	3.12	2.92	1.14	1.02	-6.98E-01	1.58E-01		-4.95E-01	3.58E-01		8.88E-02	8.63E-01		-6.00E-04	9.95E-01		-1.36E+00	2.27E-03		-1.51E+00	5.47E-04	Down	Unigene16772_All//gi|222820580|gb|ACM67640.1|//2.00E-52//BTB-POZ and MATH domain protein [Capsicum annuum]	Unigene16772_All//7.00E-43//AT3G03740| ATBPM4 (BTB-POZ and MATH domain 4); protein binding	Unigene16772_All//0.00E+00//gi|48828323|gb|CO126713.1|CO126713				nr +
Unigene16777_All	525	52.42	88.99	51.93	56.84	50.51	70.28	39.22	93.62	62.15	7.63E-01	8.44E-22		-1.35E-02	9.22E-01		-1.70E-01	1.04E-01		3.06E-01	4.70E-04		1.26E+00	9.52E-63	Up	6.64E-01	2.36E-15		Unigene16777_All//gi|119360109|gb|ABL66783.1|//8.00E-16//At5g49710 [Arabidopsis thaliana]	Unigene16777_All//3.00E-13//AT5G49710| unknown protein	Unigene16777_All//0.00E+00//gi|84167470|gb|DR456118.1|DR456118				nr -
Unigene16779_All	660	82.76	23.03	29.53	93.14	76.18	80.75	80.33	39.01	41.17	-1.85E+00	2.64E-100	Down	-1.49E+00	2.77E-71	Down	-2.90E-01	2.99E-06		-2.06E-01	2.45E-03		-1.04E+00	1.84E-50	Down	-9.65E-01	8.92E-46		Unigene16779_All//gi|209967449|gb|ACJ02353.1|//2.00E-76//60S ribosomal protein L27A [Vernicia fordii]	Unigene16779_All//4.00E-76//AT1G70600| structural constituent of ribosome	Unigene16779_All//0.00E+00//TC154004		ko03010|Ribosome		nr -
Unigene16780_All	369	4.40	5.63	5.20	6.88	8.03	2.33	7.91	8.16	4.32	3.57E-01	4.24E-01		2.41E-01	6.24E-01		2.21E-01	5.97E-01		-1.57E+00	1.37E-04	Down	4.48E-02	9.09E-01		-8.72E-01	5.68E-03					Unigene16780_All//1.00E-38//DT460718				
Unigene16782_All	727	2.66	4.39	5.71	6.78	6.06	4.22	1.28	1.09	1.48	7.22E-01	3.81E-02		1.10E+00	4.78E-04	Up	-1.62E-01	5.96E-01		-6.83E-01	1.09E-02		-2.28E-01	7.18E-01		2.10E-01	7.09E-01		Unigene16782_All//gi|115521215|gb|ABJ09073.1|//2.00E-24//heat shock transcription factor 1 [Medicago sativa] >gi|115521221|gb|ABJ09076.1| heat shock transcription factor 1 [Medicago sativa]	Unigene16782_All//3.00E-12//AT4G17750| HSF1 (HEAT SHOCK FACTOR 1); DNA binding / protein binding / transcription factor	Unigene16782_All//0.00E+00//gi|78336572|gb|DT556846.1|DT556846	HSF			nr +
Unigene16783_All	1118	0.89	2.04	1.86	1.38	3.02	1.78	2.69	1.31	2.85	1.20E+00	5.65E-03		1.06E+00	2.44E-02		1.13E+00	6.03E-04	Up	3.64E-01	4.81E-01		-1.04E+00	1.36E-03		8.63E-02	7.85E-01		Unigene16783_All//gi|87240899|gb|ABD32757.1|//2.00E-29//Integrase, catalytic region [Medicago truncatula]	Unigene16783_All//2.00E-17//AT1G21280| unknown protein	Unigene16783_All//3.00E-155//gi|13245564|gb|BE052981.2|BE052981				nr +
Unigene16784_All	712	13.01	8.68	7.40	11.26	8.61	11.16	19.42	12.21	8.84	-5.83E-01	2.00E-03		-8.13E-01	3.57E-05		-3.88E-01	5.62E-02		-1.29E-02	9.47E-01		-6.69E-01	6.71E-07		-1.14E+00	3.51E-16	Down	Unigene16784_All//gi|297851452|ref|XP_002893607.1|//4.00E-07//ATINT2 [Arabidopsis lyrata subsp. lyrata] >gi|297339449|gb|EFH69866.1| ATINT2 [Arabidopsis lyrata subsp. lyrata]	Unigene16784_All//2.00E-07//AT1G30220| INT2 (INOSITOL TRANSPORTER 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene16784_All//3.00E-154//TC172867				nr -
Unigene16791_All	775	52.59	8.50	43.22	15.17	7.91	2.45	0.60	2.86	0.31	-2.63E+00	1.89E-116	Down	-2.83E-01	1.27E-03		-9.40E-01	8.36E-10		-2.63E+00	6.76E-37	Down	2.25E+00	4.40E-07	Up	-9.60E-01	3.13E-01		Unigene16791_All//gi|163955602|gb|ABV49799.1|//7.00E-18//membrane receptor-like protein 1 [Capsicum annuum]	Unigene16791_All//2.00E-05//AT1G67000| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene16791_All//3.00E-142//TC150336				nr +
Unigene16796_All	424	15.92	9.20	10.80	25.02	29.97	29.93	80.17	42.39	39.09	-7.91E-01	4.68E-04		-5.60E-01	1.81E-02		2.60E-01	1.19E-01		2.58E-01	1.34E-01		-9.20E-01	1.14E-26		-1.04E+00	2.60E-33	Down				Unigene16796_All//0.00E+00//TC161225				
Unigene16799_All	750	7.39	8.17	9.73	6.24	8.03	8.61	8.85	7.36	3.72	1.45E-01	5.93E-01		3.96E-01	8.66E-02		3.64E-01	1.51E-01		4.64E-01	5.09E-02		-2.67E-01	2.30E-01		-1.25E+00	1.88E-09	Down	Unigene16799_All//gi|297823385|ref|XP_002879575.1|//1.00E-50//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325414|gb|EFH55834.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene16799_All//3.00E-45//AT2G35795| DNAJ heat shock N-terminal domain-containing protein	Unigene16799_All//0.00E+00//gi|164311353|gb|ES848499.1|ES848499				nr +
Unigene1680_All	2356	11.77	10.28	11.21	80.92	73.39	58.79	17.71	10.89	7.25	-1.95E-01	7.36E-02		-7.03E-02	5.90E-01		-1.41E-01	6.12E-05		-4.61E-01	2.38E-38		-7.01E-01	9.64E-21		-1.29E+00	2.95E-57	Down	Unigene1680_All//gi|297817274|ref|XP_002876520.1|//1.00E-153//IQ-domain 13 [Arabidopsis lyrata subsp. lyrata] >gi|297322358|gb|EFH52779.1| IQ-domain 13 [Arabidopsis lyrata subsp. lyrata]	Unigene1680_All//5.00E-112//AT3G59690| IQD13 (IQ-domain 13); calmodulin binding	Unigene1680_All//0.00E+00//TC163100				nr -
Unigene16800_All	419	18.73	10.40	9.15	23.42	17.26	25.65	7.77	5.99	4.28	-8.49E-01	4.66E-05		-1.03E+00	2.37E-06	Down	-4.41E-01	1.22E-02		1.31E-01	5.35E-01		-3.77E-01	2.40E-01		-8.61E-01	3.68E-03		Unigene16800_All//gi|4097569|gb|AAD09513.1|//6.00E-28//GMFP4 [Glycine max]	Unigene16800_All//2.00E-25//AT1G32400| TOM2A (TOBAMOVIRUS MULTIPLICATION 2A); protein binding	Unigene16800_All//0.00E+00//TC152981				nr +
Unigene16802_All	520	1.81	2.05	2.46	3.64	2.98	2.43	5.69	7.72	13.48	1.76E-01	7.74E-01		4.40E-01	4.71E-01		-2.89E-01	5.64E-01		-5.82E-01	2.31E-01		4.39E-01	1.19E-01		1.24E+00	9.04E-10	Up	Unigene16802_All//gi|224122896|ref|XP_002318943.1|//2.00E-27//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222857319|gb|EEE94866.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene16802_All//4.00E-19//AT1G61310| ATP binding / protein binding	Unigene16802_All//1.00E-85//TC162123		ko04626|Plant-pathogen interaction		nr +
Unigene16805_All	604	12.21	10.65	5.55	9.81	13.45	10.69	3.99	4.15	3.76	-1.97E-01	3.78E-01		-1.14E+00	6.76E-07	Down	4.55E-01	2.36E-02		1.24E-01	6.50E-01		5.74E-02	8.88E-01		-8.58E-02	8.09E-01									
Unigene16807_All	709	61.69	46.17	70.82	44.33	58.09	34.78	2.92	1.30	0.62	-4.18E-01	1.77E-07		1.99E-01	1.36E-02		3.90E-01	4.31E-07		-3.50E-01	2.16E-04		-1.17E+00	3.81E-03		-2.24E+00	6.31E-07	Down	Unigene16807_All//gi|124359162|gb|ABN05685.1|//8.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene16807_All//1.00E-05//AT3G09510| nucleic acid binding	Unigene16807_All//0.00E+00//gi|73851026|gb|DT460046.1|DT460046				nr +
Unigene1681_All	1909	67.53	46.18	49.32	58.71	74.81	61.49	7.02	22.31	11.98	-5.48E-01	4.15E-33		-4.54E-01	9.59E-23		3.50E-01	3.57E-19		6.66E-02	2.40E-01		1.67E+00	5.52E-83	Up	7.71E-01	4.87E-14		Unigene1681_All//gi|30678541|ref|NP_191916.3|//1.00E-104//UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75299638|sp|Q8GZ38.1|UNE10_ARATH RecName: Full=Transcription factor UNE10; AltName: Full=Protein UNFERTILIZED EMBRYO SAC 10; AltName: Full=Transcription factor EN 108; AltName: Full=bHLH transcription factor bHLH016; AltName: Full=Basic helix-loop-helix protein 16; Short=bHLH 16; Short=AtbHLH16 >gi|109134123|gb|AB625060.1| At4g00050 [Arabidopsis thaliana]	Unigene1681_All//3.00E-80//AT4G00050| UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor	Unigene1681_All//0.00E+00//TC146895	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr -
Unigene16810_All	673	7.31	3.46	5.54	7.55	6.86	9.46	7.10	8.76	3.20	-1.08E+00	9.20E-05	Down	-4.00E-01	1.68E-01		-1.39E-01	6.31E-01		3.26E-01	1.98E-01		3.03E-01	1.95E-01		-1.15E+00	2.74E-06	Down	Unigene16810_All//gi|15218861|ref|NP_171861.1|//1.00E-57//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana]	Unigene16810_All//6.00E-59//AT1G03650| GCN5-related N-acetyltransferase (GNAT) family protein					nr -
Unigene16812_All	564	44.16	28.66	20.68	214.63	146.11	133.97	84.86	74.03	39.98	-6.24E-01	1.15E-08		-1.09E+00	1.61E-20	Down	-5.55E-01	1.46E-38		-6.80E-01	4.78E-49		-1.97E-01	5.60E-03		-1.09E+00	3.82E-50	Down	Unigene16812_All//gi|224135763|ref|XP_002322154.1|//6.00E-55//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222869150|gb|EEF06281.1| nucleobase ascorbate transporter [Populus trichocarpa]	Unigene16812_All//6.00E-54//AT5G62890| permease, putative	Unigene16812_All//0.00E+00//gi|164290906|gb|ES802600.1|ES802600				nr -
Unigene16813_All	678	233.36	121.14	129.28	411.96	316.57	275.44	108.13	82.24	51.83	-9.46E-01	6.12E-104		-8.52E-01	1.80E-84		-3.80E-01	3.90E-44		-5.81E-01	4.55E-85		-3.95E-01	3.58E-13		-1.06E+00	1.49E-73	Down	Unigene16813_All//gi|225428888|ref|XP_002262882.1|//2.00E-72//PREDICTED: serine/threonine kinase-like [Vitis vinifera]	Unigene16813_All//2.00E-69//AT1G12310| calmodulin, putative	Unigene16813_All//0.00E+00//TC145740		ko04626|Plant-pathogen interaction		nr +
Unigene16814_All	574	38.10	36.28	41.10	42.00	38.33	37.06	19.08	18.35	8.81	-7.06E-02	6.20E-01		1.09E-01	3.96E-01		-1.32E-01	3.06E-01		-1.81E-01	1.40E-01		-5.62E-02	7.51E-01		-1.11E+00	1.23E-12	Down	Unigene16814_All//gi|42565703|ref|NP_190365.3|//3.00E-51//MAG1 (MAIGO 1); hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|42572609|ref|NP_974400.1| MAG1 (MAIGO 1); hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|145362475|ref|NP_974399.2| MAG1 (MAIGO 1); hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|222424363|dbj|BAH20137.1| AT3G47810 [Arabidopsis thaliana]	Unigene16814_All//2.00E-52//AT3G47810| MAG1 (MAIGO 1); hydrolase/ protein serine/threonine phosphatase	Unigene16814_All//0.00E+00//TC143151				nr +
Unigene16815_All	414	4.17	12.24	10.55	4.81	5.82	5.67	23.59	27.96	13.86	1.55E+00	6.56E-08	Up	1.34E+00	1.90E-05	Up	2.75E-01	5.56E-01		2.37E-01	6.36E-01		2.45E-01	1.26E-01		-7.68E-01	1.66E-06		Unigene16815_All//gi|93693071|gb|AAF87120.1|AC006434_16 F10A5.27 [Arabidopsis thaliana] >gi|11692842|gb|AAG40024.1|AF324673_1 At1g75700 [Arabidopsis thaliana] >gi|39545896|gb|AAR28011.1| TFIIF-beta 2 [Arabidopsis thaliana]	Unigene16815_All//1.00E-15//AT1G75510| transcription initiation factor IIF beta subunit (TFIIF-beta) family protein	Unigene16815_All//1.00E-158//TC158776		ko03022|Basal transcription factors		nr +
Unigene16816_All	536	47.64	72.03	139.68	82.44	82.68	95.89	265.12	39.61	84.14	5.97E-01	4.96E-12		1.55E+00	2.73E-104	Up	4.30E-03	9.64E-01		2.18E-01	3.70E-03		-2.74E+00	0.00E+00	Down	-1.66E+00	4.37E-281	Down	Unigene16816_All//gi|153805696|gb|ABS82573.1|//4.00E-97//chalcone synthase [Gossypium hirsutum]	Unigene16816_All//2.00E-80//AT5G13930| TT4 (TRANSPARENT TESTA 4); naringenin-chalcone synthase	Unigene16816_All//0.00E+00//TC130077		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr +
Unigene16817_All	464	339.41	430.69	602.85	286.22	325.21	244.60	131.49	426.97	226.24	3.44E-01	7.03E-22		8.29E-01	1.78E-142		1.84E-01	2.47E-06		-2.27E-01	1.64E-07		1.70E+00	0.00E+00	Up	7.83E-01	7.17E-63		Unigene16817_All//gi|5263319|gb|AAD41421.1|AC007727_10//3.00E-50//ESTs gb|N86028, gb|F14286, gb|T20680, gb|F14443, gb|AA657300 and gb|N65244 come from this gene [Arabidopsis thaliana]	Unigene16817_All//2.00E-51//AT1G21680| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole, plant-type cell wall; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40-like Beta Propeller (InterPro:IPR011659), Six-bladed beta-propeller, TolB-like (InterPro:IPR011042); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21670.1); Has 6869 Blast hits to 3873 proteins in 790 species: Archae - 41; Bacteria - 3697; Metazoa - 41; Fungi - 39; Plants - 64; Viruses - 0; Other Eukaryotes - 2987 (source: NCBI BLink).	Unigene16817_All//0.00E+00//gi|78325244|gb|DT545518.1|DT545518				nr +

Unigene16819_All	560	13.45	12.67	9.79	69.92	42.68	31.94	37.45	37.17	30.23	-8.69E-02	6.91E-01		-4.58E-01	4.22E-02		-7.12E-01	1.04E-19		-1.13E+00	1.02E-37	Down	-1.08E-02	9.56E-01		-3.09E-01	3.52E-03		Unigene16819_All//gi|297850988|ref|XP_002893375.1|//6.00E-11//dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339217|gb|EFH69634.1|dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16819_All//4.00E-12//AT1G26850| dehydration-responsive family protein	Unigene16819_All//0.00E+00//TC146658				nr -
Unigene1682_All	1937	3.05	2.25	1.73	2.21	2.31	1.96	0.22	1.92	0.60	-4.40E-01	7.51E-02		-8.18E-01	1.28E-03		6.34E-02	8.49E-01		-1.75E-01	6.28E-01		3.14E+00	4.53E-16	Up	1.45E+00	1.09E-02		Unigene1682_All//gi|30678541|ref|NP_191916.3|//1.00E-113//UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75299638|sp|Q8GZ38.1|UNE10_ARATH RecName: Full=Transcription factor UNE10; AltName: Full=Protein UNFERTILIZED EMBRYO SAC 10; AltName: Full=Transcription factor EN 108; AltName: Full=bHLH transcription factor bHLH016; AltName: Full=Basic helix-loop-helix protein 16; Short=bHLH 16; Short=AtbHLH16 >gi|109134123|gb|ABG25060.1|At4g00050 [Arabidopsis thaliana]	Unigene1682_All//7.00E-85//AT4G00050| UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor	Unigene1682_All//0.00E+00//TC146895	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr -
Unigene16820_All	679	3.24	0.75	0.47	3.89	6.95	5.12	1.87	1.11	0.82	-2.12E+00	1.67E-05	Down	-2.78E+00	7.59E-07	Down	8.37E-01	1.72E-03		3.98E-01	2.67E-01		-7.54E-01	1.63E-01		-1.19E+00	2.28E-02		Unigene16820_All//gi|297607851|ref|NP_001060746.2|//8.00E-29//Os07g0695700 [Oryza sativa Japonica Group] >gi|255678086|dbj|BAF22660.2|Os07g0695700 [Oryza sativa Japonica Group]	Unigene16820_All//1.00E-53//AT3G09430| unknown protein	Unigene16820_All//0.00E+00//gi|78334525|gb|DT554799.1|DT554799				nr -
Unigene16821_All	998	1.21	0.56	0.37	2.20	1.38	1.54	2.84	0.34	0.68	-1.11E+00	7.50E-02		-1.69E+00	1.44E-02		-6.70E-01	1.11E-01		-5.13E-01	2.58E-01		-3.08E+00	3.10E-12	Down	-2.06E+00	2.30E-08	Down	Unigene16821_All//gi|297607851|ref|NP_001060746.2|//1.00E-30//Os07g0695700 [Oryza sativa Japonica Group] >gi|255678086|dbj|BAF22660.2|Os07g0695700 [Oryza sativa Japonica Group]	Unigene16821_All//4.00E-75//AT3G09430| unknown protein	Unigene16821_All//0.00E+00//gi|78334525|gb|DT554799.1|DT554799				nr +
Unigene16822_All	644	2.44	5.04	4.30	4.72	7.81	4.07	2.23	3.57	6.12	1.05E+00	2.71E-03		8.19E-01	3.85E-02		7.26E-01	4.96E-03		-2.14E-01	6.16E-01		6.77E-01	7.39E-02		1.46E+00	3.22E-07	Up	Unigene16822_All//gi|34365743|gb|AAQ65183.1|//9.00E-30//At5g58020 [Arabidopsis thaliana]	Unigene16822_All//8.00E-24//AT5G58020| unknown protein	Unigene16822_All//4.00E-147//gi|78353673|gb|DT573947.1|DT573947				nr -
Unigene16823_All	765	0.41	2.65	0.70	1.95	1.31	1.12	2.76	2.68	3.02	2.69E+00	1.81E-06	Up	7.62E-01	4.53E-01		-5.82E-01	2.89E-01		-8.00E-01	1.48E-01		-4.58E-02	9.27E-01		1.28E-01	7.34E-01		Unigene16823_All//gi|22327146|ref|NP_198205.2|//2.00E-11//FRS10 (FAR1-related sequence 10); zinc ion binding [Arabidopsis thaliana] >gi|257051024|sp|Q9LKR4.2|FRS10_ARATH RecName: Full=Putative protein FAR1-RELATED SEQUENCE 10	Unigene16823_All//8.00E-11//AT5G28530| FRS10 (FAR1-related sequence 10); zinc ion binding	Unigene16823_All//5.00E-73//ES806201				nr +
Unigene16825_All	369	50.34	105.05	73.60	89.50	127.29	247.85	70.24	184.17	169.61	1.06E+00	3.65E-31	Up	5.48E-01	3.04E-07		5.08E-01	1.03E-12		1.47E+00	1.87E-129	Up	1.39E+00	3.71E-101	Up	1.27E+00	4.23E-83	Up	Unigene16825_All//gi|172045782|sp|Q9X129.2|Y1540_ARATH//9.00E-23//RecName: Full=Uncharacterized protein At1g15400	Unigene16825_All//4.00E-24//AT1G15400| unknown protein	Unigene16825_All//0.00E+00//gi|109871853|gb|DW500829.1|DW500829				nr +
Unigene16826_All	379	11.87	10.03	24.59	16.30	17.08	17.99	23.32	26.69	42.15	-2.44E-01	4.04E-01		1.05E+00	1.30E-07	Up	6.77E-02	8.39E-01		1.43E-01	6.15E-01		1.95E-01	2.77E-01		8.54E-01	7.55E-12		Unigene16826_All//gi|93280150|gb|ABF06703.1|//5.00E-10//Joka2 [Nicotiana plumbaginifolia]	Unigene16826_All//9.00E-09//AT4G24690| ubiquitin-associated (UBA)/TS-N domain-containing protein / octicosapeptide/Phox/Bem1 (PB1) domain-containing protein	Unigene16826_All//6.00E-145//BF268707				nr +
Unigene16827_All	641	1.06	3.87	3.99	4.20	5.21	4.23	0.92	3.85	8.14	1.87E+00	2.75E-05	Up	1.91E+00	2.62E-05	Up	3.12E-01	4.12E-01		1.06E-02	9.79E-01		2.06E+00	4.61E-07	Up	3.14E+00	8.91E-23	Up	Unigene16827_All//gi|297834156|ref|XP_002884960.1|//1.00E-23//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297330800|gb|EFH61219.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene16827_All//7.00E-25//AT3G13310| DNAJ heat shock N-terminal domain-containing protein	Unigene16827_All//0.00E+00//TC165849				nr -
Unigene16829_All	1054	0.79	0.34	1.52	1.37	1.27	1.20	2.49	1.51	0.68	-1.24E+00	1.15E-01		9.32E-01	8.84E-02		-1.05E-01	8.32E-01		-1.92E-01	7.24E-01		-7.23E-01	3.83E-02		-1.87E+00	5.91E-07	Down	Unigene16829_All//gi|15223802|ref|NP_173449.1|//1.00E-123//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|193806503|sp|Q9LNU6.2|PPR53_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g20230	Unigene16829_All//2.00E-124//AT1G20230| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene1683_All	1553	7.61	19.41	9.40	7.73	11.75	14.05	5.17	6.51	4.10	1.35E+00	2.24E-35	Up	3.03E-01	5.52E-02		6.04E-01	5.64E-07		8.62E-01	1.32E-13		3.32E-01	4.54E-02		-3.34E-01	6.66E-02		Unigene1683_All//gi|75282642|sp|Q501G6.1|U49G7_ARATH//5.00E-73//RecName: Full=UPF0497 membrane protein At5g62820 >gi|63003768|gb|AAY25413.1|At5g62820 [Arabidopsis thaliana] >gi|66841362|gb|AAY57318.1|At5g62820 [Arabidopsis thaliana]	Unigene1683_All//1.00E-50//AT5G62820| integral membrane protein, putative	Unigene1683_All//0.00E+00//gi|78329830|gb|DT550104.1|DT550104		ko00910|Nitrogen metabolism		nr +
Unigene16830_All	931	25.85	18.23	29.97	14.87	17.53	17.08	4.68	3.23	1.41	-5.04E-01	5.54E-06		2.13E-01	5.85E-02		2.37E-01	1.03E-01		1.99E-01	2.05E-01		-5.33E-01	4.16E-02		-1.73E+00	5.83E-10	Down	Unigene16830_All//gi|158828210|gb|ABR81088.1|//1.00E-86//TRL10 [Cleome spinosa]	Unigene16830_All//2.00E-79//AT1G07440| tropinone reductase, putative / tropine dehydrogenase, putative	Unigene16830_All//0.00E+00//TC142536		ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis		nr -
Unigene16832_All	529	0.00	0.00	0.00	0.00	0.78	0.00	2.56	0.79	0.60	null	null		null	null		9.61E+00	1.25E-02		null	null		-1.69E+00	1.96E-03		-2.09E+00	1.85E-04	Down	Unigene16832_All//gi|48310064|gb|AAT41746.1|//2.00E-09//At4g28840 [Arabidopsis thaliana] >gi|50198849|gb|AAT70453.1|At4g28840 [Arabidopsis thaliana]	Unigene16832_All//6.00E-05//AT4G28840| unknown protein	Unigene16832_All//3.00E-18//DW498405				nr -
Unigene16833_All	701	0.07	0.00	0.00	4.19	1.77	2.38	3.20	2.21	1.65	-6.22E+00	6.13E-01		-6.22E+00	6.25E-01		-1.25E+00	2.98E-04	Down	-8.15E-01	2.52E-02		-5.35E-01	1.71E-01		-9.56E-01	9.46E-03		Unigene16833_All//gi|48310064|gb|AAT41746.1|//8.00E-25//At4g28840 [Arabidopsis thaliana] >gi|50198849|gb|AAT70453.1|At4g28840 [Arabidopsis thaliana]	Unigene16833_All//3.00E-17//AT4G28840| unknown protein	Unigene16833_All//2.00E-17//TC136618				nr +
Unigene16836_All	420	2.12	3.98	1.65	1.90	2.30	1.94	5.74	1.19	2.28	9.11E-01	7.45E-02		-3.62E-01	6.32E-01		2.75E-01	7.47E-01		2.85E-02	9.71E-01		-2.26E+00	1.02E-07	Down	-1.33E+00	2.65E-04	Down	Unigene16836_All//gi|15233171|ref|NP_191723.1|//4.00E-21//AGP20 [Arabidopsis thaliana] >gi|75183616|sp|Q9M373.1|AGP20_ARATH RecName: Full=Arabinogalactan peptide 20; Short=AG-peptide 20; Flags: Precursor >gi|98960995|gb|ABF58981.1|At3g61640 [Arabidopsis thaliana]	Unigene16836_All//3.00E-16//AT3G61640| AGP20	Unigene16836_All//0.00E+00//DW503904				nr -
Unigene16837_All	453	1.39	1.12	2.12	2.31	1.82	0.40	2.61	0.09	0.53	-3.09E-01	7.01E-01		6.10E-01	3.86E-01		-3.40E-01	5.96E-01		-2.53E+00	1.22E-03		-4.82E+00	2.83E-07	Down	-2.31E+00	2.04E-04	Down	Unigene16837_All//gi|15233171|ref|NP_191723.1|//4.00E-21//AGP20 [Arabidopsis thaliana] >gi|75183616|sp|Q9M373.1|AGP20_ARATH RecName: Full=Arabinogalactan peptide 20; Short=AG-peptide 20; Flags: Precursor >gi|98960995|gb|ABF58981.1|At3g61640 [Arabidopsis thaliana]	Unigene16837_All//3.00E-16//AT3G61640| AGP20	Unigene16837_All//0.00E+00//DW503904				nr +
Unigene1684_All	1948	0.64	4.01	4.76	2.71	3.66	39.41	1.82	0.73	4.05	2.64E+00	1.33E-22	Up	2.88E+00	1.54E-28	Up	4.33E-01	4.88E-02		3.86E+00	0.00E+00	Up	-1.32E+00	1.21E-05	Down	1.15E+00	9.91E-10	Up	Unigene1684_All//gi|75282642|sp|Q501G6.1|U49G7_ARATH//7.00E-73//RecName: Full=UPF0497 membrane protein At5g62820 >gi|63003768|gb|AAY25413.1|At5g62820 [Arabidopsis thaliana] >gi|66841362|gb|AAY57318.1|At5g62820 [Arabidopsis thaliana]	Unigene1684_All//3.00E-61//AT5G14740| CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding	Unigene1684_All//0.00E+00//gi|78329830|gb|DT550104.1|DT550104		ko00910|Nitrogen metabolism		nr -
Unigene16841_All	1156	1.86	2.85	1.66	32.41	29.07	10.74	2.41	0.61	0.34	6.19E-01	7.09E-02		-1.62E-01	7.11E-01		-1.57E-01	9.14E-02		-1.59E+00	6.80E-61	Down	-1.97E+00	1.53E-07	Down	-2.81E+00	1.82E-11	Down	Unigene16841_All//gi|166487779|gb|ACL25380.1|//2.00E-48//At1g69160/F4N2_9 [Arabidopsis thaliana]	Unigene16841_All//7.00E-31//AT1G69160| unknown protein	Unigene16841_All//0.00E+00//TC1328810				nr -
Unigene16842_All	868	15.97	16.58	20.12	10.90	11.86	9.37	4.43	1.16	1.29	5.36E-02	7.31E-01		3.33E-01	1.83E-02		1.22E-01	5.81E-01		-2.19E-01	3.01E-01		-1.94E+00	6.56E-10	Down	-1.79E+00	2.81E-09	Down	Unigene16842_All//gi|20198054|gb|AAD21779.2|//6.00E-15//expressed protein [Arabidopsis thaliana] >gi|10738048|gb|ABF83621.1|At2g01870 [Arabidopsis thaliana]	Unigene16842_All//2.00E-16//AT2G01870| unknown protein	Unigene16842_All//2.00E-08//ES803021				nr +
Unigene16844_All	997	3.99	3.76	3.95	8.29	8.12	7.57	9.20	4.86	3.96	-8.47E-02	7.77E-01		-1.30E-02	9.91E-01		-3.12E-02	8.91E-01		-1.33E-01	5.97E-01		-9.20E-01	8.41E-08		-1.22E+00	3.06E-12	Down	Unigene16844_All//gi|15230653|ref|NP_187269.1|//2.00E-76//structural constituent of ribosome [Arabidopsis thaliana] >gi|62867643|gb|AAY17425.1|At3g06180 [Arabidopsis thaliana] >gi|90962960|gb|ABE02401.1|At3g06180 [Arabidopsis thaliana]	Unigene16844_All//9.00E-56//AT3G06180| structural constituent of ribosome	Unigene16844_All//0.00E+00//gi|78340478|gb|DT560752.1|DT560752		ko03040|Spliceosome		nr +
Unigene16845_All	944	7.26	6.92	9.25	1.27	1.61	0.53	0.18	6.07	31.31	-6.85E-02	7.66E-01		3.50E-01	9.64E-02		3.42E-01	5.76E-01		-1.27E+00	4.58E-02		5.08E+00	2.09E-34	Up	7.45E+00	5.95E-204	Up	Unigene16845_All//gi|124359694|gb|ABD32361.2|//2.00E-24//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene16845_All//5.00E-15//AT4G20970| basic helix-loop-helix (bHLH) family protein	Unigene16845_All//0.00E+00//TC151428	bHLH			nr -
Unigene16846_All	1765	19.24	52.88	24.74	31.27	66.53	93.06	4.67	10.11	41.55	1.46E+00	1.68E-121	Up	3.63E-01	1.25E-05		1.09E+00	2.11E-115	Up	1.57E+00	7.51E-257	Up	1.11E+00	2.07E-19	Up	3.15E+00	0.00E+00	Up	Unigene16846_All//gi|40218371|gb|AAR83118.1|//0.00E+00//secretory laccase [Gossypium arboreum]	Unigene16846_All//3.00E-147//AT5G09360| LAC14 (laccase 14); laccase	Unigene16846_All//0.00E+00//TC156527		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene16847_All	1634	0.58	0.68	0.81	1.62	1.69	1.82	9.81	16.45	99.84	2.43E-01	6.82E-01		4.99E-01	3.93E-01		6.13E-02	8.94E-01		1.75E-01	6.75E-01		7.46E-01	4.29E-15		3.35E+00	0.00E+00	Up	Unigene16847_All//gi|30690453|ref|NP_182185.2|//1.00E-152//AAA-type ATPase family protein [Arabidopsis thaliana]	Unigene16847_All//1.00E-133//AT2G46620| AAA-type ATPase family protein	Unigene16847_All//0.00E+00//gi|78331014|gb|DT551288.1|DT551288				nr -
Unigene1685_All	627	1.75	6.14	5.10	5.24	3.08	4.47	2.76	2.20	2.67	1.81E+00	1.73E-07	Up	1.54E+00	5.58E-05	Up	-7.70E-01	1.75E-02		-2.32E-01	5.54E-01		-3.30E-01	4.90E-01		-5.10E-02	9.21E-01		Unigene1685_All//gi|86440327|gb|ABC96116.1|//6.00E-12//sterol glucosyltransferase [Withania somnifera]	Unigene1685_All//2.00E-09//AT1G43620| UDP-glucose:sterol glucosyltransferase, putative	Unigene1685_All//0.00E+00//TC149348				nr +

Unigene16851_All	904	1.27	2.52	1.35	4.57	2.29	4.40	3.93	5.32	3.22	9.86E-01	2.07E-02		8.95E-02	8.83E-01		-1.00E+00	3.35E-04	Down	-5.70E-02	8.69E-01		4.37E-01	8.27E-02		-2.88E-01	3.39E-01		Unigene16851_All//gi|115456583|ref|NP_001051892.1|//7.00E-86//0s03g0848300 [Oryza sativa Japonica Group] >gi|113550363|dbj|BAF13806.1| 0s03g0848300 [Oryza sativa Japonica Group] >gi|149390857|gb|ABR25446.1| actin-related protein 2/3 complex subunit 4 [Oryza sativa Indica Group]	Unigene16851_All//5.00E-85//AT4G14147| ARPC4; protein binding	Unigene16851_All//0.00E+00//gi|21098646|gb|BQ410959.1|BQ410959				nr +
Unigene16852_All	1523	0.00	0.13	0.00	3.27	3.78	1.84	3.03	1.43	2.12	7.06E+00	1.37E-01		null	null		2.07E-01	4.72E-01		-8.31E-01	1.70E-03		-1.08E+00	2.08E-05	Down	-5.14E-01	3.48E-02		Unigene16852_All//gi|71041096|gb|AAZ20436.1|//4.00E-94//MYB20 [Malus x domestica]	Unigene16852_All//4.00E-61//AT3G08500| MYB83 (myb domain protein 83); DNA binding / transcription factor	Unigene16852_All//0.00E+00//DW226305	MYB			nr -
Unigene16853_All	1786	0.00	0.11	0.00	0.00	0.08	0.00	62.80	3.93	5.22	6.83E+00	1.37E-01		null	null		6.27E+00	3.19E-01		null	null		-4.00E+00	0.00E+00	Down	-3.59E+00	0.00E+00	Down	Unigene16853_All//gi|224127426|ref|XP_002322071.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222860844|gb|EEE98386.1| cytochrome P450 [Populus trichocarpa]	Unigene16853_All//2.00E-174//AT2G45510| CYP704A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene16853_All//8.00E-40//TC178534		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene16855_All	516	3.45	9.62	7.74	9.46	7.47	8.32	4.18	3.32	5.87	1.48E+00	2.68E-07	Up	1.17E+00	3.21E-04	Up	-3.40E-01	2.28E-01		-1.86E-01	5.61E-01		-3.32E-01	4.22E-01		4.90E-01	1.18E-01					Unigene16855_All//3.00E-86//gi|78343974|gb|DT564248.1|DT564248				
Unigene16857_All	1047	0.20	1.69	0.10	10.66	21.28	18.12	6.58	4.83	14.69	3.08E+00	1.81E-06	Up	-9.75E-01	6.21E-01		9.98E-01	3.53E-19		7.66E-01	7.70E-10		-4.47E-01	2.74E-02		1.16E+00	2.68E-18	Up	Unigene16857_All//gi|30685840|ref|NP_173276.2|//8.00E-56//BEE1 (BR Enhanced Expression 1); transcription factor [Arabidopsis thaliana] >gi|75299631|sp|Q8GZ13.1|BEE1_ARATH RecName: Full=Transcription factor BEE 1; AltName: Full=Protein Brassinosteroid enhanced expression 1; AltName: Full=Transcription factor EN 77; AltName: Full=bHLH transcription factor bHLH044; AltName: Full=Basic helix-loop-helix protein 44; Short=bHLH 44; Short=AtbHLH44 >gi|28950817|gb|AAO63332.1| At1g18400 [Arabidopsis thaliana]	Unigene16857_All//3.00E-46//AT1G18400| BEE1 (BR Enhanced Expression 1); transcription factor	Unigene16857_All//0.00E+00//TC150221	bHLH	ko04712|Circadian rhythm - plant		nr +
Unigene16858_All	862	1.76	5.23	2.72	3.41	4.23	6.34	1.77	7.18	5.64	1.57E+00	3.11E-07	Up	6.27E-01	1.48E-01		3.13E-01	3.85E-01		8.95E-01	4.05E-04		2.02E+00	2.81E-16	Up	1.68E+00	1.84E-10	Up	Unigene16858_All//gi|15724294|gb|AAL06540.1|AF412087_1//2.00E-24//AT3g45210/T14D3_150 [Arabidopsis thaliana] >gi|20334744|gb|AAM16233.1| AT3g45210/T14D3_150 [Arabidopsis thaliana]	Unigene16858_All//2.00E-24//AT5G03230| unknown protein	Unigene16858_All//0.00E+00//gi|109880034|gb|DW509004.1|DW509004				nr -
Unigene16859_All	891	28.95	9.16	3.35	49.93	17.74	8.52	14.05	5.25	4.69	-1.66E+00	3.10E-41	Down	-3.11E+00	7.32E-85	Down	-1.49E+00	2.22E-75	Down	-2.55E+00	5.76E-134	Down	-1.42E+00	7.29E-20	Down	-1.58E+00	6.47E-24	Down	Unigene16859_All//gi|189303780|gb|ACD85810.1|//2.00E-60//cystcine proteinase inhibitor [Gossypium hirsutum]	Unigene16859_All//6.00E-18//AT2G31980| cysteine proteinase inhibitor-related	Unigene16859_All//0.00E+00//TC164239				nr +
Unigene16686_All	2517	2.83	7.25	4.38	3.76	3.52	3.52	5.48	4.80	3.85	1.36E+00	7.19E-22	Up	6.31E-01	3.73E-04		-9.69E-02	6.55E-01		-9.65E-02	6.69E-01		-1.90E-01	2.06E-01		-5.10E-01	1.03E-04		Unigene16686_All//gi|86440327|gb|ABC96116.1|//0.00E+00//sterol glucosyltransferase [Withania somnifera]	Unigene16686_All//0.00E+00//AT1G43620| UDP-glucose:sterol glucosyltransferase, putative	Unigene16686_All//0.00E+00//gi|78327640|gb|DT547914.1|DT547914				nr -
Unigene16860_All	596	238.69	272.14	277.06	177.94	127.17	131.63	13.76	38.78	2.81	1.89E-01	2.74E-06		2.15E-01	1.40E-07		-4.85E-01	1.75E-26		-4.35E-01	1.85E-19		1.49E+00	8.46E-39	Up	-2.29E+00	8.98E-26	Down	Unigene16860_All//gi|115479571|ref|NP_001063379.1|//1.00E-08//Os09g0458900 [Oryza sativa Japonica Group] >gi|113631612|dbj|BAF25293.1| Os09g0458900 [Oryza sativa Japonica Group]	Unigene16860_All//2.00E-07//AT2G43290| MSS3 (multicopy suppressors of snf4 deficiency in yeast 3); calcium ion binding	Unigene16860_All//0.00E+00//TC162504		ko04626|Plant-pathogen interaction		nr +
Unigene16861_All	1169	3.54	1.91	3.83	7.54	9.46	6.41	3.40	2.50	0.75	-8.91E-01	2.98E-03		1.14E-01	7.01E-01		3.26E-01	6.21E-02		-2.34E-01	2.84E-01		-4.42E-01	1.18E-01		-2.18E+00	3.58E-12	Down	Unigene16861_All//gi|297808203|ref|XP_002871985.1|//1.00E-101//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317822|gb|EFH48244.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16861_All//3.00E-87//AT5G22050| protein kinase family protein			ko04626|Plant-pathogen interaction		nr -
Unigene16863_All	836	2.69	2.61	1.40	3.87	3.91	4.75	7.38	9.85	17.39	-4.62E-02	9.22E-01		-9.41E-01	3.61E-02		1.48E-02	9.76E-01		2.96E-01	4.01E-01		4.16E-01	2.34E-02		1.24E+00	3.85E-19	Up				Unigene16863_All//0.00E+00//gi|21103648|gb|BQ415961.1|BQ415961				
Unigene16864_All	1192	0.31	8.37	0.49	0.88	1.42	6.44	1.31	7.82	8.99	4.77E+00	5.84E-47	Up	6.77E-01	4.83E-01		6.90E-01	1.87E-01		2.88E+00	7.10E-26	Up	2.57E+00	3.76E-32	Up	2.78E+00	9.21E-41	Up	Unigene16864_All//gi|5031277|gb|AAD38144.1|AF139497_1//5.00E-38//homeobox leucine zipper protein [Prunus armeniaca]	Unigene16864_All//4.00E-28//AT3G61890| ATHB-12 (ARABIDOPSIS THALIANA HOMEOBOX 12); transcription activator/ transcription factor	Unigene16864_All//6.00E-163//TC176718	HB			nr +
Unigene16866_All	397	1.58	0.00	0.00	0.75	0.35	0.68	0.75	2.21	2.31	-1.06E+01	7.92E-04	Down	-1.06E+01	1.41E-03		-1.12E+00	4.24E-01		-1.41E-01	9.21E-01		1.57E+00	2.54E-02		1.63E+00	1.45E-02		Unigene16866_All//gi|2443889|gb|AAB71482.1|//6.00E-24//similar to S-linalool synthase gb|U58314|1491939 [Arabidopsis thaliana]	Unigene16866_All//3.00E-25//AT1G61120| TPS04 (TERPENE SYNTHASE 04); (E,E)-geranyllinalool synthase	Unigene16866_All//5.00E-07//CO128297				nr -
Unigene16867_All	946	1.38	0.05	2.25	2.05	1.20	1.77	1.61	7.11	2.86	-4.69E+00	1.63E-06	Down	7.04E-01	1.31E-01		-7.74E-01	8.43E-02		-2.17E-01	6.69E-01		2.14E+00	5.93E-19	Up	8.32E-01	1.19E-02		Unigene16867_All//gi|2443889|gb|AAB71482.1|//3.00E-54//similar to S-linalool synthase gb|U58314|1491939 [Arabidopsis thaliana]	Unigene16867_All//1.00E-55//AT1G61120| TPS04 (TERPENE SYNTHASE 04); (E,E)-geranyllinalool synthase	Unigene16867_All//7.00E-08//CO128297		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis		nr +
Unigene16868_All	683	9.88	6.68	8.42	8.90	9.58	9.13	2.54	3.61	5.31	-5.66E-01	1.24E-02		-2.31E-01	3.72E-01		1.07E-01	7.13E-01		3.64E-02	9.08E-01		5.09E-01	1.70E-01		1.06E+00	1.86E-04	Up	Unigene16868_All//gi|224072218|ref|XP_002303658.1|//6.00E-30//f-box family protein [Populus trichocarpa] >gi|222841090|gb|EEE78637.1| f-box family protein [Populus trichocarpa]	Unigene16868_All//2.00E-27//AT4G10925| F-box family protein	Unigene16868_All//0.00E+00//gi|78323596|gb|DT543870.1|DT543870				nr -
Unigene16871_All	981	0.11	0.26	0.00	0.91	0.39	1.10	5.04	1.32	10.44	1.28E+00	4.35E-01		-6.74E+00	3.95E-01		-1.24E+00	8.18E-02		2.74E-01	6.70E-01		-1.93E+00	1.77E-12	Down	1.05E+00	8.86E-11	Up	Unigene16871_All//gi|18406255|ref|NP_564730.1|//8.00E-33//ZW2 [Arabidopsis thaliana] >gi|88979941|gb|AAP82255.1|AC008051_6 Identical to gene ZW2 from Arabidopsis thaliana gb|AB028196 >gi|6520154|dbj|BAA87938.1| ZW2 [Arabidopsis thaliana] >gi|94442517|gb|ABF19046.1| At1g58330 [Arabidopsis thaliana]	Unigene16871_All//4.00E-34//AT1G58330| ZW2					nr -
Unigene16872_All	1038	0.50	1.27	0.05	0.67	1.26	1.22	3.30	2.05	13.28	1.33E+00	2.73E-02		-3.30E+00	2.40E-02		9.08E-01	1.35E-01		8.59E-01	1.71E-01		-6.84E-01	2.18E-02		2.01E+00	8.27E-36	Up	Unigene16872_All//gi|225439404|ref|XP_002263705.1|//1.00E-36//PREDICTED: similar to transcription factor-related [Vitis vinifera]	Unigene16872_All//3.00E-34//AT1G58330| ZW2					nr +
Unigene16874_All	1385	0.83	3.29	0.65	9.32	12.38	10.40	4.73	4.10	7.71	1.99E+00	8.70E-10	Up	-3.47E-01	6.16E-01		4.11E-01	1.39E-03		1.59E-01	3.64E-01		-2.05E-01	3.81E-01		7.04E-01	3.87E-06		Unigene16874_All//gi|75151444|sp|Q8GY22.1|Y2608_ARATH//2.00E-58//RecName: Full=B3 domain-containing protein At2g36080; AltName: Full=Protein AUXIN RESPONSIVE FACTOR 31	Unigene16874_All//3.00E-54//AT3G11580| DNA-binding protein, putative	Unigene16874_All//9.00E-64//gi|78341852|gb|DT562126.1|DT562126	ABI3VP1			nr +
Unigene16875_All	1150	2.82	4.49	4.45	2.38	2.93	2.40	0.74	0.65	3.74	6.72E-01	1.07E-02		6.56E-01	1.76E-02		3.01E-01	4.24E-01		8.00E-03	9.85E-01		-1.69E-01	7.99E-01		2.35E+00	4.75E-14	Up	Unigene16875_All//gi|15010592|gb|AAK23055.1|//4.00E-28//F25118.1/F25118.1 [Arabidopsis thaliana] >gi|20196850|gb|AAB80643.2| Expressed protein [Arabidopsis thaliana] >gi|20196853|gb|AAM14805.1| Expressed protein [Arabidopsis thaliana] >gi|20453327|gb|AAM19902.1| At2g33250/F25118.1 [Arabidopsis thaliana]	Unigene16875_All//2.00E-22//AT2G33250| unknown protein	Unigene16875_All//0.00E+00//FL576383				nr -
Unigene16876_All	354	5.03	1.43	2.11	3.10	1.95	1.66	0.84	0.47	0.23	-1.81E+00	6.59E-04	Down	-1.25E+00	1.68E-02		-6.70E-01	3.06E-01		-9.00E-01	1.81E-01		-8.24E-01	5.40E-01		-1.89E+00	1.68E-01					Unigene16876_All//9.00E-30//DT458249				
Unigene1688_All	1599	6.25	15.50	4.13	10.56	10.88	24.32	9.92	36.18	101.03	1.31E+00	6.75E-28	Up	-5.98E-01	1.47E-03		4.23E-02	8.26E-01		1.20E+00	8.53E-41	Up	1.87E+00	1.63E-131	Up	3.35E+00	0.00E+00	Up	Unigene1688_All//gi|90900944|gb|ABE01834.1|//1.00E-147//NAK-type protein kinase [Nicotiana tabacum]	Unigene1688_All//5.00E-131//AT5G47070| protein kinase, putative	Unigene1688_All//0.00E+00//TC144153				nr +
Unigene16880_All	1371	4.85	11.60	7.03	7.34	8.59	9.09	10.08	8.29	6.28	1.26E+00	3.74E-17	Up	5.37E-01	5.31E-03		2.27E-01	2.10E-01		3.09E-01	6.71E-02		-2.82E-01	4.47E-02		-6.84E-01	2.18E-07		Unigene16880_All//gi|225424099|ref|XP_002283125.1|//7.00E-66//PREDICTED: similar to ubiquitin-related [Vitis vinifera]	Unigene16880_All//8.00E-48//AT1G68185| ubiquitin-related	Unigene16880_All//0.00E+00//TC160657				nr +
Unigene16883_All	678	53.86	42.08	43.43	48.79	39.62	46.16	196.75	85.81	64.75	-3.56E-01	5.87E-05		-3.11E-01	8.23E-04		-3.00E-01	7.23E-04		-7.97E-02	4.92E-01		-1.20E+00	3.36E-157	Down	-1.60E+00	6.31E-252	Down	Unigene16883_All//gi|211906476|gb|ACJ11731.1|//2.00E-43//ascorbate peroxidase [Gossypium hirsutum] >gi|254036190|gb|ACT56517.1| cytosolic ascorbate peroxidase [Gossypium hirsutum]	Unigene16883_All//7.00E-29//AT1G07890| APX1 (ascorbate peroxidase 1); L-ascorbate peroxidase	Unigene16883_All//0.00E+00//TC160853		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene16884_All	1070	4.16	6.49	8.86	2.65	4.80	3.21	1.11	0.66	0.41	6.42E-01	3.92E-03		1.09E+00	3.45E-08	Up	8.54E-01	7.66E-04		2.74E-01	4.74E-01		-7.37E-01	1.94E-01		-1.43E+00	9.72E-03		Unigene16884_All//gi|117970379|dbj|BAF36749.1|//3.00E-84//telomere binding protein [Solanum lycopersicum]	Unigene16884_All//5.00E-76//AT3G12560| TRFL9 (TRF-LIKE 9); DNA bending/ DNA binding / telomeric DNA binding	Unigene16884_All//0.00E+00//CO105837	MYB-related			nr +
Unigene16887_All	425	0.00	0.00	0.00	0.00	0.00	1.81	2.79	3.74	27.37	null	null		null	null		null	null		1.08E+01	1.27E-04	Up	4.24E-01	4.00E-01		3.30E+00	3.13E-52	Up	Unigene16887_All//gi|15217709|ref|NP_176647.1|//1.00E-63//ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase [Arabidopsis thaliana] >gi|6633821|gb|AAF19680.1|AC009519_14 F1N19.23 [Arabidopsis thaliana] >gi|16226491|gb|AAL16181.1|AF428413_1 At1g64660/F1N19_22 [Arabidopsis thaliana] >gi|15450932|gb|AAK96737.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana] >gi|30387533|gb|AAP31932.1| At1g64660 [Arabidopsis thaliana] >gi|110740851|dbj|BAE98522.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana]	Unigene16887_All//7.00E-65//AT1G64660| ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase	Unigene16887_All//2.00E-74//TC130861		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -

Unigene16888_All	1562	0.00	0.00	0.00	0.00	0.04	0.95	16.86	20.04	20.61	null	null		null	null		5.46E+00	6.10E-01		9.90E+00	7.04E-09	Up	2.49E-01	4.89E-03		2.89E-01	5.47E-04		Unigene16888_All//gi|15217709|ref|NP_176647.1|//0.00E+00//ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase [Arabidopsis thaliana] >gi|6633821|gb|AAF19680.1|AC009519_14 F1N19.23 [Arabidopsis thaliana] >gi|16226491|gb|AAL16181.1|AF428413_1 At1g64660/F1N19_22 [Arabidopsis thaliana] >gi|15450932|gb|AAK96737.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana] >gi|30387333|gb|AAP31932.1| At1g64660 [Arabidopsis thaliana] >gi|110740851|dbj|BAE98522.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana]	Unigene16888_All//3.00E-174//AT1G64660| ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase	Unigene16888_All//0.00E+00//TC138839		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -
Unigene1689_All	1480	0.85	1.30	0.47	1.78	1.12	2.17	1.29	3.73	12.27	6.17E-01	1.90E-01		-8.59E-01	1.74E-01		-6.76E-01	7.16E-02		2.80E-01	4.82E-01		1.54E+00	3.19E-10	Up	3.26E+00	2.81E-80	Up	Unigene1689_All//gi|90900944|gb|ABE01834.1|//4.00E-79//NAK-type protein kinase [Nicotiana tabacum]	Unigene1689_All//2.00E-66//AT5G47070| protein kinase, putative	Unigene1689_All//0.00E+00//TC144153				nr -
Unigene16891_All	907	2.83	12.29	2.99	0.88	1.75	0.80	0.79	0.97	3.03	2.12E+00	7.00E-25	Up	8.31E-02	8.31E-01		9.91E-01	6.19E-02		-1.42E-01	8.60E-01		2.88E-01	6.58E-01		1.94E+00	1.89E-07	Up	Unigene16891_All//gi|124359163|gb|ABN05686.1|//4.00E-20//Zinc finger, CCHC-type [Medicago truncatula]	Unigene16891_All//2.00E-07//AT2G01050| nucleic acid binding / zinc ion binding	Unigene16891_All//2.00E-23//ES817039				nr -
Unigene16892_All	733	1.86	1.66	2.40	4.42	5.26	1.85	1.67	2.74	1.47	-1.62E-01	7.58E-01		3.69E-01	4.72E-01		2.52E-01	4.83E-01		-1.26E+00	2.89E-04	Down	7.10E-01	8.37E-02		-1.89E-01	7.12E-01		Unigene16892_All//gi|159465411|ref|XP_001690916.1|//3.00E-06//extracellular matrix protein [Chlamydomonas reinhardtii] >gi|158279602|gb|EDP05362.1| extracellular matrix protein [Chlamydomonas reinhardtii]		Unigene16892_All//6.00E-14//C0116827				nr +
Unigene16893_All	1109	1.60	2.83	1.15	12.89	14.66	11.57	13.19	5.16	1.80	8.20E-01	1.97E-02		-4.77E-01	3.67E-01		1.85E-01	2.27E-01		-1.57E-01	3.75E-01		-1.35E+00	1.54E-21	Down	-2.88E+00	1.96E-58	Down	Unigene16893_All//gi|9454584|gb|AAF87907.1|AC015447_17//1.00E-34//Hypothetical protein [Arabidopsis thaliana]	Unigene16893_All//1.00E-22//AT1G21510| unknown protein					nr +
Unigene16894_All	1108	5.48	1.97	1.44	15.11	6.06	8.76	7.02	2.19	10.21	-1.48E+00	8.92E-09	Down	-1.93E+00	8.20E-12	Down	-1.32E+00	1.37E-23	Down	-7.86E-01	3.24E-09		-1.68E+00	5.40E-16	Down	5.40E-01	2.31E-04		Unigene16894_All//gi|15239865|ref|NP_199155.1|//8.00E-88//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565310|sp|Q9LSW9.1|ATL5K_ARATH RecName: Full=RING-H2 finger protein ATL5K; AltName: Full=RING-H2 finger protein ATL16 >gi|30725342|gb|AAP37693.1| At5g43420 [Arabidopsis thaliana]	Unigene16894_All//1.00E-78//AT5G43420| zinc finger (C3HC4-type RING finger) family protein	Unigene16894_All//0.00E+00//gi|48790107|gb|C0091421.1|C0091421				nr -
Unigene16895_All	1143	9.20	7.27	6.24	6.84	7.41	8.14	12.10	15.50	30.25	-3.40E-01	6.01E-02		-5.60E-01	2.22E-03		1.15E-01	6.16E-01		2.51E-01	2.33E-01		3.58E-01	2.60E-03		1.32E+00	3.97E-49	Up	Unigene16895_All//gi|46418371|gb|AAS99667.1|//4.00E-34//At5g54850 [Arabidopsis thaliana] >gi|48310353|gb|AAT41804.1| At5g54850 [Arabidopsis thaliana]	Unigene16895_All//6.00E-27//AT5G54850| unknown protein	Unigene16895_All//0.00E+00//TC158985				nr -
Unigene16896_All	659	2.62	4.92	3.64	6.12	5.49	3.29	6.29	4.88	2.18	9.09E-01	8.62E-03		4.73E-01	2.77E-01		-1.58E-01	6.25E-01		-8.96E-01	2.82E-03		-3.65E-01	1.96E-01		-1.53E+00	3.88E-08	Down	Unigene16896_All//gi|47606185|sp|Q8LFJ5.1|T112A_ARATH//3.00E-41//RecName: Full=TRM112-like protein At1g22270 >gi|30102552|gb|AAP21194.1| At1g22270 [Arabidopsis thaliana]	Unigene16896_All//4.00E-24//AT1G22270| unknown protein	Unigene16896_All//0.00E+00//gi|13245084|gb|BE054257.2|BE054257				nr +
Unigene16897_All	833	5.53	5.78	4.28	4.49	6.53	3.90	0.00	0.25	1.48	6.41E-02	8.18E-01		-3.68E-01	2.33E-01		5.42E-01	3.21E-02		-2.00E-01	5.95E-01		7.97E+00	7.85E-02		1.05E+01	6.29E-09	Up	Unigene16897_All//gi|224061845|ref|XP_002300627.1|//1.00E-46//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842353|gb|EEE79900.1| NAC domain protein, IPR003441 [Populus trichocarpa]		Unigene16897_All//0.00E+00//TC168317				nr +
Unigene16898_All	495	0.21	0.72	0.43	0.40	1.60	0.46	1.37	4.48	3.14	1.76E+00	2.18E-01		1.03E+00	5.92E-01		1.99E+00	2.46E-02		1.81E-01	9.35E-01		1.71E+00	3.46E-05	Up	1.20E+00	1.02E-02		Unigene16898_All//gi|115479571|ref|NP_001063379.1|//9.00E-08//Os09g0458900 [Oryza sativa Japonica Group] >gi|113631612|dbj|BAF25293.1| Os09g0458900 [Oryza sativa Japonica Group]		Unigene16898_All//3.00E-15//DW514872				nr +
Unigene16899_All	665	1.34	6.10	5.85	2.17	5.23	4.89	2.73	7.67	2.28	2.19E+00	7.93E-10	Up	2.13E+00	8.51E-09	Up	1.27E+00	9.94E-05	Up	1.17E+00	7.65E-04	Up	1.49E+00	4.14E-09	Up	-2.64E-01	5.57E-01		Unigene16899_All//gi|115479571|ref|NP_001063379.1|//1.00E-07//Os09g0458900 [Oryza sativa Japonica Group] >gi|113631612|dbj|BAF25293.1| Os09g0458900 [Oryza sativa Japonica Group]		Unigene16899_All//3.00E-15//DW514872		ko04626|Plant-pathogen interaction		nr -
Unigene1690_All	2431	19.59	6.00	8.76	17.19	10.30	17.13	34.00	12.22	32.53	-1.71E+00	1.65E-78	Down	-1.16E+00	1.55E-42	Down	-7.39E-01	2.02E-22		-5.30E-03	9.50E-01		-1.48E+00	1.39E-134	Down	-6.38E-02	2.75E-01		Unigene1690_All//gi|297800138|ref|XP_002867953.1|//0.00E+00//early-responsive to dehydration 3 [Arabidopsis lyrata subsp. lyrata] >gi|297313789|gb|EFH44212.1| early-responsive to dehydration 3 [Arabidopsis lyrata subsp. lyrata]	Unigene1690_All//0.00E+00//AT4G19120| ERD3 (early-responsive to dehydration 3)	Unigene1690_All//0.00E+00//TC135215				nr +
Unigene16900_All	1442	4.43	0.95	0.92	7.15	9.07	4.92	1.96	0.26	0.58	-2.22E+00	1.74E-15	Down	-2.26E+00	4.38E-15	Down	3.44E-01	2.75E-02		-5.40E-01	2.07E-03		-2.91E+00	1.31E-11	Down	-1.76E+00	6.35E-07	Down	Unigene16900_All//gi|6091551|gb|AAF01764.2|AF184277_1//2.00E-81//homeodomain-leucine zipper protein 56 [Glycine max]	Unigene16900_All//8.00E-54//AT2G22430| ATHB6; DNA binding / protein binding / sequence-specific DNA binding / transcription activator/ transcription factor	Unigene16900_All//0.00E+00//TC134486	HB			nr -
Unigene16903_All	1035	11.07	11.16	9.88	3.03	6.29	15.49	6.37	22.65	38.57	1.18E-02	9.69E-01		-1.64E-01	3.92E-01		1.05E+00	2.06E-06	Up	2.35E+00	4.96E-43	Up	1.83E+00	2.86E-52	Up	2.60E+00	1.73E-139	Up								
Unigene16904_All	727	37.57	31.08	15.53	359.80	409.96	410.45	12.15	38.98	10.25	-2.73E-01	1.02E-02		-1.27E+00	1.90E-28	Down	1.88E-01	1.75E-12		1.90E-01	1.39E-11		1.68E+00	4.48E-56	Up	-2.46E-01	1.68E-01		Unigene16904_All//gi|73921138|sp|Q9FX81.1|Y5258_ARATH//5.00E-36//RecName: Full=Uncharacterized protein At5g22580 >gi|40889664|pdb|1RJJ|A Chain A, Solution Structure Of A Homodimeric Hypothetical Protein, At5g22580, A Structural Genomics Target From Arabidopsis Thaliana >gi|40889665|pdb|1RJJ|B Chain B, Solution Structure Of A Homodimeric Hypothetical Protein, At5g22580, A Structural Genomics Target From Arabidopsis Thaliana >gi|14190417|gb|AAK55689.1|AF378886_1 AT5g22580/MQJ16_12 [Arabidopsis thaliana] >gi|15215901|gb|AAK91494.1| AT5g22580/MQJ16_12 [Arabidopsis thaliana]	Unigene16904_All//2.00E-29//AT5G22580| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Stress responsive alpha-beta barrel (InterPro:IPR013097), Dimeric alpha-beta barrel (InterPro:IPR011008); BEST Arabidopsis thaliana protein match is: HS1 (HEAT STABLE PROTEIN 1) (TAIR:AT3G17210.1); Has 231 Blast hits to 231 proteins in 57 species: Archae - 0; Bacteria - 89; Metazoa - 0; Fungi - 4; Plants - 98; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink).	Unigene16904_All//0.00E+00//TC169149				nr +
Unigene16905_All	1062	15.47	9.73	7.37	19.94	16.96	13.86	18.35	8.62	7.84	-6.69E-01	1.12E-06		-1.07E+00	2.96E-13	Down	-2.33E-01	5.58E-02		-5.24E-01	6.12E-06		-1.09E+00	1.84E-20	Down	-1.23E+00	2.70E-25	Down	Unigene16905_All//gi|18396594|ref|NP_566210.1|//3.00E-34//SWIB complex BAF60b domain-containing protein [Arabidopsis thaliana] >gi|28372894|gb|AAO39929.1| At3g03590 [Arabidopsis thaliana]	Unigene16905_All//3.00E-32//AT3G03590| SWIB complex BAF60b domain-containing protein	Unigene16905_All//0.00E+00//TC1319145				nr +
Unigene16906_All	602	103.08	52.77	71.29	435.01	348.59	309.02	237.81	106.36	92.25	-9.66E-01	1.31E-42		-5.32E-01	7.20E-15		-3.20E-01	6.08E-30		-4.93E-01	1.96E-59		-1.16E+00	1.29E-160	Down	-1.37E+00	5.93E-213	Down	Unigene16906_All//gi|211906466|gb|ACJ11726.1|//1.00E-116//serine hydroxymethyltransferase [Gossypium hirsutum]	Unigene16906_All//6.00E-111//AT4G13930| SHM4 (serine hydroxymethyltransferase 4); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene16906_All//0.00E+00//TC175310		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr -
Unigene16907_All	1164	9.35	9.75	11.39	394.06	336.96	320.37	15.91	4.60	5.58	6.06E-02	7.30E-01		2.85E-01	9.03E-02		-2.26E-01	4.78E-27		-2.99E-01	6.19E-41		-1.79E+00	2.32E-40	Down	-1.51E+00	8.37E-33	Down	Unigene16907_All//gi|124360377|gb|ABN08390.1|//3.00E-51//Harpin-induced 1 [Medicago truncatula]	Unigene16907_All//1.00E-42//AT5G11890| FUNCTIONS IN: molecular_function unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17620.1); Has 455 Blast hits to 454 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 453; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene16907_All//0.00E+00//TC154558				nr +
Unigene16908_All	1009	6.95	22.45	23.54	21.53	28.39	74.17	2257.82	1858.69	2273.17	1.69E+00	5.17E-37	Up	1.76E+00	8.27E-40	Up	4.00E-01	2.58E-05		1.78E+00	5.76E-140	Up	-2.81E-01	2.20E-202		9.80E-03	3.87E-01		Unigene16908_All//gi|224137856|ref|XP_002326457.1|//1.00E-123//aquaporin, MIP family, TIP subfamily [Populus trichocarpa] >gi|222823779|gb|EEE72256.1| aquaporin, MIP family, TIP subfamily [Populus trichocarpa]	Unigene16908_All//4.00E-103//AT4G17340| TIP2;2 (TONOPLAST INTRINSIC PROTEIN 2;2); water channel	Unigene16908_All//0.00E+00//TC152333				nr -
Unigene16909_All	1627	0.84	1.53	0.72	1.13	0.72	0.97	10.45	11.17	26.64	8.68E-01	3.16E-02		-2.16E-01	7.04E-01		-6.55E-01	1.64E-01		-2.22E-01	6.73E-01		9.72E-02	4.90E-01		1.35E+00	2.47E-63	Up	Unigene16909_All//gi|42566766|ref|NP_193135.2|//1.00E-132//exostosin family protein [Arabidopsis thaliana]	Unigene16909_All//5.00E-132//AT4G13990| exostosin family protein	Unigene16909_All//5.00E-07//TC130442				nr -
Unigene16910_All	1100	12.60	5.07	9.05	24.23	16.72	5.58	6.34	1.94	6.66	-1.31E+00	4.21E-16	Down	-4.78E-01	2.37E-03		-5.35E-01	2.55E-08		-2.12E+00	4.51E-64	Down	-1.71E+00	9.55E-15	Down	7.14E-02	7.31E-01		Unigene16910_All//gi|15237049|ref|NP_194461.1|//3.00E-40//zinc finger (B-box type) family protein [Arabidopsis thaliana]	Unigene16910_All//2.00E-28//AT5G54470| zinc finger (B-box type) family protein	Unigene16910_All//7.00E-172//DW507629	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr -
Unigene16912_All	1173	5.22	0.17	3.86	0.25	0.53	0.31	10.20	11.01	21.02	-4.92E+00	9.67E-30	Down	-4.36E-01	8.65E-02		1.05E+00	2.99E-01		2.74E-01	8.33E-01		1.10E-01	5.17E-01		1.04E+00	1.71E-24	Up	Unigene16912_All//gi|37544101|gb|AAQ93035.1|//4.00E-82//gibberellin 2-oxidase [Populus alba x Populus tremuloides]	Unigene16912_All//2.00E-64//AT1G02400| GA2OX6 (GIBBERELLIN 2-OXIDASE 6); gibberellin 2-beta-dioxygenase	Unigene16912_All//0.00E+00//gi|78324168|gb|DT544442.1|DT544442		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr -

Unigene16913_All	954	3.56	3.13	3.13	5.33	1.95	1.89	10.90	7.45	8.14	-1.86E-01	6.17E-01			-1.90E-01	6.25E-01		-1.45E+00	1.32E-08	Down	-1.49E+00	5.45E-08	Down	-5.50E-01	4.85E-04		-4.21E-01	6.40E-03		Unigene16913_All//gi|297807125|ref|XP_002871446.1|//4.00E-37//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317283|gb|EFH47705.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene16913_All//3.00E-36//AT5G10970| zinc finger (C2H2 type) family protein	Unigene16913_All//4.00E-25//TC163558	C2H2			nr -
Unigene16915_All	1035	0.86	1.57	1.13	5.20	13.18	5.93	0.74	1.98	1.50	8.66E-01	9.50E-02			3.97E-01	5.45E-01		1.34E+00	1.03E-18	Up	1.91E-01	4.88E-01		1.43E+00	6.34E-04	Up	1.03E+00	2.56E-02		Unigene16915_All//gi|24461867|gb|AN62354.1|AF506028_23//3.00E-40//CTV_22 [Citrus trifoliata]	Unigene16915_All//2.00E-33//AT1G15780| unknown protein	Unigene16915_All//0.00E+00//TC159919				nr -
Unigene16918_All	1075	4.23	3.54	4.90	2.87	2.98	1.22	1.81	1.17	0.59	-2.60E-01	3.78E-01			2.12E-01	4.57E-01		5.23E-02	9.04E-01		-1.24E+00	5.07E-04	Down	-6.33E-01	1.35E-01		-1.61E+00	1.60E-04	Down	Unigene16918_All//gi|14285713|sp|P82244.1|RK34_SPIOL//9.00E-42//RecName: Full=50S ribosomal protein L34, chloroplastic; AltName: Full=CL34; Flags: Precursor >gi|189096152|pdb|3BB0|4 Chain 4, Homology Model For The Spinach Chloroplast 50s Subunit Fitted To 9.4a Cryo-Em Map Of The 70s Chlororibosome >gi|7578860|gb|AAF64157.1|AF238221_1 plastid ribosomal protein L34 precursor [Spinacia oleracea]	Unigene16918_All//2.00E-21//AT1G29070| ribosomal protein L34 family protein	Unigene16918_All//8.00E-153//TC157238				nr -
Unigene16919_All	989	3.33	3.13	0.81	6.90	9.54	11.46	3.16	2.03	1.25	-9.28E-02	7.78E-01			-2.05E+00	3.53E-07	Down	4.67E-01	1.04E-02		7.32E-01	9.68E-06		-6.41E-01	4.19E-02		-1.34E+00	2.27E-05	Down	Unigene16919_All//gi|18394953|ref|NP_564135.1|//5.00E-54//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|111074298|gb|ABH04522.1| At1g21090 [Arabidopsis thaliana]	Unigene16919_All//2.00E-47//AT1G21090| hydroxyproline-rich glycoprotein family protein	Unigene16919_All//0.00E+00//DW240318				nr -
Unigene1692_All	411	1.27	14.05	2.72	0.61	2.01	1.65	1.13	0.20	0.78	3.46E+00	6.79E-22	Up		1.10E+00	1.10E-01		1.73E+00	3.97E-02		1.44E+00	1.28E-01		-2.48E+00	3.38E-02		-5.45E-01	5.66E-01		Unigene1692_All//gi|68300884|gb|AAY89374.1|//7.00E-17//beta-amylase 1 [Nicotiana langsdorffii x Nicotiana sanderae]	Unigene1692_All//3.00E-16//AT3G23920| BAM1 (BETA-AMYLASE 1); beta-amylase	Unigene1692_All//1.00E-59//TC177376		ko00500|Starch and sucrose metabolism		nr -
Unigene16920_All	935	0.78	2.01	0.80	4.74	4.46	4.11	0.81	2.41	2.39	1.36E+00	5.88E-03			2.54E-02	9.95E-01		-8.96E-02	8.03E-01		-2.08E-01	5.29E-01		1.57E+00	9.44E-05	Up	1.55E+00	8.57E-05	Up	Unigene16920_All//gi|115472049|ref|NP_001059623.1|//5.00E-59//Os02g0475800 [Oryza sativa Japonica Group] >gi|113611159|dbj|BAF21537.1| Os02g0475800 [Oryza sativa Japonica Group]	Unigene16920_All//1.00E-59//AT3G22660| rRNA processing protein-related	Unigene16920_All//2.00E-32//ES793919				nr -
Unigene16922_All	915	6.92	3.99	2.85	6.53	8.96	8.34	15.34	9.46	8.05	-7.95E-01	6.90E-04			-1.28E+00	4.26E-07	Down	4.55E-01	2.27E-02		3.53E-01	1.16E-01		-6.98E-01	1.81E-07		-9.30E-01	4.54E-12		Unigene16922_All//gi|297812685|ref|XP_002874226.1|//1.00E-112//methyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297320063|gb|EFH50485.1| methyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene16922_All//5.00E-113//AT5G24840| tRNA (guanine-N7-)-methyltransferase	Unigene16922_All//0.00E+00//gi|164364170|gb|ES850389.1|ES850389				nr -
Unigene16923_All	1172	0.67	0.22	1.09	4.08	2.41	2.47	4.62	2.39	1.87	-1.63E+00	5.37E-02			7.04E-01	2.54E-01		-7.60E-01	3.18E-03		-7.26E-01	7.68E-03		-9.51E-01	3.66E-05		-1.30E+00	2.46E-08	Down	Unigene16923_All//gi|240254592|ref|NP_181219.4|//6.00E-84//binding [Arabidopsis thaliana]	Unigene16923_All//3.00E-85//AT2G36810| binding	Unigene16923_All//0.00E+00//ES792803				nr -
Unigene16924_All	1566	15.44	10.13	15.54	1.11	0.48	0.58	8.15	2.35	0.61	-6.08E-01	4.26E-08			9.70E-03	9.57E-01		-1.20E+00	1.07E-02		-9.49E-01	5.80E-02		-1.80E+00	3.79E-28	Down	-3.74E+00	5.58E-65	Down	Unigene16924_All//gi|224086763|ref|XP_002307954.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222853930|gb|EEE91477.1| cytochrome P450 [Populus trichocarpa]	Unigene16924_All//3.00E-168//AT3G56630| CYP94D2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene16924_All//0.00E+00//TC147270		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene16925_All	1929	0.49	0.47	0.55	8.96	5.80	5.13	2.37	1.17	0.54	-4.62E-02	9.60E-01			1.78E-01	7.74E-01		-6.27E-01	2.88E-07		-8.05E-01	6.91E-10		-1.02E+00	6.50E-05	Down	-2.14E+00	1.47E-13	Down	Unigene16925_All//gi|15237490|ref|NP_199482.1|//2.00E-92//TRN2 (TORNADO 2) [Arabidopsis thaliana] >gi|9758506|dbj|BAB08914.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] >gi|56381915|gb|AAV85676.1| At5g46700 [Arabidopsis thaliana] >gi|110740669|dbj|BAE98437.1| senescence-associated protein 5-like protein [Arabidopsis thaliana]	Unigene16925_All//8.00E-94//AT5G46700| TRN2 (TORNADO 2)	Unigene16925_All//0.00E+00//TC151053				nr +
Unigene16927_All	661	5.54	2.15	2.34	7.69	7.50	5.06	4.86	4.11	5.24	-1.37E+00	4.36E-05	Down		-1.25E+00	2.90E-04	Down	-3.52E-02	9.02E-01		-6.04E-01	2.30E-02		-2.42E-01	4.78E-01		1.09E-01	7.17E-01					Unigene16927_All//0.00E+00//DW496376				
Unigene1693_All	2074	89.48	765.37	247.84	42.27	88.50	194.13	26.09	51.75	110.81	3.10E+00	0.00E+00	Up		1.47E+00	0.00E+00	Up	1.07E+00	2.38E-174	Up	2.20E+00	0.00E+00	Up	9.88E-01	9.49E-93		2.09E+00	0.00E+00	Up	Unigene1693_All//gi|68300884|gb|AAY89374.1|//0.00E+00//beta-amylase 1 [Nicotiana langsdorffii x Nicotiana sanderae]	Unigene1693_All//0.00E+00//AT3G23920| BAM1 (BETA-AMYLASE 1); beta-amylase	Unigene1693_All//0.00E+00//TC146925		ko00500|Starch and sucrose metabolism		nr -
Unigene16931_All	987	4.88	4.98	4.69	10.50	7.36	13.41	2.61	3.22	36.00	3.01E-02	9.29E-01			-5.52E-02	8.50E-01		-5.12E-01	2.16E-03		3.53E-01	2.64E-02		3.01E-01	3.81E-01		3.78E+00	4.70E-178	Up								ESTscan +
Unigene16933_All	669	3.99	5.07	2.07	1.64	2.37	5.06	10.81	8.50	3.04	3.47E-01	3.22E-01			-9.47E-01	1.97E-02		5.32E-01	3.40E-01		1.63E+00	4.44E-06	Up	-3.47E-01	8.61E-02		-1.83E+00	3.00E-17	Down				Unigene16933_All//0.00E+00//CO072977				
Unigene16935_All	868	10.73	3.97	16.32	7.52	9.28	8.06	0.39	0.24	0.87	-1.43E+00	1.59E-12	Down		6.05E-01	8.59E-05		3.04E-01	1.61E-01		1.01E-01	6.73E-01		-6.95E-01	5.78E-01		1.16E+00	1.06E-01		Unigene16935_All//gi|15224360|ref|NP_181908.1|//5.00E-33//formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] >gi|75097595|sp|Q22824.1|FH2_ARATH RecName: Full=Formin-like protein 2; Short=AtFH2; Short=AtFORMIN-2; Flags: Precursor		Unigene16935_All//1.00E-12//CO103513				nr +
Unigene16936_All	1258	1.08	0.16	0.55	1.23	2.22	2.05	6.86	1.30	2.47	-2.75E+00	1.08E-04	Down		-9.75E-01	1.09E-01		8.53E-01	2.13E-02		7.37E-01	6.76E-02		-2.40E+00	1.16E-27	Down	-1.47E+00	3.56E-15	Down	Unigene16936_All//gi|297810843|ref|XP_002873305.1|//1.00E-126//tudor domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319142|gb|EFH49564.1| tudor domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene16936_All//9.00E-107//AT5G07350| tudor domain-containing protein / nuclease family protein	Unigene16936_All//2.00E-169//TC137583				nr -
Unigene16937_All	784	20.09	20.36	38.10	4.96	5.45	3.23	6.96	1.33	0.51	1.93E-02	9.11E-01			9.24E-01	1.08E-18		1.36E-01	7.05E-01		-6.19E-01	4.72E-02		-2.38E+00	1.38E-17	Down	-3.78E+00	2.57E-28	Down	Unigene16937_All//gi|225431780|ref|XP_002271732.1|//3.00E-50//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene16937_All//4.00E-41//AT3G06840| unknown protein	Unigene16937_All//0.00E+00//gi|109870518|gb|DW499494.1|DW499494				nr -
Unigene16938_All	644	23.24	17.62	15.05	40.38	28.18	34.15	55.74	23.10	18.99	-3.99E-01	6.23E-03			-6.27E-01	2.73E-05		-5.19E-01	1.03E-07		-2.42E-01	2.98E-02		-1.27E+00	5.63E-47	Down	-1.55E+00	2.71E-65	Down	Unigene16938_All//gi|115469972|ref|NP_001058585.1|//2.00E-53//Os06g0715500 [Oryza sativa Japonica Group] >gi|113596625|dbj|BAF20499.1| Os06g0715500 [Oryza sativa Japonica Group]	Unigene16938_All//8.00E-45//AT2G21160| translocon-associated protein alpha (TRAP alpha) family protein	Unigene16938_All//0.00E+00//gi|84167716|gb|DR456364.1|DR456364		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene16939_All	779	1.01	4.88	2.39	11.64	10.83	9.97	7.44	2.47	4.50	2.28E+00	1.13E-09	Up		1.25E+00	1.41E-02		-1.04E-01	6.32E-01		-2.23E-01	3.05E-01		-1.59E+00	3.06E-11	Down	-7.24E-01	6.68E-04		Unigene16939_All//gi|297843986|ref|XP_002889874.1|//9.00E-44//T23J18.22 [Arabidopsis lyrata subsp. lyrata] >gi|297335716|gb|EFH66133.1| T23J18.22 [Arabidopsis lyrata subsp. lyrata]	Unigene16939_All//2.00E-43//AT1G11570| nuclear transport factor 2 (NTF2), putative					nr +
Unigene1694_All	1947	12.58	6.95	7.79	21.90	21.90	20.88	19.63	9.45	18.33	-8.56E-01	3.12E-14			-6.90E-01	1.38E-09		-3.00E-04	9.94E-01		-6.91E-02	5.01E-01		-1.06E+00	2.36E-37	Down	-9.86E-02	2.49E-01		Unigene1694_All//gi|297839313|ref|XP_002887538.1|//0.00E+00//galactosyl transferase GMA12/MNN10 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333379|gb|EFH63797.1| galactosyl transferase GMA12/MNN10 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1694_All//0.00E+00//AT1G74380| XXT5 (XYLOGLUCAN XYLOSYLTRANSFERASE 5); transferase/ transferase, transferring glycosyl groups / xyloglucan 6-xylosyltransferase	Unigene1694_All//0.00E+00//TC150744				nr +
Unigene16940_All	1310	0.96	91.94	173.41	5.06	7.68	2.62	0.26	0.13	0.18	6.58E+00	0.00E+00	Up		7.50E+00	0.00E+00	Up	6.02E-01	4.43E-04		-9.49E-01	2.44E-05		-1.02E+00	4.00E-01		-5.01E-01	6.49E-01		Unigene16940_All//gi|161610920|gb|ABX75139.1|//1.00E-178//lipase [Gossypium hirsutum]	Unigene16940_All//2.00E-147//AT5G33370| GDSL-motif lipase/hydrolase family protein	Unigene16940_All//0.00E+00//TC131468				nr +
Unigene16943_All	1067	0.59	8.64	2.65	0.56	4.16	7.20	2.30	10.22	15.12	3.88E+00	6.19E-38	Up		2.17E+00	1.09E-06	Up	2.89E+00	3.21E-16	Up	3.68E+00	2.37E-32	Up	2.15E+00	1.96E-30	Up	2.72E+00	1.18E-59	Up		Unigene16943_All//1.00E-06//AT1G45249| ABF2 (ABSCISIC ACID RESPONSIVE ELEMENTS-BINDING FACTOR 2); DNA binding / protein binding / transcription activator/ transcription factor	Unigene16943_All//7.00E-33//TC173371	bZIP			nr +
Unigene16946_All	1345	1.17	0.72	1.07	3.59	0.56	0.97	181.22	38.97	21.47	-7.05E-01	1.80E-01			-1.27E-01	8.07E-01		-2.67E+00	4.52E-18	Down	-1.88E+00	2.26E-10	Down	-2.22E+00	0.00E+00	Down	-3.08E+00	0.00E+00	Down	Unigene16946_All//gi|237687961|gb|ACR14981.1|//2.00E-80//FIT1 [Arabidopsis halleri subsp. gemmifera]	Unigene16946_All//6.00E-64//AT2G28160| FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor	Unigene16946_All//6.00E-34//CA994022	bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene16948_All	2086	0.00	0.19	0.00	2.15	1.93	2.14	5.84	7.63	37.24	7.60E+00	1.36E-02			null	null		-1.54E-01	6.18E-01		-3.90E-03	9.85E-01		3.87E-01	2.07E-03		2.67E+00	9.20E-280	Up	Unigene16948_All//gi|115466740|ref|NP_001056969.1|//1.00E-166//Os06g0179500 [Oryza sativa Japonica Group] >gi|24413990|dbj|BAC22241.1| pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa Japonica Group] >gi|113595009|dbj|BAF18883.1| Os06g0179500 [Oryza sativa Japonica Group]	Unigene16948_All//1.00E-136//AT3G02650| pentatricopeptide (PPR) repeat-containing protein	Unigene16948_All//0.00E+00//TC154413				nr -
Unigene16950_All	1047	14.29	5.47	10.38	15.51	10.36	19.67	24.39	11.50	7.65	-1.39E+00	1.03E-18	Down		-4.62E-01	2.16E-03		-5.82E-01	4.51E-06		3.43E-01	5.00E-03		-1.09E+00	2.37E-26	Down	-1.67E+00	6.57E-52	Down	Unigene16950_All//gi|4510390|gb|AAD21478.1|//2.00E-80//expressed protein [Arabidopsis thaliana] >gi|14596215|gb|AAK68835.1| Unknown protein [Arabidopsis thaliana] >gi|20197529|gb|AAM15115.1| expressed protein [Arabidopsis thaliana]	Unigene16950_All//1.00E-69//AT2G35790| unknown protein	Unigene16950_All//0.00E+00//TC131990				nr +
Unigene16951_All	1115	0.38	0.09	0.57	10.90	9.60	6.36	2.24	0.52	0.64	-2.05E+00	1.21E-01			6.10E-01	5.09E-01		-1.83E-01	3.07E-01		-7.78E-01	9.11E-07		-2.09E+00	2.75E-07	Down	-1.80E+00	2.33E-06	Down	Unigene16951_All//gi|15219751|ref|NP_176853.1|//5.00E-62//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75262243|sp|Q9C9N3.1|C3H14_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 14; Short=AtC3H14	Unigene16951_All//1.00E-57//AT1G66810| zinc finger (CCCH-type) family protein		C3H			nr +
Unigene16953_All	1076	5.06	5.04	7.82	5.05	13.22	4.99	0.71	0.54	1.30	-5.20E-03	9.80E-01			6.29E-01	2.39E-03		1.39E+00	1.57E-20	Up	-1.48E-02	9.49E-01		-3.79E-01	6.35E-01		8.74E-01	7.41E-02		Unigene16953_All//gi|92893902|gb|ABE91952.1|//4.00E-15//Zinc finger, CCHC-type [Medicago truncatula]	Unigene16953_All//5.00E-16//AT2G01050| nucleic acid binding / zinc ion binding	Unigene16953_All//1.00E-19//TC175764				nr -
Unigene16954_All	541	14.70	10.21	8.46	20.99	11.08	16.28	29.70	19.62	13.11	-5.26E-01	1.07E-02			-7.96E-01	2.02E-04		-9.23E-01	3.23E-09		-3.67E-01	3.36E-02		-5.98E-01	1.34E-06		-1.18E+00	8.56E-20	Down				Unigene16954_All//0.00E+00//gi|21100384|gb|BQ412697.1|BQ412697				

Unigene16956_All	656	2.95	5.48	1.79	3.19	2.78	2.41	72.57	86.78	533.15	8.94E-01	6.08E-03		-7.25E-01	1.38E-01		-1.97E-01	6.76E-01		-4.04E-01	3.93E-01		2.58E-01	4.09E-05		2.88E+00	0.00E+00	Up	Unigene16956_All//gi|29468498|gb|AA085554.1|//4.00E-13//3-hydroxy-3-methylglutaryl-CoA reductase [Nicotiana attenuata]	Unigene16956_All//1.00E-12//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene16956_All//8.00E-44//TC159539		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene16957_All	1381	2.27	1.36	1.31	6.46	4.94	7.36	5.91	8.84	29.11	-7.44E-01	3.38E-02		-7.94E-01	3.07E-02		-3.87E-01	4.19E-02		1.89E-01	3.72E-01		5.81E-01	5.50E-05		2.30E+00	5.71E-122	Up	Unigene16957_All//gi|297797667|ref|XP_002866718.1|//1.00E-103//MAPKKK19 [Arabidopsis lyrata subsp. lyrata] >gi|297312553|gb|EFH42977.1|MAPKKK19 [Arabidopsis lyrata subsp. lyrata]	Unigene16957_All//2.00E-95//AT4G36950| MAPKKK21; ATP binding / protein kinase/ protein serine/threonine kinase	Unigene16957_All//0.00E+00//DW492589		ko04626|Plant-pathogen interaction		nr +
Unigene16960_All	1641	17.09	18.74	6.23	6.04	9.46	26.39	1.19	0.28	0.51	1.33E-01	2.15E-01		-1.46E+00	1.19E-35	Down	6.48E-01	9.98E-07		2.13E+00	2.79E-102	Up	-2.08E+00	8.32E-06	Down	-1.22E+00	2.83E-03		Unigene16960_All//gi|225451804|ref|XP_002281338.1|//0.00E+00//PREDICTED: brassinosteroid-6-oxidase [Vitis vinifera]	Unigene16960_All//0.00E+00//AT3G30180| BR6OX2 (BRASSINOSTEROID-6-OXIDASE 2); monooxygenase/ oxygen binding	Unigene16960_All//0.00E+00//TC166913		ko00905|Brassinosteroid biosynthesis		nr +
Unigene16962_All	731	30.99	33.55	21.78	14.58	24.73	29.53	5.44	14.35	8.50	1.14E-01	3.71E-01		-5.09E-01	1.79E-05		7.62E-01	4.16E-10		1.02E+00	1.32E-17	Up	1.40E+00	1.96E-16	Up	6.45E-01	1.67E-03		Unigene16962_All//gi|119720804|gb|ABL97972.1|//1.00E-09//serine-rich protein [Brassica rapa]	Unigene16962_All//2.00E-10//AT5G11090| serine-rich protein-related	Unigene16962_All//2.00E-23//gi|109836412|gb|DW234973.1|DW234973				nr -
Unigene16963_All	1396	21.78	4.83	10.38	7.21	7.23	4.01	0.00	0.06	0.00	-2.17E+00	2.02E-69	Down	-1.07E+00	5.03E-24	Down	3.90E-03	9.89E-01		-8.45E-01	1.69E-06		5.90E+00	4.02E-01		null	null		Unigene16963_All//gi|42569882|ref|NP_181827.2|//1.00E-128//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75116667|sp|Q67Z19.1|GDL48_ARATH RecName: Full=GDSL esterase/lipase At2g42990; AltName: Full=Extracellular lipase At2g42990; Flags: Precursor	Unigene16963_All//6.00E-128//AT2G42990| GDSL-motif lipase/hydrolase family protein	Unigene16963_All//0.00E+00//TC167143				nr -
Unigene16964_All	1484	0.81	0.34	0.43	2.82	0.86	5.48	3.48	7.69	11.87	-1.25E+00	4.69E-02		-9.13E-01	1.57E-01		-1.72E+00	4.74E-09	Down	9.58E-01	2.08E-06		1.15E+00	3.06E-13	Up	1.77E+00	1.47E-38	Up	Unigene16964_All//gi|224146393|ref|XP_002325991.1|//1.00E-114//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222862866|gb|EEF00373.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene16964_All//1.00E-83//AT1G71930| VND7 (VASCULAR RELATED NAC-DOMAIN PROTEIN 7); transcription activator/ transcription factor/ transcription regulator	Unigene16964_All//8.00E-12//gi|109882837|gb|DW511807.1|DW511807	NAC			nr -
Unigene16966_All	1640	17.00	27.71	33.38	20.38	31.52	36.63	0.00	0.00	0.53	7.05E-01	1.45E-18		9.73E-01	7.74E-37		6.29E-01	3.03E-20		8.46E-01	2.25E-35		null	null		9.06E+00	2.05E-06	Up	Unigene16966_All//gi|75265643|gb|AB418631.1|//1.00E-177//L-6-rhamnosyltransferase [Citrus sinensis]	Unigene16966_All//3.00E-95//AT5G54010| glycosyltransferase family protein	Unigene16966_All//0.00E+00//CO081406		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis		nr +
Unigene16967_All	1457	0.00	0.00	0.15	30.19	7.94	2.26	9.40	10.64	5.96	null	null		7.19E+00	1.41E-01		-1.93E+00	8.60E-108	Down	-3.74E+00	3.55E-193	Down	1.79E-01	2.07E-01		-6.58E-01	6.78E-07		Unigene16967_All//gi|15225480|ref|NP_181483.1|//1.00E-130//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|3355480|gb|AAC27842.1| nodulin-like protein [Arabidopsis thaliana] >gi|30017241|gb|AAP12854.1| At2g39510 [Arabidopsis thaliana] >gi|110743791|dbj|BAE99731.1| nodulin-like protein [Arabidopsis thaliana]	Unigene16967_All//9.00E-119//AT2G39510| nodulin MtN21 family protein	Unigene16967_All//0.00E+00//DW499133				nr +
Unigene16969_All	658	5.41	4.70	8.66	8.93	4.55	4.74	7.58	5.65	3.75	-2.03E-01	5.63E-01		6.79E-01	8.70E-03		-9.72E-01	1.84E-05		-9.16E-01	1.41E-04		-4.24E-01	8.62E-02		-1.01E+00	1.76E-05	Down	Unigene16969_All//gi|4803949|gb|AAD29822.1|//7.00E-38//expressed protein [Arabidopsis thaliana] >gi|20197701|gb|AAM15213.1| expressed protein [Arabidopsis thaliana] >gi|106879159|gb|ABF82609.1| At2g20940 [Arabidopsis thaliana]	Unigene16969_All//1.00E-31//AT2G20940| unknown protein	Unigene16969_All//0.00E+00//gi|109874725|gb|DW503699.1|DW503699				nr -
Unigene16970_All	1450	3.43	9.57	5.47	8.28	7.17	11.15	13.88	13.95	14.45	1.48E+00	4.49E-19	Up	6.75E-01	1.62E-03		-2.07E-01	2.44E-01		4.30E-01	1.81E-03		7.40E-03	9.86E-01		5.83E-02	6.45E-01		Unigene16970_All//gi|15230124|ref|NP_189092.1|//5.00E-48//transcription factor [Arabidopsis thaliana]	Unigene16970_All//8.00E-40//AT5G24490| transcription factor	Unigene16970_All//0.00E+00//TC157245	Trihelix			nr +
Unigene16971_All	726	61.55	42.64	57.94	60.11	65.41	69.67	97.20	70.98	39.40	-5.29E-01	2.67E-11		-8.70E-02	3.75E-01		1.22E-01	1.57E-01		2.13E-01	5.13E-03		-4.53E-01	3.61E-16		-1.30E+00	5.94E-98	Down	Unigene16971_All//gi|18401879|ref|NP_566608.1|//4.00E-31//NADH-ubiquinone oxidoreductase-related [Arabidopsis thaliana] >gi|186510194|ref|NP_001118655.1| NADH-ubiquinone oxidoreductase-related [Arabidopsis thaliana] >gi|14336154|gb|AAK59857.1| AT3g18410/MYF24_I2 [Arabidopsis thaliana] >gi|186535069|gb|AAL76140.1| AT3g18410/MYF24_I2 [Arabidopsis thaliana]	Unigene16971_All//2.00E-32//AT3G18410| NADH-ubiquinone oxidoreductase-related	Unigene16971_All//0.00E+00//TC160830		ko00190|Oxidative phosphorylation		nr -
Unigene16972_All	1364	0.31	0.11	0.16	4.93	2.42	1.46	5.46	5.12	19.07	-1.46E+00	2.34E-01		-9.74E-01	4.12E-01		-1.02E+00	1.13E-06	Down	-1.76E+00	5.37E-13	Down	-9.24E-02	6.66E-01		1.81E+00	4.59E-58	Up	Unigene16972_All//gi|224064167|ref|XP_002301396.1|//2.00E-72//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222843122|gb|EEE80669.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene16972_All//2.00E-44//AT3G61630| CRF6 (CYTOKININ RESPONSE FACTOR 6); DNA binding / transcription factor	Unigene16972_All//0.00E+00//TC140582	AP2-EREBP			nr +
Unigene16976_All	770	15.76	14.54	10.65	12.03	16.55	16.54	6.75	0.92	1.76	-1.16E-01	5.27E-01		-5.66E-01	7.82E-04		4.60E-01	2.50E-03		4.59E-01	3.59E-03		-2.87E+00	1.73E-20	Down	-1.94E+00	1.33E-13	Down	Unigene16976_All//gi|115462353|ref|NP_001054776.1|//2.00E-26//Os05g0171900 [Oryza sativa Japonica Group] >gi|113578327|dbj|BAF16690.1| Os05g0171900 [Oryza sativa Japonica Group]	Unigene16976_All//5.00E-27//AT1G15380| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene16976_All//0.00E+00//TC146059				nr +
Unigene16977_All	861	29.72	24.83	26.66	30.66	36.60	42.44	6.92	0.49	1.57	-2.59E-01	1.97E-02		-1.57E-01	2.07E-01		2.55E-01	7.23E-03		4.69E-01	4.97E-08		-3.83E+00	3.44E-30	Down	-2.14E+00	1.96E-17	Down	Unigene16977_All//gi|226500126|ref|NP_001149571.1|//9.00E-41//lactoylglutathione lyase [Zea mays] >gi|195628124|gb|ACG35892.1| lactoylglutathione lyase [Zea mays]	Unigene16977_All//6.00E-37//AT1G15380| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene16977_All//0.00E+00//TC146059				nr -
Unigene16979_All	721	1.45	0.35	1.18	29.71	29.95	23.05	4.46	8.64	12.60	-2.05E+00	6.29E-03		-2.97E-01	6.42E-01		1.15E-02	9.52E-01		-3.66E-01	1.91E-03		9.55E-01	7.59E-06		1.50E+00	3.60E-16	Up	Unigene16979_All//gi|8096279|dbj|BAA95794.1|//7.00E-16//DC1.2 homologue [Nicotiana tabacum]	Unigene16979_All//9.00E-16//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene16979_All//7.00E-134//TC151282		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene1698_All	2603	12.48	15.03	17.33	13.74	23.83	31.34	4.45	4.98	4.48	2.68E-01	2.08E-03		4.73E-01	5.16E-09		7.94E-01	3.44E-36		1.19E+00	1.51E-83	Up	1.62E-01	3.14E-01		1.09E-02	9.66E-01		Unigene1698_All//gi|224130624|ref|XP_002320887.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222861660|gb|EEE99202.1| cytochrome P450 [Populus trichocarpa]	Unigene1698_All//0.00E+00//AT3G61880| CYP78A9 (CYTOCHROME P450 78A9); monooxygenase/ oxygen binding	Unigene1698_All//0.00E+00//TC154566		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene16980_All	1314	2.07	5.13	2.31	7.70	5.95	2.92	0.87	0.13	2.18	1.31E+00	4.00E-08	Up	1.58E-01	6.63E-01		-3.71E-01	3.61E-02		-1.40E+00	6.24E-14	Down	-2.77E+00	7.62E-05	Down	1.33E+00	6.91E-05	Up	Unigene16980_All//gi|254935149|gb|ACT87982.1|//1.00E-153//gibberellin 2-oxidase [Jatropha curcas]	Unigene16980_All//8.00E-125//AT1G30040| ATGA2OX2 (GIBBERELLIN 2-OXIDASE); gibberellin 2-beta-dioxygenase	Unigene16980_All//0.00E+00//DW508045		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene16981_All	830	10.65	10.13	12.00	15.12	21.99	11.86	6.27	11.18	2.21	-7.21E-02	7.26E-01		1.71E-01	3.90E-01		5.40E-01	8.40E-06		-3.51E-01	3.20E-02		8.35E-01	8.35E-07		-1.50E+00	9.03E-10	Down	Unigene16981_All//gi|20197722|gb|AAM15224.1|//3.00E-12//Expressed protein [Arabidopsis thaliana]		Unigene16981_All//0.00E+00//TC163180				nr -
Unigene16982_All	1521	4.40	1.33	1.37	9.37	11.32	11.79	12.06	7.06	3.14	-1.72E+00	8.34E-12	Down	-1.69E+00	6.04E-11	Down	2.73E-01	4.51E-02		3.32E-01	1.28E-02		-7.73E-01	3.43E-11		-1.94E+00	6.83E-46	Down	Unigene16982_All//gi|15234049|ref|NP_192013.1|//1.00E-103//glycosyl hydrolase family 18 protein [Arabidopsis thaliana]	Unigene16982_All//1.00E-97//AT4G01040| glycosyl hydrolase family 18 protein	Unigene16982_All//0.00E+00//gi|78334114|gb|DT554388.1|DT554388				nr +
Unigene16985_All	763	7.20	15.74	14.03	13.91	30.82	29.24	0.33	0.11	0.21	1.13E+00	3.73E-11	Up	9.62E-01	1.42E-07		1.15E+00	2.81E-25	Up	1.07E+00	9.83E-20	Up	-1.60E+00	3.11E-01		-6.71E-01	6.05E-01		Unigene16985_All//gi|192910830|gb|ACF06523.1|//1.00E-93//vacuolar ATP synthase subunit E [Elaeis guineensis]	Unigene16985_All//7.00E-86//AT3G08560| VHA-E2 (VACUOLAR H+-ATPASE SUBUNIT E ISOFORM 2); hydrogen-exporting ATPase, phosphorylative mechanism / proton-transporting ATPase, rotational mechanism	Unigene16985_All//0.00E+00//DW225406		ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene16986_All	463	11.87	28.78	18.63	17.54	22.39	18.92	75.34	158.25	96.28	1.28E+00	8.32E-15	Up	6.51E-01	1.41E-03		3.52E-01	4.96E-02		1.10E-01	6.34E-01		1.07E+00	1.96E-72	Up	3.54E-01	3.67E-07		Unigene16986_All//gi|226506006|ref|NP_001152306.1|//2.00E-46//glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a [Zea mays] >gi|195654913|gb|ACG46924.1| glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a [Zea mays]	Unigene16986_All//2.00E-36//AT3G06860| MFP2 (MULTIFUNCTIONAL PROTEIN 2); 3-hydroxyacyl-CoA dehydrogenase/ enoyl-CoA hydratase	Unigene16986_All//5.00E-140//gi|164329559|gb|ES830892.1|ES830892		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene16987_All	380	15.97	36.67	21.86	14.55	25.55	26.62	54.63	124.29	62.27	1.20E+00	4.79E-14	Up	4.53E-01	3.30E-02		8.13E-01	2.93E-06		8.72E-01	9.14E-07		1.19E+00	3.21E-55	Up	1.89E-01	6.80E-02		Unigene16987_All//gi|167962162|dbj|BAG09370.1|//1.00E-56//peroxisomal fatty acid beta-oxidation multifunctional protein [Glycine max]	Unigene16987_All//3.00E-56//AT3G06860| MFP2 (MULTIFUNCTIONAL PROTEIN 2); 3-hydroxyacyl-CoA dehydrogenase/ enoyl-CoA hydratase	Unigene16987_All//0.00E+00//gi|164329559|gb|ES830892.1|ES830892		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene16989_All	767	173.20	126.18	115.25	233.74	199.56	322.21	219.78	122.50	94.17	-4.57E-01	1.16E-24		-5.88E-01	3.24E-37		-2.28E-01	4.91E-11		4.63E-01	9.66E-50		-8.43E-01	1.38E-111		-1.22E+00	5.63E-211	Down	Unigene16989_All//gi|62287477|sp|Q96SM1.1|RS11_DIPES//2.00E-85//RecName: Full=40S ribosomal protein S11 >gi|6984142|gb|AAF34771.1|AF227626_1 40S ribosomal protein S11 [Euphorbia esula]	Unigene16989_All//3.00E-74//AT5G23740| RPS11-BETA (RIBOSOMAL PROTEIN S11-BETA); structural constituent of ribosome	Unigene16989_All//0.00E+00//gi|13353640|gb|BG443988.1|BG443988		ko03010|Ribosome		nr -
Unigene16990_All	622	4.79	0.49	0.77	12.89	13.90	18.66	27.19	68.74	73.34	-3.29E+00	3.33E-11	Down	-2.64E+00	1.23E-08	Down	1.08E-01	6.42E-01		5.33E-01	1.20E-03		1.34E+00	2.66E-60	Up	1.43E+00	1.15E-72	Up	Unigene16990_All//gi|124360185|gb|ABN08198.1|//3.00E-16//Glutamine amidotransferase, class I, active site [Medicago truncatula]	Unigene16990_All//9.00E-14//AT3G12670| emb2742 (embryo defective 2742); CTP synthase/ catalytic	Unigene16990_All//0.00E+00//TC176389		ko00240|Pyrimidine metabolism		nr +
Unigene16992_All	1366	4.94	4.90	6.39	11.41	9.08	9.52	16.22	5.14	7.70	-1.31E-02	9.76E-01		3.72E-01	7.69E-02		-3.31E-01	1.68E-02		-2.62E-01	8.07E-02		-1.66E+00	3.06E-43	Down	-1.07E+00	2.54E-23	Down	Unigene16992_All//gi|209976078|gb|ACJ04083.1|//1.00E-133//cyclopropyl isomerase [Solanum lycopersicum]	Unigene16992_All//5.00E-134//AT5G50375| CPI1 (CYCLOPROPYL ISOMERASE); cycloeucalenol cycloisomerase	Unigene16992_All//0.00E+00//gi|164360110|gb|ES833819.1|ES833819		ko00100|Steroid biosynthesis		nr -
Unigene16996_All	728	1.01	192.59	13.39	23.40	13.58	16.01	12.84	19.92	30.37	7.58E+00	0.00E+00	Up	3.73E+00	5.94E-38	Up	-7.86E-01	2.07E-10		-5.48E-01	2.82E-05		6.34E-01	1.30E-06		1.24E+00	7.00E-29	Up	Unigene16996_All//gi|20197506|gb|AAM15100.1|//3.00E-19//Expressed protein [Arabidopsis thaliana]	Unigene16996_All//6.00E-21//AT2G25625| unknown protein	Unigene16996_All//0.00E+00//TC178393				nr +
Unigene16997_All	2269	0.25	0.27	0.14	0.18	0.15	0.20	19.38	23.23	55.85	7.97E-02	9.41E-01		-8.49E-01	3.97E-01		-2.10E-01	8.25E-01		1.81E-01	8.84E-01		2.61E-01	6.71E-05		1.53E+00	1.09E-220	Up	Unigene16997_All//gi|148362072|gb|ABQ59612.1|//0.00E+00//L1XX4 [Glycine max]	Unigene16997_All//4.00E-144//AT2G23770| protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	Unigene16997_All//6.00E-174//TC157480		ko04626|Plant-pathogen interaction		nr +

Unigene16998_All	1338	0.35	0.68	1.00	3.31	2.93	6.14	3.95	29.83	7.95	9.54E-01	1.96E-01		1.50E+00	1.84E-02		-1.76E-01	5.85E-01		8.91E-01	8.29E-06		2.92E+00	3.83E-155	Up	1.01E+00	1.59E-10	Up	Unigene16998_All//gi|297803740|ref|XP_002869754.1|//1.00E-155//UDP-D-glucose/UDP-D-galactose 4-epimerase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297315590|gb|EFH46013.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene16998_All//8.00E-148//AT4G23920| UGE2 (UDP-D-glucose/UDP-D-galactose 4-epimerase 2); UDP-glucose 4-epimerase/ protein dimerization	Unigene16998_All//4.00E-44//TC132041		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism		nr -
Unigene17_All	2081	0.73	0.90	1.66	1.56	1.64	1.43	5.63	4.02	2.14	3.05E-01	5.31E-01		1.19E+00	7.37E-04	Up	7.44E-02	8.46E-01		-1.19E-01	7.42E-01		-4.87E-01	1.00E-03		-1.39E+00	1.03E-18	Down	Unigene17_All//gi|140072141|gb|ABO84808.1|//1.00E-138//Chaperonin Cpn60/TCP-1; Phosphatidylinositol-4-phosphate 5-kinase; Zinc finger, FYVE/PHD-type [Medicago truncatula]	Unigene17_All//1.00E-112//AT4G33240| 1-phosphatidylinositol-4-phosphate 5-kinase/ ATP binding / phosphatidylinositol phosphate kinase/ protein binding / zinc ion binding	Unigene17_All//3.00E-166//C0129735		ko04145|Phagosome//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene1700_All	354	2.07	1.43	2.71	7.32	3.99	1.79	7.41	3.07	1.01	-5.32E-01	5.13E-01		3.88E-01	6.08E-01		-8.76E-01	1.86E-02		-2.03E+00	2.14E-06	Down	-1.27E+00	3.66E-04	Down	-2.87E+00	4.82E-11	Down	Unigene1700_All//gi|73761697|gb|AAZ83348.1|//6.00E-56//CDPK-related protein kinase [Gossypium hirsutum]	Unigene1700_All//3.00E-54//AT3G50530| CRK (CDPK-related kinase); ATP binding / calcium ion binding / calcium-dependent protein serine/threonine phosphatase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene1700_All//1.00E-31//ES806800				nr +
Unigene17001_All	629	1.66	2.26	3.13	14.18	18.12	13.93	8.87	1.66	8.49	4.39E-01	4.26E-01		9.13E-01	5.88E-02		3.54E-01	3.63E-02		-2.53E-02	9.25E-01		-2.42E+00	2.92E-18	Down	-6.41E-02	7.84E-01		Unigene17001_All//gi|18390998|ref|NP_563839.1|//6.00E-34//transcription factor [Arabidopsis thaliana] >gi|75278846|sp|Q80482.1|BH149_ARATH RecName: Full=Transcription factor bHLH149; AltName: Full=Transcription factor EN 144; AltName: Full=bHLH transcription factor bHLH149; AltName: Full=Basic helix-loop-helix protein 149; Short=bHLH 149; Short=AtbHLH149 >gi|3249098|gb|AAC24081.1| ESTs gb|T04610, gb|N38459, gb|T45174, gb|R30181 and gb|N64971 come from this gene [Arabidopsis thaliana] >gi|27764992|gb|AAO23617.1| At1g09250 [Arabidopsis thaliana]	Unigene17001_All//4.00E-31//AT1G09250| transcription factor	Unigene17001_All//2.00E-133//gi|109836342|gb|DW234903.1|DW234903				nr -
Unigene17003_All	1279	5.03	18.54	6.45	1.21	1.53	2.33	0.00	0.00	0.50	1.88E+00	9.47E-45	Up	3.59E-01	9.77E-02		3.46E-01	5.18E-01		9.49E-01	9.14E-03		null	null		8.96E+00	9.33E-05	Up	Unigene17003_All//gi|226491140|ref|NP_001148789.1|//1.00E-123//ER lumen protein retaining receptor C28H8. 4 [Zea mays] >gi|195622166|gb|ACG32913.1| ER lumen protein retaining receptor C28H8. 4 [Zea mays]	Unigene17003_All//5.00E-115//AT1G75760| ER lumen protein retaining receptor family protein	Unigene17003_All//0.00E+00//gi|78323142|gb|DT543416.1|DT543416				nr -
Unigene17004_All	2061	0.15	0.15	0.36	18.39	5.71	10.61	7.96	0.93	7.91	-4.62E-02	9.85E-01		1.25E+00	1.54E-01		-1.69E+00	5.55E-77	Down	-7.94E-01	1.77E-20		-3.09E+00	3.80E-68	Down	-9.80E-03	9.63E-01		Unigene17004_All//gi|294471310|gb|ADE80897.1|//0.00E+00//9-cis-epoxycarotenoid dioxygenase [Camelina sativa]	Unigene17004_All//0.00E+00//AT3G24220| NCED6 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 6); 9-cis-epoxycarotenoid dioxygenase	Unigene17004_All//2.00E-07//TC149428		ko00906|Carotenoid biosynthesis		nr -
Unigene17009_All	943	0.55	4.89	0.56	3.28	2.30	2.39	12.15	12.10	8.70	3.14E+00	3.86E-16	Up	2.55E-02	9.99E-01		-5.10E-01	1.50E-01		-4.52E-01	2.28E-01		-6.00E-03	1.01E+00		-4.82E-01	9.36E-04		Unigene17009_All//gi|10177960|dbj|BAB11343.1|//1.00E-129//cytochrome c1 precursor [Arabidopsis thaliana]	Unigene17009_All//2.00E-130//AT5G40810| cytochrome c1, putative	Unigene17009_All//0.00E+00//gi|109868749|gb|DW497725.1|DW497725		ko00190|Oxidative phosphorylation		nr -
Unigene1701_All	2241	4.97	2.40	3.49	23.74	19.61	9.45	10.41	3.21	3.59	-1.05E+00	1.96E-09	Down	-5.10E-01	4.09E-03		-2.76E-01	4.77E-05		-1.33E+00	8.21E-66	Down	-1.70E+00	4.22E-47	Down	-1.54E+00	4.49E-42	Down	Unigene1701_All//gi|224081597|ref|XP_002306462.1|//0.00E+00//CPK related kinase 5 [Populus trichocarpa] >gi|222855911|gb|EEE93458.1| CPK related kinase 5 [Populus trichocarpa]	Unigene1701_All//0.00E+00//AT3G50530| CRK (CDPK-related kinase); ATP binding / calcium ion binding / calcium-dependent protein serine/threonine phosphatase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene1701_All//0.00E+00//TC173197				nr -
Unigene17010_All	828	2.34	16.65	6.43	0.24	0.79	0.98	0.05	0.86	1.97	2.83E+00	1.30E-42	Up	1.46E+00	2.68E-07	Up	1.72E+00	8.17E-02		2.03E+00	2.17E-02		4.07E+00	3.51E-04	Up	5.27E+00	1.93E-10	Up	Unigene17010_All//gi|15234593|ref|NP_192419.1|//8.00E-73//AtMYB74 (myb domain protein 74); DNA binding / transcription factor [Arabidopsis thaliana] >gi|14423390|gb|AAK62377.1|AF38693 2_1 Unknown protein [Arabidopsis thaliana] >gi|7267269|emb|CAB81052.1| MYB-like protein [Arabidopsis thaliana] >gi|24899709|gb|AAN65069.1| Unknown protein [Arabidopsis thaliana]	Unigene17010_All//3.00E-64//AT4G05100| AtMYB74 (myb domain protein 74); DNA binding / transcription factor	Unigene17010_All//3.00E-10//TC138320	MYB			nr -
Unigene17013_All	973	58.88	16.82	37.21	8.91	8.03	5.89	0.17	0.21	0.04	-1.81E+00	3.03E-102	Down	-6.62E-01	4.31E-20		-1.49E-01	5.26E-01		-5.96E-01	2.04E-03		3.06E-01	8.36E-01		-2.09E+00	3.14E-01		Unigene17013_All//gi|297596400|ref|NP_001042519.2|//7.00E-35//Os01g0235100 [Oryza sativa Japonica Group] >gi|255673036|dbj|BAF04433.2| Os01g0235100 [Oryza sativa Japonica Group]	Unigene17013_All//1.00E-30//AT5G42070| unknown protein	Unigene17013_All//0.00E+00//C0087575				nr +
Unigene17014_All	826	0.38	0.43	1.55	28.16	28.68	33.13	6.65	1.37	4.73	1.76E-01	8.83E-01		2.03E+00	3.44E-03		2.63E-02	8.50E-01		2.35E-01	3.10E-02		-2.28E+00	7.25E-17	Down	-4.94E-01	2.51E-02		Unigene17014_All//gi|254554078|gb|ACT67415.1|//1.00E-131//cellulose synthase [Shorea parvifolia subsp. parvifolia]	Unigene17014_All//8.00E-95//AT5G17420| IRX3 (IRREGULAR XYLEM 3); cellulose synthase	Unigene17014_All//0.00E+00//TC149449				nr +
Unigene17015_All	892	1.06	1.53	1.01	2.74	3.28	2.53	1.94	2.16	4.15	5.39E-01	3.59E-01		-5.70E-02	9.49E-01		2.62E-01	5.48E-01		-1.12E-01	7.93E-01		1.49E-01	7.32E-01		1.10E+00	1.03E-04	Up	Unigene17015_All//gi|224097301|ref|XP_002310900.1|//2.00E-49//histone acetyltransferase [Populus trichocarpa] >gi|222853803|gb|EEE91350.1| histone acetyltransferase [Populus trichocarpa]	Unigene17015_All//7.00E-43//AT1G16710| HAC12 (histone acetyltransferase of the CBP family 12); H3/H4 histone acetyltransferase/ histone acetyltransferase/ transcription cofactor	Unigene17015_All//1.00E-175//TC133849	TAZ			nr +
Unigene17017_All	736	6.04	1.17	1.09	4.47	2.48	5.52	2.07	0.85	1.19	-2.37E+00	8.12E-12	Down	-2.48E+00	8.20E-12	Down	-8.49E-01	8.29E-03		3.06E-01	3.71E-01		-1.28E+00	9.01E-03		-7.96E-01	8.34E-02		Unigene17017_All//gi|297598779|ref|NP_001046223.2|//2.00E-28//Os02g0201000 [Oryza sativa Japonica Group] >gi|255670693|dbj|BAF08137.2| Os02g0201000 [Oryza sativa Japonica Group]	Unigene17017_All//2.00E-47//AT5G25360| unknown protein	Unigene17017_All//0.00E+00//DW517506				nr -
Unigene17020_All	564	108.63	73.49	71.66	201.46	150.44	217.01	161.77	82.48	58.84	-5.64E-01	6.05E-17		-6.00E-01	4.14E-18		-4.21E-01	5.87E-22		1.07E-01	3.32E-02		-9.72E-01	5.81E-77		-1.46E+00	3.52E-150	Down	Unigene17020_All//gi|297820930|ref|XP_002878348.1|//2.00E-24//40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata] >gi|297324186|gb|EFH54607.1| 40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata]	Unigene17020_All//1.00E-25//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene17020_All//0.00E+00//TC148254		ko03010|Ribosome		nr -
Unigene17021_All	740	0.28	0.96	0.22	1.88	2.05	2.38	0.29	0.11	1.99	1.76E+00	5.61E-02		-3.89E-01	8.07E-01		1.19E-01	8.39E-01		3.37E-01	5.42E-01		-1.34E+00	4.30E-01		2.80E+00	2.86E-06	Up	Unigene17021_All//gi|15236498|ref|NP_193179.1|//2.00E-57//IBR10 (INDOLE-3-BUTYRIC ACID RESPONSE 10); catalytic/ dodecenoyl-CoA delta-isomerase [Arabidopsis thaliana] >gi|14190481|gb|AAK55721.1|AF38064 0_1 AT4g14430/d13255c [Arabidopsis thaliana] >gi|2241799|emb|CAB10222.1| carnitine racemase like protein [Arabidopsis thaliana] >gi|7268149|emb|CAB78485.1| carnitine racemase like protein [Arabidopsis thaliana] >gi|15810107|gb|AAL06979.1| AT4g14430/d13255c [Arabidopsis thaliana] >gi|110738734|dbj|BAF01291.1| carnitine racemase like protein [Arabidopsis thaliana]	Unigene17021_All//9.00E-51//AT4G14430| IBR10 (INDOLE-3-BUTYRIC ACID RESPONSE 10); catalytic/ dodecenoyl-CoA delta-isomerase	Unigene17021_All//1.00E-89//TC170892				nr -
Unigene17022_All	596	2.28	1.53	1.43	2.26	1.73	2.35	3.55	1.47	0.80	-5.77E-01	3.19E-01		-6.75E-01	2.58E-01		-3.81E-01	5.36E-01		5.79E-02	9.39E-01		-1.27E+00	1.68E-03		-2.14E+00	1.01E-06	Down		Unigene17022_All//5.00E-14//TC169622					
Unigene17024_All	562	2.14	5.32	0.95	2.84	0.86	1.13	6.09	7.73	7.58	1.31E+00	4.54E-04	Up	-1.18E+00	7.58E-02		-1.73E+00	7.76E-04	Down	-1.33E+00	1.23E-02		3.44E-01	2.14E-01		3.16E-01	2.39E-01		Unigene17024_All//gi|256535772|gb|ACR20504.2|//1.00E-79//NADH dehydrogenase subunit 4 [Carica papaya]	Unigene17024_All//2.00E-58//ATMG00580| NADH dehydrogenase subunit 4	Unigene17024_All//0.00E+00//gi|109829152|gb|DW227746.1|DW227746		ko00190|Oxidative phosphorylation		nr -
Unigene17025_All	609	0.09	2.58	0.96	1.15	1.13	2.22	0.69	1.44	1.11	4.91E+00	8.63E-08	Up	3.49E+00	1.21E-02		-1.81E-02	9.61E-01		9.58E-01	1.09E-01		1.05E+00	1.23E-01		6.80E-01	3.71E-01		Unigene17025_All//gi|30685543|ref|NP_173224.2|//1.00E-29//phosphoinositide binding [Arabidopsis thaliana] >gi|34098829|gb|AAQ56797.1| At1g17820 [Arabidopsis thaliana]	Unigene17025_All//8.00E-28//AT1G17820| phosphoinositide binding	Unigene17025_All//0.00E+00//TC157353				nr +
Unigene17026_All	563	29.83	51.30	21.75	48.58	54.25	115.92	181.44	244.39	445.02	7.82E-01	2.50E-14		-4.56E-01	1.24E-03		1.60E-01	1.35E-01		1.25E+00	9.10E-73	Up	4.30E-01	6.89E-28		1.29E+00	0.00E+00	Up	Unigene17026_All//gi|15242536|ref|NP_198817.1|//1.00E-78//AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene17026_All//1.00E-74//AT5G40010| AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene17026_All//0.00E+00//TC133425				nr -
Unigene17027_All	936	5.76	2.54	2.96	1.60	1.32	1.30	1.13	0.76	0.60	-1.18E+00	8.34E-06	Down	-9.61E-01	3.64E-04		-2.70E-01	6.17E-01		-2.93E-01	6.38E-01		-5.73E-01	3.60E-01		-9.22E-01	1.08E-01		Unigene17027_All//gi|124359531|gb|ABN08953.1|//5.00E-98//nodulin-like protein, related [Medicago truncatula]	Unigene17027_All//1.00E-77//AT4G19450| nodulin-related	Unigene17027_All//0.00E+00//DW240181				nr -
Unigene17029_All	1488	0.95	0.95	0.07	3.08	3.17	2.73	0.77	0.62	0.27	6.20E-03	9.91E-01		-3.73E+00	8.90E-06	Down	4.18E-02	9.05E-01		-1.73E-01	6.16E-01		-3.12E-01	6.25E-01		-1.52E+00	7.91E-03		Unigene17029_All//gi|115486399|ref|NP_001068343.1|//2.00E-47//Os11g0639300 [Oryza sativa Japonica Group] >gi|77552177|gb|ABA94974.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113645565|dbj|BAF28706.1| Os11g0639300 [Oryza sativa Japonica Group]	Unigene17029_All//2.00E-26//AT5G45530| unknown protein					nr +
Unigene17030_All	2144	0.20	0.00	0.50	7.13	3.20	2.40	5.25	0.80	0.61	-7.61E+00	1.05E-02		1.35E+00	6.01E-02		-1.16E+00	1.22E-17	Down	-1.57E+00	1.21E-24	Down	-2.71E+00	4.50E-41	Down	-3.10E+00	1.58E-48	Down	Unigene17030_All//gi|240255733|ref|NP_192232.4|//0.00E+00//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene17030_All//0.00E+00//AT4G03230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene17030_All//0.00E+00//DT048478		ko04626|Plant-pathogen interaction		nr +

Unigene17031_All	628	21.24	30.01	20.27	33.55	26.98	27.40	31.31	21.70	14.72	4.99E-01	8.75E-05		-6.81E-02	6.95E-01		-3.15E-01	6.61E-03		-2.92E-01	1.71E-02		-5.29E-01	1.71E-06		-1.09E+00	3.20E-21	Down	Unigene17031_All//gi|115446855|ref|NP_001047207.1|//7.00E-24//0s02g0574600 [Oryza sativa Japonica Group] >gi|113536738|dbj|BAF09121.1| 0s02g0574600 [Oryza sativa Japonica Group]	Unigene17031_All//3.00E-27//AT4G39860| unknown protein	Unigene17031_All//0.00E+00//gi|48818607|gb|CO119920.1|CO119920				nr -
Unigene17032_All	701	0.15	1.59	0.53	1.35	1.92	2.83	5.25	5.54	10.00	3.41E+00	1.24E-04	Up	1.83E+00	2.13E-01		5.05E-01	4.23E-01		1.07E+00	2.21E-02		7.96E-02	7.93E-01		9.31E-01	1.93E-06					Unigene17032_All//7.00E-69//ES818370				
Unigene17033_All	1263	1.16	2.69	1.39	1.14	0.49	0.43	5.82	3.57	1.26	1.21E+00	4.37E-04	Up	2.62E-01	6.33E-01		-1.22E+00	2.11E-02		-1.41E+00	1.29E-02		-7.05E-01	2.32E-04		-2.21E+00	3.67E-22	Down	Unigene17033_All//gi|297833634|ref|XP_002884699.1|//1.00E-144//D-alanine--D-alanine ligase family [Arabidopsis lyrata subsp. lyrata] >gi|297330539|gb|EFH60958.1| D-alanine--D-alanine ligase family [Arabidopsis lyrata subsp. lyrata]	Unigene17033_All//2.00E-142//AT3G08840| D-alanine--D-alanine ligase family	Unigene17033_All//0.00E+00//gi|21097660|gb|BQ409973.1|BQ409973				nr -
Unigene17035_All	570	4.22	9.07	4.39	5.77	6.89	5.94	6.75	6.38	6.36	1.10E+00	4.25E-05	Up	5.64E-02	8.94E-01		2.56E-01	4.67E-01		4.30E-02	9.26E-01		-8.15E-02	7.87E-01		-8.58E-02	7.59E-01						Unigene17035_All//0.00E+00//gi|78348710|gb|DT568984.1|DT568984				
Unigene17036_All	415	7.56	20.88	7.96	30.25	24.31	35.26	32.30	47.84	43.49	1.46E+00	5.54E-12	Up	7.27E-02	8.35E-01		-3.15E-01	4.75E-02		2.21E-01	1.72E-01		5.67E-01	2.65E-07		4.29E-01	1.58E-04					Unigene17036_All//1.00E-158//BQ407140				
Unigene17038_All	1028	26.36	20.26	13.93	1.94	1.00	3.38	1.11	0.89	5.12	-3.80E-01	2.74E-04		-9.20E-01	7.12E-17		-9.48E-01	2.96E-02		8.04E-01	1.56E-02		-3.12E-01	6.25E-01		2.20E+00	8.18E-16	Up	Unigene17038_All//gi|224120536|ref|XP_002318354.1|//5.00E-90//predicted protein [Populus trichocarpa] >gi|222859027|gb|EEE96574.1| predicted protein [Populus trichocarpa]	Unigene17038_All//4.00E-37//AT5G52900| unknown protein	Unigene17038_All//0.00E+00//TC138536				nr +
Unigene17039_All	747	10.37	7.39	8.84	13.67	13.55	23.10	1.53	0.06	3.41	-4.88E-01	2.03E-02		-2.30E-01	3.33E-01		-1.25E-02	9.60E-01		7.57E-01	7.71E-09		-4.77E+00	5.39E-07	Down	1.16E+00	9.35E-04	Up	Unigene17039_All//gi|224135829|ref|XP_002327314.1|//5.00E-73//UDP-glucose:flavonoid 3-o-glucosyltransferase [Populus trichocarpa] >gi|222835684|gb|EEE74119.1| UDP-glucose:flavonoid 3-o-glucosyltransferase [Populus trichocarpa]	Unigene17039_All//7.00E-65//AT5G17050| UGT78D2 (UDP-GLUCOSYL TRANSFERASE 78D2); UDP-glycosyltransferase/ anthocyanidin 3-O-glucosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene17039_All//0.00E+00//gi|109859804|gb|DW488783.1|DW488783		ko00944|Flavone and flavonol biosynthesis//ko00942|Anthocyanin biosynthesis		nr +
Unigene17041_All	531	6.60	9.73	5.11	4.03	4.93	5.53	26.44	24.87	12.53	5.60E-01	3.44E-02		-3.68E-01	3.04E-01		2.89E-01	5.28E-01		4.55E-01	2.40E-01		-8.79E-02	6.10E-01		-1.08E+00	3.75E-15	Down	Unigene17041_All//gi|15724312|gb|AL06549.1|AF412096.1|7.00E-39//AT4g28060/T13J8_170 [Arabidopsis thaliana] >gi|21360507|gb|AAM47369.1| AT4g28060/T13J8_170 [Arabidopsis thaliana]	Unigene17041_All//4.00E-40//AT5G57815| cytochrome c oxidase subunit 6b, putative	Unigene17041_All//0.00E+00//TC162941		ko00190|Oxidative phosphorylation		nr -
Unigene17044_All	330	0.00	2.15	1.13	0.00	0.10	1.51	16.91	26.47	39.96	1.11E+01	3.33E-04	Up	1.01E+01	2.50E-02		6.70E+00	8.30E-01		1.06E+01	4.38E-03		6.46E-01	1.99E-04		1.24E+00	1.57E-17	Up				Unigene17044_All//7.00E-55//TC172706				
Unigene17045_All	357	4.40	3.26	3.73	2.23	6.46	11.64	92.50	232.63	67.96	-4.30E-01	4.03E-01		-2.38E-01	6.42E-01		1.53E+00	3.26E-04	Up	2.38E+00	1.27E-11	Up	1.33E+00	1.95E-115	Up	-4.45E-01	5.13E-08		Unigene17045_All//gi|297610489|ref|NP_001064615.2|//6.00E-27//0s10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| 0s10g0419100 [Oryza sativa Japonica Group]	Unigene17045_All//4.00E-21//AT1G60690| aldo/keto reductase family protein	Unigene17045_All//3.00E-100//TC172706		ko00053|Ascorbate and aldarate metabolism		nr -
Unigene17048_All	894	6.38	10.94	33.47	17.77	6.32	7.93	2.36	0.09	1.38	7.78E-01	2.39E-05		2.39E+00	2.22E-74	Up	-1.49E+00	4.43E-27	Down	-1.16E+00	2.33E-16	Down	-4.66E+00	1.89E-12	Down	-7.76E-01	4.06E-02					Unigene17048_All//0.00E+00//ES820211				
Unigene17050_All	203	43.04	58.91	43.54	28.96	33.93	59.40	66.44	60.33	48.47	4.53E-01	6.01E-03		1.67E-02	9.54E-01		2.29E-01	3.65E-01		1.04E+00	2.24E-10	Up	-1.39E-01	3.91E-01		-4.55E-01	6.25E-04		Unigene17050_All//gi|222424610|dbj|BAH20260.1|//8.00E-33//AT4G38510 [Arabidopsis thaliana]	Unigene17050_All//3.00E-34//AT4G38510| vacuolar ATP synthase subunit B, putative / V-ATPase B subunit, putative / vacuolar proton pump B subunit, putative / V-ATPase 57 kDa subunit, putative	Unigene17050_All//3.00E-111//TC172498		ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr +
Unigene17051_All	1239	1.44	1.51	2.28	7.88	9.12	8.71	1.23	0.34	0.58	7.57E-02	8.74E-01		6.66E-01	8.85E-02		2.10E-01	2.68E-01		1.45E-01	4.80E-01		-1.86E+00	3.50E-04	Down	-1.09E+00	1.94E-02		Unigene17051_All//gi|270342120|gb|ACZ74703.1|//1.00E-130//carboxilic ester hydrolase [Phaseolus vulgaris]	Unigene17051_All//2.00E-104//AT5G14450| GDSL-motif lipase/hydrolase family protein	Unigene17051_All//0.00E+00//TC163551				nr +
Unigene17054_All	550	18.07	7.92	1.84	21.65	10.77	7.23	12.07	0.53	4.42	-1.19E+00	3.58E-10	Down	-3.30E+00	1.27E-34	Down	-1.01E+00	4.34E-11	Down	-1.58E+00	1.63E-19	Down	-4.50E+00	1.88E-37	Down	-1.45E+00	1.27E-11	Down	Unigene17054_All//gi|255570300|ref|XP_002526110.1|//1.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223534607|gb|EEF36304.1| conserved hypothetical protein [Ricinus communis]		Unigene17054_All//0.00E+00//TC157898				nr -
Unigene17058_All	959	26.02	14.53	26.49	3.38	5.92	4.05	0.62	0.74	1.87	-8.41E-01	4.42E-14		2.54E-02	8.39E-01		8.11E-01	6.75E-04		2.63E-01	4.58E-01		2.64E-01	7.21E-01		1.60E+00	3.75E-04	Up	Unigene17058_All//gi|22327397|ref|NP_198461.2|//2.00E-46//CCB3 (COFACTOR ASSEMBLY, COMPLEX C (B6F),) [Arabidopsis thaliana]	Unigene17058_All//8.00E-48//AT5G36120| CCB3 (COFACTOR ASSEMBLY, COMPLEX C (B6F),)	Unigene17058_All//0.00E+00//TC136839				nr +
Unigene17059_All	448	14.95	21.04	17.12	28.24	26.60	14.42	45.02	29.11	20.90	4.93E-01	8.77E-03		1.95E-01	3.93E-01		-8.67E-02	6.38E-01		-9.70E-01	6.42E-10		-6.29E-01	9.09E-09		-1.11E+00	2.58E-22	Down	Unigene17059_All//gi|195628156|gb|ACG35908.1|//8.00E-12//U6 snRNA-associated Sm-like protein LSm3 [Zea mays] >gi|195643108|gb|ACG41022.1| U6 snRNA-associated Sm-like protein LSm3 [Zea mays]	Unigene17059_All//1.00E-12//AT1G21190| small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative	Unigene17059_All//0.00E+00//TC158824		ko03040|Spliceosome//ko03018|RNA degradation		nr -
Unigene1706_All	1094	1.82	2.18	1.36	1.46	3.15	1.24	4.95	2.02	2.00	2.60E-01	5.48E-01		-4.15E-01	3.93E-01		1.11E+00	6.18E-04	Up	-2.35E-01	6.80E-01		-1.29E+00	6.54E-08	Down	-1.30E+00	2.46E-08	Down	Unigene1706_All//gi|297810135|ref|XP_002872951.1|//1.00E-118//At4g00460 [Arabidopsis lyrata subsp. lyrata] >gi|297318788|gb|EFH49210.1| At4g00460 [Arabidopsis lyrata subsp. lyrata]	Unigene1706_All//4.00E-103//AT4G00460| Rho guanyl-nucleotide exchange factor	Unigene1706_All//8.00E-82//TC141986				nr -
Unigene17061_All	394	0.80	0.00	0.00	1.14	0.87	2.29	1.93	0.00	0.51	-9.64E+00	3.66E-02		-9.64E+00	4.92E-02		-3.81E-01	7.22E-01		1.01E+00	1.96E-01		-1.09E+01	1.68E-05	Down	-1.93E+00	1.14E-02		Unigene17061_All//gi|124109177|gb|ABM91064.1|//2.00E-51//xyloglucan endotransglycosylase/hydrolase precursor XTH-38 [Populus tremula x Populus tremuloides]	Unigene17061_All//4.00E-50//AT1G10550| XTH33; hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase					nr +
Unigene17062_All	966	1.03	0.00	0.22	2.89	1.03	2.57	3.63	0.17	0.25	-1.00E+01	7.46E-06	Down	-2.22E+00	7.49E-03		-1.48E+00	4.00E-05	Down	-1.67E-01	6.94E-01		-4.39E+00	1.06E-19	Down	-3.88E+00	8.45E-19	Down	Unigene17062_All//gi|124109177|gb|ABM91064.1|//1.00E-125//xyloglucan endotransglycosylase/hydrolase precursor XTH-38 [Populus tremula x Populus tremuloides]	Unigene17062_All//6.00E-110//AT1G10550| XTH33; hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase					nr +
Unigene17063_All	444	9.19	7.30	3.00	9.99	9.93	12.51	23.90	16.47	11.84	-3.32E-01	2.89E-01		-1.62E+00	1.56E-06	Down	-8.40E-03	9.67E-01		3.25E-01	2.33E-01		-5.37E-01	5.70E-04		-1.01E+00	1.22E-10	Down	Unigene17063_All//gi|25091502|sp|Q9LKA5.1|UMP1_ARATH//5.00E-06//RecName: Full=Uncharacterized protein At3g15000, mitochondrial >gi|16226543|gb|AAL16196.1|AF424827_1 AT3g15000/K1DM2_14 [Arabidopsis thaliana] >gi|53828643|gb|AAU94431.1| At3g15000 [Arabidopsis thaliana]		Unigene17063_All//0.00E+00//gi|164365928|gb|ES812556.1|ES812556				nr +
Unigene17065_All	630	9.63	2.17	10.31	3.16	0.87	1.79	5.10	3.25	1.20	-2.15E+00	3.47E-14	Down	9.81E-02	6.94E-01		-1.85E+00	4.61E-05	Down	-8.20E-01	7.58E-02		-6.50E-01	3.63E-02		-2.09E+00	1.71E-09	Down	Unigene17065_All//gi|297834664|ref|XP_002885214.1|//3.00E-32//cbl-interacting protein kinase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297331054|gb|EFH61473.1| cbl-interacting protein kinase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene17065_All//4.00E-33//AT3G17510| CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding	Unigene17065_All//0.00E+00//TC133196				nr +
Unigene17067_All	1480	0.67	1.54	1.01	25.04	0.42	0.06	5.40	0.40	4.39	1.20E+00	5.65E-03		5.85E-01	3.07E-01		-5.90E+00	4.63E-255	Down	-8.68E+00	1.28E-233	Down	-3.77E+00	8.65E-40	Down	-2.99E-01	1.06E-01		Unigene17067_All//gi|75099771|sp|Q80494.1|P2B15_ARATH//2.00E-40//RecName: Full=F-box protein PP2-B15; AltName: Full=Protein PHLOEM PROTEIN 2-LIKE B15; Short=AtPP2-B15 >gi|3249107|gb|AAC21090.1| Contains similarity to phloem-specific lectin PP2 gb|Z17331 from Cucubita maxima [Arabidopsis thaliana]	Unigene17067_All//4.00E-42//AT1G09155| AtPP2-B15 (Phloem protein 2-B15); carbohydrate binding	Unigene17067_All//4.00E-171//C0107905				nr +
Unigene17068_All	686	0.69	2.81	1.09	5.74	7.03	5.66	4.31	2.56	2.79	2.03E+00	1.13E-04	Up	6.63E-01	4.19E-01		2.93E-01	3.25E-01		-1.89E-02	9.44E-01		-7.54E-01	2.01E-02		-6.30E-01	4.37E-02		Unigene17068_All//gi|297608014|ref|NP_001061066.2|//6.00E-26//0s08g0163600 [Oryza sativa Japonica Group] >gi|255678169|dbj|BAF22980.2| 0s08g0163600 [Oryza sativa Japonica Group]	Unigene17068_All//2.00E-41//AT5G45320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: inflorescence meristem, flower, root; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G26350.1); Has 162 Blast hits to 162 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 162; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene17068_All//0.00E+00//DW510998				nr -
Unigene17071_All	1457	2.30	0.77	0.80	19.76	8.27	3.41	1.10	0.89	0.60	-1.59E+00	1.13E-05	Down	-1.52E+00	4.63E-05	Down	-1.26E+00	1.93E-37	Down	-2.54E+00	3.82E-86	Down	-3.10E-01	5.40E-01		-8.74E-01	4.99E-02		Unigene17071_All//gi|22329388|ref|NP_172200.2|//1.00E-56//ATP-dependent Clp protease ClpB protein-related [Arabidopsis thaliana] >gi|30725704|gb|AAP37874.1| At1g07200 [Arabidopsis thaliana]	Unigene17071_All//1.00E-57//AT1G07200| ATP-dependent Clp protease ClpB protein-related	Unigene17071_All//0.00E+00//gi|48744255|gb|CO074774.1|CO074774				nr +
Unigene17073_All	599	28.30	17.51	20.71	108.03	94.80	102.84	60.14	15.77	23.21	-6.93E-01	2.99E-07		-4.50E-01	1.34E-03		-1.89E-01	3.17E-03		-7.10E-02	3.90E-01		-1.93E+00	4.01E-86	Down	-1.37E+00	1.27E-54	Down	Unigene17073_All//gi|15230209|ref|NP_188511.1|//5.00E-08//protein kinase family protein [Arabidopsis thaliana]		Unigene17073_All//0.00E+00//gi|72269153|gb|DT047018.1|DT047018				nr -
Unigene17074_All	951	2.09	0.59	1.06	1.99	2.53	4.08	1.38	1.89	3.23	-1.83E+00	2.47E-04	Down	-9.75E-01	4.46E-02		3.49E-01	4.48E-01		1.04E+00	8.50E-04	Up	4.55E-01	3.20E-01		1.23E+00	1.14E-04	Up	Unigene17074_All//gi|238479361|ref|NP_001154534.1|//1.00E-69//binding [Arabidopsis thaliana] >gi|240254532|ref|NP_180101.4| binding [Arabidopsis thaliana]	Unigene17074_All//1.00E-65//AT5G20360| octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein					nr -
Unigene17075_All	616	0.93	1.48	0.43	1.37	0.84	0.81	3.78	2.78	1.42	6.64E-01	3.75E-01		-1.11E+00	2.79E-01		-7.13E-01	3.36E-01		-7.69E-01	3.34E-01		-4.40E-01	2.56E-01		-1.41E+00	1.83E-04	Down				Unigene17075_All//3.00E-34//TC136062				
Unigene17076_All	955	66.84	12.15	43.27	11.06	6.60	2.93	0.18	0.18	0.13	-2.46E+00	8.79E-169	Down	-6.27E-01	2.41E-20		-7.45E-01	4.00E-06		-1.92E+00	1.55E-22	Down	-1.64E-02	1.02E+00		-5.02E-01	7.46E-01									

Unigene17077_All	1393	0.71	0.87	1.45	2.86	1.78	1.36	4.86	1.74	4.15	2.91E-01	6.04E-01		1.03E+00	3.20E-02		-6.85E-01	1.84E-02		-1.07E+00	4.17E-04	Down	-1.48E+00	8.89E-12	Down	-2.28E-01	2.80E-01		Unigene17077_All//gi|225459358|ref|XP_002284225.1|//1.00E-148//PREDICTED: similar to F28K19.26 [Vitis vinifera]	Unigene17077_All//4.00E-129//AT1G22170| phosphoglycerate/bisphosphoglycerate mutase family protein	Unigene17077_All//0.00E+00//TC175641		ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene17079_All	409	266.98	138.88	157.80	141.65	113.49	120.80	143.90	64.48	48.80	-9.43E-01	1.46E-71		-7.59E-01	6.75E-48		-3.20E-01	5.17E-07		-2.30E-01	9.29E-04		-1.16E+00	3.35E-66	Down	-1.56E+00	3.29E-107	Down	Unigene17079_All//gi|2506277|sp|P08927.2|RUBB_PEA//1.00E-66//RecName: Full=RuBisCO large subunit-binding protein subunit beta, chloroplastic; AltName: Full=60 kDa chaperonin subunit beta; AltName: Full=CPN-60 beta; Flags: Precursor >gi|806808|gb|AAA66365.1| chaperonin precursor [Pisum sativum]	Unigene17079_All//7.00E-61//AT5G56500| ATP binding / protein binding	Unigene17079_All//0.00E+00//TC145566		ko03018|RNA degradation		nr +
Unigene17080_All	824	0.89	1.23	0.65	2.60	2.42	2.58	4.36	23.48	7.49	4.68E-01	4.89E-01		-4.60E-01	6.02E-01		-1.01E-01	8.20E-01		-1.30E-02	9.68E-01		2.43E+00	8.63E-62	Up	7.81E-01	1.62E-04		Unigene17080_All//gi|21992|emb|CAA46283.1|//2.00E-07//extensin [Volvox carteri]						nr -
Unigene17084_All	494	0.32	6.05	1.94	2.42	4.25	7.13	1.88	1.35	1.45	4.25E+00	2.19E-13	Up	2.61E+00	3.45E-03		8.13E-01	6.93E-02		1.56E+00	5.86E-06	Up	-4.76E-01	4.76E-01		-3.75E-01	5.57E-01		Unigene17084_All//gi|116744390|dbj|BAF35859.1|//2.00E-82//soluble acid invertase [Pyrus pyrifolia var. culta] >gi|186397269|dbj|BAG30920.1| soluble acid invertase [Pyrus pyrifolia]	Unigene17084_All//4.00E-82//AT1G12240| ATBETAFRUCT4; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene17084_All//5.00E-171//TC146217		ko00500|Starch and sucrose metabolism/ko00052|Galactose metabolism		nr -
Unigene17085_All	580	11.73	38.96	25.52	1.98	7.07	2.26	0.00	0.00	0.00	1.73E+00	3.69E-38	Up	1.12E+00	5.97E-13	Up	1.84E+00	5.61E-09	Up	1.93E-01	7.47E-01		null	null		null	null		Unigene17085_All//gi|224085165|ref|XP_002307511.1|//3.00E-59//one helix protein 2 [Populus trichocarpa] >gi|222856960|gb|EEE94507.1| one helix protein 2 [Populus trichocarpa]	Unigene17085_All//5.00E-34//AT1G34000| OHP2 (ONE-HELIX PROTEIN 2)	Unigene17085_All//0.00E+00//DW515940				nr +
Unigene17086_All	740	8.98	7.67	7.63	7.74	7.49	8.79	12.51	12.26	5.28	-2.28E-01	3.60E-01		-2.35E-01	3.65E-01		-4.72E-02	8.59E-01		1.83E-01	4.97E-01		-2.99E-02	8.86E-01		-1.25E+00	9.26E-13	Down	Unigene17086_All//gi|115452009|ref|NP_001049605.1|//5.00E-38//Os03g0257900 [Oryza sativa Japonica Group] >gi|108707263|gb|ABF95058.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548076|dbj|BAF11519.1| Os03g0257900 [Oryza sativa Japonica Group]	Unigene17086_All//3.00E-35//AT5G16060| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Cytochrome c oxidase biogenesis protein Cmc1-like (InterPro:IPR013892); Has 47 Blast hits to 47 proteins in 24 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 17; Plants - 21; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene17086_All//0.00E+00//TC168107				nr +
Unigene17087_All	916	3.88	5.09	1.86	6.74	6.09	2.61	0.00	0.00	0.09	3.90E-01	1.74E-01		-1.06E+00	2.06E-03		-1.47E-01	5.86E-01		-1.37E+00	1.76E-08	Down	null	null		6.44E+00	4.05E-01		Unigene17087_All//gi|57282652|emb|CAE75664.1|//1.00E-128//long chain fatty acid elongation enzyme [Gossypium hirsutum]	Unigene17087_All//5.00E-73//AT3G06470| GNS1/SUR4 membrane family protein	Unigene17087_All//0.00E+00//TC130848				nr +
Unigene17088_All	793	5.28	13.61	7.45	12.19	12.77	12.53	15.41	17.45	8.24	1.37E+00	2.33E-13	Up	4.98E-01	5.25E-02		6.71E-02	7.90E-01		4.00E-02	8.63E-01		1.79E-01	2.33E-01		-9.03E-01	3.65E-10		Unigene17088_All//gi|122831045|gb|ABM66812.1|//1.00E-107//auxin-binding protein 1 [Gossypium hirsutum] >gi|222840504|gb|ACM68695.1| auxin-binding protein 1 [Gossypium hirsutum]	Unigene17088_All//9.00E-77//AT4G02980| ABP1 (ENDOPLASMIC RETICULUM AUXIN BINDING PROTEIN 1); auxin binding	Unigene17088_All//0.00E+00//gi|109882647|gb|DW511617.1|DW511617				nr -
Unigene17089_All	255	1.64	16.69	12.11	7.03	12.02	9.21	24.04	34.09	23.59	3.35E+00	8.44E-16	Up	2.88E+00	8.48E-10	Up	7.73E-01	2.79E-02		3.89E-01	3.87E-01		5.04E-01	4.04E-03		-2.73E-02	9.20E-01				Unigene17089_All//4.00E-142//gi|78352605|gb|DT572879.1|DT572879				
Unigene1709_All	2847	0.86	1.94	0.84	2.01	1.97	1.54	3.27	2.10	5.12	1.17E+00	7.92E-06	Up	-3.72E-02	9.43E-01		-2.95E-02	9.11E-01		-3.87E-01	1.37E-01		-6.38E-01	1.40E-04		6.49E-01	4.31E-07		Unigene1709_All//gi|297810135|ref|XP_002872951.1|//1.00E-101//At4g00460 [Arabidopsis lyrata subsp. lyrata] >gi|297318788|gb|EFH49210.1| At4g00460 [Arabidopsis lyrata subsp. lyrata]	Unigene1709_All//2.00E-86//AT4G00460| Rho guanyl-nucleotide exchange factor	Unigene1709_All//0.00E+00//gi|18098661|gb|BM357915.1|BM357915				nr -
Unigene17090_All	503	4.78	3.73	2.96	8.02	5.07	3.86	6.05	3.57	0.87	-3.60E-01	3.87E-01		-6.91E-01	1.10E-01		-6.63E-01	2.15E-02		-1.06E+00	4.58E-04	Down	-7.60E-01	1.71E-02		-2.80E+00	2.18E-12	Down	Unigene17090_All//gi|224089729|ref|XP_002308804.1|//3.00E-17//predicted protein [Populus trichocarpa] >gi|222854780|gb|EEE92327.1| predicted protein [Populus trichocarpa]						nr +
Unigene17091_All	523	1.50	20.15	2.24	3.62	4.08	4.75	3.56	4.16	22.32	3.75E+00	3.46E-42	Up	5.78E-01	3.90E-01		1.74E-01	7.53E-01		3.92E-01	3.82E-01		2.24E-01	6.20E-01		2.65E+00	3.44E-42	Up	Unigene17091_All//gi|224038408|gb|ACN38308.1|//6.00E-11//AHG05 [Brassica rapa subsp. pekinensis]		Unigene17091_All//0.00E+00//gi|109874162|gb|DW503136.1|DW503136				nr +
Unigene17092_All	715	0.73	1.20	1.12	2.23	0.87	0.82	3.37	1.40	1.39	7.19E-01	3.48E-01		6.10E-01	4.41E-01		-1.36E+00	6.51E-03		-1.44E+00	7.26E-03		-1.26E+00	7.20E-04	Down	-1.27E+00	4.48E-04	Down			Unigene17092_All//1.00E-101//BQ408590				
Unigene17093_All	359	4.37	18.35	6.97	4.30	4.41	5.79	0.82	1.98	2.00	2.07E+00	1.53E-14	Up	6.73E-01	1.10E-01		3.67E-02	9.59E-01		4.28E-01	3.90E-01		1.26E+00	1.07E-01		1.28E+00	8.79E-02								
Unigene17094_All	1105	1.18	0.92	1.69	2.80	3.09	3.80	1.38	0.15	0.58	-3.68E-01	5.31E-01		5.11E-01	3.12E-01		1.43E-01	7.34E-01		4.44E-01	1.56E-01		-3.19E+00	4.80E-07	Down	-1.26E+00	7.68E-03		Unigene17094_All//gi|18076679|emb|CAC84774.1|//1.00E-81//P70 protein [Nicotiana tabacum]	Unigene17094_All//2.00E-65//AT2G37080| myosin heavy chain-related	Unigene17094_All//5.00E-34//TC142405		ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis		nr -
Unigene17095_All	479	37.79	154.76	91.60	40.35	63.48	89.48	32.92	63.00	79.18	2.03E+00	9.92E-154	Up	1.28E+00	1.09E-45	Up	6.54E-01	6.76E-13		1.15E+00	9.00E-42	Up	9.36E-01	1.94E-24		1.27E+00	2.47E-50	Up	Unigene17095_All//gi|222423852|dbj|BAH19891.1|//3.00E-10//AT5G64170 [Arabidopsis thaliana]	Unigene17095_All//2.00E-11//AT5G64170| dentin sialophosphoprotein-related	Unigene17095_All//0.00E+00//gi|48827491|gb|CO125881.1|CO125881				nr +
Unigene17096_All	864	1.33	0.12	1.05	2.36	3.15	1.36	0.88	0.53	2.40	-3.51E+00	6.57E-05	Down	-3.47E-01	6.16E-01		4.14E-01	3.10E-01		-7.99E-01	7.94E-02		-7.27E-01	3.32E-01		1.44E+00	3.77E-04	Up	Unigene17096_All//gi|115451389|ref|NP_001049295.1|//8.00E-10//Os03g0201100 [Oryza sativa Japonica Group] >gi|113547766|dbj|BAF11209.1| Os03g0201100 [Oryza sativa Japonica Group]	Unigene17096_All//9.00E-18//AT5G67530| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	Unigene17096_All//1.00E-18//gi|84163786|gb|DR452434.1|DR452434		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene17098_All	1010	2.90	3.41	6.22	5.47	5.22	4.07	2.51	2.77	4.10	2.34E-01	5.03E-01		1.10E+00	9.95E-06	Up	-6.97E-02	8.32E-01		-4.28E-01	1.04E-01		1.43E-01	6.91E-01		7.08E-01	6.18E-03		Unigene17098_All//gi|124359343|gb|ABD28505.2|//3.00E-09//RNA-directed DNA polymerase (Reverse transcriptase): Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene17098_All//7.00E-05//AT3G24255| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G23910.1); Has 2302 Blast hits to 2235 proteins in 74 species: Archae - 4; Bacteria - 15; Metazoa - 871; Fungi - 12; Plants - 1295; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).	Unigene17098_All//0.00E+00//AW536058				nr +
Unigene17099_All	738	1.28	0.41	0.79	0.68	1.03	4.16	8.25	3.06	30.93	-1.63E+00	3.13E-02		-6.85E-01	3.69E-01		6.05E-01	5.14E-01		2.62E+00	1.17E-09	Up	-1.43E+00	3.41E-10	Down	1.91E+00	6.71E-55	Up	Unigene17099_All//gi|224087552|ref|XP_002308188.1|//7.00E-27//predicted protein [Populus trichocarpa] >gi|222854164|gb|EEE91711.1| predicted protein [Populus trichocarpa]	Unigene17099_All//5.00E-06//AT3G09280| unknown protein	Unigene17099_All//0.00E+00//gi|78333794|gb|DT554068.1|DT554068				nr -
Unigene1710_All	2415	8.80	18.51	11.64	25.12	27.09	25.88	33.54	39.84	34.66	1.07E+00	1.86E-36	Up	4.04E-01	1.33E-04		1.09E-01	1.30E-01		4.29E-02	6.44E-01		2.48E-01	1.48E-07		4.72E-02	4.33E-01		Unigene1710_All//gi|297839267|ref|XP_002887515.1|//0.00E+00//lipase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333356|gb|EFH63774.1| lipase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1710_All//0.00E+00//AT1G73920| lipase family protein	Unigene1710_All//0.00E+00//TC140683				nr -
Unigene17100_All	769	2.31	0.46	0.90	2.33	8.73	8.10	24.14	128.05	73.15	-2.33E+00	4.65E-05	Down	-1.36E+00	1.01E-02		1.90E+00	3.66E-15	Up	1.80E+00	3.50E-12	Up	2.41E+00	0.00E+00	Up	1.60E+00	3.44E-105	Up	Unigene17100_All//gi|297825169|ref|XP_002880467.1|//2.00E-12//VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297326306|gb|EFH56726.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]		Unigene17100_All//0.00E+00//gi|109879400|gb|DW508370.1|DW508370				nr +
Unigene17101_All	649	2.90	6.01	3.20	10.67	8.60	5.92	6.84	6.25	4.73	1.05E+00	8.22E-04	Up	1.41E-01	7.48E-01		-3.12E-01	1.75E-01		-8.51E-01	9.80E-05		-1.31E-01	6.31E-01		-5.33E-01	3.18E-02		Unigene17101_All//gi|115486948|ref|NP_001065961.1|//6.00E-29//Os12g0110000 [Oryza sativa Japonica Group] >gi|113648468|dbj|BAF28980.1| Os12g0110000 [Oryza sativa Japonica Group]	Unigene17101_All//5.00E-28//AT3G08850| RAPTOR1: nucleotide binding / protein binding	Unigene17101_All//2.00E-106//gi|13352657|gb|BG443005.1|BG443005				nr -
Unigene17102_All	737	20.87	8.39	20.88	5.20	6.68	3.80	6.88	8.11	2.05	-1.32E+00	8.61E-18	Down	6.00E-04	9.96E-01		3.60E-01	2.12E-01		-4.54E-01	1.65E-01		2.36E-01	3.27E-01		-1.74E+00	1.30E-11	Down	Unigene17102_All//gi|224127754|ref|XP_002329169.1|//2.00E-34//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870950|gb|EEF08081.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene17102_All//3.00E-29//AT5G36930| disease resistance protein (TIR-NBS-LRR class), putative	Unigene17102_All//9.00E-152//BG441725				nr +
Unigene17103_All	610	1.72	2.08	3.84	8.57	7.51	2.81	0.83	0.89	0.72	2.76E-01	6.17E-01		1.16E+00	8.48E-03		-1.92E-01	5.30E-01		-1.61E+00	4.41E-09	Down	9.89E-02	9.21E-01		-2.11E-01	7.92E-01		Unigene17103_All//gi|15226168|ref|NP_178215.1|//5.00E-11//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene17103_All//3.00E-12//AT2G01050| nucleic acid binding / zinc ion binding	Unigene17103_All//5.00E-11//DW516140				nr -

Unigene17105_All	419	3.87	6.77	11.69	35.90	38.54	29.97	2.32	2.79	1.52	8.07E-01	3.04E-02		1.59E+00	1.31E-07	Up	1.02E-01	5.46E-01		-2.61E-01	8.88E-02		2.67E-01	6.28E-01		-6.09E-01	3.16E-01		Unigene17105_All//gi|15450826|gb|AB96684.1|/1.00E-07//Unknown protein [Arabidopsis thaliana] >gi|88196723|gb|ABD43004.1| At5g42570 [Arabidopsis thaliana]	Unigene17105_All//7.00E-09//AT5G42570| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular protein transport; LOCATED IN: endoplasmic reticulum, plasma membrane; EXPRESSED IN: 26 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: B-cell receptor-associated 31-like (InterPro:IPR008417); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G11905.1); Has 311 Blast hits to 268 proteins in 81 species: Archae - 2; Bacteria - 2; Metazoa - 134; Fungi - 41; Plants - 73; Viruses - 0; Other Eukaryotes - 59 (source: NCBI BLink).	Unigene17105_All//1.00E-164//gi|84155996|gb|DN817222.1|DN817222				nr +
Unigene17106_All	669	12.83	23.48	15.52	26.28	27.54	38.95	18.14	38.67	24.65	8.72E-01	1.16E-09		2.75E-01	1.54E-01		6.72E-02	6.81E-01		5.68E-01	4.25E-08		1.09E+00	6.35E-27	Up	4.43E-01	2.07E-04		Unigene17106_All//gi|48958497|gb|AT47801.1|/7.00E-21//At5g35732 [Arabidopsis thaliana] >gi|51536514|gb|AAU05510.1| At5g35732 [Arabidopsis thaliana]	Unigene17106_All//1.00E-20//AT5G35732| unknown protein	Unigene17106_All//0.00E+00//DW509953				nr -
Unigene1711_All	1884	6.80	2.80	4.01	6.72	5.12	7.89	68.51	85.14	75.93	-1.28E+00	2.08E-14	Down	-7.62E-01	3.20E-06		-3.92E-01	1.03E-02		2.32E-01	1.43E-01		3.14E-01	2.55E-18		1.48E-01	1.07E-04		Unigene1711_All//gi|183239022|gb|ACC60969.1|//0.00E+00//phytochrome A [Vitis riparia]	Unigene1711_All//0.00E+00//AT1G09570| PHYA (PHYTOCHROME A); G-protein coupled photoreceptor/ protein histidine kinase/ red or far-red light photoreceptor/ signal transducer	Unigene1711_All//0.00E+00//TC177478		ko04712|Circadian rhythm - plant		nr -
Unigene17111_All	512	5.31	1.39	4.37	12.26	9.62	11.82	21.39	12.82	18.99	-1.94E+00	5.15E-06	Down	-2.83E-01	4.93E-01		-3.50E-01	1.47E-01		-5.26E-02	8.50E-01		-7.39E-01	1.52E-06		-1.72E-01	3.00E-01		Unigene17111_All//gi|297792941|ref|XP_002864355.1|//3.00E-12//glucose-6-phosphate transporter 1 [Arabidopsis lyrata subsp. lyrata] >gi|297310190|gb|EFH40614.1| glucose-6-phosphate transporter 1 [Arabidopsis lyrata subsp. lyrata]	Unigene17111_All//2.00E-12//AT5G54800| GPT1; antiporter/ glucose-6-phosphate transmembrane transporter	Unigene17111_All//0.00E+00//gi|164243631|gb|ES792398.1|ES792398				nr -
Unigene17112_All	760	7.64	8.40	8.48	4.85	6.43	8.14	1.50	6.43	7.81	1.37E-01	6.11E-01		1.50E-01	5.83E-01		4.08E-01	1.52E-01		7.47E-01	1.49E-03		2.10E+00	1.29E-13	Up	2.38E+00	2.20E-19	Up			Unigene17112_All//0.00E+00//gi|13355077|gb|BG445509.1|BG445509				
Unigene17113_All	855	6.43	6.93	3.67	6.87	5.32	6.29	3.07	4.50	7.36	1.10E-01	6.59E-01		-8.06E-01	2.33E-03		-3.71E-01	1.37E-01		-1.29E-01	6.48E-01		5.53E-01	4.97E-02		1.26E+00	4.70E-09	Up	Unigene17113_All//gi|124359981|gb|ABN07997.1|//2.00E-08//contains similarity to reverse transcriptase, related [Medicago truncatula]	Unigene17113_All//2.00E-06//AT3G09510| nucleic acid binding	Unigene17113_All//0.00E+00//gi|13355077|gb|BG445509.1|BG445509				nr +
Unigene17114_All	434	34.12	20.43	33.37	41.89	52.37	46.62	62.54	36.50	24.88	-7.40E-01	4.03E-07		-3.18E-02	8.48E-01		3.22E-01	3.99E-03		1.54E-01	2.78E-01		-7.77E-01	2.61E-16		-1.33E+00	1.97E-39	Down	Unigene17114_All//gi|55979111|gb|AY690919.1|//3.00E-23//NADH:cytochrome b5 reductase [Vernicia fordii] >gi|55979115|gb|AAY69021.1| NADH:cytochrome b5 reductase [Vernicia fordii]	Unigene17114_All//2.00E-12//AT5G17770| ATCBR (ARABIDOPSIS THALIANA NADH:CYTOCHROME B5 REDUCTASE 1); cytochrome-b5 reductase	Unigene17114_All//0.00E+00//gi|21095508|gb|BQ407821.1|BQ407821		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene17116_All	573	1.46	1.06	1.39	5.22	3.06	1.58	13.58	8.53	2.50	-4.61E-01	5.43E-01		-6.77E-02	9.40E-01		-7.67E-01	2.54E-02		-1.73E+00	5.70E-06	Down	-6.70E-01	3.02E-04		-2.44E+00	2.66E-26	Down	Unigene17116_All//gi|224068646|ref|XP_002302790.1|//4.00E-12//predicted protein [Populus trichocarpa] >gi|222844516|gb|EEE82063.1| predicted protein [Populus trichocarpa]						nr +
Unigene17119_All	1107	4.54	0.37	0.48	7.06	4.11	1.06	2.94	0.34	0.32	-3.63E+00	4.63E-20	Down	-3.24E+00	2.30E-17	Down	-7.83E-01	4.60E-05		-2.74E+00	9.84E-26	Down	-3.11E+00	4.29E-14	Down	-3.18E+00	6.57E-15	Down	Unigene17119_All//gi|18400507|ref|NP_566491.1|//3.00E-94//PHD finger family protein [Arabidopsis thaliana] >gi|21618148|gb|AAM67198.1| similar to zinc-finger protein [Arabidopsis thaliana]	Unigene17119_All//2.00E-93//AT3G14740| PHD finger family protein	Unigene17119_All//0.00E+00//CO128798				nr -
Unigene17125_All	914	2.40	10.20	6.93	3.87	8.74	7.12	0.32	0.96	0.92	2.09E+00	1.72E-20	Up	1.53E+00	4.14E-09	Up	1.18E+00	3.74E-09	Up	8.79E-01	1.20E-04		1.57E+00	2.54E-02		1.50E+00	3.06E-02		Unigene17125_All//gi|224142619|ref|XP_002324652.1|//4.00E-73//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222866086|gb|EEF03217.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene17125_All//2.00E-46//AT1G15360| SHN1 (SHINE 1); DNA binding / sequence-specific DNA binding / transcription factor	Unigene17125_All//1.00E-114//ES805836	AP2-EREBP			nr +
Unigene17126_All	1271	0.70	0.56	0.13	12.86	3.82	1.46	1.50	0.69	0.31	-3.26E-01	6.22E-01		-2.48E+00	7.18E-03		-1.75E+00	3.99E-35	Down	-3.14E+00	1.65E-61	Down	-1.12E+00	8.54E-03		-2.26E+00	1.81E-06	Down	Unigene17126_All//gi|56121894|gb|AAT42228.1|/2.00E-56//At3g60670 [Arabidopsis thaliana] >gi|57222190|gb|AAW39002.1| At3g60670 [Arabidopsis thaliana]	Unigene17126_All//1.00E-49//AT3G60670| zinc-binding protein, putative	Unigene17126_All//3.00E-17//BG439997	PLATZ			nr +
Unigene17127_All	924	1.30	3.40	0.46	12.56	10.06	10.56	9.93	4.84	4.23	1.38E+00	1.62E-04	Up	-1.50E+00	2.71E-02		-3.20E-01	5.51E-02		-2.51E-01	1.67E-01		-1.04E+00	2.49E-09	Down	-1.23E+00	1.86E-12	Down	Unigene17127_All//gi|48310159|gb|AAT41765.1|/4.00E-41//At3g59680 [Arabidopsis thaliana] >gi|50198864|gb|AAT70459.1| At3g59680 [Arabidopsis thaliana]	Unigene17127_All//2.00E-45//AT3G59680| unknown protein	Unigene17127_All//0.00E+00//TC133510				nr +
Unigene17129_All	953	6.09	0.00	0.00	11.81	1.55	2.75	55.19	13.51	12.67	-1.26E+01	1.23E-33	Down	-1.26E+01	4.21E-32	Down	-2.93E+00	3.81E-46	Down	-2.10E+00	4.39E-27	Down	-2.03E+00	4.81E-134	Down	-2.12E+00	2.79E-146	Down	Unigene17129_All//gi|75099990|sp|Q80920.1|PYL4_ARATH//1.00E-66//RecName: Full=Abscisic acid receptor PYL4; AltName: Full=PYR1-like protein 4; AltName: Full=ABI1-binding protein 2; AltName: Full=Regulatory components of ABA receptor 10 >gi|3395441|gb|AAC28773.1| expressed protein [Arabidopsis thaliana] >gi|14517502|gb|AAK62641.1| At2g38310/T19C21.20 [Arabidopsis thaliana] >gi|15809748|gb|AAL06802.1| At2g38310/T19C21.20 [Arabidopsis thaliana]	Unigene17129_All//3.00E-67//AT2G38310| unknown protein	Unigene17129_All//5.00E-52//gi|109881683|gb|DW510653.1|DW510653				nr +
Unigene1713_All	826	3.74	11.23	8.51	5.43	6.21	9.02	6.55	13.00	9.98	1.59E+00	2.87E-14	Up	1.19E+00	4.81E-07	Up	1.95E-01	5.47E-01		7.33E-01	5.08E-04		9.89E-01	5.00E-10		6.08E-01	5.18E-04		Unigene1713_All//gi|297824297|ref|XP_002880031.1|//2.00E-55//UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325870|gb|EFH56290.1| UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene1713_All//2.00E-43//AT2G43210| UBX domain-containing protein	Unigene1713_All//0.00E+00//DR463169				nr -
Unigene17131_All	254	15.04	12.37	13.63	11.37	8.95	2.49	9.99	8.72	12.70	-2.82E-01	3.86E-01		-1.42E-01	6.60E-01		-3.46E-01	3.72E-01		-2.19E+00	1.06E-07	Down	-1.96E-01	6.43E-01		3.47E-01	2.65E-01				Unigene17131_All//2.00E-45//TC132851				
Unigene17132_All	882	1.78	2.13	3.44	5.42	3.12	2.77	21.19	8.25	13.14	2.56E-01	6.17E-01		9.51E-01	1.13E-02		-7.96E-01	1.97E-03		-9.72E-01	3.50E-04		-1.36E+00	1.51E-27	Down	-6.89E-01	8.87E-10		Unigene17132_All//gi|16226275|gb|AAL16121.1|AF425289_1//5.00E-10//AT5g57340/MJB24_15 [Arabidopsis thaliana]	Unigene17132_All//2.00E-10//AT5G57340| unknown protein	Unigene17132_All//0.00E+00//TC164221				nr +
Unigene17135_All	1164	0.09	0.57	0.18	3.12	2.84	8.54	2.91	1.87	1.54	2.65E+00	1.50E-02		1.03E+00	5.92E-01		-1.38E-01	7.10E-01		1.45E+00	3.27E-14	Up	-6.38E-01	3.41E-02		-9.16E-01	1.64E-03		Unigene17135_All//gi|18413388|ref|NP_567366.1|//1.00E-80//nodulin MtN3 family protein [Arabidopsis thaliana] >gi|21592843|gb|AAM64793.1| contains similarity to Medicago truncatula MtN3 (GB:U08726) [Arabidopsis thaliana] >gi|117168151|gb|ABK32158.1| At4g10850 [Arabidopsis thaliana]	Unigene17135_All//5.00E-82//AT4G10850| nodulin MtN3 family protein	Unigene17135_All//0.00E+00//gi|164244029|gb|ES821113.1|ES821113				nr +
Unigene17136_All	780	3.29	2.53	2.12	3.13	1.15	2.61	0.76	0.27	1.58	-3.76E-01	3.63E-01		-6.35E-01	1.30E-01		-1.45E+00	2.01E-04	Down	-2.64E-01	5.67E-01		-1.50E+00	9.13E-02		1.06E+00	4.50E-02		Unigene17136_All//gi|115334948|gb|AB194060.1|//2.00E-59//ripening-related expansin [Cucumis melo]	Unigene17136_All//6.00E-57//AT2G28950| ATEXPA6 (ARABIDOPSIS THALIANA EXPANSIN A6)	Unigene17136_All//0.00E+00//TC177828				nr +
Unigene17138_All	674	0.16	0.00	1.42	2.73	1.33	11.06	74.02	30.39	41.14	-7.28E+00	3.73E-01		3.19E+00	1.03E-03		-1.04E+00	2.21E-02		2.02E+00	9.22E-17	Up	-1.28E+00	4.28E-66	Down	-8.47E-01	7.68E-35		Unigene17138_All//gi|15857720|emb|CAC67501.1|//4.00E-93//selenium binding protein [Medicago sativa]	Unigene17138_All//2.00E-89//AT4G14040| SBP2 (SELENIUM-BINDING PROTEIN 2); selenium binding	Unigene17138_All//0.00E+00//gi|48802261|gb|CO103575.1|CO103575				nr +
Unigene17139_All	1108	1.04	2.24	1.97	6.29	4.01	4.08	2.25	1.09	0.29	1.11E+00	6.72E-03		9.23E-01	4.33E-02		-6.51E-01	1.69E-03		-6.27E-01	4.22E-03		-1.04E+00	3.86E-03		-2.97E+00	6.99E-11	Down	Unigene17139_All//gi|115486791|ref|NP_001068539.1|//8.00E-35//Os11g0703600 [Oryza sativa Japonica Group] >gi|77552699|gb|ABA95496.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|77552700|gb|ABA95497.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113645761|dbj|BAF28802.1| Os11g0703600 [Oryza sativa Japonica Group]	Unigene17139_All//1.00E-31//AT5G59350| unknown protein	Unigene17139_All//0.00E+00//TC151964				nr -
Unigene1714_All	1923	9.96	26.06	14.37	12.20	16.47	18.44	11.76	23.28	15.60	1.39E+00	7.89E-61	Up	5.29E-01	5.95E-07		4.33E-01	1.16E-06		5.96E-01	1.06E-11		9.85E-01	6.13E-39		4.07E-01	2.24E-06		Unigene1714_All//gi|297824297|ref|XP_002880031.1|//1.00E-117//UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325870|gb|EFH56290.1| UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene1714_All//4.00E-95//AT2G43210| UBX domain-containing protein	Unigene1714_All//0.00E+00//gi|21094702|gb|BQ407015.1|BQ407015				nr +
Unigene17142_All	782	0.67	2.72	1.02	2.74	3.30	3.47	1.68	4.44	1.02	2.02E+00	4.61E-05	Up	6.10E-01	4.41E-01		2.70E-01	5.44E-01		3.39E-01	4.22E-01		1.40E+00	5.62E-06	Up	-7.18E-01	1.54E-01				Unigene17142_All//2.00E-140//DW492196				
Unigene17145_All	356	17.20	17.08	5.53	19.17	17.80	31.97	29.57	35.34	32.56	-9.70E-03	9.86E-01		-1.64E+00	1.24E-09	Down	-1.07E-01	6.82E-01		7.38E-01	7.87E-06		2.57E-01	8.86E-02		1.39E-01	3.97E-01		Unigene17145_All//gi|61661324|gb|AAX51268.1|//6.00E-14//FLK [Arabidopsis thaliana] >gi|61661326|gb|AAX51269.1| FLK [Arabidopsis thaliana]		Unigene17145_All//0.00E+00//gi|13355924|gb|BG446212.1|BG446212			GO:0003676//GO:0009908//GO:0043231	nr -
Unigene17151_All	746	270.30	82.12	108.93	356.58	184.96	125.74	34.23	17.65	6.52	-1.72E+00	0.00E+00	Down	-1.31E+00	4.50E-217	Down	-9.47E-01	1.43E-216		-1.50E+00	0.00E+00	Down	-9.56E-01	1.54E-21		-2.39E+00	1.08E-82	Down	Unigene17151_All//gi|297796233|ref|XP_002866001.1|//3.00E-12//hypothetical protein ARALYDRAFT_918490 [Arabidopsis lyrata subsp. lyrata] >gi|297311836|gb|EFH42260.1| hypothetical protein ARALYDRAFT_918490 [Arabidopsis lyrata subsp. lyrata]		Unigene17151_All//0.00E+00//gi|82756670|gb|DV850232.1|DV850232			GO:0016020//GO:0043231	nr +

Unigene17153_All	672	1.17	3.47	1.66	4.67	4.20	4.50	0.88	0.68	1.36	1.57E+00	4.09E-04	Up	5.11E-01	4.34E-01		-1.52E-01	6.98E-01		-5.26E-02	9.03E-01		-3.64E-01	6.48E-01		6.30E-01	3.25E-01		Unigene17153_All//gi|15237955|ref|NP_197241.1|//5.00E-38//universal stress protein (USP) family protein [Arabidopsis thaliana]	Unigene17153_All//2.00E-21//AT5G17390| universal stress protein (USP) family protein	Unigene17153_All//0.00E+00//DW519995			GO:0048764//GO:0050896	nr +
Unigene17154_All	512	8.99	31.57	20.18	6.91	9.62	17.38	13.79	26.94	47.46	1.81E+00	3.41E-29	Up	1.17E+00	9.01E-10	Up	4.78E-01	8.21E-02		1.33E+00	2.65E-11	Up	9.66E-01	3.41E-12		1.78E+00	2.23E-53	Up	Unigene17154_All//gi|255630702|gb|ACU15712.1|//1.00E-06//unknown [Glycine max]	Unigene17154_All//5.00E-06//AT4G28290| unknown protein	Unigene17154_All//1.00E-180//TC174774				nr -
Unigene17155_All	1127	1.90	1.93	0.57	6.45	6.36	3.89	2.74	0.78	0.85	2.25E-02	9.79E-01		-1.75E+00	4.05E-04	Down	-2.21E-02	9.30E-01		-7.31E-01	5.75E-04		-1.81E+00	1.82E-07	Down	-1.69E+00	4.14E-07	Down	Unigene17155_All//gi|115451511|ref|NP_001049356.1|//3.00E-63//Os03g0212600 [Oryza sativa Japonica Group] >gi|108706817|gb|ABF94612.1| Targeting protein for Xklp2 containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547827|dbj|BAF11270.1| Os03g0212600 [Oryza sativa Japonica Group]	Unigene17155_All//8.00E-74//AT5G15510| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01015.1); Has 992 Blast hits to 819 proteins in 107 species: Archae - 0; Bacteria - 11; Metazoa - 477; Fungi - 40; Plants - 169; Viruses - 3; Other Eukaryotes - 292 (source: NCBI BLink).					nr -
Unigene17156_All	411	54.36	53.87	112.46	88.24	59.91	58.57	34.56	26.24	15.90	-1.29E-02	9.36E-01		1.05E+00	3.18E-35	Up	-5.59E-01	5.50E-12		-5.91E-01	6.78E-12		-3.98E-01	2.98E-03		-1.12E+00	2.81E-16	Down			Unigene17156_All//3.00E-33//TC177728				
Unigene17157_All	338	54.64	19.94	23.47	80.62	86.39	106.63	115.83	57.99	54.93	-1.45E+00	1.35E-24	Down	-1.22E+00	3.92E-18	Down	9.99E-02	4.15E-01		4.03E-01	3.52E-06		-9.98E-01	5.91E-35		-1.08E+00	1.28E-40	Down	Unigene17157_All//gi|15238099|ref|NP_198967.1|//1.00E-54//40S ribosomal protein S10 (RPS10B) [Arabidopsis thaliana] >gi|20139725|sp|Q9FFS8.1|RS102_ARATH RecName: Full=40S ribosomal protein S10-2 >gi|14030699|gb|AAK53024.1|AF37544_1 AT5g41520/MBK23_4 [Arabidopsis thaliana] >gi|14335122|gb|AAK59840.1| AT5g41520/MBK23_4 [Arabidopsis thaliana] >gi|16974521|gb|AAL31170.1| AT5g41520/MBK23_4 [Arabidopsis thaliana]	Unigene17157_All//3.00E-25//AT5G41520| 40S ribosomal protein S10 (RPS10B)	Unigene17157_All//0.00E+00//gi|13352960|gb|BG443308.1|BG443308		ko03010|Ribosome	GO:0009536//GO:0010467//GO:0015935//GO:0030312	nr +
Unigene17158_All	1300	1.61	4.01	4.30	12.76	11.50	9.69	10.08	8.55	6.40	1.32E+00	1.55E-06	Up	1.42E+00	2.47E-07	Up	-1.51E-01	3.24E-01		-3.97E-01	3.54E-03		-2.38E-01	1.12E-01		-6.55E-01	1.37E-06		Unigene17158_All//gi|224133542|ref|XP_002321600.1|//1.00E-116//f-box family protein [Populus trichocarpa] >gi|222868596|gb|EEF05727.1| f-box family protein [Populus trichocarpa]	Unigene17158_All//1.00E-55//AT5G62940| Dof-type zinc finger domain-containing protein	Unigene17158_All//1.00E-22//TC170824	C2C2-Dof		GO:0003676//GO:0010468//GO:0046914	nr -
Unigene17159_All	355	22.25	6.99	18.15	24.70	18.72	22.39	28.35	16.25	12.79	-1.67E+00	3.21E-13	Down	-2.94E-01	1.97E-01		-4.00E-01	3.68E-02		-1.41E-01	5.49E-01		-8.03E-01	6.78E-07		-1.15E+00	3.23E-12	Down	Unigene17159_All//gi|224081865|ref|XP_002306607.1|//2.00E-16//porin/voltage-dependent anion-selective channel protein [Populus trichocarpa] >gi|222855956|gb|EEE93503.1| porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	Unigene17159_All//3.00E-17//AT5G67500| VDAC2 (VOLTAGE DEPENDENT ANION CHANNEL 2); voltage-gated anion channel	Unigene17159_All//0.00E+00//gi|5045296|gb|AI726444.1|AI726444			GO:0005244//GO:0006811//GO:0009526//GO:0030312//GO:0031966//GO:0051707	nr -
Unigene17160_All	362	1.59	16.66	6.91	6.74	8.94	15.97	5.84	17.78	23.55	3.39E+00	2.07E-22	Up	2.12E+00	7.34E-06	Up	4.07E-01	2.75E-01		1.24E+00	7.15E-07	Up	1.61E+00	1.54E-12	Up	2.01E+00	1.70E-22	Up			Unigene17160_All//2.00E-86//TC138386				
Unigene17166_All	657	2.15	0.77	1.86	3.64	2.36	1.10	2.96	0.51	0.91	-1.48E+00	1.15E-02		-2.06E-01	7.06E-01		-6.26E-01	1.19E-01		-1.73E+00	6.61E-05	Down	-2.54E+00	3.67E-07	Down	-1.70E+00	7.95E-05	Down	Unigene17166_All//gi|38344244|emb|CAD41337.2|//7.00E-12//OJ991113_30.21 [Oryza sativa (japonica cultivar-group)]		Unigene17166_All//2.00E-19//TC133982			GO:0003676//GO:0016772//GO:0044238//GO:0044260	nr +
Unigene17168_All	464	5.86	1.86	4.48	4.08	4.30	2.34	3.46	0.90	2.58	-1.66E+00	5.09E-05	Down	-3.90E-01	3.51E-01		7.74E-02	8.87E-01		-8.04E-01	9.25E-02		-1.94E+00	1.42E-04	Down	-4.27E-01	3.59E-01				Unigene17168_All//0.00E+00//gi|109868929|gb|DW497905.1|DW497905				
Unigene1717_All	2615	1.30	4.48	2.14	3.94	6.37	5.82	16.02	13.75	15.77	1.78E+00	6.95E-21	Up	7.17E-01	6.17E-03		6.93E-01	5.17E-08		5.62E-01	6.16E-05		-2.21E-01	3.49E-03		-2.31E-02	7.86E-01		Unigene1717_All//gi|145567026|gb|ABR81863.1|//0.00E+00//LATE BLOOMER 1 [Pisum sativum]	Unigene1717_All//0.00E+00//AT1G22770| GI (GIGANTEA)	Unigene1717_All//0.00E+00//gi|78334501|gb|DT554775.1|DT554775		ko04712|Circadian rhythm - plant		nr +
Unigene17170_All	497	177.60	76.77	73.39	283.35	196.57	312.33	274.86	120.26	108.21	-1.21E+00	9.58E-87	Down	-1.27E+00	4.61E-91	Down	-5.28E-01	6.56E-41		1.41E-01	7.52E-04		-1.19E+00	5.18E-160	Down	-1.34E+00	2.14E-198	Down	Unigene17170_All//gi|196658063|gb|ACG48499.1|//1.00E-28//40S ribosomal protein S5 [Zea mays]	Unigene17170_All//4.00E-29//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	Unigene17170_All//0.00E+00//TC140019		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0032279	nr +
Unigene17171_All	555	112.09	50.58	60.64	177.90	154.87	160.07	101.17	65.14	52.90	-1.15E+00	1.86E-56	Down	-8.86E-01	9.59E-36		-2.00E-01	4.83E-05		-1.52E-01	4.55E-03		-6.35E-01	2.64E-23		-9.35E-01	4.83E-46		Unigene17171_All//gi|257215078|emb|CAB64523.1|//1.00E-14//nuclear RNA binding protein [Solanum tuberosum]		Unigene17171_All//6.00E-149//DT052712				nr -
Unigene17173_All	616	0.68	0.33	4.58	5.18	3.91	3.37	3.84	1.09	1.42	-1.05E+00	3.66E-01		2.75E+00	1.32E-08	Up	-4.03E-01	2.62E-01		-6.18E-01	7.96E-02		-1.82E+00	6.14E-06	Down	-1.43E+00	1.25E-04	Down			Unigene17173_All//2.00E-53//TC179501				
Unigene17174_All	287	65.26	23.30	18.37	59.53	46.67	73.96	118.59	39.32	38.31	-1.49E+00	1.03E-25	Down	-1.83E+00	4.67E-33	Down	-3.51E-01	6.68E-03		3.13E-01	9.89E-03		-1.59E+00	2.29E-62	Down	-1.63E+00	2.12E-66	Down	Unigene17174_All//gi|297827541|ref|XP_002881653.1|//1.00E-17//Os04g0376000 [Arabidopsis lyrata subsp. lyrata] >gi|297327492|gb|EFH57912.1| Os04g0376000 [Arabidopsis lyrata subsp. lyrata]	Unigene17174_All//5.00E-19//AT5G02610| 60S ribosomal protein L35 (RPL35D)	Unigene17174_All//4.00E-161//gi|164355283|gb|ES816324.1|ES816324		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0003181	nr +
Unigene17177_All	376	16.28	6.33	21.81	28.75	14.20	9.01	7.53	4.00	0.85	-1.36E+00	6.49E-08	Down	4.22E-01	4.90E-02		-1.02E+00	2.75E-10	Down	-1.67E+00	3.22E-19	Down	-9.13E-01	6.11E-03		-3.15E+00	5.98E-13	Down	Unigene17177_All//gi|145334659|ref|NP_001078675.1|//9.00E-37//PDLP7 (PLASMODESMATA-LOCATED PROTEIN 7) [Arabidopsis thaliana] >gi|122242482|sp|Q0WPN8.1|CRR60_ARATH RecName: Full=Cysteine-rich repeat secretory protein 60; Flags: Precursor	Unigene17177_All//2.00E-23//AT5G37660| PDLP7 (PLASMODESMATA-LOCATED PROTEIN 7)	Unigene17177_All//1.00E-47//gi|78336855|gb|DT557129.1|DT557129			GO:0005488//GO:0005911	nr +
Unigene17179_All	1318	0.48	0.31	0.28	4.61	2.59	0.99	6.06	0.60	5.17	-6.31E-01	4.75E-01		-7.52E-01	4.11E-01		-8.34E-01	1.77E-04		-2.21E+00	8.41E-16	Down	-3.33E+00	7.17E-36	Down	-2.30E-01	2.28E-01		Unigene17179_All//gi|18423110|ref|NP_568721.1|//1.00E-125//short-chain dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] >gi|20260276|gb|AAM13036.1| ribitol dehydrogenase-like [Arabidopsis thaliana]	Unigene17179_All//3.00E-120//AT5G50130| short-chain dehydrogenase/reductase (SDR) family protein	Unigene17179_All//0.00E+00//DW240553		ko00051|Fructose and mannose metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism//ko00860|Porphyrin and chlorophyll metabolism	GO:0008152//GO:0016491	nr +
Unigene1718_All	527	2.38	0.19	1.62	4.92	2.09	1.71	5.94	7.30	2.27	-3.63E+00	2.00E-05	Down	-5.60E-01	3.87E-01		-1.23E+00	8.91E-04	Down	-1.52E+00	1.69E-04	Down	2.98E-01	3.28E-01		-1.39E+00	1.30E-05	Down	Unigene1718_All//gi|79365227|ref|NP_175775.2|//3.00E-15//hydrolase/protein serine/threonine phosphatase [Arabidopsis thaliana]	Unigene1718_All//2.00E-16//AT1G53710| hydrolase/ protein serine/threonine phosphatase	Unigene1718_All//0.00E+00//gi|72268610|gb|DT046814.1|DT046814				nr -
Unigene17184_All	3320	0.25	0.21	0.00	0.30	0.17	0.05	10.67	19.24	13.62	-2.38E-01	7.25E-01		-7.98E+00	1.19E-04	Down	-8.54E-01	2.05E-01		-2.46E+00	2.07E-03		8.50E-01	2.76E-43		3.52E-01	3.51E-07		Unigene17184_All//gi|18405700|ref|NP_564709.1|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana]	Unigene17184_All//0.00E+00//AT1G56140| leucine-rich repeat family protein / protein kinase family protein	Unigene17184_All//0.00E+00//gi|109826453|gb|DW225167.1|DW225167			GO:0004674//GO:0006464//GO:0016020//GO:0031410//GO:0032559	nr -
Unigene17186_All	633	40.67	17.53	24.98	7.48	6.58	6.78	0.00	0.00	0.00	-1.21E+00	6.50E-26	Down	-7.03E-01	2.38E-10		-1.84E-01	5.56E-01		-1.41E-01	6.56E-01		null	null		null	null		Unigene17186_All//gi|15010676|gb|AAK73992.1|//6.00E-68//At1g64150/F22C12_10 [Arabidopsis thaliana] >gi|23565909|gb|AAN28814.1| At1g64150/F22C12_10 [Arabidopsis thaliana]	Unigene17186_All//4.00E-69//AT1G64150| unknown protein	Unigene17186_All//0.00E+00//gi|48741316|gb|CO071835.1|CO071835			GO:0031224//GO:0043231	nr -
Unigene17187_All	347	7.84	1.17	7.52	13.35	4.47	7.55	3.78	5.54	3.67	-2.75E+00	1.03E-08	Down	-6.03E-02	8.82E-01		-1.58E+00	6.71E-09	Down	-8.23E-01	2.94E-03		5.53E-01	1.99E-01		-4.00E-02	9.54E-01				Unigene17187_All//7.00E-160//TC173256				
Unigene17191_All	501	2.92	3.14	3.08	8.85	9.07	9.38	18.90	9.51	9.14	1.01E-01	8.43E-01		7.60E-02	8.89E-01		3.60E-02	9.23E-01		8.33E-02	7.91E-01		-9.91E-01	5.60E-09		-1.05E+00	4.35E-10	Down	Unigene17191_All//gi|33945873|emb|CAE45585.1|//4.00E-56//coatomer alpha subunit-like protein [Lotus japonicus]	Unigene17191_All//1.00E-51//AT2G21390| coatomer protein complex, subunit alpha, putative	Unigene17191_All//3.00E-169//gi|54122603|gb|CO498112.1|CO498112			GO:0004683//GO:0005488//GO:0015031//GO:0030120//GO:0031461//GO:0048193	nr +
Unigene17192_All	1506	1.25	4.54	1.03	1.52	0.62	5.67	5.47	20.45	17.27	1.86E+00	3.35E-13	Up	-2.87E-01	5.83E-01		-1.30E+00	1.16E-03		1.90E+00	1.04E-17	Up	1.90E+00	4.49E-72	Up	1.66E+00	1.29E-51	Up	Unigene17192_All//gi|259121423|gb|ACV92031.1|//2.00E-89//WRKY transcription factor 29 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene17192_All//2.00E-49//AT4G18170| WRKY28; transcription factor	Unigene17192_All//0.00E+00//TC131145	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0006350//GO:0006952//GO:0009725//GO:0010468//GO:0034014//GO:0043231	nr +
Unigene17193_All	242	3.46	8.58	2.42	1.24	6.26	13.06	22.54	28.32	24.20	1.31E+00	4.47E-03		-5.15E-01	5.15E-01		2.34E+00	1.15E-04	Up	3.40E+00	1.19E-12	Up	3.30E-01	1.18E-01		1.03E-01	6.55E-01		Unigene17193_All//gi|297841455|ref|XP_002888609.1|//7.00E-23//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334450|gb|EFH64868.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17193_All//3.00E-24//AT1G67580| protein kinase family protein	Unigene17193_All//4.00E-120//TC177473			GO:0004674//GO:0006464//GO:0032559//GO:0044444	nr -
Unigene17195_All	412	48.38	26.81	51.70	77.74	63.52	49.99	7.90	4.97	2.90	-8.52E-01	1.22E-11		9.56E-02	5.01E-01		-2.92E-01	1.35E-03		-6.37E-01	5.25E-12		-6.69E-01	2.97E-02		-1.45E+00	4.08E-06	Down							
Unigene17196_All	630	0.83	3.62	0.93	5.85	15.96	35.49	36.64	25.67	55.08	2.12E+00	1.18E-05	Up	1.63E-01	8.50E-01		1.45E+00	1.67E-15	Up	2.60E+00	3.73E-67	Up	-5.13E-01	4.00E-07		5.88E-01	2.82E-13		Unigene17196_All//gi|224078888|ref|XP_002305667.1|//4.00E-10//predicted protein [Populus trichocarpa] >gi|222848631|gb|EEE86178.1| predicted protein [Populus trichocarpa]		Unigene17196_All//4.00E-147//gi|164339157|gb|ES851336.1|ES851336				nr +
Unigene17197_All	590	17.91	1400.80	117.60	10.13	97.94	95.69	0.93	1.49	2.03	6.29E+00	0.00E+00	Up	2.71E+00	3.54E-199	Up	3.27E+00	2.87E-237	Up	3.24E+00	4.57E-212	Up	6.75E-01	3.28E-01		1.12E+00	3.88E-02		Unigene17197_All//gi|126080|sp|P13939.1|LEAD7_GOSHI//8.00E-43//RecName: Full=Late embryogenesis abundant protein D-7; Short=LEA D-7 >gi|18497|emb|CAA33194.1| D 29 protein [Gossypium hirsutum] >gi|18505|emb|CAA31589.1| D-7 Lea protein [Gossypium hirsutum] >gi|226551|prf||1601521A Lea D-7 gene	Unigene17197_All//6.00E-09//AT3G15670| late embryogenesis abundant protein, putative / LEA protein, putative	Unigene17197_All//4.00E-110//TC169652			GO:0043231	nr +
Unigene17198_All	569	4.32	4.01	6.93	1.75	0.54	0.40	3.42	1.47	0.77	-1.09E-01	7.80E-01		6.80E-01	3.47E-02		-1.68E+00	1.36E-02		-2.14E+00	5.32E-03		-1.22E+00	3.87E-03		-2.15E+00	2.89E-06	Down			Unigene17198_All//1.00E-08//DW508553				
Unigene17199_All	1089	2.40	0.79	1.12	1.69	0.28	0.12	4.93	1.38	0.59	-1.60E+00	1.16E-04	Down	-1.09E+00	8.04E-03		-2.57E+00	7.33E-07	Down	-3.77E+00	2.03E-08	Down	-1.84E+00	1.26E-12	Down	-3.07E+00	2.23E-23	Down			Unigene17199_All//0.00E+00//DW508553				
Unigene17201_All	539	5.05	9.21	40.90	34.20	5.88	14.08	205.75	275.20	133.49	8.68E-01	1.33E-03		3.02E+00	9.35E-71	Up	-2.54E+00	2.08E-64	Down	-1.28E+00	7.28E-22	Down	4.20E-01	9.74E-29		-6.24E-01	4.25E-45		Unigene17201_All//gi|44888879|gb|AAS48177.1|//9.00E-13//merlot proline-rich protein 2 [Vitis vinifera]		Unigene17201_All//0.00E+00//DN827784				nr -
Unigene17202_All	348	25.26	25.04	19.43	33.35	19.00	22.97	40.09	18.02	18.55	-1.23E-02	9.72E-01		-3.78E-01	7.01E-02		-8.12E-01	1.15E-07		-5.38E-01	1.01E-03		-1.15E+00	3.20E-16	Down	-1.11E+00	7.99E-16	Down			Unigene17202_All//8.00E-98//TC164165				
Unigene17203_All	1758	0.00	0.12	0.12	0.06	1.10	7.04	4.18	21.49	68.21	6.85E+00	1.37E-01		6.92E+00	1.41E-01		4.27E+00	1.23E-09	Up	6.96E+00	1.06E-71	Up	2.36E+00	4.46E-116	Up	4.03E+00	0.00E+00	Up	Unigene17203_All//gi|115466824|ref|NP_001057011.1|//7.00E-48//Os06g0186600 [Oryza sativa Japonica Group] >gi|113595051|dbj|BAF18925.1| Os06g0186600 [Oryza sativa Japonica Group]	Unigene17203_All//9.00E-47//AT2G24100| unknown protein	Unigene17203_All//9.00E-160//TC160784		ko03022|Basal transcription factors		nr -
Unigene17204_All	281	0.56	4.51	0.00	1.06	0.98	0.48	0.00	0.30	3.12	3.01E+00	1.02E-04	Up	-9.13E+00	2.45E-01		-1.18E-01	9.01E-01		-1.14E+00	4.58E-01		8.22E+00	4.02E-01		1.16E+01	2.05E-06	Up							
Unigene17205_All	619	1.86	5.57	0.95	1.69	1.17	1.46	0.96	1.55	1.03	1.58E+00	9.34E-06	Up	-9.75E-01	1.46E-01		-5.33E-01	4.27E-01		-2.12E-01	7.44E-01		7.00E-01	2.78E-01		1.07E-01	9.02E-01				Unigene17205_All//5.00E-48//TC177566				
Unigene17206_All	523	43.32	122.85	113.83	101.82	74.20	248.61	40.74	121.47	71.30	1.50E+00	1.12E-87	Up	1.39E+00	1.02E-70	Up	-4.56E-01	3.86E-12		1.29E+00	1.31E-150	Up	1.58E+00	8.15E-114	Up	8.07E-01	4.16E-24				Unigene17206_All//0.00E+00//TC159699				

Unigene17208_All	267	7.05	11.39	21.94	16.23	20.64	18.61	20.59	23.95	22.98	6.91E-01	5.37E-02		1.64E+00	2.75E-09	Up	3.46E-01	1.99E-01		1.97E-01	5.32E-01		2.18E-01	3.55E-01		1.59E-01	4.97E-01		Unigene17208_All//gi|12697589|dbj|BAB21595.1|//4.00E-13//Tat binding protein like protein [Brassica rapa]	Unigene17208_All//5.00E-14//AT3G05530| RPT5A (REGULATORY PARTICLE TRIPLE-A ATPASE 5A); ATPase/ calmodulin binding	Unigene17208_All//1.00E-117//gi|84152660|gb|DN802015.1|DN802015		ko03050|Proteasome	GO:0005515//GO:0000838//GO:0009757//GO:0016020//GO:0019941//GO:0032559//GO:0042623//GO:0043231//GO:0048229	nr -
Unigene17209_All	668	8.54	11.07	6.22	5.00	4.48	2.03	0.19	0.38	0.42	3.75E-01	8.74E-02		-4.57E-01	8.40E-02		-1.56E-01	6.77E-01		-1.30E+00	1.41E-04	Down	9.83E-01	5.17E-01		1.14E+00	3.99E-01		Unigene17209_All//gi|115457076|ref|NP_001052138.1|//4.00E-60//Os04g0166600 [Oryza sativa Japonica Group] >gi|113563709|dbj|BAF14052.1|Os04g0166600 [Oryza sativa Japonica Group]	Unigene17209_All//6.00E-41//AT1G19330| unknown protein	Unigene17209_All//0.00E+00//TC173699				nr +
Unigene17210_All	1410	0.07	0.36	1.51	0.42	0.66	3.72	8.76	2.40	14.75	2.28E+00	6.23E-02		4.35E+00	1.94E-09	Up	6.37E-01	4.18E-01		3.13E+00	2.79E-19	Up	-1.87E+00	1.10E-28	Down	7.52E-01	2.34E-12		Unigene17210_All//gi|115476924|ref|NP_001062058.1|//5.00E-77//Os08g0480200 [Oryza sativa Japonica Group] >gi|113624027|dbj|BAF23972.1|Os08g0480200 [Oryza sativa Japonica Group]	Unigene17210_All//6.00E-65//AT2G36690| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene17210_All//0.00E+00//TC155102		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr +
Unigene17211_All	382	6.44	9.68	8.78	12.52	9.38	9.46	36.75	17.94	10.53	5.89E-01	6.68E-02		4.48E-01	2.18E-01		-4.17E-01	1.33E-01		-4.04E-01	1.63E-01		-1.03E+00	8.62E-14	Down	-1.80E+00	5.15E-32	Down	Unigene17211_All//gi|57471698|gb|AAW50980.1|//8.00E-06//ribosomal protein L36 [Triticum aestivum]	Unigene17211_All//1.00E-06//AT3G53740| 60S ribosomal protein L36 (RPL36B)	Unigene17211_All//0.00E+00//TC154576		ko03010|Ribosome		nr -
Unigene17213_All	381	38.04	47.34	55.07	35.82	20.16	53.46	36.29	40.70	8.16	3.16E-01	1.78E-02		5.34E-01	1.58E-05		-8.30E-01	3.10E-09		5.78E-01	1.16E-06		1.66E-01	2.42E-01		-2.15E+00	1.01E-39	Down			Unigene17213_All//5.00E-93//TC161094				
Unigene17214_All	1328	29.98	7.86	33.08	8.48	10.42	6.22	0.13	0.25	0.06	-1.93E+00	6.53E-78	Down	1.42E-01	1.22E-01		2.98E-01	5.29E-02		-4.46E-01	8.48E-03		9.84E-01	4.24E-01		-1.09E+00	5.53E-01		Unigene17214_All//gi|6554181|gb|AAF16627.1|AC011661_5//1.00E-146//T23J18.8 [Arabidopsis thaliana]	Unigene17214_All//1.00E-143//AT1G11410| S-locus protein kinase, putative					nr +
Unigene17216_All	507	39.42	17.39	20.59	43.03	39.67	50.33	96.15	36.93	40.23	-1.18E+00	1.90E-19	Down	-9.37E-01	5.48E-13		-1.18E-01	3.93E-01		2.26E-01	4.76E-02		-1.38E+00	4.38E-72	Down	-1.26E+00	2.77E-64	Down	Unigene17216_All//gi|82623429|gb|AB887129.1|//5.00E-55//60S ribosomal protein L7A-like [Solanum tuberosum]	Unigene17216_All//1.00E-47//AT3G62870| 60S ribosomal protein L7A (RPL7aB)	Unigene17216_All//5.00E-174//TC150688		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0046914	nr +
Unigene17217_All	1607	0.42	0.63	1.16	1.80	1.97	1.57	3.45	7.39	6.62	5.75E-01	3.83E-01		1.45E+00	4.96E-03		1.33E-01	7.70E-01		-1.92E-01	6.34E-01		1.10E+00	6.34E-13	Up	9.42E-01	1.76E-09								
Unigene17219_All	722	1.81	1.82	1.25	2.14	0.38	1.00	1.76	3.18	1.43	1.03E-02	9.84E-01		-5.31E-01	3.86E-01		-2.49E+00	1.27E-05	Down	-1.10E+00	4.18E-02		8.58E-01	2.27E-02		-2.92E-01	5.99E-01		Unigene17219_All//gi|297814614|ref|XP_002875190.1|//2.00E-48//CAAX amino terminal protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321028|gb|EFH51449.1| CAAX amino terminal protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17219_All//7.00E-48//AT2G03140| CAAX amino terminal protease family protein				GO:0043231	nr +
Unigene17221_All	528	1.98	1.54	1.51	3.02	1.57	2.14	3.12	0.55	0.68	-3.68E-01	5.90E-01		-3.90E-01	5.89E-01		-9.48E-01	5.80E-02		-4.98E-01	3.77E-01		-2.49E+00	4.58E-06	Down	-2.20E+00	1.44E-05	Down	Unigene17221_All//gi|18398417|ref|NP_564399.1|//7.00E-58//TOM2A (TOBAMOVIRUS MULTIPLICATION 2A); protein binding [Arabidopsis thaliana] >gi|42571723|ref|NP_973952.1|TOM2A (TOBAMOVIRUS MULTIPLICATION 2A); protein binding [Arabidopsis thaliana] >gi|79319067|ref|NP_001031127.1|TOM2A (TOBAMOVIRUS MULTIPLICATION 2A); protein binding [Arabidopsis thaliana] >gi|14326469|gb|AAK60280.1|AF385687_1 Atlg32400/F5O14_22 [Arabidopsis thaliana] >gi|25006245|dbj|BAC24019.1|tobamovirus multiplication 2A [Arabidopsis thaliana]	Unigene17221_All//4.00E-59//AT1G32400| TOM2A (TOBAMOVIRUS MULTIPLICATION 2A); protein binding	Unigene17221_All//5.00E-168//C0105516		ko03420|Nucleotide excision repair//ko03022|Basal transcription factors	GO:0005488//GO:0022415//GO:0031224//GO:0031410//GO:0043231	nr +
Unigene17225_All	680	2.62	0.89	1.80	3.88	2.38	1.53	0.68	0.37	0.70	-1.55E+00	2.66E-03		-5.39E-01	3.00E-01		-7.06E-01	5.83E-02		-1.35E+00	6.28E-04	Down	-8.91E-01	3.84E-01		3.97E-02	9.76E-01		Unigene17225_All//gi|195622042|gb|ACG32851.1|//3.00E-58//IQD1 [Zea mays]	Unigene17225_All//1.00E-47//AT5G03040| iqd2 (IQ-domain 2); calmodulin binding	Unigene17225_All//0.00E+00//gi|78325675|gb|DT545949.1|DT545949			GO:0016020	nr -
Unigene17227_All	245	13.03	10.34	5.87	14.64	9.28	15.67	48.49	22.35	11.38	-3.33E-01	3.65E-01		-1.15E+00	1.83E-03		-6.58E-01	3.42E-02		9.81E-02	7.74E-01		-1.12E+00	2.83E-13	Down	-2.09E+00	5.20E-33	Down			Unigene17227_All//9.00E-134//BQ412756				
Unigene1723_All	2623	64.43	66.57	78.42	64.53	117.64	93.56	41.86	65.31	120.03	4.71E-02	3.04E-01		2.84E-01	2.84E-15		8.66E-01	3.59E-208		5.36E-01	2.42E-64		6.42E-01	1.19E-70		1.52E+00	0.00E+00	Up	Unigene1723_All//gi|15239925|ref|NP_199176.1|//6.00E-60//TZP; DNA binding / binding / nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene1723_All//2.00E-57//AT5G43630| TZP; DNA binding / nucleic acid binding / zinc ion binding	Unigene1723_All//4.00E-64//gi|84151078|gb|DN800433.1|DN800433				nr -
Unigene17230_All	332	26.95	18.01	29.19	32.56	44.60	42.03	76.66	39.66	26.64	-5.82E-01	2.50E-03		1.15E-01	6.05E-01		4.54E-01	1.08E-03		3.69E-01	1.60E-02		-9.51E-01	2.67E-21		-1.53E+00	2.50E-45	Down	Unigene17230_All//gi|162955861|gb|ABY25306.1|//1.00E-52//pyrophosphate-dependent phosphofructokinase beta subunit [Citrus sinensis x Poncirus trifoliata]	Unigene17230_All//2.00E-53//AT1G12000| pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative	Unigene17230_All//0.00E+00//TC140186		ko00051|Fructose and mannose metabolism	GO:0006007//GO:0008443//GO:0010038//GO:0010316//GO:0030312//GO:0032559//GO:0043231	nr -
Unigene17231_All	397	2.11	6.76	3.35	3.51	3.04	2.84	0.85	2.84	0.90	1.68E+00	5.21E-05	Up	6.69E-01	2.69E-01		-2.11E-01	7.29E-01		-3.05E-01	6.38E-01		1.74E+00	4.63E-03		8.40E-02	9.57E-01								
Unigene17232_All	1140	0.32	0.22	0.19	0.96	1.27	0.99	1.59	0.44	1.26	-5.32E-01	6.27E-01		-7.82E-01	5.53E-01		4.00E-01	5.30E-01		4.30E-02	9.43E-01		-1.86E+00	7.83E-05	Down	-3.42E-01	4.25E-01		Unigene17232_All//gi|10257491|dbj|BAB11613.1|//1.00E-150//cleavage and polyadenylation specificity factor subunit [Arabidopsis thaliana]	Unigene17232_All//2.00E-144//AT5G51660| CPSF160; nucleic acid binding				GO:0044464	nr +
Unigene17233_All	339	6.79	16.14	10.21	6.91	8.84	8.26	36.54	43.89	29.97	1.25E+00	2.45E-06	Up	5.88E-01	9.15E-02		3.56E-01	3.69E-01		2.58E-01	5.49E-01		2.64E-01	5.20E-02		-2.86E-01	4.64E-02		Unigene17233_All//gi|547478|emb|CAA85733.1|//3.00E-11//guanine nucleotide regulatory protein [Vicia faba] >gi|1098297|prf||2115367E small GTP-binding protein	Unigene17233_All//1.00E-08//AT4G19640| ARA7; GTP binding	Unigene17233_All//3.00E-177//gi|21090115|gb|BQ402428.1|BQ402428		ko04145|Phagosome//ko04144|Endocytosis	GO:0006810//GO:0016020//GO:0032561//GO:0035556	nr -
Unigene17236_All	734	1.35	1.73	1.09	1.49	1.27	0.98	3.80	2.62	1.25	3.50E-01	5.68E-01		-3.16E-01	6.27E-01		-2.37E-01	7.30E-01		-6.01E-01	3.90E-01		-5.37E-01	1.18E-01		-1.61E+00	4.09E-06	Down			Unigene17236_All//9.00E-07//EX172003				
Unigene1724_All	2387	7.39	10.76	9.03	8.85	9.36	11.16	19.02	29.50	40.37	5.43E-01	4.09E-07		2.91E-01	2.19E-02		8.15E-02	5.81E-01		3.35E-01	1.42E-03		6.33E-01	7.72E-29		1.09E+00	2.53E-99	Up	Unigene1724_All//gi|15220275|ref|NP_172572.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|75317752|sp|Q04086.1|Y1105_ARATH RecName: Full=Probable receptor-like protein kinase At1g11050; Flags: Precursor >gi|1931642|gb|AAB65477.1| Ser/Thr protein kinase isolog; 46094-44217 [Arabidopsis thaliana]	Unigene1724_All//0.00E+00//AT1G11050| protein kinase family protein	Unigene1724_All//0.00E+00//gi|164320817|gb|ES826479.1|ES826479		ko04626|Plant-pathogen interaction		nr +
Unigene17240_All	410	29.48	18.17	26.24	49.94	31.41	34.81	42.38	17.33	24.78	-6.98E-01	1.77E-05		-1.68E-01	3.81E-01		-6.69E-01	1.80E-09		-5.21E-01	1.04E-05		-1.29E+00	1.08E-23	Down	-7.75E-01	4.98E-11		Unigene17240_All//gi|51340062|gb|AAU00727.1|//1.00E-70//glucose-6-phosphate isomerase [Solanum lycopersicum]	Unigene17240_All//9.00E-67//AT4G24620| PGI1 (PHOSPHOGLUCOSE ISOMERASE 1); glucose-6-phosphate isomerase	Unigene17240_All//0.00E+00//TC156417		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway	GO:0002376//GO:0003676//GO:0006007//GO:0006073//GO:0009526//GO:0009532//GO:0009908//GO:0016861//GO:0032559	nr +
Unigene17245_All	1195	2.15	3.14	2.09	6.09	3.80	4.23	7.47	5.88	3.50	5.49E-01	8.47E-02		-3.47E-02	9.47E-01		-6.78E-01	7.69E-04		-5.24E-01	1.57E-02		-3.45E-01	5.28E-02		-1.09E+00	3.62E-10	Down	Unigene17245_All//gi|145324100|ref|NP_001077639.1|//1.00E-62//RECQL2 (ARABIDOPSIS RECQ HELICASE L2); 3'-5' DNA helicase/ ATP-dependent helicase/ four-way junction helicase/ protein binding [Arabidopsis thaliana]	Unigene17245_All//5.00E-62//AT1G31360| RECQL2 (ARABIDOPSIS RECQ HELICASE L2); 3'-5' DNA helicase/ ATP-dependent helicase/ four-way junction helicase/ protein binding	Unigene17245_All//0.00E+00//C0080049			GO:0004003//GO:0005622//GO:0006259//GO:0032559	nr +
Unigene17248_All	1013	11.67	7.65	13.77	2.90	2.82	1.61	0.83	0.12	0.31	-6.09E-01	2.10E-04		2.39E-01	1.48E-01		-4.03E-02	9.10E-01		-8.54E-01	1.88E-02		-2.75E+00	9.73E-04	Down	-1.41E+00	3.70E-02		Unigene17248_All//gi|87116636|gb|ABD19682.1|//4.00E-75//At2g32500 [Arabidopsis thaliana]	Unigene17248_All//1.00E-70//AT2G32500| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Stress responsive alpha-beta barrel (InterPro:IPR013097), Dimeric alpha-beta barrel (InterPro:IPR011008); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G31670.1); Has 36 Blast hits to 33 proteins in 10 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene17248_All//0.00E+00//D8458963			GO:0043231//GO:0044444	nr -
Unigene17249_All	552	15.73	13.77	16.50	209.73	121.33	214.94	52.77	135.68	119.59	-1.93E-01	3.76E-01		6.82E-02	7.43E-01		-7.90E-01	5.28E-69		3.54E-02	5.82E-01		1.36E+00	5.42E-108	Up	1.18E+00	5.72E-78	Up	Unigene17249_All//gi|10444366|gb|AAG17877.1|AF293404_1//4.00E-09//suspensor-specific protein [Phaseolus coccineus] >gi|131731417|gb|AAK14318.1|AF325187_2 suspensor-specific protein [Phaseolus coccineus]		Unigene17249_All//0.00E+00//DW501838				nr -
Unigene1725_All	2207	2.44	7.32	1.95	6.03	9.19	7.33	7.30	16.80	18.05	1.58E+00	2.73E-24	Up	-3.21E-01	2.47E-01		6.09E-01	8.66E-08		2.82E-01	5.26E-02		1.20E+00	1.81E-44	Up	1.31E+00	2.04E-55	Up	Unigene1725_All//gi|260408334|gb|ACX37460.1|//0.00E+00//calcium dependent protein kinase 32 [Gossypium hirsutum]	Unigene1725_All//0.00E+00//AT3G57530| CPK32 (CALCIUM-DEPENDENT PROTEIN KINASE 32); calcium-dependent protein kinase C/ calmodulin-dependent protein kinase/ kinase/ protein binding	Unigene1725_All//0.00E+00//TC166163		ko04626|Plant-pathogen interaction		nr +
Unigene17250_All	444	8.25	11.53	19.67	8.86	8.22	6.61	2.57	3.01	3.77	4.83E-01	7.15E-02		1.25E+00	2.70E-09	Up	-1.09E-01	7.75E-01		-4.23E-01	1.93E-01		2.29E-01	6.60E-01		5.52E-01	2.14E-01		Unigene17250_All//gi|224105377|ref|XP_002313789.1|//3.00E-37//phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa] >gi|222850197|gb|EEE87744.1|phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa]	Unigene17250_All//2.00E-28//AT4G34540| isoflavone reductase family protein	Unigene17250_All//0.00E+00//TC144170		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism	GO:0008152//GO:0016628//GO:0019740	nr -

Unigene17251_All	1132	1.20	5.37	1.03	2.38	3.29	7.46	2.09	3.40	4.72	2.16E+00	3.46E-14	Up	-2.16E-01	7.04E-01		4.67E-01	1.57E-01		1.65E+00	1.46E-14	Up	7.00E-01	1.20E-02		1.17E+00	4.80E-07	Up	Unigene17251_All//gi|30017323|gb|AAP12895.1|//2.00E-93//At2g38500 [Arabidopsis thaliana]	Unigene17251_All//1.00E-86//AT2G38500| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 7 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: DTA4 (DOWNSTREAM TARGET OF AGL15-4) (TAIR:AT1G79760.1); Has 26 Blast hits to 26 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene17251_All//0.00E+00//gi|78323593|gb|DT543867.1|DT543867				nr -
Unigene17252_All	739	100.39	180.39	171.13	137.98	117.80	168.80	132.45	296.53	178.01	8.46E-01	2.07E-72		7.70E-01	7.17E-57		-2.28E-01	1.61E-06		2.91E-01	5.56E-11		1.16E+00	7.52E-246	Up	4.27E-01	5.03E-27		Unigene17252_All//gi|223452524|gb|ACM89589.1|//2.00E-36//leucine-rich repeat protein [Glycine max]	Unigene17252_All//1.00E-36//AT5G21090| leucine-rich repeat protein, putative	Unigene17252_All//0.00E+00//gi|13357113|gb|BG447461.1|BG447461	ko04626|Plant-pathogen interaction	GO:0005488//GO:0008152//GO:0016628//GO:0016772//GO:0023060//GO:0044464	nr -
Unigene17253_All	545	42.14	2.88	44.36	8.50	4.61	1.99	0.70	0.61	0.15	-3.87E+00	7.13E-95	Down	7.39E-02	5.95E-01		-8.82E-01	7.26E-04		-2.10E+00	2.19E-11	Down	-1.87E-01	8.57E-01		-2.26E+00	6.49E-02		Unigene17253_All//gi|297795877|ref|XP_002865823.1|//2.00E-49//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311658|gb|EFH42082.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17253_All//2.00E-48//AT5G50790| nodulin MtN3 family protein	Unigene17253_All//1.00E-97//ES816336			GO:0031224//GO:0031410	nr +
Unigene17255_All	663	15.23	11.31	6.99	17.81	13.14	14.24	51.53	30.95	19.05	-4.29E-01	1.81E-02		-1.12E+00	4.85E-09	Down	-4.38E-01	5.26E-03		-3.23E-01	6.05E-02		-7.35E-01	1.56E-18		-1.44E+00	2.13E-55	Down	Unigene17255_All//gi|297602611|ref|NP_001052638.2|//2.00E-54//Os04g0390000 [Oryza sativa Japonica Group] >gi|255675403|dbj|BAF14552.2| Os04g0390000 [Oryza sativa Japonica Group]	Unigene17255_All//3.00E-53//AT5G65750| 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative	Unigene17255_All//0.00E+00//gi|164345754|gb|ES832017.1|ES832017	ko00380|Tryptophan metabolism/ko00020|Citrate cycle (TCA cycle)//ko00310|Lysine degradation	GO:0006607//GO:0016624//GO:0019842//GO:0043231	nr +
Unigene17256_All	413	19.26	100.97	62.28	38.11	68.54	75.02	61.94	142.39	165.05	2.39E+00	6.48E-106	Up	1.69E+00	8.10E-41	Up	8.47E-01	1.45E-18		9.77E-01	2.01E-23		1.20E+00	6.15E-70	Up	1.41E+00	3.13E-106	Up	Unigene17256_All//gi|158827648|gb|ABR81001.1|//1.00E-16//PI-phospholipase C PLC3 [Solanum lycopersicum]	Unigene17256_All//4.00E-16//AT5G58700| phosphoinositide-specific phospholipase C family protein	Unigene17256_All//3.00E-153//gi|48745911|gb|CO076430.1|CO076430	ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0004629//GO:0023060//GO:0044238//GO:0046872//GO:0060089	nr +
Unigene17257_All	743	1.69	2.25	1.72	4.02	4.96	3.10	2.11	0.56	1.07	4.13E-01	4.09E-01		2.55E-02	9.86E-01		3.02E-01	3.98E-01		-3.76E-01	3.38E-01		-1.90E+00	2.25E-04	Down	-9.73E-01	3.21E-02		Unigene17257_All//gi|115478697|ref|NP_001062942.1|//5.00E-07//Os09g0346900 [Oryza sativa Japonica Group] >gi|113631175|dbj|BAF24856.1| Os09g0346900 [Oryza sativa Japonica Group]	Unigene17257_All//1.00E-07//AT3G18380| sequence-specific DNA binding / transcription factor	Unigene17257_All//0.00E+00//gi|164255412|gb|ES799198.1|ES799198			nr +
Unigene17265_All	1398	0.00	1.88	0.08	0.21	0.39	0.39	2.27	4.28	2.45	1.09E+01	5.45E-15	Up	6.25E+00	3.99E-01		8.82E-01	4.21E-01		8.59E-01	4.23E-01		9.14E-01	2.61E-05		1.12E-01	7.16E-01		Unigene17265_All//gi|5814093|gb|AAD52097.1|AF088885|//1.00E-125//receptor-like kinase CHRK1 [Nicotiana tabacum]	Unigene17265_All//1.00E-92//AT4G23290| protein kinase family protein	Unigene17265_All//6.00E-28//DT468549	ko04626|Plant-pathogen interaction		nr +
Unigene17268_All	567	5.44	9.56	8.36	10.63	12.69	12.43	6.41	11.57	14.61	8.13E-01	1.55E-03		6.19E-01	3.28E-02		2.56E-01	2.96E-01		2.25E-01	3.81E-01		8.52E-01	3.41E-05		1.19E+00	1.17E-10	Up			Unigene17268_All//7.00E-10//ES831118				
Unigene17269_All	1190	1.01	1.06	0.90	1.76	0.75	1.06	6.50	13.49	10.51	7.41E-02	9.06E-01		-1.76E-01	7.68E-01		-1.22E+00	3.72E-03		-7.26E-01	1.09E-01		1.05E+00	4.58E-16	Up	6.93E-01	7.14E-07		Unigene17269_All//gi|8816459|emb|CAA71739.1|//7.00E-85//DEFH125 protein [Antirrhinum majus]	Unigene17269_AGL16//8.00E-83//AT3G57230| AGL16 (AGAMOUS-LIKE 16); transcription factor	Unigene17269_All//4.00E-115//CO107078	MADS		GO:0001071//GO:0003677//GO:0006351//GO:0010374//GO:0010468//GO:0016628//GO:0043231	nr +
Unigene1727_All	694	0.60	2.04	0.38	4.09	4.32	10.48	27.90	33.00	91.56	1.76E+00	3.72E-03		-6.53E-01	5.94E-01		7.74E-02	8.52E-01		1.36E+00	1.33E-09	Up	2.42E-01	2.29E-02		1.71E+00	5.83E-131	Up	Unigene1727_All//gi|297840607|ref|XP_002888185.1|//3.00E-72//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334026|gb|EFH64444.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1727_All//2.00E-73//AT1G59740| proton-dependent oligopeptide transport (POT) family protein	Unigene1727_All//0.00E+00//TC162019			nr +
Unigene17270_All	598	1.49	4.66	1.69	16.41	15.32	11.71	70.35	79.54	35.71	1.65E+00	4.82E-05	Up	1.86E-01	7.75E-01		-9.94E-02	6.33E-01		-4.87E-01	7.49E-03		1.77E-01	1.43E-02		-9.78E-01	2.33E-37		Unigene17270_All//gi|8778315|gb|AAF79324.1|AC002304_17//1.00E-14//F14J16.29 [Arabidopsis thaliana]		Unigene17270_All//5.00E-11//DW515642			nr +
Unigene17272_All	288	144.25	90.43	136.27	104.82	113.71	108.83	75.75	33.52	46.34	-6.74E-01	7.68E-16		-8.21E-02	3.94E-01		1.18E-01	2.88E-01		5.42E-02	6.59E-01		-1.18E+00	1.21E-25	Down	-7.09E-01	8.37E-12		Unigene17272_All//gi|296687231|gb|ADG27841.1|//2.00E-50//triosephosphate isomerase [Gossypium hirsutum]	Unigene17272_All//7.00E-47//AT2G21170| TIM (TRIOSEPHOSPHATE ISOMERASE); catalytic/ triose-phosphate isomerase	Unigene17272_All//9.00E-162//TC147088	ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00562|Inositol phosphate metabolism/ko00051|Fructose and mannose metabolism	GO:0000003//GO:0005488//GO:0005576//GO:0006071//GO:0006641//GO:0009526//GO:0009657//GO:0015977//GO:0016861//GO:0019682//GO:0048364	nr -
Unigene17273_All	616	47.39	43.43	15.13	17.87	21.63	13.49	52.23	34.20	192.92	-1.26E-01	2.56E-01		-1.65E+00	2.22E-44	Down	2.76E-01	8.42E-02		-4.06E-01	1.94E-02		-6.11E-01	7.40E-13		1.89E+00	1.97E-278	Up	Unigene17273_All//gi|224115182|ref|XP_002316965.1|//2.00E-22//histone H2 [Populus trichocarpa] >gi|222860030|gb|EEE97577.1| histone H2 [Populus trichocarpa]	Unigene17273_All//9.00E-22//AT4G27230| HTA2 (histone H2A); DNA binding	Unigene17273_All//8.00E-161//gi|21093785|gb|BQ406098.1|BQ406098			GO:0000785//GO:0003676//GO:0006950//GO:0009292//GO:0030312//GO:0031981//GO:0034728//GO:0051707	nr -
Unigene17275_All	521	5.52	12.35	3.88	9.94	7.07	8.67	19.96	18.69	11.24	1.16E+00	1.32E-06	Up	-5.08E-01	1.97E-01		-4.92E-01	5.55E-02		-1.98E-01	5.09E-01		-9.50E-02	6.41E-01		-8.29E-01	1.04E-07				Unigene17275_All//3.00E-132//DW520086				
Unigene17276_All	239	15.76	32.22	19.38	33.77	24.78	39.31	71.29	94.61	62.84	1.03E+00	1.52E-06	Up	2.98E-01	3.38E-01		-4.46E-01	2.41E-02		2.19E-01	3.08E-01		4.08E-01	7.11E-05		-1.82E-01	1.48E-01		Unigene17276_All//gi|297798906|ref|XP_002867337.1|//5.00E-35//signal recognition particle receptor alpha subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313173|gb|EFH43596.1| signal recognition particle receptor alpha subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17276_All//2.00E-36//AT4G30600| signal recognition particle receptor alpha subunit family protein	Unigene17276_All//1.00E-132//TC159941	ko03060|Protein export	GO:0000270//GO:0003723//GO:0004871//GO:0006613//GO:0017111//GO:0030167//GO:0031224//GO:0032561//GO:0048500	nr +
Unigene17277_All	1014	0.00	14.04	0.42	0.05	0.03	0.80	4.59	2.43	4.60	1.38E+01	9.26E-82	Up	8.71E+00	1.38E-02		-5.30E-01	8.25E-01		4.03E+00	5.91E-04	Up	-9.15E-01	2.53E-04		3.20E-03	9.90E-01		Unigene17277_All//gi|116265932|gb|ABJ91214.1|//1.00E-104//CBL-interacting protein kinase 7 [Populus trichocarpa] >gi|116265934|gb|ABJ91215.1| CBL-interacting protein kinase 8 [Populus trichocarpa]	Unigene17277_All//8.00E-100//AT4G30960| SIP3 (SOS3-INTERACTING PROTEIN 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene17277_All//5.00E-83//TC131456			GO:0004672//GO:0006464//GO:0006972//GO:0009926//GO:0023060//GO:0032501//GO:0032559	nr +
Unigene17278_All	284	3.50	3.39	5.81	8.77	5.70	3.18	1.79	0.00	4.35	-4.62E-02	9.58E-01		7.32E-01	1.71E-01		-6.22E-01	1.12E-01		-1.46E+00	3.75E-04	Down	-1.08E+01	8.89E-04	Down	1.28E+00	1.71E-02		Unigene17278_All//gi|297812423|ref|XP_002874095.1|//5.00E-06//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319932|gb|EFH50354.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17278_All//2.00E-07//AT5G22840| protein kinase family protein	Unigene17278_All//9.00E-122//CO109739			nr +
Unigene1728_All	2235	3.07	10.27	6.19	20.44	14.39	35.69	78.60	115.96	307.21	1.74E+00	4.25E-39	Up	1.01E+00	2.07E-10	Up	-5.06E-01	1.39E-12		8.04E-01	5.55E-43		5.61E-01	7.58E-84		1.97E+00	0.00E+00	Up	Unigene1728_All//gi|15218903|ref|NP_176183.1|//0.00E+00//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana]	Unigene1728_All//0.00E+00//AT1G59740| proton-dependent oligopeptide transport (POT) family protein	Unigene1728_All//0.00E+00//TC162019			nr -
Unigene17280_All	475	1.10	4.59	2.80	4.09	4.49	2.95	2.76	1.67	0.67	2.06E+00	2.93E-05	Up	1.35E+00	3.17E-02		1.36E-01	8.19E-01		-4.73E-01	3.42E-01		-7.23E-01	1.73E-01		-2.04E+00	3.01E-04	Down	Unigene17280_All//gi|297841517|ref|XP_002888640.1|//6.00E-68//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297334481|gb|EFH64899.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene17280_All//9.00E-67//AT1G68080| iron ion binding / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene17280_All//0.00E+00//CO119968			GO:0016705//GO:0019842//GO:0043170//GO:0043231//GO:0046914	nr -
Unigene17281_All	891	60.07	51.81	51.70	75.92	69.33	64.48	55.04	26.50	23.56	-2.14E-01	4.00E-03		-2.17E-01	4.96E-03		-1.31E-01	4.98E-02		-2.36E-01	1.90E-04		-1.05E+00	1.25E-47	Down	-1.22E+00	4.66E-62	Down	Unigene17281_All//gi|17380185|sp|Q82531.1|PSB1_PETHY//1.00E-116//RecName: Full=Proteasome subunit beta type-1; AltName: Full=20S proteasome alpha subunit F; AltName: Full=20S proteasome subunit beta-6 >gi|3608485|gb|AAC35983.1| proteasome beta subunit [Petunia x hybrida]	Unigene17281_All//5.00E-110//AT3G60820| PBF1; peptidase/ threonine-type endopeptidase	Unigene17281_All//0.00E+00//TC141766		ko03050|Proteasome	GO:0000502//GO:0004175//GO:0006508	nr -
Unigene17282_All	406	2.19	4.12	2.10	2.70	4.24	3.78	8.23	4.32	3.04	9.11E-01	7.45E-02		-6.21E-02	9.45E-01		6.52E-01	2.12E-01		4.87E-01	3.95E-01		-9.28E-01	2.16E-03		-1.44E+00	3.40E-06	Down	Unigene17282_All//gi|224057862|ref|XP_002299361.1|//6.00E-48//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene17282_All//9.00E-43//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene17282_All//3.00E-153//TC169017			GO:0009314//GO:0009526//GO:0009725//GO:0016881//GO:0048878	nr +
Unigene17283_All	1097	54.85	5.31	18.20	3.27	2.26	1.15	0.00	0.00	0.00	-3.37E+00	8.93E-221	Down	-1.59E+00	1.08E-86	Down	-5.33E-01	9.43E-02		-1.50E+00	6.83E-06	Down	null	null		null	null		Unigene17283_All//gi|57282652|emb|CAE75664.1|//1.00E-158//long chain fatty acid elongation enzyme [Gossypium hirsutum]	Unigene17283_All//2.00E-69//AT3G06470| CNS1/SUR4 membrane family protein	Unigene17283_All//0.00E+00//TC129693			GO:0016020//GO:0043231	nr -
Unigene17284_All	848	1.05	1.79	2.26	2.17	4.51	2.13	3.59	1.28	3.29	7.73E-01	1.48E-01		1.11E+00	2.53E-02		1.05E+00	5.36E-04	Up	-2.90E-02	9.56E-01		-1.49E+00	9.46E-06	Down	-1.26E-01	6.90E-01		Unigene17284_All//gi|238479965|ref|NP_001154663.1|//2.00E-72//ribonuclease III family protein [Arabidopsis thaliana]	Unigene17284_All//2.00E-71//AT3G43920| ribonuclease III family protein	Unigene17284_All//1.00E-24//gi|78344108|gb|DT564382.1|DT564382			GO:0003723//GO:0006259//GO:0016891//GO:0017111//GO:0030422//GO:0031981//GO:0035195	nr -
Unigene17288_All	1300	1.17	0.43	0.25	5.02	3.87	2.08	4.16	1.90	1.16	-1.45E+00	9.80E-03		-2.25E+00	5.02E-04	Down	-3.76E-01	1.04E-01		-1.27E+00	5.18E-08	Down	-1.13E+00	1.29E-06	Down	-1.84E+00	3.51E-13	Down			Unigene17288_All//9.00E-33//CO087482				
Unigene17289_All	359	12.97	5.36	15.28	27.20	10.65	13.84	2.47	1.86	1.22	-1.27E+00	1.10E-05	Down	2.36E-01	3.84E-01		-1.35E+00	1.69E-14	Down	-9.75E-01	7.38E-08		-4.09E-01	5.62E-01		-1.02E+00	1.09E-01		Unigene17289_All//gi|297721589|ref|NP_001173157.1|//3.00E-20//Os02g0762900 [Oryza sativa Japonica Group] >gi|255671268|dbj|BAH91886.1| Os02g0762900 [Oryza sativa Japonica Group]		Unigene17289_All//0.00E+00//TC174249			GO:0046872	nr +
Unigene17291_All	320	2.29	1.11	2.50	2.18	2.15	0.56	9.38	7.58	3.98	-1.05E+00	2.14E-01		1.25E-01	8.66E-01		-1.81E-02	9.61E-01		-1.95E+00	3.91E-02		-3.08E-01	3.83E-01		-1.24E+00	1.13E-04	Down			Unigene17291_All//6.00E-151//TC153952				
Unigene17294_All	392	22.16	55.19	16.98	52.74	39.62	45.97	37.64	59.60	41.16	1.32E+00	1.21E-24	Up	-3.84E-01	6.75E-02		-4.13E-01	2.62E-04		-1.98E-01	1.34E-01		6.63E-01	6.48E-11		1.29E-01	3.54E-01		Unigene17294_All//gi|75319500|sp|Q39828.1|SDL5A_SOYBN//2.00E-23//RecName: Full=Dynamin-related protein 5A; AltName: Full=Soybean dynamin-like protein 5A; Short=SDL5A >gi|1218004|gb|AAC49183.1| SDL5A [Glycine max]	Unigene17294_All//6.00E-22//AT5G42080| ADL1 (ARABIDOPSIS DYNAMIN-LIKE PROTEIN); GTP binding / GTPase/ protein binding	Unigene17294_All//0.00E+00//gi|73859009|gb|DT461748.1|DT461748			GO:0000904//GO:0000919//GO:0003002//GO:0003006//GO:0006897//GO:0009534//GO:0015630//GO:0016020//GO:0017111//GO:0019901//GO:0032561	nr -
Unigene17295_All	400	2.35	7.09	5.59	5.60	4.48	6.32	2.01	3.03	4.28	1.59E+00	6.48E-05	Up	1.25E+00	6.33E-03		-3.24E-01	4.77E-01		1.74E-01	6.79E-01		5.93E-01	2.96E-01		1.09E+00	1.26E-02								
Unigene17296_All	378	49.69	19.97	20.00	59.04	34.62	71.81	112.52	101.50	99.18	-1.31E+00	1.50E-21	Down	-1.31E+00	1.28E-20	Down	-7.70E-01	4.83E-13		2.83E-01	7.77E-03		-1.49E-01	6.04E-02		-1.82E-01	1.40E-02		Unigene17296_All//gi|211906496|gb|ACJ11741.1|//1.00E-65//heat shock protein 70 [Gossypium hirsutum]	Unigene17296_All//1.00E-60//AT5G02500| HSC70-1 (HEAT SHOCK COGNATE PROTEIN 70-1); ATP binding	Unigene17296_All//0.00E+00//gi|11203148|gb|BF272153.1|BF272153		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr +

Unigene17297_All	908	1.61	0.22	0.70	3.13	1.25	2.49	7.45	1.66	3.51	-2.85E+00	3.60E-05	Down	-1.20E+00	4.21E-02		-1.32E+00	1.81E-04	Down	-3.30E-01	4.14E-01		-2.17E+00	2.31E-19	Down	-1.09E+00	7.50E-08	Down	Unigene17297_All//gi|30698866|ref|NP_565040.2|//1.00E-115//ALAAT2 (ALANINE AMINOTRANSFERASE 2); ATP binding / L-alanine:2-oxoglutarate aminotransferase [Arabidopsis thaliana] >gi|9082268|gb|AAF82781.1|AF275371_1 alanine aminotransferase [Arabidopsis thaliana]	Unigene17297_All//3.00E-116//AT1G72330| ALAAT2 (ALANINE AMINOTRANSFERASE 2); ATP binding / L-alanine:2-oxoglutarate aminotransferase	Unigene17297_All//0.00E+00//TC161140		ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene17300_All	385	39.82	115.82	34.58	32.74	31.22	27.33	76.76	106.06	110.31	1.54E+00	3.31E-63	Up	-2.04E-01	2.09E-01		-6.86E-02	7.38E-01		-2.60E-01	1.30E-01		4.66E-01	3.55E-10		5.23E-01	3.65E-13		Unigene17300_All//gi|297831216|ref|XP_002883490.1|//5.00E-08//transaminase [Arabidopsis lyrata subsp. lyrata] >gi|297329330|gb|EFH59719.1|transaminase [Arabidopsis lyrata subsp. lyrata]	Unigene17300_All//2.00E-09//AT3G24090| glutamine-fructose-6-phosphate transaminase (isomerizing)/ sugar binding / transaminase	Unigene17300_All//3.00E-153//gi|109870871|gb|DW499847.1|DW499847		ko00520|Amino sugar and nucleotide sugar metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene17302_All	1197	0.04	0.13	0.04	5.66	5.29	1.89	6.04	4.96	3.13	1.54E+00	5.31E-01		2.62E-02	9.95E-01		-9.66E-02	7.26E-01		-1.59E+00	2.30E-11	Down	-2.85E-01	1.69E-01		-9.49E-01	7.46E-07		Unigene17302_All//gi|20269071|emb|CAD29733.1|//4.00E-53//pectin methylesterase [Sesbania rostrata]	Unigene17302_All//1.00E-37//AT1G11580| PMEPCRA (METHYLESTERASE PCR A); enzyme inhibitor/ pectinesterase	Unigene17302_All//4.00E-50//ES812870		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0016020//GO:0016787//GO:0030312	nr +
Unigene17303_All	512	155.02	72.44	33.28	710.63	825.37	687.86	162.18	54.61	46.30	-1.10E+00	7.25E-67	Down	-2.22E+00	3.37E-179	Down	2.16E-01	1.08E-22		-4.70E-02	1.27E-01		-1.57E+00	4.14E-148	Down	-1.81E+00	3.02E-186	Down	Unigene17303_All//gi|112350249|gb|AB115167.1|//3.00E-06/6A5A-like protein [Gossypium hirsutum]	Unigene17303_All//2.00E-22//AT5G14920| gibberellin-regulated family protein	Unigene17303_All//0.00E+00//TC178161			GO:0005488//GO:0044464	nr -
Unigene17305_All	748	0.00	0.00	0.00	0.00	0.00	0.00	5.82	14.08	23.65	null	null		null	null		null	null		null	null		1.27E+00	2.21E-14	Up	2.02E+00	4.16E-46	Up	Unigene17305_All//gi|75096924|sp|Q40084.1|SCP31_ARATH//2.00E-48//RecName: Full=Serine carboxypeptidase-like 31; Flags: Precursor >gi|19316400|gb|AAB65475.1| Serine carboxypeptidase isolog; 30227-33069 [Arabidopsis thaliana]	Unigene17305_All//6.00E-42//AT1G11080| scpl31 (serine carboxypeptidase-like 31); serine-type carboxypeptidase	Unigene17305_All//1.00E-61//TC160828			GO:0004180//GO:0016538//GO:0044464	nr +
Unigene17306_All	1722	0.00	0.35	0.19	0.06	0.36	0.63	11.17	21.04	57.49	8.46E+00	1.17E-03		7.54E+00	4.53E-02		2.64E+00	1.99E-02		3.44E+00	1.20E-04	Up	9.14E-01	4.85E-28		2.36E+00	0.00E+00	Up	Unigene17306_All//gi|42561909|ref|NP_172575.2|//0.00E+00//scpl31 (serine carboxypeptidase-like 31); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|133778908|gb|AB038794.1|At1g11080 [Arabidopsis thaliana]	Unigene17306_All//6.00E+00//AT1G11080| scpl31 (serine carboxypeptidase-like 31); serine-type carboxypeptidase	Unigene17306_All//0.00E+00//TC160828			GO:0004180//GO:0016538//GO:0044464	nr +
Unigene17309_All	446	2.23	2.27	2.03	3.80	5.33	5.57	7.77	2.72	3.31	2.78E-02	9.86E-01		-1.35E-01	8.38E-01		4.88E-01	2.69E-01		5.53E-01	1.96E-01		-1.52E+00	1.31E-06	Down	-1.23E+00	2.96E-05	Down			Unigene17309_All//4.00E-100//TC158952				
Unigene17310_All	301	160.27	62.45	59.97	188.00	162.22	286.74	155.64	56.79	55.46	-1.36E+00	4.47E-57	Down	-1.42E+00	1.05E-58	Down	-2.13E-01	1.71E-03		6.09E-01	9.41E-29		-1.45E+00	6.31E-75	Down	-1.49E+00	7.83E-80	Down	Unigene17310_All//gi|192910724|gb|ACF06470.1|//1.00E-37//cytoplasmic ribosomal protein S15a [Elaeis guineensis] >gi|192910726|gb|ACF06471.1|cytoplasmic ribosomal protein S15a [Elaeis guineensis]	Unigene17310_All//5.00E-39//AT5G59850| 40S ribosomal protein S15A (RPS15aF)	Unigene17310_All//4.00E-167//gi|109888297|gb|DW517266.1|DW517266		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0043231	nr +
Unigene17313_All	445	17.64	4.21	2.75	3.92	4.80	22.02	26.60	3.48	40.55	-2.07E+00	2.76E-17	Down	-2.68E+00	2.48E-22	Down	2.92E-01	5.58E-01		2.49E+00	3.09E-28	Up	-2.94E+00	7.01E-47	Down	6.08E-01	9.69E-08		Unigene17313_All//gi|297793011|ref|XP_002864390.1|//2.00E-47//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310225|gb|EFH40649.1|protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17313_All//4.00E-18//AT5G55410| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene17313_All//0.00E+00//DW512993				nr -
Unigene17314_All	463	20.79	17.51	19.90	13.34	19.19	7.71	57.17	38.00	15.66	-2.48E-01	2.09E-01		-6.35E-02	7.52E-01		5.24E-01	5.03E-03		-7.92E-01	6.94E-04		-5.89E-01	4.32E-10		-1.87E+00	1.44E-62	Down	Unigene17314_All//gi|38566498|gb|AAR24139.1|//2.00E-07//At4g33960 [Arabidopsis thaliana] >gi|40823521|gb|AAR92287.1|At4g33960 [Arabidopsis thaliana]		Unigene17314_All//7.00E-96//CD486319				nr -
Unigene17315_All	688	11.26	5.82	4.10	21.07	18.62	23.50	19.48	11.30	5.73	-9.52E-01	6.93E-06		-1.46E+00	2.98E-10	Down	-1.78E-01	2.79E-01		1.58E-01	3.33E-01		-7.86E-01	1.28E-08		-1.76E+00	9.65E-30	Down	Unigene17315_All//gi|12230639|sp|Q9SMU7.1|SRP09_ARATH//6.00E-47//RecName: Full=Signal recognition particle 9 kDa protein; Short=SRP9 >gi|6522556|emb|CAB62000.1| signal recognition particle subunit 9-like [Arabidopsis thaliana] >gi|21553473|gb|AAM62566.1| signal recognition particle 9 kDa protein SRP9 [Arabidopsis thaliana] >gi|28466801|gb|AAO44009.1|At3g49100 [Arabidopsis thaliana] >gi|110736135|dbj|BAF00039.1|signal recognition particle subunit 9 - like [Arabidopsis thaliana]	Unigene17315_All//3.00E-48//AT3G49100| signal recognition particle 9 kDa protein, putative / SRP9, putative	Unigene17315_All//0.00E+00//TC162000		ko03060|Protein export	GO:0003723//GO:0006448//GO:0006613//GO:0048500	nr +
Unigene17316_All	372	37.69	15.39	13.31	58.38	37.86	55.36	124.57	51.46	39.30	-1.29E+00	7.27E-16	Down	-1.50E+00	6.71E-19	Down	-6.25E-01	6.24E-09		-7.67E-02	6.28E-01		-1.28E+00	8.93E-61	Down	-1.66E+00	8.30E-93	Down	Unigene17316_All//gi|76161014|gb|AB404470.1|//2.00E-15//ribosomal protein S6-like protein [Solanum tuberosum]	Unigene17316_All//7.00E-14//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome	Unigene17316_All//0.00E+00//gi|164331513|gb|EV492694.1|EV492694		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene17319_All	398	116.87	56.78	101.82	47.69	51.48	32.79	5.31	1.68	2.50	-1.04E+00	2.77E-36	Down	-1.99E-01	1.87E-02		1.10E-01	4.49E-01		-5.40E-01	1.15E-05		-1.66E+00	7.98E-05	Down	-1.09E+00	4.70E-03		Unigene17319_All//gi|295684201|gb|ADG27450.1|//1.00E-67//ADP glucose pyrophosphorylase small subunit 1-like protein [Malus x domestica]	Unigene17319_All//4.00E-65//AT5G48300| ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE 1); glucose-1-phosphate adenylyltransferase	Unigene17319_All//0.00E+00//TC163706		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0032559//GO:0070566	nr -
Unigene17321_All	475	38.66	69.12	34.53	62.19	51.04	78.73	52.69	77.26	128.57	8.38E-01	3.95E-18		-1.63E-01	2.69E-01		-2.85E-01	2.94E-03		3.40E-01	7.77E-05		5.52E-01	3.02E-12		1.29E+00	1.40E-82	Up	Unigene17321_All//gi|255573949|ref|XP_002527893.1|//1.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223532744|gb|EEF34524.1|conserved hypothetical protein [Ricinus communis]	Unigene17321_All//3.00E-06//AT3G54020| phosphatidic acid phosphatase-related / PAP2-related	Unigene17321_All//0.00E+00//gi|48744548|gb|CO075067.1|CO075067				nr -
Unigene17324_All	446	44.70	41.47	69.49	17.76	18.07	11.65	82.76	170.65	80.03	-1.08E-01	4.30E-01		6.37E-01	1.79E-10		2.48E-02	9.30E-01		-6.09E-01	2.77E-03		1.04E+00	3.30E-72	Up	-4.83E-02	6.03E-01				Unigene17324_All//0.00E+00//gi|164291453|gb|ES812333.1|ES812333				
Unigene17325_All	1293	67.98	71.13	88.63	7.51	8.28	6.57	5.33	0.78	1.20	6.52E-02	3.03E-01		3.83E-01	5.59E-15		1.41E-01	5.14E-01		-1.94E-01	3.63E-01		-2.78E+00	4.58E-26	Down	-2.15E+00	3.72E-20	Down	Unigene17325_All//gi|225427213|ref|XP_002280380.1|//1.00E-143//PREDICTED: similar to mitochondrial carrier protein isoform 1 [Vitis vinifera] >gi|225427215|ref|XP_002280391.1|PREDICTED: similar to mitochondrial carrier protein isoform 2 [Vitis vinifera]	Unigene17325_All//1.00E-126//AT5G46800| BOU (A BOUT DE SOUFFLE); binding / transporter	Unigene17325_All//0.00E+00//TC149308				nr -
Unigene17327_All	612	2.56	9.44	3.65	4.80	5.12	4.87	8.36	7.92	8.85	1.88E+00	2.11E-11	Up	5.11E-01	2.54E-01		9.25E-02	8.22E-01		2.03E-02	9.53E-01		-7.75E-02	7.66E-01		8.28E-02	7.33E-01				Unigene17327_All//3.00E-92//gi|21102004|gb|BQ414317.1|BQ414317				
Unigene17329_All	832	2.26	2.25	3.71	2.81	6.08	4.18	3.30	3.01	3.54	-6.80E-03	9.84E-01		7.13E-01	5.41E-02		1.11E+00	1.60E-05	Up	5.71E-01	9.44E-02		-1.32E-01	7.21E-01		1.01E-01	7.55E-01		Unigene17329_All//gi|296082099|emb|CBI21104.3|//8.00E-18//unnamed protein product [Vitis vinifera]	Unigene17329_All//0.00E+00//CO105283				nr -
Unigene1733_All	325	8.69	1.40	3.28	11.50	18.86	12.78	8.72	1.80	4.54	-2.63E+00	1.19E-08	Down	-1.41E+00	5.17E-04	Down	7.14E-01	1.82E-03		1.53E-01	6.57E-01		-2.28E+00	5.37E-09	Down	-9.42E-01	3.44E-03		Unigene1733_All//gi|290578970|gb|ADD51363.1|//9.00E-37//B2-type cyclin [Malus x domestica]	Unigene1733_All//1.00E-34//AT2G17620| CYCB2;1 (Cyclin B2;1); cyclin-dependent protein kinase regulator	Unigene1733_All//1.00E-111//CO126417				nr -
Unigene17331_All	470	10.91	10.03	4.99	17.70	12.75	19.31	34.72	20.19	17.80	-1.22E-01	6.46E-01		-1.13E+00	5.67E-05	Down	-4.73E-01	1.39E-02		1.26E-01	6.04E-01		-7.83E-01	2.99E-10		-9.64E-01	1.06E-14				Unigene17331_All//0.00E+00//gi|21089110|gb|BQ401423.1|BQ401423				
Unigene17332_All	409	54.11	114.72	83.98	43.85	46.39	64.05	26.46	49.66	31.17	1.08E+00	7.18E-39	Up	6.34E-01	1.87E-11		8.14E-02	6.12E-01		5.47E-01	1.20E-07		9.08E-01	6.29E-16		2.36E-01	1.04E-01		Unigene17332_All//gi|182407860|gb|ACB87921.1|//3.00E-45//ubiquitin conjugating enzyme 3 [Malus x domestica]	Unigene17332_All//9.00E-45//AT4G27960| UBC9 (UBIQUITIN CONJUGATING ENZYME 9); ubiquitin-protein ligase	Unigene17332_All//0.00E+00//gi|109882405|gb|DW511375.1|DW511375		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0019787//GO:0032559//GO:0060255//GO:0070646	nr +
Unigene17333_All	486	17.87	14.60	8.11	21.42	23.31	19.61	68.73	40.68	32.38	-2.92E-01	1.51E-01		-1.14E+00	4.92E-08	Down	1.22E-01	5.51E-01		-1.28E-01	5.55E-01		-7.57E-01	5.04E-19		-1.09E+00	2.88E-35	Down	Unigene17333_All//gi|106879617|emb|CAJ38392.1|//6.00E-20//cytochrome c oxidase subunit 5b [Plantago major]	Unigene17333_All//1.00E-09//AT3G15640| cytochrome c oxidase family protein	Unigene17333_All//0.00E+00//gi|21096789|gb|BQ409102.1|BQ409102		ko00190|Oxidative phosphorylation	GO:0009534//GO:0015002//GO:0031967//GO:0046914	nr -
Unigene17336_All	398	36.81	15.28	14.58	86.49	68.61	99.75	133.85	52.61	60.46	-1.27E+00	4.25E-16	Down	-1.34E+00	1.25E-16	Down	-3.34E-01	9.68E-05		2.06E-01	2.03E-02		-1.35E+00	7.54E-76	Down	-1.15E+00	9.25E-61	Down	Unigene17336_All//gi|1173256|sp|P46299.1|RS4_GOSHI//1.00E-30//RecName: Full=40S ribosomal protein S4 >gi|488739|emb|CAA55882.1|ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene17336_All//4.00E-28//AT5G07090| 40S ribosomal protein S4 (RPS4B)	Unigene17336_All//0.00E+00//gi|48804125|gb|CO105439.1|CO105439		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0015935//GO:0016020//GO:0031981	nr +
Unigene17337_All	1255	1.79	1.78	0.85	5.40	6.06	4.53	2.73	0.27	1.17	-1.31E-02	9.90E-01		-1.08E+00	1.68E-02		1.68E-01	5.15E-01		-2.52E-01	3.20E-01		-3.36E+00	8.33E-16	Down	-1.22E+00	4.18E-05	Down	Unigene17337_All//gi|15238111|ref|NP_199561.1|//1.00E-161//pectinesterase family protein [Arabidopsis thaliana] >gi|75301651|sp|Q8LFP3.1|PME68_ARATH RecName: Full=Probable pectinesterase 68; Short=PE 68; AltName: Full=Pectin methylesterase 68; Short=AtPME68; Flags: Precursor >gi|20856815|gb|AAM26686.1|At5g47500/MXJ7_9 [Arabidopsis thaliana] >gi|23308329|gb|AAN18134.1|At5g47500/MXJ7_9 [Arabidopsis thaliana]	Unigene17337_All//3.00E-162//AT5G47500| pectinesterase family protein	Unigene17337_All//0.00E+00//ES831995		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0016787	nr -
Unigene1734_All	1714	13.37	10.11	6.77	26.16	30.58	26.40	26.62	3.66	11.53	-4.03E-01	4.25E-04		-9.81E-01	6.38E-16		2.25E-01	1.51E-03		1.35E-02	9.06E-01		-2.86E+00	1.89E-174	Down	-1.21E+00	1.52E-56	Down	Unigene1734_All//gi|780267|emb|CAA55272.1|//1.00E-146//B-like cyclin [Medicago sativa subsp. x varia]	Unigene1734_All//3.00E-127//AT2G17620| CYCB2;1 (Cyclin B2;1); cyclin-dependent protein kinase regulator	Unigene1734_All//0.00E+00//gi|73850447|gb|DT459467.1|DT459467				nr +
Unigene17340_All	673	5.21	1.43	3.16	18.21	20.16	4.16	4.65	2.92	1.48	-1.86E+00	3.46E-07	Down	-7.19E-01	3.75E-02		1.47E-01	4.17E-01		-2.13E+00	6.64E-30	Down	-6.72E-01	3.30E-02		-1.65E+00	5.47E-07	Down								
Unigene17341_All	625	6.36	8.27	7.58	10.52	12.84	12.93	3.65	1.61	1.08	3.78E-01	1.61E-01		2.53E-01	3.88E-01		2.87E-01	1.91E-01		2.98E-01	1.81E-01		-1.19E+00	1.96E-03		-1.75E+00	1.02E-05	Down	Unigene17341_All//gi|224057575|ref|XP_002299275.1|//1.00E-10//predicted protein [Populus trichocarpa] >gi|222846533|gb|EEE84080.1|predicted protein [Populus trichocarpa]						nr +
Unigene17342_All	938	2.73	2.00	2.27	4.04	4.59	2.55	4.10	1.60	2.55	-4.52E-01	2.56E-01		-2.67E-01	5.32E-01		1.85E-01	5.85E-01		-6.61E-01	3.65E-02		-1.35E+00	2.99E-06	Down	-6.87E-01	1.04E-02		Unigene17342_All//gi|225448193|ref|XP_002265586.1|//6.00E-92//PREDICTED: similar to DNA Helicase [Vitis vinifera]	Unigene17342_All//6.00E+00//AT1G60930| ATRECQ4B (ARABIDOPSIS RECQ HELICASE L4B); ATP binding / ATP-dependent helicase/ DNA helicase/ catalytic/ helicase/ nucleic acid binding / nucleotide binding	Unigene17342_All//0.00E+00//DT465159		ko03440|Homologous recombination	GO:0000725//GO:0004003//GO:0006996//GO:0009409//GO:0009737//GO:0032559//GO:0044464	nr -

Unigene17343_All	1017	10.34	35.92	34.03	0.59	1.73	0.80	0.08	0.16	0.20	1.80E+00	1.86E-64	Up	1.72E+00	5.87E-56	Up	1.55E+00	2.14E-03		4.44E-01	6.21E-01		9.84E-01	6.34E-01		1.24E+00	4.69E-01		Unigene17343_All//gi|109390302|gb|ABG33750.1|//1.00E-130//cysteine protease [Hevea brasiliensis]	Unigene17343_All//3.00E-116//AT5G43060| cysteine proteinase, putative / thiol protease, putative	Unigene17343_All//7.00E-113//gi|164366957|gb|ES827221.1|ES827221				nr -
Unigene17344_All	901	2.21	0.34	0.41	2.93	2.06	3.66	11.83	3.06	0.53	-2.71E+00	1.84E-06	Down	-2.42E+00	1.88E-05	Down	-5.06E-01	1.93E-01		3.21E-01	3.94E-01		-1.95E+00	2.63E-26	Down	-4.48E+00	9.69E-62	Down	Unigene17344_All|gi|18390725|ref|NP_563780.1|//6.00E-69//LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6) [Arabidopsis thaliana] >gi|56236136|gb|AAV84524.1| At1g07090 [Arabidopsis thaliana] >gi|88190786|gb|ABD42982.1| At1g07090 [Arabidopsis thaliana]	Unigene17344_All//2.00E-69//AT1G07090| LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6)	Unigene17344_All//8.00E-131//TC160760			GO:0043231	nr -
Unigene17345_All	727	91.54	56.87	69.22	334.58	242.18	202.77	220.42	220.59	92.66	-6.87E-01	9.79E-26		-4.03E-01	7.98E-10		-4.66E-01	3.22E-56		-7.23E-01	3.72E-109		1.20E-03	1.02E+00		-1.25E+00	1.09E-207	Down	Unigene17345_All|gi|92885091|gb|AB87611.1|//1.00E-70//Phosphoribosyltransferase; Orotidine 5-phosphate decarboxylase [Medicago truncatula]	Unigene17345_All//9.00E-59//AT3G54470| uridine 5'-monophosphate synthase / UMP synthase (PYRE-F) (UMPS)	Unigene17345_All//0.00E+00//gi|109826704|gb|DW225414.1|DW225414		ko00240|Pyrimidine metabolism	GO:0006221//GO:0009267//GO:0010038//GO:0016763//GO:0016831//GO:0019856//GO:0043231	nr -
Unigene17346_All	983	1.76	0.36	1.90	3.24	2.77	2.16	4.47	2.21	1.78	-2.28E+00	7.67E-05	Down	1.10E-01	8.12E-01		-2.29E-01	5.44E-01		-5.87E-01	9.87E-02		-1.02E+00	9.24E-05	Down	-1.33E+00	4.27E-07	Down	Unigene17346_All|gi|119391879|emb|CAF04055.2|//1.00E-130//S-adenosylmethionine transporter [Nicotiana benthamiana]	Unigene17346_All//9.00E-104//AT1G34065| SAMC2 (S-adenosylmethionine carrier 2); binding	Unigene17346_All//1.00E-126//DR460656				nr -
Unigene17347_All	708	6.80	2.50	2.11	9.15	9.53	12.89	1.91	2.95	3.43	-1.44E+00	6.94E-07	Down	-1.69E+00	4.75E-08	Down	5.97E-02	8.26E-01		4.94E-01	9.76E-03		6.27E-01	1.22E-01		8.45E-01	1.64E-02		Unigene17347_All|gi|21536721|gb|AM61053.1|//4.00E-60//AtPH1-like protein [Arabidopsis thaliana]	Unigene17347_All//7.00E-61//AT5G05710| pleckstrin homology (PH) domain-containing protein	Unigene17347_All//0.00E+00//TC152077				nr +
Unigene17348_All	612	6.41	3.39	3.57	18.23	14.63	8.19	13.47	7.58	6.44	-9.18E-01	3.02E-03		-8.46E-01	8.65E-03		-3.18E-01	6.36E-02		-1.15E+00	1.63E-11	Down	-8.30E-01	4.40E-06		-1.06E+00	4.25E-09	Down	Unigene17348_All|gi|16930439|gb|AL31905.1|AF419573_1//5.00E-52//AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|15912261|gb|AAL08264.1| AT4g27720/T29A15_210 [Arabidopsis thaliana] >gi|27764934|gb|AAO23588.1| At4g27720/T29A15_210 [Arabidopsis thaliana]	Unigene17348_All//3.00E-53//AT4G27720| LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G46650.1); Has 496 Blast hits to 491 proteins in 183 species: Archae - 5; Bacteria - 234; Metazoa - 75; Fungi - 33; Plants - 96; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink).	Unigene17348_All//0.00E+00//gi|48808727|gb|CO110041.1|CO110041			GO:0044464	nr +
Unigene1735_All	1702	1.91	1.67	0.59	2.96	5.34	2.87	9.76	0.91	4.05	-1.93E-01	6.11E-01		-1.68E+00	1.34E-05	Down	8.54E-01	2.34E-06		-4.48E-02	8.92E-01		-3.43E+00	7.47E-76	Down	-1.27E+00	7.77E-23	Down	Unigene1735_All|gi|780267|emb|CAA55272.1|//1.00E-156//B-like cyclin [Medicago sativa subsp. x varia]	Unigene1735_All//1.00E-137//AT2G17620| CYCB2;1 (Cyclin B2;1); cyclin-dependent protein kinase regulator	Unigene1735_All//0.00E+00//gi|73850447|gb|DT459467.1|DT459467				nr -
Unigene17350_All	667	8.16	45.05	6.87	7.39	8.57	11.17	23.20	57.65	143.47	2.47E+00	2.98E-79	Up	-2.49E-01	3.95E-01		2.13E-01	4.55E-01		5.96E-01	5.12E-03		1.31E+00	8.90E-53	Up	2.63E+00	0.00E+00	Up	Unigene17350_All|gi|255590379|ref|XP_002535252.1|//4.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223523639|gb|EEF27131.1| conserved hypothetical protein [Ricinus communis]		Unigene17350_All//0.00E+00//BG445214				nr +
Unigene17351_All	296	28.81	11.81	27.16	36.52	36.18	54.62	40.42	25.42	27.46	-1.29E+00	6.95E-10	Down	-8.49E-02	6.97E-01		-1.35E-02	9.54E-01		5.81E-01	1.76E-05		-6.69E-01	4.39E-06		-5.58E-01	8.38E-05		Unigene17351_All|gi|75336159|sp|Q9MAX9.1|PS10B_ARATH//8.00E-21//RecName: Full=26S protease regulatory subunit S10B homolog B; AltName: Full=26S proteasome subunit S10B homolog B; AltName: Full=26S proteasome AAA-ATPase subunit RPT4b; AltName: Full=Regulatory particle triple-A ATPase subunit 4b >gi|7767657|gb|AAF69154.1|AC007915_6 F27F5.8 [Arabidopsis thaliana] >gi|17065266|gb|AAL32787.1| similar to 26S proteasome AAA-ATPase subunit RPT4a [Arabidopsis thaliana] >gi|21387177|gb|AAM47992.1| 26S proteasome AAA-ATPase subunit RPT4a-like protein [Arabidopsis thaliana]	Unigene17351_All//3.00E-22//AT1G45000| 26S proteasome regulatory complex subunit pt2D, putative	Unigene17351_All//3.00E-152//gi|13350110|gb|BG440459.1|BG440459		ko03050|Proteasome	GO:0005838//GO:0016020//GO:0019941//GO:0030312//GO:0031981//GO:0032559//GO:0042623	nr -
Unigene17355_All	531	33.50	20.52	20.36	48.03	55.19	56.48	119.04	53.60	71.05	-7.08E-01	7.99E-08		-7.19E-01	1.25E-07		2.00E-01	5.39E-02		2.34E-01	2.32E-02		-1.15E+00	2.33E-70	Down	-7.45E-01	2.75E-35		Unigene17355_All|gi|3914771|sp|P93779.1|RL5_SOLME//9.00E-45//RecName: Full=60S ribosomal protein L5 >gi|1881380|dbj|BAA19415.1| ribosomal protein L5 [Solanum melongena]	Unigene17355_All//2.00E-69//AT1G07090| LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6)	Unigene17355_All//0.00E+00//TC140994		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0019843//GO:0030529	nr +
Unigene17356_All	838	2.31	2.84	2.35	5.94	8.30	6.90	2.07	2.99	13.07	2.99E-01	4.81E-01		2.54E-02	9.76E-01		4.82E-01	2.87E-02		2.15E-01	4.57E-01		5.33E-01	1.44E-01		2.66E+00	8.25E-40	Up	Unigene17356_All|gi|225469602|ref|XP_002263108.1|//1.00E-38//PREDICTED: similar to phosphoinositide phosphatase family protein, partial [Vitis vinifera]	Unigene17356_All//1.00E-31//AT3G51460| RHD4 (ROOT HAIR DEFECTIVE4); phosphatidylinositol-4,5-bisphosphate 5-phosphatase/ phosphatidylinositol-4-phosphate phosphatase	Unigene17356_All//4.00E-34//TC160371			GO:0000904//GO:0009826//GO:0034593//GO:0044459	nr +
Unigene17357_All	942	0.56	1.29	0.96	12.85	5.81	3.88	2.38	2.17	0.55	1.22E+00	5.24E-02		7.91E-01	3.04E-01		-1.14E+00	8.47E-14	Down	-1.73E+00	2.16E-22	Down	-1.30E-01	7.42E-01		-2.11E+00	5.78E-07	Down	Unigene17357_All|gi|44681338|gb|AS47609.1|//3.00E-07//At1g34010 [Arabidopsis thaliana] >gi|45773854|gb|AAS76731.1| At1g34010 [Arabidopsis thaliana]	Unigene17357_All//1.00E-08//AT1G34010| unknown protein				GO:0016020	nr -
Unigene17358_All	742	0.00	0.55	0.07	0.27	0.09	0.12	2.22	1.01	0.43	9.09E+00	1.36E-02		6.17E+00	6.36E-01		-1.53E+00	4.16E-01		-1.14E+00	5.69E-01		-1.13E+00	1.43E-02		-2.37E+00	5.20E-06	Down	Unigene17358_All|gi|297822505|ref|XP_002879135.1|//3.00E-28//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324974|gb|EFH55394.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene17358_All//6.00E-29//AT5G27300| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G27800.1); Has 7681 Blast hits to 2370 proteins in 97 species: Archae - 2; Bacteria - 0; Metazoa - 93; Fungi - 4; Plants - 7452; Viruses - 0; Other Eukaryotes - 130 (source: NCBI BLink).	Unigene17358_All//3.00E-68//TC140645				nr -
Unigene17360_All	1432	0.84	0.99	0.48	0.07	0.05	0.22	0.89	5.49	24.43	2.38E-01	6.50E-01		-7.98E-01	2.25E-01		-5.33E-01	8.17E-01		1.67E+00	3.09E-01		2.63E+00	7.44E-28	Up	4.79E+00	2.68E-205	Up	Unigene17360_All|gi|15241862|ref|NP_201058.1|//6.00E-66//SM05 (SIMILAR TO RCD ONE 5); NAD+ ADP-ribosyltransferase [Arabidopsis thaliana] >gi|17386160|gb|AAL38626.1|AF446893_1 AT5g62520/K19B1_13 [Arabidopsis thaliana] >gi|15450639|gb|AAK96591.1| AT5g62520/K19B1_13 [Arabidopsis thaliana]	Unigene17360_All//3.00E-68//AT5G62520| SM05 (SIMILAR TO RCD ONE 5); NAD+ ADP-ribosyltransferase	Unigene17360_All//0.00E+00//TC170283			GO:0006970//GO:0043231//GO:0044237	nr -
Unigene17361_All	975	2.74	0.73	2.62	8.69	7.56	3.15	3.08	0.00	1.02	-1.91E+00	8.10E-06	Down	-6.21E-02	8.80E-01		-2.01E-01	3.64E-01		-1.46E+00	1.45E-12	Down	-1.16E+01	3.14E-21	Down	-1.59E+00	1.94E-06	Down	Unigene17361_All|gi|115434250|ref|NP_001041883.1|//3.00E-18//Os01g0123000 [Oryza sativa Japonica Group] >gi|113531414|dbj|BAF03797.1| Os01g0123000 [Oryza sativa Japonica Group]		Unigene17361_All//0.00E+00//gi|13244053|gb|BE053132.2|BE053132				nr +
Unigene17362_All	1079	1.12	0.19	0.10	1.75	1.31	0.88	0.78	0.15	0.41	-2.57E+00	5.35E-04	Down	-3.50E+00	8.78E-05	Down	-4.23E-01	3.84E-01		-9.97E-01	3.60E-02		-2.34E+00	2.95E-03		-9.49E-01	1.47E-01		Unigene17362_All|gi|2865437|gb|AAC02672.1|//2.00E-16//polyprotein [Arabidopsis arenosa]		Unigene17362_All//0.00E+00//gi|13244053|gb|BE053132.2|BE053132				nr -
Unigene17367_All	546	2.68	3.62	1.85	2.65	2.14	2.90	1.78	1.61	4.60	4.32E-01	3.69E-01		-5.34E-01	3.66E-01		-3.03E-01	5.95E-01		1.30E-01	8.14E-01		-1.48E-01	8.13E-01		1.37E+00	1.54E-04	Up			Unigene17367_All//6.00E-07//DW237756				
Unigene17369_All	586	5.27	3.03	2.45	102.86	70.05	47.48	37.37	11.13	9.38	-8.00E-01	2.39E-02		-1.10E+00	3.31E-03		-5.54E-01	2.37E-19		-1.12E+00	1.42E-56	Down	-1.75E+00	5.02E-46	Down	-1.99E+00	1.34E-56	Down	Unigene17369_All|gi|110648737|emb|CAJ77893.1|//1.00E-54//GASA [Fagus sylvatica]	Unigene17369_All//5.00E-41//AT5G15230| GASA4 (GAST1 PROTEIN HOMOLOG 4)	Unigene17369_All//0.00E+00//gi|109877611|gb|DW506584.1|DW506584			GO:0005488//GO:0010476	nr +
Unigene17373_All	1152	0.77	0.75	0.60	4.76	0.21	1.37	36.78	15.31	9.03	-4.63E-02	9.62E-01		-3.62E-01	6.32E-01		-4.51E+00	1.42E-32	Down	-1.79E+00	5.69E-11	Down	-1.26E+00	7.07E-55	Down	-2.03E+00	4.50E-111	Down	Unigene17373_All|gi|44681336|gb|AS47608.1|//6.00E-06//At3g51100 [Arabidopsis thaliana] >gi|45773864|gb|AAS76736.1| At3g51100 [Arabidopsis thaliana]	Unigene17373_All//3.00E-07//AT3G51100| unknown protein	Unigene17373_All//0.00E+00//DT047875				nr +
Unigene17374_All	725	18.47	7.90	8.59	11.20	8.07	9.97	2.68	1.73	1.59	-1.23E+00	4.72E-14	Down	-1.10E+00	1.82E-11	Down	-4.72E-01	1.58E-02		-1.68E-01	4.74E-01		-6.33E-01	1.35E-01		-7.51E-01	5.89E-02		Unigene17374_All|gi|164564752|dbj|BAF98232.1|//9.00E-54//CM0545.540.nc [Lotus japonicus]	Unigene17374_All//1.00E-49//AT2G32650| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; CONTAINS InterPro DOMAIN/s: Cupin, RmlC-type (InterPro:IPR010651), Protein of unknown function DUF861, cupin-3 (InterPro:IPR008579), RmlC-like jelly roll fold (InterPro:IPR014710); BEST Arabidopsis thaliana protein match is: PTAC18 (PLASTID TRANSCRIPTIONALLY ACTIVE 18) (TAIR:AT2G32180.1); Has 169 Blast hits to 169 proteins in 46 species: Archae - 0; Bacteria - 71; Metazoa - 0; Fungi - 0; Plants - 81; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink).	Unigene17374_All//0.00E+00//gi|109875275|gb|DW504249.1|DW504249			GO:0000229//GO:0043231	nr +
Unigene17375_All	408	0.51	3.10	0.00	0.73	2.11	3.21	3.11	21.21	2.54	2.60E+00	3.59E-04	Up	-9.00E+00	1.46E-01		1.53E+00	5.80E-02		2.13E+00	1.28E-03		2.77E+00	2.51E-32	Up	-2.92E-01	5.99E-01		Unigene17375_All|gi|226500876|ref|NP_001149790.1|//1.00E-16//LOC100283417 [Zea mays] >gi|195634685|gb|ACG36811.1| peptidyl-prolyl isomerase [Zea mays]	Unigene17375_All//7.00E-05//AT5G48570| peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative	Unigene17375_All//8.00E-126//gi|13246247|gb|BE052552.2|BE052552			GO:0016853//GO:0044267	nr +

Unigene17376_All	399	0.52	7.62	5.47	3.62	5.18	6.45	1.06	5.76	0.40	3.86E+00	9.17E-13	Up	3.38E+00	4.02E-08	Up	5.16E-01	2.83E-01		8.34E-01	3.73E-02		2.44E+00	5.47E-08	Up	-1.41E+00	1.74E-01		Unigene17376_All//gi|226500876|ref|NP_001149790.1|//1.00E-16//LOC100283417 [Zea mays]>gi|195634685|gb|ACG36811.1|peptidyl-prolyl isomerase [Zea mays]	Unigene17376_All//7.00E-05//AT5G38570| peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative	Unigene17376_All//3.00E-178//gi|13246247|gb|BE052552.2|BE052552			GO:0016853//GO:0044267	nr -
Unigene17377_All	651	13.26	47.95	48.75	17.91	15.66	9.99	7.08	5.39	37.15	1.85E+00	1.43E-57	Up	1.88E+00	5.27E-58	Up	-1.94E-01	2.98E-01		-8.42E-01	2.26E-07		-3.93E-01	1.35E-01		2.39E+00	3.97E-77	Up	Unigene17377_All|gi|197209736|dbj|BAG68910.1|//4.00E-08//GDSL-motif lipase [Arabidopsis thaliana]	Unigene17377_All//2.00E-09//AT3G43550| carboxylesterase/ hydrolase, acting on ester bonds / lipase	Unigene17377_All//8.00E-50//FL577336			GO:0016788//GO:0044238//GO:0044464	nr -
Unigene17379_All	830	2.02	0.37	1.48	20.47	12.53	13.77	6.93	3.78	1.49	-2.46E+00	4.49E-05	Down	-4.51E-01	3.99E-01		-7.08E-01	9.75E-09		-5.72E-01	1.25E-05		-8.75E-01	7.71E-05		-2.22E+00	1.31E-17	Down	Unigene17379_All|gi|2500196|sp|Q41254.1|RAC9_GOSHI//1.00E-108//RecName: Full=Rac-like GTP-binding protein RAC9; Flags: Precursor>gi|1087113|gb|AAB35094.1|mammalian rac protein homolog [Gossypium hirsutum]	Unigene17379_All//1.00E-91//AT5G45970| ARAC2 (ARABIDOPSIS RAC-LIKE 2); GTP binding	Unigene17379_All//0.00E+00//TC143761		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity	GO:0004620//GO:0032561//GO:0035556//GO:0044424	nr +
Unigene17380_All	562	0.93	10.19	3.22	2.30	8.52	14.30	1.66	0.00	14.67	3.45E+00	1.22E-21	Up	1.79E+00	1.06E-03		1.89E+00	9.23E-11	Up	2.63E+00	1.06E-24	Up	-1.07E+01	1.14E-06	Down	3.15E+00	1.10E-35	Up				Unigene17380_All//0.00E+00//DW503756					
Unigene17381_All	543	2.31	28.83	12.94	0.92	6.28	3.91	1.71	3.16	0.73	3.64E+00	4.73E-61	Up	2.48E+00	1.53E-18	Up	2.77E+00	5.50E-12	Up	2.09E+00	2.20E-05	Up	8.82E-01	4.98E-02		-1.22E+00	5.14E-02		Unigene17381_All|gi|14589311|emb|CAC43238.1|//6.00E-06//calcium binding protein [Sesbania rostrata]		Unigene17381_All//0.00E+00//gi|109885902|gb|DW514872.1|DW514872				nr -
Unigene17383_All	1180	0.62	1.42	0.54	0.17	1.34	0.69	1.76	7.40	98.21	1.19E+00	2.17E-02		-1.97E-01	7.99E-01		2.99E+00	4.00E-06	Up	2.03E+00	2.17E-02		2.08E+00	1.97E-23	Up	5.81E+00	0.00E+00	Up	Unigene17383_All|gi|14249015|gb|AK57698.1|AF377316_1//1.00E-110//myb-like transcription factor Myb 5 [Gossypium hirsutum]	Unigene17383_All//9.00E-61//AT2G47190| MYB2 (MYB DOMAIN PROTEIN 2); DNA binding / calmodulin binding / transcription activator/ transcription factor	Unigene17383_All//0.00E+00//TC156512	MYB			nr -
Unigene17386_All	501	2.82	0.61	1.06	1.59	0.89	1.35	1.10	0.58	0.72	-2.22E+00	5.59E-04	Down	-1.41E+00	2.12E-02		-8.32E-01	2.88E-01		-2.35E-01	7.54E-01		-9.10E-01	3.19E-01		-6.16E-01	4.68E-01		Unigene17386_All|gi|115438518|ref|NP_001043559.1|//5.00E-31//Os01g0612800 [Oryza sativa Japonica Group]>gi|113533090|dbj|BAF05473.1|Os01g0612800 [Oryza sativa Japonica Group]		Unigene17386_All//5.00E-146//C0124240			GO:0005515//GO:0043231//GO:0044267	nr -
Unigene17387_All	554	133.73	114.14	95.93	152.05	139.79	195.57	239.18	165.67	116.78	-2.29E-01	1.97E-04		-4.79E-01	1.08E-14		-1.21E-01	4.11E-02		3.63E-01	2.68E-14		-5.30E-01	4.16E-39		-1.03E+00	7.27E-127	Down	Unigene17387_All|gi|295687227|gb|ADG27839.1|//4.00E-68//eukaryotic translation initiation factor 5A [Gossypium hirsutum]	Unigene17387_All//2.00E-63//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor	Unigene17387_All//0.00E+00//TC156388			GO:0006448//GO:0006449//GO:0008135//GO:0018205//GO:0043021	nr -
Unigene17388_All	452	49.43	17.26	23.21	69.98	73.59	81.53	46.86	19.51	47.24	-1.52E+00	1.74E-31	Down	-1.09E+00	2.33E-18	Down	7.26E-02	5.58E-01		2.20E-01	1.61E-02		-1.26E+00	7.84E-28	Down	1.16E-02	9.45E-01		Unigene17388_All|gi|44681380|gb|AS47630.1|//2.00E-79//At1g64650 [Arabidopsis thaliana]>gi|45723902|gb|AAS76755.1|At1g64650 [Arabidopsis thaliana]	Unigene17388_All//1.00E-80//AT1G64650| LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27720.1); Has 565 Blast hits to 562 proteins in 197 species: Archae - 7; Bacteria - 312; Metazoa - 76; Fungi - 39; Plants - 85; Viruses - 0; Other Eukaryotes - 46 (source: NCBI BLink).	Unigene17388_All//0.00E+00//gi|164255500|gb|EX170191.1|EX170191			GO:0031410	nr -
Unigene17389_All	538	3.79	15.82	8.81	14.26	13.25	11.58	26.64	32.47	20.44	2.06E+00	1.70E-18	Up	1.22E+00	3.82E-05	Up	-1.06E-01	6.62E-01		-3.00E-01	1.90E-01		2.86E-01	1.98E-02		-3.82E-01	3.12E-03					Unigene17389_All//0.00E+00//TC157968					
Unigene1739_All	3297	0.89	2.70	2.12	5.50	4.67	5.92	12.07	45.62	19.82	1.61E+00	5.63E-14	Up	1.25E+00	1.53E-07	Up	-2.36E-01	7.79E-02		1.06E-01	4.86E-01		1.92E+00	0.00E+00	Up	7.16E-01	6.75E-34	Up	Unigene1739_All//gi|224142043|ref|XP_002324368.1|//0.00E+00//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]>gi|222865802|gb|EEF02933.1|glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene1739_All//0.00E+00//AT2G29110| ATGLR2.8; intracellular ligand-gated ion channel					nr +
Unigene17390_All	670	4.30	12.93	10.73	14.50	17.01	14.56	29.72	95.57	74.98	1.59E+00	2.03E-13	Up	1.32E+00	2.29E-08	Up	2.31E-01	2.11E-01		6.10E-03	9.75E-01		1.69E+00	3.12E-126	Up	1.34E+00	5.46E-72	Up	Unigene17390_All|gi|297810727|ref|XP_002872247.1|//6.00E-62//carboxy-lyase [Arabidopsis lyrata subsp. lyrata]>gi|297319084|gb|EFH49506.1|carboxy-lyase [Arabidopsis lyrata subsp. lyrata]	Unigene17390_All//3.00E-63//AT5G06300| carboxy-lyase	Unigene17390_All//0.00E+00//TC178682			GO:0016830//GO:0043231//GO:0044444	nr +
Unigene17391_All	1169	0.09	0.09	0.18	0.60	0.85	0.31	2.17	7.15	86.36	-4.59E-02	9.89E-01		1.03E+00	5.92E-01		5.18E-01	5.07E-01		-9.49E-01	2.88E-01		1.72E+00	1.29E-17	Up	5.31E+00	0.00E+00	Up	Unigene17391_All|gi|16648773|gb|AAL25577.1|//6.00E-30//At1g68440/T2E12_1 [Arabidopsis thaliana]>gi|21700823|gb|AAM70535.1|At1g68440/T2E12_1 [Arabidopsis thaliana]	Unigene17391_All//2.00E-21//AT1G68440| unknown protein	Unigene17391_All//3.00E-20//gi|164252644|gb|ES830191.1|ES830191				nr +
Unigene17392_All	569	56.55	33.48	30.79	55.68	55.74	30.72	1.34	1.25	4.06	-7.56E-01	4.62E-15		-8.77E-01	2.00E-18		1.50E-03	9.92E-01		-8.58E-01	1.44E-19		-9.91E-02	8.96E-01		1.60E+00	3.97E-05	Up	Unigene17392_All|gi|224075319|ref|XP_002304592.1|//3.00E-25//AP2/ERF domain-containing transcription factor [Populus trichocarpa]>gi|222842024|gb|EEE79571.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene17392_All//1.00E-16//AT4G17500| ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene17392_All//0.00E+00//gi|109873110|gb|DW502085.1|DW502085	AP2-EREBP		GO:0006350//GO:0050896	nr -
Unigene17393_All	829	15.65	10.64	6.74	28.96	20.94	27.08	13.41	7.01	7.54	-5.58E-01	3.52E-04		-1.21E+00	7.54E-13	Down	-4.68E-01	4.96E-06		-9.72E-02	4.70E-01		-9.37E-01	1.54E-09		-8.30E-01	3.33E-08					Unigene17393_All//1.00E-144//gi|13248570|gb|BF276214.2|BF276214					
Unigene17396_All	799	63.65	180.36	136.82	74.38	67.06	93.55	67.10	107.24	58.49	1.50E+00	9.27E-196	Up	1.10E+00	5.85E-90	Up	-1.49E-01	3.38E-02		3.31E-01	1.50E-08		6.76E-01	3.77E-39		-1.98E-01	2.14E-03		Unigene17396_All|gi|87240982|gb|ABD32840.1|//1.00E-58//Peptidase C1A, papain; Somatotropin hormone; Peptidase C1, propeptide [Medicago truncatula]	Unigene17396_All//1.00E-59//AT4G01610| cathepsin B-like cysteine protease, putative	Unigene17396_All//0.00E+00//gi|13243636|gb|BE054781.2|BE054781			GO:0004175//GO:0019222//GO:0019538//GO:0043231	nr -
Unigene17397_All	621	1.10	0.98	0.09	1.76	1.66	1.02	4.63	0.94	4.11	-1.62E-01	8.32E-01		-3.68E+00	4.81E-03		-8.53E-02	8.79E-01		-7.94E-01	2.34E-01		-2.30E+00	3.24E-09	Down	-1.73E-01	6.11E-01		Unigene17397_All|gi|22091622|emb|CAD43141.1|//7.00E-12//cyclin D2 [Daucus carota]		Unigene17397_All//3.00E-129//gi|78333898|gb|DT554172.1|DT554172			GO:0009987//GO:0043231	nr +
Unigene17400_All	728	6.25	3.20	3.07	6.64	5.82	4.47	10.11	4.82	3.61	-9.66E-01	7.04E-04		-1.03E+00	5.87E-04	Down	-1.90E-01	5.57E-01		-5.71E-01	3.85E-02		-1.07E+00	5.70E-08	Down	-1.48E+00	3.26E-13	Down	Unigene17400_All|gi|18391101|ref|NP_563858.1|//2.00E-61//ERG28 (Arabidopsis homolog of yeast ergosterol28) [Arabidopsis thaliana]>gi|152112226|sp|Q80594.2|ERG28_ARATH RecName: Full=Ergosterol biosynthetic protein 28>gi|31711712|gb|AAP68212.1|At1g10030 [Arabidopsis thaliana]	Unigene17400_All//8.00E-53//AT1G10030| ERG28 (Arabidopsis homolog of yeast ergosterol28)	Unigene17400_All//0.00E+00//gi|109870895|gb|DW499871.1|DW499871			GO:0031224//GO:0043231	nr -
Unigene17401_All	832	1.13	1.46	0.83	1.62	1.82	1.79	1.27	1.16	4.12	3.69E-01	5.56E-01		-4.44E-01	5.54E-01		1.72E-01	8.06E-01		1.48E-01	7.88E-01		-1.37E-01	8.15E-01		1.70E+00	9.69E-08	Up	Unigene17401_All|gi|42563023|ref|NP_176917.2|//2.00E-16//ATREV3 (ARABIDOPSIS THALIANA RECOVERY PROTEIN 3); DNA binding / DNA-directed DNA polymerase [Arabidopsis thaliana]>gi|34330129|dbj|BAC82450.1|catalytic subunit of polymerase zeta [Arabidopsis thaliana]	Unigene17401_All//1.00E-17//AT1G67500| ATREV3 (ARABIDOPSIS THALIANA RECOVERY PROTEIN 3); DNA binding / DNA-directed DNA polymerase					nr -
Unigene17402_All	795	2.76	3.25	0.67	1.82	2.77	2.56	5.74	2.68	2.76	2.34E-01	5.78E-01		-2.05E+00	5.31E-05	Down	6.09E-01	1.69E-01		4.93E-01	3.11E-01		-1.10E+00	1.82E-05	Down	-1.06E+00	2.12E-05	Down	Unigene17402_All|gi|225470966|ref|XP_002267122.1|//4.00E-45//PREDICTED: similar to Os02g0672700 [Vitis vinifera]	Unigene17402_All//2.00E-33//AT4G07950| DNA-directed RNA polymerase III family protein	Unigene17402_All//0.00E+00//gi|109888645|gb|DW517614.1|DW517614		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0034062//GO:0043231//GO:0046914	nr +
Unigene17403_All	1232	2.12	0.08	1.17	0.08	0.31	1.21	23.37	55.98	71.40	-4.69E+00	1.34E-12	Down	-8.64E-01	3.52E-02		1.93E+00	1.94E-01		3.90E+00	8.60E-07	Up	1.26E+00	2.90E-88	Up	1.61E+00	8.88E-166	Up	Unigene17403_All|gi|211906456|gb|ACJ11721.1|//1.00E-115//quinone oxidoreductase [Gossypium hirsutum]	Unigene17403_All//3.00E-102//AT1G23740| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene17403_All//0.00E+00//TC139017		ko00062|Fatty acid elongation in mitochondria	GO:0003824//GO:0005488//GO:0008152	nr +
Unigene17406_All	756	0.42	0.34	0.00	0.26	0.82	1.02	24.72	29.74	11.17	-3.09E-01	7.89E-01		-8.70E+00	4.92E-02		1.64E+00	1.06E-01		1.95E+00	3.23E-02		2.67E-01	1.22E-02		-1.15E+00	7.15E-22	Down	Unigene17406_All|gi|124359568|gb|ABD28696.2|//2.00E-39//NAD-dependent epimerase/dehydratase [Medicago truncatula]	Unigene17406_All//3.00E-23//AT4G27250| dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family			ko00941|Flavonoid biosynthesis	GO:0008152//GO:0016616//GO:0048037	nr +
Unigene17407_All	564	0.65	2.96	1.42	0.35	2.56	1.28	1.57	3.19	4.03	2.19E+00	1.76E-04	Up	1.12E+00	1.80E-01		2.86E+00	2.11E-05	Up	1.86E+00	4.71E-02		1.02E+00	2.02E-02		1.35E+00	3.86E-04	Up				Unigene17407_All//7.00E-07//gi|164259175|gb|ES794754.1|ES794754					
Unigene17408_All	501	46.68	102.75	101.72	32.71	65.57	83.66	30.47	71.41	80.39	1.14E+00	5.19E-46	Up	1.12E+00	2.49E-43	Up	1.00E+00	2.18E-28	Up	1.35E+00	1.06E-52	Up	1.23E+00	2.05E-44	Up	1.40E+00	3.65E-62	Up	Unigene17408_All|gi|15238156|ref|NP_199575.1|//2.00E-15//NF-YB2 (NUCLEAR FACTOR Y, SUBUNIT B2); transcription factor [Arabidopsis thaliana]>gi|75262442|sp|Q9FGJ3.1|NFYB2_ARATH RecName: Full=Nuclear transcription factor Y subunit B-2; Short=AtNF-YB-2; AltName: Full=Transcriptional activator HAP2B>gi|14326580|gb|AAK60334.1|AF385744_1 AT5g47640/MNJ7_23 [Arabidopsis thaliana]>gi|18700234|gb|AAL77727.1|AT5g47640/MNJ7_23 [Arabidopsis thaliana]	Unigene17408_All//1.00E-16//AT5G47640| NF-YB2 (NUCLEAR FACTOR Y, SUBUNIT B2); transcription factor	Unigene17408_All//5.00E-72//gi|109886828|gb|DW515797.1|DW515797	CCAAT		GO:0001071//GO:0003677//GO:0006351//GO:0043231	nr +
Unigene17409_All	401	41.62	54.08	27.49	75.78	69.21	71.97	118.62	200.64	56.93	3.78E-01	1.44E-03		-5.99E-01	2.05E-05		-1.31E-01	2.34E-01		-7.44E-02	5.52E-01		7.58E-01	8.81E-45		-1.06E+00	6.83E-48	Down	Unigene17409_All|gi|38154485|gb|AAR12194.1|//1.00E-68//molecular chaperone Hsp90-2 [Nicotiana benthamiana]	Unigene17409_All//1.00E-68//AT5G56010| HSP81-3; ATP binding / unfolded protein binding	Unigene17409_All//0.00E+00//gi|78331215|gb|DT551489.1|DT551489		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr +
Unigene1741_All	2244	4.13	8.31	10.89	0.67	2.69	1.15	3.86	2.33	2.36	1.01E+00	3.09E-14	Up	1.40E+00	1.79E-29	Up	2.01E+00	1.31E-14	Up	7.85E-01	4.98E-02		-7.30E-01	2.92E-05		-7.10E-01	3.06E-05		Unigene1741_All|gi|124359309|gb|ABD28458.2|//0.00E+00//Beta-lactamase, class A; SPX, N-terminal; Major facilitator superfamily MFS_1 [Medicago truncatula]	Unigene1741_All//0.00E+00//AT4G22990| SPX (SYG1/Pho81/XPR1) domain-containing protein	Unigene1741_All//0.00E+00//TC136673				nr +
Unigene17410_All	748	24.76	35.43	16.94	9.26	19.61	11.29	0.11	0.00	0.00	5.17E-01	9.34E-07		-5.47E-01	3.69E-05		1.08E+00	1.64E-14	Up	2.87E-01	1.90E-01		-6.82E+00	4.04E-01		-6.82E+00	3.59E-01		Unigene17410_All|gi|117650697|gb|ABK54298.1|//1.00E-84//glycine-rich protein [Gossypium hirsutum]		Unigene17410_All//6.00E-125//gi|18101497|gb|BM360751.1|BM360751				nr -

Unigene17411_All	770	12.16	23.10	28.08	25.17	47.32	30.21	0.38	0.76	0.31	9.25E-01	7.01E-12		1.21E+00	7.28E-21	Up	9.11E-01	7.30E-27		2.63E-01	2.52E-02		9.83E-01	2.59E-01		-3.09E-01	7.75E-01		Unigene17411_All//gi|110736225|dbj|BAF00083.1|//1.00E-50//cytochrome P450 [Arabidopsis thaliana]	Unigene17411_All//5.00E-52//AT4G36380| ROT3 (ROTUNDIFOLIA 3); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding / steroid hydroxylase	Unigene17411_All//5.00E-101//gi|54120519|gb|CO496028.1|CO496028		ko00905|Brassinosteroid biosynthesis	GO:0004497//GO:0005506//GO:0006091//GO:0009826//GO:0009887//GO:0016129//GO:0018437//GO:0048827//GO:0048878	nr +
Unigene17412_All	1466	0.00	1.18	0.29	1.22	1.13	0.77	4.64	1.11	2.26	1.02E+01	7.99E-10	Up	8.18E+00	1.38E-02		-1.18E-01	8.38E-01		-6.68E-01	1.86E-01		-2.06E+00	2.56E-18	Down	-1.04E+00	1.94E-07	Down	Unigene17412_All//gi|42569297|ref|NP_180077.3|//1.00E-143//formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] >gi|160013996|sp|Q9SK28.2|FH18_ARATH RecName: Full=Formin-like protein 18; Short=AtFH18	Unigene17412_All//6.00E-137//AT2G25050| formin homology 2 domain-containing protein / FH2 domain-containing protein	Unigene17412_All//0.00E+00//D8454686				nr +
Unigene17413_All	433	48.33	26.33	27.92	50.16	47.00	73.95	123.13	65.16	38.00	-8.76E-01	9.55E-13		-7.92E-01	2.36E-10		-9.38E-02	5.25E-01		5.60E-01	1.38E-09		-9.18E-01	2.84E-41		-1.70E+00	1.42E-109	Down	Unigene17413_All//gi|192913024|gb|ACF06620.1|//3.00E-35//ribosomal protein S14 [Elaeis guineensis]	Unigene17413_All//5.00E-19//AT3G52580| 40S ribosomal protein S14 (RPS14C)	Unigene17413_All//0.00E+00//TC154908		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene17414_All	495	2.43	3.58	1.29	12.38	6.61	5.93	27.33	15.11	5.96	5.59E-01	2.54E-01		-9.13E-01	1.57E-01		-9.05E-01	4.31E-05		-1.06E+00	7.31E-06	Down	-8.55E-01	6.50E-10		-2.20E+00	6.90E-40	Down			Unigene17414_All//1.00E-119//gi|48817227|gb|CO118540.1|CO118540				
Unigene17415_All	706	2.08	0.86	0.98	4.80	2.63	1.79	3.47	2.96	1.47	-1.27E+00	2.39E-02		-1.08E+00	6.36E-02		-8.65E-01	6.08E-03		-1.42E+00	3.31E-05	Down	-2.31E-01	5.75E-01		-1.24E+00	5.26E-04	Down			Unigene17415_All//5.00E-113//TC179175				
Unigene17416_All	868	4.88	3.62	4.29	0.29	0.75	0.62	0.00	0.72	0.92	-4.32E-01	1.47E-01		-1.85E-01	5.86E-01		1.39E+00	1.51E-01		1.12E+00	3.05E-01		9.50E+00	1.47E-04	Up	9.84E+00	7.36E-06	Up	Unigene17416_All//gi|115455581|ref|NP_001051391.1|//3.00E-46//Os03g0767900 [Oryza sativa Japonica Group] >gi|113549862|dbj|BAF13305.1|Os03g0767900 [Oryza sativa Japonica Group]	Unigene17416_All//2.00E-28//AT1G49405| integral membrane protein, putative				GO:0043231	nr +
Unigene17417_All	278	101.44	51.22	43.48	146.75	164.87	269.19	189.04	100.58	111.06	-9.86E-01	1.97E-20		-1.22E+00	1.59E-27	Down	1.68E-01	3.97E-02		8.75E-01	1.47E-46		-9.10E-01	4.02E-40		-7.67E-01	4.92E-31		Unigene17417_All//gi|6688812|emb|CAB65281.1|//1.00E-43//L3 Ribosomal protein [Medicago sativa subsp. x varia]	Unigene17417_All//9.00E-36//AT1G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	Unigene17417_All//8.00E-156//gi|78339263|gb|DT559537.1|DT559537		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene17419_All	1086	0.58	0.14	1.08	5.69	1.97	4.41	10.86	2.35	1.03	-2.05E+00	4.46E-02		9.00E-01	1.70E-01		-1.53E+00	3.35E-11	Down	-3.68E-01	1.42E-01		-2.21E+00	5.23E-34	Down	-3.40E+00	1.70E-55	Down	Unigene17419_All//gi|15232846|ref|NP_186859.1|//1.00E-103//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana]	Unigene17419_All//1.00E-98//AT3G02100| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene17419_All//7.00E-30//gi|164360397|gb|ES819042.1|ES819042		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene1742_All	2102	16.45	14.66	14.03	16.61	18.91	20.78	38.46	55.16	83.03	-1.67E-01	8.75E-02		-2.29E-01	2.04E-02		1.87E-01	3.24E-02		3.23E-01	4.50E-05		5.20E-01	3.24E-33		1.11E+00	6.87E-186	Up	Unigene1742_All//gi|18146966|dbj|BAB82502.1|//4.00E-56//cig3 [Nicotiana tabacum]	Unigene1742_All//6.00E-47//AT5G19400| SMG7	Unigene1742_All//0.00E+00//TC147499				nr +
Unigene17420_All	272	5.00	0.93	1.96	13.55	15.57	20.92	32.33	24.89	29.00	-2.42E+00	3.35E-04	Down	-1.35E+00	2.93E-02		2.00E-01	5.62E-01		6.26E-01	1.20E-02		-3.77E-01	3.41E-02		-1.57E-01	3.98E-01		Unigene17420_All//gi|297798874|ref|XP_002867321.1|//2.00E-39//cytosol aminopeptidase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313157|gb|EFH43580.1| cytosol aminopeptidase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17420_All//2.00E-34//AT4G30920| cytosol aminopeptidase family protein	Unigene17420_All//5.00E-123//DW510931		ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism	GO:0008237//GO:0008238//GO:0009536//GO:0010038//GO:0019538//GO:0046914	nr -
Unigene17421_All	1291	4.05	0.71	0.62	3.70	2.43	1.15	3.14	0.26	0.46	-2.52E+00	9.08E-15	Down	-2.71E+00	3.24E-15	Down	-6.10E-01	2.00E-02		-1.68E+00	7.18E-09	Down	-3.60E+00	9.52E-20	Down	-2.76E+00	4.39E-16	Down	Unigene17421_All//gi|224120882|ref|XP_002318442.1|//1.00E-146//SET domain protein [Populus trichocarpa] >gi|222859115|gb|EEE96662.1| SET domain protein [Populus trichocarpa]	Unigene17421_All//9.00E-139//AT5G24330| ATXR6; DNA binding / protein binding	Unigene17421_All//0.00E+00//gi|78332107|gb|DT552381.1|DT552381				nr +
Unigene17422_All	517	0.61	2.06	1.96	1.45	1.53	1.05	3.76	2.51	1.16	1.76E+00	1.43E-02		1.69E+00	2.74E-02		8.40E-02	9.45E-01		-4.63E-01	6.06E-01		-5.86E-01	1.65E-01		-1.70E+00	7.95E-05	Down			Unigene17422_All//4.00E-08//DN803760				
Unigene17424_All	600	0.70	1.52	0.36	2.99	4.13	6.17	5.99	7.87	2.99	1.12E+00	1.30E-01		-9.75E-01	4.12E-01		4.67E-01	2.80E-01		1.05E+00	1.07E-03		3.94E-01	1.28E-01		-1.00E+00	3.90E-04	Down			Unigene17424_All//7.00E-07//TC173653				
Unigene17428_All	1615	0.06	0.19	0.00	0.00	0.06	0.00	16.94	36.46	23.66	1.54E+00	3.23E-01		-6.02E+00	3.95E-01		6.00E+00	4.56E-01		null	null		1.11E+00	1.68E-61	Up	4.82E-01	2.09E-10		Unigene17428_All//gi|224127726|ref|XP_002329162.1|//4.00E-62//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene17428_All//2.00E-20//AT4G12010| disease resistance protein (TIR-NBS-LRR class), putative	Unigene17428_All//1.00E-87//CO115408		ko04626|Plant-pathogen interaction		nr +
Unigene1743_All	1979	5.29	7.58	7.51	7.05	8.80	7.10	6.69	9.59	22.79	5.19E-01	3.19E-04		5.06E-01	7.79E-04		3.21E-01	1.48E-02		1.01E-02	9.48E-01		5.20E-01	4.02E-06		1.77E+00	2.71E-97	Up									
Unigene17431_All	756	1.11	3.89	3.03	3.82	2.82	5.26	1.96	4.75	10.70	1.81E+00	6.68E-06	Up	1.45E+00	1.55E-03		-4.36E-01	2.44E-01		4.60E-01	1.53E-01		1.28E+00	1.84E-05	Up	2.45E+00	4.94E-27	Up	Unigene17431_All//gi|3256068|emb|CAA74397.1|//3.00E-27//Heat Shock Factor 3 [Arabidopsis thaliana]	Unigene17431_All//2.00E-26//AT5G16820| HSF3 (HEAT SHOCK FACTOR 3); DNA binding / transcription factor	Unigene17431_All//0.00E+00//ES845267	HSF		GO:0001071//GO:0003677//GO:0006351//GO:0006950//GO:0043231	nr -
Unigene17433_All	1565	9.09	24.22	17.93	0.00	0.13	0.03	0.00	0.00	0.00	1.41E+00	2.01E-47	Up	9.80E-01	2.37E-19		7.04E+00	1.57E-01		4.85E+00	6.96E-01		null	null		null	null		Unigene17433_All//gi|22854880|gb|AAN09798.1|//1.00E-150//benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Nicotiana tabacum]	Unigene17433_All//2.00E-114//AT5G17540| transferase family protein	Unigene17433_All//5.00E-84//gi|48806574|gb|CO107888.1|CO107888		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene17434_All	504	0.31	1.41	1.69	1.58	2.12	2.33	7.13	3.73	2.69	2.18E+00	2.50E-02		2.44E+00	9.10E-03		4.22E-01	5.72E-01		5.59E-01	4.04E-01		-9.34E-01	1.28E-03		-1.41E+00	1.95E-06	Down			Unigene17434_All//0.00E+00//DW478898				
Unigene17435_All	1029	0.86	1.38	0.57	2.18	2.11	2.15	2.38	0.61	2.28	6.74E-01	2.31E-01		-6.03E-01	4.18E-01		-4.73E-02	9.09E-01		-1.86E-02	9.56E-01		-1.97E+00	1.08E-06	Down	-6.12E-02	8.73E-01		Unigene17435_All//gi|296086263|emb|CBI31704.3|//1.00E-137//unnamed protein product [Vitis vinifera]	Unigene17435_All//1.00E-116//AT3G12590| unknown protein	Unigene17435_All//5.00E-157//TC133580			GO:0043231	nr +
Unigene17436_All	981	1.17	9.30	3.58	0.10	0.70	0.18	1.51	0.72	0.00	2.99E+00	6.34E-30	Up	1.61E+00	1.02E-05	Up	2.79E+00	9.45E-03		8.58E-01	6.95E-01		-1.06E+00	3.15E-02		-1.06E+01	5.85E-11	Down	Unigene17436_All//gi|33519172|gb|AAQ20901.1|//2.00E-39//WRKY1 [Oryza sativa Japonica Group] >gi|46394288|tpg|DA005082.1| TPA_inf: WRKY transcription factor 17 [Oryza sativa (japonica cultivar-group)]	Unigene17436_All//3.00E-39//AT5G43290| WRKY49; transcription factor	Unigene17436_All//0.00E+00//CO093329	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0006350//GO:0010468//GO:0043231	nr +
Unigene17437_All	506	4.65	4.81	2.42	6.60	6.12	2.68	4.68	2.81	5.04	4.69E-02	9.20E-01		-9.43E-01	3.08E-02		-1.07E-01	8.01E-01		-1.30E+00	1.41E-04	Down	-7.37E-01	4.67E-02		1.07E-01	7.62E-01				Unigene17437_All//5.00E-109//ES847203				
Unigene17439_All	616	3.57	1.40	3.46	2.91	2.80	2.05	1.24	0.14	0.65	-1.35E+00	2.48E-03		-4.50E-02	9.31E-01		-5.87E-02	8.99E-01		-5.04E-01	3.30E-01		-3.19E+00	7.93E-04	Down	-9.34E-01	1.82E-01									
Unigene1744_All	1843	28.47	18.70	21.29	91.36	90.26	119.46	43.27	19.23	25.20	-6.07E-01	1.38E-16		-4.19E-01	1.99E-08		-1.74E-02	7.67E-01		3.87E-01	5.64E-32		-1.17E+00	7.21E-91	Down	-7.80E-01	6.93E-48		Unigene1744_All//gi|124360348|gb|AB008361.1|//1.00E-119//Hypothetical plant protein [Medicago truncatula]	Unigene1744_All//7.00E-169//AT1G51630| unknown protein	Unigene1744_All//0.00E+00//TC178491				nr +
Unigene17441_All	736	0.64	2.48	1.66	1.62	2.57	1.84	2.64	3.01	1.95	1.95E+00	2.77E-04	Up	1.38E+00	3.74E-02		6.64E-01	1.70E-01		1.81E-01	7.57E-01		1.88E-01	6.32E-01		-4.40E-01	2.84E-01									
Unigene17443_All	852	0.43	0.77	3.25	2.28	2.38	2.07	1.89	1.42	1.08	8.47E-01	3.48E-01		2.92E+00	6.14E-09	Up	6.46E-02	9.08E-01		-1.41E-01	7.62E-01		-4.07E-01	3.95E-01		-8.10E-01	6.84E-02									
Unigene17444_All	595	6.33	8.52	7.34	3.27	7.06	6.53	7.67	1.76	1.07	4.28E-01	1.17E-01		2.13E-01	5.09E-01		1.11E+00	1.11E-04	Up	1.00E+00	1.29E-03		-2.13E+00	5.23E-13	Down	-2.84E+00	1.66E-18	Down			Unigene17444_All//0.00E+00//TC152737				
Unigene17445_All	854	0.80	1.19	0.00	8.87	4.72	2.70	1.19	0.88	2.05	5.75E-01	3.83E-01		-9.64E+00	7.65E-04	Down	-9.10E-01	3.34E-06		-1.72E+00	4.25E-14	Down	-4.32E-01	5.03E-01		7.89E-01	6.43E-02		Unigene17445_All//gi|225441862|ref|XP_002284216.1|//9.00E-89//PREDICTED: similar to AT-HSFB3 (Arabidopsis thaliana heat shock transcription factor B3); DNA binding / transcription factor [Vitis vinifera]	Unigene17445_All//2.00E-53//AT2G41690| AT-HSFB3; DNA binding / transcription factor	Unigene17445_All//3.00E-10//TC139160	HSF		GO:0001071//GO:0003677//GO:0006351//GO:0010038//GO:0043231	nr +
Unigene17447_All	517	0.91	0.20	1.44	1.73	1.47	1.40	3.27	0.49	1.85	-2.22E+00	7.76E-02		6.63E-01	4.19E-01		-2.43E-01	7.53E-01		-3.11E-01	6.88E-01		-2.75E+00	8.02E-07	Down	-8.23E-01	5.74E-02		Unigene17447_All//gi|62318912|dbj|BAB93993.1|//2.00E-31//receptor lectin kinase -like protein [Arabidopsis thaliana]	Unigene17447_All//2.00E-20//AT3G53380| lectin protein kinase family protein	Unigene17447_All//0.00E+00//gi|48829083|gb|CO127473.1|CO127473			GO:0004672//GO:0004871//GO:0006464//GO:0016020//GO:0030246//GO:0031410//GO:0032559	nr +
Unigene1745_All	2656	5.16	2.48	4.65	12.38	12.99	20.80	12.51	10.04	7.77	-1.06E+00	1.71E-11	Down	-1.50E-01	3.91E-01		6.97E-02	5.43E-01		7.49E-01	1.66E-26		-3.18E-01	1.51E-04		-6.87E-01	1.27E-16		Unigene1745_All//2.00E-112//AT1G08760| unknown protein	Unigene1745_All//0.00E+00//TC166596				nr +
Unigene17450_All	1505	2.92	0.00	0.42	0.00	0.05	0.24	11.18	5.92	1.83	-1.15E+01	2.07E-25	Down	-2.78E+00	3.38E-13	Down	5.52E+00	6.10E-01		7.91E+00	2.37E-02		-9.19E-01	1.36E-13		-2.61E+00	1.48E-60	Down	Unigene17450_All//gi|15240534|ref|NP_199780.1|//1.00E-125//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|8978266|dbj|BAA98157.1| anthocyanidin-3-glucoside rhamnosyltransferase-like [Arabidopsis thaliana] >gi|28851061|gb|AAO63451.1| At5g49690 [Arabidopsis thaliana]	Unigene17450_All//9.00E-120//AT5G49690| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene17450_All//0.00E+00//TC165913		ko00908|Zeatin biosynthesis		nr +
Unigene17451_All	278	35.76	16.95	19.15	94.97	87.82	53.77	77.72	28.72	29.38	-1.08E+00	8.68E-09	Down	-9.01E-01	2.12E-06		-1.13E-01	3.60E-01		-8.21E-01	3.08E-15		-1.44E+00	2.45E-34	Down	-1.40E+00	3.40E-34	Down	Unigene17451_All//gi|12585316|sp|Q9M4G4.1|PGMC_SOLTU//2.00E-38//RecName: Full=Phosphoglucomutase, cytoplasmic; Short=PGM; AltName: Full=Glucose phosphomutase >gi|8250624|emb|CAB93681.1| cytosolic phosphoglucomutase [Solanum tuberosum]	Unigene17451_All//8.00E-38//AT1G23190| phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative	Unigene17451_All//2.00E-153//gi|21090922|gb|BQ403235.1|BQ403235		ko00500|Starch and sucrose metabolism//ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway	GO:0009536//GO:0010038//GO:0016020//GO:0016868//GO:0019318//GO:0046872	nr +
Unigene17452_All	479	54.83	113.50	73.59	39.62	40.11	38.94	245.12	208.80	125.84	1.05E+00	1.15E-42	Up	4.25E-01	5.02E-06		1.78E-02	9.14E-01		-2.51E-02	8.80E-01		-2.31E-01	5.22E-08		-9.62E-01	7.38E-100		Unigene17452_All//gi|211906454|gb|ACJ11720.1|//5.00E-38//peroxiredoxin [Gossypium hirsutum]	Unigene17452_All//3.00E-32//AT1G65980| TPX1 (thioredoxin-dependent peroxidase 1); antioxidant/ oxidoreductase	Unigene17452_All//0.00E+00//gi|21103700|gb|BQ416013.1|BQ416013		ko04146|Peroxisome	GO:0005506//GO:0006950//GO:0008152//GO:0009536//GO:0010038//GO:0016020//GO:0016209//GO:0016705//GO:0019725	nr +
Unigene17453_All	972	1.61	0.94	0.93	3.28	3.58	3.07	3.52	1.08	0.98	-7.83E-01	1.36E-01		-7.94E-01	1.48E-01		1.26E-01	7.72E-01		-9.70E-02	7.96E-01		-1.71E+00	1.23E-07	Down	-1.84E+00	1.16E-08	Down	Unigene17453_All//gi|83319215|dbj|BAE53712.1|//4.00E-22//At3g21480 [Arabidopsis thaliana]	Unigene17453_All//1.00E-20//AT3G21480| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: intracellular; CONTAINS InterPro DOMAIN/s: BRCT (InterPro:IPR001357); BEST Arabidopsis thaliana protein match is: transcription coactivator (TAIR:AT4G03130.1); Has 489 Blast hits to 455 proteins in 115 species: Archae - 2; Bacteria - 37; Metazoa - 270; Fungi - 30; Plants - 45; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).	Unigene17453_All//0.00E+00//CO108894				nr -
Unigene17457_All	1038	0.10	0.00	0.10	2.64	0.00	0.00	29.29	35.88	19.46	-6.66E+00	3.73E-01		2.55E-02	1.00E+00		-1.14E+01	1.49E-20	Down	-1.14E+01	3.34E-17	Down	2.93E-01	2.13E-04		-5.90E-01	7.41E-12		Unigene17457_All//gi|18202454|sp|P92997.1|GL113_ARATH//3.00E-90//RecName: Full=Germin-like protein subfamily 1 member 13; Flags: Precursor >gi|1755166|gb|AAB51572.1| germin-like protein [Arabidopsis thaliana]	Unigene17457_All//5.00E-91//AT5G39110| germin-like protein, putative	Unigene17457_All//0.00E+00//TC153262			GO:0005576//GO:0044464//GO:0046914	nr +

Unigene17459_All	2182	0.00	0.00	0.07	0.00	0.06	0.04	16.24	15.34	44.18	null	null		6.19E+00	2.39E-01		5.98E+00	3.19E-01		5.37E+00	4.77E-01		-8.18E-02	4.01E-01		1.44E+00	9.64E-155	Up	Unigene17459_All//gi|15240142|ref|NP_196292.1|//0.00E+00//lectin protein kinase family protein [Arabidopsis thaliana] >gi|9759302|dbj|BAB09808.1|lectin-like protein kinase [Arabidopsis thaliana]	Unigene17459_All//0.00E+00//AT5G06740| lectin protein kinase family protein	Unigene17459_All//0.00E+00//TC171186		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0030246	nr +
Unigene17462_All	567	49.64	19.30	32.03	80.83	68.81	91.52	267.25	88.60	111.58	-1.36E+00	1.06E-33	Down	-6.32E-01	1.87E-09		-2.32E-01	2.23E-03		1.79E-01	2.01E-02		-1.59E+00	1.86E-275	Down	-1.26E+00	6.51E-199	Down	Unigene17462_All//gi|2780194|emb|CAA05979.1|//1.00E-33//adenine nucleotide translocator [Lupinus albus]	Unigene17462_All//2.00E-31//AT3G08580| AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/binding	Unigene17462_All//0.00E+00//TC177362			GO:0006862//GO:0009526//GO:0015300//GO:0019866//GO:0030312//GO:0031224//GO:0031981//GO:0046914	nr -
Unigene17464_All	447	66.72	22.33	83.27	152.90	102.69	70.52	8.89	4.96	2.76	-1.58E+00	2.81E-44	Down	3.20E-01	4.84E-04		-5.74E-01	2.55E-23		-1.12E+00	3.54E-64	Down	-8.43E-01	1.99E-03		-1.69E+00	6.96E-09	Down			Unigene17464_All//2.00E-108//TC173770					
Unigene17469_All	497	2.00	5.30	2.68	2.21	2.84	0.82	3.06	0.84	0.96	1.41E+00	5.42E-04	Up	4.21E-01	4.84E-01		3.65E-01	5.62E-01		-1.43E+00	3.46E-02		-1.86E+00	3.50E-04	Down	-1.67E+00	7.06E-04	Down								
Unigene1747_All	2232	7.24	4.36	5.46	12.94	9.53	10.68	8.90	3.71	3.94	-7.33E-01	1.38E-07		-4.07E-01	5.08E-03		-4.41E-01	1.88E-06		-2.77E-01	6.70E-03		-1.26E+00	3.79E-26	Down	-1.17E+00	4.24E-24	Down	Unigene1747_All//gi|297819430|ref|XP_002877598.1|//0.00E+00//anaphase-promoting complex/cyclosome 8 [Arabidopsis lyrata subsp. lyrata] >gi|297323436|gb|EFH53857.1|anaphase-promoting complex/cyclosome 8 [Arabidopsis lyrata subsp. lyrata]	Unigene1747_All//0.00E+00//AT3G48150| APC8 (ANAPHASE-PROMOTING COMPLEX SUBUNIT 8); binding	Unigene1747_All//0.00E+00//gi|164263618|gb|ES851929.1|ES851929		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene17470_All	481	15.88	11.06	24.69	12.22	11.60	10.42	9.14	38.49	20.79	-5.22E-01	1.36E-02		6.37E-01	1.82E-04		-7.55E-02	8.14E-01		-2.30E-01	4.05E-01		2.07E+00	8.27E-49	Up	1.19E+00	1.24E-12	Up			Unigene17470_All//1.00E-128//TC161037					
Unigene17473_All	633	187.96	388.71	199.12	25.18	67.62	82.34	0.07	0.00	0.00	1.05E+00	1.82E-190	Up	8.32E-02	1.20E-01		1.43E+00	1.01E-63	Up	1.71E+00	7.18E-92	Up	-6.06E+00	6.58E-01		-6.06E+00	6.13E-01		Unigene17473_All//gi|119888002|gb|ABM05953.1|//1.00E-108//proline-rich protein [Gossypium hirsutum]	Unigene17473_All//3.00E-19//AT4G16380| metal ion binding	Unigene17473_All//0.00E+00//TC148094				nr +
Unigene17474_All	1825	0.66	0.97	0.73	0.11	0.17	0.10	10.26	32.61	27.35	5.59E-01	2.54E-01		1.46E-01	7.94E-01		6.37E-01	6.95E-01		-1.42E-01	9.35E-01		1.67E+00	1.06E-115	Up	1.41E+00	5.09E-78	Up	Unigene17474_All//gi|3892714|emb|CAA22164.1|//1.00E-147//trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana] >gi|7269105|emb|CAB79214.1|trehalose-6-phosphate phosphatase-like protein [Arabidopsis thaliana] >gi|62321206|dbj|BAD94370.1|trehalose-6-phosphate phosphatase - like protein [Arabidopsis thaliana] >gi|222422885|dbj|BAH19429.1|AT4G22590 [Arabidopsis thaliana]	Unigene17474_All//1.00E-150//AT4G12430| trehalose-6-phosphate phosphatase, putative	Unigene17474_All//0.00E+00//ES822355		ko00500|Starch and sucrose metabolism		nr +
Unigene17476_All	584	1.79	0.17	0.18	2.73	1.65	1.08	4.63	1.79	1.16	-3.37E+00	2.13E-04	Down	-3.30E+00	4.59E-04	Down	-7.25E-01	1.57E-01		-1.33E+00	1.23E-02		-1.37E+00	1.05E-04	Down	-2.00E+00	9.91E-08	Down	Unigene17476_All//gi|79553691|ref|NP_178730.2|//2.00E-39//binding [Arabidopsis thaliana]	Unigene17476_All//1.00E-40//AT2G07170| binding	Unigene17476_All//1.00E-14//ES795474				nr +
Unigene17478_All	723	1.23	0.14	0.66	5.03	3.00	0.87	13.57	11.39	6.45	-3.13E+00	1.19E-03		-8.92E-01	2.47E-01		-7.45E-01	1.45E-02		-2.52E+00	3.37E-11	Down	-2.53E-01	1.49E-01		-1.07E+00	8.43E-11	Down	Unigene17478_All//gi|18407534|ref|NP_566126.1|//6.00E-31//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|84778472|dbj|BAE73263.1|xylogen like protein 7 [Arabidopsis thaliana]	Unigene17478_All//2.00E-14//AT3G22600| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene17478_All//0.00E+00//DW507812			GO:0005488//GO:0006810//GO:0031410	nr -
Unigene17748_All	1877	11.74	7.34	9.96	14.33	13.50	12.54	3.13	0.87	1.25	-6.77E-01	7.79E-09		-2.37E-01	6.42E-02		-8.59E-02	5.15E-01		-1.93E-01	8.82E-02		-1.85E+00	6.88E-14	Down	-1.32E+00	3.79E-09	Down	Unigene1748_All//gi|34365753|gb|AAQ65188.1|//0.00E+00//At3g26950 [Arabidopsis thaliana]	Unigene1748_All//1.00E-173//AT3G26950| unknown protein	Unigene1748_All//0.00E+00//TC171095				nr +
Unigene17481_All	434	42.68	92.23	45.52	135.44	121.79	171.29	62.54	45.74	54.62	1.11E+00	1.27E-34	Up	9.31E-02	5.33E-01		-1.53E-01	3.00E-02		3.39E-01	7.30E-09		-4.51E-01	1.12E-06		-1.96E-01	3.99E-02		Unigene17481_All//gi|21536547|gb|AM60879.1|//3.00E-10//farnesylated protein (ATFP6) [Arabidopsis thaliana]	Unigene17481_All//2.00E-11//AT4G38580| ATFP6 (FARNESYLATED PROTEIN 6); metal ion binding	Unigene17481_All//2.00E-148//gi|78346088|gb|DT566362.1|DT566362			GO:0006812//GO:0009408//GO:0016020//GO:0043169	nr +
Unigene17482_All	794	0.07	0.00	0.27	3.07	1.60	2.05	2.18	1.26	0.55	-6.04E+00	6.13E-01		2.03E+00	3.61E-01		-9.38E-01	1.46E-02		-5.86E-01	1.62E-01		-7.89E-01	7.73E-02		-1.98E+00	3.36E-05	Down	Unigene17482_All//gi|115456403|ref|NP_001061802.1|//3.00E-49//Os03g0832500 [Oryza sativa Japonica Group] >gi|108711927|gb|ABF99722.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550273|dbj|BAF13716.1|Os03g0832500 [Oryza sativa Japonica Group]	Unigene17482_All//3.00E-55//AT3G17030| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nucleic acid-binding, OB-fold-like (InterPro:IPR016027); Has 10 Blast hits to 10 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene17482_All//0.00E+00//ES832170			GO:0043231	nr -
Unigene17485_All	493	14.22	12.64	3.78	20.71	26.96	21.25	12.95	135.90	18.34	-1.70E-01	4.77E-01		-1.91E+00	1.96E-13	Down	3.80E-01	1.23E-02		3.71E-02	8.67E-01		3.39E+00	7.68E-301	Up	5.02E-01	2.54E-03		Unigene17485_All//gi|255644406|gb|ACU22708.1|//2.00E-06//unknown [Glycine max]		Unigene17485_All//0.00E+00//gi|62295979|gb|DN779354.1|DN779354				nr +
Unigene17486_All	362	4.19	9.52	5.44	9.50	5.80	5.36	17.05	25.17	26.30	1.18E+00	5.21E-04	Up	3.77E-01	4.28E-01		-7.11E-01	2.49E-02		-8.24E-01	1.28E-02		5.62E-01	9.47E-04		6.25E-01	1.10E-04				Unigene17486_All//4.00E-47//TC177524					
Unigene17488_All	397	3.43	0.51	2.01	11.79	8.76	7.17	7.14	10.21	3.21	-2.75E+00	1.08E-04	Down	-7.68E-01	2.06E-01		-4.29E-01	1.24E-01		-7.19E-01	9.23E-03		5.17E-01	5.93E-02		-1.15E+00	4.37E-04	Down	Unigene17488_All//gi|20799733|gb|AAM28629.1|AF503771.1|/6.00E-16//acyl-CoA synthetase-like protein [Arabidopsis thaliana]	Unigene17488_All//3.00E-17//AT3G23790| AMP-binding protein, putative	Unigene17488_All//5.00E-167//DT047957		ko04146|Peroxisome//ko00071|Fatty acid metabolism	GO:0006633//GO:0009526//GO:0015645	nr +
Unigene17490_All	429	6.34	2.24	3.10	4.64	2.25	7.47	2.27	0.39	0.46	-1.50E+00	1.89E-04	Down	-1.03E+00	1.04E-02		-1.05E+00	1.59E-02		6.86E-01	5.12E-02		-2.54E+00	6.41E-04	Down	-2.29E+00	9.84E-04	Down			Unigene17490_All//9.00E-163//TC149795					
Unigene17491_All	1156	0.81	0.70	0.64	4.74	2.80	1.99	3.36	1.63	1.00	-2.16E-01	7.32E-01		-3.37E-01	6.16E-01		-7.59E-01	1.37E-03		-1.25E+00	1.07E-06	Down	-1.05E+00	1.75E-04	Down	-1.75E+00	3.85E-09	Down	Unigene17491_All//gi|297851732|ref|XP_002893747.1|//1.00E-148//galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339589|gb|EFH70006.1|galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17491_All//2.00E-136//AT1G32930| galactosyltransferase family protein	Unigene17491_All//0.00E+00//TC167878				nr +
Unigene17492_All	389	18.02	13.94	9.45	32.40	12.13	2.90	4.35	0.43	0.72	-3.71E-01	1.02E-01		-9.32E-01	5.70E-05		-1.42E+00	5.90E-20	Down	-3.48E+00	3.38E-52	Down	-3.34E+00	4.60E-08	Down	-2.60E+00	9.91E-07	Down			Unigene17492_All//5.00E-10//ES836479					
Unigene17493_All	1219	0.04	0.25	0.31	1.14	1.61	2.45	2.74	1.17	3.37	2.54E+00	1.51E-01		2.83E+00	9.31E-02		4.93E-01	3.16E-01		1.10E+00	2.69E-03		-1.23E+00	6.80E-05	Down	2.97E-01	2.82E-01		Unigene17493_All//gi|9759492|dbj|BAB10497.1|//1.00E-142//nuclear pore protein-like [Arabidopsis thaliana]	Unigene17493_All//4.00E-144//AT5G40480| EMB3012 (embryo defective 3012)				GO:0005488//GO:0031410	nr +
Unigene17495_All	999	3.25	2.64	2.29	3.79	4.31	8.91	7.83	1.13	0.20	-3.00E-01	3.83E-01		-5.03E-01	1.67E-01		1.85E-01	5.85E-01		1.23E+00	4.16E-10	Up	-2.79E+00	1.23E-29	Down	-5.30E+00	9.39E-50	Down	Unigene17495_All//gi|297824545|ref|XP_002880155.1|//2.00E-90//CYCP3_1 [Arabidopsis lyrata subsp. lyrata] >gi|297325994|gb|EFH56414.1|CYCP3_1 [Arabidopsis lyrata subsp. lyrata]	Unigene17495_All//1.00E-82//AT2G45080| cycp3;1 (cyclin p3;1); cyclin-dependent protein kinase	Unigene17495_All//0.00E+00//TC133126			GO:0005488//GO:0007049	nr -
Unigene17497_All	337	0.16	3.46	3.63	3.25	2.76	4.56	8.66	9.18	4.14	4.48E+00	1.19E-05	Up	4.55E+00	1.02E-05	Up	-2.37E-01	7.30E-01		4.87E-01	3.95E-01		8.43E-02	8.05E-01		-1.07E+00	8.64E-04	Down								
Unigene17498_All	408	1.67	1.61	2.48	4.64	4.22	1.66	23.94	12.81	11.81	-4.63E-02	9.70E-01		5.73E-01	4.04E-01		-1.37E-01	8.10E-01		-1.48E+00	2.25E-03		-9.03E-01	5.14E-08		-1.02E+00	6.00E-10	Down	Unigene17498_All//gi|224078968|ref|XP_002305699.1|//6.00E-06//predicted protein [Populus trichocarpa] >gi|118486666|gb|ABK95170.1|unknown [Populus trichocarpa] >gi|222848663|gb|EEE86210.1|predicted protein [Populus trichocarpa]	Unigene17498_All//7.00E-65//AT3G27430| PBB1; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene17498_All//1.00E-146//gi|164354945|gb|ES839681.1|ES839681		ko03050|Proteasome		nr -
Unigene17499_All	662	19.52	28.40	25.18	18.21	37.19	34.73	0.38	0.44	0.06	5.41E-01	2.14E-05		3.67E-01	1.07E-02		1.03E+00	2.77E-22	Up	9.31E-01	3.18E-16		2.06E-01	8.68E-01		-2.67E+00	1.15E-01		Unigene17499_All//gi|12231178|dbj|BAB20972.1|//1.00E-57//aspartic proteinase 4 [Nepenthes alata]	Unigene17499_All//1.00E-51//AT1G11910| aspartyl protease family protein	Unigene17499_All//0.00E+00//TC157826			GO:0000323//GO:0004175//GO:0006643//GO:0019538	nr -
Unigene1750_All	583	3.23	0.70	0.82	5.04	3.13	6.12	3.70	1.08	1.91	-2.22E+00	4.65E-05	Down	-1.97E+00	3.20E-04	Down	-6.87E-01	4.92E-02		2.80E-01	4.51E-01		-1.78E+00	2.50E-05	Down	-9.51E-01	1.16E-02		Unigene1750_All//gi|18416749|ref|NP_567746.1|//4.00E-42//CSN6B [Arabidopsis thaliana] >gi|55976549|sp|Q8W1P0.2|CSN6B_ARATH RecName: Full=COP9 signalosome complex subunit 6b; Short=Signalosome subunit 6b; Short=AtCSN6b >gi|18056667|gb|AAL58107.1|AF395064_1 CSN complex subunit 6B [Arabidopsis thaliana] >gi|21593149|gb|AAM65098.1|transcription factor-like [Arabidopsis thaliana]	Unigene1750_All//2.00E-35//AT4G26430| CSN6B	Unigene1750_All//7.00E-118//gi|109834448|gb|DW233013.1|DW233013				nr +
Unigene17500_All	387	5.68	0.92	4.40	4.12	6.05	2.22	2.51	0.54	0.41	-2.63E+00	7.09E-07	Down	-3.67E-01	4.12E-01		5.55E-01	2.02E-01		-8.94E-01	9.15E-02		-2.22E+00	1.82E-03		-2.61E+00	3.35E-04	Down								
Unigene17502_All	624	11.57	2.60	4.52	14.37	8.33	10.78	18.70	9.71	13.73	-2.15E+00	8.44E-17	Down	-1.36E+00	1.10E-08	Down	-7.86E-01	9.43E-06		-4.14E-01	3.49E-02		-9.45E-01	4.11E-10		-4.46E-01	2.00E-03		Unigene17502_All//gi|65998365|gb|AAS73001.2|//4.00E-57//dirigent-like protein [Gossypium barbadense]	Unigene17502_All//7.00E-40//AT2G21110| disease resistance-responsive family protein	Unigene17502_All//0.00E+00//ES791694			GO:0006950//GO:0044464	nr +
Unigene17503_All	973	3.98	11.30	9.91	0.92	1.84	1.30	0.17	0.56	0.45	1.51E+00	1.32E-15	Up	1.32E+00	6.16E-11	Up	9.98E-01	4.19E-02		4.96E-01	4.48E-01		1.68E+00	7.92E-02		1.37E+00	1.82E-01		Unigene17503_All//gi|15236113|ref|NP_196718.1|//6.00E-50//epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related [Arabidopsis thaliana] >gi|46395895|sp|Q8LG36.2|CAP16_ARATH RecName: Full=Putative clathrin assembly protein At4g40080 >gi|119360027|gb|ABL66742.1|At4g40080 [Arabidopsis thaliana]	Unigene17503_All//9.00E-45//AT4G40080| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	Unigene17503_All//0.00E+00//gi|109887705|gb|DW516674.1|DW516674				nr +
Unigene17504_All	1328	0.99	0.23	0.48	6.00	2.05	1.33	3.22	0.91	1.26	-2.11E+00	1.46E-03		-1.03E+00	9.64E-02		-1.55E+00	1.44E-14	Down	-2.18E+00	3.66E-20	Down	-1.82E+00	4.59E-10	Down	-1.35E+00	4.32E-07	Down	Unigene17504_All//gi|124360755|gb|ABN08732.1|//1.00E-167//Transcriptional factor B3; Auxin response factor [Medicago truncatula]	Unigene17504_All//3.00E-135//AT2G33860| ETT (ETTIN); DNA binding / transcription factor	Unigene17504_All//5.00E-102//gi|109839849|gb|DW238410.1|DW238410	ARF			nr +
Unigene17506_All	828	2.09	0.49	1.09	2.41	2.66	0.55	6.74	4.14	3.99	-2.09E+00	1.98E-04	Down	-9.32E-01	7.71E-02		1.45E-01	8.02E-01		-2.14E+00	2.33E-05	Down	-7.04E-01	1.70E-03		-7.55E-01	5.24E-04		Unigene17506_All//gi|126773|sp|P17815.1|MASY_RICCO//1.00E-10//RecName: Full=Malate synthase, glyoxysomal	Unigene17506_All//3.00E-11//AT5G03860| MLS (MALATE SYNTHASE); malate synthase	Unigene17506_All//1.00E-30//TC135600		ko00620|Pyruvate metabolism//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene17509_All	620	3.21	4.58	4.38	0.64	3.28	1.60	3.48	4.99	2.89	5.13E-01	1.73E-01		4.50E-01	2.65E-01		2.35E+00	3.87E-06	Up	1.32E+00	7.15E-02		5.20E-01	1.07E-01		-2.66E-01	5.07E-01		Unigene17509_All//gi|224139858|ref|XP_002323311.1|//5.00E-23//predicted protein [Populus trichocarpa] >gi|222867941|gb|EEF05072.1|predicted protein [Populus trichocarpa]	Unigene17509_All//1.00E-14//AT3G52105| unknown protein	Unigene17509_All//0.00E+00//gi|13248419|gb|BF275788.2|BF275788			GO:0031410	nr -

Unigene17510_All	713	1.76	0.99	1.27	1.89	2.08	2.28	3.68	2.76	1.06	-8.24E-01	1.69E-01		-4.72E-01	4.42E-01		1.39E-01	8.24E-01		2.74E-01	6.20E-01		-4.16E-01	2.51E-01		-1.79E+00	1.30E-06	Down	Unigene17510_All//gi|297807523|ref|XP_002871645.1|//1.00E-59//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317482|gb|EFH47904.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene17510_All//4.00E-58//AT5G15010| pentatricopeptide (PPR) repeat-containing protein	Unigene17510_All//0.00E+00//gi|164239692|gb|ES808300.1|ES808300			GO:0043231	nr +
Unigene17511_All	742	2.19	0.27	0.29	3.56	2.04	0.67	3.42	1.86	0.75	-3.00E+00	6.72E-06	Down	-2.93E+00	1.92E-05	Down	-8.01E-01	3.00E-02		-2.41E+00	7.14E-08	Down	-8.29E-01	1.32E-02		-2.19E+00	4.48E-08	Down								
Unigene17512_All	588	1.78	6.55	5.25	3.39	3.57	2.00	2.16	3.77	0.54	1.88E+00	7.67E-08	Up	1.56E+00	6.40E-05	Up	7.62E-02	8.85E-01		-7.63E-01	1.01E-01		8.01E-01	3.70E-02		-1.99E+00	4.87E-04	Down			Unigene17512_All//6.00E-38//TC170570				
Unigene17514_All	460	0.46	26.11	1.85	1.52	2.62	11.19	5.79	17.35	58.20	5.84E+00	5.28E-62	Up	2.03E+00	2.24E-02		7.89E-01	2.24E-01		2.88E+00	1.62E-17	Up	1.58E+00	4.58E-15	Up	3.33E+00	1.77E-120	Up	Unigene17514_All//gi|89111818|gb|AB060681.1|//1.00E-07//At1g67920 [Arabidopsis thaliana]	Unigene17514_All//3.00E-08//AT1G67920| unknown protein	Unigene17514_All//1.00E-174//gi|109876625|gb|DW505599.1|DW505599				nr +
Unigene17515_All	742	1.27	1.91	2.01	1.68	1.81	4.32	2.17	1.52	1.34	5.91E-01	2.94E-01		6.63E-01	2.44E-01		1.09E-01	8.71E-01		1.36E+00	1.27E-04	Up	-5.10E-01	2.90E-01		-6.90E-01	1.21E-01				Unigene17515_All//1.00E-123//ES821741				
Unigene17516_All	836	37.24	17.64	27.90	47.55	41.27	26.36	0.00	0.10	0.00	-1.08E+00	6.60E-26	Down	-4.17E-01	3.02E-05		-2.04E-01	1.60E-02		-8.51E-01	4.54E-24		6.64E+00	4.02E-01		null	null		Unigene17516_All//gi|15228530|ref|NP_189534.1|//7.00E-61//AtHB34 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 34); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene17516_All//1.00E-29//AT3G28920| AtHB34 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 34); DNA binding / transcription factor	Unigene17516_All//0.00E+00//gi|78327881|gb|DT548155.1|DT548155	zf-HD		GO:0001071//GO:0003676//GO:0006351//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene17517_All	991	0.53	1.53	0.38	0.15	1.18	7.16	0.77	6.62	5.87	1.54E+00	6.71E-03		-4.89E-01	6.32E-01		2.97E+00	1.37E-04	Up	5.57E+00	3.09E-38	Up	3.11E+00	1.20E-27	Up	2.93E+00	9.99E-24	Up	Unigene17517_All//gi|1769897|emb|CAA69271.1|//2.00E-48//lectin receptor kinase [Arabidopsis thaliana]	Unigene17517_All//2.00E-08//AT1G48720| unknown protein	Unigene17517_All//9.00E-97//DT468735			GO:0003676//GO:0006259	nr -
Unigene17519_All	502	347.49	168.46	312.18	103.99	126.77	82.68	1.18	0.92	1.83	-1.04E+00	6.56E-135	Down	-1.55E-01	1.48E-04		2.86E-01	3.41E-06		-3.31E-01	3.31E-06		-3.65E-01	6.48E-01		6.30E-01	3.25E-01		Unigene17519_All//gi|115485721|ref|NP_001068004.1|//7.00E-24//Os11g0528500 [Oryza sativa Japonica Group] >gi|77551234|gb|ABA94031.1| Rubredoxin family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113645226|dbj|BAF28367.1| Os11g0528500 [Oryza sativa Japonica Group]	Unigene17519_All//7.00E-24//AT5G51010| rubredoxin family protein	Unigene17519_All//0.00E+00//gi|164311170|gb|EX168371.1|EX168371			GO:0043169//GO:0043231	nr +
Unigene1752_All	3742	1.96	0.77	1.14	3.94	3.40	4.08	6.34	2.71	3.99	-1.34E+00	3.92E-09	Down	-7.82E-01	4.96E-04		-2.11E-01	1.74E-01		5.00E-02	7.63E-01		-1.22E+00	1.46E-29	Down	-6.67E-01	1.52E-11		Unigene1752_All//gi|30696088|ref|NP_199979.2|//0.00E+00//CPSF160; nucleic acid binding [Arabidopsis thaliana] >gi|290457637|sp|Q9FG80.2|CPSF1_ARATH RecName: Full=Cleavage and polyadenylation specificity factor subunit 1; AltName: Full=Cleavage and polyadenylation specificity factor 160 kDa subunit; Short=CPSF 160 kDa subunit; Short=AtCPSF160	Unigene1752_All//0.00E+00//AT5G51660| CPSF160; nucleic acid binding	Unigene1752_All//0.00E+00//ES807267		ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair		nr +
Unigene17521_All	389	0.40	8.08	0.96	3.07	2.83	6.62	11.63	22.67	50.08	4.32E+00	3.43E-14	Up	1.25E+00	3.66E-01		-1.18E-01	8.27E-01		1.11E+00	5.59E-03		9.63E-01	4.75E-08		2.11E+00	2.15E-53	Up	Unigene17521_All//gi|225904441|gb|ACO33539.1|//5.00E-08//phosphofructokinase [Elaeis oleifera]	Unigene17521_All//1.00E-08//AT4G29220| PFK1 (PHOSPHOFRUCTOKINASE 1); 6-phosphofructokinase	Unigene17521_All//2.00E-34//gi|109881203|gb|DW510173.1|DW510173		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway	GO:0006007//GO:0008443//GO:0016020//GO:0032559//GO:0043234//GO:0044444	nr +
Unigene17523_All	1148	11.67	1.99	1.25	13.76	6.93	5.08	4.09	0.51	0.56	-2.55E+00	2.12E-37	Down	-3.22E+00	1.41E-45	Down	-9.89E-01	3.89E-14		-1.44E+00	2.21E-22	Down	-3.00E+00	2.20E-19	Down	-2.88E+00	2.90E-19	Down	Unigene17523_All//gi|224141937|ref|XP_002324317.1|//2.00E-69//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222865751|gb|EEF02882.1| AP2/EBP domain-containing transcription factor [Populus trichocarpa]	Unigene17523_All//5.00E-43//AT5G25190| ethylene-responsive element-binding protein, putative	Unigene17523_All//0.00E+00//TC146159	AP2-EREBP		GO:0000160//GO:0000171//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene17525_All	641	2.37	1.98	6.23	3.96	2.85	1.34	0.00	0.00	0.00	-2.60E-01	6.19E-01		1.40E+00	2.49E-05	Up	-4.77E-01	2.34E-01		-1.57E+00	1.37E-04	Down	null	null		null	null									
Unigene17526_All	1342	1.91	0.98	1.43	23.13	4.29	2.93	0.09	0.34	0.00	-9.61E-01	1.52E-02		-4.19E-01	3.27E-01		-2.43E+00	6.61E-103	Down	-2.98E+00	9.77E-111	Down	1.86E+00	8.80E-02		-6.56E+00	2.00E-01		Unigene17526_All//gi|224144932|ref|XP_002325466.1|//1.00E-156//auxin efflux carrier component [Populus trichocarpa] >gi|222862341|gb|EEE99847.1| auxin efflux carrier component [Populus trichocarpa]	Unigene17526_All//6.00E-138//AT5G16530| PIN5 (PIN-FORMED 5); auxin:hydrogen symporter/ transporter	Unigene17526_All//1.00E-96//gi|109889648|gb|DW518616.1|DW518616				nr -
Unigene17529_All	461	62.42	42.87	25.99	126.21	95.91	102.38	90.43	52.77	42.69	-5.42E-01	7.20E-08		-1.26E+00	1.43E-29	Down	-3.96E-01	2.90E-10		-3.02E-01	7.34E-06		-7.77E-01	1.29E-24		-1.08E+00	1.32E-43	Down	Unigene17529_All//gi|75319500|sp|Q39828.1|SDL5A_SOYBN//2.00E-23//RecName: Full=Dynamin-related protein 5A; AltName: Full=Soybean dynamin-like protein 5A; Short=SDL5A >gi|1218004|gb|AAC49183.1| SDL5A [Glycine max]	Unigene17529_All//7.00E-22//AT5G42080| ADL1 (ARABIDOPSIS DYNAMIN-LIKE PROTEIN); GTP binding / GTPase/ protein binding	Unigene17529_All//0.00E+00//gi|21103621|gb|BQ415934.1|BQ415934			GO:0000904//GO:0000919//GO:0003002//GO:0003006//GO:0043897//GO:0009534//GO:0015630//GO:0016020//GO:0017111//GO:0019901//GO:0032561	nr -
Unigene1753_All	575	0.91	0.71	1.30	2.17	0.78	0.94	17.13	17.15	5.68	-3.68E-01	6.83E-01		5.11E-01	5.47E-01		-1.48E+00	1.18E-02		-1.20E+00	5.16E-02		1.80E-03	1.01E+00		-1.59E+00	3.38E-19	Down	Unigene1753_All//gi|297806847|ref|XP_002871307.1|//2.00E-37//SYP132 [Arabidopsis lyrata subsp. lyrata] >gi|297317144|gb|EFH47566.1| SYP132 [Arabidopsis lyrata subsp. lyrata]	Unigene1753_All//5.00E-31//AT5G08080| SYP132 (SYNTAXIN OF PLANTS 132); SNAP receptor	Unigene1753_All//7.00E-47//ES818953		ko04130|SNARE interactions in vesicular transport		nr +
Unigene17530_All	798	12.20	27.49	9.41	2.93	2.63	7.30	0.00	0.10	0.00	1.17E+00	5.81E-21	Up	-3.74E-01	5.71E-02		-1.57E-01	7.42E-01		1.32E+00	1.75E-07	Up	6.71E+00	4.02E-01		null	null									
Unigene17532_All	1907	0.36	0.00	0.06	1.57	0.79	0.83	11.40	12.16	5.87	-8.48E+00	4.10E-04	Down	-2.68E+00	1.69E-02		-9.80E-01	3.87E-03		-9.19E-01	1.05E-02		9.41E-02	4.35E-01		-9.57E-01	4.67E-19		Unigene17532_All//gi|224058659|ref|XP_002299589.1|//1.00E-176//GRAS family transcription factor [Populus trichocarpa] >gi|66947640|emb|CAJ00014.1| Nodulation Signaling Pathway 1 protein homologue 1 [Populus trichocarpa] >gi|222846847|gb|EEE84394.1| GRAS family transcription factor [Populus trichocarpa]	Unigene17532_All//1.00E-102//AT3G13840| scarecrow transcription factor family protein	Unigene17532_All//0.00E+00//TC153709	GRAS			nr -
Unigene17534_All	664	2.36	0.31	2.81	3.08	2.64	2.04	0.13	0.00	0.12	-2.95E+00	1.18E-05	Down	2.48E-01	6.19E-01		-2.18E-01	6.36E-01		-5.92E-01	2.07E-01		-6.99E+00	4.04E-01		-8.52E-02	9.72E-01									
Unigene17537_All	409	6.78	4.83	3.65	1.71	3.45	2.98	4.03	1.33	1.36	-4.89E-01	2.02E-01		-8.95E-01	2.39E-02		1.02E+00	7.53E-02		8.06E-01	2.11E-01		-1.60E+00	8.96E-04	Down	-1.56E+00	7.74E-04	Down	Unigene17537_All//gi|15724353|gb|AL06569.1|AF412117_1//7.00E-31//AT3g07910/F17A17_25 [Arabidopsis thaliana] >gi|16974541|gb|AAL31180.1| AT3g07910/F17A17_25 [Arabidopsis thaliana]	Unigene17537_All//6.00E-17//AT3G07910| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Reactive oxygen species modulator 1 (InterPro:IPR018450); Has 146 Blast hits to 146 proteins in 65 species: Archae - 0; Bacteria - 0; Metazoa - 110; Fungi - 6; Plants - 24; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink).	Unigene17537_All//6.00E-139//DW502606			GO:0044464	nr -
Unigene17538_All	898	2.51	4.85	6.34	4.94	10.55	8.15	0.09	0.19	0.22	9.54E-01	1.14E-03		1.34E+00	6.58E-07	Up	1.09E+00	1.13E-09	Up	7.23E-01	7.01E-04		9.83E-01	6.34E-01		1.24E+00	4.69E-01		Unigene17538_All//gi|15240044|ref|NP_196824.1|//8.00E-69//GRAM domain-containing protein / ABA-responsive protein-related [Arabidopsis thaliana] >gi|75181135|sp|Q9LYV6.1|GEML5_ARATH RecName: Full=GEM-like protein 5 >gi|7529275|emb|CAB86627.1| ABA-responsive protein-like [Arabidopsis thaliana] >gi|38454154|gb|AAR20771.1| At5g13200 [Arabidopsis thaliana] >gi|46402484|gb|AAS92344.1| At5g13200 [Arabidopsis thaliana] >gi|110738428|dbj|BAF01140.1| ABA-responsive protein - like [Arabidopsis thaliana]	Unigene17538_All//4.00E-70//AT5G13200| GRAM domain-containing protein / ABA-responsive protein-related	Unigene17538_All//0.00E+00//gi|109890027|gb|DW518995.1|DW518995				nr +
Unigene17539_All	258	27.78	45.56	52.84	33.21	62.73	102.41	95.54	56.21	548.63	7.14E-01	1.65E-05		9.27E-01	6.21E-09		9.18E-01	2.78E-12		1.62E+00	1.54E-43	Up	-7.65E-01	1.61E-14		2.52E+00	0.00E+00	Up	Unigene17539_All//gi|225451968|ref|XP_002279750.1|//3.00E-19//PREDICTED: similar to mangrin [Vitis vinifera]	Unigene17539_All//7.00E-13//AT3G25780| AOC3 (ALLENE OXIDE CYCLASE 3); allene-oxide cyclase	Unigene17539_All//5.00E-126//TC136584		ko00592|alpha-Linolenic acid metabolism	GO:0009536//GO:0009975	nr +
Unigene17540_All	484	6.49	3.45	5.72	0.72	1.85	3.55	0.96	0.69	1.15	-9.09E-01	9.75E-03		-1.81E-01	6.06E-01		1.36E+00	8.06E-02		2.30E+00	6.28E-05	Up	-4.76E-01	6.60E-01		2.62E-01	7.46E-01		Unigene17540_All//gi|167017602|gb|ABZ04772.1|//2.00E-11//At1g04360 [Arabidopsis thaliana] >gi|167017606|gb|ABZ04774.1| At1g04360 [Arabidopsis thaliana] >gi|167017622|gb|ABZ04782.1| At1g04360 [Arabidopsis thaliana] >gi|167017642|gb|ABZ04792.1| At1g04360 [Arabidopsis thaliana] >gi|167017644|gb|ABZ04793.1| At1g04360 [Arabidopsis thaliana] >gi|167017650|gb|ABZ04796.1| At1g04360 [Arabidopsis thaliana] >gi|167017654|gb|ABZ04798.1| At1g04360 [Arabidopsis thaliana]	Unigene17540_All//2.00E-12//AT1G04360| zinc finger (C3HC4-type RING finger) family protein	Unigene17540_All//0.00E+00//TC165167				nr +

Unigene17542_All	776	1.35	3.13	0.27	3.08	2.75	1.16	2.51	1.62	3.34	1.22E+00	3.60E-03		-2.30E+00	4.70E-03		-1.63E-01	7.23E-01		-1.40E+00	8.07E-04	Down	-6.33E-01	1.35E-01		4.13E-01	2.39E-01		Unigene17542_All//gi|3367537|gb|AAC28522.1|//1.00E-52//Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi|485107 from Caenorhabditis elegans cosmid gb|U00049. This gene is continued from unannotated gene on BAC F19K23 gb|AC000375 [Arabidopsis thaliana]	Unigene17542_All//4.00E-37//AT1G62050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: apoplast; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Ankyrin (InterPro:IPR002110); BEST Arabidopsis thaliana protein match is: ankyrin repeat family protein (TAIR:AT1G11740.1); Has 967 Blast hits to 722 proteins in 118 species: Archae - 0; Bacteria - 24; Metazoa - 556; Fungi - 45; Plants - 193; Viruses - 2; Other Eukaryotes - 147 (source: NCBI BLink).	Unigene17542_All//5.00E-144//gi|164364581|gb|ES840298.1|ES840298			GO:0005576//GO:0043231	nr -
Unigene17544_All	371	5.36	2.32	2.01	6.58	5.57	5.36	11.17	10.70	4.83	-1.21E+00	9.79E-03		-1.42E+00	4.48E-03		-2.41E-01	5.89E-01		-2.97E-01	5.03E-01		-6.15E-02	8.36E-01		-1.21E+00	6.03E-06	Down			Unigene17544_All//5.00E-121//gi|164255625|gb|ES817925.1|ES817925				
Unigene17545_All	395	1.19	2.18	0.27	3.66	2.01	1.60	2.78	6.98	3.83	8.71E-01	2.45E-01		-2.14E+00	1.03E-01		-8.67E-01	1.04E-01		-1.19E+00	3.43E-02		1.33E+00	1.41E-04	Up	4.62E-01	3.38E-01		Unigene17545_All//gi|145358912|ref|NP_199419.2|//1.00E-21//GTP binding / GTPase [Arabidopsis thaliana]	Unigene17545_All//2.00E-20//AT5G46070| GTP binding / GTPase	Unigene17545_All//0.00E+00//TC159557			GO:0017111//GO:0032561	nr +
Unigene17548_All	1051	0.85	0.00	0.20	3.79	1.93	1.89	2.29	4.02	1.74	-9.73E+00	2.86E-05	Down	-2.06E+00	1.78E-02		-9.72E-01	6.55E-04		-1.00E+00	9.11E-04	Down	8.09E-01	2.15E-03		-3.95E-01	2.78E-01		Unigene17548_All//gi|224061479|ref|XP_002300500.1|//2.00E-88//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222847758|gb|EEE85305.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene17548_All//2.00E-16//AT2G46770| EMB2301 (EMBRYO DEFECTIVE 2301); transcription activator/ transcription factor	Unigene17548_All//1.00E-43//CO495847	NAC		GO:0008152//GO:0032501	nr -
Unigene17549_All	1570	0.00	0.00	0.00	0.06	0.04	0.06	2.48	5.00	12.69	null	null		null	null		-5.33E-01	8.17E-01		-1.43E-01	9.51E-01		1.01E+00	7.75E-08	Up	2.36E+00	1.45E-62	Up	Unigene17549_All//gi|12003396|gb|AAG43555.1|AF211537_1//2.00E-85//Avr9/Cf-9 rapidly elicited protein 137 [Nicotiana tabacum]	Unigene17549_All//1.00E-61//AT3G23160| unknown protein	Unigene17549_All//1.00E-22//TC143545				nr -
Unigene17550_All	319	4.92	3.65	7.34	8.90	4.64	5.80	2.52	0.79	0.37	-4.30E-01	4.03E-01		5.78E-01	1.88E-01		-9.39E-01	7.35E-03		-6.17E-01	1.05E-01		-1.68E+00	2.46E-02		-2.75E+00	9.43E-04	Down			Unigene17550_All//4.00E-07//gi|164247859|gb|ES793306.1|ES793306				
Unigene17553_All	485	2.05	1.46	0.00	11.71	17.25	12.01	9.76	9.74	10.19	-4.87E-01	4.72E-01		-1.10E+01	1.77E-05	Down	5.59E-01	3.71E-03		3.69E-02	9.11E-01		-3.80E-03	1.02E+00		6.10E-02	8.08E-01		Unigene17553_All//gi|116787921|gb|ABK24691.1|//4.00E-07//unknown [Picea sitchensis]						nr -
Unigene17555_All	407	35.35	33.86	83.34	51.04	151.19	121.18	37.09	75.27	129.50	-6.21E-02	6.93E-01		1.24E+00	1.02E-33	Up	1.57E+00	3.43E-105	Up	1.25E+00	1.37E-54	Up	1.02E+00	1.60E-28	Up	1.80E+00	1.08E-116	Up	Unigene17555_All//gi|283132359|dbj|BAI63585.1|//5.00E-48//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene17555_All//5.00E-46//AT4G38470| protein kinase family protein	Unigene17555_All//0.00E+00//gi|164320010|gb|ES845270.1|ES845270			GO:0004672//GO:0006464//GO:0031406//GO:0032559//GO:0043231//GO:0044444	nr +
Unigene17556_All	2800	0.13	0.14	0.21	0.30	0.14	0.10	10.00	4.49	1.48	1.47E-01	8.98E-01		6.78E-01	4.83E-01		-1.16E+00	1.16E-01		-1.64E+00	4.18E-02		-1.15E+00	1.03E-31	Down	-2.76E+00	2.98E-106	Down	Unigene17556_All//gi|22329112|ref|NP_195035.2|//0.00E+00//APM1 (AMINOPEPTIDASE M1): aminopeptidase [Arabidopsis thaliana] >gi|17473511|gb|AAL38379.1|AT4g33090/F4110_20 [Arabidopsis thaliana] >gi|24209879|gb|AAN41401.1|aminopeptidase M [Arabidopsis thaliana] >gi|29028734|gb|AAO64746.1|At4g33090/F4110_20 [Arabidopsis thaliana] >gi|110742477|dbj|BAE99157.1|aminopeptidase like protein [Arabidopsis thaliana]	Unigene17556_All//0.00E+00//AT4G33090| APM1 (AMINOPEPTIDASE M1); aminopeptidase	Unigene17556_All//2.00E-41//ES790685			GO:0016020//GO:0019538//GO:0046914//GO:0060918//GO:0070011	nr +
Unigene17557_All	475	0.00	2.56	0.34	1.26	1.01	1.71	1.60	2.11	7.38	1.13E+01	5.48E-07	Up	8.39E+00	2.39E-01		-3.10E-01	7.41E-01		4.44E-01	6.21E-01		3.98E-01	5.45E-01		2.20E+00	8.42E-11	Up			Unigene17557_All//4.00E-60//DT047201				
Unigene17558_All	564	0.65	5.84	2.27	9.45	6.66	6.41	4.72	6.52	18.51	3.17E+00	8.77E-12	Up	1.80E+00	7.48E-03		-5.06E-01	4.35E-02		-5.61E-01	3.10E-02		4.66E-01	1.14E-01		1.97E+00	1.20E-26	Up	Unigene17558_All//gi|255630702|gb|ACU15712.1|//1.00E-09//unknown [Glycine max]	Unigene17558_All//3.00E-05//AT4G28290| unknown protein	Unigene17558_All//4.00E-122//DT047201				nr -
Unigene17560_All	532	2.46	5.24	1.70	2.06	5.37	6.62	3.10	1.81	4.42	1.09E+00	4.25E-03		-5.31E-01	3.86E-01		1.38E+00	1.84E-04	Up	1.68E+00	1.42E-06	Up	-7.78E-01	9.04E-02		5.11E-01	1.60E-01		Unigene17560_All//gi|297798672|ref|XP_002867220.1|//8.00E-62//glycine-rich protein [Arabidopsis lyrata subsp. lyrata] >gi|297313056|gb|EFH43479.1|glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	Unigene17560_All//4.00E-49//AT4G32920| glycine-rich protein			ko03040|Spliceosome	GO:0031410//GO:0043231	nr -
Unigene17564_All	1947	0.11	0.05	0.19	0.51	0.44	0.12	2.91	6.53	4.17	-1.05E+00	5.65E-01		8.32E-01	5.16E-01		-2.11E-01	7.79E-01		-2.14E+00	5.32E-03		1.17E+00	4.91E-15	Up	5.21E-01	3.22E-03		Unigene17564_All//gi|31616519|gb|AAP55748.1|//0.00E+00//calcium-dependent protein kinase 3 [Capsicum annuum]	Unigene17564_All//2.00E-155//AT2G17290| CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene17564_All//0.00E+00//CO103829		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene17565_All	719	0.95	0.14	1.41	3.19	1.01	1.51	0.18	0.81	0.39	-2.75E+00	1.06E-02		5.73E-01	4.04E-01		-1.66E+00	5.25E-05	Down	-1.08E+00	1.06E-02		2.21E+00	2.34E-02		1.14E+00	3.99E-01		Unigene17565_All//gi|224087431|ref|XP_002308164.1|//8.00E-66//laccase 110b [Populus trichocarpa] >gi|222854140|gb|EEE91687.1|laccase 110b [Populus trichocarpa]	Unigene17565_All//9.00E-54//AT5G60020| LAC17 (laccase 17); laccase	Unigene17565_All//0.00E+00//DW238356		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr +
Unigene17566_All	469	1.90	2.16	0.91	23.47	18.94	24.94	1.44	4.72	10.70	1.88E-01	7.64E-01		-1.06E+00	1.76E-01		-3.09E-01	7.49E-02		8.75E-02	6.69E-01		1.71E+00	3.46E-05	Up	2.89E+00	2.80E-20	Up			Unigene17566_All//0.00E+00//TC178812				
Unigene17567_All	752	1.81	0.81	0.21	4.31	6.78	2.64	4.89	0.83	3.44	-1.16E+00	4.51E-02		-3.09E+00	7.28E-05	Down	6.54E-01	1.13E-02		-7.04E-01	4.15E-02		-2.55E+00	5.12E-13	Down	-5.06E-01	6.80E-02		Unigene17567_All//gi|30102914|gb|AAP21375.1|//2.00E-14//At3g61920 [Arabidopsis thaliana]	Unigene17567_All//2.00E-10//AT3G61920| unknown protein	Unigene17567_All//2.00E-20//DW499016				nr -
Unigene17568_All	534	0.69	1.52	2.79	1.87	1.29	0.51	1.66	1.72	4.25	1.15E+00	1.48E-01		2.03E+00	1.33E-03		-5.33E-01	4.45E-01		-1.88E+00	1.18E-02		5.05E-02	9.61E-01		1.35E+00	3.86E-04	Up							
Unigene17570_All	380	25.47	126.94	66.84	59.12	94.79	103.52	48.51	114.61	135.45	2.32E+00	5.80E-118	Up	1.39E+00	2.43E-30	Up	6.81E-01	2.67E-16		8.08E-01	1.20E-21		1.24E+00	1.15E-54	Up	1.48E+00	3.79E-86	Up	Unigene17570_All//gi|194719375|gb|ACF93733.1|//2.00E-58//phospholipase C [Spinacia oleracea]	Unigene17570_All//2.00E-58//AT3G53940| phosphoinositide-specific phospholipase C, putative	Unigene17570_All//0.00E+00//TC136366		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0004629//GO:0016020//GO:0023033//GO:0023060//GO:0044238//GO:0046872//GO:0060089	nr +
Unigene17572_All	1194	0.39	0.17	0.13	1.08	2.65	1.89	3.19	0.77	2.60	-1.22E+00	2.72E-01		-1.56E+00	2.04E-01		1.29E+00	1.83E-04	Up	8.02E-01	6.55E-02		-2.05E+00	1.76E-10	Down	-2.92E-01	3.13E-01		Unigene17572_All//gi|225445342|ref|XP_002281542.1|//1.00E-176//PREDICTED: similar to GRV2 (KATAMARI2); binding / heat shock protein binding [Vitis vinifera]	Unigene17572_All//4.00E-159//AT2G26890| GRV2 (GRAVITROPISM DEFECTIVE 2); binding / heat shock protein binding				GO:0003006//GO:0005515//GO:0005768//GO:0006605//GO:0006950//GO:0009630//GO:0009657//GO:0016192//GO:0031090//GO:0042598//GO:0044267//GO:0044431	nr -
Unigene17573_All	563	0.74	8.28	3.69	3.72	3.91	2.97	0.90	0.89	2.41	3.48E+00	8.04E-18	Up	2.31E+00	1.92E-05	Up	7.50E-02	8.83E-01		-3.24E-01	4.99E-01		-1.66E-02	1.02E+00		1.42E+00	6.15E-03								
Unigene17574_All	474	1.77	1.50	1.80	2.10	2.40	2.10	4.19	1.76	1.09	-2.39E-01	7.25E-01		2.54E-02	9.93E-01		1.90E-01	8.14E-01		-3.90E-03	9.88E-01		-1.25E+00	2.79E-03		-1.94E+00	1.06E-05	Down			Unigene17574_All//3.00E-39//gi|72278960|gb|DT051793.1|DT051793				
Unigene17575_All	465	120.51	76.82	109.71	164.55	200.84	131.80	69.29	60.94	26.39	-6.50E-01	8.03E-20		-1.36E-01	8.88E-02		2.88E-01	6.15E-09		-3.20E-01	2.76E-08		-1.85E-01	4.01E-02		-1.39E+00	5.58E-50	Down	Unigene17575_All//gi|4433048|dbj|BAA21017.1|//2.00E-56//DNA-binding protein [Daucus carota]	Unigene17575_All//4.00E-46//AT2G22430| ATHB6; DNA binding / protein binding / sequence-specific DNA binding / transcription activator/ transcription factor	Unigene17575_All//0.00E+00//TC132407	HB		GO:0001071//GO:0003677//GO:0006351//GO:0006950//GO:0009738//GO:0010468//GO:0010557//GO:0030528//GO:0043231	nr -
Unigene17577_All	777	3.84	16.11	9.80	4.04	3.24	1.28	0.22	0.00	0.15	2.07E+00	5.10E-27	Up	1.35E+00	4.02E-09	Up	-3.20E-01	3.92E-01		-1.66E+00	6.19E-06	Down	-7.77E+00	1.35E-01		-5.01E-01	7.46E-01		Unigene17577_All//gi|38567727|emb|CAE76015.1|//7.00E-47//B1292H11.4|Oryza sativa (japonica cultivar-group)|	Unigene17577_All//5.00E-40//AT3G47090| leucine-rich repeat transmembrane protein kinase, putative	Unigene17577_All//0.00E+00//DR452354		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016491//GO:0031224//GO:0032559	nr -
Unigene17578_All	647	3.88	106.04	12.84	3.77	6.28	3.42	0.26	0.39	4.62	4.77E+00	0.00E+00	Up	1.73E+00	7.05E-14	Up	7.35E-01	1.26E-02		-1.41E-01	7.34E-01		5.68E-01	6.74E-01		4.14E+00	1.73E-16	Up	Unigene17578_All//gi|225431477|ref|XP_002280908.1|//4.00E-15//PREDICTED: similar to Os12g0187800 [Vitis vinifera]	Unigene17578_All//7.00E-08//AT4G33467| unknown protein					nr -
Unigene1758_All	1247	10.32	44.90	17.12	13.98	15.96	21.22	9.02	18.23	10.86	2.12E+00	1.19E-122	Up	7.30E-01	2.85E-09		1.91E-01	1.57E-01		6.02E-01	4.64E-09		1.02E+00	3.45E-21	Up	2.68E-01	5.17E-02		Unigene1758_All//gi|79582138|ref|NP_683288.2|//9.00E-97//SF2/ASF-like splicing modulator (SRP30) [Arabidopsis thaliana] >gi|4775271|emb|CAB42558.1|SF2/ASF-like splicing modulator Srp30, variant 1 [Arabidopsis thaliana]	Unigene1758_All//8.00E-73//AT1G09140| SF2/ASF-like splicing modulator (SRP30)	Unigene1758_All//0.00E+00//gi|78338162|gb|DT558436.1|DT558436		ko03040|Spliceosome		nr +
Unigene17580_All	554	0.66	2.01	4.61	2.34	0.37	1.55	4.81	5.36	2.23	1.61E+00	1.95E-02		2.80E+00	5.59E-08	Up	-2.65E+00	4.08E-05	Down	-5.94E-01	3.41E-01		1.56E-01	6.47E-01		-1.11E+00	1.03E-03		Unigene17580_All//gi|55168340|gb|AAV44205.1|//5.00E-29//unknow protein [Oryza sativa Japonica Group]		Unigene17580_All//5.00E-134//TC149394			GO:0009536	nr -
Unigene17583_All	610	1.37	9.80	4.10	10.21	7.00	5.92	77.84	15.28	10.58	2.84E+00	7.83E-19	Up	1.58E+00	3.47E-04	Up	-5.44E-01	1.61E-02		-7.85E-01	7.25E-04		-2.35E+00	2.83E-145	Down	-2.88E+00	2.33E-188	Down			Unigene17583_All//0.00E+00//gi|195983984|gb|FL577607.1|FL577607				
Unigene17584_All	643	0.73	3.39	5.05	1.55	3.00	3.93	5.72	10.27	5.89	2.21E+00	1.14E-05	Up	2.79E+00	6.07E-10	Up	9.53E-01	4.18E-02		1.34E+00	1.01E-03		8.44E-01	3.72E-05		4.11E-02	9.04E-01		Unigene17584_All//gi|297727017|ref|NP_001175872.1|//9.00E-09//Os09g0458800 [Oryza sativa Japonica Group] >gi|255678954|dbj|BAH94600.1|Os09g0458800 [Oryza sativa Japonica Group]	Unigene17584_All//5.00E-07//AT1G76640| calmodulin-related protein, putative	Unigene17584_All//0.00E+00//gi|109886179|gb|DW515149.1|DW515149		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0046872	nr -
Unigene17585_All	721	4.35	1.97	3.84	12.37	8.93	4.82	0.00	0.12	0.00	-1.15E+00	1.33E-03		-1.81E-01	6.06E-01		-4.70E-01	1.10E-02		-1.36E+00	7.43E-12	Down	6.86E+00	4.02E-01		null	null		Unigene17585_All//gi|225453452|ref|XP_002273974.1|//1.00E-37//PREDICTED: similar to TINY-like protein [Vitis vinifera]	Unigene17585_All//2.00E-32//AT3G60190| AP2 domain-containing transcription factor TINY, putative	Unigene17585_All//4.00E-18//TC177300	AP2-EREBP		GO:0043231	nr +
Unigene17588_All	872	2.16	1.22	2.50	1.89	1.50	0.41	0.15	0.00	0.18	-8.24E-01	7.98E-02		2.13E-01	6.16E-01		-3.29E-01	5.61E-01		-2.19E+00	1.26E-04	Down	-7.18E+00	2.36E-01		3.29E-01	8.51E-01		Unigene17588_All//gi|92893902|gb|ABE91952.1|//4.00E-26//Zinc finger, CONC-type [Medicago truncatula]	Unigene17588_All//4.00E-24//AT2G01050| nucleic acid binding / zinc ion binding	Unigene17588_All//1.00E-77//DN817643				nr +
Unigene1759_All	622	0.25	2.20	1.03	1.44	0.78	0.73	1.09	0.67	0.58	3.12E+00	3.45E-05	Up	2.03E+00	5.59E-02		-8.95E-01	2.14E-01		-9.89E-01	1.96E-01		-6.95E-01	3.94E-01		-9.16E-01	2.21E-01		Unigene1759_All//gi|79582138|ref|NP_683288.2|//7.00E-77//SF2/ASF-like splicing modulator (SRP30) [Arabidopsis thaliana] >gi|4775271|emb|CAB42558.1|SF2/ASF-like splicing modulator Srp30, variant 1 [Arabidopsis thaliana]	Unigene1759_All//7.00E-67//AT1G09140| SF2/ASF-like splicing modulator (SRP30)	Unigene1759_All//0.00E+00//gi|78338162|gb|DT558436.1|DT558436		ko03040|Spliceosome		nr -
Unigene17592_All	682	1.84	1.56	1.33	4.24	2.52	2.25	2.11	2.14	0.41	-2.39E-01	6.68E-01		-4.72E-01	4.42E-01		-7.47E-01	3.35E-02		-9.12E-01	1.29E-02		2.52E-02	9.93E-01		-2.37E+00	2.52E-05	Down	Unigene17592_All//gi|224133496|ref|XP_002321582.1|//1.00E-45//rna-dependent RNA polymerase [Populus trichocarpa] >gi|222868578|gb|EEF05709.1| rna-dependent RNA polymerase [Populus trichocarpa]	Unigene17592_All//6.00E-37//AT4G11130| RDR2 (RNA-DEPENDENT RNA POLYMERASE 2); RNA-directed RNA polymerase	Unigene17592_All//0.00E+00//gi|78342621|gb|DT562895.1|DT562895			GO:0007154//GO:0010033//GO:0016246//GO:0031981	nr +
Unigene17593_All	908	0.92	0.11	0.12	0.82	1.90	2.88	2.93	4.37	8.16	-3.05E+00	2.11E-03		-2.97E+00	3.83E-03		1.20E+00	1.67E-02		1.81E+00	1.68E-05	Up	5.76E-01	3.68E-02		1.48E+00	4.59E-13	Up	Unigene17593_All//gi|14954332|gb|ABP04242.1|//5.00E-36//calmodulin binding protein-like [Elaeis guineensis]	Unigene17593_All//1.00E-30//AT5G42380| CML37 (CALMODULIN LIKE 37); calcium ion binding	Unigene17593_All//5.00E-15//TC139274		ko04626|Plant-pathogen interaction	GO:0046872	nr -

Unigene17596_All	504	9.65	1.91	3.28	8.60	8.88	10.66	1.09	0.91	3.56	-2.34E+00	1.11E-12	Down	-1.56E+00	2.56E-07	Down	4.67E-02	8.95E-01		3.11E-01	2.74E-01		-2.58E-01	7.60E-01		1.71E+00	1.83E-04	Up	Unigene17596_All//gi|18394846|ref|NP_564110.1|//9.00E-25//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75174883|sp|Q9LN22.1|PPR54_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g20300, mitochondrial; Flags: Precursor >gi|17386104|gb|AAL38598.1|AF446865_1 At1g20300/F14O10_8 [Arabidopsis thaliana] >gi|15450347|gb|AAX96467.1| At1g20300/F14O10_8 [Arabidopsis thaliana]	Unigene17596_All//2.00E-18//AT1G20300| pentatricopeptide (PPR) repeat-containing protein	Unigene17596_All//0.00E+00//gi|78338963|gb|DT559237.1|DT559237				nr -
Unigene17598_All	469	52.54	305.75	90.26	56.19	200.88	72.03	25.96	43.31	87.58	2.54E+00	0.00E+00	Up	7.81E-01	7.53E-20		1.84E+00	3.68E-201	Up	3.58E-01	8.07E-05		7.38E-01	2.03E-11		1.75E+00	1.16E-87	Up	Unigene17598_All//gi|115445141|ref|NP_001046350.1|//1.00E-07//Os02g0227100 (Oryza sativa Japonica Group) >gi|113535881|dbj|BAF08264.1| Os02g0227100 (Oryza sativa Japonica Group)		Unigene17598_All//2.00E-62//DW519596			GO:0006950//GO:0010038//GO:0016604	nr -
Unigene176_All	2004	2.48	4.17	3.80	5.12	7.84	6.56	6.48	5.71	16.94	7.50E-01	1.83E-04		6.15E-01	5.04E-03		6.14E-01	3.14E-06		3.57E-01	2.50E-02		-1.81E-01	2.44E-01		1.39E+00	8.54E-52	Up	Unigene176_All//gi|297851170|ref|XP_002893466.1|//1.00E-97//GYF domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297339308|gb|EFH69725.1| GYF domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene176_All//4.00E-80//AT1G24300| LOCATED IN: chloroplast; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: GYF (InterPro:IPR003169); BEST Arabidopsis thaliana protein match is: GYF domain-containing protein (TAIR:AT1G27430.1); Has 21766 Blast hits to 10819 proteins in 514 species: Archae - 0; Bacteria - 738; Metazoa - 8216; Fungi - 1952; Plants - 1070; Viruses - 89; Other Eukaryotes - 9701 (source: NCBI BLink).				nr -
Unigene1760_All	742	3.10	14.96	4.74	3.22	3.62	3.59	2.22	3.83	1.88	2.27E+00	6.85E-27	Up	6.10E-01	7.84E-02		1.68E-01	7.21E-01		1.56E-01	7.01E-01		7.85E-01	1.81E-02		-2.42E-01	5.92E-01		Unigene1760_All//gi|5815235|gb|AAD52609.1|AF173640_1//3.00E-18//splicing factor SR1 [Arabidopsis thaliana]		Unigene1760_All//0.00E+00//gi|78338162|gb|DT558436.1|DT558436		ko03040|Spliceosome		nr +
Unigene17601_All	440	23.07	19.12	20.45	29.21	32.01	28.43	64.86	42.75	29.79	-2.71E-01	1.47E-01		-1.74E-01	3.97E-01		1.32E-01	4.60E-01		-3.89E-02	8.38E-01		-6.02E-01	3.33E-11		-1.12E+00	6.84E-32	Down	Unigene17601_All//gi|164652942|gb|ABV65004.1|//4.00E-09//14-3-3e protein [Gossypium hirsutum]	Unigene17601_All//2.00E-05//AT5G38480| GRF3 (GENERAL REGULATORY FACTOR 3); ATP binding / protein binding / protein phosphorylated amino acid binding	Unigene17601_All//0.00E+00//TC154208				nr -
Unigene17603_All	1681	0.22	0.00	0.13	1.63	2.48	1.50	3.77	0.57	1.09	-7.77E+00	1.97E-02		-7.82E-01	5.53E-01		6.05E-01	4.10E-02		-1.15E-01	7.69E-01		-2.72E+00	1.64E-23	Down	-1.79E+00	8.43E-15	Down	Unigene17603_All//gi|30694961|ref|NP_849791.1|//1.00E-72//myosin-related [Arabidopsis thaliana]	Unigene17603_All//6.00E-67//AT1G51405| myosin-related	Unigene17603_All//0.00E+00//TC144982				nr +
Unigene17604_All	519	0.60	0.29	0.00	2.21	0.53	1.65	9.04	4.19	4.99	-1.05E+00	4.43E-01		-9.24E+00	4.92E-02		-2.06E+00	1.49E-03		-4.17E-01	5.42E-01		-1.11E+00	1.12E-05	Down	-8.58E-01	3.74E-04		Unigene17604_All//gi|37202048|gb|AAQ88639.1|//1.00E-29//At3g04300 [Arabidopsis thaliana]	Unigene17604_All//1.00E-30//AT5G04300| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Cupin, RmlC-type (InterPro:IPR011051), Protein of unknown function DUF861, cupin-3 (InterPro:IPR008579), RmlC-like jelly roll fold (InterPro:IPR014710); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10300.1); Has 364 Blast hits to 364 proteins in 91 species: Archae - 0; Bacteria - 191; Metazoa - 0; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 95 (source: NCBI BLink).	Unigene17604_All//7.00E-124//DT047812				nr +
Unigene17609_All	383	1.91	5.16	5.01	1.30	3.51	4.48	0.00	1.09	2.39	1.43E+00	2.92E-03		1.39E+00	6.13E-03		1.43E+00	1.64E-02		1.78E+00	9.22E-04	Up	1.01E+01	3.65E-03		1.12E+01	1.08E-06	Up	Unigene17609_All//gi|115473321|ref|NP_001060259.1|//2.00E-22//Os07g0613900 (Oryza sativa Japonica Group) >gi|113611795|dbj|BAF22173.1| Os07g0613900 (Oryza sativa Japonica Group)	Unigene17609_All//6.00E-19//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative			GO:0031410//GO:0043231	nr +
Unigene17610_All	710	51.88	41.39	54.53	2.03	5.48	1.78	0.12	0.00	0.00	-3.26E-01	2.37E-04		7.18E-02	4.92E-01		1.43E+00	3.74E-06	Up	-1.92E-01	7.24E-01		-6.90E+00	4.04E-01		-6.90E+00	3.59E-01		Unigene17610_All//gi|209917183|gb|ACI96103.1|//1.00E-25//ICE1 transcription factor [Vitis amurensis]	Unigene17610_All//6.00E-15//AT3G26744| ICE1 (INDUCER OF CBF EXPRESSION 1); DNA binding / transcription activator/ transcription factor	Unigene17610_All//0.00E+00//gi|78328021|gb|DT548295.1|DT548295	bHLH			nr +
Unigene17612_All	455	3.10	2.67	3.04	5.47	1.59	5.36	2.23	2.30	5.52	-2.16E-01	6.80E-01		-2.91E-02	9.80E-01		-1.78E+00	6.81E-06	Down	-3.04E-02	9.43E-01		4.23E-02	9.70E-01		1.31E+00	2.73E-04	Up							
Unigene17613_All	707	2.44	6.81	3.77	5.21	6.77	6.52	0.84	0.24	0.17	1.48E+00	4.36E-07	Up	6.25E-01	1.27E-01		3.77E-01	1.95E-01		3.22E-01	3.05E-01		-1.82E+00	4.72E-02		-2.31E+00	1.36E-02		Unigene17613_All//gi|224067214|ref|XP_002302412.1|//4.00E-20//predicted protein [Populus trichocarpa] >gi|222844138|gb|EEE81685.1| predicted protein [Populus trichocarpa]		Unigene17613_All//0.00E+00//gi|11207873|gb|BF276803.1|BF276803				nr +
Unigene17614_All	1256	0.08	0.00	0.25	1.39	2.77	1.65	0.77	0.63	3.11	-6.38E+00	3.73E-01		1.61E+00	3.05E-01		9.96E-01	1.97E-03		2.53E-01	6.37E-01		-2.92E-01	6.31E-01		2.01E+00	1.08E-10	Up	Unigene17614_All//gi|188509950|gb|ACD66636.1|//3.00E-97//disease resistance related protein [Gossypium raimondii]	Unigene17614_All//2.00E-30//AT1G12210| RFL1 (RPS5-like 1); ATP binding / protein binding	Unigene17614_All//0.00E+00//ES814556		ko04626|Plant-pathogen interaction	GO:0000166	nr +
Unigene17617_All	1041	0.85	0.83	1.23	2.49	1.19	0.91	0.77	0.68	0.23	-4.62E-02	9.62E-01		5.23E-01	3.99E-01		-1.06E+00	4.04E-03		-1.45E+00	3.06E-04	Down	-1.77E-01	7.93E-01		-1.75E+00	1.55E-02		Unigene17617_All//gi|115437912|ref|NP_001043411.1|//1.00E-57//Os01g0581400 (Oryza sativa Japonica Group) >gi|53793429|dbj|BAD53152.1| serine threonine kinase 1-like [Oryza sativa Japonica Group] >gi|113532942|dbj|BAF05325.1| Os01g0581400 (Oryza sativa Japonica Group)	Unigene17617_All//3.00E-58//AT1G17540| kinase			ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0032559//GO:0050896	nr +
Unigene17619_All	979	0.53	0.72	0.54	0.97	1.30	1.94	0.95	3.29	0.85	4.39E-01	6.16E-01		2.54E-02	9.99E-01		4.29E-01	5.32E-01		1.00E+00	3.75E-02		1.79E+00	1.30E-07	Up	-1.53E-01	7.93E-01		Unigene17619_All//gi|12322504|gb|AAG51258.1|AC025782_3/3.00E-08//Ty1/copia-element polyprotein [Arabidopsis thaliana]	Unigene17619_All//6.00E-05//AT1G21280| unknown protein	Unigene17619_All//1.00E-09//ES822910			GO:0003676//GO:0003824//GO:0006259	nr -
Unigene1762_All	1224	2.65	0.70	0.22	3.38	4.47	4.10	6.25	2.73	2.02	-1.91E+00	6.49E-07	Down	-3.61E+00	2.06E-12	Down	4.05E-01	1.24E-01		2.78E-01	3.60E-01		-1.19E+00	9.80E-10	Down	-1.63E+00	1.30E-15	Down	Unigene1762_All//gi|47497094|dbj|BAD19145.1|//3.00E-87//peroxisomal membrane protein-like [Oryza sativa Japonica Group]	Unigene1762_All//1.00E-103//AT4G14310| INVOLVED IN: biological_process unknown; LOCATED IN: cell wall; EXPRESSED IN: male gametophyte; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046); Has 1571 Blast hits to 1320 proteins in 206 species: Archae - 6; Bacteria - 142; Metazoa - 581; Fungi - 102; Plants - 66; Viruses - 5; Other Eukaryotes - 669 (source: NCBI BLink).	Unigene1762_All//0.00E+00//ES811982				nr -
Unigene17621_All	240	18.31	31.67	29.95	18.68	25.83	25.03	89.67	191.74	120.18	7.90E-01	1.92E-04		7.10E-01	1.72E-03		4.67E-01	4.89E-02		4.22E-01	9.43E-02		1.10E+00	1.48E-47	Up	4.23E-01	1.56E-06		Unigene17621_All//gi|226506006|ref|NP_001152306.1|//7.00E-36//glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a [Zea mays] >gi|195654913|gb|ACG46924.1| glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a [Zea mays]	Unigene17621_All//5.00E-37//AT3G06860| MFP2 (MULTIFUNCTIONAL PROTEIN 2); 3-hydroxyacyl-CoA dehydrogenase/ enoyl-CoA hydratase	Unigene17621_All//8.00E-131//TC139991		ko00592|alpha-Linolenic acid metabolism	GO:0005777//GO:0009062//GO:0016616//GO:0016836//GO:0016856//GO:0016863//GO:0030312//GO:0031410//GO:0031981//GO:0048037	nr +
Unigene17623_All	562	0.74	1.89	1.14	4.08	4.60	3.70	5.57	2.38	1.13	1.35E+00	5.00E-02		6.10E-01	5.09E-01		1.73E-01	7.18E-01		-1.41E-01	7.44E-01		-1.23E+00	1.34E-04	Down	-2.30E+00	2.50E-10	Down			Unigene17623_All//0.00E+00//gi|13350280|gb|BG410629.1|BG410629				
Unigene17624_All	1159	0.41	0.26	0.09	2.28	1.75	0.86	1.86	0.32	0.48	-6.31E-01	5.54E-01		-2.14E+00	1.03E-01		-3.78E-01	3.45E-01		-1.41E+00	3.66E-04	Down	-2.52E+00	8.42E-08	Down	-1.95E+00	3.72E-06	Down	Unigene17624_All//gi|30699000|ref|NP_177564.2|//1.00E-149//mitochondrial substrate carrier family protein [Arabidopsis thaliana]	Unigene17624_All//3.00E-144//AT1G74240| mitochondrial substrate carrier family protein	Unigene17624_All//0.00E+00//TC159665			GO:0006810//GO:0031224//GO:0043231	nr -
Unigene17625_All	245	66.84	31.44	26.95	102.47	93.75	89.22	77.66	30.88	36.10	-1.09E+00	3.40E-14	Down	-1.31E+00	5.33E-18	Down	-1.28E-01	3.09E-01		-2.00E-01	8.88E-02		-1.33E+00	4.38E-27	Down	-1.11E+00	4.81E-21	Down	Unigene17625_All//gi|124360667|gb|ABN08656.1|//3.00E-22//Ribosomal protein S10, eukaryotic and archaeal form [Medicago truncatula]	Unigene17625_All//1.00E-21//AT3G47370| 40S ribosomal protein S20 (RPS20B)	Unigene17625_All//2.00E-131//gi|164364886|gb|EX171445.1|EX171445		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0031981	nr +
Unigene17627_All	751	0.14	0.67	0.57	0.40	0.83	1.98	53.60	54.48	51.83	2.28E+00	6.23E-02		2.03E+00	1.40E-01		1.05E+00	2.99E-01		2.32E+00	2.17E-04	Up	2.37E-02	7.95E-01		-4.84E-02	6.10E-01		Unigene17627_All//gi|15233117|ref|NP_191705.1|//6.00E-45//BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|297820998|ref|XP_002878382.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata] >gi|4689366|gb|AAD27870.1|AF134155_1 BRH1 RING finger protein [Arabidopsis thaliana] >gi|6850837|emb|CAB71076.1| RING finger protein [Arabidopsis thaliana] >gi|21554590|gb|AAM63625.1| RING finger protein [Arabidopsis thaliana] >gi|297324220|gb|EFH54641.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata]	Unigene17627_All//2.00E-41//AT3G61460| BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding	Unigene17627_All//6.00E-48//gi|109843402|gb|DW241960.1|DW241960			GO:0009725//GO:0009743//GO:0046914	nr -

Unigene17628_All	803	1.37	4.29	6.63	4.71	2.23	1.91	0.26	0.10	0.00	1.65E+00	4.66E-06	Up	2.28E+00	7.90E-13	Up	-1.08E+00	2.44E-04	Down	-1.30E+00	4.17E-05	Down	-1.34E+00	4.30E-01		-8.04E+00	5.80E-02		Unigene17628_All//gi|223452302|gb|ACM89479.1|//2.00E-87//cysteine-rich protein [Glycine max]	Unigene17628_All//3.00E-84//AT4G23180| CRK10 (CYSTEINE-RICH RLK(10): ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene17628_All//0.00E+00//DW503492		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene17629_All	498	1.47	1.22	2.78	19.71	10.03	4.90	3.74	4.28	6.88	-2.69E-01	7.19E-01		9.18E-01	1.27E-01		-9.75E-01	9.06E-09		-2.01E+00	2.56E-22	Down	1.96E-01	6.23E-01		8.81E-01	2.35E-03		Unigene17629_All//gi|6580148|emb|CAB63152.1|//6.00E-36//LS1-like protein [Arabidopsis thaliana]	Unigene17629_All//1.00E-35//AT3G51660| macrophage migration inhibitory factor family protein / MIF family protein	Unigene17629_All//0.00E+00//TC162649			GO:0006952//GO:0009536//GO:0009607//GO:0042579	nr +
Unigene1763_All	3040	2.77	1.40	0.26	4.83	5.27	4.10	7.26	2.17	2.18	-9.85E-01	1.19E-06		-3.40E+00	3.47E-30	Down	1.24E-01	4.58E-01		-2.37E-01	1.32E-01		-1.74E+00	4.14E-46	Down	-1.74E+00	1.91E-47	Down	Unigene1763_All//gi|47497094|dbj|BAD19145.1|//1.00E-172//peroxisomal membrane protein-like [Oryza sativa Japonica Group]	Unigene1763_All//0.00E+00//AT4G14310| INVOLVED IN: biological_process unknown; LOCATED IN: cell wall; EXPRESSED IN: male gametophyte; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046); Has 1571 Blast hits to 1320 proteins in 206 species: Archae - 6; Bacteria - 142; Metazoa - 581; Fungi - 102; Plants - 66; Viruses - 5; Other Eukaryotes - 669 (source: NCBI BLink).	Unigene1763_All//0.00E+00//ES811982				nr +
Unigene17633_All	312	4.86	4.06	5.12	3.67	2.10	5.21	20.60	5.09	7.92	-2.60E-01	6.19E-01		7.43E-02	8.89E-01		-8.08E-01	1.92E-01		5.05E-01	3.72E-01		-2.02E+00	7.32E-17	Down	-1.38E+00	1.58E-10	Down			Unigene17633_All//4.00E-87//gi|18098618|gb|BM357872.1|BM357872				
Unigene17634_All	1390	0.00	0.00	0.08	0.00	0.00	3.13	20.00	59.99	null	null			6.26E+00	3.99E-01		null	null		null	null		2.67E+00	1.19E-98	Up	4.26E+00	0.00E+00	Up	Unigene17634_All//gi|240255381|ref|NP_188833.4|//2.00E-79//methyltransferase [Arabidopsis thaliana] >gi|9279749|dbj|BAB01375.1| S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase-like protein; floral nectary-specific protein-like [Arabidopsis thaliana]	Unigene17634_All//3.00E-81//AT3G21950| methyltransferase			ko00592|alpha-Linolenic acid metabolism	GO:0008168//GO:0010038	nr +
Unigene17635_All	854	1.72	1.07	2.00	3.73	1.49	2.54	0.99	1.62	2.66	-6.84E-01	2.15E-01		2.18E-01	6.56E-01		-1.32E+00	6.00E-05	Down	-5.56E-01	1.20E-01		7.06E-01	1.71E-01		1.43E+00	2.14E-04	Up	Unigene17635_All//gi|144923530|gb|ABE80159.2|//8.00E-60//Tetratricopeptide-like helical [Medicago truncatula]	Unigene17635_All//3.00E-59//AT1G63080| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene17636_All	1683	0.19	6.80	0.00	0.00	0.45	0.00	0.23	4.57	14.72	5.19E+00	3.05E-56	Up	-7.54E+00	4.92E-02		8.81E+00	1.17E-04	Up	null	null		4.34E+00	3.90E-42	Up	6.03E+00	1.63E-161	Up	Unigene17636_All//gi|224123482|ref|XP_002330325.1|//4.00E-56//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222871360|gb|EEF08491.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene17636_All//1.00E-26//AT4G34410| RRTF1 (REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor	Unigene17636_All//0.00E+00//gi|78325194|gb|DT545468.1|DT545468	AP2-EREBP			nr +
Unigene17637_All	1311	1.28	0.15	0.41	16.41	15.68	22.84	7.16	5.64	5.01	-3.05E+00	3.81E-06	Down	-1.65E+00	3.47E-03		-6.60E-02	6.42E-01		4.77E-01	6.89E-07		-3.43E-01	4.71E-02		-5.14E-01	1.55E-03		Unigene17637_All//gi|30689857|ref|NP_189653.2|//1.00E-101//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|9294338|dbj|BAB02235.1| nodulin-like protein [Arabidopsis thaliana]	Unigene17637_All//1.00E-92//AT3G30340| nodulin MtN21 family protein	Unigene17637_All//0.00E+00//DR462450			GO:0031410	nr -
Unigene17638_All	529	0.00	0.77	1.11	4.61	4.75	4.78	0.88	1.03	3.01	9.58E+00	1.36E-02		1.01E+01	2.17E-03		4.24E-02	9.43E-01		5.12E-02	9.24E-01		2.24E-01	7.92E-01		1.78E+00	3.04E-04	Up	Unigene17638_All//gi|297834432|ref|XP_002885098.1|//2.00E-61//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330938|gb|EFH61357.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17638_All//1.00E-62//AT3G15610| transducin family protein / WD-40 repeat family protein	Unigene17638_All//3.00E-138//TC136037			GO:0004871//GO:0016772//GO:0031461	nr -
Unigene17640_All	644	18.28	88.67	18.85	41.00	50.96	121.18	15.49	57.05	44.23	2.28E+00	9.95E-137	Up	4.45E-02	8.05E-01		3.14E-01	4.75E-04		1.56E+00	4.71E-121	Up	1.88E+00	1.49E-84	Up	1.51E+00	1.46E-49	Up	Unigene17640_All//gi|92897781|gb|ABE93893.1|//5.00E-26//Heavy metal transport/detoxification protein [Medicago truncatula]	Unigene17640_All//8.00E-13//AT5G52740| heavy-metal-associated domain-containing protein	Unigene17640_All//2.00E-118//TC150290				nr -
Unigene17641_All	755	0.90	0.00	0.00	2.38	1.32	1.91	27.22	51.15	22.90	-9.82E+00	4.10E-04	Down	-9.82E+00	7.65E-04	Down	-8.45E-01	7.10E-02		-3.11E-01	5.66E-01		9.10E-01	1.17E-29		-2.49E-01	2.22E-02		Unigene17641_All//gi|115488582|ref|NP_001066778.1|//4.00E-47//0s12g0484700 [Oryza sativa Japonica Group] >gi|113649285|dbj|BAF29797.1| 0s12g0484700 [Oryza sativa Japonica Group]	Unigene17641_All//2.00E-47//AT4G27745| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Yippee-like protein (InterPro:IPR004910); BEST Arabidopsis thaliana protein match is: yippee family protein (TAIR:AT5G53940.1); Has 697 Blast hits to 697 proteins in 149 species: Archae - 0; Bacteria - 0; Metazoa - 401; Fungi - 132; Plants - 110; Viruses - 0; Other Eukaryotes - 54 (source: NCBI BLink).	Unigene17641_All//0.00E+00//DW512678				nr +
Unigene17642_All	405	16.67	30.03	56.54	7.26	22.70	46.84	31.84	20.85	110.96	8.49E-01	2.32E-07		1.76E+00	1.85E-38	Up	1.65E+00	5.32E-17	Up	2.69E+00	3.55E-59	Up	-6.11E-01	1.21E-05		1.80E+00	2.21E-99	Up	Unigene17642_All//gi|164472579|gb|ABY58971.1|//1.00E-06//jasmonate ZIM-domain protein 3 [Solanum lycopersicum]	Unigene17642_All//2.00E-07//AT1G70700| TIFY7	Unigene17642_All//0.00E+00//DW234777	Tify	ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene17643_All	1264	0.50	0.32	0.34	4.41	2.75	7.86	6.05	10.88	81.13	-6.31E-01	4.75E-01		-5.60E-01	5.54E-01		-6.82E-01	3.93E-03		8.33E-01	3.26E-06		8.46E-01	7.01E-10		3.74E+00	0.00E+00	Up	Unigene17643_All//gi|62867641|gb|AAY17424.1|//3.00E-53//At2g01340 [Arabidopsis thaliana] >gi|94412481|gb|ABF19028.1| At2g01340 [Arabidopsis thaliana]	Unigene17643_All//7.00E-53//AT2G01340| unknown protein	Unigene17643_All//3.00E-128//FF403790				nr -
Unigene17645_All	394	7.57	24.18	18.65	8.98	15.91	14.90	7.73	4.56	5.56	1.68E+00	9.20E-16	Up	1.30E+00	2.34E-08	Up	8.25E-01	2.42E-04		7.31E-01	2.61E-03		-7.60E-01	1.71E-02		-4.74E-01	1.28E-01		Unigene17645_All//gi|20197329|gb|AAC63841.2|//3.00E-12//expressed protein [Arabidopsis thaliana] >gi|98960999|gb|ABF58983.1| At2g31090 [Arabidopsis thaliana]		Unigene17645_All//6.00E-136//TC159218				nr -
Unigene17646_All	617	2.20	0.99	2.07	1.53	2.07	0.88	9.25	9.96	4.39	-1.16E+00	4.51E-02		-9.01E-02	8.77E-01		4.29E-01	5.32E-01		-8.04E-01	2.77E-01		1.06E-01	6.49E-01		-1.08E+00	1.14E-06	Down	Unigene17646_All//gi|108385354|gb|ABF85773.1|//5.00E-15//At5g13890 [Arabidopsis thaliana]	Unigene17646_All//3.00E-16//AT5G13890| unknown protein					nr +
Unigene17647_All	897	0.58	0.00	1.01	2.33	2.88	1.51	7.87	1.91	1.95	-9.19E+00	2.93E-03		7.91E-01	3.04E-01		3.04E-01	5.05E-01		-6.27E-01	1.72E-01		-2.04E+00	9.40E-19	Down	-2.01E+00	5.39E-19	Down	Unigene17647_All//gi|11762174|gb|AAG40365.1|AF325013_1|2.00E-58//At1g17620 [Arabidopsis thaliana]	Unigene17647_All//4.00E-50//AT1G17620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G11890.1); Has 539 Blast hits to 538 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 539; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene17647_All//0.00E+00//DW520567				nr -
Unigene1765_All	1536	51.06	42.46	39.59	88.28	78.65	74.13	56.26	28.76	16.52	-2.66E-01	6.32E-06		-3.67E-01	1.02E-09		-1.67E-01	6.96E-05		-2.52E-01	3.12E-09		-9.68E-01	1.83E-72		-1.77E+00	9.09E-188	Down	Unigene1765_All//gi|166407425|gb|AB187519.1|//1.00E-176//Hsp70-interacting protein 1 [Vitis labrusca]	Unigene1765_All//1.00E-91//AT4G22670| AtHip1 (Arabidopsis thaliana Hsp70-interacting protein 1); binding	Unigene1765_All//0.00E+00//TC159319				nr -
Unigene17650_All	938	100.68	92.64	117.74	6.11	14.13	6.36	0.09	0.00	0.00	-1.20E-01	3.58E-02		2.26E-01	9.16E-06		1.21E+00	1.34E-15	Up	5.75E-02	8.42E-01		-6.49E+00	4.04E-01		-6.49E+00	3.59E-01		Unigene17650_All//gi|224069184|ref|XP_002326295.1|//1.00E-120//light-harvesting complex I protein Lhca6 [Populus trichocarpa] >gi|222833488|gb|EEE71965.1| light-harvesting complex I protein Lhca6 [Populus trichocarpa]	Unigene17650_All//1.00E-115//AT1G19150| LHCA6; chlorophyll binding	Unigene17650_All//0.00E+00//TC139182		ko00196|Photosynthesis - antenna proteins		nr +
Unigene17651_All	630	5.48	27.51	10.90	4.19	2.84	6.67	35.17	121.27	100.17	2.33E+00	6.09E-43	Up	9.92E-01	2.41E-05		-5.60E-01	1.45E-01		6.70E-01	2.50E-02		1.79E+00	2.84E-163	Up	1.51E+00	1.84E-108	Up	Unigene17651_All//gi|270309002|dbj|BAI52954.1|//7.00E-09//sigma factor binding protein 1 [Citrullus lanatus subsp. vulgaris]	Unigene17651_All//9.00E-07//AT3G56710| SIB1 (SIGMA FACTOR BINDING PROTEIN 1); binding / protein binding	Unigene17651_All//0.00E+00//gi|109868289|gb|DW497265.1|DW497265				nr +
Unigene17652_All	562	1.21	8.48	1.99	1.33	0.86	2.17	50.86	91.55	188.84	2.81E+00	5.70E-15	Up	7.17E-01	2.87E-01		-6.32E-01	4.37E-01		7.07E-01	2.77E-01		8.48E-01	6.68E-35		1.89E+00	4.35E-250	Up	Unigene17652_All//gi|259121401|gb|ACV92020.1|//2.00E-28//WRKY transcription factor 18 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene17652_All//2.00E-18//AT5G13080| WRKY75; transcription factor	Unigene17652_All//4.00E-39//TC149403	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene17653_All	451	8.70	9.55	9.33	8.84	3.28	3.81	15.37	15.11	2.83	1.34E-01	6.45E-01		1.00E-01	7.45E-01		-1.43E+00	1.02E-06	Down	-1.22E+00	7.24E-05	Down	-2.54E-02	9.25E-01		-2.44E+00	1.43E-23	Down	Unigene17653_All//gi|224081184|ref|XP_002306325.1|//2.00E-26//cytochrome P450 [Populus trichocarpa] >gi|222855774|gb|EEE93321.1| cytochrome P450 [Populus trichocarpa]	Unigene17653_All//2.00E-22//AT3G03470| CYP89A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene17653_All//2.00E-123//gi|164361500|gb|ES833872.1|ES833872		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene17654_All	600	2.27	4.56	3.37	3.65	4.13	1.05	2.18	2.58	2.46	1.01E+00	8.65E-03		5.73E-01	2.38E-01		1.78E-01	7.14E-01		-1.79E+00	9.25E-05	Down	2.39E-01	6.35E-01		1.69E-01	7.19E-01		Unigene17654_All//gi|18390462|ref|NP_563724.1|//5.00E-42//lipid-binding serum glycoprotein family protein [Arabidopsis thaliana] >gi|7211993|gb|AAF40464.1|AC004809_22 ESTs gb|T76367 and gb|AA404955 come from this gene [Arabidopsis thaliana]	Unigene17654_All//5.00E-41//AT1G04970| lipid-binding serum glycoprotein family protein	Unigene17654_All//0.00E+00//CO093400				nr -
Unigene17655_All	767	17.33	122.74	53.81	12.60	68.92	67.24	18.08	59.72	46.69	2.82E+00	9.63E-288	Up	1.63E+00	4.25E-62	Up	2.45E+00	1.93E-161	Up	2.42E+00	3.58E-142	Up	1.72E+00	1.96E-93	Up	1.37E+00	1.51E-53	Up	Unigene17655_All//gi|32364482|gb|AAO61674.1|//4.00E-38//AKIN gamma [Medicago truncatula]	Unigene17655_All//6.00E-36//AT3G48530| KING1 (SNF1-RELATED PROTEIN KINASE REGULATORY SUBUNIT GAMMA 1)	Unigene17655_All//0.00E+00//gi|164267206|gb|ES808003.1|ES808003				nr +

Unigene17657_All	699	1.27	0.36	1.52	1.21	0.64	1.03	4.96	9.27	0.91	-1.81E+00	2.38E-02		2.60E-01	6.82E-01		-9.20E-01	2.17E-01		-2.29E-01	7.51E-01		9.02E-01	1.42E-05		-2.44E+00	3.58E-12	Down	Unigene17657_All//gi|115460536|ref|NP_001053868.1|//1.00E-14//Os04g0615200 [Oryza sativa Japonica Group] >gi|38344255|emb|CAE04335.2|OSJNBa0008M17.8 [Oryza sativa (japonica cultivar-group)] >gi|113565439|dbj|BAF15782.1|Os04g0615200 [Oryza sativa Japonica Group]		Unigene17657_All//0.00E+00//gi|109890655|gb|DW519619.1|DW519619				nr -
Unigene17658_All	1092	2.78	0.56	0.68	5.47	3.28	3.27	11.31	1.38	1.68	-2.32E+00	4.26E-08	Down	-2.03E+00	1.39E-06	Down	-7.39E-01	1.05E-03		-7.45E-01	1.78E-03		-3.04E+00	1.63E-50	Down	-2.75E+00	3.42E-47	Down	Unigene17658_All//gi|15222796|ref|NP_175985.1|//2.00E-96//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75174230|sp|Q9LG23.1|PPR82_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g55890, mitochondrial; Flags: Precursor >gi|8778306|gb|AAF79315.1|AC002304_8 F14J16.14 [Arabidopsis thaliana] >gi|186550654|gb|AAL75896.1|At1g55890/F14J16_4 [Arabidopsis thaliana] >gi|53828645|gb|AAU94432.1|At1g55890 [Arabidopsis thaliana]	Unigene17658_All//8.00E-98//AT1G55890| pentatricopeptide (PPR) repeat-containing protein				nr +
Unigene17659_All	406	0.90	4.12	1.05	0.61	2.21	2.34	4.69	3.19	2.16	2.19E+00	1.76E-04	Up	2.18E-01	8.31E-01		1.85E+00	2.15E-02		1.93E+00	1.48E-02		-5.54E-01	2.00E-01		-1.12E+00	6.32E-03			Unigene17659_All//2.00E-12//BF268565				
Unigene17660_All	769	0.20	0.00	0.00	0.06	0.54	0.18	2.80	2.07	6.27	-7.67E+00	2.16E-01		-7.67E+00	2.45E-01		3.05E+00	5.68E-02		1.44E+00	6.38E-01		-4.41E-01	2.79E-01		1.16E+00	2.36E-06	Up	Unigene17660_All//gi|3056591|gb|AAC13902.1|AAC13902//1.00E-51//TIF9.12 [Arabidopsis thaliana]	Unigene17660_All//9.00E-53//AT1G61390| S-locus protein kinase, putative	Unigene17660_All//4.00E-55//AW187355			nr +
Unigene17664_All	439	3.58	1.50	2.43	8.06	5.57	4.94	5.49	3.24	1.72	-1.25E+00	1.98E-02		-5.60E-01	3.18E-01		-5.33E-01	9.77E-02		-7.06E-01	3.12E-02		-7.62E-01	3.75E-02		-1.67E+00	1.18E-05	Down		Unigene17664_All//2.00E-06//AT3G58500| PP2A-3 (PROTEIN PHOSPHATASE 2A-3); protein serine/threonine phosphatase	Unigene17664_All//6.00E-53//BF268787			kegg -
Unigene17665_All	268	3.12	6.05	4.57	5.95	3.73	3.71	23.51	12.63	9.22	9.54E-01	6.65E-02		5.49E-01	3.86E-01		-6.75E-01	1.88E-01		-6.82E-01	2.07E-01		-8.96E-01	2.12E-05		-1.35E+00	4.86E-10	Down	Unigene17665_All//gi|297845688|ref|XP_002890725.1|//4.00E-06//60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata] >gi|297336567|gb|EFH66984.1| 60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata]		Unigene17665_All//2.00E-134//TC151369	ko03010|Ribosome		nr -
Unigene17666_All	472	11.75	37.68	16.02	21.95	24.81	30.71	36.91	55.26	42.54	1.68E+00	5.99E-29	Up	4.47E-01	4.60E-02		1.76E-01	3.51E-01		4.85E-01	8.55E-04		5.82E-01	9.22E-10		2.05E-01	6.93E-02		Unigene17666_All//gi|15233464|ref|NP_194645.1|//7.00E-18//SNF7.1 [Arabidopsis thaliana] >gi|145334175|ref|NP_001078468.1|SNF7.1 [Arabidopsis thaliana] >gi|75213588|sp|Q9SZE4.1|VPS22_ARATH RecName: Full=Vacuolar protein sorting-associated protein 32 homolog 2; Short=AtVPS32-2; AltName: Full=Charged multivesicular body protein 4 homolog 2; AltName: Full=ESCRT-III complex subunit VPS32 homolog 2		Unigene17666_All//4.00E-85//TC159631	ko04144|Endocytosis		nr -
Unigene17668_All	784	77.41	91.84	68.74	115.07	118.46	126.62	244.03	210.58	121.80	2.47E-01	7.18E-05		-1.72E-01	2.02E-02		4.19E-02	5.47E-01		1.38E-01	1.13E-02		-2.13E-01	8.80E-11		-1.00E+00	1.06E-173	Down	Unigene17668_All//gi|156972239|gb|ABU88948.1|//2.00E-62//GDP-dissociation inhibitor [Lupinus albus]	Unigene17668_All//8.00E-54//AT3G59920| ATGDI2 (RAB GDP DISSOCIATION INHIBITOR 2); RAB GDP-dissociation inhibitor	Unigene17668_All//0.00E+00//TC157366			nr -
Unigene17669_All	639	2.95	46.70	28.08	10.13	7.06	11.03	0.20	0.26	0.19	3.99E+00	1.40E-124	Up	3.25E+00	6.44E-62	Up	-5.22E-01	1.88E-02		1.22E-01	6.38E-01		3.98E-01	8.14E-01		-8.61E-02	9.69E-01		Unigene17669_All//gi|297817478|ref|XP_002876622.1|//3.00E-70//delta-8 sphingolipid desaturase [Arabidopsis lyrata subsp. lyrata] >gi|297322460|gb|EFH52881.1|delta-8 sphingolipid desaturase [Arabidopsis lyrata subsp. lyrata]	Unigene17669_All//4.00E-69//AT3G61580| delta-8 sphingolipid desaturase (SLD1)	Unigene17669_All//2.00E-10//TC132986	ko00910|Nitrogen metabolism		nr +
Unigene1767_All	1841	1.99	1.49	3.64	4.82	5.26	5.18	2.76	1.27	1.21	-4.21E-01	2.01E-01		8.73E-01	2.21E-04		1.26E-01	5.78E-01		1.04E-01	6.39E-01		-1.12E+00	4.09E-06	Down	-1.19E+00	6.74E-07	Down	Unigene1767_All//gi|213495894|gb|ACJ49167.1|//1.00E-166//protection of telomeres 1 protein [Gossypium hirsutum]		Unigene1767_All//0.00E+00//TC166493			nr -
Unigene17673_All	555	23.00	32.32	27.54	17.95	18.86	8.54	0.00	0.00	0.00	4.91E-01	1.74E-04		2.60E-01	9.70E-02		7.14E-02	7.71E-01		-1.07E+00	3.08E-09	Down	null	null		null	null		Unigene17673_All//gi|5915839|sp|O48923.1|CT1DA_SOYBN//2.00E-55//RecName: Full=Cytochrome P450 71D10 >gi|2739000|gb|AAB94588.1|CYP71D10p [Glycine max]	Unigene17673_All//5.00E-37//AT3G26230| CYP71B24; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene17673_All//0.00E+00//gi|31073140|gb|CA993419.1|CA993419	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene17674_All	478	2.30	0.42	1.78	6.15	5.98	6.24	4.60	2.36	1.08	-2.44E+00	1.50E-03		-3.67E-01	6.01E-01		-4.03E-02	9.10E-01		2.03E-02	9.53E-01		-9.62E-01	1.28E-02		-2.09E+00	9.49E-07	Down	Unigene17674_All//gi|18087513|gb|AALS8891.1|AF462768.1|//1.00E-21//AT5g18480/F20L16_200 [Arabidopsis thaliana] >gi|23506001|gb|AAN28860.1|At5g18480/F20L16_200 [Arabidopsis thaliana]	Unigene17674_All//7.00E-23//AT5G18480| PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene17674_All//2.00E-136//TC171918			nr -
Unigene17675_All	449	6.53	9.14	8.66	8.99	11.43	10.46	6.87	8.28	16.06	4.86E-01	1.11E-01		4.08E-01	2.26E-01		3.47E-01	2.22E-01		2.19E-01	4.91E-01		2.69E-01	3.97E-01		1.22E+00	8.57E-10	Up	Unigene17675_All//gi|15233948|ref|NP_194205.1|//1.00E-24//AFC2 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 2); kinase/ protein kinase [Arabidopsis thaliana] >gi|1703200|sp|P51567.1|AFC2_ARATH RecName: Full=Serine/threonine-protein kinase AFC2 >gi|601789|gb|AAA57118.1| protein kinase [Arabidopsis thaliana] >gi|642130|dbj|BAA08214.1| protein kinase [Arabidopsis thaliana] >gi|4220516|emb|CAA22989.1|protein kinase (AFC2) [Arabidopsis thaliana] >gi|7269325|emb|CAB79384.1|protein kinase (AFC2) [Arabidopsis thaliana] >gi|109134165|gb|ABG25080.1|At4g24740 [Arabidopsis thaliana] >gi|110742385|dbj|BAE99115.1|protein kinase [Arabidopsis thaliana]	Unigene17675_All//7.00E-25//AT4G24740| AFC2 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 2); kinase/ protein kinase	Unigene17675_All//4.00E-162//gi|78344868|gb|DT565142.1|DT565142			nr -
Unigene17678_All	977	1.18	0.41	1.20	4.89	5.15	4.76	1.86	0.77	0.61	-1.51E+00	2.31E-02		2.54E-02	9.88E-01		7.22E-02	8.22E-01		-3.99E-02	9.08E-01		-1.27E+00	3.87E-03		-1.61E+00	2.86E-04	Down	Unigene17678_All//gi|79557632|ref|NP_179585.3|//1.00E-107//GC1 (Golgin Candidate 1) [Arabidopsis thaliana] >gi|85681038|sp|Q8SSN9.2|GOGC1_ARATH RecName: Full=Golgin candidate 1; Short=AtGC1; AltName: Full=Golgin-84 >gi|44917433|gb|AAS49041.1|At2g19950 [Arabidopsis thaliana]	Unigene17678_All//3.00E-97//AT2G19950| GC1 (Golgin Candidate 1)	Unigene17678_All//0.00E+00//gi|78352485|gb|DT572759.1|DT572759			nr -
Unigene1768_All	2251	22.62	33.20	36.55	39.97	40.31	48.19	20.19	14.39	8.81	5.54E-01	7.87E-20		6.93E-01	5.47E-31		1.23E-02	8.61E-01		2.70E-01	1.87E-08		-4.89E-01	3.60E-12		-1.20E+00	1.59E-55	Down	Unigene1768_All//gi|229609827|gb|ACQ83529.1|//0.00E+00//CBL-interacting protein kinase 13 [Vitis vinifera]	Unigene1768_All//6.00E-152//AT5G58380| SIP1 (SOS3-INTERACTING PROTEIN 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene1768_All//0.00E+00//TC143167	ko04140|Regulation of autophagy		nr -
Unigene17685_All	662	2.45	0.92	0.48	1.81	2.24	2.59	2.81	0.82	1.56	-1.42E+00	8.26E-03		-2.34E+00	1.96E-04	Down	3.09E-01	5.98E-01		5.22E-01	3.34E-01		-1.78E+00	1.11E-04	Down	-8.45E-01	3.89E-02		Unigene17685_All//gi|297841461|ref|XP_002888612.1|//1.00E-27//DNA polymerase alpha subunit B family [Arabidopsis lyrata subsp. lyrata] >gi|297334453|gb|EFH64871.1| DNA polymerase alpha subunit B family [Arabidopsis lyrata subsp. lyrata]	Unigene17685_All//2.00E-29//AT1G67630| POLA2 (DNA POLYMERASE ALPHA 2); DNA binding / DNA-directed DNA polymerase	Unigene17685_All//0.00E+00//TC134289	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03030|DNA replication		nr +
Unigene17687_All	788	0.66	6.94	3.85	2.28	2.14	1.66	54.03	12.04	1.52	3.39E+00	2.26E-20	Up	2.54E+00	1.77E-08	Up	-8.79E-02	8.47E-01		-4.53E-01	3.94E-01		-2.17E+00	5.90E-118	Down	-5.15E+00	6.81E-266	Down			Unigene17687_All//2.00E-109//FL576500			
Unigene17689_All	1301	0.44	38.64	0.94	0.80	1.35	1.84	2.60	1.29	3.28	6.45E+00	2.13E-268	Up	1.09E+00	9.19E-02		7.47E-01	1.40E-01		1.19E+00	4.36E-03		-1.02E+00	7.56E-04	Down	3.34E-01	2.08E-01		Unigene17689_All//gi|166359608|gb|ABU88896.1|//1.00E-41//LEA-like protein [Thellungiella halophila]	Unigene17689_All//5.00E-34//AT5G06760| late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein				nr -
Unigene17692_All	886	0.41	0.34	0.00	2.02	1.59	1.27	3.20	1.18	1.03	-2.69E-01	8.01E-01		-8.69E+00	2.78E-02		-3.45E-01	5.12E-01		-6.68E-01	1.86E-01		-1.44E+00	3.44E-05	Down	-1.63E+00	2.69E-06	Down	Unigene17692_All//gi|297823265|ref|XP_002876515.1|//9.00E-23//EMB1611/MEE22 [Arabidopsis lyrata subsp. lyrata] >gi|297323354|gb|EFH55774.1|EMB1611/MEE22 [Arabidopsis lyrata subsp. lyrata]	Unigene17692_All//2.00E-20//AT2G34780| MEE22 (MATERNAL EFFECT EMBRYO ARREST 22)				nr +
Unigene17693_All	347	36.04	11.83	30.38	39.48	29.67	24.34	12.31	13.25	15.61	-1.61E+00	1.91E-19	Down	-2.46E-01	1.61E-01		-4.12E-01	4.41E-03		-6.98E-01	2.32E-06		1.07E-01	7.04E-01		3.43E-01	1.35E-01				Unigene17693_All//5.00E-90//TC158192			
Unigene17694_All	838	1.69	2.12	0.76	0.30	0.29	0.92	3.23	5.99	9.18	3.28E-01	5.12E-01		-1.14E+00	5.55E-02		-4.74E-02	9.51E-01		1.62E+00	6.61E-02		8.90E-01	2.03E-04		1.51E+00	6.51E-14	Up			Unigene17694_All//1.00E-126//TC136934			
Unigene17695_All	1399	0.71	0.76	1.37	18.27	16.57	12.91	2.48	0.57	0.71	9.81E-02	8.80E-01		9.47E-01	5.40E-02		-1.41E-01	2.42E-01		-5.00E-01	1.63E-06		-2.13E+00	4.85E-10	Down	-1.80E+00	1.61E-08	Down	Unigene17695_All//gi|115481414|ref|NP_001064300.1|//1.00E-62//Os10g0200700 [Oryza sativa Japonica Group] >gi|78708039|gb|ABB47014.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113638909|dbj|BAF26214.1|Os10g0200700 [Oryza sativa Japonica Group]	Unigene17695_All//6.00E-65//AT2G41610| unknown protein	Unigene17695_All//0.00E+00//TC130968			nr -
Unigene17696_All	729	1.51	0.42	0.58	5.47	2.55	3.53	0.64	0.92	0.66	-1.85E+00	8.99E-03		-1.37E+00	5.32E-02		-1.10E+00	1.20E-04	Down	-6.30E-01	4.01E-02		5.24E-01	5.26E-01		3.97E-02	9.76E-01		Unigene17696_All//gi|222637128|gb|EEE67260.1|//4.00E-09//hypothetical protein Os_24426 [Oryza sativa Japonica Group]					nr +
Unigene17698_All	1024	7.05	3.86	2.34	5.79	14.33	6.97	0.12	0.20	0.08	-8.69E-01	6.98E-05		-1.59E+00	7.57E-11	Down	1.31E+00	2.43E-19	Up	2.68E-01	2.73E-01		7.20E-01	6.32E-01		-6.71E-01	7.20E-01		Unigene17698_All//gi|13752458|gb|AAK38665.1|//1.00E-101//stem secoisolariciresinol dehydrogenase [Forsythia x intermedia]	Unigene17698_All//3.00E-62//AT1G52340| ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase	Unigene17698_All//0.00E+00//TC133162	ko00906|Carotenoid biosynthesis		nr -
Unigene17700_All	999	2.51	5.33	2.24	2.39	1.24	1.72	0.85	1.30	0.68	1.08E+00	4.24E-05	Up	-1.67E-01	6.79E-01		-9.48E-01	1.49E-02		-4.79E-01	2.72E-01		6.16E-01	2.53E-01		-3.20E-01	6.25E-01								
Unigene17702_All	223	68.51	42.72	30.09	110.57	81.22	136.91	98.97	80.03	42.88	-6.82E-01	1.88E-06		-1.19E+00	1.65E-14	Down	-4.45E-01	1.13E-05		3.08E-01	1.63E-03		-3.06E-01	3.86E-03		-1.21E+00	8.34E-28	Down	Unigene17702_All//gi|240254411|ref|NP_178110.6|//7.00E-31//ATP binding [Arabidopsis thaliana]	Unigene17702_All//3.00E-32//AT1G79920| ATP binding	Unigene17702_All//4.00E-114//TC162926			nr -

Unigene17704_All	1275	1.85	0.00	0.50	13.64	6.35	7.86	1.96	1.44	2.97	-1.09E+01	1.33E-13	Down	-1.88E+00	7.74E-05	Down	-1.10E+00	1.65E-18	Down	-7.94E-01	1.02E-09		-4.40E-01	2.38E-01		6.01E-01	2.74E-02		Unigene17704_All//gi|71534908|gb|AA32858.1|/8.00E-45//BURP domain-containing protein [Medicago sativa]	Unigene17704_All//2.00E-42//AT1G49320| BURP domain-containing protein	Unigene17704_All//0.00E+00//TC134385				nr -
Unigene17706_All	582	3.69	1.22	2.38	1.71	1.30	2.02	2.03	2.08	4.24	-1.60E+00	6.02E-04	Down	-6.32E-01	1.70E-01		-3.95E-01	5.73E-01		2.37E-01	7.09E-01		3.40E-02	9.80E-01		1.06E+00	2.68E-03		Unigene17706_All//gi|5903034|gb|AAD55593.1|AC008016.3//2.00E-16//F6D8.3 [Arabidopsis thaliana] >gi|28466819|gb|AAO44018.1|At1g52720 [Arabidopsis thaliana]	Unigene17706_All//3.00E-16//AT1G52720| unknown protein	Unigene17706_All//0.00E+00//gi|109880988|gb|DW509958.1|DW509958				nr +
Unigene17707_All	419	1.00	3.27	1.02	1.78	5.59	5.17	3.83	6.28	4.37	1.71E+00	5.54E-03		2.53E-02	1.00E+00		1.65E+00	1.17E-04	Up	1.54E+00	7.57E-04	Up	7.13E-01	4.06E-02		1.90E-01	6.51E-01					Unigene17707_All//2.00E-154//gi|109880300|gb|DW509270.1|DW509270				
Unigene17708_All	397	39.93	39.44	27.23	66.13	82.23	50.40	37.59	101.70	79.08	-1.80E-02	9.19E-01		-5.52E-01	1.37E-04		3.14E-01	4.82E-04		-3.92E-01	1.66E-04		1.44E+00	2.47E-63	Up	1.07E+00	2.50E-32	Up	Unigene17708_All//gi|124359162|gb|ABN05685.1|/5.00E-08//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene17708_All//3.00E-128//TC151939				nr +
Unigene17709_All	377	1.67	3.63	6.92	7.93	6.49	6.23	2.36	1.11	0.00	1.12E+00	5.30E-02		2.06E+00	7.13E-06	Up	-2.90E-01	4.51E-01		-3.48E-01	3.87E-01		-1.09E+00	1.07E-01		-1.12E+01	1.10E-06	Down	Unigene17709_All//gi|115443701|ref|NP_001045630.1|/5.00E-19//Os02g0106800 [Oryza sativa Japonica Group] >gi|113535161|dbj|BAF07544.1|Os02g0106800 [Oryza sativa Japonica Group]	Unigene17709_All//4.00E-21//AT1G33230| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: TMP17-like (InterPro:IPR012926); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10430.3); Has 198 Blast hits to 198 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 148; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink).	Unigene17709_All//6.00E-102//DT457800				nr +
Unigene1771_All	945	8.30	3.32	5.18	15.71	12.94	13.33	8.14	6.81	7.42	-1.32E+00	1.65E-09	Down	-6.80E-01	1.61E-03		-2.80E-01	5.64E-02		-2.36E-01	1.32E-01		-2.58E-01	2.07E-01		-1.34E-01	5.23E-01		Unigene1771_All//gi|16930693|gb|AAL32012.1|AF436830_1//7.00E-50//AT3g07810/F17A17_15 [Arabidopsis thaliana]	Unigene1771_All//1.00E-35//AT3G07810| heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative	Unigene1771_All//0.00E+00//TC140732		ko03040|Spliceosome		nr -
Unigene17711_All	434	27.37	7.47	6.99	47.63	34.36	51.41	74.04	25.04	31.85	-1.87E+00	9.45E-23	Down	-1.97E+00	2.90E-23	Down	-4.71E-01	2.48E-05		1.10E-01	4.37E-01		-1.56E+00	2.07E-57	Down	-1.22E+00	1.36E-40	Down	Unigene17711_All//gi|224104989|ref|XP_002313645.1|/2.00E-07//histone deacetylase [Populus trichocarpa] >gi|222850053|gb|EEE87600.1|histone deacetylase [Populus trichocarpa]	Unigene17711_All//6.00E-06//AT3G44750| HDA3 (HISTONE DEACETYLASE 3); histone deacetylase/ nucleic acid binding / zinc ion binding	Unigene17711_All//0.00E+00//gi|164286796|gb|EV499310.1|EV499310	C2H2			nr +
Unigene17712_All	317	23.44	67.45	35.44	31.59	53.45	64.68	32.54	73.31	41.60	1.53E+00	3.27E-30	Up	5.97E-01	6.79E-04		7.59E-01	1.95E-09		1.03E+00	3.60E-17	Up	1.17E+00	4.63E-27	Up	3.54E-01	9.50E-03		Unigene17712_All//gi|254681442|gb|ACT78956.1|/2.00E-35//zinc finger protein [Gossypium arboreum]	Unigene17712_All//2.00E-22//AT1G61200| zinc finger (AN1-like) family protein	Unigene17712_All//5.00E-179//TC176112				nr -
Unigene17714_All	1048	4.39	3.67	4.83	9.98	6.51	4.01	1.61	0.56	0.27	-2.58E-01	3.81E-01		1.36E-01	6.22E-01		-6.18E-01	1.58E-04		-1.32E+00	3.47E-13	Down	-1.53E+00	1.16E-03		-2.60E+00	9.91E-07	Down	Unigene17714_All//gi|124359162|gb|ABN05685.1|/8.00E-11//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene17714_All//1.00E-126//gi|73850269|gb|DT459289.1|DT459289				nr -
Unigene17716_All	654	1.76	0.16	0.00	12.42	9.11	6.91	7.76	5.62	4.51	-3.51E+00	6.57E-05	Down	-1.08E+01	2.60E-06	Down	-4.47E-01	2.33E-02		-8.46E-01	2.18E-05		-4.64E-01	5.49E-02		-7.83E-01	6.55E-04		Unigene17716_All//gi|15231680|ref|NP_190845.1|/7.00E-17//ZPR3 (LITTLE ZIPPER 3); protein binding [Arabidopsis thaliana]	Unigene17716_All//3.00E-14//AT3G52770| ZPR3 (LITTLE ZIPPER 3); protein binding					nr +
Unigene17717_All	636	0.00	2.23	1.51	1.33	2.27	4.33	12.10	28.06	21.92	1.11E+01	4.06E-08	Up	1.06E+01	2.46E-05	Up	7.72E-01	1.76E-01		1.70E+00	2.42E-05	Up	1.21E+00	3.96E-22	Up	8.58E-01	1.62E-10		Unigene17717_All//gi|297729351|ref|NP_001177039.1|/2.00E-07//Os12g0594800 [Oryza sativa Japonica Group] >gi|77556385|gb|ABA99181.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255670448|dbj|BAH95767.1|Os12g0594800 [Oryza sativa Japonica Group]		Unigene17717_All//0.00E+00//gi|109887362|gb|DW516331.1|DW516331				nr -
Unigene17718_All	1274	4.72	0.28	0.79	24.32	17.92	7.55	0.63	1.61	0.28	-4.08E+00	3.94E-26	Down	-2.57E+00	1.77E-16	Down	-4.41E-01	7.31E-07		-1.69E+00	8.70E-55	Down	1.35E+00	1.13E-03		-1.16E+00	8.85E-02		Unigene17718_All//gi|30695554|ref|NP_199696.2|/1.00E-109//ATSD11 (SULPHUR DEFICIENCY-INDUCED 1); binding [Arabidopsis thaliana] >gi|28950875|gb|AAO63361.1|At5g48850 [Arabidopsis thaliana]	Unigene17718_All//1.00E-109//AT5G48850| ATSD11 (SULPHUR DEFICIENCY-INDUCED 1); binding	Unigene17718_All//0.00E+00//TC156515				nr -
Unigene17719_All	400	0.92	16.47	1.46	0.75	1.55	2.37	4.12	3.24	1.59	4.17E+00	1.23E-28	Up	6.78E-01	4.83E-01		1.05E+00	2.99E-01		1.67E+00	3.07E-02		-3.48E-01	4.75E-01		-1.37E+00	2.58E-03					Unigene17719_All//4.00E-69//TC171420				
Unigene17721_All	795	2.24	1.85	1.07	5.33	4.24	2.22	2.34	1.63	0.90	-2.76E-01	5.91E-01		-1.06E+00	4.11E-02		-3.27E-01	2.98E-01		-1.27E+00	2.04E-05	Down	-5.22E-01	2.33E-01		-1.38E+00	1.21E-03		Unigene17721_All//gi|300827400|gb|ADK36642.1|/1.00E-108//MAPKKKe [Solanum lycopersicum]	Unigene17721_All//2.00E-109//AT3G13530| MAPKKK7; ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene17721_All//0.00E+00//gi|109823233|gb|DW008101.1|DW008101				nr +
Unigene17722_All	683	0.08	0.00	0.00	4.38	1.41	1.12	15.85	14.07	9.04	-6.26E+00	6.13E-01		-6.26E+00	6.25E-01		-1.63E+00	3.38E-06	Down	-1.96E+00	5.66E-07	Down	-1.71E-01	3.35E-01		-8.10E-01	1.03E-07					Unigene17722_All//8.00E-38//TC178205				
Unigene17723_All	471	2.22	4.63	2.49	2.64	2.92	1.53	5.12	7.99	14.13	1.06E+00	1.60E-02		1.63E-01	7.82E-01		1.45E-01	8.22E-01		-7.83E-01	2.08E-01		6.42E-01	2.31E-02		1.47E+00	1.07E-11	Up				Unigene17723_All//3.00E-21//DW511220				
Unigene17724_All	778	6.66	7.23	5.48	3.39	3.76	3.95	4.29	1.83	2.05	1.19E-01	6.39E-01		-2.82E-01	3.37E-01		1.49E-01	7.50E-01		2.18E-01	6.14E-01		-1.23E+00	6.80E-05	Down	-1.07E+00	3.16E-04	Down	Unigene17724_All//gi|15239024|ref|NP_196695.1|/4.00E-42//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|8953396|emb|CAB96669.1|separation anxiety protein-like [Arabidopsis thaliana] >gi|28416617|gb|AAO42839.1|At5g11340 [Arabidopsis thaliana] >gi|110743265|dbj|BAE99523.1|separation anxiety protein - like [Arabidopsis thaliana]	Unigene17724_All//2.00E-43//AT5G11340| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene17724_All//0.00E+00//DW518876				nr -
Unigene17726_All	333	39.59	40.32	16.95	45.63	61.84	41.50	243.27	196.68	85.42	2.63E-02	8.82E-01		-1.22E+00	3.37E-13	Down	4.39E-01	1.26E-04		-1.37E-01	4.20E-01		-3.07E-01	2.59E-09		-1.51E+00	2.24E-140	Down				Unigene17726_All//0.00E+00//TC170333				
Unigene17727_All	817	0.64	1.61	0.39	4.69	10.28	5.53	6.26	8.13	6.00	1.33E+00	2.73E-02		-7.11E-01	4.97E-01		1.13E+00	4.55E-09	Up	2.38E-01	4.77E-01		3.71E-01	7.39E-02		-6.22E-02	8.00E-01					Unigene17727_All//0.00E+00//FL576688				
Unigene17728_All	408	8.08	17.26	10.57	3.91	2.19	3.99	113.99	40.87	52.83	1.10E+00	1.37E-06	Up	3.88E-01	2.23E-01		-8.32E-01	9.85E-02		2.85E-02	9.53E-01		-1.48E+00	2.61E-76	Down	-1.11E+00	1.82E-50	Down	Unigene17728_All//gi|115478292|ref|NP_001062741.1|/6.00E-06//Os09g0272600 [Oryza sativa Japonica Group] >gi|113630974|dbj|BAF24655.1|Os09g0272600 [Oryza sativa Japonica Group]		Unigene17728_All//7.00E-148//TC170895				nr +
Unigene17729_All	1535	0.00	0.92	0.00	0.13	0.09	1.41	228.95	58.27	91.85	9.85E+00	4.06E-08	Up	null	null		-5.33E-01	7.49E-01		3.44E+00	7.19E-09	Up	-1.97E+00	0.00E+00	Down	-1.32E+00	0.00E+00	Down	Unigene17729_All//gi|18558997|gb|AAL73112.1|/1.00E-140//bacterial-induced peroxidase [Gossypium hirsutum]	Unigene17729_All//2.00E-109//AT5G39580| peroxidase, putative	Unigene17729_All//0.00E+00//TC171015		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene17732_All	333	3.61	3.80	2.56	5.39	6.10	6.10	2.03	6.65	3.95	7.40E-02	9.06E-01		-4.98E-01	4.26E-01		1.80E-01	7.49E-01		1.81E-01	7.01E-01		1.71E+00	3.46E-05	Up	9.59E-01	5.89E-02					Unigene17732_All//2.00E-21//DW492149				
Unigene17733_All	493	2.02	0.41	0.22	2.43	2.31	2.75	1.63	2.97	2.42	-2.29E+00	4.05E-03		-3.22E+00	7.83E-04	Down	-7.32E-02	8.95E-01		1.81E-01	7.57E-01		8.65E-01	8.03E-02		5.73E-01	2.93E-01		Unigene17733_All//gi|297835244|ref|XP_002885504.1|/8.00E-33//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331344|gb|EFH61763.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene17733_All//3.00E-33//AT1G12700| helicase domain-containing protein / pentatricopeptide (PPR) repeat-containing protein	Unigene17733_All//1.00E-103//TC144858				nr +
Unigene17734_All	650	1.29	0.86	1.47	3.22	2.81	1.46	10.93	25.98	7.42	-5.87E-01	4.26E-01		1.95E-01	7.70E-01		-1.97E-01	6.76E-01		-1.14E+00	1.08E-02		1.25E+00	6.45E-22	Up	-5.59E-01	3.19E-03					Unigene17734_All//5.00E-125//gi|21094366|gb|BQ406679.1|BQ406679				
Unigene17739_All	307	4.09	0.66	3.99	3.08	5.05	3.09	1.79	1.50	1.43	-2.63E+00	3.16E-04	Down	-3.60E-02	9.71E-01		7.11E-01	1.98E-01		3.00E-03	9.98E-01		-2.58E-01	7.60E-01		-3.27E-01	6.72E-01					Unigene17739_All//2.00E-24//gi|78348710|gb|DT568984.1|DT568984				
Unigene1774_All	2614	3.68	12.25	5.19	8.10	12.07	15.57	16.58	25.68	20.47	1.73E+00	6.94E-54	Up	4.96E-01	1.76E-03		5.75E-01	9.63E-11		9.43E-01	7.22E-29		6.31E-01	2.21E-27		3.04E-01	1.52E-06		Unigene1774_All//gi|115480291|ref|NP_001063739.1|/0.00E+00//Os09g0528800 [Oryza sativa Japonica Group] >gi|113631972|dbj|BAF25653.1|Os09g0528800 [Oryza sativa Japonica Group]	Unigene1774_All//6.00E-172//AT5G41940| RabGAP/TBC domain-containing protein	Unigene1774_All//0.00E+00//gi|164253627|gb|ES826444.1|ES826444				nr -
Unigene17741_All	327	0.32	2.63	1.30	1.07	2.74	1.10	2.59	1.41	8.41	3.04E+00	1.94E-03		2.03E+00	1.40E-01		1.36E+00	8.05E-02		5.12E-02	9.69E-01		-8.79E-01	2.07E-01		1.70E+00	2.16E-06	Up								
Unigene17743_All	867	2.41	0.35	0.61	2.30	2.18	2.03	2.19	0.58	0.87	-2.78E+00	6.12E-07	Down	-1.97E+00	1.29E-04	Down	-7.32E-02	8.67E-01		-1.78E-01	7.00E-01		-1.92E+00	3.20E-05	Down	-1.33E+00	1.45E-03		Unigene17743_All//gi|225030812|gb|ACN79519.1|/7.00E-46//reduced leaflet 1 [Lotus japonicus]	Unigene17743_All//3.00E-29//AT5G23570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene17743_All//0.00E+00//ES850628				nr -
Unigene17744_All	1826	6.96	2.25	10.99	0.85	0.32	0.15	0.14	0.00	0.09	-1.63E+00	3.62E-20	Down	6.59E-01	1.99E-07		-1.40E+00	6.23E-03		-2.51E+00	4.81E-05	Down	-7.12E+00	4.04E-02		-6.70E-01	6.05E-01		Unigene17744_All//gi|21537161|gb|AAM61502.1|/1.00E-154//prolylcarboxypeptidase-like protein [Arabidopsis thaliana]	Unigene17744_All//6.00E-155//AT5G22860| serine carboxypeptidase S28 family protein	Unigene17744_All//0.00E+00//gi|78344203|gb|DT564477.1|DT564477				nr +
Unigene17746_All	596	2.28	4.85	4.38	3.59	3.64	4.70	4.89	2.03	7.82	1.09E+00	3.72E-03		9.40E-01	2.21E-02		1.83E-02	9.79E-01		3.87E-01	3.49E-01		-1.27E+00	1.57E-04	Down	6.76E-01	5.11E-03									
Unigene17747_All	1286	0.81	0.12	1.16	8.48	6.43	4.67	6.05	0.42	1.73	-2.78E+00	8.21E-04	Down	5.11E-01	3.81E-01		-4.01E-01	1.65E-02		-8.61E-01	3.46E-07		-3.84E+00	2.75E-39	Down	-1.80E+00	4.14E-18	Down	Unigene17747_All//gi|115461492|ref|NP_001054346.1|/8.00E-91//Os04g0689500 [Oryza sativa Japonica Group] >gi|113565917|dbj|BAF16260.1|Os04g0689500 [Oryza sativa Japonica Group]	Unigene17747_All//4.00E-74//AT1G45688| unknown protein	Unigene17747_All//0.00E+00//TC146950				nr -
Unigene17748_All	1529	0.51	0.60	0.63	8.83	6.10	4.73	1.05	0.38	0.21	2.17E-01	7.42E-01		2.88E-01	6.65E-01		-5.33E-01	1.77E-04		-9.02E-01	2.15E-09		-1.46E+00	2.51E-03		-2.33E+00	8.81E-06	Down	Unigene17748_All//gi|38344244|emb|CAD41337.2|/1.00E-20//OJ991113_30.21 [Oryza sativa (japonica cultivar-group)]	Unigene17748_All//1.00E-06//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene17748_All//3.00E-45//TC177419				nr -
Unigene17749_All	1691	0.19	0.00	0.06	53.67	25.03	15.14	0.53	0.52	0.09	-7.54E+00	3.66E-02		-1.56E+00	3.30E-01		-1.10E+00	5.52E-95	Down	-1.83E+00	1.77E-178	Down	-1.69E-02	1.02E+00		-2.48E+00	9.93E-04	Down	Unigene17749_All//gi|225444460|ref|XP_002271944.1|/1.00E-146//PREDICTED: similar to homeodomain protein ARBOKNOX1 [Vitis vinifera]	Unigene17749_All//2.00E-114//AT1G62360| STM (SHOOT MERISTEMLESS); transcription factor	Unigene17749_All//2.00E-111//TC154278	HB			nr -
Unigene17750_All	496	5.70	0.82	7.84	14.36	12.98	12.38	2.05	0.93	2.57	-2.80E+00	3.39E-09	Down	4.60E-01	1.60E-01		-1.46E-01	5.69E-01		-2.14E-01	3.86E-01		-1.14E+00	6.62E-02		3.29E-01	5.52E-01									ESTscan +
Unigene17751_All	823	0.51	9.11	1.81	4.54	16.36	14.93	1.28	4.77	1.94	4.16E+00	1.59E-32	Up	1.83E+00	2.94E-03		1.85E+00	5.00E-29	Up	1.72E+00	4.00E-22	Up	1.89E+00	8.65E-10	Up	5.92E-01	1.95E-01		Unigene17751_All//gi|19911573|dbj|BAB88980.1|/1.00E-113//syringolide-induced protein 19-1-5 [Glycine max]		Unigene17751_All//2.00E-35//TC171552				nr +
Unigene17752_All	535	2.35	3.79	2.99	1.68	1.61	8.86	1.03	1.48	2.09	6.91E-01	1.29E-01		3.47E-01	5.29E-01		-5.88E-02	9.22E-01		2.40E+00	2.48E-13	Up	5.31E-01	4.67E-01		1.02E+00	6.87E-02					Unigene17752_All//1.00E-51//TC158364				
Unigene17753_All	607	0.86	0.42	0.26	12.15	14.18	12.05	2.37	0.48	0.00	-1.05E+00	3.11E-01		-1.71E+00	1.40E-01		2.24E-01	3.18E-01		-1.10E-02	9.55E-01		-2.30E+00	5.89E-05	Down	-1.12E+01	1.19E-10	Down								
Unigene17754_All	706	2.67	5.74	2.49	0.14	0.24	0.83	2.22	4.08	1.75	1.11E+00	3.41E-04	Up	-1.00E-01	8.30E-01		7.90E-01	7.71E-01		2.56E+00	2.87E-02		8.83E-01	7.39E-03		-3.41E-01	4.71E-01		Unigene17754_All//gi|292385868|gb|ADE22249.1|/4.00E-56//somatic embryogenesis receptor-like kinase 1 [Ageratina adenophora]	Unigene17754_All//5.00E-46//AT4G33430| BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE); kinase/ protein binding / protein heterodimerization/ protein serine/threonine kinase	Unigene17754_All//3.00E-74//DT466374		ko04626|Plant-pathogen interaction		nr +

Unigene17755_All	378	2.77	3.75	2.96	3.82	2.46	2.75	2.13	1.66	0.32	4.39E-01	4.26E-01		9.58E-02	8.80E-01		-6.36E-01	2.46E-01		-4.76E-01	4.15E-01		-3.58E-01	6.49E-01		-2.75E+00	9.43E-04	Down	Unigene17755_All//gi|209977652|gb|ACJ04334.1|//2.00E-12//ubiquitin specific protease 12 [Nicotiana tabacum]	Unigene17755_All//1.00E-12//AT5G06600| UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene17755_All//7.00E-49//DW508225				nr -
Unigene17757_All	423	36.86	61.57	62.44	55.23	126.02	87.12	73.87	180.62	249.77	7.40E-01	6.94E-12		7.60E-01	4.37E-12		1.19E+00	2.62E-60	Up	6.58E-01	2.32E-14		1.29E+00	2.58E-101	Up	1.76E+00	5.25E-225	Up	Unigene17757_All//gi|283132359|dbj|BAI63585.1|//6.00E-08//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene17757_All//3.00E-41//AT4G38470| protein kinase family protein	Unigene17757_All//0.00E+00//gi|73860670|gb|DT463409.1|DT463409				nr -
Unigene17758_All	612	28.21	71.45	31.85	14.98	18.12	40.88	66.81	141.37	218.46	1.34E+00	1.86E-50	Up	1.75E-01	2.25E-01		2.75E-01	1.28E-01		1.45E+00	5.71E-35	Up	1.08E+00	8.93E-87	Up	1.71E+00	1.02E-273	Up	Unigene17758_All//gi|115474397|ref|NP_001060795.1|//3.00E-21//Os08g0107100 [Oryza sativa Japonica Group] >gi|113622764|dbj|BAF22709.1|Os08g0107100 [Oryza sativa Japonica Group]	Unigene17758_All//4.00E-07//AT5G44860| unknown protein	Unigene17758_All//0.00E+00//C0123638				nr +
Unigene17759_All	458	7.20	5.86	1.28	7.18	3.53	9.17	6.83	7.12	15.66	-2.96E-01	3.87E-01		-2.49E+00	5.99E-09	Down	-1.02E+00	1.40E-03		3.53E-01	2.76E-01		5.93E-02	8.63E-01		1.20E+00	1.97E-09	Up			Unigene17759_All//1.00E-155//TC166327				
Unigene17776_All	2451	6.94	0.99	2.93	14.41	12.80	11.59	5.64	2.32	2.88	-2.81E+00	2.02E-52	Down	-1.24E+00	3.16E-17	Down	-1.71E-01	7.06E-02		-3.14E-01	4.38E-04		-1.28E+00	7.69E-19	Down	-9.71E-01	9.67E-13		Unigene17776_All//gi|270342119|gb|ACZ74702.1|//0.00E+00//kinesin light chain-like protein [Phaseolus vulgaris]	Unigene17776_All//0.00E+00//AT3G27960| kinesin light chain-related	Unigene17776_All//0.00E+00//TC150541				nr -
Unigene17762_All	305	27.62	24.75	33.17	43.12	25.06	14.07	25.23	21.10	27.30	-1.58E-01	4.64E-01		2.64E-01	1.83E-01		-7.83E-01	4.12E-08		-1.62E+00	3.85E-22	Down	-2.58E-01	2.07E-01		1.14E-01	5.86E-01				Unigene17762_All//8.00E-33//TC142624				
Unigene17763_All	672	0.55	0.00	0.00	4.08	4.61	1.21	4.53	4.29	2.19	-9.09E+00	1.97E-02		-9.09E+00	2.78E-02		1.78E-01	6.62E-01		-1.75E+00	1.25E-05	Down	-7.80E-02	8.19E-01		-1.05E+00	7.86E-04	Down	Unigene17763_All//gi|48310269|gb|AAT41787.1|//2.00E-08//At3g09032 [Arabidopsis thaliana] >gi|52627121|gb|AAU84687.1|At3g09032 [Arabidopsis thaliana]	Unigene17763_All//1.00E-05//AT5G01225| unknown protein	Unigene17763_All//0.00E+00//DW506648				nr +
Unigene17764_All	316	5.96	51.95	21.40	6.46	21.58	22.44	26.89	34.52	27.36	3.12E+00	7.14E-56	Up	1.84E+00	1.93E-12	Up	1.74E+00	1.14E-13	Up	1.80E+00	8.99E-14	Up	3.60E-01	2.22E-02		2.47E-02	9.14E-01				Unigene17764_All//1.00E-124//TC155600				
Unigene17766_All	505	67.97	29.30	78.77	23.87	26.66	19.59	0.67	0.17	1.50	-1.21E+00	2.58E-34	Down	2.13E-01	2.06E-02		1.60E-01	3.71E-01		-2.86E-01	9.94E-02		-2.02E+00	1.36E-01		1.16E+00	1.06E-01		Unigene17766_All//gi|297812049|ref|XP_002873908.1|//6.00E-24//pale-green and chlorophyll B reduced 2 [Arabidopsis lyrata subsp. lyrata] >gi|297319745|gb|EFH50167.1| pale-green and chlorophyll B reduced 2 [Arabidopsis lyrata subsp. lyrata]	Unigene17766_All//1.00E-24//AT5G18660| PCR2 (PALE-GREEN AND CHLOROPHYLL B REDUCED 2); 3,8-divinyl protochlorophyllide a 8-vinyl reductase	Unigene17766_All//0.00E+00//gi|84149481|gb|DN780781.1|DN780781				nr +
Unigene17769_All	353	0.30	3.44	2.11	0.42	1.85	3.71	2.40	3.55	3.27	3.54E+00	4.02E-05	Up	2.83E+00	8.52E-03		2.13E+00	3.78E-02		3.13E+00	3.90E-05	Up	5.68E-01	3.10E-01		4.50E-01	4.17E-01								
Unigene1777_All	1788	46.35	230.79	121.93	44.24	72.18	97.85	36.06	123.07	88.01	2.32E+00	0.00E+00	Up	1.40E+00	7.61E-259	Up	7.06E-01	2.18E-61		1.15E+00	1.90E-168	Up	1.77E+00	0.00E+00	Up	1.29E+00	1.11E-211	Up	Unigene1777_All//gi|195638452|gb|ACG38694.1|//1.00E-109//protein disulfide isomerase [Zea mays]	Unigene1777_All//7.00E-71//AT1G60420| DC1 domain-containing protein	Unigene1777_All//0.00E+00//TC164458				nr -
Unigene17770_All	586	1.61	2.25	6.54	2.72	1.65	4.78	2.38	1.00	1.77	4.84E-01	3.94E-01		2.03E+00	3.40E-08	Up	-7.25E-01	1.57E-01		8.13E-01	3.23E-02		-1.25E+00	1.49E-02		-4.30E-01	3.86E-01				Unigene17770_All//7.00E-07//ES852324				
Unigene17772_All	1103	0.19	0.18	0.00	37.44	19.39	11.22	2.07	0.15	0.33	-4.56E-02	9.89E-01		-7.57E+00	1.46E-01		-9.49E-01	6.34E-34		-1.74E+00	5.02E-76	Down	-3.77E+00	9.58E-12	Down	-2.67E+00	4.62E-09	Down	Unigene17772_All//gi|166203230|gb|ABY84655.1|//4.00E-83//transcription factor [Glycine max]	Unigene17772_All//7.00E-57//AT2G44745| WRKY family transcription factor	Unigene17772_All//0.00E+00//TC154949	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene17775_All	448	3.04	7.69	5.47	2.78	4.46	1.21	1.23	1.21	1.60	1.34E+00	1.09E-04	Up	8.49E-01	4.54E-02		6.81E-01	1.48E-01		-1.20E+00	5.16E-02		-1.67E-02	1.02E+00		3.84E-01	5.96E-01		Unigene17775_All//gi|74474915|dbj|BAE44441.1|//1.00E-12//dual specificity protein tyrosine phosphatase 1 [Solanum tuberosum]	Unigene17775_All//5.00E-13//AT3G06110| MKP2 (MAPK PHOSPHATASE 2); MAP kinase phosphatase/ protein tyrosine/serine/threonine phosphatase	Unigene17775_All//3.00E-101//gi|84174254|gb|DR462902.1|DR462902				nr -
Unigene17776_All	586	194.02	425.93	355.39	197.22	239.34	259.81	92.35	217.97	187.84	1.13E+00	1.57E-219	Up	8.73E-01	5.10E-116		2.79E-01	1.70E-12		3.98E-01	2.07E-23		1.24E+00	1.22E-158	Up	1.02E+00	3.76E-103	Up	Unigene17776_All//gi|38016527|gb|AB07599.1|//7.00E-58//fiber protein Fb37 [Gossypium barbadense] >gi|66271037|gb|AAY43796.1| Fb37 [Gossypium hirsutum]	Unigene17776_All//5.00E-20//AT2G27580| zinc finger (AN1-like) family protein	Unigene17776_All//0.00E+00//gi|73818451|gb|DT457471.1|DT457471				nr +
Unigene17778_All	999	0.37	0.20	0.32	3.99	1.52	1.31	11.98	7.95	6.46	-8.53E-01	4.89E-01		-1.97E-01	8.66E-01		-1.40E+00	1.67E-06	Down	-1.61E+00	4.72E-07	Down	-5.91E-01	4.81E-05		-8.91E-01	9.27E-10		Unigene17778_All//gi|15221378|ref|NP_177003.1|//1.00E-56//zinc finger protein-related [Arabidopsis thaliana] >gi|117958743|gb|ABK59680.1|At1g68360 [Arabidopsis thaliana]	Unigene17778_All//3.00E-39//AT1G68360| zinc finger protein-related		C2H2	ko03040|Spliceosome		nr +
Unigene17779_All	1517	0.00	0.13	0.00	0.13	0.23	0.06	33.97	8.57	12.55	7.06E+00	1.37E-01		null	null		7.90E-01	5.96E-01		-1.14E+00	5.69E-01		-1.99E+00	1.04E-127	Down	-1.44E+00	3.30E-83	Down	Unigene17779_All//gi|110559373|gb|ABG75942.1|//1.00E-135//coniferyl alcohol acyltransferase [Petunia x hybrida]	Unigene17779_All//2.00E-74//AT1G78990| transferase family protein	Unigene17779_All//7.00E-43//DW488553		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene1778_All	2317	7.14	5.36	7.15	5.68	5.23	4.27	2.23	0.70	2.01	-4.13E-01	2.63E-03		2.40E-03	1.00E+00		-1.18E-01	5.39E-01		-4.11E-01	8.28E-03		-1.66E+00	1.08E-10	Down	-1.46E-01	5.79E-01		Unigene1778_All//gi|186523322|ref|NP_197122.2|//1.00E-135//CRS1 (ARABIDOPSIS ORTHOLOG OF MAIZE CHLOROPLAST SPLICING FACTOR CRS1); RNA splicing factor, transesterification mechanism [Arabidopsis thaliana]	Unigene1778_All//3.00E-122//AT5G16180| CRS1 (ARABIDOPSIS ORTHOLOG OF MAIZE CHLOROPLAST SPLICING FACTOR CRS1); RNA splicing factor, transesterification mechanism	Unigene1778_All//0.00E+00//C0090314				nr +
Unigene17783_All	852	8.54	2.32	7.50	2.34	1.98	4.77	1.44	1.77	1.26	-1.88E+00	2.84E-14	Down	-1.87E-01	4.36E-01		-2.40E-01	6.05E-01		1.03E+00	6.76E-04	Up	2.95E-01	5.82E-01		-1.89E-01	7.12E-01		Unigene17783_All//gi|18404212|ref|NP_566749.1|//1.00E-107//ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase [Arabidopsis thaliana] >gi|118595574|sp|Q56YU0.2|AL2C4_ARATH RecName: Full=Aldehyde dehydrogenase family 2 member C4; AltName: Full=ALDH1a; AltName: Full=Protein REDUCED EPIDERMAL FLUORESCENCE 1 >gi|9294041|dbj|BAB01998.1| aldehyde dehydrogenase [Arabidopsis thaliana] >gi|15912241|gb|AAL08254.1| aldehyde dehydrogenase [Arabidopsis thaliana] >gi|20530143|gb|AAM27004.1| aldehyde dehydrogenase ALDH1a [Arabidopsis thaliana]	Unigene17783_All//5.00E-106//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene17783_All//0.00E+00//TC157786		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene17785_All	519	10.59	4.78	10.98	2.30	1.99	1.57	0.81	0.81	1.54	-1.15E+00	1.11E-05	Down	5.26E-02	8.43E-01		-2.11E-01	7.52E-01		-5.56E-01	3.87E-01		-1.66E-02	1.02E+00		9.14E-01	1.85E-01		Unigene17785_All//gi|224142135|ref|XP_002324414.1|//3.00E-10//predicted protein [Populus trichocarpa] >gi|222865848|gb|EEF02979.1| predicted protein [Populus trichocarpa]		Unigene17785_All//6.00E-121//DW235236				nr +
Unigene17787_All	756	1.18	0.80	0.56	20.36	14.85	16.97	21.25	10.12	8.12	-5.49E-01	4.42E-01		-1.06E+00	1.76E-01		-4.55E-01	6.34E-04		-2.63E-01	8.09E-02		-1.07E+00	1.55E-16	Down	-1.39E+00	2.90E-25	Down	Unigene17787_All//gi|15228868|ref|NP_191182.1|//1.00E-73//speckle-type POZ protein-related [Arabidopsis thaliana] >gi|45825155|gb|AAS77485.1|At3g56230 [Arabidopsis thaliana]	Unigene17787_All//1.00E-66//AT3G56230| speckle-type POZ protein-related	Unigene17787_All//0.00E+00//C0080816				nr +
Unigene17789_All	727	2.02	5.51	3.44	1.78	1.18	1.93	1.80	2.53	1.21	1.45E+00	7.12E-06	Up	7.73E-01	6.55E-02		-5.89E-01	3.13E-01		1.12E-01	8.61E-01		4.89E-01	2.72E-01		-5.81E-01	2.51E-01		Unigene17789_All//gi|19715640|gb|AAL91640.1|//2.00E-25//At1g47330/T3F24_2 [Arabidopsis thaliana] >gi|22137130|gb|AAM91410.1|At1g47330/T3F24_2 [Arabidopsis thaliana]	Unigene17789_All//2.00E-14//AT1G47330| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF21 (InterPro:IPR002550), Cystathionine beta-synthase, core (InterPro:IPR000644); BEST Arabidopsis thaliana protein match is: CBS domain-containing protein (TAIR:AT2G14520.1); Has 6970 Blast hits to 6717 proteins in 1361 species: Archae - 64; Bacteria - 4382; Metazoa - 390; Fungi - 183; Plants - 125; Viruses - 0; Other Eukaryotes - 1826 (source: NCBI BLink).	Unigene17789_All//5.00E-79//gi|48804120|gb|C0105434.1|C0105434				nr -
Unigene17790_All	561	17.16	9.12	6.07	23.09	21.73	23.59	66.70	28.46	19.60	-9.12E-01	1.12E-06		-1.50E+00	4.08E-13	Down	-8.74E-02	6.28E-01		3.10E-02	8.78E-01		-1.23E+00	1.78E-46	Down	-1.77E+00	1.18E-81	Down	Unigene17790_All//gi|195605918|gb|ACG24789.1|//5.00E-07//60S ribosomal protein L2 [Zea mays] >gi|195606274|gb|ACG24967.1| 60S ribosomal protein L2 [Zea mays]		Unigene17790_All//7.00E-127//gi|164288827|gb|ES837658.1|ES837658		ko03010|Ribosome		nr -
Unigene17791_All	1325	2.17	2.18	1.49	3.27	2.94	3.61	1.82	3.31	10.19	5.20E-03	9.88E-01		-5.47E-01	1.59E-01		-1.55E-01	6.16E-01		1.44E-01	6.53E-01		8.65E-01	8.10E-04		2.49E+00	2.18E-45	Up	Unigene17791_All//gi|16323145|gb|AAL15307.1|//4.00E-92//AT5g11000/T30N20_270 [Arabidopsis thaliana] >gi|21436003|gb|AAM51579.1|AT5g11000/T30N20_270 [Arabidopsis thaliana]	Unigene17791_All//7.00E-72//AT5G11000| unknown protein	Unigene17791_All//0.00E+00//ES804072				nr +
Unigene17792_All	786	0.13	0.00	0.00	2.09	0.31	0.40	261.43	170.37	56.92	-7.06E+00	3.73E-01		-7.06E+00	3.95E-01		-2.77E+00	1.18E-06	Down	-2.38E+00	4.74E-05	Down	-6.18E-01	3.97E-79		-2.20E+00	0.00E+00	Down								
Unigene17794_All	428	0.37	3.20	0.50	1.63	2.09	2.74	13.63	47.85	26.06	3.12E+00	3.45E-05	Up	4.41E-01	7.75E-01		3.61E-01	6.55E-01		7.52E-01	2.53E-01		1.81E+00	3.93E-45	Up	9.35E-01	8.53E-10		Unigene17794_All//gi|224137306|ref|XP_002327093.1|//1.00E-30//cytochrome P450 [Populus trichocarpa] >gi|222835408|gb|EEE73843.1| cytochrome P450 [Populus trichocarpa]	Unigene17794_All//9.00E-25//AT4G31950| CYP82C3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene17794_All//1.00E-137//TC154227		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene17795_All	373	12.48	7.61	5.71	35.79	24.93	34.75	60.08	23.64	22.64	-7.15E-01	1.04E-02		-1.13E+00	1.42E-04	Down	-5.22E-01	2.68E-04		-4.26E-02	8.12E-01		-1.35E+00	2.72E-32	Down	-1.41E+00	1.36E-35	Down	Unigene17795_All//gi|225427377|ref|XP_002282974.1|//4.00E-23//PREDICTED: similar to protein synthesis initiation factor-like [Vitis vinifera]	Unigene17795_All//2.00E-23//AT3G10950| 60S ribosomal protein L37a (RPL37aB)	Unigene17795_All//0.00E+00//TC169290		ko03010|Ribosome		nr -
Unigene17798_All	520	24.15	16.66	17.41	30.85	28.48	33.79	7.97	4.90	3.45	-5.35E-01	7.63E-04		-4.72E-01	4.57E-03		-1.15E-01	4.93E-01		1.31E-01	4.05E-01		-7.01E-01	8.50E-03		-1.21E+00	6.03E-06	Down			Unigene17798_All//0.00E+00//DT458249				
Unigene17801_All	790	2.12	1.48	2.83	3.85	5.54	5.89	2.25	2.06	5.65	-5.23E-01	3.08E-01		4.18E-01	3.69E-01		5.25E-01	7.23E-02		6.14E-01	2.97E-02		-1.24E-01	7.82E-01		1.33E+00	3.90E-07	Up	Unigene17801_All//gi|87240899|gb|ABO32757.1|//2.00E-35//Integrase, catalytic region [Medicago truncatula]	Unigene17801_All//6.00E-15//AT1G21280| unknown protein	Unigene17801_All//5.00E-110//BE052981				nr -
Unigene17802_All	1020	0.00	0.10	0.00	1.17	1.42	1.42	2.03	3.97	0.66	6.64E+00	3.87E-01		null	null		2.75E-01	6.54E-01		2.74E-01	6.49E-01		9.69E-01	3.63E-04		-1.61E+00	8.90E-05	Down	Unigene17802_All//gi|300793630|tpg|DAA33874.1|//1.00E-117//TPA: TPA_inf: aquaporin NIP1;1 [Gossypium hirsutum]	Unigene17802_All//1.00E-85//AT4G18910| NIP1;2 (NOD26-LIKE INTRINSIC PROTEIN 1;2); arsenite transmembrane transporter/ water channel	Unigene17802_All//0.00E+00//gi|109860518|gb|DW489497.1|DW489497				nr -

Unigene17803_All	914	0.92	1.44	1.28	1.58	1.05	1.38	15.27	36.54	10.46	6.54E-01	2.62E-01		4.85E-01	4.47E-01		-5.83E-01	2.98E-01		-1.92E-01	7.24E-01		1.26E+00	4.38E-43	Up	-5.45E-01	2.89E-05		Unigene17803_All//gi|297800796|ref|XP_002868282.1|//5.00E-77//enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314118|gb|EFH44541.1| enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17803_All//1.00E-77//AT4G14430| IBR10 (INDOLE-3-BUTYRIC ACID RESPONSE 10); catalytic/ dodecenoyl-CoA delta-isomerase	Unigene17803_All//0.00E+00//gi|78325409|gb|DT545683.1|DT545683		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism		nr +
Unigene17804_All	3408	0.21	0.24	0.13	0.58	0.39	1.35	3.05	17.21	20.68	1.47E-01	8.39E-01		-7.82E-01	3.80E-01		-5.69E-01	2.13E-01		1.21E+00	2.14E-05	Up	2.50E+00	5.48E-192	Up	2.76E+00	8.55E-263	Up	Unigene17804_All//gi|224102125|ref|XP_002312557.1|//0.00E+00//autoinhibited calcium ATPase [Populus trichocarpa] >gi|222852377|gb|EEE89924.1| autoinhibited calcium ATPase [Populus trichocarpa]	Unigene17804_All//0.00E+00//AT3G22910| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA13)	Unigene17804_All//2.00E-66//EX164158				nr +
Unigene17806_All	907	1.10	2.01	0.59	4.72	3.49	1.29	5.83	2.90	2.42	8.76E-01	7.03E-02		-9.01E-01	2.22E-01		-4.35E-01	1.40E-01		-1.87E+00	3.67E-09	Down	-1.01E+00	1.80E-05	Down	-1.27E+00	7.24E-08	Down	Unigene17806_All//gi|42567992|ref|NP_197554.2|//9.00E-95//ATBRXL4 (BREVIS RADIX-LIKE 4) [Arabidopsis thaliana] >gi|75151601|sp|Q8GZ92.1|BRXL4_ARATH RecName: Full=Protein Brevis radix-like 4; Short=AtBRXL4	Unigene17806_All//2.00E-76//AT5G20540| ATBRXL4 (BREVIS RADIX-LIKE 4)	Unigene17806_All//0.00E+00//gi|109834080|gb|DW232645.1|DW232645				nr -
Unigene17808_All	276	7.77	45.53	27.20	2.53	9.23	16.69	0.77	3.48	5.05	2.55E+00	9.13E-35	Up	1.81E+00	2.15E-13	Up	1.87E+00	7.42E-06	Up	2.72E+00	7.85E-15	Up	2.19E+00	2.24E-03		2.72E+00	8.11E-06	Up								
Unigene17809_All	753	1.74	10.83	6.29	2.71	4.12	8.76	0.45	2.44	4.39	2.64E+00	1.19E-23	Up	1.86E+00	5.66E-09	Up	6.02E-01	9.21E-02		1.69E+00	7.31E-12	Up	2.44E+00	1.59E-06	Up	3.29E+00	2.79E-15	Up	Unigene17809_All//gi|269314023|gb|ACZ36914.1|//1.00E-19//MADS-box transcription factor 1 [Hevea brasiliensis]	Unigene17809_All//3.00E-19//AT1G22130| AGL104 (AGAMOUS-LIKE 104); DNA binding / transcription factor	Unigene17809_All//3.00E-62//DR457055	MADS			nr -
Unigene1781_All	1070	1.52	1.04	0.75	4.24	2.35	4.05	3.08	1.41	0.97	-5.41E-01	2.98E-01		-1.02E+00	6.14E-02		-8.51E-01	1.30E-03		-6.42E-02	8.42E-01		-1.13E+00	2.47E-04	Down	-1.67E+00	1.99E-07	Down	Unigene1781_All//gi|222424346|dbj|BAH20129.1|//1.00E-73//AT4G35920 [Arabidopsis thaliana]	Unigene1781_All//7.00E-75//AT4G35920| MCA1 (mid1-complementing activity 1)	Unigene1781_All//0.00E+00//BF268714				nr +
Unigene17810_All	858	0.24	39.51	0.37	0.58	2.37	3.47	3.55	4.04	14.30	7.34E+00	7.35E-187	Up	6.11E-01	6.25E-01		2.03E+00	3.18E-05	Up	2.58E+00	3.15E-09	Up	1.89E-01	5.87E-01		2.01E+00	5.25E-32	Up	Unigene17810_All//gi|115439245|ref|NP_001043902.1|//2.00E-09//Os01g0686000 [Oryza sativa Japonica Group] >gi|113533433|dbj|BAF05816.1| Os01g0686000 [Oryza sativa Japonica Group]	Unigene17810_All//7.00E-09//AT3G03280| unknown protein	Unigene17810_All//0.00E+00//gi|109869941|gb|DW498917.1|DW498917				nr -
Unigene17811_All	1843	0.00	0.00	0.00	0.05	0.00	0.02	30.81	182.67	58.75	null	null		null	null		-5.76E+00	3.13E-01		-1.14E+00	6.77E-01		2.57E+00	0.00E+00	Up	9.31E-01	8.82E-87		Unigene17811_All//gi|15221473|ref|NP_174357.1|//0.00E+00//FAD-binding domain-containing protein [Arabidopsis thaliana] >gi|16930507|gb|AAL31939.1|AF41960 7_1 At1g30700/T518_15 [Arabidopsis thaliana] >gi|34098889|gb|AAQ56827.1| At1g30700 [Arabidopsis thaliana]	Unigene17811_All//0.00E+00//AT1G30700| FAD-binding domain-containing protein	Unigene17811_All//1.00E-17//gi|48880964|gb|CO131986.1|CO131986				nr -
Unigene17812_All	1684	0.03	0.78	0.06	0.38	0.55	0.40	19.33	36.16	39.01	4.65E+00	1.91E-06	Up	1.02E+00	7.03E-01		5.22E-01	5.25E-01		6.49E-02	9.50E-01		9.03E-01	1.01E-45		1.01E+00	8.73E-61	Up	Unigene17812_All//gi|115479143|ref|NP_001063165.1|//1.00E-40//Os09g0413600 [Oryza sativa Japonica Group] >gi|113631398|dbj|BAF25079.1| Os09g0413600 [Oryza sativa Japonica Group]	Unigene17812_All//1.00E-28//AT3G01175| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: stem, root; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1666 (InterPro:IPR012870); BEST Arabidopsis thaliana protein match is: structural constituent of ribosome (TAIR:AT5G39785.2); Has 100 Blast hits to 98 proteins in 28 species: Archae - 0; Bacteria - 8; Metazoa - 5; Fungi - 5; Plants - 48; Viruses - 0; Other Eukaryotes - 34 (source: NCBI BLink).					nr +
Unigene17813_All	501	3.34	4.45	3.08	2.59	3.51	4.78	31.56	16.18	11.21	4.13E-01	3.54E-01		-1.17E-01	8.14E-01		4.39E-01	4.18E-01		8.86E-01	3.37E-02		-9.64E-01	7.99E-14		-1.49E+00	1.22E-27	Down			Unigene17813_All//1.00E-168//gi|21090292|gb|BQ402605.1|BQ402605				
Unigene17814_All	515	2.13	0.89	1.55	6.67	2.14	6.23	9.03	4.87	8.82	-1.27E+00	5.68E-02		-4.60E-01	4.97E-01		-1.64E+00	4.27E-07	Down	-1.00E-01	7.77E-01		-8.91E-01	3.62E-04		-3.43E-02	9.09E-01		Unigene17814_All//gi|15227038|ref|NP_180478.1|//1.00E-17//APUM3 (Arabidopsis Pumilio 3); RNA binding / binding [Arabidopsis thaliana]	Unigene17814_All//9.00E-19//AT2G29140| APUM3 (Arabidopsis Pumilio 3); RNA binding / binding	Unigene17814_All//5.00E-177//TC179003				nr +
Unigene17815_All	712	1.03	0.14	0.15	4.34	2.03	4.00	2.79	1.88	2.13	-2.85E+00	6.26E-03		-2.78E+00	1.05E-02		-1.09E+00	9.95E-04	Down	-1.18E-01	7.50E-01		-5.71E-01	1.72E-01		-3.93E-01	3.41E-01		Unigene17815_All//gi|35187466|gb|AAQ84324.1|//8.00E-07//fiber protein Fb32 [Gossypium barbadense]	Unigene17815_All//4.00E-05//AT2G31130| unknown protein	Unigene17815_All//0.00E+00//TC162998				nr -
Unigene17817_All	1266	0.83	0.56	1.43	2.95	2.34	2.25	2.84	0.86	0.79	-5.61E-01	3.82E-01		7.91E-01	1.21E-01		-3.35E-01	3.10E-01		-3.93E-01	2.42E-01		-1.73E+00	4.72E-08	Down	-1.85E+00	4.08E-09	Down	Unigene17817_All//gi|15233209|ref|NP_191737.1|//7.00E-23//emb1703 (embryo defective 1703) [Arabidopsis thaliana]	Unigene17817_All//3.00E-24//AT3G61780| emb1703 (embryo defective 1703)	Unigene17817_All//0.00E+00//EE592415				nr +
Unigene17818_All	469	2.01	3.24	2.95	2.97	3.45	3.18	2.70	0.89	0.59	6.91E-01	2.02E-01		5.56E-01	3.62E-01		2.15E-01	7.32E-01		9.56E-02	8.79E-01		-1.60E+00	4.42E-03		-2.19E+00	1.97E-04	Down	Unigene17818_All//gi|30683442|ref|NP_850805.1|//1.00E-33//pre-mRNA cleavage complex-related [Arabidopsis thaliana] >gi|42573337|ref|NP_974765.1| pre-mRNA cleavage complex-related [Arabidopsis thaliana]	Unigene17818_All//7.00E-35//AT5G11010| pre-mRNA cleavage complex-related	Unigene17818_All//0.00E+00//DR461669				nr +
Unigene17819_All	458	3.31	8.41	4.30	4.79	2.56	5.92	2.12	0.73	1.30	1.34E+00	3.71E-05	Up	3.77E-01	4.28E-01		-9.05E-01	2.79E-02		3.06E-01	4.66E-01		-1.54E+00	1.90E-02		-7.02E-01	2.43E-01				Unigene17819_All//2.00E-40//TC177006				
Unigene1782_All	1870	4.92	4.77	4.53	20.78	16.22	12.58	10.67	3.00	4.13	-4.63E-02	8.16E-01		-1.21E-01	5.94E-01		-3.57E-01	6.79E-06		-7.24E-01	6.40E-18		-1.83E+00	8.20E-45	Down	-1.37E+00	1.72E-30	Down	Unigene1782_All//gi|222424346|dbj|BAH20129.1|//1.00E-173//AT4G35920 [Arabidopsis thaliana]	Unigene1782_All//6.00E-174//AT4G35920| MCA1 (mid1-complementing activity 1)	Unigene1782_All//0.00E+00//gi|109875806|gb|DR504780.1|DR504780				nr +
Unigene17822_All	691	2.42	0.44	0.00	0.00	0.10	0.92	2.57	2.24	2.36	-2.46E+00	4.49E-05	Down	-1.12E+01	3.83E-09	Down	6.64E+00	6.10E-01		9.84E+00	7.60E-04	Up	-2.00E-01	6.53E-01		-1.21E-01	7.73E-01		Unigene17822_All//gi|15237426|ref|NP_199445.1|//1.00E-42//FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / kinase/ protein binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase [Arabidopsis thaliana] >gi|75262640|sp|Q9FL28.1|FLS2_ARATH RecName: Full=LRR receptor-like serine/threonine-protein kinase FLS2; AltName: Full=Protein FLAGELLIN-SENSING 2; AltName: Full=Protein FLAGELLIN-SENSITIVE 2; Flags: Precursor >gi|10177714|dbj|BAB11088.1| receptor protein kinase [Arabidopsis thaliana] >gi|224589703|gb|ACN59383.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene17822_All//1.00E-43//AT5G46330| FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / kinase/ protein binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr -
Unigene17823_All	1381	2.39	0.33	0.69	0.58	0.20	2.39	3.58	1.21	2.60	-2.85E+00	8.12E-11	Down	-1.78E+00	4.29E-06	Down	-1.53E+00	4.83E-02		2.05E+00	7.46E-08	Up	-1.57E+00	1.68E-09	Down	-4.64E-01	4.83E-02		Unigene17823_All//gi|297794625|ref|XP_002865197.1|//1.00E-126//flagellin-sensitive 2 [Arabidopsis lyrata subsp. lyrata] >gi|297311032|gb|EFH41456.1| flagellin-sensitive 2 [Arabidopsis lyrata subsp. lyrata]	Unigene17823_All//1.00E-116//AT5G46330| FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / kinase/ protein binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr +
Unigene17824_All	585	0.36	13.60	5.46	1.53	1.35	2.16	0.00	0.29	0.00	5.25E+00	2.48E-39	Up	3.93E+00	4.02E-13	Up	-1.79E-01	8.15E-01		4.96E-01	4.48E-01		8.16E+00	1.39E-01		null	null		Unigene17824_All//gi|115475027|ref|NP_001061110.1|//1.00E-11//Os08g0174900 [Oryza sativa Japonica Group] >gi|75133775|sp|Q6Z4U2.1|CAF1M_ORYSJ RecName: Full=CRS2-associated factor 1, mitochondrial; Flags: Precursor >gi|113623079|dbj|BAF23024.1| Os08g0174900 [Oryza sativa Japonica Group]	Unigene17824_All//1.00E-06//AT4G31010| RNA binding					nr +
Unigene17825_All	393	3.20	4.77	3.39	3.42	3.50	4.60	3.55	91.46	1.01	5.78E-01	2.26E-01		8.43E-02	8.85E-01		3.44E-02	9.63E-01		4.26E-01	4.19E-01		4.69E+00	2.81E-205	Up	-1.81E+00	6.10E-04	Down	Unigene17825_All//gi|59896631|gb|AAX11684.1|//5.00E-06//peraksine reductase [Rauvolfia serpentina]		Unigene17825_All//1.00E-96//gi|48815215|gb|CO116528.1|CO116528				nr -
Unigene17827_All	331	141.16	13.78	25.26	157.27	58.68	51.17	32.96	96.98	21.30	-3.36E+00	5.47E-171	Down	-2.48E+00	1.09E-120	Down	-1.42E+00	6.07E-82	Down	-1.62E+00	1.44E-86	Down	1.56E+00	7.24E-57	Up	-6.29E-01	2.57E-05				Unigene17827_All//6.00E-157//gi|11201377|gb|BF270382.1|BF270382				
Unigene17828_All	435	56.53	158.53	113.72	109.93	135.29	151.38	295.18	307.37	316.79	1.49E+00	1.40E-92	Up	1.01E+00	2.44E-35	Up	2.99E-01	2.97E-06		4.62E-01	1.39E-13		5.83E-02	2.19E-01		1.02E-01	1.20E-02		Unigene17828_All//gi|87201358|gb|AAX07458.2|//2.00E-81//ethylene-responsive element binding protein ERF2 [Gossypium hirsutum]	Unigene17828_All//9.00E-36//AT3G14230| RAP2.2; DNA binding / transcription factor	Unigene17828_All//0.00E+00//TC134515	AP2-EREBP			nr +
Unigene17829_All	752	0.42	3.37	1.70	2.78	4.08	5.77	2.53	0.78	0.74	3.01E+00	8.44E-09	Up	2.03E+00	3.44E-03		5.51E-01	1.32E-01		1.05E+00	3.11E-04	Up	-1.70E+00	1.53E-04	Down	-1.77E+00	5.92E-05	Down	Unigene17829_All//gi|224133732|ref|XP_002321647.1|//8.00E-26//predicted protein [Populus trichocarpa] >gi|222868643|gb|EEF05774.1| predicted protein [Populus trichocarpa]						nr -
Unigene1783_All	1260	3.99	1.73	3.04	4.59	5.71	4.37	6.07	4.11	5.28	-1.20E+00	1.24E-05	Down	-3.90E-01	1.75E-01		3.17E-01	1.67E-01		-6.86E-02	7.98E-01		-5.62E-01	2.74E-03		-2.02E-01	3.14E-01		Unigene1783_All//gi|42572291|ref|NP_974492.1|//4.00E-69//methionine adenosyltransferase regulatory beta subunit-related [Arabidopsis thaliana] >gi|124301070|gb|ABN04787.1| At4g00560 [Arabidopsis thaliana]	Unigene1783_All//2.00E-70//AT4G00560| methionine adenosyltransferase regulatory beta subunit-related	Unigene1783_All//0.00E+00//TC151595		ko00523|Polyketide sugar unit biosynthesis		nr +
Unigene17832_All	317	4.29	1.60	7.39	90.99	79.73	68.81	102.43	45.62	184.99	-1.42E+00	1.66E-02		7.84E-01	7.27E-02		-1.91E-01	7.01E-02		-4.03E-01	4.20E-05		-1.17E+00	2.53E-37	Down	8.53E-01	5.57E-41		Unigene17832_All//gi|297833008|ref|XP_002884386.1|//2.00E-24//phosphoesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330026|gb|EFH60645.1| phosphoesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17832_All//1.00E-25//AT3G03520| phosphoesterase family protein	Unigene17832_All//1.00E-161//TC166303		ko00564|Glycerophospholipid metabolism//ko00562|Inositol phosphate metabolism//ko00565|Ether lipid metabolism		nr +
Unigene17833_All	440	1.07	3.92	2.54	2.38	2.66	2.05	7.21	5.32	8.51	1.87E+00	6.55E-04	Up	1.25E+00	7.15E-02		1.63E-01	8.20E-01		-2.12E-01	7.44E-01		-4.38E-01	1.75E-01		2.40E-01	4.12E-01		Unigene17833_All//gi|222423964|dbj|BAH19944.1|//4.00E-15//AT1G10660 [Arabidopsis thaliana]	Unigene17833_All//3.00E-16//AT1G10660| unknown protein	Unigene17833_All//3.00E-172//DR453316				nr -
Unigene17838_All	519	2.72	3.81	2.57	3.65	3.32	2.96	1.47	4.19	1.23	4.84E-01	3.02E-01		-8.57E-02	8.81E-01		-1.37E-01	8.10E-01		-3.02E-01	5.68E-01		1.51E+00	2.06E-04	Up	-2.56E-01	6.97E-01				Unigene17838_All//2.00E-117//gi|164268400|gb|ES831129.1|ES831129				

Unigene17839_All	522	0.90	2.33	0.00	1.62	3.89	5.02	1.46	3.04	3.05	1.37E+00	3.15E-02			-9.82E+00	8.66E-03			1.26E+00	5.34E-03			1.63E+00	7.58E-05	Up	1.06E+00	2.45E-02			1.07E+00	1.93E-02		Unigene17839_All//gi|217793962|gb|ACK56115.1|//3.00E-23//ELF4-like protein [Ipomoea nil]	Unigene17839_All//1.00E-14//AT2G29950| ELF4-L1 (ELF4-Like 1)	Unigene17839_All//0.00E+00//gi|84165413|gb|DR454061.1|DR454061				nr -
Unigene17842_All	1876	0.22	0.00	0.17	8.60	8.37	1.61	0.72	0.58	0.68	-7.80E+00	1.05E-02			-3.90E-01	7.17E-01			-3.96E-02	8.07E-01			-2.42E+00	8.88E-46	Down	-3.16E-01	5.76E-01			-8.57E-02	8.66E-01		Unigene17842_All//gi|115436122|ref|XP_001042819.1|//1.00E-175//Os01g0300900 [Oryza sativa Japonica Group] >gi|113532350|dbj|BAF04733.1|Os01g0300900 [Oryza sativa Japonica Group]	Unigene17842_All//1.00E-46//AT1G74150| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Galactose oxidase/kelch, beta-propeller (InterPro:IPR011043), Kelch repeat type 1 (InterPro:IPR006652), Kelch repeat type 2 (InterPro:IPR011498), Kelch-type beta propeller (InterPro:IPR015915); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G18610.1); Has 8525 Blast hits to 4249 proteins in 295 species: Archae - 10; Bacteria - 313; Metazoa - 3989; Fungi - 839; Plants - 1220; Viruses - 19; Other Eukaryotes - 2115 (source: NCBI BLink).	Unigene17842_All//1.00E-66//TC175999		ko04712|Circadian rhythm - plant		nr +
Unigene17843_All	1179	0.00	22.73	0.00	0.25	1.99	0.15	0.43	3.44	59.91	1.45E+01	1.86E-154	Up	null	null			2.97E+00	7.31E-09	Up	-7.27E-01	6.39E-01		3.00E+00	9.68E-17	Up	7.12E+00	0.00E+00	Up				Unigene17843_All//gi|224123482|ref|XP_002330325.1|//3.00E-59//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222871360|gb|EEF08491.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene17843_All//3.00E-29//AT4G34410| RRTF1 (REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor	Unigene17843_All//0.00E+00//TC148230	AP2-EREBP			nr +
Unigene17850_All	1167	0.63	0.22	0.27	2.39	3.10	3.56	1.56	0.39	1.02	-1.53E+00	7.78E-02			-1.20E+00	1.80E-01			3.74E-01	2.90E-01			5.75E-01	5.99E-02		-1.98E+00	3.39E-05	Down	-6.05E-01	1.46E-01		Unigene17850_All//gi|115483022|ref|NP_001065104.1|//7.00E-06//Os10g0524000 [Oryza sativa Japonica Group] >gi|113639713|dbj|BAF27018.1|Os10g0524000 [Oryza sativa Japonica Group]	Unigene17850_All//2.00E-57//AT5G03670| unknown protein	Unigene17850_All//0.00E+00//gi|78348117|gb|DT568391.1|DT568391				nr -
Unigene17852_All	680	1.77	2.76	1.57	0.73	0.91	0.53	4.91	2.64	0.64	6.40E-01	1.80E-01			-1.76E-01	7.68E-01			3.15E-01	7.84E-01			-4.64E-01	6.59E-01		-8.94E-01	3.09E-03		-2.93E+00	3.75E-14	Down	Unigene17852_All//gi|255572391|ref|XP_002527134.1|//9.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223533557|gb|EEF35297.1|conserved hypothetical protein [Ricinus communis]		Unigene17852_All//0.00E+00//gi|21093657|gb|BQ405970.1|BQ405970				nr +
Unigene17853_All	737	1.70	1.38	1.45	0.74	1.64	1.41	1.78	1.64	5.35	-3.09E-01	6.21E-01			-2.38E-01	6.85E-01			1.14E+00	7.32E-02			9.23E-01	1.96E-01		-1.13E-01	8.32E-01		1.59E+00	4.38E-08	Up	Unigene17853_All//gi|59896631|gb|AAX11684.1|//3.00E-10//perakine reductase [Rauvolfia serpentina]	Unigene17853_All//1.00E-08//AT1G60680| aldo/keto reductase family protein	Unigene17853_All//0.00E+00//TC166516				nr -
Unigene17855_All	1070	7.24	0.28	0.70	17.13	9.14	17.35	12.88	0.35	1.23	-4.67E+00	1.64E-36	Down	-3.38E+00	1.29E-27	Down	-9.07E-01	3.71E-14			1.80E-02	9.25E-01		-5.20E+00	1.17E-83	Down	-3.39E+00	1.59E-64	Down	Unigene17855_All//gi|42562941|ref|NP_176645.3|//1.00E-42//plastocyanin-like domain-containing protein [Arabidopsis thaliana] >gi|45773786|gb|AAS76697.1|At1g64640 [Arabidopsis thaliana] >gi|46359847|gb|AAS88787.1|At1g64640 [Arabidopsis thaliana]	Unigene17855_All//3.00E-41//AT1G64640| plastocyanin-like domain-containing protein	Unigene17855_All//0.00E+00//DW500755				nr -
Unigene17857_All	637	0.49	0.16	0.00	18.92	6.70	8.93	0.27	3.22	1.44	-1.63E+00	2.77E-01			-8.94E+00	4.92E-02			-1.50E+00	9.90E-21	Down		-1.08E+00	3.08E-11	Down	3.60E+00	3.47E-10	Up	2.44E+00	1.06E-03		Unigene17857_All//gi|297793777|ref|XP_002864773.1|//2.00E-26//peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297310608|gb|EFH41032.1|peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene17857_All//1.00E-27//AT5G62150| peptidoglycan-binding LysM domain-containing protein	Unigene17857_All//0.00E+00//TC153770				nr -
Unigene1786_All	907	3.35	1.28	1.41	7.63	9.11	4.98	14.40	6.04	11.86	-1.38E+00	2.10E-04	Down	-1.25E+00	1.13E-03			2.55E-01	2.48E-01			-6.17E-01	5.13E-03		-1.25E+00	2.81E-17	Down	-2.81E-01	4.45E-02		Unigene1786_All//gi|224113081|ref|XP_002316384.1|//1.00E-97//amino acid transporter [Populus trichocarpa] >gi|222865424|gb|EEF02555.1| amino acid transporter [Populus trichocarpa]	Unigene1786_All//1.00E-98//AT2G39130| amino acid transporter family protein	Unigene1786_All//0.00E+00//TC169226				nr -
Unigene17861_All	1617	0.00	0.06	0.00	0.18	0.28	0.28	36.11	3.52	12.66	5.97E+00	3.87E-01		null	null			5.83E-01	6.26E-01			5.96E-01	6.40E-01		-3.36E+00	5.36E-261	Down	-1.51E+00	1.42E-101	Down	Unigene17861_All//gi|30685446|ref|NP_197067.2|//0.00E+00//IRX6 [Arabidopsis thaliana] >gi|34222647|sp|Q9LFW3.2|COBL4_ARATH RecName: Full=COBRA-like protein 4; Flags: Precursor >gi|48525349|gb|AAT44976.1|At5g15630 [Arabidopsis thaliana] >gi|56790214|gb|AAW30024.1|At5g15630 [Arabidopsis thaliana]	Unigene17861_All//0.00E+00//AT5G15630| IRX6	Unigene17861_All//0.00E+00//C0087606				nr -
Unigene17862_All	695	1.58	1.09	2.45	3.73	2.28	1.69	1.76	1.74	0.40	-5.32E-01	3.95E-01		6.33E-01	2.37E-01			-7.10E-01	6.00E-02			-1.14E+00	3.69E-03		-1.66E-02	1.01E+00		-2.14E+00	3.24E-04	Down			Unigene17862_All//3.00E-31//gi|48795736|gb|CO097050.1|CO097050				nr -
Unigene17863_All	374	106.18	28.72	29.62	245.34	293.71	206.62	165.16	75.43	83.19	-1.89E+00	2.78E-75	Down	-1.84E+00	2.25E-70	Down	2.60E-01	1.12E-08			-2.48E-01	2.76E-06		-1.13E+00	7.50E-67	Down	-9.89E-01	1.91E-55		Unigene17863_All//gi|134035502|gb|AB047739.1|//5.00E-67//alpha-tubulin [Gossypium hirsutum]	Unigene17863_All//3.00E-56//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene17863_All//0.00E+00//TC132831		ko04145|Phagosome		nr -
Unigene17864_All	768	0.00	0.00	0.00	1.10	0.90	1.00	34.85	26.12	12.14	null	null		null	null			-2.98E-01	6.93E-01			-1.42E-01	8.54E-01		-4.16E-01	8.71E-06		-1.52E+00	1.85E-47	Down	Unigene17864_All//gi|75337341|sp|Q9SK86.1|ADHL1_ARATH//3.00E-66//RecName: Full=Alcohol dehydrogenase-like 1 >gi|6587845|gb|AAF18534.1|AC006551_20 Very similar to alcohol dehydrogenase [Arabidopsis thaliana]	Unigene17864_All//2.00E-67//AT1G22430| alcohol dehydrogenase, putative	Unigene17864_All//0.00E+00//TC162394		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr +
Unigene17865_All	373	11.64	4.48	3.43	17.63	9.69	12.47	36.27	14.23	9.93	-1.38E+00	6.27E-06	Down	-1.76E+00	9.88E-08	Down	-8.63E-01	4.84E-05			-4.99E-01	3.11E-02		-1.35E+00	6.56E-20	Down	-1.87E+00	2.09E-32	Down			Unigene17865_All//1.00E-179//gi|164272887|gb|ES843432.1|ES843432				
Unigene17866_All	578	0.91	0.79	0.83	3.28	3.22	3.75	5.56	1.95	2.48	-1.98E-01	8.20E-01		-1.27E-01	8.98E-01		-2.57E-02	9.58E-01			1.96E-01	6.94E-01		-1.51E+00	3.78E-06	Down	-1.16E+00	1.41E-04	Down	Unigene17866_All//gi|15224916|ref|NP_181989.1|//6.00E-35//RABA4; GTP binding / protein binding [Arabidopsis thaliana] >gi|75318653|sp|Q80501.1|RBH1B_ARATH RecName: Full=Ras-related protein RABH1B >gi|107738267|gb|ABF83670.1|At2g44610 [Arabidopsis thaliana] >gi|741994|prf||2008312A GTP-binding protein	Unigene17866_All//2.00E-28//AT2G44610| RABA4; GTP binding / protein binding	Unigene17866_All//0.00E+00//TC152322				nr +
Unigene17867_All	403	0.52	1.01	1.45	2.23	3.85	3.36	1.36	0.93	4.55	9.54E-01	4.14E-01		1.48E+00	1.53E-01		7.89E-01	1.51E-01			5.96E-01	3.36E-01		-5.47E-01	5.52E-01		1.74E+00	1.22E-04	Up							
Unigene17868_All	551	0.76	1.20	2.03	3.16	5.44	3.11	1.92	1.06	4.84	6.54E-01	4.48E-01		1.42E+00	4.40E-02		7.81E-01	2.85E-02			-2.27E-02	9.53E-01		-8.53E-01	1.55E-01		1.34E+00	1.23E-04	Up	Unigene17868_All//gi|126843144|gb|AB027626.1|//9.00E-24//BR11 protein [Solanum pimpinellifolium]	Unigene17868_All//5.00E-12//AT4G39400| BRI1 (BRASSINOSTEROID INSENSITIVE 1); kinase/ protein binding / protein heterodimerization/ protein homodimerization/ protein kinase/ protein serine/threonine kinase	Unigene17868_All//2.00E-41//DW477121				nr -
Unigene17869_All	1452	0.00	0.07	0.00	0.10	0.19	0.19	64.61	46.78	4.66	6.13E+00	3.87E-01		null	null		8.83E-01	5.95E-01			8.59E-01	6.31E-01		-4.66E-01	2.80E-22		-3.79E+00	0.00E+00	Down	Unigene17869_All//gi|28932880|gb|AA060108.1|//0.00E+00//nodulin-like protein [Gossypium hirsutum]	Unigene17869_All//2.00E-115//AT1G69380| integral membrane family protein / nodulin MtN21-related	Unigene17869_All//0.00E+00//TC137794				nr +
Unigene1787_All	2198	5.71	4.45	3.17	24.16	25.94	12.04	24.29	7.40	22.24	-3.61E-01	2.59E-02		-8.48E-01	3.31E-07		1.03E-01	1.95E-01			-1.00E+00	4.09E-42	Down	-1.72E+00	2.56E-108	Down	-1.28E-01	6.01E-02		Unigene1787_All//gi|224097816|ref|XP_002311078.1|//0.00E+00//amino acid transporter [Populus trichocarpa] >gi|222850898|gb|EEE88445.1| amino acid transporter [Populus trichocarpa]	Unigene1787_All//0.00E+00//AT2G39130| amino acid transporter family protein	Unigene1787_All//0.00E+00//TC154047				nr -
Unigene17870_All	2342	1.07	0.30	1.09	10.38	8.44	3.82	0.36	0.04	0.19	-1.82E+00	3.11E-05	Down	2.55E-02	9.68E-01		-2.99E-01	5.31E-03		-1.44E+00	2.49E-34	Down	-3.34E+00	2.51E-04	Down	-9.49E-01	1.47E-01		Unigene17870_All//gi|148362066|gb|AB429641.1|//0.00E+00//LYK10 [Glycine max]	Unigene17870_All//1.00E-119//AT3G01840| protein kinase family protein			ko04626|Plant-pathogen interaction		nr +
Unigene17871_All	417	180.43	109.12	119.01	200.33	237.08	236.86	330.23	157.76	181.71	-7.26E-01	7.34E-32		-6.00E-01	4.11E-22		2.43E-01	5.36E-07			2.42E-01	2.08E-06		-1.07E+00	1.12E-134	Down	-8.62E-01	2.54E-97		Unigene17871_All//gi|192910782|gb|ACF06199.1|//3.00E-70//ribosomal protein [Elaeis guineensis]	Unigene17871_All//1.00E-70//AT3G53870| 40S ribosomal protein S3 (RPS3B)	Unigene17871_All//0.00E+00//DR454528		ko03010|Ribosome		nr +
Unigene17872_All	1118	0.42	0.54	0.76	21.30	15.15	13.41	0.23	1.57	0.25	3.69E-01	6.60E-01		8.56E-01	2.80E-01		-4.91E-01	1.77E-06			-6.67E-01	8.28E-10		2.79E+00	4.04E-07	Up	1.36E-01	9.29E-01		Unigene17872_All//gi|79549667|ref|NP_178303.2|//2.00E-33//nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana]	Unigene17872_All//1.00E-23//AT2G01940| nucleic acid binding / transcription factor/ zinc ion binding	Unigene17872_All//2.00E-91//ES817490	C2H2			nr +
Unigene17875_All	222	39.36	18.72	17.51	120.95	116.80	96.43	56.56	29.93	28.17	-1.07E+00	8.98E-08	Down	-1.17E+00	2.25E-08	Down	-5.03E-02	7.12E-01			-3.27E-01	1.76E-03		-9.18E-01	2.42E-10		-1.01E+00	2.74E-12	Down	Unigene17875_All//gi|288300148|gb|ADC45377.1|//3.00E-37//S-adenosylmethionine synthetase [Cleistogenes songorica]	Unigene17875_All//5.00E-37//AT4G01850| SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase	Unigene17875_All//4.00E-120//gi|78330892|gb|DT551166.1|DT551166		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr +
Unigene17879_All	1657	0.38	0.28	0.26	0.12	0.19	0.95	5.08	7.04	11.54	-4.61E-01	6.19E-01		-5.60E-01	5.54E-01		6.36E-01	6.95E-01			2.99E+00	7.30E-06	Up	4.71E-01	1.53E-03		1.18E+00	2.44E-23	Up	Unigene17879_All//gi|27728718|gb|AA018666.1|//1.00E-111//wax synthase isoform 3 [Vitis vinifera]	Unigene17879_All//6.00E-75//AT5G55360| long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein	Unigene17879_All//2.00E-09//TC168826				nr -
Unigene17880_All	1236	2.67	0.78	1.08	5.60	3.40	2.74	0.17	0.10	0.16	-1.78E+00	2.03E-06	Down	-1.31E+00	3.67E-04	Down	-7.21E-01	4.93E-04			-1.03E+00	2.87E-06	Down	-7.54E-01	6.32E-01		-8.51E-02	9.61E-01		Unigene17880_All//gi|297801906|ref|XP_002868837.1|//2.00E-99//ATEXPA20 [Arabidopsis lyrata subsp. lyrata] >gi|297314673|gb|EFH45096.1|ATEXPA20 [Arabidopsis lyrata subsp. lyrata]	Unigene17880_All//2.00E-89//AT4G38210| ATEXPA20 (ARABIDOPSIS THALIANA EXPANSIN A20)	Unigene17880_All//2.00E-123//gi|189098414|gb|FG551566.1|FG551566				nr +
Unigene17881_All	794	1.78	4.02	1.34	3.33	4.03	4.95	1.49	0.79	0.35	1.18E+00	9.53E-04	Up	-4.08E-01	4.86E-01		2.79E-01	4.84E-01			5.74E-01	7.04E-02		-9.17E-01	1.03E-01		-2.09E+00	5.32E-04	Down	Unigene17881_All//gi|109676352|gb|AB637658.1|//1.00E-17//integrase [Populus trichocarpa]						nr +
Unigene17882_All	334	10.97	7.28	2.55	23.42	19.90	20.55	4.56	0.50	0.36	-5.91E-01	6.67E-02		-2.10E+00	3.53E-08	Down	-2.35E-01	3.05E-01			-1.88E-01	4.35E-01		-3.19E+00	4.80E-07	Down	-3.67E+00	3.49E-08	Down			Unigene17882_All//2.00E-135//C0096875				

Unigene17883_All	637	0.16	0.00	0.33	2.11	2.76	5.39	1.46	0.92	3.56	-7.36E+00	3.73E-01		1.03E+00	5.92E-01		3.85E-01	4.89E-01		1.35E+00	7.63E-05	Up	-6.69E-01	3.12E-01		1.29E+00	6.77E-04	Up	Unigene17883_All//gi|297794721|ref|XP_002865245.1|//8.00E-08//predicted protein [Arabidopsis lyrata subsp. lyrata] >gi|297311080|gb|EFH41504.1|predicted protein [Arabidopsis lyrata subsp. lyrata]						nr +
Unigene17886_All	515	19.30	12.69	8.48	4.16	5.48	2.63	0.16	0.00	0.00	-6.05E-01	8.38E-04		-1.19E+00	1.18E-09	Down	3.99E-01	3.14E-01		-6.61E-01	1.40E-01		-7.36E+00	4.04E-01		-7.36E+00	3.59E-01			Unigene17886_All//0.00E+00//DW517658					
Unigene17887_All	535	35.70	48.21	48.17	38.55	84.45	71.50	0.40	0.47	0.15	4.34E-01	5.09E-05		4.33E-01	9.50E-05		1.13E+00	3.19E-47	Up	8.91E-01	8.76E-25		2.46E-01	8.53E-01		-1.41E+00	3.80E-01		Unigene17887_All//gi|82623417|gb|AB88123.1|//1.00E-81//aspartic protease precursor-like [Solanum tuberosum]	Unigene17887_All//7.00E-75//AT1G11910| aspartyl protease family protein	Unigene17887_All//0.00E+00//gi|48821016|gb|CO122329.1|CO122329				nr -
Unigene1789_All	1009	2.96	1.41	7.60	1.68	0.96	1.61	8.80	23.11	8.29	-1.07E+00	3.38E-03		1.36E+00	2.81E-09	Up	-8.13E-01	9.38E-02		-5.89E-02	9.21E-01		1.39E+00	2.62E-35	Up	-8.58E-02	6.39E-01		Unigene1789_All//gi|18400838|ref|NP_566519.1|//1.00E-104//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|11994333|dbj|BAB02292.1| WD-40 repeat protein-like [Arabidopsis thaliana] >gi|25083282|gb|AAN72058.1|expressed protein [Arabidopsis thaliana] >gi|28059687|gb|AAO30083.1|Unknown protein [Arabidopsis thaliana]	Unigene1789_All//4.00E-102//AT3G15610| transducin family protein / WD-40 repeat family protein	Unigene1789_All//0.00E+00//TC136037				nr -
Unigene17890_All	547	2.77	6.39	5.26	6.28	11.14	16.43	0.23	0.38	0.29	1.20E+00	3.79E-04	Up	9.22E-01	1.71E-02		8.26E-01	3.02E-04		1.39E+00	4.15E-12	Up	7.20E-01	6.32E-01		3.29E-01	8.51E-01		Unigene17890_All//gi|56542451|gb|AAV82890.1|//4.00E-31//Avr9/Cf-9 rapidly elicited protein 20 [Nicotiana tabacum]	Unigene17890_All//7.00E-23//AT4G27280| calcium-binding EF hand family protein			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr +
Unigene17892_All	678	1.23	3.59	2.67	2.42	3.35	3.60	4.43	3.21	2.76	1.54E+00	3.68E-04	Up	1.11E+00	3.00E-02		4.67E-01	3.10E-01		5.69E-01	1.85E-01		-4.66E-01	1.59E-01		-6.81E-01	2.77E-02		Unigene17892_All//gi|195626992|gb|ACG35326.1|//7.00E-12//serine/threonine-protein kinase AFC3 [Zea mays]	Unigene17892_All//5.00E-11//AT4G32660| AME3; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene17892_All//0.00E+00//TC131516				nr +
Unigene17895_All	849	5.55	7.76	1.76	0.06	0.57	0.16	5.58	12.01	0.56	4.84E-01	3.66E-02		-1.66E+00	1.07E-07	Down	3.27E+00	2.69E-02		1.44E+00	6.38E-01		1.11E+00	2.52E-11	Up	-3.31E+00	3.96E-22	Down	Unigene17895_All|gi|226531666|ref|NP_001151973.1|//7.00E-35//LOC100285610 [Zea mays] >gi|195651453|gb|ACG45194.1|chaperone protein dnaJ [Zea mays]	Unigene17895_All//3.00E-26//AT1G56300| DNAJ heat shock N-terminal domain-containing protein	Unigene17895_All//0.00E+00//TC166994				nr -
Unigene17896_All	500	1.36	0.81	2.13	2.39	3.03	2.08	4.48	0.84	1.83	-7.47E-01	3.80E-01		6.47E-01	3.62E-01		3.42E-01	5.76E-01		-2.03E-01	7.36E-01		-2.42E+00	9.24E-08	Down	-1.29E+00	6.63E-04	Down	Unigene17896_All//gi|297817406|ref|XP_002876586.1|//1.00E-55//guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322424|gb|EFH52845.1|guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17896_All//1.00E-56//AT3G60860| guanine nucleotide exchange family protein	Unigene17896_All//0.00E+00//TC176014				nr +
Unigene17897_All	617	6.95	1.64	6.90	13.16	8.54	4.76	1.78	5.55	3.87	-2.08E+00	7.46E-10	Down	-1.02E-02	9.97E-01		-6.24E-01	1.01E-03		-1.47E+00	4.01E-12	Down	1.64E+00	3.21E-07	Up	1.12E+00	1.97E-03		Unigene17897_All|gi|163955602|gb|ABY49799.1|//7.00E-13//membrane receptor-like protein 1 [Capsicum annuum]	Unigene17897_All//3.00E-07//AT1G67000| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene17897_All//1.00E-137//TC150336				nr +
Unigene17898_All	431	26.59	45.03	17.42	21.27	23.17	25.36	11.77	9.70	5.55	7.60E-01	1.89E-09		-6.10E-01	4.52E-04		1.24E-01	5.80E-01		2.54E-01	1.81E-01		-2.80E-01	2.77E-01		-1.09E+00	4.14E-06	Down		Unigene17898_All//0.00E+00//TC173863					
Unigene17899_All	245	0.43	16.34	10.87	4.68	2.81	2.58	4.31	3.92	5.37	5.26E+00	6.36E-20	Up	4.67E+00	3.28E-12	Up	-7.34E-01	2.38E-01		-8.58E-01	1.93E-01		-1.37E-01	8.15E-01		3.15E-01	5.59E-01			Unigene17899_All//8.00E-17//BM461060					
Unigene17901_All	320	8.67	0.32	3.00	12.76	7.75	5.08	10.31	0.78	6.35	-4.77E+00	1.87E-13	Down	-1.53E+00	2.23E-04	Down	-7.20E-01	1.14E-02		-1.33E+00	1.31E-05	Down	-3.72E+00	1.52E-16	Down	-6.99E-01	1.70E-02			Unigene17901_All//3.00E-171//TC175805					ESTscan +
Unigene17904_All	470	4.12	17.25	4.42	12.08	3.44	12.20	114.70	297.91	111.89	2.07E+00	1.04E-17	Up	1.01E-01	8.18E-01		-1.81E+00	4.84E-13	Down	1.44E-02	9.53E-01		1.38E+00	1.18E-204	Up	-3.58E-02	6.49E-01		Unigene17904_All//gi|19911211|dbj|BAB86932.1|//4.00E-60//glucosyltransferase-14 [Vigna angularis]	Unigene17904_All//7.00E-59//AT3G53160| UGT73C7 (UDP-glucosyl transferase 73C7); UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene17904_All//0.00E+00//TC162356	ko00908|Zeatin biosynthesis			nr -
Unigene17905_All	1034	0.00	0.29	0.00	7.47	4.10	18.34	549.11	115.56	138.47	8.20E+00	4.44E-02		null	null		-8.66E-01	7.54E-06		1.30E+00	1.39E-22	Up	-2.25E+00	0.00E+00	Down	-1.99E+00	0.00E+00	Down	Unigene17905_All//gi|28625017|emb|CAD66064.1|//8.00E-72//carbonic anhydrase [Lotus japonicus]	Unigene17905_All//5.00E-67//AT5G14740| CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding	Unigene17905_All//0.00E+00//TC155629	ko00910|Nitrogen metabolism			nr +
Unigene17906_All	263	14.72	9.25	7.09	20.83	15.84	18.20	67.68	22.25	19.69	-6.71E-01	3.06E-02		-1.05E+00	1.29E-03		-3.95E-01	1.23E-01		-1.95E-01	5.01E-01		-1.61E+00	2.42E-33	Down	-1.78E+00	1.02E-39	Down	Unigene17906_All//gi|195606082|gb|ACG24871.1|//3.00E-17//40S ribosomal protein S23 [Zea mays] >gi|195618728|gb|ACG33194.1| 40S ribosomal protein S23 [Zea mays] >gi|195619636|gb|ACG31648.1| 40S ribosomal protein S23 [Zea mays] >gi|195625318|gb|ACG34489.1| 40S ribosomal protein S23 [Zea mays] >gi|195628702|gb|ACG36181.1| 40S ribosomal protein S23 [Zea mays] >gi|195657679|gb|ACG48307.1| 40S ribosomal protein S23 [Zea mays]	Unigene17906_All//5.00E-15//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene17906_All//2.00E-113//gi|13246960|gb|BE053119.2|BE053119	ko03010|Ribosome			nr -
Unigene17912_All	1059	187.74	352.82	529.94	136.84	209.41	415.94	0.52	0.32	0.08	9.10E-01	1.13E-228		1.50E+00	0.00E+00	Up	6.14E-01	2.09E-82		1.60E+00	0.00E+00	Up	-7.17E-01	4.22E-01		-2.79E+00	7.96E-03		Unigene17912_All//gi|18461098|dbj|BAB84352.1|//1.00E-157//lipoxygenase [Citrus jambhiri]	Unigene17912_All//2.00E-137//AT3G45140| LOX2 (LIPOXYGENASE 2); lipoxygenase	Unigene17912_All//0.00E+00//TC134680	ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism			nr +
Unigene17913_All	638	0.16	0.16	0.00	4.22	1.73	1.49	15.77	6.35	10.62	-4.65E-02	9.89E-01		-7.36E+00	3.95E-01		-1.29E+00	4.00E-04	Down	-1.50E+00	1.38E-04	Down	-1.31E+00	2.15E-14	Down	-5.71E-01	2.53E-04			Unigene17913_All//0.00E+00//TC165252					
Unigene17914_All	356	46.74	216.77	111.29	238.30	290.09	360.80	103.09	120.22	89.64	2.21E+00	3.30E-178	Up	1.25E+00	5.10E-40	Up	2.84E-01	1.35E-09		5.98E-01	3.00E-41		2.22E-01	3.03E-03		-2.02E-01	1.15E-02		Unigene17914_All//gi|55419648|gb|AAV51937.1|//3.00E-32//AP2/EREBP transcription factor ERF-2 [Gossypium hirsutum]	Unigene17914_All//4.00E-06//AT3G16770| ATEBP (ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN); DNA binding / protein binding / transcription activator/ transcription factor	Unigene17914_All//1.00E-142//EX164257	AP2-EREBP			nr +
Unigene17915_All	597	18.40	10.61	14.18	9.76	7.21	5.22	15.23	8.40	4.74	-7.95E-01	4.06E-06		-3.76E-01	4.06E-02		-4.37E-01	7.19E-02		-9.03E-01	1.86E-04		-8.58E-01	5.78E-07		-1.68E+00	3.37E-19	Down	Unigene17915_All//gi|166863714|gb|AB201673.1|//4.00E-21//ADP-glucose pyrophosphorylase small subunit ADPGp-1 [Gossypium hirsutum]	Unigene17915_All//1.00E-21//AT5G48300| ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE 1); glucose-1-phosphate adenylyltransferase	Unigene17915_All//5.00E-168//TC163846		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene17919_All	350	25.71	9.12	7.76	43.84	33.75	49.29	95.92	39.17	33.12	-1.50E+00	7.49E-13	Down	-1.73E+00	5.76E-15	Down	-3.77E-01	5.77E-03		1.69E-01	2.71E-01		-1.29E+00	3.95E-45	Down	-1.53E+00	5.16E-60	Down	Unigene17919_All|gi|192908658|gb|ACF06432.1|//4.00E-15//ribosomal L28-like protein [Elaeis guineensis]	Unigene17919_All//8.00E-13//AT2G19730| 60S ribosomal protein L28 (RPL28A)	Unigene17919_All//2.00E-166//TC163958	ko03010|Ribosome			nr +
Unigene17920_All	442	13.02	40.47	21.57	5.75	14.57	4.80	0.00	0.00	0.18	1.64E+00	5.00E-28	Up	7.28E-01	1.60E-04		1.34E+00	4.87E-09	Up	-2.59E-01	5.66E-01		null	null		7.49E+00	4.05E-01		Unigene17920_All|gi|145332933|ref|NP_001078332.1|//2.00E-08//RTFL14 (ROTUNDIFOLIA LIKE 14) [Arabidopsis thaliana] >gi|42822061|tpg|BAA02285.1|TPA_exp: DVL14 [Arabidopsis thaliana]	Unigene17920_All//1.00E-09//AT3G63088| RTFL14 (ROTUNDIFOLIA LIKE 14)	Unigene17920_All//8.00E-154//DW499853				nr +
Unigene17921_All	499	188.84	224.10	202.86	366.67	332.41	271.52	191.07	108.47	40.24	2.47E-01	4.09E-07		1.03E-01	7.97E-02		-1.42E-01	8.44E-05		-4.33E-01	6.08E-33		-8.17E-01	4.12E-60		-2.25E+00	2.68E-284	Down	Unigene17921_All|gi|297835378|ref|XP_002885571.1|//9.00E-11//dienelactone hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331411|gb|EFH61830.1|dienelactone hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene17921_All//5.00E-11//AT3G23600| dienelactone hydrolase family protein	Unigene17921_All//0.00E+00//TC171208				nr +
Unigene17922_All	2435	0.34	0.08	0.00	0.45	0.44	0.26	2.19	12.80	12.14	-2.05E+00	1.68E-02		-8.43E+00	1.19E-04	Down	-3.80E-02	9.49E-01		-7.93E-01	2.34E-01		2.55E+00	7.49E-105	Up	2.47E+00	7.84E-98	Up	Unigene17922_All|gi|15231294|ref|NP_187969.1|//0.00E+00//calmodulin-binding family protein [Arabidopsis thaliana]	Unigene17922_All//2.00E-180//AT3G13600| calmodulin-binding family protein	Unigene17922_All//0.00E+00//TC156520				nr +
Unigene17923_All	529	1.09	0.57	0.00	0.19	0.85	1.71	1.36	1.66	1.81	-9.21E-01	3.43E-01		-1.01E+01	2.60E-03		2.17E+00	1.06E-01		3.18E+00	9.74E-04	Up	2.88E-01	6.58E-01		4.12E-01	5.18E-01		Unigene17923_All//gi|15221226|ref|NP_177580.1|//2.00E-41//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75169846|sp|Q9CA73.1|PP119_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At1g74400	Unigene17923_All//1.00E-42//AT1G74400| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene17926_All	1019	5.08	1.29	2.51	1.61	3.38	3.01	0.25	0.00	0.00	-1.98E+00	5.02E-11	Down	-1.02E+00	2.31E-04	Down	1.07E+00	9.95E-04	Up	9.02E-01	1.16E-02		-7.96E+00	4.04E-02		-7.96E+00	3.04E-02		Unigene17926_All|gi|224114479|ref|XP_002332364.1|//1.00E-121//GRAS family transcription factor [Populus trichocarpa] >gi|222874681|gb|EEF11812.1| GRAS family transcription factor [Populus trichocarpa]	Unigene17926_All//2.00E-78//AT4G37650| SHR (SHORT ROOT); protein binding / sequence-specific DNA binding / transcription factor	Unigene17926_All//0.00E+00//gi|164285084|gb|ES814639.1|ES814639	GRAS			nr -
Unigene17928_All	343	108.30	302.24	297.61	98.47	169.87	150.90	139.41	148.90	52.03	1.48E+00	6.28E-138	Up	1.46E+00	1.37E-129	Up	7.87E-01	1.76E-33		6.16E-01	8.25E-18		9.50E-02	2.19E-01		-1.42E+00	4.32E-76	Down	Unigene17928_All|gi|18417155|ref|NP_567802.1|//1.00E-12//wound-responsive protein-related [Arabidopsis thaliana] >gi|15215820|gb|AAK91455.1|AT4g28240/F26K10_120 [Arabidopsis thaliana]	Unigene17928_All//9.00E-13//AT4G28240| wound-responsive protein-related	Unigene17928_All//7.00E-166//gi|164345621|gb|EX169134.1|EX169134				nr +
Unigene17929_All	1752	0.15	0.58	0.15	1.11	0.96	1.57	23.77	16.32	10.07	1.95E+00	1.01E-02		2.59E-02	1.00E+00		-2.03E-01	6.79E-01		5.04E-01	2.10E-01		-5.43E-01	2.10E-13		-1.24E+00	8.29E-54	Down	Unigene17929_All|gi|224111880|ref|XP_002316010.1|//1.00E-170//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1|cytochrome P450 [Populus trichocarpa]	Unigene17929_All//4.00E-85//AT3G14630| CYP72A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene17929_All//0.00E+00//gi|48741823|gb|CO072342.1|CO072342		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr -
Unigene17930_All	459	687.01	270.79	456.74	106.25	98.05	89.64	1.11	2.82	1.65	-1.34E+00	0.00E+00	Down	-5.89E-01	4.02E-88		-1.16E-01	1.66E-01		-2.45E-01	1.27E-03		1.35E+00	1.28E-02		5.77E-01	4.12E-01		Unigene17930_All|gi|18400342|ref|NP_565556.1|//1.00E-23//YCF37 (Arabidopsis homolog of Synechocystis YCF37) [Arabidopsis thaliana] >gi|3152615|gb|AAC17094.1|expressed protein [Arabidopsis thaliana] >gi|16648702|gb|AAL25543.1|At2g23670/F26B6.32 [Arabidopsis thaliana] >gi|20197003|gb|AAM14867.1|expressed protein [Arabidopsis thaliana] >gi|20334912|gb|AAM16212.1|At2g23670/F26B6.32 [Arabidopsis thaliana] >gi|206748360|gb|ACI22363.1|YCF37-like protein [Arabidopsis thaliana]	Unigene17930_All//4.00E-16//AT2G23670| YCF37 (Arabidopsis homolog of Synechocystis YCF37)	Unigene17930_All//0.00E+00//TC158076				nr +

Unigene17931_All	2922	0.00	0.07	0.04	0.02	0.14	0.00	15.83	9.93	4.13	6.12E+00	1.37E-01		5.19E+00	3.99E-01		3.06E+00	5.68E-02		-4.09E+00	6.36E-01		-6.73E-01	2.31E-21		-1.94E+00	2.88E-114	Down	Unigene17931_All//gi|115435462|ref|NP_001042489.1|//1.00E-171//0s01g0229700 [Oryza sativa Japonica Group] >gi|113532020|dbj|BAF04403.1| Os01g0229700 [Oryza sativa Japonica Group]	Unigene17931_All//1.00E-63//AT3G06880| nucleotide binding					nr -
Unigene17932_All	341	9.51	7.43	6.40	8.62	4.95	4.64	68.81	30.15	23.02	-3.57E-01	3.20E-01		-5.71E-01	1.18E-01		-8.01E-01	2.04E-02		-8.95E-01	1.37E-02		-1.19E+00	4.82E-28	Down	-1.58E+00	4.76E-44	Down			Unigene17932_All//7.00E-166//gi|11199643|gb|BF268648.1|BF268648				
Unigene17934_All	1020	5.39	0.40	1.04	1.42	1.01	1.15	1.41	0.66	0.31	-3.76E+00	1.67E-22	Down	-2.37E+00	9.32E-14	Down	-4.84E-01	3.92E-01		-2.99E-01	6.38E-01		-1.10E+00	2.77E-02		-2.17E+00	6.89E-05	Down	Unigene17934_All//gi|224143055|ref|XP_002324836.1|//1.00E-112//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222866270|gb|EEF03401.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene17934_All//3.00E-62//AT1G62790| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene17934_All//0.00E+00//gi|78330146|gb|DT550420.1|DT550420		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene17936_All	601	3.83	6.66	2.84	5.55	3.84	2.40	1.13	0.35	0.20	7.98E-01	8.98E-03		-4.34E-01	3.41E-01		-5.33E-01	1.09E-01		-1.21E+00	3.75E-04	Down	-1.69E+00	4.19E-02		-2.50E+00	4.78E-03				Unigene17936_All//3.00E-123//DW498310				
Unigene17937_All	477	2.63	0.00	0.89	2.19	1.44	0.28	1.68	1.14	1.34	-1.14E+01	2.54E-07	Down	-1.56E+00	1.90E-02		-6.03E-01	3.67E-01		-2.95E+00	3.82E-04	Down	-5.64E-01	4.30E-01		-3.34E-01	6.19E-01		Unigene17937_All//gi|75191658|sp|Q9M9X9.1|PPR18_ARATH//1.00E-61//RecName: Full=Pentatricopeptide repeat-containing protein At1g06710, mitochondrial; Flags: Precursor >gi|7523709|gb|AAF63148.1|AC011001_18 Hypothetical protein [Arabidopsis thaliana]	Unigene17937_All//3.00E-63//AT1G06710| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene17940_All	760	0.14	0.67	0.56	1.31	0.86	1.43	30.54	91.24	106.20	2.28E+00	6.23E-02		2.03E+00	1.40E-01		-6.07E-01	3.81E-01		1.22E-01	8.66E-01		1.58E+00	1.71E-124	Up	1.80E+00	1.63E-177	Up	Unigene17940_All//gi|224111870|ref|XP_002316008.1|//2.00E-27//cytochrome P450 [Populus trichocarpa] >gi|222865048|gb|EEF02179.1| cytochrome P450 [Populus trichocarpa]	Unigene17940_All//8.00E-21//AT3G14630| CYP72A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene17940_All//0.00E+00//DT463377		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +
Unigene17941_All	670	0.23	0.00	0.32	1.86	2.06	1.62	3.28	0.44	1.72	-7.87E+00	2.16E-01		4.40E-01	7.75E-01		1.45E-01	8.22E-01		-2.00E-01	7.33E-01		-2.91E+00	3.84E-09	Down	-9.28E-01	1.26E-02		Unigene17941_All//gi|30693719|ref|NP_566973.2|//1.00E-17//KIPK (KCBP-interacting protein kinase); kinase/ protein binding / protein kinase [Arabidopsis thaliana] >gi|30693721|ref|NP_850687.1| KIPK (KCBP-interacting protein kinase); kinase/ protein binding / protein kinase [Arabidopsis thaliana] >gi|7529713|emb|CAB58893.1| protein kinase-like [Arabidopsis thaliana] >gi|21703143|gb|AAM74511.1| AT3g52890/F8J2_60 [Arabidopsis thaliana] >gi|25090422|gb|AAN72297.1| At3g52890/F8J2_60 [Arabidopsis thaliana]	Unigene17941_All//2.00E-19//AT2G36350| protein kinase, putative	Unigene17941_All//2.00E-32//gi|109855879|gb|DW484858.1|DW484858				nr +
Unigene17942_All	468	8.05	14.07	18.32	17.24	24.28	33.39	5.42	3.84	1.11	8.06E-01	4.53E-04		1.19E+00	1.96E-08	Up	4.94E-01	2.27E-03		9.53E-01	1.22E-11		-4.97E-01	1.73E-01		-2.29E+00	1.64E-08	Down	Unigene17942_All//gi|28416781|gb|AA042921.1|//9.00E-28//At4g16146 [Arabidopsis thaliana]	Unigene17942_All//5.00E-28//AT4G16146| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Lg106-like (InterPro:IPR012282); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G69510.3); Has 94 Blast hits to 94 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 94; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene17942_All//1.00E-180//DW498176				nr -
Unigene17943_All	514	88.66	41.40	34.81	150.51	142.43	168.09	261.33	129.78	100.84	-1.10E+00	9.81E-39	Down	-1.35E+00	1.96E-51	Down	-7.96E-02	2.49E-01		1.59E-01	5.83E-03		-1.01E+00	2.56E-120	Down	-1.37E+00	1.44E-201	Down	Unigene17943_All//gi|161377377|gb|ABX71676.1|//1.00E-29//60S ribosomal protein L6-like protein [Panax quinquefolius]	Unigene17943_All//7.00E-13//AT1G74060| 60S ribosomal protein L6 (RPL6B)	Unigene17943_All//0.00E+00//gi|109837325|gb|DW235886.1|DW235886		ko03010|Ribosome		nr +
Unigene17947_All	1244	0.00	0.45	0.00	0.00	0.17	0.00	6.53	18.45	153.08	8.81E+00	2.18E-03		null	null		7.38E+00	1.57E-01		null	null		1.50E+00	1.08E-38	Up	4.55E+00	0.00E+00	Up	Unigene17947_All//gi|15234693|ref|NP_193934.1|//1.00E-107//F-box family protein [Arabidopsis thaliana]	Unigene17947_All//4.00E-94//AT4G22030| F-box family protein	Unigene17947_All//0.00E+00//gi|78325351|gb|DT545625.1|DT545625				nr -
Unigene17948_All	354	15.22	39.79	23.47	11.96	26.36	21.56	2.15	0.71	1.58	1.39E+00	1.43E-17	Up	6.24E-01	2.78E-03		1.14E+00	3.87E-10	Up	8.50E-01	4.40E-05		-1.60E+00	3.70E-02		-4.48E-01	5.31E-01		Unigene17948_All//gi|87240373|gb|AB032231.1|//2.00E-31//Calcium-binding EF-hand [Medicago truncatula]	Unigene17948_All//1.00E-24//AT4G27280| calcium-binding EF hand family protein	Unigene17948_All//6.00E-43//TC152910				nr -
Unigene17795_All	1783	4.25	2.70	4.75	7.74	6.72	5.83	2.80	1.05	1.52	-6.56E-01	1.88E-03		1.58E-01	4.82E-01		-2.04E-01	2.17E-01		-4.10E-01	6.76E-03		-1.41E+00	2.68E-08	Down	-8.81E-01	1.61E-04		Unigene1795_All//gi|115465159|ref|NP_001056179.1|//1.00E-151//Os05g0540100 [Oryza sativa Japonica Group] >gi|62510701|sp|Q9SXQ6.1|FEN1A_ORYSJ RecName: Full=Flap endonuclease 1a; AltName: Full=OsFEN-1a >gi|4587225|dbj|BAA36171.1| FEN-1 [Oryza sativa Japonica Group] >gi|113579730|dbj|BAF18093.1| Os05g0540100 [Oryza sativa Japonica Group]	Unigene1795_All//3.00E-139//AT5G26680| endonuclease, putative	Unigene1795_All//0.00E+00//TC168917		ko03410|Base excision repair//ko03030|DNA replication//ko03450|Non-homologous end-joining		nr +
Unigene17950_All	397	3.03	13.53	4.16	5.02	4.86	8.99	66.78	95.59	74.96	2.16E+00	1.35E-12	Up	4.56E-01	3.96E-01		-4.72E-02	9.11E-01		8.40E-01	1.01E-02		5.18E-01	2.45E-11		1.67E-01	7.00E-02		Unigene17950_All//gi|224096760|ref|XP_002334672.1|//3.00E-28//cytochrome P450 [Populus trichocarpa] >gi|222874188|gb|EEF11319.1| cytochrome P450 [Populus trichocarpa]	Unigene17950_All//4.00E-21//AT2G45580| CYP76C3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene17950_All//1.00E-115//gi|48795523|gb|CO096837.1|CO096837		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +
Unigene17951_All	967	1.03	0.47	1.16	4.69	2.07	2.80	0.44	0.39	0.21	-1.12E+00	1.09E-01		1.70E-01	7.78E-01		-1.18E+00	9.00E-06	Down	-7.42E-01	8.27E-03		-1.69E-01	8.65E-01		-1.09E+00	2.82E-01		Unigene17951_All//gi|115446781|ref|NP_001047170.1|//2.00E-13//Os02g0566300 [Oryza sativa Japonica Group] >gi|113536701|dbj|BAF09084.1| Os02g0566300 [Oryza sativa Japonica Group]	Unigene17951_All//1.00E-13//AT3G25270| nucleic acid binding					nr -
Unigene17952_All	1764	0.00	0.00	0.00	0.17	0.00	0.10	43.05	10.66	5.13	null	null		null	null		-7.40E+00	2.02E-02		-7.26E-01	6.39E-01		-2.01E+00	3.77E-191	Down	-3.07E+00	0.00E+00	Down	Unigene17952_All//gi|226490390|dbj|BAH56488.1|//1.00E-180//polygalacturonase 1 [Prunus persica]	Unigene17952_All//1.00E-147//AT5G14650| polygalacturonase, putative / pectinase, putative	Unigene17952_All//2.00E-22//TC160646		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene17953_All	372	28.69	59.25	43.80	54.50	79.89	91.18	16.71	29.10	20.35	1.05E+00	1.21E-17	Up	6.10E-01	1.79E-05		5.52E-01	1.87E-09		7.42E-01	2.88E-16		8.01E-01	2.60E-07		2.84E-01	1.39E-01		Unigene17953_All//gi|46931230|gb|AAT06419.1|//2.00E-11//At1g55340 [Arabidopsis thaliana] >gi|48310451|gb|AAT41823.1| At1g55340 [Arabidopsis thaliana]	Unigene17953_All//2.00E-11//AT1G55340| unknown protein	Unigene17953_All//3.00E-119//TC132069				nr +
Unigene17957_All	503	2.70	2.82	6.25	8.32	6.09	1.44	2.61	0.50	0.79	6.06E-02	9.22E-01		1.21E+00	1.21E-03		-4.49E-01	1.31E-01		-2.53E+00	7.23E-13	Down	-2.39E+00	9.40E-05	Down	-1.72E+00	1.48E-03								
Unigene17960_All	362	14.02	7.84	14.56	24.36	16.36	6.24	0.23	0.00	0.00	-8.39E-01	1.62E-03		5.48E-02	8.43E-01		-5.74E-01	1.60E-03		-1.97E+00	1.53E-19	Down	-7.87E+00	4.01E-01		-7.87E+00	3.59E-01				Unigene17960_All//3.00E-85//TC153480				
Unigene17961_All	627	1.08	0.81	1.02	2.15	1.54	0.36	3.03	2.47	1.46	-4.25E-01	5.97E-01		-9.01E-02	9.22E-01		-4.80E-01	4.15E-01		-2.57E+00	1.41E-04	Down	-2.99E-01	5.16E-01		-1.05E+00	9.64E-03				Unigene17961_All//1.00E-70//DW236094				
Unigene17962_All	467	28.12	50.13	38.31	33.92	25.66	37.91	184.87	446.06	78.23	8.34E-01	4.87E-13		4.46E-01	1.05E-03		-4.03E-01	2.46E-03		1.60E-01	2.97E-01		1.27E+00	7.85E-269	Up	-1.24E+00	6.11E-111	Down	Unigene17962_All//gi|195640314|gb|ACG39625.1|//9.00E-33//phospholipid hydroperoxide glutathione peroxidase [Zea mays]	Unigene17962_All//3.00E-33//AT4G11600| ATGPX6 (GLUTATHIONE PEROXIDASE 6); glutathione peroxidase	Unigene17962_All//0.00E+00//gi|72282656|gb|DT053588.1|DT053588		ko00480|Glutathione metabolism//ko00590|Arachidonic acid metabolism		nr -
Unigene17964_All	1438	0.47	0.32	1.04	1.00	0.48	0.63	3.26	3.52	1.27	-5.77E-01	4.94E-01		1.13E+00	4.89E-02		-1.07E+00	4.31E-02		-6.78E-01	2.32E-01		1.08E-01	6.81E-01		-1.36E+00	9.58E-08	Down	Unigene17964_All//gi|255595753|ref|XP_002536384.1|//3.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223519886|gb|EEF25999.1| conserved hypothetical protein [Ricinus communis]		Unigene17964_All//0.00E+00//TC179345				nr -
Unigene17965_All	383	2.32	1.19	6.81	7.15	4.14	4.01	0.88	0.33	1.66	-9.64E-01	1.95E-01		1.55E+00	3.07E-04	Up	-7.91E-01	2.88E-02		-8.35E-01	2.79E-02		-1.43E+00	2.58E-01		9.14E-01	2.47E-01				Unigene17965_All//1.00E-32//ES848018				
Unigene17967_All	1261	0.00	0.72	0.00	19.67	17.29	9.31	7.21	5.00	4.80	9.50E+00	2.62E-05	Up	null	null		-1.87E-01	1.06E-01		-1.08E+00	2.23E-22	Down	-5.26E-01	2.00E-03		-5.86E-01	3.87E-04		Unigene17967_All//gi|297728401|ref|NP_001176564.1|//4.00E-91//Os11g0521000 [Oryza sativa Japonica Group] >gi|77551166|gb|ABA93963.1| GDSL-like Lipase/Acylhydrolase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255680130|dbj|BAH95292.1| Os11g0521000 [Oryza sativa Japonica Group]	Unigene17967_All//1.00E-69//AT1G28590| lipase, putative	Unigene17967_All//0.00E+00//TC161576				nr -
Unigene17974_All	1369	0.61	0.81	0.86	15.76	12.93	8.05	5.19	8.24	1.43	4.13E-01	5.26E-01		4.85E-01	4.47E-01		-2.85E-01	1.40E-02		-9.69E-01	1.91E-16		6.68E-01	9.30E-06		-1.86E+00	2.39E-17	Down	Unigene17974_All//gi|224115540|ref|XP_002317059.1|//1.00E-157//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222860124|gb|EEE97671.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene17974_All//8.00E-85//AT2G46770| EMB2301 (EMBRYO DEFECTIVE 2301); transcription activator/ transcription factor	Unigene17974_All//0.00E+00//gi|54120338|gb|CO495847.1|CO495847	NAC			nr -
Unigene17978_All	682	0.92	0.15	0.23	1.83	1.67	0.79	1.74	0.31	1.11	-2.63E+00	1.78E-02		-1.97E+00	6.50E-02		-1.32E-01	8.17E-01		-1.20E+00	5.16E-02		-2.50E+00	1.47E-04	Down	-6.45E-01	2.30E-01		Unigene17978_All//gi|164499139|gb|ABY59139.1|//3.00E-49//At3g03680 [Arabidopsis thaliana] >gi|164499153|gb|ABY59146.1| At3g03680 [Arabidopsis thaliana]	Unigene17978_All//4.00E-35//AT3G03680| C2 domain-containing protein	Unigene17978_All//2.00E-103//TC150401				nr -
Unigene17979_All	380	1.65	0.80	1.26	3.15	2.54	1.78	4.34	4.73	1.47	-1.05E+00	2.50E-01		-3.90E-01	6.46E-01		-3.10E-01	6.07E-01		-8.20E-01	1.99E-01		1.24E-01	7.80E-01		-1.56E+00	7.74E-04	Down	Unigene17979_All//gi|156972237|gb|ABR98947.1|//5.00E-23//dynein light chain [Lupinus albus]	Unigene17979_All//5.00E-23//AT4G15930| microtubule motor	Unigene17979_All//1.00E-62//CO112297				nr +
Unigene17980_All	497	1.68	1.22	2.36	1.60	1.04	0.27	3.91	5.72	11.22	-4.61E-01	5.43E-01		4.85E-01	4.47E-01		-6.26E-01	4.24E-01		-2.56E+00	6.01E-03		5.47E-01	1.06E-01		1.52E+00	1.91E-10	Up			Unigene17980_All//2.00E-16//TC179065				
Unigene17981_All	609	1.80	1.66	2.10	4.01	2.37	1.78	2.50	1.17	0.39	-1.17E-01	8.44E-01		2.18E-01	7.02E-01		-7.55E-01	5.22E-02		-1.17E+00	4.10E-03		-1.10E+00	2.32E-02		-2.67E+00	2.74E-06	Down	Unigene17981_All//gi|149392202|gb|ABR25951.1|//3.00E-07//heat- and acid-stable phosphoprotein [Oryza sativa Indica Group]		Unigene17981_All//1.00E-85//gi|109873630|gb|DW502605.1|DW502605				nr -

Unigene17983_All	318	9.38	1.75	3.68	21.46	9.75	22.30	8.91	4.99	4.64	-2.42E+00	2.44E-08	Down	-1.35E+00	5.59E-04	Down	-1.14E+00	6.06E-08	Down	5.52E-02	8.32E-01		-8.35E-01	1.20E-02		-9.43E-01	3.44E-03		Unigene17983_All//gi|90654201|gb|AB069575.1|//6.00E-12//mitochondrial import receptor-like protein [Nicotiana tabacum]	Unigene17983_All//2.00E-10//AT3G20000| TOM40; P-P-bond-hydrolysis-driven protein transmembrane transporter/ voltage-gated anion channel	Unigene17983_All//6.00E-160//TC132010				nr +
Unigene17984_All	641	0.98	0.63	1.08	2.64	1.34	1.27	2.11	0.33	1.18	-6.31E-01	4.75E-01		1.41E-01	8.60E-01		-9.76E-01	4.19E-02		-1.06E+00	3.78E-02		-2.69E+00	1.77E-05	Down	-8.38E-01	8.98E-02		Unigene17984_All//gi|225458161|ref|XP_002281008.1|//4.00E-41//PREDICTED: similar to tetrapyrrole methylase family protein [Vitis vinifera]	Unigene17984_All//7.00E-39//AT1G45110| tetrapyrrole methylase family protein	Unigene17984_All//2.00E-180//TC147319				nr +
Unigene17985_All	1313	22.47	414.23	210.53	9.86	11.49	14.52	0.42	0.06	0.06	4.20E+00	0.00E+00	Up	3.23E+00	0.00E+00	Up	2.20E-01	1.57E-01		5.57E-01	6.23E-06		-2.72E+00	1.22E-02		-2.79E+00	7.96E-03		Unigene17985_All//gi|15222901|ref|NP_177718.1|//1.00E-125//family II extracellular lipase 3 (EXL3) [Arabidopsis thaliana] >gi|75166254|sp|Q94CH6.1|EXL3_ARATH RecName: Full=GDSL esterase/lipase EXL3; AltName: Full=Family II extracellular lipase 3; Short=Family II lipase EXL3; Flags: Precursor >gi|15054386|gb|AAK30018.1| family II lipase EXL3 [Arabidopsis thaliana]	Unigene17985_All//2.00E-126//AT1G75900| family II extracellular lipase 3 (EXL3)	Unigene17985_All//0.00E+00//TC138369				nr -
Unigene17986_All	1331	0.12	0.00	0.24	0.30	0.21	0.00	4.29	1.88	2.78	-6.88E+00	2.16E-01		1.03E+00	4.71E-01		-5.32E-01	6.16E-01		-8.23E+00	1.11E-02		-1.19E+00	2.17E-07	Down	-6.24E-01	3.65E-03		Unigene17986_All//gi|15217948|ref|NP_176133.1|//1.00E-127//RXF12; endo-1,4-beta-xylanase/ hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|8979937|gb|AAF82251.1|AC008051_2 identical to gene RXF12 from Arabidopsis thaliana gb|AB008015 and contains three Cellulose binding PF|02018 domains and is a member of Glycosyl hydrolase PF|00331 family >gi|6566263|dbj|BAA88262.1| RXF12 [Arabidopsis thaliana] >gi|18181931|dbj|BAB83869.1| xylan endohydrolase [Arabidopsis thaliana]	Unigene17986_All//3.00E-128//AT1G68370| RXF12; endo-1,4-beta-xylanase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene17986_All//0.00E+00//TC177581				nr +
Unigene17989_All	638	2.05	3.10	0.00	4.53	4.21	2.12	1.86	1.70	0.75	5.95E-01	2.01E-01		-1.10E+01	3.71E-07	Down	-1.05E-01	8.17E-01		-1.09E+00	2.96E-03		-1.24E-01	8.25E-01		-1.31E+00	1.69E-02		Unigene17989_All//gi|18491247|gb|AAL69448.1|//3.00E-26//At2g44600/F16B22.9 [Arabidopsis thaliana]	Unigene17989_All//2.00E-23//AT2G44600| unknown protein	Unigene17989_All//6.00E-23//TC163309				nr +
Unigene1799_All	1707	66.73	30.99	66.82	42.46	31.09	40.22	6.98	34.18	55.20	-1.11E+00	6.28E-97	Down	2.00E-03	9.96E-01		-4.50E-01	6.23E-16		-7.84E-02	2.92E-01		2.29E+00	1.29E-172	Up	2.98E+00	0.00E+00	Up	Unigene1799_All//gi|297827173|ref|XP_002881469.1|//1.00E-159//don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297327308|gb|EFH57728.1| don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene1799_All//1.00E-150//AT2G36790| UGT73C6 (UDP-glucosyl transferase 73C6); UDP-glucosyltransferase/ UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene1799_All//0.00E+00//TC145149		ko00908|Zeatin biosynthesis		nr +
Unigene17991_All	350	2.39	8.11	5.17	4.84	6.10	6.19	2.90	4.30	4.33	1.76E+00	1.53E-05	Up	1.11E+00	3.00E-02		3.34E-01	5.11E-01		3.56E-01	4.64E-01		5.68E-01	2.50E-01		5.77E-01	2.20E-01			Unigene17991_All//4.00E-07//DT468925					
Unigene17995_All	399	2.49	6.10	8.27	3.37	3.28	3.96	0.74	0.21	0.30	1.29E+00	2.16E-03		1.73E+00	6.46E-06	Up	-3.96E-02	9.41E-01		2.33E-01	6.96E-01		-1.82E+00	2.11E-01		-1.31E+00	3.13E-01		Unigene17995_All//gi|224109720|ref|XP_002315289.1|//4.00E-16//global transcription factor group [Populus trichocarpa] >gi|222864329|gb|EEF01460.1| global transcription factor group [Populus trichocarpa]	Unigene17995_All//1.00E-08//AT3G52280| GTE6 (GENERAL TRANSCRIPTION FACTOR GROUP E6); DNA binding / H3/H4 histone acetyltransferase	Unigene17995_All//3.00E-51//CO070884				nr -
Unigene17997_All	816	0.58	2.17	0.00	3.85	2.53	1.77	1.81	1.02	0.83	1.91E+00	4.28E-04	Up	-9.17E+00	8.65E-03		-6.03E-01	7.71E-02		-1.12E+00	1.40E-03		-8.24E-01	9.30E-02		-1.13E+00	1.72E-02		Unigene17997_All//gi|42570641|ref|NP_973394.1|//9.00E-72//PDLP6 (PLASMODESMATA-LOCATED PROTEIN 6) [Arabidopsis thaliana]	Unigene17997_All//5.00E-73//AT2G01660| PDLP6 (PLASMODESMATA-LOCATED PROTEIN 6)	Unigene17997_All//3.00E-87//TC138285				nr +
Unigene17998_All	394	1.06	5.66	0.54	13.91	12.59	6.65	18.78	18.88	1.72	2.41E+00	2.46E-06	Up	-9.75E-01	4.12E-01		-1.44E-01	6.04E-01		-1.06E+00	2.43E-05	Down	7.90E-03	1.01E+00		-3.45E+00	1.78E-35	Down	Unigene17998_All//gi|226495823|ref|NP_001147508.1|//3.00E-09//hydrophobic protein LTI6B [Zea mays] >gi|195611860|gb|ACG27760.1| hydrophobic protein LTI6B [Zea mays]	Unigene17998_All//3.00E-06//AT3G05890| RCI2B (RARE-COLD-INDUCIBLE 2B)	Unigene17998_All//0.00E+00//TC163108				nr -
Unigene17999_All	724	0.65	0.07	0.00	0.83	0.48	0.87	2.22	7.91	1.87	-3.22E+00	2.73E-02		-9.35E+00	8.65E-03		-7.96E-01	3.88E-01		8.10E-02	9.45E-01		1.83E+00	2.30E-13	Up	-2.46E-01	6.20E-01		Unigene17999_All//gi|224082420|ref|XP_002306687.1|//1.00E-09//predicted protein [Populus trichocarpa] >gi|222856136|gb|EEE93683.1| predicted protein [Populus trichocarpa]						nr -
Unigene1800_All	2201	21.68	11.19	16.67	11.97	12.03	12.25	8.01	7.35	21.16	-9.54E-01	2.72E-32		-3.79E-01	1.57E-06		7.00E-03	9.60E-01		3.31E-02	7.90E-01		-1.24E-01	3.77E-01		1.40E+00	7.38E-72	Up	Unigene1800_All//gi|226425257|gb|AC053628.1|//0.00E+00//bHLH domain protein [Gossypium hirsutum]	Unigene1800_All//1.00E-129//AT4G17880| basic helix-loop-helix (bHLH) family protein	Unigene1800_All//0.00E+00//TC152010	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene18001_All	339	74.39	199.84	87.18	60.39	83.09	118.97	99.15	115.52	85.08	1.43E+00	2.19E-85	Up	2.29E-01	3.47E-02		4.60E-01	1.27E-06		9.78E-01	2.15E-30		2.21E-01	5.15E-03		-2.21E-01	7.94E-03		Unigene18001_All//gi|111038269|gb|AB803531.1|//1.00E-53//class II knotted-like homeobox protein [Prunus persica] >gi|215983122|gb|ACJ71731.1| class II knotted-like homeobox transcription factor [Prunus persica]	Unigene18001_All//4.00E-45//AT5G11060| KNAT4 (KNOTTED1-LIKE HOMEOBOX GENE 4); transcription activator/ transcription factor	Unigene18001_All//0.00E+00//gi|11201779|gb|BF270784.1|BF270784	HB			nr -
Unigene18003_All	812	2.64	8.67	9.71	0.37	0.51	0.67	7.65	12.15	23.40	1.72E+00	3.27E-12	Up	1.88E+00	9.62E-15	Up	4.67E-01	7.42E-01		8.59E-01	4.23E-01		6.66E-01	4.05E-05		1.61E+00	1.74E-36	Up	Unigene18003_All//gi|224139090|ref|XP_002326765.1|//1.00E-20//predicted protein [Populus trichocarpa] >gi|222834087|gb|EEE72564.1| predicted protein [Populus trichocarpa]		Unigene18003_All//3.00E-31//DW243014				nr +
Unigene18004_All	542	67.19	37.02	47.36	73.62	56.04	128.66	128.01	63.93	32.34	-8.60E-01	6.09E-21		-5.05E-01	3.04E-08		-3.94E-01	3.86E-07		8.05E-01	9.50E-38		-1.00E+00	1.07E-61	Down	-1.98E+00	1.45E-176	Down	Unigene18004_All//gi|115488728|ref|NP_001066851.1|//3.00E-26//Os12g0508300 [Oryza sativa Japonica Group] >gi|297722587|ref|NP_001173657.1| Os03g0773150 [Oryza sativa Japonica Group] >gi|113649358|dbj|BAF29870.1| Os12g0508300 [Oryza sativa Japonica Group] >gi|149391293|gb|ABR25664.1| 40S ribosomal protein S29 [Oryza sativa Indica Group] >gi|255674934|dbj|BAH92385.1| Os03g0773150 [Oryza sativa Japonica Group]	Unigene18004_All//7.00E-27//AT4G33865| 40S ribosomal protein S29 (RPS29C)	Unigene18004_All//0.00E+00//gi|13245301|gb|BE053032.2|BE053032		ko03010|Ribosome		nr +
Unigene18005_All	471	215.62	105.96	50.31	159.70	140.52	142.68	95.87	43.48	44.49	-1.02E+00	2.14E-76	Down	-2.10E+00	1.05E-213	Down	-1.85E-01	1.60E-03		-1.63E-01	9.32E-03		-1.14E+00	9.00E-50	Down	-1.11E+00	7.00E-49	Down		Unigene18005_All//2.00E-06//AT5G59970| histone H4	Unigene18005_All//0.00E+00//TC158380				kegg +
Unigene18008_All	935	6.49	0.92	7.75	4.16	4.49	2.27	0.00	0.00	0.09	-2.82E+00	3.75E-19	Down	2.55E-01	2.91E-01		1.13E-01	7.76E-01		-8.72E-01	4.49E-03		null	null		6.41E+00	4.05E-01		Unigene18008_All//gi|22452315|gb|AC089483.1|//1.00E-56//receptor-like kinase [Glycine max]	Unigene18008_All//6.00E-51//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene18008_All//6.00E-67//TC133874				nr +
Unigene18009_All	1562	0.00	0.13	0.10	0.06	0.04	0.17	30.80	7.63	5.38	7.02E+00	1.37E-01		6.68E+00	2.39E-01		-5.33E-01	8.17E-01		1.44E+00	4.09E-01		-2.01E+00	2.27E-121	Down	-2.52E+00	1.27E-164	Down	Unigene18009_All//gi|15225475|ref|NP_182067.1|//1.00E-100//DNA-binding protein-related [Arabidopsis thaliana] >gi|50198795|gb|AAT70431.1| At2g45430 [Arabidopsis thaliana] >gi|56121926|gb|AAV74244.1| At2g45430 [Arabidopsis thaliana] >gi|119657388|tpd|FAA00293.1| TPA: AT-hook motif nuclear localized protein 22 [Arabidopsis thaliana]	Unigene18009_All//1.00E-50//AT2G45430| DNA-binding protein-related	Unigene18009_All//5.00E-10//gi|48789593|gb|CO090907.1|CO090907				nr +
Unigene1801_All	1006	6.35	3.43	4.98	8.07	5.82	7.59	14.33	2.24	5.35	-8.90E-01	1.49E-04		-3.51E-01	1.62E-01		-4.72E-01	1.58E-02		-8.93E-02	6.89E-01		-2.68E+00	1.18E-51	Down	-1.42E+00	1.43E-23	Down	Unigene1801_All//gi|5725356|emb|CAA10382.2|//2.00E-89//alpha-D-xylosidase [Tropaeolum majus]	Unigene1801_All//1.00E-77//AT1G68560| XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Unigene1801_All//0.00E+00//TC152199		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr +
Unigene18010_All	700	0.60	0.14	1.22	1.00	1.97	1.29	5.44	2.57	2.79	-2.05E+00	1.21E-01		1.03E+00	2.04E-01		9.82E-01	9.11E-02		3.73E-01	6.26E-01		-1.08E+00	1.36E-04	Down	-9.63E-01	4.22E-04			Unigene18010_All//0.00E+00//TC155270					
Unigene18011_All	424	90.94	37.76	32.90	90.82	77.24	118.45	143.09	53.03	53.18	-1.27E+00	3.84E-41	Down	-1.47E+00	2.04E-49	Down	-2.34E-01	5.56E-03		3.83E-01	1.22E-07		-1.43E+00	1.30E-94	Down	-1.43E+00	5.94E-97	Down	Unigene18011_All//gi|255549179|ref|XP_002515644.1|//3.00E-17//60S ribosomal protein L44 [Ricinus communis] >gi|223545238|gb|EEF46746.1| 60S ribosomal protein L44 [Ricinus communis]	Unigene18011_All//3.00E-16//AT4G14320| 60S ribosomal protein L36a/L44 (RPL36aB)	Unigene18011_All//0.00E+00//gi|13353524|gb|BG443872.1|BG443872		ko03010|Ribosome		nr -
Unigene18012_All	674	3.80	8.87	9.32	11.01	22.99	22.51	0.00	0.00	0.00	1.22E+00	1.21E-06	Up	1.29E+00	3.51E-07	Up	1.06E+00	7.67E-15	Up	1.03E+00	8.23E-13	Up	null	null		null	null		Unigene18012_All//gi|83853809|gb|ABC47842.1|//1.00E-57//membrane protein-like protein [Glycine max]	Unigene18012_All//1.00E-39//AT2G25737| unknown protein	Unigene18012_All//0.00E+00//ES815271				nr +
Unigene18016_All	511	2.76	0.20	1.77	1.56	1.82	0.35	1.90	0.74	0.16	-3.80E+00	3.23E-06	Down	-6.42E-01	2.75E-01		2.22E-01	8.13E-01		-2.14E+00	1.54E-02		-1.37E+00	3.41E-02		-3.61E+00	2.14E-05	Down	Unigene18016_All//gi|683502|emb|CAA57528.1|//2.00E-40//protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]	Unigene18016_All//1.00E-41//AT3G25800| PP2AA2 (PROTEIN PHOSPHATASE 2A SUBUNIT A2); protein phosphatase type 2A regulator	Unigene18016_All//7.00E-59//TC131383				nr -
Unigene18019_All	764	20.54	23.28	15.61	137.45	104.03	98.60	124.52	72.32	53.14	1.80E-01	2.10E-01		-3.96E-01	7.44E-03		-4.02E-01	1.22E-18		-4.79E-01	6.36E-23		-7.84E-01	6.34E-56		-1.23E+00	2.79E-120	Down	Unigene18019_All//gi|974782|emb|CAA89019.1|//2.00E-27//cobalamine-independent methionine synthase [Solenostemon scutellarioides]	Unigene18019_All//1.00E-25//AT5G17920| ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase	Unigene18019_All//0.00E+00//gi|21097601|gb|BQ409914.1|BQ409914		ko00270|Cysteine and methionine metabolism		nr +
Unigene1802_All	1035	15.01	8.13	10.44	25.85	23.99	25.92	30.60	7.83	12.32	-8.86E-01	7.96E-10		-5.24E-01	3.57E-04		-1.08E-01	3.86E-01		4.10E-03	9.71E-01		-1.97E+00	1.39E-77	Down	-1.31E+00	5.96E-45	Down	Unigene1802_All//gi|5725356|emb|CAA10382.2|//1.00E-144//alpha-D-xylosidase [Tropaeolum majus]	Unigene1802_All//5.00E-132//AT1G68560| XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Unigene1802_All//0.00E+00//TC135325		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene18021_All	309	1.35	1.97	5.34	2.10	1.00	2.19	2.60	4.33	6.58	5.39E-01	5.63E-01		1.98E+00	8.06E-04	Up	-1.06E+00	2.26E-01		6.51E-02	9.50E-01		7.35E-01	1.60E-01		1.34E+00	9.75E-04	Up		Unigene18021_All//7.00E-138//TC139685					
Unigene18022_All	418	4.26	16.36	5.86	0.95	0.91	0.22	2.12	1.40	3.34	1.94E+00	6.05E-14	Up	4.62E-01	2.84E-01		-7.33E-02	9.26E-01		-2.14E+00	1.26E-01		-6.02E-01	3.85E-01		6.51E-01	1.87E-01			Unigene18022_All//5.00E-84//DR502777					
Unigene18024_All	600	4.62	1.69	3.64	19.43	13.43	14.75	4.79	4.25	4.18	-1.43E+00	2.37E-04	Down	-3.45E-01	3.95E-01		-5.33E-01	5.87E-04		-3.97E-01	1.82E-02		-1.73E-01	6.31E-01		-1.96E-01	5.84E-01								ESTscan +
Unigene18025_All	426	2.58	3.21	4.63	1.75	3.48	2.01	0.10	0.78	1.59	3.16E-01	5.98E-01		8.43E-01	8.11E-02		9.87E-01	7.54E-02		2.00E-01	7.89E-01		2.98E+00	5.73E-02		4.00E+00	4.29E-04	Up		Unigene18025_All//0.00E+00//gi|84165097|gb|DR453745.1|DR453745					

Unigene18026_All	383	42.62	33.07	23.64	60.09	57.99	74.53	237.12	130.19	98.82	-3.66E-01	8.69E-03		-8.51E-01	3.33E-09		-5.13E-02	7.34E-01		3.11E-01	2.26E-03		-8.65E-01	4.07E-63		-1.26E+00	6.66E-120	Down	Unigene18026_All//gi|225462164|ref|XP_002266780.1|//4.00E-67//PREDICTED: similar to elongation factor 2 [Vitis vinifera]	Unigene18026_All//2.00E-67//AT3G12915| GTP binding / GTPase	Unigene18026_All//0.00E+00//gi|164320211|gb|ES792326.1|ES792326				nr -
Unigene18027_All	781	3.01	21.67	11.52	3.32	4.41	4.28	0.43	0.48	0.46	2.85E+00	1.79E-52	Up	1.93E+00	2.02E-17	Up	4.11E-01	2.46E-01		3.68E-01	3.23E-01		1.53E-01	8.90E-01		8.41E-02	9.57E-01		Unigene18027_All//gi|124359471|gb|ABN65909.1|//1.00E-61//Peptidase S26A, signal peptidase I; AAA ATPase; Peptidase M, neutral zinc metallopeptidases, zinc-binding site; Peptidase M41, FtsH extracellular [Medicago truncatula]	Unigene18027_All//9.00E-52//AT5G15250| FTSH6 (FTSH PROTEASE 6); ATP-dependent peptidase/ ATPase/ metallopeptidase/ peptidase/ zinc ion binding					nr +
Unigene18028_All	401	16.31	12.89	25.36	213.29	178.19	88.64	0.21	0.31	0.00	-3.40E-01	1.51E-01		6.37E-01	6.08E-04		-2.59E-01	5.88E-07		-1.27E+00	4.78E-98	Down	5.68E-01	7.82E-01		-7.72E+00	3.59E-01					Unigene18028_All//2.00E-55//ES843168				ESTscan +
Unigene18031_All	698	0.00	0.00	0.00	5.99	1.73	0.84	66.99	15.09	5.54	null	null		null	null		-1.80E+00	1.27E-09	Down	-2.83E+00	1.79E-14	Down	-2.15E+00	2.46E-128	Down	-3.60E+00	4.06E-229	Down	Unigene18031_All//gi|182410392|gb|ACB88202.1|//7.00E-50//PR1 protein [Solanum lycopersicum]	Unigene18031_All//4.00E-42//AT4G33720| pathogenesis-related protein, putative	Unigene18031_All//0.00E+00//DW510800		ko04626|Plant-pathogen interaction		nr +
Unigene18032_All	407	3.09	3.49	0.00	2.33	3.89	8.66	0.00	0.00	0.00	1.76E-01	7.33E-01		-1.16E+01	7.11E-07	Down	7.43E-01	1.67E-01		1.90E+00	1.30E-07	Up	null	null		null	null		Unigene18032_All//gi|224125188|ref|XP_002329915.1|//3.00E-08//predicted protein [Populus trichocarpa] >gi|222871152|gb|EEF08283.1| predicted protein [Populus trichocarpa]						nr -
Unigene18033_All	710	5.67	1.43	1.05	3.23	3.20	8.46	0.00	0.12	0.00	-1.99E+00	8.05E-09	Down	-2.43E+00	1.51E-10	Down	-1.18E-02	9.62E-01		1.39E+00	2.57E-08	Up	6.88E+00	4.02E-01		null	null		Unigene18033_All//gi|224125188|ref|XP_002329915.1|//3.00E-21//predicted protein [Populus trichocarpa] >gi|222871152|gb|EEF08283.1| predicted protein [Populus trichocarpa]						nr +
Unigene18035_All	428	7.82	7.22	7.34	24.33	20.36	25.54	11.36	4.69	11.08	-1.16E-01	7.26E-01		-9.20E-02	7.91E-01		-2.57E-01	1.64E-01		7.01E-02	7.21E-01		-1.28E+00	4.25E-07	Down	-3.65E-02	8.99E-01					Unigene18035_All//3.00E-141//ES831747				
Unigene18039_All	1160	0.63	0.26	0.23	3.91	3.95	3.11	0.58	0.32	0.03	-1.27E+00	1.36E-01		-1.46E+00	1.12E-01		1.48E-02	9.67E-01		-3.27E-01	2.92E-01		-8.47E-01	2.88E-01		-4.09E+00	3.10E-04	Down	Unigene18039_All//gi|115434250|ref|NP_001041883.1|//8.00E-17//Os01g0123000 [Oryza sativa Japonica Group] >gi|113531414|dbj|BAF03797.1| Os01g0123000 [Oryza sativa Japonica Group]		Unigene18039_All//3.00E-63//ES812834				nr -
Unigene18043_All	586	2.14	2.59	0.55	6.46	6.64	2.08	0.94	0.14	0.14	2.76E-01	5.98E-01		-1.97E+00	4.63E-03		3.96E-02	9.22E-01		-1.63E+00	6.84E-07	Down	-2.72E+00	1.22E-02		-2.79E+00	7.96E-03		Unigene18043_All//gi|295815790|gb|AGG36380.1|//3.00E-50//promoter-binding protein SPL9 [Vitis vinifera]	Unigene18043_All//2.00E-13//AT2G42200| SPL9 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9); transcription factor	Unigene18043_All//0.00E+00//gi|78342369|gb|DT562643.1|DT562643	SBP			nr -
Unigene18044_All	837	117.27	47.95	71.32	29.88	37.77	27.95	0.05	0.00	0.00	-1.29E+00	1.45E-106	Down	-7.18E-01	3.79E-39		3.38E-01	2.03E-04		-9.61E-02	4.81E-01		-5.66E+00	6.58E-01		-5.66E+00	6.13E-01		Unigene18044_All//gi|75097110|sp|Q0461K.1|Y4115_ARATH//2.00E-25//RecName: Full=Uncharacterized protein At4g01150, chloroplastic; Flags: Precursor >gi|14488088|gb|AAK63864.1|AF38929_2_1 AT4g01150/F2N1_18 [Arabidopsis thaliana] >gi|2191138|gb|AAB61025.1| A_IG002N01.18 gene product [Arabidopsis thaliana] >gi|20147123|gb|AAM10278.1| AT4g01150/F2N1_18 [Arabidopsis thaliana]	Unigene18044_All//2.00E-27//AT4G01150| unknown protein	Unigene18044_All//5.00E-104//gi|164244746|gb|ES795246.1|ES795246				nr +
Unigene18046_All	679	1.08	0.45	1.02	0.15	0.10	2.06	1.56	5.48	0.00	-1.27E+00	1.36E-01		-8.16E-02	9.29E-01		-5.33E-01	8.17E-01		3.81E+00	2.63E-06	Up	1.82E+00	7.83E-09	Up	-1.06E+01	6.72E-08	Down	Unigene18046_All//gi|224138650|ref|XP_002322867.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222867497|gb|EEF04628.1| predicted protein [Populus trichocarpa]		Unigene18046_All//9.00E-19//TC179144				nr -
Unigene18047_All	634	6.02	2.32	4.79	2.20	1.52	1.92	0.00	0.00	0.13	-1.38E+00	2.56E-05	Down	-3.32E-01	3.38E-01		-5.33E-01	3.45E-01		-1.94E-01	7.27E-01		null	null		6.97E+00	4.05E-01		Unigene18047_All//gi|115473321|ref|NP_001060259.1|//4.00E-07//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene18047_All//5.00E-05//AT2G02650| reverse transcriptase-related	Unigene18047_All//3.00E-142//TC162319				nr -
Unigene18048_All	550	6.28	26.44	12.97	51.72	35.25	138.53	81.64	328.67	225.63	2.07E+00	2.17E-31	Up	1.05E+00	5.78E-06	Up	-5.53E-01	2.39E-09		1.42E+00	1.08E-102	Up	2.01E+00	0.00E+00	Up	1.47E+00	1.29E-203	Up	Unigene18048_All//gi|224111880|ref|XP_002316010.1|//2.00E-46//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene18048_All//2.00E-30//AT1G17060| CYP72C1 (CYTOCHROME P450 72C1); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene18048_All//1.00E-103//TC139537		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +
Unigene1805_All	390	0.40	0.78	0.00	0.64	1.24	0.69	2.17	0.86	0.20	9.54E-01	5.03E-01		-8.65E+00	2.45E-01		9.53E-01	4.24E-01		1.22E-01	9.44E-01		-1.34E+00	5.68E-02		-3.41E+00	1.35E-04	Down	Unigene1805_All//gi|115439477|ref|NP_001014018.1|//1.00E-15//Os01g0706700 [Oryza sativa Japonica Group] >gi|113533549|dbj|BAF05932.1| Os01g0706700 [Oryza sativa Japonica Group]	Unigene1805_All//1.00E-11//AT1G73020| unknown protein	Unigene1805_All//4.00E-60//TC161008				nr -
Unigene18051_All	528	38.15	34.07	71.00	67.17	75.72	189.81	63.10	55.57	75.68	-1.63E-01	2.22E-01		8.96E-01	3.49E-22		1.73E-01	5.00E-02		1.50E+00	5.36E-146	Up	-1.83E-01	3.88E-02		2.62E-01	4.41E-04		Unigene18051_All//gi|6983690|emb|CAB75356.1|//1.00E-49//AE9 stearoyl-ACP desaturase [Gossypium hirsutum]	Unigene18051_All//9.00E-27//AT2G43710| SSI2; acyl-[acyl-carrier-protein] desaturase/ stearoyl-CoA 9-desaturase	Unigene18051_All//7.00E-161//TC143831		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis		nr +
Unigene18054_All	410	61.64	26.20	39.35	17.25	14.36	18.62	1.65	0.61	0.00	-1.23E+00	4.19E-26	Down	-6.47E-01	6.86E-09		-2.65E-01	2.64E-01		1.10E-01	6.66E-01		-1.43E+00	7.84E-02		-1.07E+01	3.56E-05	Down	Unigene18054_All//gi|209973101|gb|ACJ03840.1|//2.00E-26//ADP-glucose pyrophosphorylase small subunit ADPGp-2 [Gossypium hirsutum]	Unigene18054_All//5.00E-17//AT5G48300| ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE 1); glucose-1-phosphate adenylyltransferase	Unigene18054_All//0.00E+00//TC163706		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene18055_All	797	5.05	2.03	3.34	1.25	1.08	0.45	0.00	0.00	0.10	-1.31E+00	3.13E-05	Down	-5.98E-01	6.12E-02		-2.11E-01	7.79E-01		-1.46E+00	4.18E-02		null	null		6.64E+00	4.05E-01		Unigene18055_All//gi|237682450|gb|ACR10272.1|//5.00E-46//sulfotransferase 5b [Brassica rapa subsp. pekinensis]	Unigene18055_All//2.00E-46//AT1G74100| SOT16 (SULFOTRANSFERASE 16); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene18055_All//8.00E-137//TC148002		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr -
Unigene18056_All	426	67.43	24.98	36.13	150.14	141.62	156.27	157.61	87.42	83.98	-1.43E+00	4.94E-37	Down	-9.00E-01	3.11E-17		-8.43E-02	2.75E-01		5.77E-02	4.76E-01		-8.50E-01	1.51E-45		-9.08E-01	2.83E-52		Unigene18056_All//gi|297829086|ref|XP_002882425.1|//1.00E-37//60S ribosomal protein L22-2 [Arabidopsis lyrata subsp. lyrata] >gi|297328265|gb|EFH58684.1| 60S ribosomal protein L22-2 [Arabidopsis lyrata subsp. lyrata]	Unigene18056_All//3.00E-23//AT3G05560| 60S ribosomal protein L22-2 (RPL22B)	Unigene18056_All//0.00E+00//TC152213		ko03010|Ribosome		nr +
Unigene18058_All	346	14.82	37.78	14.62	26.92	26.97	24.67	14.17	10.63	9.33	1.35E+00	9.48E-16	Up	-1.95E-02	9.64E-01		2.60E-03	9.97E-01		-1.26E-01	5.91E-01		-4.15E-01	9.60E-02		-6.04E-01	9.74E-03					Unigene18058_All//2.00E-150//gi|21103908|gb|BQ416221.1|BQ416221				
Unigene1806_All	2487	3.03	1.43	1.67	5.45	6.47	5.28	6.12	3.43	4.16	-1.09E+00	6.02E-07	Down	-8.59E-01	1.05E-04		2.47E-01	8.83E-02		-4.40E-02	8.02E-01		-8.36E-01	1.13E-10		-5.55E-01	8.00E-06		Unigene1806_All//gi|116831666|gb|AB628785.1|//0.00E+00//expressed protein [Arabidopsis thaliana]	Unigene1806_All//0.00E+00//AT1G73020| unknown protein	Unigene1806_All//0.00E+00//TC161008				nr +
Unigene18062_All	413	168.74	71.53	30.69	185.39	162.75	134.72	222.87	69.32	107.84	-1.24E+00	3.76E-71	Down	-2.46E+00	4.69E-178	Down	-1.88E-01	1.14E-03		-4.61E-01	9.96E-16		-1.68E+00	1.46E-181	Down	-1.05E+00	3.46E-90	Down	Unigene18062_All//gi|297826349|ref|XP_002881057.1|//2.00E-75//tubulin beta-7 chain [Arabidopsis lyrata subsp. lyrata] >gi|297326896|gb|EFH57316.1| tubulin beta-7 chain [Arabidopsis lyrata subsp. lyrata]	Unigene18062_All//1.00E-76//AT2G29550| TUB7; structural constituent of cytoskeleton	Unigene18062_All//0.00E+00//TC129600		ko04145|Phagosome		nr +
Unigene18063_All	571	4.86	1.77	11.38	3.75	1.93	5.06	0.96	0.15	0.42	-1.45E+00	2.37E-04	Down	1.23E+00	6.97E-07	Up	-9.59E-01	2.10E-02		4.32E-01	2.77E-01		-2.72E+00	1.22E-02		-1.20E+00	1.64E-01		Unigene18063_All//gi|255573965|ref|XP_002527900.1|//4.00E-08//enzyme inhibitor, putative [Ricinus communis] >gi|223532675|gb|EEF34457.1| enzyme inhibitor, putative [Ricinus communis]		Unigene18063_All//0.00E+00//TC157935				nr -
Unigene18066_All	503	5.30	25.59	6.67	5.94	6.78	9.61	1.43	2.49	1.35	2.27E+00	4.17E-31	Up	3.30E-01	3.79E-01		1.90E-01	6.11E-01		6.93E-01	1.13E-02		8.03E-01	1.39E-01		-8.59E-02	9.11E-01		Unigene18066_All//gi|225460967|ref|XP_002280046.1|//2.00E-34//PREDICTED: similar to Os12g0143100 [Vitis vinifera]	Unigene18066_All//6.00E-35//AT5G42300| UBL5 (UBIQUITIN-LIKE PROTEIN 5)	Unigene18066_All//0.00E+00//TC164960				nr +
Unigene18067_All	386	105.05	30.32	44.01	438.13	293.95	380.50	387.64	185.48	148.00	-1.79E+00	1.04E-71	Down	-1.26E+00	5.00E-41	Down	-5.76E-01	1.61E-57		-2.04E-01	9.55E-08		-1.06E+00	8.97E-146	Down	-1.39E+00	2.83E-228	Down	Unigene18067_All//gi|211905341|gb|ACJ11250.1|//5.00E-63//S-adenosyl-L-homocysteine hydrolase [Gossypium hirsutum]	Unigene18067_All//1.00E-59//AT4G13940| MEE58 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding	Unigene18067_All//0.00E+00//gi|13351744|gb|BG442092.1|BG442092		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr +
Unigene18069_All	360	3.63	2.25	0.00	2.49	4.50	3.26	2.23	0.93	1.77	-6.90E-01	2.32E-01		-1.18E+01	3.71E-07	Down	8.52E-01	1.06E-01		3.89E-01	5.80E-01		-1.26E+00	7.98E-02		-3.34E-01	6.19E-01		Unigene18069_All//gi|297848412|ref|XP_002892087.1|//7.00E-10//T25K16.10 [Arabidopsis lyrata subsp. lyrata] >gi|297337929|gb|EFH68346.1| T25K16.10 [Arabidopsis lyrata subsp. lyrata]		Unigene18069_All//4.00E-81//TC159633				nr +
Unigene18071_All	406	2.06	1.37	0.00	4.29	1.78	0.45	1.35	0.72	0.98	-5.87E-01	4.26E-01		-1.10E+01	1.19E-04	Down	-1.27E+00	7.23E-03		-3.27E+00	3.65E-07	Down	-9.10E-01	3.19E-01		-4.64E-01	5.97E-01									
Unigene18073_All	280	1.49	7.06	6.09	1.25	3.57	2.90	8.00	5.37	2.56	2.24E+00	2.78E-05	Up	2.03E+00	5.20E-04	Up	1.52E+00	3.74E-02		1.22E+00	1.40E-01		-5.75E-01	1.39E-01		-1.64E+00	3.26E-05	Down				Unigene18073_All//2.00E-144//DT469030				
Unigene18078_All	824	1.78	0.31	0.19	1.09	2.09	2.30	1.18	0.76	1.50	-2.53E+00	1.19E-04	Down	-3.20E+00	2.45E-05	Down	9.41E-01	6.16E-02		1.08E+00	2.47E-02		-6.33E-01	3.28E-01		3.45E-01	5.38E-01		Unigene18078_All//gi|15241467|ref|NP_196974.1|//2.00E-61//cinnamoyl-CoA reductase-related [Arabidopsis thaliana] >gi|7573319|emb|CAB87637.1| cinnamoyl CoA reductase-like protein [Arabidopsis thaliana]	Unigene18078_All//1.00E-62//AT5G14700| cinnamoyl-CoA reductase-related	Unigene18078_All//0.00E+00//TC147810		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene1808_All	1527	2.26	4.68	1.39	1.11	1.24	1.27	3.93	3.07	10.23	1.05E+00	2.82E-06	Up	-6.97E-01	4.49E-02		1.61E-01	7.95E-01		1.97E-01	6.75E-01		-3.59E-01	1.11E-01		1.38E+00	4.22E-24	Up	Unigene1808_All//gi|171921111|gb|ACB59209.1|//1.00E-123//group I formin [Brassica oleracea]	Unigene1808_All//1.00E-102//AT1G70140| ATFH8 (formin 8); actin binding / actin filament binding / profilin binding	Unigene1808_All//9.00E-24//TC149034				nr +
Unigene18081_All	564	3.06	0.81	2.27	1.06	1.77	1.52	0.45	0.74	0.28	-1.92E+00	4.67E-04	Down	-4.34E-01	3.93E-01		7.40E-01	3.10E-01		5.22E-01	5.23E-01		7.20E-01	5.07E-01		-6.71E-01	6.05E-01					Unigene18081_All//0.00E+00//BE053935				
Unigene18082_All	298	16.68	16.32	10.54	23.74	27.62	23.34	58.88	15.71	23.80	-3.12E-02	9.23E-01		-6.62E-01	1.87E-02		2.19E-01	3.31E-01		-2.44E-02	9.34E-01		-1.91E+00	1.33E-41	Down	-1.31E+00	3.87E-25	Down	Unigene18082_All//gi|1762945|gb|AAC49975.1|//3.00E-15//ORF; able to induce HR-like lesions [Nicotiana tabacum]	Unigene18082_All//6.00E-14//AT4G14420| lesion inducing protein-related	Unigene18082_All//3.00E-118//BQ402658				nr +
Unigene18084_All	426	3.07	2.74	2.75	0.35	1.37	2.65	3.18	1.57	1.12	-1.67E-01	7.57E-01		-1.59E-01	7.76E-01		1.97E+00	7.04E-02		2.92E+00	3.03E-04	Up	-1.02E+00	4.99E-02		-1.50E+00	3.72E-03					Unigene18084_All//3.00E-73//TC165866				
Unigene18085_All	1430	0.40	0.21	0.52	1.71	0.96	0.76	6.39	16.10	7.24	-9.21E-01	3.43E-01		3.73E-01	6.23E-01		-8.26E-01	3.28E-02		-1.17E+00	4.10E-03		1.33E+00	1.06E-32	Up	1.82E-01	2.86E-01		Unigene18085_All//gi|15226168|ref|NP_178215.1|//2.00E-30//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene18085_All//1.00E-31//AT2G01050| nucleic acid binding / zinc ion binding	Unigene18085_All//2.00E-104//BF277456				nr -
Unigene18086_All	418	1.13	0.48	5.48	4.41	1.73	2.49	1.92	1.20	4.96	-1.22E+00	2.72E-01		2.28E+00	7.35E-06	Up	-1.35E+00	3.22E-03		-8.27E-01	8.81E-02		-6.80E-01	3.53E-01		1.37E+00	6.87E-04	Up				Unigene18086_All//2.00E-12//DW508224				

Unigene18087_All	419	17.86	8.10	10.93	21.99	12.16	25.76	92.13	57.06	32.42	-1.14E+00	2.17E-07	Down	-7.08E-01	1.39E-03		-8.55E-01	1.01E-06		2.28E-01	2.35E-01		-6.91E-01	8.81E-19		-1.51E+00	4.25E-67	Down			Unigene18087_All//0.00E+00//gi|21089865|gb|BQ402190.1|BQ402190				
Unigene18089_All	1200	0.17	0.08	0.18	7.97	7.06	2.45	0.92	0.14	0.13	-1.05E+00	5.65E-01		2.54E-02	1.00E+00		-1.75E-01	4.09E-01		-1.70E+00	1.74E-17	Down	-2.72E+00	1.31E-04	Down	-2.79E+00	6.37E-05	Down	Unigene18089_All//gi|193870483|gb|ACF22898.1|//9.00E-27//At4g33740|[Arabidopsis thaliana]	Unigene18089_All//1.00E-26//AT2G22795| unknown protein	Unigene18089_All//2.00E-30//gi|164251773|gb|ES843804.1|ES843804		ko03040|Spliceosome		nr -
Unigene1809_All	2781	1.75	2.73	0.92	0.72	1.15	0.60	1.17	1.61	5.95	6.43E-01	2.32E-03		-9.29E-01	1.14E-03		6.85E-01	4.69E-02		-2.54E-01	6.35E-01		4.58E-01	7.97E-02		2.34E+00	9.55E-52	Up	Unigene1809_All//gi|171921111|gb|AC859209.1|//1.00E-138//group I formin [Brassica oleracea]	Unigene1809_All//3.00E-141//AT1G70140| ATFH8 (formin 8); actin binding / actin filament binding / profilin binding	Unigene1809_All//0.00E+00//gi|78330425|gb|DT550699.1|DT550699		ko03040|Spliceosome		nr -
Unigene18092_All	418	0.13	0.85	2.42	1.31	1.24	3.89	3.84	1.60	1.72	2.76E+00	9.60E-02		4.27E+00	1.19E-04	Up	-8.52E-02	9.07E-01		1.57E+00	3.98E-03		-1.26E+00	7.61E-03		-1.16E+00	1.02E-02				Unigene18092_All//1.00E-171//TC162323				
Unigene18093_All	1188	0.09	0.00	0.54	24.95	7.42	6.46	34.66	6.83	7.18	-6.46E+00	3.73E-01		2.61E+00	2.33E-02		-1.75E+00	1.80E-63	Down	-1.95E+00	6.68E-64	Down	-2.34E+00	8.75E-126	Down	-2.27E+00	8.08E-125	Down	Unigene18093_All//gi|31559526|dbj|BAC77521.1|//1.00E-172//cysteine proteinase [Glycine max] >gi|31559528|dbj|BAC77522.1| cysteine proteinase [Glycine max]	Unigene18093_All//3.00E-158//AT5G50260| cysteine proteinase, putative	Unigene18093_All//0.00E+00//TC131795				nr -
Unigene18094_All	1304	2.85	2.02	1.23	8.14	5.33	5.02	0.39	0.03	0.28	-4.96E-01	1.22E-01		-1.22E+00	3.40E-04	Down	-6.09E-01	1.73E-04		-6.96E-01	4.55E-05		-3.60E+00	5.77E-03		-5.01E-01	5.83E-01		Unigene18094_All//gi|15231703|ref|NP_191512.1|//1.00E-173//strictosidine synthase family protein [Arabidopsis thaliana] >gi|42572733|ref|NP_974462.1| strictosidine synthase family protein [Arabidopsis thaliana]	Unigene18094_All//4.00E-160//AT3G59530| strictosidine synthase family protein	Unigene18094_All//0.00E+00//TC137417		ko00901|Indole alkaloid biosynthesis		nr +
Unigene18095_All	440	5.83	2.19	3.75	8.60	3.76	5.23	0.96	1.52	0.00	-1.41E+00	5.96E-04	Down	-6.35E-01	1.30E-01		-1.20E+00	5.35E-05	Down	-7.17E-01	2.25E-02		6.61E-01	4.02E-01		-9.91E+00	2.14E-03				Unigene18095_All//1.00E-38//gi|78329315|gb|DT549589.1|DT549589				
Unigene18096_All	892	0.18	0.28	1.31	2.62	4.05	3.34	3.70	2.53	3.66	6.90E-01	6.27E-01		2.90E+00	4.34E-04	Up	6.27E-01	5.15E-02		3.48E-01	3.94E-01		-5.47E-01	7.66E-02		-1.36E-02	9.71E-01		Unigene18096_All//gi|224127726|ref|XP_002329162.1|//9.00E-61//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene18096_All//3.00E-50//AT4G12020| WRKY19; transcription factor	Unigene18096_All//6.00E-141//C0115409	WRKY			nr -
Unigene181_All	1529	9.41	19.59	14.07	14.11	11.15	13.71	30.47	47.84	55.76	1.06E+00	4.20E-24	Up	5.80E-01	1.90E-06		-3.40E-01	2.63E-03		-4.16E-02	7.64E-01		6.51E-01	2.31E-31		8.72E-01	2.22E-61		Unigene181_All//gi|225457017|ref|XP_002279079.1|//1.00E-129//PREDICTED: similar to ATPANK2 (PANTOTHENATE KINASE 2); pantothenate kinase [Vitis vinifera]	Unigene181_All//5.00E-125//AT4G32180| ATPANK2 (PANTOTHENATE KINASE 2); pantothenate kinase	Unigene181_All//0.00E+00//TC135571		ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene18100_All	1939	0.00	0.05	0.00	0.05	0.11	0.00	3.60	16.25	4.56	5.71E+00	3.87E-01		null	null		1.05E+00	6.12E-01		-5.68E+00	4.01E-01		2.18E+00	1.01E-87	Up	3.42E-01	4.71E-02		Unigene18100_All//gi|54290279|dbj|BAD61224.1|//1.00E-170//conserved transmembrane protein-like [Oryza sativa Japonica Group]	Unigene18100_All//8.00E-167//AT4G18540| unknown protein					nr +
Unigene18101_All	444	0.94	0.00	0.72	4.04	7.99	6.41	3.33	0.75	1.62	-9.88E+00	1.05E-02		-3.90E-01	7.17E-01		9.84E-01	1.97E-03		6.66E-01	7.97E-02		-2.15E+00	9.69E-05	Down	-1.05E+00	2.65E-02		Unigene18101_All//gi|2811226|gb|AAB97844.1|//2.00E-45//fimbrin 2 [Arabidopsis thaliana] >gi|2811232|gb|AAB97847.1| fimbrin 2 [Arabidopsis thaliana] >gi|8777376|dbj|BAA96966.1| fimbrin 2 [Arabidopsis thaliana]	Unigene18101_All//2.00E-46//AT5G48460| fimbrin-like protein, putative	Unigene18101_All//0.00E+00//TC165166				nr +
Unigene18103_All	316	2.65	14.27	9.44	6.46	3.92	4.72	13.38	12.96	22.06	2.43E+00	3.27E-12	Up	1.83E+00	8.61E-06	Up	-7.20E-01	9.93E-02		-4.55E-01	3.46E-01		-4.58E-02	8.81E-01		7.22E-01	1.83E-04		Unigene18103_All//gi|225463384|ref|XP_002271705.1|//3.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene18103_All//1.00E-65//AT5G46410| NLI interacting factor (NIF) family protein	Unigene18103_All//3.00E-32//TC167376				nr -
Unigene18104_All	1211	0.60	0.33	0.22	18.80	7.71	2.91	6.77	0.90	1.18	-8.54E-01	3.05E-01		-1.46E+00	1.12E-01		-1.29E+00	8.61E-31	Down	-2.69E+00	6.10E-73	Down	-2.92E+00	1.91E-32	Down	-2.52E+00	1.14E-28	Down	Unigene18104_All//gi|18403760|ref|NP_565797.1|//1.00E-124//EXL1 (EXORDIUM LIKE 1) [Arabidopsis thaliana] >gi|20197218|gb|AAC61821.2| Expressed protein [Arabidopsis thaliana]	Unigene18104_All//2.00E-109//AT2G35150| EXL1 (EXORDIUM LIKE 1)	Unigene18104_All//0.00E+00//TC143675				nr -
Unigene18105_All	752	1.04	1.55	1.35	1.66	1.51	1.32	3.43	1.22	0.42	5.70E-01	3.77E-01		3.67E-01	6.21E-01		-1.32E-01	8.17E-01		-3.26E-01	6.41E-01		-1.49E+00	5.35E-05	Down	-3.02E+00	2.15E-11	Down			Unigene18105_All//9.00E-07//ES808004				
Unigene18109_All	323	99.94	120.95	97.27	178.59	138.06	203.72	107.73	91.61	48.35	2.75E-01	1.52E-03		-3.92E-02	7.22E-01		-3.71E-01	4.39E-09		1.90E-01	4.12E-03		-2.34E-01	5.29E-03		-1.16E+00	1.67E-40	Down			Unigene18109_All//4.00E-161//TC138668				ESTscan -
Unigene1811_All	1730	10.10	6.80	13.27	10.94	8.52	7.96	4.67	3.04	1.91	-5.72E-01	1.52E-05		3.93E-01	9.50E-04		-3.61E-01	2.89E-03		-4.59E-01	2.25E-04		-6.17E-01	6.80E-04		-1.29E+00	8.53E-12	Down	Unigene1811_All//gi|108705664|gb|AB93459.1|//5.00E-53//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene1811_All//1.00E-97//AT5G46560| unknown protein	Unigene1811_All//0.00E+00//ES817727				nr +
Unigene18114_All	512	1.43	1.68	0.00	3.41	2.62	2.21	1.24	2.53	4.20	2.34E-01	7.28E-01		-1.05E+01	4.13E-04	Down	-3.77E-01	4.65E-01		-6.27E-01	2.22E-01		1.03E+00	5.33E-02		1.76E+00	2.14E-05	Up			Unigene18114_All//5.00E-131//DW501891				ESTscan -
Unigene18115_All	299	12.77	17.62	14.60	11.66	12.78	13.75	54.44	33.83	23.72	4.64E-01	7.74E-02		1.93E-01	5.54E-01		1.33E-01	7.39E-01		2.37E-01	4.86E-01		-6.87E-01	2.63E-08		-1.20E+00	1.57E-20	Down			Unigene18115_All//3.00E-143//gi|21091803|gb|BQ404116.1|BQ404116				
Unigene1812_All	1212	25.94	17.94	20.34	18.62	13.15	12.71	15.63	5.52	5.29	-5.33E-01	2.80E-08		-3.51E-01	4.63E-04		-5.01E-01	2.19E-06		-5.51E-01	8.05E-07		-1.50E+00	3.15E-32	Down	-1.56E+00	3.78E-35	Down	Unigene1812_All//gi|75333830|sp|Q9FH04.1|ADHL7_ARATH//1.00E-111//RecName: Full=Alcohol dehydrogenase-like 7 >gi|10177010|dbj|BAB10198.1| alcohol dehydrogenase [Arabidopsis thaliana] >gi|19698971|gb|AAL91221.1| alcohol dehydrogenase [Arabidopsis thaliana] >gi|22136298|gb|AAM91227.1| alcohol dehydrogenase [Arabidopsis thaliana]	Unigene1812_All//2.00E-101//AT5G42250| alcohol dehydrogenase, putative	Unigene1812_All//0.00E+00//gi|109826538|gb|DW225251.1|DW225251		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr -
Unigene18120_All	737	0.85	1.58	0.00	7.50	9.67	2.33	1.55	0.91	0.59	8.92E-01	1.56E-01		-9.73E+00	1.41E-03		3.66E-01	1.05E-01		-1.69E+00	3.27E-10	Down	-7.71E-01	1.81E-01		-1.38E+00	1.42E-02									
Unigene18123_All	618	0.85	0.49	0.17	0.64	0.22	1.75	0.96	3.38	1.48	-7.83E-01	4.22E-01		-2.30E+00	6.77E-02		-1.53E+00	2.06E-01		1.44E+00	3.84E-02		1.82E+00	2.66E-05	Up	6.30E-01	3.24E-01		Unigene18123_All//gi|15226168|ref|NP_178215.1|//9.00E-10//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene18123_All//2.00E-11//AT2G01050| nucleic acid binding / zinc ion binding					nr -
Unigene18124_All	307	94.93	28.06	26.71	120.07	92.99	115.48	155.07	54.87	77.34	-1.76E+00	2.33E-50	Down	-1.83E+00	3.11E-51	Down	-3.69E-01	6.11E-06		-5.62E-02	6.40E-01		-1.50E+00	1.32E-79	Down	-1.00E+00	6.00E-44	Down	Unigene18124_All//gi|1173256|sp|P46299.1|RS4_GOSHI//5.00E-53//RecName: Full=40S ribosomal protein S4 >gi|498739|emb|CAA55882.1| ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene18124_All//4.00E-39//AT5G58420| 40S ribosomal protein S4 (RPS4D)	Unigene18124_All//4.00E-173//TC133120		ko03010|Ribosome		nr -
Unigene18125_All	590	24.65	17.43	26.90	29.55	28.42	27.33	29.88	36.06	75.83	-5.00E-01	6.51E-04		1.26E-01	4.31E-01		-5.61E-02	7.50E-01		-1.13E-01	4.78E-01		2.71E-01	1.35E-02		1.34E+00	8.04E-65	Up	Unigene18125_All//gi|183848854|gb|ACC63895.1|//1.00E-107//MAP kinase [Gossypium raimondii]	Unigene18125_All//2.00E-104//AT3G14720| ATMPK19; MAP kinase	Unigene18125_All//0.00E+00//gi|78330530|gb|DT550804.1|DT550804		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene18126_All	2098	0.05	0.00	0.20	0.19	0.00	0.00	22.27	30.72	222.11	-5.64E+00	3.73E-01		2.03E+00	1.40E-01		-7.57E+00	4.39E-03		-7.57E+00	1.11E-02		4.64E-01	1.92E-15		3.32E+00	0.00E+00	Up	Unigene18126_All//gi|2501025|sp|Q43716.1|SYK_SOLLC//0.00E+00//RecName: Full=Lysyl-tRNA synthetase; AltName: Full=Lysine--tRNA ligase; Short=LysRS >gi|11475883|emb|CAA64223.1| Lysyl-tRNA synthetase [Solanum lycopersicum]	Unigene18126_All//0.00E+00//AT3G11710| ATKRS-1 (ARABIDOPSIS THALIANA LYSYL-TRNA SYNTHETASE 1); ATP binding / aminoacyl-tRNA ligase/ lysine-tRNA ligase/ nucleic acid binding / nucleotide binding	Unigene18126_All//0.00E+00//TC166126		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene18127_All	1472	0.25	1.03	0.29	2.44	1.26	0.89	4.48	0.48	0.27	2.05E+00	6.90E-04	Up	2.18E-01	8.31E-01		-9.48E-01	1.82E-03		-1.45E+00	1.24E-05	Down	-3.21E+00	9.03E-29	Down	-4.05E+00	6.13E-36	Down								
Unigene18129_All	524	0.60	2.80	2.74	2.19	1.58	1.90	1.21	0.64	0.38	2.23E+00	4.29E-04	Up	2.20E+00	8.73E-04	Up	-4.71E-01	4.64E-01		-2.06E-01	7.39E-01		-9.24E-01	2.63E-01		-1.67E+00	4.29E-02		Unigene18129_All//gi|53370641|gb|AU89136.1|//5.00E-08//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene18129_All//3.00E-07//AT3G09510| nucleic acid binding	Unigene18129_All//7.00E-90//gi|78333787|gb|DT554061.1|DT554061				nr -
Unigene1813_All	1529	21.76	18.72	16.40	17.01	12.27	10.01	14.21	5.63	4.46	-2.17E-01	2.50E-02		-4.08E-01	2.27E-05		-4.71E-01	1.56E-06		-7.64E-01	2.39E-13		-1.34E+00	5.27E-31	Down	-1.67E+00	2.57E-44	Down	Unigene1813_All//gi|75333830|sp|Q9FH04.1|ADHL7_ARATH//1.00E-168//RecName: Full=Alcohol dehydrogenase-like 7 >gi|10177010|dbj|BAB10198.1| alcohol dehydrogenase [Arabidopsis thaliana] >gi|19698971|gb|AAL91221.1| alcohol dehydrogenase [Arabidopsis thaliana] >gi|22136298|gb|AAM91227.1| alcohol dehydrogenase [Arabidopsis thaliana]	Unigene1813_All//1.00E-159//AT5G42250| alcohol dehydrogenase, putative	Unigene1813_All//0.00E+00//gi|78341133|gb|DT561407.1|DT561407		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr -
Unigene18132_All	451	1.39	8.31	2.01	3.87	5.80	7.31	0.66	0.56	0.27	2.58E+00	6.25E-11	Up	5.28E-01	4.79E-01		5.86E-01	1.45E-01		9.19E-01	7.24E-03		-2.39E-01	8.40E-01		-1.31E+00	3.13E-01		Unigene18132_All//gi|15238923|ref|NP_199044.1|//2.00E-25//transcription activator-related [Arabidopsis thaliana] >gi|45752626|gb|AAS76211.1| At5g42290 [Arabidopsis thaliana] >gi|52218820|gb|AAU29480.1| At5g42290 [Arabidopsis thaliana]	Unigene18132_All//2.00E-25//AT5G42290| transcription activator-related					nr -
Unigene18133_All	765	0.68	0.53	0.90	10.35	6.71	4.55	7.02	10.11	9.01	-3.68E-01	6.83E-01		4.04E-01	6.09E-01		-6.26E-01	1.14E-03		-1.19E+00	1.03E-08	Down	5.26E-01	4.95E-03		3.60E-01	6.93E-02		Unigene18133_All//gi|224122332|ref|XP_002330597.1|//2.00E-08//predicted protein [Populus trichocarpa] >gi|222872155|gb|EEF09286.1| predicted protein [Populus trichocarpa]						nr -
Unigene18135_All	836	0.25	0.24	0.00	2.62	6.63	3.57	9.86	4.80	6.24	-4.63E-02	9.89E-01		-7.97E+00	1.46E-01		1.34E+00	8.02E-08	Up	4.44E-01	2.50E-01		-1.04E+00	1.71E-08	Down	-6.60E-01	1.59E-04		Unigene18135_All//gi|144925056|gb|ABP03854.1|//6.00E-79//Longin-like [Medicago truncatula]	Unigene18135_All//6.00E-73//AT4G37150| ATVAMP711 (ARABIDOPSIS THALIANA VESICLE-ASSOCIATED MEMBRANE PROTEIN 711)	Unigene18135_All//6.00E-76//DW504159		ko04130|SNARE interactions in vesicular transport		nr +
Unigene18136_All	319	6.56	3.49	2.34	11.87	8.20	4.53	1.33	0.52	1.12	-9.09E-01	4.11E-02		-1.49E+00	2.21E-03		-5.33E-01	8.42E-02		-1.39E+00	1.44E-05	Down	-1.34E+00	2.24E-01		-2.38E-01	7.88E-01				Unigene18136_All//7.00E-55//DW513049				
Unigene18137_All	870	0.54	0.29	3.00	1.83	1.42	1.87	1.12	0.67	0.18	-8.94E-01	3.89E-01		2.47E+00	3.62E-07	Up	-3.63E-01	5.18E-01		2.85E-02	9.53E-01		-7.33E-01	2.48E-01		-2.61E+00	3.35E-04	Down	Unigene18137_All//gi|295815790|gb|ADG36380.1|//2.00E-31//promoter-binding protein SPL9 [Vitis vinifera]	Unigene18137_All//2.00E-21//AT2G42200| SPL9 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9); transcription factor	Unigene18137_All//0.00E+00//gi|78351672|gb|DT571946.1|DT571946	SBP			nr +
Unigene18138_All	971	1.24	0.83	0.44	10.26	9.08	3.53	0.26	0.17	1.15	-5.70E-01	3.65E-01		-1.50E+00	2.71E-02		-1.77E-01	3.91E-01		-1.54E+00	9.36E-16	Down	-6.02E-01	6.48E-01		2.14E+00	7.62E-04	Up			Unigene18138_All//2.00E-17//DR459020				ESTscan +
Unigene18139_All	644	2.19	0.16	1.57	5.11	1.82	1.40	0.72	1.17	0.62	-3.80E+00	3.23E-06	Down	-4.82E-01	3.97E-01		-1.49E+00	5.64E-06	Down	-1.86E+00	3.73E-07	Down	6.94E-01	3.66E-01		-2.23E-01	7.90E-01		Unigene18139_All//gi|114384141|gb|AB173972.1|//2.00E-61//transcription factor MYB36 [Glycine max]	Unigene18139_All//3.00E-59//AT5G57620| MYB36 (myb domain protein 36); DNA binding / transcription factor	Unigene18139_All//2.00E-19//NP524476	MYB			nr +
Unigene1814_All	387	3.38	0.26	2.06	5.79	5.87	6.42	4.92	0.00	3.71	-3.69E+00	1.09E-05	Down	-7.12E-01	2.42E-01		1.99E-02	9.74E-01		1.48E-01	7.27E-01		-1.23E+01	1.81E-13	Down	-4.08E-01	3.33E-01				Unigene1814_All//3.00E-82//TC157735				
Unigene18140_All	465	7.20	12.31	4.70	10.28	9.92	10.00	6.36	2.25	5.83	7.74E-01	1.86E-03		-6.17E-01	8.28E-02		-5.15E-02	8.59E-01		-3.99E-02	9.08E-01		-1.50E+00	1.09E-05	Down	-1.28E-01	6.92E-01				Unigene18140_All//3.00E-110//TC151451				
Unigene18141_All	523	8.80	20.44	16.90	23.24	32.07	25.82	0.16	0.32	0.15	1.22E+00	3.57E-11	Up	9.41E-01	3.60E-06		4.64E-01	3.05E-04		1.52E-01	3.98E-01		9.83E-01	6.34E-01		-8.64E-02	9.72E-01				Unigene18141_All//7.00E-22//DR519451				
Unigene18143_All	901	0.75	0.45	0.47	1.05	0.99	0.80	29.38	52.65	14.55	-7.47E-01	3.80E-01		-6.75E-01	4.41E-01		-8.02E-02	8.94E-01		-3.89E-01	6.28E-01		8.42E-01	7.58E-32		-1.01E+00	3.06E-25	Down	Unigene18143_All//gi|65998365|gb|AAS73001.2|//4.00E-43//dirigent-like protein [Gossypium barbadense]	Unigene18143_All//2.00E-37//AT3G21110| disease resistance-responsive family protein	Unigene18143_All//2.00E-14//ES791694				nr -
Unigene18145_All	268	5.86	14.18	4.17	8.36	6.94	6.57	31.87	36.65	25.42	1.28E+00	9.00E-05	Up	-4.89E-01	3.92E-01		-2.70E-01	5.54E-01		-3.48E-01	4.57E-01		2.02E-01	2.65E-01		-3.26E-01	6.40E-02				Unigene18145_All//4.00E-68//TC155685				
Unigene18146_All	1078	0.34	0.47	0.40	20.24	5.62	2.64	0.00	0.00	0.00	4.68E-01	6.11E-01		2.18E-01	8.31E-01		-1.85E+00	1.58E-50	Down	-2.94E+00	9.03E-77	Down	null	null		null	null		Unigene18146_All//gi|75174963|sp|Q9LNG5.1|PPP7L_ARATH//2.00E-23//RecName: Full=Serine/threonine-protein phosphatase 7 long form homolog >gi|8778513|gb|AAF79521.1|AC023673.9 F21D18.16 [Arabidopsis thaliana]	Unigene18146_All//4.00E-26//AT1G17930| unknown protein					nr -

Unigene18147_All	432	1.45	0.82	2.34	2.88	1.20	3.03	3.72	0.87	3.23	-8.24E-01	3.75E-01		6.88E-01	3.42E-01		-1.27E+00	2.92E-02		7.27E-02	9.24E-01		-2.09E+00	5.87E-05	Down	-2.04E-01	6.42E-01		Unigene18147_All//gi|268053527|gb|ACY92425.1|//5.00E-21//exportin-1 [Solanum lycopersicum]	Unigene18147_All//7.00E-20//AT5G17020| XPO1A; protein binding / protein transporter/ receptor				GO:0000904//GO:0004871//GO:0005488//GO:0005635//GO:0006605//GO:0009856//GO:0022857//GO:0022892//GO:0031224//GO:0048229	nr +
Unigene18148_All	385	9.11	1.71	9.27	7.50	3.49	3.99	1.54	0.43	0.62	-2.41E+00	1.20E-09	Down	2.54E-02	9.57E-01		-1.11E+00	1.41E-03		-9.12E-01	1.29E-02		-1.82E+00	4.72E-02		-1.31E+00	1.15E-01		Unigene18148_All//gi|15242697|ref|NP_201134.1|//1.00E-25//coproporphyrinogen oxidase-related [Arabidopsis thaliana] >gi|10177310|dbj|BAB10571.1| oxygen-independent coproporphyrinogen-like protein [Arabidopsis thaliana] >gi|115311487|gb|ABI93924.1| At5g63290 [Arabidopsis thaliana]	Unigene18148_All//8.00E-27//AT5G63290| coproporphyrinogen oxidase-related			ko00860|Porphyrin and chlorophyll metabolism	GO:0005737//GO:0006778//GO:0016634//GO:0043231//GO:0051540	nr -
Unigene18149_All	1806	0.58	1.43	1.36	0.41	0.97	1.05	1.40	2.64	6.09	1.30E+00	1.34E-03		1.23E+00	4.53E-03		1.23E+00	1.31E-02		1.34E+00	5.78E-03		9.09E-01	2.31E-04		2.12E+00	1.19E-30	Up	Unigene18149_All//gi|13377502|gb|AK20740.1|//1.00E-115//LR633 [Triticum aestivum]	Unigene18149_All//2.00E-96//AT1G66920| serine/threonine protein kinase, putative	Unigene18149_All//0.00E+00//DT462272		ko04626|Plant-pathogen interaction		nr -
Unigene1815_All	824	1.84	2.46	1.49	1.03	1.55	0.77	5.59	1.37	3.82	4.18E-01	3.77E-01		-3.09E-01	5.99E-01		5.89E-01	3.55E-01		-4.22E-01	6.18E-01		-2.03E+00	2.12E-12	Down	-5.50E-01	2.35E-02				Unigene1815_All//0.00E+00//gi|11206302|gb|BF275232.1|BF275232				
Unigene18150_All	530	1.28	2.68	1.71	4.23	4.94	2.81	5.74	15.77	4.51	1.06E+00	6.14E-02		4.12E-01	5.94E-01		2.23E-01	6.04E-01		-5.89E-01	1.85E-01		1.46E+00	5.06E-14	Up	-3.49E-01	2.77E-01				Unigene18150_All//6.00E-07//TC171858				
Unigene18151_All	507	14.34	9.69	22.79	11.00	4.14	0.89	1.67	0.00	0.00	-5.65E-01	9.07E-03		6.68E-01	1.10E-04		-1.41E+00	5.14E-09	Down	-3.63E+00	4.47E-24	Down	-1.07E+01	4.39E-06	Down	-1.07E+01	2.21E-06	Down							
Unigene18153_All	820	1.15	1.54	0.26	4.68	2.14	2.26	1.03	0.31	0.39	4.28E-01	4.74E-01		-2.14E+00	1.16E-02		-1.13E+00	1.18E-04	Down	-1.05E+00	7.07E-04	Down	-1.75E+00	1.64E-02		-1.41E+00	3.70E-02		Unigene18153_All//gi|18423810|ref|NP_568834.1|//2.00E-78//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|30696669|ref|NP_851197.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene18153_All//2.00E-70//AT5G35970| zinc finger (C3HC4-type RING finger) family protein	Unigene18153_All//4.00E-123//TC173249			GO:0044464//GO:0046914	nr -
Unigene18155_All	863	0.73	4.64	2.34	5.54	14.64	8.06	0.64	0.58	0.78	2.67E+00	4.60E-12	Up	1.69E+00	8.47E-04	Up	1.40E+00	1.59E-18	Up	5.40E-01	1.57E-02		-1.32E-01	8.80E-01		3.01E-01	6.71E-01		Unigene18155_All//gi|222635925|gb|EEE66057.1|//2.00E-02//hypothetical protein Osj_22054 [Oryza sativa Japonica Group]		Unigene18155_All//9.00E-35//CO115808				nr -
Unigene18159_All	920	4.04	3.80	9.03	0.70	1.01	0.49	0.00	0.00	0.00	-8.75E-02	7.78E-01		1.16E+00	6.11E-08	Up	5.22E-01	5.25E-01		-5.20E-01	5.88E-01		null	null		null	null		Unigene18159_All//gi|134252244|gb|AB064854.1|//2.00E-70//methionine-R-sulfoxide reductase B1 protein [Capsicum annuum]	Unigene18159_All//2.00E-64//AT4G21860| MSRB2 (methionine sulfoxide reductase B 2); peptide-methionine-(S)-S-oxide reductase	Unigene18159_All//1.00E-108//gi|48796540|gb|CO097854.1|CO097854			GO:0006950//GO:0008152//GO:0009532//GO:0016671	nr +
Unigene1816_All	693	2.34	4.39	5.30	2.23	2.39	1.56	0.85	0.90	1.26	9.06E-01	1.16E-02		1.18E+00	5.30E-04	Up	9.81E-02	8.68E-01		-5.11E-01	3.72E-01		8.30E-02	9.32E-01		5.66E-01	3.85E-01				Unigene1816_All//3.00E-74//FL577098				
Unigene18160_All	1053	8.05	7.55	22.76	0.57	0.36	0.13	0.00	0.00	0.00	-9.15E-02	6.57E-01		1.50E+00	5.67E-32	Up	-6.58E-01	4.78E-01		-2.14E+00	4.39E-02		null	null		null	null		Unigene18160_All//gi|154000865|gb|ABS37001.1|//1.00E-70//phototropin-2 [Solanum lycopersicum]	Unigene18160_All//1.00E-62//AT5G58140| PHOT2 (PHOTOTROPIN 2); FMN binding / blue light photoreceptor/ kinase/ protein serine/threonine kinase	Unigene18160_All//0.00E+00//TC152542		ko04712|Circadian rhythm - plant	GO:0000166//GO:0004674//GO:0005515//GO:0006468//GO:0009416//GO:0009606//GO:0009658//GO:0009881//GO:0010360//GO:0016020//GO:0023060//GO:0043231	nr +
Unigene18162_All	337	31.21	13.23	4.42	19.66	12.06	8.44	42.15	15.63	15.01	-1.24E+00	2.35E-11	Down	-2.82E+00	1.96E-31	Down	-7.05E-01	9.08E-04		-1.22E+00	1.11E-07	Down	-1.43E+00	9.78E-23	Down	-1.49E+00	7.85E-25	Down			Unigene18162_All//1.00E-71//TC136052				
Unigene18164_All	868	0.12	0.12	0.37	0.63	0.95	1.35	3.99	2.31	0.23	-4.74E-02	9.89E-01		1.61E+00	3.05E-01		5.93E-01	4.93E-01		1.10E+00	9.17E-02		-7.89E-01	7.48E-03		-4.12E+00	2.15E-19	Down	Unigene18164_All//gi|71043507|dbj|BAE16174.1|//1.00E-77//polyamine oxidase [Nicotiana tabacum]	Unigene18164_All//1.00E-63//AT5G13700| ATPAO1 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 1); FAD binding / polyamine oxidase	Unigene18164_All//3.00E-93//TC159959			GO:0008152//GO:0016647//GO:0031410	nr +
Unigene18167_All	296	23.86	85.08	43.18	55.54	80.04	70.03	59.14	92.63	62.32	1.83E+00	6.96E-46	Up	8.56E-01	1.96E-07		5.27E-01	4.35E-07		3.35E-01	6.05E-03		6.47E-01	3.53E-12		7.56E-02	5.87E-01		Unigene18167_All//gi|15425733|dbj|BAB64344.1|//2.00E-31//EIN3-like protein [Cucumis melo]	Unigene18167_All//7.00E-23//AT3G20770| EIN3 (ETHYLENE-INSENSITIVE3); transcription factor	Unigene18167_All//2.00E-159//gi|164282440|gb|ES815287.1|ES815287	EIL			nr +
Unigene18168_All	746	1.26	3.46	1.78	0.93	4.62	4.00	0.45	0.22	0.05	1.46E+00	4.25E-04	Up	4.99E-01	3.93E-01		2.30E+00	6.12E-10	Up	2.10E+00	2.41E-07	Up	-1.02E+00	4.00E-01		-3.09E+00	3.92E-02		Unigene18168_All//gi|224139280|ref|XP_002323035.1|//4.00E-33//predicted protein [Populus trichocarpa] >gi|222867665|gb|EEF04796.1| predicted protein [Populus trichocarpa]						nr -
Unigene18169_All	587	2.14	148.04	40.37	2.29	4.81	4.39	1.22	0.71	0.41	6.11E+00	0.00E+00	Up	4.24E+00	2.78E-101	Up	1.07E+00	3.51E-03		9.37E-01	1.87E-02		-7.82E-01	3.10E-01		-1.59E+00	3.62E-02		Unigene18169_All//gi|15219811|ref|NP_176873.1|//8.00E-14//ZFP6 (ZINC FINGER PROTEIN 6); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|27923892|sp|Q39265.1|ZFP6_ARATH RecName: Full=Zinc finger protein 6 >gi|9755451|gb|AAF98212.1|AC007152_8 zinc finger protein zep6 [Arabidopsis thaliana] >gi|790683|gb|AAA87302.1| zinc finger protein [Arabidopsis thaliana] >gi|15215717|gb|AAK91404.1| At1g67030/F1019_5 [Arabidopsis thaliana] >gi|20147413|gb|AAM10416.1| At1g67030/F1019_5 [Arabidopsis thaliana]	Unigene18169_All//3.00E-13//AT1G67030| ZFP6 (ZINC FINGER PROTEIN 6); nucleic acid binding / transcription factor/ zinc ion binding		C2H2		GO:0005622	nr -
Unigene1817_All	796	3.02	1.27	1.07	6.20	9.56	5.50	4.89	1.37	2.75	-1.25E+00	2.94E-03		-1.50E+00	8.47E-04	Down	6.26E-01	1.99E-03		-1.71E-01	6.03E-01		-1.84E+00	2.22E-09	Down	-8.28E-01	1.97E-03				Unigene1817_All//3.00E-68//TC157735				
Unigene18171_All	516	0.00	0.29	1.03	1.93	1.60	4.29	4.02	5.27	0.85	8.20E+00	2.35E-01		1.00E+01	4.04E-03		-2.70E-01	7.00E-01		1.15E+00	8.64E-03		3.91E-01	2.77E-01		-2.24E+00	6.30E-07	Down	Unigene18171_All//gi|14253163|emb|CAC39319.1|//2.00E-07//YMP4 protein [Volvox carteri f. nagariensis]				ko04626|Plant-pathogen interaction//ko03040|Spliceosome		nr -
Unigene18172_All	920	2.22	0.33	0.23	2.38	2.13	2.41	6.71	1.68	1.34	-2.75E+00	1.06E-06	Down	-3.26E+00	2.37E-07	Down	-1.59E-01	7.48E-01		1.39E-02	9.75E-01		-2.00E+00	4.99E-16	Down	-2.32E+00	7.18E-20	Down	Unigene18172_All//gi|224093923|ref|XP_002310048.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222852951|gb|EEE90498.1| predicted protein [Populus trichocarpa]		Unigene18172_All//0.00E+00//BE053521				nr -
Unigene18173_All	272	56.36	62.22	125.29	56.41	68.49	118.72	0.00	0.00	0.29	1.43E-01	3.50E-01		1.15E+00	2.50E-30	Up	2.80E-01	3.05E-02		1.07E+00	2.21E-28	Up	null	null		8.19E+00	4.05E-01		Unigene18173_All//gi|213876486|gb|ACJ54281.1|//7.00E-29//lipoxygenase [Camellia sinensis]	Unigene18173_All//1.00E-14//AT3G45140| LOX2 (LIPOXYGENASE 2); lipoxygenase	Unigene18173_All//2.00E-147//TC149425		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0006633//GO:0016702//GO:0046914	nr +
Unigene18175_All	530	1.88	4.59	0.30	11.65	2.53	3.24	0.88	0.63	0.60	1.29E+00	2.16E-03		-2.64E+00	2.71E-03		-2.20E+00	2.83E-18	Down	-1.85E+00	8.71E-13	Down	-4.76E-01	6.60E-01		-5.45E-01	5.66E-01				Unigene18175_All//2.00E-127//gi|109874105|gb|DW503080.1|DW503080				
Unigene18176_All	433	0.24	0.00	0.00	8.63	2.86	2.82	2.25	0.97	1.47	-7.92E+00	3.73E-01		-7.92E+00	3.95E-01		-1.59E+00	2.35E-07	Down	-1.62E+00	1.05E-06	Down	-1.22E+00	5.68E-02		-6.09E-01	3.16E-01		Unigene18176_All//gi|255557669|ref|XP_002519864.1|//6.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223540910|gb|EEF42468.1| conserved hypothetical protein [Ricinus communis]		Unigene18176_All//4.00E-60//gi|21097632|gb|BQ409945.1|BQ409945				nr +
Unigene1818_All	1821	15.40	62.55	19.62	40.84	37.67	63.89	67.24	301.89	367.25	2.02E+00	3.34E-234	Up	3.50E-01	1.77E-04		-1.17E-01	7.13E-02		6.46E-01	9.78E-43		2.17E+00	0.00E+00	Up	2.45E+00	0.00E+00	Up	Unigene1818_All//gi|224103363|ref|XP_002334060.1|//1.00E-180//cytochrome P450 [Populus trichocarpa] >gi|222869629|gb|EEF06760.1| cytochrome P450 [Populus trichocarpa]	Unigene1818_All//2.00E-124//AT4G37370| CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene1818_All//0.00E+00//TC133718		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene18180_All	379	26.92	10.70	13.21	49.68	47.79	49.81	64.03	15.44	29.54	-1.33E+00	2.85E-12	Down	-1.03E+00	5.57E-08	Down	-5.60E-02	7.39E-01		3.70E-03	9.79E-01		-2.05E+00	4.67E-63	Down	-1.12E+00	5.14E-27	Down	Unigene18180_All//gi|297810925|ref|XP_002873346.1|//3.00E-30//ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319183|gb|EFH49605.1| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene18180_All//4.00E-26//AT5G08180| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	Unigene18180_All//4.00E-155//gi|164303846|gb|ES808562.1|ES808562			GO:0005488//GO:0022613//GO:0031981//GO:0032991	nr -
Unigene18181_All	901	1.10	0.34	1.54	2.10	2.75	2.61	2.67	1.16	0.40	-1.71E+00	2.09E-02		4.78E-01	4.06E-01		3.89E-01	3.80E-01		3.11E-01	5.02E-01		-1.21E+00	1.19E-03		-2.75E+00	8.51E-10	Down	Unigene18181_All//gi|22330953|ref|NP_187629.2|//7.00E-65//kinesin motor protein-related [Arabidopsis thaliana]	Unigene18181_All//2.00E-41//AT3G10180| kinesin motor protein-related				GO:0000166//GO:0003774//GO:0009987//GO:0015630	nr -
Unigene18183_All	1144	1.42	0.71	1.26	1.57	2.35	1.26	2.99	2.74	1.18	-1.00E+00	5.37E-02		-1.74E-01	7.29E-01		5.83E-01	1.40E-01		-3.11E-01	5.66E-01		-1.28E-01	6.93E-01		-1.34E+00	8.81E-06	Down	Unigene18183_All//gi|224125406|ref|XP_002319578.1|//3.00E-39//predicted protein [Populus trichocarpa] >gi|222857954|gb|EEE95501.1| predicted protein [Populus trichocarpa]	Unigene18183_All//9.00E-07//AT2G32910| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61910.3); Has 954 Blast hits to 804 proteins in 137 species: Archae - 0; Bacteria - 69; Metazoa - 446; Fungi - 64; Plants - 191; Viruses - 0; Other Eukaryotes - 184 (source: NCBI BLink).	Unigene18183_All//0.00E+00//TC138778				nr +
Unigene18184_All	676	0.77	0.08	0.08	7.59	5.04	4.54	3.63	1.11	1.83	-3.37E+00	1.58E-02		-3.30E+00	2.40E-02		-5.90E-01	1.96E-02		-7.40E-01	4.55E-03		-1.70E+00	1.20E-05	Down	-9.90E-01	4.75E-03		Unigene18184_All//gi|224119654|ref|XP_002331213.1|//3.00E-37//SAUR family protein [Populus trichocarpa] >gi|222873334|gb|EEF10465.1| SAUR family protein [Populus trichocarpa]	Unigene18184_All//9.00E-29//AT1G72430| auxin-responsive protein-related	Unigene18184_All//0.00E+00//TC141673			GO:0005515//GO:0009755//GO:0043231	nr +
Unigene18185_All	710	1.25	4.57	1.58	0.70	0.87	0.00	1.61	1.41	0.22	1.87E+00	1.15E-06	Up	3.30E-01	6.40E-01		3.15E-01	7.84E-01		-9.45E+00	2.98E-03		-1.87E-01	7.39E-01		-2.84E+00	3.60E-05	Down	Unigene18185_All//gi|164604830|dbj|BAF98467.1|//2.00E-71//cytochrome P450 [Coptis japonica var. dissecta]	Unigene18185_All//1.00E-43//AT4G37370| CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene18185_All//7.00E-23//TC157347		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016709	nr +
Unigene18186_All	317	24.26	12.79	6.72	35.99	24.22	32.20	69.22	29.01	18.47	-9.24E-01	1.31E-05		-1.85E+00	4.22E-14	Down	-5.71E-01	2.54E-04		-1.60E-01	4.12E-01		-1.25E+00	1.76E-28	Down	-1.91E+00	2.01E-53	Down			Unigene18186_All//8.00E-144//TC137522				

Unigene18187_All	737	1.35	0.55	0.00	4.26	5.05	2.51	4.53	0.23	1.41	-1.29E+00	6.74E-02		-1.04E+01	1.77E-05	Down	2.45E-01	5.16E-01		-7.61E-01	3.01E-02		-4.32E+00	1.38E-18	Down	-1.69E+00	1.29E-07	Down	Unigene18187_All//gi|115451511|ref|NP_001049356.1|//3.00E-64//Os03g0212600 [Oryza sativa Japonica Group] >gi|108706817|gb|ABF94612.1| Targeting protein for Xklp2 containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547827|dbj|BAF11270.1| Os03g0212600 [Oryza sativa Japonica Group]	Unigene18187_All//3.00E-73//AT5G15510| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01015.1); Has 992 Blast hits to 819 proteins in 107 species: Archae - 0; Bacteria - 11; Metazoa - 477; Fungi - 40; Plants - 169; Viruses - 3; Other Eukaryotes - 292 (source: NCBI BLink).					nr +
Unigene1819_All	2379	3.63	1.75	2.60	6.01	5.05	3.57	7.43	3.27	3.95	-1.06E+00	1.65E-07	Down	-4.83E-01	1.96E-02		-2.51E-01	1.03E-01		-7.52E-01	1.97E-07		-1.18E+00	3.63E-21	Down	-9.11E-01	1.75E-14		Unigene1819_All//gi|2191167|gb|AAB61053.1|//1.00E-79//Hypothetical protein F2P16.18 [Arabidopsis thaliana]	Unigene1819_All//3.00E-35//AT3G05750| unknown protein	Unigene1819_All//0.00E+00//TC164831				nr -
Unigene18190_All	922	1.19	4.73	2.43	0.27	0.30	0.10	2.75	2.09	0.95	1.99E+00	2.16E-09	Up	1.03E+00	2.31E-02		1.46E-01	9.62E-01		-1.46E+00	4.07E-01		-4.00E-01	2.85E-01		-1.53E+00	2.53E-05	Down	Unigene18190_All//gi|72255633|gb|AA266951.1|//3.00E-87//117M18_32 [Brassica rapa]	Unigene18190_All//4.00E-86//AT5G10530| lectin protein kinase, putative	Unigene18190_All//0.00E+00//TC159627		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004713//GO:0006464//GO:0030246//GO:0032559	nr -
Unigene18191_All	587	3.03	0.35	2.90	13.83	10.85	7.62	77.79	33.89	20.90	-3.13E+00	1.20E-06	Down	-6.21E-02	9.06E-01		-3.50E-01	8.66E-02		-8.61E-01	1.59E-05		-1.20E+00	2.13E-54	Down	-1.90E+00	1.55E-109	Down	Unigene18191_All//gi|74273314|gb|AB401325.1|//1.00E-53//VDR66 [Gossypium hirsutum] >gi|83356301|gb|ABC16635.1| bet v1 [Gossypium hirsutum]	Unigene18191_All//3.00E-41//AT1G70830| MLP28 (MLP-LIKE PROTEIN 28)	Unigene18191_All//6.00E-177//EX168667			GO:0006950//GO:0009536	nr -
Unigene18192_All	553	0.09	0.00	0.29	1.44	1.68	2.53	27.91	3.25	1.87	-6.56E+00	6.13E-01		1.61E+00	5.11E-01		2.22E-01	8.13E-01		8.13E-01	1.67E-01		-3.10E+00	2.52E-64	Down	-3.90E+00	5.45E-81	Down	Unigene18192_All//gi|74273314|gb|AB401325.1|//1.00E-71//VDR66 [Gossypium hirsutum] >gi|83356301|gb|ABC16635.1| bet v1 [Gossypium hirsutum]	Unigene18192_All//6.00E-48//AT1G70830| MLP28 (MLP-LIKE PROTEIN 28)	Unigene18192_All//4.00E-178//EX168667			GO:0006950//GO:0009536	nr -
Unigene18194_All	418	25.03	18.79	21.02	39.09	33.36	26.36	128.86	50.69	48.42	-4.14E-01	2.02E-02		-2.52E-01	2.01E-01		-2.28E-01	1.12E-01		-5.68E-01	2.20E-05		-1.35E+00	1.41E-76	Down	-1.41E+00	9.58E-85	Down	Unigene18194_All//gi|6446577|gb|AAD39534.2|//5.00E-13//cellulose synthase catalytic subunit [Gossypium hirsutum]	Unigene18194_All//3.00E-12//AT5G05170| CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene18194_All//0.00E+00//TC162053			GO:0009250//GO:0016759//GO:0031224//GO:0045229//GO:0046914	nr -
Unigene18198_All	658	1.83	0.69	0.16	2.04	4.13	1.85	3.53	1.46	1.39	-1.40E+00	2.81E-02		-3.50E+00	8.78E-05	Down	1.02E+00	6.73E-03		-1.41E-01	8.01E-01		-1.27E+00	8.52E-04	Down	-1.34E+00	3.20E-04	Down	Unigene18198_All//gi|217426816|gb|ACK44524.1|//1.00E-21//AT5G10010-like protein [Arabidopsis arenosa]	Unigene18198_All//2.00E-22//AT5G10010| unknown protein	Unigene18198_All//0.00E+00//TC172687			GO:0031981	nr -
Unigene18199_All	1919	0.22	0.13	0.28	0.16	0.48	0.28	48.47	20.82	22.90	-7.25E-01	5.26E-01		3.48E-01	7.06E-01		1.64E+00	3.35E-02		8.58E-01	4.23E-01		-1.22E+00	5.43E-113	Down	-1.08E+00	4.56E-96	Down	Unigene18199_All//gi|38636547|dbj|BAD02939.1|//0.00E+00//high-affinity nitrate transporter [Prunus persica] >gi|88673347|dbj|BAD22821.1| nitrate transporter [Prunus persica]	Unigene18199_All//0.00E+00//AT1G08090| AINRT2;1 (NITRATE TRANSPORTER 2;1); nitrate transmembrane transporter	Unigene18199_All//1.00E-38//CB074791			GO:0006810//GO:0044464	nr -
Unigene18200_All	502	18.86	19.18	15.27	43.07	47.88	34.55	1.94	0.08	0.71	2.37E-02	9.18E-01		-3.05E-01	1.39E-01		1.53E-01	2.24E-01		-3.18E-01	7.68E-03		-4.54E+00	6.92E-06	Down	-1.44E+00	2.09E-02		Unigene18200_All//gi|21615415|emb|CAD32927.1|//4.00E-40/nitrate transporter [Cicer arietinum]	Unigene18200_All//6.00E-15//AT3G26690| nitrate transporter (NTP2)	Unigene18200_All//0.00E+00//TC170563			GO:0006950//GO:0009719//GO:0015833//GO:0031224	nr -
Unigene18202_All	578	3.71	0.79	2.12	2.07	0.83	1.88	0.15	0.07	0.62	-2.23E+00	1.05E-05	Down	-8.09E-01	7.86E-02		-1.31E+00	2.84E-02		-1.41E-01	8.16E-01		-1.02E+00	7.25E-01		2.08E+00	1.01E-01		Unigene18202_All//gi|30682358|ref|NP_850050.1|//3.00E-77//serine carboxypeptidase S28 family protein [Arabidopsis thaliana] >gi|16648801|gb|AAL25591.1| At2g24280/F27D4.19 [Arabidopsis thaliana] >gi|22655366|gb|AAM98275.1| At2g24280/F27D4.19 [Arabidopsis thaliana]	Unigene18202_All//2.00E-78//AT2G24280| serine carboxypeptidase S28 family protein	Unigene18202_All//0.00E+00//CO127170			GO:0000323//GO:0008238//GO:0019538//GO:0031410	nr +
Unigene18203_All	485	83.71	140.20	65.22	9.96	9.44	4.00	0.17	0.43	0.00	7.44E-01	4.85E-30		-3.60E-01	3.19E-05		-7.73E-02	8.22E-01		-1.32E+00	2.03E-06	Down	1.31E+00	4.47E-01		-7.45E+00	3.59E-01		Unigene18203_All//gi|21322711|emb|CAD22154.1|//3.00E-25//pherophorin-dz1 protein [Volvox carteri f. nagariensis]		Unigene18203_All//3.00E-144//TC173158		ko03040|Spliceosome		nr +
Unigene18204_All	518	0.81	0.39	2.78	6.92	4.45	2.70	7.18	8.15	1.92	-1.05E+00	3.66E-01		1.78E+00	4.43E-03		-6.37E-01	4.14E-02		-1.36E+00	3.78E-05	Down	1.82E-01	5.50E-01		-1.90E+00	1.01E-09	Down	Unigene18204_All//gi|1173351|sp|P42552.1|S1FA_SPIOL//3.00E-14//RecName: Full=DNA-binding protein S1FA >gi|498705|emb|CAA56077.1| s1Fa [Spinacia oleracea]		Unigene18204_All//0.00E+00//gi|21101488|gb|BQ413801.1|BQ413801			GO:0003676//GO:0010468//GO:0043231	nr +
Unigene18205_All	295	5.32	16.32	8.30	3.21	5.25	9.65	16.63	38.40	29.44	1.62E+00	5.93E-08	Up	6.42E-01	1.36E-01		7.11E-01	1.98E-01		1.59E+00	4.77E-05	Up	1.21E+00	3.15E-14	Up	8.24E-01	1.70E-06					Unigene18205_All//1.00E-120//DW235566				
Unigene18206_All	300	16.39	24.66	22.90	25.07	23.65	21.98	38.76	21.73	15.14	5.89E-01	6.12E-03		4.82E-01	4.18E-02		-8.46E-02	7.53E-01		-1.90E-01	4.42E-01		-8.35E-01	2.54E-08	Down	-1.36E+00	6.80E-18	Down			Unigene18206_All//1.00E-157//gi|11202357|gb|BF271362.1|BF271362				
Unigene18208_All	656	2.07	2.09	2.68	6.07	3.94	2.41	1.16	0.83	0.00	8.20E-03	9.87E-01		3.69E-01	4.72E-01		-6.26E-01	3.25E-02		-1.33E+00	1.62E-05	Down	-4.86E-01	5.25E-01		-1.02E+01	8.87E-06	Down	Unigene18208_All//gi|15226086|ref|NP_179133.1|//1.00E-53//ATARFB1A (ADP-ribosylation factor B1A); GTP binding [Arabidopsis thaliana] >gi|11131351|sp|Q9SH|5.3|ARF4_ARATH RecName: Full=Probable ADP-ribosylation factor At2g15310	Unigene18208_All//2.00E-55//AT2G15310| ATARFB1A (ADP-ribosylation factor B1A); GTP binding	Unigene18208_All//2.00E-149//TC179291			GO:0006464//GO:0015031//GO:0016020//GO:0032561//GO:0035556//GO:0043231//GO:0046914//GO:0060089//GO:0060229	nr -
Unigene18209_All	275	11.23	15.29	17.04	16.12	20.66	51.73	65.50	73.86	66.64	4.46E-01	1.36E-01		6.02E-01	3.95E-02		3.58E-01	1.70E-01		1.68E+00	7.91E-25	Up	1.74E-01	1.48E-01		2.50E-02	8.55E-01		Unigene18209_All//gi|77176929|gb|AB464563.1|//5.00E-40//geranylgeranyl pyrophosphate synthase [Carica papaya]	Unigene18209_All//3.00E-36//AT4G36810| GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltranstransferase	Unigene18209_All//5.00E-154//TC130518		ko00900|Terpenoid backbone biosynthesis	GO:0004659//GO:0009536//GO:0016109//GO:0043169	nr +
Unigene1821_All	2607	9.45	3.05	1.86	9.36	8.16	7.05	18.36	5.60	6.08	-1.63E+00	1.94E-38	Down	-2.35E+00	1.20E-59	Down	-1.98E-01	8.52E-02		-4.09E-01	1.55E-04		-1.71E+00	4.90E-97	Down	-1.59E+00	4.41E-90	Down	Unigene1821_All//gi|224099067|ref|XP_002311364.1|//0.00E+00//anion exchanger family protein [Populus trichocarpa] >gi|222851184|gb|EEE88731.1| anion exchanger family protein [Populus trichocarpa]	Unigene1821_All//0.00E+00//AT2G47160| BOR1 (REQUIRES HIGH BORON 1); anion exchanger/ boron transporter	Unigene1821_All//0.00E+00//TC177631				nr +
Unigene18210_All	1203	0.74	0.42	0.44	1.66	1.72	2.33	1.23	1.49	2.75	-8.12E-01	2.68E-01		-7.40E-01	3.48E-01		5.23E-02	9.31E-01		4.91E-01	2.20E-01		2.80E-01	5.60E-01		1.16E+00	1.27E-04	Up	Unigene18210_All//gi|183604839|gb|ACC64519.1|//1.00E-131//neuroblastoma-amplified gene [Nicotiana benthamiana]	Unigene18210_All//1.00E-134//AT5G24350| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Secretory pathway Sec39 (InterPro:IPR013224); Has 170 Blast hits to 130 proteins in 45 species: Archae - 0; Bacteria - 5; Metazoa - 90; Fungi - 13; Plants - 54; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink).				GO:0000166//GO:0003676//GO:0016787	nr +
Unigene18212_All	305	36.20	15.12	15.71	33.65	41.10	46.05	74.72	45.08	41.67	-1.26E+00	3.45E-12	Down	-1.20E+00	7.02E-11	Down	2.89E-01	8.11E-02		4.53E-01	2.36E-03		-7.29E-01	1.85E-12		-8.43E-01	2.97E-16		Unigene18212_All//gi|297821200|ref|XP_002878483.1|//2.00E-48/60S ribosomal protein L7A [Arabidopsis lyrata subsp. lyrata] >gi|297324321|gb|EFH54742.1| 60S ribosomal protein L7A [Arabidopsis lyrata subsp. lyrata]	Unigene18212_All//9.00E-50//AT2G47610| 60S ribosomal protein L7A (RPL7aA)	Unigene18212_All//4.00E-167//TC138582		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0031981	nr +
Unigene18213_All	434	0.00	4.09	2.21	1.38	1.90	1.46	2.05	1.06	1.74	1.20E+01	4.14E-10	Up	1.11E+01	2.46E-05	Up	4.67E-01	5.85E-01		8.10E-02	9.45E-01		-9.50E-01	1.55E-01		-2.30E-01	7.05E-01				Unigene18213_All//0.00E+00//TC158363				
Unigene18216_All	1034	0.20	0.39	0.62	2.84	2.63	1.35	1.59	1.13	0.35	9.54E-01	4.14E-01		1.61E+00	1.11E-01		-1.12E-01	8.07E-01		-1.07E+00	3.25E-03		-4.95E-01	3.00E-01		-2.20E+00	1.44E-05	Down	Unigene18216_All//gi|124359162|gb|ABN05685.1|//2.00E-07//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene18216_All//2.00E-11//CD777482			GO:0003676	nr +
Unigene18217_All	789	6.70	6.68	6.01	1.14	3.58	2.63	0.32	0.85	1.11	-4.00E-03	9.84E-01		-1.57E-01	6.08E-01		1.66E+00	1.53E-05	Up	1.21E+00	7.99E-03		1.40E+00	8.81E-02		1.79E+00	1.04E-02		Unigene18217_All//gi|87162616|gb|ABD28411.1|//7.00E-08//C336B.2 , related [Medicago truncatula]		Unigene18217_All//1.00E-18//TC178635				nr +
Unigene18219_All	641	1.71	4.43	4.15	3.73	5.00	8.17	0.59	0.20	0.50	1.37E+00	4.19E-04	Up	1.28E+00	2.02E-03		4.22E-01	2.56E-01		1.13E+00	1.63E-05	Up	-1.60E+00	1.81E-01		-2.56E-01	7.85E-01				Unigene18219_All//0.00E+00//DR456939				
Unigene1822_All	1573	2.46	0.29	0.41	5.00	5.45	2.53	2.26	0.98	0.71	-3.09E+00	1.45E-13	Down	-2.60E+00	6.80E-11	Down	1.24E-01	6.08E-01		-9.86E-01	1.42E-06		-1.20E+00	5.71E-05	Down	-1.67E+00	6.19E-08	Down	Unigene1822_All//gi|9743345|gb|AAF97969.1|AC000103_19//6.00E-89//F21J9.30 [Arabidopsis thaliana]	Unigene1822_All//4.00E-26//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene1822_All//3.00E-88//TC144919				nr -
Unigene18223_All	817	0.00	0.00	0.00	1.34	0.00	0.33	2.02	2.81	4.05	null	null		null	null		-1.04E+01	4.06E-08	Down	-2.02E+00	4.74E-03		4.79E-01	2.23E-01		1.00E+00	7.62E-04	Up							
Unigene18224_All	727	0.29	0.14	0.88	14.39	6.25	8.08	5.93	4.60	8.27	-1.05E+00	5.65E-01		1.61E+00	1.11E-01		-1.20E+00	6.07E-13	Down	-8.33E-01	1.40E-06		-3.67E-01	1.81E-01		4.80E-01	2.25E-02		Unigene18224_All//gi|22597162|gb|AN03468.1|//4.00E-31//bZIP transcription factor ATB2 [Glycine max]	Unigene18224_All//9.00E-25//AT4G34590| GBF6 (G-BOX BINDING FACTOR 6); DNA binding / protein heterodimerization/ transcription factor	Unigene18224_All//0.00E+00//TC149576	bZIP	ko04626|Plant-pathogen interaction/ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0043231	nr -
Unigene18225_All	996	0.42	0.00	0.16	1.90	1.80	1.54	3.01	0.88	1.52	-8.71E+00	1.05E-02		-1.39E+00	2.80E-01		-8.01E-02	8.58E-01		-3.02E-01	5.68E-01		-1.77E+00	4.37E-07	Down	-9.88E-01	1.58E-03		Unigene18225_All//gi|42569372|ref|NP_180280.2|//1.00E-111//TIL2 (TILTED 2); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding / zinc ion binding [Arabidopsis thaliana]	Unigene18225_All//2.00E-111//AT2G27120| TIL2 (TILTED 2); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding / zinc ion binding			ko00230|Purine metabolism/ko00240|Pyrimidine metabolism/ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication	GO:0000109//GO:0003006//GO:0003676//GO:0006576//GO:0006259//GO:0009090//GO:0034061//GO:0046914//GO:0048581	nr +
Unigene18227_All	369	1.13	4.39	4.62	4.86	2.71	2.94	3.44	2.04	1.62	1.95E+00	6.79E-04	Up	2.03E+00	5.19E-04	Up	-8.45E-01	7.10E-02		-7.26E-01	1.44E-01		-7.54E-01	1.63E-01		-1.09E+00	3.58E-02									
Unigene18228_All	424	54.67	59.15	73.34	12.10	12.59	9.69	3.79	2.96	0.19	1.14E-01	3.67E-01		4.24E-01	2.14E-05		5.70E-02	8.51E-01		-3.20E-01	2.66E-01		-3.58E-01	4.67E-01		-4.33E+00	1.41E-09	Down	Unigene18228_All//gi|115462755|ref|NP_001051977.1|//2.00E-122//Os05g0230900 [Oryza sativa Japonica Group] >gi|113578528|dbj|BAF16891.1| Os05g0230900 [Oryza sativa Japonica Group]	Unigene18228_All//1.00E-11//AT1G67280| lactoylglutathione lyase, putative / glyoxalase I, putative	Unigene18228_All//0.00E+00//gi|109870736|gb|DW499712.1|DW499712				nr +
Unigene1823_All	985	2.82	1.44	0.92	4.30	3.67	1.74	3.26	1.15	1.46	-9.67E-01	1.06E-02		-1.62E+00	1.17E-04	Down	-2.28E-01	4.92E-01		-1.30E+00	1.23E-05	Down	-1.51E+00	3.77E-06	Down	-1.16E+00	1.41E-04	Down	Unigene1823_All//gi|32396102|gb|AAP43918.1|//3.00E-69//integrase [Gossypium hirsutum]		Unigene1823_All//7.00E-70//TC129990				nr -
Unigene18230_All	631	1.16	2.01	4.73	1.82	3.33	6.44	1.88	0.66	26.64	7.90E-01	1.89E-01		2.03E+00	1.66E-06	Up	8.75E-01	4.87E-02		1.83E+00	2.64E-08	Up	-1.50E+00	9.69E-03		3.83E+00	3.09E-85	Up	Unigene18230_All//gi|18397376|ref|NP_564349.1|//3.00E-19//JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8) [Arabidopsis thaliana] >gi|75155014|sp|Q8LBM2.1|TIF5A_ARATH RecName: Full=Protein TIFY 5A; AltName: Full=Jasmonate ZIM domain-containing protein 8 >gi|109946551|gb|ABG48454.1| Atlg30135 [Arabidopsis thaliana]	Unigene18230_All//2.00E-15//AT1G30135| JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8)	Unigene18230_All//6.00E-23//ES819370	Tify		GO:0005488//GO:0009719//GO:0009743	nr +

Unigene18231_All	662	6.88	5.66	5.31	3.76	1.40	3.07	0.38	0.51	0.24	-2.80E-01	3.56E-01		-3.73E-01	2.29E-01		-1.42E+00	2.12E-04	Down	-2.93E-01	5.03E-01		3.99E-01	7.24E-01		-6.71E-01	6.05E-01		Unigene18231_All//gi|164449260|gb|ABV56089.1|//9.00E-44//proton gradient regulation 5 [Cucumis melo] >gi|164449273|gb|ABV56101.1| proton gradient regulation 5 [Cucumis sativus]	Unigene18231_All//2.00E-43//AT2G05620| PGR5 (proton gradient regulation 5); electron carrier	Unigene18231_All//0.00E+00//TC143581			GO:0006950//GO:0009534//GO:0009642//GO:0009767	nr +
Unigene18232_All	1054	5.76	2.74	1.36	4.49	4.21	5.70	5.62	3.37	2.87	-1.07E+00	1.22E-05	Down	-2.08E+00	5.53E-13	Down	-9.13E-02	7.97E-01		3.44E-01	1.90E-01		-7.37E-01	6.74E-04		-9.67E-01	6.30E-06		Unigene18232_All//gi|18398046|ref|NP_566318.1|//1.00E-119//3' exoribonuclease family domain 1-containing protein [Arabidopsis thaliana] >gi|30680427|ref|NP_850537.1| 3' exoribonuclease family domain 1-containing protein [Arabidopsis thaliana] >gi|11762184|gb|AAG40370.1|AF325018_1 AT3g07750 [Arabidopsis thaliana] >gi|56744222|gb|AAW28551.1| At3g07750 [Arabidopsis thaliana]	Unigene18232_All//2.00E-108//AT3G07750| 3' exoribonuclease family domain 1-containing protein	Unigene18232_All//0.00E+00//DT467685		ko03018|RNA degradation	GO:0003676//GO:0008408//GO:0010467	nr -
Unigene18234_All	707	1.78	8.17	7.53	0.92	5.89	1.85	0.24	0.00	0.45	2.20E+00	8.10E-14	Up	2.08E+00	1.51E-11	Up	2.69E+00	3.92E-14	Up	1.02E+00	9.48E-02		-7.90E+00	1.35E-01		9.14E-01	4.53E-01		Unigene18234_All//gi|225440556|ref|XP_002273450.1|//2.00E-30//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene18234_All//7.00E-29//CO082632				nr +
Unigene18235_All	1121	6.53	5.51	3.04	8.09	3.96	6.20	4.19	7.01	1.74	-2.45E-01	2.85E-01		-1.10E+00	1.44E-06	Down	-1.03E+00	7.27E-09	Down	-3.82E-01	5.18E-02		7.44E-01	5.73E-05		-1.27E+00	4.77E-07	Down	Unigene18235_All//gi|223452468|gb|ACM89561.1|//1.00E-126//receptor-like protein kinase precusor-like protein [Glycine max] >gi|223452568|gb|ACM89611.1| receptor-like protein kinase [Glycine max]	Unigene18235_All//3.00E-118//AT4G00340| RLK4 (RECEPTOR-LIKE PROTEIN KINASE 4); protein kinase/ sugar binding	Unigene18235_All//0.00E+00//gi|164360172|gb|ES850125.1|ES850125		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0009987//GO:0031410//GO:0043231	nr -
Unigene18236_All	657	0.72	3.70	3.65	6.07	5.19	2.41	7.98	6.55	4.55	2.37E+00	1.02E-06	Up	2.35E+00	2.76E-06	Up	-2.25E-01	5.19E-01		-1.33E+00	1.62E-05	Down	-2.84E-01	2.57E-01		-8.11E-01	3.32E-04										
Unigene18238_All	262	4.39	8.90	5.28	2.66	5.91	5.69	2.26	0.00	0.30	1.02E+00	1.57E-02		2.66E-01	6.23E-01		1.15E+00	3.22E-02		1.10E+00	5.01E-02		-1.11E+01	2.39E-04	Down	-2.89E+00	4.53E-03				Unigene18238_All//1.00E-123//gi|48809935|gb|CO111249.1|CO111249					
Unigene18239_All	520	8.85	6.14	5.73	13.60	11.26	10.77	76.92	35.12	24.75	-5.28E-01	6.19E-02		-6.27E-01	3.38E-02		-2.73E-01	2.42E-01		-3.37E-01	1.49E-01		-1.13E+00	1.41E-43	Down	-1.64E+00	2.71E-78	Down			Unigene18239_All//0.00E+00//TC130288					
Unigene1824_All	1986	13.88	4.75	5.09	21.02	17.63	9.21	6.28	1.37	1.36	-1.55E+00	7.32E-40	Down	-1.45E+00	9.96E-35	Down	-2.53E-01	1.38E-03		-1.19E+00	1.32E-43	Down	-2.20E+00	1.07E-35	Down	-2.20E+00	6.25E-37	Down	Unigene1824_All//gi|71480741|gb|AAK85402.2|//0.00E+00//beta-1,3-glucanase [Camellia sinensis]	Unigene1824_All//0.00E+00//AT1G66250| glycosyl hydrolase family 17 protein	Unigene1824_All//0.00E+00//TC132814		ko00500|Starch and sucrose metabolism		nr -
Unigene18240_All	354	2.66	0.00	6.02	1.41	1.46	1.02	10.03	5.67	4.95	-1.14E+01	1.46E-05	Down	1.18E+00	1.19E-02		5.23E-02	9.80E-01		-4.63E-01	6.59E-01		-8.24E-01	4.65E-03		-1.02E+00	3.53E-04	Down									
Unigene18241_All	638	2.30	1.83	3.26	0.31	1.03	2.27	0.40	0.13	0.62	-3.30E-01	5.56E-01		5.04E-01	2.86E-01		1.72E+00	8.17E-02		2.86E+00	3.35E-05	Up	-1.60E+00	3.11E-01		6.51E-01	5.45E-01		Unigene18241_All//gi|297727859|ref|NP_001176293.1|//1.00E-28//Os11g0100300 [Oryza sativa Japonica Group] >gi|77548278|gb|ABA91075.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255679678|dbj|BAH95021.1| Os11g0100300 [Oryza sativa Japonica Group]	Unigene18241_All//6.00E-42//AT2G28780| unknown protein					nr -
Unigene18243_All	529	5.84	3.74	2.82	4.80	3.84	5.29	1.92	0.55	0.38	-6.44E-01	6.91E-02		-1.05E+00	4.96E-03		-3.23E-01	4.48E-01		1.40E-01	7.24E-01		-1.79E+00	6.30E-03		-2.35E+00	5.84E-04	Down			Unigene18243_All//6.00E-07//DN802407					
Unigene18244_All	1794	0.47	0.17	0.24	0.47	0.38	0.28	12.02	4.05	8.04	-1.46E+00	6.69E-02		-9.74E-01	2.37E-01		-2.98E-01	6.93E-01		-7.69E-01	3.34E-01		-1.57E+00	6.45E-39	Down	-5.80E-01	1.89E-08		Unigene18244_All//gi|45825141|gb|AAS77478.1|//5.00E-47//At5g22540 [Arabidopsis thaliana]	Unigene18244_All//1.00E-59//AT2G36430| unknown protein					nr -
Unigene18246_All	967	0.00	0.00	0.00	0.00	0.00	0.00	2.54	2.38	18.21	null	null		null	null		null	null		null	null		-9.32E-02	8.08E-01		2.84E+00	3.23E-68	Up	Unigene18246_All//gi|15238564|ref|NP_200800.1|//3.00E-23//ULI3; diacylglycerol binding / heme binding [Arabidopsis thaliana] >gi|17225050|gb|AAL37222.1|AF329199_1 ULI3 [Arabidopsis thaliana]	Unigene18246_All//1.00E-24//AT5G39920| ULI3; diacylglycerol binding / heme binding	Unigene18246_All//2.00E-66//TC145328				nr +
Unigene18248_All	647	217.94	86.54	166.09	52.66	58.39	29.60	0.33	0.19	0.92	-1.33E+00	1.22E-160	Down	-3.92E-01	4.39E-19		1.49E-01	1.14E-01		-8.31E-01	6.33E-20		-7.53E-01	6.32E-01		1.50E+00	7.88E-02		Unigene18248_All//gi|124360655|gb|ABN08644.1|//2.00E-50//Rhodanese-like [Medicago truncatula]	Unigene18248_All//1.00E-49//AT2G42220| rhodanese-like domain-containing protein	Unigene18248_All//0.00E+00//gi|109879692|gb|DW508662.1|DW508662			GO:0009534	nr +
Unigene18251_All	491	4.80	0.52	0.98	3.75	2.81	4.23	0.43	0.17	2.19	-3.22E+00	8.66E-09	Down	-2.30E+00	5.12E-06	Down	-4.20E-01	3.95E-01		1.73E-01	7.13E-01		-1.34E+00	4.30E-01		2.35E+00	4.46E-04	Up	Unigene18251_All//gi|21314549|gb|AAM47000.1|AF512542_1//2.00E-73//alpha-expansin precursor [Gossypium hirsutum]	Unigene18251_All//6.00E-66//AT2G28950| ATEXPA6 (ARABIDOPSIS THALIANA EXPANSIN A6)	Unigene18251_All//0.00E+00//gi|78334324|gb|DT554598.1|DT554598			GO:0007047//GO:0044464	nr +
Unigene18253_All	706	32.90	16.29	15.16	1.69	2.54	1.66	0.00	0.24	0.00	-1.01E+00	9.72E-18	Down	-1.12E+00	8.03E-20	Down	5.83E-01	2.59E-01		-2.60E-02	9.54E-01		7.89E+00	1.39E-01		null	null		Unigene18253_All//gi|115458314|ref|NP_001052757.1|//1.00E-16//Os04g0415000 [Oryza sativa Japonica Group] >gi|32479729|emb|CAE01516.1| OJ991214_12.5 [Oryza sativa (japonica cultivar-group)] >gi|113564328|dbj|BAF14671.1| Os04g0415000 [Oryza sativa Japonica Group] >gi|116309338|emb|CAH66422.1| H0622F05.5 [Oryza sativa (indica cultivar-group)]	Unigene18253_All//2.00E-23//AT5G06270| unknown protein	Unigene18253_All//0.00E+00//gi|84163730|gb|DR452378.1|DR452378				nr +
Unigene18256_All	605	5.10	3.18	3.96	1.89	3.47	0.90	2.38	0.97	0.59	-6.81E-01	5.42E-02		-3.65E-01	3.48E-01		8.75E-01	4.87E-02		-1.08E+00	9.66E-02		-1.30E+00	1.07E-02		-2.00E+00	1.70E-04	Down			Unigene18256_All//7.00E-07//CO131797					
Unigene18258_All	747	0.42	2.44	1.57	3.60	2.03	2.66	0.28	1.06	0.37	2.54E+00	1.40E-05	Up	1.90E+00	8.12E-03		-8.28E-01	2.29E-02		-4.37E-01	2.88E-01		1.91E+00	1.37E-02		4.00E-01	7.43E-01				Unigene18258_All//8.00E-75//TC164608					
Unigene18259_All	783	1.54	1.04	0.00	3.69	3.17	0.98	4.97	1.17	1.07	-5.70E-01	3.65E-01		-1.06E+01	1.36E-06	Down	-2.21E-01	5.88E-01		-1.91E+00	1.47E-06	Down	-2.08E+00	6.76E-11	Down	-2.22E+00	3.70E-12	Down	Unigene18259_All//gi|23197634|gb|AAN15344.1|//9.00E-18//Unknown protein [Arabidopsis thaliana]	Unigene18259_All//5.00E-43//AT2G23690| unknown protein	Unigene18259_All//0.00E+00//DN758474			GO:0005488	nr -
Unigene18261_All	656	11.96	10.12	24.84	3.34	3.46	2.20	0.32	0.38	0.18	-2.42E-01	2.72E-01		1.05E+00	6.92E-13	Up	5.23E-02	9.25E-01		-6.01E-01	1.81E-01		2.46E-01	8.53E-01		-8.23E-01	5.99E-01		Unigene18261_All//gi|87162753|gb|ABD28548.1|//6.00E-34//Protein kinase; Type I EGF [Medicago truncatula]	Unigene18261_All//2.00E-30//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase	Unigene18261_All//5.00E-11//CA994149			GO:0016301	nr -
Unigene18262_All	376	13.22	1.08	2.83	3.44	1.47	1.20	0.45	0.00	0.00	-3.62E+00	8.62E-20	Down	-2.22E+00	1.27E-11	Down	-1.23E+00	2.99E-02		-1.52E+00	1.32E-02		-8.81E+00	1.35E-01		-8.81E+00	1.08E-01		Unigene18262_All//gi|15240499|ref|NP_200348.1|//2.00E-24//long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein [Arabidopsis thaliana] >gi|75170973|sp|Q9FJ73.1|WAXS2_ARATH RecName: Full=Probable long-chain-alcohol O-fatty-acyltransferase 2; AltName: Full=Wax synthase 2 >gi|9758169|dbj|BAB08554.1| wax synthase-like protein [Arabidopsis thaliana]	Unigene18262_All//1.00E-25//AT5G55370| long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein	Unigene18262_All//0.00E+00//gi|6461333|gb|AW186897.1|AW186897			GO:0016747	nr +
Unigene18263_All	426	0.25	1.67	3.25	0.00	0.81	2.97	4.17	1.57	3.55	2.76E+00	9.15E-03		3.73E+00	1.05E-05	Up	9.66E+00	3.01E-02		1.15E+01	1.55E-07	Up	-1.41E+00	1.85E-03		-2.30E-01	5.97E-01										
Unigene18264_All	397	2.64	3.45	2.15	4.89	2.00	3.75	9.05	3.68	2.71	3.87E-01	5.01E-01		-2.97E-01	6.42E-01		-1.29E+00	3.45E-03		-3.82E-01	4.51E-01		-1.30E+00	1.46E-05	Down	-1.74E+00	1.92E-08	Down			Unigene18264_All//6.00E-65//BF278735					
Unigene18266_All	479	11.47	15.23	15.79	1.46	4.24	5.94	0.44	0.52	0.00	4.09E-01	6.34E-02		4.61E-01	4.00E-02		1.54E+00	8.41E-04	Up	2.03E+00	8.90E-07	Up	2.46E-01	8.53E-01		-8.79E+00	5.80E-02		Unigene18266_All//gi|9759309|dbj|BAB09815.1|//4.00E-14//non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	Unigene18266_All//8.00E-08//AT5G42905| nucleic acid binding / ribonuclease H					nr +
Unigene18267_All	313	176.19	126.43	167.24	109.02	178.23	123.37	476.70	255.98	212.94	-4.79E-01	1.38E-11		-7.52E-02	3.98E-01		7.09E-01	7.38E-27		1.78E-01	5.33E-02		-8.97E-01	1.03E-109		-1.16E+00	1.79E-172	Down	Unigene18267_All//gi|225380880|gb|ACN88681.1|//1.00E-49//VTC2-like protein [Malus x domestica]	Unigene18267_All//1.00E-45//AT4G26850| VTC2 (vitamin c defective 2); GDP-D-glucose phosphorylase/ GDP-galactose:glucose-1-phosphate guanyltransferase/ GDP-galactose:mannose-1-phosphate guanyltransferase/ GDP-galactose:myoinositol-1-phosphate guanyltransferase/ galactose-1-phosphate guanylyltra	Unigene18267_All//1.00E-176//gi|13353248|gb|BG443596.1|BG443596			GO:0004645//GO:0005488//GO:0008905//GO:0009719//GO:0019852//GO:0035251//GO:0042221//GO:0052482	nr +
Unigene18268_All	1098	0.57	0.78	0.39	2.36	3.86	3.50	6.58	1.60	0.62	4.56E-01	5.46E-01		-5.60E-01	5.54E-01		7.09E-01	1.38E-02		5.68E-01	7.63E-02		-2.04E+00	3.53E-19	Down	-3.42E+00	2.17E-34	Down	Unigene18268_All//gi|5103824|gb|AAD39654.1|AC007591_19//7.00E-13//EST gb|N65467 comes from this gene [Arabidopsis thaliana]	Unigene18268_All//3.00E-14//AT1G15260| unknown protein					nr -
Unigene18269_All	684	114.66	182.38	355.00	101.96	176.86	336.74	0.12	0.37	0.23	6.70E-01	1.93E-45		1.63E+00	0.00E+00	Up	7.95E-01	1.74E-70		1.72E+00	0.00E+00	Up	1.57E+00	3.26E-01		9.15E-01	6.24E-01		Unigene18269_All//gi|213876486|gb|ACJ54281.1|//6.00E-91//lipoxygenase [Camellia sinensis]	Unigene18269_All//2.00E-62//AT3G45140| LOX2 (LIPOXYGENASE 2); lipoxygenase	Unigene18269_All//0.00E+00//gi|109856617|gb|DW485596.1|DW485596		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0006633//GO:0016702//GO:0046914	nr -
Unigene1827_All	1612	65.69	53.25	48.46	220.55	193.54	107.87	38.27	13.07	19.50	-3.03E-01	1.27E-09		-4.39E-01	1.00E-17		-1.89E-01	5.82E-15		-1.03E+00	2.49E-292	Down	-1.55E+00	3.98E-108	Down	-9.73E-01	7.51E-54		Unigene1827_All//gi|190896584|gb|ACE96805.1|//1.00E-157//aspartyl protease [Populus tremula] >gi|190896586|gb|ACE96806.1| aspartyl protease [Populus tremula] >gi|190896588|gb|ACE96807.1| aspartyl protease [Populus tremula] >gi|190896590|gb|ACE96808.1| aspartyl protease [Populus tremula] >gi|190896592|gb|ACE96809.1| aspartyl protease [Populus tremula] >gi|190896594|gb|ACE96810.1| aspartyl protease [Populus tremula] >gi|190896596|gb|ACE96811.1| aspartyl protease [Populus tremula] >gi|190896598|gb|ACE96812.1| aspartyl protease [Populus tremula] >gi|190896600|gb|ACE96813.1| aspartyl protease [Populus tremula] >gi|190896602|gb|ACE96814.1| aspartyl protease [Populus tremula]	Unigene1827_All//5.00E-142//AT1G69250| chloroplast nucleoid DNA-binding protein-related	Unigene1827_All//0.00E+00//TC131527				nr -
Unigene18271_All	1577	3.02	0.58	1.15	0.69	0.28	0.57	9.01	0.74	0.63	-2.38E+00	1.07E-12	Down	-1.39E+00	3.44E-06	Down	-1.29E+00	4.07E-02		-2.79E-01	6.89E-01		-3.60E+00	9.08E-68	Down	-3.83E+00	1.13E-73	Down	Unigene18271_All//gi|10953887|gb|AAC25643.1|AF303396_1//1.00E-120//UDP-glucosyltransferase HRA25 [Phaseolus vulgaris]	Unigene18271_All//2.00E-119//AT3G02100| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene18271_All//0.00E+00//TC144434		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene18272_All	277	6.04	1.46	7.11	8.27	4.10	5.71	0.46	0.60	0.29	-2.05E+00	3.19E-04	Down	2.35E-01	6.29E-01		-1.01E+00	1.11E-02		-5.36E-01	2.24E-01		3.98E-01	8.14E-01		-6.71E-01	7.20E-01										

Unigene18274_All	525	169.12	81.55	69.07	199.45	164.44	244.31	298.22	151.90	165.35	-1.05E+00	8.39E-70	Down	-1.29E+00	1.68E-93	Down	-2.79E-01	1.58E-09		2.93E-01	2.09E-11		-9.73E-01	7.33E-132		-8.51E-01	3.73E-108		Unigene18274_All//gi|3885884|gb|AAC78102.1|//5.00E-56//60S ribosomal protein L21 [Oryza sativa Japonica Group]	Unigene18274_All//6.00E-53//AT1G09690| 60S ribosomal protein L21 (RPL21C)	Unigene18274_All//0.00E+00//gi|164300882|gb|ES806928.1|ES806928		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene18275_All	2667	0.08	0.04	0.04	0.07	0.03	0.07	19.93	43.99	12.70	-1.05E+00	5.65E-01		-9.76E-01	6.21E-01		-1.53E+00	4.16E-01		-1.42E-01	9.35E-01		1.14E+00	3.09E-128	Up	-6.50E-01	1.09E-23		Unigene18275_All//gi|15223460|ref|NP_176009.1|//1.00E-144//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|263711285|sp|C0LGH2.2|Y156L_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g56130; Flags: Precursor	Unigene18275_All//9.00E-131//AT1G56130| leucine-rich repeat family protein / protein kinase family protein	Unigene18275_All//0.00E+00//gi|109890700|gb|DW519664.1|DW519664		ko04626|Plant-pathogen interaction	GO:0005515//GO:0009755//GO:0010468//GO:0016628//GO:0043231	nr +
Unigene18277_All	778	0.20	0.00	0.00	1.73	1.64	0.81	2.23	0.27	0.82	-7.66E+00	2.16E-01		-7.66E+00	2.45E-01		-7.81E-02	8.79E-01		-1.09E+00	6.42E-02		-3.05E+00	1.18E-07	Down	-1.44E+00	1.20E-03		Unigene18277_All//gi|164605533|dbj|BAP98599.1|//2.00E-37//CM0545.320.nc [Lotus japonicus]	Unigene18277_All//7.00E-09//AT5G02440| unknown protein	Unigene18277_All//0.00E+00//TC155634				nr -
Unigene18279_All	753	0.21	0.00	0.35	0.60	0.37	0.66	2.47	6.16	14.50	-7.70E+00	2.16E-01		7.63E-01	6.44E-01		-7.03E-01	5.30E-01		1.48E-01	9.06E-01		1.32E+00	4.26E-07	Up	2.55E+00	6.28E-38	Up	Unigene18279_All//gi|30697422|ref|NP_176860.2|//1.00E-13//serine/threonine protein kinase family protein [Arabidopsis thaliana]	Unigene18279_All//3.00E-14//AT1G66880| serine/threonine protein kinase family protein	Unigene18279_All//3.00E-96//gi|109860838|gb|DW489817.1|DW489817				nr +
Unigene1828_All	2235	2.79	1.75	1.33	22.40	28.98	21.64	89.48	123.14	126.98	-6.74E-01	4.25E-03		-1.06E+00	2.16E-05	Down	3.72E-01	5.67E-10		-4.96E-02	6.33E-01		4.61E-01	2.20E-62		5.05E-01	9.49E-78		Unigene1828_All//gi|224137294|ref|XP_002327090.1|//1.00E-104//cytochrome P450 [Populus trichocarpa] >gi|222835405|gb|EEE73840.1| cytochrome P450 [Populus trichocarpa]	Unigene1828_All//2.00E-75//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene1828_All//0.00E+00//TC135606		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene18282_All	585	23.34	23.65	17.57	31.25	31.08	38.22	49.58	28.79	21.93	1.86E-02	9.24E-01		-4.10E-01	1.05E-02		-7.90E-03	9.54E-01		2.90E-01	1.46E-02		-7.84E-01	1.24E-17		-1.18E+00	7.02E-35	Down	Unigene18282_All//gi|195623644|gb|ACG33652.1|//3.00E-80//proteasome subunit alpha type 2 [Zea mays] >gi|195659247|gb|ACG49091.1| proteasome subunit alpha type 2 [Zea mays]	Unigene18282_All//5.00E-80//AT1G16470| PAB1 (PROTEASOME SUBUNIT PAB1); endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene18282_All//0.00E+00//ES852339		ko03050|Proteasome	GO:0004175//GO:0008539//GO:0005840//GO:0006952//GO:0008135//GO:0010038//GO:0019941//GO:0043231	nr +
Unigene18285_All	400	0.52	2.53	0.13	1.37	0.86	2.94	2.33	0.10	1.10	2.28E+00	4.10E-03		-1.97E+00	3.81E-01		-6.70E-01	4.97E-01		1.10E+00	9.17E-02		-4.48E+00	1.30E-05	Down	-1.09E+00	8.05E-02										
Unigene18286_All	231	0.45	0.00	4.38	1.51	1.49	0.00	0.00	0.00	0.00	-8.82E+00	3.73E-01		3.27E+00	5.93E-04	Up	-1.81E-02	9.58E-01		-1.06E+01	2.13E-02		null	null		null	null										
Unigene18287_All	342	2.14	6.52	8.56	1.02	1.31	0.66	0.00	0.00	0.00	1.61E+00	4.50E-04	Up	2.00E+00	2.63E-06	Up	3.60E-01	8.07E-01		-6.27E-01	6.21E-01		null	null		null	null										
Unigene18292_All	787	0.27	3.61	0.00	0.76	0.48	0.63	7.20	6.96	5.62	3.76E+00	1.00E-11	Up	-8.05E+00	1.46E-01		-6.58E-01	4.78E-01		-2.67E-01	7.57E-01		-4.93E-02	8.46E-01		-3.58E-01	1.08E-01				Unigene18292_All//9.00E-07//EX164488					
Unigene18293_All	568	0.00	0.36	0.00	2.98	6.67	23.77	3.57	5.30	9.19	8.48E+00	1.37E-01		null	null		1.16E+00	1.57E-04	Up	3.00E+00	3.69E-47	Up	5.68E-01	8.08E-02		1.36E+00	1.75E-08	Up									ESTscan -
Unigene18295_All	725	0.14	0.28	0.73	5.43	4.70	3.49	2.68	0.00	0.49	9.54E-01	6.22E-01		2.35E+00	5.88E-02		-2.07E-01	5.39E-01		-6.38E-01	3.96E-02		-1.14E+01	9.14E-14	Down	-2.44E+00	3.73E-07	Down	Unigene18295_All//gi|297798488|ref|XP_002867128.1|//9.00E-59//hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297312964|gb|EFH43387.1| hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene18295_All//2.00E-73//AT3G53010| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF303, acetylesterase putative (InterPro:IPR005181); BEST Arabidopsis thaliana protein match is: hydrolase (TAIR:AT4G34215.2); Has 199 Blast hits to 199 proteins in 58 species: Archae - 0; Bacteria - 119; Metazoa - 0; Fungi - 1; Plants - 56; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).	Unigene18295_All//0.00E+00//gi|78343875|gb|DT564149.1|DT564149			GO:0003824//GO:0043231	nr -
Unigene18296_All	436	5.28	7.09	5.37	8.34	6.95	8.91	32.00	17.35	10.87	4.25E-01	2.34E-01		2.54E-02	9.71E-01		-2.63E-01	4.48E-01		9.50E-02	7.82E-01		-8.83E-01	9.86E-11		-1.56E+00	5.29E-26	Down			Unigene18296_All//6.00E-170//TC131772					
Unigene18299_All	537	150.43	135.40	140.61	197.59	157.81	166.61	266.20	235.99	129.31	-1.52E-01	1.24E-02		-9.74E-02	1.46E-01		-3.24E-01	1.01E-12		-2.46E-01	4.56E-07		-1.74E-01	7.30E-06		-1.04E+00	2.07E-138	Down	Unigene18299_All//gi|300167371|gb|EFJ33976.1|//3.00E-60//ARF family GTPase [Selaginella moellendorffii] >gi|300170884|gb|EFJ37485.1| ARF family GTPase [Selaginella moellendorffii]	Unigene18299_All//1.00E-60//AT3G62290| ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding	Unigene18299_All//0.00E+00//TC143645			GO:0032561//GO:0035556//GO:0043231//GO:0060229	nr +
Unigene18300_All	501	3.24	2.02	1.17	5.27	1.92	1.44	6.08	2.17	0.72	-6.79E-01	1.89E-01		-1.47E+00	9.26E-03		-1.45E+00	9.29E-05	Down	-1.87E+00	6.88E-06	Down	-1.49E+00	9.46E-06	Down	-3.09E+00	1.33E-13	Down	Unigene18300_All//gi|145334659|ref|NP_001078675.1|//1.00E-36//PDLP7 (PLASMODESMATA-LOCATED PROTEIN 7) [Arabidopsis thaliana] >gi|122242482|sp|Q9FPN8.1|CRR60_ARATH RecName: Full=Cysteine-rich repeat secretory protein 60; Flags: Precursor	Unigene18300_All//1.00E-31//AT5G37660| PDLP7 (PLASMODESMATA-LOCATED PROTEIN 7)	Unigene18300_All//8.00E-34//gi|13353093|gb|BG443441.1|BG443441			GO:0005488//GO:0005911	nr -
Unigene18302_All	314	0.17	2.90	0.85	1.43	1.10	2.01	0.81	0.27	2.03	4.12E+00	2.34E-04	Up	2.35E+00	2.39E-01		-3.81E-01	7.22E-01		4.96E-01	6.37E-01		-1.60E+00	3.11E-01		1.33E+00	1.00E-01										
Unigene18303_All	336	3.74	2.56	1.90	3.85	4.41	3.49	30.20	12.94	9.96	-5.44E-01	3.75E-01		-9.75E-01	1.29E-01		1.93E-01	7.84E-01		-1.41E-01	8.06E-01		-1.22E+00	4.25E-13	Down	-1.60E+00	6.92E-20	Down			Unigene18303_All//2.00E-39//TC144674					
Unigene18307_All	749	0.35	0.14	0.28	0.47	1.52	2.05	10.56	10.27	91.30	-1.37E+00	3.83E-01		-2.97E-01	8.32E-01		1.70E+00	1.20E-02		2.14E+00	3.75E-01	Up	-4.00E-02	8.54E-01		3.16E+00	4.06E-302	Up									
Unigene18310_All	372	3.09	5.58	13.60	2.01	3.33	3.40	0.00	0.00	0.21	8.52E-01	5.74E-02		2.14E+00	2.51E-11	Up	7.30E-01	2.54E-01		7.59E-01	2.30E-01		null	null		7.74E+00	4.05E-01				Unigene18310_All//7.00E-09//DN803920					
Unigene18312_All	1088	0.10	0.00	0.00	8.61	2.63	10.71	0.27	0.58	2.16	-6.59E+00	3.73E-01		-6.59E+00	3.95E-01		-1.71E+00	1.20E-19	Down	3.15E-01	7.15E-02		1.08E+00	1.99E-01		2.99E+00	3.58E-10	Up	Unigene18312_All//gi|30689857|ref|NP_189653.2|//3.00E-96//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|9294338|dbj|BAB02235.1| nodulin-like protein [Arabidopsis thaliana]	Unigene18312_All//6.00E-90//AT4G01440| nodulin MtN21 family protein	Unigene18312_All//0.00E+00//TC139894			GO:0031410	nr -
Unigene18315_All	301	777.34	151.84	213.00	107.41	40.61	17.11	21.63	3.19	3.44	-2.36E+00	0.00E+00	Down	-1.87E+00	0.00E+00	Down	-1.40E+00	6.82E-50	Down	-2.65E+00	1.03E-101	Down	-2.76E+00	1.79E-24	Down	-2.65E+00	2.83E-24	Down	Unigene18315_All//gi|15236175|ref|NP_194362.1|//7.00E-10//AGP13 (arabinogalactan protein 13) [Arabidopsis thaliana] >gi|152007711|sp|Q9STQ3.1|AGP13_ARATH RecName: Full=Arabinogalactan peptide 13; Short=AG-peptide 13; Flags: Precursor >gi|10880503|gb|AAG24281.1|AF195894_1 arabinogalactan protein [Arabidopsis thaliana] >gi|89111816|gb|ABD60880.1| At4g26320 [Arabidopsis thaliana]		Unigene18315_All//2.00E-98//gi|6461432|gb|AW186996.1|AW186996			GO:0031224	nr +
Unigene18319_All	496	58.65	8.99	27.91	10.65	11.04	12.57	0.17	0.00	0.32	-2.71E+00	6.38E-86	Down	-1.07E+00	4.52E-23	Down	5.23E-02	8.63E-01		2.39E-01	3.83E-01		-7.41E+00	4.04E-01		9.14E-01	6.24E-01		Unigene18319_All//gi|224140415|ref|XP_002323578.1|//3.00E-53//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222868208|gb|EEF05339.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene18319_All//2.00E-42//AT3G51860| CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	Unigene18319_All//0.00E+00//gi|78342464|gb|DT562738.1|DT562738			GO:0000325//GO:0005488//GO:0006875//GO:0006970//GO:0009409//GO:0010038//GO:0015368//GO:0015672//GO:0030005//GO:0031090//GO:0031224//GO:0044237//GO:0046873//GO:0051707//GO:0070838	nr -
Unigene18321_All	516	2.84	0.39	1.24	6.76	7.94	4.90	2.29	1.62	1.39	-2.85E+00	3.60E-05	Down	-1.20E+00	4.21E-02		2.33E-01	5.15E-01		-4.63E-01	1.83E-01		-5.02E-01	3.95E-01		-7.23E-01	1.77E-01		Unigene18321_All//gi|291513244|emb|CBL42917.1|//2.00E-22//kaurene synthase [Helianthus annuus] >gi|298357288|emb|CBM82409.1| kaurene synthase [Helianthus annuus]	Unigene18321_All//5.00E-19//AT1G79460| GA2 (GA REQUIRING 2); ent-kaurene synthase	Unigene18321_All//0.00E+00//TC137031		ko00904|Diterpenoid biosynthesis	GO:0009532//GO:0009685//GO:0010333//GO:0010476//GO:0043692//GO:0046872	nr +
Unigene18322_All	251	136.12	224.28	259.67	34.73	44.86	69.63	0.34	0.50	0.48	7.20E-01	1.12E-23		9.32E-01	9.34E-41		3.69E-01	2.92E-02		1.00E+00	4.82E-14	Up	5.69E-01	7.82E-01		4.99E-01	8.08E-01				Unigene18322_All//6.00E-107//TC158902					
Unigene18323_All	752	0.63	1.01	0.78	0.79	1.37	3.48	0.06	1.78	0.32	6.91E-01	3.76E-01		3.15E-01	7.19E-01		7.89E-01	2.74E-01		2.13E+00	1.19E-06	Up	4.98E+00	3.03E-08	Up	2.50E+00	1.59E-01		Unigene18323_All//gi|159025705|emb|CAN88853.1|//9.00E-44//D1-type cyclin [Populus trichocarpa]	Unigene18323_All//2.00E-34//AT1G70210| CYCD1;1 (CYCLIN D1;1); cyclin-dependent protein kinase regulator	Unigene18323_All//0.00E+00//TC131651			GO:0009987	nr +
Unigene18325_All	484	2.49	0.42	0.44	0.72	1.14	2.71	1.75	0.52	1.56	-2.57E+00	5.35E-04	Down	-2.50E+00	1.15E-03		6.60E-01	5.44E-01		1.91E+00	3.05E-03		-1.75E+00	1.64E-02		-1.60E-01	7.94E-01		Unigene18325_All//gi|297841913|ref|XP_002888838.1|//1.00E-56//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297334679|gb|EFH65097.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene18325_All//4.00E-56//AT1G71460| pentatricopeptide (PPR) repeat-containing protein	Unigene18325_All//2.00E-127//TC170725			GO:0043231	nr +
Unigene18326_All	632	1.08	0.00	1.10	2.60	0.87	0.79	1.94	3.64	0.63	-1.01E+01	4.10E-04	Down	2.54E-02	9.96E-01		-1.58E+00	1.53E-03		-1.73E+00	1.40E-03		9.07E-01	1.62E-02		-1.62E+00	3.49E-03										
Unigene18329_All	691	0.15	0.15	0.08	1.15	0.90	0.13	3.98	1.75	1.84	-4.55E-02	9.89E-01		-9.74E-01	7.21E-01		-3.63E-01	6.23E-01		-3.14E+00	1.88E-03		-1.18E+00	6.00E-04	Down	-1.11E+00	8.40E-04	Down	Unigene18329_All//gi|222066100|emb|CAX28558.1|//3.00E-69//NBS-LLR resistance protein [Gossypium arboreum]	Unigene18329_All//9.00E-26//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene18329_All//1.00E-116//gi|73865644|gb|DT468382.1|DT468382		ko04626|Plant-pathogen interaction	GO:0006950//GO:0012501//GO:0032559	nr -
Unigene18331_All	852	0.12	1.31	0.75	2.81	1.37	1.38	0.94	0.05	0.42	3.41E+00	1.24E-04	Up	2.61E+00	2.33E-02		-1.03E+00	8.02E-03		-1.03E+00	1.26E-02		-4.26E+00	8.48E-05	Down	-1.16E+00	8.85E-02		Unigene18331_All//gi|44021989|gb|AAS46633.1|//4.00E-06//At2g04495 [Arabidopsis thaliana] >gi|45773862|gb|AAS76735.1| At2g04495 [Arabidopsis thaliana]	Unigene18331_All//9.00E-16//AT3G13130| unknown protein	Unigene18331_All//7.00E-17//DW224569				nr +
Unigene18332_All	1127	0.19	0.00	0.28	0.71	0.76	0.56	3.00	5.12	6.75	-7.54E+00	1.22E-01		6.10E-01	6.25E-01		1.11E-01	9.04E-01		-3.34E-01	6.86E-01		7.70E-01	4.70E-04		1.17E+00	1.23E-09	Up	Unigene18332_All//gi|82697971|gb|ABB89020.1|//6.00E-99//CXE carboxylesterase [Actinidia deliciosa]	Unigene18332_All//8.00E-96//AT5G23530| AtCXE18 (Arabidopsis thaliana carboxyesterase 18); carboxylesterase	Unigene18332_All//2.00E-08//BQ413709			GO:0000904	nr +
Unigene18334_All	659	0.48	0.08	0.65	1.36	1.62	0.96	4.68	0.51	1.27	-2.63E+00	1.31E-01		4.40E-01	6.77E-01		2.52E-01	7.58E-01		-5.04E-01	5.11E-01		-3.21E+00	9.47E-14	Down	-1.88E+00	4.13E-08	Down	Unigene18334_All//gi|22328346|ref|NP_567288.2|//5.00E-24//Met-10+ like family protein / kelch repeat-containing protein [Arabidopsis thaliana] >gi|75162488|sp|Q8W4R1.1|TYW23_ARATH RecName: Full=tRNA wybutosine-synthesizing protein 2/3/4; Includes: RecName: Full=tRNA wybutosine-synthesizing protein 3 homolog; Includes: RecName: Full=tRNA wybutosine synthesizing protein 2 homolog >gi|17064868|gb|AAL32588.1| Unknown protein [Arabidopsis thaliana] >gi|30725408|gb|AAP37726.1| At4g04670 [Arabidopsis thaliana]	Unigene18334_All//1.00E-23//AT4G04670| Met-10+ like family protein / kelch repeat-containing protein	Unigene18334_All//1.00E-168//gi|3326728|gb|AI055614.1|AI055614				nr -
Unigene18335_All	563	1.39	0.72	0.85	4.25	2.51	1.60	1.80	0.59	0.57	-9.53E-01	2.33E-01		-7.12E-01	3.89E-01		-7.60E-01	5.37E-02		-1.40E+00	8.07E-04	Down	-1.60E+00	1.27E-02		-1.67E+00	7.35E-03				Unigene18335_All//1.00E-17//TC131237					
Unigene18336_All	670	32.41	17.47	8.90	0.30	1.44	1.08	0.00	0.00	0.00	-8.92E-01	1.47E-13		-1.86E+00	2.99E-39	Down	2.27E+00	4.58E-03		1.86E+00	4.71E-02		null	null		null	null		Unigene18336_All//gi|15238336|ref|NP_196102.1|//9.00E-29//OFP13 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 13) [Arabidopsis thaliana]	Unigene18336_All//4.00E-19//AT5G04820| OFP13 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 13)	Unigene18336_All//0.00E+00//TC135536			GO:0044464	nr -

Unigene18337_A11	693	3.93	3.95	2.07	7.84	8.10	6.19	1.16	0.36	3.85	8.20E-03	9.80E-01		-9.20E-01	2.18E-02		4.79E-02	8.77E-01		-3.40E-01	2.19E-01		-1.68E+00	2.46E-02		1.73E+00	2.28E-06	Up	Unigene18337_A11//gi|30691739|ref|NP_198216.2|//5.00E-40//AN3 (ANGUSTIFOLIA 3); protein binding / transcription coactivator [Arabidopsis thaliana] >gi|215398890|gb|AAM52881.1| GRF1-interacting factor 1 [Arabidopsis thaliana]	Unigene18337_A11//1.00E-34//AT5G28640| AN3 (ANGUSTIFOLIA 3); protein binding / transcription coactivator	Unigene18337_A11//0.00E+00//gi|78335725|gb|DT555999.1|DT555999			GO:0005515//GO:0048827	nr -
Unigene18338_A11	266	60.58	47.05	48.85	59.55	67.96	64.01	82.81	62.07	30.25	-3.65E-01	9.45E-03		-3.11E-01	3.75E-02		1.91E-01	1.80E-01		1.04E-01	5.33E-01		-4.16E-01	6.48E-05		-1.45E+00	1.16E-36	Down	Unigene18338_A11//gi|8401879|ref|NP_566608.1|//1.00E-13//NADH-ubiquinone oxidoreductase-related [Arabidopsis thaliana] >gi|186510194|ref|NP_001118655.1| NADH-ubiquinone oxidoreductase-related [Arabidopsis thaliana] >gi|14335154|gb|AAK59857.1| AT3g18410/MYF24_12 [Arabidopsis thaliana] >gi|18655369|gb|AAL76140.1| AT3g18410/MYF24_12 [Arabidopsis thaliana]	Unigene18338_A11//4.00E-15//AT3G18410| NADH-ubiquinone oxidoreductase-related	Unigene18338_A11//9.00E-131//TC160830		ko00190|Oxidative phosphorylation	GO:0005746//GO:0030964//GO:0043094	nr +
Unigene18341_A11	590	0.35	0.17	0.36	3.55	0.64	1.76	1.29	0.64	1.69	-1.05E+00	5.65E-01		2.54E-02	1.00E+00		-2.47E+00	2.22E-07	Down	-1.01E+00	2.37E-02		-1.02E+00	1.69E-01		3.88E-01	5.38E-01		Unigene18341_A11//gi|224083434|ref|XP_002307025.1|//3.00E-45//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222856474|gb|EEE94021.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene18341_A11//1.00E-13//AT1G61190| disease resistance protein (CC-NBS-LRR class), putative			ko04626|Plant-pathogen interaction		nr -
Unigene18342_A11	574	1.91	0.18	0.74	0.69	0.60	1.18	1.92	1.02	0.42	-3.44E+00	1.19E-04	Down	-1.37E+00	5.32E-02		-2.11E-01	8.25E-01		7.65E-01	4.10E-01		-9.10E-01	1.24E-01		-2.20E+00	5.66E-04	Down	Unigene18342_A11//gi|976284|gb|AAB48350.1|//1.00E-20//reverse transcriptase [Arabidopsis thaliana]	Unigene18342_A11//2.00E-08//AT4G20520| RNA binding / RNA-directed DNA polymerase					nr +
Unigene18343_A11	636	1.23	2.07	1.17	3.37	0.54	0.85	86.09	95.03	22.30	7.47E-01	2.05E-01		-7.41E-02	9.35E-01		-2.64E+00	4.13E-08	Down	-1.98E+00	3.06E-05	Down	1.43E-01	2.78E-02		-1.95E+00	3.94E-136	Down	Unigene18343_A11//gi|224127726|ref|XP_002329162.1|//2.00E-10//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene18343_A11//3.00E-08//AT5G36930| disease resistance protein (TIR-NBS-LRR class), putative	Unigene18343_A11//0.00E+00//TC154501				nr +
Unigene18345_A11	554	17.19	12.44	7.88	7.37	18.59	9.21	0.00	0.15	0.14	-4.67E-01	1.26E-02		-1.12E+00	1.43E-08	Down	1.33E+00	4.35E-14	Up	3.21E-01	2.70E-01		7.24E+00	4.02E-01		7.17E+00	4.05E-01		Unigene18345_A11//gi|195636998|gb|AC537967.1|//3.00E-24//lipid transfer protein [Zea mays]	Unigene18345_A11//5.00E-23//AT1G55260| lipid binding	Unigene18345_A11//3.00E-163//gi|13355927|gb|BG446215.1|BG446215			GO:0006810//GO:0031410	nr +
Unigene18346_A11	558	2.25	6.17	3.24	2.50	2.41	5.02	0.15	0.00	0.07	1.46E+00	3.39E-05	Up	5.28E-01	3.04E-01		-5.46E-02	9.11E-01		1.01E+00	7.85E-03		-7.24E+00	4.04E-01		-1.09E+00	6.77E-01		Unigene18346_A11//gi|6633825|gb|AAF19684.1|AC009519.18/4.00E-30//F1N19.24 [Arabidopsis thaliana]	Unigene18346_A11//7.00E-28//AT1G64670| BDG1 (BODYGUARD1); hydrolase	Unigene18346_A11//0.00E+00//gi|78325607|gb|DT545881.1|DT545881			GO:0030312	nr -
Unigene18347_A11	480	1.31	5.28	1.55	2.49	0.79	3.58	1.76	3.13	2.41	2.01E+00	7.53E-06	Up	2.48E-01	7.45E-01		-1.66E+00	6.44E-03		5.22E-01	3.34E-01		8.31E-01	8.77E-02		4.50E-01	4.17E-01					Unigene18347_A11//1.00E-100//DW483208					
Unigene18349_A11	331	4.58	5.51	0.64	22.57	1.04	2.87	1.79	1.39	2.53	2.66E-01	6.07E-01		-2.83E+00	5.52E-05	Down	-4.44E+00	5.42E-44	Down	-2.98E+00	7.44E-27	Down	-3.65E-01	6.48E-01		4.99E-01	4.61E-01		Unigene18349_A11//gi|94807648|gb|ABF47121.1|//4.00E-08//At5g02220 [Arabidopsis thaliana]	Unigene18349_A11//7.00E-05//AT5G02220| unknown protein					nr -
Unigene18350_A11	534	5.88	0.47	1.59	23.69	17.22	11.84	10.77	4.46	6.71	-3.63E+00	9.98E-13	Down	-1.97E+00	1.37E-06	Down	-4.61E-01	2.10E-03		-1.00E+00	2.07E-10	Down	-1.27E+00	3.37E-08	Down	-6.81E-01	1.42E-03					Unigene18350_A11//9.00E-145//DW519524				
Unigene18352_A11	662	1.98	5.59	2.98	1.28	1.98	1.50	0.00	0.00	0.00	1.50E+00	9.99E-06	Up	5.91E-01	2.29E-01		6.28E-01	3.11E-01		2.31E-01	7.41E-01		null	null		null	null					Unigene18352_A11//4.00E-24//TC176710				
Unigene18355_A11	729	5.02	0.83	0.58	2.60	6.66	3.22	0.70	0.00	0.00	-2.59E+00	7.66E-11	Down	-3.10E+00	2.70E-12	Down	1.36E+00	4.73E-07	Up	3.11E-01	5.02E-01		-9.44E+00	8.89E-04	Down	-9.44E+00	5.54E-04	Down	Unigene18355_A11//gi|15227458|ref|NP_181107.1|//9.00E-46//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	Unigene18355_A11//5.00E-47//AT2G35640| hydroxyproline-rich glycoprotein family protein	Unigene18355_A11//0.00E+00//gi|21095194|gb|BQ407507.1|BQ407507			GO:0010468//GO:0043231	nr -
Unigene18358_A11	421	2.49	3.13	0.25	4.26	3.60	2.04	2.51	0.99	0.76	3.32E-01	5.83E-01		-3.30E+00	4.59E-04	Down	-2.43E-01	6.16E-01		-1.06E+00	3.03E-02		-1.34E+00	2.90E-02		-1.73E+00	4.76E-03									
Unigene18360_A11	1236	0.00	0.70	0.26	0.32	0.06	0.37	3.69	6.19	8.96	9.44E+00	4.95E-05	Up	8.01E+00	4.53E-02		-2.53E+00	5.80E-02		1.81E-01	8.84E-01		7.44E-01	7.28E-05		1.28E+00	1.57E-15	Up	Unigene18360_A11//gi|34452085|gb|AAQ72499.1|//2.00E-89//MADS-box protein 14 [Petunia x hybrida]	Unigene18360_A11//1.00E-81//AT2G14210| AGL44 (AGAMOUS-LIKE 44); DNA binding / transcription factor	Unigene18360_A11//3.00E-26//C0107078	MADS		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0016628//GO:0031667//GO:0043231//GO:0048528	nr +
Unigene18361_A11	329	3.82	3.23	0.97	1.21	1.05	1.92	8.22	9.40	31.00	-2.39E-01	6.68E-01		-1.97E+00	4.63E-03		-2.11E-01	8.25E-01		6.66E-01	4.92E-01		1.93E-01	6.07E-01		1.91E+00	4.16E-25	Up	Unigene18361_A11//gi|18398327|ref|NP_566341.1|//1.00E-41//protein kinase family protein [Arabidopsis thaliana]	Unigene18361_A11//6.00E-43//AT3G09010| protein kinase family protein	Unigene18361_A11//1.00E-176//ES810755			GO:0004672//GO:0006464//GO:0032559//GO:0043231	nr -
Unigene18363_A11	573	1.92	1.77	1.58	3.48	1.92	0.39	3.76	0.15	0.97	-1.17E-01	8.44E-01		-2.80E-01	6.54E-01		-8.55E-01	5.06E-02		-3.14E+00	7.59E-08	Down	-4.69E+00	9.88E-13	Down	-1.95E+00	3.72E-06	Down	Unigene18363_A11//gi|297606239|ref|NP_001058153.2|//8.00E-29//Os06g0638500 [Oryza sativa Japonica Group] >gi|255677259|dbj|BAF20067.2| Os06g0638500 [Oryza sativa Japonica Group]	Unigene18363_A11//2.00E-27//AT2G23300| leucine-rich repeat transmembrane protein kinase, putative	Unigene18363_A11//7.00E-84//gi|48879433|gb|CO130455.1|CO130455		ko04626|Plant-pathogen interaction	GO:0004871//GO:0006464//GO:0007167//GO:0016301//GO:0016628//GO:0031224//GO:0032559	nr +
Unigene18366_A11	528	6.04	16.41	23.40	0.57	1.24	2.22	0.00	0.24	0.00	1.44E+00	1.03E-11	Up	1.95E+00	5.06E-24	Up	1.13E+00	2.38E-01		1.97E+00	4.50E-03		7.89E+00	2.40E-01		null	null		Unigene18366_A11//gi|297810439|ref|XP_002873103.1|//7.00E-28//permease, cytosine/purines, uracil, thiamine, allantoin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318940|gb|EFH49362.1| permease, cytosine/purines, uracil, thiamine, allantoin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene18366_A11//2.00E-28//AT5G03555| permease, cytosine/purines, uracil, thiamine, allantoin family protein	Unigene18366_A11//7.00E-50//C0081242			GO:0006810//GO:0015932//GO:0044464	nr +
Unigene18367_A11	656	1.04	0.23	0.00	2.13	1.52	0.41	1.29	1.34	0.91	-2.16E+00	2.84E-02		-1.00E+01	7.64E-04	Down	-4.82E-01	4.04E-01		-2.36E+00	2.38E-04	Down	5.38E-02	9.58E-01		-5.01E-01	4.47E-01					Unigene18367_A11//0.00E+00//gi|164287207|gb|ES837615.1|ES837615					
Unigene18368_A11	723	0.00	1.05	0.29	1.10	1.19	1.12	26.20	11.04	68.11	1.00E+01	1.77E-04	Up	8.20E+00	1.41E-01		1.11E-01	9.04E-01		2.85E-02	9.71E-01		-1.25E+00	1.90E-24	Down	1.38E+00	4.57E-74	Up	Unigene18368_A11//gi|15227891|ref|NP_181744.1|//2.00E-26//VQ motif-containing protein [Arabidopsis thaliana] >gi|18491279|gb|AAL69464.1| At2g42140/T24P15.5 [Arabidopsis thaliana]	Unigene18368_A11//7.00E-11//AT2G42140| VQ motif-containing protein				GO:0043231	nr +
Unigene1837_A11	2980	25.83	18.30	23.32	69.52	73.20	61.30	25.44	8.92	14.34	-4.97E-01	5.98E-17		-1.47E-01	2.48E-02		7.44E-02	4.26E-02		-1.82E-01	1.28E-07		-1.51E+00	5.80E-128	Down	-8.27E-01	2.62E-50		Unigene1837_A11//gi|119507459|dbj|BAF42037.1|//0.00E+00//cellulase2 [Pyrus communis]	Unigene1837_A11//0.00E+00//AT1G75680| AtGH9B7 (Arabidopsis thaliana glycosyl hydrolase 9B7); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene1837_A11//0.00E+00//TC162981		ko00500|Starch and sucrose metabolism		nr -
Unigene18372_A11	888	2.36	3.42	0.18	4.54	2.44	2.19	6.76	15.81	13.86	5.39E-01	1.36E-01		-3.71E+00	2.55E-08	Down	-8.95E-01	1.58E-03		-1.06E+00	4.58E-04	Down	1.23E+00	7.49E-18	Up	1.04E+00	1.57E-12	Up				Unigene18372_A11//0.00E+00//gi|109826632|gb|DW225342.1|DW225342					
Unigene18375_A11	576	1.27	1.23	0.37	5.28	2.51	1.49	1.69	1.31	0.28	-4.63E-02	9.68E-01		-1.78E+00	6.00E-02		-1.07E+00	1.41E-03		-1.82E+00	1.74E-06	Down	-3.70E-01	5.87E-01		-2.61E+00	3.35E-04	Down	Unigene18375_A11//gi|297724159|ref|NP_001174443.1|//2.00E-36//Os05g0434000 [Oryza sativa Japonica Group] >gi|255676397|dbj|BAH93171.1| Os05g0434000 [Oryza sativa Japonica Group]	Unigene18375_A11//2.00E-08//ATMG01250| hypothetical protein				GO:0003676//GO:0006260//GO:0034061//GO:0043231	nr -
Unigene18377_A11	866	5.92	2.05	2.46	5.00	3.26	9.70	0.73	0.87	2.76	-1.53E+00	6.75E-08	Down	-1.27E+00	8.25E-06	Down	-6.18E-01	2.65E-02		9.55E-01	1.43E-06		2.46E-01	7.32E-01		1.91E+00	1.69E-06	Up	Unigene18377_A11//gi|292668955|gb|ADE41132.1|//1.00E-68//AP2 domain class transcription factor [Malus x domestica]	Unigene18377_A11//5.00E-49//AT5G11590| TINY2 (TINY2); DNA binding / transcription factor	Unigene18377_A11//0.00E+00//TC153571	AP2-EREBP		GO:0006350//GO:0010468	nr -
Unigene18378_A11	664	7.72	3.05	1.44	38.11	56.48	8.23	0.00	0.13	0.00	-1.34E+00	1.32E-06	Down	-2.42E+00	3.38E-13	Down	5.67E-01	2.15E-12		-2.21E+00	2.76E-64	Down	6.98E+00	4.02E-01		null	null		Unigene18378_A11//gi|15241393|ref|NP_199929.1|//2.00E-15//ankyrin repeat family protein [Arabidopsis thaliana] >gi|45825143|gb|AAS77479.1| At5g51160 [Arabidopsis thaliana]	Unigene18378_A11//1.00E-16//AT3G51160| ankyrin repeat family protein	Unigene18378_A11//0.00E+00//gi|109880897|gb|DW509867.1|DW509867				nr +
Unigene1838_A11	2296	40.38	33.17	14.91	66.41	43.85	28.03	21.62	4.53	5.95	-2.84E-01	1.26E-07		-1.44E+00	7.78E-115	Down	-5.99E-01	1.16E-55		-1.24E+00	9.99E-170	Down	-2.25E+00	2.08E-144	Down	-1.86E+00	4.71E-116	Down	Unigene1838_A11//gi|209962339|gb|ACJQ2090.1|//4.00E-98//AG-motif binding protein [Garcinia mangostana]	Unigene1838_A11//1.00E-53//AT3G54810| zinc finger (GATA type) family protein	Unigene1838_A11//0.00E+00//TC160551	C2C2-GATA			nr +
Unigene18380_A11	928	0.00	0.22	0.23	11.00	9.68	5.99	3.37	1.13	1.16	7.77E+00	1.37E-01		7.84E+00	1.41E-01		-1.84E-01	3.56E-01		-8.78E-01	5.55E-07		-1.58E+00	2.24E-06	Down	-1.54E+00	2.10E-06	Down	Unigene18380_A11//gi|71041096|gb|AAZ20436.1|//2.00E-78//MYB20 [Malus x domestica]	Unigene18380_A11//4.00E-56//AT3G08500| MYB83 (myb domain protein 83); DNA binding / transcription factor	Unigene18380_A11//7.00E-116//DN802716	MYB		GO:0001071//GO:0003676//GO:0006351//GO:0009832//GO:0010033//GO:0010468//GO:0043231	nr +
Unigene18381_A11	987	0.64	0.41	0.00	0.00	0.07	1.01	21.29	8.17	11.30	-6.31E-01	4.75E-01		-9.31E+00	1.41E-03		6.13E+00	6.10E-01		9.98E+00	6.15E-06	Up	-1.38E+00	1.53E-31	Down	-9.14E-01	3.82E-17		Unigene18381_A11//gi|226503055|ref|NP_001147033.1|//6.00E-52//pathogenesis-related protein PRB1-3 [Zea mays] >gi|195606704|gb|ACG25182.1| pathogenesis-related protein PRB1-3 precursor [Zea mays]	Unigene18381_A11//2.00E-51//AT5G66590| allergen V5/Tpx-1-related family protein	Unigene18381_A11//1.00E-46//TC144633		ko04626|Plant-pathogen interaction	GO:0044464	nr +
Unigene18382_A11	1024	0.26	0.54	0.94	2.48	1.45	0.62	0.99	0.78	0.62	1.09E+00	2.74E-01		1.87E+00	2.06E-02		-7.79E-01	4.02E-02		-2.01E+00	3.48E-06	Down	-3.54E-01	5.99E-01		-6.71E-01	2.53E-01		Unigene18382_A11//gi|124359163|gb|ABN05686.1|//1.00E-17//Zinc finger, CCHC-type [Medicago truncatula]	Unigene18382_A11//3.00E-05//AT3G47920| unknown protein	Unigene18382_A11//7.00E-33//gi|164323926|gb|ES801532.1|ES801532				nr -
Unigene18384_A11	1270	0.00	0.00	0.00	0.08	0.00	0.07	2.30	3.09	4.71	null	null		null	null		-6.29E+00	3.13E-01		-1.41E-01	9.51E-01		4.29E-01	1.34E-01		1.03E+00	1.61E-06	Up	Unigene18384_A11//gi|18700171|gb|AAL77697.1|//3.00E-82//AT5g20480/F7C8_70 [Arabidopsis thaliana] >gi|29028752|gb|AAO64755.1| At5g20480/F7C8_70 [Arabidopsis thaliana]	Unigene18384_A11//3.00E-74//AT5G20480| EFR (EF-TU RECEPTOR); ATP binding / kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction	GO:0004672//GO:0009987//GO:0023033//GO:0045087//GO:0050776	nr +
Unigene18385_A11	385	0.14	0.00	0.83	1.29	1.61	0.94	6.70	3.26	2.69	-7.09E+00	6.13E-01		2.61E+00	1.46E-01		3.15E-01	7.84E-01		-4.63E-01	6.59E-01		-1.04E+00	3.25E-03		-1.32E+00	1.79E-04	Down				Unigene18385_A11//4.00E-07//AI055087					
Unigene18387_A11	376	130.11	50.40	131.14	101.62	140.12	78.92	1.01	0.22	0.21	-1.37E+00	2.01E-58	Down	1.14E-02	9.07E-01		4.64E-01	4.33E-12		-3.65E-01	1.53E-05		-2.19E+00	8.75E-02		-2.26E+00	6.49E-02		Unigene18387_A11//gi|151176133|gb|ABN42183.2|//2.00E-61//phototropin-1 [Solanum lycopersicum]	Unigene18387_A11//1.00E-60//AT3G45780| PHOT1 (PHOTOTROPIN 1); RNA binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase	Unigene18387_A11//0.00E+00//TC177868		ko04712|Circadian rhythm - plant	GO:0004673//GO:0004674//GO:0005515//GO:0006351//GO:0006468//GO:0009416//GO:0009606//GO:0009881//GO:0009902//GO:0010118//GO:0010360//GO:0015992//GO:0023060//GO:0032559//GO:0043231//GO:0044459	nr +
Unigene18389_A11	410	1.53	1.24	0.52	1.34	2.86	3.64	2.78	1.43	0.58	-3.09E-01	7.01E-01		-1.56E+00	1.29E-01		1.10E+00	8.96E-02		1.44E+00	1.11E-02		-9.64E-01	9.33E-02		-2.26E+00	3.40E-04	Down	Unigene18389_A11//gi|115444033|ref|NP_001045796.1|//6.00E-12//Os02g0132200 [Oryza sativa Japonica Group] >gi|113535327|dbj|BAF07710.1| Os02g0132200 [Oryza sativa Japonica Group]	Unigene18389_A11//2.00E-16//AT5G05240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP030365 (InterPro:IPR016953); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G40630.1); Has 24 Blast hits to 24 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene18389_A11//1.00E-63//DT052433			GO:0009536	nr +

Unigene1839_A11	621	0.42	3.43	1.72	3.13	1.55	2.69	1.70	0.94	0.90	3.02E+00	1.63E-07	Up	2.03E+00	8.68E-03		-1.01E+00	2.18E-02		-2.17E-01	6.69E-01		-8.53E-01	1.55E-01		-9.22E-01	1.08E-01		Unigene1839_A11//gi|15221582|ref|NP_177064.1|//2.00E-18//BIM2 (BES1-interacting Myc-like protein 2); DNA binding / transcription factor [Arabidopsis thaliana] >gi|61211674|sp|Q9CAA4.1|BIM2_ARATH RecName: Full=Transcription factor BIM2; AltName: Full=BES1-interacting Myc-like protein 2; AltName: Full=Transcription factor EN 125; AltName: Full=bHLH transcription factor bHLH102; AltName: Full=Basic helix-loop-helix protein 102; Short=bHLH 102; Short=AtbHLH102	Unigene1839_A11//1.00E-19//AT1G69010| BIM2 (BES1-interacting Myc-like protein 2); DNA binding / transcription factor	Unigene1839_A11//3.00E-160//TC134011	bHLH			nr -
Unigene18391_A11	1550	5.27	1.99	18.62	0.13	0.58	0.29	1.04	0.13	0.39	-1.40E+00	1.04E-10	Down	1.82E+00	1.19E-50	Up	2.17E+00	9.20E-03		1.18E+00	3.38E-01		-2.94E+00	6.45E-07	Down	-1.43E+00	2.13E-03		Unigene18391_A11//gi|34850945|dbj|BAC87845.1|//1.00E-102//leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	Unigene18391_A11//3.00E-90//AT4G08850| kinase	Unigene18391_A11//0.00E+00//DR462992		ko03410|Base excision repair		nr +
Unigene18394_A11	1068	1.32	0.52	0.55	0.84	0.55	0.72	3.25	2.31	1.23	-1.34E+00	2.00E-02		-1.27E+00	3.55E-02		-6.15E-01	4.02E-01		-2.24E-01	7.50E-01		-4.92E-01	1.05E-01		-1.40E+00	3.45E-06	Down	Unigene18394_A11//gi|115455585|ref|NP_001051393.1|//4.00E-61//0s03g0769000 [Oryza sativa Japonica Group] >gi|113549864|dbj|BAF13307.1|Os03g0769000 [Oryza sativa Japonica Group]	Unigene18394_A11//2.00E-82//AT5G66600| unknown protein	Unigene18394_A11//0.00E+00//gi|31073688|gb|CA993967.1|CA993967				nr -
Unigene18395_A11	814	1.09	0.87	0.39	7.89	5.67	3.44	0.57	0.51	1.08	-3.26E-01	6.22E-01		-1.48E+00	6.99E-02		-4.78E-01	3.41E-02		-1.20E+00	2.77E-07	Down	-1.54E-01	8.70E-01		9.14E-01	1.59E-01		Unigene18395_A11//gi|225348641|gb|ACN87282.1|//1.00E-104//with no lysine kinase [Glycine max]	Unigene18395_A11//8.00E-105//AT5G41990| WNK8 (WITH NO LYSINE (K) KINASE 8); kinase/ protein kinase	Unigene18395_A11//0.00E+00//gi|78336011|gb|DT556285.1|DT556285		ko04712|Circadian rhythm - plant		nr -
Unigene18396_A11	447	1.17	0.00	0.00	2.79	2.47	1.82	5.20	1.68	1.07	-1.02E+01	2.93E-03		-1.02E+01	4.76E-03		-1.77E-01	7.95E-01		-6.15E-01	3.33E-01		-1.63E+00	4.15E-05	Down	-2.28E+00	7.89E-08	Down				Unigene18396_A11//5.00E-07//BG441850				
Unigene18398_A11	698	0.30	2.47	0.84	0.57	0.30	0.78	3.51	10.00	1.83	3.04E+00	3.13E-06	Up	1.49E+00	1.53E-01		-9.48E-01	4.21E-01		4.44E-01	6.78E-01		1.51E+00	2.00E-12	Up	-9.44E-01	6.97E-03									
Unigene184_A11	1602	2.25	3.04	1.63	3.08	3.27	3.58	3.72	2.79	7.88	4.30E-01	1.21E-01		-4.68E-01	1.73E-01		8.59E-02	8.15E-01		2.18E-01	4.50E-01		-4.15E-01	6.20E-02		1.08E+00	9.95E-14	Up	Unigene184_A11//gi|11094369|gb|AAG29595.1|AF196288_1//1.00E-169//Ser/Thr specific protein phosphatase 2A B regulatory subunit alpha isoform [Medicago sativa subsp. x varia]	Unigene184_A11//8.00E-150//AT1G17720| ATB BETA; nucleotide binding / protein phosphatase type 2A regulator	Unigene184_A11//0.00E+00//ES817351				nr +
Unigene18401_A11	561	3.08	1.81	1.14	4.35	2.95	15.70	2.94	0.37	1.35	-7.69E-01	1.21E-01		-1.43E+00	8.21E-03		-5.62E-01	1.62E-01		1.85E+00	1.11E-17	Up	-2.98E+00	3.67E-07	Down	-1.12E+00	1.16E-02		Unigene18401_A11//gi|297833855|ref|XP_002887309.1|//1.00E-54//allinase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333150|gb|EFH63568.1|allinase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene18401_A11//5.00E-55//AT1G23320| TAR1 (TRYPTOPHAN AMINOTRANSFERASE RELATED 1); L-tryptophan:2-oxoglutarate aminotransferase/ L-tryptophan:pyruvate aminotransferase/ carbon-sulfur lyase	Unigene18401_A11//0.00E+00//TC149881			GO:0009630//GO:0009639//GO:0009683//GO:0009725//GO:0009793//GO:0009888//GO:0010015//GO:0010051//GO:0010326//GO:0016846//GO:0044424//GO:0017635//GO:0048037//GO:0048138//GO:0048827//GO:0070529//GO:0070546//GO:0070547	nr +
Unigene18404_A11	875	0.24	0.23	0.12	0.63	0.71	0.26	4.20	2.67	31.01	-4.66E-02	9.88E-01		-9.75E-01	6.21E-01		1.78E-01	8.64E-01		-1.28E+00	2.24E-01		-6.52E-01	2.26E-02		2.88E+00	3.15E-106	Up	Unigene18404_A11//gi|115468004|ref|NP_001057601.1|//2.00E-60//0s06g0358800 [Oryza sativa Japonica Group] >gi|75254269|sp|Q69KJ0.1|RTL3_ORYSJ RecName: Full=Ribonuclease 3-like protein 3; AltName: Full=Ribonuclease III-like protein 3; Short=RNase III-like protein 3 >gi|51091751|dbj|BAD36550.1| CAF protein-like [Oryza sativa Japonica Group] >gi|113596641|dbj|BAF19515.1|Os06g0358800 [Oryza sativa Japonica Group]	Unigene18404_A11//2.00E-39//AT4G15417| ATRTL1 (ARABIDOPSIS THALIANA RNASEIII-LIKE 1); RNA binding / ribonuclease III	Unigene18404_A11//1.00E-46//AI729675			GO:0003676//GO:0010467//GO:0016891//GO:0043231	nr -
Unigene18406_A11	813	661.06	319.54	440.15	160.41	174.76	179.82	20.54	6.12	8.18	-1.05E+00	0.00E+00	Down	-5.87E-01	5.20E-149		1.24E-01	4.10E-03		1.65E-01	9.69E-05		-1.75E+00	2.93E-35	Down	-1.33E+00	1.54E-24	Down	Unigene18406_A11//gi|15217777|ref|NP_174116.1|//2.00E-42//LTPG1 (GLYCOSYLPHOSPHATIDYLINOSITOL-ANCHORED LIPID PROTEIN TRANSFER 1) [Arabidopsis thaliana] >gi|38258836|sp|Q9C7F7.1|UGP15_ARATH RecName: Full=Uncharacterized GPI-anchored protein At1g27950; Flags: Precursor	Unigene18406_A11//2.00E-37//AT1G27950| LTPG1 (GLYCOSYLPHOSPHATIDYLINOSITOL-ANCHORED LIPID PROTEIN TRANSFER 1)	Unigene18406_A11//0.00E+00//TC166241			GO:0006810//GO:0031225//GO:0031410	nr -
Unigene18410_A11	964	1.79	10.51	3.20	0.47	0.57	0.80	5.79	19.99	12.94	2.55E+00	3.53E-28	Up	8.39E-01	2.37E-02		2.97E-01	8.18E-01		7.76E-01	3.78E-01		1.79E+00	9.52E-42	Up	1.16E+00	4.84E-15	Up				Unigene18410_A11//3.00E-16//TC157819				
Unigene18411_A11	546	0.00	0.00	0.00	1.28	1.07	1.32	6.50	6.35	1.39	null	null		null	null		-2.53E-01	7.78E-01		5.13E-02	9.48E-01		-3.39E-02	9.30E-01		-2.23E+00	3.02E-11	Down								
Unigene18414_A11	354	2.66	0.72	0.90	2.25	1.36	0.00	0.48	1.53	0.56	-1.89E+00	1.53E-02		-1.56E+00	4.90E-02		-7.23E-01	3.47E-01		-1.11E-01	4.90E-05	Down	1.68E+00	7.92E-02		2.36E-01	8.83E-01					Unigene18414_A11//5.00E-99//CO093194				
Unigene18415_A11	602	33.63	10.52	18.49	6.37	4.69	4.50	1.26	0.56	0.40	-1.68E+00	6.04E-33	Down	-8.63E-01	1.57E-11		-4.42E-01	1.61E-01		-5.01E-01	1.21E-01		-1.19E+00	1.12E-01		-1.67E+00	2.39E-02					Unigene18415_A11//0.00E+00//TC163121				
Unigene18416_A11	379	6.76	11.90	6.18	2.50	5.36	9.06	3.12	4.96	7.67	8.15E-01	4.25E-03		-1.30E-01	7.45E-01		1.10E+00	1.46E-02		1.86E+00	2.97E-07	Up	6.68E-01	1.21E-01		1.30E+00	8.58E-05	Up				Unigene18416_A11//1.00E-90//gi|78323949|gb|DT544223.1|DT544223				
Unigene18418_A11	675	0.16	0.00	0.00	7.01	3.93	1.87	4.45	7.80	3.36	-7.28E+00	3.73E-01		-7.28E+00	3.95E-01		-8.36E-01	1.20E-03		-1.90E+00	2.60E-10	Down	8.11E-01	4.78E-04		-4.03E-01	2.05E-01		Unigene18418_A11//gi|2808682|emb|CAA05267.1|//4.00E-37//Hcr9-4C [Solanum habrochaites]	Unigene18418_A11//2.00E-24//AT3G11080| AtRLP35 (Receptor Like Protein 35); kinase/ protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene1842_A11	2021	5.67	3.23	3.08	7.00	6.46	5.39	6.36	2.83	3.33	-8.10E-01	1.60E-06		-8.79E-01	5.22E-07		-1.16E-01	5.26E-01		-3.78E-01	1.19E-02		-1.17E+00	2.99E-15	Down	-9.33E-01	3.45E-11		Unigene1842_A11//gi|15238875|ref|NP_199615.1|//1.00E-130//ubiquitin thiolesterase [Arabidopsis thaliana]	Unigene1842_A11//2.00E-131//AT5G48040| ubiquitin thiolesterase	Unigene1842_A11//0.00E+00//gi|164295615|gb|ES813880.1|ES813880				nr -
Unigene18420_A11	930	0.00	0.00	0.00	1.39	1.26	0.00	8.77	11.19	4.16	null	null		null	null		-1.46E-01	8.22E-01		-1.04E+01	4.24E-08	Down	3.51E-01	3.09E-02		-1.08E+00	3.39E-09	Down	Unigene18420_A11//gi|157955935|gb|ABR06391.1|//2.00E-88//CBL8 [Gossypium hirsutum]	Unigene18420_A11//8.00E-73//AT1G64480| CBL8 (CALCINEURIN B-LIKE PROTEIN 8); calcium ion binding	Unigene18420_A11//8.00E-94//TC156917		ko04650|Natural killer cell mediated cytotoxicity	GO:0004722//GO:0006875//GO:0006971//GO:0008287//GO:0009503//GO:0019932//GO:0044424//GO:0046872	nr -
Unigene18421_A11	831	0.00	0.12	0.00	0.00	0.00	0.00	48.74	18.86	27.61	6.93E+00	3.87E-01		null	null		null	null		null	null		-1.37E+00	2.52E-59	Down	-8.20E-01	6.19E-27		Unigene18421_A11//gi|575603|dbj|BAA07663.1|//4.00E-86//cationic peroxidase isozyme 38K precursor [Nicotiana tabacum]	Unigene18421_A11//4.00E-73//AT3G30400| peroxidase, putative	Unigene18421_A11//4.00E-52//FG548240		ko00940|Phenylpropanoid biosynthesis/ko00360|Phenylalanine metabolism	GO:0003824//GO:0016209//GO:0046872	nr -
Unigene18422_A11	288	114.82	241.74	92.45	120.90	77.96	95.50	69.73	391.40	238.48	1.07E+00	1.65E-56	Up	-3.13E-01	1.45E-03		-6.33E-01	2.48E-14		-3.40E-01	1.42E-04		2.49E+00	0.00E+00	Up	1.77E+00	2.24E-148	Up	Unigene18422_A11//gi|224075517|ref|XP_002304662.1|//3.00E-33//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842094|gb|EEE79641.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene18422_A11//6.00E-11//AT5G13180| ANAC083 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 83); transcription factor	Unigene18422_A11//1.00E-154//TC132151	NAC		GO:0003676//GO:0010087//GO:0010468//GO:0030528	nr +
Unigene18423_A11	565	0.83	3.59	1.51	0.88	1.77	0.88	3.82	4.14	3.67	2.11E+00	4.59E-05	Up	8.56E-01	2.80E-01		1.00E+00	1.65E-01		-3.90E-03	9.87E-01		1.18E-01	7.65E-01		-5.78E-02	8.90E-01									
Unigene18425_A11	474	63.36	51.63	47.52	90.80	106.21	95.57	130.50	70.72	62.70	-2.95E-01	3.19E-03		-4.15E-01	4.68E-05		2.26E-01	1.88E-03		7.38E-02	4.58E-01		-8.84E-01	7.90E-45		-1.06E+00	7.41E-62	Down	Unigene18425_A11//gi|192910792|gb|ACF06504.1|//2.00E-15//60S ribosomal protein L28 [Elaeis guineensis]	Unigene18425_A11//6.00E-11//AT2G19730| 60S ribosomal protein L28 (RPL28A)	Unigene18425_A11//1.00E-103//TC144564		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene18427_A11	294	2.49	0.34	0.36	7.62	2.69	5.38	3.88	0.71	0.68	-2.85E+00	6.26E-03		-2.78E+00	1.05E-02		-1.50E+00	2.60E-04	Down	-5.04E-01	2.61E-01		-2.45E+00	2.46E-04	Down	-2.52E+00	1.20E-04	Down								
Unigene18428_A11	397	18.85	55.26	18.24	35.26	57.68	174.51	108.42	58.11	100.45	1.55E+00	9.01E-32	Up	-4.70E-02	8.40E-01		7.10E-01	2.81E-11		2.31E+00	9.34E-181	Up	-9.00E-01	2.28E-32		-1.10E-01	1.62E-01		Unigene18428_A11//gi|164668308|gb|ABK60195.2|//4.00E-22//PIP2 protein [Gossypium hirsutum]	Unigene18428_A11//1.00E-17//AT3G53420| PIP2A (PLASMA MEMBRANE INTRINSIC PROTEIN 2A); water channel	Unigene18428_A11//4.00E-146//TC157513			GO:0006810//GO:0031224	nr +
Unigene18429_A11	503	0.31	0.20	0.53	1.19	0.27	0.54	2.35	3.66	5.94	-6.31E-01	7.28E-01		7.62E-01	6.44E-01		-2.12E+00	3.06E-02		-1.14E+00	2.43E-01		6.35E-01	1.44E-01		1.34E+00	4.35E-05	Up				Unigene18429_A11//1.00E-38//TC171826				
Unigene18431_A11	544	1.92	1.21	0.88	2.38	2.79	1.74	2.02	0.38	0.95	-6.68E-01	3.23E-01		-1.13E+00	1.17E-01		2.26E-01	7.27E-01		-4.50E-01	4.84E-01		-2.39E+00	4.11E-04	Down	-1.09E+00	5.40E-02		Unigene18431_A11//gi|55793838|gb|AAV65493.1|//5.00E-51//calmodulin-binding heat shock protein [Gossypium hirsutum]	Unigene18431_A11//5.00E-41//AT3G49050| lipase class 3 family protein / calmodulin-binding heat-shock protein, putative	Unigene18431_A11//2.00E-149//TC129597			GO:0004091//GO:0005515//GO:0006629//GO:0031410//GO:0050896	nr +
Unigene18433_A11	1182	0.66	0.69	0.86	2.40	1.92	1.57	1.04	2.09	2.26	4.68E-02	9.69E-01		3.66E-01	6.21E-01		-3.21E-01	4.19E-01		-6.17E-01	1.05E-01		1.01E+00	5.47E-03		1.12E+00	9.68E-04	Up				Unigene18433_A11//0.00E+00//gi|13248530|gb|BF276070.2|BF276070				
Unigene18434_A11	611	1.88	1.91	4.18	4.40	4.17	1.85	1.59	0.27	0.13	1.79E-02	9.91E-01		1.15E+00	6.07E-03		-7.81E-02	8.33E-01		-1.25E+00	1.20E-03		-2.54E+00	6.41E-04	Down	-3.61E+00	2.14E-05	Down								
Unigene18435_A11	450	0.47	0.00	0.00	0.44	1.22	0.50	2.91	4.09	60.47	-8.86E+00	1.22E-01		-8.86E+00	1.46E-01		1.47E+00	1.77E-01		1.81E-01	9.35E-01		4.89E-01	2.72E-01		4.38E+00	2.30E-151	Up	Unigene18435_A11//gi|288557882|emb|CBJ49377.1|//1.00E-24//pathogenesis-related protein 10.5 [Vitis vinifera]		Unigene18435_A11//2.00E-133//TC170165			GO:0006950	nr +
Unigene18436_A11	898	8.74	42.66	29.83	2.44	8.36	9.76	0.09	0.00	0.18	2.29E+00	2.59E-92	Up	1.77E+00	3.14E-45	Up	1.78E+00	1.92E-15	Up	2.00E+00	2.00E-19	Up	-6.56E+00	4.04E-01		9.14E-01	6.24E-01		Unigene18436_A11//gi|15220875|ref|NP_173229.1|//4.00E-38//EGY3 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN-LIKE 3) [Arabidopsis thaliana] >gi|9665065|gb|AAF97267.1|AC034106_10 F2H15.10 [Arabidopsis thaliana]	Unigene18436_A11//2.00E-39//AT1G17670| EGY3 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN-LIKE 3)	Unigene18436_A11//0.00E+00//gi|78340731|gb|DT561005.1|DT561005			GO:0000302//GO:0009642//GO:0043231	nr -
Unigene18438_A11	611	0.26	0.33	0.70	9.46	10.09	5.54	2.77	0.41	1.04	3.69E-01	8.17E-01		1.44E+00	2.53E-01		9.32E-02	7.71E-01		-7.71E-01	1.51E-03		-2.75E+00	8.02E-07	Down	-1.41E+00	1.77E-03		Unigene18438_A11//gi|3047082|gb|AAC13595.1|//1.00E-71//similar to Vigna radiata pectinacetylesterase precursor (GB:X99248) [Arabidopsis thaliana]	Unigene18438_A11//2.00E-68//AT5G26670| pectinacetylesterase, putative	Unigene18438_A11//3.00E-123//TC157856			GO:0044464	nr +
Unigene18439_A11	999	6.13	2.13	5.81	0.75	0.48	0.45	0.00	0.00	0.08	-1.52E+00	3.20E-09	Down	-7.68E-02	7.64E-01		-6.32E-01	4.37E-01		-7.26E-01	3.90E-01		null	null		6.32E+00	4.05E-01		Unigene18439_A11//gi|224077016|ref|XP_002305094.1|//1.00E-104//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222848058|gb|EEE85605.1|glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene18439_A11//3.00E-32//AT2G29110| ATGLR2.8; intracellular ligand-gated ion channel				GO:0005231//GO:0006810//GO:0008066//GO:0030313//GO:0031224	nr +
Unigene18440_A11	1310	0.16	0.04	0.24	0.27	0.18	0.07	29.37	13.11	12.89	-2.05E+00	3.34E-01		6.10E-01	6.25E-01		-5.33E-01	6.46E-01		-1.95E+00	1.96E-01		-1.16E+00	7.29E-44	Down	-1.19E+00	1.25E-46	Down	Unigene18440_A11//gi|115463027|ref|NP_001055113.1|//2.00E-15//0s05g0295800 [Oryza sativa Japonica Group] >gi|113578664|dbj|BAF17027.1|Os05g0295800 [Oryza sativa Japonica Group]	Unigene18440_A11//5.00E-16//AT1G08110| lactoylglutathione lyase, putative / glyoxalase I, putative	Unigene18440_A11//4.00E-47//gi|109881061|gb|DW510031.1|DW510031		ko00620|Pyruvate metabolism		nr -
Unigene18441_A11	348	23.30	8.44	10.86	3.15	0.99	0.52	0.00	0.00	0.00	-1.46E+00	2.53E-11	Down	-1.10E+00	3.58E-07	Down	-1.67E+00	9.38E-03		-2.60E+00	7.14E-04	Down	null	null		null	null					Unigene18441_A11//0.00E+00//ES843283				
Unigene18442_A11	483	0.65	1.36	0.66	3.61	0.71	3.27	3.59	6.14	2.80	1.07E+00	2.37E-01		2.55E-02	1.00E+00		-2.34E+00	6.96E-06	Down	-1.41E-01	7.77E-01		7.76E-01	1.67E-02		-3.56E-01	4.17E-01		Unigene18442_A11//gi|145335397|ref|NP_172597.2|//2.00E-36//ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene18442_A11//1.00E-37//AT1G11300| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene18442_A11//2.00E-90//CO081719		ko00270|Cysteine and methionine metabolism		nr -
Unigene18444_A11	329	6.68	21.87	6.31	3.18	4.92	3.71	43.82	61.61	20.59	1.71E+00	2.01E-12	Up	-8.15E-02	8.52E-01		6.30E-01	2.47E-01		2.21E-01	7.22E-01		4.92E-01	6.19E-06		-1.09E+00	7.96E-16	Down				Unigene18444_A11//7.00E-95//TC175202				
Unigene18445_A11	328	182.64	126.83	97.57	203.36	117.58	169.64	49.76	217.01	87.69	-5.26E-01	1.00E-14		-9.05E-01	1.27E-35		-7.90E-01	6.24E-40		-2.62E-01	3.33E-05		2.12E+00	1.27E-191	Up	8.18E-01	3.41E-19		Unigene18445_A11//gi|39841350|gb|AAR31185.1|//5.00E-53//serine O-acetyltransferase 1 [Glycine max]	Unigene18445_A11//4.00E-51//AT3G55920| ATSERAT2;1 (SERINE ACETYLTRANSFERASE 2;1); serine O-acetyltransferase	Unigene18445_A11//2.00E-178//TC165199		ko00270|Cysteine and methionine metabolism//ko00920|Sulfur metabolism	GO:0006563//GO:0009267//GO:0009536//GO:0010468//GO:0016412	nr -
Unigene18446_A11	1334	1.22	3.30	1.12	0.37	0.77	0.07	15.25	9.78	11.50	1.44E+00	2.39E-06	Up	-1.22E-01	8.10E-01		1.05E+00	1.37E-01		-2.46E+00	4.83E-02		-6.41E-01	4.14E-09		-4.07E-01	1.28E-04		Unigene18446_A11//gi|149728036|gb|ABR28343.1|//1.00E-107//MYB transcription factor MYB64 [Medicago truncatula]	Unigene18446_A11//6.00E-85//AT5G37620| MYB36 (myb domain protein 36); DNA binding / transcription factor	Unigene18446_A11//0.00E+00//TC144511	MYB		GO:0003676//GO:0006350//GO:0010468//GO:0043231	nr +

Unigene18448_All	775	0.00	0.26	0.14	10.67	5.55	3.61	5.67	1.51	4.99	8.03E+00	1.37E-01		7.10E+00	3.99E-01		-9.42E-01	4.34E-07		-1.56E+00	1.80E-13	Down	-1.91E+00	5.22E-11	Down	-1.86E-01	5.00E-01		Unigene18448_All//gi|149944305|gb|ABR46195.1|//1.00E-19//At1g36940 [Arabidopsis thaliana]	Unigene18448_All//4.00E-18//AT1G36940| unknown protein	Unigene18448_All//8.00E-29//TC177104				nr -
Unigene1845_All	443	2.48	6.41	2.40	10.57	10.65	13.56	8.78	11.98	18.53	1.37E+00	4.19E-04	Up	-4.50E-02	9.61E-01		1.08E-02	9.79E-01		3.59E-01	1.64E-01		4.49E-01	5.76E-02		1.08E+00	3.72E-09	Up	Unigene1845_All//gi|224106822|ref|XP_002314297.1|//2.00E-16//ABC transporter family protein [Populus trichocarpa] >gi|222850705|gb|EEE88252.1| ABC transporter family protein [Populus trichocarpa]		Unigene1845_All//0.00E+00//TC142867				nr -
Unigene18451_All	479	29.16	8.04	13.01	37.23	33.86	43.56	146.17	48.08	47.24	-1.86E+00	2.24E-26	Down	-1.16E+00	6.04E-13	Down	-1.37E-01	3.65E-01		2.27E-01	7.87E-02		-1.60E+00	6.79E-129	Down	-1.63E+00	1.10E-135	Down	Unigene18451_All//gi|76161008|gb|AB440467.1|//1.00E-28//glycoprotein-like protein [Solanum tuberosum]	Unigene18451_All//3.00E-29//AT4G27090| 60S ribosomal protein L14 (RPL14B)	Unigene18451_All//3.00E-138//TC150918		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0031981	nr -
Unigene18452_All	609	3.78	4.74	8.31	9.00	8.88	8.16	9.37	10.16	7.92	3.27E-01	3.89E-01		1.14E+00	5.79E-05	Up	-1.94E-02	9.51E-01		-1.41E-01	6.22E-01		1.16E-01	6.35E-01		-2.44E-01	2.93E-01		Unigene18452_All//gi|56382015|gb|AA985726.1|//5.00E-07//At3g09180 [Arabidopsis thaliana]	Unigene18452_All//6.00E-12//AT3G09180| unknown protein	Unigene18452_All//1.00E-159//gi|84154188|gb|DN803543.1|DN803543				nr +
Unigene18453_All	1642	0.19	9.60	0.19	0.55	0.27	0.17	4.63	17.51	64.56	5.65E+00	2.70E-80	Up	2.54E-02	1.00E+00		-1.00E+00	1.61E-01		-1.73E+00	2.81E-02		1.92E+00	4.28E-68	Up	3.80E+00	0.00E+00	Up	Unigene18453_All//gi|14582200|gb|AAK69401.1|AF274564_1//1.00E-148//immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] >gi|14582202|gb|AAK69402.1|AF274565_1 immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum]	Unigene18453_All//4.00E-93//AT5G37490| U-box domain-containing protein	Unigene18453_All//0.00E+00//TC150442				nr +
Unigene18454_All	850	0.49	0.72	0.25	6.15	3.52	1.75	1.84	1.08	0.42	5.39E-01	5.63E-01		-9.74E-01	4.12E-01		-8.04E-01	9.54E-04		-1.81E+00	1.24E-10	Down	-7.67E-01	1.07E-01		-2.13E+00	3.93E-05	Down	Unigene18454_All//gi|115454717|ref|NP_001050959.1|//3.00E-45//Os03g0692100 [Oryza sativa Japonica Group] >gi|50428646|gb|AAT76997.1| expressed protein [Oryza sativa Japonica Group] >gi|113549430|dbj|BAF12873.1| Os03g0692100 [Oryza sativa Japonica Group]	Unigene18454_All//6.00E-60//AT2G28150| unknown protein	Unigene18454_All//7.00E-165//TC178050			GO:0016020	nr -
Unigene18455_All	263	45.76	13.29	9.31	25.95	33.91	21.64	39.87	24.95	26.81	-1.78E+00	1.36E-21	Down	-2.30E+00	1.47E-28	Down	3.86E-01	4.66E-02		-2.62E-01	2.96E-01		-6.76E-01	1.63E-05		-5.72E-01	1.76E-04		Unigene18455_All//gi|300681467|emb|CBH32561.1|//3.00E-17//histone H3, expressed [Triticum aestivum]	Unigene18455_All//1.00E-18//AT5G65360| histone H3	Unigene18455_All//3.00E-112//gi|109877514|gb|DW506487.1|DW506487			GO:0000785//GO:0003676//GO:0006810//GO:0009536//GO:0031224//GO:0031981//GO:0034728	nr -
Unigene18456_All	332	1.89	1.68	1.44	6.90	2.90	3.13	3.06	2.64	0.60	-1.72E-01	8.29E-01		-3.90E-01	6.46E-01		-1.25E+00	1.29E-03		-1.14E+00	7.01E-03		-2.09E-01	7.31E-01		-2.35E+00	5.84E-04	Down			Unigene18456_All//2.00E-67//ES832749				
Unigene18462_All	286	13.90	6.56	4.28	9.75	6.62	3.32	44.79	11.25	10.03	-1.08E+00	4.77E-04	Down	-1.70E+00	8.45E-07	Down	-5.59E-01	1.33E-01		-1.56E+00	6.14E-05	Down	-1.99E+00	2.16E-32	Down	-2.16E+00	5.55E-37	Down			Unigene18462_All//2.00E-138//TC170160				
Unigene18463_All	908	0.69	1.00	0.06	1.87	1.71	0.50	2.00	0.41	0.66	5.39E-01	4.49E-01		-3.56E+00	8.32E-03		-1.28E-01	8.22E-01		-1.91E+00	4.25E-04	Down	-2.27E+00	5.13E-06	Down	-1.61E+00	2.86E-04	Down	Unigene18463_All//gi|115451337|ref|NP_001049269.1|//2.00E-82//Os03g0197100 [Oryza sativa Japonica Group] >gi|113547740|dbj|BAF11183.1| Os03g0197100 [Oryza sativa Japonica Group]	Unigene18463_All//3.00E-64//AT3G18830| ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann	Unigene18463_All//0.00E+00//TC154069			GO:0005215//GO:0006810//GO:0016020//GO:0016491	nr -
Unigene18465_All	596	0.70	2.38	1.43	2.42	0.98	1.06	2.55	1.40	0.40	1.76E+00	3.72E-03		1.03E+00	2.04E-01		-1.30E+00	1.41E-02		-1.19E+00	3.43E-02		-8.65E-01	7.38E-02		-2.67E+00	2.74E-06	Down	Unigene18465_All//gi|44917499|gb|AS49074.1|//2.00E-43//At1g44414 [Arabidopsis thaliana]	Unigene18465_All//2.00E-41//AT1G44414| unknown protein	Unigene18465_All//0.00E+00//DR453636				nr +
Unigene18466_All	396	2.77	9.47	2.42	1.01	2.17	1.94	0.53	0.21	1.91	1.77E+00	4.02E-07	Up	-1.97E-01	7.50E-01		1.11E+00	1.63E-01		9.46E-01	2.73E-01		-1.34E+00	4.30E-01		1.84E+00	1.64E-02		Unigene18466_All//gi|195480059|gb|AAL87393.1|//4.00E-16//AT5g41810/K16L22_9 [Arabidopsis thaliana]	Unigene18466_All//2.00E-16//AT1G64340| unknown protein					nr +
Unigene18467_All	334	3.45	8.50	2.71	4.03	3.71	2.70	0.76	0.38	0.00	1.30E+00	7.29E-04	Up	-3.47E-01	6.16E-01		-1.18E-01	8.29E-01		-5.74E-01	3.45E-01		-1.02E+00	4.95E-01		-9.57E+00	3.04E-02								
Unigene18468_All	939	0.56	0.86	0.11	1.96	1.65	1.92	21.21	2.09	4.62	6.32E-01	4.02E-01		-2.30E+00	6.77E-02		-2.50E-01	6.04E-01		-2.90E-02	9.56E-01		-3.34E+00	8.04E-89	Down	-2.20E+00	2.71E-58	Down	Unigene18468_All//gi|157812633|gb|ABV80356.1|//1.00E-145//phosphoenolpyruvate carboxylase [Gossypium hirsutum]	Unigene18468_All//1.00E-132//AT3G14940| ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase	Unigene18468_All//0.00E+00//TC131208		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene18469_All	751	0.56	0.88	0.00	1.46	1.05	1.56	2.81	1.00	2.33	6.54E-01	4.48E-01		-9.12E+00	1.56E-02		-4.69E-01	4.83E-01		9.96E-02	8.93E-01		-1.49E+00	3.03E-04	Down	-2.70E-01	5.05E-01		Unigene18469_All//gi|240256033|ref|NP_193913.4|//2.00E-37//binding / calmodulin binding [Arabidopsis thaliana]	Unigene18469_All//1.00E-34//AT4G21820| binding / calmodulin binding	Unigene18469_All//2.00E-07//ES816091				nr +
Unigene18476_All	821	2.74	2.04	0.13	8.92	8.26	4.13	2.32	1.02	0.58	-4.28E-01	3.28E-01		-4.40E+00	5.90E-10	Down	-1.10E-01	6.55E-01		-1.11E+00	2.32E-07	Down	-1.19E+00	5.40E-03		-1.99E+00	1.17E-05	Down	Unigene18476_All//gi|145345425|ref|NP_194388.2|//9.00E-48//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene18476_All//1.00E-39//AT4G26580| protein binding / zinc ion binding	Unigene18476_All//5.00E-138//DT047652			GO:0009536//GO:0046914	nr +
Unigene18479_All	375	40.46	35.81	34.65	43.04	32.23	46.85	68.32	49.15	29.32	-1.76E-01	2.56E-01		-2.24E-01	1.59E-01		-4.17E-01	1.43E-03		1.22E-01	4.48E-01		-4.75E-01	6.72E-07		-1.22E+00	1.07E-32	Down	Unigene18479_All//gi|211906468|gb|ACJ11727.1|//2.00E-10//20S proteasome subunit alpha-1 [Gossypium hirsutum]	Unigene18479_All//2.00E-69//AT5G35590| PAA1 (PROTEASOME ALPHA SUBUNIT A 1); endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene18479_All//0.00E+00//gi|13246985|gb|BF268248.2|BF268248		ko03050|Proteasome		nr -
Unigene18484_All	482	11.40	15.77	15.58	18.71	17.79	18.27	46.75	31.65	21.16	4.68E-01	2.80E-02		4.51E-01	4.50E-02		-7.25E-02	7.72E-01		-3.39E-02	8.90E-01		-5.63E-01	4.27E-08		-1.14E+00	4.04E-26	Down			Unigene18484_All//4.00E-159//TC162368				
Unigene18485_All	983	1.22	0.21	0.60	1.06	1.44	0.83	2.19	0.43	0.49	-2.57E+00	5.35E-04	Down	-1.04E+00	1.14E-01		4.33E-01	4.94E-01		-3.64E-01	6.33E-01		-2.37E+00	2.59E-07	Down	-2.17E+00	6.08E-07	Down	Unigene18485_All//gi|15220980|ref|NP_176725.1|//6.00E-80//FAS1 (FASCIATA 1); histone binding [Arabidopsis thaliana] >gi|4887626|dbj|BAA77811.1| FAS1 [Arabidopsis thaliana] >gi|22022526|gb|AAM83221.1| At1g65470/F5I14_33 [Arabidopsis thaliana]	Unigene18485_All//4.00E-33//AT1G65470| FAS1 (FASCIATA 1); histone binding	Unigene18485_All//9.00E-94//ES848513		ko03040|Spliceosome	GO:0000725//GO:0006338//GO:0009933//GO:0034728//GO:0035315//GO:0043234//GO:0048229//GO:0048827//GO:0051726	nr -
Unigene18486_All	600	2.79	8.53	4.08	4.90	3.90	3.01	0.07	0.00	0.13	1.61E+00	2.23E-08	Up	5.49E-01	2.03E-01		-3.28E-01	3.96E-01		-7.02E-01	5.61E-02		-6.14E+00	6.58E-01		9.14E-01	7.50E-01		Unigene18486_All//gi|9502420|gb|AAF88119.1|AC021043_12//8.00E-43//Unknown protein [Arabidopsis thaliana] >gi|15529248|gb|AAK97718.1| At1g29190/F28N24_12 [Arabidopsis thaliana] >gi|16974401|gb|AAL31126.1| At1g29190/F28N24_12 [Arabidopsis thaliana]	Unigene18486_All//1.00E-39//AT1G29195| unknown protein	Unigene18486_All//7.00E-47//gi|48811319|gb|C0112632.1|C0112632			GO:0009536	nr +
Unigene18487_All	565	2.96	2.42	0.75	3.70	3.29	1.36	3.52	2.29	1.97	-2.91E-01	5.79E-01		-1.97E+00	7.75E-04	Down	-1.70E-01	7.32E-01		-1.45E+00	1.50E-03		-6.17E-01	1.38E-01		-8.33E-01	3.41E-02		Unigene18487_All//gi|88010816|gb|ABD38857.1|//4.00E-18//At5g40960 [Arabidopsis thaliana]	Unigene18487_All//8.00E-08//AT5G40960| unknown protein				GO:0031224//GO:0031410	nr -
Unigene18490_All	715	0.59	0.85	0.30	1.46	3.76	1.90	3.31	1.52	1.84	5.39E-01	5.63E-01		-9.75E-01	4.12E-01		1.36E+00	3.86E-04	Up	3.73E-01	5.63E-01		-1.12E+00	2.64E-03		-8.49E-01	1.68E-02		Unigene18490_All//gi|224132248|ref|XP_002321292.1|//9.00E-78//SET domain protein [Populus trichocarpa] >gi|222862065|gb|EEE99607.1| SET domain protein [Populus trichocarpa]	Unigene18490_All//3.00E-73//AT1G04050| SUVR1 (ARABIDOPSIS HOMOLOG OF SU(VAR)3-9 1); histone-lysine N-methyltransferase/ zinc ion binding	Unigene18490_All//0.00E+00//DW504954		ko00310|Lysine degradation	GO:0006325//GO:0016279//GO:0031981//GO:0046914	nr -
Unigene18491_All	1452	0.00	0.52	0.07	0.62	0.47	0.84	1.14	9.12	2.74	9.03E+00	1.77E-04	Up	6.20E+00	3.99E-01		-3.81E-01	6.05E-01		4.44E-01	5.00E-01		3.01E+00	1.86E-53	Up	1.27E+00	4.22E-06	Up	Unigene18491_All//gi|16507125|gb|AAL24049.1|AF426451_1//5.00E-98//cytochrome P450 [Citrus sinensis]	Unigene18491_All//3.00E-70//AT3G26320| CYP71B36; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene18491_All//0.00E+00//gi|164256613|gb|ES819737.1|ES819737		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016709	nr -
Unigene18492_All	317	58.43	49.55	77.27	349.33	413.33	358.74	126.04	73.04	47.50	-2.38E-01	7.81E-02		4.03E-01	4.27E-04		2.43E-01	4.45E-09		3.84E-02	5.51E-01		-7.87E-01	3.97E-24		-1.41E+00	8.96E-63	Down	Unigene18492_All//gi|262181539|gb|ACY29660.1|//2.00E-06//3-deoxy-D-arabino-heptulosonate-7-phosphate synthase 02 [Vitis vinifera]		Unigene18492_All//7.00E-132//gi|109887960|gb|DW516929.1|DW516929		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene18496_All	378	1.66	0.80	0.56	2.90	1.09	0.72	2.80	0.33	1.16	-1.05E+00	2.50E-01		-1.56E+00	1.29E-01		-1.41E+00	2.62E-02		-2.02E+00	4.74E-03		-3.08E+00	6.12E-05	Down	-1.27E+00	2.97E-02		Unigene18496_All//gi|71068360|gb|AAZ23107.1|//9.00E-10//plastid ATP/ADP transport protein 2 [Manihot esculenta]	Unigene18496_All//4.00E-07//AT1G80300| NTT1 (NUCLEOTIDE TRANSPORTER 1); ATP:ADP antiporter	Unigene18496_All//4.00E-109//TC137400			GO:0005488//GO:0009526//GO:0016020	nr -
Unigene18497_All	415	9.08	8.67	7.06	20.29	18.67	31.34	134.18	61.54	50.11	-6.64E-02	8.34E-01		-3.63E-01	2.88E-01		-1.20E-01	6.12E-01		6.28E-01	4.09E-05		-1.12E+00	7.82E-60	Down	-1.42E+00	2.19E-88	Down	Unigene18497_All//gi|19773452|dbj|BAB86847.1|//3.00E-74//elongation factor EF-2 [Pisum sativum]	Unigene18497_All//3.00E-70//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene18497_All//0.00E+00//TC152459			GO:0006950//GO:0008135//GO:0009536//GO:0016020//GO:0017111//GO:0031981//GO:0032561//GO:0046914	nr +
Unigene18498_All	415	16.89	5.98	11.55	23.41	27.38	40.70	131.32	53.38	46.85	-1.50E+00	3.36E-10	Down	-5.49E-01	1.79E-02		2.26E-01	2.23E-01		7.98E-01	1.92E-09		-1.30E+00	2.31E-73	Down	-1.49E+00	1.36E-92	Down	Unigene18498_All//gi|19773452|dbj|BAB86847.1|//5.00E-75//elongation factor EF-2 [Pisum sativum]	Unigene18498_All//1.00E-70//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene18498_All//0.00E+00//TC136473			GO:0006950//GO:0008135//GO:0009536//GO:0016020//GO:0017111//GO:0031981//GO:0032561//GO:0046914	nr +
Unigene18499_All	757	3.18	3.08	7.74	1.97	5.05	3.40	0.17	0.00	0.63	-4.62E-02	9.19E-01		1.28E+00	1.15E-06	Up	1.35E+00	1.25E-05	Up	7.85E-01	4.98E-02		-7.39E+00	2.36E-01		1.91E+00	6.30E-02		Unigene18499_All//gi|115445371|ref|NP_001046465.1|//9.00E-44//Os02g0255700 [Oryza sativa Japonica Group] >gi|113535996|dbj|BAF08379.1| Os02g0255700 [Oryza sativa Japonica Group]	Unigene18499_All//3.00E-30//AT1G15290| binding	Unigene18499_All//3.00E-179//gi|109851526|gb|DW480505.1|DW480505			GO:0008135	nr +
Unigene1850_All	1803	2.12	1.10	0.27	3.20	3.57	1.58	4.76	1.25	1.79	-9.51E-01	2.52E-03		-2.99E+00	2.20E-12	Down	1.56E-01	5.76E-01		-1.02E+00	2.82E-05	Down	-1.93E+00	5.07E-21	Down	-1.41E+00	3.20E-14	Down	Unigene1850_All//gi|115463947|ref|NP_001065635.1|//0.00E+00//Os11g0128400 [Oryza sativa Japonica Group] >gi|77548491|gb|ABA91288.1| CDC45-like protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113644339|dbj|BAF27480.1| Os11g0128400 [Oryza sativa Japonica Group]	Unigene1850_All//0.00E+00//AT3G25100| CDC45 (cell division cycle 45)	Unigene1850_All//0.00E+00//TC172693				nr +
Unigene18500_All	1187	0.00	0.00	0.09	0.08	0.52	0.95	11.58	15.32	27.66	null	null		6.49E+00	3.99E-01		2.64E+00	1.99E-02		3.50E+00	7.03E-05	Up	4.04E-01	5.11E-04		1.26E+00	3.53E-43	Up	Unigene18500_All//gi|297829824|ref|XP_002882794.1|//1.00E-137//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328634|gb|EFH59053.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene18500_All//6.00E-134//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene18500_All//3.00E-20//TC134433		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0009699//GO:0012501//GO:0016705	nr +
Unigene18502_All	473	1.99	1.50	1.35	1.69	2.40	1.72	2.95	0.35	0.67	-4.09E-01	5.67E-01		-5.60E-01	4.39E-01		5.12E-01	4.65E-01		2.86E-02	9.71E-01		-3.06E+00	2.69E-06	Down	-2.13E+00	1.13E-04	Down			Unigene18502_All//3.00E-101//gi|3325769|gb|AI054655.1|AI054655				
Unigene18503_All	582	37.49	127.20	49.22	46.73	102.60	131.30	25.86	79.28	57.70	1.76E+00	1.20E-126	Up	3.93E-01	1.79E-04		1.13E+00	1.23E-62	Up	1.49E+00	1.68E-110	Up	1.62E+00	6.59E-86	Up	1.16E+00	6.37E-39	Up	Unigene18503_All//gi|18400003|ref|NP_564469.1|//3.00E-75//WD-40 repeat family protein [Arabidopsis thaliana] >gi|11074418|gb|AB404582.1| At1g36070 [Arabidopsis thaliana]	Unigene18503_All//2.00E-76//AT1G36070| WD-40 repeat family protein	Unigene18503_All//0.00E+00//gi|73865550|gb|DT468288.1|DT468288			GO:0019897//GO:0031461	nr -
Unigene18504_All	920	0.06	1.16	0.00	0.00	0.04	0.00	2.07	1.45	5.98	4.35E+00	3.95E-05	Up	-5.83E+00	6.25E-01		5.23E+00	8.30E-01		null	null		-5.09E-01	2.40E-01		1.53E+00	2.08E-10	Up			Unigene18504_All//1.00E-18//ES841761				

Unigene18505_A11	824	2.79	0.06	0.71	7.19	4.68	2.69	0.00	0.20	0.00	-5.51E+00	5.91E-12	Down	-1.97E+00	5.20E-05	Down	-6.20E-01	6.95E-03		-1.42E+00	1.28E-08	Down	7.66E+00	1.39E-01		null	null		Unigene18505_A11//gi|15225658|ref|NP_181549.1|//5.00E-41//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75315012|sp|Q9XEF0.1|BH051_ARATH RecName: Full=Transcription factor bHLH51; AltName: Full=Transcription factor EN 57; AltName: Full=bHLH transcription factor bHLH051; AltName: Full=Basic helix-loop-helix protein 51; Short=bHLH 51; Short=AtbHLH51 >gi|124300966|gb|ABN04735.1| At2g40200 [Arabidopsis thaliana] >gi|124301074|gb|ABN04789.1| At2g40200 [Arabidopsis thaliana]	Unigene18505_A11//9.00E-42//AT2G40200| basic helix-loop-helix (bHLH) family protein	Unigene18505_A11//2.00E-44//DW234183	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0010468//GO:0043231	nr -
Unigene18506_A11	314	8.33	2.90	5.94	2.70	6.36	4.89	0.00	0.53	0.00	-1.52E+00	2.21E-04	Down	-4.89E-01	2.38E-01		1.24E+00	6.86E-03		8.59E-01	1.21E-01		9.06E+00	1.39E-01		null	null								
Unigene18507_A11	382	81.91	34.35	30.95	83.72	88.52	107.00	245.71	116.85	112.22	-1.25E+00	6.33E-33	Down	-1.40E+00	1.19E-37	Down	8.05E-02	4.91E-01		3.54E-01	1.44E-05		-1.07E+00	6.22E-93	Down	-1.13E+00	4.65E-104	Down	Unigene18507_A11//gi|6094040|sp|O65743.1|RL24_CICAR//1.00E-20//RecName: Full=60S ribosomal protein L24 >gi|2961300|emb|CAA12358.1| ribosomal protein L24 [Cicer arietinum]		Unigene18507_A11//3.00E-147//gi|21099650|gb|BQ411963.1|BQ411963		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr -
Unigene18509_A11	301	0.70	0.34	0.35	1.16	2.29	3.90	8.29	3.89	3.04	-1.05E+00	5.65E-01		-9.75E-01	6.21E-01		9.82E-01	2.98E-01		1.75E+00	9.86E-03		-1.09E+00	2.53E-03		-1.44E+00	7.03E-05	Down			Unigene18509_A11//7.00E-104//gi|21095717|gb|BQ408030.1|BQ408030				
Unigene18512_A11	740	1.70	0.68	1.15	7.54	3.82	3.48	1.49	0.96	0.32	-1.31E+00	3.41E-02		-5.60E-01	3.87E-01		-9.83E-01	2.71E-05		-1.12E+00	8.52E-06	Down	-6.30E-01	2.93E-01		-2.20E+00	5.66E-04	Down	Unigene18512_A11//gi|90265044|emb|CAH67640.1|//1.00E-11//BD102C09.1 [Oryza sativa (indica cultivar-group)]		Unigene18512_A11//4.00E-49//TC133450				nr -
Unigene18513_A11	393	3.59	2.84	8.67	4.56	5.61	2.76	4.30	1.70	0.00	-3.42E-01	5.48E-01		1.27E+00	3.90E-04	Up	2.97E-01	5.67E-01		-7.26E-01	1.44E-01		-1.34E+00	3.80E-03		-1.21E+01	1.70E-12	Down			Unigene18513_A11//1.00E-07//DR458512				
Unigene18514_A11	556	0.56	2.73	3.16	4.39	5.64	3.98	0.76	0.83	3.15	2.28E+00	2.68E-04	Up	2.48E+00	4.72E-05	Up	3.60E-01	3.43E-01		-1.41E-01	7.34E-01		1.21E-01	9.07E-01		2.05E+00	2.29E-05	Up							
Unigene18516_A11	304	3.79	3.33	5.96	6.39	6.00	2.53	2.36	0.00	0.66	-1.84E-01	7.48E-01		6.53E-01	2.02E-01		-9.01E-02	8.35E-01		-1.34E+00	4.60E-03		-1.12E+01	3.26E-05	Down	-1.85E+00	1.78E-02								
Unigene18517_A11	689	117.02	82.73	94.83	12.58	17.14	16.13	3.99	4.13	1.50	-5.00E-01	6.81E-18		-3.03E-01	3.55E-07		4.47E-01	5.20E-03		3.58E-01	4.21E-02		4.85E-02	9.02E-01		-1.41E+00	4.02E-05	Down	Unigene18517_A11//gi|18417346|ref|NP_568299.1|//6.00E-44//30S ribosomal protein S13, chloroplast (CS13) [Arabidopsis thaliana] >gi|1173194|sp|P42732.1|RR13_ARATH RecName: Full=30S ribosomal protein S13, chloroplastic; AltName: Full=CS13; Flags: Precursor >gi|16767|emb|CAA79013.1| chloroplast 30S ribosomal protein S13 [Arabidopsis thaliana] >gi|662869|emb|CAA88028.1| chloroplast ribosomal protein S13 [Arabidopsis thaliana] >gi|1107483|emb|CAA63021.1| 30S ribosomal protein S13 [Arabidopsis thaliana] >gi|1515107|emb|CAA60413.1| plastid ribosomal protein S13 [Arabidopsis thaliana] >gi|14517397|gb|AAK62589.1| AT5g14320/F18022_110 [Arabidopsis thaliana] >gi|15450549|gb|AAK96452.1| AT5g14320/F18022_110 [Arabidopsis thaliana]	Unigene18517_A11//3.00E-45//AT5G14320| 30S ribosomal protein S13, chloroplast (CS13)	Unigene18517_A11//1.00E-172//TC169238		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009526//GO:0010467//GO:0033279	nr -
Unigene18518_A11	408	0.00	0.00	0.00	13.80	0.17	0.33	31.19	35.75	31.54	null	null		null	null		-6.35E+00	2.02E-39	Down	-5.38E+00	3.98E-31	Down	1.97E-01	1.71E-01		1.60E-02	9.40E-01		Unigene18518_A11//gi|145408590|ref|XP_001152214.1|//9.00E-10//O8F124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| O8F124 [Pinus koraiensis]		Unigene18518_A11//5.00E-16//TC135460				nr -
Unigene18519_A11	336	0.31	0.00	0.00	7.41	4.92	2.29	75.00	2.24	5.34	-8.28E+00	3.73E-01		-8.28E+00	3.95E-01		-5.92E-01	1.35E-01		-1.70E+00	5.56E-05	Down	-5.07E+00	7.04E-151	Down	-3.81E+00	1.05E-129	Down	Unigene18519_A11//gi|255557347|ref|XP_002519704.1|//6.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223541121|gb|EEF42677.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene18521_A11	793	0.92	1.53	0.27	4.96	6.64	5.35	5.81	0.53	0.95	7.31E-01	2.35E-01		-1.78E+00	6.00E-02		4.21E-01	1.16E-01		1.09E-01	7.32E-01		-3.46E+00	1.23E-21	Down	-2.61E+00	4.42E-17	Down	Unigene18521_A11//gi|298707512|emb|CBJ30114.1|//4.00E-07//human PTB (hnRNP) homolog family member (ptb-1) [Ectocarpus siliculosus]				ko04146|Peroxisome	GO:0003824	nr +
Unigene18522_A11	254	14.01	62.44	31.87	40.01	38.64	60.28	90.55	233.33	87.52	2.16E+00	7.07E-36	Up	1.19E+00	5.39E-08	Up	-5.03E-02	8.40E-01		5.91E-01	2.25E-05		1.37E+00	6.67E-86	Up	-4.92E-02	6.68E-01		Unigene18522_A11//gi|241740196|gb|ACS68205.1|//2.00E-40//ubiquitin 10.2 [Brassica napus]	Unigene18522_A11//7.00E-42//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene18522_A11//9.00E-137//DW238310			GO:0044424	nr +
Unigene18523_A11	1804	0.00	0.06	0.00	0.08	0.15	0.10	39.51	15.08	122.98	5.81E+00	3.87E-01		null	null		8.83E-01	5.95E-01		2.74E-01	9.05E-01		-1.39E+00	4.04E-106	Down	1.64E+00	0.00E+00	Up	Unigene18523_A11//gi|209954731|dbj|BAG80556.1|//0.00E+00//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene18523_A11//1.00E-175//AT4G01070| GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene18523_A11//1.00E-162//TC131390			GO:0035251	nr -
Unigene18524_A11	489	0.43	3.11	1.09	1.43	1.27	1.66	0.52	0.94	1.06	2.86E+00	2.69E-05	Up	1.35E+00	2.25E-01		-1.70E-01	8.21E-01		2.21E-01	7.78E-01		8.58E-01	3.96E-01		1.03E+00	2.53E-01				Unigene18524_A11//6.00E-124//ES852051				
Unigene18525_A11	1261	0.54	0.08	0.25	4.50	2.62	0.93	3.62	0.50	1.64	-2.75E+00	1.06E-02		-1.09E+00	2.39E-01		-7.81E-01	7.66E-04		-2.27E+00	2.83E-15	Down	-2.86E+00	5.04E-18	Down	-1.14E+00	5.69E-06	Down	Unigene18525_A11//gi|297816708|ref|XP_002876237.1|//1.00E-176//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322075|gb|EFH52496.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene18525_A11//8.00E-173//AT3G54030| protein kinase family protein	Unigene18525_A11//0.00E+00//TC163694		ko04626|Plant-pathogen interaction	GO:0004871//GO:0006464//GO:0016301//GO:0032559	nr -
Unigene18527_A11	5202	0.00	23.59	9.22	0.00	0.03	0.00	0.00	0.00	0.00	1.45E+01	0.00E+00	Up	1.32E+01	9.24E-273	Up	4.73E+00	3.19E-01		null	null		null	null		null	null		Unigene18527_A11//gi|15219766|ref|NP_171954.1|//1.00E-113//XIA (MYOSIN XI A); motor/ protein binding [Arabidopsis thaliana]	Unigene18527_A11//3.00E-105//AT3G19960| ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor			ko03440|Homologous recombination//ko03450|Non-homologous end-joining		nr +
Unigene18528_A11	649	0.81	14.60	50.38	2.30	1.33	0.56	0.00	0.06	0.00	4.18E+00	4.13E-41	Up	5.97E+00	4.09E-167	Up	-7.96E-01	1.31E-01		-2.05E+00	5.54E-04	Down	6.01E+00	6.35E-01		null	null				Unigene18528_A11//0.00E+00//TC167008				
Unigene1853_A11	1740	4.54	35.59	12.18	40.60	57.97	54.40	26.32	16.60	62.71	2.97E+00	1.87E-199	Up	1.42E+00	2.93E-26	Up	5.14E-01	2.14E-27		4.22E-01	1.87E-16		-6.65E-01	1.03E-20		1.25E+00	6.01E-141	Up	Unigene1853_A11//gi|297381026|gb|AD39634.1|//2.00E-69//plastid jasmonates ZIM-domain protein [Hevea brasiliensis]	Unigene1853_A11//3.00E-49//AT1G19180| JAZ1 (JASMONATE-ZIM-DOMAIN PROTEIN 1); protein binding	Unigene1853_A11//0.00E+00//TC178533	Tify	ko04626|Plant-pathogen interaction		nr +
Unigene18530_A11	392	1.87	3.75	1.36	4.07	2.99	2.19	2.27	0.32	0.71	1.00E+00	6.92E-02		-4.60E-01	6.02E-01		-4.45E-01	4.08E-01		-8.94E-01	9.15E-02		-2.82E+00	5.65E-04	Down	-1.67E+00	1.33E-02				Unigene18530_A11//1.00E-10//gi|164307321|gb|EV495891.1|EV495891				
Unigene18531_A11	694	0.98	0.37	0.15	4.74	2.13	3.12	2.92	1.32	2.58	-1.42E+00	1.16E-01		-2.67E+00	1.69E-02		-1.15E+00	3.34E-04	Down	-6.01E-01	8.32E-02		-1.14E+00	5.27E-03		-1.79E-01	6.47E-01		Unigene18531_A11//gi|186532557|ref|NP_200612.2|//7.00E-74//ATF1P1[V] (Arabidopsis homolog of yeast Fip1 [V]); RNA binding / protein binding [Arabidopsis thaliana]	Unigene18531_A11//4.00E-75//AT5G58040| ATF1P1[V] (Arabidopsis homolog of yeast Fip1 [V]); RNA binding / protein binding	Unigene18531_A11//4.00E-141//TC147880			GO:0001071//GO:0003677//GO:0005515//GO:0010468//GO:0017111//GO:0003013//GO:0032559//GO:0043231//GO:0043623	nr +
Unigene18535_A11	519	0.30	0.20	1.13	3.26	2.85	3.05	1.30	0.32	0.00	-6.31E-01	7.28E-01		1.90E+00	8.48E-02		-1.94E-01	7.24E-01		-9.96E-02	8.54E-01		-2.02E+00	1.98E-02		-1.03E+01	3.56E-05	Down							
Unigene18537_A11	444	1.30	2.40	5.28	2.92	2.71	3.97	2.76	1.79	1.44	8.87E-01	1.85E-01		2.03E+00	2.96E-05	Up	-1.04E-01	8.43E-01		4.44E-01	4.05E-01		-6.27E-01	2.59E-01		-9.44E-01	7.14E-02								
Unigene18539_A11	549	2.86	37.10	8.44	0.18	0.63	0.16	343.40	429.22	283.22	3.70E+00	2.44E-80	Up	1.56E+00	4.93E-07	Up	1.79E+00	2.58E-01		-1.42E-01	9.51E-01		3.22E-01	8.09E-28		-2.78E-01	1.08E-17		Unigene18539_A11//gi|19699035|gb|AL91002.1|//5.00E-14//asparagine synthetase [Securigera parviflora]	Unigene18539_A11//2.00E-14//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene18539_A11//0.00E+00//TC130302		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0000166//GO:0006528//GO:0009267//GO:0009642//GO:0009746//GO:0016884//GO:0034285	nr +
Unigene18543_A11	782	0.13	0.45	0.00	5.67	2.60	1.33	2.81	0.80	0.20	1.76E+00	2.18E-01		-7.06E+00	3.95E-01		-1.13E+00	2.85E-05	Down	-2.09E+00	6.60E-11	Down	-1.81E+00	1.62E-05	Down	-3.79E+00	8.31E-12	Down							
Unigene18545_A11	2588	0.04	20.73	7.18	0.00	0.05	0.00	0.00	0.00	0.00	9.00E+00	5.46E-305	Up	7.47E+00	8.68E-101	Up	5.73E+00	3.19E-01		null	null		null	null		null	null		Unigene18545_A11//sp|Q9V496|APLP_DROME//0.00E+00//Apolipophorins OS=Drosophila melanogaster GN=RfaHg PE=1 SV=2						swissprot +
Unigene1855_A11	673	11.89	20.48	8.07	12.51	7.88	3.76	11.56	8.45	11.42	7.84E-01	2.79E-07		-5.60E-01	8.99E-03		-6.67E-01	3.12E-04		-1.73E+00	7.74E-16	Down	-4.53E-01	1.62E-02		-1.69E-02	9.52E-01				Unigene1855_A11//0.00E+00//TC175526				
Unigene18551_A11	429	0.73	6.61	1.49	0.46	2.89	6.74	7.19	7.89	17.46	3.18E+00	2.99E-10	Up	1.03E+00	2.81E-01		2.64E+00	2.32E-04	Up	3.86E+00	9.04E-13	Up	1.33E-01	6.79E-01		1.28E+00	8.61E-11	Up	Unigene18551_A11//gi|255586588|ref|XP_002533928.1|//2.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223526108|gb|EEF28457.1| conserved hypothetical protein [Ricinus communis]	Unigene18551_A11//3.00E-06//AT5G65207| unknown protein	Unigene18551_A11//3.00E-156//gi|109891391|gb|DW520354.1|DW520354				nr -
Unigene18554_A11	1790	0.00	0.08	0.00	0.00	0.00	0.66	2.67	9.50	22.55	6.41E+00	2.35E-01		null	null		null	null		9.36E+00	5.32E-07	Up	1.83E+00	3.45E-38	Up	3.08E+00	1.79E-168	Up	Unigene18554_A11//gi|3399777|gb|AAC32828.1|//1.00E-50//symbiotic ammonium transporter [Glycine max]	Unigene18554_A11//1.00E-49//AT2G22760| basic helix-loop-helix (bHLH) family protein	Unigene18554_A11//0.00E+00//TC134717	bHLH	ko04626|Plant-pathogen interaction	GO:0010468//GO:0016628//GO:0043231	nr -
Unigene18555_A11	809	7.76	4.95	4.08	10.90	13.37	14.68	13.38	5.68	4.97	-6.49E-01	5.72E-03		-9.27E-01	1.70E-04		2.94E-01	1.04E-01		4.30E-01	9.41E-03		-1.24E+00	4.03E-14	Down	-1.43E+00	5.31E-18	Down	Unigene18555_A11//gi|4206124|gb|AAD11431.1|//4.00E-91//T-complex protein 1 epsilon subunit [Mesembryanthemum crystallinum]	Unigene18555_A11//2.00E-90//AT1G24510| T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative	Unigene18555_A11//0.00E+00//gi|48818503|gb|CO119816.1|CO119816			GO:0005515//GO:0016020//GO:0032559//GO:0044267//GO:0044424	nr +
Unigene18557_A11	805	1.30	0.00	0.13	1.24	3.94	1.29	1.00	0.26	1.24	-1.03E+01	3.80E-06	Down	-3.30E+00	4.58E-04	Down	1.67E+00	3.14E-06	Up	6.03E-02	9.47E-01		-1.94E+00	1.17E-02		3.10E-01	6.09E-01		Unigene18557_A11//gi|75174963|sp|Q9LN26.1|PPP7L_ARATH//9.00E-13//RecName: Full=Serine/threonine-protein phosphatase 7 long form homolog >gi|87785133|gb|AAF79521.1|AC023673_9 F21D18.16 [Arabidopsis thaliana]	Unigene18557_A11//5.00E-14//AT1G48120| calcineurin-like phosphoesterase family protein					nr -
Unigene18559_A11	333	0.00	1.83	0.00	0.15	1.14	0.54	0.38	2.76	2.27	1.08E+01	1.17E-03		null	null		2.93E+00	8.16E-02		1.86E+00	4.58E-01		2.86E+00	4.09E-04	Up	2.58E+00	2.45E-03				Unigene18559_A11//5.00E-25//gi|78329431|gb|DT549705.1|DT549705				
Unigene1856_A11	1240	42.19	76.17	31.01	43.15	41.68	20.98	17.12	13.31	24.22	8.52E-01	3.52E-52		-4.45E-01	2.74E-09		-4.97E-02	5.85E-01		-1.04E+00	6.58E-45	Down	-3.63E-01	7.12E-04		5.01E-01	6.31E-09		Unigene1856_A11//gi|15237049|ref|NP_194461.1|//3.00E-40//zinc finger (B-box type) family protein [Arabidopsis thaliana]	Unigene1856_A11//1.00E-27//AT4G27310| zinc finger (B-box type) family protein	Unigene1856_A11//0.00E+00//gi|164329459|gb|ES803529.1|ES803529	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene18561_A11	566	1.76	1.25	1.13	8.10	0.73	0.56	0.75	1.40	0.70	-4.87E-01	4.72E-01		-6.38E-01	3.90E-01		-3.47E+00	2.65E-22	Down	-3.86E+00	8.26E-21	Down	9.09E-01	2.11E-01		-8.57E-02	9.39E-01		Unigene18561_A11//gi|295393250|gb|ADG03462.1|//1.00E-67//9-cis-epoxycarotenoid dioxygenase [Gossypium hirsutum]	Unigene18561_A11//1.00E-16//AT3G14440| NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	Unigene18561_A11//6.00E-29//gi|164251625|gb|ES833984.1|ES833984		ko00906|Carotenoid biosynthesis		nr -
Unigene18562_A11	564	0.00	0.00	0.19	1.41	0.55	0.48	4.12	2.30	1.48	null	null		7.56E+00	3.99E-01		-1.36E+00	7.74E-02		-1.56E+00	6.27E-02		-8.44E-01	2.37E-02		-1.47E+00	1.01E-04	Down							
Unigene18565_A11	603	11.02	17.81	17.04	7.27	7.99	8.84	15.99	46.79	31.71	6.93E-01	6.81E-05		6.29E-01	6.54E-04		1.37E-01	6.74E-01		2.82E-01	3.33E-01		1.55E+00	1.04E-49	Up	9.88E-01	1.25E-17		Unigene18565_A11//gi|75299765|sp|Q8H154.1|ACO3_ARATH//9.00E-15//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 4	Unigene18565_A11//2.00E-16//AT1G06650| 2-oxoglutarate-dependent dioxygenase, putative				GO:0016706	nr -
Unigene18566_A11	2491	0.17	0.08	0.17	0.08	0.10	0.13	3.50	3.91	7.40	-1.05E+00	3.66E-01		2.55E-02	1.00E+00		2.75E-01	8.95E-01		6.66E-01	6.48E-01		1.61E-01	4.05E-01		1.08E+00	1.23E-19	Up	Unigene18566_A11//gi|209970622|gb|ACJ03072.1|//1.00E-165//HB06p [Malus floribunda]	Unigene18566_A11//3.00E-89//AT2G34930| disease resistance family protein	Unigene18566_A11//5.00E-08//TC178304		ko04626|Plant-pathogen interaction		nr -
Unigene18567_A11	418	17.40	16.24	12.61	22.88	28.34	27.55	69.89	67.79	31.26	-9.91E-02	6.56E-01		-4.64E-01	4.37E-02		3.09E-01	6.85E-02		2.68E-01	1.37E-01		-4.40E-02	6.83E-01		-1.16E+00	2.22E-34	Down	Unigene18567_A11//gi|40287472|gb|AR83850.1|//1.00E-16//hyom protein [Capsicum annuum]	Unigene18567_A11//3.00E-17//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome	Unigene18567_A11//3.00E-113//TC153690		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0022613//GO:0030312//GO:0043169	nr -

Unigene18569_All	283	131.26	30.44	30.29	76.57	45.26	85.22	0.00	0.00	0.00	-2.11E+00	1.58E-81	Down	-2.12E+00	5.21E-79	Down	-7.58E-01	2.36E-12		1.54E-01	2.25E-01		null	null		null	null		Unigene18569_All//gi|27735191|sp|P27483.2|GRP1_ARATH//5.00E-07//RecName: Full=Glycine-rich cell wall structural protein; Flags: Precursor						nr +
Unigene18857_All	591	2.30	3.09	2.88	0.51	1.05	2.29	1.29	0.64	1.55	4.23E-01	3.85E-01		3.25E-01	5.44E-01		1.05E+00	2.99E-01		2.18E+00	8.25E-04	Up	-1.02E+00	1.69E-01		2.68E-01	6.61E-01		Unigene18857_All//gi|109676318|gb|AB637641.1|/3.00E-46//auxin-regulated protein-like protein [Populus trichocarpa]	Unigene1857_All//2.00E-42//AT3G23280| zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein	Unigene1857_All//5.00E-54//TC150289			nr +
Unigene18571_All	384	0.95	5.41	1.11	0.00	0.54	3.65	2.64	1.31	2.80	2.50E+00	3.59E-06	Up	2.18E-01	8.31E-01		9.07E+00	1.57E-01		1.18E+01	2.43E-08	Up	-1.02E+00	1.00E-01		8.41E-02	8.95E-01		Unigene18571_All//gi|297725265|ref|NP_001174996.1|/6.00E-32//Os06g0716200 [Oryza sativa Japonica Group] >gi|255673398|dbj|BAH93724.1| Os06g0716200 [Oryza sativa Japonica Group]	Unigene18571_All//4.00E-33//AT4G36010| pathogenesis-related thaumatin family protein	Unigene18571_All//2.00E-40//C0131262			GO:0009607//GO:0031224//GO:0031410	nr +
Unigene18572_All	1171	0.00	0.00	0.00	0.00	0.00	0.00	20.22	87.09	6.02	null	null		null	null		null	null		null	null		2.11E+00	2.15E-271	Up	-1.75E+00	3.41E-51	Down	Unigene18572_All//gi|117957301|gb|ABK59093.1|/1.00E-113//peroxidase 1 [Sesbania rostrata]	Unigene18572_All//1.00E-88//AT5G05340| peroxidase, putative	Unigene18572_All//2.00E-14//DN817134		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0031410//GO:0046872	nr -
Unigene18573_All	984	3.24	0.72	3.03	1.37	1.64	0.41	0.52	0.09	0.20	-2.17E+00	7.11E-08	Down	-9.80E-02	7.81E-01		2.67E-01	6.37E-01		-1.73E+00	4.68E-03		-2.60E+00	2.05E-02		-1.35E+00	1.40E-01		Unigene18573_All//gi|42571043|ref|NP_973595.1|//1.00E-116//MEE18 (maternal effect embryo arrest 18) [Arabidopsis thaliana]	Unigene18573_All//1.00E-111//AT2G34090| MEE18 (maternal effect embryo arrest 18)	Unigene18573_All//0.00E+00//gi|84164544|gb|DR453192.1|DR453192			nr +
Unigene18574_All	1366	0.08	0.07	0.62	0.07	0.05	0.00	47.94	20.90	23.91	-4.59E-02	9.89E-01		3.03E+00	3.01E-03		-5.33E-01	8.17E-01		-6.19E+00	4.01E-01		-1.20E+00	1.28E-77	Down	-1.00E+00	4.23E-60	Down	Unigene18574_All//gi|15219988|ref|NP_173145.1|//1.00E-117//SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors [Arabidopsis thaliana] >gi|75220747|sp|Q39224.1|SRG1_ARATH RecName: Full=Protein SRG1; Short=AtSRG1; AltName: Full=Protein SENESCENCE-RELATED GENE 1 >gi|5734767|gb|AAD50032.1|AC007651_27 SRG1 Protein [Arabidopsis thaliana] >gi|479047|emb|CAA55654.1| SRG1 [Arabidopsis thaliana] >gi|15081819|gb|AAK82564.1| F6I1.30/F6I1.30 [Arabidopsis thaliana] >gi|22655018|gb|AAM98100.1| At1g17020/F6I1.30 [Arabidopsis thaliana]	Unigene18574_All//4.00E-108//AT1G17020| SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc			ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr +
Unigene18575_All	391	60.75	169.11	139.05	88.16	81.73	97.72	153.98	71.41	34.13	1.48E+00	7.43E-88	Up	1.19E+00	6.53E-51	Up	-1.09E-01	3.09E-01		1.49E-01	1.25E-01		-1.11E+00	3.58E-63	Down	-2.17E+00	2.19E-172	Down				Unigene18575_All//9.00E-138//TC179152				
Unigene18576_All	349	21.89	8.71	11.14	32.12	27.53	25.75	118.48	31.74	39.50	-1.33E+00	2.34E-09	Down	-9.75E-01	1.06E-05		-2.22E-01	2.26E-01		-3.19E-01	7.35E-02		-1.90E+00	1.13E-96	Down	-1.58E+00	2.66E-77	Down	Unigene18576_All//gi|7340791|emb|CAA63107.1|/3.00E-14//ribosomal protein L23 [Spinacia oleracea]	Unigene18576_All//3.00E-15//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene18576_All//3.00E-156//gi|13248073|gb|BF273985.2|BF273985		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene18577_All	407	60.29	55.15	30.09	101.83	92.48	111.08	242.36	122.00	121.18	-1.29E-01	2.98E-01		-1.00E+00	1.34E-17	Down	-1.39E-01	1.20E-01		1.25E-01	1.64E-01		-9.90E-01	9.50E-86		-1.00E+00	1.43E-89	Down				Unigene18577_All//0.00E+00//BQ402096				
Unigene18858_All	1840	3.30	7.52	5.50	1.11	1.76	1.28	2.05	1.36	1.78	1.19E+00	9.11E-14	Up	7.37E-01	7.66E-05		6.64E-01	5.33E-02		2.02E-01	6.69E-01		-5.86E-01	3.94E-02		-2.04E-01	4.94E-01		Unigene18858_All//gi|109676318|gb|AB637641.1|/1.00E-156//auxin-regulated protein-like protein [Populus trichocarpa]	Unigene1858_All//1.00E-122//AT3G23280| zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein	Unigene18858_All//0.00E+00//TC150289		ko04144|Endocytosis		nr +
Unigene18582_All	817	1.73	0.31	0.00	3.17	3.03	2.60	2.54	1.07	1.22	-2.48E+00	2.00E-04	Down	-1.08E+01	1.01E-07	Down	-6.32E-02	8.71E-01		-2.87E-01	5.03E-01		-1.24E+00	2.35E-03		-1.06E+00	6.48E-03		Unigene18582_All//gi|108707760|gb|ABF96555.1|/2.00E-06//Fip1 motif family protein, expressed [Oryza sativa (japonica cultivar-group)]						nr -
Unigene18584_All	313	2.84	0.81	2.55	7.32	6.16	2.89	2.97	0.67	0.38	-1.81E+00	2.38E-02		-1.55E-01	8.24E-01		-2.49E-01	5.87E-01		-1.34E+00	1.70E-03		-2.15E+00	2.95E-03		-2.96E+00	1.72E-04	Down								
Unigene18589_All	259	10.71	6.46	25.91	5.58	9.71	6.80	0.49	0.81	0.92	-7.30E-01	5.23E-02		1.27E+00	1.80E-07	Up	7.99E-01	4.43E-02		2.86E-01	6.26E-01		7.21E-01	6.32E-01		9.14E-01	5.42E-01					Unigene18589_All//4.00E-34//C0100563				
Unigene18859_All	2551	1.56	1.45	1.21	4.90	5.59	4.37	6.31	0.98	2.20	-1.04E-01	7.26E-01		-3.65E-01	2.69E-01		1.89E-01	2.57E-01		-1.65E-01	3.87E-01		-2.68E+00	7.94E-58	Down	-1.52E+00	7.24E-29	Down	Unigene1859_All//gi|18399229|ref|NP_564445.1|//1.00E-82//forkhead-associated domain-containing protein / FHA domain-containing protein [Arabidopsis thaliana] >gi|212283380|gb|ACJ23185.1| parallel spindle 1 [Arabidopsis thaliana]	Unigene1859_All//5.00E-62//AT1G34355| forkhead-associated domain-containing protein / FHA domain-containing protein	Unigene1859_All//0.00E+00//gi|161264978|gb|ES796256.1|ES796256				nr -
Unigene18592_All	752	0.00	0.00	0.00	0.13	0.09	1.86	2.02	10.73	1.38	null	null		null	null		-5.33E-01	8.17E-01		3.81E+00	2.63E-06	Up	2.41E+00	7.20E-26	Up	-5.55E-01	2.34E-01		Unigene18592_All//gi|224148856|ref|XP_002336723.1|/6.00E-67//cytochrome P450 [Populus trichocarpa] >gi|222836601|gb|EEE74994.1| cytochrome P450 [Populus trichocarpa]	Unigene18592_All//9.00E-52//AT4G31950| CYP82C3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene18592_All//1.00E-61//DR462245		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506	nr -
Unigene18594_All	624	3.35	0.81	0.85	2.79	2.92	3.98	4.61	2.75	2.94	-2.05E+00	4.33E-05	Down	-1.97E+00	1.29E-04	Down	6.60E-02	9.10E-01		5.11E-01	2.34E-01		-7.47E-01	2.35E-02		-6.50E-01	4.06E-02		Unigene18594_All//gi|15238313|ref|NP_201300.1|//1.00E-50//mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana]	Unigene18594_All//7.00E-52//AT5G64950| mitochondrial transcription termination factor-related / mTERF-related	Unigene18594_All//0.00E+00//ES795481			GO:0044464	nr -
Unigene18595_All	281	37.24	17.13	20.85	45.38	49.63	58.34	70.57	43.28	47.92	-1.12E+00	9.23E-10	Down	-8.37E-01	5.27E-06		1.29E-01	4.79E-01		3.62E-01	9.16E-03		-7.05E-01	2.22E-10		-5.58E-01	2.23E-07		Unigene18595_All//gi|195622026|gb|ACG32843.1|/1.00E-15//40S ribosomal protein S23 [Zea mays]	Unigene18595_All//1.00E-13//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene18595_All//1.00E-102//gi|109886312|gb|DW515282.1|DW515282		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene18597_All	831	0.13	0.12	0.38	1.68	0.54	0.00	2.65	4.12	1.87	-4.66E-02	9.89E-01		1.61E+00	3.05E-01		-1.64E+00	3.03E-03		-1.07E+01	1.01E-08	Down	6.41E-01	3.23E-02		-5.01E-01	1.85E-01									
Unigene18598_All	1119	0.00	0.00	0.00	0.67	1.60	2.14	0.23	4.67	0.82	null	null		null	null		1.26E+00	1.02E-02		1.68E+00	1.19E-04	Up	4.36E+00	7.12E-29	Up	1.85E+00	6.88E-03		Unigene18598_All//gi|87162727|gb|ABD28522.1|/3.00E-81//Cupin, RmlC-type [Medicago truncatula]	Unigene18598_All//9.00E-57//AT5G15120| unknown protein	Unigene18598_All//0.00E+00//PF403788			GO:0045333	nr -
Unigene18599_All	676	1.32	2.55	2.13	2.80	5.86	4.34	0.50	0.49	0.53	9.54E-01	5.77E-02		6.93E-01	2.40E-01		1.06E+00	3.45E-04	Up	6.33E-01	9.15E-02		-1.68E-02	1.02E+00		8.40E-02	9.57E-01		Unigene18599_All//gi|111146892|gb|ABH07384.1|/2.00E-27//CMR1 [Phaseolus vulgaris]	Unigene18599_All//5.00E-24//AT4G12020| WRKY19; transcription factor	Unigene18599_All//3.00E-68//DR461902		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene18601_All	705	1.04	1.01	0.30	2.47	0.29	2.24	11.33	25.14	11.81	-4.63E-02	9.68E-01		-1.78E+00	6.00E-02		-3.08E+00	8.67E-08	Down	-1.41E-01	7.77E-01		1.15E+00	3.23E-20	Up	5.93E-02	7.56E-01		Unigene18601_All//gi|224120764|ref|XP_002318411.1|/1.00E-19//predicted protein [Populus trichocarpa] >gi|222859084|gb|EEE96631.1| predicted protein [Populus trichocarpa]		Unigene18601_All//0.00E+00//gi|21101008|gb|BQ413321.1|BQ413321			GO:0006350	nr +
Unigene18602_All	278	5.83	34.81	6.51	26.70	6.19	20.31	95.21	313.47	126.39	2.58E+00	3.27E-27	Up	1.59E-01	7.37E-01		-2.11E+00	1.03E-20	Down	-3.95E-01	7.41E-02		1.72E+00	1.60E-176	Up	4.09E-01	2.34E-07		Unigene18602_All//gi|297827173|ref|XP_002881469.1|/1.00E-37//don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297327308|gb|EFH57728.1| don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene18602_All//9.00E-39//AT2G36750| UGT73C1 (UDP-GLUCOSYL TRANSFERASE 73C1); UDP-glucosyltransferase/ UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene18602_All//3.00E-146//gi|164309302|gb|ES850990.1|ES850990		ko00908|Zeatin biosynthesis	GO:0009411//GO:0016128//GO:0035251//GO:0044464//GO:0051553	nr -
Unigene18603_All	831	0.13	1.16	0.64	2.46	3.61	2.99	0.76	0.55	1.29	3.20E+00	6.55E-04	Up	2.35E+00	5.88E-02		5.53E-01	1.37E-01		2.83E-01	5.37E-01		-4.64E-01	5.93E-01		7.62E-01	1.85E-01		Unigene18603_All//gi|157169067|gb|ABU25893.1|/6.00E-58//starch synthase isoform I [Manihot esculenta]	Unigene18603_All//3.00E-50//AT5G24300| SSI1 (SUPPRESSOR OF SALICYLIC ACID INSENSITIVITY 1); starch synthase/ transferase, transferring glycosyl groups	Unigene18603_All//0.00E+00//C0112519		ko00500|Starch and sucrose metabolism	GO:0005982//GO:0009250//GO:0009532//GO:0016757//GO:0023033//GO:0051707	nr -
Unigene18605_All	444	2.95	0.00	0.36	9.42	2.71	1.63	1.14	0.94	1.79	-1.15E+01	1.28E-07	Down	-3.03E+00	1.24E-04	Down	-1.80E+00	1.27E-09	Down	-2.53E+00	7.23E-13	Down	-2.80E-01	7.49E-01		6.51E-01	3.53E-01		Unigene18605_All//gi|224139782|ref|XP_002323274.1|/2.00E-37//cytokinin oxidase [Populus trichocarpa] >gi|222867904|gb|EEF05035.1| cytokinin oxidase [Populus trichocarpa]	Unigene18605_All//1.00E-28//AT2G41510| CKX1 (CYTOKININ OXIDASE/DEHYDROGENASE 1); cytokinin dehydrogenase			ko00908|Zeatin biosynthesis	GO:0009690//GO:0009888//GO:0016645//GO:0043231	nr -
Unigene18606_All	953	1.65	0.90	0.89	5.28	5.49	2.56	0.13	0.00	0.08	-8.66E-01	9.97E-02		-8.82E-01	1.13E-01		5.70E-02	8.53E-01		-1.04E+00	7.90E-05	Down	-7.06E+00	2.36E-01		-6.71E-01	7.20E-01		Unigene18606_All//gi|38566628|gb|AR824204.1|/3.00E-34//At1g32690 [Arabidopsis thaliana] >gi|40824115|gb|AAM62349.1| At1g32690 [Arabidopsis thaliana]	Unigene18606_All//9.00E-26//AT1G32690| unknown protein	Unigene18606_All//0.00E+00//gi|78327039|gb|DT547313.1|DT547313			GO:0016020	nr +
Unigene18607_All	543	0.00	0.75	0.20	0.83	2.22	1.83	29.51	42.33	13.50	9.54E+00	1.36E-02		7.62E+00	3.99E-01		1.43E+00	2.58E-02		1.15E+00	1.16E-01		5.21E-01	2.94E-07		-1.13E+00	1.93E-18	Down				Unigene18607_All//7.00E-13//ES822458				
Unigene18610_All	333	19.33	134.51	13.43	15.11	27.71	27.26	30.09	57.23	136.98	2.80E+00	9.11E-136	Up	-5.25E-01	3.17E-02		8.75E-01	1.06E-06		8.51E-01	6.26E-06		9.28E-01	1.67E-15		2.19E+00	5.69E-130	Up	Unigene18610_All//gi|297792903|ref|XP_002864336.1|/5.00E-10//pinoid-binding protein 1 [Arabidopsis lyrata subsp. lyrata] >gi|297310171|gb|EFH60595.1| pinoid-binding protein 1 [Arabidopsis lyrata subsp. lyrata]	Unigene18610_All//3.00E-11//AT5G54490| PBP1 (PINOID-BINDING PROTEIN 1); calcium ion binding / protein binding	Unigene18610_All//4.00E-152//TC171215			GO:0009725//GO:0043231//GO:0044267//GO:0044464//GO:0046914	nr +
Unigene18611_All	1150	0.86	1.01	3.70	4.76	8.89	4.67	0.22	0.07	0.07	2.29E-01	6.94E-01		2.10E+00	1.97E-09	Up	9.00E-01	1.05E-07		-2.79E-02	9.33E-01		-1.60E+00	3.11E-01		-1.67E+00	2.56E-01		Unigene18611_All//gi|60459560|gb|AAX18166.2|/1.00E-131//CNGC2 [Gossypium hirsutum]	Unigene18611_All//3.00E-112//AT5G15410| DND1 (DEFENSE NO DEATH 1); calcium channel/ calmodulin binding / cation channel/ cyclic nucleotide binding / intracellular cAMP activated cation channel/ intracellular cyclic nucleotide activated cation channel/ inward rectifier potassium channel	Unigene18611_All//1.00E-16//TC129570		ko04626|Plant-pathogen interaction		nr +
Unigene18612_All	342	0.76	1.93	1.25	1.89	1.21	1.58	3.83	12.34	2.80	1.33E+00	1.45E-01		7.04E-01	5.54E-01		-6.48E-01	4.60E-01		-2.57E-01	7.57E-01		1.69E+00	4.82E-09	Up	-4.55E-01	3.76E-01		Unigene18612_All//gi|229893932|gb|ACQ90305.1|/1.00E-09//dormancy-associated protein 1 [Brassica rapa subsp. pekinensis]	Unigene18612_All//2.00E-10//AT1G28330| DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)	Unigene18612_All//9.00E-39//gi|164312489|gb|ES814705.1|ES814705			GO:0003824//GO:0009746//GO:0009755//GO:0034285	nr -
Unigene18613_All	325	2.90	26.50	15.24	9.96	10.49	9.17	45.40	60.44	30.03	3.19E+00	3.77E-30	Up	2.39E+00	1.13E-12	Up	7.43E-02	8.46E-01		-1.19E-01	7.42E-01		4.13E-01	2.05E-04		-5.96E-01	2.52E-06					Unigene18613_All//1.00E-22//gi|84164595|gb|DR453243.1|DR453243				
Unigene18614_All	419	1.62	0.24	0.00	2.73	1.89	2.16	1.11	0.60	1.43	-2.75E+00	1.06E-02		-1.07E+01	7.64E-04	Down	-5.33E-01	4.08E-01		-3.43E-01	6.37E-01		-8.91E-01	3.84E-01		3.62E-01	6.37E-01									

Unigene18615_All	785	0.93	4.32	2.24	0.89	1.93	1.09	276.41	674.96	726.48	2.21E+00	1.90E-08	Up	1.26E+00	1.66E-02		1.12E+00	4.05E-02		2.99E-01	6.87E-01		1.29E+00	0.00E+00	Up	1.39E+00	0.00E+00	Up	Unigene18615_All//gi|197312909|gb|ACH83235.1|//3.00E-60//alcohol dehydrogenase [Rheum australe]	Unigene18615_All//4.00E-61//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene18615_All//2.00E-60//TC157786		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0004030//GO:0009698	nr +
Unigene18617_All	969	0.22	0.63	0.33	0.62	0.85	1.03	1.09	10.09	5.10	1.54E+00	1.22E-01		6.10E-01	6.25E-01		4.67E-01	5.85E-01		7.33E-01	3.21E-01		3.21E+00	3.57E-42	Up	2.22E+00	4.57E-15	Up	Unigene18617_All//gi|151303117|gb|ABR92761.1|//3.00E-47//transcription factor TF2 [Gossypium hirsutum]	Unigene18617_All//3.00E-33//AT2G38250| DNA-binding protein-related	Unigene18617_All//6.00E-21//DW513921	Trihelix			nr +
Unigene18618_All	477	1.97	2.02	3.35	4.07	1.30	1.14	0.62	1.75	1.67	3.17E-02	9.83E-01		7.62E-01	1.60E-01		-1.65E+00	2.73E-04	Down	-1.84E+00	2.00E-04	Down	1.50E+00	3.73E-02		1.43E+00	4.39E-02					Unigene18618_All//4.00E-08//CO110739				
Unigene18619_All	360	14.53	11.12	6.06	18.82	13.97	17.94	62.01	26.70	19.03	-3.86E-01	1.46E-01		-1.26E+00	7.13E-06	Down	-4.30E-01	5.20E-02		-6.90E-02	7.85E-01		-1.22E+00	1.38E-27	Down	-1.70E+00	1.17E-46	Down	Unigene18619_All//gi|73761683|gb|AZ83341.1|//3.00E-33//ubiquitin extension protein [Gossypium hirsutum]	Unigene18619_All//6.00E-30//AT2G47110| UBQ6; protein binding	Unigene18619_All//3.00E-128//gi|13245821|gb|BE052928.2|BE052928		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene18620_All	381	12.91	2.66	4.47	1.70	1.27	2.13	0.00	0.00	0.10	-2.28E+00	1.91E-12	Down	-1.53E+00	3.36E-07	Down	-4.26E-01	6.08E-01		3.28E-01	7.01E-01		null	null		6.71E+00	6.45E-01		Unigene18620_All//gi|225460761|ref|XP_002276224.1|//1.00E-16//PREDICTED: similar to mitochondrial transcription termination factor family protein / mTERF family protein [Vitis vinifera]	Unigene18620_All//2.00E-05//AT5G55580| mitochondrial transcription termination factor family protein / mTERF family protein				nr +
Unigene18621_All	474	16.12	4.70	8.09	22.60	19.69	22.68	74.66	26.98	29.16	-1.78E+00	6.72E-14	Down	-9.95E-01	7.18E-06		-1.99E-01	3.08E-01		5.20E-03	9.78E-01		-1.47E+00	1.38E-57	Down	-1.36E+00	1.16E-52	Down	Unigene18621_All//gi|76161008|gb|AB40467.1|//2.00E-19//glycoprotein-like protein [Solanum tuberosum]	Unigene18621_All//1.00E-19//AT4G27090| 60S ribosomal protein L14 (RPL14B)	Unigene18621_All//0.00E+00//TC171368		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0031981	nr +
Unigene18624_All	512	3.58	8.02	9.78	1.36	2.08	2.65	0.66	1.47	0.62	1.16E+00	1.59E-04	Up	1.45E+00	7.69E-07	Up	6.14E-01	3.94E-01		9.58E-01	1.09E-01		1.15E+00	1.26E-01		-8.57E-02	9.47E-01					Unigene18624_All//4.00E-14//CO130441				
Unigene18625_All	723	0.58	3.36	2.28	5.37	4.14	4.44	1.29	0.98	1.32	2.54E+00	3.29E-07	Up	1.98E+00	8.05E-04	Up	-3.75E-01	2.40E-01		-2.77E-01	4.20E-01		-3.89E-01	5.75E-01		3.97E-02	9.67E-01		Unigene18625_All//gi|87162794|gb|AB028589.1|//4.00E-86//2OG-Fe(II) oxygenase [Medicago truncatula]	Unigene18625_All//6.00E-82//AT2G22260| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene18625_All//0.00E+00//TC168253			GO:0003824	nr -
Unigene18626_All	673	1.40	4.07	2.85	6.14	3.84	7.05	1.95	2.11	1.24	1.54E+00	1.40E-04	Up	1.03E+00	3.81E-02		-6.79E-01	1.69E-02		1.98E-01	5.44E-01		1.17E-01	8.18E-01		-6.48E-01	1.98E-01		Unigene18626_All//gi|297819638|ref|XP_002877702.1|//2.00E-27//bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323540|gb|EFH53961.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene18626_All//9.00E-26//AT2G22850| Atb2ZIP6 (Arabidopsis thaliana basic leucine-zipper 6); DNA binding / transcription factor	Unigene18626_All//0.00E+00//ES838565	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0003677//GO:0043231	nr -
Unigene18628_All	1449	0.00	0.35	0.07	6.81	4.35	1.78	0.85	0.66	0.33	8.45E+00	4.05E-03		6.20E+00	3.99E-01		-6.46E-01	1.28E-04		-1.94E+00	2.07E-21	Down	-3.51E-01	5.48E-01		-1.36E+00	1.18E-02		Unigene18628_All//gi|224107955|ref|XP_002314667.1|//0.00E+00//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222863707|gb|EEF00838.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene18628_All//0.00E+00//AT3G51895| SULTR3;1 (SULFATE TRANSPORTER 3;1); secondary active sulfate transmembrane transporter/ sulfate transmembrane transporter/ transporter	Unigene18628_All//0.00E+00//TC161844			GO:0015291//GO:0015698//GO:0031224	nr +
Unigene18631_All	625	62.37	2.35	7.50	7.65	5.40	0.58	0.14	0.13	0.13	-4.73E+00	3.26E-184	Down	-3.06E+00	6.27E-126	Down	-5.03E-01	6.13E-02		-3.73E+00	3.93E-21	Down	-1.72E-02	1.01E+00		-8.57E-02	9.72E-01									
Unigene18632_All	290	5.23	3.84	3.67	6.36	4.99	4.20	5.54	0.58	1.37	-4.45E-01	3.94E-01		-5.11E-01	3.80E-01		-3.50E-01	4.94E-01		-5.96E-01	2.34E-01		-3.26E+00	1.49E-07	Down	-2.01E+00	5.95E-05	Down				Unigene18632_All//2.00E-70//TC175948				
Unigene18634_All	302	5.54	0.84	1.06	1.65	2.39	2.69	0.84	1.66	1.85	-2.72E+00	1.40E-05	Down	-2.39E+00	1.21E-04	Down	5.38E-01	5.64E-01		7.07E-01	3.93E-01		9.83E-01	3.11E-01		1.14E+00	1.92E-01									
Unigene18637_All	793	81.29	108.75	147.06	73.43	145.17	620.61	932.62	1033.19	632.04	4.20E-01	5.02E-14		8.55E-01	7.35E-63		9.83E-01	7.86E-96		3.08E+00	0.00E+00	Up	1.48E-01	7.59E-22		-5.61E-01	1.41E-244		Unigene18637_All//gi|19569160|gb|AL92037.1|AF488309_1//1.00E-82//apoplastic anionic gaiacol peroxidase [Gossypium hirsutum]	Unigene18637_All//7.00E-52//AT5G06730| peroxidase, putative	Unigene18637_All//0.00E+00//TC159680		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0016209//GO:0042743	nr +
Unigene18638_All	514	0.10	7.69	1.24	6.40	4.02	4.66	1.81	2.20	0.85	6.24E+00	6.27E-21	Up	3.61E+00	6.98E-03		-6.70E-01	4.08E-02		-4.58E-01	2.03E-01		2.79E-01	6.41E-01		-1.09E+00	8.05E-02		Unigene18638_All//gi|224101607|ref|XP_002312350.1|//2.00E-13//predicted protein [Populus trichocarpa] >gi|222852170|gb|EEE89717.1| predicted protein [Populus trichocarpa]	Unigene18638_All//6.00E-05//AT3G25590| unknown protein	Unigene18638_All//1.00E-69//gi|78351933|gb|DT572207.1|DT572207				nr +
Unigene18639_All	617	0.17	11.00	0.60	3.15	2.68	3.22	0.55	1.76	0.19	6.02E+00	1.83E-35	Up	1.83E+00	2.13E-01		-2.33E-01	6.16E-01		3.26E-02	9.56E-01		1.68E+00	6.96E-03		-1.50E+00	2.11E-01		Unigene18639_All//gi|27311725|gb|AA000828.1|//9.00E-06//unknown protein [Arabidopsis thaliana] >gi|30725702|gb|AAP37873.1| At3g25590 [Arabidopsis thaliana]	Unigene18639_All//5.00E-07//AT3G25590| unknown protein	Unigene18639_All//2.00E-133//gi|78351933|gb|DT572207.1|DT572207				nr +
Unigene1864_All	2011	73.86	52.94	69.38	50.63	38.56	38.94	35.57	46.10	14.11	-4.81E-01	4.46E-30		-9.04E-02	5.88E-02		-3.93E-01	2.38E-17		-3.79E-01	1.37E-14		3.74E-01	6.58E-15		-1.33E+00	4.79E-103	Down	Unigene1864_All//gi|79383745|ref|NP_177879.3|//0.00E+00//protein binding / tubulin-tyrosine ligase [Arabidopsis thaliana] >gi|47550675|gb|AAT35236.1| At1g77550 [Arabidopsis thaliana]	Unigene1864_All//0.00E+00//AT1G77550| protein binding / tubulin-tyrosine ligase	Unigene1864_All//0.00E+00//gi|13351935|gb|BG442283.1|BG442283				nr -
Unigene18640_All	554	0.28	0.00	0.10	4.14	3.17	1.96	2.44	1.43	0.29	-8.15E+00	2.16E-01		-1.56E+00	5.33E-01		-3.84E-01	3.86E-01		-1.08E+00	1.06E-02		-7.69E-01	1.39E-01		-3.09E+00	1.97E-06	Down	Unigene18640_All//gi|225626259|gb|ACN97179.1|//8.00E-26//MYB transcription factor [Populus trichocarpa]	Unigene18640_All//6.00E-16//AT1G73410| MYB54 (MYB DOMAIN PROTEIN 54); DNA binding / transcription factor	Unigene18640_All//0.00E+00//gi|11201602|gb|BF270511.1|BF270511	MYB			nr -
Unigene18642_All	1079	1.45	23.81	8.19	1.02	0.93	3.77	0.12	0.54	0.37	4.03E+00	3.45E-108	Up	2.49E+00	2.67E-23	Up	-1.34E-01	8.25E-01		1.89E+00	1.14E-08	Up	2.21E+00	2.34E-02		1.65E+00	1.40E-01		Unigene18642_All//gi|6119723|gb|AAF04193.1|AF053638_1//3.00E-76//short-chain alcohol dehydrogenase [Pisum sativum]	Unigene18642_All//7.00E-62//AT2G47140| short-chain dehydrogenase/reductase (SDR) family protein	Unigene18642_All//0.00E+00//TC130774		ko00906|Carotenoid biosynthesis	GO:0008152//GO:0016616	nr +
Unigene18646_All	595	224.85	111.39	178.90	15.74	22.22	10.93	0.00	0.56	0.74	-1.01E+00	1.36E-98	Down	-3.30E-01	2.68E-13		4.98E-01	7.34E-04		-5.26E-01	4.71E-03		9.13E+00	1.27E-02		9.52E+00	2.13E-03		Unigene18646_All//gi|297849676|ref|XP_002892719.1|//2.00E-78//GAPA-2 [Arabidopsis lyrata subsp. lyrata] >gi|297338561|gb|EFH68978.1| GAPA-2 [Arabidopsis lyrata subsp. lyrata]	Unigene18646_All//1.00E-61//AT1G12900| GAPA-2 (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT 2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene18646_All//0.00E+00//TC158530		ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene18647_All	393	15.98	6.83	8.81	32.83	23.13	21.26	20.87	22.12	18.55	-1.23E+00	5.36E-07	Down	-8.59E-01	4.73E-04		-5.05E-01	5.69E-04		-6.27E-01	4.12E-05		8.39E-02	6.74E-01		-1.70E-01	3.80E-01		Unigene18647_All//gi|195636324|gb|ACG37630.1|//9.00E-15//derlin-2 [Zea mays]	Unigene18647_All//6.00E-16//AT4G21810| DER2.1 (DERLIN-2.1)	Unigene18647_All//9.00E-138//TC167249				nr +
Unigene18648_All	798	0.33	0.38	0.67	30.21	23.91	13.07	2.86	1.62	0.50	2.17E-01	8.65E-01		1.03E+00	3.42E-01		-3.38E-01	1.38E-03		-1.21E+00	5.21E-26	Down	-8.17E-01	3.07E-02		-2.52E+00	1.53E-08	Down	Unigene18648_All//gi|115475680|ref|NP_001061436.1|//8.00E-77//Os08g0277900 [Oryza sativa Japonica Group] >gi|113623405|dbj|BAF23350.1| Os08g0277900 [Oryza sativa Japonica Group]	Unigene18648_All//2.00E-70//AT1G16240| SYP51 (SYNTAXIN OF PLANTS 51); SNAP receptor	Unigene18648_All//0.00E+00//DW499770		ko04130|SNARE interactions in vesicular transport		nr -
Unigene18649_All	1026	0.31	0.30	0.00	0.00	0.17	0.44	2.47	2.93	8.23	-4.65E-02	9.85E-01		-8.26E+00	4.92E-02		7.39E+00	2.27E-01		8.78E+00	7.75E-03		2.46E-01	4.90E-01		1.74E+00	2.05E-18	Up	Unigene18649_All//gi|53370641|gb|AB089136.1|//2.00E-17//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene18649_All//4.00E-15//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative					nr +
Unigene1865_All	1539	0.17	0.00	0.35	1.23	0.65	0.88	1.46	0.92	0.60	-7.41E+00	6.71E-02		1.03E+00	3.42E-01		-9.23E-01	4.06E-02		-4.82E-01	3.38E-01		-6.57E-01	8.80E-02		-1.29E+00	6.63E-04	Down	Unigene1865_All//gi|79383745|ref|NP_177879.3|//0.00E+00//protein binding / tubulin-tyrosine ligase [Arabidopsis thaliana] >gi|47550675|gb|AAT35236.1| At1g77550 [Arabidopsis thaliana]	Unigene1865_All//0.00E+00//AT1G77550| protein binding / tubulin-tyrosine ligase	Unigene1865_All//0.00E+00//gi|13351935|gb|BG442283.1|BG442283				nr +
Unigene18650_All	658	0.56	3.00	0.49	0.76	0.79	0.82	2.63	2.48	5.81	2.43E+00	9.73E-06	Up	-1.97E-01	8.66E-01		5.22E-02	9.80E-01		1.22E-01	9.21E-01		-8.88E-02	8.49E-01		1.14E+00	4.19E-05	Up				Unigene18650_All//0.00E+00//DR458108				
Unigene18652_All	426	1.84	0.83	0.00	1.05	1.37	1.17	1.59	0.69	0.37	-1.15E+00	1.53E-01		-1.08E+01	2.22E-04	Down	3.85E-01	7.33E-01		1.48E-01	9.06E-01		-1.21E+00	1.34E-01		-2.09E+00	1.27E-02									
Unigene18653_All	582	0.54	0.00	0.00	0.94	1.54	0.78	4.07	0.50	1.51	-9.08E+00	3.66E-02		-9.08E+00	4.92E-02		7.08E-01	3.74E-01		-2.79E-01	7.57E-01		-3.02E+00	3.98E-10	Down	-1.43E+00	1.25E-04	Down	Unigene18653_All//gi|224065140|ref|XP_002301687.1|//2.00E-46//leucine-rich repeat transmembrane protein [Populus trichocarpa] >gi|222843413|gb|EEE80960.1| leucine-rich repeat transmembrane protein [Populus trichocarpa]	Unigene18653_All//1.00E-35//AT5G16590| LRR1; ATP binding / kinase/ protein serine/threonine kinase	Unigene18653_All//6.00E-66//gi|78328262|gb|DT548536.1|DT548536		ko04626|Plant-pathogen interaction		nr -
Unigene18654_All	500	0.00	0.00	0.00	7.37	3.03	1.72	3.55	1.25	0.72	null	null		null	null		-1.28E+00	2.19E-05	Down	-2.10E+00	3.29E-09	Down	-1.50E+00	1.01E-03		-2.31E+00	3.08E-06	Down				Unigene18654_All//1.00E-103//DW499917				
Unigene18655_All	931	0.56	0.65	1.60	0.54	0.92	0.92	14.85	2.11	3.38	2.17E-01	7.93E-01		1.51E+00	1.11E-02		7.89E-01	3.21E-01		7.85E-01	3.33E-01		-2.82E+00	2.52E-52	Down	-2.14E+00	2.67E-39	Down	Unigene18655_All//gi|283136126|gb|ADB11382.1|//8.00E-97//phi class glutathione transferase GSTF3 [Populus trichocarpa]	Unigene18655_All//5.00E-75//AT3G62760| ATGSTF13; glutathione transferase	Unigene18655_All//0.00E+00//TC154053		ko00480|Glutathione metabolism		nr -
Unigene18656_All	282	315.59	138.53	91.58	282.63	364.01	168.80	344.69	116.05	132.51	-1.19E+00	5.93E-85	Down	-1.78E+00	9.14E-151	Down	3.65E-01	4.85E-15		-7.44E-01	6.47E-38		-1.57E+00	2.61E-173	Down	-1.38E+00	6.45E-147	Down	Unigene18656_All//gi|298712420|emb|CBJ33198.1|//2.00E-32//histone H4 [Ectocarpus siliculosus]	Unigene18656_All//9.00E-21//AT5G59970| histone H4	Unigene18656_All//8.00E-156//TC179248				nr +
Unigene18657_All	1566	0.00	0.00	0.00	0.00	0.02	0.17	3.59	12.73	31.98	null	null		null	null		4.46E+00	8.30E-01		7.43E+00	7.03E-02		1.83E+00	1.99E-44	Up	3.15E+00	6.20E-214	Up	Unigene18657_All//gi|115446269|ref|NP_001046914.1|//1.00E-121//Os02g0504900 [Oryza sativa Japonica Group] >gi|48716191|dbj|BAD23231.1| kelch repeat-containing F-box protein-like [Oryza sativa Japonica Group] >gi|113536445|dbj|BAF08828.1| Os02g0504900 [Oryza sativa Japonica Group]	Unigene18657_All//9.00E-109//AT1G67480| kelch repeat-containing F-box family protein	Unigene18657_All//1.00E-78//gi|13350497|gb|BG440845.1|BG440845				nr -
Unigene18658_All	1229	0.17	0.00	0.00	0.16	0.45	0.48	11.66	4.73	6.03	-7.41E+00	1.22E-01		-7.41E+00	1.46E-01		1.47E+00	1.77E-01		1.56E+00	1.36E-01		-1.30E+00	5.72E-20	Down	-9.52E-01	9.12E-13		Unigene18658_All//gi|42568214|ref|NP_198840.2|//1.00E-75//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|10177511|dbj|BAB10905.1| nodulin-like protein [Arabidopsis thaliana] >gi|30725298|gb|AAP37671.1| At5g40240 [Arabidopsis thaliana]	Unigene18658_All//9.00E-82//AT4G15540| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: nodulin-related (TAIR:AT5G40230.1); Has 1698 Blast hits to 1688 proteins in 326 species: Archae - 14; Bacteria - 809; Metazoa - 6; Fungi - 0; Plants - 633; Viruses - 0; Other Eukaryotes - 236 (source: NCBI BLink).	Unigene18658_All//3.00E-17//TC169820				nr -

Unigene18659_All	320	0.00	1.27	0.00	1.25	3.44	2.54	4.89	11.36	6.85	1.03E+01	1.36E-02		null	null		1.47E+00	3.09E-02		1.03E+00	2.17E-01		1.22E+00	3.71E-05	Up	4.86E-01	2.01E-01		Unigene18659_All//gi|297849980|ref|XP_002892871.1|//3.00E-08//ATPDR12/PDR12 [Arabidopsis lyrata subsp. lyrata] >gi|297338713|gb|EFH69130.1|ATPDR12/PDR12 [Arabidopsis lyrata subsp. lyrata]	Unigene18659_All//1.00E-09//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene18659_All//1.00E-127//gi|48745945|gb|CO076464.1|CO076464				nr +
Unigene18661_All	306	4.96	2.65	0.70	6.51	2.14	2.66	0.14	0.41	0.91	-9.04E-01	9.22E-02		-2.83E+00	5.52E-05	Down	-1.61E+00	3.01E-04	Down	-1.29E+00	5.33E-03		1.57E+00	5.45E-01		2.72E+00	9.93E-02		Unigene18661_All//gi|15230127|ref|NP_189095.1|//6.00E-25//AT-HSFC1; DNA binding / transcription factor [Arabidopsis thaliana] >gi|75311616|sp|Q9LV52.1|HSFC1_ARATH RecName: Full=Heat stress transcription factor C-1; Short=AtHsfC1; AltName: Full=AtHsf-08 >gi|15810194|gb|AAL06998.1|AT3g24520/MOB24_5 [Arabidopsis thaliana] >gi|18252249|gb|AAL62005.1|AT3g24520/MOB24_5 [Arabidopsis thaliana]	Unigene18661_All//6.00E-16//AT3G24520| AT-HSFC1; DNA binding / transcription factor	Unigene18661_All//2.00E-33//TC139160	HSF			nr -
Unigene18662_All	514	0.20	0.79	0.73	2.13	2.61	1.32	3.95	0.65	0.85	1.95E+00	1.44E-01		1.83E+00	2.13E-01		2.93E-01	6.42E-01		-6.94E-01	3.11E-01		-2.60E+00	1.27E-07	Down	-2.21E+00	1.05E-06	Down	Unigene18662_All//gi|9280691|gb|AAF86560.1|AC069252_19//3.00E-41//F2E2.13 [Arabidopsis thaliana]	Unigene18662_All//7.00E-42//AT1G22060| LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT1G22000.1); Has 67094 Blast hits to 30189 proteins in 1408 species: Archae - 880; Bacteria - 6261; Metazoa - 35085; Fungi - 5326; Plants - 2622; Viruses - 293; Other Eukaryotes - 16627 (source: NCBI BLink).					nr -
Unigene18664_All	387	26.63	9.56	22.29	66.55	72.87	73.17	0.44	0.00	0.00	-1.48E+00	2.21E-14	Down	-2.57E-01	1.94E-01		1.31E-01	2.66E-01		1.37E-01	2.43E-01		-8.77E+00	1.35E-01		-8.77E+00	1.08E-01		Unigene18664_All//gi|150022156|gb|ABR57406.1|//7.00E-33//alpha-expansin 3 [Gossypium arboreum] >gi|150022168|gb|ABR57412.1|alpha-expansin 3 [Gossypium raimondii]	Unigene18664_All//6.00E-13//AT1G26770| ATEXPA10 (ARABIDOPSIS THALIANA EXPANSIN A 10); structural constituent of cell wall	Unigene18664_All//3.00E-110//ES819675				nr +
Unigene18665_All	449	1.40	2.37	2.25	1.55	1.23	1.91	0.94	3.63	6.74	7.61E-01	2.48E-01		6.88E-01	3.42E-01		-3.40E-01	6.80E-01		2.99E-01	6.87E-01		1.95E+00	1.26E-04	Up	2.84E+00	2.69E-12	Up	Unigene18665_All//gi|34365641|gb|AAQ65132.1|//2.00E-15//At3g48180 [Arabidopsis thaliana]	Unigene18665_All//2.00E-18//AT1G19020| unknown protein	Unigene18665_All//4.00E-122//TC168117				nr -
Unigene18667_All	453	65.95	62.41	98.86	23.86	42.42	28.31	2.05	9.87	4.05	-7.95E-02	4.88E-01		5.84E-01	8.17E-13		8.30E-01	2.54E-12		2.47E-01	1.50E-01		2.27E+00	1.10E-13	Up	9.78E-01	1.92E-02		Unigene18667_All//gi|56122682|gb|AAV74404.1|//1.00E-08//chloroplast oxygen-evolving enhancer protein [Manihot esculenta]	Unigene18667_All//8.00E-07//AT4G05180| PSBQ-2; calcium ion binding	Unigene18667_All//2.00E-123//gi|109881796|gb|DW510766.1|DW510766		ko00195|Photosynthesis		nr +
Unigene18668_All	601	0.26	0.08	0.35	1.41	0.11	1.20	1.69	1.46	1.59	-1.63E+00	4.89E-01		4.40E-01	7.75E-01		-3.62E+00	1.47E-04	Down	-2.29E-01	7.51E-01		-2.09E-01	7.31E-01		-8.58E-02	8.88E-01		Unigene18668_All//gi|75183398|sp|Q9MZY6.1|Y3972_ARATH//7.00E-10//RecName: Full=Uncharacterized protein At3g49720 >gi|222424727|dbj|BAH20317.1|AT3G49720 [Arabidopsis thaliana]	Unigene18668_All//3.00E-11//AT3G49720| unknown protein	Unigene18668_All//9.00E-96//CO096399				nr -
Unigene1867_All	1492	3.51	4.21	3.53	11.89	11.36	10.14	54.41	124.35	64.86	2.64E-01	2.90E-01		1.09E-02	9.91E-01		-6.59E-02	6.87E-01		-2.29E-01	1.07E-01		1.19E+00	9.54E-217	Up	2.53E-01	4.04E-08		Unigene1867_All//gi|119748|sp|P14766.2|F16P2_SPIOL//1.00E-173//RecName: Full=Fructose-1,6-bisphosphatase, cytosolic; Short=FBPase; AltName: Full=D-fructose-1,6-bisphosphate 1-phosphohydrolase >gi|212245|emb|CAA43860.1|fructose-bisphosphatase [Spinacia oleracea]	Unigene1867_All//6.00E-168//AT1G43670| fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	Unigene1867_All//0.00E+00//CO109076		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene18672_All	530	0.59	2.96	2.21	5.08	6.24	4.60	2.23	1.03	1.28	2.32E+00	1.67E-04	Up	1.90E+00	8.12E-03		2.97E-01	4.38E-01		-1.41E-01	7.22E-01		-1.12E+00	4.65E-02		-8.06E-01	1.31E-01		Unigene18672_All//gi|297598061|ref|NP_001045008.2|//2.00E-42//Os01g0882400 [Oryza sativa Japonica Group] >gi|255673930|dbj|BAF06922.2|Os01g0882400 [Oryza sativa Japonica Group]	Unigene18672_All//3.00E-09//AT4G24310| unknown protein					nr -
Unigene18674_All	598	1.05	0.00	0.27	0.00	1.55	0.30	8.48	7.27	13.32	-1.00E+01	7.92E-04	Down	-1.97E+00	6.50E-02		1.06E+01	1.03E-05	Up	8.24E+00	1.94E-01		-2.23E-01	3.97E-01		6.51E-01	2.67E-04					Unigene18674_All//1.00E-08//DT458988				
Unigene18675_All	670	0.39	0.98	2.46	2.08	1.64	2.43	1.07	0.56	1.72	1.33E+00	1.45E-01		2.66E+00	4.26E-05	Up	-3.40E-01	5.62E-01		2.21E-01	6.77E-01		-9.34E-01	2.26E-01		6.85E-01	2.12E-01					Unigene18675_All//3.00E-142//CO124882				
Unigene18678_All	340	87.10	329.20	211.43	118.24	193.45	302.86	26.86	102.65	93.27	1.92E+00	1.16E-214	Up	1.28E+00	7.95E-75	Up	7.10E-01	1.06E-31		1.36E+00	2.71E-129	Up	1.93E+00	1.99E-83	Up	1.80E+00	4.41E-70	Up	Unigene18678_All//gi|195626006|gb|ACG34833.1|//2.00E-06//ZmMybst1 [Zea mays]	Unigene18678_All//1.00E-07//AT5G47390| myb family transcription factor	Unigene18678_All//5.00E-136//gi|78343565|gb|DT563839.1|DT563839	MYB-related			nr +
Unigene18679_All	253	0.21	1.20	1.89	3.15	0.68	0.36	9.02	3.63	3.46	2.54E+00	1.51E-01		3.20E+00	3.48E-02		-2.21E+00	7.35E-03		-3.14E+00	1.88E-03		-1.31E+00	7.08E-04	Down	-1.38E+00	2.68E-04	Down				Unigene18679_All//6.00E-141//gi|164322178|gb|ES826526.1|ES826526				
Unigene1868_All	1287	23.94	22.99	18.66	44.59	44.17	44.36	72.41	24.55	24.55	-5.86E-02	5.93E-01		-3.60E-01	3.79E-04		-1.35E-02	8.75E-01		-7.50E-03	9.44E-01		-1.56E+00	1.37E-164	Down	-1.56E+00	2.19E-169	Down	Unigene1868_All//gi|115485231|ref|NP_001067759.1|//1.00E-120//Os11g0312400 [Oryza sativa Japonica Group] >gi|88533|sp|Q08480.1|KAD2_ORYSJ RecName: Full=Adenylate kinase B; Short=AK B; AltName: Full=ATP-AMP transphosphorylase B >gi|391879|dbj|BAA01181.1|adenylate kinase-b [Oryza sativa] >gi|62734015|gb|AAX96124.1|adenylate kinase b (ec 2.7.4.3) (atp-amp transphosphorylase) [Oryza sativa Japonica Group] >gi|113641981|dbj|BAF28122.1|Os11g0312400 [Oryza sativa Japonica Group]	Unigene1868_All//3.00E-110//AT5G50370| adenylate kinase, putative	Unigene1868_All//0.00E+00//TC139805		ko00230|Purine metabolism		nr -
Unigene18686_All	548	8.69	1.66	7.19	7.18	3.39	1.40	0.15	0.08	1.09	-2.38E+00	1.07E-12	Down	-2.73E-01	3.80E-01		-1.08E+00	1.72E-04	Down	-2.36E+00	3.39E-11	Down	-1.02E+00	7.25E-01		2.82E+00	5.65E-03		Unigene18686_All//gi|297811343|ref|XP_002873355.1|//2.00E-30//dihydropyrimidinase [Arabidopsis lyrata subsp. lyrata] >gi|297319392|gb|EFH49814.1|dihydropyrimidinase [Arabidopsis lyrata subsp. lyrata]	Unigene18686_All//9.00E-31//AT5G12200| dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2)	Unigene18686_All//0.00E+00//gi|164242868|gb|ES807046.1|ES807046		ko00240|Pyrimidine metabolism//ko00410|beta-Alanine metabolism//ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene18690_All	1777	0.00	0.17	0.00	0.95	0.81	0.94	8.92	1.69	7.15	7.42E+00	4.44E-02		null	null		-2.28E-01	6.59E-01		-1.94E-02	9.59E-01		-2.40E+00	3.98E-50	Down	-3.19E-01	9.79E-03		Unigene18690_All//gi|224062770|ref|XP_002306986.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222842612|gb|EEE80159.1|cytochrome P450 [Populus trichocarpa]	Unigene18690_All//0.00E+00//AT5G09970| CYP78A7; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene18691_All	1861	0.06	2.42	0.09	0.29	0.07	0.07	2.68	18.39	3.13	5.43E+00	1.01E-22	Up	6.10E-01	7.48E-01		-1.99E+00	5.12E-02		-2.02E+00	7.05E-02		2.78E+00	1.66E-126	Up	2.21E-01	3.46E-01		Unigene18691_All//gi|18422823|ref|NP_568687.1|//1.00E-83//ATNUDT2 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 2); ADP-ribose diphosphatase/ NAD or NADH binding / hydrolase [Arabidopsis thaliana] >gi|68565924|sp|Q9ZB74.1|NUDT2_ARATH RecName: Full=Nudix hydrolase 2; Short=ATNUDT2; AltName: Full=ADP-ribose pyrophosphatase; AltName: Full=NADH pyrophosphatase >gi|14596037|gb|AAK68746.1| MutT domain protein-like [Arabidopsis thaliana] >gi|17978727|gb|AAL47357.1| MutT domain protein-like [Arabidopsis thaliana]	Unigene18691_All//4.00E-86//AT5G47650| ATNUDT2 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 2); ADP-ribose diphosphatase/ NAD or NADH binding / hydrolase	Unigene18691_All//1.00E-140//DR458609				nr +
Unigene18694_All	404	41.05	9.53	17.53	10.48	4.35	16.99	0.00	0.41	0.00	-2.11E+00	1.10E-36	Down	-1.23E+00	1.60E-16	Down	-1.27E+00	5.18E-06	Down	6.97E-01	1.65E-03		8.69E+00	1.39E-01		null	null		Unigene18694_All//gi|147795075|emb|CAN60855.1|//3.00E-06//hypothetical protein [Vitis vinifera] >gi|296082535|emb|CBI21540.3|unnamed protein product [Vitis vinifera]						nr -
Unigene18695_All	476	1.32	0.00	0.67	3.03	1.37	2.56	1.33	0.97	0.33	-1.04E+01	7.92E-04	Down	-9.75E-01	3.16E-01		-1.14E+00	3.09E-02		-2.45E-01	6.84E-01		-4.64E-01	5.93E-01		-1.99E+00	2.04E-02		Unigene18695_All//gi|227462996|gb|ACP39950.1|//4.00E-54//pentatricopeptide repeat protein [Gossypium hirsutum] >gi|227462998|gb|ACP39951.1|pentatricopeptide repeat protein [Gossypium hirsutum]	Unigene18695_All//1.00E-12//AT2G22410| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene18697_All	1760	0.00	0.00	0.00	0.00	0.00	0.00	59.65	12.82	4.57	null	null		null	null		null	null		null	null		-2.22E+00	7.39E-299	Down	-3.71E+00	0.00E+00	Down	Unigene18697_All//gi|224139824|ref|XP_002323294.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222867924|gb|EEF05055.1|cytochrome P450 [Populus trichocarpa]	Unigene18697_All//3.00E-130//AT5G06900| CYP93D1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene18697_All//1.00E-07//CO076520		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene18699_All	351	5.96	12.56	12.74	7.66	13.05	11.58	8.67	4.52	3.75	1.07E+00	2.52E-04	Up	1.10E+00	2.88E-04	Up	7.68E-01	4.93E-03		5.96E-01	5.30E-02		-9.39E-01	3.29E-03		-1.21E+00	1.31E-04	Down	Unigene18699_All//gi|20197329|gb|AAC63841.2|//5.00E-13//expressed protein [Arabidopsis thaliana] >gi|98960999|gb|ABF58983.1|At2g31090 [Arabidopsis thaliana]		Unigene18699_All//6.00E-145//TC169072				nr -
Unigene18700_All	746	0.00	0.20	0.86	2.74	3.28	2.06	2.21	0.95	0.37	7.67E+00	2.35E-01		9.74E+00	1.16E-03		2.60E-01	5.83E-01		-4.12E-01	3.91E-01		-1.21E+00	9.00E-03		-2.56E+00	1.72E-06	Down	Unigene18700_All//gi|15230158|ref|NP_188497.1|//1.00E-78//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene18700_All//8.00E-80//AT3G18670| ankyrin repeat family protein	Unigene18700_All//0.00E+00//CO110760				nr -
Unigene18702_All	750	47.65	29.19	38.70	1.13	0.41	0.06	0.00	0.11	0.32	-7.07E-01	6.86E-15		-3.00E-01	1.44E-03		-1.45E+00	5.13E-02		-4.23E+00	2.18E-04	Down	6.80E+00	4.01E-01		8.32E+00	4.39E-02		Unigene18702_All//gi|18396089|ref|NP_566164.1|//1.00E-37//PTF1 (PLASTID TRANSCRIPTION FACTOR 1); transcription factor [Arabidopsis thaliana]	Unigene18702_All//6.00E-32//AT3G02150| PTF1 (PLASTID TRANSCRIPTION FACTOR 1); transcription factor	Unigene18702_All//0.00E+00//gi|78337379|gb|DT557653.1|DT557653	TCP			nr +
Unigene18704_All	706	3.04	3.66	0.45	0.99	1.17	1.47	0.30	0.36	0.73	2.69E-01	5.11E-01		-2.75E+00	1.29E-06	Down	2.45E-01	8.03E-01		5.75E-01	4.27E-01		2.47E-01	8.53E-01		1.29E+00	1.59E-01		Unigene18704_All//gi|91806405|gb|ABE65930.1|//8.00E-78//exocyst subunit EXO70 family protein [Arabidopsis thaliana]	Unigene18704_All//6.00E-73//AT3G09520| ATEX070H4 (exocyst subunit EXO70 family protein H4); protein binding	Unigene18704_All//0.00E+00//gi|109878907|gb|DW507877.1|DW507877				nr -
Unigene18707_All	520	4.53	1.36	3.69	7.47	7.09	4.69	1.06	1.77	1.00	-1.73E+00	1.14E-04	Down	-2.97E-01	5.08E-01		-7.66E-02	8.17E-01		-6.72E-01	3.04E-02		7.42E-01	2.60E-01		-8.58E-02	9.27E-01					Unigene18707_All//5.00E-94//CO123449				

Unigene18709_All	399	0.26	1.65	2.54	1.50	1.81	1.81	0.85	1.89	3.20	2.65E+00	1.50E-02		3.27E+00	5.93E-04	Up	2.75E-01	8.01E-01		2.74E-01	7.43E-01		1.15E+00	1.26E-01		1.91E+00	7.76E-04	Up	Unigene18709_All//gi|238479758|ref|NP_001154613.1|//4.00E-12//protein binding [Arabidopsis thaliana]	Unigene18709_All//2.00E-13//AT3G13225| protein binding					nr -
Unigene1871_All	563	5.48	5.67	3.50	5.93	5.32	7.54	16.15	5.49	5.24	4.84E-02	8.99E-01		-6.48E-01	8.21E-02		-1.56E-01	6.77E-01		3.47E-01	2.84E-01		-1.56E+00	1.15E-16	Down	-1.62E+00	2.82E-18	Down	Unigene1871_All//gi|15242719|ref|NP_198865.1|//5.00E-14//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|22531255|gb|AAM97131.1| ribonucleoprotein-like [Arabidopsis thaliana]		Unigene1871_All//0.00E+00//TC140628		ko03040|Spliceosome		nr -
Unigene18710_All	316	65.57	67.02	53.08	69.52	62.88	98.62	115.60	66.93	45.64	3.17E-02	8.10E-01		-3.05E-01	1.82E-02		-1.45E-01	2.76E-01		5.04E-01	7.57E-08		-7.89E-01	3.36E-22		-1.34E+00	2.07E-53	Down	Unigene18710_All//gi|192910708|gb|ACF06462.1|//2.00E-39//24 kDa seed maturation protein [Elaeis guineensis]	Unigene18710_All//1.00E-23//AT4G23630| BTI1 (VIRB2-INTERACTING PROTEIN 1)	Unigene18710_All//5.00E-176//TC151737				nr -
Unigene18711_All	534	0.98	3.04	0.80	1.87	2.26	0.17	1.27	0.86	2.09	1.63E+00	3.13E-03		-2.97E-01	7.50E-01		2.75E-01	7.00E-01		-3.46E+00	1.73E-04	Down	-5.57E-01	4.89E-01		7.22E-01	2.00E-01		Unigene18711_All//gi|37780047|gb|AAP32196.1|//5.00E-41//cysteine protease 8 [Trifolium repens]	Unigene18711_All//4.00E-22//AT5G45890| SAG12 (SENESCENCE-ASSOCIATED GENE 12); cysteine-type peptidase					nr -
Unigene18712_All	546	116.33	87.98	79.88	125.72	127.46	199.84	178.88	99.13	64.65	-4.03E-01	7.65E-10		-5.42E-01	9.82E-16		1.98E-02	8.41E-01		6.69E-01	1.17E-42		-8.52E-01	4.74E-66		-1.47E+00	3.17E-162	Down	Unigene18712_All//gi|32400865|gb|AAP86664.1|AF479045_1|/3.00E-27//S28 ribosomal protein [Triticum aestivum]	Unigene18712_All//7.00E-19//AT5G41410| RPS28 (RIBOSOMAL PROTEIN S28); structural constituent of ribosome	Unigene18712_All//0.00E+00//TC167949		ko03010|Ribosome		nr +
Unigene18713_All	1051	0.00	0.00	0.00	0.00	0.00	0.00	11.59	58.06	2.73	null	null		null	null		null	null		null	null		2.33E+00	8.66E-184	Up	-2.09E+00	1.04E-33	Down	Unigene18713_All//gi|124361158|gb|ABN09130.1|//1.00E-37//DC1: C1-like [Medicago truncatula]	Unigene18713_All//3.00E-32//AT2G16050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: DC1 (InterPro:IPR004146); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G20990.1); Has 719 Blast hits to 448 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 717; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene18713_All//3.00E-29//CA992648				nr -
Unigene18715_All	650	2.25	0.55	1.88	4.45	2.07	0.97	1.50	1.35	0.86	-2.05E+00	8.60E-04	Down	-2.58E-01	6.23E-01		-1.11E+00	1.41E-03		-2.19E+00	1.06E-07	Down	-1.48E-01	8.13E-01		-8.02E-01	1.83E-01				Unigene18715_All//6.00E-165//TC154776				
Unigene18716_All	717	0.00	0.00	1.04	0.76	0.19	0.63	0.12	0.35	0.00	null	null		1.00E+01	3.28E-04	Up	-1.99E+00	5.12E-02		-2.79E-01	7.57E-01		1.57E+00	3.26E-01		-6.88E+00	3.59E-01		Unigene18716_All//gi|124359982|gb|ABN07998.1|//5.00E-06//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]		Unigene18716_All//1.00E-159//gi|109836996|gb|DW235557.1|DW235557				nr -
Unigene18717_All	675	0.39	2.18	0.95	1.48	2.09	2.41	7.33	7.18	17.06	2.49E+00	1.51E-04	Up	1.29E+00	1.86E-01		5.03E-01	4.15E-01		7.07E-01	1.95E-01		-2.90E-02	9.29E-01		1.22E+00	5.08E-15	Up	Unigene18717_All//gi|297848650|ref|XP_002892206.1|//7.00E-09//thioesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338048|gb|EFH68465.1| thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene18717_All//2.00E-05//AT1G04290| thioesterase family protein	Unigene18717_All//2.00E-47//DT464347				nr -
Unigene18718_All	519	2.32	2.64	2.36	9.79	8.43	7.48	1.79	0.40	0.31	1.85E-01	7.28E-01		2.54E-02	9.87E-01		-2.16E-01	4.64E-01		-3.88E-01	1.68E-01		-2.15E+00	2.95E-03		-2.55E+00	5.79E-04	Down	Unigene18718_All//gi|18409814|ref|NP_566984.1|//1.00E-12//transcriptional factor B3 family protein [Arabidopsis thaliana] >gi|75154861|sp|Q8LAV5.1|REM20_ARATH RecName: Full=B3 domain-containing protein REM20; AltName: Full=Protein REPRODUCTIVE MERISTEM 20 >gi|106879195|gb|ABF82627.1| At3g53310 [Arabidopsis thaliana]	Unigene18718_All//3.00E-10//AT3G53310| transcriptional factor B3 family protein		ABI3VP1			nr -
Unigene18720_All	1147	0.46	0.18	0.09	0.39	1.29	1.14	3.58	0.33	2.54	-1.37E+00	1.97E-01		-2.30E+00	6.77E-02		1.72E+00	2.61E-03		1.55E+00	1.29E-02		-3.45E+00	3.04E-19	Down	-4.96E-01	5.82E-02		Unigene18720_All//gi|6635236|dbj|BAA88636.1|//7.00E-58//elicitor-inducible LRR receptor-like protein EILP [Nicotiana tabacum]	Unigene18720_All//1.00E-41//AT5G46330| FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / kinase/ protein binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr -
Unigene18722_All	1158	0.00	0.44	0.00	0.00	0.00	1.79	11.10	25.08	61.24	8.77E+00	4.05E-03		null	null		null	null		1.08E+01	2.08E-12	Up	1.18E+00	7.71E-34	Up	2.46E+00	6.35E-233	Up	Unigene18722_All//gi|259121411|gb|ACV92025.1|//4.00E-44//WRKY transcription factor 23 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene18722_All//1.00E-34//AT4G01250| WRKY22; transcription factor	Unigene18722_All//4.00E-13//gi|78325567|gb|DT545841.1|DT545841	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene18723_All	922	20.54	0.66	1.39	0.49	0.67	0.15	1.47	1.09	1.34	-4.96E+00	5.64E-92	Down	-3.89E+00	1.33E-75	Down	4.67E-01	6.35E-01		-1.73E+00	1.61E-01		-4.32E-01	4.16E-01		-1.32E-01	7.85E-01		Unigene18723_All//gi|264664506|sp|COLG89.1|Y4312_ARATH//6.00E-93//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g31250; Flags: Precursor >gi|224589643|gb|ACN59354.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene18723_All//1.00E-87//AT4G31250| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction		nr -
Unigene18725_All	327	11.52	27.27	18.89	17.06	14.32	22.65	41.63	63.14	31.68	1.24E+00	9.23E-10	Up	7.13E-01	3.92E-03		-2.53E-01	3.52E-01		4.09E-01	6.67E-02		6.01E-01	2.62E-08		-3.94E-01	3.02E-03				Unigene18725_All//2.00E-101//TC174686				
Unigene18727_All	380	1.38	0.00	1.96	6.82	3.72	4.87	6.45	3.96	1.26	-1.04E+01	2.93E-03		5.11E-01	5.47E-01		-8.76E-01	1.86E-02		-4.84E-01	2.37E-01		-7.05E-01	5.26E-02		-2.36E+00	1.64E-08	Down	Unigene18727_All//gi|224106557|ref|XP_002314207.1|//3.00E-09//predicted protein [Populus trichocarpa] >gi|222850615|gb|EEE88162.1| predicted protein [Populus trichocarpa]		Unigene18727_All//2.00E-120//TC138716				nr +
Unigene18728_All	521	1.91	7.20	12.47	2.01	8.66	8.76	0.00	0.00	0.08	1.92E+00	7.88E-08	Up	2.71E+00	7.40E-19	Up	2.11E+00	1.18E-11	Up	2.12E+00	3.87E-11	Up	null	null		6.26E+00	6.45E-01		Unigene18728_All//gi|11120557|gb|AAG30923.1|AF306349_1|/2.00E-20//MADS box protein AP2L [Eucalyptus globulus]	Unigene18728_All//1.00E-09//AT5G60910| AGL8 (agamous-like 8); transcription factor	Unigene18728_All//0.00E+00//TC179334	MADS			nr +
Unigene18729_All	302	11.43	3.52	4.76	2.80	3.76	1.50	0.14	0.00	0.00	-1.70E+00	2.46E-06	Down	-1.26E+00	3.85E-04	Down	4.24E-01	5.47E-01		-9.07E-01	2.47E-01		-7.13E+00	6.58E-01		-7.13E+00	6.13E-01									
Unigene1873_All	2921	9.83	2.98	4.78	12.88	8.42	4.92	19.63	2.58	6.60	-1.72E+00	3.56E-48	Down	-1.04E+00	8.38E-22	Down	-6.13E-01	1.32E-14		-1.39E+00	6.55E-50	Down	-2.93E+00	2.02E-224	Down	-1.57E+00	1.25E-105	Down	Unigene1873_All//gi|75335557|sp|Q9LVM0.1|Y5830_ARATH//0.00E+00//RecName: Full=Probable inactive receptor kinase At5g58300; Flags: Precursor >gi|8777331|dbj|BAA96921.1| receptor-like protein kinase [Arabidopsis thaliana] >gi|24797034|gb|AAN64529.1| At5g58299/At5g58299 [Arabidopsis thaliana] >gi|224589729|gb|ACN59396.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene1873_All//3.00E-144//AT5G58300| leucine-rich repeat transmembrane protein kinase, putative	Unigene1873_All//0.00E+00//gi|109862082|gb|DW491059.1|DW491059				nr -
Unigene18730_All	1114	0.00	0.09	0.29	0.63	0.12	0.49	2.88	7.62	4.29	6.51E+00	3.87E-01		8.16E+00	4.53E-02		-2.34E+00	1.01E-02		-3.64E-01	6.81E-01		1.40E+00	1.90E-13	Up	5.73E-01	1.62E-02		Unigene18730_All//gi|297820104|ref|XP_002877935.1|//3.00E-88//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323773|gb|EFH54194.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene18730_All//3.00E-87//AT3G53690| zinc finger (C3HC4-type RING finger) family protein					nr -
Unigene18731_All	276	2.46	7.53	0.77	1.80	2.62	2.29	1.99	1.51	1.01	1.61E+00	7.32E-04	Up	-1.68E+00	8.71E-02		5.38E-01	5.64E-01		3.44E-01	6.99E-01		-3.95E-01	6.34E-01		-9.79E-01	2.50E-01		Unigene18731_All//gi|124359162|gb|ABN05685.1|//1.00E-07//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene18731_All//7.00E-33//BQ409652				nr +
Unigene18736_All	374	37.77	63.95	42.00	141.32	145.94	124.62	127.63	88.40	54.54	7.60E-01	1.90E-11		1.53E-01	3.58E-01		4.64E-02	6.00E-01		-1.81E-01	1.69E-02		-5.30E-01	1.25E-14		-1.23E+00	1.27E-60	Down	Unigene18736_All//gi|300793582|tpg|DAA33858.1|//8.00E-67//TPA: TPA inf: aquaporin PIP1;4 [Gossypium hirsutum]	Unigene18736_All//2.00E-59//AT4G00430| PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel	Unigene18736_All//0.00E+00//TC142602				nr +
Unigene18737_All	814	0.39	0.00	0.00	2.63	3.34	2.77	1.14	0.10	0.00	-8.59E+00	3.66E-02		-8.59E+00	4.92E-02		3.45E-01	4.17E-01		7.62E-02	8.80E-01		-3.48E+00	7.79E-05	Down	-1.02E+01	5.48E-07	Down	Unigene18737_All//gi|30684813|ref|NP_188445.2|//5.00E-67//transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|27808590|gb|AAO24575.1| At3g18170 [Arabidopsis thaliana]	Unigene18737_All//3.00E-68//AT3G18170| transferase, transferring glycosyl groups	Unigene18737_All//0.00E+00//gi|54120918|gb|CO496427.1|CO496427				nr +
Unigene18738_All	350	35.73	350.92	33.62	103.61	196.77	206.59	130.22	182.35	244.61	3.30E+00	0.00E+00	Up	-8.76E-02	6.12E-01		9.25E-01	6.53E-52		9.96E-01	1.08E-55		4.86E-01	1.47E-16		9.10E-01	3.78E-66		Unigene18738_All//gi|292668949|gb|ADE41129.1|//2.00E-28//AP2 domain class transcription factor [Malus x domestica]	Unigene18738_All//3.00E-24//AT1G68840| RAV2 (REGULATOR OF THE ATPASE OF THE VACUOLAR MEMBRANE); DNA binding / transcription factor/ transcription repressor	Unigene18738_All//3.00E-156//DW520147	AP2-EREBP			nr -
Unigene18741_All	699	0.30	0.15	0.30	3.14	1.28	0.90	218.42	233.20	159.30	-1.05E+00	5.65E-01		2.53E-02	1.00E+00		-1.29E+00	1.69E-03		-1.79E+00	9.25E-05	Down	9.44E-02	1.40E-02		-4.55E-01	3.22E-35		Unigene18741_All//gi|30102554|gb|AAP21195.1|//4.00E-11//At2g16386 [Arabidopsis thaliana]	Unigene18741_All//3.00E-09//AT2G16385| unknown protein					nr +
Unigene18744_All	409	4.35	1.12	1.30	0.24	1.18	2.21	0.31	0.00	0.00	-1.96E+00	2.97E-04	Down	-1.74E+00	1.58E-03		2.27E+00	7.83E-02		3.18E+00	9.74E-04	Up	-8.28E+00	2.36E-01		-8.28E+00	2.00E-01		Unigene18744_All//gi|224091126|ref|XP_002309188.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222855164|gb|EEE92711.1| predicted protein [Populus trichocarpa]	Unigene18744_All//2.00E-05//AT5G01910| unknown protein	Unigene18744_All//0.00E+00//DW510148				nr +
Unigene18745_All	996	0.00	0.20	0.00	0.00	0.21	0.00	26.32	8.48	5.40	7.67E+00	1.37E-01		null	null		7.70E+00	1.57E-01		null	null		-1.63E+00	5.10E-50	Down	-2.29E+00	2.85E-80	Down	Unigene18745_All//gi|15225223|ref|NP_180789.1|//3.00E-41//UCC1 (UCLACYANIN 1); copper ion binding / electron carrier [Arabidopsis thaliana] >gi|3399767|gb|AAC32038.1| uclacyanin I [Arabidopsis thaliana]	Unigene18745_All//2.00E-30//AT2G32300| UCC1 (UCLACYANIN 1); copper ion binding / electron carrier			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene18746_All	493	1.70	0.10	2.48	1.92	1.12	4.67	1.11	0.25	0.81	-4.05E+00	4.66E-04	Down	5.49E-01	3.86E-01		-7.81E-01	2.68E-01		1.28E+00	2.91E-03		-2.13E+00	3.31E-02		-4.64E-01	5.97E-01		Unigene18746_All//gi|297847728|ref|XP_002891745.1|//5.00E-40//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297337587|gb|EFH68004.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene18746_All//1.00E-40//AT1G53330| pentatricopeptide (PPR) repeat-containing protein					nr -

Unigene18748_All	1542	0.00	0.07	0.00	0.00	0.04	0.00	64.11	8.97	12.66	6.04E+00	3.87E-01		null	null		5.48E+00	6.10E-01		null	null		-2.84E+00	0.00E+00	Down	-2.34E+00	0.00E+00	Down	Unigene18748_All//gi|22854880|gb|AAN09798.1|//1.00E-154//benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Nicotiana tabacum]	Unigene18748_All//3.00E-111//AT5G17540| transferase family protein	Unigene18748_All//8.00E-15//TC135891		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene18753_All	597	0.26	11.03	1.16	0.58	2.02	1.29	3.33	7.98	9.21	5.39E+00	5.45E-33	Up	2.14E+00	3.67E-02		1.79E+00	6.51E-03		1.14E+00	1.89E-01		1.26E+00	7.63E-07	Up	1.47E+00	7.70E-10	Up	Unigene18753_All//gi|162462869|ref|NP_001105794.1|//1.00E-26//alkaline alpha galactosidase 2 [Zea mays] >gi|68270845|gb|AAQ07252.2|AF197511_1 alkaline alpha galactosidase 2 [Zea mays]	Unigene18753_All//1.00E-27//AT5G20250| DIX10 (DARK INDUCIBLE 10); hydrolase, hydrolyzing O-glycosyl compounds	Unigene18753_All//2.00E-136//TC178471		ko00052|Galactose metabolism		nr +
Unigene18755_All	436	0.24	4.07	1.95	1.49	2.37	1.35	3.30	1.05	2.38	4.08E+00	6.27E-08	Up	3.03E+00	3.01E-03		6.74E-01	3.49E-01		-1.41E-01	8.73E-01		-1.64E+00	1.74E-03		-4.73E-01	3.37E-01		Unigene18755_All//gi|297738723|emb|CBI27968.3|//4.00E-10//unnamed protein product [Vitis vinifera]	Unigene18755_All//9.00E-07//AT2G19810| zinc finger (CCCH-type) family protein	Unigene18755_All//0.00E+00//gi|109827931|gb|DW226584.1|DW226584	C3H			nr +
Unigene18756_All	492	1.06	1.44	1.08	6.88	3.29	4.77	0.95	1.02	0.65	4.39E-01	6.16E-01		2.54E-02	9.99E-01		-1.07E+00	7.04E-04	Down	-5.28E-01	1.28E-01		1.09E-01	9.15E-01		-5.45E-01	5.66E-01		Unigene18756_All//gi|225437965|ref|XP_002269712.1|//4.00E-14//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene18757_All	872	2.10	0.00	0.00	1.83	0.16	0.00	22.16	5.42	11.56	-1.10E+01	1.34E-10	Down	-1.10E+01	5.33E-10	Down	-3.53E+00	4.59E-08	Down	-1.08E+01	5.79E-10	Down	-2.03E+00	9.98E-50	Down	-9.39E-01	1.55E-16		Unigene18757_All//gi|224120536|ref|XP_002318354.1|//3.00E-50//predicted protein [Populus trichocarpa] >gi|222859027|gb|EEE96574.1|predicted protein [Populus trichocarpa]	Unigene18757_All//9.00E-27//AT5G52900| unknown protein	Unigene18757_All//2.00E-14//TC138536				nr -
Unigene18758_All	1137	0.18	0.89	0.28	0.70	1.39	1.35	21.27	3.12	3.61	2.28E+00	4.10E-03		6.10E-01	6.25E-01		9.91E-01	6.19E-02		9.46E-01	8.51E-02		-2.77E+00	1.99E-89	Down	-2.56E+00	1.14E-84	Down	Unigene18758_All//gi|296917225|gb|AGS38899.1|//2.00E-91//annexin 11 [Glycine max]	Unigene18758_All//8.00E-67//AT2G38750| ANNAT4 (ANNEXIN ARABIDOPSIS 4); calcium ion binding / calcium-dependent phospholipid binding	Unigene18758_All//3.00E-07//EX169267				nr +
Unigene18759_All	379	0.14	0.00	0.00	3.55	0.36	0.72	1.34	2.10	2.21	-7.11E+00	6.13E-01		-7.11E+00	6.25E-01		-3.29E+00	1.81E-06	Down	-2.31E+00	4.01E-04	Down	6.46E-01	3.83E-01		7.22E-01	2.82E-01									
Unigene18761_All	492	115.81	54.99	110.18	8.00	6.65	5.14	0.00	0.00	0.00	-1.07E+00	1.45E-46	Down	-7.19E-02	3.96E-01		-2.67E-01	4.23E-01		-6.38E-01	3.96E-02		null	null		null	null									
Unigene18762_All	713	0.59	0.57	0.30	0.63	0.48	0.13	4.09	4.81	1.34	-4.62E-02	9.80E-01		-9.75E-01	4.12E-01		-3.81E-01	7.22E-01		-2.31E+00	7.81E-02		2.32E-01	4.84E-01		-1.61E+00	2.29E-06	Down	Unigene18762_All//gi|297802534|ref|XP_002869151.1|//8.00E-54//extra-large GTP-binding protein 2 [Arabidopsis lyrata subsp. lyrata] >gi|297314987|gb|EFH45410.1|extra-large GTP-binding protein 2 [Arabidopsis lyrata subsp. lyrata]	Unigene18762_All//3.00E-54//AT4G34390| XLG2 (extra-large GTP-binding protein 2); guanyl nucleotide binding / signal transducer	Unigene18762_All//1.00E-55//ES846620				nr +
Unigene18763_All	883	2.61	0.98	0.60	2.14	3.59	1.48	0.05	0.24	1.58	-1.42E+00	1.19E-03		-2.11E+00	2.16E-05	Down	7.43E-01	3.13E-02		-5.31E-01	2.87E-01		2.31E+00	2.40E-01		5.04E+00	8.10E-09	Up								
Unigene18764_All	522	27.76	15.82	4.69	30.73	24.67	7.01	0.00	1.36	0.46	-8.11E-01	4.69E-08		-2.56E+00	5.21E-39	Down	-3.17E-01	2.05E-02		-2.13E+00	4.49E-39	Down	1.04E+01	3.98E-05	Up	8.84E+00	4.39E-02				Unigene18764_All//1.00E-168//ES821663				
Unigene18765_All	339	125.01	43.79	79.01	43.79	44.59	18.92	0.00	0.37	0.82	-1.51E+00	6.77E-59	Down	-6.62E-01	5.05E-15		2.62E-02	8.86E-01		-1.21E+00	2.85E-16	Down	8.53E+00	2.40E-01		9.68E+00	2.43E-02				Unigene18765_All//2.00E-64//gi|82755052|gb|DV848614.1|DV848614				
Unigene18767_All	942	23.27	2.80	11.98	16.13	6.36	3.21	0.85	0.36	0.72	-3.06E+00	1.32E-73	Down	-9.58E-01	1.13E-14		-1.34E+00	4.52E-22	Down	-2.33E+00	2.87E-41	Down	-1.26E+00	7.98E-02		-2.46E-01	7.00E-01		Unigene18767_All//gi|115485799|ref|NP_001068043.1|//2.00E-28//Os11g0543300 [Oryza sativa Japonica Group] >gi|113645265|dbj|BAF28406.1|Os11g0543300 [Oryza sativa Japonica Group]	Unigene18767_All//2.00E-19//AT3G50150| unknown protein	Unigene18767_All//4.00E-25//ES800152				nr +
Unigene18769_All	372	445.01	251.58	449.62	408.02	424.24	334.84	329.38	90.67	148.11	-8.23E-01	5.57E-86		1.49E-02	7.56E-01		5.62E-02	2.44E-01		-2.85E-01	8.20E-13		-1.86E+00	2.23E-277	Down	-1.15E+00	6.57E-140	Down	Unigene18769_All//gi|3334113|sp|Q39779.1|ACBP_GOSHI//6.00E-28//RecName: Full=Acyl-CoA-binding protein; Short=ACBP >gi|1006831|gb|AAB67736.1| acyl-CoA-binding protein [Gossypium hirsutum]	Unigene18769_All//1.00E-21//AT1G31812| ACBP6 (acyl-CoA-binding protein 6); acyl-CoA binding / phosphatidylcholine binding	Unigene18769_All//3.00E-119//TC165743				nr +
Unigene18770_All	421	0.25	0.48	0.51	0.24	1.15	0.32	25.61	3.87	7.57	9.53E-01	6.22E-01		1.03E+00	5.92E-01		2.28E+00	7.83E-02		4.44E-01	8.62E-01		-2.73E+00	1.42E-39	Down	-1.76E+00	5.69E-24	Down								
Unigene18771_All	676	0.00	13.12	1.65	0.15	4.33	3.34	1.38	3.65	15.97	1.37E+01	9.33E-51	Up	1.07E+01	3.43E-06	Up	4.88E+00	1.04E-15	Up	4.50E+00	4.66E-11	Up	1.41E+00	1.76E-04	Up	3.54E+00	1.43E-51	Up	Unigene18771_All//gi|124359646|gb|ABD32321.2|//1.00E-08//Ribonuclease H [Medicago truncatula]						nr -
Unigene18772_All	655	1.28	0.46	0.08	7.23	3.47	2.14	3.55	0.45	0.00	-1.46E+00	6.69E-02		-3.97E+00	9.08E-04	Down	-1.06E+00	4.18E-05	Down	-1.76E+00	2.66E-09	Down	-2.99E+00	7.04E-10	Down	-1.18E+01	3.99E-17	Down	Unigene18772_All//gi|297800188|ref|XP_002867978.1|//1.00E-57//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313814|gb|EFH44237.1|leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene18772_All//5.00E-48//AT4G18760| AtRLP51 (Receptor Like Protein 51); protein binding	Unigene18772_All//6.00E-134//AI728852		ko04626|Plant-pathogen interaction		nr -
Unigene18773_All	225	36.28	20.04	4.26	17.49	25.86	11.84	53.93	14.12	5.49	-8.56E-01	2.72E-05		-3.09E+00	8.08E-27	Down	5.64E-01	1.95E-02		-5.63E-01	7.28E-02		-1.93E+00	1.53E-29	Down	-3.30E+00	1.81E-55	Down		Unigene18773_All//4.00E-05//AT5G59970| histone H4	Unigene18773_All//2.00E-116//TC169994				
Unigene18774_All	325	549.93	218.74	140.58	305.02	358.02	181.63	0.52	0.00	0.49	-1.33E+00	6.75E-203	Down	-1.97E+00	0.00E+00	Down	2.31E-01	1.90E-07		-7.48E-01	1.68E-47		-9.02E+00	1.35E-01		-8.60E-02	9.66E-01		Unigene18774_All//gi|117650697|gb|ABK54298.1|//1.00E-27//glycine-rich protein [Gossypium hirsutum]		Unigene18774_All//5.00E-179//gi|109884127|gb|DW513097.1|DW513097				nr -
Unigene18775_All	355	0.74	2.85	0.00	0.42	0.39	0.38	1.31	5.77	2.36	1.95E+00	1.01E-02		-9.53E+00	8.58E-02		-1.18E-01	9.11E-01		-1.41E-01	9.43E-01		2.14E+00	3.04E-06	Up	8.47E-01	2.03E-01		Unigene18775_All//gi|119942653|dbj|BAB01436.1|//7.00E-09//GDSL-motif lipase/hydrolase-like protein [Arabidopsis thaliana]	Unigene18775_All//3.00E-10//AT3G14225| GLIP4; carboxylesterase/ lipase	Unigene18775_All//5.00E-90//gi|109827634|gb|DW226308.1|DW226308				nr -
Unigene18778_All	725	0.14	0.49	0.00	0.14	0.29	0.50	0.87	2.71	1.32	1.76E+00	2.18E-01		-7.17E+00	3.95E-01		1.05E+00	6.12E-01		1.86E+00	2.20E-01		1.63E+00	1.97E-04	Up	5.92E-01	3.46E-01		Unigene18778_All//gi|147795291|emb|CAN61989.1|//5.00E-06//hypothetical protein [Vitis vinifera] >gi|297741273|emb|CBI32404.3|unnamed protein product [Vitis vinifera]		Unigene18778_All//2.00E-168//FL577132				nr -
Unigene18779_All	429	2.32	0.00	0.87	2.55	4.74	6.74	2.86	0.88	1.95	-1.12E+01	7.46E-06	Down	-1.42E+00	6.08E-02		8.91E-01	4.93E-02		1.40E+00	2.27E-04	Up	-1.70E+00	3.32E-03		-5.52E-01	3.01E-01		Unigene18779_All//gi|5263327|gb|AAD41429.1|AC007727_18//3.00E-30//EST gb|T20649 comes from this gene [Arabidopsis thaliana]	Unigene18779_All//4.00E-21//AT1G77500| unknown protein	Unigene18779_All//1.00E-168//DW512205				nr +
Unigene18780_All	759	0.48	0.53	0.14	6.96	2.50	1.13	1.89	1.10	0.42	1.47E-01	8.98E-01		-1.78E+00	2.34E-01		-1.48E+00	3.56E-09	Down	-2.62E+00	1.00E-16	Down	-7.82E-01	1.20E-01		-2.17E+00	6.88E-05	Down	Unigene18780_All//gi|124359162|gb|ABN05685.1|//1.00E-42//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene18780_All//7.00E-26//AT4G00310| hypothetical protein	Unigene18780_All//1.00E-36//TC144919				nr +
Unigene18781_All	704	2.01	31.24	22.92	0.00	0.00	0.00	0.00	0.00	0.00	3.96E+00	1.98E-91	Up	3.51E+00	1.13E-59	Up	null	null		null	null		null	null		null	null		Unigene18781_All//gi|224054404|ref|XP_002298243.1|//4.00E-54//histidine phosphotransfer protein [Populus trichocarpa] >gi|222845501|gb|EEE83048.1|histidine phosphotransfer protein [Populus trichocarpa]	Unigene18781_All//7.00E-43//AT3G16360| AHP4 (HPT PHOSPHOTRANSMITTER 4); histidine phosphotransfer kinase/ transferase, transferring phosphorus-containing groups	Unigene18781_All//0.00E+00//TC164475				nr -
Unigene18782_All	446	5.75	12.38	7.16	0.89	1.70	1.82	0.00	0.00	0.00	1.11E+00	2.01E-05	Up	3.18E-01	3.96E-01		9.27E-01	2.97E-01		1.03E+00	2.17E-01		null	null		null	null		Unigene18782_All//gi|224067116|ref|XP_002302363.1|//1.00E-11//predicted protein [Populus trichocarpa] >gi|222844089|gb|EEE81636.1|predicted protein [Populus trichocarpa]		Unigene18782_All//1.00E-50//TC137044				nr -
Unigene18786_All	555	0.28	1.73	1.92	0.54	0.93	0.24	2.89	0.45	0.43	2.62E+00	2.34E-03		2.76E+00	1.23E-03		7.89E-01	4.98E-01		-1.14E+00	4.58E-01		-2.68E+00	2.38E-06	Down	-2.75E+00	8.92E-07	Down	Unigene18786_All//gi|26451087|dbj|BAC42648.1|//1.00E-23//GP1-anchored protein [Arabidopsis thaliana] >gi|28416735|gb|AAO42898.1|At5g63500 [Arabidopsis thaliana]	Unigene18786_All//7.00E-25//AT5G63500| unknown protein	Unigene18786_All//2.00E-25//DW507367				nr +
Unigene18787_All	305	4.12	5.15	4.89	2.12	1.58	3.11	0.00	0.41	1.96	3.23E-01	5.52E-01		2.48E-01	6.34E-01		-4.26E-01	6.08E-01		5.51E-01	4.82E-01		8.68E+00	2.40E-01		1.09E+01	1.75E-04	Up								
Unigene18788_All	1447	0.14	0.25	0.07	0.14	0.26	0.25	1.99	6.93	7.93	7.61E-01	5.57E-01		-9.74E-01	6.21E-01		9.27E-01	5.23E-01		8.59E-01	5.42E-01		1.80E+00	2.42E-22	Up	2.00E+00	1.04E-29	Up	Unigene18788_All//gi|12718822|dbj|BAB32403.1|//1.00E-112//NQK1 MAPKK [Nicotiana tabacum]	Unigene18788_All//2.00E-101//AT5G56580| MKK6 (MAP KINASE KINASE 6); MAP kinase kinase/ kinase	Unigene18788_All//2.00E-55//TC178168		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene18790_All	671	0.16	1.06	1.11	0.45	0.10	0.54	1.70	39.30	41.74	2.76E+00	9.15E-03		2.83E+00	8.52E-03		-2.12E+00	1.65E-01		2.74E-01	8.33E-01		4.53E+00	1.30E-147	Up	4.62E+00	4.69E-161	Up	Unigene18790_All//gi|2346978|dbj|BAA21923.1|//2.00E-43//ZPT2-14 [Petunia x hybrida]	Unigene18790_All//2.00E-29//AT2G37430| zinc finger (C2H2 type) family protein (ZAT11)	Unigene18790_All//0.00E+00//TC168337	C2H2			nr -
Unigene18791_All	651	6.67	24.98	25.11	18.29	20.95	23.38	6.75	20.22	53.55	1.91E+00	2.12E-31	Up	1.91E+00	8.53E-31	Up	1.96E-01	2.49E-01		3.54E-01	1.52E-02		1.58E+00	2.58E-24	Up	2.99E+00	2.58E-141	Up	Unigene18791_All//gi|224100869|ref|XP_002312046.1|//7.00E-38//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222861866|gb|EEE89413.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene18791_All//2.00E-33//AT4G36920| AP2 (APETALA 2); transcription factor	Unigene18791_All//8.00E-158//TC174285	AP2-EREBP			nr -
Unigene18795_All	1779	0.00	0.00	0.00	0.06	0.00	0.00	4.30	15.34	5.20	null	null		null	null		-5.81E+00	3.13E-01		-5.81E+00	4.01E-01		1.83E+00	6.23E-61	Up	2.72E-01	1.13E-01		Unigene18795_All//gi|224140467|ref|XP_002323604.1|//1.00E-143//GRAS family transcription factor [Populus trichocarpa] >gi|222868234|gb|EEF05365.1| GRAS family transcription factor [Populus trichocarpa]	Unigene18795_All//1.00E-15//AT2G01570| RGA1 (REPRESSOR OF GA1-3 1); protein binding / transcription factor		GRAS			nr -
Unigene18799_All	720	1.60	1.48	0.44	2.21	3.78	4.27	4.93	8.30	12.23	-1.13E-01	8.45E-01		-1.85E+00	1.07E-02		7.71E-01	4.17E-02		9.46E-01	8.12E-03		7.51E-01	4.98E-04		1.31E+00	5.70E-13	Up			Unigene18799_All//6.00E-51//TC152976				
Unigene1880_All	2510	4.38	4.82	3.71	3.95	3.43	6.15	18.93	63.14	61.25	1.40E-01	4.28E-01		-2.38E-01	2.20E-01		-2.04E-01	3.18E-01		6.40E-01	3.99E-06		1.74E+00	0.00E+00	Up	1.69E+00	0.00E+00	Up	Unigene1880_All//gi|223452282|gb|ACM89469.1|//1.00E-146//serine/threonine protein kinase family protein [Glycine max]	Unigene1880_All//1.00E-139//AT1G18390| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene1880_All//0.00E+00//EX164434		ko04626|Plant-pathogen interaction		nr +
Unigene18808_All	297	2.11	0.17	1.26	2.35	0.93	4.26	54.10	18.72	13.95	-3.63E+00	5.07E-03		-7.52E-01	4.11E-01		-1.34E+00	1.09E-01		8.59E-01	1.71E-01		-1.53E+00	3.21E-28	Down	-1.96E+00	1.10E-40	Down			Unigene18808_All//1.00E-160//gi|84150720|gb|DN800075.1|DN800075				
Unigene18810_All	607	0.00	0.50	0.00	0.00	0.06	0.00	19.22	7.16	11.95	8.97E+00	4.44E-02		null	null		5.83E+00	8.30E-01		null	null		-1.42E+00	1.09E-18	Down	-6.87E-01	2.06E-06		Unigene18810_All//gi|226713612|sp|A7QF77.1|U4971_VITVI//2.00E-54//RecName: Full=UPF0497 membrane protein 1	Unigene18810_All//2.00E-42//AT5G06200| integral membrane family protein					nr +
Unigene18812_All	766	3.96	1.32	2.22	0.91	0.49	0.59	0.61	0.11	0.36	-1.58E+00	3.37E-05	Down	-8.33E-01	2.63E-02		-8.81E-01	3.00E-01		-6.27E-01	4.76E-01		-2.48E+00	3.38E-02		-7.38E-01	4.26E-01		Unigene18812_All//gi|19715622|gb|AAL91632.1|//6.00E-39//AT4g37080/CTA10_280 [Arabidopsis thaliana] >gi|23463049|gb|AAN33194.1|At4g37080/CTA10_280 [Arabidopsis thaliana]	Unigene18812_All//5.00E-34//AT4G37080| unknown protein	Unigene18812_All//2.00E-75//TC176896				nr +
Unigene18813_All	362	1.16	1.12	0.15	3.03	2.47	2.50	2.10	0.23	0.44	-4.63E-02	9.80E-01		-2.97E+00	6.46E-02		-2.92E-01	6.47E-01		-2.79E-01	6.89E-01		-3.19E+00	7.93E-04	Down	-2.26E+00	4.68E-03				Unigene18813_All//4.00E-07//DR456136				
Unigene18815_All	1546	0.17	0.30	0.07	0.26	0.27	0.73	1.29	4.00	1.78	8.02E-01	4.60E-01		-1.30E+00	4.36E-01		5.22E-02	9.89E-01		1.50E+00	2.74E-02		1.64E+00	2.11E-12	Up	4.68E-01	1.61E-01		Unigene18815_All//gi|223452371|gb|ACM89513.1|//1.00E-12//wall-associated kinase [Glycine max]	Unigene18815_All//4.00E-13//AT1G25390| protein kinase family protein	Unigene18815_All//0.00E+00//TC156074				nr +

Unigene18816_All	419	2.37	0.00	0.89	1.31	1.23	1.83	1.41	0.40	0.95	-1.12E+01	7.46E-06	Down	-1.42E+00	6.08E-02		-8.52E-02	9.07E-01		4.87E-01	5.91E-01		-1.82E+00	4.72E-02		-5.71E-01	4.78E-01		Unigene18816_All//gi|15227619|ref|NP_180537.1|//4.00E-48//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75100656|sp|Q82380.1|PP175_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g29760, chloroplastic; Flags: Precursor	Unigene18816_All//2.00E-49//AT2G29760| pentatricopeptide (PPR) repeat-containing protein	Unigene18816_All//3.00E-175//DR453173				nr -
Unigene18820_All	508	0.72	0.40	1.26	1.96	1.83	0.18	2.41	2.96	1.65	-8.54E-01	4.89E-01		8.03E-01	3.88E-01		-9.97E-02	8.68E-01		-3.46E+00	1.73E-04	Down	2.95E-01	5.82E-01		-5.51E-01	3.01E-01									
Unigene18821_All	647	3.32	1.10	3.62	0.00	1.06	0.70	0.00	0.00	0.00	-1.60E+00	6.02E-04	Down	1.27E-01	7.59E-01		1.01E+01	3.05E-04	Up	9.45E+00	7.75E-03		null	null		null	null					Unigene18821_All//2.00E-78//gi|109882461|gb|DR511431.1|DR511431				
Unigene18823_All	423	3.34	0.12	1.64	2.83	3.17	1.82	1.10	0.00	0.28	-4.80E+00	4.49E-07	Down	-1.03E+00	8.34E-02		1.68E-01	8.23E-01		-6.39E-01	3.24E-01		-1.01E+01	1.71E-03		-1.96E+00	5.82E-02					Unigene18823_All//0.00E+00//gi|48790927|gb|CO092241.1|CO092241				
Unigene18824_All	535	131.63	38.26	33.94	67.60	48.60	55.46	0.00	0.00	0.00	-1.78E+00	3.70E-123	Down	-1.96E+00	4.73E-135	Down	-4.76E-01	4.71E-09		-2.86E-01	1.35E-03		null	null		null	null		Unigene18824_All//gi|21322711|emb|CAD22154.1|//3.00E-49//phenylsporin-dsl protein [Volvox carteri f. nagariensis]	Unigene18824_All//4.00E-116//gi|78346810|gb|DT567084.1|DT567084				nr -
Unigene18825_All	517	0.00	0.00	0.00	201.76	123.42	49.62	2.78	0.57	0.08	null	null		null	null		-7.09E-01	1.55E-51		-2.02E+00	1.06E-235	Down	-2.30E+00	5.89E-05	Down	-5.17E+00	2.09E-09	Down	Unigene18825_All//gi|225626279|gb|ACN97189.1|//6.00E-79//KNOX transcription factor [Populus trichocarpa]	Unigene18825_All//3.00E-52//AT4G08150| KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor	Unigene18825_All//0.00E+00//gi|109870442|gb|DW499418.1|DW499418	HB			nr +
Unigene18826_All	429	0.98	2.36	0.74	4.30	2.01	1.26	3.06	1.85	0.28	1.28E+00	6.99E-02		-3.90E-01	7.17E-01		-1.10E+00	1.59E-02		-1.77E+00	4.90E-04	Down	-7.23E-01	1.73E-01		-3.46E+00	7.84E-07	Down								
Unigene18827_All	502	0.83	0.40	0.00	8.24	4.87	6.03	2.36	0.75	0.48	-1.05E+00	3.66E-01		-9.70E+00	1.56E-02		-7.58E-01	7.10E-03		-4.50E-01	1.48E-01		-1.65E+00	5.03E-03		-2.31E+00	2.01E-04	Down				Unigene18827_All//4.00E-42//TC160212				
Unigene18830_All	869	0.24	0.12	0.00	0.63	0.55	0.78	1.61	2.36	4.03	-1.05E+00	5.65E-01		-7.91E+00	1.46E-01		-1.85E-01	8.25E-01		3.06E-01	7.22E-01		5.54E-01	1.80E-01		1.33E+00	8.67E-06	Up								
Unigene18833_All	483	126.63	441.97	249.49	109.63	135.60	217.21	123.60	147.89	92.71	1.80E+00	0.00E+00	Up	9.78E-01	2.38E-81		3.07E-01	3.41E-07		9.86E-01	2.05E-79		2.59E-01	3.06E-06		-4.15E-01	3.29E-12		Unigene18833_All//gi|15220426|ref|NP_176904.1|//1.00E-21//rubber elongation factor (REF) family protein [Arabidopsis thaliana] >gi|30697500|ref|NP_849856.1| rubber elongation factor (REF) family protein [Arabidopsis thaliana] >gi|14424100|sp|Q9FYF7.1|Y1736_ARATH RecName: Full=REF/SRPP-like protein At1g67360 >gi|9828625|gb|AAG00248.1|AC002130_13 F1N21.18 [Arabidopsis thaliana]	Unigene18833_All//9.00E-23//AT1G67360| rubber elongation factor (REF) family protein	Unigene18833_All//3.00E-132//DR453849				nr -
Unigene18836_All	461	0.34	0.22	0.46	5.19	3.14	0.69	5.50	0.36	2.42	-6.32E-01	7.28E-01		4.40E-01	7.75E-01		-7.25E-01	6.73E-02		-2.92E+00	1.02E-08	Down	-3.92E+00	2.33E-13	Down	-1.19E+00	6.98E-04	Down	Unigene18836_All//gi|157313304|gb|ABV32545.1|//2.00E-44//beta-galactosidase protein 2 [Prunus persica]	Unigene18836_All//2.00E-43//AT3G13750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene18836_All//7.00E-96//CO499423		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series		nr +
Unigene18838_All	1172	0.09	0.39	0.55	0.09	0.00	0.08	171.75	19.72	103.44	2.12E+00	9.59E-02		2.61E+00	2.33E-02		-6.41E+00	3.13E-01		-1.41E-01	9.51E-01		-3.12E+00	0.00E+00	Down	-7.32E-01	4.12E-107		Unigene18838_All//gi|290760236|gb|AD054643.1|//1.00E-146//peroxidase [Bruguiera gymnorhiza]	Unigene18838_All//2.00E-131//AT2G18980| peroxidase, putative	Unigene18838_All//4.00E-10//ES814322		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene18839_All	545	4.90	9.58	13.58	1.74	1.52	1.91	2.17	1.23	0.95	9.68E-01	2.56E-04		1.47E+00	5.26E-10	Up	-1.96E-01	8.04E-01		1.34E-01	8.58E-01		-8.24E-01	1.42E-01		-1.19E+00	2.80E-02		Unigene18839_All//gi|27652184|gb|AA01757 3.1|//7.00E-10//carbonic anhydrase 2 [Flaveria bidentis]	Unigene18839_All//2.00E-07//AT1G70410| carbonic anhydrase, putative / carbonate dehydratase, putative	Unigene18839_All//4.00E-42//ES838914		ko00910|Nitrogen metabolism		nr -
Unigene1884_All	1710	1.81	2.16	1.53	5.13	2.17	1.85	7.32	6.23	5.34	2.61E-01	4.26E-01		-2.43E-01	5.32E-01		-1.24E+00	2.08E-11	Down	-1.47E+00	4.30E-13	Down	-2.32E-01	1.34E-01		-4.56E-01	1.01E-03		Unigene1884_All//gi|269859041|gb|ACZ52187.1|//1.00E-79//ribosomal protein L10 [Citrus sinensis]		Unigene1884_All//0.00E+00//gi|84145391|gb|DN759633.1|DN759633				nr +
Unigene18840_All	419	21.73	26.12	36.86	5.23	9.20	24.14	307.36	139.25	197.29	2.66E-01	1.39E-01		7.62E-01	2.23E-07		8.15E-01	7.15E-03		2.21E+00	2.79E-25	Up	-1.14E+00	6.95E-141	Down	-6.40E-01	1.70E-54		Unigene18840_All//gi|196259706|dbj|BAG68661.1|//4.00E-24//plasma membrane intrinsic protein [Tulipa gesneriana]	Unigene18840_All//1.00E-23//AT5G60660| PIP2;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;4); water channel	Unigene18840_All//4.00E-168//TC175923				nr -
Unigene18841_All	1489	0.04	9.56	3.72	0.00	0.00	0.00	0.00	0.00	0.00	8.09E+00	1.28E-79	Up	6.73E+00	3.87E-29	Up	null	null		null	null		null	null		null	null		Unigene18841_All//gi|166627|gb|AAC36485.1|//1.00E-147//nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]	Unigene18841_All//2.00E-148//AT1G76030| vacuolar ATP synthase subunit B / V-ATPase B subunit / vacuolar proton pump B subunit / V-ATPase 57 kDa subunit	Unigene18841_All//1.00E-29//TC130388		ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr +
Unigene18844_All	633	0.25	1.60	1.18	2.60	0.38	1.64	76.88	141.10	66.15	2.69E+00	1.41E-03		2.25E+00	2.35E-02		-2.77E+00	1.18E-06	Down	-6.62E-01	2.13E-01		8.76E-01	2.39E-63		-2.17E-01	1.33E-03		Unigene18844_All//gi|8272626|gb|AAF74286.1|AF261774_1//3.00E-33//OBFX [Solanum lycopersicum] >gi|27413995|gb|AA012185.1| fw2.2 [Solanum lycopersicum] >gi|27413997|gb|AA012186.1| fw2.2 [Solanum lycopersicum] >gi|27413999|gb|AA012187.1| fw2.2 [Solanum lycopersicum] >gi|27414001|gb|AA012188.1| fw2.2 [Solanum lycopersicum]	Unigene18844_All//1.00E-30//AT1G14870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: plasma membrane; EXPRESSED IN: callus; CONTAINS InterPro DOMAIN/s: EGF-type aspartate/asparagine hydroxylation conserved site (InterPro:IPR000152), Protein of unknown function Cys-rich (InterPro:IPR006461); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35525.1); Has 492 Blast hits to 491 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 93; Fungi - 76; Plants - 297; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink).	Unigene18844_All//8.00E-10//TC153460				nr -
Unigene18845_All	898	0.00	0.00	0.12	0.00	0.15	0.25	7.63	4.05	3.24	null	null		6.89E+00	3.99E-01		7.26E+00	3.19E-01		7.97E+00	1.19E-01		-9.14E-01	5.76E-06		-1.24E+00	1.48E-09	Down	Unigene18845_All//gi|110931832|gb|ABH02915.1|//1.00E-53//MYB transcription factor MYB94 [Glycine max]	Unigene18845_All//3.00E-49//AT5G52260| AtMYB19 (myb domain protein 19); DNA binding / transcription factor	Unigene18845_All//1.00E-52//TC175799	MYB			nr +
Unigene18847_All	291	1.08	2.44	0.18	4.96	2.13	2.17	4.50	2.44	0.96	1.18E+00	1.75E-01		-2.56E+00	1.59E-01		-1.22E+00	2.11E-02		-1.19E+00	3.43E-02		-8.83E-01	9.43E-02		-2.23E+00	1.19E-04	Down				Unigene18847_All//1.00E-43//gi|195983254|gb|FL577268.1|FL577268				
Unigene18848_All	436	2.88	2.21	2.44	3.43	5.61	5.39	0.48	1.53	2.56	-3.83E-01	5.26E-01		-2.38E-01	6.85E-01		7.10E-01	8.31E-02		6.52E-01	1.32E-01		1.66E+00	4.76E-02		2.40E+00	2.76E-04	Up				Unigene18848_All//4.00E-125//CO088448				
Unigene18852_All	356	0.88	1.57	0.00	1.96	0.77	1.52	2.38	3.64	10.18	8.28E-01	3.81E-01		-9.78E+00	4.92E-02		-1.34E+00	1.09E-01		-3.64E-01	6.81E-01		6.16E-01	2.53E-01		2.10E+00	1.53E-10	Up								
Unigene18853_All	341	0.00	1.49	0.00	1.46	1.11	3.31	4.22	0.49	0.35	1.05E+01	4.05E-03		null	null		-3.95E-01	6.89E-01		1.18E+00	7.75E-02		-3.10E+00	1.52E-06	Down	-3.59E+00	1.22E-07	Down								
Unigene18854_All	401	1.44	10.49	2.92	2.86	3.18	5.18	16.87	37.21	18.58	2.87E+00	1.42E-13	Up	1.03E+00	1.24E-01		1.53E-01	8.22E-01		8.59E-01	6.02E-02		1.14E+00	5.68E-17	Up	1.39E-01	5.14E-01					Unigene18854_All//3.00E-122//gi|109890681|gb|DW519645.1|DW519645				
Unigene18855_All	1080	0.73	1.03	0.69	0.97	0.61	0.17	3.09	0.46	3.95	5.06E-01	4.22E-01		-7.41E-02	9.35E-01		-6.77E-01	3.14E-01		-2.53E+00	1.22E-03		-2.74E+00	9.26E-13	Down	3.52E-01	1.85E-01		Unigene18855_All//gi|224110774|ref|XP_002315633.1|//1.00E-108//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222864673|gb|EEF01804.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene18855_All//2.00E-87//AT3G13090| ATMRP5; ATPase, coupled to transmembrane movement of substances			ko02010|ABC transporters		nr -
Unigene18859_All	451	2.20	1.57	0.00	1.55	0.99	1.10	2.62	0.19	0.80	-4.87E-01	4.72E-01		-1.11E+01	1.77E-05	Down	-6.40E-01	4.54E-01		-4.89E-01	5.98E-01		-3.82E+00	2.12E-06	Down	-1.72E+00	2.66E-03		Unigene18859_All//gi|255555188|ref|XP_002518631.1|//8.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223542230|gb|EEF43773.1| conserved hypothetical protein [Ricinus communis]		Unigene18859_All//6.00E-16//ES834845				nr -
Unigene1886_All	1802	125.63	80.87	102.16	165.48	173.36	203.84	207.79	125.90	93.34	-6.36E-01	6.37E-75		-2.99E-01	2.24E-18		6.72E-02	2.58E-02		3.01E-01	3.32E-33		-7.23E-01	2.03E-189		-1.15E+00	0.00E+00	Down	Unigene1886_All//gi|15235280|ref|NP_194568.1|//0.00E+00//AAC3 (ADP/ATP CARRIER 3); ATP:ADP antiporter/ binding [Arabidopsis thaliana] >gi|2842480|emb|CAA16877.1| ADP, ATP carrier-like protein [Arabidopsis thaliana] >gi|7269693|emb|CAB79641.1| ADP, ATP carrier-like protein [Arabidopsis thaliana]	Unigene1886_All//4.00E-165//AT4G28390| AAC3 (ADP/ATP CARRIER 3); ATP:ADP antiporter/ binding	Unigene1886_All//0.00E+00//TC137488				nr -
Unigene18860_All	399	0.26	3.05	0.53	0.00	0.00	0.23	2.33	1.68	1.60	3.54E+00	4.02E-05	Up	1.03E+00	5.92E-01		null	null		7.82E+00	4.77E-01		-4.76E-01	4.76E-01		-5.45E-01	3.80E-01		Unigene18860_All//gi|3914374|sp|Q42670.1|PLSC_COCNU//8.00E-17//RecName: Full=1-acyl-sn-glycerol-3-phosphate acyltransferase; Short=1-AGP acyltransferase; Short=1-AGPAT; AltName: Full=Lysophosphatidic acid acyltransferase; Short=LPAAT >gi|1098605|gb|AAC49119.1| lysophosphatidic acid acyltransferase [Cocos nucifera] >gi|1588836|prf|2204401A 1-acyl-sn-glycerol-3-phosphate acyltransferase						nr +
Unigene18861_All	306	2.05	2.15	0.00	0.16	1.13	2.80	0.00	0.00	0.00	6.92E-02	9.50E-01		-1.10E+01	1.41E-03		2.79E+00	1.14E-01		4.11E+00	3.40E-04	Up	null	null		null	null									
Unigene18864_All	577	2.72	0.18	1.11	3.11	2.09	2.27	2.49	1.96	0.76	-3.95E+00	5.06E-07	Down	-1.30E+00	2.26E-02		-5.73E-01	2.36E-01		-4.53E-01	3.94E-01		-3.49E-01	5.14E-01		-1.71E+00	8.25E-04	Down	Unigene18864_All//gi|18700123|gb|AAL77673.1|//1.00E-25//At2g39560/F12L6.22 [Arabidopsis thaliana] >gi|21464575|gb|AAM52242.1| At2g39560/F12L6.22 [Arabidopsis thaliana]	Unigene18864_All//4.00E-12//AT2G39560| unknown protein	Unigene18864_All//0.00E+00//ES831321				nr -
Unigene18865_All	542	0.39	1.03	0.00	3.68	0.83	0.58	4.68	3.16	2.21	1.41E+00	1.69E-01		-8.59E+00	1.46E-01		-2.15E+00	4.73E-06	Down	-2.66E+00	1.04E-06	Down	-5.66E-01	1.18E-01		-1.09E+00	1.73E-03		Unigene18865_All//gi|238478855|ref|NP_001154422.1|//7.00E-64//BRX-LIKE3 (BREVIS RADIX-LIKE 3) [Arabidopsis thaliana]	Unigene18865_All//4.00E-59//AT1G54180| BRX-LIKE3 (BREVIS RADIX-LIKE 3)	Unigene18865_All//0.00E+00//ES814955				nr -
Unigene18866_All	1155	0.32	0.18	0.37	13.89	9.00	2.23	0.18	0.11	0.17	-8.54E-01	4.89E-01		2.18E-01	8.31E-01		-6.25E-01	9.52E-07		-2.64E+00	2.26E-50	Down	-7.53E-01	6.32E-01		-8.52E-02	9.61E-01		Unigene18866_All//gi|30689857|ref|NP_189653.2|//6.00E-90//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|9294338|dbj|BAB02235.1| nodulin-like protein [Arabidopsis thaliana]	Unigene18866_All//1.00E-81//AT4G01440| nodulin MtN21 family protein	Unigene18866_All//9.00E-45//gi|109889892|gb|DW518860.1|DW518860				nr +
Unigene18868_All	967	1.14	0.94	0.22	8.71	5.06	4.06	7.26	3.24	2.93	-2.69E-01	6.51E-01		-2.37E+00	2.97E-03		-7.84E-01	2.06E-05		-1.10E+00	3.21E-08	Down	-1.16E+00	1.18E-08	Down	-1.31E+00	1.26E-10	Down	Unigene18868_All//gi|42567992|ref|NP_197554.2|//2.00E-08//ATBRXL4 (BREVIS RADIX-LIKE 4) [Arabidopsis thaliana] >gi|75151601|sp|Q8GZ92.1|BRXL4_ARATH RecName: Full=Protein Brevis radix-like 4; Short=AtBRXL4	Unigene18868_All//9.00E-10//AT5G20540| ATBRXL4 (BREVIS RADIX-LIKE 4)	Unigene18868_All//0.00E+00//DW498166				nr -
Unigene18870_All	274	0.38	5.73	1.36	2.18	6.66	3.79	0.00	0.00	0.00	3.91E+00	6.83E-07	Up	1.83E+00	2.13E-01		1.61E+00	1.19E-03		7.97E-01	2.63E-01		null	null		null	null		Unigene18870_All//gi|225424709|ref|XP_002265150.1|//4.00E-08//PREDICTED: hypothetical protein [Vitis vinifera]						nr +

Unigene18871_All	1023	0.00	0.00	0.00	0.49	0.27	0.26	175.44	50.05	30.61	null	null		null	null		-8.54E-01	4.07E-01		-8.78E-01	4.20E-01		-1.81E+00	0.00E+00	Down	-2.52E+00	0.00E+00	Down	Unigene18871_All//gi|3287835|sp|Q43714.1|DCS3_GOSAR//7.00E-75//RecName: Full=(+)-delta-cadinene synthase isozyme A; Short=D-cadinene synthase A >gi|1002523|gb|AAB41259.1| (+)-delta-cadinene synthase isozyme A [Gossypium arboreum] >gi|1217956|emb|CAA65289.1| (+)-delta-cadinene synthase [Gossypium arboreum]	Unigene18871_All//3.00E-43//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene18871_All//0.00E+00//TC142314		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis		nr -
Unigene18872_All	607	0.17	0.00	0.00	3.53	1.02	0.74	1.74	0.00	0.07	-7.43E+00	3.73E-01		-7.43E+00	3.94E-01		-1.79E+00	3.64E-05	Down	-2.25E+00	5.08E-06	Down	-1.08E+01	1.51E-07	Down	-4.73E+00	8.85E-07	Down	Unigene18872_All//gi|297727333|ref|XP_001176030.1|//1.00E-44//Os10g0155733 [Oryza sativa Japonica Group] >gi|18542897|gb|AAL75739.1|AC091724_12 Putative receptor-like protein kinase [Oryza sativa Japonica Group] >gi|31430260|gb|AAP52200.1| Leucine Rich Repeat family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255679221|dbj|BAH94758.1| Os10g0155733 [Oryza sativa Japonica Group]	Unigene18872_All//4.00E-23//AT1G73080| PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase			ko03410|Base excision repair		nr -
Unigene18874_All	400	0.00	2.03	1.33	2.12	2.58	2.26	0.32	0.21	0.90	1.10E+01	9.39E-05	Up	1.04E+01	4.04E-03		2.87E-01	7.18E-01		9.31E-02	9.20E-01		-6.01E-01	7.66E-01		1.50E+00	2.04E-01		Unigene18874_All//gi|224137316|ref|XP_002322527.1|//9.00E-13//predicted protein [Populus trichocarpa] >gi|222867157|gb|EEF04288.1| predicted protein [Populus trichocarpa]		Unigene18874_All//0.00E+00//ES795276				nr -
Unigene18878_All	259	5.66	1.57	1.23	2.31	3.59	2.44	1.14	1.61	0.00	-1.85E+00	1.97E-03		-2.20E+00	7.90E-04	Down	6.37E-01	4.18E-01		8.10E-02	9.45E-01		4.98E-01	6.33E-01		-1.02E+01	1.58E-02				Unigene18878_All//5.00E-86//gi|164251356|gb|ES809766.1|ES809766				
Unigene18879_All	337	3.42	1.95	3.16	3.99	3.17	0.54	1.13	0.25	0.47	-8.05E-01	2.03E-01		-1.12E-01	8.56E-01		-3.33E-01	5.81E-01		-2.90E+00	4.29E-05	Down	-2.19E+00	8.75E-02		-1.26E+00	2.48E-01				Unigene18879_All//4.00E-07//TC161150				
Unigene1888_All	1106	12.68	4.63	4.14	14.55	14.20	16.95	32.04	15.30	21.54	-1.45E+00	7.60E-19	Down	-1.61E+00	6.03E-21	Down	-3.52E-02	8.18E-01		2.20E-01	1.14E-01		-1.07E+00	3.20E-35	Down	-5.73E-01	5.25E-13		Unigene1888_All//gi|224075846|ref|XP_002304794.1|//2.00E-70//type-a response regulator [Populus trichocarpa] >gi|222842226|gb|EEE79773.1| type-a response regulator [Populus trichocarpa]	Unigene1888_All//8.00E-56//AT2G41310| ATR3 (RESPONSE REGULATOR 3); transcription regulator/ two-component response regulator	Unigene1888_All//0.00E+00//TC158199	ARR-B	ko04712|Circadian rhythm - plant		nr +
Unigene18882_All	830	21.18	0.24	3.21	1.62	0.29	0.22	0.00	0.00	0.00	-6.44E+00	5.39E-95	Down	-2.72E+00	1.76E-50	Down	-2.48E+00	5.92E-05	Down	-2.90E+00	4.29E-05	Down	null	null		null	null		Unigene18882_All//gi|22329164|ref|NP_196179.2|//3.00E-45//CIB1 (CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75299602|sp|Q8GY61.1|BH063_ARATH RecName: Full=Transcription factor bHLH063; AltName: Full=Transcription factor EN 84; AltName: Full=bHLH transcription factor bHLH063; AltName: Full=Basic helix-loop-helix protein 63; Short=bHLH 63; Short=AtbHLH63 >gi|38850907|gb|AAO63377.1| At4g34530 [Arabidopsis thaliana]	Unigene18882_All//2.00E-44//AT4G34530| CIB1 (CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1); DNA binding / transcription factor	Unigene18882_All//2.00E-82//TC167832	bHLH	ko04712|Circadian rhythm - plant		nr +
Unigene18884_All	440	95.37	52.05	76.49	147.74	113.64	112.91	198.52	123.30	75.33	-8.74E-01	1.20E-24		-3.18E-01	2.03E-04		-3.79E-01	1.58E-10		-3.88E-01	5.94E-10		-6.87E-01	4.92E-41		-1.40E+00	7.52E-135	Down	Unigene18884_All//gi|123379|sp|P26585.1|HMG1_SOYBN//3.00E-12//RecName: Full=HMG1/2-like protein; AltName: Full=Protein SB11 >gi|18645|emb|CAA41200.1| HMG-I like protein gene [Glycine max]		Unigene18884_All//1.00E-171//TC137591		ko03410|Base excision repair		nr -
Unigene18886_All	895	0.23	0.45	0.12	0.56	0.88	0.56	0.94	3.64	4.58	9.54E-01	4.14E-01		-9.74E-01	6.21E-01		6.69E-01	4.42E-01		-3.90E-03	9.87E-01		1.95E+00	1.59E-08	Up	2.28E+00	5.36E-13	Up							
Unigene18887_All	1404	0.11	0.22	0.00	0.00	0.05	0.13	5.24	3.10	12.77	9.53E-01	5.03E-01		-6.80E+00	2.45E-01		5.62E+00	6.10E-01		7.01E+00	1.94E-01		-7.59E-01	7.50E-05		1.29E+00	8.42E-25	Up	Unigene18887_All//gi|79344495|ref|NP_172900.2|//6.00E-51//protein binding [Arabidopsis thaliana]	Unigene18887_All//5.00E-52//AT1G14480| protein binding	Unigene18887_All//0.00E+00//gi|78354461|gb|DT574735.1|DT574735				nr +
Unigene18889_All	453	0.23	0.00	0.00	15.29	3.27	2.89	0.00	0.00	0.18	-7.85E+00	3.73E-01		-7.85E+00	3.94E-01		-2.23E+00	1.00E-20	Down	-2.40E+00	9.30E-20	Down	null	null		7.46E+00	4.05E-01		Unigene18889_All//gi|297814648|ref|XP_002875207.1|//3.00E-21//myb family transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297321045|gb|EFH51466.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene18889_All//2.00E-14//AT2G03500| myb family transcription factor	Unigene18889_All//4.00E-17//ES826836	G2-like			nr -
Unigene1889_All	3731	0.62	1.10	0.61	3.28	3.26	3.14	6.95	3.13	4.74	8.34E-01	5.63E-03		-7.70E-03	1.00E+00		-1.17E-02	9.59E-01		-6.71E-02	7.13E-01		-1.15E+00	2.29E-29	Down	-5.51E-01	3.61E-09		Unigene1889_All//gi|6692688|gb|AAF24822.1|AC007592_15//0.00E+00//F12K11.17 [Arabidopsis thaliana]	Unigene1889_All//0.00E+00//AT1G06490| ATGSL07 (glucan synthase-like 7); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups	Unigene1889_All//0.00E+00//DV849328				nr +
Unigene18890_All	661	0.00	3.37	0.48	0.15	0.16	0.00	0.58	1.52	1.93	1.17E+01	1.09E-12	Up	8.92E+00	4.53E-02		5.26E-02	9.67E-01		-7.24E+00	4.01E-01		1.40E+00	2.82E-02		1.74E+00	1.73E-03								
Unigene18891_All	335	0.47	1.82	3.34	0.89	1.54	0.67	3.16	1.50	1.31	1.95E+00	6.04E-02		2.83E+00	7.34E-04	Up	7.89E-01	4.98E-01		-4.04E-01	7.51E-01		-1.08E+00	7.50E-02		-1.27E+00	2.97E-02		Unigene18891_All//gi|297796605|ref|XP_002866187.1|//1.00E-33//ATLIG4 [Arabidopsis lyrata subsp. lyrata] >gi|297312022|gb|EFH42446.1| ATLIG4 [Arabidopsis lyrata subsp. lyrata]	Unigene18891_All//5.00E-35//AT5G57160| ATLIG4; DNA ligase (ATP)/ protein binding			ko03450|Non-homologous end-joining		nr +
Unigene18892_All	661	1.35	1.69	0.08	1.81	5.16	3.14	0.06	0.00	0.00	3.26E-01	5.99E-01		-4.06E+00	5.15E-04	Down	1.51E+00	7.24E-06	Up	7.97E-01	8.12E-02		-6.00E+00	6.58E-01		-6.00E+00	6.13E-01		Unigene18892_All//gi|224057862|ref|XP_002299361.1|//1.00E-66//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene18892_All//6.00E-65//AT4G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene18892_All//0.00E+00//TC147747				nr -
Unigene18894_All	423	21.77	11.38	7.30	2.00	2.52	1.60	0.40	0.00	0.28	-9.36E-01	1.12E-06		-1.58E+00	1.72E-13	Down	3.34E-01	6.42E-01		-3.22E-01	6.87E-01		-8.64E+00	1.35E-01		-5.01E-01	7.46E-01		Unigene18894_All//gi|297814490|ref|XP_002875128.1|//2.00E-26//ANAC034/ANAC035 [Arabidopsis lyrata subsp. lyrata] >gi|297320966|gb|EFH51387.1| ANAC034/ANAC035 [Arabidopsis lyrata subsp. lyrata]	Unigene18894_All//9.00E-25//AT2G02450| ANAC035 (Arabidopsis NAC domain containing protein 35); transcription factor		NAC			nr -
Unigene18895_All	722	1.01	1.68	1.03	0.48	1.00	0.56	0.64	2.61	2.21	7.31E-01	2.35E-01		2.54E-02	9.95E-01		1.05E+00	2.40E-01		2.21E-01	8.63E-01		2.02E+00	1.98E-05	Up	1.78E+00	3.04E-04	Up							
Unigene18896_All	681	0.15	0.07	0.31	0.80	1.21	1.19	2.67	0.49	1.35	-1.05E+00	6.85E-01		1.03E+00	5.92E-01		5.93E-01	4.93E-01		5.69E-01	4.96E-01		-2.44E+00	1.77E-06	Down	-9.89E-01	1.76E-02		Unigene18896_All//gi|18415500|ref|NP_567601.1|//2.00E-64//subtilase family protein [Arabidopsis thaliana]	Unigene18896_All//3.00E-47//AT4G20430| subtilase family protein	Unigene18896_All//0.00E+00//gi|78327722|gb|DT547996.1|DT547996				nr +
Unigene18899_All	292	2.33	3.47	0.00	2.90	1.18	0.77	1.16	0.72	0.68	5.75E-01	3.83E-01		-1.12E+01	7.64E-04	Down	-1.30E+00	8.01E-02		-1.91E+00	2.14E-02		-6.95E-01	5.78E-01		-7.64E-01	5.01E-01				Unigene18899_All//6.00E-18//TC147074				
Unigene1890_All	836	26.10	38.00	26.31	67.39	127.16	82.22	14.31	3.80	6.10	5.42E-01	1.39E-08		1.15E-02	9.48E-01		9.16E-01	1.03E-78		2.87E-01	3.27E-06		-1.91E+00	9.65E-29	Down	-1.23E+00	6.20E-16	Down	Unigene1890_All//1.00E-35//AT3G18440| AtALMT9 (aluminum-activated malate transporter 9); anion channel [Arabidopsis thaliana]	Unigene1890_All//3.00E-07//TC154916				nr +
Unigene18900_All	406	10.57	25.09	27.81	897.51	626.11	516.38	36.87	80.19	57.70	1.25E+00	4.33E-11	Up	1.40E+00	7.64E-14	Up	-5.20E-01	1.26E-102		-7.98E-01	6.09E-194		1.12E+00	4.26E-35	Up	6.46E-01	8.65E-11		Unigene18900_All//gi|147795447|emb|CAN65839.1|//1.00E-06//hypothetical protein [Vitis vinifera] >gi|297742394|emb|CBI34543.3| unnamed protein product [Vitis vinifera]		Unigene18900_All//0.00E+00//TC178121				nr +
Unigene18903_All	906	0.35	2.24	0.65	12.10	27.97	27.22	0.00	0.60	0.26	2.69E+00	1.81E-06	Up	9.00E-01	3.77E-01		1.21E+00	1.67E-29	Up	1.17E+00	6.11E-25	Up	9.23E+00	5.36E-04	Up	8.04E+00	4.39E-02		Unigene18903_All//gi|297729361|ref|NP_001177044.1|//1.00E-41//Os12g0596300 [Oryza sativa Japonica Group] >gi|255670454|dbj|BAH95772.1| Os12g0596300 [Oryza sativa Japonica Group]	Unigene18903_All//4.00E-110//AT2G16050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: DC1 (InterPro:IPR004146); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G20990.1); Has 719 Blast hits to 448 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 717; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr +
Unigene18907_All	1007	0.31	162.88	135.48	0.49	0.27	0.67	0.21	0.00	0.32	9.03E+00	0.00E+00	Up	8.76E+00	0.00E+00	Up	-8.55E-01	4.07E-01		4.43E-01	6.22E-01		-7.71E+00	7.45E-02		5.93E-01	6.13E-01		Unigene18907_All//gi|268053557|ref|YP_003288916.1|//2.00E-55//NADH dehydrogenase subunit 4 [Saccharina japonica] >gi|268053596|ref|YP_003288954.1| NADH dehydrogenase subunit 4 [Saccharina religiosa] >gi|268053635|ref|YP_003288992.1| NADH dehydrogenase subunit 4 [Saccharina ochotensis] >gi|268053674|ref|YP_003289069.1| NADH dehydrogenase subunit 4 [Saccharina diabolica] >gi|268053713|ref|YP_003289120.1| NADH dehydrogenase subunit 4 [Saccharina longipedalis] >gi|262318177|dbj|BAI48502.1| NADH dehydrogenase subunit 4 [Saccharina japonica] >gi|262318216|dbj|BAI48540.1| NADH dehydrogenase subunit 4 [Saccharina religiosa] >gi|262318255|dbj|BAI48578.1| NADH dehydrogenase subunit 4 [Saccharina ochotensis] >gi|262318294|dbj|BAI48616.1| NADH dehydrogenase subunit 4 [Saccharina diabolica] >gi|262318333|dbj|BAI48654.1| NADH dehydrogenase subunit 4	Unigene18907_All//6.00E-28//ATMG00580| NADH dehydrogenase subunit 4				ko00190|Oxidative phosphorylation		nr -

Unigene18909_All	335	4.22	0.76	4.77	2.97	0.93	0.81	0.00	0.00	0.24	-2.48E+00	2.00E-04	Down	1.77E-01	7.24E-01		-1.68E+00	1.36E-02		-1.88E+00	1.18E-02		null	null		7.89E+00	4.05E-01			Unigene18909_All//4.00E-07//TC173330					
Unigene1891_All	2074	15.79	18.23	16.41	31.10	59.59	45.86	6.87	2.02	3.78	2.07E-01	2.28E-02		5.50E-02	6.24E-01		9.38E-01	3.40E-95		5.60E-01	2.63E-27		-1.77E+00	1.05E-30	Down	-8.60E-01	7.53E-11		Unigene1891_All//gi|15229641|ref|NP_188473.1|//1.00E-142//AtALMT9 (aluminum-activated malate transporter 9); anion channel [Arabidopsis thaliana]	Unigene1891_All//2.00E-138//AT3G18440| AtALMT9 (aluminum-activated malate transporter 9); anion channel	Unigene1891_All//0.00E+00//AI729912				nr -
Unigene18910_All	1924	0.00	0.00	0.00	0.00	0.00	0.00	8.83	3.24	5.26	null	null		null	null		null	null		null	null		-1.45E+00	1.63E-27	Down	-7.48E-01	3.12E-10		Unigene18910_All//gi|282721270|gb|ADA83723.1|//0.00E+00//PT1 [Manihot esculenta]	Unigene18910_All//0.00E+00//AT2G32830| PHT5; inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter	Unigene18910_All//2.00E-40//gi|78339058|gb|DT559332.1|DT559332				nr +
Unigene18912_All	747	2.17	10.04	5.42	2.87	2.35	1.69	56.60	82.92	180.26	2.21E+00	8.21E-18	Up	1.32E+00	5.24E-05	Up	-2.87E-01	5.61E-01		-7.60E-01	8.66E-02		5.51E-01	5.00E-20		1.67E+00	4.96E-267	Up	Unigene18912_All//gi|224137294|ref|XP_002327090.1|//6.00E-62//cytochrome P450 [Populus trichocarpa] >gi|222835405|gb|EEE73840.1| cytochrome P450 [Populus trichocarpa]	Unigene18912_All//7.00E-41//AT2G25160| CYP92F1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene18912_All//0.00E+00//gi|48821562|gb|CO122875.1|CO122875		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene18913_All	776	0.00	0.07	0.00	0.06	0.62	0.29	107.44	20.95	27.31	6.03E+00	6.17E-01		null	null		3.27E+00	2.69E-02		2.18E+00	3.23E-01		-2.36E+00	5.29E-256	Down	-1.98E+00	8.49E-211	Down	Unigene18913_All//gi|211906536|gb|ACJ11761.1|//1.00E-105//class III peroxidase [Gossypium hirsutum]	Unigene18913_All//1.00E-84//AT1G05260| RC13 (RARE COLD INDUCIBLE GENE 3); peroxidase	Unigene18913_All//0.00E+00//gi|48792117|gb|CO093431.1|CO093431		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene18914_All	614	0.77	3.22	3.38	1.05	0.73	0.81	0.28	0.00	0.13	2.07E+00	7.23E-05	Up	2.14E+00	5.02E-05	Up	-5.33E-01	5.39E-01		-3.82E-01	6.78E-01		-8.11E+00	1.35E-01		-1.09E+00	5.53E-01		Unigene18914_All//gi|145465815|ref|NP_001056507.1|//4.00E-13//Os05g0594500 [Oryza sativa Japonica Group] >gi|113580058|dbj|BAF18421.1| Os05g0594500 [Oryza sativa Japonica Group]	Unigene18914_All//2.00E-10//AT3G48200| unknown protein					nr -
Unigene18916_All	710	0.00	0.14	0.00	1.19	1.55	0.57	2.02	0.53	1.80	7.16E+00	3.87E-01		null	null		3.80E-01	6.01E-01		-1.06E+00	1.81E-01		-1.93E+00	3.78E-04	Down	-1.73E-01	7.13E-01		Unigene18916_All//gi|145338697|ref|NP_188535.4|//7.00E-56//POK2 (PHRAGMOPLAST ORIENTING KINESIN 2); ATP binding / microtubule motor [Arabidopsis thaliana] >gi|89160909|gb|ABD62997.1| kinesin POK2 [Arabidopsis thaliana]	Unigene18916_All//2.00E-52//AT3G19050| POK2 (PHRAGMOPLAST ORIENTING KINESIN 2); ATP binding / microtubule motor					nr +
Unigene18917_All	625	1.17	5.76	3.49	0.24	1.05	1.37	0.07	0.00	0.00	2.30E+00	2.76E-09	Up	1.58E+00	9.82E-04	Up	2.13E+00	3.78E-02		2.52E+00	5.47E-03		-6.08E+00	6.58E-01		-6.08E+00	6.13E-01		Unigene18917_All//gi|115440093|ref|NP_001044326.1|//6.00E-26//Os01g0762300 [Oryza sativa Japonica Group] >gi|113533857|dbj|BAF06240.1| Os01g0762300 [Oryza sativa Japonica Group]	Unigene18917_All//2.00E-31//AT5G55570| unknown protein	Unigene18917_All//0.00E+00//TC172743				nr +
Unigene18919_All	609	0.77	0.83	0.87	0.16	0.11	0.00	2.08	2.95	6.48	1.06E-01	9.23E-01		1.78E-01	8.45E-01		-5.33E-01	8.17E-01		-7.35E+00	4.01E-01		5.03E-01	2.62E-01		1.64E+00	2.15E-08	Up			Unigene18919_All//7.00E-07//CO498882				
Unigene18920_All	313	7.19	4.53	4.59	2.39	2.53	1.59	0.54	0.80	3.31	-6.65E-01	1.20E-01		-6.46E-01	1.46E-01		8.40E-02	9.45E-01		-5.89E-01	4.87E-01		5.68E-01	6.74E-01		2.61E+00	2.37E-04	Up	Unigene18920_All//gi|297814053|ref|XP_002874910.1|//8.00E-25//TOC159 [Arabidopsis lyrata subsp. lyrata] >gi|297320747|gb|EFH51169.1| TOC159 [Arabidopsis lyrata subsp. lyrata]	Unigene18920_All//5.00E-26//AT4G02510| TOC159 (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 159); transmembrane receptor	Unigene18920_All//1.00E-77//gi|48753565|gb|CO084084.1|CO084084				nr -
Unigene18921_All	610	1.37	4.24	1.66	0.49	1.52	0.74	0.55	1.16	0.00	1.63E+00	1.16E-04	Up	2.73E-01	6.75E-01		1.64E+00	3.35E-02		5.96E-01	6.40E-01		1.07E+00	1.67E-01		-9.12E+00	8.15E-03		Unigene18921_All//gi|2342690|gb|AAB70417.1|//3.00E-30//Similar to Homo copine I (gb|U83246) [Arabidopsis thaliana]	Unigene18921_All//8.00E-31//AT1G08860| BON3 (BONZAI 3); calcium-dependent phospholipid binding	Unigene18921_All//7.00E-07//CO492732				nr -
Unigene18922_All	371	3.67	1.23	3.88	4.97	10.58	8.64	0.00	0.00	0.00	-1.58E+00	9.14E-03		7.98E-02	8.87E-01		1.09E+00	2.71E-04	Up	7.99E-01	2.22E-02		null	null		null	null		Unigene18922_All//gi|75205771|sp|Q9SUP6.2|GDL10_ARATH//6.00E-40//RecName: Full=GDSL esterase/lipase At1g28610; AltName: Full=Extracellular lipase At1g28610; Flags: Precursor >gi|10764857|gb|AAG22835.1|AC00750 8_11 F1K23.16 [Arabidopsis thaliana]	Unigene18922_All//3.00E-41//AT1G28610| GDSL-motif lipase, putative	Unigene18922_All//0.00E+00//EX169996				nr +
Unigene18924_All	347	2.26	0.88	2.15	2.87	3.87	2.47	4.14	1.57	1.26	-1.37E+00	9.60E-02		-7.41E-02	9.35E-01		4.31E-01	5.15E-01		-2.15E-01	7.45E-01		-1.40E+00	6.15E-03		-1.71E+00	8.25E-04	Down	Unigene18924_All//gi|297829270|ref|XP_002882517.1|//4.00E-09//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328357|gb|EFH58776.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene18924_All//7.00E-10//AT3G07290| zinc finger (C3HC4-type RING finger) family protein	Unigene18924_All//4.00E-35//ES791979				nr +
Unigene18926_All	460	1.82	3.52	2.66	0.54	2.84	0.69	1.93	2.82	1.65	9.54E-01	6.65E-02		5.49E-01	3.86E-01		2.39E+00	3.51E-04	Up	3.44E-01	7.97E-01		5.45E-01	3.22E-01		-2.30E-01	7.05E-01				Unigene18926_All//5.00E-07//TC171361				
Unigene18929_All	392	18.02	12.80	18.34	13.47	14.41	19.13	13.59	5.22	6.30	-4.94E-01	2.55E-02		2.54E-02	9.26E-01		9.70E-02	7.73E-01		5.06E-01	1.87E-02		-1.38E+00	1.44E-08	Down	-1.11E+00	1.47E-06	Down	Unigene18929_All//gi|297736542|emb|CBI25413.3|//5.00E-06//unnamed protein product [Vitis vinifera]		Unigene18929_All//6.00E-102//gi|84154478|gb|DN803833.1|DN803833				nr -
Unigene1893_All	1833	12.70	22.47	13.25	165.99	70.90	116.69	66.08	88.08	48.14	8.23E-01	6.97E-22		6.06E-02	6.24E-01		-1.23E+00	0.00E+00	Down	-5.08E-01	7.27E-73		4.15E-01	1.55E-30		-4.57E-01	2.57E-28		Unigene1893_All//gi|73647513|gb|AAZ79355.1|//0.00E+00//aldehyde dehydrogenase [Vitis pseudoreticulata]	Unigene1893_All//0.00E+00//AT1G23800| ALDH2B7; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)	Unigene1893_All//0.00E+00//TC132936		ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr -
Unigene18931_All	335	13.74	161.54	387.21	0.45	1.03	3.77	1.01	0.12	7.97	3.56E+00	4.15E-206	Up	4.82E+00	0.00E+00	Up	1.20E+00	4.26E-01		3.08E+00	6.55E-05	Up	-3.02E+00	5.30E-02		2.98E+00	1.99E-11	Up	Unigene18931_All//gi|416662|sp|P32765.1|ASP_THECC//6.00E-30//RecName: Full=21 kDa seed protein; Flags: Precursor >gi|99954|pir|S16252 trypsin inhibitor homolog - soybean >gi|21909|emb|CAA39860.1| 21 kDa seed protein [Theobroma cacao]		Unigene18931_All//5.00E-167//gi|109826306|gb|DW225027.1|DW225027				nr +
Unigene18932_All	657	1.67	1.00	0.49	3.64	2.73	1.24	0.45	0.57	1.03	-7.38E-01	2.50E-01		-1.78E+00	1.57E-02		-4.17E-01	3.15E-01		-1.56E+00	2.50E-04	Down	3.46E-01	7.38E-01		1.19E+00	1.20E-01		Unigene18932_All//gi|171854669|dbj|BAG16524.1|//2.00E-61//C2 domain-containing protein [Capsicum chinense]	Unigene18932_All//3.00E-42//AT4G34150| C2 domain-containing protein	Unigene18932_All//8.00E-41//gi|5049708|gb|AI730856.1|AI730856		ko03040|Spliceosome		nr -
Unigene18933_All	245	39.93	18.82	32.17	163.88	171.75	92.72	88.70	54.42	42.44	-1.09E+00	9.23E-09	Down	-3.12E-01	1.19E-01		6.77E-02	5.28E-01		-8.22E-01	6.38E-23		-7.05E-01	2.74E-11		-1.06E+00	1.62E-22	Down	Unigene18933_All//sp|P30165|ACT2_PEA//7.00E-06//Actin-2 OS=Pisum sativum PE=2 SV=1	Unigene18933_All//2.00E-06//AT5G59370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene18933_All//2.00E-131//gi|109859493|gb|DW488472.1|DW488472		ko04145|Phagosome		swissprot -
Unigene18935_All	795	0.92	1.08	0.67	4.76	2.21	0.57	2.45	0.47	0.95	2.34E-01	7.28E-01		-4.60E-01	6.02E-01		-1.11E+00	1.70E-04	Down	-3.07E+00	3.39E-14	Down	-2.37E+00	1.13E-06	Down	-1.36E+00	1.00E-03		Unigene18935_All//gi|297830924|ref|XP_002883344.1|//2.00E-21//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329184|gb|EFH59603.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene18935_All//2.00E-22//AT3G22150| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene18936_All	726	0.29	0.42	1.69	0.96	1.42	1.31	3.20	1.09	1.70	5.39E-01	6.72E-01		2.55E+00	8.25E-04	Up	5.67E-01	4.45E-01		4.44E-01	5.74E-01		-1.55E+00	8.14E-05	Down	-9.13E-01	1.12E-02		Unigene18936_All//gi|30690149|ref|NP_851029.1|//2.00E-66//NOL1/NOP2/sun family protein [Arabidopsis thaliana] >gi|30690152|ref|NP_197990.2| NOL1/NOP2/sun family protein [Arabidopsis thaliana]	Unigene18936_All//8.00E-58//AT5G26180| NOL1/NOP2/sun family protein	Unigene18936_All//0.00E+00//gi|78354140|gb|DT574414.1|DT574414				nr -
Unigene18938_All	443	14.17	18.64	20.19	8.88	9.48	8.46	27.49	19.81	9.44	3.96E-01	5.42E-02		5.11E-01	1.13E-02		9.43E-02	8.20E-01		-7.01E-02	8.38E-01		-4.72E-01	1.11E-03		-1.54E+00	1.77E-22	Down			Unigene18938_All//4.00E-168//TC174907				
Unigene18940_All	237	7.95	3.21	5.62	3.99	5.38	5.72	42.46	23.10	11.60	-1.31E+00	7.13E-03		-5.01E-01	3.23E-01		4.29E-01	5.32E-01		5.18E-01	4.01E-01		-8.78E-01	6.77E-08		-1.87E+00	2.23E-24	Down			Unigene18940_All//2.00E-66//TC142541				
Unigene18942_All	275	39.19	138.56	61.00	54.52	141.87	284.12	23.83	85.11	71.56	1.82E+00	1.69E-68	Up	6.38E-01	5.18E-06		1.38E+00	2.29E-55	Up	2.38E+00	1.01E-211	Up	1.84E+00	1.95E-52	Up	1.59E+00	6.65E-37	Up	Unigene18942_All//gi|224073168|ref|XP_002304005.1|//3.00E-35//f-box family protein [Populus trichocarpa] >gi|222841437|gb|EEE78984.1| f-box family protein [Populus trichocarpa]	Unigene18942_All//1.00E-21//AT2G44130| kelch repeat-containing F-box family protein	Unigene18942_All//1.00E-151//gi|78325802|gb|DT546076.1|DT546076				nr -
Unigene18943_All	645	3.49	1.89	5.12	3.63	0.59	0.84	0.59	0.78	0.19	-8.88E-01	3.72E-02		5.53E-01	1.27E-01		-2.63E+00	8.62E-09	Down	-2.11E+00	4.32E-06	Down	3.98E-01	6.53E-01		-1.67E+00	1.40E-01		Unigene18943_All//gi|212717133|gb|ACJ37468.1|//7.00E-30//PK-LRR-TM resistance protein [Glycine max]	Unigene18943_All//1.00E-18//AT4G13810| ArRLP47 (Receptor Like Protein 47); protein binding	Unigene18943_All//2.00E-118//TC158869				nr -
Unigene18946_All	1050	0.30	0.10	0.20	3.99	2.69	1.42	1.01	0.52	0.38	-1.63E+00	2.77E-01		-5.59E-01	6.64E-01		-5.67E-01	4.79E-02		-1.49E+00	1.12E-06	Down	-9.60E-01	1.12E-01		-1.41E+00	1.72E-02		Unigene18946_All//gi|9758157|dbj|BAB08714.1|//3.00E-11//non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]		Unigene18946_All//2.00E-14//TC137548				nr -
Unigene18947_All	711	6.26	8.41	7.41	7.50	4.55	20.52	430.24	470.57	1018.32	4.27E-01	8.23E-02		2.45E-01	3.93E-01		-7.20E-01	2.96E-03		1.45E+00	1.14E-20	Up	1.29E-01	1.90E-07		1.24E+00	0.00E+00	Up	Unigene18947_All//gi|89258498|gb|ABD65462.1|//5.00E-57//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene18947_All//5.00E-39//AT1G52340| ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase	Unigene18947_All//0.00E+00//gi|48780267|gb|CO089633.1|CO089633		ko00906|Carotenoid biosynthesis		nr -
Unigene18949_All	461	3.29	6.70	10.86	1.08	2.17	2.45	0.55	0.45	0.60	1.03E+00	4.13E-03		1.72E+00	1.42E-08	Up	1.00E+00	1.65E-01		1.18E+00	7.75E-02		-2.80E-01	8.29E-01		1.37E-01	9.29E-01		Unigene18949_All//gi|115473321|ref|NP_001060259.1|//9.00E-11//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene18949_All//1.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative					nr -
Unigene1895_All	853	0.80	2.26	3.56	1.46	3.51	2.28	1.19	2.89	1.45	1.50E+00	2.28E-03		2.16E+00	4.13E-07	Up	1.27E+00	3.78E-04	Up	6.41E-01	1.91E-01		1.28E+00	5.37E-04	Up	2.83E-01	5.98E-01				Unigene1895_All//2.00E-48//DN803649				
Unigene18951_All	620	0.68	0.25	0.26	2.33	1.28	1.09	1.57	0.27	0.90	-1.46E+00	2.34E-01		-1.39E+00	2.80E-01		-8.67E-01	1.04E-01		-1.09E+00	5.14E-02		-2.54E+00	6.41E-04	Down	-8.02E-01	1.83E-01		Unigene18951_All//gi|147882995|gb|AB451814.1|//1.00E-71//RAN GTPase-activating protein 1 [Nicotiana benthamiana]	Unigene18951_All//6.00E-62//AT3G63130| RANGAP1 (RAN GTPASE ACTIVATING PROTEIN 1); RAN GTPase activator/ protein binding	Unigene18951_All//4.00E-98//TC174264				nr -
Unigene18954_All	526	0.00	0.48	0.20	0.66	0.00	1.20	2.09	4.93	1.14	8.91E+00	7.86E-02		7.66E+00	3.99E-01		-9.37E+00	9.45E-03		8.59E-01	3.90E-01		1.24E+00	5.53E-04	Up	-8.79E-01	1.15E-01								
Unigene18959_All	375	20.09	83.50	46.72	29.09	49.22	54.92	27.85	59.52	80.00	2.06E+00	3.97E-66	Up	1.22E+00	3.05E-17	Up	7.59E-01	3.11E-10		9.17E-01	3.13E-14		1.10E+00	1.88E-23	Up	1.52E+00	1.34E-52	Up	Unigene18959_All//gi|297794475|ref|XP_002865122.1|//6.00E-54//myb family transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297310957|gb|EFH41381.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene18959_All//7.00E-46//AT5G47390| myb family transcription factor	Unigene18959_All//0.00E+00//TC158509	MYB-related			nr +

Unigene18960_All	901	0.46	0.22	0.53	1.16	0.61	1.20	1.22	9.70	3.14	-1.05E+00	3.66E-01		1.95E-01	8.39E-01		-9.25E-01	1.56E-01		5.13E-02	9.47E-01		2.99E+00	2.89E-35	Up	1.36E+00	5.48E-05	Up	Unigene18960_All//gi|79565313|ref|NP_180417.2|//3.00E-54//LBD11 (LOB DOMAIN-CONTAINING PROTEIN 11) [Arabidopsis thaliana]	Unigene18960_All//7.00E-52//AT1G07900| LBD1 (LOB DOMAIN-CONTAINING PROTEIN 1)	Unigene18960_All//6.00E-76//gi|73862495|gb|DT465234.1|DT465234		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene18962_All	454	0.00	0.89	0.00	0.77	2.35	0.99	4.56	6.26	10.79	9.80E+00	1.36E-02		null	null		1.61E+00	2.12E-02		3.73E-01	7.32E-01		4.56E-01	1.86E-01		1.24E+00	4.55E-07	Up									
Unigene18965_All	383	4.23	4.76	6.67	5.33	2.52	0.47	0.66	0.33	0.21	1.70E-01	7.15E-01		6.56E-01	1.15E-01		-1.08E+00	1.13E-02		-3.50E+00	8.72E-09	Down	-1.02E+00	4.95E-01		-1.67E+00	2.56E-01										
Unigene18966_All	583	1.79	0.35	0.64	22.98	3.13	2.32	1.31	0.43	0.68	-2.37E+00	2.49E-03		-1.49E+00	4.42E-02		-2.88E+00	6.68E-54	Down	-3.31E+00	5.57E-53	Down	-1.60E+00	3.70E-02		-9.34E-01	1.82E-01		Unigene18966_All//gi|297802294|ref|XP_002869031.1|//2.00E-26//At4g36570 [Arabidopsis lyrata subsp. lyrata] >gi|385664194|gb|AAR24137.1| At4g36570 [Arabidopsis thaliana] >gi|40823588|gb|AAR92291.1| At4g36570 [Arabidopsis thaliana] >gi|297314867|gb|EFH45290.1| At4g36570 [Arabidopsis lyrata subsp. lyrata]	Unigene18966_All//4.00E-21//AT1G19510| ATRL5 (ARABIDOPSIS RAD-LIKE 5); DNA binding / transcription factor	Unigene18966_All//0.00E+00//gi|109887456|gb|DW516425.1|DW516425	MYB-related			nr -
Unigene18967_All	1276	0.00	0.00	0.00	0.00	0.00	0.00	13.59	17.95	1.06	null	null		null	null		null	null		null	null		4.02E-01	8.24E-05		-3.68E+00	7.74E-87	Down	Unigene18967_All//gi|297836874|ref|XP_002886319.1|//3.00E-09//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332159|gb|EFH62578.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene18967_All//6.00E-43//gi|109860680|gb|DW489659.1|DW489659				nr -
Unigene18968_All	387	1.49	3.54	0.00	1.42	0.09	0.00	5.68	11.02	1.75	1.25E+00	3.35E-02		-1.05E+01	2.60E-03		-3.99E+00	2.60E-03		-1.05E+01	1.52E-03		9.55E-01	2.92E-04		-1.70E+00	2.47E-05	Down			Unigene18968_All//8.00E-52//TC177048				
Unigene1897_All	2193	3.03	4.48	2.55	4.32	7.21	3.73	22.92	21.29	141.33	5.65E-01	2.01E-03		-2.49E-01	3.33E-01		7.40E-01	1.75E-08		-2.11E-01	3.19E-01		-1.07E-01	1.58E-01		2.62E+00	0.00E+00	Up	Unigene1897_All//gi|224115010|ref|XP_002316916.1|//0.00E+00//+white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222859988|gb|EEE97528.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene1897_All//0.00E+00//AT4G2740 20| ABC transporter family protein	Unigene1897_All//9.00E-65//C0101469		ko03040|Spliceosome//ko02010|ABC transporters		nr +
Unigene18970_All	285	1.65	1.42	0.37	1.92	1.81	2.06	6.38	0.73	1.40	-2.16E-01	8.17E-01		-2.14E+00	1.03E-01		-8.52E-02	9.07E-01		9.96E-02	9.36E-01		-3.12E+00	3.72E-08	Down	-2.19E+00	5.01E-06	Down			Unigene18970_All//2.00E-135//DT049961				
Unigene18971_All	207	69.00	35.98	32.93	115.03	116.78	129.60	138.48	114.48	101.81	-9.39E-01	5.81E-10		-1.07E+00	1.44E-11	Down	2.18E-02	8.75E-01		1.72E-01	1.38E-01		-2.75E-01	2.91E-03		-4.44E-01	4.67E-07				Unigene18971_All//1.00E-113//TC143391				ESTscan -
Unigene18972_All	660	0.95	0.61	0.16	235.71	88.54	45.44	5.51	1.14	1.21	-6.31E-01	4.75E-01		-2.56E+00	2.72E-02		-1.41E+00	3.13E-242	Down	-2.38E+00	0.00E+00	Down	-2.27E+00	2.46E-11	Down	-2.19E+00	2.94E-11	Down	Unigene18972_All//gi|297592173|gb|ADI46957.1|//1.00E-11//HPR6|m [Volvox carteri f. nagariensis]		Unigene18972_All//5.00E-162//DW498546		ko03040|Spliceosome		nr -
Unigene18973_All	296	0.71	4.45	0.00	1.68	1.63	1.68	1.71	0.71	0.27	2.65E+00	2.16E-04	Up	-9.47E+00	1.46E-01		-4.72E-02	9.49E-01		-3.90E-03	9.87E-01		-1.28E+00	1.86E-01		-2.67E+00	1.37E-02		Unigene18973_All//gi|224106455|ref|XP_002314172.1|//4.00E-37//GRAS family transcription factor [Populus trichocarpa] >gi|222850580|gb|EEE88127.1| GRAS family transcription factor [Populus trichocarpa]	Unigene18973_All//2.00E-32//AT1G07530| SCL14 (SCARECROW-LIKE 14); transcription factor	Unigene18973_All//1.00E-52//gi|78330552|gb|DT550826.1|DT550826	GRAS			nr -
Unigene18978_All	1243	9.01	18.55	9.98	0.08	0.06	0.29	0.00	0.00	0.06	1.04E+00	2.65E-18	Up	1.48E-01	4.09E-01		-5.34E-01	8.17E-01		1.86E+00	2.20E-01		null	null		6.00E+00	4.05E-01		Unigene18978_All//gi|3776569|gb|AAC64886.1|//1.00E-19//ESTs gb|H65549 and gb|AA651123 come from this gene [Arabidopsis thaliana]	Unigene18978_All//1.00E-17//AT1G54740| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: structural constituent of ribosome (TAIR:AT1G22110.1); Has 479 Blast hits to 317 proteins in 60 species: Archae - 0; Bacteria - 23; Metazoa - 81; Fungi - 16; Plants - 88; Viruses - 0; Other Eukaryotes - 269 (source: NCBI BLink).				nr +
Unigene18981_All	500	0.42	0.20	0.00	3.49	3.37	1.45	8.03	3.01	23.58	-1.05E+00	5.65E-01		-8.71E+00	1.46E-01		-4.72E-02	9.17E-01		-1.27E+00	1.14E-02		-1.42E+00	6.85E-07	Down	1.55E+00	8.23E-22	Up	Unigene18981_All//gi|224128221|ref|XP_002329111.1|//8.00E-28//predicted protein [Populus trichocarpa] >gi|222869780|gb|EEF06911.1| predicted protein [Populus trichocarpa]	Unigene18981_All//6.00E-19//AT3G15518| unknown protein				nr +
Unigene18982_All	348	115.32	124.20	311.39	121.10	180.69	292.52	0.12	0.00	0.23	1.07E-01	2.33E-01		1.43E+00	5.29E-134	Up	5.77E-01	3.89E-21		1.27E+00	8.73E-116	Up	-6.92E+00	6.58E-01		9.14E-01	7.50E-01		Unigene18982_All//gi|71999171|gb|AAZ57445.1|//8.00E-17//lipoxygenase LOX2 [Populus deltoides]		Unigene18982_All//3.00E-162//TC149425		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr -
Unigene18983_All	613	56.93	31.66	42.74	12.11	3.88	4.94	0.76	1.09	0.45	-8.47E-01	1.35E-19		-4.14E-01	1.01E-05		-1.64E+00	9.01E-15	Down	-1.29E+00	2.67E-09	Down	5.24E-01	5.26E-01		-7.38E-01	4.26E-01		Unigene18983_All//gi|116310418|emb|CAH67426.1|//1.00E-20//OS10G0150F01.6 [Oryza sativa (indica cultivar-group)]	Unigene18983_All//5.00E-12//AT4G05030| heavy-metal-associated domain-containing protein				nr -
Unigene18987_All	533	0.00	0.00	0.00	2.06	1.36	0.85	0.24	1.65	1.35	null	null		null	null		-6.00E-01	3.53E-01		-1.28E+00	5.68E-02		2.79E+00	6.97E-04	Up	2.50E+00	4.03E-03		Unigene18987_All//gi|225448970|ref|XP_002269698.1|//2.00E-32//PREDICTED: similar to SEC8 (secretion 8) isoform 2 [Vitis vinifera]	Unigene18987_All//3.00E-29//AT3G10380| SEC8 (SUBUNIT OF EXOCYST COMPLEX 8)	Unigene18987_All//4.00E-88//C0117802				nr -
Unigene18990_All	343	37.83	91.59	117.21	138.84	77.50	90.46	59.41	89.81	73.17	1.28E+00	8.49E-34	Up	1.63E+00	2.48E-60	Up	-8.41E-01	8.03E-32		-6.18E-01	1.17E-16		5.96E-01	7.86E-12		3.01E-01	1.74E-03				Unigene18990_All//7.00E-123//TC169192				
Unigene18993_All	1079	0.48	0.28	0.30	10.48	15.16	13.18	0.59	0.15	0.00	-7.83E-01	4.22E-01		-7.12E-01	4.97E-01		5.33E-01	3.80E-05		3.31E-01	3.09E-02		-1.92E+00	3.09E-02		-9.20E+00	7.11E-05	Down			Unigene18993_All//6.00E-21//DR459827				
Unigene18997_All	541	52.61	38.49	37.90	23.85	30.23	24.13	69.63	27.58	41.83	-4.51E-01	8.39E-06		-4.73E-01	5.99E-06		3.42E-01	1.16E-02		1.67E-02	9.42E-01		-1.34E+00	3.41E-53	Down	-7.35E-01	5.81E-21		Unigene18997_All//gi|62286683|sp|Q9W531.1|H2A_EUPES//3.00E-30//RecName: Full=Histone H2A >gi|7649159|gb|AAF65769.1|AF242311| histone H2A [Euphorbia esula]	Unigene18997_All//7.00E-12//AT5G02560| HTA12; DNA binding	Unigene18997_All//1.00E-116//TC146106				nr -
Unigene19000_All	499	2.41	0.10	2.35	1.40	0.97	2.90	2.97	0.50	1.20	-4.57E+00	5.88E-06	Down	-3.87E-02	9.68E-01		-5.33E-01	5.45E-01		1.05E+00	6.64E-02		-2.56E+00	1.18E-05	Down	-1.31E+00	6.57E-03		Unigene19000_All//gi|18415647|ref|NP_568185.1|//1.00E-27//mitochondrial transcription termination factor family protein / mTERF family protein [Arabidopsis thaliana]	Unigene19000_All//9.00E-29//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene19000_All//0.00E+00//TC155366				nr -
Unigene19001_All	632	0.00	0.00	0.00	1.73	0.60	0.21	1.14	0.93	2.33	null	null		null	null		-1.53E+00	1.61E-02		-3.02E+00	2.14E-04	Down	-2.97E-01	6.85E-01		1.04E+00	2.97E-02		Unigene19001_All//gi|110738885|dbj|BAF01364.1|//2.00E-40//DnaJ like protein [Arabidopsis thaliana]	Unigene19001_All//3.00E-42//AT2G22360| DNAJ heat shock family protein	Unigene19001_All//0.00E+00//CO131948				nr -
Unigene19003_All	332	21.28	24.88	24.22	31.51	28.21	24.49	26.11	15.61	12.60	2.26E-01	2.99E-01		1.87E-01	4.05E-01		-1.60E-01	4.30E-01		-3.64E-01	4.50E-02		-7.42E-01	2.20E-05		-1.05E+00	2.37E-09	Down	Unigene19003_All//gi|115439979|ref|NP_001044269.1|//8.00E-22//Os01g0752800 [Oryza sativa Japonica Group] >gi|113533800|dbj|BAF06183.1| Os01g0752800 [Oryza sativa Japonica Group]	Unigene19003_All//2.00E-07//AT5G46020| unknown protein	Unigene19003_All//1.00E-118//gi|13350285|gb|BG440634.1|BG440634				nr -
Unigene19004_All	591	0.00	0.09	0.00	1.10	2.04	0.84	1.14	2.26	3.10	6.42E+00	6.17E-01		null	null		8.96E-01	1.61E-01		-3.82E-01	6.78E-01		9.84E-01	5.99E-02		1.44E+00	9.58E-04	Up	Unigene19004_All//gi|297822593|ref|XP_002879179.1|//5.00E-30//copper-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325018|gb|EFH55438.1| copper-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene19004_All//4.00E-27//AT2G37390| heavy-metal-associated domain-containing protein	Unigene19004_All//2.00E-44//TC156654				nr +
Unigene19005_All	245	13.03	6.00	5.22	3.05	6.89	7.37	1.21	0.34	0.00	-1.12E+00	1.52E-03		-1.32E+00	4.23E-04	Down	1.18E+00	2.09E-02		1.27E+00	1.08E-02		-1.82E+00	2.11E-01		-1.02E+01	1.58E-02				Unigene19005_All//3.00E-50//DW505338				
Unigene19007_All	839	0.75	0.48	0.25	1.01	1.44	1.02	1.31	0.80	4.70	-6.31E-01	4.75E-01		-1.56E+00	1.29E-01		5.09E-01	4.57E-01		1.92E-02	9.82E-01		-7.17E-01	2.30E-01		1.84E+00	9.63E-10	Up			Unigene19007_All//2.00E-152//TC143363				
Unigene19013_All	844	0.31	2.34	2.21	0.35	0.65	0.86	1.65	6.19	0.00	2.92E+00	8.36E-07	Up	2.83E+00	5.06E-06	Up	8.83E-01	4.21E-01		1.27E+00	1.56E-01		1.90E+00	7.25E-13	Up	-1.07E+01	2.40E-10	Down	Unigene19013_All//gi|124359962|gb|ABN07978.1|//2.00E-84//GRAS transcription factor [Medicago truncatula]	Unigene19013_All//4.00E-34//AT3G03450| RGL2 (RGA-LIKE 2); transcription factor		GRAS			nr -
Unigene19014_All	732	0.71	0.00	0.00	2.25	0.99	2.71	1.96	0.46	1.25	-9.48E+00	2.93E-03		-9.48E+00	4.76E-03		-1.18E+00	1.54E-02		2.74E-01	6.17E-01		-2.10E+00	1.56E-04	Down	-6.50E-01	1.74E-01		Unigene19014_All//gi|15231338|ref|NP_187348.1|//1.00E-112//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75186627|sp|Q9M907.1|PP217_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g06920	Unigene19014_All//2.00E-113//AT3G06920| pentatricopeptide (PPR) repeat-containing protein	Unigene19014_All//0.00E+00//ES831798				nr +
Unigene19018_All	537	6.53	3.21	2.18	0.09	0.00	0.00	0.08	1.32	0.15	-1.02E+00	2.04E-03		-1.58E+00	1.48E-05	Down	-6.54E+00	5.56E-01		-6.54E+00	6.36E-01		4.07E+00	3.51E-04	Up	9.15E-01	7.50E-01		Unigene19018_All//gi|116311010|emb|CAH67943.1|//1.00E-16//H0303A11-B0406H05.3 [Oryza sativa (indica cultivar-group)]	Unigene19018_All//9.00E-17//AT4G10190| oxidoreductase, 2OG-Fe(II) oxygenase family protein					nr -
Unigene19019_All	442	2.25	0.00	0.00	10.37	8.10	3.99	1.82	0.47	0.36	-1.11E+01	7.46E-06	Down	-1.11E+01	1.77E-05	Down	-3.56E-01	2.25E-01		-1.38E+00	1.55E-06	Down	-1.94E+00	1.17E-02		-2.33E+00	2.82E-03		Unigene19019_All//gi|297729395|ref|XP_001177061.1|//3.00E-12//Os12g0615000 [Oryza sativa Japonica Group] >gi|255670482|dbj|BAH95789.1| Os12g0615000 [Oryza sativa Japonica Group]	Unigene19019_All//3.00E-07//AT1G16090| WAKL7 (wall associated kinase-like 7); protein serine/threonine kinase	Unigene19019_All//1.00E-72//DT467466				nr +
Unigene19026_All	1094	0.33	0.00	0.00	0.18	0.03	0.12	1.89	2.45	0.76	-8.39E+00	1.97E-02		-8.39E+00	2.78E-02		-2.53E+00	2.34E-01		-5.57E-01	7.33E-01		3.69E-01	3.16E-01		-1.31E+00	9.85E-04	Down	Unigene19026_All//gi|66730858|dbj|BAD98961.1|//4.00E-58//2-oxoglutarate-dependent dioxygenase [Solanum lycopersicum]	Unigene19026_All//1.00E-55//AT1G06640| 2-oxoglutarate-dependent dioxygenase, putative	Unigene19026_All//0.00E+00//gi|164282550|gb|ES829272.1|ES829272		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene19027_All	713	0.44	2.42	0.00	1.33	2.32	0.95	1.72	0.76	0.95	2.46E+00	3.84E-05	Up	-8.78E+00	4.92E-02		8.04E-01	1.24E-01		-4.83E-01	5.19E-01		-1.17E+00	3.41E-02		-8.56E-01	1.02E-01		Unigene19027_All//gi|87241328|gb|AB033186.1|//2.00E-10//Helix-loop-helix DNA-binding [Medicago truncatula]						nr -
Unigene1903_All	2616	3.02	2.29	2.04	4.91	4.83	2.21	6.92	1.93	4.87	-4.02E-01	5.59E-02		-5.69E-01	8.36E-03		-2.43E-02	8.95E-01		-1.15E+00	3.84E-13	Down	-1.84E+00	6.94E-41	Down	-5.05E-01	7.83E-06		Unigene1903_All//gi|75156737|sp|Q8LLE5.1|PPP_SOLLC//1.00E-159//RecName: Full=Filament-like plant protein; Short=LePPP >gi|22652089|gb|AAN03605.1|AF405309_1 coiled-coil protein [Solanum lycopersicum]	Unigene1903_All//1.00E-85//AT3G05270| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF869, plant (InterPro:IPR008587); BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT1G77580.2); Has 97002 Blast hits to 49715 proteins in 2003 species: Archae - 1158; Bacteria - 12418; Metazoa - 49297; Fungi - 7501; Plants - 3801; Viruses - 453; Other Eukaryotes - 22374 (source: NCBI BLink).	Unigene1903_All//0.00E+00//TC165553				nr -

Unigene19031_All	303	2.24	0.33	0.00	4.11	2.39	1.79	0.84	0.28	1.18	-2.75E+00	1.06E-02		-1.11E+01	7.64E-04	Down	-7.84E-01	1.82E-01		-1.20E+00	5.16E-02		-1.60E+00	3.11E-01		4.99E-01	6.27E-01		Unigene19031_All//gi|115450303|ref|NP_001048752.1|//3.00E-12//0s03g0115400 [Oryza sativa Japonica Group] >gi|108705849|gb|ABF93644.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547223|dbj|BAF10666.1| Os03g0115400 [Oryza sativa Japonica Group]	Unigene19031_All//2.00E-12//AT5G54200| WD-40 repeat family protein	Unigene19031_All//4.00E-161//DT458374				nr +
Unigene19033_All	1002	0.10	0.56	0.37	0.80	0.62	0.32	2.53	2.09	1.11	2.41E+00	3.93E-02		1.83E+00	2.13E-01		-3.63E-01	6.23E-01		-1.33E+00	1.06E-01		-2.80E-01	4.67E-01		-1.19E+00	6.98E-04	Down				Unigene19033_All//2.00E-100//CO116968				
Unigene19034_All	537	133.68	83.03	73.88	224.67	184.36	218.75	690.18	315.61	267.30	-6.87E-01	1.02E-27		-8.56E-01	8.33E-39		-2.85E-01	2.18E-11		-3.85E-02	5.33E-01		-1.13E+00	0.00E+00	Down	-1.37E+00	0.00E+00	Down	Unigene19034_All//gi|158144895|gb|ABW21688.1|//7.00E-99//enolase [Gossypium hirsutum]	Unigene19034_All//6.00E-92//AT2G36530| LOS2; copper ion binding / phosphopyruvate hydratase	Unigene19034_All//0.00E+00//gi|21091570|gb|BQ403883.1|BQ403883		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation		nr +
Unigene19038_All	343	0.61	1.18	1.55	0.87	0.40	3.42	2.96	6.58	7.90	9.54E-01	4.14E-01		1.35E+00	2.25E-01		-1.12E+00	4.24E-01		1.97E+00	4.50E-03		1.15E+00	2.78E-03		1.42E+00	4.79E-05	Up				Unigene19038_All//2.00E-114//gi|109851619|gb|DW480598.1|DW480598				
Unigene19039_All	438	0.00	2.08	1.34	3.18	1.34	1.96	0.48	0.29	1.46	1.10E+01	2.62E-05	Up	1.04E+01	2.17E-03		-1.25E+00	2.07E-02		-7.01E-01	2.32E-01		-7.54E-01	6.32E-01		1.59E+00	5.48E-02					Unigene19039_All//6.00E-161//DN779890				ESTscan -
Unigene19040_All	312	1.01	4.38	2.73	1.28	1.10	0.58	0.00	2.01	1.40	2.12E+00	1.09E-03		1.44E+00	8.23E-02		-2.11E-01	8.25E-01		-1.14E+00	3.79E-01		1.10E+01	1.47E-04	Up	1.05E+01	2.13E-03		Unigene19040_All//gi|30689668|ref|NP_197875.2|//2.00E-34//zinc finger (B-box type) family protein [Arabidopsis thaliana]	Unigene19040_All//9.00E-36//AT5G24930| zinc finger (B-box type) family protein	Unigene19040_All//6.00E-18//gi|164258126|gb|ES791664.1|ES791664	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr -
Unigene19041_All	721	0.22	0.00	0.52	0.55	0.91	1.06	1.11	0.46	2.93	-7.77E+00	2.16E-01		1.25E+00	3.66E-01		7.15E-01	4.65E-01		9.46E-01	2.73E-01		-1.26E+00	7.98E-02		1.39E+00	4.85E-04	Up	Unigene19041_All//gi|296082528|emb|CBI21533.3|//3.00E-55//unnamed protein product [Vitis vinifera]	Unigene19041_All//4.00E-33//AT4G39420| unknown protein					nr -
Unigene19042_All	401	3.39	7.96	1.06	6.09	10.22	11.38	10.65	10.42	7.95	1.23E+00	5.85E-04	Up	-1.68E+00	8.97E-03		7.47E-01	1.07E-02		9.02E-01	1.36E-03		-3.10E-02	9.30E-01		-4.22E-01	1.03E-01		Unigene19042_All//gi|92897782|gb|ABE93894.1|//3.00E-07//Heavy metal transport/detoxification protein [Medicago truncatula]	Unigene19042_All//4.00E-05//AT1G01490| heavy-metal-associated domain-containing protein	Unigene19042_All//5.00E-47//gi|109826680|gb|DW225390.1|DW225390				nr -
Unigene19043_All	413	0.00	1.84	0.26	0.00	0.00	0.87	1.64	4.45	5.02	1.08E+01	1.77E-04	Up	8.01E+00	3.99E-01		null	null		9.77E+00	2.37E-02		1.44E+00	1.20E-03		1.61E+00	1.01E-04	Up				Unigene19043_All//5.00E-07//CO112509				
Unigene19044_All	1130	4610.39	2923.00	4829.16	947.00	1150.47	863.74	14.22	41.09	18.90	-6.57E-01	0.00E+00		6.69E-02	6.20E-24		2.81E-01	3.22E-114		-1.33E-01	2.96E-20		1.53E+00	5.87E-80	Up	4.10E-01	7.50E-05		Unigene19044_All//gi|297846544|ref|XP_002891153.1|//3.00E-97//Atlg31330/T19E23_1 [Arabidopsis lyrata subsp. lyrata] >gi|297336995|gb|EFH67412.1| Atlg31330/T19E23_1 [Arabidopsis lyrata subsp. lyrata]	Unigene19044_All//1.00E-79//AT1G31330| PSAF (photosystem I subunit F)	Unigene19044_All//0.00E+00//TC130361		ko00195|Photosynthesis		nr -
Unigene19047_All	1207	0.78	0.13	0.53	0.12	0.29	0.34	2.84	1.84	0.83	-2.63E+00	2.38E-03		-5.60E-01	4.39E-01		1.20E+00	4.26E-01		1.44E+00	2.82E-01		-6.29E-01	3.57E-02		-1.78E+00	2.53E-08	Down	Unigene19047_All//gi|124359649|gb|ABD32334.2|//2.00E-23//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene19047_All//2.00E-08//AT1G21280| unknown protein	Unigene19047_All//4.00E-50//FL576451				nr -
Unigene19054_All	1318	0.44	4.50	3.27	0.04	0.08	0.03	0.13	0.10	0.00	3.36E+00	6.62E-22	Up	2.91E+00	1.33E-13	Up	1.05E+00	8.08E-01		-1.40E-01	9.53E-01		-4.32E-01	7.93E-01		-7.00E+00	1.08E-01		Unigene19054_All//gi|125537847|gb|EAY84242.1|//1.00E-32//hypothetical protein Os1_05624 [Oryza sativa Indica Group]		Unigene19054_All//3.00E-119//gi|109852087|gb|DW481066.1|DW481066				nr +
Unigene19055_All	375	3.63	0.00	0.43	1.20	1.29	0.84	2.14	1.11	0.32	-1.18E+01	6.50E-08	Down	-3.09E+00	7.28E-05	Down	1.05E-01	9.55E-01		-5.04E-01	6.49E-01		-9.43E-01	1.88E-01		-2.75E+00	9.43E-04	Down				Unigene19055_All//2.00E-09//TC179204				
Unigene19058_All	545	4.03	0.56	1.86	5.58	5.12	4.56	0.47	3.83	9.72	-2.85E+00	2.01E-07	Down	-1.12E+00	1.46E-02		-1.24E-01	7.74E-01		-2.91E-01	4.68E-01		3.04E+00	4.79E-09	Up	4.38E+00	6.79E-30	Up				Unigene19058_All//6.00E-75//gi|164283196|gb|EV482234.1|EV482234				
Unigene19060_All	999	0.10	0.00	0.00	1.40	0.79	0.59	2.33	4.39	34.49	-6.71E+00	3.73E-01		-6.71E+00	3.94E-01		-8.17E-01	1.37E-01		-1.25E+00	3.03E-02		9.16E-01	4.01E-04		3.89E+00	2.26E-176	Up	Unigene19060_All//gi|297820344|ref|XP_002878055.1|//1.00E-111//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297323893|gb|EFH54314.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene19060_All//3.00E-112//AT5G05600| oxidoreductase, 20G-Fe(II) oxygenase family protein	Unigene19060_All//3.00E-118//TC170018		ko00941|Flavonoid biosynthesis		nr -
Unigene19062_All	394	0.66	0.00	0.54	0.76	0.96	0.69	8.69	3.29	1.92	-9.38E+00	6.71E-02		-2.97E-01	8.32E-01		3.42E-01	8.36E-01		-1.41E-01	9.21E-01		-1.40E+00	6.54E-06	Down	-2.18E+00	1.40E-10	Down				Unigene19062_All//1.00E-161//TC151844				
Unigene19064_All	632	1.41	0.24	0.34	4.10	2.29	2.00	4.28	1.52	1.70	-2.55E+00	4.05E-03		-2.06E+00	1.78E-02		-8.41E-01	2.39E-02		-1.03E+00	8.32E-03		-1.49E+00	3.15E-05	Down	-1.33E+00	1.03E-04	Down	Unigene19064_All//gi|254789789|sp|B9GL38.1|RBR_POPTR//1.00E-92//RecName: Full=Retinoblastoma-related protein	Unigene19064_All//6.00E-87//AT3G12280| RBR1 (RETINOBLASTOMA-RELATED 1); transcription factor binding	Unigene19064_All//1.00E-172//gi|109853471|gb|DW482450.1|DW482450				nr +
Unigene19065_All	672	3.89	1.06	2.38	1.11	0.05	0.27	0.19	0.12	0.00	-1.88E+00	1.28E-05	Down	-7.12E-01	8.25E-02		-4.44E+00	1.31E-04	Down	-2.05E+00	2.45E-02		-6.02E-01	7.66E-01		-7.56E+00	2.00E-01		Unigene19065_All//gi|5814093|gb|AAD52097.1|AF088885|//2.00E-46//receptor-like kinase CHRK1 [Nicotiana tabacum]	Unigene19065_All//3.00E-38//AT4G19810| glycosyl hydrolase family 18 protein	Unigene19065_All//0.00E+00//CA994240				nr -
Unigene19067_All	855	403.57	384.20	149.16	669.43	377.22	1004.95	841.75	1441.39	700.13	-7.10E-02	1.45E-02		-1.44E+00	0.00E+00	Down	-8.28E-01	0.00E+00		5.86E-01	1.28E-263		7.76E-01	0.00E+00		-2.66E-01	1.09E-59		Unigene19067_All//gi|211906504|gb|ACJ11745.1|//1.00E-159//heat shock protein 70 [Gossypium hirsutum]	Unigene19067_All//1.00E-139//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene19067_All//0.00E+00//gi|78354603|gb|DT574877.1|DT574877		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr +
Unigene19068_All	686	0.00	0.00	0.00	0.15	0.20	0.33	4.07	9.93	26.83	null	null		null	null		4.68E-01	8.77E-01		1.18E+00	5.49E-01		1.29E+00	9.97E-10	Up	2.72E+00	4.79E-68	Up	Unigene19068_All//gi|259016184|sp|Q9FLT0.2|BH120_ARATH//1.00E-22//RecName: Full=Transcription factor bHLH120; AltName: Full=Transcription factor EN 4; AltName: Full=bHLH transcription factor bHLH120; AltName: Full=Basic helix-loop-helix protein 120; Short=bHLH 120; Short=AtbHLH120	Unigene19068_All//3.00E-23//AT4G25410| DNA binding / transcription factor	Unigene19068_All//5.00E-82//ES805839	bHLH			nr -
Unigene1907_All	4787	0.47	0.40	1.05	1.76	1.50	0.72	0.57	0.32	0.66	-2.25E-01	5.92E-01		1.15E+00	5.03E-05	Up	-2.33E-01	2.87E-01		-1.29E+00	1.83E-10	Down	-8.07E-01	1.82E-02		2.18E-01	5.14E-01		Unigene1907_All//gi|29467228|dbj|BAC67060.1|//0.00E+00//DNA methyltransferase [Nicotiana tabacum]	Unigene1907_All//1.00E-167//AT5G14620| DRM2 (DOMAINS REARRANGED METHYLTRANSFERASE 2); N-methyltransferase	Unigene1907_All//0.00E+00//TC131482				nr +
Unigene19075_All	447	0.00	0.00	0.00	0.67	0.00	0.00	78.60	46.66	22.99	null	null		null	null		-9.39E+00	2.01E-02		-9.39E+00	4.00E-02		-7.52E-01	8.77E-20		-1.77E+00	4.15E-77	Down	Unigene19075_All//gi|224111880|ref|XP_002316010.1|//4.00E-49//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene19075_All//2.00E-20//AT3G14680| CYP72A14; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene19075_All//6.00E-158//TC179190		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +
Unigene19077_All	452	1.50	2.91	1.41	3.53	2.51	4.40	0.75	1.94	5.64	9.54E-01	1.06E-01		-9.01E-02	9.22E-01		-4.88E-01	3.53E-01		3.18E-01	5.38E-01		1.38E+00	4.62E-02		2.91E+00	1.01E-10	Up								
Unigene19078_All	483	73.12	16.16	42.78	6.50	5.49	0.56	0.00	0.00	0.00	-2.18E+00	8.69E-81	Down	-7.73E-01	2.23E-16		-2.43E-01	5.41E-01		-3.53E+00	2.13E-13	Down	null	null		null	null					Unigene19078_All//2.00E-176//DW509238				ESTscan -
Unigene1908_All	1713	112.12	64.45	67.83	143.83	202.35	317.99	150.98	105.28	249.85	-7.99E-01	1.01E-94		-7.25E-01	1.20E-77		4.93E-01	1.12E-86		1.14E+00	0.00E+00	Up	-5.20E-01	4.34E-73		7.27E-01	4.05E-223		Unigene1908_All//gi|297810275|ref|XP_002873021.1|//1.00E-178//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318858|gb|EFH49280.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1908_All//1.00E-179//AT5G01210| transferase family protein	Unigene1908_All//0.00E+00//TC132174		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene19081_All	520	0.20	3.12	1.84	0.96	1.13	0.09	0.00	0.00	0.00	3.95E+00	3.77E-07	Up	3.20E+00	1.03E-03		2.33E-01	8.26E-01		-3.46E+00	1.61E-02		null	null		null	null										ESTscan +
Unigene19082_All	231	6.79	14.70	17.29	6.90	6.56	7.23	50.88	8.50	7.59	1.11E+00	1.14E-03		1.35E+00	4.36E-05	Up	-7.32E-02	8.77E-01		6.81E-02	9.17E-01		-2.58E+00	1.33E-40	Down	-2.75E+00	7.54E-45	Down	Unigene19082_All//gi|224171013|ref|XP_002339450.1|//1.00E-11//flavonone 3-hydroxylase [Populus trichocarpa] >gi|222875131|gb|EEF12262.1| flavonone 3-hydroxylase [Populus trichocarpa]	Unigene19082_All//8.00E-08//AT3G51240| F3H (FLAVANONE 3-HYDROXYLASE); naringenin 3-dioxygenase	Unigene19082_All//2.00E-113//TC129624		ko00941|Flavonoid biosynthesis		nr +
Unigene19084_All	402	0.78	3.40	4.24	1.36	0.26	1.24	0.00	0.00	0.00	2.12E+00	1.09E-03		2.44E+00	7.80E-05	Up	-2.41E+00	2.44E-02		-1.41E-01	8.85E-01		null	null		null	null		Unigene19084_All//gi|224120698|ref|XP_002318395.1|//7.00E-23//predicted protein [Populus trichocarpa] >gi|222859068|gb|EEE96615.1| predicted protein [Populus trichocarpa]	Unigene19084_All//1.00E-08//AT1G37113| unknown protein					nr -
Unigene19086_All	663	0.00	0.46	0.00	0.30	0.05	1.36	40.37	78.55	341.96	8.84E+00	4.44E-02		null	null		-2.53E+00	2.34E-01		2.18E+00	9.49E-03		9.60E-01	2.31E-43		3.08E+00	0.00E+00	Up	Unigene19086_All//gi|224143055|ref|XP_002324836.1|//3.00E-16//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222866270|gb|EEF03401.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene19086_All//6.00E-12//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene19086_All//0.00E+00//TC142413		ko00904|Diterpenoid biosynthesis		nr +
Unigene19090_All	384	1.09	1.85	1.39	1.30	1.08	0.24	2.53	4.35	6.02	7.61E-01	3.62E-01		3.47E-01	7.06E-01		-2.70E-01	8.02E-01		-2.46E+00	4.83E-02		7.82E-01	8.76E-02		1.25E+00	8.33E-04	Up								
Unigene19092_All	453	1.16	0.00	0.94	1.43	2.43	1.40	1.12	2.86	0.00	-1.02E+01	2.93E-03		-2.97E-01	7.50E-01		7.67E-01	2.69E-01		-3.44E-02	9.53E-01		1.35E+00	1.28E-02		-1.01E+01	5.54E-04	Down	Unigene19092_All//gi|224135613|ref|XP_002322117.1|//2.00E-13//predicted protein [Populus trichocarpa] >gi|222869113|gb|EEF06244.1| predicted protein [Populus trichocarpa]	Unigene19092_All//1.00E-06//AT1G31840| LOCATED IN: endomembrane system; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT3G22470.1); Has 23098 Blast hits to 5773 proteins in 180 species: Archae - 3; Bacteria - 16; Metazoa - 407; Fungi - 450; Plants - 21304; Viruses - 0; Other Eukaryotes - 918 (source: NCBI BLink).					nr -
Unigene19093_All	385	1.77	1.45	0.00	0.00	0.00	0.00	3.07	1.95	2.17	-2.87E-01	7.10E-01		-1.08E+01	7.64E-04	Down	null	null		null	null		-6.54E-01	2.47E-01		-5.01E-01	3.52E-01					Unigene19093_All//3.00E-17//ES835447				
Unigene19094_All	1170	0.09	0.09	0.18	0.09	0.00	0.77	97.35	10.43	33.64	-4.59E-02	9.89E-01		1.03E+00	5.92E-01		-6.41E+00	3.13E-01		3.18E+00	9.74E-04	Up	-3.22E+00	0.00E+00	Down	-1.53E+00	1.50E-201	Down	Unigene19094_All//gi|124360461|gb|ABN08471.1|//1.00E-101//Haem peroxidase, plant/fungal/bacterial [Medicago truncatula]	Unigene19094_All//7.00E-96//AT4G26010| peroxidase, putative	Unigene19094_All//0.00E+00//BE053812		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene19095_All	427	3.68	5.34	9.85	1.75	1.45	1.48	0.10	0.59	0.37	5.39E-01	2.11E-01		1.42E+00	1.04E-05	Up	-2.70E-01	7.48E-01		-2.41E-01	7.56E-01		2.57E+00	1.53E-01		1.91E+00	3.77E-01					Unigene19095_All//5.00E-44//gi|109836362|gb|DW234923.1|DW234923				
Unigene19102_All	540	9.88	37.72	17.06	16.05	23.72	24.92	15.03	17.88	18.00	1.93E+00	6.62E-40	Up	7.88E-01	6.29E-05		5.64E-01	1.53E-04		6.35E-01	2.32E-05		2.50E-01	1.57E-01		2.60E-01	1.21E-01		Unigene19102_All//gi|15235657|ref|NP_195483.1|//5.00E-17//HHP4 (heptahelical protein 4); receptor [Arabidopsis thaliana]	Unigene19102_All//9.00E-14//AT4G37680| HHP4 (heptahelical protein 4); receptor	Unigene19102_All//9.00E-179//DW504056				nr +
Unigene19103_All	284	80.51	69.40	176.81	78.40	60.50	60.59	1.49	1.03	0.56	-2.14E-01	7.64E-02		1.14E+00	2.15E-43	Up	-3.74E-01	6.30E-04		-3.72E-01	1.23E-03		-5.31E-01	6.34E-01		-1.41E+00	1.74E-01		Unigene19103_All//gi|255548265|ref|XP_002515189.1|//3.00E-07//Calcium-activated outward-rectifying potassium channel, putative [Ricinus communis] >gi|223545669|gb|EEF47173.1| Calcium-activated outward-rectifying potassium channel, putative [Ricinus communis]		Unigene19103_All//4.00E-65//gi|11207896|gb|BF276826.1|BF276826				nr +
Unigene19104_All	743	0.14	0.68	0.00	0.27	0.60	0.43	0.63	2.70	2.14	2.28E+00	6.23E-02		-7.14E+00	3.94E-01		1.17E+00	3.47E-01		6.66E-01	6.48E-01		2.11E+00	4.88E-06	Up	1.78E+00	3.04E-04	Up								
Unigene1911_All	4474	0.37	0.89	0.08	1.25	1.32	1.30	5.02	4.18	3.86	1.26E+00	6.78E-05	Up	-2.17E+00	3.27E-04	Down	7.78E-02	8.13E-01		6.25E-02	8.26E-01		-2.65E-01	1.28E-02		-3.77E-01	1.86E-04		Unigene1911_All//gi|15232498|ref|NP_188130.1|//1.00E-153//AAA-type ATPase family protein [Arabidopsis thaliana]	Unigene1911_All//2.00E-152//AT3G15120| AAA-type ATPase family protein	Unigene1911_All//0.00E+00//TC129770				nr +
Unigene19110_All	266	0.20	5.14	0.40	2.43	2.07	1.02	2.86	1.10	8.09	4.71E+00	1.03E-06	Up	1.03E+00	7.03E-01		-2.33E-01	8.07E-01		-1.28E+00	1.83E-01		-1.38E+00	6.73E-02		1.50E+00	1.81E-04	Up				Unigene19110_All//2.00E-42//TC150438				

Unigene19111_All	748	0.00	0.00	0.00	0.13	0.37	0.00	5.82	1.68	3.41	null	null		null	null		1.47E+00	4.20E-01		-7.06E+00	4.00E-01		-1.80E+00	4.20E-10	Down	-7.72E-01	2.04E-03		Unigene19111_All//gi|15236702|ref|NP_191919.1|//3.00E-40//UNE11 (unfertilized embryo sac 11); enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor [Arabidopsis thaliana] >gi|31993325|gb|AAC19307.1| contains similarity to pectinesterases [Arabidopsis thaliana] >gi|30017225|gb|AAP12846.1| At4g00080 [Arabidopsis thaliana]	Unigene19111_All//7.00E-38//AT4G00080| UNE11 (unfertilized embryo sac 11); enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene19114_All	568	1.11	0.18	0.00	8.59	15.46	3.02	1.27	1.18	0.70	-2.63E+00	1.78E-02		-1.01E+01	1.41E-03		8.47E-01	4.36E-06		-1.51E+00	8.16E-08	Down	-1.04E-01	8.93E-01		-8.51E-01	2.39E-01		Unigene19114_All//gi|255558520|ref|XP_002520285.1|//1.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223540504|gb|EEF42071.1| conserved hypothetical protein [Ricinus communis]		Unigene19114_All//8.00E-22//gi|78350064|gb|DT570338.1|DT570338				nr -
Unigene19116_All	2400	0.00	96.74	36.30	0.04	0.03	0.00	0.00	0.00	0.00	1.66E+01	0.00E+00	Up	1.51E+01	0.00E+00	Up	-5.32E-01	8.17E-01		-5.38E+00	4.00E-01		null	null		null	null		Unigene19116_All//sp|P18522|POL1_BRSV//8.00E-10//RNA1 polyprotein OS=Beet ringspot virus PE=3 SV=1						swissprot +
Unigene19119_All	245	45.70	47.98	43.90	51.64	51.02	53.64	156.18	107.82	69.92	7.02E-02	6.88E-01		-5.79E-02	7.57E-01		-1.75E-02	9.27E-01		5.48E-02	7.60E-01		-5.35E-01	4.50E-12		-1.16E+00	1.15E-44	Down	Unigene19119_All//gi|130775702|gb|AB032474.1|//9.00E-21//unknown [Gossypium hirsutum]		Unigene19119_All//2.00E-122//TC174473				nr +
Unigene1912_All	1638	13.19	2.10	2.80	57.69	32.23	19.58	57.82	42.51	16.15	-2.65E+00	1.76E-62	Down	-2.24E+00	1.96E-49	Down	-8.40E-01	9.56E-63		-1.56E+00	2.16E-148	Down	-4.44E-01	1.31E-20		-1.84E+00	2.02E-217	Down	Unigene1912_All//gi|224085766|ref|XP_002307691.1|//0.00E+00//mtn21-like protein [Populus trichocarpa] >gi|222855140|gb|EEE94687.1| mtn21-like protein [Populus trichocarpa]	Unigene1912_All//4.00E-150//AT1G75500| nodulin MtN21 family protein	Unigene1912_All//0.00E+00//TC133250				nr -
Unigene19122_All	582	1.80	0.17	0.18	2.23	2.37	0.78	0.58	0.93	1.23	-3.37E+00	2.13E-04	Down	-3.30E+00	4.58E-04	Down	8.88E-02	8.98E-01		-1.52E+00	1.32E-02		6.84E-01	4.49E-01		1.08E+00	1.41E-01		Unigene19122_All//gi|297831082|ref|XP_002883423.1|//8.00E-56//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329263|gb|EFH59682.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene19122_All//1.00E-56//AT3G23330| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene19125_All	270	4.84	2.06	7.30	2.58	3.44	1.67	32.10	24.61	14.90	-1.23E+00	3.96E-02		5.91E-01	2.29E-01		4.15E-01	6.06E-01		-6.27E-01	4.76E-01		-3.83E-01	3.27E-02		-1.11E+00	4.26E-10	Down			Unigene19125_All//2.00E-104//gi|109845370|gb|DW243928.1|DW243928				
Unigene19126_All	876	0.12	1.27	0.12	0.23	0.31	0.62	11.10	13.22	216.98	3.41E+00	1.24E-04	Up	2.51E-02	1.00E+00		4.67E-01	8.17E-01		1.44E+00	1.93E-01		2.52E-01	1.15E-01		4.29E+00	0.00E+00	Up							ESTscan +
Unigene19131_All	595	2.11	10.05	2.33	1.17	0.58	1.37	1.14	1.69	20.96	2.25E+00	1.17E-14	Up	1.41E-01	7.97E-01		-1.02E+00	2.25E-01		2.21E-01	7.78E-01		5.68E-01	3.79E-01		4.20E+00	8.66E-68	Up	Unigene19131_All//gi|15233117|ref|NP_191705.1|//2.00E-30//BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|297820998|ref|XP_002878382.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata] >gi|4689366|gb|AAD27870.1|AF134155_1 BRH1 RING finger protein [Arabidopsis thaliana] >gi|6850837|emb|CAB71076.1| RING finger protein [Arabidopsis thaliana] >gi|21554590|gb|AAM63625.1| RING finger protein [Arabidopsis thaliana] >gi|297324220|gb|EFH54641.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata]	Unigene19131_All//1.00E-26//AT3G61460| BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding	Unigene19131_All//2.00E-25//gi|109831400|gb|DW229959.1|DW229959		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene19136_All	482	1.30	0.63	0.66	1.24	0.57	1.12	2.19	0.17	0.58	-1.05E+00	2.50E-01		-9.75E-01	3.16E-01		-1.12E+00	2.26E-01		-1.41E-01	8.79E-01		-3.66E+00	1.31E-05	Down	-1.92E+00	2.21E-03		Unigene19136_All//gi|225463317|ref|XP_002267748.1|//2.00E-11//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene19136_All//6.00E-06//AT3G23740| unknown protein	Unigene19136_All//3.00E-126//ES835012				nr -
Unigene19139_All	394	1.73	1.54	1.62	2.15	1.31	0.00	0.75	0.64	0.61	-1.62E-01	8.32E-01		-9.01E-02	9.22E-01		-7.13E-01	3.36E-01		-1.11E+01	2.43E-05	Down	-2.39E-01	8.40E-01		-3.08E-01	7.75E-01		Unigene19139_All//gi|5802244|gb|AAD51625.1|AF169022_1/3.00E-65//seed maturation protein PM37 [Glycine max]	Unigene19139_All//2.00E-62//AT3G44110| ATJ3; protein binding	Unigene19139_All//0.00E+00//ES791525		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene1914_All	606	6.73	3.68	3.69	39.79	22.22	9.39	4.88	4.41	2.50	-8.72E-01	3.89E-03		-8.68E-01	5.93E-03		-8.41E-01	2.78E-16		-2.08E+00	8.57E-57	Down	-1.46E-01	6.73E-01		-9.67E-01	2.12E-03		Unigene1914_All//gi|33465891|gb|AAQ19327.1|//1.00E-11//bZIP-like protein [Oryza sativa Japonica Group]		Unigene1914_All//6.00E-106//ES821533				nr -
Unigene19141_All	1645	0.00	0.00	0.00	0.00	0.00	0.05	18.92	4.42	11.29	null	null		null	null		null	null		5.78E+00	4.77E-01		-2.10E+00	6.26E-83	Down	-7.45E-01	7.34E-18		Unigene19141_All//gi|38344537|emb|CAD40973.2|//1.00E-118//OSJNBa0027P08.5 [Oryza sativa (japonica cultivar-group)]	Unigene19141_All//8.00E-76//AT3G05390| unknown protein					nr +
Unigene19143_All	399	0.13	4.32	5.47	172.54	292.40	178.96	26.81	49.23	39.14	5.04E+00	1.32E-08	Up	5.38E+00	9.85E-11	Up	7.61E-01	3.84E-63		5.27E-02	5.03E-01		8.77E-01	1.36E-14		5.46E-01	8.95E-06		Unigene19143_All//gi|33111959|emb|CAE12163.1|//9.00E-53//expansin-like protein [Quercus robur]	Unigene19143_All//4.00E-28//AT4G38400| ATEXLA2 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A2)	Unigene19143_All//0.00E+00//gi|54122976|gb|CO498485.1|CO498485			GO:0000003//GO:0000902//GO:0005618//GO:0009827	nr -
Unigene19144_All	565	0.00	0.09	0.00	6.97	3.23	3.36	10.78	10.95	15.23	6.49E+00	6.17E-01		null	null		-1.11E+00	1.19E-04	Down	-1.05E+00	5.70E-04	Down	2.29E-02	9.43E-01		4.99E-01	3.57E-03		Unigene19144_All//gi|196990035|gb|AAL91002.1|//2.00E-59//asparagine synthetase [Securigera parviflora]	Unigene19144_All//1.00E-57//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene19144_All//6.00E-106//gi|84158770|gb|DN827834.1|DN827834		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0006528//GO:0009064//GO:0009267//GO:0009642//GO:0009746//GO:0016884//GO:0032559//GO:0034285	nr +
Unigene19145_All	483	0.54	0.00	0.55	1.75	0.21	0.28	2.89	0.35	1.65	-9.08E+00	6.71E-02		2.53E-02	1.00E+00		-3.04E+00	5.54E-04	Down	-2.64E+00	3.54E-03		-3.06E+00	2.69E-06	Down	-8.08E-01	9.58E-02		Unigene19145_All//gi|115450855|ref|NP_001049028.1|//8.00E-17//Os03g0159200 (Oryza sativa Japonica Group) >gi|108706291|gb|ABF94086.1| XS domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547499|dbj|BAF10942.1| Os03g0159200 [Oryza sativa Japonica Group]	Unigene19145_All//7.00E-12//AT3G22435| XS domain-containing protein					nr +
Unigene19146_All	353	0.59	0.00	0.00	1.13	0.78	1.79	0.36	1.42	2.48	-9.21E+00	1.22E-01		-9.21E+00	1.46E-01		-5.33E-01	6.16E-01		6.66E-01	4.92E-01		1.98E+00	5.74E-02		2.79E+00	5.37E-04	Up							
Unigene19147_All	541	0.00	0.00	0.00	0.09	0.00	0.00	26.02	3.71	9.20	null	null		null	null		-6.53E+00	5.56E-01		-6.53E+00	6.36E-01		-2.81E+00	3.42E-53	Down	-1.50E+00	7.45E-25	Down	Unigene19147_All//gi|224137856|ref|XP_002326457.1|//1.00E-14//aquaporin, MIP family, TIP subfamily [Populus trichocarpa] >gi|222833779|gb|EEE72256.1| aquaporin, MIP family, TIP subfamily [Populus trichocarpa]	Unigene19147_All//6.00E-07//AT5G47450| AtTIP2;3; ammonia transporter/ methylammonium transmembrane transporter/ water channel	Unigene19147_All//4.00E-42//TC145045			GO:0006810//GO:0031090//GO:0031224//GO:0031410//GO:0042995//GO:0043231	nr -
Unigene19148_All	366	18.87	11.08	36.66	15.65	11.67	13.20	1.39	0.34	0.00	-7.69E-01	5.66E-04		9.58E-01	2.92E-09		-4.24E-01	8.41E-02		-2.45E-01	3.90E-01		-2.02E+00	5.20E-02		-1.04E+01	5.54E-04	Down	Unigene19148_All//gi|224081367|ref|XP_002306384.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222855833|gb|EEE93380.1| predicted protein [Populus trichocarpa]						nr -
Unigene1915_All	1326	1.34	0.38	0.88	8.26	4.41	2.76	1.66	0.95	1.20	-1.81E+00	6.59E-04	Down	-6.03E-01	2.42E-01		-9.05E-01	1.22E-08		-1.58E+00	5.25E-18	Down	-8.10E-01	3.61E-02		-4.64E-01	2.20E-01		Unigene1915_All//gi|124359162|gb|AB005685.1|//6.00E-19//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene1915_All//1.00E-06//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene1915_All//1.00E-87//ES821533				nr +
Unigene19150_All	320	0.49	0.32	0.00	8.41	3.23	2.26	1.45	0.00	0.12	-6.31E-01	7.28E-01		-8.94E+00	2.45E-01		-1.38E+00	1.60E-04	Down	-1.90E+00	4.31E-06	Down	-1.05E+01	1.71E-03		-3.55E+00	6.86E-03				Unigene19150_All//2.00E-95//ES822077				
Unigene19154_All	1216	14.84	10.25	6.74	0.78	0.42	0.45	0.03	0.07	0.07	-5.34E-01	3.91E-05		-1.14E+00	5.69E-16	Down	-8.74E-01	2.10E-01		-8.04E-01	2.77E-01		9.81E-01	7.31E-01		9.12E-01	7.50E-01		Unigene19154_All//gi|33411520|dbj|BAC81420.1|//1.00E-157//nitrate transporter [Prunus persica]	Unigene19154_All//2.00E-106//AT1G12110| NRT1.1; nitrate transmembrane transporter/ transporter	Unigene19154_All//6.00E-151//TC165574				nr -
Unigene19156_All	386	0.27	1.05	0.28	0.90	0.54	1.87	1.42	5.20	0.93	1.95E+00	1.44E-01		2.53E-02	1.00E+00		-7.55E-01	5.67E-01		1.05E+00	2.35E-01		1.87E+00	2.84E-05	Up	-6.16E-01	4.68E-01		Unigene19156_All//gi|30678996|ref|NP_567218.2|//3.00E-07//systemic acquired resistance (SAR) regulator protein NIMIN-1-related [Arabidopsis thaliana] >gi|12057175|emb|CAC19852.1| NIMIN-1b protein [Arabidopsis thaliana] >gi|109916491|gb|ABG48424.1| At4g01895 [Arabidopsis thaliana]		Unigene19156_All//5.00E-13//gi|48753792|gb|CO084311.1|CO084311				nr -
Unigene19157_All	369	1.56	3.43	7.07	2.57	1.40	0.61	0.69	0.23	0.22	1.14E+00	6.20E-02		2.18E+00	2.86E-06	Up	-8.74E-01	2.10E-01		-2.07E+00	8.57E-03		-1.60E+00	3.11E-01		-1.67E+00	2.56E-01				Unigene19157_All//4.00E-07//DW494026				
Unigene19158_All	282	0.37	0.36	0.00	5.48	1.22	4.00	5.40	16.30	2.40	-4.62E-02	9.89E-01		-8.54E+00	3.94E-01		-2.16E+00	7.69E-05	Down	-4.52E-01	4.24E-01		1.89E+00	4.35E-09	Up	-1.17E+00	1.25E-02								
Unigene19159_All	926	1.02	0.00	0.29	1.13	0.74	1.66	0.59	0.27	0.99	-9.99E+00	1.46E-05	Down	-1.82E+00	2.53E-02		-6.03E-01	3.67E-01		5.54E-01	3.36E-01		-1.13E+00	2.18E-01		7.37E-01	2.43E-01		Unigene19159_All//gi|297821058|ref|XP_002878412.1|//3.00E-51//EMB1703 [Arabidopsis lyrata subsp. lyrata] >gi|297324250|gb|EFH54671.1| EMB1703 [Arabidopsis lyrata subsp. lyrata]	Unigene19159_All//2.00E-39//AT3G61780| emb1703 (embryo defective 1703)				GO:0005488//GO:0032502	nr +
Unigene1916_All	1198	1.09	0.55	1.11	4.74	3.51	1.92	1.06	0.63	0.86	-9.90E-01	9.23E-02		2.54E-02	9.85E-01		-4.35E-01	7.84E-02		-1.30E+00	2.53E-07	Down	-7.54E-01	1.63E-01		-2.92E-01	5.99E-01		Unigene1916_All//gi|124359162|gb|AB005685.1|//9.00E-19//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene1916_All//1.00E-07//AT3G09510| nucleic acid binding	Unigene1916_All//1.00E-105//ES821533				nr +
Unigene19160_All	422	0.00	0.00	0.00	0.00	0.00	0.11	5.01	1.78	54.66	null	null		null	null		null	null		6.74E+00	6.96E-01		-1.49E+00	3.03E-04	Down	3.45E+00	3.75E-107	Up	Unigene19160_All//gi|224121846|ref|XP_002318687.1|//1.00E-26//cytochrome P450 [Populus trichocarpa] >gi|222859360|gb|EEE96907.1| cytochrome P450 [Populus trichocarpa]	Unigene19160_All//9.00E-22//AT3G53290| CYP71B30P; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene19160_All//1.00E-72//gi|109825823|gb|DW224545.1|DW224545		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016020//GO:0016491//GO:0031410//GO:0043231	nr +
Unigene19161_All	448	4.79	14.70	8.68	0.56	1.61	1.31	0.19	0.19	0.09	1.62E+00	1.26E-10	Up	8.58E-01	8.06E-03		1.54E+00	8.92E-02		1.24E+00	2.31E-01		-1.69E-02	1.01E+00		-1.09E+00	6.76E-01		Unigene19161_All//gi|221065988|ref|XP_002301993.1|//2.00E-27//cytochrome P450 [Populus trichocarpa] >gi|222843719|gb|EEE91266.1| cytochrome P450 [Populus trichocarpa]	Unigene19161_All//2.00E-17//AT4G31500| CYP83B1 (CYTOCHROME P450 MONOOXYGENASE 83B1); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding	Unigene19161_All//1.00E-112//TC135538		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0004497//GO:0005506	nr -
Unigene19163_All	797	0.07	1.02	4.94	0.00	0.00	0.40	53.58	29.63	8.20	3.95E+00	7.52E-04	Up	6.24E+00	2.76E-20	Up	null	null		8.63E+00	4.08E-02		-8.55E-01	1.64E-29		-2.71E+00	9.94E-159	Down	Unigene19163_All//gi|145408590|ref|XP_001152214.1|//2.00E-18//O8F124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| O8F124 [Pinus koraiensis]		Unigene19163_All//1.00E-39//DW502679			GO:0009536	nr -

Unigene19164_All	586	0.54	0.00	0.00	3.66	0.24	2.31	2.96	0.50	1.63	-9.07E+00	3.66E-02		-9.07E+00	4.92E-02		-3.96E+00	1.02E-11	Down	-6.61E-01	1.40E-01		-2.57E+00	1.60E-06	Down	-8.58E-01	4.40E-02		Unigene19164_All//gi|15232315|ref|NP_188700.1|//1.00E-12//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|75299591|sp|Q8GX73.1|BH123_ARATH RecName: Full=Transcription factor bHLH123; AltName: Full=Transcription factor EN 63; AltName: Full=bHLH transcription factor bHLH123; AltName: Full=Basic helix-loop-helix protein 123; Short=bHLH 123; Short=AtbHLH123	Unigene19164_All//8.00E-12//AT3G20640| ethylene-responsive protein -related	Unigene19164_All//1.00E-88//gi|109891292|gb|DW520255.1|DW520255	bHLH			nr +
Unigene19165_All	2658	0.00	41.35	13.32	0.04	0.05	0.00	0.02	0.00	0.00	1.53E+01	0.00E+00	Up	1.37E+01	5.63E-201	Up	4.66E-01	8.77E-01		-5.23E+00	4.00E-01		-3.99E+00	6.58E-01		-3.99E+00	6.13E-01		Unigene19165_All//gi|298711838|emb|CBJ32863.1|//0.00E+00//EF2, translation elongation factor 2 [Ectocarpus siliculosus]	Unigene19165_All//2.00E-16//TC161459				GO:0000166//GO:0006950//GO:0008135//GO:0009536//GO:0016020//GO:0031981//GO:0046914	nr +
Unigene19168_All	527	2.88	0.00	0.00	1.70	1.50	1.03	2.73	0.00	0.23	-1.15E+01	8.33E-09	Down	-1.15E+01	2.73E-08	Down	-1.79E-01	8.15E-01		-7.26E-01	3.45E-01		-1.14E+01	3.33E-10	Down	-3.59E+00	1.22E-07	Down	Unigene19168_All//gi|84405469|ref|NP_566822.1|//3.00E-27//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene19168_All//1.00E-13//AT3G27640| transducin family protein / WD-40 repeat family protein	Unigene19168_All//0.00E+00//gi|21099819|gb|BQ412132.1|BQ412132			GO:0031461//GO:0043231	nr +
Unigene19170_All	387	0.54	0.00	0.00	0.51	0.18	1.98	1.97	7.56	9.99	-9.08E+00	1.22E-01		-9.08E+00	1.46E-01		-1.53E+00	4.16E-01		1.95E+00	3.23E-02		1.94E+00	1.05E-07	Up	2.34E+00	1.11E-12	Up								ESTscan -
Unigene19172_All	423	2.84	4.43	7.43	2.24	0.90	0.32	3.30	4.94	1.41	6.40E-01	1.80E-01		1.38E+00	2.65E-04	Up	-1.32E+00	5.61E-02		-2.80E+00	1.18E-03		5.83E-01	1.49E-01		-1.22E+00	1.33E-02					Unigene19172_All//3.00E-76//gi|109877926|gb|DW506899.1|DW506899					
Unigene19177_All	522	0.20	0.00	0.10	5.73	6.60	3.46	2.75	0.80	0.46	-7.65E+00	3.73E-01		-9.75E-01	7.21E-01		2.04E-01	5.96E-01		-7.26E-01	4.49E-02		-1.78E+00	8.40E-04	Down	-2.59E+00	8.29E-06	Down								
Unigene19182_All	243	3.66	1.25	1.75	3.69	5.53	3.35	12.01	5.33	3.77	-1.55E+00	4.56E-02		-1.06E+00	1.76E-01		5.83E-01	3.42E-01		-1.41E-01	8.48E-01		-1.17E+00	4.27E-04	Down	-1.67E+00	1.14E-06	Down				Unigene19182_All//2.00E-23//gi|11202143|gb|BF271148.1|BF271148					
Unigene19183_All	924	0.00	1.37	0.12	0.32	0.30	0.10	17.48	7.78	11.81	1.04E+01	2.86E-07	Up	6.85E+00	3.99E-01		-1.18E-01	9.01E-01		-1.73E+00	2.89E-01		-1.17E+00	5.45E-19	Down	-5.65E-01	2.71E-06		Unigene19183_All//gi|255575239|ref|XP_002528523.1|//2.00E-21//conserved hypothetical protein [Ricinus communis] >gi|223532025|gb|EEF33835.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene19184_All	897	0.00	1.07	5.52	0.00	0.54	0.10	0.00	0.00	0.00	1.01E+01	1.38E-05	Up	1.24E+01	1.53E-27	Up	9.07E+00	5.07E-03		6.65E+00	4.77E-01		null	null		null	null		Unigene19184_All//gi|84508536|ref|YP_448700.1|//1.00E-117//cytochrome c oxidase subunit I [Dictyota dichotoma] >gi|45925704|gb|AAS79085.1| cytochrome oxidase subunit I [Dictyota dichotoma]	Unigene19184_All//3.00E-89//ATMG01360| cytochrome c oxidase subunit 1	Unigene19184_All//2.00E-08//TC149581		ko00190|Oxidative phosphorylation		nr +
Unigene19185_All	696	0.15	0.44	0.00	0.14	0.00	0.00	44.04	36.27	16.20	1.54E+00	3.23E-01		-7.23E+00	3.94E-01		-7.16E+00	3.13E-01		-7.16E+00	4.00E-01		-2.80E-01	1.57E-03		-1.44E+00	3.57E-50	Down	Unigene19185_All//gi|30725288|gb|AAF37666.1|//1.00E-11//At3g14280 [Arabidopsis thaliana]	Unigene19185_All//7.00E-13//AT3G14280| unknown protein	Unigene19185_All//2.00E-16//gi|109877131|gb|DW506105.1|DW506105				nr +
Unigene19187_All	637	2.30	0.00	0.33	5.63	2.70	1.77	0.33	0.26	0.06	-1.12E+01	1.65E-08	Down	-2.78E+00	9.28E-05	Down	-1.06E+00	4.95E-04	Down	-1.67E+00	9.86E-07	Down	-3.38E-01	8.12E-01		-2.41E+00	1.95E-01									
Unigene19189_All	327	0.00	2.79	0.00	0.61	0.63	1.52	0.39	1.15	0.97	1.14E+01	2.62E-05	Up	null	null		5.23E-02	9.89E-01		1.32E+00	2.52E-01		1.57E+00	1.95E-01		1.33E+00	2.93E-01		Unigene19189_All//gi|224125160|ref|XP_002329908.1|//8.00E-16//predicted protein [Populus trichocarpa] >gi|222871145|gb|EEF08276.1| predicted protein [Populus trichocarpa]		Unigene19189_All//1.00E-87//TC178449				nr +
Unigene19191_All	415	0.50	0.49	1.41	3.72	1.16	1.41	3.97	1.61	1.25	-4.62E-02	9.88E-01		1.48E+00	1.53E-01		-1.68E+00	1.27E-03		-1.40E+00	1.06E-02		-1.30E+00	5.42E-03		-1.67E+00	3.93E-04	Down	Unigene19191_All//gi|269927077|gb|ACZ52907.1|//3.00E-33//proliferating cell nuclear antigen gene-controlling element binding factor [Pisum sativum]	Unigene19191_All//3.00E-29//AT5G23280| TCP family transcription factor, putative	Unigene19191_All//6.00E-102//gi|13248361|gb|BF275435.2|BF275435	TCP		GO:0010468	nr -
Unigene19192_All	621	0.67	0.16	3.34	1.44	0.78	4.87	0.41	1.62	0.13	-2.05E+00	1.21E-01		2.31E+00	1.92E-05	Up	-8.95E-01	2.14E-01		1.75E+00	4.98E-06	Up	1.98E+00	3.46E-03		-1.67E+00	2.56E-01		Unigene19192_All//gi|297802216|ref|XP_002869007.1|//4.00E-50//PLA IVA/PLP1 [Arabidopsis lyrata subsp. lyrata] >gi|297314843|gb|EFH45266.1| PLA IVA/PLP1 [Arabidopsis lyrata subsp. lyrata]	Unigene19192_All//3.00E-48//AT4G37070| patatin, putative	Unigene19192_All//1.00E-48//gi|48827706|gb|CO126096.1|CO126096			GO:0008152	nr +
Unigene19195_All	382	0.27	0.13	0.14	1.30	0.00	0.71	4.10	3.94	4.07	-1.05E+00	6.85E-01		-9.74E-01	7.21E-01		-1.03E+01	8.98E-04	Down	-8.78E-01	4.20E-01		-5.61E-02	9.21E-01		-9.90E-03	9.76E-01									
Unigene19197_All	406	2.06	1.50	1.71	2.58	0.25	0.22	1.25	0.82	0.79	-4.61E-01	5.43E-01		-2.74E-01	7.05E-01		-3.34E+00	3.42E-05	Down	-3.53E+00	9.34E-05	Down	-6.02E-01	5.31E-01		-6.71E-01	4.48E-01					Unigene19197_All//2.00E-40//gi|11199855|gb|BF268860.1|BF268860					
Unigene19198_All	626	112.33	225.75	204.49	238.17	200.29	259.87	124.61	546.08	76.43	1.01E+00	1.19E-102	Up	8.64E-01	3.35E-70		-2.50E-01	6.03E-11		1.26E-01	2.27E-03		2.13E+00	0.00E+00	Up	-7.05E-01	1.73E-39		Unigene19198_All//gi|157781191|gb|ABV71991.1|//7.00E-46//thioredoxin h1 [Glycine max]	Unigene19198_All//1.00E-45//AT3G51030| ATTRX1; oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	Unigene19198_All//0.00E+00//gi|21095736|gb|BQ408049.1|BQ408049			GO:0006091//GO:0015036//GO:0018904//GO:0019725//GO:0030234//GO:0044093//GO:0044444//GO:0051234	nr -
Unigene1920_All	1036	17.73	14.92	21.95	8.17	8.68	7.85	2.04	0.77	1.73	-2.49E-01	6.52E-02		3.08E-01	1.16E-02		8.59E-02	7.32E-01		-5.89E-02	7.88E-01		-1.41E+00	5.54E-04	Down	-2.38E-01	5.66E-01		Unigene1920_All//gi|20453183|gb|AAM19832.1|//1.00E-130//At2g23390/F26B6.4 [Arabidopsis thaliana] >gi|25090334|gb|AAN72279.1| At2g23390/F26B6.4 [Arabidopsis thaliana]	Unigene1920_All//2.00E-125//AT2G23390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF482 (InterPro:IPR007434), Acyl-CoA N-acyltransferase (InterPro:IPR016181); Has 1806 Blast hits to 1806 proteins in 374 species: Archae - 0; Bacteria - 707; Metazoa - 0; Fungi - 0; Plants - 15; Viruses - 0; Other Eukaryotes - 1084 (source: NCBI BLink).	Unigene1920_All//0.00E+00//DT460339				nr +
Unigene19200_All	303	1.04	2.68	1.58	5.75	1.59	3.13	1.40	1.66	1.31	1.37E+00	9.21E-02		6.10E-01	5.87E-01		-1.85E+00	1.66E-04	Down	-8.78E-01	7.90E-02		2.46E-01	7.84E-01		-8.58E-02	9.39E-01					Unigene19200_All//2.00E-101//ES833858					
Unigene19201_All	513	1.84	0.20	1.25	6.99	4.43	1.76	0.91	1.22	0.23	-3.22E+00	6.77E-04	Down	-5.60E-01	4.39E-01		-6.58E-01	3.42E-02		-1.99E+00	2.14E-08	Down	4.31E-01	6.32E-01		-1.96E+00	5.82E-02									
Unigene19204_All	819	0.26	0.00	0.78	1.34	1.98	0.44	11.77	8.17	4.67	-8.00E+00	1.22E-01		1.61E+00	1.11E-01		5.63E-01	3.15E-01		-1.60E+00	1.95E-02		-5.28E-01	1.37E-03		-1.33E+00	1.25E-14	Down	Unigene19204_All//gi|255580497|ref|XP_002531073.1|//2.00E-40//conserved hypothetical protein [Ricinus communis] >gi|223529319|gb|EEF31287.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene19205_All	1453	0.00	14.19	4.98	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	1.15E-118	Up	1.23E+01	1.78E-40	Up	null	null		null	null		null	null		null	null		Unigene19205_All//gi|301120388|ref|XP_002907921.1|//1.00E-124//polyadenylate-binding protein 1-B [Phytophthora infestans T30-4] >gi|262102952|gb|EE761004.1| polyadenylate-binding protein 1-B [Phytophthora infestans T30-4]	Unigene19205_All//6.00E-113//AT1G49760| PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor			ko03040|Spliceosome		nr -
Unigene19209_All	395	9.01	13.08	21.84	13.24	22.23	17.38	12.52	12.59	13.62	5.39E-01	4.21E-02		1.28E+00	1.91E-09	Up	7.47E-01	4.98E-05		3.92E-01	9.45E-02		7.80E-03	1.01E+00		1.21E-01	6.29E-01		Unigene19209_All//gi|115453347|ref|NP_001050274.1|//7.00E-30//Os03g0390200 [Oryza sativa Japonica Group] >gi|71153740|sp|Q75LK7.1|SAPK1_ORYSJ RecName: Full=Serine/threonine-protein kinase SAPK1; AltName: Full=Osmotic stress/abscisic acid-activated protein kinase 1 >gi|37981924|gb|AAR06370.1| abscisic acid-inducible protein kinase [Oryza sativa Japonica Group] >gi|46917330|dbj|BAD17997.1| serine/threonine protein kinase SAPK1 [Oryza sativa Japonica Group] >gi|113548745|dbj|BAF12188.1| Os03g0390200 [Oryza sativa Japonica Group]	Unigene19209_All//3.00E-30//AT4G40010| SNRK2.7 (SNF1-RELATED PROTEIN KINASE 2.7); kinase	Unigene19209_All//6.00E-142//TC172077			GO:0000166//GO:0004672	nr -
Unigene19210_All	801	0.39	0.38	0.27	0.00	0.09	0.28	4.43	5.27	8.90	-4.64E-02	9.85E-01		-5.60E-01	6.64E-01		6.43E+00	6.10E-01		8.14E+00	1.19E-01		2.49E-01	4.04E-01		1.01E+00	2.61E-07	Up	Unigene19210_All//gi|42572503|ref|NP_974347.1|//6.00E-06//NADK1 (NAD KINASE 1); NAD+ kinase/ NADH kinase/ calmodulin binding [Arabidopsis thaliana] >gi|94717660|sp|Q56YN3.2|NADK1_ARATH RecName: Full=NAD(H) kinase 1; Short=AtNADK-1 >gi|39843359|gb|AAR32133.1| NADK1 [Arabidopsis thaliana]	Unigene19210_All//3.00E-07//AT3G21070| NADK1 (NAD KINASE 1); NAD+ kinase/ NADH kinase/ calmodulin binding	Unigene19210_All//6.00E-39//gi|73864229|gb|DT466968.1|DT466968		ko00760|Nicotinate and nicotinamide metabolism		nr -
Unigene19212_All	738	9.07	1.99	1.30	1.96	1.68	0.86	0.23	0.68	0.00	-2.19E+00	6.37E-16	Down	-2.80E+00	4.79E-20	Down	-2.21E-01	7.05E-01		-1.19E+00	3.43E-02		1.57E+00	1.18E-01		-7.84E+00	1.08E-01					Unigene19212_All//4.00E-09//TC141372					
Unigene19213_All	415	3.53	1.22	3.98	8.04	3.90	8.60	2.04	1.11	0.67	-1.53E+00	7.80E-03		1.72E-01	7.27E-01		-1.04E+00	9.95E-04	Down	9.63E-02	7.90E-01		-8.79E-01	2.07E-01		-1.60E+00	2.02E-02		Unigene19213_All//gi|297805312|ref|XP_002870540.1|//4.00E-17//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297316376|gb|EFH46799.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene19213_All//1.00E-09//AT5G37570| pentatricopeptide (PPR) repeat-containing protein	Unigene19213_All//3.00E-147//BM360671				nr +
Unigene19219_All	251	3.75	0.81	1.91	4.37	3.29	1.44	3.71	0.83	0.48	-2.22E+00	6.65E-03		-9.75E-01	2.00E-01		-4.07E-01	5.61E-01		-1.60E+00	1.95E-02		-2.15E+00	2.95E-03		-2.96E+00	1.72E-04	Down				Unigene19219_All//3.00E-22//TC132184					
Unigene19221_All	666	398.30	390.29	518.67	32.24	48.81	36.89	1.33	0.19	0.78	-2.93E-02	4.29E-01		3.81E-01	1.18E-43		5.98E-01	7.88E-12		1.95E-01	1.06E-01		-2.82E+00	5.65E-04	Down	-7.78E-01	2.20E-01		Unigene19221_All//gi|224101127|ref|XP_002312153.1|//1.00E-77//light-harvesting complex II protein Lhcb8 [Populus trichocarpa] >gi|222851973|gb|EEE89520.1| light-harvesting complex II protein Lhcb8 [Populus trichocarpa]	Unigene19221_All//4.00E-78//AT2G40100| LHCB4.3 (light harvesting complex PSII); chlorophyll binding	Unigene19221_All//0.00E+00//gi|109877290|gb|DW506263.1|DW506263		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009534//GO:0009639//GO:0043234//GO:0046906	nr +
Unigene19222_All	366	29.31	33.36	26.63	73.63	39.14	41.96	249.87	204.87	75.43	1.87E-01	2.88E-01		-1.38E-01	4.91E-01		-9.12E-01	8.32E-21		-8.12E-01	2.93E-15		-2.87E-01	3.04E-09		-1.73E+00	2.09E-192	Down				Unigene19222_All//5.00E-161//gi|164286470|gb|ES797040.1|ES797040					
Unigene19225_All	273	608.68	621.40	538.55	119.15	157.67	116.63	62.88	30.31	43.20	2.98E-02	5.39E-01		-1.77E-01	1.92E-05		4.04E-01	7.34E-08		-3.09E-02	7.90E-01		-1.05E+00	3.76E-17	Down	-5.42E-01	3.29E-06		Unigene19225_All//gi|121353|sp|P15102.1|GLNA4_PHAVU//2.00E-49//RecName: Full=Glutamine synthetase leaf isozyme, chloroplastic; AltName: Full=Isozyme delta; AltName: Full=Glutamate--ammonia ligase; Flags: Precursor	Unigene19225_All//1.00E-47//AT5G35630| GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase	Unigene19225_All//8.00E-153//gi|109836985|gb|DW235546.1|DW235546		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006541//GO:0009536//GO:0016211//GO:0032559//GO:0071941	nr -

Unigene19227_All	568	1.66	0.00	0.66	12.28	10.19	0.95	2.38	0.15	0.35	-1.07E+01	1.46E-05	Down	-1.34E+00	8.48E-02		-2.70E-01	2.56E-01		-3.69E+00	2.02E-30	Down	-4.02E+00	1.80E-07	Down	-2.76E+00	7.51E-06	Down	Unigene19227_All//gi|297842271|ref|XP_002889017.1|//6.00E-24//myb family transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297334858|gb|EFH65276.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene19227_All//4.00E-25//AT1G19510| ATRL5 (ARABIDOPSIS RAD-LIKE 5); DNA binding / transcription factor	Unigene19227_All//0.00E+00//gi|109879490|gb|DW508460.1|DW508460	MYB-related		GO:0001071//GO:0000676//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene19228_All	775	3.11	0.46	1.44	1.22	2.18	1.34	0.98	0.92	1.39	-2.76E+00	7.95E-08	Down	-1.11E+00	1.09E-02		8.34E-01	1.04E-01		1.34E-01	8.58E-01		-9.91E-02	8.96E-01		4.99E-01	3.90E-01		Unigene19228_All//gi|225426243|ref|XP_002264080.1|//2.00E-42//PREDICTED: similar to ABIL3 (ABL INTERACTOR-LIKE PROTEIN 3) [Vitis vinifera]	Unigene19228_All//7.00E-36//AT3G49290| ABIL2 (ABL INTERACTOR-LIKE PROTEIN 2)	Unigene19228_All//0.00E+00//CO113243			GO:0048513	nr -
Unigene19229_All	253	32.47	48.87	27.15	80.14	139.24	352.74	76.87	46.42	128.33	5.90E-01	2.38E-04		-2.58E-01	2.45E-01		7.97E-01	8.13E-21		2.14E+00	6.75E-212	Up	-7.28E-01	9.99E-11		7.39E-01	2.93E-18		Unigene19229_All//gi|164668308|gb|ABK60195.2|//3.00E-41//PIP2 protein [Gossypium hirsutum]	Unigene19229_All//2.00E-38//AT2G37170| PIP2B (PLASMA MEMBRANE INTRINSIC PROTEIN 2); water channel	Unigene19229_All//6.00E-141//gi|80999917|gb|BM359171.1|BM359171			GO:0006810//GO:0031224	nr +
Unigene19923_All	2694	6.64	4.19	5.51	2.61	3.22	2.36	10.31	4.98	5.96	-6.63E-01	4.15E-07		-2.68E-01	5.93E-02		3.05E-01	1.41E-01		-1.41E-01	6.08E-01		-1.05E+00	3.85E-27	Down	-7.91E-01	1.09E-17		Unigene19923_All//gi|115454097|ref|NP_001050649.1|//0.00E+00//Os03g0609800 [Oryza sativa Japonica Group] >gi|113549120|dbj|BAF12563.1|Os03g0609800 [Oryza sativa Japonica Group]	Unigene19923_All//3.00E-180//AT2G14820| NPY2 (NAKED PINS IN YUC MUTANTS 2); protein binding / signal transducer	Unigene19923_All//0.00E+00//TC161734				nr +
Unigene19232_All	517	2.73	1.08	0.00	3.18	3.40	1.92	1.72	1.13	1.23	-1.34E+00	2.00E-02		-1.14E+01	1.01E-07	Down	9.54E-02	8.67E-01		-7.26E-01	1.68E-01		-6.02E-01	3.85E-01		-4.78E-01	4.57E-01		Unigene19232_All//gi|145350620|ref|NP_194868.2|//7.00E-31//DNA-directed DNA polymerase/ damaged DNA binding [Arabidopsis thaliana] >gi|156254746|gb|ABL62813.1|cohesion establishment factor 7 [Arabidopsis thaliana]	Unigene19232_All//4.00E-29//AT4G31400| DNA-directed DNA polymerase/ damaged DNA binding	Unigene19232_All//6.00E-84//CO088747			GO:0003677//GO:0006259//GO:0034061	nr -
Unigene19233_All	1065	0.00	7.09	4.15	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	3.63E-43	Up	1.20E+01	1.55E-24	Up	null	null		null	null		null	null		null	null		Unigene19233_All//gi|558652|emb|CAA57646.1|//5.00E-21//Voltage dependent anion channel (VDAC) [Triticum aestivum]	Unigene19233_All//5.00E-20//AT5G15090| VDAC3 (VOLTAGE DEPENDENT ANION CHANNEL 3); voltage-gated anion channel					nr +
Unigene19235_All	469	1.78	0.11	1.48	2.23	1.40	2.50	0.45	0.45	1.27	-4.05E+00	4.66E-04	Down	-2.74E-01	7.05E-01		-6.77E-01	3.14E-01		1.67E-01	7.91E-01		-1.64E-02	1.02E+00		1.50E+00	7.88E-02				Unigene19235_All//3.00E-42//TC178837				
Unigene19237_All	252	85.54	95.51	275.34	171.38	142.39	184.78	113.08	25.87	55.17	1.59E-01	1.92E-01		1.69E+00	5.85E-109	Up	-2.67E-01	5.16E-04		1.09E-01	2.28E-01		-2.13E+00	2.07E-77	Down	-1.04E+00	5.04E-28	Down	Unigene19237_All//gi|197259944|gb|ACH56521.1|//1.00E-20//chalcone synthase [Gossypium hirsutum]	Unigene19237_All//3.00E-12//AT5G13930| TT4 (TRANSPARENT TESTA 4); naringenin-chalcone synthase	Unigene19237_All//5.00E-126//gi|109837795|gb|DW236356.1|DW236356		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant	GO:0009699//GO:0016747	nr -
Unigene19239_All	1804	0.20	0.76	0.94	0.28	0.23	0.10	1.90	5.28	9.56	1.90E+00	2.58E-03		2.22E+00	2.12E-04	Up	-2.69E-01	8.02E-01		-1.46E+00	1.93E-01		1.48E+00	3.59E-16	Up	2.33E+00	1.23E-53	Up	Unigene19239_All//gi|224138292|ref|XP_002326566.1|//0.00E+00//nbs-lrr resistance protein [Populus trichocarpa] >gi|222833888|gb|EEE72365.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene19239_All//6.00E-60//AT3G07040| RPM1 (RESISTANCE TO P. SYRINGAE PV MACULICOLA 1); nucleotide binding / protein binding	Unigene19239_All//0.00E+00//DT461721		ko04626|Plant-pathogen interaction	GO:0000166	nr +
Unigene1924_All	2034	86.12	49.67	52.73	28.46	28.19	26.80	18.44	8.71	5.99	-7.94E-01	1.50E-85		-7.08E-01	6.36E-68		-1.38E-02	8.76E-01		-8.66E-02	3.03E-01		-1.08E+00	4.04E-38	Down	-1.62E+00	1.65E-72	Down	Unigene1924_All//gi|297798488|ref|XP_002867128.1|//5.00E-84//hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297312964|gb|EFH43387.1|hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene1924_All//6.00E-77//AT4G34215| hydrolase	Unigene1924_All//0.00E+00//TC165136				nr +
Unigene19240_All	433	0.48	0.00	0.00	1.38	3.82	0.63	4.20	0.58	9.66	-8.92E+00	1.22E-01		-8.92E+00	1.46E-01		1.47E+00	5.01E-03		-1.14E+00	2.43E-01		-2.86E+00	1.53E-07	Down	1.20E+00	6.75E-06	Up	Unigene19240_All//gi|162280537|gb|ABX82929.1|//1.00E-10//LO4 [Solanum pennellii]	Unigene19240_All//1.00E-07//AT3G28860| ABCB19; ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter	Unigene19240_All//4.00E-32//gi|78347390|gb|DT567664.1|DT567664			GO:0006810//GO:0015405//GO:0017111//GO:0031224//GO:0032559	nr -
Unigene19241_All	343	1.98	0.00	0.31	0.73	2.51	1.32	1.36	0.24	2.44	-1.10E+01	4.10E-04	Down	-2.68E+00	1.69E-02		1.79E+00	2.95E-02		8.59E-01	4.69E-01		-2.48E+00	3.38E-02		8.47E-01	2.03E-01		Unigene19241_All//gi|257831433|gb|ACV71017.1|//4.00E-34//UPA17 [Capsicum annuum]	Unigene19241_All//2.00E-29//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene19241_All//4.00E-164//TC169730	GRF		GO:0010468//GO:0016817//GO:0030528//GO:0032559//GO:0043231//GO:0048827	nr -
Unigene19244_All	603	1.21	0.42	0.53	1.82	1.94	1.27	2.24	0.42	1.65	-1.53E+00	7.78E-02		-1.20E+00	1.80E-01		9.54E-02	9.01E-01		-5.13E-01	4.58E-01		-2.43E+00	5.63E-05	Down	-4.42E-01	3.81E-01		Unigene19244_All//gi|296086263|emb|CBI31704.3|//1.00E-77//unnamed protein product [Vitis vinifera]	Unigene19244_All//2.00E-67//AT3G12590| unknown protein				GO:0043231	nr +
Unigene19246_All	422	35.96	12.37	10.09	61.15	41.94	58.33	197.17	56.35	67.03	-1.54E+00	4.61E-22	Down	-1.83E+00	6.19E-27	Down	-5.44E-01	2.72E-08		-6.81E-02	6.37E-01		-1.81E+00	4.80E-181	Down	-1.56E+00	9.08E-151	Down	Unigene19246_All//gi|195658063|gb|ACG48499.1|//7.00E-29//40S ribosomal protein S5 [Zea mays]	Unigene19246_All//3.00E-29//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	Unigene19246_All//0.00E+00//gi|21103007|gb|BQ415320.1|BQ415320		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene19248_All	399	92.84	82.93	60.19	289.65	232.68	119.08	126.52	20.32	37.34	-1.63E-01	8.29E-02		-6.25E-01	5.31E-12		-3.16E-01	3.58E-13		-1.28E+00	6.74E-135	Down	-2.64E+00	1.14E-176	Down	-1.76E+00	2.39E-109	Down	Unigene19248_All//gi|255571590|ref|XP_002526741.1|//2.00E-09//conserved hypothetical protein [Ricinus communis] >gi|223533930|gb|EEF35655.1|conserved hypothetical protein [Ricinus communis]		Unigene19248_All//8.00E-123//TC170152				nr +
Unigene19249_All	484	1.08	1.99	0.88	3.91	3.49	1.12	0.17	0.09	0.00	8.80E-01	2.13E-01		-2.97E-01	7.50E-01		-1.66E-01	7.56E-01		-1.80E+00	3.14E-04	Down	-1.02E+00	7.25E-01		-7.45E+00	3.59E-01								
Unigene19250_All	624	0.50	0.16	0.17	1.44	1.16	1.88	0.54	0.27	3.32	-1.63E+00	2.76E-01		-1.56E+00	3.30E-01		-3.10E-01	6.65E-01		3.89E-01	5.80E-01		-1.02E+00	4.00E-01		2.61E+00	5.56E-08	Up			Unigene19250_All//0.00E+00//BE054419				
Unigene19251_All	1023	0.00	0.59	0.68	0.29	2.69	1.85	1.61	0.08	3.66	9.22E+00	1.17E-03		9.40E+00	6.17E-04	Up	3.20E+00	4.11E-11	Up	2.67E+00	3.00E-06	Up	-4.30E+00	2.19E-09	Down	1.18E+00	2.94E-05	Up	Unigene19251_All//gi|297848820|ref|XP_002892291.1|//1.00E-127//type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 [Arabidopsis lyrata subsp. lyrata] >gi|297338133|gb|EFH68550.1| type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 [Arabidopsis lyrata subsp. lyrata]	Unigene19251_All//9.00E-125//AT2G32010| endonuclease/exonuclease/phosphatase family protein	Unigene19251_All//0.00E+00//gi|13248190|gb|BF274611.2|BF274611				nr -
Unigene19253_All	420	8.10	19.42	21.05	14.59	17.38	20.00	13.79	13.93	26.75	1.26E+00	3.42E-09	Up	1.38E+00	8.92E-11	Up	2.53E-01	2.98E-01		4.55E-01	2.48E-02		1.46E-02	9.83E-01		9.56E-01	3.41E-10		Unigene19253_All//gi|15233948|ref|NP_194205.1|//3.00E-28//AFC2 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 2); kinase/ protein kinase [Arabidopsis thaliana] >gi|1703200|sp|P51567.1|AFC2_ARATH RecName: Full=Serine/threonine-protein kinase AFC2 >gi|601789|gb|AAA57118.1| protein kinase [Arabidopsis thaliana] >gi|642130|dbj|BAA08214.1| protein kinase [Arabidopsis thaliana] >gi|4220516|emb|CAA22989.1|protein kinase (AFC2) [Arabidopsis thaliana] >gi|7269325|emb|CAB79384.1|protein kinase (AFC2) [Arabidopsis thaliana] >gi|109134165|gb|ABG25080.1|At4g24740 [Arabidopsis thaliana] >gi|110742385|dbj|BAE99115.1|protein kinase [Arabidopsis thaliana]	Unigene19253_All//2.00E-29//AT4G24740| AFC2 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 2); kinase/ protein kinase	Unigene19253_All//0.00E+00//TC152286			GO:0000166//GO:0004672//GO:0006396	nr -
Unigene19254_All	376	0.28	0.40	1.42	3.58	2.11	5.77	3.60	0.89	3.39	5.39E-01	7.79E-01		2.35E+00	5.88E-02		-7.64E-01	1.72E-01		6.89E-01	1.28E-01		-2.02E+00	4.01E-04	Down	-8.58E-02	8.66E-01		Unigene19254_All//gi|212292507|gb|ACJ24185.1|//1.00E-16//CAPRICE [Gossypium hirsutum] >gi|212292511|gb|ACJ24187.1|CAPRICE [Gossypium hirsutum] >gi|212292515|gb|ACJ24189.1|CAPRICE [Gossypium hirsutum] >gi|212292519|gb|ACJ24191.1|CAPRICE [Gossypium hirsutum]	Unigene19254_All//5.00E-14//AT2G46410| CPC (CAPRICE); DNA binding / transcription factor	Unigene19254_All//5.00E-19//TC166877	MYB-related		GO:0001071//GO:0003676//GO:0006351//GO:0009719//GO:0010033//GO:0010057//GO:0010468//GO:0043231	nr +
Unigene19255_All	218	8.88	12.78	13.19	6.63	5.05	8.91	14.55	28.76	29.79	5.26E-01	1.66E-01		5.71E-01	1.42E-01		-3.91E-01	5.05E-01		4.27E-01	3.94E-01		9.83E-01	3.90E-06		1.03E+00	5.24E-07	Up			Unigene19255_All//1.00E-52//gi|164337150|gb|ES829901.1|ES829901				
Unigene19256_All	480	1.09	0.11	0.00	0.93	1.15	1.13	1.85	0.17	0.25	-3.37E+00	1.58E-02		-1.01E+01	4.75E-03		2.97E-01	8.18E-01		2.74E-01	7.83E-01		-3.41E+00	1.40E-04	Down	-2.89E+00	3.04E-04	Down	Unigene19256_All//gi|224090869|ref|XP_002309106.1|//2.00E-50//predicted protein [Populus trichocarpa] >gi|222855082|gb|EEE92629.1|predicted protein [Populus trichocarpa]	Unigene19256_All//5.00E-34//AT2G37960| unknown protein	Unigene19256_All//0.00E+00//TC167277				nr -
Unigene19257_All	378	0.55	0.00	1.41	15.95	22.50	6.09	16.11	12.27	8.33	-9.11E+00	1.22E-01		1.35E+00	2.25E-01		4.97E-01	1.01E-02		-1.39E+00	1.83E-08	Down	-3.92E-01	7.58E-02		-9.52E-01	6.16E-06				Unigene19257_All//2.00E-15//ES845654				
Unigene19258_All	445	0.71	0.34	0.00	1.90	3.02	1.12	6.65	1.50	2.95	-1.05E+00	4.43E-01		-9.46E+00	4.92E-02		6.65E-01	2.81E-01		-7.69E-01	3.34E-01		-2.15E+00	9.07E-09	Down	-1.17E+00	2.57E-04	Down	Unigene19258_All//gi|224105375|ref|XP_002333828.1|//2.00E-22//BED finger-nbs resistance protein [Populus trichocarpa] >gi|222838647|gb|EEE77012.1| BED finger-nbs resistance protein [Populus trichocarpa]	Unigene19258_All//1.00E-08//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene19258_All//5.00E-72//CO080429		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene19259_All	1154	0.05	0.44	0.00	0.86	1.43	1.29	0.84	0.76	2.07	3.28E+00	2.11E-02		-5.50E+00	6.25E-01		7.30E-01	1.67E-01		5.81E-01	3.18E-01		-1.48E-01	8.13E-01		1.30E+00	4.29E-04	Up	Unigene19259_All//gi|225464348|ref|XP_002272127.1|//2.00E-48//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene19259_All//8.00E-20//AT4G31570| unknown protein					nr -
Unigene1926_All	2623	19.63	15.94	24.83	3.82	3.01	3.08	9.28	1.69	3.05	-3.01E-01	4.78E-05		3.39E-01	3.68E-07		-3.45E-01	5.64E-02		-3.09E-01	1.08E-01		-2.46E+00	6.22E-79	Down	-1.60E+00	1.06E-46	Down	Unigene1926_All//gi|224072274|ref|XP_002303684.1|//0.00E+00//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222841116|gb|EEE78663.1|oligopeptide transporter OPT family [Populus trichocarpa]	Unigene1926_All//0.00E+00//AT4G10770| OPT7 (OLIGOPEPTIDE TRANSPORTER 7); oligopeptide transporter	Unigene1926_All//0.00E+00//gi|48799015|gb|CO100329.1|CO100329				nr +
Unigene19260_All	572	1.01	0.00	0.00	2.53	1.81	1.82	4.66	0.51	0.56	-9.97E+00	1.52E-03		-9.97E+00	2.60E-03		-4.84E-01	3.92E-01		-4.76E-01	4.15E-01		-3.19E+00	6.93E-12	Down	-3.06E+00	6.55E-12	Down			Unigene19260_All//2.00E-145//BG442356				
Unigene19261_All	789	0.07	39.05	14.98	0.00	0.00	0.00	0.00	0.00	0.00	9.20E+00	3.58E-175	Up	7.82E+00	2.00E-64	Up	null	null		null	null		null	null		null	null		Unigene19261_All//gi|301119741|ref|XP_002907598.1|//2.00E-42//60S ribosomal protein L23a [Phytophthora infestans T30-4] >gi|262106110|gb|EEY64162.1| 60S ribosomal protein L23a [Phytophthora infestans T30-4]	Unigene19261_All//1.00E-38//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene19264_All	466	0.34	0.98	0.00	1.07	0.07	0.00	0.73	3.05	2.05	1.54E+00	1.96E-01		-8.40E+00	2.45E-01		-3.85E+00	5.32E-03		-1.01E+01	2.98E-03		2.07E+00	2.12E-04	Up	1.50E+00	1.93E-02		Unigene19264_All//gi|224055709|ref|XP_002298614.1|//3.00E-06//predicted protein [Populus trichocarpa] >gi|222845872|gb|EEE83419.1|predicted protein [Populus trichocarpa]						nr -
Unigene19265_All	544	0.19	0.00	0.00	0.09	0.00	0.25	11.04	2.23	25.70	-7.59E+00	3.73E-01		-7.59E+00	3.94E-01		-6.52E+00	5.56E-01		1.44E+00	6.38E-01		-2.31E+00	1.38E-18	Down	1.22E+00	4.46E-18	Up	Unigene19265_All//gi|297597194|ref|NP_001043549.2|//3.00E-15//Os01g0611000 [Oryza sativa Japonica Group] >gi|255673458|dbj|BAF05463.2|Os01g0611000 [Oryza sativa Japonica Group]	Unigene19265_All//9.00E-56//AT5G14150| unknown protein	Unigene19265_All//4.00E-42//CK640457			GO:0031224	nr +

Unigene19267_All	474	720.13	333.73	1030.85	3457.25	2541.89	2570.31	135.67	143.90	69.59	-1.11E+00	1.06E-290	Down	5.18E-01	3.95E-108		-4.44E-01	0.00E+00		-4.28E-01	1.98E-284		8.50E-02	1.99E-01		-9.63E-01	3.37E-55		Unigene19267_All//gi|223029879|gb|ACM78621.1|//1.00E-29//non-specific lipid-transfer protein type 2 [Tamarix hispida]	Unigene19267_All//7.00E-17//AT3G18280| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene19267_All//2.00E-157//gi|109826722|gb|DW225432.1|DW225432			GO:0005488//GO:0006810//GO:0044464	nr +
Unigene19268_All	444	0.82	0.00	0.00	2.13	2.71	0.81	1.71	0.09	0.54	-9.69E+00	1.97E-02		-9.69E+00	2.78E-02		3.49E-01	5.95E-01		-1.39E+00	6.08E-02		-4.19E+00	1.57E-04	Down	-1.67E+00	2.39E-02		Unigene19268_All//gi|62632823|gb|AA389382.1|//6.00E-41//NB-LRR type disease resistance protein Rps1-k-1 [Glycine max]	Unigene19268_All//3.00E-33//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene19268_All//2.00E-114//ES846109		ko04626|Plant-pathogen interaction	GO:0000166	nr -
Unigene19270_All	271	0.19	14.02	2.16	37.31	42.19	135.16	26.37	47.04	97.02	6.18E+00	4.47E-20	Up	3.48E+00	1.21E-02		1.77E-01	3.57E-01		1.86E+00	1.86E-72	Up	8.35E-01	4.79E-09		1.88E+00	6.29E-62	Up	Unigene19270_All//gi|224112567|ref|XP_002316230.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222865270|gb|EEF02401.1| predicted protein [Populus trichocarpa]	Unigene19270_All//7.00E-07//AT2G39980| transferase family protein	Unigene19270_All//1.00E-34//DR461983				nr -
Unigene19271_All	583	0.36	17.12	0.37	0.26	0.59	0.46	0.00	0.00	0.00	5.58E+00	1.27E-50	Up	2.55E-02	1.00E+00		1.20E+00	4.26E-01		8.59E-01	6.31E-01		null	null		null	null								
Unigene19272_All	401	0.26	2.40	2.12	1.99	1.63	0.79	0.95	1.04	1.29	3.20E+00	6.55E-04	Up	3.03E+00	3.01E-03		-2.85E-01	7.21E-01		-1.33E+00	1.06E-01		1.35E-01	8.99E-01		4.45E-01	6.12E-01		Unigene19272_All//gi|15451126|gb|AA96834.1|//2.00E-07//Unknown protein [Arabidopsis thaliana]	Unigene19272_All//1.00E-08//AT1G70480| unknown protein	Unigene19272_All//5.00E-44//TC155290			GO:0000166	nr -
Unigene19274_All	584	0.54	1.48	2.37	0.77	0.77	0.85	0.87	4.29	1.64	1.46E+00	6.59E-02		2.14E+00	1.38E-03		-2.30E-03	9.69E-01		1.48E-01	9.06E-01		2.31E+00	3.91E-08	Up	9.14E-01	1.38E-01								
Unigene19276_All	380	1.38	1.07	1.68	30.02	24.56	9.03	3.00	0.66	3.98	-3.68E-01	6.83E-01		2.88E-01	7.25E-01		-2.90E-01	9.10E-02		-1.73E+00	3.08E-21	Down	-2.19E+00	6.83E-04	Down	4.07E-01	3.98E-01		Unigene19276_All//gi|223452546|gb|ACM89600.1|//2.00E-11//leucine-rich repeat family protein / extensin family protein [Glycine max]		Unigene19276_All//4.00E-63//TC161203			GO:0003824//GO:0023060	nr -
Unigene19277_All	458	0.00	0.00	0.00	0.00	0.00	0.00	13.20	3.92	1.74	null	null		null	null		null	null		null	null		-1.75E+00	2.81E-13	Down	-2.92E+00	5.54E-25	Down	Unigene19277_All//gi|73622719|gb|AAZ78398.1|//2.00E-64//elongation factor 1-alpha [Diaspidiotus sp. GEM-2005c] >gi|73622775|gb|AAZ78426.1| elongation factor 1-alpha [Hemiberlesia rapax] >gi|73622777|gb|AAZ78427.1| elongation factor 1-alpha [Hemiberlesia rapax] >gi|73622819|gb|AAZ78448.1| elongation factor 1-alpha [Octaspidiotus multipori] >gi|73622869|gb|AAZ78473.1| elongation factor 1-alpha [Targionia fabianae]	Unigene19277_All//2.00E-49//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene19277_All//6.00E-16//TC166357			GO:0008135//GO:0017111//GO:0032561	nr +
Unigene19278_All	266	0.79	0.38	0.60	56.74	55.02	38.37	1.43	0.63	14.23	-1.05E+00	5.65E-01		-3.90E-01	8.07E-01		-4.45E-02	8.20E-01		-5.64E-01	5.64E-05		-1.19E+00	3.09E-01		3.31E+00	1.65E-17	Up	Unigene19278_All//gi|5731998|gb|AAD48912.1|AF139532_1//6.00E-16//aldehyde 5-hydroxylase [Liquidambar styraciflua]	Unigene19278_All//2.00E-05//AT5G04330| cytochrome P450, putative / ferulate-5-hydroxylase, putative	Unigene19278_All//1.00E-74//TC152108		ko00940|Phenylpropanoid biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr -
Unigene19279_All	376	20.04	23.31	14.87	23.85	23.81	18.02	125.27	66.58	49.69	2.18E-01	3.00E-01		-4.30E-01	5.66E-02		-2.20E-03	9.87E-01		-4.04E-01	3.96E-02		-9.12E-01	3.94E-36		-1.33E+00	4.53E-68	Down			Unigene19279_All//5.00E-161//gi|164276410|gb|ES813867.1|ES813867				
Unigene19283_All	447	1.05	0.00	0.48	1.45	1.46	1.62	2.46	1.31	0.53	-1.00E+01	5.56E-03		-1.14E+00	3.32E-01		1.49E-02	9.91E-01		1.58E-01	8.59E-01		-9.10E-01	1.24E-01		-2.20E+00	5.66E-04	Down	Unigene19283_All//gi|22331920|ref|NP_191889.2|//2.00E-53//phosphoinositide binding [Arabidopsis thaliana]	Unigene19283_All//6.00E-28//AT3G63300| phosphoinositide binding	Unigene19283_All//6.00E-53//CK640436			GO:0005543//GO:0023060	nr +
Unigene19284_All	695	0.45	0.15	0.15	2.58	1.39	3.38	2.31	0.24	0.57	-1.63E+00	2.76E-01		-1.56E+00	3.30E-01		-8.95E-01	5.47E-02		3.89E-01	3.87E-01		-3.26E+00	1.49E-07	Down	-2.01E+00	5.95E-05	Down	Unigene19284_All//gi|15239101|ref|NP_196157.1|//2.00E-52//PRA1.B3 (PRENYLATED RAB ACCEPTOR 1.B3) [Arabidopsis thaliana] >gi|75171434|sp|Q9FLB6.1|PR1B3_ARATH RecName: Full=PRA1 family protein B3; Short=AtPRA1.B3; AltName: Full=Prenylated Rab acceptor 2 >gi|94442493|gb|ABF19034.1| At5g05380 [Arabidopsis thaliana]	Unigene19284_All//4.00E-35//AT2G38360| PRA1.B4 (PRENYLATED RAB ACCEPTOR 1.B4)	Unigene19284_All//0.00E+00//DN818198			GO:0006810//GO:0043231	nr -
Unigene19287_All	938	5.97	1.89	4.03	0.37	0.37	0.00	0.09	0.00	0.00	-1.66E+00	1.70E-09	Down	-5.66E-01	3.20E-02		-1.80E-02	9.58E-01		-8.54E+00	2.13E-02		-6.49E+00	4.04E-01		-6.49E+00	3.59E-01				Unigene19287_All//0.00E+00//TC173196				
Unigene19288_All	220	62.07	41.23	58.09	29.21	30.84	14.16	0.00	0.00	0.18	-5.90E-01	9.85E-05		-9.56E-02	6.12E-01		7.82E-02	8.09E-01		-1.04E+00	5.71E-06	Down	null	null		7.50E+00	6.45E-01				Unigene19288_All//2.00E-94//TC145690				
Unigene19293_All	645	0.00	0.00	0.00	0.15	0.11	0.00	1.57	13.80	47.31	null	null		null	null		-5.33E-01	8.17E-01		-7.27E+00	4.00E-01		3.13E+00	1.40E-37	Up	4.91E+00	1.06E-181	Up	Unigene19293_All//gi|255569385|ref|XP_002525660.1|//8.00E-58//Pre-mRNA-splicing factor ini1 [Ricinus communis] >gi|223535096|gb|EEF36778.1| Pre-mRNA-splicing factor ini1 [Ricinus communis]	Unigene19293_All//8.00E-59//AT2G30000| LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: PHF5-like (InterPro:IPR005345); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G07170.2); Has 292 Blast hits to 292 proteins in 142 species: Archae - 0; Bacteria - 0; Metazoa - 110; Fungi - 75; Plants - 47; Viruses - 0; Other Eukaryotes - 60 (source: NCBI BLink).	Unigene19293_All//2.00E-62//EX167914		ko03040|Spliceosome	nr +
Unigene19296_All	253	0.83	2.00	5.89	4.53	2.99	9.64	2.51	4.13	2.36	1.28E+00	2.31E-01		2.83E+00	6.17E-05	Up	-5.97E-01	3.41E-01		1.09E+00	8.21E-03		7.20E-01	2.38E-01		-8.58E-02	9.19E-01								
Unigene19297_All	1588	0.53	0.13	0.40	1.51	0.98	0.40	10.12	3.74	7.70	-2.05E+00	1.68E-02		-3.90E-01	6.41E-01		-6.26E-01	1.19E-01		-1.92E+00	1.46E-05	Down	-1.44E+00	9.63E-26	Down	-3.94E-01	1.16E-03		Unigene19297_All//gi|28300299|gb|AAO37645.1|//2.00E-64//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene19297_All//9.00E-25//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene19297_All//1.00E-177//TC176736			GO:0016787	nr +
Unigene19298_All	407	0.39	1.99	3.14	1.71	2.37	1.78	2.70	0.92	2.15	2.37E+00	1.01E-02		3.03E+00	1.48E-04	Up	4.67E-01	5.47E-01		5.13E-02	9.48E-01		-1.55E+00	1.12E-02		-3.27E-01	5.82E-01		Unigene19298_All//gi|1491931|gb|AACA49393.1|//3.00E-09//kinesin-like protein [Nicotiana tabacum]		Unigene19298_All//6.00E-59//TC129553			GO:0003774//GO:0007017//GO:0032559//GO:0043232	nr +
Unigene1930_All	1433	25.70	22.91	28.20	15.33	18.86	16.92	22.63	19.75	11.23	-1.66E-01	7.78E-02		1.34E-01	1.62E-01		2.99E-01	3.24E-03		1.43E-01	2.68E-01		-1.97E-01	2.75E-02		-1.01E+00	1.45E-30	Down	Unigene1930_All//gi|297804004|ref|XP_002869886.1|//1.00E-102//vesicle-associated membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315722|gb|EFH46145.1| vesicle-associated membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1930_All//3.00E-94//AT4G21450| vesicle-associated membrane family protein / VAMP family protein	Unigene1930_All//0.00E+00//gi|48748588|gb|CO079107.1|CO079107				nr -
Unigene19300_All	1478	0.00	0.31	0.00	0.00	0.05	0.24	34.16	338.13	21.11	8.27E+00	7.44E-03		null	null		5.54E+00	6.10E-01		7.93E+00	2.37E-02		3.31E+00	0.00E+00	Up	-6.95E-01	3.21E-25		Unigene19300_All//gi|209954707|dbj|BAG80544.1|//1.00E-136//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene19300_All//3.00E-108//AT4G15550| IAGLU (INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE); UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene19300_All//0.00E+00//CO074711		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr +
Unigene19301_All	253	29.99	17.42	19.15	56.11	65.06	45.16	129.01	33.37	101.88	-7.83E-01	2.14E-04		-6.47E-01	3.30E-03		2.13E-01	1.51E-01		-3.13E-01	4.18E-02		-1.95E+00	3.68E-79	Down	-3.41E-01	3.52E-05				Unigene19301_All//7.00E-73//TC130640				
Unigene19302_All	617	0.59	0.57	1.47	1.21	1.95	1.17	0.69	0.68	2.39	-4.62E-02	9.82E-01		1.31E+00	9.77E-02		6.90E-01	2.98E-01		-4.82E-02	9.50E-01		-1.67E-02	1.02E+00		1.80E+00	4.81E-04	Up	Unigene19302_All//gi|9954728|gb|AAG90851.1|AC026237_2//5.00E-12//Similar to tRNA-splicing endonuclease positive effector SEN1 [Arabidopsis thaliana]	Unigene19302_All//3.00E-13//AT1G16800| tRNA-splicing endonuclease positive effector-related				GO:0008187	nr -
Unigene19304_All	655	0.64	0.00	0.00	1.29	0.11	0.83	1.10	0.00	0.24	-9.32E+00	1.05E-02		-9.32E+00	1.56E-02		-3.62E+00	1.47E-04	Down	-6.44E-01	4.15E-01		-1.01E+01	3.26E-05	Down	-2.17E+00	7.75E-03		Unigene19304_All//gi|42561571|ref|NP_195783.3|//2.00E-72//BRCA2B (BRCA2-LIKE B); protein binding / single-stranded DNA binding [Arabidopsis thaliana] >gi|31335362|emb|CAD32572.1| breast cancer susceptibility protein 2b [Arabidopsis thaliana]	Unigene19304_All//8.00E-64//AT5G01630| BRCA2B (BRCA2-LIKE B); protein binding / single-stranded DNA binding	Unigene19304_All//3.00E-52//gi|78347639|gb|DT567913.1|DT567913		ko03440|Homologous recombination	GO:0000084//GO:0000725//GO:0003006//GO:0043231//GO:0043566//GO:0048299//GO:0048598	nr -
Unigene19305_All	407	0.64	0.12	0.26	3.55	1.86	0.00	1.56	0.82	0.69	-2.37E+00	2.14E-01		-1.30E+00	4.36E-01		-9.31E-01	8.04E-02		-1.18E+01	4.97E-09	Down	-9.24E-01	2.63E-01		-1.19E+00	1.33E-01		Unigene19305_All//gi|42561571|ref|NP_195783.3|//3.00E-46//BRCA2B (BRCA2-LIKE B); protein binding / single-stranded DNA binding [Arabidopsis thaliana] >gi|31335362|emb|CAD32572.1| breast cancer susceptibility protein 2b [Arabidopsis thaliana]	Unigene19305_All//2.00E-47//AT5G01630| BRCA2B (BRCA2-LIKE B); protein binding / single-stranded DNA binding			ko03440|Homologous recombination	GO:0000084//GO:0000725//GO:0003006//GO:0043231//GO:0043566//GO:0048299//GO:0048598	nr -
Unigene19306_All	426	0.00	8.80	0.00	1.52	4.53	5.41	2.18	0.00	0.00	1.31E+01	2.40E-21	Up	null	null		1.57E+00	9.99E-04	Up	1.83E+00	5.63E-05	Up	-1.11E+01	1.14E-06	Down	-1.11E+01	5.48E-07	Down			Unigene19306_All//2.00E-40//BQ404688				
Unigene19308_All	975	0.00	0.21	0.00	0.05	0.00	0.00	3.77	1.20	2.25	7.70E+00	1.37E-01		null	null		-5.68E+00	5.56E-01		-5.68E+00	6.36E-01		-1.65E+00	8.80E-08	Down	-7.47E-01	6.65E-03		Unigene19308_All//gi|297814267|ref|XP_002875017.1|//1.00E-123//dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320854|gb|EFH51276.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene19308_All//1.00E-123//AT4G00750| dehydration-responsive family protein	Unigene19308_All//3.00E-69//ES801170				nr +
Unigene19309_All	660	0.32	2.00	0.81	0.60	0.89	0.89	1.99	4.12	7.36	2.65E+00	2.16E-04	Up	1.35E+00	2.25E-01		5.55E-01	5.99E-01		5.59E-01	6.01E-01		1.05E+00	2.22E-03		1.89E+00	3.36E-12	Up			Unigene19309_All//8.00E-07//TC155839				
Unigene1931_All	2301	2.93	1.70	2.78	5.98	8.53	5.83	6.08	1.71	2.37	-7.91E-01	4.68E-04		-7.89E-02	7.45E-01		5.14E-01	1.03E-05		-3.56E-02	8.49E-01		-1.83E+00	1.23E-31	Down	-1.36E+00	2.06E-21	Down	Unigene1931_All//gi|263430169|sp|C0LGH8.1|Y1634_ARATH//0.00E+00//Rec Name: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g63430; Flags: Precursor >gi|224589459|gb|ACN59263.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene1931_All//0.00E+00//AT1G63430| leucine-rich repeat transmembrane protein kinase, putative	Unigene1931_All//0.00E+00//TC138084				nr -
Unigene19310_All	380	18.59	6.13	17.10	13.76	20.66	27.81	77.77	21.89	61.75	-1.60E+00	3.14E-11	Down	-1.21E-01	6.32E-01		5.86E-01	3.32E-03		1.01E+00	7.09E-09	Up	-1.83E+00	8.20E-66	Down	-3.33E-01	1.31E-04		Unigene19310_All//gi|292653525|gb|ADE34280.1|//6.00E-18//aquaporin PIP1;11 [Gossypium hirsutum]	Unigene19310_All//1.00E-16//AT4G00430| PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel	Unigene19310_All//8.00E-58//DW241297				nr -
Unigene19313_All	528	0.00	0.10	0.61	1.42	0.26	0.26	6.17	1.74	0.83	6.59E+00	6.17E-01		9.24E+00	4.53E-02		-2.44E+00	5.60E-03		-2.46E+00	1.02E-02		-1.82E+00	6.91E-08	Down	-2.89E+00	1.21E-13	Down			Unigene19313_All//1.00E-146//gi|195983426|gb|FL576920.1|FL576920				
Unigene19314_All	714	0.66	0.14	0.15	1.95	0.82	1.01	0.06	0.12	13.67	-2.22E+00	7.76E-02		-2.14E+00	1.03E-01		-1.25E+00	2.07E-02		-9.49E-01	9.91E-02		9.84E-01	7.31E-01		7.85E+00	6.47E-68	Up	Unigene19314_All//gi|15241779|ref|NP_198189.1|//2.00E-26//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene19314_All//7.00E-22//AT3G61520| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene19316_All	281	1.68	0.00	0.95	4.79	1.23	0.32	0.15	2.83	0.28	-1.07E+01	5.56E-03		-8.23E-01	4.57E-01		-1.97E+00	7.30E-04	Down	-3.90E+00	2.12E-06	Down	4.23E+00	1.05E-04	Up	9.14E-01	7.50E-01								

Unigene19319_All	1045	0.00	0.00	0.00	0.00	0.00	0.00	32.41	47.16	13.19	null	null	null	null	null	null	null	null	null	null	5.41E-01	1.31E-15		-1.30E+00	3.95E-47	Down	Unigene19319_All//gi|30683908|ref|NP_193436.2|//7.00E-73//ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1) [Arabidopsis thaliana] >gi|22095652|sp|O23547.2|EXLB1_ARATH RecName: Full=Expansin-like B1; Short=AtEXLB1; Short=At-EXPR1; Short=AtEXPR1; AltName: Full=Ath-Exp|beta-3.1; Flags: Precursor >gi|29028846|gb|AAO64802.1|At4g17030 [Arabidopsis thaliana] >gi|110736418|dbj|BAF00176.1|Expansin-like protein [Arabidopsis thaliana]	Unigene19319_All//3.00E-74//AT4G17030| ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1)	Unigene19319_All//4.00E-170//CD486015				nr -
Unigene1932_All	2429	1.72	1.42	1.21	2.42	3.32	2.03	1.51	0.31	0.62	-2.81E-01	3.60E-01		-5.15E-01	1.02E-01		4.55E-01	2.44E-02		-2.56E-01	3.53E-01		-2.29E+00	1.48E-11	Down	-1.28E+00	8.40E-06	Down	Unigene1932_All//gi|263430169|sp|C0LGH8.1|Y1634_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g63430; Flags: Precursor >gi|224589459|gb|ACN59263.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene1932_All//0.00E+00//AT1G63430| leucine-rich repeat transmembrane protein kinase, putative	Unigene1932_All//0.00E+00//TC138084		ko04626|Plant-pathogen interaction		nr -
Unigene19320_All	1181	0.93	0.00	0.27	0.30	0.76	0.46	21.84	17.16	10.09	-9.86E+00	1.95E-06	Down	-1.78E+00	1.57E-02		1.36E+00	8.05E-02		6.36E-01	5.61E-01		-3.48E-01	3.02E-04		-1.11E+00	1.40E-28	Down	Unigene19320_All//gi|15226210|ref|NP_180334.1|//5.00E-57//DC1 domain-containing protein [Arabidopsis thaliana]	Unigene19320_All//4.00E-56//AT2G27660| DC1 domain-containing protein					nr +
Unigene19323_All	392	0.13	2.84	0.00	0.76	1.05	0.58	1.83	2.13	4.27	4.41E+00	2.17E-05	Up	-7.06E+00	6.25E-01		4.67E-01	7.41E-01		-4.04E-01	7.51E-01		2.18E-01	7.44E-01		1.22E+00	6.57E-03					Unigene19323_All//5.00E-07//TC147202				
Unigene19324_All	1555	0.20	1.60	0.14	0.42	0.58	0.76	1.01	1.53	15.50	2.98E+00	1.46E-08	Up	-5.60E-01	6.64E-01		4.67E-01	5.72E-01		8.58E-01	1.95E-01		6.07E-01	1.05E-01		3.95E+00	8.06E-125	Up	Unigene19324_All//gi|115455147|ref|NP_001051174.1|//1.00E-20//Os03g0733600 [Oryza sativa Japonica Group] >gi|50540720|gb|AAT77876.1|expressed protein [Oryza sativa Japonica Group] >gi|108710922|gb|ABF98717.1| SSXT protein containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549645|dbj|BAF13088.1|Os03g0733600 [Oryza sativa Japonica Group]	Unigene19324_All//5.00E-11//AT5G28640| AN3 (ANGUSTIFOLIA 3); protein binding / transcription coactivator	Unigene19324_All//8.00E-163//gi|78335725|gb|DT555999.1|DT555999			GO:0005488	nr -
Unigene19325_All	366	0.00	0.00	0.00	2.18	0.66	0.49	2.08	60.64	0.00	null	null		null	null		-1.73E+00	2.86E-02		-2.14E+00	1.54E-02		4.87E+00	1.58E-129	Up	-1.10E+01	8.87E-06	Down	Unigene19325_All//gi|30698042|ref|NP_201258.2|//3.00E-35//XND1; transcription factor [Arabidopsis thaliana] >gi|107738104|gb|ABF83636.1|At5g64530 [Arabidopsis thaliana]	Unigene19325_All//4.00E-28//AT5G64530| XND1; transcription factor	Unigene19325_All//2.00E-43//TC150692	NAC		GO:0001071//GO:0003676//GO:0010087//GO:0010468//GO:0012501//GO:0048513	nr +
Unigene19327_All	273	2.30	0.00	1.17	6.75	5.55	2.98	0.00	1.22	1.31	-1.12E+01	7.92E-04	Down	-9.75E-01	3.16E-01		-2.83E-01	5.82E-01		-1.18E+00	1.47E-02		1.03E+01	1.27E-02		1.04E+01	7.28E-03									
Unigene19329_All	278	11.67	6.01	5.17	11.11	7.06	9.91	35.59	10.52	7.31	-9.56E-01	5.68E-03		-1.17E+00	1.35E-03		-6.54E-01	5.53E-02		-1.65E-01	6.83E-01		-1.76E+00	2.31E-21	Down	-2.28E+00	9.12E-31	Down				Unigene19329_All//6.00E-64//gi|13248500|gb|BF277112.2|BF277112				
Unigene19333_All	966	0.00	0.37	0.11	11.29	21.00	34.60	0.39	0.26	0.49	8.52E+00	2.46E-02		6.78E+00	3.99E-01		8.95E-01	1.13E-14		1.62E+00	1.63E-54	Up	-6.02E-01	6.13E-01		3.29E-01	7.07E-01		Unigene19333_All//gi|294847482|gb|ADF13752.1|//7.00E-85//MYB [Camellia sinensis]	Unigene19333_All//5.00E-74//AT1G68320| MYB62 (myb domain protein 62); DNA binding / transcription factor	Unigene19333_All//0.00E+00//ES803758	MYB		GO:0006350//GO:0009267//GO:0009685//GO:0010033//GO:0010468//GO:0043134	nr +
Unigene19336_All	492	5.21	4.94	2.92	10.02	6.16	3.03	0.95	0.68	0.57	-7.60E-02	8.43E-01		-8.34E-01	4.48E-02		-7.03E-01	5.68E-03		-1.73E+00	1.90E-09	Down	-4.76E-01	6.60E-01		-7.38E-01	4.26E-01		Unigene19336_All//gi|226532058|ref|NP_001148752.1|//3.00E-17//CREG1 protein [Zea mays] >gi|195621884|gb|ACG32772.1| CREG1 protein precursor [Zea mays]	Unigene19336_All//4.00E-14//AT2G04690| cellular repressor of E1A-stimulated genes (CREG) family	Unigene19336_All//8.00E-34//DW502057			GO:0000166//GO:0003676//GO:0043231	nr +
Unigene19337_All	670	0.16	0.76	0.00	0.89	0.98	1.89	1.14	3.62	3.15	2.28E+00	6.23E-02		-7.29E+00	3.94E-01		1.30E-01	9.05E-01		1.08E+00	8.18E-02		1.67E+00	1.89E-05	Up	1.47E+00	2.63E-04	Up	Unigene19337_All//gi|15234831|ref|NP_194799.1|//5.00E-24//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75208664|sp|Q9SUH6.1|PP341_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g30700; AltName: Full=Protein DYW9	Unigene19337_All//1.00E-22//AT3G49170| EMB2261 (embryo defective 2261)	Unigene19337_All//8.00E-07//ES795077				nr -
Unigene19343_All	379	2.07	0.53	1.12	6.31	1.36	1.67	2.45	0.11	1.16	-1.95E+00	2.62E-02		-8.82E-01	2.95E-01		-2.21E+00	2.20E-07	Down	-1.92E+00	1.46E-05	Down	-4.48E+00	1.30E-05	Down	-1.09E+00	8.05E-02		Unigene19343_All//gi|301349383|gb|ADK74335.1|//1.00E-13//chromatin assembly factor-1 [Arabidopsis thaliana]	Unigene19343_All//6.00E-15//AT1G65470| FAS1 (FASCIATA 1); histone binding				GO:0000725//GO:0006338//GO:0009933//GO:0034728//GO:0035315//GO:0048234//GO:0048229//GO:0048827//GO:0051726	nr -
Unigene1935_All	2551	7.79	7.65	8.91	19.10	14.00	10.60	21.05	18.53	10.48	-2.74E-02	8.42E-01		1.94E-01	1.36E-01		-4.48E-01	8.59E-11		-8.49E-01	3.04E-29		-1.84E-01	6.11E-03		-1.01E+00	1.16E-49	Down	Unigene1935_All//gi|62732972|gb|AAX95091.1|//7.00E-66//expressed protein [Oryza sativa Japonica Group] >gi|77548862|gb|ABA91659.1|expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene1935_All//2.00E-134//AT3G18770| LOCATED IN: chloroplast; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Autophagy-related protein 13 (InterPro:IPR018731); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G49590.2); Has 376 Blast hits to 291 proteins in 100 species: Archae - 0; Bacteria - 15; Metazoa - 70; Fungi - 108; Plants - 62; Viruses - 7; Other Eukaryotes - 114 (source: NCBI BLink).	Unigene1935_All//0.00E+00//TC164533				nr +
Unigene19352_All	931	0.00	0.05	0.00	0.43	0.85	0.29	4.36	0.54	1.03	5.77E+00	6.17E-01		null	null		9.91E-01	2.40E-01		-5.56E-01	6.38E-01		-3.02E+00	6.47E-17	Down	-2.09E+00	8.87E-12	Down	Unigene19352_All//gi|223452544|gb|ACM89599.1|//6.00E-54//receptor-kinase like protein [Glycine max]	Unigene19352_All//1.00E-32//AT3G56370| leucine-rich repeat transmembrane protein kinase, putative				GO:0005488//GO:0016772	nr +
Unigene19353_All	1122	1.59	0.00	0.52	0.13	0.03	0.08	2.71	2.31	2.91	-1.06E+01	2.68E-10	Down	-1.60E+00	3.12E-03		-2.12E+00	3.86E-01		-7.27E-01	7.15E-01		-2.32E-01	5.17E-01		1.02E-01	7.47E-01		Unigene19353_All//gi|79570100|ref|NP_181364.2|//1.00E-45//DNA binding / transcription factor [Arabidopsis thaliana]	Unigene19353_All//2.00E-39//AT2G38300| DNA binding / transcription factor	Unigene19353_All//9.00E-14//TC148270	G2-like		GO:0001071//GO:0010468	nr +
Unigene19354_All	420	2.12	3.14	3.68	10.44	14.76	4.41	14.70	24.98	19.16	5.67E-01	3.41E-01		7.96E-01	1.50E-01		5.00E-01	3.38E-02		-1.24E+00	1.88E-05	Down	7.65E-01	1.22E-06		3.83E-01	3.40E-02		Unigene19354_All//gi|297813757|ref|XP_002874762.1|//7.00E-18//At4g12320 [Arabidopsis lyrata subsp. lyrata] >gi|297320599|gb|EFH51021.1|At4g12320 [Arabidopsis lyrata subsp. lyrata]	Unigene19354_All//4.00E-09//AT4G12310| CYP706A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene19354_All//4.00E-91//TC179067		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0004497//GO:0005506	nr -
Unigene19355_All	376	1.95	3.10	3.68	5.56	0.73	2.28	0.79	0.11	1.80	6.70E-01	2.88E-01		9.19E-01	1.27E-01		-2.92E+00	8.07E-09	Down	-1.29E+00	4.31E-03		-2.82E+00	8.85E-02		1.19E+00	1.20E-01		Unigene19355_All//gi|171921105|gb|ACB59203.1|//7.00E-12//RNase H domain-containing protein [Brassica oleracea]	Unigene19355_All//2.00E-11//AT1G24090| RNase H domain-containing protein	Unigene19355_All//2.00E-144//TC137067			GO:0043231	nr -
Unigene19357_All	742	0.00	0.00	0.00	0.27	0.00	0.00	24.16	91.20	262.44	null	null		null	null		-8.07E+00	8.43E-02		-8.07E+00	1.34E-01		1.92E+00	3.25E-159	Up	3.44E+00	0.00E+00	Up	Unigene19357_All//gi|4006869|emb|CAB16787.1|//1.00E-55//patatin-like protein [Arabidopsis thaliana] >gi|7270656|emb|CAB80373.1|patatin-like protein [Arabidopsis thaliana] >gi|119035875|gb|ABM06020.1|At4g37070 [Arabidopsis thaliana]	Unigene19357_All//9.00E-49//AT4G37070| patatin, putative	Unigene19357_All//2.00E-07//TC144881			GO:0010102//GO:0016298//GO:0044238	nr +
Unigene19358_All	312	13.25	2.76	9.05	11.50	4.41	3.33	0.41	0.13	0.00	-2.26E+00	1.76E-10	Down	-5.51E-01	8.13E-02		-1.38E+00	7.99E-06	Down	-1.79E+00	2.35E-07	Down	-1.60E+00	5.34E-01		-8.67E+00	2.00E-01					Unigene19358_All//2.00E-15//ES804220				
Unigene19360_All	1511	0.45	0.07	0.00	10.95	6.13	2.87	0.11	0.14	0.05	-2.75E+00	1.06E-02		-8.81E+00	7.64E-04	Down	-8.36E-01	3.21E-11		-1.93E+00	2.01E-35	Down	3.06E-01	8.36E-01		-1.09E+00	5.53E-01		Unigene19360_All//gi|15226313|ref|NP_180366.1|//8.00E-37//BLH8 (BEL1-LIKE HOMEODOMAIN 8); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75265949|sp|Q8SJ3.1|BLH8_ARATH RecName: Full=BEL1-like homeodomain protein 8; Short=BEL1-like protein 8; AltName: Full=Protein POUND-FOOLISH >gi|29028954|gb|AAO64856.1|At2g27990 [Arabidopsis thaliana]	Unigene19360_All//4.00E-38//AT2G27990| BLH8 (BEL1-LIKE HOMEODOMAIN 8); DNA binding / transcription factor	Unigene19360_All//9.00E-98//TC137565	HB		GO:0003006//GO:0005488//GO:0007389//GO:0009791//GO:0010074//GO:0010346	nr -
Unigene19361_All	416	1.38	0.97	0.64	2.87	0.58	1.95	3.15	1.51	1.34	-5.06E-01	6.00E-01		-1.11E+00	2.79E-01		-2.31E+00	3.71E-04	Down	-5.56E-01	3.87E-01		-1.06E+00	4.42E-02		-1.23E+00	1.61E-02		Unigene19361_All//gi|298204697|emb|CBI25195.3|//5.00E-10//unnamed protein product [Vitis vinifera]		Unigene19361_All//8.00E-15//CO128299				nr -
Unigene19362_All	319	56.75	19.22	36.72	160.22	144.76	113.55	23.59	9.43	17.11	-1.56E+00	1.00E-26	Down	-6.28E-01	2.94E-06		-1.46E-01	5.93E-02		-4.97E-01	3.30E-12		-1.32E+00	4.25E-11	Down	-4.64E-01	1.21E-02		Unigene19362_All//gi|224145979|ref|XP_002325835.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222862710|gb|EEF00217.1|predicted protein [Populus trichocarpa]	Unigene19362_All//1.00E-05//AT3G03960| chaperonin, putative	Unigene19362_All//6.00E-123//gi|164248466|gb|ES835376.1|ES835376				nr -
Unigene19364_All	1119	0.00	0.45	0.19	0.36	1.60	1.45	7.90	11.65	40.69	8.82E+00	4.05E-03		7.57E+00	1.41E-01		2.17E+00	5.21E-05	Up	2.03E+00	3.98E-04	Up	5.61E-01	5.22E-05		2.37E+00	9.11E-143	Up	Unigene19364_All//gi|224066255|ref|XP_002302049.1|//3.00E-72//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222843775|gb|EEES1322.1|AP2/EBP domain-containing transcription factor [Populus trichocarpa]	Unigene19364_All//8.00E-43//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene19364_All//0.00E+00//EX167849	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene19365_All	508	0.00	0.00	0.21	2.16	0.88	0.36	2.16	1.15	0.94	null	null		7.71E+00	3.99E-01		-1.29E+00	4.07E-02		-2.60E+00	7.14E-04	Down	-9.10E-01	1.24E-01		-1.20E+00	3.41E-02		Unigene19365_All//gi|22327888|ref|NP_200462.2|//2.00E-29//APUM12 (ARABIDOPSIS PUMILIO 12); RNA binding / binding [Arabidopsis thaliana]	Unigene19365_All//1.00E-30//AT5G56510| APUM12 (ARABIDOPSIS PUMILIO 12); RNA binding / binding				GO:0005488	nr -
Unigene19366_All	701	0.07	0.00	0.61	0.85	1.13	1.16	0.60	0.60	2.73	-6.22E+00	6.13E-01		3.03E+00	5.73E-02		4.06E-01	6.32E-01		4.44E-01	6.21E-01		-1.66E-02	1.02E+00		2.18E+00	3.66E-06	Up	Unigene19366_All//gi|115449221|ref|NP_001048390.1|//1.00E-103//Os02g0796600 [Oryza sativa Japonica Group] >gi|113537921|dbj|BAF10304.1|Os02g0796600 [Oryza sativa Japonica Group]	Unigene19366_All//2.00E-103//AT4G31020| unknown protein	Unigene19366_All//5.00E-119//CO104600			GO:0003824	nr -

Unigene19368_A11	567	0.00	0.00	0.00	0.79	0.73	0.40	3.65	1.25	0.70	null	null		null	null		-1.18E-01	8.86E-01		-9.89E-01	3.94E-01		-1.54E+00	2.37E-04	Down	-2.38E+00	2.25E-07	Down	Unigene19368_A11//gi|115441063|ref|NP_001044811.1|//1.00E-06//0s01g0850000 [Oryza sativa Japonica Group] >gi|113534342|dbj|BAF06725.1|Os01g0850000 [Oryza sativa Japonica Group]	Unigene19368_A11//3.00E-13//AT4G02830| unknown protein				nr +
Unigene19369_A11	530	5.82	7.36	8.64	6.77	8.06	24.80	79.22	169.86	417.70	3.38E-01	2.94E-01		5.69E-01	5.48E-02		2.52E-01	4.59E-01		1.87E+00	1.42E-26	Up	1.10E+00	7.54E-93	Up	2.40E+00	0.00E+00	Up	Unigene19369_A11//gi|5915843|sp|O81972.1|CR2A2_SOYBN//1.00E-14//RecName: Full=Cytochrome P450 82A2; AltName: Full=Cytochrome P450 CP4		Unigene19369_A11//1.00E-88//TC132245		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0016491	nr +
Unigene19370_A11	491	30.26	28.48	39.48	28.10	29.88	28.51	187.81	155.10	80.89	-8.75E-02	6.16E-01		3.83E-01	3.52E-03		8.83E-02	6.11E-01		2.10E-02	9.24E-01		-2.76E-01	9.74E-09		-1.22E+00	1.28E-114	Down	Unigene19370_A11//gi|14423520|gb|AA662442.1|AF386997_1//2.00E-13//Unknown protein [Arabidopsis thaliana] >gi|30102918|gb|AAP21377.1|At1g17970 [Arabidopsis thaliana]		Unigene19370_A11//0.00E+00//gi|13355966|gb|BG446254.1|BG446254			GO:0044444	nr -
Unigene19372_A11	432	126.08	2310.39	1302.78	38.28	44.88	128.07	1.47	1.55	0.74	4.20E+00	0.00E+00	Up	3.37E+00	0.00E+00	Up	2.29E-01	8.10E-02		1.74E+00	3.84E-100	Up	7.65E-02	9.37E-01		-9.93E-01	2.02E-01		Unigene19372_A11//gi|49615303|gb|AT66913.1|//3.00E-82//dehydration-induced protein RD22-like protein 2 [Gossypium arboreum]		Unigene19372_A11//0.00E+00//gi|13354393|gb|BG444741.1|BG444741			GO:0006970//GO:0009725	nr +
Unigene19373_A11	967	19.64	2.93	13.33	0.26	0.07	0.28	0.00	0.00	0.00	-2.74E+00	4.21E-57	Down	-5.60E-01	1.87E-05		-1.86E+00	2.75E-01		1.21E-01	9.44E-01		null	null		null	null		Unigene19373_A11//gi|50253476|gb|AAT71940.1|//8.00E-30//At2g25770 [Arabidopsis thaliana] >gi|56381959|gb|AAV85698.1|At2g25770 [Arabidopsis thaliana]	Unigene19373_A11//1.00E-28//AT2G25770| unknown protein				nr -
Unigene19374_A11	643	0.65	1.65	0.99	1.39	2.14	1.33	2.70	0.33	1.67	1.35E+00	5.00E-02		6.10E-01	5.09E-01		6.19E-01	3.14E-01		-6.34E-02	9.39E-01		-3.05E+00	1.18E-07	Down	-6.88E-01	1.07E-01		Unigene19374_A11//gi|297809371|ref|XP_002872569.1|//3.00E-40//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318406|gb|EFH48828.1|transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene19374_A11//8.00E-40//AT4G11270| transducin family protein / WD-40 repeat family protein	Unigene19374_A11//0.00E+00//gi|109860790|gb|DW489769.1|DW489769			GO:0044444	nr +
Unigene19375_A11	506	3.31	3.00	0.63	7.48	6.53	5.89	0.17	0.17	0.00	-1.39E-01	7.69E-01		-2.39E+00	1.21E-04	Down	-1.96E-01	5.82E-01		-3.45E-01	3.14E-01		-1.65E-02	1.01E+00		-7.38E+00	3.59E-01		Unigene19375_A11//gi|224078010|ref|XP_002305474.1|//5.00E-39//SAUR family protein [Populus trichocarpa] >gi|222848438|gb|EEE85985.1| SAUR family protein [Populus trichocarpa]	Unigene19375_A11//2.00E-36//AT4G34770| auxin-responsive family protein	Unigene19375_A11//4.00E-11//CO102462			nr -
Unigene19377_A11	1491	0.21	33.54	31.21	0.00	0.23	0.18	0.00	0.00	0.08	7.32E+00	1.19E-275	Up	7.21E+00	1.51E-251	Up	7.85E+00	3.01E-02		7.51E+00	7.03E-02		null	null		6.33E+00	2.43E-01		Unigene19377_A11//gi|89276321|gb|AB066517.1|//1.00E-169//EF-1 alpha [Gymnadenia conopsea]	Unigene19377_A11//3.00E-158//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene19377_A11//6.00E-28//gi|13355123|gb|BG445555.1|BG445555			nr -
Unigene19380_A11	427	2.45	0.00	1.50	3.62	2.74	5.08	0.69	0.20	1.21	-1.13E+01	3.80E-06	Down	-7.12E-01	3.15E-01		-3.99E-01	4.68E-01		4.89E-01	2.99E-01		-1.82E+00	2.11E-01		8.07E-01	3.66E-01				Unigene19380_A11//1.00E-13//TC178241				
Unigene19386_A11	313	7.19	9.23	1.53	0.64	1.10	0.58	0.41	0.13	1.78	3.60E-01	3.51E-01		-2.23E+00	1.32E-05	Down	7.89E-01	5.96E-01		-1.41E-01	9.35E-01		-1.60E+00	5.34E-01		2.14E+00	2.64E-02								
Unigene19388_A11	364	2.30	0.14	1.46	0.68	0.38	1.24	0.00	0.00	0.00	-4.05E+00	4.65E-04	Down	-6.53E-01	3.96E-01		-8.55E-01	5.74E-01		8.59E-01	4.69E-01		null	null		null	null								
Unigene19389_A11	345	1.52	0.73	1.23	11.84	3.29	2.36	1.23	0.48	0.35	-1.05E+00	3.11E-01		-2.97E-01	7.50E-01		-1.85E+00	9.40E-10	Down	-2.33E+00	1.93E-11	Down	-1.34E+00	2.24E-01		-1.82E+00	9.22E-02								
Unigene1939_A11	2429	4.76	16.10	10.22	1.89	9.12	8.55	3.13	3.60	4.17	1.76E+00	5.77E-67	Up	1.10E+00	1.06E-20	Up	2.27E+00	7.99E-62	Up	2.18E+00	9.30E-51	Up	1.99E-01	3.11E-01		4.11E-01	9.00E-03		Unigene1939_A11//gi|46518489|gb|AAS99726.1|//0.00E+00//At1g56230 [Arabidopsis thaliana]	Unigene1939_A11//0.00E+00//AT1G56230| unknown protein	Unigene1939_A11//0.00E+00//gi|109835674|gb|DW234237.1|DW234237			nr -
Unigene19390_A11	999	0.16	0.20	0.00	0.05	0.38	0.72	4.27	0.17	1.08	3.69E-01	8.17E-01		-7.30E+00	2.45E-01		2.93E+00	8.16E-02		3.86E+00	1.75E-03		-4.67E+00	9.12E-25	Down	-1.99E+00	1.16E-11	Down	Unigene19390_A11//gi|15234257|ref|NP_192072.1|//1.00E-109//ATEXPA17 (ARABIDOPSIS THALIANA EXPANSIN A17) [Arabidopsis thaliana] >gi|20138096|sp|Q9ZSI1.1|EXP17_ARATH RecName: Full=Putative expansin-A17; Short=AtEXPA17; AltName: Full=Alpha-expansin-17; Short=At-EXP17; Short=AtEx17; AltName: Full=Ath-ExpAlpha-1.13; Flags: Precursor >gi|38859592|gb|AAC72858.1|contains similarity to expansins [Arabidopsis thaliana]	Unigene19390_A11//3.00E-105//AT4G01630| ATEXPA17 (ARABIDOPSIS THALIANA EXPANSIN A17)	Unigene19390_A11//2.00E-14//gi|78335807|gb|DT556081.1|DT556081			GO:0007047//GO:0044464	nr +
Unigene19393_A11	540	0.58	0.00	0.10	2.77	1.34	0.59	0.31	0.00	0.00	-9.18E+00	3.66E-02		-2.56E+00	1.59E-01		-1.05E+00	4.31E-02		-2.24E+00	2.25E-04	Down	-8.29E+00	1.34E-01		-8.29E+00	1.08E-01		Unigene19393_A11//gi|224113471|ref|XP_002332583.1|//9.00E-43//f-box family protein [Populus trichocarpa] >gi|222832921|gb|EEE71398.1| f-box family protein [Populus trichocarpa]	Unigene19393_A11//5.00E-18//AT3G55370| OBP3 (OBF-BINDING PROTEIN 3); DNA binding / transcription factor	Unigene19393_A11//1.00E-42//gi|109852418|gb|DW481397.1|DW481397	C2C2-Dof			nr -
Unigene19398_A11	609	0.17	0.00	0.17	1.72	1.87	1.48	2.22	0.62	0.59	-7.42E+00	3.73E-01		2.58E-02	1.00E+00		1.20E-01	8.71E-01		-2.12E-01	7.44E-01		-1.85E+00	9.22E-04	Down	-1.92E+00	4.37E-04	Down	Unigene19398_A11//gi|115454717|ref|NP_001050959.1|//6.00E-06//Os03g0692400 [Oryza sativa Japonica Group] >gi|50428646|gb|AAT76997.1|expressed protein [Oryza sativa Japonica Group] >gi|113549430|dbj|BAF12873.1|Os03g0692400 [Oryza sativa Japonica Group]	Unigene19398_A11//2.00E-06//AT2G28150| unknown protein	Unigene19398_A11//0.00E+00//CO117872			nr -
Unigene19399_A11	431	131.71	86.06	77.34	1.96	6.87	1.36	0.00	0.00	0.00	-6.14E-01	3.10E-18		-7.68E-01	1.14E-25		1.81E+00	1.85E-06	Up	-5.28E-01	5.03E-01		null	null		null	null		Unigene19399_A11//gi|296443|emb|CAA49341.1|//6.00E-51//ADR11 [Glycine max]	Unigene19399_A11//1.00E-26//AT2G10940| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene19399_A11//0.00E+00//TC137736			GO:0005488//GO:0005576//GO:0006810//GO:0009534//GO:0031410	nr -
Unigene194_A11	1146	3.42	2.08	4.32	6.13	5.50	7.68	5.13	2.52	3.75	-7.21E-01	1.93E-02		3.36E-01	2.47E-01		-1.57E-01	5.60E-01		3.26E-01	1.16E-01		-1.03E+00	3.51E-06	Down	-4.50E-01	3.49E-02		Unigene194_A11//gi|30690154|ref|NP_182112.2|//2.00E-97//BAM7 (BETA-AMYLASE 7); beta-amylase/ catalytic/ cation binding [Arabidopsis thaliana] >gi|294956510|sp|O80831.2|BAM7_ARATH RecName: Full=Beta-amylase 7; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Beta-amylase 4	Unigene194_A11//5.00E-69//AT2G45880| BAM7 (BETA-AMYLASE 7); beta-amylase/ catalytic/ cation binding				nr -
Unigene19400_A11	628	0.00	15.25	6.27	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	7.52E-55	Up	1.26E+01	7.62E-22	Up	null	null		null	null		null	null		null	null		Unigene19400_A11//gi|2493971|sp|Q41346.1|CYC_STELP//1.00E-39//RecName: Full=Cytochrome c >gi|440586|emb|CAA79708.1|mitochondrial cytochrome c [Stellaria longipes]	Unigene19400_A11//1.00E-36//AT1G22840| CYTC-1 (CYTOCHROME C-1); electron carrier/ heme binding / iron ion binding				GO:0005506//GO:0006091//GO:0031980//GO:0044425//GO:0051234	nr -
Unigene19402_A11	538	1.17	0.19	1.68	3.61	1.15	1.43	0.94	0.54	0.81	-2.63E+00	1.78E-02		5.28E-01	4.79E-01		-1.65E+00	2.73E-04	Down	-1.34E+00	4.60E-03		-7.94E-01	4.02E-01		-2.12E-01	7.92E-01								
Unigene19403_A11	1035	0.10	10.28	4.32	0.00	0.07	0.00	0.00	0.00	0.00	6.67E+00	2.86E-57	Up	5.42E+00	6.65E-22	Up	6.06E+00	6.10E-01		null	null		null	null		null	null		Unigene19403_A11//sp|Q9VXY7|LSD2_DROME//9.00E-126//Lipid storage droplets surface-binding protein 2 OS=Drosophila melanogaster GN=Lsd-2 PE=1 SV=1					swissprot -
Unigene19405_A11	1011	0.41	0.35	0.16	0.39	0.68	0.45	1.21	3.35	3.35	-2.39E-01	8.10E-01		-1.39E+00	2.80E-01		7.89E-01	4.04E-01		1.80E-01	8.84E-01		1.47E+00	3.51E-06	Up	1.47E+00	2.27E-06	Up							
Unigene19407_A11	313	2.67	2.59	0.68	2.71	0.22	0.29	1.22	1.20	1.27	-4.63E-02	9.64E-01		-1.97E+00	2.71E-02		-3.62E+00	1.47E-04	Down	-3.23E+00	1.04E-03		-1.66E-02	1.02E+00		6.62E-02	9.66E-01		Unigene19407_A11//gi|225470293|ref|XP_002266300.1|//5.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene19407_A11//1.00E-158//TC163843				nr +
Unigene1941_A11	2521	0.64	1.73	3.74	1.48	2.54	3.78	9.58	5.02	3.56	1.43E+00	3.46E-06	Up	2.54E+00	2.53E-25	Up	7.78E-01	4.66E-04		1.35E+00	2.49E-12	Up	-9.31E-01	1.47E-19		-1.43E+00	3.76E-39	Down	Unigene1941_A11//gi|225470869|ref|XP_002269732.1|//1.00E-163//PREDICTED: (-)-a-terpineol synthase [Vitis vinifera]	Unigene1941_A11//6.00E-119//AT3G25830| ATTPS-CIN (terpene synthase-like sequence-1,8-cineole); (E)-beta-ocimene synthase/ myrcene synthase	Unigene1941_A11//0.00E+00//gi|164361450|gb|ES820998.1|ES820998		ko00902|Monoterpenoid biosynthesis		nr +
Unigene19414_A11	551	0.00	6.99	6.19	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	6.32E-22	Up	1.26E+01	7.39E-19	Up	null	null		null	null		null	null		null	null		Unigene19414_A11//gi|15232536|ref|NP_191019.1|//4.00E-49//HTA11; DNA binding [Arabidopsis thaliana] >gi|297816752|ref|XP_002876259.1|histone H2A.F/Z [Arabidopsis lyrata subsp. lyrata] >gi|75277395|sp|Q23628.1|H2AV1_ARATH RecName: Full=Histone H2A variant 1; AltName: Full=H2A.F/Z 1; AltName: Full=HTA11; AltName: Full=H2AvAt >gi|2407800|emb|CAA73155.1|histone H2A.F/Z [Arabidopsis thaliana] >gi|7258359|emb|CAB77576.1|histone H2A.F/Z [Arabidopsis thaliana] >gi|21592838|gb|AAM64788.1|histone H2A.F/Z [Arabidopsis thaliana] >gi|28950691|gb|AAO63269.1|At3g54560 [Arabidopsis thaliana] >gi|110736078|dbj|BAF00012.1|histone H2A.F/Z [Arabidopsis thaliana] >gi|297322097|gb|EFH52518.1|histone H2A.F/Z [Arabidopsis lyrata subsp. lyrata]	Unigene19414_A11//1.00E-43//AT1G52740| HTA9 (HISTONE H2A PROTEIN 9); DNA binding	Unigene19414_A11//4.00E-14//TC149922			GO:0000785//GO:0003676//GO:0006952//GO:0009266//GO:0009908//GO:0034728//GO:0043231	nr -
Unigene19415_A11	1348	0.00	0.00	0.00	0.04	0.00	0.00	2.70	4.34	6.83	null	null		null	null		-5.21E+00	5.56E-01		-5.21E+00	6.36E-01		6.86E-01	1.67E-03		1.34E+00	5.80E-14	Up							
Unigene19416_A11	297	0.00	0.85	0.00	0.17	0.00	0.00	1.28	5.35	2.01	9.74E+00	7.86E-02		null	null		-7.39E+00	5.56E-01		-7.39E+00	6.36E-01		2.06E+00	8.20E-05	Up	6.51E-01	4.23E-01								
Unigene19417_A11	376	0.28	0.27	0.00	0.79	0.64	2.64	4.05	1.22	2.12	-4.64E-02	9.89E-01		-8.12E+00	3.94E-01		-3.10E-01	8.20E-01		1.73E+00	2.14E-02		-1.73E+00	7.56E-04	Down	-9.34E-01	4.27E-02								
Unigene1942_A11	689	6.38	2.28	2.78	5.42	8.65	5.05	13.19	3.46	4.97	-1.48E+00	1.31E-06	Down	-1.20E+00	1.03E-04	Down	6.73E-01	4.01E-03		-1.03E-01	7.57E-01		-1.93E+00	2.72E-22	Down	-1.41E+00	5.87E-15	Down	Unigene1942_A11//gi|15222993|ref|NP_172250.1|//1.00E-45//ankyrin repeat family protein [Arabidopsis thaliana] >gi|8439897|gb|AAF75083.1|AC007583_19 It contains Ank repeat PF|00023. EST gb|AI996003 comes from this gene [Arabidopsis thaliana]	Unigene1942_A11//7.00E-47//AT1G07710| ankyrin repeat family protein	Unigene1942_A11//0.00E+00//gi|78337246|gb|DT557520.1|DT557520			nr +
Unigene19420_A11	254	214.43	202.08	267.51	23.14	27.79	7.65	0.67	0.66	0.31	-8.56E-02	2.98E-01		3.19E-01	1.04E-06		2.64E-01	2.80E-01		-1.60E+00	4.79E-10	Down	-1.66E-02	1.02E+00		-1.09E+00	5.53E-01				Unigene19420_A11//2.00E-137//gi|164318244|gb|EX167144.1|EX167144				
Unigene19427_A11	531	0.69	4.01	1.00	0.66	2.79	1.36	0.00	0.16	0.00	2.54E+00	2.15E-06	Up	5.40E-01	6.10E-01		2.09E+00	4.64E-04	Up	1.05E+00	2.35E-01		7.30E+00	4.01E-01		null	null		Unigene19427_A11//gi|115443667|ref|NP_001045613.1|//2.00E-35//Os02g0104500 [Oryza sativa Japonica Group] >gi|113535144|dbj|BAF07527.1|Os02g0104500 [Oryza sativa Japonica Group]	Unigene19427_A11//1.00E-32//AT1G76890| GTZ; transcription factor	Unigene19427_A11//0.00E+00//TC137904	Trihelix		GO:0003676//GO:0010468	nr +

Unigene1943_All	2431	6.69	2.79	2.74	7.68	9.07	6.22	10.66	5.73	3.54	-1.26E+00	1.23E-17	Down	-1.29E+00	1.82E-17	Down	2.39E-01	4.65E-02		-3.04E-01	2.04E-02		-8.97E-01	1.00E-19		-1.59E+00	5.01E-49	Down	Unigene1943_All//gi|15222993|ref|NP_172250.1|//0.00E+00//ankyrin repeat family protein [Arabidopsis thaliana] >gi|8439897|gb|AAF75083.1|AC007583_19 It contains Ank repeat PF|00023. EST gb|AI996003 comes from this gene [Arabidopsis thaliana]	Unigene1943_All//0.00E+00//AT1G07710| ankyrin repeat family protein	Unigene1943_All//0.00E+00//gi|78337246|gb|DT557520.1|DT557520				nr -
Unigene19431_All	301	14.25	37.37	4.95	0.50	1.60	6.45	0.00	1.25	0.53	1.39E+00	3.03E-14	Up	-1.52E+00	2.44E-06	Down	1.69E+00	1.66E-01		3.70E+00	1.99E-08	Up	1.03E+01	6.86E-03		9.05E+00	1.40E-01				Unigene19431_All//9.00E-82//DT461512				
Unigene19434_All	560	0.93	3.35	2.28	1.42	0.61	0.97	2.11	0.90	1.14	1.84E+00	4.09E-04	Up	1.29E+00	4.48E-02		-1.21E+00	1.14E-01		-5.57E-01	4.98E-01		-1.24E+00	2.93E-02		-8.93E-01	9.53E-02		Unigene19434_All//gi|77553423|gb|AB496219.1|//5.00E-07//expressed protein [Oryza sativa (japonica cultivar-group)]		Unigene19434_All//0.00E+00//TC132296				nr -
Unigene19435_All	330	4.76	2.15	0.65	1.21	1.04	1.78	0.13	0.00	0.00	-1.15E+00	3.18E-02		-2.88E+00	3.27E-05	Down	-2.11E-01	8.25E-01		5.59E-01	6.01E-01		-7.00E+00	6.58E-01		-7.00E+00	6.13E-01		Unigene19435_All//gi|229609833|gb|ACQ83532.1|//9.00E-21//CBL-interacting protein kinase 16 [Vitis vinifera]	Unigene19435_All//1.00E-20//AT5G45820| CIPK20 (CBL-INTERACTING PROTEIN KINASE 20); kinase/ protein serine/threonine kinase	Unigene19435_All//6.00E-154//C0096311		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0023060//GO:0032559	nr -
Unigene19436_All	266	249.21	135.44	147.34	345.14	392.90	348.23	240.01	99.93	155.01	-8.80E-01	5.71E-39		-7.58E-01	3.04E-29		1.87E-01	1.10E-04		1.29E-02	8.58E-01		-1.26E+00	2.70E-82	Down	-6.31E-01	7.94E-27		Unigene19436_All//gi|12580867|emb|CAC27142.1|//7.00E-34//60S ribosomal protein L13E [Picea abies]	Unigene19436_All//1.00E-34//AT3G49010| ATIBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome	Unigene19436_All//2.00E-141//gi|21092341|gb|BQ404654.1|BQ404654		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene19438_All	349	1.20	0.29	2.14	2.85	1.78	1.81	0.73	3.23	1.71	-2.05E+00	1.21E-01		8.33E-01	3.39E-01		-6.85E-01	3.11E-01		-6.56E-01	3.71E-01		2.15E+00	8.74E-04	Up	1.24E+00	1.39E-01		Unigene19438_All//gi|15240591|ref|NP_196831.1|//1.00E-31//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75181128|sp|Q9LY19.1|PP378_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g13270, chloroplastic; Flags: Precursor	Unigene19438_All//4.00E-33//AT5G13270| pentatricopeptide (PPR) repeat-containing protein			GO:0003006	nr -
Unigene19439_All	626	1.92	0.00	1.53	4.77	5.89	3.82	1.69	0.47	3.12	-1.09E+01	5.01E-07	Down	-3.28E-01	6.27E-01		3.02E-01	3.98E-01		-3.20E-01	4.17E-01		-1.85E+00	4.09E-03		8.85E-01	2.73E-02		Unigene19439_All//gi|13877625|gb|AK43890.1|AF370513_1//5.00E-27//Unknown protein [Arabidopsis thaliana] >gi|23198280|gb|AAN15667.1|Unknown protein [Arabidopsis thaliana] >gi|62320689|dbj|BAD95357.1|receptor-like serine/threonine kinase [Arabidopsis thaliana]	Unigene19439_All//2.00E-28//AT1G07650| leucine-rich repeat transmembrane protein kinase, putative	Unigene19439_All//4.00E-113//TC137537		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152	nr -
Unigene1944_All	1573	6.72	9.08	5.69	6.81	11.43	16.88	12.98	20.75	23.17	4.35E-01	3.56E-03		-2.41E-01	2.25E-01		7.47E-01	9.90E-10		1.31E+00	6.59E-32	Up	6.77E-01	1.96E-15		8.36E-01	5.54E-25		Unigene1944_All//gi|45861623|gb|AAS78640.1|//2.00E-72//MAP3Ka [Solanum lycopersicum]	Unigene1944_All//2.00E-56//AT1G53570| MAP3KA; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene1944_All//0.00E+00//TC162325		ko04626|Plant-pathogen interaction		nr +
Unigene19442_All	393	1.86	2.84	5.69	0.51	1.49	2.07	0.11	0.53	0.20	6.06E-01	3.59E-01		1.61E+00	6.62E-04	Up	1.55E+00	1.41E-01		2.03E+00	2.17E-02		2.31E+00	2.40E-01		9.14E-01	7.50E-01		Unigene19442_All//gi|255573995|ref|XP_002527915.1|//4.00E-22//anthranilate phosphoribosyltransferase, putative [Ricinus communis] >gi|223532690|gb|EEF34472.1|anthranilate phosphoribosyltransferase, putative [Ricinus communis]	Unigene19442_All//4.00E-23//AT1G70570| anthranilate phosphoribosyltransferase, putative	Unigene19442_All//9.00E-21//TC152961			GO:0009536//GO:0016763	nr -
Unigene19444_All	339	0.15	0.45	0.79	0.15	0.61	0.40	2.87	0.00	1.53	1.54E+00	5.31E-01		2.35E+00	2.39E-01		2.05E+00	3.95E-01		1.44E+00	6.38E-01		-1.15E+01	5.83E-07	Down	-9.09E-01	1.31E-01		Unigene19444_All//gi|56759682|gb|AAT77693.2|//2.00E-27//hexose transporter HT2 [Vitis vinifera]	Unigene19444_All//2.00E-25//AT1G34580| monosaccharide transporter, putative	Unigene19444_All//3.00E-143//gi|78341149|gb|DT561423.1|DT561423			GO:0006810//GO:0008152//GO:0016628//GO:0022891//GO:0031224	nr +
Unigene19447_All	734	0.00	0.00	0.00	0.00	0.00	0.00	3.11	9.05	6.02	null	null		null	null		null	null		null	null		1.54E+00	3.24E-12	Up	9.54E-01	1.58E-04				Unigene19447_All//0.00E+00//TC141618				
Unigene19450_All	391	3.88	0.00	0.54	0.64	0.97	3.35	0.87	0.43	1.02	-1.19E+01	8.33E-09	Down	-2.83E+00	5.52E-05	Down	6.05E-01	6.59E-01		2.39E+00	4.71E-04	Up	-1.02E+00	4.00E-01		2.36E-01	8.04E-01		Unigene19450_All//gi|240254313|ref|NP_176555.4|//8.00E-54//MURE; ATP binding / acid-amino acid ligase/ ligase [Arabidopsis thaliana]	Unigene19450_All//1.00E-48//AT1G63680| MURE; ATP binding / acid-amino acid ligase/ ligase	Unigene19450_All//3.00E-144//C0081352			GO:0000270//GO:0016740//GO:0016881//GO:0032559//GO:0042546//GO:0043231//GO:0065008	nr -
Unigene19456_All	377	2.78	0.81	0.71	1.19	1.19	1.08	3.81	0.44	1.69	-1.78E+00	1.36E-02		-1.97E+00	1.13E-02		-2.20E-03	9.69E-01		-1.41E-01	9.00E-01		-3.10E+00	1.52E-06	Down	-1.17E+00	1.53E-02				Unigene19456_All//3.00E-125//gi|13245010|gb|BE053808.2|BE053808				
Unigene19457_All	486	0.00	0.21	0.22	0.21	0.99	0.74	3.65	12.21	4.51	7.70E+00	3.87E-01		7.78E+00	3.99E-01		2.27E+00	7.83E-02		1.86E+00	2.20E-01		1.74E+00	6.31E-13	Up	3.03E-01	4.42E-01		Unigene19457_All//gi|194466169|gb|ACF74315.1|//1.00E-13//lactoylglutathione lyase [Arachis hypogaea]	Unigene19457_All//1.00E-12//AT1G80160| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene19457_All//3.00E-126//gi|109882048|gb|DW511018.1|DW511018			GO:0003824//GO:0044238//GO:0044464	nr +
Unigene19459_All	462	1.13	7.35	2.88	0.32	0.60	1.66	0.09	0.00	0.09	2.70E+00	2.01E-10	Up	1.35E+00	3.17E-02		8.82E-01	5.95E-01		2.36E+00	1.34E-02		-6.52E+00	6.58E-01		-8.61E-02	9.72E-01				Unigene19459_All//9.00E-12//ES838169				
Unigene1946_All	1386	9.97	2.71	6.88	19.30	14.48	8.21	3.33	1.93	1.38	-1.88E+00	1.68E-26	Down	-5.35E-01	6.36E-04		-4.14E-01	2.05E-05		-1.23E+00	1.05E-29	Down	-7.85E-01	1.71E-03		-1.27E+00	5.80E-07	Down	Unigene1946_All//gi|71905585|gb|AAZ52770.1|//1.00E-118//expressed protein [Arabidopsis thaliana]	Unigene1946_All//5.00E-96//AT5G42690| unknown protein	Unigene1946_All//0.00E+00//gi|3326055|gb|AI054941.1|AI054941				nr -
Unigene19460_All	512	6.13	0.69	1.04	2.34	1.88	1.23	0.83	0.98	1.40	-3.15E+00	2.66E-11	Down	-2.56E+00	8.65E-09	Down	-3.10E-01	6.07E-01		-9.19E-01	1.46E-01		2.46E-01	7.84E-01		7.62E-01	3.02E-01		Unigene19460_All//gi|15223699|ref|NP_173419.1|//3.00E-50//glyoxal oxidase-related [Arabidopsis thaliana] >gi|16604507|gb|AAL24259.1|At1g19900/F6F9_4 [Arabidopsis thaliana]	Unigene19460_All//1.00E-50//AT1G75620| glyoxal oxidase-related	Unigene19460_All//0.00E+00//TC176842			GO:0016491//GO:0031410	nr +
Unigene19462_All	425	0.25	1.67	0.50	0.00	0.65	0.21	0.30	0.20	2.06	2.76E+00	9.15E-03		1.03E+00	5.92E-01		9.34E+00	7.02E-02		7.73E+00	4.77E-01		-6.01E-01	7.66E-01		2.79E+00	5.37E-04	Up			Unigene19462_All//2.00E-37//gi|78345912|gb|DT566186.1|DT566186				
Unigene19464_All	481	1.85	0.21	1.11	3.31	1.65	0.47	1.41	0.52	0.41	-3.13E+00	1.19E-03		-7.40E-01	3.48E-01		-1.01E+00	4.26E-02		-2.82E+00	8.55E-06	Down	-1.43E+00	7.84E-02		-1.76E+00	2.80E-02		Unigene19464_All//gi|10177699|dbj|BAB11025.1|//5.00E-17//pattern formation protein [Arabidopsis thaliana]	Unigene19464_All//3.00E-18//AT5G39500| pattern formation protein, putative	Unigene19464_All//5.00E-38//TC143189			GO:0000578//GO:0000902//GO:0001738//GO:0003006//GO:0009926//GO:0015300//GO:0032386//GO:0033205//GO:0042802//GO:0045229//GO:0048527//GO:0048764	nr -
Unigene19469_All	383	0.82	0.79	0.56	0.00	1.17	0.83	0.99	2.07	4.26	-4.61E-02	9.85E-01		-5.60E-01	6.64E-01		1.02E+01	8.01E-03		9.69E+00	4.08E-02		1.06E+00	1.41E-01		2.10E+00	3.51E-05	Up			Unigene19469_All//4.00E-07//TC165318				
Unigene19470_All	282	0.93	14.55	2.27	1.41	1.10	3.04	1.95	1.33	1.27	3.97E+00	2.03E-17	Up	1.29E+00	1.86E-01		-3.63E-01	7.54E-01		1.11E+00	1.67E-01		-5.47E-01	5.52E-01		-6.16E-01	4.68E-01				Unigene19470_All//9.00E-122//TC162104				
Unigene19471_All	892	0.00	0.00	0.00	0.00	0.00	0.00	7.73	15.04	0.31	null	null		null	null		null	null		null	null		9.61E-01	8.62E-12		-4.63E+00	6.54E-41	Down	Unigene19471_All//gi|242068411|ref|XP_002449482.1|//5.00E-12//hypothetical protein SORBIDRAFT_05g016430 [Sorghum bicolor] >gi|241935325|gb|EES08470.1|hypothetical protein SORBIDRAFT_05g016430 [Sorghum bicolor]		Unigene19471_All//2.00E-29//TC142721				nr +
Unigene19475_All	3662	0.01	0.00	0.00	0.01	0.05	0.00	1.69	0.50	6.82	-3.84E+00	6.13E-01		-3.84E+00	6.25E-01		1.79E+00	5.21E-01		-3.77E+00	6.36E-01		-1.75E+00	1.66E-13	Down	2.02E+00	1.48E-64	Up	Unigene19475_All//gi|34761721|gb|AAQ82033.1|//1.00E-117//gag/pol polyprotein [Pisum sativum]		Unigene19475_All//0.00E+00//TC142701				nr +
Unigene19476_All	272	1.54	0.00	2.35	4.40	1.77	0.83	0.00	0.31	0.29	-1.06E+01	1.05E-02		6.10E-01	5.09E-01		-1.31E+00	2.84E-02		-2.40E+00	7.07E-04	Down	8.26E+00	4.01E-01		8.19E+00	4.04E-01								
Unigene19479_All	1543	0.64	0.20	0.21	0.03	0.00	0.00	24.94	9.53	12.75	-1.71E+00	2.09E-02		-1.64E+00	3.43E-02		-5.01E+00	5.56E-01		-5.01E+00	6.36E-01		-1.39E+00	1.87E-57	Down	-9.67E-01	1.29E-33		Unigene19479_All//gi|15226375|ref|NP_178299.1|//1.00E-156//endonuclease/exonuclease/phosphatase family protein [Arabidopsis thaliana]	Unigene19479_All//4.00E-152//AT2G01900| endonuclease/exonuclease/phosphatase family protein					nr -
Unigene19480_All	723	0.00	0.14	0.29	0.41	0.10	1.00	1.52	3.53	1.93	7.13E+00	3.87E-01		8.20E+00	1.41E-01		-2.12E+00	1.65E-01		1.27E+00	1.56E-01		1.21E+00	7.71E-04	Up	3.43E-01	5.03E-01		Unigene19480_All//gi|9759309|dbj|BAB09815.1|//5.00E-07//non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]		Unigene19480_All//4.00E-09//DN799902			GO:0005488	nr +
Unigene19481_All	429	0.00	0.00	0.00	2.67	0.48	3.05	5.62	6.24	3.06	null	null		null	null		-2.47E+00	2.73E-04	Down	1.93E-01	7.47E-01		1.51E-01	6.79E-01		-8.74E-01	1.30E-02				Unigene19481_All//2.00E-59//CD485516				
Unigene19485_All	438	0.00	0.35	0.49	0.34	0.31	2.47	1.64	1.72	1.46	8.44E+00	2.35E-01		8.93E+00	1.41E-01		-1.18E-01	9.11E-01		2.88E+00	4.98E-04	Up	6.58E-02	9.46E-01		-1.73E-01	7.94E-01								
Unigene19489_All	426	0.37	1.43	0.13	1.75	1.70	2.12	1.19	0.69	7.58	1.95E+00	6.04E-02		-1.56E+00	5.33E-01		-4.72E-02	9.43E-01		2.74E-01	7.10E-01		-7.94E-01	4.02E-01		2.67E+00	2.78E-12	Up	Unigene19489_All//gi|15239795|ref|NP_199723.1|//2.00E-26//senescence-associated protein-related [Arabidopsis thaliana]	Unigene19489_All//1.00E-21//AT5G49120| senescence-associated protein-related	Unigene19489_All//3.00E-175//TC169776				nr +
Unigene1949_All	1961	2.51	0.54	1.14	7.72	4.90	2.65	1.36	0.90	0.87	-2.21E+00	5.32E-12	Down	-1.14E+00	7.74E-05	Down	-6.57E-01	6.17E-07		-1.54E+00	8.21E-24	Down	-6.02E-01	8.47E-02		-6.37E-01	5.56E-02		Unigene1949_All//gi|19715622|gb|AAL91632.1|//1.00E-144//AT4g37080/CTA10_280 [Arabidopsis thaliana] >gi|23463049|gb|AAN33194.1|At4g37080/CTA10_280 [Arabidopsis thaliana]	Unigene1949_All//3.00E-120//AT4G37080| unknown protein	Unigene1949_All//0.00E+00//gi|3326055|gb|AI054941.1|AI054941				nr -
Unigene19496_All	233	0.22	1.09	0.46	0.00	0.44	0.19	17.96	3.41	6.84	2.28E+00	2.34E-01		1.03E+00	7.03E-01		8.79E+00	4.56E-01		7.60E+00	6.96E-01		-2.40E+00	9.55E-14	Down	-1.39E+00	2.97E-07	Down							
Unigene19499_All	338	0.31	0.00	3.31	1.92	1.02	1.74	0.00	0.00	0.24	-8.27E+00	3.73E-01		3.42E+00	1.92E-04	Up	-9.11E-01	3.04E-01		-1.41E-01	8.73E-01		null	null		7.88E+00	4.04E-01								
Unigene195_All	798	1.18	2.10	0.47	1.50	0.78	0.96	3.87	2.15	1.65	8.28E-01	1.04E-01		-1.34E+00	8.48E-02		-9.48E-01	1.12E-01		-6.39E-01	3.24E-01		-8.49E-01	7.21E-03		-1.23E+00	9.25E-05	Down	Unigene195_All//gi|115480765|ref|NP_001063976.1|//5.00E-29//Os09g0569200 [Oryza sativa Japonica Group] >gi|113632209|dbj|BAF25890.1|Os09g0569200 [Oryza sativa Japonica Group]	Unigene195_All//1.00E-46//AT4G00490| BAM2 (BETA-AMYLASE 2); beta-amylase	Unigene195_All//1.00E-49//CA993976		ko00500|Starch and sucrose metabolism		nr +
Unigene1950_All	1627	57.85	26.88	55.44	27.56	28.06	22.04	1.14	1.57	2.62	-1.11E+00	3.69E-80	Down	-6.14E-02	3.60E-01		2.64E-02	8.21E-01		-3.22E-01	3.37E-05		4.55E-01	2.20E-01		1.20E+00	5.92E-06	Up	Unigene1950_All//gi|22329383|ref|NP_172182.2|//1.00E-155//calcineurin-like phosphoesterase family protein [Arabidopsis thaliana] >gi|30725626|gb|AAP37835.1|At1g07010 [Arabidopsis thaliana]	Unigene1950_All//3.00E-152//AT1G07010| calcineurin-like phosphoesterase family protein	Unigene1950_All//0.00E+00//C0085877				nr -
Unigene19502_All	2160	0.00	0.00	0.00	0.09	0.03	0.38	10.61	10.33	25.73	null	null		null	null		-1.53E+00	4.16E-01		2.03E+00	2.17E-02		-3.81E-02	7.57E-01		1.28E+00	1.96E-74	Up	Unigene19502_All//gi|223452302|gb|ACM89479.1|//1.00E-161//cysteine-rich protein [Glycine max]	Unigene19502_All//8.00E-158//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene19502_All//5.00E-171//DT469086		ko04626|Plant-pathogen interaction		nr -
Unigene19504_All	479	0.76	0.00	0.11	2.39	2.30	0.57	2.38	0.09	0.75	-9.58E+00	1.97E-02		-2.78E+00	1.03E-01		-5.62E-02	9.17E-01		-2.08E+00	2.95E-03		-4.77E+00	5.39E-07	Down	-1.67E+00	4.10E-03		Unigene19504_All//gi|115463745|ref|NP_001055472.1|//5.00E-67//Os05g0398100 [Oryza sativa Japonica Group] >gi|113579023|dbj|BAF17386.1|Os05g0398100 [Oryza sativa Japonica Group]	Unigene19504_All//5.00E-68//AT5G19330| armadillo/beta-catenin repeat family protein / BTB/POZ domain-containing protein	Unigene19504_All//0.00E+00//gi|109860278|gb|DW489257.1|DW489257			GO:0005488	nr +
Unigene19506_All	359	0.73	0.14	0.30	3.05	0.29	0.88	2.00	1.05	0.89	-2.37E+00	2.14E-01		-1.30E+00	4.36E-01		-3.41E+00	1.67E-05	Down	-1.79E+00	1.01E-02		-9.34E-01	2.26E-01		-1.17E+00	1.09E-01								

Unigene19508_All	381	0.27	0.00	0.98	1.70	1.54	1.78	5.22	0.22	1.57	-8.10E+00	3.73E-01		1.83E+00	2.13E-01		-1.46E-01	8.39E-01		6.51E-02	9.50E-01		-4.57E+00	1.31E-11	Down	-1.73E+00	5.14E-05	Down	Unigene19508_All//gi|18700095|gb|AAL77659.1|/6.00E-35//AT3g27230/K17E12_5 [Arabidopsis thaliana]	Unigene19508_All//3.00E-36//AT3G27230| LOCATED IN: Golgi apparatus; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: methyltransferase (TAIR:AT5G40830.2); Has 184 Blast hits to 183 proteins in 14 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 182; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene19508_All//2.00E-24//gi|21089442|gb|BQ401755.1|BQ401755			GO:0016741	nr +
Unigene19511_All	406	0.00	0.37	0.00	0.00	0.17	0.67	0.94	2.16	3.53	8.55E+00	2.35E-01		null	null		7.41E+00	6.10E-01		9.38E+00	7.03E-02		1.21E+00	7.78E-02		1.91E+00	3.23E-04	Up			Unigene19511_All//5.00E-07//TC162985				
Unigene19517_All	353	1.04	1.72	1.21	6.77	5.17	5.89	6.71	3.43	2.71	7.31E-01	4.16E-01		2.18E-01	8.31E-01		-3.90E-01	3.59E-01		-2.03E-01	6.52E-01		-9.66E-01	9.12E-03		-1.31E+00	3.80E-04	Down	Unigene19517_All//gi|224144486|ref|XP_002325306.1|/2.00E-10//BED finger-nhs-lrr resistance protein [Populus trichocarpa] >gi|222862181|gb|EEE99687.1| BED finger-nhs-lrr resistance protein [Populus trichocarpa]		Unigene19517_All//3.00E-91//CO080430			GO:0005488	nr +
Unigene19518_All	405	0.13	0.00	0.00	0.00	0.00	0.00	1.77	1.24	10.03	-7.01E+00	6.13E-01		-7.01E+00	6.25E-01		null	null		null	null		-5.19E-01	5.08E-01		2.50E+00	2.95E-14	Up								
Unigene19521_All	363	1.30	0.98	0.59	4.39	2.28	0.50	1.86	0.69	0.66	-4.09E-01	6.69E-01		-1.14E+00	3.32E-01		-9.48E-01	5.80E-02		-3.14E+00	2.25E-06	Down	-1.43E+00	7.84E-02		-1.50E+00	5.44E-02				Unigene19521_All//4.00E-07//ES852216				
Unigene19524_All	267	64.08	51.24	58.04	1680.25	1216.84	800.93	41.49	28.96	20.44	-3.23E-01	1.85E-02		-1.43E-01	3.71E-01		-4.66E-01	2.98E-103		-1.07E+00	0.00E+00	Down	-5.19E-01	6.58E-04		-1.02E+00	3.32E-11	Down	Unigene19524_All//gi|256010122|gb|ACU55134.1|/5.00E-21//H6-like protein [Gossypium hirsutum]		Unigene19524_All//1.00E-142//gi|21095127|gb|BQ407440.1|BQ407440				nr +
Unigene19953_All	2578	4.77	3.52	6.28	25.68	19.54	12.23	12.68	7.05	3.03	-4.39E-01	6.80E-03		3.97E-01	6.34E-03		-3.94E-01	1.67E-11		-1.07E+00	4.24E-58	Down	-8.46E-01	2.09E-22		-2.07E+00	5.38E-88	Down	Unigene19953_All//gi|87240964|gb|ABD32822.1|/0.00E+00//Protein kinase; U box [Medicago truncatula]	Unigene19953_All//7.00E-174//AT2G45910| protein kinase family protein / U-box domain-containing protein	Unigene19953_All//0.00E+00//TC140383		ko04626|Plant-pathogen interaction	GO:0016301	nr +
Unigene19530_All	447	0.59	0.00	0.00	1.11	1.39	1.01	3.69	0.19	0.27	-9.19E+00	6.71E-02		-9.19E+00	8.58E-02		3.15E-01	7.84E-01		-1.41E-01	8.93E-01		-4.30E+00	2.19E-09	Down	-3.79E+00	5.22E-09	Down								
Unigene19532_All	295	1.95	0.00	0.72	3.04	0.70	1.38	2.58	0.28	1.35	-1.09E+01	1.52E-03		-1.43E+00	1.76E-01		-2.12E+00	5.22E-03		-1.14E+00	1.31E-01		-3.19E+00	7.93E-04	Down	-9.34E-01	1.82E-01									
Unigene19534_All	1853	0.00	0.08	0.00	0.05	0.00	0.00	0.80	1.13	22.49	6.36E+00	2.35E-01		null	null		-5.75E+00	3.13E-01		-5.75E+00	4.00E-01		4.98E-01	2.30E-01		4.82E+00	2.06E-245	Up	Unigene19534_All//gi|79537392|ref|NP_200360.2|//1.00E-172//GEX1 (GAMETE EXPRESSED PROTEIN 1) [Arabidopsis thaliana]	Unigene19534_All//5.00E-1615//AT6G55490| GEX1 (GAMETE EXPRESSED PROTEIN 1)	Unigene19534_All//0.00E+00//gi|164326953|gb|EX165246.1|EX165246				nr +
Unigene19535_All	323	133.47	119.85	191.90	154.53	123.14	208.62	129.20	149.58	61.42	-1.55E-01	7.40E-02		5.24E-01	1.77E-14		-3.28E-01	2.19E-06		4.33E-01	2.05E-12		2.11E-01	2.59E-03		-1.07E+00	5.37E-43	Down	Unigene19535_All//5.00E-27//AT4G22310| unknown protein	Unigene19535_All//1.00E-114//TC157196			GO:0043231	nr -
Unigene19541_All	552	0.85	0.37	0.77	6.41	0.00	0.00	1.15	0.15	0.14	-1.22E+00	2.72E-01		-1.45E-01	8.90E-01		-1.26E+01	1.19E-26	Down	-1.26E+01	2.81E-22	Down	-2.92E+00	4.19E-03		-2.99E+00	2.58E-03				Unigene19541_All//1.00E-23//gi|164348583|gb|ES815657.1|ES815657				
Unigene19543_All	620	2.28	0.90	0.09	2.89	2.67	1.02	0.61	0.54	1.03	-1.34E+00	2.00E-02		-4.73E+00	1.31E-06	Down	-1.18E-01	8.38E-01		-1.50E+00	2.75E-03		-1.86E-01	8.57E-01		7.44E-01	3.53E-01		Unigene19543_All//gi|225431996|ref|XP_002273306.1|/1.00E-24//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene19545_All	491	0.00	0.00	0.00	0.00	0.00	0.00	16.02	20.17	2.11	null	null		null	null		null	null		null	null		3.33E-01	4.78E-02		-2.92E+00	2.77E-32	Down	Unigene19545_All//gi|238014838|gb|ACR38454.1|/5.00E-11//unknown [Zea mays]		Unigene19545_All//2.00E-19//TC152959				nr +
Unigene19546_All	358	0.00	0.00	0.00	0.00	0.00	0.00	1.18	1.05	8.90	null	null		null	null		null	null		null	null		-1.69E-01	8.65E-01		2.91E+00	3.15E-13	Up			Unigene19546_All//2.00E-74//CA993849				
Unigene19548_All	863	0.00	0.00	0.00	0.12	0.00	0.00	7.54	3.54	9.14	null	null		null	null		-6.85E+00	3.13E-01		-6.85E+00	4.00E-01		-1.09E+00	2.12E-07	Down	2.77E-01	1.41E-01		Unigene19548_All//gi|71041098|gb|AAZ20437.1|/2.00E-41//MYB21 [Malus x domestica]	Unigene19548_All//5.00E-39//AT4G05100| AtMYB74 (myb domain protein 74); DNA binding / transcription factor	Unigene19548_All//3.00E-93//gi|73861444|gb|DT464183.1|DT464183	MYB		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene19552_All	689	4.40	1.77	2.01	1.52	0.40	0.13	0.12	0.36	0.81	-1.32E+00	3.63E-04	Down	-1.13E+00	2.86E-03		-1.93E+00	4.39E-03		-3.53E+00	9.34E-05	Down	1.57E+00	3.26E-01		2.72E+00	9.38E-03		Unigene19552_All//gi|15233144|ref|NP_191714.1|/7.00E-57//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565321|sp|Q9M313.1|ATL3K_ARATH RecName: Full=RING-H2 finger protein ATL3K >gi|16226239|gb|AAL16112.1|AF428280_1 AT3g61550/F2A19_150 [Arabidopsis thaliana] >gi|21436049|gb|AAM51602.1| AT3g61550/F2A19_150 [Arabidopsis thaliana]	Unigene19552_All//4.00E-49//AT3G61550| zinc finger (C3HC4-type RING finger) family protein	Unigene19552_All//0.00E+00//TC174018			GO:0046914	nr -
Unigene19557_All	389	2.15	0.00	0.41	5.12	3.45	2.09	0.33	0.21	0.41	-1.11E+01	5.57E-05	Down	-2.39E+00	1.14E-02		-5.69E-01	2.13E-01		-1.29E+00	5.33E-03		-6.02E-01	7.66E-01		3.29E-01	8.51E-01		Unigene19557_All//gi|255563066|ref|XP_002522537.1|/1.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223538228|gb|EEF39837.1| conserved hypothetical protein [Ricinus communis]		Unigene19557_All//8.00E-89//TC178703				nr -
Unigene19559_All	445	2.23	1.71	1.32	7.16	5.49	4.57	22.80	13.90	9.31	-3.87E-01	5.79E-01		-7.63E-01	2.94E-01		-3.83E-01	2.95E-01		-6.50E-01	6.53E-02		-7.14E-01	8.08E-06		-1.29E+00	1.16E-14	Down			Unigene19559_All//3.00E-156//TC175227				
Unigene19560_All	982	0.00	0.00	0.00	0.00	0.00	0.00	99.37	103.43	33.51	null	null		null	null		null	null		null	null		5.77E-02	3.04E-01		-1.57E+00	1.26E-178	Down	Unigene19560_All//gi|226453528|gb|EEH50839.1|/1.00E-19//senescence-associated protein [Micromonas pusilla CCMP1545]		Unigene19560_All//1.00E-55//ES840408				nr -
Unigene19563_All	340	296.54	179.43	202.51	570.81	477.94	448.58	584.46	269.34	192.75	-7.25E-01	2.23E-42		-5.50E-01	2.96E-25		-2.56E-01	9.12E-15		-3.48E-01	2.56E-23		-1.12E+00	1.29E-209	Down	-1.60E+00	0.00E+00	Down	Unigene19563_All//gi|575942|dbj|BAA07681.1|/5.00E-85//stearoyl-acyl carrier protein desaturase [Sesamum indicum]	Unigene19563_All//1.00E-47//AT2G43710| SSI2; acyl-[acyl-carrier-protein] desaturase/ stearoyl-CoA 9-desaturase	Unigene19563_All//0.00E+00//gi|164346720|gb|ES810840.1|ES810840		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0002252//GO:0006633//GO:0006952//GO:0009532//GO:0009694//GO:0009863//GO:0009867//GO:0016215//GO:0046872	nr +
Unigene19574_All	224	1.64	10.63	4.28	9.34	4.00	7.06	11.70	29.11	20.45	2.70E+00	1.63E-07	Up	1.39E+00	7.12E-02		-1.22E+00	3.72E-03		-4.04E-01	3.93E-01		1.31E+00	1.28E-09	Up	8.06E-01	1.01E-03				Unigene19574_All//1.00E-86//TC170973				
Unigene19575_All	237	0.00	0.00	0.00	0.21	0.44	0.19	28.90	140.38	58.50	null	null		null	null		1.05E+00	8.08E-01		-1.41E-01	9.53E-01		2.28E+00	4.27E-98	Up	1.02E+00	1.28E-13	Up	Unigene19575_All//gi|153805698|gb|ABS52574.1|//4.00E-33//nodulin family protein [Gossypium hirsutum]	Unigene19575_All//3.00E-22//AT1G44800| nodulin MtN21 family protein	Unigene19575_All//1.00E-83//TC142141			GO:0044464	nr -
Unigene19577_All	339	0.00	2.24	0.00	1.47	1.52	1.33	1.75	2.84	1.18	1.11E+01	1.77E-04	Up	null	null		5.24E-02	9.80E-01		-1.41E-01	8.93E-01		7.00E-01	2.78E-01		-5.71E-01	4.78E-01									
Unigene19958_All	2185	12.98	12.41	15.45	9.51	13.40	5.79	0.27	0.82	1.48	-6.50E-02	6.01E-01		2.52E-01	1.11E-02		4.95E-01	9.42E-08		-7.16E-01	1.07E-09		1.60E+00	4.89E-04	Up	2.45E+00	3.21E-11	Up	Unigene19958_All//gi|42567960|ref|NP_197451.2|//0.00E+00//tryptophan/ tyrosine permease family protein [Arabidopsis thaliana] >gi|56236058|gb|AAV84485.1| At5g19500 [Arabidopsis thaliana] >gi|56790240|gb|AAW30037.1| At5g19500 [Arabidopsis thaliana]	Unigene19958_All//7.00E-174//AT5G19500| tryptophan/tyrosine permease family protein	Unigene19958_All//0.00E+00//TC175866			GO:0015837//GO:0044464	nr +
Unigene19580_All	445	0.00	0.46	0.12	0.22	0.00	0.00	46.08	211.14	140.46	8.83E+00	1.37E-01		6.90E+00	6.36E-01		-7.81E+00	3.13E-01		-7.81E+00	4.00E-01		2.20E+00	1.53E-263	Up	1.61E+00	1.14E-117	Up								
Unigene19581_All	1582	0.00	0.00	0.00	0.03	0.04	0.00	12.72	4.10	7.93	null	null		null	null		4.66E-01	9.58E-01		-4.98E+00	6.36E-01		-1.64E+00	1.32E-38	Down	-6.81E-01	2.79E-10		Unigene19581_All//gi|119331584|gb|ABL63118.1|/1.00E-102//AT-hook DNA-binding protein [Catharanthus roseus]	Unigene19581_All//2.00E-65//AT4G22810| DNA-binding protein-related	Unigene19581_All//0.00E+00//gi|48789593|gb|CO090907.1|CO090907				nr +
Unigene19584_All	455	2.30	0.00	3.51	0.66	1.29	0.30	0.56	0.00	0.26	-1.12E+01	3.80E-06	Down	6.10E-01	2.61E-01		9.70E-01	3.47E-01		-1.14E+00	4.58E-01		-9.12E+00	4.04E-02		-1.09E+00	4.28E-01		Unigene19584_All//gi|15218422|ref|NP_177979.1|/6.00E-37//ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE): alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75213463|sp|Q9SYM4.1|TPS1_ARATH RecName: Full=Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1; AltName: Full=Trehalose-6-phosphate synthase 1; Short=AtTPS1 >gi|4836875|gb|AAD30578.1|AC007260_9 trehalose-6-phosphate synthase [Arabidopsis thaliana]	Unigene19584_All//2.00E-34//AT1G78580| ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE): alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups	Unigene19584_All//1.00E-13//TC134419		ko00500|Starch and sucrose metabolism	GO:0003006//GO:0005991//GO:0007275//GO:0009756//GO:0035251//GO:0042546	nr +
Unigene19586_All	898	0.52	0.85	0.59	0.00	0.12	0.00	1.27	5.17	1.42	6.91E-01	3.76E-01		1.77E-01	8.45E-01		6.85E+00	4.56E-01		null	null		2.02E+00	2.16E-12	Up	1.59E-01	7.53E-01		Unigene19586_All//gi|23505399|gb|AAN37688.1|/7.00E-12//elicitor-like mating protein M81 [Phytophthora infestans] >gi|37930527|gb|AAP74661.1| elicitor-like transglutaminase M81 [Phytophthora infestans]	Unigene19586_All//3.00E-07//AT5G56330| ACA8 (ALPHA CARBONIC ANHYDRASE 8); carbonate dehydratase/ zinc ion binding			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene19587_All	486	0.22	0.00	0.00	0.72	0.28	0.28	9.13	2.84	1.39	-7.75E+00	3.73E-01		-7.75E+00	3.94E-01		-1.34E+00	3.08E-01		-1.36E+00	3.37E-01		-1.69E+00	1.74E-09	Down	-2.71E+00	3.45E-17	Down	Unigene19587_All//gi|224065443|ref|XP_002301820.1|/1.00E-32//predicted protein [Populus trichocarpa] >gi|222843546|gb|EEE81093.1| predicted protein [Populus trichocarpa]						nr +
Unigene19589_All	568	0.00	0.89	1.13	0.35	0.55	0.72	1.86	0.59	0.35	9.80E+00	4.05E-03		1.01E+01	1.16E-03		6.37E-01	6.95E-01		1.03E+00	4.29E-01		-1.66E+00	8.55E-03		-2.41E+00	3.46E-04	Down			Unigene19589_All//4.00E-48//TC178008				
Unigene19590_All	451	0.00	0.56	1.53	1.33	0.92	0.70	0.56	0.28	1.68	9.13E+00	7.86E-02		1.06E+01	6.17E-04	Up	-5.33E-01	5.62E-01		-9.19E-01	3.51E-01		-1.02E+00	4.95E-01		1.58E+00	3.40E-02				Unigene19590_All//3.00E-138//ES820501				
Unigene19592_All	340	12.16	40.98	16.13	15.68	13.07	16.21	142.51	256.68	200.48	1.75E+00	5.56E-24	Up	4.08E-01	1.39E-01		-2.63E-01	3.42E-01		4.79E-02	8.80E-01		8.49E-01	1.00E-38		4.92E-01	1.56E-18				Unigene19592_All//4.00E-127//TC148532				
Unigene19594_All	484	0.97	0.00	0.44	33.66	40.13	25.85	1.92	0.69	0.00	-9.93E+00	5.56E-03		-1.14E+00	3.32E-01		2.54E-01	4.78E-02		-3.81E-01	5.83E-03		-1.48E+00	2.77E-02		-1.09E+01	5.48E-07	Down								
Unigene19596_All	468	0.00	0.00	1.14	0.11	0.15	2.32	347.55	154.05	304.75	null	null		1.02E+01	4.04E-03		4.68E-01	9.58E-01		4.44E+00	2.02E-05	Up	-1.17E+00	1.17E-185	Down	-1.90E-01	7.39E-08		Unigene19596_All//gi|297794291|ref|XP_002865030.1|/8.00E-43//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310865|gb|EFH41289.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene19596_All//3.00E-40//AT5G67050| lipase class 3 family protein	Unigene19596_All//7.00E-28//TC151789			GO:0016787	nr -
Unigene19597_All	636	0.00	0.00	0.00	0.00	0.00	0.00	5.32	2.37	1.57	null	null		null	null		null	null		null	null		-1.17E+00	1.31E-04	Down	-1.76E+00	3.96E-08	Down	Unigene19597_All//gi|297795963|ref|XP_002865866.1|/4.00E-09//AT5g51550/K17N15_10 [Arabidopsis lyrata subsp. lyrata] >gi|297311701|gb|EFH42125.1| AT5g51550/K17N15_10 [Arabidopsis lyrata subsp. lyrata]	Unigene19597_All//2.00E-10//AT5G51550| EXL3 (EXORDIUM LIKE 3)					nr -
Unigene19598_All	522	0.00	0.00	0.00	0.00	0.00	0.00	68.04	373.76	155.00	null	null		null	null		null	null		null	null		2.46E+00	0.00E+00	Up	1.19E+00	2.27E-96	Up	Unigene19598_All//gi|183585187|gb|ACC63885.1|/5.00E-61//caffeic acid 3-O-methyltransferase [Populus trichocarpa]	Unigene19598_All//1.00E-12//AT4G35160| O-methyltransferase family 2 protein	Unigene19598_All//0.00E+00//CD486717		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005515//GO:0008171	nr +
Unigene19599_All	462	1.36	1.32	1.61	4.21	1.42	1.08	0.00	0.18	0.00	-4.63E-02	9.72E-01		2.48E-01	7.45E-01		-1.57E+00	4.84E-04	Down	-1.97E+00	9.06E-05	Down	7.50E+00	4.01E-01		null	null									
Unigene196_All	1056	1.93	1.97	2.67	1.84	2.64	2.35	1.88	0.55	0.79	2.59E-02	9.74E-01		4.68E-01	2.38E-01		5.22E-01	1.80E-01		3.55E-01	4.23E-01		-1.76E+00	6.52E-05	Down	-1.25E+00	2.01E-03		Unigene196_All//gi|30690154|ref|NP_182112.2|/4.00E-53//BAM7 (BETA-AMYLASE 7); beta-amylase/ catalytic/ cation binding [Arabidopsis thaliana] >gi|294956510|sp|Q60831.2|BAM7_ARATH RecName: Full=Beta-amylase 7; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Beta-amylase 4	Unigene196_All//9.00E-30//AT2G45880| BAM7 (BETA-AMYLASE 7); beta-amylase/ catalytic/ cation binding					nr +
Unigene19605_All	351	0.00	0.00	0.00	0.00	0.00	0.00	87.33	82.40	9.19	null	null		null	null		null	null		null	null		-8.38E-02	4.22E-01		-3.25E+00	2.95E-137	Down			Unigene19605_All//2.00E-18//gi|73864682|gb|DT467421.1|DT467421				

Unigene19607_All	310	0.00	0.33	0.52	0.00	0.00	0.87	18.82	84.13	23.90	8.35E+00	3.87E-01		9.01E+00	2.39E-01		null	null		9.77E+00	7.03E-02		2.16E+00	4.48E-72	Up	3.45E-01	7.08E-02		Unigene19607_All//gi|297849106|ref|XP_002892434.1|//2.00E-09//carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338276|gb|EFH68693.1|carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene19607_All//8.00E-11//AT1G08080| ACA7 (ALPHA CARBONIC ANHYDRASE 7); carbonate dehydratase/ zinc ion binding	Unigene19607_All//3.00E-134//FF403747		ko00910|Nitrogen metabolism	GO:0005515//GO:0016020//GO:0016836//GO:0018829//GO:0031410//GO:0044237//GO:0046914//GO:0051707	nr -
Unigene19608_All	762	0.00	0.67	0.00	0.00	0.00	0.00	16.04	4.83	1.57	9.38E+00	4.05E-03		null	null		null	null		null	null		-1.73E+00	1.09E-25	Down	-3.35E+00	9.95E-57	Down	Unigene19608_All//gi|124360168|gb|ABN08184.1|//8.00E-42//General substrate transporter [Medicago truncatula] >gi|124361038|gb|ABN09010.1|General substrate transporter [Medicago truncatula]	Unigene19608_All//1.00E-41//AT4G04750| carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene19608_All//5.00E-73//TC135009			GO:0006810//GO:0022891//GO:0044464	nr -
Unigene1961_All	1833	3.88	1.02	0.58	15.93	8.36	13.11	18.04	5.22	23.34	-1.92E+00	2.11E-14	Down	-2.74E+00	9.14E-21	Down	-9.30E-01	2.95E-23		-2.81E-01	5.60E-03		-1.79E+00	2.58E-71	Down	3.72E-01	1.71E-07		Unigene1961_All//gi|28416677|gb|AA042869.1|//1.00E-103//At5g42860 [Arabidopsis thaliana]	Unigene1961_All//2.00E-90//AT1G45688| unknown protein	Unigene1961_All//0.00E+00//TC167582				nr +
Unigene19615_All	601	0.26	0.67	0.62	0.99	1.15	0.60	2.04	0.97	0.53	1.37E+00	2.74E-01		1.25E+00	3.66E-01		2.04E-01	8.21E-01		-7.26E-01	4.60E-01		-1.07E+00	5.31E-02		-1.94E+00	7.80E-04	Down			Unigene19615_All//7.00E-07//CO071818				
Unigene19618_All	332	95.34	47.77	62.71	97.38	92.83	123.52	244.13	97.94	92.88	-9.97E-01	2.99E-23		-6.04E-01	8.82E-10		-6.90E-02	5.60E-01		3.43E-01	2.62E-05		-1.32E+00	3.45E-111	Down	-1.39E+00	1.12E-124	Down	Unigene19618_All//gi|1170898|sp|P46487.1|MDMH_EUCGL//9.00E-53//RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor >gi|473206|emb|CAA55383.1|mitochondrial malate dehydrogenase [Eucalyptus gunnii]	Unigene19618_All//5.00E-51//AT1G53240| malate dehydrogenase (NAD), mitochondrial	Unigene19618_All//0.00E+00//EX169900		ko00620|Pyruvate metabolism/ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0006007//GO:0009060//GO:0016615//GO:0031980//GO:0043648	nr +
Unigene19619_All	481	2.39	0.00	0.55	1.35	1.72	0.75	0.62	0.35	0.33	-1.12E+01	9.91E-07	Down	-2.11E+00	4.75E-03		3.52E-01	6.87E-01		-8.42E-01	3.75E-01		-8.24E-01	5.40E-01		-8.93E-01	4.71E-01		Unigene19619_All//gi|15223858|ref|NP_177842.1|//1.00E-12//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|122215262|sp|Q3ECB8.1|PP128_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g77170	Unigene19619_All//7.00E-14//AT1G77170| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene19624_All	296	0.00	0.51	0.18	0.17	0.12	1.68	1.29	4.52	5.25	9.00E+00	2.35E-01		7.49E+00	6.36E-01		-5.33E-01	8.25E-01		3.32E+00	2.31E-02		1.81E+00	1.20E-03		2.03E+00	8.65E-05	Up							
Unigene19630_All	292	220.93	550.60	318.41	106.28	79.72	100.23	72.40	81.73	30.70	1.32E+00	4.64E-179	Up	5.27E-01	1.15E-21		-4.15E-01	3.31E-06		-8.46E-02	4.75E-01		1.75E-01	1.09E-01		-1.24E+00	1.01E-27	Down			Unigene19630_All//1.00E-157//gi|164346299|gb|EX168441.1|EX168441				
Unigene19632_All	283	4.81	2.33	0.94	0.00	0.73	2.39	0.90	0.00	0.28	-1.05E+00	6.97E-02		-2.35E+00	7.63E-04	Down	9.51E+00	1.57E-01		1.12E+01	4.18E-04	Up	-9.81E+00	4.04E-02		-1.67E+00	2.56E-01								
Unigene19634_All	687	0.00	0.00	0.00	0.00	0.00	0.00	1.60	1.46	0.00	null	null		null	null		null	null		null	null		-1.32E-01	8.19E-01		-1.06E+01	3.33E-08	Down	Unigene19634_All//sp|Q58A42|DD3_DICDI//2.00E-17//Protein DD3-3 OS=Dictyostelium discoideum GN=DD3-3 PE=2 SV=1						swissprot -
Unigene19635_All	479	0.00	0.00	0.00	0.00	0.00	0.00	143.70	22.77	176.40	null	null		null	null		null	null		null	null		-2.66E+00	1.07E-242	Down	2.96E-01	2.31E-09		Unigene19635_All//gi|1015937|emb|CAA62943.1|//2.00E-39//extensin class 1 protein [Vigna unguiculata]		Unigene19635_All//6.00E-07//BQ402955		ko03040|Spliceosome		nr +
Unigene19964_All	3140	12.21	30.00	17.74	16.34	19.03	17.39	15.24	12.67	9.64	1.30E+00	1.50E-102	Up	5.38E-01	1.03E-13		2.20E-01	8.59E-04		8.98E-02	3.00E-01		-2.67E-01	1.15E-04		-6.61E-01	5.24E-22		Unigene1964_All//gi|22795060|gb|AAN05432.1|//0.00E+00//phospholipase D delta isoform 1b [Gossypium hirsutum]	Unigene1964_All//0.00E+00//AT4G35790| ATPLDDELTA; phospholipase D	Unigene1964_All//0.00E+00//TC168809		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism	GO:0004620//GO:0006650//GO:0044464//GO:0046872	nr -
Unigene19640_All	399	0.00	0.00	0.00	0.25	0.69	0.23	3.50	0.63	1.80	null	null		null	null		1.47E+00	4.20E-01		-1.41E-01	9.51E-01		-2.48E+00	3.36E-05	Down	-9.60E-01	4.80E-02		Unigene19640_All//gi|224112158|ref|XP_002332820.1|//7.00E-15//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834208|gb|EEE72685.1| cc-nbs-lrr resistance protein [Populus trichocarpa]						nr -
Unigene19642_All	516	0.00	9.23	4.85	0.00	0.00	0.09	0.00	0.49	0.46	1.32E+01	3.83E-27	Up	1.22E+01	8.33E-14	Up	null	null		6.45E+00	6.96E-01		8.92E+00	4.31E-02		8.86E+00	4.39E-02				Unigene19642_All//5.00E-134//CA993777				
Unigene19643_All	911	0.00	0.00	0.00	0.00	0.00	0.00	5.71	2.39	0.92	null	null		null	null		null	null		null	null		-1.26E+00	2.19E-07	Down	-2.64E+00	2.07E-19	Down	Unigene19643_All//gi|79326918|ref|NP_001031831.1|//3.00E-63//NAMT1; S-adenosylmethionine-dependent methyltransferase [Arabidopsis thaliana] >gi|110741225|dbj|BAF02163.1| S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase-like protein [Arabidopsis thaliana]	Unigene19643_All//3.00E-65//AT5G04370| NAMT1; S-adenosylmethionine-dependent methyltransferase			ko00592|alpha-Linolenic acid metabolism		nr +
Unigene19644_All	308	5.78	1.15	1.90	1.62	0.22	0.00	0.55	0.27	0.00	-2.33E+00	4.65E-05	Down	-1.60E+00	3.12E-03		-2.85E+00	1.78E-02		-1.07E+01	2.97E-03		-1.02E+00	6.14E-01		-9.10E+00	1.08E-01								
Unigene19647_All	790	0.00	0.13	0.00	6.43	2.01	1.43	0.00	0.05	0.20	7.00E+00	3.87E-01		null	null		-1.68E+00	1.38E-10	Down	-2.17E+00	5.64E-13	Down	5.73E+00	6.35E-01		7.66E+00	1.40E-01		Unigene19647_All//gi|18395562|ref|NP_027544.1|//3.00E-46//myb family transcription factor [Arabidopsis thaliana] >gi|16974544|gb|AAL31188.1|At2g03500/T4M8.7 [Arabidopsis thaliana] >gi|20197737|gb|AAD17450.2|expressed protein [Arabidopsis thaliana] >gi|22137230|gb|AAM91460.1|At2g03500/T4M8.7 [Arabidopsis thaliana]	Unigene19647_All//1.00E-47//AT2G03500| myb family transcription factor	Unigene19647_All//4.00E-43//gi|78349622|gb|DT569896.1|DT569896	G2-like			nr -
Unigene1965_All	1661	3.94	3.97	2.79	4.38	4.50	3.10	4.25	1.66	7.68	1.03E-02	9.86E-01		-4.97E-01	4.10E-02		3.91E-02	8.81E-01		-4.98E-01	2.22E-02		-1.36E+00	7.74E-11	Down	8.52E-01	1.33E-09		Unigene1965_All//gi|22326749|ref|NP_196783.2|//3.00E-84//lasl-like family protein [Arabidopsis thaliana]	Unigene1965_All//2.00E-72//AT5G12220| lasl-like family protein	Unigene1965_All//0.00E+00//gi|164324016|gb|ES829867.1|ES829867				nr -
Unigene19655_All	1213	0.00	0.00	0.00	0.00	0.00	0.00	2.68	2.03	1.02	null	null		null	null		null	null		null	null		-4.01E-01	2.15E-01		-1.40E+00	7.35E-06	Down	Unigene19655_All//gi|209967430|gb|ACJ02343.1|//6.00E-18//U-box domain-containing protein [Helianthus annuus]	Unigene19655_All//1.00E-14//AT3G06880| nucleotide binding					nr -
Unigene1966_All	2996	18.27	10.84	11.32	39.19	26.76	18.78	8.74	5.02	2.42	-7.53E-01	7.00E-25		-6.90E-01	1.22E-20		-5.51E-01	6.77E-37		-1.06E+00	2.93E-101	Down	-7.99E-01	1.78E-16		-1.85E+00	3.73E-61	Down	Unigene1966_All//gi|124359162|gb|ABN05685.1|//1.00E-139//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene1966_All//4.00E-40//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene1966_All//0.00E+00//TC153354				nr +
Unigene19667_All	383	0.27	32.81	3.06	1.69	4.23	1.53	0.00	0.00	0.00	6.91E+00	3.06E-68	Up	3.48E+00	1.09E-04	Up	1.32E+00	1.19E-02		-1.41E-01	8.73E-01		null	null		null	null									
Unigene19670_All	335	1.56	3.78	0.95	2.83	1.44	0.27	0.38	0.25	0.36	1.28E+00	3.83E-02		-7.12E-01	4.97E-01		-9.73E-01	1.60E-01		-3.39E+00	3.18E-04	Down	-6.02E-01	7.66E-01		-8.56E-02	9.69E-01				Unigene19670_All//3.00E-60//TC152633				ESTscan +
Unigene19678_All	245	2.35	4.34	2.39	8.34	9.56	4.42	10.35	5.63	2.44	8.87E-01	1.85E-01		2.54E-02	9.98E-01		1.97E-01	6.84E-01		-9.14E-01	4.37E-02		-8.79E-01	1.32E-02		-2.09E+00	1.16E-07	Down			Unigene19678_All//2.00E-125//TC155555				
Unigene1968_All	1579	12.82	9.69	8.60	10.63	10.73	10.35	9.88	3.84	4.21	-4.04E-01	9.91E-04		-5.76E-01	4.87E-06		1.32E-02	9.51E-01		-3.82E-02	8.11E-01		-1.36E+00	3.42E-23	Down	-1.23E+00	1.74E-20	Down	Unigene1968_All//gi|297845538|ref|XP_002890650.1|//1.00E-138//aspartate/glutamate/uridylate kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336492|gb|EFH66909.1|aspartate/glutamate/uridylate kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene1968_All//2.00E-128//AT1G26640| aspartate/glutamate/uridylate kinase family protein	Unigene1968_All//0.00E+00//TC137793			GO:0003824//GO:0006520	nr -
Unigene19685_All	945	0.00	0.21	0.00	0.16	0.00	0.00	2.51	0.44	3.46	7.74E+00	1.37E-01		null	null		-7.30E+00	1.66E-01		-7.30E+00	2.33E-01		-2.50E+00	1.92E-08	Down	4.64E-01	1.23E-01		Unigene19685_All//gi|15226598|ref|NP_179755.1|//1.00E-98//pectinesterase family protein [Arabidopsis thaliana] >gi|75306124|sp|Q9SLJ9.1|PME11_ARATH RecName: Full=Putative pectinesterase 11; Short=PE 11; AltName: Full=Pectin methylesterase 11; Short=AtPME11	Unigene19685_All//2.00E-100//AT2G21610| pectinesterase family protein			ko00500|Starch and sucrose metabolism/ko00040|Pentose and glucuronate interconversions		nr +
Unigene19688_All	302	3.29	0.00	2.64	14.52	3.19	2.09	0.84	1.11	0.00	-1.17E+01	7.46E-06	Down	-3.16E-01	6.27E-01		-2.18E+00	5.89E-13	Down	-2.79E+00	6.30E-15	Down	3.99E-01	7.24E-01		-9.71E+00	3.04E-02		Unigene19688_All//gi|240255417|ref|NP_199740.4|//2.00E-08//protein binding [Arabidopsis thaliana]	Unigene19688_All//5.00E-06//AT5G49290| protein binding	Unigene19688_All//2.00E-21//ES845121		ko04626|Plant-pathogen interaction		nr -
Unigene1969_All	793	9.90	20.19	17.93	22.30	20.97	22.27	29.86	36.26	19.69	1.03E+00	1.08E-12	Up	8.57E-01	3.21E-08		-8.85E-02	5.87E-01		-2.10E-03	9.86E-01		2.80E-01	2.28E-03		-6.00E-01	1.03E-09		Unigene1969_All//gi|224068086|ref|XP_002302662.1|//1.00E-115//cpk-related protein kinase 3 [Populus trichocarpa] >gi|222844388|gb|EEE81935.1| cpk-related protein kinase 3 [Populus trichocarpa]	Unigene1969_All//6.00E-99//AT2G46700| calcium-dependent protein kinase, putative / CDPK, putative	Unigene1969_All//0.00E+00//TC131981			GO:0000278//GO:0001411//GO:0002521//GO:0004672//GO:0006464//GO:0007017//GO:0009593//GO:0015630//GO:0016059//GO:0016461//GO:0032028//GO:0032412//GO:0032559//GO:0042993//GO:0042995//GO:0046872//GO:0051276	nr -
Unigene19690_All	303	11.05	10.03	11.60	11.18	9.21	7.01	34.33	16.14	11.18	-1.39E-01	6.76E-01		6.98E-02	8.37E-01		-2.80E-01	4.41E-01		-6.74E-01	4.56E-02		-1.09E+00	2.85E-11	Down	-1.62E+00	1.09E-20	Down	Unigene19690_All//gi|145910320|gb|ABP98813.1|//8.00E-08//chloroplast biotin carboxylase [Gossypium hirsutum]		Unigene19690_All//6.00E-160//gi|11206695|gb|BF275625.1|BF275625				nr -
Unigene19692_All	405	108.39	53.80	41.42	188.19	181.95	121.89	283.75	85.14	95.61	-1.01E+00	1.16E-32	Down	-1.39E+00	9.47E-52	Down	-4.86E-02	5.39E-01		-6.27E-01	5.91E-27		-1.74E+00	1.82E-236	Down	-1.57E+00	1.89E-210	Down	Unigene19692_All//gi|218202930|gb|ACK76232.1|//7.00E-73//alpha-tubulin [Dimocarpus longan]	Unigene19692_All//8.00E-73//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene19692_All//4.00E-174//EV483777		ko04145|Phagosome		nr +
Unigene19693_All	368	4.12	0.96	0.87	6.36	1.87	1.72	1.38	0.23	1.30	-2.10E+00	5.39E-04	Down	-2.25E+00	5.02E-04	Down	-1.77E+00	1.69E-05	Down	-1.89E+00	2.33E-05	Down	-2.60E+00	2.05E-02		-8.58E-02	9.30E-01		Unigene19693_All//gi|42568733|ref|NP_201147.2|//2.00E-54//emb2746 (embryo defective 2746): DNA binding / catalytic/ hydrolase [Arabidopsis thaliana]	Unigene19693_All//7.00E-56//AT5G63420| emb2746 (embryo defective 2746); DNA binding / catalytic/ hydrolase	Unigene19693_All//1.00E-38//TC176938	Trihelix			nr +
Unigene19695_All	336	7.47	0.60	9.98	1.33	1.84	1.08	0.00	0.12	0.24	-3.63E+00	2.75E-10	Down	4.18E-01	2.42E-01		4.67E-01	6.35E-01		-3.11E-01	7.57E-01		6.96E+00	6.35E-01		7.89E+00	4.04E-01								
Unigene19697_All	385	2.85	0.00	0.83	3.11	3.31	0.70	1.65	0.43	0.52	-1.15E+01	1.95E-06	Down	-1.78E+00	1.57E-02		9.18E-02	9.00E-01		-2.14E+00	1.81E-03		-1.92E+00	3.09E-02		-1.67E+00	4.29E-02		Unigene19697_All//gi|42571239|ref|NP_973693.1|//7.00E-31//oxidoreductase family protein [Arabidopsis thaliana]	Unigene19697_All//4.00E-32//AT2G45630| oxidoreductase family protein	Unigene19697_All//6.00E-173//gi|21095657|gb|BQ407970.1|BQ407970		ko00620|Pyruvate metabolism/ko00260|Glycine, serine and threonine metabolism/ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene19698_All	736	1.00	0.00	0.29	0.00	0.05	0.00	3.10	0.17	1.41	-9.96E+00	2.11E-04	Down	-1.78E+00	6.00E-02		5.55E+00	8.30E-01		null	null		-4.19E+00	1.33E-12	Down	-1.14E+00	2.03E-03		Unigene19698_All//gi|115468064|ref|NP_001057631.1|//8.00E-57//Os06g0474300 (Oryza sativa Japonica Group) >gi|113595671|dbj|BAF19545.1|Os06g0474300 (Oryza sativa Japonica Group)	Unigene19698_All//5.00E-67//AT3G05390| unknown protein	Unigene19698_All//0.00E+00//gi|109846368|gb|DW244926.1|DW244926				nr -
Unigene1970_All	959	1.25	4.33	1.22	2.96	4.27	2.50	7.98	11.99	7.93	1.79E+00	6.67E-08	Up	-3.87E-02	9.68E-01		5.29E-01	8.20E-02		-2.46E-01	5.62E-01		5.87E-01	8.11E-05		-8.20E-03	9.76E-01		Unigene1970_All//gi|224068086|ref|XP_002302662.1|//3.00E-42//cpk-related protein kinase 3 [Populus trichocarpa] >gi|222844388|gb|EEE81935.1| cpk-related protein kinase 3 [Populus trichocarpa]	Unigene1970_All//1.00E-36//AT2G46700| calcium-dependent protein kinase, putative / CDPK, putative	Unigene1970_All//0.00E+00//gi|164246355|gb|ES842418.1|ES842418			GO:0000278//GO:0001411//GO:0002521//GO:0004672//GO:0006464//GO:0007017//GO:0009593//GO:0015630//GO:0016059//GO:0016461//GO:0032028//GO:0032412//GO:0032559//GO:0042993//GO:0042995//GO:0046872//GO:0051276	nr +
Unigene19700_All	406	2.06	0.75	1.05	6.26	4.75	7.23	6.66	11.12	13.93	-1.46E+00	6.69E-02		-9.75E-01	2.37E-01		-3.98E-01	3.25E-01		2.09E-01	6.38E-01		7.38E-01	3.57E-03		1.06E+00	1.81E-06	Up	Unigene19700_All//gi|115187640|gb|ABI84264.1|//6.00E-53//ubiquitin-conjugating enzyme [Arachis hypogaea]	Unigene19700_All//7.00E-53//AT3G46160| UBC13 (ubiquitin-conjugating enzyme 13); ubiquitin-protein ligase	Unigene19700_All//5.00E-152//gi|84169243|gb|DR457891.1|DR457891		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -

Unigene19701_All	773	10.69	16.78	9.09	14.56	17.37	33.83	305.97	525.12	1224.74	6.50E-01	3.27E-05		-2.34E-01	3.02E-01		2.55E-01	1.16E-01		1.22E+00	4.87E-28	Up	7.79E-01	1.17E-233		2.00E+00	0.00E+00	Up	Unigene19701_All//gi|224148856|ref|XP_002336723.1|//2.00E-63//cytochrome P450 [Populus trichocarpa] >gi|222836601|gb|EEE74994.1|cytochrome P450 [Populus trichocarpa]	Unigene19701_All//7.00E-58//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene19701_All//0.00E+00//CD485674		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene19703_All	352	0.00	0.00	0.30	1.42	1.37	0.64	49.97	193.19	73.34	null	null		8.24E+00	3.99E-01		-4.73E-02	9.49E-01		-1.14E+00	3.07E-01		1.95E+00	7.36E-164	Up	5.54E-01	3.65E-09		Unigene19703_All//gi|153805698|gb|ABS52574.1|//3.00E-06//nodulin family protein [Gossypium hirsutum]		Unigene19703_All//7.00E-160//TC176912				nr +
Unigene19706_All	961	0.00	0.00	0.33	0.00	0.07	2.63	0.26	0.96	0.87	null	null		8.38E+00	4.52E-02		6.16E+00	6.10E-01		1.14E+01	3.83E-15	Up	1.86E+00	8.33E-03		1.72E+00	1.56E-02		Unigene19706_All//gi|121489775|emb|CAK18859.1|//2.00E-30//Putative RING-H2 finger protein precursor [Phillyrea latifolia]	Unigene19706_All//6.00E-30//AT5G53110| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: zinc finger (C3HC4-type RING finger) family protein (TAIR:AT2G46495.1); Has 118 Blast hits to 116 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 118; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene19710_All	349	0.90	92.05	76.90	0.00	0.20	0.26	0.24	0.00	0.23	6.68E+00	3.58E-173	Up	6.42E+00	1.90E-140	Up	7.62E+00	6.10E-01		8.02E+00	4.77E-01		-7.92E+00	4.04E-01		-8.59E-02	9.72E-01		Unigene19710_All//gi|170514772|gb|ACB15018.1|//8.00E-48//cytochrome c oxidase [Lepidothamnus laxifolius] >gi|170514784|gb|ACB15024.1|cytochrome c oxidase [Microstrobos fitzgeraldii]	Unigene19710_All//2.00E-38//ATMG01360| cytochrome c oxidase subunit 1			ko00190|Oxidative phosphorylation		nr -
Unigene19712_All	559	0.00	0.00	0.00	0.71	1.11	1.54	2.57	0.75	1.28	null	null		null	null		6.37E-01	5.49E-01		1.11E+00	1.67E-01		-1.78E+00	8.40E-04	Down	-1.00E+00	3.60E-02		Unigene19712_All//gi|224077026|ref|XP_002305098.1|//1.00E-53//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222848062|gb|EEE85609.1|AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene19712_All//1.00E-21//AT4G18450| ethylene-responsive factor, putative		AP2-EREBP			nr +
Unigene19715_All	412	0.76	0.25	2.59	2.78	1.42	1.10	0.72	1.93	11.99	-1.63E+00	2.76E-01		1.76E+00	1.85E-02		-9.69E-01	1.14E-01		-1.34E+00	4.01E-02		1.42E+00	5.34E-02		4.06E+00	1.51E-26	Up			Unigene19715_All//5.00E-07//DN816857					
Unigene19716_All	272	0.96	0.00	1.57	1.10	3.29	0.00	3.42	0.61	0.00	-9.91E+00	6.71E-02		7.04E-01	5.54E-01		1.58E+00	4.38E-02		-1.01E+01	4.00E-02		-2.48E+00	1.07E-03		-1.17E+01	5.48E-07	Down			Unigene19716_All//5.00E-123//TC175873					
Unigene19717_All	668	0.00	0.23	0.00	2.39	2.63	0.34	0.13	0.25	0.06	7.83E+00	2.35E-01		null	null		1.40E-01	8.32E-01		-2.82E+00	8.55E-06	Down	9.83E-01	6.34E-01		-1.09E+00	6.76E-01		Unigene19717_All//gi|18406405|ref|NP_566003.1|//9.00E-72//OEP37; ion channel [Arabidopsis thaliana] >gi|20197072|gb|AAC23403.2|expressed protein [Arabidopsis thaliana]	Unigene19717_All//2.00E-68//AT2G43950| OEP37; ion channel	Unigene19717_All//5.00E-147//gi|78328168|gb|DT548442.1|DT548442				nr +
Unigene19718_All	320	0.00	2.22	0.50	2.02	2.91	2.82	1.06	0.13	0.37	1.11E+01	3.33E-04	Up	8.96E+00	2.39E-01		5.22E-01	5.25E-01		4.80E-01	5.50E-01		-3.02E+00	5.30E-02		-1.50E+00	2.11E-01										
Unigene19719_All	369	11.20	4.39	9.52	2.70	2.89	3.18	0.34	0.34	0.43	-1.35E+00	1.53E-05	Down	-2.34E-01	4.73E-01		9.96E-02	9.02E-01		2.37E-01	7.09E-01		-1.65E-02	1.02E+00		3.30E-01	8.51E-01										
Unigene19722_All	380	149.53	2055.45	797.07	192.57	515.44	438.92	139.30	257.48	758.93	3.78E+00	0.00E+00	Up	2.41E+00	0.00E+00	Up	1.42E+00	2.39E-290	Up	1.19E+00	2.39E-170	Up	8.86E-01	1.13E-70		2.45E+00	0.00E+00	Up	Unigene19722_All//gi|38049670|gb|AAR10466.1|//1.00E-06//chloroplast outer envelope protein translocator Toc12 [Pisum sativum]	Unigene19722_All//3.00E-07//AT1G80920| J8; heat shock protein binding / unfolded protein binding	Unigene19722_All//0.00E+00//TC139195				nr -
Unigene19723_All	499	232.25	87.63	89.11	184.88	191.43	321.30	314.43	253.79	415.47	-1.41E+00	2.11E-143	Down	-1.38E+00	2.85E-135	Down	5.02E-02	4.51E-01		7.97E-01	1.01E-84		-3.09E-01	1.70E-17		4.02E-01	8.75E-38		Unigene19723_All//gi|300790610|tpg|DAA33870.1|//1.00E-52//TPA: TPA_inf: aquaporin TIP1;8 [Gossypium hirsutum]	Unigene19723_All//9.00E-42//AT2G36830| GAMMA-TIP (GAMMA TONOPLAST INTRINSIC PROTEIN); water channel	Unigene19723_All//4.00E-113//TC147846				nr +
Unigene19728_All	256	0.61	0.99	0.00	0.39	0.67	0.00	25.60	11.59	9.18	6.91E-01	6.27E-01		-9.26E+00	2.45E-01		7.89E-01	7.71E-01		-8.60E+00	4.00E-01		-1.14E+00	6.22E-08	Down	-1.48E+00	8.27E-12	Down									
Unigene19729_All	335	0.00	0.00	0.00	0.00	0.00	0.00	43.79	7.61	13.32	null	null		null	null		null	null		null	null		-2.52E+00	2.79E-49	Down	-1.72E+00	2.75E-31	Down	Unigene19729_All//gi|225544167|ref|YP_002720156.1|//7.00E-10//ORF126 [Jatropha curcas] >gi|225544183|ref|YP_002720173.1|ORF126 [Jatropha curcas] >gi|224979608|gb|ACN72735.1|ORF126 [Jatropha curcas] >gi|224979624|gb|ACN72751.1|ORF126 [Jatropha curcas]		Unigene19729_All//4.00E-16//TC155879				nr +
Unigene1973_All	291	2.88	0.00	0.18	1.20	0.47	0.62	1.60	0.57	1.28	-1.15E+01	5.57E-05	Down	-3.97E+00	9.08E-04	Down	-1.34E+00	3.08E-01		-9.49E-01	4.81E-01		-1.48E+00	1.53E-01		1.55E-01	8.60E-01										
Unigene19731_All	244	18.44	8.72	16.37	5.92	7.90	11.11	0.87	0.34	0.33	-1.08E+00	1.90E-04	Down	-1.72E-01	6.04E-01		4.17E-01	4.19E-01		9.08E-01	1.87E-02		-1.34E+00	4.30E-01		-1.41E+00	3.80E-01										
Unigene19734_All	292	0.54	1.21	1.09	0.17	0.35	0.31	3.62	2.72	0.82	1.18E+00	3.73E-01		1.03E+00	4.71E-01		1.05E+00	8.08E-01		8.58E-01	7.95E-01		-4.13E-01	5.15E-01		-2.14E+00	9.36E-04	Down									
Unigene19735_All	631	0.17	3.05	0.93	0.87	3.22	2.15	2.14	1.66	2.97	4.20E+00	1.02E-08	Up	2.49E+00	3.75E-02		1.89E+00	7.96E-05	Up	1.31E+00	2.93E-02		-3.73E-01	4.95E-01		4.69E-01	2.63E-01		Unigene19735_All//gi|110289472|gb|ABB47924.2|//1.00E-56//amine oxidase, flavin-containing family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene19735_All//4.00E-53//AT4G16310| LDL3 (LSD1-LIKE3); amine oxidase/ electron carrier/ oxidoreductase					nr -
Unigene19736_All	325	0.00	0.00	0.33	1.84	0.95	0.83	2.99	0.51	0.25	null	null		8.36E+00	3.99E-01		-9.48E-01	3.09E-01		-1.14E+00	2.43E-01		-2.54E+00	6.41E-04	Down	-3.61E+00	2.14E-05	Down			Unigene19736_All//4.00E-121//TC175222					
Unigene19738_All	541	0.00	0.00	0.00	0.00	0.00	0.00	22.74	5.79	1.62	null	null		null	null		null	null		null	null		-1.97E+00	9.97E-31	Down	-3.81E+00	1.39E-63	Down									
Unigene19739_All	563	0.84	0.18	0.19	0.80	1.22	0.56	1.20	0.00	0.57	-2.22E+00	7.76E-02		-2.14E+00	1.03E-01		6.19E-01	5.30E-01		-5.04E-01	6.49E-01		-1.02E+01	6.34E-05	Down	-1.09E+00	1.50E-01		Unigene19739_All//gi|297841913|ref|XP_002888838.1|//3.00E-61//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297334679|gb|EFH65097.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene19739_All//3.00E-61//AT1G71460| pentatricopeptide (PPR) repeat-containing protein	Unigene19739_All//0.00E+00//TC153897				nr -
Unigene19740_All	1474	0.00	6.67	1.95	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.60E-56	Up	1.09E+01	6.96E-16	Up	null	null		null	null		null	null		null	null		Unigene19740_All//gi|297604406|ref|NP_001055367.2|//1.00E-48//0s05g0373400 [Oryza sativa Japonica Group] >gi|255676313|dbj|BAF17281.2|Os05g0373400 [Oryza sativa Japonica Group]	Unigene19740_All//5.00E-26//AT1G03457| RNA-binding protein, putative					nr +
Unigene19741_All	279	3.94	45.04	10.50	1.07	0.37	0.81	1.67	1.95	0.43	3.82E+00	1.12E-47	Up	1.41E+00	3.58E-04	Up	-1.53E+00	2.98E-01		-4.04E-01	7.51E-01		2.24E-01	7.92E-01		-1.96E+00	5.82E-02		Unigene19741_All//gi|50725163|dbj|BAD33780.1|//4.00E-08//ORF82 [Oryza sativa Japonica Group] >gi|51091519|dbj|BAD36252.1| ORF82 [Oryza sativa Japonica Group] >gi|226650|prf||1603356CA ORF 82		Unigene19741_All//1.00E-28//TC129710				nr +
Unigene19750_All	478	2.85	2.97	6.68	7.30	9.94	4.06	1.06	0.26	1.33	6.07E-02	9.22E-01		1.23E+00	8.83E-04	Up	4.47E-01	1.15E-01		-8.44E-01	1.00E-02		-2.02E+00	5.20E-02		3.29E-01	6.60E-01										
Unigene19757_All	345	0.91	0.00	0.46	0.72	0.50	1.44	2.70	2.30	0.12	-9.83E+00	3.66E-02		-9.75E-01	5.06E-01		-5.33E-01	7.13E-01		9.96E-01	3.94E-01		-2.28E-01	7.18E-01		-4.54E+00	6.41E-06	Down	Unigene19757_All//gi|45752630|gb|AAS76213.1|//5.00E-37//At3g08000 [Arabidopsis thaliana] >gi|46359799|gb|AAS88763.1|At3g08000 [Arabidopsis thaliana]	Unigene19757_All//1.00E-36//AT3G08000| RNA-binding protein, putative			ko03010|Ribosome//ko03040|Spliceosome		nr +
Unigene19759_All	481	0.44	0.84	1.44	0.72	0.86	0.56	0.88	0.78	3.15	9.54E-01	4.14E-01		1.73E+00	7.67E-02		2.45E-01	8.53E-01		-3.64E-01	7.55E-01		-1.69E-01	8.65E-01		1.84E+00	3.16E-04	Up	Unigene19759_All//gi|15221621|ref|NP_176479.1|//3.00E-30//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene19759_All//1.00E-31//AT1G62910| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene19760_All	454	0.23	0.11	0.12	1.65	0.61	0.10	1.21	0.18	0.26	-1.05E+00	6.85E-01		-9.75E-01	7.21E-01		-1.44E+00	7.43E-02		-4.05E+00	7.75E-04	Down	-2.72E+00	1.22E-02		-2.20E+00	2.24E-02		Unigene19760_All//gi|75149121|sp|Q84Z01.1|CSLCA_ORYSJ//2.00E-71//RecName: Full=Putative xyloglucan glycosyltransferase 10; AltName: Full=Cellulose synthase-like protein C10; AltName: Full=OsCslC10 >gi|171769907|sp|A2IHR9.1|CSLCA_ORYSI RecName: Full=Putative xyloglucan glycosyltransferase 10; AltName: Full=Cellulose synthase-like protein C10; AltName: Full=OsCslC10	Unigene19760_All//8.00E-62//AT4G07960| ATCSLC12 (CELLULOSE-SYNTHASE LIKE C12); cellulose synthase/ transferase, transferring glycosyl groups	Unigene19760_All//3.00E-107//TC149633				nr -
Unigene19765_All	993	0.11	0.00	0.32	0.35	0.07	0.00	2.34	0.34	1.44	-6.72E+00	3.73E-01		1.61E+00	3.05E-01		-2.34E+00	1.01E-01		-8.46E+00	2.13E-02		-2.80E+00	2.78E-09	Down	-6.97E-01	5.22E-02		Unigene19765_All//gi|297848412|ref|XP_002892087.1|//8.00E-47//T25K16.10 [Arabidopsis lyrata subsp. lyrata] >gi|297337929|gb|EFH68346.1|T25K16.10 [Arabidopsis lyrata subsp. lyrata]	Unigene19765_All//2.00E-42//AT1G01110| IQD18 (IQ-domain 18)					nr +
Unigene19767_All	405	0.00	0.00	0.39	4.06	0.51	1.12	0.00	0.00	0.00	null	null		8.62E+00	2.39E-01		-2.99E+00	3.56E-07	Down	-1.86E+00	6.76E-04	Down	null	null		null	null				Unigene19767_All//5.00E-19//DN500741					
Unigene19769_All	262	27.76	26.50	53.45	13.31	14.98	19.13	11.30	7.02	5.17	-6.72E-02	7.63E-01		9.45E-01	1.96E-09		1.71E-01	6.20E-01		5.24E-01	5.63E-02		-6.87E-01	3.47E-02		-1.13E+00	4.06E-04	Down	Unigene19769_All//gi|18407113|ref|NP_566081.1|//8.00E-22//pyridoxine 5'-phosphate oxidase-related [Arabidopsis thaliana] >gi|20197772|gb|AAD20168.2|expressed protein [Arabidopsis thaliana] >gi|90568006|gb|ABD94073.1|At2g46580 [Arabidopsis thaliana]	Unigene19769_All//3.00E-23//AT2G46580| pyridoxine 5'-phosphate oxidase-related	Unigene19769_All//8.00E-119//TC144927				nr +
Unigene1977_All	1285	20.81	32.53	41.85	14.38	15.17	19.08	37.84	27.32	20.00	6.45E-01	9.10E-15		1.01E+00	2.24E-38	Up	7.67E-02	6.12E-01		4.08E-01	1.64E-04		-4.70E-01	4.09E-12		-9.20E-01	6.29E-39		Unigene1977_All//gi|225428995|ref|XP_002265518.1|//3.00E-94//PREDICTED: similar to APK (APS KINASE): ATP binding / kinase/ transferase, transferring phosphorus-containing groups [Vitis vinifera]	Unigene1977_All//7.00E-93//AT2G14750| APK (APS KINASE); ATP binding / adenylylsulfate kinase/ kinase/ transferase, transferring phosphorus-containing groups	Unigene1977_All//0.00E+00//gi|109872588|gb|DN501563.1|DN501563		ko00230|Purine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0000097//GO:0006796//GO:0007226//GO:0009536//GO:0010675//GO:0016101//GO:0032559	nr -
Unigene19770_All	364	0.43	1.39	3.36	1.09	2.55	1.99	0.58	0.57	0.66	1.69E+00	1.34E-01		2.96E+00	2.55E-04	Up	1.22E+00	1.05E-01		8.59E-01	3.42E-01		-1.67E-02	1.02E+00		1.77E-01	9.09E-01										
Unigene19771_All	416	78.36	30.82	46.72	2.16	5.88	1.85	0.00	0.00	0.00	-1.35E+00	3.26E-38	Down	-7.46E-01	2.80E-14		1.45E+00	4.00E-04	Up	-2.24E-01	7.50E-01		null	null		null	null		Unigene19771_All//gi|41745642|gb|AAS10178.1|//8.00E-53//YABBY-like transcription factor PROLONGATA [Antirrhinum majus]	Unigene19771_All//1.00E-52//AT2G26580| YAB5 (YABBY5); transcription factor	Unigene19771_All//6.00E-99//TC139496	C2C2-YABBY			nr -

Unigene19775_All	1287	0.00	6.02	2.85	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.47E-44	Up	1.15E+01	2.39E-20	Up	null	null		null	null		null	null		null	null		Unigene19775_All//gi|301107582|ref|XP_002902873.1|//4.00E-06//metalloprotease family M01, putative [Phytophthora infestans T30-4] >gi|262097991|gb|EE156043.1| metalloprotease family M01, putative [Phytophthora infestans T30-4]							nr +
Unigene19778_All	897	0.00	0.00	0.00	0.00	0.00	0.00	5.51	0.51	0.44	null	null		null	null		null	null		null	null		-3.43E+00	5.53E-23	Down	-3.63E+00	5.49E-25	Down								
Unigene1978_All	2248	3.40	1.80	2.56	18.79	16.62	8.46	5.98	2.34	2.68	-9.14E-01	1.71E-05		-4.10E-01	6.89E-02		-1.77E-01	3.50E-02		-1.15E+00	7.18E-42	Down	-1.35E+00	7.68E-20	Down	-1.16E+00	2.72E-16	Down	Unigene1978_All//gi|75163506|sp|Q93YU6.1|Y5720_ARATH//0.00E+00//RecName: Full=Probable inactive receptor kinase At5g67200; Flags: Precursor >gi|16649055|gb|AAL24379.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|28059128|gb|AAO30018.1| receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene1978_All//0.00E+00//AT5G67200| leucine-rich repeat transmembrane protein kinase, putative	Unigene1978_All//0.00E+00//TC130259		ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016020//GO:0032559	nr -
Unigene19783_All	407	4.11	3.24	12.56	0.00	1.61	1.89	0.00	0.00	0.00	-3.46E-01	4.98E-01		1.61E+00	5.18E-08	Up	1.07E+01	4.92E-04	Up	1.09E+01	1.27E-04	Up	null	null		null	null		Unigene19783_All//gi|114059563|gb|ABI49431.1|//5.00E-24//At3g16120 [Arabidopsis thaliana]	Unigene19783_All//8.00E-36//AT4G27360| dynein light chain, putative						nr +
Unigene19784_All	319	25.09	66.08	73.95	43.88	46.96	62.44	20.54	38.13	30.47	1.40E+00	3.21E-26	Up	1.56E+00	2.54E-33	Up	9.78E-02	5.82E-01		5.09E-01	2.44E-05		8.92E-01	1.34E-09		5.69E-01	3.66E-04				Unigene19784_All//3.00E-60//TC145076					
Unigene19785_All	903	0.00	0.00	0.00	0.00	0.00	0.20	4.03	2.55	1.41	null	null		null	null		null	null		7.64E+00	1.94E-01		-6.62E-01	2.17E-02		-1.51E+00	3.92E-07	Down	Unigene19785_All//gi|281333033|gb|ADA60971.1|//2.00E-47//stylish [Brassica rapa subsp. pekinensis]	Unigene19785_All//2.00E-38//AT3G51060| STY1 (STYLISH 1); protein heterodimerization/ transcription factor		SRS				nr +
Unigene19786_All	328	100.49	143.20	161.86	88.69	54.49	128.88	227.13	852.23	38.62	5.11E-01	3.97E-11		6.88E-01	6.01E-20		-7.03E-01	2.00E-14		5.39E-01	1.14E-11		1.91E+00	0.00E+00	Up	-2.56E+00	3.97E-259	Down	Unigene19786_All//gi|125620186|gb|ABN49883.1|//2.00E-153//glutathione peroxidase [Nelumbo nucifera]	Unigene19786_All//5.00E-13//AT4G11600| ATGPX6 (GLUTATHIONE PEROXIDASE 6); glutathione peroxidase	Unigene19786_All//1.00E-99//gi|13353956|gb|BG444304.1|BG444304		ko00480|Glutathione metabolism//ko00590|Arachidonic acid metabolism		nr -
Unigene19787_All	726	0.43	0.98	0.88	1.10	1.23	0.81	2.56	2.25	0.60	1.18E+00	1.75E-01		1.03E+00	2.81E-01		1.68E-01	8.32E-01		-4.41E-01	6.14E-01		-1.91E-01	6.62E-01		-2.09E+00	7.81E-06	Down								
Unigene19788_All	399	19.41	18.29	27.36	41.07	48.24	33.28	0.11	0.31	2.00	-8.58E-02	6.90E-01		4.95E-01	5.90E-03		2.32E-01	7.77E-02		-3.04E-01	3.24E-02		1.57E+00	5.45E-01		4.24E+00	7.42E-05	Up			Unigene19788_All//1.00E-167//TC179226					
Unigene19793_All	517	0.00	0.00	0.00	3.18	0.60	1.14	1.39	0.97	1.16	null	null		null	null		-2.41E+00	9.47E-06	Down	-1.49E+00	4.95E-03		-5.19E-01	5.08E-01		-2.66E-01	6.93E-01		Unigene19793_All//gi|18405136|ref|NP_565910.1|//9.00E-15//RTFL8 (ROTUNDIFOLIA LIKE 8) [Arabidopsis thaliana] >gi|20197045|gb|AAM14893.1| Expressed protein [Arabidopsis thaliana] >gi|42822055|tpg|DAA02282.1| TPA_exp: DVL11 [Arabidopsis thaliana]	Unigene19793_All//2.00E-14//AT2G39705| RTFL8 (ROTUNDIFOLIA LIKE 8)	Unigene19793_All//1.00E-103//BE054358				nr -
Unigene198_All	2117	2.60	2.58	3.17	6.54	6.18	6.19	4.15	2.05	2.94	-5.60E-03	9.78E-01		2.88E-01	2.42E-01		-8.18E-02	6.45E-01		-8.04E-02	6.64E-01		-1.02E+00	1.02E-08	Down	-5.01E-01	2.96E-03		Unigene198_All//gi|30690154|ref|NP_182112.2|//0.00E+00//BAM7 (BETA-AMYLASE 7); beta-amylase/ catalytic/ cation binding [Arabidopsis thaliana] >gi|294956510|sp|O80831.2|BAM7_ARATH RecName: Full=Beta-amylase 7; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Beta-amylase 4	Unigene198_All//2.00E-164//AT2G45880| BAM7 (BETA-AMYLASE 7); beta-amylase/ catalytic/ cation binding	Unigene198_All//1.00E-131//gi|13350033|gb|BG440382.1|BG440382		ko00500|Starch and sucrose metabolism		nr -
Unigene1980_All	1642	6.91	8.83	7.75	16.81	16.90	39.11	29.97	39.58	36.30	3.52E-01	1.89E-02		1.65E-01	3.76E-01		8.20E-03	9.49E-01		1.22E+00	2.01E-68	Up	4.01E-01	4.34E-12		2.76E-01	3.85E-06		Unigene1980_All//gi|18412659|ref|NP_567142.1|//1.00E-135//PLP9 (PATATIN-LIKE PROTEIN 9); nutrient reservoir [Arabidopsis thaliana] >gi|15912227|gb|AAL08247.1| AT3g63200/F16M2_50 [Arabidopsis thaliana] >gi|24111291|gb|AAN46769.1| At3g63200/F16M2_50 [Arabidopsis thaliana]	Unigene1980_All//1.00E-152//AT3G63200| PLP9 (PATATIN-LIKE PROTEIN 9); nutrient reservoir	Unigene1980_All//0.00E+00//TC153637				nr +
Unigene19802_All	540	2.52	7.69	8.48	0.55	0.38	0.59	0.00	0.00	0.15	1.61E+00	6.13E-07	Up	1.75E+00	4.52E-08	Up	-5.33E-01	6.79E-01		8.11E-02	9.50E-01		null	null		7.21E+00	4.04E-01		Unigene19802_All//gi|297742411|emb|CBI34560.3|//6.00E-06//unnamed protein product [Vitis vinifera]		Unigene19802_All//0.00E+00//gi|109877138|gb|DW506112.1|DW506112				nr +
Unigene19805_All	751	0.84	0.88	0.28	1.72	5.32	3.91	0.45	0.17	0.05	6.92E-02	9.50E-01		-1.56E+00	1.29E-01		1.62E+00	1.78E-07	Up	1.18E+00	1.42E-03		-1.43E+00	2.58E-01		-3.09E+00	3.92E-02		Unigene19805_All//gi|224071740|ref|XP_002303566.1|//7.00E-92//cytochrome P450 [Populus trichocarpa] >gi|222840998|gb|EEE78545.1| cytochrome P450 [Populus trichocarpa]	Unigene19805_All//7.00E-86//AT1G12740| CYP87A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene19805_All//8.00E-177//gi|3326060|gb|AI054946.1|AI054946		ko00906|Carotenoid biosynthesis//ko00905|Brassinosteroid biosynthesis		nr -
Unigene19808_All	218	0.96	5.35	1.95	2.74	3.32	2.07	0.19	0.77	0.91	2.48E+00	9.80E-04	Up	1.03E+00	3.97E-01		2.75E-01	8.01E-01		-4.05E-01	6.73E-01		1.98E+00	3.79E-01		2.24E+00	2.49E-01									
Unigene1981_All	4504	0.26	0.30	0.22	3.84	2.02	1.73	11.26	4.69	3.80	2.49E-01	6.39E-01		-1.87E-01	7.59E-01		-9.27E-01	7.06E-14		-1.15E+00	2.62E-17	Down	-1.26E+00	1.66E-65	Down	-1.57E+00	6.73E-93	Down	Unigene1981_All//gi|15222751|ref|NP_175957.1|//0.00E+00//BRL1 (BRI 1 LIKE); kinase [Arabidopsis thaliana] >gi|186491196|ref|NP_001117501.1| BRL1 (BRI 1 LIKE); kinase [Arabidopsis thaliana] >gi|57012628|sp|Q9ZWC8.1|BRL1_ARATH RecName: Full=Serine/threonine-protein kinase BRI1-like 1; AltName: Full=BRASSINOSTEROID INSENSITIVE 1-like protein 1; Flags: Precursor >gi|8778502|gb|AAF79510.1|AC002328_18 F20N2.4 [Arabidopsis thaliana] >gi|224589444|gb|ACN59256.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene1981_All//0.00E+00//AT1G55610| BRL1 (BRI 1 LIKE); kinase	Unigene1981_All//0.00E+00//TC131112			GO:0005515//GO:0016020//GO:0016301	nr -
Unigene19811_All	609	0.00	15.48	0.00	0.16	0.62	2.15	0.00	0.62	0.52	1.39E+01	5.67E-54	Up	null	null		1.93E+00	1.94E-01		3.72E+00	7.96E-06	Up	9.27E+00	6.86E-03		9.03E+00	1.34E-02		Unigene19811_All//gi|78499709|gb|ABB45861.1|//6.00E-95//DRE-binding protein 3b [Gossypium hirsutum]	Unigene19811_All//1.00E-30//AT5G52020| AP2 domain-containing protein	Unigene19811_All//0.00E+00//TC130704	AP2-EREBP			nr +
Unigene19813_All	464	0.45	0.55	0.92	1.07	0.96	0.00	0.82	3.15	0.69	2.76E-01	8.43E-01		1.03E+00	3.97E-01		-1.54E-01	8.50E-01		-1.01E+01	2.97E-03		1.94E+00	3.23E-04	Up	-2.56E-01	7.85E-01									
Unigene19818_All	493	0.00	0.62	0.00	0.91	1.33	0.27	2.23	0.00	0.73	9.27E+00	4.44E-02		null	null		5.45E-01	5.86E-01		-1.73E+00	1.61E-01		-1.11E+01	7.67E-08	Down	-1.62E+00	6.27E-03		Unigene19818_All//gi|297834964|ref|XP_002885364.1|//1.00E-49//extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata] >gi|297331204|gb|EFH61623.1| extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata]	Unigene19818_All//7.00E-41//AT3G20300| unknown protein	Unigene19818_All//0.00E+00//gi|78335352|gb|DT555626.1|DT555626				nr +
Unigene19819_All	501	0.94	1.42	0.74	0.89	1.10	0.00	2.19	1.00	0.48	5.91E-01	4.78E-01		-3.37E-01	7.34E-01		2.97E-01	8.18E-01		-9.81E+00	5.79E-03		-1.13E+00	5.52E-02		-2.20E+00	5.66E-04	Down								
Unigene1982_All	1071	16.07	12.77	22.42	17.07	17.78	12.06	3.20	1.87	1.00	-3.31E-01	1.49E-02		4.80E-01	2.88E-05		5.88E-02	7.30E-01		-5.01E-01	7.12E-05		-7.72E-01	9.48E-03		-1.67E+00	1.11E-07	Down	Unigene1982_All//gi|110740865|dbj|BAE98529.1|//3.00E-67//quinone reductase-like protein [Arabidopsis thaliana]	Unigene1982_All//8.00E-117//AT3G56460| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene1982_All//0.00E+00//DR458669			GO:0008152//GO:0016655//GO:0042579//GO:0046914	nr -
Unigene19824_All	338	2.17	0.00	1.89	0.59	1.63	1.07	0.88	0.25	0.83	-1.11E+01	2.11E-04	Down	-1.97E-01	7.99E-01		1.47E+00	1.77E-01		8.59E-01	5.42E-01		-1.82E+00	2.11E-01		-8.57E-02	9.52E-01									
Unigene19825_All	828	0.00	0.73	0.00	0.36	0.25	0.16	4.34	6.71	1.35	9.52E+00	1.17E-03		null	null		-5.33E-01	6.79E-01		-1.14E+00	4.58E-01		6.29E-01	5.19E-03		-1.69E+00	4.01E-08	Down								
Unigene19826_All	342	1.22	2.37	1.25	2.62	4.33	3.96	16.81	2.08	2.21	9.54E-01	2.26E-01		2.54E-02	1.00E+00		7.24E-01	2.03E-01		5.96E-01	3.36E-01		-3.02E+00	1.05E-23	Down	-2.93E+00	8.30E-24	Down	Unigene19826_All//gi|283837097|emb|CBH19893.1|//2.00E-16//cell division control 20 [Solanum lycopersicum var. cerasiforme]	Unigene19826_All//3.00E-17//AT4G33260| CDC20.2; signal transducer	Unigene19826_All//3.00E-171//gi|84174756|gb|DR463404.1|DR463404		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene19830_All	485	0.00	0.00	0.00	0.00	0.00	0.00	2.01	1.72	0.25	null	null		null	null		null	null		null	null		-2.18E-01	7.24E-01		-3.02E+00	9.60E-05	Down								
Unigene19831_All	1229	0.00	6.14	2.08	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	3.63E-43	Up	1.10E+01	4.21E-14	Up	null	null		null	null		null	null		null	null		Unigene19831_All//gi|159491160|ref|XP_001703541.1|//6.00E-07//flagellar associated protein [Chlamydomonas reinhardtii] >gi|158280465|gb|EDP06223.1| flagellar associated protein [Chlamydomonas reinhardtii]						nr -
Unigene19832_All	550	3.61	8.38	15.59	0.45	2.07	0.41	0.00	0.23	0.36	1.21E+00	2.90E-05	Up	2.11E+00	1.57E-18	Up	2.19E+00	2.15E-03		-1.42E-01	9.29E-01		7.83E+00	2.40E-01		8.50E+00	7.89E-02									
Unigene19833_All	1245	0.00	0.00	0.00	0.00	0.06	0.00	5.94	13.06	4.58	null	null		null	null		5.79E+00	6.10E-01		null	null		1.14E+00	2.75E-18	Up	-3.77E-01	4.58E-02		Unigene19833_All//gi|5690095|emb|CAB51950.1|//6.00E-07//transposase related protein [Zea mays]		Unigene19833_All//2.00E-18//gi|164302204|gb|ES806978.1|ES806978				nr -
Unigene19841_All	871	1.56	3.20	3.55	2.69	3.48	5.39	11.75	19.67	18.30	1.03E+00	6.58E-03		1.18E+00	1.67E-03		3.72E-01	3.34E-01		1.00E+00	2.96E-04	Up	7.44E-01	7.00E-10		6.39E-01	1.70E-07				Unigene19841_All//2.00E-11//gi|109877736|gb|DW506709.1|DW506709					
Unigene19840_All	684	0.00	0.00	0.00	0.00	0.00	0.00	1.61	2.14	0.00	null	null		null	null		null	null		null	null		4.12E-01	4.19E-01		-1.07E+01	3.33E-08	Down	Unigene19840_All//gi|300268380|gb|EFJ52561.1|//7.00E-85//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene19840_All//3.00E-80//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	Unigene19840_All//2.00E-16//gi|21101234|gb|BQ413547.1|BQ413547		ko03010|Ribosome		nr -
Unigene19843_All	354	0.74	2.43	4.06	2.11	3.31	1.66	1.91	4.13	1.58	1.72E+00	3.49E-02		2.46E+00	3.26E-04	Up	6.48E-01	3.26E-01		-3.48E-01	6.84E-01		1.11E+00	2.51E-02		-2.79E-01	6.89E-01				Unigene19843_All//2.00E-166//gi|78331277|gb|DT551551.1|DT551551					
Unigene19845_All	472	0.00	0.43	0.00	0.00	0.07	0.00	0.72	5.14	1.43	8.75E+00	1.37E-01		null	null		6.19E+00	8.30E-01		null	null		2.84E+00	9.30E-10	Up	1.00E+00	1.91E-01									
Unigene19849_All	380	0.00	0.00	3.50	0.79	2.99	0.83	0.89	0.55	0.21	null	null		1.18E+01	2.40E-07	Up	1.93E+00	5.40E-03		8.11E-02	9.50E-01		-6.95E-01	5.78E-01		-2.09E+00	1.07E-01		Unigene19845_All//gi|28558781|gb|AA045752.1|//1.00E-13//pol protein [Cucumis melo]						nr +
Unigene19851_All	561	0.56	2.44	0.38	0.36	0.55	0.00	3.54	1.34	1.78	2.12E+00	1.09E-03		-5.60E-01	6.64E-01		6.37E-01	6.95E-01		-8.47E+00	1.34E-01		-1.40E+00	9.38E-04	Down	-9.97E-01	1.18E-02		Unigene19849_All//gi|297596195|ref|NP_001042168.2|//8.00E-52//Os01g0175000 [Oryza sativa Japonica Group] >gi|255672923|dbj|BAF04082.2| Os01g0175000 [Oryza sativa Japonica Group]	Unigene19849_All//4.00E-52//AT5G20060| phospholipase/carboxylesterase family protein	Unigene19849_All//5.00E-97//TC148670		ko00564|Glycerophospholipid metabolism		nr +
Unigene19852_All	353	0.00	0.00	0.00	0.00	0.00	0.00	57.97	26.29	5.19	null	null		null	null		null	null		null	null		-1.14E+00	5.25E-23	Down	-3.48E+00	9.18E-98	Down								ESTscan +
Unigene19853_All	587	0.18	0.35	0.45	0.42	0.70	0.00	6.05	3.28	2.31	9.54E-01	6.22E-01		1.35E+00	4.09E-01		7.31E-01	5.86E-01		-8.73E+00	7.34E-02		-8.85E-01	2.39E-03		-1.39E+00	2.86E-06	Down			Unigene19852_All//2.00E-10//TC153505					
Unigene19856_All	243	0.43	0.21	0.00	0.00	0.57	0.00	2.78	10.49	18.85	-1.05E+00	6.85E-01		-8.75E+00	3.94E-01		9.15E+00	3.19E-01		null	null		1.91E+00	1.09E-06	Up	2.76E+00	9.95E-18	Up								
Unigene19857_All	404	1.17	0.13	0.00	0.99	0.85	2.46	3.45	0.83	2.76	-3.22E+00	2.73E-02		-1.02E+01	8.65E-03		-2.11E-01	8.25E-01		1.32E+00	7.15E-02		-2.06E+00	2.51E-04	Down	-3.23E-01	5.30E-01		Unigene19856_All//gi|297799708|ref|XP_002867738.1|//2.00E-48//SPX domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297313574|gb|EFH43997.1| SPX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene19856_All//4.00E-49//AT4G22990| SPX (SYG1/Pho81/XPR1) domain-containing protein	Unigene19856_All//2.00E-101//gi|78352026|gb|DT572300.1|DT572300				nr -
Unigene19857_All	254	174.27	81.59	95.18	197.30	220.17	187.41	585.76	150.23	174.41	-1.09E+00	1.93E-37	Down	-8.73E-01	6.37E-25		1.58E-01	3.01E-02		-7.42E-02	4.23E-01		-1.96E+00	0.00E+00	Down	-1.75E+00	0.00E+00	Down	Unigene19857_All//gi|211906518|gb|ACJ11752.1|//1.00E-43//glyceraldehyde-3-phosphate dehydrogenase C subunit [Gossypium hirsutum]	Unigene19857_All//4.00E-32//AT3G04120| GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene19857_All//2.00E-141//EV495962		ko00010|Glycolysis / Gluconeogenesis		nr -

Unigene19858_All	470	0.45	0.65	0.91	1.91	1.39	1.25	1.71	1.60	0.00	5.39E-01	6.72E-01		1.03E+00	3.97E-01		-4.55E-01	5.58E-01		-6.11E-01	4.26E-01		-9.46E-02	8.99E-01		-1.07E+01	4.43E-06	Down							
Unigene19859_All	1065	0.00	0.00	0.00	0.00	0.00	8.73	4.94	3.10	null	null		null	null		null	null		null	null		-8.21E-01	1.19E-06		-1.49E+00	1.34E-16	Down	Unigene19859_All//gi|115482584|ref|XP_001064885.1|//6.00E-80//Os10g0483400 (Oryza sativa Japonica Group)|gi|113639494|dbj|BAF26799.1|Os10g0483400 (Oryza sativa Japonica Group)	Unigene19859_All//2.00E-62//AT1G56120| kinase			ko04626|Plant-pathogen interaction		nr +
Unigene1986_All	2643	8.14	11.35	14.97	5.94	10.92	6.89	1.06	0.82	0.38	4.80E-01	1.06E-06		8.80E-01	1.12E-22		8.79E-01	3.94E-20		2.14E-01	1.34E-01		-3.61E-01	3.15E-01		-1.49E+00	1.49E-05	Down	Unigene1986_All//gi|226502156|ref|NP_001147894.1|//1.00E-170//CSLE6 - cellulose synthase-like family E [Zea mays]|gi|195614436|gb|ACG29048.1| CSLE6 - cellulose synthase-like family E [Zea mays]	Unigene1986_All//6.00E-162//AT1G55850| ATCSLE1; cellulose synthase| transferase, transferring glycosyl groups	Unigene1986_All//0.00E+00//TC148137			GO:0009987//GO:0016020//GO:0016757	nr +
Unigene19861_All	542	0.19	0.56	0.00	2.85	7.69	5.25	0.16	0.69	0.37	1.54E+00	3.23E-01		-7.59E+00	3.94E-01		1.43E+00	1.43E-06	Up	8.82E-01	1.87E-02		2.15E+00	9.45E-02		1.24E+00	4.69E-01		Unigene19861_All|gi|140053482|gb|AB080459.1|//2.00E-07//RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H [Medicago truncatula]		Unigene19861_All//5.00E-57//ES801598				nr +
Unigene19863_All	418	25.53	11.52	7.26	21.21	14.50	28.20	38.03	28.80	20.40	-1.15E+00	2.56E-10	Down	-1.81E+00	7.82E-19	Down	-5.49E-01	2.57E-03		4.11E-01	1.40E-02		-4.01E-01	1.38E-03		-8.99E-01	7.40E-13		Unigene19863_All|gi|217073218|gb|ACJ84968.1|//4.00E-09//unknown [Medicago truncatula]	Unigene19863_All//8.00E-07//AT3G57290| EIF3E (EUKARYOTIC TRANSLATION INITIATION FACTOR 3E); translation initiation factor	Unigene19863_All//4.00E-143//TC150595				nr +
Unigene19866_All	428	0.37	2.60	0.25	0.93	1.85	1.06	0.69	1.17	0.19	2.83E+00	5.03E-04	Up	-5.60E-01	7.76E-01		9.91E-01	2.40E-01		1.81E-01	8.84E-01		7.61E-01	4.22E-01		-1.89E+00	1.68E-01								
Unigene19867_All	305	0.00	0.66	0.17	0.82	1.13	11.70	12.20	14.39	34.09	9.38E+00	1.37E-01		7.45E+00	6.36E-01		4.67E-01	7.80E-01		3.84E+00	1.20E-15	Up	2.38E-01	4.04E-01		1.48E+00	4.20E-18	Up	Unigene19867_All|gi|116518570|gb|ABJ99502.1|//3.00E-41//1-aminocyclopropane-1-carboxylate synthase [Gossypium hirsutum]	Unigene19867_All//9.00E-36//AT4G11280| ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase	Unigene19867_All//2.00E-51//EX166586		ko00270|Cysteine and methionine metabolism		nr -
Unigene19869_All	759	1.17	0.40	0.70	2.63	5.44	1.67	0.33	0.00	0.00	-1.55E+00	4.56E-02		-7.40E-01	3.48E-01		1.05E+00	2.84E-04	Up	-6.56E-01	1.63E-01		-8.38E+00	4.04E-02		-8.38E+00	3.04E-02		Unigene19869_All|gi|15226011|ref|NP_182180.1|//3.00E-87//LAC6 (laccase 6); laccase [Arabidopsis thaliana]|gi|75338836|sp|Q9ZPY2.1|LAC6_ARATH RecName: Full=Laccase-6; AltName: Full=Benzenediol:oxygen oxidoreductase 6; AltName: Full=Urishiol oxidase 6; AltName: Full=Diphenol oxidase 6; Flags: Precursor	Unigene19869_All//2.00E-88//AT2G46570| LAC6 (laccase 6); laccase	Unigene19869_All//0.00E+00//gi|164316261|gb|ES823250.1|ES823250		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene19871_All	668	0.47	0.15	0.48	0.82	0.72	0.14	6.65	1.13	4.06	-1.63E+00	2.76E-01		2.56E-02	1.00E+00		-1.85E-01	8.25E-01		-2.60E+00	2.93E-02		-2.56E+00	1.27E-15	Down	-7.13E-01	3.96E-03		Unigene19871_All|gi|159025707|emb|CAN88854.1|//1.00E-82//D2/4-type cyclin [Populus trichocarpa]	Unigene19871_All//9.00E-55//AT5G65420| CYCD4;1 (CYCLIN D4;1); cyclin-dependent protein kinase regulator	Unigene19871_All//0.00E+00//gi|78352283|gb|DT572557.1|DT572557				nr -
Unigene19872_All	405	0.65	0.00	0.53	0.12	1.53	2.56	0.42	1.55	2.07	-9.34E+00	6.71E-02		-2.97E-01	8.32E-01		3.64E+00	5.37E-03		4.38E+00	3.58E-05	Up	1.89E+00	3.49E-02		2.31E+00	2.74E-03								
Unigene19877_All	465	0.00	0.00	0.00	0.64	0.96	0.10	4.09	1.17	3.77	null	null		null	null		5.83E-01	6.26E-01		-2.73E+00	1.37E-01		-1.81E+00	7.19E-05	Down	-1.18E-01	7.68E-01		Unigene19877_All|gi|224090677|ref|XP_002309054.1|//9.00E-20//predicted protein [Populus trichocarpa]|gi|222855030|gb|EEE92577.1|predicted protein [Populus trichocarpa]		Unigene19877_All//4.00E-14//TC166172				nr +
Unigene19878_All	584	4.30	1.13	0.73	0.34	0.29	0.00	0.22	0.14	1.02	-1.93E+00	1.39E-05	Down	-2.56E+00	3.86E-07	Down	-2.11E-01	8.59E-01		-8.41E+00	1.34E-01		-6.02E-01	7.66E-01		2.24E+00	1.67E-02								
Unigene19879_All	1218	0.00	7.95	6.38	0.00	0.08	0.04	0.14	0.00	0.00	1.30E+01	1.96E-55	Up	1.26E+01	1.71E-43	Up	6.41E+00	4.56E-01		5.21E+00	6.96E-01		-7.12E+00	1.34E-01		-7.12E+00	1.08E-01		Unigene19879_All|gi|301120388|ref|XP_002907921.1|//2.00E-47//polyadenylate-binding protein 1-B [Phytophthora infestans T30-4]|gi|262102952|gb|EEY61004.1|polyadenylate-binding protein 1-B [Phytophthora infestans T30-4]	Unigene19879_All//3.00E-35//AT1G49760| PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor			ko03040|Spliceosome		nr +
Unigene19888_All	297	1.06	0.51	0.36	4.03	2.90	2.28	3.13	0.14	1.07	-1.05E+00	4.43E-01		-1.56E+00	3.30E-01		-4.74E-01	4.58E-01		-8.20E-01	1.99E-01		-4.48E+00	1.30E-05	Down	-1.55E+00	1.68E-02								
Unigene19882_All	433	3.38	0.23	0.74	5.18	5.25	1.15	0.29	0.00	0.46	-3.85E+00	1.75E-06	Down	-2.20E+00	7.90E-04	Down	1.99E-02	9.74E-01		-2.17E+00	4.72E-06	Down	-8.19E+00	2.36E-01		6.51E-01	6.65E-01		Unigene19882_All|gi|85069287|gb|ABC69715.1|//1.00E-31//auxin response factor 4 [Solanum lycopersicum]	Unigene19882_All//3.00E-06//AT5G60450| ARF4 (AUXIN RESPONSE FACTOR 4); transcription factor	Unigene19882_All//2.00E-176//C0114066	ARF			nr +
Unigene19883_All	240	13.73	11.82	26.85	9.13	5.45	8.84	21.32	11.67	5.31	-2.16E-01	5.52E-01		9.67E-01	7.00E-05		-7.44E-01	7.45E-02		-4.62E-02	9.33E-01		-8.69E-01	2.36E-04		-2.00E+00	6.08E-14	Down			Unigene19883_All//4.00E-117//TC153292				
Unigene19885_All	334	3.60	0.30	0.32	5.52	2.78	1.35	1.01	0.00	0.24	-3.57E+00	3.63E-05	Down	-3.50E+00	8.78E-05	Down	-9.87E-01	3.05E-02		-2.03E+00	1.02E-04	Down	-9.98E+00	1.17E-02		-2.09E+00	1.07E-01			Unigene19885_All//7.00E-05//AT1G06900| catalytic/ metal ion binding / metalloendopeptidase/ zinc ion binding	Unigene19885_All//2.00E-30//TC177733				
Unigene19886_All	620	1.01	0.16	0.52	14.30	7.28	3.13	1.02	0.88	0.64	-2.63E+00	1.78E-02		-9.75E-01	3.16E-01		-9.75E-01	5.57E-08		-2.19E+00	1.53E-22	Down	-2.23E-01	7.74E-01		-6.71E-01	3.86E-01		Unigene19886_All|gi|297851290|ref|XP_002893526.1|//9.00E-38//kinase family protein [Arabidopsis lyrata subsp. lyrata]|gi|297339368|gb|EFH69785.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene19886_All//8.00E-37//AT1G28390| protein kinase family protein	Unigene19886_All//0.00E+00//BQ405997		ko04626|Plant-pathogen interaction		nr -
Unigene19887_All	292	2.33	20.82	14.77	10.58	9.55	8.97	27.95	44.09	21.56	3.16E+00	3.10E-21	Up	2.66E+00	1.84E-12	Up	-1.47E-01	7.14E-01		-2.38E-01	5.58E-01		6.58E-01	2.66E-06		-3.75E-01	3.61E-02				Unigene19887_All//8.00E-110//gi|164250801|gb|ES848347.1|ES848347				
Unigene19888_All	1261	0.00	0.00	0.00	0.00	0.00	0.00	11.80	1.13	13.27	null	null		null	null		null	null		null	null		-3.39E+00	2.39E-67	Down	1.69E-01	1.93E-01		Unigene19888_All|gi|4808524|gb|AAD29842.1|AF064694_1//1.00E-95//catechol O-methyltransferase [Thalictrum tuberosum]	Unigene19888_All//3.00E-88//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene19888_All//0.00E+00//TC131997		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene1989_All	1689	2.73	0.57	0.88	3.80	3.36	2.59	0.93	0.40	0.33	-2.26E+00	1.44E-11	Down	-1.63E+00	2.38E-07	Down	-1.78E-01	5.15E-01		-5.53E-01	1.74E-02		-1.23E+00	1.07E-02		-1.49E+00	1.74E-03		Unigene1989_All|gi|33090189|gb|AAP93893.1|//1.00E-82//NBS-type resistance protein [Gossypium barbadense]	Unigene1989_All//5.00E-57//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene1989_All//0.00E+00//NP831319		ko04626|Plant-pathogen interaction	GO:0012501//GO:0032559	nr +
Unigene19891_All	745	0.00	0.88	0.00	0.74	0.42	0.00	239.95	46.51	90.96	9.79E+00	6.26E-04	Up	null	null		-8.22E-01	3.96E-01		-9.52E+00	1.52E-03		-2.37E+00	0.00E+00	Down	-1.40E+00	1.14E-275	Down	Unigene19891_All|gi|31580853|dbj|BAC77531.1|//8.00E-85//plasma membrane H+-ATPase [Sesbania rostrata]	Unigene19891_All//8.00E-77//AT2G24520| AHA5 (Arabidopsis H(+)-ATPase 5); ATPase	Unigene19891_All//0.00E+00//gi|13351158|gb|BG441506.1|BG441506		ko00190|Oxidative phosphorylation		nr +
Unigene19895_All	768	0.00	9.10	4.02	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	5.87E-40	Up	1.20E+01	4.51E-17	Up	null	null		null	null		null	null		null	null		Unigene19895_All|gi|240254284|ref|NP_176000.4|//1.00E-06//binding / protein binding / ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene19895_All//6.00E-08//AT1G56040| binding / protein binding / ubiquitin-protein ligase					nr -
Unigene19897_All	538	0.00	0.00	0.00	0.00	0.00	0.00	1.96	3.42	0.15	null	null		null	null		null	null		null	null		7.99E-01	6.40E-02		-3.73E+00	6.13E-06	Down	Unigene19897_All|gi|38230174|gb|AAR14182.1|//3.00E-67//Rho family GTPase [Fucus distichus]	Unigene19897_All//1.00E-53//AT5G45970| ARAC2 (ARABIDOPSIS RAC-LIKE 2); GTP binding	Unigene19897_All//6.00E-07//EX169558		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene19898_All	423	0.49	0.24	0.25	0.94	0.00	1.28	2.30	0.69	6.50	-1.05E+00	5.65E-01		-9.75E-01	6.21E-01		-9.88E+00	4.39E-03		4.44E-01	6.78E-01		-1.73E+00	9.67E-03		1.50E+00	1.77E-05	Up	Unigene19898_All|gi|20197360|gb|AAM15041.1|//4.00E-12//Expressed protein [Arabidopsis thaliana]|gi|20197508|gb|AAM15101.1|Expressed protein [Arabidopsis thaliana]	Unigene19898_All//3.00E-13//AT2G25735| unknown protein					nr +
Unigene19899_All	662	0.00	0.00	0.48	0.00	0.00	0.14	1.47	9.72	47.78	null	null		8.91E+00	4.52E-02		null	null		7.09E+00	4.77E-01		2.73E+00	8.07E-24	Up	5.02E+00	1.35E-190	Up	Unigene19899_All|gi|182702251|sp|A0Z293.1|YCF1_GOSBA//2.00E-06//RecName: Full=Putative membrane protein ycf1|gi|119224919|dbj|BAF41305.1|Hypothetical protein [Gossypium barbadense]	Unigene19899_All//2.00E-07//ATMG00370| hypothetical protein	Unigene19899_All//2.00E-41//TC176151				nr +
Unigene199_All	2224	2.63	1.16	1.44	3.90	3.00	3.11	5.04	2.59	3.03	-1.18E+00	2.92E-06	Down	-8.75E-01	6.21E-04		-3.76E-01	5.32E-02		-3.27E-01	1.17E-01		-9.58E-01	6.08E-10		-7.35E-01	7.33E-07		Unigene199_All|gi|297814281|ref|XP_002875024.1|//0.00E+00//beta-amylase 9 [Arabidopsis lyrata subsp. lyrata]|gi|297320861|gb|EFH51283.1| beta-amylase 9 [Arabidopsis lyrata subsp. lyrata]	Unigene199_All//0.00E+00//AT4G00490| BAM2 (BETA-AMYLASE 2); beta-amylase	Unigene199_All//0.00E+00//gi|13350033|gb|BG440382.1|BG440382		ko00500|Starch and sucrose metabolism		nr -
Unigene19901_All	607	1.12	0.50	0.00	1.89	0.79	8.26	1.11	1.51	0.59	-1.16E+00	1.89E-01		-1.01E+01	7.64E-04	Down	-1.25E+00	4.15E-02		2.13E+00	3.17E-12	Up	4.43E-01	5.19E-01		-9.16E-01	2.21E-01		Unigene19901_All|gi|115646849|gb|ABJ17139.1|//1.00E-10//At5g64980 [Arabidopsis thaliana]	Unigene19901_All//8.00E-12//AT5G64980| unknown protein	Unigene19901_All//5.00E-156//DW507199				nr -
Unigene19903_All	341	2.76	0.00	5.78	2.19	4.65	1.32	0.99	0.00	0.23	-1.14E+01	1.46E-05	Down	1.06E+00	2.84E-02		1.08E+00	4.10E-02		-7.26E-01	3.90E-01		-9.95E+00	1.17E-02		-2.09E+00	1.07E-01								
Unigene19905_All	498	4.10	4.68	4.49	9.50	13.97	7.26	8.66	13.18	17.52	1.92E-01	6.30E-01		1.32E-01	7.55E-01		5.56E-01	1.01E-02		-3.89E-01	1.88E-01		6.06E-01	3.10E-03		1.02E+00	6.90E-09	Up			Unigene19905_All//5.00E-66//TC152800				
Unigene19906_All	268	0.20	4.35	0.00	2.23	1.93	2.02	2.52	2.50	0.74	4.48E+00	1.19E-05	Up	-7.61E+00	6.25E-01		-2.11E-01	8.23E-01		-1.41E-01	8.79E-01		-1.66E-02	1.02E+00		-1.76E+00	2.80E-02		Unigene19906_All|gi|224071143|ref|XP_002303364.1|//4.00E-14//AP2/ERF domain-containing transcription factor [Populus trichocarpa]|gi|148372077|gb|ABQ62970.1| TINY-like protein [Populus trichocarpa]|gi|222840796|gb|EEE78343.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene19906_All//1.00E-65//AT2G35700| ERF38 (ERF FAMILY PROTEIN 38); DNA binding / transcription factor	Unigene19906_All//1.00E-120//gi|109883890|gb|DW512860.1|DW512860	AP2-EREBP			nr -
Unigene19908_All	755	0.00	8.12	4.73	0.00	0.05	0.00	0.00	0.00	0.11	1.30E+01	5.27E-35	Up	1.22E+01	9.42E-20	Up	5.51E+00	8.30E-01		null	null		null	null		6.72E+00	4.04E-01		Unigene19908_All|gi|159471131|ref|XP_001693710.1|//2.00E-92//ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii]|gi|269969596|sp|A8HS48.1|RS3A_CHLRE RecName: Full=40S ribosomal protein S3a|gi|158283213|gb|EDP08964.1|ribosomal protein S3a [Chlamydomonas reinhardtii]	Unigene19908_All//5.00E-88//AT4G34670| 40S ribosomal protein S3A (RPS3aB)			ko03010|Ribosome		nr -
Unigene19917_All	210	1.74	1.93	0.00	0.71	1.48	0.00	0.81	4.18	12.71	1.46E-01	8.98E-01		-1.08E+01	2.78E-02		1.05E+00	5.31E-01		-9.47E+00	2.33E-01		2.38E+00	2.18E-03		3.98E+00	2.12E-14	Up			Unigene19917_All//1.00E-27//gi|73863828|gb|DT466567.1|DT466567				
Unigene19918_All	486	0.00	66.20	22.35	0.00	0.43	0.00	0.00	0.00	0.00	1.60E+01	1.45E-185	Up	1.44E+01	5.10E-61	Up	8.73E+00	1.57E-01		null	null		null	null		null	null								ESTscan +
Unigene19919_All	407	6.43	9.71	13.61	0.86	0.68	0.22	0.00	0.00	0.00	5.95E-01	5.35E-02		1.08E+00	5.11E-05	Up	-3.40E-01	7.86E-01		-1.95E+00	1.96E-01		null	null		null	null				Unigene19919_All//1.00E-29//CO094217				
Unigene1992_All	919	2.11	3.31	1.74	1.84	2.89	1.47	38.65	65.17	118.69	6.51E-01	6.92E-02		-2.77E-01	5.92E-01		6.47E-01	9.95E-02		-3.22E-01	5.65E-01		7.54E-01	3.22E-33		1.62E+00	8.15E-207	Up	Unigene1992_All|gi|2245019|emb|CAB10429.1|//2.00E-69//proteinase like protein [Arabidopsis thaliana]|gi|7268414|emb|CAB78706.1|proteinase like protein [Arabidopsis thaliana]	Unigene1992_All//2.00E-69//AT4G16640| matrix metalloproteinase, putative				GO:0004175//GO:0019538//GO:0031224//GO:0031410//GO:0044421//GO:0046914	nr -
Unigene19922_All	528	0.00	0.00	0.00	0.00	0.00	0.00	2.72	4.67	9.58	null	null		null	null		null	null		null	null		7.79E-01	3.14E-02		1.82E+00	4.89E-12	Up							
Unigene19923_All	720	0.15	173.75	72.70	0.14	0.14	0.00	0.00	0.00	0.00	1.02E+01	0.00E+00	Up	8.97E+00	1.22E-292	Up	5.22E-02	9.67E-01		-7.11E+00	4.00E-01		null	null		null	null		Unigene19923_All|gi|220966698|gb|ACL97363.1|//2.00E-20//elongation factor-1 alpha [Ignatius tetrasporus]	Unigene19923_All//5.00E-15//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene19923_All//3.00E-19//DW516522				nr -
Unigene19924_All	333	0.31	2.13	2.88	14.51	10.44	4.20	0.63	1.26	0.48	2.76E+00	9.15E-03		3.20E+00	1.03E-03		-4.74E-01	7.84E-02		-1.79E+00	1.07E-09	Down	9.83E-01	3.73E-01		-4.08E-01	7.55E-01								

Unigene19926_All	634	1.24	0.00	0.17	4.24	2.55	1.28	0.60	0.46	0.25	-1.03E+01	1.09E-04	Down	-2.88E+00	6.35E-03		-7.33E-01	4.55E-02		-1.73E+00	1.94E-05	Down	-3.79E-01	7.23E-01		-1.26E+00	2.48E-01		Unigene19926_All//gi|3810594|gb|AAC69376.1|//1.00E-52//expressed protein [Arabidopsis thaliana] >gi|199941293|gb|ABR46189.1| At2g14660 [Arabidopsis thaliana]	Unigene19926_All//2.00E-46//AT2G14660| unknown protein	Unigene19926_All//0.00E+00//TC146733				nr +
Unigene1993_All	911	781.31	728.28	843.29	101.32	136.91	102.97	10.07	33.08	22.00	-1.01E-01	6.34E-08		1.10E-01	2.11E-09		4.34E-01	5.99E-25		2.32E-02	7.27E-01		1.72E+00	2.67E-61	Up	1.13E+00	1.27E-22	Up	Unigene1993_All//gi|136707|sp|P26291.1|CCRIA_PEA//1.00E-102//RecName: Full=Cytochrome b6-f complex iron-sulfur subunit, chloroplastic; AltName: Full=Rieske iron-sulfur protein; Short=RISP; Short=ISP; AltName: Full=Plastohydroquinone:plastocyan in oxidoreductase iron-sulfur protein; Flags: Precursor >gi|20832|emb|CAA45151.1| chloroplast Rieske FeS protein [Pisum sativum]	Unigene1993_All//7.00E-92//AT4G03280| PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C); electron transporter, transferring electrons from cytochrome b6/f complex of photosystem II	Unigene1993_All//0.00E+00//TC134204		ko00195|Photosynthesis	GO:0006091//GO:0006952//GO:0009055//GO:0009416//GO:0009526//GO:0009534//GO:0015078//GO:0016679//GO:0031224//GO:0034357//GO:0043169//GO:0043234//GO:0051234//GO:0051536	nr +
Unigene19931_All	509	2.16	1.00	1.88	0.29	2.03	1.24	0.25	0.00	0.08	-1.12E+00	8.94E-02		-1.97E-01	7.50E-01		2.79E+00	6.87E-04	Up	2.08E+00	4.69E-02		-7.96E+00	2.36E-01		-1.67E+00	4.77E-01					Unigene19931_All//7.00E-16//TC136860				
Unigene19933_All	1034	0.00	0.00	0.00	0.00	0.00	0.09	2.17	1.46	4.62	null	null		null	null		null	null		6.45E+00	4.77E-01		-5.75E-01	1.39E-01		1.09E+00	8.21E-06	Up							
Unigene19934_All	600	0.35	4.31	0.80	0.42	0.34	1.13	2.25	1.04	3.65	3.63E+00	1.94E-10	Up	1.20E+00	3.03E-01		-2.69E-01	8.23E-01		1.44E+00	1.28E-01		-1.11E+00	3.31E-02		6.96E-01	6.30E-02				Unigene19934_All//4.00E-101//gi|73862500|gb|DT465239.1|DT465239				
Unigene19935_All	641	0.00	46.56	14.87	0.00	0.11	0.00	0.00	0.00	0.00	1.55E+01	4.54E-172	Up	1.39E+01	1.86E-53	Up	6.75E+00	6.10E-01		null	null		null	null		null	null		Unigene19935_All//gi|226490975|ref|NP_001147262.1|//4.00E-61//60S ribosomal protein L13a-2 [Zea mays] >gi|195609234|gb|ACZ26447.1| 60S ribosomal protein L13a-2 [Zea mays]	Unigene19935_All//7.00E-59//AT4G13170| 60S ribosomal protein L13A (RPL13aC)			ko03010|Ribosome		nr +
Unigene19936_All	671	0.00	0.00	0.00	0.74	0.56	0.00	5.86	2.55	4.51	null	null		null	null		-3.95E-01	6.89E-01		-9.54E+00	2.97E-03		-1.20E+00	2.08E-05	Down	-3.77E-01	1.68E-01		Unigene19936_All//gi|75299757|sp|Q8HUB9.1|AMO_ARATH//1.00E-84//RecName: Full=Primary amine oxidase; AltName: Full=Amine oxidase [copper-containing]; Flags: Precursor >gi|23297202|gb|AAN12916.1| At1g62810/F23N19_18 [Arabidopsis thaliana]	Unigene19936_All//6.00E-86//AT1G62810| copper amine oxidase, putative	Unigene19936_All//4.00E-21//ES822112		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr +
Unigene19937_All	330	0.00	2.92	0.32	0.00	0.10	0.96	1.15	4.05	1.57	1.15E+01	1.38E-05	Up	8.33E+00	3.99E-01		6.70E+00	8.30E-01		9.90E+00	4.08E-02		1.81E+00	1.20E-03		4.45E-01	6.12E-01								
Unigene19939_All	292	0.72	1.39	1.46	1.02	2.71	1.55	1.01	1.72	4.23	9.54E-01	4.14E-01		1.03E+00	3.97E-01		1.41E+00	9.66E-02		5.96E-01	6.40E-01		7.61E-01	4.22E-01		2.06E+00	5.00E-04	Up			Unigene19939_All//2.00E-51//CO104492				
Unigene1994_All	639	210.68	162.95	243.00	65.48	66.88	43.96	3.11	8.83	8.23	-3.71E-01	3.48E-17		2.06E-01	1.19E-06		3.04E-02	8.08E-01		-5.75E-01	5.45E-13		1.51E+00	3.69E-10	Up	1.40E+00	6.76E-09	Up	Unigene1994_All//gi|158935079|emb|CAME7107.1|//1.00E-45//Rieske iron-sulphur protein precursor [Glycine max]	Unigene1994_All//1.00E-38//AT4G03280| PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C); electron transporter, transferring electrons from cytochrome b6/f complex of photosystem II	Unigene1994_All//0.00E+00//gi|164317975|gb|ES845215.1|ES845215		ko00195|Photosynthesis	GO:0006091//GO:0006952//GO:0009055//GO:0009416//GO:0009526//GO:0009534//GO:0015078//GO:0016679//GO:0031224//GO:0034357//GO:0043169//GO:0043234//GO:0051234//GO:0051536	nr -
Unigene19940_All	286	1.28	4.25	8.56	3.66	3.61	5.05	11.97	7.45	68.12	1.73E+00	8.94E-03		2.74E+00	1.65E-07	Up	-1.81E-02	9.61E-01		4.66E-01	4.40E-01		-6.84E-01	2.18E-02		2.51E+00	8.79E-66	Up	Unigene19940_All//gi|16416376|dbj|BAB21610.2|//1.00E-10//mangrin [Bruguiera sexangula]		Unigene19940_All//2.00E-153//gi|164243868|gb|ES802442.1|ES802442		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene19942_All	467	0.00	0.43	0.68	0.96	0.15	4.26	5.88	7.34	5.29	8.76E+00	1.37E-01		9.42E+00	4.52E-02		-2.70E+00	3.24E-02		2.15E+00	3.16E-05	Up	3.19E-01	3.25E-01		-1.54E-01	6.44E-01				Unigene19942_All//6.00E-53//gi|78341239|gb|DT561513.1|DT561513				
Unigene19943_All	380	0.96	0.27	0.00	1.84	1.00	0.00	1.89	0.00	0.00	-1.85E+00	1.87E-01		-9.91E+00	2.78E-02		-8.81E-01	3.00E-01		-1.08E+01	1.96E-04	Down	-1.09E+01	3.26E-05	Down	-1.09E+01	1.78E-05	Down							
Unigene19947_All	612	0.51	0.83	0.17	0.49	1.24	1.40	0.41	0.48	1.95	6.91E-01	4.99E-01		-1.56E+00	3.30E-01		1.34E+00	1.23E-01		1.52E+00	6.17E-02		2.06E-01	8.68E-01		2.24E+00	3.02E-04	Up	Unigene19947_All//gi|224131232|ref|XP_002321033.1|//8.00E-39//glutaredoxin [Populus trichocarpa] >gi|222861806|gb|EEE99348.1| glutaredoxin [Populus trichocarpa]	Unigene19947_All//2.00E-36//AT1G03020| glutaredoxin family protein	Unigene19947_All//0.00E+00//gi|164342338|gb|ES843871.1|ES843871				nr -
Unigene19949_All	540	0.39	0.38	0.00	2.03	1.47	0.50	0.94	0.00	0.00	-4.65E-02	9.88E-01		-8.60E+00	1.46E-01		-4.69E-01	4.83E-01		-2.02E+00	4.74E-03		-9.88E+00	8.89E-04	Down	-9.88E+00	5.54E-04	Down	Unigene19949_All//gi|297536190|ref|XP_002885977.1|//1.00E-16//calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297331817|gb|EFH62236.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene19949_All//1.00E-15//AT2G26530| AR781					nr +
Unigene1995_All	1418	20.52	26.30	25.91	5.80	8.96	3.95	0.66	2.09	2.75	3.58E-01	4.45E-05		3.37E-01	2.49E-04		6.29E-01	2.42E-05		-5.54E-01	5.76E-03		1.67E+00	1.64E-06	Up	2.07E+00	4.23E-11	Up	Unigene1995_All//gi|136707|sp|P26291.1|CCRIA_PEA//2.00E-48//RecName: Full=Cytochrome b6-f complex iron-sulfur subunit, chloroplastic; AltName: Full=Rieske iron-sulfur protein; Short=RISP; Short=ISP; AltName: Full=Plastohydroquinone:plastocyan in oxidoreductase iron-sulfur protein; Flags: Precursor >gi|20832|emb|CAA45151.1| chloroplast Rieske FeS protein [Pisum sativum]	Unigene1995_All//5.00E-48//AT4G03280| PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C); electron transporter, transferring electrons from cytochrome b6/f complex of photosystem II	Unigene1995_All//0.00E+00//gi|48748671|gb|CO079190.1|CO079190			GO:0006091//GO:0009534//GO:0015078//GO:0016679//GO:0031224//GO:0034357//GO:0043169//GO:0051234//GO:0051536	nr +
Unigene19950_All	507	0.00	0.00	0.00	0.00	0.00	0.00	7.26	6.27	20.98	null	null		null	null		null	null		null	null		-2.12E-01	5.15E-01		1.53E+00	2.28E-19	Up	Unigene19950_All//gi|224128946|ref|XP_002320460.1|//2.00E-16//predicted protein [Populus trichocarpa] >gi|222861233|gb|EEE98775.1| predicted protein [Populus trichocarpa]	Unigene19950_All//5.00E-05//AT3G21680| unknown protein					nr +
Unigene19951_All	556	0.00	4.65	2.68	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.06E-14	Up	1.14E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene19951_All//gi|300264478|gb|EFJ48674.1|//7.00E-16//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene19951_All//2.00E-14//AT3G06680| 60S ribosomal protein L29 (RPL29B)			ko03010|Ribosome		nr +
Unigene19953_All	776	1.89	0.20	0.55	0.64	0.09	0.35	1.85	2.26	0.31	-3.27E+00	8.97E-06	Down	-1.78E+00	4.08E-03		-2.85E+00	1.78E-02		-8.78E-01	4.20E-01		2.88E-01	5.52E-01		-2.59E+00	8.29E-06	Down	Unigene19953_All//sp|Q8MP30|Y7791_DICDI//4.00E-07//Uncharacterized histidine-rich protein DDB_G0274557 OS=Dictyostelium discoideum GN=DDB_G0274557 PE=4 SV=1						swissprot -
Unigene19955_All	354	0.89	6.30	2.56	1.69	1.65	4.72	1.31	2.24	6.75	2.83E+00	2.19E-07	Up	1.53E+00	5.77E-02		-3.01E-02	9.50E-01		1.48E+00	5.30E-03		7.72E-01	2.88E-01		2.36E+00	3.39E-08	Up			Unigene19955_All//8.00E-24//gi|48817659|gb|CO118972.1|CO118972				
Unigene19957_All	454	0.35	0.11	0.47	0.66	0.83	0.30	2.42	1.01	0.44	-1.63E+00	4.89E-01		4.41E-01	7.75E-01		3.42E-01	8.36E-01		-1.14E+00	4.58E-01		-1.26E+00	3.46E-02		-2.46E+00	2.04E-04	Down			Unigene19957_All//1.00E-10//TC174282				
Unigene19958_All	235	0.22	4.74	0.00	0.64	1.47	0.19	2.16	0.71	0.17	4.41E+00	2.17E-05	Up	-7.80E+00	6.25E-01		1.20E+00	4.26E-01		-1.73E+00	5.01E-01		-1.60E+00	1.07E-01		-3.67E+00	3.75E-03								
Unigene1996_All	1220	3.22	2.45	2.92	13.68	13.58	5.37	3.29	1.99	1.37	-3.92E-01	2.13E-01		-1.37E-01	6.66E-01		-1.08E-02	9.55E-01		-1.35E+00	1.75E-21	Down	-7.29E-01	7.16E-03		-1.26E+00	3.83E-06	Down	Unigene1996_All//gi|30697804|ref|NP_177017.3|//1.00E-41//squamosa promoter-binding protein-like 6 (SPL6) [Arabidopsis thaliana] >gi|67461542|sp|Q94JW8.2|SPL6_ARATH RecName: Full=Squamosa promoter-binding-like protein 6 >gi|12325078|gb|AAG52487.1|AC018364_5 squamosa promoter binding protein-like 6; 91282-89867 [Arabidopsis thaliana] >gi|5931683|emb|CAB56595.1| squamosa promoter binding protein-like 6 [Arabidopsis thaliana] >gi|5931685|emb|CAB56596.1| squamosa promoter binding protein-like 6 [Arabidopsis thaliana] >gi|30102652|gb|AAP21244.1| At1g69170 [Arabidopsis thaliana] >gi|110735912|dbj|BAE99931.1| squamosa promoter binding protein-like 6 [Arabidopsis thaliana]	Unigene1996_All//8.00E-41//AT1G69170| squamosa promoter-binding protein-like 6 (SPL6)	Unigene1996_All//0.00E+00//TC171981	SBP		GO:0003676//GO:0043231	nr +
Unigene19960_All	459	4381.50	1966.84	5099.70	844.45	974.39	749.08	2.40	1.27	0.69	-1.16E+00	0.00E+00	Down	2.19E-01	7.39E-103		2.07E-01	4.77E-22		-1.73E-01	1.64E-12		-9.10E-01	1.24E-01		-1.79E+00	3.08E-03		Unigene19960_All//gi|255547954|ref|XP_002515034.1|//1.00E-36//photosystem II core complex proteins psbY, chloroplast precursor [Ricinus communis] >gi|223546085|gb|EEF47588.1| photosystem II core complex proteins psbY, chloroplast precursor [Ricinus communis]	Unigene19960_All//1.00E-06//AT1G67740| PSBY	Unigene19960_All//0.00E+00//gi|31073029|gb|CA993308.1|CA993308		ko00195|Photosynthesis		nr -
Unigene19964_All	337	18.16	37.44	32.71	46.86	53.95	44.36	3.26	1.24	1.42	1.04E+00	2.19E-10	Up	8.49E-01	1.98E-06		2.03E-01	1.49E-01		-7.91E-02	6.42E-01		-1.40E+00	2.04E-02		-1.20E+00	3.41E-02		Unigene19964_All//gi|224054176|ref|XP_002298129.1|//2.00E-16//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene19964_All//1.00E-15//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene19964_All//8.00E-138//TC129823		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene19966_All	250	67.39	93.43	150.80	21.92	47.38	30.71	26.04	23.91	18.49	4.71E-01	2.96E-05		1.16E+00	6.29E-34	Up	1.11E+00	2.76E-12	Up	4.87E-01	2.22E-02		-1.24E-01	6.33E-01		-4.95E-01	1.34E-02				Unigene19966_All//2.00E-134//DR453628				
Unigene19968_All	313	0.67	1.62	4.42	1.43	0.88	0.43	1.89	1.07	1.53	1.28E+00	2.31E-01		2.73E+00	1.78E-04	Up	-7.03E-01	5.30E-01		-1.73E+00	1.61E-01		-8.24E-01	3.48E-01		-3.08E-01	6.79E-01								
Unigene19969_All	1087	0.10	0.00	0.00	0.23	0.22	0.58	3.31	7.50	16.97	-6.59E+00	3.73E-01		-6.59E+00	3.94E-01		-4.67E-02	9.51E-01		1.34E+00	1.74E-01		1.18E+00	3.92E-10	Up	2.36E+00	4.37E-58	Up	Unigene19969_All//gi|124359713|gb|ABD32380.2|//8.00E-56//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene19969_All//6.00E-51//AT1G72210| basic helix-loop-helix (bHLH) family protein (bHLH096)	Unigene19969_All//2.00E-113//DW239968	bHLH			nr +
Unigene1997_All	1386	2.42	1.24	2.46	11.61	8.22	4.33	4.09	2.14	1.32	-9.59E-01	4.72E-03		2.54E-02	9.59E-01		-4.97E-01	1.13E-04		-1.42E+00	2.12E-22	Down	-9.33E-01	3.16E-05		-1.63E+00	9.49E-12	Down	Unigene1997_All//gi|6730637|gb|AAF27058.1|AC008262_7//3.00E-42//F4N2.13 [Arabidopsis thaliana]	Unigene1997_All//1.00E-37//AT1G69170| squamosa promoter-binding protein-like 6 (SPL6)	Unigene1997_All//0.00E+00//gi|164272834|gb|ES839900.1|ES839900	SBP		GO:0003676//GO:0043231	nr +
Unigene1998_All	1652	4.59	2.24	4.93	12.85	19.59	21.90	25.39	36.23	34.99	-1.04E+00	1.58E-06	Down	1.03E-01	6.33E-01		6.09E-01	3.80E-12		7.70E-01	2.18E-18		5.13E-01	3.96E-17		4.63E-01	2.98E-14		Unigene1998_All//gi|30689895|ref|NP_850429.1|//4.00E-09//EMB2766 (EMBRYO DEFECTIVE 2766); structural constituent of nuclear pore [Arabidopsis thaliana]	Unigene1998_All//1.00E-08//AT1G20970| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole; EXPRESSED IN: guard cell, cultured cell; BEST Arabidopsis thaliana protein match is: PP11 (PROTON PUMP INTERACTOR 1); protein binding (TAIR:AT4G27500.1); Has 53409 Blast hits to 33585 proteins in 1572 species: Archae - 464; Bacteria - 7066; Metazoa - 25076; Fungi - 5173; Plants - 1740; Viruses - 257; Other Eukaryotes - 13633 (source: NCBI BLink).	Unigene1998_All//0.00E+00//TC134993				nr +

Unigene19980_All	323	3.24	0.31	0.99	1.08	1.39	1.82	0.92	1.04	0.37	-3.37E+00	2.13E-04	Down	-1.71E+00	2.35E-02		3.60E-01	8.07E-01		7.52E-01	4.67E-01		1.76E-01	8.80E-01		-1.31E+00	3.13E-01		Unigene19980_All//gi|297842491|ref|XP_002889127.1|//1.00E-37//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331968|gb|EFH65386.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene19980_All//9.00E-39//AT1G77170| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene19986_All	377	0.97	0.00	0.71	0.53	2.01	3.71	0.90	0.11	1.06	-9.92E+00	1.97E-02		-4.60E-01	6.97E-01		1.93E+00	3.36E-02		2.81E+00	5.55E-05	Up	-3.02E+00	5.30E-02		2.36E-01	8.04E-01		Unigene19986_All//gi|62956018|gb|AY23354.1|//2.00E-29//3-ketoacyl-CoA reductase I [Gossypium hirsutum]	Unigene19986_All//3.00E-29//AT1G67730| YBR159: ketoreductase/ oxidoreductase	Unigene19986_All//0.00E+00//ES824093				nr +
Unigene19994_All	1737	0.00	0.00	0.00	0.00	0.00	0.00	2.77	4.36	1.35	null	null		null	null		null	null		null	null		6.50E-01	5.58E-04		-1.04E+00	1.76E-05	Down	Unigene19994_All//gi|110816488|sp|Q3BA12.1|YC91_PHAO//3.00E-20//RecName: Full=Uncharacterized protein 0RF91		Unigene19994_All//3.00E-39//gi|11207696|gb|BF276626.1|BF276626				nr +
Unigene19995_All	606	0.78	1.09	0.00	2.22	0.68	1.34	4.19	0.00	0.85	4.84E-01	5.90E-01		-9.60E+00	8.65E-03		-1.70E+00	2.73E-03		-7.26E-01	2.23E-01		-1.20E+01	6.10E-18	Down	-2.29E+00	1.64E-08	Down	Unigene19995_All//gi|28416791|gb|AA042926.1|//8.00E-09//At4g39300 [Arabidopsis thaliana]	Unigene19995_All//4.00E-08//AT1G55205| unknown protein	Unigene19995_All//0.00E+00//DW518952				nr +
Unigene19997_All	580	0.27	0.00	0.00	0.43	1.19	0.62	6.12	1.23	4.05	-8.08E+00	2.16E-01		-8.08E+00	2.45E-01		1.47E+00	1.16E-01		5.37E-01	6.94E-01		-2.32E+00	2.35E-11	Down	-5.96E-01	3.44E-02		Unigene19997_All//gi|28300299|gb|AA037645.1|//8.00E-29//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene19997_All//2.00E-19//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene19997_All//4.00E-113//TC177573		ko04626|Plant-pathogen interaction		nr -
Unigene19998_All	550	0.00	4.61	3.29	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.05E-14	Up	1.17E+01	5.70E-10	Up	null	null		null	null		null	null		null	null		Unigene19998_All//gi|255089925|ref|XP_002506884.1|//2.00E-37//autophagy-related protein 8 [Micromonas sp. RCC299] >gi|226522157|gb|ACO68142.1| autophagy-related protein 8 [Micromonas sp. RCC299]	Unigene19998_All//3.00E-36//AT2G05630| autophagy 8d (APG8d)			ko04140|Regulation of autophagy		nr +
Unigene2000_All	1645	2.16	2.03	2.23	4.48	3.45	4.31	2.44	3.23	1.19	-8.94E-02	7.78E-01		4.65E-02	8.94E-01		-3.76E-01	8.10E-02		-5.63E-02	8.17E-01		4.02E-01	9.24E-02		-1.04E+00	9.61E-05	Down	Unigene2000_All//gi|48958489|gb|AAT47797.1|//1.00E-27//At1g02290 [Arabidopsis thaliana] >gi|51536560|gb|AAU05518.1| At1g02290 [Arabidopsis thaliana]	Unigene2000_All//7.00E-28//AT1G02290| unknown protein	Unigene2000_All//0.00E+00//TC141556				nr -
Unigene20000_All	218	1.44	2.32	1.22	11.65	7.42	2.28	0.97	0.00	0.00	6.91E-01	4.99E-01		-2.38E-01	8.50E-01		-6.51E-01	9.07E-02		-2.35E+00	2.09E-07	Down	-9.92E+00	7.44E-02		-9.92E+00	5.80E-02				Unigene20000_All//6.00E-36//gi|84172947|gb|DR461595.1|DR461595				
Unigene20001_All	654	0.00	0.00	0.00	0.00	0.00	0.00	16.81	4.79	1.40	null	null		null	null		null	null		null	null		-1.81E+00	1.33E-24	Down	-3.58E+00	3.94E-54	Down	Unigene20001_All//gi|145408591|ref|YP_001152215.1|//6.00E-08//0RF441 [Pinus koraiensis] >gi|145048840|gb|ABP35457.1| 0RF441 [Pinus koraiensis]		Unigene20001_All//4.00E-30//DW479422				nr +
Unigene20002_All	745	0.00	3.74	1.50	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.43E-16	Up	1.06E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene20002_All//gi|15320813|ref|NP_196370.1|//4.00E-07//GRP17 (GLYCINE RICH PROTEIN 17); lipid binding [Arabidopsis thaliana] >gi|7576191|emb|CAB87942.1| glycine-rich protein atGRP-7 [Arabidopsis thaliana] >gi|110739545|dbj|BAF01681.1| glycine-rich protein atGRP-7 [Arabidopsis thaliana]						nr -
Unigene20003_All	383	29.78	15.35	15.15	34.73	23.38	28.89	94.72	39.39	30.58	-9.57E-01	2.42E-08		-9.75E-01	3.64E-08		-5.71E-01	6.28E-05		-2.66E-01	1.09E-01		-1.27E+00	3.48E-47	Down	-1.63E+00	9.08E-71	Down			Unigene20003_All//0.00E+00//TC166453				
Unigene20004_All	450	0.12	0.45	0.00	1.11	0.61	0.50	0.19	0.19	1.95	1.95E+00	3.75E-01		-6.86E+00	6.25E-01		-8.55E-01	4.07E-01		-1.14E+00	3.07E-01		-1.62E-02	1.01E+00		3.37E+00	1.32E-04	Up			Unigene20004_All//5.00E-07//TC136502				
Unigene20006_All	400	0.65	1.65	0.00	0.25	0.00	0.00	1.37	10.87	8.57	1.33E+00	1.45E-01		-9.35E+00	8.58E-02		-7.96E-00	3.13E-01		-7.96E-00	4.00E-01		2.98E-00	8.06E-18	Up	2.64E+00	7.51E-13	Up							
Unigene20007_All	869	0.00	1.40	1.23	0.34	0.36	0.00	4.23	3.75	5.55	1.05E+01	5.48E-07	Up	1.03E+01	6.62E-06	Up	5.23E-02	9.98E-01		-8.43E+00	4.00E-02		-1.74E-01	6.12E-01		3.90E-01	1.08E-01		Unigene20007_All//gi|54261723|gb|AAV31165.1|//1.00E-30//At3g03280 [Arabidopsis thaliana] >gi|57222180|gb|AAW38997.1| At3g03280 [Arabidopsis thaliana]	Unigene20007_All//3.00E-29//AT5G17350| unknown protein					nr +
Unigene20008_All	581	0.00	0.00	0.00	0.69	0.65	1.48	80.92	1.15	1.92	null	null		null	null		-7.31E-02	9.26E-01		1.11E+00	1.67E-01		-6.14E+00	2.06E-305	Down	-5.40E+00	3.82E-300	Down	Unigene20008_All//gi|156153185|gb|ABU54827.1|//3.00E-39//ferric reductase [Malus xiaojinensis]	Unigene20008_All//1.00E-28//AT1G01580| FRO2 (FERRIC REDUCTION OXIDASE 2); ferric-chelate reductase	Unigene20008_All//0.00E+00//CO089158				nr +
Unigene20009_All	1510	0.00	0.10	0.11	0.03	0.05	0.00	1.23	1.74	7.28	6.65E+00	2.35E-01		6.73E+00	2.39E-01		4.67E-01	9.58E-01		-5.04E+00	6.36E-01		5.01E-01	1.59E-01		2.56E+00	2.26E-38	Up	Unigene20009_All//gi|3894385|gb|AAC78592.1|//1.00E-64//Hcr2-0A [Solanum lycopersicum]	Unigene20009_All//2.00E-53//AT3G28890| AtRLP43 (Receptor Like Protein 43); kinase/ protein binding	Unigene20009_All//1.00E-41//ES795055		ko04626|Plant-pathogen interaction		nr +
Unigene20010_All	520	0.91	0.88	0.72	0.10	0.07	0.00	8.37	4.98	1.84	-4.63E-02	9.78E-01		-3.37E-01	7.34E-01		-5.33E-01	8.25E-01		-6.58E+00	6.36E-01		-7.49E-01	3.75E-03		-2.19E+00	2.64E-13	Down	Unigene20010_All//gi|224105499|ref|XP_002333808.1|//3.00E-17//predicted protein [Populus trichocarpa] >gi|222838546|gb|EEE76911.1| predicted protein [Populus trichocarpa]	Unigene20010_All//1.00E-09//AT1G77765| unknown protein					nr -
Unigene20017_All	656	6.62	2.63	1.14	5.62	5.20	4.89	0.26	0.25	0.55	-1.33E+00	1.09E-05	Down	-2.54E+00	7.10E-12	Down	-1.13E-01	7.73E-01		-2.01E-01	5.97E-01		-1.63E-02	1.02E+00		1.08E+00	3.50E-01		Unigene20017_All//gi|226529630|ref|XP_001152607.1|//4.00E-31//growth-regulating factor [Zea mays] >gi|195658087|gb|ACG48511.1| growth-regulating factor [Zea mays]	Unigene20017_All//3.00E-25//AT2G45480| AtGRF9 (GROWTH-REGULATING FACTOR 9); transcription activator	Unigene20017_All//0.00E+00//gi|78354490|gb|DT574764.1|DT574764	GRF			nr +
Unigene2002_All	295	0.18	3.09	1.08	1.69	5.37	2.14	3.30	2.41	2.43	4.12E+00	2.34E-04	Up	2.61E+00	1.46E-01		1.67E+00	2.24E-03		3.44E-01	6.99E-01		-4.53E-01	4.90E-01		-4.40E-01	4.73E-01		Unigene2002_All//gi|224113543|ref|XP_002332559.1|//4.00E-34//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222835043|gb|EEE73492.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene2002_All//2.00E-35//AT5G47230| ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5); DNA binding / transcription activator/ transcription factor	Unigene2002_All//7.00E-135//TC138684	AP2-EREBP		GO:0000160//GO:0001071//GO:0003676//GO:0006351//GO:0006950//GO:0009743//GO:0010468//GO:0030528//GO:0043231	nr +
Unigene20021_All	309	1.35	0.98	0.34	3.22	1.89	0.29	0.27	0.14	0.52	-4.61E-01	6.50E-01		-1.97E+00	1.51E-01		-7.67E-01	2.60E-01		-3.46E+00	1.73E-04	Down	-1.02E+00	7.25E-01		9.14E-01	6.24E-01									
Unigene20022_All	543	0.00	0.56	0.00	0.00	0.00	0.00	1.40	8.93	22.74	9.13E+00	4.43E-02		null	null		null	null		null	null		2.67E+00	1.01E-17	Up	4.02E+00	4.40E-65	Up	Unigene20022_All//gi|224056587|ref|XP_002298924.1|//2.00E-17//predicted protein [Populus trichocarpa] >gi|222846182|gb|EEE83729.1| predicted protein [Populus trichocarpa]	Unigene20022_All//5.00E-05//AT1G06137| unknown protein	Unigene20022_All//0.00E+00//DN817555				nr +
Unigene20026_All	502	1.67	4.64	6.89	0.20	0.62	0.00	0.00	0.00	0.00	1.48E+00	7.76E-04	Up	2.05E+00	1.49E-07	Up	1.64E+00	3.21E-01		-7.63E+00	4.00E-01		null	null		null	null				Unigene20026_All//0.00E+00//gi|109866400|gb|DW495376.1|DW495376				
Unigene20028_All	941	0.00	0.22	0.00	0.00	0.15	0.19	6.16	1.82	4.66	7.75E+00	1.37E-01		null	null		7.19E+00	3.19E-01		7.59E+00	1.94E-01		-1.76E+00	8.10E-13	Down	-4.03E-01	6.32E-02				Unigene20028_All//8.00E-20//DT468594				
Unigene2003_All	1061	1.33	7.59	1.20	11.78	21.49	11.15	14.43	21.04	51.48	2.51E+00	4.00E-22	Up	-1.45E-01	7.90E-01		8.67E-01	1.31E-15		-7.95E-02	6.90E-01		5.44E-01	1.36E-07		1.84E+00	8.98E-124	Up	Unigene2003_All//gi|224113543|ref|XP_002332559.1|//2.00E-73//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222835043|gb|EEE73492.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene2003_All//6.00E-48//AT5G47230| ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5); DNA binding / transcription activator/ transcription factor	Unigene2003_All//0.00E+00//TC138684	AP2-EREBP		GO:0006350//GO:0010033	nr +
Unigene20031_All	629	1.91	1.21	1.61	0.32	1.81	1.22	0.87	0.47	0.70	-6.63E-01	2.79E-01		-2.50E-01	6.75E-01		2.51E+00	7.35E-04	Up	1.95E+00	3.23E-02		-9.10E-01	3.19E-01		-3.27E-01	6.72E-01		Unigene20031_All//gi|117940128|sp|Q3ECP7.2|ERDL5_ARATH//4.00E-39//RecName: Full=Sugar transporter ERD6-like 5	Unigene20031_All//5.00E-27//AT1G54730| sugar transporter, putative	Unigene20031_All//0.00E+00//gi|48814398|gb|CO115711.1|CO115711				nr +
Unigene20032_All	460	0.00	0.00	0.00	0.00	0.00	0.00	21.32	5.09	11.78	null	null		null	null		null	null		null	null		-2.07E+00	3.74E-26	Down	-8.56E-01	1.08E-07		Unigene20032_All//gi|255568317|ref|XP_002525133.1|//4.00E-13//conserved hypothetical protein [Ricinus communis] >gi|223535592|gb|EEF37260.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene20034_All	944	0.00	0.11	0.11	0.00	0.15	0.57	2.11	1.33	39.12	6.75E+00	3.87E-01		6.82E+00	3.99E-01		7.19E+00	3.19E-01		9.17E+00	2.46E-03		-6.64E-01	1.09E-01		4.22E+00	2.60E-200	Up	Unigene20034_All//gi|114208|sp|P25317.1|GSTXA_TOBAC//1.00E-86//RecName: Full=Probable glutathione S-transferase parA; AltName: Full=Auxin-regulated protein parA; AltName: Full=STR246C protein >gi|170283|gb|AAA67894.1| par peptide [Nicotiana tabacum] >gi|530740|emb|CAA56790.1| STR246C [Nicotiana tabacum]	Unigene20034_All//4.00E-74//AT1G17180| ATGSTU25 (GLUTATHIONE S-TRANSFERASE TAU 25); glutathione transferase	Unigene20034_All//0.00E+00//TC141007		ko00480|Glutathione metabolism		nr +
Unigene20035_All	561	0.00	4.97	4.94	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.43E-16	Up	1.23E+01	2.75E-15	Up	null	null		null	null		null	null		null	null		Unigene20035_All//gi|298709187|emb|CBJ31130.1|//1.00E-17//Villin villin [Ectocarpus siliculosus]	Unigene20035_All//2.00E-14//AT2G29890| VLN1 (VILLIN-LIKE 1); actin binding / actin filament binding					nr -
Unigene20036_All	441	0.00	0.92	0.00	0.34	0.23	0.31	1.34	5.31	2.17	9.84E+00	1.36E-02		null	null		-5.33E-01	7.85E-01		-1.42E-01	9.43E-01		1.98E+00	1.85E-06	Up	6.92E-01	2.60E-01		Unigene20036_All//gi|57900026|dbj|BAD88068.1|//2.00E-15//KI domain interacting kinase 1-like protein [Oryza sativa Japonica Group] >gi|57900510|dbj|BAD88105.1| KI domain interacting kinase 1-like protein [Oryza sativa Japonica Group]	Unigene20036_All//2.00E-12//AT4G03230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene20036_All//6.00E-59//DT464066				nr +
Unigene20037_All	1894	0.00	0.16	0.00	0.00	0.02	0.00	0.27	3.91	5.03	7.33E+00	4.43E-02		null	null		4.19E+00	8.30E-01		null	null		3.87E+00	1.99E-37	Up	4.23E+00	4.25E-52	Up	Unigene20037_All//gi|242199342|gb|ACS87992.1|//1.00E-150//UDP-glucosyltransferase family 1 protein [Citrus sinensis]	Unigene20037_All//1.00E-132//AT2G36780| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene20037_All//0.00E+00//TC173077		ko00908|Zeatin biosynthesis		nr -
Unigene20040_All	380	0.14	0.53	0.14	5.51	8.88	1.78	0.00	0.22	0.31	1.95E+00	3.75E-01		2.49E-02	9.95E-01		6.90E-01	3.91E-02		-1.63E+00	4.42E-04	Down	7.78E+00	4.01E-01		8.30E+00	2.43E-01		Unigene20040_All//gi|62734468|gb|AAY96577.1|//2.00E-12//wall-associated protein kinase [Oryza sativa Japonica Group] >gi|77552660|gb|ABA95457.1| Protein kinase domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene20040_All//4.00E-09//AT1G19390| wall-associated kinase, putative	Unigene20040_All//2.00E-108//DT467466				nr +

Unigene20041_All	766	0.27	10.91	9.87	0.00	0.13	0.00	2.15	0.93	0.05	5.32E+00	1.40E-41	Up	5.18E+00	2.94E-36	Up	7.08E+00	4.56E-01		null	null		-1.21E+00	9.00E-03		-5.37E+00	6.97E-11	Down	Unigene20041_All//gi|4501883|ref|NP_001604.1|//1.00E-138//actin, aortic smooth muscle [Homo sapiens] >gi|6671507|ref|NP_031418.1| actin, aortic smooth muscle [Mus musculus] >gi|78045238|ref|NP_001029674.1| actin, aortic smooth muscle [Bos taurus] >gi|110625958|ref|NP_112266.1| actin, aortic smooth muscle [Rattus norvegicus] >gi|156119362|ref|NP_001095152.1| actin, aortic smooth muscle [Oryctolagus cuniculus] >gi|197097944|ref|NP_001126814.1| actin, aortic smooth muscle [Pongo abelii] >gi|213688375|ref|NP_001135417.1| actin, aortic smooth muscle [Homo sapiens] >gi|257470979|ref|NP_001158122.1| actin, aortic smooth muscle [Sus scrofa] >gi|73996085|ref|XP_534781.2| PREDICTED: similar to Actin, aortic smooth muscle (Alpha-actin 2) [Canis familiaris] >gi|114631685|ref|XP_521550.2|	Unigene20041_All//1.00E-134//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene20041_All//0.00E+00//TC153744		ko04145|Phagosome		nr +
Unigene20043_All	987	0.00	22.54	7.50	0.00	0.00	0.00	0.00	0.00	1.45E+01	4.76E-128	Up	1.29E+01	2.22E-41	Up	null	null		null	null		null	null		null	null		Unigene20043_All//sp|Q26643|TRF_SARPE//8.00E-145//Transferrin OS=Sarcophaga peregrina PE=1 SV=1						swissprot -
Unigene20044_All	484	0.43	0.84	1.43	0.62	0.43	3.17	1.92	6.48	2.47	9.54E-01	4.14E-01		1.73E+00	7.67E-02		-5.33E-01	6.79E-01		2.36E+00	1.37E-04	Up	1.75E+00	3.07E-07	Up	3.62E-01	5.21E-01		Unigene20044_All//gi|225454743|ref|XP_002273566.1|//1.00E-17//PREDICTED: similar to S-norcoclaurine synthase 2 [Vitis vinifera]		Unigene20044_All//0.00E+00//FF403697				nr -
Unigene20046_All	1278	0.20	0.04	0.25	0.43	0.35	0.07	29.41	2.16	4.33	-2.37E+00	2.14E-01		2.88E-01	8.10E-01		-2.92E-01	7.70E-01		-2.60E+00	2.93E-02		-3.77E+00	2.45E-185	Down	-2.76E+00	7.61E-143	Down	Unigene20046_All//gi|297828624|ref|XP_002882194.1|//1.00E-103//peroxidase 27 [Arabidopsis lyrata subsp. lyrata] >gi|297328034|gb|EFH58453.1| peroxidase 27 [Arabidopsis lyrata subsp. lyrata]	Unigene20046_All//6.00E-98//AT3G01190| peroxidase 27 (PER27) (P27) (PRXR7)	Unigene20046_All//1.00E-78//gi|54118297|gb|CO493806.1|CO493806		ko00940|Phenylpropanoid biosynthesis/ko00360|Phenylalanine metabolism		nr -
Unigene20047_All	1242	0.00	0.00	0.00	0.08	0.00	0.00	9.91	3.23	0.19	null	null		null	null		-6.33E+00	3.13E-01		-6.33E+00	4.00E-01		-1.62E+00	1.62E-23	Down	-5.69E+00	1.73E-80	Down	Unigene20047_All//gi|110816488|sp|Q38A12.1|YC391_PHAAO//2.00E-11//RecName: Full=Uncharacterized protein 0@391		Unigene20047_All//1.00E-43//TC172353				nr +
Unigene20049_All	625	0.25	0.73	0.17	2.23	0.44	1.30	2.37	1.07	0.13	1.54E+00	1.96E-01		-5.59E-01	7.76E-01		-2.34E+00	8.15E-05	Down	-7.79E-01	1.82E-01		-1.15E+00	2.04E-02		-4.21E+00	1.00E-08	Down	Unigene20049_All//gi|297603914|ref|NP_001054768.2|//7.00E-67//Os05g0170300 [Oryza sativa Japonica Group] >gi|255676063|dbj|BAF16682.2| Os05g0170300 [Oryza sativa Japonica Group]	Unigene20049_All//0.00E+00//AT4G20140| GS01 (GASSH01); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene20049_All//0.00E+00//ES840883				nr +
Unigene20050_All	450	0.93	0.68	0.24	0.00	1.99	0.80	1.69	5.20	21.25	-4.61E-01	6.50E-01		-1.97E+00	1.51E-01		1.10E+01	1.69E-05	Up	9.65E+00	2.37E-02		1.62E+00	4.26E-05	Up	3.65E+00	6.00E-47	Up	Unigene20050_All//gi|297603684|ref|NP_001054437.2|//2.00E-08//Os05g0110000 [Oryza sativa Japonica Group] >gi|255675945|dbj|BAF16351.2| Os05g0110000 [Oryza sativa Japonica Group]	Unigene20050_All//5.00E-09//AT4G11370| RHA1A; protein binding / zinc ion binding	Unigene20050_All//0.00E+00//TC153849				nr +
Unigene20051_All	601	0.00	0.00	0.00	0.00	0.00	0.00	11.12	16.34	41.89	null	null		null	null		null	null		null	null		5.56E-01	6.37E-04		1.91E+00	8.73E-61	Up	Unigene20051_All//gi|297803276|ref|XP_002869522.1|//2.00E-11//nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315358|gb|EFH45781.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene20051_All//1.00E-12//AT4G28040| nodulin MtN21 family protein					nr +
Unigene20054_All	272	0.00	0.00	0.00	0.00	0.00	0.00	23.32	7.84	8.06	null	null		null	null		null	null		null	null		-1.57E+00	4.79E-12	Down	-1.53E+00	4.96E-12	Down			Unigene20054_All//6.00E-21//DW504131				
Unigene20055_All	354	0.15	3.72	0.00	0.56	0.68	3.19	2.51	0.47	0.45	4.65E+00	1.91E-06	Up	-7.21E+00	6.25E-01		2.75E-01	8.95E-01		2.50E+00	1.01E-03		-2.41E+00	1.79E-03		-2.48E+00	9.93E-04	Down			Unigene20055_All//2.00E-67//TC147796				
Unigene20057_All	398	1.31	5.22	1.87	1.63	2.68	0.68	2.12	0.32	0.40	1.99E+00	7.20E-05	Up	5.11E-01	5.47E-01		7.21E-01	3.14E-01		-1.26E+00	1.83E-01		-2.75E+00	9.73E-04	Down	-2.41E+00	1.68E-03		Unigene20057_All//gi|87162732|gb|ABD28527.1|//4.00E-35//Protein kinase [Medicago truncatula]	Unigene20057_All//6.00E-35//AT3G03770| leucine-rich repeat transmembrane protein kinase, putative	Unigene20057_All//0.00E+00//TC146287		ko04626|Plant-pathogen interaction		nr +
Unigene20058_All	332	183.12	61.96	79.07	197.16	175.18	186.37	191.79	95.17	139.56	-1.56E+00	2.57E-88	Down	-1.21E+00	5.07E-58	Down	-1.71E-01	8.34E-03		-8.12E-02	3.04E-01		-1.01E+00	1.58E-57	Down	-4.59E-01	2.04E-15		Unigene20058_All//gi|15225613|ref|NP_181530.1|//2.00E-45//60S acidic ribosomal protein P0 (RPP0A) [Arabidopsis thaliana] >gi|12229886|sp|O04204.1|RLA01_ARATH RecName: Full=60S acidic ribosomal protein P0-1 >gi|2088654|gb|AAB95286.1| 60S acidic ribosomal protein P0 [Arabidopsis thaliana]	Unigene20058_All//7.00E-47//AT2G40010| 60S acidic ribosomal protein P0 (RPP0A)	Unigene20058_All//0.00E+00//TC145797		ko03010|Ribosome		nr +
Unigene20059_All	319	0.49	0.79	0.33	0.00	0.00	0.28	31.15	19.00	1.75	6.91E-01	6.27E-01		-5.59E-01	7.76E-01		null	null		8.15E+00	4.77E-01		-7.13E-01	1.05E-05		-4.16E+00	7.76E-55	Down		Unigene20059_All//3.00E-05//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene20059_All//1.00E-59//ES822054				
Unigene20061_All	1582	0.00	16.82	4.78	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	2.76E-153	Up	1.22E+01	2.76E-42	Up	null	null		null	null		null	null		null	null		Unigene20061_All//sp|Q9GPM3|ATFC_BOMMO//1.00E-17//Activating transcription factor of chaperone OS=Bombyx mori GN=ATFC PE=2 SV=1						swissprot +
Unigene20063_All	1379	0.00	10.03	5.29	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	2.03E-79	Up	1.24E+01	8.90E-41	Up	null	null		null	null		null	null		null	null		Unigene20063_All//gi|299472499|emb|CBN77284.1|//5.00E-06//hypothetical protein [Ectocarpus siliculosus]						nr -
Unigene20065_All	739	0.00	5.21	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	6.32E-22	Up	1.07E+01	9.13E-07	Up	null	null		null	null		null	null		null	null		Unigene20065_All//gi|297592144|gb|ADI46928.1|//5.00E-07//CRD1m [Volvox carteri f. nagariensis]						nr -
Unigene20068_All	317	0.50	0.00	0.67	0.31	0.00	0.00	78.29	101.26	161.49	-8.95E+00	2.16E-01		4.41E-01	7.75E-01		-8.30E+00	3.13E-01		-8.30E+00	4.00E-01		3.71E-01	1.23E-05		1.04E+00	5.55E-50	Up							ESTscan -
Unigene20071_All	935	0.00	37.01	13.95	0.00	0.07	0.00	0.00	0.00	0.00	1.52E+01	1.20E-199	Up	1.38E+01	1.96E-73	Up	6.20E+00	6.10E-01		null	null		null	null		null	null								ESTscan +
Unigene20072_All	630	0.00	2.41	1.94	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.10E-08	Up	1.09E+01	9.13E-07	Up	null	null		null	null		null	null		null	null								
Unigene20073_All	391	5.08	1.43	3.54	2.68	1.59	0.35	0.32	0.43	0.41	-1.83E+00	2.47E-04	Down	-5.22E-01	2.81E-01		-7.55E-01	2.53E-01		-2.95E+00	3.82E-04	Down	3.99E-01	8.14E-01		3.29E-01	8.51E-01		Unigene20073_All//gi|255537533|ref|XP_002509833.1|//3.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223549732|gb|EEF51220.1| conserved hypothetical protein [Ricinus communis]		Unigene20073_All//0.00E+00//gi|164281238|gb|ES852132.1|ES852132				nr -
Unigene20074_All	601	0.17	0.67	0.62	0.00	0.00	0.15	4.43	14.19	17.43	1.95E+00	1.44E-01		1.83E+00	2.13E-01		null	null		7.23E+00	4.77E-01		1.68E+00	2.29E-17	Up	1.98E+00	7.70E-27	Up							
Unigene20076_All	423	0.00	1.20	0.00	0.24	0.00	0.00	4.40	1.78	0.19	1.02E+01	4.05E-03		null	null		-7.88E+00	3.13E-01		-7.88E+00	4.00E-01		-1.31E+00	2.76E-03		-4.54E+00	2.65E-11	Down	Unigene20076_All//gi|133711974|gb|AB036677.1|//1.00E-19//vicilin [Pistacia vera]		Unigene20076_All//0.00E+00//gi|72276242|gb|DT050537.1|DT050537				nr +
Unigene20077_All	372	1.41	0.00	0.29	14.19	10.18	5.71	1.70	0.56	0.64	-1.05E+01	2.93E-03		-2.30E+00	6.76E-02		-4.79E-01	5.96E-02		-1.31E+00	5.97E-07	Down	-1.60E+00	6.27E-02		-1.41E+00	7.94E-02								
Unigene20082_All	308	2.21	1.65	0.69	1.62	0.00	0.29	4.53	4.48	3.10	-4.25E-01	5.97E-01		-1.67E+00	8.70E-02		-1.07E+01	8.98E-04	Down	-2.46E+00	4.83E-02		-1.66E-02	1.01E+00		-5.45E-01	2.66E-01				Unigene20082_All//1.00E-09//TC133606				
Unigene20088_All	1297	0.20	0.16	0.25	0.15	0.21	0.14	0.65	0.45	1.66	-3.68E-01	7.78E-01		2.88E-01	8.10E-01		4.68E-01	8.17E-01		-1.41E-01	9.35E-01		-5.31E-01	4.45E-01		1.35E+00	6.13E-04	Up	Unigene20088_All//gi|15232716|ref|NP_187567.1|//1.00E-145//lipin family protein [Arabidopsis thaliana] >gi|42572345|ref|NP_974268.1| lipin family protein [Arabidopsis thaliana] >gi|186509922|ref|NP_001118604.1| lipin family protein [Arabidopsis thaliana]	Unigene20088_All//5.00E-147//AT3G09560| lipin family protein	Unigene20088_All//0.00E+00//TC139778				nr -
Unigene20091_All	807	0.00	0.00	0.00	0.00	0.00	0.00	4.45	1.66	1.78	null	null		null	null		null	null		null	null		-1.43E+00	2.66E-06	Down	-1.33E+00	6.00E-06	Down	Unigene20091_All//gi|2341043|gb|AAB70448.1|//1.00E-110//Strong similarity to Arabidopsis REV3C (gb|X62461) [Arabidopsis thaliana] >gi|111074216|gb|ABH04481.1| AtlG04280 [Arabidopsis thaliana]	Unigene20091_All//6.00E-112//AT1G04280| unknown protein	Unigene20091_All//2.00E-140//gi|48791093|gb|CO092407.1|CO092407				nr +
Unigene20096_All	639	0.98	2.78	1.92	0.94	1.72	0.99	1.39	3.86	0.12	1.50E+00	3.72E-03		9.64E-01	1.38E-01		8.82E-01	1.94E-01		8.10E-02	9.45E-01		1.47E+00	9.56E-05	Up	-3.48E+00	7.34E-05	Down	Unigene20096_All//gi|297819638|ref|XP_002877702.1|//5.00E-26//bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323540|gb|EFH53961.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene20096_All//3.00E-13//AT3G49760| AthZIP5 (Arabidopsis thaliana basic leucine-zipper 5); DNA binding / transcription factor	Unigene20096_All//0.00E+00//EX168376	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene20097_All	537	0.49	0.85	0.30	0.74	1.09	0.34	1.10	2.57	5.34	8.02E-01	4.60E-01		-7.12E-01	6.22E-01		5.55E-01	5.99E-01		-1.14E+00	3.79E-01		1.22E+00	1.86E-02		2.28E+00	2.62E-09	Up			Unigene20097_All//6.00E-07//TC172770				

Unigene20098_All	458	0.00	0.00	0.00	0.00	0.00	0.00	48.47	49.92	5.57	null	null		null	null		null	null		null	null		4.26E-02	7.30E-01		-3.12E+00	7.03E-96	Down	Unigene20098_All//gi|253759964|ref|XP_002488956.1|//5.00E-10//hypothetical protein SORBIDRAFT_1211s002020 [Sorghum bicolor] >gi|253759995|ref|XP_002488958.1| hypothetical protein SORBIDRAFT_1184s002010 [Sorghum bicolor] >gi|253761162|ref|XP_002489054.1| hypothetical protein SORBIDRAFT_0208s002040 [Sorghum bicolor] >gi|253761217|ref|XP_002489066.1| hypothetical protein SORBIDRAFT_0177s002020 [Sorghum bicolor] >gi|253761435|ref|XP_002489115.1| hypothetical protein SORBIDRAFT_0057s002020 [Sorghum bicolor] >gi|253761554|ref|XP_002489154.1| hypothetical protein SORBIDRAFT_0016s002500 [Sorghum bicolor] >gi|253761556|ref|XP_002489155.1| hypothetical protein SORBIDRAFT_0016s002510 [Sorghum bicolor] >gi|253761558|ref|XP_002489156.1|		Unigene20098_All//4.00E-20//gi|78348172|gb|DT568446.1|DT568446				nr +
Unigene20099_All	611	0.17	0.00	0.00	1.22	0.23	0.74	0.28	0.27	2.61	-7.42E+00	3.73E-01		-7.42E+00	3.94E-01		-2.44E+00	5.60E-03		-7.26E-01	3.90E-01		-1.68E-02	1.02E+00		3.24E+00	1.34E-07	Up	Unigene20099_All//gi|224104489|ref|XP_002313453.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222849861|gb|EEE87408.1| predicted protein [Populus trichocarpa]	Unigene20099_All//1.00E-07//AT2G28690| unknown protein					nr -
Unigene20103_All	454	0.23	0.89	0.94	1.65	1.29	0.99	1.96	0.28	0.18	1.95E+00	1.44E-01		2.03E+00	1.39E-01		-3.52E-01	6.51E-01		-7.26E-01	3.90E-01		-2.82E+00	5.65E-04	Down	-3.48E+00	7.33E-05	Down			Unigene20103_All//5.00E-75//ES835359				
Unigene20104_All	630	0.00	0.16	0.00	1.19	3.50	1.65	0.00	0.73	0.25	7.33E+00	3.87E-01		null	null		1.56E+00	3.91E-04	Up	4.75E-01	5.12E-01		9.51E+00	1.94E-03		7.98E+00	1.40E-01		Unigene20104_All//gi|224105989|ref|XP_002314005.1|//3.00E-08//predicted protein [Populus trichocarpa] >gi|222850413|gb|EEE87960.1| predicted protein [Populus trichocarpa]						nr +
Unigene20105_All	347	0.60	3.65	0.31	1.58	0.99	0.78	1.95	1.45	2.07	2.60E+00	3.59E-04	Up	-9.75E-01	6.21E-01		-6.70E-01	4.97E-01		-1.02E+00	3.30E-01		-4.32E-01	6.12E-01		8.42E-02	9.24E-01		Unigene20105_All//gi|115473217|ref|NP_001060207.1|//9.00E-26//Os07g0602700 [Oryza sativa Japonica Group] >gi|113611743|dbj|BAF22121.1| Os07g0602700 [Oryza sativa Japonica Group]	Unigene20105_All//6.00E-17//AT3G02130| RPK2 (RECEPTOR-LIKE PROTEIN KINASE 2); ATP binding / kinase/ protein serine/threonine kinase					nr +
Unigene20106_All	658	0.00	0.00	0.00	0.00	0.00	0.00	3.98	3.24	0.00	null	null		null	null		null	null		null	null		-2.98E-01	4.22E-01		-1.20E+01	2.73E-19	Down	Unigene20106_All//gi|299473651|emb|CBN78045.1|//3.00E-67//poly(A) binding protein [Ectocarpus siliculosus]	Unigene20106_All//1.00E-60//AT4G34110| PAB2 (POLY(A) BINDING 2); RNA binding / translation initiation factor			ko03040|Spliceosome		nr -
Unigene20110_All	527	0.00	0.29	0.00	0.00	0.00	0.00	96.76	16.26	81.87	8.17E+00	2.35E-01		null	null		null	null		null	null		-2.57E+00	1.67E-173	Down	-2.41E-01	2.31E-04		Unigene20110_All//gi|30725324|gb|AAP37684.1|//4.00E-28//At3g01680 [Arabidopsis thaliana]	Unigene20110_All//3.00E-29//AT3G01680| unknown protein	Unigene20110_All//8.00E-65//TC134810				nr +
Unigene20111_All	939	0.00	29.89	13.67	0.00	0.00	0.00	0.00	0.00	0.00	1.49E+01	8.55E-162	Up	1.37E+01	3.18E-72	Up	null	null		null	null		null	null		null	null		Unigene20111_All//sp|O18920|ANGP1_BOVIN//2.00E-19//Angiopoietin-1 OS=Bos taurus GN=ANGPT1 PE=2 SV=3						swissprot -
Unigene20113_All	446	0.23	2.50	0.48	0.34	0.93	0.91	0.00	0.66	0.27	3.41E+00	1.24E-04	Up	1.03E+00	5.92E-01		1.47E+00	2.80E-01		1.44E+00	2.82E-01		9.36E+00	2.35E-02		8.07E+00	2.43E-01								
Unigene20114_All	345	109.04	45.38	58.19	170.81	177.77	235.11	281.13	165.12	174.48	-1.26E+00	5.45E-40	Down	-9.06E-01	1.27E-22		5.76E-02	5.14E-01		4.61E-01	1.47E-16		-7.68E-01	5.12E-55		-6.88E-01	7.41E-47		Unigene20114_All//gi|55976189|sp|Q6UNT2.1|RL5_CUCSA//7.00E-53//RecName: Full=60S ribosomal protein L5 >gi|34484312|gb|AAQ72789.1| 60S ribosomal protein L5 [Cucumis sativus]	Unigene20114_All//8.00E-53//AT5G39740| 60S ribosomal protein L5 (RPL5B)	Unigene20114_All//0.00E+00//gi|13352810|gb|BG443158.1|BG443158		ko03010|Ribosome		nr +
Unigene20115_All	694	0.00	0.00	0.00	0.00	0.00	0.00	28.82	12.23	3.39	null	null		null	null		null	null		null	null		-1.24E+00	1.82E-25	Down	-3.09E+00	1.50E-85	Down							ESTscan -
Unigene20116_All	1282	0.12	0.40	0.00	0.35	0.05	0.07	0.92	0.33	3.51	1.69E+00	1.34E-01		-6.94E+00	2.45E-01		-2.70E+00	3.24E-02		-2.31E+00	7.81E-02		-1.50E+00	9.69E-03		1.93E+00	1.25E-11	Up	Unigene20116_All//gi|115485947|ref|NP_001068117.1|//3.00E-73//Os11g0569500 [Oryza sativa Japonica Group] >gi|113645339|dbj|BAF28480.1| Os11g0569500 [Oryza sativa Japonica Group]	Unigene20116_All//2.00E-48//AT5G46330| FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / kinase/ protein binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase	Unigene20116_All//1.00E-47//TC151383		ko04626|Plant-pathogen interaction		nr -
Unigene20117_All	390	3.89	0.91	2.59	0.51	0.53	1.39	0.65	0.21	0.41	-2.10E+00	5.39E-04	Down	-5.85E-01	3.05E-01		5.24E-02	9.89E-01		1.44E+00	1.93E-01		-1.60E+00	3.11E-01		-6.71E-01	6.05E-01		Unigene20117_All//gi|15241651|ref|NP_196468.1|//3.00E-22//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75171895|sp|Q9FN7.1|PP371_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g08510 >gi|50897238|gb|AAT85758.1| At5g08510 [Arabidopsis thaliana]	Unigene20117_All//2.00E-23//AT5G08510| pentatricopeptide (PPR) repeat-containing protein	Unigene20117_All//4.00E-106//C0092688				nr -
Unigene20122_All	1202	0.09	0.51	0.13	14.34	9.91	6.88	0.60	0.07	0.13	2.54E+00	2.46E-02		6.10E-01	7.48E-01		-5.33E-01	1.54E-05		-1.06E+00	2.70E-15	Down	-3.11E+00	1.40E-03		-2.17E+00	7.75E-03		Unigene20122_All//gi|166203230|gb|ABY84655.1|//1.00E-56//transcription factor [Glycine max]	Unigene20122_All//8.00E-33//AT2G44745| WRKY family transcription factor	Unigene20122_All//4.00E-59//TC154949	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene20123_All	618	0.34	0.66	0.69	0.24	0.11	0.51	2.12	1.49	103.08	9.54E-01	4.14E-01		1.03E+00	3.97E-01		-1.12E+00	5.84E-01		1.08E+00	4.76E-01		-5.11E-01	3.55E-01		5.60E+00	0.00E+00	Up							
Unigene20124_All	263	0.20	1.93	0.61	1.89	1.70	2.40	4.50	1.59	1.06	3.28E+00	2.11E-02		1.61E+00	5.11E-01		-1.54E-01	8.50E-01		3.44E-01	6.99E-01		-1.50E+00	9.69E-03		-2.09E+00	5.32E-04	Down			Unigene20124_All//6.00E-67//TC158859				
Unigene20125_All	1053	0.35	1.25	0.40	0.43	0.59	0.73	2.33	1.27	6.43	1.85E+00	3.97E-03		2.18E-01	8.31E-01		4.67E-01	6.35E-01		7.76E-01	3.78E-01		-8.75E-01	1.57E-02		1.47E+00	6.75E-12	Up	Unigene20125_All//gi|87240796|gb|AB032654.1|//9.00E-57//Zinc finger, RING-type [Medicago truncatula]	Unigene20125_All//2.00E-41//AT4G03965| protein binding / zinc ion binding	Unigene20125_All//4.00E-16//TC154064		ko04120|Ubiquitin mediated proteolysis//ko04146|Peroxisome		nr -
Unigene20128_All	517	0.00	4.12	0.00	0.58	2.73	5.07	0.00	0.00	0.85	1.20E+01	4.10E-12	Up	null	null		2.24E+00	3.44E-04	Up	3.13E+00	8.03E-10	Up	null	null		9.73E+00	2.13E-03		Unigene20128_All//gi|41351515|dbj|BAD08339.1|//6.00E-64//flowering locus T like protein [Populus nigra] >gi|50199496|dbj|BAD27481.1| flowering locus T like protein [Populus nigra]	Unigene20128_All//2.00E-52//AT5G62040| brother of FT and TFL1 protein (BFT)					nr +
Unigene20130_All	904	0.00	0.62	0.00	0.00	0.23	0.10	0.56	1.90	2.12	9.27E+00	2.18E-03		null	null		7.84E+00	1.57E-01		6.64E+00	4.77E-01		1.76E+00	2.63E-04	Up	1.91E+00	2.33E-05	Up							
Unigene20131_All	1468	0.00	0.00	0.00	0.00	0.05	0.00	11.23	7.74	4.45	null	null		null	null		5.55E+00	6.10E-01		null	null		-5.37E-01	1.06E-05		-1.34E+00	1.89E-24	Down	Unigene20131_All//gi|22345248|gb|AC089551.1|//0.00E+00//protein kinase [Glycine max]	Unigene20131_All//2.00E-166//AT1G61590| protein kinase, putative	Unigene20131_All//4.00E-07//EX168622		ko04626|Plant-pathogen interaction		nr -
Unigene20133_All	908	0.17	0.33	0.82	0.60	0.53	0.05	4.19	5.25	1.18	9.53E-01	5.03E-01		2.25E+00	2.35E-02		-1.85E-01	8.25E-01		-3.60E+00	8.98E-03		3.24E-01	2.20E-01		-1.82E+00	2.03E-09	Down	Unigene20133_All//gi|301016726|dbj|BAJ11784.1|//2.00E-10//dehydration responsive protein [Corchorus olitorius]		Unigene20133_All//6.00E-36//TC152783				nr -
Unigene20134_All	456	0.11	1.56	0.82	1.09	1.21	0.50	2.23	0.00	1.66	3.76E+00	2.36E-03		2.83E+00	9.31E-02		1.46E-01	9.05E-01		-1.14E+00	3.07E-01		-1.11E+01	2.97E-07	Down	-4.23E-01	4.77E-01				Unigene20134_All//2.00E-166//TC168534				
Unigene20135_All	1035	0.00	97.81	33.65	0.00	0.00	0.00	0.00	0.00	0.00	1.66E+01	0.00E+00	Up	1.50E+01	1.24E-197	Up	null	null		null	null		null	null		null	null			Unigene20135_All//gi|11465624|ref|NP_049295.1|//1.00E-106//apocytochrome b [Porphyra purpurea] >gi|4106931|gb|AAD03098.1| apocytochrome b [Porphyra purpurea]	Unigene20135_All//3.00E-84//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.			ko00190|Oxidative phosphorylation		nr +
Unigene20137_All	329	2.54	1.08	0.00	3.03	3.56	0.82	4.24	0.76	0.61	-1.24E+00	1.15E-01		-1.13E+01	1.19E-04	Down	2.33E-01	7.69E-01		-1.88E+00	1.18E-02		-2.48E+00	3.36E-05	Down	-2.81E+00	4.25E-06	Down							ESTscan +
Unigene20140_All	853	0.00	19.13	14.36	0.23	0.00	0.00	0.00	0.00	0.00	1.42E+01	9.21E-94	Up	1.38E+01	6.86E-69	Up	-7.87E+00	8.43E-02		-7.87E+00	1.34E-01		null	null		null	null		Unigene20140_All//gi|145343056|ref|XP_001416282.1|//7.00E-06//Plastid ribosomal protein L10, imported to chloroplast, large ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|144576507|gb|ABO94575.1| Plastid ribosomal protein L10, imported to chloroplast, large ribosomal subunit [Ostreococcus lucimarinus CCE9901]				ko03010|Ribosome		nr -
Unigene20146_All	466	0.22	0.22	0.91	9.94	8.72	4.75	86.01	82.87	166.28	-4.63E-02	9.89E-01		2.03E+00	1.39E-01		-1.89E-01	5.44E-01		-1.07E+00	1.26E-04	Down	-5.36E-02	5.90E-01		9.51E-01	1.55E-64		Unigene20146_All//gi|224111870|ref|XP_002316008.1|//1.00E-33//cytochrome P450 [Populus trichocarpa] >gi|222865048|gb|EEF02179.1| cytochrome P450 [Populus trichocarpa]	Unigene20146_All//9.00E-27//AT3G14620| CYP72A8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene20146_All//3.00E-92//TC171728		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr -
Unigene20148_All	548	0.95	0.00	0.00	2.82	0.94	0.91	1.77	1.07	0.00	-9.90E+00	2.93E-03		-9.90E+00	4.75E-03		-1.58E+00	2.26E-03		-1.64E+00	3.26E-03		-7.33E-01	2.48E-01		-1.08E+01	2.72E-07	Down	Unigene20148_All//gi|124360549|gb|ABD33126.2|//4.00E-29//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene20148_All//2.00E-10//ATMG01250| hypothetical protein	Unigene20148_All//1.00E-42//ES822996				nr +
Unigene2015_All	1873	7.49	15.69	17.63	8.11	5.42	16.28	86.07	240.64	345.28	1.07E+00	5.02E-24	Up	1.24E+00	9.28E-33	Up	-5.81E-01	1.07E-05		1.00E+00	4.02E-24	Up	1.48E+00	0.00E+00	Up	2.00E+00	0.00E+00	Up	Unigene2015_All//0.00E+00//AT1G24400| LHT2 (LYSINE HISTIDINE TRANSPORTER 2); acidic amino acid transmembrane transporter/ amino acid transmembrane transporter/ neutral amino acid transmembrane transporter	Unigene2015_All//0.00E+00//TC158865			GO:0031224	nr +
Unigene20153_All	459	0.80	1.77	1.04	2.39	0.45	0.89	2.49	0.73	4.86	1.15E+00	1.48E-01		3.88E-01	6.97E-01		-2.41E+00	5.06E-04	Down	-1.43E+00	3.46E-02		-1.77E+00	3.71E-03		9.67E-01	9.38E-03		Unigene20153_All//gi|225456555|ref|XP_002264294.1|//1.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene20153_All//3.00E-98//gi|78340583|gb|DT560857.1|DT560857				nr -

Unigene20155_All	290	5.41	20.09	0.73	4.98	6.06	4.98	0.00	0.72	0.69	1.89E+00	1.36E-11	Up	-2.88E+00	3.27E-05	Down	2.82E-01	5.96E-01		6.00E-04	9.96E-01		9.49E+00	7.85E-02		9.42E+00	7.89E-02		Unigene20155_All//gi|159138941|gb|ABW89470.1|//4.00E-25//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene20155_All//5.00E-23//AT3G46230| ATHSP17.4	Unigene20155_All//4.00E-124//DN800613				nr +
Unigene20158_All	756	0.00	0.00	0.00	0.00	0.00	0.00	6.66	3.81	0.26	null	null		null	null		null	null		null	null		-8.03E-01	7.43E-04		-4.66E+00	4.05E-30	Down	Unigene20158_All//gi|168259042|gb|ACA23209.1|//4.00E-24//serine protease [Phytophthora infestans]						nr +
Unigene20159_All	883	2.07	8.21	10.67	0.11	0.16	0.00	0.00	0.00	0.00	1.98E+00	4.02E-15	Up	2.36E+00	2.46E-23	Up	4.68E-01	8.77E-01		-6.82E+00	4.00E-01		null	null		null	null		Unigene20159_All//gi|56392765|gb|AAV87151.1|//6.00E-85//methyl jasmonate esterase [Solanum tuberosum]	Unigene20159_All//1.00E-59//AT3G50440| MES10 (METHYL ESTERASE 10); hydrolase/ hydrolase, acting on ester bonds / methyl jasmonate esterase			ko00901|Indole alkaloid biosynthesis		nr -
Unigene2016_All	1368	3.82	2.59	2.76	8.16	9.26	8.12	6.46	6.84	13.34	-5.61E-01	3.23E-02		-4.69E-01	9.13E-02		1.84E-01	3.15E-01		-6.20E-03	9.69E-01		8.34E-02	6.60E-01		1.05E+00	2.00E-18	Up	Unigene2016_All//gi|224145649|ref|XP_002325717.1|//1.00E-56//nbs-lrr resistance protein [Populus trichocarpa] >gi|222862592|gb|EEF00099.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene2016_All//5.00E-07//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene2016_All//4.00E-115//TC171799			GO:0005488	nr -
Unigene20162_All	263	0.80	4.24	5.47	1.14	1.31	1.37	0.64	2.07	4.09	2.41E+00	1.59E-03		2.78E+00	1.05E-04	Up	2.04E-01	9.01E-01		2.74E-01	8.33E-01		1.68E+00	7.92E-02		2.67E+00	1.42E-04	Up	Unigene20162_All//gi|21425669|emb|CAC35022.1|//6.00E-11//mitochondrial RNA polymerase [Nicotiana tabacum]	Unigene20162_All//4.00E-10//AT1G68990| DNA-directed RNA polymerase, mitochondrial (RPOMT)	Unigene20162_All//3.00E-41//ES830875				nr -
Unigene20163_All	1947	0.00	0.00	0.00	0.00	0.00	0.00	7.17	10.60	0.27	null	null		null	null		null	null		null	null		5.65E-01	1.56E-07		-4.75E+00	1.28E-83	Down	Unigene20163_All//gi|299115393|emb|CBN74223.1|//5.00E-18//EsV-1-166 [Ectocarpus siliculosus]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene20164_All	649	0.00	0.00	0.00	0.00	0.11	0.00	102.54	23.76	21.79	null	null		null	null		6.73E+00	6.10E-01		null	null		-2.11E+00	5.42E-178	Down	-2.23E+00	3.54E-197	Down								
Unigene20165_All	437	0.00	0.00	0.12	2.17	1.50	0.72	1.45	0.00	0.55	null	null		6.93E+00	6.36E-01		-5.33E-01	4.51E-01		-1.58E+00	3.51E-02		-1.05E+01	1.23E-04	Down	-1.41E+00	7.94E-02		Unigene20165_All//gi|297729423|ref|NP_001177075.1|//5.00E-06//Os12g0633900 [Oryza sativa Japonica Group] >gi|77557155|gb|ABA99951.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255670513|dbj|BAH95803.1| Os12g0633900 [Oryza sativa Japonica Group]		Unigene20165_All//3.00E-08//TC164813				nr +
Unigene20166_All	1494	0.00	0.00	0.07	0.00	0.18	0.18	46.10	11.86	35.49	null	null		6.16E+00	3.99E-01		7.53E+00	7.02E-02		7.50E+00	7.03E-02		-1.96E+00	3.28E-167	Down	-3.77E-01	7.87E-12		Unigene20166_All//gi|15230349|ref|NP_188563.1|//1.00E-115//leucine-rich repeat family protein [Arabidopsis thaliana]	Unigene20166_All//2.00E-115//AT3G19320| leucine-rich repeat family protein	Unigene20166_All//5.00E-13//TC137730		ko04626|Plant-pathogen interaction		nr -
Unigene2017_All	1393	4.13	4.29	4.32	13.70	16.22	12.09	12.99	13.26	26.08	5.50E-02	8.27E-01		6.42E-02	8.02E-01		2.44E-01	3.88E-02		-1.80E-01	2.07E-01		2.98E-02	8.30E-01		1.01E+00	1.25E-33	Up	Unigene2017_All//gi|224132366|ref|XP_002328251.1|//6.00E-59//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837766|gb|EEE76131.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene2017_All//7.00E-17//AT1G69545| leucine-rich repeat family protein	Unigene2017_All//0.00E+00//ES828802			GO:0005488	nr -
Unigene20170_All	385	28.00	47.25	43.57	30.41	44.10	41.64	134.97	142.97	708.92	7.55E-01	8.14E-09		6.38E-01	5.18E-06		5.36E-01	2.23E-05		4.54E-01	9.81E-04		8.31E-02	2.67E-01		2.39E+00	0.00E+00	Up	Unigene20170_All//gi|67483357|gb|AAY68034.1|//1.00E-54//3-hydroxy-methylglutaryl coenzyme A reductase [Tilia miqueliana]	Unigene20170_All//1.00E-29//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene20170_All//0.00E+00//TC164133		ko00900|Terpenoid backbone biosynthesis		nr +
Unigene20171_All	336	0.31	4.98	2.06	1.33	0.21	4.03	116.65	298.79	551.58	4.00E+00	2.08E-07	Up	2.73E+00	1.40E-02		-2.70E+00	3.24E-02		1.60E+00	9.06E-03		1.36E+00	1.15E-143	Up	2.24E+00	0.00E+00	Up			Unigene20171_All//8.00E-141//TC150997				
Unigene20173_All	520	0.50	0.00	0.20	1.44	4.24	2.52	0.00	0.80	1.46	-8.97E+00	6.71E-02		-1.30E+00	4.36E-01		1.56E+00	3.91E-04	Up	8.10E-01	1.91E-01		9.65E+00	3.65E-03		1.05E+01	1.39E-05	Up	Unigene20173_All//gi|115446837|ref|NP_001047198.1|//9.00E-42//Os02g0572900 [Oryza sativa Japonica Group] >gi|113536729|dbj|BAF09112.1| Os02g0572900 [Oryza sativa Japonica Group]	Unigene20173_All//6.00E-42//AT1G34370| STOP1 (sensitive to proton rhizotoxicity 1); nucleic acid binding / transcription factor/ zinc ion binding	Unigene20173_All//2.00E-96//TC174797	C2H2			nr +
Unigene20175_All	662	0.32	158.74	64.03	0.00	0.21	0.00	0.00	0.00	0.00	8.97E+00	0.00E+00	Up	7.66E+00	8.60E-232	Up	7.70E+00	3.19E-01		null	null		null	null		null	null									ESTscan -
Unigene20176_All	659	0.16	0.54	0.00	0.00	0.16	0.21	0.45	1.59	2.42	1.76E+00	2.18E-01		-7.31E+00	3.94E-01		7.29E+00	4.56E-01		7.68E+00	3.11E-01		1.82E+00	5.04E-03		2.43E+00	7.10E-06	Up	Unigene20176_All//gi|224100749|ref|XP_002334340.1|//7.00E-63//cytochrome P450 [Populus trichocarpa] >gi|222871210|gb|EEF08341.1| cytochrome P450 [Populus trichocarpa]	Unigene20176_All//1.00E-48//AT4G39490| CYP96A10; electron carrier/ heme binding / iron ion binding / monooxygenase	Unigene20176_All//0.00E+00//gi|164364331|gb|EX164025.1|EX164025		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene20177_All	666	0.71	0.91	0.88	6.43	5.12	3.46	2.79	0.38	0.96	3.69E-01	6.60E-01		3.15E-01	7.19E-01		-3.30E-01	2.91E-01		-8.95E-01	1.99E-03		-2.89E+00	8.75E-08	Down	-1.55E+00	3.64E-04	Down	Unigene20177_All//gi|297848532|ref|XP_002892147.1|//4.00E-75//kinase interacting family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337989|gb|EFH68406.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata]	Unigene20177_All//5.00E-70//AT1G60080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053), KIP1-like (InterPro:IPR011684); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT3G22790.1); Has 169162 Blast hits to 69460 proteins in 2232 species: Archae - 2114; Bacteria - 24914; Metazoa - 82448; Fungi - 11850; Plants - 6375; Viruses - 760; Other Eukaryotes - 40701 (source: NCBI BLink).					nr +
Unigene20179_All	392	2.54	1.16	2.31	2.80	7.64	2.88	1.19	0.11	0.00	-1.12E+00	1.09E-01		-1.35E-01	8.38E-01		1.45E+00	6.03E-05	Up	4.30E-02	9.42E-01		-3.48E+00	1.03E-02		-1.02E+01	1.09E-03		Unigene20179_All//gi|10172593|dbj|BAB01397.1|//6.00E-32//protein kinase-like protein [Arabidopsis thaliana]	Unigene20179_All//9.00E-18//AT3G13065| SRF4 (STRUBBELIG-RECEPTOR FAMILY 4); ATP binding / kinase/ protein serine/threonine kinase	Unigene20179_All//0.00E+00//gi|78325523|gb|DT545797.1|DT545797				nr +
Unigene20181_All	689	0.00	0.00	0.00	0.00	0.00	0.00	7.92	3.94	7.46	null	null		null	null		null	null		null	null		-1.01E+00	1.27E-05	Down	-8.58E-02	7.21E-01		Unigene20181_All//gi|297724625|ref|NP_001174676.1|//5.00E-56//Os06g0231050 [Oryza sativa Japonica Group] >gi|75116473|sp|Q67X40.1|U4974_ORYSJ RecName: Full=UPF0497 membrane protein Os06g0231050 >gi|51535409|dbj|BAD37279.1| integral membrane family protein-like [Oryza sativa Japonica Group] >gi|255676859|dbj|BAH93404.1| Os06g0231050 [Oryza sativa Japonica Group]	Unigene20181_All//7.00E-43//AT5G15290| integral membrane family protein					nr -
Unigene20184_All	303	0.00	0.00	0.00	0.49	0.00	1.04	16.74	47.18	20.25	null	null		null	null		-8.95E+00	1.66E-01		1.08E+00	4.76E-01		1.49E+00	2.78E-24	Up	2.74E-01	2.10E-01				Unigene20184_All//4.00E-50//FF403697				
Unigene20189_All	740	1.06	2.12	3.53	1.08	1.07	0.31	0.00	0.00	0.00	1.00E+00	5.98E-02		1.73E+00	7.95E-05	Up	-9.10E-03	9.67E-01		-1.82E+00	3.32E-02		null	null		null	null		Unigene20189_All//gi|15146264|gb|AAK83615.1|//5.00E-61//At1g10080/T27I1_10 [Arabidopsis thaliana]	Unigene20189_All//7.00E-63//AT1G10090| unknown protein	Unigene20189_All//1.00E-21//TC172450				nr +
Unigene2019_All	2047	1.81	1.44	3.64	1.48	0.94	1.30	2.64	2.92	1.48	-3.38E-01	3.08E-01		1.01E+00	7.59E-06	Up	-6.56E-01	5.68E-02		-1.90E-01	6.27E-01		1.43E-01	5.82E-01		-8.38E-01	1.67E-04		Unigene2019_All//gi|297800334|ref|XP_002868051.1|//1.00E-141//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313887|gb|EFH44310.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2019_All//7.00E-113//AT4G17570| zinc finger (GATA type) family protein	Unigene2019_All//0.00E+00//ES801507	C2C2-GATA		GO:0001071//GO:0003677//GO:0006351//GO:0043231//GO:0046914	nr +
Unigene20191_All	527	0.30	0.00	0.00	0.28	2.35	0.69	0.08	0.40	1.59	-8.22E+00	2.16E-01		-8.22E+00	2.45E-01		3.05E+00	6.03E-05	Up	1.27E+00	3.82E-01		2.31E+00	2.40E-01		4.31E+00	4.10E-05	Up	Unigene20191_All//gi|34850945|dbj|BAC87845.1|//2.00E-51//leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	Unigene20191_All//5.00E-51//AT4G08850| kinase	Unigene20191_All//6.00E-112//DR462992		ko03410|Base excision repair		nr +
Unigene20198_All	529	0.00	1.15	0.10	0.09	0.52	0.85	1.36	1.50	0.15	1.02E+01	1.17E-03		6.65E+00	6.36E-01		2.47E+00	2.23E-01		3.18E+00	3.79E-02		1.44E-01	8.36E-01		-3.17E+00	8.09E-04	Down			Unigene20198_All//2.00E-158//C0107461				
Unigene20201_All	301	142.36	116.15	97.30	156.72	140.60	125.59	143.98	67.48	77.43	-2.94E-01	3.40E-04		-5.49E-01	4.76E-11		-1.57E-01	5.13E-02		-3.20E-01	2.33E-05		-1.09E+00	1.09E-44	Down	-8.95E-01	3.02E-33		Unigene20201_All//gi|7387726|sp|O22582.3|H2B_GOSHI//4.00E-29//RecName: Full=Histone H2B >gi|2558962|gb|AAB97163.1| histone H2B1 [Gossypium hirsutum]		Unigene20201_All//1.00E-130//gi|109826256|gb|DW224977.1|DW224977				nr +
Unigene20202_All	690	10.24	4.63	7.18	0.00	0.05	0.00	0.00	0.12	0.00	-1.15E+00	4.53E-07	Down	-5.12E-01	2.70E-02		5.64E+00	8.30E-01		null	null		6.92E+00	4.01E-01		null	null		Unigene20202_All//gi|18409132|ref|NP_564944.1|//6.00E-20//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75336852|sp|Q9SY71.1|BHLH30_ARATH RecName: Full=Transcription factor bHLH30; AltName: Full=Transcription factor EN 53; AltName: Full=bHLH transcription factor bHLH030; AltName: Full=Basic helix-loop-helix protein 30; Short=bHLH 30; Short=AtbHLH30	Unigene20202_All//1.00E-18//AT1G68810| basic helix-loop-helix (bHLH) family protein	Unigene20202_All//7.00E-69//CK640462	bHLH			nr +
Unigene20203_All	461	0.45	1.65	1.50	1.95	5.60	3.53	0.92	1.72	0.95	1.86E+00	3.73E-02		1.73E+00	7.67E-02		1.53E+00	1.27E-04	Up	8.59E-01	1.08E-01		9.09E-01	2.11E-01		5.18E-02	9.74E-01				Unigene20203_All//9.00E-52//gi|13350148|gb|BG440497.1|BG440497				
Unigene20205_All	215	7.79	9.90	8.42	1.16	1.28	3.15	5.31	6.61	0.74	3.46E-01	4.34E-01		1.13E-01	8.10E-01		1.45E-01	9.62E-01		1.44E+00	1.28E-01		3.16E-01	5.63E-01		-2.84E+00	3.60E-05	Down			Unigene20205_All//3.00E-99//ES840423				
Unigene20209_All	1032	0.00	0.00	0.00	0.00	0.00	0.00	2.62	2.03	0.00	null	null		null	null		null	null		null	null		-3.73E-01	3.08E-01		-1.14E+01	6.55E-20	Down	Unigene20209_All//sp|Q5SA42|DO3_DICDI//4.00E-70//Protein DO3-3 OS=Dictyostelium discoideum GN=DO3-3 PE=2 SV=1						swissprot +
Unigene20212_All	770	1.09	17.04	16.94	2.07	1.39	0.47	0.00	0.00	0.21	3.97E+00	8.48E-55	Up	3.96E+00	3.84E-53	Up	-5.78E-01	2.71E-01		-2.14E+00	2.07E-04	Down	null	null		7.69E+00	1.40E-01		Unigene20212_All//gi|116310040|emb|CAH67063.1|//5.00E-12//H0112G12.8 [Oryza sativa (indica cultivar-group)]	Unigene20212_All//6.00E-05//AT5G26690| heavy-metal-associated domain-containing protein					nr +
Unigene20213_All	447	316.62	171.96	153.56	415.90	314.23	426.07	105.09	68.82	46.43	-8.81E-01	1.43E-82		-1.04E+00	4.93E-106	Down	-4.04E-01	4.32E-33		3.49E-02	4.75E-01		-6.11E-01	2.29E-18		-1.18E+00	4.91E-56	Down	Unigene20213_All//gi|80973462|gb|AB853472.1|//9.00E-24//GDP-D-mannose-3',5'-epimerase [Malpighia glabra]	Unigene20213_All//6.00E-23//AT5G28840| GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-mannose 3,5-epimerase/ NAD or NADH binding / catalytic	Unigene20213_All//0.00E+00//DW227800		ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene20216_All	410	17.99	5.44	22.47	0.49	1.18	0.88	0.00	0.00	0.00	-1.73E+00	5.97E-13	Down	3.21E-01	1.21E-01		1.27E+00	2.92E-01		8.59E-01	5.42E-01		null	null		null	null		Unigene20216_All//gi|124359343|gb|ABD28505.2|//2.00E-09//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene20216_All//2.00E-09//AT5G42905| nucleic acid binding / ribonuclease H					nr -

Unigene2022_All	505	3.00	3.61	0.53	5.82	2.52	2.33	4.27	2.15	0.63	2.66E-01	6.07E-01			-2.51E+00	1.79E-04	Down	-1.21E+00	4.51E-04	Down	-1.32E+00	3.33E-04	Down	-9.89E-01	1.17E-02		-2.76E+00	7.15E-09	Down	Unigene2022_All//gi|297814281|ref|XP_002875024.1|//4.00E-23//beta-amylase 9 [Arabidopsis lyrata subsp. lyrata] >gi|297320861|gb|EFH51283.1| beta-amylase 9 [Arabidopsis lyrata subsp. lyrata]	Unigene2022_All//4.00E-23//AT4G00490| BAM2 (BETA-AMYLASE 2); beta-amylase	Unigene2022_All//0.00E+00//ES825440			GO:0005976//GO:0016160//GO:0043167//GO:0043231	nr +
Unigene20224_All	697	0.00	0.00	0.00	0.14	0.10	0.06	3.15	8.40	11.89	null	null			null	null		-5.32E-01	8.17E-01		-1.14E+00	6.77E-01		1.41E+00	1.26E-09	Up	1.91E+00	1.50E-20	Up	Unigene20224_All//gi|115445017|ref|NP_001046288.1|//1.00E-32//Os02g0215500 [Oryza sativa Japonica Group] >gi|113535819|dbj|BAF08202.1| Os02g0215500 [Oryza sativa Japonica Group]	Unigene20224_All//2.00E-29//AT3G47580| leucine-rich repeat transmembrane protein kinase, putative	Unigene20224_All//8.00E-78//TC132784		ko04626|Plant-pathogen interaction		nr -
Unigene20225_All	701	0.45	0.29	0.76	1.35	1.38	0.06	1.81	0.42	2.22	-6.31E-01	6.22E-01			7.62E-01	4.53E-01		2.67E-02	9.88E-01		-4.39E+00	5.96E-05	Down	-2.12E+00	4.17E-04	Down	2.93E-01	5.53E-01									
Unigene20227_All	715	0.00	0.00	0.00	2.79	1.71	0.00	0.06	0.11	null	null				null	null		2.00E+00	4.50E-05	Up	1.29E+00	4.33E-02		5.87E+00	6.35E-01		6.80E+00	4.04E-01		Unigene20227_All//gi|224126905|ref|XP_002329502.1|//1.00E-42//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870182|gb|EEF07313.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene20227_All//5.00E-33//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene20227_All//0.00E+00//ES812318		ko04626|Plant-pathogen interaction		nr -
Unigene2023_All	2287	3.50	2.26	3.59	6.19	4.13	3.89	3.81	2.08	1.55	-6.31E-01	2.06E-03			3.48E-02	8.80E-01		-5.84E-01	2.13E-05		-6.69E-01	3.95E-06		-8.70E-01	7.49E-07		-1.30E+00	9.02E-13	Down	Unigene2023_All//gi|297814281|ref|XP_002875024.1|//0.00E+00//beta-amylase 9 [Arabidopsis lyrata subsp. lyrata] >gi|297320861|gb|EFH51283.1| beta-amylase 9 [Arabidopsis lyrata subsp. lyrata]	Unigene2023_All//0.00E+00//AT4G00490| BAM2 (BETA-AMYLASE 2); beta-amylase	Unigene2023_All//0.00E+00//DR454733		ko00500|Starch and sucrose metabolism	GO:0005976//GO:0016160//GO:0043167//GO:0043231	nr -
Unigene20233_All	479	0.22	0.63	0.00	0.42	1.58	1.98	1.06	2.79	4.24	1.54E+00	3.23E-01			-7.77E+00	3.94E-01		1.93E+00	3.36E-02		2.25E+00	6.12E-03		1.40E+00	9.01E-03		2.00E+00	6.22E-06	Up				Unigene20233_All//6.00E-16//TC159677					
Unigene20234_All	761	0.00	0.00	0.00	0.52	0.45	0.18	7.72	2.25	4.71	null	null			null	null		-2.11E-01	8.25E-01		-1.56E+00	2.31E-01		-1.78E+00	3.40E-13	Down	-7.13E-01	7.34E-04		Unigene20234_All//gi|87240970|gb|AB032828.1|//3.00E-19//[, related [Medicago truncatula]	Unigene20234_All//2.00E-13//AT1G63670| unknown protein	Unigene20234_All//2.00E-17//gi|21097661|gb|BQ409974.1|BQ409974				nr +
Unigene20236_All	613	0.60	0.17	0.09	0.16	0.34	0.59	3.17	5.80	6.82	-1.85E+00	1.87E-01			-2.78E+00	1.03E-01		1.05E+00	6.12E-01		1.86E+00	2.20E-01		8.69E-01	2.89E-03		1.10E+00	2.88E-05	Up								
Unigene20239_All	669	5.08	3.56	7.96	42.67	2.11	0.34	1.52	0.00	1.49	-5.14E-01	1.28E-01			6.47E-01	1.65E-02		-4.34E+00	6.47E-166	Down	-6.98E+00	3.94E-173	Down	-1.06E+01	2.97E-07	Down	-2.70E-02	9.74E-01									
Unigene2024_All	2383	3.69	2.42	1.85	6.25	6.03	5.17	4.84	2.07	1.79	-6.06E-01	1.82E-03			-9.92E-01	1.29E-06		-5.28E-02	7.91E-01		-2.73E-01	7.43E-02		-1.23E+00	7.48E-15	Down	-1.44E+00	2.53E-19	Down	Unigene2024_All//gi|23329527|ref|NP_172762.2|//1.00E-115//sphere organelles protein-related [Arabidopsis thaliana]	Unigene2024_All//2.00E-98//AT1G13030| sphere organelles protein-related	Unigene2024_All//0.00E+00//TC160541				nr +
Unigene20241_All	318	0.82	2.07	0.84	0.16	2.82	0.57	0.80	0.66	0.75	1.33E+00	1.45E-01			2.54E-02	1.00E+00		4.17E+00	1.67E-04	Up	1.86E+00	4.58E-01		-2.80E-01	8.29E-01		-8.57E-02	9.57E-01									
Unigene20243_All	383	0.00	0.53	0.00	0.00	0.45	0.59	239.88	34.48	66.88	9.05E+00	1.37E-01			null	null		8.81E+00	2.27E-01		9.20E+00	1.19E-01		-2.80E+00	0.00E+00	Down	-1.84E+00	2.45E-211	Down	Unigene20243_All//gi|224137856|ref|XP_002326457.1|//9.00E-26//aquaporin, MIP family, TIP subfamily [Populus trichocarpa] >gi|222823779|gb|EEE72256.1| aquaporin, MIP family, TIP subfamily [Populus trichocarpa]	Unigene20243_All//1.00E-12//AT4G17340| TIP2;2 (TONOPLAST INTRINSIC PROTEIN 2;2); water channel	Unigene20243_All//1.00E-44//TC152333				nr +
Unigene20245_All	292	4.66	0.69	3.65	2.56	2.12	4.18	0.43	0.86	0.82	-2.75E+00	1.08E-04	Down	-3.53E-01	5.65E-01		-2.70E-01	7.48E-01		7.07E-01	2.77E-01		9.83E-01	5.17E-01		9.14E-01	5.42E-01									
Unigene20246_All	837	0.31	0.24	0.13	2.26	1.56	2.75	1.01	0.05	0.43	-3.68E-01	7.78E-01			-1.30E+00	4.36E-01		-5.33E-01	2.63E-01		2.83E-01	5.56E-01		-4.34E+00	4.55E-05	Down	-1.24E+00	6.26E-02		Unigene20246_All//gi|15229471|ref|NP_187413.1|//3.00E-65//DNA binding [Arabidopsis thaliana]	Unigene20246_All//1.00E-66//AT3G07565| DNA binding	Unigene20246_All//0.00E+00//CO083492				nr -
Unigene2025_All	1529	32.82	11.73	20.76	25.02	17.81	19.82	47.06	66.04	13.94	-1.48E+00	1.21E-67	Down	-6.61E-01	1.28E-17		-4.90E-01	4.89E-10		-3.36E-01	7.35E-05		4.89E-01	5.35E-26		-1.76E+00	6.20E-155	Down	Unigene2025_All//gi|224065731|ref|XP_002301953.1|//1.00E-172//cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa] >gi|222843679|gb|EEE81226.1| cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa]	Unigene2025_All//5.00E-117//AT4G39330| CAD9 (CINNAMYL ALCOHOL DEHYDROGENASE 9); binding / catalytic/ oxidoreductase/ zinc ion binding	Unigene2025_All//0.00E+00//TC142512		ko00940|Phenylpropanoid biosynthesis	GO:0008152//GO:0016616//GO:0046914	nr -
Unigene20250_All	640	6.29	5.15	5.91	8.48	5.43	4.16	1.32	2.22	1.31	-2.91E-01	3.73E-01			-9.16E-02	7.74E-01		-6.43E-01	7.83E-03		-1.03E+00	4.94E-05	Down	7.49E-01	1.39E-01		-1.55E-02	9.71E-01					Unigene20250_All//3.00E-157//TC152831					
Unigene20251_All	579	0.00	0.00	0.00	0.00	0.00	0.00	4.60	3.39	0.14	null	null			null	null		null	null		null	null		-4.39E-01	2.21E-01		-5.06E+00	7.12E-17	Down	Unigene20251_All//gi|52077156|dbj|BAD46202.1|//1.00E-06//hypothetical protein [Oryza sativa Japonica Group]		Unigene20251_All//2.00E-16//ES810795				nr -
Unigene20252_All	320	6.21	0.00	8.15	0.78	0.00	7.62	0.00	2.87	0.00	-1.26E+01	1.70E-11	Down	3.92E-01	3.60E-01		-9.60E+00	4.18E-02		3.29E+00	1.43E-09	Up	1.15E+01	1.48E-06	Up	null	null					Unigene20252_All//2.00E-12//ES803332					
Unigene20257_All	453	0.12	7.38	3.64	0.00	0.00	0.10	3.73	0.28	0.35	6.00E+00	1.58E-17	Up	4.98E+00	6.48E-08	Up	null	null		6.64E+00	6.96E-01		-3.75E+00	8.32E-09	Down	-3.41E+00	1.56E-08	Down	Unigene20257_All//gi|224104365|ref|XP_002313412.1|//5.00E-43//copper transporter [Populus trichocarpa] >gi|222849820|gb|EEE87367.1| copper transporter [Populus trichocarpa]	Unigene20257_All//6.00E-34//AT5G59030| COPT1 (copper transporter 1); copper ion transmembrane transporter	Unigene20257_All//2.00E-12//BQ404364				nr -
Unigene20258_All	232	6.31	5.68	16.30	3.65	4.16	2.73	1.82	4.68	3.61	-1.53E-01	7.62E-01		1.37E+00	5.97E-05	Up	1.87E-01	8.11E-01		-4.22E-01	6.18E-01		1.36E+00	2.43E-02		9.85E-01	1.40E-01					Unigene20258_All//2.00E-91//gi|54120132|gb|CO495641.1|CO495641					
Unigene2026_All	2520	17.92	8.22	12.78	7.73	9.22	8.87	2.94	1.31	1.15	-1.12E+00	8.83E-40	Down	-4.87E-01	1.83E-09		2.55E-01	2.62E-02		1.99E-01	1.19E-01		-1.16E+00	4.30E-09	Down	-1.35E+00	1.35E-11	Down	Unigene2026_All//gi|117557160|gb|AB635757.1|//0.00E+00//sulfate transporter [Populus tremula x Populus alba]	Unigene2026_All//0.00E+00//AT5G13550| SULTR4;1; sulfate transmembrane transporter	Unigene2026_All//0.00E+00//ES831922			GO:0015103//GO:0015291//GO:0015698//GO:0031224//GO:0043231	nr -
Unigene20260_All	822	0.00	0.00	0.00	0.48	0.17	0.00	2.98	7.12	0.44	null	null			null	null		-1.53E+00	2.05E-01		-8.92E+00	1.11E-02		1.25E+00	3.66E-08	Up	-2.77E+00	4.81E-10	Down	Unigene20260_All//gi|15222073|ref|NP_175349.1|//2.00E-45//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565178|sp|Q6NQG7.1|ATL1L_ARATH RecName: Full=RING-H2 finger protein ATL1L >gi|34365601|gb|AAQ65112.1| Atlg49230 [Arabidopsis thaliana]	Unigene20260_All//8.00E-46//AT1G49230| zinc finger (C3HC4-type RING finger) family protein					nr +
Unigene20261_All	234	2.46	1.30	1.59	3.19	1.18	0.19	0.72	0.36	0.17	-9.21E-01	3.43E-01		-6.27E-01	5.27E-01		-1.44E+00	7.43E-02		-4.05E+00	7.75E-04	Down	-1.02E+00	6.14E-01		-2.09E+00	3.13E-01					Unigene20261_All//3.00E-41//BF278159					
Unigene20262_All	615	1.79	0.33	0.17	2.35	1.23	0.51	0.14	0.00	0.00	-2.44E+00	1.50E-03		-3.37E+00	2.67E-04	Down	-9.31E-01	8.04E-02		-2.19E+00	3.74E-04	Down	-7.10E+00	4.04E-01		-7.10E+00	3.59E-01					Unigene20262_All//7.00E-07//DW227626					
Unigene20271_All	673	0.00	54.58	19.86	0.00	0.10	0.00	0.00	0.00	0.00	1.57E+01	5.65E-212	Up	1.43E+01	3.00E-75	Up	6.68E+00	6.10E-01		null	null		null	null		null	null			Unigene20271_All//gi|192912960|gb|AC096588.1|//3.00E-57//ribosomal protein L17 [Elaeis guineensis]	Unigene20271_All//1.00E-56//AT1G27400| 60S ribosomal protein L17 (RPL17A)		ko03010|Ribosome		nr -
Unigene20272_All	467	0.22	0.00	0.00	2.88	6.86	4.55	0.72	1.16	0.43	-7.81E+00	3.73E-01		-7.81E+00	3.94E-01		1.25E+00	2.50E-04	Up	6.58E-01	1.50E-01		6.84E-01	4.49E-01		-7.64E-01	5.01E-01		Unigene20272_All//gi|110737098|dbj|BAF00501.1|//1.00E-07//zinc finger like protein [Arabidopsis thaliana]		Unigene20272_All//3.00E-18//BE053154				nr -
Unigene20273_All	424	0.37	0.00	0.00	0.94	1.46	0.64	2.09	0.00	0.66	-8.53E+00	2.16E-01		-8.53E+00	2.45E-01		6.37E-01	5.49E-01		-5.57E-01	6.38E-01		-1.10E+01	2.24E-06	Down	-1.67E+00	1.33E-02		Unigene20273_All//gi|27529848|dbj|BAC53939.1|//6.00E-56//NCW protein-like protein [Nicotiana tabacum]	Unigene20273_All//7.00E-46//AT1G44900| ATP binding / DNA binding / DNA-dependent ATPase	Unigene20273_All//0.00E+00//gi|48822810|gb|CO124123.1|CO124123		ko03030|DNA replication		nr -
Unigene20275_All	266	22.23	76.39	26.83	40.64	35.99	40.07	79.00	158.38	80.43	1.78E+00	1.06E-35	Up	2.71E-01	2.58E-01		-1.75E-01	3.71E-01		-2.03E-02	9.35E-01		1.00E+00	7.75E-38	Up	2.59E-02	8.34E-01		Unigene20275_All//gi|1279590|emb|CAB96432.1|//5.00E-13//ras-related small GTP-binding protein [Nicotiana plumbaginifolia]	Unigene20275_All//2.00E-11//AT1G02130| ARA-5 (ARABIDOPSIS RAS 5); GTP binding	Unigene20275_All//1.00E-132//gi|21098112|gb|BQ410425.1|BQ410425				nr -
Unigene20278_All	418	1.00	0.00	0.76	3.58	5.03	8.86	0.30	0.00	0.00	-9.97E+00	1.03E-02		-3.90E-01	7.17E-01		4.91E-01	3.07E-01		1.31E+00	5.81E-05	Up	-8.25E+00	2.36E-01		-8.25E+00	2.00E-01					Unigene20278_All//5.00E-07//CO122679					
Unigene20280_All	707	0.00	0.00	0.00	0.14	0.00	0.13	3.89	0.47	3.49	null	null			null	null		-7.14E+00	3.13E-01		-1.41E-01	9.50E-01		-3.04E+00	9.79E-12	Down	-1.54E-01	6.44E-01		Unigene20280_All//gi|62867641|gb|AY117424.1|//6.00E-49//At2g01340 [Arabidopsis thaliana] >gi|94442481|gb|ABF19028.1| At2g01340 [Arabidopsis thaliana]	Unigene20280_All//1.00E-35//AT2G01340| unknown protein	Unigene20280_All//3.00E-09//PF403790				nr +
Unigene20282_All	587	456.80	2045.51	1407.27	398.09	1098.70	2126.53	176.61	392.04	250.77	2.16E+00	0.00E+00	Up	1.62E+00	0.00E+00	Up	1.46E+00	0.00E+00	Up	2.42E+00	0.00E+00	Up	1.15E+00	8.46E-254	Up	5.06E-01	7.12E-41		Unigene20282_All//gi|162462310|ref|NP_001106048.1|//6.00E-33//major facilitator superfamily protein [Zea mays] >gi|148372339|gb|ABQ63093.1| major facilitator superfamily protein [Zea mays] >gi|148791581|gb|ABR12535.1| major facilitator superfamily protein [Zea mays] >gi|195617444|gb|ACG30552.1| synaptic vesicle 2-related protein [Zea mays]	Unigene20282_All//2.00E-34//AT3G13050| transporter-related	Unigene20282_All//0.00E+00//gi|164366391|gb|ES801673.1|ES801673				nr -
Unigene20284_All	772	0.00	0.46	1.66	0.00	0.62	0.53	0.66	3.74	2.84	8.84E+00	2.46E-02		1.07E+01	4.69E-07	Up	9.29E+00	5.07E-03		9.04E+00	1.36E-02		2.51E+00	4.00E-10	Up	2.11E+00	1.02E-06	Up	Unigene20284_All//gi|240254229|ref|NP_849783.4|//1.00E-57//phosphoinositide binding [Arabidopsis thaliana]	Unigene20284_All//8.00E-91//AT4G17140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pleckstrin homology (InterPro:IPR001849); BEST Arabidopsis thaliana protein match is: phosphoinositide binding (TAIR:AT1G48090.2); Has 1924 Blast hits to 1182 proteins in 161 species: Archae - 0; Bacteria - 16; Metazoa - 911; Fungi - 304; Plants - 271; Viruses - 0; Other Eukaryotes - 422 (source: NCBI BLink).	Unigene20284_All//8.00E-140//TC149294				nr +
Unigene20285_All	1022	0.05	0.10	0.00	0.00	0.40	0.49	1.78	2.86	7.37	9.54E-01	7.26E-01		-5.68E+00	6.25E-01		8.66E+00	1.25E-02		8.93E+00	4.38E-03		6.86E-01	3.63E-02		2.05E+00	1.96E-20	Up	Unigene20285_All//gi|15220732|ref|NP_174326.1|//1.00E-115//lipase class 3 family protein [Arabidopsis thaliana]	Unigene20285_All//1.00E-116//AT1G30370| lipase class 3 family protein	Unigene20285_All//7.00E-107//TC175119				nr -
Unigene20286_All	281	0.56	0.54	0.57	9.40	4.04	7.07	0.75	1.34	0.14	-4.62E-02	9.89E-01		2.53E-02	1.00E+00		-1.22E+00	9.07E-04	Down	-4.10E-01	3.27E-01		8.32E-01	4.67E-01		-2.41E+00	1.95E-01										ESTscan +
Unigene20287_All	228	4.82	0.00	8.41	5.03	3.02	10.30	0.19	0.73	1.22	-1.22E+01	1.95E-06	Down	8.03E-01	1.02E-01		-7.34E-01	2.38E-01		1.04E+00	1.40E-02		1.98E+00	3.79E-01		2.72E+00	9.93E-02		Unigene20287_All//gi|224077524|ref|XP_002305285.1|//1.00E-07//predicted protein [Populus trichocarpa] >gi|222848249|gb|EEE85796.1| predicted protein [Populus trichocarpa]	Unigene20287_All//3.00E-06//AT1G52640| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene20288_All	915	0.00	0.66	0.23	0.22	0.11	0.00	9.84	15.62	1.87	9.38E+00	1.17E-03		7.86E+00	1.41E-01		-9.48E-01	5.88E-01		-7.77E+00	1.34E-01		6.67E-01	4.73E-07		-2.39E+00	1.12E-29	Down	Unigene20288_All//gi|45752748|gb|AS76272.1|//7.00E-36//At5g06790 [Arabidopsis thaliana]	Unigene20288_All//6.00E-33//AT5G06790| unknown protein					nr +
Unigene20289_All	609	0.00	0.17	0.00	11.94	8.54	1.33	0.14	0.00	0.00	7.38E+00	3.87E-01		null	null		-4.84E-01	2.02E-02		-3.16E+00	1.03E-27	Down	-7.12E+00	4.04E-01		-7.12E+00	3.59E-01		Unigene20289_All//gi|297725163|ref|NP_001174945.1|//1.00E-30//Os06g0666500 [Oryza sativa Japonica Group] >gi|52076527|dbj|BAD45404.1| RING zinc finger protein-like [Oryza sativa Japonica Group] >gi|255677304|dbj|BAH93673.1| Os06g0666500 [Oryza sativa Japonica Group]	Unigene20289_All//6.00E-23//AT5G05280| zinc finger (C3HC4-type RING finger) family protein	Unigene20289_All//0.00E+00//TC145820				nr +
Unigene2029_All	705	1.78	3.88	2.19	3.67	3.08	3.33	6.48	8.60	15.94	1.12E+00	3.73E-03		2.98E-01	6.09E-01		-2.56E-01	5.41E-01		-1.41E-01	7.26E-01		4.08E-01	6.42E-02		1.30E+00	4.09E-16	Up				Unigene2029_All//8.00E-07//FL576534					
Unigene20292_All	384	0.41	0.53	0.55	1.56	0.54	1.41	5.62	1.09	1.35	3.69E-01	8.16E-01		4.40E-01	7.75E-01		-1.53E+00	1.01E-01		-1.41E-01	8.79E-01		-2.37E+00	2.59E-07	Down	-2.06E+00	1.55E-06	Down				Unigene20292_All//2.00E-111//CO112619					

Unigene20293_A11	1472	0.00	0.03	0.07	0.00	0.00	0.12	0.98	7.18	17.00	5.10E+00	6.17E-01		6.18E+00	3.99E-01		null	null		6.94E+00	1.94E-01		2.88E+00	5.68E-41	Up	4.12E+00	1.06E-133	Up	Unigene20293_A11//gi|297833972|ref|XP_002884868.1|//9.00E-86//U-box domain-containing protein 24 [Arabidopsis lyrata subsp. lyrata] >gi|297330708|gb|EFH61127.1| U-box domain-containing protein 24 [Arabidopsis lyrata subsp. lyrata]	Unigene20293_A11//1.00E-82//AT2G35930| PUR23 (PLANT U-BOX 23); ubiquitin-protein ligase			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene20297_A11	944	1.77	0.48	0.11	0.95	0.66	0.19	2.28	0.58	1.18	-1.88E+00	7.32E-04	Down	-3.97E+00	4.71E-07	Down	-5.33E-01	4.70E-01		-2.31E+00	5.79E-03		-1.99E+00	4.81E-06	Down	-9.51E-01	1.16E-02		Unigene20297_A11//gi|79313291|ref|NP_001030725.1|//3.00E-89//ARC6H [Arabidopsis thaliana]	Unigene20297_A11//2.00E-78//AT3G19180| ARC6H	Unigene20297_A11//0.00E+00//ES794680				nr +
Unigene20298_A11	406	2.58	10.48	5.25	0.12	2.04	1.00	0.10	0.00	0.00	2.02E+00	2.16E-09	Up	1.03E+00	2.70E-02		4.05E+00	4.06E-04	Up	3.03E+00	6.03E-02		-6.70E+00	6.58E-01		-6.70E+00	6.13E-01		Unigene20298_A11//gi|15231450|ref|NP_187390.1|//3.00E-19//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75313804|sp|Q9SRT2.1|BHO62_ARATH RecName: Full=Transcription factor bHLH62; AltName: Full=Transcription factor EN 85; AltName: Full=bHLH transcription factor bHLH062; AltName: Full=Basic helix-loop-helix protein 62; Short=bHLH 62; Short=AtbHLH62 >gi|111074462|gb|ABH04604.1| At3g07340 [Arabidopsis thaliana]	Unigene20298_A11//2.00E-20//AT3G07340| basic helix-loop-helix (bHLH) family protein	Unigene20298_A11//7.00E-40//ES838051	bHLH			nr -
Unigene20299_A11	499	0.21	0.71	1.28	5.09	1.45	4.07	0.51	0.34	0.16	1.76E+00	2.18E-01		2.61E+00	2.33E-02		-1.81E+00	4.01E-06	Down	-3.22E-01	4.64E-01		-6.02E-01	6.48E-01		-1.67E+00	2.56E-01					Unigene20299_A11//7.00E-53//DW518489				
Unigene2030_A11	1193	1.36	3.44	1.56	2.80	3.06	1.97	7.48	12.09	16.56	1.34E+00	2.02E-05	Up	2.00E-01	6.69E-01		1.29E-01	7.55E-01		-5.07E-01	1.47E-01		6.93E-01	1.50E-07		1.15E+00	6.13E-23	Up				Unigene2030_A11//0.00E+00//FL576534				
Unigene20300_A11	366	0.00	0.00	0.00	0.00	0.00	0.00	44.94	16.22	48.66	null	null		null	null		null	null		null	null		-1.47E+00	3.08E-27	Down	1.15E-01	3.79E-01									
Unigene20302_A11	606	0.09	0.00	0.18	3.95	5.06	1.49	0.70	0.28	0.13	-6.43E+00	6.13E-01		1.03E+00	7.03E-01		3.58E-01	3.55E-01		-1.40E+00	8.07E-04	Down	-1.34E+00	2.24E-01		-2.41E+00	3.94E-02		Unigene20302_A11//gi|224107955|ref|XP_002314667.1|//2.00E-73//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222863707|gb|EEF00838.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene20302_A11//2.00E-63//AT3G51895| SULTR3;1 (SULFATE TRANSPORTER 3;1); secondary active sulfate transmembrane transporter/ sulfate transmembrane transporter/ transporter	Unigene20302_A11//0.00E+00//TC139441				nr -
Unigene20304_A11	406	3.09	0.87	1.05	5.03	0.93	0.22	0.62	1.03	0.20	-1.82E+00	5.22E-03		-1.56E+00	1.90E-02		-2.43E+00	4.21E-07	Down	-4.50E+00	2.02E-10	Down	7.21E-01	5.07E-01		-1.67E+00	2.56E-01		Unigene20304_A11//gi|115463957|ref|NP_001055578.1|//2.00E-52//Os05g0420600 [Oryza sativa Japonica Group] >gi|122169096|sp|Q0DI31.1|CYC_ORYSJ RecName: Full=Cytochrome c >gi|152013457|sp|A2V4S9.1|CYC_ORYSI RecName: Full=Cytochrome c >gi|169786|gb|AAA63515.1| cytochrome c [Oryza sativa Indica Group] >gi|218249|dbj|BAA02159.1| cytochrome C [Oryza sativa Japonica Group] >gi|48475175|gb|AAT44244.1| Cytochrome c [Oryza sativa Japonica Group] >gi|113579129|dbj|BAF17492.1| Os05g0420600 [Oryza sativa Japonica Group]	Unigene20304_A11//1.00E-52//AT4G10040| CYTC-2 (cytochrome c-2); electron carrier/ heme binding / iron ion binding	Unigene20304_A11//0.00E+00//DW498962				nr -
Unigene20307_A11	281	0.00	0.00	0.00	0.00	0.37	2.57	0.30	1.34	2.13	null	null		null	null		8.52E+00	4.56E-01		1.13E+01	2.31E-04	Up	2.15E+00	9.45E-02		2.82E+00	5.65E-03									
Unigene20309_A11	527	0.00	1.06	0.20	0.85	0.39	0.94	6.10	45.29	50.42	1.00E+01	2.18E-03		7.66E+00	3.99E-01		-1.12E+00	3.15E-01		1.48E-01	9.06E-01		2.89E+00	3.62E-92	Up	3.05E+00	4.87E-110	Up	Unigene20309_A11//gi|151301818|gb|ABN50365.2|//3.00E-47//ethylene responsive element binding protein 1 [Gossypium barbadense]	Unigene20309_A11//1.00E-24//AT4G17500| ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene20309_A11//4.00E-48//TC178747	AP2-EREBP			nr -
Unigene20310_A11	576	0.64	1.94	1.11	0.52	0.42	3.06	1.25	0.15	6.57	1.61E+00	1.95E-02		8.03E-01	3.88E-01		-3.10E-01	8.20E-01		2.56E+00	1.29E-05	Up	-3.10E+00	1.40E-03		2.40E+00	9.69E-13	Up	Unigene20310_A11//gi|297836999|ref|XP_002886381.1|//8.00E-11//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322222|gb|EFH62640.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene20310_A11//7.00E-12//AT1G63840| zinc finger (C3HC4-type RING finger) family protein	Unigene20310_A11//0.00E+00//DW506660				nr +
Unigene20316_A11	899	0.70	0.45	0.53	11.91	9.42	7.33	0.94	0.00	0.00	-6.31E-01	4.75E-01		-3.90E-01	6.46E-01		-3.38E-01	5.12E-02		-7.00E-01	3.77E-05		-9.88E+00	4.39E-06	Down	-9.88E+00	2.21E-06	Down	Unigene20316_A11//gi|4544369|gb|AAD22280.1|//3.00E-38//expressed protein [Arabidopsis thaliana] >gi|115311445|gb|ABI93903.1| At2g15440 [Arabidopsis thaliana]	Unigene20316_A11//1.00E-64//AT4G24910| unknown protein	Unigene20316_A11//0.00E+00//TC174280				nr -
Unigene20317_A11	290	0.00	1.22	3.67	3.61	3.92	4.67	0.00	0.00	0.14	1.03E+01	2.46E-02		1.18E+01	6.62E-06	Up	1.19E-01	8.71E-01		3.73E-01	5.63E-01		null	null		7.10E+00	6.45E-01									
Unigene20318_A11	248	11.60	4.49	6.87	33.54	19.58	14.39	32.90	20.06	17.51	-1.37E+00	3.57E-04	Down	-7.56E-01	5.03E-02		-7.77E-01	2.78E-05		-1.22E+00	1.67E-09	Down	-7.14E-01	7.64E-05		-9.10E-01	3.65E-07					Unigene20318_A11//2.00E-67//gi|13355208|gb|BG445460.1|BG445460				
Unigene20319_A11	368	0.28	0.41	0.58	0.54	0.66	1.35	0.57	0.57	2.81	5.39E-01	7.79E-01		1.03E+00	5.92E-01		2.75E-01	8.95E-01		1.32E+00	2.52E-01		-1.67E-02	1.02E+00		2.29E+00	7.17E-04	Up	Unigene20319_A11//gi|8778477|gb|AAF79485.1|AC022492_29//8.00E-16//F1L3.14 [Arabidopsis thaliana]	Unigene20319_A11//6.00E-16//AT1G17450| FUNCTIONS IN: molecular_function unknown; CONTAINS InterPro DOMAIN/s: B-block binding subunit of TFIIIC (InterPro:IPR007309); BEST Arabidopsis thaliana protein match is: transcription factor-related (TAIR:AT1G59453.1); Has 39 Blast hits to 33 proteins in 8 species: Archae - 0; Bacteria - 3; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene20319_A11//8.00E-51//gi|13355741|gb|BG446089.1|BG446089				nr -
Unigene20320_A11	227	0.00	0.00	0.00	1.76	1.06	0.80	2.24	0.00	0.00	null	null		null	null		-7.25E-01	5.47E-01		-1.14E+00	3.79E-01		-1.11E+01	8.89E-04	Down	-1.11E+01	5.54E-04	Down	Unigene20320_A11//gi|71905597|gb|AAZ52776.1|//3.00E-16//expressed protein [Arabidopsis thaliana]	Unigene20320_A11//1.00E-17//AT5G46060| unknown protein	Unigene20320_A11//4.00E-123//TC163177				nr +
Unigene20321_A11	243	38.54	32.53	31.56	60.27	51.02	75.83	24.88	23.74	12.30	-2.45E-01	2.18E-01		-2.89E-01	1.58E-01		-2.41E-01	1.14E-01		3.31E-01	1.14E-02		-6.80E-02	7.79E-01		-1.02E+00	1.77E-06	Down				Unigene20321_A11//8.00E-51//gi|13355741|gb|BG446089.1|BG446089				
Unigene20325_A11	558	4.50	6.17	9.35	2.14	3.89	1.05	2.73	2.62	2.71	4.56E-01	1.78E-01		1.06E+00	1.30E-04	Up	8.60E-01	4.80E-02		-1.03E+00	1.06E-01		-5.73E-02	9.20E-01		-7.80E-03	9.80E-01					Unigene20325_A11//4.00E-36//TC157882				
Unigene20326_A11	275	23.21	9.03	13.36	22.28	14.28	21.68	64.11	23.25	21.73	-1.36E+00	3.21E-08	Down	-7.97E-01	1.04E-03		-6.42E-01	4.22E-03		-3.95E-02	8.96E-01		-1.46E+00	6.25E-29	Down	-1.56E+00	9.79E-33	Down				Unigene20326_A11//1.00E-123//gi|21100689|gb|BQ413002.1|BQ413002				
Unigene20328_A11	294	2.49	0.34	0.00	4.41	2.11	1.08	1.44	0.00	0.41	-2.85E+00	6.26E-03		-1.13E+01	4.13E-04	Down	-1.06E+00	6.06E-02		-2.03E+00	1.62E-03		-1.05E+01	3.25E-03		-1.82E+00	9.22E-02		Unigene20328_A11//gi|89001003|gb|ABD59091.1|//4.00E-08//At3g48490 [Arabidopsis thaliana]	Unigene20328_A11//2.00E-09//AT3G48490| unknown protein					nr +
Unigene20331_A11	422	2.11	0.00	1.89	0.12	0.41	0.00	0.10	0.00	0.00	-1.10E+01	2.86E-05	Down	-1.55E-01	8.24E-01		1.79E+00	5.20E-01		-6.88E+00	6.36E-01		-6.65E+00	6.58E-01		-6.65E+00	6.13E-01		Unigene20331_A11//sp|Q1QME5|TATA_NITHX//5.00E-09//Sec-independent protein translocase protein tatA/E homolog OS=Nitrobacter hamburgensis (strain X14 / DSM 10229) GN=tatA PE=3 SV=1						swissprot +
Unigene20332_A11	459	1.37	0.66	3.60	0.33	0.30	0.10	5.80	1.73	10.42	-1.05E+00	2.50E-01		1.39E+00	1.19E-02		-1.18E-01	9.11E-01		-1.73E+00	5.01E-01		-1.75E+00	2.99E-06	Down	8.44E-01	4.29E-04		Unigene20332_A11//gi|8778443|gb|AAF79451.1|AC025808.33//9.00E-33//F18014.11 [Arabidopsis thaliana]	Unigene20332_A11//6.00E-34//AT1G19390| wall-associated kinase, putative	Unigene20332_A11//1.00E-35//DT462731		ko04626|Plant-pathogen interaction		nr +
Unigene20333_A11	393	0.53	0.52	0.14	2.79	2.45	0.23	0.00	0.00	0.00	-4.62E-02	9.88E-01		-1.97E+00	3.81E-01		-1.85E-01	8.01E-01		-3.60E+00	5.02E-05	Down	null	null		null	null					Unigene20333_A11//1.00E-07//DW518561				
Unigene20337_A11	303	0.35	1.00	0.00	0.00	0.34	2.09	2.51	0.69	1.18	1.54E+00	3.23E-01		-8.43E+00	3.94E-01		8.41E+00	4.56E-01		1.10E-01	7.60E-04	Up	-1.86E+00	1.82E-02		-1.09E+00	1.21E-01									
Unigene20338_A11	204	0.77	0.00	0.00	0.00	0.00	0.00	77.51	224.75	103.50	-9.59E+00	2.16E-01		-9.59E+00	2.45E-01		null	null		null	null		1.54E+00	2.60E-79	Up	4.17E-01	6.33E-05		Unigene20338_A11//gi|124360970|gb|ABN08942.1|//2.00E-28//Quinonprotein alcohol dehydrogenase-like [Medicago truncatula]						nr +
Unigene2034_A11	3049	2.23	1.96	0.82	11.70	13.38	7.33	19.14	5.51	11.11	-1.86E-01	4.34E-01		-1.44E+00	5.81E-09	Down	1.94E-01	2.23E-02		-6.74E-01	1.26E-14		-1.80E+00	4.52E-126	Down	-7.85E-01	1.08E-35		Unigene2034_A11//gi|190016004|gb|ACR62890.1|//5.00E-59//At3g63430 [Arabidopsis thaliana]	Unigene2034_A11//4.00E-60//AT3G63430| unknown protein	Unigene2034_A11//0.00E+00//TC174030				nr +
Unigene20340_A11	247	0.00	4.72	1.08	0.00	0.28	0.00	0.00	0.00	0.00	1.22E+01	1.05E-06	Up	1.01E+01	8.02E-02		8.12E+00	6.10E-01		null	null		null	null		null	null									
Unigene20343_A11	445	0.00	2.73	0.72	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	5.47E-07	Up	9.49E+00	4.52E-02		null	null		null	null		null	null		null	null									
Unigene20344_A11	367	0.29	2.76	1.02	2.17	1.31	0.62	1.27	0.57	0.33	3.28E+00	3.79E-04	Up	1.83E+00	2.13E-01		-7.25E-01	3.47E-01		-1.82E+00	3.32E-02		-1.15E+00	2.53E-01		-1.96E+00	5.82E-02		Unigene20344_A11//gi|116563475|gb|ABJ99759.1|//6.00E-30//PHD1 [Medicago truncatula]	Unigene20344_A11//8.00E-23//AT1G14510| AL7 (ALFIN-LIKE 7); DNA binding / methylated histone residue binding	Unigene20344_A11//2.00E-145//ES821348	Alfin-like			nr +
Unigene20345_A11	435	0.00	4.19	0.00	0.80	0.32	0.00	0.10	0.58	1.37	1.20E+01	2.14E-10	Up	null	null		-1.34E+00	3.08E-01		-9.65E+00	2.13E-02		2.57E+00	1.53E-01		3.82E+00	1.35E-03									
Unigene20346_A11	254	0.00	1.80	1.68	3.53	11.52	6.76	1.00	0.49	1.10	1.08E+01	7.44E-03		1.07E+01	1.38E-02		1.71E+00	5.92E-06	Up	9.37E-01	6.89E-02		-1.02E+00	4.95E-01		1.37E-01	9.29E-01					Unigene20346_A11//3.00E-07//DR453012				
Unigene20350_A11	397	0.00	12.00	3.76	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	3.83E-27	Up	1.19E+01	3.22E-08	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene20351_A11	337	0.31	0.00	1.58	0.44	1.43	3.08	0.00	0.37	0.47	-8.28E+00	3.73E-01		2.35E+00	5.87E-02		1.69E+00	1.66E-01		2.80E+00	8.13E-04	Up	8.54E+00	2.40E-01		8.89E+00	1.40E-01		Unigene20351_A11//gi|21537297|gb|AAM61638.1|//3.00E-36//DNA-damage inducible protein DDI1-like [Arabidopsis thaliana]	Unigene20351_A11//5.00E-32//AT3G13235| ubiquitin family protein	Unigene20351_A11//1.00E-31//EX168719				nr -
Unigene20353_A11	272	0.00	0.93	0.00	0.00	0.13	1.99	0.31	2.15	2.78	9.86E+00	7.86E-02		null	null		6.98E+00	8.30E-01		1.10E+01	2.46E-03		2.79E+00	8.26E-03		3.16E+00	6.83E-04	Up				Unigene20353_A11//3.00E-07//TC139061				
Unigene20358_A11	378	0.00	0.00	0.00	0.26	0.36	0.12	4.81	0.44	1.05	null	null		null	null		4.67E-01	8.77E-01		-1.14E+00	6.77E-01		-3.44E+00	7.71E-09	Down	-2.19E+00	5.01E-06	Down								
Unigene20359_A11	335	0.00	2.27	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.77E-04	Up	9.90E+00	4.52E-02		null	null		null	null		null	null		null	null		Unigene20359_A11//gi|297852396|ref|XP_002894079.1|//2.00E-06//hypothetical protein ARALYDRAFT_336913 [Arabidopsis lyrata subsp. lyrata] >gi|297339921|gb|EFH70338.1| hypothetical protein ARALYDRAFT_336913 [Arabidopsis lyrata subsp. lyrata]	Unigene20359_A11//1.00E-06//AT1G47900| unknown protein					nr -
Unigene2036_A11	3648	0.92	5.72	1.17	5.89	6.80	11.22	10.87	18.88	47.55	2.64E+00	1.20E-59	Up	3.47E-01	2.74E-01		2.08E-01	7.03E-02		9.30E-01	2.06E-28		7.96E-01	8.68E-42		2.13E+00	0.00E+00	Up	Unigene2036_A11//gi|115465817|ref|NP_001056508.1|//0.00E+00//Os05g0594700 [Oryza sativa Japonica Group] >gi|113580059|dbj|BAF18422.1| Os05g0594700 [Oryza sativa Japonica Group]	Unigene2036_A11//0.00E+00//AT4G22120| early-responsive to dehydration protein-related / ERD protein-related	Unigene2036_A11//0.00E+00//TC156729		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0016020//GO:0031410	nr +
Unigene20360_A11	413	0.00	0.00	0.00	0.00	0.00	0.00	3.99	1.62	0.77	null	null		null	null		null	null		null	null		-1.30E+00	5.42E-03		-2.37E+00	5.20E-06	Down				Unigene20360_A11//8.00E-12//DW479422				
Unigene20362_A11	289	0.36	0.35	0.55	1.38	0.60	1.72	1.61	6.22	3.03	-4.62E-02	9.89E-01		6.10E-01	7.48E-01		-1.21E+00	3.14E-01		3.18E-01	7.58E-01		1.95E+00	4.90E-05	Up	9.14E-01	1.59E-01					Unigene20362_A11//3.00E-07//AI054601				

Unigene20370_A11	573	0.00	1.50	1.12	3.13	3.55	3.70	0.15	0.00	0.00	1.06E+01	4.95E-05	Up	1.01E+01	1.16E-03		1.80E-01	7.49E-01		2.43E-01	6.07E-01		-7.21E+00	4.04E-01		-7.21E+00	3.59E-01		Unigene20370_A11//gi|225451583|ref|XP_002275555.1|//2.00E-19//PREDICTED: similar to KIP1-like [Vitis vinifera]	Unigene20370_A11//4.00E-13//AT2G22560| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: KIP1-like (InterPro:IPR011684); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT5G10500.1); Has 47807 Blast hits to 30104 proteins in 1314 species: Archae - 612; Bacteria - 5009; Metazoa - 22214; Fungi - 3986; Plants - 1654; Viruses - 215; Other Eukaryotes - 14117 (source: NCBI BLink).	Unigene20370_A11//7.00E-41//TC172942				nr -
Unigene20376_A11	276	168.15	153.11	176.73	115.69	127.64	125.18	51.17	46.49	23.24	-1.35E-01	1.12E-01		7.18E-02	4.23E-01		1.42E-01	1.56E-01		1.14E-01	2.97E-01		-1.38E-01	3.80E-01		-1.14E+00	1.39E-16	Down	Unigene20376_A11//gi|223047850|gb|ACM79935.1|//5.00E-21//eIF5A1 [Populus deltoides]	Unigene20376_A11//9.00E-20//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor	Unigene20376_A11//5.00E-114//gi|11201470|gb|BF270559.1|BF270559				nr -
Unigene20377_A11	369	0.00	0.27	0.00	0.14	0.65	0.73	0.00	0.34	1.94	8.10E+00	3.87E-01		null	null		2.27E+00	3.05E-01		2.44E+00	2.22E-01		8.41E+00	2.40E-01		1.09E+01	2.63E-05	Up									
Unigene20381_A11	240	0.00	5.70	16.42	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.80E-08	Up	1.40E+01	7.61E-22	Up	null	null		null	null		null	null		null	null		Unigene20381_A11//gi|195637630|gb|ACG38283.1|//1.00E-09//cystatin-1 precursor [Zea mays]	Unigene20381_A11//3.00E-09//AT2G40880| ATCYSA (CYSTATIN A); cysteine-type endopeptidase inhibitor					nr +
Unigene20384_A11	360	1.45	4.64	8.28	0.00	0.00	0.00	0.23	0.12	0.00	1.68E+00	2.13E-03		2.51E+00	2.98E-08	Up	null	null		null	null		-1.02E+00	7.25E-01		-7.88E+00	3.59E-01		Unigene20384_A11//gi|62956020|gb|AY23355.1|//8.00E-62//3-ketoacyl-CoA reductase 2 [Gossypium hirsutum]	Unigene20384_A11//8.00E-43//AT1G24470| short-chain dehydrogenase/reductase (SDR) family protein	Unigene20384_A11//0.00E+00//BG446279				nr +
Unigene20397_A11	298	0.00	0.00	0.36	0.67	0.35	0.91	1.99	12.34	3.61	null	null		8.48E+00	3.99E-01		-9.48E-01	5.88E-01		4.44E-01	7.64E-01		2.64E+00	2.05E-13	Up	8.62E-01	1.32E-01				Unigene20397_A11//1.00E-148//gi|6481314|gb|AW187099.2|AW187099					
Unigene20403_A11	247	0.42	1.64	0.00	1.21	0.28	1.83	0.17	0.17	3.39	1.95E+00	1.44E-01		-8.73E+00	3.94E-01		-2.12E+00	1.65E-01		5.96E-01	6.40E-01		-1.70E-02	1.00E+00		4.31E+00	4.10E-05	Up	Unigene20403_A11//gi|296088679|emb|CBI32314.3|//3.00E-32//unnamed protein product [Vitis vinifera]	Unigene20403_A11//8.00E-27//AT2G48060| unknown protein	Unigene20403_A11//1.00E-31//TC164370				nr -
Unigene20404_A11	330	0.00	6.30	3.07	0.00	0.31	0.00	0.00	0.00	0.00	1.26E+01	7.95E-12	Up	1.16E+01	1.27E-05	Up	8.29E+00	4.56E-01		null	null		null	null		null	null		Unigene20404_A11//sp|076217|PE1_ANOGA//5.00E-08//Peritrophin-1 OS=Anopheles gambiae GN=Aper1 PE=2 SV=2						swissprot -
Unigene20406_A11	278	0.00	0.55	2.49	0.90	0.62	1.14	0.91	0.30	1.15	9.09E+00	2.35E-01		1.13E+01	6.17E-04	Up	-5.33E-01	7.13E-01		3.44E-01	7.97E-01		-1.60E+00	3.11E-01		3.29E-01	7.63E-01		Unigene20406_A11//gi|224053426|ref|XP_002297813.1|//8.00E-17//f-box family protein [Populus trichocarpa] >gi|222845071|gb|EEE82618.1| f-box family protein [Populus trichocarpa]	Unigene20406_A11//2.00E-11//AT2G02240| MEE66 (maternal effect embryo arrest 66)					nr -
Unigene20407_A11	698	0.15	0.58	0.00	0.14	0.00	0.19	0.48	1.14	3.31	1.95E+00	1.44E-01		-7.23E+00	3.94E-01		-7.16E+00	3.13E-01		4.44E-01	8.62E-01		1.23E+00	9.04E-02		2.77E+00	2.46E-09	Up	Unigene20407_A11//gi|5263313|gb|AAD41415.1|AC007727_4//1.00E-14//Contains similarity to gb|U07707 epidermal growth factor receptor substrate (eps15) from Homo sapiens and contains 2 PF|00036 EF hand domains. ESTs gb|T44428 and gb|AA395440 come from this gene [Arabidopsis thaliana]	Unigene20407_A11//8.00E-11//AT1G21630| calcium-binding EF hand family protein	Unigene20407_A11//4.00E-52//gi|164342121|gb|ES807814.1|ES807814				nr +
Unigene20408_A11	725	0.07	0.49	0.22	0.41	0.05	0.44	1.22	0.98	4.78	2.76E+00	9.59E-02		1.61E+00	5.11E-01		-3.12E+00	7.56E-02		8.10E-02	9.50E-01		-3.22E-01	6.33E-01		1.96E+00	2.36E-09	Up	Unigene20408_A11//gi|225457017|ref|XP_002279079.1|//2.00E-07//PREDICTED: similar to ATPANK2 (PANTOTHENATE KINASE 2); pantothenate kinase [Vitis vinifera]	Unigene20408_A11//6.00E-08//AT4G32180| ATPANK2 (PANTOTHENATE KINASE 2); pantothenate kinase	Unigene20408_A11//8.00E-35//TC135571		ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene20410_A11	1687	0.00	7.18	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.81E-69	Up	1.07E+01	5.43E-15	Up	null	null		null	null		null	null		null	null		Unigene20410_A11//gi|115476300|ref|NP_001061146.1|//5.00E-70//Os08g0398700 [Oryza sativa Japonica Group] >gi|113623715|dbj|BAF23660.1| Os08g0398700 [Oryza sativa Japonica Group]	Unigene20410_A11//6.00E-64//AT4G33090| APM1 (AMINOPEPTIDASE M1); aminopeptidase			ko00590|Arachidonic acid metabolism		nr -
Unigene20412_A11	263	8.36	32.56	6.88	21.02	24.48	17.00	14.63	21.61	24.39	1.96E+00	1.68E-17	Up	-2.80E-01	5.53E-01		2.20E-01	4.12E-01		-3.07E-01	2.68E-01		5.63E-01	1.17E-02		7.37E-01	2.66E-04				Unigene20412_A11//2.00E-85//TC177002					
Unigene20414_A11	327	0.00	0.00	0.81	0.46	0.84	4.14	0.65	1.02	1.95	null	null		9.67E+00	8.02E-02		8.83E-01	5.95E-01		3.18E+00	2.31E-05	Up	6.61E-01	6.09E-01		1.59E+00	5.48E-02		Unigene20414_A11//gi|297836072|ref|XP_002885918.1|//9.00E-20//CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331758|gb|EFH62177.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene20414_A11//2.00E-05//AT2G14520| CBS domain-containing protein	Unigene20414_A11//2.00E-33//CO099327				nr -
Unigene20423_A11	274	0.00	0.00	0.00	0.00	0.00	0.00	2.31	1.98	0.00	null	null		null	null		null	null		null	null		-2.23E-01	7.74E-01		-1.12E+01	7.11E-05	Down	Unigene20423_A11//gi|168063705|ref|XP_001783810.1|//2.00E-07//predicted protein [Physcomitrella patens subsp. patens] >gi|162664692|gb|EDQ51402.1| predicted protein [Physcomitrella patens subsp. patens]				ko00600|Sphingolipid metabolism		nr +
Unigene20425_A11	323	0.00	38.28	17.31	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	6.26E-71	Up	1.41E+01	3.82E-31	Up	null	null		null	null		null	null		null	null		Unigene20425_A11//gi|9256636|ref|NP_061348.1|//3.00E-06//60S ribosomal protein L41 [Mus musculus] >gi|10863875|ref|NP_066927.1| 60S ribosomal protein L41 [Homo sapiens] >gi|20806115|ref|NP_620783.1| 60S ribosomal protein L41 [Rattus norvegicus] >gi|78217384|ref|NP_001030344.1| 60S ribosomal protein L41 [Homo sapiens] >gi|114326422|ref|NP_001041622.1| 60S ribosomal protein L41 [Felis catus] >gi|197100322|ref|NP_001124641.1| 60S ribosomal protein L41 [Pongo abelii] >gi|159476032|ref|XP_001696118.1| ribosomal protein L41, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|51701777|sp|Q6YLX4.1|RL41_CYPCA RecName: Full=60S ribosomal protein L41 >gi|51701779|sp|Q71H53.1|RL41_EPIC0 RecName: Full=60S ribosomal protein L41				ko03010|Ribosome		nr -
Unigene20429_A11	332	0.00	3.51	0.32	0.00	0.93	0.68	0.00	0.76	1.08	1.18E+01	1.05E-06	Up	8.33E+00	3.99E-01		9.87E+00	4.54E-02		9.41E+00	1.19E-01		9.56E+00	4.31E-02		1.01E+01	7.28E-03									
Unigene20430_A11	228	0.00	1.11	3.27	0.00	0.30	0.20	0.00	0.00	0.00	1.01E+01	7.86E-02		1.17E+01	3.28E-04	Up	8.24E+00	6.10E-01		7.63E+00	6.96E-01		null	null		null	null										ESTscan +
Unigene20433_A11	266	0.00	2.86	2.60	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.77E-04	Up	1.13E+01	6.17E-04	Up	null	null		null	null		null	null		null	null		Unigene20433_A11//gi|298711838|emb|CBJ32863.1|//2.00E-24//EF2, translation elongation factor 2 [Ectocarpus siliculosus]	Unigene20433_A11//3.00E-21//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding					nr -
Unigene20434_A11	303	1.04	3.34	0.35	0.33	0.45	1.04	0.56	5.10	1.18	1.69E+00	2.14E-02		-1.56E+00	3.30E-01		4.67E-01	8.77E-01		1.67E+00	3.09E-01		3.19E+00	3.93E-07	Up	1.08E+00	3.50E-01				Unigene20434_A11//4.00E-10//gi|21090181|gb|BQ402494.1|BQ402494					
Unigene20435_A11	253	0.62	3.40	13.89	0.00	0.00	0.00	0.00	0.00	0.00	2.46E+00	6.27E-03		4.48E+00	1.11E-15	Up	null	null		null	null		null	null		null	null											
Unigene20436_A11	309	1.19	0.33	2.24	0.00	0.22	0.00	1.64	0.00	0.00	-1.85E+00	1.87E-01		9.18E-01	3.11E-01		7.80E+00	6.10E-01		null	null		-1.07E+01	8.89E-04	Down	-1.07E+01	5.54E-04	Down									
Unigene20437_A11	391	0.80	3.37	4.22	0.25	0.18	0.46	1.08	0.64	0.61	2.07E+00	1.71E-03		2.39E+00	1.28E-04	Up	-5.33E-01	8.17E-01		8.59E-01	6.95E-01		-7.54E-01	4.77E-01		-8.23E-01	3.99E-01				Unigene20437_A11//6.00E-136//TC165774					
Unigene20444_A11	338	0.15	0.30	0.00	0.15	0.20	0.80	3.63	3.34	0.94	9.54E-01	7.26E-01		-7.27E+00	6.25E-01		4.67E-01	9.58E-01		2.44E+00	2.22E-01		-1.20E-01	8.28E-01		-1.94E+00	7.80E-04	Down			Unigene20444_A11//7.00E-160//ESS20444					
Unigene20447_A11	264	14.47	14.97	13.51	26.04	12.78	7.19	25.94	32.61	29.73	4.93E-02	8.81E-01		-9.83E-02	7.62E-01		-1.03E+00	7.89E-07	Down	-1.86E+00	2.87E-14	Down	3.30E-01	7.23E-02		1.96E-01	3.24E-01				Unigene20447_A11//4.00E-59//TC177450					
Unigene20452_A11	306	9.23	0.33	6.96	0.98	0.23	0.44	0.00	0.00	0.00	-4.80E+00	9.65E-14	Down	-4.08E-01	3.12E-01		-2.12E+00	1.65E-01		-1.14E+00	4.58E-01		null	null		null	null		Unigene20452_A11//gi|223452526|gb|ACM89590.1|//3.00E-19//disease resistance protein [Glycine max]	Unigene20452_A11//3.00E-14//AT1G74190| AtRLP15 (Receptor Like Protein 15); protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene20457_A11	226	6.25	0.90	4.71	27.11	19.81	5.40	196.25	198.25	53.41	-2.80E+00	6.22E-05	Down	-4.08E-01	4.86E-01		-4.53E-01	5.29E-02		-2.33E+00	6.50E-17	Down	1.47E-02	8.74E-01		-1.88E+00	5.02E-105	Down			Unigene20457_A11//6.00E-107//gi|164344114|gb|ES843921.1|ES843921					
Unigene2046_A11	2174	2.24	6.67	3.06	3.69	3.22	6.07	3.05	3.75	2.82	1.57E+00	1.18E-21	Up	4.52E-01	6.10E-02		-1.98E-01	3.88E-01		7.18E-01	2.30E-06		2.96E-01	1.25E-01		-1.14E-01	6.07E-01		Unigene2046_A11//gi|297822749|ref|XP_002879257.1|//1.00E-132//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325096|gb|EFH55516.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2046_A11//1.00E-125//AT2G30160| mitochondrial substrate carrier family protein	Unigene2046_A11//0.00E+00//TC161159				nr -
Unigene20462_A11	258	0.00	2.75	2.89	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.33E-04	Up	1.15E+01	3.28E-04	Up	null	null		null	null		null	null		null	null										
Unigene20463_A11	432	0.24	0.00	1.48	2.31	0.32	0.42	0.59	0.10	0.37	-7.92E+00	3.73E-01		2.61E+00	2.33E-02		-2.85E+00	2.37E-04	Down	-2.46E+00	2.07E-03		-2.60E+00	1.44E-01		-6.71E-01	6.05E-01		Unigene20463_A11//gi|118487984|gb|AB836813.1|//6.00E-06//unknown [Populus trichocarpa]						nr -
Unigene20467_A11	319	0.49	0.16	0.00	3.75	1.94	0.28	0.93	0.92	1.37	-1.63E+00	4.89E-01		-8.94E+00	2.45E-01		-9.48E-01	1.12E-01		-3.73E+00	1.43E-05	Down	-1.67E-02	1.02E+00		5.66E-01	5.78E-01									
Unigene20470_A11	257	0.41	5.13	2.90	3.10	3.48	1.58	0.16	0.00	0.16	3.65E+00	1.28E-05	Up	2.83E+00	8.52E-03		1.68E-01	8.32E-01		-9.72E-01	2.30E-01		-7.36E+00	6.58E-01		-8.58E-02	9.72E-01		Unigene20470_A11//gi|32396100|gb|AAP43917.1|//3.00E-29//integrase [Gossypium hirsutum]						nr +
Unigene20474_A11	586	0.00	0.26	0.00	3.83	1.12	0.92	0.29	0.43	0.07	8.02E+00	2.35E-01		null	null		-1.78E+00	2.49E-05	Down	-2.05E+00	1.16E-05	Down	5.68E-01	6.74E-01		-2.09E+00	3.13E-01				Unigene20474_A11//0.00E+00//TC161671					ESTscan -
Unigene20477_A11	228	3.67	0.44	0.93	4.37	3.93	0.20	1.48	1.10	0.35	-3.05E+00	2.11E-03		-1.97E+00	2.71E-02		-1.54E-01	8.40E-01		-1.46E+00	3.09E-05	Down	-4.32E-01	7.03E-01		-2.09E+00	1.02E-01									
Unigene20483_A11	423	0.00	0.84	0.88	0.12	2.04	0.75	0.40	0.10	0.09	9.71E+00	2.46E-02		9.78E+00	2.50E-02		4.11E+00	2.60E-04	Up	2.67E+00	1.44E-01		-2.02E+00	3.67E-01		-2.09E+00	3.13E-01				Unigene20483_A11//5.00E-07//TC143788					
Unigene20485_A11	210	1.74	7.72	1.52	1.19	1.48	0.65	10.47	3.58	4.93	2.15E+00	2.79E-04	Up	-1.97E-01	8.66E-01		3.15E-01	8.38E-01		-8.78E-01	6.16E-01		-1.55E+00	1.39E-04	Down	-1.09E+00	3.88E-03				Unigene20485_A11//8.00E-66//TC143225					
Unigene20488_A11	331	1.90	6.58	5.47	3.76	5.62	3.68	2.17	1.39	2.17	1.80E+00	1.58E-04	Up	1.53E+00	4.03E-03		5.78E-01	2.50E-01		-3.04E-02	9.47E-01		-6.45E-01	4.01E-01		-3.30E-03	9.90E-01				Unigene20488_A11//1.00E-34//gi|11201485|gb|BF270574.1|BF270574					
Unigene20493_A11	764	0.00	16.45	3.90	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	4.23E-72	Up	1.19E+01	1.77E-16	Up	null	null		null	null		null	null		null	null		Unigene20493_A11//gi|149067212|gb|EDM16945.1|//1.00E-82//solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3, isoform CRA_c [Rattus norvegicus]	Unigene20493_A11//2.00E-56//AT3G48850| mitochondrial phosphate transporter, putative					nr -

Unigene2050_All	2579	3.21	3.03	3.55	8.17	12.31	13.50	19.38	18.05	43.16	-8.33E-02	6.89E-01		1.48E-01	4.99E-01		5.91E-01	2.46E-11		7.25E-01	5.06E-16		-1.02E-01	1.84E-01		1.16E+00	1.41E-126	Up	Unigene2050_All//gi|226425257|gb|AC053628.1|//0.00E+00//bHLH domain protein [Gossypium hirsutum]	Unigene2050_All//1.00E-145//AT1G32640| MYC2; DNA binding / transcription activator/ transcription factor	Unigene2050_All//0.00E+00//TC174376	bHLH	ko04626|Plant-pathogen interaction	GO:0010468//GO:0016628//GO:0043231	nr -
Unigene20506_All	230	12.51	3.97	7.64	10.61	9.43	17.28	22.98	11.81	6.41	-1.66E+00	2.95E-05	Down	-7.12E-01	6.64E-02		-1.70E-01	7.04E-01		7.03E-01	2.25E-02		-9.60E-01	3.93E-05		-1.84E+00	6.25E-13	Down	Unigene20506_All//gi|54039313|sp|P62302.1|RS13_SOYBN//1.00E-10//RecName: Full=40S ribosomal protein S13 >gi|44662862|gb|AAS47510.1| ribosomal protein S13 [Glycine max] >gi|161367348|gb|ABX71080.1| ribosomal protein S13 [Glycine max]	Unigene20506_All//4.00E-10//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene20506_All//7.00E-85//gi|84169912|gb|DR458560.1|DR458560		ko03010|Ribosome		nr +
Unigene20507_All	374	1.26	1.90	6.41	0.13	1.57	1.57	0.45	0.11	1.49	5.91E-01	4.78E-01		2.35E+00	2.76E-06	Up	3.55E+00	8.14E-03		3.56E+00	8.48E-03		-2.02E+00	3.67E-01		1.72E+00	5.91E-02					Unigene20507_All//9.00E-33//TC150993				
Unigene20508_All	245	0.00	0.00	0.87	5.29	6.47	3.69	4.49	0.85	4.23	null	null		9.76E+00	1.41E-01		2.91E-01	6.10E-01		-5.20E-01	4.01E-01		-2.40E+00	4.11E-04	Down	-8.58E-02	8.84E-01									
Unigene2051_All	2672	2.19	1.21	1.77	8.84	6.25	3.55	6.44	1.97	2.24	-8.54E-01	5.08E-04		-3.06E-01	2.49E-01		-5.00E-01	1.28E-06		-1.32E+00	4.81E-29	Down	-1.71E+00	3.43E-35	Down	-1.53E+00	5.97E-31	Down	Unigene2051_All//gi|42566272|ref|NP_192248.2|//0.00E+00//SRF3 (STRUBBELIG-RECEPTOR FAMILY 3); ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|75127761|sp|Q8GZK3.1|SRF3_ARATH RecName: Full=Protein STRUBBELIG-RECEPTOR FAMILY 3; AltName: Full=Leucine-rich repeat receptor kinase-like protein SRF3; Flags: Precursor >gi|41323405|gb|AAR99871.1| strubbelig receptor family 3 [Arabidopsis thaliana] >gi|224589608|gb|ACN59337.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene2051_All//2.00E-172//AT1G11130| SUB (STRUBBELIG); protein binding / receptor signaling protein serine/threonine kinase	Unigene2051_All//0.00E+00//TC175510		ko04626|Plant-pathogen interaction	GO:0003006//GO:0004672//GO:0004871//GO:0005488//GO:0010056//GO:0010057//GO:0016020//GO:0023060//GO:0032989	nr +
Unigene20511_All	529	0.00	0.19	0.00	0.38	0.07	1.20	0.56	1.42	4.90	7.58E+00	3.87E-01		null	null		-2.53E+00	2.34E-01		1.67E+00	9.80E-02		1.35E+00	7.61E-02		3.13E+00	1.33E-11	Up	Unigene20511_All//gi|75171229|sp|Q9FKD7.1|SINL7_ARATH//9.00E-10//RecName: Full=E3 ubiquitin-protein ligase SINA-like 7; AltName: Full=Seven in absentia-like protein 7	Unigene20511_All//5.00E-11//AT5G37890| seven in absentia (SINA) protein, putative	Unigene20511_All//6.00E-07//TC169388				nr -
Unigene20518_All	589	0.09	0.00	0.09	0.42	0.06	0.31	0.29	2.13	1.35	-6.47E+00	6.13E-01		2.58E-02	9.95E-01		-2.85E+00	1.37E-01		-4.64E-01	7.45E-01		2.89E+00	1.97E-05	Up	2.24E+00	4.37E-03									
Unigene2052_All	873	3.96	1.74	1.71	3.25	5.40	2.59	2.28	3.06	1.64	-1.18E+00	4.86E-04	Down	-1.21E+00	6.25E-04	Down	7.33E-01	6.43E-03		-3.30E-01	4.14E-01		4.29E-01	2.37E-01		-4.71E-01	2.44E-01		Unigene2052_All//gi|115469942|ref|NP_001058570.1|//3.00E-32//Os06g0714000 [Oryza sativa Japonica Group] >gi|113596610|dbj|BAF20484.1| Os06g0714000 [Oryza sativa Japonica Group]	Unigene2052_All//1.00E-31//AT3G51130| unknown protein	Unigene2052_All//2.00E-45//TC135459				nr +
Unigene20525_All	308	0.00	0.00	0.00	0.00	0.00	0.00	1.65	2.04	0.00	null	null		null	null		null	null		null	null		3.05E-01	7.04E-01		-1.07E+01	5.54E-04	Down	Unigene20525_All//gi|12229935|sp|Q9SM13.1|RS12_CYAPA//2.00E-30//RecName: Full=40S ribosomal protein S12 >gi|6012956|emb|CAB57311.1| 40s ribosomal protein S12 [Cyanophora paradoxa]	Unigene20525_All//8.00E-24//AT1G15930| 40S ribosomal protein S12 (RPS12A)			ko03010|Ribosome		nr -
Unigene20526_All	240	6.76	10.98	4.88	3.94	3.59	2.45	19.20	7.66	5.31	7.00E-01	7.23E-02		-4.69E-01	3.87E-01		-1.37E-01	8.18E-01		-6.89E-01	3.58E-01		-1.33E+00	4.05E-07	Down	-1.85E+00	1.78E-11	Down				Unigene20526_All//8.00E-91//gi|13245946|gb|BE055536.2|BE055536					
Unigene20529_All	429	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.68	2.23	null	null		null	null		null	null		null	null		9.41E+00	2.35E-02		1.11E+01	5.69E-07	Up	Unigene20529_All//gi|297728489|ref|NP_001176608.1|//1.00E-27//Os11g0559200 [Oryza sativa Japonica Group] >gi|77551507|gb|ABA94304.1| Leucine Rich Repeat family protein [Oryza sativa (Japonica cultivar-group)] >gi|255680191|dbj|BAH95336.1| Os11g0559200 [Oryza sativa Japonica Group]	Unigene20529_All//4.00E-07//AT3G47580| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction		nr -
Unigene20532_All	265	0.00	0.00	0.00	1.13	2.86	1.70	3.19	0.63	0.00	null	null		null	null		1.34E+00	1.23E-01		5.96E-01	6.40E-01		-2.34E+00	2.95E-03		-1.16E+01	2.21E-06	Down				Unigene20532_All//5.00E-43//CO102451				
Unigene20533_All	394	0.00	1.67	1.89	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	6.26E-04	Up	1.09E+01	3.28E-04	Up	null	null		null	null		null	null		null	null									
Unigene20537_All	446	2.58	0.23	0.60	1.90	1.85	0.81	1.80	0.00	0.45	-3.51E+00	6.57E-05	Down	-2.11E+00	4.75E-03		-3.51E-02	9.55E-01		-1.23E+00	1.20E-01		-1.08E+01	8.58E-06	Down	-2.01E+00	7.11E-03		Unigene20537_All//gi|15234116|ref|NP_192036.1|//7.00E-12//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene20537_All//3.00E-13//AT4G01270| zinc finger (C3HC4-type RING finger) family protein	Unigene20537_All//0.00E+00//DT463420				nr -
Unigene20541_All	667	0.00	1.29	0.00	0.00	0.00	0.14	0.00	0.50	6.15	1.03E+01	4.95E-05	Up	null	null		null	null		7.08E+00	4.77E-01		8.97E+00	1.27E-02		1.26E+01	2.33E-29	Up				Unigene20541_All//5.00E-08//TC178414				
Unigene20542_All	448	0.00	8.60	2.50	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	6.32E-22	Up	1.13E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene20542_All//sp|P02518|HSP27_DROME//2.00E-54//Heat shock protein 27 OS=Drosophila melanogaster GN=Hsp27 PE=1 SV=2								swissprot -
Unigene20546_All	278	0.00	0.00	1.15	1.08	1.73	5.20	0.00	0.00	0.57	null	null		1.02E+01	4.52E-02		6.90E-01	5.67E-01		2.27E+00	3.41E-04	Up	null	null		9.16E+00	1.40E-01									
Unigene20549_All	540	0.10	0.00	0.10	0.55	0.00	0.92	2.43	0.62	3.39	-6.60E+00	6.13E-01		2.51E-02	9.95E-01		-9.11E+00	2.01E-02		7.33E-01	5.16E-01		-1.97E+00	6.34E-04	Down	4.84E-01	2.54E-01		Unigene20549_All//gi|19920130|gb|AAM08562.1|AC092749_15//3.00E-34//Putative retroelement [Oryza sativa Japonica Group] >gi|20087076|gb|AAM10749.1|AC112514_2 Putative retroelement [Oryza sativa Japonica Group]	Unigene20549_All//2.00E-09//AT4G23160| protein kinase family protein					nr -
Unigene2055_All	3564	1.32	3.10	2.26	9.64	9.87	5.89	9.50	8.37	6.58	1.23E+00	1.01E-11	Up	7.72E-01	2.82E-04		3.40E-02	8.03E-01		-7.11E-01	1.90E-15		-1.83E-01	3.79E-02		-5.29E-01	6.12E-11		Unigene2055_All//gi|47834703|gb|AAT39005.1|//0.00E+00//AML1 [Solanum lycopersicum]	Unigene2055_All//3.00E-155//AT5G61960| AML1 (ARABIDOPSIS ME12-LIKE PROTEIN 1); RNA binding / protein binding	Unigene2055_All//0.00E+00//TC178052		ko03040|Spliceosome		nr +
Unigene20553_All	404	0.00	3.01	1.19	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.47E-07	Up	1.02E+01	7.49E-03		null	null		null	null		null	null		null	null		Unigene20553_All//gi|224009464|ref|XP_002293690.1|//4.00E-54//eukaryotic translation initiation factor 4A [Thalassiosira pseudonana CCMP1335] >gi|220970362|gb|EED88699.1| eukaryotic translation initiation factor 4A [Thalassiosira pseudonana CCMP1335]	Unigene20553_All//2.00E-52//AT1G72730| eukaryotic translation initiation factor 4A, putative / eIF-4A, putative					nr +
Unigene20556_All	354	0.00	4.01	2.56	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.06E-08	Up	1.13E+01	4.71E-05	Up	null	null		null	null		null	null		null	null		Unigene20556_All//gi|159490596|ref|XP_001703259.1|//1.00E-17//chaperonin 10 [Chlamydomonas reinhardtii] >gi|158280183|gb|EDP05941.1| chaperonin 10 [Chlamydomonas reinhardtii]	Unigene20556_All//1.00E-16//AT1G23100| 10 kDa chaperonin, putative					nr +
Unigene20559_All	280	0.00	0.00	0.00	0.00	0.00	0.32	0.45	2.69	3.98	null	null		null	null		null	null		8.33E+00	4.77E-01		2.57E+00	3.32E-03		3.14E+00	2.19E-05	Up								
Unigene2056_All	1596	46.39	60.86	31.76	76.97	45.37	70.29	10.70	18.07	84.00	3.92E-01	6.82E-14		-5.46E-01	1.82E-18		-7.62E-01	6.99E-69		-1.31E-01	6.74E-03		7.56E-01	1.75E-16		2.97E+00	0.00E+00	Up	Unigene2056_All//gi|15226223|ref|NP_178238.1|//1.00E-105//ribose-5-phosphate isomerase [Arabidopsis thaliana] >gi|6226027|sp|Q9ZU38.1|RPIA_ARATH RecName: Full=Probable ribose-5-phosphate isomerase; AltName: Full=Phosphoriboisomerase >gi|15809810|gb|AAL06833.1| At2g01290/F10A8.17 [Arabidopsis thaliana] >gi|17978867|gb|AAL47405.1| At2g01290/F10A8.17 [Arabidopsis thaliana]	Unigene2056_All//3.00E-106//AT2G01290| ribose-5-phosphate isomerase	Unigene2056_All//0.00E+00//TC175773		ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway	GO:0006098//GO:0009250//GO:0016861//GO:0004124//GO:0016108	nr +
Unigene20560_All	404	0.00	0.00	0.00	0.00	0.00	0.00	19.47	0.93	1.18	null	null		null	null		null	null		null	null		-4.39E+00	1.44E-43	Down	-4.04E+00	1.14E-42	Down	Unigene20560_All//gi|29539332|dbj|BAC67667.1|//7.00E-55//elongation factor-1alpha [Cyanidioschyzon merolae]	Unigene20560_All//6.00E-47//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene20560_All//2.00E-12//TC173271				nr +
Unigene20567_All	499	0.00	0.61	5.76	0.00	0.00	0.00	0.00	0.00	0.00	9.25E+00	4.43E-02		1.25E+01	6.96E-16	Up	null	null		null	null		null	null		null	null		Unigene20567_All//gi|225440324|ref|XP_002263599.1|//9.00E-81//PREDICTED: similar to HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding isoform 1 [Vitis vinifera]	Unigene20567_All//2.00E-72//AT3G09440| heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3)	Unigene20567_All//1.00E-63//TC143358		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -
Unigene2057_All	2173	5.97	24.83	15.41	11.94	14.67	15.01	10.86	14.27	12.54	2.06E+00	1.26E-113	Up	1.37E+00	7.69E-39	Up	2.97E-01	1.25E-03		3.29E-01	4.26E-04		3.95E-01	4.90E-06		2.08E-01	2.78E-02		Unigene2057_All//gi|82791812|gb|AB890835.1|//0.00E+00//YHS and GAT domain protein [Glycine max]	Unigene2057_All//8.00E-140//AT4G32760| protein transporter	Unigene2057_All//0.00E+00//CO113624		ko03040|Spliceosome		nr +
Unigene20573_All	384	0.95	1.32	4.99	0.91	0.54	0.35	0.00	0.00	0.21	4.68E-01	6.11E-01		2.39E+00	3.03E-05	Up	-7.55E-01	5.67E-01		-1.36E+00	3.37E-01		null	null		7.70E+00	4.04E-01									
Unigene20575_All	241	0.00	0.00	0.00	0.00	0.00	0.00	3.86	3.82	0.00	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		-1.19E+01	5.47E-07	Down	Unigene20575_All//gi|159489791|ref|XP_001702878.1|//1.00E-20//ribosomal protein L38, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|27497793|gb|AAO13217.1| 60S ribosomal protein L38 [Chlamydomonas reinhardtii] >gi|158271006|gb|EDO96835.1| ribosomal protein L38 [Chlamydomonas reinhardtii]	Unigene20575_All//4.00E-20//AT3G59540| 60S ribosomal protein L38 (RPL38B)			ko03010|Ribosome		nr +
Unigene20583_All	281	0.00	4.87	3.60	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.80E-08	Up	1.18E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene20583_All//gi|193848502|gb|ACF22693.1|//3.00E-49//ring box protein [Brachypodium distachyon]	Unigene20583_All//5.00E-50//AT5G26570| RBX1 (RING-BOX 1); protein binding	Unigene20583_All//2.00E-08//DW498285		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair		nr -
Unigene20587_All	471	0.00	0.00	0.11	1.48	4.46	0.86	0.09	0.00	0.25	null	null		6.82E+00	6.36E-01		1.59E+00	4.65E-04	Up	-7.79E-01	3.93E-01		-6.49E+00	6.58E-01		1.50E+00	5.58E-01			Unigene20587_All//3.00E-06//AT2G46620| AAA-type ATPase family protein	Unigene20587_All//7.00E-22//gi|78328297|gb|DT548571.1|DT548571				
Unigene20588_All	294	0.36	0.00	3.80	0.34	0.35	0.00	1.15	0.43	0.68	-8.48E+00	3.73E-01		3.42E+00	1.92E-04	Up	5.23E-02	9.67E-01		-8.40E+00	4.00E-01		-1.43E+00	2.58E-01		-7.61E-01	5.01E-01									
Unigene20591_All	268	0.00	2.65	2.58	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.33E-04	Up	1.13E+01	6.17E-04	Up	null	null		null	null		null	null		null	null									
Unigene20594_All	362	0.29	2.80	2.94	0.00	0.00	0.00	0.00	0.00	0.00	3.28E+00	3.79E-04	Up	3.35E+00	3.36E-04	Up	null	null		null	null		null	null		null	null		Unigene20594_All//gi|56669638|gb|AAD46404.1|AF096248_1//3.00E-12//ethylene-responsive RNA helicase [Solanum lycopersicum]	Unigene20594_All//3.00E-08//AT1G55150| DEAD box RNA helicase, putative (RH20)			ko03040|Spliceosome		nr +

Unigene206_All	503	1.04	0.20	0.11	0.50	0.62	1.35	1.51	4.57	6.42	-2.37E+00	4.76E-02		-3.30E+00	2.40E-02		3.15E-01	8.38E-01		1.44E+00	1.28E-01		1.59E+00	6.35E-05	Up	2.08E+00	2.18E-09	Up	Unigene206_All//gi|224145028|ref|XP_002325500.1|//3.00E-16//nbs-lrr resistance protein [Populus trichocarpa] >gi|222862375|gb|EEE99881.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene206_All//2.00E-10//AT4G19510| disease resistance protein (TIR-NBS-LRR class), putative					nr -
Unigene20604_All	282	0.74	1.44	1.70	1.06	0.24	0.64	2.40	0.44	0.00	9.54E-01	4.14E-01		1.20E+00	3.03E-01		-2.12E+00	1.65E-01		-7.26E-01	6.39E-01		-2.43E+00	7.76E-03		-1.12E+01	3.56E-05	Down	Unigene20604_All//gi|255538714|ref|XP_002510422.1|//4.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223551123|gb|EEF52609.1| conserved hypothetical protein [Ricinus communis]		Unigene20604_All//8.00E-11//TC161475				nr +
Unigene20607_All	684	0.00	3.26	0.62	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.09E-12	Up	9.28E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene20607_All//gi|115446121|ref|NP_001046840.1|//6.00E-12//Os02g0474700 [Oryza sativa Japonica Group] >gi|113536371|dbj|BAF08754.1| Os02g0474700 [Oryza sativa Japonica Group]						nr +
Unigene20608_All	240	0.00	24.91	114.04	0.62	0.29	0.00	0.18	0.00	0.00	1.46E+01	3.95E-34	Up	1.68E+01	4.73E-155	Up	-1.12E+00	5.84E-01		-9.28E+00	2.33E-01		-7.46E+00	6.58E-01		-7.46E+00	6.13E-01		Unigene20608_All//gi|55168340|gb|AAV44205.1|//5.00E-26//unknow protein [Oryza sativa Japonica Group]		Unigene20608_All//2.00E-54//gi|109856262|gb|DW485241.1|DW485241				nr -
Unigene2061_All	950	4.90	2.56	2.35	22.65	14.21	7.65	10.99	2.55	5.54	-9.37E-01	8.50E-04		-1.06E+00	3.32E-04	Down	-6.73E-01	5.00E-10		-1.57E+00	2.62E-34	Down	-2.11E+00	1.81E-28	Down	-9.90E-01	3.98E-10		Unigene2061_All//gi|15217901|ref|NP_174156.1|//2.00E-74//AtRLP4 (Receptor Like Protein 4); protein binding [Arabidopsis thaliana]	Unigene2061_All//1.00E-64//AT1G28340| AtRLP4 (Receptor Like Protein 4); protein binding	Unigene2061_All//0.00E+00//gi|84151272|gb|DN800627.1|DN800627		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016772//GO:0023060//GO:0044464	nr -
Unigene20611_All	395	1.59	0.00	0.81	1.64	1.48	1.14	2.25	0.74	0.61	-1.06E+01	7.92E-04	Down	-9.75E-01	3.16E-01		-1.46E-01	8.39E-01		-5.20E-01	5.88E-01		-1.60E+00	2.18E-02		-1.89E+00	6.34E-03									
Unigene20613_All	213	99.24	74.22	43.50	265.91	221.97	407.53	94.09	74.37	61.35	-4.19E-01	4.56E-04		-1.19E+00	6.40E-20	Down	-2.61E-01	7.63E-05		6.16E-01	1.68E-29		-3.39E-01	2.28E-03		-6.17E-01	9.86E-09		Unigene20613_All//gi|194462393|gb|ACF72671.1|//1.00E-14//Ran-binding protein 1 [Cucumis melo var. cantalupensis]	Unigene20613_All//4.00E-10//AT2G30060| Ran-binding protein 1b (RanBP1b)	Unigene20613_All//4.00E-117//gi|13350120|gb|BG440469.1|BG440469				nr +
Unigene20614_All	400	0.00	2.28	0.00	0.25	0.69	0.34	2.54	5.12	1.39	1.12E+01	2.62E-05	Up	null	null		1.47E+00	4.20E-01		4.43E-01	8.62E-01		1.01E+00	1.23E-02		-8.63E-01	1.40E-01		Unigene20614_All//gi|224144595|ref|XP_002325344.1|//2.00E-18//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222862219|gb|EEE99725.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene20614_All//4.00E-05//AT1G62630| disease resistance protein (CC-NBS-LRR class), putative	Unigene20614_All//1.00E-16//CO080430				nr -
Unigene20615_All	429	0.00	9.57	5.59	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	2.25E-23	Up	1.24E+01	3.24E-13	Up	null	null		null	null		null	null		null	null		Unigene20615_All//sp|Q2PQM7|IDGF4_GLOMM//4.00E-39//Chitinase-like protein Idgf4 OS=Glossina morsitans morsitans GN=Idgf4 PE=2 SV=1						swissprot -
Unigene20616_All	333	1180.91	398.96	908.29	312.50	229.57	164.24	0.00	0.00	0.00	-1.57E+00	0.00E+00	Down	-3.79E-01	4.76E-49		-4.45E-01	3.01E-22		-9.28E-01	5.88E-72		null	null		null	null		Unigene20616_All//gi|3334277|sp|O24418.1|NLTP6_GOSHI//4.00E-33//RecName: Full=Non-specific lipid-transfer protein 6; Short=LTP; Flags: Precursor >gi|2338124|gb|AAB66990?.1| lipid transfer protein [Gossypium hirsutum]	Unigene20616_All//3.00E-09//AT5G58310| LTP4 (LIPID TRANSFER PROTEIN 4); lipid binding	Unigene20616_All//3.00E-162//gi|109867390|gb|DW496366.1|DW496366				nr +
Unigene2062_All	2362	1.62	0.64	1.04	5.44	3.64	2.01	4.08	1.40	2.55	-1.33E+00	4.44E-05	Down	-6.41E-01	5.07E-02		-5.78E-01	7.05E-05		-1.44E+00	2.58E-18	Down	-1.55E+00	1.79E-17	Down	-6.80E-01	2.23E-05		Unigene2062_All//gi|15217901|ref|NP_174156.1|//0.00E+00//AtRLP4 (Receptor Like Protein 4); protein binding [Arabidopsis thaliana]	Unigene2062_All//0.00E+00//AT1G28340| AtRLP4 (Receptor Like Protein 4); protein binding	Unigene2062_All//0.00E+00//TC136368		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016772//GO:0023060//GO:0044464	nr -
Unigene20623_All	252	0.00	1.01	0.42	0.59	1.50	0.90	2.52	1.00	0.16	9.97E+00	7.86E-02		8.72E+00	3.99E-01		1.34E+00	3.40E-01		5.96E-01	7.21E-01		-1.34E+00	1.13E-01		-3.99E+00	5.82E-04	Down			Unigene20623_All//8.00E-128//DT459330				
Unigene20624_All	246	0.00	3.09	2.38	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.77E-04	Up	1.12E+01	2.17E-03		null	null		null	null		null	null		null	null									
Unigene20628_All	272	0.00	0.00	0.00	0.00	0.00	0.00	2.49	1.69	9.52	null	null		null	null		null	null		null	null		-5.57E-01	4.89E-01		1.94E+00	4.54E-07	Up								
Unigene20629_All	255	1.64	1.59	6.68	1.76	2.97	4.25	0.50	0.33	1.25	-4.63E-02	9.80E-01		2.03E+00	5.19E-04	Up	7.57E-01	3.95E-01		1.27E+00	6.54E-02		-6.02E-01	7.66E-01		1.33E+00	2.93E-01									
Unigene2063_All	2822	24.03	5.53	15.17	11.14	10.85	5.76	0.00	0.15	0.03	-2.12E+00	2.28E-149	Down	-6.63E-01	9.11E-24		-3.81E-02	7.79E-01		-9.51E-01	5.34E-23		7.21E+00	3.65E-03		4.82E+00	4.04E-01		Unigene2063_All//gi|240256087|ref|NP_194459.4|//0.00E+00//ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene2063_All//0.00E+00//AT4G27300| S-locus protein kinase, putative	Unigene2063_All//0.00E+00//TC154318		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674//GO:0004871//GO:0009987	nr -
Unigene20630_All	276	6.07	0.73	3.28	0.36	0.00	0.33	0.31	0.00	0.43	-3.05E+00	3.81E-06	Down	-8.87E-01	9.63E-02		-8.50E+00	3.13E-01		-1.41E-01	9.50E-01		-8.26E+00	4.04E-01		4.99E-01	8.08E-01									
Unigene20631_All	242	0.00	0.63	0.88	0.62	0.71	1.31	7.69	17.27	9.55	9.29E+00	2.35E-01		9.78E+00	1.41E-01		2.04E-01	9.50E-01		1.08E+00	4.76E-01		1.17E+00	1.70E-05	Up	3.13E-01	4.08E-01				Unigene20631_All//4.00E-09//TC174988				
Unigene20632_All	419	0.00	0.00	0.00	0.00	0.00	0.00	1.51	2.89	0.00	null	null		null	null		null	null		null	null		9.35E-01	9.20E-02		-1.06E+01	7.11E-05	Down	Unigene20632_All//gi|114159828|gb|ABI53721.1|//5.00E-72//polyubiquitin [Porphyra yezoensis]	Unigene20632_All//3.00E-72//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene20632_All//2.00E-62//BM359461				nr +
Unigene20633_All	338	0.31	3.30	2.05	0.59	0.20	0.40	2.75	0.25	1.77	3.41E+00	1.24E-04	Up	2.73E+00	1.40E-02		-1.53E+00	4.16E-01		-5.56E-01	7.33E-01		-3.48E+00	7.79E-05	Down	-6.38E-01	3.08E-01			Unigene20633_All//1.00E-06//AT5G63570| GSA1 (GLUTAMATE-1-SEMIALDEHYDE-2,1-AMINOMUTASE); glutamate-1-semialdehyde 2,1-aminomutase	Unigene20633_All//6.00E-09//gi|78334136|gb|DT554410.1|DT554410		ko00860|Porphyrin and chlorophyll metabolism		kegg +
Unigene20638_All	481	0.00	0.00	0.00	0.00	1.07	0.00	0.88	3.22	0.99	null	null		null	null		1.01E+01	3.21E-03		null	null		1.87E+00	3.06E-04	Up	1.77E-01	8.46E-01									
Unigene20639_All	222	3.30	1.14	4.56	6.73	0.93	2.85	1.90	0.75	0.90	-1.53E+00	7.78E-02		4.66E-01	5.12E-01		-2.85E+00	2.83E-06	Down	-1.24E+00	2.45E-02		-1.34E+00	2.24E-01		-1.09E+00	2.82E-01									
Unigene20640_All	441	30.97	23.55	25.96	8.58	13.20	8.71	3.83	9.48	12.74	-3.95E-01	1.02E-02		-2.54E-01	1.33E-01		6.20E-01	9.45E-03		2.01E-02	9.48E-01		1.31E+00	2.20E-06	Up	1.73E+00	1.72E-12	Up	Unigene20640_All//gi|15240250|ref|NP_200949.1|//3.00E-14//RPE; catalytic/ ribulose-phosphate 3-epimerase [Arabidopsis thaliana] >gi|30697525|ref|NP_851240.1| RPE; catalytic/ ribulose-phosphate 3-epimerase [Arabidopsis thaliana] >gi|4102703|gb|AAD09954.1| ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana] >gi|9757862|dbj|BAB08496.1| ribulose-5-phosphate-3-epimerase [Arabidopsis thaliana]	Unigene20640_All//1.00E-15//AT5G61410| RPE; catalytic/ ribulose-phosphate 3-epimerase	Unigene20640_All//2.00E-56//TC160697		ko00710|Carbon fixation in photosynthetic organisms//ko00040|Pentose and glucuronate interconversions//ko00030|Pentose phosphate pathway		nr -
Unigene20641_All	250	2.72	0.00	1.92	0.20	0.00	0.00	0.00	0.00	0.00	-1.14E+01	4.10E-04	Down	-5.05E-01	5.82E-01		-7.64E+00	5.56E-01		-7.64E+00	6.36E-01		null	null		null	null									ESTscan +
Unigene20646_All	227	76.06	34.82	87.26	51.35	57.19	40.79	0.19	0.00	0.00	-1.13E+00	9.47E-16	Down	1.98E-01	1.50E-01		1.55E-01	3.97E-01		-3.32E-01	5.37E-02		-7.54E+00	6.58E-01		-7.54E+00	6.13E-01				Unigene20646_All//6.00E-107//TC158448				
Unigene20647_All	705	0.15	0.07	0.00	0.42	0.20	0.00	2.52	0.42	3.79	-1.05E+00	6.84E-01		-7.21E+00	3.94E-01		-1.12E+00	4.24E-01		-8.73E+00	4.00E-02		-2.60E+00	9.39E-07	Down	5.88E-01	7.89E-02		Unigene20647_All//gi|269819290|gb|ACZ44833.1|//7.00E-51//glycosyltransferase [Malus x domestica]	Unigene20647_All//3.00E-49//AT2G29730| UGT71D1 (UDP-GLUCOSYL TRANSFERASE 71D1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene20647_All//0.00E+00//AI726414				nr -
Unigene20649_All	478	0.00	0.00	0.00	0.00	0.00	0.19	0.18	0.70	2.33	null	null		null	null		null	null		7.56E+00	4.77E-01		1.98E+00	1.44E-01		3.72E+00	4.35E-06	Up								
Unigene20651_All	505	2.80	0.40	2.43	0.79	0.89	0.98	0.50	0.33	0.47	-2.80E+00	6.22E-05	Down	-2.06E-01	7.06E-01		1.68E-01	9.04E-01		3.18E-01	7.58E-01		-6.01E-01	6.48E-01		-8.58E-02	9.57E-01		Unigene20651_All//gi|124360436|gb|ABN08446.1|//2.00E-64//Emr1, related [Medicago truncatula]	Unigene20651_All//3.00E-52//AT5G23570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene20651_All//1.00E-152//gi|78353936|gb|DT574210.1|DT574210				nr -
Unigene20656_All	393	1.33	17.53	0.27	0.76	1.05	0.34	0.00	0.00	2.13	3.72E+00	1.46E-27	Up	-2.30E+00	6.76E-02		4.67E-01	7.41E-01		-1.14E+00	4.57E-01		null	null		1.11E+01	3.88E-06	Up	Unigene20656_All//gi|42571085|ref|NP_973616.1|//8.00E-16//ROT4 (ROTUNDIFOLIA4) [Arabidopsis thaliana] >gi|42822065|tpg|DAA02287.1| TPA_exp: DVL16 [Arabidopsis thaliana] >gi|109134191|gb|ABG25093.1| At2g36985 [Arabidopsis thaliana]	Unigene20656_All//4.00E-17//AT2G36985| ROT4 (ROTUNDIFOLIA4)					nr -
Unigene20657_All	246	0.00	6.18	3.03	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.10E-08	Up	1.16E+01	3.28E-04	Up	null	null		null	null		null	null		null	null		Unigene20657_All//sp|P37159|LYSE_DROME//8.00E-26//Lysozyme E OS=Drosophila melanogaster GN=LysE PE=2 SV=2						swissprot -
Unigene2066_All	1182	5.89	5.70	4.51	2.40	4.87	6.53	5.90	4.38	5.49	-4.63E-02	8.43E-01		-3.86E-01	1.06E-01		1.02E+00	1.86E-05	Up	1.44E+00	4.24E-11	Up	-4.29E-01	3.36E-02		-1.03E-01	6.35E-01		Unigene2066_All//gi|240256130|ref|NP_974671.4|//4.00E-62//aminoacyl-tRNA hydrolase [Arabidopsis thaliana]	Unigene2066_All//7.00E-52//AT4G32900| aminoacyl-tRNA hydrolase	Unigene2066_All//0.00E+00//BF274661			GO:0004091//GO:0010467	nr +
Unigene20661_All	252	2.49	9.85	5.49	12.85	8.06	8.96	3.86	7.80	3.48	1.98E+00	1.18E-05	Up	1.14E+00	5.84E-02		-6.72E-01	4.14E-02		-5.20E-01	1.44E-01		1.01E+00	1.45E-02		-1.50E-01	7.92E-01									
Unigene20662_All	264	0.00	4.99	1.41	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.50E-07	Up	1.05E+01	2.50E-02		null	null		null	null		null	null		null	null									
Unigene20663_All	433	0.00	0.00	0.00	6.10	2.07	0.63	0.88	0.39	0.92	null	null		null	null		-1.56E+00	3.20E-05	Down	-3.28E+00	1.17E-10	Down	-1.19E+00	3.09E-01		6.63E-02	9.66E-01		Unigene20663_All//gi|62866924|gb|AAY17358.1|//5.00E-60//lipase	Unigene20663_All//7.00E-49//AT5G14180| MPL1 (MYZUS PERSICAE-INDUCED LIPASE 1); catalytic	Unigene20663_All//1.00E-41//TC140358				nr +
Unigene20666_All	259	2.83	0.39	8.43	1.73	1.33	1.40	0.00	0.16	0.00	-2.85E+00	6.26E-03		1.58E+00	9.82E-04	Up	-3.81E-01	7.22E-01		-3.11E-01	7.57E-01		7.33E+00	6.35E-01		null	null		Unigene20666_All//gi|224058117|ref|XP_002299451.1|//4.00E-08//predicted protein [Populus trichocarpa] >gi|222846709|gb|EEE84256.1| predicted protein [Populus trichocarpa]		Unigene20666_All//6.00E-107//ES798634				nr -
Unigene20670_All	256	2.45	0.00	0.00	2.72	4.17	3.00	0.00	0.00	0.00	-1.13E+01	7.92E-04	Down	-1.13E+01	1.41E-03		6.14E-01	3.94E-01		1.39E-01	8.78E-01		null	null		null	null				Unigene20670_All//5.00E-126//DR457234				ESTscan +
Unigene20671_All	448	2.45	1.13	2.26	3.34	2.31	1.41	6.70	7.37	3.11	-1.12E+00	8.94E-02		-1.19E-01	8.50E-01		-5.33E-01	3.21E-01		-1.24E+00	2.45E-02		1.37E-01	6.73E-01		-1.11E+00	4.59E-04	Down	Unigene20671_All//gi|140055592|gb|AB080947.1|//5.00E-30//Ankyrin [Medicago truncatula]	Unigene20671_All//1.00E-23//AT2G47070| SPL1 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 1); DNA binding / transcription factor	Unigene20671_All//3.00E-144//DR455289	SBP			nr +
Unigene20673_All	248	0.00	12.26	3.01	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	2.67E-17	Up	1.16E+01	3.28E-04	Up	null	null		null	null		null	null		null	null									
Unigene2068_All	2352	10.74	8.92	11.55	10.38	13.05	9.03	10.41	6.81	5.00	-2.69E-01	1.57E-02		1.04E-01	3.82E-01		3.30E-01	3.83E-04		-2.02E-01	9.12E-02		-6.13E-01	5.01E-10		-1.06E+00	4.55E-25	Down	Unigene2068_All//gi|108712095|gb|ABF99890.1|//1.00E-170//Ser/Thr protein phosphatase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|108712097|gb|ABF99892.1| Ser/Thr protein phosphatase family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene2068_All//0.00E+00//ES804808	Unigene2068_All//0.00E+00//TC136368			GO:0016831//GO:0048037	nr +
Unigene20680_All	321	0.00	0.00	2.65	1.40	0.75	0.14	1.05	1.30	0.74	null	null		1.14E+01	9.03E-05	Up	-8.95E-01	4.13E-01		-3.31E+00	2.84E-02		3.05E-01	7.57E-01		-5.01E-01	6.49E-01				Unigene20680_All//1.00E-56//CO104791				
Unigene20681_All	310	0.00	0.00	0.00	0.32	2.11	5.54	0.00	0.27	0.90	null	null		null	null		2.72E+00	1.37E-02		4.11E+00	5.03E-08	Up	8.07E+00	4.01E-01		9.81E+00	2.43E-02		Unigene20681_All//gi|302142163|emb|CBI19366.3|//8.00E-08//unnamed protein product [Vitis vinifera]						nr -
Unigene2069_All	3331	2.10	0.81	0.67	2.65	1.47	1.14	9.35	7.89	8.75	-1.38E+00	3.72E-09	Down	-1.65E+00	4.62E-11	Down	-8.51E-01	2.07E-06		-1.22E+00	5.62E-10	Down	-2.45E-01	5.80E-03		-9.56E-02	3.29E-01		Unigene2069_All//gi|33468530|emb|CAE30324.1|//0.00E+00//NIN-like protein 1 [Lotus japonicus]	Unigene2069_All//0.00E+00//AT1G22640| RWP-RK domain-containing protein	Unigene2069_All//0.00E+00//DT464058	RWP-RK		GO:0010468	nr +
Unigene20694_All	227	2.30	15.40	5.40	0.88	3.34	1.79	0.37	0.37	0.00	2.74E+00	6.92E-11	Up	1.23E+00	6.00E-02		1.93E+00	3.36E-02		1.03E+00	4.29E-01		-1.68E-02	1.01E+00		-8.54E+00	3.59E-01									
Unigene20695_All	262	4.19	5.03	2.24	5.32	8.15	6.55	10.81	10.53	4.87	2.62E-01	6.27E-01		-9.08E-01	1.87E-01		6.14E-01	1.75E-01		2.99E-01	6.11E-01		-3.83E-02	9.30E-01		-1.15E+00	4.37E-04	Down			Unigene20695_All//3.00E-53//DR459498				
Unigene20696_All	403	0.00	117.43	43.74	0.00	0.09	0.00	0.21	0.00	0.00	1.68E+01	2.43E-273	Up	1.54E+01	1.66E-99	Up	6.42E+00	8.30E-01		null	null		-7.71E+00	4.04E-01		-7.71E+00	3.59E-01		Unigene20696_All//gi|157011451|gb|ABV00887.1|//2.00E-67//actin [Rhodomonas sp. CCMP768]	Unigene20696_All//3.00E-65//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene20696_All//2.00E-111//TC153744		ko04145|Phagosome		nr +
Unigene20697_All	980	0.11	0.26	0.76	1.22	0.56	0.37	4.75	2.43	1.99	1.28E+00	4.35E-01		2.83E+00	8.52E-03		-1.12E+00	6.04E-02		-1.73E+00	8.52E-03		-9.65E-01	1.21E-04		-1.25E+00	6.79E-07	Down	Unigene20697_All//gi|145339954|ref|NP_567251.2|//8.00E-96//binding / catalytic/ oxidoreductase [Arabidopsis thaliana]	Unigene20697_All//6.00E-98//AT4G03140| binding / catalytic/ oxidoreductase	Unigene20697_All//9.00E-97//TC138997		ko00906|Carotenoid biosynthesis		nr +

Unigene20698_All	335	1.25	1.21	1.75	2.97	0.41	0.81	0.25	0.75	0.24	-4.63E-02	9.80E-01		4.85E-01	6.30E-01		-2.85E+00	2.37E-04	Down	-1.88E+00	1.18E-02		1.57E+00	3.26E-01		-8.60E-02	9.72E-01		Unigene20698_All//gi|225445549|ref|XP_002282244.1|//8.00E-08//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene20698_All//1.00E-10//gi|164273372|gb|ES813805.1|ES813805				nr -
Unigene20703_All	285	0.18	0.71	4.30	1.05	0.73	0.00	2.23	1.03	2.66	1.95E+00	3.75E-01		4.55E+00	1.02E-05	Up	-5.33E-01	6.79E-01		-1.00E+01	4.00E-02		-1.12E+00	1.80E-01		2.55E-01	7.07E-01								
Unigene20704_All	222	2.12	0.00	2.40	1.57	2.17	1.42	0.38	3.77	0.18	-1.11E+01	5.56E-03		1.77E-01	8.45E-01		4.67E-01	7.04E-01		-1.41E-01	9.12E-01		3.31E+00	3.10E-04	Up	-1.09E+00	6.76E-01			Unigene20704_All//2.00E-07//TC150710				
Unigene20706_All	324	0.00	0.00	0.00	0.00	0.11	0.00	1.57	0.26	0.00	null	null		null	null		6.73E+00	8.30E-01		null	null		-2.60E+00	2.05E-02		-1.06E+01	5.54E-04	Down	Unigene20706_All//gi|34223515|gb|AAQ63000.1|//1.00E-17//oil palm polygalacturonase allergen PEST643 [Elaeis guineensis]	Unigene20706_All//5.00E-19//AT1G02790| PGA4 (POLYGALACTURONASE 4); polygalacturonase	Unigene20706_All//6.00E-86//TC158815		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene20712_All	225	0.00	0.00	0.00	0.00	0.00	0.00	2.82	2.60	0.00	null	null		null	null		null	null		null	null		-1.16E-01	8.88E-01		-1.15E+01	7.11E-05	Down							
Unigene20713_All	431	0.00	0.00	1.98	1.50	0.08	0.00	0.00	0.00	0.00	null	null		1.09E+01	9.03E-05	Up	-4.23E+00	5.94E-04	Down	-1.06E+01	3.90E-04	Down	null	null		null	null		Unigene20713_All//gi|40950550|gb|AB97905.1|//1.00E-84//catalase [Solanum tuberosum]	Unigene20713_All//4.00E-68//AT1G20620| CAT3 (CATALASE 3); catalase	Unigene20713_All//4.00E-26//EV485883		ko04146|Peroxisome//ko00380|Tryptophan metabolism		nr -
Unigene20719_All	645	106.10	22.55	128.71	0.31	0.11	0.63	0.00	0.00	0.00	-2.23E+00	3.90E-161	Down	2.79E-01	2.21E-06		-1.53E+00	4.16E-01		1.03E+00	4.28E-01		null	null		null	null		Unigene20719_All//gi|3193326|gb|AAC19308.1|//7.00E-22//contains similarity to transcriptional activators such as Rx-like and myc-like regulatory R proteins [Arabidopsis thaliana]	Unigene20719_All//4.00E-08//AT4G00050| UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor	Unigene20719_All//4.00E-18//TC148000	bHLH	ko04712|Circadian rhythm - plant		nr -
Unigene2072_All	1985	3.53	2.02	1.85	6.58	5.26	5.10	9.84	4.55	5.34	-8.09E-01	2.61E-04		-9.32E-01	5.70E-05		-3.23E-01	3.73E-02		-3.68E-01	2.06E-02		-1.11E+00	3.51E-21	Down	-8.82E-01	3.90E-15		Unigene2072_All//gi|297811479|ref|XP_002873623.1|//0.00E+00//aba-overly sensitive 1 [Arabidopsis lyrata subsp. lyrata] >gi|297319460|gb|EFH49882.1| aba-overly sensitive 1 [Arabidopsis lyrata subsp. lyrata]	Unigene2072_All//0.00E+00//AT5G13680| ABO1 (ABA-OVERLY SENSITIVE 1); transcription elongation regulator	Unigene2072_All//0.00E+00//TC167829		GO:0040007		nr -
Unigene20720_All	234	0.00	0.00	0.00	0.00	0.00	0.00	4.34	4.11	0.68	null	null		null	null		null	null		null	null		-7.80E-02	9.08E-01		-2.67E+00	1.94E-04	Down							
Unigene20724_All	357	0.29	2.98	0.30	0.70	0.96	0.63	0.36	0.82	1.00	3.35E+00	2.17E-04	Up	2.54E-02	1.00E+00		4.67E-01	7.80E-01		-1.42E-01	9.29E-01		1.21E+00	3.92E-01		1.50E+00	2.04E-01		Unigene20724_All//gi|18399097|ref|NP_564433.1|//1.00E-49//transporter-related [Arabidopsis thaliana] >gi|10086480|gb|AAG12540.1|AC015446_21 Unknown protein [Arabidopsis thaliana] >gi|193788740|gb|ACF20469.1|Atig34020 [Arabidopsis thaliana]	Unigene20724_All//5.00E-51//AT1G34020| transporter-related	Unigene20724_All//6.00E-108//TC176616				nr +
Unigene20726_All	236	0.00	2.15	0.68	1.27	0.44	1.34	0.90	4.25	9.62	1.11E+01	4.05E-03		9.40E+00	2.39E-01		-1.53E+00	2.98E-01		8.10E-02	9.50E-01		2.25E+00	1.39E-03		3.43E+00	4.71E-11	Up							
Unigene2073_All	2944	0.78	0.43	0.87	2.40	2.26	1.72	3.03	1.42	2.15	-8.62E-01	4.02E-02		1.51E-01	7.04E-01		-8.99E-02	7.44E-01		-4.84E-01	2.94E-02		-1.09E+00	7.54E-10	Down	-4.94E-01	3.14E-03		Unigene2073_All//gi|297811479|ref|XP_002873623.1|//0.00E+00//aba-overly sensitive 1 [Arabidopsis lyrata subsp. lyrata] >gi|297319460|gb|EFH49882.1| aba-overly sensitive 1 [Arabidopsis lyrata subsp. lyrata]	Unigene2073_All//0.00E+00//AT5G13680| ABO1 (ABA-OVERLY SENSITIVE 1); transcription elongation regulator	Unigene2073_All//0.00E+00//TC167829		GO:0040007		nr +
Unigene20738_All	259	0.00	0.00	1.64	2.31	0.00	0.00	0.00	0.00	0.00	null	null		1.07E+01	1.38E-02		-1.12E+01	1.78E-04	Down	-1.12E+01	7.71E-04	Down	null	null		null	null		Unigene20738_All//gi|218931460|gb|ACL12359.1|//9.00E-42//ATP synthase beta subunit [Myosotidium hortensia]	Unigene20738_All//1.00E-42//ATCG00480| chloroplast-encoded gene for beta subunit of ATP synthase	Unigene20738_All//1.00E-89//TC176987		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr -
Unigene2074_All	2406	2.91	7.94	8.59	19.32	8.54	7.96	11.55	6.98	9.42	1.45E+00	4.56E-25	Up	1.56E+00	3.02E-29	Up	-1.18E+00	2.66E-54	Down	-1.28E+00	2.83E-54	Down	-7.25E-01	6.94E-15		-2.93E-01	1.20E-03		Unigene2074_All//gi|42741727|gb|AAS45124.1|//0.00E+00//WAK-like kinase [Solanum lycopersicum]	Unigene2074_All//2.00E-169//AT2G23450| protein kinase family protein	Unigene2074_All//0.00E+00//DW506334		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674//GO:0008152	nr -
Unigene20743_All	237	7.73	1.50	10.56	1.05	3.78	1.33	0.18	0.00	0.00	-2.37E+00	2.79E-05	Down	4.51E-01	2.91E-01		1.85E+00	2.15E-02		3.44E-01	7.97E-01		-7.48E+00	6.57E-01		-7.48E+00	6.13E-01			Unigene20743_All//5.00E-55//gi|78326061|gb|DT546335.1|DT546335				
Unigene20744_All	469	0.00	7.56	2.50	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	3.46E-20	Up	1.13E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene20744_All//gi|739124966|dbj|BAE20328.1|//6.00E-25//omega-5 gliadin [Triticum aestivum]				ko03022|Basal transcription factors		nr +
Unigene20748_All	299	82.59	45.08	61.62	145.61	175.98	178.24	232.89	103.16	108.46	-8.74E-01	7.93E-15		-4.23E-01	2.03E-04		2.73E-01	7.53E-05		2.92E-01	4.15E-05		-1.17E+00	5.60E-80	Down	-1.10E+00	2.35E-74	Down	Unigene20748_All//gi|233955399|gb|ACQ91203.1|//5.00E-53//calreticulin [Carica papaya]	Unigene20748_All//2.00E-52//AT1G56340| CRT1 (CALRETICULIN 1); calcium ion binding / unfolded protein binding	Unigene20748_All//3.00E-168//EV496536		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr -
Unigene20749_All	282	0.00	1.08	3.21	0.18	0.85	2.88	0.90	0.59	0.28	1.01E+01	4.43E-02		1.16E+01	4.71E-05	Up	2.28E+00	3.05E-01		4.03E+00	5.91E-04	Up	-6.02E-01	6.48E-01		-1.67E+00	2.56E-01		Unigene20749_All//gi|297835572|ref|XP_002885568.1|//8.00E-22//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331408|gb|EFH61827.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene20749_All//3.00E-23//AT3G23560| ALF5 (ABERRANT LATERAL ROOT FORMATION 5); antiporter/ drug transporter/ transporter	Unigene20749_All//2.00E-17//TC152494				nr +
Unigene20757_All	415	0.88	4.76	1.15	4.68	5.48	4.35	7.03	12.49	10.85	2.43E+00	9.73E-06	Up	3.88E-01	6.97E-01		2.26E-01	6.27E-01		-1.05E-01	8.28E-01		8.29E-01	4.07E-04		6.26E-01	1.11E-02			Unigene20757_All//2.00E-37//TC176311				
Unigene20759_All	472	10.97	6.98	4.96	24.38	23.49	17.13	10.48	10.89	11.73	-6.53E-01	1.28E-02		-1.14E+00	4.21E-05	Down	-5.35E-02	8.17E-01		-5.09E-01	2.03E-03		5.55E-02	8.35E-01		1.63E-01	5.12E-01			Unigene20759_All//1.00E-118//DR463469				
Unigene20760_All	358	0.00	0.00	0.00	0.00	0.00	0.00	1.89	5.02	0.00	null	null		null	null		null	null		null	null		1.41E+00	1.74E-03		-1.09E+01	3.56E-05	Down		Unigene20760_All//2.00E-18//gi|84067512|gb|DW177377.1|DW177377				
Unigene20762_All	483	0.33	1.99	1.21	1.44	1.14	0.75	3.76	2.94	1.24	2.62E+00	2.34E-03		1.90E+00	8.48E-02		-3.40E-01	6.80E-01		-9.49E-01	2.88E-01		-3.56E-01	4.32E-01		-1.61E+00	2.86E-04	Down	Unigene20762_All//gi|2262118|gb|AAB63626.1|//3.00E-14//cell division protein isolog [Arabidopsis thaliana] >gi|4972098|emb|CAB43894.1| cell division protein-like [Arabidopsis thaliana] >gi|7269243|emb|CAB81312.1| cell division protein-like [Arabidopsis thaliana]	Unigene20762_All//2.00E-07//AT4G23940| FtsH protease, putative	Unigene20762_All//1.00E-78//TC177172				nr +
Unigene20763_All	652	0.16	1.09	0.08	0.92	0.00	0.00	0.91	0.51	4.95	2.76E+00	9.13E-03		-9.74E-01	7.21E-01		-9.84E+00	1.78E-04	Down	-9.84E+00	7.71E-04	Down	-8.24E-01	3.48E-01		2.45E+00	3.21E-11	Up	Unigene20763_All//gi|15217867|ref|NP_176697.1|//2.00E-10//DC1 domain-containing protein [Arabidopsis thaliana] >gi|4646199|gb|AAD26872.1|AC007230_6 EST gb|T22166 comes from this gene [Arabidopsis thaliana]	Unigene20763_All//4.00E-12//AT1G65180| DC1 domain-containing protein	Unigene20763_All//5.00E-14//gi|164256937|gb|ES846398.1|ES846398				nr +
Unigene20764_All	409	0.64	1.12	0.39	3.78	1.09	0.99	0.31	0.20	0.88	8.02E-01	4.60E-01		-7.12E-01	6.22E-01		-1.79E+00	6.85E-04	Down	-1.93E+00	7.77E-04	Down	-6.01E-01	7.66E-01		1.50E+00	2.04E-01		Unigene20764_All//gi|240254197|ref|NP_564436.4|//1.00E-06//SAMC2 (S-adenosylmethionine carrier 2); binding [Arabidopsis thaliana]		Unigene20764_All//4.00E-38//DR460656				nr -
Unigene20767_All	349	1.20	0.29	0.00	3.00	1.97	1.16	3.15	0.24	0.23	-2.05E+00	1.21E-01		-1.02E+01	1.56E-02		-6.03E-01	3.67E-01		-1.36E+00	4.89E-02		-3.72E+00	7.15E-06	Down	-3.79E+00	3.27E-06	Down	Unigene20767_All//gi|2500197|sp|Q41253.1|RAC13_GOSHI//3.00E-52//RecName: Full=Rac-like GTP-binding protein RAC13; Flags: Precursor >gi|1087111|gb|AAB35093.1| pea Rho1 protein homolog/mammalian rac protein homolog [Gossypium hirsutum]	Unigene20767_All//3.00E-42//AT5G45970| ARAC2 (ARABIDOPSIS RAC-LIKE 2); GTP binding	Unigene20767_All//1.00E-96//TC169212		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene20769_All	367	0.00	3.87	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.06E-08	Up	1.05E+01	4.04E-03		null	null		null	null		null	null		null	null		Unigene20769_All//sp|P02516|HSP23_DROME//3.00E-10//Heat shock protein 23 OS=Drosophila melanogaster GN=Hsp23 PE=1 SV=2						swissprot -
Unigene20770_All	218	0.96	0.00	0.00	4.11	0.63	1.24	0.00	0.38	0.37	-9.91E+00	1.22E-01		-9.91E+00	1.46E-01		-2.70E+00	8.77E-04	Down	-1.73E+00	2.81E-02		8.58E+00	4.01E-01		8.51E+00	4.04E-01								
Unigene20776_All	259	0.20	4.89	1.23	0.38	0.00	0.35	0.00	0.00	0.00	4.60E+00	3.52E-06	Up	2.61E+00	1.46E-01		-8.59E+00	3.13E-01		-1.41E-01	9.50E-01		null	null		null	null		Unigene20776_All//COG2837//1.00E-06//Predicted iron-dependent peroxidase						cog +
Unigene20778_All	492	43.71	27.81	41.78	151.77	113.80	59.58	134.75	90.47	19.27	-6.52E-01	3.70E-08		-6.51E-02	6.21E-01		-4.15E-01	3.33E-14		-1.35E+00	2.09E-94	Down	-5.75E-01	5.10E-23		-2.81E+00	1.01E-255	Down		Unigene20778_All//1.00E-177//gi|109874684|gb|DW503658.1|DW503658				
Unigene20779_All	261	0.00	6.60	3.47	0.00	0.00	0.00	0.00	0.00	0.31	1.27E+01	7.99E-10	Up	1.18E+01	4.71E-05	Up	null	null		null	null		null	null		8.25E+00	4.04E-01		Unigene20779_All//gi|66270189|gb|AAY43424.1|//1.00E-18//ribosomal protein L39 [Phytophthora infestans]	Unigene20779_All//5.00E-18//AT3G02190| 60S ribosomal protein L39 (RPL39B)			ko03010|Ribosome		nr -
Unigene20782_All	325	0.00	6.70	3.28	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.11E-12	Up	1.17E+01	6.62E-06	Up	null	null		null	null		null	null		null	null		Unigene20782_All//gi|4185855|emb|CAA10660.1|//2.00E-25//Ca2+-ATPase [Arabidopsis thaliana]	Unigene20782_All//2.00E-16//AT1G10130| ECA3 (ENDOPLASMIC RETICULUM-TYPE CALCIUM-TRANSPORTING ATPASE 3); calcium-transporting ATPase/ calmodulin binding / manganese-transporting ATPase/ peroxidase					nr +
Unigene20784_All	439	0.12	0.58	0.00	0.45	0.31	0.21	4.33	2.09	0.82	2.28E+00	2.34E-01		-6.90E+00	6.25E-01		-5.33E-01	7.49E-01		-1.14E+00	5.69E-01		-1.05E+00	1.31E-02		-2.41E+00	6.35E-07	Down							
Unigene20785_All	235	0.00	8.41	1.13	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	2.97E-11	Up	1.01E+01	8.02E-02		null	null		null	null		null	null		null	null								ESTscan +
Unigene20790_All	342	0.00	0.15	0.00	0.73	0.40	0.79	0.49	0.98	3.26	7.21E+00	6.17E-01		null	null		-8.55E-01	5.74E-01		1.22E-01	9.44E-01		9.83E-01	4.24E-01		2.72E+00	8.54E-05	Up			Unigene20790_All//4.00E-07//BF369090				
Unigene20794_All	272	0.58	0.56	0.39	1.83	2.28	0.33	0.47	1.08	3.37	-4.62E-02	9.89E-01		-5.60E-01	7.76E-01		3.15E-01	7.84E-01		-2.46E+00	4.83E-02		1.21E+00	3.92E-01		2.85E+00	3.18E-04	Up		Unigene20794_All//2.00E-45//TC142195				
Unigene20796_All	347	0.00	11.10	10.28	0.00	0.10	0.00	0.00	0.00	0.00	1.34E+01	6.32E-22	Up	1.33E+01	9.42E-20	Up	6.63E+00	8.30E-01		null	null		null	null		null	null		Unigene20796_All//gi|15718687|ref|NP_000996.2|//2.00E-54//40S ribosomal protein S3 [Homo sapiens] >gi|77404290|ref|NP_001029219.1|40S ribosomal protein S3 [Bos taurus] >gi|113205854|ref|NP_001038066.1|40S ribosomal protein S3 [Sus scrofa] >gi|109107963|ref|XP_001086020.1|PREDICTED: 40S ribosomal protein S3 [Macaca mulatta] >gi|417719|sp|P23396.2|RS3_HUMAN RecName: Full=40S ribosomal protein S3 >gi|91207641|sp|Q3T169.1|RS3_BOVIN RecName: Full=40S ribosomal protein S3 >gi|115502828|sp|Q028U2.1|RS3_PIG RecName: Full=40S ribosomal protein S3 >gi|187609257|pdb|2ZKQ|CC Chain c, Structure Of A Mammalian Ribosomal 40s Subunit Within An 80s Complex Obtained By Docking Homology Models Of The Rna And Proteins Into An 8.7 A Cryo-Em Map >gi|555941|gb|AAB60336.1| ribosomal protein S3 [Homo	Unigene20796_All//6.00E-49//AT5G35530| 40S ribosomal protein S3 (RPS3C)			ko03010|Ribosome		nr +
Unigene20799_All	699	0.00	0.00	0.00	0.00	0.00	0.26	0.79	1.26	3.08	null	null		null	null		null	null		8.01E+00	1.94E-01		6.75E-01	3.28E-01		1.97E+00	4.04E-06	Up	Unigene20799_All//gi|297726167|ref|NP_001175447.1|//4.00E-70//Os08g0230800 [Oryza sativa Japonica Group] >gi|255678252|dbj|BAH94175.1|Os08g0230800 [Oryza sativa Japonica Group]	Unigene20799_All//1.00E-54//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene20799_All//8.00E-07//TC175564				nr -

Unigene2080_All	2904	12.34	5.09	7.10	18.87	13.86	10.82	9.10	2.56	2.87	-1.28E+00	1.12E-38	Down	-7.98E-01	1.64E-17		-4.45E-01	6.39E-12		-8.02E-01	8.07E-30		-1.83E+00	6.74E-59	Down	-1.67E+00	2.28E-53	Down	Unigene2080_All//gi|15222569|ref|NP_174489.1|//0.00E+00//early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana]	Unigene2080_All//0.00E+00//AT1G3290| early-responsive to dehydration protein-related / ERD protein-related	Unigene2080_All//0.00E+00//TC159145			GO:0016020//GO:0031410	nr +
Unigene20804_All	284	0.00	0.00	0.00	0.35	0.00	0.00	2.83	0.74	0.00	null	null		null	null		-8.45E+00	3.13E-01		-8.45E+00	4.00E-01		-1.94E+00	1.17E-02		-1.15E+01	4.43E-06	Down			Unigene20804_All//2.00E-58//DW503765				
Unigene2081_All	1908	24.57	13.84	14.21	27.78	21.87	20.69	34.97	12.97	18.04	-8.29E-01	3.85E-25		-7.90E-01	2.38E-22		-3.45E-01	2.26E-07		-4.25E-01	1.20E-09		-1.43E+00	7.22E-104	Down	-9.55E-01	2.01E-56	Down	Unigene2081_All//gi|15224592|ref|NP_180654.1|//0.00E+00//ASP1 (ASPARTATE AMINOTRANSFERASE 1); L-aspartate:2-oxoglutarate aminotransferase [Arabidopsis thaliana] >gi|186504418|ref|NP_001118421.1|ASP1 (ASPARTATE AMINOTRANSFERASE 1); L-aspartate:2-oxoglutarate aminotransferase [Arabidopsis thaliana] >gi|1168256|sp|P46643.1|AAT1_ARATHRecName: Full=Aspartate aminotransferase, mitochondrial; AltName: Full=Transaminase A; Flags: Precursor >gi|693688|gb|AAA79369.1|aspartate aminotransferase [Arabidopsis thaliana] >gi|3201622|gb|AAC20731.1|aspartate aminotransferase (AAT1) [Arabidopsis thaliana] >gi|16619085|gb|AAL24394.1|aspartate aminotransferase (AAT1) [Arabidopsis thaliana] >gi|22136256|gb|AAM91206.1|aspartate aminotransferase AAT1 [Arabidopsis thaliana]	Unigene2081_All//0.00E+00//AT2G3090| ASP1 (ASPARTATE AMINOTRANSFERASE 1); L-aspartate:2-oxoglutarate aminotransferase	Unigene2081_All//0.00E+00//TC157731		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism//ko00350|Tyrosine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0006519//GO:0008483//GO:0010038//GO:0043231//GO:0046914//GO:0048037	nr -
Unigene20810_All	243	0.00	0.00	0.44	1.03	0.57	0.00	2.09	0.34	0.00	null	null		8.78E+00	3.99E-01		-8.55E-01	5.74E-01		-1.00E+01	7.34E-02		-2.60E+00	2.05E-02		-1.10E+01	5.54E-04	Down							
Unigene20811_All	315	35.21	22.52	27.55	45.86	48.76	55.06	14.50	36.62	26.81	-6.45E-01	1.53E-04		-3.54E-01	5.30E-02		8.83E-02	6.02E-01		2.64E-01	6.17E-02		1.34E+00	8.00E-17	Up	8.87E-01	4.60E-07				Unigene20811_All//1.00E-87//TC155685				
Unigene2812_All	264	0.00	0.00	0.00	0.00	0.00	0.00	4.00	0.48	1.06	null	null		null	null		null	null		null	null		-3.08E+00	6.12E-05	Down	-1.92E+00	2.21E-03									
Unigene2082_All	292	2.51	3.82	2.55	1.36	2.12	3.40	7.38	2.72	15.83	6.06E-01	3.59E-01		2.54E-02	9.95E-01		6.37E-01	5.49E-01		1.32E+00	7.15E-02		-1.44E+00	3.83E-04	Down	1.10E+00	1.08E-05	Up	Unigene2082_All//gi|224080231|ref|XP_002306063.1|//9.00E-10//predicted protein [Populus trichocarpa] >gi|222849027|gb|EEE86574.1|predicted protein [Populus trichocarpa]		Unigene2082_All//4.00E-50//C0083773				nr +
Unigene20822_All	425	0.00	0.00	0.00	0.00	0.00	0.00	2.19	6.49	0.00	null	null		null	null		null	null		null	null		1.57E+00	1.23E-05	Up	-1.11E+01	5.47E-07	Down							ESTscan -
Unigene20826_All	276	0.00	4.77	2.12	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.50E-07	Up	1.11E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene20826_All//gi|297605712|ref|NP_001057499.2|//4.00E-13//Os06g0317400 [Oryza sativa Japonica Group] >gi|255676992|dbj|BAF19413.2|Os06g0317400 [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr +
Unigene2083_All	2067	8.68	11.57	9.97	11.42	13.69	12.04	15.55	11.10	40.92	4.14E-01	2.09E-04		2.00E-01	1.40E-01		2.62E-01	9.54E-03		7.58E-02	6.00E-01		-4.86E-01	9.24E-09		1.40E+00	3.83E-129	Up	Unigene2083_All//gi|44681378|gb|AAS47629.1|//8.00E-54//At1g26580 [Arabidopsis thaliana] >gi|45773908|gb|AAS76758.1|At1g26580 [Arabidopsis thaliana]	Unigene2083_All//8.00E-55//AT1G26580| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: myb family transcription factor / ELM2 domain-containing protein (TAIR:AT2G03470.1); Has 82 Blast hits to 82 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 78; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene2083_All//0.00E+00//TC178755				nr +
Unigene20834_All	847	0.00	0.00	0.00	0.00	0.00	0.00	3.00	1.92	0.00	null	null		null	null		null	null		null	null		-6.38E-01	7.45E-02		-1.15E+01	1.14E-18	Down	Unigene20834_All//gi|156987840|gb|ABU99898.1|//1.00E-122//translation elongation factor 1-alpha [Pythium vexans]	Unigene20834_All//2.00E-111//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene20834_All//6.00E-42//CD809343				nr +
Unigene2084_All	671	0.31	0.91	1.11	0.52	0.51	0.27	1.07	0.81	4.39	1.54E+00	1.22E-01		1.83E+00	5.05E-02		-1.82E-02	9.58E-01		-9.49E-01	4.81E-01		-4.04E-01	6.23E-01		2.04E+00	2.04E-08	Up	Unigene2084_All//gi|225452966|ref|XP_002279146.1|//3.00E-18//PREDICTED: hypothetical protein [Vitis vinifera] >gi|147800960|emb|CAN60122.1|hypothetical protein [Vitis vinifera] >gi|296082992|emb|CBI22293.3|unnamed protein product [Vitis vinifera]		Unigene2084_All//3.00E-114//C0083773				nr +
Unigene20841_All	376	0.14	2.02	3.40	0.66	0.82	0.36	0.00	0.00	0.00	3.86E+00	1.33E-03		4.61E+00	5.51E-06	Up	3.15E-01	8.38E-01		-8.79E-01	6.16E-01		null	null		null	null		Unigene20841_All//gi|558629|emb|CAA57551.1|//4.00E-10//chloroplast RNA binding protein [Phaseolus vulgaris]	Unigene20841_All//7.00E-11//AT1G60000| 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	Unigene20841_All//2.00E-52//TC141634				nr +
Unigene20843_All	223	0.23	3.64	0.72	1.79	3.24	0.81	2.28	1.50	4.29	3.95E+00	7.52E-04	Up	1.61E+00	5.11E-01		8.60E-01	3.36E-01		-1.14E+00	3.79E-01		-6.02E-01	5.31E-01		9.14E-01	1.38E-01				Unigene20843_All//7.00E-94//TC173886				
Unigene20847_All	835	0.00	0.00	0.00	0.00	0.00	0.00	4.86	0.00	1.15	null	null		null	null		null	null		null	null		-1.22E+01	1.02E-28	Down	-2.09E+00	8.87E-12	Down	Unigene20847_All//gi|297801316|ref|XP_002868542.1|//1.00E-45//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314378|gb|EFH44801.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene20847_All//1.00E-45//AT5G37800| basic helix-loop-helix (bHLH) family protein		bHLH		ko04712|Circadian rhythm - plant		nr +
Unigene20849_All	263	0.40	4.43	0.40	6.63	5.63	4.12	3.38	1.75	0.45	3.48E+00	7.08E-05	Up	2.52E-02	1.00E+00		-2.36E-01	6.37E-01		-6.86E-01	1.81E-01		-9.50E-01	1.55E-01		-2.89E+00	3.04E-04	Down			Unigene20849_All//3.00E-10//TC177419				
Unigene2085_All	2383	0.11	0.34	0.09	0.44	0.23	0.34	0.92	0.54	2.96	1.63E+00	5.05E-02		-2.97E-01	8.32E-01		-9.25E-01	1.56E-01		-3.64E-01	6.33E-01		-7.63E-01	4.86E-02		1.68E+00	7.06E-15	Up	Unigene2085_All//gi|115453611|ref|NP_001050406.1|//2.00E-50//Os03g0425800 [Oryza sativa Japonica Group] >gi|113548877|dbj|BAF12320.1|Os03g0425800 [Oryza sativa Japonica Group]	Unigene2085_All//2.00E-50//AT1G26580| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: myb family transcription factor / ELM2 domain-containing protein (TAIR:AT2G03470.1); Has 82 Blast hits to 82 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 78; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene2085_All//0.00E+00//TC178755				nr -
Unigene20851_All	437	0.00	1.62	3.17	0.00	0.79	0.00	0.00	0.00	0.00	1.07E+01	3.33E-04	Up	1.16E+01	1.23E-07	Up	9.62E+00	3.01E-02		null	null		null	null		null	null		Unigene20851_All//gi|297830964|ref|XP_002883364.1|//4.00E-37//imidazoleglycerol-phosphate dehydratase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297329204|gb|EFH59623.1|imidazoleglycerol-phosphate dehydratase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene20851_All//6.00E-38//AT3G22425| IGPD; imidazoleglycerol-phosphate dehydratase			ko00340|Histidine metabolism		nr +
Unigene20852_All	279	3.38	0.00	2.86	2.14	1.48	1.30	0.61	1.20	0.57	-1.17E+01	1.46E-05	Down	-2.38E-01	7.23E-01		-5.33E-01	5.62E-01		-7.26E-01	4.60E-01		9.83E-01	4.24E-01		-8.58E-02	9.66E-01				Unigene20852_All//3.00E-100//TC177318				
Unigene20853_All	224	0.00	4.52	9.03	0.00	0.00	2.22	0.00	0.00	0.00	1.21E+01	7.26E-06	Up	1.31E+01	3.80E-11	Up	null	null		1.11E+01	4.38E-03		null	null		null	null		Unigene20853_All//gi|226502080|ref|NP_001147639.1|//7.00E-30//chlorophyll a-b binding protein 1, chloroplastic precursor [Zea mays] >gi|195612774|gb|ACG28217.1|chlorophyll a-b binding protein 2 [Zea mays]	Unigene20853_All//7.00E-30//AT2G34420| LHB1B2; chlorophyll binding	Unigene20853_All//2.00E-42//gi|109842107|gb|DW240667.1|DW240667		ko00196|Photosynthesis - antenna proteins		nr +
Unigene20858_All	300	0.00	30.06	14.38	0.33	0.00	0.00	0.00	0.00	0.00	1.49E+01	1.24E-51	Up	1.38E+01	6.13E-24	Up	-8.38E+00	3.13E-01		-8.38E+00	4.00E-01		null	null		null	null		Unigene20858_All//gi|160895838|ref|YP_001561420.1|//3.00E-41//elongation factor Tu [Delftia acidovorans SPH-1] >gi|160361422|gb|ABX33035.1|translation elongation factor Tu [Delftia acidovorans SPH-1]	Unigene20858_All//2.00E-28//AT4G20360| ATRABE1B (ARABIDOPSIS RAB GTPASE HOMOLOG E1B); GTP binding / GTPase/ translation elongation factor			ko04626|Plant-pathogen interaction		nr +
Unigene20860_All	243	0.00	0.00	0.00	0.00	0.00	0.00	4.35	1.38	0.00	null	null		null	null		null	null		null	null		-1.66E+00	8.55E-03		-1.21E+01	6.72E-08	Down	Unigene20860_All//gi|12229935|sp|Q9SM13.1|RS12_CYAPA//2.00E-13//RecName: Full=40S ribosomal protein S12 >gi|6012956|emb|CAB57311.1| 40s ribosomal protein S12 [Cyanophora paradoxa]				ko03010|Ribosome		nr +
Unigene20864_All	398	0.00	12.99	5.35	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.81E-29	Up	1.24E+01	9.78E-12	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene20865_All	343	0.00	0.00	0.00	0.00	0.00	0.00	4.31	10.60	0.00	null	null		null	null		null	null		null	null		1.30E+00	1.31E-05	Up	-1.21E+01	5.85E-11	Down	Unigene20865_All//gi|297836874|ref|XP_002886319.1|//5.00E-07//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332159|gb|EFH62578.1|expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene20865_All//4.00E-10//ES813141				nr +
Unigene20867_All	227	0.00	0.00	0.00	0.00	0.30	0.00	40.42	34.43	219.73	null	null		null	null		8.25E+00	6.10E-01		null	null		-2.31E-01	2.15E-01		2.44E+00	2.40E-162	Up							
Unigene20870_All	383	0.00	3.70	3.34	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.06E-08	Up	1.17E+01	4.69E-07	Up	null	null		null	null		null	null		null	null		Unigene20870_All//gi|254558248|gb|ACT67906.1|//2.00E-37//heat shock protein 70 [Ulva prolifera]	Unigene20870_All//3.00E-36//AT5G28540| BIP1; ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03060|Protein export		nr +
Unigene20872_All	1127	0.14	0.00	0.00	12.82	0.58	0.72	1.76	0.52	0.57	-7.12E+00	2.16E-01		-7.12E+00	2.45E-01		-4.46E+00	1.65E-85	Down	-4.15E+00	9.38E-69	Down	-1.76E+00	6.52E-05	Down	-1.64E+00	1.05E-04	Down	Unigene20872_All//gi|226497282|ref|NP_001148515.1|//4.00E-33//pro-resilin [Zea mays] >gi|195619956|gb|ACG31808.1| pro-resilin precursor [Zea mays]	Unigene20872_All//2.00E-25//AT3G06130| heavy-metal-associated domain-containing protein	Unigene20872_All//1.00E-164//TC148013		ko04144|Endocytosis		nr -
Unigene20873_All	607	0.00	0.00	0.35	0.00	0.00	0.15	0.42	1.24	13.98	null	null		8.45E+00	1.41E-01		null	null		7.22E+00	4.77E-01		1.57E+00	4.21E-02		5.06E+00	1.38E-51	Up			Unigene20873_All//1.00E-85//DT466717				

Unigene20875_All	291	0.00	0.00	0.00	0.00	0.47	1.40	0.00	0.29	3.42	null	null		null	null		8.89E+00	3.19E-01		1.04E+01	1.36E-02		8.17E+00	4.01E-01		1.17E+01	3.00E-07	Up	Unigene20875_All//gi|62867613|gb|AAY17410.1|/2.00E-08//At1g29290 [Arabidopsis thaliana]	Unigene20875_All//6.00E-09//AT1G29290| unknown protein	Unigene20875_All//2.00E-156//EX164543				nr +
Unigene20876_All	249	0.00	0.20	2.78	1.00	0.69	1.09	1.02	0.34	0.32	7.67E+00	6.17E-01		1.14E+01	6.17E-04	Up	-5.33E-01	7.13E-01		1.22E-01	9.44E-01		-1.60E+00	3.10E-01		-1.67E+00	2.56E-01						Unigene20876_All//2.00E-70//TC152047				
Unigene20878_All	243	0.00	13.14	9.86	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	3.64E-18	Up	1.33E+01	3.24E-13	Up	null	null		null	null		null	null		null	null		Unigene20878_All//sp|Q3YX76|RS15_SHISS/1.00E-22//30S ribosomal protein S15 OS=Shigella sonnei (strain Ss046) GN=rpsO PE=3 SV=1						swissprot -
Unigene20882_All	251	97.55	48.45	46.04	53.39	56.25	43.72	68.56	32.80	26.98	-1.01E+00	1.58E-18	Down	-1.08E+00	7.37E-20	Down	7.53E-02	6.92E-01		-2.88E-01	7.45E-02		-1.06E+00	1.81E-17	Down	-1.35E+00	9.38E-26	Down	Unigene20882_All//gi|2506277|sp|P08927.2|RUBB_PEA//2.00E-28//RecName: Full=RuBisCO large subunit-binding protein subunit beta, chloroplastic; AltName: Full=60 kDa chaperonin subunit beta; AltName: Full=CPN-60 beta; Flags: Precursor >gi|806808|gb|AAA66365.1| chaperonin precursor [Pisum sativum]	Unigene20882_All//4.00E-24//AT1G55490| CPN60B (CHAPERONIN 60 BETA); ATP binding / protein binding	Unigene20882_All//2.00E-113//gi|82756701|gb|DV850263.1|DV850263		ko03018|RNA degradation		nr +
Unigene20883_All	382	0.00	4.64	2.37	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.14E-10	Up	1.12E+01	4.71E-05	Up	null	null		null	null		null	null		null	null		Unigene20883_All//gi|226456765|gb|EEH54065.1|/3.00E-09//glycosyltransferase family 35 protein [Micromonas pusilla CCMP1545]	Unigene20883_All//7.00E-06//AT3G46970| PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups		ko00500|Starch and sucrose metabolism		nr +
Unigene20887_All	212	153.75	87.72	82.39	149.21	126.05	155.73	459.90	153.58	156.54	-8.10E-01	4.57E-17		-9.00E-01	1.82E-19		-2.43E-01	9.91E-03		6.17E-02	6.32E-01		-1.58E+00	9.86E-176	Down	-1.55E+00	3.03E-176	Down	Unigene20887_All//gi|211906490|gb|AC111738.1|/9.00E-36//malate dehydrogenase [Gossypium hirsutum]	Unigene20887_All//6.00E-28//AT5G43330| malate dehydrogenase, cytosolic, putative	Unigene20887_All//1.00E-116//BF271167		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene20889_All	2193	12.36	7.21	8.52	20.08	25.52	17.20	10.55	8.25	4.21	-7.78E-01	2.07E-13		-5.36E-01	5.76E-07		3.46E-01	1.17E-07		-2.24E-01	6.28E-03		-3.54E-01	5.34E-04		-1.32E+00	1.82E-33	Down	Unigene20889_All//gi|15238817|ref|NP_199591.1|/0.00E+00//phototropic-responsive NPH3 family protein [Arabidopsis thaliana] >gi|10177916|dbj|BAB11327.1| photoreceptor-interacting protein-like [Arabidopsis thaliana] >gi|110736956|dbj|BAF00434.1| photoreceptor-interacting like protein [Arabidopsis thaliana]	Unigene20889_All//0.00E+00//AT5G47800| phototropic-responsive NPH3 family protein	Unigene20889_All//0.00E+00//TC158646			GO:0005488//GO:0009314//GO:0060089	nr +
Unigene20890_All	977	0.00	0.00	0.00	0.00	0.00	0.00	2.81	2.05	0.00	null	null		null	null		null	null		null	null		-4.54E-01	1.98E-01		-1.15E+01	3.21E-20	Down	Unigene20890_All//gi|117606903|gb|ABK42021.1|/3.00E-11//vegetative cell wall protein [Chlamydomonas incerta]						nr +
Unigene20893_All	519	0.50	0.10	0.21	1.25	0.73	0.96	2.28	0.48	1.23	-2.37E+00	2.14E-01		-1.30E+00	4.36E-01		-7.74E-01	3.81E-01		-3.83E-01	6.78E-01		-2.24E+00	4.21E-04	Down	-8.93E-01	9.53E-02		Unigene20893_All//gi|4678941|emb|CAB41332.1|/2.00E-14//gamma response I protein [Arabidopsis thaliana]	Unigene20893_All//9.00E-16//AT3G22115| ATGR1 (ARABIDOPSIS THALIANA GAMMA RESPONSE GENE 1)					nr +
Unigene20894_All	381	0.00	0.00	0.00	0.00	0.00	0.00	1.78	2.19	0.00	null	null		null	null		null	null		null	null		3.05E-01	6.47E-01		-1.08E+01	3.56E-05	Down								
Unigene20895_All	273	0.58	0.56	1.56	1.82	0.38	1.32	0.00	2.76	0.88	-4.64E-02	9.89E-01		1.44E+00	2.53E-01		-2.27E+00	4.22E-02		-4.63E-01	6.59E-01		1.14E+01	2.07E-05	Up	9.77E+00	4.39E-02						Unigene20895_All//3.00E-07//EX166628				
Unigene20897_All	1226	0.09	0.25	0.00	0.41	0.11	0.29	0.79	7.19	0.26	1.54E+00	3.23E-01		-6.42E+00	3.94E-01		-1.85E+00	8.43E-02		-4.63E-01	6.59E-01		3.18E+00	9.13E-38	Up	-1.61E+00	1.12E-02		Unigene20897_All//gi|71041092|gb|AAZ20434.1|/2.00E-87//MYB18 [Malus x domestica]	Unigene20897_All//1.00E-66//AT4G28110| AtMYB41 (myb domain protein 41); DNA binding / transcription factor	Unigene20897_All//3.00E-72//NP524448	MYB			nr +
Unigene20901_All	238	0.00	55.99	23.05	0.00	0.00	0.00	0.00	0.00	0.00	1.58E+01	1.72E-76	Up	1.45E+01	1.52E-30	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene20905_All	390	0.40	1.04	3.69	0.13	0.26	0.00	0.00	0.00	0.00	1.37E+00	2.74E-01		3.20E+00	2.79E-05	Up	1.05E+00	8.08E-01		-7.00E+00	6.36E-01		null	null		null	null		Unigene20905_All//gi|168047204|ref|XP_001776061.1|/1.00E-10//SWIRM domain protein [Physcomitrella patens subsp. patens] >gi|162672571|gb|EDQ59106.1| SWIRM domain protein [Physcomitrella patens subsp. patens]	Unigene20905_All//7.00E-10//AT3G10390| FLD (FLOWERING LOCUS D); amine oxidase/ electron carrier/ oxidoreductase					nr -
Unigene20911_All	318	0.99	0.96	0.00	0.00	0.87	2.98	0.93	1.45	0.13	-4.63E-02	9.85E-01		-9.95E+00	4.91E-02		9.76E+00	7.02E-02		1.15E+01	1.13E-05	Up	6.36E-01	5.36E-01		-2.89E+00	6.77E-02									
Unigene20914_All	430	1.10	0.00	0.00	0.81	0.64	0.84	0.30	1.07	3.98	-1.01E+01	5.55E-03		-1.01E+01	8.65E-03		-3.40E-01	7.86E-01		5.12E-02	9.69E-01		1.86E+00	8.80E-02		3.76E+00	4.38E-09	Up								
Unigene20915_All	320	0.00	0.32	1.50	1.56	0.11	0.28	0.00	2.22	0.62	8.31E+00	3.87E-01		1.05E+01	7.49E-03		-3.85E+00	5.31E-03		-2.46E+00	4.83E-02		1.11E+01	3.98E-05	Up	9.28E+00	7.89E-02									
Unigene20916_All	240	101.37	29.77	22.63	107.10	67.15	115.17	170.53	88.82	60.42	-1.77E+00	1.86E-42	Down	-2.16E+00	2.59E-53	Down	-6.74E-01	6.72E-12		1.05E-01	4.01E-01		-9.41E-01	3.51E-33		-1.50E+00	2.06E-70	Down			Unigene20916_All//3.00E-133//gi|21095440|gb|BQ407753.1|BQ407753				
Unigene20918_All	208	2.01	0.73	0.51	0.24	3.64	1.95	1.02	0.20	0.96	-1.46E+00	2.34E-01		-1.97E+00	1.51E-01		3.93E+00	9.79E-04	Up	3.03E+00	6.03E-02		-2.34E+00	2.37E-01		-8.58E-02	9.61E-01		Unigene20918_All//gi|6685538|sp|Q40554.1|EIF3A_TOBAC//3.00E-22//RecName: Full=Eukaryotic translation initiation factor 3 subunit A; Short=eIF3a; AltName: Full=Eukaryotic translation initiation factor 3 subunit 10; AltName: Full=eIF-3-theta; AltName: Full=Eukaryotic translation initiation factor 3 large subunit; AltName: Full=PNLA-35	Unigene20918_All//9.00E-22//AT4G11420| EIF3A (EUKARYOTIC TRANSLATION INITIATION FACTOR 3A); translation initiation factor	Unigene20918_All//7.00E-54//gi|78329831|gb|DT550105.1|DT550105				nr -
Unigene2092_All	3219	0.59	0.47	0.56	0.74	1.68	0.98	1.05	0.79	1.45	-3.09E-01	5.23E-01		-5.71E-02	9.13E-01		1.18E+00	2.33E-06	Up	4.03E-01	2.89E-01		-4.08E-01	1.95E-01		4.63E-01	5.85E-02		Unigene2092_All//gi|51477379|gb|AAU04752.1|/0.00E+00//DRP [Cucumis melo]	Unigene2092_All//0.00E+00//AT1G10290| ADL6 (DYNAMIN-LIKE PROTEIN 6); GTPase	Unigene2092_All//0.00E+00//TC149214		ko04144|Endocytosis	GO:0005515//GO:0006892//GO:0006897//GO:0016020//GO:0017111//GO:0030139//GO:0032561	nr +
Unigene20923_All	329	1.43	0.00	0.32	3.79	1.88	0.55	11.31	9.02	17.80	-1.05E+01	5.55E-03		-2.14E+00	1.03E-01		-1.01E+00	8.39E-02		-2.79E+00	1.35E-04	Down	-3.26E-01	2.83E-01		6.54E-01	2.04E-03				Unigene20923_All//2.00E-12//DV849456				
Unigene20924_All	926	0.00	0.00	0.12	0.32	1.26	0.83	0.55	0.54	5.46	null	null		6.85E+00	3.99E-01		1.97E+00	3.92E-03		1.36E+00	1.18E-01		-1.67E-02	1.02E+00		3.32E+00	3.25E-23	Up	Unigene20924_All//gi|224082982|ref|XP_002306917.1|/2.00E-63//SAUR family protein [Populus trichocarpa] >gi|222856366|gb|EEE93913.1| SAUR family protein [Populus trichocarpa]	Unigene20924_All//4.00E-56//AT1G75590| auxin-responsive family protein	Unigene20924_All//0.00E+00//gi|13349587|gb|BG439930.1|BG439930				nr +
Unigene20926_All	317	0.00	0.00	0.00	0.00	0.00	0.00	2.27	1.98	0.00	null	null		null	null		null	null		null	null		-1.97E-01	7.84E-01		-1.11E+01	1.78E-05	Down	Unigene20926_All//gi|156554296|ref|XP_001602465.1|/2.00E-44//PREDICTED: similar to S14e ribosomal protein [Nasonia vitripennis]	Unigene20926_All//9.00E-39//AT3G52580| 40S ribosomal protein S14 (RPS14C)			ko03010|Ribosome		nr +
Unigene20928_All	300	0.00	0.34	0.18	0.00	0.00	0.00	3.24	0.42	1.33	8.40E+00	3.87E-01		7.47E+00	6.36E-01		null	null		null	null		-2.96E+00	1.89E-04	Down	-1.29E+00	3.62E-02		Unigene20928_All//gi|225469701|ref|XP_002269421.1|/1.00E-16//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene20929_All	398	0.00	2.29	1.74	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.62E-05	Up	1.08E+01	6.17E-04	Up	null	null		null	null		null	null		null	null		Unigene20929_All//gi|75220641|sp|Q32904.1|CB23_PEA//2.00E-70//RecName: Full=Chlorophyll a-b binding protein 3, chloroplastic; AltName: Full=LHCII type III CAB-3; Flags: Precursor >gi|309673|gb|AAA84545.1| light harvesting protein [Pisum sativum]	Unigene20929_All//2.00E-71//AT1G61520| LHCA3; chlorophyll binding	Unigene20929_All//6.00E-25//TC177640		ko00196|Photosynthesis - antenna proteins		nr +
Unigene2093_All	3203	0.29	0.55	0.35	0.95	0.54	0.94	1.32	0.60	0.62	9.13E-01	6.42E-02		2.48E-01	6.90E-01		-8.20E-01	1.54E-02		-6.10E-03	9.82E-01		-1.14E+00	2.32E-05	Down	-1.09E+00	3.10E-05	Down	Unigene2093_All//gi|6625788|gb|AAF19398.1|AF203882.1|/0.00E+00//dynamin homolog [Astragalus sinicus]	Unigene2093_All//0.00E+00//AT1G59610| ADL3 (ARABIDOPSIS DYNAMIN-LIKE 3); GTPase	Unigene2093_All//0.00E+00//TC153961		ko04144|Endocytosis	GO:0005515//GO:0006892//GO:0006897//GO:0016020//GO:0017111//GO:0030139//GO:0032561	nr -
Unigene20930_All	467	0.11	0.54	0.91	1.17	0.74	0.39	1.81	0.54	0.17	2.28E+00	2.34E-01		3.03E+00	5.73E-02		-6.70E-01	4.97E-01		-1.60E+00	1.32E-01		-1.75E+00	1.64E-02		-3.41E+00	1.35E-04	Down	Unigene20930_All//gi|18395013|ref|NP_564145.1|/7.00E-12//NADK2; NAD+ kinase/ calmodulin binding [Arabidopsis thaliana] >gi|75169003|sp|Q9C5W3.1|NADK2_ARATH RecName: Full=NAD kinase 2, chloroplastic; Short=AtNADK-2; Flags: Precursor	Unigene20930_All//3.00E-11//AT1G21640| NADK2; NAD+ kinase/ calmodulin binding	Unigene20930_All//1.00E-29//ES843723				nr -
Unigene20931_All	224	9.11	0.00	0.95	0.67	0.92	0.00	0.00	0.37	1.07	-1.32E+01	8.50E-12	Down	-3.26E+00	2.37E-07	Down	4.67E-01	8.25E-01		-9.38E+00	2.33E-01		8.54E+00	4.01E-01		1.01E+01	4.39E-02				Unigene20931_All//3.00E-07//TC146102				
Unigene20936_All	497	0.00	3.16	0.64	1.00	0.07	0.82	2.47	1.51	1.60	1.16E+01	5.70E-09	Up	9.33E+00	4.52E-02		-3.85E+00	5.31E-03		-2.94E-01	7.57E-01		-7.05E-01	2.06E-01		-6.22E-01	2.39E-01		Unigene20936_All//gi|145335397|ref|NP_172597.2|/2.00E-35//ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene20936_All//1.00E-36//AT1G11300| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene20936_All//2.00E-87//CO081719				nr +
Unigene20938_All	264	0.00	12.67	4.64	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	4.95E-19	Up	1.22E+01	9.12E-07	Up	null	null		null	null		null	null		null	null		Unigene20938_All//gi|115487986|ref|NP_001066480.1|/4.00E-10//Os12g0242100 [Oryza sativa Japonica Group] >gi|113648887|dbj|BAF29499.1| Os12g0242100 [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr +
Unigene20941_All	216	0.00	74.13	21.69	0.46	0.32	0.42	0.00	0.00	0.00	1.62E+01	5.27E-92	Up	1.44E+01	4.86E-26	Up	-5.33E-01	8.17E-01		-1.41E-01	9.50E-01		null	null		null	null		Unigene20941_All//gi|145354534|ref|XP_001421538.1|/7.00E-13//Ribosomal protein L24, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901] >gi|144581775|gb|AB099831.1| Ribosomal protein L24, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901]	Unigene20941_All//2.00E-13//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene20942_All	472	0.44	0.21	0.00	3.59	3.06	0.96	0.90	0.62	0.51	-1.05E+00	5.65E-01		-8.79E+00	1.46E-01		-2.28E-01	6.59E-01		-1.91E+00	4.25E-04	Down	-5.31E-01	6.34E-01		-8.23E-01	3.99E-01		Unigene20942_All//gi|124359163|gb|ABN06588.1|/7.00E-15//Zinc finger, CCHC-type [Medicago truncatula]		Unigene20942_All//6.00E-07//ES792407				nr +
Unigene20943_All	250	0.00	2.03	1.07	0.40	0.28	0.00	63.25	30.26	67.57	1.10E+01	4.03E-03		1.01E+01	8.02E-02		-5.33E-01	8.17E-01		-8.64E+00	4.00E-01		-1.06E+00	4.03E-16	Down	9.52E-02	4.92E-01				Unigene20943_All//6.00E-27//TC129587				
Unigene2095_All	1852	8.64	29.60	2.90	5.51	8.74	5.58	89.81	20.63	53.13	1.78E+00	6.56E-95	Up	-1.57E+00	5.31E-23	Down	6.64E-01	2.76E-07		1.83E-02	9.44E-01		-2.12E+00	0.00E+00	Down	-7.57E-01	4.18E-94		Unigene2095_All//gi|86129698|gb|ABC86558.1|/0.00E+00//abscisic acid 8'-hydroxylase [Phaseolus vulgaris]	Unigene2095_All//0.00E+00//AT4G19230| CYP707A1; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	Unigene2095_All//0.00E+00//TC134461		ko00906|Carotenoid biosynthesis	GO:0003006//GO:0005506//GO:0006952//GO:0009416//GO:0009687//GO:0016109	nr +
Unigene20955_All	256	1.23	0.20	2.70	0.78	1.48	0.35	1.98	0.00	0.00	-2.63E+00	1.31E-01		1.14E+00	2.18E-01		9.27E-01	5.23E-01		-1.14E+00	5.69E-01		-1.10E+01	8.89E-04	Down	-1.10E+01	5.54E-04	Down								
Unigene20956_All	575	1.18	0.44	0.00	0.87	0.36	0.00	2.57	0.29	0.55	-1.42E+00	1.16E-01		-1.02E+01	7.64E-04	Down	-1.27E+00	2.22E-01		-9.76E+00	2.97E-03		-3.15E+00	8.54E-07	Down	-2.22E+00	4.14E-05	Down								
Unigene20960_All	637	0.00	2.07	2.17	0.00	0.00	0.00	0.00	0.00	0.06	1.10E+01	1.50E-07	Up	1.11E+01	1.23E-07	Up	null	null		null	null		null	null		5.97E+00	6.45E-01		Unigene20960_All//gi|255977231|dbj|BAH97107.1|/3.00E-67//heat shock protein of Hsp90 [Chara braunii]	Unigene20960_All//3.00E-35//AT5G52640| AtHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -

Unigene20963_All	301	0.00	2.36	1.24	0.00	0.00	0.75	0.00	0.00	0.00	1.12E+01	3.33E-04	Up	1.03E+01	2.50E-02		null	null		9.55E+00	1.19E-01		null	null		null	null		Unigene20963_All//gi|194476850|ref|YP_002049029.1|//2.00E-10//t-RNA synthetase, class Ia:Valyl-tRNA [Paulinella chromatophora] >gi|171191857|gb|ACB42819.1| t-RNA synthetase, class Ia:Valyl-tRNA [Paulinella chromatophora]	Unigene20963_All//2.00E-09//ATIG16610| TWN2 (TWIN 2); ATP binding / aminoacyl-tRNA ligase/ nucleotide binding / valine-tRNA ligase			ko00970|Aminoacyl-tRNA biosynthesis//ko00290|Valine, leucine and isoleucine biosynthesis		nr -
Unigene20967_All	458	0.00	0.33	0.12	0.22	0.15	0.10	0.46	2.46	2.09	8.37E+00	2.35E-01		6.86E+00	6.36E-01		-5.32E-01	8.17E-01		-1.14E+00	6.77E-01		2.42E+00	3.17E-04	Up	2.18E+00	1.83E-03		Unigene20967_All//gi|15232500|ref|NP_188131.1|//2.00E-06//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|218546753|sp|P0C898.1|PP232_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At3g15130	Unigene20967_All//6.00E-06//AT3G15130| pentatricopeptide (PPR) repeat-containing protein	Unigene20967_All//1.00E-149//DT458401				nr +
Unigene20972_All	510	0.00	30.60	15.87	0.00	0.00	0.00	0.00	0.00	1.49E+01	1.16E-89	Up	1.40E+01	2.65E-45	Up	null	null		null	null		null	null		null	null		Unigene20972_All//gi|295913728|gb|ADG58103.1|//8.00E-45//transcription factor [Lycoris longituba]	Unigene20972_All//6.00E-07//AT3G55770| LIM domain-containing protein		LIM			nr -
Unigene20974_All	264	0.00	2.69	1.01	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.33E-04	Up	9.98E+00	8.02E-02		null	null		null	null		null	null		null	null		Unigene20974_All//gi|115451633|ref|NP_001049417.1|//2.00E-14//Os03g0222100 [Oryza sativa Japonica Group] >gi|113547888|dbj|BAF11331.1| Os03g0222100 [Oryza sativa Japonica Group]	Unigene20974_All//3.00E-15//AT4G24800| MA3 domain-containing protein					nr -
Unigene20977_All	460	0.00	0.00	0.00	0.00	0.00	1.84	3.54	0.00	null	null		null	null		null	null		null	null		9.47E-01	4.07E-02		-1.08E+01	2.21E-06	Down	Unigene20977_All//gi|298705189|emb|CBJ28620.1|//6.00E-37//Ribosomal protein L3 [Ectocarpus siliculosus]	Unigene20977_All//2.00E-32//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene20977_All//3.00E-08//TC149894		ko03010|Ribosome		nr -
Unigene2098_All	1391	1.35	1.35	1.45	0.93	1.04	1.14	1.16	4.39	4.64	-6.70E-03	9.84E-01		1.03E-01	8.17E-01		1.59E-01	8.26E-01		2.88E-01	6.43E-01		1.93E+00	4.20E-15	Up	2.01E+00	3.66E-17	Up	Unigene2098_All//gi|115439213|ref|NP_001043886.1|//9.00E-51//Os01g0682500 [Oryza sativa Japonica Group] >gi|56202305|dbj|BAD73764.1| phosphoribulokinase/uridine kinase-like [Oryza sativa Japonica Group] >gi|56784876|dbj|BAD82147.1| phosphoribulokinase/uridine kinase-like [Oryza sativa Japonica Group] >gi|113533417|dbj|BAF05800.1| Os01g0682500 [Oryza sativa Japonica Group]	Unigene2098_All//9.00E-46//AT1G80380| phosphoribulokinase/uridine kinase-related	Unigene2098_All//0.00E+00//gi|109847833|gb|DW476813.1|DW476813			GO:0009526//GO:0009532//GO:0016301//GO:0032559//GO:0043094	nr -
Unigene20981_All	203	71.65	19.72	35.94	117.79	115.86	155.51	53.53	59.50	52.99	-1.86E+00	1.76E-27	Down	-9.96E-01	1.44E-10		-2.38E-02	8.58E-01		4.01E-01	1.92E-05		1.53E-01	3.71E-01		-1.46E-02	9.52E-01		Unigene20981_All//gi|7208784|emb|CAB76914.1|//5.00E-26//60S ribosomal protein L6 [Cicer arietinum]	Unigene20981_All//2.00E-11//AT1G74060| 60S ribosomal protein L6 (RPL6B)	Unigene20981_All//2.00E-94//ES816401		ko03010|Ribosome		nr -
Unigene20983_All	528	0.00	2.88	2.62	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.10E-08	Up	1.14E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene20983_All//gi|115476996|ref|NP_001062094.1|//9.00E-21//Os08g0486200 [Oryza sativa Japonica Group] >gi|113624063|dbj|BAF24008.1| Os08g0486200 [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr +
Unigene20984_All	475	0.00	62.94	25.11	0.00	0.29	0.00	0.00	0.00	0.00	1.59E+01	2.31E-172	Up	1.46E+01	4.52E-67	Up	8.18E+00	3.19E-01		null	null		null	null		null	null		Unigene20984_All//gi|242068415|ref|XP_002449484.1|//5.00E-06//hypothetical protein SORBIDRAFT_05g016450 [Sorghum bicolor] >gi|241935327|gb|EES08472.1| hypothetical protein SORBIDRAFT_05g016450 [Sorghum bicolor]		Unigene20984_All//2.00E-28//DV849020				nr -
Unigene20985_All	567	0.00	0.00	0.00	0.00	0.00	0.00	6.64	4.72	0.49	null	null		null	null		null	null		null	null		-4.92E-01	8.76E-02		-3.75E+00	1.21E-19	Down	Unigene20985_All//gi|226492324|ref|NP_001142207.1|//3.00E-09//hypothetical protein LOC100274375 [Zea mays] >gi|194707598|gb|ACF87883.1| unknown [Zea mays]						nr +
Unigene20987_All	581	8.65	1.05	4.86	1.37	0.83	1.09	0.00	0.00	0.00	-3.05E+00	3.21E-17	Down	-8.32E-01	2.90E-03		-7.25E-01	3.47E-01		-3.34E-01	6.86E-01		null	null		null	null		Unigene20987_All//gi|297827609|ref|XP_002881687.1|//3.00E-54//peroxisomal membrane protein [Arabidopsis lyrata subsp. lyrata] >gi|297327526|gb|EFH57946.1| peroxisomal membrane protein [Arabidopsis lyrata subsp. lyrata]	Unigene20987_All//1.00E-54//AT2G39970| peroxisomal membrane protein (PMP36)	Unigene20987_All//3.00E-120//BG440716		ko04146|Peroxisome		nr +
Unigene20988_All	837	0.00	0.00	0.00	0.00	0.00	0.00	5.71	1.40	1.76	null	null		null	null		null	null		null	null		-2.03E+00	7.99E-13	Down	-1.70E+00	1.36E-10	Down	Unigene20988_All//gi|298706692|emb|CBJ34222.1|//2.00E-09//conserved unknown protein [Ectocarpus siliculosus] >gi|298713886|emb|CBJ33762.1| conserved unknown protein [Ectocarpus siliculosus]		Unigene20988_All//1.00E-24//ES794483				nr -
Unigene2099_All	1615	6.32	5.27	4.12	1.73	1.68	2.13	1.26	4.81	3.03	-2.61E-01	1.64E-01		-6.16E-01	9.08E-04		-3.62E-02	9.24E-01		2.99E-01	4.21E-01		1.94E+00	3.38E-19	Up	1.27E+00	2.67E-07	Up	Unigene2099_All//gi|115439213|ref|NP_001043886.1|//1.00E-139//Os01g0682500 [Oryza sativa Japonica Group] >gi|56202305|dbj|BAD73764.1| phosphoribulokinase/uridine kinase-like [Oryza sativa Japonica Group] >gi|56784876|dbj|BAD82147.1| phosphoribulokinase/uridine kinase-like [Oryza sativa Japonica Group] >gi|113533417|dbj|BAF05800.1| Os01g0682500 [Oryza sativa Japonica Group]	Unigene2099_All//7.00E-121//AT1G80380| phosphoribulokinase/uridine kinase-related	Unigene2099_All//0.00E+00//DW500600				nr -
Unigene20990_All	1199	0.00	0.00	0.00	0.00	0.00	0.00	3.03	3.63	0.00	null	null		null	null		null	null		null	null		2.58E-01	3.75E-01		-1.16E+01	9.77E-27	Down	Unigene20990_All//gi|226498304|ref|NP_001147852.1|//7.00E-22//kelch motif family protein [Zea mays] >gi|195614132|gb|ACG28896.1| kelch motif family protein [Zea mays]	Unigene20990_All//8.00E-28//AT1G74150| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Galactose oxidase/kelch, beta-propeller (InterPro:IPR011043), Kelch repeat type 1 (InterPro:IPR006652), Kelch repeat type 2 (InterPro:IPR011498), Kelch-type beta propeller (InterPro:IPR015915); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G18610.1); Has 8525 Blast hits to 4249 proteins in 295 species: Archae - 10; Bacteria - 313; Metazoa - 3989; Fungi - 859; Plants - 1220; Viruses - 19; Other Eukaryotes - 2115 (source: NCBI BLink).				ko04712|Circadian rhythm - plant		nr +
Unigene20997_All	641	0.24	0.00	0.00	0.00	0.00	0.00	4.02	1.63	0.06	-7.94E+00	2.16E-01		-7.94E+00	2.45E-01		null	null		null	null		-1.30E+00	3.05E-04	Down	-6.02E+00	1.74E-17	Down								
Unigene2100_All	2740	2.29	2.98	2.20	5.27	6.89	3.94	11.54	1.92	3.29	3.78E-01	6.88E-02		-6.13E-02	8.07E-01		3.86E-01	1.60E-03		-4.21E-01	4.18E-03		-2.59E+00	2.02E-108	Down	-1.81E+00	1.32E-71	Down	Unigene2100_All//gi|240254101|ref|NP_173290.4|//0.00E+00//ATP binding / microtubule motor [Arabidopsis thaliana]	Unigene2100_All//0.00E+00//AT1G18550| ATP binding / microtubule motor	Unigene2100_All//0.00E+00//ES824255			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr +
Unigene21007_All	278	0.00	0.18	1.15	1.08	1.24	0.81	2.28	0.00	2.01	7.51E+00	6.17E-01		1.02E+01	4.52E-02		2.04E-01	9.01E-01		-4.04E-01	7.51E-01		-1.12E+01	1.23E-04	Down	-1.85E-01	7.94E-01									
Unigene21009_All	656	0.00	0.00	0.00	0.00	0.00	0.00	1.74	3.19	0.00	null	null		null	null		null	null		null	null		8.72E-01	2.88E-02		-1.08E+01	1.65E-08	Down	Unigene21009_All//gi|15240947|ref|NP_198672.1|//8.00E-08//protein kinase family protein [Arabidopsis thaliana] >gi|15983497|gb|AAL11616.1|AF424623_1 AT5g38560/MBB18_10 [Arabidopsis thaliana] >gi|18700153|gb|AAL77688.1| AT5g38560/MBB18_10 [Arabidopsis thaliana] >gi|21360463|gb|AAM47347.1| AT5g38560/MBB18_10 [Arabidopsis thaliana]						nr +
Unigene2101_All	540	57.07	76.75	95.55	39.94	58.99	55.95	7.52	5.81	2.43	4.28E-01	2.22E-07		7.44E-01	3.60E-22		5.62E-01	1.96E-10		4.86E-01	3.53E-07		-3.73E-01	1.90E-01		-1.63E+00	1.21E-08	Down	Unigene2101_All//gi|10764491|gb|AAG22740.1|AF282850_1//9.00E-69//allergenic isoflavone reductase-like protein Bet v 6.0102 [Betula pendula]	Unigene2101_All//3.00E-61//AT1G75280| isoflavone reductase, putative	Unigene2101_All//0.00E+00//gi|109873586|gb|DW502561.1|DW502561		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism	GO:0008152//GO:0016628	nr +
Unigene21011_All	279	0.38	3.09	0.00	0.36	0.74	6.64	1.52	3.75	4.71	3.04E+00	1.94E-03		-8.55E+00	3.94E-01		1.05E+00	6.12E-01		4.22E+00	8.95E-09	Up	1.31E+00	3.44E-02		1.64E+00	2.41E-03		Unigene21011_All//gi|124360934|gb|ABN08906.1|//2.00E-13//Ankyrin [Medicago truncatula]	Unigene21011_All//5.00E-11//AT5G54620| ankyrin repeat family protein					nr -
Unigene21013_All	477	0.00	10.41	6.14	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	2.63E-28	Up	1.26E+01	3.52E-16	Up	null	null		null	null		null	null		null	null		Unigene21013_All//sp|Q24407|ATP5J_DROME//4.00E-40//ATP synthase-coupling factor 6, mitochondrial OS=Drosophila melanogaster GN=ATPsyn-CF6 PE=1 SV=1						swissprot -
Unigene21016_All	334	0.00	0.00	0.00	0.45	0.00	0.27	8.86	0.00	3.58	null	null		null	null		-8.81E+00	1.66E-01		-7.27E-01	7.15E-01		-1.31E+01	6.25E-21	Down	-1.31E+00	5.75E-05	Down			Unigene21016_All//7.00E-169//TC171064				
Unigene21017_All	527	0.30	0.00	1.41	1.32	1.11	0.17	2.09	0.16	0.00	-8.22E+00	2.16E-01		2.25E+00	2.35E-02		-2.53E-01	7.78E-01		-2.95E+00	5.84E-03		-3.72E+00	7.15E-06	Down	-1.10E+01	3.33E-08	Down	Unigene21017_All//gi|2739004|gb|AAB94590.1|//2.00E-36//CYP82C1p [Glycine max]	Unigene21017_All//3.00E-25//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene21017_All//6.00E-07//TC141877		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +

Unigene21018_All	391	0.00	0.52	0.00	0.00	0.00	2.19	0.22	0.11	1.53	9.02E+00	1.37E-01		null	null		null	null		1.11E+01	3.79E-05	Up	-1.02E+00	7.25E-01		2.82E+00	5.65E-03		Unigene21018_All//gi|224066257|ref|XP_002302050.1|//2.00E-42//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222843776|gb|EEE81323.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene21018_All//7.00E-20//AT3G23220| DNA binding / transcription factor	Unigene21018_All//5.00E-10//DW237308	AP2-EREBP			nr +
Unigene2102_All	2471	28.44	35.66	32.82	32.05	40.93	36.37	9.03	5.02	3.72	3.27E-01	3.03E-09		2.07E-01	7.04E-04		3.53E-01	6.31E-14		1.82E-01	9.91E-04		-8.47E-01	1.39E-15		-1.28E+00	1.07E-30	Down	Unigene2102_All//gi|124488476|gb|ABV12322.1|//1.00E-143//phenylcoumaran benzylic ether reductase-like protein [Gossypium hirsutum]	Unigene2102_All//6.00E-126//AT4G39230| isoflavone reductase, putative	Unigene2102_All//0.00E+00//TC145561		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism		nr -
Unigene21025_All	449	0.00	0.00	0.00	0.00	0.08	0.00	241.53	44.31	120.31	null	null		null	null		6.26E+00	8.30E-01		null	null		-2.45E+00	0.00E+00	Down	-1.01E+00	2.83E-99	Down	Unigene21025_All//gi|224110984|ref|XP_002315705.1|//1.00E-31//high affinity inorganic phosphate transporter [Populus trichocarpa] >gi|222864745|gb|EEF01876.1| high affinity inorganic phosphate transporter [Populus trichocarpa]	Unigene21025_All//1.00E-27//AT2G38940| ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter					nr +
Unigene21028_All	672	0.00	0.00	0.00	4.45	1.13	1.21	0.13	0.00	0.00	null	null		null	null		-1.98E+00	5.91E-08	Down	-1.88E+00	1.27E-06	Down	-6.98E+00	4.04E-01		-6.98E+00	3.59E-01		Unigene21028_All//gi|107738065|gb|ABF83626.1|//9.00E-08//At4g33800 [Arabidopsis thaliana]	Unigene21028_All//1.00E-06//AT4G33800| unknown protein					nr -
Unigene2103_All	664	1.73	1.76	0.88	1.73	1.66	1.70	1.66	1.95	3.96	1.79E-02	9.91E-01		-9.75E-01	1.46E-01		-5.63E-02	9.17E-01		-2.11E-02	9.62E-01		2.37E-01	6.52E-01		1.26E+00	2.97E-04	Up	Unigene2103_All//gi|297597177|ref|NP_001043529.2|//1.00E-90//Os01g0607200 [Oryza sativa Japonica Group] >gi|255673448|dbj|BAF05443.2| Os01g0607200 [Oryza sativa Japonica Group]	Unigene2103_All//4.00E-87//AT2G01170| BAT1 (BIDIRECTIONAL AMINO ACID TRANSPORTER 1); amino acid transmembrane transporter	Unigene2103_All//1.00E-125//ES846180			GO:0015172//GO:0015174//GO:0015179//GO:0015837//GO:0031224	nr -
Unigene21033_All	973	0.00	0.21	0.00	0.15	0.04	0.37	1.87	2.66	8.31	7.70E+00	1.37E-01		null	null		-2.12E+00	3.86E-01		1.27E+00	3.82E-01		5.11E-01	1.53E-01		2.15E+00	3.03E-23	Up	Unigene21033_All//gi|145335895|ref|NP_173359.3|//1.00E-118//FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase [Arabidopsis thaliana] >gi|75174733|sp|Q9LMA1.1|FMO1_ARATH RecName: Full=Probable flavin-containing monooxygenase 1 >gi|89540062|gb|AAR82235.1|AC069143_11 Contains similarity to a dimethylaniline monooxygenase (N-oxide forming) 2 (pulmonary flavin-containing monooxygenase 2) (FMO 2) (Dimethylaniline oxidase 2) (FMO 1B1) from Oryctolagus cuniculus gi|120434 and contains a flavin-binding monooxygenase-like PF|00743 domain [Arabidopsis thaliana]	Unigene21033_All//4.00E-120//AT1G19250| FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase					nr +
Unigene21035_All	785	0.20	127.22	42.13	0.00	0.00	0.00	0.00	0.00	0.00	9.31E+00	0.00E+00	Up	7.72E+00	6.67E-181	Up	null	null		null	null		null	null		null	null		Unigene21035_All//sp|Q04691|FBP1_DROME//1.00E-25//Fat-body protein 1 OS=Drosophila melanogaster GN=Fbp1 PE=2 SV=2						swissprot +
Unigene21036_All	488	1.39	1.35	0.87	2.65	6.77	5.83	0.78	0.86	0.57	-4.63E-02	9.70E-01		-6.75E-01	4.41E-01		1.35E+00	6.34E-05	Up	1.14E+00	2.54E-03		1.35E-01	8.99E-01		-4.48E-01	6.41E-01		Unigene21036_All//gi|29029014|gb|AA064886.1|//8.00E-57//At4g13370 [Arabidopsis thaliana]	Unigene21036_All//5.00E-58//AT4G13370| unknown protein	Unigene21036_All//0.00E+00//DW504002				nr +
Unigene21037_All	373	0.00	10.05	4.28	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	2.40E-21	Up	1.21E+01	8.44E-09	Up	null	null		null	null		null	null		null	null									
Unigene21038_All	1143	0.64	0.27	0.70	0.04	0.15	0.04	18.75	3.88	1.50	-1.27E+00	1.36E-01		1.25E-01	8.66E-01		1.79E+00	5.20E-01		-1.43E-01	9.53E-01		-2.27E+00	2.03E-63	Down	-3.65E+00	1.78E-106	Down	Unigene21038_All//gi|145408594|ref|YP_001152218.1|//5.00E-17//ORF82c [Pinus koraiensis] >gi|145048843|gb|ABP35459.1| ORF82c [Pinus koraiensis]		Unigene21038_All//2.00E-45//gi|84148798|gb|DN780098.1|DN780098				nr +
Unigene21039_All	298	0.00	0.00	0.00	0.00	0.00	0.00	5.39	0.98	12.97	null	null		null	null		null	null		null	null		-2.46E+00	7.71E-06	Down	1.27E+00	6.65E-06	Up	Unigene21039_All//gi|42567516|ref|NP_195582.2|//1.00E-10//disease resistance-responsive family protein [Arabidopsis thaliana]	Unigene21039_All//4.00E-12//AT4G38700| disease resistance-responsive family protein	Unigene21039_All//3.00E-32//ES800335				nr -
Unigene2104_All	2029	4.38	1.90	1.76	4.10	2.94	2.27	10.38	8.03	19.79	-1.21E+00	2.20E-09	Down	-1.32E+00	3.89E-10	Down	-4.82E-01	1.22E-02		-8.53E-01	1.45E-05		-3.69E-01	5.87E-04		9.32E-01	9.41E-33		Unigene2104_All//gi|18379164|ref|NF_565254.1|//0.00E+00//BAT1 (BIDIRECTIONAL AMINO ACID TRANSPORTER 1); amino acid transmembrane transporter [Arabidopsis thaliana]	Unigene2104_All//0.00E+00//AT2G01170| BAT1 (BIDIRECTIONAL AMINO ACID TRANSPORTER 1); amino acid transmembrane transporter	Unigene2104_All//0.00E+00//ES846180			GO:0015172//GO:0015174//GO:0015179//GO:0015837//GO:0031224	nr -
Unigene21040_All	457	0.00	0.44	0.00	1.42	3.32	1.09	3.42	1.19	1.05	8.79E+00	1.37E-01		null	null		1.23E+00	2.48E-02		-3.82E-01	6.78E-01		-1.53E+00	1.98E-03		-1.71E+00	4.59E-04	Down	Unigene21040_All//gi|184014891|ref|NP_566576.1|//6.00E-56//meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana]	Unigene21040_All//4.00E-57//AT3G17380| meprin and TRAF homology domain-containing protein / MATH domain-containing protein	Unigene21040_All//3.00E-27//CO077682				nr -
Unigene21042_All	222	3.77	5.25	7.68	4.94	2.79	0.81	0.95	1.13	1.79	4.77E-01	4.39E-01		1.03E+00	5.24E-02		-8.22E-01	1.96E-01		-2.60E+00	7.13E-04	Down	2.46E-01	8.53E-01		9.14E-01	3.86E-01								
Unigene21043_All	523	3.40	1.65	1.83	2.10	4.35	2.59	3.56	1.44	1.22	-1.05E+00	3.39E-02		-8.92E-01	8.34E-02		1.05E+00	1.23E-02		3.06E-01	6.14E-01		-1.31E+00	2.76E-03		-1.55E+00	3.64E-04	Down	Unigene21043_All//gi|90399226|emb|CAH68301.1|//5.00E-45//B0811B10.1 [Oryza sativa (indica cultivar-group)] >gi|116308857|emb|CAH65994.1| H1005F08.23 [Oryza sativa (indica cultivar-group)]	Unigene21043_All//3.00E-44//AT1G78690| phospholipid/glycerol acyltransferase family protein	Unigene21043_All//0.00E+00//TC171452		ko00564|Glycerophospholipid metabolism		nr +
Unigene21045_All	635	0.00	8.46	6.88	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.24E-30	Up	1.27E+01	3.08E-24	Up	null	null		null	null		null	null		null	null		Unigene21045_All//gi|115487186|ref|NP_001066080.1|//2.00E-11//Os12g0132300 [Oryza sativa Japonica Group] >gi|122234179|sp|Q0IQB6.1|CML3_ORYSJ RecName: Full=Calmodulin-like protein 3 >gi|113648587|dbj|BAF29099.1| Os12g0132300 [Oryza sativa Japonica Group]	Unigene21045_All//6.00E-10//AT5G37780| CAM1 (CALMODULIN 1); calcium ion binding			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene21046_All	762	0.00	5.85	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.11E-25	Up	1.07E+01	9.12E-07	Up	null	null		null	null		null	null		null	null		Unigene21046_All//gi|130750612|gb|AB032293.1|//2.00E-09//75k gamma secalin [Secale sylvestre]						nr -
Unigene21049_All	455	0.00	7.35	3.39	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	4.95E-19	Up	1.17E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene21049_All//gi|111609767|gb|ABH11436.1|//4.00E-60//cytosolic glucose-6-phosphate isomerase [Pavlova lutheri]	Unigene21049_All//7.00E-37//AT5G42740| glucose-6-phosphate isomerase, cytosolic (PGIC)			ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene2105_All	2561	4.05	7.64	6.20	11.05	9.86	10.39	8.67	31.53	19.43	9.17E-01	8.38E-13		6.15E-01	2.04E-05		-1.65E-01	1.34E-01		-8.90E-02	4.73E-01		1.86E+00	8.19E-183	Up	1.16E+00	9.15E-58	Up	Unigene2105_All//gi|297833884|ref|XP_002884824.1|//0.00E+00//xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330064|gb|EFH61083.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2105_All//0.00E+00//AT3G10960| xanthine/uracil permease family protein	Unigene2105_All//0.00E+00//TC156149			GO:0006863//GO:0043231	nr +
Unigene21053_All	451	0.00	5.06	2.13	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.64E-13	Up	1.11E+01	2.46E-05	Up	null	null		null	null		null	null		null	null		Unigene21053_All//sp|P08962|CD63_HUMAN//2.00E-77//CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2						swissprot -
Unigene21055_All	535	4.60	0.95	5.47	1.30	2.70	0.42	0.55	0.08	0.15	-2.28E+00	1.43E-06	Down	2.52E-01	5.27E-01		1.05E+00	6.14E-02		-1.63E+00	7.45E-02		-2.82E+00	8.85E-02		-1.89E+00	1.68E-01				Unigene21055_All//6.00E-07//TC131834				
Unigene21056_All	428	0.98	0.71	0.37	5.24	3.30	1.06	1.98	1.27	0.84	-4.61E-01	6.50E-01		-1.39E+00	2.80E-01		-6.67E-01	1.08E-01		-2.31E+00	1.80E-06	Down	-6.38E-01	3.70E-01		-1.24E+00	6.26E-02		Unigene21056_All//gi|255537141|ref|XP_002509637.1|//2.00E-06//ESC, putative [Ricinus communis] >gi|223549536|gb|EEF51024.1| ESC, putative [Ricinus communis]		Unigene21056_All//0.00E+00//TC130630				nr +
Unigene2106_All	4214	0.06	0.07	0.47	7.84	3.64	2.10	9.40	2.85	2.14	2.15E-01	8.65E-01		2.91E+00	1.70E-06	Up	-1.11E+00	4.53E-35	Down	-1.90E+00	9.15E-69	Down	-1.72E+00	4.68E-81	Down	-2.14E+00	2.73E-111	Down	Unigene2106_All//gi|224133676|ref|XP_002327653.1|//0.00E+00//histidine kinase osmosensor protein [Populus trichocarpa] >gi|222836738|gb|EEE75131.1| histidine kinase osmosensor protein [Populus trichocarpa]	Unigene2106_All//0.00E+00//AT2G17820| ATHK1 (histidine kinase 1); histidine phosphotransfer kinase/ osmosensor/ protein histidine kinase	Unigene2106_All//9.00E-48//DW512893	Orphans	ko04712|Circadian rhythm - plant	GO:0004673//GO:0004888//GO:0006351//GO:0006468//GO:0006950//GO:0023060//GO:0032559//GO:0044464//GO:0048316	nr -
Unigene21060_All	638	0.16	123.81	46.91	0.00	0.00	0.00	0.00	0.00	0.00	9.56E+00	0.00E+00	Up	8.16E+00	4.65E-165	Up	null	null		null	null		null	null		null	null		Unigene21060_All//gi|300170214|gb|EFJ36815.1|//4.00E-09//hypothetical protein SELMODRAFT_437890 [Selaginella moellendorffii]						nr +
Unigene21061_All	468	0.00	5.85	5.58	0.00	0.00	0.10	0.00	0.00	0.17	1.25E+01	1.44E-15	Up	1.24E+01	2.12E-14	Up	null	null		6.59E+00	6.96E-01		null	null		7.41E+00	4.04E-01		Unigene21061_All//gi|297812013|ref|XP_002873890.1|//2.00E-59//40S ribosomal protein S16 [Arabidopsis lyrata subsp. lyrata] >gi|297319727|gb|EFH50149.1| 40S ribosomal protein S16 [Arabidopsis lyrata subsp. lyrata]	Unigene21061_All//9.00E-59//AT5G18380| 40S ribosomal protein S16 (RPS16C)			ko03010|Ribosome		nr -
Unigene21062_All	419	0.00	0.00	0.00	0.00	0.00	0.00	3.63	4.29	0.00	null	null		null	null		null	null		null	null		2.40E-01	6.34E-01		-1.18E+01	2.88E-11	Down	Unigene21062_All//gi|62287478|sp|Q9M5Z9.1|RS23_EUPES//2.00E-56//RecName: Full=40S ribosomal protein S23 >gi|6716785|gb|AAF26742.1|AF220539_1 40s ribosomal protein S23 [Euphorbia esula]	Unigene21062_All//1.00E-55//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene21062_All//1.00E-32//CD486290		ko03010|Ribosome		nr -
Unigene21063_All	1096	0.00	0.00	0.00	0.00	0.00	0.00	7.79	5.15	0.00	null	null		null	null		null	null		null	null		-5.98E-01	6.76E-04		-1.29E+01	7.14E-63	Down	Unigene21063_All//gi|3219280|dbj|BAA28834.1|//8.00E-98//delta-9 fatty acid desaturase [Cyanidioschyzon merolae]	Unigene21063_All//1.00E-26//AT1G06080| ADS1 (DELTA 9 DESATURASE 1); oxidoreductase			ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene21064_All	460	0.23	10.57	6.95	0.00	0.00	0.00	0.00	0.00	0.00	5.54E+00	1.09E-24	Up	4.93E+00	5.03E-15	Up	null	null		null	null		null	null		null	null		Unigene21064_All//gi|301121610|ref|XP_002908532.1|//8.00E-66//60S ribosomal protein L23 [Phytophthora infestans T30-4] >gi|66270163|gb|AAY43411.1| ribosomal protein L23 [Phytophthora infestans] >gi|262103563|gb|EEY61615.1| 60S ribosomal protein L23 [Phytophthora infestans T30-4]	Unigene21064_All//7.00E-59//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene21064_All//2.00E-12//gi|13246889|gb|BE052234.2|BE052234		ko03010|Ribosome		nr -
Unigene21065_All	373	2.81	1.63	0.29	2.40	1.94	1.33	0.45	0.56	0.85	-7.83E-01	2.34E-01		-3.30E+00	4.58E-04	Down	-3.10E-01	6.65E-01		-8.52E-01	2.63E-01		3.05E-01	8.36E-01		9.14E-01	4.53E-01				Unigene21065_All//1.00E-152//FL577049				

Unigene21067_All	1054	0.00	0.00	0.00	0.00	0.00	0.00	13.56	14.35	5.22	null	null		null	null		null	null		null	null		8.23E-02	6.21E-01		-1.38E+00	2.58E-22	Down	Unigene21067_All//gi|224123754|ref|XP_002319156.1|//3.00E-65//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222857532|gb|EEE95079.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene21067_All//7.00E-24//AT5G19790| RAP2.11 (related to AP2 11); DNA binding / transcription factor	Unigene21067_All//8.00E-08//gi|11206528|gb|BF275458.1|BF275458	AP2-EREBP			nr -
Unigene2107_All	2131	16.92	8.68	7.65	29.52	19.75	23.61	42.58	18.20	18.32	-9.63E-01	6.22E-25		-1.15E+00	1.14E-31	Down	-5.80E-01	6.69E-22		-3.23E-01	5.08E-07		-1.23E+00	3.11E-111	Down	-1.22E+00	5.26E-113	Down	Unigene2107_All//gi|15226618|ref|NP_182273.1|//0.00E+00//FUM1 (FUMARASE 1); catalytic/ fumarate hydratase [Arabidopsis thaliana] >gi|14531433|ref|NP_001078975.1| FUM1 (FUMARASE 1); catalytic/ fumarate hydratase [Arabidopsis thaliana] >gi|399931311|sp|P93033.2|FUM1_ARATH RecName: Full=Fumarate hydratase 1, mitochondrial; Short=Fumarase 1; Flags: Precursor >gi|2443751|gb|AAR71399.1| fumarase [Arabidopsis thaliana] >gi|15809968|gb|AAL06911.1| At2g47510/T30B22.19 [Arabidopsis thaliana]	Unigene2107_All//0.00E+00//AT2G47510| FUM1 (FUMARASE 1); catalytic/ fumarate hydratase	Unigene2107_All//0.00E+00//TC137905		ko00020|Citrate cycle (TCA cycle)	GO:0003006//GO:0005488//GO:0006970//GO:0009060//GO:0016836//GO:0043231//GO:0043648	nr +
Unigene21071_All	226	3.70	0.00	0.47	4.19	7.62	1.60	1.31	1.29	0.18	-1.19E+01	5.57E-05	Down	-2.97E+00	3.83E-03		8.63E-01	8.70E-02		-1.39E+00	6.08E-02		-1.66E-02	1.02E+00		-2.89E+00	6.76E-02									
Unigene21072_All	380	0.00	0.27	2.80	0.26	0.73	0.12	0.00	0.00	0.00	8.06E+00	3.87E-01		1.15E+01	6.62E-06	Up	1.47E+00	4.20E-01		-1.14E+00	6.77E-01		null	null		null	null		Unigene21072_All//gi|222834359|gb|EEE72836.1|//5.00E-18//predicted protein [Populus trichocarpa]						nr -
Unigene21077_All	540	0.19	0.00	0.00	0.28	0.13	0.25	6.97	3.56	1.18	-7.60E+00	3.73E-01		-7.60E+00	3.94E-01		-1.12E+00	5.84E-01		-1.41E-01	9.43E-01		-9.69E-01	6.21E-04		-2.56E+00	7.87E-14	Down	Unigene21077_All//gi|152925784|gb|ABS32110.1|//4.00E-55//aldehyde oxidase 3 [Pisum sativum]	Unigene21077_All//2.00E-51//AT1G04580| AAO4 (ARABIDOPSIS ALDEHYDE OXIDASE 4); aldehyde oxidase/ aryl-aldehyde oxidase	Unigene21077_All//3.00E-18//gi|5046767|gb|AI727915.1|AI727915		ko00230|Purine metabolism//ko04146|Peroxisome//ko00906|Carotenoid biosynthesis//ko00232|Caffeine metabolism		nr -
Unigene21079_All	456	0.00	0.00	0.00	0.00	0.00	0.00	4.36	3.57	0.00	null	null		null	null		null	null		null	null		-2.86E-01	5.28E-01		-1.21E+01	1.18E-14	Down	Unigene21079_All//gi|20140683|sp|Q94472.1|TCTP_SOYBN//2.00E-13//RecName: Full=Translationally-controlled tumor protein homolog; Short=TCTP >gi|16417595|gb|AAL18814.1|AF421558_1 translationally controlled tumor-like protein [Glycine max]	Unigene21079_All//1.00E-13//AT3G05540| INVOLVED IN: biological_process unknown; LOCATED IN: cytoplasm; CONTAINS InterPro DOMAIN/s: Translationally controlled tumour protein (InterPro:IPR018105), Translationally controlled tumour-associated TCTP (InterPro:IPR001983), Mss4/translationally controlled tumour-associated TCTP (InterPro:IPR011323), Translationally controlled tumour protein, conserved site (InterPro:IPR018103), Mss4-like (InterPro:IPR010657); BEST Arabidopsis thaliana protein match is: TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN) (TAIR:AT3G16640.1); Has 640 Blast hits to 640 proteins in 231 species: Archae - 0; Bacteria - 0; Metazoa - 343; Fungi - 110; Plants - 105; Viruses - 0; Other Eukaryotes - 82 (source: NCBI BLink).					nr -
Unigene21080_All	618	1.02	0.00	0.17	2.34	3.62	0.44	0.68	0.00	0.52	-9.99E+00	7.92E-04	Down	-2.56E+00	2.72E-02		6.32E-01	1.53E-01		-2.41E+00	1.41E-04	Down	-9.42E+00	3.25E-03		-4.08E-01	6.54E-01		Unigene21080_All//gi|15221989|ref|NP_175318.1|//1.00E-14//WD-40 repeat family protein [Arabidopsis thaliana] >gi|918805951|gb|ABE65704.1| WD-40 repeat family protein [Arabidopsis thaliana]	Unigene21080_All//1.00E-14//AT1G48870| WD-40 repeat family protein	Unigene21080_All//0.00E+00//TC147273				nr -
Unigene21081_All	895	0.00	16.19	6.49	0.00	0.00	0.05	0.00	0.00	0.00	1.40E+01	3.17E-83	Up	1.27E+01	2.41E-32	Up	null	null		5.66E+00	6.96E-01		null	null		null	null		Unigene21081_All//gi|195606690|gb|ACG25175.1|//3.00E-24//60S ribosomal protein L22-2 [Zea mays] >gi|195619566|gb|ACG31613.1| 60S ribosomal protein L22-2 [Zea mays]	Unigene21081_All//5.00E-18//AT3G05560| 60S ribosomal protein L22-2 (RPL22B)			ko03010|Ribosome		nr -
Unigene21084_All	414	2.02	1.47	2.06	14.32	9.40	6.11	0.92	1.01	0.48	-4.61E-01	5.43E-01		2.54E-02	9.93E-01		-6.07E-01	8.34E-03		-1.23E+00	5.12E-07	Down	1.36E-01	8.99E-01		-9.34E-01	3.79E-01		Unigene21084_All//gi|255546387|ref|XP_002514253.1|//5.00E-10//protein phosphatase 2c, putative [Ricinus communis] >gi|223546709|gb|EEF48207.1| protein phosphatase 2c, putative [Ricinus communis]		Unigene21084_All//2.00E-86//TC162642				nr +
Unigene21085_All	435	0.00	0.00	0.00	0.00	0.00	0.00	19.15	16.72	1.28	null	null		null	null		null	null		null	null		-1.96E-01	3.36E-01		-3.90E+00	5.21E-44	Down	Unigene21085_All//gi|147791048|emb|CAN65763.1|//2.00E-09//hypothetical protein [Vitis vinifera]		Unigene21085_All//2.00E-25//ES810763				nr +
Unigene21088_All	393	0.67	0.00	0.41	3.04	1.14	0.57	1.40	0.74	0.00	-9.38E+00	6.71E-02		-7.12E-01	6.22E-01		-1.42E+00	1.82E-02		-2.40E+00	7.07E-04	Down	-9.10E-01	3.19E-01		-1.04E+01	2.80E-04	Down								
Unigene21089_All	484	0.00	0.00	0.00	0.00	0.00	0.00	0.44	2.33	1.40	null	null		null	null		null	null		null	null		2.42E+00	3.17E-04	Up	1.68E+00	3.70E-02				Unigene21089_All//1.00E-20//ES819249				
Unigene21091_All	502	0.00	41.18	23.65	0.00	0.00	0.00	0.00	0.00	0.00	1.53E+01	5.87E-119	Up	1.45E+01	9.08E-67	Up	null	null		null	null		null	null		null	null		Unigene21091_All//gi|73761683|gb|AZ83341.1|//6.00E-71//ubiquitin extension protein [Gossypium hirsutum]	Unigene21091_All//4.00E-50//AT3G62250| UBQ5 (ubiquitin 5); protein binding / structural constituent of ribosome	Unigene21091_All//1.00E-14//TC153198		ko03010|Ribosome		nr -
Unigene21092_All	503	0.00	5.74	4.34	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.97E-16	Up	1.21E+01	4.95E-12	Up	null	null		null	null		null	null		null	null		Unigene21092_All//gi|50508930|dbj|BAD31835.1|//9.00E-06//putative high-affinity potassium transporter [Oryza sativa Japonica Group] >gi|215694830|dbj|BAG90021.1| unnamed protein product [Oryza sativa Japonica Group]						nr +
Unigene21094_All	512	0.61	0.99	1.14	0.39	1.01	0.71	0.91	4.08	7.24	6.91E-01	4.99E-01		9.00E-01	3.77E-01		1.37E+00	2.26E-01		8.59E-01	5.42E-01		2.17E+00	1.89E-06	Up	2.99E+00	1.16E-15	Up	Unigene21094_All//gi|226510391|ref|NP_001150862.1|//1.00E-09//LOC100284495 [Zea mays] >gi|195642440|gb|ACG40688.1| helix-loop-helix DNA-binding domain containing protein [Zea mays]	Unigene21094_All//6.00E-07//AT2G42280| basic helix-loop-helix (bHLH) family protein	Unigene21094_All//4.00E-39//TC132550	bHLH			nr +
Unigene21098_All	381	0.00	6.38	2.80	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	7.73E-14	Up	1.14E+01	6.62E-06	Up	null	null		null	null		null	null		null	null		Unigene21098_All//sp|Q9UNL2|SSRG_HUMAN//1.00E-29//Translocon-associated protein subunit gamma OS=Homo sapiens GN=SSR3 PE=1 SV=1						swissprot -
Unigene211_All	2786	8.34	13.09	13.72	14.38	22.58	24.30	4.57	5.64	12.35	6.51E-01	3.34E-13		7.19E-01	1.15E-15		6.52E-01	3.99E-26		7.57E-01	5.05E-33		3.04E-01	1.88E-02		1.44E+00	2.88E-55	Up	Unigene211_All//gi|224145021|ref|XP_002325498.1|//1.00E-104//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222862373|gb|EEE99879.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene211_All//2.00E-81//AT1G27180| disease resistance protein (TIR-NBS-LRR class), putative	Unigene211_All//1.00E-147//DW507651		ko04626|Plant-pathogen interaction		nr -
Unigene2110_All	2125	3.79	2.72	2.66	144.59	150.72	134.30	17.63	10.03	7.44	-4.80E-01	1.96E-02		-5.14E-01	1.66E-02		5.99E-02	4.87E-02		-1.07E-01	2.48E-04		-8.13E-01	5.99E-24		-1.24E+00	8.18E-49	Down	Unigene2110_All//gi|224139028|ref|XP_002322962.1|//0.00E+00//laccase 1b [Populus trichocarpa] >gi|222867592|gb|EEF04723.1| laccase 1b [Populus trichocarpa]	Unigene2110_All//0.00E+00//AT2G38080| IRX12 (IRREGULAR XYLEM 12); laccase	Unigene2110_All//0.00E+00//TC178660		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0009832//GO:0016682//GO:0031410//GO:0016914	nr +
Unigene21100_All	354	0.15	0.00	0.00	0.14	0.00	0.13	1.19	13.34	1.80	-7.21E+00	6.13E-01		-7.21E+00	6.25E-01		-7.14E+00	5.56E-01		-1.41E-01	9.53E-01		3.48E+00	3.55E-22	Up	5.92E-01	4.53E-01				Unigene21100_All//3.00E-125//BQ408652				
Unigene21101_All	425	0.00	17.64	9.52	0.12	0.00	0.00	0.00	0.00	0.19	1.41E+01	7.11E-43	Up	1.32E+01	1.92E-22	Up	-6.87E+00	5.56E-01		-6.87E+00	6.36E-01		null	null		7.55E+00	4.04E-01		Unigene21101_All//gi|301105188|ref|XP_002901678.1|//2.00E-47//60S ribosomal protein L32-1 [Phytophthora infestans T30-4] >gi|262100682|gb|EEY38734.1| 60S ribosomal protein L32-1 [Phytophthora infestans T30-4]	Unigene21101_All//1.00E-41//AT4G18100| 60S ribosomal protein L32 (RPL32A)			ko03010|Ribosome		nr -
Unigene21102_All	575	0.00	7.49	4.35	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.56E-24	Up	1.21E+01	8.33E-14	Up	null	null		null	null		null	null		null	null		Unigene21102_All//gi|15239735|ref|NP_200288.1|//4.00E-86//THI1; protein homodimerization [Arabidopsis thaliana] >gi|2501188|sp|Q38814.1|THI4_ARATH RecName: Full=Thiazole biosynthetic enzyme, chloroplastic; AltName: Full=ARA6; Flags: Precursor >gi|16226384|gb|AAL16153.1|AF428385_1 AT5g54770/MBG8_3 [Arabidopsis thaliana] >gi|16226866|gb|AAL16285.1|AF428355_1 AT5g54770/MBG8_3 [Arabidopsis thaliana] >gi|16930501|gb|AAL31936.1|AF419604_1 AT5g54770/MBG8_3 [Arabidopsis thaliana] >gi|1113783|gb|AAC97124.1| Thi1 protein [Arabidopsis thaliana] >gi|9758257|dbj|BAB08756.1| thiazole biosynthetic enzyme precursor (ARA6) [Arabidopsis thaliana] >gi|15809897|gb|AAL06876.1| AT5g54770/MBG8_3 [Arabidopsis thaliana] >gi|16604392|gb|AAL24202.1| AT5g54770/MBG8_3 [Arabidopsis thaliana]	Unigene21102_All//9.00E-79//AT5G54770| THI1; protein homodimerization	Unigene21102_All//2.00E-81//TC129728				nr +
Unigene21103_All	881	0.06	0.00	0.12	0.34	0.00	0.10	0.96	0.71	5.52	-5.89E+00	6.13E-01		1.03E+00	7.03E-01		-8.41E+00	2.01E-02		-1.73E+00	2.89E-01		-4.32E-01	5.47E-01		2.52E+00	4.40E-17	Up	Unigene21103_All//gi|222622434|gb|EEE56566.1|//4.00E-06//hypothetical protein Os_05904 [Oryza sativa Japonica Group]		Unigene21103_All//1.00E-37//gi|78324200|gb|DT544475.1|DT544475				nr -

Unigene21104_All	375	0.00	0.14	0.43	0.13	0.46	0.60	1.13	3.01	7.54	7.08E+00	6.17E-01		8.73E+00	2.39E-01		1.79E+00	5.20E-01		2.18E+00	3.23E-01		1.42E+00	1.72E-02		2.74E+00	3.79E-11	Up	Unigene21104_All//gi|30684587|ref|NP_180603.2|//2.00E-11//chloroplast thylakoidal processing peptidase [Arabidopsis thaliana] >gi|75276837|sp|Q04348.2|TPP1_ARATH RecName: Full=Thylakoidal processing peptidase 1, chloroplastic; AltName: Full=Signal peptidase I-1; Flags: Precursor >gi|2769566|emb|CAA71502.1| chloroplast thylakoidal processing peptidase [Arabidopsis thaliana] >gi|58652110|gb|AAW80880.1| At2g30440 [Arabidopsis thaliana]	Unigene21104_All//1.00E-12//AT1G06870| signal peptidase, putative	Unigene21104_All//5.00E-124//C0093587		ko03060|Protein export		nr +
Unigene21106_All	365	2.29	1.94	0.88	3.14	2.36	1.36	6.83	2.86	3.49	-2.39E-01	7.25E-01		-1.39E+00	9.66E-02		-4.12E-01	5.39E-01		-1.21E+00	6.46E-02		-1.26E+00	6.09E-04	Down	-9.69E-01	5.22E-03		Unigene21106_All//gi|40823305|gb|AA892274.1|//3.00E-16//At3g49310 [Arabidopsis thaliana] >gi|46518411|gb|AAS99687.1| At3g49310 [Arabidopsis thaliana]	Unigene21106_All//2.00E-17//AT3G49310| LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27720.1); Has 550 Blast hits to 545 proteins in 201 species: Archae - 5; Bacteria - 285; Metazoa - 85; Fungi - 33; Plants - 99; Viruses - 0; Other Eukaryotes - 43 (source: NCBI BLink).	Unigene21106_All//3.00E-51//TC154592				nr -
Unigene2111_All	216	1.70	0.00	0.74	2.08	1.28	1.05	3.52	2.13	0.37	-1.07E+01	1.97E-02		-1.20E+00	3.96E-01		-7.03E-01	5.30E-01		-9.90E-01	3.94E-01		-7.27E-01	3.32E-01		-3.26E+00	4.48E-04	Down			Unigene2111_All//3.00E-19//TC164314				
Unigene21119_All	399	0.13	0.76	2.67	1.12	0.78	1.25	2.12	1.47	0.90	2.54E+00	1.51E-01		4.35E+00	6.46E-05	Up	-5.33E-01	5.96E-01		1.48E-01	9.06E-01		-5.31E-01	4.45E-01		-1.24E+00	6.26E-02		Unigene21119_All//gi|37624222|gb|AAQ95646.1|//2.00E-28//transposase [Coix aquatica]	Unigene21119_All//2.00E-16//AT5G41980| unknown protein	Unigene21119_All//2.00E-123//ES838001				nr -
Unigene2112_All	1122	31.38	32.06	27.38	39.03	33.48	29.55	16.28	9.98	4.23	3.09E-02	7.57E-01		-1.97E-01	4.83E-02		-2.21E-01	5.01E-03		-4.02E-01	2.46E-07		-7.05E-01	1.24E-09		-1.95E+00	7.50E-46	Down			Unigene2112_All//4.00E-59//TC164314				
Unigene21121_All	455	0.00	0.45	3.51	3.28	1.36	0.69	1.30	0.92	0.53	8.80E+00	1.37E-01		1.18E+01	8.44E-09	Up	-1.27E+00	1.45E-02		-2.24E+00	2.25E-04	Down	-5.02E-01	5.74E-01		-1.31E+00	1.15E-01		Unigene21121_All//gi|16323222|gb|AAL15345.1|//4.00E-54//AT4g24430/T22A6_260 [Arabidopsis thaliana]	Unigene21121_All//3.00E-55//AT4G24430| lyase					nr -
Unigene21123_All	450	0.00	5.40	3.31	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.73E-14	Up	1.17E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene21123_All//gi|225440326|ref|XP_002263672.1|//3.00E-68//PREDICTED: similar to HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding isoform 2 [Vitis vinifera]	Unigene21123_All//6.00E-68//AT3G12580| HSP70 (heat shock protein 70); ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -
Unigene21125_All	637	0.00	12.81	7.69	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	1.14E-46	Up	1.29E+01	3.05E-27	Up	null	null		null	null		null	null		null	null		Unigene21125_All//sp|Q9VAJ4|OB99A_DROME//2.00E-23//General odorant-binding protein 99a OS=Drosophila melanogaster GN=Obp99a PE=1 SV=2						swissprot -
Unigene2113_All	2474	16.16	31.21	20.45	25.79	26.71	24.10	30.54	26.74	14.72	9.50E-01	2.98E-51		3.40E-01	9.54E-06		5.04E-02	5.39E-01		-9.81E-02	1.99E-01		-1.92E-01	4.84E-04		-1.05E+00	7.48E-75	Down	Unigene2113_All//gi|18410148|ref|NP_565045.1|//1.00E-113//TRFL6 (TRF-LIKE 6); DNA binding / transcription factor [Arabidopsis thaliana] >gi|15010654|gb|AAK73986.1| At1g72650/F28P22_16 [Arabidopsis thaliana] >gi|21700907|gb|AAM70577.1| At1g72650/F28P22_16 [Arabidopsis thaliana] >gi|416190044|gb|AAS10010.1| MYB transcription factor [Arabidopsis thaliana]	Unigene2113_All//7.00E-109//AT1G72650| TRFL6 (TRF-LIKE 6); DNA binding / transcription factor	Unigene2113_All//0.00E+00//TC178726	MYB-related		GO:0043229	nr -
Unigene21130_All	406	0.00	17.60	6.16	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	7.81E-41	Up	1.26E+01	8.33E-14	Up	null	null		null	null		null	null		null	null		Unigene21130_All//gi|145352014|ref|XP_001420354.1|//1.00E-21//Ribosomal protein L38, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901] >gi|144580588|gb|AB098647.1| Ribosomal protein L38, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901]	Unigene21130_All//1.00E-20//AT3G59540| 60S ribosomal protein L38 (RPL38B)			ko03010|Ribosome		nr -
Unigene21131_All	586	0.00	0.35	0.00	0.00	0.00	0.00	2.81	3.64	0.00	8.43E+00	1.37E-01		null	null		null	null		null	null		3.70E-01	3.84E-01		-1.15E+01	3.45E-12	Down	Unigene21131_All//gi|55168340|gb|AAV44205.1|//1.00E-24//unknow protein [Oryza sativa Japonica Group]		Unigene21131_All//6.00E-38//gi|109824085|gb|DW008930.1|DW008930				nr -
Unigene21132_All	327	0.00	5.89	2.93	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.73E-11	Up	1.15E+01	2.46E-05	Up	null	null		null	null		null	null		null	null								
Unigene21134_All	396	0.00	2.69	0.94	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.81E-06	Up	9.88E+00	2.50E-02		null	null		null	null		null	null		null	null								ESTscan +
Unigene21136_All	419	0.00	0.00	0.00	0.00	0.00	0.00	6.76	11.27	0.00	null	null		null	null		null	null		null	null		7.38E-01	2.82E-03		-1.27E+01	7.69E-21	Down			Unigene21136_All//8.00E-09//gi|11208661|gb|BF277591.1|BF277591				
Unigene21138_All	309	0.00	7.05	2.07	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.11E-12	Up	1.10E+01	1.16E-03		null	null		null	null		null	null		null	null								
Unigene2114_All	1453	6.63	5.27	6.23	15.84	11.28	4.82	14.64	35.29	7.90	-3.31E-01	8.06E-02		-8.88E-02	6.59E-01		-4.90E-01	2.98E-06		-1.72E+00	8.16E-42	Down	1.27E+00	1.29E-66	Up	-8.90E-01	1.23E-16		Unigene2114_All//gi|30682289|ref|NP_187876.2|//1.00E-33//aspartyl protease family protein [Arabidopsis thaliana] >gi|119944412|dbj|BAB02414.1| chloroplast nucleoid DNA binding protein-like [Arabidopsis thaliana]	Unigene2114_All//3.00E-31//AT3G12700| aspartyl protease family protein				GO:0016787	nr +
Unigene21142_All	383	0.00	0.00	0.00	0.00	0.00	0.00	4.08	4.69	0.00	null	null		null	null		null	null		null	null		2.00E-01	6.50E-01		-1.20E+01	1.42E-11	Down	Unigene21142_All//gi|297794223|ref|XP_002864996.1|//3.00E-34//60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|297310831|gb|EFH41255.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene21142_All//4.00E-35//AT3G49910| 60S ribosomal protein L26 (RPL26A)			ko03010|Ribosome		nr -
Unigene21145_All	561	0.00	6.23	3.13	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	6.73E-20	Up	1.16E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene21145_All//gi|300260051|gb|EFJ44273.1|//4.00E-06//hypothetical protein VOLCADRAFT_121342 [Volvox carteri f. nagariensis]						nr -
Unigene21146_All	906	0.06	0.00	0.00	0.55	0.15	0.15	1.73	0.37	0.88	-5.85E+00	6.13E-01		-5.85E+00	6.24E-01		-1.85E+00	8.43E-02		-1.88E+00	1.08E-01		-2.23E+00	3.66E-05	Down	-9.73E-01	3.21E-02		Unigene21146_All//gi|16326|emb|CAA49263.1|//2.00E-22//HAT 3.1 [Arabidopsis thaliana]	Unigene21146_All//1.00E-23//AT3G19510| HAT3.1; DNA binding / sequence-specific DNA binding / transcription activator/ transcription factor	Unigene21146_All//0.00E+00//TC178282	HB			nr +
Unigene2115_All	1812	6.70	5.42	4.56	14.27	10.41	2.89	26.39	54.16	9.54	-3.04E-01	6.96E-02		-5.57E-01	9.65E-04		-4.54E-01	3.97E-06		-2.30E+00	4.67E-69	Down	1.04E+00	6.65E-92	Up	-1.47E+00	9.04E-80	Down	Unigene2115_All//gi|30682289|ref|NP_187876.2|//1.00E-126//aspartyl protease family protein [Arabidopsis thaliana] >gi|119944412|dbj|BAB02414.1| chloroplast nucleoid DNA binding protein-like [Arabidopsis thaliana]	Unigene2115_All//1.00E-127//AT3G12700| aspartyl protease family protein	Unigene2115_All//0.00E+00//gi|11210072|gb|BF279002.1|BF279002				nr +
Unigene21150_All	618	0.00	0.00	0.00	0.00	0.00	0.00	5.06	10.42	3.16	null	null		null	null		null	null		null	null		1.04E+00	8.24E-07	Up	-6.81E-01	2.43E-02				Unigene21150_All//2.00E-139//TC142576				
Unigene21154_All	521	1.51	1.26	0.41	0.86	0.79	0.17	9.33	2.09	0.38	-2.53E-01	7.26E-01		-1.88E+00	4.13E-02		-1.18E-01	8.86E-01		-2.31E+00	7.81E-02		-2.16E+00	4.59E-14	Down	-4.61E+00	6.03E-29	Down	Unigene21154_All//gi|115450457|ref|NP_001048829.1|//3.00E-08//Os03g0126900 [Oryza sativa Japonica Group] >gi|113547300|dbj|BAF10743.1| Os03g0126900 [Oryza sativa Japonica Group]						nr -
Unigene21157_All	656	0.00	2.32	11.20	0.15	0.84	0.28	0.00	0.00	0.00	1.12E+01	1.10E-08	Up	1.35E+01	4.46E-41	Up	2.47E+00	4.05E-02		8.58E-01	6.95E-01		null	null		null	null		Unigene21157_All//gi|225703022|dbj|BAH00233.1|//3.00E-43//cytochrome c oxidase subunit II [Haptoglossa sp. SZ03]	Unigene21157_All//2.00E-19//ATMG00160| cytochrome c oxidase subunit 2			ko00190|Oxidative phosphorylation		nr +
Unigene21159_All	459	0.00	62.37	21.00	0.00	0.00	0.00	0.00	0.00	0.00	1.59E+01	5.05E-165	Up	1.44E+01	4.64E-54	Up	null	null		null	null		null	null		null	null		Unigene21159_All//gi|247421835|gb|ACS96145.1|//2.00E-58//S18.A ribosomal protein [Jatropha curcas]	Unigene21159_All//1.00E-58//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome	Unigene21159_All//1.00E-13//gi|18100852|gb|BM360106.1|BM360106		ko03010|Ribosome		nr +
Unigene21160_All	491	0.00	0.00	0.00	0.00	0.00	0.00	2.67	1.87	0.00	null	null		null	null		null	null		null	null		-5.11E-01	3.55E-01		-1.14E+01	9.85E-10	Down	Unigene21160_All//gi|301122631|ref|XP_002909042.1|//7.00E-43//40S ribosomal protein S6 [Phytophthora infestans T30-4] >gi|262099804|gb|EEY57856.1| 40S ribosomal protein S6 [Phytophthora infestans T30-4]	Unigene21160_All//2.00E-37//AT5G10360| EMB3010 (embryo defective 3010); structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene21163_All	549	0.38	14.40	16.97	0.18	0.63	0.41	2.08	0.46	0.36	5.24E+00	4.75E-39	Up	5.48E+00	7.31E-46	Up	1.79E+00	2.58E-01		1.18E+00	5.49E-01		-2.19E+00	6.83E-04	Down	-2.52E+00	1.20E-04	Down	Unigene21163_All//gi|238014838|gb|ACR38454.1|//6.00E-22//unknown [Zea mays]		Unigene21163_All//4.00E-33//TC144228				nr -
Unigene21164_All	504	0.42	4.73	0.63	0.49	0.68	1.25	0.67	1.58	1.58	3.51E+00	2.01E-09	Up	6.10E-01	6.25E-01		4.67E-01	7.29E-01		1.34E+00	1.74E-01		1.23E+00	9.04E-02		1.24E+00	7.69E-02				Unigene21164_All//2.00E-31//DW499420				
Unigene21166_All	416	0.50	0.49	0.77	3.11	0.66	0.33	0.41	0.20	0.29	-4.63E-02	9.88E-01		6.10E-01	6.25E-01		-2.23E+00	2.69E-04	Down	-3.26E+00	1.98E-05	Down	-1.02E+00	6.14E-01		-5.01E-01	7.46E-01				Unigene21166_All//5.00E-07//ES833590				
Unigene21167_All	304	0.00	0.00	0.00	0.33	0.00	0.00	4.45	5.50	1.18	null	null		null	null		-8.36E+00	3.13E-01		-8.36E+00	4.00E-01		3.05E-01	5.39E-01		-1.92E+00	4.37E-04	Down							
Unigene21170_All	384	0.00	0.00	0.00	0.00	0.00	0.00	8.92	4.24	0.73	null	null		null	null		null	null		null	null		-1.07E+00	3.71E-04	Down	-3.62E+00	1.97E-17	Down	Unigene21170_All//gi|79313961|ref|NP_001030789.1|//7.00E-12//AAA-type ATPase family protein [Arabidopsis thaliana]	Unigene21170_All//1.00E-10//AT3G28540| AAA-type ATPase family protein					nr +

Unigene21177_All	513	0.10	0.00	0.42	0.19	0.00	0.18	0.66	3.42	5.59	-6.67E+00	6.13E-01		2.03E+00	3.61E-01		-7.60E+00	3.13E-01		-1.41E-01	9.50E-01		2.38E+00	4.38E-06	Up	3.08E+00	1.30E-12	Up	Unigene21177_All//gi|124361158|gb|ABN09130.1|//2.00E-08//DC1; C1-like [Medicago truncatula]	Unigene21177_All//2.00E-11//AT2G16050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: DC1 (InterPro:IPR004146); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G20990.1); Has 719 Blast hits to 448 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 717; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).				nr +
Unigene21180_All	457	20.61	7.54	32.16	2.07	1.58	2.87	0.00	0.09	0.09	-1.45E+00	7.40E-13	Down	6.42E-01	2.06E-05		-3.88E-01	5.85E-01		4.69E-01	4.67E-01		6.52E+00	6.35E-01		6.45E+00	6.45E-01		Unigene21180_All//gi|159895667|gb|ABX10444.1|//3.00E-23//phosphoethanolamine N-methyltransferase [Gossypium hirsutum]	Unigene21180_All//8.00E-22//AT3G18000| XPL1 (XIPOTL 1); methyltransferase/ phosphoethanolamine N-methyltransferase	Unigene21180_All//2.00E-74//gi|13352266|gb|BG442614.1|BG442614		ko00564|Glycerophospholipid metabolism		nr +
Unigene21182_All	1231	0.00	0.00	0.09	9.83	9.62	3.96	0.00	0.10	0.00	null	null		6.43E+00	3.99E-01		-3.12E-02	8.67E-01		-1.31E+00	4.46E-15	Down	6.67E+00	2.40E-01		null	null		Unigene21182_All//gi|254935149|gb|ACT87982.1|//1.00E-129//gibberellin 2-oxidase [Jatropha curcas]	Unigene21182_All//1.00E-117//AT1G30040| ATGA2OX2 (GIBBERELLIN 2-OXIDASE); gibberellin 2-beta-dioxygenase	Unigene21182_All//3.00E-54//DW508045		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr -
Unigene21183_All	363	0.00	0.00	0.00	0.00	0.00	0.00	2.10	2.42	0.00	null	null		null	null		null	null		null	null		2.06E-01	7.54E-01		-1.10E+01	8.87E-06	Down	Unigene21183_All//gi|255071745|ref|XP_002499547.1|//2.00E-36//ribosomal protein L37e [Micromonas sp. RCC299] >gi|226514809|gb|ACO60805.1| ribosomal protein L37e [Micromonas sp. RCC299]	Unigene21183_All//6.00E-28//AT1G32300| 60S ribosomal protein L37 (RPL37B)			ko03010|Ribosome		nr -
Unigene21185_All	220	8.32	5.53	5.08	10.64	8.14	9.65	26.52	16.15	12.13	-5.91E-01	2.19E-01		-7.12E-01	1.56E-01		-3.87E-01	3.73E-01		-1.41E-01	7.41E-01		-7.16E-01	1.05E-03		-1.13E+00	2.81E-07	Down			Unigene21185_All//1.00E-110//gi|18098696|gb|BM357950.1|BM357950				
Unigene21186_All	351	2.24	0.00	1.37	3.12	0.49	0.90	0.12	0.00	0.11	-1.11E+01	1.09E-04	Down	-7.12E-01	3.89E-01		-2.67E+00	1.89E-04	Down	-1.79E+00	1.01E-02		-6.91E+00	6.57E-01		-8.63E-02	9.72E-01									
Unigene21189_All	285	1.47	0.00	0.00	5.42	3.02	1.27	1.63	0.15	0.84	-1.05E+01	1.05E-02		-1.05E+01	1.56E-02		-8.43E-01	1.01E-01		-2.10E+00	3.41E-04	Down	-3.48E+00	1.03E-02		-9.60E-01	3.13E-01		Unigene21189_All//gi|297828041|ref|XP_002881903.1|//1.00E-24//3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327742|gb|EFH58162.1| 3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene21189_All//4.00E-26//AT2G43420| 3-beta hydroxysteroid dehydrogenase/isomerase family protein	Unigene21189_All//4.00E-68//gi|78345401|gb|DT565675.1|DT565675		ko00100|Steroid biosynthesis		nr -
Unigene21190_All	340	0.00	2.68	2.51	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.62E-05	Up	1.13E+01	9.03E-05	Up	null	null		null	null		null	null		null	null		Unigene21190_All//gi|224013014|ref|XP_002295159.1|//5.00E-06//chitinase [Thalassiosira pseudonana CCMP1335] >gi|220969121|gb|EED87463.1| chitinase [Thalassiosira pseudonana CCMP1335]						nr -
Unigene21191_All	274	0.00	82.66	43.34	0.00	0.25	0.00	0.00	0.00	0.00	1.63E+01	2.14E-130	Up	1.54E+01	9.07E-67	Up	7.97E+00	6.10E-01		null	null		null	null		null	null		Unigene21191_All//gi|4139170|gb|AAD03711.1|//2.00E-35//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene21191_All//3.00E-33//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene21191_All//5.00E-43//TC166357				nr +
Unigene2120_All	1891	2.41	5.79	3.44	2.63	1.71	2.67	2.46	3.56	2.11	1.27E+00	4.08E-12	Up	5.13E-01	3.48E-02		-6.22E-01	1.49E-02		2.21E-02	9.48E-01		5.33E-01	8.59E-03		-2.23E-01	3.93E-01		Unigene2120_All//gi|15236546|ref|NP_194913.1|//1.00E-145//PGR3 (PROTON GRADIENT REGULATION 3) [Arabidopsis thaliana] >gi|75213543|sp|Q9SZ52.1|PP344_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g31850, chloroplastic; AltName: Full=Protein PROTON GRADIENT REGULATION 3; Flags: Precursor	Unigene2120_All//9.00E-146//AT4G31850| PGR3 (PROTON GRADIENT REGULATION 3)	Unigene2120_All//0.00E+00//TC145494				nr -
Unigene21200_All	1518	0.00	0.00	0.00	0.00	0.09	0.00	4.96	0.17	1.36	null	null		null	null		6.50E+00	3.19E-01		null	null		-4.91E+00	1.60E-44	Down	-1.86E+00	2.66E-18	Down	Unigene21200_All//gi|115474639|ref|NP_001060916.1|//1.00E-96//Os08g0129600 (Oryza sativa Japonica Group) >gi|29467527|dbj|BAC66716.1| proline-rich protein family-like [Oryza sativa Japonica Group] >gi|113622885|dbj|BAF22830.1| Os08g0129600 (Oryza sativa Japonica Group)	Unigene21200_All//5.00E-41//AT4G18570| proline-rich family protein					nr +
Unigene21201_All	318	0.66	0.32	0.00	0.78	1.62	0.57	1.99	0.13	0.63	-1.05E+00	5.65E-01		-9.36E+00	1.46E-01		1.05E+00	3.49E-01		-4.63E-01	7.44E-01		-3.92E+00	9.81E-04	Down	-1.67E+00	4.29E-02		Unigene21201_All//gi|122232354|sp|Q2ABE5.1|RBR_CAMSI//2.00E-38//RecName: Full=Retinoblastoma-related protein >gi|89111303|dbj|BAE80326.1| retinoblastoma related protein [Camellia sinensis]	Unigene21201_All//2.00E-33//AT3G12280| RBR1 (RETINOBLASTOMA-RELATED 1); transcription factor binding	Unigene21201_All//3.00E-165//TC134014				nr -
Unigene21202_All	1076	0.00	35.13	13.56	0.05	0.00	0.00	0.00	0.00	0.00	1.51E+01	3.87E-218	Up	1.37E+01	3.22E-82	Up	-5.53E+00	5.56E-01		-5.53E+00	6.36E-01		null	null		null	null		Unigene21202_All//gi|226457728|gb|EEH55026.1|//2.00E-13//glycoside hydrolase family 13 protein [Micromonas pusilla CCMP1545]	Unigene21202_All//3.00E-05//AT2G39930| ISA1 (ISOAMYLASE 1); alpha-amylase/ isoamylase			ko00500|Starch and sucrose metabolism		nr +
Unigene21203_All	645	0.00	29.85	0.50	2.01	1.39	6.23	0.00	0.00	0.06	1.49E+01	9.35E-111	Up	8.95E+00	4.52E-02		-5.33E-01	3.71E-01		1.63E+00	3.93E-07	Up	null	null		5.95E+00	6.45E-01		Unigene21203_All//gi|224056198|ref|XP_002298751.1|//2.00E-12//predicted protein [Populus trichocarpa] >gi|222846009|gb|EEE83556.1| predicted protein [Populus trichocarpa]		Unigene21203_All//0.00E+00//DW499583				nr +
Unigene21204_All	577	0.00	52.43	17.26	0.00	0.00	0.00	0.00	0.00	0.00	1.57E+01	2.04E-174	Up	1.41E+01	7.07E-56	Up	null	null		null	null		null	null		null	null		Unigene21204_All//gi|112253389|gb|AB114282.1|//8.00E-72//cyclophilin-like protein [Pfiesteria piscicida] >gi|112253391|gb|AB114283.1| cyclophilin-like protein [Pfiesteria piscicida] >gi|112253393|gb|AB114284.1| cyclophilin-like protein [Pfiesteria piscicida]	Unigene21204_All//2.00E-69//AT4G38740| ROC1 (ROTAMASE CYP 1); peptidyl-prolyl cis-trans isomerase	Unigene21204_All//5.00E-11//gi|48739115|gb|CO069634.1|CO069634				nr +
Unigene21205_All	562	0.00	5.41	3.98	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.67E-17	Up	1.20E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene21205_All//gi|158341664|ref|NP_001103449.1|//3.00E-36//ras-related protein Rab-1B [Rattus norvegicus] >gi|149042337|gb|EDL96044.1| rCG63295 [Rattus norvegicus] >gi|149062037|gb|EDM12460.1| rCG48149, isoform CRA_b [Rattus norvegicus]	Unigene21205_All//3.00E-35//AT1G02130| ARA-5 (ARABIDOPSIS RAS 5); GTP binding	Unigene21205_All//3.00E-15//gi|48798482|gb|CO099796.1|CO099796				nr -
Unigene21206_All	542	0.19	0.00	0.00	6.53	4.13	1.33	0.00	0.08	0.15	-7.59E+00	3.72E-01		-7.59E+00	3.94E-01		-6.60E-01	3.53E-02		-2.29E+00	8.64E-10	Down	6.27E+00	6.35E-01		7.20E+00	4.04E-01		Unigene21206_All//gi|225450273|ref|XP_002267267.1|//4.00E-24//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene21206_All//6.00E-10//AT2G31930| unknown protein	Unigene21206_All//0.00E+00//TC165623				nr -
Unigene21216_All	432	0.24	1.06	0.00	0.92	0.96	1.15	2.25	0.10	4.24	2.12E+00	9.59E-02		-7.92E+00	3.94E-01		5.22E-02	9.89E-01		3.18E-01	7.58E-01		-4.54E+00	6.92E-06	Down	9.14E-01	2.82E-02		Unigene21216_All//gi|224071947|ref|XP_002303599.1|//2.00E-59//tir-nbs resistance protein [Populus trichocarpa] >gi|222841031|gb|EEE78578.1| tir-nbs resistance protein [Populus trichocarpa]	Unigene21216_All//1.00E-55//AT4G23440| nucleoside-triphosphatase/ nucleotide binding / transmembrane receptor					nr +
Unigene21218_All	378	0.00	1.88	0.00	1.05	0.82	0.84	0.56	0.77	1.48	1.09E+01	3.33E-04	Up	null	null		-3.63E-01	7.54E-01		-3.34E-01	7.57E-01		4.69E-01	7.06E-01		1.40E+00	1.12E-01									
Unigene2122_All	1538	260.58	221.42	146.04	96.84	173.43	161.92	15.01	6.55	21.08	-2.35E-01	2.41E-21		-8.35E-01	1.49E-206		8.41E-01	4.89E-171		7.42E-01	6.02E-116		-1.20E+00	8.12E-28	Down	4.90E-01	3.14E-09		Unigene2122_All//gi|164472579|gb|AB158971.1|//7.00E-51//jasmonate ZIM-domain protein 3 [Solanum lycopersicum]	Unigene2122_All//2.00E-38//AT3G17860| JAZ3 (JASMONATE-ZIM-DOMAIN PROTEIN 3)	Unigene2122_All//0.00E+00//TC134684	Tify	ko04626|Plant-pathogen interaction		nr -
Unigene21221_All	224	0.00	0.45	0.00	4.67	3.07	0.60	0.19	0.00	0.18	8.82E+00	3.87E-01		null	null		-6.03E-01	3.67E-01		-2.95E+00	3.82E-04	Down	-7.56E+00	6.57E-01		-8.58E-02	9.72E-01									
Unigene21222_All	605	0.00	1.17	0.18	0.33	0.23	0.00	1.19	3.39	2.44	1.02E+01	3.33E-04	Up	7.46E+00	3.99E-01		-5.33E-01	7.49E-01		-8.36E+00	1.34E-01		1.51E+00	3.42E-04	Up	1.04E+00	2.97E-02		Unigene21222_All//gi|255584505|ref|XP_002532981.1|//3.00E-64//conserved hypothetical protein [Ricinus communis] >gi|223527245|gb|EEF29405.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene21227_All	368	0.71	5.78	5.79	0.00	0.37	0.00	0.00	0.00	0.00	3.02E+00	1.63E-07	Up	3.03E+00	3.19E-07	Up	8.55E+00	3.19E-01		null	null		null	null		null	null				Unigene21227_All//2.00E-132//gi|78332505|gb|DT552779.1|DT552779				
Unigene2123_All	1432	18.27	12.77	13.42	26.65	28.62	22.64	19.13	11.06	8.96	-5.16E-01	1.10E-06		-4.45E-01	5.18E-05		1.03E-01	2.99E-01		-2.35E-01	8.05E-03		-7.90E-01	6.35E-17		-1.09E+00	1.82E-29	Down	Unigene2123_All//gi|15237607|ref|NP_196026.1|//1.00E-159//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75181220|sp|Q9LZA4.1|PMT7_ARATH RecName: Full=Probable methyltransferase PMT7 >gi|18086557|gb|AAL57703.1| AT5g04060/F8F6_270 [Arabidopsis thaliana]	Unigene2123_All//2.00E-153//AT5G04060| dehydration-responsive protein-related	Unigene2123_All//0.00E+00//TC170620				nr -
Unigene21230_All	365	0.00	23.46	15.03	0.00	0.00	0.12	0.00	0.00	0.00	1.45E+01	5.27E-49	Up	1.39E+01	1.52E-30	Up	null	null		6.95E+00	6.96E-01		null	null		null	null		Unigene21230_All//gi|115470525|ref|NP_001058861.1|//4.00E-07//Os07g0139600 (Oryza sativa Japonica Group) >gi|113610397|dbj|BAF20775.1| Os07g0139600 (Oryza sativa Japonica Group)		Unigene21230_All//2.00E-09//DW511047		ko03010|Ribosome		nr -
Unigene21231_All	304	0.00	2.17	0.88	0.00	0.45	0.00	0.00	0.00	0.00	1.11E+01	6.26E-04	Up	9.77E+00	8.02E-02		8.82E+00	3.19E-01		null	null		null	null		null	null									ESTscan -
Unigene21232_All	263	0.80	0.00	1.21	0.19	0.65	0.34	13.66	19.86	3.79	-9.64E+00	1.22E-01		6.10E-01	6.25E-01		1.79E+00	5.20E-01		8.59E-01	7.94E-01		5.40E-01	2.18E-02		-1.85E+00	4.08E-09	Down								

Unigene21238_All	475	0.00	0.00	0.00	0.00	0.00	0.00	5.96	5.90	0.17	null	null		null	null		null	null		null	null		-1.66E-02	9.96E-01		-5.15E+00	4.64E-18	Down	Unigene21238_All//gi|301111414|ref|XP_002904786.1|//4.00E-56//ribosomal protein L27 [Phytophthora infestans T30-4] >gi|66270187|gb|AAY43423.1| ribosomal protein L27 [Phytophthora infestans] >gi|262095116|gb|EEY53168.1| ribosomal protein L27 [Phytophthora infestans T30-4]	Unigene21238_All//1.00E-38//AT1G70600| structural constituent of ribosome			ko03010|Ribosome		nr -
Unigene2124_All	2381	8.44	3.92	6.53	13.79	15.72	16.20	8.86	5.49	5.50	-1.11E+00	1.02E-17	Down	-3.70E-01	4.14E-03		1.89E-01	3.60E-02		2.33E-01	8.53E-03		-6.90E-01	1.34E-10		-6.87E-01	7.19E-11		Unigene2124_All//gi|15237607|ref|NP_196026.1|//0.00E+00//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75181220|sp|Q9LZA4.1|PMT7_ARATH RecName: Full=Probable methyltransferase PMT7 >gi|18086552|gb|AAL57703.1| AT5g04060/F8F6_270 [Arabidopsis thaliana]	Unigene2124_All//0.00E+00//AT3G10200| dehydration-responsive protein-related	Unigene2124_All//0.00E+00//gi|164249419|gb|ES828952.1|ES828952		GO:0043231	nr -
Unigene21242_All	364	1.01	0.56	0.00	1.37	2.18	0.74	3.14	0.34	1.75	-8.54E-01	4.89E-01		-9.97E+00	2.78E-02		6.69E-01	4.42E-01		-8.78E-01	4.20E-01		-3.19E+00	1.96E-05	Down	-8.41E-01	1.23E-01		Unigene21242_All//gi|297828838|ref|XP_002882301.1|//2.00E-41//C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328414|gb|EFH58560.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene21242_All//9.00E-43//AT3G03680| C2 domain-containing protein	Unigene21242_All//7.00E-09//gi|78330459|gb|DT550733.1|DT550733				nr +
Unigene21245_All	328	0.64	0.00	0.65	7.75	2.83	1.10	0.00	0.00	0.00	-9.32E+00	1.22E-01		2.53E-02	1.00E+00		-1.45E+00	1.36E-04	Down	-2.81E+00	6.58E-09	Down	null	null		null	null		Unigene21245_All//gi|133925931|gb|AB043717.1|//3.00E-50//profilin [Gossypium hirsutum] >gi|133925933|gb|AB043718.1| profilin [Gossypium hirsutum] >gi|133925935|gb|AB043719.1| profilin [Gossypium hirsutum] >gi|260871353|gb|ACX53268.1| profilin [Gossypium raimondii] >gi|260871355|gb|ACX53269.1| profilin [Gossypium arboreum]	Unigene21245_All//7.00E-42//AT4G29340| PRF4 (PROFILIN 4); actin binding	Unigene21245_All//2.00E-80//TC154043				nr +
Unigene21246_All	456	0.57	0.00	0.00	0.44	0.45	0.40	2.32	2.84	0.44	-9.16E+00	6.71E-02		-9.16E+00	8.58E-02		5.22E-02	9.89E-01		-1.41E-01	9.35E-01		2.94E-01	6.23E-01		-2.41E+00	3.46E-04	Down		Unigene21246_All//5.00E-07//DW482420					
Unigene21248_All	1182	0.00	0.00	0.00	0.00	0.00	0.00	4.97	7.35	0.00	null	null		null	null		null	null		null	null		5.65E-01	1.21E-03		-1.23E+01	3.15E-43	Down	Unigene21248_All//gi|4139170|gb|AAD03711.1|//1.00E-134//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene21248_All//1.00E-130//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene21248_All//2.00E-24//CD809343				nr -
Unigene21250_All	450	0.23	0.00	0.00	3.99	2.60	0.60	0.38	0.19	0.00	-7.86E+00	3.72E-01		-7.86E+00	3.94E-01		-6.15E-01	2.02E-01		-2.73E+00	2.99E-06	Down	-1.02E+00	6.14E-01		-8.55E+00	1.08E-01		Unigene21250_All//gi|255563510|ref|XP_002522757.1|//2.00E-17//conserved hypothetical protein [Ricinus communis] >gi|223537995|gb|EEF39608.1| conserved hypothetical protein [Ricinus communis]		Unigene21250_All//0.00E+00//TC169521				nr +
Unigene21253_All	614	0.77	0.41	0.52	2.68	0.62	1.10	0.90	0.41	0.00	-8.94E-01	3.89E-01		-5.59E-01	6.28E-01		-2.12E+00	5.46E-05	Down	-1.28E+00	1.42E-02		-1.13E+00	2.18E-01		-9.81E+00	2.80E-04	Down	Unigene21253_All//gi|124359162|gb|ABN05685.1|//2.00E-36//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene21253_All//3.00E-12//ATMG01250| hypothetical protein					nr +
Unigene21254_All	540	0.68	0.66	0.59	0.37	0.45	0.25	1.80	3.48	5.09	-4.63E-02	9.82E-01		-1.97E-01	8.66E-01		2.75E-01	8.95E-01		-5.57E-01	7.33E-01		9.52E-01	2.51E-02		1.50E+00	1.77E-05	Up		Unigene21254_All//6.00E-07//TC175034					
Unigene21259_All	1283	0.00	0.00	0.00	0.00	0.00	0.00	4.32	4.92	0.00	null	null		null	null		null	null		null	null		1.88E-01	4.22E-01		-1.21E+01	9.82E-41	Down	Unigene21259_All//gi|222836332|gb|EEE74739.1|//6.00E-06//predicted protein [Populus trichocarpa]		Unigene21259_All//4.00E-10//TC152783				nr -
Unigene21260_All	584	0.00	14.06	14.50	0.00	0.06	0.00	0.07	0.00	0.00	1.38E+01	5.84E-47	Up	1.38E+01	2.05E-47	Up	5.88E+00	8.30E-01		null	null		-6.18E+00	6.57E-01		-6.18E+00	6.13E-01		Unigene21260_All//gi|226530763|ref|NP_001151702.1|//4.00E-81//60S ribosomal protein L11 [Zea mays] >gi|195649157|gb|ACG44046.1| 60S ribosomal protein L11 [Zea mays]	Unigene21260_All//2.00E-68//AT2G42740| RPL16A; structural constituent of ribosome	Unigene21260_All//1.00E-08//EV498971		ko03010|Ribosome		nr -
Unigene21261_All	845	0.00	0.00	0.00	0.00	0.00	0.00	10.06	0.74	4.29	null	null		null	null		null	null		null	null		-3.76E+00	3.44E-42	Down	-1.23E+00	1.49E-11	Down	Unigene21261_All//gi|38564292|gb|AAR23725.1|//5.00E-40//At5g62280 [Arabidopsis thaliana] >gi|45592914|gb|AAS68111.1| At5g62280 [Arabidopsis thaliana]	Unigene21261_All//2.00E-37//AT5G62280| unknown protein					nr -
Unigene21262_All	1651	0.60	0.00	0.13	0.15	0.10	0.19	5.35	0.51	1.57	-9.23E+00	7.46E-06	Down	-2.22E+00	7.49E-03		-5.33E-01	7.13E-01		3.44E-01	7.97E-01		-3.40E+00	2.37E-40	Down	-1.77E+00	5.48E-20	Down	Unigene21262_All//gi|88433803|dbj|BAS97351.1|//0.00E+00//protein kinase [Arabidopsis thaliana]	Unigene21262_All//0.00E+00//AT5G40030| protein kinase, putative	Unigene21262_All//0.00E+00//TC171959				nr +
Unigene21263_All	529	0.00	76.53	34.63	0.00	0.00	0.00	0.00	0.00	0.00	1.62E+01	1.08E-233	Up	1.51E+01	1.89E-103	Up	null	null		null	null		null	null		null	null		Unigene21263_All//gi|50843988|gb|AT84169.1|//1.00E-36//60S ribosomal protein L27 [Chara globularis]	Unigene21263_All//3.00E-26//AT2G32220| 60S ribosomal protein L27 (RPL27A)			ko03010|Ribosome		nr -
Unigene21266_All	295	0.35	2.92	6.32	0.51	2.33	1.99	0.00	0.00	0.00	3.04E+00	1.94E-03		4.15E+00	4.39E-08	Up	2.20E+00	2.71E-02		1.97E+00	7.00E-02		null	null		null	null		Unigene21266_All//gi|255586613|ref|XP_002533939.1|//3.00E-06//Metalloendoproteinase 1 precursor, putative [Ricinus communis] >gi|223526094|gb|EEF28446.1| Metalloendoproteinase 1 precursor, putative [Ricinus communis]						nr -
Unigene21267_All	460	0.34	2.64	1.50	0.22	0.07	0.00	0.00	0.00	0.00	2.95E+00	1.75E-04	Up	2.14E+00	3.67E-02		-1.53E+00	5.86E-01		-7.76E+00	4.00E-01		null	null		null	null		Unigene21267_All//gi|170576371|ref|XP_001890602.1|//2.00E-06//resolvase [Brugia malayi] >gi|37496517|emb|CAD50592.1| resolvase [Cloning vector pUvBBAC] >gi|158600296|gb|EDP37566.1| resolvase [Brugia malayi]						nr +
Unigene21269_All	1162	0.00	0.00	0.00	0.26	0.00	0.00	47.01	0.50	4.01	null	null		null	null		-8.01E+00	2.01E-02		-8.01E+00	4.00E-02		-6.54E+00	0.00E+00	Down	-3.55E+00	1.19E-264	Down	Unigene21269_All//gi|18379010|ref|NP_563662.1|//1.00E-142//pectinesterase family protein [Arabidopsis thaliana] >gi|75313808|sp|Q9SRX4.1|PME7_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 7; Includes: RecName: Full=Pectinesterase inhibitor 7; AltName: Full=Pectin methylesterase inhibitor 7; Includes: RecName: Full=Pectinesterase 7; Short=PE 7; AltName: Full=Pectin methylesterase 7; AltName: Full=Pectin methylesterase 1; Short=AtPME1; Flags: Precursor >gi|6056422|gb|AAF02886.1|AC009525_20 Similar to pectinesterases [Arabidopsis thaliana] >gi|133778888|gb|ABO38784.1| At1g02810 [Arabidopsis thaliana]	Unigene21269_All//2.00E-143//AT1G02810| pectinesterase family protein	Unigene21269_All//5.00E-139//TC138774		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene21270_All	715	0.00	213.52	73.28	0.00	0.10	0.00	0.00	0.00	0.00	1.77E+01	0.00E+00	Up	1.62E+01	4.98E-298	Up	6.59E+00	6.10E-01		null	null		null	null		null	null		Unigene21270_All//sp|Q04691|FBP1_DROME//2.00E-18//Fat-body protein 1 OS=Drosophila melanogaster GN=Fbp1 PE=2 SV=2						swissprot +
Unigene21272_All	216	11.38	5.16	4.44	12.22	5.58	0.84	2.74	1.35	0.00	-1.14E+00	5.46E-03		-1.36E+00	1.89E-03		-1.13E+00	1.99E-03		-3.87E+00	3.85E-12	Down	-1.02E+00	2.40E-01		-1.14E+01	1.41E-04	Down		Unigene21272_All//5.00E-30//EX163928					
Unigene21277_All	562	0.09	8.57	2.46	0.00	0.00	0.00	0.00	0.00	0.00	6.52E+00	8.98E-26	Up	4.73E+00	1.57E-06	Up	null	null		null	null		null	null		null	null		Unigene21277_All//gi|194476620|ref|YP_002048799.1|//2.00E-21//tRNA (guanine-N(1)-)-methyltransferase [Pauliinella chromatophora] >gi|171191627|gb|ACB42589.1| tRNA (guanine-N(1)-)-methyltransferase [Pauliinella chromatophora]						nr +
Unigene21278_All	313	0.00	16.19	5.78	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	6.88E-29	Up	1.25E+01	5.69E-10	Up	null	null		null	null		null	null		null	null		Unigene21278_All//gi|299117091|emb|CBN73862.1|//3.00E-12//Novel Sm-like protein with long N-and C-terminal domains. [Ectocarpus siliculosus]	Unigene21278_All//3.00E-13//AT1G26110| unknown protein					nr -
Unigene21279_All	311	0.00	4.07	0.51	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.86E-07	Up	9.00E+00	2.39E-01		null	null		null	null		null	null		null	null		Unigene21279_All//gi|298711480|emb|CBJ26568.1|//5.00E-07//Fatty acid elongase [Ectocarpus siliculosus]						nr -
Unigene2128_All	430	110.00	230.84	177.21	153.61	124.21	161.54	268.43	599.04	335.29	1.07E+00	1.00E-79	Up	6.88E-01	2.02E-28		-3.07E-01	2.36E-07		7.26E-02	3.51E-01		1.16E+00	4.59E-287	Up	3.21E-01	1.01E-17		Unigene2128_All//gi|4150974|emb|CAA11899.1|//1.00E-21//cystatin [Castanea sativa]	Unigene2128_All//4.00E-17//AT2G40880| ATCYSA (CYSTATIN A); cysteine-type endopeptidase inhibitor	Unigene2128_All//0.00E+00//gi|84169186|gb|DR457834.1|DR457834			GO:0004866//GO:0016787	nr +
Unigene21286_All	448	0.00	12.10	9.98	0.00	0.15	0.00	0.00	0.00	0.18	1.36E+01	6.35E-31	Up	1.33E+01	7.76E-25	Up	7.26E+00	6.10E-01		null	null		null	null		7.47E+00	4.04E-01		Unigene21286_All//gi|301095995|ref|XP_002897096.1|//2.00E-55//40S ribosomal protein S15a [Phytophthora infestans T30-4] >gi|262107415|gb|EEY65467.1| 40S ribosomal protein S15a [Phytophthora infestans T30-4]	Unigene21286_All//2.00E-55//AT5G59850| 40S ribosomal protein S15A (RPS15aF)	Unigene21286_All//8.00E-09//EX170100		ko03010|Ribosome		nr -
Unigene21287_All	986	0.00	16.08	3.78	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	3.99E-91	Up	1.19E+01	1.20E-20	Up	null	null		null	null		null	null		null	null		Unigene21287_All//gi|115446071|ref|NP_001046815.1|//2.00E-14//Os02g0467200 [Oryza sativa Japonica Group] >gi|113536346|dbj|BAF08729.1| Os02g0467200 [Oryza sativa Japonica Group]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene21288_All	344	43.20	37.56	18.11	35.33	33.03	45.69	103.86	38.52	24.32	-2.02E-01	1.97E-01		-1.25E+00	2.41E-15	Down	-9.71E-02	6.01E-01		3.71E-01	9.14E-03		-1.43E+00	5.78E-56	Down	-2.09E+00	7.34E-98	Down	Unigene21288_All//gi|40287504|gb|AAR83866.1|//1.00E-07//40S ribosomal protein S17 [Capsicum annuum]	Unigene21288_All//4.00E-05//AT5G04800| 40S ribosomal protein S17 (RPS17D)	Unigene21288_All//3.00E-97//gi|11201772|gb|BF270777.1|BF270777		ko03010|Ribosome		nr +
Unigene21289_All	390	116.58	68.08	126.84	0.77	4.50	2.08	0.00	0.00	0.00	-7.76E-01	6.85E-22		1.22E-01	1.58E-01		2.55E+00	7.87E-06	Up	1.44E+00	8.45E-02		null	null		null	null		Unigene21289_All//gi|22531014|gb|AAM97011.1|//4.00E-41//expressed protein [Arabidopsis thaliana] >gi|231997966|gb|AAN15510.1| expressed protein [Arabidopsis thaliana]	Unigene21289_All//7.00E-41//AT1G08380| PSAO (photosystem I subunit O)	Unigene21289_All//2.00E-135//TC178284				nr +
Unigene2129_All	2336	1.43	5.42	1.44	2.37	1.56	2.15	9.41	14.94	11.68	1.92E+00	7.66E-25	Up	2.70E-03	9.92E-01		-5.99E-01	1.27E-02		-1.41E-01	6.20E-01		6.67E-01	4.86E-16		3.12E-01	6.43E-04			Unigene2129_All//0.00E+00//CO113753					
Unigene21291_All	460	9.21	31.72	12.97	6.17	18.64	19.05	8.18	23.71	13.94	1.78E+00	7.04E-26	Up	4.93E-01	5.40E-02		1.59E+00	3.37E-15	Up	1.63E+00	8.93E-15	Up	1.54E+00	1.89E-19	Up	7.69E-01	1.45E-04			Unigene21291_All//2.00E-117//gi|164348505|gb|EX165275.1|EX165275					

Unigene21292_A11	932	0.00	0.00	0.00	0.00	0.00	0.00	0.54	2.51	4.66	null	null		null	null		null	null		null	null		2.21E+00	2.81E-07	Up	3.10E+00	8.00E-19	Up	Unigene21292_A11//gi|15223140|ref|NP_177795.1|//4.00E-96//OPR2 [Arabidopsis thaliana] >gi|62900694|sp|Q8GYB8.2|OPR2_ARATH RecName: Full=12-oxophytodienoate reductase 2; AltName: Full=12-oxophytodienoate-10,11-reductase 2; Short=OPDA-reductase 2; Short=AtOPR2 >gi|6143903|gb|AAF04449.1|AC010718_18 12-oxophytodienoate reductase (OPR2); 15748-17127 [Arabidopsis thaliana] >gi|3882356|gb|AAC78441.1| 12-oxophytodienoate reductase OPR2 [Arabidopsis thaliana] >gi|94442433|gb|ABF19004.1| At1g76690 [Arabidopsis thaliana]	Unigene21292_A11//5.00E-98//AT1G76690| OPR2	Unigene21292_A11//8.00E-14//TC146365		ko00592|alpha-Linolenic acid metabolism		nr -
Unigene21293_A11	347	0.00	1.02	0.00	0.00	0.00	0.26	0.12	2.53	1.95	1.00E+01	2.46E-02		null	null		null	null		8.02E+00	4.77E-01		4.38E+00	3.08E-05	Up	4.00E+00	4.29E-04	Up								
Unigene21298_A11	467	0.00	8.68	8.21	0.00	0.00	0.00	0.00	0.00	0.09	1.31E+01	4.39E-23	Up	1.30E+01	3.02E-21	Up	null	null		null	null		null	null		6.41E+00	6.45E-01		Unigene21298_A11//gi|145344703|ref|XP_001416866.1|//3.00E-45//Ribosomal protein S20, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901] >gi|144577092|gb|ABO95159.1| Ribosomal protein S20, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901]	Unigene21298_A11//5.00E-43//AT5G62300| 40S ribosomal protein S20 (RPS20C)	Unigene21298_A11//9.00E-09//TC162279		ko03010|Ribosome		nr +
Unigene21299_A11	825	0.00	0.00	0.00	0.00	0.00	0.00	4.77	7.40	0.19	null	null		null	null		null	null		null	null		6.34E-01	2.95E-03		-4.62E+00	1.50E-23	Down				Unigene21299_A11//2.00E-07//TC154839				
Unigene213_A11	911	5.74	4.12	4.85	8.15	10.17	12.49	18.80	8.40	14.69	-4.81E-01	6.82E-02		-2.43E-01	3.82E-01		3.20E-01	1.04E-01		6.17E-01	1.92E-04		-1.16E+00	5.95E-20	Down	-3.55E-01	2.50E-03		Unigene213_A11//9.00E-87//AT2G05710| aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative	Unigene213_A11//0.00E+00//TC149649		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene21300_A11	290	0.18	0.00	0.00	0.00	1.90	3.43	0.29	0.43	0.96	-7.50E+00	6.12E-01		-7.50E+00	6.24E-01		1.09E+01	2.02E-03		1.17E+01	6.14E-06	Up	5.68E-01	7.82E-01		1.72E+00	2.30E-01									
Unigene21302_A11	810	0.45	0.00	0.53	0.37	0.94	0.22	12.74	1.50	0.39	-8.82E+00	1.97E-02		2.18E-01	8.31E-01		-3.12E+00	7.56E-02		-7.27E-01	6.39E-01		-3.09E+00	5.02E-43	Down	-5.02E+00	8.78E-64	Down				Unigene21302_A11//1.00E-52//TC134383				
Unigene21304_A11	606	0.00	0.00	0.00	0.08	0.00	0.00	12.42	5.24	0.99	null	null		null	null		-6.36E+00	5.56E-01		-6.36E+00	6.36E-01		-1.24E+00	3.60E-10	Down	-3.65E+00	7.43E-38	Down	Unigene21304_A11//gi|115450457|ref|NP_001048829.1|//2.00E-09//Os03g0126900 [Oryza sativa Japonica Group] >gi|113547300|dbj|BAF10743.1| Os03g0126900 [Oryza sativa Japonica Group]						nr -
Unigene21305_A11	389	0.00	0.00	0.00	0.00	0.00	0.00	2.50	2.58	0.00	null	null		null	null		null	null		null	null		4.48E-02	9.67E-01		-1.13E+01	2.72E-07	Down	Unigene21305_A11//gi|112253642|gb|ABI14406.1|//5.00E-45//40S ribosomal S14 [Prorocentrum minimum]	Unigene21305_A11//1.00E-38//AT3G11510| 40S ribosomal protein S14 (RPS14B)	Unigene21305_A11//1.00E-07//CD485874		ko03010|Ribosome		nr -
Unigene21310_A11	294	0.89	2.24	0.36	3.22	1.29	0.15	1.29	1.42	0.68	1.33E+00	1.45E-01		-1.30E+00	4.36E-01		-1.32E+00	5.61E-02		-4.39E+00	5.96E-05	Down	1.35E-01	8.99E-01		-9.34E-01	3.79E-01		Unigene21310_A11//gi|297727877|ref|NP_001176302.1|//9.00E-06//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1| Os11g0106066 [Oryza sativa Japonica Group]		Unigene21310_A11//9.00E-14//gi|21103110|gb|BQ415423.1|BQ415423				nr -
Unigene21315_A11	371	0.00	0.00	0.00	0.00	0.00	0.00	4.67	1.58	0.32	null	null		null	null		null	null		null	null		-1.57E+00	7.86E-04	Down	-3.86E+00	1.46E-09	Down	Unigene21315_A11//gi|159474294|ref|XP_001695264.1|//3.00E-52//heat shock protein 90A [Chlamydomonas reinhardtii] >gi|158276198|gb|EDP01972.1| heat shock protein 90A [Chlamydomonas reinhardtii]	Unigene21315_A11//2.00E-52//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Unigene21315_A11//1.00E-07//TC167157		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene21322_A11	530	0.00	19.69	8.04	0.00	0.00	0.00	0.00	0.00	0.00	1.43E+01	8.09E-60	Up	1.30E+01	1.22E-23	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene21325_A11	352	0.00	0.29	0.00	0.00	0.00	0.26	2.28	0.12	2.15	8.17E+00	3.87E-01		null	null		null	null		8.00E+00	4.77E-01		-4.27E+00	8.48E-05	Down	-8.58E-02	9.05E-01		Unigene21325_A11//gi|115474509|ref|NP_001060851.1|//1.00E-08//Os08g0115200 [Oryza sativa Japonica Group] >gi|42409298|dbj|BAD10560.1| calmodulin-binding protein family-like [Oryza sativa Japonica Group] >gi|113622820|dbj|BAF22765.1| Os08g0115200 [Oryza sativa Japonica Group]						nr +
Unigene21326_A11	390	0.00	0.00	0.00	0.00	0.00	0.00	4.55	1.61	0.41	null	null		null	null		null	null		null	null		-1.50E+00	1.01E-03		-3.48E+00	4.53E-09	Down	Unigene21326_A11//gi|18408550|ref|NP_564878.1|//4.00E-47//60S ribosomal protein L10 (RPL10C) [Arabidopsis thaliana] >gi|297838747|ref|XP_002887255.1| 60S ribosomal protein L10 [Arabidopsis lyrata subsp. lyrata] >gi|75249285|sp|Q93Z22.1|RL10J_ARATH RecName: Full=60S ribosomal protein L10-3 >gi|14194141|gb|AAK56265.1|AF36727_1 At1g66580/T12I7_3 [Arabidopsis thaliana] >gi|15777885|gb|AAL05903.1| At1g66580/T12I7_3 [Arabidopsis thaliana] >gi|297333096|gb|EFH63514.1| 60S ribosomal protein L10 [Arabidopsis lyrata subsp. lyrata]	Unigene21326_A11//1.00E-44//AT1G66580| 60S ribosomal protein L10 (RPL10C)	Unigene21326_A11//3.00E-08//TC145515		ko03010|Ribosome		nr +
Unigene21327_A11	828	0.19	0.12	0.00	0.24	0.00	0.00	12.56	1.41	3.66	-6.31E-01	7.28E-01		-7.57E+00	2.45E-01		-7.91E+00	8.43E-02		-7.91E+00	1.34E-01		-3.15E+00	3.30E-44	Down	-1.78E+00	1.51E-23	Down	Unigene21327_A11//gi|226529589|ref|NP_001151813.1|//7.00E-16//EF hand family protein [Zea mays] >gi|195649869|gb|ACG44402.1| EF hand family protein [Zea mays]	Unigene21327_A11//2.00E-14//AT5G44460| calcium-binding protein, putative			ko04626|Plant-pathogen interaction		nr +
Unigene2133_A11	272	70.21	59.61	64.41	50.55	67.73	77.38	30.47	79.75	84.22	-2.36E-01	7.50E-02		-1.24E-01	3.82E-01		4.22E-01	5.78E-04		6.14E-01	1.40E-07		1.39E+00	1.01E-32	Up	1.47E+00	2.93E-38	Up	Unigene2133_A11//gi|297827267|ref|XP_002881516.1|//3.00E-25//sodium- and lithium-tolerant 1 [Arabidopsis lyrata subsp. lyrata] >gi|297327355|gb|EFH57775.1| sodium-and lithium-tolerant 1 [Arabidopsis lyrata subsp. lyrata]	Unigene2133_A11//3.00E-26//AT2G37570| SLT1 (sodium- and lithium-tolerant 1)	Unigene2133_A11//7.00E-150//gi|75324913|gb|DT545187.1|DT545187			GO:0006972	nr -
Unigene21334_A11	416	161.36	116.69	107.40	235.18	220.52	243.73	540.60	243.64	235.68	-4.68E-01	2.22E-13		-5.87E-01	4.66E-19		-9.29E-02	1.05E-01		5.15E-02	4.30E-01		-1.15E+00	3.44E-248	Down	-1.20E+00	3.36E-272	Down	Unigene21334_A11//gi|242129046|gb|ACS83602.1|//1.00E-72//ATP synthase beta subunit 1 [Gossypium hirsutum]	Unigene21334_A11//2.00E-72//AT5G08690| ATP synthase beta chain 2, mitochondrial	Unigene21334_A11//0.00E+00//TC129973		ko00190|Oxidative phosphorylation		nr -
Unigene21335_A11	321	0.00	2.05	2.65	0.78	1.39	0.28	0.13	0.26	0.25	1.10E+01	6.26E-04	Up	1.14E+01	9.03E-05	Up	8.46E-01	5.14E-01		-1.46E+00	4.07E-01		9.84E-01	7.31E-01		9.14E-01	7.50E-01					Unigene21335_A11//1.00E-13//AW186767				
Unigene21337_A11	628	1.58	0.00	0.59	0.00	0.27	0.07	0.00	0.00	0.00	-1.06E+01	7.46E-06	Down	-1.42E+00	6.08E-02		8.10E+00	2.27E-01		6.17E+00	6.96E-01		null	null		null	null									nr -
Unigene21340_A11	727	3.60	7.25	6.15	0.14	0.00	0.37	0.00	0.12	0.00	1.01E+00	1.31E-04	Up	7.74E-01	9.38E-03		-7.10E+00	3.13E-01		1.44E+00	4.09E-01		6.85E+00	4.01E-01		null	null		Unigene21340_A11//gi|124359343|gb|AB028505.2|//2.00E-17//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene21340_A11//5.00E-14//AT5G42905| nucleic acid binding / ribonuclease H					nr -
Unigene21343_A11	258	39.75	52.24	67.08	2.32	2.80	2.63	10.00	28.51	45.71	3.94E-01	1.09E-02		7.55E-01	4.65E-08		2.75E-01	8.01E-01		1.81E-01	8.45E-01		1.51E+00	4.35E-13	Up	2.19E+00	2.76E-34	Up				Unigene21343_A11//9.00E-100//gi|109836377|gb|DW234938.1|DW234938				
Unigene21345_A11	458	0.00	0.22	0.00	0.00	0.00	0.00	1.66	1.73	0.17	7.79E+00	3.87E-01		null	null		null	null		null	null		6.14E-02	9.50E-01		-3.26E+00	4.48E-04	Down	Unigene21345_A11//gi|115476630|ref|NP_001061911.1|//4.00E-10//Os08g0441700 [Oryza sativa Japonica Group] >gi|113623880|dbj|BAF23825.1| Os08g0441700 [Oryza sativa Japonica Group]						nr -
Unigene21347_A11	891	0.00	0.34	0.24	0.39	1.04	0.71	2.47	1.08	1.03	8.41E+00	4.43E-02		7.90E+00	1.41E-01		1.41E+00	6.25E-02		8.58E-01	3.90E-01		-1.19E+00	2.33E-03		-1.26E+00	9.51E-04	Down	Unigene21347_A11//gi|115467098|ref|NP_001057148.1|//5.00E-85//Os06g0216800 [Oryza sativa Japonica Group] >gi|113595188|dbj|BAF19062.1| Os06g0216800 [Oryza sativa Japonica Group]	Unigene21347_A11//5.00E-61//AT2G15790| SQN (SQUINT); peptidyl-prolyl cis-trans isomerase	Unigene21347_A11//0.00E+00//TC177390				nr +
Unigene21348_A11	533	0.00	0.00	0.00	0.00	0.13	0.00	10.79	2.35	5.61	null	null		null	null		7.01E+00	6.10E-01		null	null		-2.20E+00	7.95E-17	Down	-9.45E-01	1.36E-05	Down	Unigene21348_A11//gi|238055378|sp|B9SCX0.1|U4975_RICCO//3.00E-40//RecName: Full=UPF0497 membrane protein 5	Unigene21348_A11//1.00E-11//AT5G06200| integral membrane family protein					nr -
Unigene2135_A11	1775	6.04	2.80	3.84	3.99	4.11	3.21	2.14	2.05	1.26	-1.11E+00	7.31E-10	Down	-6.54E-01	2.90E-04		4.55E-02	8.60E-01		-3.14E-01	1.88E-01		-6.55E-02	8.32E-01		-7.70E-01	4.33E-03		Unigene2135_A11//gi|90265189|emb|CAH67660.1|//1.00E-146//BO410608.15 [Oryza sativa (indica cultivar-group)]					GO:0043231//GO:0048037	nr +
Unigene21350_A11	224	0.00	0.00	0.00	1.78	0.31	0.00	2.64	0.56	0.00	null	null		null	null		-2.53E+00	5.80E-02		-1.08E+01	1.11E-02		-2.24E+00	2.07E-02		-1.14E+01	1.41E-04	Down				Unigene21350_A11//7.00E-14//PL576500				
Unigene21353_A11	610	0.00	53.83	24.38	0.00	0.00	0.00	0.00	0.00	0.00	1.57E+01	2.23E-189	Up	1.46E+01	9.83E-84	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene21355_A11	580	35.27	10.92	10.28	73.95	57.12	66.27	70.78	50.30	31.18	-1.69E+00	1.09E-33	Down	-1.78E+00	1.03E-34	Down	-3.73E-01	6.11E-07		-1.58E-01	7.26E-02		-4.93E-01	3.11E-11		-1.18E+00	2.29E-49	Down	Unigene21355_A11//gi|115474635|ref|NP_001060914.1|//2.00E-36//Os08g0129200 [Oryza sativa Japonica Group] >gi|113622883|dbj|BAF22828.1| Os08g0129200 [Oryza sativa Japonica Group] >gi|187609563|gb|ACD13289.1| cold shock domain protein 2 [Oryza sativa Japonica Group]		Unigene21355_A11//0.00E+00//TC175227		ko03040|Spliceosome		nr -
Unigene21356_A11	263	1.59	7.90	5.26	1.89	4.06	1.89	0.32	0.00	0.15	2.31E+00	1.07E-05	Up	1.73E+00	6.71E-03		1.10E+00	1.09E-01		-3.90E-03	9.87E-01		-8.33E+00	4.04E-01		-1.09E+00	6.76E-01					Unigene21356_A11//1.00E-61//TC145896				

Unigene21359_All	751	0.14	0.54	0.00	0.27	0.28	0.00	2.65	5.57	1.96	1.95E+00	1.44E-01		-7.12E+00	3.94E-01		5.23E-02	9.89E-01		-8.05E+00	1.34E-01		1.07E+00	6.71E-05	Up	-4.31E-01	2.89E-01		Unigene21359_All//gi|32395577|gb|AAP37970.1|//8.00E-35//seed specific protein Bn15D17A [Brassica napus]	Unigene21359_All//2.00E-34//AT1G68510| LBD42 (LOB DOMAIN-CONTAINING PROTEIN 42)	Unigene21359_All//0.00E+00//DR455668				nr -
Unigene21361_All	1112	0.00	5.51	4.26	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.27E-35	Up	1.21E+01	2.44E-26	Up	null	null		null	null		null	null		null	null		Unigene21361_All//gi|145652387|gb|AEP88248.1|//5.00E-06//transcription factor bZIP10 [Glycine max]						nr +
Unigene21363_All	570	0.00	56.80	25.50	0.00	0.00	0.00	0.00	0.00	0.00	1.58E+01	9.72E-187	Up	1.46E+01	6.43E-82	Up	null	null		null	null		null	null		null	null		Unigene21363_All//gi|225431804|ref|XP_002272727.1|//6.00E-61//PREDICTED: similar to 60S ribosomal protein L19 [Vitis vinifera]	Unigene21363_All//1.00E-47//AT3G16780| 60S ribosomal protein L19 (RPL19B)			ko03010|Ribosome		nr -
Unigene21366_All	237	0.00	4.49	3.37	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.81E-06	Up	1.17E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene21366_All//gi|16224244|gb|AAL15648.1|AF411551.1|//6.00E-22//plastidic aldolase [Medicago sativa]	Unigene21366_All//3.00E-09//AT2G21330| fructose-bisphosphate aldolase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene21367_All	327	0.48	0.16	0.33	10.36	8.74	2.62	0.00	0.00	0.00	-1.63E+00	4.89E-01		-5.60E-01	7.76E-01		-2.45E-01	5.19E-01		-1.98E+00	6.38E-08	Down	null	null		null	null					Unigene21367_All//8.00E-70//TC174457				ESTscan +
Unigene21368_All	390	0.00	2.60	0.82	0.26	0.18	0.46	3.47	0.21	0.20	1.13E+01	7.26E-06	Up	9.68E+00	4.52E-02		-5.33E-01	8.16E-01		8.58E-01	6.95E-01		-4.02E+00	1.80E-07	Down	-4.09E+00	7.07E-08	Down	Unigene21368_All//gi|15227801|ref|NP_179319.1|//5.00E-41//mitochondrial substrate carrier family protein [Arabidopsis thaliana] >gi|33589804|gb|AAQ22668.1| At2g17270 [Arabidopsis thaliana]	Unigene21368_All//5.00E-35//AT2G17270| mitochondrial substrate carrier family protein					nr -
Unigene21369_All	669	0.00	53.85	19.58	0.00	0.00	0.00	0.00	0.00	0.00	1.57E+01	7.25E-208	Up	1.43E+01	9.77E-74	Up	null	null		null	null		null	null		null	null		Unigene21369_All//gi|157093371|gb|ABV22340.1|//3.00E-20//calponin domain-containing protein [Noctiluca scintillans]	Unigene21369_All//8.00E-06//AT5G27000| ATK4 (ARABIDOPSIS THALIANA KINESIN 4); ATPase/ microtubule binding / microtubule motor	Unigene21369_All//6.00E-20//DV849622				nr -
Unigene21370_All	460	0.00	1.65	1.50	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	1.77E-04	Up	1.06E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene21370_All//sp|P15311|EZRI_HUMAN//1.00E-77//Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4						swissprot -
Unigene21372_All	590	0.00	29.20	15.52	0.00	0.00	0.00	0.00	0.00	0.00	1.48E+01	4.93E-99	Up	1.39E+01	2.42E-51	Up	null	null		null	null		null	null		null	null		Unigene21372_All//gi|206573535|gb|ACI14379.1|//2.00E-63//40S ribosomal protein S15-like protein [Forsythia suspensa]	Unigene21372_All//1.00E-48//AT5G09510| 40S ribosomal protein S15 (RPS15D)	Unigene21372_All//3.00E-18//gi|109830543|gb|DW229102.1|DW229102		ko03010|Ribosome		nr -
Unigene21373_All	1064	0.00	0.00	0.00	0.00	0.00	0.08	1.31	3.69	1.20	null	null		null	null		null	null		6.41E+00	4.77E-01		1.49E+00	3.14E-07	Up	-1.30E-01	7.83E-01		Unigene21373_All//gi|223452302|gb|ACM89479.1|//3.00E-97//cysteine-rich protein [Glycine max]	Unigene21373_All//5.00E-96//AT4G21390| B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding	Unigene21373_All//5.00E-09//TC154318		ko04626|Plant-pathogen interaction		nr -
Unigene21378_All	471	0.00	5.59	4.86	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.45E-15	Up	1.22E+01	1.27E-12	Up	null	null		null	null		null	null		null	null		Unigene21378_All//gi|115464699|ref|NP_001055949.1|//4.00E-30//Os05g0498400 [Oryza sativa Japonica Group] >gi|113579500|dbj|BAF17863.1| Os05g0498400 [Oryza sativa Japonica Group]	Unigene21378_All//5.00E-30//AT1G54290| eukaryotic translation initiation factor SUI1, putative					nr +
Unigene21379_All	334	0.00	3.03	1.12	0.60	0.00	1.49	0.13	0.13	0.00	1.16E+01	7.26E-06	Up	1.01E+01	2.50E-02		-9.22E+00	8.43E-02		1.32E+00	2.52E-01		-1.72E-02	1.00E+00		-6.98E+00	6.13E-01		Unigene21379_All//gi|85068670|gb|ABBC69415.1|//7.00E-28//CYP71AH2 [Nicotiana tabacum]	Unigene21379_All//5.00E-17//AT1G13080| CYP71B2 (CYTOCHROME P450 71B2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene21379_All//7.00E-163//TC130557		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene21382_All	522	0.00	0.00	0.00	0.00	0.00	0.00	2.43	2.56	0.00	null	null		null	null		null	null		null	null		7.65E-02	8.93E-01		-1.12E+01	1.99E-09	Down	Unigene21382_All//gi|297723953|ref|NP_001174340.1|//8.00E-08//Os05g0313600 [Oryza sativa Japonica Group] >gi|255676232|dbj|BAH93068.1| Os05g0313600 [Oryza sativa Japonica Group]						nr -
Unigene21384_All	1100	0.00	11.15	4.45	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.40E-70	Up	1.21E+01	3.05E-27	Up	null	null		null	null		null	null		null	null		Unigene21384_All//gi|13160397|emb|CAC32834.1|//2.00E-72//aldose reductase [Digitalis purpurea]	Unigene21384_All//8.00E-72//AT2G37790| aldo/keto reductase family protein			ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene21385_All	449	0.00	0.00	0.00	0.00	0.00	0.00	5.18	4.38	0.18	null	null		null	null		null	null		null	null		-2.43E-01	5.62E-01		-4.87E+00	1.64E-14	Down	Unigene21385_All//gi|159484538|ref|XP_001700313.1|//2.00E-61//ribosomal protein L40, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|82244|emb|CAA43216.1| ubiquitin extension protein (UbCEP52) [Chlamydomonas reinhardtii] >gi|158272480|gb|EDO98280.1| ribosomal protein L40 [Chlamydomonas reinhardtii]	Unigene21385_All//5.00E-62//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene21385_All//4.00E-26//CD486028		ko03010|Ribosome		nr -
Unigene21386_All	429	40.73	21.26	29.67	51.90	39.17	37.16	87.62	91.29	28.32	-9.38E-01	5.49E-12		-4.57E-01	9.11E-04		-4.06E-01	1.79E-04		-4.82E-01	1.97E-05		5.92E-02	5.45E-01		-1.63E+00	3.51E-73	Down			Unigene21386_All//6.00E-173//TC177017				
Unigene21394_All	345	0.00	3.97	5.87	0.87	0.70	0.00	0.25	0.24	0.00	1.20E+01	7.80E-08	Up	1.25E+01	3.80E-11	Up	-3.10E-01	8.20E-01		-9.76E+00	4.00E-02		-1.66E-02	1.01E+00		-7.94E+00	3.59E-01				Unigene21394_All//5.00E-28//CD095570				
Unigene21395_All	457	0.00	58.65	24.70	0.00	0.00	0.00	0.00	0.00	0.00	1.58E+01	1.86E-154	Up	1.46E+01	1.93E-63	Up	null	null		null	null		null	null		null	null		Unigene21395_All//gi|298713887|emb|CBJ33763.1|//1.00E-11//conserved unknown protein [Ectocarpus siliculosus]		Unigene21395_All//8.00E-37//TC143817				nr -
Unigene21397_All	319	0.00	1.91	2.17	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	1.17E-03		1.11E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene21397_All//gi|159478278|ref|XP_001697231.1|//3.00E-30//20S proteasome alpha subunit E [Chlamydomonas reinhardtii] >gi|158274705|gb|EDP00486.1| 20S proteasome alpha subunit E [Chlamydomonas reinhardtii]	Unigene21397_All//1.00E-27//AT1G53850| PAE1; endopeptidase/ peptidase/ threonine-type endopeptidase			ko03050|Proteasome		nr +
Unigene21398_All	473	0.00	0.00	0.00	0.00	0.15	0.00	4.11	6.89	0.17	null	null		null	null		7.19E+00	6.10E-01		null	null		7.45E-01	1.50E-02		-4.61E+00	6.97E-12	Down	Unigene21398_All//gi|226460767|gb|EEH58061.1|//2.00E-24//profilin [Micromonas pusilla CCMP1545]	Unigene21398_All//2.00E-22//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding					nr +
Unigene21400_All	460	0.00	0.00	0.00	7.15	4.34	1.18	2.30	0.00	0.17	null	null		null	null		-7.19E-01	2.71E-02		-2.60E+00	1.67E-10	Down	-1.12E+01	1.51E-07	Down	-3.73E+00	6.13E-06	Down	Unigene21400_All//gi|115455585|ref|NP_001051393.1|//2.00E-13//Os03g0769000 [Oryza sativa Japonica Group] >gi|113549864|dbj|BAF13307.1| Os03g0769000 [Oryza sativa Japonica Group]	Unigene21400_All//4.00E-13//AT5G66600| unknown protein	Unigene21400_All//4.00E-131//TC172096				nr +
Unigene21401_All	662	0.08	0.15	0.00	0.38	0.16	0.20	9.20	11.93	3.85	9.55E-01	7.26E-01		-6.30E+00	6.24E-01		-1.27E+00	4.24E-01		-8.78E-01	6.16E-01		3.76E-01	4.78E-02		-1.26E+00	8.68E-09	Down			Unigene21401_All//4.00E-175//FL576717				
Unigene21402_All	530	0.00	12.05	3.62	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	1.85E-36	Up	1.18E+01	1.47E-10	Up	null	null		null	null		null	null		null	null		Unigene21402_All//gi|224069720|ref|XP_002326400.1|//1.00E-44//argonaute protein group [Populus trichocarpa] >gi|222833593|gb|EEE72070.1| argonaute protein group [Populus trichocarpa]	Unigene21402_All//2.00E-44//AT2G27880| AGO5 (ARGONAUTE 5); nucleic acid binding					nr -
Unigene21406_All	635	0.00	0.00	0.00	0.00	0.00	0.00	2.86	2.57	0.00	null	null		null	null		null	null		null	null		-1.58E-01	7.23E-01		-1.15E+01	2.03E-13	Down	Unigene21406_All//gi|33326375|gb|AAQ08597.1|//9.00E-94//heat shock protein [Hevea brasiliensis]	Unigene21406_All//6.00E-80//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene21406_All//2.00E-16//gi|31072433|gb|CA992712.1|CA992712		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene21408_All	738	0.00	12.22	5.56	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	1.24E-51	Up	1.24E+01	9.64E-23	Up	null	null		null	null		null	null		null	null		Unigene21408_All//gi|148612407|gb|ABQ96119.1|//2.00E-08//alpha-gliadin [Aegilops tauschii]				ko03022|Basal transcription factors		nr -
Unigene21409_All	205	3.83	0.74	2.34	4.13	2.69	4.41	8.66	2.45	1.75	-2.37E+00	1.09E-02		-7.12E-01	3.89E-01		-6.20E-01	4.13E-01		9.31E-02	9.20E-01		-1.82E+00	1.22E-04	Down	-2.31E+00	3.08E-06	Down			Unigene21409_All//2.00E-57//gi|161256764|gb|ES837017.1|ES837017				
Unigene21411_All	524	1.10	1.35	0.10	5.70	3.42	1.90	0.89	0.80	0.08	3.02E-01	6.93E-01		-3.43E+00	1.41E-02		-7.39E-01	3.17E-02		-1.59E+00	2.21E-05	Down	-1.54E-01	8.70E-01		-3.55E+00	6.85E-03		Unigene21411_All//gi|38345009|emb|CAE01608.2|//1.00E-23//OSJNBa0052021.12 [Oryza sativa (japonica cultivar-group)]	Unigene21411_All//3.00E-10//ATMG01250| hypothetical protein	Unigene21411_All//2.00E-28//gi|163334098|gb|ES836566.1|ES836566				nr +
Unigene21414_All	805	0.13	0.13	0.40	0.37	0.09	0.22	5.36	12.15	11.78	-4.62E-02	9.89E-01		1.61E+00	3.05E-01		-2.12E+00	1.65E-01		-7.27E-01	6.39E-01		1.18E+00	5.31E-12	Up	1.14E+00	2.64E-11	Up	Unigene21414_All//gi|224082796|ref|XP_002306842.1|//5.00E-35//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222856291|gb|EEE93838.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene21414_All//5.00E-25//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene21414_All//3.00E-10//EX167849	AP2-EREBP			nr -
Unigene21417_All	307	0.00	0.00	0.00	0.00	0.00	0.00	1.79	3.40	0.00	null	null		null	null		null	null		null	null		9.27E-01	1.30E-01		-1.08E+01	2.80E-04	Down							ESTscan +
Unigene21423_All	772	7.59	4.46	2.69	0.00	0.13	0.00	0.00	0.05	0.00	-7.66E-01	1.74E-03		-1.50E+00	3.26E-08	Down	7.06E+00	4.56E-01		null	null		5.76E+00	6.35E-01		null	null									
Unigene21424_All	332	2.36	0.00	0.00	0.45	0.10	0.00	1.66	0.76	0.12	-1.12E+01	1.09E-04	Down	-1.12E+01	2.22E-04	Down	-2.12E+00	3.86E-01		-8.81E+00	2.33E-01		-1.13E+00	2.18E-01		-3.79E+00	2.03E-03				Unigene21424_All//5.00E-108//DW502471				
Unigene2143_All	1470	3.42	19.44	2.61	2.61	2.06	4.67	6.10	15.33	21.22	2.51E+00	6.43E-77	Up	-3.90E-01	1.75E-01		-3.40E-01	3.06E-01		8.40E-01	1.47E-04		1.33E+00	7.80E-32	Up	1.80E+00	4.04E-69	Up	Unigene2143_All//gi|30687005|ref|NP_194310.3|//1.00E-65//calmodulin-binding protein [Arabidopsis thaliana] >gi|145334135|ref|NP_001078448.1| calmodulin-binding protein [Arabidopsis thaliana]	Unigene2143_All//6.00E-67//AT4G25800| calmodulin-binding protein	Unigene2143_All//0.00E+00//TC149602		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005515	nr -
Unigene21430_All	477	0.00	0.00	0.00	0.00	0.00	0.00	2.39	3.07	0.00	null	null		null	null		null	null		null	null		3.58E-01	4.96E-01		-1.12E+01	1.65E-08	Down	Unigene21430_All//gi|1703148|sp|P53491.1|ACT_ACECL//1.00E-34//RecName: Full=Actin >gi|2654377|emb|CAA82272.1| actin [Acetabularia peniculus]	Unigene21430_All//5.00E-35//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene21430_All//5.00E-38//gi|31406833|gb|CD485868.1|CD485868		ko04145|Phagosome		nr -
Unigene21431_All	470	0.00	77.94	35.46	0.00	0.15	0.00	0.00	0.00	0.00	1.63E+01	2.18E-211	Up	1.51E+01	4.82E-94	Up	7.19E+00	6.10E-01		null	null		null	null		null	null		Unigene21431_All//gi|301121610|ref|XP_002908532.1|//1.00E-63//60S ribosomal protein L23 [Phytophthora infestans T30-4] >gi|662701653|gb|AAY43411.1| ribosomal protein L23 [Phytophthora infestans] >gi|262103563|gb|EE161615.1| 60S ribosomal protein L23 [Phytophthora infestans T30-4]	Unigene21431_All//6.00E-63//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene21431_All//2.00E-13//DW230604		ko03010|Ribosome		nr +
Unigene21434_All	476	0.88	0.85	3.69	0.00	0.29	1.04	0.00	0.00	0.00	-4.62E-02	9.80E-01		2.07E+00	3.29E-04	Up	8.18E+00	3.19E-01		1.00E+01	4.38E-03		null	null		null	null		Unigene21434_All//gi|116059997|emb|CAL56056.1|//1.00E-20//Cnx2, molybdenum cofactor biosynthesis protein (IC) (Ostreococcus tauri]	Unigene21434_All//8.00E-21//AT2G31955| CNX2 (COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 2); catalytic					nr +
Unigene21435_All	634	0.08	0.00	0.17	12.34	5.87	2.71	0.00	0.00	0.00	-6.37E+00	6.12E-01		1.03E+00	7.03E-01		-1.07E+00	3.16E-08	Down	-2.19E+00	6.59E-20	Down	null	null		null	null									

Unigene21437_All	594	0.00	0.00	0.00	0.00	0.00	0.00	3.63	5.77	0.00	null	null		null	null		null	null		null	null		6.69E-01	2.50E-02		-1.18E+01	6.89E-16	Down	Unigene21437_All//gi|300175904|emb|CBK21900.2|//8.00E-43//Ribosomal protein L18e [Blastocystis hominis]	Unigene21437_All//5.00E-41//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome			ko03010|Ribosome		nr -
Unigene2144_All	2343	1.32	7.94	1.05	1.17	0.68	1.60	3.43	4.89	5.90	2.59E+00	4.34E-52	Up	-3.34E-01	4.00E-01		-7.90E-01	2.88E-02		4.52E-01	1.79E-01		5.12E-01	6.26E-04		7.83E-01	4.61E-09		Unigene2144_All//gi|226499068|ref|NP_001152440.1|//6.00E-87//calmodulin binding protein [Zea mays]	Unigene2144_All//1.00E-87//AT4G25800| calmodulin-binding protein	Unigene2144_All//0.00E+00//TC149602		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005515	nr -
Unigene21440_All	517	0.30	0.49	0.21	0.29	0.07	0.17	0.82	2.99	2.16	6.91E-01	6.27E-01		-5.60E-01	7.76E-01		-2.12E+00	3.86E-01		-7.27E-01	7.15E-01		1.87E+00	3.06E-04	Up	1.40E+00	1.56E-02									
Unigene21441_All	395	2.91	1.28	0.81	3.78	0.96	0.00	0.21	0.00	0.00	-1.18E+00	6.62E-02		-1.85E+00	1.07E-02		-1.98E+00	2.94E-04	Down	-1.19E+01	2.43E-09	Down	-7.74E+00	4.04E-01		-7.74E+00	3.59E-01		Unigene21441_All//gi|22331260|ref|NP_188894.2|//8.00E-09//senescence-associated protein-related [Arabidopsis thaliana]	Unigene21441_All//4.00E-10//AT3G22550| senescence-associated protein-related	Unigene21441_All//5.00E-13//TC142940				nr -
Unigene21443_All	1112	0.19	0.46	0.48	2.02	1.98	0.73	0.61	0.11	0.43	1.28E+00	2.31E-01		1.35E+00	2.25E-01		-2.45E-02	9.58E-01		-1.46E+00	8.28E-04	Down	-2.43E+00	7.76E-03		-5.01E-01	5.07E-01		Unigene21443_All//gi|224115064|ref|XP_002332228.1|//6.00E-78//nramp transporter [Populus trichocarpa] >gi|222831841|gb|EEE70318.1| nramp transporter [Populus trichocarpa]	Unigene21443_All//1.00E-71//AT2G23150| NRAMP3 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 3); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter	Unigene21443_All//2.00E-141//TC161061				nr +
Unigene21446_All	457	0.00	0.00	0.00	0.00	0.00	2.68	4.39	0.00	null	null		null	null		null	null		null	null		7.10E-01	8.37E-02		-1.14E+01	4.03E-09	Down	Unigene21446_All//gi|145345768|ref|XP_001417372.1|//3.00E-39//Ribosomal protein S17, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901] >gi|144577599|gb|ABO95665.1| Ribosomal protein S17, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901]	Unigene21446_All//1.00E-35//AT5G04800| 40S ribosomal protein S17 (RPS17D)	Unigene21446_All//3.00E-08//EX167574		ko03010|Ribosome		nr -
Unigene21448_All	704	0.30	2.16	1.21	3.25	7.43	2.18	0.00	0.48	0.11	2.86E+00	2.69E-05	Up	2.03E+00	2.24E-02		1.19E+00	2.77E-06	Up	-5.78E-01	1.90E-01		8.89E+00	1.27E-02		6.82E+00	4.04E-01		Unigene21448_All//gi|38566598|gb|AAR24189.1|//3.00E-29//At5g14690 [Arabidopsis thaliana] >gi|40824071|gb|AAR92338.1| At5g14690 [Arabidopsis thaliana]	Unigene21448_All//8.00E-28//AT5G14690| unknown protein	Unigene21448_All//0.00E+00//DW009333				nr +
Unigene21456_All	1014	0.00	0.00	0.00	0.00	0.00	0.00	15.97	19.46	0.24	null	null		null	null		null	null		null	null		2.85E-01	1.25E-02		-6.08E+00	1.47E-108	Down	Unigene21456_All//gi|4139170|gb|AAD03711.1|//1.00E-131//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene21456_All//3.00E-122//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene21456_All//1.00E-49//ES811919				nr -
Unigene21458_All	380	0.00	0.00	0.00	0.00	0.00	0.00	1.78	1.10	0.00	null	null		null	null		null	null		null	null		-6.95E-01	3.94E-01		-1.08E+01	3.56E-05	Down	Unigene21458_All//gi|301120388|ref|XP_002907921.1|//1.00E-12//polyadenylate-binding protein 1-B [Phytophthora infestans T30-4] >gi|262102952|gb|EEY61004.1| polyadenylate-binding protein 1-B [Phytophthora infestans T30-4]	Unigene21458_All//7.00E-11//AT1G22760| PAB3 (POLY(A) BINDING PROTEIN 3); RNA binding / translation initiation factor					nr -
Unigene21461_All	407	0.00	4.36	1.05	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	4.14E-10	Up	1.00E+01	1.38E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene21465_All	477	0.00	0.00	0.00	0.00	0.00	0.00	14.09	11.39	0.08	null	null		null	null		null	null		null	null		-3.07E-01	1.51E-01		-7.40E+00	1.49E-47	Down	Unigene21465_All//gi|115451717|ref|NP_001049459.1|//8.00E-06//Os03g0231300 [Oryza sativa Japonica Group] >gi|108706989|gb|ABF94784.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547930|dbj|BAF11373.1| Os03g0231300 [Oryza sativa Japonica Group]		Unigene21465_All//6.00E-07//gi|84158120|gb|DN827167.1|DN827167				nr +
Unigene2147_All	812	4.19	4.18	3.54	5.15	4.37	5.17	5.83	3.71	2.31	-2.50E-03	9.91E-01		-2.42E-01	5.12E-01		-2.39E-01	4.65E-01		5.40E-03	9.87E-01		-6.54E-01	8.00E-03		-1.34E+00	1.15E-07	Down	Unigene2147_All//gi|224136205|ref|XP_002322271.1|//1.00E-65//f-box family protein [Populus trichocarpa] >gi|222869267|gb|EEF06398.1| f-box family protein [Populus trichocarpa]	Unigene2147_All//4.00E-42//AT5G63520| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Cyclin-like F-box (InterPro:IPR001810), FIST domain, N-terminal (InterPro:IPR013702); Has 96 Blast hits to 96 proteins in 46 species: Archae - 0; Bacteria - 72; Metazoa - 6; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene2147_All//0.00E+00//TC171773				nr +
Unigene21470_All	226	25.23	9.86	18.85	1.54	1.52	2.00	0.00	0.55	0.53	-1.36E+00	2.24E-07	Down	-4.21E-01	1.15E-01		-1.81E-02	9.58E-01		3.73E-01	7.32E-01		9.12E+00	2.40E-01		9.05E+00	2.43E-01		Unigene21470_All//gi|224090875|ref|XP_002309107.1|//2.00E-06//cytochrome P450 [Populus trichocarpa] >gi|222855083|gb|EEE92630.1| cytochrome P450 [Populus trichocarpa]		Unigene21470_All//3.00E-105//TC169554				nr +
Unigene21473_All	278	1.32	0.18	1.34	8.06	1.49	0.81	0.00	0.00	0.00	-2.85E+00	7.80E-02		2.54E-02	1.00E+00		-2.44E+00	8.82E-08	Down	-3.31E+00	3.54E-09	Down	null	null		null	null		Unigene21473_All//gi|298105240|gb|ADI55168.1|//2.00E-38//AS1 [Gossypium hirsutum]	Unigene21473_All//6.00E-14//AT4G08685| SAM7	Unigene21473_All//4.00E-108//TC141513				nr -
Unigene21475_All	374	0.00	0.00	0.00	0.00	0.00	0.00	4.07	0.45	1.92	null	null		null	null		null	null		null	null		-3.19E+00	4.80E-07	Down	-1.09E+00	1.94E-02		Unigene21475_All//gi|38566620|gb|AAR24200.1|//1.00E-08//At5g01790 [Arabidopsis thaliana] >gi|40824035|gb|AAR92330.1| At5g01790 [Arabidopsis thaliana]		Unigene21475_All//3.00E-113//DT464192				nr -
Unigene21477_All	571	0.46	0.36	0.28	1.66	4.28	2.93	0.37	0.37	0.91	-3.68E-01	7.78E-01		-7.12E-01	6.22E-01		1.37E+00	7.53E-04	Up	8.20E-01	1.19E-01		-1.65E-02	1.02E+00		1.29E+00	1.59E-01		Unigene21477_All//gi|152926166|gb|ABS32237.1|//2.00E-35//asymmetric leaves 2 [Carica papaya]	Unigene21477_All//7.00E-37//AT1G65620| AS2 (ASYMMETRIC LEAVES 2); protein binding			ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene21478_All	418	0.00	0.00	0.00	0.00	0.00	0.00	3.54	3.80	0.00	null	null		null	null		null	null		null	null		1.02E-01	8.34E-01		-1.18E+01	5.85E-11	Down	Unigene21478_All//gi|195609320|gb|ACG26490.1|//3.00E-46//40S ribosomal protein S16 [Zea mays] >gi|195615434|gb|ACG29547.1| 40S ribosomal protein S16 [Zea mays] >gi|195621150|gb|ACG32405.1| 40S ribosomal protein S16 [Zea mays] >gi|195626368|gb|ACG35014.1| 40S ribosomal protein S16 [Zea mays] >gi|195643186|gb|ACG41061.1| 40S ribosomal protein S16 [Zea mays] >gi|195658147|gb|ACG48541.1| 40S ribosomal protein S16 [Zea mays]	Unigene21478_All//9.00E-46//AT3G04230| 40S ribosomal protein S16 (RPS16B)			ko03010|Ribosome		nr -
Unigene21479_All	701	0.00	17.20	8.20	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	3.54E-69	Up	1.30E+01	4.81E-32	Up	null	null		null	null		null	null		null	null		Unigene21479_All//gi|224006323|ref|XP_002292122.1|//8.00E-12//trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972641|gb|EED90973.1| trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]						nr -
Unigene21484_All	361	0.00	0.00	0.00	0.00	0.00	0.00	7.26	9.15	0.66	null	null		null	null		null	null		null	null		3.33E-01	3.10E-01		-3.46E+00	5.23E-13	Down			Unigene21484_All//8.00E-21//TC142576				
Unigene21488_All	491	0.00	11.66	4.34	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	1.13E-32	Up	1.21E+01	9.78E-12	Up	null	null		null	null		null	null		null	null									
Unigene2149_All	1853	3.87	3.25	4.54	6.40	4.89	8.02	5.41	5.23	2.69	-2.50E-01	2.80E-01		2.31E-01	3.04E-01		-3.89E-01	1.48E-02		3.26E-01	2.96E-02		-4.74E-02	7.99E-01		-1.01E+00	4.91E-10	Down	Unigene2149_All//gi|224136205|ref|XP_002322271.1|//1.00E-159//f-box family protein [Populus trichocarpa] >gi|222869267|gb|EEF06398.1| f-box family protein [Populus trichocarpa]	Unigene2149_All//9.00E-102//AT5G63520| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Cyclin-like F-box (InterPro:IPR001810), FIST domain, N-terminal (InterPro:IPR013702); Has 96 Blast hits to 96 proteins in 46 species: Archae - 0; Bacteria - 72; Metazoa - 6; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene2149_All//0.00E+00//TC159431				nr +
Unigene21491_All	225	1.16	0.00	0.24	2.88	1.99	0.60	2.44	0.00	1.77	-1.02E+01	6.71E-02		-2.30E+00	2.43E-01		-5.33E-01	5.39E-01		-2.26E+00	2.76E-02		-1.13E+01	4.61E-04	Down	-4.64E-01	5.97E-01				Unigene21491_All//3.00E-07//TC155752				
Unigene21492_All	327	0.00	0.00	0.00	0.00	0.00	0.00	1.94	2.68	0.12	null	null		null	null		null	null		null	null		4.69E-01	5.04E-01		-3.99E+00	5.82E-04	Down	Unigene21492_All//gi|297824233|ref|XP_002876999.1|//6.00E-16//ATMBF1A/MBF1A [Arabidopsis lyrata subsp. lyrata] >gi|297325838|gb|EFH56258.1| ATMBF1A/MBF1A [Arabidopsis lyrata subsp. lyrata]	Unigene21492_All//3.00E-17//AT2G42680| MBF1A (MULTIPROTEIN BRIDGING FACTOR 1A); DNA binding / transcription coactivator					nr -
Unigene21495_All	451	2.09	0.45	1.18	1.77	1.30	2.80	1.59	0.00	0.71	-2.22E+00	6.65E-03		-8.23E-01	2.71E-01		-4.45E-01	5.73E-01		6.66E-01	2.99E-01		-1.06E+01	3.26E-05	Down	-1.17E+00	1.09E-01		Unigene21495_All//gi|15218160|ref|NP_172993.1|//5.00E-17//aspartate-glutamate racemase family [Arabidopsis thaliana] >gi|5103839|gb|AAD39669.1|AC007591_34 is a member of the PF|01177 Aspartate-glutamate racemase family. EST gb|T43554 comes from this gene [Arabidopsis thaliana]	Unigene21495_All//4.00E-14//AT1G15410| aspartate-glutamate racemase family	Unigene21495_All//0.00E+00//gi|164313116|gb|ES828103.1|ES828103				nr +
Unigene21496_All	233	0.22	0.00	0.00	1.92	7.98	4.07	2.90	7.18	2.91	-7.81E+00	6.12E-01		-7.81E+00	6.24E-01		2.05E+00	6.94E-05	Up	1.08E+00	1.48E-01		1.31E+00	5.02E-03		1.60E-03	9.97E-01		Unigene21496_All//gi|255556083|ref|XP_002519076.1|//3.00E-09//Dehydration-responsive protein RD22 precursor, putative [Ricinus communis] >gi|223541739|gb|EEF43287.1| Dehydration-responsive protein RD22 precursor, putative [Ricinus communis]		Unigene21496_All//3.00E-115//TC155039				nr -
Unigene21497_All	390	0.00	5.20	1.64	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.54E-11	Up	1.07E+01	1.16E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene21503_All	764	0.14	0.13	0.00	0.07	0.05	0.00	94.08	376.44	117.80	-4.71E-02	9.89E-01		-7.10E+00	3.94E-01		-5.32E-01	8.25E-01		-6.03E+00	6.36E-01		2.00E+00	0.00E+00	Up	3.24E-01	1.27E-11		Unigene21503_All//gi|124360970|gb|ABN08942.1|//7.00E-62//Quinonprotein alcohol dehydrogenase-like [Medicago truncatula]						nr +

Unigene21509_All	1155	0.00	11.49	4.84	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	3.37E-76	Up	1.22E+01	3.82E-31	Up	null	null		null	null		null	null		null	null		Unigene21509_All//gi|224129832|ref|XP_002320682.1|//7.00E-99//endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa] >gi|222861455|gb|EEE98997.1| endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa]	Unigene21509_All//9.00E-92//ATIG10130| ECA3 (ENDOPLASMIC RETICULUM-TYPE CALCIUM-TRANSPORTING ATPASE 3); calcium-transporting ATPase/ calmodulin binding / manganese-transporting ATPase/ peroxidase					nr -
Unigene2151_All	1353	76.37	96.47	109.26	140.68	125.65	125.11	116.97	56.75	36.89	3.37E-01	4.52E-14		5.17E-01	6.83E-33		-1.63E-01	2.35E-06		-1.69E-01	3.00E-06		-1.04E+00	1.89E-149	Down	-1.66E+00	0.00E+00	Down	Unigene2151_All//gi|18411317|ref|NP_565146.1|//1.00E-162//ACR3; amino acid binding [Arabidopsis thaliana] >gi|30699222|ref|NP_849896.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|30699224|ref|NP_849897.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|79321337|ref|NP_001031289.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|186495930|ref|NP_001117608.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|28299923|gb|AC006631.1| Similar to uridylyl transferases [Arabidopsis thaliana] >gi|22138096|gb|AAM93428.1| ACR3 [Arabidopsis thaliana] >gi|222424164|dbj|BAH20041.1| AT1G76990 [Arabidopsis thaliana]	Unigene2151_All//4.00E-163//AT1G76990| ACR3; amino acid binding	Unigene2151_All//0.00E+00//TC152223		ko00500|Starch and sucrose metabolism	GO:0031406	nr +
Unigene21511_All	437	0.00	0.00	0.00	0.23	0.47	0.83	1.55	2.30	10.12	null	null		null	null		1.05E+00	6.12E-01		1.86E+00	2.19E-01		5.68E-01	3.79E-01		2.71E+00	8.17E-17	Up	Unigene21511_All//gi|224127987|ref|XP_002320213.1|//6.00E-66//endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa] >gi|222860986|gb|EEE98528.1| endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa]	Unigene21511_All//3.00E-60//AT4G00900| ECA2 (ER-TYPE CA2+-ATPASE 2); calcium-transporting ATPase	Unigene21511_All//5.00E-78//DR456990				nr -
Unigene21513_All	526	0.00	0.19	0.00	0.00	0.00	0.34	0.24	6.75	9.69	7.59E+00	3.87E-01		null	null		null	null		8.42E+00	1.94E-01		4.81E+00	6.80E-21	Up	5.33E+00	6.72E-32	Up								
Unigene21514_All	397	3.95	0.38	1.21	2.76	0.87	0.68	0.00	0.00	0.00	-3.37E+00	2.77E-06	Down	-1.71E+00	3.82E-03		-1.67E+00	9.38E-03		-2.02E+00	4.74E-03		null	null		null	null										
Unigene21515_All	286	0.73	5.49	0.37	0.52	0.24	0.00	2.96	1.75	0.56	2.91E+00	1.58E-05	Up	-9.75E-01	6.21E-01		-1.12E+00	5.84E-01		-9.03E+00	2.33E-01		-7.54E-01	2.78E-01		-2.41E+00	1.68E-03				Unigene21515_All//3.00E-07//gi|109871161|gb|DW500137.1|DW500137					
Unigene21516_All	709	0.00	0.00	0.00	0.21	0.00	0.13	5.13	0.53	4.83	null	null		null	null		-7.72E+00	1.66E-01		-7.27E-01	7.15E-01		-3.27E+00	2.19E-16	Down	-8.58E-02	7.66E-01		Unigene21516_All//gi|89274163|gb|AB065602.1|//8.00E-34//At1g06980 [Arabidopsis thaliana]	Unigene21516_All//9.00E-38//AT2G30230| unknown protein	Unigene21516_All//4.00E-24//DW509989				nr -
Unigene21518_All	689	0.00	10.15	6.03	0.00	0.00	0.13	0.00	0.00	0.00	1.33E+01	5.87E-40	Up	1.26E+01	4.83E-23	Up	null	null		7.03E+00	4.77E-01		null	null		null	null		Unigene21518_All//gi|29539344|dbj|BAC67673.1|//4.00E-69//ribosomal protein S8 [Cyanidioschyzon merolae]	Unigene21518_All//4.00E-69//AT5G39240| 40S ribosomal protein S8 (RPS8B)			ko03010|Ribosome		nr +
Unigene21519_All	555	0.19	0.00	0.00	0.36	0.00	0.33	0.46	1.36	3.30	-7.56E+00	3.72E-01		-7.56E+00	3.94E-01		-8.49E+00	8.43E-02		-1.41E-01	9.35E-01		1.57E+00	4.21E-02		2.85E+00	9.46E-08	Up	Unigene21519_All//gi|224142053|ref|XP_002324373.1|//1.00E-21//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222865807|gb|EEF02938.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene21519_All//2.00E-18//AT2G29120| ATGLR2.7; intracellular ligand-gated ion channel					nr +
Unigene21522_All	716	0.00	0.00	0.00	0.00	0.00	0.00	1.95	1.93	0.00	null	null		null	null		null	null		null	null		-1.67E-02	1.01E+00		-1.09E+01	2.40E-10	Down	Unigene21522_All//gi|297612310|ref|NP_001068397.2|//8.00E-07//Os11g0657400 [Oryza sativa Japonica Group] >gi|255680330|dbj|BAF28760.2| Os11g0657400 [Oryza sativa Japonica Group]						nr +
Unigene21524_All	520	0.00	1.17	1.23	4.79	2.72	0.52	3.41	0.00	0.15	1.02E+01	1.17E-03		1.03E+01	1.16E-03		-8.19E-01	3.21E-02		-3.20E+00	7.46E-10	Down	-1.17E+01	1.41E-12	Down	-4.48E+00	1.00E-10	Down	Unigene21524_All//gi|18411885|ref|NP_565175.1|//1.00E-09//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|21537200|gb|AAM61541.1| RNA recognition motif-containing protein SEB-4 [Arabidopsis thaliana] >gi|124300976|gb|ABN04740.1| At1g78260 [Arabidopsis thaliana]		Unigene21524_All//0.00E+00//gi|109888753|gb|DW517722.1|DW517722				nr +
Unigene21526_All	467	0.00	3.80	1.71	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.14E-10	Up	1.07E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene21526_All//gi|297724159|ref|NP_001174443.1|//9.00E-42//Os05g0434000 [Oryza sativa Japonica Group] >gi|255676397|dbj|BAH93171.1| Os05g0434000 [Oryza sativa Japonica Group]	Unigene2154_All//1.00E-18//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene2154_All//1.00E-143//TC177566			GO:0005488//GO:0016772	nr -
Unigene21540_All	629	0.00	6.04	4.57	0.00	0.16	0.14	0.00	0.00	0.00	1.26E+01	1.23E-21	Up	1.22E+01	6.96E-16	Up	7.36E+00	4.56E-01		7.17E+00	4.77E-01		null	null		null	null		Unigene21540_All//gi|224004208|ref|XP_002286755.1|//4.00E-31//calmodulin [Thalassiosira pseudonana CCMP1335] >gi|209585787|gb|ACI64472.1| calmodulin [Thalassiosira pseudonana CCMP1335]	Unigene21540_All//1.00E-29//AT3G56800| CAM3 (CALMODULIN 3); calcium ion binding			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene21541_All	550	1.71	10.78	6.49	0.18	0.13	1.31	0.00	0.08	0.00	2.65E+00	1.90E-17	Up	1.92E+00	3.36E-07	Up	-5.33E-01	8.16E-01		2.86E+00	7.12E-03		6.25E+00	6.35E-01		null	null		Unigene21541_All//gi|51849627|dbj|BAD42345.1|//6.00E-68//sorbitol transporter [Malus x domestica]	Unigene21541_All//9.00E-49//AT2G16130| mannitol transporter, putative	Unigene21541_All//6.00E-38//ES816133				nr -
Unigene21542_All	502	0.00	8.88	3.39	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.11E-25	Up	1.17E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene21542_All//gi|149067212|gb|EDM16945.1|//9.00E-46//solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 3, isoform CRA_c [Rattus norvegicus]	Unigene21542_All//2.00E-30//AT5G14040| mitochondrial phosphate transporter					nr +
Unigene21547_All	594	0.00	6.91	5.11	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.25E-23	Up	1.23E+01	8.92E-17	Up	null	null		null	null		null	null		null	null		Unigene21547_All//gi|21322711|emb|CAD22154.1|//3.00E-28//pherophorin-dz1 protein [Volvox carteri f. nagariensis]						nr -
Unigene21548_All	453	0.00	0.00	0.00	0.00	0.00	0.00	4.20	0.83	2.64	null	null		null	null		null	null		null	null		-2.34E+00	1.88E-06	Down	-6.71E-01	9.77E-02									
Unigene2155_All	1672	1.60	4.49	1.24	0.60	1.17	0.73	0.46	0.67	1.00	1.49E+00	9.94E-11	Up	-3.62E-01	3.99E-01		9.78E-01	3.42E-02		2.91E-01	6.61E-01		5.68E-01	3.44E-01		1.14E+00	1.07E-02		Unigene2155_All//gi|297724159|ref|NP_001174443.1|//3.00E-40//Os05g0434000 [Oryza sativa Japonica Group] >gi|255676397|dbj|BAH93171.1| Os05g0434000 [Oryza sativa Japonica Group]	Unigene2155_All//1.00E-27//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene2155_All//1.00E-143//TC177566			GO:0003676//GO:0006260//GO:0034061//GO:0043231	nr -
Unigene21557_All	392	0.27	12.15	2.99	0.13	0.00	0.00	0.00	0.00	0.00	5.51E+00	3.99E-24	Up	3.49E+00	1.09E-04	Up	-6.99E+00	5.55E-01		-6.99E+00	6.36E-01		null	null		null	null										
Unigene21560_All	373	0.00	9.37	2.57	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	6.73E-20	Up	1.13E+01	2.46E-05	Up	null	null		null	null		null	null		null	null		Unigene21560_All//gi|298706463|emb|CBJ29450.1|//3.00E-12//protein tyrosine phosphatase [Ectocarpus siliculosus]						nr +
Unigene21561_All	383	0.00	8.47	4.03	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.88E-18	Up	1.20E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene21561_All//gi|297838641|ref|XP_002887202.1|//6.00E-12//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297333043|gb|EFH63461.1| expressed protein [Arabidopsis lyrata subsp. lyrata]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene21563_All	287	3.46	5.12	0.37	3.99	8.40	9.13	1.18	0.00	1.80	5.64E-01	3.11E-01		-3.22E+00	7.83E-04	Down	1.07E+00	8.04E-03		1.19E+00	2.63E-03		-1.02E+01	1.17E-02		6.15E-01	4.94E-01				Unigene21563_All//2.00E-48//gi|73865869|gb|DT468607.1|DT468607					
Unigene21564_All	455	0.23	2.45	2.34	0.11	0.15	0.79	0.00	0.00	0.00	3.41E+00	1.24E-04	Up	3.35E+00	3.36E-04	Up	4.67E-01	9.58E-01		2.86E+00	9.45E-02		null	null		null	null										ESTscan -
Unigene21565_All	353	0.00	0.00	0.00	0.00	0.00	0.00	4.43	2.25	1.35	null	null		null	null		null	null		null	null		-9.78E-01	3.94E-02		-1.71E+00	4.59E-04	Down									
Unigene21570_All	269	0.00	0.00	0.00	1.30	1.28	1.51	2.04	0.00	1.33	null	null		null	null		-1.81E-02	9.58E-01		2.21E-01	8.63E-01		-1.10E+01	4.61E-04	Down	-6.16E-01	4.68E-01		Unigene21570_All//gi|225432149|ref|XP_002274818.1|//7.00E-13//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene21570_All//3.00E-16//DT527500				nr -
Unigene21571_All	424	1.36	0.00	0.88	4.46	0.57	0.96	4.49	2.46	1.03	-1.04E+01	1.52E-03		-6.27E-01	5.27E-01		-2.97E+00	3.79E-08	Down	-2.22E+00	2.53E-05	Down	-8.65E-01	4.03E-02		-2.12E+00	4.75E-06	Down			Unigene21571_All//5.00E-13//TC160912					
Unigene21572_All	319	0.33	3.49	1.34	0.16	0.86	1.42	0.53	0.13	0.37	3.41E+00	1.24E-04	Up	2.03E+00	1.39E-01		2.47E+00	2.23E-01		3.18E+00	3.79E-02		-2.02E+00	3.67E-01		-5.01E-01	7.46E-01									
Unigene21576_All	277	0.19	1.10	0.19	3.24	1.99	0.16	1.07	0.75	0.58	2.54E+00	1.51E-01		2.50E-02	9.95E-01		-7.03E-01	3.25E-01		-4.31E+00	1.14E-04	Down	-5.02E-01	6.78E-01		-8.93E-01	4.71E-01		Unigene21576_All//gi|115481730|ref|NP_001064458.1|//3.00E-10//Os10g0370500 [Oryza sativa Japonica Group] >gi|19920182|gb|AAM08614.1|AC10731 4_5 Putative Glucan 1,3-beta-glucosidase precursor [Oryza sativa Japonica Group] >gi|20043013|gb|AAM08821.1|AC11333 5_1 Putative Glucan 1,3-beta-glucosidase precursor [Oryza sativa Japonica Group] >gi|31431628|gb|AAP53379.1| Cellulase containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639067|dbj|BAF26372.1| Os10g0370500 [Oryza sativa Japonica Group]		Unigene21576_All//5.00E-49//TC148256		ko00500|Starch and sucrose metabolism		nr -

Unigene21577_All	776	0.00	1.89	3.43	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	2.11E-08	Up	1.17E+01	1.07E-14	Up	null	null		null	null		null	null		null	null		Unigene21577_All//gi|17221648|dbj|BAB78478.1|//7.00E-21//preproMP73 [Cucurbita maxima]				ko03040|Spliceosome//ko03022|Basal transcription factors		nr -
Unigene21578_All	618	0.00	5.49	4.91	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.55E-19	Up	1.23E+01	8.92E-17	Up	null	null		null	null		null	null		null	null		Unigene21578_All//gi|2388584|gb|AAB71465.1|//1.00E-17//EST gb|ATTS1136 comes from this gene [Arabidopsis thaliana]				ko00270|Cysteine and methionine metabolism		nr -
Unigene21579_All	312	0.00	1.14	6.49	2.08	4.53	6.51	0.68	1.21	1.02	1.02E+01	2.46E-02		1.27E+01	3.80E-11	Up	1.12E+00	4.87E-02		1.65E+00	5.82E-04	Up	8.31E-01	4.67E-01		5.92E-01	6.13E-01					Unigene21579_All//4.00E-127//TC157475				
Unigene21582_All	264	70.75	22.26	58.90	7.74	17.22	14.03	0.00	0.00	0.00	-1.67E+00	3.19E-30	Down	-2.65E-01	5.73E-02		1.15E+00	2.80E-05	Up	8.59E-01	7.14E-03		null	null		null	null					Unigene21582_All//5.00E-15//ESS30911				
Unigene21583_All	368	0.00	1.79	3.33	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	6.25E-04	Up	1.17E+01	9.12E-07	Up	null	null		null	null		null	null		null	null		Unigene21583_All//sp|P15514|AREG_HUMAN//4.00E-68//Amphiregulin OS=Homo sapiens GN=AREG PE=1 SV=2						swissprot +
Unigene21585_All	259	0.00	0.00	0.41	3.27	3.32	0.70	4.41	0.81	0.92	null	null		8.68E+00	3.99E-01		2.37E-02	9.92E-01		-2.23E+00	9.53E-03		-2.45E+00	2.46E-04	Down	-2.26E+00	3.40E-04	Down	Unigene21585_All//gi|2509617|pir|PC_DROME//9.00E-07//Polycomb group protein Pc OS=Drosophila melanogaster GN=Pc PE=1 SV=1			Unigene21585_All//5.00E-09//DT466780			swissprot -
Unigene2159_All	1666	4.05	4.65	5.37	17.94	18.79	14.96	11.95	7.28	5.62	2.00E-01	3.72E-01		4.07E-01	4.71E-02		6.66E-02	5.85E-01		-2.62E-01	9.53E-03		-7.16E-01	1.09E-10		-1.09E+00	1.75E-21	Down	Unigene2159_All//gi|75266736|sp|Q9SZ53.1|P2C60_ARATH//1.00E-162//RecName: Full=Probable protein phosphatase 2C 60; Short=AtPP2C60 >gi|4584525|emb|CAB40756.1| protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi|7270089|emb|CAB79904.1| protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi|16209698|gb|AAL14406.1| AT4g31860/F11C18_60 [Arabidopsis thaliana] >gi|21360433|gb|AAM47332.1| AT4g31860/F11C18_60 [Arabidopsis thaliana]	Unigene2159_All//1.00E-163//AT4G31860| protein phosphatase 2C, putative / PP2C, putative	Unigene2159_All//0.00E+00//TC162207			nr +
Unigene21591_All	795	0.00	0.00	0.00	0.00	0.09	0.00	3.72	1.00	0.35	null	null		null	null		6.44E+00	6.10E-01		null	null		-1.90E+00	1.36E-07	Down	-3.41E+00	1.95E-14	Down	Unigene21591_All//gi|156763856|emb|CA099130.1|//2.00E-59//berberine bridge enzyme like protein [Nicotiana tabacum]	Unigene21591_All//3.00E-39//AT4G20860| FAD-binding domain-containing protein					nr +
Unigene21592_All	502	0.31	0.00	0.00	0.20	0.14	0.72	1.94	0.58	0.16	-8.29E+00	2.16E-01		-8.29E+00	2.45E-01		-5.33E-01	8.16E-01		1.86E+00	2.19E-01		-1.73E+00	9.67E-03		-3.61E+00	2.14E-05	Down				Unigene21592_All//2.00E-127//gi|109869959|gb|DW498935.1|DW498935				
Unigene21593_All	375	0.00	0.00	0.00	0.00	0.00	0.00	5.86	1.67	0.96	null	null		null	null		null	null		null	null		-1.81E+00	1.62E-05	Down	-2.62E+00	1.41E-08	Down	Unigene21593_All//gi|186517638|ref|NP_001119144.1|//4.00E-21//40S ribosomal protein S25 (RPS25E) [Arabidopsis thaliana]	Unigene21593_All//2.00E-22//AT4G39200| 40S ribosomal protein S25 (RPS25E)			ko03010|Ribosome		nr +
Unigene21594_All	259	0.00	0.00	0.00	0.00	0.00	0.00	1.14	6.29	20.00	null	null		null	null		null	null		null	null		2.46E+00	6.63E-06	Up	4.13E+00	4.03E-28	Up				Unigene21594_All//2.00E-14//gi|109828500|gb|DW227123.1|DW227123				
Unigene21596_All	269	0.19	0.94	3.96	3.15	1.92	0.00	0.94	0.16	0.59	2.28E+00	2.34E-01		4.35E+00	6.46E-05	Up	-7.13E-01	3.36E-01		-1.16E+01	2.43E-05	Down	-2.60E+00	1.44E-01		-6.71E-01	6.05E-01					Unigene21596_All//1.00E-46//ES811843				
Unigene21597_All	257	6.31	751.56	150.43	11.24	32.56	194.54	0.16	0.00	1.71	6.90E+00	0.00E+00	Up	4.58E+00	9.34E-174	Up	1.53E+00	4.55E-14	Up	4.11E+00	2.29E-228	Up	-7.36E+00	6.57E-01		3.37E+00	1.26E-02		Unigene21597_All//gi|35187464|gb|AAQ84323.1|//8.00E-27//fiber protein Fb31 [Gossypium barbadense]	Unigene21597_All//3.00E-22//AT5G13170| SAG29 (SENESCENCE-ASSOCIATED PROTEIN 29)	Unigene21597_All//6.00E-33//TC163895				nr -
Unigene21598_All	260	0.60	0.00	0.00	1.34	1.32	0.35	2.76	0.16	0.46	-9.24E+00	2.16E-01		-9.24E+00	2.45E-01		-1.82E-02	9.58E-01		-1.95E+00	1.96E-01		-4.10E+00	2.91E-04	Down	-2.59E+00	2.81E-03		Unigene21598_All//gi|5107822|gb|AAD40135.1|AF149413_16//3.00E-19//contains similarity to retrotransposon Ta11-1 [Arabidopsis thaliana]	Unigene21598_All//9.00E-12//ATMG01250| hypothetical protein					nr -
Unigene21600_All	322	0.00	0.00	0.17	0.93	0.86	6.17	0.13	0.13	0.00	null	null		7.37E+00	6.36E-01		-1.18E-01	9.00E-01		2.73E+00	1.12E-06	Up	-1.66E-02	1.00E+00		-7.04E+00	6.13E-01					Unigene21600_All//4.00E-07//DR453175				
Unigene21602_All	439	0.00	7.16	3.03	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	7.08E-18	Up	1.16E+01	2.40E-07	Up	null	null		null	null		null	null		null	null		Unigene21602_All//gi|222446344|dbj|BAH20802.1|//5.00E-21//protein disulfide isomerase [Triticum aestivum]	Unigene21602_All//8.00E-19//AT1G77510| ATPDIL1-2 (PDI-LIKE 1-2); protein disulfide isomerase	Unigene21602_All//1.00E-10//DR454021		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene21603_All	313	0.33	3.72	0.00	1.11	0.33	1.15	2.57	1.07	1.65	3.48E+00	7.08E-05	Up	-8.39E+00	3.94E-01		-1.75E+00	1.90E-01		5.11E-02	9.69E-01		-1.26E+00	7.98E-02		-6.33E-01	3.56E-01					Unigene21603_All//8.00E-39//DN817052				
Unigene21604_All	267	0.59	0.00	0.40	4.48	3.48	0.68	1.58	1.25	1.19	-9.20E+00	2.16E-01		-5.60E-01	7.76E-01		-3.63E-01	5.70E-01		-2.73E+00	2.36E-04	Down	-3.39E-01	7.30E-01		-4.08E-01	6.54E-01									
Unigene21605_All	260	0.40	1.56	0.00	4.60	3.18	0.35	0.00	0.48	0.31	1.95E+00	1.44E-01		-8.65E+00	3.94E-01		-5.33E-01	3.93E-01		-3.73E+00	1.43E-05	Down	8.91E+00	2.40E-01		8.26E+00	4.04E-01					Unigene21605_All//3.00E-07//gi|164287566|gb|ES798386.1|ES798386				
Unigene21606_All	224	2.10	1.58	0.95	0.22	0.92	1.41	0.57	0.00	5.69	-4.09E-01	6.69E-01		-1.14E+00	3.32E-01		2.05E+00	3.95E-01		2.67E+00	1.44E-01		-9.15E+00	2.35E-01		3.33E+00	2.39E-06	Up	Unigene21606_All//gi|240256003|ref|NP_193602.4|//5.00E-10//protein binding / structural constituent of cell wall [Arabidopsis thaliana] >gi|300681244|sp|Q9SN46.2|LRX5_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 5; Short=LRR/EXTENSIN5; Short=AtLRX5; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor	Unigene21606_All//2.00E-11//AT4G18670| protein binding / structural constituent of cell wall	Unigene21606_All//4.00E-37//TC135314				nr +
Unigene21610_All	301	5.01	0.84	0.53	1.99	2.17	0.75	3.65	1.25	0.40	-2.58E+00	7.04E-05	Down	-3.25E+00	1.40E-05	Down	1.30E-01	9.05E-01		-1.40E+00	1.58E-01		-1.55E+00	1.12E-02		-3.20E+00	1.63E-05	Down				Unigene21610_All//3.00E-20//TC147879				
Unigene21612_All	282	0.00	32.52	10.95	0.00	0.00	0.00	0.00	0.00	0.00	1.50E+01	1.63E-52	Up	1.34E+01	4.51E-17	Up	null	null		null	null		null	null		null	null										
Unigene21613_All	712	0.66	0.14	0.00	1.61	1.16	1.40	0.30	3.76	2.24	-2.22E+00	7.76E-02		-9.37E+00	8.65E-03		-4.71E-01	4.64E-01		-2.06E-01	7.39E-01		3.66E+00	2.58E-13	Up	2.91E+00	5.82E-07	Up	Unigene21613_All//gi|115187640|gb|AB184264.1|//3.00E-32//ubiquitin-conjugating enzyme [Arachis hypogaea]	Unigene21613_All//1.00E-32//AT5G59300| UBC7 (UBIQUITIN CARRIER PROTEIN 7); protein binding / ubiquitin-protein ligase	Unigene21613_All//4.00E-157//EX163878		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene21617_All	546	0.00	10.21	3.02	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	8.50E-32	Up	1.16E+01	4.31E-09	Up	null	null		null	null		null	null		null	null		Unigene21617_All//gi|159489456|ref|XP_001702713.1|//1.00E-11//nuclear ribonucleoprotein [Chlamydomonas reinhardtii] >gi|158280735|gb|EDP06492.1| nuclear ribonucleoprotein [Chlamydomonas reinhardtii]				ko03040|Spliceosome		nr +
Unigene21618_All	399	0.39	0.64	1.07	0.50	3.02	3.28	1.91	2.51	2.70	6.91E-01	6.27E-01		1.44E+00	2.53E-01		2.60E+00	3.41E-04	Up	2.72E+00	1.49E-04	Up	3.98E-01	5.45E-01		4.99E-01	3.90E-01		Unigene21618_All//gi|225459685|ref|XP_002285888.1|//8.00E-46//PREDICTED: similar to BTB/POZ domain-containing protein [Vitis vinifera]	Unigene21618_All//4.00E-45//AT4G08455| BTB/POZ domain-containing protein	Unigene21618_All//2.00E-80//gi|109826126|gb|DW224847.1|DW224847				nr -
Unigene21620_All	291	0.00	0.00	0.73	0.34	0.36	2.48	104.61	122.66	294.89	null	null		9.52E+00	1.41E-01		5.21E-02	9.67E-01		2.86E+00	7.12E-03		2.30E-01	5.55E-03		1.50E+00	4.46E-145	Up	Unigene21620_All//gi|256538309|gb|ACU82514.1|//4.00E-46//pleiotropic drug resistance protein [Cucumis sativus]	Unigene21620_All//4.00E-45//AT1G59870| PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	Unigene21620_All//8.00E-116//TC177387		ko03040|Spliceosome//ko02010|ABC transporters		nr +
Unigene21627_All	306	0.00	2.82	1.91	0.16	0.00	0.44	0.00	0.00	0.00	1.15E+01	4.95E-05	Up	1.09E+01	2.17E-03		-7.35E+00	5.55E-01		1.44E+00	6.38E-01		null	null		null	null		Unigene21627_All//gi|224139854|ref|XP_002323309.1|//1.00E-44//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222867939|gb|EEF05070.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene21627_All//2.00E-31//AT3G57600| AP2 domain-containing transcription factor, putative	Unigene21627_All//1.00E-167//ES811974	AP2-EREBP			nr -
Unigene21628_All	292	0.00	0.00	0.00	1.19	1.18	0.15	2.17	0.14	0.00	null	null		null	null		-1.81E-02	9.58E-01		-2.95E+00	8.30E-02		-3.92E+00	9.81E-04	Down	-1.11E+01	7.11E-05	Down				Unigene21628_All//2.00E-33//TC149919				
Unigene21630_All	288	4.54	1.94	0.55	0.69	1.43	0.63	0.29	0.87	0.28	-1.23E+00	3.96E-02		-3.03E+00	1.24E-04	Down	1.05E+00	4.26E-01		-1.41E-01	9.35E-01		1.57E+00	3.26E-01		-8.55E-02	9.72E-01		Unigene21630_All//gi|255548087|ref|XP_002515100.1|//5.00E-11//hypothetical protein RCOM_1340820 [Ricinus communis] >gi|223545580|gb|EEF47084.1| hypothetical protein RCOM_1340820 [Ricinus communis]						nr -
Unigene21635_All	342	0.00	3.26	3.27	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.00E-06	Up	1.17E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene21635_All//sp|P09211|GSTP1_HUMAN//8.00E-45//Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2				ko00480|Glutathione metabolism		swissprot -
Unigene21637_All	297	0.35	4.44	0.00	0.00	2.20	0.46	0.57	0.99	0.27	3.65E+00	1.28E-05	Up	-8.46E+00	3.94E-01		1.11E+01	4.92E-04	Up	8.83E+00	3.11E-01		7.91E-01	5.63E-01		-1.09E+00	5.53E-01										
Unigene21638_All	292	1.61	2.43	2.01	5.29	2.83	1.24	0.14	0.00	0.00	5.91E-01	4.78E-01		3.15E-01	7.19E-01		-9.02E-01	7.78E-02		-2.10E+00	3.41E-04	Down	-7.18E+00	6.57E-01		-7.18E+00	6.13E-01					Unigene21638_All//3.00E-07//BM359553				
Unigene21639_All	940	0.00	8.79	3.34	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.98E-47	Up	1.17E+01	2.28E-17	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene21640_All	542	0.00	8.41	1.67	0.00	0.13	0.00	0.00	0.00	0.00	1.30E+01	5.54E-26	Up	1.07E+01	4.71E-05	Up	6.99E+00	6.10E-01		null	null		null	null		null	null		Unigene21640_All//sp|Q98EB3|HLYE_ECO57//2.00E-14//Hemolysin E OS=Escherichia coli O157:H7 GN=hlyE PE=3 SV=3						swissprot -
Unigene21642_All	212	0.00	0.00	0.00	0.00	0.32	5.97	0.20	4.34	1.88	null	null		null	null		8.34E+00	6.10E-01		1.25E+01	1.55E-07	Up	4.44E+00	1.66E-05	Up	3.24E+00	2.14E-02										
Unigene21643_All	356	0.00	4.55	2.69	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.97E-09	Up	1.14E+01	2.46E-05	Up	null	null		null	null		null	null		null	null		Unigene21643_All//sp|Q04691|FBP1_DROME//5.00E-18//Fat-body protein 1 OS=Drosophila melanogaster GN=Fbp1 PE=2 SV=2						swissprot -
Unigene21646_All	294	0.00	4.14	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.47E-07	Up	1.03E+01	2.50E-02		null	null		null	null		null	null		null	null										
Unigene21648_All	305	0.00	0.00	0.00	3.92	1.02	0.00	0.00	0.00	0.00	null	null		null	null		-1.95E+00	1.81E-03		-1.19E-01	1.76E-07	Down	null	null		null	null										
Unigene21649_All	271	0.39	3.93	2.75	4.23	2.16	1.67	2.18	0.31	0.74	3.35E+00	2.17E-04	Up	2.83E+00	8.52E-03		-9.69E-01	1.14E-01		-1.34E+00	4.01E-02		-2.82E+00	7.17E-03		-1.57E+00	6.49E-02		Unigene21649_All//gi|15226168|ref|NP_178215.1|//6.00E-09//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene21649_All//2.00E-10//AT2G01050| nucleic acid binding / zinc ion binding	Unigene21649_All//5.00E-52//DW516140				nr -
Unigene2165_All	474	2.98	1.28	2.13	1.79	0.94	0.29	6.96	4.67	0.67	-1.22E+00	3.33E-02		-4.82E-01	3.97E-01		-9.20E-01	2.17E-01		-2.64E+00	3.54E-03		-5.74E-01	6.21E-02		-3.37E+00	7.22E-16	Down	Unigene2165_All//gi|115479373|ref|NP_001063280.1|//2.00E-35//Os09g0440200 [Oryza sativa Japonica Group] >gi|113631513|dbj|BAF25194.1| Os09g0440200 [Oryza sativa Japonica Group]	Unigene2165_All//1.00E-37//AT3G42930| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: intracellular; EXPRESSED IN: stem; CONTAINS InterPro DOMAIN/s: BRCT (InterPro:IPR001357); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G26270.1); Has 208 Blast hits to 206 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 118; Fungi - 52; Plants - 24; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink).				GO:0044464	nr -
Unigene21658_All	323	0.00	2.35	0.16	0.15	0.53	0.42	3.27	2.07	1.11	1.12E+01	1.77E-04	Up	7.37E+00	6.36E-01		1.79E+00	5.20E-01		1.44E+00	6.38E-01		-6.61E-01	2.78E-01		-1.56E+00	9.40E-03		Unigene21658_All//gi|224107569|ref|XP_002333494.1|//5.00E-08//predicted protein [Populus trichocarpa] >gi|222837063|gb|EEE75442.1| predicted protein [Populus trichocarpa]						nr +

Unigene2166_All	1030	0.56	0.39	0.72	0.63	0.33	0.26	3.69	0.32	0.31	-5.06E-01	6.00E-01		3.73E-01	6.23E-01		-9.11E-01	3.04E-01		-1.26E+00	1.83E-01		-3.51E+00	3.68E-18	Down	-3.58E+00	4.00E-19	Down	Unigene2166_All//gi|115479373|ref|NP_001063280.1|//1.00E-34//Os09g0440200 [Oryza sativa Japonica Group] >gi|113631513|dbj|BAF25194.1|Os09g0440200 [Oryza sativa Japonica Group]	Unigene2166_All//1.00E-36//AT3G43930| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: intracellular; EXPRESSED IN: stem; CONTAINS InterPro DOMAIN/s: BRCT (InterPro:IPR001357); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G26270.1); Has 208 Blast hits to 206 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 118; Fungi - 52; Plants - 24; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink).				GO:0044464	nr -
Unigene21660_All	492	0.53	0.00	0.54	0.41	1.40	0.55	2.06	1.36	0.40	-9.05E+00	6.71E-02		2.55E-02	1.00E+00		1.79E+00	6.10E-02		4.44E-01	7.64E-01		-6.02E-01	3.45E-01		-2.35E+00	5.84E-04	Down		Unigene21660_All//0.00E+00//gi|21095170|gb|BQ407483.1|BQ407483					
Unigene21661_All	365	2.72	1.11	0.00	0.41	1.60	0.62	1.51	1.37	0.87	-1.29E+00	6.74E-02		-1.14E+01	1.77E-05	Down	1.97E+00	7.04E-02		5.96E-01	7.21E-01		-1.32E-01	8.80E-01		-7.86E-01	3.62E-01		Unigene21661_All//gi|15228894|ref|NP_191192.1|//1.00E-42//N2,N2-dimethylguanosine tRNA methyltransferase family protein [Arabidopsis thaliana] >gi|7572931|emb|CAB87432.1| N2,N2-dimethylguanosine tRNA methyltransferases-like protein [Arabidopsis thaliana]	Unigene21661_All//1.00E-40//AT3G36330| N2,N2-dimethylguanosine tRNA methyltransferase family protein	Unigene21661_All//1.00E-149//ES800657				nr -
Unigene21662_All	313	0.00	0.00	0.00	0.00	0.00	0.00	32.82	5.34	8.53	null	null		null	null		null	null		null	null		-2.62E+00	3.69E-36	Down	-1.94E+00	3.93E-26	Down								
Unigene21663_All	269	0.00	0.00	0.00	2.59	1.28	0.00	0.31	0.00	0.00	null	null		null	null		-1.02E+00	2.25E-01		-1.13E+01	1.96E-04	Down	-8.30E+00	4.04E-01		-8.30E+00	3.58E-01									
Unigene21664_All	595	0.00	2.13	1.97	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	2.86E-07	Up	1.09E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene21664_All//sp|P05787|K2C8_HUMAN//7.00E-60//Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7								swissprot -
Unigene21666_All	288	0.00	0.00	0.00	0.35	1.43	1.88	0.00	0.00	1.94	null	null		null	null		2.05E+00	1.47E-01		2.44E+00	4.41E-02		null	null		1.09E+01	3.28E-04	Up	Unigene21666_All//gi|145362122|ref|NP_973484.2|//1.00E-37//LCV3 (like cov 3) [Arabidopsis thaliana]	Unigene21666_All//4.00E-39//AT2G18460| LCV3 (like cov 3)	Unigene21666_All//3.00E-07//gi|48778652|gb|CO088018.1|CO088018				nr -
Unigene21667_All	325	0.32	0.00	0.00	0.31	0.32	0.00	1.17	2.31	4.54	-8.33E+00	3.72E-01		-8.33E+00	3.94E-01		5.27E-02	9.67E-01		-8.26E+00	4.00E-01		9.83E-01	1.89E-01		1.95E+00	2.09E-04	Up								
Unigene21668_All	341	0.31	0.89	3.12	0.58	0.71	0.00	0.00	0.00	0.00	1.54E+00	3.23E-01		3.35E+00	3.36E-04	Up	2.75E-01	8.95E-01		-9.19E+00	1.34E-01		null	null		null	null									ESTscan +
Unigene2167_All	2054	5.99	7.33	8.79	13.85	10.86	7.37	30.16	13.33	5.31	2.92E-01	5.01E-02		5.54E-01	3.78E-05		-3.50E-01	2.39E-04		-9.11E-01	1.93E-19		-1.18E+00	1.58E-71	Down	-2.50E+00	1.52E-210	Down	Unigene2167_All//gi|115479373|ref|NP_001063280.1|//1.00E-165//Os09g0440200 [Oryza sativa Japonica Group] >gi|113631513|dbj|BAF25194.1|Os09g0440200 [Oryza sativa Japonica Group]	Unigene2167_All//1.00E-142//AT2G26270| unknown protein	Unigene2167_All//0.00E+00//gi|164342689|gb|ES830952.1|ES830952			GO:0044464	nr -
Unigene21671_All	996	0.11	0.41	0.05	0.25	0.24	0.14	0.47	1.64	5.96	1.95E+00	1.44E-01		-9.74E-01	7.21E-01		-4.75E-02	9.51E-01		-8.79E-01	6.16E-01		1.81E+00	2.86E-04	Up	3.67E+00	1.61E-29	Up								
Unigene21682_All	318	2.96	0.00	0.00	2.35	3.47	3.12	1.20	0.26	0.00	-1.15E+01	1.46E-05	Down	-1.15E+01	3.35E-05	Down	5.61E-01	4.27E-01		4.11E-01	6.02E-01		-2.19E+00	8.75E-02		-1.02E+01	4.19E-03			Unigene21682_All//4.00E-130//CO115486					
Unigene21684_All	231	1.13	6.14	0.00	1.29	2.39	1.17	1.10	1.63	1.03	2.44E+00	2.48E-04	Up	-1.01E+01	8.57E-02		8.82E-01	4.21E-01		-1.41E-01	9.21E-01		5.68E-01	6.37E-01		-8.58E-02	9.57E-01		Unigene21684_All//gi|91806656|gb|AB666055.1|//1.00E-18//ARID/BRIGHT DNA-binding domain-containing protein/ELM2 domain-containing protein/Myb-like DNA-binding domain-containing protein [Arabidopsis thaliana]	Unigene21684_All//6.00E-20//AT4G11400| ARID/BRIGHT DNA-binding domain-containing protein / ELM2 domain-containing protein / Myb-like DNA-binding domain-containing protein	Unigene21684_All//3.00E-87//TC160340				nr +
Unigene21687_All	1271	0.12	0.16	0.29	0.00	0.03	0.00	4.92	2.17	0.97	3.69E-01	8.16E-01		1.25E+00	3.66E-01		4.76E+00	8.30E-01		null	null		-1.18E+00	5.57E-08	Down	-2.34E+00	2.50E-20	Down	Unigene21687_All//gi|6692128|gb|AAF24593.1|AC007654_9//7.00E-81//T19E23.14 [Arabidopsis thaliana]	Unigene21687_All//4.00E-79//AT1G31350| F-box family protein					nr +
Unigene21691_All	730	0.00	0.00	0.00	0.00	0.00	0.00	1.56	1.66	0.00	null	null		null	null		null	null		null	null		8.65E-02	8.83E-01		-1.06E+01	1.65E-08	Down								ESTscan +
Unigene21694_All	226	0.23	2.02	4.48	1.98	1.83	0.40	0.00	0.37	0.00	3.12E+00	3.58E-02		4.27E+00	1.19E-04	Up	-1.18E-01	8.86E-01		-2.31E+00	7.81E-02		8.53E+00	4.01E-01		null	null			Unigene21694_All//9.00E-109//gi|48810753|gb|CO112066.1|CO112066					
Unigene21696_All	569	0.00	0.53	0.00	0.00	0.12	0.56	1.63	0.66	3.92	9.06E+00	4.43E-02		null	null		6.92E+00	6.10E-01		9.12E+00	4.07E-02		-1.31E+00	4.81E-02		1.26E+00	9.46E-04	Up	Unigene21696_All//gi|297851466|ref|XP_002893614.1|//2.00E-45//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339456|gb|EFH69873.1|lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene21696_All//2.00E-44//AT1G30370| lipase class 3 family protein	Unigene21696_All//3.00E-24//TC175119				nr +
Unigene21705_All	294	0.36	2.07	0.00	3.73	3.75	0.61	0.72	0.71	0.41	2.54E+00	2.46E-02		-8.48E+00	3.94E-01		7.90E-03	9.92E-01		-2.60E+00	7.13E-04	Down	-1.67E-02	1.02E+00		-8.23E-01	5.99E-01								
Unigene21706_All	280	0.00	2.90	2.85	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.39E-05	Up	1.15E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene21706_All//gi|3719443|gb|AAC6337.2|//3.00E-22//lipid transfer protein [Brassica oleracea]	Unigene21706_All//4.00E-20//AT2G38530| LTP2 (LIPID TRANSFER PROTEIN 2); lipid binding					nr -
Unigene21707_All	999	0.10	5.38	2.40	0.00	0.00	0.00	0.00	0.00	0.00	5.68E+00	1.66E-27	Up	4.52E+00	8.08E-11	Up	null	null		null	null		null	null		null	null		Unigene21707_All//gi|255072339|ref|XP_002499844.1|//3.00E-09//alpha-2 macroglobulin family-like protein [Micromonas sp. RCC299] >gi|226515106|gb|ACO61102.1|alpha-2 macroglobulin family-like protein [Micromonas sp. RCC299]						nr -
Unigene21709_All	273	0.00	6.87	3.51	0.00	0.25	0.00	0.00	0.00	0.00	1.27E+01	1.11E-10	Up	1.18E+01	2.46E-05	Up	7.98E+00	6.10E-01		null	null		null	null		null	null		Unigene21709_All//gi|148443410|gb|ABH11435.2|//5.00E-30//cytosolic glucose-6-phosphate isomerase [Emiliania huxleyi]	Unigene21709_All//3.00E-15//AT5G42740| glucose-6-phosphate isomerase, cytosolic (PGIC)			ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene21720_All	279	0.75	7.45	0.19	0.18	1.11	0.32	2.58	6.59	6.85	3.31E+00	6.32E-08	Up	-1.97E+00	3.81E-01		2.64E+00	1.61E-01		8.59E-01	7.94E-01		1.36E+00	2.16E-03		1.41E+00	8.61E-04	Up								
Unigene21722_All	400	0.00	0.00	0.40	0.00	0.43	0.23	0.42	2.61	1.59	null	null		8.64E+00	2.39E-01		8.75E+00	2.27E-01		7.82E+00	4.77E-01		2.63E+00	2.86E-04	Up	1.91E+00	2.60E-02									
Unigene21724_All	656	0.00	0.00	0.00	0.15	0.00	0.00	2.19	1.15	0.30	null	null		null	null		-7.25E+00	3.13E-01		-7.25E+00	4.00E-01		-9.34E-01	6.12E-02		-2.85E+00	2.40E-06	Down	Unigene21724_All//gi|226505956|ref|NP_001149335.1|//4.00E-39//LOC100282958 [Zea mays] >gi|195626474|gb|ACG35062.1|auxin-induced protein PCNT115 [Zea mays]	Unigene21724_All//1.00E-35//AT1G60710| ATB2; oxidoreductase	Unigene21724_All//3.00E-15//CO080482			ko00053|Ascorbate and aldarate metabolism	nr +
Unigene21728_All	254	21.42	13.17	16.77	18.63	23.05	26.67	54.10	20.08	24.00	-7.02E-01	5.88E-03		-3.53E-01	2.06E-01		3.07E-01	2.48E-01		5.18E-01	2.33E-02		-1.43E+00	5.50E-22	Down	-1.17E+00	6.70E-17	Down		Unigene21728_All//5.00E-129//gi|21093515|gb|BQ405828.1|BQ405828					
Unigene21733_All	416	0.00	16.81	7.55	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	5.86E-40	Up	1.29E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene21733_All//gi|20140684|sp|Q944W6.1|TCTP_BRAOL//2.00E-144//RecName: Full=Translationally-controlled tumor protein homolog; Short=TCTP >gi|16033628|gb|AAL13303.1|AF418663_1 translationally controlled tumor protein [Brassica oleracea]	Unigene21733_All//4.00E-15//AT3G16640| TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN)					nr +
Unigene21737_All	347	2.41	0.29	0.00	1.15	2.48	1.17	0.00	0.60	0.69	-3.05E+00	2.11E-03		-1.12E+01	1.19E-04	Down	1.11E+00	1.63E-01		2.85E-02	9.85E-01		9.23E+00	7.85E-02		9.43E+00	4.39E-02		Unigene21737_All//gi|15241158|ref|NP_197471.1|//4.00E-37//MATE efflux protein-related [Arabidopsis thaliana] >gi|67633808|gb|AAY78828.1| MATE efflux protein-related [Arabidopsis thaliana]	Unigene21737_All//7.00E-33//AT5G19700| MATE efflux protein-related	Unigene21737_All//5.00E-28//gi|78347917|gb|DT568191.1|DT568191				nr -
Unigene21742_All	234	0.00	9.53	5.23	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.09E-12	Up	1.24E+01	9.12E-07	Up	null	null		null	null		null	null		null	null		Unigene21742_All//gi|17473703|gb|AAL38307.1|//1.00E-28//germin-like protein [Arabidopsis thaliana] >gi|20148495|gb|AAM10138.1|germin-like protein [Arabidopsis thaliana]	Unigene21742_All//8.00E-22//AT1G72610| GER1 (GERMIN-LIKE PROTEIN 1); oxalate oxidase					nr +
Unigene21743_All	241	28.66	12.40	36.46	27.08	26.86	15.55	0.18	0.00	0.33	-1.21E+00	1.82E-07	Down	3.47E-01	9.77E-02		-1.15E-02	9.58E-01		-8.00E-01	4.02E-04		-7.45E+00	6.57E-01		9.14E-01	7.50E-01									
Unigene21749_All	433	0.00	1.87	2.58	0.35	0.32	0.21	0.00	0.00	0.00	1.09E+01	9.39E-05	Up	1.13E+01	3.43E-06	Up	-1.18E-01	9.11E-01		-7.26E-01	7.15E-01		null	null		null	null									
Unigene21751_All	676	11.15	1.20	3.15	0.00	0.20	0.00	0.13	0.00	0.00	-3.22E+00	7.08E-27	Down	-1.82E+00	1.55E-13	Down	7.67E+00	3.19E-01		null	null		-6.97E+00	4.04E-01		-6.97E+00	3.58E-01			Unigene21751_All//1.00E-27//FL577251					
Unigene21754_All	364	0.14	0.28	0.59	0.14	0.76	0.50	4.88	6.89	67.20	9.54E-01	7.26E-01		2.03E+00	3.61E-01		2.47E+00	2.23E-01		1.86E+00	4.58E-01		4.98E-01	1.76E-01		3.78E+00	1.09E-122	Up	Unigene21754_All//gi|3287834|sp|Q39760.1|DCS2_GOSAR//2.00E-52//RecName: Full=(+)-delta-cadinene synthase isozyme XC14; Short=D-cadinene synthase XC14 >gi|1043314|gb|AAA93065.1| (+)-delta-cadinene synthase isozyme XC14 [Gossypium arboreum]	Unigene21754_All//1.00E-23//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene21754_All//4.00E-143//TC129587	ko00904|Diterpenoid biosynthesis		nr +
Unigene2176_All	638	47.81	16.52	41.31	60.04	67.20	113.12	53.61	72.06	52.33	-1.53E+00	2.19E-43	Down	-2.11E-01	4.90E-02		1.62E-01	5.77E-02		9.14E-01	2.90E-48		4.27E-01	9.30E-10		-3.50E-02	7.10E-01		Unigene2176_All//gi|82621166|gb|AB586271.1|//4.00E-82//adenine phosphoribosyltransferase-like [Solanum tuberosum]	Unigene2176_All//6.00E-51//AT1G27450| APT1 (ADENINE PHOSPHORIBOSYL TRANSFERASE 1); adenine phosphoribosyltransferase	Unigene2176_All//0.00E+00//gi|21103660|gb|BQ415973.1|BQ415973	ko00230|Purine metabolism	GO:0005618//GO:0009536//GO:0010038//GO:0016020//GO:0016763//GO:0043096	nr -
Unigene21761_All	393	0.00	0.00	0.00	0.13	1.66	2.07	0.75	0.74	0.10	null	null		null	null		3.71E+00	3.55E-03		4.03E+00	5.91E-04	Up	-1.66E-02	1.02E+00		-2.89E+00	6.76E-02									
Unigene21773_All	450	0.00	0.00	0.24	0.00	0.23	0.50	1.41	3.81	10.00	null	null		7.89E+00	3.99E-01		7.84E+00	4.56E-01		8.97E+00	1.19E-01		1.43E+00	1.99E-03		2.83E+00	7.34E-18	Up	Unigene21773_All//gi|28416869|gb|AA042965.1|//2.00E-09//At2g35290 [Arabidopsis thaliana]	Unigene21773_All//1.00E-10//AT2G35290| unknown protein	Unigene21773_All//0.00E+00//TC150538				nr +
Unigene21774_All	837	0.00	3.39	1.65	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.83E-16	Up	1.07E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene21774_All//sp|P11153|LIPL_CAVPO//1.00E-24//Lipoprotein lipase OS=Cavia porcellus GN=LPL PE=2 SV=1								swissprot -
Unigene2178_All	2221	4.66	9.88	3.98	5.07	9.88	12.06	21.24	21.19	39.78	1.08E+00	1.58E-18	Up	-2.29E-01	2.43E-01		9.62E-01	7.97E-18		1.25E+00	5.78E-30	Up	-3.80E-03	1.00E+00		9.05E-01	1.07E-67		Unigene2178_All//gi|15210142|ref|NP_196292.1|//0.00E+00//lectin protein kinase family protein [Arabidopsis thaliana] >gi|9759302|dbj|BAB09808.1|lectin-like protein kinase [Arabidopsis thaliana]	Unigene2178_All//0.00E+00//AT5G06740| lectin protein kinase family protein	Unigene2178_All//0.00E+00//TC157540	ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0030246	nr -
Unigene21780_All	315	0.00	0.64	0.00	1.90	0.00	0.00	0.67	0.00	0.00	9.33E+00	1.37E-01		null	null		-1.09E+01	1.78E-04	Down	-1.09E-01	7.70E-04	Down	-9.39E+00	7.44E-02		-9.39E+00	5.80E-02									
Unigene21781_All	285	0.00	0.00	0.00	0.00	0.00	0.00	6.08	11.59	0.00	null	null		null	null		null	null		null	null		9.30E-01	2.30E-03		-1.26E+01	8.37E-13	Down								ESTscan -
Unigene21784_All	413	0.00	2.82	6.58	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.05E-06	Up	1.27E+01	5.43E-15	Up	null	null		null	null		null	null		null	null		Unigene21784_All//sp|P01857|IGHG1_HUMAN//1.00E-71//Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1								swissprot -
Unigene21786_All	269	3.89	0.00	0.00	0.37	3.07	1.18	0.31	0.47	0.30	-1.19E+01	3.80E-06	Down	-1.19E+01	9.32E-06	Down	3.05E+00	1.99E-03		1.67E+00	3.09E-01		5.68E-01	7.82E-01		-8.60E-02	9.72E-01		Unigene21786_All//gi|22795064|gb|AAN05433.1|//9.00E-31//phospholipase D delta isoform Ia [Gossypium hirsutum]	Unigene21786_All//1.00E-28//AT4G35790| ATPLDDELTA; phospholipase D		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr +
Unigene21787_All	287	14.04	5.83	3.90	14.23	9.24	25.18	22.98	10.63	6.11	-1.27E+00	5.26E-05	Down	-1.85E+00	1.20E-07	Down	-6.23E-01	3.07E-02		8.23E-01	1.26E-04		-1.11E+00	1.14E-07	Down	-1.91E+00	1.04E-16	Down	Unigene21787_All//gi|192910906|gb|ACF06561.1|//1.00E-13//ribosomal protein L18a [Elaeis guineensis]	Unigene21787_All//1.00E-13//AT2G34480| 60S ribosomal protein L18A (RPL18aB)	Unigene21787_All//2.00E-55//ES844049	ko03010|Ribosome		nr +
Unigene21788_All	378	0.00	3.08	3.10	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.05E-06	Up	1.16E+01	1.77E-06	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene21789_All	400	0.13	2.28	0.00	0.62	0.34	0.23	2.75	4.18	0.40	4.12E+00	2.34E-04	Up	-7.03E+00	6.24E-01		-8.55E-01	5.73E-01		-1.46E+00	4.07E-01		6.05E-01	1.94E-01		-2.79E+00	6.37E-05	Down								

Unigene2179_All	2597	3.81	5.01	2.69	2.51	3.00	2.33	5.73	8.76	35.36	3.97E-01	1.20E-02		-5.03E-01	8.25E-03		2.54E-01	2.73E-01		-1.09E-01	6.93E-01		6.11E-01	2.50E-09		2.63E+00	0.00E+00	Up	Unigene2179_All//gi|15227189|ref|NP_182322.1|//1.00E-173//RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase [Arabidopsis thaliana] >gi|75319082|sp|P93050.1|RKF3_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase RKF3; AltName: Full=Receptor-like kinase in flowers 3; Flags: Precursor >gi|1785621|emb|CAB06335.1| At1g22324 [Arabidopsis thaliana] >gi|2465927|gb|AAC50045.1| receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi|14335116|gb|AAK59837.1| At2g48010/T9J23.16 [Arabidopsis thaliana] >gi|23308235|gb|AAN18087.1| At2g48010/T9J23.16 [Arabidopsis thaliana]	Unigene2179_All//0.00E+00//AT2G4801 0| RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase	Unigene2179_All//0.00E+00//TC155154		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene21795_All	294	0.00	5.17	2.54	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.10E-08	Up	1.13E+01	3.28E-04	Up	null	null		null	null		null	null		null	null		Unigene21795_All//gi|1216391|gb|AAC49182.1|//1.00E-28//myrosinase-associated protein [Brassica napus] >gi|1589010|prf|2209432B myrosinase-associated protein:ISOTYPE=4	Unigene21795_All//3.00E-26//AT3G14210| ESM1 (epithiospecifier modifier 1); carboxylesterase/ hydrolase, acting on ester bonds					nr +
Unigene21796_All	406	0.26	1.00	3.67	0.00	0.93	0.56	0.00	0.00	0.00	1.95E+00	1.44E-01		3.83E+00	3.20E-06	Up	9.87E+00	1.96E-02		9.12E+00	1.19E-01		null	null		null	null		Unigene21796_All//gi|15228003|ref|NP_181807.1|//2.00E-20//CSY3 (citrate synthase 3); citrate (SI)-synthase [Arabidopsis thaliana] >gi|73917790|sp|Q9SJH7.1|CISY3_ARATH RecName: Full=Citrate synthase 3, peroxisomal; Flags: Precursor >gi|15081644|gb|AAK82477.1| At2g42790/F7D19.21 [Arabidopsis thaliana] >gi|21700853|gb|AAMU0550.1| At2g42790/F7D19.21 [Arabidopsis thaliana]	Unigene21796_All//1.00E-21//AT2G42790| CSY3 (citrate synthase 3); citrate (SI)-synthase			ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene2180_All	2253	1.16	0.99	0.95	3.18	2.34	2.41	4.20	1.08	1.61	-2.31E-01	5.78E-01		-2.97E-01	4.77E-01		-4.45E-01	3.67E-02		-4.05E-01	7.34E-02		-1.97E+00	1.02E-23	Down	-1.39E+00	3.40E-15	Down	Unigene2180_All//gi|159461700|gb|AB96888.1|//0.00E+00//CMT-type DNA-methyltransferase [Elaeis guineensis]	Unigene2180_All//5.00E-157//AT1G80740| CMT1 (CHROMOMETHYLASE 1); DNA binding / chromatin binding	Unigene2180_All//1.00E-159//TC166584		ko00270|Cysteine and methionine metabolism	GO:0005488//GO:0008757//GO:0009793//GO:0016458//GO:0032776//GO:0034968//GO:0043229	nr -
Unigene21800_All	570	0.00	0.53	0.00	0.09	0.60	0.79	0.37	0.95	4.12	9.06E+00	4.43E-02		null	null		2.79E+00	1.14E-01		3.18E+00	3.79E-02		1.36E+00	1.44E-01		3.47E+00	1.50E-11	Up							
Unigene21801_All	810	0.06	0.00	0.00	0.37	0.47	0.56	0.57	0.93	2.51	-6.01E+00	6.12E-01		-6.01E+00	6.24E-01		3.42E-01	8.36E-01		5.96E-01	6.40E-01		6.94E-01	3.66E-01		2.13E+00	2.44E-06	Up	Unigene21801_All//gi|297598339|ref|NP_001045426.2|//3.00E-41//Os01g0953100 [Oryza sativa Japonica Group] >gi|255674080|dbj|BAF07340.2| Os01g0953100 [Oryza sativa Japonica Group]	Unigene21801_All//8.00E-30//AT5G45470| unknown protein					nr -
Unigene21807_All	417	0.50	0.49	0.13	1.08	1.57	1.30	0.41	0.80	7.74	-4.64E-02	9.88E-01		-1.97E+00	3.81E-01		5.45E-01	5.86E-01		2.74E-01	7.83E-01		9.83E-01	4.24E-01		4.25E+00	4.59E-18	Up			Unigene21807_All//6.00E-25//DT462517				
Unigene21808_All	302	8.32	5.87	20.28	2.80	1.60	0.30	0.00	0.00	0.26	-5.02E-01	2.17E-01		1.29E+00	5.83E-07	Up	-8.13E-01	2.80E-01		-3.23E+00	1.04E-03		null	null		8.04E+00	4.04E-01								
Unigene21809_All	252	1.25	1.61	0.42	0.00	0.27	0.00	4.53	2.65	0.00	3.69E-01	7.24E-01		-1.56E+00	3.30E-01		8.09E+00	6.10E-01		null	null		-7.72E-01	1.81E-01		-1.21E+01	1.65E-08	Down			Unigene21809_All//2.00E-08//FL684450				
Unigene2181_All	2284	7.49	5.30	7.83	10.60	10.86	7.99	9.16	5.23	2.65	-4.99E-01	1.96E-04		6.46E-02	6.59E-01		3.44E-02	8.34E-01		-4.08E-01	1.75E-04		-8.08E-01	1.34E-13		-1.79E+00	7.74E-47	Down	Unigene2181_All//gi|115453945|ref|NP_001050573.1|//0.00E+00//Os03g0586900 [Oryza sativa Japonica Group] >gi|108709563|gb|ABF97358.1| DNA helicase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549044|dbj|BAF12487.1| Os03g0586900 [Oryza sativa Japonica Group]	Unigene2181_All//0.00E+00//AT2G03270| DNA-binding protein, putative	Unigene2181_All//0.00E+00//TC174377		ko03030|DNA replication	GO:0003676//GO:0016462//GO:0032559	nr -
Unigene21811_All	412	0.00	0.00	0.00	0.00	0.00	0.00	4.31	1.62	0.87	null	null		null	null		null	null		null	null		-1.41E+00	1.85E-03		-2.31E+00	3.08E-06	Down	Unigene21811_All//gi|300266195|gb|EFJ50383.1|//3.00E-36//ribosomal protein L18A component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene21811_All//3.00E-35//AT2G34480| 60S ribosomal protein L18A (RPL18aB)			ko03010|Ribosome		nr +
Unigene21816_All	317	0.00	0.00	0.34	0.63	0.87	1.28	2.40	0.53	9.05	null	null		8.39E+00	3.99E-01		4.67E-01	8.17E-01		1.03E+00	4.28E-01		-2.19E+00	7.77E-03		1.91E+00	1.22E-07	Up			Unigene21816_All//3.00E-131//gi|28352665|gb|DT572939.1|DT572939				
Unigene21819_All	250	0.42	0.00	5.11	2.39	1.38	3.97	1.86	0.50	1.12	-8.71E+00	3.72E-01		3.61E+00	3.41E-05	Up	-7.96E-01	3.88E-01		7.33E-01	3.21E-01		-1.89E+00	8.00E-02		-7.38E-01	4.26E-01				Unigene21819_All//3.00E-07//TC137480				
Unigene21821_All	566	0.00	6.62	1.41	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.40E-21	Up	1.05E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene21821_All//gi|116060901|emb|CAL57379.1|//2.00E-20//protein synthesis initiation factor eIF2 beta (ISS) [Ostreococcus tauri]	Unigene21821_All//2.00E-07//AT5G20920| EIF2 BETA; translation initiation factor					nr +
Unigene21822_All	965	0.00	5.67	1.82	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	3.25E-31	Up	1.08E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene21822_All//gi|159491160|ref|XP_001703541.1|//1.00E-08//flagellar associated protein [Chlamydomonas reinhardtii] >gi|158280465|gb|EDP06223.1| flagellar associated protein [Chlamydomonas reinhardtii]						nr -
Unigene21823_All	363	0.00	7.40	1.91	0.55	0.19	1.37	0.00	0.00	0.11	1.29E+01	2.81E-15	Up	1.09E+01	6.16E-04	Up	-1.53E+00	4.16E-01		1.32E+00	2.52E-01		null	null		6.78E+00	6.45E-01								
Unigene21824_All	354	0.15	0.00	0.90	4.08	0.97	0.51	0.00	0.12	0.00	-7.21E+00	6.12E-01		2.61E+00	1.46E-01		-2.07E+00	2.41E-04	Down	-3.00E+00	1.34E-05	Down	6.88E+00	6.35E-01		null	null				Unigene21824_All//4.00E-07//TC153175				
Unigene21827_All	326	1.60	0.31	0.00	3.36	0.74	0.55	0.65	0.26	0.37	-2.37E+00	4.76E-02		-1.06E+01	4.75E-03		-2.18E+00	1.20E-03		-2.60E+00	7.13E-04	Down	-1.34E+00	4.30E-01		-8.23E-01	5.99E-01		Unigene21827_All//gi|11072009|gb|AG28888.1|AC008113.4/7.00E-28//F12A21.8 [Arabidopsis thaliana]	Unigene21827_All//3.00E-29//AT1G67790| unknown protein					nr +
Unigene21828_All	421	0.00	2.53	2.53	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.81E-06	Up	1.13E+01	6.62E-06	Up	null	null		null	null		null	null		null	null								
Unigene2183_All	1104	17.63	49.06	14.23	98.82	156.24	113.07	25.12	58.83	183.53	1.48E+00	4.74E-72	Up	-3.09E-01	2.08E-02		6.61E-01	5.06E-73		1.94E-01	1.89E-05		1.23E+00	7.41E-80	Up	2.87E+00	0.00E+00	Up	Unigene2183_All//gi|15450373|gb|AAK96480.1|//3.00E-65//AT4g32480/F8B4_180 [Arabidopsis thaliana] >gi|16974485|gb|AAL31246.1| AT4g32480/F8B4_180 [Arabidopsis thaliana]	Unigene2183_All//8.00E-64//AT4G32480| unknown protein	Unigene2183_All//0.00E+00//TC141876				nr -
Unigene21830_All	321	2.44	0.00	0.00	2.95	0.43	0.00	0.13	0.78	0.00	-1.13E+01	1.09E-04	Down	-1.13E+01	2.22E-04	Down	-2.78E+00	4.58E-04	Down	-1.15E+01	6.01E-06	Down	2.57E+00	1.53E-01		-7.04E+00	6.13E-01				Unigene21830_All//3.00E-128//CK640433				
Unigene21833_All	675	0.16	0.00	0.47	0.52	0.87	0.74	2.88	5.08	0.53	-7.28E+00	3.72E-01		1.61E+00	3.05E-01		7.48E-01	4.81E-01		5.11E-01	6.41E-01		8.17E-01	6.02E-03		-2.44E+00	3.73E-07	Down	Unigene21833_All//gi|219879368|gb|ACL51016.1|//4.00E-12//squamosa promoter-binding protein [Citrus trifoliata]	Unigene21833_All//6.00E-11//AT5G50570| squamosa promoter-binding protein, putative	Unigene21833_All//8.00E-41//TC140706	SBP			nr +
Unigene21835_All	330	0.00	0.00	3.71	0.45	1.25	0.14	0.00	0.00	0.00	null	null		1.19E+01	9.12E-07	Up	1.47E+00	2.80E-01		-1.73E+00	5.01E-01		null	null		null	null		Unigene21835_All//gi|255596472|ref|XP_002536547.1|//2.00E-07//Transcription elongation factor greA, putative [Ricinus communis] >gi|223519331|gb|EEF25837.1| Transcription elongation factor greA, putative [Ricinus communis]						nr -
Unigene21836_All	258	0.00	26.71	11.15	0.00	0.00	0.00	0.00	0.00	0.00	1.47E+01	2.25E-39	Up	1.34E+01	6.96E-16	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene2184_All	1978	36.90	13.60	21.13	32.61	50.33	48.89	17.59	2.68	17.58	-1.44E+00	8.67E-94	Down	-8.04E-01	1.60E-35		6.26E-01	2.20E-38		5.84E-01	7.31E-30		-2.71E+00	1.04E-125	Down	-7.00E-04	9.92E-01		Unigene2184_All//gi|18404228|ref|NP_566752.1|//0.00E+00//AAA-type ATPase family protein / ankyrin repeat family protein [Arabidopsis thaliana]	Unigene2184_All//0.00E+00//AT3G24530| AAA-type ATPase family protein / ankyrin repeat family protein	Unigene2184_All//0.00E+00//TC155840			GO:0009536//GO:0017111//GO:0032559//GO:0043170	nr +
Unigene21840_All	290	0.00	0.00	0.00	0.00	0.00	0.00	34.12	129.86	0.27	null	null		null	null		null	null		null	null		1.92E+00	1.28E-89	Up	-6.96E+00	5.14E-69	Down							
Unigene21841_All	380	0.00	2.27	2.10	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	4.95E-05	Up	1.10E+01	1.72E-04	Up	null	null		null	null		null	null		null	null								swissprot -
Unigene21842_All	563	0.00	0.00	0.00	0.00	0.00	0.00	1.05	2.30	5.94	null	null		null	null		null	null		null	null		1.13E+00	3.49E-02		2.50E+00	7.13E-12	Up	Unigene21842_All//gi|209970607|gb|ACJ03066.1|//1.00E-19//M18S-3Δp [Malus floribunda]	Unigene21842_All//5.00E-10//AT1G74190| AtRLP15 (Receptor Like Protein 15); protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene21844_All	368	0.00	1.79	0.43	0.00	0.00	0.12	0.34	5.45	2.27	1.08E+01	6.25E-04	Up	8.76E+00	2.39E-01		null	null		6.94E+00	6.96E-01		3.98E+00	9.80E-11	Up	2.72E+00	8.98E-04	Up	Unigene21844_All//gi|288310302|gb|ADC45390.1|//1.00E-13//branched chain amino acid transaminase [Curcumis melo]	Unigene21844_All//3.00E-10//AT1G10070| ATBCAT-2 (ARABIDOPSIS THALIANA BRANCHED-CHAIN AMINO ACID TRANSAMINASE 2); branched-chain-amino-acid transaminase/ catalytic	Unigene21844_All//1.00E-62//TC159597		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene21849_All	375	1.81	6.22	1.56	0.00	0.28	0.36	0.00	0.11	1.17	1.78E+00	9.75E-05	Up	-2.16E-01	7.88E-01		8.11E+00	4.56E-01		8.50E+00	3.11E-01		6.80E+00	6.35E-01		1.02E+01	2.13E-03		Unigene21849_All//gi|297839707|ref|XP_002887735.1|//5.00E-11//VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333576|gb|EFH63994.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene21849_All//2.00E-06//AT1G78410| VQ motif-containing protein	Unigene21849_All//4.00E-174//DV850067				nr -
Unigene2185_All	501	33.00	10.92	42.62	30.43	29.83	18.75	2.62	2.09	1.11	-1.60E+00	3.31E-25	Down	3.69E-01	3.04E-03		-2.85E-02	8.63E-01		-6.98E-01	5.22E-07		-3.27E-01	5.67E-01		-1.23E+00	1.61E-02				Unigene2185_All//8.00E-31//TC172880				
Unigene21850_All	301	0.35	0.17	0.00	0.83	1.03	1.20	8.29	1.25	1.72	-1.05E+00	6.84E-01		-8.44E+00	3.94E-01		3.15E-01	8.38E-01		5.37E-01	6.94E-01		-2.73E+00	1.13E-09	Down	-2.27E+00	2.76E-08	Down			Unigene21850_All//6.00E-09//ES839848				ESTscan +
Unigene21852_All	645	0.00	0.00	0.00	0.00	0.00	0.00	1.90	2.92	0.19	null	null		null	null		null	null		null	null		6.17E-01	1.50E-01		-3.36E+00	2.67E-06	Down	Unigene21852_All//gi|301091801|ref|XP_002896076.1|//5.00E-58//ras protein let-60 [Phytophthora infestans T30-4] >gi|301118482|ref|XP_002906969.1| ras protein let-60 [Phytophthora infestans T30-4] >gi|262094999|gb|EEY53051.1| ras protein let-60 [Phytophthora infestans T30-4] >gi|262108318|gb|EEY66370.1| ras protein let-60 [Phytophthora infestans T30-4]	Unigene21852_All//5.00E-20//AT1G43890| ATRAB18 (ARABIDOPSIS RAB GTPASE HOMOLOG B18); GTP binding					nr +
Unigene21856_All	210	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.20	3.60	null	null		null	null		null	null		null	null		7.64E+00	6.35E-01		1.18E+01	1.39E-05	Up	Unigene21856_All//gi|110931846|gb|ABH02922.1|//1.00E-25//MYB transcription factor MYB122 [Glycine max]	Unigene21856_All//7.00E-21//AT5G61250| ArMYB17 (myb domain protein 17); DNA binding / transcription factor	Unigene21856_All//2.00E-41//DN817124	MYB			nr -

Unigene21858_All	674	0.00	31.20	11.93	0.00	0.00	0.00	0.00	0.00	0.00	1.49E+01	5.20E-121	Up	1.35E+01	5.31E-45	Up	null	null		null	null		null	null		null	null		Unigene21858_All//gi|6978859|ref|NP_036980.1|//2.00E-16//ferritin heavy chain [Rattus norvegicus] >gi|309233|gb|AAA37612.1| ferritin heavy chain [Mus musculus] >gi|1433203|gb|AAB39890.1| ferritin-H submit [Rattus norvegicus] >gi|127799856|gb|AAH81845.2| Ferritin, heavy polypeptide 1 [Rattus norvegicus] >gi|149062360|gb|EDM12783.1| rCG47136, isoform CRA_a [Rattus norvegicus]	Unigene21858_All//2.00E-14//AT2G40300| ATFER4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal ion binding			ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene2186_All	1720	26.98	11.11	29.97	22.01	25.85	10.71	3.20	2.07	0.93	-1.28E+00	3.89E-50	Down	1.52E-01	6.64E-02		2.32E-01	3.02E-03		-1.04E+00	7.39E-32	Down	-6.30E-01	5.44E-03		-1.79E+00	6.79E-13	Down	Unigene2186_All//gi|124359162|gb|AB005685.1|//6.00E-10//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene2186_All//5.00E-75//TC168408				nr -
Unigene21860_All	265	0.79	3.25	0.80	0.19	1.30	0.51	0.48	0.63	3.91	2.04E+00	1.59E-02		2.55E-02	1.00E+00		2.79E+00	1.14E-01		1.44E+00	6.38E-01		3.99E-01	8.14E-01		3.03E+00	6.50E-05	Up			Unigene21860_All//5.00E-18//TC158642				
Unigene21861_All	248	0.63	0.82	0.00	0.20	1.11	0.55	0.00	0.00	3.05	3.69E-01	8.16E-01		-9.31E+00	2.45E-01		2.47E+00	2.23E-01		1.44E+00	6.38E-01		null	null		1.16E+01	1.39E-05	Up	Unigene21861_All//gi|223452546|gb|ACM89600.1|//3.00E-29//leucine-rich repeat family protein / extensin family protein [Glycine max]	Unigene21861_All//2.00E-30//AT4G29240| leucine-rich repeat family protein / extensin family protein	Unigene21861_All//3.00E-133//TC178003		ko04626|Plant-pathogen interaction		nr -
Unigene21862_All	427	0.00	4.03	4.61	0.00	0.00	0.21	0.00	0.00	0.00	1.20E+01	7.99E-10	Up	1.22E+01	7.46E-11	Up	null	null		7.72E+00	4.77E-01		null	null		null	null		Unigene21862_All//gi|195612198|gb|ACG27929.1|//1.00E-28//fructose-bisphosphate aldolase, cytoplasmic isozyme 1 [Zea mays]	Unigene21862_All//6.00E-29//AT4G26530| fructose-bisphosphate aldolase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene21863_All	433	64.65	75.59	83.63	711.20	449.73	277.55	0.78	0.87	0.46	2.26E-01	2.08E-02		3.71E-01	5.58E-05		-6.61E-01	3.58E-134		-1.36E+00	0.00E+00	Down	1.53E-01	8.90E-01		-7.64E-01	5.01E-01		Unigene21863_All//gi|224108579|ref|XP_002314897.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222863937|gb|EEF01068.1| predicted protein [Populus trichocarpa]		Unigene21863_All//0.00E+00//gi|31072761|gb|CA993040.1|CA993040				nr -
Unigene21864_All	713	0.00	0.00	0.00	0.14	0.00	0.00	1.90	5.51	0.00	null	null		null	null		-7.13E+00	3.13E-01		-7.13E+00	4.00E-01		1.54E+00	1.64E-07	Up	-1.09E+01	4.86E-10	Down							ESTscan -
Unigene21865_All	934	0.06	0.00	0.00	0.37	0.33	2.13	0.54	1.16	1.75	-5.81E+00	6.12E-01		-5.81E+00	6.24E-01		-1.70E-01	8.58E-01		2.51E+00	3.78E-06	Up	1.10E+00	6.53E-02		1.69E+00	4.33E-04	Up	Unigene21865_All//gi|42569036|ref|NP_179058.3|//1.00E-119//CBS domain-containing protein [Arabidopsis thaliana]	Unigene21865_All//1.00E-115//AT4G33700| CBS domain-containing protein	Unigene21865_All//0.00E+00//TC133787				nr -
Unigene21867_All	370	0.00	3.83	1.87	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.06E-08	Up	1.09E+01	6.16E-04	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene21869_All	364	0.43	0.97	5.85	0.14	0.57	1.99	0.23	0.23	0.66	1.18E+00	3.72E-01		3.76E+00	1.35E-08	Up	2.05E+00	3.95E-01		3.86E+00	1.75E-03		-1.69E-02	1.01E+00		1.50E+00	3.39E-01				Unigene21869_All//4.00E-07//TC176819				
Unigene2187_All	1733	23.61	37.80	30.30	45.99	65.21	127.78	532.05	656.38	1837.89	6.79E-01	8.22E-25		3.60E-01	1.59E-06		5.04E-01	1.35E-29		1.47E+00	0.00E+00	Up	3.03E-01	4.31E-117		1.79E+00	0.00E+00	Up	Unigene2187_All//gi|18252325|gb|AAL66194.1|AF386512_1//1.00E-150//cytochrome P450 [Pyrus communis]	Unigene2187_All//3.00E-94//AT5G07990| TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	Unigene2187_All//0.00E+00//TC148903		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene21872_All	296	0.18	3.08	0.00	0.17	0.00	0.15	1.00	0.99	2.69	4.12E+00	2.34E-04	Up	-7.47E+00	6.24E-01		-7.39E+00	5.55E-01		-1.41E-01	9.53E-01		-1.67E-02	1.02E+00		1.43E+00	4.39E-02									
Unigene21878_All	332	0.00	0.00	0.00	0.30	0.00	0.00	4.97	0.00	7.44	null	null		null	null		-8.23E+00	3.13E-01		-8.23E+00	4.00E-01		-1.23E+01	1.09E-11	Down	5.83E-01	9.75E-02		Unigene21878_All//gi|42567516|ref|NP_195582.2|//4.00E-26//disease resistance-responsive family protein [Arabidopsis thaliana]	Unigene21878_All//2.00E-27//AT4G38700| disease resistance-responsive family protein	Unigene21878_All//2.00E-89//EX172002				nr +
Unigene21880_All	328	1.28	1.70	1.95	0.91	3.67	4.54	0.00	0.13	0.24	4.13E-01	6.37E-01		6.10E-01	5.09E-01		2.01E+00	2.81E-03		2.32E+00	2.17E-04	Up	6.99E+00	6.35E-01		7.92E+00	4.04E-01								
Unigene21882_All	711	0.00	0.00	0.00	0.00	0.00	0.00	1.90	2.29	0.00	null	null		null	null		null	null		null	null		2.69E-01	6.10E-01		-1.09E+01	4.86E-10	Down	Unigene21882_All//gi|300123088|emb|CBK24095.2|//8.00E-08//unnamed protein product [Blastocystis hominis]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene21883_All	322	0.00	0.00	0.00	0.00	0.00	0.00	116.20	19.21	81.16	null	null		null	null		null	null		null	null		-2.60E+00	9.18E-129	Down	-5.18E-01	1.48E-11	Down	Unigene21883_All//gi|559237|gb|AAA98492.1|//5.00E-43//tyrosine-rich hydroxyproline-rich glycoprotein [Petroselinum crispum]		Unigene21883_All//6.00E-09//gi|109886900|gb|DW515869.1|DW515869				nr +
Unigene21885_All	378	0.14	0.00	0.00	0.13	0.46	0.48	2.01	5.86	10.54	-7.11E+00	6.12E-01		-7.11E+00	6.24E-01		1.79E+00	5.20E-01		1.86E+00	4.58E-01		1.54E+00	1.40E-04	Up	2.39E+00	2.56E-13	Up			Unigene21885_All//3.00E-20//gi|112044487|gb|BF273417.1|BF273417				
Unigene21887_All	533	0.00	0.00	0.00	0.00	0.00	0.00	1.75	3.06	0.00	null	null		null	null		null	null		null	null		8.09E-01	8.07E-02		-1.08E+01	5.47E-07	Down	Unigene21887_All//gi|225435082|ref|XP_002284448.1|//1.00E-22//PREDICTED: similar to 60S ribosomal protein L23A isoform 2 [Vitis vinifera] >gi|225435084|ref|XP_002284445.1| PREDICTED: similar to 60S ribosomal protein L23A isoform 1 [Vitis vinifera]	Unigene21887_All//3.00E-23//AT2G39460| RPL23AA (RIBOSOMAL PROTEIN L23AA); RNA binding / nucleotide binding / structural constituent of ribosome			ko03010|Ribosome		nr -
Unigene21892_All	229	0.00	3.32	5.35	0.22	0.30	0.00	0.18	0.55	0.00	1.17E+01	1.77E-04	Up	1.24E+01	9.12E-07	Up	4.67E-01	9.58E-01		-7.76E+00	6.35E-01		1.57E+00	5.45E-01		-7.53E+00	6.13E-01				Unigene21892_All//4.00E-86//TC169822				
Unigene21894_All	264	0.99	0.38	0.00	70.57	31.44	22.07	0.32	0.95	0.00	-1.37E+00	3.83E-01		-9.95E+00	8.57E-02		-1.17E+00	1.17E-21	Down	-1.68E+00	7.71E-33	Down	1.57E+00	3.26E-01		-8.32E+00	3.58E-01		Unigene21894_All//gi|224075387|ref|XP_002304612.1|//4.00E-07//predicted protein [Populus trichocarpa] >gi|222842044|gb|EEE79591.1| predicted protein [Populus trichocarpa]						nr -
Unigene21898_All	846	0.43	0.18	0.00	0.59	0.20	0.21	12.04	0.84	1.98	-1.27E+00	3.36E-01		-8.76E+00	2.78E-02		-1.53E+00	1.45E-01		-1.46E+00	1.93E-01		-3.84E+00	2.53E-51	Down	-2.61E+00	7.51E-37	Down	Unigene21898_All//gi|5262758|emb|CAB45906.1|//7.00E-49//pathogenesis-related protein homolog [Arabidopsis thaliana] >gi|7270050|emb|CAB79865.1| pathogenesis-related protein homolog [Arabidopsis thaliana]	Unigene21898_All//6.00E-50//AT4G31470| pathogenesis-related protein, putative	Unigene21898_All//0.00E+00//gi|164345926|gb|EX164581.1|EX164581		ko04626|Plant-pathogen interaction		nr +
Unigene2190_All	905	24.57	32.42	33.42	9.25	20.05	10.63	0.23	0.28	0.40	4.00E-01	6.22E-05		4.44E-01	1.15E-05		1.12E+00	9.69E-19	Up	2.01E-01	3.47E-01		2.46E-01	8.53E-01		7.62E-01	4.99E-01		Unigene2190_All//gi|18447767|gb|AAL67994.1|//1.00E-137//acyltransferase-like protein [Gossypium hirsutum]	Unigene2190_All//7.00E-123//AT5G23940| EMB3009 (embryo defective 3009); transferase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene2190_All//0.00E+00//TC136175		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016740	nr -
Unigene21901_All	527	5.56	2.31	2.93	8.03	8.63	6.60	9.47	3.41	4.61	-1.27E+00	7.30E-04	Down	-9.24E-01	1.59E-02		1.02E-01	7.89E-01		-2.84E-01	3.98E-01		-1.47E+00	7.92E-09	Down	-1.04E+00	1.17E-05	Down	Unigene21901_All//gi|3947719|emb|CAA10101.1|//3.00E-25//ribosomal protein S28 [Prunus persica] >gi|3947721|emb|CAA10102.1| ribosomal protein S28 [Prunus persica] >gi|3947723|emb|CAA10103.1| ribosomal protein S28 [Prunus persica]	Unigene21901_All//2.00E-23//AT5G64140| RPS28 (RIBOSOMAL PROTEIN S28); structural constituent of ribosome	Unigene21901_All//4.00E-150//BF275781		ko03010|Ribosome		nr -
Unigene21906_All	398	0.00	4.20	2.01	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.54E-09	Up	1.10E+01	1.72E-04	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene21908_All	807	0.00	4.14	1.65	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.95E-19	Up	1.07E+01	2.40E-07	Up	null	null		null	null		null	null		null	null		Unigene21908_All//gi|951453|gb|AAA74724.1|//2.00E-14//initiation factor (iso)4F p82 subunit [Triticum aestivum]	Unigene21908_All//7.00E-08//AT5G57870| eukaryotic translation initiation factor 4F, putative / eIF-4F, putative					nr -
Unigene21909_All	360	115.40	286.85	146.59	19.23	40.94	73.01	37.00	66.06	109.78	1.31E+00	1.10E-114	Up	3.45E-01	4.06E-06		1.09E+00	1.02E-14	Up	1.92E+00	1.21E-54	Up	8.36E-01	3.31E-16		1.57E+00	4.09E-72	Up	Unigene21909_All//gi|73761689|gb|AZ83344.1|//7.00E-37//ACC oxidase 3 [Gossypium hirsutum]	Unigene21909_All//3.00E-25//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene21909_All//2.00E-151//TC179511		ko00270|Cysteine and methionine metabolism		nr -
Unigene2191_All	2006	10.75	11.01	11.36	46.16	42.45	37.78	27.27	10.46	9.20	3.54E-02	7.79E-01		8.04E-02	5.70E-01		-1.21E-01	3.07E-02		-2.89E-01	2.86E-08		-1.38E+00	5.23E-81	Down	-1.57E+00	1.65E-100	Down	Unigene2191_All//gi|30693062|ref|NP_190430.2|//0.00E+00//phosphoesterase family protein [Arabidopsis thaliana] >gi|24417137|dbj|BAC22511.1| phosphatidylglycerol-specific phospholipase C [Arabidopsis thaliana]	Unigene2191_All//0.00E+00//AT3G48610| phosphoesterase family protein	Unigene2191_All//0.00E+00//gi|164277851|gb|ES809488.1|ES809488		ko00564|Glycerophospholipid metabolism//ko00562|Inositol phosphate metabolism//ko00565|Ether lipid metabolism	GO:0004629	nr -
Unigene21910_All	539	0.78	0.56	0.10	8.87	0.26	0.00	2.59	0.00	0.30	-4.62E-01	6.50E-01		-2.97E+00	6.46E-02		-5.12E+00	1.35E-30	Down	-1.31E+01	3.10E-30	Down	-1.13E+01	6.58E-10	Down	-3.13E+00	1.09E-06	Down							
Unigene21911_All	748	0.00	0.68	0.00	0.13	0.00	0.42	0.85	1.84	7.78	9.40E+00	4.04E-03		null	null		-7.06E+00	3.13E-01		1.67E+00	3.09E-01		1.12E+00	2.98E-02		3.20E+00	1.00E-25	Up	Unigene21911_All//gi|82400126|gb|ABB72802.1|//1.00E-17//L-allo-threonine aldolase-related protein [Solanum tuberosum]	Unigene21911_All//2.00E-17//AT3G04520| THA2 (threonine Aldolase 2); threonine aldolase	Unigene21911_All//1.00E-73//TC139061		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene21914_All	699	0.15	5.29	2.67	0.00	0.00	0.00	0.00	0.00	0.00	5.14E+00	2.97E-18	Up	4.15E+00	4.39E-08	Up	null	null		null	null		null	null		null	null		Unigene21914_All//sp|Q58876|ITM2B_PONAB//6.00E-110//Integral membrane protein 2B OS=Pongo abelii GN=ITM2B PE=2 SV=1						swissprot +
Unigene21916_All	332	0.00	0.00	0.00	0.00	0.00	0.00	6.49	4.78	0.00	null	null		null	null		null	null		null	null		-4.41E-01	2.79E-01		-1.27E+01	6.89E-16	Down			Unigene21916_All//8.00E-27//TC146753				
Unigene21917_All	539	0.10	0.38	0.00	0.37	0.38	1.17	0.16	3.64	12.27	1.95E+00	3.75E-01		-6.60E+00	6.24E-01		5.21E-02	9.89E-01		1.67E+00	9.79E-02		4.54E+00	2.20E-11	Up	6.29E+00	7.34E-44	Up	Unigene21917_All//gi|255635283|gb|ACU17995.1|//2.00E-06//unknown [Glycine max]	Unigene21917_All//8.00E-05//AT5G56630| PFK7 (PHOSPHOFRUCTOKINASE 7); 6-phosphofructokinase	Unigene21917_All//4.00E-36//TC169193				nr +
Unigene21918_All	1034	0.00	0.00	0.00	0.00	0.00	0.00	7.24	2.71	0.23	null	null		null	null		null	null		null	null		-1.42E+00	3.45E-12	Down	-4.97E+00	3.68E-46	Down	Unigene21918_All//gi|3980198|emb|CAA46863.1|//2.00E-51//thiolprotease [Pisum sativum]	Unigene21918_All//2.00E-39//AT1G09850| XBCP3 (xylem bark cysteine peptidase 3); cysteine-type endopeptidase/ cysteine-type peptidase					nr -
Unigene21919_All	562	0.00	0.00	0.00	0.09	0.00	0.00	2.63	0.74	1.49	null	null		null	null		-6.47E+00	5.55E-01		-6.47E+00	6.35E-01		-1.82E+00	5.43E-04	Down	-8.23E-01	7.86E-02		Unigene21919_All//gi|240254246|ref|NP_175634.5|//8.00E-23//ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana]	Unigene21919_All//1.00E-23//AT1G52240| ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor	Unigene21919_All//0.00E+00//gi|48816718|gb|CO118031.1|CO118031				nr +
Unigene2192_All	1413	66.10	41.49	54.42	3.63	5.24	22.25	2.87	3.87	3.47	-6.72E-01	1.74E-34		-2.81E-01	3.65E-07		5.29E-01	1.14E-02		2.62E+00	6.42E-95	Up	4.32E-01	6.40E-02		2.72E-01	2.79E-01		Unigene2192_All//gi|21615407|emb|CAD33923.1|//1.00E-124//alpha-expansin 3 [Cicer arietinum]	Unigene2192_All//3.00E-110//AT1G69530| ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1)	Unigene2192_All//0.00E+00//TC131830				nr -
Unigene21921_All	484	0.00	0.00	0.00	0.00	0.00	0.00	0.52	2.42	4.20	null	null		null	null		null	null		null	null		2.21E+00	5.41E-04	Up	3.00E+00	6.43E-09	Up			Unigene21921_All//6.00E-07//DW519568				
Unigene21922_All	474	0.66	0.53	0.45	4.41	2.62	1.14	0.80	0.44	0.25	-3.09E-01	7.89E-01		-5.60E-01	6.64E-01		-7.55E-01	7.83E-02		-1.95E+00	4.94E-05	Down	-8.65E-01	4.41E-01		-1.67E+00	1.40E-01								
Unigene21923_All	970	6.04	0.52	2.91	0.51	0.57	0.19	0.09	0.00	0.00	-3.53E+00	8.42E-23	Down	-1.05E+00	4.59E-05	Down	1.46E-01	9.05E-01		-1.46E+00	1.93E-01		-6.45E+00	4.04E-01		-6.45E+00	3.58E-01		Unigene21923_All//gi|42572013|ref|NP_974097.1|//8.00E-23//protein kinase-related [Arabidopsis thaliana] >gi|79320834|ref|NP_001031244.1| protein kinase-related [Arabidopsis thaliana]	Unigene21923_All//8.00E-20//AT1G66880| serine/threonine protein kinase family protein					nr +
Unigene21924_All	435	5.89	0.23	3.67	0.00	0.08	0.00	0.19	0.00	0.00	-4.66E+00	2.58E-12	Down	-6.82E-01	1.00E-01		6.31E+00	8.30E-01		null	null		-7.60E+00	4.04E-01		-7.60E+00	3.58E-01				Unigene21924_All//1.00E-16//ES835962				
Unigene21928_All	366	0.71	2.08	0.58	0.82	2.63	0.74	0.92	1.03	4.14	1.54E+00	7.40E-02		-2.97E-01	8.32E-01		1.69E+00	2.52E-02		-1.41E-01	9.21E-01		1.53E-01	8.90E-01		2.16E+00	5.30E-05	Up			Unigene21928_All//2.00E-33//TC168963				
Unigene2193_All	2049	3.52	2.28	1.43	12.11	10.10	6.06	6.36	3.35	3.71	-6.31E-01	3.66E-03		-1.30E+00	3.30E-08	Down	-2.62E-01	1.57E-02		-9.98E-01	9.38E-20		-9.26E-01	7.73E-11		-7.75E-01	1.67E-08		Unigene2193_All//gi|110676572|gb|ABG85154.1|//1.00E-144//RhoGAP1 [Nicotiana tabacum]	Unigene2193_All//6.00E-136//AT5G22400| rac GTPase activating protein, putative	Unigene2193_All//0.00E+00//TC132086				nr -

Unigene21933_All	420	0.25	1.45	0.00	0.24	1.07	0.22	0.30	1.09	3.13	2.54E+00	2.46E-02		-7.96E+00	3.94E-01		2.17E+00	1.06E-01		-1.41E-01	9.50E-01		1.86E+00	8.80E-02		3.37E+00	1.37E-06	Up								
Unigene21934_All	441	0.00	0.00	0.00	0.00	0.00	0.00	1.44	2.18	0.00	null	null		null	null		null	null		null	null		6.00E-01	3.67E-01		-1.05E+01	7.11E-05	Down	Unigene21934_All//gi|57791555|gb|AA56553.1|/4.00E-54//ubiquitin/s27a 40s ribosomal protein [Nicotiana benthamiana]	Unigene21934_All//1.00E-22//AT3G62250| UBQ5 (ubiquitin 5); protein binding / structural constituent of ribosome	Unigene21934_All//4.00E-17//BF277514		ko03010|Ribosome		nr -
Unigene21935_All	722	0.00	8.07	2.21	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	2.96E-33	Up	1.11E+01	8.44E-09	Up	null	null		null	null		null	null		null	null		Unigene21935_All//gi|300122978|emb|CBK23985.2|/4.00E-15//unnamed protein product [Blastocystis hominis]						nr -
Unigene21939_All	679	6.94	0.90	4.71	0.07	0.10	0.07	0.00	0.00	0.06	-2.95E+00	1.04E-15	Down	-5.60E-01	5.56E-02		4.66E-01	9.58E-01		-1.42E-01	9.53E-01		null	null		5.88E+00	6.45E-01		Unigene21939_All//gi|186478326|ref|NP_001117258.1|/4.00E-20//transcription regulator [Arabidopsis thaliana] >gi|5091554|gb|AAD39583.1|AC007067_23 T10024.23 [Arabidopsis thaliana]	Unigene21939_All//2.00E-21//AT1G10586| transcription regulator	Unigene21939_All//0.00E+00//ES797065				nr +
Unigene2194_All	2035	10.39	5.93	6.49	6.98	6.80	7.52	4.20	1.91	2.27	-8.10E-01	2.43E-11		-6.79E-01	3.79E-08		-3.64E-02	8.24E-01		1.09E-01	5.39E-01		-1.14E+00	5.31E-10	Down	-8.86E-01	3.63E-07		Unigene2194_All//gi|15230719|ref|NP_187294.1|//0.00E+00//EMB2750 (embryo defective 2750) [Arabidopsis thaliana] >gi|75207273|sp|Q9SQU6.1|PP216_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g06430, chloroplastic; AltName: Full=Protein EMBRYO DEFECTIVE 2750; Flags: Precursor >gi|30387593|gb|AAP31962.1|At3g06430 [Arabidopsis thaliana]	Unigene2194_All//0.00E+00//AT3G06430| EMB2750 (embryo defective 2750)	Unigene2194_All//0.00E+00//ES800872	GO:0003006		nr +
Unigene21940_All	481	0.87	1.05	1.00	0.31	1.22	0.00	0.35	0.70	2.07	2.76E-01	7.64E-01		1.95E-01	8.39E-01		1.97E+00	7.03E-02		-8.28E+00	2.33E-01		9.83E-01	4.24E-01		2.56E+00	3.91E-04	Up	Unigene21940_All//gi|115455657|ref|NP_001051429.1|/3.00E-07//Os03g0775300 [Oryza sativa Japonica Group] >gi|113549900|dbj|BAF13343.1|Os03g0775300 [Oryza sativa Japonica Group]	Unigene21940_All//6.00E-06//AT1G75200| flavodoxin family protein / radical SAM domain-containing protein	Unigene21940_All//4.00E-153//gi|78351317|gb|DT571591.1|DT571591				nr -
Unigene21941_All	280	0.00	0.00	0.00	2.31	0.98	0.32	0.00	1.94	0.28	null	null		null	null		-1.23E+00	1.60E-01		-2.84E+00	1.02E-02		1.09E+01	5.36E-04	Up	8.15E+00	4.04E-01									
Unigene21942_All	470	0.00	8.41	3.06	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.66E-22	Up	1.16E+01	6.30E-08	Up	null	null		null	null		null	null		null	null		Unigene21942_All//gi|6094476|sp|O23787.1|THI4_CITSI//7.00E-66//RecName: Full=Thiazole biosynthetic enzyme, chloroplastic; Flags: Precursor >gi|2582665|emb|CAB05370.1| thi [Citrus sinensis]	Unigene21942_All//2.00E-53//ES849692	Unigene21942_All//2.00E-53//ES849692				nr +
Unigene21943_All	334	2.35	4.10	0.00	4.92	4.33	3.52	0.89	1.00	0.00	8.02E-01	1.60E-01		-1.12E+01	2.22E-04	Down	-1.85E-01	7.46E-01		-4.85E-01	3.82E-01		1.76E-01	8.80E-01		-9.79E+00	1.58E-02				Unigene21943_All//3.00E-103//gi|78332099|gb|DT552373.1|DT552373					
Unigene21944_All	431	0.24	0.71	0.49	0.69	2.08	0.94	0.39	0.78	3.97	1.54E+00	3.23E-01		1.03E+00	5.92E-01		1.58E+00	4.38E-02		4.44E-01	7.01E-01		9.83E-01	4.24E-01		3.34E+00	2.49E-08	Up	Unigene21944_All//gi|17064892|gb|AAL32600.1|/8.00E-11//Unknown protein [Arabidopsis thaliana] >gi|30102842|gb|AAP21339.1|At4g22000 [Arabidopsis thaliana]	Unigene21944_All//5.00E-12//AT4G22000| unknown protein	Unigene21944_All//5.00E-87//gi|109834182|gb|DW232747.1|DW232747				nr +
Unigene21945_All	678	0.00	10.99	1.89	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.39E-42	Up	1.09E+01	4.69E-07	Up	null	null		null	null		null	null		null	null		Unigene21945_All//gi|6015063|sp|O81918.3|EF1D_BETVU//6.00E-17//RecName: Full=Elongation factor 1-delta; Short=EF-1-delta; AltName: Full=Elongation factor 1B-beta; AltName: Full=eEF-1B beta >gi|3288113|emb|CAB09803.1|elongation factor 1-beta [Beta vulgaris subsp. vulgaris]	Unigene21945_All//1.00E-05//AT5G19510| elongation factor 1B alpha-subunit 2 (eEF1Balpha2)					nr -
Unigene21948_All	743	0.00	0.68	0.00	0.00	0.09	0.12	0.00	1.58	4.61	9.41E+00	4.04E-03		null	null		6.53E+00	6.10E-01		6.93E+00	4.77E-01		1.06E+01	2.73E-08	Up	1.22E+01	1.63E-24	Up	Unigene21948_All//gi|183904108|ref|NP_563710.1|//8.00E-69//AWPM-19-like membrane family protein [Arabidopsis thaliana] >gi|2494121|gb|AAB80630.1| Strong similarity to Triticum ABA induced membrane protein (gb|U80037). EST gb|Z27032 comes from this gene [Arabidopsis thaliana]	Unigene21948_All//1.00E-61//AT1G04560| AWPM-19-like membrane family protein					nr +
Unigene2195_All	1870	10.86	9.46	14.01	11.06	10.31	9.27	3.44	2.41	1.66	-1.99E-01	1.27E-01		3.68E-01	8.94E-04		-1.00E-01	5.01E-01		-2.53E-01	4.55E-02		-5.10E-01	1.46E-02		-1.05E+00	3.89E-07	Down	Unigene2195_All//gi|297792071|ref|XP_002863920.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297309755|gb|EFH40179.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2195_All//0.00E+00//AT5G48730| pentatricopeptide (PPR) repeat-containing protein	Unigene2195_All//0.00E+00//gi|164354426|gb|ES824727.1|ES824727				nr +
Unigene21955_All	333	0.00	0.00	0.00	8.53	0.93	3.39	0.00	0.00	0.00	null	null		null	null		-3.20E+00	6.72E-13	Down	-1.33E+00	4.10E-04	Down	null	null		null	null									ESTscan +
Unigene21956_All	775	0.00	0.00	0.00	0.00	0.00	0.00	4.42	1.35	0.46	null	null		null	null		null	null		null	null		-1.71E+00	1.23E-07	Down	-3.26E+00	5.76E-16	Down			Unigene21956_All//1.00E-18//TC164196					
Unigene21957_All	349	0.00	0.00	0.00	0.00	0.00	0.00	2.67	0.84	27.05	null	null		null	null		null	null		null	null		-1.67E+00	1.45E-02		3.34E+00	4.73E-43	Up	Unigene21957_All//gi|28300299|gb|AAO37645.1|/8.00E-19//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene21957_All//4.00E-05//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene21957_All//4.00E-38//gi|164297689|gb|EX168250.1|EX168250				nr +
Unigene21959_All	492	0.00	0.00	0.00	0.00	0.00	0.00	41.85	103.98	105.35	null	null		null	null		null	null		null	null		1.31E+00	6.01E-70	Up	1.33E+00	5.55E-74	Up	Unigene21959_All//gi|13359451|dbj|BAB33421.1|//2.00E-18//putative senescence-associated protein [Pisum sativum]		Unigene21959_All//1.00E-41//gi|84157109|gb|DN826156.1|DN826156				nr +
Unigene21962_All	311	406.62	270.94	238.17	496.54	360.96	470.95	238.32	231.02	117.85	-5.86E-01	1.61E-36		-7.72E-01	4.62E-57		-4.60E-01	6.41E-35		-7.63E-02	1.03E-01		-4.49E-02	5.25E-01		-1.02E+00	2.78E-69	Down	Unigene21962_All//gi|13540405|gb|AAK29456.1|AF352253_1//2.00E-21//histone H1 [Lens culinaris]		Unigene21962_All//1.00E-157//gi|11207145|gb|BF276075.1|BF276075				nr +
Unigene21963_All	333	0.00	1.22	0.00	0.15	0.10	1.76	0.00	2.64	0.12	1.02E+01	1.36E-02		null	null		-5.33E-01	8.25E-01		3.56E+00	8.48E-03		1.14E+01	2.86E-06	Up	6.90E+00	6.45E-01		Unigene21963_All//gi|31324528|gb|AAP47579.1|//5.00E-28//receptor kinase Lecrk [Gossypium hirsutum]	Unigene21963_All//2.00E-23//AT2G37710| RLK (receptor lectin kinase); kinase	Unigene21963_All//4.00E-16//ES797969				nr -
Unigene21965_All	542	0.00	20.47	6.48	0.00	0.00	0.17	0.16	0.00	0.00	1.43E+01	1.28E-63	Up	1.27E+01	1.87E-19	Up	null	null		7.38E+00	4.77E-01		-7.29E+00	4.04E-01		-7.29E+00	3.58E-01		Unigene21965_All//gi|226532341|ref|NP_001147384.1|/3.00E-52//60S ribosomal protein L9 [Zea mays] >gi|195610798|gb|ACG27229.1| 60S ribosomal protein L9 [Zea mays]	Unigene21965_All//4.00E-49//AT1G33140| PGY2 (PIGGYBACK2); structural constituent of ribosome	Unigene21965_All//2.00E-07//ES846343		ko03010|Ribosome		nr -
Unigene21967_All	419	0.75	0.36	3.43	0.12	0.33	0.00	0.00	0.00	0.00	-1.05E+00	4.43E-01		2.20E+00	8.73E-04	Up	1.47E+00	6.19E-01		-6.89E+00	6.35E-01		null	null		null	null		Unigene21967_All//gi|255604647|ref|XP_002538258.1|//1.00E-17//Bactoprenol glucosyl transferase, putative [Ricinus communis] >gi|223513033|gb|EEF24124.1|Bactoprenol glucosyl transferase, putative [Ricinus communis]						nr +
Unigene2197_All	422	0.99	5.40	7.95	2.24	3.10	3.64	9.02	4.95	1.04	2.45E+00	1.50E-06	Up	3.00E+00	5.10E-11	Up	4.67E-01	4.71E-01		6.98E-01	2.15E-01		-8.65E-01	2.01E-03		-3.12E+00	5.44E-17	Down	Unigene2197_All//gi|5733879|gb|AAD49767.1|AC007932_15//3.00E-122//ESTs gb|N97074, gb|T13943 and gb|R89965 come from this gene [Arabidopsis thaliana]		Unigene2197_All//1.00E-115//EX166960		GO:0016740		nr -
Unigene21971_All	418	0.63	6.79	1.66	0.36	0.49	0.97	0.20	0.00	0.86	3.44E+00	5.93E-11	Up	1.40E+00	1.39E-01		4.67E-01	8.25E-01		1.44E+00	2.82E-01		-7.66E+00	4.04E-01		2.08E+00	1.01E-01				Unigene21971_All//3.00E-162//TC163008					
Unigene21972_All	349	0.00	0.00	0.00	0.00	0.00	0.00	2.91	6.83	0.34	null	null		null	null		null	null		null	null		1.23E+00	1.05E-03		-3.09E+00	5.36E-05	Down			Unigene21972_All//1.00E-07//TC134836					ESTscan +
Unigene21974_All	416	1.26	0.00	2.69	2.63	0.50	1.63	0.71	0.20	0.00	-1.03E+01	2.93E-03		1.10E+00	1.10E-01		-2.41E+00	5.06E-04	Down	-6.94E-01	3.11E-01		-1.82E+00	2.11E-01		-9.47E+00	1.58E-02		Unigene21974_All//gi|115452767|ref|NP_001049984.1|//1.00E-11//Os03g0325500 [Oryza sativa Japonica Group] >gi|113548455|dbj|BAF11898.1|Os03g0325500 [Oryza sativa Japonica Group]	Unigene21974_All//9.00E-12//AT5G18240| MYB1 (MYB-related protein 1); transcription factor	Unigene21974_All//5.00E-47//ES794788	G2-like			nr -
Unigene21975_All	347	2.26	4.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9.54E-01	7.82E-02		-1.11E+01	2.22E-04	Down	null	null		null	null		null	null		null	null		Unigene21975_All//gi|115481958|ref|NP_001064572.1|//5.00E-54//Os10g0409400 [Oryza sativa Japonica Group] >gi|75141703|sp|Q7XES5.1|BURFG_ORYSJ RecName: Full=BURP domain-containing protein 16; Short=OsBURP16; AltName: Full=Protein WGP1; Short=OsWGP1; Flags: Precursor >gi|31432021|gb|AAP53713.1| BURP domain containing protein, expressed {Oryza sativa (japonica cultivar-group)} >gi|113639181|dbj|BAF26486.1|Os10g0409400 [Oryza sativa Japonica Group] >gi|149287280|gb|ABR23532.1| cell wall protein WGP1 [Oryza sativa Japonica Group]						nr -
Unigene21979_All	603	0.00	1.76	0.62	0.00	0.57	0.00	0.00	0.00	0.00	1.08E+01	3.81E-06	Up	9.27E+00	2.50E-02		9.16E+00	3.01E-02		null	null		null	null		null	null		Unigene21979_All//COG1215//3.00E-11//Glycosyltransferases, probably involved in cell wall biogenesis						cog +
Unigene2198_All	1444	53.66	208.19	208.98	119.98	129.04	166.80	121.95	145.47	45.96	1.96E+00	0.00E+00	Up	1.96E+00	0.00E+00	Up	1.05E-01	5.32E-03		4.75E-01	7.72E-51		2.55E-01	3.11E-16		-1.41E+00	4.97E-274	Down	Unigene2198_All//gi|5733879|gb|AAD49767.1|AC007932_15//2.00E-54//ESTs gb|N97074, gb|T13943 and gb|R89965 come from this gene [Arabidopsis thaliana]	Unigene2198_All//3.00E-25//AT1G48300| unknown protein	Unigene2198_All//0.00E+00//TC135504				nr +
Unigene21981_All	1124	0.00	0.09	0.00	0.00	0.12	0.16	0.94	2.90	18.18	6.50E+00	3.87E-01		null	null		6.94E+00	3.18E-01		7.33E+00	1.94E-01		1.62E+00	8.02E-07	Up	4.27E+00	4.96E-112	Up	Unigene21981_All//gi|170660047|gb|ACB28472.1|//4.00E-23//polyprotein [Ananas comosus]	Unigene21981_All//6.00E-09//AT5G42905| nucleic acid binding / ribonuclease H					nr +
Unigene21983_All	331	0.00	1.99	2.90	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.25E-04	Up	1.15E+01	2.46E-05	Up	null	null		null	null		null	null		null	null		Unigene21983_All//sp|P42226|STAT6_HUMAN//3.00E-61//Signal transducer and activator of transcription 6 OS=Homo sapiens GN=STAT6 PE=1 SV=1	Unigene21983_All//7.00E-05//AT4G27850| proline-rich family protein					swissprot -
Unigene21986_All	288	0.00	0.00	0.00	0.00	0.00	0.00	10.13	0.87	3.32	null	null		null	null		null	null		null	null		-3.54E+00	3.75E-14	Down	-1.61E+00	2.28E-06	Down								
Unigene21987_All	392	0.00	10.47	6.38	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.25E-23	Up	1.26E+01	8.32E-14	Up	null	null		null	null		null	null		null	null		Unigene21987_All//gi|299470138|emb|CBN78167.1|//2.00E-24//ribosomal protein L34 [Ectocarpus siliculosus]	Unigene21987_All//3.00E-19//AT1G26880| 60S ribosomal protein L34 (RPL34A)			ko03010|Ribosome		nr +
Unigene21989_All	569	0.00	189.05	105.28	0.26	0.06	0.64	20.21	18.88	3.99	1.75E+01	0.00E+00	Up	1.67E+01	0.00E+00	Up	-2.12E+00	3.86E-01		1.27E+00	3.82E-01		-9.85E-02	6.04E-01		-2.34E+00	1.09E-36	Down	Unigene21989_All//gi|145408591|ref|XP_001152215.1|//3.00E-07//ORF441 [Pinus koraiensis] >gi|145048840|gb|ABP35457.1|ORF441 [Pinus koraiensis]		Unigene21989_All//2.00E-28//DW479422				nr +
Unigene21991_All	394	1.59	1.80	0.95	6.45	2.45	3.21	3.54	0.42	1.82	1.76E-01	8.17E-01		-7.52E-01	4.11E-01		-1.40E+00	2.24E-04	Down	-1.01E+00	1.11E-02		-3.06E+00	2.69E-06	Down	-9.60E-01	4.80E-02				Unigene21991_All//9.00E-24//TC175187					
Unigene21993_All	285	0.00	45.87	18.68	0.00	0.00	0.00	0.00	0.00	0.00	1.55E+01	5.01E-75	Up	1.42E+01	1.21E-29	Up	null	null		null	null		null	null		null	null										

Unigene21994_All	300	1.57	2.70	1.78	0.17	1.61	4.52	0.00	0.00	0.00	7.84E-01	3.23E-01		1.77E-01	8.45E-01		3.28E+00	2.69E-02		4.77E+00	6.28E-07	Up	null	null		null	null		Unigene21994_All//gi|224105309|ref|XP_002313762.1|//1.00E-33//cytochrome P450 probable 5-hydroxylase for coniferaldehyde, coniferyl alcohol and ferulic acid [Populus trichocarpa] >gi|222850170|gb|EEE87717.1| cytochrome P450 probable 5-hydroxylase for coniferaldehyde, coniferyl alcohol and ferulic acid [Populus trichocarpa]	Unigene21994_All//5.00E-32//AT4G36220| FAH1 (FERULIC ACID 5-HYDROXYLASE 1); ferulate 5-hydroxylase/ monooxygenase	Unigene21994_All//2.00E-156//BE052825		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene21995_All	372	0.00	3.13	4.01	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.05E-06	Up	1.20E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene21995_All//gi|224000023|ref|XP_002289684.1|//5.00E-10//asparaginyl-trna synthetase [Thalassiosira pseudonana CCMP1335] >gi|220974892|gb|EED93221.1| asparaginyl-trna synthetase [Thalassiosira pseudonana CCMP1335]	Unigene21995_All//1.00E-06//AT4G17300| NS1; asparagine-tRNA ligase			ko00970|Aminoacyl-tRNA biosynthesis		nr +
Unigene22_All	688	1.37	2.95	2.79	4.78	3.20	3.54	9.40	14.88	21.02	1.11E+00	1.62E-02		1.03E+00	3.81E-02		-5.77E-01	8.35E-02		-4.31E-01	2.29E-01		6.63E-01	3.08E-05		1.16E+00	2.53E-17	Up			Unigene22_All//0.00E+00//ES833096				
Unigene22001_All	352	0.00	0.00	0.00	3.96	1.86	0.51	0.00	0.00	0.00	null	null		null	null		-1.09E+00	4.31E-02		-2.95E+00	2.40E-05	Down	null	null		null	null		Unigene22001_All//gi|124360558|gb|ABN08564.1|//9.00E-13//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene22001_All//1.00E-05//AT1G43760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706), Endonuclease/exonuclease/phosphatase (InterPro:IPR005135); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40390.1); Has 2614 Blast hits to 2551 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 1517; Fungi - 2; Plants - 1086; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene22001_All//5.00E-19//DT049173				nr +
Unigene22002_All	286	61.47	60.06	69.45	22.12	23.72	18.32	56.77	21.48	25.91	-3.34E-02	8.15E-01		1.76E-01	2.14E-01		1.01E-01	7.29E-01		-2.72E-01	2.98E-01		-1.40E+00	4.33E-25	Down	-1.13E+00	9.36E-19	Down	Unigene22002_All//gi|224113699|ref|XP_002316546.1|//2.00E-07//precursor of carboxylase t-protein 1, glycine decarboxylase complex [Populus trichocarpa] >gi|222859611|gb|EEE97158.1| precursor of carboxylase t-protein 1, glycine decarboxylase complex [Populus trichocarpa]	Unigene22002_All//3.00E-06//AT1G11860| aminomethyltransferase, putative	Unigene22002_All//5.00E-148//gi|164295970|gb|EX171014.1|EX171014		ko00910|Nitrogen metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr -
Unigene22003_All	742	0.00	0.00	0.00	0.00	0.00	0.00	3.87	1.58	0.00	null	null		null	null		null	null		null	null		-1.30E+00	1.31E-04	Down	-1.19E+01	3.77E-21	Down	Unigene22003_All//gi|15236171|ref|NP_195193.1|//4.00E-60//40S ribosomal protein S3A (RPS3aB) [Arabidopsis thaliana] >gi|19884297|sp|Q42262.3|RS3A2_ARATH RecName: Full=40S ribosomal protein S3a-2 >gi|2661422|emb|CAA04689.1| Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi|3096936|emb|CAA18846.1| Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi|7270417|emb|CAB80184.1| Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi|17064848|gb|AAL32578.1| Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]	Unigene22003_All//6.00E-62//AT4G34670| 40S ribosomal protein S3A (RPS3aB)	Unigene22003_All//9.00E-10//gi|21089744|gb|BQ402057.1|BQ402057		ko03010|Ribosome		nr -
Unigene22004_All	530	0.00	6.02	2.51	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	3.64E-18	Up	1.13E+01	2.40E-07	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene22007_All	396	0.00	0.00	0.00	0.00	0.00	0.00	2.56	0.00	1.51	null	null		null	null		null	null		null	null		-1.13E+01	2.97E-07	Down	-7.64E-01	1.95E-01		Unigene22007_All//gi|6730632|gb|AAF27053.1|AC008262_2//2.00E-07//FAN2.3 [Arabidopsis thaliana]	Unigene22007_All//6.00E-06//AT1G69050| unknown protein					nr +
Unigene2201_All	2241	17.04	21.91	16.87	1.71	1.44	1.71	6.45	5.78	15.40	3.62E-01	1.57E-06		-1.47E-02	8.92E-01		-2.45E-01	4.78E-01		1.20E-03	1.00E+00		-1.58E-01	2.91E-01		1.25E+00	3.11E-45	Up	Unigene2201_All//gi|295841585|dbj|BAJ07173.1|//1.00E-118//MdTCP2A [Malus x domestica]	Unigene2201_All//2.00E-49//AT4G18390| TCP family transcription factor, putative	Unigene2201_All//0.00E+00//TC169763	TCP		GO:0032502	nr +
Unigene22010_All	389	0.00	5.21	3.83	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.54E-11	Up	1.19E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene22010_All//gi|159474092|ref|XP_001695163.1|//4.00E-33//dihydrolipoyl dehydrogenase [Chlamydomonas reinhardtii] >gi|158276097|gb|EDP01871.1| dihydrolipoyl dehydrogenase [Chlamydomonas reinhardtii]	Unigene22010_All//8.00E-30//AT3G17240| mtLPD2 (LIPOAMIDE DEHYDROGENASE 2); ATP binding / dihydrolipoyl dehydrogenase			ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00020|Citrate cycle (TCA cycle)//ko00260|Glycine, serine and threonine metabolism		nr -
Unigene22014_All	310	1.52	0.00	0.00	1.93	1.33	0.00	0.00	0.13	0.26	-1.06E+01	5.55E-03		-1.06E+01	8.65E-03		-5.33E-01	5.62E-01		-1.09E+01	7.70E-04	Down	7.07E+00	6.35E-01		8.01E+00	4.04E-01		Unigene22014_All//gi|30678079|ref|NP_178475.2|//7.00E-07//18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|42570677|ref|NP_973412.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|79316683|ref|NP_001030966.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|186499149|ref|NP_001118260.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana]		Unigene22014_All//1.00E-43//TC172722				nr +
Unigene22015_All	336	179.39	81.73	193.03	71.31	175.05	53.36	1.01	0.37	2.49	-1.13E+00	1.16E-53	Down	1.06E-01	1.59E-01		1.30E+00	7.52E-76	Up	-4.18E-01	1.27E-04		-1.43E+00	2.58E-01		1.31E+00	5.56E-02		Unigene22015_All//gi|70609692|gb|AA205071.1|//6.00E-48//cytochrome P450 [Citrus sinensis]	Unigene22015_All//6.00E-45//AT5G05690| CPD (CONSTITUTIVE PHOTOMORPHOGENIC DWARF); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene22015_All//0.00E+00//ES790679		ko00905|Brassinosteroid biosynthesis		nr -
Unigene22019_All	1139	0.00	10.85	2.76	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	6.26E-71	Up	1.14E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene22019_All//sp|Q9V496|APLP_DROME//7.00E-103//Apolipophorins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2						swissprot -
Unigene2202_All	689	1.90	1.25	5.72	6.07	3.45	3.34	6.81	4.13	4.86	-6.03E-01	3.07E-01		1.59E+00	3.16E-06	Up	-8.17E-01	3.34E-03		-8.61E-01	3.35E-03		-7.24E-01	3.46E-03		-4.88E-01	4.35E-02				Unigene2202_All//0.00E+00//gi|164244044|gb|ES821458.1|ES821458				
Unigene22020_All	549	0.00	0.00	0.00	0.00	0.00	0.00	7.62	7.00	1.02	null	null		null	null		null	null		null	null		-1.22E-01	6.71E-01		-2.91E+00	2.01E-17	Down	Unigene22020_All//gi|301016726|dbj|BAJ11184.1|//7.00E-15//dehydration responsive protein [Corchorus olitorius]		Unigene22020_All//8.00E-25//TC171825				nr +
Unigene22023_All	352	0.00	13.10	9.83	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	2.84E-26	Up	1.33E+01	3.72E-19	Up	null	null		null	null		null	null		null	null									
Unigene22024_All	301	2.43	0.00	2.30	2.32	1.37	0.30	0.00	0.56	0.00	-1.12E+01	2.11E-04	Down	-8.15E-02	9.29E-01		-7.55E-01	3.69E-01		-2.95E+00	5.84E-03		9.12E+00	1.39E-01		null	null									
Unigene22027_All	310	0.84	0.16	3.26	3.86	3.22	0.73	1.09	1.08	0.90	-2.37E+00	2.14E-01		1.95E+00	1.37E-02		-2.60E-01	6.78E-01		-2.40E+00	7.07E-04	Down	-1.66E-02	1.02E+00		-2.78E-01	7.81E-01				Unigene22027_All//4.00E-07//TC163819				
Unigene22033_All	427	0.00	7.59	4.12	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.88E-18	Up	1.20E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene22033_All//sp|Q64424|LIPR2_MYOCO//1.00E-06//Pancreatic lipase-related protein 2 OS=Myocastor coypus GN=PNLIPRP2 PE=1 SV=1						swissprot +
Unigene22035_All	289	0.00	0.00	0.00	0.00	0.00	0.00	2.63	1.30	0.00	null	null		null	null		null	null		null	null		-1.02E+00	1.69E-01		-1.14E+01	8.87E-06	Down	Unigene22035_All//gi|301165845|ref|XP_002902006.1|//2.00E-36//heat shock 70 kDa protein [Phytophthora infestans T30-4] >gi|262099344|gb|EEY57396.1| heat shock 70 kDa protein [Phytophthora infestans T30-4]	Unigene22035_All//1.00E-35//AT3G12580| HSP70 (heat shock protein 70); ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -
Unigene22048_All	334	0.00	1.97	1.28	2.09	5.98	2.97	0.00	0.00	0.00	1.09E+01	6.25E-04	Up	1.03E+01	1.38E-02		1.52E+00	1.12E-03		5.11E-01	4.92E-01		null	null		null	null				Unigene22048_All//5.00E-139//gi|78331690|gb|DT551964.1|DT551964				
Unigene22049_All	631	0.00	3.85	2.53	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.73E-14	Up	1.13E+01	8.44E-09	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene22050_All	234	0.67	0.00	0.00	0.00	0.00	0.00	3.98	1.79	0.00	-9.39E+00	2.16E-01		-9.39E+00	2.45E-01		null	null		null	null		-1.15E+00	7.87E-02		-1.20E+01	5.47E-07	Down			Unigene22050_All//5.00E-64//FL576677				
Unigene22051_All	618	0.00	0.00	0.00	0.00	0.00	0.00	1.85	3.18	0.00	null	null		null	null		null	null		null	null		7.83E-01	5.87E-02		-1.09E+01	1.65E-08	Down	Unigene22051_All//gi|300268126|gb|EFJ52307.1|//7.00E-85//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene22051_All//1.00E-70//AT4G16720| 60S ribosomal protein L15 (RPL15A)	Unigene22051_All//8.00E-13//CD485862		ko03010|Ribosome		nr +
Unigene22054_All	376	111.32	81.80	62.74	108.77	103.95	75.91	97.04	42.46	52.02	-4.45E-01	5.96E-08		-8.27E-01	1.34E-21		-6.54E-02	5.48E-01		-5.19E-01	1.16E-10		-1.19E+00	2.83E-43	Down	-9.00E-01	2.29E-28		Unigene22054_All//gi|224087383|ref|XP_002308145.1|//7.00E-13//histone 2 [Populus trichocarpa] >gi|222854121|gb|EEE91668.1| histone 2 [Populus trichocarpa]		Unigene22054_All//9.00E-138//gi|164285666|gb|ES832576.1|ES832576				nr +
Unigene22055_All	388	0.00	2.35	1.24	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.62E-05	Up	1.03E+01	7.49E-03		null	null		null	null		null	null		null	null		Unigene22055_All//gi|300151997|gb|EFJ18641.1|//7.00E-06//hypothetical protein SELMODRAFT_112245 [Selaginella moellendorffii]						nr +

Unigene22056_All	421	3.11	0.48	0.89	1.30	1.96	2.15	2.41	0.20	1.42	-2.69E+00	1.84E-04	Down	-1.81E+00	6.66E-03		5.93E-01	4.93E-01		7.21E-01	3.62E-01		-3.60E+00	2.38E-05	Down	-7.64E-01	1.95E-01		Unigene22056_All//gi|75332302|sp|Q94KE0.1|ERDL3_ARATH//3.00E-36//RecName: Full=Sugar transporter ERD6-like 3; AltName: Full=Sugar transporter-like protein 2 >gi|41494109|gb|AAK56249.1|AF36726 0_1 At1g08920/F7G19_20 [Arabidopsis thaliana] >gi|22137064|gb|AAM91377.1| At1g08920/F7G19_20 [Arabidopsis thaliana] >gi|169403716|emb|CAQ16329.1| hexose transporter-like protein [Arabidopsis thaliana]	Unigene22056_All//5.00E-30//AT1G08920| sugar transporter, putative	Unigene22056_All//4.00E-94//TC147217				nr -
Unigene22057_All	462	1.59	0.11	0.00	1.08	2.46	2.54	0.00	0.00	0.00	-3.85E+00	1.56E-03		-1.06E+01	4.13E-04	Down	1.19E+00	7.15E-02		1.24E+00	5.89E-02		null	null		null	null		Unigene22057_All//gi|16304001|gb|AAL16905.1|AF420013_1//2.00E-08//auxin efflux carrier protein [Narcissus pseudonarcissus]	Unigene22057_All//6.00E-08//AT1G23080| PIN7 (PIN-FORMED 7); auxin efflux transmembrane transporter/ auxin:hydrogen symporter/ transporter					nr -
Unigene2206_All	1492	46.25	95.29	63.46	61.20	70.65	55.46	47.66	48.46	56.13	1.04E+00	2.37E-109	Up	4.56E-01	4.64E-17		2.07E-01	1.30E-05		-1.42E-01	1.25E-02		2.40E-02	7.28E-01		2.36E-01	2.42E-06		Unigene2206_All//gi|30027167|gb|AAP06759.1|//4.00E-94//auxin response factor-like protein [Mangifera indica]	Unigene2206_All//2.00E-66//AT5G62000| ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Unigene2206_All//0.00E+00//TC152154	ARF		GO:0005488//GO:0006355//GO:0008283//GO:0009900//GO:0009908//GO:0010260	nr -
Unigene22062_All	288	0.00	3.52	2.03	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.26E-06	Up	1.10E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene22062_All//sp|Q9V3S0|CP4G1_DROME//2.00E-07//Cytochrome P450 4g1 OS=Drosophila melanogaster GN=Cyp4g1 PE=2 SV=1						swissprot +
Unigene22063_All	546	0.00	6.68	3.02	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	9.11E-21	Up	1.16E+01	4.30E-09	Up	null	null		null	null		null	null		null	null		Unigene22063_All//sp|Q29GR8|MOEH_DROPS//1.00E-65//Moesin/ezrin/radixin homolog 1 OS=Drosophila pseudoobscura pseudoobscura GN=Moe PE=3 SV=3						swissprot +
Unigene22064_All	332	52.16	123.16	67.20	140.74	167.09	158.21	138.81	198.53	115.08	1.24E+00	6.83E-42	Up	3.66E-01	2.63E-03		2.48E-01	2.54E-04		1.69E-01	2.91E-02		5.16E-01	5.51E-19		-2.71E-01	8.34E-05		Unigene22064_All//gi|10559491|gb|ABG76000.1|//1.00E-22//GRP-like protein 2 [Gossypium hirsutum]	Unigene22064_All//1.00E-12//AT5G15650| RGP2 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 2); transferase, transferring hexosyl groups	Unigene22064_All//0.00E+00//gi|11208552|gb|BF277482.1|BF277482				nr +
Unigene22068_All	251	0.00	0.00	0.42	0.20	0.55	0.18	2.02	0.00	0.48	null	null		8.73E+00	3.99E-01		1.47E+00	6.19E-01		-1.42E-01	9.53E-01		-1.10E+01	8.89E-04	Down	-2.09E+00	3.64E-02		Unigene22068_All//gi|15240531|ref|NP_200365.1|//5.00E-23//TRN1 (TORNADO 1) [Arabidopsis thaliana]	Unigene22068_All//2.00E-24//AT5G55540| TRN1 (TORNADO 1)					nr -
Unigene2207_All	2565	0.96	1.38	1.74	1.79	2.30	2.17	5.72	2.64	3.11	5.28E-01	1.11E-01		8.63E-01	3.84E-03		3.62E-01	1.59E-01		2.78E-01	3.28E-01		-1.12E+00	3.72E-16	Down	-8.81E-01	1.46E-11		Unigene2207_All//gi|30680985|ref|NP_567345.2|//0.00E+00//MLH1 (MUTL-HOMOLOGUE 1); protein binding, bridging [Arabidopsis thaliana] >gi|3893081|emb|CAA10163.1| MLH1 protein [Arabidopsis thaliana] >gi|7267357|emb|CAB78038.1| MLH1 protein [Arabidopsis thaliana]	Unigene2207_All//0.00E+00//AT4G09140| MLH1 (MUTL-HOMOLOGUE 1); protein binding, bridging			ko03430|Mismatch repair	GO:0000785//GO:0003690//GO:0005515//GO:0006281//GO:0006310//GO:0009791//GO:0032559//GO:0043231//GO:0048229//GO:0048608	nr -
Unigene22070_All	316	0.00	2.57	0.34	0.32	0.98	2.14	0.40	2.38	2.14	1.13E+01	9.38E-05	Up	8.40E+00	3.99E-01		1.64E+00	3.21E-01		2.77E+00	1.14E-02		2.57E+00	3.32E-03		2.42E+00	6.57E-03				Unigene22070_All//4.00E-07//TC164754					
Unigene22071_All	558	0.00	0.00	0.00	0.00	0.12	0.00	0.38	3.15	1.78	null	null		null	null		6.95E+00	6.10E-01		null	null		3.05E+00	1.02E-07	Up	2.24E+00	1.15E-03		Unigene22071_All//gi|18408863|ref|NP_561907.1|//1.00E-67//copine-related [Arabidopsis thaliana] >gi|42572019|ref|NP_974100.1| copine-related [Arabidopsis thaliana] >gi|145326680|ref|NP_001077787.1| copine-related [Arabidopsis thaliana] >gi|119935848|gb|ABM06011.1| At1g67800 [Arabidopsis thaliana]	Unigene22071_All//4.00E-63//AT3G01650| RGLG1 (RING domain Ligase1); protein binding / zinc ion binding	Unigene22071_All//6.00E-143//gi|78340190|gb|DT560464.1|DT560464				nr +
Unigene22072_All	528	0.20	3.07	0.20	0.38	0.13	0.26	0.48	0.40	1.36	3.95E+00	3.77E-07	Up	2.53E-02	1.00E+00		-1.53E+00	4.16E-01		-5.57E-01	7.33E-01		-2.80E-01	8.29E-01		1.50E+00	4.94E-02		Unigene22072_All//gi|164605528|dbj|BAF98594.1|//2.00E-34//CM0545.410.nc [Lotus japonicus]	Unigene22072_All//7.00E-29//AT3G56650| AtRLP32 (Receptor Like Protein 32); kinase/ protein binding					nr -
Unigene22075_All	310	0.00	11.11	2.40	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.31E-19	Up	1.12E+01	3.28E-04	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene22077_All	1918	0.00	17.41	7.22	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	1.33E-192	Up	1.28E+01	5.55E-78	Up	null	null		null	null		null	null		null	null		Unigene22077_All//gi|226461026|gb|EEH58319.1|//0.00E+00//ATP synthase [Micromonas pusilla CCMP1545]	Unigene22077_All//0.00E+00//AT2G07698| ATP synthase alpha chain, mitochondrial, putative	Unigene22077_All//1.00E-23//DW505421		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr +
Unigene22079_All	358	0.00	0.00	0.00	0.00	0.00	0.00	1.06	1.63	10.13	null	null		null	null		null	null		null	null		6.21E-01	4.78E-01		3.25E+00	1.58E-16	Up									
Unigene2208_All	1728	241.77	133.42	255.40	87.29	72.94	42.76	35.11	49.44	3.73	-8.58E-01	5.86E-232		7.91E-02	2.27E-03		-2.59E-01	7.87E-12		-1.03E+00	9.78E-124	Down	4.94E-01	1.61E-22		-3.23E+00	5.15E-270	Down	Unigene2208_All//gi|5430771|gb|AAD43171.1|AC007504_26//3.00E-75//Unknown Protein [Arabidopsis thaliana] >gi|105830110|gb|ABF74714.1| At1g49470 [Arabidopsis thaliana]	Unigene2208_All//5.00E-53//AT1G49470| unknown protein	Unigene2208_All//0.00E+00//TC159523			GO:0008152//GO:0043234//GO:0044464	nr -
Unigene22080_All	851	0.12	10.78	12.83	0.00	0.08	0.00	0.00	0.00	0.00	6.45E+00	6.41E-49	Up	6.70E+00	1.31E-57	Up	6.34E+00	6.10E-01		null	null		null	null		null	null		Unigene22080_All//gi|300156386|gb|EFJ23015.1|//2.00E-06//hypothetical protein SELMODRAFT_443049 [Selaginella moellendorffii]						nr +
Unigene22081_All	1598	0.20	0.19	0.27	0.06	0.00	0.25	4.79	11.59	7.58	-4.63E-02	9.85E-01		4.41E-01	6.77E-01		-5.96E+00	3.13E-01		2.03E+00	1.49E-01		1.27E+00	1.08E-24	Up	6.62E-01	3.09E-06		Unigene22081_All//gi|42567622|ref|NP_195977.2|//1.00E-170//ATIREG2 (IRON-REGULATED PROTEIN 2); nickel ion transmembrane transporter [Arabidopsis thaliana]	Unigene22081_All//5.00E-163//AT5G03570| ATIREG2 (IRON-REGULATED PROTEIN 2); nickel ion transmembrane transporter	Unigene22081_All//0.00E+00//TC176717				nr -
Unigene22083_All	473	0.88	0.00	1.13	2.21	0.29	0.19	2.41	1.06	0.59	-9.79E+00	1.05E-02		3.47E-01	7.06E-01		-2.93E+00	1.21E-04	Down	-3.53E+00	9.34E-05	Down	-1.19E+00	4.02E-02		-2.03E+00	8.64E-04	Down			Unigene22083_All//3.00E-18//TC175612					
Unigene22085_All	474	0.55	0.64	0.00	0.21	0.73	0.10	2.77	0.09	0.50	2.17E-01	8.63E-01		-9.11E+00	8.57E-02		1.79E+00	2.58E-01		-1.14E+00	6.77E-01		-4.97E+00	4.05E-08	Down	-2.46E+00	4.22E-05	Down			Unigene22085_All//6.00E-07//ES814768					
Unigene22087_All	297	0.18	0.85	0.72	9.06	1.86	0.15	0.00	0.14	0.13	2.28E+00	2.34E-01		2.03E+00	3.61E-01		-2.29E+00	1.39E-08	Down	-5.90E+00	1.92E-15	Down	7.14E+00	6.35E-01		7.07E+00	6.45E-01		Unigene22087_All//gi|222423788|dbj|BAH19860.1|//1.00E-12//AT4G12040 [Arabidopsis thaliana]	Unigene22087_All//6.00E-14//AT4G12040| zinc finger (AN1-like) family protein	Unigene22087_All//2.00E-51//TC164159				nr +
Unigene22088_All	319	0.33	1.27	0.00	0.16	0.00	0.00	0.40	2.62	18.36	1.95E+00	1.44E-01		-8.36E+00	3.94E-01		-7.29E+00	5.55E-01		-7.29E+00	6.35E-01		2.72E+00	1.18E-03		5.53E+00	3.74E-37	Up	Unigene22088_All//gi|255554831|ref|XP_002518453.1|//2.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223542298|gb|EEF43840.1| conserved hypothetical protein [Ricinus communis]		Unigene22088_All//3.00E-137//gi|78325351|gb|DT545625.1|DT545625				nr -
Unigene22091_All	342	0.00	0.00	0.78	0.15	0.00	0.53	0.62	4.16	3.03	null	null		9.60E+00	8.02E-02		-7.19E+00	5.55E-01		1.86E+00	4.58E-01		2.75E+00	8.33E-06	Up	2.29E+00	7.17E-04	Up	Unigene22091_All//gi|18403744|ref|NP_564599.1|//7.00E-10//cryptdin protein-related [Arabidopsis thaliana] >gi|91805957|gb|ABE65707.1| cryptdin protein-like protein [Arabidopsis thaliana]		Unigene22091_All//3.00E-137//DN779269				nr +
Unigene22093_All	335	0.62	0.00	0.00	3.12	0.31	1.89	2.27	0.87	0.71	-9.29E+00	1.22E-01		-9.29E+00	1.46E-01		-3.34E+00	3.42E-05	Down	-7.26E-01	3.02E-01		-1.38E+00	6.73E-02		-1.67E+00	2.39E-02									
Unigene22097_All	348	1.20	1.75	0.61	0.29	0.59	0.00	0.24	0.00	2.75	5.39E-01	5.63E-01		-9.75E-01	4.12E-01		1.05E+00	6.12E-01		-8.16E+00	4.00E-01		-7.92E+00	4.04E-01		3.50E+00	4.29E-05	Up								
Unigene22099_All	307	0.00	0.00	12.32	12.82	0.00	0.00	0.00	0.00	0.00	null	null		1.36E+01	6.02E-21	Up	-1.36E+01	1.03E-29	Down	-1.36E+01	8.06E-25	Down	null	null		null	null		Unigene22099_All//gi|541682|emb|CAA54561.1|//7.00E-45//cell wall protein [Solanum lycopersicum]						nr -
Unigene22100_All	1075	0.00	0.00	0.00	0.00	0.00	0.00	1.77	5.02	0.04	null	null		null	null		null	null		null	null		1.50E+00	1.02E-09	Up	-5.58E+00	1.14E-12	Down	Unigene22100_All//gi|298705968|emb|CBJ29089.1|//4.00E-15//WORN repeat variant family protein [Ectocarpus siliculosus]	Unigene22100_All//2.00E-16//AT1G21980| ATPIPSK1 (PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE 1); 1-phosphatidylinositol-4-phosphate 5-kinase/ actin filament binding / actin monomer binding / phosphatidylinositol phosphate kinase					nr +
Unigene22102_All	614	0.00	6.44	2.25	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.66E-22	Up	1.11E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene22102_All//sp|Q9VGX3|FAU_DROME//8.00E-06//Protein anoxia up-regulated OS=Drosophila melanogaster GN=fau PE=1 SV=3						swissprot +
Unigene22103_All	418	2.00	0.00	1.02	1.07	1.98	1.08	1.62	0.50	3.05	-1.10E+01	5.57E-05	Down	-9.75E-01	2.37E-01		8.82E-01	2.93E-01		1.06E-02	1.00E+00		-1.69E+00	4.19E-02		9.14E-01	7.70E-02									
Unigene22105_All	262	0.00	4.25	2.85	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.00E-06	Up	1.15E+01	3.28E-04	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene22109_All	338	1.24	0.00	1.26	0.29	1.73	0.27	2.50	0.12	0.35	-1.03E+01	1.05E-02		2.54E-02	1.00E+00		2.55E+00	2.84E-02		-1.42E-01	9.50E-01		-4.34E+00	4.55E-05	Down	-2.82E+00	5.38E-04	Down	Unigene22109_All//gi|186531517|ref|NP_200071.2|//2.00E-06//RAB GTPase activator [Arabidopsis thaliana]	Unigene22109_All//6.00E-08//AT5G52580| RAB GTPase activator	Unigene22109_All//5.00E-31//gi|48739768|gb|CO070287.1|CO070287				nr -
Unigene22110_All	352	0.00	0.00	0.00	0.00	0.00	0.00	1.68	2.85	0.00	null	null		null	null		null	null		null	null		7.61E-01	2.28E-01		-1.07E+01	1.41E-04	Down								ESTscan +
Unigene22111_All	310	0.17	0.00	0.00	1.29	0.67	0.58	2.73	2.56	0.26	-7.40E+00	6.12E-01		-7.40E+00	6.24E-01		-9.48E-01	4.21E-01		-1.14E+00	3.79E-01		-9.06E-02	9.01E-01		-3.41E+00	1.35E-04	Down								
Unigene22112_All	1036	0.00	0.00	0.00	0.00	0.00	0.00	4.90	0.28	2.88	null	null		null	null		null	null		null	null		-4.12E+00	4.10E-27	Down	-7.64E-01	8.83E-04		Unigene22112_All//gi|297833034|ref|XP_002884399.1|//1.00E-77//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330239|gb|EFH60658.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22112_All//1.00E-78//AT3G03620| MATE efflux family protein	Unigene22112_All//3.00E-07//gi|21097225|gb|BQ409538.1|BQ409538				nr +
Unigene22114_All	478	0.00	5.19	2.56	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.98E-14	Up	1.13E+01	9.12E-07	Up	null	null		null	null		null	null		null	null		Unigene22114_All//sp|Q29IK8|SAP30_DROPS//6.00E-57//Histone deacetylase complex subunit SAP30 homolog OS=Drosophila pseudoobscura pseudoobscura GN=Sap30 PE=3 SV=1						swissprot -
Unigene22115_All	433	0.00	1.99	2.58	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	4.95E-05	Up	1.13E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene22115_All//gi|186479105|ref|NP_174461.3|//3.00E-06//actin binding [Arabidopsis thaliana] >gi|166215071|sp|Q9C6S1.3|FH14_ARATH RecName: Full=Formin-like protein 14; Short=AtFH14						nr +
Unigene22116_All	381	0.27	65.30	18.17	0.00	0.00	0.00	0.00	0.00	0.00	7.89E+00	7.61E-139	Up	6.05E+00	2.37E-35	Up	null	null		null	null		null	null		null	null										
Unigene22117_All	457	0.00	0.00	0.00	0.65	0.00	0.20	5.64	0.18	2.96	null	null		null	null		-9.35E+00	2.01E-02		-1.73E+00	2.89E-01		-4.95E+00	1.46E-15	Down	-9.29E-01	6.22E-03		Unigene22117_All//gi|221068552|ref|XP_002326143.1|//2.00E-32//SAUR family protein [Populus trichocarpa] >gi|222833336|gb|EEE71813.1| SAUR family protein [Populus trichocarpa]	Unigene22117_All//4.00E-18//AT5G20810| auxin-responsive protein, putative / small auxin up RNA (SAUR_B)	Unigene22117_All//1.00E-13//ES826125				nr -
Unigene22122_All	306	1.03	10.43	3.83	2.28	0.68	1.92	4.15	37.42	5.34	3.35E+00	5.56E-12	Up	1.90E+00	8.12E-03		-1.76E+00	4.11E-02		-2.48E-01	7.56E-01		3.17E+00	8.92E-49	Up	3.65E-01	4.27E-01				Unigene22122_All//2.00E-95//TC170894					
Unigene22128_All	305	0.69	0.33	0.00	0.33	1.02	0.00	1.94	6.71	8.36	-1.05E+00	5.65E-01		-9.42E+00	1.46E-01		1.64E+00	3.21E-01		-8.33E+00	4.00E-01		1.79E+00	4.09E-05	Up	2.11E+00	1.13E-07	Up	Unigene22128_All//gi|223452359|gb|ACM89507.1|//2.00E-25//NAK-type protein kinase [Glycine max]	Unigene22128_All//5.00E-24//AT5G47070| protein kinase, putative	Unigene22128_All//7.00E-30//DR459121		ko04626|Plant-pathogen interaction		nr +
Unigene2213_All	342	15.15	24.30	22.42	0.29	1.81	2.77	1.98	0.98	3.49	6.82E-01	6.84E-04		5.66E-01	9.88E-03		2.64E+00	1.99E-02		3.25E+00	5.84E-04	Up	-1.02E+00	2.04E-01		8.21E-01	1.26E-01		Unigene2213_All//gi|124359969|gb|AB007985.1|//5.00E-18//Sterol desaturase [Medicago truncatula]	Unigene2213_All//5.00E-16//AT1G02205| CER1 (ECERIFERUM 1); octadecanal decarbonylase	Unigene2213_All//2.00E-153//gi|195983482|gb|FL576456.1|FL576456			GO:0003824//GO:0006631//GO:0031224//GO:0043231//GO:0046914	nr +

Unigene22135_All	305	31.39	12.96	16.59	107.47	127.92	110.76	91.08	47.41	44.93	-1.28E+00	6.97E-11	Down	-9.20E-01	2.15E-06		2.51E-01	2.61E-03		4.35E-02	6.91E-01		-9.42E-01	8.32E-23		-1.02E+00	1.14E-26	Down	Unigene22135_All//gi|48085530|gb|AAD29845.1|AF064692_1//1.00E-50//O-methyltransferase [Thalictrum tuberosum]	Unigene22135_All//2.00E-48//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene22135_All//7.00E-172//gi|78325889|gb|DT546163.1|DT546163		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene2214_All	2040	153.32	154.74	221.69	9.45	20.37	77.55	7.48	3.03	8.98	1.33E-02	6.90E-01		5.32E-01	3.00E-105		1.11E+00	4.60E-42	Up	3.04E+00	0.00E+00	Up	-1.30E+00	3.23E-21	Down	2.64E-01	2.28E-02		Unigene2214_All//gi|87162521|gb|AB028316.1|//0.00E+00//Sterol desaturase [Medicago truncatula]	Unigene2214_All//9.00E-136//AT1G02205| CER1 (ECERIFERUM 1); octadecanal decarbonylase	Unigene2214_All//0.00E+00//TC143408		ko00100|Steroid biosynthesis	GO:0003006//GO:0006633//GO:0016020//GO:0043231//GO:0043667	nr -
Unigene22140_All	956	0.11	0.69	0.06	0.63	2.92	1.13	2.17	0.74	3.21	2.65E+00	1.50E-02		-9.75E-01	7.21E-01		2.22E+00	8.47E-08	Up	8.59E-01	2.17E-01		-1.54E+00	2.37E-04	Down	5.66E-01	6.67E-02		Unigene22140_All//gi|225461945|ref|XP_002268896.1|//9.00E-55//PREDICTED: similar to E3 ubiquitin-protein ligase UPL1 [Vitis vinifera]	Unigene22140_All//1.00E-52//AT1G70320| UPL2 (UBIQUITIN-PROTEIN LIGASE 2); ubiquitin-protein ligase	Unigene22140_All//4.00E-173//TC151320		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene22147_All	593	0.97	0.51	0.18	2.60	1.39	1.29	2.14	0.28	1.14	-9.21E-01	3.43E-01		-2.43E+00	4.40E-02		-9.02E-01	7.78E-02		-1.01E+00	6.16E-02		-2.92E+00	1.46E-05	Down	-9.05E-01	7.78E-02		Unigene22147_All//gi|297848532|ref|XP_002892147.1|//3.00E-53//kinase interacting family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337989|gb|EFH68406.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22147_All//1.00E-35//AT1G03080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053), KIP1-like (InterPro:IPR011684); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT3G22790.1); Has 169162 Blast hits to 69460 proteins in 2232 species: Archae - 2114; Bacteria - 24914; Metazoa - 82448; Fungi - 11850; Plants - 6375; Viruses - 760; Other Eukaryotes - 40701 (source: NCBI BLink).				GO:0016020	nr -
Unigene22148_All	1543	1.12	0.85	1.38	5.55	7.70	8.34	2.41	0.95	1.55	-3.90E-01	4.27E-01		3.03E-01	5.19E-01		4.72E-01	2.88E-03		5.87E-01	1.40E-04		-1.35E+00	5.02E-06	Down	-6.38E-01	1.96E-02		Unigene22148_All//gi|297848532|ref|XP_002892147.1|//1.00E-155//kinase interacting family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337989|gb|EFH68406.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22148_All//5.00E-155//AT1G03080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053), KIP1-like (InterPro:IPR011684); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT3G22790.1); Has 169162 Blast hits to 69460 proteins in 2232 species: Archae - 2114; Bacteria - 24914; Metazoa - 82448; Fungi - 11850; Plants - 6375; Viruses - 760; Other Eukaryotes - 40701 (source: NCBI BLink).				GO:0016020	nr -
Unigene22151_All	4873	4.60	3.06	3.48	20.99	19.14	20.51	19.57	9.01	6.36	-5.88E-01	3.58E-07		-4.03E-01	8.22E-04		-1.33E-01	9.80E-03		-3.31E-02	6.07E-01		-1.12E+00	2.79E-101	Down	-1.62E+00	2.54E-183	Down	Unigene22151_All//gi|297848532|ref|XP_002892147.1|//1.00E-145//kinase interacting family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337989|gb|EFH68406.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22151_All//4.00E-121//AT1G03080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053), KIP1-like (InterPro:IPR011684); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT3G22790.1); Has 169162 Blast hits to 69460 proteins in 2232 species: Archae - 2114; Bacteria - 24914; Metazoa - 82448; Fungi - 11850; Plants - 6375; Viruses - 760; Other Eukaryotes - 40701 (source: NCBI BLink).	Unigene22151_All//0.00E+00//TC135486				nr -
Unigene22152_All	5192	1.56	4.14	2.40	6.08	4.50	6.85	16.07	17.38	33.89	1.41E+00	5.89E-27	Up	6.20E-01	1.82E-04		-4.34E-01	8.43E-07		1.71E-01	8.18E-02		1.13E-01	3.38E-02		1.08E+00	3.47E-178	Up	Unigene22152_All//gi|297848532|ref|XP_002892147.1|//0.00E+00//kinase interacting family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337989|gb|EFH68406.1| kinase interacting family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22152_All//0.00E+00//AT1G03080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053), KIP1-like (InterPro:IPR011684); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT3G22790.1); Has 169162 Blast hits to 69460 proteins in 2232 species: Archae - 2114; Bacteria - 24914; Metazoa - 82448; Fungi - 11850; Plants - 6375; Viruses - 760; Other Eukaryotes - 40701 (source: NCBI BLink).	Unigene22152_All//0.00E+00//gi|164358751|gb|ES835307.1|ES835307				nr -
Unigene22153_All	524	0.80	3.58	0.81	1.71	1.84	1.38	5.97	5.66	8.44	2.16E+00	7.11E-05	Up	2.54E-02	1.00E+00		1.05E-01	9.03E-01		-3.11E-01	6.88E-01		-7.63E-02	8.21E-01		4.99E-01	4.67E-02		Unigene22153_All//gi|225428015|ref|XP_002278452.1|//2.00E-69//PREDICTED: similar to KAK (KAKTUS) isoform 2 [Vitis vinifera]	Unigene22153_All//2.00E-56//AT4G38600| KAK (KAKTUS); ubiquitin-protein ligase	Unigene22153_All//0.00E+00//ES810035		ko04120|Ubiquitin mediated proteolysis	GO:0000904//GO:0006261//GO:0016020//GO:0016879//GO:0043412	nr +
Unigene22156_All	2290	0.55	2.41	0.70	0.70	1.35	2.41	1.70	4.23	20.88	2.14E+00	8.78E-13	Up	3.47E-01	5.29E-01		9.59E-01	5.51E-03		1.79E+00	9.04E-11	Up	1.32E+00	5.70E-14	Up	3.62E+00	6.20E-231	Up	Unigene22156_All//gi|225428013|ref|XP_002278408.1|//0.00E+00//PREDICTED: similar to KAK (KAKTUS) isoform 1 [Vitis vinifera]	Unigene22156_All//0.00E+00//AT4G38600| KAK (KAKTUS); ubiquitin-protein ligase	Unigene22156_All//0.00E+00//TC129866		ko04120|Ubiquitin mediated proteolysis	GO:0000904//GO:0006261//GO:0016020//GO:0016879//GO:0043412	nr -
Unigene22157_All	2997	1.47	3.28	2.20	3.92	5.19	6.16	8.01	4.81	11.22	1.16E+00	1.13E-09	Up	5.87E-01	1.39E-02		4.05E-01	3.04E-03		6.52E-01	2.07E-07		-7.36E-01	2.71E-13		4.86E-01	2.20E-09		Unigene22157_All//gi|300158422|gb|EFJ25045.1|//0.00E+00//ubiquitin-protein ligase, UPL3 [Selaginella moellendorffii]	Unigene22157_All//4.00E-162//AT4G38600| KAK (KAKTUS); ubiquitin-protein ligase	Unigene22157_All//0.00E+00//TC163055		ko04120|Ubiquitin mediated proteolysis	GO:0000904//GO:0006261//GO:0016020//GO:0016879//GO:0043412	nr +
Unigene22158_All	4378	1.33	2.95	2.13	3.39	3.85	5.04	12.76	10.25	18.79	1.15E+00	2.38E-12	Up	6.82E-01	4.74E-04		1.82E-01	2.26E-01		5.73E-01	4.47E-07		-3.15E-01	5.47E-07		5.59E-01	1.16E-27		Unigene22158_All//gi|225428013|ref|XP_002278408.1|//0.00E+00//PREDICTED: similar to KAK (KAKTUS) isoform 1 [Vitis vinifera]	Unigene22158_All//0.00E+00//AT4G38600| KAK (KAKTUS); ubiquitin-protein ligase	Unigene22158_All//0.00E+00//TC129866		ko04120|Ubiquitin mediated proteolysis	GO:0000904//GO:0006261//GO:0016020//GO:0016879//GO:0043412	nr +
Unigene2216_All	1914	1.59	1.01	0.45	3.75	2.61	2.60	3.25	1.83	2.23	-6.56E-01	6.70E-02		-1.83E+00	7.38E-06	Down	-5.23E-01	1.21E-02		-5.30E-01	1.52E-02		-8.24E-01	9.68E-05		-5.44E-01	7.87E-03		Unigene2216_All//gi|30680203|ref|NP_195998.2|//2.00E-14//TRFL10 (TRF-LIKE 10); DNA binding [Arabidopsis thaliana]	Unigene2216_All//9.00E-16//AT5G03780| TRFL10 (TRF-LIKE 10); DNA binding	Unigene2216_All//2.00E-16//C0131071	MYB-related	ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0010033	nr +
Unigene22161_All	680	3.54	4.47	2.51	8.06	5.72	3.85	7.83	7.74	6.56	3.37E-01	3.73E-01		-4.98E-01	2.46E-01		-4.94E-01	4.56E-02		-1.06E+00	2.43E-05	Down	-1.66E-02	9.77E-01		-2.56E-01	2.86E-01		Unigene22161_All//gi|224100259|ref|XP_002311805.1|//8.00E-25//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222851625|gb|EEE89172.1| chromatin remodeling complex subunit [Populus trichocarpa]		Unigene22161_All//7.00E-177//gi|48814371|gb|CO115684.1|CO115684				nr +
Unigene2217_All	916	3.08	1.22	2.09	5.76	3.87	5.08	4.29	2.56	2.61	-1.34E+00	5.15E-04	Down	-5.60E-01	1.52E-01		-5.74E-01	2.08E-02		-1.83E-01	5.49E-01		-7.48E-01	6.34E-03		-7.18E-01	6.74E-03		Unigene2217_All//gi|186492817|ref|NP_176551.3|//1.00E-132//kinesin motor protein-related [Arabidopsis thaliana]	Unigene2217_All//6.00E-134//AT1G63640| kinesin motor protein-related	Unigene2217_All//0.00E+00//TC162561				nr -
Unigene22172_All	3649	2.88	6.22	3.06	5.45	7.55	8.54	18.32	11.32	14.67	1.11E+00	6.71E-20	Up	8.86E-02	6.28E-01		4.71E-01	9.63E-07		6.49E-01	5.78E-12		-6.95E-01	3.33E-32		-3.20E-01	1.08E-08		Unigene22172_All//gi|87241276|gb|ABD33134.1|//0.00E+00//Nucleic acid binding NABP [Medicago truncatula]	Unigene22172_All//0.00E+00//AT2G29190| APUM2 (Arabidopsis Pumilio 2); RNA binding / binding	Unigene22172_All//0.00E+00//TC151891			GO:0003723//GO:0016020	nr +
Unigene22173_All	906	0.35	0.00	0.00	1.76	2.28	4.24	4.95	1.34	5.41	-8.44E+00	3.66E-02		-8.44E+00	4.91E-02		3.74E-01	4.58E-01		1.27E+00	6.59E-05	Up	-1.89E+00	4.89E-11	Down	1.29E-01	6.25E-01		Unigene22173_All//gi|5902365|gb|AAD55467.1|AC009322_7//1.00E-171//Putative splicing factor Prp8 [Arabidopsis thaliana]	Unigene22173_All//4.00E-172//AT1G80070| SUS2 (ABNORMAL SUSPENSOR 2)	Unigene22173_All//3.00E-56//TC137004		ko03040|Spliceosome		nr +
Unigene22174_All	1101	2.57	2.49	2.81	3.26	7.01	6.48	4.53	2.28	5.79	-4.62E-02	9.10E-01		1.29E-01	7.17E-01		1.10E+00	4.49E-08	Up	9.93E-01	5.24E-06		-9.92E-01	4.05E-05		3.54E-01	9.01E-02		Unigene22174_All//gi|5902365|gb|AAD55467.1|AC009322_7//1.00E-179//Putative splicing factor Prp8 [Arabidopsis thaliana]	Unigene22174_All//9.00E-145//AT1G80070| SUS2 (ABNORMAL SUSPENSOR 2)	Unigene22174_All//0.00E+00//TC137004		ko03040|Spliceosome		nr -
Unigene22175_All	1387	1.21	0.22	1.23	1.90	3.85	1.92	2.29	0.81	2.21	-2.46E+00	4.49E-05	Down	2.55E-02	9.79E-01		1.02E+00	4.39E-05	Up	1.34E-02	9.73E-01		-1.49E+00	5.56E-06	Down	-4.78E-02	8.90E-01		Unigene22175_All//gi|5902365|gb|AAD55467.1|AC009322_7//0.00E+00//Putative splicing factor Prp8 [Arabidopsis thaliana]	Unigene22175_All//0.00E+00//AT1G80070| SUS2 (ABNORMAL SUSPENSOR 2)	Unigene22175_All//0.00E+00//TC137004		ko03040|Spliceosome	GO:0000377//GO:0005618//GO:0005985//GO:0006073//GO:0006950//GO:0009536//GO:0030529//GO:0035251//GO:0048316	nr -
Unigene2218_All	3888	4.88	3.77	4.70	12.17	11.96	8.83	8.53	3.95	5.39	-3.75E-01	3.32E-03		-5.64E-02	6.97E-01		-2.57E-02	8.15E-01		-4.63E-01	4.60E-10		-1.11E+00	2.73E-35	Down	-6.62E-01	1.47E-15		Unigene2218_All//gi|186492817|ref|NP_176551.3|//0.00E+00//kinesin motor protein-related [Arabidopsis thaliana]	Unigene2218_All//0.00E+00//AT1G63640| kinesin motor protein-related	Unigene2218_All//0.00E+00//TC162561			GO:0003774//GO:0005506//GO:0007017//GO:0015630//GO:0016020//GO:0032559	nr -
Unigene22180_All	2057	3.38	1.06	1.86	7.29	4.64	6.15	15.58	4.41	6.00	-1.68E+00	8.83E-12	Down	-8.60E-01	2.07E-04		-6.53E-01	8.32E-07		-2.46E-01	1.15E-01		-1.82E+00	7.03E-71	Down	-1.38E+00	8.10E-49	Down	Unigene22180_All//gi|18420660|ref|NP_568428.1|//0.00E+00//PYRD (pyrimidine d); dihydroorotate dehydrogenase [Arabidopsis thaliana] >gi|26454657|sp|P32746.2|PYRD_ARATH RecName: Full=Dihydroorotate dehydrogenase, mitochondrial; Short=DHOdehase; AltName: Full=Dihydroorotate oxidase; Flags: Precursor >gi|24753785|gb|AAN64025.1|AF454729_1 dihydroorotate dehydrogenase [Arabidopsis thaliana] >gi|110736302|dbj|BAF00121.1| dihydroorotate dehydrogenase [Arabidopsis thaliana] >gi|111074516|gb|ABH04631.1| At5g23300 [Arabidopsis thaliana]	Unigene22180_All//0.00E+00//AT5G23300| PYRD (pyrimidine d); dihydroorotate dehydrogenase	Unigene22180_All//0.00E+00//TC167246		ko00240|Pyrimidine metabolism	GO:0004152//GO:0009174//GO:0016020//GO:0019856//GO:0043231	nr +

Unigene22184_All	519	0.10	1.76	1.74	0.48	0.60	1.04	1.79	1.37	1.46	4.12E+00	2.34E-04	Up	4.11E+00	3.91E-04	Up	3.15E-01	8.38E-01		1.12E+00	3.05E-01		-3.89E-01	5.75E-01		-2.97E-01	6.31E-01		Unigene22184_All//gi|297811289|ref|XP_002873528.1|//7.00E-73//glycine-rich protein [Arabidopsis lyrata subsp. lyrata] >gi|297319365|gb|EFH49787.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	Unigene22184_All//5.00E-48//AT5G11700| glycine-rich protein			ko03040|Spliceosome	GO:0043231	nr +
Unigene22185_All	1010	0.73	1.91	0.47	1.28	0.95	0.49	1.00	0.83	2.96	1.39E+00	4.12E-03		-6.12E-01	4.70E-01		-4.26E-01	4.87E-01		-1.38E+00	2.30E-02		-2.80E-01	6.37E-01		1.56E+00	3.58E-06	Up	Unigene22185_All//gi|297811289|ref|XP_002873528.1|//1.00E-149//glycine-rich protein [Arabidopsis lyrata subsp. lyrata] >gi|297319365|gb|EFH49787.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	Unigene22185_All//3.00E-115//AT5G11700| glycine-rich protein	Unigene22185_All//4.00E-56//ES843086		ko03040|Spliceosome		nr -
Unigene22188_All	866	0.48	2.87	1.41	5.46	3.86	5.79	5.61	7.05	14.12	2.57E+00	1.98E-07	Up	1.55E+00	2.13E-02		-5.03E-01	6.33E-02		8.31E-02	7.82E-01		3.28E-01	1.45E-01		1.33E+00	4.26E-18	Up	Unigene22188_All//gi|297832462|ref|XP_002884113.1|//2.00E-70//PHD finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329953|gb|EFH60372.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22188_All//7.00E-71//AT2G18090| PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein	Unigene22188_All//0.00E+00//CO098346			GO:0003676//GO:0006351//GO:0043231//GO:0046914	nr +
Unigene22191_All	2169	1.06	1.12	1.08	2.55	2.03	3.52	3.24	3.08	7.93	7.92E-02	8.44E-01		2.53E-02	9.71E-01		-3.27E-01	2.17E-01		4.65E-01	3.02E-02		-6.97E-02	7.54E-01		1.29E+00	4.30E-24	Up	Unigene22191_All//gi|30680213|ref|NP_849971.1|//8.00E-75//PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein [Arabidopsis thaliana] >gi|13877655|gb|AAK43905.1|AF37058 6_1 Unknown protein [Arabidopsis thaliana]	Unigene22191_All//1.00E-76//AT2G18090| PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein	Unigene22191_All//6.00E-109//CO098346			GO:0003676//GO:0006351//GO:0043231//GO:0046872	nr +
Unigene22192_All	3509	3.65	15.19	2.61	6.16	12.83	14.20	16.01	18.33	24.70	2.06E+00	3.11E-112	Up	-4.85E-01	3.17E-03		1.06E+00	2.91E-42	Up	1.20E+00	3.40E-52	Up	1.95E-01	1.16E-03		6.26E-01	2.00E-35		Unigene22192_All//gi|240255591|ref|NP_190681.6|//2.00E-76//DNA binding / nucleic acid binding / protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene22192_All//3.00E-67//AT2G18090| PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein	Unigene22192_All//0.00E+00//TC148899			GO:0005488	nr -
Unigene22195_All	687	0.99	1.77	1.55	0.51	1.15	2.17	2.71	1.52	2.73	8.38E-01	1.73E-01		6.47E-01	3.62E-01		1.18E+00	1.61E-01		2.10E+00	5.79E-04	Up	-8.32E-01	5.15E-02		9.30E-03	9.81E-01		Unigene22195_All//gi|18418260|ref|NP_567931.1|//1.00E-94//DRP3A (DYNAMIN-RELATED PROTEIN 3A); GTP binding / GTPase/ phosphoinositide binding [Arabidopsis thaliana] >gi|60392233|sp|Q8S944.2|DRP3A_ARATH RecName: Full=Dynamin-related protein 3A; AltName: Full=Dynamin-like protein 2a; AltName: Full=Dynamin-like protein 2 >gi|3549667|emb|CAA20578.1| Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana] >gi|7270313|emb|CAB80082.1| Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana] >gi|19032335|dbj|BAB85643.1| dynamin like protein 2a [Arabidopsis thaliana]	Unigene22195_All//7.00E-96//AT4G33650| DRP3A (DYNAMIN-RELATED PROTEIN 3A); GTP binding / GTPase/ phosphoinositide binding	Unigene22195_All//6.00E-54//TC164775		ko04144|Endocytosis	GO:0005543//GO:0007005//GO:0007031//GO:0007275//GO:0009526//GO:0009657//GO:0016020//GO:0017111//GO:0032561//GO:0042579	nr +
Unigene22198_All	2234	1.59	2.22	3.67	4.15	3.64	3.94	3.77	4.40	4.74	4.81E-01	7.82E-02		1.20E+00	2.80E-08	Up	-1.89E-01	3.73E-01		-7.32E-02	7.30E-01		2.23E-01	2.15E-01		3.33E-01	3.24E-02		Unigene22198_All//gi|18418260|ref|NP_567931.1|//4.00E-58//DRP3A (DYNAMIN-RELATED PROTEIN 3A); GTP binding / GTPase/ phosphoinositide binding [Arabidopsis thaliana] >gi|60392233|sp|Q8S944.2|DRP3A_ARATH RecName: Full=Dynamin-related protein 3A; AltName: Full=Dynamin-like protein 2a; AltName: Full=Dynamin-like protein 2 >gi|3549667|emb|CAA20578.1| Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana] >gi|7270313|emb|CAB80082.1| Arabidopsis dynamin-like protein ADL2 [Arabidopsis thaliana] >gi|19032335|dbj|BAB85643.1| dynamin like protein 2a [Arabidopsis thaliana]	Unigene22198_All//2.00E-53//AT4G33650| DRP3A (DYNAMIN-RELATED PROTEIN 3A); GTP binding / GTPase/ phosphoinositide binding	Unigene22198_All//0.00E+00//TC177479		ko04144|Endocytosis	GO:0005543//GO:0007005//GO:0007031//GO:0007275//GO:0009526//GO:0009657//GO:0016020//GO:0017111//GO:0032561//GO:0042579	nr +
Unigene2220_All	937	5.70	3.57	3.86	4.78	2.21	2.51	2.89	1.47	1.57	-6.74E-01	8.94E-03		-5.60E-01	4.00E-02		-1.12E+00	2.87E-05	Down	-9.33E-01	9.35E-04		-9.72E-01	4.54E-03		-8.76E-01	7.81E-03		Unigene2220_All//gi|297797517|ref|XP_002866643.1|//6.00E-87//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312478|gb|EFH42902.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2220_All//2.00E-80//AT5G64970| mitochondrial substrate carrier family protein	Unigene2220_All//0.00E+00//CO111785		ko04146|Peroxisome	GO:0019866//GO:0031224//GO:0043231//GO:0046907	nr -
Unigene22208_All	1044	5.06	1.36	5.71	4.34	4.12	1.99	0.45	0.24	0.73	-1.90E+00	1.09E-10	Down	1.75E-01	5.25E-01		-7.47E-02	8.40E-01		-1.13E+00	6.75E-05	Down	-8.91E-01	3.84E-01		7.03E-01	3.27E-01		Unigene22208_All//gi|224150180|ref|XP_002336919.1|//3.00E-84//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837129|gb|EEE75508.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene22208_All//3.00E-73//AT1G50180| disease resistance protein (CC-NBS-LRR class), putative	Unigene22208_All//1.00E-166//TC172834		ko04626|Plant-pathogen interaction	GO:0016787	nr -
Unigene2221_All	1889	7.04	3.62	4.79	6.96	6.31	3.99	4.28	1.70	2.07	-9.58E-01	1.30E-09		-5.54E-01	5.42E-04		-1.42E-01	4.27E-01		-8.02E-01	1.25E-07		-1.33E+00	6.51E-12	Down	-1.05E+00	9.64E-09	Down	Unigene2221_All//gi|297797517|ref|XP_002866643.1|//1.00E-147//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312478|gb|EFH42902.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2221_All//8.00E-132//AT5G64970| mitochondrial substrate carrier family protein	Unigene2221_All//0.00E+00//TC138175				nr -
Unigene22211_All	1692	2.01	1.83	1.73	9.10	10.85	9.26	3.95	2.72	1.70	-1.38E-01	6.77E-01		-2.16E-01	5.67E-01		2.54E-01	5.66E-02		2.59E-02	8.92E-01		-5.39E-01	8.04E-03		-1.22E+00	3.61E-09	Down	Unigene22211_All//gi|29839624|sp|Q9FJX8.1|RPS4_ARATH//8.00E-56//RecName: Full=Probable disease resistance RPP8-like protein 4 >gi|10177352|dbj|BAB10695.1| disease resistance protein [Arabidopsis thaliana] >gi|29029048|gb|AAO64903.1| At5g48620 [Arabidopsis thaliana]	Unigene22211_All//1.00E-55//AT5G48620| disease resistance protein (CC-NBS-LRR class), putative	Unigene22211_All//3.00E-107//ES848802		ko04626|Plant-pathogen interaction		nr +
Unigene22216_All	2155	2.28	2.52	1.63	5.96	5.40	6.20	11.71	5.55	6.23	1.41E-01	5.99E-01		-4.85E-01	9.14E-02		-1.43E-01	4.33E-01		5.68E-02	7.51E-01		-1.08E+00	8.43E-26	Down	-9.11E-01	2.61E-20		Unigene22216_All//gi|15217579|ref|NP_171698.1|//0.00E+00//EDA10 (embryo sac development arrest 10); ARF guanyl-nucleotide exchange factor/ binding / guanyl-nucleotide exchange factor [Arabidopsis thaliana] >gi|8570447|gb|AAF76474.1|AC020622_8 Contains similarity to a guanine nucleotide exchange factor from Homo sapiens gb|AF111162 and contains a Sec7 PF|01369 domain [Arabidopsis thaliana]	Unigene22216_All//0.00E+00//AT1G01960| EDA10 (embryo sac development arrest 10); ARF guanyl-nucleotide exchange factor/ binding / guanyl-nucleotide exchange factor	Unigene22216_All//0.00E+00//CO497609		ko04626|Plant-pathogen interaction	GO:0005083//GO:0009536//GO:0009553//GO:0032011	nr -
Unigene22217_All	3475	2.65	1.84	2.99	6.98	6.80	7.16	8.15	3.88	5.10	-5.28E-01	5.35E-03		1.73E-01	3.90E-01		-3.84E-02	8.07E-01		3.67E-02	7.82E-01		-1.07E+00	1.79E-28	Down	-6.76E-01	6.39E-14		Unigene22217_All//gi|15232969|ref|NP_191645.1|//0.00E+00//guanine nucleotide exchange family protein [Arabidopsis thaliana] >gi|7329696|emb|CAB82690.1| guanine nucleotide exchange factor-like protein [Arabidopsis thaliana]	Unigene22217_All//0.00E+00//AT3G60860| guanine nucleotide exchange family protein	Unigene22217_All//0.00E+00//CO497609		ko04626|Plant-pathogen interaction	GO:0005083//GO:0009553//GO:0032011//GO:0043231//GO:0044444	nr -
Unigene2222_All	1785	69.64	29.35	7.04	126.89	74.18	8.86	201.38	50.93	28.88	-1.25E+00	9.25E-128	Down	-3.31E+00	0.00E+00	Down	-7.75E-01	1.56E-130		-3.84E+00	0.00E+00	Down	-1.98E+00	0.00E+00	Down	-2.80E+00	0.00E+00	Down	Unigene2222_All//gi|15219226|ref|NP_173089.1|//0.00E+00//ATOCT3 (ARABIDOPSIS THALIANA ORGANIC CATION/CARNITINE TRANSPORTER 3); carbohydrate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|4966360|gb|AAD34691.1|AC006341_19 Is a member of the PF|00083 sugar transporter family [Arabidopsis thaliana] >gi|18958009|gb|AAL79578.1| At1g16390/F309_19 [Arabidopsis thaliana] >gi|23507793|gb|AAN38700.1| At1g16390/F309_19 [Arabidopsis thaliana]	Unigene2222_All//9.00E-177//AT1G16390| ATOCT3 (ARABIDOPSIS THALIANA ORGANIC CATION/CARNITINE TRANSPORTER 3); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene2222_All//0.00E+00//TC144198			GO:0006810//GO:0022891//GO:0031224	nr -
Unigene22221_All	3102	3.53	1.70	1.87	5.38	4.78	4.35	4.47	3.10	4.70	-1.05E+00	2.85E-09	Down	-9.14E-01	3.99E-07		-1.69E-01	2.67E-01		-3.05E-01	2.94E-02		-5.29E-01	8.04E-05		7.23E-02	6.30E-01		Unigene22221_All//gi|9294489|dbj|BAB02708.1|//0.00E+00//IRE homolog; protein kinase-like protein [Arabidopsis thaliana]	Unigene22221_All//0.00E+00//AT3G17850| protein kinase, putative	Unigene22221_All//0.00E+00//gi|109862286|gb|DW491263.1|DW491263			GO:0004674//GO:0006464//GO:0032559	nr +
Unigene22223_All	1077	1.36	2.92	1.29	3.05	3.74	6.21	7.18	10.67	20.16	1.10E+00	2.06E-03		-8.15E-02	8.85E-01		2.93E-01	3.88E-01		1.02E+00	6.27E-06	Up	5.71E-01	1.26E-04		1.49E+00	4.34E-37	Up	Unigene22223_All//gi|224116170|ref|XP_002317230.1|//1.00E-100//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222860295|gb|EEE97842.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene22223_All//3.00E-78//AT1G61140| EDA16 (embryo sac development arrest 16); ATP binding / DNA binding / helicase/ nucleic acid binding / protein binding / zinc ion binding					nr +
Unigene22224_All	2251	2.51	3.80	1.68	4.12	3.99	6.40	15.08	27.46	39.22	6.00E-01	2.39E-03		-5.80E-01	2.71E-02		-4.39E-02	8.29E-01		6.37E-01	1.02E-05		8.65E-01	3.97E-43		1.38E+00	3.20E-132	Up	Unigene22224_All//gi|224116170|ref|XP_002317230.1|//0.00E+00//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222860295|gb|EEE97842.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene22224_All//0.00E+00//AT1G61140| EDA16 (embryo sac development arrest 16); ATP binding / DNA binding / helicase/ nucleic acid binding / protein binding / zinc ion binding	Unigene22224_All//0.00E+00//TC148116		ko03420|Nucleotide excision repair		nr -

Unigene22225_All	4531	1.70	2.82	1.62	3.55	3.82	4.07	11.64	13.84	39.54	7.31E-01	3.92E-06		-6.58E-02	7.74E-01		1.06E-01	5.30E-01		1.96E-01	1.74E-01		2.50E-01	2.85E-05		1.76E+00	0.00E+00	Up	Unigene22225_All|gi|224116170|ref|XP_002317230.1|//0.00E+00//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222860295|gb|EEE97842.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene22225_All//0.00E+00//AT1G61140| EDA16 (embryo sac development arrest 16); ATP binding / DNA binding / helicase/ nucleic acid binding / protein binding / zinc ion binding	Unigene22225_All//0.00E+00//TC148116		ko03420|Nucleotide excision repair		nr +
Unigene22226_All	5012	1.98	3.51	1.81	4.02	4.19	6.61	8.22	18.64	20.09	8.23E-01	8.86E-10		-1.35E-01	5.22E-01		6.18E-02	6.89E-01		7.18E-01	5.00E-15		1.18E+00	7.16E-108	Up	1.29E+00	3.29E-136	Up	Unigene22226_All|gi|224116170|ref|XP_002317230.1|//0.00E+00//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222860295|gb|EEE97842.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene22226_All//0.00E+00//AT1G61140| EDA16 (embryo sac development arrest 16); ATP binding / DNA binding / helicase/ nucleic acid binding / protein binding / zinc ion binding	Unigene22226_All//0.00E+00//ES793074				nr -
Unigene22231_All	867	4.35	3.51	1.78	6.66	7.07	8.70	10.09	12.34	20.82	-3.09E-01	3.56E-01		-1.29E+00	1.51E-04	Down	8.51E-02	7.99E-01		3.84E-01	8.29E-02		2.90E-01	7.65E-02		1.04E+00	3.51E-18	Up	Unigene22231_All|gi|297816498|ref|XP_002876132.1|//1.00E-65//myb family transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297321970|gb|EFH52391.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene22231_All//1.00E-62//AT3G52250| DNA binding / transcription factor	Unigene22231_All//0.00E+00//DN781589	MYB			nr +
Unigene22232_All	668	2.19	4.32	3.99	4.70	7.37	6.63	2.78	2.94	10.44	9.79E-01	8.37E-03		8.62E-01	3.32E-02		6.50E-01	1.38E-02		4.96E-01	9.66E-02		7.85E-02	8.58E-01		1.91E+00	2.52E-17	Up	Unigene22232_All|gi|224097993|ref|XP_002311103.1|//6.00E-10//predicted protein [Populus trichocarpa] >gi|222850923|gb|EEE88470.1| predicted protein [Populus trichocarpa]		Unigene22232_All//6.00E-137//gi|109860131|gb|DW489110.1|DW489110				nr -
Unigene22235_All	344	8.67	14.43	6.35	9.99	20.32	9.06	19.30	21.26	15.98	7.36E-01	6.35E-03		-4.50E-01	2.44E-01		1.02E+00	1.41E-06	Up	-1.41E-01	6.80E-01		1.40E-01	5.42E-01		-2.72E-01	1.94E-01		Unigene22235_All|gi|297613682|gb|ADI48274.1|//5.00E-58//uridine cytidine kinase [Carica papaya]	Unigene22235_All//2.00E-51//AT1G55810| uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative	Unigene22235_All//0.00E+00//TC173927		ko00240|Pyrimidine metabolism		nr +
Unigene22239_All	1227	6.14	16.97	10.29	9.26	11.00	9.35	32.43	40.88	37.79	1.47E+00	7.84E-28	Up	7.44E-01	6.16E-06		2.49E-01	1.25E-01		1.44E-02	9.48E-01		3.34E-01	5.35E-07		2.21E-01	1.46E-03		Unigene22239_All|gi|297847946|ref|XP_002891854.1|//4.00E-54//F20N2.19 [Arabidopsis lyrata subsp. lyrata] >gi|297337696|gb|EFH68113.1| F20N2.19 [Arabidopsis lyrata subsp. lyrata]	Unigene22239_All//1.00E-54//AT4G26510| ATP binding / kinase/ phosphotransferase, alcohol group as acceptor / uracil phosphoribosyltransferase	Unigene22239_All//0.00E+00//TC147483		ko00240|Pyrimidine metabolism		nr +
Unigene22240_All	1227	1.75	4.75	2.99	10.31	12.85	11.01	7.68	2.21	5.81	1.44E+00	3.94E-08	Up	7.76E-01	2.04E-02		3.18E-01	2.36E-02		9.39E-02	6.41E-01		-1.80E+00	5.61E-21	Down	-4.03E-01	1.38E-02		Unigene22240_All|gi|110737140|dbj|BAF00520.1|//1.00E-150//uracil phosphoribosyl transferase like protein [Arabidopsis thaliana]	Unigene22240_All//4.00E-143//AT4G26510| ATP binding / kinase/ phosphotransferase, alcohol group as acceptor / uracil phosphoribosyltransferase	Unigene22240_All//0.00E+00//TC162638		ko00240|Pyrimidine metabolism		nr -
Unigene22242_All	2491	8.49	30.63	20.54	9.54	7.84	13.72	41.24	65.92	59.37	1.85E+00	1.03E-139	Up	1.28E+00	4.11E-53	Up	-2.83E-01	9.66E-03		5.25E-01	3.89E-09		6.77E-01	2.59E-74		5.25E-01	6.14E-44		Unigene22242_All|gi|300680944|sp|B5W8Z8.1|FAO1_LOTJA//0.00E+00//RecName: Full=Long-chain-alcohol oxidase FAO1; AltName: Full=Long-chain fatty alcohol oxidase 1 >gi|209570220|emb|CAP15762.1| long chain fatty alcohol oxidase FAO1 [Lotus japonicus]	Unigene22242_All//0.00E+00//AT3G23410| alcohol oxidase-related	Unigene22242_All//0.00E+00//TC155689				nr -
Unigene22243_All	371	7.47	6.28	1.58	13.56	11.97	13.76	14.02	16.45	17.50	-2.51E-01	5.25E-01		-2.24E+00	8.38E-07	Down	-1.80E-01	5.50E-01		2.06E-02	9.53E-01		2.31E-01	3.35E-01		3.20E-01	1.23E-01				Unigene22243_All//0.00E+00//gi|18098642|gb|BM357896.1|BM357896				
Unigene22245_All	1416	1.03	1.22	1.99	3.10	3.77	2.87	2.63	2.24	5.40	2.34E-01	6.17E-01		9.46E-01	1.56E-02		2.84E-01	3.16E-01		-1.09E-01	7.24E-01		-2.28E-01	4.68E-01		1.04E+00	3.66E-08	Up	Unigene22245_All|gi|115473879|ref|NP_001060538.1|//1.00E-10//Os07g0661500 [Oryza sativa Japonica Group] >gi|113612074|dbj|BAF22452.1| Os07g0661500 [Oryza sativa Japonica Group]	Unigene22245_All//5.00E-31//AT5G12400| PHD finger transcription factor, putative	Unigene22245_All//0.00E+00//gi|109859697|gb|DW488676.1|DW488676				nr -
Unigene22247_All	748	2.73	2.98	2.56	6.99	8.24	10.69	12.44	5.03	8.10	1.28E-01	7.57E-01		-9.01E-02	8.43E-01		2.37E-01	3.82E-01		6.12E-01	2.66E-03		-1.31E+00	2.75E-13	Down	-6.19E-01	1.48E-04		Unigene22247_All|gi|30685230|ref|NP_193817.2|//1.00E-114//TPP2 (TRIPEPTIDYL PEPTIDASE II); tripeptidyl-peptidase [Arabidopsis thaliana]	Unigene22247_All//1.00E-115//AT4G20850| TPP2 (TRIPEPTIDYL PEPTIDASE II); tripeptidyl-peptidase	Unigene22247_All//3.00E-127//TC154462				nr -
Unigene2225_All	2238	69.08	142.52	96.08	7.70	13.49	12.77	12.32	16.02	9.11	1.04E+00	2.04E-245	Up	4.76E-01	4.64E-41		8.09E-01	2.37E-18		7.30E-01	2.01E-13		3.80E-01	1.99E-06		-4.35E-01	1.36E-06		Unigene2225_All|gi|111038269|gb|ABH03531.1|//1.00E-173//class II knotted-like homeobox protein [Prunus persica] >gi|215983122|gb|ACJ71731.1| class II knotted-like homeobox transcription factor [Prunus persica]	Unigene2225_All//6.00E-141//AT5G25220| KNAT3 (KNOTTED1-LIKE HOMEOBOX GENE 3); transcription activator/ transcription factor	Unigene2225_All//0.00E+00//TC133921	HB		GO:0010071//GO:0000677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene22251_All	4332	1.94	1.58	2.11	3.65	4.29	3.62	6.89	2.59	4.69	-3.00E-01	1.45E-01		1.21E-01	5.96E-01		2.36E-01	7.85E-02		-1.09E-02	9.52E-01		-1.41E+00	4.62E-46	Down	-5.55E-01	1.53E-10		Unigene22251_All|gi|30685230|ref|NP_193817.2|//0.00E+00//TPP2 (TRIPEPTIDYL PEPTIDASE II); tripeptidyl-peptidase [Arabidopsis thaliana]	Unigene22251_All//0.00E+00//AT4G20850| TPP2 (TRIPEPTIDYL PEPTIDASE II); tripeptidyl-peptidase	Unigene22251_All//0.00E+00//TC134152				nr -
Unigene22254_All	268	0.39	2.27	2.38	0.93	5.14	2.70	4.58	5.77	9.66	2.54E+00	2.46E-02		2.61E+00	2.33E-02		2.47E+00	1.66E-04	Up	1.54E+00	9.17E-02		3.35E-01	5.17E-01		1.08E+00	1.75E-03									ESTscan -
Unigene2226_All	1603	13.06	15.90	7.14	35.27	22.26	18.85	25.40	2.32	3.21	2.84E-01	1.00E-02		-8.70E-01	4.75E-12		-6.64E-01	4.82E-25		-9.04E-01	1.23E-37		-3.45E+00	1.63E-186	Down	-2.99E+00	8.85E-168	Down	Unigene2226_All|gi|37572443|dbj|BAC98491.1|//2.00E-88//AG-motif binding protein-1 [Nicotiana tabacum]	Unigene2226_All//8.00E-60//AT3G54810| zinc finger (GATA type) family protein	Unigene2226_All//0.00E+00//TC158948	C2C2-GATA		GO:0005488//GO:0032501//GO:0048511	nr -
Unigene22262_All	1163	13.59	2.22	3.62	32.04	20.46	9.32	4.29	2.48	4.04	-2.61E+00	3.93E-45	Down	-1.91E+00	1.33E-29	Down	-6.47E-01	6.79E-16		-1.78E+00	5.24E-71	Down	-7.91E-01	9.43E-04		-8.58E-02	7.31E-01		Unigene22262_All|gi|224101241|ref|XP_002312197.1|//3.00E-82//dicer-like protein [Populus trichocarpa] >gi|222852017|gb|EEE89564.1| dicer-like protein [Populus trichocarpa]	Unigene22262_All//9.00E-71//AT3G03300| DCL2 (DICER-LIKE 2); ATP binding / ATP-dependent helicase/ RNA binding / double-stranded RNA binding / helicase/ nucleic acid binding / ribonuclease III	Unigene22262_All//0.00E+00//TC171206				nr +
Unigene22263_All	3678	5.51	1.98	2.71	15.83	12.40	6.73	5.38	2.50	4.92	-1.47E+00	2.22E-27	Down	-1.02E+00	4.02E-15	Down	-3.53E-01	2.20E-08		-1.23E+00	3.22E-64	Down	-1.11E+00	3.27E-21	Down	-1.30E-01	2.87E-01		Unigene22263_All|gi|224109196|ref|XP_002315119.1|//0.00E+00//dicer-like protein [Populus trichocarpa] >gi|222864159|gb|EEF01290.1| dicer-like protein [Populus trichocarpa]	Unigene22263_All//0.00E+00//AT3G03300| DCL2 (DICER-LIKE 2); ATP binding / ATP-dependent helicase/ RNA binding / double-stranded RNA binding / helicase/ nucleic acid binding / ribonuclease III	Unigene22263_All//0.00E+00//TC171206				nr +
Unigene22264_All	4515	3.55	2.83	3.22	8.51	7.21	5.41	5.09	2.24	3.05	-3.26E-01	2.17E-02		-1.39E-01	3.88E-01		-2.39E-01	4.47E-03		-6.53E-01	7.29E-15		-1.19E+00	2.57E-27	Down	-7.39E-01	3.02E-13		Unigene22264_All|gi|224109196|ref|XP_002315119.1|//0.00E+00//dicer-like protein [Populus trichocarpa] >gi|222864159|gb|EEF01290.1| dicer-like protein [Populus trichocarpa]	Unigene22264_All//0.00E+00//AT3G03300| DCL2 (DICER-LIKE 2); ATP binding / ATP-dependent helicase/ RNA binding / double-stranded RNA binding / helicase/ nucleic acid binding / ribonuclease III	Unigene22264_All//0.00E+00//TC171206				nr +
Unigene22266_All	802	0.26	0.00	0.00	0.06	0.04	0.00	7.38	0.73	2.43	-8.03E+00	1.22E-01		-8.03E+00	1.46E-01		-5.34E-01	8.25E-01		-5.96E+00	6.35E-01		-3.34E+00	9.00E-27	Down	-1.60E+00	5.88E-12	Down	Unigene22266_All|gi|15241569|ref|NP_199290.1|//2.00E-33//DC1 domain-containing protein [Arabidopsis thaliana] >gi|9758381|dbj|BAB08830.1| CHP-rich zinc finger protein-like [Arabidopsis thaliana] >gi|67633858|gb|AAY78853.1| DC1 domain-containing protein [Arabidopsis thaliana]	Unigene22266_All//8.00E-35//AT5G44770| DC1 domain-containing protein	Unigene22266_All//0.00E+00//TC171911				nr +
Unigene22270_All	1936	1.03	3.87	0.72	3.63	7.52	3.24	6.55	9.52	17.80	1.92E+00	6.03E-15	Up	-5.22E-01	2.81E-01		1.05E+00	8.88E-14	Up	-1.62E-01	5.36E-01		5.39E-01	2.54E-06		1.44E+00	1.07E-55	Up	Unigene22270_All|gi|29029012|gb|AA064885.1|//9.00E-57//At5g22355 [Arabidopsis thaliana]	Unigene22270_All//4.00E-58//AT5G22355| DC1 domain-containing protein	Unigene22270_All//0.00E+00//TC171911				nr -
Unigene22272_All	688	2.89	2.65	6.66	6.37	10.46	6.96	3.32	2.79	2.20	-1.24E-01	7.75E-01		1.20E+00	6.25E-05	Up	7.15E-01	5.72E-04		1.27E-01	7.00E-01		-2.48E-01	5.57E-01		-5.93E-01	1.05E-01		Unigene22272_All|gi|223452309|gb|ACM89482.1|//7.00E-90//receptor-like kinase [Glycine max]	Unigene22272_All//3.00E-83//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene22272_All//1.00E-132//TC130439				nr -
Unigene22273_All	1719	6.76	4.10	2.91	18.78	10.96	8.09	11.26	2.53	4.31	-7.22E-01	1.46E-05		-1.21E+00	1.46E-11	Down	-7.77E-01	5.91E-19		-1.21E+00	6.51E-35	Down	-2.16E+00	1.10E-53	Down	-1.39E+00	3.60E-30	Down	Unigene22273_All|gi|163717541|gb|ABV40731.1|//0.00E+00//FERONIA receptor-like kinase [Citrus trifoliata]	Unigene22273_All//0.00E+00//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene22273_All//0.00E+00//gi|78346422|gb|DT566696.1|DT566696		ko04626|Plant-pathogen interaction		nr +
Unigene22274_All	3566	3.83	2.37	1.43	9.96	7.89	5.51	6.32	1.63	3.15	-6.91E-01	5.65E-06		-1.42E+00	5.91E-17	Down	-3.36E-01	6.34E-05		-8.54E-01	1.04E-21		-1.96E+00	4.74E-55	Down	-1.00E+00	2.67E-21	Down	Unigene22274_All|gi|155242124|gb|ABI18696.1|//0.00E+00//FERONIA receptor-like kinase [Arabidopsis lyrata]	Unigene22274_All//0.00E+00//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene22274_All//0.00E+00//gi|164344389|gb|ES815140.1|ES815140		ko04626|Plant-pathogen interaction		nr -
Unigene22275_All	3155	10.71	9.56	4.81	12.28	9.31	7.84	35.91	17.92	22.12	-1.65E-01	9.60E-02		-1.16E+00	4.06E-30	Down	-4.00E-01	3.85E-07		-6.47E-01	8.88E-15		-1.00E+00	1.99E-100	Down	-6.99E-01	4.35E-56		Unigene22275_All|gi|223452393|gb|ACM89524.1|//0.00E+00//FERONIA receptor-like kinase [Glycine max]	Unigene22275_All//0.00E+00//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene22275_All//0.00E+00//TC130439		ko04626|Plant-pathogen interaction		nr -
Unigene2228_All	1861	21.20	13.42	19.20	40.10	32.23	30.07	39.44	18.84	15.37	-6.59E-01	1.51E-14		-1.43E-01	1.40E-01		-3.15E-01	1.22E-08		-4.15E-01	8.88E-13		-1.07E+00	4.15E-72	Down	-1.36E+00	9.87E-109	Down	Unigene2228_All|gi|16930463|gb|AAL31917.1|AF419885_1//1.00E-150//AT5g14250/F18O22_40 [Arabidopsis thaliana] >gi|21360467|gb|AAM47349.1| AT5g14250/F18O22_40 [Arabidopsis thaliana]	Unigene2228_All//2.00E-145//AT5G14250| COP13 (CONSTITUTIVE PHOTOMORPHOGENIC 13); protein binding	Unigene2228_All//0.00E+00//TC154658			GO:0043234	nr +
Unigene22292_All	2516	0.52	1.05	0.63	2.97	2.92	2.78	3.95	3.80	11.21	1.01E+00	1.01E-02		2.88E-01	6.16E-01		-2.68E-02	9.11E-01		-9.41E-02	6.85E-01		-5.40E-02	7.73E-01		1.51E+00	1.05E-48	Up	Unigene22292_All|gi|224112851|ref|XP_002316309.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222865349|gb|EEF02480.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene22292_All//0.00E+00//AT2G39480| PGP6 (P-GLYCOPROTEIN 6); ATPase, coupled to transmembrane movement of substances	Unigene22292_All//0.00E+00//DT462892		ko02010|ABC transporters		nr +
Unigene22293_All	632	4.39	7.78	7.75	14.98	10.41	14.86	8.03	10.25	16.96	8.26E-01	2.37E-03		8.21E-01	3.71E-03		-5.25E-01	2.83E-03		-1.08E-02	9.50E-01		3.53E-01	1.02E-01		1.08E+00	1.03E-11	Up	Unigene22293_All|gi|224098270|ref|XP_002311144.1|//1.00E-102//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222850964|gb|EEE88511.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene22293_All//1.00E-96//AT3G55320| PGP20 (P-GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances	Unigene22293_All//0.00E+00//ES812024		ko02010|ABC transporters		nr -
Unigene22295_All	1562	0.57	0.97	0.99	0.83	0.66	1.39	1.35	0.94	5.69	7.73E-01	1.48E-01		7.96E-01	1.50E-01		-3.26E-01	5.86E-01		7.43E-01	9.72E-02		-5.31E-01	1.91E-01		2.07E+00	2.84E-24	Up	Unigene22295_All|gi|224112851|ref|XP_002316309.1|//1.00E-179//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222865349|gb|EEF02480.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene22295_All//0.00E+00//AT2G39480| PGP6 (P-GLYCOPROTEIN 6); ATPase, coupled to transmembrane movement of substances	Unigene22295_All//0.00E+00//DT462892		ko02010|ABC transporters		nr +

Unigene22296_All	3297	2.86	2.69	1.81	5.36	5.19	5.81	9.48	11.93	19.93	-8.69E-02	6.56E-01			-6.59E-01	6.90E-04		-4.72E-02	8.00E-01			1.15E-01	4.56E-01		3.32E-01	1.31E-05		1.07E+00	1.26E-66	Up	Unigene22296_All//gi|224112851|ref|XP_002316309.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222865349|gb|EEF02480.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene22296_All//0.00E+00//AT2G39480| PGP6 (P-GLYCOPROTEIN 6); ATPase, coupled to transmembrane movement of substances	Unigene22296_All//0.00E+00//ES812024		ko02010|ABC transporters		nr -
Unigene22297_All	5084	1.78	2.62	1.27	5.24	5.25	4.02	8.61	9.11	20.73	5.58E-01	2.91E-04			-4.90E-01	1.46E-02		2.00E-03	9.90E-01			-3.85E-01	1.96E-04		8.17E-02	3.33E-01		1.27E+00	1.11E-138	Up	Unigene22297_All//gi|224112851|ref|XP_002316309.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222865349|gb|EEF02480.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene22297_All//0.00E+00//AT3G55320| PGP20 (P-GLYCOPROTEIN 20); ATPase, coupled to transmembrane movement of substances	Unigene22297_All//0.00E+00//gi|73860154|gb|DT462893.1|DT462893		ko02010|ABC transporters		nr +
Unigene22299_All	645	3.65	1.73	4.87	3.94	5.02	5.67	3.54	1.30	0.56	-1.08E+00	1.01E-02			4.16E-01	2.64E-01		3.50E-01	3.51E-01			5.26E-01	1.17E-01		-1.45E+00	2.26E-04	Down	-2.67E+00	4.62E-09	Down	Unigene22299_All//gi|77554105|gb|AB496901.1|//5.00E-26//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene22299_All//2.00E-34//AT3G01810| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: nucleolar protein gar2-related (TAIR:AT2G42320.2); Has 1293 Blast hits to 384 proteins in 97 species: Archae - 2; Bacteria - 96; Metazoa - 212; Fungi - 99; Plants - 59; Viruses - 0; Other Eukaryotes - 825 (source: NCBI BLink).	Unigene22299_All//0.00E+00//DR457157				nr -
Unigene2230_All	1017	21.25	5.33	9.27	18.03	13.65	9.95	12.60	3.29	3.17	-1.99E+00	2.16E-44	Down	-1.20E+00	1.54E-20	Down	-4.02E-01	9.77E-04		-8.58E-01	1.46E-11				-1.94E+00	3.09E-31	Down	-1.99E+00	2.42E-33	Down	Unigene2230_All//gi|51557078|gb|AAU06309.1|//5.00E-55//MYB transcription factor [Hevea brasiliensis]	Unigene2230_All//1.00E-35//AT2G38090| myb family transcription factor	Unigene2230_All//0.00E+00//TC166199	MYB-related			nr -
Unigene22301_All	4320	11.24	7.44	9.17	11.52	11.41	11.42	5.03	2.50	3.10	-5.96E-01	6.24E-15			-2.93E-01	2.17E-04		-1.32E-02	8.90E-01		-1.30E-02	9.06E-01			-1.01E+00	3.56E-20	Down	-6.99E-01	1.70E-11		Unigene22301_All//gi|77554105|gb|AB496901.1|//0.00E+00//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene22301_All//0.00E+00//AT3G01810| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: nucleolar protein gar2-related (TAIR:AT2G42320.2); Has 1293 Blast hits to 384 proteins in 97 species: Archae - 2; Bacteria - 96; Metazoa - 212; Fungi - 99; Plants - 59; Viruses - 0; Other Eukaryotes - 825 (source: NCBI BLink).	Unigene22301_All//0.00E+00//TC149061		ko00230|Purine metabolism		nr +
Unigene22303_All	592	3.09	2.65	1.35	0.67	1.86	0.84	3.21	1.13	2.15	-2.21E-01	6.22E-01		-1.20E+00	1.99E-02		1.47E+00	3.09E-02		3.18E-01	7.58E-01		-1.51E+00	5.93E-04	Down	-5.78E-01	1.56E-01		Unigene22303_All//gi|42569411|ref|NP_180399.2|//5.00E-63//pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein [Arabidopsis thaliana]	Unigene22303_All//3.00E-51//AT2G28320| pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein	Unigene22303_All//0.00E+00//DW487933				nr +
Unigene22305_All	1526	1.89	3.02	0.91	2.91	3.32	3.58	5.54	2.63	3.26	6.80E-01	1.55E-02		-1.06E+00	6.82E-03		1.91E-01	5.63E-01		3.02E-01	2.87E-01		-1.08E+00	3.80E-09	Down	-7.64E-01	1.03E-05		Unigene22305_All//gi|42569411|ref|NP_180399.2|//1.00E-116//pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein [Arabidopsis thaliana]	Unigene22305_All//6.00E-118//AT2G28320| pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein	Unigene22305_All//0.00E+00//EX164741				nr -
Unigene22306_All	1816	5.45	3.15	4.87	3.37	3.89	3.98	4.40	1.17	3.88	-7.88E-01	1.59E-05		-1.62E-01	4.26E-01		2.04E-01	4.22E-01		2.38E-01	3.37E-01		-1.91E+00	2.36E-19	Down	-1.80E-01	3.55E-01		Unigene22306_All//gi|42569411|ref|NP_180399.2|//0.00E+00//pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein [Arabidopsis thaliana]	Unigene22306_All//0.00E+00//AT2G28320| pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein	Unigene22306_All//0.00E+00//TC175659				nr -
Unigene2231_All	1486	9.40	1.57	4.95	9.79	7.44	7.14	5.01	1.04	1.47	-2.58E+00	1.78E-39	Down	-9.27E-01	4.14E-09		-3.96E-01	4.76E-03		-4.55E-01	1.73E-03		-2.27E+00	2.22E-22	Down	-1.76E+00	7.06E-17	Down	Unigene2231_All//gi|51557078|gb|AAU06309.1|//1.00E-114//MYB transcription factor [Hevea brasiliensis]	Unigene2231_All//2.00E-86//AT2G38090| myb family transcription factor	Unigene2231_All//0.00E+00//TC166199	MYB		GO:0001071//GO:0003676//GO:0010468//GO:0043231	nr +
Unigene22310_All	495	4.02	0.51	4.52	5.74	6.96	4.74	7.17	1.94	5.79	-2.97E+00	5.00E-07	Down	1.70E-01	6.95E-01		2.78E-01	4.58E-01		-2.74E-01	5.03E-01		-1.89E+00	6.81E-09	Down	-3.08E-01	3.02E-01		Unigene22310_All//gi|9294023|dbj|BAB01926.1|//3.00E-57//multispanning membrane protein-like [Arabidopsis thaliana]	Unigene22310_All//2.00E-58//AT3G13772| endomembrane protein 70, putative	Unigene22310_All//3.00E-144//CO116561				nr +
Unigene22314_All	1496	3.15	3.29	2.88	6.96	6.19	6.46	3.84	1.37	2.16	6.18E-02	8.24E-01		-1.27E-01	6.63E-01		-1.69E-01	4.05E-01		-1.07E-01	6.39E-01		-1.49E+00	3.30E-10	Down	-8.34E-01	1.07E-04		Unigene22314_All//gi|297850472|ref|XP_002893117.1|//2.00E-74//F2D10.3 [Arabidopsis lyrata subsp. lyrata] >gi|297338959|gb|EFH69376.1| F2D10.3 [Arabidopsis lyrata subsp. lyrata]	Unigene22314_All//4.00E-72//AT1G20550| unknown protein	Unigene22314_All//0.00E+00//ES819285				nr -
Unigene22315_All	1085	3.95	2.01	1.13	5.00	4.73	4.37	5.07	2.35	3.34	-9.78E-01	9.23E-04		-1.81E+00	6.92E-08	Down	-8.17E-02	8.10E-01		-1.95E-01	5.02E-01		-1.11E+00	1.72E-06	Down	-6.00E-01	6.15E-03		Unigene22315_All//gi|297850472|ref|XP_002893117.1|//1.00E-139//F2D10.3 [Arabidopsis lyrata subsp. lyrata] >gi|297338959|gb|EFH69376.1| F2D10.3 [Arabidopsis lyrata subsp. lyrata]	Unigene22315_All//3.00E-141//AT1G76270| unknown protein	Unigene22315_All//0.00E+00//ES819285				nr -
Unigene22316_All	1688	5.95	5.52	3.91	13.19	11.20	11.26	12.62	6.09	6.96	-1.08E-01	6.12E-01		-6.05E-01	1.23E-03		-2.36E-01	4.48E-02		-2.28E-01	6.56E-02		-1.05E+00	4.68E-21	Down	-8.59E-01	1.00E-15		Unigene22316_All//gi|6573718|gb|AAF17638.1|AC009978_14//1.00E-137//T23E18.20 [Arabidopsis thaliana]	Unigene22316_All//5.00E-133//AT1G76270| unknown protein	Unigene22316_All//0.00E+00//ES831274				nr +
Unigene2232_All	1794	2.25	0.90	1.72	4.28	4.59	3.98	3.11	1.86	2.53	-1.31E+00	3.13E-05	Down	-3.83E-01	2.42E-01		1.01E-01	6.83E-01		-1.04E-01	6.80E-01		-7.39E-01	9.71E-04		-2.97E-01	1.94E-01		Unigene2232_All//gi|18410975|ref|NP_567068.1|//1.00E-171//ubiquitin thiolesterase [Arabidopsis thaliana] >gi|15810016|gb|AAL06935.1| AT3g58520/F14P22_110 [Arabidopsis thaliana] >gi|22135767|gb|AAM91040.1| AT3g58520/F14P22_110 [Arabidopsis thaliana]	Unigene2232_All//7.00E-169//AT3G58520| ubiquitin thiolesterase	Unigene2232_All//0.00E+00//TC163192				nr +
Unigene22321_All	3760	10.33	8.53	11.56	66.75	63.23	62.16	28.80	12.02	14.39	-2.76E-01	1.54E-03		1.63E-01	7.22E-02		-7.81E-02	1.89E-02		-1.03E-01	1.80E-03		-1.26E+00	1.43E-138	Down	-1.00E+00	2.05E-98	Down	Unigene22321_All//gi|1685087|gb|AAC49536.1|//0.00E-000//diphenol oxidase [Nicotiana tabacum]	Unigene22321_All//0.00E+00//AT2G38080| IRX12 (IRREGULAR XYLEM 12); laccase	Unigene22321_All//0.00E+00//TC178577		ko04130|SNARE interactions in vesicular transport		nr -
Unigene22327_All	913	8.65	6.66	6.77	10.42	9.77	7.72	6.34	2.66	10.87	-3.78E-01	7.38E-02		-3.55E-01	1.13E-01		-9.33E-02	6.71E-01		-4.33E-01	2.12E-02		-1.26E+00	4.03E-08	Down	7.76E-01	1.15E-06		Unigene22327_All//gi|30690202|ref|NP_850444.1|//2.00E-72//transmembrane protein-related [Arabidopsis thaliana]	Unigene22327_All//1.00E-73//AT2G46060| transmembrane protein-related	Unigene22327_All//0.00E+00//TC178493				nr +
Unigene22328_All	1379	3.26	8.60	3.36	6.39	5.14	5.80	24.22	58.34	31.35	1.40E+00	4.36E-15	Up	4.21E-02	8.92E-01		-3.14E-01	1.14E-01		-1.41E-01	5.47E-01		1.27E+00	6.79E-104	Up	3.72E-01	1.46E-07		Unigene22328_All//gi|30690202|ref|NP_850444.1|//1.00E-106//transmembrane protein-related [Arabidopsis thaliana]	Unigene22328_All//3.00E-106//AT2G46060| transmembrane protein-related	Unigene22328_All//0.00E+00//DT526806				nr +
Unigene22335_All	549	0.95	1.66	1.16	1.81	1.38	0.90	3.77	1.22	1.31	8.02E-01	2.71E-01		2.88E-01	7.25E-01		-3.95E-01	5.73E-01		-1.00E+00	1.57E-01		-1.63E+00	1.21E-04	Down	-1.53E+00	1.72E-04	Down	Unigene22335_All//gi|297833636|ref|XP_002884700.1|//7.00E-22//RAPTOR1B [Arabidopsis lyrata subsp. lyrata] >gi|297330540|gb|EFH60959.1| RAPTOR1B [Arabidopsis lyrata subsp. lyrata]	Unigene22335_All//4.00E-23//AT3G08850| RAPTOR1; nucleotide binding / protein binding	Unigene22335_All//0.00E+00//TC168723				nr +
Unigene2234_All	2061	3.02	1.60	2.30	25.31	27.00	11.90	62.02	107.16	36.28	-9.19E-01	1.15E-04		-3.94E-01	1.24E-01		9.35E-02	2.58E-01		-1.09E+00	3.88E-47	Down	7.89E-01	3.69E-130		-7.73E-01	3.59E-75		Unigene2234_All//gi|224077380|ref|XP_002305237.1|//0.00E+00//acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa] >gi|222848201|gb|EEE85748.1| acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]	Unigene2234_All//0.00E+00//AT1G66120| acyl-activating enzyme 11 (AAE11)	Unigene2234_All//0.00E+00//TC134902		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0016405//GO:0019758	nr +
Unigene22350_All	822	2.93	2.28	2.92	3.82	4.86	3.57	3.60	3.15	9.74	-3.60E-01	3.87E-01		-6.30E-03	9.96E-01		3.48E-01	3.00E-01		-9.63E-02	7.90E-01		-1.92E-01	6.16E-01		1.44E+00	1.61E-13	Up	Unigene22350_All//gi|30686918|ref|NP_850847.1|//2.00E-12//CHR17 (CHROMATIN REMODELING FACTOR17): ATP binding / DNA binding / DNA-dependent ATPase/ helicase/ hydrolase, acting on on d anhydrides, in phosphorus-containing anhydrides / nucleic acid binding / nucleosome binding [Arabidopsis thaliana]	Unigene22350_All//2.00E-11//AT5G44090| calcium-binding EF hand family protein, putative / protein phosphatase 2A 62 kDa B'' regulatory subunit, putative	Unigene22350_All//1.00E-61//ES791217				nr -
Unigene22352_All	3106	17.42	24.36	16.60	7.39	13.16	9.32	9.30	11.18	35.62	4.84E-01	7.47E-16		-6.98E-02	4.11E-01		8.32E-01	6.87E-26		3.34E-01	8.38E-04		2.66E-01	1.31E-03		1.94E+00	5.27E-269	Up	Unigene22352_All//gi|5533379|gb|AAD45158.1|AF165429_1//0.00E+00//protein phosphatase 2A 62 kDa B'' regulatory subunit [Arabidopsis thaliana] >gi|9759510|dbj|BAB10976.1| protein phosphatase 2A 62 kDa B'' regulatory subunit [Arabidopsis thaliana] >gi|20466175|gb|AAM20405.1| protein phosphatase 2A 62 kDa B regulatory subunit [Arabidopsis thaliana] >gi|25083926|gb|AAN72135.1| protein phosphatase 2A 62 kDa B regulatory subunit [Arabidopsis thaliana] >gi|42740920|gb|AAS44556.1| protein phosphatase 2A alpha [Arabidopsis thaliana]	Unigene22352_All//0.00E+00//AT5G44090| calcium-binding EF hand family protein, putative / protein phosphatase 2A 62 kDa B'' regulatory subunit, putative	Unigene22352_All//0.00E+00//TC143696				nr -

Unigene22353_All	1003	1.04	1.16	1.81	4.92	4.81	2.75	7.67	2.83	10.49	1.55E-01	7.88E-01		7.91E-01	1.21E-01		-3.28E-02	9.10E-01		-8.40E-01	1.61E-03		-1.44E+00	9.61E-13	Down	4.51E-01	3.30E-03		Unigene22353_All//gi|13384201|gb|AAK21311.1|//1.00E-144//myosin subfamily XI heavy chain [Petroselinum crispum]	Unigene22353_All//1.00E-134//AT5G43900| MYA2 (ARABIDOPSIS MYOSIN 2); GTP-dependent protein binding / Rab GTPase binding / motor	Unigene22353_All//0.00E+00//TC176117				nr +
Unigene22355_All	2629	1.27	1.62	1.46	5.89	6.56	4.31	8.36	3.74	5.67	3.46E-01	2.53E-01		1.95E-01	5.85E-01		1.55E-01	3.06E-01		-4.51E-01	1.28E-03		-1.16E+00	2.23E-25	Down	-5.61E-01	3.78E-08		Unigene22355_All//gi|42561681|ref|NP_171912.2|//0.00E+00//XI B (MYOSIN XI B); motor [Arabidopsis thaliana]	Unigene22355_All//0.00E+00//AT1G04160| XIB (MYOSIN XI B); motor	Unigene22355_All//0.00E+00//TC172345				nr +
Unigene22357_All	3281	25.37	15.98	15.42	45.52	51.12	39.01	30.50	6.68	17.61	-6.67E-01	2.12E-30		-7.19E-01	2.33E-33		1.68E-01	6.69E-06		-2.23E-01	4.26E-08		-2.19E+00	8.51E-281	Down	-7.93E-01	1.31E-61		Unigene22357_All//gi|57232107|gb|AW47739.1|//0.00E+00//beta-galactosidase [Prunus persica]	Unigene22357_All//0.00E+00//AT4G36360| BGAL3 (beta-galactosidase 3); beta-galactosidase/ catalytic/ cation binding / sugar binding	Unigene22357_All//0.00E+00//TC157192		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series		nr +
Unigene22358_All	3578	25.71	23.85	31.42	63.61	76.22	80.00	29.38	9.31	8.55	-1.08E-01	6.58E-02		2.89E-01	5.81E-09		2.61E-01	4.66E-21		3.31E-01	5.40E-31		-1.66E+00	1.52E-202	Down	-1.78E+00	1.64E-230	Down	Unigene22358_All//gi|57232107|gb|AW47739.1|//0.00E+00//beta-galactosidase [Prunus persica]	Unigene22358_All//0.00E+00//AT4G36360| BGAL3 (beta-galactosidase 3); beta-galactosidase/ catalytic/ cation binding / sugar binding	Unigene22358_All//0.00E+00//TC133401		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series		nr -
Unigene22362_All	1184	6.50	9.20	8.86	14.22	26.64	18.42	7.61	3.07	6.70	5.02E-01	3.72E-03		4.48E-01	1.56E-02		9.06E-01	4.38E-23		3.74E-01	1.39E-03		-1.31E+00	6.36E-13	Down	-1.84E-01	3.17E-01		Unigene22362_All//gi|42569975|ref|NP_182176.2|//2.00E-69//ARF11 (AUXIN RESPONSE FACTOR 11); transcription factor [Arabidopsis thaliana] >gi|110739886|dbj|BAF01750.1| ARF1 family auxin responsive transcription factor like protein [Arabidopsis thaliana]	Unigene22362_All//6.00E-69//AT2G46530| ARF11 (AUXIN RESPONSE FACTOR 11); transcription factor	Unigene22362_All//0.00E+00//gi|78336702|gb|DT556976.1|DT556976	ARF			nr +
Unigene22363_All	2684	5.15	8.53	7.24	9.19	15.97	12.44	16.05	7.94	8.10	7.30E-01	2.64E-10		4.93E-01	1.40E-04		7.98E-01	2.59E-25		4.37E-01	1.42E-06		-1.02E+00	1.86E-39	Down	-9.86E-01	9.94E-39		Unigene22363_All//gi|299118178|gb|ADJ10892.1|//1.00E-177//auxin response factor 1 [Solanum lycopersicum]	Unigene22363_All//1.00E-147//AT3G61830| ARF18 (AUXIN RESPONSE FACTOR 18); transcription factor	Unigene22363_All//0.00E+00//gi|78336702|gb|DT556976.1|DT556976	ARF			nr -
Unigene22368_All	2681	2.48	8.35	3.93	2.12	2.49	2.80	2.68	4.15	3.00	1.75E+00	1.92E-38	Up	6.66E-01	2.52E-04		2.34E-01	3.59E-01		4.01E-01	7.03E-02		6.29E-01	3.37E-05		1.63E-01	4.05E-01		Unigene22368_All//gi|224124478|ref|XP_002330033.1|//0.00E+00//ferroportin protein family [Populus trichocarpa] >gi|222871458|gb|EEF08589.1| ferroportin protein family [Populus trichocarpa]	Unigene22368_All//0.00E+00//AT5G26820| AT1REG3 (IRON-REGULATED PROTEIN 3)	Unigene22368_All//0.00E+00//TC173362				nr +
Unigene2237_All	506	0.21	0.00	0.00	0.20	0.61	0.89	3.09	10.16	3.39	-7.69E+00	3.72E-01		-7.69E+00	3.94E-01		1.64E+00	3.21E-01		2.18E+00	1.03E-01		1.72E+00	4.30E-11	Up	1.31E-01	7.63E-01		Unigene2237_All//gi|51457952|gb|AAU03265.1|//2.00E-42//alpha/beta fold family protein [Solanum lycopersicum]	Unigene2237_All//6.00E-39//AT4G36610| hydrolase, alpha/beta fold family protein	Unigene2237_All//0.00E+00//gi|18101438|gb|BM360692.1|BM360692			GO:0003824	nr +
Unigene22371_All	3130	7.41	8.86	5.36	14.04	11.66	13.04	30.23	19.00	14.40	2.58E-01	1.50E-02		-4.67E-01	7.08E-05		-2.68E-01	4.51E-04		-1.06E-01	2.63E-01		-6.70E-01	1.82E-42		-1.07E+00	4.81E-96	Down	Unigene22371_All//gi|75172888|sp|Q9FWR2.1|AVPX_ARATH//0.00E+00//RecName: Full=Pyrophosphate-energized membrane proton pump 3; AltName: Full=Pyrophosphate-energized inorganic pyrophosphatase 3; Short=H(+)-PPase 3; AltName: Full=AVP1-like protein 2 >gi|99547727|gb|AAG96080.1|AC026237_1 Putative vacuolar-type H+-translocating inorganic pyrophosphatase [Arabidopsis thaliana]	Unigene22371_All//0.00E+00//AT1G16780| vacuolar-type H+-translocating inorganic pyrophosphatase, putative	Unigene22371_All//0.00E+00//TC136422		ko00190|Oxidative phosphorylation		nr +
Unigene22373_All	398	2.89	3.56	2.41	5.38	4.15	5.67	6.80	1.68	2.40	3.02E-01	6.11E-01		-2.64E-01	6.64E-01		-3.74E-01	4.16E-01		7.62E-02	8.80E-01		-2.02E+00	1.61E-07	Down	-1.50E+00	1.78E-05	Down	Unigene22373_All//gi|225456018|ref|XP_002279561.1|//7.00E-10//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297734247|emb|CBI15494.3| unnamed protein product [Vitis vinifera]	Unigene22373_All//5.00E-06//AT4G21460| unknown protein	Unigene22373_All//2.00E-105//ES844337				nr -
Unigene22375_All	749	3.84	5.21	5.97	7.78	6.25	6.39	1.81	2.40	4.41	4.39E-01	1.62E-01		6.36E-01	3.37E-02		-3.16E-01	2.22E-01		-2.84E-01	2.98E-01		4.10E-01	3.80E-01		1.29E+00	2.70E-05	Up	Unigene22375_All//gi|15231294|ref|NP_187969.1|//1.00E-09//calmodulin-binding family protein [Arabidopsis thaliana]	Unigene22375_All//6.00E-11//AT3G13600| calmodulin-binding family protein	Unigene22375_All//2.00E-72//ES844337				nr +
Unigene22376_All	1500	12.00	11.92	10.69	19.10	14.49	20.50	21.70	9.75	14.95	-9.00E-03	9.70E-01		-1.67E-01	2.59E-01		-3.99E-01	2.12E-05		1.03E-01	3.97E-01		-1.15E+00	8.89E-37	Down	-5.38E-01	7.98E-11		Unigene22376_All//gi|11692818|gb|AAG40012.1|AF324661_1/1.00E-151//AT3g18240 [Arabidopsis thaliana] >gi|222422869|dbj|BAH19421.1| AT3G18240 [Arabidopsis thaliana]	Unigene22376_All//2.00E-138//AT3G18240| unknown protein	Unigene22376_All//0.00E+00//TC174502				nr +
Unigene2238_All	1217	16.16	14.41	16.10	13.14	15.11	15.22	2.02	7.25	3.24	-1.66E-01	2.19E-01		-5.60E-03	9.92E-01		2.02E-01	1.50E-01		2.12E-01	1.31E-01		1.85E+00	2.29E-20	Up	6.86E-01	9.86E-03		Unigene2238_All//gi|18398716|ref|NP_565437.1|//1.00E-79//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|13605611|gb|AAK32799.1|AF36163_1 At2g18360/T3D06.13 [Arabidopsis thaliana] >gi|20197805|gb|AAD15501.2| expressed protein [Arabidopsis thaliana] >gi|21360541|gb|AAM47467.1| At2g18360/T3D06.13 [Arabidopsis thaliana]	Unigene2238_All//9.00E-80//AT2G18360| hydrolase, alpha/beta fold family protein	Unigene2238_All//0.00E+00//gi|18101438|gb|BM360692.1|BM360692			GO:0003824	nr -
Unigene22381_All	3057	0.60	0.63	1.41	1.08	0.81	0.93	1.56	2.09	1.54	7.23E-02	8.79E-01		1.24E+00	7.49E-05	Up	-4.07E-01	2.45E-01		-2.09E-01	6.10E-01		4.21E-01	4.81E-02		-2.34E-02	9.47E-01		Unigene22381_All//gi|15241481|ref|NP_196415.1|//7.00E-90//dentin sialophosphoprotein-related [Arabidopsis thaliana]	Unigene22381_All//9.00E-86//AT5G07980| dentin sialophosphoprotein-related	Unigene22381_All//0.00E+00//ES807799				nr +
Unigene22383_All	1086	2.41	2.47	2.84	4.22	3.27	3.16	6.11	6.47	2.42	3.78E-02	9.37E-01		2.40E-01	5.37E-01		-3.70E-01	2.03E-01		-4.17E-01	1.59E-01		8.11E-02	7.24E-01		-1.34E+00	2.27E-10	Down	Unigene22383_All//gi|297800334|ref|XP_002868051.1|//1.00E-84//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313887|gb|EFH44310.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22383_All//1.00E-67//AT4G17570| zinc finger (GATA type) family protein	Unigene22383_All//0.00E+00//gi|78338694|gb|DT558968.1|DT558968	C2C2-GATA			nr +
Unigene22384_All	1959	4.33	3.44	3.59	11.60	9.56	6.04	6.95	5.23	2.34	-3.31E-01	1.07E-01		-2.70E-01	2.25E-01		-2.78E-01	1.38E-02		-9.41E-01	1.74E-16		-4.11E-01	2.70E-03		-1.57E+00	1.03E-25	Down	Unigene22384_All//gi|297800334|ref|XP_002868051.1|//1.00E-118//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313887|gb|EFH44310.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22384_All//5.00E-102//AT4G17570| zinc finger (GATA type) family protein	Unigene22384_All//0.00E+00//gi|78338694|gb|DT558968.1|DT558968	C2C2-GATA			nr +
Unigene22386_All	1034	0.56	3.14	1.70	3.18	3.43	2.27	2.17	1.29	2.58	2.49E+00	3.21E-09	Up	1.61E+00	3.13E-03		1.09E-01	8.02E-01		-4.85E-01	1.74E-01		-7.45E-01	5.20E-02		2.52E-01	4.80E-01		Unigene22386_All//gi|22329893|ref|NP_174433.2|//1.00E-118//SGR2 (SHOOT GRAVITROPISM 2); phospholipase A1 [Arabidopsis thaliana] >gi|16904659|dbj|BAB71959.1| shoot gravitropism 2 [Arabidopsis thaliana]	Unigene22386_All//2.00E-118//AT1G31480| SGR2 (SHOOT GRAVITROPISM 2); phospholipase A1	Unigene22386_All//0.00E+00//CO127587				nr -
Unigene22387_All	2974	1.74	3.78	2.22	3.47	3.08	3.14	5.54	4.61	4.25	1.12E+00	2.28E-10	Up	3.50E-01	1.54E-01		-1.71E-01	3.99E-01		-1.41E-01	4.98E-01		-2.66E-01	3.71E-02		-3.85E-01	1.29E-03		Unigene22387_All//gi|22329893|ref|NP_174433.2|//1.00E-160//SGR2 (SHOOT GRAVITROPISM 2); phospholipase A1 [Arabidopsis thaliana] >gi|16904659|dbj|BAB71959.1| shoot gravitropism 2 [Arabidopsis thaliana]	Unigene22387_All//4.00E-162//AT1G31480| SGR2 (SHOOT GRAVITROPISM 2); phospholipase A1	Unigene22387_All//0.00E+00//TC147416				nr -
Unigene2239_All	1276	0.90	2.06	1.21	1.64	1.65	1.49	0.33	1.61	1.00	1.19E+00	2.69E-03		4.24E-01	4.35E-01		5.70E-03	9.98E-01		-1.41E-01	7.55E-01		2.28E+00	1.12E-06	Up	1.59E+00	3.57E-03		Unigene2239_All|gi|18398716|ref|NP_565437.1|//1.00E-55//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|13605611|gb|AAK32799.1|AF36163_1 At2g18360/T3D06.13 [Arabidopsis thaliana] >gi|20197805|gb|AAD15501.2| expressed protein [Arabidopsis thaliana] >gi|21360541|gb|AAM47467.1| At2g18360/T3D06.13 [Arabidopsis thaliana]	Unigene2239_All//6.00E-57//AT2G18360| hydrolase, alpha/beta fold family protein	Unigene2239_All//0.00E+00//gi|18101438|gb|BM360692.1|BM360692			GO:0003824	nr -
Unigene2240_All	1949	8.35	22.23	6.61	17.43	16.80	33.07	24.88	48.25	57.77	1.41E+00	4.30E-54	Up	-3.37E-01	2.24E-02		-5.30E-02	6.37E-01		9.24E-01	6.26E-44		9.55E-01	5.30E-77		1.22E+00	1.26E-138	Up	Unigene2240_All//gi|4138265|emb|CAA06925.1|//0.00E+00//Avr9 elicitor response protein [Nicotiana tabacum]	Unigene2240_All//4.00E-178//AT1G77810| galactosyltransferase family protein	Unigene2240_All//0.00E+00//TC176993			GO:0006464//GO:0031224//GO:0035250//GO:0043231	nr +
Unigene22405_All	2206	1.40	3.81	2.00	15.42	15.70	12.96	23.34	18.23	23.68	1.45E+00	1.89E-11	Up	5.18E-01	8.81E-02		2.60E-02	8.25E-01		-2.51E-01	7.53E-03		-3.57E-01	5.22E-08		2.03E-02	7.90E-01		Unigene22405_All//gi|240256093|ref|NP_194529.4|//0.00E+00//ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene22405_All//0.00E+00//AT4G28000| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene22405_All//0.00E+00//ES846800				nr -
Unigene22407_All	2678	0.78	3.01	1.63	10.62	8.95	8.52	12.14	10.05	9.02	1.94E+00	2.56E-16	Up	1.06E+00	5.15E-04	Up	-2.47E-01	1.39E-02		-3.19E-01	1.66E-03		-2.73E-01	1.50E-03		-4.30E-01	1.80E-07		Unigene22407_All//gi|297796103|ref|XP_002865936.1|//0.00E+00//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297311771|gb|EFH42195.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene22407_All//0.00E+00//AT4G28000| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene22407_All//0.00E+00//TC145862				nr -
Unigene22411_All	3213	1.73	1.03	0.53	9.09	6.57	8.24	8.92	10.88	4.59	-7.52E-01	2.90E-03		-1.70E+00	2.92E-09	Down	-4.68E-01	3.42E-07		-1.41E-01	2.20E-01		2.86E-01	5.04E-04		-9.60E-01	5.84E-25		Unigene22411_All//gi|79336607|ref|NP_172105.3|//1.00E-156//transcription factor [Arabidopsis thaliana] >gi|193806610|sp|P0C7P8.1|Y1615_ARATH RecName: Full=Uncharacterized basic helix-loop-helix protein At1g06150	Unigene22411_All//5.00E-154//AT1G06150| transcription factor	Unigene22411_All//0.00E+00//TC177863				nr +

Unigene22414_All	837	3.13	5.27	3.12	13.09	9.30	11.71	14.30	7.09	8.14	7.53E-01	9.11E-03		-3.70E-03	9.92E-01		-4.94E-01	2.30E-03		-1.61E-01	4.22E-01		-1.01E+00	1.75E-11	Down	-8.13E-01	1.77E-08		Unigene22414_All//gi|224110590|ref|XP_002315568.1|//1.00E-130//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222864608|gb|EEF01739.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene22414_All//1.00E-129//AT3G06400| CHR11 (CHROMATIN-REMODELING PROTEIN 11); ATP binding / DNA binding / DNA-dependent ATPase/ helicase/ hydrolase, acting on acid anhydrides, in phosphorus-containing anhydrides / nucleic acid binding / nucleosome binding	Unigene22414_All//0.00E+00//ES850311				nr -
Unigene22418_All	1472	8.28	2.82	2.24	19.09	14.90	11.90	29.90	12.32	11.77	-1.55E+00	4.36E-18	Down	-1.88E+00	1.50E-22	Down	-3.57E-01	1.94E-04		-6.81E-01	7.37E-12		-1.28E+00	5.34E-58	Down	-1.34E+00	1.89E-64	Down	Unigene22418_All//gi|168035589|ref|XP_001770292.1|//1.00E-158//SNF2 family DNA-dependent ATPase [Physcomitrella patens subsp. patens] >gi|162678509|gb|EDQ64967.1| SNF2 family DNA-dependent ATPase [Physcomitrella patens subsp. patens]	Unigene22418_All//1.00E-145//AT5G18620| CHR17 (CHROMATIN REMODELING FACTOR17); ATP binding / DNA binding / DNA-dependent ATPase/ helicase/ hydrolase, acting on acid anhydrides, in phosphorus-containing anhydrides / nucleic acid binding / nucleosome binding	Unigene22418_All//0.00E+00//TC158674				nr +
Unigene22422_All	4351	5.18	2.35	1.63	12.69	10.28	7.45	24.35	7.59	9.76	-1.14E+00	1.11E-20	Down	-1.67E+00	4.69E-35	Down	-3.03E-01	4.02E-06		-7.67E-01	7.10E-28		-1.68E+00	1.94E-208	Down	-1.32E+00	1.65E-149	Down	Unigene22422_All//gi|224128722|ref|XP_002328950.1|//0.00E+00//glycosyltransferase, CAZy family GT2 [Populus trichocarpa] >gi|222839184|gb|EEE77535.1| glycosyltransferase, CAZy family GT2 [Populus trichocarpa]	Unigene22422_All//0.00E+00//AT3G03050| CSLD3 (CELLULOSE SYNTHASE-LIKE D3); cellulose synthase/ transferase, transferring glycosyl groups	Unigene22422_All//0.00E+00//TC140260		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene22423_All	3976	3.50	7.95	1.98	4.00	4.11	4.62	14.29	22.22	17.02	1.18E+00	2.55E-30	Up	-8.20E-01	1.62E-07		3.86E-02	8.23E-01		2.10E-01	1.36E-01		6.37E-01	2.45E-36		2.52E-01	6.55E-06		Unigene22423_All//gi|224128722|ref|XP_002328950.1|//0.00E+00//glycosyltransferase, CAZy family GT2 [Populus trichocarpa] >gi|222839184|gb|EEE77535.1| glycosyltransferase, CAZy family GT2 [Populus trichocarpa]	Unigene22423_All//0.00E+00//AT3G03050| CSLD3 (CELLULOSE SYNTHASE-LIKE D3); cellulose synthase/ transferase, transferring glycosyl groups	Unigene22423_All//0.00E+00//TC143295		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene22427_All	3561	0.65	1.08	0.82	1.48	1.49	1.43	2.20	2.52	5.43	7.42E-01	1.73E-02		3.47E-01	3.91E-01		6.20E-03	9.89E-01		-4.91E-02	8.74E-01		2.00E-01	3.00E-01		1.30E+00	2.84E-27	Up	Unigene22427_All//gi|22655793|gb|AAN04210.1|//0.00E+00//Putative ubiquitin carboxyl terminal hydrolase [Oryza sativa Japonica Group]	Unigene22427_All//0.00E+00//AT2G40930| UBP5 (UBIQUITIN-SPECIFIC PROTEASE 5); ubiquitin-specific protease	Unigene22427_All//0.00E+00//TC166611				nr +
Unigene22429_All	816	2.63	7.08	9.53	5.62	13.97	15.28	9.69	27.61	50.24	1.43E+00	5.67E-08	Up	1.86E+00	2.35E-14	Up	1.31E+00	3.18E-15	Up	1.44E+00	1.40E-17	Up	1.51E+00	2.00E-38	Up	2.37E+00	3.64E-129	Up	Unigene22429_All//gi|283132359|dbj|BAI63585.1|//2.00E-76//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene22429_All//9.00E-74//AT4G38470| protein kinase family protein	Unigene22429_All//0.00E+00//TC130901				nr -
Unigene2243_All	2965	1.54	0.97	0.66	5.06	6.10	3.75	6.16	1.31	2.47	-6.56E-01	2.01E-02		-1.21E+00	6.46E-05	Down	2.70E-01	4.17E-02		-4.33E-01	2.52E-03		-2.23E+00	6.42E-53	Down	-1.32E+00	1.96E-26	Down	Unigene2243_All//gi|115444855|ref|NP_001046207.1|//0.00E+00//Os02g0198400 [Oryza sativa Japonica Group] >gi|113535738|dbj|BAF08121.1| Os02g0198400 [Oryza sativa Japonica Group]	Unigene2243_All//0.00E+00//AT5G48310| unknown protein			G0:0009987	nr +
Unigene22430_All	1195	10.64	13.44	16.98	11.01	36.08	24.91	21.41	35.71	72.48	3.37E-01	1.73E-02		6.74E-01	8.88E-08		1.71E+00	1.45E-83	Up	1.18E+00	2.48E-30	Up	7.38E-01	4.44E-23		1.76E+00	7.71E-185	Up	Unigene22430_All//gi|283132359|dbj|BAI63585.1|//1.00E-120//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene22430_All//1.00E-104//AT4G38470| protein kinase family protein	Unigene22430_All//0.00E+00//gi|164320010|gb|ES845270.1|ES845270				nr -
Unigene22431_All	2093	1.00	5.79	1.55	3.07	6.37	8.14	5.78	27.10	61.73	2.53E+00	2.90E-33	Up	6.34E-01	7.85E-02		1.05E+00	1.23E-12	Up	1.41E+00	6.45E-23	Up	2.23E+00	2.58E-162	Up	3.42E+00	0.00E+00	Up	Unigene22431_All//gi|283132359|dbj|BAI63585.1|//0.00E+00//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene22431_All//0.00E+00//AT4G38470| protein kinase family protein	Unigene22431_All//0.00E+00//TC130901				nr +
Unigene22433_All	752	1.60	1.08	5.59	8.28	11.54	10.69	6.86	2.72	11.65	-5.70E-01	3.65E-01		1.81E+00	9.31E-08	Up	4.79E-01	1.25E-02		3.69E-01	8.54E-02		-1.33E+00	6.18E-08	Down	7.65E-01	7.30E-06		Unigene22433_All//gi|22330351|ref|NP_176286.2|//7.00E-22//phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] >gi|75158988|sp|Q8RY89.1|PI5K8_ARATH RecName: Full=Phosphatidylinositol-4-phosphate 5-kinase 8; Short=AtPIP5K8; AltName: Full=1-phosphatidylinositol-4-phosphate kinase 8; AltName: Full=PtdIns(4)P-5-kinase 8; AltName: Full=Diphosphoinositide kinase 8	Unigene22433_All//4.00E-23//AT1G60890| phosphatidylinositol-4-phosphate 5-kinase family protein	Unigene22433_All//6.00E-42//ES793975				nr -
Unigene22434_All	2896	2.78	3.95	5.79	19.01	21.59	13.96	23.72	12.07	25.78	5.07E-01	2.56E-03		1.06E+00	2.54E-13	Up	1.84E-01	5.29E-03		-4.46E-01	7.77E-11		-9.76E-01	1.68E-58		1.20E-01	3.37E-02		Unigene22434_All//gi|22330351|ref|NP_176286.2|//0.00E+00//phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] >gi|75158988|sp|Q8RY89.1|PI5K8_ARATH RecName: Full=Phosphatidylinositol-4-phosphate 5-kinase 8; Short=AtPIP5K8; AltName: Full=1-phosphatidylinositol-4-phosphate kinase 8; AltName: Full=PtdIns(4)P-5-kinase 8; AltName: Full=Diphosphoinositide kinase 8	Unigene22434_All//0.00E+00//AT1G60890| phosphatidylinositol-4-phosphate 5-kinase family protein	Unigene22434_All//0.00E+00//ES840099		ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene22439_All	2617	8.76	12.80	9.46	28.40	22.38	26.46	42.93	19.31	16.75	5.48E-01	3.78E-09		1.12E-01	3.86E-01		-3.44E-01	4.80E-10		-1.02E-01	1.36E-01		-1.15E+00	9.34E-125	Down	-1.36E+00	9.51E-166	Down	Unigene22439_All//gi|54606850|gb|AAV34773.1|//1.00E-145//At1g73390 [Arabidopsis thaliana]	Unigene22439_All//6.00E-130//AT1G73390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: B801 (InterPro:IPR004328); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17940.1); Has 95 Blast hits to 95 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 19; Fungi - 23; Plants - 53; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene22439_All//0.00E+00//TC151263				nr +
Unigene22444_All	2286	15.27	2.93	5.73	47.48	31.18	34.02	53.51	22.84	37.50	-2.38E+00	4.19E-89	Down	-1.41E+00	2.27E-42	Down	-6.07E-01	1.20E-40		-4.81E-01	7.75E-24		-1.23E+00	3.51E-150	Down	-5.13E-01	4.48E-35		Unigene22444_All//gi|30690755|ref|NP_174240.2|//0.00E+00//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|79318852|ref|NP_001031109.1| dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75223284|sp|Q6NF87.1|PMT0_ARATH RecName: Full=Probable methyltransferase PMT24 >gi|38564284|gb|AAR23721.1| At1g29470 [Arabidopsis thaliana]	Unigene22444_All//0.00E+00//AT1G29470| dehydration-responsive protein-related	Unigene22444_All//0.00E+00//TC172357				nr -
Unigene22445_All	2989	6.70	5.76	6.93	15.28	12.96	13.07	13.88	8.38	5.78	-2.18E-01	9.31E-02		4.78E-02	7.24E-01		-2.38E-01	1.71E-03		-2.26E-01	4.82E-03		-7.28E-01	5.72E-22		-1.26E+00	3.45E-55	Down	Unigene22445_All//gi|30690755|ref|NP_174240.2|//0.00E+00//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|79318852|ref|NP_001031109.1| dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75223284|sp|Q6NF87.1|PMT0_ARATH RecName: Full=Probable methyltransferase PMT24 >gi|38564284|gb|AAR23721.1| At1g29470 [Arabidopsis thaliana]	Unigene22445_All//0.00E+00//AT1G29470| dehydration-responsive protein-related	Unigene22445_All//0.00E+00//TC137646				nr +
Unigene22446_All	1983	6.17	2.68	3.92	8.19	8.37	8.02	3.58	3.16	3.03	-1.20E+00	1.53E-12	Down	-6.55E-01	9.00E-05		3.15E-02	8.51E-01		-3.07E-02	8.63E-01		-1.80E-01	4.12E-01		-2.40E-01	2.40E-01		Unigene22446_All//gi|297794385|ref|XP_002865077.1|//0.00E+00//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310912|gb|EFH41336.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22446_All//0.00E+00//AT5G66310| kinesin motor family protein	Unigene22446_All//0.00E+00//CO132658				nr -
Unigene22447_All	3388	3.01	2.98	2.47	10.47	10.97	9.02	5.05	0.90	2.86	-1.70E-02	9.46E-01		-2.87E-01	1.42E-01		6.71E-02	5.43E-01		-2.14E-01	2.27E-02		-2.49E+00	1.80E-56	Down	-8.23E-01	5.59E-12		Unigene22447_All//gi|297794385|ref|XP_002865077.1|//0.00E+00//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310912|gb|EFH41336.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22447_All//0.00E+00//AT5G66310| kinesin motor family protein	Unigene22447_All//0.00E+00//TC146089				nr +
Unigene22448_All	3098	0.41	0.41	0.38	0.61	0.78	0.61	0.78	0.13	0.36	1.28E-02	9.80E-01		-1.00E-01	8.66E-01		3.49E-01	4.48E-01		3.10E-03	9.99E-01		-2.53E+00	1.13E-08	Down	-1.11E+00	1.88E-03		Unigene22448_All//gi|297794385|ref|XP_002865077.1|//0.00E+00//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310912|gb|EFH41336.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22448_All//0.00E+00//AT5G66310| kinesin motor family protein	Unigene22448_All//0.00E+00//TC146089				nr +
Unigene22449_All	3537	16.92	7.26	11.73	16.75	19.66	15.42	8.70	7.03	5.32	-1.22E+00	8.05E-60	Down	-5.29E-01	3.13E-14		2.31E-01	1.10E-04		-1.19E-01	1.25E-01		-3.08E-01	4.52E-04		-7.11E-01	2.36E-16		Unigene22449_All//gi|297794385|ref|XP_002865077.1|//0.00E+00//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310912|gb|EFH41336.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22449_All//0.00E+00//AT5G66310| kinesin motor family protein	Unigene22449_All//0.00E+00//TC177682				nr -
Unigene22455_All	2346	12.96	55.10	5.47	46.67	91.48	29.15	42.93	32.92	102.91	2.09E+00	4.98E-277	Up	-1.24E+00	1.87E-30	Down	9.71E-01	5.31E-175		-6.79E-01	2.48E-44		-3.83E-01	8.02E-17		1.26E+00	0.00E+00	Up	Unigene22455_All//gi|171452362|dbj|BAG15872.1|//0.00E+00//transcription factor [Bruguiera gymnorhiza]	Unigene22455_All//3.00E-164//AT2G40140| CZF1; transcription factor	Unigene22455_All//0.00E+00//TC137552	C3H			nr +
Unigene22456_All	1887	27.37	83.03	21.84	34.66	72.72	33.27	33.39	50.23	77.95	1.60E+00	1.82E-233	Up	-3.25E-01	1.90E-05		1.07E+00	6.62E-131	Up	-5.92E-02	4.80E-01		5.90E-01	5.16E-34		1.22E+00	8.37E-183	Up	Unigene22456_All//gi|171452362|dbj|BAG15872.1|//0.00E+00//transcription factor [Bruguiera gymnorhiza]	Unigene22456_All//2.00E-139//AT2G40140| CZF1; transcription factor	Unigene22456_All//0.00E+00//TC148465	C3H			nr +

Unigene22457_All	1398	1.80	3.08	1.52	3.49	4.04	3.65	9.01	6.49	2.68	7.78E-01	7.79E-03		-2.38E-01	5.95E-01		2.10E-01	4.69E-01		6.40E-02	8.36E-01		-4.74E-01	8.40E-04		-1.75E+00	1.06E-27	Down	Unigene22457_All//gi|297607888|ref|NP_001060844.2|//4.00E-11//Os08g0113800 [Oryza sativa Japonica Group] >gi|255678106|dbj|BAF22758.2|Os08g0113800 [Oryza sativa Japonica Group]	Unigene22457_All//7.00E-57//AT2G23093| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G49310.1); Has 251 Blast hits to 248 proteins in 89 species: Archae - 0; Bacteria - 66; Metazoa - 68; Fungi - 18; Plants - 79; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink).	Unigene22457_All//0.00E+00//TC175935				nr -
Unigene22460_All	2630	18.26	9.40	16.44	24.93	19.54	16.91	18.63	6.29	6.74	-9.58E-01	1.07E-32		-1.52E-01	7.91E-02		-3.52E-01	2.68E-09		-5.59E-01	4.48E-19		-1.57E+00	2.59E-87	Down	-1.47E+00	1.17E-81	Down	Unigene22460_All//gi|223452450|gb|ACM89552.1|//0.00E+00//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene22460_All//0.00E+00//AT2G35620| FEI2 (FEI 2); kinase	Unigene22460_All//0.00E+00//TC175305				nr +
Unigene22461_All	2743	33.55	19.97	24.31	50.45	49.26	47.81	27.64	15.27	13.75	-7.49E-01	5.86E-41		-4.65E-01	3.67E-17		-3.44E-02	5.39E-01		-7.74E-02	1.22E-01		-8.56E-01	6.58E-52		-1.01E+00	8.44E-70	Down	Unigene22461_All//gi|223452450|gb|ACM89552.1|//0.00E+00//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene22461_All//0.00E+00//AT1G31420| FEI1 (FEI 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene22461_All//0.00E+00//TC159590				nr -
Unigene22463_All	776	7.28	4.90	10.98	4.04	6.43	3.32	2.18	3.61	5.03	-5.72E-01	2.22E-02		5.92E-01	3.99E-03		6.70E-01	1.03E-02		-2.86E-01	4.68E-01		7.28E-01	3.04E-02		1.21E+00	1.37E-05	Up	Unigene22463_All//gi|115465219|ref|NP_001056209.1|//5.00E-16//Os05g0545000 [Oryza sativa Japonica Group] >gi|113579760|dbj|BAF18123.1|Os05g0545000 [Oryza sativa Japonica Group]	Unigene22463_All//3.00E-11//AT1G19650| SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative	Unigene22463_All//5.00E-172//TC157145				nr -
Unigene22464_All	2417	5.04	2.18	5.57	7.50	6.87	6.61	4.11	2.75	4.07	-1.21E+00	1.31E-12	Down	1.44E-01	4.01E-01		-1.28E-01	4.03E-01		-1.82E-01	2.17E-01		-5.80E-01	3.28E-04		-1.40E-02	9.57E-01		Unigene22464_All//gi|14486705|gb|AK63247.1|AF367433_1|//0.00E+00//phosphatidylinositol transfer-like protein III [Lotus japonicus]	Unigene22464_All//0.00E+00//AT2G21520| transporter	Unigene22464_All//0.00E+00//CO499841				nr +
Unigene22465_All	2371	22.07	16.41	25.76	9.62	15.53	12.67	6.06	10.47	13.37	-4.27E-01	4.27E-09		2.23E-01	1.73E-03		6.90E-01	4.90E-17		3.97E-01	4.00E-05		7.88E-01	2.50E-15		1.14E+00	5.45E-36	Up	Unigene22465_All//gi|115439423|ref|NP_001043991.1|//1.00E-163//Os01g0701900 [Oryza sativa Japonica Group] >gi|113533522|dbj|BAF05905.1|Os01g0701900 [Oryza sativa Japonica Group]	Unigene22465_All//2.00E-108//AT2G21520| transporter	Unigene22465_All//0.00E+00//TC157145				nr -
Unigene22467_All	1680	3.36	3.71	3.07	3.77	4.26	3.01	3.70	2.11	1.30	1.41E-01	6.00E-01		-1.30E-01	6.19E-01		1.79E-01	4.93E-01		-3.23E-01	2.02E-01		-8.07E-01	1.33E-04		-1.50E+00	1.67E-11	Down	Unigene22467_All//gi|15010784|gb|AK74051.1|//1.00E-174//AT4g38500/F20M13_60 [Arabidopsis thaliana] >gi|28660679|gb|AAO43564.1|At4g38500/F20M13_60 [Arabidopsis thaliana]	Unigene22467_All//0.00E+00//AT4G38500| unknown protein	Unigene22467_All//0.00E+00//TC176745				nr +
Unigene22468_All	3743	14.64	16.34	15.69	9.38	9.32	7.28	10.55	5.95	4.31	1.59E-01	2.47E-02		1.01E-01	2.17E-01		-9.70E-03	9.37E-01		-3.67E-01	3.36E-05		-8.26E-01	7.57E-26		-1.29E+00	1.89E-54	Down	Unigene22468_All//gi|15010784|gb|AK74051.1|//0.00E+00//AT4g38500/F20M13_60 [Arabidopsis thaliana] >gi|28660679|gb|AAO43564.1|At4g38500/F20M13_60 [Arabidopsis thaliana]	Unigene22468_All//0.00E+00//AT4G38500| unknown protein	Unigene22468_All//0.00E+00//TC176745		ko00906|Carotenoid biosynthesis		nr -
Unigene2247_All	2961	13.59	34.22	17.86	18.84	12.34	9.20	6.50	1.99	9.61	1.33E+00	4.61E-115	Up	3.94E-01	1.18E-07		-6.11E-01	2.61E-21		-1.03E+00	2.10E-46	Down	-1.71E+00	3.31E-39	Down	5.64E-01	2.53E-10		Unigene2247_All//gi|255560673|ref|XP_002521350.1|//0.00E+00//Phosphatidylcholine: Diacylglycerol Acyltransferase [Ricinus communis] >gi|223539428|gb|EEF41018.1|Phosphatidylcholine: Diacylglycerol Acyltransferase [Ricinus communis]	Unigene2247_All//0.00E+00//AT5G13640| ATPDAT; phosphatidylcholine-sterol O-acyltransferase	Unigene2247_All//0.00E+00//TC164250		ko00561|Glycerolipid metabolism	GO:0008080//GO:0008374//GO:0044238	nr -
Unigene22470_All	634	0.00	0.32	0.00	0.16	0.00	0.07	2.87	2.51	0.31	8.32E+00	1.37E-01		null	null		-7.30E+00	3.13E-01		-1.14E+00	6.77E-01		-1.95E-01	6.57E-01		-3.19E+00	1.20E-08	Down	Unigene22470_All//gi|297719563|ref|NP_001172143.1|//1.00E-23//Os01g0116166 [Oryza sativa Japonica Group] >gi|255672802|dbj|BAH90873.1|Os01g0116166 [Oryza sativa Japonica Group]		Unigene22470_All//4.00E-76//FL576972				nr -
Unigene22471_All	1158	1.94	0.61	1.10	0.60	0.48	0.23	5.26	1.34	2.20	-1.67E+00	2.65E-04	Down	-8.16E-01	6.87E-02		-3.40E-01	6.80E-01		-1.36E+00	1.31E-01		-1.98E+00	1.27E-15	Down	-1.26E+00	8.68E-09	Down	Unigene22471_All//gi|42568214|ref|NP_198840.2|//2.00E-36//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|10177511|dbj|BAB10905.1|nodulin-like protein [Arabidopsis thaliana] >gi|30725298|gb|AAP37671.1|At5g40240 [Arabidopsis thaliana]	Unigene22471_All//9.00E-31//AT5G40240| nodulin MtN21 family protein	Unigene22471_All//0.00E+00//TC135150				nr +
Unigene22479_All	2964	9.00	4.58	7.02	12.08	10.03	7.98	9.02	5.51	4.10	-9.75E-01	5.11E-19		-3.58E-01	1.14E-03		-2.69E-01	1.76E-03		-5.98E-01	5.57E-12		-7.09E-01	7.80E-14		-1.14E+00	1.63E-30	Down	Unigene22479_All//gi|15230685|ref|NP_187914.1|//0.00E+00//CBS domain-containing protein / transporter associated domain-containing protein [Arabidopsis thaliana]	Unigene22479_All//3.00E-178//AT3G13070| CBS domain-containing protein / transporter associated domain-containing protein	Unigene22479_All//0.00E+00//TC146946				nr -
Unigene22481_All	3495	2.22	1.99	0.84	3.02	4.13	2.44	7.06	2.03	2.46	-1.58E-01	4.88E-01		-1.40E+00	1.00E-09	Down	4.50E-01	1.43E-03		-3.07E-01	9.80E-02		-1.80E+00	8.53E-54	Down	-1.52E+00	8.04E-44	Down	Unigene22481_All//gi|15208453|gb|AK91815.1|AF272752_1|//0.00E+00//kinesin heavy chain [Zea mays]	Unigene22481_All//0.00E+00//AT3G45850| kinesin motor protein-related	Unigene22481_All//0.00E+00//ES798429				nr +
Unigene22482_All	3391	1.60	1.24	0.42	3.58	3.30	2.70	5.02	1.13	2.01	-3.72E-01	1.54E-01		-1.92E+00	1.30E-10	Down	-1.19E-01	5.57E-01		-4.07E-01	1.28E-02		-2.15E+00	4.11E-47	Down	-1.32E+00	7.15E-25	Down	Unigene22482_All//gi|11132775|sp|O23826.1|K125_TOBAC//0.00E+00//RecName: Full=125 kDa kinesin-related protein >gi|2582971|dbj|BAA23159.1|TKRP125 [Nicotiana tabacum]	Unigene22482_All//0.00E+00//AT2G36200| kinesin motor protein-related	Unigene22482_All//0.00E+00//DV849928				nr -
Unigene22483_All	3667	3.57	1.60	0.91	5.91	6.15	4.57	13.11	2.42	5.21	-1.15E+00	1.49E-12	Down	-1.96E+00	1.73E-25	Down	5.78E-02	7.02E-01		-3.71E-01	1.52E-03		-2.44E+00	7.42E-154	Down	-1.33E+00	3.82E-69	Down	Unigene22483_All//gi|11132775|sp|O23826.1|K125_TOBAC//0.00E+00//RecName: Full=125 kDa kinesin-related protein >gi|2582971|dbj|BAA23159.1|TKRP125 [Nicotiana tabacum]	Unigene22483_All//0.00E+00//AT2G36200| kinesin motor protein-related	Unigene22483_All//0.00E+00//ES798429				nr -
Unigene22493_All	1167	5.07	2.17	2.69	11.18	12.39	13.24	13.41	11.46	12.90	-1.22E+00	1.29E-06	Down	-9.12E-01	3.45E-04		1.48E-01	3.94E-01		2.43E-01	1.15E-01		-2.26E-01	9.35E-02		-5.50E-02	6.91E-01		Unigene22493_All//gi|3435196|gb|AAC36469.1|//5.00E-89//glutamyl-tRNA synthetase [Arabidopsis thaliana] >gi|20466052|gb|AAM20443.1|glutamyl-tRNA synthetase [Arabidopsis thaliana] >gi|23198080|gb|AAN15567.1|glutamyl-tRNA synthetase [Arabidopsis thaliana] >gi|110740992|dbj|BAE98590.1|glutamyl-tRNA synthetase [Arabidopsis thaliana]	Unigene22493_All//7.00E-81//AT5G26710| glutamate-tRNA ligase, putative / glutamyl-tRNA synthetase, putatuve / GluRS, putative	Unigene22493_All//0.00E+00//ES808752		ko00970|Aminoacyl-tRNA biosynthesis//ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene22494_All	1396	4.65	3.30	2.44	8.31	6.98	9.32	23.93	19.64	11.76	-4.93E-01	3.44E-02		-9.29E-01	1.24E-04		-2.52E-01	1.51E-01		1.64E-01	3.79E-01		-2.85E-01	7.20E-04		-1.03E+00	3.58E-32	Down	Unigene22494_All//gi|115481716|ref|NP_001064451.1|//0.00E+00//Os10g0369000 [Oryza sativa Japonica Group] >gi|20043025|gb|AAM08833.1|AC113335_13 Putative glutamyl-tRNA synthetase [Oryza sativa Japonica Group] >gi|31431616|gb|AAP53367.1|glutamyl-tRNA synthetase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639060|dbj|BAF26365.1|Os10g0369000 [Oryza sativa Japonica Group]	Unigene22494_All//0.00E+00//AT5G26710| glutamate-tRNA ligase, putative / glutamyl-tRNA synthetase, putatuve / GluRS, putative	Unigene22494_All//0.00E+00//TC156181		ko00970|Aminoacyl-tRNA biosynthesis//ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene22496_All	2856	1.08	1.08	0.19	3.02	3.11	3.27	6.00	3.59	3.31	1.70E-03	9.97E-01		-2.54E+00	1.45E-08	Down	4.39E-02	8.50E-01		1.17E-01	6.32E-01		-7.42E-01	7.73E-10		-8.59E-01	8.05E-13		Unigene22496_All//gi|226530698|ref|NP_001147450.1|//0.00E+00//glutamyl-tRNA synthetase, cytoplasmic [Zea mays] >gi|195611488|gb|ACG27574.1|glutamyl-tRNA synthetase, cytoplasmic [Zea mays]	Unigene22496_All//0.00E+00//AT5G26710| glutamate-tRNA ligase, putative / glutamyl-tRNA synthetase, putatuve / GluRS, putative	Unigene22496_All//0.00E+00//TC156181		ko00970|Aminoacyl-tRNA biosynthesis//ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene22497_All	596	0.70	1.36	1.07	1.34	0.12	0.61	2.91	2.59	3.68	9.54E-01	2.26E-01		6.10E-01	5.09E-01		-3.53E+00	3.03E-04	Down	-1.14E+00	1.63E-01		-1.65E-01	7.27E-01		3.38E-01	3.88E-01		Unigene22497_All//gi|115478156|ref|NP_001062673.1|//4.00E-65//Os09g0249600 [Oryza sativa Japonica Group] >gi|113630906|dbj|BAF24587.1|Os09g0249600 [Oryza sativa Japonica Group]	Unigene22497_All//5.00E-57//AT1G28060| small nuclear ribonucleoprotein family protein / snRNP family protein	Unigene22497_All//6.00E-137//gi|48817622|gb|CO118935.1|CO118935		ko03040|Spliceosome		nr +
Unigene2250_All	2947	0.66	0.62	1.10	2.37	1.40	1.64	6.46	7.13	2.84	-8.57E-02	8.47E-01		7.47E-01	3.82E-02		-7.55E-01	2.40E-04		-5.29E-01	1.72E-02		1.44E-01	2.35E-01		-1.19E+00	1.93E-23	Down	Unigene2250_All//gi|297596537|ref|NP_001042723.2|//0.00E+00//Os01g0275900 [Oryza sativa Japonica Group] >gi|255673109|dbj|BAF04637.2|Os01g0275900 [Oryza sativa Japonica Group]		Unigene2250_All//0.00E+00//TC131083				nr +
Unigene22500_All	1064	1.18	1.81	0.90	1.83	3.79	3.18	7.19	12.53	20.26	6.17E-01	1.90E-01		-3.90E-01	5.38E-01		1.05E+00	3.50E-04	Up	8.02E-01	1.76E-02		8.01E-01	7.90E-09		1.49E+00	5.21E-37	Up	Unigene22500_All//gi|10120421|gb|AAG13046.1|AC011807_5|//3.00E-08//Putative RNA binding protein [Arabidopsis thaliana]	Unigene22500_All//0.00E+00//AT3G19130| ATRBP47B (RNA-binding protein 47B); RNA binding	Unigene22500_All//0.00E+00//gi|164241127|gb|ES851840.1|ES851840				nr +
Unigene22501_All	658	0.56	0.31	0.00	2.20	1.31	2.75	2.83	4.64	5.87	-8.54E-01	4.89E-01		-9.12E+00	2.78E-02		-7.47E-01	1.63E-01		3.23E-01	5.57E-01		7.14E-01	2.52E-02		1.05E+00	1.23E-04	Up	Unigene22501_All//gi|110681486|emb|CAL25353.1|//4.00E-29//ACBF-like dna binding protein [Platanus x acerifolia]	Unigene22501_All//2.00E-24//AT1G49600| ATRBP42A (Arabidopsis thaliana RNA-binding protein 47a); RNA binding	Unigene22501_All//0.00E+00//ES813259				nr +
Unigene22503_All	1689	21.84	13.62	10.88	54.65	53.82	64.82	33.19	20.66	28.78	-6.81E-01	2.03E-14		-1.01E+00	2.62E-26	Down	-2.20E-02	7.85E-01		2.46E-01	2.98E-07		-6.84E-01	2.06E-26		-2.06E-01	1.03E-03		Unigene22503_All//gi|15230291|ref|NP_188544.1|//1.00E-155//ATRBP47B (RNA-binding protein 47B); RNA binding [Arabidopsis thaliana] >gi|11107446|gb|AR004596.1|At3g19130 [Arabidopsis thaliana]	Unigene22503_All//2.00E-126//AT3G19130| ATRBP47B (RNA-binding protein 47B); RNA binding	Unigene22503_All//0.00E+00//TC136197		ko03040|Spliceosome		nr -

Unigene22504_All	544	3.46	6.52	5.87	8.97	6.08	9.55	8.78	11.52	18.97	9.13E-01	5.51E-03		7.62E-01	3.61E-02		-5.62E-01	3.15E-02		8.94E-02	7.57E-01		3.92E-01	7.17E-02		1.11E+00	8.13E-12	Up	Unigene22504_All//gi|6664305|gb|AAF22887.1|AC006932_4//8.00E-63//T2767.7 [Arabidopsis thaliana]	Unigene22504_All//2.00E-63//AT1G08370| DCP1 (decapping 1); ap7G(5')pppN diphosphatase/ protein homodimerization	Unigene22504_All//0.00E+00//gi|78341015|gb|BT561289.1|BT561289				nr +
Unigene22507_All	1242	17.27	5.71	13.63	20.13	16.86	18.98	33.40	55.90	62.61	-1.60E+00	1.54E-32	Down	-3.41E-01	6.41E-03		-2.56E-01	1.78E-02		-8.50E-02	5.34E-01		7.43E-01	1.94E-37		9.07E-01	7.14E-60		Unigene22507_All//gi|15236300|ref|NP_193087.1|//0.00E+00//AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter [Arabidopsis thaliana] >gi|1703292|sp|P54144.1|AMT11_ARATH RecName: Full=Ammonium transporter 1 member 1; Short=AtAMT1;1 >gi|551219|emb|CAA53473.1| amt1 [Arabidopsis thaliana] >gi|4678377|emb|CAB41109.1| ammonium transport protein (AMT1) [Arabidopsis thaliana] >gi|7268054|emb|CAB78393.1| ammonium transport protein (AMT1) [Arabidopsis thaliana]	Unigene22507_All//3.00E-152//AT4G13510| AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter	Unigene22507_All//0.00E+00//gi|78336379|gb|BT556653.1|BT556653				nr -
Unigene22508_All	1767	15.31	5.62	12.57	5.72	8.34	5.78	75.47	156.99	63.35	-1.45E+00	2.23E-35	Down	-2.85E-01	1.05E-02		5.44E-01	7.55E-05		1.34E-02	9.57E-01		1.06E+00	1.28E-266	Up	-2.52E-01	8.62E-11		Unigene22508_All//gi|38684027|gb|AB278052.1|//0.00E+00//ammonium transporter [Triticum aestivum]	Unigene22508_All//2.00E-105//AT4G13510| AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter	Unigene22508_All//0.00E+00//DW496501				nr -
Unigene2251_All	3413	4.32	1.90	1.12	9.15	10.11	7.09	6.32	1.27	2.89	-1.19E+00	1.19E-14	Down	-1.94E+00	2.43E-28	Down	1.44E-01	1.57E-01		-3.68E-01	1.02E-04		-2.31E+00	5.17E-65	Down	-1.13E+00	1.98E-24	Down	Unigene2251_All//gi|15221443|ref|NP_174345.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|75336895|sp|Q9SA72.1|Y1357_ARATH RecName: Full=Probable receptor-like protein kinase At1g30570; Flags: Precursor >gi|4587513|gb|AAD25744.1|AC007060_2 Contains eukaryotic protein kinase domain PF|00069 [Arabidopsis thaliana]	Unigene2251_All//0.00E+00//AT1G30570| protein kinase family protein	Unigene2251_All//0.00E+00//gi|164350233|gb|ES805185.1|ES805185		ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0031410//GO:0032559	nr +
Unigene22510_All	674	4.04	2.33	1.90	9.09	8.23	13.54	12.67	3.84	5.50	-7.93E-01	3.72E-02		-1.09E+00	6.96E-03		-1.44E-01	5.98E-01		5.74E-01	2.37E-03		-1.72E+00	5.02E-18	Down	-1.20E+00	2.82E-11	Down	Unigene22510_All//gi|115463121|ref|NP_001055160.1|//7.00E-82//Os05g0311000 [Oryza sativa Japonica Group] >gi|122169274|sp|Q0DJ99.1|COPD2_ORYSJ RecName: Full=Coatomer subunit delta-2; AltName: Full=Delta-coat protein 2; Short=Delta-COP 2 >gi|113578711|dbj|BAF17074.1|Os05g0311000 [Oryza sativa Japonica Group]	Unigene22510_All//9.00E-82//AT5G05010| clathrin adaptor complexes medium subunit-related	Unigene22510_All//0.00E+00//gi|164321297|gb|ES829783.1|ES829783				nr +
Unigene22511_All	579	24.40	19.17	18.95	34.50	32.35	32.37	74.70	35.66	32.75	-3.48E-01	2.19E-02		-3.65E-01	2.15E-02		-9.27E-02	5.57E-01		-9.19E-02	5.53E-01		-1.07E+00	6.77E-43	Down	-1.19E+00	1.91E-52	Down	Unigene22511_All//gi|15451156|gb|AK96849.1|//3.00E-67//coatomer delta subunit (delta-coat protein) (delta-COP) [Arabidopsis thaliana]	Unigene22511_All//3.00E-68//AT5G05010| clathrin adaptor complexes medium subunit-related	Unigene22511_All//0.00E+00//gi|21097066|gb|BQ409379.1|BQ409379				nr +
Unigene22516_All	1801	1.69	1.46	0.68	2.30	2.39	2.31	3.80	3.34	3.19	-2.04E-01	6.01E-01		-1.31E+00	6.75E-04	Down	5.81E-02	8.68E-01		7.10E-03	9.83E-01		-1.87E-01	4.01E-01		-2.56E-01	2.14E-01		Unigene22516_All//gi|187884338|gb|ACD37257.1|//1.00E-123//tousled-like protein [Solanum lycopersicum]	Unigene22516_All//3.00E-96//AT5G20930| TSL (TOUSLED); kinase/ protein serine/threonine kinase	Unigene22516_All//0.00E+00//TC170455				nr -
Unigene22519_All	647	6.95	4.93	2.80	12.16	7.29	7.05	9.61	8.46	8.87	-4.95E-01	8.40E-02		-1.31E+00	1.94E-05	Down	-7.38E-01	1.17E-04		-7.87E-01	1.03E-04		-1.83E-01	4.42E-01		-1.16E-01	6.15E-01		Unigene22519_All//gi|297812297|ref|XP_002874032.1|//1.00E-51//La domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319869|gb|EFH50291.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene22519_All//3.00E-52//AT5G21160| La domain-containing protein / proline-rich family protein	Unigene22519_All//8.00E-155//gi|78333249|gb|DT553523.1|DT553523				nr +
Unigene2252_All	1060	1.09	0.05	0.00	2.73	2.34	0.94	6.66	3.47	3.12	-4.51E+00	1.11E-05	Down	-1.01E+01	2.60E-06	Down	-2.21E-01	5.88E-01		-1.54E+00	5.05E-05	Down	-9.41E-01	2.15E-06		-1.09E+00	2.99E-08	Down	Unigene2252_All//gi|7269936|emb|CAB81029.1|//1.00E-153//cyclic nucleotide and calmodulin-regulated ion channel-like protein [Arabidopsis thaliana]	Unigene2252_All//5.00E-145//AT4G30360| ATCNGC17; calmodulin binding / cyclic nucleotide binding / ion channel	Unigene2252_All//1.00E-59//gi|164307600|gb|ES833254.1|ES833254		ko04626|Plant-pathogen interaction		nr +
Unigene22520_All	535	0.98	0.76	1.49	1.49	1.16	2.53	7.03	2.89	3.28	-3.68E-01	6.83E-01		6.10E-01	4.41E-01		-3.63E-01	6.23E-01		7.65E-01	2.05E-01		-1.28E+00	1.05E-05	Down	-1.10E+00	7.52E-05	Down	Unigene22520_All//gi|297812297|ref|XP_002874032.1|//1.00E-34//La domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319869|gb|EFH50291.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene22520_All//9.00E-36//AT5G21160| La domain-containing protein / proline-rich family protein	Unigene22520_All//1.00E-140//gi|78333249|gb|DT553523.1|DT553523				nr +
Unigene22525_All	3739	5.14	2.44	3.53	16.95	15.92	11.39	11.91	13.16	53.74	-1.07E+00	3.54E-16	Down	-5.40E-01	3.28E-05		-8.98E-02	2.35E-01		-5.73E-01	2.92E-19		1.44E-01	4.86E-02		2.17E+00	0.00E+00	Up	Unigene22525_All//gi|110737733|dbj|BAF00805.1|//1.00E-150//IFA-binding protein [Arabidopsis thaliana]	Unigene22525_All//3.00E-118//AT1G70750| unknown protein	Unigene22525_All//0.00E+00//TC168249				nr +
Unigene22527_All	3641	0.24	0.14	0.16	0.52	0.37	0.30	0.78	0.62	2.35	-8.12E-01	2.68E-01		-6.03E-01	4.18E-01		-4.95E-01	3.07E-01		-8.04E-01	9.25E-02		-3.28E-01	3.67E-01		1.60E+00	1.12E-16	Up	Unigene22527_All//gi|110737733|dbj|BAF00805.1|//1.00E-150//IFA-binding protein [Arabidopsis thaliana]	Unigene22527_All//2.00E-119//AT1G70750| unknown protein	Unigene22527_All//0.00E+00//TC168249				nr +
Unigene22528_All	625	3.35	2.11	0.51	3.35	4.08	2.31	4.26	4.28	5.74	-6.68E-01	1.33E-01		-2.71E+00	2.17E-06	Down	2.85E-01	5.45E-01		-5.34E-01	2.49E-01		6.10E-03	1.02E+00		4.29E-01	1.36E-01		Unigene22528_All//gi|42565391|ref|NP_189910.2|//5.00E-71//ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis thaliana] >gi|34849889|gb|AAQ82841.1|At3g43240 [Arabidopsis thaliana]	Unigene22528_All//3.00E-71//AT3G43240| ARID/BRIGHT DNA-binding domain-containing protein	Unigene22528_All//0.00E+00//TC174386				nr +
Unigene22529_All	1212	3.54	1.55	1.85	5.18	3.24	2.61	3.70	3.24	4.73	-1.19E+00	7.09E-05	Down	-9.40E-01	2.19E-03		-6.77E-01	2.11E-03		-9.89E-01	2.07E-05		-1.90E-01	5.16E-01		3.56E-01	1.08E-01		Unigene22529_All//gi|42565391|ref|NP_189910.2|//1.00E-159//ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis thaliana] >gi|34849889|gb|AAQ82841.1|At3g43240 [Arabidopsis thaliana]	Unigene22529_All//3.00E-153//AT3G43240| ARID/BRIGHT DNA-binding domain-containing protein	Unigene22529_All//0.00E+00//TC174386				nr -
Unigene2253_All	2624	0.78	0.52	0.43	3.08	1.55	0.96	16.48	10.70	8.06	-5.77E-01	2.05E-01		-8.68E-01	6.77E-02		-9.90E-01	1.73E-07		-1.67E+00	1.77E-14	Down	-6.23E-01	1.48E-17		-1.03E+00	7.69E-42	Down	Unigene2253_All//gi|30682497|ref|NP_850056.1|//0.00E+00//ATCNGC14; calmodulin binding / cyclic nucleotide binding / ion channel [Arabidopsis thaliana] >gi|38502238|sp|Q9SJA4.2|CNG14_ARATH RecName: Full=Probable cyclic nucleotide-gated ion channel 14; AltName: Full=Cyclic nucleotide- and calmodulin-regulated ion channel 14	Unigene2253_All//3.00E+00//AT2G26210| ATCNGC14; calmodulin binding / cyclic nucleotide binding / ion channel	Unigene2253_All//0.00E+00//TC136176		ko04626|Plant-pathogen interaction	GO:0005267//GO:0030001//GO:0031224	nr +
Unigene22533_All	1115	7.88	3.00	3.58	9.83	11.74	12.84	32.46	15.89	16.11	-1.39E+00	2.14E-11	Down	-1.14E+00	4.21E-08	Down	2.56E-01	1.20E-01		3.86E-01	1.01E-02		-1.03E+00	4.58E-34	Down	-1.01E+00	5.50E-34	Down	Unigene22533_All//gi|10176814|dbj|BAB10022.1|//0.00E+00//endosomal protein-like [Arabidopsis thaliana]	Unigene22533_All//0.00E+00//AT5G35160| LOCATED IN: integral to membrane, Golgi apparatus; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nonaspanin (TM9SF) (InterPro:IPR004240); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12650.1); Has 1053 Blast hits to 1004 proteins in 163 species: Archae - 0; Bacteria - 0; Metazoa - 478; Fungi - 143; Plants - 250; Viruses - 0; Other Eukaryotes - 182 (source: NCBI BLink).	Unigene22533_All//0.00E+00//TC148478				nr -
Unigene22535_All	2621	11.70	6.77	6.58	18.63	17.33	20.49	37.09	15.44	17.19	-7.90E-01	1.87E-15		-8.30E-01	4.74E-16		-1.04E-01	2.27E-01		1.38E-01	8.29E-02		-1.26E+00	5.24E-125	Down	-1.11E+00	1.80E-104	Down	Unigene22535_All//gi|10176814|dbj|BAB10022.1|//0.00E+00//endosomal protein-like [Arabidopsis thaliana]	Unigene22535_All//0.00E+00//AT5G35160| LOCATED IN: integral to membrane, Golgi apparatus; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nonaspanin (TM9SF) (InterPro:IPR004240); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12650.1); Has 1053 Blast hits to 1004 proteins in 163 species: Archae - 0; Bacteria - 0; Metazoa - 478; Fungi - 143; Plants - 250; Viruses - 0; Other Eukaryotes - 182 (source: NCBI BLink).	Unigene22535_All//0.00E+00//TC151676				nr -
Unigene22536_All	489	2.14	1.87	2.94	3.97	1.13	5.36	6.48	16.07	3.01	-1.98E-01	7.41E-01		4.58E-01	4.15E-01		-1.82E+00	7.81E-05	Down	4.31E-01	3.11E-01		1.31E+00	2.29E-11	Up	-1.11E+00	3.07E-04	Down	Unigene22536_All//gi|297823297|ref|XP_002879531.1|//8.00E-20//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325370|gb|EFH55790.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22536_All//6.00E-21//AT2G35050| protein kinase family protein	Unigene22536_All//8.00E-108//gi|164274664|gb|ES792524.1|ES792524				nr -
Unigene22539_All	275	60.69	28.01	33.69	106.51	102.05	100.51	145.75	49.55	75.91	-1.12E+00	5.16E-15	Down	-8.49E-01	2.28E-09		-6.17E-02	6.07E-01		-8.37E-02	5.00E-01		-1.56E+00	6.23E-71	Down	-9.41E-01	1.83E-33		Unigene22539_All//gi|6446577|gb|AAD39534.2|//9.00E-45//cellulose synthase catalytic subunit [Gossypium hirsutum]	Unigene22539_All//3.00E-42//AT5G05170| CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene22539_All//3.00E-149//TC131422				nr +
Unigene22540_All	332	26.48	16.48	15.40	38.86	44.08	36.32	98.95	43.05	51.60	-6.84E-01	4.29E-04		-7.82E-01	1.11E-04		1.82E-01	2.75E-01		-9.75E-02	6.38E-01		-1.20E+00	1.86E-39	Down	-9.39E-01	1.65E-27		Unigene22540_All//gi|6446577|gb|AAD39534.2|//2.00E-60//cellulose synthase catalytic subunit [Gossypium hirsutum]	Unigene22540_All//1.00E-57//AT5G05170| CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene22540_All//0.00E+00//TC131422				nr +
Unigene22541_All	3115	36.30	20.92	31.92	59.83	60.42	57.47	67.69	26.02	37.46	-7.95E-01	1.34E-55		-1.86E-01	2.85E-04		1.44E-02	8.06E-01		-5.79E-02	1.95E-01		-1.38E+00	0.00E+00	Down	-8.54E-01	3.59E-146		Unigene22541_All//gi|6446577|gb|AAD39534.2|//0.00E+00//cellulose synthase catalytic subunit [Gossypium hirsutum]	Unigene22541_All//0.00E+00//AT5G05170| CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene22541_All//0.00E+00//TC131422				nr +

Unigene22542_All	1098	4.67	4.11	2.09	7.80	10.38	9.05	12.25	3.08	8.35	-1.85E-01	5.15E-01			-1.16E+00	3.60E-05	Down	4.12E-01	1.26E-02		2.14E-01	3.06E-01		-1.99E+00	6.93E-34	Down	-5.53E-01	3.22E-05		Unigene22542_All//gi|15233583|ref|NP_193859.1|//1.00E-127//ATK1 (ARABIDOPSIS THALIANA KINESIN 1); microtubule motor/ minus-end-directed microtubule motor [Arabidopsis thaliana] >gi|1170619|sp|Q07970.1|ATK1_ARATH RecName: Full=Kinesin-1; AltName: Full=Kinesin-like protein A >gi|303502|dbj|BAA01972.1| kinesin-like motor protein heavy chain [Arabidopsis thaliana] >gi|2911084|emb|CAA17546.1| kinesin-related protein katA [Arabidopsis thaliana] >gi|7268924|emb|CAB79127.1| kinesin-related protein katA [Arabidopsis thaliana]	Unigene22542_All//3.00E-118//AT4G21270| ATK1 (ARABIDOPSIS THALIANA KINESIN 1); microtubule motor/ minus-end-directed microtubule motor	Unigene22542_All//0.00E+00//TC173031				nr -
Unigene22543_All	3000	3.40	2.45	1.60	6.94	9.05	7.77	11.19	1.67	4.37	-4.74E-01	8.36E-03			-1.09E+00	1.02E-08	Down	3.82E-01	1.04E-04		1.63E-01	2.08E-01		-2.74E+00	9.42E-123	Down	-1.36E+00	4.81E-50	Down	Unigene22543_All//gi|15233583|ref|NP_193859.1|//0.00E+00//ATK1 (ARABIDOPSIS THALIANA KINESIN 1); microtubule motor/ minus-end-directed microtubule motor [Arabidopsis thaliana] >gi|1170619|sp|Q07970.1|ATK1_ARATH RecName: Full=Kinesin-1; AltName: Full=Kinesin-like protein A >gi|303502|dbj|BAA01972.1| kinesin-like motor protein heavy chain [Arabidopsis thaliana] >gi|2911084|emb|CAA17546.1| kinesin-related protein katA [Arabidopsis thaliana] >gi|7268924|emb|CAB79127.1| kinesin-related protein katA [Arabidopsis thaliana]	Unigene22543_All//0.00E+00//AT4G21270| ATK1 (ARABIDOPSIS THALIANA KINESIN 1); microtubule motor/ minus-end-directed microtubule motor	Unigene22543_All//0.00E+00//TC173031				nr -
Unigene22544_All	2863	1.96	1.70	1.00	4.56	6.53	4.70	6.62	1.59	4.69	-2.03E-01	4.43E-01			-9.61E-01	2.69E-04		5.19E-01	1.48E-05		4.43E-02	8.05E-01		-2.06E+00	1.76E-49	Down	-4.97E-01	6.69E-06		Unigene22544_All//gi|15233583|ref|NP_193859.1|//0.00E+00//ATK1 (ARABIDOPSIS THALIANA KINESIN 1); microtubule motor/ minus-end-directed microtubule motor [Arabidopsis thaliana] >gi|1170619|sp|Q07970.1|ATK1_ARATH RecName: Full=Kinesin-1; AltName: Full=Kinesin-like protein A >gi|303502|dbj|BAA01972.1| kinesin-like motor protein heavy chain [Arabidopsis thaliana] >gi|2911084|emb|CAA17546.1| kinesin-related protein katA [Arabidopsis thaliana] >gi|7268924|emb|CAB79127.1| kinesin-related protein katA [Arabidopsis thaliana]	Unigene22544_All//0.00E+00//AT4G21270| ATK1 (ARABIDOPSIS THALIANA KINESIN 1); microtubule motor/ minus-end-directed microtubule motor	Unigene22544_All//0.00E+00//ES846869				nr -
Unigene22550_All	954	2.14	5.90	3.13	5.64	4.76	8.95	6.96	7.49	11.44	1.46E+00	4.97E-08	Up	5.47E-01	1.48E-01		-2.43E-01	3.89E-01		6.66E-01	6.44E-04		1.07E-01	6.40E-01		7.18E-01	1.95E-06		Unigene22550_All//gi|297821923|ref|XP_002878844.1|//4.00E-71//octicosapeptide/Phox/Bem1p domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297324683|gb|EFH55103.1| octicosapeptide/Phox/Bem1p domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene22550_All//1.00E-58//AT4G32070| octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein	Unigene22550_All//0.00E+00//TC175249				nr -
Unigene22554_All	1716	11.53	12.84	11.08	22.73	25.28	28.50	32.30	39.73	79.65	1.56E-01	2.21E-01		-5.71E-02	6.86E-01		1.54E-01	7.41E-02		3.27E-01	1.05E-05		2.99E-01	1.33E-07		1.30E+00	2.97E-187	Up	Unigene22554_All//gi|223452480|gb|ACM89567.1|//0.00E+00//serine/threonine protein kinase [Glycine max]	Unigene22554_All//8.00E-163//AT3G62220| serine/threonine protein kinase, putative	Unigene22554_All//0.00E+00//TC177382		ko04626|Plant-pathogen interaction		nr +
Unigene22559_All	2116	2.94	7.14	2.26	14.01	14.37	13.21	10.13	11.32	6.46	1.28E+00	1.13E-16	Up	-3.78E-01	1.38E-01		3.69E-02	8.02E-01		-8.44E-02	4.91E-01		1.60E-01	1.46E-01		-6.50E-01	4.42E-10		Unigene22559_All//gi|63115354|gb|AY33856.1|//0.00E+00//class III HD-zip protein [Gossypium barbadense]	Unigene22559_All//0.00E+00//AT5G60690| REV (REVOLUTA); DNA binding / lipid binding / transcription factor	Unigene22559_All//0.00E+00//gi|78348557|gb|DT568831.1|DT568831	HB			nr +
Unigene2256_All	1602	13.62	18.47	16.39	10.82	18.72	28.78	15.70	18.99	11.51	4.40E-01	9.33E-06		2.67E-01	1.92E-02		7.91E-01	1.51E-17		1.41E+00	1.24E-61	Up	2.74E-01	2.08E-03		-4.48E-01	2.17E-06		Unigene2256_All//gi|224109590|ref|XP_002315247.1|//2.00E-76//metal tolerance protein [Populus trichocarpa] >gi|145452064|gb|ABF68858.1| Mn-specific cation diffusion facilitator transporter [Populus trichocarpa] >gi|222864287|gb|EEF01418.1| metal tolerance protein [Populus trichocarpa]	Unigene2256_All//2.00E-70//AT2G39450| MTP11; cation transmembrane transporter/ manganese ion transmembrane transporter/ manganese:hydrogen antiporter	Unigene2256_All//0.00E+00//gi|78336165|gb|DT556439.1|DT556439			GO:0005768//GO:0006811//GO:0010038//GO:0015082//GO:0030005//GO:0051139	nr +
Unigene22560_All	1231	2.93	3.87	3.81	10.48	9.06	9.94	37.61	26.72	12.30	4.00E-01	1.55E-01		3.76E-01	2.14E-01		-2.10E-01	2.19E-01		-7.61E-02	6.98E-01		-4.93E-01	1.43E-12		-1.61E+00	1.20E-88	Down	Unigene22560_All//gi|297833762|ref|XP_002884763.1|//1.00E-107//PIP5K9 [Arabidopsis lyrata subsp. lyrata] >gi|297330603|gb|EFH61022.1| PIP5K9 [Arabidopsis lyrata subsp. lyrata]	Unigene22560_All//4.00E-109//AT3G09920| PIP5K9 (PHOSPHATIDYL INOSITOL MONOPHOSPHATE 5 KINASE); 1-phosphatidylinositol-4-phosphate 5-kinase/ ATP binding / phosphatidylinositol phosphate kinase	Unigene22560_All//0.00E+00//DW511509				nr +
Unigene22561_All	2235	6.44	8.80	8.96	24.47	25.81	30.35	69.26	46.04	26.43	4.50E-01	2.94E-04		4.77E-01	1.81E-04		7.66E-02	3.61E-01		3.11E-01	5.11E-07		-5.89E-01	5.46E-55		-1.39E+00	3.13E-236	Down	Unigene22561_All//gi|297833762|ref|XP_002884763.1|//0.00E+00//PIP5K9 [Arabidopsis lyrata subsp. lyrata] >gi|297330603|gb|EFH61022.1| PIP5K9 [Arabidopsis lyrata subsp. lyrata]	Unigene22561_All//0.00E+00//AT3G09920| PIP5K9 (PHOSPHATIDYL INOSITOL MONOPHOSPHATE 5 KINASE); 1-phosphatidylinositol-4-phosphate 5-kinase/ ATP binding / phosphatidylinositol phosphate kinase	Unigene22561_All//0.00E+00//TC153098		ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene22563_All	448	3.97	3.51	4.40	2.00	4.07	7.56	1.42	2.24	1.25	-1.80E-01	6.96E-01		1.47E-01	7.47E-01		1.03E+00	3.41E-02		1.92E+00	1.92E-07	Up	6.62E-01	2.97E-01		-1.85E-01	7.94E-01		Unigene22563_All//gi|6706418|emb|CAB66104.1|//5.00E-43//protease-like protein [Arabidopsis thaliana]	Unigene22563_All//1.00E-42//AT2G41790| peptidase M16 family protein / insulinase family protein	Unigene22563_All//0.00E+00//TC150844				nr -
Unigene22567_All	350	0.00	0.29	0.00	0.71	0.98	2.45	1.21	3.58	4.33	8.18E+00	3.87E-01		null	null		4.67E-01	7.79E-01		1.78E+00	3.19E-02		1.57E+00	5.58E-03		1.84E+00	3.16E-04	Up	Unigene22567_All//gi|35187447|gb|AQ84315.1|//5.00E-19//fiber protein Fb26 [Gossypium barbadense]	Unigene22567_All//2.00E-14//AT1G74040| IMS1 (2-ISOPROPYLMALATE SYNTHASE 1); 2-isopropylmalate synthase	Unigene22567_All//6.00E-77//TC143072		ko00620|Pyruvate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis		nr -
Unigene22568_All	2330	14.73	4.96	9.90	21.98	18.41	22.16	21.03	11.52	14.64	-1.57E+00	1.75E-50	Down	-5.74E-01	1.13E-09		-2.55E-01	2.70E-04		1.16E-02	9.17E-01		-8.69E-01	1.10E-34		-5.23E-01	4.16E-15		Unigene22568_All//gi|75707983|gb|ABA26446.1|//0.00E+00//2-isopropylmalate synthase 1 [Brassica insularis]	Unigene22568_All//0.00E+00//AT1G74040| IMS1 (2-ISOPROPYLMALATE SYNTHASE 1); 2-isopropylmalate synthase	Unigene22568_All//0.00E+00//TC158445		ko00620|Pyruvate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis		nr +
Unigene22569_All	2360	16.12	11.40	17.55	27.10	41.94	82.90	17.99	35.30	36.04	-5.00E-01	7.58E-09		1.23E-01	2.03E-01		6.30E-01	1.44E-38		1.61E+00	0.00E+00	Up	9.73E-01	2.55E-70		1.00E+00	3.67E-77	Up	Unigene22569_All//gi|171921096|gb|ACB59195.1|//0.00E+00//2-isopropylmalate synthase [Brassica oleracea]	Unigene22569_All//0.00E+00//AT1G74040| IMS1 (2-ISOPROPYLMALATE SYNTHASE 1); 2-isopropylmalate synthase	Unigene22569_All//0.00E+00//TC169650		ko00620|Pyruvate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis		nr +
Unigene22574_All	1273	2.01	2.11	1.38	3.64	2.71	2.24	9.37	6.01	4.63	6.70E-02	8.64E-01		-5.45E-01	1.94E-01		-4.28E-01	1.28E-01		-7.03E-01	1.14E-02		-6.41E-01	1.14E-05		-1.02E+00	6.73E-12	Down	Unigene22574_All//gi|224141351|ref|XP_002324036.1|//0.00E+00//high mobility group family [Populus trichocarpa] >gi|222867038|gb|EEF04169.1| high mobility group family [Populus trichocarpa]	Unigene22574_All//0.00E+00//AT3G28730| ATHMG (ARABIDOPSIS THALIANA HIGH MOBILITY GROUP); transcription factor	Unigene22574_All//0.00E+00//gi|11207893|gb|BF276823.1|BF276823				nr +
Unigene22581_All	1693	5.72	6.40	2.67	7.74	8.30	7.10	20.45	11.31	16.61	1.64E-01	3.87E-01		-1.10E+00	2.22E-08	Down	1.01E-01	5.84E-01		-1.25E-01	4.99E-01		-8.55E-01	4.15E-24		-3.00E-01	1.80E-04		Unigene22581_All//gi|15221817|ref|NP_175847.1|//1.00E-171//calcium-binding EF-hand family protein [Arabidopsis thaliana] >gi|4585988|gb|AAD25624.1|AC005287_26 Similar to phosphoprotein phosphatase 2A regulatory subunit [Arabidopsis thaliana]	Unigene22581_All//2.00E-172//AT1G54450| calcium-binding EF-hand family protein	Unigene22581_All//0.00E+00//TC168457				nr +
Unigene22582_All	1865	3.42	2.39	2.06	3.66	3.36	4.02	5.96	3.09	2.71	-5.18E-01	2.69E-02		-7.35E-01	2.45E-03		-1.23E-01	6.19E-01		1.36E-01	6.17E-01		-9.47E-01	1.06E-09		-1.14E+00	3.34E-13	Down	Unigene22582_All//gi|15221817|ref|NP_175847.1|//0.00E+00//calcium-binding EF-hand family protein [Arabidopsis thaliana] >gi|4585988|gb|AAD25624.1|AC005287_26 Similar to phosphoprotein phosphatase 2A regulatory subunit [Arabidopsis thaliana]	Unigene22582_All//0.00E+00//AT1G54450| calcium-binding EF-hand family protein	Unigene22582_All//0.00E+00//TC149879				nr -
Unigene22589_All	1700	52.60	127.99	51.97	31.38	17.34	18.30	91.08	91.85	51.18	1.28E+00	2.12E-232	Up	-1.74E-02	7.91E-01		-8.56E-01	1.08E-36		-7.78E-01	1.37E-27		1.22E-02	7.92E-01		-8.32E-01	7.20E-103		Unigene22589_All//gi|91208926|ref|YP_538961.1|//1.00E-91//ATP-dependent Clp protease proteolytic subunit [Gossypium hirsutum] >gi|122201402|sp|Q2L926.1|CLPP_GOSHI RecName: Full=ATP-dependent Clp protease proteolytic subunit; AltName: Full=Endopeptidase Clp >gi|85687440|gb|ABC73652.1| clp protease proteolytic subunit [Gossypium hirsutum]	Unigene22589_All//5.00E-84//ATCG00670| Encodes the only ClpP (caseinolytic protease) encoded within the plastid genome. Contains a highly conserved catalytic triad of Ser-type proteases (Ser-His-Asp). Part of the 350 kDa chloroplast Clp complex. The name reflects nomenclature described in Adam et. al (2001).	Unigene22589_All//0.00E+00//TC138780				nr +
Unigene2259_All	2056	8.55	9.49	7.17	14.39	12.51	15.97	13.90	13.44	5.13	1.50E-01	2.75E-01		-2.53E-01	8.03E-02		-2.02E-01	4.70E-02		1.50E-01	1.55E-01		-4.90E-02	6.47E-01		-1.44E+00	1.51E-46	Down	Unigene2259_All//gi|186550639|gb|AAL75889.1|//0.00E+00//AT4g27020/F10M23_360 [Arabidopsis thaliana] >gi|23505979|gb|AAN28849.1| At4g27020/F10M23_360 [Arabidopsis thaliana]	Unigene2259_All//0.00E+00//AT4G27020| unknown protein	Unigene2259_All//0.00E+00//TC137209			GO:0031410//GO:0043231	nr +
Unigene22592_All	2738	5.04	5.09	3.68	6.15	5.71	6.65	12.08	6.78	34.89	1.26E-02	9.58E-01		-4.57E-01	3.85E-03		-1.07E-01	5.23E-01		1.12E-01	4.71E-01		-8.33E-01	4.28E-22		1.53E+00	4.09E-167	Up	Unigene22592_All//gi|224112289|ref|XP_002316143.1|//0.00E+00//integral membrane single C2 domain protein [Populus trichocarpa] >gi|222865183|gb|EEF02314.1| integral membrane single C2 domain protein [Populus trichocarpa]	Unigene22592_All//0.00E+00//AT3G19830| NTMC2T5.2	Unigene22592_All//0.00E+00//TC140519				nr +
Unigene22599_All	1477	26.18	25.83	23.58	63.04	52.43	48.13	17.98	21.96	36.68	-1.92E-02	8.45E-01		-1.51E-01	1.25E-01		-2.66E-01	7.57E-08		-3.89E-01	4.57E-14		2.89E-01	7.43E-04		1.03E+00	1.38E-51	Up	Unigene22599_All//gi|3157952|gb|AAC17635.1|//2.00E-45//F12F1.11 [Arabidopsis thaliana]	Unigene22599_All//4.00E-29//AT1G12020| unknown protein	Unigene22599_All//0.00E+00//TC136348				nr -

Unigene226_All	504	16.71	5.43	6.55	63.75	73.38	58.16	138.75	34.08	78.10	-1.62E+00	1.66E-13	Down	-1.35E+00	5.54E-10	Down	2.03E-01	2.35E-02		-1.33E-01	2.27E-01		-2.03E+00	1.91E-177	Down	-8.29E-01	9.92E-47		Unigene226_All//gi|224066625|ref|XP_002302169.1|//6.00E-83//cellulose synthase [Populus trichocarpa] >gi|222843895|gb|EEE81442.1|cellulose synthase [Populus trichocarpa]	Unigene226_All//1.00E-42//AT2G21770| CESA9 (CELLULOSE SYNTHASE A9); cellulose synthase/ transferase, transferring glycosyl groups	Unigene226_All//0.00E+00//TC170744				nr +
Unigene2260_All	361	5.22	3.79	4.87	1.10	3.72	0.75	9.14	3.13	3.09	-4.61E-01	3.40E-01		-1.00E-01	8.30E-01		1.75E+00	4.15E-03		-5.57E-01	6.38E-01		-1.55E+00	1.72E-06	Down	-1.56E+00	7.77E-07	Down	Unigene2260_All//gi|18401175|ref|NP_566554.1|//2.00E-10//protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] >gi|75274292|sp|Q9LUS8.1|P2C40_ARATH RecName: Full=Probable protein phosphatase 2C 40; Short=AtPP2C40; AltName: Full=Protein phosphatase 2C homolog 1 >gi|22531239|gb|AAM97123.1|expressed protein [Arabidopsis thaliana] >gi|31711894|gb|AAP68303.1|At3g16560 [Arabidopsis thaliana]	Unigene2260_All//1.00E-10//AT3G16560| protein phosphatase 2C-related / PP2C-related	Unigene2260_All//2.00E-151//CA994014		GO:0004721	nr -
Unigene22600_All	4958	3.56	1.82	1.22	5.18	4.69	5.72	10.44	4.73	5.46	-9.67E-01	1.12E-12		-1.54E+00	1.81E-24	Down	-1.45E-01	2.27E-01		1.42E-01	2.26E-01		-1.14E+00	4.82E-57	Down	-9.36E-01	1.49E-42		Unigene22600_All//gi|30684028|ref|NP_172938.2|//0.00E+00//NUP155; nucleocytoplasmic transporter [Arabidopsis thaliana]	Unigene22600_All//0.00E+00//AT1G14850| NUP155; nucleocytoplasmic transporter	Unigene22600_All//0.00E+00//gi|164286684|gb|ES833188.1|ES833188				nr +
Unigene22605_All	1073	1.22	2.08	3.47	6.64	7.77	6.82	7.25	9.43	8.39	7.69E-01	7.33E-02		1.51E+00	1.48E-05	Up	2.26E-01	3.09E-01		3.86E-02	8.92E-01		3.79E-01	2.09E-02		2.11E-01	2.42E-01		Unigene22605_All//gi|10177232|dbj|BAB10606.1|//1.00E-112//protease-like protein [Arabidopsis thaliana]	Unigene22605_All//5.00E-102//AT5G22850| aspartyl protease family protein	Unigene22605_All//1.00E-157//gi|13350746|gb|BG441094.1|BG441094				nr +
Unigene22606_All	1628	1.61	1.06	1.64	4.68	4.04	2.44	3.06	2.28	0.95	-6.03E-01	1.22E-01		2.54E-02	9.67E-01		-2.13E-01	3.61E-01		-9.39E-01	6.01E-06		-4.24E-01	8.62E-02		-1.68E+00	6.56E-11	Down	Unigene22606_All//gi|10177232|dbj|BAB10606.1|//1.00E-172//protease-like protein [Arabidopsis thaliana]	Unigene22606_All//3.00E-160//AT5G22850| aspartyl protease family protein	Unigene22606_All//0.00E+00//ES802226				nr +
Unigene22608_All	1830	9.35	27.33	10.59	23.55	27.19	29.89	27.38	45.59	24.82	1.55E+00	2.70E-71	Up	1.80E-01	2.09E-01		2.08E-01	5.20E-03		3.44E-01	7.09E-07		7.36E-01	4.72E-44		-1.42E-01	4.14E-02		Unigene22608_All//gi|10177232|dbj|BAB10606.1|//0.00E+00//protease-like protein [Arabidopsis thaliana]	Unigene22608_All//0.00E+00//AT5G22850| aspartyl protease family protein	Unigene22608_All//0.00E+00//CO090406				nr +
Unigene22609_All	352	0.15	0.00	0.00	4.10	1.17	0.13	5.16	7.36	6.56	-7.22E+00	6.12E-01		-7.22E+00	6.24E-01		-1.81E+00	9.96E-04	Down	-5.00E+00	7.44E-08	Down	5.11E-01	1.53E-01		3.46E-01	3.61E-01		Unigene22609_All//gi|31580853|dbj|BAC77531.1|//1.00E-33//plasma membrane H+-ATPase [Sesbania rostrata]	Unigene22609_All//2.00E-30//AT4G30190| AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	Unigene22609_All//1.00E-90//gi|164365854|gb|ES802372.1|ES802372		ko00190|Oxidative phosphorylation		nr +
Unigene2261_All	3940	10.01	9.59	9.04	7.47	6.24	5.46	9.80	4.58	6.69	-6.17E-02	5.43E-01		-1.47E-01	1.32E-01		-2.60E-01	7.72E-03		-4.54E-01	2.71E-06		-1.10E+00	4.58E-40	Down	-5.50E-01	3.80E-13		Unigene2261_All//gi|18401175|ref|NP_566554.1|//1.00E-161//protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] >gi|75274292|sp|Q9LUS8.1|P2C40_ARATH RecName: Full=Probable protein phosphatase 2C 40; Short=AtPP2C40; AltName: Full=Protein phosphatase 2C homolog 1 >gi|22531239|gb|AAM97123.1|expressed protein [Arabidopsis thaliana] >gi|31711894|gb|AAP68303.1|At3g16560 [Arabidopsis thaliana]	Unigene2261_All//7.00E-139//AT3G16560| protein phosphatase 2C-related / PP2C-related	Unigene2261_All//0.00E+00//TC151953				nr +
Unigene22610_All	479	0.22	0.00	0.22	4.26	2.30	1.79	15.89	19.20	6.32	-7.77E+00	3.72E-01		2.49E-02	1.00E+00		-8.90E-01	3.87E-02		-1.25E+00	6.06E-03		2.73E-01	1.34E-01		-1.33E+00	1.10E-11	Down			Unigene22610_All//9.00E-09//CO071267				
Unigene22611_All	1311	0.24	0.08	0.00	0.04	0.16	0.03	79.50	14.09	38.59	-1.63E+00	2.76E-01		-7.90E+00	4.91E-02		2.05E+00	3.95E-01		-1.44E-01	9.53E-01		-2.50E+00	0.00E+00	Down	-1.04E+00	2.84E-101	Down	Unigene22611_All//gi|7105717|gb|AAB84202.2|//0.00E+00//plasma membrane proton ATPase [Kosteletzkya virginica]	Unigene22611_All//0.00E+00//AT4G30190| AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	Unigene22611_All//0.00E+00//CO071267		ko00190|Oxidative phosphorylation		nr +
Unigene22612_All	3405	37.91	12.69	10.07	242.17	171.92	193.73	416.38	446.02	193.13	-1.58E+00	1.53E-189	Down	-1.91E+00	3.08E-240	Down	-4.94E-01	7.07E-212		-3.22E-01	2.66E-84		9.92E-02	1.09E-18		-1.11E+00	0.00E+00	Down	Unigene22612_All//gi|31580853|dbj|BAC77531.1|//0.00E+00//plasma membrane H+-ATPase [Sesbania rostrata]	Unigene22612_All//0.00E+00//AT2G24520| AHA5 (Arabidopsis H(+)-ATPase 5); ATPase	Unigene22612_All//0.00E+00//TC145549		ko00190|Oxidative phosphorylation		nr +
Unigene22615_All	1896	50.55	28.22	52.24	95.42	50.15	36.68	26.54	7.54	6.16	-8.41E-01	5.88E-52		4.73E-02	4.59E-01		-9.28E-01	2.01E-142		-1.38E+00	3.40E-236	Down	-1.82E+00	2.01E-110	Down	-2.11E+00	1.19E-138	Down	Unigene22615_All//gi|284519840|gb|ADB92670.1|//0.00E+00//amino acid permease 6 [Populus tremula x Populus alba]	Unigene22615_All//0.00E+00//AT5G49630| AAP6 (AMINO ACID PERMEASE 6); acidic amino acid transmembrane transporter/ amino acid transmembrane transporter/ neutral amino acid transmembrane transporter	Unigene22615_All//0.00E+00//TC162144				nr -
Unigene22616_All	2081	9.78	1.87	3.79	37.44	24.85	17.51	15.26	5.12	3.47	-2.38E+00	3.47E-52	Down	-1.37E+00	9.70E-24	Down	-5.91E-01	6.28E-28		-1.10E+00	5.80E-71	Down	-1.58E+00	2.64E-57	Down	-2.14E+00	2.11E-89	Down	Unigene22616_All//gi|224102121|ref|XP_002312555.1|//0.00E+00//argonaute protein group [Populus trichocarpa] >gi|222852375|gb|EEE89922.1|argonaute protein group [Populus trichocarpa]	Unigene22616_All//0.00E+00//AT5G43810| ZLL (ZWILLE); translation initiation factor	Unigene22616_All//0.00E+00//TC134355				nr +
Unigene22617_All	3582	4.09	5.23	5.47	16.90	26.73	35.96	15.53	14.54	13.92	3.56E-01	5.91E-03		4.20E-01	1.21E-03		6.62E-01	1.14E-40		1.09E+00	1.45E-114	Up	-9.55E-02	1.91E-01		-1.58E-01	1.46E-02		Unigene22617_All//gi|224102121|ref|XP_002312555.1|//0.00E+00//argonaute protein group [Populus trichocarpa] >gi|222852375|gb|EEE89922.1|argonaute protein group [Populus trichocarpa]	Unigene22617_All//0.00E+00//AT5G43810| ZLL (ZWILLE); translation initiation factor	Unigene22617_All//0.00E+00//gi|11200612|gb|BF269617.1|BF269617				nr -
Unigene22618_All	1441	38.96	16.63	21.43	13.00	15.25	11.78	49.91	28.80	40.09	-1.23E+00	1.05E-56	Down	-8.62E-01	7.55E-31		2.30E-01	5.75E-02		-1.41E-01	3.49E-01		-7.93E-01	2.46E-43		-3.16E-01	4.35E-09		Unigene22618_All//gi|45479863|gb|AAS66771.1|//0.00E+00//PPase [Hevea brasiliensis]	Unigene22618_All//0.00E+00//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene22618_All//0.00E+00//TC168590		ko00190|Oxidative phosphorylation		nr -
Unigene22619_All	1640	58.64	34.82	28.74	19.50	17.91	14.21	83.37	59.38	62.55	-7.52E-01	4.38E-43		-1.03E+00	1.83E-70	Down	-1.23E-01	2.59E-01		-4.57E-01	7.51E-07		-4.90E-01	4.83E-35		-4.15E-01	9.68E-27		Unigene22619_All//gi|45479863|gb|AAS66771.1|//0.00E+00//PPase [Hevea brasiliensis]	Unigene22619_All//0.00E+00//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene22619_All//0.00E+00//TC168590		ko00190|Oxidative phosphorylation		nr -
Unigene2262_All	1729	19.19	18.37	14.94	33.51	31.43	25.00	14.11	6.74	4.59	-6.23E-02	5.81E-01		-3.61E-01	1.99E-04		-9.24E-02	2.47E-01		-4.23E-01	2.24E-10		-1.06E+00	1.78E-24	Down	-1.62E+00	1.75E-47	Down	Unigene2262_All//gi|15232856|ref|NP_189427.1|//2.00E-76//NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN reductase [Arabidopsis thaliana] >gi|75273736|sp|Q9LK88.1|NQR_ARATH RecName: Full=NADPH:quinone oxidoreductase >gi|11994494|dbj|BAB02535.1|NADPH:quinone oxidoreductase [Arabidopsis thaliana] >gi|88193780|gb|ABD42979.1|At3g27890 [Arabidopsis thaliana]	Unigene2262_All//7.00E-78//AT3G27890| NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN reductase	Unigene2262_All//0.00E+00//TC145508			GO:0006952//GO:0006970//GO:0008152//GO:0009532//GO:0016020//GO:0016646//GO:0016655//GO:0042579//GO:0046914	nr +
Unigene22623_All	1840	4.07	9.42	5.38	7.34	16.86	12.98	4.85	4.66	7.38	1.21E+00	1.46E-17	Up	4.05E-01	3.65E-02		1.20E+00	1.19E-35	Up	8.24E-01	8.60E-14		-5.82E-02	7.67E-01		6.07E-01	5.03E-06		Unigene22623_All//gi|12324937|gb|AAG52416.1|AC011622_4//0.00E+00//GMP synthase: 61700-64653 [Arabidopsis thaliana] >gi|56381989|gb|AAV85713.1|At1g63660 [Arabidopsis thaliana]	Unigene22623_All//0.00E+00//AT1G63660| GMP synthase (glutamine-hydrolyzing), putative / glutamine amidotransferase, putative	Unigene22623_All//0.00E+00//TC156263		ko00230|Purine metabolism		nr -
Unigene22624_All	2081	14.13	3.09	5.55	14.94	9.88	18.43	23.91	9.86	11.85	-2.19E+00	6.87E-68	Down	-1.35E+00	2.76E-33	Down	-5.97E-01	1.39E-11		3.03E-01	4.14E-04		-1.28E+00	2.09E-65	Down	-1.01E+00	1.38E-46	Down	Unigene22624_All//gi|12324937|gb|AAG52416.1|AC011622_4//0.00E+00//GMP synthase: 61700-64653 [Arabidopsis thaliana] >gi|56381989|gb|AAV85713.1|At1g63660 [Arabidopsis thaliana]	Unigene22624_All//0.00E+00//AT1G63660| GMP synthase (glutamine-hydrolyzing), putative / glutamine amidotransferase, putative	Unigene22624_All//0.00E+00//TC146253		ko00230|Purine metabolism		nr -
Unigene22625_All	1904	9.18	5.54	3.75	11.75	12.59	8.23	11.72	8.23	4.41	-7.30E-01	4.44E-08		-1.29E+00	8.96E-19	Down	9.97E-02	4.65E-01		-5.13E-01	4.98E-06		-5.10E-01	7.45E-07		-1.41E+00	1.64E-35	Down	Unigene22625_All//gi|32478841|gb|AAP83637.1|//0.00E+00//katanin [Gossypium hirsutum]	Unigene22625_All//0.00E+00//AT1G80350| ERH3 (ECTOPIC ROOT HAIR 3); ATP binding / nucleoside-triphosphatase/ nucleotide binding	Unigene22625_All//0.00E+00//TC129612				nr +
Unigene22627_All	1363	0.00	0.00	0.00	6.76	3.44	3.61	1.83	1.35	0.53	null	null		null	null		-9.77E-01	2.72E-08		-9.05E-01	1.17E-06		-4.40E-01	2.38E-01		-1.80E+00	2.33E-06	Down	Unigene22627_All//gi|224094448|ref|XP_002310162.1|//0.00E+00//multicopper oxidase [Populus trichocarpa] >gi|222853065|gb|EEE90612.1|multicopper oxidase [Populus trichocarpa]	Unigene22627_All//2.00E-179//AT5G66920| ska17 (SKU5 Similar 17); copper ion binding / oxidoreductase	Unigene22627_All//0.00E+00//TC152935		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene22628_All	3900	4.88	4.50	0.59	10.93	6.29	5.56	10.16	1.44	6.52	-1.19E-01	3.84E-01		-3.06E+00	1.40E-61	Down	-7.98E-01	4.28E-26		-9.76E-01	2.37E-32		-2.82E+00	2.82E-149	Down	-6.40E-01	1.98E-17		Unigene22628_All//gi|224094448|ref|XP_002310162.1|//0.00E+00//multicopper oxidase [Populus trichocarpa] >gi|222853065|gb|EEE90612.1|multicopper oxidase [Populus trichocarpa]	Unigene22628_All//0.00E+00//AT5G66920| ska17 (SKU5 Similar 17); copper ion binding / oxidoreductase	Unigene22628_All//0.00E+00//TC164381		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene22629_All	1907	46.48	18.09	15.36	173.97	97.47	51.13	64.19	19.42	38.40	-1.36E+00	1.71E-104	Down	-1.60E+00	2.59E-128	Down	-8.36E-01	3.95E-218		-1.77E+00	0.00E+00	Down	-1.72E+00	2.03E-249	Down	-7.41E-01	5.78E-67		Unigene22629_All//gi|224094448|ref|XP_002310162.1|//0.00E+00//multicopper oxidase [Populus trichocarpa] >gi|222853065|gb|EEE90612.1|multicopper oxidase [Populus trichocarpa]	Unigene22629_All//0.00E+00//AT5G66920| ska17 (SKU5 Similar 17); copper ion binding / oxidoreductase	Unigene22629_All//0.00E+00//TC160479		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene2263_All	984	5.58	6.54	2.60	8.40	6.93	7.11	27.54	26.97	18.18	2.28E-01	3.72E-01		-1.10E+00	4.16E-05	Down	-2.78E-01	1.88E-01		-2.40E-01	2.89E-01		-3.02E-02	7.89E-01		-5.99E-01	5.90E-11		Unigene2263_All//gi|240256121|ref|NP_191990.4|//1.00E-102//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|240256123|ref|NP_001119101.4|protein binding / zinc ion binding [Arabidopsis thaliana] >gi|259016138|sp|Q9M081.2|SC24B_ARATH RecName: Full=Protein transport protein Sec24-like At4g32640	Unigene2263_All//1.00E-91//AT4G32640| protein binding / zinc ion binding	Unigene2263_All//0.00E+00//TC178996			GO:0006950//GO:0009536//GO:0012507//GO:0015031//GO:0046914//GO:0048193	nr -
Unigene22632_All	2079	6.34	6.70	7.35	11.12	10.58	17.94	14.42	12.12	37.23	7.97E-02	6.13E-01		2.13E-01	1.83E-01		-7.10E-02	5.96E-01		6.91E-01	8.67E-16		-2.50E-01	5.79E-03		1.37E+00	9.49E-115	Up	Unigene22632_All//gi|15236164|ref|NP_194360.1|//0.00E+00//embl027 (embryo defective 1027); ATP binding / aminoacyl-tRNA ligase/ arginine-tRNA ligase/ nucleotide binding [Arabidopsis thaliana] >gi|2632105|emb|CAB11468.1|arginyl-tRNA synthetase [Arabidopsis thaliana] >gi|4539426|emb|CAB38959.1|arginyl-tRNA synthetase [Arabidopsis thaliana] >gi|7269482|emb|CAB79485.1|arginyl-tRNA synthetase [Arabidopsis thaliana]	Unigene22632_All//0.00E+00//AT4G26300| emb1027 (embryo defective 1027); ATP binding / aminoacyl-tRNA ligase/ arginine-tRNA ligase/ nucleotide binding	Unigene22632_All//0.00E+00//TC165896		ko00970|Aminoacyl-tRNA biosynthesis		nr -

Unigene22633_All	253	1.65	2.00	2.10	3.54	1.36	4.28	5.85	10.41	25.35	2.76E-01	7.64E-01		3.47E-01	7.06E-01		-1.38E+00	5.39E-02		2.74E-01	6.70E-01		8.31E-01	1.68E-02		2.12E+00	3.30E-18	Up	Unigene22633_All//gi|224064438|ref|XP_002301476.1|//3.00E-38//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222843202|gb|EEE80749.1|multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene22633_All//8.00E-35//AT3G62700| ATMRP10; ATPase, coupled to transmembrane movement of substances			ko02010|ABC transporters		nr +
Unigene22634_All	4853	4.97	4.23	4.20	8.55	5.05	5.94	24.12	37.72	86.00	-2.33E-01	4.37E-02		-2.42E-01	4.53E-02		-7.59E-01	2.69E-23		-5.26E-01	4.53E-11		6.46E-01	3.37E-76		1.83E+00	0.00E+00	Up	Unigene22634_All//gi|224064438|ref|XP_002301476.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222843202|gb|EEE80749.1|multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene22634_All//0.00E+00//AT2G47800| ATMRP4 (ARABIDOPSIS THALIANA MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 4); ATPase, coupled to transmembrane movement of substances / folic acid transporter	Unigene22634_All//0.00E+00//TC130271		ko02010|ABC transporters		nr -
Unigene22636_All	648	3.23	2.35	1.40	4.84	3.45	2.16	5.81	3.93	4.37	-4.61E-01	3.09E-01		-1.21E+00	1.09E-02		-4.88E-01	1.65E-01		-1.16E+00	9.08E-04	Down	-5.62E-01	4.85E-02		-4.12E-01	1.40E-01		Unigene22636_All//gi|108706753|gb|AB894548.1|//1.00E-31//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene22636_All//3.00E-41//AT1G49890| unknown protein	Unigene22636_All//0.00E+00//gi|109825988|gb|DW224709.1|DW224709				nr +
Unigene22637_All	1279	3.11	1.94	2.33	4.21	4.66	3.46	6.58	2.97	5.26	-6.80E-01	2.59E-02		-4.15E-01	2.11E-01		1.47E-01	5.94E-01		-2.82E-01	3.24E-01		-1.15E+00	5.45E-10	Down	-3.22E-01	7.04E-02		Unigene22637_All//gi|108706753|gb|AB894548.1|//1.00E-78//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene22637_All//3.00E-91//AT1G49890| unknown protein	Unigene22637_All//0.00E+00//TC149421				nr -
Unigene22638_All	2251	2.28	1.87	3.12	6.17	6.79	10.11	5.39	2.36	6.87	-2.86E-01	3.06E-01		4.55E-01	5.11E-02		1.38E-01	4.19E-01		7.12E-01	2.27E-10		-1.19E+00	6.19E-15	Down	3.49E-01	5.18E-03		Unigene22638_All//gi|297600512|ref|NP_001049317.2|//1.00E-88//Os03g0206100 [Oryza sativa Japonica Group] >gi|255674297|dbj|BAF11231.2|Os03g0206100 [Oryza sativa Japonica Group]	Unigene22638_All//2.00E-150//AT1G49890| unknown protein	Unigene22638_All//0.00E+00//TC146302				nr -
Unigene2264_All	614	1.53	3.47	1.91	2.11	2.47	4.93	7.64	7.28	5.19	1.18E+00	8.94E-03		3.15E-01	6.23E-01		2.26E-01	7.27E-01		1.22E+00	7.75E-04	Up	-6.96E-02	7.99E-01		-5.58E-01	2.02E-02		Unigene2264_All//gi|240256121|ref|NP_194990.4|//6.00E-31//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|240256123|ref|NP_001119101.4|protein binding / zinc ion binding [Arabidopsis thaliana] >gi|259016138|sp|Q9M081.2|SC24B_ARATH RecName: Full=Protein transport protein Sec24-like At4g32640	Unigene2264_All//3.00E-32//AT4G32640| protein binding / zinc ion binding	Unigene2264_All//0.00E+00//DT527084			GO:0006950//GO:0009536//GO:0012507//GO:0015031//GO:0046914//GO:0048193	nr -
Unigene22640_All	3082	0.56	2.86	1.12	2.65	2.72	2.14	5.02	2.83	3.15	2.35E+00	2.01E-22	Up	1.00E+00	3.98E-03		3.46E-02	8.91E-01		-3.09E-01	1.54E-01		-8.25E-01	1.30E-10		-6.71E-01	6.49E-08		Unigene22640_All//gi|115434984|ref|NP_001042250.1|//0.00E+00//Os01g0187400 [Oryza sativa Japonica Group] >gi|113531781|dbj|BAF04164.1|Os01g0187400 [Oryza sativa Japonica Group]	Unigene22640_All//0.00E+00//AT5G11700| glycine-rich protein	Unigene22640_All//4.00E-160//EE593111				nr +
Unigene22641_All	4664	0.70	5.50	2.15	3.62	5.12	3.24	4.39	3.19	3.37	2.98E+00	3.75E-83	Up	1.63E+00	2.63E-15	Up	5.01E-01	1.46E-06		-1.59E-01	3.11E-01		-4.60E-01	2.16E-05		-3.83E-01	3.09E-04		Unigene22641_All//gi|115434984|ref|NP_001042250.1|//0.00E+00//Os01g0187400 [Oryza sativa Japonica Group] >gi|113531781|dbj|BAF04164.1|Os01g0187400 [Oryza sativa Japonica Group]	Unigene22641_All//0.00E+00//AT5G11700| glycine-rich protein	Unigene22641_All//0.00E+00//EE593111		ko03040|Spliceosome		nr -
Unigene22643_All	1478	2.90	3.98	1.73	5.02	4.85	7.24	4.78	6.59	9.62	4.54E-01	6.68E-02		-7.47E-01	1.45E-02		-5.14E-02	8.17E-01		5.28E-01	2.24E-03		4.64E-01	4.92E-03		1.01E+00	8.44E-14	Up	Unigene22643_All//gi|18086381|gb|AAL57650.1|//1.00E-124//AT3g18790/WVE11_17 [Arabidopsis thaliana] >gi|19699138|gb|AAL90935.1|AT3g18790/WVE11_17 [Arabidopsis thaliana] >gi|227202802|dbj|BAH56874.1|AT3G18790 [Arabidopsis thaliana]	Unigene22643_All//1.00E-81//AT3G18790| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Isy1-like splicing (InterPro:IPR009360); Has 1075 Blast hits to 879 proteins in 176 species: Archae - 8; Bacteria - 11; Metazoa - 379; Fungi - 177; Plants - 27; Viruses - 9; Other Eukaryotes - 464 (source: NCBI BLink).	Unigene22643_All//0.00E+00//TC163036		ko03040|Spliceosome		nr -
Unigene22645_All	946	13.77	11.52	11.65	21.06	25.59	11.70	9.16	1.94	3.37	-2.58E-01	1.17E-01		-2.41E-01	1.61E-01		2.81E-01	1.06E-02		-8.49E-01	2.65E-12		-2.24E+00	1.53E-25	Down	-1.44E+00	8.12E-15	Down	Unigene22645_All//gi|222424070|dbj|BAH19995.1|//2.00E-54//AT4G28760 [Arabidopsis thaliana]	Unigene22645_All//4.00E-41//AT4G28760| unknown protein	Unigene22645_All//0.00E+00//gi|164304692|gb|ES808593.1|ES808593				nr +
Unigene22647_All	3768	14.15	10.37	9.53	24.13	28.34	14.50	9.49	2.63	4.70	-4.49E-01	4.68E-10		-5.71E-01	1.55E-14		2.32E-01	6.23E-07		-7.34E-01	3.05E-42		-1.85E+00	7.08E-81	Down	-1.01E+00	1.00E-33	Down	Unigene22647_All//gi|222424070|dbj|BAH19995.1|//0.00E+00//AT4G28760 [Arabidopsis thaliana]	Unigene22647_All//0.00E+00//AT4G28760| unknown protein	Unigene22647_All//0.00E+00//TC137304				nr -
Unigene22652_All	1045	1.60	0.78	0.82	3.86	2.97	2.94	10.48	3.68	4.50	-1.05E+00	4.04E-02		-9.75E-01	6.91E-02		-3.81E-01	2.25E-01		-3.94E-01	2.23E-01		-1.51E+00	4.21E-19	Down	-1.22E+00	1.79E-14	Down	Unigene22652_All//gi|224141943|ref|XP_002324320.1|//1.00E-117//type-b response regulator [Populus trichocarpa] >gi|222865754|gb|EEF02885.1| type-b response regulator [Populus trichocarpa]	Unigene22652_All//4.00E-88//AT2G25180| ARR12 (ARABIDOPSIS RESPONSE REGULATOR 12); transcription factor/ two-component response regulator	Unigene22652_All//0.00E+00//DR453553	ARR-B	ko04712|Circadian rhythm - plant		nr +
Unigene22653_All	2485	1.43	2.79	1.93	1.80	1.86	2.89	8.06	2.93	4.06	9.64E-01	1.93E-05		4.30E-01	1.43E-01		4.16E-02	9.06E-01		6.80E-01	1.65E-03		-1.46E+00	9.33E-33	Down	-9.92E-01	1.16E-18		Unigene22653_All//gi|224089346|ref|XP_002308698.1|//1.00E-166//type-b response regulator [Populus trichocarpa] >gi|222854674|gb|EEE92221.1| type-b response regulator [Populus trichocarpa]	Unigene22653_All//3.00E-85//AT2G25180| ARR12 (ARABIDOPSIS RESPONSE REGULATOR 12); transcription factor/ two-component response regulator	Unigene22653_All//0.00E+00//DW508344	ARR-B	ko04712|Circadian rhythm - plant		nr -
Unigene22654_All	2343	0.56	0.30	0.91	1.30	1.12	0.54	3.66	1.53	1.55	-8.83E-01	1.32E-01		7.03E-01	1.31E-01		-2.15E-01	5.87E-01		-1.26E+00	4.43E-04	Down	-1.26E+00	1.22E-11	Down	-1.24E+00	7.40E-12	Down	Unigene22654_All//gi|224089346|ref|XP_002308698.1|//1.00E-155//type-b response regulator [Populus trichocarpa] >gi|222854674|gb|EEE92221.1| type-b response regulator [Populus trichocarpa]	Unigene22654_All//7.00E-104//AT2G25180| ARR12 (ARABIDOPSIS RESPONSE REGULATOR 12); transcription factor/ two-component response regulator	Unigene22654_All//0.00E+00//DR453553	ARR-B	ko04712|Circadian rhythm - plant		nr +
Unigene22655_All	2339	1.70	1.39	0.71	3.15	2.09	1.68	14.73	4.72	3.83	-2.94E-01	3.69E-01		-1.27E+00	1.13E-04	Down	-5.92E-01	3.38E-03		-9.08E-01	1.70E-05		-1.64E+00	5.43E-66	Down	-1.94E+00	1.37E-85	Down	Unigene22655_All//gi|224141943|ref|XP_002324320.1|//1.00E-172//type-b response regulator [Populus trichocarpa] >gi|222865754|gb|EEF02885.1| type-b response regulator [Populus trichocarpa]	Unigene22655_All//9.00E-90//AT2G25180| ARR12 (ARABIDOPSIS RESPONSE REGULATOR 12); transcription factor/ two-component response regulator	Unigene22655_All//0.00E+00//DR453553	ARR-B	ko04712|Circadian rhythm - plant		nr +
Unigene22656_All	1239	7.05	3.56	3.61	0.60	1.03	2.73	3.31	4.93	23.76	-9.87E-01	6.87E-07		-9.66E-01	2.49E-06		7.70E-01	2.20E-01		2.18E+00	1.16E-08	Up	5.73E-01	7.36E-03		2.84E+00	1.32E-113	Up	Unigene22656_All//gi|297806091|ref|XP_002870929.1|//1.00E-147//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316766|gb|EFH47188.1|mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22656_All//2.00E-147//AT5G01340| mitochondrial substrate carrier family protein	Unigene22656_All//0.00E+00//TC145877				nr -
Unigene22657_All	2603	30.77	119.34	43.12	44.32	40.16	51.44	70.41	145.14	45.49	1.96E+00	0.00E+00	Up	4.87E-01	1.39E-22		-1.42E-01	2.68E-03		2.15E-01	6.97E-07		1.04E+00	0.00E+00	Up	-6.30E-01	3.12E-75		Unigene22657_All//gi|5802244|gb|AAD51625.1|AF169022_1//0.00E+00//seed maturation protein PM37 [Glycine max]	Unigene22657_All//2.00E-172//AT3G44110| ATJ3; protein binding	Unigene22657_All//0.00E+00//TC136321		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene22658_All	1003	5.84	31.32	8.28	15.55	18.44	23.73	11.30	14.46	9.21	2.42E+00	3.59E-81	Up	5.04E-01	1.68E-02		2.46E-01	6.51E-02		6.10E-01	2.14E-08		3.56E-01	7.65E-03		-2.94E-01	5.18E-02		Unigene22658_All//gi|15241456|ref|NP_196409.1|//1.00E-171//DGK1 (DIACYLGLYCEROL KINASE1); calcium ion binding / diacylglycerol kinase [Arabidopsis thaliana] >gi|20141593|sp|Q39017.2|DGK1_ARATH RecName: Full=Diacylglycerol kinase 1; Short=DAG kinase 1; AltName: Full=Diglyceride kinase 1; Short=DGK 1 >gi|6562306|emb|CAB62604.1|diacylglycerol kinase (ATDGK1) [Arabidopsis thaliana] >gi|10176726|dbj|BAB09956.1|diacylglycerol kinase ATDGK1 homolog [Arabidopsis thaliana]	Unigene22658_All//3.00E-168//AT5G07920| DGK1 (DIACYLGLYCEROL KINASE1); calcium ion binding / diacylglycerol kinase	Unigene22658_All//0.00E+00//gi|78335430|gb|DT555704.1|DT555704		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr -
Unigene22659_All	505	2.18	3.91	3.16	4.24	1.23	4.65	1.93	3.97	2.68	8.47E-01	6.71E-02		5.40E-01	3.30E-01		-1.79E+00	3.64E-05	Down	1.33E-01	7.61E-01		1.04E+00	1.10E-02		4.78E-01	3.55E-01		Unigene22659_All//gi|1374772|dbj|BAA09856.1|//1.00E-14//diacylglycerol kinase [Arabidopsis thaliana]	Unigene22659_All//6.00E-16//AT5G07920| DGK1 (DIACYLGLYCEROL KINASE1); calcium ion binding / diacylglycerol kinase	Unigene22659_All//0.00E+00//gi|78333226|gb|DT553500.1|DT553500		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr -
Unigene2266_All	1721	2.16	3.27	1.83	3.07	3.46	3.10	5.45	3.74	2.62	5.98E-01	1.72E-02		-2.42E-01	4.87E-01		1.74E-01	5.39E-01		1.33E-02	9.59E-01		-5.44E-01	1.12E-03		-1.06E+00	3.50E-10	Down	Unigene2266_All//gi|297800708|ref|XP_002868238.1|//1.00E-113//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314074|gb|EFH44497.1|mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2266_All//3.00E-98//AT4G15010| mitochondrial substrate carrier family protein	Unigene2266_All//0.00E+00//gi|21097161|gb|BQ409474.1|BQ409474			GO:0006810//GO:0016020	nr -
Unigene22661_All	2865	1.04	29.16	3.29	4.76	9.30	9.16	4.04	3.34	4.31	4.81E+00	0.00E+00	Up	1.66E+00	7.24E-15	Up	9.66E-01	1.05E-21		9.43E-01	8.10E-19		-2.76E-01	7.91E-02		9.22E-02	5.90E-01		Unigene22661_All//gi|15241456|ref|NP_196409.1|//0.00E+00//DGK1 (DIACYLGLYCEROL KINASE1); calcium ion binding / diacylglycerol kinase [Arabidopsis thaliana] >gi|20141593|sp|Q39017.2|DGK1_ARATH RecName: Full=Diacylglycerol kinase 1; Short=DAG kinase 1; AltName: Full=Diglyceride kinase 1; Short=DGK 1 >gi|6562306|emb|CAB62604.1|diacylglycerol kinase (ATDGK1) [Arabidopsis thaliana] >gi|10176726|dbj|BAB09956.1|diacylglycerol kinase ATDGK1 homolog [Arabidopsis thaliana]	Unigene22661_All//0.00E+00//AT5G07920| DGK1 (DIACYLGLYCEROL KINASE1); calcium ion binding / diacylglycerol kinase	Unigene22661_All//0.00E+00//gi|78335430|gb|DT555704.1|DT555704		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr -

Unigene22665_All	879	3.27	0.75	1.94	5.10	6.27	4.88	7.60	2.90	3.90	-2.13E+00	5.14E-07	Down	-7.56E-01	5.03E-02		2.97E-01	2.91E-01		-6.34E-02	8.46E-01		-1.39E+00	1.17E-10	Down	-9.63E-01	1.54E-06		Unigene22665_All//gi|145344920|ref|XP_001416972.1|//7.00E-12//NCS1 family transporter: cytosine/purines/uracil/thiamine/allantoin [Ostreococcus lucimarinus CE5901] >gi|144577198|gb|AB095265.1| NCS1 family transporter: cytosine/purines/uracil/thiamine/allantoin [Ostreococcus lucimarinus CE5901]	Unigene22665_All//1.00E-18//AT5G55820| unknown protein			ko03022|Basal transcription factors		nr -
Unigene22666_All	2651	0.69	0.23	0.08	2.16	1.65	1.98	4.85	1.96	2.01	-1.59E+00	1.79E-03		-3.10E+00	2.21E-06	Down	-3.89E-01	1.19E-01		-1.29E-01	6.53E-01		-1.31E+00	3.83E-18	Down	-1.27E+00	8.01E-18	Down	Unigene22666_All//gi|295831199|gb|ADG39268.1|//5.00E-11//AT5G55820-like protein [Capsella grandiflora]	Unigene22666_All//2.00E-46//AT5G55820| unknown protein			ko03040|Spliceosome		nr -
Unigene22667_All	3529	1.38	0.76	0.71	2.82	3.13	2.79	5.40	2.17	2.44	-8.57E-01	1.67E-03		-9.59E-01	7.86E-04		1.50E-01	4.59E-01		-1.71E-02	9.48E-01		-1.32E+00	9.30E-27	Down	-1.15E+00	2.31E-22	Down	Unigene22667_All//gi|295831201|gb|ADG39269.1|//7.00E-14//AT5G55820-like protein [Capsella grandiflora]	Unigene22667_All//7.00E-55//AT5G55820| unknown protein	Unigene22667_All//1.00E-160//DW235394		ko03040|Spliceosome		nr +
Unigene22668_All	2253	1.63	1.98	1.65	2.94	4.20	11.15	5.54	3.90	11.67	2.84E-01	3.55E-01		2.54E-02	9.55E-01		5.15E-01	4.22E-03		1.92E+00	3.89E-52	Up	-5.07E-01	3.74E-04		1.08E+00	2.38E-27	Up	Unigene22668_All//gi|15147869|dbj|BAB62845.1|//0.00E+00//Ndr kinase [Arabidopsis thaliana]	Unigene22668_All//0.00E+00//AT5G09890| protein kinase, putative	Unigene22668_All//0.00E+00//C0117524				nr +
Unigene2267_All	602	4.61	8.84	5.57	6.70	6.06	4.58	22.12	15.90	47.12	9.40E-01	3.23E-04		2.75E-01	4.44E-01		-1.45E-01	6.67E-01		-5.51E-01	7.41E-02		-4.77E-01	5.31E-04		1.09E+00	4.51E-30	Up	Unigene2267_All//gi|297727983|ref|NP_001176355.1|//2.00E-25//Os11g0150450 [Oryza sativa Japonica Group] >gi|255679794|dbj|BAH95083.1|Os11g0150450 [Oryza sativa Japonica Group]	Unigene2267_All//2.00E-15//AT4G10150| zinc finger (C3HC4-type RING finger) family protein	Unigene2267_All//0.00E+00//TC151362			GO:0031410//GO:0046872	nr +
Unigene22670_All	1269	3.30	1.08	0.92	3.85	4.42	3.45	1.93	0.59	0.60	-1.61E+00	4.84E-07	Down	-1.84E+00	7.35E-08	Down	2.01E-01	5.00E-01		-1.56E-01	6.42E-01		-1.70E+00	1.19E-05	Down	-1.70E+00	7.66E-06	Down	Unigene22670_All//gi|115450547|ref|NP_001048874.1|//1.00E-169//Os03g0133300 [Oryza sativa Japonica Group] >gi|113547345|dbj|BAF10788.1|Os03g0133300 [Oryza sativa Japonica Group]	Unigene22670_All//1.00E-177//AT1G42430| unknown protein	Unigene22670_All//0.00E+00//DW498257				nr +
Unigene22671_All	2617	30.77	45.79	25.50	21.03	71.53	73.52	15.67	32.31	38.09	5.74E-01	2.56E-33		-2.71E-01	6.19E-06		1.77E+00	0.00E+00	Up	1.81E+00	0.00E+00	Up	1.04E+00	4.18E-80	Up	1.28E+00	2.26E-133	Up	Unigene22671_All//gi|22758282|gb|AAN05510.1|//1.00E-175//Hypothetical protein [Oryza sativa Japonica Group] >gi|108706037|gb|ABF93832.1|expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene22671_All//0.00E+00//AT1G42430| unknown protein	Unigene22671_All//0.00E+00//gi|78332737|gb|DT553011.1|DT553011				nr -
Unigene22675_All	559	8.05	3.08	2.48	15.33	10.97	9.78	13.54	2.24	4.99	-1.39E+00	3.67E-06	Down	-1.70E+00	1.27E-07	Down	-4.83E-01	1.04E-02		-6.49E-01	8.03E-04		-2.59E+00	1.61E-26	Down	-1.44E+00	5.21E-13	Down	Unigene22675_All//gi|21536697|gb|AAM61029.1|//9.00E-35//ankyrin-like protein [Arabidopsis thaliana]	Unigene22675_All//5.00E-36//AT1G04430| dehydration-responsive protein-related	Unigene22675_All//0.00E+00//TC137071				nr +
Unigene22676_All	1123	7.36	1.99	3.60	15.39	10.61	9.57	19.88	2.12	6.70	-1.89E+00	3.02E-16	Down	-1.03E+00	1.27E-06	Down	-5.37E-01	1.27E-05		-6.85E-01	1.26E-07		-3.23E+00	2.14E-96	Down	-1.57E+00	1.73E-41	Down	Unigene22676_All//gi|21536697|gb|AAM61029.1|//1.00E-117//ankyrin-like protein [Arabidopsis thaliana]	Unigene22676_All//4.00E-107//AT1G04430| dehydration-responsive protein-related	Unigene22676_All//0.00E+00//TC137071				nr +
Unigene22677_All	2577	28.00	12.19	13.39	43.05	33.15	37.93	42.44	13.66	16.02	-1.20E+00	4.60E-70	Down	-1.06E+00	6.32E-56	Down	-3.77E-01	1.76E-17		-1.83E-01	1.84E-04		-1.64E+00	8.51E-207	Down	-1.41E+00	3.77E-170	Down	Unigene22677_All//gi|18414198|ref|NP_567427.1|//0.00E+00//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|79325109|ref|NP_001031639.1|dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75249435|sp|Q93YV7.1|PMT3_ARATH RecName: Full=Probable methyltransferase PMT3	Unigene22677_All//0.00E+00//AT4G14360| dehydration-responsive protein-related	Unigene22677_All//0.00E+00//TC146232				nr -
Unigene22681_All	1754	11.34	5.89	12.60	15.99	15.75	12.77	16.42	7.15	9.34	-9.44E-01	1.17E-13		1.53E-01	2.51E-01		-2.22E-02	8.57E-01		-3.24E-01	1.47E-03		-1.20E+00	1.26E-34	Down	-8.14E-01	3.38E-19		Unigene22681_All//gi|18424970|ref|NP_569013.1|//0.00E+00//peptidase M3 family protein / thimet oligopeptidase family protein [Arabidopsis thaliana]	Unigene22681_All//0.00E+00//AT5G65620| peptidase M3 family protein / thimet oligopeptidase family protein	Unigene22681_All//0.00E+00//TC141141				nr +
Unigene22692_All	2016	38.12	25.71	27.07	11.29	12.91	8.13	2.92	3.07	1.38	-5.68E-01	2.41E-21		-4.94E-01	4.89E-16		1.94E-01	8.50E-02		-4.74E-01	2.19E-05		7.38E-02	7.57E-01		-1.08E+00	7.62E-07	Down	Unigene22692_All//gi|225436223|ref|XP_002273602.1|//0.00E+00//PREDICTED: similar to SIGB (SIGMA FACTOR B); DNA binding / DNA-directed RNA polymerase/ transcription factor [Vitis vinifera]	Unigene22692_All//1.00E-115//AT1G08540| SIG2 (DNA POLYMERASE SIGMA SUBUNIT 2); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor	Unigene22692_All//0.00E+00//TC134562	Sigma70-like			nr -
Unigene22694_All	4266	5.95	2.55	3.58	4.75	4.27	6.73	5.57	2.91	5.58	-1.22E+00	9.56E-26	Down	-7.32E-01	6.63E-11		-1.54E-01	2.61E-01		5.03E-01	3.05E-07		-9.37E-01	1.84E-19		1.30E-03	9.89E-01		Unigene22694_All//gi|297852484|ref|XP_002894123.1|//0.00E+00//helicase domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297339965|gb|EFH70382.1|helicase domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene22694_All//0.00E+00//AT1G48650| helicase domain-containing protein	Unigene22694_All//0.00E+00//TC152226				nr +
Unigene22696_All	1459	23.02	2.01	11.13	0.82	0.59	0.31	0.06	0.14	0.03	-3.51E+00	4.20E-128	Down	-1.05E+00	1.16E-25	Down	-4.74E-01	4.58E-01		-1.40E+00	2.82E-02		1.30E+00	4.47E-01		-1.09E+00	6.76E-01		Unigene22696_All//gi|224112939|ref|XP_002332682.1|//1.00E-143//cytochrome P450 [Populus trichocarpa] >gi|222838808|gb|EEE77159.1|cytochrome P450 [Populus trichocarpa]	Unigene22696_All//2.00E-95//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene22696_All//9.00E-141//TC131128		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene22697_All	1019	0.00	0.00	0.00	0.59	0.61	4.21	1.87	10.62	3.01	null	null		null	null		5.24E-02	9.72E-01		2.84E+00	1.87E-14	Up	2.51E+00	3.66E-36	Up	6.89E-01	2.49E-02		Unigene22697_All//gi|224149471|ref|XP_002336813.1|//1.00E-73//cytochrome P450 [Populus trichocarpa] >gi|222836945|gb|EEE75338.1|cytochrome P450 [Populus trichocarpa]	Unigene22697_All//2.00E-46//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene22697_All//3.00E-146//TC131128		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene22698_All	1698	2.34	10.27	5.52	10.12	7.24	6.36	1.99	2.02	1.22	2.13E+00	8.03E-39	Up	1.24E+00	9.82E-10	Up	-4.83E-01	1.00E-04		-6.71E-01	2.49E-07		1.90E-02	9.84E-01		-7.07E-01	1.43E-02		Unigene22698_All//gi|224112939|ref|XP_002332682.1|//1.00E-167//cytochrome P450 [Populus trichocarpa] >gi|222838808|gb|EEE77159.1|cytochrome P450 [Populus trichocarpa]	Unigene22698_All//8.00E-121//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene22698_All//5.00E-180//DR462245		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene22699_All	1698	0.00	0.12	0.06	6.51	4.50	21.70	25.60	160.07	51.43	6.90E+00	1.36E-01		5.97E+00	3.99E-01		-5.33E-01	8.67E-04		1.74E+00	1.60E-66	Up	2.64E+00	0.00E+00	Up	1.01E+00	1.04E-79	Up	Unigene22699_All//gi|224112939|ref|XP_002332682.1|//1.00E-174//cytochrome P450 [Populus trichocarpa] >gi|222838808|gb|EEE77159.1|cytochrome P450 [Populus trichocarpa]	Unigene22699_All//3.00E-131//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene22699_All//0.00E+00//TC131128		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene227_All	1895	6.32	2.33	3.48	25.34	29.20	25.31	63.05	14.58	43.16	-1.44E+00	5.02E-16	Down	-8.60E-01	4.72E-07		2.05E-01	3.38E-03		-1.70E-03	9.82E-01		-2.11E+00	0.00E+00	Down	-5.47E-01	1.97E-38		Unigene227_All//gi|224066625|ref|XP_002302169.1|//0.00E+00//cellulose synthase [Populus trichocarpa] >gi|222843895|gb|EEE81442.1|cellulose synthase [Populus trichocarpa]	Unigene227_All//0.00E+00//AT4G39350| CESA2 (CELLULOSE SYNTHASE A2); cellulose synthase/ transferase, transferring glycosyl groups	Unigene227_All//0.00E+00//gi|48809797|gb|CO111111.1|CO111111				nr -
Unigene2270_All	2740	15.22	10.78	11.60	36.22	34.70	42.69	28.70	18.81	12.13	-4.97E-01	1.51E-09		-3.92E-01	4.10E-06		-6.17E-02	3.15E-01		2.37E-01	3.13E-07		-6.10E-01	4.21E-30		-1.24E+00	2.09E-101	Down	Unigene2270_All//gi|124359883|gb|AB006173.1|//4.00E-26//Transcriptional factor B3 [Medicago truncatula]	Unigene2270_All//2.00E-24//AT3G18990| VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor	Unigene2270_All//0.00E+00//TC167787	ABI3VP1			nr +
Unigene22701_All	2516	3.06	4.17	2.96	4.24	5.27	4.18	2.81	3.85	6.00	4.48E-01	1.18E-02		-4.50E-02	8.45E-01		3.15E-01	4.46E-02		-1.87E-02	9.41E-01		4.58E-01	5.70E-03		1.10E+00	1.48E-16	Up	Unigene22701_All//gi|145331109|ref|NP_001078046.1|//1.00E-143//FPA; RNA binding [Arabidopsis thaliana] >gi|145331111|ref|NP_001078047.1|FPA; RNA binding [Arabidopsis thaliana] >gi|145331113|ref|NP_001078048.1|FPA; RNA binding [Arabidopsis thaliana] >gi|290463421|sp|Q8LPQ9.2|FPA_ARATH RecName: Full=Flowering time control protein FPA	Unigene22701_All//2.00E-133//AT2G43410| FPA; RNA binding	Unigene22701_All//0.00E+00//CO095058				nr -
Unigene22704_All	1499	1.36	1.86	3.59	1.86	1.95	1.51	2.14	2.73	2.21	4.50E-01	2.34E-01		1.40E+00	6.03E-07	Up	6.93E-02	8.73E-01		-3.05E-01	4.67E-01		3.50E-01	2.23E-01		4.13E-02	9.11E-01		Unigene22704_All//gi|186519877|ref|NP_196001.2|//2.00E-30//carboxylesterase/ hydrolase, acting on ester bonds / lipase [Arabidopsis thaliana] >gi|75170264|sp|Q9FF70.1|GDL72_ARATH RecName: Full=GDSL esterase/lipase At5g03810; AltName: Full=Extracellular lipase At5g03810; Flags: Precursor >gi|9758010|dbj|BAB08607.1|proline-rich protein APG-like [Arabidopsis thaliana]	Unigene22704_All//9.00E-32//AT5G03810| carboxylesterase/ hydrolase, acting on ester bonds / lipase	Unigene22704_All//6.00E-170//gi|21091985|gb|BQ404298.1|BQ404298				nr -
Unigene22707_All	3404	2.15	3.86	4.58	6.70	9.37	5.43	4.78	4.17	5.24	8.41E-01	9.17E-08		1.09E+00	4.85E-13	Up	4.83E-01	4.64E-08		-3.05E-01	8.72E-03		-1.96E-01	1.44E-01		1.33E-01	3.06E-01		Unigene22707_All//gi|124359162|gb|ABN05685.1|//1.00E-111//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene22707_All//2.00E-26//AT4G29690| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene22707_All//0.00E+00//BF270759				nr +
Unigene22708_All	1809	1.53	8.12	6.12	6.97	9.16	17.68	9.79	4.00	8.79	2.41E+00	5.99E-38	Up	2.00E+00	3.10E-22	Up	3.94E-01	2.81E-03		1.34E+00	8.35E-40	Up	-1.29E+00	3.30E-24	Down	-1.56E-01	2.13E-01		Unigene22708_All//gi|115473401|ref|NP_001060299.1|//0.00E+00//Os07g0620300 [Oryza sativa Japonica Group] >gi|113611835|dbj|BAF22213.1|Os07g0620300 [Oryza sativa Japonica Group]	Unigene22708_All//0.00E+00//AT4G24550| clathrin adaptor complexes medium subunit family protein	Unigene22708_All//0.00E+00//TC164504				nr +
Unigene2271_All	1578	9.48	2.41	3.88	95.43	64.77	47.74	50.91	15.97	20.80	-1.98E+00	1.39E-30	Down	-1.29E+00	4.24E-16	Down	-5.59E-01	1.37E-48		-9.99E-01	1.39E-117		-1.67E+00	7.05E-157	Down	-1.29E+00	7.33E-110	Down	Unigene2271_All//gi|224085766|ref|XP_002307691.1|//0.00E+00//mtn21-like protein [Populus trichocarpa] >gi|222857140|gb|EEE94687.1|mtn21-like protein [Populus trichocarpa]	Unigene2271_All//3.00E-156//AT1G75500| nodulin MtN21 family protein	Unigene2271_All//0.00E+00//TC137784			GO:0044464	nr -
Unigene22715_All	1453	7.24	18.34	14.48	11.93	12.47	17.00	12.28	9.55	10.99	1.34E+00	4.77E-31	Up	1.00E+00	3.82E-15	Up	6.33E-02	7.11E-01		5.11E-01	1.69E-06		-3.63E-01	2.16E-03		-1.60E-01	2.00E-01		Unigene22715_All//gi|222423063|dbj|BAH19513.1|//9.00E-72//AT3G04240 [Arabidopsis thaliana]	Unigene22715_All//4.00E-73//AT3G04240| SEC (secret agent); transferase, transferring glycosyl groups	Unigene22715_All//0.00E+00//ES793997				nr -

Unigene22716_All	2183	10.14	26.41	21.05	16.13	17.15	28.20	24.58	24.95	20.79	1.38E+00	2.03E-69	Up	1.05E+00	2.62E-35	Up	8.79E-02	4.15E-01		8.06E-01	2.14E-33		2.15E-02	7.86E-01		-2.42E-01	1.44E-04		Unigene22716_All//gi|15229253|ref|NP_187074.1|//0.00E+00//SEC (secret agent); transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75336082|sp|Q9SE70.1|SEC_ARATH RecName: Full=Probable UDP-N-acetylglucosamine—peptide N-acetylglucosaminyltransferase SEC; AltName: Full=Protein SECRET AGENT >gi|18139887|gb|AAL60196.1|AF441079_1 O-linked N-acetyl glucosamine transferase [Arabidopsis thaliana] >gi|110742062|dbj|BAE98963.1| O-linked GlcNAc transferase like protein [Arabidopsis thaliana]	Unigene22716_All//0.00E+00//AT3G04240| SEC (secret agent); transferase, transferring glycosyl groups	Unigene22716_All//0.00E+00//TC151850				nr -
Unigene22717_All	1225	1.20	1.03	1.39	7.28	8.15	6.45	5.25	3.82	1.82	-2.10E-01	6.84E-01		2.18E-01	6.56E-01		1.63E-01	4.46E-01		-1.74E-01	4.42E-01		-4.57E-01	3.00E-02		-1.53E+00	4.17E-12	Down	Unigene22717_All//gi|297798030|ref|XP_002866899.1|//1.00E-112//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312735|gb|EFH43158.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22717_All//5.00E-113//AT4G39955| hydrolase, alpha/beta fold family protein	Unigene22717_All//0.00E+00//TC139638				nr -
Unigene22718_All	1436	22.48	40.01	62.45	4.09	4.20	9.25	4.30	7.22	6.80	8.32E-01	9.38E-31		1.47E+00	1.09E-115	Up	3.59E-02	9.06E-01		1.18E+00	8.84E-14	Up	7.48E-01	2.40E-06		6.61E-01	3.50E-05		Unigene22718_All//gi|297798030|ref|XP_002866899.1|//1.00E-113//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312735|gb|EFH43158.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22718_All//5.00E-114//AT4G39955| hydrolase, alpha/beta fold family protein	Unigene22718_All//2.00E-138//TC139638				nr -
Unigene22719_All	1788	3.57	7.00	11.88	0.59	0.67	1.31	1.89	1.73	2.18	9.71E-01	2.97E-09		1.73E+00	5.98E-35	Up	2.04E-01	8.01E-01		1.17E+00	5.81E-03		-1.29E-01	6.91E-01		2.07E-01	4.79E-01		Unigene22719_All//gi|145357815|ref|NP_196505.2|//2.00E-78//hydrolase [Arabidopsis thaliana] >gi|67633792|gb|AAY78820.1| hydrolase [Arabidopsis thaliana]	Unigene22719_All//1.00E-79//AT5G09430| hydrolase	Unigene22719_All//4.00E-128//TC139638				nr +
Unigene22720_All	2589	2.47	2.02	3.68	9.43	8.21	5.98	1.34	1.78	0.65	-2.91E-01	2.36E-01		5.79E-01	2.76E-03		-2.00E-01	8.24E-02		-6.56E-01	9.27E-10		4.07E-01	1.20E-01		-1.05E+00	2.88E-04	Down	Unigene22720_All//gi|297798030|ref|XP_002866899.1|//6.00E-91//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312735|gb|EFH43158.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22720_All//4.00E-92//AT4G39955| hydrolase, alpha/beta fold family protein	Unigene22720_All//0.00E+00//TC139638				nr -
Unigene22722_All	541	1.55	0.00	0.69	3.31	1.91	2.50	1.33	0.39	0.88	-1.06E+01	5.57E-05	Down	-1.17E+00	1.52E-01		-7.96E-01	8.93E-02		-4.05E-01	4.43E-01		-1.78E+00	2.79E-02		-5.88E-01	4.09E-01		Unigene22722_All//gi|145333717|ref|NP_001078426.1|//2.00E-20//ubiquitin thiolesterase/ zinc ion binding [Arabidopsis thaliana]	Unigene22722_All//6.00E-13//AT4G22285| ubiquitin thiolesterase/ zinc ion binding	Unigene22722_All//1.00E-85//TC157707		ko03040|Spliceosome	GO:0016787	nr +
Unigene22727_All	817	5.76	2.23	3.58	6.34	3.96	7.85	4.92	1.79	1.90	-1.37E+00	2.61E-06	Down	-6.85E-01	1.82E-02		-6.79E-01	6.07E-03		3.08E-01	2.27E-01		-1.46E+00	3.75E-07	Down	-1.37E+00	7.63E-07	Down	Unigene22727_All//gi|28200788|emb|CAD45375.1|//1.00E-88//potyviral helper component protease-interacting protein 2 [Solanum tuberosum subsp. andigena]	Unigene22727_All//2.00E-76//AT4G27060| TOR1 (TORTIFOLIA 1); microtubule binding	Unigene22727_All//0.00E+00//TC169095			GO:0000902//GO:0015631//GO:0016787//GO:0050879//GO:0055028	nr +
Unigene22728_All	2220	2.90	1.42	0.77	3.19	3.32	2.58	3.89	2.32	2.94	-1.03E+00	1.19E-05	Down	-1.92E+00	2.01E-12	Down	5.90E-02	8.22E-01		-3.02E-01	2.05E-01		-7.47E-01	2.07E-05		-4.01E-01	2.00E-02		Unigene22728_All//gi|42567178|ref|NP_194136.2|//1.00E-169//TOR1 (TORTIFOLIA 1); microtubule binding [Arabidopsis thaliana] >gi|83288274|sp|Q9T041.2|MAPT_ARATH RecName: Full=Microtubule-associated protein TORTIFOLIA1; AltName: Full=Microtubule-associated protein SPIRAL2; AltName: Full=Protein CONVOLUTA >gi|51870567|emb|CAC80696.2| TORTIFOLIA1 microtubule-associated protein [Arabidopsis thaliana] >gi|53791209|dbj|BAD54701.1| microtubule associated protein SPIRAL2 [Arabidopsis thaliana]	Unigene22728_All//6.00E-150//AT4G27060| TOR1 (TORTIFOLIA 1); microtubule binding	Unigene22728_All//0.00E+00//TC169095				nr +
Unigene22729_All	2340	4.74	3.14	2.71	5.64	5.65	3.22	7.55	1.84	2.13	-5.94E-01	4.84E-04		-8.08E-01	5.45E-06		2.40E-03	9.94E-01		-8.08E-01	9.74E-08		-2.04E+00	1.09E-45	Down	-1.83E+00	7.81E-41	Down	Unigene22729_All//gi|28200788|emb|CAD45375.1|//0.00E+00//potyviral helper component protease-interacting protein 2 [Solanum tuberosum subsp. andigena]	Unigene22729_All//9.00E-167//AT4G27060| TOR1 (TORTIFOLIA 1); microtubule binding	Unigene22729_All//0.00E+00//CO092484			GO:0000902//GO:0015631//GO:0050879//GO:0055028	nr -
Unigene2273_All	1269	2.56	5.23	5.75	11.31	11.72	4.98	1.17	0.99	1.22	1.03E+00	9.15E-06	Up	1.17E+00	3.98E-07	Up	5.23E-02	8.07E-01		-1.18E+00	3.55E-15	Down	-2.39E-01	6.20E-01		7.04E-02	8.93E-01		Unigene2273_All//gi|34925093|sp|P93788.1|REMO_SOLTU//1.00E-35//RecName: Full=Remorin; AltName: Full=pp34 >gi|1881585|gb|AAB49425.1| remorin [Solanum tuberosum]	Unigene2273_All//3.00E-15//AT5G23750| remorin family protein	Unigene2273_All//0.00E+00//gi|84164567|gb|DR453215.1|DR453215			GO:0007154//GO:0016020//GO:0043168//GO:0051234	nr +
Unigene22731_All	4081	8.91	4.67	3.46	4.38	3.59	3.39	9.33	6.73	18.07	-9.33E-01	7.13E-24		-1.37E+00	6.71E-42	Down	-2.89E-01	2.62E-02		-3.72E-01	4.54E-03		-4.72E-01	9.34E-10		9.53E-01	1.16E-61		Unigene22731_All//gi|253971327|gb|AC737432.1|//1.00E-178//type-1 phosphatidic acid phosphohydrolase 2 [Arabidopsis thaliana]	Unigene22731_All//1.00E-179//AT5G42870| lipin family protein	Unigene22731_All//0.00E+00//TC148394				nr -
Unigene22732_All	854	3.49	11.99	5.05	8.34	7.30	7.14	7.38	9.94	28.36	1.78E+00	2.70E-18	Up	5.32E-01	8.42E-02		-1.93E-01	4.35E-01		-2.25E-01	3.75E-01		4.30E-01	1.69E-02		1.94E+00	1.15E-59	Up	Unigene22732_All//gi|20269057|emb|CAC84709.1|//2.00E-63//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene22732_All//3.00E-34//AT4G28640| IAA11 (INDOLE-3-ACETIC ACID INDUCIBLE 11); transcription factor	Unigene22732_All//0.00E+00//TC142252			GO:0009725//GO:0009987	nr +
Unigene22733_All	905	1.33	2.07	2.65	4.13	2.47	2.05	2.52	2.72	6.52	6.40E-01	1.80E-01		9.94E-01	2.16E-02		-7.39E-01	1.37E-02		-1.01E+00	1.29E-03		1.11E-01	7.70E-01		1.37E+00	1.56E-09	Up	Unigene22733_All//gi|224107521|ref|XP_002314509.1|//2.00E-07//predicted protein [Populus trichocarpa] >gi|222863549|gb|EEF00680.1| predicted protein [Populus trichocarpa]	Unigene22733_All//0.00E+00//TC152524			GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr +
Unigene22734_All	1532	3.01	7.77	5.67	7.54	7.37	6.25	4.80	5.02	18.62	1.37E+00	9.93E-15	Up	9.15E-01	7.95E-06		-3.31E-02	8.60E-01		-2.72E-01	1.32E-01		6.40E-02	7.67E-01		1.96E+00	1.07E-70	Up	Unigene22734_All//gi|20269057|emb|CAC84709.1|//5.00E-72//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene22734_All//8.00E-38//AT4G28640| IAA11 (INDOLE-3-ACETIC ACID INDUCIBLE 11); transcription factor	Unigene22734_All//0.00E+00//TC142252			GO:0003002//GO:0005515//GO:0009725//GO:0009790//GO:0009987//GO:0010467//GO:0030528//GO:0048513	nr -
Unigene22735_All	3810	3.58	2.55	2.17	8.46	6.05	4.45	9.54	3.38	3.20	-4.89E-01	1.29E-03		-7.26E-01	4.02E-06		-4.84E-01	2.25E-08		-9.28E-01	1.19E-22		-1.50E+00	6.44E-61	Down	-1.58E+00	1.45E-67	Down	Unigene22735_All//gi|7269720|emb|CAB81453.1|//0.00E+00//receptor protein kinase-like protein [Arabidopsis thaliana] >gi|224589634|gb|ACN59350.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene22735_All//0.00E+00//AT4G28650| leucine-rich repeat transmembrane protein kinase, putative	Unigene22735_All//0.00E+00//gi|109884107|gb|DW513077.1|DW513077			GO:0004672//GO:0005488//GO:0031410	nr -
Unigene22736_All	1567	22.84	9.51	17.64	21.97	20.88	14.84	7.07	3.49	3.05	-1.26E+00	4.55E-38	Down	-3.73E-01	5.88E-05		-7.34E-02	5.31E-01		-5.66E-01	1.68E-10		-1.02E+00	8.99E-11	Down	-1.21E+00	1.71E-14	Down	Unigene22736_All//gi|18424871|ref|NP_568996.1|//1.00E-146//LIP1 (Light Insensitive Period1); GTPase [Arabidopsis thaliana] >gi|29839609|sp|Q9C5J9.1|Y5483_ARATH RecName: Full=Uncharacterized GTP-binding protein At5g64813	Unigene22736_All//5.00E-119//AT5G64813| LIP1 (Light Insensitive Period1); GTPase	Unigene22736_All//0.00E+00//gi|21094765|gb|BQ407078.1|BQ407078				nr +
Unigene22738_All	5424	6.08	3.83	4.48	11.79	12.09	8.12	10.87	5.02	6.21	-6.66E-01	1.71E-12		-4.41E-01	4.92E-06		3.57E-02	6.75E-01		-5.39E-01	1.98E-17		-1.11E+00	2.25E-62	Down	-8.09E-01	5.88E-38		Unigene22738_All//gi|115473349|ref|NP_001060273.1|//4.00E-98//Os07g0616000 [Oryza sativa Japonica Group] >gi|113611809|dbj|BAF22187.1| Os07g0616000 [Oryza sativa Japonica Group]	Unigene22738_All//8.00E-108//AT3G14172| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: COP1-interacting protein-related (TAIR:AT1G72410.1); Has 2665 Blast hits to 1956 proteins in 215 species: Archae - 2; Bacteria - 189; Metazoa - 878; Fungi - 141; Plants - 132; Viruses - 5; Other Eukaryotes - 1318 (source: NCBI BLink).	Unigene22738_All//0.00E+00//TC173525				nr +
Unigene22739_All	905	3.01	0.95	2.18	4.90	4.26	2.74	1.54	0.51	1.14	-1.66E+00	5.09E-05	Down	-4.66E-01	2.47E-01		-2.01E-01	5.49E-01		-8.36E-01	3.23E-03		-1.60E+00	2.61E-03		-4.30E-01	3.86E-01		Unigene22739_All//gi|75334257|sp|Q9FRL3.1|ERDL6_ARATH//1.00E-68//RecName: Full=Sugar transporter ERD6-like 6 >gi|15724240|gb|AAL06513.1|AF412060_1 At1g75220/F22H5_6 [Arabidopsis thaliana] >gi|21700861|gb|AAM70554.1| At1g75220/F22H5_6 [Arabidopsis thaliana]	Unigene22739_All//5.00E-58//AT1G75220| integral membrane protein, putative	Unigene22739_All//0.00E+00//gi|54119024|gb|CO494533.1|CO494533			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr -
Unigene22740_All	1631	2.50	0.62	1.31	1.62	2.32	1.63	5.24	1.82	2.27	-2.01E+00	5.04E-09	Down	-9.38E-01	3.00E-03		5.21E-01	1.04E-01		1.33E-02	9.73E-01		-1.53E+00	2.79E-15	Down	-1.20E+00	2.82E-11	Down	Unigene22740_All//gi|1209756|gb|AAB53155.1|//0.00E+00//integral membrane protein [Beta vulgaris]	Unigene22740_All//0.00E+00//AT1G75220| integral membrane protein, putative	Unigene22740_All//0.00E+00//TC152037			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr -
Unigene22741_All	1798	5.70	17.64	7.94	4.10	5.98	5.22	5.27	3.98	3.86	1.63E+00	6.56E-49	Up	4.77E-01	2.04E-03		5.43E-01	1.05E-03		3.50E-01	7.45E-02		-4.06E-01	1.64E-02		-4.50E-01	5.52E-03		Unigene22741_All//gi|75334257|sp|Q9FRL3.1|ERDL6_ARATH//0.00E+00//RecName: Full=Sugar transporter ERD6-like 6 >gi|15724240|gb|AAL06513.1|AF412060_1 At1g75220/F22H5_6 [Arabidopsis thaliana] >gi|21700861|gb|AAM70554.1| At1g75220/F22H5_6 [Arabidopsis thaliana]	Unigene22741_All//0.00E+00//AT1G75220| integral membrane protein, putative	Unigene22741_All//0.00E+00//TC173761			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr +
Unigene22744_All	1616	4.01	17.15	6.23	5.09	6.20	9.89	11.15	15.13	29.31	2.09E+00	4.85E-60	Up	6.34E-01	6.99E-04		2.86E-01	1.35E-01		9.60E-01	5.06E-12		4.41E-01	7.13E-06		1.40E+00	1.40E-72	Up	Unigene22744_All//gi|9279693|dbj|BAB01250.1|//1.00E-161//kinase-like protein [Arabidopsis thaliana]	Unigene22744_All//3.00E-157//AT3G22750| protein kinase, putative	Unigene22744_All//0.00E+00//gi|109865723|gb|DW494699.1|DW494699				nr +
Unigene22745_All	2042	30.49	15.26	25.61	41.81	44.20	34.53	10.83	5.18	5.89	-9.99E-01	3.81E-45		-2.52E-01	3.08E-04		8.01E-02	2.05E-01		-2.76E-01	4.27E-07		-1.06E+00	3.05E-22	Down	-8.78E-01	6.96E-17		Unigene22745_All//gi|9279693|dbj|BAB01250.1|//1.00E-163//kinase-like protein [Arabidopsis thaliana]	Unigene22745_All//1.00E-164//AT3G22750| protein kinase, putative	Unigene22745_All//0.00E+00//TC132657				nr +

Unigene22749_All	1126	1.30	4.90	4.97	6.24	5.93	5.33	4.43	1.71	5.17	1.91E+00	3.47E-11	Up	1.93E+00	5.11E-11	Up	-7.23E-02	8.08E-01		-2.26E-01	3.76E-01		-1.38E+00	4.81E-08	Down	2.21E-01	3.46E-01		Unigene22749_All//gi|297839541|ref|XP_002887652.1|//1.00E-112//tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333493|gb|EFH63911.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene22749_All//2.00E-105//AT1G76630| tetratricopeptide repeat (TPR)-containing protein	Unigene22749_All//0.00E+00//TC135613		ko03018|RNA degradation		nr -
Unigene22751_All	2210	14.02	7.84	6.14	15.98	13.28	11.10	23.49	17.19	48.71	-8.38E-01	3.44E-17		-1.19E+00	6.04E-29	Down	-2.68E-01	2.07E-03		-5.26E-01	1.61E-09		-4.51E-01	5.46E-12		1.05E+00	2.39E-105	Up	Unigene22751_All//gi|11132838|sp|O64967.1|HMDR2_GOSHI//0.00E+00//Rec Name: Full=3-hydroxy-3-methylglutaryl-coenzyme A reductase 2; Short=HMG-CoA reductase 2 >gi|2935300|gb|AAC05089.1| 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 [Gossypium hirsutum]	Unigene22751_All//0.00E+00//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene22751_All//0.00E+00//TC140749		ko00900|Terpenoid backbone biosynthesis	GO:0000166//GO:0005740//GO:0006720//GO:0006732//GO:0009526//GO:0016616//GO:0031090//GO:0031224//GO:0048037	nr -
Unigene22752_All	2108	5.36	41.70	16.80	5.77	5.05	7.18	10.55	32.52	25.66	2.96E+00	5.08E-282	Up	1.65E+00	6.24E-54	Up	-1.92E-01	2.91E-01		3.16E-01	3.39E-02		1.62E+00	3.56E-128	Up	1.28E+00	7.19E-73	Up	Unigene22752_All//gi|67483357|gb|AY68034.1|//0.00E+00//3-hydroxy-methylglutaryl coenzyme A reductase [Tilia miqueliana]	Unigene22752_All//0.00E+00//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene22752_All//0.00E+00//TC147118		ko00900|Terpenoid backbone biosynthesis	GO:0000166//GO:0005740//GO:0006720//GO:0006732//GO:0009526//GO:0016616//GO:0031090//GO:0031224//GO:0048037	nr +
Unigene22755_All	1964	1.04	3.69	3.61	3.78	5.87	6.81	10.81	10.90	15.66	1.83E+00	1.25E-13	Up	1.80E+00	1.48E-12	Up	6.36E-01	5.36E-05		8.49E-01	2.23E-08		1.18E-02	9.47E-01		5.35E-01	3.69E-10		Unigene22755_All//gi|22655246|gb|AAM88213.1|//1.00E-149//protein kinase ATN1-like protein [Arabidopsis thaliana] >gi|25084113|gb|AAN72179.1| protein kinase ATN1-like protein [Arabidopsis thaliana]	Unigene22755_All//2.00E-150//AT5G01850| protein kinase, putative	Unigene22755_All//0.00E+00//gi|164331811|gb|ES840586.1|ES840586				nr +
Unigene2276_All	2202	7.10	3.06	3.53	15.11	9.01	11.40	13.86	12.22	3.22	-1.22E+00	4.59E-16	Down	-1.01E+00	1.49E-11	Down	-7.47E-01	3.17E-18		-4.06E-01	7.47E-06		-1.82E-01	5.24E-02		-2.11E+00	2.59E-84	Down	Unigene2276_All//gi|224365621|ref|YP_002608349.1|//3.00E-98//orf185 [Vitis vinifera] >gi|209954145|emb|CAQ77575.1| orf185 [Vitis vinifera] >gi|239764756|gb|ACS15226.1| 00F185 [Vitis vinifera]	Unigene2276_All//6.00E-11//ATMG00510| NADH dehydrogenase subunit 7	Unigene2276_All//0.00E+00//TC134352		ko00190|Oxidative phosphorylation	GO:0000166//GO:0006091//GO:0016491//GO:0043231//GO:0048037	nr +
Unigene22764_All	591	5.58	4.12	2.88	4.47	2.56	4.74	15.31	13.51	6.54	-4.39E-01	2.10E-01		-9.52E-01	7.85E-03		-8.01E-01	3.00E-02		8.49E-02	8.43E-01		-1.81E-01	3.61E-01		-1.23E+00	3.22E-12	Down			Unigene22764_All//6.00E-177//TC145370				
Unigene22765_All	1078	20.19	12.13	20.25	19.55	16.87	18.77	38.36	17.41	20.55	-7.36E-01	5.44E-10		4.40E-03	9.97E-01		-2.13E-01	8.65E-02		-5.86E-02	7.04E-01		-1.14E+00	1.38E-45	Down	-9.01E-01	4.31E-32		Unigene22765_All//gi|162464059|ref|NP_001104914.1|//1.00E-117//pyruvate dehydrogenase2 [Zea mays] >gi|385899|gb|AAC72192.1| pyruvate dehydrogenase E1 beta subunit isoform 1 [Zea mays]	Unigene22765_All//6.00E-116//AT5G50850| MAB1 (MACCI-BOU): catalytic/ pyruvate dehydrogenase (acetyl-transferring)	Unigene22765_All//0.00E+00//TC149969		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)//ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis		nr -
Unigene22768_All	2167	4.61	2.90	1.28	9.29	4.39	8.29	12.57	6.87	7.08	-6.70E-01	2.10E-04		-1.85E+00	3.79E-18	Down	-1.08E+00	1.03E-20	Down	-1.63E-01	2.41E-01		-8.72E-01	9.54E-20		-8.28E-01	1.05E-18		Unigene22768_All//gi|75328082|sp|Q84T03.1|RH27_ORYSJ//0.00E+00//RecN ame: Full=DEAD-box ATP-dependent RNA helicase 27	Unigene22768_All//0.00E+00//AT3G18600| DEAD/DEAH box helicase, putative	Unigene22768_All//0.00E+00//TC169797			GO:0031981//GO:0032559//GO:0042623	nr +
Unigene22770_All	739	5.66	3.36	9.73	3.77	4.15	3.12	7.09	4.47	36.60	-7.54E-01	1.10E-02		7.80E-01	5.77E-04		1.36E-01	7.69E-01		-2.76E-01	5.03E-01		-6.67E-01	4.09E-03		2.37E+00	3.66E-85	Up	Unigene22770_All//gi|224057862|ref|XP_002299361.1|//5.00E-57//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene22770_All//9.00E-54//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene22770_All//6.00E-17//ES827343			GO:0000902//GO:0009536//GO:0009581//GO:0009755//GO:0016881//GO:0032787//GO:0042742//GO:0048878	nr +
Unigene22771_All	2019	3.24	0.00	0.00	9.13	2.83	2.08	3.48	0.99	2.21	-1.17E+01	6.57E-38	Down	-1.17E+01	3.30E-36	Down	-1.69E+00	1.31E-37	Down	-2.13E+00	7.28E-45	Down	-1.81E+00	6.11E-16	Down	-6.54E-01	6.18E-04		Unigene22771_All//gi|224057862|ref|XP_002299361.1|//1.00E-173//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene22771_All//2.00E-147//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene22771_All//7.00E-56//CO097810				nr +
Unigene22772_All	2015	7.01	3.07	2.99	3.39	1.93	1.43	7.39	5.58	27.58	-1.19E+00	3.56E-14	Down	-1.23E+00	3.19E-14	Down	-8.11E-01	9.68E-05		-1.24E+00	4.43E-08	Down	-4.05E-01	1.89E-03		1.90E+00	5.15E-132	Up	Unigene22772_All//gi|224057862|ref|XP_002299361.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene22772_All//9.00E-174//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene22772_All//3.00E-52//CO097810				nr +
Unigene22777_All	1871	11.21	23.80	16.02	25.03	20.52	23.87	21.47	22.29	13.99	1.09E+00	4.90E-37	Up	5.15E-01	3.76E-07		-2.86E-01	8.38E-05		-6.81E-02	4.81E-01		5.45E-02	5.70E-01		-6.18E-01	1.26E-16		Unigene22777_All//gi|226500876|ref|NP_001149790.1|//0.00E+00//LOC100283417 [Zea mays] >gi|195634685|gb|ACG36811.1| peptidyl-prolyl isomerase [Zea mays]	Unigene22777_All//0.00E+00//AT3G25230| ROF1 (ROTAMASE FKBP 1); FK506 binding / calmodulin binding / peptidyl-prolyl cis-trans isomerase	Unigene22777_All//0.00E+00//TC141230			GO:0003824//GO:0005515//GO:0005527//GO:0006950//GO:0010038//GO:0043231//GO:0044267	nr +
Unigene22778_All	2119	5.85	23.82	7.59	13.78	11.99	16.52	7.04	34.79	4.64	2.03E+00	3.23E-104	Up	3.75E-01	1.05E-02		-2.00E-01	5.20E-02		2.62E-01	4.46E-03		2.30E+00	1.45E-219	Up	-6.01E-01	1.83E-06		Unigene22778_All//gi|226500876|ref|NP_001149790.1|//0.00E+00//LOC100283417 [Zea mays] >gi|195634685|gb|ACG36811.1| peptidyl-prolyl isomerase [Zea mays]	Unigene22778_All//0.00E+00//AT3G25230| ROF1 (ROTAMASE FKBP 1); FK506 binding / calmodulin binding / peptidyl-prolyl cis-trans isomerase	Unigene22778_All//0.00E+00//TC135788			GO:0005515//GO:0005527//GO:0006950//GO:0010038//GO:0016859//GO:0043231//GO:0044267	nr +
Unigene22779_All	599	4.89	2.54	3.38	3.49	7.13	4.00	2.12	1.67	3.92	-9.47E-01	9.80E-03		-5.34E-01	1.65E-01		1.03E+00	2.90E-04	Up	1.94E-01	6.79E-01		-3.39E-01	5.58E-01		8.90E-01	1.34E-02		Unigene22779_All//gi|297795621|ref|XP_002865695.1|//2.00E-28//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311530|gb|EFH41954.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22779_All//1.00E-29//AT5G48970| mitochondrial substrate carrier family protein	Unigene22779_All//8.00E-50//DW505809			GO:0019866//GO:0031224//GO:0046907	nr +
Unigene22783_All	818	3.01	0.68	5.53	2.98	2.44	2.98	1.14	0.82	2.53	-2.14E+00	3.81E-06	Down	8.80E-01	2.99E-03		-2.89E-01	5.21E-01		-1.30E-03	9.93E-01		-4.76E-01	4.76E-01		1.16E+00	3.38E-03		Unigene22783_All//gi|15239754|ref|NP_199708.1|//1.00E-49//mitochondrial substrate carrier family protein [Arabidopsis thaliana] >gi|10177187|dbj|BAB10321.1| mitochondrial carrier protein-like [Arabidopsis thaliana] >gi|30017309|gb|AAP12888.1| At5g48970 [Arabidopsis thaliana]	Unigene22783_All//2.00E-44//AT5G48970| mitochondrial substrate carrier family protein	Unigene22783_All//0.00E+00//DW488429			GO:0019866//GO:0031224//GO:0046907	nr -
Unigene22784_All	1292	4.05	1.45	2.18	2.39	1.84	2.17	3.80	2.33	2.99	-1.48E+00	1.09E-07	Down	-8.91E-01	1.12E-03		-3.78E-01	3.11E-01		-1.41E-01	7.01E-01		-7.05E-01	3.50E-03		-3.44E-01	1.56E-01		Unigene22784_All//gi|15239754|ref|NP_199708.1|//1.00E-152//mitochondrial substrate carrier family protein [Arabidopsis thaliana] >gi|10177187|dbj|BAB10321.1| mitochondrial carrier protein-like [Arabidopsis thaliana] >gi|30017309|gb|AAP12888.1| At5g48970 [Arabidopsis thaliana]	Unigene22784_All//6.00E-143//AT5G48970| mitochondrial substrate carrier family protein	Unigene22784_All//0.00E+00//DW505809			GO:0016020	nr +
Unigene22785_All	1626	0.16	0.53	0.88	0.46	0.40	0.92	1.51	0.72	1.35	1.72E+00	3.49E-02		2.46E+00	3.26E-04	Up	-1.91E-01	8.21E-01		9.96E-01	7.46E-02		-1.07E+00	3.41E-03		-1.62E-01	6.47E-01		Unigene22785_All//gi|15239754|ref|NP_199708.1|//1.00E-154//mitochondrial substrate carrier family protein [Arabidopsis thaliana] >gi|10177187|dbj|BAB10321.1| mitochondrial carrier protein-like [Arabidopsis thaliana] >gi|30017309|gb|AAP12888.1| At5g48970 [Arabidopsis thaliana]	Unigene22785_All//1.00E-155//AT5G48970| mitochondrial substrate carrier family protein	Unigene22785_All//0.00E+00//gi|84172800|gb|DR461448.1|DR461448			GO:0006810//GO:0016020	nr +
Unigene22786_All	2016	14.35	14.38	15.50	30.99	27.36	23.95	28.59	19.14	12.05	2.50E-03	9.80E-01		1.12E-01	3.35E-01		-1.79E-01	6.45E-03		-3.72E-01	6.67E-09		-5.79E-01	2.21E-20		-1.25E+00	8.80E-75	Down	Unigene22786_All//gi|33945873|emb|CAE45585.1|//0.00E+00//coatomer alpha subunit-like protein [Lotus japonicus]	Unigene22786_All//0.00E+00//AT2G21390| coatomer protein complex, subunit alpha, putative	Unigene22786_All//0.00E+00//TC136284			GO:0004683//GO:0005488//GO:0015031//GO:0030120//GO:0031461//GO:0048193	nr -
Unigene22787_All	2942	9.21	7.77	5.32	19.30	17.02	14.83	24.34	15.44	9.89	-2.46E-01	2.25E-02		-7.92E-01	3.25E-13		-1.82E-01	9.10E-03		-3.80E-01	1.75E-08		-6.57E-01	2.97E-31		-1.30E+00	4.07E-99	Down	Unigene22787_All//gi|164605514|dbj|BAF98580.1|//0.00E+00//CM0216.440.nc [Lotus japonicus]	Unigene22787_All//0.00E+00//AT1G62020| coatomer protein complex, subunit alpha, putative	Unigene22787_All//0.00E+00//TC138546			GO:0004683//GO:0005488//GO:0015031//GO:0030120//GO:0031461//GO:0048193	nr -
Unigene22788_All	801	4.96	7.72	6.12	4.60	7.57	4.17	2.16	0.94	0.40	6.37E-01	7.35E-03		3.01E-01	3.15E-01		7.17E-01	1.87E-03		-1.41E-01	7.05E-01		-1.20E+00	7.57E-03		-2.44E+00	1.80E-06	Down	Unigene22788_All//gi|87240442|gb|AB032300.1|//6.00E-68//TGF-beta receptor, type I/II extracellular region [Medicago truncatula]	Unigene22788_All//5.00E-58//AT3G16180| proton-dependent oligopeptide transport (POT) family protein	Unigene22788_All//3.00E-90//ES817506			GO:0006810//GO:0016020	nr +
Unigene22789_All	1996	1.76	1.52	1.33	1.02	0.76	0.32	9.43	3.46	2.26	-2.06E-01	5.61E-01		-3.97E-01	2.58E-01		-4.31E-01	3.48E-01		-1.69E+00	3.48E-04	Down	-1.45E+00	2.35E-30	Down	-2.06E+00	6.26E-51	Down	Unigene22789_All//gi|297834490|ref|XP_002885127.1|//1.00E-161//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330967|gb|EFH61386.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22789_All//3.00E-152//AT1G52190| proton-dependent oligopeptide transport (POT) family protein	Unigene22789_All//5.00E-97//ES817506				nr -
Unigene22790_All	3592	2.69	3.27	3.54	4.96	6.38	3.22	1.07	0.33	0.08	2.80E-01	1.05E-01		3.95E-01	1.82E-02		3.63E-01	9.07E-04		-6.25E-01	9.10E-07		-1.72E+00	1.63E-08	Down	-3.79E+00	3.35E-20	Down	Unigene22790_All//gi|224092304|ref|XP_002309850.1|//1.00E-156//glycosyl transferase [Populus trichocarpa] >gi|222855526|gb|EEE93073.1| glycosyl transferase [Populus trichocarpa]	Unigene22790_All//1.00E-137//AT1G52190| proton-dependent oligopeptide transport (POT) family protein	Unigene22790_All//0.00E+00//ES817506				nr -
Unigene22794_All	731	1.15	1.66	1.89	3.07	3.30	2.84	1.74	2.69	3.81	5.39E-01	3.76E-01		7.26E-01	2.28E-01		1.05E-01	8.24E-01		-1.10E-01	8.00E-01		6.31E-01	1.35E-01		1.14E+00	6.21E-04	Up			Unigene22794_All//6.00E-48//TC160781				
Unigene22796_All	3056	2.05	1.71	3.28	5.67	4.71	3.46	3.09	4.84	14.70	-2.67E-01	2.82E-01		6.73E-01	3.27E-04		-2.68E-01	4.53E-02		-7.14E-01	3.65E-08		6.50E-01	5.42E-07		2.25E+00	7.42E-133	Up	Unigene22796_All//gi|4160292|emb|CAA77084.1|//0.00E+00//alpha-N-acetylglucosaminidase [Nicotiana tabacum]	Unigene22796_All//0.00E+00//AT5G13690| alpha-N-acetylglucosaminidase family / NAGLU family	Unigene22796_All//0.00E+00//TC134398		ko00531|Glycosaminoglycan degradation	GO:0031410	nr +
Unigene22797_All	4517	0.94	0.84	1.14	0.89	1.14	1.85	1.28	4.75	18.25	-1.57E-01	6.04E-01		2.86E-01	3.30E-01		3.56E-01	2.04E-01		1.05E+00	1.59E-07	Up	1.89E+00	6.49E-50	Up	3.83E+00	0.00E+00	Up	Unigene22797_All//gi|297807393|ref|XP_002871580.1|//0.00E+00//alpha-N-acetylglucosaminidase family [Arabidopsis lyrata subsp. lyrata] >gi|297317417|gb|EFH47839.1| alpha-N-acetylglucosaminidase family [Arabidopsis lyrata subsp. lyrata]	Unigene22797_All//0.00E+00//AT5G13690| alpha-N-acetylglucosaminidase family / NAGLU family	Unigene22797_All//0.00E+00//TC134398		ko00531|Glycosaminoglycan degradation	GO:0008152//GO:0016647//GO:0016798//GO:0031410	nr -
Unigene228_All	2537	27.06	25.01	38.66	97.49	161.06	140.26	72.14	19.67	66.33	-1.14E-01	9.95E-02		5.15E-01	6.97E-22		7.24E-01	5.62E-203		5.25E-01	1.19E-89		-1.87E+00	0.00E+00	Down	-1.21E-01	3.51E-04		Unigene228_All//gi|224066625|ref|XP_002302169.1|//0.00E+00//cellulose synthase [Populus trichocarpa] >gi|222843895|gb|EEE81442.1| cellulose synthase [Populus trichocarpa]	Unigene228_All//0.00E+00//AT5G64740| CESA6 (CELLULOSE SYNTHASE 6); cellulose synthase/ transferase, transferring glycosyl groups	Unigene228_All//0.00E+00//TC170744				nr +

Unigene22801_All	2085	5.52	2.60	3.68	6.43	6.80	6.35	7.62	3.33	4.51	-1.09E+00	3.54E-10	Down	-5.86E-01	7.31E-04		8.24E-02	6.49E-01		-1.81E-02	9.36E-01		-1.20E+00	2.12E-19	Down	-7.58E-01	7.99E-10		Unigene22801_All//gi|193104969|gb|AAL84969.1|//1.00E-144//AT5g20600/F7C8_190 [Arabidopsis thaliana] >gi|28416463|gb|AAO42762.1| At5g20600/F7C8_190 [Arabidopsis thaliana]	Unigene22801_All//1.00E-121//AT5G20600| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: rRNA processing; LOCATED IN: preribosome, small subunit precursor; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nucleolar, Nop52 (InterPro:IPR010301); Has 444 Blast hits to 431 proteins in 151 species: Archae - 0; Bacteria - 10; Metazoa - 196; Fungi - 114; Plants - 27; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink).	Unigene22801_All//0.00E+00//C0117186				nr +
Unigene22802_All	4797	1.97	0.91	0.85	5.60	5.37	3.45	6.63	1.66	2.57	-1.12E+00	6.63E-09	Down	-1.21E+00	1.82E-09	Down	-5.99E-02	6.35E-01		-7.00E-01	6.88E-12		-1.99E+00	2.30E-79	Down	-1.36E+00	7.81E-48	Down	Unigene22802_All//gi|15240200|ref|NP_201511.1|//0.00E+00//ICU2 (INCURVATA2); DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|75170581|sp|Q9FHA3.1|DPOLA_ARATH RecName: Full=DNA polymerase alpha catalytic subunit >gi|10177597|dbj|BAB10944.1| DNA polymerase alpha 1 [Arabidopsis thaliana]	Unigene22802_All//0.00E+00//AT5G67100| ICU2 (INCURVATA2); DNA-directed DNA polymerase	Unigene22802_All//0.00E+00//TC154637		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03030|DNA replication	GO:0003676//GO:0003899//GO:0004527//GO:0006271//GO:0009887//GO:0009908//GO:0034061//GO:0043231	nr +
Unigene22804_All	2615	1.46	3.53	2.44	4.95	4.65	5.15	6.08	9.24	8.64	1.27E+00	2.12E-10	Up	7.42E-01	2.17E-03		-9.15E-02	6.12E-01		5.54E-02	7.56E-01		6.04E-01	1.17E-09		5.07E-01	4.62E-07		Unigene22804_All//gi|225434110|ref|XP_002273984.1|//0.00E+00//PREDICTED: similar to C2 domain-containing protein / GRAM domain-containing protein [Vitis vinifera]	Unigene22804_All//0.00E+00//AT3G59660| C2 domain-containing protein / GRAM domain-containing protein	Unigene22804_All//0.00E+00//EX165561			GO:0044464	nr +
Unigene22805_All	1628	0.64	1.68	1.18	2.72	3.49	2.39	1.97	2.03	1.05	1.39E+00	4.77E-04	Up	8.73E-01	7.66E-02		3.58E-01	1.70E-01		-1.91E-01	5.71E-01		3.92E-02	9.19E-01		-9.08E-01	2.41E-03		Unigene22805_All//gi|225434110|ref|XP_002273984.1|//0.00E+00//PREDICTED: similar to C2 domain-containing protein / GRAM domain-containing protein [Vitis vinifera]	Unigene22805_All//2.00E-177//AT3G59660| C2 domain-containing protein / GRAM domain-containing protein	Unigene22805_All//0.00E+00//TC169424			GO:0044464	nr +
Unigene22811_All	736	0.21	0.41	0.43	1.29	1.54	0.68	4.02	5.79	13.15	9.54E-01	5.03E-01		1.03E+00	4.71E-01		2.64E-01	7.30E-01		-9.30E-01	2.07E-01		5.27E-01	4.75E-02		1.71E+00	1.42E-20	Up			Unigene22811_All//1.00E-98//gi|73861728|gb|DT464467.1|DT464467				
Unigene22812_All	752	24.70	30.93	28.04	64.26	151.66	154.23	122.12	320.53	340.91	3.24E-01	4.80E-03		1.83E-01	1.75E-01		1.24E+00	2.33E-137	Up	1.26E+00	2.15E-130	Up	1.39E+00	0.00E+00	Up	1.48E+00	0.00E+00	Up	Unigene22812_All//gi|224115832|ref|XP_002332068.1|//9.00E-87//hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase [Populus trichocarpa] >gi|183385183|gb|ACC63883.1| quinate O-hydroxycinnamoyltransferase/shikimate O-hydroxycinnamoyltransferase [Populus trichocarpa] >gi|222831954|gb|EEE70431.1| hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase [Populus trichocarpa]	Unigene22812_All//2.00E-84//AT5G48930| HCT (HYDROXYCINNAMOYL-COA SHIKIMATE/QUINATE HYDROXYCINNAMOYL TRANSFERASE); quinate O-hydroxycinnamoyltransferase/ shikimate O-hydroxycinnamoyltransferase/ transferase	Unigene22812_All//0.00E+00//gi|73861728|gb|DT464467.1|DT464467		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0009813//GO:0048878//GO:0050737	nr +
Unigene22813_All	3048	19.29	28.59	18.99	49.98	98.27	113.53	123.32	307.98	279.24	5.68E-01	5.50E-24		-2.29E-02	7.75E-01		9.75E-01	3.60E-246		1.18E+00	0.00E+00	Up	1.32E+00	0.00E+00	Up	1.18E+00	0.00E+00	Up	Unigene22813_All//gi|21536883|gb|AAM61215.1|//1.00E-151//anthranilate N-benzoyltransferase [Arabidopsis thaliana]	Unigene22813_All//6.00E-147//AT5G48930| HCT (HYDROXYCINNAMOYL-COA SHIKIMATE/QUINATE HYDROXYCINNAMOYL TRANSFERASE); quinate O-hydroxycinnamoyltransferase/ shikimate O-hydroxycinnamoyltransferase/ transferase	Unigene22813_All//0.00E+00//TC150287		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene22816_All	1852	21.84	9.44	17.19	11.05	10.45	8.05	5.98	2.73	2.45	-1.21E+00	4.11E-40	Down	-3.45E-01	7.38E-05		-8.12E-02	5.85E-01		-4.58E-01	1.15E-04		-1.13E+00	1.17E-12	Down	-1.29E+00	8.06E-16	Down	Unigene22816_All//gi|75101048|sp|P93115.1|MGDG_CUCSA//0.00E+00//RecName: Full=Monogalactosyldiacylglycerol synthase, chloroplastic; Short=CsMGD1; Flags: Precursor >gi|1805254|gb|AAC49624.1| monogalactosyldiacylglycerol synthase [Cucumis sativus]	Unigene22816_All//0.00E+00//AT4G31780| MGD1 (MONOGALACTOSYL DIACYLGLYCEROL SYNTHASE 1); 1,2-diacylglycerol 3-beta-galactosyltransferase/ UDP-galactosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene22816_All//0.00E+00//gi|164240089|gb|ES852419.1|ES852419		ko00561|Glycerolipid metabolism	GO:0005488//GO:0007275//GO:0009247//GO:0009528//GO:0009668//GO:0009941//GO:0030258//GO:0035250	nr +
Unigene22817_All	1735	2.17	1.23	3.96	4.51	3.47	2.11	2.07	0.99	20.02	-8.24E-01	9.03E-03		8.67E-01	2.02E-04		-3.76E-01	6.97E-02		-1.10E+00	1.19E-07	Down	-1.07E+00	2.61E-04	Down	3.27E+00	9.03E-154	Up	Unigene22817_All//gi|75101048|sp|P93115.1|MGDG_CUCSA//0.00E+00//RecName: Full=Monogalactosyldiacylglycerol synthase, chloroplastic; Short=CsMGD1; Flags: Precursor >gi|1805254|gb|AAC49624.1| monogalactosyldiacylglycerol synthase [Cucumis sativus]	Unigene22817_All//0.00E+00//AT4G31780| MGD1 (MONOGALACTOSYL DIACYLGLYCEROL SYNTHASE 1); 1,2-diacylglycerol 3-beta-galactosyltransferase/ UDP-galactosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene22817_All//0.00E+00//CO120414		ko00561|Glycerolipid metabolism	GO:0005488//GO:0007275//GO:0009247//GO:0009528//GO:0009668//GO:0009941//GO:0030258//GO:0035250	nr -
Unigene22818_All	1644	4.84	4.56	4.31	3.64	3.71	2.75	7.43	5.14	71.27	-8.47E-02	6.90E-01		-1.67E-01	4.70E-01		2.80E-02	9.33E-01		-4.04E-01	1.10E-01		-5.33E-01	2.12E-04		3.26E+00	0.00E+00	Up	Unigene22818_All//gi|75173455|sp|Q9FZL4.1|MGDG_SOYBN//0.00E+00//RecName: Full=Probable monogalactosyldiacylglycerol synthase, chloroplastic; Short=GmMGD1; AltName: Full=MGDG synthase type A; Flags: Precursor >gi|9884651|dbj|BAB11979.1| MGDG synthase type A [Glycine max]	Unigene22818_All//0.00E+00//AT4G31780| MGD1 (MONOGALACTOSYL DIACYLGLYCEROL SYNTHASE 1); 1,2-diacylglycerol 3-beta-galactosyltransferase/ UDP-galactosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene22818_All//0.00E+00//TC164348		ko00561|Glycerolipid metabolism	GO:0005488//GO:0007275//GO:0009247//GO:0009528//GO:0009668//GO:0009941//GO:0030258//GO:0035250	nr +
Unigene22827_All	614	14.15	5.36	5.55	9.17	6.06	10.67	15.70	8.37	5.19	-1.40E+00	2.53E-11	Down	-1.35E+00	2.95E-10	Down	-5.98E-01	1.20E-02		2.18E-01	4.07E-01		-9.07E-01	5.56E-08		-1.60E+00	7.10E-19	Down	Unigene22827_All//gi|28412960|gb|AA040252.1|//1.00E-82//aminoimidazolecarboximide ribonucleotide transformylase/inosine monophosphate cyclohydrolase [Vigna unguiculata]	Unigene22827_All//5.00E-78//AT2G35040| AICARFT/IMPCHase bienzyme family protein	Unigene22827_All//0.00E+00//TC152488		ko00230|Purine metabolism//ko00670|One carbon pool by folate	GO:0006950//GO:0009168//GO:0009526//GO:0009532//GO:0016742//GO:0019238	nr -
Unigene22828_All	862	3.34	2.06	1.48	5.03	3.36	2.10	4.37	1.60	2.17	-6.98E-01	5.83E-02		-1.17E+00	2.86E-03		-5.83E-01	3.77E-02		-1.26E+00	1.64E-05	Down	-1.45E+00	1.08E-06	Down	-1.01E+00	2.63E-04	Down	Unigene22828_All//gi|28412960|gb|AA040252.1|//1.00E-111//aminoimidazolecarboximide ribonucleotide transformylase/inosine monophosphate cyclohydrolase [Vigna unguiculata]	Unigene22828_All//1.00E-110//AT2G35040| AICARFT/IMPCHase bienzyme family protein	Unigene22828_All//0.00E+00//TC152488		ko00230|Purine metabolism//ko00670|One carbon pool by folate	GO:0009168//GO:0016742//GO:0019238	nr -
Unigene22829_All	2146	10.22	3.90	5.63	13.02	11.49	9.70	16.59	5.63	6.33	-1.39E+00	3.32E-27	Down	-8.59E-01	2.50E-12		-1.81E-01	9.42E-02		-4.25E-01	2.11E-05		-1.56E+00	3.02E-63	Down	-1.39E+00	5.77E-55	Down	Unigene22829_All//gi|28412960|gb|AA040252.1|//0.00E+00//aminoimidazolecarboximide ribonucleotide transformylase/inosine monophosphate cyclohydrolase [Vigna unguiculata]	Unigene22829_All//0.00E+00//AT2G35040| AICARFT/IMPCHase bienzyme family protein	Unigene22829_All//0.00E+00//TC152488		ko00230|Purine metabolism//ko00670|One carbon pool by folate	GO:0006950//GO:0009168//GO:0009526//GO:0009532//GO:0016742//GO:0019238	nr -
Unigene2283_All	1231	1.83	2.68	1.69	3.48	3.58	2.42	2.71	1.15	1.81	5.50E-01	1.11E-01		-1.16E-01	7.85E-01		4.11E-02	9.11E-01		-5.23E-01	8.01E-02		-1.23E+00	6.80E-05	Down	-5.82E-01	4.60E-02				Unigene2283_All//0.00E+00//gi|78328857|gb|DT549131.1|DT549131				ESTscan +
Unigene22831_All	555	8.48	6.76	3.84	12.57	15.08	10.90	15.01	11.15	11.99	-3.29E-01	2.50E-01		-1.14E+00	1.05E-04	Down	2.63E-01	2.26E-01		-2.05E-01	4.19E-01		-4.29E-01	1.82E-02		-3.24E-01	6.95E-02		Unigene22831_All//gi|13605613|gb|AK32800.1|AF361632_1//2.00E-80//At3g21211 [Arabidopsis thaliana] >gi|23505943|gb|AAN28831.1| At3g21211/At3g21211 [Arabidopsis thaliana] >gi|222423570|dbj|BAH19754.1| AT3G21215 [Arabidopsis thaliana]	Unigene22831_All//1.00E-61//AT3G21215| RNA-binding protein, putative	Unigene22831_All//0.00E+00//gi|78322907|gb|DT543181.1|DT543181			GO:0003676//GO:0031410//GO:0043231	nr +
Unigene22835_All	498	13.13	16.38	11.66	29.01	25.10	27.12	30.05	36.17	9.36	3.19E-01	1.31E-01		-1.72E-01	5.11E-01		-2.09E-01	1.87E-01		-9.73E-02	6.12E-01		2.67E-01	2.75E-02		-1.68E+00	4.99E-31	Down	Unigene22835_All//gi|224106565|ref|XP_002314209.1|//6.00E-42//endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa] >gi|222850617|gb|EEE88164.1| endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa]	Unigene22835_All//1.00E-39//AT1G07810| ECA1 (ER-TYPE CA2+-ATPASE 1); calcium-transporting ATPase	Unigene22835_All//0.00E+00//TC136400			GO:0000041//GO:0009206//GO:0010038//GO:0016757//GO:0019829//GO:0030005//GO:0031227//GO:0032559//GO:0070838	nr +
Unigene22836_All	3767	10.06	10.59	8.89	17.23	13.04	13.12	47.29	47.38	17.12	7.41E-02	4.44E-01		-1.78E-01	6.65E-02		-4.03E-01	1.00E-11		-3.94E-01	3.40E-10		2.80E-03	9.80E-01		-1.47E+00	1.68E-294	Down	Unigene22836_All//gi|297849064|ref|XP_002892413.1|//0.00E+00//endoplasmic reticulum-type calcium-transporting ATPase 4 [Arabidopsis lyrata subsp. lyrata] >gi|297338255|gb|EFH68672.1| endoplasmic reticulum-type calcium-transporting ATPase 4 [Arabidopsis lyrata subsp. lyrata]	Unigene22836_All//0.00E+00//AT1G07670| calcium-transporting ATPase	Unigene22836_All//0.00E+00//TC136400			GO:0000041//GO:0009206//GO:0010038//GO:0016757//GO:0019829//GO:0030005//GO:0031227//GO:0032559//GO:0070838	nr +
Unigene22838_All	5719	0.42	0.43	0.54	1.11	1.08	1.11	2.44	1.08	2.41	4.49E-02	9.23E-01		3.60E-01	3.57E-01		-3.75E-02	8.82E-01		9.50E-03	9.68E-01		-1.17E+00	1.23E-16	Down	-1.76E-02	9.24E-01		Unigene22838_All//gi|297596233|ref|XP_001042222.2|//1.00E-108//Os01g0182900 [Oryza sativa Japonica Group] >gi|255672945|dbj|BAF04136.2| Os01g0182900 [Oryza sativa Japonica Group]	Unigene22838_All//0.00E+00//AT4G39450| unknown protein	Unigene22838_All//0.00E+00//CO071382			GO:0003676//GO:0006260//GO:0034061	nr -
Unigene22840_All	3576	7.55	6.73	6.81	6.21	7.03	9.46	10.20	10.04	5.07	-1.66E-01	1.39E-01		-1.50E-01	2.17E-01		1.78E-01	1.30E-01		6.07E-01	1.52E-11		-2.33E-02	8.13E-01		-1.01E+00	3.34E-34	Down	Unigene22840_All//gi|92870993|gb|AB830154.1|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene22840_All//0.00E+00//AT1G73660| protein kinase family protein	Unigene22840_All//0.00E+00//gi|164336552|gb|ES847576.1|ES847576			GO:0000166//GO:0004702//GO:0006970	nr +
Unigene22844_All	2495	0.13	0.39	0.43	0.70	0.72	1.76	1.53	2.51	8.81	1.62E+00	3.15E-02		1.76E+00	1.85E-02		3.85E-02	9.50E-01		1.33E+00	7.21E-06	Up	7.20E-01	5.94E-04		2.53E+00	6.28E-75	Up	Unigene22844_All//gi|28874836|emb|CAC84087.1|//0.00E+00//ZIK1 protein [Medicago sativa]	Unigene22844_All//3.00E-169//AT3G48260| WNK3; kinase/ protein kinase	Unigene22844_All//4.00E-30//TC156787		ko04712|Circadian rhythm - plant	GO:0004672	nr +
Unigene2285_All	2340	9.77	5.44	10.45	1.47	3.86	3.30	0.04	0.14	0.07	-8.46E-01	4.24E-13		9.63E-02	4.57E-01		1.39E+00	3.48E-13	Up	1.17E+00	3.48E-08	Up	1.98E+00	1.44E-01		9.16E-01	6.24E-01		Unigene2285_All//gi|115446743|ref|NP_001047151.1|//0.00E+00//Os02g0562300 [Oryza sativa Japonica Group] >gi|113536682|dbj|BAF09065.1| Os02g0562300 [Oryza sativa Japonica Group]	Unigene2285_All//6.00E-176//AT5G57580| calmodulin-binding protein	Unigene2285_All//0.00E+00//TC172469		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005515	nr +
Unigene22851_All	1709	14.73	56.98	26.55	55.24	53.84	59.83	50.64	54.54	42.47	1.95E+00	2.97E-191	Up	8.50E-01	1.70E-24		-3.69E-02	5.93E-01		1.15E-01	3.77E-02		1.07E-01	4.12E-02		-2.54E-01	2.17E-07		Unigene22851_All//gi|55419648|gb|AAV51937.1|//1.00E-113//AP2/EREBP transcription factor ERF-2 [Gossypium hirsutum]	Unigene22851_All//8.00E-40//AT3G16770| ATEBP (ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN); DNA binding / protein binding / transcription activator/ transcription factor	Unigene22851_All//0.00E+00//TC129792	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0009607//GO:0009725//GO:0010468//GO:0016020//GO:0030528//GO:0043231	nr +

Unigene22852_All	1511	12.12	8.45	9.55	39.89	28.19	17.66	15.00	15.66	8.38	-5.20E-01	5.40E-05		-3.44E-01	1.22E-02		-5.01E-01	3.79E-16		-1.18E+00	1.71E-61	Down	6.19E-02	6.47E-01		-8.39E-01	4.64E-16		Unigene22852_All//gi|224121930|ref|XP_002318708.1|//1.00E-168//acyl:coa ligase [Populus trichocarpa] >gi|222859381|gb|EEE96928.1|acyl:coa ligase [Populus trichocarpa]	Unigene22852_All//2.00E-140//AT5G63380| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene22852_All//0.00E+00//gi|164278657|gb|ES814857.1|ES814857		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene22854_All	890	3.76	1.94	4.01	9.79	12.15	9.18	2.00	0.52	0.94	-9.59E-01	4.72E-03		9.15E-02	7.82E-01		3.11E-01	8.27E-02		-9.28E-02	6.98E-01		-1.95E+00	5.37E-05	Down	-1.09E+00	1.06E-02		Unigene22854_All//gi|237688244|gb|ACR15118.1|//2.00E-82//choline monooxygenase [Lycium barbarum]	Unigene22854_All//7.00E-81//AT4G29890| choline monooxygenase, putative (CMO-like)	Unigene22854_All//0.00E+00//gi|48740717|gb|C0071236.1|C0071236		ko00260|Glycine, serine and threonine metabolism	GO:0004497//GO:0006725//GO:0009536//GO:0016705//GO:0046914//GO:0051536	nr -
Unigene22856_All	1232	3.82	2.88	2.68	7.24	5.79	3.52	8.10	6.79	9.99	-4.09E-01	1.46E-01		-5.12E-01	8.11E-02		-3.23E-01	1.00E-01		-1.04E+00	5.59E-08	Down	-2.55E-01	1.40E-01		3.03E-01	3.53E-02		Unigene22856_All//gi|42573375|ref|NP_974784.1|//2.00E-14//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene22856_All//1.00E-15//AT5G15550| transducin family protein / WD-40 repeat family protein	Unigene22856_All//2.00E-150//TC176838			GO:0019897//GO:0031461//GO:0031981	nr -
Unigene22858_All	1544	6.61	7.09	7.04	8.03	9.23	8.22	11.50	44.91	4.18	1.01E-01	6.21E-01		9.05E-02	6.25E-01		2.01E-01	2.23E-01		3.30E-02	8.71E-01		1.97E+00	1.07E-168	Up	-1.46E+00	6.03E-30	Down	Unigene22858_All//gi|237688244|gb|ACR15118.1|//2.00E-96//choline monooxygenase [Lycium barbarum]	Unigene22858_All//3.00E-91//AT4G29890| choline monooxygenase, putative (CMO-like)	Unigene22858_All//0.00E+00//TC153189		ko00480|Glutathione metabolism//ko00260|Glycine, serine and threonine metabolism	GO:0006725//GO:0009536//GO:0016713//GO:0046914//GO:0051536	nr +
Unigene22859_All	601	0.78	0.67	1.06	2.74	0.52	1.65	1.41	0.90	2.25	-2.16E-01	8.17E-01		4.40E-01	6.23E-01		-2.41E+00	9.47E-06	Down	-7.26E-01	1.68E-01		-6.38E-01	3.70E-01		6.80E-01	1.74E-01		Unigene22859_All//gi|30689066|ref|NP_194882.2|//1.00E-10//ATEX070G1 (exocyst subunit EX070 family protein G1); protein binding [Arabidopsis thaliana] >gi|32347268|gb|AAP31853.1| EX070-G1 protein [Arabidopsis thaliana]	Unigene22859_All//1.00E-119//TC158086			GO:0005488//GO:0043234//GO:0044444//GO:0048278	nr +
Unigene2286_All	2747	1.35	3.06	2.60	2.50	2.76	2.61	3.34	3.35	12.33	1.18E+00	1.42E-08	Up	9.42E-01	3.96E-05		1.40E-01	5.87E-01		6.29E-02	7.97E-01		3.20E-03	1.02E+00		1.88E+00	9.00E-80	Up	Unigene2286_All//gi|225439890|ref|XP_002275005.1|//1.00E-79//PREDICTED: similar to ribonuclease P family protein [Vitis vinifera]	Unigene2286_All//2.00E-79//AT1G18590| SOT17 (SULFOTRANSFERASE 17); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene2286_All//0.00E+00//TC179009		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0004549//GO:0006396//GO:0008146//GO:0019758//GO:0030677//GO:0034660	nr -
Unigene22863_All	624	2.93	6.50	2.22	1.52	3.37	2.97	21.68	24.45	13.60	1.15E+00	2.16E-04	Up	-4.04E-01	4.14E-01		1.15E+00	9.33E-03		9.68E-01	4.73E-02		1.73E-01	2.30E-01		-6.73E-01	4.53E-07		Unigene22863_All//gi|297721091|ref|NP_001172908.1|//3.00E-23//Os02g0294600 [Oryza sativa Japonica Group] >gi|255670813|dbj|BAH91637.1|Os02g0294600 [Oryza sativa Japonica Group]	Unigene22863_All//5.00E-22//AT5G08560| transducin family protein / WD-40 repeat family protein	Unigene22863_All//1.00E-168//TC155903				nr +
Unigene22865_All	1172	6.56	13.53	14.04	22.10	23.06	42.31	2.78	11.20	8.70	1.04E+00	7.20E-13	Up	1.10E+00	7.71E-14	Up	6.15E-02	6.30E-01		9.37E-01	1.02E-34		2.01E+00	1.80E-33	Up	1.65E+00	1.44E-20	Up	Unigene22865_All//gi|84453182|dbj|BAE71188.1|//2.00E-50//BEL1-like homeodomain transcription factor [Trifolium pratense]	Unigene22865_All//3.00E-28//AT2G35940| BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene22865_All//4.00E-161//TC153181	HB		GO:0000741//GO:0003677//GO:0006350//GO:0009608//GO:0009725//GO:0010218//GO:0010468//GO:0042802//GO:0043231//GO:0046983	nr -
Unigene22866_All	2852	7.19	21.11	12.83	22.08	24.20	34.65	6.03	27.52	17.91	1.55E+00	3.66E-86	Up	8.35E-01	2.86E-19		1.32E-01	4.59E-02		6.50E-01	7.69E-37		2.19E+00	2.04E-219	Up	1.57E+00	5.40E-93	Up	Unigene22866_All//gi|84453182|dbj|BAE71188.1|//0.00E+00//BEL1-like homeodomain transcription factor [Trifolium pratense]	Unigene22866_All//7.00E-146//AT2G35940| BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene22866_All//0.00E+00//TC145692	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene22867_All	1407	0.07	0.22	0.38	2.34	3.84	5.30	4.06	3.21	9.12	1.54E+00	3.23E-01		2.35E+00	5.87E-02		7.18E-01	3.72E-03		1.18E+00	4.81E-08	Up	-3.39E-01	1.45E-01		1.17E+00	1.28E-15	Up	Unigene22867_All//gi|224101393|ref|XP_002312260.1|//1.00E-128//phol-like protein [Populus trichocarpa] >gi|222852080|gb|EEE89627.1| phol-like protein [Populus trichocarpa]	Unigene22867_All//1.00E-116//AT1G14040| LOCATED IN: integral to membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03240.1); Has 732 Blast hits to 696 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 238; Fungi - 246; Plants - 151; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink).	Unigene22867_All//9.00E-27//gi|78327673|gb|DT547947.1|DT547947				nr +
Unigene22869_All	1390	0.00	0.00	0.00	0.65	1.07	0.75	0.73	1.38	2.61	null	null		null	null		7.24E-01	2.03E-01		2.12E-01	7.55E-01		9.22E-01	2.79E-02		1.84E+00	5.51E-09	Up	Unigene22869_All//gi|224101393|ref|XP_002312260.1|//1.00E-114//phol-like protein [Populus trichocarpa] >gi|222852080|gb|EEE89627.1| phol-like protein [Populus trichocarpa]	Unigene22869_All//3.00E-108//AT1G14040| LOCATED IN: integral to membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03240.1); Has 732 Blast hits to 696 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 238; Fungi - 246; Plants - 151; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink).	Unigene22869_All//9.00E-27//gi|78327673|gb|DT547947.1|DT547947				nr +
Unigene22870_All	1699	0.22	0.51	0.53	3.55	3.77	4.44	7.39	2.56	3.12	1.23E+00	1.12E-01		1.31E+00	9.77E-02		8.76E-02	7.85E-01		3.23E-01	1.56E-01		-1.53E+00	3.27E-22	Down	-1.24E+00	5.71E-17	Down	Unigene22870_All//gi|224101393|ref|XP_002312260.1|//2.00E-13//phol-like protein [Populus trichocarpa] >gi|222852080|gb|EEE89627.1| phol-like protein [Populus trichocarpa]	Unigene22870_All//1.00E-10//AT1G14040| LOCATED IN: integral to membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03240.1); Has 732 Blast hits to 696 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 238; Fungi - 246; Plants - 151; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink).	Unigene22870_All//4.00E-54//TC136942			GO:0031224	nr +
Unigene22871_All	2575	0.43	0.67	0.48	2.53	3.41	5.24	6.21	2.74	5.89	6.49E-01	1.97E-01		1.57E-01	7.86E-01		4.28E-01	2.68E-02		1.05E+00	9.18E-12	Up	-1.18E+00	4.74E-19	Down	-7.44E-02	5.98E-01		Unigene22871_All//gi|224141421|ref|XP_002324071.1|//0.00E+00//phol-like protein [Populus trichocarpa] >gi|222867073|gb|EEF04204.1| phol-like protein [Populus trichocarpa]	Unigene22871_All//0.00E+00//AT3G29060| LOCATED IN: integral to membrane; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: EXS, C-terminal (InterPro:IPR004342), SPX, N-terminal (InterPro:IPR004331); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G14040.1); Has 970 Blast hits to 889 proteins in 159 species: Archae - 2; Bacteria - 5; Metazoa - 379; Fungi - 260; Plants - 176; Viruses - 28; Other Eukaryotes - 120 (source: NCBI BLink).	Unigene22871_All//0.00E+00//gi|3326353|gb|AI055239.1|AI055239				nr +
Unigene22872_All	395	5.83	5.90	4.99	4.67	1.22	2.29	0.96	4.55	2.32	1.79E-02	9.86E-01		-2.25E-01	6.42E-01		-1.93E+00	5.68E-05	Down	-1.03E+00	3.31E-02		2.24E+00	7.60E-06	Up	1.27E+00	4.87E-02		Unigene22872_All//gi|27464259|gb|AA016018.1|//4.00E-19//chloroplast biogenesis protein [Lotus japonicus]	Unigene22872_All//2.00E-18//AT5G24290| cytochrome c biogenesis protein family	Unigene22872_All//4.00E-100//TC132626		ko04144|Endocytosis	GO:0008152//GO:0017004//GO:0042651//GO:0043231	nr +
Unigene2288_All	2036	5.09	25.71	11.04	2.42	2.22	4.81	1.89	3.39	4.72	2.34E+00	2.77E-129	Up	1.12E+00	3.24E-19	Up	-1.29E-01	6.75E-01		9.91E-01	5.51E-08		8.42E-01	2.51E-05		1.32E+00	3.26E-14	Up	Unigene2288_All//gi|3142300|gb|AAC16751.1|//1.00E-166//Contains similarity to pre-mRNA processing protein PRP39 gb|L29224 from S. cerevisiae. ESTs gb|R64908 and gb|T88158, gb|N38703 and gb|AA651043 come from this gene [Arabidopsis thaliana]	Unigene2288_All//4.00E-167//AT1G04090| unknown protein	Unigene2288_All//0.00E+00//TC151462				nr +
Unigene22881_All	774	2.84	2.42	1.44	3.80	3.69	3.62	4.15	9.18	6.02	-2.29E-01	6.22E-01		-9.75E-01	3.25E-02		-4.03E-02	9.10E-01		-6.99E-02	8.63E-01		1.14E+00	1.53E-08	Up	5.37E-01	2.70E-02		Unigene22881_All//gi|224054324|ref|XP_002298203.1|//3.00E-96//amidase family protein [Populus trichocarpa] >gi|222845461|gb|EEE83008.1|amidase family protein [Populus trichocarpa]	Unigene22881_All//6.00E-74//AT5G09420| ATTOC64-V (ARABIDOPSIS THALIANA TRANSLOCON AT THE OUTER MEMBRANE OF CHLOROPLASTS 64-V); amidase/ binding / carbon-nitrogen ligase, with glutamine as amido-N-donor	Unigene22881_All//0.00E+00//CO081528		ko00970|Aminoacyl-tRNA biosynthesis	GO:0005488//GO:0016879	nr -
Unigene22882_All	711	3.68	4.35	5.32	6.38	7.22	5.59	9.51	21.99	14.68	2.41E-01	5.19E-01		5.31E-01	1.11E-01		1.79E-01	5.70E-01		-1.90E-01	5.67E-01		1.21E+00	2.36E-19	Up	6.26E-01	4.69E-05							Unigene22882_All//0.00E+00//CO111046				
Unigene22884_All	317	2.31	0.32	2.35	0.16	0.76	1.71	1.07	1.19	4.52	-2.85E+00	6.26E-03		2.54E-02	9.95E-01		2.28E+00	3.05E-01		3.44E+00	1.40E-02		1.53E-01	8.90E-01		2.08E+00	1.33E-04	Up	Unigene22884_All//gi|115460722|ref|NP_001053961.1|//2.00E-33//Os04g0628600 [Oryza sativa Japonica Group] >gi|113565532|dbj|BAF15875.1|Os04g0628600 [Oryza sativa Japonica Group]	Unigene22884_All//2.00E-38//AT3G20720| unknown protein	Unigene22884_All//3.00E-32//TC153934				nr +
Unigene22886_All	608	50.43	30.17	25.49	96.35	102.06	93.37	48.75	21.38	44.56	-7.41E-01	6.35E-14		-9.85E-01	3.24E-21		8.30E-02	3.00E-01		-4.53E-02	6.40E-01		-1.19E+00	3.77E-35	Down	-1.30E-01	1.75E-01		Unigene22886_All//gi|15809886|gb|AAL06871.1|//3.00E-75//AT5g20890/F22D1_60 [Arabidopsis thaliana] >gi|17065150|gb|AAL32729.1|Unknown protein [Arabidopsis thaliana] >gi|21537317|gb|AAM61658.1| T-complex protein 1, beta subunit [Arabidopsis thaliana] >gi|25083652|gb|AAN72101.1|Unknown protein [Arabidopsis thaliana]	Unigene22886_All//2.00E-76//AT5G20890| chaperonin, putative	Unigene22886_All//0.00E+00//gi|21093107|gb|BQ405420.1|BQ405420			GO:0004672//GO:0005515//GO:0006464//GO:0030312//GO:0031225//GO:0032559//GO:0044424	nr -
Unigene22888_All	1559	2.55	7.41	2.84	17.57	14.84	16.34	19.15	39.89	39.81	1.54E+00	7.30E-17	Up	1.53E-01	6.34E-01		-2.44E-01	1.82E-02		-1.05E-01	3.98E-01		1.06E+00	1.60E-60	Up	1.06E+00	1.70E-61	Up	Unigene22888_All//gi|292698371|dbj|BA199728.1|//1.00E-100//heat stress transcription factor [Carica papaya]	Unigene22888_All//2.00E-80//AT4G36990| HSF4 (HEAT SHOCK FACTOR 4); DNA binding / transcription factor/ transcription repressor	Unigene22888_All//0.00E+00//TC179388	HSF		GO:0001071//GO:0003677//GO:0006350//GO:0006950//GO:0010468//GO:0030528	nr -

Unigene22889_All	1738	11.53	13.56	12.19	37.98	35.49	51.17	89.45	210.16	282.42	2.34E-01	4.65E-02		8.08E-02	5.87E-01		-9.79E-02	1.75E-01		4.30E-01	5.33E-16		1.23E+00	0.00E+00	Up	1.66E+00	0.00E+00	Up	Unigene22889_All//gi|292698371|dbj|BAI99728.1|//1.00E-106//heat stress transcription factor [Carica papaya]	Unigene22889_All//0.00E+00//AT5G64890| HSF4 (HEAT SHOCK FACTOR 4); DNA binding / transcription factor/ transcription repressor	Unigene22889_All//0.00E+00//TC145788	HSF		GO:0001071//GO:0003677//GO:0006350//GO:0006950//GO:0010468//GO:0030528	nr -
Unigene2289_All	2137	3.67	19.09	10.12	1.70	2.05	4.99	0.73	1.23	1.83	2.38E+00	5.94E-103	Up	1.46E+00	7.56E-28	Up	2.66E-01	4.18E-01		1.55E+00	9.81E-17	Up	7.51E-01	3.10E-02		1.32E+00	2.74E-06	Up	Unigene2289_All//gi|15450691|gb|AAK96617.1|//0.00E+00//AT3g04350/T6K12_3 [Arabidopsis thaliana] >gi|21360521|gb|AAM47376.1| AT3g04350/T6K12_3 [Arabidopsis thaliana]	Unigene2289_All//0.00E+00//AT3G04350| unknown protein	Unigene2289_All//0.00E+00//gi|164304452|gb|ES850573.1|ES850573				nr +
Unigene22890_All	1133	9.05	1.21	3.29	8.18	8.39	11.92	8.77	2.47	3.52	-2.91E+00	5.39E-33	Down	-1.46E+00	1.97E-13	Down	3.67E-02	8.74E-01		5.43E-01	3.05E-04		-1.83E+00	1.38E-22	Down	-1.32E+00	8.42E-15	Down	Unigene22890_All//gi|297609887|ref|NP_001063818.2|//3.00E-77//Os09g0542000 [Oryza sativa Japonica Group] >gi|255679102|dbj|BAF25732.2| Os09g0542000 [Oryza sativa Japonica Group]	Unigene22890_All//3.00E-49//AT1G76010| nucleic acid binding	Unigene22890_All//2.00E-141//TC174580			GO:0005488//GO:0031410	nr +
Unigene22891_All	1000	4.97	0.86	0.69	4.73	2.48	5.60	1.86	0.75	0.40	-2.53E+00	4.11E-14	Down	-2.84E+00	3.37E-15	Down	-9.33E-01	2.93E-04		2.43E-01	3.90E-01		-1.31E+00	2.76E-03		-2.22E+00	3.02E-06	Down	Unigene22891_All//gi|297609887|ref|NP_001063818.2|//1.00E-71//Os09g0542000 [Oryza sativa Japonica Group] >gi|255679102|dbj|BAF25732.2| Os09g0542000 [Oryza sativa Japonica Group]	Unigene22891_All//1.00E-45//AT1G76010| nucleic acid binding	Unigene22891_All//0.00E+00//TC174580			GO:0005488	nr -
Unigene22892_All	1214	36.63	53.72	31.41	46.90	49.92	96.09	52.55	126.28	51.98	5.52E-01	2.60E-17		-2.22E-01	9.48E-03		9.01E-02	2.54E-01		1.03E+00	1.85E-95	Up	1.26E+00	1.53E-196	Up	-1.58E-02	8.20E-01		Unigene22892_All//gi|297609887|ref|NP_001063818.2|//2.00E-52//Os09g0542000 [Oryza sativa Japonica Group] >gi|255679102|dbj|BAF25732.2| Os09g0542000 [Oryza sativa Japonica Group]	Unigene22892_All//3.00E-22//AT1G20220| nucleic acid binding	Unigene22892_All//0.00E+00//TC174580		ko03040|Spliceosome	GO:0005488	nr +
Unigene22894_All	1269	3.92	3.75	4.57	4.00	5.67	4.88	3.20	0.96	0.53	-6.15E-02	8.21E-01		2.24E-01	3.99E-01		5.02E-01	1.92E-02		2.84E-01	2.83E-01		-1.74E+00	4.06E-09	Down	-2.58E+00	5.41E-15	Down	Unigene22894_All//gi|7444442|pir||T02087//8.00E-11//gag/pol polyprotein - maize retrotransposon Hopscotch >gi|531389|gb|AAA57005.1| copia-like retrotransposon Hopscotch polyprotein [Zea mays]					GO:0003676	nr +
Unigene22895_All	2385	5.55	4.27	6.97	5.10	5.50	3.65	4.18	2.79	1.69	-3.78E-01	1.58E-02		3.28E-01	2.45E-02		1.10E-01	5.66E-01		-4.80E-01	2.83E-03		-5.86E-01	2.74E-04		-1.31E+00	1.00E-14	Down	Unigene22895_All//gi|38346107|emb|CAE04585.2|//7.00E-55//OSJNBb0006N15.2 [Oryza sativa (japonica cultivar-group)]	Unigene22895_All//7.00E-36//AT4G23160| protein kinase family protein				GO:0005488	nr +
Unigene22896_All	2215	15.38	8.17	9.59	87.44	42.80	62.09	52.19	127.90	92.30	-9.13E-01	1.18E-21		-6.81E-01	8.66E-13		-1.03E+00	8.59E-182	Down	-4.94E-01	3.46E-44		1.29E+00	0.00E+00	Up	8.23E-01	2.14E-132		Unigene22896_All//gi|297821018|ref|XP_002883391.1|//1.00E-146//chl-interacting protein kinase 7 [Arabidopsis lyrata subsp. lyrata] >gi|297329231|gb|EFH59650.1| chl-interacting protein kinase 7 [Arabidopsis lyrata subsp. lyrata]	Unigene22896_All//1.00E-133//AT3G23000| CIPK7 (CBL-INTERACTING PROTEIN KINASE 7); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene22896_All//0.00E+00//gi|164282369|gb|ES809936.1|ES809936		ko04140|Regulation of autophagy		nr -
Unigene22897_All	1495	4.06	13.96	5.63	9.36	7.81	8.52	4.19	4.14	2.27	1.78E+00	1.07E-36	Up	4.71E-01	2.46E-02		-2.62E-01	8.84E-02		-1.36E-01	4.51E-01		-1.66E-02	9.71E-01		-8.86E-01	1.74E-05		Unigene22897_All//gi|115442463|ref|NP_001045511.1|//7.00E-20//Os01g0967700 [Oryza sativa Japonica Group] >gi|113535042|dbj|BAF07425.1| Os01g0967700 [Oryza sativa Japonica Group]	Unigene22897_All//2.00E-21//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene22897_All//0.00E+00//gi|109860341|gb|DW489320.1|DW489320			GO:0044464	nr +
Unigene22898_All	3772	0.68	3.56	1.12	2.60	2.10	2.16	1.63	2.15	1.45	2.39E+00	1.91E-34	Up	7.15E-01	2.10E-02		-3.09E-01	9.69E-02		-2.72E-01	1.72E-01		4.03E-01	2.99E-02		-1.68E-01	4.68E-01		Unigene22898_All//gi|33465891|gb|AAQ19327.1|//1.00E-138//bZIP-like protein [Oryza sativa Japonica Group]	Unigene22898_All//3.00E-22//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene22898_All//0.00E+00//gi|109860341|gb|DW489320.1|DW489320				nr +
Unigene22899_All	885	3.07	2.00	6.02	2.31	3.35	1.89	1.19	2.98	3.65	-6.17E-01	1.06E-01		9.69E-01	3.50E-04		5.36E-01	1.55E-01		-2.90E-01	5.68E-01		1.32E+00	2.33E-04	Up	1.61E+00	7.06E-07	Up	Unigene22899_All//gi|224117488|ref|XP_002331687.1|//2.00E-87//SET domain protein [Populus trichocarpa] >gi|222874165|gb|EEF11296.1| SET domain protein [Populus trichocarpa]	Unigene22899_All//2.00E-80//AT5G14260| SET domain-containing protein	Unigene22899_All//3.00E-149//gi|5047905|gb|AI729053.1|AI729053			GO:0009536	nr +
Unigene22901_All	1430	3.66	11.76	3.65	8.78	9.51	17.34	9.08	17.62	57.39	1.68E+00	1.67E-27	Up	-3.80E-03	9.97E-01		1.16E-01	5.53E-01		9.82E-01	5.18E-19		9.57E-01	2.70E-21		2.66E+00	6.12E-294	Up	Unigene22901_All//gi|115487746|ref|NP_001066360.1|//1.00E-119//Os12g0197500 [Oryza sativa Japonica Group] >gi|122205634|sp|Q2QWE9.1|SGS3_ORYSJ RecName: Full=Protein SUPPRESSOR OF GENE SILENCING 3 homolog; Short=OsSGS3 >gi|77553859|gb|ABA96655.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113648867|dbj|BAF29379.1| Os12g0197500 [Oryza sativa Japonica Group]	Unigene22901_All//4.00E-105//AT5G23570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene22901_All//0.00E+00//gi|21095780|gb|BQ408093.1|BQ408093			GO:0005737//GO:0016787//GO:0044238//GO:0050789	nr +
Unigene22902_All	373	51.62	42.93	59.10	98.16	91.49	103.40	103.38	45.27	46.35	-2.66E-01	4.11E-02		1.95E-01	1.40E-01		-1.02E-01	3.19E-01		7.51E-02	4.82E-01		-1.19E+00	1.27E-45	Down	-1.16E+00	7.24E-45	Down	Unigene22902_All//gi|225030812|gb|ACN79519.1|//2.00E-56//reduced leaflet 1 [Lotus japonicus]	Unigene22902_All//3.00E-50//AT5G23570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene22902_All//0.00E+00//TC176927			GO:0002697//GO:0009791//GO:0016787//GO:0030422//GO:0044444	nr +
Unigene22903_All	2225	0.73	5.10	1.46	1.86	2.21	4.18	2.72	8.28	39.52	2.81E+00	7.25E-35	Up	1.00E+00	5.55E-03		2.52E-01	4.16E-01		1.17E+00	9.25E-10	Up	1.61E+00	1.60E-34	Up	3.86E+00	0.00E+00	Up	Unigene22903_All//gi|152377789|ref|NP_197747.1|//1.00E-153//SGS3 (SUPPRESSOR OF GENE SILENCING 3) [Arabidopsis thaliana] >gi|75173862|sp|Q6QLD1.1|SGS3_ARATH RecName: Full=Protein SUPPRESSOR OF GENE SILENCING 3; Short=AtSGS3 >gi|8164030|gb|AAF73960.1| SGS3 [Arabidopsis thaliana]	Unigene22903_All//2.00E-148//AT5G23570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene22903_All//0.00E+00//TC138155				nr -
Unigene22904_All	1868	9.86	4.61	6.73	11.76	11.26	7.37	6.38	6.20	4.18	-1.10E+00	4.77E-16	Down	-5.51E-01	3.41E-05		-6.23E-02	6.64E-01		-6.73E-01	3.08E-09		-4.24E-02	8.04E-01		-6.11E-01	1.79E-05		Unigene22904_All//gi|297843468|ref|XP_002889615.1|//1.00E-149//pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335457|gb|EFH65874.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene22904_All//7.00E-149//AT1G06730| pfkB-type carbohydrate kinase family protein	Unigene22904_All//0.00E+00//TC166790		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism	GO:0003676//GO:0006260//GO:0034061	nr -
Unigene22905_All	1995	3.28	2.26	2.40	3.82	3.68	3.31	1.87	0.71	1.08	-5.36E-01	2.00E-02		-4.49E-01	6.68E-02		-5.54E-02	8.17E-01		-2.09E-01	3.98E-01		-1.39E+00	2.84E-06	Down	-7.90E-01	3.91E-03		Unigene22905_All//gi|15222179|ref|NP_172158.1|//1.00E-149//pfkB-type carbohydrate kinase family protein [Arabidopsis thaliana] >gi|13605673|gb|AAK32830.1|AF361817_1 At1g06730/F4H5_22 [Arabidopsis thaliana]	Unigene22905_All//3.00E-151//AT1G06730| pfkB-type carbohydrate kinase family protein	Unigene22905_All//0.00E+00//TC166790		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism	GO:0003676//GO:0006260//GO:0034061	nr -
Unigene22913_All	1745	12.47	6.30	8.67	26.43	22.32	27.90	20.76	9.84	10.09	-9.85E-01	6.33E-16		-5.25E-01	1.46E-05		-2.44E-01	1.14E-03		7.79E-02	4.06E-01		-1.08E+00	1.33E-36	Down	-1.04E+00	1.06E-35	Down	Unigene22913_All//gi|21593999|gb|AAM65917.1|//1.00E-166//ATP phosphoribosyl transferase [Arabidopsis thaliana]	Unigene22913_All//5.00E-167//AT1G09795| ATATP-PRT2 (ATP PHOSPHORIBOSYL TRANSFERASE 2); ATP phosphoribosyltransferase	Unigene22913_All//0.00E+00//TC139042		ko00340|Histidine metabolism		nr +
Unigene22914_All	1663	11.77	8.32	8.65	10.09	8.49	8.77	3.25	2.74	1.46	-5.00E-01	5.62E-05		-4.45E-01	5.98E-04		-2.50E-01	7.26E-02		-2.03E-01	1.80E-01		-2.48E-01	3.28E-01		-1.16E+00	4.86E-07	Down	Unigene22914_All//gi|297840697|ref|XP_002888230.1|//1.00E-141//chloroplast ATP phosphoribosyl transferase [Arabidopsis lyrata subsp. lyrata] >gi|297334071|gb|EFH64489.1| chloroplast ATP phosphoribosyl transferase [Arabidopsis lyrata subsp. lyrata]	Unigene22914_All//1.00E-124//AT1G68080| ATATP-PRT1 (ATP PHOSPHORIBOSYL TRANSFERASE 1); ATP phosphoribosyltransferase	Unigene22914_All//0.00E+00//TC139042		ko00340|Histidine metabolism		nr -
Unigene22915_All	5095	7.27	6.32	7.43	11.12	12.87	10.99	9.58	20.61	14.51	-2.03E-01	2.68E-02		3.15E-02	7.54E-01		2.11E-01	7.56E-04		-1.63E-02	8.59E-01		1.10E+00	9.23E-109	Up	5.99E-01	4.07E-28		Unigene22915_All//gi|186495165|ref|NP_565074.2|//9.00E-39//calmodulin binding [Arabidopsis thaliana]	Unigene22915_All//4.00E-40//AT1G73805| calmodulin binding	Unigene22915_All//0.00E+00//TC153024		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene22923_All	1916	7.51	7.93	6.59	32.24	30.09	24.59	14.08	5.82	13.22	7.93E-02	6.20E-01		-1.89E-01	2.55E-01		-9.97E-02	1.85E-01		-3.91E-01	1.28E-09		-1.27E+00	1.29E-35	Down	-9.03E-02	3.95E-01		Unigene22923_All//gi|131054094|gb|AB032773.1|//1.00E-118//MYB transcription factor MYB34 [Medicago truncatula]	Unigene22923_All//9.00E-69//AT1G32240| KAN2 (KANADI 2); DNA binding / transcription factor	Unigene22923_All//0.00E+00//TC153796	G2-like		GO:0009943//GO:0010468//GO:0048437	nr -
Unigene22924_All	1817	6.88	7.31	6.74	15.74	11.41	10.39	5.70	3.91	2.57	8.63E-02	6.13E-01		-3.00E-02	8.71E-01		-4.64E-01	5.82E-07		-5.99E-01	1.01E-09		-5.44E-01	5.74E-04		-1.15E+00	1.28E-12	Down	Unigene22924_All//gi|131054094|gb|AB032773.1|//1.00E-117//MYB transcription factor MYB34 [Medicago truncatula]	Unigene22924_All//5.00E-69//AT1G32240| KAN2 (KANADI 2); DNA binding / transcription factor	Unigene22924_All//0.00E+00//TC170910	G2-like		GO:0009943//GO:0010468//GO:0048437	nr +
Unigene22927_All	580	4.87	3.23	6.15	6.53	1.72	5.14	4.37	4.83	4.05	-5.92E-01	1.15E-01		3.37E-01	3.50E-01		-1.92E+00	1.43E-09	Down	-3.45E-01	3.14E-01		1.43E-01	6.91E-01		-1.10E-01	7.50E-01		Unigene22927_All//gi|62816284|emb|CAD47810.2|//4.00E-10//hydroxyphenylpyruvate reductase (HPPR) [Solenostemon scutellarioides]	Unigene22927_All//5.00E-10//AT1G79870| oxidoreductase family protein	Unigene22927_All//0.00E+00//gi|78323257|gb|DT543531.1|DT543531			GO:0000166//GO:0008152//GO:0016616	nr -
Unigene22929_All	4447	5.14	9.22	6.14	44.52	32.01	26.12	38.59	101.82	39.30	8.42E-01	1.29E-22		2.57E-01	2.19E-02		-4.76E-01	1.63E-47		-7.69E-01	4.23E-99		1.40E+00	0.00E+00	Up	2.63E-02	5.51E-01		Unigene22929_All//gi|170282492|gb|ACB12194.1|//0.00E+00//PH02 [Nicotiana benthamiana]	Unigene22929_All//0.00E+00//AT2G33770| PH02 (PHOSPHATE 2); ubiquitin-protein ligase	Unigene22929_All//0.00E+00//TC161860		ko04120|Ubiquitin mediated proteolysis	GO:0009267//GO:0009639//GO:0015698//GO:0019787//GO:0055061	nr +
Unigene22930_All	875	5.26	18.47	13.63	7.57	12.12	10.37	7.63	13.33	10.97	1.81E+00	3.41E-29	Up	1.37E+00	2.96E-14	Up	6.79E-01	3.95E-05		4.54E-01	1.89E-02		8.04E-01	7.29E-08		5.23E-01	1.14E-03		Unigene22930_All//gi|6730631|gb|AAF27052.1|AC008262_1//5.00E-28//F4N2.2 [Arabidopsis thaliana]	Unigene22930_All//3.00E-28//AT3G01990| ACR6; amino acid binding	Unigene22930_All//0.00E+00//gi|48752163|gb|CO082682.1|CO082682			GO:0003006//GO:0004672//GO:0006520//GO:0008356//GO:0009725//GO:0010102//GO:0016020//GO:0016023//GO:0031406//GO:0042802	nr +
Unigene22932_All	1878	5.52	19.18	16.16	10.69	12.63	13.56	8.42	14.67	15.78	1.80E+00	1.21E-63	Up	1.55E+00	2.02E-42	Up	2.41E-01	3.52E-02		3.44E-01	1.41E-03		8.01E-01	2.36E-17		9.07E-01	2.32E-23		Unigene22932_All//gi|15232835|ref|NP_186848.1|//1.00E-174//ACR6; amino acid binding [Arabidopsis thaliana] >gi|22138102|gb|AAM93431.1| ACR6 [Arabidopsis thaliana]	Unigene22932_All//2.00E-175//AT3G01990| ACR6; amino acid binding	Unigene22932_All//0.00E+00//TC141278			GO:0031406	nr +
Unigene22934_All	352	1.19	0.86	0.30	1.42	0.88	0.38	11.53	10.57	3.85	-4.61E-01	6.50E-01		-1.97E+00	1.51E-01		-6.85E-01	5.15E-01		-1.88E+00	1.08E-01		-1.26E-01	6.66E-01		-1.58E+00	2.38E-08	Down	Unigene22934_All//gi|115444017|ref|NP_001045788.1|//1.00E-06//Os02g0131100 [Oryza sativa Japonica Group] >gi|113535319|dbj|BAF07702.1| Os02g0131100 [Oryza sativa Japonica Group]		Unigene22934_All//3.00E-165//DW517273				nr +
Unigene22935_All	3676	35.68	16.72	15.43	113.57	82.01	57.85	123.53	102.93	102.84	-1.09E+00	1.88E-109	Down	-1.21E+00	1.58E-124	Down	-4.70E-01	1.10E-97		-9.73E-01	0.00E+00		-2.63E-01	2.49E-36		-2.65E-01	1.15E-37		Unigene22935_All//gi|116309878|emb|CAH66915.1|//2.00E-23//OSIGBa0126B18.8 [Oryza sativa (indica cultivar-group)]	Unigene22935_All//3.00E-18//AT5G40450| unknown protein	Unigene22935_All//0.00E+00//TC129721				nr +
Unigene22937_All	664	7.72	6.94	3.61	18.01	10.22	13.88	10.89	5.67	6.72	-1.53E-01	6.08E-01		-1.10E+00	8.88E-05	Down	-8.18E-01	5.75E-08		-3.76E-01	2.41E-02		-9.43E-01	1.52E-06		-6.96E-01	2.14E-04		Unigene22937_All//gi|12407755|gb|AG53638.1|AF291714_1//3.00E-63//initiation factor 3d [Arabidopsis thaliana]	Unigene22937_All//2.00E-55//AT4G20980| eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative	Unigene22937_All//0.00E+00//TC165584			GO:0006412//GO:0008135//GO:0009536	nr +

Unigene2294_All	2322	3.06	2.64	1.28	3.93	5.07	4.08	7.12	4.09	4.68	-2.15E-01	3.75E-01			-1.25E+00	1.10E-07	Down	3.70E-01	2.47E-02		5.71E-02	7.96E-01		-8.01E-01	9.12E-11		-6.04E-01	4.03E-07		Unigene2294_All//gi|115472381|ref|NP_001059789.1|//1.00E-127//0s07g0517300 [Oryza sativa Japonica Group] >gi|113611325|dbj|BAF21703.1|Os07g0517300 [Oryza sativa Japonica Group]	Unigene2294_All//2.00E-87//AT3G16730| unknown protein	Unigene2294_All//0.00E+00//TC177827				nr -
Unigene22940_All	608	7.40	9.58	8.23	10.98	9.46	9.58	6.88	5.57	3.15	3.73E-01	1.37E-01			1.54E-01	6.28E-01		-2.15E-01	3.94E-01		-1.96E-01	4.56E-01		-3.06E-01	2.84E-01		-1.13E+00	1.77E-05	Down	Unigene22940_All//gi|4104242|gb|AAD01982.1|//1.00E-103//palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]	Unigene22940_All//2.00E-98//AT1G08510| FATB (fatty acyl-ACP thioesterases B); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase	Unigene22940_All//0.00E+00//gi|78350239|gb|DT570513.1|DT570513		ko00061|Fatty acid biosynthesis	GO:0006631//GO:0016297//GO:0022892//GO:0043231	nr +
Unigene22941_All	1074	17.64	40.81	22.96	20.32	21.93	24.56	14.57	5.53	7.05	1.21E+00	3.09E-43	Up		3.80E-01	8.86E-04		1.10E-01	4.18E-01		2.74E-01	1.16E-02		-1.40E+00	4.13E-24	Down	-1.05E+00	4.50E-16	Down	Unigene22941_All//gi|4104242|gb|AAD01982.1|//1.00E-152//palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]	Unigene22941_All//3.00E-136//AT1G08510| FATB (fatty acyl-ACP thioesterases B); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase	Unigene22941_All//0.00E+00//TC138795		ko00061|Fatty acid biosynthesis		nr +
Unigene22944_All	2808	4.81	3.27	2.07	7.86	5.43	5.50	7.09	6.15	7.12	-5.58E-01	2.58E-04			-1.22E+00	2.15E-13	Down	-5.33E-01	6.28E-07		-5.15E-01	5.49E-06		-2.06E-01	8.13E-02		6.10E-03	9.69E-01		Unigene22944_All//gi|225429526|ref|XP_002279005.1|//0.00E+00//PREDICTED: similar to ftsH-like protease [Vitis vinifera]	Unigene22944_All//0.00E+00//AT2G26140| ftsh4 (FtsH protease 4); ATP-dependent peptidase/ ATPase/ metallopeptidase	Unigene22944_All//0.00E+00//TC168149			GO:0004175//GO:0009057//GO:0019538//GO:0032559//GO:0042623//GO:0043231	nr +
Unigene22945_All	5074	1.55	1.17	0.93	4.22	4.10	3.86	4.04	1.19	7.33	-4.05E-01	5.50E-02			-7.28E-01	7.35E-04		-4.24E-02	8.03E-01		-1.28E-01	3.71E-01		-1.77E+00	7.78E-44	Down	8.58E-01	1.42E-26		Unigene22945_All//gi|17065024|gb|AAL32666.1|//1.00E-178//Unknown protein [Arabidopsis thaliana]	Unigene22945_All//1.00E-161//AT5G12430| DNAJ heat shock N-terminal domain-containing protein	Unigene22945_All//0.00E+00//ES828148		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene22948_All	1787	16.51	32.41	22.74	13.32	17.27	15.54	2.30	7.44	11.66	9.73E-01	3.85E-40			4.61E-01	7.50E-08		3.74E-01	4.36E-05		2.22E-01	4.09E-02		1.70E+00	4.94E-27	Up	2.34E+00	4.95E-65	Up	Unigene22948_All//gi|229609817|gb|ACQ83524.1|//1.00E-163//CBL-interacting protein kinase 08 [Vitis vinifera]	Unigene22948_All//3.00E-124//AT5G01820| ATSR1 (ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene22948_All//0.00E+00//gi|78346462|gb|DT566736.1|DT566736				nr -
Unigene22949_All	1544	62.66	52.21	62.63	41.30	32.47	41.95	6.85	4.11	2.58	-2.63E-01	5.69E-07			-6.00E-04	9.91E-01		-3.47E-01	7.63E-09		2.25E-02	7.84E-01		-7.35E-01	2.73E-06		-1.41E+00	2.99E-17	Down	Unigene22949_All//gi|229609817|gb|ACQ83524.1|//1.00E-171//CBL-interacting protein kinase 08 [Vitis vinifera]	Unigene22949_All//3.00E-141//AT5G01820| ATSR1 (ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene22949_All//0.00E+00//TC141742		ko04140|Regulation of autophagy		nr +
Unigene22950_All	1806	4.66	17.17	11.20	4.77	9.04	8.20	1.47	1.71	6.66	1.88E+00	2.81E-58	Up		1.26E+00	5.29E-21	Up	9.21E-01	1.82E-12		7.82E-01	4.36E-08		2.16E-01	5.47E-01		2.18E+00	1.27E-34	Up	Unigene22950_All//gi|229609817|gb|ACQ83524.1|//1.00E-167//CBL-interacting protein kinase 08 [Vitis vinifera]	Unigene22950_All//4.00E-135//AT5G01820| ATSR1 (ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene22950_All//2.00E-161//gi|78346462|gb|DT566736.1|DT566736		ko04140|Regulation of autophagy		nr +
Unigene22953_All	2654	64.76	17.37	23.41	90.53	76.23	45.86	15.53	10.05	8.02	-1.90E+00	0.00E+00	Down		-1.47E+00	1.30E-219	Down	-2.48E-01	4.16E-17		-9.81E-01	8.88E-182		-6.29E-01	5.01E-17		-9.54E-01	3.49E-35		Unigene22953_All//gi|15795122|dbj|BAB02500.1|//1.00E-74//IojAP protein-like [Arabidopsis thaliana] >gi|22655076|gb|AAM98129.1| expressed protein [Arabidopsis thaliana] >gi|27311971|gb|AAO00951.1| expressed protein [Arabidopsis thaliana]	Unigene22953_All//7.00E-76//AT3G12930| INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Iojap-related protein (InterPro:IPR004394); Has 2517 Blast hits to 2517 proteins in 833 species: Archae - 0; Bacteria - 1551; Metazoa - 22; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 909 (source: NCBI BLink).	Unigene22953_All//0.00E+00//TC147216			GO:0009536	nr -
Unigene2296_All	1340	63.92	59.40	79.00	76.47	53.17	61.61	14.01	34.37	19.06	-1.06E-01	8.46E-02			3.06E-01	2.48E-09		-5.24E-01	1.61E-29		-3.12E-01	2.29E-10		1.29E+00	9.98E-62	Up	4.44E-01	2.29E-06		Unigene2296_All//gi|297839773|ref|XP_002887768.1|//9.00E-77//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297333609|gb|EFH64027.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene2296_All//8.00E-58//AT1G79110| protein binding / zinc ion binding	Unigene2296_All//0.00E+00//gi|78341645|gb|DT561919.1|DT561919			GO:0043231	nr -
Unigene22961_All	712	12.05	4.84	13.31	10.91	11.46	5.46	1.72	1.41	0.78	-1.32E+00	2.84E-10	Down		1.44E-01	5.06E-01		7.07E-02	8.10E-01		-1.00E+00	1.21E-06	Down	-2.90E-01	6.39E-01		-1.14E+00	3.17E-02		Unigene22961_All//gi|242036241|ref|XP_002465515.1|//4.00E-07//hypothetical protein SORBIDRAFT_01g040340 [Sorghum bicolor] >gi|241919369|gb|EER92513.1| hypothetical protein SORBIDRAFT_01g040340 [Sorghum bicolor]		Unigene22961_All//2.00E-174//CD485974				nr +
Unigene22962_All	762	11.54	7.85	10.90	8.24	6.42	2.84	1.89	0.60	0.68	-5.56E-01	4.22E-03			-8.15E-02	6.98E-01		-3.60E-01	1.34E-01		-1.53E+00	4.20E-10	Down	-1.64E+00	1.74E-03		-1.47E+00	3.08E-03		Unigene22962_All//gi|242085688|ref|XP_002443269.1|//1.00E-05//hypothetical protein SORBIDRAFT_08g016660 [Sorghum bicolor] >gi|241943962|gb|EES17107.1| hypothetical protein SORBIDRAFT_08g016660 [Sorghum bicolor]		Unigene22962_All//2.00E-112//CD485974				nr +
Unigene22963_All	1192	10.71	9.86	8.89	7.06	8.29	4.21	2.41	1.47	1.04	-1.19E-01	5.01E-01			-2.69E-01	1.24E-01		2.31E-01	2.51E-01		-7.48E-01	1.25E-04		-7.12E-01	3.12E-02		-1.22E+00	1.94E-04	Down	Unigene22963_All//gi|124359162|gb|ABN05685.1|//6.00E-21//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene22963_All//6.00E-17//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene22963_All//5.00E-142//CD485974			GO:0005488//GO:0044464	nr +
Unigene22966_All	1099	4.24	9.36	7.90	8.57	6.08	5.79	7.69	6.16	5.73	1.14E+00	7.43E-10	Up		8.98E-01	1.13E-05		-4.95E-01	5.31E-03		-5.64E-01	2.24E-03		-3.21E-01	8.44E-02		-4.26E-01	1.41E-02		Unigene22966_All//gi|222423701|dbj|BAH19817.1|//1.00E-137//AT3G14830 [Arabidopsis thaliana]	Unigene22966_All//4.00E-138//AT3G14830| unknown protein	Unigene22966_All//0.00E+00//gi|48751131|gb|C0081650.1|C0081650				nr -
Unigene22967_All	1062	6.26	20.66	14.84	9.99	13.26	12.33	14.97	29.79	28.17	1.72E+00	8.42E-37	Up		1.25E+00	3.92E-16	Up	4.09E-01	4.85E-03		3.04E-01	6.38E-02		9.93E-01	3.94E-28		9.12E-01	8.12E-24		Unigene22967_All//gi|222423701|dbj|BAH19817.1|//1.00E-120//AT3G14830 [Arabidopsis thaliana]	Unigene22967_All//4.00E-122//AT3G14830| unknown protein	Unigene22967_All//0.00E+00//TC147594				nr -
Unigene22968_All	2184	7.59	15.50	12.22	10.36	13.94	14.97	12.31	19.71	21.32	1.03E+00	5.37E-26	Up		6.86E-01	2.72E-10		4.29E-01	2.60E-06		5.32E-01	5.80E-09		6.79E-01	3.30E-20		7.92E-01	5.72E-29		Unigene22968_All//gi|222423701|dbj|BAH19817.1|//1.00E-177//AT3G14830 [Arabidopsis thaliana]	Unigene22968_All//2.00E-167//AT3G14830| unknown protein	Unigene22968_All//0.00E+00//gi|48751131|gb|C0081650.1|C0081650				nr +
Unigene22970_All	816	2.76	5.65	3.98	6.04	7.43	7.97	3.11	9.68	4.10	1.04E+00	2.86E-04	Up		5.30E-01	1.45E-01		2.97E-01	2.57E-01		3.99E-01	9.92E-02		1.64E+00	1.25E-15	Up	4.00E-01	1.86E-01		Unigene22970_All//gi|30682967|ref|NP_193208.2|//2.00E-11//PPD2; dioxygenase/ metal ion binding [Arabidopsis thaliana] >gi|75151364|sp|Q8GY55.1|TIF4B_ARATH RecName: Full=Protein TIFY 4B; AltName: Full=Protein PEAPOD 2	Unigene22970_All//2.00E-11//AT4G14720| PPD2; dioxygenase/ metal ion binding	Unigene22970_All//0.00E+00//gi|73863881|gb|DT466620.1|DT466620	Tify		GO:0005488//GO:0008283//GO:0048827	nr +
Unigene22974_All	3353	0.50	0.41	0.81	2.20	1.02	0.51	8.99	2.19	3.47	-2.91E-01	5.79E-01			6.98E-01	8.10E-02		-1.11E+00	3.07E-08	Down	-2.10E+00	6.80E-18	Down	-2.03E+00	2.61E-77	Down	-1.37E+00	7.14E-46	Down	Unigene22974_All//gi|224143990|ref|XP_002325148.1|//0.00E+00//type-b response regulator [Populus trichocarpa] >gi|222866582|gb|EEF03713.1| type-b response regulator [Populus trichocarpa]	Unigene22974_All//3.00E-96//AT5G58080| ARR18 (ARABIDOPSIS RESPONSE REGULATOR 18); transcription factor/ two-component response regulator	Unigene22974_All//0.00E+00//gi|109885001|gb|DW513971.1|DW513971	ARR-B	ko04712|Circadian rhythm - plant	GO:0006350//GO:0010468	nr -
Unigene22975_All	2523	2.53	4.60	4.41	5.27	10.65	27.24	11.73	18.75	34.63	8.62E-01	3.20E-07			8.02E-01	5.91E-06		1.01E+00	1.14E-23	Up	2.37E+00	3.58E-185	Up	6.77E-01	5.21E-22		1.56E+00	2.13E-157	Up	Unigene22975_All//gi|224143990|ref|XP_002325148.1|//0.00E+00//type-b response regulator [Populus trichocarpa] >gi|222866582|gb|EEF03713.1| type-b response regulator [Populus trichocarpa]	Unigene22975_All//2.00E-98//AT2G25180| ARR12 (ARABIDOPSIS RESPONSE REGULATOR 12); transcription factor/ two-component response regulator	Unigene22975_All//0.00E+00//gi|189098372|gb|FG551524.1|FG551524	ARR-B	ko04712|Circadian rhythm - plant	GO:0006350//GO:0010468	nr +
Unigene22976_All	2137	5.12	2.21	1.30	12.35	9.59	6.95	19.80	4.46	7.72	-1.21E+00	1.88E-11	Down		-1.98E+00	1.21E-21	Down	-3.66E-01	2.24E-04		-8.29E-01	1.65E-15		-2.15E+00	3.08E-116	Down	-1.36E+00	4.77E-63	Down	Unigene22976_All//gi|10177316|dbj|BAB10642.1|//0.00E+00//kinesin-like protein [Arabidopsis thaliana]	Unigene22976_All//9.00E-156//AT5G60930| chromosome-associated kinesin, putative	Unigene22976_All//0.00E+00//TC129989			GO:0000166//GO:0003774	nr -
Unigene22977_All	4215	2.15	1.49	0.67	4.44	4.67	3.18	9.51	1.98	4.10	-5.27E-01	5.98E-03			-1.68E+00	1.69E-14	Down	7.26E-02	6.28E-01		-4.82E-01	1.12E-04		-2.26E+00	3.38E-117	Down	-1.21E+00	3.62E-50	Down	Unigene22977_All//gi|10177316|dbj|BAB10642.1|//0.00E+00//kinesin-like protein [Arabidopsis thaliana]	Unigene22977_All//0.00E+00//AT5G60930| chromosome-associated kinesin, putative	Unigene22977_All//0.00E+00//TC129989			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr +
Unigene22978_All	3507	11.32	27.94	7.12	16.48	24.15	22.85	52.65	35.59	96.43	1.30E+00	1.60E-107	Up		-6.69E-01	2.24E-14		5.52E-01	3.50E-26		4.72E-01	4.95E-17		-5.65E-01	8.89E-61		8.73E-01	9.12E-242		Unigene22978_All//gi|225438996|ref|XP_002284429.1|//0.00E+00//PREDICTED: similar to ACA1 (autoinhibited Ca2+ -ATPase 1); calmodulin binding isoform 1 [Vitis vinifera]	Unigene22978_All//0.00E+00//AT4G37640| ACA2 (CALCIUM ATPASE 2); calcium ion transmembrane transporter/ calcium-transporting ATPase/ calmodulin binding	Unigene22978_All//0.00E+00//TC135305			GO:0005261//GO:0005515//GO:0009206//GO:0009628//GO:0009532//GO:0016836//GO:0019829//GO:0031224//GO:0032559//GO:0046873//GO:0046914//GO:0070838	nr +
Unigene22979_All	1222	1.88	5.72	3.49	4.97	2.56	2.77	7.96	10.40	7.79	1.60E+00	4.35E-11	Up		8.88E-01	3.87E-03		-9.56E-01	1.76E-05		-8.43E-01	3.45E-04		3.86E-01	7.05E-03		-3.04E-02	8.74E-01		Unigene22979_All//gi|255633684|gb|ACU17202.1|//1.00E-06//unknown [Glycine max]		Unigene22979_All//9.00E-39//DT466058				nr +
Unigene22984_All	1599	7.04	7.70	6.89	12.49	10.27	6.36	11.08	7.55	4.73	1.30E-01	4.64E-01			-2.93E-02	8.82E-01		-2.82E-01	2.05E-02		-9.75E-01	1.97E-15		-5.53E-01	2.37E-06		-1.23E+00	4.62E-23	Down	Unigene22984_All//gi|18401727|ref|NP_029426.1|//2.00E-82//SAND family protein [Arabidopsis thaliana] >gi|15983791|gb|AAL10492.1| At2g28390/T1B3.9 [Arabidopsis thaliana] >gi|20197735|gb|AAD20687.2| expressed protein [Arabidopsis thaliana] >gi|22137018|gb|AAM91354.1| At2g28390/T1B3.9 [Arabidopsis thaliana]	Unigene22984_All//6.00E-84//AT2G28390| SAND family protein	Unigene22984_All//0.00E+00//TC179153			GO:0044464	nr -
Unigene22988_All	4144	5.25	4.55	4.07	11.40	11.52	10.17	18.22	8.55	10.72	-2.08E-01	9.58E-02			-3.67E-01	2.95E-03		1.53E-02	8.76E-01		-1.64E-01	4.67E-02		-1.09E+00	4.72E-77	Down	-7.66E-01	5.18E-44		Unigene22988_All//gi|115489008|ref|NP_001066991.1|//0.00E+00//Os12g0554400 [Oryza sativa Japonica Group] >gi|77556742|gb|ABA99538.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649498|dbj|BAF30010.1| Os12g0554400 [Oryza sativa Japonica Group]	Unigene22988_All//5.00E-51//AT5G54440| unknown protein	Unigene22988_All//0.00E+00//TC169501				nr -
Unigene22992_All	722	5.58	1.75	1.18	1.93	1.10	2.44	1.29	0.81	1.43	-1.67E+00	4.18E-07	Down		-2.24E+00	1.29E-09	Down	-8.17E-01	1.37E-01		3.37E-01	5.42E-01		-6.69E-01	3.12E-01		1.55E-01	7.86E-01		Unigene22992_All//gi|297840127|ref|XP_002887945.1|//1.00E-122//PDE316 [Arabidopsis lyrata subsp. lyrata] >gi|297333786|gb|EFH64204.1| PDE316 [Arabidopsis lyrata subsp. lyrata]	Unigene22992_All//5.00E-123//AT1G63680| MURE; ATP binding / acid-amino acid ligase/ ligase	Unigene22992_All//9.00E-161//C0081352			GO:0000270//GO:0016879//GO:0032559//GO:0042546//GO:0043231//GO:0065008	nr -
Unigene22993_All	2270	4.98	3.64	4.46	29.23	22.48	19.86	6.71	1.36	3.14	-4.52E-01	7.68E-03			-1.60E-01	3.95E-01		-3.79E-01	9.73E-11		-5.58E-01	3.28E-19		-2.30E+00	8.09E-46	Down	-1.09E+00	9.56E-17	Down	Unigene22993_All//gi|297840127|ref|XP_002887945.1|//0.00E+00//PDE316 [Arabidopsis lyrata subsp. lyrata] >gi|297333786|gb|EFH64204.1| PDE316 [Arabidopsis lyrata subsp. lyrata]	Unigene22993_All//0.00E+00//AT1G63680| MURE; ATP binding / acid-amino acid ligase/ ligase	Unigene22993_All//0.00E+00//gi|78339123|gb|DT559397.1|DT559397			GO:0000270//GO:0016881//GO:0032559//GO:0042546//GO:0044424//GO:0065008	nr +

Unigene22997_All	240	1.74	1.27	0.22	0.62	0.86	2.07	0.00	3.83	3.15	-4.61E-01	6.50E-01		-2.97E+00	6.46E-02		4.67E-01	8.25E-01		1.73E+00	1.45E-01		1.19E+01	1.48E-06	Up	1.16E+01	1.39E-05	Up	Unigene22997_All//gi|222422961|dbj|BAH19465.1|//6.00E-25//AT5G51180|unknown protein [Arabidopsis thaliana]	Unigene22997_All//2.00E-26//AT5G51180| unknown protein	Unigene22997_All//3.00E-115//CO103613				nr +
Unigene22999_All	1643	1.62	4.19	1.43	2.55	2.62	3.00	4.61	8.32	8.39	1.37E+00	7.98E-09	Up	-1.88E-01	6.24E-01		4.08E-02	9.10E-01		2.34E-01	4.55E-01		8.53E-01	5.88E-10		8.65E-01	1.51E-10		Unigene22999_All//gi|222422961|dbj|BAH19465.1|//1.00E-140//AT5G51180|Arabidopsis thaliana]	Unigene22999_All//1.00E-141//AT5G51180| unknown protein	Unigene22999_All//0.00E+00//CO103613				nr -
Unigene2300_All	664	12.92	3.89	10.18	8.85	5.45	4.63	3.76	3.90	3.48	-1.73E+00	5.30E-15	Down	-3.44E-01	1.08E-01		-7.01E-01	2.16E-03		-9.37E-01	9.98E-05		5.49E-02	8.91E-01		-1.11E-01	7.52E-01				Unigene2300_All//0.00E+00//gi|21102407|gb|BQ414720.1|BQ414720				
Unigene23001_All	2301	6.39	19.18	9.03	8.20	8.92	10.50	5.88	5.92	8.19	1.59E+00	2.97E-65	Up	4.98E-01	6.30E-05		1.21E-01	4.09E-01		3.56E-01	1.29E-03		1.02E-02	9.79E-01		4.78E-01	1.62E-05		Unigene23001_All//gi|297848430|ref|XP_002892096.1|//1.00E-122//endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337938|gb|EFH68355.1|endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23001_All//4.00E-123//AT1G02270|endonuclease/exonuclease/phosphatase family protein / calcium-binding EF hand family protein	Unigene23001_All//0.00E+00//TC160489		ko03018|RNA degradation		nr +
Unigene23003_All	2706	14.33	10.07	6.65	3.41	2.57	3.27	13.41	11.95	16.12	-5.08E-01	2.93E-09		-1.11E+00	3.16E-32	Down	-4.06E-01	2.83E-02		-5.80E-02	7.90E-01		-1.65E-01	5.35E-02		2.66E-01	1.80E-04		Unigene23003_All//gi|295841585|dbj|BAJ07173.1|//1.00E-119//MdTCP2A [Malus x domestica]	Unigene23003_All//2.00E-34//AT4G18390| TCP family transcription factor, putative	Unigene23003_All//0.00E+00//TC140289	TCP			nr +
Unigene23009_All	2467	11.81	6.80	11.29	47.71	53.14	48.44	55.05	199.32	40.45	-7.97E-01	5.95E-15		-6.55E-02	6.09E-01		1.55E-01	3.46E-04		2.18E-02	7.13E-01		1.86E+00	0.00E+00	Up	-4.45E-01	4.27E-30		Unigene23009_All//gi|113203757|gb|ABI33979.1|//0.00E+00//phenylalanine ammonia lyase [Jatropha curcas]	Unigene23009_All//0.00E+00//AT2G37040| pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase	Unigene23009_All//0.00E+00//TC131092		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00910|Nitrogen metabolism	GO:0006558//GO:0006575//GO:0016840//GO:0044424	nr -
Unigene2301_All	980	1.92	0.31	0.43	0.61	0.46	0.37	0.60	0.17	0.73	-2.63E+00	5.43E-06	Down	-2.14E+00	1.32E-04	Down	-4.17E-01	6.27E-01		-7.26E-01	4.60E-01		-1.82E+00	4.71E-02		2.77E-01	6.90E-01		Unigene2301_All//gi|297845704|ref|XP_002890733.1|//6.00E-52//T17H3.9 [Arabidopsis lyrata subsp. lyrata] >gi|297336575|gb|EFH66692.1|T17H3.9 [Arabidopsis lyrata subsp. lyrata]	Unigene2301_All//2.00E-49//AT1G27590| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: LP.06 six leaves visible, 4 anthesis, petal differentiation and expansion stage, E expanded cotyledon stage; BEST Arabidopsis thaliana protein match is: phosphatidylinositol 3- and 4-kinase family protein (TAIR:AT1G27570.1); Has 81 Blast hits to 81 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 59; Fungi - 4; Plants - 17; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene2301_All//0.00E+00//gi|21102407|gb|BQ414720.1|BQ414720			GO:0009987//GO:0010167	nr +
Unigene23010_All	3294	50.03	51.85	58.21	118.59	134.40	87.12	94.92	34.91	78.87	5.16E-02	2.54E-01		2.18E-01	6.24E-09		1.81E-01	6.33E-17		-4.45E-01	3.24E-73		-1.44E+00	0.00E+00	Down	-2.67E-01	9.80E-27		Unigene23010_All//gi|148299083|gb|ABQ58079.1|//0.00E+00//subtilisin-like protease [Nicotiana tabacum]	Unigene23010_All//0.00E+00//AT5G67360| ARA12; serine-type endopeptidase	Unigene23010_All//0.00E+00//TC141200			GO:0003006//GO:0004175//GO:0005515//GO:0005576//GO:0005618//GO:0009845//GO:0010191//GO:0019538//GO:0031410//GO:0044092	nr -
Unigene23013_All	1073	1.76	2.13	1.49	2.74	0.55	0.38	18.80	48.03	332.45	2.76E-01	5.29E-01		-2.38E-01	6.05E-01		-2.33E+00	1.59E-09	Down	-2.85E+00	2.24E-10	Down	1.35E+00	8.62E-74	Up	4.14E+00	0.00E+00	Up	Unigene23013_All//gi|15228034|ref|NP_181216.1|//5.00E-85//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana]	Unigene23013_All//9.00E-84//AT2G36780| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene23013_All//3.00E-100//gi|164268063|gb|EX164988.1|EX164988		ko00908|Zeatin biosynthesis	GO:0008194//GO:0016758	nr +
Unigene23014_All	1893	13.68	14.59	8.07	1.61	1.44	1.43	0.00	0.93	0.08	9.26E-02	4.24E-01		-7.61E-01	7.40E-12		-1.60E-01	6.86E-01		-1.65E-01	6.86E-01		9.86E+00	2.29E-12	Up	6.40E+00	1.40E-01		Unigene23014_All//gi|297827169|ref|XP_002881467.1|//1.00E-151//UDP-glucosyl transferase 72C1 [Arabidopsis lyrata subsp. lyrata] >gi|297327306|gb|EFH57726.1| UDP-glucosyl transferase 72C1 [Arabidopsis lyrata subsp. lyrata]	Unigene23014_All//4.00E-150//AT2G36750| UGT73C1 (UDP-GLUCOSYL TRANSFERASE 73C1); UDP-glycosyltransferase/ UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene23014_All//0.00E+00//TC157080		ko00908|Zeatin biosynthesis		nr +
Unigene23015_All	1743	1.47	1.02	1.62	2.14	0.59	1.11	12.10	33.28	255.28	-5.32E-01	1.81E-01		1.39E-01	7.15E-01		-1.85E+00	5.08E-09	Down	-9.44E-01	2.66E-03		1.46E+00	6.66E-93	Up	4.40E+00	0.00E+00	Up	Unigene23015_All//gi|297827173|ref|XP_002881469.1|//1.00E-142//dongluconolactonase [Arabidopsis lyrata subsp. lyrata] >gi|297327308|gb|EFH57728.1| dongluconolactonase [Arabidopsis lyrata subsp. lyrata]	Unigene23015_All//3.00E-142//AT2G36800| DOGT1 (DON-GLUCOSYLTRANSFERASE 1); UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transf	Unigene23015_All//0.00E+00//TC132849		ko00908|Zeatin biosynthesis		nr +
Unigene23016_All	441	1.66	1.03	5.80	0.56	1.41	2.36	1.82	1.71	0.45	-6.84E-01	3.86E-01		1.80E+00	5.75E-05	Up	1.32E+00	1.88E-01		2.06E+00	6.55E-03		-9.47E-02	8.99E-01		-2.01E+00	7.11E-03		Unigene23016_All//gi|206114257|gb|AC105256.1|//5.00E-16//type 1 MADS box transcription factor [Petunia x hybrida]	Unigene23016_All//8.00E-17//AT5G48670| AGL80 (AGAMOUS-LIKE 80); DNA binding / transcription factor	Unigene23016_All//5.00E-72//TC144524	MADS		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene23017_All	1059	29.79	26.36	29.67	36.93	34.96	19.96	5.27	3.12	1.39	-1.76E-01	8.43E-02		-6.00E-03	9.79E-01		-7.91E-02	4.54E-01		-8.88E-01	2.07E-25		-7.57E-01	7.27E-04		-1.92E+00	2.39E-14	Down	Unigene23017_All//gi|53370641|gb|AAU89136.1|//4.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene23017_All//0.00E+00//gi|109865951|gb|DW494927.1|DW494927				nr +
Unigene23018_All	1473	4.58	3.34	1.99	8.66	7.95	5.55	6.06	5.11	1.79	-4.58E-01	4.44E-02		-1.20E+00	6.53E-07	Down	-1.23E-01	5.23E-01		-6.42E-01	3.04E-05		-2.46E-01	1.89E-01		-1.76E+00	4.80E-20	Down	Unigene23018_All//gi|206114257|gb|AC105256.1|//5.00E-30//type 1 MADS box transcription factor [Petunia x hybrida]	Unigene23018_All//8.00E-28//AT5G48670| AGL80 (AGAMOUS-LIKE 80); DNA binding / transcription factor	Unigene23018_All//1.00E-164//gi|84172254|gb|DR460902.1|DR460902	MADS		GO:0005488//GO:0006350//GO:0043231	nr +
Unigene23019_All	1329	1.26	1.56	0.88	2.66	2.00	1.19	1.46	0.53	0.45	3.11E-01	4.96E-01		-5.15E-01	3.44E-01		-4.16E-01	2.15E-01		-1.16E+00	3.83E-04	Down	-1.45E+00	7.53E-04	Down	-1.70E+00	7.95E-05	Down	Unigene23019_All//gi|206114257|gb|AC105256.1|//1.00E-36//type 1 MADS box transcription factor [Petunia x hybrida]	Unigene23019_All//1.00E-34//AT5G48670| AGL80 (AGAMOUS-LIKE 80); DNA binding / transcription factor	Unigene23019_All//0.00E+00//TC172008	MADS		GO:0003677//GO:0006350//GO:0010468//GO:0043231	nr -
Unigene23021_All	856	7.40	3.20	7.28	15.89	11.10	7.12	1.93	1.12	0.88	-1.21E+00	6.26E-07	Down	-2.31E-02	9.43E-01		-5.17E-01	2.67E-04		-1.16E+00	5.86E-14	Down	-7.79E-01	9.04E-02		-1.12E+00	1.16E-02				Unigene23021_All//0.00E+00//TC169069				
Unigene23023_All	4172	1.71	1.51	2.53	3.03	2.25	2.19	90.96	36.34	33.35	-1.80E-01	4.41E-01		5.67E-01	1.88E-03		-4.29E-01	4.55E-03		-4.72E-01	2.67E-03		-1.32E+00	0.00E+00	Down	-1.45E+00	0.00E+00	Down	Unigene23023_All//gi|297850284|ref|XP_002893023.1|//0.00E+00//F14D16.3 [Arabidopsis lyrata subsp. lyrata] >gi|297338865|gb|EFH69282.1|F14D16.3 [Arabidopsis lyrata subsp. lyrata]	Unigene23023_All//0.00E+00//AT1G18910| protein binding / zinc ion binding	Unigene23023_All//0.00E+00//DR463206		ko04120|Ubiquitin mediated proteolysis	GO:0005488	nr -
Unigene23024_All	426	2.95	1.07	2.00	5.85	4.61	5.19	20.64	20.11	6.36	-1.46E+00	1.95E-02		-5.60E-01	3.87E-01		-3.44E-01	4.20E-01		-1.71E-01	6.71E-01		-3.76E-02	8.53E-01		-1.70E+00	8.10E-19	Down	Unigene23024_All//gi|109676312|gb|AB637638.1|//2.00E-08//transposase [Populus trichocarpa]		Unigene23024_All//0.00E+00//TC160367				nr +
Unigene23026_All	3363	4.36	3.69	3.86	6.59	7.65	5.49	5.58	2.77	4.29	-2.39E-01	1.21E-01		-1.73E-01	3.05E-01		2.15E-01	5.37E-02		-2.63E-01	2.93E-02		-1.01E+00	1.63E-17	Down	-3.80E-01	6.29E-04		Unigene23026_All//gi|189409278|gb|ACO69970.1|//0.00E+00//phytochrome B [Vitis riparia]	Unigene23026_All//0.00E+00//AT2G18790| PHYB (PHYTOCHROME B); G-protein coupled photoreceptor/ protein histidine kinase/ red or far-red light photoreceptor/ signal transducer	Unigene23026_All//0.00E+00//TC141542		ko04712|Circadian rhythm - plant	GO:0004673//GO:0004930//GO:0006351//GO:0006468//GO:0007602//GO:0010468//GO:0032559//GO:0042802//GO:0044464//GO:0050877	nr +
Unigene23031_All	291	0.00	2.26	0.73	3.94	2.25	1.24	5.67	4.45	1.78	1.11E+01	6.25E-04	Up	9.52E+00	1.41E-01		-8.08E-01	1.92E-01		-1.67E+00	1.29E-02		-3.48E-01	4.75E-01		-1.67E+00	3.93E-04	Down	Unigene23031_All//gi|227206370|dbj|BAH57240.1|//1.00E-08//AT4G35750|Arabidopsis thaliana]	Unigene23031_All//9.00E-07//AT4G35750| Rho-GTPase-activating protein-related	Unigene23031_All//2.00E-91//gi|109857633|gb|DW486612.1|DW486612				nr -
Unigene23032_All	796	18.93	12.09	19.73	81.92	64.63	52.20	73.99	60.86	33.23	-6.46E-01	7.00E-06		6.00E-02	7.02E-01		-3.42E-01	8.27E-09		-6.50E-01	1.13E-24		-2.82E-01	4.38E-06		-1.15E+00	7.76E-68	Down	Unigene23032_All//gi|15237117|ref|NP_195300.1|//2.00E-75//Rho-GTPase-activating protein-related [Arabidopsis thaliana] >gi|30725562|gb|AAP37803.1|At4g35750 [Arabidopsis thaliana]	Unigene23032_All//9.00E-77//AT4G35750| Rho-GTPase-activating protein-related	Unigene23032_All//0.00E+00//TC138858				nr -
Unigene23037_All	1480	0.46	0.41	0.14	7.44	5.35	6.13	2.29	1.24	0.78	-1.62E-01	8.32E-01		-1.68E+00	8.70E-02		-4.75E-01	3.42E-03		-2.78E-01	1.32E-01		-8.79E-01	3.35E-03		-1.55E+00	6.56E-07	Down	Unigene23037_All//gi|89357197|gb|AB072481.1|//1.00E-165//TCP domain-like protein I [Gossypium barbadense]	Unigene23037_All//4.00E-46//AT3G47620| AcTCP14 (TEOSINTE BRANCHED1, CYCLOIDEA AND PCF (TCP) 14); transcription factor	Unigene23037_All//0.00E+00//gi|78327899|gb|DT548173.1|DT548173	TCP		GO:0009725	nr -
Unigene23039_All	2707	22.79	55.29	25.04	43.58	64.34	62.60	4.65	9.03	3.33	1.28E+00	2.98E-159	Up	1.36E-01	5.63E-02		5.62E-01	2.25E-55		5.23E-01	1.32E-42		9.57E-01	1.18E-20		-4.85E-01	4.41E-04		Unigene23039_All//gi|224138036|ref|XP_002326502.1|//1.00E-167//pseudo response regulator [Populus trichocarpa] >gi|222833824|gb|EEE72201.1|pseudo response regulator [Populus trichocarpa]	Unigene23039_All//1.00E-114//AT4G18020| APRR2; transcription factor/ two-component response regulator	Unigene23039_All//0.00E+00//TC132471	ARR-B	ko04712|Circadian rhythm - plant	GO:0006355	nr +
Unigene2304_All	2325	8.06	18.57	9.30	14.21	13.36	14.80	15.73	20.60	17.03	1.20E+00	2.79E-42	Up	2.07E-01	1.17E-01		-8.86E-02	4.34E-01		5.94E-02	6.35E-01		3.89E-01	1.13E-08		1.15E-01	1.64E-01		Unigene2304_All//gi|297728499|ref|NP_001176613.1|//1.00E-107//Os11g0568700 [Oryza sativa Japonica Group] >gi|108864521|gb|ABA94317.2|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108864522|gb|ABG22532.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108864524|gb|ABG22534.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255680198|dbj|BAH95341.1|Os11g0568700 [Oryza sativa Japonica Group]	Unigene2304_All//1.00E-112//AT5G06440| unknown protein	Unigene2304_All//0.00E+00//TC177622			GO:0043231	nr +
Unigene23041_All	4109	3.13	2.60	1.97	7.63	6.58	6.36	8.37	3.81	5.23	-2.68E-01	1.03E-01		-6.69E-01	3.90E-05		-2.13E-01	2.88E-02		-2.61E-01	7.85E-03		-1.13E+00	1.12E-37	Down	-6.79E-01	8.32E-17		Unigene23041_All//gi|18395372|ref|NP_565285.1|//0.00E+00//STI (STICHEL); ATP binding / DNA binding / DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|8980710|gb|AAF82285.1|AF264023_1 STICHEL [Arabidopsis thaliana] >gi|20197093|gb|AAC18938.2|similar to prokaryotic DNA polymerase III gamma subunit [Arabidopsis thaliana]	Unigene23041_All//0.00E+00//AT2G02480| STI (STICHEL); ATP binding / DNA binding / DNA-directed DNA polymerase	Unigene23041_All//0.00E+00//TC161794		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03430|Mismatch repair	GO:0000904//GO:0006259//GO:0016020//GO:0016462//GO:0032559//GO:0034061//GO:0035315//GO:0042575	nr -
Unigene23043_All	2398	2.99	1.99	3.00	6.96	6.91	4.29	7.44	5.87	3.11	-5.90E-01	6.91E-03		4.20E-03	1.00E+00		-1.08E-02	9.55E-01		-6.97E-01	1.41E-07		-3.41E-01	4.09E-03		-1.26E+00	3.53E-24	Down	Unigene23043_All//gi|18422318|ref|NP_568624.1|//5.00E-87//COP1-interacting protein-related [Arabidopsis thaliana]	Unigene23043_All//9.00E-64//AT5G43310| COP1-interacting protein-related	Unigene23043_All//0.00E+00//TC131438			GO:0044464	nr +
Unigene23047_All	1019	0.51	0.30	0.63	3.42	3.55	4.96	0.95	1.44	4.14	-7.84E-01	4.22E-01		2.88E-01	7.25E-01		5.23E-02	8.96E-01		5.37E-01	4.83E-02		5.89E-01	2.39E-01		2.12E+00	2.82E-12	Up	Unigene23047_All//gi|297821204|ref|XP_002878485.1|//5.00E-31//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324323|gb|EFH54744.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene23047_All//3.00E-25//AT3G62900| zinc ion binding	Unigene23047_All//8.00E-45//DW501509				nr +
Unigene2305_All	1908	35.35	7.99	13.87	48.72	44.70	28.78	3.74	2.02	2.48	-2.14E+00	7.86E-151	Down	-1.35E+00	5.05E-76	Down	-1.24E-01	2.55E-02		-7.59E-01	9.69E-46		-8.94E-01	5.37E-06		-5.92E-01	1.73E-03		Unigene2305_All//gi|152406633|ref|NP_190850.1|//1.00E-105//IQ011 (IQ-domain 11); calmodulin binding [Arabidopsis thaliana]	Unigene2305_All//8.00E-105//AT5G13460| IQ011 (IQ-domain 11); calmodulin binding	Unigene2305_All//0.00E+00//TC151171				nr -

Unigene23051_All	1367	3.67	7.71	6.23	7.80	8.29	6.31	11.29	11.07	9.30	1.07E+00	3.94E-09	Up	7.62E-01	2.09E-04		8.78E-02	6.74E-01		-3.06E-01	9.82E-02		-2.85E-02	8.54E-01		-2.80E-01	2.73E-02		Unigene23051_All//gi|255576262|ref|XP_002529024.1|//6.00E-38//protein binding protein, putative [Ricinus communis] >gi|223531504|gb|EEF33335.1| protein binding protein, putative [Ricinus communis]	Unigene23051_All//9.00E-07//AT5G55390| EDM2; transcription factor	Unigene23051_All//0.00E+00//TC138017				nr -
Unigene23053_All	3552	0.25	1.13	0.31	0.76	0.67	0.67	0.98	0.54	0.59	2.17E+00	1.27E-09	Up	3.30E-01	6.40E-01		-1.79E-01	6.62E-01		-1.68E-01	6.99E-01		-8.51E-01	3.97E-03		-7.16E-01	1.20E-02		Unigene23053_All//gi|145359280|ref|NP_200350.2|//0.00E+00//EDM2; transcription factor [Arabidopsis thaliana]	Unigene23053_All//0.00E+00//AT5G55390| EDM2; transcription factor	Unigene23053_All//0.00E+00//TC138017		ko00310|Lysine degradation		nr +
Unigene23054_All	1630	5.78	1.24	4.51	15.22	12.97	5.21	27.21	19.33	16.30	-2.22E+00	1.85E-22	Down	-3.58E-01	7.65E-02		-2.31E-01	3.76E-02		-1.55E+00	8.45E-39	Down	-4.93E-01	4.49E-12		-7.39E-01	1.00E-24		Unigene23054_All//gi|229002575|dbj|BAH57745.1|//0.00E+00//lipoxygenase [Actinidia arguta]	Unigene23054_All//0.00E+00//AT3G22400| LOX5; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene23054_All//1.00E-161//TC153291		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0006633//GO:0016702//GO:0046914//GO:0048527	nr +
Unigene23055_All	4973	57.66	80.14	38.92	15.54	12.87	12.57	11.56	5.93	5.42	4.75E-01	1.07E-77		-5.67E-01	7.67E-75		-2.71E-01	7.42E-07		-3.06E-01	1.02E-07		-9.63E-01	4.99E-48		-1.09E+00	1.25E-60	Down	Unigene23055_All//gi|33235471|emb|CAE17327.1|//0.00E+00//lipoxygenase [Fragaria x ananassa]	Unigene23055_All//0.00E+00//AT3G22400| LOX5; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene23055_All//0.00E+00//TC129578		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0006633//GO:0016702//GO:0046914//GO:0048527	nr +
Unigene23057_All	1142	30.42	18.64	21.50	60.28	61.75	71.30	53.35	21.92	32.55	-7.07E-01	1.70E-14		-5.01E-01	8.40E-08		3.48E-02	6.70E-01		2.42E-01	1.99E-05		-1.28E+00	2.11E-80	Down	-7.13E-01	1.26E-31		Unigene23057_All//gi|195616008|gb|ACG29834.1|//1.00E-160//eukaryotic translation initiation factor 3 subunit 6-interacting protein [Zea mays]	Unigene23057_All//1.00E-173//AT5G25757| unknown protein	Unigene23057_All//0.00E+00//TC136128				nr +
Unigene23058_All	1213	20.06	8.77	13.70	25.09	20.35	24.05	28.69	11.47	11.82	-1.19E+00	6.88E-24	Down	-5.50E-01	1.35E-06		-3.02E-01	1.22E-03		-6.10E-02	6.07E-01		-1.32E+00	2.08E-48	Down	-1.28E+00	2.28E-47	Down	Unigene23058_All//gi|195616008|gb|ACG29834.1|//1.00E-158//eukaryotic translation initiation factor 3 subunit 6-interacting protein [Zea mays]	Unigene23058_All//1.00E-171//AT5G25757| unknown protein	Unigene23058_All//0.00E+00//gi|78351280|gb|DT571554.1|DT571554				nr -
Unigene2306_All	511	3.07	8.33	0.94	3.22	3.64	5.30	6.45	13.17	5.77	1.44E+00	3.87E-06	Up	-1.71E+00	3.82E-03		1.78E-01	7.69E-01		7.21E-01	6.52E-02		1.03E+00	5.74E-07	Up	-1.62E-01	6.10E-01		Unigene2306_All//gi|255549978|ref|XP_002516040.1|//9.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223544945|gb|EEF46460.1| conserved hypothetical protein [Ricinus communis]		Unigene2306_All//2.00E-158//gi|48817347|gb|CO118660.1|CO118660				nr +
Unigene23060_All	2178	1.51	2.09	1.47	5.97	8.22	5.33	6.99	1.06	3.00	4.68E-01	1.03E-01		-4.50E-02	9.07E-01		4.62E-01	1.90E-04		-1.64E-01	3.78E-01		-2.73E+00	1.23E-55	Down	-1.22E+00	8.93E-20	Down	Unigene23060_All//gi|224058599|ref|XP_002299559.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222846817|gb|EEE84364.1| GRAS family transcription factor [Populus trichocarpa]	Unigene23060_All//4.00E-178//AT1G63100| scarecrow transcription factor family protein	Unigene23060_All//3.00E-80//gi|109870218|gb|DW499194.1|DW499194	GRAS		GO:0010468	nr +
Unigene23061_All	2198	0.95	0.97	0.51	4.37	3.73	2.38	4.12	0.68	1.49	2.40E-02	9.77E-01		-9.04E-01	5.29E-02		-2.30E-01	2.50E-01		-8.76E-01	1.39E-06		-2.59E+00	1.67E-31	Down	-1.47E+00	7.88E-16	Down	Unigene23061_All//gi|224058599|ref|XP_002299559.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222846817|gb|EEE84364.1| GRAS family transcription factor [Populus trichocarpa]	Unigene23061_All//0.00E+00//AT1G63100| scarecrow transcription factor family protein	Unigene23061_All//0.00E+00//gi|109870218|gb|DW499194.1|DW499194	GRAS		GO:0010468	nr -
Unigene23062_All	2137	1.47	1.33	0.92	3.94	5.27	4.04	5.82	0.92	2.24	-1.46E-01	6.72E-01		-6.72E-01	6.85E-02		4.20E-01	1.14E-02		3.52E-02	8.92E-01		-2.66E+00	2.22E-44	Down	-1.38E+00	1.57E-19	Down	Unigene23062_All//gi|224058599|ref|XP_002299559.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222846817|gb|EEE84364.1| GRAS family transcription factor [Populus trichocarpa]	Unigene23062_All//0.00E+00//AT1G63100| scarecrow transcription factor family protein	Unigene23062_All//3.00E-89//gi|109870218|gb|DW499194.1|DW499194	GRAS		GO:0010468	nr -
Unigene23064_All	2095	2.42	1.14	0.69	4.38	3.19	1.19	4.42	0.74	1.84	-1.09E+00	5.58E-05	Down	-1.82E+00	2.76E-09	Down	-4.56E-01	1.24E-02		-1.88E+00	3.35E-19	Down	-2.58E+00	3.85E-32	Down	-1.26E+00	5.56E-13	Down	Unigene23064_All//gi|31711982|gb|AA96834Z.1|//1.00E-160//At5g12900 [Arabidopsis thaliana] >gi|47847287|dbj|BAD21351.1| IRK-interacting protein [Arabidopsis thaliana]	Unigene23064_All//6.00E-152//AT5G12900| unknown protein	Unigene23064_All//0.00E+00//TC149269				nr -
Unigene23065_All	3215	221.29	227.09	264.54	20.27	29.25	24.12	12.68	38.75	16.13	3.73E-02	7.09E-02		2.58E-01	3.44E-51		5.29E-01	5.82E-27		2.51E-01	1.59E-05		1.61E+00	4.34E-230	Up	3.48E-01	5.98E-08		Unigene23065_All//gi|145408582|ref|YP_001152206.1|//5.00E-51//ORF137 [Pinus koraiensis] >gi|145048833|gb|ABP35449.1| ORF137 [Pinus koraiensis]		Unigene23065_All//0.00E+00//TC175763			GO:0004175//GO:0009536//GO:0019538//GO:0046914	nr +
Unigene23066_All	1372	13.77	5.84	4.74	14.41	9.34	8.20	15.07	7.19	5.89	-1.24E+00	8.44E-20	Down	-1.54E+00	3.25E-26	Down	-6.27E-01	3.24E-08		-8.14E-01	2.00E-11		-1.07E+00	5.93E-21	Down	-1.35E+00	4.58E-31	Down	Unigene23066_All//gi|5123836|emb|CAB45387.1|//1.00E-133//NAD-malate dehydrogenase [Nicotiana tabacum]	Unigene23066_All//4.00E-116//AT3G47520| MDH (MALATE DEHYDROGENASE); L-malate dehydrogenase/ binding / catalytic/ malate dehydrogenase/ oxidoreductase/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	Unigene23066_All//0.00E+00//TC133370		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene23067_All	1789	6.11	1.78	2.02	8.91	5.27	6.19	24.46	7.87	6.57	-1.78E+00	1.39E-19	Down	-1.59E+00	3.58E-16	Down	-7.57E-01	3.47E-09		-5.27E-01	1.10E-04		-1.64E+00	4.56E-83	Down	-1.90E+00	4.56E-105	Down	Unigene23067_All//gi|5123836|emb|CAB45387.1|//1.00E-156//NAD-malate dehydrogenase [Nicotiana tabacum]	Unigene23067_All//2.00E-116//AT3G47520| MDH (MALATE DEHYDROGENASE); L-malate dehydrogenase/ binding / catalytic/ malate dehydrogenase/ oxidoreductase/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	Unigene23067_All//0.00E+00//TC169263		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene23068_All	1811	8.73	4.48	3.12	6.22	4.92	3.92	13.10	5.61	4.40	-9.63E-01	2.32E-11		-1.49E+00	6.77E-21	Down	-3.36E-01	4.56E-02		-6.67E-01	5.36E-05		-1.22E+00	1.46E-29	Down	-1.57E+00	2.92E-44	Down	Unigene23068_All//gi|5123836|emb|CAB45387.1|//0.00E+00//NAD-malate dehydrogenase [Nicotiana tabacum]	Unigene23068_All//9.00E-156//AT3G47520| MDH (MALATE DEHYDROGENASE); L-malate dehydrogenase/ binding / catalytic/ malate dehydrogenase/ oxidoreductase/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	Unigene23068_All//0.00E+00//TC133370		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0009536//GO:0016615//GO:0043648//GO:0044238	nr -
Unigene23073_All	816	1.41	0.00	1.17	1.59	0.76	0.66	4.46	1.95	2.73	-1.05E+01	9.91E-07	Down	-2.64E-01	6.64E-01		-1.06E+00	6.06E-02		-1.26E+00	3.78E-02		-1.19E+00	4.81E-05	Down	-7.05E-01	1.09E-02		Unigene23073_All//gi|297722809|ref|NP_001173768.1|//4.00E-63//Os04g0169500 [Oryza sativa Japonica Group] >gi|255675175|dbj|BAH92496.1| Os04g0169500 [Oryza sativa Japonica Group]	Unigene23073_All//3.00E-68//AT3G23160| unknown protein	Unigene23073_All//0.00E+00//CK640597			GO:0043231	nr -
Unigene23074_All	2149	0.56	1.01	0.47	1.81	2.64	1.66	1.71	3.07	7.86	8.56E-01	4.88E-02		-2.50E-01	6.75E-01		5.48E-01	2.58E-02		-1.23E-01	7.10E-01		8.44E-01	3.72E-05		2.20E+00	6.07E-49	Up	Unigene23074_All//gi|297722809|ref|NP_001173768.1|//5.00E-86//Os04g0169500 [Oryza sativa Japonica Group] >gi|255675175|dbj|BAH92496.1| Os04g0169500 [Oryza sativa Japonica Group]	Unigene23074_All//4.00E-92//AT3G23160| unknown protein	Unigene23074_All//6.00E-35//CK640597			GO:0043231	nr +
Unigene23075_All	2068	1.70	0.37	1.16	2.46	1.96	2.38	3.56	1.11	3.33	-2.21E+00	9.68E-09	Down	-5.49E-01	1.16E-01		-3.22E-01	2.47E-01		-4.56E-02	8.88E-01		-1.68E+00	4.07E-15	Down	-9.41E-02	6.40E-01		Unigene23075_All//gi|57834005|emb|CAI44602.1|//1.00E-123//P0650D04.6 [Oryza sativa (japonica cultivar-group)]	Unigene23075_All//7.00E-177//AT3G23160| unknown protein	Unigene23075_All//6.00E-35//CK640597				nr -
Unigene23078_All	900	4.77	4.56	3.91	4.48	3.60	7.23	1.08	2.41	5.49	-6.40E-02	8.28E-01		-2.88E-01	3.82E-01		-3.18E-01	3.19E-01		6.89E-01	2.64E-03		1.16E+00	3.26E-03		2.34E+00	5.30E-16	Up	Unigene23078_All//gi|297809607|ref|XP_002872687.1|//3.00E-39//malonyl-CoA decarboxylase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318524|gb|EFH48946.1| malonyl-CoA decarboxylase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23078_All//1.00E-33//AT4G04320| malonyl-CoA decarboxylase family protein			ko04146|Peroxisome//ko00640|Propanoate metabolism//ko00410|beta-Alanine metabolism	GO:0000166//GO:0004672//GO:0006631//GO:0016831//GO:0042579//GO:0043170	nr +
Unigene2308_All	2478	2.49	0.98	1.68	7.28	4.17	7.60	7.59	3.34	3.54	-1.34E+00	7.84E-08	Down	-5.72E-01	2.20E-02		-8.04E-01	2.07E-11		6.27E-02	7.02E-01		-1.18E+00	1.75E-22	Down	-1.10E+00	9.91E-21	Down	Unigene2308_All//gi|18401257|ref|NP_566559.1|//0.00E+00//APUM24 (Arabidopsis Pumilio 24); RNA binding / binding [Arabidopsis thaliana] >gi|15010674|gb|AAK73996.1| AT3g16810/K2019_3 [Arabidopsis thaliana]	Unigene2308_All//0.00E+00//AT3G16810| APUM24 (Arabidopsis Pumilio 24); RNA binding / binding	Unigene2308_All//0.00E+00//ES795540			GO:0003676//GO:0031981	nr -
Unigene23088_All	984	10.21	7.52	8.60	8.25	8.82	6.93	3.35	3.70	0.93	-4.41E-01	1.52E-02		-2.47E-01	2.25E-01		9.59E-02	6.96E-01		-2.52E-01	2.65E-01		1.41E-01	6.45E-01		-1.85E+00	2.06E-08	Down	Unigene23088_All//gi|115447627|ref|NP_001047593.1|//7.00E-69//Os02g0651300 [Oryza sativa Japonica Group] >gi|49387879|dbj|BAD26566.1| chaperone protein dnaJ-like [Oryza sativa Japonica Group] >gi|113537124|dbj|BAF09507.1| Os02g0651300 [Oryza sativa Japonica Group]	Unigene23088_All//7.00E-64//AT5G61670| Encodes a close homolog of the Cauliflower OR (Orange) protein. The function of OR is to induce the differentiation of proplastids or other noncolored plastids into chromoplasts for carotenoid accumulation. Both proteins contain a Cysteine-rich zinc finger domain that is highly specific to DnaJ-like molecular chaperons.	Unigene23088_All//0.00E+00//gi|109825420|gb|DW224153.1|DW224153			GO:0005515//GO:0009657//GO:0016117//GO:0043231//GO:0044267	nr +
Unigene23089_All	1269	36.32	23.96	38.52	27.64	36.77	19.40	5.33	3.85	2.54	-6.00E-01	2.12E-14		8.47E-02	3.62E-01		4.12E-01	9.20E-09		-5.11E-01	5.45E-09		-4.68E-01	2.17E-02		-1.07E+00	1.15E-07	Down	Unigene23089_All//gi|20453124|gb|AAM19804.1|//1.00E-134//AT5g61670/k11j9_190 [Arabidopsis thaliana] >gi|23506191|gb|AAX31107.1| At5g61670/k11j9_190 [Arabidopsis thaliana]	Unigene23089_All//1.00E-119//AT5G61670| Encodes a close homolog of the Cauliflower OR (Orange) protein. The function of OR is to induce the differentiation of proplastids or other noncolored plastids into chromoplasts for carotenoid accumulation. Both proteins contain a Cysteine-rich zinc finger domain that is highly specific to DnaJ-like molecular chaperons.	Unigene23089_All//0.00E+00//TC135419				nr +
Unigene23092_All	3175	8.12	3.78	5.25	10.79	7.88	8.31	7.16	3.70	2.41	-1.10E+00	2.22E-22	Down	-6.30E-01	1.15E-08		-4.53E-01	6.62E-08		-3.78E-01	2.43E-05		-9.54E-01	3.30E-19		-1.57E+00	2.00E-42	Down	Unigene23092_All//gi|223452422|gb|ACM89538.1|//0.00E+00//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene23092_All//0.00E+00//AT1G72180| leucine-rich repeat transmembrane protein kinase, putative	Unigene23092_All//0.00E+00//TC162959			GO:0004672//GO:0005488//GO:0044464	nr +

Unigene23093_All	250	0.21	1.22	0.00	0.80	2.07	1.99	3.38	0.50	0.80	2.54E+00	1.51E-01			-7.71E+00	6.24E-01		1.37E+00	2.26E-01		1.32E+00	2.52E-01		-2.75E+00	9.73E-04	Down	-2.09E+00	4.37E-03		Unigene23093_All|gi|115446991|ref|NP_001047275.1|//4.00E-21//0s02g0588500 [Oryza sativa Japonica Group] >gi|113536806|dbj|BAF09189.1|0s02g0588500 [Oryza sativa Japonica Group]	Unigene23093_All//6.00E-19//AT1G66970| SVL2 (SHV3-LIKE 2); glycerophosphodiester phosphodiesterase/ kinase	Unigene23093_All//4.00E-139//EY198122			GO:0005576//GO:0008081//GO:0009536//GO:0016772//GO:0019400//GO:0032425//GO:0031410	nr +
Unigene23094_All	2708	29.79	4.66	6.57	44.33	32.16	17.28	28.46	5.45	12.12	-2.68E+00	9.18E-235	Down	-2.18E+00	3.06E-178	Down	-4.63E-01	1.50E-27		-1.36E+00	2.31E-153	Down	-2.39E+00	6.57E-240	Down	-1.23E+00	5.84E-98	Down	Unigene23094_All|gi|115500890|dbj|BAF34116.1|//0.00E+00//glycerophosphodiesterase-like protein [Nicotiana tabacum]	Unigene23094_All//0.00E+00//AT5G55480| SVL1 (SHV3-LIKE 1); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase	Unigene23094_All//0.00E+00//TC152032		ko00564|Glycerophospholipid metabolism	GO:0000904//GO:0005576//GO:0005618//GO:0008081//GO:0009536//GO:0009826//GO:0010383//GO:0016772//GO:0019400//GO:0031225//GO:0031410//GO:0035315//GO:0048764	nr -
Unigene23095_All	725	2.31	0.77	1.98	1.79	2.47	2.68	4.67	1.73	1.59	-1.59E+00	3.09E-03		-2.20E-01	6.59E-01		4.67E-01	3.80E-01		5.85E-01	2.29E-01		-1.43E+00	5.24E-06	Down	-1.55E+00	6.56E-07	Down	Unigene23095_All|gi|22329062|ref|NP_194909.2|//9.00E-86//enoyl-CoA hydratase/isomerase family protein [Arabidopsis thaliana] >gi|75247660|sp|Q8RXN4.1|HIBC5_ARATH RecName: Full=3-hydroxyisobutyryl-CoA hydrolase-like protein 2, mitochondrial; Flags: Precursor	Unigene23095_All//2.00E-79//AT4G31810| enoyl-CoA hydratase/isomerase family protein	Unigene23095_All//0.00E+00//ES841318		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism	GO:0009062//GO:0016289//GO:0016836//GO:0043231	nr -
Unigene23096_All	1784	3.37	1.90	2.81	4.61	4.54	3.14	4.50	1.31	2.14	-8.26E-01	6.28E-04		-2.66E-01	3.27E-01		-2.25E-02	9.23E-01		-5.54E-01	5.76E-03		-1.78E+00	8.97E-18	Down	-1.07E+00	5.67E-09	Down	Unigene23096_All|gi|22329062|ref|NP_194909.2|//1.00E-163//enoyl-CoA hydratase/isomerase family protein [Arabidopsis thaliana] >gi|75247660|sp|Q8RXN4.1|HIBC5_ARATH RecName: Full=3-hydroxyisobutyryl-CoA hydrolase-like protein 2, mitochondrial; Flags: Precursor	Unigene23096_All//1.00E-158//AT4G31810| enoyl-CoA hydratase/isomerase family protein	Unigene23096_All//0.00E+00//ES841318		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism		nr -
Unigene23098_All	1995	10.12	5.13	5.53	61.48	42.00	21.03	21.15	5.57	5.67	-9.81E-01	1.01E-14		-8.74E-01	1.01E-11		-5.50E-01	1.98E-38		-1.55E+00	2.08E-190	Down	-1.92E+00	2.74E-100	Down	-1.90E+00	1.66E-101	Down	Unigene23098_All|gi|30679432|ref|NP_187173.2|//1.00E-117//heavy-metal-associated domain-containing protein [Arabidopsis thaliana]	Unigene23098_All//4.00E-27//AT3G06130| heavy-metal-associated domain-containing protein	Unigene23098_All//8.00E-173//DR456194		ko03040|Spliceosome		nr +
Unigene23099_All	595	0.35	0.34	1.07	0.00	0.81	1.06	1.99	2.39	4.42	-4.63E-02	9.88E-01		1.61E+00	1.11E-01		9.66E+00	5.07E-03		1.01E+01	7.60E-04	Up	2.63E-01	6.49E-01		1.15E+00	8.15E-04	Up	Unigene23099_All|gi|224103591|ref|XP_002313114.1|//2.00E-65//predicted protein [Populus trichocarpa] >gi|222849522|gb|EEES7069.1|predicted protein [Populus trichocarpa]	Unigene23099_All//9.00E-43//AT3G19190| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: ATG2, C-terminal (InterPro:IPR015412); Has 603 Blast hits to 514 proteins in 156 species: Archae - 0; Bacteria - 19; Metazoa - 326; Fungi - 168; Plants - 38; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).					nr +
Unigene2310_All	2003	1.07	3.72	2.98	2.98	3.51	2.55	2.24	1.15	0.70	1.80E+00	1.13E-13	Up	1.48E+00	3.26E-08	Up	2.33E-01	3.45E-01		-2.28E-01	4.04E-01		-9.63E-01	1.71E-04		-1.68E+00	6.76E-10	Down	Unigene2310_All|gi|15237681|ref|NP_201241.1|//6.00E-35//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|30698003|ref|NP_851265.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|79332130|ref|NP_001032136.1|DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|134031896|gb|AB045685.1|At5g64360 [Arabidopsis thaliana] >gi|222423220|dbj|BAH19587.1|AT5G64360 [Arabidopsis thaliana]	Unigene2310_All//3.00E-36//AT5G64360| DNAJ heat shock N-terminal domain-containing protein	Unigene2310_All//0.00E+00//TC161868			GO:0005515	nr -
Unigene23100_All	5785	1.17	3.08	1.83	2.26	2.23	3.22	7.79	10.60	15.31	1.40E+00	2.03E-22	Up	6.51E-01	3.34E-04		-2.47E-02	8.93E-01		5.10E-01	4.69E-05		4.44E-01	1.21E-13		9.75E-01	1.20E-76		Unigene23100_All|gi|115467502|ref|NP_001057350.1|//1.00E-113//0s06g0267600 [Oryza sativa Japonica Group] >gi|53791759|dbj|BAD53524.1|potential autophagy related protein-like [Oryza sativa Japonica Group] >gi|113595390|dbj|BAF19264.1|0s06g0267600 [Oryza sativa Japonica Group]	Unigene23100_All//0.00E+00//AT3G19190| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: ATG2, C-terminal (InterPro:IPR015412); Has 603 Blast hits to 514 proteins in 156 species: Archae - 0; Bacteria - 19; Metazoa - 326; Fungi - 168; Plants - 38; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene23100_All//0.00E+00//gi|164339363|gb|ES823266.1|ES823266				nr -
Unigene23102_All	1139	3.03	2.40	2.48	3.32	3.02	2.30	2.04	1.58	0.80	-3.36E-01	3.33E-01		-2.91E-01	4.06E-01		-1.37E-01	7.04E-01		-5.31E-01	1.00E-01		-3.72E-01	3.57E-01		-1.34E+00	3.20E-04	Down	Unigene23102_All|gi|15222660|ref|NP_173944.1|//1.00E-105//phosphoribulokinase/uridine kinase family protein [Arabidopsis thaliana]	Unigene23102_All//2.00E-98//AT1G26190| phosphoribulokinase/uridine kinase family protein	Unigene23102_All//0.00E+00//TC169509			GO:0006139//GO:0009058//GO:0016772//GO:0032559	nr +
Unigene23103_All	2126	4.21	5.17	2.43	3.77	3.34	3.42	3.48	1.97	1.09	2.97E-01	9.55E-02		-7.93E-01	7.68E-05		-1.77E-01	4.52E-01		-1.41E-01	5.68E-01		-8.24E-01	1.73E-05		-1.68E+00	1.01E-15	Down	Unigene23103_All|gi|15222660|ref|NP_173944.1|//0.00E+00//phosphoribulokinase/uridine kinase family protein [Arabidopsis thaliana]	Unigene23103_All//0.00E+00//AT1G26190| phosphoribulokinase/uridine kinase family protein	Unigene23103_All//0.00E+00//ES797197		ko00240|Pyrimidine metabolism	GO:0006164//GO:0006397//GO:0009975//GO:0019204//GO:0019206//GO:0032559//GO:0034708	nr +
Unigene23104_All	1230	31.69	32.63	39.70	15.43	21.73	17.40	13.20	7.71	6.45	4.20E-02	6.55E-01		3.25E-01	3.44E-05		4.94E-01	4.29E-07		1.74E-01	1.94E-01		-7.75E-01	4.78E-10		-1.03E+00	2.53E-16	Down	Unigene23104_All|gi|115436372|ref|NP_001042944.1|//4.00E-91//0s01g0338600 [Oryza sativa Japonica Group] >gi|53792377|dbj|BAD53130.1|cyanobacteria-specific protein-like [Oryza sativa Japonica Group] >gi|113532475|dbj|BAF04858.1|0s01g0338600 [Oryza sativa Japonica Group]	Unigene23104_All//5.00E-97//AT2G43945| unknown protein	Unigene23104_All//0.00E+00//CO077261			GO:0008172//GO:0009536	nr -
Unigene23105_All	2240	2.38	2.40	2.59	2.45	2.29	1.92	2.17	1.57	0.78	9.20E-03	9.90E-01		1.21E-01	6.37E-01		-9.48E-02	7.69E-01		-3.53E-01	1.94E-01		-4.70E-01	5.78E-02		-1.47E+00	6.35E-09	Down	Unigene23105_All|gi|115436372|ref|NP_001042944.1|//1.00E-65//0s01g0338600 [Oryza sativa Japonica Group] >gi|53792377|dbj|BAD53130.1|cyanobacteria-specific protein-like [Oryza sativa Japonica Group] >gi|113532475|dbj|BAF04858.1|0s01g0338600 [Oryza sativa Japonica Group]	Unigene23105_All//1.00E-71//AT2G43945| unknown protein	Unigene23105_All//0.00E+00//CO119087			GO:0008172//GO:0009536	nr +
Unigene23106_All	1226	74.21	35.75	46.47	119.50	119.77	52.09	32.69	11.22	7.12	-1.05E+00	1.11E-71	Down	-6.75E-01	1.05E-32		3.20E-03	9.53E-01		-1.20E+00	1.54E-153	Down	-1.54E+00	4.63E-70	Down	-2.20E+00	9.91E-117	Down	Unigene23106_All|gi|15242118|ref|NP_199968.1|//1.00E-165//EXL3 (EXORDIUM LIKE 3) [Arabidopsis thaliana] >gi|16226762|gb|AAL16255.1|AF428325_1 AT5g51550/K17N15_10 [Arabidopsis thaliana]	Unigene23106_All//1.00E-156//AT5G51550| EXL3 (EXORDIUM LIKE 3)	Unigene23106_All//0.00E+00//TC134506				nr -
Unigene23107_All	1399	7.78	5.65	4.76	35.07	18.76	10.40	5.35	1.25	1.22	-4.61E-01	7.76E-03		-7.09E-01	7.41E-05		-9.03E-01	5.50E-37		-1.75E+00	2.00E-91	Down	-2.09E+00	2.00E-20	Down	-2.13E+00	1.51E-21	Down	Unigene23107_All|gi|16604527|gb|AL243269.1|//1.00E-154//AT5g51550/K17N15_10 [Arabidopsis thaliana] >gi|21655293|gb|AAM65358.1|AT5g51550/K17N15_10 [Arabidopsis thaliana]	Unigene23107_All//3.00E-142//AT5G51550| EXL3 (EXORDIUM LIKE 3)	Unigene23107_All//0.00E+00//gi|78349671|gb|DT569945.1|DT569945				nr -
Unigene23108_All	1501	4.08	2.53	2.45	6.77	5.41	1.59	3.61	2.09	1.01	-6.88E-01	3.94E-03		-7.36E-01	3.07E-03		-3.23E-01	7.51E-02		-2.09E+00	3.11E-24	Down	-7.88E-01	5.56E-04		-1.84E+00	3.51E-13	Down	Unigene23108_All|gi|15242118|ref|NP_199968.1|//1.00E-165//EXL3 (EXORDIUM LIKE 3) [Arabidopsis thaliana] >gi|16226762|gb|AAL16255.1|AF428325_1 AT5g51550/K17N15_10 [Arabidopsis thaliana]	Unigene23108_All//4.00E-156//AT5G51550| EXL3 (EXORDIUM LIKE 3)	Unigene23108_All//0.00E+00//TC134506				nr -
Unigene23110_All	2538	7.11	39.91	11.31	11.01	20.26	31.50	43.23	74.72	119.34	2.49E+00	4.89E-269	Up	6.69E-01	1.39E-10		8.80E-01	1.15E-35		1.52E+00	1.52E-118	Up	7.89E-01	6.13E-112		1.47E+00	0.00E+00	Up	Unigene23110_All|gi|33637487|gb|AAQ23899.1|//0.00E+00//RSH2 [Nicotiana tabacum]	Unigene23110_All//0.00E+00//AT3G14650| RSH2 (RELA-SPOT HOMOLOG 2); GTP diphosphokinase	Unigene23110_All//0.00E+00//TC151760			GO:0006950//GO:0008617//GO:0009536//GO:0009725//GO:0015291//GO:0015893//GO:0016020//GO:0016778//GO:0016294	nr -
Unigene23114_All	1974	3.66	1.49	2.54	1.77	1.62	1.30	2.98	5.61	9.71	-1.30E+00	1.38E-08	Down	-5.29E-01	2.07E-02		-1.23E-01	7.55E-01		-4.38E-01	2.10E-01		9.14E-01	3.77E-09		1.71E+00	9.22E-40	Up	Unigene23114_All|gi|297814950|ref|XP_002875358.1|//1.00E-126//peptidase M48 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321196|gb|EFH51617.1|peptidase M48 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23114_All//2.00E-120//AT3G27110| peptidase M48 family protein	Unigene23114_All//0.00E+00//gi|78340335|gb|DT560609.1|DT560609			GO:0004175//GO:0019538//GO:0044464	nr -
Unigene23117_All	1054	10.67	27.02	15.31	24.77	21.27	17.35	20.86	31.09	24.42	1.34E+00	4.56E-33	Up	5.20E-01	2.89E-04		-2.20E-01	4.23E-02		-5.13E-01	6.46E-07		5.76E-01	7.92E-12		2.27E-01	1.88E-02		Unigene23117_All|gi|15233464|ref|NP_194645.1|//2.00E-96//SNF7.1 [Arabidopsis thaliana] >gi|145334175|ref|NP_001078468.1|SNF7.1 [Arabidopsis thaliana] >gi|75213588|sp|Q9SZE4.1|VPS22_ARATH RecName: Full=Vacuolar protein sorting-associated protein 32 homolog 2; Short=AtVPS32-2; AltName: Full=Charged multivesicular body protein 4 homolog 2; AltName: Full=ESCRT-III complex subunit VPS32 homolog 2	Unigene23117_All//3.00E-58//AT4G29160| SNF7.1	Unigene23117_All//0.00E+00//gi|78336388|gb|DT556662.1|DT556662		ko04144|Endocytosis	GO:0006810//GO:0010008	nr +
Unigene23119_All	683	5.44	4.45	2.73	18.01	13.31	7.41	3.47	0.43	1.40	-2.89E-01	3.80E-01		-9.95E-01	2.95E-03		-4.37E-01	4.39E-03		-1.28E+00	8.16E-15	Down	-3.02E+00	3.98E-10	Down	-1.31E+00	3.80E-04	Down	Unigene23119_All|gi|109509138|gb|ABG34278.1|//1.00E-76//polygalacturonase [Eucalyptus globulus subsp. globulus]	Unigene23119_All//9.00E-71//AT3G62110| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene23119_All//0.00E+00//TC158871		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553//GO:0031410//GO:0043231//GO:0044238//GO:0045229	nr +

Unigene2312_A11	1149	7.15	16.80	6.26	31.52	57.57	53.65	133.13	143.32	275.89	1.23E+00	5.45E-20	Up	-1.92E-01	4.00E-01		8.69E-01	6.25E-45		7.68E-01	8.34E-31		1.06E-01	4.68E-03		1.05E+00	0.00E+00	Up	Unigene2312_A11//gi|18400517|ref|NP_566493.1|//3.00E-95//nodulin MtN3 family protein [Arabidopsis thaliana] >gi|11994587|dbj|BAB02642.1| MtN3-like protein [Arabidopsis thaliana] >gi|15809923|gb|AAL06889.1| AT3g14770/T21E2_2 [Arabidopsis thaliana] >gi|17978879|gb|AAL47411.1| AT3g14770/T21E2_2 [Arabidopsis thaliana]	Unigene2312_A11//2.00E-78//AT3G14770| nodulin MtN3 family protein	Unigene2312_A11//0.00E+00//TC176376			GO:0031224//GO:0031410	nr +
Unigene23120_A11	568	2.76	1.43	1.50	8.16	5.82	1.83	3.05	0.81	1.61	-9.53E-01	7.08E-02		-8.82E-01	1.13E-01		-4.87E-01	7.74E-02		-2.16E+00	8.64E-12	Down	-1.91E+00	8.45E-05	Down	-9.20E-01	3.10E-02		Unigene23120_A11//gi|109509138|gb|ABG34278.1|//2.00E-56//polygalacturonase [Eucalyptus globulus subsp. globulus]	Unigene23120_A11//2.00E-42//AT3G62110| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene23120_A11//0.00E+00//TC158871			GO:0004553//GO:0031410//GO:0043231//GO:0044238//GO:0045229	nr +
Unigene23121_A11	1852	3.39	0.90	3.71	7.69	6.77	3.41	3.29	0.50	0.77	-1.91E+00	1.16E-12	Down	1.30E-01	6.30E-01		-1.85E-01	2.62E-01		-1.17E+00	7.03E-15	Down	-2.73E+00	1.21E-22	Down	-2.09E+00	2.91E-17	Down	Unigene23121_A11//gi|297817560|ref|XP_002876663.1|//0.00E+00//glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] >gi|297322501|gb|EFH52922.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	Unigene23121_A11//0.00E+00//AT3G62110| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene23121_A11//0.00E+00//TC158871		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553//GO:0043231//GO:0044238//GO:0045229	nr -
Unigene23122_A11	1499	3.66	1.55	1.53	13.69	12.43	7.80	2.71	2.12	1.09	-1.24E+00	2.64E-06	Down	-1.26E+00	3.85E-06	Down	-1.40E-01	3.08E-01		-8.11E-01	9.37E-12		-3.54E-01	2.19E-01		-1.31E+00	1.59E-06	Down	Unigene23122_A11//gi|109509138|gb|ABG34278.1|//1.00E-120//polygalacturonase [Eucalyptus globulus subsp. globulus]	Unigene23122_A11//1.00E-115//AT3G62110| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene23122_A11//0.00E+00//TC158871		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0008152//GO:0016798	nr +
Unigene23123_A11	1057	2.77	0.86	1.21	26.91	11.79	22.52	36.60	40.25	22.69	-1.68E+00	1.95E-05	Down	-1.20E+00	2.12E-03		-1.19E+00	6.06E-34	Down	-2.57E-01	1.36E-02		1.37E-01	8.76E-02		-6.90E-01	2.57E-19		Unigene23123_A11//gi|15217543|ref|NP_177315.1|//1.00E-103//ATCK1 (CHOLINE KINASE 1); choline kinase [Arabidopsis thaliana] >gi|30725296|gb|AAP37670.1| At1g71697 [Arabidopsis thaliana] >gi|110739418|dbj|BAF01619.1| choline kinase like protein [Arabidopsis thaliana] >gi|110741310|dbj|BAF02205.1| choline kinase like protein [Arabidopsis thaliana]	Unigene23123_A11//4.00E-99//AT1G71697| ATCK1 (CHOLINE KINASE 1); choline kinase	Unigene23123_A11//0.00E+00//TC156508		ko00564|Glycerophospholipid metabolism	GO:0016301	nr +
Unigene23124_A11	1526	4.87	40.14	4.89	34.41	24.62	34.57	22.28	43.80	306.20	3.04E+00	3.35E-202	Up	4.90E-03	1.00E+00		-4.83E-01	3.08E-13		6.80E-03	9.47E-01		9.75E-01	7.81E-57		3.78E+00	0.00E+00	Up	Unigene23124_A11//gi|1438881|gb|AAC49375.1|//1.00E-144//GmCK2p [Glycine max]	Unigene23124_A11//7.00E-143//AT1G71697| ATCK1 (CHOLINE KINASE 1); choline kinase	Unigene23124_A11//0.00E+00//TC141931		ko00564|Glycerophospholipid metabolism		nr +
Unigene23127_A11	2809	5.29	6.30	7.77	3.92	6.15	8.79	5.89	5.65	14.51	2.51E-01	6.82E-02		5.55E-01	4.35E-06		6.51E-01	1.71E-07		1.17E+00	7.42E-25	Up	-5.78E-02	6.89E-01		1.30E+00	2.28E-56	Up	Unigene23127_A11//gi|60652321|gb|AX33233.1|//0.00E+00//plastid alpha-amylase [Actinidia chinensis]	Unigene23127_A11//0.00E+00//AT1G69830| AMY3 (ALPHA-AMYLASE-LIKE 3); alpha-amylase	Unigene23127_A11//0.00E+00//TC157834		ko00500|Starch and sucrose metabolism	GO:0005982//GO:0009532//GO:0016160//GO:0046872	nr +
Unigene23128_A11	1028	2.65	0.89	1.45	5.86	5.53	5.45	6.83	2.68	4.96	-1.58E+00	1.00E-04	Down	-8.68E-01	3.01E-02		-8.52E-02	7.85E-01		-1.06E-01	6.80E-01		-1.35E+00	1.11E-10	Down	-4.61E-01	1.64E-02		Unigene23128_A11//gi|20138095|sp|Q92V77.1|XPO2_ARATH//3.00E-96//RecName: Full=Exportin-2; Short=Exp2; AltName: Full=Importin-alpha re-exporter; AltName: Full=Cellular apoptosis susceptibility protein homolog >gi|18077710|emb|CAC83300.1| cellular apoptosis susceptibility protein homologue [Arabidopsis thaliana]	Unigene23128_A11//7.00E-86//AT2G46520| cellular apoptosis susceptibility protein, putative / importin-alpha re-exporter, putative	Unigene23128_A11//0.00E+00//gi|109858347|gb|DW487326.1|DW487326			GO:0005049//GO:0006635//GO:0006606//GO:0022892	nr -
Unigene2313_A11	1556	4.54	4.04	4.14	8.71	8.01	7.87	8.61	4.86	4.17	-1.69E-01	4.78E-01		-1.33E-01	6.18E-01		-1.20E-01	5.19E-01		-1.47E-01	4.13E-01		-8.25E-01	2.65E-09		-1.05E+00	7.37E-14	Down	Unigene2313_A11//gi|2213536|emb|CAA67290.1|//2.00E-88//DNA-binding protein PD1 [Pisum sativum] >gi|119657408|tpd|FAA00303.1| TPA: AT-hook motif nuclear localized protein 1 [Pisum sativum]	Unigene2313_A11//1.00E-84//AT1G63470| DNA-binding family protein	Unigene2313_A11//0.00E+00//TC171768				nr -
Unigene23135_A11	3503	4.17	1.53	2.54	5.90	3.87	3.12	8.38	5.25	5.64	-1.44E+00	2.32E-19	Down	-7.15E-01	2.46E-06		-6.08E-01	3.92E-08		-9.20E-01	1.64E-14		-6.74E-01	6.98E-14		-5.70E-01	7.38E-11		Unigene23135_A11//gi|79507158|ref|NP_196044.2|//7.00E-90//ELF6 (EARLY FLOWERING 6); transcription factor [Arabidopsis thaliana] >gi|50513175|gb|AAT77780.1| early flowering 6 [Arabidopsis thaliana]	Unigene23135_A11//5.00E-85//AT5G04240| ELF6 (EARLY FLOWERING 6); transcription factor	Unigene23135_A11//8.00E-162//gi|13349643|gb|BG439993.1|BG439993	Jumonji		GO:0000902//GO:0009725//GO:0010468//GO:0043231//GO:0046914//GO:0048581//GO:0070076	nr -
Unigene23137_A11	1916	3.88	8.20	9.25	3.56	4.48	4.38	5.43	6.68	6.28	1.08E+00	1.96E-13	Up	1.26E+00	2.87E-18	Up	3.29E-01	1.08E-01		3.00E-01	1.66E-01		2.98E-01	4.16E-02		2.10E-01	1.68E-01		Unigene23137_A11//gi|297808941|ref|XP_002871904.1|//0.00E+00//peptidase M28 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317741|gb|EFH48163.1| peptidase M28 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23137_A11//0.00E+00//AT5G19740| peptidase M28 family protein				GO:0008238//GO:0019538//GO:0043231	nr -
Unigene23139_A11	1683	0.19	0.00	0.44	0.56	0.25	0.35	6.10	19.12	23.01	-7.54E+00	3.66E-02		1.25E+00	1.54E-01		-1.20E+00	8.32E-02		-6.89E-01	3.58E-01		1.65E+00	8.71E-62	Up	1.91E+00	4.54E-93	Up	Unigene23139_A11//gi|15219169|ref|NP_175713.1|//1.00E-168//protein kinase family protein [Arabidopsis thaliana] >gi|9454540|gb|AAF87863.1|AC022520_7 similar to cdc2 protein kinase [Arabidopsis thaliana]	Unigene23139_A11//5.00E-165//AT1G53050| protein kinase family protein	Unigene23139_A11//0.00E+00//TC137973			GO:0000166//GO:0004674//GO:0009987	nr -
Unigene2314_A11	474	6.29	2.46	3.26	9.46	4.29	7.91	0.62	1.50	0.84	-1.36E+00	3.03E-04	Down	-9.50E-01	1.25E-02		-1.14E+00	1.96E-05	Down	-2.58E-01	4.18E-01		1.26E+00	1.07E-01		4.29E-01	6.62E-01		Unigene2314_A11//gi|115187393|gb|AB184250.1|//8.00E-32//thiamine biosynthetic enzyme [Arachis hypogaea]	Unigene2314_A11//1.00E-21//AT5G54770| THI1; protein homodimerization	Unigene2314_A11//0.00E+00//TC140898			GO:0006772//GO:0009507	nr +
Unigene23140_A11	2936	6.31	26.40	7.15	9.13	9.86	10.86	33.54	47.58	55.78	2.07E+00	5.40E-164	Up	1.80E-01	1.86E-01		1.12E-01	3.42E-01		2.51E-01	1.06E-02		5.04E-01	1.05E-37		7.34E-01	2.36E-87		Unigene23140_A11//gi|15219169|ref|NP_175713.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|9454540|gb|AAF87863.1|AC022520_7 similar to cdc2 protein kinase [Arabidopsis thaliana]	Unigene23140_A11//0.00E+00//AT1G53050| protein kinase family protein	Unigene23140_A11//0.00E+00//TC137973			GO:0004674//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene23142_A11	1604	4.40	2.72	5.38	7.27	5.43	3.89	3.16	2.58	1.17	-6.97E-01	1.52E-03		2.88E-01	1.81E-01		-4.20E-01	8.38E-03		-9.03E-01	3.18E-08		-2.94E-01	2.47E-01		-1.44E+00	5.47E-09	Down	Unigene23142_A11//gi|195625620|gb|AC034640.1|//1.00E-28//HT1 protein kinase [Zea mays]	Unigene23142_A11//2.00E-23//AT1G62400| HT1 (high leaf temperature 1); kinase/ protein serine/threonine/tyrosine kinase	Unigene23142_A11//0.00E+00//TC172815			GO:0004672//GO:0006464//GO:0010118//GO:0032559	nr +
Unigene23144_A11	1192	0.09	0.04	0.13	17.64	2.05	9.28	143.41	121.78	90.64	-1.05E+00	6.84E-01		6.10E-01	7.48E-01		-3.10E+00	1.42E-91	Down	-9.26E-01	6.53E-15		-2.36E-01	1.12E-11		-6.62E-01	1.69E-76		Unigene23144_A11//gi|15241268|ref|NP_200470.1|//1.00E-115//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|75171106|sp|Q9FJU9.1|E1313_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 13; AltName: Full=(1->3)-beta-glucan endohydrolase 13; Short=(1->3)-beta-glucanase 13; AltName: Full=Beta-1,3-endoglucanase 13; Short=Beta-1,3-glucanase 13; Flags: Precursor >gi|10176762|dbj|BAB09876.1| beta-1,3-glucanase-like protein [Arabidopsis thaliana] >gi|19715572|gb|AAL91612.1| AT5g56590/MIK19_3 [Arabidopsis thaliana] >gi|22137244|gb|AAM91467.1| AT5g56590/MIK19_3 [Arabidopsis thaliana]	Unigene23144_A11//2.00E-113//AT5G56590| glycosyl hydrolase family 17 protein	Unigene23144_A11//7.00E-166//gi|84158432|gb|DN827479.1|DN827479		ko00500|Starch and sucrose metabolism	GO:0016798//GO:0031225	nr +
Unigene23145_A11	1927	63.64	18.25	95.03	29.65	14.28	27.98	16.65	33.51	14.08	-1.80E+00	2.04E-217	Down	5.78E-01	9.14E-50		-1.05E+00	9.39E-56	Down	-8.35E-02	3.24E-01		1.01E+00	4.66E-58	Up	-2.42E-01	4.21E-03		Unigene23145_A11//gi|225445059|ref|XP_002283473.1|//1.00E-148//PREDICTED: similar to beta-1,3-glucanase [Vitis vinifera]	Unigene23145_A11//4.00E-135//AT5G56590| glycosyl hydrolase family 17 protein	Unigene23145_A11//0.00E+00//DN827506		ko00500|Starch and sucrose metabolism		nr -
Unigene23146_A11	1788	6.73	5.87	3.60	4.01	9.86	5.71	15.75	31.49	25.60	-1.98E-01	2.57E-01		-9.01E-01	1.30E-07		1.30E+00	6.29E-23	Up	5.09E-01	4.33E-03		1.00E+00	5.80E-50		7.01E-01	3.37E-23		Unigene23146_A11//gi|15082058|gb|AB84008.1|AF393847_1|//0.00E+00//beta-amylase PCT-BMY1 [Solanum tuberosum]	Unigene23146_A11//0.00E+00//AT4G17090| CT-BMY (CHLOROPLAST BETA-AMYLASE); beta-amylase	Unigene23146_A11//0.00E+00//TC133811		ko00500|Starch and sucrose metabolism	GO:0000023//GO:0005982//GO:0006950//GO:0009532//GO:0016160//GO:0043167	nr +
Unigene23147_A11	1867	16.09	4.32	10.07	15.24	19.46	7.38	47.15	122.68	145.48	-1.90E+00	1.44E-57	Down	-6.76E-01	3.23E-11		3.53E-01	2.38E-05		-1.05E+00	2.44E-24	Down	1.38E+00	0.00E+00	Up	1.63E+00	0.00E+00	Up	Unigene23147_A11//gi|15082058|gb|AB84008.1|AF393847_1|//0.00E+00//beta-amylase PCT-BMY1 [Solanum tuberosum]	Unigene23147_A11//0.00E+00//AT4G17090| CT-BMY (CHLOROPLAST BETA-AMYLASE); beta-amylase	Unigene23147_A11//0.00E+00//TC176569		ko00500|Starch and sucrose metabolism	GO:0000023//GO:0005982//GO:0006950//GO:0009532//GO:0016160//GO:0043167	nr -
Unigene23148_A11	1198	2.66	0.76	1.60	3.95	3.39	2.49	2.47	1.54	1.26	-1.81E+00	2.26E-06	Down	-7.35E-01	4.42E-02		-2.20E-01	4.78E-01		-6.67E-01	1.55E-02		-6.87E-01	3.47E-02		-9.67E-01	2.12E-03		Unigene23148_A11//gi|92893902|gb|AB591952.1|//3.00E-13//Zinc finger, CCHC-type [Medicago truncatula]	Unigene23148_A11//6.00E-12//AT2G01050| nucleic acid binding / zinc ion binding	Unigene23148_A11//1.00E-31//DW516140				nr -
Unigene23149_A11	1157	13.43	3.63	7.55	5.08	4.32	3.79	2.12	2.46	1.34	-1.89E+00	8.05E-30	Down	-8.31E-01	1.74E-08		-2.35E-01	3.84E-01		-4.24E-01	9.42E-02		2.13E-01	5.77E-01		-6.58E-01	5.85E-02		Unigene23149_A11//gi|158828302|gb|ABW81177.1|//3.00E-27//gag non-LTR retrotransposase [Arabidopsis cebennensis]	Unigene23149_A11//2.00E-24//AT2G01050| nucleic acid binding / zinc ion binding	Unigene23149_A11//7.00E-30//DW516140				nr -
Unigene2315_A11	1487	42.15	22.22	19.37	67.33	43.54	36.02	0.71	1.15	0.32	-9.24E-01	5.24E-40		-1.12E+00	6.37E-53	Down	-6.29E-01	5.00E-40		-9.03E-01	4.37E-66		6.97E-01	1.25E-01		-1.14E+00	4.77E-02		Unigene2315_A11//gi|58201024|gb|AAW66657.1|//1.00E-155//thiamine biosynthetic enzyme [Picrorhiza kurroa]	Unigene2315_A11//8.00E-144//AT5G54770| THI1; protein homodimerization	Unigene2315_A11//0.00E+00//TC136283				nr +
Unigene23153_A11	517	1.01	1.27	1.13	3.66	2.46	2.62	23.14	10.99	2.08	3.32E-01	6.80E-01		1.63E-01	8.50E-01		-5.71E-01	2.26E-01		-4.82E-01	3.38E-01		-1.07E+00	1.41E-12	Down	-3.48E+00	2.45E-57	Down	Unigene23153_A11//gi|240255793|ref|NP_192969.4|//1.00E-32//CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|51536592|gb|AAU05534.1| At4g12320 [Arabidopsis thaliana]	Unigene23153_A11//7.00E-34//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene23153_A11//7.00E-170//TC179067		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506	nr -
Unigene23154_A11	1422	1.55	4.38	3.18	10.02	9.93	9.85	40.91	33.51	7.76	1.50E+00	3.75E-09	Up	1.04E+00	4.87E-04	Up	-1.31E-02	9.49E-01		-2.52E-02	9.01E-01		-2.88E-01	3.08E-06		-2.40E+00	5.67E-188	Down	Unigene23154_A11//gi|240255793|ref|NP_192969.4|//3.00E-92//CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|51536592|gb|AAU05534.1| At4g12320 [Arabidopsis thaliana]	Unigene23154_A11//5.00E-82//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene23154_A11//0.00E+00//TC141023		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0016491//GO:0046872	nr +

Unigene23155_All	1224	7.82	9.44	7.66	20.39	29.06	18.60	54.37	52.42	16.47	2.71E-01	1.21E-01		-3.09E-02	8.86E-01		5.11E-01	7.59E-10		-1.33E-01	3.03E-01		-5.28E-02	4.61E-01		-1.72E+00	1.21E-139	Down	Unigene23155_All|gi|224131390|ref|XP_002328527.1|/1.00E-104//cytochrome P450 [Populus trichocarpa]>gi|222838242|gb|EEE76607.1|cytochrome P450 [Populus trichocarpa]	Unigene23155_All//1.00E-99//AT4G12300| CYP706A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene23155_All//0.00E+00//TC141023		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene23156_All	728	2.37	2.51	0.59	3.15	3.55	2.23	2.50	0.92	0.99	7.92E-02	8.69E-01		-2.02E+00	5.05E-04	Down	1.73E-01	7.18E-01		-4.95E-01	2.65E-01		-1.44E+00	1.28E-03		-1.34E+00	1.76E-03		Unigene23156_All|gi|62286891|sp|Q8L3X9.1|KASM_ARATH//8.00E-73//RecName: Full=3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial; AltName: Full=Beta-ketoacyl-ACP synthase; AltName: Full=mtKAS; Flags: Precursor>gi|20373025|dbj|BAB91181.1| 3-ketoacyl-acyl carrier protein synthase [Arabidopsis thaliana]>gi|20466243|gb|AAM20439.1| 3-oxoacyl carrier protein synthase [Arabidopsis thaliana]>gi|22136308|gb|AAM91232.1| 3-oxoacyl carrier protein synthase [Arabidopsis thaliana]	Unigene23156_All//2.00E-54//AT2G04540| 3-oxoacyl-(acyl-carrier-protein) synthase II, putative	Unigene23156_All//0.00E+00//TC139385		ko00061|Fatty acid biosynthesis	GO:0004312//GO:0006631//GO:0043231	nr -
Unigene23158_All	650	3.86	3.98	2.79	7.36	4.72	2.71	4.23	5.21	1.47	4.12E-02	9.31E-01		-4.72E-01	2.64E-01		-6.42E-01	1.39E-02		-1.44E+00	3.30E-07	Down	3.01E-01	3.65E-01		-1.52E+00	1.19E-05	Down	Unigene23158_All|gi|124359752|gb|ABN06084.1|//2.00E-17//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene23158_All//3.00E-12//AT3G25270| nucleic acid binding	Unigene23158_All//0.00E+00//BQ413841				nr -
Unigene23159_All	1583	23.24	17.76	18.77	30.08	27.87	27.93	14.77	9.51	6.67	-3.87E-01	1.11E-05		-3.08E-01	8.78E-04		-1.11E-01	2.02E-01		-1.07E-01	2.28E-01		-6.36E-01	3.27E-10		-1.15E+00	3.46E-27	Down	Unigene23159_All|gi|297612697|ref|NP_001066197.2|//8.00E-16//Os12g0156200 [Oryza sativa Japonica Group]>gi|255670064|dbj|BAF29216.2|Os12g0156200 [Oryza sativa Japonica Group]	Unigene23159_All//1.00E-12//AT4G28090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene23159_All//0.00E+00//gi|21101528|gb|BQ413841.1|BQ413841				nr +
Unigene2316_All	2427	4.40	5.99	5.18	12.79	9.15	9.47	28.94	9.16	6.99	4.46E-01	2.48E-03		2.36E-01	1.84E-01		-4.83E-01	4.95E-08		-4.33E-01	4.12E-06		-1.66E+00	1.11E-135	Down	-2.05E+00	2.55E-186	Down	Unigene2316_All|gi|224127816|ref|XP_002320171.1|/0.00E+00//f-box family protein [Populus trichocarpa]>gi|222860944|gb|EEE98486.1| f-box family protein [Populus trichocarpa]	Unigene2316_All//2.00E-155//AT3G61590| HFS (HAWAIIAN SKIRT); ubiquitin-protein ligase	Unigene2316_All//0.00E+00//gi|164315206|gb|ES823231.1|ES823231				nr +
Unigene23160_All	1280	7.07	7.32	5.20	11.91	8.39	10.06	3.37	2.61	0.93	5.05E-02	7.99E-01		-4.43E-01	2.82E-02		-5.05E-01	1.45E-04		-2.44E-01	1.15E-01		-3.67E-01	1.81E-01		-1.85E+00	9.00E-11	Down	Unigene23160_All|gi|115473321|ref|NP_001060259.1|/7.00E-14//Os07g0613900 [Oryza sativa Japonica Group]>gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene23160_All//1.00E-12//AT3G09510| nucleic acid binding	Unigene23160_All//0.00E+00//gi|21101528|gb|BQ413841.1|BQ413841				nr -
Unigene23165_All	342	5.97	1.48	3.11	1.60	2.11	2.11	0.49	0.24	0.35	-2.01E+00	6.90E-05	Down	-9.38E-01	4.84E-02		4.00E-01	6.64E-01		3.99E-01	6.51E-01		-1.02E+00	6.14E-01		-5.01E-01	7.46E-01		Unigene23165_All|gi|149798881|gb|ABR32118.1|//2.00E-26//waxy [Parrotia persica]	Unigene23165_All//7.00E-26//AT1G32900| starch synthase, putative	Unigene23165_All//1.00E-108//TC166217		ko00500|Starch and sucrose metabolism	GO:0005977//GO:0035251	nr +
Unigene23167_All	2354	607.02	322.61	450.59	181.80	218.52	221.83	58.16	24.61	24.23	-9.12E-01	0.00E+00		-4.30E-01	1.42E-224		2.65E-01	1.04E-40		2.87E-01	4.74E-43		-1.24E+00	1.11E-170	Down	-1.26E+00	2.19E-180	Down	Unigene23167_All|gi|258489621|gb|ACV72639.1|//0.00E+00//granule-bound starch synthase 1 [Gossypium hirsutum]	Unigene23167_All//0.00E+00//AT1G32900| starch synthase, putative	Unigene23167_All//0.00E+00//TC139259		ko00500|Starch and sucrose metabolism	GO:0005488//GO:0005977//GO:0005982//GO:0009536//GO:0046527	nr +
Unigene23168_All	3000	2.01	3.04	1.40	3.97	3.24	2.71	7.03	3.29	2.92	6.00E-01	1.64E-03		-5.16E-01	4.31E-02		-2.94E-01	7.83E-02		-5.50E-01	6.29E-04		-1.10E+00	2.77E-22	Down	-1.27E+00	1.12E-28	Down	Unigene23168_All|gi|297814345|ref|XP_002875056.1|/0.00E+00//ATRNL [Arabidopsis lyrata subsp. lyrata]>gi|297320893|gb|EFH51315.1| ATRNL [Arabidopsis lyrata subsp. lyrata]	Unigene23168_All//0.00E+00//AT1G07910| RNL (RNA LIGASE); 2',3'-cyclic-nucleotide 3'-phosphodiesterase/ RNA ligase (ATP)/ polynucleotide kinase	Unigene23168_All//0.00E+00//TC168479			GO:0000394//GO:0004112//GO:0008452//GO:0016773	nr +
Unigene2317_All	787	5.45	4.64	2.44	9.87	6.74	3.44	10.85	9.77	8.86	-2.34E-01	4.41E-01		-1.16E+00	1.91E-04	Down	-5.51E-01	5.16E-03		-1.52E+00	3.25E-12	Down	-1.51E-01	4.56E-01		-2.93E-01	1.01E-01		Unigene2317_All|gi|108711330|gb|ABF99125.1|//1.00E-08//expressed protein [Oryza sativa (Japonica cultivar-group)]	Unigene2317_All//2.00E-10//AT3G50815| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF59 (InterPro:IPR002744); BEST Arabidopsis thaliana protein match is: vacuolar sorting signal binding (TAIR:AT1G68310.2); Has 415 Blast hits to 414 proteins in 153 species: Archae - 0; Bacteria - 0; Metazoa - 216; Fungi - 86; Plants - 41; Viruses - 0; Other Eukaryotes - 72 (source: NCBI BLink).	Unigene2317_All//1.00E-166//AI732021			GO:0005048	nr +
Unigene23172_All	2340	2.10	5.72	2.59	8.58	8.55	12.99	7.91	8.00	21.47	1.44E+00	9.95E-18	Up	3.04E-01	2.43E-01		-4.90E-03	9.66E-01		5.98E-01	3.34E-10		1.59E-02	9.22E-01		1.44E+00	1.24E-80	Up	Unigene23172_All|gi|297840517|ref|XP_002888140.1|//0.00E+00//dynamin family protein [Arabidopsis lyrata subsp. lyrata]>gi|297333981|gb|EFH94399.1|dynamin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23172_All//7.00E-138//AT1G60500| dynamin family protein	Unigene23172_All//0.00E+00//CO097917		ko04144|Endocytosis	GO:0017111//GO:0032561	nr -
Unigene23173_All	2218	17.22	7.97	9.34	14.22	14.02	11.93	12.39	18.71	14.53	-1.11E+00	3.67E-33	Down	-8.83E-01	5.36E-22		-2.02E-02	8.62E-01		-2.53E-01	1.01E-02		5.95E-01	1.36E-15		2.30E-01	6.86E-03		Unigene23173_All|gi|224100869|ref|XP_002312046.1|/1.00E-122//AP2 domain-containing transcription factor [Populus trichocarpa]>gi|222861866|gb|EEE89413.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene23173_All//9.00E-71//AT2G28550| RAP2.7 (RELATED TO AP2.7); DNA binding / transcription factor	Unigene23173_All//0.00E+00//TC175425	AP2-EREBP		GO:0003006//GO:0003676//GO:0006351//GO:0009653//GO:0043231	nr +
Unigene23176_All	3249	6.20	7.27	5.70	4.29	4.60	4.99	17.83	36.12	71.50	2.29E-01	5.12E-02		-1.20E-01	3.86E-01		9.96E-02	5.85E-01		2.17E-01	1.53E-01		1.02E+00	1.35E-106	Up	2.00E+00	0.00E+00	Up	Unigene23176_All|gi|74474913|dbj|BAE44440.1|//0.00E+00//MAP kinase phosphatase 1 [Solanum tuberosum]	Unigene23176_All//3.00E-143//AT3G55270| MKP1 (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 1); MAP kinase tyrosine/serine/threonine phosphatase	Unigene23176_All//0.00E+00//gi|78351570|gb|DT571844.1|DT571844			GO:0016791	nr -
Unigene23177_All	2483	7.46	2.73	4.18	10.89	9.85	13.79	27.62	28.21	17.04	-1.45E+00	1.69E-24	Down	-8.35E-01	4.74E-10		-1.46E-01	2.09E-01		3.40E-01	1.77E-04		3.06E-02	6.53E-01		-6.97E-01	4.04E-34		Unigene23177_All|gi|255552335|ref|XP_002517212.1|//0.00E+00//Acyl-CoA synthetase [Ricinus communis]>gi|83320525|gb|ABC02881.1| ACS2 [Ricinus communis]>gi|223543847|gb|EEF45375.1| Acyl-CoA synthetase [Ricinus communis]	Unigene23177_All//0.00E+00//AT3G05970| LACS6 (long-chain acyl-CoA synthetase 6); long-chain-fatty-acid-CoA ligase	Unigene23177_All//0.00E+00//gi|109848121|gb|DW477101.1|DW477101		ko04146|Peroxisome//ko00071|Fatty acid metabolism	GO:0015645//GO:0044464	nr -
Unigene23179_All	2074	1.97	4.72	6.44	2.83	2.31	2.87	6.81	9.39	5.55	1.26E+00	7.56E-11	Up	1.71E+00	9.47E-22	Up	-2.96E-01	2.52E-01		2.03E-02	9.48E-01		4.64E-01	3.07E-05		-2.95E-01	2.66E-02		Unigene23179_All|gi|115483686|ref|NP_001065513.1|//0.00E+00//Os10g0580400 [Oryza sativa Japonica Group] >gi|31433710|gb|AAP55189.1|SSS sodium solute transporter superfamily protein, expressed [Oryza sativa (japonica cultivar-group)]>gi|39545690|gb|AAR27948.1| DUR3 [Oryza sativa Japonica Group]>gi|113640045|dbj|BAF27350.1|Os10g0580400 [Oryza sativa Japonica Group]	Unigene23179_All//0.00E+00//AT5G45380| sodium:solute symporter family protein	Unigene23179_All//0.00E+00//gi|48790607|gb|CO091921.1|CO091921			GO:0030001//GO:0031224	nr +
Unigene23191_All	4682	3.27	6.59	3.65	7.16	9.52	5.57	10.70	19.22	16.23	1.01E+00	4.81E-23	Up	1.57E-01	3.14E-01		4.12E-01	2.20E-08		-3.64E-01	6.39E-05		8.45E-01	4.83E-60		6.01E-01	4.84E-29		Unigene23191_All|gi|179331110|gb|AL48201.1|AF378084.1|/1.00E-120//PNCBP [Solanum tuberosum]	Unigene23191_All//4.00E-58//AT5G04020| calmodulin binding	Unigene23191_All//0.00E+00//CA993885				nr +
Unigene23192_All	3176	6.11	5.87	3.07	13.58	15.50	17.33	18.90	23.21	39.73	-5.80E-02	6.71E-01		-9.94E-01	7.30E-14		1.91E-01	1.20E-02		3.52E-01	3.48E-07		2.96E-01	4.66E-08		1.07E+00	4.61E-127	Up	Unigene23192_All|gi|224063557|ref|XP_002301203.1|//0.00E+00//nbs-lrr resistance protein [Populus trichocarpa]>gi|222842929|gb|EEE80476.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene23192_All//0.00E+00//AT4G33300| ADR1-L1 (ADR1-like 1); ATP binding / protein binding	Unigene23192_All//0.00E+00//gi|164286086|gb|ES814667.1|ES814667		ko04626|Plant-pathogen interaction	GO:0005576//GO:0006950//GO:0009607//GO:0012501//GO:0016462//GO:0016772//GO:0032559	nr -
Unigene23194_All	1352	3.75	4.98	4.06	6.12	4.76	4.41	8.66	6.37	4.24	4.09E-01	7.67E-02		1.12E-01	6.77E-01		-3.61E-01	7.38E-02		-4.72E-01	2.00E-02		-4.44E-01	2.82E-03		-1.03E+00	6.06E-12	Down	Unigene23194_All|gi|18415901|ref|NP_567660.1|//1.00E-121//ATCES1; catalytic/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in linear amides [Arabidopsis thaliana]>gi|14488266|dbj|BAB60897.1| Acyl-CoA independent ceramide synthase [Arabidopsis thaliana]	Unigene23194_All//1.00E-115//AT4G22330| ATCES1; catalytic/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	Unigene23194_All//0.00E+00//CO099189		ko00600|Sphingolipid metabolism		nr -
Unigene23197_All	1478	15.04	6.55	23.20	7.89	6.29	5.96	11.70	19.12	17.17	-1.20E+00	4.26E-22	Down	6.25E-01	3.64E-11		-3.26E-01	4.88E-02		-4.04E-01	1.59E-02		7.08E-01	1.58E-14		5.53E-01	5.10E-09		Unigene23197_All|gi|115469074|ref|NP_001058136.1|//1.00E-99//Os06g0634300 [Oryza sativa Japonica Group]>gi|51535777|dbj|BAD37816.1| MutT domain protein-like [Oryza sativa Japonica Group]>gi|51535894|dbj|BAD37977.1| MutT domain protein-like [Oryza sativa Japonica Group]>gi|113596176|dbj|BAF20050.1|Os06g0634300 [Oryza sativa Japonica Group]	Unigene23197_All//3.00E-97//AT5G47650| ATNUDT2 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 2); ADP-ribose diphosphatase/ NAD or NADH binding / hydrolase	Unigene23197_All//0.00E+00//TC163797			GO:0003824	nr +
Unigene2320_All	1452	1.66	1.74	2.35	4.97	2.66	2.43	4.60	4.75	5.24	7.41E-02	8.51E-01		5.02E-01	1.53E-01		-9.05E-01	6.80E-06		-1.04E+00	1.50E-06	Down	4.59E-02	8.41E-01		1.88E-01	3.61E-01		Unigene2320_All|gi|18425006|ref|NP_569021.1|//2.00E-63//BSD domain-containing protein [Arabidopsis thaliana]	Unigene2320_All//1.00E-47//AT5G65910| BSD domain-containing protein	Unigene2320_All//0.00E+00//DW510935				nr -
Unigene23200_All	3333	5.35	3.83	4.49	17.59	13.60	7.41	8.04	3.24	2.87	-4.83E-01	2.26E-04		-2.54E-01	7.85E-02		-3.72E-01	3.10E-09		-1.25E+00	1.10E-65	Down	-1.31E+00	4.05E-37	Down	-1.49E+00	5.56E-46	Down	Unigene23200_All|gi|15235439|ref|NP_195427.1|//0.00E+00//catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana]	Unigene23200_All//0.00E+00//AT4G37100| catalytic/ pyridoxal phosphate binding	Unigene23200_All//0.00E+00//TC147380			GO:0016020	nr +
Unigene23201_All	697	3.60	5.09	3.82	1.93	5.58	3.76	7.10	8.64	11.37	4.98E-01	1.33E-01		8.43E-02	8.30E-01		1.53E+00	9.42E-07	Up	9.62E-01	1.46E-02		2.83E-01	2.26E-01		6.81E-01	1.47E-04		Unigene23201_All|gi|297832820|ref|XP_002884292.1|//4.00E-18//structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]>gi|297330132|gb|EFH60551.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	Unigene23201_All//1.00E-07//AT3G01170| structural constituent of ribosome	Unigene23201_All//0.00E+00//TC167180			GO:0005622	nr +

Unigene23206_All	1950	0.30	0.34	0.74	0.43	0.46	0.63	1.63	0.75	0.59	1.95E-01	8.07E-01		1.32E+00	2.70E-02		8.01E-02	9.41E-01		5.26E-01	4.24E-01		-1.12E+00	4.03E-04	Down	-1.46E+00	4.89E-06	Down	Unigene23206_All//gi|225460573|ref|XP_002278721.1|//0.00E+00//PREDICTED: similar to SP1a/RYanodine receptor (SPRY) domain-containing protein [Vitis vinifera]	Unigene23206_All//8.00E-173//AT1G35470| SP1a/RYanodine receptor (SPRY) domain-containing protein	Unigene23206_All//0.00E+00//TC140476				nr +
Unigene23207_All	3904	1.66	0.93	0.70	3.64	3.45	3.20	8.38	3.37	3.39	-8.31E-01	3.33E-04		-1.26E+00	4.45E-07	Down	-7.65E-02	6.70E-01		-1.83E-01	2.85E-01		-1.31E+00	3.91E-45	Down	-1.31E+00	4.10E-46	Down	Unigene23207_All//gi|3551249|dbj|BAS2823.1|//1.00E-79//184 [Daucus carota]	Unigene23207_All//2.00E-69//AT2G04235| unknown protein	Unigene23207_All//0.00E+00//CO132717				nr +
Unigene23209_All	210	5.23	1.45	2.54	3.80	1.15	3.23	5.44	11.94	19.35	-1.85E+00	8.99E-03		-1.05E+00	1.35E-01		-1.73E+00	2.86E-02		-2.35E-01	7.54E-01		1.14E+00	1.71E-03		1.83E+00	6.15E-10	Up	Unigene23209_All//gi|2501578|sp|Q39963.1|PDX1_HEVBR//1.00E-19//RecName: Full=Probable pyridoxal biosynthesis protein PDX1; AltName: Full=Ethylene-inducible protein HEVER >gi|1209317|gb|AAA91063.1| ethylene-inducible protein [Hevea brasiliensis]	Unigene23209_All//4.00E-20//AT5G01410| RSR4 (REDUCED SUGAR RESPONSE 4); protein heterodimerization/ protein homodimerization	Unigene23209_All//2.00E-100//TC168383		ko00750|Vitamin B6 metabolism	GO:0006519//GO:0006778//GO:0006972//GO:0008614//GO:0009108//GO:0016020//GO:0033194//GO:0042364//GO:0042802//GO:0044444//GO:0046983	nr -
Unigene23210_All	1161	17.98	4.54	9.04	2.10	1.48	0.82	2.91	5.29	6.14	-1.99E+00	1.15E-42	Down	-9.93E-01	7.84E-15		-5.04E-01	2.20E-01		-1.36E+00	9.53E-04	Down	8.61E-01	5.43E-05		1.08E+00	4.65E-08	Up	Unigene23210_All//gi|2501578|sp|Q39963.1|PDX1_HEVBR//1.00E-157//RecName: Full=Probable pyridoxal biosynthesis protein PDX1; AltName: Full=Ethylene-inducible protein HEVER >gi|1209317|gb|AAA91063.1| ethylene-inducible protein [Hevea brasiliensis]	Unigene23210_All//1.00E-138//AT5G01410| RSR4 (REDUCED SUGAR RESPONSE 4); protein heterodimerization/ protein homodimerization	Unigene23210_All//0.00E+00//TC159235		ko00750|Vitamin B6 metabolism		nr -
Unigene23211_All	1711	165.34	97.96	145.71	87.87	89.16	166.85	40.92	178.37	273.10	-7.55E-01	2.23E-126		-1.82E-01	2.92E-09		2.10E-02	7.18E-01		9.25E-01	9.48E-194		2.12E+00	0.00E+00	Up	2.74E+00	0.00E+00	Up	Unigene23211_All//gi|2501578|sp|Q39963.1|PDX1_HEVBR//1.00E-164//RecName: Full=Probable pyridoxal biosynthesis protein PDX1; AltName: Full=Ethylene-inducible protein HEVER >gi|1209317|gb|AAA91063.1| ethylene-inducible protein [Hevea brasiliensis]	Unigene23211_All//9.00E-145//AT5G01410| RSR4 (REDUCED SUGAR RESPONSE 4); protein heterodimerization/ protein homodimerization	Unigene23211_All//0.00E+00//TC146066		ko00750|Vitamin B6 metabolism		nr -
Unigene23212_All	1854	17.69	35.47	24.70	29.45	28.36	37.56	35.28	47.77	45.83	1.00E+00	7.46E-48	Up	4.81E-01	2.09E-09		-5.42E-02	5.47E-01		3.51E-01	7.02E-09		4.37E-01	8.01E-19		3.78E-01	2.31E-14		Unigene23212_All//gi|124359459|gb|ABD02255.2|//1.00E-170//Esterase/lipase/thioesterase [Medicago truncatula]	Unigene23212_All//2.00E-135//AT4G24760| unknown protein	Unigene23212_All//0.00E+00//gi|78354245|gb|DT574519.1|DT574519				nr -
Unigene23213_All	773	3.32	1.11	4.34	3.74	4.86	4.79	1.97	2.97	5.88	-1.57E+00	1.74E-04	Down	3.88E-01	2.85E-01		3.78E-01	2.71E-01		3.58E-01	3.09E-01		5.95E-01	1.21E-01		1.58E+00	4.30E-09	Up			Unigene23213_All//1.00E-178//gi|3326725|gb|AI055611.1|AI055611				
Unigene23214_All	1959	6.38	8.56	11.34	5.24	7.80	8.18	3.22	3.24	7.71	4.24E-01	1.90E-03		8.28E-01	8.59E-12		5.75E-01	1.76E-05		6.44E-01	2.16E-06		1.22E-02	9.92E-01		1.26E+00	1.92E-20	Up	Unigene23214_All//gi|169264899|dbj|BAG12293.1|//4.00E-59//S locus F-box protein with the low allelic sequence polymorphism 1-S2 [Prunus avium]	Unigene23214_All//4.00E-30//AT3G06240| F-box family protein	Unigene23214_All//0.00E+00//TC177799				nr +
Unigene23216_All	1377	0.76	1.47	0.46	0.87	2.15	1.18	7.92	4.46	8.33	9.54E-01	3.64E-02		-7.11E-01	3.15E-01		1.31E+00	2.76E-04	Up	4.44E-01	4.29E-01		-8.28E-01	9.15E-08		7.29E-02	6.55E-01		Unigene23216_All//gi|262192731|gb|AC330433.1|//2.00E-08//apetala 2-like protein [Nicotiana tabacum]		Unigene23216_All//0.00E+00//TC149345			GO:0008152	nr +
Unigene23219_All	2663	4.58	5.37	6.28	28.49	21.70	17.33	61.27	17.69	15.15	2.29E-01	1.43E-01		4.56E-01	1.25E-03		-3.93E-01	4.84E-13		-7.17E-01	6.53E-34		-1.79E+00	0.00E+00	Down	-2.02E+00	0.00E+00	Down	Unigene23219_All//gi|224130916|ref|XP_002320956.1|//0.00E+00//anion exchanger family protein [Populus trichocarpa] >gi|222861729|gb|EEE99271.1| anion exchanger family protein [Populus trichocarpa]	Unigene23219_All//0.00E+00//AT2G47160| BOR1 (REQUIRES HIGH BORON 1); anion exchanger/ boron transporter	Unigene23219_All//0.00E+00//gi|78340795|gb|DT561069.1|DT561069			GO:0006811//GO:0010035//GO:0015301//GO:0015562//GO:0031224//GO:0043231//GO:0043673//GO:0044459	nr +
Unigene23221_All	1023	1.02	0.94	0.68	3.21	2.22	1.06	3.84	2.12	3.31	-1.20E-01	8.43E-01		-5.96E-01	3.93E-01		-5.33E-01	1.13E-01		-1.60E+00	6.54E-06	Down	-8.55E-01	1.84E-03		-2.16E-01	4.56E-01		Unigene23221_All//gi|89540052|gb|AAF82225.1|AC069143_1//3.00E-45//Contains similarity to a HSPC326 mRNA from Homo sapiens gb|AF161444. EST gb|AI997162 comes from this gene [Arabidopsis thaliana]	Unigene23221_All//1.00E-45//AT1G19140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ubiquinone biosynthetic process; LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: COQ9 (InterPro:IPR013718), Ubiquinone biosynthesis protein COQ9 (InterPro:IPR012762); Has 598 Blast hits to 598 proteins in 175 species: Archae - 0; Bacteria - 149; Metazoa - 114; Fungi - 60; Plants - 22; Viruses - 0; Other Eukaryotes - 253 (source: NCBI BLink).	Unigene23221_All//5.00E-43//TC149082			GO:0006350//GO:0006743//GO:0016564//GO:0043231	nr -
Unigene23222_All	2382	0.62	1.51	1.14	6.71	3.70	2.73	17.11	4.02	4.83	1.30E+00	1.18E-04	Up	8.91E-01	2.58E-02		-8.59E-01	2.34E-11		-1.30E+00	1.96E-19	Down	-2.09E+00	5.74E-108	Down	-1.82E+00	7.64E-93	Down	Unigene23222_All//gi|18396193|ref|NP_565330.1|//0.00E+00//subtilase family protein [Arabidopsis thaliana]	Unigene23222_All//0.00E+00//AT2G05920| subtilase family protein	Unigene23222_All//0.00E+00//gi|164277689|gb|ES792111.1|ES792111			GO:0003006//GO:0004175//GO:0005515//GO:0005576//GO:0005618//GO:0009845//GO:0010191//GO:0019538//GO:0031410//GO:0044092	nr -
Unigene23223_All	2994	0.17	0.25	0.09	2.53	1.53	1.13	6.91	1.40	1.24	5.39E-01	5.02E-01		-9.75E-01	3.76E-01		-7.25E-01	2.17E-04		-1.16E+00	4.45E-08	Down	-2.31E+00	3.13E-62	Down	-2.48E+00	6.10E-70	Down	Unigene23223_All//gi|18396193|ref|NP_565330.1|//0.00E+00//subtilase family protein [Arabidopsis thaliana]	Unigene23223_All//0.00E+00//AT2G05920| subtilase family protein	Unigene23223_All//0.00E+00//TC140297			GO:0003006//GO:0004175//GO:0005515//GO:0005576//GO:0005618//GO:0009845//GO:0010191//GO:0019538//GO:0031410//GO:0044092	nr -
Unigene23224_All	3492	60.11	54.86	64.92	38.87	34.07	29.28	87.35	98.62	30.71	-1.32E-01	2.41E-04		1.11E-01	2.30E-03		-1.90E-01	3.83E-06		-4.09E-01	4.09E-22		1.75E-01	3.84E-13		-1.51E+00	0.00E+00	Down	Unigene23224_All//gi|225456641|ref|XP_002270344.1|//0.00E+00//PREDICTED: similar to plasma membrane H+ ATPase [Vitis vinifera]	Unigene23224_All//0.00E+00//AT3G47950| AHA4; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	Unigene23224_All//0.00E+00//TC153731		ko00190|Oxidative phosphorylation	GO:0006811//GO:0006818//GO:0006970//GO:0009206//GO:0015662//GO:0033124//GO:0032559//GO:0043169	nr +
Unigene23225_All	796	7.43	5.67	5.89	11.95	13.50	8.79	8.23	36.60	17.57	-3.91E-01	1.19E-01		-3.35E-01	2.10E-01		1.75E-01	3.84E-01		-4.43E-01	1.83E-02		2.15E+00	4.68E-80	Up	1.09E+00	2.50E-15	Up	Unigene23225_All//gi|225465815|ref|XP_002263159.1|//1.00E-71//PREDICTED: similar to TGA-type basic leucine zipper protein TGA2.1 [Vitis vinifera]	Unigene23225_All//8.00E-48//AT5G06950| AHBP-1B; DNA binding / transcription activator/ transcription factor/ transcription repressor	Unigene23225_All//0.00E+00//TC136987	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0009627//GO:0030528//GO:0042221//GO:0043231	nr +
Unigene23226_All	1279	4.99	3.61	4.21	10.59	12.38	8.30	3.07	12.68	6.35	-4.69E-01	4.57E-02		-2.47E-01	3.51E-01		2.25E-01	1.34E-01		-3.52E-01	2.37E-02		2.04E+00	4.71E-42	Up	1.05E+00	1.03E-08	Up	Unigene23226_All//gi|225465815|ref|XP_002263159.1|//3.00E-57//PREDICTED: similar to TGA-type basic leucine zipper protein TGA2.1 [Vitis vinifera]	Unigene23226_All//3.00E-26//AT3G12250| TGA6 (TGACG MOTIF-BINDING FACTOR 6); DNA binding / transcription factor	Unigene23226_All//0.00E+00//DV849344	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0009536//GO:0009814//GO:0010468//GO:0042221	nr -
Unigene23227_All	1938	0.81	0.65	1.18	1.18	1.71	1.89	3.12	7.18	4.77	-3.09E-01	5.67E-01		5.45E-01	2.27E-01		5.29E-01	1.31E-01		6.75E-01	3.84E-02		1.20E+00	3.35E-17	Up	6.12E-01	1.94E-04		Unigene23227_All//gi|225465815|ref|XP_002263159.1|//1.00E-104//PREDICTED: similar to TGA-type basic leucine zipper protein TGA2.1 [Vitis vinifera]	Unigene23227_All//2.00E-71//AT3G12250| TGA6 (TGACG MOTIF-BINDING FACTOR 6); DNA binding / transcription factor	Unigene23227_All//0.00E+00//TC152059	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0009908//GO:0043231	nr -
Unigene23233_All	2235	0.75	2.61	0.79	4.93	6.42	5.33	21.55	15.07	25.74	1.80E+00	7.05E-11	Up	6.97E-02	8.91E-01		3.83E-01	8.02E-03		1.15E-01	5.75E-01		-5.16E-01	4.50E-14		2.57E-01	2.71E-05		Unigene23233_All//gi|226502985|ref|NP_001149075.1|//3.00E-36//nuclear transcription factor Y subunit A-3 [Zea mays] >gi|195624530|gb|ACG34095.1| nuclear transcription factor Y subunit A-3 [Zea mays]	Unigene23233_All//2.00E-28//AT1G30500| NF-YA7 (NUCLEAR FACTOR Y, SUBUNIT A7); specific transcriptional repressor/ transcription factor	Unigene23233_All//1.00E-177//DN817884	CCAAT		GO:0043231	nr +
Unigene23234_All	4002	8.48	7.32	6.56	14.03	14.52	10.25	20.32	9.75	10.33	-2.13E-01	2.62E-02		-3.71E-01	1.04E-04		4.93E-02	5.87E-01		-4.53E-01	2.27E-11		-1.06E+00	6.24E-79	Down	-9.75E-01	5.18E-71		Unigene23234_All//gi|2191175|gb|AAB61061.1|//0.00E+00//Hypothetical protein F2P16.24 [Arabidopsis thaliana]	Unigene23234_All//0.00E+00//AT5G268S0| INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: cyclin-related (TAIR:AT2G41830.1); Has 199 Blast hits to 197 proteins in 66 species: Archae - 0; Bacteria - 0; Metazoa - 113; Fungi - 19; Plants - 59; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink).	Unigene23234_All//0.00E+00//TC144903			GO:0043231	nr +
Unigene23238_All	3399	5.77	13.52	7.60	7.11	3.99	4.08	7.30	13.35	10.24	1.23E+00	2.52E-46	Up	3.97E-01	3.62E-04		-8.33E-01	4.69E-16		-8.01E-01	1.87E-13		8.71E-01	2.81E-32		4.89E-01	8.84E-10		Unigene23238_All//gi|124360233|gb|ABN08246.1|//1.00E-165//Solute carrier family 35 member B3, related [Medicago truncatula]	Unigene23238_All//4.00E-152//AT1G12600| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf whorl, petal, male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: UAA transporter (InterPro:IPR013657); BEST Arabidopsis thaliana protein match is: UDP-galactose transporter-related (TAIR:AT4G23010.1); Has 943 Blast hits to 943 proteins in 196 species: Archae - 2; Bacteria - 55; Metazoa - 506; Fungi - 148; Plants - 112; Viruses - 0; Other Eukaryotes - 120 (source: NCBI BLink).	Unigene23238_All//0.00E+00//CO130465		ko04626|Plant-pathogen interaction		nr +
Unigene2324_All	2300	1.05	0.90	1.32	2.75	3.07	2.10	5.02	0.49	0.94	-2.12E-01	6.02E-01		3.35E-01	4.02E-01		1.58E-01	5.43E-01		-3.89E-01	1.14E-01		-3.35E+00	6.93E-52	Down	-2.42E+00	2.34E-38	Down	Unigene2324_All//gi|9989057|gb|AAG10820.1|AC011808_8//6.00E-48//Hypothetical protein [Arabidopsis thaliana] >gi|38603812|gb|AAR24651.1| At1g16630 [Arabidopsis thaliana] >gi|11073871|dbj|BAF01309.1| Hypothetical protei [Arabidopsis thaliana]	Unigene2324_All//7.00E-42//AT2G16270| unknown protein	Unigene2324_All//0.00E+00//TC145425				nr +
Unigene23241_All	1936	0.70	1.10	0.91	3.06	4.29	2.59	6.62	2.25	1.77	6.46E-01	1.41E-01		3.69E-01	4.72E-01		4.85E-01	1.36E-02		-2.42E-01	3.88E-01		-1.56E+00	2.99E-23	Down	-1.90E+00	1.80E-31	Down	Unigene23241_All//gi|224099703|ref|XP_002311584.1|//0.00E+00//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222851404|gb|EEE88951.1| nucleobase ascorbate transporter [Populus trichocarpa]	Unigene23241_All//0.00E+00//AT1G60030| xanthine/uracil permease family protein	Unigene23241_All//3.00E-89//ES844484			GO:0005215//GO:0006810//GO:0030312//GO:0043231	nr -
Unigene23242_All	1575	5.28	3.57	5.54	8.29	8.35	5.82	6.31	3.03	3.01	-5.65E-01	4.87E-03		7.01E-02	7.41E-01		1.13E-02	9.55E-01		-5.10E-01	8.87E-04		-1.06E+00	2.21E-10	Down	-1.07E+00	7.72E-11	Down	Unigene23242_All//gi|15419985|gb|AAK97227.1|AF302013_1//0.00E+00//CDK-activating kinase [Medicago sativa subsp. x varia]	Unigene23242_All//5.00E-151//AT1G18040| CDKD1;3 (CYCLIN-DEPENDENT KINASE D1;3); kinase/ protein kinase	Unigene23242_All//0.00E+00//TC174948		ko03420|Nucleotide excision repair	GO:0004672//GO:0006464//GO:0032559	nr +

Unigene23243_All	1804	14.70	12.30	8.15	14.94	12.24	11.04	11.67	10.50	64.62	-2.57E-01	1.79E-02		-8.52E-01	1.37E-14		-2.88E-01	4.41E-03		-4.36E-01	1.82E-05		-1.53E-01	2.05E-01		2.47E+00	0.00E+00	Up	Unigene23243_All//gi|15419985|gb|AB97227.1|AF302013_1//0.00E+00//CDK-activating kinase [Medicago sativa subsp. x varia]	Unigene23243_All//1.00E-169//AT1G18040| CDKD1;3 (CYCLIN-DEPENDENT KINASE D1;3); kinase/ protein kinase	Unigene23243_All//0.00E+00//TC155002		ko03420|Nucleotide excision repair	GO:0004674//GO:0006464//GO:0032559	nr -
Unigene23248_All	2374	1.94	11.25	5.47	9.65	23.69	43.36	31.95	58.15	86.44	2.54E+00	8.34E-73	Up	1.50E+00	1.58E-17	Up	1.30E+00	1.75E-72	Up	2.17E+00	1.41E-248	Up	8.64E-01	3.08E-95		1.44E+00	0.00E+00	Up	Unigene23248_All//gi|21928129|gb|AAM78092.1|//1.00E-151//At4g17080/d14570w [Arabidopsis thaliana] >gi|27764944|gb|AAO23593.1| At4g17080/d14570w [Arabidopsis thaliana]	Unigene23248_All//5.00E-127//AT4G17080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MORN motif (InterPro:IPR003409); BEST Arabidopsis thaliana protein match is: MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein /phosphatidylinositol-4-phosphate 5-kinase-related (TAIR:AT2G35170.1); Has 18005 Blast hits to 5199 proteins in 343 species: Archae - 0; Bacteria - 1726; Metazoa - 3046; Fungi - 93; Plants - 653; Viruses - 0; Other Eukaryotes - 12487 (source: NCBI BLink).	Unigene23248_All//0.00E+00//ES843631		ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene2325_All	579	0.99	4.38	3.04	2.41	1.78	1.64	4.89	2.82	22.91	2.14E+00	3.00E-06	Up	1.61E+00	3.13E-03		-4.33E-01	4.50E-01		-5.56E-01	3.52E-01		-7.97E-01	1.65E-02		2.23E+00	3.28E-39	Up	Unigene2325_All//gi|223452353|gb|ACM89504.1|//2.00E-13//protein kinase family protein [Glycine max]	Unigene2325_All//4.00E-10//AT5G40380| protein kinase family protein	Unigene2325_All//0.00E+00//TC159599			GO:0004672//GO:0006464//GO:0032559	nr +
Unigene23251_All	1961	3.50	2.79	1.28	3.91	3.86	2.44	6.02	7.25	4.69	-3.25E-01	1.60E-01		-1.45E+00	4.03E-09	Down	-1.81E-02	9.45E-01		-6.80E-01	9.69E-04		2.69E-01	5.41E-02		-3.58E-01	1.35E-02		Unigene23251_All//gi|297825135|ref|XP_002880450.1|//5.00E-95//transferase [Arabidopsis lyrata subsp. lyrata] >gi|297326289|gb|EFH56709.1| transferase [Arabidopsis lyrata subsp. lyrata]	Unigene23251_All//4.00E-67//AT2G22530| catalytic/ transferase	Unigene23251_All//0.00E+00//TC172136				nr +
Unigene23254_All	795	0.99	0.57	0.60	1.50	3.51	2.73	2.34	1.58	5.56	-7.83E-01	3.28E-01		-7.12E-01	3.89E-01		1.22E+00	9.93E-04	Up	8.59E-01	5.30E-02		-5.69E-01	1.93E-01		1.25E+00	1.64E-06	Up	Unigene23254_All//gi|225431806|ref|XP_002272864.1|//1.00E-133//PREDICTED: similar to PLDP1 (PHOSPHOLIPASE D ZETA1); phospholipase D [Vitis vinifera]	Unigene23254_All//1.00E-117//AT3G16785| PLDP1 (PHOSPHOLIPASE D P1); phospholipase D	Unigene23254_All//2.00E-29//TC164151		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism/ko00565|Ether lipid metabolism		nr +
Unigene23255_All	2827	0.26	0.82	0.64	0.60	1.15	0.54	1.18	1.18	2.06	1.67E+00	2.05E-04	Up	1.31E+00	1.21E-02		9.35E-01	5.47E-03		-1.41E-01	7.81E-01		1.60E-03	9.95E-01		8.00E-01	1.88E-04		Unigene23255_All//gi|225431806|ref|XP_002272864.1|//0.00E+00//PREDICTED: similar to PLDP1 (PHOSPHOLIPASE D ZETA1); phospholipase D [Vitis vinifera]	Unigene23255_All//0.00E+00//AT3G16785| PLDP1 (PHOSPHOLIPASE D P1); phospholipase D	Unigene23255_All//0.00E+00//TC167292		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism	GO:0004620//GO:0005488//GO:0006644//GO:0009247//GO:0009267//GO:0009725//GO:0016628//GO:0043231//GO:0048513//GO:0050794	nr +
Unigene23256_All	3374	17.62	6.61	9.61	13.26	14.04	8.34	12.44	6.37	7.84	-1.41E+00	1.67E-74	Down	-8.74E-01	2.20E-33		8.30E-02	3.76E-01		-6.69E-01	5.81E-18		-9.67E-01	1.56E-35		-6.66E-01	1.05E-19		Unigene23256_All//gi|297829916|ref|XP_002882840.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328680|gb|EFH59099.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23256_All//0.00E+00//AT3G13690| protein kinase family protein	Unigene23256_All//0.00E+00//TC143516		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016020//GO:0032559//GO:0043231	nr +
Unigene23257_All	3614	8.32	3.36	4.44	5.84	4.61	3.34	7.12	4.82	3.90	-1.31E+00	9.18E-34	Down	-9.08E-01	2.78E-18		-3.42E-01	2.79E-03		-8.09E-01	5.08E-12		-5.63E-01	3.87E-09		-8.69E-01	3.62E-19		Unigene23257_All//gi|297829916|ref|XP_002882840.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328680|gb|EFH59099.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23257_All//0.00E+00//AT3G13690| protein kinase family protein	Unigene23257_All//0.00E+00//TC143516		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016020//GO:0032559//GO:0043231	nr +
Unigene23258_All	3772	0.93	9.94	1.84	5.20	9.16	27.86	19.28	38.15	116.27	3.42E+00	3.88E-138	Up	9.82E-01	2.66E-05		8.15E-01	3.29E-21		2.42E+00	2.67E-290	Up	9.85E-01	1.94E-123		2.59E+00	0.00E+00	Up	Unigene23258_All//gi|30681478|ref|NP_850942.1|//0.00E+00//LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|17065208|gb|AAL32758.1| Unknown protein [Arabidopsis thaliana] >gi|224589386|gb|ACN59227.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23258_All//0.00E+00//AT1G09970| LRR XI-23; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene23258_All//0.00E+00//DV849207			GO:0003006//GO:0004672//GO:0004871//GO:0006464//GO:0008238//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene2326_All	2045	0.38	0.82	0.21	0.80	1.03	0.84	5.04	1.43	5.24	1.09E+00	3.43E-02		-8.82E-01	2.95E-01		3.54E-01	4.78E-01		6.22E-02	9.25E-01		-1.82E+00	2.87E-23	Down	5.49E-02	7.50E-01		Unigene2326_All//gi|15223170|ref|NP_177210.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|75333658|sp|Q9CAL2.1|CRK3_ARATH RecName: Full=Cysteine-rich receptor-like protein kinase 3; Short=Cysteine-rich RLK3; Flags: Precursor	Unigene2326_All//0.00E+00//AT1G70530| protein kinase family protein	Unigene2326_All//0.00E+00//TC130015		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene23262_All	3259	4.40	2.66	4.93	3.93	4.72	3.88	1.30	1.15	2.71	-7.27E-01	9.91E-07		1.66E-01	3.02E-01		2.66E-01	7.15E-02		-1.77E-02	9.37E-01		-1.69E-01	5.90E-01		1.06E+00	1.24E-09	Up	Unigene23262_All//gi|145335021|ref|NP_171815.3|//0.00E+00//FZL (FZO-LIKE); GTP binding / GTPase/ thiamin-phosphate diphosphorylase [Arabidopsis thaliana] >gi|92911702|gb|ABE96616.1| FZL [Arabidopsis thaliana]	Unigene23262_All//0.00E+00//AT1G03160| FZL (FZO-LIKE); GTP binding / GTPase/ thiamin-phosphate diphosphorylase	Unigene23262_All//0.00E+00//CO086171			GO:0003006//GO:0003824//GO:0008152//GO:0009668//GO:0009941//GO:0032561	nr +
Unigene23267_All	759	12.61	8.75	5.54	19.16	18.65	10.77	9.80	7.32	7.93	-5.29E-01	4.35E-03		-1.19E+00	2.55E-09	Down	-3.95E-02	8.21E-01		-8.31E-01	7.38E-09		-4.21E-01	3.06E-02		-3.07E-01	1.09E-01		Unigene23267_All//gi|145334843|ref|NP_001078767.1|//4.00E-54//protein kinase-related [Arabidopsis thaliana]	Unigene23267_All//2.00E-55//AT5G59010| protein kinase-related	Unigene23267_All//0.00E+00//gi|164348940|gb|ES819867.1|ES819867			GO:0004672//GO:0004871//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene23269_All	2896	7.71	6.88	3.84	13.14	11.59	9.22	24.03	27.61	38.38	-1.66E-01	1.89E-01		-1.01E+00	3.78E-16	Down	-1.81E-01	4.22E-02		-5.12E-01	9.80E-10		2.00E-01	1.56E-04		6.76E-01	1.28E-51		Unigene23269_All//gi|224141469|ref|XP_002324094.1|//0.00E+00//glycosyltransferase [Populus trichocarpa] >gi|222867096|gb|EEF04227.1| glycosyltransferase [Populus trichocarpa]	Unigene23269_All//0.00E+00//AT3G01040| GAUT13 (Galacturonosyltransferase 13); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene23269_All//0.00E+00//gi|73859382|gb|DT462121.1|DT462121			GO:0005975//GO:0008194	nr -
Unigene2327_All	950	1.43	1.28	1.46	0.94	1.70	2.09	3.12	2.16	18.75	-1.62E-01	7.58E-01		2.55E-02	9.84E-01		8.52E-01	1.06E-01		1.15E+00	1.42E-02		-5.31E-01	1.09E-01		2.59E+00	2.24E-62	Up	Unigene2327_All//gi|223452353|gb|ACM89504.1|//8.00E-38//protein kinase family protein [Glycine max]	Unigene2327_All//3.00E-32//AT1G70530| protein kinase family protein	Unigene2327_All//0.00E+00//TC159599		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene23270_All	381	4.26	1.86	2.24	3.01	4.25	4.39	8.66	6.91	3.66	-1.19E+00	2.32E-02		-9.29E-01	8.76E-02		4.98E-01	3.75E-01		5.45E-01	3.17E-01		-3.25E-01	3.25E-01		-1.24E+00	4.39E-05	Down	Unigene23270_All//gi|75228574|sp|Q7F8R0.1|C3H14_ORYSJ//2.00E-36//RecName: Full=Zinc finger CCCH domain-containing protein 14; Short=OsC3H14 >gi|46389843|dbj|BAD15406.1| KH domain-containing protein-like [Oryza sativa Japonica Group]	Unigene23270_All//2.00E-33//AT3G12130| KH domain-containing protein / zinc finger (CCCH type) family protein	Unigene23270_All//0.00E+00//TC147901	C3H		GO:0003676//GO:0046914	nr -
Unigene23272_All	1337	25.59	13.57	12.94	24.85	20.40	18.82	29.69	12.94	15.88	-9.16E-01	7.50E-22		-9.84E-01	1.42E-23		-2.85E-01	1.41E-03		-4.01E-01	9.83E-06		-1.20E+00	2.27E-47	Down	-9.03E-01	5.66E-31		Unigene23272_All//gi|75228574|sp|Q7F8R0.1|C3H14_ORYSJ//7.00E-95//RecName: Full=Zinc finger CCCH domain-containing protein 14; Short=OsC3H14 >gi|46389843|dbj|BAD15406.1| KH domain-containing protein-like [Oryza sativa Japonica Group]	Unigene23272_All//2.00E-81//AT5G06770| KH domain-containing protein / zinc finger (CCCH type) family protein	Unigene23272_All//0.00E+00//TC139821	C3H		GO:0005488	nr +
Unigene23275_All	350	6.58	7.24	13.39	10.11	5.80	15.10	16.67	14.21	8.88	1.38E-01	7.26E-01		1.03E+00	4.59E-04	Up	-8.00E-01	9.48E-03		5.79E-01	2.76E-02		-2.30E-01	3.51E-01		-9.09E-01	2.30E-05		Unigene23275_All//gi|224095950|ref|XP_002310510.1|//2.00E-08//predicted protein [Populus trichocarpa] >gi|222853413|gb|EEE90960.1| predicted protein [Populus trichocarpa]		Unigene23275_All//0.00E+00//gi|164367064|gb|ES844718.1|ES844718				nr -
Unigene2328_All	1651	0.70	0.37	0.06	1.57	0.67	1.01	1.66	0.61	1.81	-9.21E-01	1.43E-01		-3.43E+00	1.54E-04	Down	-1.23E+00	8.91E-04	Down	-6.33E-01	1.16E-01		-1.45E+00	3.99E-05	Down	1.21E-01	7.13E-01		Unigene2328_All//gi|15226343|ref|NP_178283.1|//9.00E-88//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75216739|sp|Q9ZUA2.1|PP141_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g01740	Unigene2328_All//6.00E-89//AT2G01740| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene23281_All	2900	0.23	0.00	0.00	0.21	0.32	0.23	11.05	10.45	15.32	-7.87E+00	4.10E-04	Down	-7.87E+00	7.64E-04	Down	6.37E-01	4.18E-01		1.81E-01	8.45E-01		-8.09E-02	4.30E-01		4.71E-01	1.70E-11		Unigene23281_All//gi|75164734|sp|Q948T9.1|RBOHB_SOLTU//0.00E+00//RecName: Full=Respiratory burst oxidase homolog protein B; AltName: Full=NADPH oxidase RBOHB; AltName: Full=StRBOHB >gi|16519089|dbj|BAB70751.1| respiratory burst oxidase homolog [Solanum tuberosum]	Unigene23281_All//0.00E+00//AT1G09090| ATRBOHB (respiratory burst oxidase homolog B) ; FAD binding / calcium ion binding / electron carrier/ iron ion binding / oxidoreductase/ oxidoreductase, acting on NADH or NADPH, with oxygen as acceptor / peroxidase	Unigene23281_All//0.00E+00//TC130743		ko04626|Plant-pathogen interaction	GO:0006950//GO:0008152//GO:0016209//GO:0030554//GO:0031224//GO:0032501//GO:0046914//GO:0050664	nr +
Unigene23283_All	1305	1.48	2.52	1.55	3.70	3.03	2.91	6.80	8.39	3.21	7.67E-01	2.46E-02		6.39E-02	8.93E-01		-2.87E-01	3.17E-01		-3.49E-01	2.31E-01		3.03E-01	5.92E-02		-1.09E+00	4.97E-10	Down	Unigene23283_All//gi|42561843|ref|NP_172383.3|//4.00E-23//ATRBOHB (respiratory burst oxidase homolog B); FAD binding / calcium ion binding / electron carrier/ iron ion binding / oxidoreductase/ oxidoreductase, acting on NADH or NADPH, with oxygen as acceptor / peroxidase [Arabidopsis thaliana]	Unigene23283_All//9.00E-25//AT1G09090| ATRBOHB (respiratory burst oxidase homolog B) ; FAD binding / calcium ion binding / electron carrier/ iron ion binding / oxidoreductase/ oxidoreductase, acting on NADH or NADPH, with oxygen as acceptor / peroxidase	Unigene23283_All//2.00E-126//gi|78344592|gb|DT564866.1|DT564866		ko04626|Plant-pathogen interaction	GO:0006950//GO:0008152//GO:0016209//GO:0030554//GO:0031224//GO:0032501//GO:0046914//GO:0050664	nr -
Unigene23285_All	1375	8.64	11.90	4.30	15.61	9.09	12.78	37.36	39.52	31.26	4.63E-01	7.85E-04		-1.01E+00	6.69E-09	Down	-7.80E-01	7.56E-13		-2.89E-01	1.72E-02		8.09E-02	2.89E-01		-2.57E-01	7.53E-05		Unigene23285_All//gi|145332907|ref|NP_001078319.1|//2.00E-97//EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G) ; translation initiation factor [Arabidopsis thaliana]	Unigene23285_All//2.00E-88//AT3G60240| EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G); translation initiation factor	Unigene23285_All//0.00E+00//TC143728			GO:0051707	nr +

Unigene23288_All	590	3.28	4.55	2.08	3.04	5.14	4.21	5.73	5.38	2.63	4.72E-01	2.27E-01		-6.61E-01	1.77E-01		7.57E-01	3.28E-02		4.70E-01	2.77E-01		-9.06E-02	7.81E-01		-1.12E+00	1.49E-04	Down	Unigene23288_All//gi|297847224|ref|XP_002891493.1|//4.00E-32//pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337335|gb|EFH67752.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23288_All//2.00E-23//AT1G49350| pfkB-type carbohydrate kinase family protein	Unigene23288_All//3.00E-163//ES835866			GO:0016773//GO:0019321//GO:0042254//GO:0043231	nr -
Unigene2329_All	2595	0.97	0.59	0.78	2.55	2.06	1.90	1.89	0.72	1.18	-7.24E-01	6.91E-02		-3.12E-01	4.62E-01		-3.12E-01	1.89E-01		-4.29E-01	6.91E-02		-1.38E+00	5.62E-08	Down	-6.77E-01	3.76E-03		Unigene2329_All//gi|15226343|ref|NP_178283.1|//1.00E-161//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75216739|sp|Q9ZUA2.1|PP141_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g01740	Unigene2329_All//2.00E-152//AT2G01740| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene23291_All	5042	4.29	0.87	0.82	5.90	4.66	3.13	13.62	5.06	6.57	-2.29E+00	6.93E-53	Down	-2.38E+00	3.31E-53	Down	-3.39E-01	2.81E-04		-9.16E-01	1.73E-20		-1.43E+00	2.04E-106	Down	-1.05E+00	7.41E-68	Down	Unigene23291_All//gi|224144433|ref|XP_002325288.1|//0.00E+00//DNA methyltransferase [Populus trichocarpa] >gi|222862163|gb|EEE99669.1| DNA methyltransferase [Populus trichocarpa]	Unigene23291_All//0.00E+00//AT5G49160| MET1 (METHYLTRANSFERASE 1); methyltransferase	Unigene23291_All//0.00E+00//ES834976		ko00270|Cysteine and methionine metabolism	GO:0003676//GO:0006305//GO:0008757//GO:0016747//GO:0043231	nr -
Unigene23295_All	1182	1.99	5.44	3.24	3.50	4.20	4.55	6.47	7.14	5.26	1.45E+00	5.65E-09	Up	7.04E-01	3.12E-02		2.62E-01	3.88E-01		3.78E-01	1.69E-01		1.42E-01	4.98E-01		-3.00E-01	1.12E-01		Unigene23295_All//gi|145652379|gb|ABP88244.1|//2.00E-42//transcription factor bZIP87 [Glycine max]	Unigene23295_All//1.00E-24//AT2G35530| bZIP transcription factor family protein	Unigene23295_All//0.00E+00//gi|109856215|gb|DW485194.1|DW485194	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene23302_All	2743	3.40	4.16	3.38	9.03	10.66	8.86	3.45	0.59	1.90	2.92E-01	9.55E-02		-7.40E-03	9.95E-01		2.40E-01	1.72E-02		-2.71E-02	8.45E-01		-2.54E+00	3.01E-32	Down	-8.60E-01	1.67E-07		Unigene23302_All//gi|158302693|dbj|BAF85832.1|//0.00E+00//alpha-1,2-fucosidase [Lilium longiflorum]	Unigene23302_All//0.00E+00//AT4G34260| FUC95A; 1,2-alpha-L-fucosidase	Unigene23302_All//0.00E+00//TC164493			GO:0004560//GO:0044464	nr -
Unigene23305_All	1566	3.37	3.72	1.50	9.19	5.96	13.87	6.43	6.54	6.97	1.41E-01	6.18E-01		-1.17E+00	2.27E-05	Down	-6.25E-01	4.03E-06		5.94E-01	2.22E-07		2.52E-02	9.03E-01		1.17E-01	5.00E-01		Unigene23305_All//gi|297852984|ref|XP_002894323.1|//1.00E-151//FMN binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297340165|gb|EFH70582.1| FMN binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene23305_All//6.00E-146//AT1G51560| FMN binding	Unigene23305_All//0.00E+00//TC145460				nr +
Unigene23308_All	2949	3.90	2.54	3.21	3.09	3.02	2.24	1.38	0.64	1.53	-6.18E-01	2.10E-04		-2.80E-01	1.30E-01		-3.16E-02	8.82E-01		-4.67E-01	1.46E-02		-1.11E+00	5.17E-05	Down	1.49E-01	6.06E-01		Unigene23308_All//gi|30678102|ref|NP_850987.1|//0.00E+00//RNEE/G (RNASE E/G-LIKE); endoribonuclease [Arabidopsis thaliana] >gi|25991183|gb|AAN76770.1|AF45047 9_1 endoribonuclease [Arabidopsis thaliana]	Unigene23308_All//0.00E+00//AT2G04270| RNEE/G (RNASE E/G-LIKE); endoribonuclease	Unigene23308_All//0.00E+00//ES832096			GO:0004519//GO:0005488//GO:0009657//GO:0010467//GO:0044238//GO:0044424	nr +
Unigene23311_All	528	18.83	11.71	18.96	26.04	33.91	27.97	49.49	18.21	16.37	-6.85E-01	1.56E-04		1.01E-02	9.81E-01		3.81E-01	2.55E-03		1.03E-01	5.74E-01		-1.44E+00	1.25E-41	Down	-1.60E+00	1.21E-49	Down	Unigene23311_All//gi|222422853|dbj|BAH19413.1|//4.00E-85//AT5G62890 [Arabidopsis thaliana]	Unigene23311_All//3.00E-79//AT5G62890| permease, putative	Unigene23311_All//0.00E+00//gi|164361102|gb|ES820984.1|ES820984			GO:0005215//GO:0006810//GO:0030312//GO:0043231	nr -
Unigene23312_All	1546	9.81	5.74	8.78	28.16	28.42	17.47	37.19	23.22	16.29	-7.75E-01	8.05E-08		-1.60E-01	3.41E-01		1.33E-02	9.02E-01		-6.89E-01	2.11E-18		-6.80E-01	8.97E-27		-1.19E+00	1.35E-69	Down	Unigene23312_All//gi|297795771|ref|XP_002865770.1|//0.00E+00//xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311605|gb|EFH42029.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23312_All//0.00E+00//AT5G49990| xanthine/uracil permease family protein	Unigene23312_All//0.00E+00//TC141209			GO:0005215//GO:0006810//GO:0044464	nr -
Unigene23313_All	456	9.64	5.78	17.52	19.45	13.37	17.13	3.06	4.67	6.99	-7.38E-01	1.03E-02		8.62E-01	5.63E-05		-5.41E-01	3.03E-03		-1.83E-01	4.12E-01		6.11E-01	1.28E-01		1.19E+00	1.21E-04	Up			Unigene23313_All//1.00E-38//ES825867				
Unigene23316_All	3786	7.03	13.32	13.05	41.72	34.25	25.13	10.79	8.56	4.09	9.21E-01	5.05E-32		8.92E-01	7.55E-29		-2.85E-01	1.07E-14		-7.31E-01	1.66E-72		-3.34E-01	7.27E-06		-1.40E+00	1.72E-63	Down	Unigene23316_All//gi|18402202|ref|NP_565689.1|//0.00E+00//heat shock protein-related [Arabidopsis thaliana] >gi|3420054|gb|AAC31855.1| expressed protein [Arabidopsis thaliana]	Unigene23316_All//3.00E-175//AT2G29970| heat shock protein-related	Unigene23316_All//0.00E+00//ES851486				nr -
Unigene2332_All	1948	3.95	1.14	2.51	11.28	5.96	3.55	7.08	2.64	3.25	-1.79E+00	4.31E-14	Down	-6.51E-01	2.87E-03		-9.21E-01	2.57E-17		-1.67E+00	2.31E-38	Down	-1.42E+00	6.91E-22	Down	-1.12E+00	7.63E-16	Down	Unigene2332_All//gi|100865521|gb|AAG12581.1|AC022522.14|//8.00E-26//Hypothetical protein [Arabidopsis thaliana]	Unigene2332_All//4.00E-27//AT1G12120| unknown protein	Unigene2332_All//0.00E+00//TC149874				nr +
Unigene23322_All	2976	1.23	1.82	3.01	1.67	2.50	1.82	4.73	4.35	2.36	5.66E-01	2.75E-02		1.29E+00	6.84E-10	Up	5.78E-01	5.10E-03		1.22E-01	6.97E-01		-1.20E-01	4.43E-01		-1.01E+00	1.13E-13	Down	Unigene23322_All//gi|158828300|gb|ABW81175.1|//3.00E-59//non-LTR retrotransposon transposase [Arabidopsis cebennensis]	Unigene23322_All//5.00E-13//AT3G24255| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G23910.1); Has 2302 Blast hits to 2235 proteins in 74 species: Archae - 4; Bacteria - 15; Metazoa - 871; Fungi - 12; Plants - 1295; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).	Unigene23322_All//0.00E+00//TC166871				nr +
Unigene23327_All	1626	27.25	57.21	34.48	34.25	52.99	44.80	22.02	35.37	21.19	1.07E+00	8.34E-75	Up	3.40E-01	2.82E-06		6.30E-01	1.37E-33		3.87E-01	5.35E-11		6.83E-01	5.12E-27		-5.55E-02	5.71E-01		Unigene23327_All//gi|158516792|gb|ABW70159.1|//1.00E-167//SINA1 [Medicago truncatula]	Unigene23327_All//9.00E-160//AT3G61790| seven in absentia (SINA) family protein	Unigene23327_All//0.00E+00//TC141983		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene23328_All	2857	17.78	11.35	15.12	18.33	15.22	13.09	17.48	8.72	8.32	-6.48E-01	5.88E-18		-2.34E-01	2.96E-03		-2.68E-01	9.96E-05		-4.86E-01	5.32E-12		-1.00E+00	9.81E-45	Down	-1.07E+00	4.60E-51	Down	Unigene23328_All//gi|75150628|sp|Q8GU14.1|UGP16_ARATH//1.00E-160//RecName: Full=Uncharacterized GPI-anchored protein At1g61900; Flags: Precursor >gi|27311769|gb|AAO00850.1| Unknown protein [Arabidopsis thaliana] >gi|30387511|gb|AAP31921.1| At1g61900 [Arabidopsis thaliana]	Unigene23328_All//4.00E-150//AT1G61900| unknown protein	Unigene23328_All//0.00E+00//TC156473		ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene23329_All	1662	18.86	14.27	22.52	4.05	5.12	5.22	50.45	5.00	2.09	-4.02E-01	2.86E-05		2.56E-01	5.91E-03		3.39E-01	9.85E-02		3.67E-01	7.27E-02		-3.33E+00	0.00E+00	Down	-4.60E+00	0.00E+00	Down	Unigene23329_All//gi|73624747|gb|AA279231.1|//2.00E-95//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene23329_All//3.00E-86//AT4G35850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene23329_All//0.00E+00//TC146329			GO:0016740	nr +
Unigene23330_All	2347	9.05	6.07	13.02	1.76	2.04	2.25	12.07	0.91	0.75	-5.77E-01	1.20E-06		5.25E-01	1.64E-07		2.11E-01	5.21E-01		3.54E-01	2.08E-01		-3.73E+00	1.09E-138	Down	-4.01E+00	1.35E-151	Down	Unigene23330_All//gi|30686386|ref|NP_567692.2|//1.00E-112//ATCSLG2; cellulose synthase/ transferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75161526|sp|Q8VYR4.1|CSLG2_ARATH RecName: Full=Cellulose synthase-like protein G2; Short=AtCsl2G	Unigene23330_All//2.00E-113//AT4G24000| ATCSLG2; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	Unigene23330_All//0.00E+00//TC133279			GO:0009987//GO:0016020//GO:0016757	nr -
Unigene23333_All	2571	6.90	4.53	4.70	13.70	13.58	7.66	11.79	5.43	5.95	-6.06E-01	3.92E-06		-5.53E-01	4.71E-05		-1.24E-02	9.11E-01		-8.39E-01	6.95E-21		-1.12E+00	1.14E-32	Down	-9.87E-01	1.50E-27		Unigene23333_All//gi|129563703|gb|AB033100.1|//0.00E+00//ovule receptor-like kinase 28 [Solanum chacoense]	Unigene23333_All//0.00E+00//AT1G53730| SRF6 (STRUBBELIG-RECEPTOR FAMILY 6); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene23333_All//0.00E+00//TC132078		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004871//GO:0006464//GO:0007167//GO:0031224//GO:0031410//GO:0032559//GO:0043231	nr +
Unigene23337_All	956	0.33	0.00	0.00	3.39	2.45	1.61	2.21	0.61	2.08	-8.36E+00	3.66E-02		-8.36E+00	4.91E-02		-4.68E-01	1.75E-01		-1.08E+00	1.71E-03		-1.85E+00	1.76E-05	Down	-8.58E-02	8.24E-01				Unigene23337_All//1.00E-37//gi|109873271|gb|DW502246.1|DW502246				
Unigene23338_All	623	0.00	0.00	0.00	8.88	2.93	4.35	2.04	1.07	1.22	null	null		null	null		-1.60E+00	1.06E-10	Down	-1.03E+00	3.98E-05	Down	-9.24E-01	8.68E-02		-7.45E-01	1.46E-01				Unigene23338_All//2.00E-63//gi|109873271|gb|DW502246.1|DW502246				
Unigene23339_All	2637	1.03	0.86	0.77	34.70	17.60	11.77	7.52	4.03	10.70	-2.55E-01	5.22E-01		-4.27E-01	2.98E-01		-9.79E-01	7.36E-79		-1.56E+00	7.33E-144	Down	-9.01E-01	2.11E-15		5.08E-01	1.23E-08		Unigene23339_All//gi|281333041|gb|ADA60975.1|//1.00E-102//lateral root primordium 1 [Brassica rapa subsp. pekinensis]	Unigene23339_All//1.00E-64//AT5G12330| LRP1 (LATERAL ROOT PRIMORDIUM 1); protein homodimerization	Unigene23339_All//0.00E+00//TC178472	SRS		GO:0009725//GO:0042802//GO:0048513	nr -
Unigene2334_All	1391	5.34	3.97	6.16	10.28	11.49	8.70	6.84	3.46	2.89	-4.28E-01	4.79E-02		2.07E-01	3.63E-01		1.60E-01	3.11E-01		-2.40E-01	1.33E-01		-9.85E-01	6.25E-09		-1.24E+00	5.13E-13	Down	Unigene2334_All//gi|42571467|ref|NP_973824.1|//1.00E-38//IQ028 (IQ67 DOMAIN PROTEIN 28); calmodulin binding [Arabidopsis thaliana]	Unigene2334_All//4.00E-19//AT1G74690| IQD31 (IQ-domain 31); calmodulin binding	Unigene2334_All//0.00E+00//C0131160			GO:0044464	nr +
Unigene23343_All	1276	9.06	24.18	19.24	8.12	9.34	15.15	32.44	39.54	78.80	1.42E+00	7.46E-39	Up	1.09E+00	4.94E-20	Up	2.02E-01	2.77E-01		9.00E-01	5.38E-13		2.85E-01	1.96E-05		1.28E+00	2.00E-134	Up	Unigene23343_All//gi|145338102|ref|NP_187095.2|//2.00E-86//transcription factor [Arabidopsis thaliana]	Unigene23343_All//3.00E-57//AT3G04450| transcription factor	Unigene23343_All//0.00E+00//TC146436	G2-like		GO:0001071//GO:0003676//GO:0010468//GO:0043231	nr -
Unigene23344_All	1908	7.49	19.39	13.62	5.53	8.83	9.66	14.09	18.31	39.80	1.37E+00	2.47E-44	Up	8.63E-01	1.20E-14		6.73E-01	1.01E-07		8.03E-01	2.40E-10		3.78E-01	3.06E-06		1.50E+00	8.92E-129	Up	Unigene23344_All//gi|6942190|gb|AAF32350.1|AF219972_1//8.00E-85//CDPK substrate protein 1 [Mesembryanthemum crystallinum]	Unigene23344_All//9.00E-85//AT5G29000| myb family transcription factor	Unigene23344_All//0.00E+00//TC146436	G2-like		GO:0043231	nr +
Unigene23345_All	1817	23.04	10.68	22.19	32.84	31.23	30.03	20.73	5.50	6.47	-1.11E+00	3.60E-36	Down	-5.43E-02	6.10E-01		-7.26E-02	3.82E-01		-1.29E-01	8.44E-02		-1.92E+00	4.88E-89	Down	-1.68E+00	1.21E-76	Down	Unigene23345_All//gi|18650600|gb|AAL75900.1|//1.00E-169//AT4g33220/F20D10_340 [Arabidopsis thaliana]	Unigene23345_All//9.00E-170//AT4G38220| aminoacylase, putative / N-acyl-L-amino-acid amidohydrolase, putative	Unigene23345_All//0.00E+00//TC176358		ko00330|Arginine and proline metabolism	GO:0005488//GO:0006519//GO:0016811//GO:0019538//GO:0044424//GO:0070011	nr +
Unigene23346_All	761	4.26	4.73	3.57	5.56	5.97	5.99	5.17	3.24	1.36	1.49E-01	6.40E-01		-2.56E-01	4.95E-01		1.02E-01	7.89E-01		1.07E-01	7.29E-01		-6.73E-01	1.43E-02		-1.92E+00	2.23E-10	Down	Unigene23346_All//gi|18406554|ref|NP_566018.1|//1.00E-27//p21Cip1-binding protein-related [Arabidopsis thaliana] >gi|75099252|sp|Q64885.2|BCCIP_ARATH RecName: Full=Protein BCCIP homolog >gi|15010574|gb|AAK73946.1| At2g44510/F411.32 [Arabidopsis thaliana] >gi|20197194|gb|AAC16097.2| Expressed protein [Arabidopsis thaliana] >gi|21360495|gb|AAM47363.1| At2g44510/F411.32 [Arabidopsis thaliana]	Unigene23346_All//4.00E-20//AT2G44510| p21Cip1-binding protein-related	Unigene23346_All//0.00E+00//TC176879			GO:0031981	nr -
Unigene2335_All	2015	6.36	4.00	3.14	9.94	10.51	8.34	7.30	3.46	23.41	-6.70E-01	2.06E-05		-1.02E+00	1.08E-09	Down	8.07E-02	5.85E-01		-2.53E-01	4.98E-02		-1.08E+00	2.53E-15	Down	1.68E+00	9.64E-95	Up	Unigene2335_All//gi|297827153|ref|XP_002881459.1|//0.00E+00//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327298|gb|EFH57718.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2335_All//0.00E+00//AT2G36670| aspartyl protease family protein	Unigene2335_All//0.00E+00//ES851936			GO:0004175//GO:0019538//GO:0044464	nr -

Unigene23350_All	791	8.47	23.06	20.13	15.93	15.37	17.99	5.35	6.60	7.76	1.45E+00	5.87E-24	Up	1.25E+00	2.36E-16	Up	-5.21E-02	8.13E-01		1.75E-01	3.08E-01		3.05E-01	2.26E-01		5.37E-01	9.48E-03		Unigene23350_All//gi|225441272|ref|XP_002274851.1|//3.00E-14//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene23350_All//2.00E-14//AT3G57062| unknown protein	Unigene23350_All//0.00E+00//TC162640			GO:0044464	nr -
Unigene23351_All	1797	4.34	5.64	11.05	5.07	5.50	4.55	3.69	5.00	2.35	3.78E-01	3.89E-02		1.35E+00	9.43E-23	Up	1.17E-01	5.99E-01		-1.57E-01	4.78E-01		4.37E-01	1.18E-02		-6.53E-01	9.25E-04					Unigene23351_All//0.00E+00//DW225314				
Unigene23352_All	2245	3.92	3.68	2.16	5.84	5.11	5.59	5.50	2.49	2.84	-8.98E-02	6.57E-01		-8.59E-01	2.32E-05		-1.92E-01	2.64E-01		-6.14E-02	7.31E-01		-1.14E+00	3.47E-14	Down	-9.54E-01	3.73E-11		Unigene23352_All//gi|297801602|ref|XP_002868685.1|//0.00E+00//GTP-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314521|gb|EFH41944.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23352_All//0.00E+00//AT5G39960| GTP-binding family protein	Unigene23352_All//0.00E+00//TC153344			GO:0032561//GO:0043231	nr +
Unigene23353_All	1321	9.86	8.02	6.65	5.54	5.53	2.77	1.79	1.04	0.48	-2.99E-01	6.43E-02		-5.68E-01	4.45E-04		-4.40E-03	9.78E-01		-1.00E+00	2.63E-06	Down	-7.80E-01	3.51E-02		-1.89E+00	1.88E-06	Down	Unigene23353_All//gi|297827989|ref|XP_002881877.1|//1.00E-122//ATMPK20 [Arabidopsis lyrata subsp. lyrata] >gi|297327716|gb|EFH58136.1| ATMPK20 [Arabidopsis lyrata subsp. lyrata]	Unigene23353_All//2.00E-114//AT2G42880| ATMPK20; MAP kinase	Unigene23353_All//0.00E+00//TC149504		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene23355_All	432	16.11	17.48	8.75	9.11	19.45	14.85	15.27	11.03	11.80	1.18E-01	6.03E-01		-8.80E-01	1.49E-04		1.09E+00	1.25E-08	Up	7.05E-01	2.26E-03		-4.69E-01	2.32E-02		-3.71E-01	6.62E-02		Unigene23355_All//gi|15242296|ref|NP_197048.1|//9.00E-42//EDL1 (EID1-like 1) [Arabidopsis thaliana] >gi|50198779|gb|AAT70423.1| At5g15440 [Arabidopsis thaliana]	Unigene23355_All//6.00E-43//AT5G15440| EDL1 (EID1-like 1)	Unigene23355_All//0.00E+00//gi|84167068|gb|DR455716.1|DR455716				nr -
Unigene23358_All	2340	81.01	112.21	28.42	46.39	49.36	69.79	79.75	138.18	157.87	4.70E-01	1.86E-50		-1.51E+00	6.75E-253	Down	8.95E-02	8.71E-02		5.89E-01	6.61E-51		7.93E-01	7.22E-192		9.85E-01	0.00E+00		Unigene23358_All//gi|40645472|dbj|BAD06581.1|//0.00E+00//arginine decarboxylase [Nicotiana tabacum]	Unigene23358_All//0.00E+00//AT2G16500| ADC1 (ARGININE DECARBOXYLASE 1); arginine decarboxylase	Unigene23358_All//0.00E+00//TC159427		ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism	GO:0006525//GO:0006596//GO:0006970//GO:0009725//GO:0009791//GO:0016831	nr -
Unigene2336_All	1906	0.58	0.11	0.28	0.63	0.38	0.78	0.89	0.24	1.40	-2.44E+00	1.50E-03		-1.05E+00	1.35E-01		-7.25E-01	2.33E-01		3.18E-01	6.18E-01		-1.88E+00	1.33E-04	Down	6.58E-01	4.85E-02		Unigene2336_All//gi|297827153|ref|XP_002881459.1|//0.00E+00//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327298|gb|EFH57718.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2336_All//0.00E+00//AT2G36670| aspartyl protease family protein	Unigene2336_All//0.00E+00//ES851936			GO:0004175//GO:0019538//GO:0044464	nr +
Unigene23360_All	998	0.58	2.54	1.71	3.04	3.07	2.22	6.65	9.42	6.03	2.14E+00	3.00E-06	Up	1.57E+00	4.57E-03		1.23E-02	9.84E-01		-4.58E-01	2.26E-01		5.03E-01	2.71E-03		-1.42E-01	5.33E-01		Unigene23360_All//gi|115447285|ref|NP_001047422.1|//4.00E-13//Os02g0614100 [Oryza sativa Japonica Group] >gi|113536953|dbj|BAF09336.1| Os02g0614100 [Oryza sativa Japonica Group]	Unigene23360_All//8.00E-17//AT4G32272| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter-related (TAIR:AT4G31600.1); Has 1302 Blast hits to 1300 proteins in 174 species: Archae - 0; Bacteria - 4; Metazoa - 376; Fungi - 239; Plants - 567; Viruses - 0; Other Eukaryotes - 116 (source: NCBI BLink).	Unigene23360_All//2.00E-98//gi|13247739|gb|BF272057.2|BF272057			GO:0031224	nr +
Unigene23361_All	1440	2.33	5.14	2.81	2.87	3.32	3.14	7.96	12.92	8.44	1.14E+00	2.59E-07	Up	2.73E-01	3.93E-01		2.11E-01	5.21E-01		1.27E-01	6.72E-01		6.99E-01	1.23E-09		8.47E-02	6.05E-01		Unigene23361_All//gi|255084806|ref|XP_002504834.1|//3.00E-68//Drug/Metabolite transporter superfamily [Micromonas sp. RCC299] >gi|226520103|gb|ACO66092.1| Drug/Metabolite transporter superfamily [Micromonas sp. RCC299]	Unigene23361_All//3.00E-109//AT4G32272| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter-related (TAIR:AT4G31600.1); Has 1302 Blast hits to 1300 proteins in 174 species: Archae - 0; Bacteria - 4; Metazoa - 376; Fungi - 239; Plants - 567; Viruses - 0; Other Eukaryotes - 116 (source: NCBI BLink).	Unigene23361_All//0.00E+00//gi|13247739|gb|BF272057.2|BF272057			GO:0016020	nr -
Unigene23362_All	1918	31.32	20.42	26.54	48.15	52.46	40.05	38.47	17.26	16.97	-6.17E-01	2.13E-19		-2.39E-01	8.45E-04		1.24E-01	2.01E-02		-2.66E-01	4.04E-07		-1.16E+00	1.36E-82	Down	-1.18E+00	8.61E-88	Down	Unigene23362_All//gi|18650600|gb|AAL75900.1|//1.00E-172//AT4g38220/F20D10_340 [Arabidopsis thaliana]	Unigene23362_All//8.00E-174//AT4G38220| aminoacylase, putative / N-acyl-L-amino-acid amidohydrolase, putative	Unigene23362_All//0.00E+00//TC140255		ko00330|Arginine and proline metabolism	GO:0005488//GO:0006519//GO:0016811//GO:0019538//GO:0044424//GO:0070011	nr +
Unigene23366_All	3014	3.35	3.35	3.07	8.25	7.21	3.63	11.53	4.09	3.65	-2.10E-03	9.89E-01		-1.24E-01	5.60E-01		-1.94E-01	8.95E-02		-1.19E+00	5.26E-26	Down	-1.50E+00	4.34E-58	Down	-1.66E+00	1.43E-69	Down	Unigene23366_All//gi|193237591|dbj|BAG50072.1|//1.00E-156//transcription factor CPP [Lotus japonicus]	Unigene23366_All//8.00E-104//AT4G14770| TCX2 (TESMIN/TSO1-LIKE CXC 2); transcription factor	Unigene23366_All//0.00E+00//gi|164240752|gb|ES808313.1|ES808313	CPP			nr -
Unigene23367_All	2139	0.71	1.11	0.95	2.86	1.79	1.08	1.80	0.74	1.10	6.50E-01	1.18E-01		4.15E-01	3.85E-01		-6.81E-01	2.31E-03		-1.41E+00	8.43E-09	Down	-1.28E+00	8.89E-06	Down	-7.11E-01	8.01E-03		Unigene23367_All//gi|193237591|dbj|BAG50072.1|//1.00E-168//transcription factor CPP [Lotus japonicus]	Unigene23367_All//3.00E-108//AT4G14770| TCX2 (TESMIN/TSO1-LIKE CXC 2); transcription factor	Unigene23367_All//0.00E+00//TC159632	CPP			nr +
Unigene23369_All	779	8.46	11.06	11.01	15.03	13.75	11.13	11.89	5.85	4.76	3.86E-01	5.49E-02		3.79E-01	7.37E-02		-1.28E-01	5.24E-01		-4.33E-01	9.08E-03		-1.02E+00	3.16E-09	Down	-1.32E+00	6.73E-14	Down	Unigene23369_All//gi|94442918|emb|CAJ91134.1|//4.00E-56//tubby protein [Platanus x acerifolia]	Unigene23369_All//3.00E-56//AT2G47900| AtTLP3 (TUBBY LIKE PROTEIN 3); phosphoric diester hydrolase/ transcription factor	Unigene23369_All//0.00E+00//TC167425	TUB		GO:0010468//GO:0042578	nr -
Unigene23370_All	1553	10.31	9.30	13.68	13.25	11.46	8.70	8.52	3.79	5.59	-1.49E-01	3.41E-01		4.08E-01	1.00E-03		-2.09E-01	1.01E-01		-6.07E-01	2.39E-07		-1.17E+00	1.09E-15	Down	-6.08E-01	6.21E-06		Unigene23370_All//gi|224107205|ref|XP_002314408.1|//1.00E-148//f-box family protein [Populus trichocarpa] >gi|222863448|gb|EEF00579.1| f-box family protein [Populus trichocarpa]	Unigene23370_All//2.00E-141//AT2G47900| AtTLP3 (TUBBY LIKE PROTEIN 3); phosphoric diester hydrolase/ transcription factor	Unigene23370_All//0.00E+00//TC167425	TUB			nr +
Unigene23372_All	1644	1.15	1.33	1.94	4.09	1.95	2.17	6.22	3.69	4.24	2.10E-01	6.10E-01		7.62E-01	3.61E-02		-1.07E+00	3.93E-07	Down	-9.14E-01	3.98E-05		-7.56E-01	2.21E-06		-5.54E-01	3.44E-04		Unigene23372_All//gi|124359891|gb|ABN06178.1|//5.00E-62//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene23372_All//2.00E-54//AT2G27230| LHW (LONESOME HIGHWAY); protein homodimerization/ transcription activator/ transcription factor	Unigene23372_All//3.00E-08//DW232932	bHLH		GO:0010468//GO:0043231	nr +
Unigene23373_All	1620	2.20	2.75	1.71	2.37	1.64	1.20	5.48	5.50	11.56	3.26E-01	2.74E-01		-3.62E-01	3.08E-01		-5.33E-01	8.18E-02		-9.82E-01	1.51E-03		3.80E-03	1.02E+00		1.08E+00	9.58E-20	Up	Unigene23373_All//gi|124359891|gb|ABN06178.1|//2.00E-60//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene23373_All//5.00E-47//AT2G27230| LHW (LONESOME HIGHWAY); protein homodimerization/ transcription activator/ transcription factor	Unigene23373_All//0.00E+00//DW232932	bHLH		GO:0010468//GO:0043231	nr +
Unigene23374_All	2613	1.00	21.10	0.59	2.36	6.84	9.18	3.66	23.79	87.62	4.40E+00	3.46E-246	Up	-7.61E-01	6.33E-02		1.53E+00	1.10E-29	Up	1.96E+00	5.37E-51	Up	2.70E+00	1.83E-222	Up	4.58E+00	0.00E+00	Up	Unigene23374_All//gi|224126261|ref|XP_002319796.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222858172|gb|EEE95719.1| GRAS family transcription factor [Populus trichocarpa]	Unigene23374_All//5.00E-139//AT5G48150| PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor	Unigene23374_All//0.00E+00//gi|78329092|gb|DT549366.1|DT549366	GRAS		GO:0010468	nr -
Unigene23377_All	1138	12.60	9.57	14.74	18.17	13.01	15.32	26.86	17.19	12.50	-3.96E-01	7.98E-03		2.27E-01	1.37E-01		-4.81E-01	1.61E-05		-2.46E-01	5.35E-02		-6.44E-01	2.23E-13		-1.10E+00	3.32E-33	Down	Unigene23377_All//gi|15236549|ref|NP_193484.1|//4.00E-95//UCH3 (UBIQUITIN C-TERMINAL HYDROLASE 3); ubiquitin thiolesterase [Arabidopsis thaliana]	Unigene23377_All//2.00E-96//AT4G17510| UCH3 (UBIQUITIN C-TERMINAL HYDROLASE 3); ubiquitin thiolesterase	Unigene23377_All//0.00E+00//TC153479			GO:0016790//GO:0019941//GO:0044464	nr +
Unigene23378_All	1171	5.81	7.01	7.91	8.25	9.62	6.90	11.66	6.67	5.10	2.71E-01	2.07E-01		4.46E-01	2.50E-02		2.21E-01	2.36E-01		-2.58E-01	2.03E-01		-8.05E-01	4.15E-09		-1.19E+00	3.14E-17	Down	Unigene23378_All//gi|15236549|ref|NP_193484.1|//6.00E-92//UCH3 (UBIQUITIN C-TERMINAL HYDROLASE 3); ubiquitin thiolesterase [Arabidopsis thaliana]	Unigene23378_All//3.00E-93//AT4G17510| UCH3 (UBIQUITIN C-TERMINAL HYDROLASE 3); ubiquitin thiolesterase	Unigene23378_All//0.00E+00//TC142864			GO:0016790//GO:0019941//GO:0044464	nr +
Unigene23379_All	3859	2.59	3.52	4.76	33.08	28.64	23.32	18.32	67.59	19.82	4.42E-01	3.96E-03		8.78E-01	7.74E-11		-2.08E-01	8.02E-07		-5.04E-01	2.03E-30		1.88E+00	0.00E+00	Up	1.14E-01	4.24E-02		Unigene23379_All//gi|8777306|dbj|BAA96896.1|//0.00E+00//receptor-like protein kinase [Arabidopsis thaliana] >gi|224589747|gb|ACN59405.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23379_All//0.00E+00//AT5G63930| leucine-rich repeat transmembrane protein kinase, putative	Unigene23379_All//0.00E+00//TC166002		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene2338_All	1499	4.47	2.23	1.60	4.95	6.20	4.49	12.58	8.34	9.65	-1.00E+00	1.38E-05	Down	-1.48E+00	3.55E-09	Down	3.25E-01	9.58E-02		-1.41E-01	5.92E-01		-5.94E-01	1.62E-07		-3.83E-01	5.60E-04		Unigene2338_All//gi|124360656|gb|AB008645.1|//1.00E-161//Tubulin binding cofactor C [Medicago truncatula]	Unigene2338_All//4.00E-156//AT3G57890| tubulin-specific chaperone C-related	Unigene2338_All//0.00E+00//TC148286				nr -
Unigene23380_All	3657	0.54	0.32	0.33	3.42	1.84	2.52	1.43	6.64	1.10	-7.71E-01	9.16E-02		-6.99E-01	1.44E-01		-8.97E-01	1.21E-09		-4.41E-01	5.69E-03		2.21E+00	3.85E-69	Up	-3.82E-01	9.90E-02		Unigene23380_All//gi|8777306|dbj|BAA96896.1|//0.00E+00//receptor-like protein kinase [Arabidopsis thaliana] >gi|224589747|gb|ACN59405.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23380_All//0.00E+00//AT5G63930| leucine-rich repeat transmembrane protein kinase, putative	Unigene23380_All//0.00E+00//TC155976		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0007167//GO:0016020//GO:0032559	nr -
Unigene23381_All	573	0.00	1.33	1.21	0.43	1.56	1.50	4.50	5.91	6.33	1.04E+01	1.77E-04	Up	1.02E+01	6.16E-04	Up	1.85E+00	2.15E-02		1.78E+00	3.19E-02		3.93E-01	2.16E-01		4.91E-01	8.19E-02		Unigene23381_All//gi|2842757|sp|Q99090.2|CPRF2_PETCR//2.00E-41//RecName: Full=Light-inducible protein CPRF2; AltName: Full=Common plant regulatory factor 2; Short=CPRF-2 >gi|1806261|emb|CAA41453.1| DNA-binding protein; bZIP type [Petroselinum crispum]	Unigene23381_All//1.00E-27//AT3G54620| BZIP25 (BASIC LEUCINE ZIPPER 25); protein heterodimerization/ transcription factor	Unigene23381_All//5.00E-134//gi|78345534|gb|DT565808.1|DT565808	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0002239//GO:0003677//GO:0033554//GO:0044424//GO:0046983	nr +
Unigene23382_All	1172	1.52	3.72	2.00	5.44	5.41	10.75	12.81	16.01	12.34	1.29E+00	1.90E-05	Up	3.97E-01	3.82E-01		-9.10E-03	9.67E-01		9.83E-01	5.85E-10		3.22E-01	5.49E-03		-5.37E-02	7.08E-01		Unigene23382_All//gi|16797791|gb|AL27150.1|//1.00E-73//bZIP transcription factor [Nicotiana tabacum]	Unigene23382_All//3.00E-54//AT3G54620| BZIP25 (BASIC LEUCINE ZIPPER 25); protein heterodimerization/ transcription factor	Unigene23382_All//0.00E+00//TC132621	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0002239//GO:0003677//GO:0033554//GO:0044424//GO:0046983	nr -
Unigene23385_All	1452	0.97	2.02	2.49	2.64	3.27	4.29	5.77	5.15	4.17	1.06E+00	4.21E-03		1.36E+00	9.94E-05	Up	3.09E-01	3.14E-01		7.00E-01	2.85E-03		-1.62E-01	4.23E-01		-4.67E-01	7.18E-03		Unigene23385_All//gi|16797791|gb|AL27150.1|//2.00E-78//bZIP transcription factor [Nicotiana tabacum]	Unigene23385_All//8.00E-65//AT3G54620| BZIP25 (BASIC LEUCINE ZIPPER 25); protein heterodimerization/ transcription factor	Unigene23385_All//0.00E+00//TC178172	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0002239//GO:0003677//GO:0033554//GO:0044424//GO:0046983	nr -
Unigene23387_All	1362	6.30	2.60	8.05	5.19	2.98	2.12	1.83	1.26	0.70	-1.27E+00	8.23E-10	Down	3.54E-01	5.40E-02		-8.00E-01	8.58E-05		-1.29E+00	7.37E-09	Down	-5.42E-01	1.39E-01		-1.38E+00	1.26E-04	Down	Unigene23387_All//gi|145333011|ref|NP_001078371.1|//3.00E-39//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene23387_All//2.00E-40//AT4G10720| ankyrin repeat family protein	Unigene23387_All//0.00E+00//DW517242			GO:0010033	nr -

Unigene23388_All	1659	4.38	5.59	3.66	15.31	17.91	10.40	1.91	2.92	0.60	3.51E-01	7.08E-02		-2.61E-01	2.77E-01		2.26E-01	2.45E-02		-5.58E-01	9.33E-08		6.13E-01	1.21E-02		-1.67E+00	3.56E-07	Down	Unigene23388_All//gi|42566408|ref|NP_192810.2|//1.00E-59//ankyrin repeat family protein [Arabidopsis thaliana] >gi|66792696|gb|AAY56450.1|At4g10720 [Arabidopsis thaliana]	Unigene23388_All//5.00E-55//AT4G10720| ankyrin repeat family protein	Unigene23388_All//0.00E+00//TC138470			GO:0010033	nr +
Unigene23389_All	3669	8.23	21.34	12.23	9.14	10.92	15.78	21.02	38.55	23.00	1.37E+00	2.54E-93	Up	5.72E-01	2.08E-12		2.57E-01	1.74E-03		7.88E-01	2.61E-30		8.75E-01	1.16E-99		1.30E-01	1.28E-02		Unigene23389_All//gi|15237392|ref|NP_199430.1|//0.00E+00//delta-OAT; ornithine-oxo-acid transaminase [Arabidopsis thaliana] >gi|9757738|dbj|BAB08263.1|ornithine aminotransferase [Arabidopsis thaliana] >gi|66792620|gb|AAY56412.1|At5g46180 [Arabidopsis thaliana] >gi|115646724|gb|ABJ17095.1|At5g46180 [Arabidopsis thaliana]	Unigene23389_All//0.00E+00//AT5G46180| delta-OAT; ornithine-oxo-acid transaminase	Unigene23389_All//0.00E+00//TC149137		ko00330|Arginine and proline metabolism	GO:0006527//GO:0006560//GO:0006591//GO:0006972//GO:0008483//GO:0043231//GO:0046914//GO:0048037	nr -
Unigene2339_All	203	1.29	1.25	0.26	0.49	0.51	0.00	21.24	12.56	4.71	-4.63E-02	9.87E-01		-2.30E+00	2.43E-01		5.22E-02	9.67E-01		-8.94E+00	4.00E-01		-7.58E-01	3.52E-03		-2.17E+00	4.39E-13	Down			Unigene2339_All//6.00E-79//TC173771				
Unigene23391_All	477	1.86	0.53	0.78	4.60	3.32	1.61	3.19	3.07	0.67	-1.81E+00	2.38E-02		-1.25E+00	1.17E-01		-4.69E-01	2.94E-01		-1.51E+00	6.85E-04	Down	-5.73E-02	9.20E-01		-2.26E+00	2.48E-05	Down	Unigene23391_All//gi|297820264|ref|XP_002878015.1|//2.00E-22//SET domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297323853|gb|EFH54274.1| SET domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene23391_All//2.00E-23//AT3G35080| SET domain-containing protein	Unigene23391_All//2.00E-93//TC177694			GO:0008757	nr -
Unigene23394_All	2257	5.52	11.99	8.16	11.21	9.08	10.83	6.65	11.11	5.45	1.12E+00	6.79E-24	Up	5.65E-01	2.10E-05		-3.05E-01	3.46E-03		-5.06E-02	6.87E-01		7.41E-01	5.70E-14		-2.86E-01	2.62E-02		Unigene23394_All//186531917|ref|NP_200071.2|//0.00E+00//RAB GTPase activator [Arabidopsis thaliana]	Unigene23394_All//0.00E+00//AT5G52580| RAB GTPase activator	Unigene23394_All//0.00E+00//TC169379			GO:0005099//GO:0032318//GO:0044464	nr -
Unigene23400_All	4176	4.41	12.04	4.78	7.63	6.61	7.39	14.45	20.02	21.49	1.45E+00	4.97E-65	Up	1.17E-01	4.07E-01		-2.07E-01	3.24E-02		-4.76E-02	7.03E-01		4.70E-01	2.96E-20		5.73E-01	1.85E-31		Unigene23400_All//gi|8978348|dbj|BAA98201.1|//0.00E+00//human RAN binding protein 16-like [Arabidopsis thaliana]	Unigene23400_All//0.00E+00//AT5G06120| Ran-binding protein, putative	Unigene23400_All//0.00E+00//TC140102			GO:0015031//GO:0022892	nr -
Unigene23401_All	2198	9.85	21.00	13.88	19.94	19.55	25.07	26.78	38.45	26.68	1.09E+00	1.13E-38	Up	4.94E-01	8.58E-07		-2.86E-02	8.06E-01		3.30E-01	1.89E-06		5.22E-01	1.40E-24		-5.20E-03	9.62E-01		Unigene23401_All//gi|224105833|ref|XP_002313948.1|//0.00E+00//sugar transporter/spinster transmembrane protein [Populus trichocarpa] >gi|222850356|gb|EEE87903.1| sugar transporter/spinster transmembrane protein [Populus trichocarpa]	Unigene23401_All//2.00E-172//AT5G64500| membrane protein-related	Unigene23401_All//0.00E+00//TC149005			GO:0006810//GO:0031224	nr -
Unigene23402_All	2256	6.33	13.90	6.87	7.11	8.55	8.37	18.31	19.68	12.66	1.13E+00	3.64E-28	Up	1.18E-01	4.75E-01		2.66E-01	3.80E-02		2.35E-01	8.45E-02		1.04E-01	2.10E-01		-5.32E-01	2.91E-13		Unigene23402_All//gi|89257426|gb|AB064918.1|//6.00E-50//bax inhibitor-like protein [Brassica oleracea]	Unigene23402_All//2.00E-33//AT5G47120| ATBI1 (BAX INHIBITOR 1)	Unigene23402_All//0.00E+00//TC162692			GO:0005488//GO:0006631//GO:0006950//GO:0006984//GO:0012505//GO:0031224//GO:0043066//GO:0043231	nr +
Unigene23403_All	1758	1.85	4.93	5.51	3.34	3.74	2.08	1.39	0.64	0.95	1.42E+00	1.90E-11	Up	1.58E+00	2.99E-14	Up	1.62E-01	5.51E-01		-6.84E-01	4.60E-03		-1.12E+00	2.21E-03		-5.51E-01	1.15E-01		Unigene23403_All//gi|115433970|ref|NP_001041743.1|//2.00E-12//Os01g0101600 [Oryza sativa Japonica Group] >gi|52076599|dbj|BAD45501.1|nuclear protein -like [Oryza sativa Japonica Group] >gi|113531274|dbj|BAF03657.1|Os01g0101600 [Oryza sativa Japonica Group]	Unigene23403_All//4.00E-07//AT3G23900| RNA recognition motif (RRM)-containing protein	Unigene23403_All//0.00E+00//TC162692			GO:0005488	nr -
Unigene23404_All	2534	259.37	125.53	194.26	65.86	86.02	61.69	12.60	10.80	12.47	-1.05E+00	0.00E+00	Down	-4.17E-01	9.28E-98		3.85E-01	7.71E-35		-9.44E-02	2.70E-02		-2.22E-01	1.24E-02		-1.50E-02	8.91E-01		Unigene23404_All//gi|2495155|sp|P93311.1|HEM11_CUCSA//0.00E-00//RecName: Full=Glutamyl-tRNA reductase 1, chloroplastic; Short=GluTR; Flags: Precursor >gi|1694926|dbj|BAA08910.1|glutamyl-tRNA reductase [Cucumis sativus]	Unigene23404_All//0.00E+00//AT1G58290| HEMA1; glutamyl-tRNA reductase	Unigene23404_All//0.00E+00//TC179097		ko00860|Porphyrin and chlorophyll metabolism	GO:0000166//GO:0006779//GO:0006950//GO:0009314//GO:0009536//GO:0016616//GO:0016620	nr -
Unigene23406_All	384	4.36	3.56	2.50	4.02	4.21	2.94	7.60	5.12	3.53	-2.91E-01	5.79E-01		-8.05E-01	1.35E-01		6.77E-02	9.17E-01		-4.52E-01	4.24E-01		-5.71E-01	8.53E-02		-1.11E+00	5.60E-04	Down	Unigene23406_All//gi|226499046|ref|NP_001147290.1|//4.00E-48//inner membrane protein ybaL [Zea mays] >gi|195609554|gb|ACG26607.1| inner membrane protein ybaL [Zea mays]	Unigene23406_All//1.00E-35//AT5G11800| KEA6; potassium ion transmembrane transporter/ potassium:hydrogen antiporter				GO:0005451//GO:0030001//GO:0031224//GO:0043231//GO:0046873	nr -
Unigene23410_All	1200	7.72	12.50	17.57	16.15	13.60	11.40	22.66	20.51	11.75	6.96E-01	1.56E-06		1.19E+00	7.48E-20	Up	-2.48E-01	5.15E-02		-5.02E-01	3.90E-05		-1.43E-01	1.69E-01		-9.47E-01	3.24E-23		Unigene23410_All//gi|16118856|gb|AL14629.1|AF417576_1//1.00E-165//growth-on protein G8010 [Euphorbia esula]	Unigene23410_All//8.00E-142//AT1G63690| protease-associated (PA) domain-containing protein	Unigene23410_All//0.00E+00//gi|48822757|gb|CO124070.1|CO124070				nr -
Unigene23411_All	1421	36.23	9.73	18.47	31.97	32.13	31.81	14.28	5.97	7.43	-1.90E+00	4.20E-98	Down	-9.72E-01	1.59E-34		7.30E-03	9.56E-01		-7.10E-03	9.47E-01		-1.26E+00	1.66E-26	Down	-9.43E-01	1.94E-17		Unigene23411_All//gi|16118856|gb|AL14629.1|AF417576_1//1.00E-166//growth-on protein G8010 [Euphorbia esula]	Unigene23411_All//5.00E-148//AT1G63690| protease-associated (PA) domain-containing protein	Unigene23411_All//0.00E+00//TC143970				nr -
Unigene23413_All	1017	52.94	10.11	18.12	17.00	9.82	9.37	2.91	3.86	4.58	-2.39E+00	1.61E-137	Down	-1.55E+00	1.75E-74	Down	-7.92E-01	1.09E-10		-8.59E-01	5.70E-11		4.09E-01	1.52E-01		6.55E-01	6.69E-03		Unigene23413_All//gi|30677926|ref|NP_178254.2|//1.00E-125//ATMPK17; MAP kinase [Arabidopsis thaliana] >gi|79316341|ref|NP_001030939.1|ATMPK17; MAP kinase [Arabidopsis thaliana] >gi|79316349|ref|NP_001030940.1|ATMPK17; MAP kinase [Arabidopsis thaliana] >gi|79316359|ref|NP_001030941.1|ATMPK17; MAP kinase [Arabidopsis thaliana] >gi|75327927|sp|Q84M93.1|MPK17_ARATH RecName: Full=Mitogen-activated protein kinase 17; Short=MAP kinase 17; Short=AtMPK17 >gi|30102718|gb|AAP21277.1|At2g01450 [Arabidopsis thaliana] >gi|222423803|dbj|BAH19867.1|AT2G01450 [Arabidopsis thaliana]	Unigene23413_All//1.00E-117//AT2G01450| ATMPK17; MAP kinase	Unigene23413_All//0.00E+00//TC146869		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene23414_All	2499	35.51	8.23	12.44	11.06	6.04	5.66	2.52	3.56	2.53	-2.11E+00	4.28E-194	Down	-1.51E+00	1.26E-118	Down	-8.74E-01	6.94E-20		-9.68E-01	7.04E-21		4.99E-01	3.92E-03		7.90E-03	9.67E-01		Unigene23414_All//gi|30677926|ref|NP_178254.2|//0.00E+00//ATMPK17; MAP kinase [Arabidopsis thaliana] >gi|79316341|ref|NP_001030939.1|ATMPK17; MAP kinase [Arabidopsis thaliana] >gi|79316349|ref|NP_001030940.1|ATMPK17; MAP kinase [Arabidopsis thaliana] >gi|79316359|ref|NP_001030941.1|ATMPK17; MAP kinase [Arabidopsis thaliana] >gi|75327927|sp|Q84M93.1|MPK17_ARATH RecName: Full=Mitogen-activated protein kinase 17; Short=MAP kinase 17; Short=AtMPK17 >gi|30102718|gb|AAP21277.1|At2g01450 [Arabidopsis thaliana] >gi|222423803|dbj|BAH19867.1|AT2G01450 [Arabidopsis thaliana]	Unigene23414_All//0.00E+00//AT2G01450| ATMPK17; MAP kinase	Unigene23414_All//0.00E+00//TC146869		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0009755//GO:0023060//GO:0032559//GO:0043231//GO:0044444	nr -
Unigene23418_All	2783	11.58	78.73	20.44	21.69	40.91	99.53	31.21	142.69	322.49	2.77E+00	0.00E+00	Up	8.19E-01	9.80E-29		9.15E-01	3.66E-84		2.20E+00	0.00E+00	Up	2.19E+00	0.00E+00	Up	3.37E+00	0.00E+00	Up	Unigene23418_All//gi|224061351|ref|XP_002300437.1|//0.00E+00//integral membrane single C2 domain protein [Populus trichocarpa] >gi|222847695|gb|EEE85242.1|integral membrane single C2 domain protein [Populus trichocarpa]	Unigene23418_All//0.00E+00//AT3G14590| NTMC2T6.2; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: C2 membrane targeting protein (InterPro:IPR018029), C2 calcium/lipid-binding region, CaLB (InterPro:IPR008973), C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: NTMC2T6.1 (TAIR:AT1G53590.1); Has 3079 Blast hits to 2709 proteins in 189 species: Archae - 0; Bacteria - 2; Metazoa - 1922; Fungi - 332; Plants - 570; Viruses - 0; Other Eukaryotes - 253 (source: NCBI BLink).	Unigene23418_All//0.00E+00//TC133895			GO:0016020//GO:0031410	nr +
Unigene2342_All	5785	7.83	8.03	7.33	8.79	8.96	8.06	15.79	13.00	7.81	3.63E-02	6.81E-01		-9.62E-02	3.09E-01		2.71E-02	8.04E-01		-1.25E-01	1.35E-01		-2.80E-01	6.77E-09		-1.02E+00	3.15E-85	Down	Unigene2342_All//gi|75182350|sp|Q9M1Y3.1|SKI35_ARATH//0.00E-00//RecName: Full=F-box/ankyrin repeat protein SKIP35; AltName: Full=SKP1-interacting partner 35 >gi|30725436|gb|AAP37740.1|At3g59910 [Arabidopsis thaliana]	Unigene2342_All//0.00E+00//AT3G59910| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Ankyrin (InterPro:IPR002110); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G44090.2); Has 43 Blast hits to 43 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink).	Unigene2342_All//0.00E+00//TC150432				nr +
Unigene23422_All	459	1.60	3.31	1.62	1.74	2.70	4.03	1.20	3.82	2.78	1.05E+00	5.24E-02		2.54E-02	9.95E-01		6.37E-01	3.15E-01		1.22E+00	1.32E-02		1.68E+00	3.64E-04	Up	1.21E+00	2.09E-02		Unigene23422_All//gi|223452302|gb|ACM89479.1|//5.00E-26//cysteine-rich protein [Glycine max]	Unigene23422_All//2.00E-15//AT4G05200| protein kinase family protein	Unigene23422_All//6.00E-87//DW239571			GO:0000166//GO:0004674//GO:0004871//GO:0006952//GO:0008219//GO:0010033	nr -
Unigene23423_All	2227	14.64	35.99	15.16	19.62	40.43	45.37	2.87	18.19	24.99	1.30E+00	1.52E-87	Up	5.06E-02	6.28E-01		1.04E+00	1.33E-82	Up	1.21E+00	3.49E-106	Up	2.67E+00	5.35E-143	Up	3.12E+00	1.72E-235	Up	Unigene23423_All//gi|223452302|gb|ACM89479.1|//0.00E+00//cysteine-rich protein [Glycine max]	Unigene23423_All//0.00E+00//AT4G05200| protein kinase family protein	Unigene23423_All//0.00E+00//TC165530		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674//GO:0016020	nr +
Unigene23424_All	596	2.28	6.04	2.14	2.01	2.48	1.67	14.05	10.31	20.12	1.40E+00	3.83E-05	Up	-9.01E-02	8.77E-01		3.09E-01	5.98E-01		-2.67E-01	6.88E-01		-4.46E-01	1.33E-02		5.18E-01	2.65E-04		Unigene23424_All//gi|71493366|gb|AAZ32787.1|//6.00E-66//cellulose synthase-like protein CslE [Nicotiana tabacum]	Unigene23424_All//1.00E-34//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups				GO:0009250//GO:0016759//GO:0031224//GO:0045229	nr -
Unigene23426_All	1098	7.81	7.38	3.93	7.03	5.49	9.38	17.52	43.32	40.49	-8.19E-02	6.88E-01		-9.92E-01	1.76E-06		-3.58E-01	8.89E-02		4.15E-01	2.19E-02		1.31E+00	1.49E-64	Up	1.21E+00	8.73E-55	Up	Unigene23426_All//gi|255560551|ref|XP_002521290.1|//9.00E-18//conserved hypothetical protein [Ricinus communis] >gi|223539558|gb|EEF41146.1|conserved hypothetical protein [Ricinus communis]	Unigene23426_All//6.00E-160//BF268833				nr +

Unigene23427_All	1838	37.38	30.21	18.98	22.93	23.61	30.81	100.78	256.78	260.62	-3.07E-01	1.12E-06		-9.78E-01	2.09E-46		4.20E-02	6.95E-01		4.26E-01	2.93E-10		1.35E+00	0.00E+00	Up	1.37E+00	0.00E+00	Up	Unigene23427_All//gi|14326527|gb|AA660308.1|AF385717_1//2.00E-60//AT4g35110/M4E13_160 [Arabidopsis thaliana] >gi|22137306|gb|AAM91498.1| AT4g35110/M4E13_160 [Arabidopsis thaliana]	Unigene23427_All//1.00E-50//AT4G35110| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: Phospholipase-like, arabidopsis (InterPro:IPR007942); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G16900.1); Has 495 Blast hits to 408 proteins in 102 species: Archae - 17; Bacteria - 39; Metazoa - 132; Fungi - 34; Plants - 131; Viruses - 35; Other Eukaryotes - 107 (source: NCBI BLink).	Unigene23427_All//0.00E+00//TC133622		ko03040|Spliceosome	GO:0016020	nr -
Unigene23428_All	710	2.95	6.28	5.93	24.49	14.65	15.65	19.06	7.36	48.93	1.09E+00	1.88E-04	Up	1.01E+00	1.19E-03		-7.41E-01	1.22E-09		-6.46E-01	5.72E-07		-1.37E+00	2.09E-20	Down	1.36E+00	1.71E-51	Up	Unigene23428_All//gi|15237117|ref|NP_195300.1|//2.00E-84//Rho-GTPase-activating protein-related [Arabidopsis thaliana] >gi|30725562|gb|AAP37803.1| At4g35750 [Arabidopsis thaliana]	Unigene23428_All//1.00E-81//AT4G35750| Rho-GTPase-activating protein-related	Unigene23428_All//0.00E+00//gi|109866890|gb|DW495866.1|DW495866				nr +
Unigene23429_All	1008	1.25	2.16	1.74	13.84	5.33	9.05	16.53	7.75	42.84	7.95E-01	6.74E-02		4.85E-01	3.60E-01		-1.38E+00	4.40E-21	Down	-6.13E-01	2.82E-05		-1.09E+00	1.22E-17	Down	1.37E+00	8.90E-65	Up	Unigene23429_All//gi|15237117|ref|NP_195300.1|//7.00E-81//Rho-GTPase-activating protein-related [Arabidopsis thaliana] >gi|30725562|gb|AAP37803.1| At4g35750 [Arabidopsis thaliana]	Unigene23429_All//6.00E-79//AT4G35750| Rho-GTPase-activating protein-related	Unigene23429_All//0.00E+00//TC160214				nr -
Unigene23431_All	3540	141.07	66.64	117.03	11.71	12.80	7.11	3.60	2.13	2.25	-1.08E+00	0.00E+00	Down	-2.70E-01	6.03E-33		1.29E-01	1.40E-01		-7.20E-01	6.26E-19		-7.58E-01	8.76E-08		-6.76E-01	9.63E-07		Unigene23431_All//gi|225423855|ref|XP_002281154.1|//0.00E+00//PREDICTED: similar to CHLP1 (CHLOROPLAST UNUSUAL POSITIONING 1) [Vitis vinifera]	Unigene23431_All//0.00E+00//AT3G25690| CHLP1 (CHLOROPLAST UNUSUAL POSITIONING 1)	Unigene23431_All//0.00E+00//TC144977		ko03040|Spliceosome	GO:0009527//GO:0009658	nr +
Unigene23432_All	2151	1.80	1.32	2.28	66.37	57.30	33.41	11.26	2.39	1.63	-4.48E-01	1.53E-01		3.40E-01	2.43E-01		-2.12E-01	8.23E-08		-9.91E-01	6.94E-110		-2.24E+00	3.98E-70	Down	-2.79E+00	3.17E-93	Down	Unigene23432_All//gi|115452921|ref|NP_001050061.1|//1.00E-49//Os03g0339700 [Oryza sativa Japonica Group] >gi|108708050|gb|ABF95845.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548532|dbj|BAF11975.1| Os03g0339700 [Oryza sativa Japonica Group]	Unigene23432_All//2.00E-62//AT2G40480| unknown protein	Unigene23432_All//0.00E+00//TC173131				nr -
Unigene23433_All	2257	13.05	8.78	5.99	27.17	23.92	27.75	22.99	15.63	22.59	-5.72E-01	8.98E-09		-1.12E+00	3.66E-25	Down	-1.84E-01	5.60E-03		3.07E-02	7.06E-01		-5.56E-01	3.25E-17		-2.48E-02	7.48E-01		Unigene23433_All//gi|289541361|gb|ADD09804.1|//0.00E+00//ectoapyrase 2 [Gossypium hirsutum]	Unigene23433_All//3.00E-169//AT5G18280| ATAPY2 (ARABIDOPSIS THALIANA APYRASE 2); ATPase/ nucleotide diphosphatase	Unigene23433_All//0.00E+00//TC150263		ko00230|Purine metabolism//ko00730|Thiamine metabolism	GO:0016462	nr +
Unigene23434_All	3031	171.10	77.12	118.87	82.88	60.17	21.44	12.94	3.67	8.89	-1.15E+00	0.00E+00	Down	-5.26E-01	7.58E-118		-4.62E-01	4.31E-57		-1.95E+00	0.00E+00	Down	-1.82E+00	1.67E-86	Down	-5.43E-01	4.48E-13		Unigene23434_All//gi|24474446|gb|AAL15927.1|//0.00E+00//nitrate reductase [Tilia platyphyllos]	Unigene23434_All//0.00E+00//AT1G37130| NIA2 (NITRATE REDUCTASE 2); nitrate reductase (NADH)/ nitrate reductase	Unigene23434_All//0.00E+00//TC158081		ko00910|Nitrogen metabolism//ko00920|Sulfur metabolism	GO:0005506//GO:0008940//GO:0030554//GO:0042126	nr -
Unigene23435_All	2578	3.94	39.25	5.62	4.50	14.15	12.60	14.84	35.51	57.41	3.32E+00	0.00E+00	Up	5.13E-01	7.76E-04		1.65E+00	3.55E-67	Up	1.48E+00	6.91E-47	Up	1.26E+00	1.17E-116	Up	1.95E+00	0.00E+00	Up	Unigene23435_All//gi|30013679|gb|AAP03882.1|//0.00E+00//Avr9/Cf-9 rapidly elicited protein 276 [Nicotiana tabacum]	Unigene23435_All//0.00E+00//AT1G29340| PLB17 (PLANT U-BOX 17); ubiquitin-protein ligase	Unigene23435_All//0.00E+00//TC148106		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0012501//GO:0019787//GO:0032446//GO:0043234//GO:0050832	nr +
Unigene23436_All	1444	10.36	11.93	11.47	29.39	35.89	72.84	24.62	30.13	28.72	2.03E-01	1.53E-01		1.46E-01	3.66E-01		2.88E-01	3.16E-05		1.31E+00	4.76E-125	Up	2.91E-01	5.90E-05		2.22E-01	2.67E-03		Unigene23436_All//gi|2745902|gb|AAB94773.1|//0.00E+00//ERS-like ethylene receptor [Pisum sativum]	Unigene23436_All//6.00E-173//AT2G40940| ERS1 (ETHYLENE RESPONSE SENSOR 1); ethylene binding / protein histidine kinase/ receptor	Unigene23436_All//0.00E+00//TC174002			GO:0004673//GO:0004871//GO:0006468//GO:0023060//GO:0032559//GO:0044464	nr +
Unigene23437_All	2167	8.57	16.84	11.30	12.44	10.69	18.40	7.73	10.76	16.44	9.74E-01	1.35E-25		3.99E-01	4.92E-04		-2.18E-01	4.10E-02		5.65E-01	5.62E-12		4.78E-01	2.06E-06		1.09E+00	1.94E-37	Up	Unigene23437_All//gi|297606541|ref|NP_001058631.2|//1.00E-132//Os06g0726600 [Oryza sativa Japonica Group] >gi|54291134|dbj|BAD61807.1| MAP kinase activating protein-like [Oryza sativa Japonica Group] >gi|255677415|dbj|BAF20545.2| Os06g0726600 [Oryza sativa Japonica Group]	Unigene23437_All//1.00E-144//AT4G38360| unknown protein	Unigene23437_All//0.00E+00//ES831043				nr -
Unigene23440_All	3078	0.43	1.40	0.67	0.58	0.73	1.00	1.44	1.03	0.65	1.72E+00	8.88E-08	Up	6.67E-01	1.51E-01		3.20E-01	5.18E-01		7.76E-01	3.07E-02		-4.83E-01	6.46E-02		-1.16E+00	6.12E-06	Down	Unigene23440_All//gi|30686462|ref|NP_849551.1|//0.00E+00//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	Unigene23440_All//0.00E+00//AT4G24270| RNA recognition motif (RRM)-containing protein	Unigene23440_All//0.00E+00//TC141604		ko03040|Spliceosome	GO:0005488	nr -
Unigene23441_All	2182	12.23	44.07	15.91	8.24	11.03	18.05	17.50	47.35	51.09	1.85E+00	1.15E-175	Up	3.80E-01	5.60E-05		4.21E-01	5.91E-05		1.13E+00	1.77E-37	Up	1.44E+00	4.40E-161	Up	1.55E+00	1.13E-197	Up	Unigene23441_All//gi|223452488|gb|ACM89571.1|//1.00E-168//protein kinase [Glycine max]	Unigene23441_All//6.00E-166//AT3G09830| protein kinase, putative	Unigene23441_All//0.00E+00//TC161503				nr -
Unigene23442_All	2422	12.46	11.99	14.75	12.01	10.62	8.67	13.35	7.06	5.49	-5.63E-02	6.16E-01		2.43E-01	1.16E-02		-1.78E-01	9.30E-02		-4.70E-01	1.33E-06		-9.20E-01	1.95E-25		-1.28E+00	3.09E-44	Down	Unigene23442_All//gi|69218101|gb|AAZ04133.1|//0.00E+00//N-acylethanolamine amidohydrolase [Medicago truncatula]	Unigene23442_All//0.00E+00//AT5G64440| AtFAAH (Arabidopsis thaliana fatty acid amide hydrolase); N-(long-chain-acyl)ethanolamine deacylase/ amidase	Unigene23442_All//0.00E+00//TC166680		ko00970|Aminoacyl-tRNA biosynthesis	GO:0006952//GO:0016020//GO:0016811//GO:0016879//GO:0043231	nr -
Unigene23443_All	1660	8.57	81.10	12.80	8.70	18.44	23.67	24.94	85.45	94.92	3.24E+00	0.00E+00	Up	5.78E-01	2.44E-06		1.08E+00	6.06E-30	Up	1.44E+00	2.28E-54	Up	1.78E+00	1.16E-300	Up	1.93E+00	0.00E+00	Up	Unigene23443_All//gi|3643085|gb|AAC36698.1|//1.00E-145//protein phosphatase-2C [Mesembryanthemum crystallinum]	Unigene23443_All//2.00E-127//AT3G62260| protein phosphatase 2C, putative / PP2C, putative	Unigene23443_All//0.00E+00//TC164464	DBP			nr +
Unigene23446_All	453	6.01	8.95	5.88	20.23	13.99	16.75	22.40	11.99	9.85	5.75E-01	5.90E-02		-3.12E-02	9.54E-01		-5.33E-01	2.94E-03		-2.73E-01	1.91E-01		-9.01E-01	2.81E-08		-1.19E+00	6.48E-13	Down	Unigene23446_All//gi|224053829|ref|XP_002298000.1|//1.00E-23//calcium dependent protein kinase 3 [Populus trichocarpa] >gi|222845258|gb|EEE82805.1| calcium dependent protein kinase 3 [Populus trichocarpa]	Unigene23446_All//1.00E-22//AT4G23650| CDPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene23446_All//0.00E+00//gi|21095380|gb|BQ407693.1|BQ407693		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0006970//GO:0009755//GO:0010118//GO:0016020//GO:0032412//GO:0032559//GO:0043231//GO:0046872	nr +
Unigene2345_All	1984	10.10	4.80	7.38	15.57	14.91	14.34	10.14	6.09	6.69	-1.07E+00	8.03E-17	Down	-4.53E-01	3.92E-04		-6.23E-02	6.13E-01		-1.18E-01	3.07E-01		-7.37E-01	2.73E-11		-6.01E-01	2.07E-08		Unigene2345_All//gi|15237681|ref|NP_201241.1|//2.00E-36//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|30698003|ref|NP_851265.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|79332130|ref|NP_001032136.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|134031896|gb|ABO45685.1| At5g64360 [Arabidopsis thaliana] >gi|222423220|dbj|BAH19587.1| AT5G64360 [Arabidopsis thaliana]	Unigene2345_All//1.00E-23//AT1G62970| DNAJ heat shock N-terminal domain-containing protein	Unigene2345_All//0.00E+00//TC157118			GO:0005515	nr -
Unigene23450_All	1331	2.20	0.76	1.84	7.34	7.19	3.80	3.34	1.41	1.95	-1.53E+00	7.46E-05	Down	-2.58E-01	5.16E-01		-2.84E-02	8.93E-01		-9.49E-01	1.53E-07		-1.24E+00	2.76E-06	Down	-7.78E-01	1.69E-03		Unigene23450_All//gi|79328583|ref|NP_001031933.1|//8.00E-70//PHS1 (PROPYZAMIDE-HYPERSENSITIVE 1); phosphoprotein phosphatase/ protein tyrosine/serine/threonine phosphatase [Arabidopsis thaliana]	Unigene23450_All//8.00E-63//AT5G23720| PHS1 (PROPYZAMIDE-HYPERSENSITIVE 1); phosphoprotein phosphatase/ protein tyrosine/serine/threonine phosphatase	Unigene23450_All//0.00E+00//ES815814			GO:0004721//GO:0006464//GO:0006732//GO:0006796//GO:0007127//GO:0009642//GO:0009657//GO:0009725//GO:0010118//GO:0010467//GO:0016616//GO:0016772//GO:0030865//GO:0044424//GO:0046914	nr +
Unigene23452_All	1874	43.25	143.68	20.80	19.19	21.17	84.49	59.25	325.49	269.90	1.73E+00	0.00E+00	Up	-1.06E+00	5.31E-62	Down	1.41E-01	1.28E-01		2.14E+00	0.00E+00	Up	2.46E+00	0.00E+00	Up	2.19E+00	0.00E+00	Up	Unigene23452_All//gi|224137016|ref|XP_002322473.1|//0.00E+00//acyl:coa ligase [Populus trichocarpa] >gi|222869469|gb|EEF06600.1| acyl:coa ligase [Populus trichocarpa]	Unigene23452_All//0.00E+00//AT3G48990| AMP-dependent synthetase and ligase family protein	Unigene23452_All//0.00E+00//TC130872		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0005576//GO:0009536//GO:0010038//GO:0016405//GO:0032559	nr +
Unigene23455_All	508	0.62	0.40	0.31	0.20	0.88	0.36	1.66	3.54	5.72	-6.31E-01	6.22E-01		-9.75E-01	5.06E-01		2.17E+00	1.06E-01		8.59E-01	6.95E-01		1.09E+00	1.32E-02		1.78E+00	4.19E-07	Up		Unigene23455_All//7.00E-130//TC161628					
Unigene23456_All	3137	1.33	0.95	0.71	3.35	3.59	2.98	4.57	8.01	11.65	-4.86E-01	1.06E-01		-9.04E-01	3.67E-03		9.94E-02	6.16E-01		-1.69E-01	4.07E-01		8.10E-01	3.49E-16		1.35E+00	1.80E-53	Up	Unigene23456_All//gi|22335691|dbj|BAC10548.1|//8.00E-54//cullin-like protein1 [Pisum sativum]	Unigene23456_All//6.00E-54//AT4G02570| ATCUL1 (ARABIDOPSIS THALIANA CULLIN 1); protein binding	Unigene23456_All//0.00E+00//TC161628		ko04120|Ubiquitin mediated proteolysis	GO:0005488	nr +
Unigene23457_All	2407	38.10	83.13	51.88	54.84	73.51	110.82	78.64	107.19	115.03	1.13E+00	7.50E-174	Up	4.45E-01	2.39E-21		4.23E-01	1.52E-33		1.01E+00	4.91E-211	Up	4.47E-01	2.31E-55		5.49E-01	4.73E-88		Unigene23457_All//gi|15224204|ref|NP_181830.1|//0.00E+00//ATPAO2 (Polyamine oxidase 2); amine oxidase/ electron carrier/ oxidoreductase [Arabidopsis thaliana] >gi|75206576|sp|Q9SKX5.1|PAO2_ARATH RecName: Full=Probable polyamine oxidase 2; Short=AtPAO2; AltName: Full=Amine oxidase 1 >gi|115311507|gb|AB193934.1| At2g43020 [Arabidopsis thaliana]	Unigene23457_All//0.00E+00//AT2G43020| ATPAO2 (Polyamine oxidase 2); amine oxidase/ electron carrier/ oxidoreductase	Unigene23457_All//0.00E+00//TC150788			GO:0006595//GO:0016641//GO:0016647//GO:0016741	nr -
Unigene23459_All	765	17.44	16.16	17.26	24.29	22.87	19.01	31.50	22.73	13.49	-1.10E-01	5.32E-01		-1.48E-02	9.49E-01		-8.70E-02	5.86E-01		-3.54E-01	6.03E-03		-4.71E-01	1.90E-06		-1.22E+00	6.17E-31	Down	Unigene23459_All//gi|226500790|ref|NP_001149507.1|//1.00E-65//LOC100283133 [Zea mays] >gi|195621266|gb|ACG32463.1| trafficking protein particle complex subunit 4 [Zea mays] >gi|195627666|gb|ACG35663.1| trafficking protein particle complex subunit 4 [Zea mays]	Unigene23459_All//3.00E-72//AT5G02280| synbindin, putative	Unigene23459_All//0.00E+00//TC171579			GO:0044431//GO:0048193	nr +
Unigene23461_All	1124	9.17	5.18	7.82	7.62	8.15	10.61	1.17	4.91	3.26	-8.23E-01	4.28E-06		-2.30E-01	2.42E-01		9.64E-02	6.81E-01		4.77E-01	3.53E-03		2.07E+00	4.80E-15	Up	1.48E+00	6.20E-07	Up	Unigene23461_All//gi|22329127|ref|NP_195080.2|//1.00E-115//metallo-beta-lactamase family protein [Arabidopsis thaliana]	Unigene23461_All//2.00E-116//AT4G33540| metallo-beta-lactamase family protein	Unigene23461_All//0.00E+00//CO095189			GO:0043231	nr +
Unigene23462_All	660	11.49	2.46	11.62	3.77	1.67	1.09	0.00	0.00	0.06	-2.23E+00	2.55E-18	Down	1.54E-02	9.65E-01		-1.18E+00	1.93E-03		-1.79E+00	2.71E-05	Down	null	null		5.92E+00	6.45E-01		Unigene23462_All//gi|297802650|ref|XP_002869209.1|//9.00E-60//metallo-beta-lactamase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315045|gb|EFH45468.1| metallo-beta-lactamase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23462_All//4.00E-60//AT4G33540| metallo-beta-lactamase family protein	Unigene23462_All//0.00E+00//gi|48793875|gb|CO095189.1|CO095189			GO:0003824//GO:0009536//GO:0010035	nr +
Unigene23463_All	801	1.31	3.04	2.19	4.42	4.64	3.21	1.43	6.42	4.18	1.22E+00	3.60E-03		7.48E-01	1.45E-01		7.25E-02	8.41E-01		-4.58E-01	1.84E-01		2.17E+00	7.27E-15	Up	1.55E+00	8.88E-07	Up	Unigene23463_All//gi|22329127|ref|NP_195080.2|//2.00E-08//metallo-beta-lactamase family protein [Arabidopsis thaliana]	Unigene23463_All//1.00E-09//AT4G33540| metallo-beta-lactamase family protein	Unigene23463_All//0.00E+00//TC176228			GO:0003824//GO:0009536//GO:0010035	nr -

Unigene23464_All	1342	9.71	11.52	10.87	14.51	16.11	19.86	5.48	21.55	7.99	2.46E-01	9.85E-02		1.63E-01	3.40E-01		1.51E-01	2.63E-01		4.52E-01	1.06E-05		1.98E+00	3.41E-71	Up	5.43E-01	3.31E-04		Unigene23464_All//gi|297802650|ref|XP_002869209.1|//1.00E-116//metallo-beta-lactamase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315045|gb|EFH45468.1|metallo-beta-lactamase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23464_All//2.00E-116//AT4G33540| metallo-beta-lactamase family protein	Unigene23464_All//0.00E+00//TC176228			GO:0043231	nr +
Unigene23467_All	3309	4.25	3.11	3.41	6.74	6.10	5.34	10.34	4.76	6.63	-4.52E-01	2.55E-03		-3.18E-01	4.81E-02		-1.45E-01	2.70E-01		-3.38E-01	3.63E-03		-1.12E+00	9.98E-37	Down	-6.40E-01	3.70E-15		Unigene23467_All//gi|79586698|ref|NP_680116.2|//5.00E-67//REF6 (RELATIVE OF EARLY FLOWERING 6); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|50513173|gb|AAT77779.1|relative of early flowering 6 [Arabidopsis thaliana]	Unigene23467_All//2.00E-61//AT3G48430| REF6 (RELATIVE OF EARLY FLOWERING 6); nucleic acid binding / transcription factor/ zinc ion binding	Unigene23467_All//0.00E+00//ES822227	Jumonji		GO:0005488//GO:0005622//GO:0007275//GO:0016570//GO:0048856	nr +
Unigene23468_All	707	3.18	1.94	3.16	4.51	4.29	2.75	10.29	5.32	4.45	-7.18E-01	9.12E-02		-8.50E-03	1.00E+00		-7.32E-02	8.30E-01		-7.15E-01	4.03E-02		-9.51E-01	1.15E-06		-1.21E+00	9.02E-10	Down	Unigene23468_All//gi|224071151|ref|XP_002303365.1|//1.00E-11//predicted protein [Populus trichocarpa] >gi|222840797|gb|EEE78344.1|predicted protein [Populus trichocarpa]		Unigene23468_All//3.00E-179//CO111550			GO:0003677//GO:0006350//GO:0010468//GO:0030528	nr -
Unigene23469_All	1502	95.76	34.88	37.54	123.08	77.70	76.62	42.51	23.82	24.45	-1.46E+00	1.31E-187	Down	-1.35E+00	4.23E-162	Down	-6.64E-01	4.33E-81		-6.84E-01	2.04E-75		-8.36E-01	4.32E-42		-7.98E-01	4.97E-40		Unigene23469_All//gi|1234900|emb|CAA63222.1|//3.00E-95//homeobox-leucine zipper protein [Glycine max]	Unigene23469_All//1.00E-75//AT4G16780| ATHB-2 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 2); DNA binding / protein homodimerization/ sequence-specific DNA binding / transcription factor	Unigene23469_All//0.00E+00//TC137089	HB		GO:0000902//GO:0001071//GO:0003677//GO:0006351//GO:0009639//GO:0009755//GO:0010468//GO:0030528//GO:0042802//GO:0043231//GO:0048513	nr -
Unigene23471_All	3009	4.26	2.80	5.01	4.72	4.78	5.24	2.96	5.95	7.28	-6.08E-01	1.09E-04		2.33E-01	1.43E-01		1.99E-02	9.20E-01		1.51E-01	3.69E-01		1.00E+00	1.54E-16	Up	1.30E+00	1.62E-30	Up	Unigene23471_All//gi|15221299|ref|NP_176986.1|//2.00E-33//zinc finger (B-box type) family protein [Arabidopsis thaliana] >gi|17433041|sp|Q9C5P4.1|COLX_ARATH RecName: Full=Putative zinc finger protein At1g68190	Unigene23471_All//8.00E-35//AT1G68190| zinc finger (B-box type) family protein	Unigene23471_All//0.00E+00//TC157110	C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0010468//GO:0044464//GO:0046914	nr +
Unigene23472_All	2347	12.82	28.89	18.26	18.57	34.39	34.48	22.00	39.71	33.93	1.17E+00	3.00E-63	Up	5.11E-01	8.65E-10		8.89E-01	6.79E-57		8.93E-01	5.16E-52		8.52E-01	4.27E-63		6.25E-01	1.32E-32		Unigene23472_All//gi|11066213|gb|AAG28503.1|AF196966_1//0.00E+00//hexokinase [Citrus sinensis]	Unigene23472_All//0.00E+00//AT4G29130| HXK1 (HEXOKINASE 1); ATP binding / fructokinase/ glucokinase/ hexokinase	Unigene23472_All//0.00E+00//TC168507		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism	GO:0004396//GO:0006007//GO:0008219//GO:0009527//GO:0009757//GO:0031224//GO:0032559//GO:0046914	nr -
Unigene23475_All	660	16.57	11.67	37.03	1.74	3.97	4.45	8.90	4.43	3.74	-5.06E-01	3.34E-03		1.16E+00	3.98E-22	Up	1.19E+00	2.00E-03		1.36E+00	2.92E-04	Up	-1.01E+00	5.28E-06	Down	-1.25E+00	1.83E-08	Down				Unigene23475_All//0.00E+00//gi|109882978|gb|DW511948.1|DW511948				
Unigene23476_All	523	12.20	12.30	34.01	1.52	10.80	10.19	5.25	4.95	6.86	1.17E-02	9.82E-01		1.48E+00	2.26E-23	Up	2.82E+00	4.19E-20	Up	2.74E+00	3.29E-17	Up	-8.48E-02	8.12E-01		3.84E-01	1.88E-01					Unigene23476_All//1.00E-143//DW511948				
Unigene23477_All	658	2.31	21.33	11.98	4.09	8.11	10.57	3.41	8.38	6.05	3.21E+00	4.58E-49	Up	2.38E+00	1.04E-19	Up	9.89E-01	6.82E-05		1.37E+00	2.42E-09	Up	1.30E+00	3.93E-08	Up	8.30E-01	1.75E-03					Unigene23477_All//0.00E+00//DW508057				
Unigene23479_All	1484	5.99	3.41	1.97	11.38	8.91	11.47	8.09	4.73	3.57	-8.12E-01	2.83E-05		-1.60E+00	2.35E-13	Down	-3.53E-01	6.76E-03		1.19E-02	9.48E-01		-7.74E-01	1.26E-07		-1.18E+00	5.01E-15	Down				Unigene23479_All//1.00E-35//CO092801				
Unigene2348_All	1841	7.28	10.27	8.10	11.36	20.00	15.70	19.57	29.17	45.05	4.97E-01	9.07E-05		1.55E-01	3.65E-01		8.15E-01	1.42E-22		4.66E-01	1.94E-06		5.76E-01	7.03E-19		1.20E+00	8.87E-101	Up	Unigene2348_All//gi|115459996|ref|NP_001053598.1|//5.00E-89//Os04g0569900 [Oryza sativa Japonica Group] >gi|38567921|emb|CAE75904.1|OSJNBa0088I22.17 [Oryza sativa (japonica cultivar-group)] >gi|113565169|dbj|BAF15512.1|Os04g0569900 [Oryza sativa Japonica Group]	Unigene2348_All//9.00E-42//AT4G23060| IQD22 (IQ-domain 22); calmodulin binding	Unigene2348_All//0.00E+00//TC134574			GO:0009725	nr -
Unigene23480_All	878	1.13	1.27	0.18	2.33	3.73	1.59	2.99	0.29	1.23	1.65E-01	7.79E-01		-2.64E+00	2.71E-03		6.80E-01	4.55E-02		-5.45E-01	2.45E-01		-3.39E+00	2.52E-12	Down	-1.29E+00	2.12E-04	Down	Unigene23480_All//gi|297817550|ref|XP_002876658.1|//6.00E-64//pectinacetylesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322496|gb|EFH52917.1|pectinacetylesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23480_All//7.00E-63//AT3G62060| pectinacetylesterase family protein	Unigene23480_All//0.00E+00//CO116950			GO:0044464	nr -
Unigene23481_All	931	11.41	2.78	4.18	12.36	13.13	20.13	5.22	1.89	2.74	-2.04E+00	8.90E-23	Down	-1.45E+00	9.36E-14	Down	8.73E-02	6.59E-01		7.04E-01	1.70E-08		-1.47E+00	1.34E-08	Down	-9.31E-01	8.99E-05		Unigene23481_All//gi|297817550|ref|XP_002876658.1|//5.00E-63//pectinacetylesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322496|gb|EFH52917.1|pectinacetylesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23481_All//3.00E-64//AT2G46930| pectinacetylesterase, putative	Unigene23481_All//0.00E+00//CO101542			GO:0044464	nr +
Unigene23482_All	1692	39.58	6.47	9.79	39.86	40.87	37.29	11.67	5.58	6.00	-2.61E+00	8.54E-190	Down	-2.02E+00	1.10E-133	Down	3.59E-02	6.60E-01		-9.63E-02	1.93E-01		-1.06E+00	6.23E-20	Down	-9.59E-01	1.90E-17		Unigene23482_All//gi|109509148|gb|AB634283.1|//1.00E-169//pectin acetylesterase [Eucalyptus globulus subsp. globulus]	Unigene23482_All//5.00E-169//AT2G46930| pectinacetylesterase, putative	Unigene23482_All//0.00E+00//TC137126				nr -
Unigene23483_All	352	5.95	4.46	1.51	13.30	13.40	23.22	22.46	3.21	4.19	-4.14E-01	3.72E-01		-1.97E+00	1.29E-04	Down	1.08E-02	9.79E-01		8.04E-01	5.73E-05		-2.81E+00	4.02E-30	Down	-2.42E+00	1.63E-26	Down	Unigene23483_All//gi|21326148|gb|AAM47602.1|AF513859_1//2.00E-27//ovule/fiber cell elongation protein Ghfe1 [Gossypium hirsutum] >gi|226358404|gb|AC051065.1| fiber cell elongation protein [Gossypium hirsutum]	Unigene23483_All//8.00E-19//AT3G19820| DWF1 (DWARF 1); calmodulin binding / catalytic	Unigene23483_All//4.00E-38//TC139145		ko00100|Steroid biosynthesis	GO:0000902//GO:0003824//GO:0005515//GO:0016129//GO:0030554//GO:0031224//GO:0043231	nr +
Unigene23484_All	2153	67.75	25.51	26.88	181.30	161.88	238.61	267.21	33.68	88.04	-1.41E+00	5.90E-181	Down	-1.33E+00	3.57E-161	Down	-1.64E-01	1.54E-12		3.96E-01	2.86E-77		-2.99E+00	0.00E+00	Down	-1.60E+00	0.00E+00	Down	Unigene23484_All//gi|21326148|gb|AAM47602.1|AF513859_1//0.00E+00//ovule/fiber cell elongation protein Ghfe1 [Gossypium hirsutum] >gi|226358404|gb|AC051065.1| fiber cell elongation protein [Gossypium hirsutum]	Unigene23484_All//0.00E+00//AT3G19820| DWF1 (DWARF 1); calmodulin binding / catalytic	Unigene23484_All//0.00E+00//TC129617		ko00100|Steroid biosynthesis	GO:0000902//GO:0003824//GO:0005515//GO:0016129//GO:0030554//GO:0031224//GO:0043231	nr -
Unigene23488_All	1833	0.46	0.17	0.26	6.22	7.01	8.06	0.51	0.43	2.20	-1.46E+00	6.69E-02		-8.04E-01	3.22E-01		1.71E-01	3.39E-01		3.73E-01	1.16E-02		-2.28E-01	7.18E-01		2.11E+00	1.07E-11	Up	Unigene23488_All//gi|71905561|gb|AAZ52758.1|//1.00E-131//expressed protein [Arabidopsis thaliana] >gi|71905563|gb|AAZ52759.1|expressed protein [Arabidopsis thaliana]	Unigene23488_All//4.00E-129//AT3G06080| unknown protein	Unigene23488_All//0.00E+00//TC176247				nr -
Unigene23490_All	3220	28.27	16.22	23.38	7.09	7.18	4.01	13.18	5.66	8.95	-8.01E-01	1.69E-45		-2.74E-01	1.00E-06		1.83E-02	9.03E-01		-8.21E-01	2.96E-13		-1.22E+00	4.90E-52	Down	-5.60E-01	8.28E-15		Unigene23490_All//gi|30695748|ref|NP_199787.2|//0.00E-00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|30102752|gb|AAP21294.1|At5g49760 [Arabidopsis thaliana] >gi|224589713|gb|ACN59388.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23490_All//0.00E+00//AT5G49760| leucine-rich repeat family protein / protein kinase family protein	Unigene23490_All//0.00E+00//TC156939			GO:0000166//GO:0004674//GO:0004871//GO:0008152//GO:0016020//GO:0016491//GO:0031410//GO:0043231	nr +
Unigene23492_All	935	2.24	10.30	6.95	6.66	7.81	7.73	35.36	51.59	66.77	2.20E+00	1.37E-22	Up	1.63E+00	3.27E-10	Up	2.30E-01	3.41E-01		2.15E-01	4.04E-01		5.45E-01	1.77E-15		9.17E-01	3.92E-49					Unigene23492_All//3.00E-115//gi|78330337|gb|DT550611.1|DT550611				
Unigene23493_All	1670	11.56	55.28	33.10	45.76	46.56	52.17	61.37	98.16	119.40	2.26E+00	2.39E-218	Up	1.52E+00	1.47E-74	Up	2.51E-02	7.75E-01		1.89E-01	7.52E-04		6.78E-01	2.26E-74		9.60E-01	2.02E-167		Unigene23493_All//gi|13605601|gb|AAK32794.1|AF361626_1//7.00E-50//At1g54460/F20D21_28 [Arabidopsis thaliana] >gi|15777865|gb|AAL05893.1|At1g54460/F20D21_28 [Arabidopsis thaliana]	Unigene23493_All//gi|13605601|gb|AAK32794.1|AF361626_1//7.00E-36//AT1G54460| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: WDL1 (TAIR:AT3G01630.3); Has 393 Blast hits to 375 proteins in 76 species: Archae - 0; Bacteria - 3; Metazoa - 143; Fungi - 38; Plants - 160; Viruses - 0; Other Eukaryotes - 49 (source: NCBI BLink).	Unigene23493_All//0.00E+00//gi|109873376|gb|DW502351.1|DW502351				nr +
Unigene23494_All	3198	6.05	4.01	4.01	17.45	14.54	10.70	8.83	3.71	4.31	-5.95E-01	2.00E-06		-5.93E-01	4.51E-06		-2.63E-01	7.32E-05		-7.05E-01	2.40E-24		-1.25E+00	3.06E-36	Down	-1.03E+00	9.18E-28	Down	Unigene23494_All//gi|15219169|ref|NP_175713.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|9454540|gb|AAF87863.1|AC022520_7 similar to cdc2 protein kinase [Arabidopsis thaliana]	Unigene23494_All//0.00E+00//AT1G53050| protein kinase family protein	Unigene23494_All//0.00E+00//TC169472			GO:0004674//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene23495_All	1389	35.41	24.15	28.83	19.15	18.35	15.25	11.11	4.48	7.63	-5.52E-01	2.84E-13		-2.97E-01	1.65E-04		-6.20E-02	6.21E-01		-3.29E-01	1.75E-03		-1.31E+00	1.36E-21	Down	-5.42E-01	1.11E-05		Unigene23495_All//gi|300608168|emb|CAZ86694.1|//1.00E-131//epoxide hydrolase 3 [Prunus persica]	Unigene23495_All//8.00E-51//AT3G51000| epoxide hydrolase, putative	Unigene23495_All//0.00E+00//TC136233				nr +
Unigene23496_All	1267	18.29	7.56	13.32	58.23	49.14	26.38	63.14	17.05	11.85	-1.28E+00	3.17E-25	Down	-4.57E-01	9.89E-05		-2.45E-01	1.68E-05		-1.14E+00	7.48E-72	Down	-1.89E+00	7.28E-185	Down	-2.41E+00	3.72E-260	Down	Unigene23496_All//gi|300608168|emb|CAZ86694.1|//1.00E-131//epoxide hydrolase 3 [Prunus persica]	Unigene23496_All//1.00E-52//AT3G51000| epoxide hydrolase, putative	Unigene23496_All//0.00E+00//TC170513				nr -
Unigene23497_All	967	9.41	28.30	16.69	22.05	24.29	19.29	9.14	8.04	15.66	1.59E+00	9.24E-41	Up	8.26E-01	1.05E-08		1.40E-01	2.87E-01		-1.93E-01	1.39E-01		-1.85E-01	3.53E-01		7.77E-01	1.03E-09		Unigene23497_All//gi|158828228|gb|ABW81106.1|//1.00E-18//putRNAbp29 [Cleome spinosa]	Unigene23497_All//2.00E-11//AT1G07350| transformer serine/arginine-rich ribonucleoprotein, putative	Unigene23497_All//1.00E-166//ES831278		ko03040|Spliceosome	GO:0003676	nr +
Unigene23498_All	1763	11.60	43.89	13.83	21.11	19.90	19.67	19.62	27.78	24.34	1.92E+00	1.26E-148	Up	2.54E-01	3.42E-02		-8.47E-02	4.24E-01		-1.01E-01	3.39E-01		5.02E-01	1.16E-13		3.11E-01	1.26E-05		Unigene23498_All//gi|158828228|gb|ABW81106.1|//2.00E-53//putRNAbp29 [Cleome spinosa]	Unigene23498_All//4.00E-30//AT1G07350| transformer serine/arginine-rich ribonucleoprotein, putative	Unigene23498_All//0.00E+00//TC151542		ko03040|Spliceosome	GO:0003676//GO:0006396//GO:0043231	nr +
Unigene235_All	2922	2.81	2.24	3.34	19.04	13.73	11.81	16.74	8.40	7.73	-3.30E-01	1.16E-01		2.47E-01	2.34E-01		-4.72E-01	1.92E-13		-6.89E-01	2.18E-23		-9.96E-01	2.68E-43		-1.11E+00	1.99E-53	Down	Unigene235_All//gi|224140225|ref|XP_002323485.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222868115|gb|EEF05246.1|multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene235_All//0.00E+00//AT2G36910| ABCB1 (ATP BINDING CASSETTE SUBFAMILY B1); ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter/ calmodulin binding	Unigene235_All//0.00E+00//gi|78334666|gb|DT554940.1|DT554940		ko02010|ABC transporters		nr +

Unigene2350_All	1935	3.84	3.17	1.79	6.15	4.16	4.71	13.13	15.98	10.99	-2.77E-01	2.17E-01			-1.10E+00	1.23E-06	Down	-5.63E-01	2.19E-04		-3.84E-01	2.12E-02		2.84E-01	1.28E-03		-2.56E-01	7.72E-03		Unigene2350_All//gi|15231097|ref|NP_190767.1|//1.00E-122//protein kinase family protein [Arabidopsis thaliana] >gi|75337704|sp|Q9SV05.1|CCR35_ARATH RecName: Full=Serine/threonine-protein kinase-like protein At3g51990; AltName: Full=CRINKLY 4-related kinase; Flags: Precursor	Unigene2350_All//2.00E-123//AT3G51990| protein kinase family protein	Unigene2350_All//0.00E+00//TC174470		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr -
Unigene23502_All	1248	1.51	1.10	3.33	2.71	1.57	0.87	4.74	2.65	1.95	-4.61E-01	3.40E-01			1.14E+00	3.11E-04	Up	-7.87E-01	1.30E-02		-1.64E+00	2.80E-06	Down	-8.42E-01	1.08E-04		-1.28E+00	7.66E-09	Down	Unigene23502_All//gi|110295239|gb|AB668964.1|//1.00E-120//small GTPase [Gossypium hirsutum]	Unigene23502_All//2.00E-94//AT5G62880| ARAC10; GTP binding	Unigene23502_All//0.00E+00//TC137834		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene23504_All	1061	1.38	1.00	1.81	5.21	5.45	3.66	5.86	3.43	2.74	-4.61E-01	3.84E-01			3.88E-01	4.19E-01		6.52E-02	8.25E-01		-5.10E-01	4.70E-02		-7.73E-01	2.46E-04		-1.10E+00	2.22E-07	Down	Unigene23504_All//gi|62867605|gb|AAY17406.1|//5.00E-34//At2g37195 [Arabidopsis thaliana] >gi|66841340|gb|AAY57307.1| At2g37195 [Arabidopsis thaliana]	Unigene23504_All//1.00E-34//AT2G37195| unknown protein	Unigene23504_All//1.00E-77//DW498449				nr -
Unigene23506_All	3103	3.19	1.73	2.23	5.60	5.94	2.82	9.91	2.42	2.85	-8.81E-01	1.70E-06			-5.15E-01	6.94E-03		8.36E-02	6.05E-01		-9.89E-01	8.36E-14		-2.03E+00	1.35E-78	Down	-1.80E+00	8.12E-69	Down	Unigene23506_All//gi|224129966|ref|XP_002320715.1|//0.00E+00//tubulin folding cofactor [Populus trichocarpa] >gi|222861488|gb|EEE99030.1| tubulin folding cofactor [Populus trichocarpa]	Unigene23506_All//0.00E+00//AT3G60740| TTN1 (TITAN 1); tubulin binding	Unigene23506_All//0.00E+00//TC143765			GO:0003006//GO:0008092//GO:0043623//GO:0044267	nr +
Unigene23507_All	968	38.11	56.90	87.36	50.38	55.89	40.45	16.34	11.36	10.82	5.78E-01	5.88E-16			1.20E+00	3.08E-79	Up	1.50E-01	4.63E-02		-3.17E-01	1.95E-05		-5.25E-01	2.57E-05		-5.94E-01	1.14E-06		Unigene23507_All//gi|15225800|ref|NP_180251.1|//1.00E-50//emb|187 (embryo defective 1187); kinase/ phosphotransferase, alcohol group as acceptor [Arabidopsis thaliana] >gi|110738719|dbj|BAF01284.1| choline kinase like protein [Arabidopsis thaliana]	Unigene23507_All//6.00E-52//AT2G26830| emb|187 (embryo defective 1187); kinase/ phosphotransferase, alcohol group as acceptor	Unigene23507_All//0.00E+00//TC161826		ko00564|Glycerophospholipid metabolism	GO:0003006//GO:0016301	nr -
Unigene23508_All	1533	40.38	66.67	81.42	40.88	43.76	36.09	28.71	19.60	12.63	7.24E-01	1.07E-42			1.01E+00	4.54E-89	Up	9.82E-02	1.72E-01		-1.80E-01	8.80E-03		-5.51E-01	1.82E-14		-1.18E+00	5.17E-53	Down	Unigene23508_All//gi|15225800|ref|NP_180251.1|//1.00E-162//emb|187 (embryo defective 1187); kinase/ phosphotransferase, alcohol group as acceptor [Arabidopsis thaliana] >gi|110738719|dbj|BAF01284.1| choline kinase like protein [Arabidopsis thaliana]	Unigene23508_All//6.00E-156//AT2G26830| emb|187 (embryo defective 1187); kinase/ phosphotransferase, alcohol group as acceptor	Unigene23508_All//0.00E+00//TC152334		ko00564|Glycerophospholipid metabolism		nr +
Unigene23509_All	1453	16.20	7.78	10.04	24.55	22.87	23.93	10.21	5.12	5.68	-1.06E+00	3.08E-19	Down	-6.90E-01	3.00E-09		-1.02E-01	3.23E-01		-3.65E-02	7.34E-01		-9.96E-01	1.02E-13		-8.48E-01	5.29E-11		Unigene23509_All//gi|224471665|dbj|BAH10700.2|//0.00E+00//GDP-mannose 4,6-dehydratase [Nicotiana benthamiana]	Unigene23509_All//0.00E+00//AT3G51160| MUR1 (MURUS 1); GDP-mannose 4,6-dehydratase	Unigene23509_All//0.00E+00//TC162474		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism	GO:0000902//GO:0006013//GO:0016836//GO:0042350//GO:0044444//GO:0048037	nr +
Unigene2351_All	1991	25.96	14.81	12.68	48.44	39.50	67.17	84.48	60.44	48.34	-8.10E-01	1.31E-26			-1.03E+00	2.25E-38	Down	-2.94E-01	9.91E-10		4.72E-01	4.60E-28		-4.83E-01	6.79E-42		-8.05E-01	9.96E-106		Unigene2351_All//gi|229893773|gb|ACQ90244.1|//0.00E+00//DEAD-box RNA helicase [Glycine max]	Unigene2351_All//0.00E+00//AT1G31970| STRS1 (STRESS RESPONSE SUPPRESSOR 1); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene2351_All//0.00E+00//TC161300		ko03040|Spliceosome	GO:0032559//GO:0042623	nr +
Unigene23512_All	1384	4.42	4.28	5.08	4.97	5.62	5.25	6.63	4.05	2.79	-4.63E-02	8.53E-01			1.99E-01	4.08E-01		1.79E-01	4.63E-01		8.10E-02	7.40E-01		-7.12E-01	2.56E-05		-1.25E+00	1.13E-12	Down	Unigene23512_All//gi|42564243|ref|NP_188244.2|//1.00E-100//RNA binding / catalytic [Arabidopsis thaliana]	Unigene23512_All//2.00E-97//AT3G16230| RNA binding / catalytic	Unigene23512_All//0.00E+00//TC179450			GO:0043231	nr +
Unigene23514_All	2893	226.88	15.85	112.92	969.35	539.22	273.96	262.20	146.23	68.95	-3.84E+00	0.00E+00	Down	-1.01E+00	0.00E+00	Down	-8.46E-01	0.00E+00		-1.82E+00	0.00E+00	Down	-8.42E-01	0.00E+00		-1.93E+00	0.00E+00	Down	Unigene23514_All//gi|1771160|emb|CAA67429.1|//0.00E+00//SBT1 [Solanum lycopersicum] >gi|3687305|emb|CAA06999.1| subtilisin-like protease [Solanum lycopersicum]	Unigene23514_All//0.00E+00//AT5G67360| ARA12; serine-type endopeptidase	Unigene23514_All//0.00E+00//TC142452		ko04141|Protein processing in endoplasmic reticulum	GO:0003006//GO:0004175//GO:0005515//GO:0005576//GO:0005618//GO:0009845//GO:0010191//GO:0019538//GO:0031410//GO:0044092	nr +
Unigene23516_All	1654	2.66	8.18	3.32	3.25	4.02	3.33	23.34	39.67	20.23	1.62E+00	4.01E-21	Up	3.20E-01	2.44E-01		3.05E-01	2.16E-01		3.44E-02	9.22E-01		7.65E-01	2.92E-37		-2.06E-01	7.75E-03		Unigene23516_All//gi|145328284|ref|NP_001077888.1|//3.00E-36//ALDH6B2; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase [Arabidopsis thaliana]	Unigene23516_All//1.00E-37//AT2G14170| ALDH6B2; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase	Unigene23516_All//3.00E-147//gi|109825992|gb|DW224713.1|DW224713		ko00562|Inositol phosphate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism	GO:0006950//GO:0009081//GO:0016620//GO:0043231//GO:0046914	nr +
Unigene23519_All	2332	59.93	22.21	42.34	98.86	108.67	145.56	65.69	19.64	55.42	-1.43E+00	1.08E-177	Down	-5.01E-01	1.80E-29		1.37E-01	5.66E-06		5.58E-01	1.40E-95		-1.74E+00	0.00E+00	Down	-2.45E-01	1.20E-11		Unigene23519_All//gi|297800264|ref|XP_002868016.1|//0.00E+00//dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313852|gb|EFH44275.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23519_All//0.00E+00//AT4G18030| dehydration-responsive family protein	Unigene23519_All//0.00E+00//TC137299			GO:0005618//GO:0016020//GO:0016741//GO:0043231	nr -
Unigene23522_All	1826	28.62	35.35	35.23	18.41	27.61	35.05	61.80	211.59	182.46	3.05E-01	3.10E-06		3.00E-01	9.33E-06		5.84E-01	2.21E-17		9.29E-01	5.38E-44		1.78E+00	0.00E+00	Up	1.56E+00	0.00E+00	Up	Unigene23522_All//gi|46850513|gb|AAT02656.1|//0.00E+00//mitochondrial pyruvate dehydrogenase kinase isoform 2 [Glycine max]	Unigene23522_All//0.00E+00//AT3G06483| PDK (PYRUVATE DEHYDROGENASE KINASE); ATP binding / histidine phosphotransfer kinase/ pyruvate dehydrogenase (acetyl-transferring) kinase	Unigene23522_All//0.00E+00//TC141413			GO:0004673//GO:0004871//GO:0006468//GO:0023060//GO:0032559//GO:0043231	nr +
Unigene23523_All	3872	2.55	7.79	3.77	7.19	7.30	6.95	13.26	19.16	16.22	1.61E+00	1.12E-45	Up	5.61E-01	2.15E-04		2.19E-02	8.66E-01		-4.89E-02	6.81E-01		5.31E-01	2.28E-22		2.91E-01	5.52E-07		Unigene23523_All//gi|297725107|ref|NP_001174917.1|//5.00E-50//Os06g0631400 [Oryza sativa Japonica Group] >gi|255677249|dbj|BAH93645.1| Os06g0631400 [Oryza sativa Japonica Group]	Unigene23523_All//5.00E-75//AT4G24200| LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: TFIIS N-terminal (InterPro:IPR017923); BEST Arabidopsis thaliana protein match is: DNA binding / protein binding / transcription regulator (TAIR:AT3G48050.2); Has 1007 Blast hits to 471 proteins in 129 species: Archae - 0; Bacteria - 216; Metazoa - 191; Fungi - 150; Plants - 70; Viruses - 0; Other Eukaryotes - 380 (source: NCBI BLink).	Unigene23523_All//0.00E+00//TC166966				nr +
Unigene23524_All	2320	10.19	28.04	16.32	9.88	10.64	18.42	25.22	30.03	26.39	1.46E+00	5.51E-85	Up	6.79E-01	4.26E-14		1.08E-01	4.18E-01		8.99E-01	5.29E-28		2.52E-01	7.73E-06		6.55E-02	3.53E-01		Unigene23524_All//gi|224127622|ref|XP_002329323.1|//0.00E+00//4-coumarate-coa ligase [Populus trichocarpa] >gi|224127626|ref|XP_002329324.1| acyl:coa ligase [Populus trichocarpa] >gi|222870777|gb|EEF07908.1| 4-coumarate-coa ligase [Populus trichocarpa] >gi|222870778|gb|EEF07909.1| acyl:coa ligase [Populus trichocarpa]	Unigene23524_All//0.00E+00//AT4G05160| 4-coumarate--CoA ligase, putative / 4-coumaroyl-CoA synthase, putative	Unigene23524_All//0.00E+00//TC141057		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0009694//GO:0009850//GO:0016408//GO:0016703//GO:0042579	nr +
Unigene23529_All	477	1.65	3.82	3.01	7.94	7.72	7.48	7.36	1.23	2.59	1.22E+00	1.36E-02		8.73E-01	1.38E-01		-3.91E-02	9.05E-01		-8.56E-02	7.96E-01		-2.58E+00	1.30E-12	Down	-1.51E+00	6.97E-07	Down	Unigene23529_All//gi|283837097|emb|CBH19893.1|//1.00E-54//cell division control 20 [Solanum lycopersicum var. cerasiforme]	Unigene23529_All//2.00E-50//AT4G33270| CDC20.1; signal transducer	Unigene23529_All//0.00E+00//ES809876		ko04120|Ubiquitin mediated proteolysis	GO:0009987//GO:0019897//GO:0023060	nr +
Unigene2353_All	1468	36.00	30.96	26.70	66.03	54.98	72.58	45.91	108.62	71.26	-2.17E-01	3.55E-03		-4.31E-01	6.72E-09		-2.64E-01	4.57E-08		1.36E-01	9.27E-03		1.24E+00	8.85E-199	Up	6.34E-01	1.27E-43		Unigene2353_All//gi|90194295|gb|AAL74418.2|AF452254|//0.00E+00//ATP sulfurylase [Glycine max]	Unigene2353_All//0.00E+00//AT4G14680| APS3; sulfate adenylyltransferase (ATP)	Unigene2353_All//0.00E+00//TC137655		ko00230|Purine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0004779//GO:0006790//GO:0009536//GO:0010038//GO:0016020	nr +
Unigene23530_All	1497	8.39	7.45	5.09	20.00	23.85	17.95	29.54	6.25	5.80	-1.72E-01	3.31E-01		-7.22E-01	1.24E-05		2.54E-01	3.85E-03		-1.56E-01	1.59E-01		-2.24E+00	9.63E-128	Down	-2.35E+00	1.78E-139	Down	Unigene23530_All//gi|15234128|ref|NP_195053.1|//0.00E+00//CDC20.1; signal transducer [Arabidopsis thaliana] >gi|4490294|emb|CAB38785.1| WD-repeat protein-like protein [Arabidopsis thaliana] >gi|7270275|emb|CAB80044.1| WD-repeat protein-like protein [Arabidopsis thaliana] >gi|109946631|gb|ABG48494.1| At4g33270 [Arabidopsis thaliana]	Unigene23530_All//0.00E+00//AT4G33270| CDC20.1; signal transducer	Unigene23530_All//0.00E+00//TC149062		ko04120|Ubiquitin mediated proteolysis	GO:0009987//GO:0019897//GO:0023060	nr -
Unigene23532_All	1901	25.82	7.09	16.81	63.81	59.25	57.07	31.38	17.83	12.03	-1.86E+00	1.91E-91	Down	-6.19E-01	1.96E-15		-1.07E-01	2.81E-02		-1.61E-01	6.39E-04		-8.16E-01	8.03E-38		-1.38E+00	6.75E-91	Down	Unigene23532_All//gi|297820194|ref|XP_002877980.1|//0.00E+00//ump synthase [Arabidopsis lyrata subsp. lyrata] >gi|297323818|gb|EFH54239.1| ump synthase [Arabidopsis lyrata subsp. lyrata]	Unigene23532_All//0.00E+00//AT3G54470| uridine 5'-monophosphate synthase / UMP synthase (PYRE-F) (UMPS)	Unigene23532_All//0.00E+00//TC152509		ko00240|Pyrimidine metabolism	GO:0006221//GO:0009267//GO:0010038//GO:0016763//GO:0016831//GO:0019856	nr -
Unigene23534_All	520	1.01	1.36	1.84	2.39	2.65	3.04	3.25	1.85	0.77	4.39E-01	6.16E-01		8.73E-01	2.38E-01		1.45E-01	8.22E-01		3.44E-01	5.61E-01		-8.15E-01	7.25E-02		-2.09E+00	2.24E-05	Down	Unigene23534_All//gi|224072260|ref|XP_002303678.1|//2.00E-61//f-box family protein [Populus trichocarpa] >gi|222841110|gb|EEE78657.1| f-box family protein [Populus trichocarpa]	Unigene23534_All//4.00E-46//AT4G24060| Dof-type zinc finger domain-containing protein	Unigene23534_All//2.00E-118//gi|48823035|gb|CO124348.1|CO124348	C2C2-Dof		GO:0003676//GO:0010468//GO:0046914	nr -
Unigene23535_All	967	10.23	9.64	8.48	17.05	21.97	20.97	25.49	15.00	10.88	-8.50E-02	6.56E-01		-2.70E-01	1.79E-01		3.66E-01	1.39E-03		2.99E-01	1.74E-02		-7.65E-01	1.61E-14		-1.23E+00	8.08E-32	Down	Unigene23535_All//gi|224072260|ref|XP_002303678.1|//8.00E-97//f-box family protein [Populus trichocarpa] >gi|222841110|gb|EEE78657.1| f-box family protein [Populus trichocarpa]	Unigene23535_All//2.00E-45//AT4G24060| Dof-type zinc finger domain-containing protein	Unigene23535_All//0.00E+00//DW238568	C2C2-Dof		GO:0005488	nr -
Unigene23536_All	1773	0.18	0.11	0.27	4.66	4.21	4.38	1.12	1.27	0.29	-6.32E-01	6.22E-01		6.10E-01	5.87E-01		-1.46E-01	5.50E-01		-9.02E-02	6.81E-01		1.84E-01	6.37E-01		-1.94E+00	1.06E-05	Down	Unigene23536_All//gi|112363396|gb|AB116022.1|//5.00E-92//Dof21 [Glycine max]	Unigene23536_All//3.00E-42//AT4G24060| Dof-type zinc finger domain-containing protein	Unigene23536_All//0.00E+00//TC165484	C2C2-Dof		GO:0005488	nr -
Unigene23539_All	581	0.36	0.35	0.00	1.63	0.47	1.55	0.15	1.51	0.69	-4.64E-02	9.88E-01		-8.49E+00	1.46E-01		-1.78E+00	1.22E-02		-6.74E-02	9.34E-01		3.38E+00	1.75E-04	Up	2.24E+00	6.42E-02		Unigene23539_All//gi|259121387|gb|ACV92013.1|//4.00E-56//WRKY transcription factor 11 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene23539_All//9.00E-45//AT1G69310| WRKY57; transcription factor	Unigene23539_All//1.00E-137//TC131485	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +

Unigene2354_All	3524	2.61	0.75	1.33	8.61	5.38	7.93	10.28	3.84	5.53	-1.81E+00	5.78E-17	Down	-9.75E-01	1.01E-06		-6.77E-01	4.36E-14		-1.18E-01	3.09E-01		-1.42E+00	4.33E-56	Down	-8.95E-01	5.79E-28		Unigene2354_All//gi|108862244|gb|AB058898.2|//0.00E+00//Nrap protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene2354_All//0.00E+00//AT1G63810| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nrap protein (InterPro:IPR005554); Has 268 Blast hits to 263 proteins in 124 species: Archae - 3; Bacteria - 0; Metazoa - 116; Fungi - 89; Plants - 17; Viruses - 0; Other Eukaryotes - 43 (source: NCBI BLink).	Unigene2354_All//0.00E+00//C0128452				nr +
Unigene23540_All	1444	1.88	0.21	0.70	9.73	4.70	4.57	2.43	1.94	3.64	-3.16E+00	6.46E-10	Down	-1.43E+00	5.90E-04	Down	-1.05E+00	6.70E-14	Down	-1.09E+00	3.79E-13	Down	-3.26E-01	3.05E-01		5.84E-01	9.71E-03		Unigene23540_All//gi|151934189|gb|ABS18432.1|//3.00E-82//WRKY32 [Glycine max]	Unigene23540_All//9.00E-60//AT1G69310| WRKY57; transcription factor	Unigene23540_All//0.00E+00//TC176901	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0006350//GO:0010468//GO:0043231	nr +
Unigene23541_All	1638	6.20	1.79	5.88	6.26	5.28	4.88	1.83	1.96	1.39	-1.79E+00	2.16E-18	Down	-7.47E-02	7.04E-01		-2.48E-01	1.90E-01		-3.60E-01	4.99E-02		1.00E-01	7.65E-01		-4.03E-01	2.05E-01		Unigene23541_All//gi|151934189|gb|ABS18432.1|//5.00E-84//WRKY32 [Glycine max]	Unigene23541_All//3.00E-61//AT1G69310| WRKY57; transcription factor	Unigene23541_All//5.00E-149//TC131485	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0006350//GO:0010468//GO:0043231	nr -
Unigene23542_All	3695	3.85	2.47	3.59	8.24	5.70	5.78	18.67	6.78	8.19	-6.42E-01	1.51E-05		-1.02E-01	5.71E-01		-5.30E-01	2.85E-09		-5.11E-01	6.83E-08		-1.46E+00	5.92E-111	Down	-1.19E+00	5.17E-83	Down	Unigene23542_All//gi|30690550|ref|NP_850463.1|//0.00E+00//POL (poltergeist); protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|30690552|ref|NP_850464.1| POL (poltergeist); protein serine/threonine phosphatase [Arabidopsis thaliana]	Unigene23542_All//0.00E+00//AT2G46920| POL (poltergeist); protein serine/threonine phosphatase	Unigene23542_All//2.00E-08//DN802972			GO:0004721//GO:0008289//GO:0009933//GO:0010073//GO:0010468//GO:0016020//GO:0043231	nr -
Unigene23544_All	3433	2.97	1.77	2.08	9.50	12.76	26.64	33.39	27.70	48.69	-7.47E-01	3.05E-05		-5.16E-01	5.78E-03		4.25E-01	1.04E-08		1.49E+00	9.71E-132	Up	-2.70E-01	3.20E-10		5.44E-01	9.00E-53		Unigene23544_All//gi|225589567|gb|ACN59317.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23544_All//0.00E+00//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene23544_All//0.00E+00//TC155454		ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0016628//GO:0032559	nr +
Unigene23548_All	1352	14.01	26.57	17.09	14.81	14.70	18.94	10.48	25.97	20.18	9.24E-01	3.82E-23		2.87E-01	1.84E-02		-1.13E-02	9.48E-01		3.55E-01	9.04E-04		1.31E+00	4.65E-48	Up	9.46E-01	4.06E-23		Unigene23548_All//gi|294690000|gb|AA043182.1|//1.00E-117//peptide methionine sulfoxide reductase [Gossypium barbadense]	Unigene23548_All//2.00E-91//AT4G25130| peptide methionine sulfoxide reductase, putative	Unigene23548_All//0.00E+00//gi|78336772|gb|DT557046.1|DT557046			GO:0005488//GO:0009532//GO:0009639//GO:0016671//GO:0043412	nr +
Unigene23549_All	2057	19.38	16.87	20.61	27.15	25.16	27.01	13.44	16.82	5.50	-2.00E-01	2.36E-02		8.84E-02	3.81E-01		-1.10E-01	1.63E-01		-7.50E-03	9.45E-01		3.24E-01	7.69E-05		-1.29E+00	2.68E-38	Down	Unigene23549_All//gi|61789859|gb|ABX79677.1|//0.00E+00//GT-1 [Glycine max]	Unigene23549_All//4.00E-155//AT1G13450| DNA binding protein GT-1	Unigene23549_All//0.00E+00//gi|78342291|gb|DT562565.1|DT562565	Trihelix		GO:0003676//GO:0010468	nr -
Unigene23550_All	336	11.83	15.38	11.09	16.31	19.78	19.62	10.70	6.84	5.22	3.78E-01	1.61E-01		-9.33E-02	7.71E-01		2.78E-01	2.68E-01		2.67E-01	3.01E-01		-6.45E-01	2.63E-02		-1.04E+00	2.62E-04	Down	Unigene23550_All//gi|297824813|ref|XP_002880289.1|//2.00E-29//long-chain-fatty-acid--CoA ligase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326128|gb|EFH56548.1| long-chain-fatty-acid--CoA ligase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23550_All//7.00E-25//AT2G47240| long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein	Unigene23550_All//2.00E-160//TC156174		ko04146|Peroxisome//ko00071|Fatty acid metabolism	GO:0015645//GO:0043231	nr -
Unigene23553_All	2396	4.11	19.18	14.02	8.00	13.08	16.83	23.05	29.17	36.11	2.22E+00	6.32E-107	Up	1.77E+00	1.04E-56	Up	7.08E-01	3.26E-15		1.07E+00	2.92E-35	Up	3.40E-01	1.06E-09		6.48E-01	1.34E-37		Unigene23553_All//gi|145567026|gb|ABP81863.1|//0.00E+00//LATE BLOOMER 1 [Pisum sativum]	Unigene23553_All//0.00E+00//AT1G22770| GI (GIGANTEA)	Unigene23553_All//0.00E+00//gi|78334501|gb|DT554775.1|DT554775		ko04712|Circadian rhythm - plant	GO:0000302//GO:0005488//GO:0009266//GO:0009639//GO:0010468//GO:0031981//GO:0048511//GO:0048582	nr +
Unigene23554_All	848	1.48	6.75	0.44	1.17	1.95	1.44	12.71	16.26	17.76	2.19E+00	1.31E-13	Up	-1.75E+00	9.85E-03		7.30E-01	1.67E-01		2.92E-01	6.61E-01		3.55E-01	9.81E-03		4.82E-01	1.20E-04		Unigene23554_All//gi|225880061|gb|ACN94268.1|//9.00E-22//stress induced protein [Vitis vinifera]	Unigene23554_All//1.00E-12//AT5G62860| F-box family protein-related	Unigene23554_All//0.00E+00//TC132665				nr -
Unigene23555_All	1410	7.90	9.31	13.67	18.76	13.58	12.94	9.21	7.94	3.96	2.36E-01	1.50E-01		7.91E-01	1.41E-09		-4.66E-01	1.54E-06		-5.36E-01	1.62E-07		-2.13E-01	1.62E-01		-1.22E+00	5.79E-17	Down	Unigene23555_All//gi|132424655|gb|AB033480.1|//2.00E-93//class II KNOX homeobox transcription factor [Medicago truncatula]	Unigene23555_All//1.00E-88//AT5G11060| KNAT4 (KNOTTED1-LIKE HOMEOBOX GENE 4); transcription activator/ transcription factor	Unigene23555_All//0.00E+00//TC132665	HB		GO:0001071//GO:0003677//GO:0006350//GO:0009314//GO:0010468//GO:0030528//GO:0043231//GO:0044444	nr -
Unigene23556_All	2072	5.61	12.40	5.40	9.86	14.49	10.44	8.57	11.62	11.67	1.15E+00	1.56E-23	Up	-5.48E-02	7.67E-01		5.56E-01	1.13E-09		8.30E-02	5.88E-01		4.39E-01	9.33E-06		4.46E-01	4.14E-06		Unigene23556_All//gi|132424655|gb|AB033480.1|//1.00E-118//class II KNOX homeobox transcription factor [Medicago truncatula]	Unigene23556_All//2.00E-115//AT5G11060| KNAT4 (KNOTTED1-LIKE HOMEOBOX GENE 4); transcription activator/ transcription factor	Unigene23556_All//0.00E+00//TC132665	HB			nr +
Unigene23557_All	2753	16.67	52.47	23.06	24.39	29.58	33.30	56.10	104.95	93.55	1.65E+00	1.10E-225	Up	4.68E-01	3.48E-12		2.78E-01	1.98E-07		4.49E-01	8.26E-18		9.04E-01	3.18E-214		7.38E-01	3.91E-138		Unigene23557_All//gi|297845328|ref|XP_002890545.1|//0.00E+00//T-complex protein 11 [Arabidopsis lyrata subsp. lyrata] >gi|297336387|gb|EFH66804.1| T-complex protein 11 [Arabidopsis lyrata subsp. lyrata]	Unigene23557_All//0.00E+00//AT1G22930| T-complex protein 11	Unigene23557_All//0.00E+00//TC177792				nr -
Unigene23558_All	3033	1.52	2.64	1.39	3.78	3.83	3.77	18.64	32.88	168.02	7.98E-01	1.07E-04		-1.30E-01	6.57E-01		1.84E-02	9.41E-01		-3.90E-03	9.80E-01		8.19E-01	4.72E-63		3.17E+00	0.00E+00	Up	Unigene23558_All//gi|224106453|ref|XP_002314171.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222850579|gb|EEE88126.1| GRAS family transcription factor [Populus trichocarpa]	Unigene23558_All//2.00E-174//AT1G07530| SCL14 (SCARECROW-LIKE 14); transcription factor	Unigene23558_All//0.00E+00//gi|48828299|gb|CO126689.1|CO126689	GRAS		GO:0032583//GO:0042221//GO:0043231//GO:0044444	nr +
Unigene23563_All	1412	50.51	44.93	48.16	54.47	54.38	60.10	98.12	57.45	45.96	-1.69E-01	8.82E-03		-6.86E-02	3.75E-01		-2.30E-03	9.71E-01		1.42E-01	1.74E-02		-7.72E-01	4.87E-79		-1.09E+00	2.44E-145	Down	Unigene23563_All//gi|543867|sp|P26360.2|ATPG3_IPOBA//1.00E-151//RecName: Full=ATP synthase subunit gamma, mitochondrial; AltName: Full=F-ATPase gamma subunit; Flags: Precursor >gi|303626|dbj|BAA03526.1| F1-ATPase gamma subunit [Ipomoea batatas]	Unigene23563_All//9.00E-130//AT2G33040| ATP synthase gamma chain, mitochondrial (ATPC)	Unigene23563_All//0.00E+00//TC142755		ko00190|Oxidative phosphorylation		nr -
Unigene23565_All	3997	7.64	4.53	5.88	21.92	22.86	14.64	20.76	11.49	9.52	-7.56E-01	2.39E-14		-3.80E-01	1.79E-04		6.02E-02	3.67E-01		-5.82E-01	3.81E-27		-8.54E-01	1.84E-56		-1.13E+00	2.09E-91	Down	Unigene23565_All//gi|297826937|ref|XP_002881351.1|//0.00E+00//AIR9 protein [Arabidopsis lyrata subsp. lyrata] >gi|297327190|gb|EFH57610.1| AIR9 protein [Arabidopsis lyrata subsp. lyrata]	Unigene23565_All//0.00E+00//AT2G34680| AIR9; protein binding	Unigene23565_All//0.00E+00//CO081816			GO:0043231	nr -
Unigene23567_All	1315	18.62	11.33	12.39	51.41	42.34	50.76	36.46	21.52	17.12	-7.17E-01	1.09E-10		-5.88E-01	2.23E-07		-2.80E-01	2.12E-06		-1.82E-02	8.22E-01		-7.61E-01	3.40E-27		-1.09E+00	1.31E-50	Down	Unigene23567_All//gi|255957396|emb|CBA13552.1|//1.00E-167//cytosolic chaperonin, delta subunit [Glycine max]	Unigene23567_All//8.00E-161//AT3G18190| chaperonin, putative	Unigene23567_All//0.00E+00//TC135604				nr -
Unigene23568_All	1441	17.90	19.16	10.90	21.88	22.75	28.80	16.05	33.12	39.84	9.84E-02	3.88E-01		-7.16E-01	1.12E-10		5.61E-02	6.27E-01		3.97E-01	8.28E-07		1.05E+00	1.14E-45	Up	1.31E+00	5.65E-80	Up	Unigene23568_All//gi|22324807|gb|AAM95645.1|//0.00E+00//WD-repeat protein GhTTG3 [Gossypium hirsutum]	Unigene23568_All//2.00E-151//AT5G24520| TTG1 (TRANSPARENT TESTA GLABRA 1); DNA binding / nucleotide binding / protein binding	Unigene23568_All//0.00E+00//TC129779				nr -
Unigene2357_All	2372	4.48	3.97	4.15	7.35	6.53	7.22	4.12	0.99	1.53	-1.73E-01	3.61E-01		-1.09E-01	6.13E-01		-1.70E-01	2.48E-01		-2.66E-02	8.77E-01		-2.06E+00	6.04E-26	Down	-1.43E+00	2.30E-16	Down	Unigene2357_All//gi|297807311|ref|XP_002871539.1|//0.00E+00//C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317376|gb|EFH47798.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2357_All//0.00E+00//AT3G57880| C2 domain-containing protein	Unigene2357_All//0.00E+00//TC157516			GO:0003824//GO:0030312//GO:0043231	nr +
Unigene23573_All	2067	17.92	42.41	24.99	35.11	45.40	33.06	7.08	13.16	7.90	1.24E+00	2.02E-89	Up	4.80E-01	1.83E-10		3.71E-01	3.62E-14		-8.70E-02	2.31E-01		8.95E-01	1.42E-20		1.59E-01	2.29E-01		Unigene23573_All//gi|297819734|ref|XP_002877750.1|//1.00E-106//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323588|gb|EFH14009.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23573_All//5.00E-107//AT3G50560| short-chain dehydrogenase/reductase (SDR) family protein	Unigene23573_All//0.00E+00//TC132892		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0003824//GO:0008152	nr -
Unigene23574_All	1572	19.80	12.22	11.52	44.30	40.99	40.51	81.20	40.68	40.47	-6.97E-01	9.18E-13		-7.82E-01	8.92E-15		-1.12E-01	9.88E-02		-1.29E-01	5.93E-02		-9.97E-01	5.10E-112		-1.00E+00	1.58E-116	Down	Unigene23574_All//gi|283488489|gb|ADB24766.1|//0.00E+00//UDP-D-glucose dehydrogenase [Gossypium hirsutum]	Unigene23574_All//0.00E+00//AT3G29360| UDP-glucose 6-dehydrogenase, putative	Unigene23574_All//0.00E+00//TC132012		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions	GO:0000166//GO:0008152//GO:0016616//GO:0030312//GO:0043231//GO:0044444//GO:0048037	nr -
Unigene23575_All	834	6.34	10.33	11.05	8.18	11.97	11.43	5.22	11.43	10.13	7.05E-01	3.43E-04		8.02E-01	4.68E-05		5.49E-01	1.51E-03		4.82E-01	9.95E-03		1.13E+00	5.77E-11	Up	9.56E-01	7.03E-08		Unigene23575_All//gi|30841458|gb|AP34366.1|//1.00E-136//fiber protein Fb19 [Gossypium barbadense]	Unigene23575_All//7.00E-91//AT4G40080| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	Unigene23575_All//0.00E+00//TC138324			GO:0008289	nr -
Unigene23576_All	1263	23.41	30.89	23.95	14.12	25.25	28.93	2.14	7.71	10.41	4.00E-01	2.74E-06		3.30E-02	7.73E-01		8.38E-01	1.54E-20		1.03E+00	3.28E-30	Up	1.85E+00	1.99E-22	Up	2.28E+00	5.61E-40	Up	Unigene23576_All//gi|30841458|gb|AP34366.1|//1.00E-123//fiber protein Fb19 [Gossypium barbadense]	Unigene23576_All//9.00E-93//AT4G40080| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	Unigene23576_All//0.00E+00//gi|73866167|gb|DT468905.1|DT468905				nr +
Unigene23577_All	1304	4.90	1.28	2.41	17.61	12.44	7.00	7.39	9.39	18.24	-1.93E+00	4.61E-13	Down	-1.02E+00	3.17E-05	Down	-5.02E-01	1.68E-06		-1.33E+00	8.79E-29	Down	3.45E-01	1.97E-02		1.30E+00	2.66E-33	Up	Unigene23577_All//gi|30841458|gb|AP34366.1|//1.00E-180//fiber protein Fb19 [Gossypium barbadense]	Unigene23577_All//4.00E-109//AT4G40080| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	Unigene23577_All//0.00E+00//TC138324			GO:0008289	nr +
Unigene2358_All	1872	2.88	7.61	4.92	3.67	7.91	8.30	7.11	15.56	22.32	1.40E+00	4.84E-18	Up	7.74E-01	8.46E-05		1.11E+00	3.79E-15	Up	1.18E+00	4.82E-16	Up	1.13E+00	7.78E-32	Up	1.65E+00	7.39E-82	Up	Unigene2358_All//gi|89001001|gb|ABD59090.1|//4.00E-43//At1g76185 [Arabidopsis thaliana]	Unigene2358_All//8.00E-43//AT1G20160| unknown protein	Unigene2358_All//0.00E+00//gi|109885694|gb|DW514664.1|DW514664				nr +
Unigene23582_All	590	7.89	3.01	2.17	5.99	3.39	2.68	1.36	1.28	3.24	-1.39E+00	2.13E-06	Down	-1.87E+00	7.68E-09	Down	-8.24E-01	7.45E-03		-1.16E+00	3.83E-04	Down	-9.47E-02	8.99E-01		1.25E+00	2.65E-03		Unigene23582_All//gi|110741893|dbj|BAE98888.1|//2.00E-57//protein kinase like protein [Arabidopsis thaliana]	Unigene23582_All//9.00E-59//AT1G62950| leucine-rich repeat transmembrane protein kinase, putative	Unigene23582_All//0.00E+00//ES795267		ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene23583_All	2144	6.61	1.77	2.24	3.44	3.24	1.94	2.66	2.12	4.74	-1.90E+00	1.55E-27	Down	-1.56E+00	2.90E-20	Down	-8.39E-02	7.59E-01		-8.27E-01	8.54E-05		-3.25E-01	1.65E-01		8.32E-01	1.51E-07		Unigene23583_All//gi|8778632|gb|AAF79640.1|AC025416_14//0.00E+00//F5O11.21 [Arabidopsis thaliana]	Unigene23583_All//0.00E+00//AT1G12460| leucine-rich repeat transmembrane protein kinase, putative	Unigene23583_All//0.00E+00//ES795267			GO:0004672//GO:0005488//GO:0008152//GO:0016020	nr -
Unigene23585_All	1151	2.18	0.97	0.83	1.77	3.05	1.53	5.07	2.91	2.04	-1.17E+00	4.00E-03		-1.39E+00	1.33E-03		7.82E-01	1.52E-02		-2.14E-01	6.65E-01		-8.03E-01	2.42E-04		-1.31E+00	5.47E-09	Down	Unigene23585_All//gi|32362295|gb|AAP80175.1|//1.00E-129//At3g55350 [Arabidopsis thaliana]	Unigene23585_All//7.00E-121//AT3G55350| unknown protein	Unigene23585_All//0.00E+00//TC176207				nr +
Unigene23586_All	1518	4.00	3.81	2.67	4.43	5.67	3.18	3.84	1.79	0.94	-7.14E-02	7.71E-01		-5.85E-01	2.02E-02		3.56E-01	7.74E-02		-4.77E-01	3.82E-02		-1.10E+00	8.54E-07	Down	-2.02E+00	5.58E-16	Down	Unigene23586_All//gi|32362295|gb|AAP80175.1|//1.00E-146//At3g55350 [Arabidopsis thaliana]	Unigene23586_All//2.00E-147//AT3G55350| unknown protein	Unigene23586_All//0.00E+00//DW509629				nr +

Unigene23590_All	1565	0.80	0.71	1.36	0.48	1.06	1.85	0.49	1.42	2.21	-1.72E-01	7.55E-01			7.62E-01	9.80E-02		1.15E+00	2.64E-02		1.95E+00	1.43E-06	Up	1.54E+00	1.40E-04	Up	2.19E+00	1.35E-10	Up	Unigene23590_All//gi|224116480|ref|XP_002317311.1|//1.00E-114//global transcription factor group [Populus trichocarpa] >gi|222860376|gb|EEE97923.1|global transcription factor group [Populus trichocarpa]	Unigene23590_All//7.00E-53//AT5G46550| DNA-binding bromodomain-containing protein	Unigene23590_All//0.00E+00//gi|48829467|gb|CO127857.1|CO127857				nr -
Unigene23592_All	1556	20.38	23.87	23.20	42.48	28.42	20.87	40.16	17.03	27.60	2.28E-01	1.19E-02		1.87E-01	5.74E-02		-5.80E-01	5.52E-23		-1.03E+00	4.24E-54	Down	-1.24E+00	5.66E-78	Down	-5.41E-01	3.63E-20		Unigene23592_All|gi|79325241|ref|NP_001031706.1|//1.00E-144//ARF9 (AUXIN RESPONSE FACTOR 9); transcription factor [Arabidopsis thaliana]	Unigene23592_All//2.00E-132//AT4G23980| ARF9 (AUXIN RESPONSE FACTOR 9); transcription factor	Unigene23592_All//0.00E+00//TC152966	ARF			nr -
Unigene23593_All	2819	6.03	7.39	8.44	7.49	7.78	9.04	26.19	43.40	59.26	2.92E-01	1.79E-02		4.85E-01	2.61E-05		5.45E-02	7.32E-01		2.70E-01	1.49E-02		7.29E-01	3.41E-63		1.18E+00	1.44E-195	Up	Unigene23593_All|gi|18408017|ref|NP_564829.1|//1.00E-176//protein kinase family protein [Arabidopsis thaliana] >gi|79320679|ref|NP_001031229.1|protein kinase family protein [Arabidopsis thaliana] >gi|15983374|gb|AAL11555.1|AF424561_1 At1g64300/F15H21_13 [Arabidopsis thaliana] >gi|22655480|gb|AAM98332.1|At1g64300/F15H21_13 [Arabidopsis thaliana]	Unigene23593_All//6.00E-164//AT1G64300| protein kinase family protein	Unigene23593_All//0.00E+00//gi|164251415|gb|ES814522.1|ES814522		ko04626|Plant-pathogen interaction//ko04140|Regulation of autophagy		nr +
Unigene23594_All	3487	3.99	2.33	3.80	12.39	12.08	10.36	9.53	4.64	5.94	-7.80E-01	2.63E-07		-6.99E-02	6.77E-01		-3.64E-02	7.46E-01		-2.57E-01	1.53E-03		-1.04E+00	9.11E-32	Down	-6.82E-01	2.12E-16		Unigene23594_All|gi|297844112|ref|XP_002889937.1|//0.00E+00//T12C24.2 [Arabidopsis lyrata subsp. lyrata] >gi|297335779|gb|EFH66196.1|T12C24.2 [Arabidopsis lyrata subsp. lyrata]	Unigene23594_All//0.00E+00//AT1G12470| Pep3/Vps18/deep orange family protein	Unigene23594_All//0.00E+00//TC168180			GO:0043231//GO:0046914	nr -
Unigene23595_All	3451	23.86	4.13	7.07	21.93	20.56	14.04	8.77	3.28	5.74	-2.53E+00	4.53E-225	Down	-1.76E+00	2.43E-136	Down	-9.31E-02	1.64E-01		-6.43E-01	5.46E-28		-1.42E+00	6.53E-47	Down	-6.13E-01	1.42E-12		Unigene23595_All|gi|9795593|gb|AAF98411.1|AC026238_3/1.00E-115//Unknown protein [Arabidopsis thaliana] >gi|208566609|gb|AAM26675.1|At1g18620/F25I16_13 [Arabidopsis thaliana] >gi|32306507|gb|AAP78937.1|At1g18620 [Arabidopsis thaliana]	Unigene23595_All//0.00E+00//AT1G74160| unknown protein	Unigene23595_All//0.00E+00//TC157135				nr -
Unigene23597_All	2432	1.23	2.81	2.39	1.80	1.67	1.50	1.34	1.05	1.39	1.20E+00	2.80E-07	Up	9.61E-01	1.96E-04		-1.10E-01	7.56E-01		-2.61E-01	4.19E-01		-3.53E-01	2.79E-01		5.68E-02	8.62E-01		Unigene23597_All|gi|15223514|ref|NP_176027.1|//1.00E-147//3'-5' exonuclease domain-containing protein [Arabidopsis thaliana]	Unigene23597_All//1.00E-140//AT1G56310| 3'-5' exonuclease domain-containing protein	Unigene23597_All//0.00E+00//ES842938			GO:0004527//GO:0005488//GO:0034641//GO:0044464	nr -
Unigene236_All	4233	17.33	4.29	8.33	51.46	44.16	19.63	14.69	9.37	4.49	-2.02E+00	2.10E-151	Down	-1.06E+00	2.99E-56	Down	-2.21E-01	1.66E-12		-1.39E+00	7.39E-288	Down	-6.49E-01	1.07E-26		-1.71E+00	3.17E-129	Down	Unigene236_All|gi|224140225|ref|XP_002323485.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222868115|gb|EEF05246.1|multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene236_All//0.00E+00//AT2G36910| ABCB1 (ATP BINDING CASSETTE SUBFAMILY B1); ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter/ calmodulin binding	Unigene236_All//0.00E+00//TC144697		ko02010|ABC transporters		nr +
Unigene23600_All	559	4.31	0.63	1.05	6.77	5.85	3.55	1.82	0.15	1.28	-2.76E+00	7.95E-08	Down	-2.04E+00	2.15E-05	Down	-2.11E-01	5.41E-01		-9.30E-01	2.85E-03		-3.60E+00	2.38E-05	Down	-5.01E-01	3.99E-01		Unigene23600_All|gi|297820220|ref|XP_002877993.1|//1.00E-21//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323831|gb|EFH54252.1|F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23600_All//9.00E-15//AT3G54650| FBL17; ubiquitin-protein ligase	Unigene23600_All//0.00E+00//TC136743			GO:0005488//GO:0007067//GO:0009791//GO:0031461//GO:0043073//GO:0043161//GO:0048229	nr -
Unigene23601_All	2071	3.41	0.51	0.64	6.52	6.52	3.03	8.59	1.88	3.65	-2.73E+00	1.72E-21	Down	-2.41E+00	6.83E-18	Down	-1.00E-04	9.94E-01		-1.10E+00	6.70E-13	Down	-2.20E+00	1.56E-50	Down	-1.23E+00	2.30E-23	Down	Unigene23601_All|gi|42565930|ref|NP_567005.2|//0.00E+00//FBL17; ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75331246|sp|Q8W104.1|FBL17_ARATH RecName: Full=F-box/LRR-repeat protein 17 >gi|18087570|gb|AAL58916.1|AF462827_1 AT3g54650/T5N23_10 [Arabidopsis thaliana] >gi|22655356|gb|AAM98270.1|At3g54650/T5N23_10 [Arabidopsis thaliana]	Unigene23601_All//5.00E-163//AT3G54650| FBL17; ubiquitin-protein ligase	Unigene23601_All//0.00E+00//TC136743			GO:0005488//GO:0007067//GO:0009791//GO:0031461//GO:0043073//GO:0043161//GO:0048229	nr -
Unigene23602_All	630	6.48	4.02	2.20	7.43	5.14	3.23	244.42	104.16	41.36	-6.88E-01	2.23E-02		-1.56E+00	3.06E-06	Down	-5.33E-01	4.83E-02		-1.20E+00	1.58E-05	Down	-1.23E+00	1.95E-189	Down	-2.56E+00	0.00E+00	Down	Unigene23602_All|gi|48675345|dbj|BAD22820.1|//5.00E-51//nitrate transporter [Prunus persica]	Unigene23602_All//3.00E-32//AT1G12110| NRT1.1; nitrate transmembrane transporter/ transporter	Unigene23602_All//8.00E-155//TC161661			GO:0015833//GO:0031224//GO:0031410	nr -
Unigene23603_All	2086	9.28	3.60	6.64	18.96	15.62	9.83	334.19	116.09	84.47	-1.37E+00	1.55E-23	Down	-4.84E-01	1.95E-04		-2.80E-01	5.17E-04		-9.48E-01	1.22E-28		-1.53E+00	0.00E+00	Down	-1.98E+00	0.00E+00	Down	Unigene23603_All|gi|33411520|dbj|BAC81420.1|//1.00E-155//nitrate transporter [Prunus persica]	Unigene23603_All//9.00E-107//AT1G12110| NRT1.1; nitrate transmembrane transporter/ transporter	Unigene23603_All//0.00E+00//TC161661				nr +
Unigene23604_All	2255	2.62	2.81	1.63	5.63	4.20	3.67	10.16	6.30	4.40	9.93E-02	6.83E-01		-6.86E-01	6.96E-03		-4.24E-01	5.01E-03		-6.20E-01	5.85E-05		-6.89E-01	1.94E-11		-1.21E+00	7.06E-29	Down	Unigene23604_All|gi|224091597|ref|XP_002309295.1|//0.00E+00//tubulin gamma complex-associated protein [Populus trichocarpa] >gi|222855271|gb|EEE92818.1|tubulin gamma complex-associated protein [Populus trichocarpa]	Unigene23604_All//0.00E+00//AT5G06680| SPC98 (SPINDLE POLE BODY COMPONENT 98); tubulin binding	Unigene23604_All//0.00E+00//gi|54117650|gb|CO493159.1|CO493159			GO:0000226//GO:0012505//GO:0015630//GO:0044430//GO:0044459	nr -
Unigene23610_All	423	8.41	16.89	19.13	4.95	3.58	4.38	4.00	0.69	0.47	1.01E+00	6.49E-06	Up	1.19E+00	5.39E-08	Up	-4.66E-01	3.11E-01		-1.76E-01	6.94E-01		-2.53E+00	2.71E-06	Down	-3.09E+00	7.24E-08	Down	Unigene23610_All|gi|33772169|gb|AAQ54521.1|//1.00E-35//aldo/keto reductase [Malus x domestica]	Unigene23610_All//4.00E-36//AT2G37760| aldo/keto reductase family protein	Unigene23610_All//1.00E-134//gi|48805188|gb|CO106502.1|CO106502		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism/ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism	GO:0004033//GO:0006970//GO:0008152//GO:0010038	nr +
Unigene23611_All	1458	57.81	98.52	87.58	28.15	32.85	26.70	11.05	3.27	2.27	7.69E-01	2.29E-66		5.99E-01	4.26E-37		2.23E-01	3.04E-03		-7.64E-02	4.67E-01		-1.76E+00	2.67E-34	Down	-2.28E+00	1.30E-49	Down	Unigene23611_All|gi|297823649|ref|XP_002879707.1|//1.00E-126//aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325546|gb|EFH55966.1|aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23611_All//2.00E-127//AT2G37760| aldo/keto reductase family protein	Unigene23611_All//0.00E+00//TC139862		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism/ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr -
Unigene23613_All	2665	31.12	61.41	63.36	31.96	38.54	46.38	14.45	9.06	5.83	9.81E-01	9.45E-114		1.03E+00	3.90E-123	Up	2.70E-01	9.60E-09		5.37E-01	8.53E-33		-6.73E-01	6.42E-18		-1.31E+00	2.69E-54	Down	Unigene23613_All|gi|297834254|ref|XP_002885009.1|//0.00E+00//subtilase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330849|gb|EFH61268.1|subtilase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23613_All//0.00E+00//AT3G14067| subtilase family protein	Unigene23613_All//0.00E+00//TC145308			GO:0003006//GO:0004175//GO:0005515//GO:0005576//GO:0005618//GO:0009845//GO:0010191//GO:0016020//GO:0019538//GO:0031410//GO:0043231//GO:0044092	nr -
Unigene23615_All	2056	19.26	9.39	15.51	75.93	36.76	19.05	12.59	7.22	5.93	-1.04E+00	8.90E-31	Down	-3.12E-01	4.25E-04		-1.05E+00	2.79E-150	Down	-2.00E+00	0.00E+00	Down	-8.02E-01	2.00E-16		-1.09E+00	1.60E-27	Down	Unigene23615_All|gi|224063973|ref|XP_002301328.1|//1.00E-29//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222843054|gb|EEE80601.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene23615_All//3.00E-28//AT3G03200| anac045 (Arabidopsis NAC domain containing protein 45); transcription factor	Unigene23615_All//0.00E+00//TC157318	NAC			nr +
Unigene23616_All	478	133.87	283.24	213.11	101.61	150.42	128.88	137.54	212.21	160.27	1.08E+00	1.88E-110	Up	6.71E-01	3.48E-36		5.66E-01	2.70E-23		3.43E-01	1.28E-07		6.26E-01	2.49E-40		2.21E-01	2.77E-05		Unigene23616_All|gi|211906480|gb|ACJ11733.1|//4.00E-93//catalase [Gossypium hirsutum]	Unigene23616_All//2.00E-86//AT4G35090| CAT2 (CATALASE 2); catalase	Unigene23616_All//0.00E+00//gi|78338113|gb|DT558387.1|DT558387		ko04146|Peroxisome//ko00380|Tryptophan metabolism	GO:0004601//GO:0005506//GO:0005777//GO:0006950//GO:0042743	nr -
Unigene23617_All	464	0.90	5.13	3.21	1.40	2.15	3.31	1.09	2.07	0.86	2.51E+00	5.46E-07	Up	1.83E+00	2.94E-03		6.25E-01	4.06E-01		1.25E+00	2.40E-02		9.22E-01	1.49E-01		-3.49E-01	6.73E-01		Unigene23617_All|gi|211906480|gb|ACJ11733.1|//2.00E-18//catalase [Gossypium hirsutum]	Unigene23617_All//2.00E-17//AT4G35090| CAT2 (CATALASE 2); catalase	Unigene23617_All//1.00E-63//TC146350		ko04146|Peroxisome//ko00380|Tryptophan metabolism	GO:0004601//GO:0005506//GO:0005777//GO:0006950//GO:0042743	nr +
Unigene23618_All	1445	5.07	16.31	10.36	3.55	7.17	7.81	11.03	14.26	14.39	1.69E+00	2.79E-38	Up	1.03E+00	1.78E-11	Up	1.01E+00	2.22E-09	Up	1.14E+00	3.08E-11	Up	3.70E-01	6.63E-04		3.84E-01	2.71E-04		Unigene23618_All|gi|211906480|gb|ACJ11733.1|//0.00E+00//catalase [Gossypium hirsutum]	Unigene23618_All//0.00E+00//AT4G35090| CAT2 (CATALASE 2); catalase	Unigene23618_All//0.00E+00//gi|78330501|gb|DT550775.1|DT550775		ko04146|Peroxisome//ko00380|Tryptophan metabolism	GO:0004601//GO:0005506//GO:0005777//GO:0006950//GO:0042743	nr +
Unigene23619_All	2279	11.46	30.75	17.73	8.63	13.19	14.19	4.06	3.98	3.32	1.42E+00	3.47E-88	Up	6.31E-01	3.08E-13		6.12E-01	2.20E-11		7.17E-01	1.20E-14		-2.99E-02	8.86E-01		-2.91E-01	8.78E-02		Unigene23619_All|gi|115432144|gb|AB197349.1|//0.00E+00//cold-induced thioredoxin domain-containing protein [Ammopiptanthus mongolicus]	Unigene23619_All//0.00E+00//AT4G03200| catalytic	Unigene23619_All//0.00E+00//TC136201		ko00240|Pyrimidine metabolism	GO:0009536	nr -
Unigene23620_All	2847	5.95	19.63	10.70	4.53	6.48	7.69	1.83	1.76	0.95	1.72E+00	1.25E-92	Up	8.45E-01	1.75E-16		5.17E-01	1.86E-05		7.64E-01	3.18E-11		-5.22E-02	8.43E-01		-9.41E-01	4.09E-05		Unigene23620_All|gi|115432144|gb|AB197349.1|//0.00E+00//cold-induced thioredoxin domain-containing protein [Ammopiptanthus mongolicus]	Unigene23620_All//0.00E+00//AT4G03200| catalytic	Unigene23620_All//0.00E+00//TC136201		ko00240|Pyrimidine metabolism	GO:0009536	nr -
Unigene23621_All	2809	7.06	3.41	4.13	21.85	13.82	9.61	15.91	5.98	7.83	-1.05E+00	4.17E-16	Down	-7.73E-01	1.86E-09		-6.61E-01	6.36E-27		-1.18E+00	2.31E-63	Down	-1.41E+00	2.21E-68	Down	-1.02E+00	1.31E-42	Down	Unigene23621_All|gi|263430169|sp|C0LGB8.1|Y1634_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g63430; Flags: Precursor >gi|224589459|gb|ACN59263.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23621_All//0.00E+00//AT1G63430| leucine-rich repeat transmembrane protein kinase, putative	Unigene23621_All//0.00E+00//TC173924		ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene23623_All	1215	5.00	16.43	7.93	8.81	9.75	11.34	11.07	26.97	22.79	1.72E+00	2.13E-33	Up	6.67E-01	4.94E-04		1.45E-01	4.55E-01		3.63E-01	1.88E-02		1.29E+00	1.23E-43	Up	1.04E+00	2.41E-27	Up	Unigene23623_All|gi|15241003|ref|NP_195772.1|//9.00E-94//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|66865962|gb|AAY57615.1| RING finger family protein [Arabidopsis thaliana]	Unigene23623_All//4.00E-95//AT5G01520| zinc finger (C3HC4-type RING finger) family protein	Unigene23623_All//0.00E+00//TC178940			GO:0004659//GO:0046914	nr -
Unigene23624_All	1031	1.12	4.23	2.43	1.55	1.44	2.10	2.34	3.77	3.94	1.92E+00	5.20E-09	Up	1.12E+00	8.17E-03		-1.06E-01	8.20E-01		4.44E-01	3.51E-01		6.90E-01	1.27E-02		7.54E-01	3.96E-03		Unigene23624_All|gi|15241003|ref|NP_195772.1|//1.00E-106//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|66865962|gb|AAY57615.1| RING finger family protein [Arabidopsis thaliana]	Unigene23624_All//2.00E-102//AT5G01520| zinc finger (C3HC4-type RING finger) family protein	Unigene23624_All//0.00E+00//gi|54119577|gb|CO495086.1|CO495086				nr +
Unigene23625_All	2622	12.41	3.46	2.27	11.87	12.50	5.34	18.50	4.81	18.86	-1.84E+00	6.61E-60	Down	-2.45E+00	9.46E-83	Down	7.44E-02	5.47E-01		-1.15E+00	4.74E-31	Down	-1.94E+00	1.42E-116	Down	2.78E-02	7.22E-01		Unigene23625_All|gi|13877693|gb|AAK43924.1|AF370605_1/0.00E+00//axi 1 protein-like protein [Arabidopsis thaliana] >gi|3128192|gb|AAC16096.1| similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana]	Unigene23625_All//0.00E+00//AT2G44500| unknown protein	Unigene23625_All//0.00E+00//TC179512			GO:0009536	nr -

Unigene23628_All	3353	2.48	2.83	3.54	2.84	3.24	3.46	1.00	0.70	0.23	1.88E-01	3.67E-01		5.13E-01	2.68E-03		1.89E-01	3.30E-01		2.87E-01	1.08E-01		-5.13E-01	9.54E-02		-2.14E+00	3.83E-10	Down	Unigene23628_All//gi|61162203|dbj|BAD91083.1|//0.00E+00//beta-D-galactosidase [Pyrus pyrifolia]	Unigene23628_All//0.00E+00//AT2G28470| BGAL8 (beta-galactosidase 8); beta-galactosidase/ catalytic/ cation binding / sugar binding	Unigene23628_All//0.00E+00//TC153727		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series	GO:0015925//GO:0030246//GO:0030312//GO:0031410//GO:0043167//GO:0044238	nr -
Unigene23629_All	2675	3.44	2.03	4.86	37.78	24.78	19.84	10.23	6.27	4.08	-7.64E-01	5.61E-05		4.97E-01	2.25E-03		-6.09E-01	4.46E-38		-9.30E-01	4.32E-70		-7.07E-01	4.67E-14		-1.33E+00	1.60E-39	Down	Unigene23629_All//gi|18147596|dbj|BAB83088.1|//0.00E+00//beta-amyrin synthase [Betula platyphylla]	Unigene23629_All//0.00E+00//AT1G78955| CAS1 (Cameliol C synthase 1); beta-amyrin synthase	Unigene23629_All//4.00E-135//DW008193		ko00100|Steroid biosynthesis	GO:0016853	nr +
Unigene23630_All	2042	43.30	84.84	50.12	34.25	72.92	67.15	94.06	76.71	42.78	9.70E-01	3.00E-118		2.11E-01	7.88E-05		1.09E+00	1.40E-146	Up	9.71E-01	4.75E-101		-2.94E-01	2.13E-19		-1.14E+00	6.51E-214	Down	Unigene23630_All//gi|15224852|ref|NP_179571.1|//4.00E-94//zinc finger (CCCH-type) family protein |Arabidopsis thaliana| >gi|75220226|sp|Q82199.1|C3H20_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 20; Short=AtC3H20	Unigene23630_All//1.00E-83//AT2G19810| zinc finger (CCCH-type) family protein	Unigene23630_All//0.00E+00//TC135221	C3H		GO:0001071//GO:0010260//GO:0010468//GO:0023033//GO:0043231//GO:0046914	nr -
Unigene23631_All	2442	5.08	2.26	3.45	21.03	21.90	17.85	29.14	38.75	122.86	-1.17E+00	3.88E-12	Down	-5.60E-01	7.74E-04		5.83E-02	5.43E-01		-2.37E-01	1.41E-03		4.11E-01	5.50E-18		2.08E+00	0.00E+00	Up	Unigene23631_All//gi|15241068|ref|NP_195803.1|//0.00E+00//armadillo/beta-catenin repeat family protein / U-box domain-containing protein |Arabidopsis thaliana| >gi|75264490|sp|Q9LZW3.1|PUB16_ARATH RecName: Full=U-box domain-containing protein 16; AltName: Full=Plant U-box protein 16 >gi|51536504|gb|AAU05490.1| At5g01830 [Arabidopsis thaliana] >gi|52421307|gb|AAU45223.1| At5g01830 [Arabidopsis thaliana]	Unigene23631_All//0.00E+00//AT5G01830| armadillo/beta-catenin repeat family protein / U-box domain-containing protein	Unigene23631_All//0.00E+00//TC166205			GO:0009743//GO:0019787//GO:0032446//GO:0043234	nr +
Unigene2364_All	1566	8.02	9.03	9.18	43.58	31.20	43.49	349.26	162.54	202.42	1.71E-01	2.98E-01		1.95E-01	2.42E-01		-4.82E-01	5.16E-17		-2.90E-03	9.65E-01		-1.10E+00	0.00E+00	Down	-7.87E-01	0.00E+00		Unigene2364_All//gi|157042763|gb|AAV02033.1|//0.00E+00//glyceraldehyde 3-phosphate dehydrogenase [Nicotiana langsdorffii x Nicotiana sanderae]	Unigene2364_All//2.00E-166//AT1G13140| GAPC2 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene2364_All//0.00E+00//TC161182		ko00010|Glycolysis / Gluconeogenesis	GO:0000166//GO:0008943//GO:0019318	nr -
Unigene23642_All	2989	8.63	33.89	14.27	14.65	22.60	39.60	11.08	26.26	27.76	1.97E+00	9.50E-202	Up	7.26E-01	1.11E-17		6.26E-01	4.00E-26		1.43E+00	1.24E-161	Up	1.25E+00	1.48E-98	Up	1.33E+00	3.74E-117	Up	Unigene23642_All//gi|15131533|emb|CAC48386.1|//0.00E+00//ethylene receptor [Fragaria x ananassa]	Unigene23642_All//0.00E+00//AT3G04580| EIN4 (ETHYLENE INSENSITIVE 4); ethylene binding / glycogen synthase kinase 3/ protein histidine kinase/ receptor	Unigene23642_All//0.00E+00//TC131832	Orphans	ko04712|Circadian rhythm - plant	GO:0000160//GO:0004673//GO:0004871//GO:0006351//GO:0006468//GO:0031090//GO:0032559	nr -
Unigene23643_All	3545	1.25	3.93	1.58	1.41	2.33	4.01	1.09	2.91	2.66	1.65E+00	3.29E-22	Up	3.30E-01	2.35E-01		7.30E-01	1.32E-04		1.51E+00	2.07E-21	Up	1.42E+00	1.41E-16	Up	1.30E+00	1.27E-13	Up	Unigene23643_All//gi|15131533|emb|CAC48386.1|//0.00E+00//ethylene receptor [Fragaria x ananassa]	Unigene23643_All//0.00E+00//AT3G04580| EIN4 (ETHYLENE INSENSITIVE 4); ethylene binding / glycogen synthase kinase 3/ protein histidine kinase/ receptor	Unigene23643_All//0.00E+00//TC131832	Orphans	ko04712|Circadian rhythm - plant	GO:0000160//GO:0004673//GO:0004871//GO:0006351//GO:0006468//GO:0031090//GO:0032559	nr -
Unigene23644_All	3390	5.56	2.90	2.14	17.34	19.54	11.31	22.31	2.87	8.57	-9.38E-01	7.33E-13		-1.38E+00	2.98E-22	Down	1.73E-01	7.43E-03		-6.16E-01	2.51E-20		-2.96E+00	7.83E-299	Down	-1.38E+00	1.00E-114	Down	Unigene23644_All//gi|124360602|gb|ABN08601.1|//1.00E-165//CIP7 , disease resistance related [Medicago truncatula]	Unigene23644_All//7.00E-125//AT1G61100| disease resistance protein (TIR class), putative	Unigene23644_All//0.00E+00//TC137091				nr +
Unigene23645_All	503	0.00	0.00	0.00	2.38	0.89	0.45	1.85	4.15	1.43	null	null		null	null		-1.42E+00	1.82E-02		-2.40E+00	7.07E-04	Down	1.17E+00	3.80E-03		-3.75E-01	5.57E-01				Unigene23645_All//0.00E+00//gi|84175226|gb|DR463874.1|DR463874				
Unigene23647_All	2999	18.46	20.24	21.13	2.96	3.56	2.27	8.97	17.50	19.93	1.33E-01	6.72E-02		1.95E-01	5.89E-03		2.68E-01	1.52E-01		-3.79E-01	5.83E-02		9.65E-01	4.69E-44		1.15E+00	4.97E-68	Up	Unigene23647_All//gi|7239157|gb|AAF43095.1|AF053769_1//0.00E+00//homeodomain protein [Malus x domestica]	Unigene23647_All//7.00E-135//AT4G36870| BLH2 (BEL1-LIKE HOMEODOMAIN 2); DNA binding / transcription factor	Unigene23647_All//0.00E+00//TC174077	HB		GO:0003677//GO:0006350//GO:0010468	nr +
Unigene23652_All	1084	1.83	1.12	0.69	1.42	1.84	1.79	3.67	1.66	2.24	-7.09E-01	1.20E-01		-1.42E+00	4.48E-03		3.71E-01	4.65E-01		3.31E-01	5.22E-01		-1.15E+00	3.90E-05	Down	-7.10E-01	7.04E-03		Unigene23652_All//gi|53828635|gb|AAT94427.1|//1.00E-78//At1g58110 [Arabidopsis thaliana]	Unigene23652_All//2.00E-72//AT1G58110| bZIP family transcription factor	Unigene23652_All//2.00E-165//TC176960			GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0043231	nr +
Unigene23653_All	1509	3.09	2.05	1.98	7.99	9.04	4.79	6.42	2.05	2.67	-5.91E-01	3.47E-02		-6.43E-01	2.77E-02		1.78E-01	3.11E-01		-7.38E-01	3.35E-06		-1.65E+00	3.78E-19	Down	-1.27E+00	1.25E-13	Down	Unigene23653_All//gi|53828635|gb|AAT94427.1|//8.00E-84//At1g58110 [Arabidopsis thaliana]	Unigene23653_All//8.00E-75//AT1G58110| bZIP family transcription factor	Unigene23653_All//0.00E+00//TC176960			GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0043231	nr +
Unigene23655_All	3137	3.34	0.63	1.32	6.83	3.86	8.25	7.59	2.96	4.51	-2.40E+00	2.13E-27	Down	-1.33E+00	5.16E-12	Down	-8.21E-01	5.70E-14		2.73E-01	1.29E-02		-1.36E+00	8.80E-35	Down	-7.51E-01	4.69E-14		Unigene23655_All//gi|124360858|gb|ABN08830.1|//0.00E+00//Periodic tryptophan protein-associated region; WD40-like [Medicago truncatula]	Unigene23655_All//0.00E+00//AT1G15440| transducin family protein / WD-40 repeat family protein	Unigene23655_All//0.00E+00//gi|164251328|gb|EX171971.1|EX171971		ko03040|Spliceosome	GO:0004683	nr +
Unigene2366_All	1833	15.93	7.13	12.14	8.34	7.80	7.59	3.23	2.67	1.26	-1.16E+00	2.88E-27	Down	-3.91E-01	1.65E-04		-9.78E-02	5.74E-01		-1.37E-01	4.19E-01		-2.76E-01	2.40E-01		-1.36E+00	1.51E-09	Down	Unigene2366_All//gi|2194144|gb|AAB61119.1|//6.00E-63//F20P5.8 [Arabidopsis thaliana]	Unigene2366_All//7.00E-50//AT1G70200| RNA recognition motif (RRM)-containing protein	Unigene2366_All//0.00E+00//TC170862			GO:0005488//GO:0009536	nr +
Unigene23660_All	2470	6.93	7.36	6.10	7.72	13.90	5.32	1.93	0.30	2.39	8.84E-02	5.61E-01		-1.83E-01	2.37E-01		8.48E-01	1.71E-22		-5.38E-01	1.19E-05		-2.67E+00	1.68E-17	Down	3.03E-01	1.71E-01		Unigene23660_All//gi|9757828|dbj|BAB08265.1|//0.00E+00//receptor kinase-like protein [Arabidopsis thaliana] >gi|224589693|gb|ACN59378.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23660_All//0.00E+00//AT5G43020| leucine-rich repeat transmembrane protein kinase, putative	Unigene23660_All//0.00E+00//TC150681			GO:0004672//GO:0006464//GO:0007167//GO:0016020//GO:0032559	nr +
Unigene23663_All	585	1.16	2.94	2.18	0.68	2.59	0.93	1.73	1.21	1.91	1.34E+00	9.43E-03		9.10E-01	1.46E-01		1.93E+00	8.33E-04	Up	4.44E-01	6.78E-01		-5.14E-01	4.07E-01		1.37E-01	8.05E-01		Unigene23663_All//gi|224108163|ref|XP_002314744.1|//1.00E-87//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222863784|gb|EEF00915.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene23663_All//6.00E-84//AT2G02090| ETL1: ATP binding / DNA binding / helicase/ nucleic acid binding	Unigene23663_All//0.00E+00//CO115855			GO:0003676//GO:0009536//GO:0017111//GO:0032559	nr -
Unigene23666_All	1822	3.68	4.89	4.06	8.26	7.96	6.37	11.07	7.55	4.81	4.13E-01	3.54E-02		1.44E-01	5.64E-01		-5.34E-02	7.85E-01		-3.74E-01	9.99E-03		-5.53E-01	4.07E-07		-1.20E+00	2.44E-25	Down	Unigene23666_All//gi|42563882|ref|NP_187552.3|//1.00E-161//pectinacetylesterase family protein [Arabidopsis thaliana] >gi|119035842|gb|ABM06009.1| At3g09410 [Arabidopsis thaliana]	Unigene23666_All//1.00E-157//AT3G09410| pectinacetylesterase family protein	Unigene23666_All//0.00E+00//ES851698				nr +
Unigene23668_All	1668	1.22	0.97	1.66	4.72	4.17	5.31	47.68	193.49	64.63	-3.32E-01	4.66E-01		4.41E-01	2.72E-01		-1.78E-01	4.55E-01		1.70E-01	4.62E-01		2.02E+00	0.00E+00	Up	4.39E-01	1.80E-23		Unigene23668_All//gi|74273639|gb|AB01487.1|//1.00E-157//flavin-containing monooxygenase family protein FMO2 [Gossypium hirsutum]	Unigene23668_All//8.00E-91//AT1G62620| flavin-containing monooxygenase family protein / FMO family protein	Unigene23668_All//0.00E+00//TC129641		ko00380|Tryptophan metabolism	GO:0016491//GO:0043231	nr +
Unigene23669_All	1312	2.27	0.54	1.87	3.08	4.44	2.72	1.45	1.88	3.86	-2.07E+00	4.95E-07	Down	-2.84E-01	4.62E-01		5.28E-01	3.00E-02		-1.78E-01	6.36E-01		3.74E-01	3.34E-01		1.41E+00	1.20E-08	Up	Unigene23669_All//gi|74273639|gb|AB01487.1|//1.00E-107//flavin-containing monooxygenase family protein FMO2 [Gossypium hirsutum]	Unigene23669_All//1.00E-54//AT1G12140| FMO GS-OX5 (FLAVIN-MONOOXYGENASE GLUCOSINOLATE S-OXYGENASE 5); S-methylthiopropyl glucosinolate S-oxygenase/ flavin-containing monooxygenase/ monooxygenase	Unigene23669_All//0.00E+00//TC129641			GO:0000166//GO:0004497//GO:0008152	nr +
Unigene2367_All	1299	20.58	85.66	52.64	4.49	6.73	10.60	7.94	20.24	12.54	2.06E+00	5.65E-234	Up	1.35E+00	1.00E-77	Up	5.86E-01	1.71E-03		1.24E+00	1.72E-15	Up	1.35E+00	7.39E-38	Up	6.59E-01	5.01E-08		Unigene2367_All//gi|5262190|emb|CAB45787.1|//1.00E-104//inositol 1, 3, 4-trisphosphate 5/6-kinase-like protein [Arabidopsis thaliana] >gi|7267457|emb|CAB81153.1| inositol 1, 3, 4-trisphosphate 5/6-kinase-like protein [Arabidopsis thaliana]	Unigene2367_All//3.00E-83//AT4G08170| inositol 1,3,4-trisphosphate 5/6-kinase family protein	Unigene2367_All//0.00E+00//gi|78333889|gb|DT554163.1|DT554163		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0032559//GO:0043231//GO:0043647//GO:0046872//GO:0051765//GO:0051766	nr -
Unigene23671_All	3245	2.43	3.87	2.77	5.93	6.73	11.00	6.91	14.80	10.36	6.70E-01	2.65E-05		1.88E-01	3.86E-01		1.83E-01	1.54E-01		8.92E-01	3.56E-23		1.10E+00	7.95E-50	Up	5.85E-01	8.41E-13		Unigene23671_All//gi|224109752|ref|XP_002315300.1|//0.00E+00//p-aminobenzoate synthase [Populus trichocarpa] >gi|222864340|gb|EEF01471.1| p-aminobenzoate synthase [Populus trichocarpa]	Unigene23671_All//0.00E+00//AT2G28880| emb1997 (embryo defective 1997); anthranilate synthase/ catalytic/ oxo-acid-lyase	Unigene23671_All//0.00E+00//ES850836		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0003006//GO:0006760//GO:0009064//GO:0016833	nr +
Unigene23672_All	1717	30.17	11.13	16.28	107.11	94.66	41.85	24.55	89.85	22.62	-1.44E+00	1.07E-66	Down	-8.90E-01	4.90E-30		-1.78E-01	3.16E-07		-1.36E+00	6.94E-234	Down	1.87E+00	0.00E+00	Up	-1.18E-01	1.35E-01		Unigene23672_All//gi|86553064|gb|AAS17751.2|//0.00E+00//beta xylosidase [Fragaria x ananassa]	Unigene23672_All//0.00E+00//AT5G49360| BXL1 (BETA-XYLOSIDASE 1); hydrolase, hydrolyzing O-glycosyl compounds	Unigene23672_All//0.00E+00//TC148277		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0003006//GO:0005576//GO:0005618//GO:0015926//GO:0044238	nr -
Unigene23673_All	2461	12.59	3.75	6.04	32.93	30.10	16.39	7.39	25.93	8.00	-1.75E+00	4.82E-53	Down	-1.06E+00	4.03E-24	Down	-1.30E-01	3.00E-02		-1.01E+00	2.90E-64	Down	1.81E+00	3.43E-139	Up	1.14E-01	3.52E-01		Unigene23673_All//gi|86553064|gb|AAS17751.2|//0.00E+00//beta xylosidase [Fragaria x ananassa]	Unigene23673_All//0.00E+00//AT5G49360| BXL1 (BETA-XYLOSIDASE 1); hydrolase, hydrolyzing O-glycosyl compounds	Unigene23673_All//0.00E+00//TC135078		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0003006//GO:0005576//GO:0005618//GO:0015926//GO:0044238	nr +
Unigene23676_All	3702	1.17	2.42	1.67	2.44	2.94	2.59	4.13	2.18	3.12	1.05E+00	1.21E-07	Up	5.08E-01	4.31E-02		2.71E-01	1.39E-01		8.67E-02	6.71E-01		-9.24E-01	1.48E-12		-4.06E-01	1.10E-03		Unigene23676_All//gi|297818774|ref|XP_002877270.1|//0.00E+00//phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323108|gb|EFH53529.1| phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23676_All//0.00E+00//AT3G43220| phosphoinositide phosphatase family protein	Unigene23676_All//0.00E+00//TC166395				nr +
Unigene23679_All	2878	4.84	3.57	2.89	8.76	7.18	4.35	9.33	6.33	5.97	-4.36E-01	3.93E-03		-7.45E-01	1.82E-06		-2.87E-01	6.51E-03		-1.01E+00	1.81E-20	Down	-5.59E-01	2.20E-09		-6.45E-01	3.00E-12		Unigene23679_All//gi|280967728|gb|ACZ98534.1|//0.00E+00//LisH-SSDP-WD40 [Malus x domestica]	Unigene23679_All//4.00E-118//AT4G32551| LUG (LEUNIG); protein binding / protein heterodimerization/ transcription repressor	Unigene23679_All//0.00E+00//CO114698		ko03040|Spliceosome	GO:0005488//GO:0006350	nr -
Unigene2368_All	1540	16.10	62.45	46.51	2.10	4.05	7.80	11.17	26.57	12.86	1.96E+00	2.91E-189	Up	1.53E+00	1.05E-97	Up	9.45E-01	2.94E-05		1.89E+00	1.23E-24	Up	1.25E+00	5.26E-52	Up	2.02E-01	7.62E-02		Unigene2368_All//gi|18413088|ref|NP_567334.1|//1.00E-151//inositol 1,3,4-trisphosphate 5/6-kinase family protein [Arabidopsis thaliana] >gi|83288250|sp|Q9SUG3.2|ITPK2_ARATH RecName: Full=Inositol-tetrakisphosphate 1-kinase 2; AltName: Full=Inositol 1,3,4-trisphosphate 5/6-kinase 2; Short=Inositol-triphosphate 5/6-kinase 2; Short=Ins(1,3,4)P(3) 5/6-kinase 2; Short=AtItpk-2 >gi|15215758|gb|AAK91424.1| AT4g08170/T12G13_10 [Arabidopsis thaliana] >gi|16323320|gb|AAL15415.1| AT4g08170/T12G13_10 [Arabidopsis thaliana]	Unigene2368_All//9.00E-131//AT4G08170| inositol 1,3,4-trisphosphate 5/6-kinase family protein	Unigene2368_All//0.00E+00//TC178237		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene23682_All	1324	4.27	1.61	2.69	3.05	3.69	3.75	2.14	2.62	6.05	-1.41E+00	1.04E-07	Down	-6.63E-01	1.11E-02		2.77E-01	3.57E-01		3.00E-01	3.16E-01		2.92E-01	3.72E-01		1.50E+00	2.35E-14	Up	Unigene23682_All//gi|18405682|ref|NP_564708.1|//3.00E-55//tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana] >gi|109946435|gb|ABG48396.1| At1g56090 [Arabidopsis thaliana]	Unigene23682_All//9.00E-51//AT1G56090| tetratricopeptide repeat (TPR)-containing protein	Unigene23682_All//0.00E+00//gi|78325144|gb|DT545418.1|DT545418			GO:0050896	nr +

Unigene23683_All	1606	3.78	4.04	4.58	3.94	4.46	4.87	6.37	4.01	12.85	9.57E-02	6.85E-01			2.76E-01	2.46E-01		1.79E-01	4.93E-01			3.05E-01	1.79E-01		-6.69E-01	2.59E-05		1.01E+00	1.11E-19	Up	Unigene23683_All//gi|18405682|ref|NP_564708.1|//5.00E-73//tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana] >gi|109946435|gb|ABG48396.1|At1g56090 [Arabidopsis thaliana]	Unigene23683_All//4.00E-48//AT1G56090| tetratricopeptide repeat (TPR)-containing protein	Unigene23683_All//0.00E+00//gi|78336651|gb|DT556925.1|DT556925				nr +
Unigene23684_All	863	5.21	11.51	6.97	2.89	3.67	3.56	1.86	9.01	1.29	1.14E+00	1.57E-09	Up		4.19E-01	1.04E-01		3.47E-01	3.65E-01			3.02E-01	4.53E-01		2.27E+00	2.22E-23	Up	-5.26E-01	2.44E-01		Unigene23684_All//gi|227206278|dbj|BAH57194.1|//1.00E-111//AT2G21860| violaxanthin de-epoxidase-related [Arabidopsis thaliana]	Unigene23684_All//1.00E-112//AT2G21860| violaxanthin de-epoxidase-related	Unigene23684_All//2.00E-20//BF276101			GO:0008152//GO:0009536//GO:0016491	nr -
Unigene23685_All	2197	3.29	5.14	3.01	1.45	2.26	2.10	1.14	4.32	1.11	6.46E-01	1.31E-04			-1.29E-01	6.22E-01		6.37E-01	1.56E-02			5.31E-01	6.64E-02		1.93E+00	4.20E-23	Up	-3.77E-02	9.33E-01		Unigene23685_All//gi|18399815|ref|NP_565520.1|//0.00E+00//violaxanthin de-epoxidase-related [Arabidopsis thaliana] >gi|4417279|gb|AAD20404.1| expressed protein [Arabidopsis thaliana] >gi|14532484|gb|AAK63970.1| At2g21860/F7D8.18 [Arabidopsis thaliana]	Unigene23685_All//0.00E+00//AT2G21860| violaxanthin de-epoxidase-related	Unigene23685_All//1.00E-17//BF276101		ko00906|Carotenoid biosynthesis	GO:0043231	nr +
Unigene23688_All	2363	35.18	20.01	23.82	8.62	9.05	6.02	23.28	53.43	13.62	-8.14E-01	9.03E-43			-5.63E-01	9.11E-22		6.98E-02	6.27E-01			-5.18E-01	1.22E-05		1.20E+00	6.27E-149	Up	-7.73E-01	7.64E-33		Unigene23688_All//gi|7239157|gb|AAF43095.1|AF053769.1|//0.00E+00//homeodomain protein [Malus x domestica]	Unigene23688_All//2.00E-113//AT4G36870| BLH2 (BEL1-LIKE HOMEODOMAIN 2); DNA binding / transcription factor	Unigene23688_All//0.00E+00//CO114222	HB			nr +
Unigene23690_All	1599	48.59	69.65	66.64	117.39	138.28	146.31	19.28	73.21	31.47	5.20E-01	4.78E-26			4.56E-01	4.43E-19		2.36E-01	2.89E-14			3.18E-01	1.27E-23		1.93E+00	7.88E-277	Up	7.07E-01	8.75E-26		Unigene23690_All//gi|84453182|dbj|BAE71188.1|//1.00E-135//BEL1-like homeodomain transcription factor [Trifolium pratense]	Unigene23690_All//5.00E-100//AT2G35940| BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene23690_All//0.00E+00//CO117633	HB		GO:0003677//GO:0006350//GO:0010468	nr -
Unigene23691_All	1126	4.23	3.38	3.69	8.94	9.17	6.10	10.10	8.57	3.82	-3.25E-01	2.52E-01			-1.97E-01	5.24E-01		3.79E-02	8.60E-01			-5.52E-01	1.90E-03		-2.36E-01	1.44E-01		-1.40E+00	2.15E-18	Down	Unigene23691_All//gi|42564060|ref|NP_566388.2|//7.00E-61//Paxneb protein-related [Arabidopsis thaliana]	Unigene23691_All//8.00E-53//AT3G11220| Paxneb protein-related	Unigene23691_All//0.00E+00//TC172250			GO:0006355//GO:0040007//GO:0043234	nr +
Unigene23692_All	1469	2.67	0.93	2.54	8.68	6.84	6.21	4.32	3.44	4.20	-1.52E+00	3.62E-06	Down		-7.41E-02	8.17E-01		-3.43E-01	2.76E-02			-4.83E-01	1.96E-03		-3.27E-01	1.38E-01		-3.85E-02	8.71E-01		Unigene23692_All//gi|115469124|ref|NP_001058161.1|//1.00E-122//Os06g06390600 [Oryza sativa Japonica Group] >gi|51535593|dbj|BAD37537.1| Paxneb protein-like [Oryza sativa Japonica Group] >gi|51536358|dbj|BAD37489.1| Paxneb protein-like [Oryza sativa Japonica Group] >gi|113596200|dbj|BAF20075.1| Os06g0639600 [Oryza sativa Japonica Group]	Unigene23692_All//2.00E-102//AT3G11220| Paxneb protein-related	Unigene23692_All//0.00E+00//TC144763			GO:0006355//GO:0043234	nr -
Unigene23693_All	3376	17.20	17.80	16.15	40.39	41.79	46.89	36.14	59.13	88.21	4.93E-02	5.51E-01			-9.09E-02	2.66E-01		4.93E-02	3.51E-01			2.15E-01	4.85E-08		7.10E-01	4.12E-98		1.29E+00	0.00E+00	Up	Unigene23693_All//gi|79568805|ref|NP_181242.3|//0.00E+00//kinase [Arabidopsis thaliana]	Unigene23693_All//0.00E+00//AT2G37050| kinase	Unigene23693_All//0.00E+00//TC145147			GO:0004702//GO:0006464//GO:0016020//GO:0031410//GO:0032559	nr +
Unigene23694_All	2599	6.38	2.94	5.04	4.85	4.62	3.34	14.79	2.12	6.09	-1.12E+00	6.20E-15	Down		-3.40E-01	1.92E-02		-6.86E-02	7.38E-01			-5.40E-01	5.40E-04		-2.80E+00	1.25E-143	Down	-1.28E+00	2.29E-52	Down	Unigene23694_All//gi|145336784|ref|NP_175929.3|//0.00E+00//AE18 (ACYL-ACTIVATING ENZYME 18); catalytic/ ligase [Arabidopsis thaliana] >gi|29893268|gb|AAPO3028.1| acyl-activating enzyme 18 [Arabidopsis thaliana]	Unigene23694_All//0.00E+00//AT1G55320| AAE18 (ACYL-ACTIVATING ENZYME 18); catalytic/ ligase	Unigene23694_All//0.00E+00//TC151819		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism	GO:0016405//GO:0042445//GO:0042579	nr +
Unigene23695_All	2756	2.77	3.97	4.79	17.01	11.67	10.96	8.64	4.22	3.48	5.19E-01	2.61E-03			7.90E-01	9.08E-07		-5.43E-01	1.26E-14			-6.34E-01	4.03E-17		-1.03E+00	7.72E-23	Down	-1.31E+00	6.72E-34	Down	Unigene23695_All//gi|15231233|ref|NP_190817.1|//1.00E-168//heat shock protein-related [Arabidopsis thaliana] >gi|14917467|gb|AAS49058.1| At3g52490 [Arabidopsis thaliana]	Unigene23695_All//2.00E-152//AT3G52490| heat shock protein-related	Unigene23695_All//7.00E-106//gi|109883498|gb|DW512468.1|DW512468				nr -
Unigene23696_All	2479	8.04	7.05	6.57	36.31	37.16	37.42	13.93	4.25	7.91	-1.90E-01	1.50E-01			-2.91E-01	2.80E-02		3.33E-02	6.26E-01			4.34E-02	5.42E-01		-1.71E+00	3.44E-70	Down	-8.18E-01	5.34E-23		Unigene23696_All//gi|22328012|ref|NP_201064.2|//1.00E-143//binding [Arabidopsis thaliana] >gi|38564286|gb|AAR23722.1| At5g62580 [Arabidopsis thaliana]	Unigene23696_All//5.00E-117//AT5G62580| binding	Unigene23696_All//0.00E+00//TC174806				nr -
Unigene23697_All	3028	3.11	1.72	2.23	13.10	11.60	10.05	4.47	1.60	1.50	-8.52E-01	6.27E-06			-4.78E-01	1.51E-02		-1.75E-01	4.54E-02			-3.81E-01	3.67E-06		-1.48E+00	9.10E-23	Down	-1.57E+00	1.21E-25	Down	Unigene23697_All//gi|22328012|ref|NP_201064.2|//1.00E-145//binding [Arabidopsis thaliana] >gi|38564286|gb|AAR23722.1| At5g62580 [Arabidopsis thaliana]	Unigene23697_All//3.00E-118//AT5G62580| binding	Unigene23697_All//0.00E+00//TC174806				nr -
Unigene23698_All	2479	43.82	268.15	85.04	19.67	32.38	40.10	18.57	29.93	26.50	2.61E+00	0.00E+00	Up		9.57E-01	6.48E-137		7.19E-01	1.92E-39			1.03E+00	1.92E-80	Up	6.88E-01	4.97E-35		5.13E-01	3.38E-19		Unigene23698_All//gi|33637487|gb|AQ23899.1|//0.00E+00//RSH2 [Nicotiana tabacum]	Unigene23698_All//0.00E+00//AT3G14050| RSH2 (RELA-SPOT HOMOLOG 2); GTP diphosphokinase	Unigene23698_All//0.00E+00//gi|73851052|gb|DT460072.1|DT460072			GO:0006950//GO:0008617//GO:0009536//GO:0009725//GO:0015291//GO:0015893//GO:0016020//GO:0016278	nr +
Unigene23699_All	1863	10.36	13.25	16.46	20.62	29.72	51.93	37.97	14.18	48.35	3.54E-01	1.37E-03			6.68E-01	3.14E-11		5.28E-01	6.10E-16			1.33E+00	3.46E-118	Up	-1.42E+00	6.24E-109	Down	3.49E-01	3.39E-13		Unigene23699_All//gi|239056192|emb|CAQ68629.1|//0.00E+00//pyruvate kinase [Vitis vinifera]	Unigene23699_All//0.00E+00//AT5G08570| pyruvate kinase, putative	Unigene23699_All//0.00E+00//TC176691		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0006007//GO:0010038//GO:0016020//GO:0016301//GO:0031420//GO:0032559//GO:0044424	nr -
Unigene2370_All	939	68.42	110.57	98.33	56.02	59.63	61.47	60.02	85.24	123.80	6.92E-01	3.38E-40			5.23E-01	3.17E-21		9.00E-02	2.81E-01			1.34E-01	7.87E-02		5.06E-01	4.35E-22		1.04E+00	2.09E-112	Up	Unigene2370_All//gi|98961095|gb|AB539031.1|//9.00E-37//At1g78890 [Arabidopsis thaliana]	Unigene2370_All//6.00E-37//AT1G78890| unknown protein	Unigene2370_All//0.00E+00//TC144811				nr +
Unigene23700_All	1472	3.55	7.02	3.94	4.20	5.40	10.68	7.47	7.87	10.53	9.82E-01	6.53E-08			1.50E-01	6.06E-01		3.65E-01	8.44E-02			1.35E+00	6.60E-20	Up	7.47E-02	6.61E-01		4.95E-01	5.94E-05		Unigene23700_All//gi|51870705|dbj|BAD42432.1|//7.00E-61//bZip transcription factor [Psophocarpus tetragonolobus]	Unigene23700_All//2.00E-31//AT2G46270| GBF3 (G-BOX BINDING FACTOR 3); sequence-specific DNA binding / transcription factor	Unigene23700_All//0.00E+00//TC166186	bZIP		GO:0003677//GO:0006351//GO:0009725//GO:0010468//GO:0044444	nr +
Unigene23701_All	1084	14.00	26.88	18.03	20.50	31.16	43.58	25.74	24.75	29.81	9.41E-01	1.68E-19			3.65E-01	5.37E-03		6.05E-01	1.70E-12			1.09E+00	3.36E-42	Up	-5.65E-02	6.51E-01		2.11E-01	1.35E-02		Unigene23701_All//gi|51870705|dbj|BAD42432.1|//1.00E-114//bZip transcription factor [Psophocarpus tetragonolobus]	Unigene23701_All//5.00E-71//AT2G46270| GBF3 (G-BOX BINDING FACTOR 3); sequence-specific DNA binding / transcription factor	Unigene23701_All//0.00E+00//gi|164269221|gb|ES808495.1|ES808495	bZIP		GO:0003677//GO:0006350//GO:0009725//GO:0044444	nr -
Unigene23702_All	2221	23.96	15.44	24.79	10.59	10.48	9.23	23.17	12.61	11.17	-6.33E-01	4.52E-18			4.93E-02	5.89E-01		-1.44E-02	9.17E-01			-1.98E-01	1.08E-01		-8.78E-01	5.38E-37		-1.05E+00	3.65E-51	Down	Unigene23702_All//gi|30686602|ref|NP_194193.2|//0.00E+00//PGI1 (PHOSPHOGLUCOSE ISOMERASE 1); glucose-6-phosphate isomerase [Arabidopsis thaliana] >gi|110742488|dbj|BAE99162.1| glucose-6-phosphate isomerase [Arabidopsis thaliana]	Unigene23702_All//0.00E+00//AT4G24620| PGI1 (PHOSPHOGLUCOSE ISOMERASE 1); glucose-6-phosphate isomerase	Unigene23702_All//0.00E+00//TC158737		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway	GO:0002376//GO:0003676//GO:0006007//GO:0006073//GO:0009526//GO:0009532//GO:0009908//GO:0016861//GO:0032559	nr -
Unigene23706_All	1736	2.56	5.95	2.39	2.38	3.09	2.76	1.51	0.99	1.72	1.22E+00	7.57E-11	Up		-9.86E-02	7.43E-01		3.78E-01	1.62E-01			2.12E-01	5.01E-01		-6.13E-01	8.10E-02		1.89E-01	5.97E-01		Unigene23706_All//gi|224078898|ref|XP_002305671.1|//1.00E-109//bromodomain protein [Populus trichocarpa] >gi|222848635|gb|EEE86182.1| bromodomain protein [Populus trichocarpa]	Unigene23706_All//2.00E-89//AT1G61215| BRD4 (BROMODOMAIN 4); DNA binding	Unigene23706_All//4.00E-91//gi|78342832|gb|DT563106.1|DT563106				nr +
Unigene23709_All	2690	1.19	0.66	0.71	10.26	6.77	3.21	7.32	5.05	3.70	-8.48E-01	1.45E-02			-7.36E-01	4.42E-02		-5.99E-01	2.00E-10			-1.68E+00	1.91E-48	Down	-5.37E-01	1.18E-06		-9.84E-01	3.79E-18		Unigene23709_All//gi|115475676|ref|NP_001061434.1|//0.00E+00//Os08g0276400 [Oryza sativa Japonica Group] >gi|113623403|dbj|BAF23348.1| Os08g0276400 [Oryza sativa Japonica Group]	Unigene23709_All//0.00E+00//AT2G24230| leucine-rich repeat transmembrane protein kinase, putative	Unigene23709_All//0.00E+00//ES804750			GO:0004713//GO:0006464//GO:0016020//GO:0016791//GO:0031410//GO:0032559//GO:0043231	nr -
Unigene2371_All	520	7.35	6.82	6.55	33.15	24.44	21.71	10.90	4.98	3.91	-1.07E-01	7.25E-01			-1.64E-01	6.35E-01		-4.40E-01	4.38E-04			-6.10E-01	2.58E-06		-1.13E+00	7.68E-07	Down	-1.48E+00	2.50E-10	Down	Unigene2371_All//gi|48209969|gb|AAT40532.1|//3.00E-48//hydrolase, alpha/beta fold family protein [Solanum demissum]	Unigene2371_All//3.00E-42//AT3G09690| hydrolase, alpha/beta fold family protein	Unigene2371_All//2.00E-158//DW502330			GO:0003824	nr +
Unigene23712_All	550	1.90	1.20	2.90	2.72	1.31	0.41	0.54	0.46	0.22	-6.68E-01	3.23E-01			6.10E-01	2.61E-01		-1.05E+00	4.31E-02			-2.73E+00	2.66E-05	Down	-2.39E-01	8.40E-01		-1.31E+00	3.13E-01		Unigene23712_All//gi|264664501|sp|C0LGK9.1|Y2242_ARATH//2.00E-87//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At2g24230; Flags: Precursor >gi|224589521|gb|ACN59294.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23712_All//8.00E-88//AT2G24230| leucine-rich repeat transmembrane protein kinase, putative	Unigene23712_All//0.00E+00//gi|164250456|gb|ES826759.1|ES826759			GO:0004713//GO:0006464//GO:0007167//GO:0016791//GO:0031410//GO:0032559	nr -
Unigene23713_All	2911	0.31	0.17	0.26	1.95	1.51	1.16	2.06	1.03	0.41	-8.11E-01	2.68E-01			-2.55E-01	7.17E-01		-3.66E-01	1.53E-01			-7.46E-01	2.40E-03		-9.96E-01	4.96E-06		-2.33E+00	2.04E-19	Down	Unigene23713_All//gi|264664501|sp|C0LGK9.1|Y2242_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At2g24230; Flags: Precursor >gi|224589521|gb|ACN59294.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23713_All//0.00E+00//AT2G24230| leucine-rich repeat transmembrane protein kinase, putative	Unigene23713_All//0.00E+00//ES804750			GO:0004713//GO:0006464//GO:0007167//GO:0016020//GO:0016791//GO:0031410//GO:0032559//GO:0043231	nr +
Unigene23717_All	1952	20.93	6.96	25.86	26.31	19.58	1.62	124.98	87.75	50.80	-1.59E+00	5.31E-61	Down		3.05E-01	8.09E-05		-4.26E-01	2.21E-10			-4.02E+00	7.86E-239	Down	-5.10E-01	1.16E-66		-1.30E+00	0.00E+00	Down	Unigene23717_All//gi|15220671|ref|NP_173733.1|//1.00E-154//pectinesterase family protein [Arabidopsis thaliana] >gi|75278018|sp|Q49298.1|PME6_ARATH RecName: Full=Probable pectinesterase/pectinesterase inhibitor 6; Includes: RecName: Full=Pectinesterase inhibitor 6; AltName: Full=Pectin methylesterase inhibitor 6; Includes: RecName: Full=Pectinesterase 6; Short=PE 6; AltName: Full=Pectin methylesterase 6; Short=AtPME6; Flags: Precursor >gi|9295687|gb|AAF86993.1|AC005292_2_F26F24.2 [Arabidopsis thaliana]	Unigene23717_All//2.00E-154//AT1G23200| pectinesterase family protein	Unigene23717_All//0.00E+00//CO118188		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0030234//GO:0030312//GO:0071555	nr +
Unigene23718_All	537	5.65	3.87	5.45	10.20	12.89	13.88	7.87	11.83	16.91	-5.47E-01	1.29E-01			-5.12E-02	8.95E-01		3.37E-01	1.52E-01			4.44E-01	4.26E-02		5.87E-01	4.90E-03		1.10E+00	2.12E-10	Up	Unigene23718_All//gi|224082450|ref|XP_002306697.1|//2.00E-49//f-box family protein [Populus trichocarpa] >gi|222856146|gb|EEE93693.1| f-box family protein [Populus trichocarpa]	Unigene23718_All//3.00E-46//AT1G25280| ArTLP10 (TUBBY LIKE PROTEIN 10); phosphoric diester hydrolase/ transcription factor	Unigene23718_All//0.00E+00//gi|78337625|gb|DT557899.1|DT557899	TUB		GO:0010468//GO:0016020//GO:0042578	nr +
Unigene2372_All	1957	2.89	2.25	2.31	9.16	6.84	9.95	7.60	3.37	2.79	-3.58E-01	1.63E-01			-3.20E-01	2.41E-01		-4.21E-01	6.05E-04			1.18E-01	4.35E-01		-1.17E+00	1.15E-17	Down	-1.45E+00	6.45E-25	Down	Unigene2372_All//gi|48209969|gb|AAT40532.1|//1.00E-142//hydrolase, alpha/beta fold family protein [Solanum demissum]	Unigene2372_All//6.00E-133//AT3G09690| hydrolase, alpha/beta fold family protein	Unigene2372_All//0.00E+00//DT465562			GO:0003824	nr +

Unigene23722_All	2059	3.10	2.14	1.24	2.20	2.98	1.75	5.01	2.27	2.55	-5.34E-01	2.25E-02		-1.32E+00	1.77E-07	Down	4.35E-01	7.24E-02		-3.27E-01	2.92E-01		-1.14E+00	5.52E-12	Down	-9.72E-01	9.55E-10		Unigene23722_All//gi|225424368|ref|XP_002281246.1|//1.00E-174//PREDICTED: similar to SET domain-containing protein [Vitis vinifera]	Unigene23722_All//6.00E-162//AT1G24610| SET domain-containing protein	Unigene23722_All//0.00E+00//TC144497			GO:0043231	nr +
Unigene23724_All	943	1.44	1.88	0.68	3.70	4.38	3.40	2.11	0.75	1.14	3.83E-01	4.34E-01		-1.09E+00	7.48E-02		2.45E-01	4.78E-01		-1.21E-01	7.28E-01		-1.48E+00	5.15E-04	Down	-8.86E-01	2.45E-02		Unigene23724_All//gi|30725614|gb|AP37829.1|//3.00E-83//At5g12470 [Arabidopsis thaliana]	Unigene23724_All//1.00E-84//AT5G12470| unknown protein	Unigene23724_All//0.00E+00//TC142182			GO:0009528	nr -
Unigene23725_All	938	71.34	28.85	53.99	214.66	194.20	204.87	52.20	40.77	34.87	-1.31E+00	3.00E-74	Down	-4.02E-01	8.00E-10		-1.45E-01	2.08E-05		-6.73E-02	9.92E-02		-3.56E-01	1.24E-07		-5.82E-01	4.05E-18		Unigene23725_All//gi|30725614|gb|AP37829.1|//3.00E-72//At5g12470 [Arabidopsis thaliana]	Unigene23725_All//3.00E-65//AT5G12470| unknown protein	Unigene23725_All//0.00E+00//TC131666			GO:0009528	nr -
Unigene23728_All	3634	4.23	2.18	2.34	6.69	5.87	4.41	8.20	2.44	3.91	-9.61E-01	4.83E-11		-8.52E-01	9.68E-09		-1.90E-01	1.04E-01		-6.01E-01	2.12E-08		-1.75E+00	1.77E-62	Down	-1.07E+00	9.93E-31	Down	Unigene23728_All//gi|7529272|emb|CAB86487.1|//7.00E-49//ataxia-telangiectasia mutated protein (Atm) [Arabidopsis thaliana]	Unigene23728_All//2.00E-29//AT3G48190| ATM (ATAXIA-TELANGIECTASIA MUTATED); 1-phosphatidylinositol-3-phosphate 5-kinase	Unigene23728_All//0.00E+00//TC158560				nr -
Unigene23729_All	760	3.30	7.07	2.24	7.14	6.07	6.36	8.90	9.68	4.77	1.10E+00	3.14E-05	Up	-5.60E-01	1.86E-01		-2.35E-01	4.07E-01		-1.68E-01	5.85E-01		1.21E-01	6.11E-01		-9.00E-01	5.40E-06		Unigene23729_All//gi|18076148|emb|CAC80702.1|//4.00E-50//N-acetylglucosaminyltransferase I [Nicotiana tabacum]	Unigene23729_All//4.00E-47//AT4G38240| CGL1 (COMPLEX GLYCAN LESS 1); alpha-1,3-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase/ protein N-acetylglucosaminyltransferase/ transferase, transferring glycosyl groups	Unigene23729_All//0.00E+00//DT463328		ko00510|N-Glycan biosynthesis	GO:0006487//GO:0006970//GO:0008375//GO:0012505//GO:0031410//GO:0043231	nr +
Unigene2373_All	1617	2.46	5.17	2.01	13.28	23.17	31.76	91.12	240.82	176.40	1.07E+00	1.95E-07	Up	-2.92E-01	3.99E-01		8.03E-01	2.06E-22		1.26E+00	1.43E-57	Up	1.40E+00	0.00E+00	Up	9.53E-01	3.00E-236		Unigene2373_All//gi|15237530|ref|NP_198915.1|//1.00E-100//GLIP1 (GDSL LIPASE1); carboxylesterase/ lipase [Arabidopsis thaliana] >gi|75171498|sp|Q9FLN0.1|GLIP1_ARATH RecName: Full=GDSL esterase/lipase 1; AltName: Full=Extracellular lipase 1; Flags: Precursor >gi|9759145|dbj|BAB09701.1| GDSL-motif lipase/hydrolase-like protein [Arabidopsis thaliana]	Unigene2373_All//2.00E-101//AT5G40990| GLIP1 (GDSL LIPASE1); carboxylesterase/ lipase	Unigene2373_All//0.00E+00//TC134290				nr -
Unigene23732_All	1002	9.24	3.19	2.71	14.96	10.34	3.97	9.71	1.88	4.06	-1.54E+00	1.03E-13	Down	-1.77E+00	7.00E-16	Down	-5.33E-01	6.71E-05		-1.92E+00	8.35E-32	Down	-2.37E+00	1.34E-30	Down	-1.26E+00	1.47E-13	Down	Unigene23732_All//gi|15220206|ref|NP_178186.1|//2.00E-94//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|6503282|gb|AAF14658.1|AC011713_6 Contains similarity to gb|AF092102 G-protein beta subunit git5p from Schizosaccharomyces pombe and contains 2 PF|00400|WD domain, G-beta repeat domains [Arabidopsis thaliana]	Unigene23732_All//4.00E-95//AT1G80710| transducin family protein / WD-40 repeat family protein	Unigene23732_All//0.00E+00//gi|164355271|gb|ES808242.1|ES808242		ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair		nr -
Unigene23733_All	1089	1.78	0.56	2.59	2.52	1.42	2.24	3.61	0.69	1.10	-1.67E+00	7.92E-04	Down	5.44E-01	1.65E-01		-8.22E-01	2.23E-02		-1.68E-01	6.96E-01		-2.39E+00	6.96E-13	Down	-1.72E+00	5.21E-09	Down	Unigene23733_All//gi|297839865|ref|XP_002887814.1|//3.00E-71//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333655|gb|EFH64073.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23733_All//2.00E-71//AT1G80710| transducin family protein / WD-40 repeat family protein	Unigene23733_All//0.00E+00//ES805674				nr -
Unigene23734_All	1962	7.73	2.94	1.19	9.11	6.32	4.24	11.23	2.75	4.93	-1.39E+00	4.14E-19	Down	-2.70E+00	4.02E-43	Down	-5.29E-01	1.18E-05		-1.11E+00	6.35E-17	Down	-2.03E+00	1.61E-56	Down	-1.19E+00	5.01E-27	Down	Unigene23734_All//gi|297839865|ref|XP_002887814.1|//1.00E-144//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333655|gb|EFH64073.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23734_All//1.00E-134//AT1G80710| transducin family protein / WD-40 repeat family protein	Unigene23734_All//0.00E+00//TC149415		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair		nr -
Unigene23735_All	1176	1.65	2.67	2.67	3.77	3.46	2.65	4.64	2.77	2.24	6.99E-01	4.63E-02		6.99E-01	5.72E-02		-1.26E-01	7.05E-01		-5.09E-01	8.33E-02		-7.42E-01	1.07E-03		-1.05E+00	3.17E-06	Down	Unigene23735_All//gi|186511602|ref|NP_849538.2|//1.00E-68//kinase [Arabidopsis thaliana] >gi|281185491|sp|Q8VZG8.3|Y4885_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g08850; Flags: Precursor >gi|18086327|gb|AAL57627.1|AT4g08850/T32A17_160 [Arabidopsis thaliana] >gi|224589610|gb|ACN59338.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23735_All//7.00E-66//AT4G08850| kinase	Unigene23735_All//3.00E-140//ES811264		ko03410|Base excision repair		nr -
Unigene23736_All	2101	1.25	1.04	1.22	2.16	1.61	1.25	2.39	0.95	1.37	-2.64E-01	5.14E-01		-3.34E-02	9.49E-01		-4.26E-01	1.37E-01		-7.91E-01	4.78E-03		-1.33E+00	1.04E-07	Down	-8.11E-01	4.57E-04		Unigene23736_All//gi|16924042|gb|AAL31654.1|AC079179_9/6.00E-58//Putative protein kinase [Oryza sativa] >gi|20042880|gb|AAM08708.1|AC116601_1 Putative protein kinase [Oryza sativa Japonica Group] >gi|31429913|gb|AAP51897.1| Leucine Rich Repeat family protein [Oryza sativa (japonica cultivar-group)]	Unigene23736_All//1.00E-67//AT4G08850| kinase	Unigene23736_All//0.00E+00//ES805497		ko03410|Base excision repair	GO:0016301	nr -
Unigene23737_All	2625	25.19	12.35	13.51	20.00	20.07	46.57	23.42	54.63	38.12	-1.03E+00	3.08E-50	Down	-8.99E-01	7.05E-39		5.00E-03	9.58E-01		1.22E+00	4.46E-130	Up	1.22E+00	3.04E-174	Up	7.03E-01	6.90E-50		Unigene23737_All//gi|117557150|gb|ABK35752.1|//0.00E+00//sulfate transporter [Populus tremula x Populus alba]	Unigene23737_All//0.00E+00//AT5G13550| SULTR4;1; sulfate transmembrane transporter	Unigene23737_All//0.00E+00//TC131024			GO:0015103//GO:0015291//GO:0015698//GO:0031224//GO:0043231	nr -
Unigene23738_All	2365	27.79	8.25	12.32	109.70	72.28	30.61	40.12	19.00	12.26	-1.75E+00	2.99E-112	Down	-1.17E+00	1.23E-59	Down	-6.02E-01	1.71E-95		-1.84E+00	0.00E+00	Down	-1.08E+00	8.59E-95	Down	-1.71E+00	1.18E-196	Down	Unigene23738_All//gi|224090949|ref|XP_002309128.1|//0.00E+00//auxin influx carrier component [Populus trichocarpa] >gi|222855104|gb|EEE92651.1| auxin influx carrier component [Populus trichocarpa]	Unigene23738_All//0.00E+00//AT2G38120| AUX1 (AUXIN RESISTANT 1); amino acid transmembrane transporter/ auxin binding / auxin influx transmembrane transporter/ transporter	Unigene23738_All//0.00E+00//TC144248			GO:0001738//GO:0005275//GO:0009630//GO:0009755//GO:0010102//GO:0015291//GO:0015837//GO:0031224//GO:0048364//GO:0042562//GO:0043231//GO:0048764//GO:0051707//GO:0060918//GO:0080161	nr +
Unigene2374_All	2049	26.05	17.63	12.50	49.26	51.76	51.42	34.38	22.56	34.65	-5.63E-01	8.12E-15		-1.06E+00	3.76E-41	Down	7.16E-02	2.23E-01		6.21E-02	3.16E-01		-6.08E-01	6.90E-27		1.13E-02	8.75E-01		Unigene2374_All//gi|108711072|gb|ABF98867.1|YT521-B-like family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549735|dbj|BAF13178.1| Os03g0748000 [Oryza sativa Japonica Group]	Unigene2374_All//1.00E-110//AT5G61020| ECT3	Unigene2374_All//0.00E+00//TC162075				nr +
Unigene23741_All	671	2.42	2.42	1.19	3.93	3.49	4.24	11.15	6.85	4.33	-5.00E-04	9.97E-01		-1.02E+00	6.14E-02		-1.73E-01	6.81E-01		1.08E-01	7.91E-01		-7.03E-01	2.09E-04		-1.36E+00	6.40E-12	Down	Unigene23741_All//gi|297721981|ref|NP_001173354.1|//4.00E-17//Os03g0253800 [Oryza sativa Japonica Group] >gi|108707218|gb|ABF95013.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255674378|dbj|BAH92082.1| Os03g0253800 [Oryza sativa Japonica Group]	Unigene23741_All//4.00E-18//AT4G00026| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Mitochondrial import inner membrane translocase, subunit Tim21 (InterPro:IPR013261); Has 168 Blast hits to 168 proteins in 84 species: Archae - 0; Bacteria - 0; Metazoa - 92; Fungi - 52; Plants - 20; Viruses - 0; Other Eukarryotes - 4 (source: NCBI BLink).	Unigene23741_All//0.00E+00//TC175717			GO:0009536	nr -
Unigene23743_All	1096	4.11	3.19	2.23	6.05	4.37	7.21	4.28	1.53	2.14	-3.64E-01	2.14E-01		-8.77E-01	3.24E-03		-4.69E-01	3.46E-02		2.55E-01	2.71E-01		-1.49E+00	1.80E-08	Down	-9.98E-01	4.32E-05		Unigene23743_All//gi|297721981|ref|NP_001173354.1|//2.00E-50//Os03g0253800 [Oryza sativa Japonica Group] >gi|108707218|gb|ABF95013.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255674378|dbj|BAH92082.1| Os03g0253800 [Oryza sativa Japonica Group]	Unigene23743_All//8.00E-50//AT4G00026| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Mitochondrial import inner membrane translocase, subunit Tim21 (InterPro:IPR013261); Has 168 Blast hits to 168 proteins in 84 species: Archae - 0; Bacteria - 0; Metazoa - 92; Fungi - 52; Plants - 20; Viruses - 0; Other Eukarryotes - 4 (source: NCBI BLink).	Unigene23743_All//0.00E+00//TC175717			GO:0043231	nr -
Unigene23744_All	1147	62.68	31.94	30.41	88.99	76.86	81.70	36.01	23.32	25.39	-9.73E-01	8.04E-50		-1.04E+00	5.69E-54	Down	-2.11E-01	1.03E-05		-1.23E-01	2.40E-02		-6.27E-01	5.47E-17		-5.04E-01	4.13E-12		Unigene23744_All//gi|59956974|emb|CAI11451.1|//0.00E+00//alpha-1,6-xylosyltransferase [Gossypium raimondii]	Unigene23744_All//0.00E+00//AT4G02500| XT2 (UDP-XYLOSYLTRANSFERASE 2); UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups / xyloglucan 6-xylosyltransferase	Unigene23744_All//0.00E+00//TC149619			GO:0008194//GO:0009250//GO:0031224//GO:0042285//GO:0048588	nr -
Unigene23747_All	3715	0.04	0.49	0.32	0.08	0.32	0.18	0.40	0.69	0.35	3.54E+00	2.15E-07	Up	2.90E+00	4.34E-04	Up	1.97E+00	3.92E-03		1.18E+00	2.08E-01		7.85E-01	2.67E-02		-1.71E-01	7.13E-01		Unigene23747_All//gi|297819878|ref|XP_002877822.1|//0.00E+00//ethylene-overproduction protein 1 [Arabidopsis lyrata subsp. lyrata] >gi|297323660|gb|EFH54081.1| ethylene-overproduction protein 1 [Arabidopsis lyrata subsp. lyrata]	Unigene23747_All//0.00E+00//AT3G51770| ETO1 (ETHYLENE OVERPRODUCER 1); protein binding, bridging	Unigene23747_All//0.00E+00//ES792429			GO:0005488	nr -
Unigene2375_All	2148	8.67	5.90	6.47	61.97	50.13	35.45	22.50	8.33	14.50	-5.56E-01	1.32E-05		-4.22E-01	1.56E-03		-3.06E-01	3.21E-14		-8.06E-01	2.48E-72		-1.43E+00	1.21E-75	Down	-6.33E-01	1.12E-20		Unigene2375_All//gi|297817214|ref|XP_002876490.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323328|gb|EFH52749.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2375_All//0.00E+00//AT3G59110| protein kinase family protein	Unigene2375_All//2.00E-164//DW510835		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016020//GO:0032559	nr +

Unigene23753_All	2062	21.67	13.24	10.69	43.34	48.35	111.16	82.12	158.30	140.29	-7.10E-01	1.48E-18		-1.02E+00	1.86E-32	Down	1.58E-01	2.02E-03		1.36E+00	4.03E-288	Up	9.47E-01	1.07E-261		7.73E-01	6.73E-168		Unigene23753_All//gi|224112417|ref|XP_002316182.1|//0.00E+00//amino acid transporter [Populus trichocarpa] >gi|222865222|gb|EEF02353.1| amino acid transporter [Populus trichocarpa]	Unigene23753_All//2.00E-142//AT3G56200| amino acid transporter family protein	Unigene23753_All//0.00E+00//TC166801			GO:0031224	nr +
Unigene23755_All	2011	5.88	19.07	7.04	44.34	47.35	41.41	34.38	32.05	66.33	1.70E+00	1.49E-62	Up	2.61E-01	1.12E-01		9.47E-02	1.05E-01		-9.85E-02	1.14E-01		-1.01E-01	1.11E-01		9.48E-01	6.09E-110		Unigene23755_All//gi|15221327|ref|NP_172704.1|//1.00E-175//ACR8; amino acid binding [Arabidopsis thaliana] >gi|8778647|gb|AAF79655.1|AC025416_29 F5O11.14 [Arabidopsis thaliana] >gi|22138106|gb|AAM93433.1| ACR8 [Arabidopsis thaliana] >gi|111074504|gb|ABH04625.1| At1g12420 [Arabidopsis thaliana]	Unigene23755_All//5.00E-171//AT1G12420| ACR8; amino acid binding	Unigene23755_All//0.00E+00//TC162983			GO:0031406	nr +
Unigene2376_All	2546	5.51	4.20	3.33	12.78	18.26	9.47	12.06	2.25	3.47	-3.91E-01	9.79E-03		-7.28E-01	2.77E-06		5.15E-01	6.82E-13		-4.32E-01	2.44E-06		-2.42E+00	1.28E-97	Down	-1.80E+00	1.28E-68	Down	Unigene2376_All//gi|15231029|ref|NP_190742.1|//0.00E+00//IMK2 (INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|75302755|sp|Q9SC74.1|IMK2_ARATH RecName: Full=Probably inactive leucine-rich repeat receptor-like protein kinase IMK2; AltName: Full=Protein INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 2; Flags: Precursor >gi|13937246|gb|AAK50115.1|AF372978_1 AT3g51740/T18N14_120 [Arabidopsis thaliana] >gi|30102480|gb|AAP21158.1| At3g51740/T18N14_120 [Arabidopsis thaliana] >gi|224589600|gb|ACN59333.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene2376_All//6.00E-106//AT3G51740| IMK2 (INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene2376_All//0.00E+00//C0091793		ko04626|Plant-pathogen interaction	GO:0005618//GO:0016020//GO:0016301	nr +
Unigene23760_All	1913	7.77	5.22	6.96	13.12	14.53	14.35	5.83	12.13	5.50	-5.74E-01	7.25E-05		-1.59E-01	3.54E-01		1.47E-01	2.05E-01		1.29E-01	2.90E-01		1.06E+00	5.97E-23	Up	-8.58E-02	6.14E-01		Unigene23760_All//gi|224055111|ref|XP_002298418.1|//5.00E-42//f-box family protein [Populus trichocarpa] >gi|222845676|gb|EEE83223.1| f-box family protein [Populus trichocarpa]	Unigene23760_All//4.00E-26//AT3G23880| F-box family protein	Unigene23760_All//0.00E+00//TC176442				nr -
Unigene23761_All	1691	1.39	0.48	0.88	1.97	1.51	1.58	1.88	2.79	0.40	-1.54E+00	4.45E-04	Down	-6.59E-01	1.35E-01		-3.89E-01	2.69E-01		-3.25E-01	3.93E-01		5.75E-01	2.08E-02		-2.23E+00	4.13E-10	Down	Unigene23761_All//gi|224089629|ref|XP_002308787.1|//5.00E-32//f-box family protein [Populus trichocarpa] >gi|222854763|gb|EEE92310.1| f-box family protein [Populus trichocarpa]	Unigene23761_All//4.00E-21//AT4G12560| F-box family protein	Unigene23761_All//0.00E+00//TC176442				nr -
Unigene23765_All	2059	23.71	19.44	19.40	29.01	25.67	26.65	46.08	32.82	22.60	-2.86E-01	1.77E-04		-2.90E-01	2.55E-04		-1.76E-01	9.43E-03		-1.22E-01	1.08E-01		-4.89E-01	1.51E-24		-1.03E+00	3.77E-90	Down	Unigene23765_All//gi|222424098|dbj|BAH20009.1|//0.00E+00//AT1G80910 [Arabidopsis thaliana]	Unigene23765_All//0.00E+00//AT1G80910| unknown protein	Unigene23765_All//0.00E+00//TC138094				nr +
Unigene23766_All	2331	5.16	3.35	5.76	9.57	13.06	10.42	7.56	3.39	3.38	-6.25E-01	1.23E-04		1.57E-01	3.87E-01		4.48E-01	8.56E-07		1.23E-01	3.57E-01		-1.16E+00	2.13E-20	Down	-1.16E+00	4.33E-21	Down	Unigene23766_All//gi|225452080|ref|XP_002284052.1|//0.00E+00//PREDICTED: plastid hexose transporter [Vitis vinifera] >gi|51574116|gb|AAU07980.1| plastid hexose transporter [Vitis vinifera]	Unigene23766_All//0.00E+00//AT5G16150| PGLCT (PLASTIDIC GLC TRANSLOCATOR); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene23766_All//0.00E+00//TC167742			GO:0006810//GO:0009526//GO:0022891//GO:0031224	nr +
Unigene2377_All	2194	11.54	10.72	12.84	23.34	22.19	20.69	14.63	4.78	6.17	-1.07E-01	3.79E-01		1.54E-01	1.89E-01		-7.27E-02	4.22E-01		-1.74E-01	2.55E-02		-1.61E+00	6.32E-60	Down	-1.24E+00	5.77E-42	Down	Unigene2377_All//gi|297840355|ref|XP_002888059.1|//0.00E+00//patatin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333900|gb|EFH64318.1| patatin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2377_All//0.00E+00//AT1G61850| galactolipase/ phospholipase	Unigene2377_All//0.00E+00//TC139319			GO:0003824//GO:0005488//GO:0044238	nr -
Unigene23772_All	1017	4.58	4.14	2.04	6.86	4.94	5.77	9.89	8.67	10.50	-1.47E-01	6.13E-01		-1.17E+00	9.00E-05	Down	-4.72E-01	2.81E-02		-2.48E-01	3.18E-01		-1.90E-01	2.94E-01		8.55E-02	6.27E-01		Unigene23772_All//gi|3785977|gb|AAC67324.1|//3.00E-94//similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana] >gi|202604020|gb|AAM13108.1| similar to axi 1 protein [Arabidopsis thaliana] >gi|22136280|gb|AAM91218.1| similar to axi 1 protein [Arabidopsis thaliana] >gi|110742513|dbj|BAE99174.1| similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana]	Unigene23772_All//6.00E-95//AT2G01480| unknown protein	Unigene23772_All//0.00E+00//TC175825				nr +
Unigene23774_All	1770	47.56	71.62	38.36	51.28	54.65	57.79	77.01	157.48	110.49	5.91E-01	4.51E-37		-3.10E-01	9.32E-08		9.19E-02	1.15E-01		1.73E-01	8.44E-04		1.03E+00	1.00E-257	Up	5.21E-01	6.77E-57		Unigene23774_All//gi|224109872|ref|XP_002315338.1|//6.00E-97//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222864378|gb|EEF01509.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene23774_All//1.00E-54//AT5G04410| NAC2; transcription factor	Unigene23774_All//0.00E+00//TC163580	NAC		GO:0009642//GO:0009813//GO:0010557//GO:0030528//GO:0043231	nr -
Unigene23775_All	1866	96.34	114.86	108.04	91.06	83.45	92.96	20.89	46.25	13.81	2.54E-01	1.64E-13		1.65E-01	9.22E-06		-1.26E-01	1.01E-03		2.99E-02	5.69E-01		1.15E+00	4.39E-95	Up	-5.97E-01	3.02E-15		Unigene23775_All//gi|297800796|ref|XP_002868282.1|//3.00E-84//enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314118|gb|EFH44541.1| enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23775_All//2.00E-70//AT4G14430| IBR10 (INDOLE-3-BUTYRIC ACID RESPONSE 10); catalytic/ dodecenoyl-CoA delta-isomerase	Unigene23775_All//0.00E+00//TC130523		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism	GO:0005488//GO:0006631//GO:0009733//GO:0009850//GO:0016856//GO:0016863//GO:0042579//GO:0048588	nr -
Unigene23777_All	2193	9.28	11.88	7.07	31.05	42.08	36.25	13.19	38.14	8.85	3.56E-01	9.14E-04		-3.93E-01	2.05E-03		4.39E-01	6.94E-19		2.23E-01	1.20E-04		1.53E+00	1.33E-143	Up	-5.76E-01	6.94E-11		Unigene23777_All//gi|18409132|ref|NP_564944.1|//1.00E-103//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75336852|sp|Q9SY71.1|BH030_ARATH RecName: Full=Transcription factor bHLH30; AltName: Full=Transcription factor EN 53; AltName: Full=bHLH transcription factor bHLH030; AltName: Full=Basic helix-loop-helix protein 30; Short=bHLH 30; Short=AtbHLH30	Unigene23777_All//4.00E-73//AT1G68810| basic helix-loop-helix (bHLH) family protein	Unigene23777_All//0.00E+00//DW479206	bHLH		ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0005488//GO:0009267//GO:0009813//GO:0010468//GO:0043231//GO:0048468//GO:0048513	nr +
Unigene2378_All	2151	74.48	47.11	69.22	14.61	13.18	8.69	0.73	0.16	0.35	-6.61E-01	5.66E-57		-1.06E-01	1.83E-02		-1.49E-01	1.57E-01		-7.49E-01	1.70E-15		-2.23E+00	3.66E-05	Down	-1.05E+00	2.17E-02		Unigene2378_All//gi|22329512|ref|NP_172718.2|//0.00E+00//glucose-methanol-choline (GMC) oxidoreductase family protein [Arabidopsis thaliana] >gi|51536604|gb|AAU05540.1| At1g12570 [Arabidopsis thaliana]	Unigene2378_All//0.00E+00//AT1G12570| glucose-methanol-choline (GMC) oxidoreductase family protein	Unigene2378_All//0.00E+00//TC154931		ko00460|Cyanoamino acid metabolism	GO:0016491//GO:0016832//GO:0030554//GO:0031410//GO:0044281	nr +
Unigene23784_All	2460	5.53	14.67	8.07	21.93	16.80	17.40	21.98	26.59	6.69	1.41E+00	6.96E-45	Up	5.46E-01	1.83E-05		-3.85E-01	4.45E-09		-3.34E-01	1.79E-06		2.75E-01	2.25E-06		-1.72E+00	5.11E-113	Down	Unigene23784_All//gi|20856863|gb|AAM26687.1|//1.00E-100//AT3G50930/F18B3_210 [Arabidopsis thaliana]	Unigene23784_All//0.00E+00//AT3G50930| BCS1 (CYTOCHROME BC1 SYNTHESIS); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene23784_All//0.00E+00//gi|73863645|gb|DT466384.1|DT466384				nr +
Unigene23795_All	686	0.38	0.15	0.00	3.20	1.66	0.66	3.14	0.85	0.35	-1.37E+00	3.83E-01		-8.57E+00	8.57E-02		-9.48E-01	2.09E-02		-2.28E+00	3.02E-06	Down	-1.88E+00	1.13E-05	Down	-3.17E+00	4.41E-10	Down			Unigene23795_All//6.00E-88//gi|164288193|gb|ES802527.1|ES802527				
Unigene23796_All	386	0.95	0.00	0.41	3.10	2.50	0.82	5.15	4.55	1.03	-9.89E+00	1.97E-02		-1.20E+00	3.96E-01		-3.10E-01	6.07E-01		-1.92E+00	4.14E-03		-1.79E-01	6.74E-01		-2.32E+00	6.40E-07	Down	Unigene23796_All//gi|270309090|dbj|BAI52985.1|//3.00E-06//G1-like7 protein [Oryza sativa Japonica Group]	Unigene23796_All//7.00E-120//gi|72272245|gb|DT048554.1|DT048554					nr -
Unigene23797_All	1594	3.32	2.48	3.11	15.75	13.72	7.17	12.76	5.79	7.42	-4.19E-01	1.15E-01		-9.37E-02	7.31E-01		-1.99E-01	7.85E-02		-1.14E+00	1.50E-24	Down	-1.14E+00	8.59E-23	Down	-7.81E-01	6.15E-13		Unigene23797_All//gi|18390725|ref|NP_563780.1|//1.00E-72//LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6) [Arabidopsis thaliana] >gi|56236136|gb|AAY84524.1| At1g07090 [Arabidopsis thaliana] >gi|88193786|gb|ABD42982.1| At1g07090 [Arabidopsis thaliana]	Unigene23797_All//2.00E-69//AT1G07090| LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6)	Unigene23797_All//0.00E+00//TC160760				nr -
Unigene23798_All	3533	1.61	1.48	0.80	5.09	7.15	4.73	13.62	2.73	4.68	-1.28E-01	6.05E-01		-1.01E+00	1.07E-04	Down	4.91E-01	1.11E-06		-1.06E-01	5.02E-01		-2.32E+00	8.17E-145	Down	-1.54E+00	3.07E-86	Down	Unigene23798_All//gi|297722557|ref|NP_001173642.1|//0.00E+00//Os03g0750200 [Oryza sativa Japonica Group] >gi|108711101|gb|ABF98896.1| Kinesin motor domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255674900|dbj|BAH92370.1| Os03g0750200 [Oryza sativa Japonica Group]	Unigene23798_All//0.00E+00//AT3G44650| kinesin motor protein-related	Unigene23798_All//0.00E+00//ES801493			GO:0000166//GO:0003774//GO:0015630	nr -
Unigene23799_All	3149	2.19	1.32	1.62	4.95	4.76	3.33	5.96	2.64	2.13	-7.33E-01	9.98E-04		-4.34E-01	6.77E-02		-5.78E-02	7.59E-01		-5.73E-01	3.03E-05		-1.17E+00	3.93E-22	Down	-1.49E+00	1.75E-32	Down	Unigene23799_All//gi|87241322|gb|ABD33180.1|//5.00E-93//TGF-beta receptor, type I/II extracellular region [Medicago truncatula]	Unigene23799_All//1.00E-59//AT1G33440| proton-dependent oligopeptide transport (POT) family protein	Unigene23799_All//0.00E+00//TC150454			GO:0044464	nr +
Unigene2380_All	1762	3.09	3.13	4.02	10.43	11.49	9.56	5.02	2.18	3.26	2.15E-02	9.54E-01		3.80E-01	1.08E-01		1.40E-01	3.17E-01		-1.26E-01	4.11E-01		-1.20E+00	3.37E-11	Down	-6.23E-01	2.05E-04		Unigene2380_All//gi|115448467|ref|NP_001048013.1|//1.00E-149//Os02g0730400 [Oryza sativa Japonica Group] >gi|113537544|dbj|BAF09927.1| Os02g0730400 [Oryza sativa Japonica Group]	Unigene2380_All//1.00E-112//AT5G14890| NHL repeat-containing protein	Unigene2380_All//0.00E+00//gi|78345005|gb|DT565279.1|DT565279				nr +

Unigene23804_All	628	1.67	4.84	3.48	1.75	1.54	1.44	5.59	5.99	10.85	1.54E+00	5.28E-05	Up	1.06E+00	2.07E-02		-1.85E-01	8.01E-01		-2.79E-01	6.89E-01		1.00E-01	7.41E-01		9.57E-01	1.54E-06		Unigene23804_All//gi|225434133|ref|XP_002277485.1|//4.00E-32//PREDICTED: O-acetylserine(thiol)-lyase [Vitis vinifera]	Unigene23804_All//3.00E-33//AT3G22460| OAS A2 (O-ACETYLSERINE (THIOL) LYASE (OAS-TL) ISOFORM A1); catalytic/ cysteine synthase/ pyridoxal phosphate binding	Unigene23804_All//4.00E-132//TC138434		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0000097//GO:0006563//GO:0010038//GO:0016765//GO:0016835//GO:0048037	nr +
Unigene23807_All	543	0.77	0.56	3.53	1.19	2.03	2.00	3.04	1.69	2.35	-4.61E-01	6.50E-01		2.20E+00	8.21E-05	Up	7.67E-01	2.69E-01		7.43E-01	2.89E-01		-8.43E-01	6.70E-02		-3.71E-01	4.08E-01		Unigene23807_All//gi|66220146|gb|AY43006.1|//4.00E-24//Na+/H+ antiporter [Glycine max]	Unigene23807_All//3.00E-24//AT3G06370| NHX4 (SODIUM HYDROGEN EXCHANGER 4); sodium ion transmembrane transporter/ sodium:hydrogen antiporter	Unigene23807_All//0.00E+00//TC177520			GO:0005451//GO:0030001//GO:0031224//GO:0055067	nr -
Unigene23812_All	1295	4.36	6.10	4.44	6.00	5.61	7.32	2.58	1.84	1.26	4.84E-01	1.99E-02		2.54E-02	9.37E-01		-9.70E-02	6.97E-01		2.87E-01	1.54E-01		-4.88E-01	1.17E-01		-1.03E+00	4.78E-04	Down	Unigene23812_All//gi|76573323|gb|AB446766.1|//2.00E-82//pre-mRNA splicing factor-like protein [Solanum tuberosum]	Unigene23812_All//8.00E-69//AT3G49430| SRp34a (Ser/Arg-rich protein 34a); RNA binding / nucleic acid binding / nucleotide binding	Unigene23812_All//4.00E-121//TC178827		ko03040|Spliceosome	GO:0003676//GO:0006396//GO:0031981	nr -
Unigene23813_All	1570	1.43	3.32	2.78	2.86	2.15	1.73	1.54	2.48	1.02	1.21E+00	7.47E-06	Up	9.57E-01	1.62E-03		-4.10E-01	1.56E-01		-7.26E-01	1.03E-02		6.90E-01	1.27E-02		-5.97E-01	9.17E-02		Unigene23813_All//gi|76573323|gb|AB446766.1|//8.00E-88//pre-mRNA splicing factor-like protein [Solanum tuberosum]	Unigene23813_All//3.00E-74//AT3G49430| SRp34a (Ser/Arg-rich protein 34a); RNA binding / nucleic acid binding / nucleotide binding	Unigene23813_All//1.00E-90//gi|78341263|gb|DT561537.1|DT561537		ko03040|Spliceosome	GO:0003676//GO:0006396//GO:0031981	nr -
Unigene23814_All	731	41.01	28.21	23.75	41.43	28.97	46.03	48.30	228.19	41.75	-5.40E-01	4.18E-08		-7.88E-01	1.92E-14		-5.16E-01	8.25E-09		1.52E-01	1.43E-01		2.24E+00	0.00E+00	Up	-2.10E-01	9.64E-03		Unigene23814_All//gi|227204395|dbj|BAH57049.1|//4.00E-63//AT4G24220 [Arabidopsis thaliana]	Unigene23814_All//2.00E-64//AT4G24220| VEP1 (VEIN PATTERNING 1); binding / catalytic	Unigene23814_All//0.00E+00//TC145628			GO:0003002//GO:0006950//GO:0008152//GO:0048037	nr +
Unigene23815_All	615	1.79	5.60	1.13	4.86	1.62	8.67	54.10	406.27	34.53	1.65E+00	4.66E-06	Up	-6.67E-01	3.35E-01		-1.58E+00	6.09E-06	Down	8.34E-01	1.15E-03		2.91E+00	0.00E+00	Up	-6.48E-01	4.37E-15		Unigene23815_All//gi|227204395|dbj|BAH57049.1|//7.00E-35//AT4G24220 [Arabidopsis thaliana]	Unigene23815_All//4.00E-36//AT4G24220| VEP1 (VEIN PATTERNING 1); binding / catalytic	Unigene23815_All//0.00E+00//gi|21103566|gb|BQ415879.1|BQ415879			GO:0003002//GO:0006950//GO:0008152//GO:0048037	nr +
Unigene23816_All	634	25.75	20.22	13.86	22.71	14.12	18.31	60.89	272.53	48.64	-3.49E-01	1.27E-02		-8.94E-01	5.98E-10		-6.85E-01	4.21E-07		-3.11E-01	4.20E-02		2.16E+00	0.00E+00	Up	-3.24E-01	1.65E-05		Unigene23816_All//gi|227204395|dbj|BAH57049.1|//2.00E-34//AT4G24220 [Arabidopsis thaliana]	Unigene23816_All//1.00E-27//AT4G24220| VEP1 (VEIN PATTERNING 1); binding / catalytic	Unigene23816_All//0.00E+00//gi|109827758|gb|DW226423.1|DW226423			GO:0003002//GO:0005488//GO:0006950//GO:0008152	nr -
Unigene23817_All	3019	2.32	3.81	2.31	4.55	4.37	6.07	19.16	31.52	66.55	7.14E-01	2.06E-05		-7.30E-03	9.99E-01		-6.00E-02	7.70E-01		4.15E-01	1.19E-03		7.18E-01	3.79E-48		1.80E+00	0.00E+00	Up	Unigene23817_All//gi|224098441|ref|XP_002311175.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222850995|gb|EEE88542.1| GRAS family transcription factor [Populus trichocarpa]	Unigene23817_All//5.00E-171//AT1G07530| SCL14 (SCARECROW-LIKE 14); transcription factor	Unigene23817_All//0.00E+00//TC144114	GRAS		GO:0010468	nr -
Unigene23818_All	2744	0.11	0.44	0.21	0.31	0.14	0.33	1.96	3.15	4.40	1.95E+00	4.09E-03		9.00E-01	3.77E-01		-1.16E+00	1.16E-01		9.32E-02	9.20E-01		6.88E-01	8.22E-05		1.17E+00	9.37E-15	Up	Unigene23818_All//gi|224098441|ref|XP_002311175.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222850995|gb|EEE88542.1| GRAS family transcription factor [Populus trichocarpa]	Unigene23818_All//4.00E-171//AT1G07530| SCL14 (SCARECROW-LIKE 14); transcription factor	Unigene23818_All//0.00E+00//TC144114	GRAS		GO:0010468	nr +
Unigene2382_All	1121	25.90	29.43	28.26	23.69	24.27	34.29	21.95	90.90	33.58	1.84E-01	6.49E-02		1.26E-01	2.55E-01		3.50E-02	8.15E-01		5.34E-01	1.76E-10		2.05E+00	8.63E-262	Up	6.14E-01	2.18E-15		Unigene2382_All//gi|225456525|ref|XP_002284739.1|//1.00E-115//PREDICTED: similar to MtN19-like protein [Vitis vinifera]	Unigene2382_All//2.00E-108//AT5G61820| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Stress up-regulated Nod 19 (InterPro:IPR011692); Has 27 Blast hits to 27 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene2382_All//0.00E+00//TC168670			GO:0031410	nr +
Unigene23820_All	3149	0.47	0.23	0.79	2.61	2.18	2.57	14.00	17.68	31.12	-1.05E+00	5.84E-02		7.73E-01	6.55E-02		-2.62E-01	2.24E-01		-2.39E-02	9.34E-01		3.36E-01	9.30E-08		1.15E+00	4.72E-111	Up	Unigene23820_All//gi|297822769|ref|XP_002879267.1|//1.00E-152//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325106|gb|EFH55526.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23820_All//3.00E-153//AT2G30550| lipase class 3 family protein	Unigene23820_All//0.00E+00//gi|78327007|gb|DT547281.1|DT547281			GO:0004091//GO:0044238	nr -
Unigene23822_All	1826	12.21	25.61	14.09	12.28	16.18	21.99	1.51	3.14	4.71	1.07E+00	6.65E-38	Up	2.07E-01	8.20E-02		3.98E-01	1.95E-05		8.41E-01	1.36E-23		1.06E+00	2.66E-06	Up	1.65E+00	1.78E-17	Up	Unigene23822_All//gi|124360931|gb|ABN08903.1|//2.00E-91//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene23822_All//1.00E-39//AT2G20180| PIL5 (PHYTOCHROME INTERACTING FACTOR 3-LIKE 5); DNA binding / phytochrome binding / transcription factor	Unigene23822_All//0.00E+00//gi|48813505|gb|CO114818.1|CO114818	bHLH	ko04712|Circadian rhythm - plant	GO:0005515//GO:0006779//GO:0009640//GO:0010029//GO:0023033//GO:0051716	nr +
Unigene23824_All	568	3.96	4.55	2.25	3.24	2.97	2.07	7.74	2.94	3.30	2.00E-01	6.15E-01		-8.16E-01	6.87E-02		-1.27E-01	8.13E-01		-6.50E-01	1.92E-01		-1.40E+00	2.57E-07	Down	-1.23E+00	2.03E-06	Down	Unigene23824_All//gi|50838966|gb|AT81727.1|//9.00E-57//expressed protein, having alternative splicing products [Oryza sativa Japonica Group]	Unigene23824_All//3.00E-56//AT1G27150| binding	Unigene23824_All//0.00E+00//TC135619				nr +
Unigene23832_All	1513	1.66	1.34	1.90	3.13	3.96	2.51	2.88	1.24	2.24	-3.09E-01	4.43E-01		1.95E-01	6.23E-01		3.40E-01	1.83E-01		-3.19E-01	2.94E-01		-1.21E+00	5.41E-06	Down	-3.63E-01	1.61E-01		Unigene23832_All//gi|18424524|ref|NP_568944.1|//1.00E-172//BON1 (BONZAI 1); calcium-dependent phospholipid binding [Arabidopsis thaliana] >gi|42572762|ref|NP_974977.1| BON1 (BONZAI 1); calcium-dependent phospholipid binding [Arabidopsis thaliana] >gi|9758389|dbj|BAB08876.1| copine-like protein [Arabidopsis thaliana] >gi|17065496|gb|AAL32902.1| copine-like protein [Arabidopsis thaliana] >gi|21553477|gb|AAM62570.1| copine-like protein [Arabidopsis thaliana] >gi|34365733|gb|AAQ65178.1| At5g61900 [Arabidopsis thaliana]	Unigene23832_All//3.00E-167//AT5G61900| BON1 (BONZAI 1); calcium-dependent phospholipid binding	Unigene23832_All//0.00E+00//TC178192				nr +
Unigene23838_All	420	0.37	0.97	1.78	3.91	5.41	0.97	0.60	0.40	0.38	1.37E+00	2.74E-01		2.25E+00	2.35E-02		4.67E-01	3.10E-01		-2.02E+00	3.04E-04	Down	-6.01E-01	6.48E-01		-6.71E-01	6.05E-01		Unigene23838_All//gi|87162753|gb|AB028548.1|//9.00E-34//Protein kinase; Type I EGF [Medicago truncatula]	Unigene23838_All//2.00E-26//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase	Unigene23838_All//4.00E-17//DT467466				nr +
Unigene23839_All	774	1.15	0.79	2.68	5.02	4.58	1.81	2.51	0.92	0.21	-5.49E-01	4.42E-01		1.22E+00	1.02E-02		-1.32E-01	7.13E-01		-1.47E+00	3.73E-06	Down	-1.45E+00	7.53E-04	Down	-3.61E+00	3.72E-10	Down	Unigene23839_All//gi|15222427|ref|NP_177131.1|//1.00E-57//protein kinase family protein [Arabidopsis thaliana] >gi|75333576|sp|Q9C9L5.1|WAKLH_ARATH RecName: Full=Wall-associated receptor kinase-like 9; Flags: Precursor	Unigene23839_All//8.00E-59//AT1G69730| protein kinase family protein	Unigene23839_All//0.00E+00//TC164885		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0032559//GO:0046872	nr -
Unigene2384_All	1417	90.54	77.38	113.75	39.48	40.56	31.55	10.26	7.34	3.09	-2.27E-01	6.04E-07		3.29E-01	7.31E-16		3.90E-02	6.65E-01		-3.23E-01	2.40E-06		-4.83E-01	2.24E-04		-1.73E+00	2.34E-31	Down	Unigene2384_All//gi|75297894|sp|Q84MB3.1|ACCH1_ARATH|/1.00E-124//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene2384_All//1.00E-117//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene2384_All//8.00E-15//TC141122		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene23840_All	2638	16.24	4.03	16.13	4.89	3.43	3.13	0.59	0.70	0.27	-2.01E+00	2.62E-88	Down	-1.03E-02	9.28E-01		-5.11E-01	4.90E-04		-6.43E-01	2.61E-05		2.33E-01	6.40E-01		-1.13E+00	1.41E-02		Unigene23840_All//gi|87162753|gb|AB028548.1|//0.00E+00//Protein kinase; Type I EGF [Medicago truncatula]	Unigene23840_All//7.00E-150//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase	Unigene23840_All//0.00E+00//TC164885		ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488	nr +
Unigene23842_All	3147	7.33	16.00	9.39	9.10	11.84	12.00	16.32	28.34	15.51	1.13E+00	2.82E-44	Up	3.57E-01	5.74E-04		3.79E-01	3.54E-06		3.99E-01	2.60E-06		7.96E-01	8.10E-54		-7.40E-02	3.31E-01		Unigene23842_All//gi|42566726|ref|NP_193001.2|//0.00E+00//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	Unigene23842_All//0.00E+00//AT4G12640| RNA recognition motif (RRM)-containing protein	Unigene23842_All//0.00E+00//TC161817		ko03040|Spliceosome	GO:0005488	nr -
Unigene23843_All	3474	3.37	8.96	5.87	3.80	6.53	6.11	14.56	20.22	9.83	1.41E+00	7.46E-39	Up	7.99E-01	2.83E-10		7.82E-01	4.10E-13		6.85E-01	3.95E-09		4.75E-01	2.03E-17		-5.67E-01	7.53E-18		Unigene23843_All//gi|225030814|gb|ACN79520.1|//0.00E+00//reduced leaflet 3 [Lotus japonicus]	Unigene23843_All//0.00E+00//AT1G69440| AGO7 (ARGONAUTE7); nucleic acid binding	Unigene23843_All//0.00E+00//TC145316			GO:0008135//GO:0009791//GO:0030422//GO:0035195//GO:0044464//GO:0050793	nr +
Unigene23844_All	1561	6.80	2.17	6.31	7.85	6.31	3.18	5.31	1.23	2.27	-1.65E+00	3.57E-17	Down	-1.09E-01	6.13E-01		-3.15E-01	5.10E-02		-1.30E+00	4.19E-15	Down	-2.11E+00	9.49E-23	Down	-1.22E+00	3.13E-11	Down	Unigene23844_All//gi|124359565|gb|ABD28693.2|//1.00E-106//Glycosyltransferase sugar-binding region containing DXD motif; Alpha 1,4-glycosyltransferase conserved region [Medicago truncatula]	Unigene23844_All//8.00E-89//AT1G61050| alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein	Unigene23844_All//9.00E-18//CO495496			GO:0008378//GO:0043231//GO:0044444	nr +
Unigene23846_All	4098	11.02	6.02	7.02	13.52	12.45	12.64	20.24	5.43	7.88	-8.72E-01	2.28E-26		-6.51E-01	1.61E-15		-1.18E-01	1.27E-01		-9.67E-02	2.44E-01		-1.90E+00	3.27E-193	Down	-1.36E+00	6.68E-123	Down	Unigene23846_All//gi|18397283|ref|NP_564338.1|//0.00E+00//CARB (CARBAMOYL PHOSPHATE SYNTHETASE B); ATP binding / carbamoyl-phosphate synthase/ catalytic [Arabidopsis thaliana] >gi|9972356|gb|AAG10606.1|AC008030_6 carbamoyl phosphate synthetase large chain (carB) [Arabidopsis thaliana] >gi|14194125|gb|AAK56257.1|AF367268_1 At1g29900/F1N18_6 [Arabidopsis thaliana] >gi|1477480|gb|AAB67843.1| carbamoyl phosphate synthetase large chain [Arabidopsis thaliana] >gi|22137066|gb|AAM91378.1| At1g29900/F1N18_6 [Arabidopsis thaliana]	Unigene23846_All//0.00E+00//AT1G29900| CARB (CARBAMOYL PHOSPHATE SYNTHETASE B); ATP binding / carbamoyl-phosphate synthase/ catalytic	Unigene23846_All//0.00E+00//TC132927		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0004086//GO:0006525//GO:0009267//GO:0009532//GO:0032559	nr -
Unigene23847_All	2713	4.84	9.28	4.16	16.23	12.93	6.81	10.08	7.83	9.09	9.39E-01	6.62E-17		-2.18E-01	2.15E-01		-3.28E-01	1.06E-05		-1.25E+00	7.64E-50	Down	-3.66E-01	8.13E-05		-1.50E-01	1.27E-01		Unigene23847_All//gi|215598266|tpg|DAA06351.1|//0.00E+00//TPA_inf: ARO1-like protein 2 [Vitis vinifera]	Unigene23847_All//0.00E+00//AT5G66200| ARO2 (ARMADILLO REPEAT ONLY 2); binding	Unigene23847_All//0.00E+00//TC142355			GO:0000904//GO:0007010//GO:0016020//GO:0043231	nr +
Unigene23848_All	1914	132.39	75.66	76.23	285.22	317.37	193.75	34.92	9.06	11.91	-8.07E-01	5.01E-127		-7.96E-01	2.41E-120		1.54E-01	4.38E-17		-5.58E-01	2.44E-154		-1.95E+00	5.86E-161	Down	-1.55E+00	8.36E-121	Down	Unigene23848_All//gi|157273656|gb|ABV27482.1|//0.00E+00//fasciclin-like arabinogalactan protein 11 [Gossypium hirsutum]	Unigene23848_All//2.00E-132//AT5G55730| FLA1 (FASCICLIN-LIKE ARAB INOGALACTAN 1)	Unigene23848_All//0.00E+00//TC140451				nr +
Unigene23849_All	1811	9.13	3.97	4.47	15.68	11.37	11.05	15.18	5.59	7.85	-1.20E+00	1.25E-16	Down	-1.03E+00	1.38E-12	Down	-4.64E-01	6.64E-07		-5.05E-01	2.85E-07		-1.44E+00	1.02E-43	Down	-9.50E-01	1.35E-23		Unigene23849_All//gi|223452478|gb|ACM89566.1|//1.00E-159//protein kinase family protein [Glycine max]	Unigene23849_All//7.00E-125//AT3G26700| protein kinase family protein	Unigene23849_All//0.00E+00//ES813401		ko04626|Plant-pathogen interaction	GO:0016301//GO:0031410	nr +

Unigene2385_All	1685	21.18	5.50	5.63	16.73	10.93	8.71	13.90	3.18	6.08	-1.94E+00	1.71E-70	Down	-1.91E+00	1.54E-66	Down	-6.14E-01	4.31E-11		-9.42E-01	2.32E-20		-2.13E+00	7.59E-64	Down	-1.19E+00	5.68E-29	Down	Unigene2385_All//gi|15221371|ref|NP_172712.1|//1.00E-149//phosphate translocator-related [Arabidopsis thaliana] >gi|8778643|gb|AAF79651.1|AC025416_25 F5O11.25 [Arabidopsis thaliana] >gi|9502394|gb|AAF88101.1|AC025417_29 T12C24.5 [Arabidopsis thaliana]	Unigene2385_All//9.00E-129//AT1G12500| phosphate translocator-related	Unigene2385_All//0.00E+00//TC161688				nr +
Unigene23850_All	1734	4.44	1.93	4.33	7.99	5.74	3.70	3.54	1.08	2.34	-1.20E+00	3.68E-08	Down	-3.47E-02	8.85E-01		-4.77E-01	7.43E-04		-1.11E+00	2.49E-13	Down	-1.70E+00	5.40E-13	Down	-5.93E-01	3.97E-03		Unigene23850_All//gi|223452478|gb|ACM89566.1|//1.00E-159//protein kinase family protein [Glycine max]	Unigene23850_All//1.00E-133//AT3G26700| protein kinase family protein	Unigene23850_All//0.00E+00//ES813401			GO:0016301//GO:0031410	nr -
Unigene23852_All	3610	29.18	36.30	34.56	17.83	13.57	13.29	20.71	10.34	8.93	3.15E-01	1.55E-12		2.44E-01	2.39E-07		-3.93E-01	3.67E-11		-4.24E-01	1.57E-11		-1.00E+00	1.95E-66	Down	-1.21E+00	6.75E-93	Down	Unigene23852_All//gi|297852644|ref|XP_002894203.1|//0.00E+00//ATPREP2 [Arabidopsis lyrata subsp. lyrata] >gi|297340045|gb|EFH70462.1|ATPREP2 [Arabidopsis lyrata subsp. lyrata]	Unigene23852_All//0.00E+00//AT3G19170| ATPREP1 (PRESEQUENCE PROTEASE 1); metalloendopeptidase	Unigene23852_All//0.00E+00//TC140346			GO:0004175//GO:0005576//GO:0009526//GO:0009532//GO:0010038//GO:0016485//GO:0016914	nr -
Unigene23858_All	578	2.35	2.45	1.66	4.74	2.74	1.25	3.36	1.74	0.96	6.07E-02	9.22E-01		-5.05E-01	3.82E-01		-7.91E-01	2.88E-02		-1.92E+00	2.70E-06	Down	-9.55E-01	2.18E-02		-1.80E+00	3.78E-05	Down	Unigene23858_All//gi|224102857|ref|XP_002312830.1|//1.00E-08//transcription factor E2F [Populus trichocarpa] >gi|222849238|gb|EEE86785.1| transcription factor E2F [Populus trichocarpa]	Unigene23858_All//9.00E-102//DW476220				GO:0006350	nr -
Unigene23859_All	1956	3.85	3.29	1.77	5.96	5.92	5.36	6.98	6.52	3.63	-2.28E-01	3.23E-01		-1.12E+00	6.74E-07	Down	-1.07E-02	9.48E-01		-1.54E-01	4.32E-01		-9.94E-02	5.51E-01		-9.46E-01	4.42E-12		Unigene23859_All//gi|224132326|ref|XP_002328241.1|//0.00E+00//transcription factor E2F [Populus trichocarpa] >gi|222837756|gb|EEE76121.1| transcription factor E2F [Populus trichocarpa]	Unigene23859_All//3.00E-135//AT5G22220| E2F1; DNA binding / protein binding / transcription factor	Unigene23859_All//0.00E+00//TC151377	E2F-DP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231//GO:0043234	nr -
Unigene2386_All	1459	25.32	8.30	15.44	23.80	23.30	27.67	47.24	21.69	21.65	-1.61E+00	3.49E-56	Down	-7.14E-01	5.99E-15		-3.08E-02	8.19E-01		2.18E-01	1.22E-02		-1.12E+00	1.04E-73	Down	-1.13E+00	4.87E-76	Down	Unigene2386_All//gi|151347486|gb|AB501352.1|//0.00E+00//methionine synthase [Carica papaya]	Unigene2386_All//0.00E+00//AT5G17920| ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase	Unigene2386_All//0.00E+00//TC140906		ko00270|Cysteine and methionine metabolism	GO:0000097//GO:0005576//GO:0006970//GO:0008172//GO:0009532//GO:0010038//GO:0016020//GO:0042579//GO:0046914	nr +
Unigene23860_All	1416	9.46	113.43	35.50	18.43	67.73	84.23	56.10	88.52	68.42	3.58E+00	0.00E+00	Up	1.91E+00	1.10E-93	Up	1.88E+00	1.27E-210	Up	2.19E+00	3.30E-292	Up	6.58E-01	3.34E-54		2.86E-01	5.07E-10		Unigene23860_All//gi|15230001|ref|NP_189598.1|//7.00E-67//AFP3 (ABI FIVE BINDING PROTEIN 3) [Arabidopsis thaliana] >gi|79313999|ref|NP_001030794.1|AFP3 (ABI FIVE BINDING PROTEIN 3) [Arabidopsis thaliana] >gi|145332713|ref|NP_001078222.1|AFP3 (ABI FIVE BINDING PROTEIN 3) [Arabidopsis thaliana] >gi|75165510|sp|Q94F39.1|AFP3_ARATH RecName: Full=Ninja-family protein AFP3; AltName: Full=ABI five-binding protein 3; Short=ABI5-binding protein 3 >gi|14326674|gb|AAK60331.1|AF385741_1 AT3g29575/MWE13_2 [Arabidopsis thaliana] >gi|22137322|gb|AAM91506.1|AT3g29575/MWE13_2 [Arabidopsis thaliana] >gi|222424245|dbj|BAH20080.1|AT3G29575 [Arabidopsis thaliana]	Unigene23860_All//7.00E-55//AT3G29575| AFP3 (ABI FIVE BINDING PROTEIN 3)	Unigene23860_All//0.00E+00//TC135557			GO:0005488//GO:0009725	nr -
Unigene23861_All	1980	49.86	46.04	40.91	31.07	30.26	25.27	15.93	6.84	5.75	-1.15E-01	3.95E-02		-2.86E-01	8.89E-08		-3.81E-02	6.54E-01		-2.98E-01	5.08E-06		-1.22E+00	7.34E-39	Down	-1.47E+00	5.60E-53	Down	Unigene23861_All//gi|240255941|ref|NP_567501.4|//0.00E+00//binding [Arabidopsis thaliana]	Unigene23861_All//8.00E-180//AT4G16490| binding	Unigene23861_All//0.00E+00//gi|78346726|gb|DT567000.1|DT567000			GO:0003824	nr +
Unigene23863_All	2588	2.24	2.21	1.03	3.70	3.34	2.15	5.31	2.00	2.66	-2.05E-02	9.53E-01		-1.13E+00	1.68E-05	Down	-1.46E-01	5.11E-01		-7.84E-01	1.53E-05		-1.41E+00	1.83E-21	Down	-9.96E-01	3.71E-13		Unigene23863_All//gi|49615726|gb|AT67045.1|//0.00E+00//DNA mismatch repair protein [Petunia x hybrida]	Unigene23863_All//0.00E+00//AT4G02070| MSH6 (MUTS HOMOLOG 6); damaged DNA binding	Unigene23863_All//0.00E+00//CO110882		ko03430|Mismatch repair	GO:0003690//GO:0006281//GO:0032559//GO:0043231	nr +
Unigene23868_All	2022	7.27	8.85	7.22	9.07	14.19	23.56	34.08	26.89	145.96	2.83E-01	3.64E-02		-1.10E-02	9.67E-01		6.46E-01	6.03E-12		1.38E+00	1.99E-61	Up	-3.42E-01	1.10E-09		2.10E+00	0.00E+00	Up	Unigene23868_All//gi|224066819|ref|XP_002302231.1|//0.00E+00//iaa-amino acid hydrolase 9 [Populus trichocarpa] >gi|222843957|gb|EEE81504.1| iaa-amino acid hydrolase 9 [Populus trichocarpa]	Unigene23868_All//6.00E-173//AT1G44350| ILL6; IAA-amino acid conjugate hydrolase/ metallopeptidase	Unigene23868_All//0.00E+00//gi|164359711|gb|ES820930.1|ES820930			GO:0005488//GO:0016811	nr -
Unigene23869_All	3516	3.91	1.82	1.86	49.13	34.01	18.00	17.91	7.88	6.66	-1.11E+00	2.21E-12	Down	-1.07E+00	3.17E-11	Down	-5.31E-01	1.19E-50		-1.45E+00	4.22E-243	Down	-1.18E+00	2.90E-73	Down	-1.43E+00	2.17E-100	Down	Unigene23869_All//gi|75333913|sp|Q9FI15.1|Y5148_ARATH//0.00E+00//Rec Name: Full=Probable leucine-rich repeat receptor-like protein kinase At5g61480; Flags: Precursor >gi|10177178|dbj|BAB10447.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|224589737|gb|ACN59400.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene23869_All//0.00E+00//AT5G61480| leucine-rich repeat transmembrane protein kinase, putative	Unigene23869_All//0.00E+00//TC136236			GO:0004672//GO:0004871//GO:0006464//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene2387_All	2362	17.14	9.48	10.93	5.10	5.95	4.82	0.86	0.34	1.80	-8.55E-01	5.74E-23		-6.49E-01	6.58E-14		2.21E-01	1.70E-01		-8.30E-02	6.80E-01		-1.35E+00	1.15E-03		1.07E+00	3.95E-05	Up	Unigene2387_All//gi|297812041|ref|XP_002873904.1|//0.00E+00//GTP1/OBG family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319741|gb|EFH50163.1| GTP1/OBG family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2387_All//0.00E+00//AT5G18570| GTP1/OBG family protein	Unigene2387_All//0.00E+00//TC143230			GO:0017111//GO:0032561//GO:0043231	nr +
Unigene23873_All	2221	15.83	43.35	38.07	4.28	7.50	9.80	0.30	0.28	0.07	1.45E+00	1.32E-124	Up	1.27E+00	1.55E-86	Up	8.09E-01	2.64E-10		1.19E+00	8.76E-23	Up	-1.10E-01	8.90E-01		-2.09E+00	1.27E-02		Unigene23873_All//gi|224138238|ref|XP_002322764.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222867394|gb|EEF04525.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene23873_All//0.00E+00//AT5G06530| ABC transporter family protein	Unigene23873_All//0.00E+00//TC133240		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015098//GO:0015405//GO:0016020//GO:0017111//GO:0032559	nr -
Unigene23874_All	1557	23.62	42.73	54.07	4.83	12.21	10.76	0.08	0.03	0.05	8.55E-01	3.61E-37		1.19E+00	1.18E-78	Up	1.34E+00	7.60E-26	Up	1.16E+00	8.62E-17	Up	-1.60E+00	5.34E-01		-6.71E-01	7.20E-01		Unigene23874_All//gi|224138238|ref|XP_002322764.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222867394|gb|EEF04525.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene23874_All//0.00E+00//AT5G06530| ABC transporter family protein	Unigene23874_All//0.00E+00//TC133240		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015098//GO:0016020//GO:0017111//GO:0032559	nr +
Unigene23875_All	1674	5.72	11.96	10.69	7.05	9.01	6.12	3.21	3.07	3.00	1.06E+00	1.64E-16	Up	9.02E-01	5.04E-11		3.53E-01	1.27E-02		-2.04E-01	2.75E-01		-6.28E-02	8.07E-01		-9.72E-02	6.80E-01		Unigene23875_All//gi|297798344|ref|XP_002867056.1|//1.00E-122//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312892|gb|EFH43315.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23875_All//2.00E-123//AT4G35780| protein kinase family protein	Unigene23875_All//0.00E+00//CO081593			GO:0043231	nr -
Unigene23876_All	2300	1.96	0.95	1.25	5.15	4.90	2.51	7.08	3.69	3.60	-1.05E+00	2.90E-04	Down	-6.46E-01	3.04E-02		-7.43E-02	7.20E-01		-1.04E+00	2.46E-10	Down	-9.40E-01	1.16E-13		-9.74E-01	6.60E-15		Unigene23876_All//gi|13605521|gb|AAK32754.1|AF361586_1//1.00E-177//AT3g17900/MEB5_12 [Arabidopsis thaliana] >gi|23506057|gb|AAN28888.1| At3g17900/MEB5_12 [Arabidopsis thaliana]	Unigene23876_All//3.00E-166//AT3G17900| unknown protein	Unigene23876_All//0.00E+00//ES804027				nr -
Unigene23877_All	1180	4.83	2.53	2.17	5.53	4.52	5.70	7.20	3.65	4.83	-9.32E-01	1.99E-04		-1.16E+00	1.24E-05	Down	-2.90E-01	2.32E-01		4.43E-02	8.76E-01		-9.81E-01	5.12E-08		-5.77E-01	7.66E-04		Unigene23877_All//gi|79557286|ref|NP_179256.3|//1.00E-105//antiporter/ drug transporter [Arabidopsis thaliana]	Unigene23877_All//1.00E-101//AT2G16650| antiporter/ drug transporter	Unigene23877_All//0.00E+00//ES837663				nr +
Unigene23878_All	2098	4.69	2.29	3.58	6.58	5.97	6.72	4.11	1.45	2.73	-1.03E+00	3.68E-08	Down	-3.90E-01	4.51E-02		-1.39E-01	4.29E-01		3.03E-02	8.77E-01		-1.50E+00	4.64E-15	Down	-5.88E-01	5.43E-04		Unigene23878_All//gi|79557286|ref|NP_179256.3|//0.00E+00//antiporter/ drug transporter [Arabidopsis thaliana]	Unigene23878_All//9.00E-179//AT2G16650| antiporter/ drug transporter	Unigene23878_All//0.00E+00//ES837663			GO:0015291//GO:0015893//GO:0044464	nr +
Unigene23879_All	2512	3.92	2.72	2.37	24.35	24.25	17.84	10.45	5.21	4.19	-5.24E-01	4.10E-03		-7.22E-01	1.40E-04		-6.00E-03	9.53E-01		-4.49E-01	3.76E-12		-1.01E+00	5.66E-24	Down	-1.32E+00	9.91E-38	Down	Unigene23879_All//gi|15220862|ref|NP_178202.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|6503299|gb|AAF14675.1|AC011713_23 Contains similarity to gb|U82481 KI domain interacting kinase 1 from Zea mays and contains PF|00069 Eukaryotic protein kinase domain. ESTs gb|H77140, gb|H76842 and gb|AI994303 come from this gene [Arabidopsis thaliana]	Unigene23879_All//0.00E+00//AT1G80870| protein kinase family protein	Unigene23879_All//0.00E+00//TC178739			GO:0004672//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene23882_All	1235	1.19	4.23	1.29	3.47	3.46	5.70	4.45	13.00	26.06	1.83E+00	4.76E-10	Up	1.25E-01	8.06E-01		-4.70E-03	9.78E-01		7.18E-01	9.93E-04		1.55E+00	1.60E-28	Up	2.55E+00	2.65E-110	Up	Unigene23882_All//gi|57222120|gb|AAW38967.1|//6.00E-19//At5g65140 [Arabidopsis thaliana] >gi|57222226|gb|AAW39020.1| At5g65140 [Arabidopsis thaliana] >gi|62320350|dbj|BAD94722.1| trehalose-6-phosphate phosphatase [Arabidopsis thaliana]	Unigene23882_All//4.00E-211//AT4G39770| trehalose-6-phosphate phosphatase, putative	Unigene23882_All//0.00E+00//TC149239		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0010038//GO:0019203	nr +
Unigene23883_All	1521	3.44	18.59	8.37	18.57	30.81	54.64	15.73	46.22	141.10	2.43E+00	1.65E-73	Up	1.28E+00	1.03E-13	Up	7.31E-01	8.44E-24		1.56E+00	4.47E-128	Up	1.55E+00	2.03E-123	Up	3.16E+00	0.00E+00	Up	Unigene23883_All//gi|217426807|gb|ACX44515.1|//1.00E-131//AT4G10100-like protein [Arabidopsis arenosa]	Unigene23883_All//3.00E-136//AT4G10100| trehalose-6-phosphate phosphatase, putative	Unigene23883_All//0.00E+00//TC135974		ko00500|Starch and sucrose metabolism		nr -

Unigene23886_All	2254	2.60	1.93	3.31	9.88	4.16	2.66	1.93	2.06	0.35	-4.27E-01	8.51E-02		3.47E-01	1.37E-01		-1.25E+00	9.08E-29	Down	-1.89E+00	3.48E-46	Down	9.13E-02	7.37E-01		-2.45E+00	3.87E-15	Down	Unigene23886_All//gi|18394832|ref|NP_564107.1|//0.00E+00//ATSBT5.2; identical protein binding / serine-type endopeptidase [Arabidopsis thaliana] >gi|8778982|gb|AAF79897.1|AC022472.6 Contains similarity to p69c gene from Lycopersicon esculentum gb|Y17277 and is a member of subtilase family PF|00082. ESTs gb|T22485, gb|R65370, gb|AA651071 come from this gene [Arabidopsis thaliana]	Unigene23886_All//0.00E+00//AT1G20160| ATSBT5.2; identical protein binding / serine-type endopeptidase	Unigene23886_All//3.00E-160//TC158057		ko04141|Protein processing in endoplasmic reticulum	GO:0005576//GO:0019538//GO:0070011	nr +
Unigene23887_All	1840	6.00	5.51	7.29	12.83	11.90	11.12	16.96	20.13	4.96	-1.24E-01	5.21E-01		2.82E-01	9.23E-02		-1.09E-01	4.18E-01		-2.07E-01	8.78E-02		2.47E-01	2.13E-03		-1.77E+00	1.30E-68	Down	Unigene23887_All//gi|30686502|ref|NP_850841.1|//1.00E-129//AAA-type ATPase family protein [Arabidopsis thaliana] >gi|9759053|dbj|BAB09575.1| AAA-type ATPase-like protein [Arabidopsis thaliana]	Unigene23887_All//4.00E-124//AT5G17760| AAA-type ATPase family protein	Unigene23887_All//0.00E+00//gi|78349545|gb|DT569819.1|DT569819				nr -
Unigene23888_All	678	1.85	0.15	0.00	10.43	7.31	5.46	3.74	1.23	1.82	-3.63E+00	2.00E-05	Down	-1.09E+01	7.11E-07	Down	-5.13E-01	1.49E-02		-9.34E-01	1.60E-05		-1.60E+00	2.15E-05	Down	-1.04E+00	2.62E-03		Unigene23888_All//gi|10086489|gb|AAG12549.1|AC007797_9//5.00E-09//Unknown Protein [Arabidopsis thaliana]	Unigene23888_All//3.00E-07//AT1G19835| unknown protein	Unigene23888_All//0.00E+00//TC155764				nr +
Unigene23889_All	710	1.62	0.71	0.75	5.26	5.72	4.07	4.82	0.82	2.13	-1.18E+00	6.62E-02		-1.11E+00	9.93E-02		1.21E-01	7.58E-01		-3.70E-01	2.80E-01		-2.55E+00	3.78E-12	Down	-1.18E+00	6.79E-05	Down	Unigene23889_All//gi|10086489|gb|AAG12549.1|AC007797_9//1.00E-37//Unknown Protein [Arabidopsis thaliana]	Unigene23889_All//6.00E-34//AT1G19835| unknown protein				GO:0016020	nr +
Unigene23890_All	3635	0.39	0.70	0.40	3.80	4.47	3.34	2.81	1.22	1.71	8.43E-01	3.48E-02		2.54E-02	9.83E-01		2.36E-01	1.05E-01		-1.84E-01	2.89E-01		-1.21E+00	5.92E-13	Down	-7.19E-01	3.82E-06		Unigene23890_All//gi|205716586|sp|O65649.2|FPP5_ARATH//0.00E+00//Rec Name: Full=Filament-like plant protein 5; Short=AtFPP5	Unigene23890_All//7.00E-130//AT4G36120| unknown protein	Unigene23890_All//0.00E+00//TC155764				nr -
Unigene23891_All	2128	8.09	6.33	7.56	113.93	100.18	85.66	24.99	11.65	10.84	-3.53E-01	9.25E-03		-9.81E-02	5.41E-01		-1.86E-01	4.66E-10		-4.12E-01	1.53E-39		-1.10E+00	2.44E-55	Down	-1.21E+00	1.26E-65	Down	Unigene23891_All//gi|297817274|ref|XP_002876520.1|//1.00E-135//IQ-domain 13 [Arabidopsis lyrata subsp. lyrata] >gi|297322358|gb|EFH52779.1| IQ-domain 13 [Arabidopsis lyrata subsp. lyrata]	Unigene23891_All//4.00E-112//AT3G59690| IQ013 (IQ-domain 13); calmodulin binding	Unigene23891_All//0.00E+00//TC154019				nr -
Unigene23893_All	1450	4.37	14.36	7.86	13.91	15.32	13.52	15.54	15.02	13.41	1.72E+00	8.17E-35	Up	8.48E-01	1.29E-06		1.39E-01	3.08E-01		-4.16E-02	7.73E-01		-4.95E-02	6.89E-01		-2.13E-01	4.23E-02		Unigene23893_All//gi|222423063|dbj|BAH19513.1|//3.00E-74//AT3G04240 [Arabidopsis thaliana]	Unigene23893_All//2.00E-75//AT3G04240| SEC (secret agent); transferase, transferring glycosyl groups	Unigene23893_All//0.00E+00//ES793997			GO:0006486//GO:0016740	nr -
Unigene23894_All	1017	0.10	1.40	0.42	0.69	0.71	1.55	0.91	0.58	1.72	3.76E+00	3.98E-06	Up	2.03E+00	1.39E-01		5.25E-02	9.65E-01		1.18E+00	2.91E-02		-6.69E-01	3.12E-01		9.14E-01	3.24E-02		Unigene23894_All//gi|222423063|dbj|BAH19513.1|//2.00E-74//AT3G04240 [Arabidopsis thaliana]	Unigene23894_All//1.00E-75//AT3G04240| SEC (secret agent); transferase, transferring glycosyl groups	Unigene23894_All//0.00E+00//ES793997			GO:0016740	nr -
Unigene23896_All	1631	2.86	3.11	4.47	96.88	90.24	87.56	13.69	2.49	4.23	1.22E-01	6.50E-01		6.48E-01	3.99E-03		-1.03E-01	1.39E-02		-1.46E-01	3.69E-04		-2.46E+00	1.72E-72	Down	-1.70E+00	2.44E-46	Down	Unigene23896_All//gi|38194917|gb|AAR13305.1|//0.00E+00//phytochelatin synthetase-like protein [Phaseolus vulgaris]	Unigene23896_All//0.00E+00//AT5G15630| IRX6	Unigene23896_All//0.00E+00//TC139655			GO:0009832//GO:0016020	nr +
Unigene23897_All	658	6.84	2.31	2.75	15.75	10.15	10.36	10.60	2.54	3.39	-1.57E+00	3.14E-07	Down	-1.31E+00	1.94E-05	Down	-6.33E-01	1.15E-04		-6.03E-01	5.15E-04		-2.06E+00	9.63E-19	Down	-1.64E+00	1.83E-14	Down	Unigene23897_All//gi|290782382|gb|ADD62393.1|//1.00E-60//beta-galactosidase 3 [Prunus persica]	Unigene23897_All//7.00E-57//AT1G45130| BGAL5 (beta-galactosidase 5); beta-galactosidase/ catalytic/ cation binding	Unigene23897_All//0.00E+00//gi|21096978|gb|BQ409291.1|BQ409291		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation	GO:0015925//GO:0030246//GO:0031410//GO:0043167//GO:0043234//GO:0044238	nr +
Unigene23898_All	2530	16.79	7.19	7.03	41.51	33.13	25.10	13.10	2.59	4.80	-1.22E+00	7.68E-43	Down	-1.26E+00	5.09E-43	Down	-3.25E-01	1.17E-12		-7.26E-01	9.95E-48		-2.34E+00	5.92E-101	Down	-1.45E+00	1.87E-54	Down	Unigene23898_All//gi|61162206|dbj|BAD91084.1|//0.00E+00//beta-D-galactosidase [Pyrus pyrifolia]	Unigene23898_All//0.00E+00//AT1G45130| BGAL5 (beta-galactosidase 5); beta-galactosidase/ catalytic/ cation binding	Unigene23898_All//0.00E+00//TC139421		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series	GO:0015925//GO:0030246//GO:0043167//GO:0043234//GO:0044238//GO:0044464	nr -
Unigene23899_All	2316	25.87	15.93	20.42	62.14	60.19	61.91	37.00	18.17	17.86	-7.00E-01	5.43E-24		-3.41E-01	1.03E-06		-4.60E-02	3.86E-01		-5.20E-03	9.39E-01		-1.03E+00	4.85E-79	Down	-1.05E+00	1.45E-84	Down	Unigene23899_All//gi|297841957|ref|XP_002888860.1|//0.00E+00//SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334701|gb|EFH65119.1| SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23899_All//9.00E-162//AT1G72160| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene23899_All//0.00E+00//TC133782			GO:0044464//GO:0051234	nr +
Unigene23900_All	1872	0.89	2.17	1.34	2.05	2.94	18.31	8.92	86.56	101.62	1.28E+00	4.89E-05	Up	5.80E-01	1.67E-01		5.23E-01	3.86E-02		3.16E+00	8.45E-126	Up	3.28E+00	0.00E+00	Up	3.51E+00	0.00E+00	Up	Unigene23900_All//gi|297823360|ref|XP_002884062.1|//1.00E-155//auxin efflux carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329902|gb|EFH60321.1| auxin efflux carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23900_All//3.00E-153//AT2G17500| auxin efflux carrier family protein	Unigene23900_All//0.00E+00//TC171782				nr +
Unigene23901_All	1853	1.75	2.13	1.93	5.43	3.57	2.92	5.23	3.79	2.26	2.85E-01	3.71E-01		1.37E-01	6.83E-01		-6.06E-01	2.95E-04		-8.93E-01	4.61E-07		-4.64E-01	5.07E-03		-1.21E+00	9.34E-13	Down	Unigene23901_All//gi|119360031|gb|ABL66744.1|//2.00E-71//At1g54200 [Arabidopsis thaliana]	Unigene23901_All//5.00E-42//AT1G54200| unknown protein	Unigene23901_All//5.00E-140//gi|109836025|gb|DW234587.1|DW234587				nr +
Unigene23903_All	896	1.46	3.34	2.56	2.56	3.38	4.23	5.47	2.05	3.51	1.19E+00	1.27E-03		8.08E-01	6.77E-02		4.03E-01	3.03E-01		7.27E-01	2.15E-02		-1.42E+00	3.12E-08	Down	-6.40E-01	6.16E-03		Unigene23903_All//gi|297828497|ref|XP_002882131.1|//3.00E-94//At2g47760/F17A22.15 [Arabidopsis lyrata subsp. lyrata] >gi|297327970|gb|EFH58390.1| At2g47760/F17A22.15 [Arabidopsis lyrata subsp. lyrata]	Unigene23903_All//1.00E-91//AT2G47760| ALG3; alpha-1,3-mannosyltransferase/ catalytic	Unigene23903_All//0.00E+00//gi|84171820|gb|DR160468.1|DR160468		ko00510|N-Glycan biosynthesis	GO:0000030//GO:0006464//GO:0031224//GO:0043231	nr -
Unigene23904_All	1600	1.77	3.83	2.73	4.08	2.69	3.73	6.87	4.18	3.09	1.12E+00	5.24E-06	Up	6.28E-01	3.90E-02		-6.00E-01	5.72E-03		-1.30E-01	6.18E-01		-7.17E-01	2.82E-06		-1.15E+00	2.26E-13	Down	Unigene23904_All//gi|297828497|ref|XP_002882131.1|//1.00E-178//At2g47760/F17A22.15 [Arabidopsis lyrata subsp. lyrata] >gi|297327970|gb|EFH58390.1| At2g47760/F17A22.15 [Arabidopsis lyrata subsp. lyrata]	Unigene23904_All//1.00E-157//AT2G47760| ALG3; alpha-1,3-mannosyltransferase/ catalytic	Unigene23904_All//0.00E+00//TC171960		ko00510|N-Glycan biosynthesis	GO:0016757//GO:0031224//GO:0043231	nr +
Unigene23909_All	1850	11.96	30.98	13.01	19.93	23.51	29.78	14.79	23.86	19.10	1.37E+00	2.51E-68	Up	1.21E-01	3.65E-01		2.39E-01	2.47E-03		5.80E-01	4.75E-17		6.90E-01	2.81E-21		3.69E-01	2.82E-06		Unigene23909_All//gi|297788413|ref|XP_002862315.1|//1.00E-127//UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297307700|gb|EFH38573.1| UBX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene23909_All//3.00E-92//AT2G43210| UBX domain-containing protein	Unigene23909_All//0.00E+00//ES821958				nr +
Unigene2391_All	747	2.24	0.95	1.21	4.73	2.54	1.63	0.23	0.50	0.59	-1.24E+00	1.66E-02		-8.87E-01	9.63E-02		-9.01E-01	3.32E-03		-1.54E+00	5.55E-06	Down	1.15E+00	3.27E-01		1.37E+00	1.82E-01				Unigene2391_All//9.00E-44//TC147255				ESTscan +
Unigene23910_All	3330	1.34	1.92	1.76	5.61	3.32	2.59	8.76	3.44	3.40	5.22E-01	2.60E-02		3.97E-01	1.34E-01		-7.57E-01	1.10E-10		-1.11E+00	7.01E-18	Down	-1.35E+00	5.64E-42	Down	-1.37E+00	4.52E-44	Down	Unigene23910_All//gi|297807817|ref|XP_002871792.1|//0.00E+00//C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317629|gb|EFH48051.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene23910_All//0.00E+00//AT5G17980| C2 domain-containing protein	Unigene23910_All//0.00E+00//TC167959			GO:0016020//GO:0043231	nr -
Unigene23912_All	2491	2.42	5.23	5.07	5.82	8.42	6.65	1.19	2.63	1.74	1.11E+00	8.40E-12	Up	1.07E+00	2.44E-10	Up	5.33E-01	1.91E-06		1.93E-01	2.09E-01		1.15E+00	5.50E-08	Up	5.53E-01	2.86E-02		Unigene23912_All//gi|157313314|gb|ABV32550.1|//0.00E+00//sucrose phosphate synthase protein 2 [Prunus persica]	Unigene23912_All//0.00E+00//AT5G11110| ATSPS2F (SUCROSE PHOSPHATE SYNTHASE 2F); sucrose-phosphate synthase	Unigene23912_All//0.00E+00//TC157499		ko00500|Starch and sucrose metabolism	GO:0005984//GO:0035251	nr +
Unigene23913_All	2501	0.42	1.48	1.19	1.51	1.69	1.52	0.20	0.22	0.43	1.82E+00	2.79E-07	Up	1.51E+00	1.38E-04	Up	1.62E-01	6.27E-01		3.00E-03	9.95E-01		9.89E-02	9.21E-01		1.08E+00	5.98E-02		Unigene23913_All//gi|157313314|gb|ABV32550.1|//0.00E+00//sucrose phosphate synthase protein 2 [Prunus persica]	Unigene23913_All//0.00E+00//AT5G11110| ATSPS2F (SUCROSE PHOSPHATE SYNTHASE 2F); sucrose-phosphate synthase	Unigene23913_All//0.00E+00//TC157499		ko00500|Starch and sucrose metabolism	GO:0005984//GO:0035251	nr +
Unigene23914_All	1283	13.95	47.87	7.93	11.96	34.14	9.82	44.85	52.77	68.16	1.78E+00	1.63E-106	Up	-8.15E-01	2.29E-09		1.51E+00	3.23E-71	Up	-2.84E-01	5.73E-02		2.35E-01	4.38E-05		6.04E-01	1.36E-33		Unigene23914_All//gi|224074873|ref|XP_002304470.1|//3.00E-56//f-box family protein [Populus trichocarpa] >gi|222841902|gb|EEE79449.1| f-box family protein [Populus trichocarpa]	Unigene23914_All//2.00E-56//AT1G12710| AtPP2-A12 (Phloem protein 2-A12); carbohydrate binding	Unigene23914_All//0.00E+00//gi|78353864|gb|DT574138.1|DT574138			GO:0005488	nr +
Unigene23915_All	3450	2.09	1.60	2.49	5.88	6.60	6.43	13.76	27.68	10.01	-3.87E-01	8.06E-02		2.48E-01	2.54E-01		1.67E-01	1.88E-01		1.29E-01	3.54E-01		1.01E+00	2.06E-85	Up	-4.59E-01	9.56E-12		Unigene23915_All//gi|224124220|ref|XP_002319275.1|//8.00E-81//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222857651|gb|EEE95198.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene23915_All//1.00E-71//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene23915_All//0.00E+00//TC148928		ko04626|Plant-pathogen interaction		nr -
Unigene23920_All	349	8.10	4.94	6.41	6.85	4.64	5.56	8.60	4.07	2.51	-7.14E-01	5.52E-02		-3.37E-01	3.83E-01		-5.63E-01	1.64E-01		-3.00E-01	5.02E-01		-1.08E+00	8.90E-04	Down	-1.78E+00	2.27E-07	Down			Unigene23920_All//2.00E-107//TC141427				ESTscan +
Unigene23921_All	516	9.13	11.19	11.15	8.98	6.67	7.53	7.21	4.94	2.01	2.95E-01	2.51E-01		2.88E-01	2.90E-01		-4.28E-01	1.28E-01		-2.54E-01	4.16E-01		-5.45E-01	5.74E-02		-1.84E+00	2.29E-09	Down			Unigene23921_All//1.00E-54//EV498053				
Unigene23922_All	1005	44.93	29.04	36.82	36.68	35.91	24.58	15.94	9.23	6.50	-6.30E-01	2.69E-15		-2.87E-01	5.32E-04		-3.06E-02	8.13E-01		-5.77E-01	1.33E-11		-7.88E-01	3.39E-10		-1.29E+00	1.06E-22	Down	Unigene23922_All//gi|124359162|gb|ABV05685.1|//1.00E-18//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene23922_All//1.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene23922_All//0.00E+00//TC141427				nr +
Unigene23929_All	3369	3.20	1.91	2.75	2.68	2.41	1.77	3.04	0.84	1.42	-7.44E-01	1.85E-05		-2.18E-01	2.59E-01		-1.50E-01	5.13E-01		-5.97E-01	1.55E-03		-1.85E+00	1.37E-23	Down	-1.10E+00	1.30E-11	Down	Unigene23929_All//gi|42562825|ref|NP_176222.2|//0.00E+00//potassium transporter family protein [Arabidopsis thaliana] >gi|38502862|sp|O80739.2|POT12_ARATH RecName: Full=Putative potassium transporter 12; Short=AtPOT12	Unigene23929_All//0.00E+00//AT1G60160| potassium transporter family protein	Unigene23929_All//0.00E+00//TC141951			GO:0030001//GO:0044464//GO:0046873	nr +
Unigene23930_All	3599	0.67	0.37	0.96	0.39	0.69	0.09	1.17	0.53	0.42	-8.70E-01	3.39E-02		5.24E-01	1.39E-01		8.30E-01	3.86E-02		-2.14E+00	6.16E-04	Down	-1.14E+00	2.32E-05	Down	-1.48E+00	6.12E-08	Down	Unigene23930_All//gi|42562825|ref|NP_176222.2|//0.00E+00//potassium transporter family protein [Arabidopsis thaliana] >gi|38502862|sp|O80739.2|POT12_ARATH RecName: Full=Putative potassium transporter 12; Short=AtPOT12	Unigene23930_All//0.00E+00//AT1G60160| potassium transporter family protein	Unigene23930_All//0.00E+00//TC141951			GO:0030001//GO:0044464//GO:0046873	nr +
Unigene23933_All	1766	3.91	12.19	4.28	13.03	15.50	18.29	32.92	55.10	35.39	1.64E+00	9.51E-34	Up	1.31E-01	6.06E-01		2.50E-01	1.60E-02		4.89E-01	1.09E-07		7.43E-01	3.90E-52		1.05E-01	1.02E-01		Unigene23933_All//gi|60932254|gb|AAX37335.1|//0.00E+00//UDP-glucuronic acid decarboxylase 2 [Populus tomentosa]	Unigene23933_All//0.00E+00//AT3G62830| AUD1; UDP-glucuronate decarboxylase/ catalytic/ dTDP-glucose 4,6-dehydratase	Unigene23933_All//0.00E+00//TC138942		ko00523|Polyketide sugar unit biosynthesis	GO:0009226//GO:0012505//GO:0016020//GO:0016831//GO:0016836//GO:0019121//GO:0043231//GO:0048037	nr -

Unigene23934_All	1867	52.85	103.65	84.05	20.81	31.43	35.15	14.81	32.91	24.20	9.72E-01	2.57E-132		6.69E-01	2.76E-55		5.95E-01	8.35E-21		7.56E-01	6.19E-32		1.15E+00	2.20E-68	Up	7.08E-01	2.61E-23		Unigene23934_All//gi|15237896|ref|NP_197800.1|//0.00E+00//SIGE (SIGMA FACTOR E); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor [Arabidopsis thaliana] >gi|4033838|emb|CAA77213.1| sigma-like factor [Arabidopsis thaliana] >gi|4972299|dbj|BAA78109.1| RNA polymerase sigma subunit SigE [Arabidopsis thaliana] >gi|10178160|dbj|BAB11572.1| sigma-like factor [Arabidopsis thaliana] >gi|222423237|dbj|BAH19595.1| AT5G24120 [Arabidopsis thaliana]	Unigene23934_All//2.00E-179//AT5G24120| SIGE (SIGMA FACTOR E); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor	Unigene23934_All//0.00E+00//TC169078	Sigma70-like		GO:0000996//GO:0001071//GO:0003676//GO:0006351//GO:0009639//GO:0030162	nr +
Unigene23936_All	508	0.82	0.70	1.05	3.63	2.85	0.98	1.58	1.73	1.02	-2.39E-01	8.10E-01		3.47E-01	7.06E-01		-3.50E-01	4.93E-01		-1.89E+00	2.31E-04	Down	1.28E-01	8.49E-01		-6.33E-01	3.56E-01		Unigene23936_All//gi|115462875|ref|NP_001055037.1|//2.00E-07//Os05g0256100 [Oryza sativa Japonica Group] >gi|113578588|dbj|BAF16951.1| Os05g0256100 [Oryza sativa Japonica Group]	Unigene23936_All//1.00E-07//AT1G56145| leucine-rich repeat family protein / protein kinase family protein	Unigene23936_All//3.00E-61//ES848834			GO:0004175//GO:0004702//GO:0004713//GO:0006464//GO:0016628//GO:0031410//GO:0032559//GO:0043231	nr +
Unigene23937_All	2361	11.41	7.90	9.97	0.46	1.47	0.77	32.18	10.82	52.06	-5.31E-01	3.52E-07		-1.95E-01	9.32E-02		1.67E+00	8.82E-07	Up	7.21E-01	1.51E-01		-1.57E+00	6.73E-136	Down	6.94E-01	1.08E-59		Unigene23937_All//gi|6056376|gb|AAF02840.1|AC009894_11//0.00E+00//Similar to serine/threonine kinases [Arabidopsis thaliana]	Unigene23937_All//0.00E+00//AT1G56140| leucine-rich repeat family protein / protein kinase family protein	Unigene23937_All//3.00E-145//gi|78332832|gb|DT553106.1|DT553106		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004713//GO:0006464//GO:0016628//GO:0032559	nr +
Unigene23938_All	2103	10.18	7.49	8.58	3.48	5.32	6.79	3.48	9.48	5.23	-4.42E-01	1.95E-04		-2.45E-01	5.81E-02		6.12E-01	1.38E-04		9.63E-01	7.59E-11		1.45E+00	5.14E-32	Up	5.88E-01	8.08E-05		Unigene23938_All//gi|297802820|ref|XP_002869294.1|//1.00E-160//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315130|gb|EFH45553.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23938_All//2.00E-159//AT4G32060| calcium-binding EF hand family protein	Unigene23938_All//0.00E+00//TC154143	ko04626|Plant-pathogen interaction	GO:0046872	nr +
Unigene23939_All	2749	3.41	3.54	4.20	5.87	6.59	4.88	8.95	4.24	10.71	5.49E-02	7.78E-01		3.03E-01	9.39E-02		1.66E-01	2.59E-01		-2.67E-01	6.90E-02		-1.08E+00	3.89E-25	Down	2.59E-01	3.51E-03		Unigene23939_All//gi|297720101|ref|NP_001172412.1|//2.00E-55//Os01g0550600 [Oryza sativa Japonica Group] >gi|255673350|dbj|BAH91142.1| Os01g0550600 [Oryza sativa Japonica Group]	Unigene23939_All//1.00E-65//AT5G53020| unknown protein	Unigene23939_All//0.00E+00//TC164261				nr +
Unigene2394_All	586	4.91	1.47	2.91	29.33	26.97	16.88	6.49	17.47	2.31	-1.74E+00	1.44E-05	Down	-7.56E-01	5.03E-02		-1.21E-01	4.49E-01		-7.97E-01	1.14E-09		1.43E+00	1.61E-16	Up	-1.49E+00	2.75E-07	Down	Unigene2394_All//gi|115441793|ref|NP_001045176.1|//2.00E-06//Os01g0914000 [Oryza sativa Japonica Group] >gi|113534707|dbj|BAF07090.1| Os01g0914000 [Oryza sativa Japonica Group]	Unigene2394_All//2.00E-34//AT5G48500| unknown protein	Unigene2394_All//0.00E+00//ES799140				nr -
Unigene23942_All	1008	5.66	9.80	4.86	9.98	14.45	24.64	17.74	17.17	33.20	7.93E-01	1.50E-05		-2.19E-01	4.15E-01		5.34E-01	1.15E-04		1.30E+00	1.17E-29	Up	-4.77E-02	7.33E-01		9.04E-01	3.85E-26		Unigene23942_All//gi|125951640|sp|Q0DCM5.2|MAN6_ORYSJ//4.00E-33//RecName: Full=Mannan endo-1,4-beta-mannosidase 6; AltName: Full=Beta-mannanase 6; AltName: Full=Endo-beta-1,4-mannanase 6; AltName: Full=OsMAN6; Flags: Precursor	Unigene23942_All//5.00E-23//AT2G20680| glycosyl hydrolase family 5 protein / cellulase family protein	Unigene23942_All//0.00E+00//gi|21098172|gb|BQ410485.1|BQ410485			GO:0016798//GO:0043167//GO:0044238	nr +
Unigene23943_All	1640	4.40	8.16	5.94	6.96	11.99	17.65	13.12	13.30	33.86	8.90E-01	1.33E-08		4.33E-01	2.56E-02		7.86E-01	1.65E-11		1.34E+00	4.26E-36	Up	1.98E-02	8.84E-01		1.37E+00	1.83E-82	Up	Unigene23943_All//gi|125951640|sp|Q0DCM5.2|MAN6_ORYSJ//1.00E-143//RecName: Full=Mannan endo-1,4-beta-mannosidase 6; AltName: Full=Beta-mannanase 6; AltName: Full=Endo-beta-1,4-mannanase 6; AltName: Full=OsMAN6; Flags: Precursor	Unigene23943_All//2.00E-122//AT4G28320| glycosyl hydrolase family 5 protein / cellulase family protein	Unigene23943_All//0.00E+00//TC140198			GO:0016798//GO:0043167//GO:0044238	nr +
Unigene23944_All	2057	36.68	45.50	42.20	25.21	35.77	56.62	71.55	121.45	63.35	3.11E-01	5.67E-09		2.02E-01	5.99E-04		5.05E-01	1.81E-19		1.17E+00	1.02E-115	Up	7.63E-01	5.58E-139		-1.76E-01	2.50E-06		Unigene23944_All//gi|186495165|ref|NP_565074.2|//1.00E-125//calmodulin binding [Arabidopsis thaliana]	Unigene23944_All//5.00E-122//AT1G73805| calmodulin binding	Unigene23944_All//0.00E+00//gi|78339621|gb|DT559895.1|DT559895		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005515	nr +
Unigene23945_All	2136	32.87	12.07	19.94	34.24	24.75	12.45	3.31	1.96	1.51	-1.44E+00	9.89E-91	Down	-7.21E-01	2.20E-28		-4.68E-01	2.79E-17		-1.46E+00	4.11E-104	Down	-7.57E-01	1.15E-04		-1.13E+00	1.23E-08	Down	Unigene23945_All//gi|115479213|ref|NP_001063200.1|//0.00E+00//Os09g0420900 [Oryza sativa Japonica Group] >gi|113631433|dbj|BAF25114.1| Os09g0420900 [Oryza sativa Japonica Group]	Unigene23945_All//5.00E-169//AT4G31820| ENP (ENHANCER OF PINOID); protein binding / signal transducer	Unigene23945_All//3.00E-154//AI731519			GO:0005488//GO:0009314//GO:0060089	nr -
Unigene23948_All	1233	4.37	4.85	4.45	4.00	4.11	4.98	3.74	2.31	1.55	1.50E-01	5.81E-01		2.54E-02	9.40E-01		3.76E-02	9.09E-01		3.17E-01	2.23E-01		-6.97E-01	5.34E-03		-1.27E+00	5.80E-07	Down	Unigene23948_All//gi|30699037|ref|NP_177608.2|//1.00E-87//TRZ1 (TRNASE Z 1); 3'-tRNA processing endoribonuclease [Arabidopsis thaliana] >gi|88984765|sp|Q8LGU7.3|RNZN_ARATH RecName: Full=Nuclear ribonuclease Z; Short=RNase Z; AltName: Full=tRNase Z; AltName: Full=tRNA 3 endonuclease; AltName: Full=Zinc phosphodiesterase NUZ >gi|20975609|emb|CAD22100.1| RNase Z [Arabidopsis thaliana] >gi|90962972|gb|ABE02410.1| At1g74700 [Arabidopsis thaliana]	Unigene23948_All//5.00E-89//AT1G74700| TRZ1 (TRNASE Z 1); 3'-tRNA processing endoribonuclease	Unigene23948_All//0.00E+00//gi|78332065|gb|DT552339.1|DT552339			GO:0008033//GO:0016891	nr -
Unigene23949_All	1526	1.20	2.89	3.94	3.92	4.85	8.94	1.58	2.47	4.49	1.27E+00	2.32E-05	Up	1.72E+00	3.85E-10	Up	3.09E-01	1.74E-01		1.19E+00	2.10E-14	Up	6.42E-01	2.31E-02		1.51E+00	1.68E-12	Up	Unigene23949_All//gi|12043533|emb|CAC19789.1|//1.00E-46//MYB-like DNA-binding protein [Catharanthus roseus]	Unigene23949_All//2.00E-40//AT1G07540| TRFL2 (TRF-LIKE 2); DNA binding	Unigene23949_All//0.00E+00//TC165993	MYB-related			nr +
Unigene2395_All	794	3.10	2.17	1.14	5.71	4.99	2.56	2.24	0.89	1.66	-5.13E-01	2.12E-01		-1.44E+00	1.08E-03		-1.95E-01	5.62E-01		-1.16E+00	4.35E-05	Down	-1.32E+00	3.24E-03		-4.34E-01	3.18E-01		Unigene2395_All//gi|255572638|ref|XP_002527252.1|//1.00E-42//conserved hypothetical protein [Ricinus communis] >gi|223533345|gb|EEF35096.1| conserved hypothetical protein [Ricinus communis]	Unigene2395_All//1.00E-25//AT5G48500| unknown protein	Unigene2395_All//0.00E+00//TC138221				nr -
Unigene23950_All	2568	1.92	3.12	3.07	5.47	6.10	9.50	1.79	3.32	4.02	7.03E-01	6.18E-04		6.80E-01	1.54E-03		1.58E-01	3.24E-01		7.96E-01	2.67E-13		8.88E-01	6.46E-07		1.16E+00	1.21E-12	Up	Unigene23950_All//gi|12043533|emb|CAC19789.1|//1.00E-148//MYB-like DNA-binding protein [Catharanthus roseus]	Unigene23950_All//8.00E-122//AT1G07540| TRFL2 (TRF-LIKE 2); DNA binding	Unigene23950_All//0.00E+00//TC165993	MYB-related			nr -
Unigene23951_All	1655	21.09	10.59	6.11	76.66	73.41	51.69	29.20	14.47	19.26	-9.93E-01	2.14E-25		-1.79E+00	2.52E-59	Down	-6.26E-02	2.42E-01		-5.69E-01	1.72E-37		-1.01E+00	5.41E-44	Down	-6.01E-01	6.99E-19		Unigene23951_All//gi|19569135|gb|AAL92026.1|AF481959_1//0.00E+00//tubulin beta-1 [Gossypium hirsutum] >gi|19569609|gb|AAL92118.1|AF487511_1 beta-tubulin [Gossypium hirsutum]	Unigene23951_All//0.00E+00//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene23951_All//0.00E+00//TC176998		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene23953_All	2963	1.32	0.44	0.67	3.23	5.21	4.28	4.34	3.00	2.26	-1.57E+00	1.89E-06	Down	-9.94E-01	2.15E-03		6.90E-01	2.10E-07		4.08E-01	1.08E-02		-5.30E-01	1.53E-04		-9.41E-01	2.39E-11		Unigene23953_All//gi|224122712|ref|XP_002318907.1|//1.00E-150//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222850580|gb|EEE97127.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene23953_All//2.00E-59//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene23953_All//0.00E+00//gi|21089563|gb|BQ401876.1|BQ401876		ko04626|Plant-pathogen interaction		nr +
Unigene23955_All	1940	25.27	58.79	33.87	77.49	132.13	97.66	11.68	15.15	10.10	1.22E+00	1.31E-112	Up	4.23E-01	1.54E-10		7.70E-01	1.81E-141		3.34E-01	4.84E-21		3.75E-01	2.61E-05		-2.09E-01	4.56E-02		Unigene23955_All//gi|30684032|ref|NP_180450.2|//0.00E+00//ankyrin repeat family protein [Arabidopsis thaliana] >gi|75332072|sp|Q94B55.1|XB31_ARATH RecName: Full=Putative E3 ubiquitin-protein ligase XBAT31; AltName: Full=Ankyrin repeat domain and RING finger-containing protein XBAT31; AltName: Full=Protein XB3 homolog 1 >gi|70905107|gb|AAZ14079.1| At2g28840 [Arabidopsis thaliana]	Unigene23955_All//0.00E+00//AT2G28840| ankyrin repeat family protein	Unigene23955_All//0.00E+00//gi|164329831|gb|ES808972.1|ES808972			GO:0003824//GO:0046914	nr -
Unigene23956_All	698	4.42	3.12	4.27	4.28	4.44	5.82	5.21	3.95	2.17	-5.03E-01	1.58E-01		-4.99E-02	8.98E-01		5.23E-02	9.05E-01		4.44E-01	1.65E-01		-3.99E-01	1.86E-01		-1.26E+00	1.20E-05	Down	Unigene23956_All//gi|124361203|gb|ABN09175.1|//4.00E-17//Homeodomain-related [Medicago truncatula]	Unigene23956_All//2.00E-11//AT3G10760| myb family transcription factor	Unigene23956_All//6.00E-128//TC166200	G2-like		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene2396_All	1156	0.91	0.61	1.06	6.25	4.35	2.66	5.96	9.29	0.83	-5.61E-01	3.82E-01		2.27E-01	7.03E-01		-5.23E-01	1.17E-02		-1.23E+00	1.85E-08	Down	6.40E-01	3.50E-05		-2.85E+00	1.20E-27	Down	Unigene2396_All//gi|115441793|ref|NP_001045176.1|//3.00E-07//Os01g0914000 [Oryza sativa Japonica Group] >gi|113534707|dbj|BAF07090.1| Os01g0914000 [Oryza sativa Japonica Group]	Unigene2396_All//1.00E-28//AT5G48500| unknown protein	Unigene2396_All//0.00E+00//ES799140				nr +
Unigene23961_All	1075	1.22	2.07	3.42	1.44	3.33	1.60	6.80	5.48	16.08	7.69E-01	7.33E-02		1.49E+00	2.18E-05	Up	1.21E+00	1.40E-04	Up	1.52E-01	7.68E-01		-3.12E-01	1.27E-01		1.24E+00	9.81E-23	Up	Unigene23961_All//gi|13605841|gb|AAK32906.1|AF367319_1//1.00E-42//AT5g59960/mmn10_180 [Arabidopsis thaliana] >gi|22137192|gb|AAM91441.1| AT5g59960/mmn10_180 [Arabidopsis thaliana]	Unigene23961_All//6.00E-42//AT5G59960| unknown protein	Unigene23961_All//0.00E+00//TC136790			GO:0043231	nr -
Unigene23962_All	461	0.45	2.97	2.43	0.86	1.87	0.98	3.49	4.90	3.98	2.71E+00	1.29E-04	Up	2.42E+00	2.21E-03		1.11E+00	1.63E-01		1.81E-01	8.83E-01		4.90E-01	2.16E-01		1.90E-01	6.51E-01		Unigene23962_All//gi|115434566|ref|NP_001042041.1|//4.00E-19//Os01g0151600 [Oryza sativa Japonica Group] >gi|113531572|dbj|BAF03955.1| Os01g0151600 [Oryza sativa Japonica Group]	Unigene23962_All//2.00E-18//AT5G59960| unknown protein	Unigene23962_All//1.00E-20//TC148558			GO:0043231	nr +
Unigene23966_All	2750	6.93	3.57	4.76	12.92	12.68	10.53	7.96	16.63	2.42	-9.54E-01	2.41E-13		-5.40E-01	3.58E-05		-2.60E-02	8.16E-01		-2.95E-01	1.00E-03		1.06E+00	6.59E-45	Up	-1.72E+00	2.38E-46	Down	Unigene23966_All//gi|14335068|gb|AAK59798.1|//4.00E-80//AT5g35460/MOK9_4 [Arabidopsis thaliana] >gi|27764924|gb|AAO23583.1| At5g35460/MOK9_4 [Arabidopsis thaliana]	Unigene23966_All//3.00E-74//AT5G35460| unknown protein	Unigene23966_All//0.00E+00//TC161588			GO:0044464	nr +
Unigene23972_All	800	9.61	28.18	18.84	2.62	3.70	2.60	0.11	0.31	1.00	1.55E+00	1.26E-32	Up	9.70E-01	1.59E-10		5.01E-01	1.84E-01		-1.01E-02	9.75E-01		1.57E+00	3.26E-01		3.24E+00	3.96E-04	Up	Unigene23972_All//gi|296875326|gb|AD482116.1|//5.00E-48//violaxanthin de-epoxidase [Citrus sinensis]	Unigene23972_All//6.00E-30//AT1G08550| NPQ1 (NON-PHOTOCHEMICAL QUENCHING 1); violaxanthin de-epoxidase	Unigene23972_All//0.00E+00//TC167239		ko00906|Carotenoid biosynthesis	GO:0008152//GO:0009536//GO:0016491	nr +

Unigene23973_All	1897	22.42	59.72	31.21	7.77	7.30	7.19	0.38	0.93	1.45	1.41E+00	1.42E-140	Up	4.77E-01	8.55E-12		-9.11E-02	6.08E-01		-1.12E-01	5.27E-01		1.29E+00	4.31E-03		1.94E+00	1.89E-07	Up	Unigene23973_All//gi|296875326|gb|ADH82116.1|//0.00E+00//violaxanthin de-epoxidase [Citrus sinensis]	Unigene23973_All//1.00E-141//AT1G08550| NPQ1 (NON-PHOTOCHEMICAL QUENCHING 1); violaxanthin de-epoxidase	Unigene23973_All//0.00E+00//TC162648		ko00906|Carotenoid biosynthesis	GO:0008152//GO:0009534//GO:0016491	nr +
Unigene23975_All	1924	5.57	5.74	4.51	5.83	8.54	10.96	7.89	15.84	9.42	4.24E-02	8.16E-01		-3.05E-01	1.07E-01		5.51E-01	1.85E-05		9.12E-01	1.93E-14		1.01E+00	1.15E-27	Up	2.56E-01	2.86E-02		Unigene23975_All//gi|297822773|ref|XP_002879269.1|//1.00E-134//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325108|gb|EFH55528.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23975_All//2.00E-133//AT2G30580| DRIP2 (DREB2A-INTERACTING PROTEIN 2); protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene23975_All//0.00E+00//TC172167				nr +
Unigene23977_All	2119	1.78	1.63	0.65	1.22	2.00	1.19	5.61	1.91	3.37	-1.29E-01	6.83E-01		-1.44E+00	2.83E-05	Down	7.09E-01	1.38E-02		-3.44E-02	9.44E-01		-1.55E+00	1.85E-21	Down	-7.36E-01	3.02E-07		Unigene23977_All//gi|164605531|dbj|BAF98597.1|//0.00E+00//CM0545.360.nc [Lotus japonicus]	Unigene23977_All//0.00E+00//AT3G21620| early-responsive to dehydration protein-related / ERD protein-related	Unigene23977_All//0.00E+00//ES791798			GO:0016020//GO:0031410	nr +
Unigene23978_All	2272	21.72	56.16	28.22	9.76	14.05	15.29	6.16	12.47	7.80	1.37E+00	4.45E-151	Up	3.78E-01	1.71E-08		5.26E-01	2.49E-09		6.48E-01	3.14E-13		1.02E+00	2.67E-26	Up	3.41E-01	3.21E-03		Unigene23978_All//gi|115439195|ref|NP_001043877.1|//2.00E-59//Os01g0681000 [Oryza sativa Japonica Group] >gi|113533408|dbj|BAF05791.1|Os01g0681000 [Oryza sativa Japonica Group]	Unigene23978_All//9.00E-54//AT5G53390| unknown protein	Unigene23978_All//0.00E+00//gi|78335557|gb|DT555831.1|DT555831				nr +
Unigene23980_All	1601	10.23	28.42	22.95	9.18	10.43	49.56	13.15	11.70	37.92	1.47E+00	1.74E-60	Up	1.17E+00	3.01E-33	Up	1.85E-01	2.24E-01		2.43E+00	1.71E-220	Up	-1.69E-01	1.50E-01		1.53E+00	3.53E-106	Up	Unigene23980_All//gi|297801962|ref|XP_002868865.1|//1.00E-119//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314701|gb|EFH45124.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene23980_All//8.00E-119//AT4G38810| calcium-binding EF hand family protein	Unigene23980_All//0.00E+00//TC131229			GO:0046872	nr -
Unigene23981_All	1603	7.34	24.53	13.49	8.76	9.86	35.70	8.73	6.15	20.60	1.74E+00	2.46E-66	Up	8.77E-01	1.32E-12		1.70E-01	2.92E-01		2.03E+00	6.80E-127	Up	-5.05E-01	1.57E-04		1.24E+00	1.67E-42	Up	Unigene23981_All//gi|228481109|gb|ACQ42253.1|//1.00E-148//SsRK2 calcium sensor [Nicotiana plumbaginifolia]	Unigene23981_All//1.00E-142//AT4G38810| calcium-binding EF hand family protein	Unigene23981_All//0.00E+00//TC131229			GO:0046872	nr +
Unigene23983_All	584	8.24	10.32	10.03	10.32	4.42	16.94	18.39	30.06	7.23	3.25E-01	1.97E-01		2.83E-01	2.96E-01		-1.22E+00	7.14E-08	Down	7.15E-01	6.48E-05		7.09E-01	2.36E-09		-1.35E+00	2.00E-16	Down			Unigene23983_All//0.00E+00//gi|164304320|gb|ES824157.1|ES824157				
Unigene23985_All	1964	22.03	29.72	57.67	58.23	51.34	54.84	136.18	24.86	29.86	4.32E-01	3.14E-10		1.39E+00	1.78E-133	Up	-1.82E-01	7.00E-05		-8.65E-02	1.16E-01		-2.45E+00	0.00E+00	Down	-2.19E+00	0.00E+00	Down	Unigene23985_All//gi|197259950|gb|ACH56524.1|//0.00E+00//flavonoid 3'5'-hydroxylase [Gossypium hirsutum]	Unigene23985_All//2.00E-141//AT5G07990| TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	Unigene23985_All//0.00E+00//TC148300		ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr -
Unigene23987_All	1873	14.78	17.58	17.31	73.70	46.05	37.47	37.61	17.52	18.46	2.51E-01	9.22E-03		2.29E-01	2.56E-02		-6.78E-01	5.56E-63		-9.76E-01	1.20E-103		-1.10E+00	4.29E-73	Down	-1.03E+00	5.33E-67	Down	Unigene23987_All//gi|21616053|emb|CAC86004.1|//0.00E+00//aspartic proteinase [Theobroma cacao]	Unigene23987_All//0.00E+00//AT1G11910| aspartyl protease family protein	Unigene23987_All//0.00E+00//TC132875			GO:0004175//GO:0019538//GO:0043231	nr -
Unigene23988_All	3971	24.06	4.64	13.53	36.92	23.27	45.16	60.40	27.00	61.99	-2.37E+00	6.90E-242	Down	-8.30E-01	5.80E-49		-6.66E-01	1.15E-64		2.91E-01	1.61E-15		-1.16E+00	4.27E-269	Down	3.74E-02	2.65E-01		Unigene23988_All//gi|7630016|emb|CAB88358.1|//0.00E+00//transporter-like protein [Arabidopsis thaliana]	Unigene23988_All//0.00E+00//AT3G53960| proton-dependent oligopeptide transport (POT) family protein	Unigene23988_All//0.00E+00//TC168673			GO:0003677//GO:0006350//GO:0010468//GO:0015833//GO:0031224	nr +
Unigene23989_All	1923	10.04	4.80	6.09	22.20	21.79	23.91	14.12	15.30	13.69	-1.07E+00	4.51E-16	Down	-7.21E-01	2.93E-08		-2.67E-02	8.19E-01		1.07E-01	2.42E-01		1.16E-01	2.57E-01		-4.37E-02	6.72E-01		Unigene23989_All//gi|297813753|ref|XP_002874760.1|//0.00E+00//UDP-D-glucuronate 4-epimerase 5 [Arabidopsis lyrata subsp. lyrata] >gi|297320597|gb|EFH51019.1| UDP-D-glucuronate 4-epimerase 5 [Arabidopsis lyrata subsp. lyrata]	Unigene23989_All//2.00E-170//AT4G12250| GAE5 (UDP-D-GLUCURONATE 4-EPIMERASE 5); UDP-glucuronate 4-epimerase/ catalytic	Unigene23989_All//0.00E+00//gi|78331554|gb|DT551828.1|DT551828		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0006139//GO:0016857//GO:0044464//GO:0048037	nr +
Unigene23990_All	2009	12.58	2.72	9.22	4.56	4.25	2.25	0.93	0.08	2.02	-2.21E+00	6.28E-59	Down	-4.48E-01	6.42E-05		-1.02E-01	6.38E-01		-1.02E+00	5.87E-08	Down	-3.48E+00	4.23E-09	Down	1.13E+00	2.79E-05	Up	Unigene23990_All//gi|115465815|ref|NP_001056507.1|//1.00E-166//Os05g0594500 [Oryza sativa Japonica Group] >gi|113580058|dbj|BAF18421.1|Os05g0594500 [Oryza sativa Japonica Group]	Unigene23990_All//0.00E+00//AT3G48200| unknown protein	Unigene23990_All//0.00E+00//ES809935				nr +
Unigene23991_All	3636	6.32	1.20	4.55	2.84	2.32	1.29	0.33	0.10	1.93	-2.40E+00	2.94E-59	Down	-4.72E-01	6.30E-05		-2.90E-01	1.13E-01		-1.13E+00	2.08E-10	Down	-1.65E+00	5.03E-03		2.57E+00	9.02E-25	Up	Unigene23991_All//gi|115465815|ref|NP_001056507.1|//0.00E+00//Os05g0594500 [Oryza sativa Japonica Group] >gi|113580058|dbj|BAF18421.1|Os05g0594500 [Oryza sativa Japonica Group]	Unigene23991_All//0.00E+00//AT3G48200| unknown protein	Unigene23991_All//0.00E+00//ES809935			GO:0044464	nr +
Unigene23993_All	2668	14.04	23.44	11.32	25.13	29.54	34.26	41.06	55.99	141.05	7.39E-01	2.26E-27		-3.11E-01	6.69E-04		2.33E-01	2.60E-05		4.47E-01	1.31E-17		4.47E-01	1.76E-32		1.78E+00	0.00E+00	Up	Unigene23993_All//gi|115451711|ref|NP_001049456.1|//7.00E-55//Os03g0230300 [Oryza sativa Japonica Group] >gi|108706982|gb|ABF94777.1| Poly polymerase catalytic domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|108706983|gb|ABF94778.1| Poly polymerase catalytic domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547927|dbj|BAF11370.1|Os03g0230300 [Oryza sativa Japonica Group]	Unigene23993_All//5.00E-42//AT1G32230| RCD1 (RADICAL-INDUCED CELL DEATH1); protein binding	Unigene23993_All//0.00E+00//TC160976			GO:0006979//GO:0009628//GO:0009719//GO:0009987//GO:0010033//GO:0044424	nr -
Unigene23994_All	2102	17.75	25.31	27.74	15.48	28.52	23.31	6.74	2.70	4.02	5.12E-01	1.51E-12		6.44E-01	1.54E-19		8.82E-01	9.33E-42		5.91E-01	9.61E-16		-1.32E+00	4.58E-20	Down	-7.46E-01	1.23E-08		Unigene23994_All//gi|256997232|dbj|BAI22699.1|//1.00E-121//MurA transferase2 [Physcomitrella patens subsp. patens] >gi|256997234|dbj|BAI22700.1| MurA transferase2 [Physcomitrella patens subsp. patens]	Unigene23994_All//1.00E-06//AT1G48860| 3-phosphoshikimate 1-carboxyvinyltransferase, putative / 5-enolpyruvylshikimate-3-phosphate, putative / EPSP synthase, putative	Unigene23994_All//0.00E+00//TC147102		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0003824	nr +
Unigene23996_All	2005	22.89	13.12	15.46	43.43	39.45	26.06	32.31	12.88	10.81	-8.03E-01	2.21E-23		-5.66E-01	2.02E-12		-1.39E-01	1.41E-02		-7.37E-01	1.02E-40		-1.33E+00	6.62E-90	Down	-1.58E+00	4.65E-120	Down	Unigene23996_All//gi|75207338|sp|Q9SRE5.1|Y1666_ARATH//1.00E-138//RecName: Full=Uncharacterized protein At1g76660 >gi|28851037|gb|AAO63442.1|At1g76660 [Arabidopsis thaliana]	Unigene23996_All//3.00E-130//AT1G76660| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT5G52430.1); Has 280 Blast hits to 160 proteins in 42 species: Archae - 0; Bacteria - 4; Metazoa - 55; Fungi - 17; Plants - 64; Viruses - 4; Other Eukaryotes - 136 (source: NCBI BLink).	Unigene23996_All//0.00E+00//TC138101				nr +
Unigene23998_All	955	0.77	1.59	0.33	2.97	1.80	3.07	4.69	2.32	3.59	1.05E+00	5.24E-02		-1.20E+00	1.80E-01		-7.22E-01	4.22E-02		4.81E-02	9.22E-01		-1.02E+00	7.75E-05	Down	-3.88E-01	1.25E-01		Unigene23998_All//gi|18421489|ref|NP_568530.1|//5.00E-60//EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana]	Unigene23998_All//5.00E-59//AT2G32295| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; CONTAINS InterPro DOMAIN/s: EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: EXS family protein / ERD1/XPR1/SYG1 family protein (TAIR:AT5G35730.1); Has 582 Blast hits to 577 proteins in 138 species: Archae - 0; Bacteria - 0; Metazoa - 223; Fungi - 177; Plants - 106; Viruses - 0; Other Eukaryotes - 76 (source: NCBI BLink).	Unigene23998_All//1.00E-21//gi|78327608|gb|DT547882.1|DT547882			GO:0031224//GO:0031410	nr -
Unigene23999_All	1844	3.29	3.35	1.59	4.24	3.21	4.51	8.78	6.39	4.52	2.65E-02	9.30E-01		-1.05E+00	3.36E-05	Down	-4.01E-01	5.03E-02		8.75E-02	6.98E-01		-4.58E-01	2.04E-04		-9.60E-01	1.72E-14		Unigene23999_All//gi|18421489|ref|NP_568530.1|//0.00E+00//EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana]	Unigene23999_All//0.00E+00//AT5G35730| EXS family protein / ERD1/XPR1/SYG1 family protein	Unigene23999_All//0.00E+00//DN800699			GO:0031224//GO:0031410	nr +
Unigene24_All	752	1.95	2.76	1.27	5.83	2.98	5.10	3.88	3.06	8.74	5.04E-01	2.63E-01		-6.12E-01	2.90E-01		-9.70E-01	3.20E-04		-1.91E-01	5.73E-01		-3.44E-01	3.29E-01		1.17E+00	1.82E-08	Up	Unigene24_All//gi|297821204|ref|XP_002878485.1|//2.00E-17//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324323|gb|EFH54744.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene24_All//1.00E-18//AT3G62900| zinc ion binding	Unigene24_All//5.00E-101//TC160642				nr +
Unigene24000_All	741	2.68	7.73	1.22	7.19	25.61	10.00	18.26	22.56	18.44	1.53E+00	1.23E-08	Up	-1.14E+00	1.99E-02		1.83E+00	2.55E-40	Up	4.75E-01	2.95E-02		3.05E-01	1.44E-02		1.43E-02	9.46E-01		Unigene24000_All//gi|15241598|ref|NP_196452.1|//2.00E-52//GRAM domain-containing protein / ABA-responsive protein-related [Arabidopsis thaliana] >gi|75172412|sp|Q9FTA0.1|GEML4_ARATH RecName: Full=GEM-like protein 4	Unigene24000_All//9.00E-54//AT5G08350| GRAM domain-containing protein / ABA-responsive protein-related	Unigene24000_All//0.00E+00//ES832934				nr +
Unigene24002_All	3161	12.50	8.09	7.90	57.57	51.42	35.10	27.47	8.28	8.44	-6.27E-01	2.27E-13		-6.62E-01	4.97E-14		-1.63E-01	4.22E-06		-7.14E-01	5.37E-80		-1.73E+00	5.67E-178	Down	-1.70E+00	6.77E-179	Down	Unigene24002_All//gi|115477174|ref|NP_001062183.1|//0.00E+00//Os08g0505200 [Oryza sativa Japonica Group] >gi|113624152|dbj|BAF24097.1|Os08g0505200 [Oryza sativa Japonica Group]	Unigene24002_All//2.00E-174//AT2G42320| nucleolar protein gar2-related	Unigene24002_All//0.00E+00//TC166154		ko00310|Lysine degradation		nr -
Unigene24003_All	3054	0.67	0.45	0.49	3.36	2.45	1.64	2.27	0.86	0.59	-5.77E-01	2.05E-01		-4.53E-01	3.56E-01		-4.58E-01	7.19E-03		-1.03E+00	5.40E-09	Down	-1.40E+00	4.11E-11	Down	-1.95E+00	5.51E-18	Down	Unigene24003_All//gi|115477174|ref|NP_001062183.1|//0.00E+00//Os08g0505200 [Oryza sativa Japonica Group] >gi|113624152|dbj|BAF24097.1|Os08g0505200 [Oryza sativa Japonica Group]	Unigene24003_All//2.00E-172//AT2G42320| nucleolar protein gar2-related	Unigene24003_All//0.00E+00//TC166154		ko00310|Lysine degradation		nr -
Unigene24004_All	1859	59.53	60.35	48.72	148.24	110.60	69.87	97.11	10.12	7.07	1.97E-02	7.24E-01		-2.89E-01	8.42E-09		-4.23E-01	4.68E-53		-1.09E+00	4.02E-246	Down	-3.26E+00	0.00E+00	Down	-3.78E+00	0.00E+00	Down	Unigene24004_All//gi|79507883|ref|NP_196320.2|//1.00E-170//aspartic-type endopeptidase [Arabidopsis thaliana]	Unigene24004_All//5.00E-147//AT5G07030| aspartic-type endopeptidase	Unigene24004_All//0.00E+00//TC136921			GO:0004175//GO:0019538	nr +
Unigene24007_All	2295	0.36	0.66	0.37	0.41	0.95	1.32	0.72	0.56	0.33	8.60E-01	1.12E-01		2.51E-02	9.93E-01		1.20E+00	5.78E-03		1.68E+00	1.06E-05	Up	-3.48E-01	4.75E-01		-1.12E+00	1.16E-02		Unigene24007_All//gi|225452330|ref|XP_002272711.1|//1.00E-162//PREDICTED: similar to stpk1 protein kinase [Vitis vinifera]	Unigene24007_All//1.00E-141//AT3G27580| ATPK7; kinase/ protein serine/threonine kinase	Unigene24007_All//0.00E+00//ES801689				nr -

Unigene24009_All	2453	2.32	2.64	2.47	4.41	3.86	3.72	4.50	2.22	4.42	1.86E-01	4.51E-01		9.01E-02	7.20E-01		-1.91E-01	3.19E-01		-2.45E-01	1.99E-01		-1.02E+00	8.00E-11	Down	-2.62E-02	8.86E-01		Unigene24009_All//gi|115465695|ref|NP_001056447.1|//1.00E-159//Os05g0583500 [Oryza sativa Japonica Group] >gi|42491385|gb|AAS16891.1| unknown protein [Oryza sativa Japonica Group] >gi|113579998|dbj|BAF18361.1|Os05g0583500 [Oryza sativa Japonica Group]	Unigene24009_All//1.00E-125//AT1G15240| phox (PX) domain-containing protein	Unigene24009_All//0.00E+00//TC177204			GO:0005488//GO:0009987	nr +
Unigene2401_All	788	48.14	18.90	31.69	74.72	72.93	85.74	40.40	21.75	25.38	-1.35E+00	1.84E-44	Down	-6.03E-01	1.52E-11		-3.49E-02	7.02E-01		1.99E-01	2.17E-03		-8.94E-01	6.81E-24		-6.71E-01	2.51E-15		Unigene2401_All//gi|225444159|ref|XP_002270662.1|//2.00E-93//PREDICTED: similar to coatomer protein epsilon subunit family protein / COPE family protein [Vitis vinifera]	Unigene2401_All//1.00E-94//AT1G30630| coatomer protein epsilon subunit family protein / COPE family protein	Unigene2401_All//0.00E+00//gi|78335983|gb|DT556257.1|DT556257			GO:0005488//GO:0022892//GO:0030120//GO:0048193	nr -
Unigene24010_All	1660	2.52	2.14	2.60	5.64	9.29	8.95	56.08	25.83	32.04	-2.39E-01	4.36E-01		4.33E-02	8.93E-01		7.20E-01	6.13E-08		6.66E-01	2.66E-06		-1.12E+00	1.19E-98	Down	-8.08E-01	3.14E-59		Unigene24010_All//gi|5230728|gb|AAD40979.1|AF089851_1//0.00E+00//peroxisomal copper-containing amine oxidase [Glycine max]	Unigene24010_All//0.00E+00//AT2G42490| copper amine oxidase, putative	Unigene24010_All//0.00E+00//TC179437		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0006807//GO:0016641//GO:0042579//GO:0046914//GO:0048037	nr +
Unigene24011_All	3364	1.20	0.98	1.12	2.46	5.55	3.80	15.48	5.65	9.55	-2.91E-01	3.73E-01		-9.16E-02	7.74E-01		1.17E+00	7.82E-21	Up	6.28E-01	4.81E-05		-1.45E+00	3.63E-83	Down	-6.98E-01	3.28E-26		Unigene24011_All//gi|115315698|gb|ABI93948.1|//0.00E+00//methylputrescine oxidase [Nicotiana tabacum] >gi|134048906|dbj|BAF49519.1| N-methylputrescine oxidase [Nicotiana tabacum]	Unigene24011_All//0.00E+00//AT2G42490| copper amine oxidase, putative	Unigene24011_All//0.00E+00//gi|164267218|gb|ES808465.1|ES808465		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0006807//GO:0016641//GO:0042579//GO:0046914//GO:0048037	nr +
Unigene24012_All	3102	0.19	0.03	0.14	0.37	0.40	0.60	2.25	0.55	0.98	-2.50E+00	2.94E-02		-4.34E-01	6.23E-01		1.13E-01	8.71E-01		6.92E-01	1.64E-01		-2.03E+00	2.43E-18	Down	-1.20E+00	2.30E-09	Down	Unigene24012_All//gi|115315698|gb|ABI93948.1|//0.00E+00//methylputrescine oxidase [Nicotiana tabacum] >gi|134048906|dbj|BAF49519.1| N-methylputrescine oxidase [Nicotiana tabacum]	Unigene24012_All//0.00E+00//AT2G42490| copper amine oxidase, putative	Unigene24012_All//0.00E+00//gi|164267218|gb|ES808465.1|ES808465		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0006807//GO:0016641//GO:0042579//GO:0046914//GO:0048037	nr -
Unigene24013_All	2421	10.85	22.50	37.30	11.65	13.84	17.03	63.24	16.50	32.76	1.05E+00	6.42E-43	Up	1.78E+00	3.89E-153	Up	2.49E-01	6.68E-03		5.48E-01	9.83E-12		-1.94E+00	0.00E+00	Down	-9.49E-01	5.29E-127		Unigene24013_All//gi|113203757|gb|ABI33979.1|//0.00E+00//phenylalanine ammonia lyase [Jatropha curcas]	Unigene24013_All//0.00E+00//AT2G37040| pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase	Unigene24013_All//0.00E+00//TC135012		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00910|Nitrogen metabolism	GO:0006558//GO:0006575//GO:0016840//GO:0044424	nr +
Unigene24014_All	3584	1.90	1.50	0.98	10.13	13.70	11.81	38.80	39.45	101.81	-3.41E-01	1.39E-01		-9.53E-01	5.40E-05		4.35E-01	4.03E-10		2.21E-01	8.82E-03		2.40E-02	6.33E-01		1.39E+00	0.00E+00	Up	Unigene24014_All//gi|15220790|ref|NP_175749.1|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|264664588|sp|C0LGG9.2|Y5344_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g53440; Flags: Precursor	Unigene24014_All//0.00E+00//AT1G53440| leucine-rich repeat family protein / protein kinase family protein	Unigene24014_All//0.00E+00//TC151625		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene24016_All	2758	2.56	4.17	2.32	2.44	3.73	1.95	1.04	0.92	9.20	7.04E-01	2.70E-05		-1.45E-01	5.78E-01		6.15E-01	2.69E-04		-3.23E-01	1.86E-01		-1.73E-01	6.31E-01		3.14E+00	2.97E-108	Up	Unigene24016_All//gi|15228781|ref|NP_191154.1|//0.00E+00//CCR3 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 3); kinase [Arabidopsis thaliana] >gi|75335634|sp|Q9LY50.1|ACCR3_ARATH RecName: Full=Putative serine/threonine-protein kinase-like protein CCR3; AltName: Full=Protein CRINKLY 4 RELATED 3; Short=AtCRR3; Flags: Precursor >gi|7573490|emb|CAB87849.1|receptor kinase-like protein [Arabidopsis thaliana]	Unigene24016_All//0.00E+00//AT3G55950| CCR3 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 3); kinase	Unigene24016_All//0.00E+00//TC164649		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0042802//GO:0044464	nr +
Unigene24017_All	2527	0.29	1.80	0.40	2.31	1.69	3.23	51.98	46.46	55.92	2.64E+00	1.78E-13	Up	4.66E-01	5.12E-01		-4.49E-01	6.35E-02		4.88E-01	1.71E-02		-1.62E-01	7.17E-05		1.05E-01	8.17E-03		Unigene24017_All//gi|18399411|ref|NP_566405.1|//0.00E+00//glutaredoxin-related [Arabidopsis thaliana]	Unigene24017_All//0.00E+00//AT3G11920| glutaredoxin-related					nr -
Unigene24018_All	1982	1.29	4.65	2.63	24.30	19.09	17.18	10.00	11.28	8.38	1.85E+00	2.20E-17	Up	1.03E+00	1.94E-04	Up	-3.48E-01	7.33E-07		-5.00E-01	1.10E-11		1.73E-01	1.29E-01		-2.55E-01	2.13E-02		Unigene24018_All//gi|8096269|dbj|BAA95789.1|//2.00E-84//KED [Nicotiana tabacum]	Unigene24018_All//2.00E-05//AT1G56660| unknown protein	Unigene24018_All//6.00E-158//gi|164357054|gb|ES837724.1|ES837724		ko03040|Spliceosome		nr -
Unigene24019_All	2279	5.76	4.45	3.50	17.95	15.14	13.63	15.90	9.46	5.12	-3.74E-01	1.77E-02		-7.17E-01	8.34E-06		-2.45E-01	2.35E-03		-3.96E-01	9.45E-07		-7.49E-01	3.35E-20		-1.63E+00	6.92E-71	Down	Unigene24019_All//gi|18766642|gb|AAL79012.1|AF469649_1//0.00E+00//NIMA-related protein kinase [Populus tremula x Populus alba]	Unigene24019_All//8.00E-179//AT3G63280| ATNEK4 (NIMA-RELATED KINASE 4); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene24019_All//0.00E+00//TC174526			GO:0004702//GO:0006464//GO:0032559	nr -
Unigene24020_All	2008	1.95	1.89	2.73	3.97	4.46	2.97	2.36	1.75	4.94	-4.63E-02	8.88E-01		4.83E-01	7.37E-02		1.68E-01	4.57E-01		-4.19E-01	4.62E-02		-4.32E-01	8.87E-02		1.07E+00	9.92E-11	Up	Unigene24020_All//gi|124301088|gb|ABN04796.1|//1.00E-166//At2g47020 [Arabidopsis thaliana]	Unigene24020_All//3.00E-155//AT2G47020| peptide chain release factor, putative	Unigene24020_All//0.00E+00//TC159695				nr -
Unigene24026_All	3407	8.72	23.02	12.22	16.43	20.81	17.94	11.02	14.76	11.03	1.40E+00	3.98E-96	Up	4.87E-01	8.80E-09		3.41E-01	2.59E-09		1.26E-01	9.07E-02		4.21E-01	2.27E-10		9.00E-04	9.91E-01		Unigene24026_All//gi|15229253|ref|NP_187074.1|//0.00E+00//SEC (secret agent); transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75336082|sp|Q9M8Y0.1|SEC_ARATH RecName: Full=Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC; AltName: Full=Protein SECRET AGENT >gi|18139887|gb|AAL60196.1|AF441079_1 O-linked N-acetyl glucosamine transferase [Arabidopsis thaliana] >gi|110742062|dbj|BAE98963.1| O-linked GlcNAc transferase like protein [Arabidopsis thaliana]	Unigene24026_All//0.00E+00//AT3G04240| SEC (secret agent); transferase, transferring glycosyl groups	Unigene24026_All//0.00E+00//TC138567			GO:0006486//GO:0016740	nr +
Unigene24027_All	3488	0.98	2.30	1.50	2.31	2.88	2.15	1.24	0.96	1.44	1.24E+00	9.23E-09	Up	6.18E-01	2.42E-02		3.17E-01	8.81E-02		-1.06E-01	6.62E-01		-3.67E-01	1.81E-01		2.19E-01	3.84E-01		Unigene24027_All//gi|15229253|ref|NP_187074.1|//0.00E+00//SEC (secret agent); transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75336082|sp|Q9M8Y0.1|SEC_ARATH RecName: Full=Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC; AltName: Full=Protein SECRET AGENT >gi|18139887|gb|AAL60196.1|AF441079_1 O-linked N-acetyl glucosamine transferase [Arabidopsis thaliana] >gi|110742062|dbj|BAE98963.1| O-linked GlcNAc transferase like protein [Arabidopsis thaliana]	Unigene24027_All//0.00E+00//AT3G04240| SEC (secret agent); transferase, transferring glycosyl groups	Unigene24027_All//0.00E+00//TC138567			GO:0006486//GO:0016740	nr -
Unigene2403_All	1015	5.98	15.77	9.29	6.43	6.21	8.99	3.62	6.88	7.46	1.40E+00	3.77E-20	Up	6.35E-01	1.07E-03		-5.04E-02	8.36E-01		4.83E-01	1.16E-02		9.24E-01	3.70E-06		1.04E+00	4.21E-08	Up	Unigene2403_All//gi|14423428|gb|AAK62396.1|AF386951_1//2.00E-33//Unknown protein [Arabidopsis thaliana]	Unigene2403_All//2.00E-26//AT1G27290| unknown protein	Unigene2403_All//0.00E+00//gi|109873812|gb|DW502787.1|DW502787				nr -
Unigene24033_All	2709	0.89	1.12	1.91	2.59	3.37	3.53	2.97	5.82	1.90	3.37E-01	3.73E-01		1.10E+00	7.59E-05	Up	3.78E-01	4.94E-02		4.47E-01	1.73E-02		9.72E-01	6.04E-14		-6.44E-01	2.74E-04		Unigene24033_All//gi|297824647|ref|XP_002880206.1|//1.00E-132//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326045|gb|EFH56465.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24033_All//4.00E-115//AT2G45910| protein kinase family protein / U-box domain-containing protein	Unigene24033_All//0.00E+00//TC163265		ko04626|Plant-pathogen interaction		nr +
Unigene24037_All	1995	1.76	4.04	3.55	1.97	2.87	2.35	1.93	1.63	2.78	1.20E+00	1.84E-08	Up	1.01E+00	1.15E-05	Up	5.39E-01	2.83E-02		2.55E-01	4.16E-01		-2.39E-01	4.31E-01		5.25E-01	1.68E-02		Unigene24037_All//gi|42415865|gb|AAS15800.1|//1.00E-172//heat shock factor protein hsf8-related [Glycine max]	Unigene24037_All//2.00E-115//AT1G32330| ATHSFA1D; DNA binding / transcription factor	Unigene24037_All//0.00E+00//gi|78333922|gb|DT554196.1|DT554196	HSF		GO:0001071//GO:0003677//GO:0006351//GO:0043231//GO:0050896	nr +
Unigene24038_All	2697	4.81	18.26	5.21	17.14	23.11	21.43	11.08	11.11	14.25	1.92E+00	4.02E-95	Up	1.16E-01	5.09E-01		4.31E-01	1.66E-12		3.23E-01	1.76E-06		3.60E-03	1.01E+00		3.63E-01	1.46E-06		Unigene24038_All//gi|195976673|dbj|BAG68575.1|//0.00E+00//arginine decarboxylase [Prunus persica]	Unigene24038_All//0.00E+00//AT4G34710| ADC2 (ARGININE DECARBOXYLASE 2); arginine decarboxylase	Unigene24038_All//0.00E+00//TC144978		ko00330|Arginine and proline metabolism	GO:0006525//GO:0006596//GO:0006970//GO:0009725//GO:0009791//GO:0016831	nr +
Unigene2404_All	990	2.11	5.63	1.99	4.13	4.07	3.70	4.57	5.24	6.76	1.41E+00	1.32E-07	Up	-8.71E-02	8.46E-01		-1.99E-02	9.56E-01		-1.59E-01	6.37E-01		1.96E-01	4.56E-01		5.65E-01	4.11E-03		Unigene2404_All//gi|14423428|gb|AAK62396.1|AF386951_1//2.00E-33//Unknown protein [Arabidopsis thaliana]	Unigene2404_All//2.00E-26//AT1G27290| unknown protein	Unigene2404_All//0.00E+00//TC142303				nr +
Unigene24040_All	1214	2.93	1.38	1.36	4.97	5.33	5.47	3.10	2.96	2.49	-1.09E+00	9.97E-04	Down	-1.11E+00	1.34E-03		1.03E-01	7.29E-01		1.39E-01	6.35E-01		-6.61E-02	8.31E-01		-3.14E-01	2.73E-01		Unigene24040_All//gi|145335240|ref|NP_172254.2|//4.00E-25//RAD51D (ARABIDOPSIS HOMOLOG OF RAD51 D); ATP binding / DNA binding / DNA-dependent ATPase [Arabidopsis thaliana] >gi|83305360|sp|Q9LQQ2.2|RA51D_ARATH RecName: Full=DNA repair protein RAD51 homolog 4; Short=AtRAD51D >gi|58430742|dbj|BAD89165.1|AtRAD51D [Arabidopsis thaliana] >gi|90969171|gb|ABE02570.1| RAD51D splice variant a [Arabidopsis thaliana] >gi|90969179|gb|ABE02658.1| RAD51D splice variant a [Arabidopsis thaliana]	Unigene24040_All//5.00E-21//AT1G07745| RAD51D (ARABIDOPSIS HOMOLOG OF RAD51 D); ATP binding / DNA binding / DNA-dependent ATPase	Unigene24040_All//0.00E+00//gi|48793277|gb|CO094591.1|CO094591			GO:0003676//GO:0006310//GO:0009607	nr +
Unigene24041_All	2444	26.52	23.57	18.56	60.80	56.15	54.77	63.51	21.56	21.94	-1.70E-01	1.23E-02		-5.15E-01	1.18E-14		-1.15E-01	6.59E-03		-1.51E-01	3.69E-04		-1.56E+00	2.87E-273	Down	-1.53E+00	1.65E-274	Down	Unigene24041_All//gi|4689474|gb|AAD27910.1|//0.00E+00//expressed protein [Arabidopsis thaliana] >gi|51536602|gb|AAU05539.1|At2g04280 [Arabidopsis thaliana]	Unigene24041_All//0.00E+00//AT2G04280| unknown protein	Unigene24041_All//0.00E+00//TC142069			GO:0043231	nr +

Unigene24042_All	2120	13.57	31.31	27.53	14.97	24.32	34.58	10.69	18.87	11.20	1.21E+00	9.43E-65	Up	1.02E+00	2.11E-42	Up	7.00E-01	2.66E-24		1.21E+00	5.70E-77	Up	8.20E-01	8.19E-26		6.73E-02	5.81E-01		Unigene24042_All//gi|111038269|gb|AB803531.1|//1.00E-171//class II knotted-like homeobox protein [Prunus persica] >gi|215983122|gb|ACJ71731.1| class II knotted-like homeobox transcription factor [Prunus persica]	Unigene24042_All//7.00E-134//AT5G25220| KNAT3 (KNOTTED1-LIKE HOMEOBOX GENE 3); transcription activator/ transcription factor	Unigene24042_All//0.00E+00//TC144378	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene24045_All	2129	12.95	12.97	15.81	26.14	25.01	21.11	36.76	20.18	14.69	2.20E-03	9.83E-01		2.88E-01	3.33E-03		-6.38E-02	4.69E-01		-3.08E-01	7.82E-06		-8.65E-01	1.66E-54		-1.32E+00	3.37E-111	Down	Unigene24045_All//gi|240256211|ref|NP_195404.6|//0.00E+00//zinc ion binding [Arabidopsis thaliana]	Unigene24045_All//0.00E+00//AT4G36860| zinc ion binding	Unigene24045_All//0.00E+00//gi|164335253|gb|ES816200.1|ES816200	Orphans		GO:0046914	nr -
Unigene24046_All	1882	10.48	7.11	8.23	32.16	30.46	27.81	23.95	10.50	16.00	-5.60E-01	5.95E-06		-3.48E-01	7.91E-03		-7.81E-02	3.23E-01		-2.10E-01	2.20E-03		-1.19E+00	5.04E-53	Down	-5.82E-01	9.88E-17		Unigene24046_All//gi|297799300|ref|XP_002867534.1|//0.00E+00//galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313370|gb|EFH43793.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24046_All//5.00E-179//AT4G26940| galactosyltransferase family protein	Unigene24046_All//0.00E+00//TC156368			GO:0005488//GO:0006464//GO:0031224//GO:0035250//GO:0043231	nr -
Unigene24047_All	535	4.69	20.65	5.18	9.40	15.90	7.77	1.42	4.61	5.06	2.14E+00	6.73E-25	Up	1.41E-01	7.12E-01		7.58E-01	5.47E-05		-2.76E-01	3.57E-01		1.70E+00	1.25E-05	Up	1.83E+00	6.77E-07	Up	Unigene24047_All//gi|224980172|gb|ACN72950.1|//6.00E-07//COS11_At2g15890 [Solanum dulcamara]		Unigene24047_All//0.00E+00//TC146030			GO:0003006//GO:0006952//GO:0009536	nr +
Unigene24048_All	1165	47.25	168.23	54.07	42.72	120.66	96.45	27.04	110.07	138.80	1.83E+00	0.00E+00	Up	1.95E-01	6.16E-03		1.50E+00	2.55E-225	Up	1.18E+00	8.53E-113	Up	2.03E+00	0.00E+00	Up	2.36E+00	0.00E+00	Up	Unigene24048_All//gi|18397956|ref|NP_565383.1|//4.00E-59//MEE14 (maternal effect embryo arrest 14) [Arabidopsis thaliana] >gi|11692922|gb|AAG40064.1|AF324713_1 At2g15890 [Arabidopsis thaliana] >gi|5306244|gb|AAD41977.1| expressed protein [Arabidopsis thaliana] >gi|30725564|gb|AAP37804.1| At2g15890 [Arabidopsis thaliana]	Unigene24048_All//3.00E-56//AT2G15890| MEE14 (maternal effect embryo arrest 14)	Unigene24048_All//0.00E+00//TC168955			GO:0003006//GO:0003824//GO:0006952//GO:0009536//GO:0030554	nr -
Unigene24049_All	903	0.64	0.56	0.59	1.88	2.48	5.95	0.66	3.70	1.19	-1.84E-01	8.25E-01		-1.12E-01	9.07E-01		4.02E-01	3.92E-01		1.67E+00	1.40E-09	Up	2.50E+00	1.38E-11	Up	8.62E-01	1.32E-01		Unigene24049_All//gi|87162753|gb|AB028548.1|//2.00E-92//Protein kinase; Type I EGF [Medicago truncatula]	Unigene24049_All//4.00E-87//AT1G21250| WAK1 (CELL WALL-ASSOCIATED KINASE); kinase	Unigene24049_All//3.00E-16//DT467837		ko04626|Plant-pathogen interaction	GO:0004674//GO:0005618//GO:0006464//GO:0006952//GO:0010033//GO:0016020//GO:0023033//GO:0031410//GO:0032559//GO:0043231//GO:0046872//GO:0051707	nr +
Unigene2405_All	1442	6.60	5.76	7.90	10.23	10.77	10.30	4.54	3.51	1.82	-1.97E-01	3.35E-01		2.59E-01	1.60E-01		7.49E-02	6.73E-01		1.11E-02	9.57E-01		-3.74E-01	7.87E-02		-1.32E+00	4.74E-10	Down	Unigene2405_All//gi|227463008|gb|ACP39956.1|//2.00E-88//pentatricopeptide repeat protein [Gossypium hirsutum] >gi|227463010|gb|ACP39957.1| pentatricopeptide repeat protein [Gossypium hirsutum]	Unigene2405_All//3.00E-120//AT1G61870| PPR336 (pentatricopeptide repeat 336)	Unigene2405_All//0.00E+00//gi|78342473|gb|DT562747.1|DT562747			GO:0001071//GO:0006351//GO:0043231	nr +
Unigene24050_All	1025	5.92	7.96	12.88	1.94	1.38	0.84	0.21	1.30	0.51	4.27E-01	3.83E-02		1.12E+00	1.30E-11	Up	-4.97E-01	2.89E-01		-1.22E+00	8.56E-03		2.66E+00	2.41E-05	Up	1.29E+00	1.59E-01		Unigene24050_All//gi|87162753|gb|AB028548.1|//1.00E-103//Protein kinase; Type I EGF [Medicago truncatula]	Unigene24050_All//1.00E-96//AT1G21210| WAK4 (wall associated kinase 4); ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase	Unigene24050_All//2.00E-23//DT467814		ko04626|Plant-pathogen interaction	GO:0000902//GO:0004672//GO:0005618//GO:0005975//GO:0006464//GO:0006884//GO:0006952//GO:0010033//GO:0016020//GO:0023033//GO:0032559//GO:0043231//GO:0048528//GO:0051707	nr +
Unigene24054_All	630	1.74	4.91	4.90	6.72	4.26	7.31	3.83	4.44	2.21	1.49E+00	6.92E-05	Up	1.49E+00	1.20E-04	Up	-6.57E-01	1.95E-02		1.22E-01	6.88E-01		2.17E-01	5.73E-01		-7.89E-01	2.45E-02		Unigene24054_All//gi|18417747|ref|NP_567868.1|//3.00E-24//endonuclease V family protein [Arabidopsis thaliana] >gi|119360075|gb|ABL66766.1| At4g31150 [Arabidopsis thaliana]	Unigene24054_All//2.00E-18//AT4G31150| endonuclease V family protein	Unigene24054_All//0.00E+00//gi|78329779|gb|DT550053.1|DT550053			GO:0004519//GO:0044464	nr +
Unigene24056_All	1960	2.86	10.06	4.92	3.30	2.97	9.10	26.47	19.75	51.69	1.82E+00	1.42E-35	Up	7.84E-01	4.40E-05		-1.54E-01	5.64E-01		1.46E+00	2.10E-25	Up	-4.23E-01	9.75E-11		9.66E-01	3.00E-86		Unigene24056_All//gi|18416717|ref|NP_567742.1|//0.00E+00//PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase [Arabidopsis thaliana] >gi|75164938|sp|Q94AA4.1|K6PF3_ARATH RecName: Full=6-phosphofructokinase 3; AltName: Full=Phosphofructokinase 3; AltName: Full=Phosphohexokinase 3 >gi|15146208|gb|AAK83587.1| AT4g26270/T25K17_80 [Arabidopsis thaliana] >gi|19699124|gb|AAL90928.1| AT4g26270/T25K17_80 [Arabidopsis thaliana]	Unigene24056_AtI//0.00E+00//AT4G26270| PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase	Unigene24056_AtI//0.00E+00//TC136990		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway	GO:0006007//GO:0008443//GO:0016020//GO:0032559//GO:0043234//GO:0044444	nr +
Unigene24057_All	762	21.42	4.85	7.69	47.07	41.17	36.69	17.53	13.05	12.81	-2.14E+00	7.11E-37	Down	-1.48E+00	1.95E-21	Down	-1.93E-01	3.43E-02		-3.60E-01	4.01E-05		-4.26E-01	2.06E-03		-4.53E-01	7.04E-04		Unigene24057_All//gi|115473321|ref|NP_001060259.1|//1.00E-13//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene24057_All//2.00E-05//AT2G02650| reverse transcriptase-related	Unigene24057_All//0.00E+00//ES829277				nr -
Unigene24058_All	2337	5.26	1.30	2.42	12.75	8.22	3.83	5.32	1.82	1.14	-2.02E+00	7.03E-26	Down	-1.12E+00	7.45E-11	Down	-6.33E-01	2.61E-12		-1.74E+00	7.76E-55	Down	-1.54E+00	2.87E-22	Down	-2.22E+00	3.82E-37	Down	Unigene24058_All//gi|124360549|gb|AB033126.2|//2.00E-84//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene24058_All//1.00E-15//ATMG00310| hypothetical protein	Unigene24058_All//0.00E+00//TC158493			GO:0003676//GO:0006260//GO:0034061//GO:0043231	nr +
Unigene24059_All	2545	20.17	45.27	26.45	27.76	31.34	33.70	40.67	38.10	52.10	1.17E+00	2.96E-106	Up	3.91E-01	2.03E-09		1.75E-01	2.29E-03		2.80E-01	2.91E-07		-9.41E-02	6.15E-02		3.57E-01	7.87E-20		Unigene24059_All//gi|225446357|ref|XP_002272844.1|//1.00E-133//PREDICTED: similar to hydroxyproline-rich glycoprotein family protein [Vitis vinifera]	Unigene24059_All//4.00E-31//AT4G28300| hydroxyproline-rich glycoprotein family protein	Unigene24059_All//0.00E+00//TC143398		ko03040|Spliceosome		nr -
Unigene24064_All	1312	20.42	14.56	15.54	7.33	7.87	18.49	16.73	18.89	40.17	-4.88E-01	3.08E-06		-3.93E-01	3.10E-04		1.04E-01	6.16E-01		1.33E+00	5.06E-30	Up	1.76E-01	9.90E-02		1.26E+00	1.85E-69	Up	Unigene24064_All//gi|34550779|gb|AAQ74955.1|//1.00E-87//Gbiaa-Re [Gossypium barbadense]	Unigene24064_All//3.00E-49//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene24064_All//0.00E+00//gi|109876373|gb|DW505347.1|DW505347			GO:0001071//GO:0003676//GO:0005515//GO:0006412//GO:0009755//GO:0010468//GO:0043231	nr +
Unigene24068_All	2610	7.20	11.82	9.79	14.91	14.67	13.00	11.00	13.93	4.43	7.16E-01	3.33E-13		4.45E-01	6.43E-05		-2.29E-02	8.16E-01		-1.98E-01	2.80E-02		3.41E-01	1.78E-05		-1.31E+00	7.46E-41	Down	Unigene24068_All//gi|115484315|ref|NP_001065819.1|//2.00E-26//Os11g0160700 [Oryza sativa Japonica Group] >gi|77548797|gb|ABA91594.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113644523|dbj|BAF27664.1| Os11g0160700 [Oryza sativa Japonica Group]	Unigene24068_All//2.00E-20//AT5G03780| TRFL10 (TRF-LIKE 10); DNA binding	Unigene24068_All//0.00E+00//TC134399	MYB-related			nr +
Unigene24069_All	3081	12.48	10.71	9.89	12.35	13.91	17.22	17.13	23.40	35.57	-2.21E-01	1.31E-02		-3.36E-01	1.76E-04		1.72E-01	4.17E-02		4.80E-01	7.86E-12		4.50E-01	2.70E-16		1.05E+00	1.12E-107	Up	Unigene24069_All//gi|297849570|ref|XP_002892666.1|//0.00E+00//transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297338808|gb|EFH68925.1| transcription factor jumonji domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene24069_AtI//0.00E+00//AT1G11950| transcription factor	Unigene24069_AtI//0.00E+00//gi|78334335|gb|DT554609.1|DT554609			GO:0046872	nr -
Unigene24071_All	2333	10.05	6.28	7.44	50.41	35.56	29.64	83.80	47.99	32.50	-6.79E-01	2.13E-09		-4.33E-01	2.14E-04		-5.04E-01	1.87E-31		-7.66E-01	1.11E-58		-8.04E-01	3.21E-119		-1.37E+00	9.39E-291	Down	Unigene24071_All//gi|297792281|ref|XP_002864025.1|//9.00E-33//transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata] >gi|297309860|gb|EFH60284.1| transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata]	Unigene24071_AtI//5.00E-25//AT5G50010| transcription factor/ transcription regulator	Unigene24071_AtI//0.00E+00//TC167463	bHLH		GO:0009987	nr -
Unigene24072_All	1192	1.76	6.84	2.77	6.56	7.54	6.25	4.97	5.15	4.55	1.96E+00	1.04E-16	Up	6.58E-01	6.57E-02		2.01E-01	3.58E-01		-6.97E-02	7.62E-01		5.38E-02	8.24E-01		-1.28E-01	6.11E-01		Unigene24072_All//gi|224128312|ref|XP_002320296.1|//1.00E-126//SET domain protein [Populus trichocarpa] >gi|222861069|gb|EEE98611.1| SET domain protein [Populus trichocarpa]	Unigene24072_AtI//8.00E-83//AT4G02020| SWN (SWINGER); transcription factor	Unigene24072_AtI//0.00E+00//TC172649			GO:0003006//GO:0005488//GO:0040029//GO:0043231	nr +
Unigene24073_All	3110	4.41	11.45	10.27	14.51	14.97	11.55	12.56	9.84	6.83	1.38E+00	5.99E-43	Up	1.22E+00	3.87E-31	Up	4.48E-02	6.50E-01		-3.30E-01	1.95E-05		-3.53E-01	3.76E-06		-8.80E-01	3.23E-29		Unigene24073_All//gi|22535907|gb|AAN01115.1|AF407010_1/0.00E+00//SET domain-containing protein [Oryza sativa]	Unigene24073_AtI//9.00E-170//AT4G02020| SWN (SWINGER); transcription factor	Unigene24073_AtI//0.00E+00//TC172649			GO:0003006//GO:0005488//GO:0006479//GO:0008168//GO:0009292//GO:0009987//GO:0040029//GO:0043231	nr -
Unigene24075_All	947	1.77	3.96	3.21	42.08	32.36	35.48	11.88	2.69	4.33	1.16E+00	3.35E-04	Up	8.58E-01	2.21E-02		-3.79E-01	1.13E-06		-2.46E-01	4.10E-03		-2.14E+00	3.21E-31	Down	-1.45E+00	3.53E-19	Down	Unigene24075_All//gi|46518375|gb|AAS99669.1|//4.00E-59//At2g27740 [Arabidopsis thaliana] >gi|83310362|gb|AAT41807.1| At2g27740 [Arabidopsis thaliana]	Unigene24075_AtI//2.00E-60//AT2G27740| unknown protein	Unigene24075_AtI//0.00E+00//TC163074				nr -
Unigene24076_All	1315	42.97	24.66	32.88	76.82	63.69	61.79	101.44	47.68	30.54	-8.01E-01	1.67E-28		-3.86E-01	7.65E-08		-2.71E-01	9.51E-09		-3.14E-01	2.22E-10		-1.09E+00	3.45E-135	Down	-1.73E+00	2.73E-281	Down	Unigene24076_All//gi|210063564|gb|ACJ06541.1|//1.00E-102//cycloghilin [Camellia oleifera]	Unigene24076_AtI//2.00E-81//AT5G58710| ROC7; peptidyl-prolyl cis-trans isomerase	Unigene24076_AtI//0.00E+00//TC152827			GO:0005626//GO:0005770//GO:0009536//GO:0016859//GO:0031410//GO:0044267//GO:0044431//GO:0048513	nr -
Unigene24078_All	1296	4.93	2.31	5.38	9.19	18.92	13.38	6.95	1.74	7.56	-1.09E+00	4.55E-06	Down	1.28E-01	6.33E-01		1.04E+00	1.33E-22	Up	5.43E-01	3.08E-05		-2.00E+00	4.89E-23	Down	1.22E-01	5.08E-01		Unigene24078_All//gi|225435610|ref|XP_002283298.1|//1.00E-161//PREDICTED: similar to Callose synthase 3 [Vitis vinifera]	Unigene24078_AtI//3.00E-158//AT5G13000| ATGSL12 (glucan synthase-like 12); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups	Unigene24078_AtI//0.00E+00//TC143296				nr +
Unigene24079_All	2414	5.14	1.60	4.15	7.53	4.59	7.88	15.03	27.30	83.67	-1.69E+00	1.28E-20	Down	-3.09E-01	7.68E-02		-7.14E-01	1.95E-09		6.45E-02	6.92E-01		8.62E-01	1.16E-45		2.48E+00	0.00E+00	Up	Unigene24079_All//gi|22330270|ref|NP_175981.2|//0.00E+00//ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75161659|sp|Q8VZK9.1|CSLE1_ARATH RecName: Full=Cellulose synthase-like protein E1; Short=AtCslE1	Unigene24079_AtI//0.00E+00//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene24079_AtI//0.00E+00//CO090378			GO:0009987//GO:0016020//GO:0016757	nr -
Unigene24080_All	2402	0.11	0.02	0.40	0.41	0.16	0.68	0.51	2.44	3.91	-2.37E+00	2.14E-01		1.87E+00	2.06E-02		-1.40E+00	3.79E-02		7.07E-01	1.95E-01		2.25E+00	1.36E-17	Up	2.94E+00	5.52E-38	Up	Unigene24080_All//gi|22330270|ref|NP_175981.2|//0.00E+00//ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75161659|sp|Q8VZK9.1|CSLE1_ARATH RecName: Full=Cellulose synthase-like protein E1; Short=AtCslE1	Unigene24080_AtI//0.00E+00//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene24080_AtI//0.00E+00//TC153141			GO:0009250//GO:0016759//GO:0031224//GO:0045229//GO:0051234	nr +

Unigene24085_All	1242	84.67	88.32	67.74	43.52	66.15	63.93	18.25	37.52	15.24	6.09E-02	2.89E-01		-3.22E-01	3.76E-10		6.04E-01	8.08E-30		5.55E-01	1.66E-22		1.04E+00	2.99E-44	Up	-2.60E-01	1.12E-02		Unigene24085_All//gi|48431269|gb|AT44124.1|//4.00E-76//F3H-like protein [Saussurea medusa]	Unigene24085_All//3.00E-57//AT5G24530| DMR6 (DOWNY MILDEW RESISTANT 6); oxidoreductase/oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene24085_All//2.00E-12//TC179429		ko00941|Flavonoid biosynthesis	GO:0003824	nr +
Unigene24086_All	1639	1.66	11.59	5.23	1.06	3.36	2.78	0.90	2.78	5.40	2.80E+00	5.80E-58	Up	1.66E+00	1.58E-13	Up	1.66E+00	1.92E-10	Up	1.39E+00	1.90E-06	Up	1.62E+00	3.24E-09	Up	2.58E+00	3.20E-31	Up			Unigene24086_All//7.00E-142//gi|78346593|gb|DT566867.1|DT566867				
Unigene24088_All	364	3.45	3.62	1.02	4.79	3.97	4.34	7.09	3.56	1.64	6.92E-02	9.12E-01		-1.75E+00	9.85E-03		-2.70E-01	6.05E-01		-1.41E-01	7.77E-01		-9.93E-01	4.86E-03		-2.11E+00	7.05E-08	Down	Unigene24088_All//gi|194306662|gb|ACF41944.1|//7.00E-07//At3g48860 [Arabidopsis thaliana]	Unigene24088_All//3.00E-08//AT3G48860| unknown protein	Unigene24088_All//1.00E-152//TC143779				nr +
Unigene24089_All	2156	6.21	4.51	4.77	14.76	12.70	10.12	10.00	3.82	3.81	-4.61E-01	2.76E-03		-3.82E-01	1.90E-02		-2.18E-01	2.34E-02		-5.45E-01	3.56E-09		-1.39E+00	1.30E-32	Down	-1.39E+00	8.91E-34	Down	Unigene24089_All//gi|115441987|ref|NP_001045273.1|//1.00E-171//Os01g0928100 [Oryza sativa Japonica Group] >gi|113534804|dbj|BAF07187.1| Os01g0928100 [Oryza sativa Japonica Group]	Unigene24089_All//1.00E-167//AT5G13260| unknown protein	Unigene24089_All//0.00E+00//gi|78345821|gb|DT566095.1|DT566095				nr -
Unigene24092_All	793	6.14	2.68	5.04	10.74	10.07	7.86	17.70	4.64	4.47	-1.19E+00	2.07E-05	Down	-2.85E-01	3.52E-01		-9.25E-02	6.98E-01		-4.51E-01	2.43E-02		-1.93E+00	5.01E-34	Down	-1.99E+00	2.32E-36	Down	Unigene24092_All//gi|33415263|gb|AQ18140.1|//1.00E-117//enolase [Gossypium barbadense]	Unigene24092_All//4.00E-111//AT2G36530| LOS2; copper ion binding / phosphopyruvate hydratase	Unigene24092_All//0.00E+00//gi|78336833|gb|DT557107.1|DT557107		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation		nr -
Unigene24093_All	1626	13.26	5.64	3.57	20.25	20.92	19.17	41.92	11.39	14.85	-1.23E+00	2.42E-22	Down	-1.89E+00	8.93E-40	Down	4.72E-02	6.99E-01		-7.95E-02	4.95E-01		-1.88E+00	1.17E-156	Down	-1.50E+00	9.13E-117	Down	Unigene24093_All//gi|224482647|gb|ACN50180.1|//0.00E+00//enolase [Annona cherimola]	Unigene24093_All//0.00E+00//AT2G36530| LOS2; copper ion binding / phosphopyruvate hydratase	Unigene24093_All//0.00E+00//TC154314		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation	GO:0006007//GO:0016836//GO:0043234//GO:0044424//GO:0046872	nr -
Unigene24094_All	692	0.60	0.22	1.46	2.74	3.18	1.96	2.51	1.63	0.06	-1.46E+00	2.34E-01		1.27E+00	8.36E-02		2.19E-01	6.50E-01		-4.82E-01	3.38E-01		-6.19E-01	1.70E-01		-5.44E+00	1.77E-11	Down	Unigene24094_All//gi|113205216|gb|AAT39281.2|//2.00E-26//Integrase core domain containing protein [Solanum demissum]						nr +
Unigene24095_All	2008	2.01	2.50	2.55	6.03	7.49	3.13	4.06	2.06	1.51	3.16E-01	2.54E-01		3.44E-01	2.38E-01		3.14E-01	3.03E-02		-9.47E-01	3.60E-09		-9.80E-01	1.03E-07		-1.43E+00	8.01E-14	Down	Unigene24095_All//gi|2865437|gb|AAC02672.1|//1.00E-17//polyprotein [Arabidopsis arenosa]						nr -
Unigene24099_All	3113	1.95	0.86	1.13	6.18	3.24	3.15	10.10	1.40	4.61	-1.18E+00	2.02E-06	Down	-7.88E-01	1.62E-03		-9.30E-01	1.79E-15		-9.72E-01	8.30E-15		-2.86E+00	4.46E-120	Down	-1.13E+00	1.41E-35	Down	Unigene24099_All//gi|87162732|gb|AB028527.1|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene24099_All//0.00E+00//AT3G03770| leucine-rich repeat transmembrane protein kinase, putative	Unigene24099_All//0.00E+00//TC167802		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0007167//GO:0016628//GO:0031410//GO:0032559	nr -
Unigene24100_All	1949	16.48	8.76	9.32	19.12	22.81	25.70	29.63	28.54	68.13	-9.12E-01	2.02E-20		-8.23E-01	1.42E-16		2.55E-01	9.37E-04		4.27E-01	3.69E-09		-5.41E-02	4.90E-01		1.20E+00	2.09E-160	Up	Unigene24100_All//gi|15241252|ref|NP_197507.1|//1.00E-151//ATNUDX19 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 19); hydrolase/metal ion binding [Arabidopsis thaliana] >gi|68565923|sp|Q94A82.1|NUD19_ARATH RecName: Full=Nudix hydrolase 19, chloroplastic; Short=AtNUDT19; AltName: Full=NADH pyrophosphatase NUDT19; Flags: Precursor >gi|15146278|gb|AAK83622.1| AT5g20070/F28I16_220 [Arabidopsis thaliana] >gi|19699164|gb|AAL90948.1| AT5g20070/F28I16_220 [Arabidopsis thaliana]	Unigene24100_All//2.00E-147//AT5G20070| ATNUDX19 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 19); hydrolase/metal ion binding	Unigene24100_All//0.00E+00//TC142228		ko04146|Peroxisome//ko00760|Nicotinate and nicotinamide metabolism		nr +
Unigene24101_All	2740	1.91	6.18	3.83	16.11	14.93	10.75	8.27	10.42	7.49	1.69E+00	7.34E-28	Up	1.00E+00	6.36E-08	Up	-1.10E-01	2.27E-01		-5.84E-01	4.88E-14		3.33E-01	2.55E-04		-1.44E-01	1.95E-01		Unigene24101_All//gi|30690286|ref|NP_849565.1|//0.00E+00//TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|20453189|gb|AAM19835.1| AT4g35300/F23E12_140 [Arabidopsis thaliana]	Unigene24101_All//0.00E+00//AT4G35300| TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter	Unigene24101_All//0.00E+00//gi|164257431|gb|ES807125.1|ES807125			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr -
Unigene24105_All	2761	2.01	3.95	4.24	18.82	21.41	15.79	14.72	7.80	5.86	9.74E-01	3.44E-08		1.08E+00	8.79E-10	Up	1.87E-01	6.21E-03		-2.54E-01	5.19E-04		-9.17E-01	1.49E-31		-1.33E+00	1.67E-58	Down	Unigene24105_All//gi|297598339|ref|NP_001045426.2|//1.00E-133//Os01g0953100 [Oryza sativa Japonica Group] >gi|255674080|dbj|BAF07340.2| Os01g0953100 [Oryza sativa Japonica Group]	Unigene24105_All//0.00E+00//AT5G45530| unknown protein	Unigene24105_All//4.00E-18//TC173900			GO:0016020	nr +
Unigene24107_All	2305	0.89	0.99	2.08	26.41	21.96	19.06	5.32	2.61	1.07	1.60E-01	6.94E-01		1.23E+00	2.75E-05	Up	-2.66E-01	2.41E-05		-4.70E-01	4.28E-13		-1.03E+00	5.13E-12	Down	-2.31E+00	1.72E-38	Down	Unigene24107_All//gi|60657592|gb|AX33317.1|//0.00E+00//secondary cell wall-related glycosyltransferase family 8 [Populus tremula x Populus tremuloides]	Unigene24107_All//0.00E+00//AT3G18660| PGSIP1 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 1); transferase, transferring glycosyl groups	Unigene24107_All//0.00E+00//CO498175			GO:0008152//GO:0009536//GO:0035251	nr +
Unigene24108_All	2104	0.15	0.19	0.33	6.51	5.53	4.79	1.97	1.41	0.72	3.69E-01	7.24E-01		1.14E+00	2.18E-01		-2.35E-01	1.43E-01		-4.44E-01	3.23E-03		-4.82E-01	7.71E-02		-1.45E+00	1.35E-07	Down	Unigene24108_All//gi|60657592|gb|AX33317.1|//0.00E+00//secondary cell wall-related glycosyltransferase family 8 [Populus tremula x Populus tremuloides]	Unigene24108_All//0.00E+00//AT3G18660| PGSIP1 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 1); transferase, transferring glycosyl groups	Unigene24108_All//0.00E+00//TC160998			GO:0008152//GO:0009536//GO:0035251	nr +
Unigene24110_All	2845	8.28	0.41	1.91	4.39	3.68	2.60	19.25	3.45	4.75	-4.34E+00	1.71E-105	Down	-2.12E+00	3.47E-50	Down	-2.56E-01	1.23E-01		-7.55E-01	1.23E-06		-2.48E+00	1.87E-178	Down	-2.02E+00	1.11E-142	Down	Unigene24110_All//gi|115466984|ref|NP_001057091.1|//0.00E+00//Os06g0205600 [Oryza sativa Japonica Group] >gi|51091457|dbj|BAD36198.1| mechanosensitive ion channel domain-containing protein-like [Oryza sativa Japonica Group] >gi|113595131|dbj|BAF19005.1| Os06g0205600 [Oryza sativa Japonica Group]	Unigene24110_All//1.00E-173//AT5G12080| MSL10 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 10); mechanically-gated ion channel	Unigene24110_All//0.00E+00//TC138827			GO:0005216//GO:0006810//GO:0009612//GO:0016020//GO:0031410//GO:0043231	nr +
Unigene24112_All	3662	1.03	1.80	2.11	11.52	11.90	12.36	2.92	1.34	2.12	8.06E-01	4.53E-04		1.04E+00	2.72E-06	Up	4.72E-02	6.41E-01		1.01E-01	2.85E-01		-1.13E+00	3.20E-12	Down	-4.62E-01	2.28E-03		Unigene24112_All//gi|115482822|ref|NP_001065004.1|//1.00E-146//Os10g0504600 [Oryza sativa Japonica Group] >gi|110288363|gb|AAP54507.2| Chorion family 2 protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639613|dbj|BAF26918.1| Os10g0504600 [Oryza sativa Japonica Group]	Unigene24112_All//0.00E+00//AT1G63300| unknown protein	Unigene24112_All//3.00E-155//TC174357				nr +
Unigene24113_All	3545	1.27	1.24	0.92	15.49	11.57	7.91	9.12	3.65	4.15	-2.96E-02	9.32E-01		-4.70E-01	1.24E-01		-4.21E-01	8.29E-11		-9.69E-01	5.27E-41		-1.32E+00	6.12E-45	Down	-1.14E+00	8.72E-37	Down	Unigene24113_All//gi|223452530|gb|ACM89592.1|//0.00E+00//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene24113_All//0.00E+00//AT5G01890| leucine-rich repeat transmembrane protein kinase, putative	Unigene24113_All//0.00E+00//TC157842		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016020//GO:0016301	nr +
Unigene24117_All	2231	3.52	0.75	2.08	13.82	13.32	9.66	11.81	2.74	4.68	-2.23E+00	5.65E-19	Down	-7.61E-01	4.22E-04		-5.33E-02	6.59E-01		-5.17E-01	3.69E-08		-2.11E+00	7.71E-71	Down	-1.34E+00	1.59E-38	Down	Unigene24117_All//gi|115477084|ref|NP_001062138.1|//0.00E+00//Os08g0496900 [Oryza sativa Japonica Group] >gi|113624107|dbj|BAF24052.1| Os08g0496900 [Oryza sativa Japonica Group]	Unigene24117_All//0.00E+00//AT4G12650| LOCATED IN: integral to membrane, Golgi apparatus, plasma membrane, vacuole; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nonaspanin (TM9SF) (InterPro:IPR004240); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35160.1); Has 983 Blast hits to 980 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 434; Fungi - 144; Plants - 228; Viruses - 0; Other Eukaryotes - 177 (source: NCBI BLink).	Unigene24117_All//0.00E+00//TC172940			GO:0031224//GO:0031410	nr -
Unigene24118_All	1329	143.26	56.20	131.30	106.23	105.02	96.41	34.01	20.28	19.21	-1.35E+00	3.98E-221	Down	-1.26E-01	1.49E-03		-1.65E-02	8.05E-01		-1.40E-01	1.49E-03		-7.46E-01	8.06E-25		-8.24E-01	3.46E-30		Unigene24118_All//gi|6091551|gb|AAF01764.2|AF184277.1|//2.00E-68//homeodomain-leucine zipper protein 56 [Glycine max]	Unigene24118_All//1.00E-47//AT2G22430| ATHB6; DNA binding / protein binding / sequence-specific DNA binding / transcription activator/ transcription factor	Unigene24118_All//0.00E+00//gi|78323570|gb|DT543844.1|DT543844	HB		GO:0001071//GO:0003677//GO:0006351//GO:0006950//GO:0009648//GO:0009738//GO:0010468//GO:0010557//GO:0016049//GO:0030528//GO:0043231//GO:0048506	nr +
Unigene24119_All	2181	5.09	3.04	5.79	6.28	4.17	2.96	9.03	8.05	3.67	-7.41E-01	1.47E-05		1.86E-01	3.05E-01		-5.92E-01	2.38E-05		-1.08E+00	1.01E-12	Down	-1.67E-01	1.77E-01		-1.30E+00	7.41E-28	Down	Unigene24119_All//gi|94982942|gb|AB950224.1|//1.00E-102//Nod factor perception protein [Medicago truncatula]	Unigene24119_All//7.00E-60//AT2G33580| protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	Unigene24119_All//0.00E+00//TC176506		ko04626|Plant-pathogen interaction	GO:0043170	nr -
Unigene2412_All	3287	23.27	37.54	49.93	11.71	13.41	5.65	0.08	0.05	0.17	6.90E-01	2.52E-47		1.10E+00	2.28E-134	Up	1.95E-01	1.62E-02		-1.05E+00	4.24E-33	Down	-6.01E-01	6.48E-01		1.14E+00	1.91E-01		Unigene2412_All//gi|3024426|sp|Q42910.1|PPDK_MESCR//0.00E+00//RecName: Full=Pyruvate, phosphate dikinase, chloroplastic; AltName: Full=Pyruvate, orthophosphate dikinase; Flags: Precursor >gi|854265|emb|CAA57872.1| pyruvate,orthophosphate dikinase [Mesembryanthemum crystallinum]	Unigene2412_All//0.00E+00//AT4G15530| PPDK (pyruvate orthophosphate dikinase); kinase/ pyruvate, phosphate dikinase	Unigene2412_All//0.00E+00//TC139890		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0005982//GO:0006629//GO:0006796//GO:0009314//GO:0009532//GO:0016781//GO:0032559//GO:0043169	nr +
Unigene24120_All	1803	50.72	20.91	34.91	58.13	53.76	54.18	44.13	27.91	29.74	-1.28E+00	6.16E-98	Down	-5.39E-01	3.81E-22		-1.13E-01	3.23E-02		-1.02E-01	7.01E-02		-6.61E-01	4.98E-35		-5.69E-01	8.53E-28		Unigene24120_All//gi|18411070|ref|NP_567076.1|//1.00E-158//magnesium transporter CorA-like family protein [Arabidopsis thaliana] >gi|75163756|sp|Q93Z07.1|MRS2_4_ARATH RecName: Full=Magnesium transporter MRS2-4; AltName: Full=Magnesium Transporter 6; Short=AtMGT6 >gi|16209702|gb|AAL14408.1| AT3g58970/F17J16_20 [Arabidopsis thaliana] >gi|25090327|gb|AAN72277.1| At3g58970/F17J16_20 [Arabidopsis thaliana] >gi|25360850|gb|AAN73214.1| MRS2-4 [Arabidopsis thaliana]	Unigene24120_All//8.00E-131//AT3G58970| magnesium transporter CorA-like family protein	Unigene24120_All//0.00E+00//TC144260				nr -

Unigene24122_All	1309	2.20	1.12	4.76	6.70	7.89	2.86	3.94	2.55	1.92	-9.70E-01	8.92E-03		1.11E+00	8.70E-06	Up	2.37E-01	2.26E-01		-1.23E+00	4.92E-10	Down	-6.25E-01	7.76E-03		-1.04E+00	7.86E-06	Down	Unigene24122_All//gi|30685150|ref|NP_188529.2|//4.00E-61//VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor [Arabidopsis thaliana] >gi|75153628|sp|Q8LSW1.1|VRN1_ARATH RecName: Full=B3 domain-containing transcription factor VRN1; AltName: Full=Protein VERNALIZATION 1 >gi|21734794|gb|AAM76972.1|AF28905 1_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|21734796|gb|AAM76973.1|AF28905 2_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|89000959|gb|ABD59069.1| At3g18990 [Arabidopsis thaliana]	Unigene24122_All//2.00E-62//AT3G18990| VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor	Unigene24122_All//0.00E+00//TC139826	ABI3VP1		GO:0003676//GO:0006350//GO:0009409//GO:0009908//GO:0010468//GO:0031981	nr -
Unigene24127_All	2211	16.52	35.32	23.14	9.40	10.42	9.87	1.95	1.27	0.81	1.10E+00	2.10E-65	Up	4.87E-01	1.23E-10		1.49E-01	2.48E-01		7.06E-02	6.22E-01		-6.23E-01	1.71E-02		-1.27E+00	1.49E-06	Down	Unigene24127_All//gi|11103269|gb|AB003531.1|//1.00E-170//class II knotted-like homeobox protein [Prunus persica] >gi|215983122|gb|ACJ71731.1| class II knotted-like homeobox transcription factor [Prunus persica]	Unigene24127_All//5.00E-137//AT5G25220| KNAT3 (KNOTTED1-LIKE HOMEOBOX GENE 3); transcription activator/ transcription factor	Unigene24127_All//0.00E+00//TC159507	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene2413_All	2321	3.36	2.03	2.13	8.24	9.26	7.04	13.08	4.36	6.63	-7.26E-01	4.78E-04		-6.55E-01	2.50E-03		1.68E-01	2.03E-01		-2.27E-01	9.51E-02		-1.59E+00	2.35E-55	Down	-9.81E-01	2.42E-27		Unigene2413_All//gi|22329611|ref|NP_173083.2|//1.00E-121//CYCB3;1 (cyclin b3;1); cyclin-dependent protein kinase [Arabidopsis thaliana] >gi|147636373|sp|Q9SA32.2|CCB31_ARATH RecName: Full=Putative cyclin-B3-1; AltName: Full=G2/mitotic-specific cyclin-B3-1; Short=CycB3;1	Unigene2413_All//2.00E-116//AT1G16330| CYCB3;1 (cyclin b3;1); cyclin-dependent protein kinase	Unigene2413_All//0.00E+00//ES812657			GO:0043231	nr -
Unigene24134_All	1524	11.43	11.24	9.40	14.71	22.48	17.45	7.71	15.85	16.94	-2.48E-02	8.69E-01		-2.83E-01	4.89E-02		6.12E-01	6.13E-13		2.47E-01	2.42E-02		1.04E+00	2.67E-23	Up	1.14E+00	3.29E-29	Up	Unigene24134_All//gi|15221582|ref|NP_177064.1|//1.00E-89//BIM2 (BES1-interacting Myc-like protein 2); DNA binding / transcription factor [Arabidopsis thaliana] >gi|61211674|sp|Q9CAA4.1|BIM2_ARATH RecName: Full=Transcription factor BIM2; AltName: Full=BES1-interacting Myc-like protein 2; AltName: Full=Transcription factor EN 125; AltName: Full=bHLH transcription factor bHLH102; AltName: Full=Basic helix-loop-helix protein 102; Short=bHLH 102; Short=AtbHLH102	Unigene24134_All//5.00E-69//AT1G69010| BIM2 (BES1-interacting Myc-like protein 2); DNA binding / transcription factor	Unigene24134_All//0.00E+00//TC145596	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr +
Unigene24135_All	514	8.65	0.49	2.69	13.96	7.10	4.74	5.92	3.01	1.63	-4.13E+00	1.38E-19	Down	-1.68E+00	1.92E-07	Down	-9.75E-01	1.47E-06		-1.56E+00	1.06E-11	Down	-9.77E-01	2.26E-03		-1.86E+00	6.59E-08	Down	Unigene24135_All//gi|297794009|ref|XP_002864889.1|//1.00E-177//latex-abundant family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310724|gb|EFH41148.1| latex-abundant family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24135_All//1.00E-18//AT5G64240| AtMC3 (metacaspase 3); cysteine-type endopeptidase	Unigene24135_All//5.00E-146//TC158276				nr +
Unigene24136_All	2643	15.78	5.21	11.00	28.37	13.80	7.59	3.97	4.43	3.01	-1.60E+00	1.11E-62	Down	-5.20E-01	7.85E-10		-1.04E+00	2.00E-71	Down	-1.90E+00	4.96E-156	Down	1.58E-01	3.60E-01		-3.96E-01	1.02E-02		Unigene24136_All//gi|297794009|ref|XP_002864889.1|//1.00E-101//latex-abundant family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310724|gb|EFH41148.1| latex-abundant family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24136_All//7.00E-99//AT5G64240| AtMC3 (metacaspase 3); cysteine-type endopeptidase	Unigene24136_All//0.00E+00//TC168021			GO:0004175//GO:0012502	nr -
Unigene24137_All	1880	51.51	25.07	37.33	23.24	22.86	26.57	12.91	10.92	7.50	-1.04E+00	1.47E-74	Down	-4.65E-01	5.50E-18		-2.37E-02	8.13E-01		1.93E-01	1.31E-02		-2.42E-01	1.89E-02		-7.83E-01	2.55E-15		Unigene24137_All//gi|18398463|ref|NP_564404.1|//1.00E-172//ATNAP6 (NON-INTRINSIC ABC PROTEIN 6); protein binding / transporter [Arabidopsis thaliana] >gi|75180162|sp|Q9LQR7.1|ABT1_ARATH RecName: Full=Protein ABCI7, chloroplastic; AltName: Full=ABC transporter I family member 7; Short=ABC transporter ABCI.7; Short=AtABCI7; AltName: Full=Non-intrinsic ABC protein 6; AltName: Full=Plastid SufD-like protein; Flags: Precursor >gi|8920626|gb|AAF81348.1|AC007767_28 Contains an uncharacterized protein family (UPF0051) domain PF|01458 [Arabidopsis thaliana] >gi|11564672|gb|ABJ17094.1| At1g32500 [Arabidopsis thaliana]	Unigene24137_All//3.00E-152//AT1G32500| ATNAP6 (NON-INTRINSIC ABC PROTEIN 6); protein binding / transporter	Unigene24137_All//0.00E+00//TC148575			GO:0005488//GO:0031163	nr -
Unigene24138_All	542	10.81	11.59	12.87	9.93	4.64	4.75	37.60	36.63	29.33	1.01E-01	6.80E-01		2.52E-01	3.11E-01		-1.10E+00	4.83E-06	Down	-1.06E+00	3.03E-05	Down	-3.77E-02	7.72E-01		-3.59E-01	7.70E-04		Unigene24138_All//gi|75273870|sp|Q9LRZ4.1|P2C41_ARATH//6.00E-47//RecName: Full=Probable protein phosphatase 2C 41; Short=AtPP2C41 >gi|7939572|dbj|BAA95773.1| protein phosphatase-2C-like protein [Arabidopsis thaliana] >gi|222423684|dbj|BAH19809.1| AT3G16800 [Arabidopsis thaliana]	Unigene24138_All//3.00E-48//AT3G16800| protein phosphatase 2C, putative / PP2C, putative	Unigene24138_All//4.00E-76//gi|84171822|gb|DR460470.1|DR460470			GO:0004721//GO:0006950//GO:0043231	nr -
Unigene2414_All	1720	23.42	34.35	26.28	14.65	18.28	14.55	24.80	50.79	27.68	5.52E-01	9.14E-16		1.66E-01	5.83E-02		3.19E-01	5.26E-04		-1.07E-02	9.49E-01		1.03E+00	1.82E-81	Up	1.58E-01	2.51E-02		Unigene2414_All//gi|15239142|ref|NP_196726.1|//1.00E-158//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|7573379|emb|CAB87683.1| lysophospholipase-like protein [Arabidopsis thaliana] >gi|110738402|dbj|BAF01127.1| lysophospholipase like protein [Arabidopsis thaliana] >gi|111074320|gb|ABH04533.1| At5g11650 [Arabidopsis thaliana]	Unigene2414_All//3.00E-159//AT5G11650| hydrolase, alpha/beta fold family protein	Unigene2414_All//0.00E+00//TC162830		ko00561|Glycerolipid metabolism		nr -
Unigene24142_All	2558	3.62	1.92	3.29	30.75	29.86	20.96	10.36	16.16	4.81	-9.14E-01	1.77E-06		-1.38E-01	5.28E-01		-4.24E-02	5.82E-01		-5.53E-01	2.53E-22		6.41E-01	1.25E-17		-1.11E+00	4.98E-29	Down	Unigene24142_All//gi|42566276|ref|NP_192255.2|//4.00E-71//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene24142_All//2.00E-66//AT4G03460| ankyrin repeat family protein	Unigene24142_All//0.00E+00//DW230980				nr +
Unigene24143_All	2155	3.35	2.35	2.99	18.82	17.08	15.84	2.41	1.59	0.89	-5.11E-01	1.93E-02		-1.64E-01	5.09E-01		-1.40E-01	1.24E-01		-2.48E-01	3.43E-03		-6.02E-01	1.03E-02		-1.44E+00	3.09E-09	Down	Unigene24143_All//gi|15241713|ref|NP_195839.1|//1.00E-164//PCS1 (PROMOTION OF CELL SURVIVAL 1); aspartic-type endopeptidase/ peptidase [Arabidopsis thaliana] >gi|50897174|gb|AAT85726.1| At5g02190 [Arabidopsis thaliana] >gi|53828617|gb|AAU94418.1| At5g02190 [Arabidopsis thaliana]	Unigene24143_All//2.00E-158//AT5G02190| PCS1 (PROMOTION OF CELL SURVIVAL 1); aspartic-type endopeptidase/ peptidase	Unigene24143_All//0.00E+00//TC146281			GO:0004175//GO:0019538	nr +
Unigene24144_All	371	13.12	27.86	14.78	26.45	20.70	30.68	40.00	30.08	21.69	1.09E+00	3.42E-09	Up	1.73E-01	5.52E-01		-3.54E-01	5.14E-02		2.14E-01	2.60E-01		-4.11E-01	1.61E-03		-8.83E-01	9.95E-12		Unigene24144_All//gi|297823677|ref|XP_002879721.1|//5.00E-53//ribosome biogenesis regulatory protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325560|gb|EFH55980.1| ribosome biogenesis regulatory protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24144_All//4.00E-46//AT2G37990| ribosome biogenesis regulatory protein (RRS1) family protein	Unigene24144_All//0.00E+00//TC129757			GO:0022613//GO:0031981	nr +
Unigene24146_All	1592	7.26	32.11	5.52	12.14	31.04	18.44	28.31	65.29	31.01	2.14E+00	1.30E-113	Up	-3.96E-01	2.50E-02		1.35E+00	3.64E-68	Up	6.03E-01	5.30E-10		1.21E+00	8.24E-124	Up	1.31E-01	6.42E-02		Unigene24146_All//gi|225442186|ref|XP_002276676.1|//1.00E-156//PREDICTED: similar to mitochondrial substrate carrier family protein isoform 1 [Vitis vinifera]	Unigene24146_All//2.00E-127//AT1G72820| mitochondrial substrate carrier family protein	Unigene24146_All//0.00E+00//TC145968				nr -
Unigene24147_All	2706	0.56	1.33	0.65	3.90	3.47	3.54	4.42	4.73	3.86	1.25E+00	1.98E-04	Up	2.12E-01	6.61E-01		-1.68E-01	4.03E-01		-1.41E-01	4.96E-01		9.61E-02	5.88E-01		-1.97E-01	1.97E-01		Unigene24147_All//gi|297723429|ref|NP_001174078.1|//1.00E-175//Os04g0599650 [Oryza sativa Japonica Group] >gi|255675747|dbj|BAH92806.1| Os04g0599650 [Oryza sativa Japonica Group]		Unigene24147_All//0.00E+00//gi|84164136|gb|DR452784.1|DR452784			GO:0003676//GO:0003678//GO:0006259//GO:0032559	nr +
Unigene24148_All	1344	49.79	29.44	26.07	95.59	89.88	28.16	14.94	4.23	20.42	-7.58E-01	1.32E-30		-9.34E-01	7.15E-42		-8.88E-02	7.02E-02		-1.76E+00	1.27E-240	Down	-1.82E+00	1.10E-44	Down	4.51E-01	6.07E-07		Unigene24148_All//gi|224054710|ref|XP_002298353.1|//1.00E-141//alpha-expansin family protein [Populus trichocarpa] >gi|222845611|gb|EEE83158.1| alpha-expansin family protein [Populus trichocarpa]	Unigene24148_All//7.00E-134//AT2G39700| ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	Unigene24148_All//0.00E+00//gi|78342812|gb|DT563086.1|DT563086				nr -
Unigene2415_All	1562	16.82	11.06	9.82	14.86	14.31	9.40	9.34	4.36	4.16	-6.04E-01	1.22E-08		-7.76E-01	2.05E-12		-5.48E-02	7.08E-01		-6.61E-01	1.94E-09		-1.10E+00	1.09E-15	Down	-1.17E+00	9.13E-18	Down	Unigene2415_All//gi|297791867|ref|XP_002863818.1|//1.00E-150//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309653|gb|EFH40077.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2415_All//1.00E-144//AT5G42130| mitochondrial substrate carrier family protein	Unigene2415_All//0.00E+00//TC152848			GO:0043231	nr +
Unigene24154_All	4423	0.24	0.32	0.39	0.23	0.24	0.16	0.71	0.29	0.44	4.39E-01	4.25E-01		7.04E-01	1.81E-01		9.96E-02	9.02E-01		-4.63E-01	5.26E-01		-1.27E+00	7.99E-05	Down	-6.80E-01	2.43E-02		Unigene24154_All//gi|15229615|ref|NP_188457.1|//0.00E+00//EMB2454 (embryo defective 2454); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|20453199|gb|AAM19839.1| AT3g18290/MIE15_8 [Arabidopsis thaliana] >gi|29028750|gb|AAO64754.1| At3g18290/MIE15_8 [Arabidopsis thaliana]	Unigene24154_All//0.00E+00//AT3G18290| EMB2454 (embryo defective 2454); protein binding / zinc ion binding	Unigene24154_All//0.00E+00//TC152326		ko04120|Ubiquitin mediated proteolysis	GO:0005488	nr +

Unigene24159_All	2989	1.80	1.86	2.94	10.07	8.40	6.89	1.95	1.12	0.97	4.85E-02	8.54E-01		7.05E-01	4.77E-04		-2.61E-01	6.56E-03		-5.47E-01	9.34E-09		-8.03E-01	2.42E-04		-1.00E+00	3.55E-06	Down	Unigene24159_All|gi|4204259|gb|AAD10640.1|//0.00E+00//Similar to Kinesin proteins [Arabidopsis thaliana]	Unigene24159_All//2.00E-163//AT1G55550| ATP binding / microtubule motor	Unigene24159_All//0.00E+00//DT052538			GO:0000166//GO:0003774//GO:0009987	nr +
Unigene24163_All	3249	8.04	16.73	11.08	15.42	17.29	15.58	19.30	28.04	16.10	1.06E+00	3.13E-43	Up	4.63E-01	4.37E-07		1.65E-01	2.24E-02		1.47E-02	8.88E-01		5.39E-01	5.51E-28		-2.62E-01	7.04E-06		Unigene24163_All|gi|16973320|emb|CAC84112.1|//4.00E-20//salt inducible-like protein [Gossypium hirsutum]	Unigene24163_All//7.00E-14//AT4G14200| unknown protein	Unigene24163_All//0.00E+00//TC171910				nr -
Unigene24168_All	2188	19.42	2.78	3.31	20.35	15.71	7.22	17.16	2.60	3.53	-2.80E+00	3.22E-130	Down	-2.55E+00	2.57E-113	Down	-3.74E-01	3.16E-07		-1.49E+00	7.32E-66	Down	-2.72E+00	3.41E-136	Down	-2.28E+00	2.32E-114	Down	Unigene24168_All|gi|115451537|ref|NP_001049369.1|//0.00E+00//Os03g0214100 [Oryza sativa Japonica Group] >gi|108706832|gb|ABF94627.1| replication factor-a protein 1 containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547840|dbj|BAF11283.1| Os03g0214100 [Oryza sativa Japonica Group]	Unigene24168_All//0.00E+00//AT5G08020| RPA70B (RPA70-KDA SUBUNIT B); DNA binding / nucleic acid binding	Unigene24168_All//0.00E+00//TC130012		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair	GO:0003676//GO:0006259//GO:0009411//GO:0043231	nr -
Unigene24171_All	1689	58.86	34.35	38.65	37.52	48.46	22.14	1.75	4.50	2.31	-7.77E-01	4.50E-47		-6.07E-01	1.38E-29		3.69E-01	2.43E-12		-7.61E-01	1.86E-31		1.36E+00	1.15E-11	Up	4.00E-01	1.45E-01		Unigene24171_All|gi|115456355|ref|NP_001051778.1|//1.00E-103//Os03g0828800 [Oryza sativa Japonica Group] >gi|108711884|gb|ABF99679.1| D-mannose binding lectin family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550249|dbj|BAF13692.1| Os03g0828800 [Oryza sativa Japonica Group]	Unigene24171_All//1.00E-79//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene24171_All//0.00E+00//TC170385		ko04626|Plant-pathogen interaction		nr +
Unigene24172_All	2856	2.27	1.42	2.78	5.22	4.24	2.58	5.09	4.00	3.00	-6.79E-01	3.27E-03		2.90E-01	2.03E-01		-2.97E-01	4.04E-02		-1.02E+00	1.89E-12	Down	-3.50E-01	8.70E-03		-7.64E-01	3.52E-09		Unigene24172_All|gi|4508083|gb|AAD21427.1|//1.00E-105//hypothetical protein [Arabidopsis thaliana]	Unigene24172_All//9.00E-42//AT1G61690| phosphoinositide binding	Unigene24172_All//0.00E+00//gi|109867215|gb|DW496191.1|DW496191				nr -
Unigene24175_All	1338	14.55	17.04	18.43	17.46	15.80	11.81	21.87	12.99	10.81	2.28E-01	5.76E-02		3.41E-01	3.11E-03		-1.44E-01	2.59E-01		-5.64E-01	2.67E-07		-7.51E-01	1.49E-16		-1.02E+00	6.34E-28	Down	Unigene24175_All|gi|297814115|ref|XP_002874941.1|//1.00E-105//0s01g0254000 [Arabidopsis lyrata subsp. lyrata] >gi|297320778|gb|EFH51200.1| Os01g0254000 [Arabidopsis lyrata subsp. lyrata]	Unigene24175_All//1.00E-84//AT4G02080| ATSAR2 (ARABIDOPSIS THALIANA SECRETION-ASSOCIATED RAS SUPER FAMILY 2); GTP binding	Unigene24175_All//0.00E+00//TC154099		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene24176_All	546	17.06	15.13	12.29	9.49	4.48	6.37	1.32	0.54	0.88	-1.73E-01	3.83E-01		-4.73E-01	1.69E-02		-1.08E+00	9.99E-06	Down	-5.75E-01	2.93E-02		-1.30E+00	9.45E-02		-5.88E-01	4.09E-01		Unigene24176_All|gi|15241652|ref|NP_196469.1|//3.00E-50//myb family transcription factor [Arabidopsis thaliana] >gi|41619008|gb|AAS10002.1| MYB transcription factor [Arabidopsis thaliana]	Unigene24176_All//2.00E-51//AT5G08520| myb family transcription factor	Unigene24176_All//0.00E+00//CO131061	MYB		GO:0001071//GO:0003676//GO:0010468//GO:0043231	nr +
Unigene24179_All	2039	27.25	16.25	13.63	43.00	40.38	35.17	21.21	6.89	7.54	-7.46E-01	7.50E-25		-9.99E-01	5.70E-39		-9.06E-02	1.45E-01		-2.90E-01	6.81E-08		-1.62E+00	3.23E-81	Down	-1.49E+00	5.26E-74	Down	Unigene24179_All|gi|6093739|sp|Q43111.1|PME3_PHAVU//0.00E+00//RecName: Full=Pectinesterase 3; Short=PE 3; AltName: Full=Pectin methylesterase 3; Flags: Precursor >gi|732913|emb|CAA59482.1| pectinesterase [Phaseolus vulgaris]	Unigene24179_All//0.00E+00//AT1G53840| ATPME1; pectinesterase	Unigene24179_All//0.00E+00//TC139115		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0016020//GO:0030234//GO:0030312//GO:0045229//GO:0071555	nr -
Unigene24185_All	1263	3.15	6.90	4.09	4.81	4.53	4.65	4.42	10.03	7.25	1.13E+00	2.37E-08	Up	3.77E-01	1.83E-01		-8.84E-02	7.72E-01		-4.98E-02	8.58E-01		1.18E+00	2.56E-15	Up	7.15E-01	1.61E-05		Unigene24185_All|gi|297850116|ref|XP_002892939.1|//8.00E-24//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297338781|gb|EFH69198.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene24185_All//1.00E-24//AT1G17210| zinc ion binding	Unigene24185_All//0.00E+00//CO097905			GO:0043231//GO:0046914	nr +
Unigene24188_All	2572	15.36	10.72	6.46	22.74	21.31	16.45	15.32	6.47	5.72	-5.19E-01	9.22E-10		-1.25E+00	1.06E-39	Down	-9.33E-02	2.37E-01		-4.67E-01	1.92E-12		-1.24E+00	7.45E-50	Down	-1.42E+00	6.77E-63	Down	Unigene24188_All|gi|115454097|ref|NP_001050649.1|//0.00E+00//Os03g0609800 [Oryza sativa Japonica Group] >gi|113549120|dbj|BAF12563.1| Os03g0609800 [Oryza sativa Japonica Group]	Unigene24188_All//8.00E-177//AT2G14820| NPY2 (NAKED PINS IN YUC MUTANTS 2); protein binding / signal transducer	Unigene24188_All//0.00E+00//TC160996			GO:0005488//GO:0009314//GO:0060089	nr +
Unigene2419_All	2492	2.90	1.22	1.28	18.55	8.07	6.98	5.26	1.88	1.18	-1.25E+00	3.92E-08	Down	-1.18E+00	4.21E-07	Down	-1.20E+00	8.59E-56	Down	-1.41E+00	1.05E-62	Down	-1.49E+00	3.49E-22	Down	-2.15E+00	1.12E-37	Down	Unigene2419_All|gi|211906532|gb|AGJ11759.1|//0.00E+00//class III peroxidase [Gossypium hirsutum]	Unigene2419_All//1.00E-125//AT4G37530| peroxidase, putative	Unigene2419_All//0.00E+00//gi|164302716|gb|ES837136.1|ES837136		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209	nr +
Unigene24192_All	2848	1.18	0.84	1.14	3.24	3.19	2.60	2.09	0.69	1.64	-4.92E-01	1.47E-01		-4.39E-02	9.09E-01		-1.97E-02	9.30E-01		-3.15E-01	1.19E-01		-1.60E+00	1.19E-11	Down	-3.55E-01	1.00E-01		Unigene24192_All|gi|297826945|ref|XP_002881355.1|//1.00E-180//RNA polymerase I specific transcription initiation factor RRN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327194|gb|EFH57614.1| RNA polymerase I specific transcription initiation factor RRN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24192_All//1.00E-177//AT2G34750| RNA polymerase I specific transcription initiation factor RRN3 family protein	Unigene24192_All//0.00E+00//TC130041				nr -
Unigene24193_All	2645	4.39	2.34	2.60	8.23	9.14	6.73	9.85	3.98	3.92	-9.10E-01	7.27E-08		-7.58E-01	1.15E-05		1.51E-01	2.25E-01		-2.91E-01	1.56E-02		-1.31E+00	9.03E-36	Down	-1.33E+00	7.06E-38	Down	Unigene24193_All|gi|18394738|ref|NP_564084.1|//0.00E+00//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75174900|sp|Q9LN50.1|PMTS_ARATH RecName: Full=Probable methyltransferase PMT28 >gi|8778438|gb|AAF79446.1|AC025808_28 F18O14.20 [Arabidopsis thaliana]	Unigene24193_All//0.00E+00//AT1G19430| dehydration-responsive protein-related	Unigene24193_All//0.00E+00//TC146520		ko03040|Spliceosome	GO:0003824//GO:0005488//GO:0043231	nr -
Unigene24196_All	2725	0.96	2.36	1.56	2.23	2.22	2.77	14.03	21.37	54.65	1.30E+00	1.03E-07	Up	7.04E-01	2.22E-02		-4.00E-03	9.80E-01		3.12E-01	1.76E-01		6.07E-01	2.55E-22		1.96E+00	0.00E+00	Up	Unigene24196_All|gi|75334121|sp|Q9FNE1.1|CRK42_ARATH//0.00E+00//RecName: Full=Cysteine-rich receptor-like protein kinase 42; Short=Cysteine-rich RLK42; Flags: Precursor >gi|10178148|dbj|BAB11593.1| receptor-like serine/threonine kinase [Arabidopsis thaliana]	Unigene24196_All//0.00E+00//AT5G40380| protein kinase family protein	Unigene24196_All//0.00E+00//DT462978		ko04626|Plant-pathogen interaction	GO:0004672	nr -
Unigene24197_All	2688	5.37	1.89	3.74	5.52	3.98	4.96	15.56	15.77	16.30	-1.51E+00	1.77E-20	Down	-5.21E-01	6.58E-04		-4.71E-01	5.20E-04		-1.56E-01	3.63E-01		1.94E-02	8.33E-01		6.76E-02	4.13E-01		Unigene24197_All|gi|225452458|ref|XP_002274361.1|//0.00E+00//PREDICTED: similar to AO (L-ASPARTATE OXIDASE); L-aspartate oxidase [Vitis vinifera]	Unigene24197_All//0.00E+00//AT5G14760| AO (L-ASPARTATE OXIDASE); L-aspartate oxidase/ electron carrier/ oxidoreductase	Unigene24197_All//0.00E+00//ES824670		ko00250|Alanine, aspartate and glutamate metabolism//ko00760|Nicotinate and nicotinamide metabolism	GO:0009536//GO:0015922//GO:0019359	nr -
Unigene24199_All	1501	44.97	37.47	26.00	102.78	88.28	96.43	125.88	129.15	40.21	-2.63E-01	4.03E-05		-7.90E-01	6.39E-32		-2.19E-01	6.38E-09		-9.20E-02	4.08E-02		3.69E-02	3.77E-01		-1.65E+00	0.00E+00	Down	Unigene24199_All|gi|297821166|ref|XP_002878466.1|//1.00E-160//DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324304|gb|EFH54725.1| DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24199_All//7.00E-151//AT3G62600| ATERDJ3B; heat shock protein binding / unfolded protein binding	Unigene24199_All//0.00E+00//TC135002		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene2420_All	1333	3.77	1.18	2.80	3.92	5.40	7.59	15.29	9.38	36.67	-1.68E+00	1.01E-08	Down	-4.30E-01	1.37E-01		4.61E-01	3.36E-02		9.52E-01	9.83E-08		-7.06E-01	1.18E-10		1.26E+00	2.52E-64	Up	Unigene2420_All|gi|297803592|ref|XP_002869680.1|//1.00E-103//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297315516|gb|EFH45939.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene2420_All//1.00E-103//AT1G17020| SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc	Unigene2420_All//1.00E-136//TC138716		ko00270|Cysteine and methionine metabolism		nr +
Unigene24201_All	2134	6.30	1.90	4.47	10.74	7.26	8.17	7.19	2.60	3.32	-1.73E+00	4.45E-23	Down	-4.96E-01	1.88E-03		-5.64E-01	6.57E-08		-3.94E-01	4.56E-04		-1.47E+00	2.46E-25	Down	-1.11E+00	2.35E-17	Down	Unigene24201_All|gi|75331892|sp|Q944S1.1|RH22_ARATH//1.00E-174//RecName: Full=DEAD-box ATP-dependent RNA helicase 22 >gi|15983392|gb|AAL11564.1|AF424570_1 At1g59990/T2K10_4 [Arabidopsis thaliana] >gi|22653388|gb|AAM98286.1| At1g59990/T2K10_4 [Arabidopsis thaliana]	Unigene24201_All//9.00E-176//AT1G59990| DEAD/DEAH box helicase, putative (RH22)	Unigene24201_All//0.00E+00//TC161179			GO:0005488//GO:0017111//GO:0043231	nr +
Unigene24202_All	475	0.99	0.21	3.03	5.24	3.19	3.90	9.70	13.46	3.94	-2.22E+00	7.76E-02		1.61E+00	8.67E-03		-7.17E-01	6.35E-02		-4.28E-01	3.21E-01		4.73E-01	2.48E-02		-1.30E+00	3.44E-07	Down	Unigene24202_All|gi|255549816|ref|XP_002515959.1|//4.00E-09//Auxin-responsive protein IAA6, putative [Ricinus communis] >gi|223541864|gb|EEF46379.1| Auxin-responsive protein IAA6, putative [Ricinus communis]	Unigene24202_All//8.00E-07//AT3G16500| PAP1 (PHYTOCHROME-ASSOCIATED PROTEIN 1); transcription factor	Unigene24202_All//4.00E-119//gi|48828583|gb|CO126973.1|CO126973			GO:0009987//GO:0010467	nr +
Unigene24203_All	1376	10.00	4.20	9.64	108.79	108.54	124.69	59.89	58.81	27.94	-1.25E+00	7.07E-15	Down	-5.35E-02	7.50E-01		-3.30E-03	9.63E-01		1.97E-01	2.19E-07		-2.63E-02	6.81E-01		-1.10E+00	1.68E-87	Down	Unigene24203_All|gi|21593333|gb|AAM65282.1|//5.00E-58//phytochrome-associated protein 1 (PAP1) [Arabidopsis thaliana]	Unigene24203_All//2.00E-45//AT3G16500| PAP1 (PHYTOCHROME-ASSOCIATED PROTEIN 1); transcription factor	Unigene24203_All//0.00E+00//TC140165			GO:0001071//GO:0003676//GO:0006351//GO:0006412//GO:0006801//GO:0006970//GO:0009718//GO:0009725//GO:0010182//GO:0010468//GO:0016021//GO:0016791//GO:0019637//GO:0043231	nr +
Unigene24209_All	759	1.52	0.27	2.81	6.89	11.02	10.12	2.84	2.86	1.89	-2.51E+00	8.99E-04	Down	8.88E-01	5.42E-02		6.78E-01	3.61E-04		5.54E-01	8.42E-03		1.14E-02	1.02E+00		-5.88E-01	1.18E-01			Unigene24209_All//8.00E-72//TC166519				
Unigene2421_All	1747	4.25	2.18	3.32	6.73	6.98	7.91	8.81	3.85	4.70	-9.67E-01	8.19E-06		-3.56E-01	1.27E-01		5.23E-02	8.19E-01		2.33E-01	1.59E-01		-1.19E+00	9.62E-19	Down	-9.07E-01	1.18E-12		Unigene2421_All|gi|224103345|ref|XP_002313020.1|//1.00E-122//inner membrane protein [Populus trichocarpa] >gi|222849428|gb|EEE86975.1| inner membrane protein [Populus trichocarpa]	Unigene2421_All//4.00E-110//AT1G65080| OXA1 family protein	Unigene2421_All//0.00E+00//gi|78327069|gb|DT547343.1|DT547343		ko03060|Protein export	GO:0016020//GO:0043231	nr +
Unigene24210_All	1885	2.03	0.75	1.89	6.13	8.20	6.28	3.30	4.61	2.41	-1.43E+00	1.43E-05	Down	-9.83E-02	7.62E-01		4.20E-01	2.09E-03		3.40E-02	8.72E-01		4.84E-01	5.87E-03		-4.53E-01	2.83E-02		Unigene24210_All//sp|Q92878|RAD50_HUMAN//7.00E-06//DNA repair protein RAD50 OS=Homo sapiens GN=RAD50 PE=1 SV=1		Unigene24210_All//2.00E-71//TC166519				swissprot +

Unigene24211_All	1632	5.00	11.98	10.31	33.91	36.99	41.23	40.47	36.47	39.37	1.26E+00	6.10E-21	Up	1.04E+00	4.35E-13	Up	1.25E-01	8.51E-02		2.82E-01	6.38E-06		-1.50E-01	1.38E-02		-3.95E-02	5.88E-01		Unigene24211_All//gi|15233452|ref|NP_194639.1|//7.00E-73//ethylene-responsive family protein [Arabidopsis thaliana] >gi|75159400|sp|Q8S3D1.2|BH068_ARATH RecName: Full=Transcription factor bHLH068; AltName: Full=Transcription factor EN 60; AltName: Full=bHLH transcription factor bHLH068; AltName: Full=Basic helix-loop-helix protein 68; Short=bHLH 68; Short=AtbHLH68	Unigene24211_All//3.00E-50//AT4G29100| ethylene-responsive family protein	Unigene24211_All//0.00E+00//TC143406	bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene24212_All	487	1.07	5.41	1.97	3.48	3.39	3.99	0.43	2.75	2.13	2.33E+00	4.20E-07	Up	8.74E-01	2.38E-01		-3.52E-02	9.43E-01		1.97E-01	6.75E-01		2.66E+00	2.41E-05	Up	2.29E+00	7.17E-04	Up	Unigene24212_All//gi|219816075|gb|ACL37155.1|//2.00E-27//short-chain alcohol dehydrogenase [Panax ginseng]	Unigene24212_All//8.00E-21//AT3G01980| short-chain dehydrogenase/reductase (SDR) family protein	Unigene24212_All//3.00E-129//ES803044		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0008152//GO:0016616//GO:0042579	nr +
Unigene24213_All	1287	1.18	7.64	1.16	2.36	3.51	3.97	1.25	4.94	3.28	2.70E+00	5.22E-29	Up	-2.52E-02	9.84E-01		5.70E-01	4.37E-02		7.48E-01	4.60E-03		1.98E+00	2.71E-16	Up	1.39E+00	3.04E-07	Up	Unigene24213_All//gi|219816075|gb|ACL37155.1|//6.00E-94//short-chain alcohol dehydrogenase [Panax ginseng]	Unigene24213_All//1.00E-77//AT3G01980| short-chain dehydrogenase/reductase (SDR) family protein	Unigene24213_All//0.00E+00//ES803044		ko04146|Peroxisome//ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0008152//GO:0016491//GO:0042579	nr -
Unigene24214_All	1198	1.18	4.78	1.51	1.46	2.01	4.37	0.35	1.74	1.83	2.02E+00	2.35E-12	Up	3.58E-01	4.81E-01		4.67E-01	2.92E-01		1.59E+00	8.97E-09	Up	2.31E+00	6.82E-07	Up	2.37E+00	1.29E-07	Up	Unigene24214_All//gi|219816075|gb|ACL37155.1|//6.00E-94//short-chain alcohol dehydrogenase [Panax ginseng]	Unigene24214_All//5.00E-79//AT3G01980| short-chain dehydrogenase/reductase (SDR) family protein	Unigene24214_All//0.00E+00//gi|164344338|gb|ES803044.1|ES803044		ko04146|Peroxisome//ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0008152//GO:0016616//GO:0042579	nr -
Unigene24219_All	377	1.39	0.27	0.28	0.53	0.00	1.20	2.69	3.88	9.19	-2.37E+00	4.76E-02		-2.30E+00	6.76E-02		-9.05E+00	8.43E-02		1.18E+00	3.38E-01		5.28E-01	3.03E-01		1.77E+00	2.97E-08	Up			Unigene24219_All//7.00E-43//CO072579				
Unigene2422_All	734	4.85	3.66	8.20	5.84	6.33	6.46	8.76	18.22	15.36	-4.06E-01	2.23E-01		7.58E-01	2.51E-03		1.18E-01	7.44E-01		1.47E-01	6.47E-01		1.06E+00	1.29E-13	Up	8.11E-01	5.77E-08		Unigene2422_All//gi|115449335|ref|NP_001048441.1|//5.00E-07//Os02g0805500 [Oryza sativa Japonica Group] >gi|113537972|dbj|BAF10355.1|Os02g0805500 [Oryza sativa Japonica Group]	Unigene2422_All//4.00E-07//AT5G63980| 5AL1; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase	Unigene2422_All//0.00E+00//TC160940		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism	GO:0008252//GO:0016312//GO:0043231//GO:0044237	nr -
Unigene24220_All	1609	7.19	7.94	4.53	10.87	10.68	9.04	1.66	6.96	7.03	1.43E-01	4.00E-01		-6.65E-01	1.21E-04		-2.51E-02	8.73E-01		-2.66E-01	5.67E-02		2.07E+00	8.96E-30	Up	2.09E+00	5.62E-31	Up	Unigene24220_All//gi|4530126|gb|AAD21872.1|//3.00E-49//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene24220_All//7.00E-41//AT4G21410| protein kinase family protein	Unigene24220_All//0.00E+00//CO072579			GO:0004672	nr -
Unigene24222_All	1340	9.88	3.67	9.06	10.89	11.28	9.00	4.80	3.99	3.06	-1.43E+00	2.13E-17	Down	-1.25E-01	4.89E-01		5.07E-02	8.06E-01		-2.76E-01	7.44E-02		-2.65E-01	2.39E-01		-6.47E-01	1.24E-03		Unigene24222_All//gi|297821280|ref|XP_002878523.1|//1.00E-79//tRNA/rRNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324361|gb|EFH14782.1|tRNA/rRNA methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24222_All//9.00E-78//AT5G26880| tRNA/rRNA methyltransferase (SpoU) family protein	Unigene24222_All//0.00E+00//TC130250			GO:0003676//GO:0008168//GO:0010467//GO:0043231	nr +
Unigene24223_All	215	6.33	3.77	1.24	1.85	0.64	3.99	0.79	1.17	0.56	-7.47E-01	1.93E-01		-2.35E+00	7.63E-04	Down	-1.53E+00	2.05E-01		1.11E+00	1.67E-01		5.68E-01	6.74E-01		-5.01E-01	7.46E-01		Unigene24223_All//gi|9955568|emb|CAC05495.1|//2.00E-25//DNA gyrase subunit B-like protein [Arabidopsis thaliana]	Unigene24223_All//1.00E-12//AT5G04130| DNA topoisomerase, ATP-hydrolyzing, putative / DNA topoisomerase II, putative / DNA gyrase, putative	Unigene24223_All//6.00E-85//TC137470			GO:0003916//GO:0006259//GO:0009536//GO:0032559//GO:0043232	nr -
Unigene24224_All	2454	12.77	4.29	7.12	9.07	7.03	6.11	12.49	4.63	5.99	-1.57E+00	3.29E-46	Down	-8.44E-01	7.52E-17		-3.68E-01	7.82E-04		-5.71E-01	3.96E-07		-1.43E+00	4.01E-48	Down	-1.06E+00	3.13E-31	Down	Unigene24224_All//gi|75288399|sp|Q5YLB4.1|GYRB_NICBE//0.00E+00//RecName: Full=DNA gyrase subunit B, chloroplastic/mitochondrial; Flags: Precursor >gi|38017095|gb|AAR07943.1| DNA gyrase B subunit [Nicotiana benthamiana]	Unigene24224_All//0.00E+00//AT5G04130| DNA topoisomerase, ATP-hydrolyzing, putative / DNA topoisomerase II, putative / DNA gyrase, putative	Unigene24224_All//0.00E+00//TC156127			GO:0003916//GO:0006259//GO:0009536//GO:0032559//GO:0043232	nr +
Unigene24225_All	2140	38.78	22.87	26.87	82.29	72.04	74.86	86.60	38.48	40.81	-7.62E-01	4.28E-38		-5.29E-01	1.74E-19		-1.92E-01	6.39E-08		-1.37E-01	4.36E-04		-1.17E+00	1.82E-210	Down	-1.09E+00	1.21E-191	Down	Unigene24225_All//gi|243713053|dbj|BAC22124.1|//0.00E+00//t-complex polypeptide 1 [Bruguiera sexangula]	Unigene24225_All//0.00E+00//AT3G20050| ATTCP-1; ATP binding / protein binding / unfolded protein binding	Unigene24225_All//0.00E+00//TC145064			GO:0005515//GO:0032559//GO:0044267//GO:0044424	nr +
Unigene24226_All	1093	3.16	5.84	6.67	2.92	2.27	6.86	16.75	73.38	25.62	8.87E-01	1.62E-04		1.08E+00	2.38E-06	Up	-3.63E-01	3.13E-01		1.23E+00	1.27E-08	Up	2.13E+00	1.05E-216	Up	6.13E-01	1.13E-11		Unigene24226_All//gi|75213423|sp|Q9SYF0.1|GLIP2_ARATH//5.00E-40//RecName: Full=GDSL esterase/lipase 2; AltName: Full=Extracellular lipase 2; Flags: Precursor >gi|4587535|gb|AAD25766.1|AC006577_2 Belongs to the PF|00657 Lipase/Acylhydrolase with GDSL-motif family. EST gb|R29935 comes from this gene [Arabidopsis thaliana]	Unigene24226_All//2.00E-41//AT1G53940| GLIP2; arylesterase/ carboxylesterase/ lipase	Unigene24226_All//0.00E+00//TC173925			GO:0004091//GO:0009734//GO:0009814//GO:0044238//GO:0048583//GO:0050832	nr -
Unigene24227_All	1225	11.28	18.61	11.95	8.82	3.88	18.10	30.55	155.45	59.38	7.23E-01	4.07E-10		8.43E-02	6.24E-01		-1.19E+00	4.54E-13	Down	1.04E+00	1.35E-18	Up	2.35E+00	0.00E+00	Up	9.59E-01	1.71E-61		Unigene24227_All//gi|21358785|gb|AAM47031.1|//1.00E-111//lipase SIL1 [Brassica rapa subsp. pekinensis]	Unigene24227_All//9.00E-109//AT5G40990| GLIP1 (GDSL LIPASE1); carboxylesterase/ lipase	Unigene24227_All//0.00E+00//TC173925				nr +
Unigene24228_All	2044	6.07	3.20	1.93	5.63	4.82	4.71	10.18	3.11	6.49	-9.24E-01	1.55E-08		-1.65E+00	3.22E-19	Down	-2.25E-01	2.14E-01		-2.58E-01	1.53E-01		-1.71E+00	1.74E-42	Down	-6.49E-01	8.57E-10		Unigene24228_All//gi|18414910|ref|NP_568157.1|//0.00E+00//outer membrane OMP85 family protein [Arabidopsis thaliana] >gi|16648863|gb|AAL24283.1|Unknown protein [Arabidopsis thaliana]	Unigene24228_All//0.00E+00//AT5G05520| outer membrane OMP85 family protein	Unigene24228_All//0.00E+00//TC149876			GO:0016020//GO:0043231	nr +
Unigene2423_All	1765	3.59	2.58	2.35	5.05	6.63	6.73	16.65	33.15	35.64	-4.73E-01	4.47E-02		-6.08E-01	1.32E-02		3.93E-01	1.63E-02		4.14E-01	1.28E-02		9.94E-01	2.09E-51		1.10E+00	2.51E-66	Up	Unigene2423_All//gi|115449335|ref|NP_001048441.1|//1.00E-154//Os02g0805500 [Oryza sativa Japonica Group] >gi|113537972|dbj|BAF10355.1|Os02g0805500 [Oryza sativa Japonica Group]	Unigene2423_All//2.00E-126//AT5G54390| AHL (ARABIDOPSIS HAL2-LIKE); 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase	Unigene2423_All//0.00E+00//TC160940		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism	GO:0008252//GO:0016312//GO:0044237	nr +
Unigene24230_All	3103	3.81	3.66	3.33	4.86	4.11	4.37	7.06	3.37	3.79	-5.91E-02	7.31E-01		-1.95E-01	3.00E-01		-2.45E-01	1.01E-01		-1.56E-01	3.58E-01		-1.07E+00	3.81E-22	Down	-8.98E-01	2.40E-17		Unigene24230_All//gi|297826459|ref|XP_002881112.1|//0.00E+00//high-level expression of sugar-inducible gene 2 [Arabidopsis lyrata subsp. lyrata] >gi|297326951|gb|EFH57371.1| high-level expression of sugar-inducible gene 2 [Arabidopsis lyrata subsp. lyrata]	Unigene24230_All//0.00E+00//AT2G30470| HS12 (HIGH-LEVEL EXPRESSION OF SUGAR-INDUCIBLE GENE 2); transcription factor/ transcription repressor	Unigene24230_All//0.00E+00//TC171130	ABI3VP1	ko00310|Lysine degradation	GO:0005488//GO:0006350//GO:0009725//GO:0009815//GO:0010431//GO:0010468//GO:0030528//GO:0034285//GO:0043231	nr -
Unigene24231_All	2069	15.63	12.15	13.59	11.41	10.00	14.73	41.93	19.78	15.10	-3.64E-01	1.26E-04		-2.02E-01	5.28E-02		-1.90E-01	1.09E-01		3.69E-01	1.28E-04		-1.08E+00	1.64E-87	Down	-1.47E+00	5.25E-145	Down	Unigene24231_All//gi|224111924|ref|XP_002316024.1|//0.00E+00//precursor of dehydrogenase dihydrolipoamide dehydrogenase 4 [Populus trichocarpa] >gi|222865064|gb|EEF02195.1|precursor of dehydrogenase dihydrolipoamide dehydrogenase 4 [Populus trichocarpa]	Unigene24231_All//0.00E+00//AT4G16155| dihydrolipoyl dehydrogenase	Unigene24231_All//0.00E+00//TC154661		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00020|Citrate cycle (TCA cycle)//ko00260|Glycine, serine and threonine metabolism	GO:0006085//GO:0006091//GO:0009526//GO:0009532//GO:0016668//GO:0019725//GO:0030554//GO:0031981	nr +
Unigene24232_All	1892	34.43	119.74	71.18	31.07	36.49	41.80	5.77	14.27	17.20	1.80E+00	0.00E+00	Up	1.05E+00	9.82E-102	Up	2.32E-01	1.09E-04		4.28E-01	3.58E-14		1.31E+00	4.73E-37	Up	1.58E+00	5.65E-60	Up	Unigene24232_All//gi|162568918|gb|ABV19383.1|//0.00E+00//pheophorbide A oxygenase 2 [Nicotiana tabacum]	Unigene24232_All//6.00E-164//AT3G44880| ACD1 (ACCELERATED CELL DEATH 1); iron-sulfur cluster binding / pheophorbide a oxygenase	Unigene24232_All//0.00E+00//TC152282		ko00860|Porphyrin and chlorophyll metabolism	GO:0008152//GO:0009536//GO:0016703//GO:0043169//GO:0051536	nr +
Unigene24233_All	2120	6.22	5.35	7.49	7.26	7.93	5.97	6.96	4.36	3.48	-2.16E-01	1.94E-01		2.67E-01	7.98E-02		1.27E-01	4.36E-01		-2.84E-01	5.73E-02		-6.76E-01	2.03E-07		-1.00E+00	3.40E-14	Down	Unigene24233_All//gi|124359654|gb|ABN06026.1|//0.00E+00//Peptidase, trypsin-like serine and cysteine proteases [Medicago truncatula]	Unigene24233_All//0.00E+00//AT2G35155| catalytic	Unigene24233_All//0.00E+00//TC150671			GO:0016787	nr +
Unigene24235_All	2214	39.49	32.02	24.89	80.80	54.55	88.16	86.47	46.65	38.85	-3.03E-01	4.54E-08		-6.66E-01	1.12E-30		-5.67E-01	4.00E-59		1.26E-01	6.74E-04		-8.90E-01	7.64E-139		-1.15E+00	1.41E-218	Down	Unigene24235_All//gi|399940|sp|Q01899.1|HSP7M_PHAVU//0.00E+00//RecName: Full=Heat shock 70 kDa protein, mitochondrial; Flags: Precursor >gi|22636|emb|CAA47345.1| 70 kDa heat shock protein [Phaseolus vulgaris]	Unigene24235_All//0.00E+00//AT5G09590| MTHSC70-2 (MITOCHONDRIAL HSP70 2); ATP binding	Unigene24235_All//0.00E+00//TC143272		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03018|RNA degradation	GO:0005515//GO:0006970//GO:0009536//GO:0010038//GO:0016020//GO:0016128//GO:0030312//GO:0032559//GO:0044267//GO:0051707	nr +
Unigene24236_All	649	2.34	3.67	6.56	8.98	7.96	6.89	10.49	8.31	6.14	6.50E-01	1.18E-01		1.49E+00	3.94E-06	Up	-1.74E-01	5.51E-01		-3.82E-01	1.37E-01		-3.36E-01	1.11E-01		-7.73E-01	7.52E-05		Unigene24236_All//gi|119214865|gb|ABL61264.1|//1.00E-44//SGT1-2 [Solanum lycopersicum]	Unigene24236_All//2.00E-35//AT4G11260| SGT1B; protein binding	Unigene24236_All//0.00E+00//TC150523		ko04626|Plant-pathogen interaction	GO:0006952//GO:0009755//GO:0019941//GO:0031461	nr -
Unigene24237_All	1575	14.75	8.91	8.69	25.81	24.51	24.26	20.32	16.85	9.74	-7.27E-01	2.07E-10		-7.63E-01	9.24E-11		-7.45E-02	4.71E-01		-8.93E-02	3.93E-01		-2.70E-01	1.83E-03		-1.06E+00	1.27E-32	Down	Unigene24237_All//gi|119214865|gb|ABL61264.1|//1.00E-144//SGT1-2 [Solanum lycopersicum]	Unigene24237_All//1.00E-114//AT4G11260| SGT1B; protein binding	Unigene24237_All//0.00E+00//TC150523		ko04626|Plant-pathogen interaction		nr +
Unigene24238_All	1708	15.26	10.59	9.85	20.24	20.34	18.17	24.41	6.61	9.61	-5.27E-01	7.13E-07		-6.31E-01	9.11E-09		7.20E-03	9.49E-01		-1.56E-01	1.25E-01		-1.89E+00	2.05E-96	Down	-1.34E+00	4.26E-61	Down	Unigene24238_All//gi|115393868|gb|AB196983.1|//1.00E-72//phytocyanin-like arabinogalactan-protein [Gossypium hirsutum] >gi|115393870|gb|AB196984.1|phytocyanin-like arabinogalactan-protein [Gossypium hirsutum]	Unigene24238_All//2.00E-51//AT5G25080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Sas10/Utp3/CID (InterPro:IPR007146), Exosome-associated factor Rrp47/DNA strand repair CID (InterPro:IPR011082); Has 137 Blast hits to 137 proteins in 56 species: Archae - 0; Bacteria - 0; Metazoa - 76; Fungi - 42; Plants - 16; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink).	Unigene24238_All//0.00E+00//gi|164317288|gb|ES808080.1|ES808080			GO:0046914	nr -
Unigene24239_All	1463	27.04	29.20	26.02	38.44	33.80	41.55	31.33	30.34	14.81	1.11E-01	2.24E-01		-5.50E-02	6.18E-01		-1.86E-01	7.80E-03		1.12E-01	1.42E-01		-4.62E-02	6.30E-01		-1.08E+00	1.11E-47	Down	Unigene24239_All//gi|55419646|gb|AY519536.1|//1.00E-120//bHLH transcription factor [Gossypium hirsutum]	Unigene24239_All//7.00E-71//AT5G62610| basic helix-loop-helix (bHLH) family protein	Unigene24239_All//0.00E+00//TC136930	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0001071//GO:0010468//GO:0043231	nr +
Unigene2424_All	2184	6.66	4.29	4.73	4.08	6.78	6.10	5.69	2.56	3.67	-6.34E-01	1.52E-05		-4.94E-01	1.22E-03		7.32E-01	7.69E-08		5.79E-01	1.27E-04		-1.15E+00	1.82E-14	Down	-6.34E-01	5.25E-06		Unigene2424_All//gi|16209658|gb|AAL14389.1|//1.00E-179//At1g61350/TIF9_16 [Arabidopsis thaliana]	Unigene2424_All//4.00E-180//AT1G61350| armadillo/beta-catenin repeat family protein	Unigene2424_All//0.00E+00//TC145657			GO:0003824	nr +
Unigene24241_All	2283	2.96	6.79	3.73	15.62	11.30	11.04	33.87	19.94	24.88	1.20E+00	1.46E-15	Up	3.36E-01	1.19E-01		-4.68E-01	1.16E-08		-5.01E-01	7.64E-09		-7.65E-01	9.82E-44		-4.45E-01	1.46E-17		Unigene24241_All//gi|83284015|gb|ABC01915.1|//0.00E+00//vacuolar sorting receptor protein PV72-like protein [Solanum tuberosum]	Unigene24241_All//0.00E+00//AT3G52850| VSR1 (VACUOLAR SORTING RECEPTOR HOMOLOG 1); amino-terminal vacuolar sorting propeptide binding	Unigene24241_All//0.00E+00//TC137270			GO:0004871//GO:0006605//GO:0006892//GO:0010209//GO:0016020//GO:0031410//GO:0043234//GO:0044431//GO:0046872	nr -

Unigene24243_All	2531	0.81	0.36	0.21	3.03	4.39	3.71	4.78	3.62	6.34	-1.16E+00	1.12E-02		-1.94E+00	1.99E-04	Down	5.36E-01	9.78E-04		2.92E-01	1.48E-01		-4.02E-01	6.21E-03		4.09E-01	7.54E-04		Unigene24243_All//gi|297828377|ref|XP_002882071.1|//0.00E+00//phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327910|gb|EFH58330.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24243_All//0.00E+00//AT2G46500| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	Unigene24243_All//0.00E+00//TC170230			GO:0016772//GO:0042579	nr -
Unigene24244_All	2645	6.59	15.65	5.84	31.11	40.07	58.55	35.93	73.11	48.63	1.25E+00	7.00E-43	Up	-1.74E-01	2.46E-01		3.65E-01	1.61E-15		9.12E-01	8.81E-103		1.02E+00	6.07E-177	Up	4.37E-01	1.41E-27		Unigene24244_All//gi|15228136|ref|NP_178516.1|//0.00E+00//long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8) [Arabidopsis thaliana] >gi|30678112|ref|NP_849934.1| long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8) [Arabidopsis thaliana] >gi|20805877|gb|AAM28875.1|AF503758_1 long chain acyl-CoA synthetase 8 [Arabidopsis thaliana] >gi|25090427|gb|AAN72299.1| At2g04350/T23O15.3 [Arabidopsis thaliana]	Unigene24244_All//0.00E+00//AT2G04350| long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8)	Unigene24244_All//0.00E+00//TC156201		ko04146|Peroxisome//ko00071|Fatty acid metabolism	GO:0006631//GO:0009526//GO:0015645	nr +
Unigene24246_All	457	0.34	1.33	0.82	1.09	1.58	0.79	3.79	3.38	0.96	1.95E+00	6.04E-02		1.25E+00	3.66E-01		5.38E-01	5.64E-01		-4.63E-01	6.59E-01		-1.65E-01	7.27E-01		-1.98E+00	3.36E-05	Down	Unigene24246_All//gi|297826389|ref|XP_002881077.1|//6.00E-18//cyclophilin [Arabidopsis lyrata subsp. lyrata] >gi|297326916|gb|EFH57336.1| cyclophilin [Arabidopsis lyrata subsp. lyrata]	Unigene24246_All//2.00E-18//AT3G55920| peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative	Unigene24246_All//2.00E-154//TC146213			GO:0005626//GO:0005770//GO:0009536//GO:0016020//GO:0016859//GO:0031410//GO:0044267//GO:0044431//GO:0048513	nr +
Unigene24248_All	636	0.99	3.27	2.34	1.72	3.25	2.70	3.52	3.02	2.32	1.73E+00	3.59E-04	Up	1.25E+00	3.19E-02		9.15E-01	4.13E-02		6.47E-01	2.21E-01		-2.21E-01	6.18E-01		-6.04E-01	1.01E-01		Unigene24248_All//gi|165971819|emb|CAP69837.1|//3.00E-36//cyclophilin [Ricinus communis]	Unigene24248_All//3.00E-27//AT2G29960| CYP5 (CYCLOPHILIN 5); peptidyl-prolyl cis-trans isomerase	Unigene24248_All//1.00E-171//TC165293			GO:0016859//GO:0044267	nr +
Unigene24252_All	1884	5.17	56.08	4.95	4.71	10.64	89.25	14.50	30.99	38.44	3.44E+00	0.00E+00	Up	-6.25E-02	7.55E-01		1.18E+00	2.06E-22	Up	4.25E+00	0.00E+00	Up	1.10E+00	4.27E-60	Up	1.41E+00	5.61E-112	Up	Unigene24252_All//gi|224084123|ref|XP_002307218.1|//0.00E+00//aromatic and neutral amino acid transporter [Populus trichocarpa] >gi|222856667|gb|EEE94214.1| aromatic and neutral amino acid transporter [Populus trichocarpa]	Unigene24252_All//5.00E-154//AT4G38250| amino acid transporter family protein	Unigene24252_All//0.00E+00//TC140146			GO:0031224	nr +
Unigene24255_All	1358	4.97	5.11	5.73	31.55	29.26	14.93	7.04	5.02	3.93	4.05E-02	8.66E-01		2.04E-01	4.02E-01		-1.08E-01	2.42E-01		-1.08E+00	2.93E-38	Down	-4.88E-01	3.30E-03		-8.40E-01	2.65E-07		Unigene24255_All//gi|18412073|ref|NP_565187.1|//1.00E-122//brassinosteroid signalling positive regulator-related [Arabidopsis thaliana] >gi|61211694|sp|Q9ZV88.1|BEH4_ARATH RecName: Full=BES1/BZR1 homolog protein 4 >gi|3834322|gb|AAC83038.1| EST gb|R30300 comes from this gene [Arabidopsis thaliana] >gi|15218802|gb|AAK91446.1| At1g78700/F9K20_26 [Arabidopsis thaliana] >gi|19699252|gb|AAL90992.1| At1g78700/F9K20_26 [Arabidopsis thaliana]	Unigene24255_All//2.00E-85//AT1G78700| brassinosteroid signalling positive regulator-related	Unigene24255_All//0.00E+00//TC153559	BES1			nr +
Unigene24259_All	2195	29.89	30.10	32.44	28.82	31.94	27.22	18.20	8.59	7.97	1.01E-02	9.03E-01		1.18E-01	9.50E-02		1.48E-01	2.08E-02		-8.24E-02	3.05E-01		-1.08E+00	1.07E-40	Down	-1.19E+00	1.16E-48	Down	Unigene24259_All//gi|15226866|ref|NP_178316.1|//1.00E-128//AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding >gi|41059987|emb|CAF18564.1| ID1-like zinc finger protein 2 [Arabidopsis thaliana]	Unigene24259_All//5.00E-109//AT2G02070| AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding	Unigene24259_All//0.00E+00//TC170428	C2H2			nr +
Unigene2426_All	1671	45.59	14.16	26.99	43.43	36.58	25.30	17.64	7.90	6.44	-1.69E+00	2.88E-123	Down	-7.56E-01	2.28E-33		-2.48E-01	1.55E-05		-7.80E-01	1.64E-37		-1.16E+00	1.55E-33	Down	-1.45E+00	8.17E-19	Down	Unigene2426_All//gi|10177211|dbj|BAB10286.1|//0.00E+00//protein kinase [Arabidopsis thaliana]	Unigene2426_All//5.00E-180//AT5G50000| protein kinase, putative	Unigene2426_All//0.00E+00//TC167891			GO:0004713//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene24260_All	1889	5.32	6.09	5.10	11.58	7.89	9.25	7.74	12.13	18.47	1.95E-01	2.81E-01		-5.97E-02	7.64E-01		-5.53E-01	2.62E-07		-3.23E-01	6.20E-03		6.47E-01	2.72E-10		1.25E+00	9.82E-46	Up	Unigene24260_All//gi|297802336|ref|XP_002869052.1|//3.00E-77//La domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297314888|gb|EFH45311.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene24260_All//2.00E-50//AT4G35890| La domain-containing protein	Unigene24260_All//0.00E+00//TC175238		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene24262_All	1455	11.87	29.84	14.24	19.14	17.35	22.78	10.14	10.37	7.94	1.33E+00	1.53E-49	Up	2.63E-01	4.46E-02		-1.42E-01	2.17E-01		2.52E-01	8.58E-03		3.21E-02	8.36E-01		-3.53E-01	5.77E-03		Unigene24262_All//gi|297799940|ref|XP_002867854.1|//1.00E-132//At4g21350 [Arabidopsis lyrata subsp. lyrata] >gi|297313690|gb|EFH44113.1| At4g21350 [Arabidopsis lyrata subsp. lyrata]	Unigene24262_All//3.00E-120//AT4G21350| PUB8 (PLANT U-BOX 8); binding / protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene24262_All//0.00E+00//TC173957		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene24263_All	1835	7.70	19.55	12.62	15.31	13.15	16.54	19.38	16.35	4.69	1.34E+00	1.07E-41	Up	7.14E-01	1.26E-09		-2.19E-01	3.46E-02		1.11E-01	3.45E-01		-2.45E-01	2.97E-03		-2.05E+00	1.46E-94	Down	Unigene24263_All//gi|297817588|ref|XP_002876677.1|//3.00E-50//Os01g0254000 [Arabidopsis lyrata subsp. lyrata] >gi|297322515|gb|EFH52936.1| Os01g0254000 [Arabidopsis lyrata subsp. lyrata]	Unigene24263_All//7.00E-45//AT4G02080| ATSAR2 (ARABIDOPSIS THALIANA SECRETION-ASSOCIATED RAS SUPER FAMILY 2); GTP binding	Unigene24263_All//0.00E+00//gi|21102492|gb|BQ414805.1|BQ414805		ko04141|Protein processing in endoplasmic reticulum	GO:0015031//GO:0016020//GO:0032561//GO:0043231	nr +
Unigene24264_All	1416	28.82	35.68	34.33	22.20	32.44	21.18	14.09	6.14	11.96	3.08E-01	3.74E-05		2.53E-01	1.64E-03		5.47E-01	3.60E-14		-6.79E-02	5.92E-01		-1.20E+00	3.15E-24	Down	-2.37E-01	3.30E-02		Unigene24264_All//gi|9802596|gb|AAF99798.1|AC012463_15//3.00E-91//T22E.19 [Arabidopsis thaliana]	Unigene24264_All//2.00E-95//AT1G47740| unknown protein	Unigene24264_All//0.00E+00//TC135360			GO:0043231	nr -
Unigene24266_All	1894	2.38	2.49	1.66	3.13	2.64	3.22	6.25	4.02	2.80	6.66E-02	8.15E-01		-5.18E-01	8.60E-02		-2.48E-01	3.45E-01		4.06E-02	8.98E-01		-6.38E-01	1.32E-05		-1.16E+00	1.93E-14	Down	Unigene24266_All//gi|224055719|ref|XP_002286619.1|//0.00E+00//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222845877|gb|EEE83424.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene24266_All//0.00E+00//AT5G14170| CHC1	Unigene24266_All//0.00E+00//ES851503			GO:0048513	nr +
Unigene24269_All	3221	1.51	1.05	1.03	20.18	15.62	10.14	6.01	2.95	2.21	-5.19E-01	5.83E-02		-5.60E-01	5.04E-02		-3.70E-01	4.32E-10		-9.93E-01	1.67E-50		-1.03E+00	1.40E-18	Down	-1.44E+00	5.85E-32	Down	Unigene24269_All//gi|75333913|sp|Q9FI15.1|Y5148_ARATH/0.00E+00//RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At5g61480; Flags: Precursor >gi|10177178|dbj|BAB10447.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|224589737|gb|ACN59400.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene24269_All//0.00E+00//AT5G61480| leucine-rich repeat transmembrane protein kinase, putative	Unigene24269_All//0.00E+00//ES843870			GO:0004672//GO:0004871//GO:0006464//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene2427_All	1749	12.80	9.44	9.04	12.87	14.16	13.66	9.45	4.30	5.63	-4.39E-01	1.46E-04		-5.02E-01	2.65E-05		1.37E-01	2.80E-01		8.55E-02	5.47E-01		-1.14E+00	1.31E-18	Down	-7.49E-01	5.54E-10		Unigene2427_All//gi|297828171|ref|XP_002881968.1|//1.00E-127//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297327807|gb|EFH58227.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene2427_All//2.00E-117//AT2G44580| protein binding / zinc ion binding	Unigene2427_All//0.00E+00//TC143495				nr +
Unigene24271_All	2347	5.95	3.78	3.38	11.55	9.57	10.08	7.75	3.54	4.31	-6.56E-01	1.23E-05		-8.16E-01	1.76E-07		-2.71E-01	7.71E-03		-1.96E-01	8.21E-02		-1.13E+00	3.55E-20	Down	-8.45E-01	3.22E-13		Unigene24271_All//gi|75217862|sp|Q56X72.1|RTNL5_ARATH//2.00E-58//RecName: Full=Reticulon-like protein B21; Short=AtRTNLB21	Unigene24271_All//8.00E-44//AT5G58000| LOCATED IN: endoplasmic reticulum, chloroplast; CONTAINS InterPro DOMAIN/s: Reticulon (InterPro:IPR003388); BEST Arabidopsis thaliana protein match is: reticulon family protein (TAIR:AT4G28430.1); Has 1047 Blast hits to 1034 proteins in 125 species: Archae - 0; Bacteria - 2; Metazoa - 715; Fungi - 46; Plants - 58; Viruses - 4; Other Eukaryotes - 222 (source: NCBI BLink).	Unigene24271_All//0.00E+00//gi|21089952|gb|BQ402265.1|BQ402265			GO:0031410//GO:0043231	nr -
Unigene24274_All	1299	4.79	2.89	2.30	38.65	29.93	40.96	21.58	62.81	33.43	-7.32E-01	1.96E-03		-1.06E+00	2.16E-05	Down	-3.69E-01	6.73E-08		8.34E-02	3.47E-01		1.54E+00	2.46E-141	Up	6.31E-01	1.72E-18		Unigene24274_All//gi|21700767|gb|AG38145.1|//2.00E-55//phosphoglycerate mutase-like protein [Glycine max]	Unigene24274_All//2.00E-51//AT2G17280| phosphoglycerate/bisphosphoglycerate mutase family protein	Unigene24274_All//0.00E+00//gi|109827459|gb|DW226142.1|DW226142				nr +
Unigene24276_All	2038	0.33	0.05	0.10	3.62	2.45	2.28	1.12	2.63	2.46	-2.75E+00	1.06E-02		-1.68E+00	8.70E-02		-5.62E-01	5.62E-03		-6.64E-01	1.66E-03		1.23E+00	2.61E-07	Up	1.14E+00	2.15E-06	Up	Unigene24276_All//gi|21700767|gb|AG38145.1|//3.00E-55//phosphoglycerate mutase-like protein [Glycine max]	Unigene24276_All//3.00E-51//AT2G17280| phosphoglycerate/bisphosphoglycerate mutase family protein	Unigene24276_All//0.00E+00//gi|109827459|gb|DW226142.1|DW226142				nr +
Unigene24277_All	1381	18.41	59.51	21.40	19.19	32.39	30.22	18.16	20.19	24.84	1.69E+00	8.56E-133	Up	2.17E-01	4.61E-02		7.55E-01	4.74E-24		6.55E-01	4.43E-16		1.53E-01	1.34E-01		4.52E-01	1.71E-08		Unigene24277_All//gi|110931692|gb|AB802845.1|//1.00E-131//MYB transcription factor MYB93 [Glycine max]	Unigene24277_All//8.00E-85//AT5G47390| myb family transcription factor	Unigene24277_All//0.00E+00//TC143218	MYB-related		GO:0005488//GO:0043231	nr -
Unigene2428_All	2100	9.07	20.32	9.15	10.22	10.36	12.19	8.42	9.59	6.89	1.16E+00	1.36E-39	Up	1.35E-02	9.40E-01		1.96E-02	9.00E-01		2.54E-01	2.28E-02		1.89E-01	1.14E-01		-2.89E-01	1.35E-02		Unigene2428_All//gi|297727099|ref|NP_001175913.1|//1.00E-50//Os09g0491676 [Oryza sativa Japonica Group] >gi|255679013|dbj|BAH94641.1| Os09g0491676 [Oryza sativa Japonica Group]	Unigene2428_All//1.00E-97//AT3G57990| unknown protein	Unigene2428_All//0.00E+00//gi|78327105|gb|DT547379.1|DT547379				nr -
Unigene24280_All	555	20.27	15.06	9.79	29.26	25.81	31.74	93.63	41.19	41.06	-4.28E-01	1.22E-02		-1.05E+00	5.00E-09	Down	-1.81E-01	2.32E-01		1.17E-01	4.71E-01		-1.18E+00	1.17E-60	Down	-1.19E+00	8.57E-63	Down	Unigene24280_All//gi|283049400|gb|AD607168.1|//4.00E-70//DEAD-box RNA helicase-like protein [Prunus persica] >gi|283049402|gb|AD607169.1| DEAD-box RNA helicase-like protein [Prunus persica]	Unigene24280_All//8.00E-66//AT3G13920| EIF4A1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 4A1); ATP-dependent helicase/ translation initiation factor	Unigene24280_All//0.00E+00//gi|13245597|gb|BE053659.2|BE053659			GO:0008135//GO:0010467//GO:0032559//GO:0042623	nr -

Unigene24281_All	553	18.17	11.45	11.75	22.43	20.80	28.26	49.31	24.49	19.67	-6.65E-01	2.19E-04			-6.29E-01	7.85E-04			-1.09E-01	5.73E-01			3.33E-01	2.14E-02			-1.01E+00	4.62E-25	Down	-1.33E+00	1.94E-39	Down	Unigene24281_All//gi|283049400|gb|ADB07168.1|//7.00E-56//DEAD-box RNA helicase-like protein [Prunus persica] >gi|283049402|gb|ADB07169.1| DEAD-box RNA helicase-like protein [Prunus persica]	Unigene24281_All//4.00E-52//AT3G13920| EIF4A1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 4A1); ATP-dependent helicase/ translation initiation factor	Unigene24281_All//0.00E+00//gi|54120818|gb|CO496327.1|CO496327			GO:0008135//GO:0010467//GO:0032559//GO:0042623	nr -
Unigene24284_All	677	6.18	5.99	4.48	14.27	20.91	16.41	9.37	3.89	1.65	-4.63E-02	8.83E-01			-4.64E-01	1.43E-01			5.50E-01	8.97E-05			2.01E-01	3.07E-01			-1.27E+00	6.23E-09	Down	-2.51E+00	2.94E-22	Down	Unigene24284_All//gi|30684004|ref|NP_193466.2|//2.00E-24//phosphoinositide binding [Arabidopsis thaliana] >gi|54606846|gb|AAV34771.1| At4g17350 [Arabidopsis thaliana] >gi|98860971|gb|ABF58969.1| At4g17350 [Arabidopsis thaliana]	Unigene24284_All//1.00E-25//AT4G17350| phosphoinositide binding	Unigene24284_All//3.00E-154//TC173071			GO:0005543//GO:0023060	nr -
Unigene24285_All	1397	24.23	12.98	19.13	48.64	77.20	57.22	17.37	4.10	5.16	-9.00E-01	4.94E-21			-3.41E-01	4.04E-04			6.67E-01	2.08E-46			2.35E-01	4.61E-05			-2.08E+00	2.74E-64	Down	-1.75E+00	1.36E-52	Down	Unigene24285_All//gi|30684004|ref|NP_193466.2|//1.00E-126//phosphoinositide binding [Arabidopsis thaliana] >gi|54606846|gb|AAV34771.1| At4g17350 [Arabidopsis thaliana] >gi|98860971|gb|ABF58969.1| At4g17350 [Arabidopsis thaliana]	Unigene24285_All//1.00E-95//AT4G17350| phosphoinositide binding	Unigene24285_All//0.00E+00//TC151606			GO:0005543//GO:0023060	nr -
Unigene24288_All	3053	10.76	8.15	11.25	11.45	12.05	9.82	6.26	2.59	3.18	-4.01E-01	1.84E-05			6.39E-02	5.82E-01			7.27E-02	5.27E-01			-2.22E-01	1.86E-02			-1.27E+00	1.68E-25	Down	-9.75E-01	2.23E-17		Unigene24288_All//gi|297806463|ref|XP_002871115.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297316952|gb|EFH47374.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene24288_All//0.00E+00//AT5G04810| pentatricopeptide (PPR) repeat-containing protein	Unigene24288_All//0.00E+00//gi|109888497|gb|DW517466.1|DW517466			GO:0005488//GO:0009536	nr -
Unigene2429_All	1596	1.48	2.83	2.14	1.90	1.27	1.70	3.02	1.73	1.10	9.38E-01	1.09E-03			5.34E-01	1.35E-01			-5.81E-01	9.63E-02			-1.65E-01	6.86E-01			-8.05E-01	9.66E-04		-1.46E+00	9.43E-09	Down	Unigene2429_All//gi|297727099|ref|NP_001175913.1|//9.00E-47//Os09g0491676 [Oryza sativa Japonica Group] >gi|255679013|dbj|BAH94641.1| Os09g0491676 [Oryza sativa Japonica Group]	Unigene2429_All//3.00E-94//AT3G57990| unknown protein	Unigene2429_All//0.00E+00//gi|78327105|gb|DT547379.1|DT547379				nr -
Unigene24292_All	1603	11.65	4.71	11.79	13.02	12.18	11.21	1.77	55.69	3.21	-1.31E+00	3.07E-21	Down	1.73E-02	9.15E-01			-9.63E-02	5.22E-01			-2.16E-01	9.69E-02			4.98E+00	0.00E+00	Up	8.59E-01	1.92E-04		Unigene24292_All//gi|48431269|gb|AAT44124.1|//2.00E-79//F3H-like protein [Saussurea medusa]	Unigene24292_All//3.00E-56//AT4G10500| oxidoreductase, 20G-Fe(II) oxygenase family protein	Unigene24292_All//0.00E+00//gi|11209086|gb|BF278100.1|BF278100		ko00941|Flavonoid biosynthesis	GO:0016491	nr +
Unigene24293_All	2757	4.84	2.08	3.28	3.67	3.75	2.95	0.55	15.77	0.69	-1.22E+00	6.63E-14	Down	-5.60E-01	4.59E-04			3.08E-02	8.92E-01			-3.15E-01	9.72E-02			4.84E+00	1.06E-252	Up	3.29E-01	4.37E-01		Unigene24293_All//gi|48431269|gb|AAT44124.1|//1.00E-82//F3H-like protein [Saussurea medusa]	Unigene24293_All//2.00E-60//AT5G24530| DMR6 (DOWNY MILDEW RESISTANT 6); oxidoreductase/ oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene24293_All//0.00E+00//ES819751		ko00941|Flavonoid biosynthesis/ko00904|Diterpenoid biosynthesis		nr -
Unigene24295_All	1549	12.80	59.01	24.51	20.87	23.52	41.46	27.54	23.53	23.56	2.20E+00	6.03E-210	Up	9.37E-01	3.59E-24			1.72E-01	6.58E-02			9.90E-01	4.39E-49			-2.27E-01	2.38E-03		-2.25E-01	1.91E-03		Unigene24295_All//gi|297834964|ref|XP_002885364.1|//1.00E-126//extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata] >gi|297331204|gb|EFH61623.1| extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata]	Unigene24295_All//2.00E-110//AT4G22270| unknown protein	Unigene24295_All//0.00E+00//gi|78330714|gb|DT550988.1|DT550988				nr -
Unigene24296_All	1713	3.05	29.70	9.20	6.40	7.72	13.50	11.67	14.20	10.44	3.28E+00	1.65E-180	Up	1.59E+00	4.46E-23	Up	2.71E-01	9.32E-02			1.08E+00	1.39E-20	Up	2.83E-01	5.20E-03		-1.61E-01	1.68E-01				Unigene24296_All//gi|87240785|gb|AB032643.1|//1.00E-144//AT3g20300/MQC12_5 [Medicago truncatula]	Unigene24296_All//4.00E-133//AT4G22270| unknown protein	Unigene24296_All//0.00E+00//TC154903				nr +
Unigene24297_All	467	1.90	1.30	0.91	2.24	1.70	1.06	1.63	2.95	5.29	-5.49E-01	4.42E-01			-1.06E+00	1.76E-01			-4.01E-01	5.54E-01			-1.07E+00	1.19E-01			8.58E-01	9.44E-02		1.70E+00	8.13E-06	Up	Unigene24297_All//gi|115464107|ref|NP_001055653.1|//6.00E-14//Os05g0437500 [Oryza sativa Japonica Group] >gi|113579204|dbj|BAF17567.1| Os05g0437500 [Oryza sativa Japonica Group]	Unigene24297_All//8.00E-15//AT4G30260| integral membrane Yip1 family protein	Unigene24297_All//9.00E-123//CO101309			GO:0016020	nr -
Unigene24299_All	900	4.94	3.10	4.56	8.69	9.68	8.58	2.35	3.39	6.42	-6.74E-01	1.85E-02			-1.17E-01	7.01E-01			1.56E-01	5.18E-01			-1.82E-02	9.52E-01			5.29E-01	1.04E-01		1.45E+00	3.98E-10	Up	Unigene24299_All//gi|115464107|ref|NP_001055653.1|//4.00E-33//Os05g0437500 [Oryza sativa Japonica Group] >gi|113579204|dbj|BAF17567.1| Os05g0437500 [Oryza sativa Japonica Group]	Unigene24299_All//4.00E-30//AT4G30260| integral membrane Yip1 family protein	Unigene24299_All//6.00E-101//gi|78338551|gb|DT558825.1|DT558825			GO:0016020	nr -
Unigene24302_All	1464	2.75	0.97	1.45	12.76	16.23	4.20	32.75	2.14	3.02	-1.51E+00	3.10E-06	Down	-9.20E-01	3.88E-03			3.47E-01	1.26E-03			-1.60E+00	6.30E-31	Down	-3.94E+00	1.92E-244	Down	-3.44E+00	6.71E-226	Down	Unigene24302_All//gi|18404191|ref|NP_566747.1|//1.00E-41//copper-binding family protein [Arabidopsis thaliana]	Unigene24302_All//6.00E-43//AT3G24450| copper-binding family protein	Unigene24302_All//8.00E-129//gi|189098594|gb|FG551746.1|FG551746			GO:0000041//GO:0031410//GO:0043169//GO:0043231	nr -
Unigene24304_All	2304	2.48	1.32	1.62	10.33	5.98	4.12	6.84	4.12	3.25	-9.08E-01	2.85E-04			-6.14E-01	1.84E-02			-7.90E-01	1.74E-14			-1.33E+00	1.07E-29	Down	-7.33E-01	5.86E-09		-1.07E+00	7.64E-17	Down	Unigene24304_All//gi|115479373|ref|NP_001063280.1|//1.00E-139//Os09g0440200 [Oryza sativa Japonica Group] >gi|113631513|dbj|BAF25194.1| Os09g0440200 [Oryza sativa Japonica Group]	Unigene24304_All//7.00E-92//AT2G26270| unknown protein	Unigene24304_All//8.00E-130//TC166953			GO:0044464	nr +
Unigene24314_All	587	1.43	3.11	2.18	1.53	5.98	5.69	1.08	2.42	2.51	1.12E+00	2.19E-02			6.10E-01	3.33E-01			1.97E+00	1.95E-08	Up	1.90E+00	2.92E-07	Up	1.16E+00	2.19E-02		1.22E+00	1.17E-02		Unigene24314_All//gi|147854975|emb|CAN80266.1|//8.00E-11//hypothetical protein [Vitis vinifera]		Unigene24314_All//2.00E-62//gi|78323949|gb|DT544223.1|DT544223				nr -
Unigene24315_All	880	2.97	14.51	6.54	4.47	6.30	8.93	9.22	14.34	13.26	2.29E+00	3.81E-31	Up	1.14E+00	1.51E-05	Up	4.95E-01	5.05E-02			9.98E-01	1.34E-06			6.37E-01	6.76E-06		5.24E-01	2.80E-04		Unigene24315_All//gi|147854975|emb|CAN80266.1|//3.00E-14//hypothetical protein [Vitis vinifera]		Unigene24315_All//0.00E+00//ES809071				nr -
Unigene24317_All	2531	0.23	0.30	0.38	0.43	0.54	0.71	1.64	0.79	0.50	4.01E-01	6.01E-01			7.36E-01	3.23E-01			3.30E-01	6.09E-01			7.21E-01	1.51E-01			-1.05E+00	1.04E-04	Down	-1.70E+00	2.51E-09	Down	Unigene24317_All//gi|20473411|gb|AAM22488.1|//2.00E-62//3615.7 [Oryza sativa Japonica Group]	Unigene24317_All//8.00E-47//AT4G26190| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: NLI interacting factor (InterPro:IPR004274); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G36550.1); Has 24148 Blast hits to 14674 proteins in 713 species: Archae - 56; Bacteria - 1518; Metazoa - 9576; Fungi - 1916; Plants - 955; Viruses - 87; Other Eukaryotes - 10040 (source: NCBI BLink).	Unigene24317_All//0.00E+00//gi|109866424|gb|DW495400.1|DW495400				nr +
Unigene24319_All	2276	10.48	13.56	10.72	41.28	41.09	53.42	5.24	8.43	11.78	3.71E-01	1.38E-04			3.17E-02	8.02E-01			-6.50E-03	9.30E-01			3.72E-01	1.13E-16			6.86E-01	1.26E-09		1.17E+00	1.01E-31	Up	Unigene24319_All//gi|9858780|gb|AAG01127.1|AF273333_12//1.00E-127//BAC19.12 [Solanum lycopersicum]	Unigene24319_All//1.00E-106//AT3G50700| AtIDD2 (Arabidopsis thaliana Indeterminate(ID)-Domain 2); nucleic acid binding / transcription factor/ zinc ion binding	Unigene24319_All//0.00E+00//TC179348	C2H2			nr -
Unigene24320_All	1055	20.18	13.02	8.78	26.54	21.93	32.49	8.26	4.24	9.82	-6.33E-01	1.04E-07			-1.20E+00	2.43E-20	Down	-2.75E-01	5.78E-03			2.92E-01	1.49E-03			-9.62E-01	5.92E-08		2.50E-01	1.23E-01		Unigene24320_All//gi|15218593|ref|NP_177419.1|//2.00E-79//ATTIM23-2; P-P-bond-hydrolysis-driven protein transmembrane transporter/ protein transporter [Arabidopsis thaliana] >gi|12323775|gb|AAG51855.1|AC01092 6_18 inner mitochondrial membrane protein; 26940-26374 [Arabidopsis thaliana] >gi|603056|gb|AAA57314.1| inner mitochondrial membrane protein [Arabidopsis thaliana] >gi|14596209|gb|AAK68832.1| inner mitochondrial membrane protein [Arabidopsis thaliana] >gi|18377494|gb|AAL66913.1| inner mitochondrial membrane protein [Arabidopsis thaliana] >gi|21594303|gb|AAM65992.1| inner mitochondrial membrane protein [Arabidopsis thaliana] >gi|38628778|gb|AAR26374.1| mitochondrial inner membrane translocase TM23-2 [Arabidopsis thaliana]	Unigene24320_All//6.00E-60//AT1G72750| ATTIM23-2; P-P-bond-hydrolysis-driven protein transmembrane transporter/ protein transporter	Unigene24320_All//0.00E+00//gi|78354913|gb|DT575187.1|DT575187			GO:0005743//GO:0006605//GO:0008320//GO:0031224	nr -
Unigene24323_All	2007	26.77	49.33	38.21	9.58	12.22	12.98	20.10	42.13	22.91	8.82E-01	6.86E-58			5.13E-01	3.96E-17			3.51E-01	8.93E-04			4.39E-01	2.53E-05			1.07E+00	4.18E-83	Up	1.89E-01	7.65E-03					Unigene24323_All//0.00E+00//TC178959				
Unigene24324_All	1103	5.60	5.24	5.84	1.31	4.31	3.03	0.00	0.00	0.07	-9.60E-02	6.91E-01			6.16E-02	8.04E-01			1.72E+00	1.76E-09	Up	1.21E+00	4.20E-04	Up	null	null		6.17E+00	4.04E-01		Unigene24324_All//gi|159895661|gb|ABX10441.1|//0.00E+00//3-ketoacyl-CoA synthase 6 [Gossypium hirsutum]	Unigene24324_All//6.00E-146//AT2G28630| KCS12 (3-KETOACYL-COA SYNTHASE 12); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene24324_All//0.00E+00//TC146425			GO:0006631//GO:0016746//GO:0044464	nr +
Unigene24325_All	1766	24.29	18.71	7.03	7.79	9.57	7.52	0.07	0.00	0.27	-3.77E-01	3.31E-06			-1.79E+00	4.50E-73	Down	2.98E-01	2.83E-02			-5.03E-02	7.74E-01			-6.17E+00	2.35E-01		1.91E+00	6.30E-02		Unigene24325_All//gi|159895657|gb|ABX10439.1|//0.00E+00//3-ketoacyl-CoA synthase 3 [Gossypium hirsutum]	Unigene24325_All//0.00E+00//AT2G28630| KCS12 (3-KETOACYL-COA SYNTHASE 12); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene24325_All//0.00E+00//TC133336			GO:0006631//GO:0006950//GO:0009314//GO:0016747//GO:0043231	nr +
Unigene24330_All	2368	3.82	9.50	2.83	11.49	10.98	13.81	27.69	38.64	26.25	1.31E+00	1.69E-25	Up	-4.32E-01	3.33E-02			-6.51E-02	5.98E-01			2.66E-01	5.54E-03			4.80E-01	6.27E-23		-7.75E-02	2.33E-01		Unigene24330_All//gi|157399678|gb|ABV53463.1|//1.00E-122//pseudo-response regulator 7 [Castanea sativa]	Unigene24330_All//2.00E-62//AT5G02810| PRR7 (PSEUDO-RESPONSE REGULATOR 7); transcription regulator/ two-component response regulator	Unigene24330_All//0.00E+00//TC175188		ko04712|Circadian rhythm - plant		nr -

Unigene24333_All	2068	5.14	33.74	20.60	10.38	18.37	32.15	1.78	5.58	6.36	2.72E+00	1.55E-204	Up	2.00E+00	9.03E-85	Up	8.23E-01	1.17E-23		1.63E+00	1.40E-109	Up	1.65E+00	1.15E-22	Up	1.84E+00	1.88E-30	Up	Unigene24333_All//gi|297818318|ref|XP_002877042.1|//1.00E-178//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322880|gb|EFH53301.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24333_All//2.00E-168//AT5G40720| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF23 (InterPro:IPR008166); BEST Arabidopsis thaliana protein match is: zinc finger (C3HC4-type RING finger) family protein (TAIR:AT3G27330.1); Has 216 Blast hits to 216 proteins in 64 species: Archae - 0; Bacteria - 120; Metazoa - 2; Fungi - 4; Plants - 57; Viruses - 0; Other Eukaryotes - 33 (source: NCBI BLink).	Unigene24333_All//0.00E+00//gi|164353184|gb|ES839139.1|ES839139			GO:0046872	nr +
Unigene24336_All	1696	23.17	12.31	14.82	38.83	30.37	35.15	49.11	23.17	23.35	-9.12E-01	7.76E-25		-6.45E-01	2.31E-13		-3.54E-01	1.82E-09		-1.44E-01	3.86E-02		-1.08E+00	5.10E-84	Down	-1.07E+00	6.25E-85	Down	Unigene24336_All//gi|18425101|ref|NP_569038.1|//0.00E+00//DGL1; dolichyl-diphosphooligosaccharide-protein glycotransferase [Arabidopsis thaliana] >gi|16226812|gb|AAL16268.1|AF428338_1 AT5g66680/MSN2_7 [Arabidopsis thaliana]	Unigene24336_All//0.00E+00//AT5G66680| DGL1; dolichyl-diphosphooligosaccharide-protein glycotransferase	Unigene24336_All//0.00E+00//TC162420		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0000902//GO:0000576//GO:0005618//GO:0005789//GO:0006487//GO:0007047//GO:0009250//GO:0031410//GO:0031981	nr -
Unigene24338_All	2680	0.55	1.23	0.68	1.08	1.41	1.75	2.29	2.93	7.18	1.17E+00	8.21E-04	Up	3.06E-01	5.57E-01		3.91E-01	2.44E-01		7.01E-01	1.17E-02		3.58E-01	6.16E-02		1.65E+00	3.75E-38	Up	Unigene24338_All//gi|15227189|ref|NP_182322.1|//1.00E-165//RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase [Arabidopsis thaliana] >gi|75319082|sp|P93050.1|RKF3_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase RKF3; AltName: Full=Receptor-like kinase in flowers 3; Flags: Precursor >gi|1785621|emb|CAB06335.1|At4g22324 [Arabidopsis thaliana] >gi|2465927|gb|AAC50045.1| receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi|14335116|gb|AAK59837.1|At2g18010/T9J23.16 [Arabidopsis thaliana] >gi|23308235|gb|AAN18087.1|At2g18010/T9J23.16 [Arabidopsis thaliana]	Unigene24338_All//1.00E-166//AT2G48010| RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase	Unigene24338_All//9.00E-124//gi|84149157|gb|DN780457.1|DN780457		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr -
Unigene2434_All	584	10.84	7.64	8.94	19.19	24.29	23.05	24.25	9.95	14.53	-5.06E-01	3.19E-02		-2.79E-01	2.81E-01		3.40E-01	2.18E-02		2.64E-01	1.10E-01		-1.29E+00	2.33E-19	Down	-7.39E-01	1.63E-08		Unigene2434_All//gi|75169434|sp|Q9C827.1|COB22_ARATH//3.00E-83//RecName: Full=Coatomer subunit beta'-2; AltName: Full=Beta'-coat protein 2; Short=Beta'-COP 2	Unigene2434_All//2.00E-84//AT1G52360| coatomer protein complex, subunit beta 2 (beta prime), putative	Unigene2434_All//0.00E+00//ES826394			GO:0005488//GO:0015031//GO:0016740//GO:0030120	nr +
Unigene24347_All	1464	3.82	3.22	4.51	7.38	4.30	3.42	5.31	5.77	3.67	-2.49E-01	3.61E-01		2.38E-01	3.59E-01		-7.79E-01	1.04E-06		-1.11E+00	1.66E-10	Down	1.18E-01	5.92E-01		-5.33E-01	3.15E-03		Unigene24347_All//gi|7767672|gb|AAF69169.1|AC007915_21//9.00E-25//F22F5.21 [Arabidopsis thaliana]	Unigene24347_All//3.00E-17//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene24347_All//5.00E-53//DT464254			GO:0043229//GO:0044444	nr -
Unigene24348_All	796	7.16	4.46	3.28	6.57	5.15	3.74	2.92	3.62	1.90	-6.85E-01	5.77E-03		-1.13E+00	1.95E-05	Down	-3.52E-01	1.90E-01		-8.11E-01	1.62E-03		3.11E-01	3.92E-01		-6.19E-01	8.57E-02				Unigene24348_All//3.00E-34//TC147599				
Unigene2435_All	457	2.29	2.55	3.38	4.91	4.52	4.45	9.62	3.29	5.75	1.55E-01	7.88E-01		5.61E-01	3.19E-01		-1.18E-01	8.19E-01		-1.41E-01	7.46E-01		-1.55E+00	2.11E-08	Down	-7.42E-01	2.85E-03		Unigene2435_All//gi|71534920|gb|AAZ32864.1|//3.00E-43//coatomer protein complex subunit beta 2 [Medicago sativa]	Unigene2435_All//4.00E-44//AT1G52360| coatomer protein complex, subunit beta 2 (beta prime), putative	Unigene2435_All//0.00E+00//TC133516			GO:0004683//GO:0005488//GO:0015031//GO:0030120	nr -
Unigene24352_All	1559	4.16	57.82	7.10	7.99	11.88	17.58	39.30	172.38	206.55	3.80E+00	0.00E+00	Up	7.72E-01	1.34E-05		5.73E-01	1.75E-06		1.14E+00	1.64E-26	Up	2.13E+00	0.00E+00	Up	2.39E+00	0.00E+00	Up	Unigene24352_All//gi|206584347|gb|ACI15346.1|//1.00E-139//NAC domain protein NAC5 [Gossypium hirsutum] >gi|206584357|gb|ACI15351.1| NAC domain protein NAC5 [Gossypium hirsutum]	Unigene24352_All//1.00E-82//AT3G04070| nac047 (Arabidopsis NAC domain containing protein 47); transcription factor	Unigene24352_All//0.00E+00//TC135034	NAC			nr +
Unigene24353_All	1963	84.33	18.58	41.61	41.64	35.33	24.41	14.19	5.39	4.57	-2.18E+00	0.00E+00	Down	-1.02E+00	3.63E-119	Down	-2.37E-01	1.04E-05		-7.71E-01	2.52E-41		-1.40E+00	2.60E-42	Down	-1.64E+00	8.48E-55	Down	Unigene24353_All//gi|224121930|ref|XP_002318708.1|//0.00E+00//acyl:coa ligase [Populus trichocarpa] >gi|222859381|gb|EEE96928.1|acyl:coa ligase [Populus trichocarpa]	Unigene24353_All//3.00E-178//AT5G63380| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene24353_All//0.00E+00//TC136311		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0009694//GO:0009850//GO:0016408//GO:0016703//GO:0042579	nr +
Unigene24354_All	1790	61.21	140.09	21.06	105.00	77.09	86.59	77.33	28.81	98.35	1.19E+00	1.84E-239	Up	-1.54E+00	3.43E-150	Down	-4.46E-01	4.71E-40		-2.78E-01	5.22E-15		-1.42E+00	2.49E-213	Down	3.47E-01	1.11E-24		Unigene24354_All//gi|211906522|gb|ACJ11754.1|//0.00E+00//UDP-D-glucuronic acid 4-epimerase [Gossypium hirsutum]	Unigene24354_All//0.00E+00//AT4G30440| GAE1 (UDP-D-GLUCURONATE 4-EPIMERASE 1); UDP-glucuronate 4-epimerase/ catalytic	Unigene24354_All//0.00E+00//TC138102		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0006139//GO:0016857//GO:0048037	nr +
Unigene24357_All	906	3.70	2.68	3.06	77.25	15.66	3.19	16.24	3.41	7.56	-4.61E-01	1.78E-01		-2.74E-01	4.47E-01		-2.30E+00	6.13E-217	Down	-4.60E+00	0.00E+00	Down	-2.25E+00	3.52E-43	Down	-1.10E+00	2.05E-16	Down	Unigene24357_All//gi|60592454|gb|AAX28837.1|//3.00E-62//zinc transporter protein ZIP1 [Fragaria x ananassa]	Unigene24357_All//2.00E-35//AT3G12750| ZIP1 (ZINC TRANSPORTER 1 PRECURSOR); zinc ion transmembrane transporter	Unigene24357_All//1.00E-34//TC170125			GO:0008324//GO:0016020//GO:0016491//GO:0030001	nr -
Unigene24358_All	1361	2.23	2.76	2.23	53.88	9.03	1.46	13.73	2.79	5.68	3.05E-01	3.68E-01		3.00E-04	9.98E-01		-2.58E+00	1.31E-260	Down	-5.21E+00	0.00E+00	Down	-2.30E+00	4.98E-56	Down	-1.27E+00	1.06E-25	Down	Unigene24358_All//gi|224109078|ref|XP_002315075.1|//1.00E-119//ZIP transporter [Populus trichocarpa] >gi|222864115|gb|EEF01246.1| ZIP transporter [Populus trichocarpa]	Unigene24358_All//2.00E-69//AT3G12750| ZIP1 (ZINC TRANSPORTER 1 PRECURSOR); zinc ion transmembrane transporter	Unigene24358_All//0.00E+00//TC170125				nr +
Unigene24359_All	1848	2.89	8.39	4.52	4.74	3.35	9.34	7.05	9.70	13.47	1.54E+00	2.21E-22	Up	6.48E-01	1.83E-03		-5.00E-01	6.93E-03		9.77E-01	2.76E-13		4.61E-01	7.51E-05		9.35E-01	8.88E-21		Unigene24359_All//gi|225439231|ref|XP_002271046.1|//0.00E+00//PREDICTED: similar to 0s02g0125100 [Vitis vinifera]	Unigene24359_All//0.00E+00//AT4G13430| IIL1 (ISOPROPYL MALATE ISOMERASE LARGE SUBUNIT 1); 4 iron, 4 sulfur cluster binding / hydro-lyase/ lyase	Unigene24359_All//0.00E+00//TC149567		ko00290|Valine, leucine and isoleucine biosynthesis//ko00660|C5-Branched dibasic acid metabolism	GO:0006520//GO:0009532//GO:0010038//GO:0016836//GO:0016866//GO:0019758//GO:0051536	nr -
Unigene2436_All	647	1.62	1.96	3.62	5.47	7.03	5.72	9.41	4.26	8.00	2.76E-01	6.17E-01		1.16E+00	8.48E-03		3.62E-01	2.31E-01		6.64E-02	8.63E-01		-1.14E+00	2.04E-07	Down	-2.33E-01	2.99E-01		Unigene2436_All//gi|71534920|gb|AAZ32864.1|//6.00E-61//coatomer protein complex subunit beta 2 [Medicago sativa]	Unigene2436_All//6.00E-54//AT1G52360| coatomer protein complex, subunit beta 2 (beta prime), putative	Unigene2436_All//0.00E+00//gi|109853202|gb|DW482181.1|DW482181			GO:0012505//GO:0030117	nr -
Unigene24360_All	2600	17.67	9.35	17.06	13.30	15.20	9.92	7.35	1.95	3.16	-9.17E-01	3.59E-29		-5.05E-02	6.20E-01		1.93E-01	2.59E-02		-4.23E-01	1.81E-06		-1.92E+00	1.30E-45	Down	-1.22E+00	1.39E-24	Down	Unigene24360_All//gi|42565028|ref|NP_188606.2|//0.00E+00//ARC5 (ACCUMULATION AND REPLICATION OF CHLOROPLAST 5); GTP binding / GTPase [Arabidopsis thaliana]	Unigene24360_All//0.00E+00//AT3G19720| ARC5 (ACCUMULATION AND REPLICATION OF CHLOROPLAST 5); GTP binding / GTPase	Unigene24360_All//0.00E+00//gi|78351600|gb|DT571874.1|DT571874		ko04144|Endocytosis	GO:0017111//GO:0032561	nr +
Unigene24362_All	1708	2.79	3.03	4.24	22.40	18.33	19.33	9.53	1.59	1.77	1.18E-01	6.57E-01		6.05E-01	7.42E-03		-2.90E-01	4.07E-04		-2.13E-01	1.80E-02		-2.58E+00	5.03E-56	Down	-2.43E+00	7.59E-54	Down	Unigene24362_All//gi|15228789|ref|NP_194158.1|//0.00E+00//ESK1 (ESKIMO 1) [Arabidopsis thaliana]	Unigene24362_All//0.00E+00//AT3G55990| ESK1 (ESKIMO 1)	Unigene24362_All//3.00E-82//ES795179			GO:0006970//GO:0009409//GO:0010557	nr +
Unigene24366_All	2115	5.57	4.98	5.36	10.83	10.91	9.35	17.51	10.41	7.10	-1.60E-01	3.75E-01		-5.37E-02	7.71E-01		9.90E-03	9.60E-01		-2.12E-01	8.38E-02		-7.50E-01	1.10E-20		-1.30E+00	8.76E-52	Down	Unigene24366_All//gi|297830122|ref|XP_002882943.1|//0.00E+00//regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326783|gb|EFH59202.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24366_All//0.00E+00//AT3G15430| regulator of chromosome condensation (RCC1) family protein	Unigene24366_All//0.00E+00//TC165597		ko04120|Ubiquitin mediated proteolysis	GO:0017016	nr +
Unigene24371_All	567	2.03	0.00	0.28	3.16	2.49	0.88	2.83	0.37	1.26	-1.10E+01	9.91E-07	Down	-2.85E+00	6.02E-04	Down	-3.45E-01	5.12E-01		-1.85E+00	3.68E-04	Down	-2.94E+00	6.45E-07	Down	-1.16E+00	1.02E-02		Unigene24371_All//gi|238478855|ref|NP_001154422.1|//2.00E-07//BRX-LIKE3 (BREVIS RADIX-LIKE 3) [Arabidopsis thaliana]	Unigene24371_All//1.00E-08//AT1G54180| BRX-LIKE3 (BREVIS RADIX-LIKE 3)	Unigene24371_All//0.00E+00//DW506861				nr +
Unigene24372_All	1885	2.58	0.86	0.62	7.16	4.48	1.75	4.62	1.06	3.15	-1.59E+00	7.02E-08	Down	-2.05E+00	2.25E-10	Down	-6.78E-01	1.39E-06		-2.03E+00	5.11E-31	Down	-2.12E+00	5.12E-24	Down	-5.53E-01	1.08E-03		Unigene24372_All//gi|30682933|ref|NP_188016.2|//1.00E-139//ATBRXL2 [Arabidopsis thaliana] >gi|42572427|ref|NP_974309.1|ATBRXL2 [Arabidopsis thaliana] >gi|75151461|sp|Q8GYL9.1|BRXL2_ARATH RecName: Full=Protein Brevis radix-like 2; Short=AtBRXL2 >gi|115311461|gb|ABI93911.1|At3g14000 [Arabidopsis thaliana]	Unigene24372_All//1.00E-135//AT3G14000| ATBRXL2	Unigene24372_All//0.00E+00//gi|78335216|gb|DT555490.1|DT555490				nr +
Unigene24373_All	452	2.20	2.58	1.18	4.63	4.95	1.30	0.37	1.66	1.94	2.29E-01	6.94E-01		-9.01E-01	2.22E-01		9.74E-02	8.38E-01		-1.83E+00	1.08E-04	Down	2.15E+00	9.17E-03		2.37E+00	1.71E-03		Unigene24373_All//gi|30102910|gb|AAP21373.1|//1.00E-33//At2g38730 [Arabidopsis thaliana] >gi|45680872|gb|AAS75305.1| single domain cyclophilin type peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	Unigene24373_All//2.00E-32//AT2G38730| peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative	Unigene24373_All//1.00E-94//ES798520		ko03040|Spliceosome	GO:0016020//GO:0016859//GO:0043231//GO:0044267	nr -
Unigene24377_All	2117	3.19	1.20	1.64	11.77	8.31	9.19	4.07	2.25	2.16	-1.41E+00	4.22E-09	Down	-9.64E-01	4.84E-05		-5.01E-01	5.44E-07		-3.56E-01	1.01E-03		-8.56E-01	1.25E-06		-9.13E-01	1.49E-07		Unigene24377_All//gi|223452302|gb|ACM89479.1|//1.00E-166//cysteine-rich protein [Glycine max]	Unigene24377_All//8.00E-153//AT4G05200| protein kinase family protein	Unigene24377_All//0.00E+00//gi|78330915|gb|DT551189.1|DT551189		ko04626|Plant-pathogen interaction	GO:0004672	nr +
Unigene2438_All	414	6.45	3.43	1.16	13.00	11.98	9.71	35.64	35.13	43.50	-9.11E-01	1.83E-02		-2.48E+00	2.65E-07	Down	-1.18E-01	6.94E-01		-4.21E-01	1.18E-01		-2.08E-02	9.04E-01		2.87E-01	1.34E-02		Unigene2438_All//gi|30678278|ref|NP_563695.2|//2.00E-70//ADK1 (dual specificity kinase 1); kinase/ protein serine/threonine/tyrosine kinase [Arabidopsis thaliana] >gi|4204297|gb|AAD10678.1| ADK1 [Arabidopsis thaliana] >gi|18700077|gb|AAL77651.1|At1g03930/F21M11_14 [Arabidopsis thaliana] >gi|20852979|gb|AAM26641.1|At1g03930/F21M11_14 [Arabidopsis thaliana] >gi|62996988|gb|AAY24538.1| casein kinase 1-like protein 9b [Arabidopsis thaliana]	Unigene2438_All//9.00E-72//AT1G03930| ADK1 (dual specificity kinase 1); kinase/ protein serine/threonine/tyrosine kinase	Unigene2438_All//0.00E+00//TC175126			GO:0000902//GO:0004672//GO:0005576//GO:0006166//GO:0006464//GO:0009536//GO:0009725//GO:0010038//GO:0016020//GO:0019206//GO:0023060//GO:0032559//GO:0034285//GO:0042445//GO:0016914//GO:0048513	nr +
Unigene24381_All	2271	9.84	8.95	10.76	23.27	19.36	30.88	36.27	41.52	73.20	-1.37E-01	2.88E-01		1.30E-01	3.19E-01		-2.65E-01	1.06E-04		4.08E-01	1.25E-11		1.95E-01	5.52E-05		1.01E+00	1.16E-152	Up	Unigene24381_All//gi|297820152|ref|XP_002877959.1|//0.00E+00//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323797|gb|EFH54218.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24381_All//0.00E+00//AT3G54140| PTR1 (PEPTIDE TRANSPORTER 1); dipeptide transporter/ transporter/ tripeptide transporter	Unigene24381_All//0.00E+00//TC158352			GO:0000904//GO:0006857//GO:0008152//GO:0015198//GO:0031224	nr -

Unigene24382_A11	5559	5.83	1.67	2.64	5.81	3.92	7.00	5.19	1.84	2.59	-1.80E+00	6.46E-58	Down	-1.14E+00	2.79E-28	Down	-5.67E-01	5.51E-11		2.69E-01	1.84E-03		-1.49E+00	2.93E-48	Down	-1.00E+00	8.41E-27		Unigene24382_A11//gi|30682500|ref|NP_196478.2|//0.00E+00//DEAD box RNA helicase (RH26) [Arabidopsis thaliana] >gi|109893654|sp|Q9FNM7.2|RH26_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 26	Unigene24382_A11//0.00E+00//AT5G08610| DEAD box RNA helicase (RH26)	Unigene24382_A11//0.00E+00//TC174573			GO:0003676//GO:0006970//GO:0032559//GO:0042623//GO:0043231	nr +
Unigene24384_A11	1538	60.18	27.94	37.67	30.28	35.26	47.01	16.69	10.98	10.49	-1.11E+00	5.94E-79	Down	-6.76E-01	2.62E-33		2.20E-01	1.66E-03		6.35E-01	5.64E-26		-6.04E-01	3.18E-10		-6.70E-01	1.70E-12		Unigene24384_A11//gi|229609837|gb|ACQ83534.1|//0.00E+00//CBL-interacting protein kinase 18 [Vitis vinifera]	Unigene24384_A11//0.00E+00//AT2G26980| CIPK3 (CBL-INTERACTING PROTEIN KINASE 3); kinase/ protein kinase/ protein serine/threonine kinase	Unigene24384_A11//0.00E+00//TC141442		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0009755//GO:0023060//GO:0032559//GO:0043231	nr +
Unigene24386_A11	2576	7.78	5.92	5.35	9.24	9.60	4.91	13.29	5.78	11.66	-3.94E-01	1.43E-03		-5.39E-01	2.18E-05		5.43E-02	7.08E-01		-9.13E-01	1.97E-16		-1.20E+00	3.26E-41	Down	-1.89E-01	2.36E-02		Unigene24386_A11//gi|222424122|dbj|BAH20620.1|//2.00E-80//AT2G30990 [Arabidopsis thaliana]	Unigene24386_A11//2.00E-47//AT2G30990| unknown protein	Unigene24386_A11//0.00E+00//ES820755				nr -
Unigene24387_A11	3087	1.51	5.22	2.52	7.57	9.65	8.34	7.20	8.34	3.79	1.79E+00	1.17E-28	Up	7.40E-01	6.33E-04		3.50E-01	1.90E-04		1.40E-01	2.60E-01		2.11E-01	3.71E-02		-9.25E-01	1.87E-18		Unigene24387_A11//gi|20453164|gb|AAM19823.1|//4.00E-61//AT5g45500/MFC19_17 [Arabidopsis thaliana] >gi|23308327|gb|AAN18133.1|At5g45500/MFC19_17 [Arabidopsis thaliana]	Unigene24387_A11//2.00E-52//AT5G45500| unknown protein					nr +
Unigene24389_A11	1801	3.92	5.32	7.51	3.21	6.81	16.88	2.28	6.75	10.35	4.39E-01	1.92E-02		9.37E-01	5.14E-09		1.09E+00	3.17E-12	Up	2.40E+00	5.08E-83	Up	1.57E+00	3.01E-22	Up	2.18E+00	1.67E-53	Up	Unigene24389_A11//gi|224123490|ref|XP_002330327.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222871362|gb|EEF08493.1|cytochrome P450 [Populus trichocarpa]	Unigene24389_A11//0.00E+00//AT3G19270| CYP707A4; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	Unigene24389_A11//0.00E+00//TC169191		ko00906|Carotenoid biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr +
Unigene24391_A11	2781	16.76	61.53	25.28	15.87	11.70	14.49	9.82	8.45	8.71	1.88E+00	0.00E+00	Up	5.92E-01	2.98E-20		-4.40E-01	1.67E-09		-1.32E-01	1.43E-01		-2.18E-01	2.53E-02		-1.73E-01	7.16E-02		Unigene24391_A11//gi|18398032|ref|NP_566315.1|//0.00E+00//ABC1 family protein [Arabidopsis thaliana] >gi|30680411|ref|NP_850536.1| ABC1 family protein [Arabidopsis thaliana] >gi|222424076|dbj|BAH19998.1|AT3G07700 [Arabidopsis thaliana]	Unigene24391_A11//0.00E+00//AT3G07700| ABC1 family protein	Unigene24391_A11//0.00E+00//TC138759		ko04626|Plant-pathogen interaction	GO:0043231	nr -
Unigene24392_A11	2748	1.24	4.00	1.49	0.85	0.91	0.81	0.95	0.53	0.90	1.69E+00	2.44E-18	Up	2.70E-01	3.96E-01		1.03E-01	8.23E-01		-8.13E-02	8.61E-01		-8.42E-01	1.56E-02		-8.58E-02	8.04E-01		Unigene24392_A11//gi|18398032|ref|NP_566315.1|//0.00E+00//ABC1 family protein [Arabidopsis thaliana] >gi|30680411|ref|NP_850536.1| ABC1 family protein [Arabidopsis thaliana] >gi|222424076|dbj|BAH19998.1|AT3G07700 [Arabidopsis thaliana]	Unigene24392_A11//0.00E+00//AT3G07700| ABC1 family protein	Unigene24392_A11//0.00E+00//TC138759		ko04626|Plant-pathogen interaction	GO:0043231	nr +
Unigene24393_A11	887	13.39	3.83	2.40	17.75	15.92	12.98	6.96	2.87	2.69	-1.81E+00	1.07E-21	Down	-2.48E+00	7.89E-31	Down	-1.57E-01	3.14E-01		-4.51E-01	1.14E-03		-1.28E+00	8.68E-09	Down	-1.37E+00	4.88E-10	Down	Unigene24393_A11//gi|194244953|gb|ACF35260.1|//6.00E-90//BARD1 [Arabidopsis thaliana]	Unigene24393_A11//3.00E-91//AT1G04020| BARD1 (BREAST CANCER ASSOCIATED RING 1); DNA binding / transcription coactivator	Unigene24393_A11//3.00E-155//TC164562			GO:0005488	nr +
Unigene24394_A11	2056	2.60	0.91	1.04	2.96	3.40	2.11	3.91	1.42	1.49	-1.51E+00	4.97E-08	Down	-1.33E+00	2.16E-06	Down	2.02E-01	4.28E-01		-4.87E-01	4.53E-02		-1.46E+00	1.57E-13	Down	-1.39E+00	4.56E-13	Down	Unigene24394_A11//gi|145362227|ref|NP_973758.2|//1.00E-151//BARD1 (BREAST CANCER ASSOCIATED RING 1); DNA binding / transcription coactivator [Arabidopsis thaliana]	Unigene24394_A11//4.00E-152//AT1G04020| BARD1 (BREAST CANCER ASSOCIATED RING 1); DNA binding / transcription coactivator	Unigene24394_A11//0.00E+00//ES822772				nr +
Unigene24395_A11	1548	13.52	8.25	11.32	8.53	10.39	5.84	5.27	1.86	2.81	-7.13E-01	3.60E-09		-2.57E-01	4.90E-02		2.85E-01	4.38E-02		-5.47E-01	3.06E-04		-1.50E+00	2.62E-14	Down	-9.10E-01	3.65E-07		Unigene24395_A11//gi|16604308|gb|AAL24160.1|//1.00E-118//At1g31300/T19E23_12 [Arabidopsis thaliana] >gi|20660069|gb|AAM19956.1|At1g31300/T19E23_12 [Arabidopsis thaliana]	Unigene24395_A11//5.00E-120//AT1G31300| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: TRAM, LAG1 and CLN8 homology (InterPro:IPR006634); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G19645.2); Has 478 Blast hits to 478 proteins in 104 species: Archae - 0; Bacteria - 0; Metazoa - 269; Fungi - 98; Plants - 80; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink).	Unigene24395_A11//0.00E+00//TC163597				nr -
Unigene24396_A11	2389	3.64	3.73	3.92	6.61	5.78	4.67	14.78	9.81	7.30	3.81E-02	8.55E-01		1.10E-01	6.34E-01		-1.94E-01	2.05E-01		-5.01E-01	2.60E-04		-5.90E-01	3.09E-13		-1.02E+00	1.64E-33	Down	Unigene24396_A11//gi|224079409|ref|XP_002305854.1|//0.00E+00//histone deacetylase [Populus trichocarpa] >gi|222848818|gb|EEE86365.1|histone deacetylase [Populus trichocarpa]	Unigene24396_A11//0.00E+00//AT5G61060| HDA05 (HISTONE DEACETYLASE 5); histone deacetylase	Unigene24396_A11//0.00E+00//TC172833			GO:0003824//GO:0006476//GO:0043231	nr +
Unigene24397_A11	749	1.26	1.08	1.00	5.99	3.36	1.93	10.22	3.24	3.78	-2.16E-01	7.32E-01		-3.37E-01	6.16E-01		-8.35E-01	1.74E-03		-1.63E+00	4.88E-08	Down	-1.66E+00	1.91E-15	Down	-1.44E+00	4.34E-13	Down	Unigene24397_A11//gi|75319499|sp|Q39821.1|SDLCA_SOYBN//1.00E-110//RecName: Full=Dynamin-related protein 12A; AltName: Full=Soybean dynamin-like protein 12A; Short=SDL12A; AltName: Full=Phragmoplastin >gi|12179941|gb|AAB05992.1| SDL12A [Glycine max]	Unigene24397_A11//2.00E-100//AT5G42080| ADL1 (ARABIDOPSIS DYNAMIN-LIKE PROTEIN); GTP binding / GTPase/ protein binding	Unigene24397_A11//0.00E+00//gi|78330988|gb|DT551262.1|DT551262		ko04144|Endocytosis		nr +
Unigene24399_A11	2393	29.10	23.67	19.69	37.01	36.16	37.29	26.38	21.15	11.77	-2.98E-01	1.98E-06		-5.63E-01	2.31E-18		-3.35E-02	6.27E-01		1.09E-02	8.90E-01		-3.19E-01	6.21E-08		-1.16E+00	1.36E-73	Down	Unigene24399_A11//gi|224089817|ref|XP_002308822.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222854798|gb|EEE92345.1| GRAS family transcription factor [Populus trichocarpa]	Unigene24399_A11//1.00E-136//AT5G41920| scarecrow transcription factor family protein	Unigene24399_A11//0.00E+00//TC146031	GRAS	ko03010|Ribosome	GO:0010468	nr +
Unigene24400_A11	3280	1.90	1.41	1.41	13.21	9.43	5.89	5.65	1.95	2.32	-4.33E-01	7.09E-02		-4.27E-01	9.11E-02		-4.87E-01	3.57E-11		-1.16E+00	1.01E-43	Down	-1.53E+00	1.70E-32	Down	-1.28E+00	9.26E-26	Down	Unigene24400_A11//gi|63115354|gb|AY33856.1|//0.00E+00//class III HD-zip protein [Gossypium barbadense]	Unigene24400_A11//0.00E+00//AT5G60690| REV (REVOLUTA); DNA binding / lipid binding / transcription factor	Unigene24400_A11//0.00E+00//TC142046	HB		GO:0001071//GO:0003677//GO:0006351//GO:0009799//GO:0009933//GO:0009943//GO:0010468//GO:0043231//GO:0048869	nr +
Unigene24401_A11	1349	121.13	170.19	136.38	95.53	101.21	102.75	112.71	294.96	141.34	4.91E-01	9.26E-48		1.71E-01	1.22E-05		8.34E-02	8.32E-02		1.05E-01	2.48E-02		1.39E+00	0.00E+00	Up	3.27E-01	6.70E-24		Unigene24401_A11//gi|297846438|ref|XP_002891100.1|//1.00E-156//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336942|gb|EFH67359.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24401_A11//2.00E-143//AT1G34370| STOP1 (sensitive to proton rhizotoxicity 1); nucleic acid binding / transcription factor/ zinc ion binding	Unigene24401_A11//0.00E+00//TC150549	C2H2			nr +
Unigene24403_A11	1537	5.92	4.45	5.82	27.06	16.33	10.52	31.96	21.73	11.51	-4.12E-01	3.31E-02		-2.52E-02	9.14E-01		-7.29E-01	9.47E-22		-1.36E+00	1.31E-53	Down	-5.57E-01	2.26E-16		-1.47E+00	1.92E-82	Down	Unigene24403_A11//gi|224140225|ref|XP_002323485.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222868115|gb|EEF05246.1|multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene24403_A11//0.00E+00//AT2G36910| ABCB1 (ATP BINDING CASSETTE SUBFAMILY B1); ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter/ calmodulin binding	Unigene24403_A11//0.00E+00//TC138356		ko02010|ABC transporters	GO:0005515//GO:0009630//GO:0009639//GO:0009725//GO:0015562//GO:0019829//GO:0031224//GO:0032555//GO:0032559//GO:0043231//GO:0043479//GO:0048437//GO:0051707//GO:0060918	nr +
Unigene24404_A11	3667	3.54	2.65	2.37	10.83	13.22	9.03	14.35	2.96	5.21	-4.16E-01	8.40E-03		-5.80E-01	3.44E-04		2.88E-01	6.19E-05		-2.62E-01	2.09E-03		-2.28E+00	5.64E-155	Down	-1.46E+00	3.98E-87	Down	Unigene24404_A11//gi|224539866|ref|XP_002274736.1|//0.00E+00//PREDICTED: similar to kinesin motor protein-related [Vitis vinifera]	Unigene24404_A11//0.00E+00//AT2G37420| kinesin motor protein-related	Unigene24404_A11//1.00E-169//TC154928			GO:0003774//GO:0007017//GO:0015630//GO:0016020//GO:0032559	nr +
Unigene24405_A11	3583	0.50	0.33	0.24	1.21	1.41	0.86	1.83	0.34	0.76	-6.10E-01	2.16E-01		-1.06E+00	4.11E-02		2.24E-01	4.65E-01		-4.97E-01	9.71E-02		-2.43E+00	1.69E-21	Down	-1.27E+00	1.37E-09	Down	Unigene24405_A11//gi|224539866|ref|XP_002274736.1|//0.00E+00//PREDICTED: similar to kinesin motor protein-related [Vitis vinifera]	Unigene24405_A11//0.00E+00//AT2G37420| kinesin motor protein-related	Unigene24405_A11//4.00E-154//TC154928			GO:0003774//GO:0007017//GO:0015630//GO:0016020//GO:0032559	nr +
Unigene24406_A11	1965	5.43	8.92	7.78	8.32	13.95	13.42	29.31	55.34	101.15	7.16E-01	7.65E-08		5.18E-01	4.67E-04		7.46E-01	1.38E-14		6.91E-01	2.41E-11		9.17E-01	4.16E-83		1.79E+00	0.00E+00	Up	Unigene24406_A11//gi|297800878|ref|XP_002868323.1|//1.00E-145//AT-HSFA5 [Arabidopsis lyrata subsp. lyrata] >gi|297314159|gb|EFH44582.1| AT-HSFA5 [Arabidopsis lyrata subsp. lyrata]	Unigene24406_A11//8.00E-142//AT4G13980| AT-HSFA5; DNA binding / transcription factor	Unigene24406_A11//0.00E+00//gi|78328031|gb|DT548305.1|DT548305	HSF		GO:0001071//GO:0003677//GO:0006351//GO:0043231	nr +
Unigene24408_A11	1917	4.07	3.46	2.00	8.37	7.71	6.38	8.73	1.61	3.10	-2.32E-01	2.99E-01		-1.02E+00	3.15E-06	Down	-1.19E-01	4.73E-01		-3.90E-01	5.02E-03		-2.44E+00	6.64E-54	Down	-1.50E+00	2.71E-29	Down	Unigene24408_A11//gi|297791475|ref|XP_002863622.1|//1.00E-146//nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309457|gb|EFH39881.1|nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24408_A11//6.00E-122//AT5G43960| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene24408_A11//0.00E+00//TC132088		ko03040|Spliceosome		nr +
Unigene24409_A11	1222	165.10	153.13	159.14	59.35	40.55	38.92	109.30	99.22	43.39	-1.09E-01	3.78E-03		-5.30E-02	2.26E-01		-5.50E-01	7.37E-23		-6.09E-01	2.02E-24		-1.40E-01	6.71E-04		-1.33E+00	2.54E-191	Down	Unigene24409_A11//gi|225348627|gb|ACN87275.1|//2.00E-84//short chain dehydrogenase/reductase [Nandina domestica]	Unigene24409_A11//3.00E-76//AT3G61220| short-chain dehydrogenase/reductase (SDR) family protein	Unigene24409_A11//0.00E+00//TC143224		ko04146|Peroxisome//ko00906|Carotenoid biosynthesis	GO:0008152//GO:0016616	nr -
Unigene24414_A11	1740	17.26	11.59	14.72	29.43	28.52	35.09	51.90	16.31	16.39	-5.75E-01	5.49E-09		-2.30E-01	3.23E-02		-4.54E-02	6.18E-01		2.54E-01	1.40E-04		-1.67E+00	6.03E-176	Down	-1.66E+00	6.23E-180	Down	Unigene24414_A11//gi|20334820|gb|AAM16166.1|//0.00E+00//At1g12050/F12F1_8 [Arabidopsis thaliana]	Unigene24414_A11//0.00E+00//AT1G12050| fumarylacetoacetase, putative	Unigene24414_A11//0.00E+00//TC154980		ko00350|Tyrosine metabolism	GO:0006520//GO:0016823	nr -
Unigene24415_A11	1382	0.72	1.47	0.39	3.35	1.32	2.03	4.07	6.62	11.10	1.03E+00	2.45E-02		-9.01E-01	2.22E-01		-1.34E+00	4.42E-07	Down	-7.26E-01	8.91E-03		7.03E-01	3.35E-05		1.45E+00	2.06E-25	Up	Unigene24415_A11//gi|168988212|gb|ACA35280.1|//1.00E-88//abscisic acid insensitive [Cucumis sativus]	Unigene24415_A11//7.00E-39//AT2G36270| ABI5 (ABA INSENSITIVE 5); DNA binding / transcription activator/ transcription factor	Unigene24415_A11//7.00E-12//CO080792	bZIP		GO:0003676//GO:0006355//GO:0006950//GO:0009628//GO:0009725//GO:0009943//GO:0009845//GO:0023033//GO:0071310	nr -
Unigene24418_A11	1106	0.28	1.33	0.48	1.71	1.31	1.14	2.03	2.27	5.76	2.23E+00	4.29E-04	Up	7.63E-01	4.53E-01		-3.88E-01	4.26E-01		-5.82E-01	2.31E-01		1.62E-01	6.65E-01		1.51E+00	1.07E-11	Up	Unigene24418_A11//gi|168988212|gb|ACA35280.1|//1.00E-06//abscisic acid insensitive [Cucumis sativus]	Unigene24418_A11//4.00E-07//AT2G36270| ABI5 (ABA INSENSITIVE 5); DNA binding / transcription activator/ transcription factor		bZIP			nr +
Unigene24419_A11	1364	0.42	2.23	0.23	2.26	1.51	3.24	0.81	1.20	3.04	2.40E+00	2.40E-08	Up	-8.49E-01	3.97E-01		-5.80E-01	9.32E-02		5.19E-01	7.95E-02		5.68E-01	2.34E-01		1.91E+00	1.11E-10	Up	Unigene24419_A11//gi|168988212|gb|ACA35280.1|//1.00E-120//abscisic acid insensitive [Cucumis sativus]	Unigene24419_A11//1.00E-82//AT2G36270| ABI5 (ABA INSENSITIVE 5); DNA binding / transcription activator/ transcription factor	Unigene24419_A11//2.00E-15//CO096856	bZIP		GO:0005488//GO:0006950//GO:0009628	nr +

Unigene2442_All	568	7.18	5.44	7.31	5.44	6.00	8.19	11.54	7.28	3.79	-4.01E-01	1.96E-01		2.54E-02	9.51E-01		1.43E-01	7.34E-01		5.91E-01	3.76E-02		-6.63E-01	1.17E-03		-1.61E+00	3.21E-13	Down	Unigene2442_All//gi|297845584|ref|XP_002890673.1|//2.00E-18//metal-dependent phosphohydrolase HD domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297336615|gb|EFH66932.1| metal-dependent phosphohydrolase HD domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2442_All//3.00E-19//AT1G26160| metal-dependent phosphohydrolase HD domain-containing protein	Unigene2442_All//0.00E+00//gi|21103356|gb|BQ415669.1|BQ415669			GO:0009536	nr -
Unigene24423_All	1395	6.04	4.40	5.34	4.14	4.05	2.88	3.73	8.27	6.80	-4.58E-01	2.25E-02		-1.76E-01	4.24E-01		-3.31E-02	9.02E-01		-5.24E-01	3.59E-02		1.15E+00	1.90E-13	Up	8.67E-01	1.50E-07		Unigene24423_All//gi|224117488|ref|XP_002331687.1|//4.00E-53//SET domain protein [Populus trichocarpa] >gi|222874165|gb|EEF11296.1| SET domain protein [Populus trichocarpa]	Unigene24423_All//5.00E-52//AT5G14260| SET domain-containing protein	Unigene24423_All//4.00E-177//ES835011			GO:0009536	nr -
Unigene24426_All	2084	1.33	2.77	0.79	3.51	4.91	3.49	5.50	4.65	5.79	1.06E+00	2.67E-05	Up	-7.48E-01	5.84E-02		4.82E-01	5.32E-03		-1.02E-02	9.58E-01		-2.41E-01	1.35E-01		7.52E-02	6.31E-01									
Unigene24428_All	2048	15.18	12.99	16.95	6.28	6.39	4.39	10.18	6.90	3.46	-2.24E-01	2.54E-02		1.60E-01	1.23E-01		2.60E-02	8.97E-01		-5.16E-01	8.39E-04		-5.61E-01	1.63E-07		-1.56E+00	2.35E-38	Down	Unigene24428_All//gi|297808589|ref|XP_002872178.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297318015|gb|EFH48437.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene24428_All//9.00E-178//AT5G25630| pentatricopeptide (PPR) repeat-containing protein	Unigene24428_All//0.00E+00//TC142838				nr +
Unigene24429_All	1563	3.82	2.11	3.07	7.20	3.92	3.24	4.76	1.50	1.55	-8.57E-01	4.24E-04		-3.16E-01	2.32E-01		-8.77E-01	1.97E-08		-1.15E+00	1.31E-11	Down	-1.67E+00	3.64E-15	Down	-1.61E+00	5.45E-15	Down	Unigene24429_All//gi|8493576|gb|AAF75799.1|AC011000.2//0.00E+00//Contains weak similarity to T-type calcium channel isoform from Rattus norvegicus gb|AF125161. EST gb|H30034 comes from this gene [Arabidopsis thaliana]	Unigene24429_All//0.00E+00//AT1G62870| unknown protein	Unigene24429_All//0.00E+00//gi|48742535|gb|C0073054.1|C0073054			GO:0005488	nr +
Unigene24431_All	1018	8.38	17.42	8.58	18.40	15.39	17.52	26.04	30.14	40.43	1.06E+00	1.47E-14	Up	3.42E-02	8.78E-01		-2.58E-01	4.54E-02		-7.03E-02	6.56E-01		2.11E-01	2.11E-02		6.35E-01	1.03E-17		Unigene24431_All//gi|48958465|gb|AAT47785.1|//5.00E-40//At5g18540 [Arabidopsis thaliana] >gi|51972056|gb|AAU15132.1| At5g18540 [Arabidopsis thaliana]	Unigene24431_All//8.00E-31//AT5G18540| unknown protein	Unigene24431_All//5.00E-148//gi|84148310|gb|DN779610.1|DN779610				nr -
Unigene24438_All	2124	2.93	13.76	1.88	3.75	14.49	14.14	27.05	32.92	81.37	2.23E+00	1.72E-68	Up	-6.41E-01	9.43E-03		1.95E+00	5.65E-71	Up	1.91E+00	6.30E-62	Up	2.83E-01	4.03E-07		1.59E+00	0.00E+00	Up	Unigene24438_All//gi|224060651|ref|XP_002300248.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222847506|gb|EEE85053.1| GH3 family protein [Populus trichocarpa]	Unigene24438_All//0.00E+00//AT2G14960| GH3.1	Unigene24438_All//0.00E+00//TC132279			GO:0009725//GO:0016881//GO:0048878	nr -
Unigene2444_All	1455	3.38	4.49	3.11	17.19	19.45	13.50	9.12	3.30	21.17	4.10E-01	7.93E-02		-1.20E-01	6.75E-01		1.79E-01	1.01E-01		-3.48E-01	1.30E-03		-1.47E+00	4.91E-22	Down	1.21E+00	1.78E-38	Up	Unigene2444_All//gi|28416689|gb|AAO42875.1|//1.00E-174//At3g50340 [Arabidopsis thaliana]	Unigene2444_All//8.00E-152//AT3G50340| unknown protein	Unigene2444_All//0.00E+00//TC178575				nr +
Unigene24441_All	818	1.02	1.61	0.00	4.14	4.00	1.66	3.98	4.34	3.02	6.54E-01	2.62E-01		-1.00E+01	1.19E-04	Down	-5.03E-02	8.82E-01		-1.32E+00	9.81E-05	Down	1.26E-01	6.92E-01		-3.98E-01	1.93E-01		Unigene24441_All//gi|297806541|ref|XP_002871154.1|//5.00E-23//metal ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297316991|gb|EFH47413.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene24441_All//4.00E-15//AT5G05365| metal ion binding	Unigene24441_All//9.00E-38//DT049308			GO:0006812//GO:0043169	nr +
Unigene24446_All	545	0.77	1.30	3.03	3.02	2.09	1.99	3.65	2.91	1.46	7.61E-01	3.62E-01		1.98E+00	8.05E-04	Up	-5.33E-01	3.08E-01		-6.01E-01	2.60E-01		-3.23E-01	4.58E-01		-1.32E+00	1.19E-03		Unigene24446_All//gi|109946553|gb|ABG48455.1|//3.00E-40//At4g33925 [Arabidopsis thaliana]	Unigene24446_All//2.00E-41//AT4G33925| unknown protein	Unigene24446_All//0.00E+00//TC167523			GO:0043231//GO:0046914	nr -
Unigene24447_All	1902	0.77	21.39	0.36	2.59	21.06	22.58	44.10	138.84	204.93	4.80E+00	1.73E-191	Up	-1.08E+00	6.36E-02		3.02E+00	1.60E-152	Up	3.12E+00	8.02E-156	Up	1.65E+00	0.00E+00	Up	2.22E+00	0.00E+00	Up	Unigene24447_All//gi|226235456|dbj|BAH47640.1|//1.00E-156//progesterone 5beta reductase-A [Nicotiana tabacum]	Unigene24447_All//4.00E-137//AT4G24220| VEP1 (VEIN PATTERNING 1); binding / catalytic	Unigene24447_All//0.00E+00//TC144845				nr -
Unigene24449_All	648	1.29	0.94	0.49	1.38	1.38	1.95	1.44	0.19	0.61	-4.61E-01	5.43E-01		-1.39E+00	9.66E-02		-2.10E-03	9.78E-01		4.96E-01	4.48E-01		-2.89E+00	3.28E-04	Down	-1.22E+00	5.14E-02		Unigene24449_All//gi|30681946|ref|NP_172556.2|//5.00E-55//AGD4 (ARF-GAP domain 4); ARF GTPase activator/ protein binding / zinc ion binding [Arabidopsis thaliana] >gi|75313633|sp|Q9SMX5.2|AGD4_ARATH RecName: Full=ADP-ribosylation factor GTPase-activating protein AGD4; Short=ARF GAP AGD4; AltName: Full=Protein ARF-GAP DOMAIN 4; Short=AtAGD4; AltName: Full=GCN4-complementing protein 1 >gi|6463806|emb|CAB61505.1| GCN4-complementing protein (GCP1) [Arabidopsis thaliana]	Unigene24449_All//3.00E-56//AT1G10870| AGD4 (ARF-GAP domain 4); ARF GTPase activator/ protein binding / zinc ion binding	Unigene24449_All//3.00E-89//C0108031		ko04144|Endocytosis	GO:0003002//GO:0005083//GO:0005543//GO:0005798//GO:0008483//GO:0009085//GO:0009532//GO:0009627//GO:0009725//GO:0009887//GO:0016020//GO:0046914	nr +
Unigene24452_All	1578	0.99	28.29	7.80	7.01	12.09	17.46	13.29	46.83	34.64	4.83E+00	6.41E-211	Up	2.97E+00	6.14E-39	Up	7.87E-01	3.30E-11		1.32E+00	2.41E-33	Up	1.82E+00	9.93E-162	Up	1.38E+00	1.83E-82	Up	Unigene24452_All//gi|18394987|ref|NP_564139.1|//1.00E-158//SKP2A [Arabidopsis thaliana] >gi|9454572|gb|AAF87895.1|AC015447_5 Unknown protein [Arabidopsis thaliana] >gi|16604366|gb|AAL24189.1| At1g21410/F24J8_17 [Arabidopsis thaliana] >gi|19699206|gb|AAL90969.1| At1g21410/F24J8_17 [Arabidopsis thaliana]	Unigene24452_All//9.00E-160//AT1G21410| SKP2A	Unigene24452_All//0.00E+00//TC155040		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene24454_All	1529	8.04	11.04	7.63	45.32	31.71	31.28	24.67	44.17	10.84	4.57E-01	7.50E-04		-7.63E-02	6.67E-01		-5.15E-01	1.85E-19		-5.35E-01	1.33E-18		8.41E-01	6.75E-45		-1.19E+00	1.21E-45	Down	Unigene24454_All//gi|15233452|ref|NP_194639.1|//1.00E-63//ethylene-responsive family protein [Arabidopsis thaliana] >gi|75159400|sp|Q8S3D1.2|BH068_ARATH RecName: Full=Transcription factor bHLH68; AltName: Full=Transcription factor EN 60; AltName: Full=bHLH transcription factor bHLH068; AltName: Full=Basic helix-loop-helix protein 68; Short=bHLH 68; Short=AtbHLH68	Unigene24454_All//5.00E-59//AT4G29100| ethylene-responsive family protein	Unigene24454_All//0.00E+00//TC173656	bHLH			nr +
Unigene24456_All	1937	1.24	1.07	1.10	4.96	3.29	3.57	5.44	9.26	2.53	-2.12E-01	6.02E-01		-1.76E-01	6.68E-01		-5.94E-01	5.67E-04		-4.77E-01	9.99E-03		7.68E-01	7.63E-11		-1.10E+00	5.19E-12	Down	Unigene24456_All//gi|15233452|ref|NP_194639.1|//1.00E-73//ethylene-responsive family protein [Arabidopsis thaliana] >gi|75159400|sp|Q8S3D1.2|BH068_ARATH RecName: Full=Transcription factor bHLH68; AltName: Full=Transcription factor EN 60; AltName: Full=bHLH transcription factor bHLH068; AltName: Full=Basic helix-loop-helix protein 68; Short=bHLH 68; Short=AtbHLH68	Unigene24456_All//4.00E-69//AT4G29100| ethylene-responsive family protein	Unigene24456_All//0.00E+00//TC173656	bHLH		GO:0010468//GO:0043231	nr +
Unigene24457_All	1069	59.66	26.78	31.93	199.72	174.95	181.03	53.55	33.47	44.57	-1.16E+00	1.81E-58	Down	-9.02E-01	1.03E-37		-1.91E-01	2.05E-09		-1.42E-01	4.13E-05		-6.78E-01	1.43E-26		-2.65E-01	1.47E-05		Unigene24457_All//gi|30679432|ref|NP_187173.2|//2.00E-60//heavy-metal-associated domain-containing protein [Arabidopsis thaliana]	Unigene24457_All//3.00E-30//AT5G19090| heavy-metal-associated domain-containing protein	Unigene24457_All//1.00E-105//gi|78346467|gb|DT566741.1|DT566741			GO:0030312	nr -
Unigene24459_All	1077	61.26	28.75	47.47	70.07	62.64	46.42	34.43	14.82	9.62	-1.09E+00	3.28E-55	Down	-3.68E-01	2.51E-08		-1.62E-01	6.79E-03		-5.94E-01	2.59E-24		-1.22E+00	2.65E-45	Down	-1.84E+00	1.50E-85	Down	Unigene24459_All//gi|297814115|ref|XP_002874941.1|//1.00E-105//Os01g0254000 [Arabidopsis lyrata subsp. lyrata] >gi|297320778|gb|EFH51200.1| Os01g0254000 [Arabidopsis lyrata subsp. lyrata]	Unigene24459_All//8.00E-92//AT4G02080| ATSAR2 (ARABIDOPSIS THALIANA SECRETION-ASSOCIATED RAS SUPER FAMILY 2); GTP binding	Unigene24459_All//0.00E+00//gi|164253913|gb|EV488185.1|EV488185		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene24460_All	1559	82.56	79.34	116.10	567.22	344.26	152.18	119.65	88.95	18.35	-5.75E-02	2.75E-01		4.92E-01	9.11E-37		-7.20E-01	0.00E+00		-1.90E+00	0.00E+00	Down	-4.28E-01	3.16E-37		-2.71E+00	0.00E+00	Down	Unigene24460_All//gi|153805698|gb|ABS52574.1|//1.00E-173//nodulin family protein [Gossypium hirsutum]	Unigene24460_All//2.00E-135//AT4G08300| nodulin MtN21 family protein	Unigene24460_All//0.00E+00//TC164086				nr -
Unigene24462_All	483	4.22	1.68	2.43	0.41	0.57	0.37	14.44	3.98	1.48	-1.33E+00	4.16E-03		-8.01E-01	9.12E-02		4.68E-01	8.17E-01		-1.41E-01	9.35E-01		-1.86E+00	1.88E-16	Down	-3.28E+00	4.74E-32	Down	Unigene24462_All//gi|300193870|gb|ADJ68324.1|//8.00E-28//geraniol 10-hydroxylase [Picrorhiza kurrooa]	Unigene24462_All//1.00E-21//AT2G45570| CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene24462_All//6.00E-124//DW232478		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016712	nr -
Unigene24463_All	1570	1.30	0.19	1.59	0.06	0.00	0.00	5.60	15.81	22.36	-2.75E+00	1.06E-06	Down	2.95E-01	4.93E-01		-5.99E+00	3.13E-01		-5.99E+00	4.00E-01		1.50E+00	1.00E-41	Up	2.00E+00	3.05E-89	Up	Unigene24463_All//gi|269838629|gb|ACZ48680.1|//1.00E-148//geraniol 10-hydroxylase [Swertia mussotii]	Unigene24463_All//2.00E-118//AT2G45570| CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene24463_All//0.00E+00//TC143178		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene24464_All	1875	45.07	18.27	31.86	6.93	4.46	2.99	45.78	14.69	15.51	-1.30E+00	3.48E-93	Down	-5.00E-01	5.83E-18		-6.36E-01	9.87E-06		-1.22E+00	2.12E-14	Down	-1.64E+00	6.31E-163	Down	-1.56E+00	3.53E-156	Down	Unigene24464_All//gi|224058639|ref|XP_002296579.1|//1.00E-174//cytochrome P450 [Populus trichocarpa] >gi|222846827|gb|EEE84384.1| cytochrome P450 [Populus trichocarpa]	Unigene24464_All//2.00E-131//AT2G45570| CYP76C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene24464_All//0.00E+00//TC143178		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene24465_All	3772	0.93	1.22	0.65	5.27	9.38	4.54	3.08	0.86	1.28	3.96E-01	1.69E-01		-5.17E-01	1.38E-01		8.31E-01	2.00E-22		-2.16E-01	1.08E-01		-1.83E+00	1.91E-26	Down	-1.27E+00	2.95E-16	Down	Unigene24465_All//gi|15242952|ref|NP_200041.1|//1.00E-138//protein transport protein-related [Arabidopsis thaliana] >gi|10177394|dbj|BAB10525.1| hyaluronan mediated motility receptor-like protein [Arabidopsis thaliana] >gi|47550677|gb|AAT35237.1| At5g52280 [Arabidopsis thaliana] >gi|51970830|dbj|BAD44107.1| hyaluronan mediated motility receptor-like protein [Arabidopsis thaliana]	Unigene24465_All//0.00E+00//AT1G63300| unknown protein	Unigene24465_All//0.00E+00//ES829107				nr +

Unigene24466_All	2401	4.49	1.37	5.39	2.14	1.98	1.24	13.96	15.68	26.23	-1.71E+00	2.34E-18	Down	2.64E-01	1.29E-01		-1.11E-01	7.27E-01		-7.84E-01	2.64E-03		1.68E-01	4.48E-02		9.10E-01	6.50E-49		Unigene24466_All//gi|134032232|gb|ABN50364.2|//1.00E-127//LysM-domain containing receptor-like kinase [Sesbania rostrata]	Unigene24466_All//9.00E-100//AT2G33580| protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	Unigene24466_All//0.00E+00//CA993999		ko04626|Plant-pathogen interaction	GO:0004672//GO:0043170	nr +
Unigene24467_All	2037	8.60	3.51	3.74	6.19	4.46	5.81	3.80	3.12	2.64	-1.29E+00	1.06E-19	Down	-1.20E+00	6.81E-17	Down	-4.71E-01	1.64E-03		-9.10E-02	6.30E-01		-2.84E-01	1.52E-01		-5.25E-01	3.75E-03		Unigene24467_All//gi|115459218|ref|NP_001063209.1|//1.00E-155//Os04g0497900 [Oryza sativa Japonica Group] >gi|38345391|emb|CAD41245.2|OSJNBa0067K08.20 [Oryza sativa (japonica cultivar-group)] >gi|113564780|dbj|BAF15123.1|Os04g0497900 [Oryza sativa Japonica Group]	Unigene24467_All//1.00E-168//AT3G14900| unknown protein	Unigene24467_All//0.00E+00//CO087382			GO:0007275//GO:0009536	nr -
Unigene24469_All	2050	1.51	4.25	1.38	4.76	5.38	4.19	5.01	4.40	5.60	1.50E+00	2.01E-12	Up	-1.29E-01	7.23E-01		1.75E-01	3.82E-01		-1.86E-01	3.90E-01		-1.87E-01	3.00E-01		1.59E-01	3.32E-01		Unigene24469_All//gi|115462993|ref|NP_001055096.1|//4.00E-82//Os05g0287800 [Oryza sativa Japonica Group] >gi|113578647|dbj|BAF17010.1|Os05g0287800 [Oryza sativa Japonica Group]	Unigene24469_All//2.00E-83//AT3G54020| phosphatidic acid phosphatase-related / PAP2-related	Unigene24469_All//0.00E+00//DT051264			GO:0043231	nr -
Unigene2447_All	3572	17.75	9.49	11.70	32.87	29.04	34.34	53.70	27.99	25.47	-9.04E-01	5.31E-39		-6.01E-01	8.83E-19		-1.79E-01	7.41E-05		6.31E-02	2.61E-01		-9.40E-01	2.19E-152		-1.08E+00	1.52E-195	Down	Unigene2447_All//gi|15223829|ref|NP_172913.1|//0.00E+00//TWN2 (TWIN 2); ATP binding / aminoacyl-tRNA ligase/ nucleotide binding / valine-tRNA ligase [Arabidopsis thaliana] >gi|215424252|sp|P93736.2|SYV_ARATH RecName: Full=Valyl-tRNA synthetase; AltName: Full=Valine--tRNA ligase; Short=ValRS	Unigene2447_All//0.00E+00//AT1G14610| TWN2 (TWIN 2); ATP binding / aminoacyl-tRNA ligase/ nucleotide binding / valine-tRNA ligase	Unigene2447_All//0.00E+00//TC166486		ko00970|Aminoacyl-tRNA biosynthesis//ko00290|Valine, leucine and isoleucine biosynthesis	GO:0003006//GO:0004812//GO:0006418//GO:0009536//GO:0032559	nr +
Unigene24470_All	694	2.94	1.61	2.00	4.09	2.13	0.52	2.86	0.12	0.40	-8.72E-01	5.29E-02		-5.60E-01	2.40E-01		-9.39E-01	7.35E-03		-2.97E+00	1.91E-10	Down	-4.57E+00	1.31E-11	Down	-2.83E+00	1.91E-08	Down	Unigene24470_All//gi|297830148|ref|XP_002882956.1|//5.00E-86//phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328796|gb|EFH59215.1|phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24470_All//5.00E-80//AT3G15650| phospholipase/carboxylesterase family protein	Unigene24470_All//0.00E+00//TC141972		ko00564|Glycerophospholipid metabolism	GO:0016788	nr +
Unigene24471_All	1222	1.80	3.03	4.49	9.05	1.86	6.95	4.60	2.26	1.63	7.51E-01	1.87E-02		1.32E+00	1.57E-06	Up	-2.28E+00	5.35E-34	Down	-3.81E-01	2.89E-02		-1.03E+00	5.95E-06	Down	-1.50E+00	2.01E-10	Down	Unigene24471_All//gi|297830148|ref|XP_002882956.1|//1.00E-114//phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328796|gb|EFH59215.1|phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24471_All//6.00E-107//AT3G15650| phospholipase/carboxylesterase family protein	Unigene24471_All//0.00E+00//gi|109860509|gb|DW489488.1|DW489488		ko00564|Glycerophospholipid metabolism		nr +
Unigene24473_All	1470	10.75	11.00	8.01	18.74	19.23	17.42	22.09	14.56	9.95	3.27E-02	8.30E-01		-4.25E-01	3.81E-03		3.74E-02	8.08E-01		-1.05E-01	3.95E-01		-6.02E-01	1.24E-12		-1.15E+00	1.29E-37	Down	Unigene24473_All//gi|297807497|ref|XP_002871632.1|//1.00E-103//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297317469|gb|EFH47891.1|binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene24473_All//8.00E-104//AT5G14790| binding	Unigene24473_All//0.00E+00//TC152784				nr +
Unigene24474_All	2079	40.24	67.58	74.10	23.60	26.07	28.41	14.01	3.90	6.09	7.48E-01	6.69E-62		8.81E-01	3.71E-87		1.44E-01	5.83E-02		2.68E-01	7.46E-05		-1.85E+00	1.20E-65	Down	-1.20E+00	3.71E-36	Down	Unigene24474_All//gi|194595409|gb|ACF77017.1|//0.00E+00//ADP-glucose pyrophosphorylase large subunit [Citrus sinensis]	Unigene24474_All//0.00E+00//AT4G39210| APL3; glucose-1-phosphate adenylyltransferase	Unigene24474_All//0.00E+00//TC136795		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0032559//GO:0070566	nr -
Unigene24475_All	3181	0.44	0.41	0.42	7.83	5.86	4.44	4.77	2.15	2.32	-1.01E-01	8.47E-01		-8.57E-02	8.81E-01		-4.19E-01	3.50E-05		-8.17E-01	2.60E-14		-1.15E+00	2.07E-17	Down	-1.04E+00	1.66E-15	Down	Unigene24475_All//gi|42568402|ref|NP_196685.2|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|264664537|sp|Q5LGV0.1|Y5487_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At5g48740; Flags: Precursor >gi|224589707|gb|ACN59385.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene24475_All//0.00E+00//AT5G48740| leucine-rich repeat family protein / protein kinase family protein	Unigene24475_All//0.00E+00//ES818556		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0032559//GO:0044464	nr +
Unigene24478_All	1549	4.26	4.35	5.26	3.38	4.45	2.83	2.05	1.54	0.72	3.18E-02	9.04E-01		3.06E-01	1.66E-01		3.97E-01	8.21E-02		-2.56E-01	3.94E-01		-4.13E-01	2.08E-01		-1.51E+00	2.64E-06	Down	Unigene24478_All//gi|115442029|ref|NP_001045294.1|//0.00E+00//Os01g0931100 [Oryza sativa Japonica Group] >gi|113534825|dbj|BAF07208.1|Os01g0931100 [Oryza sativa Japonica Group]	Unigene24478_All//0.00E+00//AT5G27730| unknown protein	Unigene24478_All//0.00E+00//DW495169		ko00531|Glycosaminoglycan degradation	GO:0044464	nr -
Unigene24479_All	1465	112.11	53.61	95.30	26.45	24.75	20.62	3.78	3.40	3.73	-1.06E+00	5.44E-131	Down	-2.34E-01	9.30E-09		-9.60E-02	3.37E-01		-3.59E-01	1.80E-05		-1.55E-01	5.60E-01		-2.12E-02	9.48E-01		Unigene24479_All//gi|229609699|gb|ACQ83465.1|//9.00E-51//stress-enhanced protein 4 [Arabidopsis thaliana]	Unigene24479_All//1.00E-41//AT3G12345| unknown protein	Unigene24479_All//0.00E+00//gi|109877695|gb|DW506668.1|DW506668			GO:0043231	nr -
Unigene2448_All	2633	16.04	9.74	8.82	32.52	24.19	21.97	9.84	4.68	6.31	-7.20E-01	5.66E-18		-8.63E-01	2.32E-23		-4.27E-01	4.91E-17		-5.66E-01	3.08E-25		-1.07E+00	3.23E-26	Down	-6.42E-01	9.28E-12		Unigene2448_All//gi|145336402|ref|NP_174715.2|//0.00E+00//EMB2756 (EMBRYO DEFECTIVE 2756) [Arabidopsis thaliana]	Unigene2448_All//3.00E-176//AT4G09630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF616 (InterPro:IPR006852); BEST Arabidopsis thaliana protein match is: EMB2756 (EMBRYO DEFECTIVE 2756) (TAIR:AT1G34850.1); Has 2910 Blast hits to 2214 proteins in 235 species: Archae - 17; Bacteria - 119; Metazoa - 666; Fungi - 192; Plants - 194; Viruses - 70; Other Eukaryotes - 1652 (source: NCBI BLink).	Unigene2448_All//0.00E+00//TC159729				nr -
Unigene24482_All	2111	40.99	35.86	48.26	83.06	81.09	63.43	65.95	43.78	23.59	-1.93E-01	7.08E-04		2.35E-01	9.38E-06		-3.47E-02	4.92E-01		-3.89E-01	6.17E-26		-5.91E-01	6.96E-50		-1.48E+00	1.69E-234	Down	Unigene24482_All//gi|44917449|gb|AS49049.1|//1.00E-109//At4g14840 [Arabidopsis thaliana] >gi|46931278|gb|AAT06443.1|At4g14840 [Arabidopsis thaliana]	Unigene24482_All//4.00E-108//AT3G22520| unknown protein	Unigene24482_All//0.00E+00//TC153186				nr -
Unigene24483_All	278	2.63	2.00	2.68	3.94	5.20	7.47	5.02	1.20	1.58	-3.94E-01	6.11E-01		2.54E-02	9.95E-01		4.00E-01	5.30E-01		9.23E-01	4.23E-02		-2.06E+00	2.51E-04	Down	-1.67E+00	1.27E-03		Unigene24483_All//gi|42565391|ref|NP_189910.2|//5.00E-24//ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis thaliana] >gi|34849889|gb|AAQ82841.1|At3g43240 [Arabidopsis thaliana]	Unigene24483_All//2.00E-25//AT3G43240| ARID/BRIGHT DNA-binding domain-containing protein	Unigene24483_All//2.00E-54//gi|78333893|gb|DT554167.1|DT554167			GO:0003676//GO:0043231//GO:0046914	nr -
Unigene24485_All	1021	42.64	19.55	16.32	52.11	50.89	72.68	94.00	72.74	42.14	-1.12E+00	1.94E-38	Down	-1.39E+00	3.68E-51	Down	-3.40E-02	7.31E-01		4.80E-01	2.51E-16		-3.70E-01	4.04E-15		-1.16E+00	1.97E-110	Down	Unigene24485_All//gi|154269254|gb|ABS72187.1|//1.00E-48//acidic ribosomal protein P3 [Corchorus olitorius]	Unigene24485_All//1.00E-16//AT4G25890| 60S acidic ribosomal protein P3 (RPP3A)	Unigene24485_All//0.00E+00//TC141918		ko03010|Ribosome	GO:0005198//GO:0005840//GO:0006412//GO:0043231	nr +
Unigene24488_All	1476	14.78	8.65	5.63	36.52	27.81	21.20	28.36	10.05	12.50	-7.73E-01	7.64E-11		-1.39E+00	4.33E-26	Down	-3.93E-01	2.03E-09		-7.84E-01	2.93E-28		-1.50E+00	6.89E-70	Down	-1.18E+00	2.72E-50	Down	Unigene24488_All//gi|18417145|ref|NP_567799.1|//1.00E-110//ULT1 (ULTRAPETALA1); DNA binding [Arabidopsis thaliana] >gi|61217374|sp|Q96GZ8.1|ULT1_ARATH RecName: Full=Protein ULTRAPETALA 1 >gi|11074294|gb|AB004520.1|At4g28190 [Arabidopsis thaliana]	Unigene24488_All//4.00E-111//AT4G28190| ULT1 (ULTRAPETALA1); DNA binding	Unigene24488_All//0.00E+00//TC133354	ULT		GO:0043231//GO:0044444	nr +
Unigene24489_All	2101	2.19	2.39	1.12	3.60	1.74	2.95	18.27	15.22	33.22	1.24E-01	6.47E-01		-9.75E-01	9.65E-04		-1.05E+00	9.21E-08	Down	-2.91E-01	2.06E-01		-2.64E-01	7.52E-04		8.62E-01	1.59E-49		Unigene24489_All//gi|50198982|gb|AT70492.1|//1.00E-135//At3g05320 [Arabidopsis thaliana]	Unigene24489_All//5.00E-146//AT3G05320| unknown protein	Unigene24489_All//0.00E+00//TC138243			GO:0008417	nr -
Unigene24490_All	3176	32.65	17.85	18.74	26.57	21.22	11.01	22.25	5.07	10.39	-8.71E-01	1.45E-59		-8.01E-01	6.51E-50		-3.25E-01	3.15E-10		-1.27E+00	2.76E-97	Down	-2.13E+00	8.53E-192	Down	-1.10E+00	5.12E-75	Down	Unigene24490_All//gi|1707642|emb|CAA69028.1|//0.00E+00//TMK [Oryza sativa (indica cultivar-group)]	Unigene24490_All//0.00E+00//AT1G66150| TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase	Unigene24490_All//0.00E+00//TC159022			GO:0004713//GO:0004871//GO:0006464//GO:0031224//GO:0032559//GO:0043231	nr -
Unigene24495_All	1799	6.25	9.97	8.11	9.39	5.76	32.51	15.51	30.88	91.24	6.73E-01	2.85E-07		3.75E-01	1.55E-02		-7.04E-01	1.29E-08		1.79E+00	4.42E-110	Up	9.93E-01	8.45E-49		2.56E+00	0.00E+00	Up	Unigene24495_All//gi|16604352|gb|AL24182.1|//0.00E+00//AT5g12010/F14F18_180 [Arabidopsis thaliana] >gi|25141199|gb|AAN73294.1|At5g12010/F14F18_180 [Arabidopsis thaliana]	Unigene24495_All//0.00E+00//AT5G12010| unknown protein	Unigene24495_All//0.00E+00//TC141075			GO:0009536	nr -
Unigene24497_All	2442	4.50	12.89	6.13	5.63	8.73	7.36	9.23	11.33	6.61	1.52E+00	7.52E-44	Up	4.46E-01	3.15E-03		6.33E-01	1.07E-08		3.87E-01	3.06E-03		2.96E-01	1.55E-03		-4.82E-01	1.56E-06		Unigene24497_All//gi|20147370|gb|AAM10395.1|//1.00E-94//At5g22100/At5g22100 [Arabidopsis thaliana] >gi|23506189|gb|AAN31106.1|At5g22100 [Arabidopsis thaliana]	Unigene24497_All//3.00E-82//AT5G22120| unknown protein	Unigene24497_All//0.00E+00//TC178198				nr -
Unigene24498_All	1360	1.15	2.05	1.37	3.11	2.58	2.69	3.58	2.24	1.20	8.28E-01	2.78E-02		2.48E-01	6.19E-01		-2.70E-01	4.00E-01		-2.11E-01	5.34E-01		-6.72E-01	5.63E-03		-1.57E+00	9.35E-10	Down	Unigene24498_All//gi|20147370|gb|AAM10395.1|//1.00E-95//At5g22100/At5g22100 [Arabidopsis thaliana] >gi|23506189|gb|AAN31106.1|At5g22100 [Arabidopsis thaliana]	Unigene24498_All//3.00E-83//AT5G22120| unknown protein	Unigene24498_All//0.00E+00//TC178198				nr -
Unigene24501_All	1777	9.54	6.19	3.36	17.10	18.29	13.24	32.74	5.88	10.27	-6.25E-01	3.55E-06		-1.51E+00	7.31E-23	Down	9.73E-02	3.93E-01		-3.69E-01	1.23E-04		-2.48E+00	1.95E-189	Down	-1.67E+00	3.54E-117	Down	Unigene24501_All//gi|224139678|ref|XP_002323225.1|//1.00E-158//cyclin b [Populus trichocarpa] >gi|222867855|gb|EEF04986.1|cyclin b [Populus trichocarpa]	Unigene24501_All//4.00E-118//AT5G06150| CYCB1AT; cyclin-dependent protein kinase regulator	Unigene24501_All//0.00E+00//TC133933				nr +

Unigene24502_A11	520	2.11	7.41	0.61	1.72	3.11	4.08	3.01	9.81	12.49	1.81E+00	1.73E-07	Up	-1.78E+00	1.57E-02		8.52E-01	1.06E-01		1.24E+00	5.89E-03		1.70E+00	6.55E-11	Up	2.05E+00	9.12E-18	Up	Unigene24502_A11//gi|14517476|gb|AK62628.1|//6.00E-48//At2g43320/T1024.6 [Arabidopsis thaliana] >gi|20196858|gb|AAB64311.2| expressed protein [Arabidopsis thaliana] >gi|20197145|gb|AAM14937.1| expressed protein [Arabidopsis thaliana] >gi|22136568|gb|AAM91070.1| At2g43320/T1024.6 [Arabidopsis thaliana]	Unigene24502_A11//4.00E-49//AT2G43320| unknown protein	Unigene24502_A11//6.00E-149//DW228030			GO:0043231	nr -
Unigene24503_A11	1491	2.77	12.57	3.96	2.81	5.47	11.15	6.49	22.06	22.12	2.18E+00	6.56E-43	Up	5.16E-01	4.53E-02		9.64E-01	6.26E-07		1.99E+00	3.05E-36	Up	1.76E+00	1.73E-69	Up	1.77E+00	2.38E-71	Up	Unigene24503_A11//gi|14517476|gb|AK62628.1|//1.00E-141//At2g43320/T1024.6 [Arabidopsis thaliana] >gi|20196858|gb|AAB64311.2| expressed protein [Arabidopsis thaliana] >gi|20197145|gb|AAM14937.1| expressed protein [Arabidopsis thaliana] >gi|22136568|gb|AAM91070.1| At2g43320/T1024.6 [Arabidopsis thaliana]	Unigene24503_A11//9.00E-135//AT2G43320| unknown protein	Unigene24503_A11//0.00E+00//DW228030				nr +
Unigene24504_A11	1973	2.10	2.05	2.97	9.32	9.55	9.18	23.62	14.93	11.73	-2.82E-02	9.41E-01		5.03E-01	5.11E-02		3.52E-02	8.25E-01		-2.14E-02	9.06E-01		-6.61E-01	7.42E-21		-1.01E+00	1.99E-43	Down	Unigene24504_A11//gi|270342119|gb|ACZ74702.1|//0.00E+00//kinesin light chain-like protein [Phaseolus vulgaris]	Unigene24504_A11//0.00E+00//AT3G27960| kinesin light chain-related	Unigene24504_A11//0.00E+00//TC143247			GO:0000904//GO:0016020	nr +
Unigene24507_A11	2071	31.96	31.17	45.61	30.93	24.84	22.33	13.45	7.53	2.04	-3.60E-02	6.15E-01		5.13E-01	5.61E-21		-3.16E-01	1.48E-07		-4.70E-01	9.58E-14		-8.38E-01	6.46E-19		-2.72E+00	2.32E-104	Down	Unigene24507_A11//gi|15221382|ref|NP_177616.1|//1.00E-176//nodulin family protein [Arabidopsis thaliana] >gi|5882744|gb|AAD55297.1|AC008263_28 Strong similarity to gb|AF031243 nodule-specific protein (Nlj70) from Lotus japonicus and is a member of the PF|00083 Sugar (and other) transporter family. EST gb|Z37715 comes from this gene [Arabidopsis thaliana]	Unigene24507_A11//3.00E-154//AT1G74780| nodulin family protein	Unigene24507_A11//0.00E+00//TC178612				nr +
Unigene24508_A11	1857	1.83	4.83	3.47	8.42	6.40	6.52	5.78	5.85	3.39	1.40E+00	1.32E-11	Up	9.22E-01	1.44E-04		-3.97E-01	3.12E-03		-3.70E-01	9.21E-03		1.71E-02	9.44E-01		-7.71E-01	4.16E-07		Unigene24508_A11//gi|297828676|ref|XP_002882220.1|//0.00E+00//regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328060|gb|EFH58479.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24508_A11//0.00E+00//AT3G02300| regulator of chromosome condensation (RCC1) family protein	Unigene24508_A11//0.00E+00//CO122041		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene24509_A11	2498	7.88	16.21	15.24	30.31	23.85	28.20	54.31	69.35	51.66	1.04E+00	1.55E-31	Up	9.53E-01	6.75E-25		-3.46E-01	2.36E-10		-1.04E-01	1.27E-01		3.53E-01	2.14E-24		-7.24E-02	9.17E-02		Unigene24509_A11//gi|71153407|sp|Q8LTE3.2|VSR7_ARATH//0.00E+00//RecName: Full=Vacuolar-sorting receptor 7; Short=AtVSR7; AltName: Full=Epidermal growth factor receptor-like protein 3; Short=AtELP3; AltName: Full=BP80-like protein f; Short=AtBP80f; Flags: Precursor	Unigene24509_A11//0.00E+00//AT1G30900| vacuolar sorting receptor, putative	Unigene24509_A11//0.00E+00//TC164699			GO:0004871//GO:0031410//GO:0046872	nr +
Unigene2451_A11	1725	8.04	22.91	10.28	11.03	4.77	3.40	9.76	70.65	21.43	1.51E+00	1.46E-54	Up	3.55E-01	1.08E-02		-1.21E+00	2.10E-23	Down	-1.70E+00	4.47E-34	Down	2.86E+00	0.00E+00	Up	1.14E+00	1.78E-41	Up	Unigene2451_A11//gi|398413350|gb|AAR31185.1|//1.00E-134//serine O-acetyltransferase 1 [Glycine max]	Unigene2451_A11//0.00E+00//AT4G14880| ATSERAT2;2 (SERINE ACETYLTRANSFERASE 2;2); serine O-acetyltransferase	Unigene2451_A11//0.00E+00//gi|78341050|gb|DT561324.1|DT561324		ko00270|Cysteine and methionine metabolism//ko00920|Sulfur metabolism		nr -
Unigene24510_A11	1092	75.18	103.98	52.27	72.17	70.98	70.14	23.81	48.72	33.71	4.68E-01	4.50E-22		-5.24E-01	5.64E-19		-2.39E-02	7.84E-01		-4.10E-02	6.16E-01		1.03E+00	7.56E-50	Up	5.02E-01	9.48E-11		Unigene24510_A11//gi|224069160|ref|XP_002326289.1|//4.00E-53//copper transporter [Populus trichocarpa] >gi|222833482|gb|EEE71959.1| copper transporter [Populus trichocarpa]	Unigene24510_A11//4.00E-37//AT5G20650| COPT5; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter	Unigene24510_A11//0.00E+00//gi|109877013|gb|DW505987.1|DW505987			GO:0000041//GO:0005375//GO:0031224//GO:0043231	nr +
Unigene24511_A11	1421	12.56	4.42	7.46	17.63	12.60	12.68	137.52	49.12	33.73	-1.51E+00	5.29E-25	Down	-7.52E-01	3.24E-08		-4.85E-01	1.22E-06		-4.76E-01	6.79E-06		-1.49E+00	0.00E+00	Down	-2.03E+00	0.00E+00	Down	Unigene24511_A11//gi|151547430|gb|ABS12459.1|//1.00E-169//cysteine protease Cp [Citrus sinensis]	Unigene24511_A11//2.00E-166//AT3G45310| cysteine proteinase, putative	Unigene24511_A11//0.00E+00//TC134773				nr -
Unigene24513_A11	750	9.98	56.95	37.84	4.72	13.50	21.56	18.27	11.26	8.92	2.51E+00	5.52E-115	Up	1.92E+00	1.38E-53	Up	1.52E+00	1.09E-16	Up	2.19E+00	7.37E-40	Up	-6.98E-01	2.62E-07		-1.03E+00	6.78E-14	Down	Unigene24513_A11//gi|297828756|ref|XP_002882260.1|//8.00E-69//UPF0131 protein At3g02910 [Arabidopsis lyrata subsp. lyrata] >gi|297328100|gb|EFH58519.1| UPF0131 protein At3g02910 [Arabidopsis lyrata subsp. lyrata]	Unigene24513_A11//1.00E-69//AT3G02910| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Butirosin biosynthesis, BtrG-like (InterPro:IPR013024), AIG2-like (InterPro:IPR009288); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G46720.1); Has 210 Blast hits to 210 proteins in 66 species: Archae - 2; Bacteria - 27; Metazoa - 122; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink).	Unigene24513_A11//0.00E+00//TC145941				nr -
Unigene24514_A11	823	5.09	4.56	1.62	7.99	9.29	7.08	32.26	26.87	22.85	-1.59E-01	6.02E-01		-1.65E+00	7.05E-07	Down	2.17E-01	3.61E-01		-1.75E-01	5.10E-01		-2.64E-01	6.31E-03		-4.98E-01	6.13E-08		Unigene24514_A11//gi|17381236|gb|AL36037.1|//4.00E-66//AT3g02910/F13E7_14 [Arabidopsis thaliana] >gi|21464585|gb|AAM52247.1| AT3g02910/F13E7_14 [Arabidopsis thaliana]	Unigene24514_A11//2.00E-67//AT3G02910| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Butirosin biosynthesis, BtrG-like (InterPro:IPR013024), AIG2-like (InterPro:IPR009288); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G46720.1); Has 210 Blast hits to 210 proteins in 66 species: Archae - 2; Bacteria - 27; Metazoa - 122; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink).	Unigene24514_A11//0.00E+00//TC145941				nr -
Unigene24515_A11	796	25.37	127.88	78.94	12.64	26.78	51.92	6.64	13.44	10.66	2.33E+00	1.28E-250	Up	1.64E+00	1.25E-94	Up	1.08E+00	6.38E-21	Up	2.04E+00	2.15E-92	Up	1.02E+00	1.97E-10	Up	6.83E-01	7.63E-05		Unigene24515_A11//gi|17381236|gb|AL36037.1|//5.00E-66//AT3g02910/F13E7_14 [Arabidopsis thaliana] >gi|21464585|gb|AAM52247.1| AT3g02910/F13E7_14 [Arabidopsis thaliana]	Unigene24515_A11//4.00E-62//AT3G02910| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Butirosin biosynthesis, BtrG-like (InterPro:IPR013024), AIG2-like (InterPro:IPR009288); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G46720.1); Has 210 Blast hits to 210 proteins in 66 species: Archae - 2; Bacteria - 27; Metazoa - 122; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink).	Unigene24515_A11//0.00E+00//gi|164287999|gb|ES791418.1|ES791418				nr -
Unigene24517_A11	516	0.81	1.08	0.00	5.21	3.60	2.89	5.82	2.35	2.55	4.13E-01	6.37E-01		-9.66E+00	1.56E-02		-5.33E-01	1.63E-01		-8.52E-01	2.65E-02		-1.31E+00	7.84E-05	Down	-1.19E+00	1.84E-04	Down	Unigene24517_A11//gi|9798385|emb|CAC03532.1|//2.00E-49//non-phototropic hypocotyl 3-like protein [Arabidopsis thaliana]	Unigene24517_A11//9.00E-51//AT3G14820| protein binding / signal transducer	Unigene24517_A11//0.00E+00//gi|84171069|gb|DR459717.1|DR459717			GO:0005488//GO:0009314//GO:0060089	nr +
Unigene24519_A11	2457	1.75	1.59	1.32	9.25	6.92	3.16	5.54	3.40	5.32	-1.37E-01	6.35E-01		-4.02E-01	2.06E-01		-4.17E-01	9.47E-05		-1.55E+00	1.31E-35	Down	-7.04E-01	2.34E-07		-5.92E-02	6.90E-01		Unigene24519_A11//gi|24025550|ref|NP_190068.4|//1.00E-155//protein binding / signal transducer [Arabidopsis thaliana]	Unigene24519_A11//2.00E-148//AT3G14820| protein binding / signal transducer	Unigene24519_A11//0.00E+00//TC146301			GO:0005488//GO:0009314//GO:0060089	nr +
Unigene2452_A11	2416	4.59	6.44	6.79	17.34	16.25	18.13	14.88	1.85	7.27	4.88E-01	5.67E-04		5.64E-01	6.99E-05		-9.38E-02	3.25E-01		6.45E-02	5.32E-01		-3.01E+00	1.46E-144	Down	-1.03E+00	5.93E-35	Down	Unigene2452_A11//gi|297810457|ref|XP_002873112.1|//0.00E+00//ATCSLA09 [Arabidopsis lyrata subsp. lyrata] >gi|297318949|gb|EFH49371.1| ATCSLA09 [Arabidopsis lyrata subsp. lyrata]	Unigene2452_A11//0.00E+00//AT5G03760| ATCSLA09; mannan synthase/ transferase, transferring glycosyl groups	Unigene2452_A11//0.00E+00//TC136449				nr -
Unigene24520_A11	1712	24.97	7.52	12.10	37.36	34.64	28.02	20.82	6.32	9.19	-1.73E+00	4.91E-72	Down	-1.05E+00	2.33E-32	Down	-1.09E-01	1.31E-01		-4.15E-01	4.83E-11		-1.72E+00	9.79E-73	Down	-1.18E+00	8.40E-43	Down	Unigene24520_A11//gi|126201|sp|P29102.1|LEU3_BRANA//0.00E+00//RecName: Full=3-isopropylmalate dehydrogenase, chloroplastic; Short=3-IPM-DH; Short=IMDH; AltName: Full=Beta-IPM dehydrogenase; Flags: Precursor >gi|17827|emb|CAA42596.1| 3-isopropylmalate dehydrogenase [Brassica napus]	Unigene24520_A11//0.00E+00//AT1G80560| 3-isopropylmalate dehydrogenase, chloroplast, putative	Unigene24520_A11//0.00E+00//gi|78353335|gb|DT573609.1|DT573609		ko00290|Valine, leucine and isoleucine biosynthesis	GO:0000166//GO:0000551//GO:0008652//GO:0009536//GO:0016616//GO:0046872	nr -
Unigene24524_A11	2575	10.83	21.94	8.02	1.08	2.03	0.98	0.23	0.37	0.08	1.02E+00	3.26E-42	Up	-4.33E-01	4.54E-05		9.08E-01	2.91E-04		-1.41E-01	7.15E-01		6.99E-01	2.78E-01		-1.57E+00	6.49E-02		Unigene24524_A11//gi|297726167|ref|NP_001175417.1|//1.00E-171//Os08g0230800 (Oryza sativa Japonica Group) >gi|255678252|dbj|BAH94175.1| Os08g0230800 (Oryza sativa Japonica Group)	Unigene24524_A11//1.00E-115//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene24524_A11//0.00E+00//TC175564		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674//GO:0004871//GO:0009987	nr -

Unigene24525_All	1447	12.66	93.60	21.20	11.77	20.80	34.93	34.57	78.22	298.58	2.89E+00	0.00E+00	Up	7.44E-01	1.92E-13		8.21E-01	9.73E-19		1.57E+00	7.20E-79	Up	1.18E+00	6.02E-130	Up	3.11E+00	0.00E+00	Up	Unigene24525_All//gi|225446337|ref|XP_002272136.1|//5.00E-81//PREDICTED: similar to ring domain containing protein isoform 2 [Vitis vinifera] >gi|225446339|ref|XP_002272107.1|PREDICTED: similar to ring domain containing protein isoform 1 [Vitis vinifera]	Unigene24525_All//4.00E-53//AT4G03510| RMA1; protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene24525_All//0.00E+00//TC161722		ko04146|Peroxisome	GO:0006511//GO:0006886//GO:0006950//GO:0009725//GO:0019787//GO:0031090//GO:0032146//GO:0043231//GO:0046872//GO:0046903	nr -
Unigene24526_All	2443	11.78	14.71	18.66	4.02	5.89	6.36	0.80	6.26	11.19	3.20E-01	3.80E-04		6.64E-01	3.36E-16		5.53E-01	7.10E-05		6.63E-01	1.66E-06		2.98E+00	5.33E-61	Up	3.81E+00	7.86E-138	Up	Unigene24526_All//gi|73624747|gb|AAZ79231.1|/1.00E-131//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene24526_All//4.00E-119//AT4G24000| ATCSLG2; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	Unigene24526_All//0.00E+00//gi|73862999|gb|DT465738.1|DT465738			GO:0009987//GO:0016020//GO:0016757	nr +
Unigene24528_All	3281	2.89	1.03	1.67	10.54	9.33	5.44	8.61	3.17	3.52	-1.48E+00	2.71E-13	Down	-7.88E-01	4.86E-05		-1.75E-01	6.60E-02		-9.55E-01	2.17E-25		-1.44E+00	7.89E-45	Down	-1.29E+00	4.07E-39	Down	Unigene24528_All//gi|115452131|ref|NP_001049666.1|/1.00E-63//Os03g0267600 [Oryza sativa Japonica Group] >gi|108707365|gb|ABF95160.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548137|dbj|BAF11580.1|Os03g0267600 [Oryza sativa Japonica Group]	Unigene24528_All//3.00E-79//AT5G01030| unknown protein	Unigene24528_All//0.00E+00//TC153922				nr +
Unigene2453_All	2312	2.51	1.12	1.91	4.98	5.36	3.16	11.23	8.04	7.81	-1.17E+00	4.02E-06	Down	-3.94E-01	1.41E-01		1.07E-01	5.85E-01		-6.53E-01	6.19E-05		-4.81E-01	4.04E-07		-5.25E-01	1.80E-08		Unigene2453_All//gi|224085587|ref|XP_002307628.1|/0.00E+00//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222857077|gb|EEE94624.1|glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene2453_All//0.00E+00//AT1G06780| GAUT6 (Galacturonosyltransferase 6); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups	Unigene2453_All//0.00E+00//TC134871				nr +
Unigene24534_All	1213	22.95	13.62	20.98	10.92	11.84	11.65	4.88	2.07	4.73	-7.53E-01	4.85E-13		-1.29E-01	2.81E-01		1.16E-01	5.33E-01		9.33E-02	6.35E-01		-1.24E+00	4.06E-08	Down	-4.52E-02	8.50E-01		Unigene24534_All//gi|122194126|sp|Q1R376.1|PMM_SOYBN//1.00E-116//RecName: Full=Phosphomannomutase; AltName: Full=GmPMM >gi|90762150|gb|ABD97873.1|phosphomannomutase [Glycine max]	Unigene24534_All//4.00E-100//AT2G45790| PMM (PHOSPHOMANNOMUTASE); phosphomannomutase	Unigene24534_All//0.00E+00//TC138832		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene24535_All	1509	17.41	24.71	18.60	21.49	21.04	24.81	14.85	8.89	6.68	5.06E-01	7.50E-09		9.55E-02	4.20E-01		-3.06E-02	8.20E-01		2.07E-01	2.38E-02		-7.40E-01	1.42E-12		-1.15E+00	2.73E-26	Down			Unigene24535_All//0.00E+00//BQ405645				
Unigene24536_All	1631	4.72	5.22	3.30	5.25	5.76	8.06	4.90	3.00	1.61	1.46E-01	5.03E-01		-5.16E-01	1.92E-02		1.34E-01	5.54E-01		6.17E-01	4.98E-05		-7.09E-01	1.05E-04		-1.60E+00	6.91E-16	Down			Unigene24536_All//0.00E+00//BQ405645				
Unigene24539_All	2275	14.67	2.63	5.17	17.19	18.06	23.03	10.70	0.88	3.64	-2.48E+00	2.30E-89	Down	-1.50E+00	1.90E-44	Down	7.12E-02	5.08E-01		4.22E-01	2.29E-09		-3.60E+00	7.72E-116	Down	-1.56E+00	1.17E-44	Down	Unigene24539_All//gi|18405677|ref|NP_566835.1|//0.00E+00//ATCSLC04 (CELLULOSE-SYNTHASE LIKE C4); cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75273615|sp|Q9LJP4.1|CSLC4_ARATH RecName: Full=Xyloglucan glycosyltransferase 4; AltName: Full=Xyloglucan synthase 4; AltName: Full=Cellulose synthase-like protein C4; Short=AtCslC4 >gi|9279781|dbj|BAB01433.1|glucosyltransferase-like protein [Arabidopsis thaliana]	Unigene24539_All//0.00E+00//AT3G28180| ATCSLC04 (CELLULOSE-SYNTHASE LIKE C4); cellulose synthase/ transferase, transferring glycosyl groups	Unigene24539_All//0.00E+00//TC163491			GO:0016020//GO:0016759//GO:0043231	nr -
Unigene24542_All	1430	1.83	1.56	0.60	2.89	2.00	2.05	2.69	1.58	1.64	-2.31E-01	5.78E-01		-1.62E+00	1.90E-04	Down	-5.33E-01	6.87E-02		-4.94E-01	1.10E-01		-7.70E-01	5.61E-03		-7.11E-01	8.01E-03		Unigene24542_All//gi|224068552|ref|XP_002326143.1|/1.00E-52//SAUR family protein [Populus trichocarpa] >gi|222833336|gb|EEE71813.1| SAUR family protein [Populus trichocarpa]	Unigene24542_All//6.00E-51//AT3G43120| auxin-responsive protein-related	Unigene24542_All//0.00E+00//ES826125			GO:0005515//GO:0009725//GO:0042579	nr +
Unigene24545_All	1118	4.59	2.99	5.00	10.34	7.42	4.73	12.14	6.88	4.17	-6.17E-01	1.97E-02		1.25E-01	6.32E-01		-4.78E-01	2.42E-03		-1.13E+00	1.65E-11	Down	-8.20E-01	2.60E-09		-1.54E+00	5.80E-25	Down	Unigene24545_All//gi|157863708|gb|ABV90875.1|/1.00E-90//inositol-1,4,5-triphosphate-5-phosphatase [Solanum lycopersicum]	Unigene24545_All//1.00E-90//AT4G18010| AT5PTASE2 (MYO-INOSITOL POLYPHOSPHATE 5-PHOSPHATASE 2); inositol-polyphosphate 5-phosphatase	Unigene24545_All//0.00E+00//gi|48811631|gb|CO112944.1|CO112944			GO:0009725//GO:0016628//GO:0032501//GO:0043231//GO:0043647//GO:0046030	nr +
Unigene24546_All	1313	5.82	6.48	7.26	13.54	9.94	9.08	5.70	3.72	2.82	1.56E-01	4.70E-01		3.19E-01	1.15E-01		-4.46E-01	2.72E-04		-5.77E-01	6.16E-06		-6.14E-01	1.21E-03		-1.01E+00	8.84E-08	Down	Unigene24546_All//gi|157863708|gb|ABV90875.1|/3.00E-47//inositol-1,4,5-triphosphate-5-phosphatase [Solanum lycopersicum]	Unigene24546_All//2.00E-43//AT4G18010| AT5PTASE2 (MYO-INOSITOL POLYPHOSPHATE 5-PHOSPHATASE 2); inositol-polyphosphate 5-phosphatase	Unigene24546_All//0.00E+00//TC145892			GO:0009725//GO:0016628//GO:0032501//GO:0043231//GO:0043647//GO:0046030	nr +
Unigene24549_All	857	2.14	1.54	2.17	4.48	3.94	5.06	6.22	7.80	2.88	-4.75E-01	3.32E-01		2.54E-02	9.77E-01		-1.85E-01	5.94E-01		1.77E-01	6.28E-01		3.28E-01	1.26E-01		-1.11E+00	1.47E-06	Down			Unigene24549_All//0.00E+00//DW239666				
Unigene2455_All	1339	12.00	12.90	5.89	15.85	16.36	16.32	30.82	23.25	16.81	1.05E-01	4.88E-01		-1.03E+00	3.46E-12	Down	4.55E-02	7.86E-01		4.27E-02	7.57E-01		-4.06E-01	3.75E-08		-8.74E-01	1.63E-30		Unigene2455_All//gi|255570669|ref|XP_002526289.1|//1.00E-154//ER Phosphatidate Phosphatase [Ricinus communis] >gi|223534370|gb|EEF36078.1| ER Phosphatidate Phosphatase [Ricinus communis]	Unigene2455_All//8.00E-133//AT1G15080| LPP2 (LIPID PHOSPHATE PHOSPHATASE 2); acid phosphatase/ phosphatidate phosphatase	Unigene2455_All//0.00E+00//TC152384		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism//ko00600|Sphingolipid metabolism		nr -
Unigene24550_All	2345	5.93	4.58	4.02	6.80	8.83	6.43	6.54	4.28	2.48	-3.74E-01	1.42E-02		-5.62E-01	3.12E-04		3.77E-01	1.15E-03		-7.96E-02	6.38E-01		-6.14E-01	1.33E-06		-1.40E+00	1.88E-24	Down	Unigene24550_All//gi|297317194|gb|EFH47616.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317194|gb|EFH47616.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24550_All//4.00E-117//AT5G08750| zinc finger (C3HC4-type RING finger) family protein	Unigene24550_All//0.00E+00//TC139313			GO:0044464	nr +
Unigene24554_All	3029	22.08	66.31	48.77	8.19	14.78	16.22	19.21	14.89	49.52	1.59E+00	2.52E-295	Up	1.14E+00	1.69E-128	Up	8.52E-01	1.82E-29		9.86E-01	2.06E-37		-3.67E-01	2.18E-09		1.37E+00	3.95E-221	Up	Unigene24554_All//gi|30681308|ref|NP_566373.2|//0.00E+00//sporulation protein-related [Arabidopsis thaliana]	Unigene24554_All//0.00E+00//AT3G10420| sporulation protein-related	Unigene24554_All//0.00E+00//gi|78342146|gb|DT562420.1|DT562420			GO:0009536//GO:0016462//GO:0032559	nr -
Unigene24555_All	316	2.15	2.24	4.72	3.78	2.72	9.00	1.07	1.59	0.63	6.06E-02	9.57E-01		1.13E+00	4.89E-02		-4.74E-01	4.58E-01		1.25E+00	9.51E-04	Up	5.68E-01	5.63E-01		-7.64E-01	5.01E-01		Unigene24555_All//gi|297738153|emb|CBI27354.3|//6.00E-08//unnamed protein product [Vitis vinifera]	Unigene24555_All//6.00E-05//AT1G65950| ABC1 family protein	Unigene24555_All//2.00E-89//gi|5048826|gb|AIT29974.1|AIT29974				nr +
Unigene24557_All	1348	8.89	80.48	29.55	26.57	24.29	48.08	58.37	82.51	30.85	3.18E+00	0.00E+00	Up	1.73E+00	4.17E-65	Up	-1.29E-01	1.95E-01		8.56E-01	7.02E-39		4.99E-01	1.20E-29		-9.20E-01	2.13E-62		Unigene24557_All//gi|20196907|gb|AB67625.2|/1.00E-149//expressed protein [Arabidopsis thaliana]	Unigene24557_All//4.00E-151//AT2G34070| unknown protein	Unigene24557_All//0.00E+00//TC133530				nr -
Unigene24558_All	962	35.46	16.17	15.78	36.14	31.43	37.70	26.90	21.55	18.18	-1.13E+00	1.28E-30	Down	-1.17E+00	6.04E-31	Down	-2.02E-01	2.90E-02		6.08E-02	6.15E-01		-3.20E-01	9.20E-04		-5.65E-01	1.55E-09		Unigene24558_All//gi|297795569|ref|XP_002865669.1|/4.00E-97//60S ribosomal protein L13A [Arabidopsis lyrata subsp. lyrata] >gi|297311504|gb|EFH19928.1| 60S ribosomal protein L13A [Arabidopsis lyrata subsp. lyrata]	Unigene24558_All//1.00E-89//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene24558_All//0.00E+00//TC135282		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene24559_All	1741	8.26	6.11	6.48	19.40	12.48	18.16	31.79	20.84	15.15	-4.35E-01	3.35E-03		-3.50E-01	2.61E-02		-6.36E-01	4.87E-14		-9.53E-02	3.93E-01		-6.09E-01	2.09E-21		-1.07E+00	1.91E-56	Down	Unigene24559_All//gi|18405716|ref|NP_565950.1|//0.00E+00//GPT (UDP-GLCNAC%3ADOLICHOL+PHOSPHATE+GLCNAC-1-P+TRANSFERASE); UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis thaliana] >gi|15724328|gb|AAL06557.1|AF412104_1 T26J13.8/T26J13.8 [Arabidopsis thaliana] >gi|5804772|dbj|BAA83586.1| UDP-GlcNAc:dolichol phosphate N-acetylglucosamine-1-phosphate transferase [Arabidopsis thaliana] >gi|5804774|dbj|BAA83587.1| UDP-GlcNAc:dolichol phosphate N-acetylglucosamine-1-phosphate transferase [Arabidopsis thaliana] >gi|19699118|gb|AAL90925.1|T26J13.8/T26J13.8 [Arabidopsis thaliana]	Unigene24559_All//3.00E-158//AT2G41490| GPT (UDP-GLCNAC%3ADOLICHOL+PHOSPHATE+GLCNAC-1-P+TRANSFERASE); UDP-N-acetylglucosamine-dolichyl-phosphate N-acetylglucosaminephosphotransferase	Unigene24559_All//0.00E+00//TC158507		ko00510|N-Glycan biosynthesis	GO:0016780	nr +
Unigene24560_All	2590	3.15	2.64	2.76	23.41	18.39	9.57	3.67	0.86	0.54	-2.55E-01	2.36E-01		-1.94E-01	3.97E-01		-3.48E-01	1.70E-08		-1.29E+00	1.39E-71	Down	-2.10E+00	6.30E-26	Down	-2.77E+00	8.64E-37	Down	Unigene24560_All//gi|8778601|gb|AAF79609.1|AC027665_10//1.00E-113//F5M15.15 [Arabidopsis thaliana]	Unigene24560_All//5.00E-87//AT1G20530| unknown protein	Unigene24560_All//0.00E+00//TC159593				nr +
Unigene24561_All	776	0.40	0.26	0.69	3.34	2.04	1.28	0.82	0.65	0.21	-6.31E-01	6.22E-01		7.63E-01	4.53E-01		-7.10E-01	6.00E-02		-1.38E+00	5.34E-04	Down	-3.39E-01	6.63E-01		-1.99E+00	2.04E-02				Unigene24561_All//1.00E-83//ES819997				
Unigene24562_All	1116	82.04	48.63	70.76	375.88	279.00	160.58	145.56	112.02	77.50	-7.55E-01	2.59E-41		-2.13E-01	1.74E-04		-4.30E-01	2.32E-83		-1.23E+00	0.00E+00	Down	-3.78E-01	5.40E-26		-9.09E-01	1.73E-125		Unigene24562_All//gi|20269051|emb|CAC84706.1|//1.00E-101//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene24562_All//8.00E-64//AT2G22670| IAA8; transcription factor	Unigene24562_All//0.00E+00//TC135490			GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr +
Unigene24563_All	1896	4.08	4.60	2.19	24.96	28.99	15.48	27.43	3.20	14.58	1.71E-01	4.14E-01		-8.99E-01	3.92E-05		2.16E-01	1.91E-03		-6.89E-01	5.95E-20		-3.10E+00	1.58E-215	Down	-9.12E-01	6.23E-41		Unigene24563_All//gi|14531294|gb|AAK66160.1|/1.00E-169//pectate lyase B [Fragaria x ananassa] >gi|71390451|gb|AAZ31565.1|pectate lyase isoform 3 [Fragaria x ananassa]	Unigene24563_All//1.00E-149//AT5G48900| pectate lyase family protein	Unigene24563_All//0.00E+00//gi|78336071|gb|DT556345.1|DT556345		ko00040|Pentose and glucuronate interconversions		nr -
Unigene24564_All	1928	47.98	75.74	19.08	37.05	32.70	42.33	39.39	77.46	84.24	6.59E-01	1.41E-51		-1.33E+00	7.21E-102	Down	-1.80E-01	2.99E-03		1.92E-01	9.58E-04		9.76E-01	3.63E-126		1.10E+00	1.11E-169	Up	Unigene24564_All//gi|195976673|dbj|BAG68575.1|//3.00E-23//arginine decarboxylase [Prunus persica]	Unigene24564_All//2.00E-11//AT2G16500| ADC1 (ARGININE DECARBOXYLASE 1); arginine decarboxylase	Unigene24564_All//0.00E+00//gi|21097947|gb|BQ410260.1|BQ410260		ko00330|Arginine and proline metabolism	GO:0006596//GO:0016831	nr +
Unigene24565_All	1829	5.58	12.49	7.28	6.70	10.17	10.62	14.61	21.05	35.35	1.16E+00	1.55E-21	Up	3.84E-01	1.87E-02		6.02E-01	4.79E-07		6.64E-01	5.37E-08		5.27E-01	7.91E-12		1.27E+00	3.96E-86	Up	Unigene24565_All//gi|18406410|ref|NP_564750.1|//1.00E-143//CW14 [Arabidopsis thaliana] >gi|8778748|gb|AAF79756.1|AC009317_15 T30E16.22 [Arabidopsis thaliana] >gi|6520233|dbj|BAA87958.1| CW14 [Arabidopsis thaliana]	Unigene24565_All//1.00E-139//AT1G59650| CW14	Unigene24565_All//0.00E+00//gi|73860290|gb|DT463029.1|DT463029				nr +
Unigene2457_All	1099	1.29	137.35	45.79	5.17	40.73	78.70	23.74	48.87	232.47	6.74E+00	0.00E+00	Up	5.15E+00	8.97E-242	Up	2.98E+00	3.66E-168	Up	3.93E+00	0.00E+00	Up	1.04E+00	5.23E-51	Up	3.29E+00	0.00E+00	Up	Unigene2457_All//gi|296278600|gb|ADH04264.1|/6.00E-59//HB1 [Nicotiana benthamiana]	Unigene2457_All//6.00E-50//AT3G61890| ATHB-12 (ARABIDOPSIS THALIANA HOMEOBOX 12); transcription activator/ transcription factor	Unigene2457_All//0.00E+00//TC136825	HB			nr +
Unigene24570_All	2743	7.71	3.86	5.01	14.95	12.68	10.11	18.07	9.07	8.77	-9.97E-01	8.73E-16		-6.22E-01	4.50E-07		-2.37E-01	3.38E-03		-5.64E-01	2.49E-12		-9.95E-01	8.81E-44		-1.04E+00	1.41E-48	Down	Unigene24570_All//gi|4914320|gb|AAD32868.1|AC005489_6//0.00E+00//F14N23.6 [Arabidopsis thaliana]	Unigene24570_All//0.00E+00//AT1G10180| unknown protein	Unigene24570_All//0.00E+00//TC170182				nr +
Unigene24571_All	2091	3.93	10.44	4.33	7.98	11.84	10.80	12.25	17.47	26.06	1.41E+00	1.55E-27	Up	1.40E-01	5.27E-01		5.69E-01	2.17E-08		4.36E-01	1.14E-04		5.12E-01	9.83E-11		1.09E+00	8.26E-57	Up	Unigene24571_All//gi|3287693|gb|AAC25521.1|//0.00E+00//Similar to LIM17 gene product gb|1653769 from the genome of Synechocystis sp. gb|D90916 [Arabidopsis thaliana]	Unigene24571_All//0.00E+00//AT4G09510| beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative	Unigene24571_All//0.00E+00//TC152907			GO:0004553	nr -
Unigene24576_All	1380	10.58	6.87	11.46	3.72	9.83	8.18	8.46	7.87	4.56	-6.24E-01	2.01E-05		1.16E-01	4.79E-01		1.40E+00	6.99E-20	Up	1.14E+00	3.08E-11	Up	-1.03E-01	5.76E-01		-8.91E-01	1.54E-09		Unigene24576_All//gi|222424621|dbj|BAH20265.1|//1.00E-47//AT1G28100 [Arabidopsis thaliana]	Unigene24576_All//5.00E-49//AT1G28100| unknown protein	Unigene24576_All//8.00E-166//TC158820			GO:0016830	nr +

Unigene24580_All	1304	97.22	452.41	175.72	12.00	32.06	43.15	2.30	5.42	5.93	2.22E+00	0.00E+00	Up	8.54E-01	7.23E-123		1.42E+00	8.31E-62	Up	1.85E+00	2.26E-110	Up	1.23E+00	1.81E-09	Up	1.36E+00	3.56E-12	Up	Unigene24580_All//gi|115456091|ref|NP_001051646.1|//1.00E-51//0s03g0807900 [Oryza sativa Japonica Group] >gi|108711663|gb|ABF99458.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550117|dbj|BAF13560.1| Os03g0807900 [Oryza sativa Japonica Group]	Unigene24580_All//3.00E-50//AT5G19855| unknown protein	Unigene24580_All//0.00E+00//TC140954			GO:0043231	nr -
Unigene24581_All	1564	18.97	90.62	40.41	3.89	8.50	9.39	0.19	1.12	1.02	2.26E+00	0.00E+00	Up	1.09E+00	3.46E-51	Up	1.13E+00	4.64E-14	Up	1.27E+00	4.26E-17	Up	2.57E+00	1.41E-06	Up	2.43E+00	7.10E-06	Up	Unigene24581_All//gi|115456091|ref|NP_001051646.1|//3.00E-23//0s03g0807900 [Oryza sativa Japonica Group] >gi|108711663|gb|ABF99458.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550117|dbj|BAF13560.1| Os03g0807900 [Oryza sativa Japonica Group]	Unigene24581_All//3.00E-35//AT5G19855| unknown protein	Unigene24581_All//0.00E+00//TC133036			GO:0043231	nr +
Unigene24583_All	2158	2.06	1.13	0.64	3.95	3.24	3.96	4.08	1.84	5.58	-8.71E-01	2.44E-03		-1.68E+00	1.92E-07	Down	-2.85E-01	1.65E-01		3.00E-03	9.89E-01		-1.15E+00	1.98E-10	Down	4.52E-01	1.47E-03		Unigene24583_All//gi|95147298|gb|AB957284.1|//1.00E-155//At4g17430 [Arabidopsis thaliana]	Unigene24583_All//2.00E-145//AT4G17430| unknown protein	Unigene24583_All//0.00E+00//CO085561				nr -
Unigene24584_All	1659	10.85	25.23	10.50	21.08	49.19	26.57	21.03	29.85	48.63	1.22E+00	1.08E-41	Up	-4.77E-02	7.47E-01		1.22E+00	2.87E-96	Up	3.34E-01	2.07E-05		5.06E-01	5.65E-14		1.21E+00	7.38E-99	Up	Unigene24584_All//gi|297814706|ref|XP_002875236.1|//1.00E-176//phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321074|gb|EFH51495.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24584_All//2.00E-170//AT2G03890| phosphatidylinositol 3- and 4-kinase family protein	Unigene24584_All//0.00E+00//TC157642			GO:0016772	nr -
Unigene24585_All	1886	32.74	10.29	14.74	9.54	7.08	9.24	3.36	1.09	1.94	-1.67E+00	1.44E-98	Down	-1.15E+00	2.39E-54	Down	-4.29E-01	4.58E-04		-4.48E-02	7.68E-01		-1.63E+00	1.21E-12	Down	-7.91E-01	9.92E-05		Unigene24585_All//gi|225439231|ref|XP_002271046.1|//0.00E+00//PREDICTED: similar to 0s02g0125100 [Vitis vinifera]	Unigene24585_All//0.00E+00//AT4G13430| IIL1 (ISOPROPYL MALATE ISOMERASE LARGE SUBUNIT 1): 4 iron, 4 sulfur cluster binding / hydro-lyase/ lyase	Unigene24585_All//0.00E+00//TC152002		ko00290|Valine, leucine and isoleucine biosynthesis//ko00660|C5-Branched dibasic acid metabolism	GO:0006520//GO:0009532//GO:0010038//GO:0016836//GO:0016866//GO:0019758//GO:0051536	nr +
Unigene24590_All	2123	4.21	1.77	1.40	10.84	10.87	3.66	2.39	0.45	0.51	-1.25E+00	5.74E-10	Down	-1.59E+00	3.15E-13	Down	3.60E-03	9.82E-01		-1.57E+00	1.04E-36	Down	-2.40E+00	1.57E-16	Down	-2.24E+00	8.69E-16	Down	Unigene24590_All//gi|9757828|dbj|BAB08265.1|//0.00E+00//receptor kinase-like protein [Arabidopsis thaliana] >gi|224589693|gb|ACN59378.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene24590_All//0.00E+00//AT5G43020| leucine-rich repeat transmembrane protein kinase, putative	Unigene24590_All//0.00E+00//TC176293			GO:0004672//GO:0006464//GO:0007167//GO:0032559	nr -
Unigene24591_All	1981	1.93	0.90	2.96	5.00	3.65	2.62	1.54	6.03	6.40	-1.11E+00	5.07E-04	Down	6.17E-01	1.58E-02		-4.55E-01	8.92E-03		-9.33E-01	1.90E-07		1.97E+00	8.19E-30	Up	2.06E+00	5.58E-34	Up	Unigene24591_All//gi|115445023|ref|NP_001046291.1|//1.00E-154//0s02g0215700 [Oryza sativa Japonica Group] >gi|113535822|dbj|BAF08205.1| Os02g0215700 [Oryza sativa Japonica Group]	Unigene24591_All//5.00E-116//AT3G47090| leucine-rich repeat transmembrane protein kinase, putative	Unigene24591_All//0.00E+00//TC176293		ko04626|Plant-pathogen interaction		nr +
Unigene24594_All	1930	10.68	16.22	10.35	13.65	14.06	19.26	13.32	23.22	33.07	6.03E-01	4.35E-10		-4.59E-02	7.38E-01		4.23E-02	7.78E-01		4.96E-01	5.57E-09		8.02E-01	9.23E-28		1.31E+00	7.54E-89	Up	Unigene24594_All//gi|15237625|ref|NP_198949.1|//1.00E-160//potassium channel tetramerisation domain-containing protein [Arabidopsis thaliana] >gi|54606858|gb|AAY34777.1| At5g41330 [Arabidopsis thaliana]	Unigene24594_All//7.00E-149//AT5G41330| potassium channel tetramerisation domain-containing protein	Unigene24594_All//0.00E+00//gi|78350294|gb|DT570568.1|DT570568			GO:0005267//GO:0005488//GO:0005887//GO:0030001	nr +
Unigene24595_All	2181	2.64	3.69	2.93	7.93	6.19	5.74	4.40	3.10	15.80	4.85E-01	1.84E-02		1.51E-01	5.81E-01		-3.57E-01	5.38E-03		-4.67E-01	3.66E-04		-5.03E-01	2.36E-03		1.84E+00	7.09E-79	Up	Unigene24595_All//gi|224130712|ref|XP_002320909.1|//6.00E-23//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222861682|gb|EEE99224.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene24595_All//1.00E-18//AT2G17040| anac036 (Arabidopsis NAC domain containing protein 36); transcription factor	Unigene24595_All//0.00E+00//TC152883	NAC			nr +
Unigene24596_All	1391	13.24	39.38	42.80	24.85	35.00	46.46	9.21	8.50	18.90	1.57E+00	7.34E-80	Up	1.69E+00	5.26E-94	Up	4.94E-01	1.56E-12		9.03E-01	2.15E-42		-1.15E-01	4.94E-01		1.04E+00	8.03E-26	Up	Unigene24596_All//gi|18395805|ref|NP_566136.1|//1.00E-147//armadillo/beta-catenin repeat family protein [Arabidopsis thaliana]	Unigene24596_All//1.00E-148//AT3G01400| armadillo/beta-catenin repeat family protein	Unigene24596_All//0.00E+00//TC152526				nr -
Unigene24599_All	1567	20.17	18.17	22.67	27.78	31.86	39.69	6.04	14.51	15.08	-1.50E-01	1.47E-01		1.69E-01	9.46E-02		1.98E-01	8.25E-03		5.14E-01	1.48E-15		1.26E+00	9.66E-30	Up	1.32E+00	1.09E-33	Up	Unigene24599_All//gi|224107205|ref|XP_002314408.1|//1.00E-162//f-box family protein [Populus trichocarpa] >gi|222863448|gb|EEF00579.1| f-box family protein [Populus trichocarpa]	Unigene24599_All//9.00E-152//AT2G47900| AtTLP3 (TUBBY LIKE PROTEIN 3); phosphoric diester hydrolase/ transcription factor	Unigene24599_All//2.00E-74//TC167425	TUB			nr +
Unigene2460_All	1867	44.75	10.18	21.56	181.46	137.32	140.35	64.16	51.31	33.25	-2.14E+00	6.98E-186	Down	-1.05E+00	1.15E-63	Down	-4.02E-01	1.83E-59		-3.71E-01	2.31E-45		-3.22E-01	1.33E-14		-9.48E-01	1.69E-99		Unigene2460_All//gi|115481736|ref|NP_001064461.1|//1.00E-164//0s10g0370800 [Oryza sativa Japonica Group] >gi|19920188|gb|AAM08620.1|AC107314_11 Putative Glucan 1,3-beta-glucosidase precursor [Oryza sativa Japonica Group] >gi|31431641|gb|AAP53385.1| Cellulase containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639070|dbj|BAF26375.1| Os10g0370800 [Oryza sativa Japonica Group]		Unigene2460_All//0.00E+00//TC151069		ko00500|Starch and sucrose metabolism		nr +
Unigene24600_All	1724	11.05	8.32	14.49	4.57	5.13	4.48	2.92	1.94	1.43	-4.09E-01	1.25E-03		3.91E-01	5.68E-04		1.69E-01	4.55E-01		-2.73E-02	9.23E-01		-5.90E-01	1.36E-02		-1.03E+00	1.30E-05	Down	Unigene24600_All//gi|124360437|gb|ABN08447.1|//1.00E-143//Patatin [Medicago truncatula]	Unigene24600_All//7.00E-137//AT1G33270| patatin-related	Unigene24600_All//0.00E+00//TC144476				nr -
Unigene24601_All	492	0.85	1.54	0.76	5.06	1.89	1.38	14.95	10.87	5.02	8.61E-01	2.93E-01		-1.67E-01	8.79E-01		-1.42E+00	2.12E-04	Down	-1.88E+00	1.27E-05	Down	-4.60E-01	1.80E-02		-1.57E+00	2.49E-14	Down			Unigene24601_All//2.00E-117//TC140303				
Unigene24602_All	947	16.52	8.99	5.57	28.35	20.07	20.70	48.22	42.55	28.31	-8.78E-01	9.32E-10		-1.57E+00	2.15E-22	Down	-4.98E-01	2.03E-07		-4.54E-01	8.25E-06		-1.81E-01	1.44E-02		-7.68E-01	3.92E-27		Unigene24602_All//gi|1335862|gb|AAC49294.1|//7.00E-71//clathrin heavy chain [Glycine max]	Unigene24602_All//1.00E-37//AT3G08530| clathrin heavy chain, putative	Unigene24602_All//0.00E+00//TC140303		ko04144|Endocytosis	GO:0005488//GO:0005905//GO:0009536//GO:0012510//GO:0015031	nr +
Unigene24603_All	2389	14.76	16.44	12.50	23.42	24.69	20.76	25.18	21.82	10.11	1.55E-01	9.06E-02		-2.39E-01	1.37E-02		7.65E-02	3.53E-01		-1.74E-01	1.86E-02		-2.07E-01	8.36E-04		-1.32E+00	4.45E-85	Down	Unigene24603_All//gi|15237681|ref|NP_201241.1|//5.00E-70//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|30698003|ref|NP_851265.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|79332130|ref|NP_001032136.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|134031896|gb|ABO45685.1| At5g64360 [Arabidopsis thaliana] >gi|222423220|dbj|BAH19587.1| AT5G64360 [Arabidopsis thaliana]	Unigene24603_All//1.00E-56//AT5G64360| DNAJ heat shock N-terminal domain-containing protein	Unigene24603_All//0.00E+00//TC170325			GO:0005515	nr +
Unigene24604_All	1199	9.38	6.59	4.13	38.72	39.58	33.56	93.76	63.09	55.06	-5.09E-01	2.67E-03		-1.18E+00	8.45E-11	Down	3.15E-02	7.82E-01		-2.06E-01	1.02E-02		-5.72E-01	4.37E-38		-7.68E-01	1.84E-65		Unigene24604_All//gi|258489633|gb|ACV72640.1|//1.00E-180//sucrose synthase 1 [Gossypium hirsutum]	Unigene24604_All//0.00E+00//gi|164343484|gb|ES810477.1|ES810477	Unigene24604_All//0.00E+00//TC176293		ko00500|Starch and sucrose metabolism		nr -
Unigene24605_All	1771	11.32	8.33	3.55	16.31	20.18	10.84	13.78	1.82	4.50	-4.43E-01	3.19E-04		-1.67E+00	2.91E-31	Down	3.07E-01	3.32E-04		-5.90E-01	1.42E-09		-2.92E+00	1.67E-95	Down	-1.61E+00	3.50E-47	Down	Unigene24605_All//gi|857397|dbj|BAA09466.1|//1.00E-180//mitotic cyclin a2-type [Glycine max]	Unigene24605_All//5.00E-149//AT1G44110| CYCA1;1 (Cyclin A1;1); cyclin-dependent protein kinase regulator	Unigene24605_All//0.00E+00//gi|164363212|gb|ES846634.1|ES846634			GO:0009987//GO:0043231	nr +
Unigene24606_All	1647	6.83	0.98	3.27	71.11	23.25	27.01	8.73	3.96	2.15	-2.79E+00	1.03E-34	Down	-1.06E+00	3.28E-09	Down	-1.61E+00	1.07E-222	Down	-1.40E+00	6.76E-156	Down	-1.14E+00	2.16E-16	Down	-2.02E+00	4.76E-38	Down	Unigene24606_All//gi|115461729|ref|NP_001054464.1|//1.00E-19//0s05g0115100 [Oryza sativa Japonica Group] >gi|55168327|gb|AAV44192.1| unknown protein [Oryza sativa Japonica Group] >gi|113578015|dbj|BAF16378.1| Os05g0115100 [Oryza sativa Japonica Group]	Unigene24606_All//3.00E-28//AT3G44940| unknown protein	Unigene24606_All//0.00E+00//TC152386				nr -
Unigene24611_All	1822	34.29	18.72	18.21	84.43	66.04	59.27	185.36	65.38	60.74	-8.73E-01	2.52E-36		-9.13E-01	1.03E-37		-3.55E-01	1.66E-21		-5.11E-01	2.38E-37		-1.50E+00	0.00E+00	Down	-1.61E+00	0.00E+00	Down	Unigene24611_All//gi|2499488|sp|Q41140.1|PFPA_RICCO//0.00E+00//RecName: Full=Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit alpha; Short=PFP; AltName: Full=6-phosphofructokinase, pyrophosphate dependent; AltName: Full=Pyrophosphate-dependent 6-phosphofructose-1-kinase; AltName: Full=PPi-PFK >gi|483547|emb|CAA83682.1| pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]	Unigene24611_All//0.00E+00//AT1G20950| pyrophosphate--fructose-6-phosphate 1-phosphotransferase-related / pyrophosphate-dependent 6-phosphofructose-1-kinase-related	Unigene24611_All//0.00E+00//TC150470		ko00051|Fructose and mannose metabolism	GO:0006007//GO:0008443//GO:0009746//GO:0010316//GO:0032559//GO:0034285	nr -
Unigene24612_All	2103	3.11	2.05	3.32	2.46	2.44	3.78	2.73	2.72	17.98	-6.03E-01	8.74E-03		9.30E-02	6.99E-01		-1.39E-02	9.53E-01		6.18E-01	2.50E-03		-6.00E-03	1.02E+00		2.72E+00	7.76E-139	Up	Unigene24612_All//gi|209867508|gb|ACI90292.1|//1.00E-99//WRKY transcription factor [Picrorhiza kurroa]	Unigene24612_All//4.00E-44//AT1G62300| WRKY6; transcription factor	Unigene24612_All//0.00E+00//TC154906	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0010467	nr -
Unigene24614_All	1079	22.64	11.74	13.52	27.61	23.49	26.24	34.48	16.35	16.21	-9.48E-01	1.01E-16		-7.44E-01	8.12E-11		-2.33E-01	1.83E-02		-7.31E-02	5.68E-01		-1.08E+00	1.44E-37	Down	-1.09E+00	2.27E-39	Down	Unigene24614_All//gi|297788583|ref|XP_002862370.1|//1.00E-127//26S proteasome regulatory subunit [Arabidopsis lyrata subsp. lyrata] >gi|297827613|ref|XP_002881689.1| 26S proteasome regulatory subunit [Arabidopsis lyrata subsp. lyrata] >gi|297307815|gb|EFH38628.1| 26S proteasome regulatory subunit [Arabidopsis lyrata subsp. lyrata] >gi|297327528|gb|EFH57948.1| 26S proteasome regulatory subunit [Arabidopsis lyrata subsp. lyrata]	Unigene24614_All//8.00E-111//AT2G39990| EIF2; translation initiation factor	Unigene24614_All//0.00E+00//TC138548				nr +
Unigene24615_All	2038	34.22	5.54	21.56	13.32	7.10	5.78	6.66	2.24	6.27	-2.63E+00	1.07E-198	Down	-6.67E-01	1.20E-24		-9.09E-01	7.79E-21		-1.20E+00	4.93E-29	Down	-1.57E+00	6.24E-25	Down	-8.58E-02	5.99E-01		Unigene24615_All//gi|20197910|gb|AAD23682.2|//0.00E+00//expressed protein [Arabidopsis thaliana]	Unigene24615_All//4.00E-172//AT2G21340| antiporter/ drug transporter	Unigene24615_All//0.00E+00//CO086503			GO:0009536//GO:0015291//GO:0015893	nr -

Unigene24616_All	1047	46.12	48.64	56.71	60.23	51.67	53.53	41.96	86.51	35.46	7.65E-02	3.68E-01		2.98E-01	2.48E-05		-2.21E-01	4.62E-04		-1.70E-01	1.36E-02		1.04E+00	9.20E-86	Up	-2.43E-01	6.35E-04		Unigene24616_All//gi|14190455|gb|AK55708.1|AF380627_1//3.00E-63//AT5g53330|K19E1_13 [Arabidopsis thaliana] >gi|15809720|gb|AAL06788.1| AT5g53330|K19E1_13 [Arabidopsis thaliana]	Unigene24616_All//3.00E-59//AT5G53330| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin-associated/translation elongation factor EF1B, N-terminal, eukaryote (InterPro:IPR015940); Has 28 Blast hits to 28 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 11; Fungi - 2; Plants - 15; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene24616_All//0.00E+00//TC139406				nr +
Unigene24617_All	1145	14.12	164.97	52.32	18.19	33.02	34.59	3.47	17.63	18.20	3.55E+00	0.00E+00	Up	1.89E+00	3.68E-110	Up	8.61E-01	2.25E-25		9.28E-01	2.20E-27		2.34E+00	8.22E-62	Up	2.39E+00	1.63E-66	Up	Unigene24617_All//gi|15240044|ref|NP_196824.1|//1.00E-104//GRAM domain-containing protein / ABA-responsive protein-related [Arabidopsis thaliana] >gi|75181135|sp|Q9LYV6.1|GEML5_ARATH RecName: Full=GEM-like protein 5 >gi|7529275|emb|CAB86627.1| ABA-responsive protein-like [Arabidopsis thaliana] >gi|38454154|gb|AAR20771.1| At5g13200 [Arabidopsis thaliana] >gi|46402484|gb|AAS92344.1| At5g13200 [Arabidopsis thaliana] >gi|110738428|dbj|BAF01140.1| ABA-responsive protein - like [Arabidopsis thaliana]	Unigene24617_All//1.00E-105//AT5G13200| GRAM domain-containing protein / ABA-responsive protein-related	Unigene24617_All//0.00E+00//TC148143				nr -
Unigene24618_All	796	4.14	8.85	7.43	2.32	2.86	3.91	0.05	0.00	0.00	1.10E+00	1.37E-06	Up	8.43E-01	9.03E-04		3.02E-01	5.45E-01		7.58E-01	3.37E-02		-5.73E+00	6.57E-01		-5.73E+00	6.13E-01		Unigene24618_All//gi|4090943|gb|AAC98912.1|//1.00E-114//COP1 homolog [Solanum lycopersicum]	Unigene24618_All//5.00E-111//AT2G32950| COP1 (CONSTITUTIVE PHOTOMORPHOGENIC 1); protein binding / ubiquitin-protein ligase	Unigene24618_All//0.00E+00//DR458816		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene24619_All	2490	8.45	15.81	15.18	3.56	5.32	8.67	0.25	0.12	0.14	9.04E-01	1.91E-24		8.46E-01	2.44E-20		5.80E-01	6.77E-05		1.28E+00	3.03E-25	Up	-1.12E+00	1.80E-01		-8.23E-01	2.93E-01		Unigene24619_All//gi|15225760|ref|NP_180854.1|//0.00E+00//COP1 (CONSTITUTIVE PHOTOMORPHOGENIC 1); protein binding / ubiquitin-protein ligase [Arabidopsis thaliana] >gi|20141387|sp|P43254.2|COP1_ARATH RecName: Full=E3 ubiquitin-protein ligase COP1; AltName: Full=Constitutive photomorphogenesis protein 1 >gi|2702280|gb|AAB91983.1| COP1 regulatory protein [Arabidopsis thaliana] >gi|95147316|gb|ABF57293.1| At2g32950 [Arabidopsis thaliana]	Unigene24619_All//0.00E+00//AT2G32950| COP1 (CONSTITUTIVE PHOTOMORPHOGENIC 1); protein binding / ubiquitin-protein ligase	Unigene24619_All//0.00E+00//DR458816		ko04120|Ubiquitin mediated proteolysis	GO:0005515//GO:0006259//GO:0007602//GO:0009639//GO:0009646//GO:0009648//GO:0009812//GO:0010118//GO:0016628//GO:0019787//GO:0023033//GO:0031461//GO:0043231//GO:0046914	nr +
Unigene24620_All	1631	13.18	5.34	5.35	80.78	36.95	26.78	9.88	4.23	5.89	-1.30E+00	3.12E-24	Down	-1.30E+00	3.45E-23	Down	-1.13E+00	1.22E-143	Down	-1.59E+00	1.95E-213	Down	-1.22E+00	2.42E-20	Down	-7.47E-01	1.03E-09		Unigene24620_All//gi|60459337|gb|AA320028.1|//0.00E+00//purple acid phosphatase [Medicago truncatula]	Unigene24620_All//0.00E+00//AT2G16430| PAP10 (PURPLE ACID PHOSPHATASE 10); acid phosphatase/ protein serine/threonine phosphatase	Unigene24620_All//0.00E+00//TC142660			GO:0005618//GO:0016791//GO:0044421//GO:0046914	nr +
Unigene24621_All	1133	20.00	56.44	8.65	28.23	28.33	19.09	27.54	28.59	29.08	1.50E+00	1.10E-86	Up	-1.21E+00	7.54E-22	Down	5.10E-03	9.64E-01		-5.64E-01	9.37E-10		5.39E-02	6.36E-01		7.84E-02	4.11E-01		Unigene24621_All//gi|145049690|gb|ABP35526.1|//1.00E-115//CCR4-associated factor [Ipomoea batatas]	Unigene24621_All//2.00E-109//AT3G44260| CCR4-NOT transcription complex protein, putative	Unigene24621_All//0.00E+00//TC148665		ko03018|RNA degradation	GO:0004540//GO:0005488//GO:0016070//GO:0043231	nr -
Unigene24622_All	1710	4.86	1.24	0.72	8.77	5.98	9.03	50.07	29.31	41.77	-1.97E+00	3.42E-17	Down	-2.76E+00	1.97E-24	Down	-5.52E-01	3.47E-05		4.28E-02	7.96E-01		-7.73E-01	3.33E-49		-2.61E-01	1.09E-07		Unigene24622_All//gi|223452333|gb|ACN89494.1|//1.00E-175//kinase-like protein [Glycine max]	Unigene24622_All//1.00E-161//AT2G05940| protein kinase, putative	Unigene24622_All//0.00E+00//TC172983		ko04626|Plant-pathogen interaction		nr +
Unigene24625_All	336	2.80	2.26	3.49	10.82	11.38	8.47	11.58	3.61	7.47	-3.09E-01	6.29E-01		3.15E-01	6.23E-01		7.19E-02	8.39E-01		-3.54E-01	3.11E-01		-1.68E+00	2.23E-08	Down	-6.32E-01	1.77E-02					Unigene24625_All//6.00E-77//TC154016				
Unigene24629_All	1340	12.77	29.61	24.40	9.59	13.34	12.67	2.97	6.55	2.88	1.21E+00	2.35E-39	Up	9.34E-01	8.60E-21		4.76E-01	1.19E-04		4.02E-01	2.82E-03		1.14E+00	2.44E-10	Up	-4.05E-02	8.98E-01		Unigene24629_All//gi|301070456|gb|ADK55590.1|//1.00E-102//plastid NEP interaction protein [Nicotiana benthamiana]	Unigene24629_All//1.00E-89//AT4G35840| zinc finger (C3HC4-type RING finger) family protein	Unigene24629_All//0.00E+00//gi|78345372|gb|DT565646.1|DT565646			GO:0009743//GO:0046914	nr -
Unigene24631_All	2012	4.50	1.74	1.19	12.33	12.51	7.97	5.65	2.08	2.12	-1.37E+00	1.87E-11	Down	-1.92E+00	2.96E-17	Down	2.10E-02	8.78E-01		-6.30E-01	2.93E-09		-1.44E+00	1.36E-18	Down	-1.42E+00	1.20E-18	Down	Unigene24631_All//gi|188509929|gb|ACD56618.1|//0.00E+00//peptidoglycan-binding LysM domain-containing related protein [Gossypioides kirkii]	Unigene24631_All//5.00E-144//AT1G21880| LYM1 (LYSM DOMAIN GPI-ANCHORED PROTEIN 1 PRECURSOR)	Unigene24631_All//0.00E+00//TC153404		ko04626|Plant-pathogen interaction	GO:0009056	nr +
Unigene24634_All	1116	37.65	24.74	24.29	39.99	38.45	50.79	54.71	31.98	26.84	-6.05E-01	2.23E-13		-6.32E-01	8.72E-14		-5.69E-02	5.76E-01		3.45E-01	3.99E-07		-7.74E-01	1.89E-35		-1.03E+00	3.00E-58	Down	Unigene24634_All//gi|289540890|gb|ADD09567.1|//6.00E-81//adeninephosphoribosyl transferase [Trifolium repens] >gi|289540907|gb|ADD09581.1| adeninephosphoribosyl transferase [Trifolium repens]	Unigene24634_All//4.00E-80//AT1G27450| APT1 (ADENINE PHOSPHORIBOSYL TRANSFERASE 1); adenine phosphoribosyltransferase	Unigene24634_All//0.00E+00//TC137508		ko00230|Purine metabolism	GO:0005618//GO:0009536//GO:0010038//GO:0016020//GO:0016763//GO:0043596	nr +
Unigene24635_All	1480	14.57	10.37	6.62	26.69	24.20	18.65	14.57	8.33	7.89	-4.90E-01	3.24E-05		-1.14E+00	6.14E-19	Down	-1.42E-01	1.24E-01		-5.18E-01	2.83E-10		-8.06E-01	6.13E-14		-8.85E-01	1.04E-16		Unigene24635_All//gi|225435953|ref|XP_002269709.1|//1.00E-173//PREDICTED: similar to plectin-related [Vitis vinifera]	Unigene24635_All//2.00E-166//AT2G26770| plectin-related	Unigene24635_All//0.00E+00//TC149680				nr -
Unigene24636_All	1572	29.82	9.96	15.28	3.61	2.78	1.67	45.99	52.88	42.93	-1.58E+00	1.95E-69	Down	-9.65E-01	3.94E-31		-3.77E-01	1.37E-01		-1.12E+00	6.85E-06	Down	2.01E-01	1.01E-04		-9.94E-02	9.25E-02		Unigene24636_All//gi|6056400|gb|AAF02864.1|AC009324_13/1.00E-125//Similar to anther-specific proline-rich protein APG [Arabidopsis thaliana]	Unigene24636_All//4.00E-126//AT1G53920| GLIP5; carboxylesterase/ lipase	Unigene24636_All//2.00E-09//gi|73863828|gb|DT466567.1|DT466567				nr -
Unigene24637_All	2626	6.38	2.33	5.29	8.50	13.11	10.06	12.03	9.28	6.19	-1.45E+00	2.99E-22	Down	-2.69E-01	7.01E-02		6.26E-01	1.67E-13		2.44E-01	2.74E-02		-3.74E-01	1.23E-05		-9.58E-01	2.37E-27		Unigene24637_All//gi|2702270|gb|AAB91973.1|//1.00E-113//expressed protein [Arabidopsis thaliana]	Unigene24637_All//5.00E-99//AT2G32970| unknown protein	Unigene24637_All//0.00E+00//TC135430				nr +
Unigene24639_All	447	86.73	178.08	132.95	225.67	313.31	277.85	178.86	189.16	175.40	1.04E+00	4.93E-61	Up	6.16E-01	2.00E-18		4.73E-01	1.03E-32		3.00E-01	1.43E-11		8.07E-02	1.66E-01		-2.82E-02	6.41E-01		Unigene24639_All//gi|110559491|gb|ABG76000.1|//5.00E-85//GRP-like protein 2 [Gossypium hirsutum]	Unigene24639_All//3.00E-81//AT3G02230| RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1); cellulose synthase (UDP-forming)	Unigene24639_All//0.00E+00//gi|13351790|gb|BG442138.1|BG442138			GO:0005618//GO:0009250//GO:0035251//GO:0043231//GO:0044459//GO:0045229	nr -
Unigene24642_All	675	2.09	1.35	4.73	5.02	4.39	6.02	3.26	1.92	0.65	-6.31E-01	2.56E-01		1.18E+00	1.41E-03		-1.94E-01	6.00E-01		2.63E-01	4.46E-01		-7.63E-01	4.86E-02		-2.33E+00	1.34E-07	Down	Unigene24642_All//gi|7579025|gb|AAF64227.1|AF248647_1//2.00E-34//glucose acyltransferase [Solanum pennellii]	Unigene24642_All//5.00E-33//AT1G73300| scpl2 (serine carboxypeptidase-like 2); serine-type carboxypeptidase	Unigene24642_All//8.00E-07//TC162267		ko00940|Phenylpropanoid biosynthesis	GO:0016787	nr +
Unigene24643_All	1345	3.23	2.03	4.83	4.33	5.22	5.64	2.39	1.15	1.13	-6.66E-01	2.17E-02		5.81E-01	1.60E-02		2.69E-01	2.70E-01		3.81E-01	8.51E-02		-1.06E+00	7.09E-04	Down	-1.09E+00	3.44E-04	Down	Unigene24643_All//gi|115457130|ref|NP_001052165.1|//6.00E-60//Os04g0176400 [Oryza sativa Japonica Group] >gi|38344210|emb|CAE01973.2|OSJNBa0051N19.2 [Oryza sativa (Japonica cultivar-group)] >gi|113563736|dbj|BAF14079.1| Os04g0176400 [Oryza sativa Japonica Group]	Unigene24643_All//1.00E-57//AT1G73290| scpl5 (serine carboxypeptidase-like 5); serine-type carboxypeptidase	Unigene24643_All//2.00E-61//TC162267			GO:0004180//GO:0031410	nr -
Unigene24644_All	1394	22.41	16.54	19.37	39.20	42.49	28.25	31.39	15.56	19.52	-4.38E-01	5.24E-06		-2.10E-01	4.68E-02		1.16E-01	1.23E-01		-4.73E-01	6.32E-12		-1.01E+00	6.89E-40	Down	-6.86E-01	1.68E-21		Unigene24644_All//gi|14626935|gb|AAK70805.1|//0.00E+00//leucine-rich repeat resistance protein-like protein [Gossypium hirsutum]	Unigene24644_All//4.00E-135//AT5G61240| protein binding	Unigene24644_All//0.00E+00//TC131977		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene24648_All	2353	11.70	2.33	9.21	0.66	0.63	0.19	49.86	62.90	91.83	-2.33E+00	1.62E-68	Down	-3.45E-01	1.45E-03		-6.06E-02	9.01E-01		-1.77E+00	1.65E-03		3.35E-01	4.02E-19		8.81E-01	4.26E-157		Unigene24648_All//gi|224127989|ref|XP_002329227.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222871008|gb|EEF08139.1| cytochrome P450 [Populus trichocarpa]	Unigene24648_All//0.00E+00//AT5G24910| CYP714A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene24648_All//0.00E+00//TC144453		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00590|Arachidonic acid metabolism	GO:0005506//GO:0008152//GO:0016634	nr +
Unigene24651_All	489	7.81	12.95	10.89	12.73	14.08	6.47	15.39	10.60	7.09	7.30E-01	1.87E-03		4.79E-01	8.00E-02		1.45E-01	5.81E-01		-9.78E-01	2.76E-05		-5.38E-01	4.58E-03		-1.12E+00	5.12E-09	Down	Unigene24651_All//gi|115456507|ref|NP_001051854.1|//2.00E-38//Os03g0841800 [Oryza sativa Japonica Group] >gi|113550325|dbj|BAF13768.1| Os03g0841800 [Oryza sativa Japonica Group]	Unigene24651_All//1.00E-31//AT5G14640| SK13 (SHAGGY-LIKE KINASE 13); ATP binding / protein kinase/ protein serine/threonine kinase	Unigene24651_All//0.00E+00//ES851781			GO:0004672//GO:0006464//GO:0032559	nr +
Unigene24652_All	1919	42.45	34.72	33.77	48.13	50.19	43.87	38.07	23.13	15.80	-2.90E-01	4.72E-07		-3.30E-01	2.26E-08		6.06E-02	3.42E-01		-1.34E-01	1.95E-02		-7.19E-01	3.11E-37		-1.27E+00	2.39E-97	Down	Unigene24652_All//gi|92893880|gb|ABF91930.1|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene24652_All//0.00E+00//AT1G57870| ATSK42 (ARABIDOPSIS SHAGGY-LIKE KINASE 42); ATP binding / protein kinase/ protein serine/threonine kinase	Unigene24652_All//0.00E+00//gi|109828489|gb|DW227112.1|DW227112			GO:0004672//GO:0006464//GO:0006970//GO:0016020//GO:0032559//GO:0044444	nr -
Unigene24653_All	1690	11.05	213.77	29.15	14.97	48.11	276.67	65.12	343.12	364.65	4.27E+00	0.00E+00	Up	1.40E+00	6.94E-59	Up	1.68E+00	6.11E-154	Up	4.21E+00	0.00E+00	Up	2.40E+00	0.00E+00	Up	2.49E+00	0.00E+00	Up	Unigene24653_All//gi|18398912|ref|NP_564426.1|//0.00E+00//disease resistance protein-related / LRR protein-related [Arabidopsis thaliana]	Unigene24653_All//0.00E+00//AT1G33590| disease resistance protein-related / LRR protein-related	Unigene24653_All//0.00E+00//TC167755		ko04626|Plant-pathogen interaction	GO:0005488//GO:0005618//GO:0006950//GO:0008152//GO:0009536//GO:0016628//GO:0016772//GO:0023060	nr -
Unigene24656_All	1503	7.38	5.63	11.23	25.69	24.49	34.17	84.34	7.84	18.71	-3.91E-01	2.43E-02		6.06E-01	1.40E-05		-6.87E-02	5.36E-01		4.12E-01	8.25E-09		-3.43E+00	0.00E+00	Down	-2.17E+00	0.00E+00	Down	Unigene24656_All//gi|286294480|gb|AAO39816.1|//1.00E-161//dihydroflavonol 4-reductase [Malus x domestica]	Unigene24656_All//7.00E-146//AT5G42800| DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase	Unigene24656_All//0.00E+00//TC131472		ko00941|Flavonoid biosynthesis		nr -
Unigene24657_All	2010	13.61	9.23	17.96	76.51	76.67	100.10	39.44	12.10	19.21	-5.61E-01	5.92E-08		4.00E-01	1.37E-05		3.00E-03	9.56E-01		3.88E-01	2.20E-29		-1.70E+00	4.91E-159	Down	-1.04E+00	1.07E-76	Down	Unigene24657_All//gi|157273666|gb|ABV27487.1|//0.00E+00//fasciclin-like arabinogalactan protein 16 [Gossypium hirsutum]	Unigene24657_All//3.00E-148//AT5G06390| FLA17 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 17 PRECURSOR)	Unigene24657_All//0.00E+00//TC131368				nr +
Unigene24658_All	1195	1.88	2.50	2.50	3.67	5.45	5.52	9.48	22.28	7.50	4.10E-01	2.66E-01		4.07E-01	2.96E-01		5.70E-01	1.12E-02		5.89E-01	1.02E-02		1.23E+00	2.13E-33	Up	-3.38E-01	2.34E-02		Unigene24658_All//gi|15227225|ref|NP_179836.1|//1.00E-126//UCP5 (UNCOUPLING PROTEIN 5); binding [Arabidopsis thaliana] >gi|90567689|emb|CAJ86454.1| mitochondrial dicarboxylate carrier [Arabidopsis thaliana]	Unigene24658_All//4.00E-114//AT2G22500| UCP5 (UNCOUPLING PROTEIN 5); binding	Unigene24658_All//0.00E+00//gi|164280689|gb|ES792998.1|ES792998				nr +
Unigene24659_All	1178	57.70	66.71	28.03	129.86	126.05	145.15	94.61	222.64	213.84	2.10E-01	4.60E-04		-1.04E+00	6.56E-51	Down	-4.30E-02	4.10E-01		1.61E-01	3.42E-05		1.23E+00	0.00E+00	Up	1.18E+00	6.22E-294	Up	Unigene24659_All//gi|15227225|ref|NP_179836.1|//1.00E-111//UCP5 (UNCOUPLING PROTEIN 5); binding [Arabidopsis thaliana] >gi|90567689|emb|CAJ86454.1| mitochondrial dicarboxylate carrier [Arabidopsis thaliana]	Unigene24659_All//1.00E-93//AT2G22500| UCP5 (UNCOUPLING PROTEIN 5); binding	Unigene24659_All//0.00E+00//TC144747				nr -

Unigene2466_All	1529	0.82	2.95	0.98	2.90	2.84	2.84	5.28	6.56	4.12	1.84E+00	7.50E-09	Up	2.48E-01	6.34E-01		-3.11E-02	9.18E-01		-3.22E-02	9.35E-01		3.13E-01	6.32E-02		-3.60E-01	4.62E-02		Unigene2466_All//gi|76824324|gb|AAF62262.1|AF165186_1//1.00E-144//MAP kinase kinase [Nicotiana tabacum]	Unigene2466_All//5.00E-126//AT4G29810| ATMEK2 (ARABIDOPSIS THALIANA MAP KINASE KINASE 2); MAP kinase kinase/ kinase	Unigene2466_All//0.00E+00//gi|48747841|gb|C00783600.1|C00783600		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene24662_All	2705	1.66	4.01	3.86	24.66	23.09	24.43	13.49	8.54	9.46	1.27E+00	4.68E-12	Up	1.21E+00	1.78E-10	Up	-9.47E-02	1.93E-01		-1.36E-02	8.77E-01		-6.59E-01	2.05E-16		-5.13E-01	4.21E-11		Unigene24662_All//gi|42568160|ref|NP_198834.2|//0.00E+00//SUS5; UDP-glycosyltransferase/ sucrose synthase [Arabidopsis thaliana]	Unigene24662_All//0.00E+00//AT5G37180| SUS5; UDP-glycosyltransferase/ sucrose synthase	Unigene24662_All//0.00E+00//TC139942		ko00500|Starch and sucrose metabolism	GO:0005984//GO:0030312//GO:0035251	nr -
Unigene24666_All	1974	35.20	90.28	48.91	41.64	53.90	55.94	9.25	11.41	14.79	1.36E+00	4.79E-208	Up	4.75E-01	1.22E-18		3.73E-01	3.74E-16		4.26E-01	2.17E-19		3.03E-01	3.94E-03		6.77E-01	2.79E-14		Unigene24666_All//gi|18400571|ref|NP_565572.1|//1.00E-121//AFR (ATTENUATED FAR-RED RESPONSE) [Arabidopsis thaliana] >gi|67460122|sp|Q8LAW2.2|AFR_ARATH RecName: Full=F-box protein AFR; AltName: Full=Protein ATTENUATED FAR-RED RESPONSE; AltName: Full=SKP1-interacting partner 29 >gi|4572676|gb|AAD23891.1| expressed protein [Arabidopsis thaliana] >gi|18086659|gb|AAL57704.1| At2g24540/F25P17.16 [Arabidopsis thaliana] >gi|23507761|gb|AAX38684.1| At2g24540/F25P17.16 [Arabidopsis thaliana]	Unigene24666_All//4.00E-118//AT2G24540| AFR (ATTENUATED FAR-RED RESPONSE)	Unigene24666_All//0.00E+00//TC169295				nr +
Unigene24667_All	384	2.59	2.38	0.00	2.46	1.08	3.76	4.73	2.83	2.39	-1.24E-01	8.42E-01		-1.13E+01	1.77E-05	Down	-1.20E+00	8.32E-02		6.11E-01	3.05E-01		-7.43E-01	8.75E-02		-9.89E-01	1.76E-02		Unigene24667_All//gi|42571763|ref|NP_973972.1|//4.00E-26//ATPUP11; purine transmembrane transporter [Arabidopsis thaliana]	Unigene24667_All//2.00E-27//AT1G44750| ATPUP11; purine transmembrane transporter	Unigene24667_All//2.00E-107//TC178750			GO:0015205//GO:0015851//GO:0031224	nr +
Unigene24669_All	1430	1.83	0.92	2.38	3.27	2.72	2.46	8.93	9.27	19.03	-9.90E-01	1.16E-02		3.82E-01	2.90E-01		-2.67E-01	3.78E-01		-4.11E-01	1.61E-01		5.33E-02	7.37E-01		1.09E+00	6.45E-29	Up	Unigene24669_All//gi|42571763|ref|NP_973972.1|//1.00E-143//ATPUP11; purine transmembrane transporter [Arabidopsis thaliana]	Unigene24669_All//2.00E-117//AT1G44750| ATPUP11; purine transmembrane transporter	Unigene24669_All//0.00E+00//TC178750				nr -
Unigene24672_All	716	1.75	3.26	1.26	4.10	2.16	1.64	2.66	2.28	1.28	8.92E-01	3.35E-02		-4.72E-01	4.42E-01		-9.24E-01	7.14E-03		-1.32E+00	3.33E-04	Down	-2.23E-01	6.53E-01		-1.05E+00	9.64E-03				Unigene24672_All//0.00E+00//TC162453				
Unigene24676_All	2406	3.94	2.36	2.01	8.16	8.99	5.50	7.28	3.67	3.13	-7.39E-01	7.52E-05		-9.67E-01	8.26E-07		1.40E-01	3.12E-01		-5.69E-01	2.47E-06		-9.89E-01	7.53E-16		-1.22E+00	1.59E-22	Down	Unigene24676_All//gi|297806737|ref|XP_002871252.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317089|gb|EFH47511.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24676_All//0.00E+00//AT5G58520| protein kinase family protein	Unigene24676_All//0.00E+00//gi|78342278|gb|DT562552.1|DT562552			GO:0004713//GO:0006464//GO:0032559	nr -
Unigene24677_All	1161	5.32	4.71	6.10	9.61	8.19	7.31	2.26	0.76	1.41	-1.74E-01	4.98E-01		1.98E-01	4.08E-01		-2.32E-01	2.05E-01		-3.94E-01	2.25E-02		-1.58E+00	1.89E-05	Down	-6.83E-01	4.13E-02		Unigene24677_All//gi|168988195|gb|AC435266.1|//2.00E-87//nuclear transport family protein [Cucumis sativus]	Unigene24677_All//5.00E-54//AT5G43960| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene24677_All//0.00E+00//gi|78334459|gb|DT554733.1|DT554733			GO:0005488//GO:0051234	nr +
Unigene24678_All	1246	2.60	1.26	1.62	3.36	2.98	2.32	1.80	0.57	1.28	-1.05E+00	2.62E-03		-6.81E-01	5.92E-02		-1.70E-01	6.13E-01		-5.34E-01	7.79E-02		-1.66E+00	4.68E-05	Down	-4.92E-01	1.89E-01		Unigene24678_All//gi|168988195|gb|AC435266.1|//1.00E-108//nuclear transport family protein [Cucumis sativus]	Unigene24678_All//3.00E-60//AT5G43960| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene24678_All//0.00E+00//gi|78334459|gb|DT554733.1|DT554733		ko03040|Spliceosome	GO:0005488	nr +
Unigene2468_All	3461	2.06	1.60	0.69	5.57	6.68	6.04	12.08	3.85	7.21	-3.66E-01	1.05E-01		-1.57E+00	1.66E-10	Down	2.61E-01	2.24E-02		1.17E-01	4.17E-01		-1.65E+00	2.38E-80	Down	-7.46E-01	1.03E-23		Unigene2468_All//gi|16326135|dbj|BAB70511.1|//0.00E+00//Myb [Nicotiana tabacum]	Unigene2468_All//0.00E+00//AT5G11510| MYB3R-4 (myb domain protein 3R-4); DNA binding / transcription coactivator/ transcription factor	Unigene2468_All//0.00E+00//TC155720	MYB			nr -
Unigene24681_All	2213	3.38	3.53	2.96	3.56	4.19	3.18	0.88	2.04	0.67	6.06E-02	7.77E-01		-1.92E-01	4.11E-01		2.35E-01	2.63E-01		-1.60E-01	5.08E-01		1.21E+00	3.40E-06	Up	-4.00E-01	3.38E-01		Unigene24681_All//gi|255560673|ref|XP_002521350.1|//0.00E+00//Phosphatidylcholine: Diacylglycerol Acyltransferase [Ricinus communis] >gi|223539428|gb|EEF41018.1| Phosphatidylcholine: Diacylglycerol Acyltransferase [Ricinus communis]	Unigene24681_All//0.00E+00//AT5G13640| ATPDAT; phosphatidylcholine-sterol O-acyltransferase	Unigene24681_All//0.00E+00//ES835685		ko00561|Glycerolipid metabolism	GO:0008080//GO:0008374//GO:0044238	nr +
Unigene24682_All	1832	0.34	0.19	0.76	0.87	0.49	0.67	0.95	1.21	17.44	-8.24E-01	3.75E-01		1.14E+00	5.84E-02		-8.32E-01	9.85E-02		-3.87E-01	4.87E-01		3.54E-01	4.00E-01		4.20E+00	5.17E-173	Up	Unigene24682_All//gi|297835838|ref|XP_002885801.1|//1.00E-163//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331641|gb|EFH62060.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24682_All//5.00E-78//AT2G05810| armadillo/beta-catenin repeat family protein				GO:0003824	nr -
Unigene24683_All	2374	1.56	1.62	0.43	6.57	5.45	2.83	3.78	1.09	3.47	5.19E-02	8.75E-01		-1.88E+00	3.14E-07	Down	-2.68E-01	6.17E-02		-1.21E+00	4.30E-17	Down	-1.79E+00	6.56E-20	Down	-1.20E-01	5.41E-01		Unigene24683_All//gi|297835838|ref|XP_002885801.1|//0.00E+00//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331641|gb|EFH62060.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24683_All//4.00E-178//AT2G05810| armadillo/beta-catenin repeat family protein				GO:0003824	nr +
Unigene24687_All	1925	6.01	5.00	5.45	0.85	2.04	0.75	1.36	2.17	1.88	-2.64E-01	1.31E-01		-1.40E-01	4.60E-01		1.26E+00	3.35E-05	Up	-1.86E-01	7.15E-01		6.73E-01	1.13E-02		4.68E-01	9.95E-02		Unigene24687_All//gi|18407193|ref|NP_566089.1|//4.00E-63//NGA1 (NGATHA1); transcription factor [Arabidopsis thaliana] >gi|75100798|sp|Q82799.1|NGA1_ARATH RecName: Full=B3 domain-containing transcription factor NGA1; AltName: Full=Protein NGATHA 1	Unigene24687_All//2.00E-56//AT1G01030| NGA3 (NGATHA3); transcription factor	Unigene24687_All//3.00E-55//TC131198	ABI3VP1		GO:0006350//GO:0009791//GO:0010468//GO:0043231//GO:0048827	nr +
Unigene24689_All	2395	3.32	2.94	2.78	16.91	11.17	5.81	14.99	11.03	7.52	-1.75E-01	4.23E-01		-2.57E-01	2.57E-01		-5.98E-01	5.09E-15		-1.54E+00	9.45E-63	Down	-4.43E-01	2.73E-08		-9.95E-01	6.55E-33		Unigene24689_All//gi|224052976|ref|XP_002297645.1|//0.00E+00//f-box family protein [Populus trichocarpa] >gi|222844903|gb|EEE82450.1| f-box family protein [Populus trichocarpa]	Unigene24689_All//0.00E+00//AT1G55270| kelch repeat-containing F-box family protein	Unigene24689_All//0.00E+00//gi|164361111|gb|ES820993.1|ES820993				nr -
Unigene2469_All	1841	301.48	25.60	112.26	160.10	116.23	103.01	13.34	2.32	3.85	-3.56E+00	0.00E+00	Down	-1.43E+00	0.00E+00	Down	-4.62E-01	6.22E-67		-6.36E-01	1.25E-105		-2.53E+00	3.81E-82	Down	-1.79E+00	5.77E-55	Down	Unigene2469_All//gi|284504570|gb|ADB90475.1|//0.00E+00//pectate lyase [Gossypium herbaceum]	Unigene2469_All//0.00E+00//AT1G67750| pectate lyase family protein	Unigene2469_All//0.00E+00//TC141162		ko00040|Pentose and glucuronate interconversions		nr +
Unigene24690_All	1439	3.35	8.27	7.25	2.77	4.91	2.64	2.67	0.81	0.42	1.31E+00	9.66E-14	Up	1.12E+00	2.99E-09	Up	8.25E-01	8.27E-05		-7.10E-02	8.34E-01		-1.72E+00	1.63E-08	Down	-2.69E+00	7.56E-15	Down	Unigene24690_All//gi|61656661|emb|CAI64479.1|//2.00E-07//OSJNBa0032N05.16 [Oryza sativa (japonica cultivar-group)]	Unigene24690_All//3.00E-07//AT1G48120| calcineurin-like phosphoesterase family protein	Unigene24690_All//7.00E-12//TC173362				nr +
Unigene24691_All	586	102.50	40.38	28.08	63.59	47.25	19.19	211.26	20.18	29.57	-1.34E+00	1.15E-69	Down	-1.87E+00	2.34E-108	Down	-4.29E-01	9.25E-08		-1.73E+00	4.58E-68	Down	-3.39E+00	0.00E+00	Down	-2.84E+00	0.00E+00	Down	Unigene24691_All//gi|157273642|gb|ABV27475.1|//1.00E-73//fasciclin-like arabinogalactan protein 4 [Gossypium hirsutum]	Unigene24691_All//3.00E-27//AT2G20520| FLA6 (FASCICLIN-LIKE ARABINOGALACTAN 6)	Unigene24691_All//0.00E+00//gi|21094508|gb|BQ406821.1|BQ406821			GO:0005618//GO:0031225	nr -
Unigene24692_All	1256	102.81	30.70	31.20	90.74	71.58	25.24	86.58	7.19	15.19	-1.74E+00	1.33E-218	Down	-1.72E+00	9.63E-208	Down	-3.42E-01	4.91E-15		-1.85E+00	1.55E-227	Down	-3.59E+00	0.00E+00	Down	-2.51E+00	0.00E+00	Down	Unigene24692_All//gi|157273642|gb|ABV27475.1|//1.00E-132//fasciclin-like arabinogalactan protein 4 [Gossypium hirsutum]	Unigene24692_All//2.00E-55//AT1G03870| FLA9 (FASCICLIN-LIKE ARABINOOGALACTAN 9)	Unigene24692_All//0.00E+00//TC132198			GO:0005618//GO:0031225	nr +
Unigene24693_All	2217	4.39	2.10	3.19	8.07	5.61	4.97	2.98	0.68	0.92	-1.06E+00	1.93E-08	Down	-4.59E-01	1.78E-02		-5.25E-01	1.39E-05		-6.99E-01	4.14E-08		-2.13E+00	1.63E-18	Down	-1.70E+00	2.52E-14	Down	Unigene24693_All//gi|15220455|ref|NP_176918.1|//0.00E+00//leucine-rich repeat family protein [Arabidopsis thaliana] >gi|3176660|gb|AAC18784.1| Similar to ERECTA receptor protein kinase gb|U47029 from A. thaliana [Arabidopsis thaliana] >gi|224589465|gb|ACN59266.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene24693_All//0.00E+00//AT1G67510| leucine-rich repeat family protein	Unigene24693_All//1.00E-162//gi|164252751|gb|ES839343.1|ES839343			GO:0004672//GO:0006464//GO:0007167//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene24694_All	1760	9.78	81.45	13.83	23.01	37.17	16.37	23.04	36.98	23.45	3.06E+00	0.00E+00	Up	5.00E-01	1.16E-05		6.92E-01	3.76E-30		-4.91E-01	1.29E-09		6.83E-01	2.14E-30		2.56E-02	7.64E-01		Unigene24694_All//gi|224137264|ref|XP_002322514.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222867144|gb|EEF04275.1| GRAS family transcription factor [Populus trichocarpa]	Unigene24694_All//2.00E-143//AT4G17230| SCL13 (Scarecrow-like 13); transcription factor	Unigene24694_All//0.00E+00//TC131672	GRAS		GO:0010468	nr +
Unigene24696_All	2924	3.22	30.22	2.51	6.88	10.25	3.77	9.47	13.65	9.76	3.23E+00	0.00E+00	Up	-3.58E-01	7.65E-02		5.74E-01	3.44E-10		-8.69E-01	6.63E-13		5.27E-01	2.91E-12		4.27E-02	6.74E-01		Unigene24696_All//gi|224137264|ref|XP_002322514.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222867144|gb|EEF04275.1| GRAS family transcription factor [Populus trichocarpa]	Unigene24696_All//2.00E-172//AT4G17230| SCL13 (Scarecrow-like 13); transcription factor	Unigene24696_All//0.00E+00//TC145667	GRAS		GO:0010468	nr -
Unigene24698_All	1545	1.08	0.89	1.76	1.19	1.36	0.47	2.76	1.22	0.59	-2.91E-01	5.79E-01		6.98E-01	8.10E-02		1.89E-01	7.28E-01		-1.35E+00	5.69E-03		-1.18E+00	1.05E-05	Down	-2.22E+00	2.72E-13	Down	Unigene24698_All//gi|30680320|ref|NP_187406.2|//3.00E-39//far-red impaired responsive family protein / FAR1 family protein [Arabidopsis thaliana]	Unigene24698_All//4.00E-37//AT3G07500| far-red impaired responsive family protein / FAR1 family protein	Unigene24698_All//0.00E+00//C0128037				nr +
Unigene24699_All	2628	11.09	3.45	1.72	49.45	45.00	31.97	11.63	0.83	3.02	-1.68E+00	2.03E-47	Down	-2.69E+00	2.39E-82	Down	-1.36E-01	2.14E-03		-6.30E-01	5.73E-46		-3.81E+00	3.11E-152	Down	-1.95E+00	3.05E-76	Down	Unigene24699_All//gi|15220780|ref|NP_176434.1|//0.00E+00//LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2); protein binding / structural constituent of cell wall [Arabidopsis thaliana]	Unigene24699_All//2.00E-121//AT1G62440| LRX2 (LEUCINE-RICH REPEAT/EXTENSIN 2); protein binding / structural constituent of cell wall	Unigene24699_All//0.00E+00//gi|78350028|gb|DT570302.1|DT570302		ko04626|Plant-pathogen interaction	GO:0000902//GO:0005618//GO:0010053	nr +
Unigene24700_All	1867	17.80	16.75	18.57	12.94	10.75	15.77	4.28	9.54	1.13	-8.77E-02	4.00E-01		6.13E-02	5.97E-01		-2.67E-01	1.47E-02		2.86E-01	4.68E-03		1.16E+00	1.71E-20	Up	-1.92E+00	3.53E-20	Down	Unigene24700_All//gi|115465379|ref|NP_001056289.1|//3.00E-70//Os05g0557500 [Oryza sativa Japonica Group] >gi|113579840|dbj|BAF18203.1| Os05g0557500 [Oryza sativa Japonica Group]	Unigene24700_All//5.00E-91//AT4G21700| unknown protein	Unigene24700_All//0.00E+00//TC179303			GO:0009536	nr +
Unigene24701_All	1327	13.41	12.37	10.19	16.25	19.07	22.84	13.38	35.37	19.03	-1.16E-01	4.24E-01		-3.95E-01	4.08E-03		2.31E-01	3.76E-02		4.91E-01	2.65E-07		1.40E+00	5.85E-71	Up	5.08E-01	7.95E-08		Unigene24701_All//gi|115488050|ref|NP_001066512.1|//2.00E-23//Os12g0257500 [Oryza sativa Japonica Group] >gi|77554187|gb|ABA96983.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649019|dbj|BAF29531.1| Os12g0257500 [Oryza sativa Japonica Group]	Unigene24701_All//1.00E-37//AT3G11810| unknown protein	Unigene24701_All//0.00E+00//TC147723				nr -

Unigene24702_A11	665	47.05	5.33	11.69	20.08	27.55	21.60	6.74	1.51	1.44	-3.14E+00	1.10E-107	Down	-2.01E+00	2.74E-62	Down	4.57E-01	1.87E-04		1.05E-01	5.70E-01		-2.16E+00	5.24E-13	Down	-2.23E+00	5.69E-14	Down	Unigene24702_A11//gi|15809822|gb|AAL06839.1|//4.00E-61//AT5g25460/F18G18_200 [Arabidopsis thaliana]	Unigene24702_A11//2.00E-62//AT5G25460| unknown protein	Unigene24702_A11//0.00E+00//CO127406			GO:0005618	nr +
Unigene24703_A11	1425	223.42	35.34	74.81	100.40	146.32	101.58	21.51	5.69	6.54	-2.66E+00	0.00E+00	Down	-1.58E+00	0.00E+00	Down	5.43E-01	2.49E-62		1.69E-02	7.55E-01		-1.92E+00	9.41E-73	Down	-1.72E+00	1.92E-64	Down	Unigene24703_A11//gi|14423450|gb|AAK62407.1|AF386962_1/1.00E-155//Unknown protein [Arabidopsis thaliana] >gi|30725566|gb|AAP37805.1|At5g25460 [Arabidopsis thaliana]	Unigene24703_A11//3.00E-158//AT5G11420| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cell wall, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25460.1); Has 185 Blast hits to 157 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 185; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene24703_A11//0.00E+00//TC131401				nr +
Unigene24704_A11	943	25.52	16.44	28.12	44.11	36.92	29.45	25.92	22.25	11.58	-6.34E-01	1.23E-08		1.40E-01	2.47E-01		-2.57E-01	1.20E-03		-5.83E-01	3.24E-13		-2.20E-01	3.41E-02		-1.16E+00	5.62E-29	Down	Unigene24704_A11//gi|14326527|gb|AK660308.1|AF385717_1/8.00E-06//AT4g35110/M4E13_160 [Arabidopsis thaliana] >gi|22137306|gb|AAM91498.1|AT4g35110/M4E13_160 [Arabidopsis thaliana]	Unigene24704_A11//4.00E-136//CA993743| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: TRAF-like (InterPro:IPR008974), MATH (InterPro:IPR002083); BEST Arabidopsis thaliana protein match is: meprin and TRAF homology domain-containing protein / MATH domain-containing protein (TAIR:AT3G58210.1); Has 220 Blast hits to 198 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 215; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene24704_A11//4.00E-136//CA993743				nr -
Unigene24705_A11	1089	7.83	5.77	10.17	8.10	9.58	8.13	9.82	6.41	3.22	-4.41E-01	2.73E-02		3.77E-01	3.87E-02		2.43E-01	2.08E-01		5.70E-03	9.78E-01		-6.16E-01	7.01E-05		-1.61E+00	4.42E-21	Down	Unigene24705_A11//gi|297831622|ref|XP_002883693.1|//5.00E-06//predicted protein [Arabidopsis lyrata subsp. lyrata] >gi|297329533|gb|EFH59952.1|predicted protein [Arabidopsis lyrata subsp. lyrata]	Unigene24705_A11//1.00E-05//AT3G29080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: TRAF-like (InterPro:IPR008974), MATH (InterPro:IPR002083); BEST Arabidopsis thaliana protein match is: meprin and TRAF homology domain-containing protein / MATH domain-containing protein (TAIR:AT3G58210.1); Has 220 Blast hits to 198 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 215; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene24705_A11//3.00E-155//CA993743				nr -
Unigene24706_A11	1094	241.57	144.64	189.93	118.84	109.57	121.66	219.21	138.19	78.66	-7.40E-01	5.38E-114		-3.47E-01	3.41E-28		-1.17E-01	1.03E-02		3.38E-02	5.75E-01		-6.66E-01	3.12E-105		-1.48E+00	0.00E+00	Down	Unigene24706_A11//gi|211906460|gb|ACJ11723.1|//1.00E-138//triosephosphate isomerase [Gossypium hirsutum]	Unigene24706_A11//3.00E-104//AT3G55440| TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase	Unigene24706_A11//0.00E+00//TC1330306		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00562|Inositol phosphate metabolism//ko00051|Fructose and mannose metabolism		nr +
Unigene24708_A11	325	1.61	2.03	4.10	5.21	4.24	1.53	2.34	0.77	1.35	3.32E-01	6.80E-01		1.35E+00	3.17E-02		-2.98E-01	5.76E-01		-1.77E+00	9.00E-04	Down	-1.60E+00	3.70E-02		-7.96E-01	2.52E-01				Unigene24708_A11//1.00E-151//DT461444				
Unigene24709_A11	1857	0.73	0.68	1.12	2.66	2.30	1.85	1.00	0.27	0.71	-1.03E-01	8.47E-01		6.10E-01	1.96E-01		-2.08E-01	5.01E-01		-5.23E-01	5.72E-02		-1.89E+00	5.01E-05	Down	-5.01E-01	2.29E-01		Unigene24709_A11//gi|256002927|gb|ACU52707.1|//3.00E-98//bHLH transcription factor PTF1 [Glycine max]	Unigene24709_A11//2.00E-70//AT3G57800| basic helix-loop-helix (bHLH) family protein	Unigene24709_A11//0.00E+00//TC131322	bHLH	ko04712|Circadian rhythm - plant	GO:0010468//GO:0043231	nr +
Unigene24713_A11	1256	7.54	22.71	14.75	76.11	49.95	107.66	12.86	14.38	9.99	1.59E+00	1.36E-42	Up	9.69E-01	9.36E-13		-6.08E-01	6.45E-36		5.00E-01	1.52E-31		1.61E-01	2.23E-01		-3.64E-01	2.68E-03		Unigene24713_A11//gi|283135894|gb|ADB11338.1|//3.00E-83//theta class glutathione transferase GSTT2 [Populus trichocarpa]	Unigene24713_A11//0.00E+00//AT5G41210| ATGSTT1 (GLUTATHIONE S-TRANSFERASE THETA 1); glutathione transferase	Unigene24713_A11//0.00E+00//gi|11208807|gb|BF277737.1|BF277737		ko00480|Glutathione metabolism//ko00350|Tyrosine metabolism	GO:0009404//GO:0016765//GO:0042579	nr -
Unigene24717_A11	1773	19.03	25.83	18.59	2.42	1.51	1.53	8.78	11.69	20.60	4.41E-01	1.74E-08		-3.40E-02	7.49E-01		-6.74E-01	1.54E-02		-6.61E-01	2.40E-02		4.14E-01	1.23E-04		1.23E+00	1.70E-46	Up	Unigene24717_A11//gi|115450383|ref|NP_001048792.1|//3.00E-62//Os03g0120900 [Oryza sativa Japonica Group] >gi|75246354|sp|Q8LM89.1|Y3209_ORYSJ RecName: Full=B3 domain-containing protein Os03g0120900 >gi|24268418|gb|AAN52315.1|AC105363_4 Putative RAV-like B3 domain DNA binding protein [Oryza sativa Japonica Group] >gi|108706902|gb|ABF93697.1| B3 DNA binding domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547263|dbj|BAF10706.1|Os03g0120900 [Oryza sativa Japonica Group]	Unigene24717_A11//3.00E-58//AT2G46870| NGA1 (NGATHA1); transcription factor	Unigene24717_A11//2.00E-133//CO123445	ABI3VP1		GO:0009791//GO:0043231//GO:0048827	nr +
Unigene24718_A11	1218	32.43	32.07	57.23	82.82	47.95	29.52	2.88	65.99	1.64	-1.60E-02	8.73E-01		8.19E-01	4.25E-35		-7.89E-01	5.08E-60		-1.49E+00	7.25E-148	Down	4.52E+00	0.00E+00	Up	-8.17E-01	3.95E-03		Unigene24718_A11//gi|115449335|ref|NP_001048441.1|//1.00E-125//Os02g0805500 [Oryza sativa Japonica Group] >gi|113537972|dbj|BAF10355.1|Os02g0805500 [Oryza sativa Japonica Group]	Unigene24718_A11//3.00E-99//AT5G54390| AHL (ARABIDOPSIS HAL2-LIKE); 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase	Unigene24718_A11//0.00E+00//TC132111		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism		nr +
Unigene24720_A11	3252	1.21	0.62	1.28	19.42	14.98	10.64	6.54	1.84	2.45	-9.53E-01	2.12E-03		8.19E-02	7.91E-01		-3.74E-01	4.84E-10		-8.69E-01	2.91E-39		-1.83E+00	1.23E-47	Down	-1.42E+00	3.94E-34	Down	Unigene24720_A11//gi|115452031|ref|NP_001049616.1|//1.00E-127//Os03g0259900 [Oryza sativa Japonica Group] >gi|108707251|gb|ABF95076.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548087|dbj|BAF11530.1|Os03g0259900 [Oryza sativa Japonica Group]	Unigene24720_A11//3.00E-75//AT5G16720| unknown protein	Unigene24720_A11//0.00E+00//TC162205				nr -
Unigene24721_A11	2063	7.28	18.72	12.31	15.16	12.37	11.47	16.11	13.68	9.58	1.36E+00	9.92E-46	Up	7.58E-01	1.35E-11		-2.94E-01	1.42E-03		-4.03E-01	1.82E-05		-2.36E-01	6.01E-03		-7.50E-01	3.24E-19		Unigene24721_A11//gi|145839433|gb|ABP96799.1|//0.00E+00//purple acid phosphatase [Nicotiana tabacum]	Unigene24721_A11//0.00E+00//AT3G07130| PAP15 (PURPLE ACID PHOSPHATASE 15); acid phosphatase/ protein serine/threonine phosphatase	Unigene24721_A11//0.00E+00//gi|78351306|gb|DT571580.1|DT571580			GO:0009856//GO:0016791//GO:0032501//GO:0043169//GO:0044464	nr -
Unigene24722_A11	970	1.89	0.00	0.60	1.69	0.82	1.26	2.09	1.21	2.22	-1.09E+01	1.34E-10	Down	-1.64E+00	2.15E-03		-1.05E+00	3.11E-02		-4.31E-01	4.32E-01		-7.94E-01	5.03E-02		8.41E-02	8.33E-01		Unigene24722_A11//gi|186413970|emb|CAD22561.1|//9.00E-08//reverse transcriptase [Brassica rapa subsp. rapa]	Unigene24722_A11//2.00E-07//AT4G20520| RNA binding / RNA-directed DNA polymerase	Unigene24722_A11//4.00E-40//ES821102			GO:0003676//GO:0006260//GO:0034061	nr -
Unigene24725_A11	1295	12.28	15.30	18.71	13.12	10.88	7.88	36.40	96.24	48.61	3.17E-01	1.22E-02		6.07E-01	1.02E-07		-2.70E-01	4.61E-02		-7.35E-01	2.15E-08		1.40E+00	2.16E-187	Up	4.17E-01	6.72E-13		Unigene24725_A11//gi|2829926|gb|AAC00634.1|//2.00E-38//Hypothetical protein [Arabidopsis thaliana] >gi|38454134|gb|AAR20761.1|At1g76980 [Arabidopsis thaliana] >gi|38604022|gb|AAR24754.1|At1g76980 [Arabidopsis thaliana]	Unigene24725_A11//3.00E-28//AT1G76980| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: emb2170 (embryo defective 2170) (TAIR:AT1G21390.1); Has 33 Blast hits to 33 proteins in 14 species: Archae - 0; Bacteria - 4; Metazoa - 2; Fungi - 7; Plants - 14; Viruses - 2; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene24725_A11//0.00E+00//TC137496				nr -
Unigene24727_A11	2078	0.10	0.17	0.18	0.48	0.35	0.61	1.08	0.28	0.40	7.61E-01	5.57E-01		8.33E-01	5.16E-01		-4.62E-01	5.19E-01		3.44E-01	6.24E-01		-1.94E+00	4.55E-06	Down	-1.42E+00	2.20E-04	Down	Unigene24727_A11//gi|297804260|ref|XP_002870014.1|//0.00E+00//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315850|gb|EFH46273.1|transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24727_A11//7.00E-168//AT4G18905| transducin family protein / WD-40 repeat family protein	Unigene24727_A11//0.00E+00//TC150780			GO:0004468	nr -
Unigene2473_A11	827	2.78	0.74	2.45	4.04	3.66	4.37	13.29	13.24	21.82	-1.92E+00	3.76E-05	Down	-1.86E-01	6.58E-01		-1.39E-01	7.21E-01		1.15E-01	7.43E-01		-5.60E-03	1.01E+00		7.15E-01	5.26E-10		Unigene2473_A11//gi|224074521|ref|XP_002304384.1|//3.00E-51//neutral amino acid transport protein [Populus trichocarpa] >gi|222841816|gb|EEE79363.1|neutral amino acid transport protein [Populus trichocarpa]	Unigene2473_A11//2.00E-40//AT1G31830| amino acid permease family protein	Unigene2473_A11//0.00E+00//gi|164335631|gb|ES806224.1|ES806224				nr -
Unigene24730_A11	2269	5.93	4.60	5.26	17.76	17.44	13.85	10.32	4.97	9.29	-3.65E-01	1.91E-02		-1.73E-01	3.32E-01		-2.65E-02	8.29E-01		-3.59E-01	1.21E-05		-1.05E+00	3.88E-23	Down	-1.52E-01	1.55E-01		Unigene24730_A11//gi|115479513|ref|NP_001063350.1|//3.00E-80//Os09g0454200 [Oryza sativa Japonica Group] >gi|51535214|dbj|BAD38263.1|hydroxyproline-rich glycoprotein-like protein [Oryza sativa Japonica Group] >gi|51535954|dbj|BAD38036.1|hydroxyproline-rich glycoprotein-like protein [Oryza sativa Japonica Group] >gi|113631583|dbj|BAF25264.1|Os09g0454200 [Oryza sativa Japonica Group]	Unigene24730_A11//1.00E-50//AT1G10790| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT3G56590.2); Has 40 Blast hits to 40 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene24730_A11//0.00E+00//DW241816		ko03040|Spliceosome//ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko03020|RNA polymerase//ko00565|Ether lipid metabolism		nr +

Unigene24731_All	2306	14.25	9.21	10.88	22.53	20.61	26.40	23.93	11.76	11.96	-6.30E-01	2.31E-11		-3.90E-01	6.08E-05		-1.29E-01	1.04E-01		2.29E-01	7.15E-04		-1.02E+00	4.83E-51	Down	-1.00E+00	1.41E-50	Down	Unigene24731_All//gi|297851044|ref|XP_002893403.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297339245|gb|EFH69662.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene24731_All//0.00E+00//AT1G26460| pentatricopeptide (PPR) repeat-containing protein	Unigene24731_All//0.00E+00//TC141265			GO:0016787//GO:0043231//GO:0044238	nr -
Unigene24733_All	1333	7.85	8.48	7.03	4.30	2.14	6.10	2.63	5.96	3.59	1.11E-01	5.67E-01		-1.59E-01	4.18E-01		-1.00E+00	1.37E-05	Down	5.05E-01	1.36E-02		1.18E+00	7.43E-10	Up	4.46E-01	6.48E-02		Unigene24733_All//gi|29420155|gb|AA061856.1|//1.00E-109//glutathione S-transferase Z1 [Malva pusilla]	Unigene24733_All//6.00E-79//AT2G02390| ATGSTZ1 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE ZETA 1); catalytic/ glutathione transferase	Unigene24733_All//0.00E+00//gi|13354841|gb|BG445189.1|BG445189		ko00350|Tyrosine metabolism	GO:0006520//GO:0009404//GO:0016765//GO:0016859//GO:0044424	nr -
Unigene24734_All	2638	14.32	8.18	12.68	24.98	21.59	13.54	26.70	13.99	6.25	-8.07E-01	1.47E-19		-1.76E-01	7.01E-02		-2.11E-01	6.86E-04		-8.84E-01	3.97E-42		-9.33E-01	1.13E-55		-2.09E+00	2.83E-192	Down	Unigene24734_All//gi|297807627|ref|XP_002871697.1|//0.00E+00//nsp-interacting kinase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297317534|gb|EFH47956.1| nsp-interacting kinase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene24734_All//0.00E+00//AT5G16000| NIK1 (NSP-INTERACTING KINASE 1); kinase	Unigene24734_All//0.00E+00//TC137581		ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene24736_All	1629	3.85	2.52	3.30	5.23	4.16	2.58	6.10	4.62	6.46	-6.13E-01	9.13E-03		-2.23E-01	3.96E-01		-3.29E-01	1.03E-01		-1.02E+00	1.98E-07	Down	-4.01E-01	1.48E-02		8.21E-02	6.49E-01		Unigene24736_All//gi|297833916|ref|XP_002884840.1|//1.00E-153//organic anion transporter [Arabidopsis lyrata subsp. lyrata] >gi|297330680|gb|EFH61099.1| organic anion transporter [Arabidopsis lyrata subsp. lyrata]	Unigene24736_All//1.00E-148//AT3G11320| organic anion transmembrane transporter	Unigene24736_All//0.00E+00//TC163497				nr +
Unigene24737_All	1297	47.68	57.23	47.01	71.67	62.74	65.26	75.69	79.82	37.78	2.63E-01	1.49E-05		-2.05E-02	7.97E-01		-1.92E-01	1.80E-04		-1.35E-01	1.74E-02		7.66E-02	1.41E-01		-1.00E+00	1.60E-89	Down	Unigene24737_All//gi|449174149|gb|AES49049.1|//4.00E-70//At4g14840 [Arabidopsis thaliana] >gi|46931278|gb|AAT06443.1| At4g14840 [Arabidopsis thaliana]	Unigene24737_All//3.00E-76//AT3G22520| unknown protein	Unigene24737_All//0.00E+00//gi|164301346|gb|ES807538.1|ES807538			GO:0009526//GO:0009532	nr +
Unigene24738_All	684	5.51	2.52	9.96	5.24	4.73	3.63	2.60	3.42	2.04	-1.13E+00	4.44E-04	Down	8.56E-01	2.59E-04		-1.48E-01	6.82E-01		-5.30E-01	1.14E-01		3.98E-01	3.13E-01		-3.49E-01	4.21E-01		Unigene24738_All//gi|18401324|ref|NP_565636.1|//3.00E-19//FRS3 (FAR1-related sequence 3); zinc ion binding [Arabidopsis thaliana] >gi|30683396|ref|NP_850098.1| FRS3 (FAR1-related sequence 3); zinc ion binding [Arabidopsis thaliana] >gi|75216958|sp|Q93Y39.2|FRS3_ARATH RecName: Full=Protein FAR1-RELATED SEQUENCE 3 >gi|15982769|gb|AAL09732.1| At2g27110/T20P8.16 [Arabidopsis thaliana] >gi|20197414|gb|AAC77869.2| Mutator-like transposase [Arabidopsis thaliana] >gi|27363374|gb|AAO11606.1| At2g27110/T20P8.16 [Arabidopsis thaliana]	Unigene24738_All//5.00E-20//AT2G27110| FRS3 (FAR1-related sequence 3); zinc ion binding	Unigene24738_All//0.00E+00//TC163005				nr -
Unigene24741_All	233	4.49	0.43	0.91	4.92	0.89	12.41	11.79	78.03	30.26	-3.37E+00	2.13E-04	Down	-2.30E+00	4.70E-03		-2.47E+00	2.73E-04	Down	1.34E+00	4.05E-04	Up	2.73E+00	4.28E-66	Up	1.36E+00	3.98E-11	Up	Unigene24741_All//gi|66346995|emb|CAE00460.2|//1.00E-20//branched-chain amino acid aminotransferase [Hordeum vulgare subsp. vulgare]	Unigene24741_All//2.00E-19//AT1G50090| aminotransferase class IV family protein	Unigene24741_All//5.00E-129//TC146308		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis	GO:0006520//GO:0008483	nr -
Unigene24742_All	563	4.46	1.80	3.59	0.80	1.22	2.17	28.16	16.93	8.42	-1.31E+00	1.48E-03		-3.12E-01	4.62E-01		6.19E-01	5.30E-01		1.44E+00	2.53E-02		-7.35E-01	4.98E-09		-1.74E+00	2.09E-34	Down	Unigene24742_All//gi|255689399|gb|ACU30051.1|//3.00E-67//branched-chain amino acid aminotransferase [Glycine max]	Unigene24742_All//2.00E-67//AT1G50110| branched-chain amino acid aminotransferase 6 / branched-chain amino acid transaminase 6 (BCAT6)	Unigene24742_All//0.00E+00//gi|164242862|gb|ES807040.1|ES807040		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis	GO:0006520//GO:0008483//GO:0009536	nr -
Unigene24743_All	1322	8.75	4.06	3.71	7.23	3.41	11.44	34.57	88.87	42.46	-1.11E+00	1.67E-10	Down	-1.24E+00	7.35E-12	Down	-1.08E+00	4.12E-10	Down	6.62E-01	2.44E-06		1.36E+00	5.42E-169	Up	2.97E-01	1.51E-06		Unigene24743_All//gi|297852700|ref|XP_002894231.1|//1.00E-122//aminotransferase class IV family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340073|gb|EFH70490.1| aminotransferase class IV family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24743_All//7.00E-123//AT1G50090| aminotransferase class IV family protein	Unigene24743_All//0.00E+00//TC146308		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene24745_All	2106	17.19	19.42	24.96	31.81	31.98	36.24	9.03	3.71	5.64	1.76E-01	4.65E-02		5.38E-01	6.02E-13		7.60E-03	9.36E-01		1.88E-01	1.96E-03		-1.28E+00	1.16E-25	Down	-6.80E-01	9.57E-10		Unigene24745_All//gi|224131384|ref|XP_002321071.1|//0.00E+00//glycosyltransferase [Populus trichocarpa] >gi|222861844|gb|EEE99386.1| glycosyltransferase [Populus trichocarpa]	Unigene24745_All//0.00E+00//AT3G58790| GAUT15 (Galacturonosyltransferase 15); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene24745_All//0.00E+00//TC136551			GO:0008194	nr -
Unigene24746_All	1927	305.43	94.53	212.34	129.77	167.32	81.98	1.97	1.82	1.53	-1.69E+00	0.00E+00	Down	-5.25E-01	3.03E-133		3.67E-01	7.27E-47		-6.63E-01	2.36E-96		-1.16E-01	7.06E-01		-3.68E-01	1.90E-01		Unigene24746_All//gi|18411523|ref|NP_567209.1|//1.00E-134//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|73622092|sp|Q9M158.2|Y4105_ARATH RecName: Full=Uncharacterized protein At4g01050 >gi|15982915|gb|AAL09804.1| AT4g01050/F2N1_31 [Arabidopsis thaliana] >gi|16323194|gb|AAL15331.1| AT4g01050/F2N1_31 [Arabidopsis thaliana] >gi|21700911|gb|AAM70579.1| AT4g01050/F2N1_31 [Arabidopsis thaliana]	Unigene24746_All//6.00E-111//AT4G01050| hydroxyproline-rich glycoprotein family protein	Unigene24746_All//0.00E+00//TC133963				nr +
Unigene24749_All	1152	4.45	2.16	2.59	6.01	5.89	5.68	13.62	11.94	13.07	-1.05E+00	9.60E-05	Down	-7.82E-01	4.55E-03		-2.96E-02	9.05E-01		-8.05E-02	7.45E-01		-1.90E-01	1.69E-01		-5.88E-02	6.73E-01		Unigene24749_All//gi|297811301|ref|XP_002873534.1|//1.00E-100//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319371|gb|EFH49793.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24749_All//8.00E-100//AT5G11850| protein kinase family protein	Unigene24749_All//0.00E+00//TC152932			GO:0004702//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene24750_All	1981	3.17	0.90	1.51	3.70	3.39	3.10	6.68	3.10	2.78	-1.82E+00	5.99E-12	Down	-1.07E+00	1.61E-05	Down	-1.25E-01	6.02E-01		-2.54E-01	2.93E-01		-1.11E+00	1.76E-14	Down	-1.27E+00	2.57E-18	Down	Unigene24750_All//gi|115463921|ref|NP_001055560.1|//0.00E+00//Os05g0417100 [Oryza sativa Japonica Group] >gi|113579111|dbj|BAF17474.1| Os05g0417100 [Oryza sativa Japonica Group]	Unigene24750_All//0.00E+00//AT5G36950| DegP10 (DegP protease 10); catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase	Unigene24750_All//0.00E+00//CO132889			GO:0004175//GO:0005488//GO:0016491//GO:0019538//GO:0043231	nr -
Unigene24751_All	1347	1.17	1.69	4.51	10.39	12.42	21.56	96.86	37.82	52.97	5.39E-01	2.11E-01		1.95E+00	4.62E-12	Up	2.58E-01	6.74E-02		1.05E+00	8.58E-25	Up	-1.36E+00	8.43E-187	Down	-8.71E-01	7.09E-94		Unigene24751_All//gi|300509024|gb|ADK22418.1|//1.00E-170//cinnamyl alcohol dehydrogenase [Hibiscus cannabinus]	Unigene24751_All//5.00E-146//AT4G34230| ATCAD5 (CINNAMYL ALCOHOL DEHYDROGENASE 5); cinnamyl-alcohol dehydrogenase	Unigene24751_All//0.00E+00//gi|48792786|gb|CO094100.1|CO094100		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene24753_All	706	0.44	2.30	1.66	1.41	0.73	1.60	7.07	8.64	6.55	2.37E+00	1.02E-04	Up	1.90E+00	8.12E-03		-9.48E-01	1.58E-01		1.81E-01	7.84E-01		2.91E-01	2.08E-01		-1.11E-01	6.55E-01		Unigene24753_All//gi|30013679|gb|AAP03882.1|//2.00E-85//Avr9/Cf-9 rapidly elicited protein 276 [Nicotiana tabacum]	Unigene24753_All//4.00E-49//AT1G29340| PUB17 (PLANT U-BOX 17); ubiquitin-protein ligase	Unigene24753_All//0.00E+00//TC142062			GO:0005488//GO:0012501//GO:0019787//GO:0032446//GO:0043231//GO:0043234//GO:0050832	nr -
Unigene24755_All	1226	18.56	16.66	17.33	29.09	27.89	31.46	67.97	27.00	29.47	-1.57E-01	2.16E-01		-9.92E-02	4.61E-01		-6.08E-02	5.86E-01		1.13E-01	2.66E-01		-1.33E+00	3.22E-116	Down	-1.21E+00	2.21E-102	Down	Unigene24755_All//gi|15242792|ref|NP_201156.1|//1.00E-110//GAMMA CAL1 (GAMMA CARBONIC ANHYDRASE LIKE 1); carbonate dehydratase [Arabidopsis thaliana] >gi|25091501|sp|Q9FWV1.1|UMP7_ARATH RecName: Full=Uncharacterized protein At5g63510, mitochondrial	Unigene24755_All//1.00E-109//AT5G63510| GAMMA CAL1 (GAMMA CARBONIC ANHYDRASE LIKE 1); carbonate dehydratase	Unigene24755_All//0.00E+00//TC130052			GO:0003824	nr -
Unigene24756_All	1512	12.67	3.42	12.75	7.54	7.08	6.57	3.22	2.76	1.79	-1.89E+00	1.05E-36	Down	9.50E-03	9.66E-01		-9.11E-02	6.40E-01		-1.99E-01	3.01E-01		-2.18E-01	4.15E-01		-8.44E-01	3.53E-04		Unigene24756_All//gi|57222140|gb|AAW38977.1|//2.00E-82//At5g49800 [Arabidopsis thaliana]	Unigene24756_All//7.00E-84//AT5G49800| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, C globular stage, petal differentiation and expansion stage, D bilateral stage; CONTAINS InterPro DOMAIN/s: Lipid-binding START (InterPro:IPR002913); Has 156 Blast hits to 155 proteins in 50 species: Archae - 0; Bacteria - 14; Metazoa - 91; Fungi - 2; Plants - 15; Viruses - 0; Other Eukaryotes - 34 (source: NCBI BLink).	Unigene24756_All//0.00E+00//TC154459				nr +
Unigene24757_All	1264	5.80	5.65	7.79	5.56	7.71	4.57	7.26	2.98	3.94	-3.60E-02	8.79E-01		4.28E-01	2.66E-02		4.72E-01	8.20E-03		-2.81E-01	2.43E-01		-1.29E+00	7.88E-13	Down	-8.82E-01	1.41E-07		Unigene24757_All//gi|297829036|ref|XP_002882400.1|//1.00E-114//phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328240|gb|EFH58659.1| phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24757_All//7.00E-110//AT3G05170| phosphoglycerate/bisphosphoglycerate mutase family protein	Unigene24757_All//0.00E+00//ES792435				nr -

Unigene24758_All	1850	3.90	1.29	1.73	5.90	3.26	3.08	3.93	5.24	3.60	-1.60E+00	1.81E-11	Down	-1.18E+00	4.21E-07	Down	-8.56E-01	6.99E-08		-9.39E-01	3.24E-08		4.15E-01	1.27E-02		-1.28E-01	5.58E-01		Unigene24758_All//gi|18411962|ref|NP_567241.1|//0.00E+00//XT2 (UDP-XYLOSYLTRANSFERASE 2); UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups / xyloglucan 6-xylosyltransferase [Arabidopsis thaliana] >gi|46576207|sp|Q22775.1|GT2_ARATH RecName: Full=Putative glycosyltransferase 2; Short=AtGT2 >gi|3193287|gb|AAC19271.1|T14P8.23 [Arabidopsis thaliana] >gi|16209669|gb|AAL14393.1|AT4g02500/T10P11_20 [Arabidopsis thaliana] >gi|30387559|gb|AAP31945.1|At4g02500 [Arabidopsis thaliana]	Unigene24758_All//0.00E+00//AT4G02500| XT2 (UDP-XYLOSYLTRANSFERASE 2); UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups / xyloglucan 6-xylosyltransferase	Unigene24758_All//0.00E+00//ES828626			GO:0008194//GO:0009250//GO:0031224//GO:0042285//GO:0048588	nr -
Unigene24762_All	1996	5.27	3.66	5.31	4.77	5.28	5.61	8.18	6.26	3.89	-5.27E-01	2.72E-03		1.10E-02	9.76E-01		1.47E-01	4.89E-01		2.35E-01	2.14E-01		-3.85E-01	1.89E-03		-1.07E+00	2.57E-17	Down	Unigene24762_All//gi|297831554|ref|XP_002883659.1|//0.00E+00//ankyrin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329499|gb|EFH59918.1|ankyrin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24762_All//0.00E+00//AT2G04740| ankyrin repeat family protein	Unigene24762_All//0.00E+00//gi|78336956|gb|DT557230.1|DT557230			GO:0005488	nr +
Unigene24765_All	520	2.62	0.29	1.64	1.15	1.72	2.87	3.41	0.80	1.46	-3.16E+00	2.85E-05	Down	-6.75E-01	2.58E-01		5.83E-01	4.72E-01		1.32E+00	1.96E-02		-2.09E+00	2.21E-05	Down	-1.23E+00	4.20E-03		Unigene24765_All//gi|87162555|gb|AB028350.1|//1.00E-16//Protein phosphatase 2C-like [Medicago truncatula]	Unigene24765_All//7.00E-05//AT5G27930| protein phosphatase 2C, putative / PP2C, putative	Unigene24765_All//7.00E-50//TC168339			GO:0004721//GO:0006950	nr +
Unigene24766_All	1460	4.95	2.60	4.56	4.13	7.15	8.88	5.30	3.35	4.20	-9.26E-01	2.48E-05		-1.17E-01	6.07E-01		7.92E-01	2.02E-06		1.10E+00	3.01E-12	Up	-6.62E-01	3.71E-04		-3.35E-01	7.19E-02		Unigene24766_All//gi|87162555|gb|AB028350.1|//1.00E-161//Protein phosphatase 2C-like [Medicago truncatula]	Unigene24766_All//4.00E-144//AT5G27930| protein phosphatase 2C, putative / PP2C, putative	Unigene24766_All//0.00E+00//TC171325				nr -
Unigene24768_All	2035	1.05	4.48	1.91	1.59	1.10	2.91	12.03	30.87	41.91	2.09E+00	4.28E-20	Up	8.58E-01	8.06E-03		-5.33E-01	1.16E-01		8.70E-01	3.15E-04		1.36E+00	2.09E-90	Up	1.80E+00	5.81E-188	Up	Unigene24768_All//gi|18396768|ref|NP_564307.1|//0.00E+00//NSL1 (necrotic spotted lesions 1) [Arabidopsis thaliana] >gi|6560762|gb|AAF16762.1|AC010155_15 F3M18.18 [Arabidopsis thaliana]	Unigene24768_All//0.00E+00//AT1G28380| NSL1 (necrotic spotted lesions 1)	Unigene24768_All//0.00E+00//D8453833			GO:0006952//GO:0006970//GO:0009696//GO:0033554	nr +
Unigene24769_All	1205	45.37	12.70	20.02	65.23	72.96	52.17	77.65	33.23	80.57	-1.84E+00	8.61E-100	Down	-1.18E+00	3.97E-50	Down	1.61E-01	3.28E-03		-3.22E-01	1.35E-08		-1.22E+00	1.85E-114	Down	5.33E-02	3.37E-01		Unigene24769_All//gi|15230120|ref|NP_189091.1|//1.00E-137//leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] >gi|75334999|sp|Q9LHF1.1|LRX4_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 4; Short=LRR/EXTENSIN4; Short=AtLRX4; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|9294099|dbj|BAB01951.1|extensin-like protein [Arabidopsis thaliana]	Unigene24769_All//4.00E-131//AT3G24480| leucine-rich repeat family protein / extensin family protein	Unigene24769_All//0.00E+00//gi|109865606|gb|DW494582.1|DW494582		ko04626|Plant-pathogen interaction	GO:0005198//GO:0044464	nr +
Unigene24770_All	1889	1.19	1.85	1.10	1.45	1.86	1.84	23.39	9.45	6.16	6.36E-01	5.43E-02		-1.16E-01	7.85E-01		3.58E-01	3.12E-01		3.44E-01	3.48E-01		-1.31E+00	2.96E-60	Down	-1.93E+00	3.17E-108	Down	Unigene24770_All//gi|9719299|gb|AAF97728.1|AF176035_1//1.00E-156//potassium-sodium symporter HKT1 [Eucalyptus camaldulensis]	Unigene24770_All//1.00E-93//AT4G10310| HKT1 (HIGH-AFFINITY K+ TRANSPORTER 1); sodium ion transmembrane transporter					nr +
Unigene24776_All	1171	9.70	3.76	5.96	12.51	9.17	10.88	1.41	3.39	1.63	-1.36E+00	4.60E-14	Down	-7.03E-01	5.75E-05		-4.47E-01	1.16E-03		-2.02E-01	2.21E-01		1.27E+00	7.15E-06	Up	2.14E-01	6.18E-01		Unigene24776_All//gi|217741977|emb|CAD41785.1|//2.00E-08//OSJNBa0035M09.1 [Oryza sativa (japonica cultivar-group)] >gi|38346911|emb|CAE03883.2|OSJNBb0015N08.11 [Oryza sativa (japonica cultivar-group)]	Unigene24776_All//9.00E-08//AT3G09510| nucleic acid binding	Unigene24776_All//0.00E+00//D8519451				nr -
Unigene24777_All	1387	2.90	6.50	2.92	6.43	5.46	4.40	3.96	7.77	6.52	1.16E+00	5.89E-09	Up	6.50E-03	1.00E+00		-2.35E-01	2.62E-01		-5.48E-01	4.09E-03		9.72E-01	8.35E-10		7.18E-01	1.72E-05		Unigene24777_All//gi|15241123|ref|NP_198156.1|//5.00E-68//transcription regulator [Arabidopsis thaliana]	Unigene24777_All//1.00E-28//AT3G04930| transcription regulator	Unigene24777_All//0.00E+00//gi|78334760|gb|DT555034.1|DT555034	GeBP			nr -
Unigene24778_All	1322	20.22	49.60	19.78	14.70	22.74	22.34	11.16	12.14	12.75	1.29E+00	2.20E-71	Up	-3.22E-02	7.89E-01		6.30E-01	5.66E-12		6.04E-01	4.23E-10		1.21E-01	3.97E-01		1.92E-01	1.29E-01		Unigene24778_All//gi|115441875|ref|NP_001045217.1|//1.00E-23//Os01g0920100 [Oryza sativa Japonica Group] >gi|113534748|dbj|BAF07131.1|Os01g0920100 [Oryza sativa Japonica Group]	Unigene24778_All//2.00E-22//AT3G01860| unknown protein	Unigene24778_All//0.00E+00//TC147878				nr -
Unigene24779_All	1367	4.29	2.04	5.96	6.41	3.58	7.96	6.59	7.83	53.13	-1.07E+00	1.75E-05	Down	4.75E-01	2.61E-02		-8.42E-01	2.79E-06		3.12E-01	8.72E-02		2.49E-01	1.37E-01		3.01E+00	2.48E-296	Up	Unigene24779_All//gi|16604352|gb|AAL24182.1|//1.00E-123//AT5g12010/F14F18_180 [Arabidopsis thaliana] >gi|25141199|gb|AAN73294.1|At5g12010/F14F18_180 [Arabidopsis thaliana]	Unigene24779_All//4.00E-106//AT5G12010| unknown protein	Unigene24779_All//0.00E+00//gi|164330162|gb|ES803558.1|ES803558				nr -
Unigene2478_All	1749	28.00	37.34	25.24	26.94	33.39	56.45	21.25	45.19	27.24	4.15E-01	1.29E-10		-1.50E-01	8.01E-02		3.10E-01	1.41E-06		1.07E+00	5.82E-85	Up	1.09E+00	3.49E-80	Up	3.59E-01	9.40E-08		Unigene2478_All//gi|297806753|ref|XP_002871260.1|//1.00E-73//IQ-domain 24 [Arabidopsis lyrata subsp. lyrata] >gi|297317097|gb|EFH47519.1| IQ-domain 24 [Arabidopsis lyrata subsp. lyrata]	Unigene2478_All//1.00E-41//AT5G07240| IQD24 (IQ-domain 24); calmodulin binding	Unigene2478_All//0.00E+00//TC157310				nr -
Unigene24783_All	1714	10.04	6.59	4.72	58.56	43.32	54.07	12.28	7.73	35.89	-6.07E-01	5.37E-06		-1.09E+00	3.04E-14	Down	-4.35E-01	1.29E-20		-1.15E-01	3.99E-02		-6.68E-01	4.69E-10		1.55E+00	1.72E-109	Up	Unigene24783_All//gi|259563723|gb|ACW83060.1|//1.00E-176//glycosyltransferase family GT8 protein [Populus deltoides]	Unigene24783_All//3.00E-152//AT1G19300| PARVUS (PARVUS); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene24783_All//0.00E+00//TC153816				nr -
Unigene24785_All	2193	3.36	4.21	3.52	1.02	1.60	1.54	3.62	4.15	13.32	3.22E-01	1.01E-01		6.58E-02	7.73E-01		6.48E-01	4.73E-02		5.96E-01	8.39E-02		1.97E-01	3.06E-01		1.88E+00	1.42E-68	Up	Unigene24785_All//gi|5091545|gb|AAD39574.1|AC007067_14//5.00E-24//T10024.14 [Arabidopsis thaliana] >gi|149944329|gb|ABR46207.1|At1g10522 [Arabidopsis thaliana]	Unigene24785_All//2.00E-25//AT1G10522| unknown protein	Unigene24785_All//0.00E+00//TC144184			GO:0009536	nr +
Unigene24786_All	543	10.31	4.01	6.67	3.03	1.90	0.67	0.86	0.46	1.03	-1.36E+00	2.66E-07	Down	-6.29E-01	1.67E-02		-6.70E-01	1.82E-01		-2.19E+00	1.26E-04	Down	-8.91E-01	3.84E-01		2.62E-01	7.46E-01		Unigene24786_All//gi|5091545|gb|AAD39574.1|AC007067_14//8.00E-23//T10024.14 [Arabidopsis thaliana] >gi|149944329|gb|ABR46207.1|At1g10522 [Arabidopsis thaliana]	Unigene24786_All//4.00E-24//AT1G10522| unknown protein				GO:0009536	nr +
Unigene24787_All	1365	43.58	26.76	42.48	7.77	13.40	5.66	5.20	6.55	18.88	-7.03E-01	4.73E-24		-3.68E-02	6.42E-01		7.85E-01	9.92E-11		-4.58E-01	8.82E-03		3.33E-01	6.31E-02		1.86E+00	7.39E-60	Up	Unigene24787_All//gi|5091546|gb|AAD39575.1|AC007067_15//5.00E-33//T10024.15 [Arabidopsis thaliana]	Unigene24787_All//1.00E-34//AT1G10530| unknown protein	Unigene24787_All//0.00E+00//TC144184				nr +
Unigene24788_All	2227	3.31	1.66	4.26	4.38	4.78	8.68	38.35	15.76	58.59	-9.96E-01	5.06E-06		3.62E-01	7.13E-02		1.24E-01	5.60E-01		9.85E-01	5.02E-15		-1.28E+00	2.40E-112	Down	6.11E-01	8.97E-51		Unigene24788_All//gi|294861494|gb|ADF45509.1|//1.00E-106//type 2 ribosome-inactivating protein precursor [Camellia sinensis]		Unigene24788_All//0.00E+00//TC156855			GO:0005529//GO:0008152//GO:0016798//GO:0050794	nr +
Unigene24790_All	1782	0.82	1.34	2.63	3.69	4.56	5.53	2.09	1.41	4.29	7.01E-01	8.95E-02		1.68E+00	8.42E-08	Up	3.06E-01	1.56E-01		5.82E-01	1.25E-03		-5.69E-01	4.68E-02		1.04E+00	3.66E-08	Up	Unigene24790_All//gi|224127754|ref|XP_002329169.1|//1.00E-97//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870950|gb|EEF08081.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene24790_All//2.00E-86//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene24790_All//2.00E-99//TC140957		ko04626|Plant-pathogen interaction		nr +
Unigene24792_All	1194	3.55	1.61	3.17	2.38	2.57	2.69	3.15	2.66	3.47	-1.14E+00	1.56E-04	Down	-1.65E-01	6.37E-01		1.10E-01	8.13E-01		1.75E-01	6.57E-01		-2.44E-01	4.27E-01		1.39E-01	6.27E-01				Unigene24792_All//0.00E+00//gi|164343652|gb|ES843200.1|ES843200				ESTscan -
Unigene24796_All	2354	2.09	2.00	1.29	2.48	2.60	2.34	11.28	3.21	6.60	-6.17E-02	8.21E-01		-6.96E-01	1.37E-02		7.27E-02	8.27E-01		-8.10E-02	7.62E-01		-1.81E+00	2.02E-58	Down	-7.73E-01	2.50E-16		Unigene24796_All//gi|224092304|ref|XP_002309550.1|//1.00E-172//glycosyl transferase [Populus trichocarpa] >gi|222855526|gb|EEE93073.1|glycosyl transferase [Populus trichocarpa]	Unigene24796_All//4.00E-94//AT1G27600| glycosyl transferase family 43 protein	Unigene24796_All//0.00E+00//TC176193			GO:0015020//GO:0044464	nr -
Unigene24798_All	1496	52.01	41.25	36.41	66.06	65.51	46.31	46.35	25.03	8.71	-3.34E-01	1.33E-08		-5.14E-01	2.03E-17		-1.21E-02	8.53E-01		-5.13E-01	2.29E-24		-8.89E-01	1.30E-50		-2.41E+00	1.81E-225	Down	Unigene24798_All//gi|18402992|ref|NP_566685.1|//1.00E-152//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|29029688|gb|AAO64923.1|At3g21420 [Arabidopsis thaliana]	Unigene24798_All//2.00E-147//AT3G21420| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene24798_All//0.00E+00//TC135303		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis	GO:0007568//GO:0008152//GO:0016491	nr -
Unigene24801_All	1899	14.46	39.44	14.64	13.01	17.15	16.05	6.19	10.65	6.94	1.45E+00	1.94E-96	Up	1.71E-02	8.92E-01		3.99E-01	6.03E-06		3.03E-01	2.01E-03		7.83E-01	1.63E-12		1.66E-01	2.64E-01		Unigene24801_All//gi|195636148|gb|ACG37542.1|//0.00E+00//eukaryotic peptide chain release factor subunit 1-1 [Zea mays]	Unigene24801_All//0.00E+00//AT3G26618| ERF1-3 (eukaryotic release factor 1-3); translation release factor	Unigene24801_All//0.00E+00//TC137467			GO:0003747//GO:0006412//GO:0044424	nr +
Unigene24805_All	2529	1.61	1.82	0.88	3.33	2.19	1.30	4.63	4.02	2.35	1.76E-01	5.67E-01		-8.68E-01	5.93E-03		-6.03E-01	1.21E-03		-1.35E+00	3.72E-11	Down	-2.06E-01	2.10E-01		-9.80E-01	4.38E-11		Unigene24805_All//gi|115452215|ref|NP_001049708.1|//0.00E+00//Os03g0275500 [Oryza sativa Japonica Group] >gi|113548179|dbj|BAF11622.1|Os03g0275500 [Oryza sativa Japonica Group]	Unigene24805_All//2.00E-152//AT4G32285| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	Unigene24805_All//0.00E+00//TC151645			GO:0005515//GO:0006901//GO:0016491//GO:0030117//GO:0035091//GO:0043231	nr +
Unigene24807_All	1161	8.74	8.47	10.41	7.21	8.72	7.08	2.91	2.45	1.41	-4.63E-02	8.08E-01		2.52E-01	1.58E-01		2.75E-01	1.53E-01		-2.59E-02	9.26E-01		-2.51E-01	4.42E-01		-1.05E+00	3.51E-04	Down	Unigene24807_All//gi|15226168|ref|NP_178215.1|//2.00E-25//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene24807_All//8.00E-27//AT2G01050| nucleic acid binding / zinc ion binding	Unigene24807_All//5.00E-28//TC175764				nr -
Unigene24809_All	759	5.10	5.47	4.70	6.37	6.90	5.95	4.07	3.41	1.99	1.02E-01	7.29E-01		-1.18E-01	7.15E-01		1.15E-01	7.29E-01		-9.74E-02	7.42E-01		-2.52E-01	4.67E-01		-1.03E+00	8.73E-04	Down	Unigene24809_All//gi|6969575|gb|AAF33823.1|AF223351_1//5.00E-27//phospholipase C1 [Nicotiana tabacum]	Unigene24809_All//9.00E-25//AT3G46020| RNA-binding protein, putative	Unigene24809_All//0.00E+00//TC174884		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0004629//GO:0023060//GO:0044238//GO:0046872//GO:0060089	nr +
Unigene2481_All	2198	2.36	2.70	2.54	3.04	3.42	2.75	4.52	2.76	2.21	1.95E-01	4.50E-01		1.10E-01	6.79E-01		1.69E-01	5.13E-01		-1.41E-01	6.21E-01		-7.13E-01	1.05E-05		-1.03E+00	2.68E-10	Down	Unigene2481_All//gi|225424303|ref|XP_002280941.1|//0.00E+00//PREDICTED: similar to armadillo/beta-catenin repeat family protein [Vitis vinifera]	Unigene2481_All//8.00E-178//AT1G23180| armadillo/beta-catenin repeat family protein	Unigene2481_All//0.00E+00//C0131070				nr -
Unigene24810_All	2112	0.50	0.82	0.35	1.82	2.54	1.18	7.23	15.71	5.43	7.19E-01	1.48E-01		-4.89E-01	4.78E-01		4.86E-01	6.04E-02		-6.27E-01	4.62E-02		1.12E+00	1.01E-35	Up	-4.12E-01	9.46E-04		Unigene24810_All//gi|158827646|gb|ABR81000.1|//0.00E+00//PI-phospholipase C PLC4 [Solanum lycopersicum]	Unigene24810_All//4.00E-175//AT5G58700| phosphoinositide-specific phospholipase C family protein	Unigene24810_All//0.00E+00//TC138492		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0004629//GO:0023060//GO:0044238//GO:0046872//GO:0060089	nr -

Unigene24812_All	2854	1.32	2.66	2.18	7.82	6.49	10.92	2.21	1.98	1.93	1.01E+00	2.66E-06	Up	7.26E-01	3.16E-03		-2.69E-01	1.95E-02		4.82E-01	2.87E-07		-1.59E-01	5.18E-01		-1.97E-01	3.77E-01		Unigene24812_All//gi|115480315|ref|NP_001063751.1|//0.00E+00//Os09g0530800 [Oryza sativa Japonica Group] >gi|113631984|dbj|BAF25665.1|Os09g0530800 [Oryza sativa Japonica Group]	Unigene24812_All//0.00E+00//AT4G10550| subtilase family protein	Unigene24812_All//0.00E+00//TC170056			GO:0004175//GO:0005515//GO:0005576//GO:0019538//GO:0031410//GO:0044092	nr -
Unigene24813_All	1860	13.50	9.02	7.41	29.30	27.25	30.38	24.37	17.73	9.49	-5.83E-01	8.03E-08		-8.65E-01	3.48E-14		-1.05E-01	1.94E-01		5.21E-02	5.75E-01		-4.59E-01	6.67E-11		-1.36E+00	1.50E-67	Down	Unigene24813_All//gi|30725690|gb|AAP37867.1|//1.00E-129//At4g31080 [Arabidopsis thaliana]	Unigene24813_All//3.00E-111//AT4G31080| unknown protein	Unigene24813_All//0.00E+00//TC154343			GO:0003676//GO:0006260//GO:0034061	nr +
Unigene24814_All	1613	68.02	58.71	56.19	35.48	39.28	32.82	2.96	3.01	1.14	-2.12E-01	1.88E-05		-2.76E-01	4.74E-08		1.47E-01	3.23E-02		-1.13E-01	1.54E-01		2.12E-02	9.63E-01		-1.38E+00	4.51E-08	Down	Unigene24814_All//gi|18447767|gb|AAL67994.1|//0.00E+00//acyltransferase-like protein [Gossypium hirsutum]	Unigene24814_All//6.00E-167//AT5G23940| EMB3009 (embryo defective 3009); transferase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene24814_All//0.00E+00//TC130449		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016747	nr +
Unigene24815_All	1178	6.04	9.33	8.32	14.17	22.22	12.65	26.49	91.65	35.68	6.28E-01	2.51E-04		4.62E-01	1.64E-02		6.49E-01	4.95E-11		-1.63E-01	3.04E-01		1.79E+00	2.41E-231	Up	4.30E-01	2.26E-09		Unigene24815_All//gi|300793630|tpg|DAA33874.1|//1.00E-152//TPA: TPA_inf: aquaporin NIP1;1 [Gossypium hirsutum]	Unigene24815_All//2.00E-100//AT4G18910| NIP1;2 (NODO26-LIKE INTRINSIC PROTEIN 1;2); arsenite transmembrane transporter/ water channel	Unigene24815_All//0.00E+00//gi|164295610|gb|ES813875.1|ES813875			GO:0044464//GO:0051234	nr -
Unigene24817_All	748	11.40	16.05	6.83	18.18	11.46	12.26	16.73	11.85	7.03	4.94E-01	2.57E-03		-7.38E-01	3.29E-04		-6.65E-01	1.99E-06		-5.69E-01	1.31E-04		-4.98E-01	4.62E-04		-1.25E+00	4.88E-17	Down	Unigene24817_All//gi|297723437|ref|NP_001174082.1|//8.00E-58//Os04g0607100 [Oryza sativa Japonica Group] >gi|255675757|dbj|BAH92810.1|Os04g0607100 [Oryza sativa Japonica Group]	Unigene24817_All//8.00E-56//AT5G57270| unknown protein	Unigene24817_All//0.00E+00//TC141329			GO:0008194//GO:0043231	nr +
Unigene24818_All	1848	13.39	12.34	10.60	18.79	14.31	12.54	13.70	8.35	5.97	-1.18E-01	3.46E-01		-3.37E-01	3.52E-03		-3.93E-01	2.92E-06		-5.84E-01	3.62E-11		-7.16E-01	2.41E-13		-1.20E+00	1.95E-31	Down	Unigene24818_All//gi|17065506|gb|AAL32907.1|//1.00E-148//Unknown protein [Arabidopsis thaliana] >gi|53828653|gb|AAU94436.1|At2g19160 [Arabidopsis thaliana]	Unigene24818_All//1.00E-149//AT4G30060| unknown protein	Unigene24818_All//0.00E+00//TC141329				nr -
Unigene24819_All	855	0.92	3.50	3.99	1.34	2.42	1.16	0.30	0.44	0.42	1.93E+00	1.91E-06	Up	2.12E+00	9.57E-08	Up	8.51E-01	5.85E-02		-2.06E-01	7.39E-01		5.69E-01	6.37E-01		4.99E-01	6.27E-01		Unigene24819_All//gi|115478729|ref|NP_001062958.1|//3.00E-58//Os09g0352400 [Oryza sativa Japonica Group] >gi|50252790|dbj|BAD29024.1|bystin (51.6 kD)-like [Oryza sativa Japonica Group] >gi|50252802|dbj|BAD29035.1|bystin (51.6 kD)-like [Oryza sativa Japonica Group] >gi|113631191|dbj|BAF24872.1|Os09g0352400 [Oryza sativa Japonica Group]	Unigene24819_All//2.00E-64//AT1G31660| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Bystin (InterPro:IPR007955); Has 370 Blast hits to 362 proteins in 156 species: Archae - 0; Bacteria - 7; Metazoa - 139; Fungi - 93; Plants - 32; Viruses - 0; Other Eukaryotes - 99 (source: NCBI BLink).	Unigene24819_All//2.00E-106//C0093473			GO:0003676//GO:0006260//GO:0034061	nr -
Unigene24820_All	1986	5.82	1.56	2.52	11.36	8.91	19.81	11.26	7.98	11.55	-1.90E+00	1.21E-22	Down	-1.21E+00	2.01E-11	Down	-3.50E-01	1.36E-03		8.02E-01	2.30E-21		-4.98E-01	1.35E-06		3.70E-02	7.45E-01		Unigene24820_All//gi|115478729|ref|NP_001062958.1|//1.00E-145//Os09g0352400 [Oryza sativa Japonica Group] >gi|50252790|dbj|BAD29024.1|bystin (51.6 kD)-like [Oryza sativa Japonica Group] >gi|50252802|dbj|BAD29035.1|bystin (51.6 kD)-like [Oryza sativa Japonica Group] >gi|113631191|dbj|BAF24872.1|Os09g0352400 [Oryza sativa Japonica Group]	Unigene24820_All//5.00E-155//AT1G31660| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Bystin (InterPro:IPR007955); Has 370 Blast hits to 362 proteins in 156 species: Archae - 0; Bacteria - 7; Metazoa - 139; Fungi - 93; Plants - 32; Viruses - 0; Other Eukaryotes - 99 (source: NCBI BLink).	Unigene24820_All//0.00E+00//TC137394				nr +
Unigene24826_All	2406	5.63	4.30	2.72	7.41	6.67	5.33	7.36	13.65	11.86	-3.91E-01	1.14E-02		-1.05E+00	1.02E-10	Down	-1.52E-01	3.12E-01		-4.76E-01	2.12E-04		8.91E-01	1.78E-24		6.87E-01	2.55E-14		Unigene24826_All//gi|42741727|gb|AAS45124.1|//0.00E+00//WAK-like kinase [Solanum lycopersicum]	Unigene24826_All//2.00E-176//AT2G23450| protein kinase family protein	Unigene24826_All//0.00E+00//TC147339			GO:0000166//GO:0004672//GO:0008152//GO:0016491	nr -
Unigene2483_All	1206	15.31	29.45	18.37	21.73	48.54	27.34	62.12	47.27	39.74	9.44E-01	1.07E-23		2.62E-01	3.77E-02		1.16E+00	1.39E-63	Up	3.31E-01	3.57E-04		-3.94E-01	2.15E-13		-6.45E-01	1.62E-32		Unigene2483_All//gi|183014149|dbj|BAG24402.1|//1.00E-104//bZIP protein [Glycine max]	Unigene2483_All//7.00E-47//AT5G28770| BZO2H3; DNA binding / protein heterodimerization/ transcription factor	Unigene2483_All//0.00E+00//gi|164263464|gb|ES832952.1|ES832952	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene24830_All	1674	8.85	47.04	25.83	10.86	22.05	48.16	3.36	11.24	8.16	2.41E+00	1.26E-201	Up	1.55E+00	5.23E-60	Up	1.02E+00	8.03E-33	Up	2.15E+00	1.31E-192	Up	1.74E+00	2.37E-39	Up	1.28E+00	5.09E-19	Up	Unigene24830_All//gi|6730631|gb|AAF27052.1|AC008262_1//1.00E-127//F4N2.2 [Arabidopsis thaliana]	Unigene24830_All//2.00E-125//AT1G69040| ACR4 (ACT REPEAT 4); amino acid binding	Unigene24830_All//0.00E+00//TC142625				nr -
Unigene24833_All	2278	1.01	0.85	0.28	3.30	3.70	2.68	5.22	1.83	3.55	-2.58E-01	5.58E-01		-1.85E+00	1.18E-04	Down	1.66E-01	4.88E-01		-3.03E-01	1.90E-01		-1.51E+00	1.32E-20	Down	-5.55E-01	9.77E-05		Unigene24833_All//gi|240256033|ref|NP_193913.4|//1.00E-112//binding / calmodulin binding [Arabidopsis thaliana]	Unigene24833_All//7.00E-114//AT4G21820| binding / calmodulin binding	Unigene24833_All//6.00E-32//gi|73847296|gb|DT456316.1|DT456316				nr -
Unigene24835_All	1600	37.41	18.02	16.97	90.38	71.86	88.38	58.85	32.16	26.84	-1.05E+00	2.17E-47	Down	-1.14E+00	6.78E-52	Down	-3.31E-01	8.15E-18		-3.23E-02	5.76E-01		-8.72E-01	2.77E-66		-1.13E+00	1.16E-104	Down	Unigene24835_All//gi|224087993|ref|XP_002308283.1|//1.00E-167//nucleosome/chromatin assembly factor group [Populus trichocarpa] >gi|222854259|gb|EEE91806.1|nucleosome/chromatin assembly factor group [Populus trichocarpa]	Unigene24835_All//8.00E-114//AT2G19480| NAP1;2 (NUCLEOSOME ASSEMBLY PROTEIN 1;2); DNA binding	Unigene24835_All//0.00E+00//TC133650				nr -
Unigene24837_All	1386	0.91	0.77	2.84	1.83	1.79	1.79	2.32	1.63	2.39	-2.39E-01	6.68E-01		1.65E+00	1.60E-06	Up	-3.52E-02	9.30E-01		-3.25E-02	9.49E-01		-5.10E-01	1.07E-01		4.13E-02	9.11E-01		Unigene24837_All//gi|18397705|ref|NP_564367.1|//1.00E-140//integral membrane HRF1 family protein [Arabidopsis thaliana] >gi|145324088|ref|NP_001077633.1|integral membrane HRF1 family protein [Arabidopsis thaliana]	Unigene24837_All//1.00E-123//AT3G59500| integral membrane HRF1 family protein	Unigene24837_All//0.00E+00//TC161232				nr -
Unigene24838_All	2786	13.33	8.97	11.54	6.54	10.05	4.67	40.37	10.56	24.88	-5.73E-01	7.35E-11		-2.08E-01	3.01E-02		6.19E-01	7.51E-11		-4.87E-01	1.18E-04		-1.93E+00	2.81E-268	Down	-6.98E-01	1.49E-55		Unigene24838_All//gi|22705377|gb|ACP18876.1|//0.00E+00//subtilisin-like serine protease [Carica papaya]	Unigene24838_All//0.00E+00//AT2G04160| AIR3; serine-type endopeptidase	Unigene24838_All//0.00E+00//TC174671			GO:0004175//GO:0005515//GO:0009725//GO:0010101//GO:0016628//GO:0019538//GO:0044092//GO:0044464	nr -
Unigene24839_All	2552	8.39	7.96	11.23	1.97	3.78	3.27	1.52	1.72	3.64	-7.48E-02	6.01E-01		4.21E-01	5.65E-05		9.38E-01	8.96E-08		7.32E-01	2.07E-04		1.74E-01	5.63E-01		1.25E+00	8.26E-13	Up	Unigene24839_All//gi|264664531|sp|Q0LG68.1|Y5343_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g53430; Flags: Precursor >gi|224589438|gb|ACN59253.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene24839_All//0.00E+00//AT1G53440| leucine-rich repeat family protein / protein kinase family protein	Unigene24839_All//0.00E+00//TC151625		ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488//GO:0016020	nr +
Unigene24843_All	1359	91.71	63.76	41.81	32.99	28.58	29.21	2.27	0.83	0.79	-5.24E-01	1.30E-29		-1.13E+00	1.16E-106	Down	-2.07E-01	8.44E-03		-1.76E-01	3.79E-02		-1.45E+00	1.20E-05	Down	-1.52E+00	3.15E-06	Down	Unigene24843_All//gi|15242562|ref|NP_195909.1|//2.00E-58//transferase family protein [Arabidopsis thaliana] >gi|34098861|gb|AAQ56813.1|At5g02890 [Arabidopsis thaliana]	Unigene24843_All//9.00E-60//AT5G02890| transferase family protein	Unigene24843_All//0.00E+00//TC133643		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016740	nr -
Unigene24844_All	2215	4.46	9.04	7.00	8.10	7.46	8.07	14.95	25.72	28.87	1.02E+00	2.11E-15	Up	6.48E-01	9.53E-06		-1.18E-01	4.52E-01		-3.90E-03	9.75E-01		7.83E-01	9.97E-34		9.50E-01	2.74E-53		Unigene24844_All//gi|14517540|gb|AAG2660.1|//1.00E-115//AT3G50910|F18B3_190 [Arabidopsis thaliana] >gi|27764930|gb|AAO23586.1|At3g50910|F18B3_190 [Arabidopsis thaliana]	Unigene24844_All//5.00E-85//AT3G50910| unknown protein	Unigene24844_All//0.00E+00//TC144427				nr -
Unigene24845_All	1186	12.35	38.15	10.37	11.63	11.24	15.46	40.39	69.81	66.41	1.63E+00	2.20E-69	Up	-2.52E-01	1.20E-01		-5.02E-02	8.10E-01		4.10E-01	1.39E-03		7.90E-01	2.53E-49		7.17E-01	7.64E-41		Unigene24845_All//gi|115446743|ref|NP_001047151.1|//1.00E-83//Os02g0562300 [Oryza sativa Japonica Group] >gi|113536682|dbj|BAF09065.1|Os02g0562300 [Oryza sativa Japonica Group]	Unigene24845_All//1.00E-81//AT5G57580| calmodulin-binding protein	Unigene24845_All//0.00E+00//TC138777		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005515	nr -
Unigene24849_All	361	0.29	0.84	1.48	1.38	2.00	1.50	7.26	5.09	2.76	1.54E+00	3.23E-01		2.35E+00	5.87E-02		5.38E-01	5.64E-01		1.22E-01	9.21E-01		-5.11E-01	1.50E-01		-1.40E+00	7.11E-05	Down			Unigene24849_All//5.00E-124//gi|48747278|gb|C0077797.1|C0077797				
Unigene2485_All	706	0.44	0.86	0.08	1.27	1.95	0.77	5.87	7.10	11.85	9.54E-01	3.14E-01		-2.56E+00	1.59E-01		6.19E-01	3.14E-01		-7.27E-01	3.45E-01		2.76E-01	2.90E-01		1.01E+00	1.60E-08	Up	Unigene2485_All//gi|297807509|ref|XP_002871638.1|//5.00E-07//senescence-associated gene 101 [Arabidopsis lyrata subsp. lyrata] >gi|297317475|gb|EFH47897.1|senescence-associated gene 101 [Arabidopsis lyrata subsp. lyrata]	Unigene2485_All//5.00E-08//AT5G14930| SAG101 (SENESCENCE-ASSOCIATED GENE 101); carboxylesterase/ triacylglycerol lipase	Unigene2485_All//0.00E+00//DT462534				nr -
Unigene24851_All	2085	8.38	6.71	7.05	4.59	4.99	3.18	3.31	1.00	1.30	-3.22E-01	1.76E-02		-2.50E-01	8.53E-02		1.21E-01	5.81E-01		-5.27E-01	4.16E-03		-1.72E+00	1.06E-14	Down	-1.35E+00	7.38E-11	Down	Unigene24851_All//gi|297847780|ref|XP_002891771.1|//1.00E-148//endonuclease [Arabidopsis lyrata subsp. lyrata] >gi|297337613|gb|EFH98030.1|endonuclease [Arabidopsis lyrata subsp. lyrata]	Unigene24851_All//5.00E-125//AT1G53800| endonuclease	Unigene24851_All//0.00E+00//C0086799				nr +
Unigene24852_All	2583	14.40	7.47	8.53	26.48	34.74	18.34	19.27	6.36	8.16	-9.46E-01	5.41E-25		-7.55E-01	1.56E-16		3.92E-01	5.31E-15		-5.30E-01	4.62E-18		-1.60E+00	2.19E-91	Down	-1.24E+00	3.36E-64	Down	Unigene24852_All//gi|264664457|sp|Q0LG15.1|Y1699_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g69990; Flags: Precursor >gi|224589473|gb|ACN59270.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene24852_All//0.00E+00//AT1G27190| leucine-rich repeat transmembrane protein kinase, putative	Unigene24852_All//0.00E+00//TC157465			GO:0004871//GO:0006464//GO:0007167//GO:0016301//GO:0031224//GO:0032559	nr -
Unigene24856_All	837	0.75	0.73	0.00	3.63	2.26	0.65	1.06	2.30	0.33	-4.63E-02	9.72E-01		-9.55E+00	1.41E-03		-6.82E-01	4.63E-02		-2.49E+00	2.72E-09	Down	1.11E+00	8.32E-03		-1.67E+00	1.33E-02		Unigene24856_All//gi|15238363|ref|NP_201321.1|//9.00E-21//VQ motif-containing protein [Arabidopsis thaliana] >gi|44917435|gb|AAS49042.1|At5g65170 [Arabidopsis thaliana] >gi|46931270|gb|AAT06439.1|At5g65170 [Arabidopsis thaliana]	Unigene24856_All//1.00E-19//AT1G35830| VQ motif-containing protein	Unigene24856_All//0.00E+00//TC164060				nr +
Unigene24857_All	1148	1.82	9.18	6.68	4.82	3.06	3.42	4.86	15.98	13.29	2.33E+00	2.06E-26	Up	1.87E+00	2.54E-14	Up	-6.55E-01	6.03E-03		-4.93E-01	5.60E-02		1.72E+00	1.17E-37	Up	1.45E+00	2.27E-25	Up	Unigene24857_All//gi|297726881|ref|NP_001175804.1|//3.00E-23//Os09g0370500 [Oryza sativa Japonica Group] >gi|255678843|dbj|BAH94532.1|Os09g0370500 [Oryza sativa Japonica Group]	Unigene24857_All//1.00E-19//AT1G35830| VQ motif-containing protein	Unigene24857_All//0.00E+00//gi|109870024|gb|DW499000.1|DW499000				nr +

Unigene24858_All	1302	2.73	11.75	9.82	2.75	2.06	1.46	8.61	33.61	30.08	2.10E+00	1.31E-33	Up	1.84E+00	4.81E-23	Up	-4.17E-01	2.08E-01		-9.19E-01	4.31E-03		1.97E+00	1.06E-106	Up	1.81E+00	5.51E-87	Up	Unigene24858_All//gi|15220238|ref|NP_174819.1|//2.00E-20//VQ motif-containing protein [Arabidopsis thaliana]	Unigene24858_All//8.00E-21//AT1G35830| VQ motif-containing protein	Unigene24858_All//0.00E+00//TC155335				nr +
Unigene24861_All	1025	22.61	10.88	12.10	59.19	33.23	25.56	1.86	4.00	3.42	-1.06E+00	7.28E-19	Down	-9.02E-01	4.67E-14		-8.33E-01	8.32E-40		-1.21E+00	5.65E-65	Down	1.11E+00	5.07E-05	Up	8.82E-01	2.05E-03		Unigene24861_All//gi|15220529|ref|NP_176350.1|//1.00E-109//MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding [Arabidopsis thaliana] >gi|33112391|sp|Q9ZK87.2|MLO6_ARATH RecName: Full=MLO-like protein 6; Short=AtMlo6 >gi|4585879|gb|AAD25552.1|AC005850_9 Highly Similar to Mlo proteins [Arabidopsis thaliana] >gi|24111257|gb|AAK53799.2|AF369567.1 membrane protein Mlo6 [Arabidopsis thaliana]	Unigene24861_All//8.00E-93//AT1G61560| MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding	Unigene24861_All//0.00E+00//DW225778			GO:0009987//GO:0031224	nr -
Unigene24862_All	1198	1.00	1.52	1.51	5.86	2.47	1.58	2.47	1.47	0.90	6.00E-01	2.15E-01		5.89E-01	2.42E-01		-1.25E+00	2.43E-09	Down	-1.89E+00	6.93E-15	Down	-7.54E-01	2.01E-02		-1.46E+00	1.04E-05	Down	Unigene24862_All//gi|7767672|gb|AAF69169.1|AC007915_21//1.00E-30//F27F5.21 [Arabidopsis thaliana]	Unigene24862_All//4.00E-21//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene24862_All//1.00E-90//gi|21101771|gb|BQ414084.1|BQ414084				nr -
Unigene24863_All	653	6.73	2.25	3.18	7.48	3.69	4.08	1.55	2.18	0.24	-1.58E+00	3.64E-07	Down	-1.08E+00	3.97E-04	Down	-1.02E+00	5.81E-05	Down	-8.74E-01	1.11E-03		4.86E-01	3.60E-01		-2.67E+00	1.94E-04	Down	Unigene24863_All//gi|297725701|ref|NP_001175214.1|//9.00E-07//Os07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1|Os07g0501200 [Oryza sativa Japonica Group]	Unigene24863_All//2.00E-05//AT3G25270| nucleic acid binding	Unigene24863_All//1.00E-144//gi|109858628|gb|DW487607.1|DW487607				nr -
Unigene24864_All	1787	3.95	2.89	2.65	10.98	7.26	3.74	1.85	0.84	0.56	-4.51E-01	4.31E-02		-5.76E-01	1.25E-02		-5.96E-01	1.63E-07		-1.55E+00	5.27E-31	Down	-1.13E+00	2.47E-04	Down	-1.73E+00	9.62E-08	Down	Unigene24864_All//gi|115473321|ref|NP_001060259.1|//5.00E-26//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene24864_All//4.00E-12//AT4G06310| hypothetical protein	Unigene24864_All//5.00E-152//DR462084				nr -
Unigene24865_All	1273	31.24	40.68	40.24	16.44	19.86	9.05	0.33	2.20	0.47	3.81E-01	1.95E-07		3.65E-01	1.50E-06		2.73E-01	1.12E-02		-8.61E-01	3.33E-13		2.73E+00	9.78E-11	Up	4.99E-01	5.52E-01		Unigene24865_All//gi|115473321|ref|NP_001060259.1|//2.00E-16//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene24865_All//17.00E-17//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene24865_All//0.00E+00//gi|164307909|gb|EX171632.1|EX171632			GO:0044464	nr +
Unigene24869_All	680	3.23	2.38	0.94	2.34	4.76	5.78	1.68	1.11	1.35	-4.39E-01	3.23E-01		-1.78E+00	2.71E-04	Down	1.02E+00	2.39E-03		1.30E+00	3.48E-05	Up	-6.02E-01	3.08E-01		-3.17E-01	5.87E-01		Unigene24869_All//gi|227204199|dbj|BAH56951.1|//1.00E-58//AT4G10430 [Arabidopsis thaliana]	Unigene24869_All//2.00E-53//AT1G33230| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: TMP17-like (InterPro:IPR012926); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10430.3); Has 198 Blast hits to 198 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 148; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink).	Unigene24869_All//0.00E+00//AW186684			GO:0031224	nr -
Unigene2487_All	1871	4.36	5.71	5.58	5.22	3.11	3.21	6.67	29.78	26.55	3.89E-01	2.78E-02		3.55E-01	6.10E-02		-7.47E-01	1.00E-05		-7.01E-01	9.10E-05		2.16E+00	3.45E-153	Up	1.99E+00	8.87E-126	Up	Unigene2487_All//gi|115458514|ref|NP_001052857.1|//1.00E-67//Os04g0437300 [Oryza sativa Japonica Group] >gi|38344067|emb|CAD40819.2|OSJNBa0006820.11 [Oryza sativa (japonica cultivar-group)] >gi|113564428|dbj|BAF14771.1|Os04g0437300 [Oryza sativa Japonica Group] >gi|116310783|emb|CAH67575.1|H0315408.5 [Oryza sativa (indica cultivar-group)]	Unigene2487_All//8.00E-36//AT1G49780| PUB26 (PLANT U-BOX 26); binding / ubiquitin-protein ligase	Unigene2487_All//2.00E-25//TC151768				nr +
Unigene24871_All	827	22.59	11.33	16.61	26.99	21.40	34.19	21.78	9.70	8.33	9.95E-01	5.52E-14		-4.43E-01	8.61E-04		-3.34E-01	2.56E-03		3.41E-01	7.52E-04		-1.17E+00	4.80E-21	Down	-1.39E+00	4.00E-28	Down	Unigene24871_All//gi|18414012|ref|NP_568106.1|//9.00E-30//nucleotide binding [Arabidopsis thaliana] >gi|117168203|gb|ABK32184.1|At5g02740 [Arabidopsis thaliana]	Unigene24871_All//2.00E-30//AT5G02740| unknown protein	Unigene24871_All//0.00E+00//gi|13350392|gb|BG440740.1|BG440740				nr +
Unigene24872_All	205	8.68	2.97	5.20	3.64	2.35	13.88	0.00	2.85	0.00	-1.55E+00	2.66E-03		-7.40E-01	1.46E-01		-6.32E-01	4.37E-01		1.93E+00	2.17E-06	Up	1.15E+01	2.81E-04	Up	null	null				Unigene24872_All//5.00E-110//gi|13350392|gb|BG440740.1|BG440740				
Unigene24873_All	1089	9.85	5.30	5.57	10.98	10.53	11.03	15.34	7.75	5.05	-8.93E-01	4.02E-07		-8.21E-01	5.81E-06		-6.02E-02	7.84E-01		7.00E-03	9.68E-01		-9.84E-01	4.83E-15		-1.60E+00	3.01E-32	Down	Unigene24873_All//gi|18414012|ref|NP_568106.1|//8.00E-38//nucleotide binding [Arabidopsis thaliana] >gi|117168203|gb|ABK32184.1|At5g02740 [Arabidopsis thaliana]	Unigene24873_All//1.00E-38//AT5G02740| unknown protein	Unigene24873_All//0.00E+00//TC149599				nr +
Unigene24874_All	2118	0.02	1.34	0.20	2.63	2.94	35.46	5.21	46.28	106.93	5.76E+00	1.04E-14	Up	3.03E+00	5.73E-02		1.60E-01	5.73E-01		3.75E+00	0.00E+00	Up	3.15E+00	0.00E+00	Up	4.36E+00	0.00E+00	Up	Unigene24874_All//gi|224066615|ref|XP_002302164.1|//2.00E-98//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222843890|gb|EEE81437.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene24874_All//8.00E-24//AT5G64750| ABR1 (ABA REPRESSOR1); DNA binding / transcription factor	Unigene24874_All//6.00E-38//ES831270	AP2-EREBP		GO:0006950//GO:0009737//GO:0009987	nr -
Unigene24875_All	485	1.08	3.87	4.28	6.27	6.25	5.96	6.19	2.84	5.59	1.84E+00	4.09E-04	Up	1.99E+00	1.22E-04	Up	-4.00E-03	9.80E-01		-7.21E-02	8.59E-01		-1.12E+00	5.69E-04	Down	-1.48E-01	6.42E-01				Unigene24875_All//3.00E-55//gi|164243647|gb|ES793584.1|ES793584				
Unigene2488_All	1307	38.83	25.01	26.69	40.29	38.20	44.33	54.06	31.05	19.20	-6.35E-01	2.40E-17		-5.41E-01	1.20E-12		-7.66E-02	3.84E-01		1.38E-01	6.89E-02		-8.00E-01	3.42E-43		-1.49E+00	1.63E-120	Down	Unigene2488_All//gi|13936812|gb|AAK09417.1|AF335551_1//1.00E-178//TGF-beta receptor-interacting protein 1 [Phaseolus vulgaris]	Unigene2488_All//4.00E-161//AT2G46280| TRIP-1 (TGF-BETA RECEPTOR INTERACTING PROTEIN 1); nucleotide binding / protein binding	Unigene2488_All//0.00E+00//TC153489				nr -
Unigene24881_All	853	5.95	6.24	2.75	6.37	6.82	4.87	3.62	2.45	3.18	6.81E-02	7.97E-01		-1.12E+00	7.70E-05	Down	1.00E-01	7.59E-01		-3.86E-01	1.51E-01		-5.63E-01	7.92E-02		-1.88E-01	5.86E-01		Unigene24881_All//gi|115478358|ref|NP_001062774.1|//1.00E-112//Os09g0284200 [Oryza sativa Japonica Group] >gi|113631007|dbj|BAF24688.1|Os09g0284200 [Oryza sativa Japonica Group]	Unigene24881_All//2.00E-111//AT5G55260| PPX2 (PROTEIN PHOSPHATASE X 2); protein serine/threonine phosphatase	Unigene24881_All//0.00E+00//TC167708			GO:0016791	nr +
Unigene24883_All	2149	4.82	4.20	1.49	6.82	5.16	5.34	1.69	0.16	1.19	-2.00E-01	2.99E-01		-1.70E+00	1.00E-16	Down	-4.01E-01	4.01E-03		-3.52E-01	1.78E-02		-3.44E+00	4.14E-17	Down	-5.12E-01	6.68E-02		Unigene24883_All//gi|15230360|ref|NP_191321.1|//1.00E-152//glyoxal oxidase-related [Arabidopsis thaliana]	Unigene24883_All//6.00E-154//AT3G57620| glyoxal oxidase-related	Unigene24883_All//0.00E+00//EX165993				nr +
Unigene24884_All	1224	18.47	14.41	9.48	53.40	36.35	48.26	40.66	19.16	22.43	-3.58E-01	2.04E-03		-9.61E-01	3.31E-15		-5.55E-01	5.49E-21		-1.46E-01	3.59E-02		-1.09E+00	1.25E-50	Down	-8.58E-01	1.68E-35		Unigene24884_All//gi|15242483|ref|NP_199387.1|//1.00E-107//AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding [Arabidopsis thaliana] >gi|75171186|sp|Q9FK68.1|RAA1C_ARATH RecName: Full=Ras-related protein RABA1c >gi|9758678|dbj|BAB09217.1| Rab-type small GTP-binding protein-like [Arabidopsis thaliana]	Unigene24884_All//2.00E-108//AT5G45750| AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding	Unigene24884_All//0.00E+00//TC132701				nr +
Unigene24885_All	1049	4.64	10.43	6.60	5.98	5.71	8.01	26.48	42.35	30.91	1.17E+00	8.58E-11	Up	5.09E-01	2.98E-02		-6.70E-02	8.26E-01		4.21E-01	4.01E-02		6.78E-01	9.34E-21		2.23E-01	8.49E-03		Unigene24885_All//gi|259121397|gb|ACY92018.1|//1.00E-57//WRKY transcription factor 16 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene24885_All//3.00E-36//AT5G64810| WRKY51; transcription factor	Unigene24885_All//6.00E-163//DT469066	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0006350//GO:0010468//GO:0043231	nr +
Unigene24886_All	1823	8.81	9.56	9.49	4.29	6.93	6.12	4.66	3.85	16.94	1.18E-01	4.20E-01		1.08E-01	4.95E-01		6.92E-01	3.38E-06		5.12E-01	2.44E-03		-2.75E-01	1.44E-01		1.86E+00	1.26E-71	Up	Unigene24886_All//gi|15227228|ref|NP_182332.1|//5.00E-90//PAC (PALE CRESS) [Arabidopsis thaliana] >gi|1483213|emb|CAA65334.1| PAC [Arabidopsis thaliana] >gi|21555469|gb|AAM63866.1| pale cress protein [Arabidopsis thaliana] >gi|28950889|gb|AAO63368.1|At2g48120 [Arabidopsis thaliana]	Unigene24886_All//6.00E-69//AT2G48120| PAC (PALE CRESS)	Unigene24886_All//0.00E+00//gi|109871210|gb|DW500186.1|DW500186			GO:0006397//GO:0009536//GO:0009657//GO:0009887//GO:0016109	nr +
Unigene24887_All	1245	11.89	11.80	9.67	6.48	5.64	6.82	3.40	3.02	0.99	-1.10E-02	9.64E-01		-2.99E-01	5.72E-02		-2.00E-01	3.84E-01		7.34E-02	7.44E-01		-1.69E-01	5.90E-01		-1.78E+00	4.90E-10	Down	Unigene24887_All//gi|15227228|ref|NP_182332.1|//1.00E-113//PAC (PALE CRESS) [Arabidopsis thaliana] >gi|1483213|emb|CAA65334.1| PAC [Arabidopsis thaliana] >gi|21555469|gb|AAM63866.1| pale cress protein [Arabidopsis thaliana] >gi|28950889|gb|AAO63368.1|At2g48120 [Arabidopsis thaliana]	Unigene24887_All//6.00E-87//AT2G48120| PAC (PALE CRESS)	Unigene24887_All//3.00E-20//DW500186			GO:0043231	nr -
Unigene24889_All	2306	19.38	21.75	61.59	62.65	42.22	56.80	91.64	68.64	75.05	1.67E-01	3.49E-02		1.67E+00	1.74E-219	Up	-5.70E-01	3.46E-48		-1.41E-01	1.11E-03		-4.17E-01	3.79E-40		-2.88E-01	4.69E-21		Unigene24889_All//gi|163889366|gb|ABV48136.1|//0.00E+00//glycine-rich protein [Medicago truncatula]	Unigene24889_All//0.00E+00//AT2G22660| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1399 (InterPro:IPR009836); BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT4G37900.1); Has 257 Blast hits to 239 proteins in 58 species: Archae - 0; Bacteria - 21; Metazoa - 12; Fungi - 149; Plants - 61; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink).	Unigene24889_All//0.00E+00//TC146178			GO:0016020	nr -

Unigene2489_All	1401	3.96	3.94	5.25	3.20	2.34	1.93	1.66	0.60	0.40	-6.00E-03	9.87E-01		4.06E-01	7.87E-02		-4.55E-01	1.09E-01		-7.26E-01	1.03E-02		-1.48E+00	1.54E-04	Down	-2.06E+00	5.41E-07	Down	Unigene2489_All//gi|251764780|sp|Q8L735.2|ISOA2_ARATH//1.00E-180//RecName: Full=Isoamylase 2, chloroplastic; Short=AtISA2; AltName: Full=Protein DEBRANCHING ENZYME 1; Flags: Precursor >gi|38586573|gb|AAC72113.1| Similar to gi|1652733 glycogen operon protein GlgX from Synechocystis sp. genome gb|D90908. ESTs gb|H36690, gb|AA712462, gb|AA651230 and gb|N95932 come from this gene [Arabidopsis thaliana]	Unigene2489_All//0.00E+00//AT1G03310| isoamylase, putative / starch debranching enzyme, putative	Unigene2489_All//0.00E+00//ES817618				nr +
Unigene24893_All	1325	0.39	0.11	0.16	0.41	0.75	0.37	1.37	0.28	0.45	-1.78E+00	1.08E-01		-1.30E+00	2.42E-01		8.66E-01	2.34E-01		-1.42E-01	8.85E-01		-2.27E+00	5.13E-06	Down	-1.61E+00	2.86E-04	Down	Unigene24893_All//gi|115470967|ref|NP_001059082.1|//5.00E-23//Os07g0188800 [Oryza sativa Japonica Group] >gi|34394614|dbj|BAC83916.1| methylmalonate semi-aldehyde dehydrogenase [Oryza sativa Japonica Group] >gi|50508946|dbj|BAD31850.1| methylmalonate semi-aldehyde dehydrogenase [Oryza sativa Japonica Group] >gi|113610618|dbj|BAF20996.1| Os07g0188800 [Oryza sativa Japonica Group]	Unigene24893_All//4.00E-24//AT2G14170| ALDH6B2; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase	Unigene24893_All//0.00E+00//ES817587		ko00562|Inositol phosphate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism	GO:0006950//GO:0008152//GO:0016491//GO:0043231//GO:0046914	nr +
Unigene24896_All	1772	4.99	5.26	1.89	2.92	2.27	3.24	10.90	13.66	42.83	7.64E-02	7.00E-01		-1.40E+00	5.71E-11	Down	-3.63E-01	1.76E-01		1.47E-01	6.38E-01		3.25E-01	1.19E-03		1.97E+00	2.94E-189	Up	Unigene24896_All//gi|115447297|ref|NP_001047428.1|//8.00E-68//Os02g0614700 [Oryza sativa Japonica Group] >gi|113536959|dbj|BAF09342.1| Os02g0614700 [Oryza sativa Japonica Group]	Unigene24896_All//2.00E-42//AT4G06536| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: B302 (SPRY)-like (InterPro:IPR00015670), SPla/RYanodine receptor SPRY (InterPro:IPR003877); Has 20 Blast hits to 20 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 7; Plants - 11; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene24896_All//0.00E+00//DT468675			GO:0044464	nr -
Unigene24897_All	772	2.58	1.64	3.04	7.03	3.88	5.73	8.76	5.85	4.18	-6.50E-01	1.53E-01		2.37E-01	6.13E-01		-8.58E-01	3.05E-04		-2.95E-01	2.98E-01		-5.84E-01	3.71E-03		-1.07E+00	1.15E-07	Down	Unigene24897_All//gi|195636804|gb|AGS37870.1|//3.00E-25//choline/ethanolamine kinase [Zea mays]	Unigene24897_All//2.00E-21//AT2G26830| emb1187 (embryo defective 1187); kinase/ phosphotransferase, alcohol group as acceptor	Unigene24897_All//0.00E+00//gi|164338112|gb|ES834939.1|ES834939		ko00564|Glycerophospholipid metabolism	GO:0003006//GO:0016301	nr +
Unigene24899_All	2304	2.23	2.60	0.99	7.44	4.21	3.74	13.08	6.73	6.69	2.22E-01	3.91E-01		-1.16E+00	3.60E-05	Down	-8.19E-01	3.19E-11		-9.90E-01	1.19E-13		-9.59E-01	2.03E-25		-9.67E-01	1.52E-26		Unigene24899_All//gi|19401142|gb|AL87543.1|AF293343_1//0.00E+00//KAP-2 [Medicago truncatula]	Unigene24899_All//0.00E+00//AT1G48650| KU80; double-stranded DNA binding / protein binding	Unigene24899_All//0.00E+00//TC174101		ko03450|Non-homologous end-joining	GO:0000726//GO:0003678//GO:0043231//GO:0043566	nr -
Unigene24903_All	2228	9.16	21.40	7.27	9.55	10.43	14.82	14.92	14.95	26.88	1.22E+00	7.98E-48	Up	-3.34E-01	9.62E-03		1.28E-01	3.26E-01		6.34E-01	3.65E-12		3.40E-03	1.01E+00		8.49E-01	1.49E-41		Unigene24903_All//gi|15241899|ref|NP_201068.1|//0.00E+00//galactosyltransferase family protein [Arabidopsis thaliana] >gi|221271940|sp|Q9LV16.2|B3GTJ_ARATH RecName: Full=Probable beta-1,3-galactosyltransferase 19	Unigene24903_All//0.00E+00//AT5G62620| galactosyltransferase family protein	Unigene24903_All//0.00E+00//TC158472			GO:0006464//GO:0009536//GO:0030246//GO:0031224//GO:0035250	nr +
Unigene24905_All	453	1.04	2.91	3.88	3.52	1.98	1.69	0.28	1.57	0.97	1.48E+00	1.55E-02		1.90E+00	7.52E-04	Up	-8.32E-01	9.85E-02		-1.05E+00	4.57E-02		2.49E+00	5.53E-03		1.79E+00	9.60E-02		Unigene24905_All//gi|15234743|ref|NP_194772.1|//2.00E-19//TET9 (TETRASPANIN9) [Arabidopsis thaliana] >gi|7269944|emb|CAB79761.1| senescence-associated protein homolog [Arabidopsis thaliana]	Unigene24905_All//1.00E-20//AT4G30430| TET9 (TETRASPANIN9)	Unigene24905_All//0.00E+00//gi|78346822|gb|DT567096.1|DT567096			GO:0016020//GO:0031410//GO:0032502	nr -
Unigene24906_All	1694	58.44	223.47	119.77	110.54	117.25	174.26	20.09	79.47	34.15	1.94E+00	0.00E+00	Up	1.04E+00	3.80E-150	Up	8.51E-02	2.46E-02		6.57E-01	4.67E-111		1.98E+00	0.00E+00	Up	7.65E-01	1.01E-33		Unigene24906_All//gi|79592093|ref|NP_850045.2|//1.00E-111//TET8 (TETRASPANIN8) [Arabidopsis thaliana]	Unigene24906_All//1.00E-94//AT2G23810| TET8 (TETRASPANIN8)	Unigene24906_All//0.00E+00//gi|78342741|gb|DT563015.1|DT563015			GO:0016020//GO:0032502	nr -
Unigene24908_All	1991	4.28	10.66	8.99	4.93	7.21	9.64	8.26	10.06	9.90	1.32E+00	3.61E-24	Up	1.07E+00	2.12E-14	Up	5.49E-01	8.10E-05		9.68E-01	1.66E-14		2.84E-01	1.22E-02		2.62E-01	1.85E-02		Unigene24908_All//gi|297844364|ref|XP_002890063.1|//1.00E-125//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335905|gb|EFH66322.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24908_All//4.00E-122//AT1G14560| mitochondrial substrate carrier family protein	Unigene24908_All//0.00E+00//TC144102				nr -
Unigene24909_All	1021	76.87	163.97	76.15	114.80	211.77	229.80	42.65	59.89	47.17	1.09E+00	7.55E-139	Up	-1.36E-02	8.50E-01		8.83E-01	1.03E-150		1.00E+00	1.37E-181	Up	4.90E-01	4.00E-16		1.45E-01	4.04E-02		Unigene24909_All//gi|297797417|ref|XP_002866593.1|//6.00E-47//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312428|gb|EFH42852.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24909_All//1.00E-36//AT5G64080| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene24909_All//0.00E+00//gi|164284153|gb|ES832524.1|ES832524			GO:0005488//GO:0006810//GO:0031225	nr -
Unigene24912_All	1555	12.42	2.83	6.64	15.83	8.70	4.41	1.60	0.30	0.18	-2.13E+00	3.22E-43	Down	-9.02E-01	7.99E-12		-8.63E-01	2.37E-17		-1.84E+00	3.11E-49	Down	-2.44E+00	1.25E-08	Down	-3.16E+00	1.62E-11	Down	Unigene24912_All//gi|224146504|ref|XP_002326030.1|//1.00E-174//beta-ketoacyl-coa synthase family protein [Populus trichocarpa] >gi|222862905|gb|EEF00412.1| beta-ketoacyl-coa synthase family protein [Populus trichocarpa]	Unigene24912_All//2.00E-162//AT5G04530| KCS19 (3-KETOACYL-COA SYNTHASE 19); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene24912_All//0.00E+00//TC156017				nr +
Unigene24913_All	1484	8.29	1.54	5.27	8.59	4.83	2.43	0.00	0.03	0.08	-2.43E+00	1.70E-32	Down	-6.51E-01	9.50E-05		-8.32E-01	1.04E-08		-1.82E+00	2.58E-25	Down	4.82E+00	6.35E-01		6.33E+00	2.43E-01		Unigene24913_All//gi|224146504|ref|XP_002326030.1|//1.00E-167//beta-ketoacyl-coa synthase family protein [Populus trichocarpa] >gi|222862905|gb|EEF00412.1| beta-ketoacyl-coa synthase family protein [Populus trichocarpa]	Unigene24913_All//5.00E-152//AT5G04530| KCS19 (3-KETOACYL-COA SYNTHASE 19); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene24913_All//0.00E+00//TC156017				nr -
Unigene24915_All	428	5.38	2.37	4.23	8.26	8.13	7.70	5.33	1.46	2.42	-1.18E+00	5.68E-03		-3.47E-01	4.29E-01		-2.42E-02	9.49E-01		-1.01E-01	7.69E-01		-1.86E+00	6.67E-06	Down	-1.14E+00	2.03E-03		Unigene24915_All//gi|15219396|ref|NP_173131.1|//9.00E-13//mitochondrial 28S ribosomal protein S29-related [Arabidopsis thaliana] >gi|17064866|gb|AAL32587.1| Unknown protein [Arabidopsis thaliana]	Unigene24915_All//2.00E-69//AT1G16870| mitochondrial 28S ribosomal protein S29-related	Unigene24915_All//0.00E+00//gi|78336724|gb|DT556998.1|DT556998				nr +
Unigene24916_All	1773	8.29	1.97	3.99	11.44	11.30	11.97	16.65	3.16	4.92	-2.07E+00	6.45E-32	Down	-1.05E+00	1.18E-11	Down	-1.67E-02	9.11E-01		6.62E-02	6.57E-01		-2.40E+00	9.49E-93	Down	-1.76E+00	3.92E-64	Down	Unigene24916_All//gi|225434411|ref|XP_002271596.1|//1.00E-176//PREDICTED: similar to mitochondrial 28S ribosomal protein S29-related [Vitis vinifera]	Unigene24916_All//1.00E-166//AT1G16870| mitochondrial 28S ribosomal protein S29-related	Unigene24916_All//0.00E+00//TC152689				nr -
Unigene24917_All	2449	8.08	5.52	5.33	15.83	15.06	11.71	17.20	14.11	6.72	-5.48E-01	9.19E-06		-6.00E-01	2.65E-06		-7.16E-02	5.15E-01		-4.34E-01	1.68E-07		-2.85E-01	1.16E-04		-1.36E+00	1.77E-62	Down	Unigene24917_All//gi|219291116|gb|ACL13991.1|//1.00E-100//At2g33360 [Arabidopsis thaliana]	Unigene24917_All//1.00E-94//AT2G33360| unknown protein	Unigene24917_All//0.00E+00//TC179435			GO:0043231	nr -
Unigene24924_All	2405	10.77	5.86	5.27	22.95	16.22	13.65	25.56	17.12	8.55	-8.79E-01	1.18E-15		-1.03E+00	2.17E-19	Down	-5.01E-01	8.34E-15		-7.49E-01	9.05E-27		-5.79E-01	1.19E-21		-1.58E+00	4.50E-114	Down	Unigene24924_All//gi|205830832|sp|A8MQR0.1|WIT2_ARATH//1.00E-145//RecName: Full=WPP domain-interacting tail-anchored protein 2	Unigene24924_All//3.00E-125//AT1G68910| unknown protein	Unigene24924_All//0.00E+00//TC168308			GO:0005515	nr -
Unigene24925_All	2673	1.66	1.06	1.41	2.63	2.49	1.40	5.90	3.24	1.40	-6.48E-01	2.38E-02		-2.34E-01	4.52E-01		-7.98E-02	7.81E-01		-9.06E-01	2.99E-05		-8.66E-01	1.15E-11		-2.07E+00	4.12E-43	Down	Unigene24925_All//gi|205830832|sp|A8MQR0.1|WIT2_ARATH//1.00E-150//RecName: Full=WPP domain-interacting tail-anchored protein 2	Unigene24925_All//4.00E-130//AT1G68910| unknown protein	Unigene24925_All//0.00E+00//TC168308			GO:0005515	nr -
Unigene24927_All	1522	53.15	55.83	53.63	235.46	252.83	246.38	296.04	137.53	107.68	7.11E-02	2.74E-01		1.32E-02	8.50E-01		1.03E-01	2.78E-05		6.54E-02	1.99E-02		-1.11E+00	0.00E+00	Down	-1.46E+00	0.00E+00	Down	Unigene24927_All//gi|224084626|ref|XP_002307364.1|//0.00E+00//2-dehydro-3-deoxyphosphoheptonate aldolase/ 3-deoxy-d-arabino-heptulosonate 7-phosphate synthetase [Populus trichocarpa] >gi|222856813|gb|EEE94360.1| 2-dehydro-3-deoxyphosphoheptonate aldolase/ 3-deoxy-d-arabino-heptulosonate 7-phosphate synthetase [Populus trichocarpa]	Unigene24927_All//0.00E+00//AT1G22410| 2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, putative / DAHP synthetase, putative	Unigene24927_All//0.00E+00//TC131263		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0008652//GO:0009536//GO:0016765//GO:0019632//GO:0043650	nr -
Unigene24931_All	642	2.44	6.00	2.32	3.18	1.88	2.04	4.28	3.39	5.09	1.29E+00	6.40E-05	Up	-7.42E-02	8.92E-01		-7.61E-01	8.04E-02		-6.41E-01	1.68E-01		-3.39E-01	3.60E-01		2.49E-01	4.31E-01		Unigene24931_All//gi|124359162|gb|ABN05685.1|//8.00E-15//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene24931_All//4.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene24931_All//0.00E+00//gi|109891149|gb|DW520112.1|DW520112				nr -
Unigene24933_All	689	40.40	43.17	49.23	8.39	9.00	8.00	4.48	2.12	1.10	9.57E-02	3.83E-01		2.85E-01	3.46E-03		1.01E-01	7.44E-01		-6.86E-02	7.97E-01		-1.08E+00	7.45E-04	Down	-2.03E+00	7.46E-09	Down	Unigene24933_All//gi|115440489|ref|NP_001044524.1|//5.00E-66//Os01g0798500 [Oryza sativa Japonica Group] >gi|113534055|dbj|BAF06438.1| Os01g0798500 [Oryza sativa Japonica Group]	Unigene24933_All//9.00E-69//AT5G44650| unknown protein	Unigene24933_All//0.00E+00//gi|109890422|gb|DW519386.1|DW519386			GO:0009534	nr +
Unigene24934_All	1446	22.11	16.78	26.51	5.34	6.53	4.31	2.25	0.72	0.94	-3.97E-01	2.95E-05		2.62E-01	4.19E-03		2.89E-01	1.45E-01		-3.09E-01	1.70E-01		-1.64E+00	6.59E-07	Down	-1.27E+00	3.76E-05	Down	Unigene24934_All//gi|115440489|ref|NP_001044524.1|//2.00E-53//Os01g0798500 [Oryza sativa Japonica Group] >gi|113534055|dbj|BAF06438.1| Os01g0798500 [Oryza sativa Japonica Group]	Unigene24934_All//1.00E-56//AT5G44650| unknown protein	Unigene24934_All//0.00E+00//TC131715			GO:0009534	nr -
Unigene24935_All	763	11.11	2.92	3.35	2.22	1.90	1.89	0.33	1.97	0.10	-1.93E+00	4.74E-17	Down	-1.73E+00	3.86E-14	Down	-2.28E-01	6.59E-01		-2.29E-01	6.78E-01		2.57E+00	9.84E-06	Up	-1.67E+00	2.56E-01		Unigene24935_All//gi|119507467|dbj|BAF42041.1|//1.00E-112//pectin methylesterase 4 [Pyrus communis]	Unigene24935_All//4.00E-112//AT4G33220| enzyme inhibitor/ pectinesterase	Unigene24935_All//0.00E+00//TC144757		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0030234//GO:0030312//GO:0071555	nr -
Unigene24936_All	1815	11.91	1.65	2.96	1.78	1.37	2.21	0.75	1.61	0.09	-2.85E+00	1.12E-67	Down	-2.01E+00	4.76E-43	Down	-3.85E-01	2.86E-01		3.12E-01	3.61E-01		1.11E+00	7.66E-04	Up	-3.09E+00	1.97E-06	Down	Unigene24936_All//gi|119507467|dbj|BAF42041.1|//0.00E+00//pectin methylesterase 4 [Pyrus communis]	Unigene24936_All//0.00E+00//AT4G33220| enzyme inhibitor/ pectinesterase	Unigene24936_All//0.00E+00//gi|78325881|gb|DT546155.1|DT546155		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0030234//GO:0045229//GO:0071555	nr -

Unigene24937_All	1517	21.45	159.72	52.44	30.24	49.94	85.62	50.25	257.86	339.17	2.90E+00	0.00E+00	Up	1.29E+00	8.63E-84	Up	7.24E-01	1.17E-37		1.50E+00	1.05E-189	Up	2.36E+00	0.00E+00	Up	2.75E+00	0.00E+00	Up	Unigene24937_All//gi|206584347|gb|ACI15346.1|//0.00E+00//NAC domain protein NAC5 [Gossypium hirsutum] >gi|206584357|gb|ACI15351.1| NAC domain protein NAC5 [Gossypium hirsutum]	Unigene24937_All//2.00E-90//AT3G04070| anac047 (Arabidopsis NAC domain containing protein 47); transcription factor	Unigene24937_All//0.00E+00//TC137888	NAC		GO:0003676//GO:0010468	nr +
Unigene24939_All	921	15.00	14.74	13.24	27.85	31.78	31.19	29.24	23.14	14.53	-2.46E-02	8.88E-01		-1.80E-01	3.00E-01		1.90E-01	7.06E-02		1.63E-01	1.48E-01		-3.37E-01	3.31E-04		-1.01E+00	1.86E-25	Down	Unigene24939_All|gi|75338884|sp|Q9ZR40.1|U2A2B_NICPL//3.00E-90//RecName: Full=Splicing factor U2af large subunit B; AltName: Full=U2 small nuclear ribonucleoprotein auxiliary factor large subunit B; Short=U2 snRNP auxiliary factor large subunit B; AltName: Full=U2 auxiliary factor 65 kDa subunit B; AltName: Full=NpU2AF65b >gi|3850821|emb|CAA77135.1| U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]	Unigene24939_All//6.00E-30//AT4G36690| ATU2AF65A; RNA binding / nucleic acid binding / nucleotide binding	Unigene24939_All//1.00E-132//TC157758	ko03040|Spliceosome	GO:0000377//GO:0003676//GO:0006952//GO:0043231	nr -
Unigene2494_All	667	2.43	0.46	2.24	3.14	3.10	4.20	1.84	3.32	1.79	-2.42E+00	7.51E-05	Down	-1.21E-01	8.10E-01		-1.81E-02	9.56E-01		4.21E-01	3.05E-01		8.53E-01	2.67E-02		-3.70E-02	9.60E-01		Unigene2494_All|gi|224106127|ref|XP_002314053.1|//2.00E-60//cinnamoyl CoA reductase-like protein [Populus trichocarpa] >gi|222850461|gb|EEE88008.1| cinnamoyl CoA reductase-like protein [Populus trichocarpa]	Unigene2494_All//7.00E-55//AT5G19440| cinnamyl-alcohol dehydrogenase, putative (CAD)	Unigene2494_All//0.00E+00//TC150352		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene24940_All	1582	7.57	5.86	6.97	19.96	15.59	14.07	5.16	2.30	3.42	-3.70E-01	2.60E-02		-1.20E-01	5.33E-01		-3.57E-01	6.55E-05		-5.04E-01	5.42E-08		-1.17E+00	5.70E-10	Down	-5.91E-01	7.56E-04		Unigene24940_All//gi|115464003|ref|NP_001055601.1|//1.00E-127//Os05g0426300 [Oryza sativa Japonica Group] >gi|113579152|dbj|BAF17515.1| Os05g0426300 [Oryza sativa Japonica Group]	Unigene24940_All//1.00E-119//AT1G48880| unknown protein	Unigene24940_All//0.00E+00//TC165439				nr -
Unigene24941_All	1901	24.44	26.79	14.73	21.83	30.90	38.27	27.40	55.80	70.27	1.32E-01	1.01E-01		-7.30E-01	2.23E-19		5.02E-01	1.96E-15		8.10E-01	9.23E-40		1.03E+00	1.50E-97	Up	1.36E+00	2.61E-195	Up	Unigene24941_All|gi|224084626|ref|XP_002307364.1|//0.00E+00//2-dehydro-3-deoxyphosphoheptonate aldolase/ 3-deoxy-d-arabino-heptulosonate 7-phosphate synthetase [Populus trichocarpa] >gi|222856813|gb|EEE94360.1| 2-dehydro-3-deoxyphosphoheptonate aldolase/ 3-deoxy-d-arabino-heptulosonate 7-phosphate synthetase [Populus trichocarpa]	Unigene24941_All//0.00E+00//AT4G33510| DHS2 (3-deoxy-d-arabino-heptulosonate 7-phosphate synthase); 3-deoxy-7-phosphoheptulonate synthase	Unigene24941_All//0.00E+00//TC134528		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0005488//GO:0008652//GO:0009536//GO:0016765//GO:0019632//GO:0043650	nr +
Unigene24942_All	2053	2.27	2.27	1.14	5.46	5.87	4.31	6.55	1.91	2.81	1.50E-03	9.96E-01		-9.91E-01	7.36E-04		1.05E-01	6.01E-01		-3.41E-01	5.26E-02		-1.77E+00	3.85E-29	Down	-1.22E+00	1.52E-17	Down	Unigene24942_All|gi|115444033|ref|NP_001045796.1|//2.00E-61//Os02g0132200 [Oryza sativa Japonica Group] >gi|113535327|dbj|BAF07710.1| Os02g0132200 [Oryza sativa Japonica Group]	Unigene24942_All//1.00E-68//AT5G05240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP030365 (InterPro:IPR016953); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G40630.1); Has 24 Blast hits to 24 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene24942_All//0.00E+00//TC170923			GO:0009536	nr +
Unigene24943_All	1377	9.69	30.65	14.85	8.47	9.33	18.01	6.54	4.98	8.56	1.66E+00	1.01E-66	Up	6.16E-01	8.91E-07		1.40E-01	4.52E-01		1.09E+00	2.08E-22	Up	-3.94E-01	2.41E-02		3.89E-01	7.24E-03		Unigene24943_All|gi|21554334|gb|AM63441.1|//3.00E-25//latex-abundant protein-like [Arabidopsis thaliana]	Unigene24943_All//1.00E-26//AT5G04200| ArMC9 (metacaspase 9); cysteine-type peptidase	Unigene24943_All//4.00E-143//TC158381			GO:0008152//GO:0070011	nr -
Unigene24947_All	1871	9.40	7.18	6.77	15.07	10.67	12.31	7.82	2.08	7.60	-3.89E-01	3.53E-03		-4.72E-01	5.87E-04		-4.97E-01	9.71E-08		-2.92E-01	4.60E-03		-1.91E+00	6.01E-35	Down	-4.07E-02	7.77E-01		Unigene24947_All|gi|227204439|dbj|BAH57071.1|//1.00E-149//AT2G37860| [Arabidopsis thaliana]	Unigene24947_All//7.00E-127//AT2G37860| LCD1 (LOWER CELL DENSITY 1)	Unigene24947_All//0.00E+00//TC168858				nr +
Unigene24948_All	1274	7.10	29.23	9.45	6.61	8.08	10.00	10.06	29.36	30.11	2.04E+00	7.98E-78	Up	4.11E-01	1.69E-02		2.90E-01	1.20E-01		5.97E-01	1.17E-04		1.55E+00	1.83E-65	Up	1.58E+00	7.03E-71	Up	Unigene24948_All|gi|89111818|gb|AB060681.1|//1.00E-14//At1g67920 [Arabidopsis thaliana]	Unigene24948_All//6.00E-16//AT1G67920| unknown protein	Unigene24948_All//0.00E+00//TC156791			GO:0009536	nr -
Unigene24949_All	1181	12.40	5.62	11.45	20.46	22.01	28.49	24.38	27.43	27.26	-1.14E+00	9.46E-14	Down	-1.15E-01	5.05E-01		1.06E-01	4.16E-01		4.78E-01	1.09E-07		1.70E-01	6.26E-02		1.61E-01	6.86E-02		Unigene24949_All|gi|27805752|sp|O23429.2|VA724_ARATH//1.00E-109//RecName: Full=Vesicle-associated membrane protein 724; Short=AtVAMP724; AltName: Full=SYBL1-like protein >gi|48310135|gb|AAT41760.1| At4g15780 [Arabidopsis thaliana] >gi|50198886|gb|AAT70463.1| At4g15780 [Arabidopsis thaliana]	Unigene24949_All//5.00E-99//AT4G15780| ATVAMP724	Unigene24949_All//0.00E+00//TC137155		ko04130|SNARE interactions in vesicular transport	GO:0006810//GO:0031224	nr -
Unigene2495_All	476	6.60	17.78	7.16	33.38	19.46	61.77	1.07	0.00	0.08	1.43E+00	2.42E-11	Up	1.19E-01	7.27E-01		-7.79E-01	1.33E-09		8.88E-01	4.77E-19		-1.01E+01	8.89E-04	Down	-3.67E+00	3.75E-03		Unigene2495_All|gi|224106117|ref|XP_002314050.1|//2.00E-34//cinnamoyl CoA reductase-like protein [Populus trichocarpa] >gi|222850458|gb|EEE88005.1| cinnamoyl CoA reductase-like protein [Populus trichocarpa]	Unigene2495_All//8.00E-35//AT5G19440| cinnamyl-alcohol dehydrogenase, putative (CAD)	Unigene2495_All//1.00E-112//TC167211		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene24950_All	1543	5.43	2.36	6.04	2.91	2.23	3.01	1.62	0.79	1.11	-1.20E+00	8.85E-09	Down	1.55E-01	4.69E-01		-3.81E-01	1.93E-01		5.32E-02	8.78E-01		-1.04E+00	3.86E-03		-5.42E-01	1.18E-01		Unigene24950_All|gi|224069492|ref|XP_002302984.1|//1.00E-151//methionyl-trna formyltransferase [Populus trichocarpa] >gi|222844710|gb|EEE82257.1| methionyl-trna formyltransferase [Populus trichocarpa]	Unigene24950_All//1.00E-140//AT1G66520| pde194 (pigment defective 194); catalytic/ formyltetrahydrofolate deformylase/ hydroxymethyl-, formyl- and related transferase	Unigene24950_All//0.00E+00//EX166859		ko00970|Aminoacyl-tRNA biosynthesis//ko00670|One carbon pool by folate	GO:0016740	nr -
Unigene24951_All	1557	32.93	5.96	9.17	23.96	16.41	8.32	7.49	1.21	2.66	-2.47E+00	3.96E-136	Down	-1.85E+00	5.41E-91	Down	-5.46E-01	7.68E-12		-1.53E+00	6.09E-57	Down	-2.63E+00	3.22E-41	Down	-1.49E+00	1.22E-20	Down	Unigene24951_All|gi|124359980|gb|ABN07996.1|//1.00E-104//Thioredoxin fold [Medicago truncatula]	Unigene24951_All//2.00E-65//AT2G41330| glutaredoxin family protein	Unigene24951_All//0.00E+00//gi|78340711|gb|DT560985.1|DT560985			GO:0015036//GO:0019725	nr -
Unigene24952_All	1909	2.08	2.26	1.84	4.31	4.53	3.57	5.85	1.47	3.38	1.15E-01	6.94E-01		-1.78E-01	6.18E-01		7.25E-02	7.92E-01		-2.69E-01	2.24E-01		-1.99E+00	2.38E-28	Down	-7.90E-01	1.23E-07		Unigene24952_All|gi|115439961|ref|NP_001044260.1|//1.00E-125//Os01g0751600 [Oryza sativa Japonica Group] >gi|15623855|dbj|BAB67914.1| lipase (class 3)-like protein [Oryza sativa Japonica Group] >gi|20166583|dbj|BAB89530.1| lipase (class 3)-like protein [Oryza sativa Japonica Group] >gi|113553791|dbj|BAF06174.1| Os01g0751600 [Oryza sativa Japonica Group]	Unigene24952_All//2.00E-140//AT5G50890| LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: lipase class 3 family protein (TAIR:AT2G05260.1); Has 115 Blast hits to 115 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 115; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene24952_All//3.00E-73//DR455575				nr +
Unigene24953_All	1995	7.47	16.03	7.26	11.51	11.20	19.40	14.77	12.65	12.94	1.10E+00	2.40E-27	Up	-4.20E-02	7.97E-01		-3.92E-02	8.09E-01		7.53E-01	6.19E-19		-2.23E-01	1.62E-02		-1.91E-01	3.60E-02		Unigene24953_All|gi|15227684|ref|NP_180560.1|//0.00E+00//NDA2 (ALTERNATIVE NAD(P)H DEHYDROGENASE 2); FAD binding / NADH dehydrogenase/ oxidoreductase [Arabidopsis thaliana]	Unigene24953_All//0.00E+00//AT2G29990| NDA2 (ALTERNATIVE NAD(P)H DEHYDROGENASE 2); FAD binding / NADH dehydrogenase/ oxidoreductase	Unigene24953_All//0.00E+00//gi|78341242|gb|DT561516.1|DT561516		ko00190|Oxidative phosphorylation	GO:0005743//GO:0008152//GO:0030554//GO:0050136	nr +
Unigene24954_All	1321	11.96	4.68	6.37	5.47	5.60	4.79	2.94	1.08	1.96	-1.35E+00	4.72E-19	Down	-9.09E-01	6.46E-10		3.56E-02	8.95E-01		-1.92E-01	4.49E-01		-1.45E+00	6.35E-07	Down	-5.87E-01	2.81E-02		Unigene24954_All|gi|15242597|ref|NP_198832.1|//3.00E-94//EMB506 (embryo defective 506); protein binding [Arabidopsis thaliana] >gi|75313777|sp|Q9SQK3.1|EM506_ARATH RecName: Full=Ankyrin repeat domain-containing protein EMB506, chloroplastic; AltName: Full=Protein EMBRYO DEFECTIVE 506; Flags: Precursor >gi|5911312|gb|AAD55746.1|AF026167_1 ankyrin repeat protein EMB506 [Arabidopsis thaliana] >gi|10177503|dbj|BAB10897.1| ankyrin repeat protein EMB506 [Arabidopsis thaliana]	Unigene24954_All//3.00E-87//AT5G40160| EMB506 (embryo defective 506); protein binding	Unigene24954_All//0.00E+00//TC161729			GO:0003006//GO:0005488//GO:0009536	nr +
Unigene24955_All	2256	5.15	5.03	3.00	10.40	13.16	11.63	15.05	4.15	4.41	-3.33E-02	8.54E-01		-7.80E-01	6.39E-06		3.39E-01	3.28E-04		1.61E-01	1.80E-01		-1.86E+00	3.80E-77	Down	-1.77E+00	2.63E-74	Down	Unigene24955_All|gi|224080986|ref|XP_002306254.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222855703|gb|EEE92250.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene24955_All//0.00E+00//AT2G13610| ABC transporter family protein	Unigene24955_All//0.00E+00//TC177293		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015405//GO:0015604//GO:0017111//GO:0031224//GO:0032559//GO:0051234//GO:0051707	nr -
Unigene24956_All	497	5.58	5.00	4.61	9.12	7.76	4.27	13.70	13.71	10.74	-1.60E-01	6.64E-01		-2.76E-01	4.99E-01		-2.33E-01	4.52E-01		-1.09E+00	1.03E-04	Down	1.20E-03	9.95E-01		-3.51E-01	7.88E-02		Unigene24956_All|gi|115463143|ref|NP_001055171.1|//6.00E-44//Os05g0315200 [Oryza sativa Japonica Group] >gi|113578222|dbj|BAF17085.1| Os05g0315200 [Oryza sativa Japonica Group]	Unigene24956_All//4.00E-43//AT1G30050| unknown protein	Unigene24956_All//0.00E+00//DR511217				nr +
Unigene24957_All	1127	1.86	2.25	1.70	3.71	2.63	1.36	7.24	10.57	7.81	2.76E-01	5.02E-01		-1.27E-01	7.74E-01		-4.99E-01	8.70E-02		-1.45E+00	2.03E-06	Down	5.46E-01	1.87E-04		1.10E-01	5.90E-01		Unigene24957_All|gi|115463143|ref|NP_001055171.1|//7.00E-24//Os05g0315200 [Oryza sativa Japonica Group] >gi|113578222|dbj|BAF17085.1| Os05g0315200 [Oryza sativa Japonica Group]	Unigene24957_All//9.00E-36//AT5G01970| unknown protein	Unigene24957_All//4.00E-62//TC158862				nr -
Unigene24960_All	1413	6.70	12.12	13.42	5.25	4.65	5.63	20.89	7.39	3.64	8.55E-01	3.91E-10		1.00E+00	9.78E-14	Up	-1.74E-01	4.78E-01		9.88E-02	6.96E-01		-1.50E+00	1.40E-49	Down	-2.52E+00	1.90E-101	Down	Unigene24960_All|gi|156891145|gb|ABR96710.1|//3.00E-22//glutaredoxin [Solanum tuberosum]	Unigene24960_All//4.00E-21//AT5G40370| glutaredoxin, putative	Unigene24960_All//0.00E+00//TC159755			GO:0006091//GO:0015036//GO:0016020//GO:0019725//GO:0043231//GO:0051234	nr -

Unigene24962_All	1159	8.94	8.66	11.03	15.86	11.02	12.35	8.28	4.00	4.61	-4.63E-02	8.06E-01		3.03E-01	7.77E-02		-5.25E-01	9.99E-06		-3.61E-01	5.33E-03		-1.05E+00	6.83E-10	Down	-8.46E-01	2.05E-07		Unigene24962_All//gi|18411133|ref|NP_567078.1|//5.00E-43//TXR1 (THAXTOMIN A RESISTANT 1) [Arabidopsis thaliana] >gi|14190487|gb|AAK55724.1|AF38064 3_1 AT3g59280/F25L23_140 [Arabidopsis thaliana] >gi|15809738|gb|AAL06797.1| AT3g59280/F25L23_140 [Arabidopsis thaliana] >gi|32306447|gb|AAM63549.1| thaxtomin resistance protein TXR1 [Arabidopsis thaliana]	Unigene24962_All//2.00E-44//AT3G59280| TXR1 (THAXTOMIN A RESISTANT 1)	Unigene24962_All//3.00E-17//TC132843			GO:0005515//GO:0044464	nr +
Unigene24963_All	2551	1.46	1.53	1.44	2.01	2.15	2.89	10.03	19.50	48.62	7.08E-02	8.20E-01		-1.58E-02	9.85E-01		9.37E-02	7.85E-01		5.21E-01	1.62E-02		9.59E-01	2.24E-41		2.28E+00	0.00E+00	Up	Unigene24963_All//gi|297832266|ref|XP_002884015.1|//2.00E-92//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329855|gb|EFH60274.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24963_All//8.00E-92//AT2G16750| protein kinase family protein	Unigene24963_All//0.00E+00//DT461906		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr -
Unigene24965_All	1194	34.75	26.10	26.94	60.33	47.53	28.90	25.50	15.51	8.98	-4.13E-01	5.45E-07		-3.67E-01	1.72E-05		-3.44E-01	8.90E-10		-1.06E+00	2.37E-62	Down	-7.17E-01	6.16E-16		-1.51E+00	4.49E-53	Down	Unigene24965_All//gi|53370641|gb|AU89136.1|//6.00E-08//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene24965_All//6.00E-83//ES830147				nr -
Unigene24966_All	1197	6.43	7.28	5.83	16.81	18.70	19.39	24.62	7.09	9.15	1.80E-01	3.81E-01		-1.41E-01	5.68E-01		1.53E-01	2.39E-01		2.06E-01	9.43E-02		-1.80E+00	5.01E-64	Down	-1.43E+00	1.66E-47	Down	Unigene24966_All//gi|115480761|ref|NP_001063974.1|//5.00E-25//Os09g0568900 [Oryza sativa Japonica Group] >gi|5821432|dbj|BAA81662.2| F1F0-ATPase inhibitor protein [Oryza sativa Japonica Group] >gi|52077175|dbj|BAD46220.1| F1F0-ATPase inhibitor protein [Oryza sativa Japonica Group] >gi|113632207|dbj|BAF25888.1| Os09g0568900 [Oryza sativa Japonica Group]	Unigene24966_All//9.00E-16//AT2G27730| unknown protein	Unigene24966_All//0.00E+00//TC157141			GO:0005746//GO:0030964//GO:0031981//GO:0043094//GO:0046914	nr +
Unigene24967_All	2370	0.64	1.09	1.33	4.90	5.84	5.43	8.88	2.82	5.28	7.68E-01	5.07E-02		1.05E+00	4.45E-03		2.54E-01	1.09E-01		1.49E-01	4.23E-01		-1.65E+00	4.98E-41	Down	-7.51E-01	1.54E-12		Unigene24967_All//gi|1483177|dbj|BAA13135.1|//0.00E+00//subtilisin-like protein [Picea abies]	Unigene24967_All//1.00E-178//AT1G20160| ATSBT5.2; identical protein binding / serine-type endopeptidase	Unigene24967_All//0.00E+00//ES801496			GO:0004175//GO:0005515//GO:0005576//GO:0016628//GO:0019538//GO:0043410//GO:0044092	nr +
Unigene24972_All	976	2.09	0.31	0.98	5.41	4.45	2.17	2.43	2.40	2.16	-2.75E+00	1.06E-06	Down	-1.09E+00	2.30E-02		-2.83E-01	3.15E-01		-1.31E+00	5.97E-07	Down	-1.66E-02	1.00E+00		-1.65E-01	6.47E-01		Unigene24972_All//gi|212717133|gb|ACJ37408.1|//1.00E-24//PK-LRR-TM resistance protein [Glycine max]	Unigene24972_All//1.00E-17//AT3G25020| AtRLP42 (Receptor Like Protein 42); protein binding	Unigene24972_All//0.00E+00//gi|109881738|gb|DW510708.1|DW510708			GO:0003824	nr +
Unigene24973_All	954	2.47	2.12	2.01	3.45	3.25	2.18	1.02	3.42	1.34	-2.16E-01	5.98E-01		-2.97E-01	5.08E-01		-8.52E-02	8.11E-01		-6.62E-01	5.44E-02		1.75E+00	1.85E-07	Up	3.91E-01	4.66E-01		Unigene24973_All//gi|164605529|dbj|BAF98595.1|//1.00E-85//CM0545.400.nc [Lotus japonicus]	Unigene24973_All//1.00E-52//AT2G25440| AtRLP20 (Receptor Like Protein 20); kinase/ protein binding	Unigene24973_All//1.00E-129//TC160015				nr -
Unigene24974_All	1105	7.06	5.73	5.40	12.08	15.77	8.91	3.75	0.61	2.02	-3.00E-01	1.66E-01		-3.86E-01	8.36E-02		3.84E-01	2.75E-03		-4.39E-01	4.13E-03		-2.63E+00	4.73E-15	Down	-8.93E-01	5.66E-04		Unigene24974_All//gi|297830566|ref|XP_002883165.1|//9.00E-61//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297329005|gb|EFH59424.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene24974_All//7.00E-53//AT3G19184| DNA binding	Unigene24974_All//0.00E+00//TC155460	ABI3VP1		GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene24975_All	1045	1.60	1.84	1.12	3.96	2.44	2.25	2.51	0.44	0.57	2.02E-01	6.50E-01		-5.15E-01	3.44E-01		-6.98E-01	1.37E-02		-8.16E-01	5.83E-03		-2.51E+00	2.60E-09	Down	-2.13E+00	4.28E-08	Down	Unigene24975_All//gi|297830566|ref|XP_002883165.1|//6.00E-64//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297329005|gb|EFH59424.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene24975_All//2.00E-56//AT3G19184| DNA binding	Unigene24975_All//0.00E+00//TC155460	ABI3VP1		GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene24978_All	2568	1.10	3.93	0.91	1.63	2.28	3.31	8.28	16.08	22.63	1.84E+00	8.62E-19	Up	-2.70E-01	5.06E-01		4.84E-01	4.78E-02		1.02E+00	2.54E-07	Up	9.57E-01	2.26E-34		1.45E+00	3.30E-94	Up	Unigene24978_All//gi|224132554|ref|XP_002321349.1|//1.00E-164//pseudo response regulator [Populus trichocarpa] >gi|222868345|gb|EEF05476.1| pseudo response regulator [Populus trichocarpa]	Unigene24978_All//4.00E-109//AT5G24470| APRR5 (ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator	Unigene24978_All//0.00E+00//TC177669		ko04712|Circadian rhythm - plant		nr -
Unigene2498_All	1813	30.24	34.04	47.64	11.10	7.31	6.43	0.30	0.28	2.40	1.71E-01	1.46E-02		6.56E-01	1.50E-29		-6.02E-01	8.10E-08		-7.88E-01	5.10E-11		-1.33E-01	8.80E-01		2.98E+00	3.63E-18	Up	Unigene2498_All//gi|2501491|sp|Q40284.1|UFOG1_MANES//1.00E-127//RecName: Full=Anthocyanidin 3-O-glucosyltransferase 1; AltName: Full=Flavonol 3-O-glucosyltransferase 1; AltName: Full=UDP-glucose flavonoid 3-O-glucosyltransferase 1 >gi|453246|emb|CAA54609.1| UTP-glucose glucosyltransferase [Manihot esculenta]	Unigene2498_All//3.00E-113//AT3G21760| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene2498_All//0.00E+00//gi|109871489|gb|DW500465.1|DW500465				nr -
Unigene24980_All	1237	8.54	19.37	10.03	13.21	13.72	17.89	15.35	16.29	13.33	1.18E+00	4.41E-23	Up	2.31E-01	1.98E-01		5.52E-02	7.70E-01		4.38E-01	1.30E-04		8.57E-02	5.33E-01		-2.03E-01	8.18E-02		Unigene24980_All//gi|18413291|ref|NP_567350.1|//1.00E-118//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|14423412|gb|AAK62388.1|AF38694 3_1 lipase-like protein [Arabidopsis thaliana] >gi|20148343|gb|AAM10062.1| lipase-like protein [Arabidopsis thaliana]	Unigene24980_All//2.00E-119//AT4G10050| hydrolase, alpha/beta fold family protein	Unigene24980_All//0.00E+00//gi|164335198|gb|ES801025.1|ES801025				nr -
Unigene24981_All	1618	5.04	11.59	7.54	8.90	9.11	10.05	6.40	7.57	5.81	1.20E+00	1.18E-18	Up	5.79E-01	5.59E-04		3.39E-02	8.49E-01		1.76E-01	2.68E-01		2.42E-01	1.20E-01		-1.40E-01	4.17E-01		Unigene24981_All//gi|18413291|ref|NP_567350.1|//1.00E-151//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|14423412|gb|AAK62388.1|AF38694 3_1 lipase-like protein [Arabidopsis thaliana] >gi|20148343|gb|AAM10062.1| lipase-like protein [Arabidopsis thaliana]	Unigene24981_All//6.00E-153//AT4G10050| hydrolase, alpha/beta fold family protein	Unigene24981_All//0.00E+00//TC143524				nr +
Unigene24982_All	1542	5.56	5.29	5.63	7.11	5.23	5.95	34.19	8.10	13.82	-7.29E-02	7.28E-01		1.66E-02	9.56E-01		-4.44E-01	6.88E-03		-2.57E-01	1.69E-01		-2.08E+00	2.40E-138	Down	-1.31E+00	9.88E-74	Down	Unigene24982_All//gi|110559491|gb|AB676000.1|//0.00E+00//GDP-like protein 2 [Gossypium hirsutum]	Unigene24982_All//0.00E+00//AT3G02230| RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1); cellulose synthase (UDP-forming)	Unigene24982_All//0.00E+00//gi|78332180|gb|DT552454.1|DT552454			GO:0005618//GO:0009250//GO:0035251//GO:0043231//GO:0044159//GO:0045229	nr -
Unigene24983_All	1863	63.78	26.68	38.79	494.10	364.20	218.91	61.21	11.04	22.99	-1.26E+00	8.81E-124	Down	-7.18E-01	2.66E-47		-4.40E-01	7.01E-191		-1.17E+00	0.00E+00	Down	-2.47E+00	0.00E+00	Down	-1.41E+00	1.20E-178	Down	Unigene24983_All//gi|134035512|gb|AB047744.1|//0.00E+00//polygalacturonase-inhibiting protein [Gossypium hirsutum]	Unigene24983_All//2.00E-122//AT3G20820| leucine-rich repeat family protein	Unigene24983_All//0.00E+00//TC145226		ko04626|Plant-pathogen interaction	GO:0005488	nr -
Unigene24986_All	1239	12.58	8.34	7.95	3.18	1.36	2.62	34.02	47.73	17.65	-5.93E-01	2.58E-05		-6.62E-01	5.76E-06		-1.22E+00	2.49E-05	Down	-2.75E-01	4.20E-01		4.89E-01	1.47E-15		-9.47E-01	1.77E-35		Unigene24986_All//gi|15236657|ref|NP_193515.1|//1.00E-105//DNA-binding protein-related [Arabidopsis thaliana] >gi|17933299|gb|AAL48232.1|AF44635 9_1 AT4g17800/d14935c [Arabidopsis thaliana] >gi|20453387|gb|AAM19932.1| AT4g17800/d14935c [Arabidopsis thaliana] >gi|119657390|tpd|FAA00294.1| TPA: AT-hook motif nuclear localized protein 23 [Arabidopsis thaliana]	Unigene24986_All//1.00E-87//AT4G17800| DNA-binding protein-related	Unigene24986_All//7.00E-92//gi|78329872|gb|DT550146.1|DT550146				nr -
Unigene24987_All	1519	6.37	3.24	3.96	5.77	7.14	8.18	12.25	5.61	4.83	-9.78E-01	1.94E-07		-6.86E-01	3.34E-04		3.07E-01	8.47E-02		5.02E-01	1.55E-03		-1.13E+00	1.50E-20	Down	-1.34E+00	1.02E-27	Down	Unigene24987_All//gi|71727712|gb|AA239949.1|//0.00E+00//serine/threonine protein kinase [Gossypium hirsutum]	Unigene24987_All//3.00E-165//AT5G08160| ATPK3; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene24987_All//0.00E+00//TC141682			GO:0004672//GO:0006464//GO:0032559	nr +
Unigene24989_All	1340	39.94	29.19	41.77	7.66	4.99	4.28	35.84	14.04	13.71	-4.52E-01	3.09E-10		6.44E-02	4.47E-01		-6.19E-01	1.79E-04		-8.39E-01	1.54E-06		-1.35E+00	7.05E-69	Down	-1.39E+00	1.27E-73	Down	Unigene24989_All//gi|47716659|gb|AT37529.1|//1.00E-131//purple acid phosphatase 1 [Solanum tuberosum]	Unigene24989_All//2.00E-122//AT1G14700| PAP3 (PURPLE ACID PHOSPHATASE 3); acid phosphatase/ protein serine/threonine phosphatase	Unigene24989_All//0.00E+00//TC139837		ko00740|Riboflavin metabolism		nr +
Unigene24990_All	1068	33.02	53.28	41.93	58.49	59.68	54.00	54.95	19.76	11.00	6.90E-01	2.98E-22		3.45E-01	2.68E-05		2.91E-02	7.60E-01		-1.15E-01	1.25E-01		-1.48E+00	1.10E-95	Down	-2.32E+00	3.46E-182	Down	Unigene24990_All//gi|87162930|gb|AB028725.1|//3.00E-52//Embryo-specific 3 [Medicago truncatula]	Unigene24990_All//3.00E-50//AT5G62200| embryo-specific protein-related	Unigene24990_All//0.00E+00//gi|164334536|gb|ES849269.1|ES849269			GO:0031224	nr -
Unigene24992_All	2202	4.61	4.97	6.84	6.02	6.54	6.54	2.90	2.90	0.87	1.09E-01	5.86E-01		5.70E-01	1.28E-04		1.19E-01	5.21E-01		1.21E-01	5.00E-01		2.40E-03	1.02E+00		-1.74E+00	2.48E-14	Down	Unigene24992_All//gi|297836442|ref|XP_002886103.1|//1.00E-167//ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331943|gb|EFH62362.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene24992_All//7.00E-135//AT2G17200| ubiquitin family protein	Unigene24992_All//0.00E+00//TC138162		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene24994_All	3481	0.26	0.44	0.15	0.69	1.51	1.36	5.99	14.78	89.79	7.73E-01	1.48E-01		-7.40E-01	3.48E-01		1.14E+00	6.25E-06	Up	9.88E-01	3.41E-04		1.30E+00	1.43E-69	Up	3.91E+00	0.00E+00	Up	Unigene24994_All//gi|264661459|sp|C0LGJ1.1|Y1743_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g74360; Flags: Precursor >gi|224589485|gb|ACN59276.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene24994_All//0.00E+00//AT1G74360| leucine-rich repeat transmembrane protein kinase, putative	Unigene24994_All//0.00E+00//gi|73864329|gb|DT467068.1|DT467068			GO:0016301//GO:0043231	nr -
Unigene24996_All	1346	37.67	44.42	61.68	16.54	18.29	13.56	0.06	0.56	0.24	2.38E-01	5.70E-04		7.11E-01	9.33E-33		1.45E-01	2.44E-01		-2.87E-01	1.56E-02		3.15E+00	9.54E-04	Up	1.91E+00	1.54E-01		Unigene24996_All//gi|115435276|ref|NP_001042396.1|//1.00E-111//Os01g0215700 [Oryza sativa Japonica Group] >gi|113531927|dbj|BAF04310.1| Os01g0215700 [Oryza sativa Japonica Group]	Unigene24996_All//1.00E-97//AT5G45910| GDSL-motif lipase/hydrolase family protein	Unigene24996_All//0.00E+00//gi|164334024|gb|ES814008.1|ES814008			GO:0043231	nr -
Unigene24997_All	428	7.21	3.67	5.47	10.59	7.08	4.22	6.42	4.00	3.16	-9.75E-01	6.21E-03		-3.98E-01	2.99E-01		-5.81E-01	3.32E-02		-1.33E+00	3.85E-06	Down	-6.82E-01	4.47E-02		-1.02E+00	1.95E-03					Unigene24997_All//1.00E-115//DW497772				
Unigene24999_All	1412	6.45	4.27	4.94	5.08	5.98	3.55	3.89	1.42	1.89	-5.94E-01	1.80E-03		-3.84E-01	5.94E-02		2.34E-01	2.98E-01		-5.17E-01	1.82E-02		-1.45E+00	1.77E-09	Down	-1.04E+00	3.53E-06	Down	Unigene24999_All//gi|29028900|gb|AA064829.1|//1.00E-108//At2g26470 [Arabidopsis thaliana]	Unigene24999_All//1.00E-109//AT2G26470| unknown protein	Unigene24999_All//0.00E+00//TC148684				nr -
Unigene25_All	4196	1.80	1.70	2.01	5.02	6.52	9.00	7.50	5.50	17.54	-7.66E-02	7.25E-01		1.59E-01	4.81E-01		3.76E-01	1.28E-04		8.41E-01	3.02E-22		-4.47E-01	1.70E-07		1.23E+00	3.76E-92	Up	Unigene25_All//gi|297821204|ref|XP_002878485.1|//1.00E-118//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324323|gb|EFH54744.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene25_All//2.00E-55//AT3G62900| zinc ion binding	Unigene25_All//0.00E+00//gi|78343877|gb|DT564151.1|DT564151				nr -

Unigene25000_A11	1455	1.47	1.25	1.94	1.99	1.61	2.20	1.86	0.49	2.19	-2.34E-01	6.22E-01			3.96E-01	3.29E-01		-3.03E-01	4.44E-01			1.50E-01	6.78E-01		-1.93E+00	3.86E-07	Down	2.36E-01	4.70E-01		Unigene25000_A11//gi|297825331|ref|XP_002880548.1|//0.00E+00//PDE319/SCA3 [Arabidopsis lyrata subsp. lyrata] >gi|297326387|gb|EFH56807.1|PDE319/SCA3 [Arabidopsis lyrata subsp. lyrata]	Unigene25000_A11//5.00E-168//AT2G24120| SCA3 (SCABRA 3); DNA binding / DNA-directed RNA polymerase	Unigene25000_A11//0.00E+00//D8460653			GO:0003676//GO:0010467//GO:0034062//GO:0043231	nr -
Unigene25005_A11	461	0.45	1.54	2.89	1.08	0.52	1.96	3.94	1.63	0.95	1.76E+00	5.60E-02			2.67E+00	3.01E-04	Up	-1.05E+00	3.15E-01			8.59E-01	2.70E-01		-1.27E+00	3.87E-03		-2.05E+00	1.27E-05	Down	Unigene25005_A11//gi|227202800|dbj|BAH56873.1|//2.00E-18//AT5G25540 [Arabidopsis thaliana]	Unigene25005_A11//1.00E-19//AT5G25540| CID6 (CTC-Interacting Domain 6); protein binding	Unigene25005_A11//0.00E+00//TC159914				nr +
Unigene25006_A11	654	2.24	5.50	5.37	4.80	4.42	4.14	9.44	11.70	6.52	1.30E+00	1.18E-04	Up	1.26E+00	3.30E-04	Up	-1.18E-01	7.85E-01		-2.12E-01	6.15E-01		3.09E-01	1.21E-01		-5.34E-01	9.35E-03		Unigene25006_A11//gi|255551120|ref|XP_002516608.1|//1.00E-09//conserved hypothetical protein [Ricinus communis] >gi|223544428|gb|EEF45949.1|conserved hypothetical protein [Ricinus communis]		Unigene25006_A11//0.00E+00//gi|21102623|gb|BQ414936.1|BQ414936				nr +
Unigene25008_A11	941	12.73	10.12	15.73	8.79	9.00	8.64	6.02	4.31	2.20	-3.31E-01	4.81E-02			3.05E-01	5.11E-02		3.48E-02	8.89E-01			-2.46E-02	9.31E-01		-4.83E-01	3.26E-02		-1.45E+00	4.61E-10	Down	Unigene25008_A11//gi|15240039|ref|NP_196261.1|//1.00E-63//thioredoxin-related [Arabidopsis thaliana] >gi|38603858|gb|AAR24674.1|At5g06430 [Arabidopsis thaliana]	Unigene25008_A11//6.00E-65//AT5G06430| thioredoxin-related	Unigene25008_A11//0.00E+00//gi|109860752|gb|DW489731.1|DW489731			GO:0019725//GO:0043231	nr +
Unigene25010_A11	563	25.74	45.09	32.25	74.06	109.42	62.41	26.73	79.14	28.45	8.09E-01	2.16E-13			3.25E-01	1.87E-02		5.63E-01	7.79E-20			-2.47E-01	3.08E-03		1.57E+00	2.86E-79	Up	8.95E-02	5.41E-01		Unigene25010_A11//gi|20385508|gb|AAM21317.1|AF373100_1//6.00E-48//auxin-regulated protein [Populus tremula x Populus tremuloides]	Unigene25010_A11//1.00E-43//AT3G04730| IAA16; transcription factor	Unigene25010_A11//0.00E+00//TC146998			GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr +
Unigene25011_A11	505	109.41	144.38	115.67	332.62	409.81	314.09	54.59	184.98	80.70	4.00E-01	5.03E-11			8.03E-02	3.41E-01		3.01E-01	5.81E-21			-8.27E-02	5.82E-02		1.76E+00	1.34E-195	Up	5.64E-01	2.17E-14		Unigene25011_A11//gi|20385508|gb|AAM21317.1|AF373100_1//6.00E-32//auxin-regulated protein [Populus tremula x Populus tremuloides]	Unigene25011_A11//2.00E-26//AT3G04730| IAA16; transcription factor	Unigene25011_A11//0.00E+00//ES802080			GO:0010071//GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr +
Unigene25012_A11	1448	1.59	4.48	2.57	4.68	6.80	5.99	4.20	3.18	5.97	1.49E+00	2.07E-09	Up	6.95E-01	3.67E-02		5.40E-01	2.04E-03		3.56E-01	8.30E-02		-4.05E-01	6.57E-02		5.06E-01	3.05E-03		Unigene25012_A11//gi|15146232|gb|AA83599.1|//1.00E-132//At1g65900/F12P19_7 [Arabidopsis thaliana] >gi|19699144|gb|AAL90938.1|At1g65900/F12P19_7 [Arabidopsis thaliana]	Unigene25012_A11//8.00E-130//AT1G65900| unknown protein	Unigene25012_A11//0.00E+00//TC179049			GO:0031410//GO:0043231	nr +
Unigene25013_A11	1462	0.93	0.83	0.47	2.42	2.71	2.16	2.95	1.46	1.88	-1.62E-01	7.58E-01		-9.75E-01	1.09E-01		1.63E-01	6.41E-01		-1.62E-01	6.62E-01		-1.02E+00	1.10E-04	Down	-6.50E-01	9.70E-03		Unigene25013_A11//gi|15146232|gb|AA83599.1|//1.00E-145//At1g65900/F12P19_7 [Arabidopsis thaliana] >gi|19699144|gb|AAL90938.1|At1g65900/F12P19_7 [Arabidopsis thaliana]	Unigene25013_A11//1.00E-145//AT1G65900| unknown protein	Unigene25013_A11//0.00E+00//gi|164266226|gb|ES808453.1|ES808453			GO:0043231//GO:0044444	nr +
Unigene25014_A11	1398	2.36	9.13	6.32	25.01	16.45	6.11	49.51	35.85	5.24	1.95E+00	1.30E-25	Up	1.42E+00	2.80E-11	Up	-6.04E-01	2.85E-13		-2.03E+00	9.67E-80	Down	-4.66E-01	1.22E-16		-3.24E+00	0.00E+00	Down	Unigene25014_A11//gi|224112271|ref|XP_002316138.1|//0.00E+00//amino acid transporter [Populus trichocarpa] >gi|222865178|gb|EEF02309.1| amino acid transporter [Populus trichocarpa]	Unigene25014_A11//1.00E-101//AT3G28960| amino acid transporter family protein				GO:0031224	nr +
Unigene25018_A11	2061	0.03	5.48	0.31	0.19	1.84	25.13	11.02	73.15	164.13	7.75E+00	9.39E-63	Up	3.61E+00	6.97E-03		3.25E+00	2.07E-15	Up	7.02E+00	2.27E-302	Up	2.73E+00	0.00E+00	Up	3.90E+00	0.00E+00	Up	Unigene25018_A11//gi|224082488|ref|XP_002306712.1|//1.00E-93//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222856161|gb|EEE93708.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene25018_A11//3.00E-17//AT5G50080| DNA binding / transcription factor	Unigene25018_A11//2.00E-31//ES831270	AP2-EREBP		GO:0006950//GO:0009737//GO:0009987	nr +
Unigene25019_A11	2320	12.90	10.88	7.46	24.80	20.77	28.09	42.85	26.66	20.76	-2.46E-01	1.56E-02		-7.90E-01	1.78E-14		-2.56E-01	8.97E-05		1.80E-01	7.43E-03		-6.84E-01	3.04E-46		-1.05E+00	4.92E-97	Down	Unigene25019_A11//gi|15220511|ref|NP_176936.1|//0.00E+00//TS RNA binding [Arabidopsis thaliana] >gi|11072013|gb|AAG28892.1|AC008113_8 F12A21.17 [Arabidopsis thaliana]	Unigene25019_A11//0.00E+00//AT1G67680| TS RNA binding	Unigene25019_A11//0.00E+00//TC164434		ko03060|Protein export	GO:0003723//GO:0006259//GO:0006613//GO:0030529//GO:0031410	nr +
Unigene25021_A11	2656	2.01	0.72	0.86	2.94	4.82	2.62	4.44	0.83	2.61	-1.47E+00	9.26E-08	Down	-1.22E+00	1.02E-05	Down	7.12E-01	1.48E-06		-1.69E-01	4.80E-01		-2.41E+00	9.48E-38	Down	-7.67E-01	1.16E-07		Unigene25021_A11//gi|115452545|ref|NP_001049873.1|//1.00E-112//Os03g0302900 [Oryza sativa Japonica Group] >gi|108707707|gb|ABF95502.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548344|dbj|BAF11787.1|Os03g0302900 [Oryza sativa Japonica Group]	Unigene25021_A11//3.00E-36//AT3G05750| unknown protein	Unigene25021_A11//0.00E+00//TC168542				nr +
Unigene25022_A11	1769	4.44	2.92	2.92	0.79	0.58	2.86	35.06	70.10	77.38	-6.03E-01	3.64E-03		-6.04E-01	5.22E-03		-4.33E-01	4.50E-01		1.86E+00	2.00E-10	Up	1.00E+00	3.97E-109		1.14E+00	1.17E-152	Up	Unigene25022_A11//gi|297795735|ref|XP_002865752.1|//1.00E-163//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311587|gb|EFH42011.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25022_A11//7.00E-156//AT5G49690| UDP-glucoronosyl/UDP-glucosyl transferase family protein			ko00908|Zeatin biosynthesis		nr +
Unigene25024_A11	1020	26.47	19.57	14.77	42.59	48.14	63.63	58.24	28.89	29.96	-4.35E-01	2.93E-05		-8.41E-01	1.56E-14		1.77E-01	2.18E-02		5.79E-01	6.06E-20		-1.01E+00	8.89E-54	Down	-9.59E-01	1.04E-50		Unigene25024_A11//gi|192913036|gb|ACF06626.1|//1.00E-131//S6 ribosomal protein [Elaeis guineensis]	Unigene25024_A11//2.00E-103//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome	Unigene25024_A11//0.00E+00//TC162340		ko03010|Ribosome		nr +
Unigene25025_A11	761	26.26	57.26	28.76	28.67	33.26	37.69	110.45	168.23	67.79	1.12E+00	2.62E-38	Up	1.31E-01	3.48E-01		2.14E-01	5.69E-02		3.94E-01	7.00E-05		6.07E-01	4.60E-48		-7.04E-01	2.25E-42		Unigene25025_A11//gi|224131746|ref|XP_002328098.1|//1.00E-24//ethylene-insensitive 3b [Populus trichocarpa] >gi|222837613|gb|EEE75978.1|ethylene-insensitive 3b [Populus trichocarpa]	Unigene25025_A11//2.00E-06//AT3G20770| EIN3 (ETHYLENE-INSENSITIVE3); transcription factor	Unigene25025_A11//0.00E+00//gi|164261686|gb|ES845400.1|ES845400	EIL		GO:0000160//GO:0001071//GO:0003676//GO:0006952//GO:0009725//GO:0009733//GO:0043231//GO:0071310	nr -
Unigene25026_A11	1435	1.49	4.63	3.19	4.44	4.25	5.00	2.15	0.79	2.55	1.63E+00	8.45E-11	Up	1.09E+00	2.41E-04	Up	-6.51E-02	8.32E-01		1.72E-01	5.00E-01		-1.45E+00	1.20E-05	Down	2.48E-01	3.99E-01		Unigene25026_A11//gi|297827475|ref|XP_002881620.1|//1.00E-131//yellow-leaf-specific gene 5 [Arabidopsis lyrata subsp. lyrata] >gi|297327459|gb|EFH57879.1|yellow-leaf-specific gene 5 [Arabidopsis lyrata subsp. lyrata]	Unigene25026_A11//2.00E-116//AT2G38860| YLS5	Unigene25026_A11//0.00E+00//gi|78344620|gb|DT564894.1|DT564894				nr +
Unigene25029_A11	1630	22.02	9.14	12.81	152.13	85.10	99.47	56.83	30.49	18.82	-1.27E+00	2.26E-38	Down	-7.82E-01	6.08E-17		-8.38E-01	7.25E-164		-6.13E-01	3.13E-83		-8.99E-01	1.38E-68		-1.59E+00	9.53E-174	Down	Unigene25029_A11//gi|145332667|ref|NP_001078199.1|//8.00E-16//structural constituent of cell wall [Arabidopsis thaliana]	Unigene25029_A11//1.00E-27//AT2G46630| unknown protein	Unigene25029_A11//0.00E+00//TC133129		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene25035_A11	1753	20.36	8.44	11.91	27.68	19.11	13.84	4.39	1.29	1.07	-1.27E+00	3.22E-38	Down	-7.74E-01	1.52E-16		-5.34E-01	1.14E-14		-1.00E+00	2.92E-38	Down	-1.77E+00	6.20E-17	Down	-2.04E+00	5.29E-21	Down	Unigene25035_A11//gi|145341413|ref|NP_193960.2|//1.00E-162//ubiquitin thiolesterase [Arabidopsis thaliana] >gi|30387541|gb|AAF31936.1|At4g22290 [Arabidopsis thaliana]	Unigene25035_A11//5.00E-133//AT4G22290| ubiquitin thiolesterase	Unigene25035_A11//0.00E+00//gi|78347501|gb|DT567775.1|DT567775				nr +
Unigene25038_A11	1555	7.77	7.53	8.84	19.51	15.41	9.15	7.37	4.68	2.25	-4.63E-02	7.88E-01			1.85E-01	2.83E-01		-3.40E-01	2.22E-04		-1.09E+00	8.64E-28	Down	-6.56E-01	1.11E-05		-1.71E+00	1.88E-24	Down	Unigene25038_A11//gi|124359981|gb|ABN07997.1|//2.00E-23//contains similarity to reverse transcriptase, related [Medicago truncatula]	Unigene25038_A11//7.00E-13//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene25038_A11//0.00E+00//gi|73849193|gb|DT458213.1|DT458213				nr -
Unigene25039_A11	1571	0.73	0.68	2.14	1.01	1.78	0.89	0.57	0.45	0.15	-1.13E-01	8.45E-01			1.54E+00	3.32E-05	Up	8.07E-01	3.00E-02		-1.87E-01	7.18E-01		-3.22E-01	6.33E-01		-1.89E+00	6.34E-03		Unigene25039_A11//gi|297725701|ref|NP_001175214.1|//4.00E-29//Os07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1|Os07g0501200 [Oryza sativa Japonica Group]	Unigene25039_A11//1.00E-14//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene25039_A11//0.00E+00//gi|73849193|gb|DT458213.1|DT458213				nr +
Unigene2504_A11	2352	26.76	25.14	26.65	26.81	27.77	24.00	29.41	12.07	11.52	-9.01E-02	2.30E-01		-6.10E-03	9.56E-01		5.08E-02	5.67E-01		-1.60E-01	2.20E-02		-1.29E+00	1.97E-91	Down	-1.35E+00	1.07E-101	Down	Unigene2504_A11//gi|145358557|ref|NP_198470.3|//0.00E+00//serine-type peptidase [Arabidopsis thaliana]	Unigene2504_A11//0.00E+00//AT5G36210| serine-type peptidase	Unigene2504_A11//0.00E+00//TC153599				nr -
Unigene25042_A11	1097	2.81	9.42	3.40	7.04	7.78	8.93	14.26	41.64	34.61	1.74E+00	5.57E-18	Up	2.72E-01	4.18E-01		1.45E-01	5.62E-01		3.44E-01	7.34E-02		1.55E+00	8.59E-80	Up	1.28E+00	3.45E-51	Up	Unigene25042_A11//gi|115475257|ref|NP_001061225.1|//2.00E-66//Os08g0203700 [Oryza sativa Japonica Group] >gi|113623194|dbj|BAF23139.1|Os08g0203700 [Oryza sativa Japonica Group]	Unigene25042_A11//3.00E-57//AT1G56145| leucine-rich repeat family protein / protein kinase family protein	Unigene25042_A11//0.00E+00//TC173885			GO:0004672//GO:0005488//GO:0031410	nr +
Unigene25043_A11	1119	5.10	3.17	2.71	12.46	15.14	9.89	32.87	5.27	11.36	-6.85E-01	5.77E-03		-9.10E-01	4.72E-04		2.81E-01	4.11E-02		-3.34E-01	3.04E-02		-2.64E+00	4.69E-129	Down	-1.53E+00	1.23E-65	Down	Unigene25043_A11//gi|28950901|gb|AA063374.1|//1.00E-63//At5g66230 [Arabidopsis thaliana]	Unigene25043_A11//1.00E-50//AT5G66230| unknown protein	Unigene25043_A11//0.00E+00//TC171290				nr +
Unigene25045_A11	1755	4.89	1.33	3.85	10.13	7.57	7.87	3.90	1.98	2.22	-1.88E+00	1.02E-16	Down	-3.44E-01	1.08E-01		-4.20E-01	6.64E-04		-3.64E-01	5.77E-03		-9.81E-01	1.28E-06		-8.11E-01	3.22E-05		Unigene25045_A11//gi|15221574|ref|NP_174383.1|//1.00E-145//GTP-binding protein (ERG) [Arabidopsis thaliana] >gi|11467944|sp|O82653.2|ERG_ARATH RecName: Full=GTP-binding protein ERG >gi|9755380|gb|AAF98187.1|AC000107_10 F17F8.15 [Arabidopsis thaliana] >gi|50253492|gb|AAT71948.1|At1g30960 [Arabidopsis thaliana] >gi|53850539|gb|AAU95446.1|At1g30960 [Arabidopsis thaliana]	Unigene25045_A11//4.00E-129//AT1G30960| GTP-binding protein (ERG)	Unigene25045_A11//0.00E+00//gi|78354114|gb|DT574388.1|DT574388			GO:0000166//GO:0003676//GO:0043231	nr +
Unigene25047_A11	1371	3.55	14.82	12.78	27.65	17.21	27.70	25.57	11.07	9.94	2.06E+00	2.72E-43	Up	1.85E+00	1.69E-31	Up	-6.85E-01	8.01E-18		2.80E-03	9.76E-01		-1.21E+00	1.88E-42	Down	-1.36E+00	1.41E-52	Down	Unigene25047_A11//gi|15234751|ref|NP_194776.1|//1.00E-117//cinnamoyl-CoA reductase-related [Arabidopsis thaliana] >gi|7269948|emb|CAB79765.1|cinnamoyl-CoA reductase-like protein [Arabidopsis thaliana] >gi|14596197|gb|AAK68826.1|cinnamoyl-CoA reductase-like protein [Arabidopsis thaliana] >gi|24899703|gb|AAN65066.1|cinnamoyl-CoA reductase-like protein [Arabidopsis thaliana]	Unigene25047_A11//5.00E-114//AT4G30470| cinnamoyl-CoA reductase-related	Unigene25047_A11//0.00E+00//CO080804		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis	GO:0008152//GO:0016491	nr +

Unigene25048_All	992	0.58	1.48	1.72	2.36	1.87	1.41	0.47	1.14	5.22	1.35E+00	1.72E-02		1.57E+00	4.57E-03		-3.32E-01	4.57E-01		-7.42E-01	7.76E-02		1.28E+00	2.97E-02		3.48E+00	1.03E-24	Up	Unigene25048_All//gi|34850945|dbj|BAC87845.1|//2.00E-63//leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	Unigene25048_All//3.00E-52//AT1G35710| leucine-rich repeat transmembrane protein kinase, putative	Unigene25048_All//0.00E+00//DR458690		ko03410|Base excision repair	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene25053_All	1869	2.88	1.92	0.80	3.15	3.19	2.22	4.23	1.81	2.92	-5.83E-01	2.34E-02		-1.85E+00	4.65E-10	Down	1.93E-02	9.48E-01		-5.01E-01	4.32E-02		-1.22E+00	2.18E-10	Down	-5.35E-01	2.77E-03		Unigene25053_All//gi|28416671|gb|AA042866.1|//1.00E-126//At5g41980 [Arabidopsis thaliana]	Unigene25053_All//7.00E-128//AT5G41980| unknown protein	Unigene25053_All//0.00E+00//TC176609				nr -
Unigene25054_All	781	7.57	31.40	9.95	12.82	17.15	16.31	6.93	13.16	8.47	2.05E+00	8.06E-52	Up	3.95E-01	7.76E-02		4.20E-01	4.84E-03		3.47E-01	3.34E-02		9.26E-01	1.02E-08		2.89E-01	1.65E-01		Unigene25054_All//gi|225450271|ref|XP_002267230.1|//1.00E-44//PREDICTED: similar to Os03g0374500 [Vitis vinifera]	Unigene25054_All//7.00E-18//AT1G55310| SR33; RNA binding / protein binding	Unigene25054_All//0.00E+00//TC135803		ko03040|Spliceosome	GO:0000377//GO:0003676//GO:0016020//GO:0016604	nr -
Unigene25055_All	1117	0.75	2.86	2.43	2.14	2.03	2.39	1.82	2.99	4.14	1.93E+00	7.71E-07	Up	1.70E+00	7.11E-05	Up	-7.32E-02	8.55E-01		1.56E-01	7.01E-01		7.20E-01	1.72E-02		1.19E+00	2.56E-06	Up	Unigene25055_All//gi|225450271|ref|XP_002267230.1|//3.00E-44//PREDICTED: similar to Os03g0374500 [Vitis vinifera]	Unigene25055_All//1.00E-17//AT1G55310| SR33; RNA binding / protein binding	Unigene25055_All//0.00E+00//TC135803		ko03040|Spliceosome	GO:0000377//GO:0003676//GO:0016020//GO:0016604	nr +
Unigene25056_All	1366	12.33	24.82	14.42	19.15	19.16	32.20	28.04	44.76	73.73	1.01E+00	3.24E-25	Up	2.26E-01	9.97E-02		1.00E-03	9.98E-01		7.50E-01	2.64E-21		6.75E-01	4.74E-28		1.39E+00	2.27E-153	Up	Unigene25056_All//gi|18417680|ref|NP_568315.1|//1.00E-40//MUB2 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 2) [Arabidopsis thaliana] >gi|30685362|ref|NP_850824.1| MUB2 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 2) [Arabidopsis thaliana] >gi|75155277|sp|Q8LCS8.1|MUB2_ARATH RecName: Full=Membrane-anchored ubiquitin-fold protein 2; Short=Membrane-anchored ub-fold protein 2; Short=AtMUB2; AltName: Full=NTGP5 >gi|21554321|gb|AAM63426.1| NTGP5 [Arabidopsis thaliana]	Unigene25056_All//5.00E-36//AT5G15460| MUB2 (MEMBRANE-ANCHORED UBIQUITIN-FOLD PROTEIN 2)	Unigene25056_All//0.00E+00//TC165045			GO:0043412	nr +
Unigene25057_All	2416	3.01	1.20	0.68	5.53	4.26	5.25	12.39	3.72	4.40	-1.33E+00	5.65E-09	Down	-2.14E+00	5.13E-16	Down	-3.75E-01	1.19E-02		-7.30E-02	6.78E-01		-1.74E+00	4.87E-62	Down	-1.49E+00	1.60E-51	Down	Unigene25057_All//gi|297828702|ref|XP_002882233.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328073|gb|EFH58492.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene25057_All//0.00E+00//AT3G02490| pentatricopeptide (PPR) repeat-containing protein	Unigene25057_All//0.00E+00//TC159629				nr -
Unigene25059_All	1377	4.29	5.41	9.86	11.07	13.15	12.79	7.68	7.19	4.17	3.33E-01	1.32E-01		1.20E+00	3.33E-13	Up	2.49E-01	6.50E-02		2.09E-01	1.51E-01		-9.37E-02	6.44E-01		-8.82E-01	1.36E-08		Unigene25059_All//gi|297803996|ref|XP_002869882.1|//1.00E-141//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297315718|gb|EFH46141.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene25059_All//6.00E-142//AT4G21580| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene25059_All//0.00E+00//TC139299				nr +
Unigene25062_All	1927	4.89	2.31	2.90	6.00	6.79	16.50	9.39	8.81	8.06	-1.08E+00	2.18E-08	Down	-7.52E-01	1.09E-04		1.79E-01	3.07E-01		1.46E+00	8.06E-45	Up	-9.27E-02	5.17E-01		-2.20E-01	6.39E-02		Unigene25062_All//gi|42561755|ref|NP_172143.3|//0.00E+00//NOL1/NOP2/sun family protein [Arabidopsis thaliana] >gi|30102880|gb|AAP21258.1| At1g06560 [Arabidopsis thaliana]	Unigene25062_All//0.00E+00//AT1G06560| NOL1/NOP2/sun family protein	Unigene25062_All//0.00E+00//TC158832			GO:0003676//GO:0016741	nr +
Unigene25063_All	1400	9.08	17.01	13.05	22.24	37.71	33.23	59.25	32.99	243.58	9.05E-01	4.07E-15		5.23E-01	9.28E-05		7.62E-01	9.60E-29		5.79E-01	1.84E-14		-8.45E-01	1.75E-55		2.04E+00	0.00E+00	Up	Unigene25063_All//gi|297381026|gb|AD139634.1|//3.00E-37//plastid jasmonates ZIM-domain protein [Hevea brasiliensis]	Unigene25063_All//4.00E-31//AT1G19180| JAZ1 (JASMONATE-ZIM-DOMAIN PROTEIN 1); protein binding	Unigene25063_All//0.00E+00//gi|78326022|gb|DT546296.1|DT546296	Tify	ko04626|Plant-pathogen interaction	GO:0005488//GO:0006950//GO:0007275//GO:0009719	nr -
Unigene25064_All	2206	2.99	1.33	2.53	6.80	5.14	6.33	10.85	6.84	8.70	-1.17E+00	8.18E-07	Down	-2.38E-01	3.62E-01		-4.04E-01	3.24E-03		-1.04E-01	5.67E-01		-6.65E-01	3.08E-11		-3.18E-01	1.19E-03		Unigene25064_All//gi|2462134|emb|CAA73798.1|//1.00E-15//reverse transcriptase [Beta vulgaris subsp. vulgaris]		Unigene25064_All//4.00E-08//DN509345			GO:0003824//GO:0005488//GO:0006807//GO:0044237	nr -
Unigene25066_All	1907	2.94	9.88	6.67	15.96	20.15	17.36	10.97	5.33	8.25	1.75E+00	2.04E-32	Up	1.18E+00	3.48E-12	Up	3.36E-01	3.42E-05		1.21E-01	2.70E-01		-1.04E+00	1.94E-20	Down	-4.11E-01	8.34E-05		Unigene25066_All//gi|115474907|ref|NP_001061050.1|//1.00E-140//Os08g0161500 [Oryza sativa Japonica Group] >gi|113623019|dbj|BAF22964.1| Os08g0161500 [Oryza sativa Japonica Group]	Unigene25066_All//2.00E-125//AT1G32190| INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: plasma membrane; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 8 growth stages; CONTAINS InterPro DOMAIN/s: Alpha/beta hydrolase fold-1 (InterPro:IPR000073); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G24320.1); Has 8192 Blast hits to 4778 proteins in 522 species: Archae - 0; Bacteria - 690; Metazoa - 5331; Fungi - 155; Plants - 259; Viruses - 14; Other Eukaryotes - 1743 (source: NCBI BLink).	Unigene25066_All//0.00E+00//TC140313				nr -
Unigene2507_All	1857	16.82	4.67	9.58	4.40	2.36	2.82	10.63	20.41	9.10	-1.85E+00	8.25E-58	Down	-8.13E-01	8.60E-16		-9.02E-01	1.51E-06		-6.41E-01	1.29E-03		9.41E-01	9.48E-31		-2.25E-01	4.53E-02		Unigene2507_All//gi|297851852|ref|XP_002893807.1|//1.00E-149//allinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339649|gb|EFH70066.1| allinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2507_All//5.00E-135//AT1G34060| allinase family protein					nr +
Unigene25070_All	3140	0.68	1.16	0.56	1.27	1.01	4.63	14.39	12.65	15.71	7.66E-01	1.73E-02		-2.88E-01	5.45E-01		-3.31E-01	3.10E-01		1.87E+00	3.12E-29	Up	-1.87E-01	1.16E-02		1.26E-01	7.77E-02		Unigene25070_All//gi|18413351|ref|NP_567361.1|//0.00E+00//subtilase family protein [Arabidopsis thaliana]	Unigene25070_All//0.00E+00//AT4G10540| subtilase family protein	Unigene25070_All//0.00E+00//DN779650		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavone and flavonol biosynthesis	GO:0005576//GO:0005618//GO:0016787//GO:0019538	nr -
Unigene25071_All	2112	1.96	1.37	1.66	2.17	2.69	1.69	3.16	0.99	4.77	-5.17E-01	8.53E-02		-2.34E-01	4.73E-01		3.10E-01	2.52E-01		-3.61E-01	2.35E-01		-1.68E+00	8.84E-14	Down	5.93E-01	1.50E-04		Unigene25071_All//gi|224589671|gb|ACN59367.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene25071_All//7.00E-96//AT5G14210| leucine-rich repeat transmembrane protein kinase, putative	Unigene25071_All//0.00E+00//TC179227		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0007167//GO:0016628//GO:0032559//GO:0043231	nr -
Unigene25073_All	1703	13.30	29.34	19.20	27.00	53.10	32.83	3.33	2.38	3.16	1.14E+00	7.75E-45	Up	5.29E-01	4.28E-08		9.76E-01	2.37E-74		2.82E-01	4.81E-05		-4.83E-01	3.26E-02		-7.51E-02	7.50E-01		Unigene25073_All//gi|297810483|ref|XP_002873125.1|//4.00E-65//IQ-domain 12 [Arabidopsis lyrata subsp. lyrata] >gi|297318962|gb|EFH49384.1| IQ-domain 12 [Arabidopsis lyrata subsp. lyrata]	Unigene25073_All//8.00E-38//AT5G03960| IQD12 (IQ-domain 12); calmodulin binding	Unigene25073_All//0.00E+00//TC160733				nr +
Unigene25074_All	1900	1.82	3.63	1.93	0.94	2.39	0.88	40.61	126.05	54.08	9.97E-01	1.16E-05		8.95E-02	7.84E-01		1.34E+00	1.62E-06	Up	-1.02E-01	8.43E-01		1.63E+00	0.00E+00	Up	4.13E-01	3.90E-20		Unigene25074_All//gi|115461410|ref|NP_001054305.1|//2.00E-95//Os04g0683800 [Oryza sativa Japonica Group] >gi|32488702|emb|CAE03445.1| OSJNBa0088H09.3 [Oryza sativa (japonica cultivar-group)] >gi|113568876|dbj|BAF16219.1| Os04g0683800 [Oryza sativa Japonica Group]	Unigene25074_All//1.00E-91//AT5G12970| C2 domain-containing protein	Unigene25074_All//0.00E+00//gi|84170688|gb|DR459336.1|DR459336				nr +
Unigene25079_All	2490	0.97	0.61	1.54	5.50	6.94	8.00	22.12	8.61	9.39	-6.63E-01	1.06E-01		6.72E-01	4.05E-02		3.36E-01	1.07E-02		5.40E-01	7.30E-06		-1.36E+00	1.12E-79	Down	-1.24E+00	1.11E-70	Down	Unigene25079_All//gi|115466984|ref|NP_001057091.1|//1.00E-172//Os06g0205600 [Oryza sativa Japonica Group] >gi|51091457|dbj|BAD36198.1| mechanosensitive ion channel domain-containing protein-like [Oryza sativa Japonica Group] >gi|113595131|dbj|BAF19005.1| Os06g0205600 [Oryza sativa Japonica Group]	Unigene25079_All//1.00E-147//AT5G12080| MSL10 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 10); mechanically-gated ion channel	Unigene25079_All//0.00E+00//ES836909			GO:0004872//GO:0006810//GO:0006952//GO:0023060//GO:0044425	nr +
Unigene25081_All	1857	10.45	10.97	3.21	16.87	21.14	19.46	19.85	11.57	12.29	9.95E-02	6.12E-01		-1.70E+00	4.83E-31	Down	3.25E-01	5.30E-05		2.06E-01	2.85E-02		-7.79E-01	5.85E-22		-6.92E-01	1.57E-18		Unigene25081_All//gi|297813815|ref|XP_002874791.1|//0.00E+00//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320628|gb|EFH51050.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25081_All//0.00E+00//AT3G20290| ATEH1 (EPS15 HOMOLOGY DOMAIN 1); GTP binding / GTPase/ calcium ion binding	Unigene25081_All//0.00E+00//TC132036			GO:0016020//GO:0016192//GO:0017111//GO:0032561//GO:0042598//GO:0043231//GO:0046872	nr +
Unigene25083_All	1601	6.54	3.73	5.95	14.87	10.93	12.02	16.11	6.63	7.12	-8.08E-01	5.27E-06		-1.35E-01	5.09E-01		-4.45E-01	1.70E-05		-3.08E-01	6.50E-03		-1.28E+00	2.19E-34	Down	-1.18E+00	3.52E-31	Down	Unigene25083_All//gi|297843112|ref|XP_002889437.1|//1.00E-148//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335279|gb|EFH65696.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25083_All//7.00E-145//AT1G03110| transducin family protein / WD-40 repeat family protein	Unigene25083_All//0.00E+00//TC139087		ko03018|RNA degradation		nr +
Unigene25086_All	740	0.99	4.11	1.30	3.90	2.56	2.75	14.28	36.77	24.98	2.05E+00	5.01E-07	Up	3.88E-01	6.08E-01		-6.09E-01	8.82E-02		-5.08E-01	1.90E-01		1.36E+00	8.65E-40	Up	8.06E-01	2.22E-12		Unigene25086_All//gi|92897763|gb|AB93875.1|//5.00E-52//Leucine-rich repeat [Medicago truncatula]	Unigene25086_All//1.00E-23//AT1G74190| AtRLP15 (Receptor Like Protein 15); protein binding	Unigene25086_All//0.00E+00//TC175792		ko04626|Plant-pathogen interaction		nr +
Unigene25087_All	1445	0.22	1.02	0.41	2.41	1.69	1.63	3.07	5.78	19.74	2.23E+00	4.29E-04	Up	9.00E-01	3.77E-01		-5.12E-01	1.16E-01		-5.70E-01	9.03E-02		9.13E-01	4.37E-07		2.68E+00	1.62E-103	Up	Unigene25087_All//gi|14330716|emb|CAC40826.1|//3.00E-87//HcrVf2 protein [Malus floribunda]	Unigene25087_All//1.00E-48//AT1G74190| AtRLP15 (Receptor Like Protein 15); protein binding	Unigene25087_All//0.00E+00//TC175792				nr -
Unigene2509_All	376	1.95	0.00	0.85	0.79	1.74	2.64	1.35	1.78	1.38	-1.09E+01	2.11E-04	Down	-1.20E+00	1.80E-01		1.13E+00	2.38E-01		1.73E+00	2.14E-02		3.98E-01	6.48E-01		2.96E-02	9.70E-01		Unigene2509_All//gi|297596740|ref|NP_001042999.2|//4.00E-43//Os01g0355900 [Oryza sativa Japonica Group] >gi|255673216|dbj|BAF04913.2| Os01g0355900 [Oryza sativa Japonica Group]	Unigene2509_All//3.00E-44//AT3G06910| ULP1A (UB-LIKE PROTEASE 1A); SUMO-specific protease/ cysteine-type peptidase	Unigene2509_All//2.00E-172//gi|5044896|gb|AI726044.1|AI726044				nr -
Unigene25090_All	1133	45.44	95.39	125.06	70.92	71.33	109.82	272.23	46.15	68.95	1.07E+00	8.36E-87	Up	1.46E+00	2.77E-180	Up	8.40E-03	9.15E-01		6.31E-01	7.19E-44		-2.56E+00	0.00E+00	Down	-1.98E+00	0.00E+00	Down	Unigene25090_All//gi|74273629|gb|AB001482.1|//0.00E+00//gibberellin 20-oxidase 1 [Gossypium hirsutum]	Unigene25090_All//8.00E-165//AT3G51240| F3H (FLAVANONE 3-HYDROXYLASE); naringenin 3-dioxygenase	Unigene25090_All//0.00E+00//TC129624		ko00941|Flavonoid biosynthesis	GO:0003824//GO:0008152	nr -
Unigene25092_All	1577	8.00	4.88	3.75	35.63	23.34	21.62	13.32	11.32	11.47	-7.11E-01	7.76E-06		-1.09E+00	1.15E-10	Down	-6.10E-01	2.00E-21		-7.21E-01	1.76E-25		-2.36E-01	3.63E-02		-2.16E-01	4.73E-02		Unigene25092_All//gi|9802596|gb|AAF99798.1|AC012463_15//9.00E-92//T22E.19 [Arabidopsis thaliana]	Unigene25092_All//7.00E-96//AT1G47740| unknown protein	Unigene25092_All//0.00E+00//TC160413			GO:0043231	nr -
Unigene25093_All	834	5.52	4.01	3.13	9.44	7.18	10.23	6.13	2.91	2.63	-4.61E-01	1.06E-01		-8.19E-01	5.24E-03		-3.94E-01	5.48E-02		1.17E-01	6.09E-01		-1.08E+00	7.29E-06	Down	-1.22E+00	2.95E-07	Down	Unigene25093_All//gi|18404735|ref|NP_566786.1|//9.00E-27//transcription factor S-II (TFIIS) domain-containing protein [Arabidopsis thaliana] >gi|88011125|gb|ABD38906.1| At3g25940 [Arabidopsis thaliana]	Unigene25093_All//5.00E-28//AT3G25940| transcription factor S-II (TFIIS) domain-containing protein	Unigene25093_All//0.00E+00//TC165726		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003676//GO:0006351	nr +
Unigene25094_All	817	18.51	8.50	23.40	23.29	22.38	33.61	18.79	23.53	57.59	-1.12E+00	8.19E-14	Down	3.38E-01	1.15E-02		-5.75E-02	7.28E-01		5.29E-01	1.44E-07		3.25E-01	4.46E-03		1.62E+00	2.09E-89	Up	Unigene25094_All//gi|183584854|gb|ACC63895.1|//1.00E-67//MAP kinase [Gossypium raimondii]	Unigene25094_All//4.00E-66//AT1G53510| ATMPK18; MAP kinase	Unigene25094_All//0.00E+00//gi|78326246|gb|DT546520.1|DT546520		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0032559	nr +

Unigene25095_All	497	13.48	6.22	15.32	5.01	3.88	4.73	1.96	1.09	1.04	-1.12E+00	1.70E-06	Down	1.85E-01	4.24E-01		-3.69E-01	3.82E-01		-8.48E-02	8.47E-01		-8.40E-01	1.87E-01		-9.09E-01	1.31E-01		Unigene25095_All//gi|4732123|gb|AAD28617.1|AF129087_1//5.00E-43//mitogen-activated protein kinase homologue [Medicago sativa]	Unigene25095_All//3.00E-42//AT3G14720| ATMPK19; MAP kinase	Unigene25095_All//2.00E-161//TC177502		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0032559	nr +
Unigene25096_All	1251	2.80	4.46	1.62	3.54	6.47	14.22	122.31	254.75	347.31	6.69E-01	7.94E-03		-7.93E-01	2.15E-02		8.68E-01	7.24E-06		2.00E+00	3.75E-39	Up	1.06E+00	0.00E+00	Up	1.51E+00	0.00E+00	Up	Unigene25096_All//gi|4581119|gb|AAD24609.1|//1.00E-108//expressed protein [Arabidopsis thaliana]	Unigene25096_All//3.00E-104//AT2G16760| FUNCTIONS IN: molecular_function unknown; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Six-bladed beta-propeller, TolB-like (InterPro:IPR011042); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G47370.1); Has 78 Blast hits to 78 proteins in 24 species: Archae - 0; Bacteria - 32; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene25096_All//0.00E+00//TC160460				nr +
Unigene25100_All	1238	18.38	14.28	9.98	11.35	9.62	12.08	4.17	2.33	2.03	-3.64E-01	1.62E-03		-8.82E-01	2.54E-13		-2.38E-01	1.31E-01		8.97E-02	6.38E-01		-8.39E-01	3.57E-04		-1.04E+00	7.86E-06	Down	Unigene25100_All//gi|17065156|gb|AAL32732.1|//1.00E-109//Unknown protein [Arabidopsis thaliana] >gi|27311937|gb|AA000934.1| Unknown protein [Arabidopsis thaliana]	Unigene25100_All//2.00E-103//AT3G21200| unknown protein	Unigene25100_All//0.00E+00//TC147279		GO:0043231	nr +
Unigene25101_All	2497	19.42	28.10	32.48	10.71	16.19	20.80	20.86	21.11	52.17	5.33E-01	1.83E-17		7.42E-01	2.19E-34		5.96E-01	1.69E-14		9.57E-01	1.21E-37		1.69E-02	8.36E-01		1.32E+00	8.37E-183	Up	Unigene25101_All//gi|2501491|sp|Q40284.1|UFOG1_MANES//4.00E-94//RecName: Full=Anthocyanidin 3-O-glucosyltransferase 1; AltName: Full=Flavonol 3-O-glucosyltransferase 1; AltName: Full=UDP-glucose flavonoid 3-O-glucosyltransferase 1 >gi|453246|emb|CAA54609.1| UTP-glucose glucosyltransferase [Manihot esculenta]	Unigene25101_All//1.00E-88//AT2G29730| UGT71D1 (UDP-GLUCOSYL TRANSFERASE 71D1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene25101_All//0.00E+00//TC142661		GO:0000166//GO:0006350//GO:0016757	nr -
Unigene25102_All	2152	18.09	24.44	18.26	9.47	16.75	20.61	8.37	3.26	3.00	4.34E-01	2.22E-09		1.37E-02	8.98E-01		8.23E-01	1.71E-22		1.12E+00	1.25E-41	Up	-1.36E+00	1.67E-26	Down	-1.48E+00	5.57E-31	Down	Unigene25102_All//gi|30697152|ref|NP_851217.1|//0.00E+00//GIL1 (GRAVITROPIC IN THE LIGHT) [Arabidopsis thaliana]	Unigene25102_All//2.00E-142//AT5G58960| GIL1 (GRAVITROPIC IN THE LIGHT)	Unigene25102_All//0.00E+00//TC146888		GO:0009416//GO:0009630	nr +
Unigene25106_All	2198	4.74	2.07	3.88	7.28	6.42	5.47	7.00	9.20	2.25	-1.19E+00	1.24E-10	Down	-2.89E-01	1.40E-01		-1.80E-01	2.40E-01		-4.13E-01	2.89E-03		3.94E-01	3.18E-04		-1.61E+00	9.75E-31	Down	Unigene25106_All//gi|9294580|dbj|BAB02861.1|//0.00E+00//receptor-like protein kinase-like protein [Arabidopsis thaliana] >gi|224589583|gb|ACN59325.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene25106_All//0.00E+00//AT3G28450| leucine-rich repeat transmembrane protein kinase, putative	Unigene25106_All//0.00E+00//gi|161275576|gb|ES805887.1|ES805887		GO:0004871//GO:0006464//GO:0007167//GO:0009536//GO:0016301//GO:0031224//GO:0032559	nr -
Unigene25107_All	1009	5.96	16.12	12.61	33.87	47.06	78.91	29.75	36.20	41.58	1.43E+00	3.30E-21	Up	1.08E+00	1.33E-10	Up	4.75E-01	2.11E-11		1.22E+00	6.21E-85	Up	2.83E-01	4.09E-04		4.83E-01	2.26E-11		Unigene25107_All//gi|151549227|gb|ABS12731.1|//1.00E-92//metal tolerance protein [Cucumis sativus]	Unigene25107_All//2.00E-70//AT2G46800| ZAT (ZINC TRANSPORTER OF ARABIDOPSIS THALIANA); inorganic anion transmembrane transporter/ metal ion transmembrane transporter/ zinc ion transmembrane transporter	Unigene25107_All//1.00E-108//TC169982		GO:0000041//GO:0008509//GO:0010035//GO:0015082//GO:0016491//GO:0030005//GO:0031090//GO:0043231	nr +
Unigene25108_All	1872	4.98	2.35	2.19	6.68	7.28	5.36	11.23	2.08	4.06	-1.08E+00	2.63E-08	Down	-1.18E+00	4.75E-09	Down	1.25E-01	5.09E-01		-3.19E-01	5.53E-02		-2.43E+00	2.03E-67	Down	-1.47E+00	1.83E-35	Down	Unigene25108_All//gi|297814157|ref|XP_002874962.1|//1.00E-176//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320799|gb|EFH51221.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25108_All//8.00E-123//AT4G01730| zinc ion binding	Unigene25108_All//0.00E+00//D#502328		GO:0008152//GO:0016628//GO:0046914	nr +
Unigene2511_All	1561	52.52	114.00	36.13	26.58	38.96	59.63	2.28	7.10	2.37	1.12E+00	4.83E-153	Up	-5.40E-01	5.76E-20		5.51E-01	7.17E-19		1.17E+00	2.66E-92	Up	1.64E+00	1.20E-21	Up	6.10E-02	8.41E-01		Unigene2511_All//gi|18412129|ref|NP_565191.1|//1.00E-166//curculin-like (mannose-binding) lectin family protein [Arabidopsis thaliana] >gi|16226591|gb|AAL16208.1|AF428439_1 At1g78830/F9K20_12 [Arabidopsis thaliana] >gi|3834312|gb|AAC83028.1| Strong similarity to glycoprotein EP1 gb|L16983 Daucus carota and a member of S locus glycoprotein family PF|00954. ESTs gb|AA067487, gb|Z35737, gb|Z30815, gb|Z33550, gb|AA713171, gb|AI100553, gb|Z34248, gb|AA728536, gb|Z30816 and gb|Z35351 come from this gene [Arabidopsis thaliana]	Unigene2511_All//7.00E-160//AT1G78830| curculin-like (mannose-binding) lectin family protein	Unigene2511_All//0.00E+00//TC139408			nr +
Unigene25116_All	1196	5.82	7.24	6.10	2.87	2.62	5.97	8.70	11.85	13.76	3.16E-01	1.20E-01		6.81E-02	7.71E-01		-1.33E-01	7.32E-01		1.05E+00	1.48E-06	Up	4.46E-01	8.18E-04		6.62E-01	3.85E-08		Unigene25116_All//gi|30678415|ref|NP_849580.1|//1.00E-104//TPK1 (THIAMIN PYROPHOSPHOKINASE1); thiamin diphosphokinase [Arabidopsis thaliana] >gi|222424006|dbj|BAH19964.1| AT1G02880 [Arabidopsis thaliana]	Unigene25116_All//1.00E-102//AT1G02880| TPK1 (THIAMIN PYROPHOSPHOKINASE1); thiamin diphosphokinase	Unigene25116_All//0.00E+00//TC140607		ko00730|Thiamine metabolism	GO:0003690//GO:0006260//GO:0006281//GO:0009108//GO:0016462//GO:0016778//GO:0032559//GO:0034061//GO:0042723//GO:0043231//GO:0044444	nr +
Unigene25117_All	1333	58.88	22.12	39.43	54.04	42.62	34.12	3.24	1.91	1.40	-1.41E+00	6.50E-98	Down	-5.78E-01	1.35E-21		-3.42E-01	1.09E-09		-6.63E-01	3.60E-28		-7.58E-01	3.52E-03		-1.20E+00	4.05E-06	Down	Unigene25117_All//gi|297810811|ref|XP_002873289.1|//3.00E-77//sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319126|gb|EFH49548.1| sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25117_All//4.00E-76//AT1G74100| SOT16 (SULFOTRANSFERASE 16); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene25117_All//0.00E+00//TC175298		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism	GO:0008146	nr -
Unigene2512_All	1741	11.18	30.70	17.07	7.07	10.17	10.14	21.52	15.60	15.35	1.46E+00	9.09E-70	Up	6.10E-01	2.19E-09		5.25E-01	2.18E-05		5.21E-01	5.39E-05		-4.64E-01	2.60E-09		-4.87E-01	1.97E-10		Unigene2512_All//gi|297823847|ref|XP_002879806.1|//1.00E-150//ACT domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325645|gb|EFH56065.1| ACT domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2512_All//4.00E-149//AT2G39570| ACT domain-containing protein	Unigene2512_All//0.00E+00//TC168618			nr -
Unigene25124_All	1960	1.95	0.67	0.73	2.64	2.16	3.27	3.43	3.50	3.23	-1.54E+00	4.19E-06	Down	-1.41E+00	3.57E-05	Down	-2.91E-01	3.06E-01		3.08E-01	2.27E-01		2.80E-02	9.15E-01		-8.58E-02	6.84E-01		Unigene25124_All//gi|15235498|ref|NP_192184.1|//1.00E-113//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75213324|sp|Q9SY02.1|PP301_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g02750	Unigene25124_All//5.00E-111//AT4G02750| pentatricopeptide (PPR) repeat-containing protein	Unigene25124_All//0.00E+00//D#463308			nr -
Unigene25125_All	1626	15.22	10.88	6.03	57.23	57.52	28.41	29.38	10.46	9.58	-4.85E-01	8.97E-06		-1.34E+00	9.29E-28	Down	7.30E-03	9.23E-01		-1.01E+00	4.15E-74	Down	-1.49E+00	3.61E-79	Down	-1.62E+00	8.40E-92	Down	Unigene25125_All//gi|15230555|ref|NP_190735.1|//1.00E-177//SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|75202761|sp|Q9SCU1.1|PATL6_ARATH RecName: Full=Patellin-6 >gi|16930483|gb|AAL31927.1|AF419595_1 AT3g51670/T18N14_50 [Arabidopsis thaliana] >gi|25141223|gb|AAN73306.1| At3g51670/T18N14_50 [Arabidopsis thaliana]	Unigene25125_All//2.00E-161//AT3G51670| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene25125_All//0.00E+00//TC139830			nr -
Unigene25126_All	2669	6.06	8.45	1.58	0.67	0.28	2.35	11.31	4.13	1.27	4.80E-01	3.04E-05		-1.94E+00	5.70E-31	Down	-1.24E+00	7.41E-03		1.81E+00	2.33E-12	Up	-1.45E+00	1.95E-48	Down	-3.16E+00	1.48E-131	Down	Unigene25126_All//gi|195976673|dbj|BAG68575.1|//0.00E+00//arginine decarboxylase [Prunus persica]	Unigene25126_All//0.00E+00//AT4G34710| ADC2 (ARGININE DECARBOXYLASE 2); arginine decarboxylase	Unigene25126_All//0.00E+00//TC161329		ko00330|Arginine and proline metabolism//ko00300|Lysine biosynthesis	GO:0006525//GO:0006596//GO:0006970//GO:0009725//GO:0009791//GO:0016831	nr -
Unigene25129_All	1253	1.50	2.10	4.84	1.95	0.30	0.83	113.34	87.56	100.82	4.84E-01	2.19E-01		1.69E+00	5.26E-10	Up	-2.69E+00	2.28E-09	Down	-1.23E+00	2.60E-03		-3.72E-01	3.09E-22		-1.69E-01	9.25E-06		Unigene25129_All//gi|68271836|gb|AA989231.1|//1.00E-177//hexose transporter 1 [Juglans regia]	Unigene25129_All//7.00E-149//AT1G11260| STP1 (SUGAR TRANSPORTER 1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene25129_All//0.00E+00//TC141152			nr -
Unigene2513_All	1727	94.07	214.44	61.42	100.81	106.72	81.93	282.67	464.81	541.25	1.19E+00	0.00E+00	Up	-6.15E-01	3.20E-49		8.21E-02	4.03E-02		-2.99E-01	6.14E-16		7.18E-01	0.00E+00		9.37E-01	0.00E+00		Unigene2513_All//gi|82469976|gb|AB877236.1|//1.00E-167//patellin 1 [Cucurbita pepo]	Unigene2513_All//2.00E-120//AT1G72160| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene2513_All//0.00E+00//TC168329			nr +
Unigene25130_All	1913	10.94	6.52	8.24	5.49	3.53	2.38	4.13	2.77	1.75	-7.48E-01	6.83E-10		-4.09E-01	1.09E-03		-6.39E-01	8.59E-05		-1.20E+00	1.34E-11	Down	-5.75E-01	1.79E-03		-1.24E+00	5.92E-11	Down	Unigene25130_All//gi|42565106|ref|NP_188849.3|//1.00E-146//phototropic-responsive NPH3 protein-related [Arabidopsis thaliana]	Unigene25130_All//5.00E-137//AT3G22104| phototropic-responsive NPH3 protein-related	Unigene25130_All//0.00E+00//TC163220			GO:0005488//GO:0009314//GO:0060089	nr +

Unigene25132_A11	1368	14.61	39.56	22.34	28.62	34.41	20.40	10.17	27.47	27.29	1.44E+00	3.82E-69	Up	6.13E-01	1.06E-09		2.66E-01	3.26E-04		-4.88E-01	3.15E-09		1.43E+00	7.29E-59	Up	1.42E+00	3.61E-59	Up	Unigene25132_A11//gi|15235712|ref|NP_195493.1|//7.00E-56//HAT22; transcription factor [Arabidopsis thaliana] >gi|1170409|sp|P46604.1|HAT22_ARATH RecName: Full=Homeobox-leucine zipper protein HAT22; AltName: Full=Homeodomain-leucine zipper protein HAT22; Short=HD-ZIP protein 22 >gi|549887|gb|AAA56902.1| homeobox protein [Arabidopsis thaliana] >gi|549888|gb|AAA56903.1| homeobox protein [Arabidopsis thaliana] >gi|4490724|emb|CAB38927.1| homeobox protein HAT22 [Arabidopsis thaliana] >gi|7270762|emb|CAB80444.1| homeobox protein HAT22 [Arabidopsis thaliana] >gi|20145867|emb|CAD29653.1| homeodomain-leucine zipper protein HAT22 [Arabidopsis thaliana] >gi|21593156|gb|AAM65105.1| homeobox protein HAT22 [Arabidopsis thaliana]	Unigene25132_A11//2.00E-40//AT4G37790| HAT22; transcription factor	Unigene25132_A11//0.00E+00//gi|48793824|gb|CO095138.1|CO095138	HB		GO:0006350//GO:0009725	nr -
Unigene25133_A11	1716	23.66	18.90	18.93	15.33	16.15	19.37	29.12	14.01	12.49	-3.24E-01	1.13E-04		-3.22E-01	2.24E-04		7.58E-02	5.60E-01		3.38E-01	2.49E-04		-1.06E+00	1.19E-48	Down	-1.22E+00	5.32E-63	Down	Unigene25133_A11//gi|297851884|ref|XP_002893023.1|//0.00E+00//EMB3003 [Arabidopsis lyrata subsp. lyrata] >gi|297339665|gb|EFH70082.1| EMB3003 [Arabidopsis lyrata subsp. lyrata]	Unigene25133_A11//8.00E-175//AT1G34430| EMB3003 (embryo defective 3003); acyltransferase/ dihydrolipoyllysine-residue acetyltransferase/ protein binding	Unigene25133_A11//0.00E+00//TC133463		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)	GO:0003006//GO:0005488//GO:0005840//GO:0009526//GO:0016020//GO:0016747	nr +
Unigene25137_A11	1207	5.38	37.87	15.13	28.56	47.70	73.68	90.06	126.56	163.02	2.82E+00	1.95E-139	Up	1.49E+00	2.44E-24	Up	7.40E-01	8.14E-30		1.37E+00	5.61E-113	Up	4.91E-01	3.26E-39		8.56E-01	2.43E-136		Unigene25137_A11//gi|15234749|ref|NP_194775.1|//8.00E-39//glycine-rich protein [Arabidopsis thaliana] >gi|7269947|emb|CAB79764.1| glycine-rich protein [Arabidopsis thaliana]		Unigene25137_A11//0.00E+00//gi|109888857|gb|DW517826.1|DW517826				nr +
Unigene2514_A11	1758	7.26	6.08	6.97	6.80	9.64	10.64	10.22	21.97	19.08	-2.56E-01	1.22E-01		-5.99E-02	7.31E-01		5.03E-01	7.56E-05		6.45E-01	2.28E-07		1.10E+00	1.82E-40	Up	9.01E-01	4.84E-26		Unigene2514_A11//gi|223452446|gb|ACM89550.1|//1.00E-176//protein kinase [Glycine max]	Unigene2514_A11//3.00E-159//AT2G28940| protein kinase family protein	Unigene2514_A11//0.00E+00//gi|78353760|gb|DT574034.1|DT574034				nr +
Unigene25140_A11	1021	34.18	28.44	24.04	54.60	87.79	66.84	42.45	90.31	47.72	-2.65E-01	4.15E-03		-5.08E-01	5.29E-08		6.85E-01	1.62E-40		2.92E-01	2.37E-06		1.09E+00	1.67E-93	Up	1.69E-01	1.47E-02		Unigene25140_A11//gi|224063557|ref|XP_002301203.1|//3.00E-82//nbs-lrr resistance protein [Populus trichocarpa] >gi|222842929|gb|EEE80476.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene25140_A11//9.00E-75//AT4G33300| ADR1-L1 (ADR1-like 1); ATP binding / protein binding	Unigene25140_A11//0.00E+00//TC154725		ko04626|Plant-pathogen interaction	GO:0005576//GO:0006950//GO:0012501//GO:0016462//GO:0032559	nr +
Unigene25141_A11	2327	1.10	2.92	3.39	1.97	1.05	1.16	8.23	8.35	5.36	1.41E+00	5.03E-09	Up	1.62E+00	4.07E-12	Up	-9.06E-01	5.54E-04		-7.58E-01	6.56E-03		2.11E-02	8.83E-01		-6.19E-01	1.97E-08		Unigene25141_A11//gi|79507164|ref|NP_196165.3|//0.00E+00//hydrolase, acting on glycosyl bonds / mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase [Arabidopsis thaliana]	Unigene25141_A11//0.00E+00//AT5G05460| hydrolase, acting on glycosyl bonds / mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase	Unigene25141_A11//0.00E+00//CO097949			GO:0016798	nr +
Unigene25142_A11	1453	19.01	149.64	21.66	59.28	210.00	135.33	215.74	505.69	373.98	2.98E+00	0.00E+00	Up	1.88E-01	8.00E-02		1.82E+00	0.00E+00	Up	1.19E+00	1.88E-201	Up	1.23E+00	0.00E+00	Up	7.94E-01	0.00E+00		Unigene25142_A11//gi|240248438|gb|ACS45396.1|//1.00E-145//myo-inositol oxygenase [Solanum lycopersicum]	Unigene25142_A11//5.00E-144//AT2G19800| MIOX2 (MYO-INOSITOL OXYGENASE 2); inositol oxygenase	Unigene25142_A11//0.00E+00//TC136393		ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene25143_A11	2218	20.73	8.45	7.66	24.88	19.90	21.26	38.20	16.04	17.37	-1.29E+00	1.59E-50	Down	-1.44E+00	4.26E-57	Down	-3.22E-01	8.43E-07		-2.27E-01	1.48E-03		-1.25E+00	2.07E-107	Down	-1.14E+00	7.26E-95	Down	Unigene25143_A11//gi|6626184|gb|AAF19528.1|AF215731_1|//0.00E+00//Ran GTPase activating protein [Medicago sativa subsp. x varia]	Unigene25143_A11//0.00E+00//AT3G63130| RANGAP1 (RAN GTPASE ACTIVATING PROTEIN 1); RAN GTPase activator/ protein binding	Unigene25143_A11//0.00E+00//TC174264			GO:0005488//GO:0006605//GO:0007017//GO:0009536//GO:0012505//GO:0016020//GO:0051301	nr +
Unigene25144_A11	2363	16.83	12.35	18.41	58.37	37.26	30.89	11.33	5.52	4.67	-4.46E-01	1.22E-07		1.30E-01	1.59E-01		-6.48E-01	5.72E-58		-9.18E-01	1.38E-93		-1.04E+00	1.11E-25	Down	-1.28E+00	1.30E-36	Down	Unigene25144_A11//gi|159025697|emb|CAN88849.1|//1.00E-115//D1-type cyclin [Populus trichocarpa]	Unigene25144_A11//3.00E-83//AT1G70210| CYCD1;1 (CYCLIN D1;1); cyclin-dependent protein kinase regulator	Unigene25144_A11//0.00E+00//TC150256			GO:0005488//GO:0007049	nr +
Unigene25145_A11	403	70.11	30.68	26.43	94.93	110.65	148.60	276.87	159.72	159.65	-1.19E+00	1.36E-27	Down	-1.41E+00	3.66E-34	Down	2.21E-01	4.91E-03		6.47E-01	2.57E-22		-7.94E-01	7.26E-67		-7.94E-01	8.45E-69		Unigene25145_A11//gi|297837293|ref|XP_002886528.1|//2.00E-72//ARP2/RPL3B [Arabidopsis lyrata subsp. lyrata] >gi|297332369|gb|EFH62787.1| ARP2/RPL3B [Arabidopsis lyrata subsp. lyrata]	Unigene25145_A11//1.00E-72//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene25145_A11//0.00E+00//gi|164273459|gb|ES822007.1|ES822007		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0019219//GO:0030312//GO:0031981	nr -
Unigene25146_A11	353	60.03	25.12	33.64	92.15	81.26	134.85	235.72	103.13	117.48	-1.26E+00	1.26E-22	Down	-8.36E-01	2.03E-11		-1.81E-01	6.52E-02		5.49E-01	1.72E-13		-1.19E+00	1.01E-97	Down	-1.00E+00	2.94E-76	Down	Unigene25146_A11//gi|297837293|ref|XP_002886528.1|//7.00E-63//ARP2/RPL3B [Arabidopsis lyrata subsp. lyrata] >gi|297332369|gb|EFH62787.1| ARP2/RPL3B [Arabidopsis lyrata subsp. lyrata]	Unigene25146_A11//3.00E-64//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene25146_A11//0.00E+00//TC135584		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934	nr -
Unigene25147_A11	533	48.39	18.92	15.19	89.72	83.92	110.15	229.96	97.08	92.23	-1.36E+00	1.13E-30	Down	-1.67E+00	4.41E-40	Down	-9.64E-02	2.84E-01		2.96E-01	1.08E-05		-1.24E+00	1.59E-153	Down	-1.32E+00	1.18E-172	Down	Unigene25147_A11//gi|5762260|dbj|BAA83471.1|//3.00E-95//CsF-3 [Cucumis sativus]	Unigene25147_A11//1.00E-91//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene25147_A11//0.00E+00//TC132278		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene25148_A11	317	20.47	17.10	12.93	27.66	32.59	35.05	161.38	78.58	60.45	-2.59E-01	2.90E-01		-6.62E-01	5.99E-03		2.37E-01	2.26E-01		3.42E-01	5.45E-02		-1.04E+00	1.99E-48	Down	-1.42E+00	6.57E-81	Down	Unigene25148_A11//gi|38327504|gb|AR17783.1|//3.00E-12//ribosomal protein L3 [Solanum lycopersicum]	Unigene25148_A11//2.00E-08//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene25148_A11//6.00E-154//TC135599		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene2515_A11	1404	2.53	3.50	1.90	5.85	4.12	2.86	4.37	2.92	2.18	4.66E-01	8.95E-02		-4.18E-01	2.39E-01		-5.07E-01	8.46E-03		-1.03E+00	2.56E-07	Down	-5.82E-01	6.30E-03		-9.99E-01	2.15E-06					Unigene2515_A11//0.00E+00//TC173793				
Unigene25150_A11	377	44.41	25.54	23.31	77.83	81.66	84.34	310.43	117.41	182.71	-7.98E-01	5.95E-09		-9.30E-01	7.48E-11		6.93E-02	5.79E-01		1.16E-01	3.12E-01		-1.40E+00	2.41E-176	Down	-7.65E-01	1.37E-67		Unigene25150_A11//gi|242129046|gb|ACS83602.1|//8.00E-40//ATP synthase beta subunit 1 [Gossypium hirsutum]	Unigene25150_A11//5.00E-38//AT5G08690| ATP synthase beta chain 2, mitochondrial	Unigene25150_A11//9.00E-135//ES806872		ko00190|Oxidative phosphorylation	GO:0000275//GO:0015078//GO:0015662//GO:0015986//GO:0019829//GO:0032559	nr +
Unigene25151_A11	1163	7.87	7.76	6.91	19.36	18.12	14.72	19.70	9.78	16.65	-2.17E-02	9.28E-01		-1.87E-01	4.02E-01		-9.55E-02	5.06E-01		-3.96E-01	5.02E-04		-1.01E+00	3.08E-21	Down	-2.43E-01	1.76E-02		Unigene25151_A11//gi|115439241|ref|NP_001043900.1|//1.00E-96//Os01g0685800 [Oryza sativa Japonica Group] >gi|113533431|dbj|BAF05814.1| Os01g0685800 [Oryza sativa Japonica Group]	Unigene25151_A11//3.00E-77//AT5G08680| ATP synthase beta chain, mitochondrial, putative	Unigene25151_A11//0.00E+00//gi|78325771|gb|DT546045.1|DT546045		ko00190|Oxidative phosphorylation	GO:0000275//GO:0015078//GO:0015662//GO:0015986//GO:0019829//GO:0032559	nr -
Unigene25153_A11	860	54.02	26.04	24.40	49.24	35.36	22.21	6.34	6.61	1.76	-1.05E+00	7.00E-37	Down	-1.15E+00	9.28E-41	Down	-4.78E-01	1.44E-10		-1.15E+00	9.06E-42	Down	5.96E-02	8.14E-01		-1.85E+00	2.21E-13	Down	Unigene25153_A11//gi|124359981|gb|ABW07997.1|//8.00E-10//contains similarity to reverse trancriptase, related [Medicago truncatula]	Unigene25153_A11//3.00E-09//AT3G09510| nucleic acid binding	Unigene25153_A11//6.00E-110//TC144919				nr -
Unigene25154_A11	402	6.12	2.65	0.79	7.68	8.57	3.15	0.42	0.73	0.69	-1.21E+00	3.44E-03		-2.94E+00	5.16E-08	Down	1.57E-01	6.94E-01		-1.29E+00	3.11E-04	Down	7.91E-01	5.63E-01		7.22E-01	5.97E-01					Unigene25154_A11//5.00E-07//TC133651				
Unigene25155_A11	1016	30.18	7.18	14.10	37.46	28.50	14.80	2.08	1.15	1.02	-2.07E+00	7.31E-66	Down	-1.10E+00	2.96E-25	Down	-3.94E-01	7.53E-07		-1.34E+00	8.62E-48	Down	-8.53E-01	3.12E-02		-1.03E+00	7.19E-03		Unigene25155_A11//gi|124359162|gb|ABN05883.1|//5.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene25155_A11//2.00E-10//AT3G09510| nucleic acid binding	Unigene25155_A11//8.00E-116//TC144919				nr +
Unigene2516_A11	589	1.87	5.68	5.88	9.39	8.36	7.51	16.37	20.58	29.08	1.61E+00	1.03E-05	Up	1.66E+00	7.72E-06	Up	-1.67E-01	5.63E-01		-3.21E-01	2.38E-01		3.30E-01	2.71E-02		8.30E-01	4.57E-12		Unigene2516_A11//gi|60459371|gb|AAX20031.1|//6.00E-99//RING-finger protein [Capsicum annuum]	Unigene2516_A11//6.00E-97//AT5G14420| RGLG2 (RING domain Ligase2); ubiquitin-protein ligase	Unigene2516_A11//0.00E+00//TC139811				nr +
Unigene25161_A11	1418	12.99	15.12	10.10	16.83	14.72	19.59	14.88	11.85	7.39	2.19E-01	7.91E-02		-3.63E-01	7.62E-03		-1.93E-01	1.01E-01		2.19E-01	4.40E-02		-3.29E-01	2.41E-03		-1.01E+00	3.59E-20	Down	Unigene25161_A11//gi|115482622|ref|NP_001064904.1|//2.00E-83//Os10g0486900 [Oryza sativa Japonica Group] >gi|110289293|gb|AAF54357.2| TPR Domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639513|dbj|BAF26818.1| Os10g0486900 [Oryza sativa Japonica Group]	Unigene25161_A11//7.00E-79//AT4G30480| tetratricopeptide repeat (TPR)-containing protein	Unigene25161_A11//0.00E+00//TC141672			GO:0043231//GO:0050896	nr -
Unigene25162_A11	915	6.92	1.50	3.38	16.33	11.93	4.29	2.08	2.01	2.05	-2.21E+00	2.87E-15	Down	-1.04E+00	2.79E-05	Down	-4.53E-01	8.46E-04		-1.93E+00	5.87E-32	Down	-4.91E-02	9.25E-01		-2.31E-02	9.67E-01		Unigene25162_A11//gi|225430575|ref|XP_002263122.1|//8.00E-38//PREDICTED: similar to GDU1 [Vitis vinifera]	Unigene25162_A11//3.00E-18//AT4G25760| AtGDU2 (Arabidopsis thaliana GLUTAMINE DUMPER 2)	Unigene25162_A11//0.00E+00//TC162175			GO:0031410	nr -
Unigene25163_A11	988	2.91	1.03	0.97	6.71	4.60	2.51	1.71	1.44	1.57	-1.51E+00	1.10E-04	Down	-1.59E+00	1.05E-04	Down	-5.44E-01	1.25E-02		-1.42E+00	1.68E-09	Down	-2.51E-01	6.29E-01		-1.22E-01	7.74E-01		Unigene25163_A11//gi|225430575|ref|XP_002263122.1|//7.00E-38//PREDICTED: similar to GDU1 [Vitis vinifera]	Unigene25163_A11//3.00E-18//AT4G25760| AtGDU2 (Arabidopsis thaliana GLUTAMINE DUMPER 2)	Unigene25163_A11//0.00E+00//TC162175			GO:0031410	nr -
Unigene25164_A11	685	1.22	2.59	1.01	0.87	1.16	2.51	8.64	21.11	34.55	1.08E+00	2.92E-02		-2.74E-01	7.05E-01		4.06E-01	6.32E-01		1.52E+00	3.74E-03		1.29E+00	8.77E-20	Up	2.00E+00	1.62E-60	Up	Unigene25164_A11//gi|42565070|ref|NP_188744.3|//1.00E-43//NAD(K) (NAD KINASE 1); NAD+ kinase/ NADH kinase/ calmodulin binding [Arabidopsis thaliana]	Unigene25164_A11//2.00E-36//AT3G21070| NADK1 (NAD KINASE 1); NAD+ kinase/ NADH kinase/ calmodulin binding	Unigene25164_A11//0.00E+00//CO112509		ko00760|Nicotinate and nicotinamide metabolism	GO:0005515//GO:0006739//GO:0009108//GO:0016301//GO:0043169//GO:0044424	nr +
Unigene25165_A11	960	4.96	9.03	5.49	4.67	5.38	3.95	10.57	14.32	22.66	8.64E-01	1.29E-05		1.47E-01	6.36E-01		2.04E-01	5.20E-01		-2.41E-01	4.58E-01		4.38E-01	1.23E-03		1.10E+00	1.41E-23	Up	Unigene25165_A11//gi|227204135|dbj|BAH56919.1|//3.00E-52//AT3G21070 [Arabidopsis thaliana]	Unigene25165_A11//2.00E-45//AT3G21070| NADK1 (NAD KINASE 1); NAD+ kinase/ NADH kinase/ calmodulin binding	Unigene25165_A11//0.00E+00//ES836577		ko00760|Nicotinate and nicotinamide metabolism	GO:0005515//GO:0006739//GO:0009108//GO:0016301//GO:0043169//GO:0044424	nr -
Unigene25166_A11	2320	3.90	1.27	1.65	2.10	0.99	2.22	0.69	4.43	5.86	-1.62E+00	1.82E-14	Down	-1.24E+00	2.00E-09	Down	-1.08E+00	2.05E-05	Down	7.68E-02	7.90E-01		2.68E+00	6.01E-37	Up	3.08E+00	3.82E-57	Up	Unigene25166_A11//gi|18419847|ref|NP_568006.1|//1.00E-177//SPH12 (SEC14-LIKE 12); phosphatidylinositol transporter/ transporter [Arabidopsis thaliana] >gi|15215780|gb|AAK91435.1| CTA10_870/CTA10_870 [Arabidopsis thaliana] >gi|23463079|gb|AAN33209.1| At4g36490/CTA10_870 [Arabidopsis thaliana]	Unigene25166_A11//1.00E-162//AT4G36490| SPH12 (SEC14-LIKE 12); phosphatidylinositol transporter/ transporter	Unigene25166_A11//4.00E-172//TC134726				nr +
Unigene25167_A11	2125	11.03	5.32	7.02	39.78	25.41	20.38	13.63	3.32	5.23	-1.05E+00	5.65E-19	Down	-6.53E-01	2.08E-08		-6.47E-01	1.52E-35		-9.65E-01	1.91E-62		-2.04E+00	2.46E-74	Down	-1.38E+00	1.74E-44	Down	Unigene25167_A11//gi|30686497|ref|NP_849691.1|//0.00E+00//jacalin lectin family protein [Arabidopsis thaliana] >gi|17064842|gb|AAL32575.1| Unknown protein [Arabidopsis thaliana] >gi|19715576|gb|AAL91614.1| At1g19720/F14P1_33 [Arabidopsis thaliana] >gi|23197804|gb|AAN15429.1| Unknown protein [Arabidopsis thaliana]	Unigene25167_A11//0.00E+00//AT1G19715| jacalin lectin family protein	Unigene25167_A11//0.00E+00//ES824377				nr +

Unigene25169_All	1635	44.13	23.77	38.20	26.20	31.02	24.20	4.32	2.33	1.95	-8.93E-01	2.19E-43		-2.08E-01	1.43E-03		2.44E-01	6.63E-04		-1.15E-01	2.25E-01		-8.93E-01	6.39E-06		-1.15E+00	7.80E-09	Down	Unigene25169_All//gi|288558799|gb|ACV87307.2|//1.00E-149//glycosyltransferase [Populus deltoides]	Unigene25169_All//5.00E-124//AT3G16520| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene25169_All//0.00E+00//TC165705				nr +
Unigene25170_All	619	2.96	1.31	0.69	18.27	12.74	15.18	10.11	1.62	1.87	-1.18E+00	1.60E-02		-2.10E+00	2.07E-04	Down	-5.20E-01	1.01E-03		-2.68E-01	1.40E-01		-2.64E+00	1.77E-22	Down	-2.44E+00	2.75E-21	Down	Unigene25170_All//gi|115434736|ref|NP_001042126.1|//8.00E-07//Os01g0168100 [Oryza sativa Japonica Group] >gi|13486675|dbj|BAB39912.1| P0028E10.16 [Oryza sativa Japonica Group] >gi|15528776|dbj|BAB64818.1| kinase interacting protein 1 -like [Oryza sativa Japonica Group] >gi|20804819|dbj|BAB92502.1| kinase interacting protein 1 -like [Oryza sativa Japonica Group] >gi|113531657|dbj|BAF04040.1| Os01g0168100 [Oryza sativa Japonica Group]						nr +
Unigene25171_All	1736	5.79	2.74	1.44	29.99	25.97	20.14	11.76	3.97	2.32	-1.08E+00	7.21E-09	Down	-2.00E+00	3.20E-20	Down	-2.08E-01	3.75E-03		-5.75E-01	5.41E-16		-1.57E+00	7.79E-37	Down	-2.34E+00	1.23E-64	Down	Unigene25171_All//gi|115434736|ref|NP_001042126.1|//9.00E-24//Os01g0168100 [Oryza sativa Japonica Group] >gi|13486675|dbj|BAB39912.1| P0028E10.16 [Oryza sativa Japonica Group] >gi|15528776|dbj|BAB64818.1| kinase interacting protein 1 -like [Oryza sativa Japonica Group] >gi|20804819|dbj|BAB92502.1| kinase interacting protein 1 -like [Oryza sativa Japonica Group] >gi|113531657|dbj|BAF04040.1| Os01g0168100 [Oryza sativa Japonica Group]	Unigene25171_All//3.00E-35//AT5G05180| unknown protein	Unigene25171_All//0.00E+00//TC176354				nr -
Unigene25174_All	1267	21.80	52.35	40.52	154.95	152.50	130.18	197.65	441.58	377.67	1.26E+00	1.36E-69	Up	8.94E-01	4.65E-30		-2.30E-02	6.16E-01		-2.51E-01	5.25E-13		1.16E+00	0.00E+00	Up	9.34E-01	0.00E+00		Unigene25174_All//gi|115452497|ref|NP_001049849.1|//1.00E-37//Os03g0299600 [Oryza sativa Japonica Group] >gi|113548320|dbj|BAF11763.1| Os03g0299600 [Oryza sativa Japonica Group]	Unigene25174_All//2.00E-30//AT3G10985| SAG20 (SENESCENCE ASSOCIATED GENE 20)	Unigene25174_All//0.00E+00//TC160651			GO:0005488//GO:0032502//GO:0051707	nr +
Unigene25175_All	1310	4.87	11.80	5.57	6.58	5.60	7.72	4.58	8.71	5.47	1.28E+00	5.33E-17	Up	1.93E-01	4.15E-01		-2.33E-01	2.80E-01		2.31E-01	2.48E-01		9.26E-01	1.36E-09		2.56E-01	2.02E-01		Unigene25175_All//gi|30684602|ref|NP_850606.1|//1.00E-119//ATRBL14 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 14); zinc ion binding [Arabidopsis thaliana] >gi|75247670|sp|Q8RXW0.1|Y3761_ARATH RecName: Full=Uncharacterized protein At3g17611	Unigene25175_All//3.00E-84//AT3G17611| ATRBL14 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 14); zinc ion binding	Unigene25175_All//0.00E+00//gi|164248124|gb|ES806284.1|ES806284			GO:0031224//GO:0046914	nr -
Unigene25177_All	2512	9.21	6.47	5.49	12.08	10.19	12.69	20.15	8.10	9.77	-5.08E-01	7.42E-06		-7.46E-01	2.59E-10		-2.46E-01	1.10E-02		7.18E-02	5.61E-01		-1.31E+00	2.07E-69	Down	-1.04E+00	9.40E-50	Down	Unigene25177_All//gi|30688918|ref|NP_194841.2|//0.00E+00//SKB1 (SHK1 BINDING PROTEIN 1); protein methyltransferase [Arabidopsis thaliana] >gi|152013352|sp|Q8GWT4.2|ANM5_ARATH RecName: Full=Protein arginine N-methyltransferase 5; AltName: Full=Shk1 kinase-binding protein 1 homolog	Unigene25177_All//0.00E+00//AT4G31120| SKB1 (SHK1 BINDING PROTEIN 1); protein methyltransferase	Unigene25177_All//0.00E+00//TC170114			GO:0009908//GO:0010048//GO:0016274//GO:0016772//GO:0044424	nr +
Unigene25178_All	1070	19.61	17.47	15.43	32.64	22.43	23.68	27.90	15.90	13.11	-1.66E-01	2.06E-01		-3.46E-01	6.30E-03		-5.41E-01	6.26E-11		-4.63E-01	1.38E-07		-8.11E-01	3.60E-19		-1.09E+00	8.45E-32	Down	Unigene25178_All//gi|11452761|ref|NP_001049981.1|//1.00E-34//Os03g0324800 [Oryza sativa Japonica Group] >gi|108707909|gb|ABF95704.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548452|dbj|BAF11895.1| Os03g0324800 [Oryza sativa Japonica Group]	Unigene25178_All//1.00E-70//AT4G26410| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP022280 (InterPro:IPR016803); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G45060.1); Has 47 Blast hits to 47 proteins in 12 species: Archae - 3; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 40; Viruses - 1; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene25178_All//0.00E+00//TC138478			GO:0043231	nr +
Unigene25182_All	2176	0.70	1.84	1.25	3.00	3.61	2.59	1.77	0.83	1.52	1.40E+00	1.30E-05	Up	8.40E-01	3.58E-02		2.67E-01	2.36E-01		-2.09E-01	4.27E-01		-1.10E+00	9.99E-05	Down	-2.19E-01	4.54E-01		Unigene25182_All//gi|296082100|emb|CBI21105.3|//1.00E-27//unnamed protein product [Vitis vinifera]		Unigene25182_All//0.00E+00//DT467744				nr -
Unigene25183_All	1931	1.52	1.86	1.96	4.62	4.37	4.30	7.64	2.88	2.97	2.96E-01	3.78E-01		3.68E-01	2.79E-01		-7.98E-02	7.45E-01		-1.02E-01	6.59E-01		-1.41E+00	4.97E-23	Down	-1.36E+00	1.22E-22	Down	Unigene25183_All//gi|116309454|emb|CAH66526.1|//1.00E-160//H0502B11.6 [Oryza sativa (indica cultivar-group)]	Unigene25183_All//5.00E-157//AT5G47900| unknown protein	Unigene25183_All//0.00E+00//TC169338		ko00531|Glycosaminoglycan degradation		nr -
Unigene25184_All	1717	2.13	1.30	2.92	29.91	26.31	21.81	9.75	3.02	2.81	-7.16E-01	2.50E-02		4.51E-01	1.16E-01		-1.85E-01	1.22E-02		-4.56E-01	1.43E-10		-1.69E+00	8.31E-34	Down	-1.80E+00	7.63E-38	Down	Unigene25184_All//gi|115462313|ref|NP_001054756.1|//1.00E-119//Os05g0168700 [Oryza sativa Japonica Group] >gi|113578307|dbj|BAF16670.1| Os05g0168700 [Oryza sativa Japonica Group]	Unigene25184_All//5.00E-137//AT2G28315| LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: transporter-related (TAIR:AT1G06890.2); Has 1852 Blast hits to 1847 proteins in 207 species: Archae - 0; Bacteria - 58; Metazoa - 582; Fungi - 250; Plants - 685; Viruses - 0; Other Eukaryotes - 277 (source: NCBI BLink).	Unigene25184_All//0.00E+00//gi|54115429|gb|CO490938.1|CO490938				nr -
Unigene25186_All	2336	11.38	8.74	10.96	13.75	18.99	15.72	20.14	50.87	27.44	-3.80E-01	3.17E-04		-5.34E-02	6.56E-01		4.65E-01	2.61E-10		1.93E-01	4.04E-02		1.34E+00	5.37E-166	Up	4.46E-01	1.01E-14		Unigene25186_All//gi|62857020|dbj|BAD95895.1|//1.00E-128//Ser/Thr protein kinase [Lotus japonicus]	Unigene25186_All//2.00E-110//AT1G66930| serine/threonine protein kinase family protein	Unigene25186_All//0.00E+00//TC165421		ko04626|Plant-pathogen interaction		nr +
Unigene25187_All	2418	4.76	2.33	2.27	11.80	11.72	6.09	10.58	5.70	5.11	-1.03E+00	1.92E-09	Down	-1.07E+00	1.79E-09	Down	-1.03E-02	9.41E-01		-9.55E-01	4.42E-21		-8.91E-01	2.85E-19		-1.05E+00	7.78E-26	Down	Unigene25187_All//gi|215598266|tpg|DAA06351.1|//0.00E+00//TPA_inf: ARO1-like protein 2 [Vitis vinifera]	Unigene25187_All//0.00E+00//AT5G66200| ARO2 (ARMADILLO REPEAT ONLY 2); binding	Unigene25187_All//0.00E+00//ES807758			GO:0000904//GO:0007010//GO:0016020//GO:0043231	nr +
Unigene25188_All	3226	1.67	6.53	0.79	3.18	3.50	2.90	5.79	12.76	55.08	1.97E+00	2.91E-42	Up	-1.08E+00	7.48E-05	Down	1.38E-01	5.07E-01		-1.34E-01	5.31E-01		1.14E+00	2.64E-45	Up	3.25E+00	0.00E+00	Up	Unigene25188_All//gi|297821008|ref|XP_002878387.1|//1.00E-125//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297324225|gb|EFH54646.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene25188_All//1.00E-123//AT3G61520| pentatricopeptide (PPR) repeat-containing protein	Unigene25188_All//0.00E+00//TC142990		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene25189_All	1722	11.21	6.62	7.95	17.73	17.32	19.75	36.49	8.03	11.68	-7.60E-01	1.98E-09		-4.97E-01	1.33E-04		-3.42E-02	8.07E-01		1.55E-01	1.32E-01		-2.18E+00	1.49E-175	Down	-1.64E+00	2.88E-123	Down	Unigene25189_All//gi|38228677|emb|CAE54075.1|//0.00E+00//serine/threonine-protein kinase [Fagus sylvatica]	Unigene25189_All//4.00E-163//AT1G10940| SNRK2.4 (SNF1-RELATED PROTEIN KINASE 2.4); kinase	Unigene25189_All//0.00E+00//TC139425			GO:0004672//GO:0006464//GO:0006950//GO:0032559	nr -
Unigene25190_All	2069	0.91	0.96	0.44	16.42	8.92	6.64	7.70	2.18	2.33	6.92E-02	8.83E-01		-1.06E+00	3.51E-02		-8.80E-01	1.25E-24		-1.31E+00	3.80E-41	Down	-1.82E+00	1.34E-35	Down	-1.73E+00	3.86E-34	Down	Unigene25190_All//gi|115449257|ref|NP_001048408.1|//1.00E-174//Os02g0799300 [Oryza sativa Japonica Group] >gi|113537939|dbj|BAF10322.1| Os02g0799300 [Oryza sativa Japonica Group]	Unigene25190_All//1.00E-171//AT2G25270| unknown protein	Unigene25190_All//0.00E+00//TC178302				nr +
Unigene25193_All	1610	55.08	30.02	31.12	52.75	56.25	50.27	43.23	16.41	18.90	-8.76E-01	1.78E-51		-8.24E-01	7.42E-45		9.26E-02	1.28E-01		-6.96E-02	3.12E-01		-1.40E+00	1.57E-104	Down	-1.19E+00	3.02E-84	Down	Unigene25193_All//gi|297799514|ref|XP_002867641.1|//0.00E+00//argininosuccinate synthase family [Arabidopsis lyrata subsp. lyrata] >gi|297313477|gb|EFH43900.1| argininosuccinate synthase family [Arabidopsis lyrata subsp. lyrata]	Unigene25193_All//0.00E+00//AT4G24830| argininosuccinate synthase family	Unigene25193_All//0.00E+00//TC148602		ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006525//GO:0009532//GO:0016879//GO:0032559	nr +
Unigene25196_All	636	9.05	10.12	11.47	4.46	6.28	4.12	7.18	3.42	4.76	1.61E-01	5.29E-01		3.42E-01	1.44E-01		4.92E-01	1.14E-01		-1.16E-01	7.62E-01		-1.07E+00	2.82E-05	Down	-5.93E-01	1.50E-02		Unigene25196_All//gi|297795405|ref|XP_002865587.1|//6.00E-48//nitrogen regulation family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311422|gb|EFH41846.1| nitrogen regulation family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25196_All//2.00E-48//AT5G47970| nitrogen regulation family protein	Unigene25196_All//0.00E+00//gi|13356556|gb|BG446916.1|BG446916			GO:0006399//GO:0016627//GO:0019740//GO:0030554//GO:0043231//GO:0044444	nr +
Unigene25200_All	1724	1.61	0.65	0.59	16.70	12.14	9.48	7.50	0.68	4.39	-1.31E+00	7.32E-04	Down	-1.45E+00	4.11E-04	Down	-4.60E-01	6.77E-07		-8.17E-01	1.99E-16		-3.47E+00	8.49E-60	Down	-7.73E-01	2.01E-08		Unigene25200_All//gi|223452546|gb|ACM89600.1|//1.00E-151//leucine-rich repeat family protein / extensin family protein [Glycine max]	Unigene25200_All//1.00E-133//AT2G19780| leucine-rich repeat family protein / extensin family protein	Unigene25200_All//0.00E+00//TC139316			GO:0005488//GO:0005618//GO:0031410	nr -
Unigene25202_All	1682	5.72	5.90	7.47	10.57	9.60	5.16	0.96	0.17	0.62	4.49E-02	8.16E-01		3.85E-01	2.30E-02		-1.39E-01	3.54E-01		-1.04E+00	3.36E-15	Down	-2.46E+00	7.71E-06	Down	-6.33E-01	1.58E-01		Unigene25202_All//gi|223452546|gb|ACM89600.1|//1.00E-162//leucine-rich repeat family protein / extensin family protein [Glycine max]	Unigene25202_All//4.00E-127//AT4G29240| leucine-rich repeat family protein / extensin family protein	Unigene25202_All//0.00E+00//TC133057			GO:0023060//GO:0031410	nr +
Unigene25204_All	1258	2.66	4.63	2.50	6.41	7.06	3.45	4.34	2.16	17.20	7.99E-01	1.17E-03		-9.20E-02	7.91E-01		1.39E-01	5.50E-01		-8.96E-01	7.78E-06		-1.01E+00	1.27E-05	Down	1.99E+00	5.58E-55	Up	Unigene25204_All//gi|260424374|gb|ACX37656.1|//5.00E-57//homeodomain associated leucine zipper protein [Gossypium arboreum]	Unigene25204_All//2.00E-35//AT3G60390| HAT3 (HOMEOBOX-LEUCINE ZIPPER PROTEIN 3); transcription factor	Unigene25204_All//0.00E+00//FL577231	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0030528//GO:0043231	nr -
Unigene25205_All	1292	4.41	8.24	4.08	7.25	13.97	5.31	3.44	2.10	15.85	9.00E-01	3.97E-07		-1.13E-01	6.66E-01		9.46E-01	2.46E-14		-4.48E-01	1.78E-02		-7.09E-01	5.61E-03		2.21E+00	2.24E-59	Up	Unigene25205_All//gi|260424374|gb|ACX37656.1|//1.00E-102//homeodomain associated leucine zipper protein [Gossypium arboreum]	Unigene25205_All//8.00E-76//AT3G60390| HAT3 (HOMEOBOX-LEUCINE ZIPPER PROTEIN 3); transcription factor	Unigene25205_All//0.00E+00//TC148112	HB		GO:0001071//GO:0003677//GO:0006355//GO:0009639//GO:0009719//GO:0030528//GO:0043231	nr +
Unigene25208_All	1107	145.48	456.62	231.38	111.91	109.43	155.40	62.94	110.47	94.65	1.65E+00	0.00E+00	Up	6.69E-01	4.84E-90		-3.23E-02	5.91E-01		4.74E-01	3.17E-36		8.12E-01	5.76E-76		5.89E-01	2.54E-38		Unigene25208_All//gi|38016525|gb|AR07598.1|//1.00E-81//fiber protein Fb19 [Gossypium barbadense]	Unigene25208_All//6.00E-67//AT2G47710| universal stress protein (USP) family protein	Unigene25208_All//0.00E+00//gi|78351414|gb|DT571688.1|DT571688			GO:0043231//GO:0050896	nr -

Unigene25209_All	872	1.80	0.46	0.37	3.03	2.41	1.24	4.27	2.25	1.55	-1.95E+00	7.99E-04	Down	-2.30E+00	3.17E-04	Down	-3.30E-01	4.24E-01		-1.28E+00	1.04E-03		-9.21E-01	1.19E-03		-1.46E+00	6.07E-07	Down	Unigene25209_All//gi|75208205|sp|Q9SUC9.1|UGP17_ARATH//9.00E-30//RecName: Full=Uncharacterized GPI-anchored protein At4g28100; Flags: Precursor	Unigene25209_All//2.00E-29//AT4G28100| unknown protein	Unigene25209_All//0.00E+00//gi|48822249|gb|C0123562.1|C0123562			GO:0031225//GO:0031410	nr -
Unigene25210_All	1700	5.66	3.19	4.79	9.03	9.91	5.58	5.92	4.08	2.58	-8.28E-01	8.35E-06		-2.41E-01	2.43E-01		1.34E-01	4.05E-01		-6.94E-01	5.57E-07		-5.36E-01	8.43E-04		-1.20E+00	4.88E-13	Down	Unigene25210_All//gi|75208205|sp|Q9SUC9.1|UGP17_ARATH//1.00E-112//RecName: Full=Uncharacterized GPI-anchored protein At4g28100; Flags: Precursor	Unigene25210_All//1.00E-111//AT4G28100| unknown protein	Unigene25210_All//0.00E+00//TC148212			GO:0031410	nr -
Unigene25211_All	1817	13.99	6.16	6.21	25.28	21.70	12.85	7.75	2.30	2.59	-1.18E+00	1.30E-24	Down	-1.17E+00	2.76E-23	Down	-2.20E-01	4.02E-03		-9.76E-01	8.26E-35		-1.75E+00	5.97E-30	Down	-1.58E+00	7.82E-27	Down	Unigene25211_All//gi|213868273|gb|ACJ54183.1|//1.00E-67//PB1 domain-containing protein [Nicotiana benthamiana]	Unigene25211_All//1.00E-50//AT5G64430| octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	Unigene25211_All//0.00E+00//TC151077				nr +
Unigene25212_All	1752	0.00	0.00	0.00	85.78	59.44	40.14	8.28	9.09	5.43	null	null		null	null		-5.29E-01	6.65E-44		-1.10E+00	1.78E-136	Down	1.35E-01	3.62E-01		-6.07E-01	2.09E-06		Unigene25212_All//gi|225626279|gb|ACN97189.1|//0.00E+00//KNOX transcription factor [Populus trichocarpa]	Unigene25212_All//2.00E-120//AT4G08150| KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor	Unigene25212_All//0.00E+00//TC153771	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene25213_All	1365	1.69	0.30	0.08	2.12	1.46	1.56	4.80	4.59	2.80	-2.51E+00	7.85E-07	Down	-4.43E+00	3.18E-10	Down	-5.33E-01	1.46E-01		-4.45E-01	2.52E-01		-6.39E-02	7.79E-01		-7.77E-01	9.76E-05		Unigene25213_All//gi|18421145|ref|NP_568499.1|//2.00E-61//RECQSIM (Arabidopsis RecQ-helicase sim); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana] >gi|75309680|sp|Q9FT69.1|RQS1M_ARATH RecName: Full=ATP-dependent DNA helicase Q-like SIM; AltName: Full=RecQ-like protein SIM; Short=Similar to RecQ protein; Short=AtRecQsim >gi|11121453|emb|CAC14870.1| DNA Helicase [Arabidopsis thaliana]	Unigene25213_All//2.00E-33//AT5G27680| RECQSIM (Arabidopsis RecQ helicase sim); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene25213_All//0.00E+00//gi|6462375|gb|AW187939.1|AW187939			GO:0003678//GO:0006259//GO:0032559//GO:0042623	nr +
Unigene25216_All	1585	2.67	5.79	2.49	3.99	3.82	4.13	3.23	1.82	2.41	1.11E+00	1.53E-08	Up	-1.05E-01	7.31E-01		-6.19E-02	8.11E-01		4.98E-02	8.62E-01		-8.27E-01	4.58E-04		-4.20E-01	7.04E-02		Unigene25216_All//gi|115466278|ref|NP_001056738.1|//1.00E-106//Os06g0138200 [Oryza sativa Japonica Group] >gi|55296462|dbj|BAD68658.1| oxidoreductase, 2OG-Fe(II) oxygenase family protein-like [Oryza sativa Japonica Group] >gi|113594778|dbj|BAF18652.1| Os06g0138200 [Oryza sativa Japonica Group]	Unigene25216_All//8.00E-100//AT2G17970| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene25216_All//0.00E+00//gi|78336638|gb|DT556912.1|DT556912			GO:0003824	nr -
Unigene25217_All	1529	0.44	1.76	1.15	1.27	0.72	0.89	0.86	0.85	0.31	1.98E+00	4.79E-06	Up	1.37E+00	1.01E-02		-8.18E-01	6.69E-02		-5.20E-01	2.89E-01		-1.66E-02	1.01E+00		-1.45E+00	5.49E-03		Unigene25217_All//gi|124360274|gb|ABN08287.1|//1.00E-116//2OG-Fe(II) oxygenase [Medicago truncatula]	Unigene25217_All//2.00E-107//AT2G17970| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene25217_All//0.00E+00//gi|78336638|gb|DT556912.1|DT556912				nr -
Unigene25219_All	2015	5.53	1.79	4.04	6.92	7.74	6.32	1.93	1.43	1.09	-1.63E+00	9.06E-18	Down	-4.52E-01	1.16E-02		1.61E-01	3.16E-01		-1.31E-01	4.72E-01		-4.32E-01	1.34E-01		-8.28E-01	1.97E-03		Unigene25219_All//gi|113205348|gb|ABI34354.1|//1.00E-18//Retrotransposon gag protein [Solanum demissum]		Unigene25219_All//2.00E-179//FL577116			GO:0003676//GO:0003824//GO:0006259	nr +
Unigene25222_All	1409	36.13	8.24	14.81	34.54	27.81	21.64	2.55	1.33	0.54	-2.13E+00	3.36E-113	Down	-1.29E+00	2.22E-53	Down	-3.13E-01	9.33E-06		-6.75E-01	8.59E-20		-9.34E-01	1.28E-03		-2.25E+00	1.80E-11	Down	Unigene25222_All//gi|48310189|gb|AAT41771.1|//2.00E-78//At5g42680 [Arabidopsis thaliana] >gi|52118794|gb|AAU29467.1| At5g42680 [Arabidopsis thaliana]	Unigene25222_All//4.00E-71//AT5G42680| unknown protein	Unigene25222_All//0.00E+00//TC130400				nr -
Unigene25223_All	439	2.15	6.23	1.70	1.82	1.88	4.32	3.27	3.90	2.81	1.54E+00	1.40E-04	Up	-3.37E-01	6.16E-01		5.23E-02	9.65E-01		1.25E+00	9.82E-03		2.54E-01	6.22E-01		-2.19E-01	6.38E-01		Unigene25223_All//gi|115463925|ref|NP_001055562.1|//8.00E-22//Os05g0117300 [Oryza sativa Japonica Group] >gi|113579113|dbj|BAF17476.1| Os05g0117300 [Oryza sativa Japonica Group]	Unigene25223_All//9.00E-31//AT4G12760| unknown protein	Unigene25223_All//1.00E-161//gi|164292987|gb|ES807262.1|ES807262				nr +
Unigene25228_All	1909	1.64	7.19	2.82	5.17	4.82	5.56	3.17	3.04	3.59	2.13E+00	1.18E-30	Up	7.77E-01	3.74E-03		-1.01E-01	6.23E-01		1.06E-01	6.44E-01		-5.75E-02	8.14E-01		1.81E-01	4.03E-01		Unigene25228_All//gi|224073218|ref|XP_002304028.1|//1.00E-65//bromodomain protein [Populus trichocarpa] >gi|222841460|gb|EEE79007.1| bromodomain protein [Populus trichocarpa]	Unigene25228_All//2.00E-26//AT3G60110| DNA binding	Unigene25228_All//0.00E+00//ES850664				nr -
Unigene25230_All	356	0.29	0.57	0.60	6.86	2.61	0.13	1.31	0.47	0.22	9.54E-01	6.21E-01		1.03E+00	5.91E-01		-1.39E+00	3.28E-04	Down	-5.76E+00	6.63E-14	Down	-1.48E+00	1.53E-01		-2.55E+00	2.35E-02		Unigene25230_All//gi|115446695|ref|NP_001047127.1|//1.00E-12//Os02g0556100 [Oryza sativa Japonica Group] >gi|46389859|dbj|BAD15460.1| dehydrogenase-like protein [Oryza sativa Japonica Group] >gi|113536658|dbj|BAF09041.1| Os02g0556100 [Oryza sativa Japonica Group]	Unigene25230_All//1.00E-13//AT5G10730| binding / catalytic/ coenzyme binding	Unigene25230_All//2.00E-86//C0102313				nr -
Unigene25232_All	522	0.00	0.10	0.00	0.48	0.53	0.61	6.24	10.49	24.27	6.60E+00	6.17E-01		null	null		1.45E-01	9.61E-01		3.44E-01	7.97E-01		7.50E-01	9.41E-04		1.96E+00	5.87E-32	Up	Unigene25232_All//gi|224092694|ref|XP_002309700.1|//2.00E-42//histidine kinase cytokinin receptor [Populus trichocarpa] >gi|222855676|gb|EEE93223.1| histidine kinase cytokinin receptor [Populus trichocarpa]	Unigene25232_All//2.00E-36//AT5G10720| AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase	Unigene25232_All//2.00E-170//DT460627	Orphans			nr -
Unigene25233_All	2555	0.25	0.06	0.04	0.74	0.34	0.12	11.30	10.62	19.76	-2.05E+00	4.46E-02		-2.56E+00	2.72E-02		-1.14E+00	1.12E-02		-2.58E+00	3.16E-06	Down	-9.03E-02	4.03E-01		8.06E-01	3.33E-32		Unigene25233_All//gi|224092694|ref|XP_002309700.1|//1.00E-136//histidine kinase cytokinin receptor [Populus trichocarpa] >gi|222855676|gb|EEE93223.1| histidine kinase cytokinin receptor [Populus trichocarpa]	Unigene25233_All//3.00E-95//AT5G10720| AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase	Unigene25233_All//0.00E+00//gi|164239423|gb|ES794354.1|ES794354	Orphans			nr -
Unigene25234_All	1909	10.80	9.45	7.48	4.57	5.29	2.11	11.43	20.12	8.03	-1.93E-01	1.34E-01		-5.31E-01	2.18E-05		2.11E-01	3.05E-01		-1.12E+00	1.08E-08	Down	8.16E-01	1.22E-24		-5.08E-01	6.53E-07		Unigene25234_All//gi|18407955|ref|NP_566879.1|//1.00E-154//MLO3 (MILDEW RESISTANCE LOCUS O 3); calmodulin binding [Arabidopsis thaliana] >gi|33112392|sp|Q94KB9.1|MLO3_ARATH RecName: Full=MLO-like protein 3; Short=AtMlo3 >gi|14091576|gb|AAK53796.1|AF36956 4_1 membrane protein Mlo3 [Arabidopsis thaliana]	Unigene25234_All//1.00E-155//AT3G45290| MLO3 (MILDEW RESISTANCE LOCUS O 3); calmodulin binding	Unigene25234_All//0.00E+00//TC158683				nr +
Unigene25237_All	1891	2.55	0.62	0.76	15.65	9.45	5.56	4.81	1.66	2.04	-2.05E+00	9.52E-11	Down	-1.74E+00	2.27E-08	Down	-7.27E-01	1.50E-15		-1.49E+00	8.75E-44	Down	-1.54E+00	2.24E-16	Down	-1.23E+00	2.27E-12	Down	Unigene25237_All//gi|7672732|gb|AAF66615.1|//0.00E+00//LRR receptor-like protein kinase [Nicotiana tabacum]	Unigene25237_All//4.00E-178//AT1G66150| TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase	Unigene25237_All//0.00E+00//TC176715				nr +
Unigene25238_All	1595	3.58	6.45	8.35	3.19	2.79	5.55	20.01	56.97	37.97	8.51E-01	2.27E-06		1.22E+00	2.44E-13	Up	-1.94E-01	5.31E-01		8.01E-01	2.70E-05		1.51E+00	1.48E-152	Up	9.24E-01	2.89E-48		Unigene25238_All//gi|75297894|sp|Q84MB3.1|ACCH1_ARATH//1.00E-113//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene25238_All//4.00E-110//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene25238_All//5.00E-16//TC174072		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene2524_All	1844	12.71	11.57	10.74	3.08	2.71	3.67	11.62	25.09	8.43	-1.36E-01	2.77E-01		-2.43E-01	4.85E-02		-1.86E-01	5.23E-01		2.55E-01	3.16E-01		1.11E+00	9.44E-49	Up	-4.64E-01	6.64E-06		Unigene2524_All//gi|297833649|ref|XP_002887206.1|//2.00E-88//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333047|gb|EFH63465.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2524_All//4.00E-77//AT1G68810| basic helix-loop-helix (bHLH) family protein	Unigene2524_All//0.00E+00//ES815402	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr -
Unigene25240_All	1134	84.16	84.00	74.52	65.50	63.59	86.07	61.48	42.16	25.51	-2.60E-03	9.86E-01		-1.75E-01	1.96E-03		-4.27E-02	5.83E-01		3.94E-01	5.73E-15		-5.44E-01	5.65E-22		-1.27E+00	5.58E-93	Down	Unigene25240_All//gi|77999287|gb|ABB16990.1|//1.00E-129//proteasome-like protein alpha subunit [Solanum tuberosum]	Unigene25240_All//5.00E-112//AT5G66140| PAM2 (PROTEASOME ALPHA SUBUNIT D 2); endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene25240_All//0.00E+00//TC137305		ko03050|Proteasome		nr +
Unigene25241_All	1212	28.02	4.47	10.72	39.54	28.98	46.54	70.99	22.42	19.66	-2.65E+00	8.17E-98	Down	-1.39E+00	4.94E-40	Down	-4.48E-01	1.26E-10		2.35E-01	8.33E-04		-1.66E+00	1.16E-166	Down	-1.85E+00	1.99E-199	Down	Unigene25241_All//gi|58979188|gb|AN83328.1|//1.00E-127//mitochondrial prohibitin 1 [Petunia x hybrida]	Unigene25241_All//7.00E-112//AT3G27280| ATPHB4 (PROHIBITIN 4)	Unigene25241_All//0.00E+00//TC140471				nr +
Unigene25242_All	1873	31.82	33.09	33.06	42.42	40.12	33.85	59.46	34.05	23.06	5.64E-02	4.74E-01		5.55E-02	5.03E-01		-8.06E-02	2.33E-01		-3.25E-01	7.97E-09		-8.04E-01	3.04E-68		-1.37E+00	6.55E-166	Down	Unigene25242_All//gi|17064906|gb|AAL32607.1|//0.00E+00//Unknown protein [Arabidopsis thaliana] >gi|231978400|gb|AAN15447.1| Unknown protein [Arabidopsis thaliana]	Unigene25242_All//0.00E+00//AT5G19010| MPK16; MAP kinase	Unigene25242_All//0.00E+00//TC134704		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene25243_All	1690	63.65	30.40	49.72	60.13	53.55	43.69	23.97	13.28	9.83	-1.07E+00	3.09E-86	Down	-3.56E-01	2.05E-12		-1.67E-01	7.57E-04		-4.61E-01	1.08E-20		-8.52E-01	7.08E-28		-1.29E+00	1.84E-55	Down	Unigene25243_All//gi|62900644|sp|Q82291.1|PAP3_ARATH//1.00E-112//RecName: Full=Probable plastid-lipid-associated protein 3, chloroplastic; Short=AtPap3; AltName: Full=Fibrillin-3; Flags: Precursor	Unigene25243_All//5.00E-100//AT2G35490| plastid-lipid associated protein PAP, putative	Unigene25243_All//0.00E+00//TC145198				nr -
Unigene25244_All	2061	0.53	1.01	0.62	4.13	5.43	1.84	19.22	46.28	26.23	9.19E-01	4.07E-02		2.18E-01	7.02E-01		3.94E-01	1.93E-02		-1.17E+00	4.41E-09	Down	1.27E+00	6.36E-123	Up	4.49E-01	1.10E-12		Unigene25244_All//gi|15232096|ref|NP_186784.1|//0.00E+00//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana]	Unigene25244_All//8.00E-170//AT3G01350| proton-dependent oligopeptide transport (POT) family protein	Unigene25244_All//0.00E+00//DW511750				nr +
Unigene25245_All	1883	1.39	8.02	2.74	1.85	3.20	2.06	5.32	7.79	25.35	2.53E+00	2.85E-41	Up	9.81E-01	3.77E-04		7.89E-01	6.15E-04		1.56E-01	6.66E-01		5.50E-01	2.33E-05		2.25E+00	5.55E-141	Up	Unigene25245_All//gi|76884939|gb|ABA59556.1|//1.00E-146//U-box protein [Capsicum annuum]	Unigene25245_All//9.00E-144//AT2G35930| PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase	Unigene25245_All//0.00E+00//TC161324				nr +
Unigene25246_All	1121	35.85	12.52	22.28	13.55	8.72	6.69	1.62	1.90	19.08	-1.52E+00	4.19E-56	Down	-6.86E-01	3.62E-15		-6.36E-01	1.34E-06		-1.02E+00	9.81E-13	Down	2.30E-01	6.13E-01		3.56E+00	4.22E-102	Up	Unigene25246_All//gi|18417976|ref|NP_567891.1|//2.00E-20//IAA29 (INDOLE-3-ACETIC ACID INDUCIBLE 29); transcription factor [Arabidopsis thaliana] >gi|46396937|sp|Q93WC4.2|IAA29_ARATH RecName: Full=Auxin-responsive protein IAA29; AltName: Full=Indoleacetic acid-induced protein 29 >gi|49616375|gb|AAT67084.1| IAA29 [Arabidopsis thaliana]	Unigene25246_All//9.00E-18//AT4G32280| IAA29 (INDOLE-3-ACETIC ACID INDUCIBLE 29); transcription factor	Unigene25246_All//0.00E+00//TC149850				nr -

Unigene25247_All	1259	80.75	46.08	45.76	68.89	68.13	33.54	5.21	4.15	4.02	-8.09E-01	1.41E-51		-8.19E-01	6.92E-51		-1.59E-02	8.24E-01		-1.04E+00	2.71E-72	Down	-3.27E-01	1.33E-01		-3.73E-01	6.56E-02		Unigene25247_All//gi|224128494|ref|XP_002320346.1|//1.00E-123//f-box family protein [Populus trichocarpa] >gi|222861119|gb|EEE98661.1| f-box family protein [Populus trichocarpa]	Unigene25247_All//2.00E-108//AT4G02440| EID1 (EMPFINDLICHER IM DUNKELROTEN LICHT 1); ubiquitin-protein ligase	Unigene25247_All//0.00E+00//TC135585				nr +
Unigene25248_All	2314	1.22	0.61	0.28	2.22	2.17	1.85	4.20	4.52	2.74	-9.94E-01	8.04E-03		-2.14E+00	1.39E-06	Down	-2.93E-02	9.17E-01		-2.58E-01	3.95E-01		1.04E-01	6.03E-01		-6.18E-01	1.03E-04		Unigene25248_All//gi|115470455|ref|NP_001058826.1|//1.00E-150//Os07g0130800 [Oryza sativa Japonica Group] >gi|113610362|dbj|BAF20740.1| Os07g0130800 [Oryza sativa Japonica Group]	Unigene25248_All//0.00E+00//AT3G55550| lectin protein kinase, putative	Unigene25248_All//0.00E+00//TC157059		ko04626|Plant-pathogen interaction		nr -
Unigene25249_All	3152	0.60	1.58	0.78	9.29	10.79	8.00	9.86	3.38	5.78	1.40E+00	9.14E-07	Up	3.79E-01	3.96E-01		2.16E-01	2.05E-02		-2.17E-01	3.98E-02		-1.54E+00	1.64E-54	Down	-7.71E-01	6.95E-19		Unigene25249_All//gi|157313306|gb|ABV32546.1|//0.00E+00//beta-galactosidase protein 1 [Prunus persica]	Unigene25249_All//0.00E+00//AT3G13750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene25249_All//0.00E+00//TC140662		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series		nr +
Unigene2525_All	1413	5.07	7.14	8.52	10.58	16.96	21.96	3.95	3.31	4.96	4.92E-01	6.53E-03		7.48E-01	9.77E-06		6.82E-01	5.32E-11		1.05E+00	1.69E-26	Up	-2.54E-01	3.07E-01		3.29E-01	9.76E-02		Unigene2525_All//gi|18394792|ref|NP_564096.1|//6.00E-76//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75217972|sp|Q6X4L4.1|C3H6_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 6; Short=AtC3H6 >gi|98969983|gb|ABF58975.1| At1g19860 [Arabidopsis thaliana]	Unigene2525_All//3.00E-77//AT1G19860| zinc finger (CCCH-type) family protein	Unigene2525_All//0.00E+00//TC171927	C3H			nr +
Unigene25250_All	1721	0.64	14.43	0.56	0.58	2.10	0.60	4.91	7.80	118.40	4.50E+00	1.52E-112	Up	-1.97E-01	7.50E-01		1.86E+00	4.41E-08	Up	6.03E-02	9.47E-01		6.66E-01	1.16E-06		4.59E+00	0.00E+00	Up	Unigene25250_All//gi|14532502|gb|AAK63929.1|//1.00E-152//AT3g19970/MZE19_2 [Arabidopsis thaliana] >gi|30102458|gb|AAP21147.1| At3g19970/MZE19_2 [Arabidopsis thaliana]	Unigene25250_All//2.00E-136//AT3G19970| unknown protein	Unigene25250_All//0.00E+00//TC161959				nr -
Unigene25251_All	1101	2.80	1.75	1.06	6.33	5.50	4.14	3.92	9.30	10.06	-6.81E-01	5.42E-02		-1.40E+00	2.82E-04	Down	-2.03E-01	4.16E-01		-6.13E-01	5.25E-03		1.25E+00	1.41E-13	Up	1.36E+00	5.22E-17	Up	Unigene25251_All//gi|226532648|ref|NP_001148060.1|//1.00E-111//MAC/Perforin domain containing protein [Zea mays] >gi|195615564|gb|ACG29612.1| MAC/Perforin domain containing protein [Zea mays]	Unigene25251_All//7.00E-67//AT1G14780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24290.2); Has 119 Blast hits to 118 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 14; Fungi - 0; Plants - 105; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene25251_All//0.00E+00//gi|164331352|gb|ES822479.1|ES822479				nr +
Unigene25252_All	2229	0.73	0.82	0.24	2.41	2.26	1.40	2.83	4.39	6.13	1.69E-01	7.15E-01		-1.61E+00	5.02E-03		-9.77E-02	7.61E-01		-7.88E-01	1.87E-03		6.35E-01	9.92E-05		1.12E+00	1.70E-15	Up	Unigene25252_All//gi|226532648|ref|NP_001148060.1|//0.00E+00//MAC/Perforin domain containing protein [Zea mays] >gi|195615564|gb|ACG29612.1| MAC/Perforin domain containing protein [Zea mays]	Unigene25252_All//3.00E-136//AT1G14780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24290.2); Has 119 Blast hits to 118 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 14; Fungi - 0; Plants - 105; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene25252_All//0.00E+00//TC155025				nr -
Unigene25255_All	1052	19.69	11.27	8.00	10.56	8.87	8.41	3.98	3.06	2.42	-8.05E-01	4.91E-11		-1.30E+00	2.30E-22	Down	-2.51E-01	1.62E-01		-3.28E-01	6.63E-02		-3.79E-01	1.72E-01		-7.15E-01	5.13E-03		Unigene25255_All//gi|297827979|ref|XP_002881872.1|//2.00E-84//peroxisomal membrane 22 kDa family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327711|gb|EFH58131.1| peroxisomal membrane 22 kDa family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25255_All//8.00E-82//AT2G42770| peroxisomal membrane 22 kDa family protein	Unigene25255_All//0.00E+00//TC138471		ko04146|Peroxisome		nr +
Unigene25256_All	1360	43.40	13.93	19.11	57.62	74.24	43.40	9.51	0.74	2.84	-1.64E+00	8.61E-92	Down	-1.18E+00	2.76E-54	Down	3.66E-01	7.57E-15		-4.09E-01	5.19E-13		-3.69E+00	5.48E-63	Down	-1.74E+00	2.89E-28	Down	Unigene25256_All//gi|15225423|ref|NP_179668.1|//1.00E-104//ATEXPB1 (ARABIDOPSIS THALIANA EXPANSIN B1) [Arabidopsis thaliana] >gi|20138056|sp|Q9SKU2.1|EXPB1_ARATH RecName: Full=Expansin-B1; Short=At-EXPB1; AltName: Full=Beta-expansin-1; AltName: Full=Ath-ExpBeta-1.5; Flags: Precursor >gi|4454473|gb|AAD20920.1| beta-expansin pollen allergen protein [Arabidopsis thaliana] >gi|21536717|gb|AAM61049.1| beta-expansin 1 precursor (At-EXPB1) (Ath-ExpBeta-1.5) [Arabidopsis thaliana]	Unigene25256_All//8.00E-96//AT2G20750| ATEXPB1 (ARABIDOPSIS THALIANA EXPANSIN B1)	Unigene25256_All//0.00E+00//TC153471				nr -
Unigene25257_All	2310	7.11	5.51	6.50	8.09	6.95	5.92	8.35	3.64	4.54	-3.69E-01	7.76E-03		-1.30E-01	4.04E-01		-2.19E-01	1.01E-01		-4.49E-01	3.46E-04		-1.20E+00	2.01E-23	Down	-8.80E-01	6.99E-15		Unigene25257_All//gi|226528455|ref|NP_001150976.1|//1.00E-101//LOC100284609 [Zea mays]	Unigene25257_All//3.00E-170//AT4G14605| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Mitochodrial transcription termination factor-related (InterPro:IPR003690); BEST Arabidopsis thaliana protein match is: EMB2219 (embryo defective 2219) (TAIR:AT2G21710.1); Has 760 Blast hits to 374 proteins in 45 species: Archae - 0; Bacteria - 0; Metazoa - 99; Fungi - 0; Plants - 624; Viruses - 0; Other Eukaryotes - 37 (source: NCBI BLink).	Unigene25257_All//0.00E+00//gi|31073555|gb|CA993834.1|CA993834				nr +
Unigene25258_All	1808	20.89	20.74	23.94	32.40	31.06	32.67	16.23	10.98	7.62	-1.07E-02	9.28E-01		1.97E-01	2.57E-02		-6.08E-02	4.84E-01		1.21E-02	9.03E-01		-5.64E-01	2.57E-10		-1.09E+00	2.82E-31	Down	Unigene25258_All//gi|297812101|ref|XP_002873934.1|//1.00E-141//carbohydrate kinase family [Arabidopsis lyrata subsp. lyrata] >gi|297319771|gb|EFH50193.1| carbohydrate kinase family [Arabidopsis lyrata subsp. lyrata]	Unigene25258_All//7.00E-140//AT5G19150| carbohydrate kinase family	Unigene25258_All//0.00E+00//TC173732				nr +
Unigene25259_All	822	4.07	0.25	4.79	3.70	1.68	1.26	0.21	0.10	0.00	-4.05E+00	1.20E-14	Down	2.35E-01	4.85E-01		-1.14E+00	6.85E-04	Down	-1.55E+00	2.75E-05	Down	-1.02E+00	6.14E-01		-7.68E+00	1.08E-01		Unigene25259_All//gi|145357661|ref|NP_196152.2|//3.00E-10//DNA binding [Arabidopsis thaliana]	Unigene25259_All//4.00E-11//AT5G05330| DNA binding	Unigene25259_All//4.00E-126//gi|78329027|gb|DT549301.1|DT549301				nr +
Unigene25260_All	864	1.39	1.88	1.29	5.48	4.38	3.97	2.40	0.24	1.01	4.30E-01	3.96E-01		-1.06E-01	8.62E-01		-3.21E-01	2.75E-01		-4.63E-01	1.06E-01		-3.31E+00	1.12E-09	Down	-1.24E+00	1.64E-03		Unigene25260_All//gi|145357661|ref|NP_196152.2|//3.00E-41//DNA binding [Arabidopsis thaliana]	Unigene25260_All//1.00E-37//AT5G05330| DNA binding	Unigene25260_All//0.00E+00//ES827558		ko03410|Base excision repair		nr -
Unigene25263_All	1124	5.40	6.49	6.16	4.96	4.26	3.29	10.83	8.40	4.68	2.66E-01	2.40E-01		1.90E-01	4.39E-01		-2.21E-01	4.26E-01		-5.91E-01	1.88E-02		-3.66E-01	1.29E-02		-1.21E+00	7.94E-16	Down	Unigene25263_All//gi|11074304|gb|AB80452 5.1|//4.00E-69//At5g65400 [Arabidopsis thaliana]	Unigene25263_All//2.00E-61//AT5G65400| unknown protein	Unigene25263_All//7.00E-178//gi|164254980|gb|EV488207.1|EV488207				nr +
Unigene25264_All	1098	0.62	2.82	1.31	1.36	0.85	1.19	4.47	5.33	2.65	2.18E+00	1.21E-07	Up	1.08E+00	6.63E-02		-6.85E-01	1.99E-01		-1.90E-01	7.21E-01		2.55E-01	2.89E-01		-7.54E-01	1.27E-03		Unigene25264_All//gi|11074304|gb|AB80452 5.1|//2.00E-72//At5g65400 [Arabidopsis thaliana]	Unigene25264_All//5.00E-65//AT5G65400| unknown protein	Unigene25264_All//0.00E+00//TC160574				nr -
Unigene25265_All	2046	1.02	1.19	0.70	3.14	2.31	1.57	4.13	2.61	3.39	2.17E-01	5.93E-01		-5.42E-01	2.44E-01		-4.46E-01	5.01E-02		-1.00E+00	1.24E-05	Down	-6.61E-01	1.88E-04		-2.87E-01	1.09E-01		Unigene25265_All//gi|42567734|ref|NP_196398.2|//0.00E+00//SNF2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing protein [Arabidopsis thaliana]	Unigene25265_All//0.00E+00//AT5G07810| SNF2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing protein					nr +
Unigene25266_All	1612	7.56	6.19	9.91	12.08	12.41	8.12	6.58	3.79	2.50	-2.88E-01	8.58E-02		3.90E-01	7.80E-03		3.87E-02	8.32E-01		-5.73E-01	2.33E-06		-7.98E-01	3.65E-07		-1.40E+00	3.65E-17	Down	Unigene25266_All//gi|15235067|ref|NP_193689.1|//2.00E-63//INDL (IND1(IRON-SULFUR PROTEIN REQUIRED FOR NADH DEHYDROGENASE)-LIKE) [Arabidopsis thaliana] >gi|2853081|emb|CAA16931.1| ATP binding protein-like [Arabidopsis thaliana] >gi|7268750|emb|CAB78956.1| ATP binding protein-like [Arabidopsis thaliana] >gi|110737938|dbj|BAF00906.1| ATP binding protein - like [Arabidopsis thaliana]	Unigene25266_All//1.00E-64//AT4G19540| INDL (IND1(IRON-SULFUR PROTEIN REQUIRED FOR NADH DEHYDROGENASE)-LIKE)	Unigene25266_All//0.00E+00//TC168431				nr -

Unigene25267_All	1196	1.88	8.05	2.63	3.04	6.65	7.82	3.96	11.04	11.36	2.10E+00	2.72E-21	Up	4.82E-01	1.98E-01		1.13E+00	1.37E-08	Up	1.36E+00	2.97E-12	Up	1.48E+00	3.48E-22	Up	1.52E+00	3.03E-24	Up	Unigene25267_All//gi|297817792|ref|XP_002876779.1|//5.00E-56//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322617|gb|EFH53038.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene25267_All//1.00E-54//AT2G01818| zinc ion binding	Unigene25267_All//0.00E+00//TC142616				nr -
Unigene25268_All	888	23.51	17.75	16.19	19.19	14.70	17.09	20.71	11.25	7.22	-4.06E-01	7.64E-04		-5.38E-01	1.44E-05		-3.85E-01	2.67E-03		-1.67E-01	2.82E-01		-8.81E-01	7.99E-14		-1.52E+00	7.88E-33	Down	Unigene25268_All//gi|6056421|gb|AAF02885.1|AC009525_19//1.00E-51//Unknown protein [Arabidopsis thaliana] >gi|14423480|gb|AAK62422.1|AF38697 7_1 Unknown protein [Arabidopsis thaliana]	Unigene25268_All//5.00E-50//AT1G02816| unknown protein	Unigene25268_All//0.00E+00//gi|13352116|gb|BG442368.1|BG442368				nr +
Unigene25271_All	625	0.17	0.24	0.43	15.30	4.96	4.05	9.88	14.18	3.12	5.39E-01	7.79E-01		1.35E+00	4.09E-01		-1.63E+00	1.24E-18	Down	-1.92E+00	1.64E-20	Down	5.22E-01	2.60E-03		-1.66E+00	4.58E-13	Down		Unigene25271_All//5.00E-45//PL577709					
Unigene25276_All	1640	7.47	7.85	6.01	14.18	13.25	17.76	16.68	39.12	30.02	7.21E-02	6.69E-01		-3.14E-01	7.38E-02		-9.85E-02	4.73E-01		3.25E-01	1.18E-03		1.23E+00	4.15E-79	Up	8.48E-01	3.09E-34		Unigene25276_All//gi|90398982|emb|CAJ86254.1|//1.00E-122//HB001008.12 [Oryza sativa (indica cultivar-group)]	Unigene25276_All//2.00E-118//AT3G09010| protein kinase family protein	Unigene25276_All//0.00E+00//TC144120		ko04626|Plant-pathogen interaction		nr -
Unigene25277_All	2368	4.99	4.58	3.64	6.54	5.63	3.13	16.44	5.51	11.31	-1.25E-01	4.96E-01		-4.55E-01	8.49E-03		-2.17E-01	1.51E-01		-1.06E+00	6.78E-14	Down	-1.58E+00	2.54E-70	Down	-5.41E-01	6.88E-13		Unigene25277_All//gi|227206194|dbj|BAH57152.1|//1.00E-104//AT3G15095| unknown protein [Arabidopsis thaliana]	Unigene25277_All//2.00E-41//AT3G15095| unknown protein	Unigene25277_All//0.00E+00//gi|78346958|gb|DT567232.1|DT567232				nr -
Unigene25278_All	1446	3.69	2.07	0.85	2.82	3.64	2.53	3.13	2.25	1.32	-8.36E-01	1.22E-03		-2.12E+00	8.74E-12	Down	3.67E-01	1.80E-01		-1.59E-01	6.37E-01		-4.73E-01	6.81E-02		-1.24E+00	1.18E-06	Down	Unigene25278_All//gi|112419535|dbj|BAF02935.1|//1.00E-158//RAD51 homolog [Populus nigra]	Unigene25278_All//1.00E-154//AT5G20850| ATRAD51; ATP binding / DNA binding / DNA-dependent ATPase/ damaged DNA binding / nucleoside-triphosphatase/ nucleotide binding / protein binding / sequence-specific DNA binding	Unigene25278_All//0.00E+00//TC165721		ko03440|Homologous recombination		nr +
Unigene25279_All	1577	3.48	10.60	3.04	12.22	14.00	8.65	15.76	13.30	46.43	1.61E+00	1.42E-25	Up	-1.97E-01	4.87E-01		1.95E-01	1.18E-01		-4.99E-01	4.54E-05		-2.45E-01	1.58E-02		1.56E+00	1.21E-131	Up	Unigene25279_All//gi|156118320|gb|ABU49721.1|//5.00E-89//WRKY transcription factor 2 [Solanum tuberosum]	Unigene25279_All//2.00E-64//AT4G24240| WRKY7; calmodulin binding / transcription factor	Unigene25279_All//0.00E+00//TC139974	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene2528_All	1299	0.28	0.55	1.35	1.07	0.66	0.28	0.62	0.64	0.58	9.54E-01	2.62E-01		2.26E+00	1.32E-04	Up	-6.96E-01	2.12E-01		-1.95E+00	1.43E-03		5.74E-02	9.54E-01		-8.58E-02	9.05E-01		Unigene2528_All//gi|115466456|ref|NP_001056827.1|//5.00E-47//Os06g0151200 [Oryza sativa Japonica Group] >gi|55296621|dbj|BAD69323.1| RNA-binding protein-like [Oryza sativa Japonica Group] >gi|55297274|dbj|BAD69059.1| RNA-binding protein-like [Oryza sativa Japonica Group] >gi|113594867|dbj|BAF18741.1|Os06g0151200 [Oryza sativa Japonica Group]	Unigene2528_All//6.00E-68//AT3G13700| RNA-binding protein, putative	Unigene2528_All//0.00E+00//TC176752				nr +
Unigene25280_All	455	1.15	0.33	0.47	1.31	3.03	5.96	3.16	2.30	1.05	-1.78E+00	1.08E-01		-1.30E+00	2.42E-01		1.20E+00	3.86E-02		2.18E+00	4.91E-07	Up	-4.60E-01	3.83E-01		-1.59E+00	1.64E-03		Unigene25280_All//gi|3334147|sp|Q39799.1|CHI1_GOSHI//5.00E-83//RecName: Full=Endochitinase 1; Flags: Precursor >gi|1469788|gb|AAB67842.1| class I chitinase [Gossypium hirsutum] >gi|298106229|gb|ADI56257.1| class I chitinase [Gossypium hirsutum]	Unigene25280_All//3.00E-58//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene25280_All//0.00E+00//TC130556		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene25281_All	1376	38.21	13.74	26.01	49.38	31.08	73.82	59.89	274.59	58.08	-1.48E+00	2.63E-70	Down	-5.55E-01	1.13E-13		-6.68E-01	2.65E-30		5.80E-01	5.65E-31		2.20E+00	0.00E+00	Up	-4.42E-02	4.73E-01		Unigene25281_All//gi|3334147|sp|Q39799.1|CHI1_GOSHI//0.00E+00//RecName: Full=Endochitinase 1; Flags: Precursor >gi|1469788|gb|AAB67842.1| class I chitinase [Gossypium hirsutum] >gi|298106229|gb|ADI56257.1| class I chitinase [Gossypium hirsutum]	Unigene25281_All//8.00E-114//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene25281_All//0.00E+00//TC130556		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene25284_All	1276	15.54	5.60	9.10	8.39	10.01	7.72	2.85	2.00	2.40	-1.47E+00	7.78E-27	Down	-7.73E-01	1.86E-09		2.54E-01	1.29E-01		-1.21E-01	5.71E-01		-5.12E-01	8.01E-02		-2.45E-01	4.04E-01		Unigene25284_All//gi|74229683|gb|AB000456.1|//1.00E-149//FeSOD [Gossypium hirsutum]	Unigene25284_All//2.00E-110//AT5G23310| FSD3 (FE SUPEROXIDE DISMUTASE 3); superoxide dismutase	Unigene25284_All//0.00E+00//TC133513		ko04146|Peroxisome		nr +
Unigene25286_All	2101	10.61	8.47	12.19	40.07	17.60	16.19	33.49	23.77	32.27	-3.26E-01	5.66E-03		2.01E-01	9.29E-02		-1.19E+00	1.42E-99	Down	-1.31E+00	2.15E-101	Down	-4.94E-01	9.58E-19		-5.32E-02	4.12E-01		Unigene25286_All//gi|16930479|gb|AAL31925.1|AF419593_1 At2g39210/T16B24.15 [Arabidopsis thaliana] >gi|34020841|gb|AAC28987.1| nodulin-like protein [Arabidopsis thaliana]	Unigene25286_All//0.00E+00//AT2G39210| nodulin family protein	Unigene25286_All//0.00E+00//DW498332				nr -
Unigene25287_All	2300	2.32	0.55	1.07	17.39	8.95	5.97	1.93	1.84	0.61	-2.07E+00	4.89E-12	Down	-1.12E+00	4.20E-05	Down	-9.58E-01	2.32E-33		-1.54E+00	4.81E-62	Down	-7.27E-02	7.95E-01		-1.67E+00	1.04E-09	Down	Unigene25287_All//gi|253740260|gb|ACT34764.1|//0.00E+00//subtilisin-like protease preproenzyme [Nicotiana tabacum]	Unigene25287_All//2.00E-167//AT5G67090| subtilase family protein	Unigene25287_All//0.00E+00//TC166251				nr -
Unigene25290_All	688	13.38	15.83	8.82	13.11	11.51	15.10	20.16	12.82	5.33	2.43E-01	1.87E-01		-6.01E-01	2.27E-03		-1.87E-01	3.87E-01		2.04E-01	3.14E-01		-6.53E-01	1.17E-06		-1.92E+00	2.12E-34	Down	Unigene25290_All//gi|29468343|gb|AA085511.1|//6.00E-57//CSN8 [Nicotiana benthamiana]	Unigene25290_All//2.00E-54//AT4G14110| COP9 (CONSTITUTIVE PHOTOMORPHOGENIC 9); metalloendopeptidase/ protein binding	Unigene25290_All//0.00E+00//TC172116				nr -
Unigene25291_All	736	5.47	12.39	7.38	12.12	14.36	7.67	14.94	6.98	6.33	1.18E+00	3.14E-09	Up	4.31E-01	1.16E-01		2.46E-01	1.97E-01		-6.59E-01	4.85E-04		-1.10E+00	5.40E-12	Down	-1.24E+00	7.69E-15	Down	Unigene25291_All//gi|29468343|gb|AA085511.1|//9.00E-84//CSN8 [Nicotiana benthamiana]	Unigene25291_All//3.00E-80//AT4G14110| COP9 (CONSTITUTIVE PHOTOMORPHOGENIC 9); metalloendopeptidase/ protein binding	Unigene25291_All//0.00E+00//TC172116				nr +
Unigene25294_All	1853	4.12	4.13	1.81	12.23	11.13	16.26	11.93	39.63	17.57	2.30E-03	9.91E-01		-1.19E+00	1.41E-07	Down	-1.36E-01	3.06E-01		4.10E-01	1.99E-05		1.73E+00	2.39E-150	Up	5.58E-01	1.85E-11		Unigene25294_All//gi|84514139|gb|ABC39078.1|//0.00E+00//cytochrome P450 monooxygenase CYP72A59 [Medicago truncatula]	Unigene25294_All//5.00E-170//AT3G14690| CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene25294_All//0.00E+00//CO075207		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00906|Carotenoid biosynthesis		nr +
Unigene25298_All	1756	2.41	3.81	2.00	2.04	1.76	4.01	4.14	8.45	6.10	6.58E-01	3.79E-03		-2.70E-01	3.86E-01		-2.11E-01	5.57E-01		9.74E-01	8.84E-06		1.03E+00	2.15E-14	Up	5.59E-01	2.17E-04		Unigene25298_All//gi|42572523|ref|NP_974357.1|//1.00E-146//RSY3 (RASPBERRY 3); ATP binding / ligase, forming carbon-nitrogen bonds / nucleotide binding [Arabidopsis thaliana]	Unigene25298_All//2.00E-147//AT3G24560| RSY3 (RASPBERRY 3)					nr +
Unigene253_All	393	1.33	3.48	1.90	1.77	2.45	1.61	3.87	1.49	0.91	1.39E+00	1.95E-02		5.11E-01	5.47E-01		4.67E-01	5.47E-01		-1.41E-01	8.66E-01		-1.38E+00	5.25E-03		-2.09E+00	6.46E-05	Down	Unigene253_All//gi|18652508|gb|AAL77142.1|AC097447_8//4.00E-41//Putative myosin-like protein [Oryza sativa Japonica Group]	Unigene253_All//7.00E-36//AT1G19835| unknown protein	Unigene253_All//6.00E-139//gi|78350729|gb|DT571003.1|DT571003				nr -
Unigene2530_All	1261	27.14	50.31	29.05	29.27	38.83	33.77	34.87	33.31	16.30	8.91E-01	5.77E-38		9.85E-02	3.59E-01		4.08E-01	5.26E-09		2.06E-01	1.50E-02		-6.60E-02	4.52E-01		-1.10E+00	6.73E-47	Down	Unigene2530_All//gi|75161363|sp|Q8VXU6.1|DI194_ARATH//2.00E-71//RecName: Full=Protein DEHYDRATION-INDUCED 19 homolog 4; Short=AtDi19-4 >gi|18377875|gb|AAL67123.1|AT3g06760/F3E22_10 [Arabidopsis thaliana] >gi|22137252|gb|AAM91471.1|AT3g06760/F3E22_10 [Arabidopsis thaliana]	Unigene2530_All//4.00E-59//AT3G06760| INVOLVED IN: response to water deprivation; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Drought induced 19 (InterPro:IPR008598); BEST Arabidopsis thaliana protein match is: HRB1 (HYPERSENSITIVE TO RED AND BLUE); protein binding (TAIR:AT5G49230.1); Has 133 Blast hits to 133 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 6; Fungi - 0; Plants - 127; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene2530_All//0.00E+00//TC138461				nr +
Unigene25300_All	1021	2.41	8.09	4.17	3.95	4.86	4.78	2.32	6.18	2.89	1.75E+00	1.48E-14	Up	7.93E-01	9.73E-03		2.97E-01	3.11E-01		2.74E-01	3.80E-01		1.41E+00	2.42E-10	Up	3.16E-01	3.48E-01		Unigene25300_All//gi|9651530|gb|AAF91178.1|AF203700_1//1.00E-107//ClpB [Phaseolus lunatus]	Unigene25300_All//7.00E-98//AT2G25140| CLPB4 (CASEIN LYTIC PROTEINASE B4); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding					nr -
Unigene25301_All	1773	6.49	1.51	1.83	27.14	19.66	10.98	1.69	2.22	5.42	-2.10E+00	1.51E-25	Down	-1.83E+00	1.96E-20	Down	-4.66E-01	2.09E-11		-1.31E+00	5.45E-58	Down	3.88E-01	1.78E-01		1.68E+00	6.83E-20	Up	Unigene25301_All//gi|30684004|ref|NP_193466.2|//2.00E-87//phosphoinositide binding [Arabidopsis thaliana] >gi|54608486|gb|AAY34771.1|At4g17350 [Arabidopsis thaliana] >gi|98960971|gb|ABF58969.1|At4g17350 [Arabidopsis thaliana]	Unigene25301_All//3.00E-66//AT5G47440| phosphoinositide binding	Unigene25301_All//0.00E+00//DR457190				nr +
Unigene25303_All	1378	2.01	6.43	2.13	1.81	2.27	2.69	8.13	60.09	77.10	1.68E+00	9.69E-15	Up	7.89E-02	8.31E-01		3.31E-01	3.95E-01		5.72E-01	8.03E-02		2.89E+00	0.00E+00	Up	3.25E+00	0.00E+00	Up	Unigene25303_All//gi|297802270|ref|XP_002869019.1|//4.00E-91//transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297314855|gb|EFH45278.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene25303_All//8.00E-98//AT2G23790| unknown protein	Unigene25303_All//0.00E+00//TC149751				nr +
Unigene25304_All	2482	0.76	12.25	0.77	2.11	4.97	4.26	4.07	6.35	29.61	4.01E+00	1.59E-127	Up	2.54E-02	9.76E-01		1.24E+00	5.20E-15	Up	1.01E+00	7.09E-09	Up	6.41E-01	3.13E-07		2.86E+00	8.49E-285	Up	Unigene25304_All//gi|15228781|ref|NP_191154.1|//0.00E+00//CCR3 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 3); kinase [Arabidopsis thaliana] >gi|75335634|sp|Q9LY50.1|ACCR3_ARATH RecName: Full=Putative serine/threonine-protein kinase-like protein CCR3; AltName: Full=Protein CRINKLY 4 RELATED 3; Short=AtCRR3; Flags: Precursor >gi|7573490|emb|CAB87849.1| receptor kinase-like protein [Arabidopsis thaliana]	Unigene25304_All//0.00E+00//AT3G55950| CCR3 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 3); kinase	Unigene25304_All//0.00E+00//TC155100				nr +
Unigene25306_All	472	3.55	2.68	4.29	21.32	12.18	8.13	3.76	2.39	0.34	-4.02E-01	4.19E-01		2.73E-01	5.85E-01		-8.07E-01	1.17E-06		-1.39E+00	9.23E-14	Down	-6.54E-01	1.39E-01		-3.48E+00	4.53E-09	Down			Unigene25306_All//1.00E-106//TC149648				
Unigene25307_All	1355	9.19	5.05	4.21	52.31	35.63	16.23	6.58	1.79	1.38	-8.64E-01	9.59E-08		-1.13E+00	4.70E-11	Down	-5.54E-01	1.11E-22		-1.69E+00	5.62E-125	Down	-1.88E+00	3.96E-21	Down	-2.25E+00	2.30E-27	Down	Unigene25307_All//gi|124359162|gb|ABN05685.1|//3.00E-53//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene25307_All//7.00E-20//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene25307_All//0.00E+00//TC149648				nr -

Unigene25309_All	1330	4.13	3.39	3.72	5.62	4.74	4.31	7.15	2.67	2.67	-2.85E-01	2.85E-01		-1.50E-01	6.22E-01		-2.46E-01	2.93E-01		-3.82E-01	8.49E-02		-1.42E+00	2.54E-15	Down	-1.42E+00	7.21E-16	Down	Unigene25309_All//gi|68146569|emb|CAI91280.1|//1.00E-175//deoxyhypusine synthase [Crotalaria scassellatii]	Unigene25309_All//2.00E-168//AT5G05920| DHS (DEOXYHYPUSINE SYNTHASE)					nr +
Unigene2531_All	2253	6.41	7.11	7.26	10.24	8.76	9.84	10.55	4.49	6.37	1.49E-01	3.41E-01		1.79E-01	2.48E-01		-2.25E-01	5.30E-02		-5.67E-02	6.98E-01		-1.23E+00	6.26E-30	Down	-7.28E-01	2.39E-13		Unigene2531_All//gi|30695996|ref|NP_175965.2|//1.00E-137//SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana]	Unigene2531_All//1.00E-122//AT1G55690| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene2531_All//0.00E+00//gi|164255546|gb|ES811859.1|ES811859				nr +
Unigene25310_All	1133	4.43	4.47	4.37	133.57	122.70	103.04	38.40	8.56	11.01	1.26E-02	9.85E-01		-2.04E-02	9.62E-01		-1.23E-01	3.01E-03		-3.74E-01	5.94E-21		-2.17E+00	1.67E-120	Down	-1.80E+00	1.70E-97	Down	Unigene25310_All//gi|297797657|ref|XP_002866713.1|//1.00E-129//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297312548|gb|EFH42972.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene25310_All//9.00E-127//AT5G67210| unknown protein	Unigene25310_All//0.00E+00//TC150886				nr -
Unigene25312_All	915	7.49	18.05	10.01	35.33	42.94	66.59	59.38	66.74	70.01	1.27E+00	5.63E-18	Up	4.18E-01	3.84E-02		2.81E-01	5.80E-04		9.14E-01	7.53E-41		1.69E-01	7.35E-03		2.38E-01	3.97E-05		Unigene25312_All//gi|224056695|ref|XP_002298977.1|//2.00E-77//metal tolerance protein [Populus trichocarpa] >gi|222846235|gb|EEE83782.1| metal tolerance protein [Populus trichocarpa]	Unigene25312_All//3.00E-65//AT2G46800| ZAT (ZINC TRANSPORTER OF ARABIDOPSIS THALIANA); inorganic anion transmembrane transporter/ metal ion transmembrane transporter/ zinc ion transmembrane transporter	Unigene25312_All//0.00E+00//gi|84145696|gb|DN759938.1|DN759938				nr -
Unigene25314_All	986	4.40	11.36	3.73	6.26	6.67	7.60	5.19	11.70	11.56	1.37E+00	7.79E-14	Up	-2.41E-01	4.42E-01		9.05E-02	7.69E-01		2.79E-01	2.29E-01		1.17E+00	7.31E-14	Up	1.16E+00	9.76E-14	Up	Unigene25314_All//gi|168029039|ref|XP_001767034.1|//7.00E-61//BAH-PHD domain-containing protein [Physcomitrella patens subsp. patens] >gi|162681776|gb|EDQ68200.1| BAH-PHD domain-containing protein [Physcomitrella patens subsp. patens]	Unigene25314_All//3.00E-55//AT4G39100| SHL1 (short life); transcription factor/ zinc-mediated transcriptional activator	Unigene25314_All//0.00E+00//DW501028				nr +
Unigene25315_All	2659	8.26	4.15	6.51	15.04	11.28	6.98	2.50	0.47	0.52	-9.92E-01	2.96E-16		-3.45E-01	5.16E-03		-4.15E-01	7.46E-08		-1.11E+00	2.72E-37	Down	-2.40E+00	1.86E-21	Down	-2.25E+00	1.49E-20	Down	Unigene25315_All//gi|297720101|ref|NP_001172412.1|//1.00E-112//Os01g0550600 [Oryza sativa Japonica Group] >gi|255673350|dbj|BAH91142.1| Os01g0550600 [Oryza sativa Japonica Group]	Unigene25315_All//1.00E-135//AT5G53020| unknown protein	Unigene25315_All//0.00E+00//TC138857				nr +
Unigene25318_All	1142	37.48	44.55	48.63	75.42	68.60	77.63	86.67	67.89	39.73	2.49E-01	9.36E-04		3.76E-01	2.18E-07		-1.37E-01	1.65E-02		4.17E-02	5.72E-01		-3.52E-01	2.76E-14		-1.13E+00	7.92E-109	Down	Unigene25318_All//gi|295687227|gb|ADG27839.1|//5.00E-48//eukaryotic translation initiation factor 5A [Gossypium hirsutum]	Unigene25318_All//8.00E-43//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor	Unigene25318_All//0.00E+00//gi|13350299|gb|BG440648.1|BG440648				nr +
Unigene2532_All	2531	0.81	1.00	0.76	1.44	1.66	1.73	1.37	0.43	0.96	3.12E-01	4.38E-01		-9.01E-02	8.43E-01		2.08E-01	5.42E-01		2.69E-01	4.08E-01		-1.67E+00	1.68E-07	Down	-5.13E-01	7.46E-02		Unigene2532_All//gi|30695991|ref|NP_849815.1|//0.00E+00//SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|30695993|ref|NP_849816.1| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|63003750|gb|AAY25404.1| At1g55690 [Arabidopsis thaliana] >gi|209414534|gb|ACI46507.1| At1g55690 [Arabidopsis thaliana]	Unigene2532_All//0.00E+00//AT1G5590| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene2532_All//0.00E+00//gi|164255546|gb|ES811859.1|ES811859				nr +
Unigene25320_All	1849	0.85	0.16	0.46	3.85	6.13	4.62	7.13	2.31	2.80	-2.37E+00	1.25E-04	Down	-8.82E-01	1.13E-01		6.69E-01	2.54E-05		2.61E-01	2.29E-01		-1.63E+00	1.92E-25	Down	-1.35E+00	5.05E-20	Down	Unigene25320_All//gi|224139208|ref|XP_002326795.1|//0.00E+00//condensin complex components subunit [Populus trichocarpa] >gi|222834117|gb|EEE72594.1| condensin complex components subunit [Populus trichocarpa]	Unigene25320_All//0.00E+00//AT5G62410| SMC2 (STRUCTURAL MAINTENANCE OF CHROMOSOMES 2); transporter	Unigene25320_All//0.00E+00//gi|109850162|gb|DW479141.1|DW479141				nr -
Unigene25321_All	1001	2.35	2.58	4.31	9.11	4.54	4.74	2.70	1.09	1.47	1.34E-01	7.23E-01		8.73E-01	4.13E-03		-1.00E+00	1.42E-08	Down	-9.43E-01	5.10E-07		-1.32E+00	1.83E-04	Down	-8.76E-01	7.80E-03		Unigene25321_All//gi|124359162|gb|ABN05685.1|//2.00E-07//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene25321_All//7.00E-33//ES829487				nr +
Unigene25322_All	1454	2.34	2.20	2.97	5.41	4.14	2.14	1.08	1.29	1.12	-9.14E-02	7.78E-01		3.43E-01	2.78E-01		-3.85E-01	6.08E-02		-1.34E+00	2.73E-10	Down	2.66E-01	5.75E-01		6.23E-02	9.07E-01		Unigene25322_All//gi|140053549|gb|ABO80476.1|//1.00E-34//RNA-directed DNA polymerase , related [Medicago truncatula]	Unigene25322_All//3.00E-24//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene25322_All//1.00E-32//ES829487				nr +
Unigene25323_All	2134	29.81	11.63	23.03	31.35	30.34	18.90	4.72	3.13	3.06	-1.36E+00	6.77E-75	Down	-3.72E-01	3.23E-08		-4.74E-02	5.66E-01		-7.30E-01	6.37E-31		-5.90E-01	2.37E-04		-6.23E-01	6.73E-05		Unigene25323_All//gi|145340395|ref|NP_193399.3|//1.00E-131//MRH1 (morphogenesis of root hair 1); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|26350646|sp|C0LGQ4.1|MRH1_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase MRH1; AltName: Full=Protein MORPHOGENESIS OF ROOT HAIR 1; Flags: Precursor >gi|224589612|gb|ACN59339.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene25323_All//1.00E-117//AT5G07150| leucine-rich repeat family protein	Unigene25323_All//0.00E+00//TC152866		ko04626|Plant-pathogen interaction		nr -
Unigene25325_All	2547	85.39	29.01	44.70	27.21	23.92	19.77	16.12	10.52	10.70	-1.56E+00	0.00E+00	Down	-9.34E-01	2.10E-135		-1.86E-01	2.48E-03		-4.61E-01	2.74E-14		-6.16E-01	2.20E-16		-5.91E-01	9.28E-16		Unigene25325_All//gi|38327302|gb|AAR17698.1|//0.00E+00//GTP-binding protein TypA [Trifolium pratense]	Unigene25325_All//0.00E+00//AT5G13650| elongation factor family protein	Unigene25325_All//0.00E+00//TC152507				nr -
Unigene25326_All	1517	2.97	2.81	1.26	3.15	4.52	4.79	8.22	5.37	6.64	-8.02E-02	7.79E-01		-1.23E+00	5.45E-05	Down	5.19E-01	1.84E-02		6.05E-01	5.06E-03		-6.14E-01	1.59E-05		-3.07E-01	3.05E-02		Unigene25326_All//gi|297603691|ref|NP_001054442.2|//3.00E-40//Os05g0110700 [Oryza sativa Japonica Group] >gi|255675950|dbj|BAF16356.2| Os05g0110700 [Oryza sativa Japonica Group]	Unigene25326_All//1.00E-66//AT3G48210| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Kinetochore-Ndc80 complex, subunit Spc25 (InterPro:IPR013255); Has 142 Blast hits to 142 proteins in 51 species: Archae - 0; Bacteria - 2; Metazoa - 61; Fungi - 34; Plants - 34; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).					nr +
Unigene2533_All	2691	0.45	0.43	0.57	0.50	0.74	0.79	0.46	0.09	0.27	-4.62E-02	9.51E-01		3.60E-01	5.20E-01		5.71E-01	2.32E-01		6.58E-01	1.50E-01		-2.29E+00	2.57E-04	Down	-7.74E-01	1.40E-01		Unigene2533_All//gi|30695991|ref|NP_849815.1|//0.00E+00//SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|30695993|ref|NP_849816.1| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|63003750|gb|AAY25404.1| At1g55690 [Arabidopsis thaliana] >gi|209414534|gb|ACI46507.1| At1g55690 [Arabidopsis thaliana]	Unigene2533_All//0.00E+00//AT1G5590| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene2533_All//0.00E+00//DN804597				nr +
Unigene25330_All	250	0.00	2.84	0.00	1.99	4.13	5.78	8.46	4.68	10.20	1.15E+01	3.33E-04	Up	null	null		1.05E+00	1.37E-01		1.54E+00	8.56E-03		-8.53E-01	3.12E-02		2.70E-01	4.62E-01		Unigene25330_All//gi|111183356|gb|ABH07935.1|//1.00E-12//ethylene receptor [Ziziphus jujuba]	Unigene25330_All//4.00E-05//AT3G23150| ETR2 (ethylene response 2); ethylene binding / glycogen synthase kinase 3/ protein histidine kinase/ receptor	Unigene25330_All//1.00E-09//TC131832	Orphans			nr -
Unigene25333_All	1404	4.47	6.50	3.83	6.35	6.03	6.14	2.23	4.76	5.33	5.39E-01	4.78E-03		-2.23E-01	3.96E-01		-7.40E-02	7.72E-01		-4.78E-02	8.32E-01		1.10E+00	1.37E-07	Up	1.26E+00	1.48E-10	Up	Unigene25333_All//gi|56126414|gb|AAV76001.1|//1.00E-62//cyclin dependent kinase inhibitor [Euphorbia esula]	Unigene25333_All//4.00E-39//AT2G32710| KRP4; cyclin binding / cyclin-dependent protein kinase inhibitor	Unigene25333_All//0.00E+00//ES799800				nr -
Unigene25334_All	1475	4.86	2.10	1.88	7.84	7.84	7.84	7.74	2.86	4.54	-1.21E+00	9.05E-08	Down	-1.37E+00	8.88E-09	Down	1.70E-03	9.98E-01		6.00E-04	9.99E-01		-1.44E+00	1.71E-18	Down	-7.70E-01	1.71E-07		Unigene25334_All//gi|9294423|dbj|BAB02543.1|//1.00E-170//mitotic checkpoint protein [Arabidopsis thaliana]	Unigene25334_All//1.00E-166//AT1G49910| WD-40 repeat family protein / mitotic checkpoint protein, putative	Unigene25334_All//0.00E+00//gi|78339352|gb|DT559626.1|DT559626				nr -
Unigene25336_All	2080	1.11	1.12	0.97	9.87	11.13	9.10	5.85	2.53	1.67	1.79E-02	9.86E-01		-1.86E-01	6.58E-01		1.73E-01	1.65E-01		-1.17E-01	4.21E-01		-1.21E+00	2.71E-15	Down	-1.81E+00	4.29E-28	Down	Unigene25336_All//gi|115448541|ref|NP_001048050.1|//1.00E-134//Os02g0736100 [Oryza sativa Japonica Group] >gi|113537581|dbj|BAF09964.1| Os02g0736100 [Oryza sativa Japonica Group]	Unigene25336_All//9.00E-126//AT4G17220| ATMAP70-5 (microtubule-associated proteins 70-5); microtubule binding	Unigene25336_All//0.00E+00//gi|84145930|gb|DN760172.1|DN760172				nr -
Unigene25339_All	2037	5.32	19.23	10.01	9.10	9.60	12.62	12.83	33.90	48.46	1.85E+00	4.14E-72	Up	9.13E-01	1.01E-12		7.79E-02	6.03E-01		4.72E-01	6.53E-06		1.40E+00	5.20E-104	Up	1.92E+00	8.61E-237	Up	Unigene25339_All//gi|99646741|emb|CAK22423.1|//0.00E+00//regulator of chromosome condensation family protein [Beta vulgaris]	Unigene25339_All//4.00E-174//AT5G11580| UVB-resistance protein-related / regulator of chromosome condensation (RCC1) family protein	Unigene25339_All//0.00E+00//TC143578		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene2534_All	2296	9.30	4.13	5.66	8.37	6.87	6.71	6.92	4.79	5.19	-1.17E+00	1.77E-20	Down	-7.16E-01	5.73E-09		-2.86E-01	2.15E-02		-3.20E-01	1.22E-02		-5.32E-01	1.84E-05		-4.16E-01	6.19E-04		Unigene2534_All//gi|297843864|ref|XP_002889813.1|//0.00E+00//EMB2004 [Arabidopsis lyrata subsp. lyrata] >gi|297335655|gb|EFH66072.1| EMB2004 [Arabidopsis lyrata subsp. lyrata]	Unigene2534_All//0.00E+00//AT1G10510| emb2004 (embryo defective 2004)	Unigene2534_All//0.00E+00//TC172054				nr +
Unigene25342_All	1729	19.00	18.11	50.54	13.80	16.13	66.87	16.73	2.05	7.12	-6.94E-02	5.28E-01		1.41E+00	1.30E-105	Up	2.25E-01	3.15E-02		2.28E+00	9.56E-297	Up	-3.03E+00	3.91E-117	Down	-1.23E+00	2.44E-37	Down	Unigene25342_All//gi|255762735|gb|ACU33178.1|//0.00E+00//cytochrome P450 71 family protein [Solanum lycopersicum]	Unigene25342_All//1.00E-96//AT3G26310| CYP71B35; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene25342_All//0.00E+00//gi|164273263|gb|ES802071.1|ES802071		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene25344_All	1646	19.26	8.68	16.31	3.81	3.20	2.55	0.10	0.30	0.19	-1.15E+00	3.49E-29	Down	-2.41E-01	2.01E-02		-2.53E-01	3.19E-01		-5.80E-01	1.36E-02		1.57E+00	1.18E-01		9.15E-01	4.53E-01		Unigene25344_All//gi|225445308|ref|XP_002281353.1|//0.00E+00//FREDICTED: similar to HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101); ATP binding [Vitis vinifera]	Unigene25344_All//0.00E+00//AT3G24430| HCF101 (HIGH-CHLOROPHYLL-FLUORESCENCE 101); ATP binding	Unigene25344_All//0.00E+00//TC131767				nr +

Unigene25346_All	262	1.40	2.71	1.22	0.38	0.26	0.69	4.03	15.00	3.19	9.54E-01	2.62E-01		-1.97E-01	8.66E-01		-5.33E-01	8.16E-01		8.58E-01	6.95E-01		1.89E+00	8.65E-10	Up	-3.37E-01	5.77E-01			Unigene25346_All//1.00E-86//TC177420					
Unigene25347_All	1020	4.57	12.57	5.95	4.00	6.11	8.68	51.19	101.99	85.73	1.46E+00	2.58E-17	Up	3.83E-01	1.38E-01		6.10E-01	7.89E-03		1.12E+00	1.10E-08	Up	9.94E-01	6.74E-91		7.44E-01	3.79E-48		Unigene25347_All//gi|222423859|dbj|BAH19894.1|/2.00E-25//AT5G14420 [Arabidopsis thaliana]	Unigene25347_All//1.00E-23//AT5G14420| RGLG2 (RING domain Ligase2); ubiquitin-protein ligase	Unigene25347_All//0.00E+00//DW500485				nr -
Unigene25352_All	1124	4.98	144.75	41.64	21.94	62.44	78.84	9.40	12.83	7.16	4.86E+00	0.00E+00	Up	3.06E+00	2.24E-152	Up	1.51E+00	1.19E-113	Up	1.85E+00	1.86E-173	Up	4.48E-01	6.82E-04		-3.93E-01	1.04E-02		Unigene25352_All//gi|108385250|gb|ABF85766.1|/2.00E-45//At3g48510 [Arabidopsis thaliana]	Unigene25352_All//1.00E-26//AT5G63350| unknown protein	Unigene25352_All//0.00E+00//TC171088				nr +
Unigene25355_All	1347	2.72	2.63	1.23	5.21	6.60	6.30	12.43	12.66	14.64	-4.63E-02	8.93E-01		-1.15E+00	7.42E-04	Down	3.39E-01	8.82E-02		2.74E-01	2.11E-01		2.64E-02	8.57E-01		2.36E-01	3.57E-02		Unigene25355_All//gi|1087073|gb|AAB34987.1|/1.00E-175//calmodulin-binding heat-shock protein [Nicotiana tabacum]	Unigene25355_All//6.00E-151//AT5G37710| lipase class 3 family protein / calmodulin-binding heat-shock protein, putative	Unigene25355_All//0.00E+00//gi|109859821|gb|DW488800.1|DW488800				nr +
Unigene25356_All	1856	2.11	0.85	1.21	3.76	3.19	3.50	4.10	3.78	4.31	-1.32E+00	3.73E-05	Down	-8.11E-01	1.20E-02		-2.36E-01	3.21E-01		-1.01E-01	6.71E-01		-1.16E-01	6.23E-01		7.34E-02	7.10E-01		Unigene25356_All//gi|1087073|gb|AAB34987.1|/0.00E+00//calmodulin-binding heat-shock protein [Nicotiana tabacum]	Unigene25356_All//2.00E-173//AT5G37710| lipase class 3 family protein / calmodulin-binding heat-shock protein, putative	Unigene25356_All//0.00E+00//TC132301				nr -
Unigene2536_All	2464	3.86	25.68	4.95	5.24	8.19	9.51	25.70	29.43	85.58	2.73E+00	8.32E-187	Up	3.57E-01	3.96E-02		6.45E-01	1.56E-08		8.61E-01	1.44E-14		1.95E-01	4.98E-04		1.74E+00	0.00E+00	Up	Unigene2536_All//gi|153850908|gb|ABS52644.1|/0.00E+00//neutral invertase [Vitis vinifera]	Unigene2536_All//0.00E+00//AT3G06500| beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative	Unigene2536_All//0.00E+00//TC141310				nr -
Unigene25361_All	1337	31.27	26.79	32.26	7.19	9.43	6.76	0.98	1.75	2.89	-2.23E-01	8.76E-03		4.51E-02	6.24E-01		3.91E-01	1.25E-02		-9.00E-02	6.94E-01		8.37E-01	2.46E-02		1.56E+00	9.47E-08	Up	Unigene25361_All//gi|58531976|emb|CAE03618.3|/1.00E-132//OSJNBa0003B01.9 [Oryza sativa (japonica cultivar-group)] >gi|116310870|emb|CAH67811.1|OSIGBa0138H21-OSIGBa0138E01.2 [Oryza sativa (indica cultivar-group)]	Unigene25361_All//3.00E-118//AT2G21960| unknown protein	Unigene25361_All//0.00E+00//TC144790				nr +
Unigene25364_All	2448	4.32	1.84	0.91	56.88	30.71	20.16	10.00	5.99	6.62	-1.23E+00	2.76E-11	Down	-2.24E+00	2.15E-24	Down	-8.89E-01	7.36E-102		-1.50E+00	1.49E-205	Down	-7.39E-01	1.28E-13		-5.94E-01	7.58E-10		Unigene25364_All//gi|115439837|ref|NP_001041198.1|/1.00E-103//0s01g0739700 [Oryza sativa Japonica Group] >gi|113533729|dbj|BAF06112.1|Os01g0739700 [Oryza sativa Japonica Group]	Unigene25364_All//8.00E-97//AT4G29360| glycosyl hydrolase family 17 protein	Unigene25364_All//0.00E+00//TC130707		ko00500|Starch and sucrose metabolism		nr -
Unigene25366_All	1289	17.09	11.52	11.77	19.98	19.50	16.61	5.25	1.91	2.84	-5.69E-01	1.04E-06		-5.38E-01	7.99E-06		-3.49E-02	8.14E-01		-2.67E-01	1.54E-02		-1.46E+00	1.66E-11	Down	-8.84E-01	7.63E-06		Unigene25366_All//gi|297602586|ref|NP_001052602.2|/1.00E-109//0s04g0381400 [Oryza sativa Japonica Group] >gi|38346635|emb|CAD40743.2|OSJNBa0072D21.5 [Oryza sativa (japonica cultivar-group)] >gi|255675399|dbj|BAF14516.2|Os04g0381400 [Oryza sativa Japonica Group]	Unigene25366_All//8.00E-84//AT5G38360| catalytic					nr +
Unigene25367_All	1346	0.54	4.44	1.35	2.78	1.77	3.59	11.47	34.16	80.62	3.03E+00	4.44E-20	Up	1.31E+00	1.21E-02		-6.53E-01	3.13E-02		3.71E-01	2.09E-01		1.57E+00	1.78E-82	Up	2.81E+00	0.00E+00	Up	Unigene25367_All//gi|228480908|gb|ACQ42220.1|/2.00E-98//R2R3 transcription factor MYB108-like protein 1 [Vitis vinifera]	Unigene25367_All//6.00E-69//AT3G06490| MYB108 (myb domain protein 108); DNA binding / transcription factor	Unigene25367_All//0.00E+00//gi|78345617|gb|DT565891.1|DT565891	MYB			nr +
Unigene25369_All	1228	437.87	288.63	228.96	202.95	171.70	154.06	57.50	20.01	26.96	-6.01E-01	1.87E-160		-9.35E-01	0.00E+00		-2.41E-01	7.84E-17		-3.98E-01	3.84E-38		-1.52E+00	1.81E-120	Down	-1.09E+00	2.62E-74	Down	Unigene25369_All//gi|20269059|emb|CAC84710.1|/2.00E-97//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene25369_All//2.00E-85//AT4G14550| IAA14 (INDOLE-3-ACETIC ACID INDUCIBLE 14); protein binding / transcription factor/ transcription repressor	Unigene25369_All//0.00E+00//gi|31406891|gb|CD485926.1|CD485926				nr -
Unigene2537_All	1554	5.99	14.44	10.83	14.52	16.15	18.80	14.64	17.43	11.41	1.27E+00	3.64E-24	Up	8.53E-01	1.56E-09		1.54E-01	2.07E-01		3.73E-01	1.54E-04		2.52E-01	8.85E-03		-3.60E-01	3.33E-04		Unigene2537_All//gi|240255344|ref|NP_566479.5|/1.00E-95//oxidoreductase [Arabidopsis thaliana]	Unigene2537_All//6.00E-97//AT3G14160| oxidoreductase	Unigene2537_All//0.00E+00//gi|78327600|gb|DT547874.1|DT547874				nr +
Unigene25372_All	1820	4.48	4.59	2.81	4.54	4.92	6.55	11.27	15.04	25.85	3.47E-02	8.76E-01		-6.75E-01	1.36E-03		1.15E-01	6.12E-01		5.28E-01	1.13E-03		4.17E-01	6.40E-06		1.20E+00	3.78E-57	Up	Unigene25372_All//gi|20146108|dbj|BAB88943.1|/1.00E-153//protein phosphatase 2C [Mesembryanthemum crystallinum]	Unigene25372_All//1.00E-129//AT2G25620| protein phosphatase 2C, putative / PP2C, putative	Unigene25372_All//0.00E+00//gi|109885130|gb|DW514100.1|DW514100	DBP			nr +
Unigene25373_All	2065	7.70	7.24	6.47	11.68	12.87	11.11	64.66	21.80	104.22	-8.96E-02	5.86E-01		-2.51E-01	1.03E-01		1.41E-01	2.37E-01		-7.16E-02	6.35E-01		-1.57E+00	1.92E-237	Down	6.89E-01	1.57E-102		Unigene25373_All//gi|16417946|gb|AAL18925.1|AF429384_1/1.00E-144//mevalonate kinase [Hevea brasiliensis] >gi|164601974|dbj|BAF98283.1|mevalonate kinase [Hevea brasiliensis]	Unigene25373_All//4.00E-121//AT5G27450| MK (MEVALONATE KINASE); mevalonate kinase	Unigene25373_All//0.00E+00//TC146423		ko04146|Peroxisome//ko00900|Terpenoid backbone biosynthesis		nr -
Unigene25374_All	1630	6.61	5.72	4.31	6.27	5.73	8.40	0.75	2.51	66.11	-2.09E-01	2.60E-01		-6.17E-01	6.15E-04		-1.30E-01	5.57E-01		4.22E-01	5.58E-03		1.74E+00	3.77E-09	Up	6.46E+00	0.00E+00	Up	Unigene25374_All//gi|297843036|ref|XP_002889399.1|/1.00E-159//glycerol-3-phosphate acyltransferase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297335241|gb|EFH65658.1|glycerol-3-phosphate acyltransferase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene25374_All//3.00E-154//AT1G02390| GPAT2 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 2); acyltransferase	Unigene25374_All//0.00E+00//CO070826		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr +
Unigene25375_All	1007	27.95	34.82	25.33	43.48	39.56	41.13	16.54	11.37	8.15	3.17E-01	5.24E-04		-1.42E-01	2.35E-01		-1.36E-01	1.16E-01		-8.03E-02	4.16E-01		-5.41E-01	8.04E-06		-1.02E+00	2.10E-16	Down			Unigene25375_All//0.00E+00//ES823720				
Unigene25379_All	955	9.70	4.78	3.74	18.15	9.95	17.26	12.79	7.70	6.63	-1.02E+00	1.24E-07	Down	-1.38E+00	3.34E-11	Down	-8.67E-01	1.83E-12		-7.26E-02	6.59E-01		-7.32E-01	4.15E-07		-9.48E-01	6.03E-11		Unigene25379_All//gi|297596476|ref|NP_001042641.2|/2.00E-29//Os01g0259900 [Oryza sativa Japonica Group] >gi|255673077|dbj|BAF04555.2|Os01g0259900 [Oryza sativa Japonica Group]	Unigene25379_All//4.00E-22//AT5G64680| unknown protein	Unigene25379_All//0.00E+00//TC144870				nr +
Unigene2538_All	477	1.76	0.96	0.67	2.40	1.59	1.33	3.63	0.44	0.75	-8.76E-01	2.47E-01		-1.39E+00	9.66E-02		-5.97E-01	3.41E-01		-8.58E-01	1.93E-01		-3.05E+00	1.18E-07	Down	-2.27E+00	5.17E-06	Down	Unigene2538_All//gi|124360144|gb|AB008160.1|/2.00E-39//Heat shock protein DnaJ [Medicago truncatula]	Unigene2538_All//1.00E-35//AT3G04980| DNAJ heat shock N-terminal domain-containing protein	Unigene2538_All//3.00E-169//TC143078		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene25382_All	1104	3.89	3.81	5.45	5.78	7.27	6.83	3.75	2.50	1.80	-2.88E-02	9.38E-01		4.88E-01	5.54E-02		3.32E-01	1.20E-01		2.42E-01	3.11E-01		-5.87E-01	2.86E-02		-1.06E+00	5.80E-05	Down	Unigene25382_All//gi|115451691|ref|NP_001049446.1|/3.00E-19//Os03g0227500 [Oryza sativa Japonica Group] >gi|108706962|gb|ABF94757.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547917|dbj|BAF11360.1|Os03g0227500 [Oryza sativa Japonica Group]	Unigene25382_All//3.00E-14//AT1G20460| unknown protein	Unigene25382_All//0.00E+00//TC142501				nr +
Unigene25383_All	1250	34.99	27.89	29.86	42.32	43.64	52.50	35.99	27.35	16.57	-3.27E-01	4.84E-05		-2.29E-01	7.97E-03		4.41E-02	6.17E-01		3.11E-01	8.03E-07		-3.96E-01	1.93E-08		-1.12E+00	1.75E-49	Down	Unigene25383_All//gi|18401792|ref|NP_566599.1|/1.00E-100//MOS4 (Modifier of snc1,4) [Arabidopsis thaliana] >gi|75164860|sp|Q94959.1|SPF27_ARATH RecName: Full=Pre-mRNA-splicing factor SPF27 homolog; AltName: Full=Modifier of SNC1 member 4; AltName: Full=Protein BCAS2 homolog >gi|152014429|gb|ABS20115.1|modifier of SNC1 [Arabidopsis thaliana]	Unigene25383_All//4.00E-101//AT3G18165| MOS4 (Modifier of snc1,4)	Unigene25383_All//0.00E+00//TC144657		ko03040|Spliceosome		nr +
Unigene25385_All	1223	45.43	84.39	71.28	65.98	68.96	89.11	17.18	44.15	21.53	8.93E-01	1.16E-61		6.50E-01	2.34E-29		6.35E-02	3.56E-01		4.33E-01	9.46E-20		1.36E+00	5.38E-78	Up	3.26E-01	4.64E-04		Unigene25385_All//gi|115477851|ref|NP_001062521.1|/4.00E-65//Os08g0562600 [Oryza sativa Japonica Group] >gi|113624490|dbj|BAF24435.1|Os08g0562600 [Oryza sativa Japonica Group]	Unigene25385_All//7.00E-45//AT5G23950| C2 domain-containing protein	Unigene25385_All//0.00E+00//DW503601				nr -
Unigene25386_All	1447	2.49	1.33	1.73	7.33	5.90	3.43	1.90	2.17	1.51	-9.07E-01	5.17E-03		-5.29E-01	1.26E-01		-3.13E-01	7.72E-02		-1.09E+00	3.95E-10	Down	1.90E-01	6.11E-01		-3.27E-01	3.46E-01		Unigene25386_All//gi|239056163|emb|CAQ58594.1|/1.00E-68//KANADI like transcription factor [Vitis vinifera]	Unigene25386_All//4.00E-45//AT5G16560| KAN (KANADI); transcription factor	Unigene25386_All//0.00E+00//TC170310	G2-like			nr -
Unigene25387_All	945	31.72	69.49	43.67	32.95	58.81	89.32	50.60	61.43	65.05	1.13E+00	6.22E-58	Up	4.61E-01	5.93E-08		8.36E-01	2.08E-35		1.44E+00	7.85E-116	Up	2.80E-01	6.21E-06		3.62E-01	6.41E-10		Unigene25387_All//gi|75334257|sp|Q9FRL3.1|ERDL6_ARATH//2.00E-82//RecName: Full=Sugar transporter ERD6-like 6 >gi|15724240|gb|AAL06513.1|AF412060_1 At1g75220/F22H5_6 [Arabidopsis thaliana] >gi|21700861|gb|AAMT0554.1|At1g75220/F22H5_6 [Arabidopsis thaliana]	Unigene25387_All//2.00E-74//AT1G75220| integral membrane protein, putative	Unigene25387_All//0.00E+00//DW516027				nr -
Unigene25388_All	1705	20.01	8.44	14.34	16.36	14.26	13.35	6.15	4.61	3.67	-1.25E+00	1.78E-35	Down	-4.81E-01	3.58E-07		-1.98E-01	6.14E-02		-2.93E-01	4.59E-03		-4.16E-01	8.90E-03		-7.45E-01	1.28E-06		Unigene25388_All//gi|18415415|ref|NP_567592.1|/2.00E-53//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|15451112|gb|AAK96827.1|Unknown protein [Arabidopsis thaliana]	Unigene25388_All//3.00E-46//AT4G19985| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene25388_All//0.00E+00//TC156393				nr -
Unigene2539_All	774	1.76	0.52	2.61	4.51	2.45	1.87	2.57	1.08	1.65	-1.75E+00	4.61E-03		5.73E-01	2.38E-01		-8.81E-01	4.46E-03		-1.27E+00	1.32E-04	Down	-1.25E+00	2.79E-03		-6.40E-01	1.05E-01		Unigene2539_All//gi|102139803|gb|ABF69988.1|/5.00E-46//heat shock protein DnaJ N-terminal domain-containing protein [Musa acuminata]	Unigene2539_All//1.00E-33//AT3G06340| DNAJ heat shock N-terminal domain-containing protein	Unigene2539_All//6.00E-113//ES852177		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene25390_All	1560	1.51	4.29	2.49	18.01	18.01	16.88	7.59	1.61	1.51	1.51E+00	8.70E-10	Up	7.23E-01	2.53E-02		2.00E-04	9.98E-01		-9.36E-02	4.59E-01		-2.24E+00	1.13E-34	Down	-2.33E+00	1.36E-37	Down	Unigene25390_All//gi|162459967|ref|NP_001105928.1|/0.00E+00//brittle stalk2 [Zea mays] >gi|116563464|gb|ABJ99754.1|brittle stalk-2 [Zea mays] >gi|195635919|gb|ACG37428.1|COBRA-like protein 4 precursor [Zea mays]	Unigene25390_All//3.00E-126//AT1G09790| COBL6 (COBRA-LIKE PROTEIN 6 PRECURSOR)	Unigene25390_All//0.00E+00//TC141403				nr +
Unigene25393_All	506	0.21	0.00	0.00	0.39	0.88	2.05	1.09	12.89	2.20	-7.69E+00	3.72E-01		-7.69E+00	3.94E-01		1.17E+00	3.47E-01		2.38E+00	2.54E-03		3.57E+00	4.94E-31	Up	1.02E+00	6.87E-02		Unigene25393_All//gi|168032240|ref|XP_001768627.1|/9.00E-06//predicted protein [Physcomitrella patens subsp. patens] >gi|162680126|gb|EDQ66565.1|predicted protein [Physcomitrella patens subsp. patens]	Unigene25393_All//1.00E-65//AT3G58270| meprin and TRAF homology domain-containing protein / MATH domain-containing protein	Unigene25393_All//2.00E-19//TC178833				nr +
Unigene25394_All	1140	1.38	1.33	1.07	10.01	16.13	42.03	18.77	233.10	29.95	-4.63E-02	9.40E-01		-3.58E-01	5.20E-01		6.89E-01	1.04E-08		2.07E+00	2.60E-109	Up	3.63E+00	0.00E+00	Up	6.74E-01	1.94E-16		Unigene25394_All//gi|164605535|dbj|BAF98601.1|/1.00E-26//CM0545.290.nc [Lotus japonicus]	Unigene25394_All//3.00E-26//AT5G06600| UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene25394_All//2.00E-150//DT461777				nr +

Unigene25395_All	2541	12.21	9.91	10.90	23.86	23.43	20.74	28.30	17.09	13.88	-3.01E-01	2.17E-03		-1.64E-01	1.39E-01		-2.61E-02	7.94E-01		-2.02E-01	3.30E-03		-7.28E-01	1.93E-37		-1.03E+00	1.32E-68	Down	Unigene25395_All//gi|297844510|ref|XP_002890136.1|//0.00E+00//XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335978|gb|EFH66395.1| XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene25395_All//3.00E-161//AT1G15910| XH/XS domain-containing protein / XS zinc finger domain-containing protein	Unigene25395_All//0.00E+00//TC148433				nr -
Unigene25397_All	506	0.52	0.50	0.84	3.64	3.13	1.96	4.85	1.82	3.39	-4.62E-02	9.87E-01		7.04E-01	5.54E-01		-2.19E-01	6.59E-01		-8.91E-01	6.61E-02		-1.42E+00	1.67E-04	Down	-5.18E-01	1.41E-01		Unigene25397_All//gi|284026888|gb|AD866335.1|//9.00E-28//CC-NBS-LRR protein [Quercus suber]	Unigene25397_All//2.00E-13//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene25397_All//2.00E-121//TC176306				nr -
Unigene25399_All	600	1.57	0.42	2.57	5.48	4.19	1.51	1.48	0.91	1.53	-1.89E+00	1.53E-02		7.13E-01	2.04E-01		-3.87E-01	2.77E-01		-1.86E+00	3.73E-07	Down	-7.09E-01	2.97E-01		4.54E-02	9.63E-01		Unigene25399_All//gi|284026888|gb|AD866335.1|//4.00E-18//CC-NBS-LRR protein [Quercus suber]		Unigene25399_All//4.00E-101//TC176306				nr -
Unigene254_All	1335	1.02	2.09	1.44	4.78	4.80	7.85	4.62	1.91	4.27	1.03E+00	6.58E-03		4.95E-01	3.22E-01		6.50E-03	9.88E-01		7.17E-01	3.45E-05		-1.28E+00	8.68E-09	Down	-1.16E-01	6.15E-01		Unigene254_All//gi|75169070|sp|Q9C698.1|FPP6_ARATH//1.00E-160//RecName: Full=Filament-like plant protein 6; Short=AtFPP6 >gi|12328626|gb|AAG51782.1|AC07967 9_2 mysoin-like protein; 11013-7318 [Arabidopsis thaliana]	Unigene254_All//1.00E-150//AT1G47900| unknown protein	Unigene254_All//0.00E+00//gi|78350729|gb|DT571003.1|DT571003				nr -
Unigene2540_All	1414	0.74	0.36	0.38	2.18	1.61	1.60	3.17	0.98	0.59	-1.05E+00	1.20E-01		-9.75E-01	1.67E-01		-4.43E-01	2.21E-01		-4.52E-01	2.28E-01		-1.70E+00	1.14E-09	Down	-2.42E+00	2.36E-15	Down	Unigene2540_All//gi|297813015|ref|XP_002874391.1|//2.00E-56//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297320228|gb|EFH50650.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2540_All//1.00E-46//AT5G27240| DNAJ heat shock N-terminal domain-containing protein	Unigene2540_All//0.00E+00//TC143078		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene25401_All	1628	19.15	13.91	15.86	17.90	16.60	19.23	16.34	9.86	7.63	-4.61E-01	1.64E-06		-2.72E-01	8.25E-03		-1.08E-01	3.53E-01		1.03E-01	3.89E-01		-7.29E-01	2.16E-14		-1.10E+00	9.82E-29	Down	Unigene25401_All//gi|8439539|gb|AAF74980.1|AF082890|//0.00E+00//cystathionine beta-lyase [Solanum tuberosum]	Unigene25401_All//1.00E-176//AT3G57050| CBL (cystathionine beta-lyase); cystathionine beta-lyase	Unigene25401_All//0.00E+00//DW236740		ko00270|Cysteine and methionine metabolism//ko00910|Nitrogen metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr -
Unigene25402_All	1468	45.23	36.79	46.07	44.28	44.97	41.19	43.37	22.09	17.50	-2.98E-01	3.64E-06		2.65E-02	7.22E-01		2.21E-02	8.17E-01		-1.04E-01	1.62E-01		-9.73E-01	4.53E-54		-1.31E+00	3.90E-89	Down	Unigene25402_All//gi|12585330|sp|Q92SQ4.1|PGMC_POPTN//0.00E+00//RecName: Full=Phosphoglucomutase, cytoplasmic; Short=PGM; AltName: Full=Glucose phosphomutase >gi|4234941|gb|AAD13031.1| cytosolic phosphoglucomutase [Populus tremula x Populus tremuloides]	Unigene25402_All//0.00E+00//AT1G23190| phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative	Unigene25402_All//0.00E+00//TC131004		ko00500|Starch and sucrose metabolism//ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene25404_All	1020	14.77	130.35	20.41	47.08	36.46	95.51	171.11	173.99	118.19	3.14E+00	0.00E+00	Up	4.67E-01	1.82E-04		-3.69E-01	1.45E-07		1.02E+00	5.50E-78	Up	2.40E-02	6.14E-01		-5.34E-01	2.25E-53		Unigene25404_All//gi|167427545|gb|AB280409.1|//2.00E-83//hairpin-inducing protein [Casuarina glauca]	Unigene25404_All//6.00E-58//AT5G06320| NHL3	Unigene25404_All//0.00E+00//gi|109877916|gb|DW506889.1|DW506889		ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport		nr +
Unigene25405_All	279	3.38	3.27	0.00	4.11	3.95	1.62	0.61	0.15	0.29	-4.63E-02	9.60E-01		-1.17E+01	3.35E-05	Down	-5.62E-02	9.17E-01		-1.34E+00	4.01E-02		-2.02E+00	3.67E-01		-1.09E+00	5.53E-01		Unigene25405_All//gi|4204763|gb|AAD11483.1|//3.00E-20//peroxidase [Glycine max]	Unigene25405_All//7.00E-15//AT5G51890| peroxidase	Unigene25405_All//8.00E-45//TC147725		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene25406_All	690	5.54	6.68	7.87	64.54	79.90	47.59	8.82	3.39	4.33	2.72E-01	3.73E-01		5.08E-01	5.96E-02		3.08E-01	3.47E-06		-4.40E-01	1.07E-08		-1.38E+00	1.12E-09	Down	-1.03E+00	1.31E-06	Down	Unigene25406_All//gi|225626265|gb|ACN97182.1|//1.00E-52//peroxidase [Populus trichocarpa]	Unigene25406_All//2.00E-43//AT5G42180| peroxidase 64 (PER64) (P64) (PRX64)	Unigene25406_All//2.00E-146//TC147725		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene25407_All	1364	4.37	1.93	3.75	151.93	160.39	123.44	15.47	7.14	5.84	-1.18E+00	2.43E-06	Down	-2.23E-01	3.95E-01		7.82E-02	3.13E-02		-3.00E-01	6.59E-19		-1.12E+00	7.18E-23	Down	-1.40E+00	1.85E-33	Down	Unigene25407_All//gi|225626265|gb|ACN97182.1|//1.00E-144//peroxidase [Populus trichocarpa]	Unigene25407_All//3.00E-117//AT5G42180| peroxidase 64 (PER64) (P64) (PRX64)	Unigene25407_All//0.00E+00//TC147725		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene2541_All	2052	1.35	3.58	1.76	3.84	2.75	8.72	7.95	25.03	20.40	1.41E+00	1.04E-09	Up	3.85E-01	2.65E-01		-4.79E-01	1.61E-02		1.18E+00	1.42E-18	Up	1.65E+00	8.84E-99	Up	1.36E+00	8.37E-62	Up	Unigene2541_All//gi|86279632|gb|AB C94471.1|//0.00E+00//type 1 diacylglycerol acyltransferase [Vernicia fordii] >gi|86279634|gb|ABC94472.1| type 1 diacylglycerol acyltransferase [Vernicia fordii]	Unigene2541_All//0.00E+00//AT2G19450| TAG1 (TRIACYLGLYCEROL BIOSYNTHESIS DEFECT 1); diacylglycerol O-acyltransferase	Unigene2541_All//0.00E+00//gi|73863702|gb|DT466441.1|DT466441		ko00561|Glycerolipid metabolism		nr -
Unigene25410_All	1221	5.61	3.07	4.49	4.00	2.51	5.03	2.80	2.50	0.78	-8.70E-01	1.10E-04		-3.22E-01	1.89E-01		-6.72E-01	8.92E-03		3.31E-01	2.00E-01		-1.67E-01	6.45E-01		-1.84E+00	1.16E-08	Down	Unigene25410_All//gi|225436865|ref|XP_002272498.1|//1.00E-88//PREDICTED: similar to F16N3.14 [Vitis vinifera]	Unigene25410_All//5.00E-88//AT4G31050| lipoyltransferase (LIP2p)	Unigene25410_All//0.00E+00//AI728636		ko00785|Lipoic acid metabolism		nr -
Unigene25412_All	1401	5.34	12.41	6.69	11.31	16.20	14.80	6.22	3.85	6.11	1.22E+00	1.05E-17	Up	3.25E-01	1.11E-01		5.19E-01	1.26E-06		3.88E-01	1.22E-03		-6.92E-01	7.00E-05		-2.41E-02	9.14E-01		Unigene25412_All//gi|227202770|dbj|BAH56858.1|//3.00E-95//AT1G78150 [Arabidopsis thaliana]	Unigene25412_All//1.00E-96//AT1G78150| unknown protein	Unigene25412_All//0.00E+00//gi|78327849|gb|DT548123.1|DT548123				nr +
Unigene25415_All	1626	2.28	0.62	2.95	27.20	21.14	19.80	136.46	73.57	207.06	-1.87E+00	1.28E-07	Down	3.68E-01	2.21E-01		-3.64E-01	7.32E-07		-4.58E-01	2.89E-09		-8.91E-01	4.14E-161		6.02E-01	5.62E-126		Unigene25415_All//gi|297833008|ref|XP_002884386.1|//1.00E-171//phosphoesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330226|gb|EFH60645.1| phosphoesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25415_All//6.00E-172//AT3G03520| phosphoesterase family protein	Unigene25415_All//0.00E+00//TC150855		ko00564|Glycerophospholipid metabolism//ko00562|Inositol phosphate metabolism//ko00565|Ether lipid metabolism		nr +
Unigene25416_All	1407	4.76	4.36	4.28	16.43	18.80	12.04	17.28	8.73	8.35	-1.27E-01	5.93E-01		-1.54E-01	5.56E-01		1.94E-01	8.20E-02		-4.49E-01	5.26E-05		-9.84E-01	1.56E-21		-1.05E+00	1.57E-24	Down	Unigene25416_All//gi|20257219|gb|AAM12952.1|//1.00E-119//auxin-regulated protein [Zinnia violacea]	Unigene25416_All//3.00E-111//AT5G65670| IAA9 (INDOLE-3-ACETIC ACID INDUCIBLE 9); transcription factor	Unigene25416_All//0.00E+00//TC152754				nr -
Unigene25417_All	1528	1.75	2.82	1.67	6.39	5.97	5.08	5.81	2.54	3.21	6.91E-01	1.82E-02		-6.20E-02	8.80E-01		-9.75E-02	6.45E-01		-3.30E-01	8.60E-02		-1.19E+00	3.95E-11	Down	-8.58E-01	4.60E-07		Unigene25417_All//gi|20257219|gb|AAM12952.1|//1.00E-119//auxin-regulated protein [Zinnia violacea]	Unigene25417_All//3.00E-111//AT5G65670| IAA9 (INDOLE-3-ACETIC ACID INDUCIBLE 9); transcription factor	Unigene25417_All//0.00E+00//TC152754				nr +
Unigene25418_All	2299	0.82	1.10	1.07	5.44	4.21	2.79	15.74	13.69	4.64	4.28E-01	2.94E-01		3.79E-01	3.96E-01		-3.70E-01	1.75E-02		-9.63E-01	1.06E-09		-2.02E-01	1.56E-02		-1.76E+00	1.18E-78	Down	Unigene25418_All//gi|224102357|ref|XP_002312648.1|//1.00E-180//type-b response regulator [Populus trichocarpa] >gi|222852468|gb|EEE90015.1| type-b response regulator [Populus trichocarpa]	Unigene25418_All//1.00E-116//AT1G67710| ARR11 (RESPONSE REGULATOR 11); transcription factor/ two-component response regulator	Unigene25418_All//0.00E+00//TC162706	ARR-B	ko04712|Circadian rhythm - plant		nr -
Unigene2542_All	2295	8.14	44.93	21.09	11.94	17.62	17.16	18.68	26.97	20.15	2.46E+00	7.26E-271	Up	1.37E+00	2.65E-56	Up	5.61E-01	4.47E-13		5.24E-01	2.22E-10		5.30E-01	1.04E-18		1.10E-01	1.47E-01		Unigene2542_All//gi|22329080|ref|NP_194952.2|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|30689316|ref|NP_849560.1| protein kinase family protein [Arabidopsis thaliana] >gi|79326108|ref|NP_001031769.1| protein kinase family protein [Arabidopsis thaliana] >gi|21703136|gb|AAM74508.1| AT4g32250/F10M8_110 [Arabidopsis thaliana] >gi|24111389|gb|AAN46821.1| At4g32250/F10M8_110 [Arabidopsis thaliana]	Unigene2542_All//0.00E+00//AT4G32250| protein kinase family protein	Unigene2542_All//0.00E+00//TC136189		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene25420_All	1327	0.91	1.68	1.36	11.26	8.56	7.05	3.22	1.86	1.17	8.90E-01	3.87E-02		5.89E-01	2.42E-01		-3.95E-01	4.22E-03		-6.77E-01	1.50E-06		-7.92E-01	2.45E-03		-1.46E+00	7.58E-08	Down	Unigene25420_All//gi|18413990|ref|NP_567403.1|//1.00E-122//MEE55 (maternal effect embryo arrest 55) [Arabidopsis thaliana]	Unigene25420_All//3.00E-116//AT4G13345| MEE55 (maternal effect embryo arrest 55)				nr -
Unigene25423_All	1418	1.70	0.39	2.10	4.99	2.26	2.26	6.83	2.00	2.30	-2.11E+00	6.17E-06	Down	3.09E-01	4.13E-01		-1.14E+00	2.93E-08	Down	-1.14E+00	2.08E-07	Down	-1.77E+00	4.29E-21	Down	-1.57E+00	1.79E-18	Down	Unigene25423_All//gi|15228027|ref|NP_181819.1|//1.00E-159//ribose-phosphate pyrophosphokinase 4 / phosphoribosyl diphosphate synthetase 4 (PRS4) [Arabidopsis thaliana] >gi|62286916|sp|Q68045.2|KPRS4_ARATH RecName: Full=Ribose-phosphate pyrophosphokinase 4; AltName: Full=Phosphoribosyl pyrophosphate synthase 4 >gi|4902472|emb|CAB43553.1| phosphoribosyl diphosphate synthase [Arabidopsis thaliana]	Unigene25423_All//7.00E-161//AT2G42910| ribose-phosphate pyrophosphokinase 4 / phosphoribosyl diphosphate synthetase 4 (PRS4)	Unigene25423_All//0.00E+00//TC153487		ko00230|Purine metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene25424_All	1679	7.20	5.79	4.66	6.32	4.70	5.41	17.80	8.61	8.61	-3.13E-01	6.22E-02		-6.27E-01	2.01E-04		-4.28E-01	1.09E-02		-2.25E-01	2.46E-01		-1.05E+00	4.86E-29	Down	-1.05E+00	6.63E-30	Down	Unigene25424_All//gi|224108928|ref|XP_002315019.1|//1.00E-64//chorismate mutase [Populus trichocarpa] >gi|222864059|gb|EEF01190.1| chorismate mutase [Populus trichocarpa]	Unigene25424_All//6.00E-63//AT1G69370| CM3 (chorismate mutase 3); chorismate mutase	Unigene25424_All//0.00E+00//ES821004		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene25425_All	1378	0.87	0.07	0.23	0.40	0.50	0.33	1.17	0.97	0.64	-3.57E+00	3.63E-05	Down	-1.91E+00	7.10E-03		3.30E-01	7.52E-01		-2.79E-01	7.57E-01		-2.65E-01	6.15E-01		-8.74E-01	4.99E-02		Unigene25425_All//gi|15222292|ref|NP_177096.1|//1.00E-112//CM3 (chorismate mutase 3); chorismate mutase [Arabidopsis thaliana] >gi|28950893|gb|AAO63370.1| At1g69370 [Arabidopsis thaliana]	Unigene25425_All//5.00E-111//AT1G69370| CM3 (chorismate mutase 3); chorismate mutase	Unigene25425_All//0.00E+00//ES821004		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene25427_All	1479	21.58	90.92	9.83	56.65	59.60	89.56	34.02	34.00	49.97	2.08E+00	7.31E-286	Up	-1.13E+00	1.13E-27	Down	7.33E-02	2.65E-01		6.61E-01	1.27E-50		-1.00E-03	1.02E+00		5.55E-01	1.25E-24		Unigene25427_All//gi|110559491|gb|ABG76000.1|//0.00E+00//GRP-like protein 2 [Gossypium hirsutum]	Unigene25427_All//0.00E+00//AT3G08900| RGF3 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 3); transferase, transferring hexosyl groups	Unigene25427_All//0.00E+00//TC135534				nr +
Unigene25438_All	269	0.39	0.00	0.00	1.85	0.00	0.50	4.72	1.71	0.74	-8.60E+00	3.72E-01		-8.60E+00	3.94E-01		-1.09E+01	8.98E-04	Down	-1.88E+00	1.08E-01		-1.46E+00	8.32E-03		-2.67E+00	2.31E-05	Down			Unigene25438_All//3.00E-112//ES839469				
Unigene25439_All	2003	2.04	0.43	0.82	4.18	3.21	5.07	7.77	2.90	4.71	-2.24E+00	2.92E-10	Down	-1.31E+00	5.82E-05	Down	-3.78E-01	5.68E-02		2.80E-01	1.48E-01		-1.42E+00	1.46E-24	Down	-7.21E-01	6.68E-09		Unigene25439_All//gi|449417589|gb|ABS49119.1|//1.00E-73//At3g59670 [Arabidopsis thaliana]	Unigene25439_All//6.00E-69//AT3G59670| unknown protein	Unigene25439_All//0.00E+00//gi|164308025|gb|ES839469.1|ES839469				nr +
Unigene2544_All	2171	6.82	3.29	3.46	12.30	13.02	7.34	9.62	4.74	4.50	-1.05E+00	3.03E-12	Down	-9.80E-01	1.74E-10		8.25E-02	5.31E-01		-7.44E-01	4.28E-13		-1.02E+00	9.05E-20	Down	-1.10E+00	9.09E-23	Down	Unigene2544_All//gi|55819802|gb|AAV66096.1|//5.00E-61//At5g59830 [Arabidopsis thaliana]	Unigene2544_All//4.00E-77//AT5G13660| unknown protein	Unigene2544_All//0.00E+00//TC164794				nr -
Unigene25440_All	925	14.88	10.52	8.00	27.41	24.05	28.37	53.52	32.49	23.17	-5.00E-01	9.46E-04		-8.95E-01	1.66E-08		-1.89E-01	9.71E-02		4.95E-02	6.92E-01		-7.20E-01	1.41E-25		-1.21E+00	2.37E-61	Down	Unigene25440_All//gi|255957394|emb|CBA13551.1|//1.00E-99//cytosolic chaperonin, delta subunit [Glycine max]	Unigene25440_All//2.00E-65//AT3G18190| chaperonin, putative	Unigene25440_All//0.00E+00//TC142327				nr -
Unigene25442_All	1512	5.88	8.24	4.19	10.74	11.23	11.35	5.01	1.85	3.29	4.87E-01	2.40E-03		-4.89E-01	1.59E-02		6.40E-02	7.20E-01		7.97E-02	6.22E-01		-1.43E+00	1.63E-12	Down	-6.04E-01	9.67E-04		Unigene25442_All//gi|157400520|gb|ABV53914.1|//1.00E-122//GAGA-motif binding transcriptional activator [Populus trichocarpa]	Unigene25442_All//1.00E-103//AT2G21240| BPC4 (BASIC PENTACYSTEINE 4); DNA binding / transcription factor	Unigene25442_All//0.00E+00//TC171838	BBR/BPC			nr +
Unigene25443_All	1421	61.45	60.76	62.58	60.19	54.94	132.44	37.37	42.50	27.14	-1.63E-02	7.99E-01		2.63E-02	6.93E-01		-1.32E-01	2.23E-02		1.14E+00	2.79E-179	Up	1.86E-01	3.02E-03		-4.62E-01	3.77E-13		Unigene25443_All//gi|15235521|ref|NP_194628.1|//7.00E-66//RNA-binding protein-related [Arabidopsis thaliana] >gi|115646852|gb|ABJ17140.1| At4g28990 [Arabidopsis thaliana]	Unigene25443_All//3.00E-36//AT4G28990| RNA-binding protein-related	Unigene25443_All//0.00E+00//gi|78345677|gb|DT565951.1|DT565951				nr -

Unigene25444_All	1125	10.93	12.48	17.09	4.65	7.38	5.50	1.13	2.56	2.69	1.91E-01	2.34E-01		6.45E-01	6.77E-07		6.66E-01	4.95E-04		2.42E-01	3.78E-01		1.19E+00	4.11E-04	Up	1.26E+00	9.33E-05	Up	Unigene25444_All//gi|115457978|ref|NP_001052389.1|//3.00E-46//0s04g0379400 [Oryza sativa Japonica Group] >gi|113564160|dbj|BAF14503.1|Os04g0379400 [Oryza sativa Japonica Group]	Unigene25444_All//2.00E-46//AT4G22830| unknown protein	Unigene25444_All//0.00E+00//gi|109842812|gb|DW241370.1|DW241370				nr -
Unigene25449_All	327	0.64	3.56	1.14	1.52	1.68	1.66	0.65	0.64	0.49	2.48E+00	9.79E-04	Up	8.33E-01	5.16E-01		1.45E-01	9.05E-01		1.22E-01	9.21E-01		-1.66E-02	1.02E+00		-4.08E-01	7.55E-01					Unigene25449_All//0.00E+00//BE053793					
Unigene25451_All	472	0.78	0.97	0.79	0.63	0.36	0.77	1.52	1.06	0.17	3.17E-01	7.44E-01		2.54E-02	1.00E+00		-7.96E-01	5.57E-01		2.74E-01	8.33E-01		-5.19E-01	5.07E-01		-3.17E+00	8.09E-04	Down				Unigene25451_All//2.00E-114//BG445148					
Unigene25452_All	558	21.66	43.59	16.22	27.14	14.69	19.02	6.67	7.79	7.64	1.01E+00	2.59E-18	Up	-4.17E-01	1.51E-02		-8.86E-01	2.46E-11		-5.13E-01	2.62E-04		2.24E-01	4.31E-01		1.96E-01	4.83E-01					Unigene25452_All//0.00E+00//BG445148					
Unigene25453_All	2162	1.14	1.01	0.59	8.62	4.30	3.99	15.41	6.11	12.16	-1.75E-01	6.53E-01		-9.44E-01	2.64E-02		-1.00E+00	5.73E-17	Down	-1.11E+00	9.74E-18	Down	-1.33E+00	4.53E-47	Down	-3.42E-01	2.73E-05		Unigene25453_All//gi|22328918|ref|NP_194254.2|//0.00E+00//SKS1 (SKU5 SIMILAR 1); copper ion binding / oxidoreductase [Arabidopsis thaliana] >gi|38258619|sp|Q8VXX5.1|SKS1_ARATH RecName: Full=Monocopper oxidase-like protein SKS1; Flags: Precursor	Unigene25453_All//0.00E+00//AT4G25240| SKS1 (SKU5 SIMILAR 1); copper ion binding / oxidoreductase	Unigene25453_All//0.00E+00//gi|78343358|gb|DT563632.1|DT563632		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene25456_All	1020	25.96	39.74	35.19	94.40	238.38	118.53	10.53	42.74	5.78	6.15E-01	3.10E-13		4.39E-01	1.82E-06		1.34E+00	0.00E+00	Up	3.28E-01	2.96E-13		2.02E+00	2.97E-110	Up	-8.65E-01	1.81E-08		Unigene25456_All//gi|166203244|gb|AB184662.1|//1.00E-40//transcription factor [Glycine max]	Unigene25456_All//1.00E-34//AT3G56400| WRKY70; transcription factor/ transcription repressor	Unigene25456_All//0.00E+00//TC147331	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene25459_All	1419	14.93	9.07	13.55	11.16	9.20	8.56	6.17	2.86	2.98	-7.19E-01	2.08E-09		-1.41E-01	3.15E-01		-2.80E-01	4.70E-02		-3.83E-01	6.36E-03		-1.11E+00	6.82E-10	Down	-1.05E+00	1.94E-09	Down	Unigene25459_All//gi|14190399|gb|AK55680.1|AF378877_1//8.00E-93//AT3g06200/F28L1_14 [Arabidopsis thaliana] >gi|17386098|gb|AAL38595.1|AF446862_1 AT3g06200/F28L1_14 [Arabidopsis thaliana]	Unigene25459_All//1.00E-87//AT3G06200| guanylate kinase, putative	Unigene25459_All//0.00E+00//EE593128		ko00230|Purine metabolism		nr +
Unigene2546_All	854	12.87	8.43	3.12	27.47	19.64	19.78	27.53	13.75	11.66	-6.11E-01	3.59E-04		-2.05E+00	1.23E-22	Down	-4.85E-01	2.98E-06		-4.74E-01	1.55E-05		-1.00E+00	2.03E-21	Down	-1.24E+00	8.99E-31	Down	Unigene2546_All//gi|15236781|ref|NP_194965.1|//9.00E-62//phosphate translocator-related [Arabidopsis thaliana]	Unigene2546_All//3.00E-41//AT2G25520| phosphate translocator-related	Unigene2546_All//0.00E+00//C0103048				nr -
Unigene25460_All	2117	14.75	12.30	13.43	14.38	16.31	12.84	8.41	5.01	4.18	-2.62E-01	7.94E-03		-1.36E-01	2.32E-01		1.82E-01	5.66E-02		-1.63E-01	1.32E-01		-7.46E-01	2.80E-10		-1.01E+00	3.86E-17	Down	Unigene25460_All//gi|22327657|ref|NP_199707.2|//0.00E+00//5' nucleotidase family protein [Arabidopsis thaliana]	Unigene25460_All//0.00E+00//AT5G48960| 5' nucleotidase family protein	Unigene25460_All//0.00E+00//TC151206				nr -
Unigene25462_All	1780	8.99	18.90	8.91	13.57	11.78	13.35	12.95	13.08	19.25	1.07E+00	1.50E-27	Up	-1.28E-02	9.53E-01		-2.04E-01	7.70E-02		-2.43E-02	8.64E-01		1.48E-02	9.18E-01		5.72E-01	1.53E-12		Unigene25462_All//gi|21553404|gb|AB62497.1|//0.00E+00//26S proteasome regulatory particle chain RPT6-like protein [Arabidopsis thaliana]	Unigene25462_All//0.00E+00//AT4G27680| MSP1 protein, putative / intramitochondrial sorting protein, putative	Unigene25462_All//0.00E+00//TC140555		ko00230|Purine metabolism		nr -
Unigene25463_All	1453	3.06	2.27	1.17	6.55	6.02	4.94	7.04	3.31	3.45	-4.33E-01	1.34E-01		-1.38E+00	9.09E-06	Down	-1.21E-01	5.88E-01		-4.06E-01	3.23E-02		-1.09E+00	4.04E-11	Down	-1.03E+00	1.64E-10	Down	Unigene25463_All//gi|15240163|ref|NP_200929.1|//1.00E-100//SNAP33 (SOLUBLE N-ETHYLMALEIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding [Arabidopsis thaliana] >gi|27805727|sp|Q9STP9.1|SNP33_ARATH RecName: Full=SNAP25 homologous protein SNAP33; Short=AtSNAP33; AltName: Full=Synaptosomal-associated protein SNAP25-like 1; Short=SNAP-25-like protein 1; AltName: Full=Snap25a >gi|5731763|emb|CAB52582.1| SNAP33 protein [Arabidopsis thaliana] >gi|5731764|emb|CAB52583.1| SNAP33B protein [Arabidopsis thaliana] >gi|9759467|dbj|BAB10383.1| SNAP25A protein [Arabidopsis thaliana] >gi|16323047|gb|AAL15258.1| AT5g61210/maf19_210 [Arabidopsis thaliana] >gi|18072736|emb|CAC79615.1| SNAP-25 like protein [Arabidopsis thaliana] >gi|22655332|gb|AAM98258.1| At5g61210/maf19_210 [Arabidopsis thaliana]	Unigene25463_All//1.00E-98//AT5G61210| SNAP33 (SOLUBLE N-ETHYLMALEIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding	Unigene25463_All//8.00E-126//TC146462		ko04130|SNARE interactions in vesicular transport		nr +
Unigene25465_All	848	0.62	4.30	1.57	4.35	5.20	4.10	1.15	0.20	0.42	2.80E+00	1.40E-11	Up	1.35E+00	3.17E-02		2.58E-01	4.29E-01		-8.41E-02	8.03E-01		-2.54E+00	6.41E-04	Down	-1.44E+00	2.09E-02										ESTscan +
Unigene25466_All	848	4.07	16.43	3.58	18.68	21.36	14.43	1.70	0.94	0.80	2.01E+00	5.64E-29	Up	-1.86E-01	6.29E-01		1.93E-01	1.71E-01		-3.72E-01	8.25E-03		-8.56E-01	8.67E-02		-1.09E+00	2.39E-02		Unigene25466_All//gi|117168113|gb|ABK32139.1|//5.00E-06//At4g21865 [Arabidopsis thaliana]	Unigene25466_All//1.00E-05//AT4G21865| unknown protein					nr -
Unigene25467_All	1521	3.23	4.56	1.58	3.21	4.05	3.89	4.89	4.53	4.35	4.97E-01	2.63E-02		-1.04E+00	2.80E-04	Down	3.36E-01	1.81E-01		2.77E-01	3.13E-01		-1.10E-01	6.55E-01		-1.70E-01	4.00E-01		Unigene25467_All//gi|30686371|ref|NP_188811.2|//1.00E-108//APO4 (ACCUMULATION OF PHOTOSYSTEM ONE 4) [Arabidopsis thaliana] >gi|68565079|sp|Q8LS20.2|APO4_ARATH RecName: Full=APO protein 4, mitochondrial; Flags: Precursor >gi|108385418|gb|ABF85786.1| At3g21740 [Arabidopsis thaliana]	Unigene25467_All//1.00E-109//AT3G21740| APO4 (ACCUMULATION OF PHOTOSYSTEM ONE 4)	Unigene25467_All//0.00E+00//TC169727				nr -
Unigene25472_All	1924	6.88	2.95	3.54	0.26	0.64	0.35	53.73	33.48	31.91	-1.22E+00	7.93E-14	Down	-9.58E-01	4.09E-09		1.32E+00	3.54E-02		4.44E-01	6.22E-01		-6.83E-01	7.46E-48		-7.52E-01	4.37E-58		Unigene25472_All//gi|224148020|ref|XP_002336576.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222836229|gb|EEE74650.1| cytochrome P450 [Populus trichocarpa]	Unigene25472_All//3.00E-129//AT5G42650| AOS (ALLENE OXIDE SYNTHASE); allene oxide synthase/ hydro-lyase/ oxygen binding	Unigene25472_All//0.00E+00//TC161797		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene25473_All	2638	0.26	0.25	0.52	7.76	5.61	2.38	9.46	10.62	10.96	-4.61E-02	9.70E-01		1.03E+00	8.63E-02		-4.68E-01	3.25E-05		-1.71E+00	6.68E-37	Down	1.67E-01	9.44E-02		2.13E-01	1.91E-02		Unigene25473_All//gi|225452330|ref|XP_002272711.1|//0.00E+00//PREDICTED: similar to stpk1 protein kinase [Vitis vinifera]	Unigene25473_All//4.00E-176//AT3G27580| ATPK7; kinase/ protein serine/threonine kinase	Unigene25473_All//0.00E+00//ES849907				nr -
Unigene25474_All	1164	37.31	84.28	55.86	38.09	50.74	57.00	73.45	78.60	51.00	1.18E+00	1.17E-91	Up	5.82E-01	3.19E-18		4.14E-01	4.91E-11		5.82E-01	1.62E-20		9.79E-02	6.95E-02		-5.26E-01	5.88E-26		Unigene25474_All//gi|18390626|ref|NP_563762.1|//7.00E-58//VHS domain-containing protein / GAT domain-containing protein [Arabidopsis thaliana] >gi|8844126|gb|AAF80218.1|AC025290_7 Contains similarity to an ADP-ribosylation factor binding protein GGA1 from Homo sapiens gb|AF190882 and contains a VHS PF|00790 domain. EST gb|BE037588 comes from this gene [Arabidopsis thaliana] >gi|15450711|gb|AAK96627.1| At1g06210/F9P14_4 [Arabidopsis thaliana] >gi|23308355|gb|AAN18147.1| At1g06210/F9P14_4 [Arabidopsis thaliana]	Unigene25474_All//4.00E-59//AT1G06210| VHS domain-containing protein / GAT domain-containing protein	Unigene25474_All//0.00E+00//TC157877				nr +
Unigene25475_All	750	6.35	24.39	13.35	9.23	9.78	13.49	9.36	28.76	13.39	1.94E+00	3.96E-36	Up	1.07E+00	2.22E-08	Up	8.31E-02	7.79E-01		5.47E-01	2.15E-03		1.62E+00	1.14E-40	Up	5.16E-01	9.99E-04		Unigene25475_All//gi|297803996|ref|XP_002868882.1|//5.00E-65//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297315718|gb|EFH46141.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene25475_All//1.00E-65//AT4G21580| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene25475_All//0.00E+00//TC138973				nr +
Unigene25476_All	592	4.77	8.99	13.49	5.22	7.33	10.38	3.29	3.95	3.97	9.13E-01	4.65E-04		1.50E+00	4.99E-11	Up	4.90E-01	9.80E-02		9.92E-01	2.92E-05		2.67E-01	5.17E-01		2.73E-01	4.78E-01		Unigene25476_All//gi|76160992|gb|AB40459.1|//5.00E-31//NADPH quinone oxidoreductase-like protein [Solanum tuberosum]	Unigene25476_All//9.00E-29//AT4G21580| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene25476_All//3.00E-163//gi|164280348|gb|ES838373.1|ES838373				nr -
Unigene25477_All	1368	5.78	15.11	12.65	5.13	8.03	10.99	5.41	10.08	6.70	1.39E+00	1.74E-25	Up	1.13E+00	3.15E-15	Up	6.45E-01	6.82E-05		1.10E+00	5.36E-14	Up	8.99E-01	6.78E-11		3.09E-01	7.02E-02		Unigene25477_All//gi|297803996|ref|XP_002868882.1|//1.00E-144//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297315718|gb|EFH46141.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene25477_All//3.00E-144//AT4G21580| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene25477_All//0.00E+00//TC134426				nr -
Unigene25479_All	762	43.60	21.94	20.41	81.00	54.59	81.32	86.89	33.18	32.83	-9.91E-01	4.10E-24		-1.10E+00	3.13E-27	Down	-5.69E-01	9.09E-21		5.70E-03	9.53E-01		-1.39E+00	1.57E-98	Down	-1.40E+00	4.45E-103	Down	Unigene25479_All//gi|76161008|gb|AB40467.1|//1.00E-60//glycoprotein-like protein [Solanum tuberosum]	Unigene25479_All//3.00E-60//AT4G27090| 60S ribosomal protein L14 (RPL14B)	Unigene25479_All//0.00E+00//gi|21094401|gb|BQ406714.1|BQ406714		ko03010|Ribosome		nr +
Unigene2548_All	720	1.02	0.28	0.59	6.16	7.51	5.08	7.58	4.01	3.32	-1.85E+00	4.08E-02		-7.82E-01	3.80E-01		2.86E-01	3.06E-01		-2.77E-01	3.98E-01		-9.19E-01	5.84E-05		-1.19E+00	2.17E-07	Down	Unigene2548_All//gi|224098838|ref|XP_002311286.1|//5.00E-78//ent-kaurene synthase [Populus trichocarpa] >gi|222851106|gb|EEE88653.1| ent-kaurene synthase [Populus trichocarpa]	Unigene2548_All//4.00E-63//AT1G79460| GA2 (GA REQUIRING 2); ent-kaurene synthase	Unigene2548_All//0.00E+00//gi|164291061|gb|ES844936.1|ES844936		ko00904|Diterpenoid biosynthesis//ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis		nr -
Unigene25480_All	1563	16.60	2.66	10.94	29.67	17.10	38.81	7.22	6.12	17.15	-2.64E+00	9.49E-75	Down	-6.02E-01	4.23E-08		-7.95E-01	3.62E-28		3.87E-01	2.97E-09		-2.38E-01	1.43E-01		1.25E+00	4.58E-35	Up	Unigene25480_All//gi|15240534|ref|NP_199780.1|//1.00E-116//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|8978266|dbj|BAA98157.1| anthocyanidin-3-glucoside rhamnosyltransferase-like [Arabidopsis thaliana] >gi|28951061|gb|AAO63454.1| At5g19690 [Arabidopsis thaliana]	Unigene25480_All//7.00E-102//AT5G49690| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene25480_All//0.00E+00//TC165913		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis		nr +
Unigene25481_All	1576	82.00	17.81	42.78	128.68	79.01	109.18	1.05	3.05	0.88	-2.20E+00	1.49E-298	Down	-9.39E-01	2.75E-81		-7.04E-01	1.08E-98		-2.37E-01	4.67E-12		1.54E+00	4.59E-09	Up	-2.42E-01	5.92E-01		Unigene25481_All//gi|15240534|ref|NP_199780.1|//1.00E-125//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|8978266|dbj|BAA98157.1| anthocyanidin-3-glucoside rhamnosyltransferase-like [Arabidopsis thaliana] >gi|28951061|gb|AAO63454.1| At5g19690 [Arabidopsis thaliana]	Unigene25481_All//2.00E-121//AT5G49690| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene25481_All//0.00E+00//TC165913		ko00908|Zeatin biosynthesis		nr -

Unigene25482_All	1989	1.47	0.74	0.51	4.48	3.86	2.29	4.61	1.39	1.66	-9.96E-01	6.75E-03		-1.53E+00	1.38E-04	Down	-2.16E-01	3.15E-01		-9.67E-01	3.78E-07		-1.73E+00	1.66E-19	Down	-1.47E+00	4.44E-16	Down	Unigene25482_All//gi|115463857|ref|NP_001055528.1|//1.00E-156//Os05g0409400 [Oryza sativa Japonica Group] >gi|113579079|dbj|BAF17442.1| Os05g0409400 [Oryza sativa Japonica Group]	Unigene25482_All//3.00E-112//AT5G51600| PLE (PLEIADE); microtubule binding	Unigene25482_All//0.00E+00//ES835970				nr +
Unigene25483_All	1260	3.90	4.14	8.16	5.77	4.21	4.12	5.23	4.44	5.06	8.56E-02	7.46E-01		1.06E+00	1.77E-08	Up	-4.56E-01	3.03E-02		-4.86E-01	2.62E-02		-2.36E-01	2.97E-01		-4.93E-02	8.20E-01		Unigene25483_All//gi|124359162|gb|ABN05885.1|//5.00E-06//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene25483_All//0.00E+00//gi|21093525|gb|BQ405838.1|BQ405838				nr +
Unigene25484_All	1523	3.16	2.69	2.31	4.61	2.78	2.82	2.72	1.81	1.26	-2.30E-01	4.17E-01		-4.54E-01	1.23E-01		-7.30E-01	3.71E-04		-7.11E-01	1.04E-03		-5.87E-01	2.86E-02		-1.12E+00	2.44E-05	Down	Unigene25484_All//gi|33465891|gb|AAQ19327.1|//8.00E-18//bZIP-like protein [Oryza sativa Japonica Group]	Unigene25484_All//3.00E-10//AT4G26090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene25484_All//0.00E+00//gi|21093525|gb|BQ405838.1|BQ405838				nr +
Unigene25485_All	1475	24.94	19.51	29.75	112.39	87.24	70.06	18.23	14.08	6.13	-3.54E-01	6.21E-05		2.55E-01	2.76E-03		-3.65E-01	1.70E-24		-6.82E-01	2.35E-67		-3.72E-01	6.91E-05		-1.57E+00	5.48E-50	Down	Unigene25485_All//gi|225428877|ref|XP_002282482.1|//1.00E-156//PREDICTED: similar to leucine-rich repeat family protein [Vitis vinifera]	Unigene25485_All//9.00E-119//AT3G19320| leucine-rich repeat family protein	Unigene25485_All//0.00E+00//TC137730		ko04626|Plant-pathogen interaction		nr +
Unigene25486_All	1900	0.69	1.52	0.34	1.36	1.69	3.87	3.65	2.13	2.45	1.14E+00	2.36E-03		-1.03E+00	9.64E-02		3.06E-01	4.29E-01		1.51E+00	2.92E-11	Up	-7.74E-01	9.44E-05		-5.73E-01	2.86E-03		Unigene25486_All//gi|168988212|gb|ACA35280.1|//1.00E-116//abscisic acid insensitive [Cucumis sativus]	Unigene25486_All//5.00E-81//AT2G36270| ABI5 (ABA INSENSITIVE 5); DNA binding / transcription activator/ transcription factor	Unigene25486_All//2.00E-10//TC173371	bZIP			nr -
Unigene25488_All	1198	6.11	4.91	6.13	47.94	11.30	21.68	15.11	6.45	1.96	-3.18E-01	1.53E-01		4.60E-03	1.00E+00		-2.09E+00	1.21E-156	Down	-1.15E+00	2.99E-56	Down	-1.23E+00	7.89E-23	Down	-2.94E+00	7.24E-74	Down	Unigene25488_All//gi|297796749|ref|XP_002866259.1|//1.00E-36//ATOFP3/OFP3 [Arabidopsis lyrata subsp. lyrata] >gi|297312094|gb|EFH42518.1| ATOFP3/OFP3 [Arabidopsis lyrata subsp. lyrata]	Unigene25488_All//2.00E-24//AT5G01840| OFP1 (OVATE FAMILY PROTEIN 1); protein binding / transcription repressor	Unigene25488_All//0.00E+00//TC158072				nr -
Unigene2549_All	1975	1.43	0.31	0.86	4.87	4.31	3.29	4.50	1.93	1.88	-2.22E+00	3.19E-07	Down	-7.29E-01	6.23E-02		-1.77E-01	4.01E-01		-5.64E-01	1.97E-03		-1.22E+00	1.46E-11	Down	-1.26E+00	1.74E-12	Down	Unigene2549_All//gi|224098838|ref|XP_002311286.1|//0.00E+00//ent-kaurene synthase [Populus trichocarpa] >gi|222851106|gb|EEE88653.1| ent-kaurene synthase [Populus trichocarpa]	Unigene2549_All//2.00E-169//AT1G79460| GA2 (GA REQUIRING 2); ent-kaurene synthase	Unigene2549_All//0.00E+00//TC179422		ko00904|Diterpenoid biosynthesis		nr -
Unigene25490_All	1333	2.39	0.65	3.52	7.89	3.90	2.30	19.06	11.26	5.17	-1.89E+00	1.03E-06	Down	5.54E-01	5.83E-02		-1.02E+00	5.63E-10	Down	-1.78E+00	2.90E-20	Down	-7.60E-01	8.92E-15		-1.88E+00	1.01E-60	Down	Unigene25490_All//gi|156901569|gb|ABU96774.1|//1.00E-112//bZIP transcription factor [Brassica juncea]	Unigene25490_All//3.00E-104//AT1G22070| TGA3; DNA binding / calmodulin binding / protein binding / transcription factor	Unigene25490_All//0.00E+00//TC137533	bZIP			nr +
Unigene25492_All	226	0.46	0.45	4.95	1.76	2.59	0.80	2.81	0.74	1.41	-4.62E-02	9.89E-01		3.42E+00	1.92E-04	Up	5.55E-01	5.99E-01		-1.14E+00	3.79E-01		-1.92E+00	3.09E-02		-9.93E-01	2.02E-01		Unigene25492_All//gi|115448709|ref|NP_001048134.1|//2.00E-29//Os02g0751100 [Oryza sativa Japonica Group] >gi|46390211|dbj|BAD15642.1| aspartyl protease-like [Oryza sativa Japonica Group] >gi|113537665|dbj|BAF100048.1| Os02g0751100 [Oryza sativa Japonica Group]	Unigene25492_All//1.00E-26//AT5G10080| aspartyl protease family protein	Unigene25492_All//7.00E-125//TC140835				nr -
Unigene25495_All	1154	13.33	9.97	6.97	30.95	37.69	36.08	29.68	3.44	10.18	-4.19E-01	3.39E-03		-9.36E-01	4.06E-10		2.84E-01	2.19E-04		2.21E-01	9.25E-03		-3.11E+00	2.11E-142	Down	-1.54E+00	9.83E-62	Down	Unigene25495_All//gi|18414533|ref|NP_567477.1|//1.00E-94//binding [Arabidopsis thaliana]	Unigene25495_All//2.00E-91//AT4G15830| binding	Unigene25495_All//0.00E+00//TC140160				nr +
Unigene25496_All	1416	0.89	1.00	3.27	0.74	3.09	3.41	33.41	68.54	51.49	1.76E-01	7.33E-01		1.88E+00	6.11E-09	Up	2.06E+00	5.06E-11	Up	2.21E+00	2.56E-12	Up	1.04E+00	8.50E-91	Up	6.24E-01	8.51E-30		Unigene25496_All//gi|115461410|ref|NP_001054305.1|//1.00E-133//Os04g0683800 [Oryza sativa Japonica Group] >gi|32488702|emb|CAE03445.1| OSJNBa0088H09.3 [Oryza sativa (japonica cultivar-group)] >gi|113565876|dbj|BAF16219.1| Os04g0683800 [Oryza sativa Japonica Group]	Unigene25496_All//6.00E-112//AT4G11610| C2 domain-containing protein	Unigene25496_All//5.00E-158//ES800656				nr +
Unigene25498_All	1605	7.73	9.03	10.22	7.36	8.05	7.12	19.12	2.42	5.71	2.25E-01	1.48E-01		4.03E-01	5.07E-03		1.29E-01	5.05E-01		-4.71E-02	8.02E-01		-2.98E+00	1.69E-122	Down	-1.74E+00	6.09E-66	Down	Unigene25498_All//gi|195643822|gb|ACG41379.1|//1.00E-84//dihydroflavonol-4-reductase [Zea mays]	Unigene25498_All//5.00E-67//AT2G23910| cinnamoyl-CoA reductase-related	Unigene25498_All//0.00E+00//TC134705		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene25499_All	1824	0.29	2.14	1.34	0.79	0.98	1.86	1.72	3.25	6.49	2.90E+00	9.29E-13	Up	2.23E+00	4.62E-06	Up	3.10E-01	5.79E-01		1.23E+00	3.11E-04	Up	9.24E-01	2.36E-05		1.92E+00	4.30E-29	Up	Unigene25499_All//gi|22330342|ref|NP_176256.2|//1.00E-162//SWIM zinc finger family protein [Arabidopsis thaliana] >gi|19715655|gb|AAL91647.1| At1g60560/F8A5_10 [Arabidopsis thaliana] >gi|27363242|gb|AAO11540.1| At1g60560/F8A5_10 [Arabidopsis thaliana]	Unigene25499_All//2.00E-156//AT1G60560| SWIM zinc finger family protein					nr +
Unigene2550_All	1603	17.76	38.34	30.99	14.36	15.55	12.99	10.79	8.76	24.08	1.11E+00	1.06E-52	Up	8.04E-01	2.32E-24		1.15E-01	3.75E-01		-1.45E-01	2.74E-01		-3.00E-01	1.42E-02		1.16E+00	1.19E-44	Up	Unigene2550_All//gi|195612254|gb|ACG27957.1|//3.00E-64//salt tolerance-like protein [Zea mays]	Unigene2550_All//4.00E-60//AT4G38960| zinc finger (B-box type) family protein	Unigene2550_All//0.00E+00//gi|54117753|gb|CO493262.1|CO493262	DBB	ko04712|Circadian rhythm - plant		nr +
Unigene25502_All	1370	3.74	4.51	6.49	3.45	4.42	4.58	1.23	1.31	2.47	2.70E-01	2.82E-01		7.94E-01	7.66E-05		3.57E-01	1.58E-01		4.08E-01	9.84E-02		8.76E-02	8.49E-01		1.00E+00	6.60E-04	Up	Unigene25502_All//gi|18411296|ref|NP_567171.1|//2.00E-56//RHB1A; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|42572783|ref|NP_974488.1| RHB1A; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|88193784|gb|ABD42981.1| At4g00335 [Arabidopsis thaliana] >gi|110736762|dbj|BAF00342.1| RING-H2 finger protein RHB1a [Arabidopsis thaliana]	Unigene25502_All//1.00E-57//AT4G00335| RHB1A; protein binding / zinc ion binding	Unigene25502_All//4.00E-155//gi|48780013|gb|CO089379.1|CO089379				nr +
Unigene25503_All	1403	1.23	2.06	1.06	7.31	5.25	3.61	6.39	15.73	2.39	7.42E-01	4.35E-02		-2.12E-01	6.65E-01		-4.78E-01	4.77E-03		-1.02E+00	8.00E-09	Down	1.30E+00	3.71E-30	Up	-1.42E+00	5.77E-15	Down	Unigene25503_All//gi|219879368|gb|ACL51016.1|//1.00E-58//squamosa promoter-binding protein [Citrus trifoliata]	Unigene25503_All//3.00E-41//AT5G50570| squamosa promoter-binding protein, putative	Unigene25503_All//0.00E+00//TC140706	SBP			nr +
Unigene25507_All	1660	4.92	1.98	1.41	10.77	9.90	8.22	11.49	4.51	4.70	-1.31E+00	9.81E-10	Down	-1.80E+00	2.19E-14	Down	-1.23E-01	4.25E-01		-3.91E-01	2.70E-03		-1.35E+00	9.93E-28	Down	-1.29E+00	1.19E-26	Down	Unigene25507_All//gi|224135005|ref|XP_002327543.1|//0.00E+00//nucleosome/chromatin assembly factor group [Populus trichocarpa] >gi|222836097|gb|EEE74518.1| nucleosome/chromatin assembly factor group [Populus trichocarpa]	Unigene25507_All//0.00E+00//AT2G19520| FVE; metal ion binding	Unigene25507_All//0.00E+00//TC149733				nr +
Unigene25508_All	1274	8.99	5.57	9.11	30.62	36.52	26.16	3.02	0.89	0.88	-6.92E-01	3.65E-05		1.88E-02	9.32E-01		2.54E-01	6.90E-04		-2.27E-01	9.89E-03		-1.77E+00	7.61E-09	Down	-1.79E+00	2.81E-09	Down	Unigene25508_All//gi|15227037|ref|NP_180477.1|//1.00E-128//LAC2 (laccase 2); laccase [Arabidopsis thaliana] >gi|75318741|sp|Q81081.1|LAC2_ARATH RecName: Full=Laccase-2; AltName: Full=Benzenediol:oxygen oxidoreductase 2; AltName: Full=Urishiol oxidase 2; AltName: Full=Diphenol oxidase 2; Flags: Precursor	Unigene25508_All//6.00E-130//AT2G29130| LAC2 (laccase 2); laccase	Unigene25508_All//9.00E-79//DW497408		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene2551_All	1861	34.05	22.87	24.04	9.26	11.32	7.06	11.13	3.17	6.87	-5.74E-01	4.83E-18		-5.02E-01	9.82E-14		2.90E-01	1.49E-02		-3.91E-01	3.31E-03		-1.81E+00	7.95E-46	Down	-6.96E-01	6.36E-11		Unigene2551_All//gi|170676246|gb|ACB30362.1|//0.00E+00//transcription factor [Capsicum annuum]	Unigene2551_All//6.00E-155//AT5G54630| zinc finger protein-related	Unigene2551_All//0.00E+00//gi|164354824|gb|ES808225.1|ES808225	C2H2			nr -
Unigene25510_All	1177	3.96	21.91	2.17	8.97	19.08	13.58	33.95	117.93	301.95	2.47E+00	3.08E-68	Up	-8.65E-01	3.04E-03		1.09E+00	3.43E-22	Up	5.98E-01	1.11E-05		1.80E+00	1.13E-298	Up	3.15E+00	0.00E+00	Up	Unigene25510_All//gi|4666360|gb|AAD26942.1|AF119050_1/1.00E-62//zinc-finger protein 1 [Datisca glomerata]	Unigene25510_All//2.00E-41//AT3G19580| AZF2 (ARABIDOPSIS ZINC-FINGER PROTEIN 2); DNA binding / nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding	Unigene25510_All//0.00E+00//gi|78338833|gb|DT559107.1|DT559107	C2H2			nr +
Unigene25511_All	1595	3.77	0.89	0.93	11.59	6.69	5.78	52.70	9.98	15.89	-2.08E+00	1.47E-13	Down	-2.01E+00	2.21E-12	Down	-7.92E-01	2.13E-11		-1.00E+00	5.23E-15	Down	-2.40E+00	1.56E-263	Down	-1.73E+00	3.33E-177	Down	Unigene25511_All//gi|166343841|gb|ABY86663.1|//0.00E+00//beta-tubulin 17 [Gossypium hirsutum]	Unigene25511_All//0.00E+00//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene25511_All//0.00E+00//TC132467		ko04145|Phagosome		nr -
Unigene25513_All	1567	2.04	0.06	0.82	3.31	3.80	1.84	2.43	0.67	1.60	-4.98E+00	9.32E-16	Down	-1.32E+00	4.23E-04	Down	2.02E-01	4.78E-01		-8.42E-01	1.14E-03		-1.86E+00	2.39E-09	Down	-6.00E-01	2.64E-02		Unigene25513_All//gi|145324070|ref|NP_001077624.1|//1.00E-55//DNA binding / catalytic/ nuclease [Arabidopsis thaliana] >gi|166232400|sp|Q8L627.2|EX01_ARATH RecName: Full=Exonuclease 1	Unigene25513_All//5.00E-57//AT1G29630| nuclease	Unigene25513_All//7.00E-108//TC177650		ko03430|Mismatch repair		nr +
Unigene25518_All	860	15.03	12.43	13.56	40.03	28.79	40.44	40.41	37.96	17.83	-2.74E-01	9.43E-02		-1.48E-01	3.98E-01		-4.75E-01	1.28E-08		1.48E-02	9.12E-01		-9.04E-02	3.63E-01		-1.18E+00	8.62E-42	Down			Unigene25518_All//0.00E+00//TC159565				
Unigene25519_All	1166	17.23	12.08	19.82	123.94	95.10	132.70	49.46	14.34	19.13	-5.12E-01	2.86E-05		2.02E-01	1.12E-01		-3.82E-01	3.02E-23		9.86E-02	2.63E-02		-1.79E+00	1.07E-123	Down	-1.37E+00	1.27E-86	Down	Unigene25519_All//gi|157273640|gb|ABV27474.1|//1.00E-146//fasciclin-like arabinogalactan protein 3 [Gossypium hirsutum]	Unigene25519_All//1.00E-50//AT2G04780| FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7)	Unigene25519_All//0.00E+00//TC135086				nr +
Unigene2552_All	915	10.12	20.27	12.10	11.16	10.50	9.97	9.38	11.51	14.37	1.00E+00	5.43E-14	Up	2.58E-01	1.70E-01		-8.80E-02	6.80E-01		-1.63E-01	4.40E-01		2.95E-01	7.39E-02		6.15E-01	5.54E-06		Unigene2552_All//gi|157887047|emb|CAP03014.1|//1.00E-102//NEP1-interacting protein [Spinacia oleracea]	Unigene2552_All//3.00E-94//AT4G35840| zinc finger (C3HC4-type RING finger) family protein	Unigene2552_All//0.00E+00//gi|109884145|gb|DW513115.1|DW513115				nr +
Unigene25523_All	1875	4.24	202.81	0.97	4.86	19.06	5.78	12.04	9.94	294.10	5.58E+00	0.00E+00	Up	-2.14E+00	2.01E-17	Down	1.97E+00	1.28E-83	Up	2.50E-01	1.94E-01		-2.76E-01	8.98E-03		4.61E+00	0.00E+00	Up	Unigene25523_All//gi|195549553|gb|ACG50004.1|//1.00E-168//salt responsive protein 2 [Solanum lycopersicum]	Unigene25523_All//8.00E-161//AT4G29780| unknown protein	Unigene25523_All//0.00E+00//TC138024				nr -
Unigene25527_All	2030	14.59	7.51	11.31	33.42	27.14	21.34	15.52	6.01	8.67	-9.57E-01	1.99E-20		-3.68E-01	3.76E-04		-3.00E-01	2.86E-07		-6.48E-01	1.80E-25		-1.37E+00	3.26E-46	Down	-8.39E-01	5.71E-22		Unigene25527_All//gi|42562316|ref|NP_564237.2|//0.00E+00//leucine-rich repeat protein-related [Arabidopsis thaliana]	Unigene25527_All//0.00E+00//AT1G25570| leucine-rich repeat protein-related	Unigene25527_All//0.00E+00//TC148585		ko04626|Plant-pathogen interaction		nr -
Unigene25528_All	3705	0.62	1.56	1.09	0.95	1.23	1.85	4.17	5.62	5.71	1.33E+00	3.24E-07	Up	8.14E-01	1.00E-02		3.62E-01	2.31E-01		9.57E-01	1.66E-05		4.32E-01	5.88E-05		4.55E-01	1.23E-05		Unigene25528_All//gi|297802544|ref|XP_002869156.1|//0.00E+00//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297314992|gb|EFH45415.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene25528_All//0.00E+00//AT4G34310| unknown protein	Unigene25528_All//0.00E+00//ES827046				nr +

Unigene25529_All	1672	2.75	3.15	1.53	4.83	6.63	4.94	4.75	1.45	4.29	1.95E-01	4.86E-01		-8.49E-01	3.88E-03		4.58E-01	5.61E-03		3.44E-02	8.99E-01		-1.71E+00	9.89E-17	Down	-1.49E-01	4.61E-01		Unigene25529_All//gi|18397616|ref|NP_564360.1|//1.00E-126//SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|79318998|ref|NP_001031119.1| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|78959068|sp|Q94C39.2|PATL4_ARATH RecName: Full=Patellin-4 >gi|4587525|gb|AAD25756.1|AC007060_14 Contains the PF|00650 CRAL/TRIO phosphatidyl-inositol-transfer protein domain. ESTs gb|T76582, gb|N06574 and gb|Z25700 come from this gene [Arabidopsis thaliana] >gi|222424393|dbj|BAH20152.1| AT1G30690 [Arabidopsis thaliana]	Unigene25529_All//2.00E-120//AT1G30690| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene25529_All//0.00E+00//TC149974				nr -
Unigene25532_All	1698	1.85	3.31	4.70	15.40	19.23	18.43	0.65	0.74	0.68	8.41E-01	8.33E-04		1.35E+00	1.74E-09	Up	3.20E-01	3.71E-04		2.59E-01	8.60E-03		1.90E-01	7.28E-01		7.17E-02	9.11E-01		Unigene25532_All//gi|240256390|ref|NP_199107.5|//1.00E-103//triacylglycerol lipase [Arabidopsis thaliana]	Unigene25532_All//5.00E-105//AT5G42930| triacylglycerol lipase				nr -
Unigene25533_All	1319	23.92	28.24	24.95	7.48	12.14	8.49	1.12	3.36	2.30	2.39E-01	7.96E-03		6.08E-02	6.14E-01		6.99E-01	7.79E-08		1.83E-01	3.56E-01		1.58E+00	1.08E-08	Up	1.03E+00	1.01E-03		Unigene25533_All//gi|7547401|gb|AAB28813.2|//1.00E-143//cytochrome c1 precursor [Solanum tuberosum]	Unigene25533_All//8.00E-132//AT5G40810| cytochrome c1, putative	Unigene25533_All//0.00E+00//TC143992		ko00190|Oxidative phosphorylation		nr -
Unigene25534_All	1980	11.10	16.56	14.63	14.06	19.95	24.70	23.72	29.21	5.53	5.77E-01	8.73E-10		3.99E-01	1.30E-04		5.04E-01	1.27E-10		8.13E-01	4.88E-27		3.00E-01	1.20E-06		-2.10E+00	6.85E-129	Down	Unigene25534_All//gi|60617303|gb|AAX31279.1|//1.00E-150//phosphomannose isomerase [Cyanopsis tetragonolobus]	Unigene25534_All//1.00E-127//AT3G02570| MEE31 (MATERNAL EFFECT EMBRYO ARREST 31); mannose-6-phosphate isomerase	Unigene25534_All//0.00E+00//TC179484		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene25538_All	553	24.32	15.94	20.32	6.04	8.41	15.60	0.46	0.53	0.29	-6.09E-01	6.85E-05		-2.59E-01	1.28E-01		4.78E-01	9.25E-02		1.37E+00	1.92E-11	Up	2.06E-01	8.68E-01		-6.71E-01	6.05E-01		Unigene25538_All//gi|225438398|ref|XP_002274735.1|//3.00E-08//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296082589|emb|CBI21594.3| unnamed protein product [Vitis vinifera]	Unigene25538_All//1.00E-06//AT2G28605| Encodes a PsbP domain-OEC23 like protein localized in thylakoid (peripheral-lumenal side).	Unigene25538_All//2.00E-22//ES804853				nr -
Unigene2554_All	1125	3.86	0.32	2.51	53.36	29.23	9.15	2.59	4.76	1.17	-3.61E+00	2.39E-17	Down	-6.22E-01	4.23E-02		-8.68E-01	2.98E-42		-2.54E+00	4.68E-180	Down	8.75E-01	1.50E-04		-1.15E+00	3.57E-04	Down	Unigene2554_All//gi|15224291|ref|NP_181282.1|//1.00E-122//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|4056506|gb|AAC98072.1| nodulin-like protein [Arabidopsis thaliana] >gi|14994253|gb|AAK73261.1| nodulin-like protein [Arabidopsis thaliana]	Unigene2554_All//2.00E-110//AT2G37460| nodulin MtN21 family protein	Unigene2554_All//7.00E-104//ES836178				nr -
Unigene25542_All	2062	8.65	9.66	3.41	4.64	4.16	7.32	10.38	2.35	3.07	1.59E-01	2.36E-01		-1.34E+00	2.60E-20	Down	-1.58E-01	4.59E-01		6.57E-01	2.95E-06		-2.14E+00	9.19E-59	Down	-1.76E+00	1.20E-46	Down	Unigene25542_All//gi|15221327|ref|NP_172704.1|//1.00E-165//ACR8; amino acid binding [Arabidopsis thaliana] >gi|8778647|gb|AAF79655.1|AC025416_29 F5O11.14 [Arabidopsis thaliana] >gi|22138106|gb|AAM93433.1| ACR8 [Arabidopsis thaliana] >gi|111074504|gb|ABH94625.1| At1g12420 [Arabidopsis thaliana]	Unigene25542_All//2.00E-162//AT1G12420| ACR8; amino acid binding	Unigene25542_All//0.00E+00//TC159483				nr +
Unigene25545_All	3309	0.92	0.92	0.55	10.81	7.37	5.60	11.30	2.27	1.95	2.70E-03	9.94E-01		-7.45E-01	4.69E-02		-5.53E-01	1.30E-11		-9.50E-01	4.88E-26		-2.31E+00	2.40E-112	Down	-2.53E+00	5.22E-129	Down	Unigene25545_All//gi|223452280|gb|ACM89468.1|//0.00E+00//ATP-binding/protein serine/threonine kinase [Glycine max]	Unigene25545_All//0.00E+00//AT2G01950| BRL2 (BRI1-LIKE 2); ATP binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase	Unigene25545_All//0.00E+00//TC149159				nr +
Unigene2555_All	1556	4.00	1.14	2.84	50.42	27.38	9.46	2.36	5.64	1.41	-1.81E+00	9.35E-12	Down	-4.94E-01	4.79E-02		-8.81E-01	1.39E-56		-2.41E+00	2.65E-221	Down	1.25E+00	7.51E-12	Up	-7.47E-01	6.65E-03		Unigene2555_All//gi|15224291|ref|NP_181282.1|//1.00E-141//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|4056506|gb|AAC98072.1| nodulin-like protein [Arabidopsis thaliana] >gi|14994253|gb|AAK73261.1| nodulin-like protein [Arabidopsis thaliana]	Unigene2555_All//3.00E-130//AT2G37460| nodulin MtN21 family protein	Unigene2555_All//0.00E+00//TC173959				nr -
Unigene25550_All	1366	6.36	6.68	7.68	7.55	7.13	5.79	4.55	1.87	3.94	7.05E-02	7.23E-01		2.72E-01	1.56E-01		-8.15E-02	7.11E-01		-3.84E-01	3.51E-02		-1.29E+00	6.12E-09	Down	-2.09E-01	3.58E-01		Unigene25550_All//gi|18401489|ref|NP_566576.1|//7.00E-23//meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana]	Unigene25550_All//1.00E-23//AT3G17380| meprin and TRAF homology domain-containing protein / MATH domain-containing protein	Unigene25550_All//2.00E-147//EE592532				nr -
Unigene25554_All	1063	30.42	19.40	30.71	39.79	47.94	25.83	10.78	5.03	4.83	-6.49E-01	9.43E-12		1.37E-02	9.10E-01		2.69E-01	1.34E-04		-6.23E-01	4.56E-15		-1.10E+00	1.66E-12	Down	-1.16E+00	5.98E-14	Down	Unigene25554_All//gi|3608141|gb|AAC36174.1|//5.00E-27//expressed protein [Arabidopsis thaliana] >gi|107738167|gb|ABF83654.1| At2g35470 [Arabidopsis thaliana]	Unigene25554_All//2.00E-19//AT2G35470| unknown protein	Unigene25554_All//0.00E+00//TC134213				nr +
Unigene25557_All	858	3.66	4.31	3.23	11.03	11.76	6.95	14.44	5.16	6.18	2.37E-01	4.81E-01		-1.81E-01	6.06E-01		9.22E-02	6.78E-01		-6.67E-01	2.58E-04		-1.48E+00	5.67E-21	Down	-1.23E+00	2.31E-16	Down	Unigene25557_All//gi|2230292|sp|Q9LU93.1|MAD2_ARATH|/1.00E-77//RecName: Full=Mitotic spindle checkpoint protein MAD2 >gi|9279603|dbj|BAB01061.1| cell cycle checkpoint protein MAD2-like [Arabidopsis thaliana] >gi|37202030|gb|AAQ89630.1| At3g25980 [Arabidopsis thaliana]	Unigene25557_All//1.00E-78//AT3G25980| mitotic spindle checkpoint protein, putative (MAD2)	Unigene25557_All//0.00E+00//TC154367				nr +
Unigene25558_All	1081	3.82	3.09	1.03	9.49	10.13	8.11	5.79	2.20	3.24	-3.06E-01	3.32E-01		-1.89E+00	5.03E-08	Down	9.37E-02	6.52E-01		-2.28E-01	2.49E-01		-1.39E+00	4.56E-10	Down	-8.36E-01	4.71E-05		Unigene25558_All//gi|115459076|ref|NP_001053138.1|//1.00E-100//Os04g0486500 [Oryza sativa Japonica Group] >gi|113564709|dbj|BAF15052.1| Os04g0486500 [Oryza sativa Japonica Group]	Unigene25558_All//2.00E-100//AT3G25980| mitotic spindle checkpoint protein, putative (MAD2)	Unigene25558_All//0.00E+00//TC154367				nr +
Unigene25560_All	1168	2.02	3.60	3.65	2.56	2.06	1.70	2.64	5.30	1.53	8.37E-01	4.85E-03		8.56E-01	5.29E-03		-3.10E-01	4.22E-01		-5.89E-01	1.12E-01		1.00E+00	3.08E-06	Up	-7.84E-01	1.00E-02		Unigene25560_All//gi|113205363|gb|AAF66771.2|//3.00E-62//Putative polyprotein, identical [Solanum demissum]		Unigene25560_All//1.00E-34//FL577188				nr +
Unigene25563_All	1443	1.67	2.39	2.14	6.49	6.56	5.63	2.72	2.40	1.30	5.18E-01	1.23E-01		3.60E-01	3.57E-01		1.60E-02	9.60E-01		-2.04E-01	3.45E-01		-1.81E-01	5.74E-01		-1.07E+00	7.74E-05	Down	Unigene25563_All//gi|21322711|emb|CAD22154.1|//3.00E-95//pherophorin-dz1 protein [Volvox carteri f. nagariensis]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene25566_All	1038	82.92	87.33	99.68	15.64	19.34	16.58	2.16	1.65	0.50	7.48E-02	2.31E-01		2.66E-01	3.68E-07		3.06E-01	1.19E-02		8.35E-02	6.38E-01		-3.87E-01	3.45E-01		-2.11E+00	5.78E-07	Down	Unigene25566_All//gi|225442943|ref|XP_002266165.1|//1.00E-113//PREDICTED: similar to chloroplast post-illumination chlorophyll fluorescence increase protein isoform 1 [Vitis vinifera] >gi|225442945|ref|XP_002266207.1| PREDICTED: similar to chloroplast post-illumination chlorophyll fluorescence increase protein isoform 2 [Vitis vinifera]	Unigene25566_All//3.00E-104//AT3G15840| PIFI (post-illumination chlorophyll fluorescence increase)	Unigene25566_All//0.00E+00//TC160970				nr -
Unigene25567_All	1809	2.31	0.70	0.79	2.29	0.61	1.30	2.64	0.95	1.74	-1.72E+00	1.17E-07	Down	-1.54E+00	2.74E-06	Down	-1.91E+00	2.65E-10	Down	-8.16E-01	5.83E-03		-1.48E+00	1.55E-08	Down	-6.02E-01	1.12E-02		Unigene25567_All//gi|48525335|gb|AAT44969.1|//1.00E-115//At2g36240 [Arabidopsis thaliana] >gi|50198948|gb|AAT70477.1| At2g36240 [Arabidopsis thaliana]	Unigene25567_All//6.00E-112//AT2G36240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT1G09900.1); Has 18740 Blast hits to 5421 proteins in 159 species: Archae - 3; Bacteria - 12; Metazoa - 272; Fungi - 258; Plants - 17650; Viruses - 2; Other Eukaryotes - 543 (source: NCBI BLink).					nr -
Unigene2557_All	1832	36.01	119.01	38.83	88.86	114.26	175.01	72.21	19.10	53.10	1.72E+00	0.00E+00	Up	1.09E-01	1.32E-01		3.63E-01	6.20E-30		9.78E-01	1.49E-238		-1.92E+00	0.00E+00	Down	-4.44E-01	3.20E-29		Unigene2557_All//gi|18421660|ref|NP_568551.1|//1.00E-169//aspartyl protease family protein [Arabidopsis thaliana] >gi|15809850|gb|AAL06853.1| AT5g37540/mpa22_p_70 [Arabidopsis thaliana]	Unigene2557_All//2.00E-160//AT1G66180| aspartyl protease family protein	Unigene2557_All//0.00E+00//TC133329				nr -
Unigene25570_All	948	60.71	39.34	36.57	71.99	77.81	116.20	232.76	151.97	112.92	-6.26E-01	4.27E-19		-7.31E-01	6.13E-24		1.12E-01	8.89E-02		6.91E-01	1.46E-45		-6.15E-01	2.87E-84		-1.04E+00	6.80E-214	Down	Unigene25570_All//gi|224995910|gb|ACN76858.1|//8.00E-75//seed ripening regulated protein [Camellia oleifera]	Unigene25570_All//8.00E-40//AT2G18110| elongation factor 1-beta, putative / EF-1-beta, putative	Unigene25570_All//0.00E+00//TC130309				nr -
Unigene25573_All	2038	2.36	4.77	2.59	4.25	3.65	3.97	7.07	7.69	8.54	1.02E+00	7.27E-08	Up	1.31E-01	6.24E-01		-2.21E-01	3.11E-01		-1.01E-01	6.71E-01		1.21E-01	4.08E-01		2.72E-01	2.23E-02		Unigene25573_All//gi|224082190|ref|XP_002306596.1|//1.00E-157//f-box family protein [Populus trichocarpa] >gi|222856045|gb|EEE93592.1| f-box family protein [Populus trichocarpa]	Unigene25573_All//5.00E-155//AT1G22040| kelch repeat-containing F-box family protein	Unigene25573_All//0.00E+00//TC164799				nr -
Unigene25576_All	1257	37.71	29.06	36.64	32.93	32.98	36.04	39.29	24.04	17.34	-3.76E-01	9.88E-07		-4.14E-02	6.41E-01		2.20E-03	9.85E-01		1.30E-01	1.44E-01		-7.09E-01	8.14E-25		-1.18E+00	5.13E-59	Down	Unigene25576_All//gi|222136863|gb|ACM45081.1|//1.00E-154//3-dehydroquinate synthase [Vitis vinifera]	Unigene25576_All//3.00E-146//AT5G66120| 3-dehydroquinate synthase, putative	Unigene25576_All//0.00E+00//TC137999		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene25577_All	482	44.61	36.48	31.38	65.01	56.44	81.99	133.16	49.34	38.35	-2.91E-01	1.65E-02		-5.08E-01	3.22E-05		-2.04E-01	3.82E-02		3.35E-01	6.09E-05		-1.43E+00	4.48E-100	Down	-1.80E+00	1.08E-142	Down	Unigene25577_All//gi|225440890|ref|XP_002282641.1|//3.00E-39//PREDICTED: similar to ribosomal protein L10a [Vitis vinifera]	Unigene25577_All//3.00E-40//AT5G22440| 60S ribosomal protein L10A (RPL10aC)	Unigene25577_All//0.00E+00//TC134937		ko03010|Ribosome		nr +

Unigene25578_All	411	26.35	11.71	9.59	36.97	33.01	45.93	151.43	60.10	50.40	-1.17E+00	9.63E-11	Down	-1.46E+00	3.92E-14	Down	-1.63E-01	3.06E-01		3.13E-01	1.61E-02		-1.33E+00	4.32E-87	Down	-1.59E+00	3.55E-116	Down	Unigene25578_All//gi|225440890|ref|XP_002282641.1|//2.00E-39//PREDICTED: similar to ribosomal protein L10a [Vitis vinifera]	Unigene25578_All//2.00E-40//AT5G22410| 60S ribosomal protein L10A (RPL10aC)	Unigene25578_All//0.00E+00//gi|21091509|gb|BQ403822.1|BQ403822		ko03010|Ribosome		nr +
Unigene25580_All	1490	5.72	8.60	5.11	10.97	8.60	11.22	8.31	8.36	17.14	5.88E-01	1.85E-04		-1.64E-01	4.64E-01		-3.51E-01	8.34E-03		3.24E-02	8.52E-01		7.80E-03	9.97E-01		1.04E+00	2.41E-25	Up	Unigene25580_All//gi|18700113|gb|AAL77668.1|//1.00E-119//At2g32760/F24L7.10 [Arabidopsis thaliana] >gi|94142409|gb|ABF18992.1|At2g32760 [Arabidopsis thaliana]	Unigene25580_All//3.00E-100//AT2G32760| unknown protein	Unigene25580_All//0.00E+00//ES815631				nr +
Unigene25581_All	1018	84.60	156.79	143.38	115.09	143.36	166.68	43.19	51.90	232.22	8.90E-01	2.09E-94		7.61E-01	2.34E-64		3.17E-01	2.34E-16		5.34E-01	2.18E-44		2.65E-01	5.18E-05		2.43E+00	0.00E+00	Up	Unigene25581_All//gi|16974548|gb|AAL31190.1|//3.00E-27//AT4g32020/F10N7_170 [Arabidopsis thaliana] >gi|21928043|gb|AAM78050.1|AT4g32020/F10N7_170 [Arabidopsis thaliana]	Unigene25581_All//4.00E-22//AT4G32020| unknown protein	Unigene25581_All//0.00E+00//TC139831				nr +
Unigene25583_All	1557	10.82	7.06	7.18	1.92	2.28	1.22	1.30	3.06	1.43	-6.16E-01	5.19E-06		-5.91E-01	2.35E-05		2.47E-01	5.23E-01		-6.56E-01	7.32E-02		1.23E+00	1.28E-06	Up	1.37E-01	7.19E-01		Unigene25583_All//gi|297819654|ref|XP_002877710.1|//1.00E-110//BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297323548|gb|EFH53969.1|BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene25583_All//2.00E-100//AT3G49900| BTB/POZ domain-containing protein	Unigene25583_All//0.00E+00//gi|78334819|gb|DT555093.1|DT555093				nr -
Unigene25584_All	674	2.64	2.63	1.74	2.00	1.38	0.80	4.01	4.40	1.77	-4.40E-03	9.89E-01		-6.03E-01	2.42E-01		-5.33E-01	3.57E-01		-1.31E+00	2.66E-02		1.33E-01	7.05E-01		-1.18E+00	4.69E-04	Down	Unigene25584_All//gi|15228391|ref|NP_187698.1|//3.00E-36//MES17 (METHYL ESTERASE 17); hydrolase/ hydrolase, acting on ester bonds / methyl indole-3-acetate esterase [Arabidopsis thaliana]	Unigene25584_All//1.00E-37//AT3G10870| MES17 (METHYL ESTERASE 17); hydrolase/ hydrolase, acting on ester bonds / methyl indole-3-acetate esterase			ko00901|Indole alkaloid biosynthesis		nr +
Unigene25587_All	847	11.86	16.57	13.64	26.41	20.45	23.57	51.81	44.46	130.57	4.83E-01	1.29E-03		2.02E-01	2.84E-01		-3.69E-01	7.38E-04		-1.64E-01	2.13E-01		-2.21E-01	2.76E-03		1.33E+00	2.97E-157	Up	Unigene25587_All//gi|18390789|ref|NP_563791.1|//1.00E-115//PLL5; catalytic/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75180175|sp|Q9LQN6.1|P2C04_ARATH RecName: Full=Probable protein phosphatase 2C 4; Short=AtPP2C04; AltName: Full=Protein phosphatase 2C PLL5; Short=PP2C PLL5; AltName: Full=Protein POLTERGEIST-LIKE 5 >gi|8439909|gb|AAF75095.1|AC007583_31 It contains protein phosphatase 2C domain PF|00481. ESTs gb|H36120 and gb|36519 come from this gene [Arabidopsis thaliana]	Unigene25587_All//1.00E-116//AT1G07630| PLL5; catalytic/ protein serine/threonine phosphatase	Unigene25587_All//0.00E+00//TC141642				nr -
Unigene25589_All	952	9.40	21.40	8.17	9.47	13.56	12.76	29.27	25.86	25.19	1.19E+00	7.11E-20	Up	-2.03E-01	3.62E-01		5.18E-01	5.05E-04		4.30E-01	8.43E-03		-1.79E-01	7.20E-02		-2.16E-01	1.97E-02		Unigene25589_All//gi|30682553|ref|NP_683559.2|//4.00E-19//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]		Unigene25589_All//0.00E+00//TC172480		ko03040|Spliceosome		nr -
Unigene2559_All	1148	17.64	9.05	12.25	21.52	17.07	15.38	13.22	10.19	6.11	-9.63E-01	2.40E-14		-5.26E-01	3.05E-05		-3.35E-01	1.33E-03		-4.85E-01	5.31E-06		-3.75E-01	3.73E-03		-1.11E+00	3.51E-17	Down	Unigene2559_All//gi|79325353|ref|NP_001031741.1|//5.00E-36//zinc finger (HIT type) family protein [Arabidopsis thaliana] >gi|92856578|gb|ABE77402.1|At4g28820 [Arabidopsis thaliana]	Unigene2559_All//2.00E-37//AT4G28820| zinc finger (HIT type) family protein	Unigene2559_All//0.00E+00//TC175020				nr -
Unigene25590_All	1530	2.09	2.75	0.49	3.84	2.48	2.36	6.05	2.68	3.57	3.98E-01	1.92E-01		-2.10E+00	3.53E-07	Down	-6.34E-01	5.91E-03		-7.02E-01	3.58E-03		-1.18E+00	2.33E-11	Down	-7.63E-01	3.74E-06		Unigene25590_All//gi|115482986|ref|NP_001065086.1|//1.00E-125//Os10g0520700 [Oryza sativa Japonica Group] >gi|78708920|gb|ABB47895.1| HIT zinc finger family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639695|dbj|BAF27000.1|Os10g0520700 [Oryza sativa Japonica Group]	Unigene25590_All//3.00E-124//AT5G63830| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Zinc finger, HIT-type (InterPro:IPR007529); Has 339 Blast hits to 334 proteins in 111 species: Archae - 0; Bacteria - 0; Metazoa - 177; Fungi - 84; Plants - 29; Viruses - 0; Other Eukaryotes - 49 (source: NCBI BLink).	Unigene25590_All//0.00E+00//TC179520				nr -
Unigene25592_All	1431	1.94	0.99	1.79	2.78	3.73	2.08	2.72	0.50	3.51	-9.67E-01	1.06E-02		-1.18E-01	7.58E-01		4.22E-01	1.12E-01		-4.19E-01	1.94E-01		-2.45E+00	3.80E-13	Down	3.68E-01	1.23E-01		Unigene25592_All//gi|297843156|ref|XP_002889459.1|//1.00E-143//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335301|gb|EFH65718.1|leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25592_All//5.00E-133//AT1G03440| leucine-rich repeat family protein	Unigene25592_All//0.00E+00//gi|78351668|gb|DT571942.1|DT571942		ko04626|Plant-pathogen interaction		nr +
Unigene25593_All	1488	3.20	6.06	7.94	67.32	63.22	34.42	7.02	16.97	2.68	9.22E-01	2.18E-06		1.31E+00	3.21E-13	Up	-9.06E-02	1.11E-01		-9.68E-01	2.58E-74		1.27E+00	2.49E-33	Up	-1.39E+00	9.44E-17	Down	Unigene25593_All//gi|18396010|ref|NP_565323.1|//7.00E-98//lipase class 3 family protein [Arabidopsis thaliana] >gi|4755196|gb|AAD29063.1|expressed protein [Arabidopsis thaliana] >gi|27760040|gb|AAO23641.1|At2g05260 [Arabidopsis thaliana]	Unigene25593_All//4.00E-99//AT2G05260| lipase class 3 family protein	Unigene25593_All//0.00E+00//TC161782				nr +
Unigene25595_All	979	16.99	44.04	31.71	13.53	23.14	14.39	8.59	11.70	11.39	1.37E+00	1.23E-51	Up	9.00E-01	1.35E-18		7.74E-01	6.95E-13		8.87E-02	6.19E-01		4.45E-01	3.15E-03		4.07E-01	6.35E-03		Unigene25595_All//gi|6664314|gb|AAF22896.1|AC006932_13//4.00E-58//T27G7.21 [Arabidopsis thaliana]	Unigene25595_All//7.00E-61//AT1G08530| unknown protein	Unigene25595_All//0.00E+00//TC152997				nr +
Unigene25596_All	1169	18.84	5.37	5.74	64.09	47.46	41.76	34.25	3.68	10.74	-1.81E+00	9.46E-40	Down	-1.72E+00	1.60E-35	Down	-4.34E-01	2.16E-15		-6.18E-01	7.34E-26		-3.22E+00	5.32E-172	Down	-1.67E+00	5.92E-81	Down	Unigene25596_All//gi|124360377|gb|ABN08390.1|//3.00E-75//Harpin-induced 1 [Medicago truncatula]	Unigene25596_All//8.00E-43//AT1G17620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010084); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G11890.1); Has 539 Blast hits to 538 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 539; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene25596_All//0.00E+00//gi|78331643|gb|DT551917.1|DT551917				nr -
Unigene25597_All	2650	6.99	3.00	4.70	9.23	8.69	4.72	10.85	5.24	11.74	-1.22E+00	5.56E-19	Down	-5.72E-01	1.60E-05		-8.64E-02	5.36E-01		-9.67E-01	1.61E-18		-1.05E+00	4.17E-28	Down	1.14E-01	2.30E-01		Unigene25597_All//gi|297819644|ref|XP_002877705.1|//0.00E+00//U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297323543|gb|EFH53964.1| U-box domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene25597_All//2.00E-179//AT3G49810| U-box domain-containing protein	Unigene25597_All//0.00E+00//TC139911				nr -
Unigene25598_All	1258	4.12	7.37	5.59	1.86	2.35	1.51	1.55	4.78	1.93	8.40E-01	1.02E-05		4.40E-01	6.00E-02		3.39E-01	4.01E-01		-3.04E-01	5.02E-01		1.63E+00	5.27E-12	Up	3.21E-01	3.85E-01										
Unigene25599_All	844	17.54	5.46	13.00	29.75	27.66	14.13	11.52	11.79	35.50	-1.68E+00	2.09E-24	Down	-4.33E-01	4.45E-03		-1.05E-01	4.21E-01		-1.07E+00	1.75E-22	Down	3.27E-02	8.68E-01		1.62E+00	1.39E-57	Up	Unigene25599_All//gi|147835796|emb|CAN66251.1|//4.00E-07//hypothetical protein [Vitis vinifera]		Unigene25599_All//1.00E-154//gi|109885809|gb|DW514779.1|DW514779				nr -
Unigene256_All	3742	15.83	9.79	16.58	28.69	21.63	22.62	12.45	3.23	3.48	-6.93E-01	2.37E-23		6.69E-02	3.95E-01		-4.07E-01	1.69E-19		-3.43E-01	7.54E-13		-1.95E+00	1.83E-112	Down	-1.84E+00	3.35E-107	Down	Unigene256_All//gi|10086489|gb|AAG12549.1|AC007797_9//1.00E-128//Unknown Protein [Arabidopsis thaliana]	Unigene256_All//1.00E-117//AT1G19835| unknown protein	Unigene256_All//0.00E+00//TC155136				nr -
Unigene2560_All	1277	5.70	4.29	3.71	3.20	4.61	8.35	53.93	31.03	63.86	-4.10E-01	6.26E-02		-6.18E-01	6.23E-03		5.28E-01	2.90E-02		1.38E+00	3.27E-14	Up	-7.98E-01	6.14E-42		2.44E-01	1.51E-06		Unigene2560_All//gi|38194918|gb|AAR13306.1|//0.00E+00//reversibly glycosylated protein [Phaseolus vulgaris]	Unigene2560_All//0.00E+00//AT3G02230| RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1); cellulose synthase (UDP-forming)	Unigene2560_All//0.00E+00//gi|109839169|gb|DW237730.1|DW237730				nr -
Unigene25600_All	1115	1.31	0.86	1.53	1.25	1.48	1.22	4.25	3.97	12.29	-6.06E-01	2.68E-01		2.18E-01	6.56E-01		2.45E-01	6.73E-01		-4.18E-02	9.52E-01		-9.61E-02	7.24E-01		1.53E+00	9.72E-25	Up	Unigene25600_All//gi|147835796|emb|CAN66251.1|//6.00E-07//hypothetical protein [Vitis vinifera]		Unigene25600_All//0.00E+00//gi|109885809|gb|DW514779.1|DW514779				nr +
Unigene25602_All	1025	6.13	4.84	7.27	7.87	4.80	6.17	7.26	2.77	3.34	-3.39E-01	1.63E-01		2.48E-01	3.00E-01		-7.13E-01	1.64E-04		-3.52E-01	1.01E-01		-1.39E+00	9.04E-12	Down	-1.12E+00	6.25E-09	Down	Unigene25602_All//gi|2252850|gb|AAB62848.1|//2.00E-14//contains region of similarity to DNA binding protein [Arabidopsis thaliana]	Unigene25602_All//1.00E-12//AT4G00950| MEE47 (maternal effect embryo arrest 47); transcription factor	Unigene25602_All//0.00E+00//TC132734				nr +
Unigene25603_All	881	19.18	16.16	19.16	69.10	43.11	23.84	17.04	21.59	8.46	-2.47E-01	7.93E-02		-1.70E-03	9.90E-01		-6.81E-01	4.29E-28		-1.54E+00	1.46E-93	Down	3.41E-01	2.89E-03		-1.01E+00	1.26E-14	Down			Unigene25603_All//0.00E+00//TC166458				
Unigene25605_All	1385	20.40	8.82	10.65	41.51	38.94	47.15	57.33	25.83	23.27	-1.21E+00	3.11E-28	Down	-9.38E-01	4.10E-18		-9.22E-02	2.51E-01		1.84E-01	5.86E-03		-1.15E+00	4.38E-88	Down	-1.30E+00	7.33E-110	Down	Unigene25605_All//gi|15221511|ref|NP_172140.1|//3.00E-49//myosin heavy chain-related [Arabidopsis thaliana] >gi|6692690|gb|AAF24824.1|AC007592_17 F12K11.14 [Arabidopsis thaliana]	Unigene25605_All//9.00E-31//AT1G06530| myosin heavy chain-related	Unigene25605_All//0.00E+00//TC156464				nr +
Unigene25607_All	1819	1.90	0.75	1.11	12.49	12.55	3.82	16.11	13.40	13.82	-1.34E+00	1.06E-04	Down	-7.71E-01	2.64E-02		7.30E-03	9.62E-01		-1.71E+00	5.84E-41	Down	-2.66E-01	3.58E-03		-2.21E-01	1.39E-02		Unigene25607_All//gi|225458467|ref|XP_002282153.1|//6.00E-97//PREDICTED: similar to ATS/KAN4 (ABERRANT TESTA SHAPE); DNA binding / transcription factor [Vitis vinifera]	Unigene25607_All//1.00E-46//AT5G42630| ATS (ABERRANT TESTA SHAPE); DNA binding / transcription factor	Unigene25607_All//6.00E-13//TC178091	G2-like			nr -
Unigene25611_All	1730	3.18	1.96	1.42	13.30	15.82	13.37	8.19	5.48	6.13	-6.94E-01	6.19E-03		-1.17E+00	1.68E-05	Down	2.50E-01	1.60E-02		6.80E-03	9.54E-01		-5.78E-01	1.28E-05		-4.19E-01	1.25E-03		Unigene25611_All//gi|6692100|gb|AAF24565.1|AC007764_7//5.00E-61//F22C12.16 [Arabidopsis thaliana] >gi|98981119|gb|ABF59043.1|At1g64080 [Arabidopsis thaliana]	Unigene25611_All//4.00E-29//AT1G64080| unknown protein	Unigene25611_All//0.00E+00//TC130592				nr -

Unigene25615_All	492	130.59	25.75	48.81	20.45	37.44	17.07	2.49	1.27	3.08	-2.34E+00	2.61E-160	Down	-1.42E+00	3.18E-78	Down	8.73E-01	7.79E-13		-2.61E-01	1.89E-01		-9.68E-01	7.84E-02		3.04E-01	5.45E-01		Unigene25615_All//gi|155966601|gb|ABU41233.1|//4.00E-46//xyloglucan endotransglycosylase [Gossypium hirsutum] >gi|166343773|gb|ABY86634.1| xyloglucan endotransglycosylase/hydrolase [Gossypium arboreum]	Unigene25615_All//1.00E-31//AT4G37800| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene25615_All//8.00E-111//gi|48821533|gb|CO122846.1|CO122846				nr -
Unigene25616_All	1206	388.55	110.62	133.52	69.81	135.51	70.55	7.15	4.40	6.38	-1.81E+00	0.00E+00	Down	-1.54E+00	0.00E+00	Down	9.57E-01	3.67E-130		1.54E-02	8.36E-01		-7.00E-01	6.28E-05		-1.66E-01	3.79E-01		Unigene25616_All//gi|155966601|gb|ABU41233.1|//1.00E-123//xyloglucan endotransglycosylase [Gossypium hirsutum] >gi|166343773|gb|ABY86634.1| xyloglucan endotransglycosylase/hydrolase [Gossypium arboreum]	Unigene25616_All//6.00E-107//AT5G65730| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene25616_All//0.00E+00//TC147919				nr -
Unigene25617_All	769	8.03	6.33	6.99	4.79	5.28	6.93	1.10	2.93	3.42	-3.44E-01	1.59E-01		-1.99E-01	4.47E-01		1.41E-01	7.03E-01		5.32E-01	4.34E-02		1.42E+00	3.34E-04	Up	1.64E+00	7.17E-06	Up	Unigene25617_All//gi|224130402|ref|XP_002320828.1|//1.00E-101//ketopantoate hydroxymethyltransferase [Populus trichocarpa] >gi|222861601|gb|EEE99143.1| ketopantoate hydroxymethyltransferase [Populus trichocarpa]	Unigene25617_All//4.00E-100//AT3G61530| PANB2; 3-methyl-2-oxobutanoate hydroxymethyltransferase	Unigene25617_All//0.00E+00//gi|78342700|gb|DT562974.1|DT562974		ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene25619_All	1978	1.72	0.03	0.05	2.22	1.62	1.00	5.96	1.67	4.13	-6.07E+00	3.90E-18	Down	-5.00E+00	5.72E-16	Down	-4.53E-01	1.15E-01		-1.14E+00	7.54E-05	Down	-1.84E+00	7.27E-27	Down	-5.31E-01	2.07E-04		Unigene25619_All//gi|209970622|gb|ACJ03072.1|//1.00E-156//HB06p [Malus floribunda]	Unigene25619_All//8.00E-63//AT2G34930| disease resistance family protein	Unigene25619_All//6.00E-07//TC175792		ko04626|Plant-pathogen interaction		nr -
Unigene2562_All	1632	7.60	11.58	9.95	15.38	12.87	17.46	25.83	15.29	11.84	6.08E-01	1.70E-06		3.89E-01	7.44E-03		-2.57E-01	1.70E-02		1.83E-01	9.97E-02		-7.57E-01	8.83E-24		-1.13E+00	7.30E-47	Down	Unigene2562_All//gi|2072356|gb|AAB53764.1|//0.00E+00//aminoalcoholphosphotransferase [Brassica rapa subsp. campestris]	Unigene2562_All//0.00E+00//AT1G13560| AAPT1 (AMINOALCOHOLPHOSPHOTRANSFERASE 1); phosphatidyltransferase/ phosphotransferase, for other substituted phosphate groups	Unigene2562_All//0.00E+00//TC156563		ko00564|Glycerophospholipid metabolism/ko00565|Ether lipid metabolism		nr +
Unigene25620_All	1402	18.32	30.86	22.79	29.53	34.48	38.11	39.99	54.35	101.02	7.52E-01	9.35E-20		3.15E-01	1.66E-03		2.24E-01	2.70E-03		3.68E-01	1.50E-07		4.43E-01	1.17E-16		1.34E+00	5.15E-202	Up			Unigene25620_All//0.00E+00//gi|73863397|gb|DT466136.1|DT466136				
Unigene25621_All	352	3.12	5.18	4.84	8.07	8.32	6.67	7.21	3.56	2.72	7.31E-01	1.30E-01		6.33E-01	2.37E-01		4.38E-02	9.29E-01		-2.74E-01	5.03E-01		-1.02E+00	4.34E-03		-1.41E+00	8.57E-05	Down			Unigene25621_All//1.00E-10//TC176003				
Unigene25623_All	1447	6.83	53.44	44.97	10.36	14.66	13.80	4.21	2.02	2.29	2.97E+00	1.03E-248	Up	2.72E+00	4.76E-187	Up	5.01E-01	7.09E-06		4.13E-01	7.14E-04		-1.06E+00	1.21E-06	Down	-8.81E-01	2.56E-05		Unigene25623_All//gi|226495003|ref|NP_001147031.1|//2.00E-38//RING-H2 finger protein ATL5A [Zea mays] >gi|195606664|gb|ACG25162.1| RING-H2 finger protein ATL5A [Zea mays]	Unigene25623_All//6.00E-34//AT5G42200| zinc finger (C3HC4-type RING finger) family protein	Unigene25623_All//0.00E+00//TC160426				nr +
Unigene25624_All	394	3.98	4.12	6.89	2.28	2.45	7.57	3.00	1.80	1.31	4.69E-02	9.41E-01		7.91E-01	4.77E-02		1.05E-01	9.03E-01		1.73E+00	7.38E-06	Up	-7.37E-01	1.94E-01		-1.19E+00	2.80E-02				Unigene25624_All//5.00E-13//TC146667				
Unigene25625_All	1005	5.88	8.92	5.62	6.89	6.37	9.12	2.82	1.46	0.71	6.01E-01	1.79E-03		-6.69E-02	7.96E-01		-1.12E-01	6.58E-01		4.05E-01	3.84E-02		-9.53E-01	4.22E-03		-1.98E+00	5.62E-08	Down			Unigene25625_All//2.00E-125//gi|73851037|gb|DT460057.1|DT460057				
Unigene25626_All	1791	5.23	2.07	2.26	5.51	5.71	4.21	10.29	13.42	11.14	-1.34E+00	1.97E-11	Down	-1.21E+00	2.12E-09	Down	5.23E-02	8.09E-01		-3.87E-01	3.85E-02		3.83E-01	1.22E-04		1.15E-01	3.58E-01		Unigene25626_All//gi|42569720|ref|NP_181341.2|//0.00E+00//PHT4;2 (PHOSPHATE TRANSPORTER 4;2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ organic anion transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|187470894|sp|Q7XJK2.2|ANTR3_ARATH RecName: Full=Probable anion transporter 3, chloroplastic; AltName: Full=Phosphate transporter PHT4;2; Flags: Precursor	Unigene25626_All//0.00E+00//AT2G38060| PHT4;2 (PHOSPHATE TRANSPORTER 4;2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ organic anion transmembrane transporter/ sugar:hydrogen symporter	Unigene25626_All//0.00E+00//gi|78331539|gb|DT551813.1|DT551813				nr -
Unigene25627_All	431	0.73	0.82	2.22	2.77	1.60	0.31	3.92	1.94	1.66	1.76E-01	8.83E-01		1.61E+00	4.07E-02		-7.96E-01	1.87E-01		-3.14E+00	6.58E-05	Down	-1.02E+00	2.47E-02		-1.24E+00	5.14E-03				Unigene25627_All//8.00E-77//CO111189				
Unigene25628_All	1360	2.12	0.97	1.72	3.41	2.79	2.23	4.35	3.44	1.17	-1.13E+00	2.63E-03		-2.97E-01	4.49E-01		-2.91E-01	3.23E-01		-6.14E-01	2.87E-02		-3.39E-01	1.38E-01		-1.89E+00	6.82E-15	Down			Unigene25628_All//0.00E+00//CO111189				
Unigene25629_All	1411	5.86	8.04	7.59	57.40	26.53	14.98	45.25	17.51	13.55	4.57E-01	7.07E-03		3.73E-01	4.46E-02		-1.11E+00	2.07E-86	Down	-1.94E+00	7.64E-173	Down	-1.37E+00	4.25E-93	Down	-1.74E+00	9.06E-136	Down	Unigene25629_All//gi|224109078|ref|XP_002315075.1|//1.00E-146//ZIP transporter [Populus trichocarpa] >gi|222864115|gb|EEF01246.1| ZIP transporter [Populus trichocarpa]	Unigene25629_All//4.00E-87//AT3G12750| ZIP1 (ZINC TRANSPORTER 1 PRECURSOR); zinc ion transmembrane transporter	Unigene25629_All//0.00E+00//TC146584				nr -
Unigene2563_All	1562	3.01	2.95	3.14	6.38	5.16	6.91	9.61	4.47	3.72	-3.03E-02	9.28E-01		5.71E-02	8.42E-01		-3.06E-01	9.78E-02		1.16E-01	6.02E-01		-1.10E+00	2.92E-16	Down	-1.37E+00	3.94E-23	Down	Unigene2563_All//gi|2072356|gb|AAB53764.1|//0.00E+00//aminoalcoholphosphotransferase [Brassica rapa subsp. campestris]	Unigene2563_All//0.00E+00//AT1G13560| AAPT1 (AMINOALCOHOLPHOSPHOTRANSFERASE 1); phosphatidyltransferase/ phosphotransferase, for other substituted phosphate groups	Unigene2563_All//0.00E+00//TC156563		ko00564|Glycerophospholipid metabolism/ko00565|Ether lipid metabolism		nr -
Unigene25632_All	284	9.95	6.78	18.56	30.70	24.61	29.90	5.21	4.12	1.26	-5.53E-01	1.37E-01		9.00E-01	9.25E-04		-3.19E-01	1.10E-01		-3.80E-02	8.75E-01		-3.39E-01	5.22E-01		-2.05E+00	1.05E-04	Down			Unigene25632_All//3.00E-143//gi|109887279|gb|DW516248.1|DW516248				
Unigene25634_All	758	7.32	7.89	10.26	11.04	8.90	6.43	5.58	3.20	1.52	1.09E-01	6.62E-01		4.87E-01	2.63E-02		-3.10E-01	1.33E-01		-7.79E-01	6.87E-05		-8.03E-01	2.28E-03		-1.87E+00	1.01E-10	Down			Unigene25634_All//0.00E+00//TC173020				
Unigene25638_All	2477	6.48	4.11	4.13	16.97	15.79	30.08	13.11	35.77	32.01	-6.57E-01	2.22E-06		-6.52E-01	5.68E-06		-1.04E-01	2.77E-01		8.26E-01	4.86E-42		1.45E+00	5.78E-140	Up	1.29E+00	4.44E-107	Up	Unigene25638_All//gi|115480840|ref|NP_001064013.1|//0.00E+00//Os10g0101000 [Oryza sativa Japonica Group] >gi|18481964|gb|AAL73562.1|AC079632.6 Putative receptor-like protein kinase [Oryza sativa Japonica Group] >gi|19920204|gb|AAM08636.1|AC108883.9 Putative receptor-like protein kinase [Oryza sativa Japonica Group] >gi|31429736|gb|AAP51745.1| Protein kinase domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113638622|dbj|BAF25927.1| Os10g0101000 [Oryza sativa Japonica Group]	Unigene25638_All//3.00E-103//AT1G34300| lectin protein kinase family protein	Unigene25638_All//0.00E+00//DW233905				nr -
Unigene2564_All	1855	1.83	4.97	3.50	7.36	9.32	8.20	25.89	40.67	41.81	1.44E+00	2.13E-12	Up	9.34E-01	1.11E-04		3.41E-01	9.37E-03		1.57E-01	3.52E-01		6.51E-01	2.16E-32		6.92E-01	8.71E-38		Unigene2564_All//gi|224111880|ref|XP_002316010.1|//1.00E-161//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene2564_All//2.00E-92//AT3G14610| CYP72A10; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene2564_All//0.00E+00//TC137307		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00906|Carotenoid biosynthesis		nr +
Unigene25640_All	1456	3.41	6.19	4.46	5.41	5.01	5.86	2.93	6.11	4.43	8.60E-01	9.00E-06		3.86E-01	1.21E-01		-1.09E-01	6.45E-01		1.17E-01	6.09E-01		1.06E+00	2.29E-09	Up	5.96E-01	3.01E-03		Unigene25640_All//gi|7573596|dbj|BAB49509.1|//1.00E-152//protein kinase 1 [Populus nigra]	Unigene25640_All//3.00E-141//AT1G07870| protein kinase family protein	Unigene25640_All//0.00E+00//TC157713		ko04626|Plant-pathogen interaction		nr +
Unigene25641_All	1382	14.50	18.04	14.22	30.06	33.96	34.38	20.04	40.74	132.92	3.15E-01	4.45E-03		-2.83E-02	8.41E-01		1.76E-01	2.69E-02		1.94E-01	1.59E-02		1.02E+00	6.31E-52	Up	2.73E+00	0.00E+00	Up	Unigene25641_All//gi|124359429|gb|ABD28590.2|//9.00E-66//C2 [Medicago truncatula]	Unigene25641_All//6.00E-59//AT5G47710| C2 domain-containing protein	Unigene25641_All//0.00E+00//TC159883				nr +
Unigene25642_All	1339	6.29	11.88	8.07	11.12	15.71	12.88	16.86	31.18	91.10	9.17E-01	1.42E-10		3.60E-01	5.18E-02		4.98E-01	8.62E-06		2.12E-01	1.48E-01		8.87E-01	1.15E-30		2.43E+00	0.00E+00	Up	Unigene25642_All//gi|124359429|gb|ABD28590.2|//9.00E-66//C2 [Medicago truncatula]	Unigene25642_All//6.00E-59//AT5G47710| C2 domain-containing protein	Unigene25642_All//0.00E+00//TC159883				nr -
Unigene25644_All	1041	64.28	45.32	54.48	105.47	94.57	90.33	97.27	38.86	47.84	-5.04E-01	3.32E-15		-2.39E-01	3.85E-04		-1.57E-01	1.02E-03		-2.24E-01	3.49E-06		-1.32E+00	1.01E-139	Down	-1.02E+00	1.47E-95	Down	Unigene25644_All//gi|18404471|ref|NP_566762.1|//9.00E-62//FKBP15-1; FK506 binding / peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi|23396586|sp|Q38935.2|FKR21_ARATH RecName: Full=FK506-binding protein 2-1; AltName: Full=Peptidyl-prolyl cis-trans isomerase; Short=PPIase; AltName: Full=Rotamase; AltName: Full=15 kDa FKBP; AltName: Full=FKBP-15-1; Flags: Precursor >gi|9294179|dbj|BAB02081.1| immunophilin [Arabidopsis thaliana] >gi|17065400|gb|AAL32854.1| immunophilin [Arabidopsis thaliana] >gi|22136164|gb|AAM91160.1| immunophilin [Arabidopsis thaliana]	Unigene25644_All//3.00E-58//AT5G48580| FKBP15-2; FK506 binding / peptidyl-prolyl cis-trans isomerase	Unigene25644_All//0.00E+00//TC157862				nr -
Unigene25645_All	764	23.70	28.45	28.16	25.10	15.64	17.50	19.31	13.90	9.54	2.64E-01	3.00E-02		2.49E-01	5.31E-02		-6.83E-01	3.25E-09		-5.21E-01	2.15E-05		-4.75E-01	2.53E-04		-1.02E+00	1.54E-14	Down	Unigene25645_All//gi|300170593|gb|EFJ37194.1|//2.00E-33//ARF-like GTPase [Selaginella moellendorffii]	Unigene25645_All//3.00E-32//AT5G52210| ATG81 (ARABIDOPSIS THALIANA GTP-BINDING PROTEIN 1); GTP binding	Unigene25645_All//0.00E+00//TC137081				nr +
Unigene25646_All	937	8.93	78.74	7.44	9.36	18.89	19.42	10.06	11.29	13.27	3.14E+00	5.90E-251	Up	-2.63E-01	2.34E-01		1.01E+00	1.06E-15	Up	1.05E+00	9.13E-16	Up	1.66E-01	3.67E-01		3.99E-01	4.47E-03		Unigene25646_All//gi|257219566|gb|ACV50436.1|//2.00E-11//Avr9/Cf-9 rapidly elicited protein [Jatropha curcas]	Unigene25646_All//5.00E-08//AT1G32920| unknown protein	Unigene25646_All//0.00E+00//TC165351				nr -
Unigene25647_All	1393	7.66	5.06	4.82	56.36	77.87	141.20	103.32	24.81	33.60	-6.00E-01	5.70E-04		-6.70E-01	2.13E-04		4.66E-01	9.72E-25		1.33E+00	6.54E-238	Up	-2.06E+00	0.00E+00	Down	-1.62E+00	5.95E-276	Down	Unigene25647_All//gi|14423450|gb|AAK62407.1|AF386962_1/1.00E-148//Unknown protein [Arabidopsis thaliana] >gi|30725566|gb|AAP37805.1| At5g25460 [Arabidopsis thaliana]	Unigene25647_All//1.00E-149//AT5G25460| unknown protein	Unigene25647_All//0.00E+00//TC130426				nr -
Unigene25648_All	1256	11.62	10.21	16.62	8.53	8.80	7.30	11.38	11.81	5.33	-1.87E-01	2.32E-01		5.16E-01	3.20E-05		4.56E-02	8.29E-01		-2.24E-01	2.45E-01		5.42E-02	7.23E-01		-1.09E+00	8.65E-16	Down	Unigene25648_All//gi|115466130|ref|NP_001056664.1|//5.00E-57//Os06g0127500 [Oryza sativa Japonica Group] >gi|113594704|dbj|BAF18578.1| Os06g0127500 [Oryza sativa Japonica Group]	Unigene25648_All//3.00E-42//AT1G76940| RNA recognition motif (RRM)-containing protein	Unigene25648_All//0.00E+00//TC155388				nr -
Unigene25649_All	1186	8.25	11.45	15.54	30.12	24.68	14.62	2.85	1.52	6.05	4.73E-01	2.00E-03		9.13E-01	1.48E-11		-2.87E-01	7.72E-04		-1.04E+00	3.02E-30	Down	-9.12E-01	2.38E-03		1.08E+00	3.47E-08	Up	Unigene25649_All//gi|14005348|gb|AB080459.1|//3.00E-16//RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H [Medicago truncatula]	Unigene25649_All//1.00E-07//AT3G09510| nucleic acid binding	Unigene25649_All//0.00E+00//TC166781				nr -

Unigene2565_All	1959	5.69	3.96	3.56	2.54	3.20	2.65	11.48	16.45	23.00	-5.24E-01	2.12E-03		-6.76E-01	1.29E-04		3.31E-01	1.85E-01		6.02E-02	8.48E-01		5.19E-01	8.75E-10		1.00E+00	2.88E-41	Up	Unigene2565_All//gi|30678079|ref|NP_178475.2|//7.00E-46//18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|42570677|ref|NP_973412.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|79316683|ref|NP_001030966.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana] >gi|186499149|ref|NP_001118260.1| 18S pre-ribosomal assembly protein gar2-related [Arabidopsis thaliana]	Unigene2565_All//2.00E-37//AT2G30810| 18S pre-ribosomal assembly protein gar2-related	Unigene2565_All//0.00E+00//CO107756				nr -
Unigene25650_All	1673	8.35	10.09	4.49	29.63	29.41	18.19	24.08	9.09	16.00	2.72E-01	5.22E-02		-8.96E-01	1.22E-08		-1.04E-02	9.12E-01		-7.03E-01	1.26E-21		-1.41E+00	2.53E-61	Down	-5.90E-01	2.03E-15		Unigene25650_All//gi|259121393|gb|ACY92016.1|//1.00E-108//WRKY transcription factor 14 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene25650_All//5.00E-78//AT4G24240| WRKY7; calmodulin binding / transcription factor	Unigene25650_All//0.00E+00//gi|78350377|gb|DT570651.1|DT570651	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene25651_All	1667	5.68	3.92	3.58	45.00	21.13	17.91	27.44	15.77	13.19	-5.35E-01	4.11E-03		-6.67E-01	5.74E-04		-1.09E+00	2.43E-77	Down	-1.33E+00	1.01E-92	Down	-7.99E-01	3.21E-28		-1.06E+00	6.23E-46	Down	Unigene25651_All//gi|115464229|ref|NP_001055714.1|//1.00E-44//Os05g0453300 [Oryza sativa Japonica Group] >gi|113579265|dbj|BAF17628.1| Os05g0453300 [Oryza sativa Japonica Group]	Unigene25651_All//1.00E-33//AT3G54000| unknown protein	Unigene25651_All//0.00E+00//TC150498				nr -
Unigene25652_All	2070	3.82	7.88	9.88	3.99	8.15	8.84	3.96	1.01	0.79	1.05E+00	2.93E-13	Up	1.37E+00	5.36E-24	Up	1.03E+00	2.41E-15	Up	1.15E+00	4.92E-18	Up	-1.97E+00	9.87E-21	Down	-2.33E+00	3.12E-26	Down	Unigene25652_All//gi|297790444|ref|XP_002863113.1|//0.00E+00//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308935|gb|EFH39372.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25652_All//4.00E-177//AT1G69870| proton-dependent oligopeptide transport (POT) family protein	Unigene25652_All//0.00E+00//TC144461				nr +
Unigene25654_All	1825	0.92	0.61	0.64	3.03	2.53	2.00	3.22	1.31	1.29	-5.87E-01	2.42E-01		-5.15E-01	3.44E-01		-2.61E-01	3.34E-01		-5.96E-01	1.84E-02		-1.30E+00	1.18E-08	Down	-1.32E+00	3.79E-09	Down	Unigene25654_All//gi|297821008|ref|XP_002878387.1|//1.00E-102//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297324225|gb|EFH54646.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene25654_All//9.00E-103//AT3G61520| pentatricopeptide (PPR) repeat-containing protein	Unigene25654_All//0.00E+00//ES793082				nr -
Unigene25655_All	463	18.87	19.15	8.28	21.63	20.45	28.29	6.57	3.97	4.39	2.12E-02	9.34E-01		-1.19E+00	1.40E-08	Down	-8.04E-02	7.22E-01		3.88E-01	1.41E-02		-7.27E-01	2.25E-02		-5.83E-01	5.82E-02					Unigene25655_All//0.00E+00//DW499913				
Unigene25656_All	618	3.81	0.82	1.64	2.66	2.73	3.07	0.82	0.61	0.52	-2.22E+00	3.85E-06	Down	-1.22E+00	5.99E-03		3.76E-02	9.55E-01		2.07E-01	7.01E-01		-4.32E-01	6.18E-01		-6.71E-01	4.48E-01					Unigene25656_All//4.00E-138//DW499913				
Unigene25658_All	1885	253.58	158.08	144.41	40.27	91.69	38.57	17.50	14.04	4.90	-6.82E-01	2.65E-178		-8.12E-01	8.85E-235		1.19E+00	1.08E-194	Up	-6.22E-02	4.04E-01		-3.18E-01	1.59E-04		-1.84E+00	6.54E-76	Down	Unigene25658_All//gi|15241168|ref|NP_197478.1|//0.00E+00//TUA3; structural constituent of cytoskeleton [Arabidopsis thaliana] >gi|15241179|ref|NP_197479.1| TUA5; structural constituent of cytoskeleton [Arabidopsis thaliana] >gi|297808045|ref|XP_002871906.1| tubulin alpha-3 [Arabidopsis lyrata subsp. lyrata] >gi|297812159|ref|XP_002873963.1| tubulin alpha-3 [Arabidopsis lyrata subsp. lyrata] >gi|135406|sp|P20363.1|TBA3_ARATH RecName: Full=Tubulin alpha-3/alpha-5 chain >gi|13605805|gb|AAK32888.1|AF367301_1 AT5g19770/T29J13_190 [Arabidopsis thaliana] >gi|166912|gb|AAA32888.1| alpha-tubulin [Arabidopsis thaliana] >gi|166918|gb|AAA32891.1| alpha-5 tubulin [Arabidopsis thaliana] >gi|23565949|gb|AAN28834.1| At5g19770/T29J13_190 [Arabidopsis thaliana] >gi|297317743|gb|EFH48165.1| tubulin alpha-3 [Arabidopsis	Unigene25658_All//0.00E+00//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene25658_All//0.00E+00//TC159355		ko04145|Phagosome		nr +
Unigene25659_All	3199	1.11	3.03	0.93	0.61	0.44	0.40	3.00	4.95	9.40	1.44E+00	4.96E-13	Up	-2.55E-01	4.70E-01		-4.61E-01	3.22E-01		-6.20E-01	1.97E-01		7.23E-01	8.69E-09		1.65E+00	4.71E-59	Up	Unigene25659_All//gi|209970609|gb|ACJ03067.1|//1.00E-155//AL07-2p [Malus floribunda]	Unigene25659_All//8.00E-57//AT1G45616| AtRLP6 (Receptor Like Protein 6); protein binding	Unigene25659_All//2.00E-66//DT467122		ko04626|Plant-pathogen interaction		nr +
Unigene2566_All	1572	0.90	5.38	1.08	3.07	1.71	2.50	4.73	5.03	3.78	2.58E+00	6.31E-24	Up	2.71E-01	6.27E-01		-8.47E-01	8.83E-04		-2.98E-01	3.23E-01		8.62E-02	6.80E-01		-3.26E-01	8.80E-02		Unigene2566_All//gi|15218229|ref|NP_177937.1|//2.00E-48//UNE2 (unfertilized embryo sac 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|28416565|gb|AAO42813.1| At1g78130 [Arabidopsis thaliana] >gi|110742895|dbj|BAE99345.1| transporter like protein [Arabidopsis thaliana]	Unigene2566_All//1.00E-49//AT1G78130| UNE2 (unfertilized embryo sac 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter					nr +
Unigene25660_All	1103	2.89	2.89	2.17	1.99	4.09	2.99	5.63	12.16	3.54	3.00E-04	9.99E-01		-4.14E-01	2.64E-01		1.04E+00	1.52E-04	Up	5.89E-01	9.39E-02		1.11E+00	1.04E-14	Up	-6.71E-01	1.04E-03									
Unigene25661_All	1374	2.40	1.00	2.56	8.81	7.54	6.87	4.95	2.40	2.35	-1.27E+00	3.05E-04	Down	9.25E-02	7.81E-01		-2.24E-01	1.99E-01		-3.59E-01	3.12E-02		-1.04E+00	3.38E-07	Down	-1.08E+00	8.41E-08	Down	Unigene25661_All//gi|18402610|ref|NP_566661.1|//1.00E-102//RTL2 (RNASE THREE-LIKE PROTEIN 2); double-stranded RNA binding / ribonuclease III [Arabidopsis thaliana]	Unigene25661_All//3.00E-87//AT3G20120| RTL2 (RNASE THREE-LIKE PROTEIN 2); double-stranded RNA binding / ribonuclease III	Unigene25661_All//0.00E+00//ES819060				nr +
Unigene25664_All	1613	2.43	4.34	1.85	0.62	0.58	2.30	4.14	12.67	37.99	8.33E-01	1.80E-04		-3.96E-01	2.39E-01		-9.98E-02	8.68E-01		1.89E+00	5.77E-08	Up	1.61E+00	2.27E-38	Up	3.20E+00	5.01E-265	Up	Unigene25664_All//gi|15242536|ref|NP_188817.1|//1.00E-158//AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene25664_All//2.00E-155//AT5G40010| AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene25664_All//1.00E-26//ES840572				nr -
Unigene25665_All	830	24.77	41.94	37.79	40.87	53.11	124.99	25.78	53.53	56.30	7.60E-01	2.65E-16		6.09E-01	7.72E-10		3.78E-01	3.74E-07		1.61E+00	3.66E-168	Up	1.05E+00	3.74E-43	Up	1.13E+00	1.37E-51	Up	Unigene25665_All//gi|48958479|gb|AAT47792.1|//1.00E-32//At1g72510 [Arabidopsis thaliana] >gi|51536554|gb|AU035515.1| At1g72510 [Arabidopsis thaliana]	Unigene25665_All//1.00E-31//AT1G72510| unknown protein	Unigene25665_All//0.00E+00//gi|164290723|gb|ES791502.1|ES791502				nr -
Unigene25666_All	1798	21.16	9.41	10.75	26.85	27.66	18.01	9.48	4.70	4.96	-1.17E+00	9.36E-36	Down	-9.77E-01	7.48E-26		4.28E-02	6.56E-01		-5.76E-01	6.15E-15		-1.01E+00	4.83E-16	Down	-9.33E-01	1.52E-14		Unigene25666_All//gi|297841763|ref|XP_002888763.1|//1.00E-170//NHL repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297334604|gb|EFH65022.1| NHL repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene25666_All//7.00E-145//AT1G70280| NHL repeat-containing protein	Unigene25666_All//0.00E+00//TC159118				nr +
Unigene25667_All	1508	7.67	3.63	5.86	4.03	5.53	13.48	40.99	34.15	23.78	-1.08E+00	4.02E-10	Down	-3.88E-01	2.86E-02		4.55E-01	2.13E-02		1.74E+00	5.16E-37	Up	-2.64E-01	1.11E-05		-7.86E-01	7.91E-38		Unigene25667_All//gi|57222158|gb|AK388986.1|//1.00E-113//At4g27460 [Arabidopsis thaliana]	Unigene25667_All//2.00E-104//AT5G53750| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to wounding; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage; CONTAINS InterPro DOMAIN/s: Cystathionine beta-synthase, core (InterPro:IPR000644); BEST Arabidopsis thaliana protein match is: CBS domain-containing protein (TAIR:AT4G27460.1); Has 79 Blast hits to 78 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 79; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene25667_All//0.00E+00//TC160324				nr +
Unigene25668_All	1972	1.99	1.05	0.54	2.91	3.35	1.19	7.14	6.10	4.40	-9.18E-01	3.02E-03		-1.88E+00	1.25E-07	Down	2.07E-01	4.33E-01		-1.29E+00	2.93E-07	Down	-2.26E-01	1.17E-01		-6.97E-01	9.93E-08		Unigene25668_All//gi|257831433|gb|ACV71017.1|//1.00E-136//UPA17 [Capsicum annuum]	Unigene25668_All//2.00E-82//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene25668_All//0.00E+00//TC167794	GRF			nr +
Unigene2567_All	2083	0.73	3.11	0.82	0.86	1.42	1.37	2.46	2.15	1.87	2.10E+00	1.50E-14	Up	1.68E-01	7.31E-01		7.24E-01	4.47E-02		6.66E-01	7.97E-02		-1.94E-01	4.66E-01		-3.90E-01	9.60E-02		Unigene2567_All//gi|15218229|ref|NP_177937.1|//0.00E+00//UNE2 (unfertilized embryo sac 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|28416565|gb|AAO42813.1| At1g78130 [Arabidopsis thaliana] >gi|110742895|dbj|BAE99345.1| transporter like protein [Arabidopsis thaliana]	Unigene2567_All//0.00E+00//AT1G78130| UNE2 (unfertilized embryo sac 2); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene2567_All//2.00E-19//gi|78348752|gb|DT569026.1|DT569026				nr +
Unigene25670_All	1684	12.80	9.57	12.77	13.13	14.70	11.13	7.06	2.38	2.84	-4.20E-01	3.83E-04		-2.90E-03	1.00E+00		1.63E-01	1.77E-01		-2.39E-01	5.17E-02		-1.57E+00	9.46E-22	Down	-1.31E+00	1.99E-17	Down	Unigene25670_All//gi|226496785|ref|NP_001151692.1|//2.00E-55//erg28 like protein [Zea mays] >gi|195648941|gb|ACG43938.1| erg28 like protein [Zea mays]	Unigene25670_All//2.00E-56//AT1G10030| ERG28 (Arabidopsis homolog of yeast ergosterol28)	Unigene25670_All//0.00E+00//TC150056				nr +
Unigene25674_All	1676	8.24	5.41	25.67	9.33	4.83	4.15	3.96	6.53	1.81	-6.07E-01	5.62E-05		1.64E+00	5.59E-65	Up	-9.51E-01	3.94E-13		-1.17E+00	3.20E-16	Down	7.22E-01	2.58E-06		-1.13E+00	3.35E-08	Down	Unigene25674_All//gi|24430421|dbj|BAC23609.1|//5.00E-49//41 kD chloroplast nucleoid DNA binding protein (CND41) [Nicotiana sylvestris]	Unigene25674_All//2.00E-43//AT5G10770| chloroplast nucleoid DNA-binding protein, putative	Unigene25674_All//0.00E+00//DW505245				nr +
Unigene25675_All	545	3.55	21.48	15.34	4.39	6.13	15.41	16.14	6.90	4.97	2.60E+00	4.63E-33	Up	2.11E+00	4.17E-18	Up	4.82E-01	1.67E-01		1.81E+00	1.99E-16	Up	-1.23E+00	1.73E-11	Down	-1.70E+00	8.10E-19	Down	Unigene25675_All//gi|297794665|ref|XP_002865217.1|//2.00E-43//carboxylic ester hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297311052|gb|EFH41476.1| carboxylic ester hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene25675_All//3.00E-43//AT5G45920| carboxylesterase/ hydrolase/ hydrolase, acting on ester bonds	Unigene25675_All//0.00E+00//BF276837				nr +

Unigene25676_A11	1116	4.08	20.02	7.11	5.89	8.30	8.54	19.85	7.90	8.75	2.30E+00	2.60E-54	Up	8.02E-01	1.83E-04		4.94E-01	7.03E-03		5.35E-01	3.82E-03		-1.33E+00	2.37E-31	Down	-1.18E+00	4.72E-27	Down	Unigene25676_A11//gi|297794665|ref|XP_002865217.1|//3.00E-90//carboxylic ester hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297311052|gb|EFH11476.1| carboxylic ester hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene25676_A11//2.00E-84//AT5G45920| carboxylesterase/ hydrolase/ hydrolase, acting on ester bonds	Unigene25676_A11//0.00E+00//TC156278				nr +
Unigene25677_A11	1898	1.08	0.48	1.01	2.70	1.31	3.45	3.79	1.98	1.93	-1.16E+00	1.12E-02		-9.01E-02	8.43E-01		-1.05E+00	2.04E-05	Down	3.52E-01	1.51E-01		-9.34E-01	2.00E-06		-9.72E-01	4.70E-07		Unigene25677_A11//gi|15237977|ref|NP_199503.1|//0.00E+00//intron maturase, type II family protein [Arabidopsis thaliana]	Unigene25677_A11//0.00E+00//AT5G46920| intron maturase, type II family protein	Unigene25677_A11//0.00E+00//ES814681				nr +
Unigene25678_A11	2139	5.92	2.30	2.39	15.02	13.99	18.94	40.82	39.18	33.26	-1.37E+00	1.33E-15	Down	-1.31E+00	5.06E-14	Down	-1.03E-01	3.57E-01		3.34E-01	4.89E-05		-5.92E-02	3.34E-01		-2.95E-01	1.25E-09		Unigene25678_A11//gi|11545445|ref|NP_001050873.1|//0.00E+00//Os03g0672300 [Oryza sativa Japonica Group] >gi|113549344|dbj|BAF12787.1| Os03g0672300 [Oryza sativa Japonica Group]	Unigene25678_A11//1.00E-167//AT3G22960| PKP-ALPHA; pyruvate kinase	Unigene25678_A11//0.00E+00//gi|21091051|gb|BQ403364.1|BQ403364		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene25685_A11	1627	9.62	2.37	5.37	34.29	11.28	5.61	18.76	6.11	2.11	-2.02E+00	6.91E-33	Down	-8.41E-01	1.08E-08		-1.60E+00	3.13E-105	Down	-2.61E+00	1.42E-172	Down	-1.62E+00	2.84E-57	Down	-3.16E+00	5.44E-133	Down	Unigene25685_A11//gi|297851126|ref|XP_002893444.1|//1.00E-136//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339286|gb|EFH69703.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25685_A11//9.00E-128//AT1G24530| transducin family protein / WD-40 repeat family protein	Unigene25685_A11//0.00E+00//TC145560		ko03040|Spliceosome		nr +
Unigene25690_A11	1131	9.21	3.00	8.29	16.69	20.86	188.00	168.75	73.28	100.32	-1.62E+00	1.91E-16	Down	-1.52E-01	4.47E-01		3.21E-01	3.30E-03		3.49E+00	0.00E+00	Up	-1.20E+00	1.59E-226	Down	-7.50E-01	3.90E-106		Unigene25690_A11//gi|85540956|sp|Q8GXG1.2|ASPG2_ARATH//1.00E-159//RecName: Full=Probable isoaspartyl peptidase/L-asparaginase 2; AltName: Full=L-asparagine amidohydrolase 2; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase 2 subunit alpha; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase 2 subunit beta; Flags: Precursor >gi|9294462|dbj|BAB02681.1| l-asparaginase (l-asparagine amidohydrolase) [Arabidopsis thaliana] >gi|89000945|gb|ABD59062.1| At3g16150 [Arabidopsis thaliana]	Unigene25690_A11//2.00E-160//AT3G16150| L-asparaginase, putative / L-asparagine amidohydrolase, putative	Unigene25690_A11//0.00E+00//TC158757				nr +
Unigene25691_A11	300	36.10	13.85	17.40	54.46	43.73	49.98	6.20	5.71	4.78	-1.38E+00	1.07E-13	Down	-1.05E+00	9.40E-09	Down	-3.17E-01	1.95E-02		-1.24E-01	4.56E-01		-1.19E-01	7.87E-01		-3.75E-01	3.77E-01					Unigene25691_A11//5.00E-117//gi|78329476|gb|DT549750.1|DT549750				
Unigene25692_A11	875	8.07	11.00	7.79	12.64	9.41	12.65	13.92	6.64	7.33	4.47E-01	1.66E-02		-5.14E-02	8.31E-01		-4.26E-01	9.42E-03		8.00E-04	9.98E-01		-1.07E+00	1.13E-12	Down	-9.25E-01	1.66E-10		Unigene25692_A11//gi|18411368|ref|NP_567088.1|//7.00E-36//dihydrodipicolinate reductase family protein [Arabidopsis thaliana] >gi|75245889|sp|Q8LB01.1|DAPB2_ARATH RecName: Full=Dihydrodipicolinate reductase 2, chloroplastic; Short=DHPR 2; Flags: Precursor >gi|111074490|gb|ABH04618.1| At3g59890 [Arabidopsis thaliana]	Unigene25692_A11//3.00E-36//AT3G59890| dihydrodipicolinate reductase family protein	Unigene25692_A11//0.00E+00//gi|78329476|gb|DT549750.1|DT549750		ko00300|Lysine biosynthesis		nr -
Unigene25693_A11	578	3.35	8.94	3.69	6.38	8.34	4.30	20.55	11.79	9.37	1.42E+00	3.92E-07	Up	1.38E-01	7.50E-01		3.87E-01	1.77E-01		-5.70E-01	7.96E-02		-8.02E-01	5.51E-08		-1.13E+00	5.52E-14	Down	Unigene25693_A11//gi|154269264|gb|ABS72192.1|//3.00E-14//mitochondrial NADH-ubiquinone oxidoreductase [Corchorus olitorius]	Unigene25693_A11//3.00E-15//AT3G03070| NADH-ubiquinone oxidoreductase-related	Unigene25693_A11//3.00E-166//TC164563		ko00190|Oxidative phosphorylation		nr -
Unigene25696_A11	932	28.41	15.06	15.20	39.87	23.98	31.84	31.21	22.06	15.00	-9.16E-01	4.42E-17		-9.02E-01	5.48E-16		-7.34E-01	1.04E-19		-3.25E-01	1.74E-04		-5.00E-01	2.09E-08		-1.06E+00	1.56E-29	Down	Unigene25696_A11//gi|4557063|gb|AAD22502.1|//5.00E-25//expressed protein [Arabidopsis thaliana]		Unigene25696_A11//6.00E-175//ES808231				nr +
Unigene25697_A11	1893	1.44	4.12	0.98	1.58	1.82	2.53	5.07	5.43	4.10	1.52E+00	1.96E-11	Up	-5.46E-01	1.76E-01		2.04E-01	5.96E-01		6.80E-01	1.36E-02		9.94E-02	6.25E-01		-3.05E-01	6.52E-02		Unigene25697_A11//gi|18418116|ref|NP_567910.1|//0.00E+00//glycine-rich protein [Arabidopsis thaliana]	Unigene25697_A11//0.00E+00//AT4G32920| glycine-rich protein	Unigene25697_A11//0.00E+00//ES844225				nr +
Unigene25698_A11	1654	35.24	29.62	27.43	65.05	56.52	59.23	73.24	50.87	32.85	-2.50E-01	3.30E-04		-3.61E-01	3.26E-07		-2.03E-01	1.44E-05		-1.35E-01	9.25E-03		-5.26E-01	2.38E-35		-1.16E+00	5.54E-139	Down	Unigene25698_A11//gi|112972|sp|P28734.1|AATC_DAUCA//0.00E+00//RecName: Full=Aspartate aminotransferase, cytoplasmic; AltName: Full=Transaminase A >gi|167546|gb|AAA33134.1| aspartate aminotransferase [Daucus carota] >gi|445587|prf||1909339A Asp aminotransferase	Unigene25698_A11//0.00E+00//AT5G11520| ASP3 (ASPARTATE AMINOTRANSFERASE 3); L-aspartate:2-oxoglutarate aminotransferase	Unigene25698_A11//0.00E+00//TC146702		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism//ko00350|Tyrosine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr +
Unigene25700_A11	471	0.22	3.01	2.37	0.53	3.36	1.05	0.00	0.00	0.00	3.76E+00	3.98E-06	Up	3.42E+00	1.92E-04	Up	2.67E+00	1.61E-05	Up	9.96E-01	3.94E-01		null	null		null	null		Unigene25700_A11//gi|83853827|gb|AC47859.1|//9.00E-26//membrane protein-like protein [Glycine max]	Unigene25700_A11//4.00E-13//AT2G25737| unknown protein	Unigene25700_A11//2.00E-111//ES799196				nr +
Unigene25701_A11	1281	5.68	14.64	12.39	9.68	23.79	18.33	0.07	0.00	0.00	1.37E+00	1.19E-22	Up	1.13E+00	6.62E-14	Up	1.30E+00	2.00E-39	Up	9.21E-01	2.87E-16		-6.04E+00	4.04E-01		-6.04E+00	3.58E-01		Unigene25701_A11//gi|83853827|gb|AC47859.1|//1.00E-129//membrane protein-like protein [Glycine max]	Unigene25701_A11//3.00E-74//AT2G25737| unknown protein	Unigene25701_A11//0.00E+00//ES799196				nr -
Unigene25702_A11	1598	1.31	1.78	2.90	4.80	4.14	4.47	2.01	3.09	2.37	4.39E-01	2.43E-01		1.15E+00	1.15E-04	Up	-2.15E-01	3.52E-01		-1.04E-01	6.80E-01		6.18E-01	1.06E-02		2.36E-01	4.19E-01		Unigene25702_A11//gi|15228377|ref|NP_190412.1|//1.00E-120//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]	Unigene25702_A11//8.00E-122//AT3G48410| hydrolase, alpha/beta fold family protein	Unigene25702_A11//1.00E-41//EG036043				nr -
Unigene25706_A11	1524	5.60	14.90	6.95	6.54	4.38	3.85	1.91	3.29	5.62	1.41E+00	1.20E-28	Up	3.13E-01	9.91E-02		-5.77E-01	6.45E-04		-7.63E-01	1.63E-05		7.82E-01	1.05E-03		1.55E+00	4.49E-16	Up	Unigene25706_A11//gi|15220725|ref|NP_174322.1|//1.00E-113//remorin family protein [Arabidopsis thaliana]	Unigene25706_A11//4.00E-63//AT1G30320| remorin family protein	Unigene25706_A11//3.00E-113//ES804827				nr +
Unigene25707_A11	1805	1.10	5.59	2.60	1.85	1.37	1.95	0.77	1.97	2.56	2.34E+00	1.99E-25	Up	1.24E+00	3.26E-05	Up	-4.29E-01	2.15E-01		7.79E-02	8.35E-01		1.35E+00	8.71E-06	Up	1.73E+00	2.16E-10	Up	Unigene25707_A11//gi|15220725|ref|NP_174322.1|//1.00E-132//remorin family protein [Arabidopsis thaliana]	Unigene25707_A11//2.00E-76//AT1G30320| remorin family protein	Unigene25707_A11//3.00E-113//ES804827				nr -
Unigene25708_A11	984	3.83	3.71	5.36	4.91	4.97	10.01	5.24	5.86	3.89	-4.63E-02	8.91E-01		4.85E-01	8.00E-02		1.72E-02	9.63E-01		1.03E+00	1.83E-08	Up	1.61E-01	5.32E-01		-4.32E-01	6.11E-02		Unigene25708_A11//gi|226506158|ref|NP_001150517.1|//5.00E-60//protein SFT2 [Zea mays] >gi|195639824|gb|ACG39380.1| protein SFT2 [Zea mays]	Unigene25708_A11//2.00E-50//AT4G26550| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: SFT2-like (InterPro:IPR011691); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G56020.1); Has 452 Blast hits to 452 proteins in 136 species: Archae - 0; Bacteria - 0; Metazoa - 198; Fungi - 89; Plants - 61; Viruses - 0; Other Eukaryotes - 104 (source: NCBI BLink).	Unigene25708_A11//0.00E+00//EE592710				nr +
Unigene25709_A11	1432	2.63	3.08	1.82	2.16	0.84	0.73	4.07	3.59	3.17	2.27E-01	4.52E-01		-5.30E-01	1.14E-01		-1.36E+00	5.55E-05	Down	-1.57E+00	1.82E-05	Down	-1.83E-01	4.61E-01		-3.62E-01	9.80E-02		Unigene25709_A11//gi|42568494|ref|NP_200101.2|//6.00E-21//AT hook motif-containing protein [Arabidopsis thaliana] >gi|57222118|gb|AAK38966.1| At5g52890 [Arabidopsis thaliana] >gi|57222216|gb|AAK39015.1| At5g52890 [Arabidopsis thaliana]	Unigene25709_A11//3.00E-22//AT5G52890| AT hook motif-containing protein	Unigene25709_A11//0.00E+00//gi|78330396|gb|DT550670.1|DT550670				nr +
Unigene25712_A11	506	4.55	6.21	7.05	8.07	6.12	4.28	3.43	1.57	0.87	4.49E-01	2.14E-01		6.32E-01	6.46E-02		-3.98E-01	1.95E-01		-9.14E-01	2.15E-03		-1.13E+00	1.21E-02		-1.98E+00	3.36E-05	Down				Unigene25712_A11//1.00E-97//TC139447				
Unigene25715_A11	1613	2.34	3.30	1.62	2.69	4.68	3.25	5.66	11.30	31.32	4.98E-01	5.69E-02		-5.30E-01	1.14E-01		7.99E-01	7.31E-05		2.74E-01	3.54E-01		9.97E-01	1.20E-16		2.47E+00	2.27E-166	Up	Unigene25715_A11//gi|3378495|emb|CAA07568.1|//1.00E-107//Mitochondrial carrier protein [Ribes nigrum]	Unigene25715_A11//1.00E-126//AT2G30160| mitochondrial substrate carrier family protein	Unigene25715_A11//0.00E+00//TC168154				nr +
Unigene25719_A11	1142	0.82	1.02	0.89	1.31	3.47	2.29	1.59	1.35	2.06	3.07E-01	6.13E-01		1.03E-01	8.77E-01		1.41E+00	4.09E-06	Up	8.10E-01	4.06E-02		-2.33E-01	6.42E-01		3.71E-01	3.26E-01		Unigene25719_A11//gi|158516790|gb|ABW70158.1|//1.00E-83//vesicle-associated protein [Medicago truncatula]	Unigene25719_A11//2.00E-64//AT3G60600| VAP (VESICLE ASSOCIATED PROTEIN); protein binding	Unigene25719_A11//6.00E-120//TC167342				nr -
Unigene2572_A11	911	2.58	4.23	3.04	11.76	13.15	13.14	1.30	0.50	4.81	7.10E-01	2.30E-02		2.34E-01	5.79E-01		1.62E-01	3.96E-01		1.60E-01	4.04E-01		-1.36E+00	1.74E-02		1.89E+00	4.62E-11	Up	Unigene2572_A11//gi|113206404|gb|AB134432.1|//1.00E-13//CRY [Pisum sativum]	Unigene2572_A11//8.00E-13//AT2G01570| RGA1 (REPRESSOR OF GA1-3 1); protein binding / transcription factor	Unigene2572_A11//6.00E-178//TC169400	GRAS			nr +
Unigene25720_A11	1180	0.09	0.34	0.00	1.77	0.58	7.00	0.65	0.78	2.53	1.95E+00	1.44E-01		-6.47E+00	3.94E-01		-1.60E+00	2.04E-04	Down	1.98E+00	3.75E-18	Up	2.73E-01	6.70E-01		1.97E+00	3.27E-08	Up	Unigene25720_A11//gi|224088063|ref|XP_002308312.1|//1.00E-134//cytochrome P450 [Populus trichocarpa] >gi|222854288|gb|EEE91835.1| cytochrome P450 [Populus trichocarpa]	Unigene25720_A11//7.00E-125//AT2G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene25720_A11//3.00E-38//DW512175		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00906|Carotenoid biosynthesis		nr +
Unigene25721_A11	872	1.68	2.15	1.89	3.37	3.83	5.65	2.42	4.27	8.27	3.56E-01	4.56E-01		1.72E-01	7.27E-01		1.85E-01	6.25E-01		7.44E-01	5.80E-03		8.15E-01	4.04E-03		1.77E+00	2.90E-16	Up	Unigene25721_A11//gi|224114389|ref|XP_002332385.1|//2.00E-20//cytochrome P450 [Populus trichocarpa] >gi|222832209|gb|EEE70686.1| cytochrome P450 [Populus trichocarpa]	Unigene25721_A11//6.00E-21//AT2G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene25721_A11//2.00E-69//gi|109883205|gb|DW512175.1|DW512175		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene25725_A11	1131	13.55	27.42	12.62	34.40	52.12	31.43	42.84	37.58	32.86	1.02E+00	2.06E-23	Up	-1.03E-01	5.45E-01		6.00E-01	3.34E-21		-1.30E-01	1.85E-01		-1.89E-01	7.70E-03		-3.83E-01	8.60E-09		Unigene25725_A11//gi|263199372|gb|ACV69975.1|//4.00E-54//WRKY transcription factor [Vitis pseudoreticulata]	Unigene25725_A11//6.00E-27//AT3G56400| WRKY70; transcription factor/ transcription repressor	Unigene25725_A11//0.00E+00//gi|109842282|gb|DW240842.1|DW240842	WRKY	ko04626|Plant-pathogen interaction		nr +

Unigene25733_All	1030	52.17	46.98	57.23	73.17	72.05	71.43	96.75	67.04	41.93	-1.51E-01	4.85E-02		1.34E-01	8.50E-02		-2.24E-02	8.07E-01		-3.48E-02	6.56E-01		-5.29E-01	1.41E-29		-1.21E+00	2.10E-122	Down	Unigene25733_All//gi|18396016|ref|NP_564256.1|//2.00E-81//emp24/gp25L/p24 family protein [Arabidopsis thaliana] >gi|9295740|gb|AAF87046.1|AC006535_24 T24P13.7 [Arabidopsis thaliana]	Unigene25733_All//3.00E-64//AT1G26690| emp24/gp25L/p24 family protein	Unigene25733_All//0.00E+00//TC151261			GO:0008565//GO:0015031//GO:0031224//GO:0043231	nr +
Unigene25734_All	1223	3.76	16.03	6.40	4.52	7.26	13.48	14.97	33.66	45.83	2.09E+00	1.56E-42	Up	7.66E-01	3.87E-04		6.84E-01	1.90E-04		1.58E+00	3.44E-26	Up	1.17E+00	3.57E-47	Up	1.61E+00	3.33E-106	Up	Unigene25734_All//gi|108707569|gb|ABF95364.1|//3.00E-85//Phosphatidylinositol transfer protein, expressed [Oryza sativa (japonica cultivar-group)]		Unigene25734_All//0.00E+00//DW243278			GO:0044464//GO:0051234	nr +
Unigene25735_All	1282	2.24	468.04	3.32	2.37	8.06	32.13	45.38	220.65	300.65	7.70E+00	0.00E+00	Up	5.66E-01	6.75E-02		1.77E+00	5.56E-21	Up	3.76E+00	6.31E-176	Up	2.28E+00	0.00E+00	Up	2.73E+00	0.00E+00	Up	Unigene25735_All//gi|15223567|ref|NP_176053.1|//1.00E-155//AtGolS2 (Arabidopsis thaliana galactinol synthase 2); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups >gi|9954752|gb|AAG09103.1|AC009323_14 Putative galactinol synthase [Arabidopsis thaliana] >gi|15215762|gb|AAK91426.1|At1g56600/F25P12_16 [Arabidopsis thaliana] >gi|16323314|gb|AAL15412.1|At1g56600/F25P12_16 [Arabidopsis thaliana] >gi|17298125|dbj|BAB78531.1|galactinol synthase [Arabidopsis thaliana]	Unigene25735_All//4.00E-142//AT1G56600| AtGolS2 (Arabidopsis thaliana galactinol synthase 2); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene25735_All//0.00E+00//gi|78344359|gb|DT564633.1|DT564633				nr +
Unigene25738_All	751	0.49	2.36	2.13	1.39	0.64	1.80	5.86	5.84	4.03	2.28E+00	6.80E-05	Up	2.12E+00	5.41E-04	Up	-1.12E+00	8.44E-02		3.73E-01	5.63E-01		-2.80E-03	1.02E+00		-5.38E-01	3.10E-02		Unigene25738_All|gi|297800436|ref|XP_002868102.1|//9.00E-07//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297313938|gb|EFH44361.1|oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene25738_All//5.00E-08//AT4G16765| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene25738_All//3.00E-37//EV494750				nr -
Unigene25739_All	741	7.63	41.44	19.76	7.93	11.11	21.70	25.85	33.50	14.41	2.44E+00	4.25E-80	Up	1.37E+00	2.25E-17	Up	4.86E-01	1.41E-02		1.45E+00	1.04E-22	Up	3.74E-01	1.31E-04		-8.43E-01	8.08E-14		Unigene25739_All|gi|297800436|ref|XP_002868102.1|//8.00E-15//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297313938|gb|EFH44361.1|oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene25739_All//4.00E-16//AT4G16765| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene25739_All//0.00E+00//TC168767			GO:0008152//GO:0016706//GO:0046914	nr -
Unigene25741_All	1105	9.00	5.64	6.02	8.57	8.07	9.52	44.92	9.04	22.35	-6.74E-01	2.01E-04		-5.79E-01	2.17E-03		-8.57E-02	7.08E-01		1.53E-01	4.71E-01		-2.31E+00	4.73E-149	Down	-1.01E+00	5.03E-46	Down	Unigene25741_All//gi|82659447|gb|AB888840.1|//1.00E-141//aquaporin [Stevia rebaudiana]	Unigene25741_All//5.00E-126//AT2G37170| PIP2B (PLASMA MEMBRANE INTRINSIC PROTEIN 2); water channel	Unigene25741_All//0.00E+00//CO086106				nr +
Unigene25742_All	504	0.00	0.20	0.00	0.00	0.00	0.00	2.10	6.22	25.45	7.65E+00	3.87E-01		null	null		null	null		null	null		1.57E+00	2.66E-06	Up	3.60E+00	4.40E-62	Up	Unigene25742_All|gi|13937213|gb|AAK50099.1|AF372961_1/4.00E-58//AT3g51000/F24M12_40 [Arabidopsis thaliana] >gi|6562252|emb|CAB62622.1|epoxide hydrolase-like protein [Arabidopsis thaliana] >gi|18491129|gb|AAL69533.1|AT3g51000/F24M12_40 [Arabidopsis thaliana]	Unigene25742_All//9.00E-59//AT3G51000| epoxide hydrolase, putative	Unigene25742_All//1.00E-112//BG439973			GO:0004713//GO:0016803	nr +
Unigene25743_All	2566	10.40	8.02	8.30	12.54	11.50	14.10	8.16	6.58	17.84	-3.75E-01	3.70E-04		-3.25E-01	3.35E-03		-1.25E-01	2.45E-01		1.69E-01	8.20E-02		-3.10E-01	4.60E-03		1.13E+00	1.10E-50	Up	Unigene25743_All|gi|300608166|emb|CAZ86693.1|//4.00E-75//epoxide hydrolase 2 [Prunus persica]	Unigene25743_All//2.00E-68//AT4G02340| epoxide hydrolase, putative	Unigene25743_All//0.00E+00//gi|78354672|gb|DT574946.1|DT574946		ko03010|Ribosome	GO:0004713	nr +
Unigene25744_All	1512	1.66	8.98	6.97	10.18	6.22	2.21	1.17	0.08	0.84	2.43E+00	1.32E-35	Up	2.07E+00	3.67E-22	Up	-7.11E-01	4.92E-08		-2.20E+00	4.39E-39	Down	-3.82E+00	2.43E-09	Down	-4.78E-01	2.64E-01		Unigene25744_All|gi|240254055|ref|NP_563875.6|//0.00E+00//polygalacturonase [Arabidopsis thaliana]	Unigene25744_All//1.00E-162//AT1G10640| polygalacturonase	Unigene25744_All//0.00E+00//TC164483		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553//GO:0044238//GO:0045229	nr +
Unigene25746_All	1477	9.78	3.84	12.83	28.97	26.28	25.69	13.08	1.84	2.54	-1.35E+00	2.35E-17	Down	3.93E-01	3.11E-03		-1.41E-01	1.06E-01		-1.74E-01	4.56E-02		-2.83E+00	2.72E-73	Down	-2.37E+00	6.13E-62	Down	Unigene25746_All//gi|27765046|gb|AAG32644.1|//1.00E-86//At5g67210 [Arabidopsis thaliana]	Unigene25746_All//2.00E-67//AT2G15440| unknown protein	Unigene25746_All//0.00E+00//TC147766				nr +
Unigene25747_All	1336	5.99	21.47	10.96	14.99	16.01	12.74	4.40	8.17	1.61	1.84E+00	1.94E-52	Up	8.71E-01	1.16E-08		9.47E-02	5.31E-01		-2.34E-01	7.36E-02		8.92E-01	1.07E-08		-1.45E+00	2.17E-10	Down	Unigene25747_All//gi|115311433|gb|AB193897.1|//8.00E-35//At1g65690 [Arabidopsis thaliana] >gi|222422971|dbj|BAH19470.1|AT4G01670 [Arabidopsis thaliana]	Unigene25747_All//1.00E-31//AT4G01670| unknown protein	Unigene25747_All//0.00E+00//TC171872				nr +
Unigene25749_All	1146	21.50	10.30	12.82	41.03	36.30	35.59	38.41	23.71	33.20	-1.06E+00	3.57E-20	Down	-7.46E-01	6.04E-11		-1.77E-01	2.44E-02		-2.06E-01	1.00E-02		-6.96E-01	1.50E-21		-2.10E-01	3.39E-03		Unigene25749_All|gi|115485231|ref|NP_001067759.1|//1.00E-121//Os11g0312400 [Oryza sativa Japonica Group] >gi|585338|sp|Q08480.1|KAD2_ORYSJ RecName: Full=Adenylate kinase B; Short=AK B; AltName: Full=ATP-AMP transphosphorylase B >gi|3918579|dbj|BAA00181.1|adenylate kinase-b [Oryza sativa] >gi|62734015|gb|AAX96124.1|adenylate kinase b (ec 2.7.4.3) (atp-amp transphosphorylase) [Oryza sativa Japonica Group] >gi|113644981|dbj|BAF28122.1|Os11g0312400 [Oryza sativa Japonica Group]	Unigene25749_All//7.00E-113//AT5G63400| ADK1 (ADENYLATE KINASE 1); ATP binding / adenylate kinase/ nucleobase, nucleoside, nucleotide kinase/ nucleotide kinase/ phosphotransferase, phosphate group as acceptor	Unigene25749_All//0.00E+00//TC131414		ko00230|Purine metabolism		nr +
Unigene25752_All	1526	89.93	348.74	182.64	25.79	24.91	33.06	1.33	1.29	1.46	1.96E+00	0.00E+00	Up	1.02E+00	6.10E-202	Up	-4.99E-02	6.31E-01		3.58E-01	7.56E-07		-4.70E-02	9.26E-01		1.37E-01	7.19E-01		Unigene25752_All|gi|21593424|gb|AAM65391.1|//9.00E-86//fatty acid elongase-like protein (cer2-like) [Arabidopsis thaliana]	Unigene25752_All//1.00E-84//AT4G13840| transferase family protein	Unigene25752_All//0.00E+00//TC177789		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0006633//GO:0009534	nr +
Unigene25753_All	1303	2.29	4.74	2.00	3.94	3.12	3.12	3.41	4.62	3.94	1.05E+00	1.46E-05	Up	-1.93E-01	6.22E-01		-3.37E-01	2.22E-01		-3.36E-01	2.34E-01		4.39E-01	4.56E-02		2.11E-01	3.99E-01				Unigene25753_All//4.00E-07//BQ401821				
Unigene25755_All	1326	1.97	2.14	1.85	3.83	5.58	3.68	6.22	3.03	4.33	1.17E-01	7.46E-01		-9.49E-02	8.09E-01		5.43E-01	9.22E-03		-5.89E-02	8.48E-01		-1.04E+00	1.71E-08	Down	-5.23E-01	2.73E-03		Unigene25755_All//gi|46931320|gb|AT06464.1|//6.00E-80//At1g10600 [Arabidopsis thaliana]	Unigene25755_All//3.00E-81//AT1G10600| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ubiquitin-dependent protein catabolic process; LOCATED IN: chloroplast; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Mov34/MPN/PAD-1 (InterPro:IPR000555); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G16144.1); Has 753 Blast hits to 752 proteins in 167 species: Archae - 0; Bacteria - 0; Metazoa - 359; Fungi - 199; Plants - 115; Viruses - 0; Other Eukaryotes - 80 (source: NCBI BLink).	Unigene25755_All//0.00E+00//gi|33266646|gb|AI055532.1|AI055532		ko04144|Endocytosis	GO:0005488//GO:0006886//GO:0010638//GO:0044464//GO:0051603//GO:0070646	nr +
Unigene25757_All	1842	2.36	0.61	0.64	6.63	3.27	2.80	11.06	8.58	10.71	-1.96E+00	2.77E-09	Down	-1.89E+00	2.01E-08	Down	-1.02E+00	1.51E-11	Down	-1.25E+00	4.60E-14	Down	-3.67E-01	7.96E-04		-4.74E-02	6.97E-01		Unigene25757_All|gi|224067240|ref|XP_002302425.1|//1.00E-171//cytochrome P450 [Populus trichocarpa] >gi|222844151|gb|EEE81698.1|cytochrome P450 [Populus trichocarpa]	Unigene25757_All//7.00E-113//AT4G37240| CYP81D3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene25757_All//5.00E-146//gi|164362113|gb|EX168646.1|EX168646		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene2576_All	1767	3.32	1.03	1.60	5.27	6.61	4.40	6.80	2.34	2.53	-1.68E+00	4.20E-10	Down	-1.05E+00	4.59E-05	Down	3.26E-01	5.39E-02		-2.62E-01	2.05E-01		-1.54E+00	2.11E-21	Down	-1.43E+00	6.89E-20	Down	Unigene2576_All|gi|75331853|sp|Q94186.1|UBC37_ARATH//4.00E-73//RecName: Full=Probable ubiquitin-conjugating enzyme E2 37; AltName: Full=Ubiquitin carrier protein 37 >gi|16974491|gb|AAL31249.1|At3g24512/At3g24512 [Arabidopsis thaliana] >gi|66354482|gb|AAY44876.1|ubiquitinating enzyme [Arabidopsis thaliana]	Unigene2576_All//2.00E-74//AT3G24515| UBC37 (ubiquitin-conjugating enzyme 37); small conjugating protein ligase/ ubiquitin-protein ligase	Unigene2576_All//5.00E-152//DW502480		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene25760_All	2604	7.09	3.99	3.31	0.77	1.60	0.59	0.16	0.22	0.24	-8.30E-01	2.04E-10		-1.10E+00	1.90E-15	Down	1.06E+00	2.27E-04	Up	-3.76E-01	4.53E-01		4.68E-01	6.13E-01		5.92E-01	4.53E-01		Unigene25760_All|gi|224106201|ref|XP_002314083.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222850491|gb|EEE88038.1|white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene25760_All//0.00E+00//AT1G51460| ABC transporter family protein	Unigene25760_All//0.00E+00//TC151356		ko03040|Spliceosome//ko02010|ABC transporters	GO:0006633//GO:0006970//GO:0009725//GO:0015405//GO:0015604//GO:0017111//GO:0032559//GO:0044464	nr +
Unigene25761_All	1168	2.55	3.86	1.64	38.77	30.10	24.21	8.83	4.58	2.80	5.97E-01	3.66E-02		-6.38E-01	9.30E-02		-3.65E-01	4.86E-07		-6.80E-01	1.13E-18		-9.47E-01	4.58E-09		-1.66E+00	3.12E-21	Down	Unigene25761_All|gi|169667045|gb|ACA64095.1|//1.00E-72//WOX4 [Petunia x hybrida]	Unigene25761_All//3.00E-52//AT1G46480| WOX4 (WUSCHEL RELATED HOMEOBOX 4); transcription factor	Unigene25761_All//0.00E+00//TC135359	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene25764_All	836	22.47	145.28	24.33	41.53	93.21	56.72	44.00	71.34	96.64	2.69E+00	0.00E+00	Up	1.15E-01	4.09E-01		1.17E+00	2.20E-85	Up	4.50E-01	1.58E-09		6.97E-01	5.79E-29		1.14E+00	1.46E-89	Up	Unigene25764_All|gi|55419650|gb|AAV51938.1|//6.00E-95//AP2/EREBP transcription factor ERF-1 [Gossypium hirsutum]	Unigene25764_All//1.00E-19//AT3G15210| ERF4 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 4); DNA binding / protein binding / transcription factor/ transcription repressor	Unigene25764_All//0.00E+00//TC179612	AP2-EREBP		GO:0001071//GO:0002218//GO:0003676//GO:0006351//GO:0009743//GO:0009873//GO:0010468//GO:0030528//GO:0044451	nr -
Unigene25766_All	1570	1.67	1.07	0.81	2.79	1.60	2.42	0.73	2.05	1.19	-6.46E-01	9.73E-02		-1.03E+00	1.22E-02		-8.02E-01	3.05E-03		-2.09E-01	5.31E-01		1.50E+00	4.53E-06	Up	7.14E-01	8.20E-02		Unigene25766_All|gi|15227541|ref|NP_178413.1|//2.00E-47//CAAX amino terminal protease family protein [Arabidopsis thaliana] >gi|3548816|gb|AAC34488.1| similar to late embryogenesis abundant proteins [Arabidopsis thaliana]	Unigene25766_All//8.00E-23//AT2G03140| CAAX amino terminal protease family protein				GO:0044464	nr -
Unigene25767_All	1352	14.43	94.03	31.27	13.15	17.45	32.27	25.92	35.33	48.12	2.70E+00	0.00E+00	Up	1.12E+00	1.33E-35	Up	4.08E-01	1.25E-04		1.29E+00	3.43E-51	Up	4.47E-01	6.25E-11		8.92E-01	6.57E-49		Unigene25767_All|gi|283488487|gb|ADB24765.1|//0.00E+00//UDP-D-glucose dehydrogenase [Gossypium hirsutum]	Unigene25767_All//3.00E-172//AT5G15490| UDP-glucose 6-dehydrogenase, putative	Unigene25767_All//0.00E+00//TC147613		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions	GO:0000166//GO:0008152//GO:0016614	nr +
Unigene25768_All	1297	7.95	4.81	2.59	19.86	17.82	14.90	11.25	2.48	19.90	-7.26E-01	4.52E-05		-1.62E+00	1.32E-15	Down	-1.57E-01	1.81E-01		-4.14E-01	7.80E-05		-2.18E+00	3.40E-41	Down	8.24E-01	1.59E-17		Unigene25768_All|gi|21314549|gb|AAM47000.1|AF512542_1/1.00E-154//alpha-expansin precursor [Gossypium hirsutum]	Unigene25768_All//8.00E-132//AT2G28950| ATEXP16 (ARABIDOPSIS THALIANA EXPANSIN A6)	Unigene25768_All//0.00E+00//TC138918				nr -

Unigene2577_All	1431	3.77	3.36	3.68	3.17	2.41	1.74	2.90	1.08	1.73	-1.63E-01	5.63E-01		-3.17E-02	9.19E-01		-3.97E-01	1.65E-01		-8.68E-01	1.94E-03		-1.42E+00	4.05E-07	Down	-7.46E-01	3.74E-03		Unigene2577_All//gi|145336613|ref|NP_175542.2|//0.00E+00//tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase [Arabidopsis thaliana]	Unigene2577_All//2.00E-176//AT1G51310| tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	Unigene2577_All//0.00E+00//ES825312				nr +
Unigene25770_All	1180	8.56	6.23	2.66	17.14	14.80	12.06	3.22	3.22	7.63	-4.59E-01	1.12E-02		-1.68E+00	3.76E-16	Down	-2.12E-01	9.71E-02		-5.08E-01	2.01E-05		-7.00E-04	9.97E-01		1.24E+00	2.83E-12	Up	Unigene25770_All//gi|4512625|gb|AAD21694.1|//6.00E-07//ESTs gb|T20423, gb|AA712864, gb|H76323 and gb|Z25560 come from this gene [Arabidopsis thaliana]	Unigene25770_All//7.00E-31//AT4G16850| unknown protein					nr -
Unigene25776_All	1121	31.92	24.72	32.40	65.15	53.94	47.86	72.94	65.17	28.64	-3.69E-01	3.87E-05		2.12E-02	8.39E-01		-2.72E-01	1.50E-06		-4.45E-01	3.94E-14		-1.63E-01	2.33E-03		-1.35E+00	1.48E-119	Down	Unigene25776_All//gi|115485735|ref|NP_001068011.1|//3.00E-56//Os11g0531700 [Oryza sativa Japonica Group] >gi|113645233|dbj|BAF28374.1| Os11g0531700 [Oryza sativa Japonica Group]	Unigene25776_All//1.00E-54//AT3G26690| ATNUDX13 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 13); bis(5'-adenosyl)-pentaphosphatase/ hydrolase	Unigene25776_All//0.00E+00//DW497827			GO:0004551//GO:0043231	nr +
Unigene25777_All	916	1.14	1.88	1.74	1.96	3.12	6.75	46.11	46.86	34.01	7.19E-01	1.48E-01		6.10E-01	2.61E-01		6.72E-01	7.09E-02		1.79E+00	5.26E-12	Up	2.33E-02	7.93E-01		-4.39E-01	8.61E-10		Unigene25777_All//gi|195611428|gb|ACG27544.1|//1.00E-78//peroxisomal membrane protein PMP22 [Zea mays]	Unigene25777_All//9.00E-89//AT4G14305| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; CONTAINS InterPro DOMAIN/s: Mpv17/PMP22 (InterPro:IPR007248); BEST Arabidopsis thaliana protein match is: PMP22 (TAIR:AT4G04470.1); Has 957 Blast hits to 957 proteins in 126 species: Archae - 0; Bacteria - 0; Metazoa - 456; Fungi - 286; Plants - 164; Viruses - 0; Other Eukaryotes - 51 (source: NCBI BLink).	Unigene25777_All//0.00E+00//TC172138		ko04146|Peroxisome	GO:0031224	nr +
Unigene25778_All	1359	2.50	5.97	6.94	3.41	3.17	3.22	1.06	0.46	0.29	1.25E+00	4.78E-09	Up	1.47E+00	1.47E-12	Up	-1.06E-01	7.58E-01		-8.06E-02	7.95E-01		-1.20E+00	1.76E-02		-1.85E+00	3.87E-04	Down			Unigene25778_All//1.00E-173//C0099713				
Unigene25779_All	778	101.08	50.28	116.77	16.33	16.82	12.07	0.11	0.11	0.00	-1.01E+00	1.13E-57	Down	2.08E-01	2.76E-04		4.28E-02	8.26E-01		-4.35E-01	5.83E-03		-1.74E-02	1.01E+00		-6.76E+00	3.58E-01		Unigene25779_All//gi|38564300|gb|AAR23729.1|//3.00E-59//At2g41120 [Arabidopsis thaliana] >gi|38604032|gb|AAR24759.1| At2g41120 [Arabidopsis thaliana]	Unigene25779_All//1.00E-60//AT2G41120| unknown protein	Unigene25779_All//0.00E+00//TC131504			GO:0009536	nr -
Unigene25780_All	924	19.71	15.68	18.67	3.56	5.29	1.17	0.00	0.00	0.09	-3.29E-01	1.26E-02		-7.77E-02	6.39E-01		5.73E-01	3.32E-02		-1.60E+00	6.54E-06	Down	null	null		6.43E+00	4.04E-01		Unigene25780_All//gi|38564300|gb|AAR23729.1|//3.00E-34//At2g41120 [Arabidopsis thaliana] >gi|38604032|gb|AAR24759.1| At2g41120 [Arabidopsis thaliana]	Unigene25780_All//2.00E-35//AT2G41120| unknown protein	Unigene25780_All//0.00E+00//TC131504			GO:0043231//GO:0044444	nr -
Unigene25782_All	1594	6.07	8.68	8.12	14.72	14.84	13.43	5.09	3.49	2.07	5.15E-01	6.44E-04		4.19E-01	1.11E-02		1.19E-02	9.46E-01		-1.32E-01	3.20E-01		-5.46E-01	2.63E-03		-1.30E+00	5.95E-12	Down	Unigene25782_All//gi|148886783|sp|Q8GWK2.2|AP2L4_ARATH//1.00E-144//RecName: Full=AP2-like ethylene-responsive transcription factor At2g41710	Unigene25782_All//1.00E-128//AT2G41710| ovule development protein, putative	Unigene25782_All//0.00E+00//gi|164320821|gb|ES826483.1|ES826483	AP2-EREBP		GO:0001071//GO:0006351//GO:0010468//GO:0016491//GO:0043231	nr +
Unigene25784_All	1672	5.38	4.12	2.20	14.93	19.54	14.94	16.92	2.75	6.34	-3.85E-01	4.84E-02		-1.29E+00	5.80E-10	Down	3.89E-01	1.02E-05		1.10E-03	9.94E-01		-2.62E+00	1.70E-98	Down	-1.42E+00	4.17E-45	Down	Unigene25784_All//gi|30102712|gb|AAP21274.1|//1.00E-100//At4g28230 [Arabidopsis thaliana]	Unigene25784_All//5.00E-94//AT4G28230| unknown protein	Unigene25784_All//0.00E+00//TC158039				nr -
Unigene25787_All	1602	3.00	6.64	2.79	4.91	2.47	3.64	14.49	32.77	15.47	1.14E+00	3.49E-10	Up	-1.06E-01	7.14E-01		-9.91E-01	2.49E-07		-4.34E-01	3.96E-02		1.18E+00	1.35E-60	Up	9.43E-02	3.97E-01		Unigene25787_All//gi|9858770|gb|AAG01117.1|AF273333_2//2.00E-49//BAC19.2 [Solanum lycopersicum]	Unigene25787_All//1.00E-08//AT5G49610| F-box family protein	Unigene25787_All//0.00E+00//gi|164304705|gb|ES808606.1|ES808606				nr +
Unigene25788_All	1910	1.12	0.40	0.84	1.96	1.88	1.58	3.01	1.23	1.17	-1.50E+00	1.14E-03		-4.25E-01	3.74E-01		-6.11E-02	8.50E-01		-3.04E-01	3.96E-01		-1.30E+00	1.98E-08	Down	-1.37E+00	2.20E-09	Down	Unigene25788_All//gi|297808821|ref|XP_002872294.1|//0.00E+00//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297318131|gb|EFH48553.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene25788_All//0.00E+00//AT5G27970| binding	Unigene25788_All//9.00E-117//TC145597		ko04626|Plant-pathogen interaction		nr +
Unigene25789_All	1360	24.51	39.12	41.39	21.21	17.27	28.33	31.18	183.23	16.64	6.75E-01	4.55E-20		7.56E-01	8.06E-25		-2.97E-01	2.16E-03		4.18E-01	6.07E-07		2.55E+00	0.00E+00	Up	-9.06E-01	3.16E-33		Unigene25789_All//gi|75333650|sp|Q9CAI3.1|CAD1I_ARATH//1.00E-160//RecName: Full=Probable cinnamyl alcohol dehydrogenase 1; Short=AtCAD1 >gi|27311669|gb|AA000800.1| Unknown protein [Arabidopsis thaliana] >gi|31711846|gb|AAP68279.1| At1g72680 [Arabidopsis thaliana]	Unigene25789_All//1.00E-155//AT1G72680| cinnamyl-alcohol dehydrogenase, putative	Unigene25789_All//0.00E+00//TC130824		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene25790_All	1497	1.22	2.84	4.27	1.63	1.06	1.09	4.12	11.14	1.33	1.22E+00	6.14E-05	Up	1.80E+00	1.90E-11	Up	-6.24E-01	1.15E-01		-5.86E-01	1.62E-01		1.43E+00	1.46E-26	Up	-1.63E+00	9.25E-13	Down	Unigene25790_All//gi|75333650|sp|Q9CAI3.1|CAD1I_ARATH//1.00E-160//RecName: Full=Probable cinnamyl alcohol dehydrogenase 1; Short=AtCAD1 >gi|27311669|gb|AA000800.1| Unknown protein [Arabidopsis thaliana] >gi|31711846|gb|AAP68279.1| At1g72680 [Arabidopsis thaliana]	Unigene25790_All//1.00E-155//AT1G72680| cinnamyl-alcohol dehydrogenase, putative	Unigene25790_All//0.00E+00//TC140969		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene25791_All	2602	9.59	7.50	7.22	10.86	9.83	9.53	23.37	13.36	7.43	-3.55E-01	1.20E-03		-4.09E-01	3.08E-04		-1.43E-01	2.09E-01		-1.88E-01	8.90E-02		-8.06E-01	8.94E-38		-1.65E+00	1.92E-120	Down	Unigene25791_All//gi|42572403|ref|NP_974297.1|//0.00E+00//transcription factor [Arabidopsis thaliana] >gi|222424421|dbj|BAH20166.1| AT3G13000 [Arabidopsis thaliana]	Unigene25791_All//0.00E+00//AT3G13000| transcription factor	Unigene25791_All//0.00E+00//TC142427			GO:0010468//GO:0043231	nr +
Unigene25793_All	696	16.61	9.90	15.61	18.47	16.82	12.26	18.04	16.27	7.90	-7.47E-01	7.92E-06		-9.01E-02	6.17E-01		-1.35E-01	4.65E-01		-5.90E-01	1.20E-04		-1.49E-01	3.73E-01		-1.19E+00	6.74E-16	Down	Unigene25793_All//gi|195647116|gb|ACG43026.1|//5.00E-41//COV1-like protein [Zea mays]	Unigene25793_A1l//6.00E-39//AT1G43130| LCV2 (LIKE COV 2)	Unigene25793_A1l//0.00E+00//gi|73848986|gb|DT458006.1|DT458006				nr -
Unigene25795_All	1672	6.32	3.85	3.38	9.56	9.39	8.27	12.42	8.12	5.91	-7.16E-01	4.49E-05		-9.05E-01	8.29E-07		-2.62E-02	8.73E-01		-2.11E-01	1.72E-01		-6.12E-01	1.31E-08		-1.07E+00	8.57E-22	Down	Unigene25795_All//gi|240256386|ref|NP_196003.4|//1.00E-171//POLA3; DNA primase [Arabidopsis thaliana]	Unigene25795_All//9.00E-173//AT5G41880| POLA3; DNA primase	Unigene25795_All//0.00E+00//gi|164357660|gb|ES812850.1|ES812850		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03030|DNA replication	GO:0003899//GO:0006259	nr +
Unigene25797_All	1369	5.69	4.44	2.68	14.70	17.91	13.30	18.22	4.15	4.57	-3.59E-01	9.32E-02		-1.09E+00	8.90E-07	Down	2.85E-01	8.87E-03		-1.45E-01	3.11E-01		-2.13E+00	4.37E-68	Down	-2.00E+00	2.02E-64	Down	Unigene25797_All//gi|18414533|ref|NP_567477.1|//3.00E-89//binding [Arabidopsis thaliana]	Unigene25797_A1l//7.00E-86//AT4G15830| binding	Unigene25797_A1l//0.00E+00//TC149854			GO:0044464	nr +
Unigene25799_All	1429	26.00	11.10	14.09	78.54	60.80	97.82	56.60	17.17	17.34	-1.23E+00	9.58E-38	Down	-8.84E-01	1.84E-21		-3.69E-01	4.81E-17		3.17E-01	2.90E-14		-1.72E+00	1.78E-164	Down	-1.71E+00	2.65E-167	Down	Unigene25799_All//gi|211906514|gb|ACJ11750.1|//1.00E-159//lactoylglutathione lyase [Gossypium hirsutum]	Unigene25799_A1l//1.00E-135//AT1G11840| ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase/ metal ion binding	Unigene25799_A1l//0.00E+00//TC131783		ko00620|Pyruvate metabolism		nr -
Unigene2580_All	2023	1.84	0.73	1.87	4.51	3.68	3.93	3.89	3.68	4.02	-1.34E+00	5.24E-05	Down	2.54E-02	9.55E-01		-2.94E-01	1.37E-01		-1.98E-01	3.74E-01		-8.01E-02	7.07E-01		4.74E-02	8.07E-01		Unigene2580_All//gi|79534875|ref|NP_199967.2|//0.00E+00//metalloendopeptidase [Arabidopsis thaliana]	Unigene2580_A1l//0.00E+00//AT5G51540| metalloendopeptidase	Unigene2580_A1l//0.00E+00//TC130337				nr +
Unigene25801_All	1246	11.17	17.36	16.03	19.91	23.85	27.95	14.49	29.65	34.50	6.37E-01	7.24E-08		5.21E-01	4.22E-05		2.61E-01	7.93E-03		4.89E-01	2.97E-08		1.03E+00	7.10E-35	Up	1.25E+00	6.14E-56	Up	Unigene25801_All//gi|18700701|gb|AAL78674.1|AF458699_1//1.00E-148//ankyrin-kinase [Medicago truncatula]	Unigene25801_A1l//7.00E-143//AT2G43850| ankyrin protein kinase, putative (APK1)	Unigene25801_A1l//0.00E+00//CO069627				nr +
Unigene25806_All	1651	12.80	28.82	44.19	22.18	22.57	26.40	154.22	26.68	42.28	1.17E+00	1.74E-44	Up	1.79E+00	3.04E-124	Up	2.52E-02	8.24E-01		2.51E-01	1.98E-03		-2.53E+00	0.00E+00	Down	-1.87E+00	0.00E+00	Down	Unigene25806_All//gi|121755809|gb|ABM64802.1|//0.00E+00//anthocyanidin reductase [Gossypium hirsutum]	Unigene25806_A1l//6.00E-120//AT1G61720| BAN (BANYULS); oxidoreductase	Unigene25806_A1l//0.00E+00//TC129667		ko00941|Flavonoid biosynthesis	GO:0008152//GO:0048037	nr -
Unigene25808_All	991	10.51	11.91	14.19	50.52	57.33	39.42	13.70	1.10	3.62	1.81E-01	3.20E-01		4.33E-01	5.71E-03		1.83E-01	9.24E-03		-3.58E-01	8.12E-07		-3.64E+00	2.25E-65	Down	-1.92E+00	1.07E-33	Down	Unigene25808_All//gi|297834560|ref|XP_002885162.1|//1.00E-75//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331002|gb|EFH81421.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25808_A1l//2.00E-72//AT4G15920| INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPR018169), RAG1-activating protein 1 homologue (InterPro:IPR018179), MtN3 and saliva related transmembrane protein (InterPro:IPR004316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene25808_A1l//0.00E+00//gi|109856377|gb|DW485356.1|DW485356			GO:0031224	nr -
Unigene2581_All	1850	76.02	14.52	31.98	74.53	51.19	34.32	30.65	15.09	17.10	-2.39E+00	0.00E+00	Down	-1.25E+00	1.99E-140	Down	-5.42E-01	4.40E-42		-1.12E+00	1.64E-129	Down	-1.02E+00	3.12E-52	Down	-8.42E-01	4.85E-39		Unigene2581_All//gi|126217796|gb|AB981351.1|//0.00E+00//auxin influx transport protein [Casuarina glauca]	Unigene2581_A1l//0.00E+00//AT1G77690| LAX3 (LIKE AUX1 3); amino acid transmembrane transporter/ auxin influx transmembrane transporter/ transporter	Unigene2581_A1l//0.00E+00//TC133111				nr +
Unigene25810_All	2099	8.30	16.97	15.55	6.93	12.48	22.21	11.82	7.85	47.07	1.03E+00	1.97E-27	Up	9.06E-01	9.85E-20		8.49E-01	2.64E-17		1.68E+00	3.09E-80	Up	-5.92E-01	1.37E-09		1.99E+00	2.13E-249	Up	Unigene25810_All//gi|15239225|ref|NP_196192.1|//0.00E+00//ASA1 (ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1); anthranilate synthase [Arabidopsis thaliana] >gi|418133|sp|P32068.1|TRPE_ARATH RecName: Full=Anthranilate synthase component I-1, chloroplastic; Flags: Precursor >gi|166604|gb|AAA32738.1| anthranilate synthase alpha subunit [Arabidopsis thaliana] >gi|9759098|dbj|BAB09667.1| anthranilate synthase component I-1 precursor [Arabidopsis thaliana]	Unigene25810_A1l//0.00E+00//AT5G05730| ASA1 (ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1); anthranilate synthase	Unigene25810_A1l//0.00E+00//TC159312		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0006568//GO:0006950//GO:0008652//GO:0009536//GO:0009725//GO:0009850//GO:0016833//GO:0043234//GO:0048527	nr +

Unigene25813_All	2670	0.12	0.61	0.06	2.02	3.50	1.07	2.30	1.78	3.55	2.37E+00	1.02E-04	Up	-9.76E-01	5.06E-01		7.95E-01	7.84E-06		-9.19E-01	2.85E-04		-3.64E-01	1.01E-01		6.29E-01	1.04E-04		Unigene25813_All//gi|124359162|gb|ABN05685.1|//2.00E-40//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene25813_All//8.00E-10//AT1G43760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706), Endonuclease/exonuclease/phosphatase (InterPro:IPR005135); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40390.1); Has 2614 Blast hits to 2551 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 1517; Fungi - 2; Plants - 1086; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene25813_All//3.00E-31//TC137548			GO:0005488	nr -
Unigene25814_All	1277	10.73	25.04	14.30	20.09	23.60	37.49	42.68	80.29	62.43	1.22E+00	3.48E-32	Up	4.14E-01	2.18E-03		2.32E-01	1.95E-02		9.00E-01	2.20E-31		9.12E-01	1.34E-77		5.49E-01	5.35E-26		Unigene25814_All//gi|115446837|ref|NP_001047198.1|//2.00E-73//Os02g0572900 [Oryza sativa Japonica Group] >gi|113536729|dbj|BAF09112.1|Os02g0572900 [Oryza sativa Japonica Group]	Unigene25814_All//1.00E-60//AT1G34370| STOP1 (sensitive to proton rhizotoxicity 1); nucleic acid binding / transcription factor/ zinc ion binding	Unigene25814_All//0.00E+00//TC174797	C2H2		GO:0010468//GO:0043231//GO:0046914	nr +
Unigene25815_All	1045	2.20	4.61	2.09	26.74	10.84	9.16	2.31	2.00	1.83	1.06E+00	1.38E-04	Up	-7.65E-02	8.60E-01		-1.30E+00	1.82E-38	Down	-1.55E+00	1.39E-43	Down	-2.06E-01	6.32E-01		-3.34E-01	3.64E-01		Unigene25815_All//gi|15228868|ref|NP_191882.1|//2.00E-53//speckle-type POZ protein-related [Arabidopsis thaliana] >gi|45825155|gb|AAS77485.1|At3g56230 [Arabidopsis thaliana]	Unigene25815_All//1.00E-54//AT3G56230| speckle-type POZ protein-related	Unigene25815_All//0.00E+00//gi|21097487|gb|BQ409800.1|BQ409800		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005488//GO:0009791	nr -
Unigene25816_All	1243	0.25	2.77	1.67	12.90	4.57	5.96	1.90	2.86	3.69	3.46E+00	3.07E-13	Up	2.73E+00	2.06E-06	Up	-1.50E+00	1.84E-27	Down	-1.11E+00	1.95E-15	Down	5.85E-01	4.65E-02		9.52E-01	1.19E-04		Unigene25816_All//gi|15228868|ref|NP_191882.1|//8.00E-51//speckle-type POZ protein-related [Arabidopsis thaliana] >gi|45825155|gb|AAS77485.1|At3g56230 [Arabidopsis thaliana]	Unigene25816_All//4.00E-52//AT3G56230| speckle-type POZ protein-related	Unigene25816_All//0.00E+00//TC163218			GO:0005488//GO:0009791	nr -
Unigene25817_All	1818	0.63	0.95	0.94	1.34	1.63	0.89	4.40	3.63	12.03	5.82E-01	2.41E-01		5.66E-01	2.83E-01		2.79E-01	5.12E-01		-5.86E-01	1.62E-01		-2.75E-01	1.60E-01		1.45E+00	4.75E-36	Up	Unigene25817_All//gi|28466915|gb|AA044066.1|//4.00E-67//At5g20120 [Arabidopsis thaliana]	Unigene25817_All//1.00E-66//AT5G20120| unknown protein	Unigene25817_All//0.00E+00//gi|109873070|gb|DW502045.1|DW502045				nr +
Unigene25819_All	841	82.93	39.46	55.53	115.32	114.93	144.19	82.20	66.40	57.70	-1.07E+00	1.34E-56	Down	-5.79E-01	2.88E-19		-4.90E-03	9.53E-01		3.22E-01	7.48E-13		-3.08E-01	3.99E-08		-5.11E-01	4.46E-20		Unigene25819_All//gi|223469631|gb|ACM90156.1|//7.00E-77//40S ribosomal protein S15-like protein [Jatropha curcas]	Unigene25819_All//3.00E-71//AT5G09510| 40S ribosomal protein S15 (RPS15D)	Unigene25819_All//0.00E+00//gi|109868344|gb|DW497320.1|DW497320		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0019935//GO:0016020//GO:0031981	nr -
Unigene2582_All	1479	24.80	109.22	65.13	49.98	63.66	85.26	53.57	152.63	135.06	2.14E+00	0.00E+00	Up	1.39E+00	3.69E-114	Up	3.49E-01	9.63E-13		7.70E-01	6.64E-63		1.51E+00	0.00E+00	Up	1.33E+00	1.03E-283	Up	Unigene2582_All//gi|297809099|ref|XP_002872433.1|//2.00E-97//T-complex protein 11 [Arabidopsis lyrata subsp. lyrata] >gi|297318270|gb|EFH48692.1| T-complex protein 11 [Arabidopsis lyrata subsp. lyrata]	Unigene2582_All//4.00E-82//AT4G09150| T-complex protein 11	Unigene2582_All//0.00E+00//TC144547				nr -
Unigene25820_All	915	36.65	24.53	21.65	60.70	54.61	86.28	84.19	49.38	41.71	-5.79E-01	4.46E-10		-7.60E-01	4.00E-15		-1.53E-01	3.70E-02		5.07E-01	4.14E-19		-7.70E-01	4.57E-44		-1.01E+00	1.16E-71	Down	Unigene25820_All//gi|225431804|ref|XP_002272727.1|//1.00E-105//PREDICTED: similar to 60S ribosomal protein L19 [Vitis vinifera]	Unigene25820_All//4.00E-87//AT3G16780| 60S ribosomal protein L19 (RPL19B)	Unigene25820_All//0.00E+00//TC134161		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene25826_All	1540	3.33	12.70	1.83	11.97	11.16	10.35	10.08	24.24	37.07	1.93E+00	2.55E-38	Up	-8.61E-01	1.81E-03		-1.01E-01	5.30E-01		-2.09E-01	1.36E-01		1.27E+00	1.76E-48	Up	1.88E+00	1.51E-133	Up	Unigene25826_All//gi|15235152|ref|NP_195118.1|//1.00E-159//protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|75279001|sp|Q81760.1|P2C63_ARATH RecName: Full=Probable protein phosphatase 2C 63; Short=AtPP2C63 >gi|13937198|gb|AAK50092.1|AF372953_1 AT4g33920/F17I5_110 [Arabidopsis thaliana] >gi|19548015|gb|AAL87371.1|AT4g33920/F17I5_110 [Arabidopsis thaliana]	Unigene25826_All//4.00E-151//AT4G33920| protein phosphatase 2C family protein / PP2C family protein	Unigene25826_All//0.00E+00//gi|78331947|gb|DT552221.1|DT552221			GO:0004721//GO:0006464//GO:0043169//GO:0043234	nr -
Unigene25827_All	1454	0.65	1.25	1.68	2.71	2.46	4.57	26.98	23.08	10.17	9.54E-01	4.89E-02		1.38E+00	1.64E-03		-1.36E-01	6.98E-01		7.55E-01	8.22E-04		-2.25E-01	4.09E-03		-1.41E+00	1.03E-61	Down	Unigene25827_All//gi|225470181|ref|XP_002268244.1|//2.00E-36//PREDICTED: similar to Os04g0533900 [Vitis vinifera]	Unigene25827_All//2.00E-24//AT5G23760| heavy-metal-associated domain-containing protein	Unigene25827_All//6.00E-111//ES830932			GO:0006812//GO:0031410//GO:0043169	nr +
Unigene25829_All	1616	23.25	14.80	16.61	21.36	22.82	21.16	43.54	19.11	17.90	-6.52E-01	1.29E-13		-4.85E-01	6.10E-08		9.54E-02	3.68E-01		-1.40E-02	9.17E-01		-1.19E+00	3.40E-82	Down	-1.28E+00	2.55E-95	Down	Unigene25829_All//gi|82569446|gb|AB883365.1|//1.00E-176//enoyl-ACP reductase [Malus x domestica]	Unigene25829_All//8.00E-140//AT2G05990| MOD1 (MOSAIC DEATH 1); enoyl-[acyl-carrier-protein] reductase (NADH) / enoyl-[acyl-carrier-protein] reductase/ oxidoreductase	Unigene25829_All//0.00E+00//TC167592		ko00061|Fatty acid biosynthesis	GO:0004312//GO:0000631	nr +
Unigene2583_All	402	0.26	0.76	0.13	0.25	2.48	0.79	4.84	0.62	3.07	1.54E+00	3.23E-01		-9.74E-01	7.21E-01		3.33E+00	2.50E-04	Up	1.67E+00	3.09E-01		-2.96E+00	2.83E-08	Down	-6.55E-01	1.01E-01		Unigene2583_All//gi|297816394|ref|XP_002876080.1|//9.00E-30//proline-rich family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321918|gb|EFH52339.1|proline-rich family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2583_All//8.00E-20//AT3G51290| proline-rich family protein	Unigene2583_All//4.00E-112//ES813435				nr -
Unigene25830_All	1894	4.25	2.57	4.36	13.49	13.11	11.57	9.51	5.43	3.41	-7.28E-01	3.61E-04		3.47E-02	8.79E-01		-4.16E-02	7.85E-01		-2.22E-01	5.06E-02		-8.09E-01	7.74E-12		-1.48E+00	5.57E-31	Down	Unigene25830_All//gi|297824789|ref|XP_002880277.1|//1.00E-179//At2g47010/F14M4.16 [Arabidopsis lyrata subsp. lyrata] >gi|297326116|gb|EFH56536.1|At2g47010/F14M4.16 [Arabidopsis lyrata subsp. lyrata]	Unigene25830_All//3.00E-177//AT2G47010| unknown protein	Unigene25830_All//0.00E+00//TC163352				nr +
Unigene25831_All	1832	1.00	1.49	2.27	2.37	2.29	2.49	8.82	11.48	6.55	5.79E-01	1.30E-01		1.18E+00	1.96E-04	Up	-4.48E-02	8.82E-01		7.39E-02	8.16E-01		3.80E-01	3.99E-04		-4.30E-01	3.63E-04		Unigene25831_All//gi|224105695|ref|XP_002313902.1|//0.00E+00//neutral amino acid transport protein [Populus trichocarpa] >gi|222850310|gb|EEE87857.1|neutral amino acid transport protein [Populus trichocarpa]	Unigene25831_All//3.00E-155//AT3G19553| amino acid permease family protein	Unigene25831_All//0.00E+00//TC156430			GO:0005275//GO:0015837//GO:0031224	nr +
Unigene25832_All	984	8.19	6.85	6.93	5.97	6.72	5.97	9.54	4.04	4.62	-2.58E-01	2.34E-01		-2.41E-01	2.91E-01		1.70E-01	5.49E-01		-1.70E-03	9.92E-01		-1.24E+00	1.93E-12	Down	-1.05E+00	5.32E-10	Down	Unigene25832_All//gi|77551376|gb|AB94173.1|//7.00E-67//Maf-like protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene25832_All//2.00E-72//AT5G42770| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytoplasm; CONTAINS InterPro DOMAIN/s: Maf-like protein (InterPro:IPR003697); BEST Arabidopsis thaliana protein match is: Maf family protein (TAIR:AT5G66550.1); Has 4061 Blast hits to 4057 proteins in 1128 species: Archae - 23; Bacteria - 2744; Metazoa - 45; Fungi - 50; Plants - 61; Viruses - 0; Other Eukaryotes - 1138 (source: NCBI BLink).	Unigene25832_All//0.00E+00//TC171537			GO:0044424	nr +
Unigene25834_All	1639	0.57	0.83	0.65	2.83	3.36	3.33	2.40	0.41	1.97	5.39E-01	3.59E-01		1.77E-01	7.73E-01		2.50E-01	3.86E-01		2.38E-01	4.10E-01		-2.56E+00	6.96E-14	Down	-2.85E-01	3.14E-01		Unigene25834_All//gi|30684540|ref|NP_193617.2|//1.00E-133//ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene25834_All//2.00E-84//AT4G18820| ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding	Unigene25834_All//2.00E-68//ES816108			GO:0000166//GO:0016779//GO:0043231	nr -
Unigene25835_All	1576	23.27	50.77	26.90	133.29	134.70	116.89	19.80	25.67	16.53	1.13E+00	7.47E-70	Up	2.09E-01	1.86E-02		1.52E-02	7.72E-01		-1.89E-01	2.54E-08		3.75E-01	5.33E-07		-2.60E-01	2.36E-03		Unigene25835_All//gi|18404500|ref|NP_566763.1|//1.00E-145//auxin-responsive family protein [Arabidopsis thaliana] >gi|79313415|ref|NP_001030764.1|auxin-responsive family protein [Arabidopsis thaliana] >gi|16323200|gb|AAL15334.1|AT3g25290/MJL12_25 [Arabidopsis thaliana] >gi|25090093|gb|AAN72226.1|At3g25290/MJL12_25 [Arabidopsis thaliana]	Unigene25835_All//9.00E-147//AT3G25290| auxin-responsive family protein	Unigene25835_All//0.00E+00//TC156387				nr -
Unigene25837_All	1519	4.10	2.10	2.98	28.66	21.31	6.93	7.68	2.20	1.13	-9.64E-01	5.53E-05		-4.60E-01	6.73E-02		-4.28E-01	6.14E-09		-2.05E+00	4.15E-100	Down	-1.80E+00	6.17E-26	Down	-2.77E+00	6.36E-45	Down	Unigene25837_All//gi|115485419|ref|NP_001067853.1|//2.00E-21//Os11g0458100 [Oryza sativa Japonica Group] >gi|113645075|dbj|BAF28216.1|Os11g0458100 [Oryza sativa Japonica Group]	Unigene25837_All//1.00E-27//AT3G25130| unknown protein	Unigene25837_All//0.00E+00//TC171120		ko03040|Spliceosome	GO:0016020	nr +
Unigene25838_All	1842	27.78	52.68	33.27	14.14	5.98	7.48	7.05	10.69	1.34	9.23E-01	2.92E-61		2.60E-01	2.05E-04		-1.24E+00	2.86E-33	Down	-9.19E-01	3.92E-18		6.01E-01	5.84E-08		-2.39E+00	2.04E-42	Down	Unigene25838_All//gi|224105433|ref|XP_002313809.1|//0.00E+00//polyol transporter [Populus trichocarpa] >gi|222850217|gb|EEE87764.1|polyol transporter [Populus trichocarpa]	Unigene25838_All//3.00E-169//AT3G18830| ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann	Unigene25838_All//0.00E+00//TC142402			GO:0006810//GO:0008152//GO:0016628//GO:0022857//GO:0031224	nr +
Unigene25839_All	1860	21.55	11.39	18.41	14.89	12.81	18.84	32.35	14.00	9.60	-9.20E-01	1.15E-25		-2.27E-01	1.24E-02		-2.17E-01	3.86E-02		3.40E-01	1.45E-04		-1.21E+00	2.50E-72	Down	-1.75E+00	2.01E-129	Down	Unigene25839_All//gi|297820562|ref|XP_002878164.1|//0.00E+00//adenylosuccinate synthetase [Arabidopsis lyrata subsp. lyrata] >gi|297324002|gb|EFH54423.1|adenylosuccinate synthetase [Arabidopsis lyrata subsp. lyrata]	Unigene25839_All//0.00E+00//AT3G57610| ADSS (ADENYLOSUCCINATE SYNTHASE); adenylosuccinate synthase	Unigene25839_All//0.00E+00//TC137517		ko00230|Purine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0005576//GO:0009168//GO:0009532//GO:0010038//GO:0016879//GO:0032561//GO:0046872	nr -

Unigene2584_All	1570	3.40	1.90	1.15	4.25	4.63	2.04	4.87	0.64	2.00	-8.36E-01	1.22E-03		-1.56E+00	5.80E-08	Down	1.22E-01	6.25E-01		-1.06E+00	2.71E-06	Down	-2.93E+00	1.80E-30	Down	-1.28E+00	3.82E-11	Down	Unigene2584_All//gi|297816394|ref|XP_002876080.1|//1.00E-150//proline-rich family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321918|gb|EFH52339.1| proline-rich family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2584_All//4.00E-123//AT3G51290| proline-rich family protein	Unigene2584_All//0.00E+00//ES813435				nr +
Unigene25841_All	1641	6.95	14.14	12.01	3.73	4.47	6.30	4.05	5.43	6.48	1.02E+00	6.06E-18	Up	7.89E-01	9.80E-10		2.60E-01	2.79E-01		7.55E-01	1.49E-05		4.23E-01	1.55E-02		6.80E-01	8.21E-06		Unigene25841_All//gi|42565501|ref|NP_190002.2|//1.00E-176//chloroplast outer membrane protein-related [Arabidopsis thaliana] >gi|56121918|gb|AAV74240.1| At3g44160 [Arabidopsis thaliana] >gi|60543353|gb|AAX22274.1| At3g44160 [Arabidopsis thaliana]	Unigene25841_All//2.00E-169//AT3G44160| chloroplast outer membrane protein-related	Unigene25841_All//0.00E+00//TC168101			GO:0016020	nr -
Unigene25842_All	2421	8.06	6.20	5.32	23.62	18.52	17.85	23.52	15.47	11.01	-3.80E-01	2.51E-03		-5.99E-01	3.31E-06		-3.51E-01	3.68E-08		-4.04E-01	1.79E-09		-6.05E-01	1.01E-21		-1.10E+00	2.39E-60	Down	Unigene25842_All//gi|44917457|gb|AY89053.1|//0.00E+00//At5g57460 [Arabidopsis thaliana] >gi|56381939|gb|AAV85688.1| At5g57460 [Arabidopsis thaliana]	Unigene25842_All//0.00E+00//AT5G57460| unknown protein	Unigene25842_All//0.00E+00//TC165187			GO:0009536//GO:0016020	nr +
Unigene25843_All	1804	5.02	2.58	3.39	7.95	7.88	7.94	11.72	4.84	4.68	-9.57E-01	8.53E-07		-5.64E-01	4.71E-03		-1.26E-02	9.51E-01		-3.00E-03	9.82E-01		-1.28E+00	3.86E-28	Down	-1.32E+00	1.11E-30	Down	Unigene25843_All//gi|77552243|gb|ABA95040.1|//1.00E-167//Nuclear pore protein 84/107 containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|77552244|gb|ABA95041.1| Nuclear pore protein 84/107 containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene25843_All//0.00E+00//AT3G14120| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: transport; LOCATED IN: nuclear pore; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nuclear pore protein 84/107 (InterPro:IPR007252); Has 207 Blast hits to 206 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 123; Fungi - 57; Plants - 22; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene25843_All//0.00E+00//TC161364			GO:0005635//GO:0051234	nr +
Unigene25844_All	976	7.72	8.67	11.13	9.14	8.33	8.51	7.10	14.99	9.67	1.68E-01	4.32E-01		5.28E-01	3.35E-03		-1.34E-01	5.53E-01		-1.02E-01	6.58E-01		1.08E+00	3.05E-15	Up	4.45E-01	6.35E-03		Unigene25844_All//gi|145332026|ref|NP_001078135.1|//7.00E-13//yippee family protein [Arabidopsis thaliana]	Unigene25844_All//4.00E-14//AT3G11230| yippee family protein	Unigene25844_All//0.00E+00//TC165504			GO:0044464	nr +
Unigene25846_All	1787	1.52	1.87	2.15	3.65	2.37	2.35	7.52	1.71	7.85	2.98E-01	3.82E-01		4.95E-01	1.40E-01		-6.24E-01	3.99E-03		-6.36E-01	5.26E-03		-2.14E+00	3.75E-37	Down	6.07E-02	6.77E-01		Unigene25846_All//gi|240254028|ref|NP_172209.4|//1.00E-104//nucleotide-sugar transmembrane transporter [Arabidopsis thaliana] >gi|29329819|emb|CAD83086.1| GONST2 Golgi Nucleotide sugar transporter [Arabidopsis thaliana]	Unigene25846_All//5.00E-95//AT1G07290| nucleotide-sugar transmembrane transporter				GO:0016020	nr -
Unigene25847_All	1671	0.44	0.00	0.19	0.51	1.07	0.68	2.00	0.75	1.34	-8.78E+00	2.11E-04	Down	-1.20E+00	1.80E-01		1.08E+00	2.74E-02		4.15E-01	5.61E-01		-1.41E+00	7.62E-06	Down	-5.82E-01	4.60E-02		Unigene25847_All//gi|240254028|ref|NP_172209.4|//1.00E-136//nucleotide-sugar transmembrane transporter [Arabidopsis thaliana] >gi|29329819|emb|CAD83086.1| GONST2 Golgi Nucleotide sugar transporter [Arabidopsis thaliana]	Unigene25847_All//1.00E-127//AT1G07290| nucleotide-sugar transmembrane transporter				GO:0043231	nr +
Unigene25848_All	1735	9.29	10.05	8.13	27.16	30.45	26.40	15.43	4.79	8.01	1.13E-01	4.43E-01		-1.92E-01	2.29E-01		1.65E-01	2.79E-02		-4.13E-02	6.85E-01		-1.69E+00	2.48E-53	Down	-9.45E-01	8.69E-23		Unigene25848_All//gi|4204286|gb|AAD10667.1|//4.00E-65//Unknown protein [Arabidopsis thaliana]	Unigene25848_All//1.00E-35//AT1G04030| unknown protein	Unigene25848_All//0.00E+00//TC159120				nr +
Unigene25849_All	3007	0.61	1.43	1.31	4.11	3.16	6.13	4.96	6.74	6.24	1.23E+00	4.47E-05	Up	1.11E+00	6.68E-04	Up	-3.78E-01	1.54E-02		5.77E-01	4.42E-06		4.42E-01	5.03E-05		3.30E-01	3.29E-03		Unigene25849_All//gi|155242124|gb|ABT18096.1|//0.00E+00//FERONIA receptor-like kinase [Arabidopsis lyrata]	Unigene25849_All//0.00E+00//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene25849_All//4.00E-52//TC163657		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006468//GO:0007275//GO:0009856//GO:0016020//GO:0044426	nr +
Unigene25850_All	2442	2.51	2.18	1.11	7.57	6.04	4.77	10.98	16.62	23.83	-2.02E-01	4.18E-01		-1.17E+00	4.23E-06	Down	-3.27E-01	8.93E-03		-6.65E-01	9.98E-08		5.98E-01	2.01E-15		1.12E+00	2.90E-63	Up	Unigene25850_All//gi|37202044|gb|AAQ89637.1|//0.00E+00//At1g34320 [Arabidopsis thaliana]	Unigene25850_All//0.00E+00//AT5G08660| unknown protein	Unigene25850_All//0.00E+00//TC140989			GO:0016020	nr +
Unigene25851_All	553	1.70	0.18	0.58	1.98	2.86	3.10	4.36	8.62	6.12	-3.22E+00	6.77E-04	Down	-1.56E+00	4.90E-02		5.31E-01	3.40E-01		6.47E-01	2.21E-01		9.83E-01	7.41E-05		4.91E-01	9.60E-02		Unigene25851_All//gi|51971945|dbj|BAD14637.1|//2.00E-25//DNAJ-like protein [Arabidopsis thaliana]	Unigene25851_All//8.00E-26//AT5G49060| DNAJ heat shock N-terminal domain-containing protein	Unigene25851_All//0.00E+00//gi|164254592|gb|ES814334.1|ES814334		ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0016020//GO:0044267	nr -
Unigene25853_All	2120	33.81	25.93	16.80	5.50	8.45	4.47	0.70	0.47	0.23	-3.83E-01	4.56E-10		-1.01E+00	6.29E-51	Down	6.19E-01	3.91E-07		-2.98E-01	9.00E-02		-5.61E-01	2.61E-01		-1.63E+00	1.09E-03		Unigene25853_All//gi|41590425|gb|AAK55693.1|AF378890_1/1.00E-119//At1g68400/T2E12_5 [Arabidopsis thaliana] >gi|20857353|gb|AAM26714.1| At1g68400/T2E12_5 [Arabidopsis thaliana]	Unigene25853_All//4.00E-84//AT1G68400| leucine-rich repeat transmembrane protein kinase, putative	Unigene25853_All//0.00E+00//TC170357		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016020//GO:0016301	nr -
Unigene25856_All	1894	0.99	25.23	4.19	1.89	6.18	6.72	0.42	2.49	1.77	4.66E+00	2.58E-221	Up	2.07E+00	7.52E-17	Up	1.71E+00	1.09E-22	Up	1.83E+00	6.09E-25	Up	2.56E+00	1.73E-16	Up	2.06E+00	1.44E-09	Up	Unigene25856_All//gi|15218349|ref|NP_177355.1|//8.00E-74//late embryogenesis abundant domain-containing protein / LEA domain-containing protein [Arabidopsis thaliana]	Unigene25856_All//8.00E-75//AT1G72100| late embryogenesis abundant domain-containing protein / LEA domain-containing protein					nr -
Unigene25857_All	1911	0.16	2.23	0.25	0.52	0.47	0.71	0.09	0.22	0.10	3.76E+00	2.38E-17	Up	6.10E-01	5.87E-01		-1.54E-01	8.40E-01		4.44E-01	4.72E-01		1.31E+00	2.34E-01		2.36E-01	8.83E-01		Unigene25857_All//gi|15218349|ref|NP_177355.1|//9.00E-81//late embryogenesis abundant domain-containing protein / LEA domain-containing protein [Arabidopsis thaliana]	Unigene25857_All//9.00E-82//AT1G72100| late embryogenesis abundant domain-containing protein / LEA domain-containing protein					nr +
Unigene25858_All	1491	4.28	3.57	2.96	5.35	9.77	7.18	15.88	12.14	42.24	-2.63E-01	2.86E-01		-5.30E-01	3.06E-02		8.70E-01	3.45E-10		4.25E-01	1.60E-02		-3.88E-01	1.11E-04		1.41E+00	5.84E-98	Up	Unigene25858_All//gi|224057048|ref|XP_002299117.1|//0.00E+00//neutral amino acid transport protein [Populus trichocarpa] >gi|222846375|gb|EEE83922.1| neutral amino acid transport protein [Populus trichocarpa]	Unigene25858_All//2.00E-172//AT3G13620| amino acid permease family protein	Unigene25858_All//0.00E+00//gi|78338788|gb|DT559062.1|DT559062			GO:0015171//GO:0015837//GO:0031224	nr +
Unigene2586_All	1557	21.94	19.30	10.64	31.55	35.96	28.31	23.68	20.29	19.29	-1.85E-01	5.69E-02		-1.04E+00	5.97E-26	Down	1.89E-01	7.20E-03		-1.56E-01	5.57E-02		-2.23E-01	6.30E-03		-2.96E-01	1.35E-04		Unigene2586_All//gi|73761695|gb|AAZ83347.1|//2.00E-82//ethylene-responsive element-binding factor [Gossypium hirsutum]	Unigene2586_All//3.00E-41//AT1G56640| ERF3 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 3); DNA binding / protein binding / transcription factor/ transcription repressor	Unigene2586_All//0.00E+00//gi|78335584|gb|DT555858.1|DT555858	AP2-EREBP			nr -
Unigene25861_All	295	2.13	3.61	1.44	3.88	4.55	0.46	2.29	4.68	0.54	7.61E-01	2.48E-01		-5.60E-01	5.54E-01		2.29E-01	7.47E-01		-3.08E+00	1.19E-04	Down	1.03E+00	4.52E-02		-2.09E+00	1.27E-02				Unigene25861_All//6.00E-49//TC174169				ESTscan -
Unigene25862_All	413	1.14	1.35	0.64	1.81	0.92	0.33	2.15	2.43	0.39	2.43E-01	7.77E-01		-8.23E-01	4.57E-01		-9.80E-01	2.23E-01		-2.46E+00	1.02E-02		1.76E-01	7.73E-01		-2.48E+00	9.93E-04	Down			Unigene25862_All//7.00E-71//TC174169				ESTscan +
Unigene25863_All	1249	7.21	5.27	6.31	13.76	8.02	4.85	7.89	5.72	2.49	-4.50E-01	2.00E-02		-1.91E-01	3.95E-01		-7.78E-01	2.47E-10		-1.51E+00	5.35E-26	Down	-4.63E-01	4.70E-03		-1.66E+00	2.09E-20	Down	Unigene25863_All//gi|33465891|gb|AAQ19327.1|//5.00E-12//bZIP-like protein [Oryza sativa Japonica Group]	Unigene25863_All//3.00E-06//AT3G09510| nucleic acid binding	Unigene25863_All//2.00E-132//gi|78328462|gb|DT548736.1|DT548736				nr +
Unigene25864_All	2242	0.93	1.15	0.38	1.29	0.95	0.81	9.66	9.17	45.56	3.04E-01	4.46E-01		-1.30E+00	6.74E-03		-4.36E-01	2.44E-01		-6.77E-01	6.97E-02		-7.41E-02	5.83E-01		2.24E+00	7.25E-299	Up	Unigene25864_All//gi|224114037|ref|XP_002332458.1|//1.00E-157//cytochrome P450 [Populus trichocarpa] >gi|222832529|gb|EEE71006.1| cytochrome P450 [Populus trichocarpa]	Unigene25864_All//7.00E-102//AT3G26300| CYP71B34; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene25864_All//0.00E+00//TC133655		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene25865_All	1856	8.77	6.31	9.35	7.41	5.86	6.64	8.22	3.40	3.61	-4.75E-01	5.68E-04		9.34E-02	5.64E-01		-3.37E-01	2.33E-02		-1.57E-01	3.85E-01		-1.27E+00	1.62E-20	Down	-1.19E+00	4.47E-19	Down	Unigene25865_All//gi|115434952|ref|NP_001042234.1|//8.00E-58//Os01g0184500 [Oryza sativa Japonica Group] >gi|75321764|sp|Q5VRY0.1|RH39_ORYSJ RecName: Full=DEAD-box ATP-dependent RNA helicase 39 >gi|113531765|dbj|BAF04148.1| Os01g0184500 [Oryza sativa Japonica Group]	Unigene25865_All//7.00E-58//AT4G09730| DEAD/DEAH box helicase, putative	Unigene25865_All//0.00E+00//DW481895		ko03040|Spliceosome	GO:0005488//GO:0016787//GO:0043231	nr -
Unigene25867_All	2249	4.84	0.59	1.44	7.58	7.21	18.58	19.12	4.16	9.64	-3.05E+00	1.16E-36	Down	-1.74E+00	3.31E-18	Down	-7.09E-02	6.63E-01		1.29E+00	5.35E-49	Up	-2.20E+00	1.97E-121	Down	-9.88E-01	8.22E-39		Unigene25867_All//gi|87240677|gb|ABD32535.1|//0.00E+00//TGF-beta receptor, type I/II extracellular region [Medicago truncatula]	Unigene25867_All//0.00E+00//AT1G32450| NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	Unigene25867_All//0.00E+00//TC151543			GO:0004871//GO:0015833//GO:0044464	nr +
Unigene25868_All	1488	13.68	10.42	12.45	24.44	19.76	16.57	16.03	12.13	5.27	-3.93E-01	1.35E-03		-1.35E-01	3.52E-01		-3.06E-01	2.55E-04		-5.60E-01	6.90E-11		-4.01E-01	5.78E-05		-1.60E+00	1.09E-45	Down	Unigene25868_All//gi|226492856|ref|NP_001149901.1|//1.00E-103//LOC100283529 [Zea mays] >gi|195635353|gb|ACG37145.1| TLD family protein [Zea mays]	Unigene25868_All//1.00E-109//AT4G39870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TLDc (InterPro:IPR006571); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G05590.2); Has 2018 Blast hits to 1865 proteins in 220 species: Archae - 0; Bacteria - 39; Metazoa - 1002; Fungi - 279; Plants - 129; Viruses - 34; Other Eukaryotes - 535 (source: NCBI BLink).	Unigene25868_All//0.00E+00//CO123557				nr +
Unigene25871_All	1440	1.71	3.55	1.07	3.49	2.44	4.17	1.97	1.36	2.55	1.06E+00	8.86E-05	Up	-6.71E-01	1.16E-01		-5.18E-01	4.53E-02		2.56E-01	3.51E-01		-5.28E-01	1.22E-01		3.72E-01	1.98E-01		Unigene25871_All//gi|15236944|ref|NP_192822.1|//9.00E-74//kinesin light chain-related [Arabidopsis thaliana] >gi|3513727|gb|AAC33943.1| contains similarity to TPR domains (Pfam: TPR,hmm; score: 11.15) and kinesin motor domains (Pfam: kinesin2,hmm, score: 17.49, 20.52 and 10.94) [Arabidopsis thaliana] >gi|19699309|gb|AAL91265.1| AT4g10840/F25i24_50 [Arabidopsis thaliana]	Unigene25871_All//1.00E-67//AT4G10840| kinesin light chain-related	Unigene25871_All//0.00E+00//gi|18099885|gb|BM359139.1|BM359139			GO:0016020	nr -
Unigene25872_All	1773	8.38	10.12	11.86	21.49	17.32	21.80	54.25	8.20	8.85	2.72E-01	4.46E-02		5.01E-01	4.99E-05		-3.11E-01	1.31E-04		2.08E-02	8.57E-01		-2.73E+00	0.00E+00	Down	-2.62E+00	0.00E+00	Down	Unigene25872_All//gi|262021252|gb|ACV06905.1|//0.00E+00//flavonoid 3'-hydroxylase [Gossypium hirsutum]	Unigene25872_All//0.00E+00//AT5G07990| TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	Unigene25872_All//0.00E+00//TC149834		ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0009699//GO:0016709//GO:0031090//GO:0031224//GO:0044231	nr -

Unigene25875_A11	1985	6.80	2.50	2.39	21.53	13.86	9.15	12.89	3.52	2.33	-1.44E+00	5.76E-18	Down	-1.51E+00	2.31E-18	Down	-6.35E-01	1.33E-17		-1.24E+00	2.67E-47	Down	-1.87E+00	6.11E-59	Down	-2.47E+00	6.91E-86	Down	Unigene25875_A11//gi|15230555|ref|NP_190735.1|//1.00E-171//SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|75202761|sp|Q9SCU1.1|PATL6_ARATH RecName: Full=Patellin-6 >gi|16930483|gb|AAL31927.1|AF419595_1 AT3g51670/T18N14_50 [Arabidopsis thaliana] >gi|25141223|gb|AAN73306.1|At3g51670/T18N14_50 [Arabidopsis thaliana]	Unigene25875_A11//1.00E-172//AT3G51670| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene25875_A11//0.00E+00//TC133821				nr +
Unigene25876_A11	1788	8.49	4.73	9.26	14.26	11.75	13.64	11.33	4.51	6.19	-8.43E-01	6.70E-09		1.26E-01	4.15E-01		-2.80E-01	7.75E-03		-6.46E-02	6.23E-01		-1.33E+00	1.07E-28	Down	-8.71E-01	2.48E-15		Unigene25876_A11//gi|16604368|gb|AL24190.1|//1.00E-175//At2g19940/F6P22.3 [Arabidopsis thaliana] >gi|19699208|gb|AAL90970.1|At2g19940/F6P22.3 [Arabidopsis thaliana]	Unigene25876_A11//3.00E-176//AT2G19940| N-acetyl-gamma-glutamyl-phosphate reductase/ NAD or NADH binding / binding / catalytic/ oxidoreductase, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor / protein dimerization	Unigene25876_A11//0.00E+00//TC178877		ko00330|Arginine and proline metabolism		nr +
Unigene25878_A11	1535	6.78	11.42	7.49	10.00	14.33	15.24	9.45	22.19	27.67	7.52E-01	1.82E-08		1.44E-01	4.48E-01		5.20E-01	1.79E-06		6.09E-01	3.16E-08		1.23E+00	1.75E-42	Up	1.55E+00	4.41E-76	Up	Unigene25878_A11//gi|3256068|emb|CAA74397.1|//1.00E-106//Heat Shock Factor 3 [Arabidopsis thaliana]	Unigene25878_A11//1.00E-88//AT3G02990| ATHSFA1E; DNA binding / transcription factor	Unigene25878_A11//0.00E+00//TC153046	HSF			nr -
Unigene25880_A11	759	21.09	54.81	24.27	25.60	39.38	43.68	16.93	40.53	38.84	1.38E+00	4.84E-50	Up	2.03E-01	1.57E-01		6.22E-01	1.22E-11		7.71E-01	6.05E-17		1.26E+00	9.56E-40	Up	1.20E+00	4.11E-36	Up	Unigene25880_A11//gi|27808522|gb|AU024541.1|//6.00E-48//At4g33985 [Arabidopsis thaliana]	Unigene25880_A11//2.00E-40//AT4G33985| unknown protein	Unigene25880_A11//0.00E+00//gi|164315732|gb|ES823239.1|ES823239				nr -
Unigene25881_A11	860	1.64	0.59	0.99	5.27	0.56	0.37	1.97	1.36	0.74	-1.48E+00	1.15E-02		-7.30E-01	2.21E-01		-3.23E+00	1.16E-20	Down	-3.84E+00	1.60E-20	Down	-5.31E-01	2.50E-01		-1.41E+00	1.77E-03		Unigene25881_A11//gi|29539325O|gb|AG603462.1|//1.00E-124//9-cis-epoxycarotenoid dioxygenase [Gossypium hirsutum]	Unigene25881_A11//4.00E-96//AT1G30100| NCED5 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 5); 9-cis-epoxycarotenoid dioxygenase	Unigene25881_A11//1.00E-27//TC175846		ko00906|Carotenoid biosynthesis		nr +
Unigene25882_A11	2204	0.90	0.18	0.22	3.75	2.09	1.80	2.11	11.34	3.63	-2.29E+00	1.72E-05	Down	-2.05E+00	1.32E-04	Down	-8.42E-01	6.00E-06		-1.06E+00	1.26E-07	Down	2.43E+00	1.64E-79	Up	7.84E-01	1.25E-05		Unigene25882_A11//gi|29539325O|gb|AG603462.1|//0.00E+00//9-cis-epoxycarotenoid dioxygenase [Gossypium hirsutum]	Unigene25882_A11//0.00E+00//AT3G14440| NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	Unigene25882_A11//5.00E-85//gi|164251625|gb|ES833984.1|ES833984		ko00906|Carotenoid biosynthesis	GO:0016701	nr -
Unigene25883_A11	1503	6.13	5.50	7.51	30.23	18.42	19.98	32.74	38.29	15.11	-1.57E-01	4.42E-01		2.94E-01	1.12E-01		-7.15E-01	6.21E-23		-5.97E-01	5.34E-15		2.26E-01	3.45E-04		-1.12E+00	7.91E-54	Down	Unigene25883_A11//gi|224103919|ref|XP_002313244.1|//1.00E-140//ZIP transporter [Populus trichocarpa] >gi|222849652|gb|EEE87199.1| ZIP transporter [Populus trichocarpa]	Unigene25883_A11//8.00E-123//AT2G30080| ZIP6; cation transmembrane transporter/ metal ion transmembrane transporter	Unigene25883_A11//0.00E+00//TC176595			GO:0000041//GO:0015082//GO:0031224	nr +
Unigene25885_A11	1342	12.75	6.76	8.85	8.72	7.26	9.29	12.26	5.42	3.98	-9.16E-01	2.58E-11		-5.27E-01	1.49E-04		-2.65E-01	1.24E-01		9.06E-02	6.39E-01		-1.18E+00	1.45E-19	Down	-1.62E+00	2.43E-32	Down	Unigene25885_A11//gi|115450219|ref|NP_001048710.1|//1.00E-123//Os03g0109700 [Oryza sativa Japonica Group] >gi|108706784|gb|ABF93579.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547181|dbj|BAF10624.1|Os03g0109700 [Oryza sativa Japonica Group]	Unigene25885_A11//8.00E-117//AT2G23370| unknown protein	Unigene25885_A11//6.00E-34//C0101453				nr +
Unigene25888_A11	1148	107.56	83.73	106.13	17.57	23.16	32.65	16.35	23.99	39.98	-3.61E-01	3.93E-15		-1.93E-02	7.27E-01		3.98E-01	6.06E-05		8.94E-01	2.09E-24		5.53E-01	1.98E-09		1.29E+00	1.79E-62	Up	Unigene25888_A11//gi|82697941|gb|AB889005.1|//3.00E-87//CXE carboxylesterase [Malus pumila]	Unigene25888_A11//1.00E-62//AT3G48700| ATCXE13 (ARABIDOPSIS THALIANA CARBOXYESTERASE 13); hydrolase	Unigene25888_A11//0.00E+00//TC134739				nr -
Unigene25889_A11	1312	7.50	29.54	12.78	9.07	14.20	9.23	15.28	10.03	18.16	1.98E+00	8.81E-78	Up	7.70E-01	4.42E-08		6.46E-01	6.22E-08		2.38E-02	9.19E-01		-6.06E-01	3.27E-08		2.49E-01	1.29E-02		Unigene25889_A11//gi|29294065|gb|AAO73902.1|//1.00E-24//expressed protein [Arabidopsis thaliana] >gi|30023750|gb|AAP13408.1|At5g21940 [Arabidopsis thaliana]	Unigene25889_A11//4.00E-19//AT5G21940| unknown protein	Unigene25889_A11//0.00E+00//gi|84155850|gb|DN817076.1|DN817076			GO:0005488//GO:0043231	nr +
Unigene25890_A11	1328	10.01	256.97	74.62	35.71	66.82	58.22	17.48	11.74	9.42	4.68E+00	0.00E+00	Up	2.90E+00	3.01E-305	Up	9.04E-01	2.64E-64		7.05E-01	2.62E-33		-5.74E-01	1.37E-08		-8.92E-01	3.99E-18		Unigene25890_A11//gi|15224852|ref|NP_179571.1|//1.00E-109//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75220226|sp|O82199.1|C3H20_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 20; Short=AtC3H20	Unigene25890_A11//1.00E-101//AT2G19810| zinc finger (CCCH-type) family protein	Unigene25890_A11//0.00E+00//gi|78328330|gb|DT548604.1|DT548604	C3H		GO:0003676//GO:0044424	nr +
Unigene25892_A11	313	0.00	0.00	0.00	0.00	0.00	0.29	0.27	1.07	2.42	null	null		null	null		null	null		8.17E+00	4.77E-01		1.98E+00	1.44E-01		3.16E+00	6.82E-04	Up								
Unigene25895_A11	1170	3.58	2.99	1.46	3.19	4.83	4.05	3.61	1.71	1.53	-2.60E-01	3.89E-01		-1.30E+00	5.04E-05	Down	5.96E-01	1.48E-02		3.44E-01	2.52E-01		-1.08E+00	5.66E-05	Down	-1.24E+00	3.02E-06	Down	Unigene25895_A11//gi|297792331|ref|XP_002861050.1|//1.00E-106//EMB1006 [Arabidopsis lyrata subsp. lyrata] >gi|297309885|gb|EFH40309.1|EMB1006 [Arabidopsis lyrata subsp. lyrata]	Unigene25895_A11//2.00E-105//AT5G50280| EMB1006 (embryo defective 1006)					nr +
Unigene25896_A11	971	30.01	99.46	153.17	38.89	35.75	37.72	3.44	1.85	1.27	1.73E+00	1.16E-160	Up	2.35E+00	0.00E+00	Up	-1.21E-01	2.17E-01		-4.39E-02	7.01E-01		-8.94E-01	3.09E-03		-1.44E+00	3.39E-06	Down	Unigene25896_A11//gi|15810045|gb|AAL06949.1|//2.00E-21//AT5g05250/K18123_5 [Arabidopsis thaliana]	Unigene25896_A11//1.00E-22//AT5G05250| unknown protein	Unigene25896_A11//9.00E-26//gi|48749429|gb|C0079948.1|C0079948				nr -
Unigene25899_A11	1123	2.42	2.71	1.66	3.46	4.02	2.45	2.79	2.20	1.28	1.60E-01	6.47E-01		-5.46E-01	1.76E-01		2.15E-01	5.29E-01		-4.96E-01	1.23E-01		-3.43E-01	3.09E-01		-1.13E+00	2.73E-04	Down	Unigene25899_A11//gi|18407526|ref|NP_566124.1|//2.00E-77//exonuclease family protein [Arabidopsis thaliana] >gi|42571283|ref|NP_973715.1|exonuclease family protein [Arabidopsis thaliana] >gi|79324951|ref|NP_001031560.1|exonuclease family protein [Arabidopsis thaliana] >gi|20197555|gb|AAD13713.2|Expressed protein [Arabidopsis thaliana]	Unigene25899_A11//1.00E-78//AT2G48100| exonuclease family protein	Unigene25899_A11//0.00E+00//TC176519	C2H2		GO:0004518//GO:0005488//GO:0044464	nr +
Unigene2590_A11	1964	26.91	17.57	28.31	20.70	19.69	13.15	3.23	2.00	1.10	-6.15E-01	4.52E-17		7.32E-02	3.93E-01		-7.20E-02	4.95E-01		-6.54E-01	9.31E-16		-6.91E-01	9.06E-04		-1.56E+00	2.58E-12	Down	Unigene2590_A11//gi|297833866|ref|XP_002884815.1|//1.00E-118//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330055|gb|EFH61074.1|hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2590_A11//3.00E-104//AT3G10840| hydrolase, alpha/beta fold family protein	Unigene2590_A11//0.00E+00//TC134405				nr +
Unigene25904_A11	751	52.11	56.20	15.46	43.31	36.64	23.09	16.44	98.67	8.97	1.09E-01	2.31E-01		-1.75E+00	8.45E-65	Down	-2.42E-01	9.37E-03		-9.07E-01	5.12E-22		2.59E+00	1.41E-252	Up	-8.75E-01	9.10E-10		Unigene25904_A11//gi|87241016|gb|ABD32874.1|//1.00E-33//VQ [Medicago truncatula]	Unigene25904_A11//6.00E-22//AT3G56880| VQ motif-containing protein	Unigene25904_A11//0.00E+00//gi|109865072|gb|DW494048.1|DW494048				nr +
Unigene25905_A11	1096	28.50	32.13	21.91	47.63	42.45	67.62	58.71	201.39	70.19	1.73E-01	7.30E-02		-3.79E-01	1.53E-04		-1.66E-01	2.59E-02		5.06E-01	7.23E-18		1.78E+00	0.00E+00	Up	2.58E-01	8.03E-07		Unigene25905_A11//gi|18404500|ref|NP_566763.1|//5.00E-51//auxin-responsive family protein [Arabidopsis thaliana] >gi|79313415|ref|NP_001030764.1|auxin-responsive family protein [Arabidopsis thaliana] >gi|16323200|gb|AAL15334.1|AT3g25290/MJL12_25 [Arabidopsis thaliana] >gi|25090093|gb|AAN72226.1|At3g25290/MJL12_25 [Arabidopsis thaliana]	Unigene25905_A11//2.00E-52//AT3G25290| auxin-responsive family protein	Unigene25905_A11//0.00E+00//TC149410			GO:0016020//GO:0016491	nr +
Unigene25909_A11	2204	19.61	14.81	15.27	41.07	41.00	34.14	25.84	8.10	16.43	-4.05E-01	5.00E-07		-3.61E-01	1.59E-05		-2.50E-03	9.66E-01		-2.67E-01	4.94E-07		-1.67E+00	1.50E-111	Down	-6.53E-01	1.62E-25		Unigene25909_A11//gi|124360430|gb|ABN08440.1|//0.00E+00//Lung seven transmembrane receptor [Medicago truncatula]	Unigene25909_A11//0.00E+00//AT2G01070| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Transmembrane receptor, eukaryota (InterPro:IPR009637); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G72480.1); Has 500 Blast hits to 499 proteins in 125 species: Archae - 0; Bacteria - 0; Metazoa - 271; Fungi - 99; Plants - 97; Viruses - 0; Other Eukaryotes - 33 (source: NCBI BLink).	Unigene25909_A11//0.00E+00//TC137743			GO:0004871//GO:0031224//GO:0031410	nr -
Unigene2591_A11	1474	1.31	4.57	3.32	15.34	13.32	10.33	13.83	2.95	5.24	1.80E+00	1.80E-12	Up	1.34E+00	4.97E-06	Up	-2.04E-01	8.81E-02		-5.71E-01	3.02E-07		-2.23E+00	7.38E-59	Down	-1.40E+00	3.83E-32	Down	Unigene2591_A11//gi|292668975|gb|ADE41142.1|//2.00E-75//AP2 domain class transcription factor [Malus x domestica]	Unigene2591_A11//1.00E-48//AT5G11590| TINY2 (TINY2); DNA binding / transcription factor	Unigene2591_A11//3.00E-85//DW517601	AP2-EREBP			nr -
Unigene25915_A11	704	8.77	17.13	17.78	16.63	22.06	36.37	35.07	207.91	98.58	9.66E-01	7.18E-09		1.02E+00	1.53E-09	Up	4.08E-01	2.84E-03		1.13E+00	1.73E-24	Up	2.57E+00	0.00E+00	Up	1.49E+00	5.58E-117	Up	Unigene25915_A11//gi|52550577|gb|AAU14999.2|//5.00E-41//MtN19-like protein [Pisum sativum]	Unigene25915_A11//7.00E-40//AT5G61820| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Stress up-regulated Nod 19 (InterPro:IPR011692); Has 27 Blast hits to 27 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene25915_A11//0.00E+00//TC142135			GO:0031410//GO:0043231	nr -
Unigene25916_A11	809	7.57	16.28	13.23	3.51	4.77	2.68	0.99	1.14	0.79	1.11E+00	8.44E-12	Up	8.06E-01	8.42E-06		4.42E-01	1.71E-01		-3.89E-01	3.34E-01		1.95E-01	7.62E-01		-3.34E-01	6.19E-01			Unigene25916_A11//7.00E-05//AT5G02790| In2-1 protein, putative	Unigene25916_A11//0.00E+00//DN803806				
Unigene25920_A11	1101	63.92	125.82	80.09	125.87	125.29	153.58	30.18	125.01	36.22	9.77E-01	8.73E-96		3.26E-01	8.48E-09		-6.60E-03	9.10E-01		2.87E-01	2.53E-14		2.05E+00	0.00E+00	Up	2.63E-01	4.29E-04		Unigene25920_A11//gi|84453182|dbj|BAE71188.1|//7.00E-68//BEL1-like homeodomain transcription factor [Trifolium pratense]	Unigene25920_A11//2.00E-46//AT2G35940| BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene25920_A11//0.00E+00//TC136142	HB		GO:0000741//GO:0003677//GO:0006350//GO:0009608//GO:0009725//GO:0010218//GO:0010468//GO:0042802//GO:0043231//GO:0046983	nr +

Unigene25921_All	2669	0.80	1.01	1.84	2.61	2.04	3.94	7.83	13.30	8.90	3.24E-01	4.00E-01			1.19E+00	3.77E-05	Up	-3.58E-01	1.10E-01		5.94E-01	6.19E-04		7.65E-01	1.72E-20		1.85E-01	7.47E-02		Unigene25921_All//gi|16974605|gb|AAL31205.1|//0.00E+00//AT5g47580/MN J7_17 [Arabidopsis thaliana] >gi|23506171|gb|AAN31097.1| At5g47580/MNJ7_17 [Arabidopsis thaliana]	Unigene25921_All//3.00E-169//AT5G47580| unknown protein	Unigene25921_All//0.00E+00//gi|164242198|gb|ES851858.1|ES851858			GO:0043231	nr -
Unigene25922_All	1529	3.63	4.21	3.00	56.79	50.09	57.04	13.13	5.17	8.18	2.15E-01	3.88E-01			-2.76E-01	3.29E-01		-1.81E-01	7.73E-04		6.40E-03	9.42E-01		-1.35E+00	4.78E-29	Down	-6.83E-01	2.68E-10		Unigene25922_All//gi|27765046|gb|AAO23644.1|//1.00E-129//At5g67210 [Arabidopsis thaliana]	Unigene25922_All//9.00E-117//AT5G67210| unknown protein	Unigene25922_All//0.00E+00//TC157128				nr +
Unigene25923_All	1167	6.77	4.91	5.52	11.35	10.09	6.08	12.43	1.79	2.80	-4.65E-01	2.55E-02			-2.94E-01	1.97E-01		-1.70E-01	3.20E-01		-9.02E-01	3.06E-09		-2.79E+00	1.93E-54	Down	-2.15E+00	1.51E-41	Down	Unigene25923_All//gi|38603818|gb|AAZ46654.1|//7.00E-77//At5g56120 [Arabidopsis thaliana]	Unigene25923_All//3.00E-78//AT5G56120| unknown protein	Unigene25923_All//0.00E+00//ES849239				nr -
Unigene25927_All	888	89.56	37.60	40.48	142.94	124.25	120.08	128.60	56.15	49.80	-1.25E+00	1.65E-82	Down	-1.15E+00	2.24E-69	Down	-2.02E-01	1.97E-06		-2.51E-01	1.21E-08		-1.20E+00	2.17E-134	Down	-1.37E+00	1.67E-170	Down	Unigene25927_All//gi|115473289|ref|XP_001060243.1|//1.00E-113//Os07g0608500 [Oryza sativa Japonica Group] >gi|14192875|gb|AAK55780.1|AC07903 8_14 Putative 40S ribosomal protein; contains C-terminal domain [Oryza sativa] >gi|113611779|dbj|BAF22157.1| Os07g0608500 [Oryza sativa Japonica Group]	Unigene25927_All//3.00E-109//AT5G35530| 40S ribosomal protein S3 (RPS3C)	Unigene25927_All//0.00E+00//TC146766	ko03010|Ribosome		nr +
Unigene25928_All	570	1.47	7.56	1.12	2.36	4.59	5.86	1.63	2.64	6.36	2.36E+00	2.42E-11	Up	-3.90E-01	6.41E-01		9.60E-01	1.25E-02		1.31E+00	1.46E-04	Up	6.94E-01	1.55E-01		1.96E+00	9.85E-10	Up	Unigene25928_All//gi|74267246|dbj|BAE44121.1|//1.00E-55//protein phosphatase 2C [Nicotiana benthamiana]	Unigene25928_All//1.00E-55//AT2G30020| protein phosphatase 2C, putative / PP2C, putative	Unigene25928_All//0.00E+00//gi|78351552|gb|DT571826.1|DT571826			GO:0004721//GO:0006464//GO:0006952//GO:0009536//GO:0009755//GO:0043169//GO:0043234//GO:0051707	nr -
Unigene25929_All	1166	0.94	8.95	1.23	1.62	3.13	2.44	1.45	2.04	4.51	3.25E+00	5.20E-37	Up	3.88E-01	5.06E-01		9.47E-01	2.42E-03		5.88E-01	1.29E-01		4.94E-01	1.95E-01		1.64E+00	6.47E-11	Up	Unigene25929_All//gi|75223238|sp|O80871.1|PP2C25_ARATH//1.00E-104//RecName: Full=Probable protein phosphatase 2C 25; Short=AtPP2C25; AltName: Full=Protein phosphatase AP2C1	Unigene25929_All//5.00E-105//AT2G30020| protein phosphatase 2C, putative / PP2C, putative	Unigene25929_All//0.00E+00//TC157217			GO:0004721//GO:0006464//GO:0009536//GO:0043169//GO:0043234	nr +
Unigene25931_All	1463	9.30	12.64	11.97	5.52	5.93	4.54	1.53	0.63	0.52	4.43E-01	5.82E-04		3.65E-01	8.98E-03		1.05E-01	6.56E-01		-2.82E-01	2.06E-01		-1.29E+00	1.00E-03		-1.57E+00	6.40E-05	Down	Unigene25931_All//gi|225428995|ref|XP_002265518.1|//1.00E-86//PREDICTED: similar to APK (APS KINASE); ATP binding / kinase/ transferase, transferring phosphorus-containing groups [Vitis vinifera]	Unigene25931_All//2.00E-77//AT5G67520| adenylylsulfate kinase, putative	Unigene25931_All//0.00E+00//CO106645	ko00230|Purine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0006790//GO:0006796//GO:0007276//GO:0009536//GO:0010675//GO:0010601//GO:0032559//GO:0044249	nr -
Unigene25932_All	1012	4.34	4.36	2.21	3.99	4.29	4.64	8.36	3.18	3.03	4.40E-03	9.87E-01		-9.75E-01	1.30E-03		1.05E-01	7.89E-01		2.19E-01	4.91E-01		-1.39E+00	2.46E-13	Down	-1.46E+00	9.41E-15	Down	Unigene25932_All//gi|106879161|gb|ABF82610.1|//6.00E-28//At4g26060 [Arabidopsis thaliana]	Unigene25932_All//6.00E-25//AT4G26060| unknown protein	Unigene25932_All//0.00E+00//gi|164363572|gb|ES831797.1|ES831797				nr -
Unigene25933_All	839	11.10	22.59	17.45	13.30	16.13	15.61	22.98	23.51	15.62	1.02E+00	8.51E-15	Up	6.53E-01	1.55E-05		2.78E-01	7.93E-02		2.31E-01	1.81E-01		3.31E-02	8.03E-01		-5.57E-01	3.63E-07		Unigene25933_All//gi|283484477|gb|ADB23456.1|//5.00E-55//nuclear factor Y subunit C [Phaseolus vulgaris]	Unigene25933_All//9.00E-35//AT1G08970| NF-YC9 (NUCLEAR FACTOR Y, SUBUNIT C9); DNA binding / transcription factor	Unigene25933_All//0.00E+00//TC175556	CCAAT		GO:0001071//GO:0003677//GO:0006351//GO:0043231	nr -
Unigene25934_All	927	79.07	208.47	159.06	64.54	61.07	83.31	88.71	180.66	282.09	1.40E+00	1.14E-235	Up	1.01E+00	1.48E-104	Up	-7.97E-02	3.14E-01		3.68E-01	1.24E-10		1.03E+00	1.23E-153	Up	1.67E+00	0.00E+00	Up	Unigene25934_All//gi|33324520|gb|AAQ08000.1|//7.00E-84//dehydration responsive element binding protein [Gossypium hirsutum] >gi|37727988|gb|AAO43165.1| DRE binding protein 1 [Gossypium hirsutum]	Unigene25934_All//6.00E-38//AT1G46768| RAP2.1 (related to AP2 1); DNA binding / transcription factor	Unigene25934_All//0.00E+00//TC164889	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene25937_All	1797	0.12	1.24	0.41	1.55	1.15	1.21	0.87	0.60	1.33	3.41E+00	1.13E-08	Up	1.83E+00	5.05E-02		-4.33E-01	2.62E-01		-3.64E-01	3.82E-01		-5.26E-01	2.81E-01		6.12E-01	8.70E-02		Unigene25937_All//gi|22326836|ref|NP_197125.2|//0.00E+00//HEAT repeat-containing protein [Arabidopsis thaliana] >gi|19789899|gb|AAL47427.1| AT5g16210/T21H19_130 [Arabidopsis thaliana]	Unigene25937_All//0.00E+00//AT5G16210| HEAT repeat-containing protein	Unigene25937_All//0.00E+00//TC134516			GO:0044464	nr +
Unigene25940_All	1294	7.44	40.76	18.27	5.35	14.08	15.04	21.40	65.70	54.65	2.45E+00	4.96E-138	Up	1.30E+00	2.13E-25	Up	1.40E+00	2.15E-26	Up	1.49E+00	1.75E-28	Up	1.62E+00	5.18E-158	Up	1.35E+00	5.01E-103	Up	Unigene25940_All//gi|8131905|gb|AAF73132.1|AF149047|//1.00E-157//homogentisate 1,2-dioxygenase [Solanum lycopersicum]	Unigene25940_All//9.00E-152//AT5G54080| HGO (HOMOGENTISATE 1,2-DIOXYGENASE); homogentisate 1,2-dioxygenase	Unigene25940_All//0.00E+00//TC155472	ko00350|Tyrosine metabolism	GO:0008152	nr -
Unigene25941_All	1513	5.12	170.70	2.11	8.26	38.53	14.72	13.80	37.10	188.61	5.06E+00	0.00E+00	Up	-1.28E+00	1.62E-08	Down	2.22E+00	1.57E-158	Up	8.33E-01	4.01E-13		1.43E+00	6.72E-87	Up	3.77E+00	0.00E+00	Up	Unigene25941_All//gi|224104250|ref|XP_002313372.1|//4.00E-74//f-box family protein [Populus trichocarpa] >gi|222849780|gb|EEE87327.1| f-box family protein [Populus trichocarpa]	Unigene25941_All//2.00E-49//AT1G30200| F-box family protein	Unigene25941_All//0.00E+00//TC131903				nr +
Unigene25946_All	1149	27.59	7.67	15.85	102.06	68.21	71.93	72.16	28.99	20.14	-1.85E+00	1.61E-58	Down	-8.00E-01	1.30E-15		-5.81E-01	1.21E-40		-5.05E-01	5.06E-28		-1.32E+00	1.88E-113	Down	-1.84E+00	1.61E-190	Down	Unigene25946_All//gi|152963813|gb|ABS50234.1|//1.00E-79//Ran binding protein [Nicotiana benthamiana]	Unigene25946_All//5.00E-68//AT1G07140| SIRANBP; Ran GTPase binding	Unigene25946_All//0.00E+00//TC133315			GO:0006810//GO:0017016	nr -
Unigene25947_All	1018	5.19	2.44	2.82	24.37	14.48	24.76	12.42	13.18	2.39	-1.09E+00	3.89E-05	Down	-8.78E-01	1.22E-03		-7.51E-01	7.52E-14		2.27E-02	8.75E-01		8.58E-02	6.32E-01		-2.38E+00	4.91E-41	Down	Unigene25947_All//gi|15238973|ref|NP_196677.1|//3.00E-80//APT5 (Adenine phosphoribosyltransferase 5); adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|8953378|emb|CAB96651.1| adenine phosphoribosyltransferase-like protein [Arabidopsis thaliana]	Unigene25947_All//2.00E-81//AT5G11160| APT5 (Adenine phosphoribosyltransferase 5); adenine phosphoribosyltransferase	Unigene25947_All//0.00E+00//TC132333	ko00230|Purine metabolism	GO:0015103//GO:0016020//GO:0016763//GO:0043096//GO:0044444	nr +
Unigene25948_All	1667	0.94	1.19	1.37	1.79	1.92	1.27	2.69	5.14	5.52	3.32E-01	4.78E-01		5.45E-01	2.27E-01		9.96E-02	8.35E-01		-4.94E-01	1.95E-01		9.35E-01	1.67E-07		1.04E+00	1.28E-09	Up	Unigene25948_All//gi|224133938|ref|XP_002327716.1|//8.00E-25//f-box family protein [Populus trichocarpa] >gi|222836801|gb|EEE75194.1| f-box family protein [Populus trichocarpa]	Unigene25948_All//4.00E-12//AT2G17030| F-box family protein					nr +
Unigene25951_All	1235	1.02	1.72	0.09	2.22	2.15	2.56	6.33	4.91	9.58	7.61E-01	8.36E-02		-3.56E+00	4.96E-05	Down	-4.72E-02	9.01E-01		2.07E-01	6.32E-01		-3.68E-01	5.44E-02		5.97E-01	3.10E-05		Unigene25951_All//gi|71041112|gb|AAZ20444.1|//9.00E-73//MYBR5 [Malus x domestica]	Unigene25951_All//6.00E-60//AT5G32660| myb family transcription factor	Unigene25951_All//0.00E+00//TC135437	MYB-related	ko04712|Circadian rhythm - plant	GO:0001071//GO:0006351//GO:0006970//GO:0009725//GO:0010038//GO:0010468	nr +
Unigene25953_All	1219	2.96	6.98	5.64	3.23	1.72	2.78	9.61	13.10	8.76	1.24E+00	2.73E-09	Up	9.28E-01	7.28E-05		-9.06E-01	1.64E-03		-2.16E-01	5.42E-01		4.47E-01	3.30E-04		-1.34E-01	4.06E-01		Unigene25953_All//gi|75180423|sp|Q9LT89.1|TCP19_ARATH//4.00E-67//RecName: Full=Transcription factor TCP19 >gi|31711724|gb|AAP68218.1| At5g51910 [Arabidopsis thaliana]	Unigene25953_All//1.00E-66//AT5G51910| TCP family transcription factor, putative	Unigene25953_All//0.00E+00//TC146696	TCP		GO:0010468//GO:0043231	nr +
Unigene25954_All	831	17.06	20.85	14.03	24.52	20.10	17.83	10.74	14.69	5.13	2.89E-01	3.56E-02		-2.82E-01	8.22E-02		-2.87E-01	1.71E-02		-4.60E-01	1.13E-04		4.52E-01	1.82E-03		-1.07E+00	8.55E-10	Down	Unigene25954_All//gi|115455043|ref|NP_001051122.1|//3.00E-23//Os03g0724500 [Oryza sativa Japonica Group] >gi|37718771|gb|AAR01643.1| expressed protein [Oryza sativa Japonica Group] >gi|113549593|dbj|BAF13036.1| Os03g0724500 [Oryza sativa Japonica Group]	Unigene25954_All//2.00E-17//AT3G05570| unknown protein	Unigene25954_All//0.00E+00//TC162208				nr -
Unigene25956_All	1726	0.30	2.35	0.74	1.65	1.96	2.30	5.22	6.78	8.68	2.95E+00	1.79E-13	Up	1.29E+00	4.48E-02		2.49E-01	5.31E-01		4.85E-01	1.31E-01		3.78E-01	1.21E-02		7.34E-01	8.28E-09		Unigene25956_All//gi|297839877|ref|XP_002887820.1|//0.00E+00//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333661|gb|EFH64079.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25956_All//0.00E+00//AT1G80570| F-box family protein (FBL14)	Unigene25956_All//0.00E+00//TC145155		ko04120|Ubiquitin mediated proteolysis	GO:0003824//GO:0019941	nr +
Unigene25957_All	1809	16.80	5.91	11.01	15.86	13.99	12.73	7.62	8.57	6.08	-1.51E+00	3.40E-42	Down	-6.10E-01	1.44E-09		-1.81E-01	8.77E-02		-3.17E-01	1.67E-03		1.70E-01	2.37E-01		-3.26E-01	1.47E-02		Unigene25957_All//gi|297806753|ref|XP_002871260.1|//2.00E-72//IQ-domain 24 [Arabidopsis lyrata subsp. lyrata] >gi|297317097|gb|EFH47519.1| IQ-domain 24 [Arabidopsis lyrata subsp. lyrata]	Unigene25957_All//3.00E-40//AT5G07240| IQD24 (IQ-domain 24); calmodulin binding	Unigene25957_All//0.00E+00//TC151829				nr -
Unigene2596_All	1595	102.97	6.19	17.73	176.49	80.31	109.07	5.04	2.57	0.47	-4.06E+00	0.00E+00	Down	-2.54E+00	0.00E+00	Down	-1.14E+00	0.00E+00	Down	-6.94E-01	9.69E-118		-9.72E-01	1.63E-07		-3.41E+00	4.69E-38	Down	Unigene2596_All//gi|15222811|ref|NP_173397.1|//1.00E-128//leucine-rich repeat family protein [Arabidopsis thaliana] >gi|10120434|gb|AAG13059.1|AC01180 7_18 Unknown protein [Arabidopsis thaliana] >gi|44681384|gb|AAS47632.1| At1g49750 [Arabidopsis thaliana] >gi|45773904|gb|AAS76756.1| At1g49750 [Arabidopsis thaliana] >gi|222423160|dbj|BAH19559.1| AT1G49750 [Arabidopsis thaliana]	Unigene2596_All//1.00E-95//AT1G49750| leucine-rich repeat family protein	Unigene2596_All//0.00E+00//TC144786	ko04626|Plant-pathogen interaction		nr -
Unigene25960_All	1530	0.99	89.78	6.37	6.97	11.25	11.81	3.43	2.05	3.15	6.50E+00	0.00E+00	Up	2.68E+00	8.16E-28	Up	6.92E-01	3.08E-08		7.61E-01	2.59E-09		-7.42E-01	1.40E-03		-1.21E-01	6.29E-01		Unigene25960_All//gi|15242078|ref|NP_197587.1|//1.00E-170//glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Unigene25960_All//3.00E-163//AT5G20870| glycosyl hydrolase family 17 protein	Unigene25960_All//9.00E-95//gi|78329547|gb|DT549821.1|DT549821		ko00500|Starch and sucrose metabolism	GO:0008422//GO:0043167//GO:0044238	nr -
Unigene25965_All	863	21.40	16.20	14.99	29.73	21.71	32.55	50.51	57.29	19.57	-4.01E-01	1.92E-03		-5.13E-01	1.15E-04		-4.54E-01	4.51E-06		1.31E-01	2.74E-01		1.82E-01	9.90E-03		-1.37E+00	1.67E-65	Down	Unigene25965_All//gi|115475686|ref|NP_001061439.1|//1.00E-63//Os08g0278900 [Oryza sativa Japonica Group] >gi|37805903|dbj|BAC99752.1| Stromal cell-derived factor 2-like protein [Oryza sativa Japonica Group] >gi|37806069|dbj|BAC99520.1| Stromal cell-derived factor 2-like protein [Oryza sativa Japonica Group] >gi|113623408|dbj|BAF23353.1| Os08g0278900 [Oryza sativa Japonica Group]	Unigene25965_All//2.00E-63//AT2G25110| SDF2 (STROMAL CELL-DERIVED FACTOR 2-LIKE PROTEIN PRECURSOR)	Unigene25965_All//0.00E+00//TC161526			GO:0000030//GO:0006952//GO:0031410//GO:0043231	nr -
Unigene25969_All	695	3.31	9.48	4.83	3.80	8.13	10.53	0.61	3.79	2.41	1.52E+00	9.70E-10	Up	5.43E-01	1.31E-01		1.10E+00	5.57E-06	Up	1.47E+00	8.04E-11	Up	2.64E+00	8.37E-10	Up	1.98E+00	5.62E-05	Up	Unigene25969_All//gi|297838467|ref|XP_002887115.1|//9.00E-55//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332956|gb|EFH63374.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25969_All//1.00E-45//AT1G67340| zinc finger (MYND type) family protein / F-box family protein	Unigene25969_All//0.00E+00//ES804023			GO:0043231//GO:0046914	nr +

Unigene25970_All	1335	9.80	28.31	12.60	18.28	33.79	28.99	0.95	5.35	3.34	1.53E+00	3.32E-53	Up	3.63E-01	1.12E-02		8.86E-01	1.02E-31		6.65E-01	2.39E-15		2.49E+00	5.93E-24	Up	1.81E+00	1.05E-10	Up	Unigene25970_All//gi|224122012|ref|XP_002318728.1|//1.00E-116//f-box family protein [Populus trichocarpa] >gi|222859401|gb|EEE96948.1| f-box family protein [Populus trichocarpa]	Unigene25970_All//3.00E-97//AT1G67340| zinc finger (MYND type) family protein / F-box family protein	Unigene25970_All//0.00E+00//ES804023				nr +
Unigene25973_All	930	28.35	36.94	35.27	28.98	35.58	43.80	40.55	14.02	23.60	3.82E-01	3.13E-05		3.15E-01	1.40E-03		2.96E-01	9.98E-04		5.96E-01	2.23E-13		-1.53E+00	2.88E-65	Down	-7.81E-01	3.43E-23		Unigene25973_All//gi|255565335|ref|XP_002523659.1|//9.00E-47//Phospholipase A21 [Ricinus communis] >gi|223537111|gb|EEF38745.1| Phospholipase A21 [Ricinus communis]	Unigene25973_All//2.00E-37//AT2G06925| PLA2-ALPHA; phospholipase A2	Unigene25973_All//0.00E+00//gi|21097261|gb|BQ409574.1|BQ409574		ko00592|alpha-Linolenic acid metabolism//ko00564|Glycerophospholipid metabolism//ko00591|Linoleic acid metabolism//ko00565|Ether lipid metabolism//ko00590|Arachidonic acid metabolism	GO:0004091//GO:0006629//GO:0019637//GO:0043231//GO:0046872	nr +
Unigene25974_All	2336	0.81	1.56	0.68	4.39	4.07	3.87	4.02	1.84	2.23	9.54E-01	3.28E-03		-2.38E-01	6.05E-01		-1.11E-01	6.01E-01		-1.84E-01	3.80E-01		-1.12E+00	9.37E-11	Down	-8.47E-01	2.81E-07		Unigene25974_All//gi|15217473|ref|NP_174595.1|//0.00E+00//fringe-related protein [Arabidopsis thaliana]	Unigene25974_All//0.00E+00//AT1G33250| fringe-related protein	Unigene25974_All//0.00E+00//TC136013			GO:0016740	nr -
Unigene25975_All	1433	7.63	1.45	6.02	7.44	4.64	3.75	3.45	0.32	0.28	-2.40E+00	1.74E-28	Down	-3.42E-01	6.48E-02		-6.82E-01	2.29E-05		-9.88E-01	1.06E-08		-3.43E+00	5.53E-23	Down	-3.63E+00	5.49E-25	Down	Unigene25975_All//gi|75115359|sp|Q66Q42.1|Y5162_ARATH//3.00E-48//RecName: Full=Uncharacterized protein At5g41620 >gi|51536470|gb|AAU05473.1| At5g41620 [Arabidopsis thaliana] >gi|53850503|gb|AAU95428.1| At5g41620 [Arabidopsis thaliana]	Unigene25975_All//2.00E-45//AT5G41620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, plasma membrane; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: intracellular protein transport protein USO1-related (TAIR:AT1G64180.1); Has 2568 Blast hits to 2157 proteins in 267 species: Archae - 27; Bacteria - 258; Metazoa - 955; Fungi - 181; Plants - 134; Viruses - 0; Other Eukaryotes - 1013 (source: NCBI BLink).	Unigene25975_All//1.00E-22//TC142544			GO:0009536//GO:0016020	nr -
Unigene25976_All	646	6.56	6.12	2.80	5.55	5.44	5.45	2.09	1.36	1.17	-1.01E-01	7.27E-01		-1.23E+00	1.01E-04	Down	-3.02E-02	9.30E-01		-2.59E-02	9.44E-01		-6.24E-01	2.33E-01		-8.38E-01	8.98E-02		Unigene25976_All//gi|8886939|gb|AAF80625.1|AC069251_18//1.00E-12//F2D10.35 [Arabidopsis thaliana]	Unigene25976_All//1.00E-12//AT1G20830| unknown protein	Unigene25976_All//0.00E+00//BF270610				nr +
Unigene25977_All	1386	7.13	7.79	9.68	7.48	6.78	7.53	5.00	2.41	2.99	1.26E-01	5.16E-01		4.40E-01	6.18E-03		-1.40E-01	5.11E-01		9.90E-03	9.56E-01		-1.05E+00	2.10E-07	Down	-7.43E-01	1.18E-04		Unigene25977_All//gi|8886939|gb|AAF80625.1|AC069251_18//4.00E-99//F2D10.35 [Arabidopsis thaliana]	Unigene25977_All//3.00E-99//AT1G20830| unknown protein	Unigene25977_All//0.00E+00//gi|11201521|gb|BF270610.1|BF270610			GO:0043231	nr +
Unigene2598_All	1742	18.29	14.22	14.18	5.89	7.33	5.29	4.44	2.11	2.01	-3.63E-01	1.48E-04		-3.67E-01	2.17E-04		3.16E-01	4.85E-02		-1.56E-01	4.64E-01		-1.07E+00	2.09E-08	Down	-1.14E+00	1.57E-09	Down	Unigene2598_All//gi|297804126|ref|XP_002869947.1|//0.00E+00//PTAC14 [Arabidopsis lyrata subsp. lyrata] >gi|297315783|gb|EFH46206.1| PTAC14 [Arabidopsis lyrata subsp. lyrata]	Unigene2598_All//0.00E+00//AT4G20130| PTAC14 (PLASTID TRANSCRIPTIONALLY ACTIVE14)	Unigene2598_All//0.00E+00//TC133974				nr -
Unigene25980_All	864	9.20	7.57	6.84	7.50	6.70	4.91	3.62	1.84	1.25	-2.83E-01	1.91E-01		-4.28E-01	4.98E-02		-1.63E-01	5.61E-01		-6.09E-01	7.93E-03		-9.78E-01	1.90E-03		-1.54E+00	2.10E-06	Down	Unigene25980_All//gi|30679573|ref|NP_849599.1|//1.00E-84//GLX2-4 (glyoxalase 2-4); hydrolase/ hydroxyacylglutathione hydrolase/ zinc ion binding [Arabidopsis thaliana]	Unigene25980_All//5.00E-86//AT1G06130| GLX2-4 (glyoxalase 2-4); hydrolase/ hydroxyacylglutathione hydrolase/ zinc ion binding	Unigene25980_All//0.00E+00//TC151164	ko00620|Pyruvate metabolism	GO:0006089//GO:0009536//GO:0016790//GO:0016812//GO:0016999//GO:0046914	nr +
Unigene25982_All	1532	5.33	4.56	2.68	10.63	9.37	11.20	9.38	4.12	4.00	-2.23E-01	3.08E-01		-9.93E-01	3.31E-06		-1.82E-01	2.28E-01		7.53E-02	6.48E-01		-1.19E+00	1.98E-17	Down	-1.23E+00	6.44E-19	Down	Unigene25982_All//gi|30686117|ref|NP_181004.2|//2.00E-68//MEE21 (maternal effect embryo arrest 21) [Arabidopsis thaliana]	Unigene25982_All//7.00E-57//AT2G34570| MEE21 (maternal effect embryo arrest 21)	Unigene25982_All//0.00E+00//TC167698			GO:0003006	nr +
Unigene25983_All	1199	1.53	2.62	1.51	3.32	3.62	1.39	3.49	2.72	1.76	7.79E-01	2.64E-02		-1.64E-02	9.96E-01		1.23E-01	7.42E-01		-1.25E+00	4.47E-05	Down	-3.61E-01	1.99E-01		-9.87E-01	1.43E-04		Unigene25983_All//gi|186515828|ref|NP_567915.3|//7.00E-89//ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene25983_All//3.00E-88//AT4G33160| ubiquitin-protein ligase	Unigene25983_All//0.00E+00//gi|78340958|gb|DT561232.1|DT561232				nr +
Unigene25984_All	1726	0.91	1.09	1.42	1.50	2.09	1.15	2.16	1.48	0.97	2.56E-01	6.17E-01		6.42E-01	1.36E-01		4.81E-01	1.52E-01		-3.83E-01	3.76E-01		-5.45E-01	5.74E-02		-1.15E+00	4.24E-05	Down	Unigene25984_All//gi|224088629|ref|XP_002308504.1|//1.00E-159//f-box family protein [Populus trichocarpa] >gi|222854480|gb|EEE92027.1| f-box family protein [Populus trichocarpa]	Unigene25984_All//1.00E-57//AT4G33160| ubiquitin-protein ligase	Unigene25984_All//0.00E+00//gi|78340958|gb|DT561232.1|DT561232				nr +
Unigene25985_All	1193	3.90	2.97	2.01	3.97	6.49	9.01	9.36	11.04	17.10	-3.93E-01	1.69E-01		-9.59E-01	1.08E-03		7.11E-01	3.43E-04		1.18E+00	2.23E-11	Up	2.38E-01	1.09E-01		8.70E-01	2.59E-15		Unigene25985_All//gi|224142413|ref|XP_002324552.1|//1.00E-110//ABC transporter family protein [Populus trichocarpa] >gi|222865986|gb|EEF03117.1| ABC transporter family protein [Populus trichocarpa]	Unigene25985_All//1.00E-100//AT1G63270| ATNAP10; transporter	Unigene25985_All//0.00E+00//gi|109874279|gb|DW503253.1|DW503253		ko02010|ABC transporters	GO:0017111//GO:0030313//GO:0032559//GO:0043623	nr +
Unigene25987_All	1036	1.46	3.57	1.64	4.04	4.59	4.75	3.10	5.08	4.42	1.29E+00	1.03E-04	Up	1.67E-01	7.31E-01		1.84E-01	5.76E-01		2.34E-01	4.55E-01		7.13E-01	2.11E-03		5.12E-01	3.72E-02		Unigene25987_All//gi|300153596|gb|EFJ20234.1|//5.00E-56//ubiquitin-conjugating enzyme 19, E2 [Selaginella moellendorffii]	Unigene25987_All//3.00E-47//AT1G50490| UBC20 (ubiquitin-conjugating enzyme 20); ubiquitin-protein ligase	Unigene25987_All//0.00E+00//DR460965		ko04120|Ubiquitin mediated proteolysis	GO:0019787//GO:0019941//GO:0032446//GO:0032559//GO:0043231//GO:0060255//GO:0070646	nr +
Unigene25988_All	883	22.22	28.86	23.28	9.03	15.05	9.51	7.23	34.08	23.60	3.77E-01	4.91E-04		6.71E-02	6.18E-01		7.38E-01	3.48E-07		7.58E-02	7.38E-01		2.24E+00	9.91E-87	Up	1.71E+00	3.31E-43	Up	Unigene25988_All//gi|11137999|dbj|BAB17755.1|//8.00E-51//glycerol-3-phosphate acyltransferase [Cucurbita moschata] >gi|13429838|dbj|BAB39689.1| acyl-(acyl-carrier-protein): glycerol-3-phosphate acyltransferase [Cucurbita moschata]	Unigene25988_All//2.00E-48//AT1G32200| ATS1; glycerol-3-phosphate O-acyltransferase	Unigene25988_All//0.00E+00//gi|109852696|gb|DW481675.1|DW481675		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0003006//GO:0004497//GO:0006633//GO:0006950//GO:0006996//GO:0008374//GO:0009532//GO:0009725//GO:0016705//GO:0031224//GO:0046471//GO:0046872	nr +
Unigene25989_All	790	68.41	56.57	54.06	100.01	95.07	161.16	75.41	257.23	288.55	-2.74E-01	1.49E-04		-3.40E-01	4.40E-06		-7.31E-02	2.99E-01		6.88E-01	2.82E-52		1.77E+00	0.00E+00	Up	1.94E+00	0.00E+00	Up	Unigene25989_All//gi|192910680|gb|ACF06448.1|//6.00E-57//annexin [Elaeis guineensis]	Unigene25989_All//7.00E-37//AT1G68090| ANN5; calcium ion binding / calcium-dependent phospholipid binding	Unigene25989_All//0.00E+00//TC159094			GO:0005543//GO:0046872	nr +
Unigene2599_All	1523	11.37	7.88	16.29	35.42	28.33	33.09	99.88	10.37	25.79	-5.28E-01	7.05E-05		5.19E-01	4.05E-06		-3.22E-01	1.16E-06		-9.81E-02	2.43E-01		-3.27E+00	0.00E+00	Down	-1.95E+00	0.00E+00	Down	Unigene2599_All//gi|153805696|gb|ABS52573.1|//0.00E+00//chalcone synthase [Gossypium hirsutum]	Unigene2599_All//0.00E+00//AT5G13930| TT4 (TRANSPARENT TESTA 4); naringenin-chalcone synthase	Unigene2599_All//0.00E+00//gi|164343483|gb|ES810476.1|ES810476		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr +
Unigene25991_All	1529	4.41	19.68	2.75	1.66	3.83	6.14	1.77	3.39	2.68	2.16E+00	1.38E-67	Up	-6.82E-01	3.76E-03		1.20E+00	4.46E-07	Up	1.89E+00	2.67E-19	Up	9.38E-01	7.06E-05		6.01E-01	2.10E-02		Unigene25991_All//gi|223452315|gb|ACM89485.1|//1.00E-80//receptor-like kinase [Glycine max]	Unigene25991_All//3.00E-68//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene25991_All//0.00E+00//TC132339		ko04626|Plant-pathogen interaction	GO:0004672	nr +
Unigene25993_All	1892	10.62	5.44	5.49	13.85	16.11	11.31	7.44	0.75	1.71	-9.66E-01	2.62E-14		-9.52E-01	2.20E-13		2.18E-01	2.90E-02		-2.92E-01	6.69E-03		-3.31E+00	2.18E-62	Down	-2.13E+00	8.94E-40	Down	Unigene25993_All//gi|297798774|ref|XP_002867271.1|//1.00E-162//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313107|gb|EFH43530.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene25993_All//1.00E-153//AT4G31890| armadillo/beta-catenin repeat family protein	Unigene25993_All//0.00E+00//TC152078				nr +
Unigene25994_All	1378	9.04	18.50	15.88	17.32	21.02	20.25	27.74	33.49	33.97	1.03E+00	6.86E-20	Up	8.14E-01	2.68E-11		2.79E-01	4.55E-03		2.26E-01	3.66E-02		2.72E-01	1.15E-04		2.93E-01	1.73E-05		Unigene25994_All//gi|32470632|gb|AAP45159.1|//1.00E-115//Plant viral-response family protein [Solanum bulbocastanum] >gi|32470663|gb|AAP45189.1| Plant viral-response family protein [Solanum bulbocastanum]	Unigene25994_All//2.00E-106//AT1G32120| unknown protein	Unigene25994_All//0.00E+00//ES806512			GO:0044464	nr +
Unigene25995_All	2646	3.05	1.13	4.33	14.10	13.44	10.58	10.27	5.05	5.31	-1.43E+00	6.78E-11	Down	5.07E-01	3.77E-03		-6.89E-02	5.45E-01		-4.14E-01	1.09E-06		-1.02E+00	1.61E-25	Down	-9.51E-01	2.24E-23		Unigene25995_All//gi|15239502|ref|NP_197954.1|//0.00E+00//exostosin family protein [Arabidopsis thaliana]	Unigene25995_All//2.00E-178//AT4G32790| exostosin family protein	Unigene25995_All//0.00E+00//ES808098			GO:0044464	nr +
Unigene25998_All	1778	7.71	3.82	6.74	20.31	14.64	8.81	26.51	16.38	11.09	-1.01E+00	8.88E-11	Down	-1.94E-01	2.54E-01		-4.72E-01	6.49E-09		-1.20E+00	1.69E-38	Down	-6.94E-01	6.25E-23		-1.26E+00	3.20E-62	Down	Unigene25998_All//gi|51557078|gb|AAU06309.1|//1.00E-124//MYB transcription factor [Hevea brasiliensis]	Unigene25998_All//7.00E-100//AT2G38090| myb family transcription factor	Unigene25998_All//0.00E+00//TC136411	MYB	ko04712|Circadian rhythm - plant	GO:0003676//GO:0010468//GO:0043231	nr +
Unigene2600_All	1945	35.72	17.22	15.71	30.22	22.87	30.79	31.78	17.17	17.92	-1.05E+00	8.11E-55	Down	-1.18E+00	5.78E-64	Down	-4.02E-01	1.23E-10		2.69E-02	7.49E-01		-8.88E-01	3.60E-45		-8.26E-01	3.55E-41		Unigene2600_All//gi|255557353|ref|XP_002519707.1|//0.00E+00//50 kDa ketoacyl-ACP synthase [Ricinus communis] >gi|294668|gb|AAA33873.1| chloroplast beta-ketoacyl-ACP synthase precursor [Ricinus communis] >gi|148791249|gb|ABR12416.1| plastid 3-keto-acyl-ACP synthase I [Ricinus communis] >gi|223541124|gb|EEF42680.1| 50 kDa ketoacyl-ACP synthase [Ricinus communis]	Unigene2600_All//0.00E+00//AT5G46290| KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); catalytic/ fatty-acid synthase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene2600_All//0.00E+00//TC148793		ko00061|Fatty acid biosynthesis		nr -
Unigene26001_All	1228	4.30	5.65	12.23	19.67	8.81	9.27	9.43	11.23	6.68	3.94E-01	8.25E-02		1.51E+00	2.30E-20	Up	-1.16E+00	1.03E-27	Down	-1.09E+00	4.94E-22	Down	2.52E-01	7.88E-02		-4.97E-01	5.76E-04		Unigene26001_All//gi|2274915|emb|CAA03908.1|//1.00E-134//beta-1,3-glucanase [Citrus sinensis]	Unigene26001_All//1.00E-111//AT3G57270| BG1 (BETA-1,3-GLUCANASE 1); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene26001_All//1.00E-31//gi|3326349|gb|AI055235.1|AI055235		ko00500|Starch and sucrose metabolism		nr +
Unigene26003_All	1631	2.25	1.12	0.46	6.84	8.72	6.90	10.58	1.97	3.05	-1.01E+00	1.89E-03		-2.30E+00	4.88E-09	Down	3.50E-01	1.77E-02		1.13E-02	9.49E-01		-2.42E+00	3.86E-55	Down	-1.79E+00	7.51E-39	Down	Unigene26003_All//gi|209865484|gb|ACI89426.1|//1.00E-157//cyclin B [Populus tomentosa]	Unigene26003_All//3.00E-105//AT1G76310| CYCB2;4 (CYCLIN B2;4); cyclin-dependent protein kinase regulator	Unigene26003_All//0.00E+00//TC168094				nr -
Unigene26006_All	770	61.77	64.16	60.65	146.14	178.57	172.27	154.62	144.06	67.67	5.49E-02	5.46E-01		-2.63E-02	7.73E-01		2.89E-01	4.66E-13		2.37E-01	4.20E-08		-1.02E-01	2.54E-02		-1.19E+00	2.33E-143	Down	Unigene26006_All//gi|260751188|gb|ACX48910.1|//1.00E-132//p-coumaroyl-shikimate 3'-hydroxylase [Trifolium pratense]	Unigene26006_All//1.00E-122//AT2G40890| CYP98A3 (cytochrome P450, family 98, subfamily A, polypeptide 3); monooxygenase/ p-coumarate 3-hydroxylase	Unigene26006_All//0.00E+00//TC135543		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr -

Unigene26007_All	874	13.89	31.89	11.94	21.49	17.77	25.11	44.41	85.89	61.67	1.20E+00	2.43E-27	Up	-2.18E-01	2.38E-01		-2.74E-01	3.13E-02		2.25E-01	7.31E-02		9.52E-01	3.26E-61		4.74E-01	6.76E-14		Unigene26007_All//gi|30697970|ref|NP_201227.3|//7.00E-59//calmodulin-binding protein [Arabidopsis thaliana] >gi|79332100|ref|NP_001032135.1| calmodulin-binding protein [Arabidopsis thaliana] >gi|75324343|sp|Q6NPP4.1|CMTA2_ARATH RecName: Full=Calmodulin-binding transcription activator 2; AltName: Full=Signal-responsive protein 4; AltName: Full=Ethylene-induced calmodulin-binding protein c; Short=EICBP.c; Short=AtER66 >gi|38603814|gb|AAR24652.1| At5g64220 [Arabidopsis thaliana] >gi|110738680|dbj|BAF01265.1| Calmodulin-binding transcription activator 2 [Arabidopsis thaliana]	Unigene26007_All//8.00E-52//AT5G64220| calmodulin-binding protein	Unigene26007_All//0.00E+00//TC163953	CAMTA		GO:0003676//GO:0005515//GO:0009409//GO:0010468//GO:0016604//GO:0003528	nr -
Unigene26008_All	992	1.90	5.21	2.25	3.11	2.53	2.32	2.60	3.08	2.69	1.46E+00	2.13E-07	Up	2.48E-01	6.03E-01		-2.97E-01	4.34E-01		-4.23E-01	2.61E-01		2.43E-01	4.95E-01		4.95E-02	9.03E-01		Unigene26008_All//gi|297846628|ref|XP_002891195.1|//3.00E-90//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297337037|gb|EFH67454.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene26008_All//8.00E-92//AT1G35660| unknown protein					nr -
Unigene26009_All	985	53.49	36.88	46.98	123.25	93.97	91.79	27.09	18.03	11.32	-5.36E-01	1.77E-13		-1.87E-01	1.81E-02		-3.91E-01	1.87E-20		-4.25E-01	2.74E-21		-5.87E-01	4.20E-10		-1.26E+00	1.26E-35	Down	Unigene26009_All//gi|75185987|sp|Q9M7N6.1|MAF1_SOLLC//9.00E-35//RecName: Full=MFP1 attachment factor 1 >gi|7546725|gb|AAF63657.1|AF118113_1 MFP1 attachment factor 1 [Solanum lycopersicum]	Unigene26009_All//2.00E-33//AT1G47200| MFP2	Unigene26009_All//0.00E+00//gi|109877553|gb|DW506526.1|DW506526			GO:0000087//GO:0005488//GO:0031965//GO:0048528	nr +
Unigene2601_All	1644	11.27	2.65	5.38	10.33	8.32	13.27	15.64	3.28	5.86	-2.09E+00	1.99E-40	Down	-1.07E+00	8.18E-15	Down	-3.13E-01	1.80E-02		3.61E-01	2.09E-03		-2.25E+00	4.68E-75	Down	-1.41E+00	5.24E-41	Down	Unigene2601_All//gi|15223910|ref|NP_172934.1|//1.00E-165//semialdehyde dehydrogenase family protein [Arabidopsis thaliana] >gi|17979524|gb|AAL50097.1| At1g14810/F10B6_6 [Arabidopsis thaliana] >gi|20856224|gb|AAM26654.1| At1g14810/F10B6_6 [Arabidopsis thaliana]	Unigene2601_All//1.00E-149//AT1G14810| semialdehyde dehydrogenase family protein	Unigene2601_All//0.00E+00//TC145725		ko00270|Cysteine and methionine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00300|Lysine biosynthesis		nr -
Unigene26010_All	1038	2.87	2.44	2.00	7.01	3.82	2.52	5.87	1.97	2.73	-2.35E-01	5.35E-01		-5.22E-01	1.72E-01		-8.77E-01	1.20E-05		-1.47E+00	5.61E-11	Down	-1.57E+00	1.39E-11	Down	-1.11E+00	2.41E-07	Down	Unigene26010_All//gi|297598416|ref|NP_001045553.2|//2.00E-06//Os01g0974300 [Oryza sativa Japonica Group] >gi|255674124|dbj|BAF07467.2| Os01g0974300 [Oryza sativa Japonica Group]	Unigene26010_All//5.00E-13//AT3G12590| unknown protein	Unigene26010_All//0.00E+00//ES825126			GO:0043231	nr +
Unigene26013_All	739	2.62	0.55	1.37	2.70	2.00	0.98	2.23	1.41	0.75	-2.26E+00	2.83E-05	Down	-9.36E-01	5.62E-02		-4.28E-01	3.61E-01		-1.46E+00	1.84E-03		-6.58E-01	1.54E-01		-1.56E+00	7.74E-04	Down	Unigene26013_All//gi|15232311|ref|NP_191598.1|//2.00E-50//HAT3 (HOMEOBOX-LEUCINE ZIPPER PROTEIN 3); transcription factor [Arabidopsis thaliana] >gi|12644275|sp|P46602.2|HAT3_ARATH RecName: Full=Homeobox-leucine zipper protein HAT3; AltName: Full=Homeodomain-leucine zipper protein HAT3; Short=HD-ZIP protein 3 >gi|7287987|emb|CAB81825.1| homeobox-leucine zipper protein HAT3 [Arabidopsis thaliana] >gi|20067965|emb|CAD29465.1| homeodomain-leucine zipper protein HAT3 [Arabidopsis thaliana] >gi|20466199|gb|AAM20417.1| homeobox-leucine zipper protein HAT3 [Arabidopsis thaliana] >gi|30984526|gb|AAP42726.1| At3g60390 [Arabidopsis thaliana]	Unigene26013_All//2.00E-40//AT3G60390| HAT3 (HOMEOBOX-LEUCINE ZIPPER PROTEIN 3); transcription factor	Unigene26013_All//0.00E+00//gi|109873495|gb|DW502470.1|DW502470	HB		GO:0000902//GO:0001071//GO:0003677//GO:0006355//GO:0009639//GO:0009725//GO:0023033//GO:0030528//GO:0042802//GO:0043231//GO:0048513	nr -
Unigene26014_All	1232	3.44	0.53	0.61	2.71	1.43	0.48	2.85	1.63	1.68	-2.69E+00	6.43E-13	Down	-2.51E+00	1.98E-11	Down	-9.26E-01	3.54E-03		-2.51E+00	3.04E-10	Down	-8.07E-01	5.92E-03		-7.60E-01	7.20E-03		Unigene26014_All//gi|15232311|ref|NP_191598.1|//6.00E-88//HAT3 (HOMEOBOX-LEUCINE ZIPPER PROTEIN 3); transcription factor [Arabidopsis thaliana] >gi|12644275|sp|P46602.2|HAT3_ARATH RecName: Full=Homeobox-leucine zipper protein HAT3; AltName: Full=Homeodomain-leucine zipper protein HAT3; Short=HD-ZIP protein 3 >gi|7287987|emb|CAB81825.1| homeobox-leucine zipper protein HAT3 [Arabidopsis thaliana] >gi|20067965|emb|CAD29465.1| homeodomain-leucine zipper protein HAT3 [Arabidopsis thaliana] >gi|20466199|gb|AAM20417.1| homeobox-leucine zipper protein HAT3 [Arabidopsis thaliana] >gi|30984526|gb|AAP42726.1| At3g60390 [Arabidopsis thaliana]	Unigene26014_All//4.00E-79//AT3G60390| HAT3 (HOMEOBOX-LEUCINE ZIPPER PROTEIN 3); transcription factor	Unigene26014_All//0.00E+00//TC174274	HB		GO:0000902//GO:0001071//GO:0003677//GO:0006355//GO:0009639//GO:0009725//GO:0023033//GO:0030528//GO:0042802//GO:0043231//GO:0048513	nr +
Unigene26015_All	1029	2.34	7.73	5.80	5.28	3.25	3.47	1.07	1.10	2.75	1.72E+00	8.37E-14	Up	1.31E+00	5.73E-07	Up	-7.01E-01	3.47E-03		-6.06E-01	1.77E-02		3.79E-02	9.76E-01		1.36E+00	5.48E-05	Up	Unigene26015_All//gi|212552160|gb|ACJ31801.1|//1.00E-55//receptor-like protein kinase [Glycine max]	Unigene26015_All//5.00E-48//AT3G22060| receptor protein kinase-related	Unigene26015_All//5.00E-09//DN816929			GO:0004672	nr +
Unigene26019_All	1060	153.06	105.69	186.12	40.13	35.86	48.06	7.26	20.03	7.82	-5.34E-01	1.25E-39		2.82E-01	1.54E-14		-1.62E-01	5.67E-02		2.60E-01	4.29E-04		1.46E+00	1.18E-34	Up	1.07E-01	6.17E-01		Unigene26019_All//gi|224090769|ref|XP_002309074.1|//2.00E-35//HLIP/One helix protein [Populus trichocarpa] >gi|222855050|gb|EEE92597.1| HLIP/One helix protein [Populus trichocarpa]	Unigene26019_All//9.00E-27//AT5G02120| OHP (ONE HELIX PROTEIN)	Unigene26019_All//0.00E+00//gi|109868698|gb|DW497674.1|DW497674			GO:0009534//GO:0009642//GO:0016701//GO:0019758	nr +
Unigene26020_All	1066	9.62	24.00	16.73	9.63	7.79	19.40	18.17	26.82	14.61	1.32E+00	4.32E-29	Up	7.99E-01	4.62E-09		-3.06E-01	9.09E-02		1.01E+00	1.03E-16	Up	5.62E-01	5.13E-10		-3.14E-01	4.46E-03		Unigene26020_All//gi|18397866|ref|NP_565376.1|//5.00E-39//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|66865916|gb|AAY57592.1| RING finger family protein [Arabidopsis thaliana] >gi|49944335|gb|ABR46210.1| At2g15580 [Arabidopsis thaliana] >gi|222423846|dbj|BAH19888.1| AT2G15580 [Arabidopsis thaliana]	Unigene26020_All//3.00E-40//AT2G15580| zinc finger (C3HC4-type RING finger) family protein	Unigene26020_All//0.00E+00//gi|164303437|gb|ES808557.1|ES808557			GO:0046872	nr -
Unigene26021_All	1485	0.35	2.42	2.26	2.68	2.90	3.16	2.05	1.01	3.00	2.78E+00	2.38E-11	Up	2.68E+00	7.30E-10	Up	1.11E-01	7.76E-01		2.37E-01	4.59E-01		-1.02E+00	1.53E-03		5.52E-01	2.64E-02		Unigene26021_All//gi|297825637|ref|XP_002880701.1|//1.00E-148//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297326540|gb|EFH56960.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene26021_All//4.00E-153//AT2G25730| unknown protein				GO:0005488	nr -
Unigene26025_All	998	14.36	119.26	32.23	38.73	139.88	110.83	22.79	60.06	85.27	3.05E+00	0.00E+00	Up	1.17E+00	3.62E-29	Up	1.85E+00	2.40E-301	Up	1.52E+00	5.45E-164	Up	1.40E+00	5.65E-90	Up	1.90E+00	3.69E-202	Up	Unigene26025_All//gi|9294810|gb|AAF86687.1|//1.00E-27//MTD1 [Medicago truncatula]	Unigene26025_All//6.00E-13//AT5G21940| unknown protein	Unigene26025_All//0.00E+00//ES821674			GO:0005488	nr -
Unigene26027_All	1021	20.19	11.96	10.43	8.05	5.53	3.05	2.94	0.86	0.98	-7.55E-01	6.41E-10		-9.53E-01	9.98E-14		-5.42E-01	4.56E-03		-1.40E+00	1.88E-11	Down	-1.77E+00	4.37E-07	Down	-1.59E+00	1.94E-06	Down	Unigene26027_All//gi|124359162|gb|ABN06683.1|//2.00E-08//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene26027_All//1.00E-92//gi|164323688|gb|EV493775.1|EV493775				nr -
Unigene26028_All	1029	1.27	2.31	1.86	24.50	25.37	18.26	8.38	148.99	13.05	8.64E-01	3.65E-02		5.51E-01	2.59E-01		5.04E-02	7.28E-01		-4.24E-01	6.27E-05		4.15E+00	0.00E+00	Up	6.38E-01	1.92E-06		Unigene26028_All//gi|297242517|gb|AD124922.1|//1.00E-144//pirin [Carica papaya]	Unigene26028_All//1.00E-110//AT1G50590| pirin, putative	Unigene26028_All//0.00E+00//TC159429				nr +
Unigene26031_All	1267	7.76	4.16	2.56	4.91	4.57	4.13	3.57	7.16	12.33	-9.00E-01	1.10E-06		-1.60E+00	1.18E-14	Down	-1.06E-01	7.05E-01		-2.49E-01	3.51E-01		1.00E+00	8.82E-09	Up	1.79E+00	1.04E-34	Up	Unigene26031_All//gi|75334522|sp|Q9FYX2.1|CML25_ARATH//1.00E-24//RecName: Full=Probable calcium-binding protein CML25; AltName: Full=Calmodulin-like protein 25 >gi|9743349|gb|AAF97973.1|AC000103_23 F21J9.28 [Arabidopsis thaliana] >gi|91805849|gb|ABE65653.1| polcalcin [Arabidopsis thaliana]	Unigene26031_All//7.00E-18//AT1G24620| polcalcin, putative / calcium-binding pollen allergen, putative	Unigene26031_All//0.00E+00//TC148242		ko04626|Plant-pathogen interaction	GO:0006950//GO:0043231//GO:0046872	nr -
Unigene26032_All	937	7.09	2.87	6.71	19.72	12.24	9.54	6.54	3.93	2.25	-1.31E+00	4.73E-08	Down	-8.06E-02	7.41E-01		-6.89E-01	4.96E-09		-1.05E+00	4.83E-16	Down	-7.37E-01	5.18E-04		-1.54E+00	1.05E-11	Down			Unigene26032_All//0.00E+00//gi|78322904|gb|DT543178.1|DT543178				
Unigene26037_All	1150	3.05	0.84	3.98	4.94	4.52	3.69	3.68	2.69	4.02	-1.86E+00	3.46E-07	Down	3.86E-01	2.08E-01		-1.27E-01	6.47E-01		-4.20E-01	1.06E-01		-4.51E-01	9.51E-02		1.28E-01	6.37E-01		Unigene26037_All//gi|18396900|ref|NP_564316.1|//4.00E-85//ATNUDX15 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 15); hydrolase [Arabidopsis thaliana] >gi|42570219|ref|NP_849725.2| ATNUDX15 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 15); hydrolase [Arabidopsis thaliana] >gi|79318810|ref|NP_001031104.1| ATNUDX15 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 15); hydrolase [Arabidopsis thaliana]	Unigene26037_All//7.00E-77//AT1G28960| ATNUDX15 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 15); hydrolase	Unigene26037_All//0.00E+00//TC131846			GO:0016462//GO:0043231	nr -
Unigene26038_All	2271	0.71	2.34	0.35	1.25	1.85	1.23	6.96	3.85	15.09	1.71E+00	2.15E-09	Up	-1.02E+00	6.14E-02		5.65E-01	5.67E-02		-2.01E-02	9.49E-01		-8.56E-01	1.76E-11		1.12E+00	1.93E-37	Up	Unigene26038_All//gi|15231291|ref|NP_187969.1|//0.00E+00//calmodulin-binding family protein [Arabidopsis thaliana]	Unigene26038_All//0.00E+00//AT3G13600| calmodulin-binding family protein	Unigene26038_All//2.00E-149//gi|48881621|gb|CO132643.1|CO132643				nr +
Unigene26041_All	1061	59.96	39.11	24.44	890.41	586.02	788.25	135.49	61.96	110.77	-6.17E-01	1.77E-20		-1.29E+00	2.60E-67	Down	-6.04E-01	0.00E+00		-1.76E-01	1.34E-30		-1.13E+00	3.40E-154	Down	-2.91E-01	7.66E-15		Unigene26041_All//gi|21585695|gb|AAK65492.1|//2.00E-33//allergenic-related protein Pt2L4 [Manihot esculenta]		Unigene26041_All//0.00E+00//TC145920				nr +

Unigene26042_All	1486	18.63	41.46	32.68	3.79	3.85	2.70	0.20	0.23	0.11	1.15E+00	3.47E-56	Up	8.11E-01	3.36E-24		2.22E-02	9.57E-01		-4.86E-01	5.74E-02		1.76E-01	8.80E-01		-8.94E-01	4.71E-01		Unigene26042_All//gi|25052804|gb|AAN65180.1|//0.00E+00//mitogen-activated protein kinase 4 [Petroselinum crispum]	Unigene26042_All//0.00E+00//AT4G01370| ATMPK4 (ARABIDOPSIS THALIANA MAP KINASE 4); MAP kinase/ kinase	Unigene26042_All//0.00E+00//TC156398		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0032559	nr +
Unigene26044_All	906	203.10	139.26	166.98	71.31	51.46	79.76	34.16	17.85	14.03	-5.45E-01	2.21E-46		-2.83E-01	1.24E-13		-4.71E-01	1.88E-15		1.62E-01	1.19E-02		-9.36E-01	4.51E-25		-1.28E+00	1.68E-42	Down	Unigene26044_All//gi|15237987|ref|NP_197258.1|//3.00E-38//BolA-like family protein [Arabidopsis thaliana] >gi|98960931|gb|ABF58949.1|At5g17560 [Arabidopsis thaliana]	Unigene26044_All//1.00E-39//AT5G17560| BolA-like family protein	Unigene26044_All//0.00E+00//gi|109889453|gb|DW518421.1|DW518421			GO:0009536	nr -
Unigene26046_All	1154	1.68	2.37	1.85	0.82	1.70	1.10	1.54	3.30	0.66	4.99E-01	1.97E-01		1.38E-01	7.50E-01		1.05E+00	2.24E-02		4.18E-01	5.23E-01		1.10E+00	1.12E-04	Up	-1.23E+00	4.20E-03		Unigene26046_All//gi|297813969|ref|XP_002874868.1|//2.00E-63//translocon at the inner envelope membrane of chloroplasts 20-IV [Arabidopsis lyrata subsp. lyrata] >gi|297320705|gb|EFH51127.1|translocon at the inner envelope membrane of chloroplasts 20-IV [Arabidopsis lyrata subsp. lyrata]	Unigene26046_All//1.00E-64//AT4G03320| tic20-IV (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 20-IV)				nr +
Unigene26048_All	805	32.56	39.91	27.85	26.86	34.82	85.33	1.05	4.26	2.23	2.93E-01	2.36E-03		-2.26E-01	5.20E-02		3.75E-01	1.07E-04		1.67E+00	6.59E-117	Up	2.02E+00	2.53E-09	Up	1.08E+00	1.09E-02		Unigene26048_All//gi|48958479|gb|AT47792.1|//8.00E-28//At1g72510 [Arabidopsis thaliana] >gi|51536554|gb|AAU05515.1|At1g72510 [Arabidopsis thaliana]	Unigene26048_All//4.00E-29//AT1G72510| unknown protein	Unigene26048_All//8.00E-32//gi|109877652|gb|DW506625.1|DW506625				nr -
Unigene26049_All	924	6.00	9.05	7.66	16.82	19.60	15.64	3.02	5.52	12.12	5.92E-01	3.12E-03		3.53E-01	1.37E-01		2.21E-01	1.09E-01		-1.05E-01	5.50E-01		8.70E-01	2.44E-04		2.00E+00	3.81E-29	Up	Unigene26049_All//gi|145334901|ref|NP_001078796.1|//7.00E-13//IDL2 (INFLORESCENCE DEFICIENT IN ABSCISSION (IDA)-LIKE 2) [Arabidopsis thaliana] >gi|75120856|sp|Q6DUW9.1|IDL2_ARATH RecName: Full=Protein IDA-LIKE 2; Flags: Precursor >gi|49425314|gb|AAT66015.1| ida like-protein 2 [Arabidopsis thaliana]	Unigene26049_All//4.00E-13//AT5G64667| IDL2 (INFLORESCENCE DEFICIENT IN ABSCISSION (IDA)-LIKE 2)	Unigene26049_All//0.00E+00//TC158808			GO:0043231	nr -
Unigene26050_All	1061	1.13	4.68	1.46	3.47	5.78	8.60	22.91	30.29	26.51	2.04E+00	5.67E-11	Up	3.60E-01	5.20E-01		7.34E-01	1.33E-03		1.31E+00	2.80E-11	Up	4.03E-01	1.95E-06		2.10E-01	2.33E-02		Unigene26050_All//gi|158323776|gb|ABW34392.1|//6.00E-85//R2R3 Myb14 transcription factor [Vitis vinifera]	Unigene26050_All//5.00E-67//AT2G31180| MYB14 (MYB DOMAIN PROTEIN 14); DNA binding / transcription factor	Unigene26050_All//0.00E+00//gi|109875501|gb|DW504475.1|DW504475	MYB			nr -
Unigene26052_All	1060	2.17	6.79	4.02	1.17	0.88	1.19	4.51	2.92	1.73	1.64E+00	8.81E-12	Up	8.88E-01	3.87E-03		-4.22E-01	5.06E-01		2.21E-02	9.71E-01		-6.27E-01	1.07E-02		-1.38E+00	4.51E-08	Down	Unigene26052_All//gi|124361039|gb|ABN09011.1|//2.00E-95//General substrate transporter; Sugar transporter superfamily [Medicago truncatula]	Unigene26052_All//2.00E-85//AT1G54730| sugar transporter, putative	Unigene26052_All//0.00E+00//TC145455			GO:0006810//GO:0008152//GO:0016628//GO:0022891//GO:0031224	nr +
Unigene26056_All	1425	7.49	0.96	0.19	8.39	1.16	1.05	39.43	29.18	17.22	-2.96E+00	5.24E-35	Down	-5.33E+00	1.57E-51	Down	-2.85E+00	1.04E-47	Down	-3.00E+00	3.88E-43	Down	-4.34E-01	4.15E-12		-1.20E+00	2.29E-68	Down	Unigene26056_All//gi|75099990|sp|Q80920.1|PYL4_ARATH//2.00E-47//RecName: Full=Abscisic acid receptor PYL4; AltName: Full=PYR1-like protein 4; AltName: Full=ABA1-binding protein 2; AltName: Full=Regulatory components of ABA receptor 10 >gi|3395441|gb|AAC28773.1|expressed protein [Arabidopsis thaliana] >gi|14517502|gb|AAK62641.1|At2g38310/T19C21.20 [Arabidopsis thaliana] >gi|15809748|gb|AAL06802.1|At2g38310/T19C21.20 [Arabidopsis thaliana]	Unigene26056_All//2.00E-42//AT2G38310| unknown protein	Unigene26056_All//0.00E+00//DW481244			GO:0004871//GO:0009755//GO:0019840//GO:0043231	nr +
Unigene26057_All	738	2.20	4.05	2.24	3.85	4.48	2.14	3.49	0.00	2.32	8.82E-01	1.49E-02		2.54E-02	9.80E-01		2.19E-01	5.85E-01		-8.45E-01	2.29E-02		-1.18E+01	3.06E-18	Down	-5.90E-01	8.20E-02		Unigene26057_All//gi|224137598|ref|XP_002322597.1|//1.00E-23//global transcription factor group [Populus trichocarpa] >gi|222867227|gb|EEF04358.1|global transcription factor group [Populus trichocarpa]	Unigene26057_All//3.00E-18//AT1G65440| GTB1; RNA binding / hydrolase, acting on ester bonds / transcription elongation regulator	Unigene26057_All//6.00E-162//gi|164310796|gb|ES816080.1|ES816080			GO:0009987	nr +
Unigene26058_All	715	2.63	1.63	3.05	2.23	1.88	1.39	1.95	0.00	1.67	-6.93E-01	1.39E-01		2.13E-01	6.16E-01		-2.47E-01	6.36E-01		-6.82E-01	2.07E-01		-1.09E+01	6.58E-10	Down	-2.23E-01	6.37E-01		Unigene26058_All//gi|224057210|ref|XP_002299174.1|//6.00E-13//global transcription factor group [Populus trichocarpa] >gi|222846432|gb|EEE83979.1|global transcription factor group [Populus trichocarpa]	Unigene26058_All//1.00E-04//AT1G65440| GTB1; RNA binding / hydrolase, acting on ester bonds / transcription elongation regulator	Unigene26058_All//1.00E-104//gi|48814267|gb|CO115580.1|CO115580				nr +
Unigene26059_All	932	7.63	21.96	6.06	5.18	8.17	7.85	2.72	3.05	19.79	1.52E+00	6.16E-29	Up	-3.34E-01	1.58E-01		6.55E-01	1.16E-03		5.99E-01	5.39E-03		1.64E-01	6.34E-01		2.86E+00	6.81E-72	Up	Unigene26059_All//gi|3176675|gb|AAC18798.1|//2.00E-58//F17O7.4 [Arabidopsis thaliana] >gi|15010576|gb|AAK73947.1|At1g70420/F17O7_4 [Arabidopsis thaliana] >gi|21700801|gb|AAM70524.1|At1g70420/F17O7_4 [Arabidopsis thaliana]	Unigene26059_All//1.00E-55//AT1G70420| unknown protein	Unigene26059_All//0.00E+00//gi|82755838|gb|DV849400.1|DV849400				nr -
Unigene26060_All	1290	1.66	0.90	1.24	2.09	2.03	2.14	3.11	1.52	1.76	-8.80E-01	4.38E-02		-4.25E-01	3.74E-01		-3.96E-02	9.16E-01		3.45E-02	9.50E-01		-1.03E+00	1.66E-04	Down	-8.23E-01	1.73E-03		Unigene26060_All//gi|15232243|ref|NP_191564.1|//1.00E-101//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75181813|sp|Q9M1D8.1|PP2S8_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g60050	Unigene26060_All//5.00E-103//AT3G60050| pentatricopeptide (PPR) repeat-containing protein	Unigene26060_All//0.00E+00//TC175451			GO:0016020//GO:0043231	nr +
Unigene26061_All	1001	10.92	12.50	11.81	25.98	28.45	31.67	8.87	3.01	7.28	1.95E-01	2.57E-01		1.13E-01	5.69E-01		1.31E-01	2.62E-01		2.86E-01	3.05E-03		-1.56E+00	2.24E-16	Down	-2.84E-01	1.04E-01		Unigene26061_All//gi|124360377|gb|ABN08390.1|//1.00E-50//Harpin-induced 1 [Medicago truncatula]	Unigene26061_All//1.00E-36//AT5G11890| FUNCTIONS IN: molecular_function unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17620.1); Has 455 Blast hits to 454 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 453; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene26061_All//0.00E+00//gi|78326026|gb|DT546300.1|DT546300			GO:0016020	nr -
Unigene26062_All	849	28.04	26.92	25.03	28.22	31.84	26.49	32.87	24.96	15.39	-5.90E-02	6.25E-01		-1.64E-01	2.02E-01		1.74E-01	1.23E-01		-9.13E-02	5.03E-01		-3.97E-01	1.42E-05		-1.09E+00	5.48E-30	Down	Unigene26062_All//gi|15241303|ref|NP_199900.1|//2.00E-87//UBC27 (ubiquitin-conjugating enzyme 27); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75333893|sp|Q9FI61.1|UBC27_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 27; AltName: Full=Ubiquitin carrier protein 27 >gi|9758234|dbj|BAB08733.1|ubiquitin-conjugating enzyme-like protein [Arabidopsis thaliana] >gi|66354462|gb|AAY44866.1|ubiquitinating enzyme [Arabidopsis thaliana] >gi|110677320|gb|ABG85247.1|ubiquitin conjugating enzyme [Arabidopsis thaliana]	Unigene26062_All//5.00E-84//AT5G50870| UBC27 (ubiquitin-conjugating enzyme 27); ubiquitin-protein ligase	Unigene26062_All//0.00E+00//TC145443		ko04120|Ubiquitin mediated proteolysis	GO:0019787//GO:0019941//GO:0060255//GO:0070646	nr -
Unigene26063_All	881	4.34	5.75	3.02	13.91	14.85	12.71	6.57	1.99	2.17	4.08E-01	1.35E-01		-5.21E-01	1.18E-01		9.47E-02	6.09E-01		-1.30E-01	4.97E-01		-1.72E+00	1.73E-12	Down	-1.60E+00	1.05E-11	Down	Unigene26063_All//gi|15232662|ref|NP_188189.1|//4.00E-63//zinc finger (Ran-binding) family protein [Arabidopsis thaliana] >gi|119943400|dbj|BAB02299.1| zinc finger protein-like; Ser/Thr protein kinase-like protein [Arabidopsis thaliana] >gi|89274153|gb|ABD65597.1|At3g15680 [Arabidopsis thaliana]	Unigene26063_All//7.00E-51//AT3G15680| zinc finger (Ran-binding) family protein	Unigene26063_All//0.00E+00//gi|109869965|gb|DW498941.1|DW498941			GO:0044464//GO:0046914	nr -
Unigene26064_All	1769	1.77	1.15	0.72	2.20	2.16	2.68	3.85	1.06	1.19	-6.31E-01	7.20E-02		-1.30E+00	5.92E-04	Down	-2.36E-02	9.48E-01		2.88E-01	3.57E-01		-1.86E+00	4.97E-16	Down	-1.69E+00	1.21E-14	Down	Unigene26064_All//gi|15238313|ref|NP_201300.1|//2.00E-34//mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana]	Unigene26064_All//5.00E-36//AT5G64950| mitochondrial transcription termination factor-related / mTERF-related	Unigene26064_All//0.00E+00//ES837030				nr +
Unigene26065_All	1473	1.28	0.00	0.65	1.29	0.89	1.38	0.86	0.20	0.38	-1.03E+01	6.73E-11	Down	-9.75E-01	5.03E-02		-5.33E-01	2.63E-01		1.03E-01	8.38E-01		-2.12E+00	4.17E-04	Down	-1.19E+00	2.28E-02		Unigene26065_All//gi|297806821|ref|XP_002871294.1|//2.00E-40//mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317131|gb|EFH47553.1|mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26065_All//6.00E-40//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene26065_All//0.00E+00//ES837030				nr +
Unigene26066_All	554	3.59	6.22	8.84	2.07	1.86	1.88	2.67	1.89	1.44	7.93E-01	1.72E-02		1.30E+00	8.44E-06	Up	-1.49E-01	8.32E-01		-1.41E-01	8.21E-01		-5.02E-01	3.26E-01		-8.93E-01	5.68E-02		Unigene26066_All//gi|225445260|ref|XP_002281062.1|//1.00E-24//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297738835|emb|CBI28080.3|unnamed protein product [Vitis vinifera]		Unigene26066_All//0.00E+00//ES837270			GO:0043231	nr +
Unigene26069_All	879	40.59	52.86	37.38	36.27	39.45	50.87	82.73	183.30	79.90	3.81E-01	9.44E-07		-1.19E-01	2.52E-01		1.21E-01	2.46E-01		4.88E-01	2.27E-10		1.15E+00	3.47E-177	Up	-5.02E-02	4.37E-01		Unigene26069_All//gi|11094252|dbj|BAB17667.1|//2.00E-29//PEX14 [Arabidopsis thaliana]	Unigene26069_All//3.00E-16//AT5G62810| PEX14; protein binding / protein transporter	Unigene26069_All//0.00E+00//gi|164333679|gb|ES816866.1|ES816866		ko04146|Peroxisome	GO:0006996//GO:0016020//GO:0044444	nr -
Unigene26070_All	977	5.36	4.41	4.41	4.84	5.99	3.65	2.94	1.11	1.30	-2.81E-01	3.11E-01		-2.79E-01	3.42E-01		3.07E-01	2.48E-01		-4.08E-01	1.62E-01		-1.40E+00	4.29E-05	Down	-1.17E+00	3.14E-04	Down	Unigene26070_All//gi|18410169|ref|NP_567011.1|//3.00E-69//catalytic [Arabidopsis thaliana]	Unigene26070_All//2.00E-69//AT3G54970| catalytic					nr +

Unigene26071_All	890	24.34	13.72	23.45	25.35	21.98	19.54	29.74	20.76	14.10	-8.27E-01	5.35E-12		-5.34E-02	6.94E-01		-2.06E-01	8.46E-02		-3.76E-01	9.74E-04		-5.19E-01	3.43E-08		-1.08E+00	9.32E-28	Down	Unigene26071_All//gi|132424657|gb|AB033481.1|//7.00E-42//class II KNOX homeobox transcription factor [Medicago truncatula]	Unigene26071_All//2.00E-32//AT1G62990| KNAT7 (KNOTTED-LIKE HOMEOBOX OF ARABIDOPSIS THALIANA 7); DNA binding / transcription activator/ transcription factor	Unigene26071_All//0.00E+00//ES847552	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010087//GO:0010468//GO:0030528//GO:0043231	nr +
Unigene26072_All	2558	2.37	0.93	1.27	2.90	2.05	1.98	1.49	2.39	0.87	-1.35E+00	9.32E-08	Down	-9.02E-01	3.26E-04		-5.04E-01	1.39E-02		-5.53E-01	9.41E-03		6.81E-01	1.39E-03		-7.70E-01	4.33E-03		Unigene26072_All//gi|240255701|ref|NP_567172.4|//0.00E+00//RLK4 (RECEPTOR-LIKE PROTEIN KINASE 4); protein kinase/ sugar binding [Arabidopsis thaliana]	Unigene26072_All//0.00E+00//AT4G00340| RLK4 (RECEPTOR-LIKE PROTEIN KINASE 4); protein kinase/ sugar binding	Unigene26072_All//0.00E+00//TC169836		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0009987	nr +
Unigene26073_All	1479	15.39	6.92	8.97	25.60	14.60	23.33	24.24	16.76	15.30	-1.15E+00	3.02E-21	Down	-7.80E-01	6.44E-11		-8.10E-01	8.37E-24		-1.34E-01	1.77E-01		-5.33E-01	2.70E-11		-6.64E-01	7.40E-17		Unigene26073_All//gi|297795361|ref|XP_002865565.1|//1.00E-112//electron carrier/ protein disulfide oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297311400|gb|EFH41824.1| electron carrier/ protein disulfide oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene26073_All//2.00E-109//AT5G42150| electron carrier/ protein disulfide oxidoreductase	Unigene26073_All//0.00E+00//TC134232		ko00590|Arachidonic acid metabolism	GO:0015036//GO:0019725	nr +
Unigene26074_All	1387	4.04	4.82	1.57	4.06	4.30	3.81	8.17	6.06	9.97	2.57E-01	2.87E-01		-1.36E+00	6.65E-07	Down	8.18E-02	8.08E-01		-9.12E-02	7.38E-01		-4.32E-01	4.43E-03		2.87E-01	3.39E-02		Unigene26074_All//gi|18399730|ref|NP_566435.1|//1.00E-139//ALIS1 (ALA-INTERACTING SUBUNIT 1); phospholipid transporter [Arabidopsis thaliana] >gi|75274144|sp|Q9LTW0.1|ALIS1_ARATH RecName: Full=ALA-interacting subunit 1; Short=AtALIS1; AltName: Full=ALA3 beta-subunit 1 >gi|152942336|gb|AAV85265.1|AF410309_1 AT3g12740/MBK21_10 [Arabidopsis thaliana]	Unigene26074_All//1.00E-129//AT3G12740| ALIS1 (ALA-INTERACTING SUBUNIT 1); phospholipid transporter	Unigene26074_All//0.00E+00//TC154597				nr +
Unigene26078_All	1016	4.74	0.90	3.14	5.79	3.80	6.27	3.50	2.18	2.31	-2.40E+00	6.32E-13	Down	-5.91E-01	4.05E-02		-6.08E-01	8.62E-03		1.16E-01	6.83E-01		-6.81E-01	1.97E-02		-5.96E-01	3.44E-02		Unigene26078_All//gi|113205216|gb|AAT38281.2|//1.00E-07//Integrase core domain containing protein [Solanum demissum]		Unigene26078_All//6.00E-67//DW231553			GO:0005488	nr +
Unigene26079_All	1483	7.83	2.77	2.87	22.30	11.28	8.07	9.58	4.11	1.91	-1.50E+00	1.85E-16	Down	-1.45E+00	6.05E-15	Down	-9.83E-01	7.50E-29		-1.47E+00	1.10E-47	Down	-1.22E+00	6.28E-18	Down	-2.33E+00	7.37E-45	Down	Unigene26079_All//gi|18415796|ref|NP_568193.1|//1.00E-151//AtAGAL2 (Arabidopsis thaliana ALPHA-GALACTOSIDASE 2); alpha-galactosidase/ catalytic/ hydrolase, hydrolyzing O-glycosyl compounds >gi|196990069|gb|AAL50902.1| AT5g08370/F8L15_100 [Arabidopsis thaliana] >gi|21553660|gb|AAM62753.1| alpha-galactosidase-like protein [Arabidopsis thaliana] >gi|23308433|gb|AAN18186.1| At5g08370/F8L15_100 [Arabidopsis thaliana]	Unigene26079_All//2.00E-150//AT5G08370| AtAGAL2 (Arabidopsis thaliana ALPHA-GALACTOSIDASE 2); alpha-galactosidase/ catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene26079_All//5.00E-13//ES844509		ko00561|Glycerolipid metabolism//ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00603|Glycosphingolipid biosynthesis - globo series		nr +
Unigene26080_All	1156	2.72	0.96	0.60	10.64	5.99	5.24	11.23	5.60	2.45	-1.49E+00	5.47E-05	Down	-2.18E+00	2.17E-07	Down	-8.30E-01	2.20E-08		-1.02E+00	1.67E-10	Down	-1.00E+00	3.21E-12	Down	-2.20E+00	2.68E-38	Down	Unigene26080_All//gi|297817792|ref|XP_002876779.1|//4.00E-62//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322617|gb|EFH53038.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene26080_All//8.00E-54//AT2G01818| zinc ion binding	Unigene26080_All//0.00E+00//TC136117			GO:0044464//GO:0046914	nr -
Unigene26081_All	1262	1.99	2.57	2.28	4.46	4.01	4.51	5.19	8.84	11.59	3.69E-01	3.02E-01		1.95E-01	6.23E-01		-1.53E-01	5.90E-01		1.57E-02	9.50E-01		7.68E-01	4.74E-07		1.16E+00	1.95E-17	Up	Unigene26081_All//gi|15240723|ref|NP_196885.1|//1.00E-86//glutaredoxin family protein [Arabidopsis thaliana] >gi|14532460|gb|AAK63958.1| AT5g13810/MAC12_24 [Arabidopsis thaliana] >gi|16974533|gb|AAL31176.1| AT5g13810/MAC12_24 [Arabidopsis thaliana]	Unigene26081_All//2.00E-85//AT5G13810| glutaredoxin family protein	Unigene26081_All//0.00E+00//gi|164309145|gb|ES818885.1|ES818885			GO:0015036//GO:0019725	nr +
Unigene26083_All	1305	0.24	0.16	0.29	0.08	0.48	0.21	0.55	0.74	1.77	-6.32E-01	6.22E-01		2.47E-01	8.23E-01		2.64E+00	1.99E-02		1.44E+00	4.09E-01		4.19E-01	5.31E-01		1.68E+00	1.93E-05	Up	Unigene26083_All//gi|15240723|ref|NP_196885.1|//6.00E-86//glutaredoxin family protein [Arabidopsis thaliana] >gi|14532460|gb|AAK63958.1| AT5g13810/MAC12_24 [Arabidopsis thaliana] >gi|16974533|gb|AAL31176.1| AT5g13810/MAC12_24 [Arabidopsis thaliana]	Unigene26083_All//1.00E-84//AT5G13810| glutaredoxin family protein	Unigene26083_All//0.00E+00//gi|164309145|gb|ES818885.1|ES818885			GO:0015036//GO:0019725	nr -
Unigene26085_All	1683	32.86	16.35	25.03	18.74	20.28	18.73	12.46	6.16	6.04	-1.01E+00	9.57E-41	Down	-3.93E-01	6.40E-08		1.14E-01	2.94E-01		-4.00E-04	9.96E-01		-1.02E+00	1.14E-19	Down	-1.05E+00	3.45E-21	Down	Unigene26085_All//gi|15241601|ref|NP_196455.1|//0.00E+00//AtAGAL1 (Arabidopsis thaliana ALPHA-GALACTOSIDASE 1); alpha-galactosidase/ catalytic/ hydrolase, hydrolyzing O-glycosyl compounds >gi|10178280|emb|CAC08338.1| alpha-galactosidase-like protein [Arabidopsis thaliana]	Unigene26085_All//0.00E+00//AT5G08380| AtAGAL1 (Arabidopsis thaliana ALPHA-GALACTOSIDASE 1); alpha-galactosidase/ catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene26085_All//0.00E+00//TC157514		ko00561|Glycerolipid metabolism//ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00603|Glycosphingolipid biosynthesis - globo series	GO:0005576//GO:0005618//GO:0015925//GO:0043167//GO:0044238	nr +
Unigene26086_All	1559	13.66	11.64	11.89	16.68	16.92	14.17	13.86	5.63	8.02	-2.31E-01	6.38E-02		-2.01E-01	1.36E-01		2.06E-02	8.77E-01		-2.36E-01	3.50E-02		-1.30E+00	1.39E-29	Down	-7.88E-01	6.92E-14		Unigene26086_All//gi|115477899|ref|NP_001062545.1|//2.00E-55//Os08g0567000 [Oryza sativa Japonica Group] >gi|113624514|dbj|BAF24459.1| Os08g0567000 [Oryza sativa Japonica Group]	Unigene26086_All//4.00E-35//AT3G24160| PMP (PUTATIVE TYPE 1 MEMBRANE PROTEIN)	Unigene26086_All//0.00E+00//gi|164353568|gb|ES831659.1|ES831659			GO:0016020//GO:0043231//GO:0044444	nr -
Unigene26088_All	1189	7.92	6.22	4.70	16.05	14.57	13.37	18.60	10.72	9.05	-3.48E-01	6.96E-02		-7.52E-01	1.09E-04		-1.39E-01	3.27E-01		-2.63E-01	4.66E-02		-7.95E-01	6.16E-14		-1.04E+00	4.29E-22	Down	Unigene26088_All//gi|30690667|ref|NP_198101.2|//1.00E-141//integral membrane Yip1 family protein [Arabidopsis thaliana]	Unigene26088_All//5.00E-128//AT5G27490| integral membrane Yip1 family protein	Unigene26088_All//0.00E+00//TC144532				nr -
Unigene26093_All	1251	38.64	13.16	16.64	55.55	41.18	60.29	94.94	38.12	39.46	-1.55E+00	9.91E-70	Down	-1.22E+00	1.93E-46	Down	-4.32E-01	3.27E-14		1.18E-01	7.44E-02		-1.32E+00	2.13E-162	Down	-1.27E+00	2.59E-157	Down	Unigene26093_All//gi|161788876|dbj|BAF95072.1|//1.00E-132//voltage-dependent anion channel [Nicotiana tabacum]	Unigene26093_All//1.00E-113//AT3G01280| VDAC1 (VOLTAGE DEPENDENT ANION CHANNEL 1); voltage-gated anion channel	Unigene26093_All//0.00E+00//TC173544				nr +
Unigene26096_All	1395	26.18	21.10	23.40	26.75	31.65	24.77	16.67	12.31	7.25	-3.11E-01	4.99E-04		-1.62E-01	1.05E-01		2.43E-01	1.84E-03		-1.11E-01	2.87E-01		-4.37E-01	1.50E-05		-1.20E+00	5.20E-29	Down	Unigene26096_All//gi|14970762|emb|CAC44460.1|//1.00E-149//protein tyrosine phosphatase [Solanum lycopersicum]	Unigene26096_All//5.00E-138//AT3G52180| SEX4 (STARCH-EXCESS 4); polysaccharide binding / protein tyrosine/serine/threonine phosphatase	Unigene26096_All//0.00E+00//TC134660				nr +
Unigene261_All	3381	5.22	11.11	6.55	6.22	7.36	8.70	5.88	6.06	6.39	1.09E+00	1.56E-31	Up	3.29E-01	7.44E-03		2.44E-01	2.76E-02		4.84E-01	5.97E-07		4.35E-02	7.33E-01		1.20E-01	3.09E-01		Unigene261_All//gi|42572121|ref|NP_974151.1|//1.00E-142//pseudouridine synthase family protein [Arabidopsis thaliana] >gi|122215273|sp|Q3ECD0.1|PUS2_ARATH RecName: Full=RNA pseudourine synthase 2, chloroplastic; AltName: Full=RNA-uridine isomerase 2; AltName: Full=RNA pseudouridylate synthase 2; Flags: Precursor	Unigene261_All//4.00E-144//AT1G76050| pseudouridine synthase family protein	Unigene261_All//0.00E+00//TC149660				nr +
Unigene2610_All	2339	2.37	6.63	6.67	6.41	6.32	6.95	4.43	5.29	8.28	1.48E+00	3.05E-21	Up	1.49E+00	7.59E-21	Up	-2.15E-02	9.01E-01		1.17E-01	4.81E-01		2.56E-01	9.28E-02		9.02E-01	1.86E-15		Unigene2610_All//gi|42569297|ref|NP_180077.3|//1.00E-158//formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] >gi|160013996|sp|Q9SK28.2|FH18_ARATH RecName: Full=Formin-like protein 18; Short=AtFH18	Unigene2610_All//1.00E-142//AT2G25050| formin homology 2 domain-containing protein / FH2 domain-containing protein	Unigene2610_All//0.00E+00//gi|109850295|gb|DW479274.1|DW479274		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene26100_All	1246	100.15	139.81	144.79	38.54	43.72	29.90	12.15	5.77	4.99	4.81E-01	3.49E-35		5.32E-01	3.44E-42		1.82E-01	1.15E-02		-3.66E-01	8.01E-07		-1.07E+00	1.06E-15	Down	-1.28E+00	3.05E-21	Down	Unigene26100_All//gi|115473281|ref|NP_001060239.1|//3.00E-67//Os07g0608100 [Oryza sativa Japonica Group] >gi|113611775|dbj|BAF22153.1| Os07g0608100 [Oryza sativa Japonica Group]	Unigene26100_All//8.00E-86//AT3G32930| unknown protein	Unigene26100_All//0.00E+00//gi|109879971|gb|DW508941.1|DW508941			GO:0009526	nr -
Unigene26101_All	1635	0.86	15.77	1.34	3.02	3.37	2.73	1.22	5.37	18.37	4.19E+00	1.33E-111	Up	6.28E-01	1.66E-01		1.60E-01	5.94E-01		-1.41E-01	6.48E-01		2.14E+00	1.75E-24	Up	3.92E+00	1.22E-154	Up	Unigene26101_All//gi|87241270|gb|ABD33128.1|//2.00E-67//Zinc finger, RING-type; Thioredoxin-related [Medicago truncatula]	Unigene26101_All//7.00E-52//AT2G29720| RMC2A; protein binding / zinc ion binding	Unigene26101_All//0.00E+00//gi|78339650|gb|DT559924.1|DT559924			GO:0005488	nr -
Unigene26104_All	3824	0.22	0.08	0.15	1.22	0.59	0.86	11.82	7.67	22.46	-1.46E+00	6.69E-02		-5.15E-01	5.15E-01		-1.06E+00	4.18E-05	Down	-5.06E-01	7.46E-02		-6.23E-01	2.48E-18		9.26E-01	2.11E-68		Unigene26104_All//gi|8777306|dbj|BAA96896.1|//0.00E+00//receptor-like protein kinase [Arabidopsis thaliana] >gi|224589747|gb|ACN59405.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene26104_All//0.00E+00//AT5G63930| leucine-rich repeat transmembrane protein kinase, putative	Unigene26104_All//0.00E+00//CO115013		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0032559	nr -
Unigene26105_All	1071	1.91	1.75	2.64	8.19	3.83	2.99	6.67	4.68	6.21	-1.22E-01	7.76E-01		4.68E-01	2.38E-01		-1.10E+00	1.73E-09	Down	-1.45E+00	7.82E-13	Down	-5.11E-01	9.26E-03		-1.03E-01	6.32E-01		Unigene26105_All//gi|112982631|dbj|BAF03494.1|//2.00E-97//XRCC4 homolog [Populus nigra]	Unigene26105_All//1.00E-78//AT3G23100| XRCC4; protein C-terminus binding			ko03450|Non-homologous end-joining	GO:0003676//GO:0004812//GO:0005515//GO:0006281//GO:0006418//GO:0032559//GO:0043231//GO:0046914	nr +
Unigene26106_All	1276	1.64	1.79	0.33	5.66	3.62	4.11	9.38	15.13	8.18	1.24E-01	7.62E-01		-2.30E+00	2.03E-05	Down	-6.47E-01	1.45E-03		-4.63E-01	3.59E-02		6.91E-01	8.80E-10		-1.97E-01	1.97E-01		Unigene26106_All//gi|15232843|ref|NP_186856.1|//1.00E-99//OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|45773792|gb|AAS76700.1| At3g02070 [Arabidopsis thaliana] >gi|46402444|gb|AAS92324.1| At3g02070 [Arabidopsis thaliana] >gi|222424391|dbj|BAH20151.1| AT3G02070 [Arabidopsis thaliana]	Unigene26106_All//2.00E-95//AT3G02070| OTU-like cysteine protease family protein	Unigene26106_All//0.00E+00//DR457243			GO:0016020//GO:0043231//GO:0070011	nr +
Unigene26107_All	1520	1.41	4.27	2.42	4.78	9.65	6.06	6.65	17.10	17.11	1.60E+00	2.79E-10	Up	7.76E-01	2.04E-02		1.01E+00	4.74E-13	Up	3.41E-01	8.70E-02		1.36E+00	5.12E-38	Up	1.36E+00	6.13E-39	Up							
Unigene26108_All	1667	2.82	1.00	0.51	4.78	3.12	3.68	12.86	8.68	3.92	-1.49E+00	4.42E-07	Down	-2.47E+00	2.02E-12	Down	-6.16E-01	1.33E-03		-3.76E-01	7.80E-02		-5.68E-01	7.51E-08		-1.71E+00	3.31E-45	Down	Unigene26108_All//gi|114479586|gb|AB175147.1|//1.00E-180//malate dehydrogenase [Citrus junos]	Unigene26108_All//2.00E-162//AT3G47520| MDH (MALATE DEHYDROGENASE); L-malate dehydrogenase/ binding / catalytic/ malate dehydrogenase/ oxidoreductase/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor	Unigene26108_All//0.00E+00//gi|78329516|gb|DT549790.1|DT549790		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0016615//GO:0043648//GO:0044238	nr -

Unigene26109_All	721	15.38	6.40	5.91	14.92	7.88	5.39	16.07	8.64	6.24	-1.27E+00	2.43E-12	Down	-1.38E+00	2.31E-13	Down	-9.21E-01	9.66E-09		-1.47E+00	6.47E-16	Down	-8.96E-01	3.02E-09		-1.36E+00	5.65E-18	Down	Unigene26109_All//gi|34099829|gb|AAQ57203.1|//1.00E-70//ATP sulfurylase [Populus tremula x Populus alba]	Unigene26109_All//7.00E-69//AT1G19920| APS2; sulfate adenylyltransferase (ATP)	Unigene26109_All//0.00E+00//gi|109873753|gb|DW502728.1|DW502728		ko00230|Purine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0004779//GO:0006790//GO:0009536	nr -
Unigene2611_All	1996	3.96	0.86	2.16	119.94	117.95	111.51	19.11	4.98	6.47	-2.20E+00	9.39E-19	Down	-8.73E-01	5.18E-05		-2.41E-02	5.86E-01		-1.05E-01	1.79E-03		-1.94E+00	1.28E-91	Down	-1.56E+00	6.15E-70	Down	Unigene2611_All//gi|224139028|ref|XP_002322962.1|//0.00E+00//laccase 1b [Populus trichocarpa] >gi|222867592|gb|EEF04723.1|laccase 1b [Populus trichocarpa]	Unigene2611_All//0.00E+00//AT2G38080| IRX12 (IRREGULAR XYLEM 12); laccase	Unigene2611_All//0.00E+00//TC167308		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene26110_All	2215	18.71	12.56	12.55	16.17	11.10	10.85	10.15	4.62	4.06	-5.75E-01	4.16E-12		-5.76E-01	1.29E-11		-5.43E-01	2.92E-11		-5.76E-01	3.03E-11		-1.14E+00	5.22E-25	Down	-1.32E+00	1.73E-32	Down	Unigene26110_All//gi|1589913|gb|AAB67995.1|//0.00E+00//ATP-sulfurylase precursor [Brassica oleracea]	Unigene26110_All//0.00E+00//AT1G19920| APS2; sulfate adenylyltransferase (ATP)	Unigene26110_All//0.00E+00//TC167397		ko00230|Purine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0004779//GO:0006790//GO:0009536//GO:0010038//GO:0016020	nr -
Unigene26111_All	1186	13.19	4.27	8.13	20.37	13.09	14.78	20.36	9.48	12.53	-1.63E+00	1.51E-24	Down	-6.99E-01	1.68E-06		-6.38E-01	3.26E-10		-4.63E-01	1.78E-05		-1.10E+00	1.38E-25	Down	-7.00E-01	1.06E-12		Unigene26111_All//gi|15220092|ref|NP_178140.1|//4.00E-59//cytochrome c oxidase family protein [Arabidopsis thaliana] >gi|5902388|gb|AAD55490.1|AC009322_30 Unknown protein [Arabidopsis thaliana] >gi|30102586|gb|AAP21211.1|At1g80230 [Arabidopsis thaliana]	Unigene26111_All//1.00E-48//AT1G80230| cytochrome c oxidase family protein	Unigene26111_All//0.00E+00//TC159527		ko00190|Oxidative phosphorylation	GO:0009534//GO:0015002//GO:0031967//GO:0046914	nr +
Unigene26113_All	1290	0.65	0.43	0.74	1.24	1.20	1.61	4.36	5.61	10.65	-5.87E-01	4.26E-01		1.95E-01	7.70E-01		-4.09E-02	9.33E-01		3.82E-01	4.38E-01		3.63E-01	7.20E-02		1.29E+00	2.60E-19	Up	Unigene26113_All//gi|82623379|gb|AB887104.1|//4.00E-94//ChaC-like family protein-like [Solanum tuberosum]	Unigene26113_All//1.00E-90//AT4G31290| ChaC-like family protein	Unigene26113_All//0.00E+00//TC131188			GO:0010038//GO:0016798//GO:0044238	nr -
Unigene26116_All	2365	7.96	3.86	6.12	15.12	11.78	18.43	29.41	12.23	13.26	-1.05E+00	2.98E-15	Down	-3.79E-01	4.58E-03		-3.61E-01	1.46E-05		2.85E-01	3.72E-04		-1.27E+00	8.68E-90	Down	-1.15E+00	2.26E-79	Down	Unigene26116_All//gi|75335516|sp|Q9LUW5.1|RH53_ARATH//0.00E+00//RecName: Full=DEAD-box ATP-dependent RNA helicase 53 >gi|9293867|dbj|BAB01770.1| DEAD-Box RNA helicase-like protein [Arabidopsis thaliana] >gi|17064852|gb|AAL32580.1| DEAD-Box RNA helicase-like protein [Arabidopsis thaliana] >gi|20259816|gb|AAM13255.1| DEAD-Box RNA helicase-like protein [Arabidopsis thaliana]	Unigene26116_All//0.00E+00//AT3G22330| PMH2 (putative mitochondrial RNA helicase 2); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene26116_All//0.00E+00//gi|78354171|gb|DT574445.1|DT574445			GO:0000377//GO:0003676//GO:0006970//GO:0030312//GO:0031981//GO:0032559//GO:0032991//GO:0042623	nr +
Unigene26117_All	1738	13.52	4.29	2.97	21.12	10.84	3.25	12.80	0.34	4.26	-1.66E+00	1.69E-37	Down	-2.19E+00	3.83E-52	Down	-9.63E-01	6.62E-31		-2.70E+00	6.33E-118	Down	-5.25E+00	1.60E-135	Down	-1.59E+00	5.33E-42	Down	Unigene26117_All//gi|18411885|ref|NP_565175.1|//2.00E-73//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|21537200|gb|AAM61541.1| RNA recognition motif-containing protein SEB-4 [Arabidopsis thaliana] >gi|124300976|gb|ABN04740.1|At1g78260 [Arabidopsis thaliana]	Unigene26117_All//2.00E-39//AT1G78260| RNA recognition motif (RRM)-containing protein	Unigene26117_All//0.00E+00//gi|78344046|gb|DT564320.1|DT564320		ko03040|Spliceosome	GO:0003676	nr -
Unigene26118_All	1711	7.22	4.62	3.11	12.40	11.91	10.32	8.85	5.74	4.98	-6.44E-01	6.06E-05		-1.21E+00	3.07E-12	Down	-5.79E-02	7.04E-01		-2.65E-01	3.24E-02		-6.24E-01	1.07E-06		-8.28E-01	8.38E-11		Unigene26118_All//gi|18418335|ref|NP_567944.1|//1.00E-144//armadillo/beta-catenin repeat family protein [Arabidopsis thaliana] >gi|111074180|gb|ABH04463.1|At4g33945 [Arabidopsis thaliana]	Unigene26118_All//1.00E-145//AT4G33945| armadillo/beta-catenin repeat family protein	Unigene26118_All//0.00E+00//TC164561			GO:0046914	nr -
Unigene26122_All	1303	10.12	8.87	10.79	10.51	7.43	7.21	4.96	2.79	2.29	-1.91E-01	2.52E-01		9.25E-02	6.21E-01		-5.02E-01	3.95E-04		-5.44E-01	2.45E-04		-8.31E-01	5.82E-05		-1.11E+00	7.84E-08	Down	Unigene26122_All//gi|115488582|ref|NP_001066778.1|//2.00E-51//Os12g0484700 [Oryza sativa Japonica Group] >gi|113649285|dbj|BAF29797.1|Os12g0484700 [Oryza sativa Japonica Group]	Unigene26122_All//2.00E-47//AT4G27745| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Yippee-like protein (InterPro:IPR004910); BEST Arabidopsis thaliana protein match is: yippee family protein (TAIR:AT5G53940.1); Has 697 Blast hits to 697 proteins in 149 species: Archae - 0; Bacteria - 0; Metazoa - 401; Fungi - 132; Plants - 110; Viruses - 0; Other Eukaryotes - 54 (source: NCBI BLink).	Unigene26122_All//0.00E+00//gi|84170802|gb|DR459450.1|DR459450				nr -
Unigene26126_All	1790	4.09	0.51	1.90	8.96	9.33	10.34	9.28	2.80	4.50	-3.01E+00	1.58E-24	Down	-1.10E+00	1.44E-06	Down	5.82E-02	7.56E-01		2.07E-01	1.42E-01		-1.73E+00	1.49E-34	Down	-1.05E+00	5.55E-17	Down	Unigene26126_All//gi|225433506|ref|XP_002266154.1|//0.00E+00//PREDICTED: similar to HOG1 (HOMOLOGY-DEPENDENT GENE SILENCING 1); adenosylhomocysteinase isoform 1 [Vitis vinifera]	Unigene26126_All//0.00E+00//AT4G13940| MES8 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding	Unigene26126_All//0.00E+00//TC149941		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0003006//GO:0006342//GO:0010608//GO:0016020//GO:0016802//GO:0043231//GO:0046914//GO:0050896	nr -
Unigene26127_All	575	16.20	22.82	39.08	49.47	53.18	46.66	18.60	29.51	36.31	4.95E-01	1.49E-03		1.27E+00	1.90E-23	Up	1.04E-01	3.72E-01		-8.44E-02	4.98E-01		6.66E-01	3.32E-08		9.65E-01	1.90E-18		Unigene26127_All//gi|4220461|gb|AAD12688.1|//4.00E-25//ESTs gb|T75642 and gb|AA650997 come from this gene [Arabidopsis thaliana]	Unigene26127_All//2.00E-26//AT1G52140| unknown protein	Unigene26127_All//0.00E+00//TC148369				nr -
Unigene26131_All	466	5.95	16.53	14.74	12.83	13.74	29.37	31.66	39.37	9.15	1.47E+00	7.92E-11	Up	1.31E+00	6.38E-08	Up	9.96E-02	7.44E-01		1.19E+00	1.54E-14	Up	3.14E-01	7.62E-03		-1.79E+00	2.50E-33	Down	Unigene26131_All//gi|225441738|ref|XP_002277447.1|//6.00E-10//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene26131_All//0.00E+00//TC174483				nr -
Unigene26132_All	410	3.06	8.65	4.29	2.67	5.54	6.28	12.37	8.56	4.37	1.50E+00	1.62E-05	Up	4.85E-01	3.60E-01		1.05E+00	1.23E-02		1.23E+00	2.15E-03		-5.31E-01	2.64E-02		-1.50E+00	1.61E-09	Down	Unigene26132_All//gi|225441738|ref|XP_002277447.1|//2.00E-09//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene26132_All//5.00E-124//TC174483				nr -
Unigene26134_All	659	43.03	35.37	36.77	61.91	62.97	88.54	94.50	52.45	46.85	-2.83E-01	6.41E-03		-2.27E-01	4.14E-02		2.44E-02	8.20E-01		5.16E-01	1.01E-14		-8.49E-01	3.11E-42		-1.01E+00	5.09E-58	Down	Unigene26134_All//gi|297803476|ref|XP_002869622.1|//3.00E-57//mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315458|gb|EFH45881.1|mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26134_All//4.00E-50//AT4G26210| mitochondrial ATP synthase g subunit family protein	Unigene26134_All//0.00E+00//TC159905		ko00190|Oxidative phosphorylation	GO:0005753//GO:0006754//GO:0006818//GO:0015077	nr -
Unigene26137_All	1743	4.71	0.55	0.58	4.17	3.28	2.33	7.16	1.32	1.51	-3.09E+00	3.31E-28	Down	-3.02E+00	2.08E-26	Down	-3.47E-01	1.14E-01		-8.39E-01	7.69E-05		-2.44E+00	2.16E-40	Down	-2.25E+00	8.21E-38	Down	Unigene26137_All//gi|15215782|gb|AAB91436.1|//1.00E-142//At1g18090/T10F20_6 [Arabidopsis thaliana] >gi|21360461|gb|AAM47346.1|At1g18090/T10F20_6 [Arabidopsis thaliana]	Unigene26137_All//5.00E-139//AT1G18090| exonuclease, putative	Unigene26137_All//0.00E+00//TC156828		ko03430|Mismatch repair	GO:0016788	nr +
Unigene26138_All	887	1.59	1.54	1.14	2.02	2.68	1.43	3.24	4.05	1.30	-4.62E-02	9.45E-01		-4.82E-01	3.97E-01		4.06E-01	3.67E-01		-5.04E-01	3.30E-01		3.22E-01	3.04E-01		-1.32E+00	6.99E-05	Down	Unigene26138_All//gi|124359162|gb|ABN05685.1|//1.00E-10//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene26138_All//4.00E-46//gi|11201689|gb|BF270694.1|BF270694				nr +
Unigene26139_All	1331	10.10	4.64	8.12	18.98	23.96	14.25	11.91	12.75	4.58	-1.12E+00	2.46E-12	Down	-3.15E-01	5.71E-02		3.36E-01	2.05E-04		-4.13E-01	9.76E-05		9.80E-02	5.06E-01		-1.38E+00	1.09E-24	Down			Unigene26139_All//0.00E+00//gi|11201689|gb|BF270694.1|BF270694				
Unigene2614_All	1344	1.28	2.98	3.41	6.75	1.74	1.58	2.64	3.86	1.25	1.21E+00	1.13E-04	Up	1.41E+00	4.56E-06	Up	-1.95E+00	8.17E-23	Down	-2.09E+00	8.72E-22	Down	5.45E-01	2.09E-02		-1.09E+00	1.54E-04	Down			Unigene2614_All//6.00E-117//TC171002				ESTscan -
Unigene26140_All	1215	10.59	4.38	6.31	15.95	9.72	10.11	6.58	2.99	2.13	-1.27E+00	2.48E-14	Down	-7.47E-01	4.56E-06		-7.14E-01	4.89E-10		-6.58E-01	6.47E-08		-1.14E+00	2.06E-09	Down	-1.63E+00	3.47E-16	Down	Unigene26140_All//gi|297832962|ref|XP_002884363.1|//1.00E-121//ATEXPA13 [Arabidopsis lyrata subsp. lyrata] >gi|297330203|gb|EFH60622.1|ATEXPA13 [Arabidopsis lyrata subsp. lyrata]	Unigene26140_All//3.00E-109//AT3G03220| ATEXPA13 (ARABIDOPSIS THALIANA EXPANSIN A13)	Unigene26140_All//0.00E+00//gi|78342777|gb|DT563051.1|DT563051				nr -
Unigene26141_All	2298	8.06	7.36	7.97	13.81	14.03	13.78	22.83	17.06	9.43	-1.30E-01	3.76E-01		-1.59E-02	9.26E-01		2.25E-02	8.49E-01		-3.30E-03	9.72E-01		-4.21E-01	9.40E-11		-1.28E+00	1.02E-70	Down	Unigene26141_All//gi|115457642|ref|NP_001052421.1|//0.00E+00//Os04g0307200 [Oryza sativa Japonica Group] >gi|32483270|emb|CAE02397.1|OSJNBa0024J22.1 [Oryza sativa (japonica cultivar-group)] >gi|38347199|emb|CAD40524.2|OSJNBa0023J03.11 [Oryza sativa (japonica cultivar-group)] >gi|113563992|dbj|BAF14335.1|Os04g0307200 [Oryza sativa Japonica Group] >gi|116308827|emb|CAH66056.1|OS1GBa0125J07.5 [Oryza sativa (indica cultivar-group)]	Unigene26141_All//0.00E+00//AT1G79940| AT5DJ22A; heat shock protein binding / unfolded protein binding	Unigene26141_All//0.00E+00//TC179548		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0005515//GO:0031227//GO:0031410//GO:0044267//GO:0050896	nr -
Unigene26142_All	359	0.44	1.41	0.89	1.80	1.15	1.01	2.12	0.47	0.11	1.69E+00	1.34E-01		1.03E+00	4.71E-01		-6.48E-01	4.60E-01		-8.42E-01	3.75E-01		-2.19E+00	7.77E-03		-4.26E+00	8.65E-05	Down	Unigene26142_All//gi|7669956|emb|CAB88243.1|//2.00E-37//purple acid phosphatase-like protein [Arabidopsis thaliana]	Unigene26142_All//9.00E-39//AT3G52820| PAP22 (PURPLE ACID PHOSPHATASE 22); acid phosphatase/ protein serine/threonine phosphatase				GO:0016791//GO:0031410//GO:0043169	nr -
Unigene26143_All	735	1.42	0.34	1.88	6.37	4.87	5.10	3.68	0.91	1.14	-2.05E+00	6.29E-03		4.04E-01	4.96E-01		-3.87E-01	1.70E-01		-3.21E-01	2.93E-01		-2.02E+00	1.61E-07	Down	-1.69E+00	2.38E-06	Down	Unigene26143_All//gi|22331756|ref|NP_190850.2|//4.00E-42//PAP22 (PURPLE ACID PHOSPHATASE 22); acid phosphatase/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75247769|sp|Q8S340.1|PPA22_ARATH RecName: Full=Purple acid phosphatase 22; Flags: Precursor >gi|20257495|gb|AAM15917.1|AF492668_1 purple acid phosphatase [Arabidopsis thaliana]	Unigene26143_All//2.00E-42//AT3G52820| PAP22 (PURPLE ACID PHOSPHATASE 22); acid phosphatase/ protein serine/threonine phosphatase				GO:0016791//GO:0031410	nr -
Unigene26144_All	1466	0.54	1.42	1.02	6.22	4.72	2.59	7.73	2.08	2.15	1.40E+00	2.58E-03		9.26E-01	1.05E-01		-3.97E-01	3.35E-02		-1.26E+00	6.64E-11	Down	-1.89E+00	7.07E-27	Down	-1.85E+00	6.97E-27	Down	Unigene26144_All//gi|22331756|ref|NP_190850.2|//1.00E-173//PAP22 (PURPLE ACID PHOSPHATASE 22); acid phosphatase/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75247769|sp|Q8S340.1|PPA22_ARATH RecName: Full=Purple acid phosphatase 22; Flags: Precursor >gi|20257495|gb|AAM15917.1|AF492668_1 purple acid phosphatase [Arabidopsis thaliana]	Unigene26144_All//3.00E-173//AT3G52820| PAP22 (PURPLE ACID PHOSPHATASE 22); acid phosphatase/ protein serine/threonine phosphatase					nr +

Unigene26146_All	1316	7.24	7.51	4.94	14.35	19.10	12.84	9.70	2.60	4.84	5.33E-02	7.79E-01		-5.52E-01	4.43E-03		4.13E-01	5.36E-05		-1.61E-01	2.73E-01		-1.90E+00	2.74E-30	Down	-1.00E+00	2.03E-12	Down	Unigene26146_All//gi|53828523|gb|AU94371.1|/8.00E-38//At3g52110 [Arabidopsis thaliana] >gi|55733773|gb|AAV59283.1| At3g52110 [Arabidopsis thaliana]	Unigene26146_All//4.00E-34//AT3G52110| unknown protein	Unigene26146_All//0.00E+00//TC170636				nr +
Unigene26147_All	1295	18.50	29.70	19.66	17.96	21.57	23.37	32.06	21.85	15.75	6.83E-01	5.25E-15		8.71E-02	5.03E-01		2.64E-01	9.48E-03		3.79E-01	8.37E-05		-5.53E-01	8.34E-14		-1.03E+00	8.52E-40	Down	Unigene26147_All//gi|292630750|sp|Q11234.1|DRE2_YITV1/9.00E-89//RecName: Full=Anamorsin homolog; AltName: Full=Fe-S cluster assembly protein DRE2 homolog	Unigene26147_All//1.00E-60//AT5G18400| unknown protein	Unigene26147_All//0.00E+00//TC166323			GO:0044464	nr -
Unigene2615_All	1772	1.15	2.69	2.82	4.67	1.03	1.27	1.31	0.33	0.70	1.22E+00	1.83E-05	Up	1.29E+00	7.15E-06	Up	-2.18E+00	4.72E-24	Down	-1.87E+00	3.08E-17	Down	-1.99E+00	1.81E-06	Down	-9.13E-01	1.12E-02		Unigene2615_All//gi|297851744|ref|XP_002893753.1|/2.00E-10//ANAC014 [Arabidopsis lyrata subsp. lyrata] >gi|297339595|gb|EFH70012.1| ANAC014 [Arabidopsis lyrata subsp. lyrata]	Unigene2615_All//3.00E-11//AT1G33060| no apical meristem (NAM) family protein	Unigene2615_All//4.00E-125//DT465126	NAC			nr -
Unigene26153_All	1274	17.70	11.57	26.04	127.04	128.25	184.02	257.30	106.98	28.24	-6.13E-01	1.04E-07		5.57E-01	6.29E-09		1.37E-02	8.22E-01		5.35E-01	3.24E-61		-1.27E+00	0.00E+00	Down	-3.19E+00	0.00E+00	Down	Unigene26153_All//gi|3098571|gb|AAC15700.1|//2.00E-53//BURP domain containing protein [Brassica napus] >gi|226427141|gb|ACO54860.1| BURP domain protein [Brassica napus] >gi|226427143|gb|ACO54861.1| BURP domain protein [Brassica napus]	Unigene26153_All//4.00E-52//AT1G49320| BURP domain-containing protein	Unigene26153_All//0.00E+00//TC143958				nr +
Unigene26155_All	1348	5.55	2.22	1.78	6.13	4.04	6.40	8.00	11.50	19.86	-1.32E+00	3.98E-09	Down	-1.64E+00	1.04E-11	Down	-6.04E-01	1.33E-03		6.10E-02	7.91E-01		5.24E-01	3.21E-05		1.31E+00	8.86E-38	Up	Unigene26155_All//gi|225445404|ref|XP_002281763.1|/1.00E-154//PREDICTED: similar to zinc finger (C3HC4-type RING finger) family protein [Vitis vinifera]	Unigene26155_All//5.00E-109//AT1G11020| zinc finger (C3HC4-type RING finger) family protein	Unigene26155_All//0.00E+00//gi|78337432|gb|DT557706.1|DT557706		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene26159_All	591	1.86	1.11	0.54	1.35	0.99	2.06	6.15	6.44	19.75	-7.38E-01	2.50E-01		-1.78E+00	1.57E-02		-4.45E-01	5.73E-01		6.14E-01	3.52E-01		6.49E-02	8.35E-01		1.68E+00	4.14E-24	Up	Unigene26159_All//gi|42569943|ref|NP_182100.2|//2.00E-25//BAP2 (BON ASSOCIATION PROTEIN 2) [Arabidopsis thaliana] >gi|94442457|gb|ABF19016.1| At2g45760 [Arabidopsis thaliana]	Unigene26159_All//9.00E-27//AT2G45760| BAP2 (BON ASSOCIATION PROTEIN 2)	Unigene26159_All//0.00E+00//TC150216			GO:0006952//GO:0008289//GO:0009628//GO:0009987//GO:0010033//GO:0044464	nr +
Unigene2616_All	1293	1.90	1.10	3.09	3.54	0.67	1.57	0.82	1.13	0.49	-7.93E-01	4.88E-02		7.00E-01	2.80E-02		-2.41E+00	2.97E-15	Down	-1.17E+00	3.11E-05	Down	4.69E-01	3.70E-01		-7.30E-01	2.01E-01		Unigene2616_All//gi|224133993|ref|XP_002321956.1|/2.00E-15//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222868852|gb|EEF06083.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene2616_All//1.00E-14//AT4G35580| NTL9 (NAC transcription factor-like 9); transcription factor	Unigene2616_All//0.00E+00//TC171002	NAC			nr +
Unigene26160_All	739	3.75	3.29	3.67	4.31	6.48	6.97	11.04	12.05	43.02	-1.89E-01	6.20E-01		-3.01E-02	9.55E-01		5.86E-01	3.10E-02		6.92E-01	8.67E-03		1.26E-01	5.46E-01		1.96E+00	4.53E-79	Up	Unigene26160_All//gi|42569943|ref|NP_182100.2|//9.00E-30//BAP2 (BON ASSOCIATION PROTEIN 2) [Arabidopsis thaliana] >gi|94442457|gb|ABF19016.1| At2g45760 [Arabidopsis thaliana]	Unigene26160_All//3.00E-30//AT2G45760| BAP2 (BON ASSOCIATION PROTEIN 2)	Unigene26160_All//0.00E+00//gi|73860596|gb|DT463335.1|DT463335			GO:0006952//GO:0008289//GO:0009628//GO:0009987//GO:0010033//GO:0044464	nr -
Unigene26161_All	1338	34.02	98.69	21.57	41.85	60.09	40.17	30.34	40.36	84.17	1.54E+00	2.13E-185	Up	-6.57E-01	6.72E-16		5.22E-01	1.53E-22		-5.91E-02	5.06E-01		4.12E-01	1.18E-10		1.47E+00	6.36E-186	Up	Unigene26161_All//gi|87241270|gb|ABX33128.1|/9.00E-87//Zinc finger, RING-type; Thioredoxin-related [Medicago truncatula]	Unigene26161_All//2.00E-68//AT5G59550| zinc finger (C3HC4-type RING finger) family protein	Unigene26161_All//0.00E+00//TC135320			GO:0005488//GO:0009743	nr -
Unigene26162_All	1152	7.54	2.24	4.39	4.80	4.16	3.96	2.72	1.74	0.97	-1.75E+00	2.21E-15	Down	-7.80E-01	1.29E-04		-2.08E-01	4.60E-01		-2.78E-01	3.23E-01		-6.41E-01	4.19E-02		-1.49E+00	3.94E-06	Down	Unigene26162_All//gi|240254604|ref|NP_181402.4|//3.00E-94//5'-nucleotidase/ magnesium ion binding [Arabidopsis thaliana]	Unigene26162_All//8.00E-96//AT2G38680| 5'-nucleotidase/ magnesium ion binding	Unigene26162_All//0.00E+00//gi|48813164|gb|CO114477.1|CO114477			GO:0008252//GO:0043231//GO:0046872	nr -
Unigene26163_All	1291	2.88	1.45	2.19	1.43	1.23	0.45	2.06	0.87	0.77	-9.87E-01	2.10E-03		-3.96E-01	2.42E-01		-2.19E-01	6.59E-01		-1.65E+00	9.75E-04	Down	-1.24E+00	4.36E-04	Down	-1.42E+00	4.85E-05	Down	Unigene26163_All//gi|297601399|ref|NP_001050781.2|//1.00E-119//Os03g0648900 [Oryza sativa Japonica Group] >gi|255674748|dbj|BAF12695.2| Os03g0648900 [Oryza sativa Japonica Group]	Unigene26163_All//5.00E-119//AT2G38680| 5'-nucleotidase/ magnesium ion binding	Unigene26163_All//0.00E+00//TC136741				nr -
Unigene26165_All	1530	16.96	11.86	11.49	31.45	26.56	28.43	18.68	10.93	7.11	-5.17E-01	1.20E-06		-5.63E-01	3.04E-07		-2.44E-01	8.57E-04		-1.46E-01	8.08E-02		-7.74E-01	5.22E-17		-1.39E+00	1.69E-44	Down	Unigene26165_All//gi|115473953|ref|NP_001060575.1|/1.00E-126//Os07g0667400 [Oryza sativa Japonica Group] >gi|113612111|dbj|BAF22489.1| Os07g0667400 [Oryza sativa Japonica Group]	Unigene26165_All//5.00E-134//AT3G05100| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Methyltransferase type 12 (InterPro:IPR013217); Hss 53 Blast hits to 53 proteins in 21 species: Archae - 2; Bacteria - 27; Metazoa - 0; Fungi - 3; Plants - 11; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink).	Unigene26165_All//0.00E+00//TC169237				nr -
Unigene26169_All	1650	0.44	0.80	1.03	3.05	3.90	2.57	2.20	2.61	0.36	8.47E-01	1.46E-01		1.22E+00	2.32E-02		3.56E-01	1.44E-01		-2.45E-01	4.12E-01		2.44E-01	3.96E-01		-2.61E+00	1.25E-13	Down	Unigene26169_All//gi|116311056|emb|CAH67987.1|/8.00E-22//OSIGBa0142I02-OSIGBa0101B20.30 [Oryza sativa (indica cultivar-group)]	Unigene26169_All//1.00E-30//AT5G01150| unknown protein					nr +
Unigene2617_All	2165	151.38	111.22	135.77	152.87	163.21	114.78	65.29	41.26	21.77	-4.45E-01	6.55E-57		-1.57E-01	4.00E-08		9.44E-02	3.00E-04		-4.14E-01	2.88E-54		-6.62E-01	9.08E-62		-1.58E+00	2.32E-262	Down	Unigene2617_All//gi|63054405|gb|AAY28970.1|/0.00E+00//GIA/RGA-like gibberellin response modulator [Gossypium hirsutum]	Unigene2617_All//0.00E+00//AT2G01570| RGA1 (REPRESSOR OF GA1-3 1); protein binding / transcription factor	Unigene2617_All//0.00E+00//TC129593	GRAS			nr -
Unigene26170_All	1394	3.42	5.60	2.71	6.97	6.97	8.97	3.82	7.17	7.86	7.13E-01	6.25E-04		-3.33E-01	2.65E-01		-5.00E-04	9.92E-01		3.65E-01	2.57E-02		9.07E-01	3.14E-08		1.04E+00	2.55E-11	Up	Unigene26170_All//gi|18418491|ref|NP_567969.1|/1.00E-165//SH3 domain-containing protein 2 (SH3P2) [Arabidopsis thaliana] >gi|16974678|gb|AAL32439.1|AF36777 4_1 SH3 domain-containing protein 2 [Arabidopsis thaliana]	Unigene26170_All//1.00E-166//AT4G34660| SH3 domain-containing protein 2 (SH3P2)	Unigene26170_All//0.00E+00//TC153815		ko04144|Endocytosis		nr -
Unigene26172_All	1237	74.15	91.26	96.17	63.35	81.59	82.62	51.58	19.02	23.96	3.00E-01	5.38E-10		3.75E-01	5.43E-15		3.65E-01	8.33E-15		3.83E-01	6.79E-15		-1.44E+00	3.50E-100	Down	-1.11E+00	1.53E-68	Down	Unigene26172_All//gi|10334991|gb|AAG15839.2|AF055910_1/1.00E-155//NADPH-dependent mannose 6-phosphate reductase [Phelipanche ramosa]	Unigene26172_All//2.00E-149//AT2G21250| mannose 6-phosphate reductase (NADPH-dependent), putative	Unigene26172_All//0.00E+00//TC149512		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr -
Unigene26173_All	268	4.69	0.38	1.19	6.32	3.73	1.52	11.83	4.83	4.31	-3.63E+00	2.00E-05	Down	-1.97E+00	4.62E-03		-7.62E-01	1.18E-01		-2.06E+00	1.87E-04	Down	-1.29E+00	5.66E-05	Down	-1.46E+00	4.89E-06	Down			Unigene26173_All//2.00E-91//TC158810				
Unigene26175_All	1186	39.79	12.73	24.11	24.28	25.32	16.18	21.75	16.18	12.06	-1.64E+00	7.48E-74	Down	-7.23E-01	2.42E-19		6.06E-02	6.17E-01		-5.85E-01	2.08E-09		-4.27E-01	7.60E-06		-8.51E-01	1.46E-18		Unigene26175_All//gi|115448325|ref|NP_001047942.1|//3.00E-75//Os02g0719000 [Oryza sativa Japonica Group] >gi|113557473|dbj|BAF09856.1| Os02g0719000 [Oryza sativa Japonica Group]	Unigene26175_All//1.00E-66//AT3G07880| Rho GDP-dissociation inhibitor family protein	Unigene26175_All//0.00E+00//TC135645			GO:0005092//GO:0043231	nr +
Unigene26176_All	1746	3.03	1.74	1.40	4.28	4.63	3.88	1.24	0.67	1.44	-7.98E-01	2.15E-03		-1.11E+00	5.63E-05	Down	1.15E-01	6.27E-01		-1.41E-01	5.90E-01		-8.82E-01	2.39E-02		2.19E-01	5.68E-01		Unigene26176_All//gi|30677982|ref|NP_178323.2|//1.00E-161//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene26176_All//8.00E-163//AT2G02150| pentatricopeptide (PPR) repeat-containing protein	Unigene26176_All//5.00E-180//DR455635				nr +
Unigene26177_All	1285	28.05	61.32	52.26	25.66	24.39	26.92	22.14	27.42	26.76	1.13E+00	4.46E-69	Up	8.97E-01	2.01E-39		-7.36E-02	5.42E-01		6.91E-02	5.60E-01		3.08E-01	1.49E-04		2.73E-01	7.46E-04		Unigene26177_All//gi|14423560|gb|AAK62462.1|AF387017_1/7.00E-55//Unknown protein [Arabidopsis thaliana]	Unigene26177_All//2.00E-42//AT5G16550| unknown protein	Unigene26177_All//0.00E+00//TC149010			GO:0044464	nr +
Unigene26178_All	1490	8.36	2.24	0.43	3.38	4.14	24.46	8.91	11.98	10.94	-1.90E+00	3.22E-24	Down	-4.28E+00	2.95E-53	Down	2.93E-01	2.60E-01		2.86E+00	5.43E-121	Up	4.27E-01	2.69E-04		2.96E-01	1.59E-02		Unigene26178_All//gi|15225663|ref|NP_181552.1|//1.00E-160//transferase family protein [Arabidopsis thaliana]	Unigene26178_All//5.00E-152//AT2G40230| transferase family protein	Unigene26178_All//0.00E+00//gi|13244056|gb|BE053135.2|BE053135		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016746	nr -
Unigene2618_All	2767	12.59	5.07	4.50	25.38	22.79	16.26	13.57	2.16	7.41	-1.31E+00	3.13E-39	Down	-1.48E+00	1.87E-45	Down	-1.56E-01	1.34E-02		-6.43E-01	5.07E-26		-2.65E+00	3.15E-132	Down	-8.72E-01	1.05E-27		Unigene2618_All//gi|110739553|dbj|BAF01685.1|//0.00E+00//anthranilate phosphoribosyltransferase-like protein [Arabidopsis thaliana]	Unigene2618_All//0.00E+00//AT3G57880| C2 domain-containing protein	Unigene2618_All//0.00E+00//TC157780				nr -
Unigene26181_All	798	44.52	17.78	21.62	68.85	53.77	73.80	67.82	39.12	28.16	-1.32E+00	1.48E-40	Down	-1.04E+00	7.51E-27	Down	-3.57E-01	4.33E-08		1.00E-01	2.14E-01		-7.94E-01	7.61E-33		-1.27E+00	2.96E-72	Down	Unigene26181_All//gi|297803476|ref|XP_002860622.1|//1.00E-56//mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315458|gb|EFH45881.1| mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26181_All//3.00E-54//AT4G29480| mitochondrial ATP synthase g subunit family protein	Unigene26181_All//0.00E+00//gi|109870116|gb|DW499092.1|DW499092		ko00190|Oxidative phosphorylation	GO:0005753//GO:0006754//GO:0006818//GO:0015077	nr -
Unigene26182_All	827	3.92	8.95	5.34	6.87	7.91	8.36	8.13	8.19	6.94	1.19E+00	9.89E-08	Up	4.46E-01	1.46E-01		2.04E-01	4.45E-01		2.83E-01	2.47E-01		1.03E-02	9.98E-01		-2.29E-01	2.80E-01		Unigene26182_All//gi|13992686|gb|AAK51580.1|AC022352_16/1.00E-11//Putative retroelement [Oryza sativa Japonica Group]		Unigene26182_All//0.00E+00//gi|78334565|gb|DT554839.1|DT554839			GO:0003676//GO:0004175//GO:0006260//GO:0019538//GO:0031410//GO:0034061//GO:0043231	nr -
Unigene26184_All	858	37.56	58.11	49.59	17.71	54.54	68.64	94.71	84.81	78.47	6.30E-01	9.16E-17		4.01E-01	1.80E-06		1.62E+00	4.07E-84	Up	1.95E+00	1.37E-124	Up	-1.59E-01	3.01E-03		-2.71E-01	7.96E-08		Unigene26184_All//gi|21322711|emb|CAD22154.1|//4.00E-70//pherophorin-dz1 protein [Volvox carteri f. nagariensis]		Unigene26184_All//2.00E-88//gi|82755970|gb|DV849532.1|DV849532		ko03040|Spliceosome	GO:0031410	nr +
Unigene26185_All	1581	7.58	2.63	4.38	14.37	14.66	8.14	3.53	1.37	1.26	-1.53E+00	2.18E-17	Down	-7.91E-01	3.24E-06		2.89E-02	8.33E-01		-8.20E-01	3.63E-13		-1.36E+00	9.00E-09	Down	-1.49E+00	2.99E-10	Down	Unigene26185_All//gi|297812893|ref|XP_002874330.1|//1.00E-141//kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320167|gb|EFH50589.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26185_All//2.00E-95//AT5G26960| kelch repeat-containing F-box family protein	Unigene26185_All//0.00E+00//gi|78328020|gb|DT548294.1|DT548294		ko03040|Spliceosome		nr -
Unigene26187_All	527	6.85	6.15	16.37	8.51	1.57	2.31	3.05	10.39	2.72	-1.55E-01	6.24E-01		1.26E+00	3.19E-09	Up	-2.44E+00	3.97E-15	Down	-1.88E+00	1.24E-09	Down	1.77E+00	3.10E-12	Up	-1.64E-01	7.13E-01				Unigene26187_All//0.00E+00//DW515623				ESTscan +
Unigene26188_All	553	8.23	9.80	14.35	5.13	1.49	4.33	3.98	21.24	1.66	2.52E-01	3.63E-01		8.02E-01	1.83E-04		-1.78E+00	1.27E-06	Down	-2.46E-01	5.62E-01		2.42E+00	1.47E-37	Up	-1.26E+00	9.51E-04	Down			Unigene26188_All//3.00E-120//DW515623				
Unigene26189_All	1323	14.32	8.39	11.43	14.57	13.38	12.29	6.65	2.87	3.31	-7.71E-01	1.73E-09		-3.25E-01	1.62E-02		-1.23E-01	4.05E-01		-2.46E-01	6.54E-02		-1.21E+00	2.86E-11	Down	-1.00E+00	7.27E-09	Down	Unigene26189_All//gi|297804086|ref|XP_002869927.1|//1.00E-118//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317563|gb|EFH46186.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26189_All//9.00E-118//AT4G20760| short-chain dehydrogenase/reductase (SDR) family protein	Unigene26189_All//0.00E+00//TC146470		ko00903|Limonene and pinene degradation//ko00960|Carotenoid biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis	GO:0003824//GO:0008152	nr -

Unigene2619_All	2573	3.40	2.15	1.80	10.90	9.14	13.02	4.09	12.96	10.42	-6.62E-01	6.78E-04		-9.15E-01	7.45E-06		-2.54E-01	1.18E-02		2.57E-01	6.71E-03		1.66E+00	6.62E-65	Up	1.35E+00	2.01E-39	Up	Unigene2619_All//gi|225442633|ref|XP_002284593.1|//0.00E+00//PREDICTED: similar to BY-2 kinesin-like protein 10 [Vitis vinifera]	Unigene2619_All//0.00E+00//gi|54120253|gb|AY3G16060| kinesin motor family protein	Unigene2619_All//0.00E+00//gi|54120253|gb|CO495762.1|CO495762				nr +
Unigene26193_All	1268	34.12	4.72	16.71	47.02	27.32	19.45	2.90	2.34	1.57	-2.86E+00	3.77E-135	Down	-1.03E+00	5.68E-32	Down	-7.84E-01	3.41E-35		-1.27E+00	4.64E-69	Down	-3.10E-01	3.18E-01		-8.85E-01	1.39E-03		Unigene26193_All//gi|79484897|ref|NP_567694.2|//1.00E-137//YSL1 (YELLOW STRIPE LIKE 1): oligopeptide transporter [Arabidopsis thaliana] >gi|16035903|sp|Q683L0.2|YSL1_ARATH RecName: Full=Metal-nicotianamine transporter YSL1; AltName: Full=Protein YELLOW STRIPE LIKE 1; Short=AtYSL1	Unigene26193_All//4.00E-117//AT4G24120| YSL1 (YELLOW STRIPE LIKE 1): oligopeptide transporter	Unigene26193_All//0.00E+00//TC147689				nr -
Unigene26194_All	1191	46.83	28.76	34.02	45.00	39.96	39.97	31.81	10.81	13.81	-7.03E-01	1.35E-22		-4.61E-01	1.73E-10		-1.72E-01	1.88E-02		-1.71E-01	2.42E-02		-1.56E+00	4.06E-67	Down	-1.20E+00	7.24E-47	Down	Unigene26194_All//gi|152955225|emb|CAM59673.1|//1.00E-105//parvulin-type peptidyl prolyl cis/trans isomerase [Lotus japonicus]	Unigene26194_All//7.00E-79//AT5G19370| rhodanese-like domain-containing protein / PPIC-type PPIASE domain-containing protein	Unigene26194_All//0.00E+00//TC135589			GO:0009536//GO:0016853	nr -
Unigene26195_All	715	23.78	24.31	34.26	26.54	26.63	28.93	40.21	27.06	19.33	3.15E-02	8.30E-01		5.27E-01	3.43E-06		4.80E-03	9.78E-01		1.24E-01	3.86E-01		-5.71E-01	2.38E-10		-1.06E+00	3.48E-29	Down	Unigene26195_All//gi|0177925|dbj|BAB11336.1|//4.00E-36//NADH dehydrogenase 10.5K chain-like protein [Arabidopsis thaliana] >gi|21593502|gb|AAM65469.1| NADH dehydrogenase 10.5K chain-like protein [Arabidopsis thaliana]	Unigene26195_All//2.00E-37//AT5G47890| NADH-ubiquinone oxidoreductase B8 subunit, putative	Unigene26195_All//0.00E+00//TC158270		ko00190|Oxidative phosphorylation	GO:0008152//GO:0016651//GO:0030964//GO:0043231	nr -
Unigene26196_All	929	3.27	1.36	4.13	5.95	5.86	4.08	5.37	2.88	1.50	-1.26E+00	6.15E-04	Down	3.37E-01	3.25E-01		-2.33E-02	9.36E-01		-5.44E-01	3.32E-02		-8.99E-01	1.82E-04		-1.84E+00	3.15E-12	Down	Unigene26196_All//gi|18378607|gb|AAL68641.1|AF458765_1//4.00E-13//polyprotein [Oryza sativa Japonica Group]		Unigene26196_All//1.00E-30//ES807842			GO:0005488	nr +
Unigene26197_All	1335	11.64	73.06	7.38	11.94	33.46	17.79	19.00	45.93	28.56	2.65E+00	3.07E-278	Up	-6.58E-01	6.95E-06		1.49E+00	9.80E-71	Up	5.76E-01	1.29E-07		1.27E+00	8.05E-80	Up	5.88E-01	1.73E-14		Unigene26197_All//gi|15228302|ref|NP_188294.1|//1.00E-71//ATL2; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|68565202|sp|Q8L9T5.2|ATL3F_ARATH RecName: Full=RING-H2 finger protein ATL3F; AltName: Full=RING-H2 finger protein ATL2 >gi|11994627|dbj|BAB02764.1| RING zinc finger protein-like [Arabidopsis thaliana] >gi|17065578|gb|AAL32943.1| RING zinc finger protein-like [Arabidopsis thaliana] >gi|20148585|gb|AAM10183.1| RING zinc finger protein-like [Arabidopsis thaliana] >gi|70065095|gb|AAZ14073.1|At3g16720 [Arabidopsis thaliana]	Unigene26197_All//5.00E-52//AT3G16720| ATL2; protein binding / zinc ion binding	Unigene26197_All//0.00E+00//gi|78328199|gb|DT548473.1|DT548473			GO:0005488//GO:0006950//GO:0009743	nr +
Unigene26198_All	1754	1.61	17.45	3.19	3.52	2.98	4.63	6.53	15.13	8.06	3.44E+00	2.47E-113	Up	9.85E-01	1.90E-04		-2.39E-01	3.55E-01		3.96E-01	6.04E-02		1.21E+00	1.92E-32	Up	3.04E-01	2.22E-02		Unigene26198_All//gi|15220023|ref|NP_178108.1|//1.00E-112//BAC2; L-ornithine transmembrane transporter/ binding / carnitine:acyl carnitine antiporter [Arabidopsis thaliana]	Unigene26198_All//9.00E-106//AT1G79900| BAC2; L-ornithine transmembrane transporter/ binding / carnitine:acyl carnitine antiporter	Unigene26198_All//0.00E+00//TC164412			GO:0006810//GO:0016020	nr +
Unigene26199_All	570	7.34	2.76	3.18	7.87	7.85	5.15	10.24	6.16	5.24	-1.41E+00	6.04E-06	Down	-1.21E+00	1.39E-04	Down	-2.10E-03	9.86E-01		-6.11E-01	3.32E-02		-7.33E-01	7.92E-04		-9.66E-01	7.68E-06		Unigene26199_All//gi|297802336|ref|XP_002869052.1|//2.00E-10//La domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297314888|gb|EFH45311.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene26199_All//4.00E-11//AT4G35890| La domain-containing protein	Unigene26199_All//4.00E-175//gi|21089964|gb|BQ402277.1|BQ402277			GO:0003676//GO:0043231	nr +
Unigene262_All	2155	13.45	16.20	14.70	29.17	26.89	25.27	14.07	10.92	7.02	2.68E-01	3.82E-03		1.28E-01	2.43E-01		-1.17E-01	1.02E-01		-2.07E-01	2.03E-03		-3.66E-01	3.04E-05		-1.00E+00	3.15E-28	Down	Unigene262_All//gi|18394842|ref|NP_564109.1|//1.00E-142//oxidoreductase, 20G-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|9558598|gb|AAF88161.1|AC026234_12 Contains similarity to a prolyl 4-hydroxylase alpha subunit protein from Gallus gallus gi|212530 [Arabidopsis thaliana] >gi|90962978|gb|ABE02413.1|At1g20270 [Arabidopsis thaliana]	Unigene262_All//1.00E-130//AT1G20270| oxidoreductase, 20G-Fe(II) oxygenase family protein	Unigene262_All//0.00E+00//gi|193219586|gb|EY198048.1|EY198048		ko00190|Oxidative phosphorylation//ko04145|Phagosome//ko00330|Arginine and proline metabolism		nr -
Unigene26201_All	1160	1.58	0.87	0.46	3.78	2.55	1.60	1.93	1.33	1.99	-8.54E-01	7.59E-02		-1.78E+00	1.06E-03		-5.66E-01	4.23E-02		-1.24E+00	1.88E-05	Down	-5.35E-01	1.71E-01		4.42E-02	9.26E-01		Unigene26201_All//gi|3367537|gb|AAC28522.1|//1.00E-138//Contains similarity to ANK repeat region of Fowlpox virus BamHI-orf7 protein homolog C18F10.7 gi|485107 from Caenorhabditis elegans cosmid gb|U00049. This gene is continued from unannotated gene on BAC F19K23 gb|AC000375 [Arabidopsis thaliana]	Unigene26201_All//8.00E-158//AT1G62050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: apoplast; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Ankyrin (InterPro:IPR002110); BEST Arabidopsis thaliana protein match is: ankyrin repeat family protein (TAIR:AT1G11740.1); Has 967 Blast hits to 722 proteins in 118 species: Archae - 0; Bacteria - 24; Metazoa - 556; Fungi - 45; Plants - 193; Viruses - 2; Other Eukaryotes - 147 (source: NCBI BLink).	Unigene26201_All//0.00E+00//gi|78337038|gb|DT557312.1|DT557312			GO:0016020	nr +
Unigene26203_All	2144	1.17	3.52	1.09	7.71	8.74	9.37	6.94	2.65	3.55	1.59E+00	9.16E-12	Up	-1.00E-01	8.05E-01		1.80E-01	2.04E-01		2.81E-01	2.74E-02		-1.39E+00	9.58E-23	Down	-9.68E-01	1.44E-13		Unigene26203_All//gi|15724288|gb|AAL06537.1|AF412084_1//1.00E-132//AT5g11590|T24K9_26 [Arabidopsis thaliana]	Unigene26203_All//3.00E-128//AT3G11590| unknown protein	Unigene26203_All//0.00E+00//gi|48746571|gb|CO077090.1|CO077090				nr -
Unigene26205_All	1708	0.31	0.62	0.22	2.16	2.36	1.82	9.53	6.83	4.62	1.02E+00	1.27E-01		-4.89E-01	6.32E-01		1.28E-01	7.41E-01		-2.42E-01	5.00E-01		-4.81E-01	8.92E-05		-1.05E+00	1.23E-16	Down	Unigene26205_All//gi|224106295|ref|XP_002314117.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222850525|gb|EEE88072.1| cytochrome P450 [Populus trichocarpa]	Unigene26205_All//0.00E+00//AT5G58860| CYP86A1 (CYTOCHROME P450 86A1); fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene26205_All//0.00E+00//TC134417		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0006631//GO:0016712//GO:0016713//GO:0043231	nr -
Unigene26207_All	1817	8.12	7.17	9.91	16.89	18.44	17.00	12.22	7.82	4.80	-1.80E-01	2.51E-01		2.87E-01	4.25E-02		1.27E-01	2.29E-01		9.70E-03	9.51E-01		-6.43E-01	6.35E-10		-1.35E+00	4.94E-33	Down	Unigene26207_All//gi|226491724|ref|NP_001151279.1|//1.00E-105//transposon protein Mutator sub-class [Zea mays] >gi|195645492|gb|ACG42214.1| transposon protein Mutator sub-class [Zea mays]	Unigene26207_All//9.00E-135//AT3G52610| unknown protein	Unigene26207_All//0.00E+00//TC172103				nr +
Unigene26210_All	1529	2.12	2.68	1.01	5.02	2.34	1.51	3.37	2.21	2.68	3.39E-01	2.76E-01		-1.07E+00	3.24E-03		-1.10E+00	2.17E-08	Down	-1.74E+00	1.73E-14	Down	-6.08E-01	9.85E-03		-3.30E-01	1.63E-01		Unigene26210_All//gi|224055581|ref|XP_002298550.1|//1.00E-110//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222845808|gb|EEE83355.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene26210_All//1.00E-83//AT3G01600| anac044 (Arabidopsis NAC domain containing protein 44); transcription factor	Unigene26210_All//0.00E+00//ES811418	NAC		GO:0001071//GO:0043231	nr -
Unigene26212_All	1840	2.82	6.17	2.72	2.90	4.88	2.60	1.59	2.36	10.96	1.13E+00	1.23E-10	Up	-4.94E-02	8.63E-01		7.54E-01	3.37E-05		-1.55E-01	6.32E-01		5.75E-01	2.77E-02		2.79E+00	2.07E-76	Up	Unigene26212_All//gi|224078898|ref|XP_002305671.1|//1.00E-127//bromodomain protein [Populus trichocarpa] >gi|222848635|gb|EEE86182.1| bromodomain protein [Populus trichocarpa]	Unigene26212_All//2.00E-78//AT1G61215| BRD4 (BROMODOMAIN 4); DNA binding	Unigene26212_All//0.00E+00//gi|78333150|gb|DT553424.1|DT553424				nr +
Unigene26214_All	1114	6.90	10.37	7.17	11.58	12.58	10.26	12.18	11.56	5.83	5.87E-01	4.32E-04		5.45E-02	8.07E-01		1.19E-01	5.26E-01		-1.75E-01	3.37E-01		-7.63E-02	6.20E-01		-1.06E+00	2.14E-14	Down		Unigene26214_All//4.00E-164//gi|18099558|gb|BM358812.1|BM358812				
Unigene26216_All	1641	5.77	4.14	1.88	3.43	2.94	2.64	5.00	0.56	2.57	-4.80E-01	1.05E-02		-1.62E+00	2.38E-14	Down	-2.24E-01	4.21E-01		-3.77E-01	1.54E-01		-3.16E+00	4.80E-35	Down	-9.58E-01	9.28E-08		Unigene26216_All//gi|223452530|gb|ACM89592.1|//0.00E+00//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene26216_All//0.00E+00//AT3G56370| leucine-rich repeat transmembrane protein kinase, putative	Unigene26216_All//0.00E+00//gi|78331908|gb|DT552182.1|DT552182		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152//GO:0016020//GO:0031410	nr +
Unigene26217_All	1057	952.62	769.58	1089.08	251.19	327.31	203.26	71.36	25.82	49.56	-3.08E-01	2.09E-87		1.93E-01	6.06E-40		3.82E-01	3.12E-54		-3.06E-01	6.03E-25		-1.47E+00	1.02E-121	Down	-5.26E-01	5.60E-23		Unigene26217_All//gi|5733730|gb|AAD49734.1|AF169795_1//1.00E-136//glutamine synthetase precursor [Juglans nigra]	Unigene26217_All//3.00E-106//AT5G35630| GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase	Unigene26217_All//0.00E+00//gi|164346321|gb|EX169168.1|EX169168		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene26218_All	2132	0.56	0.00	0.00	2.73	5.30	5.13	1.59	2.45	1.10	-9.14E+00	5.01E-07	Down	-9.14E+00	1.36E-06	Down	9.55E-01	2.92E-09		9.07E-01	1.03E-07		6.27E-01	7.18E-03		-5.25E-01	7.12E-02		Unigene26218_All//gi|56609044|gb|AW03152.1|//0.00E+00//kinesin [Gossypium hirsutum]	Unigene26218_All//0.00E+00//AT5G27000| ATK4 (ARABIDOPSIS THALIANA KINESIN 4); ATPase/ microtubule binding / microtubule motor	Unigene26218_All//0.00E+00//TC129556			GO:0003774//GO:0007017//GO:0015630//GO:0015631//GO:0032559	nr -
Unigene26220_All	1305	0.84	1.36	0.45	1.60	1.90	1.07	1.39	0.42	1.59	6.91E-01	1.58E-01		-9.07E-01	1.87E-01		2.45E-01	5.94E-01		-5.80E-01	2.11E-01		-1.74E+00	1.71E-04	Down	1.88E-01	6.28E-01		Unigene26220_All//gi|115488902|ref|NP_001066938.1|//4.00E-06//Os12g0536200 [Oryza sativa Japonica Group] >gi|108862776|gb|ABA98834.2| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108862777|gb|ABG22039.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649445|dbj|BAF29957.1|Os12g0536200 [Oryza sativa Japonica Group]		Unigene26220_All//0.00E+00//gi|13354323|gb|BG444671.1|BG444671				nr -
Unigene26221_All	2114	7.38	5.92	6.37	13.13	5.85	11.52	4.14	25.96	13.17	-3.17E-01	2.83E-02		-2.11E-01	1.83E-01		-1.17E+00	4.59E-32	Down	-1.89E-01	9.07E-02		2.65E+00	2.98E-192	Up	1.67E+00	9.36E-56	Up	Unigene26221_All//gi|71738561|gb|AAZ40342.1|//1.00E-172//beta-1,3-glucanase 2 [Zizjphus jujuba]	Unigene26221_All//1.00E-167//AT5G55180| glycosyl hydrolase family 17 protein	Unigene26221_All//0.00E+00//TC172324		ko00500|Starch and sucrose metabolism		nr +
Unigene26223_All	1038	2.32	30.80	22.93	8.69	7.76	19.88	9.61	8.66	19.23	3.73E+00	7.63E-127	Up	3.31E+00	2.39E-83	Up	-1.62E-01	4.60E-01		1.19E+00	1.19E-21	Up	-1.51E-01	4.12E-01		1.00E+00	1.03E-18	Up	Unigene26223_All//gi|186479105|ref|NP_174461.3|//7.00E-06//actin binding [Arabidopsis thaliana] >gi|166215071|sp|Q9C6S1.3|FH14_ARATH RecName: Full=Formin-like protein 14; Short=AtFH14						nr +

Unigene26224_A11	1792	1.05	1.50	1.75	9.65	9.55	6.30	4.08	3.83	1.47	5.12E-01	1.90E-01			7.38E-01	4.51E-02		-1.44E-02	9.33E-01			-6.14E-01	2.12E-06		-9.37E-02	6.63E-01		-1.48E+00	4.86E-13	Down	Unigene26224_A11//gi|115445729|ref|NP_001046644.1|//7.00E-08//0s02g0307900 [Oryza sativa Japonica Group] >gi|113536175|dbj|BAF08558.1|Os02g0307900 [Oryza sativa Japonica Group]		Unigene26224_A11//0.00E+00//TC173460				nr +
Unigene26226_A11	1609	1.11	1.20	1.16	4.58	5.12	3.23	2.76	1.61	0.87	1.14E-01	7.98E-01			6.72E-02	8.92E-01		1.59E-01	5.21E-01			-5.05E-01	1.92E-02		-7.77E-01	2.38E-03		-1.67E+00	1.04E-09	Down	Unigene26226_A11//gi|15809986|gb|AAL06920.1|/1.00E-165//AT3g19540/T31J18_4 [Arabidopsis thaliana] >gi|22137022|gb|AAM91356.1|At3g19540/T31J18_4 [Arabidopsis thaliana]	Unigene26226_A11//7.00E-158//AT3G19540| unknown protein	Unigene26226_A11//0.00E+00//TC154076				nr +
Unigene26227_A11	1278	5.28	7.77	2.54	1.91	2.78	6.18	2.51	3.04	2.24	5.57E-01	2.17E-03		-1.06E+00	9.90E-06	Down	5.39E-01	1.05E-01		1.70E+00	3.67E-14	Up	2.75E-01	3.73E-01		-1.64E-01	6.11E-01		Unigene26227_A11//gi|224103505|ref|XP_002313083.1|/1.00E-123//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222849491|gb|EEE87038.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene26227_A11//6.00E-112//AT3G19000| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene26227_A11//0.00E+00//ES843724		ko00904|Diterpenoid biosynthesis		nr -
Unigene26231_A11	1141	6.51	4.84	5.37	12.49	9.17	8.91	12.19	5.82	3.95	-4.28E-01	4.79E-02		-2.79E-01	2.37E-01		-4.45E-01	1.49E-03		-4.88E-01	8.43E-04		-1.07E+00	2.55E-14	Down	-1.63E+00	1.38E-27	Down	Unigene26231_A11//gi|68449752|gb|AAY97863.1|/2.00E-86//AC113 [Solanum lycopersicum]	Unigene26231_A11//2.00E-63//AT5G51840| unknown protein	Unigene26231_A11//0.00E+00//TC153325				nr -
Unigene26233_A11	980	27.87	55.89	45.97	13.22	32.71	23.46	19.98	40.56	42.77	1.00E+00	5.31E-40	Up	7.22E-01	1.75E-18		1.31E+00	5.50E-42	Up	8.28E-01	2.10E-13		1.02E+00	8.51E-37	Up	1.10E+00	1.72E-44	Up	Unigene26233_A11//gi|15721876|dbj|BAB68392.1|/5.00E-25//CmE8 [Cucumis melo]	Unigene26233_A11//5.00E-26//AT5G39540| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene26233_A11//0.00E+00//TC174072		ko04402|Benzoxazinoid biosynthesis	GO:0008152//GO:0016706//GO:0046914	nr +
Unigene26234_A11	398	0.53	0.38	0.00	3.50	0.61	1.59	0.11	0.21	0.00	-4.61E-01	7.58E-01		-9.04E+00	1.46E-01		-2.53E+00	3.16E-05	Down	-1.14E+00	4.68E-02		9.84E-01	7.31E-01		-6.73E+00	6.13E-01		Unigene26234_A11//gi|15235981|ref|NP_193450.1|//4.00E-60//RABB1C (ARABIDOPSIS RAB GTPASE HOMOLOG B1C); GTP binding / GTPase [Arabidopsis thaliana] >gi|1765896|emb|CAA70498.1| Rab2-like protein [Arabidopsis thaliana] >gi|5281023|emb|CAB45962.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] >gi|7268468|emb|CAB80988.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] >gi|27311815|gb|AAO00873.1| GTP-binding RAB2A like protein [Arabidopsis thaliana] >gi|30023652|gb|AAP13359.1|At4g17170 [Arabidopsis thaliana]	Unigene26234_A11//1.00E-146//AT727234	Unigene26234_A11//2.00E-61//AT4G17170| RABB1C (ARABIDOPSIS RAB GTPASE HOMOLOG B1C); GTP binding / GTPase			GO:0005793//GO:0016020//GO:0032561//GO:0035556//GO:0043231//GO:0048193	nr +
Unigene26237_A11	607	1.90	1.50	0.00	1.97	3.06	0.37	3.48	1.51	0.85	-3.36E-01	6.09E-01		-1.09E+01	2.60E-06	Down	6.37E-01	1.99E-01		-2.40E+00	7.07E-04	Down	-1.20E+00	2.77E-03		-2.03E+00	2.52E-06	Down	Unigene26237_A11//gi|297849978|ref|XP_002892870.1|//9.00E-72//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338712|gb|EFH69129.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26237_A11//3.00E-67//AT1G15490| hydrolase, alpha/beta fold family protein	Unigene26237_A11//9.00E-176//ES798683			GO:0044464	nr -
Unigene26238_A11	2681	0.70	0.00	0.18	4.11	1.72	0.94	6.78	0.37	0.83	-9.46E+00	6.73E-11	Down	-1.97E+00	3.20E-04	Down	-1.25E+00	1.62E-14	Down	-2.12E+00	8.68E-27	Down	-4.18E+00	5.02E-97	Down	-3.03E+00	2.76E-76	Down	Unigene26238_A11//gi|297849978|ref|XP_002892870.1|//0.00E+00//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338712|gb|EFH69129.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26238_A11//0.00E+00//AT1G15490| hydrolase, alpha/beta fold family protein	Unigene26238_A11//0.00E+00//ES798683			GO:0003824//GO:0044464	nr -
Unigene26239_A11	2019	4.51	1.83	2.48	4.52	6.79	5.97	0.82	0.54	0.14	-1.30E+00	1.18E-10	Down	-8.63E-01	1.45E-05		5.88E-01	3.77E-05		4.04E-01	1.46E-02		-6.02E-01	2.00E-01		-2.56E+00	1.72E-06	Down	Unigene26239_A11//gi|115444583|ref|NP_001046071.1|//0.00E+00//0s02g0177800 [Oryza sativa Japonica Group] >gi|113535602|dbj|BAF07985.1|Os02g0177800 [Oryza sativa Japonica Group]	Unigene26239_A11//0.00E+00//AT5G57580| calmodulin-binding protein	Unigene26239_A11//0.00E+00//EE592665		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005515	nr +
Unigene26241_A11	2037	24.27	7.54	17.96	48.35	39.25	32.84	34.50	12.72	15.61	-1.69E+00	3.04E-80	Down	-4.35E-01	1.74E-08		-3.01E-01	2.55E-10		-5.58E-01	2.93E-28		-1.44E+00	2.70E-110	Down	-1.14E+00	1.31E-79	Down	Unigene26241_A11//gi|7271957|gb|AAF44708.1|AF242819_1//0.00E+00//wound-inducible carboxypeptidase [Solanum lycopersicum]	Unigene26241_A11//0.00E+00//AT4G12910| scp120 (serine carboxypeptidase-like 20); serine-type carboxypeptidase	Unigene26241_A11//0.00E+00//TC131195			GO:0004180//GO:0019538//GO:0042579	nr -
Unigene26244_A11	1152	13.72	17.95	11.09	27.93	34.88	24.11	13.14	9.29	87.77	3.88E-01	1.44E-03		-3.06E-01	4.35E-02		3.21E-01	5.51E-05		-2.12E-01	3.35E-02		-5.01E-01	9.02E-05		2.74E+00	0.00E+00	Up	Unigene26244_A11//gi|18403283|ref|NP_566699.1|//9.00E-13//VQ motif-containing protein [Arabidopsis thaliana]	Unigene26244_A11//5.00E-14//AT3G22160| VQ motif-containing protein	Unigene26244_A11//0.00E+00//TC162090				nr +
Unigene26245_A11	666	47.53	44.81	36.94	69.56	62.61	88.29	57.39	28.87	25.12	-8.49E-02	4.34E-01		-3.64E-01	2.64E-04		-1.52E-01	6.41E-02		3.44E-01	2.43E-07		-9.91E-01	8.99E-34		-1.19E+00	1.40E-46	Down	Unigene26245_A11//gi|282848224|gb|ADB02893.1|//2.00E-28//ubiquinol-cytochrome C reductase [Jatropha curcas]	Unigene26245_A11//3.00E-26//AT3G52730| ubiquinol-cytochrome C reductase UQCRX/QCR9-like family protein	Unigene26245_A11//0.00E+00//TC160898		ko00190|Oxidative phosphorylation	GO:0005746//GO:0015078//GO:0022904//GO:0051234	nr -
Unigene26247_A11	1744	16.02	5.08	9.34	20.34	13.72	15.30	26.59	8.39	12.11	-1.66E+00	2.03E-44	Down	-7.78E-01	3.25E-13		-5.68E-01	4.63E-12		-4.10E-01	2.72E-06		-1.66E+00	2.94E-90	Down	-1.14E+00	3.42E-52	Down	Unigene26247_A11//gi|2811029|sp|O04866.1|ARGD_ALNGL//0.00E+00//RecName: Full=Acetylornithine aminotransferase, mitochondrial; Short=ACOAT; AltName: Full=Acetylornithine transaminase; Short=AOTA; Flags: Precursor >gi|9445411|emb|CAA69806.1| acetylornithine aminotransferase [Alnus glutinosa]	Unigene26247_A11//1.00E-156//AT1G80600| WIN1 (HOPW1-1-INTERACTING 1); N2-acetyl-L-ornithine:2-oxoglutarate 5-aminotransferase/ catalytic/ pyridoxal phosphate binding / transaminase	Unigene26247_A11//0.00E+00//gi|164283027|gb|ES803715.1|ES803715		ko00330|Arginine and proline metabolism	GO:0006525//GO:0008483//GO:0043231//GO:0048037	nr -
Unigene2625_A11	1581	12.15	8.81	4.14	19.35	21.56	16.43	40.46	11.18	14.06	-4.63E-01	2.34E-04		-1.55E+00	6.09E-27	Down	1.57E-01	1.16E-01		-2.36E-01	1.96E-02		-1.86E+00	1.89E-144	Down	-1.52E+00	1.23E-112	Down	Unigene2625_A11//gi|166343839|gb|AB986662.1|//0.00E+00//beta-tubulin 16 [Gossypium hirsutum]	Unigene2625_A11//0.00E+00//AT5G23860| TUB8, structural constituent of cytoskeleton	Unigene2625_A11//0.00E+00//TC130221		ko04145|Phagosome		nr -
Unigene26251_A11	936	122.25	51.59	108.09	608.41	494.42	406.18	160.36	161.96	78.19	-1.24E+00	2.33E-117	Down	-1.78E-01	4.99E-04		-2.99E-01	2.90E-57		-5.83E-01	2.97E-174		1.43E-02	7.65E-01		-1.04E+00	4.66E-144	Down	Unigene26251_A11//gi|297820194|ref|XP_002877980.1|//1.00E-108//ump synthase [Arabidopsis lyrata subsp. lyrata] >gi|297323818|gb|EFH54239.1| ump synthase [Arabidopsis lyrata subsp. lyrata]	Unigene26251_A11//2.00E-91//AT3G54170| uridine 5'-monophosphate synthase / UMP synthase (PYRE-F) (UMPS)	Unigene26251_A11//0.00E+00//TC130176		ko00240|Pyrimidine metabolism	GO:0006220//GO:0016763//GO:0016831//GO:0019856	nr -
Unigene26252_A11	1078	16.89	16.69	14.18	32.67	51.97	79.39	6.71	9.42	14.52	-1.75E-02	9.14E-01		-2.53E-01	7.63E-02		6.70E-01	1.91E-24		1.28E+00	2.02E-98	Up	4.90E-01	2.25E-03		1.11E+00	1.44E-17	Up	Unigene26252_A11//gi|29029104|gb|AA064931.1|/9.00E-81//At5g47310 [Arabidopsis thaliana]	Unigene26252_A11//7.00E-78//AT5G47310| unknown protein	Unigene26252_A11//0.00E+00//gi|109871420|gb|DW500396.1|DW500396				nr +
Unigene26254_A11	1825	1.75	229.72	1.46	2.35	12.21	12.23	4.10	11.79	43.07	7.04E+00	0.00E+00	Up	-2.62E-01	4.88E-01		2.38E+00	1.22E-65	Up	2.38E+00	1.40E-60	Up	1.52E+00	3.16E-37	Up	3.39E+00	0.00E+00	Up	Unigene26254_A11//gi|297596267|ref|NP_001042284.2|//1.00E-82//Os01g0194000 [Oryza sativa Japonica Group] >gi|255672964|dbj|BAF04198.2|Os01g0194000 [Oryza sativa Japonica Group]	Unigene26254_A11//6.00E-84//AT5G04860| unknown protein	Unigene26254_A11//0.00E+00//TC151215			GO:0043231	nr +
Unigene26255_A11	2005	0.00	22.52	0.11	0.35	1.03	1.13	0.51	1.21	5.03	1.45E+01	1.04E-260	Up	6.73E+00	1.41E-01		1.57E+00	6.25E-04	Up	1.70E+00	1.80E-04	Up	1.26E+00	7.55E-04	Up	3.31E+00	1.56E-45	Up	Unigene26255_A11//gi|115489620|ref|NP_001067297.1|//1.00E-81//Os12g0620600 [Oryza sativa Japonica Group] >gi|77557103|gb|ABA99899.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649804|dbj|BAF30316.1|Os12g0620600 [Oryza sativa Japonica Group]	Unigene26255_A11//3.00E-80//AT3G11760| unknown protein	Unigene26255_A11//0.00E+00//TC151215			GO:0043231	nr -
Unigene26256_A11	972	38.76	42.17	48.10	41.56	61.01	50.79	28.23	20.94	10.90	1.22E-01	1.88E-01		3.12E-01	1.12E-04		5.54E-01	1.53E-18		2.89E-01	1.02E-04		-4.31E-01	2.93E-06		-1.37E+00	8.79E-42	Down	Unigene26256_A11//gi|6066609|emb|CAB58442.1|//2.00E-58//chloroplast channel forming outer membrane protein [Pisum sativum]	Unigene26256_A11//6.00E-59//AT1G20816| unknown protein	Unigene26256_A11//0.00E+00//TC145865			GO:0009526	nr +
Unigene26258_A11	749	59.66	96.54	59.22	84.60	101.74	92.80	56.90	90.57	138.88	6.94E-01	2.34E-28		-1.05E-02	9.23E-01		2.66E-01	1.83E-06		1.34E-01	4.96E-02		6.71E-01	1.07E-30		1.29E+00	3.61E-140	Up	Unigene26258_A11//gi|112455658|gb|AB118983.1|//3.00E-56//molecular chaperone DjA2 [Allium ampeloprasum]	Unigene26258_A11//5.00E-45//AT3G44110| ATJ3; protein binding	Unigene26258_A11//0.00E+00//gi|109858861|gb|DW487840.1|DW487840		ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0006950//GO:0032559//GO:0043169//GO:0044267//GO:0044424	nr +
Unigene26260_A11	1066	20.76	37.79	27.67	46.22	30.85	66.69	49.46	90.53	153.49	8.64E-01	3.43E-23		4.15E-01	5.57E-05		-5.83E-01	2.19E-17		5.29E-01	1.38E-18		8.72E-01	7.09E-68		1.63E+00	0.00E+00	Up	Unigene26260_A11//gi|33324520|gb|AAQ08000.1|/9.00E-63//dehydration responsive element binding protein [Gossypium hirsutum] >gi|37727988|gb|AO43165.1| DRE binding protein 1 [Gossypium hirsutum]	Unigene26260_A11//3.00E-38//AT2G23340| AP2 domain-containing transcription factor, putative	Unigene26260_A11//0.00E+00//DW505168	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene26261_A11	1613	7.85	7.16	7.23	9.85	10.48	12.43	16.62	8.21	9.68	-1.32E-01	4.46E-01		-1.19E-01	5.25E-01		8.95E-02	5.93E-01		3.36E-01	6.97E-03		-1.02E+00	6.56E-25	Down	-7.79E-01	1.07E-16		Unigene26261_A11//gi|21592356|gb|AAM64307.1|//1.00E-158//nuclear matrix protein 1 [Arabidopsis thaliana]	Unigene26261_A11//4.00E-159//AT5G17620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Plant nuclear matrix 1 (InterPro:IPR010604); Has 62 Blast hits to 62 proteins in 32 species: Archae - 0; Bacteria - 19; Metazoa - 8; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene26261_A11//0.00E+00//TC144809				nr -
Unigene26262_A11	1453	3.06	4.57	4.58	24.34	17.82	11.50	16.41	4.95	10.20	5.78E-01	1.15E-02		5.82E-01	1.44E-02		-4.50E-01	4.92E-08		-1.08E+00	8.45E-32	Down	-1.73E+00	2.49E-49	Down	-6.86E-01	3.76E-12		Unigene26262_A11//gi|87240518|gb|ABD32376.1|//1.00E-172//Lipolytic enzyme, G-D-S-L [Medicago truncatula] >gi|124361052|gb|ABN09024.1|Lipolytic enzyme, G-D-S-L [Medicago truncatula]	Unigene26262_A11//4.00E-158//AT1G54790| GDSL-motif lipase/hydrolase family protein	Unigene26262_A11//0.00E+00//TC165129				nr +
Unigene26265_A11	681	8.45	4.02	5.24	11.56	7.38	8.89	3.97	1.84	1.46	-1.07E+00	2.11E-05	Down	-6.90E-01	7.44E-03		-6.47E-01	8.02E-04		-3.79E-01	7.74E-02		-1.11E+00	1.31E-03		-1.44E+00	3.29E-05	Down	Unigene26265_A11//gi|53370641|gb|AAU89136.1|//1.00E-09//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene26265_A11//3.00E-43//TC173067				nr +

Unigene26267_All	787	1.46	5.79	1.62	8.61	9.10	8.72	15.10	16.84	8.45	1.99E+00	8.70E-10	Up	1.51E-01	7.90E-01		8.03E-02	7.90E-01		1.91E-02	9.47E-01		1.57E-01	3.24E-01		-8.37E-01	8.28E-09		Unigene26267_All//gi|195626278|gb|ACG33969.1|//1.00E-29//density-regulated protein [Zea mays]	Unigene26267_All//1.00E-28//AT5G11900| eukaryotic translation initiation factor SUI1 family protein	Unigene26267_All//0.00E+00//gi|164294124|gb|ES820649.1|ES820649			GO:0006412//GO:0008135	nr +
Unigene26269_All	1213	18.55	20.59	19.40	18.19	32.56	18.84	12.13	2.96	6.83	1.51E-01	2.11E-01		6.51E-02	6.32E-01		8.40E-01	1.97E-25		5.04E-02	7.11E-01		-2.03E+00	4.64E-38	Down	-8.28E-01	1.58E-10		Unigene26269_All//gi|77403837|dbj|BAE46407.1|//6.00E-50//cytochrome b561 [Citrullus lanatus]	Unigene26269_All//2.00E-40//AT1G26100| cytochrome B561 family protein	Unigene26269_All//0.00E+00//ES822973			GO:0031224	nr +
Unigene26271_All	601	23.68	21.08	20.29	44.59	32.54	40.58	29.20	20.17	13.79	-1.68E-01	3.06E-01		-2.23E-01	1.79E-01		-4.54E-01	2.47E-06		-1.36E-01	2.63E-01		-5.34E-01	5.76E-06		-1.08E+00	7.42E-19	Down	Unigene26271_All//gi|115465821|ref|NP_001056510.1|//3.00E-44//Os03g0594900 [Oryza sativa Japonica Group] >gi|113580061|dbj|BAF18424.1|Os05g0594900 [Oryza sativa Japonica Group]	Unigene26271_All//6.00E-34//AT1G65700| small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative	Unigene26271_All//0.00E+00//gi|109871616|gb|DW500592.1|DW500592		ko03040|Spliceosome//ko03018|RNA degradation	GO:0030529//GO:0043231	nr +
Unigene26273_All	1678	15.93	7.82	9.08	8.85	8.58	10.36	2.92	1.82	3.80	-1.03E+00	1.07E-20	Down	-8.12E-01	1.37E-13		-4.45E-02	8.22E-01		2.28E-01	1.16E-01		-6.85E-01	4.56E-03		3.78E-01	6.74E-02		Unigene26273_All//gi|297844480|ref|XP_002890121.1|//1.00E-110//prephenate dehydrogenase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335963|gb|EFH66380.1|prephenate dehydrogenase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26273_All//3.00E-123//AT1G15710| prephenate dehydrogenase family protein	Unigene26273_All//0.00E+00//ES799906			GO:0003824//GO:0008152	nr -
Unigene26275_All	670	12.57	54.30	9.78	8.48	6.27	11.80	22.65	34.87	126.53	2.11E+00	2.18E-79	Up	-3.63E-01	9.03E-02		-4.35E-01	7.84E-02		4.77E-01	2.29E-02		6.22E-01	7.70E-10		2.48E+00	1.12E-280	Up			Unigene26275_All//0.00E+00//TC178853				
Unigene26276_All	1716	1.10	3.87	1.09	2.18	3.19	4.18	10.23	6.65	24.26	1.82E+00	1.89E-12	Up	-1.52E-02	9.98E-01		5.51E-01	2.84E-02		9.43E-01	1.32E-05		-6.21E-01	1.43E-07		1.25E+00	7.26E-54	Up	Unigene26276_All//gi|42569649|ref|NP_565817.2|//0.00E+00//glycogenin glucosyltransferase (glycogenin)-related [Arabidopsis thaliana]	Unigene26276_All//0.00E+00//AT2G35710| glycogenin glucosyltransferase (glycogenin)-related	Unigene26276_All//0.00E+00//TC151370			GO:0005975//GO:0016757//GO:0031410	nr +
Unigene26277_All	1578	5.90	2.47	3.81	11.30	17.59	33.03	3.70	2.44	1.82	-1.26E+00	2.37E-10	Down	-6.30E-01	1.27E-03		6.38E-01	2.45E-11		1.55E+00	1.03E-79	Up	-6.02E-01	6.03E-03		-1.02E+00	2.38E-06	Down	Unigene26277_All//gi|109946617|gb|ABG48487.1|//5.00E-37//At4g00770 [Arabidopsis thaliana]	Unigene26277_All//2.00E-18//AT4G00770| unknown protein	Unigene26277_All//0.00E+00//gi|164281687|gb|ES815281.1|ES815281				nr -
Unigene26278_All	1822	7.15	5.06	4.35	14.33	11.51	15.94	14.36	6.33	10.36	-4.99E-01	1.40E-03		-7.15E-01	9.67E-06		-3.16E-01	1.91E-03		1.54E-01	1.77E-01		-1.18E+00	7.73E-31	Down	-4.71E-01	3.62E-07		Unigene26278_All//gi|297827085|ref|XP_002881425.1|//0.00E+00//attim44-2 [Arabidopsis lyrata subsp. lyrata] >gi|297337264|gb|EFH57684.1|attim44-2 [Arabidopsis lyrata subsp. lyrata]	Unigene26278_All//0.00E+00//AT2G36070| ATTIM44-2; protein-transmembrane transporting ATPase	Unigene26278_All//0.00E+00//TC129716			GO:0005743//GO:0006605//GO:0008320//GO:0042626	nr +
Unigene2628_All	1511	11.08	6.14	9.34	11.57	8.87	9.80	10.10	58.56	8.62	-8.53E-01	6.43E-10		-2.47E-01	9.86E-02		-3.84E-01	2.29E-03		-2.39E-01	9.20E-02		2.54E+00	7.15E-295	Up	-2.29E-01	7.98E-02		Unigene2628_All//gi|18405635|ref|NP_566831.1|//6.00E-79//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|13937165|gb|AAK50076.1|AF37293 6_1 AT3g28050/MMG15_6 [Arabidopsis thaliana] >gi|22137010|gb|AAM91350.1|At3g28050/MMG15_6 [Arabidopsis thaliana]	Unigene2628_All//8.00E-68//AT3G28050| nodulin MtN21 family protein	Unigene2628_All//0.00E+00//gi|164299079|gb|ES806034.1|ES806034				nr -
Unigene26282_All	978	3.96	8.19	4.52	3.72	3.91	3.60	5.23	4.66	3.71	1.05E+00	6.30E-07	Up	1.91E-01	5.57E-01		7.19E-02	8.39E-01		-4.58E-02	9.07E-01		-1.67E-01	5.44E-01		-4.97E-01	3.03E-02				Unigene26282_All//6.00E-21//DT463962				
Unigene26283_All	471	11.44	6.24	2.60	8.14	6.87	11.89	25.13	12.60	8.12	-8.75E-01	6.85E-04		-2.14E+00	5.43E-12	Down	-2.45E-01	4.78E-01		5.46E-01	3.23E-02		-9.96E-01	4.16E-11		-1.63E+00	1.17E-23	Down	Unigene26283_All//gi|12802327|gb|AK07827.1|AF297643_1/2.00E-25//mitochondrial processing peptidase beta subunit [Cucumis melo]	Unigene26283_All//2.00E-22//AT3G02090| mitochondrial processing peptidase beta subunit, putative	Unigene26283_All//1.00E-165//CK640557			GO:0004175//GO:0005746//GO:0009536//GO:0019538//GO:0030312//GO:0031980//GO:0046914	nr -
Unigene26284_All	862	29.44	16.99	15.63	38.08	31.72	29.86	79.12	41.75	37.44	-7.93E-01	5.14E-13		-9.13E-01	1.17E-15		-2.64E-01	3.76E-03		-3.51E-01	1.44E-04		-9.22E-01	5.97E-53		-1.08E+00	2.05E-70	Down	Unigene26284_All//gi|12802327|gb|AK07827.1|AF297643_1/9.00E-75//mitochondrial processing peptidase beta subunit [Cucumis melo]	Unigene26284_All//1.00E-69//AT3G02090| mitochondrial processing peptidase beta subunit, putative	Unigene26284_All//0.00E+00//TC148340			GO:0004175//GO:0005746//GO:0009536//GO:0019538//GO:0030312//GO:0031980//GO:0046914	nr +
Unigene26285_All	1096	15.75	44.47	31.09	7.18	12.22	14.92	2.55	4.84	4.36	1.50E+00	3.04E-66	Up	9.81E-01	1.95E-23		7.67E-01	1.05E-07		1.05E+00	3.09E-14	Up	9.28E-01	6.65E-05		7.77E-01	1.14E-03		Unigene26285_All//gi|115442435|ref|NP_001045497.1|//4.00E-57//Os01g0965900 [Oryza sativa Japonica Group] >gi|113535028|dbj|BAF07411.1|Os01g0965900 [Oryza sativa Japonica Group]	Unigene26285_All//6.00E-62//AT5G04830| unknown protein	Unigene26285_All//0.00E+00//gi|54117572|gb|CO493081.1|CO493081				nr -
Unigene26286_All	258	0.00	0.00	0.00	2.32	1.07	0.35	1.97	0.00	0.00	null	null		null	null		-1.12E+00	2.26E-01		-2.73E+00	1.74E-02		-1.09E+01	8.89E-04	Down	-1.09E+01	5.54E-04	Down							ESTscan +
Unigene26287_All	1269	3.55	0.00	0.50	3.89	1.87	1.00	2.50	0.13	0.38	-1.18E+01	5.12E-26	Down	-2.82E+00	1.15E-13	Down	-1.05E+00	2.92E-05	Down	-1.96E+00	3.78E-11	Down	-4.25E+00	1.79E-17	Down	-2.73E+00	1.44E-12	Down	Unigene26287_All//gi|115453985|ref|NP_001050593.1|//2.00E-32//Os03g0594700 [Oryza sativa Japonica Group] >gi|108709633|gb|ABF97428.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108709634|gb|ABF97429.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549064|dbj|BAF12507.1|Os03g0594700 [Oryza sativa Japonica Group]	Unigene26287_All//1.00E-48//AT3G56870| unknown protein	Unigene26287_All//2.00E-12//TC134831				nr +
Unigene26289_All	1419	1.73	1.96	0.60	7.30	7.26	6.37	22.91	17.50	8.79	1.80E-01	6.19E-01		-1.53E+00	5.92E-04	Down	-9.10E-03	9.59E-01		-1.98E-01	3.31E-01		-3.89E-01	3.74E-06		-1.38E+00	6.91E-50	Down	Unigene26289_All//gi|224079069|ref|XP_002305737.1|//1.00E-174//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222848701|gb|EEE86248.1|nucleobase ascorbate transporter [Populus trichocarpa]	Unigene26289_All//4.00E-166//AT2G34190| xanthine/uracil permease family protein	Unigene26289_All//0.00E+00//TC165903				nr +
Unigene2629_All	620	0.51	5.88	0.94	1.04	1.22	2.77	15.82	36.07	36.56	3.54E+00	2.96E-14	Up	9.00E-01	3.77E-01		2.26E-01	8.32E-01		1.41E+00	6.85E-03		1.19E+00	1.16E-26	Up	1.21E+00	2.33E-28	Up			Unigene2629_All//0.00E+00//TC147961				
Unigene26290_All	953	29.81	18.66	28.39	41.09	34.80	32.51	26.62	16.84	12.29	-6.76E-01	3.86E-11		-7.07E-02	5.80E-01		-2.40E-01	3.94E-03		-3.38E-01	5.41E-05		-6.61E-01	1.02E-11		-1.12E+00	3.82E-28	Down	Unigene26290_All//gi|240255892|ref|NP_193328.4|//6.00E-42//microtubule motor [Arabidopsis thaliana] >gi|28466885|gb|AAO44005L.1|At4g15930 [Arabidopsis thaliana]	Unigene26290_All//3.00E-43//AT4G15930| microtubule motor	Unigene26290_All//0.00E+00//TC158226			GO:0003774//GO:0009987//GO:0015630//GO:0042995	nr +
Unigene26293_All	1362	59.70	27.90	32.33	94.95	71.30	73.65	30.61	22.80	13.75	-1.10E+00	1.87E-68	Down	-8.85E-01	1.98E-46		-4.13E-01	4.58E-24		-3.67E-01	2.62E-17		-4.25E-01	7.22E-09		-1.15E+00	2.83E-48	Down	Unigene26293_All//gi|297809003|ref|XP_002872535.1|//1.00E-122//HpcH/HpaI aldolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318372|gb|EFH48794.1|HpcH/HpaI aldolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26293_All//4.00E-116//AT4G10750| HpcH/HpaI aldolase family protein	Unigene26293_All//0.00E+00//TC145595		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0009755//GO:0016829//GO:0043231//GO:0044237	nr -
Unigene26294_All	2168	23.12	16.38	17.46	15.12	15.47	13.19	10.59	5.03	5.73	-4.97E-01	2.70E-11		-4.05E-01	1.28E-07		3.32E-02	8.11E-01		-1.97E-01	4.83E-02		-1.07E+00	2.25E-23	Down	-8.85E-01	1.00E-17		Unigene26294_All//gi|22330580|ref|NP_565032.2|//0.00E+00//deoxynucleoside kinase family [Arabidopsis thaliana] >gi|63003832|gb|AAY25445.1|At1g72040 [Arabidopsis thaliana]	Unigene26294_All//0.00E+00//AT1G72040| deoxynucleoside kinase family	Unigene26294_All//0.00E+00//TC153222		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism	GO:0016301//GO:0032559//GO:0034641//GO:0043231	nr -
Unigene26298_All	1448	0.00	1.85	0.29	0.10	0.10	0.56	2.34	9.27	22.23	1.09E+01	2.81E-15	Up	8.20E+00	1.38E-02		-1.18E-01	9.11E-01		2.44E+00	8.58E-03		1.99E+00	1.08E-33	Up	3.25E+00	1.29E-141	Up	Unigene26298_All//gi|145822092|gb|AAK69402.1|AF274565_1 immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] >gi|145822092|gb|AAK69402.1|AF274565_1 immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum]	Unigene26298_All//5.00E-80//AT5G37490| U-box domain-containing protein			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene26299_All	2088	5.51	1.80	1.30	12.36	12.12	6.58	14.70	5.72	6.26	-1.62E+00	3.98E-18	Down	-2.08E+00	2.96E-24	Down	-2.79E-02	8.18E-01		-9.10E-01	1.12E-17		-1.36E+00	1.08E-44	Down	-1.23E+00	1.44E-39	Down	Unigene26299_All//gi|224074645|ref|XP_002304405.1|//0.00E+00//condensin complex components subunit [Populus trichocarpa] >gi|222841837|gb|EEE79384.1|condensin complex components subunit [Populus trichocarpa]	Unigene26299_All//0.00E+00//AT5G62410| SMC2 (STRUCTURAL MAINTENANCE OF CHROMOSOMES 2); transporter	Unigene26299_All//0.00E+00//TC145640			GO:0000793//GO:0006996//GO:0032559	nr -
Unigene263_All	728	2.16	2.51	2.05	4.24	3.97	3.85	2.85	0.57	2.79	2.17E-01	6.34E-01		-7.41E-02	8.92E-01		-9.45E-02	8.26E-01		-1.41E-01	7.01E-01		-2.31E+00	7.13E-07	Down	-2.81E-02	9.60E-01		Unigene263_All//2.00E-96//AT1G09010| glycoside hydrolase family 2 protein	Unigene263_All//0.00E+00//gi|48816867|gb|CO118180.1|CO118180				nr -
Unigene2630_All	639	8.68	86.11	22.92	44.12	22.63	55.98	83.37	204.47	288.78	3.31E+00	8.16E-197	Up	1.40E+00	7.08E-18	Up	-9.63E-01	7.88E-24		3.43E-01	1.00E-04		1.29E+00	1.08E-173	Up	1.79E+00	0.00E+00	Up	Unigene2630_All//gi|223029869|gb|ACR36116.1|//7.00E-22//protease inhibitor/seed storage/lipid transfer protein family protein [Tamarix hispida]	Unigene2630_All//9.00E-17//AT1G62790| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene2630_All//0.00E+00//TC147961				nr -
Unigene26301_All	1332	41.48	19.40	29.94	24.16	24.09	33.30	13.90	9.57	10.86	-1.10E+00	1.16E-46	Down	-4.70E-01	9.23E-11		-3.90E-03	9.67E-01		4.63E-01	2.13E-09		-5.39E-01	2.41E-06		-3.57E-01	1.51E-03		Unigene26301_All//gi|2501578|sp|Q39963.1|PDX1_HEVBR//1.00E-161//RecName: Full=Probable pyridoxal biosynthesis protein PDX1; AltName: Full=Ethylene-inducible protein HEVER >gi|1209317|gb|AAA91063.1|ethylene-inducible protein [Hevea brasiliensis]	Unigene26301_All//2.00E-139//AT5G01410| HSR4 (HEAT-ACCED SUGAR RESPONSE 4); protein heterodimerization/ protein homodimerization	Unigene26301_All//0.00E+00//TC154075		ko00750|Vitamin B6 metabolism		nr +
Unigene26303_All	712	14.04	67.25	30.29	50.02	45.32	45.16	27.55	32.99	31.84	2.26E+00	1.25E-113	Up	1.11E+00	2.84E-18	Up	-1.43E-01	1.47E-01		-1.48E-01	1.41E-01		2.60E-01	1.26E-02		2.09E-01	4.72E-02		Unigene26303_All//gi|15241722|ref|NP_201021.1|//4.00E-30//peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana] >gi|45518349|gb|AAS99656.1|At5g62150 [Arabidopsis thaliana] >gi|48310309|gb|AAT41795.1|At5g62150 [Arabidopsis thaliana]	Unigene26303_All//2.00E-31//AT5G62150| peptidoglycan-binding LysM domain-containing protein	Unigene26303_All//0.00E+00//TC153478			GO:0009056//GO:0044464	nr +
Unigene26304_All	771	42.07	16.50	29.42	30.95	33.18	26.77	20.13	20.22	11.68	-1.35E+00	3.18E-38	Down	-5.16E-01	1.07E-07		1.01E-01	4.45E-01		-2.09E-01	8.12E-02		6.80E-03	9.98E-01		-7.85E-01	3.64E-10		Unigene26304_All//gi|48958503|gb|AAT47804.1|//8.00E-64//At2g41945 [Arabidopsis thaliana] >gi|51536546|gb|AAU05511.1|At2g41945 [Arabidopsis thaliana]	Unigene26304_All//7.00E-52//AT2G41945| unknown protein	Unigene26304_All//0.00E+00//gi|21099173|gb|BQ111486.1|BQ111486			GO:0044464	nr +

Unigene26306_All	1358	52.17	193.35	77.99	219.80	232.68	652.21	94.71	68.48	85.57	1.89E+00	0.00E+00	Up	5.80E-01	3.78E-29		8.22E-02	4.14E-03		1.57E+00	0.00E+00	Up	-4.68E-01	1.96E-30		-1.46E-01	3.14E-04		Unigene26306_All//gi|15237656|ref|NP_201231.1|//1.00E-126//EXL2 (EXORDIUM LIKE 2) [Arabidopsis thaliana] >gi|14190477|gb|AAK55719.1|AF380638_1 AT5g64260/MSJ1_10 [Arabidopsis thaliana] >gi|9759402|dbj|BAB09857.1| phi-1-like protein [Arabidopsis thaliana] >gi|16323270|gb|AAL15369.1|AT5g64260/MSJ1_10 [Arabidopsis thaliana] >gi|21593241|gb|AAM65190.1| phi-1-like protein [Arabidopsis thaliana]	Unigene26306_All//2.00E-127//AT5G64260| EXL2 (EXORDIUM LIKE 2)	Unigene26306_All//0.00E+00//TC159697				nr +
Unigene2631_All	478	0.88	3.07	0.67	2.50	0.94	3.02	3.01	8.39	15.75	1.81E+00	2.45E-03		-3.90E-01	7.17E-01		-1.42E+00	1.82E-02		2.74E-01	6.49E-01		1.48E+00	2.77E-07	Up	2.39E+00	1.65E-24	Up	Unigene2631_All//gi|6630451|gb|AAF19539.1|AC007190_7//2.00E-08//F23N19.16 [Arabidopsis thaliana]	Unigene2631_All//4.00E-09//AT1G62790| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene2631_All//3.00E-76//DN827814				nr +
Unigene26312_All	1137	6.86	7.04	9.32	6.40	9.12	6.51	4.09	4.71	1.65	3.83E-02	8.64E-01		4.43E-01	1.62E-02		5.11E-01	2.72E-03		2.63E-02	9.35E-01		2.02E-01	4.29E-01		-1.31E+00	2.39E-07	Down	Unigene26312_All//gi|169730526|gb|ACA64829.1|//2.00E-24//SKIP interacting protein 9 [Oryza sativa]	Unigene26312_All//1.00E-10//AT1G50710| unknown protein	Unigene26312_All//9.00E-159//gi|73864261|gb|DT467000.1|DT467000				nr -
Unigene26314_All	1601	3.04	4.56	2.99	8.93	6.75	4.20	1.72	0.78	0.70	5.85E-01	6.98E-03		-2.19E-02	9.58E-01		-4.03E-01	4.38E-03		-1.09E+00	2.71E-13	Down	-1.13E+00	9.60E-04	Down	-1.30E+00	1.22E-04	Down	Unigene26314_All//gi|297727877|ref|NP_001176302.1|//1.00E-06//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1|Os11g0106066 [Oryza sativa Japonica Group]	Unigene26314_All//7.00E-05//AT3G09510| nucleic acid binding	Unigene26314_All//0.00E+00//TC175381				nr +
Unigene26315_All	1113	0.75	0.32	0.57	1.34	0.74	0.28	0.46	0.53	0.43	-1.24E+00	1.15E-01		-3.90E-01	6.41E-01		-8.55E-01	1.02E-01		-2.24E+00	2.25E-04	Down	2.06E-01	8.00E-01		-8.61E-02	9.30E-01		Unigene26315_All//gi|33465891|gb|AAQ19327.1|//7.00E-09//bZIP-like protein [Oryza sativa Japonica Group]		Unigene26315_All//0.00E+00//TC175381				nr +
Unigene26316_All	1213	5.39	9.02	2.55	5.75	5.20	5.81	5.93	5.58	5.19	7.43E-01	1.68E-05		-1.08E+00	8.82E-06	Down	-1.46E-01	5.73E-01		1.47E-02	9.48E-01		-8.62E-02	6.99E-01		-1.91E-01	3.52E-01		Unigene26316_All//gi|18411974|ref|NP_567112.1|//3.00E-97//SKIP4 (SKP1 INTERACTING PARTNER 4) [Arabidopsis thaliana] >gi|75182826|sp|Q9MZC9.1|SKIP4_ARATH RecName: Full=F-box/kelch-repeat protein SKIP4; AltName: Full=SKP1-interacting partner 4 >gi|94442421|gb|ABF18998.1|At3g61350 [Arabidopsis thaliana]	Unigene26316_All//2.00E-98//AT3G61350| SKIP4 (SKP1 INTERACTING PARTNER 4)	Unigene26316_All//0.00E+00//TC152776		GO:0006950		nr -
Unigene26318_All	1675	40.58	32.34	38.47	13.06	17.10	13.67	7.90	3.72	2.85	-3.27E-01	2.31E-07		-7.70E-02	3.20E-01		3.90E-01	4.22E-05		6.64E-02	6.40E-01		-1.09E+00	4.30E-14	Down	-1.47E+00	9.81E-23	Down	Unigene26318_All//gi|297833984|ref|NP_002884874.1|//1.00E-161//prenyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297330714|gb|EFH61133.1|prenyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene26318_All//1.00E-152//AT3G11945| homogentisate farnesyltransferase/ homogentisate geranylgeranyltransferase/ homogentisate solanesyltransferase	Unigene26318_All//0.00E+00//TC151952		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene26321_All	2028	0.57	0.22	0.32	24.69	19.66	9.80	0.88	1.50	0.51	-1.34E+00	4.03E-02		-8.49E-01	2.06E-01		-3.28E-01	2.01E-06		-1.33E+00	2.88E-62	Down	7.81E-01	1.42E-02		-7.78E-01	6.39E-02		Unigene26321_All//gi|115436122|ref|NP_001042819.1|//1.00E-170//Os01g0300900 [Oryza sativa Japonica Group] >gi|113532350|dbj|BAF04733.1|Os01g0300900 [Oryza sativa Japonica Group]	Unigene26321_All//1.00E-45//AT1G18610| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Galactose oxidase/kelch, beta-propeller (InterPro:IPR011043), Kelch repeat type 1 (InterPro:IPR006652), Kelch repeat type 2 (InterPro:IPR011498), Kelch-type beta propeller (InterPro:IPR015915); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G74150.1); Has 8761 Blast hits to 4412 proteins in 271 species: Archae - 12; Bacteria - 304; Metazoa - 4209; Fungi - 851; Plants - 1246; Viruses - 11; Other Eukaryotes - 2128 (source: NCBI BLink).	Unigene26321_All//0.00E+00//TC175999		ko04712|Circadian rhythm - plant		nr +
Unigene26322_All	1738	6.08	1.69	5.30	15.22	11.00	10.03	24.94	4.79	10.70	-1.85E+00	6.01E-20	Down	-1.98E-01	3.25E-01		-4.69E-01	1.34E-06		-6.02E-01	4.15E-09		-2.38E+00	7.64E-135	Down	-1.22E+00	1.19E-54	Down	Unigene26322_All//gi|115447469|ref|NP_001047514.1|//0.00E+00//Os02g0634700 [Oryza sativa Japonica Group] >gi|113537045|dbj|BAF09428.1|Os02g0634700 [Oryza sativa Japonica Group]	Unigene26322_All//0.00E+00//AT5G23210| SCPL34; serine-type carboxypeptidase	Unigene26322_All//2.00E-12//TC170768			GO:0004180//GO:0005618//GO:0019538//GO:0031410//GO:0043231	nr -
Unigene26323_All	1317	2.07	0.58	0.53	4.61	3.01	1.95	9.05	2.16	2.57	-1.84E+00	1.16E-05	Down	-1.97E+00	8.44E-06	Down	-6.18E-01	6.33E-03		-1.24E+00	2.90E-07	Down	-2.07E+00	1.16E-31	Down	-1.82E+00	1.36E-27	Down	Unigene26323_All//gi|15239147|ref|NP_196170.1|//6.00E-71//protein kinase-related [Arabidopsis thaliana] >gi|50253522|gb|AAT71963.1|At5g05510 [Arabidopsis thaliana] >gi|56381969|gb|AAV85703.1|At5g05510 [Arabidopsis thaliana]	Unigene26323_All//1.00E-68//AT5G05510| protein kinase-related					nr +
Unigene26324_All	1583	15.44	9.60	11.34	21.43	17.45	17.97	19.58	10.96	8.98	-6.85E-01	6.67E-10		-4.45E-01	9.88E-05		-2.97E-01	7.13E-04		-2.54E-01	6.93E-03		-8.37E-01	6.24E-21		-1.12E+00	1.31E-34	Down	Unigene26324_All//gi|87241169|gb|AB033027.1|//1.00E-146//Dual specificity protein phosphatase [Medicago truncatula]	Unigene26324_All//3.00E-38//AT4G18593| dual specificity protein phosphatase-related	Unigene26324_All//0.00E+00//ES792269			GO:0016787	nr -
Unigene26328_All	861	5.59	4.71	1.73	9.78	7.12	5.35	14.49	9.32	7.68	-2.48E-01	3.91E-01		-1.69E+00	4.75E-08	Down	-4.58E-01	1.73E-02		-8.70E-01	8.58E-06		-6.36E-01	7.80E-06		-9.15E-01	1.43E-10		Unigene26328_All//gi|75218951|sp|O04235.1|SSRP1_VICFA//1.00E-83//RecName: Full=FACT complex subunit SSRP1; AltName: Full=Facilitates chromatin transcription complex subunit SSRP1; AltName: Full=Recombination signal sequence recognition protein 1 >gi|2104679|emb|CAA66480.1|transcription factor [Vicia faba var. minor]	Unigene26328_All//1.00E-44//AT3G28730| ATHMG (ARABIDOPSIS THALIANA HIGH MOBILITY GROUP); transcription factor	Unigene26328_All//0.00E+00//gi|11208265|gb|BF277195.1|BF277195			GO:0000790//GO:0003006//GO:0003676//GO:0006259//GO:0008023//GO:0010468//GO:0016628//GO:0033554	nr +
Unigene26329_All	1292	1.05	1.41	1.73	5.78	2.43	2.55	8.90	4.59	2.71	4.23E-01	3.85E-01		7.17E-01	1.11E-01		-1.25E+00	5.38E-10	Down	-1.18E+00	3.51E-08	Down	-9.54E-01	3.99E-10		-1.71E+00	1.21E-24	Down	Unigene26329_All//gi|219879368|gb|ACL51016.1|//1.00E-65//squamosa promoter-binding protein [Citrus trifoliata]	Unigene26329_All//3.00E-45//AT5G50570| squamosa promoter-binding protein, putative	Unigene26329_All//0.00E+00//gi|78330475|gb|DT550749.1|DT550749	SBP			nr +
Unigene2633_All	2028	16.43	9.07	6.20	20.44	13.52	9.20	6.84	1.01	2.20	-8.58E-01	3.76E-19		-1.41E+00	3.32E-40	Down	-5.97E-01	2.73E-15		-1.15E+00	4.20E-41	Down	-2.76E+00	2.18E-51	Down	-1.64E+00	1.06E-27	Down	Unigene2633_All//gi|82592920|sp|P92990.2|JP650_ARATH//0.00E+00//RecName: Full=Probable polygalacturonase non-catalytic subunit JP650; AltName: Full=Aromatic-rich glycoprotein JP650; Flags: Precursor >gi|3176680|gb|AAC18803.1|Identical to polygalacuronase isoenzyme 1 beta subunit homolog mRNA gb|U83373. EST gb|AA404828 comes from this gene [Arabidopsis thaliana]	Unigene2633_All//0.00E+00//AT1G67070| BURP domain-containing protein / polygalacturonase, putative	Unigene2633_All//0.00E+00//TC138593				nr +
Unigene26330_All	2182	1.15	0.07	0.15	12.12	7.29	7.78	11.61	4.35	6.17	-4.05E+00	4.22E-11	Down	-2.97E+00	2.98E-08	Down	-7.34E-01	3.76E-14		-6.39E-01	4.41E-10		-1.42E+00	2.69E-39	Down	-9.11E-01	2.15E-20		Unigene26330_All//gi|5545339|dbj|BAA82556.1|//0.00E+00//lectin-like protein kinase [Populus nigra]	Unigene26330_All//2.00E-87//AT5G55830| lectin protein kinase, putative	Unigene26330_All//3.00E-15//TC151676			GO:0004713//GO:0006464//GO:0030246//GO:0032559	nr +
Unigene26331_All	852	42.93	32.17	18.23	53.79	39.65	88.10	60.99	67.80	55.22	-4.16E-01	2.46E-06		-1.23E+00	4.46E-36	Down	-4.40E-01	7.31E-10		7.12E-01	7.15E-33		1.53E-01	2.05E-02		-1.43E-01	3.50E-02		Unigene26331_All//gi|4589960|gb|AAD26478.1|//2.00E-63//expressed protein [Arabidopsis thaliana]	Unigene26331_All//3.00E-45//AT2G31410| unknown protein	Unigene26331_All//2.00E-180//gi|21094856|gb|BQ407169.1|BQ407169				nr -
Unigene26332_All	1115	1.78	1.23	2.87	4.42	3.21	2.31	3.72	2.10	1.18	-5.39E-01	2.35E-01		6.84E-01	5.97E-02		-4.62E-01	8.43E-02		-9.38E-01	4.34E-04		-8.24E-01	1.97E-03		-1.66E+00	5.14E-09	Down	Unigene26332_All//gi|18412499|ref|NP_567262.1|//1.00E-115//PUX4; protein binding [Arabidopsis thaliana] >gi|45862328|gb|AAS78926.1| CDC48-interacting UBX-domain protein [Arabidopsis thaliana]	Unigene26332_All//8.00E-98//AT4G04210| PUX4; protein binding	Unigene26332_All//0.00E+00//TC136320				nr -
Unigene26335_All	1551	4.89	21.10	18.16	3.37	2.22	3.00	0.33	0.59	0.26	2.11E+00	2.04E-71	Up	1.89E+00	4.76E-52	Up	-6.03E-01	1.53E-02		-1.69E-01	5.92E-01		8.58E-01	1.95E-01		-3.49E-01	6.73E-01		Unigene26335_All//gi|158706505|sp|Q6DYE5.2|U496K_ARATH//1.00E-82//RecName: Full=UPF0496 protein At1g20180 >gi|8778981|gb|AAF79896.1|AC022472_5 Contains similarity to At14a protein from Arabidopsis thaliana gi|4589123	Unigene26335_All//1.00E-73//AT1G20180| unknown protein	Unigene26335_All//2.00E-49//DN817633				nr -
Unigene26336_All	887	10.20	11.88	14.05	1.68	2.02	2.29	3.58	2.83	0.76	2.20E-01	2.38E-01		4.61E-01	5.87E-03		2.61E-01	6.21E-01		4.44E-01	3.75E-01		-3.39E-01	3.12E-01		-2.23E+00	4.13E-10	Down	Unigene26336_All//gi|18417112|ref|NP_567795.1|//1.00E-86//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|15081771|gb|AAK82540.1|AT4g28030/T13J8_140 [Arabidopsis thaliana] >gi|22137098|gb|AAM91394.1|At4g28030/T13J8_140 [Arabidopsis thaliana]	Unigene26336_All//7.00E-88//AT4G28030| GCN5-related N-acetyltransferase (GNAT) family protein				GO:0009536//GO:0016407	nr +
Unigene26337_All	295	20.93	5.32	13.54	28.03	24.05	19.90	18.20	20.26	19.85	-1.97E+00	5.30E-13	Down	-6.28E-01	1.14E-02		-2.21E-01	3.12E-01		-4.94E-01	1.43E-02		1.55E-01	5.44E-01		1.25E-01	5.97E-01		Unigene26337_All//gi|224097020|ref|XP_002310813.1|//5.00E-28//f-box family protein [Populus trichocarpa] >gi|222853716|gb|EEE91263.1| f-box family protein [Populus trichocarpa]	Unigene26337_All//6.00E-19//AT2G18280| AtTLP2 (TUBBY LIKE PROTEIN 2); phosphoric diester hydrolase/ transcription factor	Unigene26337_All//1.00E-133//ES842902	TUB		GO:0010468//GO:0042578	nr -

Unigene26338_All	651	11.98	5.29	10.22	13.39	9.47	9.64	12.79	12.01	13.52	-1.18E+00	4.95E-08	Down	-2.28E-01	3.36E-01		-5.00E-01	7.16E-03		-4.74E-01	1.58E-02		-9.18E-02	6.46E-01		8.00E-02	6.70E-01		Unigene26338_All//gi|224097020|ref|XP_002310813.1|//2.00E-27//f-box family protein [Populus trichocarpa] >gi|222853716|gb|EEE91263.1| f-box family protein [Populus trichocarpa]	Unigene26338_All//2.00E-18//AT2G18280| AtTLP2 (TUBBY LIKE PROTEIN 2); phosphoric diester hydrolase/ transcription factor	Unigene26338_All//0.00E+00//TC163351	TUB		GO:0010468//GO:0042578	nr +
Unigene26339_All	1177	29.65	44.94	52.44	19.85	18.49	13.89	1.26	0.96	0.27	6.00E-01	2.36E-16		8.23E-01	2.43E-31		-1.02E-01	4.56E-01		-5.15E-01	2.65E-06		-3.91E-01	4.42E-01		-2.22E+00	4.14E-05	Down	Unigene26339_All//gi|124360931|gb|ABN08903.1|//2.00E-69//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene26339_All//4.00E-37//AT2G20180| PIL5 (PHYTOCHROME INTERACTING FACTOR 3-LIKE 5); DNA binding / phytochrome binding / transcription factor	Unigene26339_All//0.00E+00//TC170683	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0001071//GO:0003676//GO:0005515//GO:0006779//GO:0009630//GO:0009640//GO:0010017//GO:0010029//GO:0010468//GO:0010476//GO:0043231	nr +
Unigene26340_All	1271	3.54	3.19	2.89	2.90	3.12	5.86	15.90	23.41	21.85	-1.51E-01	6.10E-01		-2.92E-01	3.59E-01		1.03E-01	8.10E-01		1.02E+00	1.86E-06	Up	5.58E-01	2.82E-10		4.58E-01	3.34E-07		Unigene26340_All//gi|21536609|gb|AM60941.1|//9.00E-57//protein kinase-like protein [Arabidopsis thaliana] >gi|51968380|dbj|BAD42882.1| protein kinase - like protein [Arabidopsis thaliana]	Unigene26340_All//4.00E-58//AT3G57750| protein kinase, putative	Unigene26340_All//0.00E+00//TC137731			GO:0016301	nr -
Unigene26344_All	1521	18.06	8.73	17.08	17.42	12.88	5.58	18.29	22.01	5.29	-1.05E+00	5.58E-22	Down	-8.00E-02	5.24E-01		-4.36E-01	7.65E-06		-1.64E+00	3.85E-45	Down	2.67E-01	1.60E-03		-1.79E+00	5.33E-62	Down	Unigene26344_All//gi|224112251|ref|XP_002316131.1|//2.00E-45//f-box family protein [Populus trichocarpa] >gi|222865171|gb|EEF02302.1| f-box family protein [Populus trichocarpa]	Unigene26344_All//2.00E-36//AT5G62430| CDF1 (CYCLING DOF FACTOR 1); DNA binding / protein binding / transcription factor	Unigene26344_All//0.00E+00//gi|109856563|gb|DW485542.1|DW485542	C2C2-Dof		GO:0003676//GO:0006350//GO:0009526//GO:0010468//GO:0048506	nr +
Unigene26347_All	1120	14.39	43.66	30.81	24.82	32.01	30.24	82.03	197.71	93.98	1.60E+00	3.03E-73	Up	1.10E+00	1.88E-28	Up	3.67E-01	1.22E-05		2.85E-01	2.13E-03		1.27E+00	3.44E-285	Up	1.96E-01	1.06E-05		Unigene26347_All//gi|34922417|sp|O49809.2|MFPA_BRANA//2.00E-47//RecName: Full=Glyoxysomal fatty acid beta-oxidation multifunctional protein MFP-a; Includes: RecName: Full=Enoyl-CoA hydratase/3-2-trans-enoyl-CoA isomerase/3-hydroxybutyryl-CoA epimerase; Includes: RecName: Full=3-hydroxyacyl-CoA dehydrogenase >gi|2832898|emb|CAA04386.1| Tetrafunctional protein of glyoxysomal fatty acid beta-oxidation [Brassica napus]	Unigene26347_All//9.00E-47//AT3G06860| MFP2 (MULTIFUNCTIONAL PROTEIN 2); 3-hydroxyacyl-CoA dehydrogenase/ enoyl-CoA hydratase	Unigene26347_All//0.00E+00//gi|18099878|gb|BM359132.1|BM359132		ko00592|alpha-Linolenic acid metabolism	GO:0005777//GO:0009062//GO:0016616//GO:0016836//GO:0016856//GO:0016863//GO:0030312//GO:0031981//GO:0048037	nr +
Unigene26349_All	1909	1.21	30.52	0.39	1.30	3.41	2.32	1.35	5.12	6.70	4.66E+00	8.76E-270	Up	-1.63E+00	5.02E-04	Down	1.39E+00	1.48E-09	Up	8.30E-01	3.82E-03		1.92E+00	1.00E-23	Up	2.31E+00	1.67E-39	Up	Unigene26349_All//gi|104294986|gb|ABF72002.1|//1.00E-111//U-box domain-containing protein [Musa acuminata]	Unigene26349_All//5.00E-09//AT1G68940| armadillo/beta-catenin repeat protein-related / U-box domain-containing protein	Unigene26349_All//0.00E+00//gi|164337459|gb|ES829921.1|ES829921			GO:0046872	nr -
Unigene26350_All	1320	36.03	5.22	20.41	3.13	2.71	2.29	0.96	0.25	0.33	-2.79E+00	9.47E-145	Down	-8.20E-01	4.31E-24		-2.07E-01	5.52E-01		-4.50E-01	1.48E-01		-1.92E+00	9.98E-04	Down	-1.53E+00	4.40E-03		Unigene26350_All//gi|124359195|gb|ABN05708.1|//1.00E-136//Short-chain dehydrogenase/reductase SDR [Medicago truncatula]	Unigene26350_All//2.00E-114//AT5G02540| short-chain dehydrogenase/reductase (SDR) family protein	Unigene26350_All//0.00E+00//TC163357		ko00051|Fructose and mannose metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism//ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene26351_All	873	1.74	1.68	2.81	4.11	3.23	1.66	2.03	0.72	0.41	-4.62E-02	9.41E-01		6.91E-01	1.04E-01		-3.45E-01	3.18E-01		-1.31E+00	6.40E-05	Down	-1.50E+00	1.01E-03		-2.31E+00	3.08E-06	Down	Unigene26351_All//gi|145308448|gb|ABF57459.1|//4.00E-77//receptor-like kinase 17 precursor [Solanum chacoense]	Unigene26351_All//3.00E-31//AT5G14210| leucine-rich repeat transmembrane protein kinase, putative	Unigene26351_All//3.00E-173//ES844822			GO:0003824	nr +
Unigene26353_All	1163	6.61	22.57	9.57	15.81	24.46	15.61	10.03	4.46	45.29	1.77E+00	1.42E-45	Up	5.33E-01	2.63E-03		6.30E-01	2.37E-11		-1.78E-02	9.24E-01		-1.17E+00	5.33E-14	Down	2.17E+00	6.74E-149	Up	Unigene26353_All//gi|107738372|gb|ABF83685.1|//4.00E-38//At2g42760 [Arabidopsis thaliana]	Unigene26353_All//2.00E-30//AT2G42760| unknown protein	Unigene26353_All//0.00E+00//TC138694				nr +
Unigene26354_All	1040	6.79	4.14	4.25	14.37	17.65	15.03	11.71	3.05	3.52	-7.14E-01	1.16E-03		-6.76E-01	3.16E-03		2.97E-01	2.17E-02		6.44E-02	6.91E-01		-1.94E+00	9.68E-30	Down	-1.73E+00	2.01E-26	Down	Unigene26354_All//gi|166343833|gb|ABU86659.1|//1.00E-180//beta-tubulin 13 [Gossypium hirsutum]	Unigene26354_All//7.00E-1622//AT1G75780| TUB1; GTP binding / GTPase/ structural molecule	Unigene26354_All//0.00E+00//TC131067		ko04145|Phagosome		nr -
Unigene26355_All	1129	4.17	25.58	3.21	36.62	109.25	29.84	626.79	365.72	157.59	2.62E+00	1.60E-81	Up	-3.79E-01	2.10E-01		1.58E+00	6.35E-213	Up	-2.95E-01	3.19E-04		-7.77E-01	0.00E+00		-1.99E+00	0.00E+00	Down	Unigene26355_All//gi|300793602|tpg|DAA33867.1|//1.00E-141//TPA: TPA_inf: aquaporin TIP1;4 [Gossypium hirsutum]	Unigene26355_All//8.00E-112//AT2G36830| GAMMA-TIP (GAMMA TONOPLAST INTRINSIC PROTEIN); water channel	Unigene26355_All//0.00E+00//TC163572				nr +
Unigene26357_All	1106	151.05	172.30	217.19	305.06	246.84	454.78	34.48	716.16	54.57	1.90E-01	2.73E-07		5.24E-01	1.56E-54		-3.06E-01	2.26E-35		5.76E-01	1.03E-149		4.38E+00	0.00E+00	Up	6.62E-01	1.67E-27		Unigene26357_All//gi|209954731|dbj|BAG80556.1|//1.00E-112//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene26357_All//2.00E-101//AT4G01070| GTZ1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene26357_All//0.00E+00//TC131390			GO:0016757	nr -
Unigene26358_All	1557	14.21	7.68	5.85	7.39	5.48	5.83	9.07	6.93	4.25	-8.88E-01	1.00E-13		-1.28E+00	2.49E-23	Down	-4.30E-01	7.19E-03		-3.42E-01	4.77E-02		-3.89E-01	3.82E-03		-1.09E+00	1.29E-15	Down	Unigene26358_All//gi|18115808|ref|NP_568196.1|//1.00E-166//lipoic acid synthase family protein [Arabidopsis thaliana] >gi|20373023|dbj|BAB91180.1| lipoic acid synthase [Arabidopsis thaliana] >gi|98960967|gb|ABF58967.1| At5g08415 [Arabidopsis thaliana]	Unigene26358_All//2.00E-159//AT5G08415| lipoic acid synthase family protein	Unigene26358_All//0.00E+00//TC131194		ko00785|Lipoic acid metabolism		nr -
Unigene26359_All	1955	2.44	1.89	1.39	9.50	11.10	6.72	5.17	2.12	1.37	-3.64E-01	2.02E-01		-8.10E-01	4.87E-03		2.24E-01	6.97E-02		-5.00E-01	6.44E-05		-1.29E+00	4.47E-14	Down	-1.92E+00	2.63E-25	Down	Unigene26359_All//gi|145361904|ref|NP_850812.2|//1.00E-137//CRN (CORYNE); ATP binding / kinase/ protein kinase [Arabidopsis thaliana] >gi|7529284|emb|CAB86636.1| protein kinase precursor-like [Arabidopsis thaliana]	Unigene26359_All//6.00E-111//AT5G13290| CRN (CORYNE); ATP binding / kinase/ protein kinase	Unigene26359_All//0.00E+00//TC146311			GO:0005488//GO:0009908//GO:0010015//GO:0010073//GO:0016020//GO:0016301	nr +
Unigene26360_All	1640	12.73	5.90	9.06	29.92	20.07	20.98	16.37	21.92	11.73	-1.11E+00	2.04E-18	Down	-4.91E-01	7.95E-05		-5.76E-01	6.18E-17		-5.12E-01	2.30E-12		4.21E-01	1.23E-07		-4.81E-01	1.42E-07		Unigene26360_All//gi|213868273|gb|ACJ54183.1|//1.00E-80//PB1 domain-containing protein [Nicotiana benthamiana]	Unigene26360_All//2.00E-63//AT5G64430| octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	Unigene26360_All//0.00E+00//TC143204				nr +
Unigene26363_All	800	2.68	4.31	5.79	7.66	8.01	4.97	10.94	7.37	5.03	6.84E-01	4.01E-02		1.11E+00	1.78E-04	Up	6.40E-02	8.21E-01		-6.25E-01	8.37E-03		-5.71E-01	1.02E-03		-1.12E+00	2.24E-10	Down	Unigene26363_All//gi|115442129|ref|NP_001045344.1|//7.00E-15//Os01g0939000 [Oryza sativa Japonica Group] >gi|113534875|dbj|BAF07258.1| Os01g0939000 [Oryza sativa Japonica Group]		Unigene26363_All//1.00E-61//gi|164264265|gb|ES811402.1|ES811402			GO:0031410	nr -
Unigene26365_All	1779	9.50	1.68	1.05	10.39	10.01	3.40	14.31	2.35	2.87	-2.50E+00	6.93E-46	Down	-3.18E+00	8.35E-57	Down	-5.39E-02	7.54E-01		-1.61E+00	9.19E-31	Down	-2.61E+00	3.92E-88	Down	-2.32E+00	2.21E-79	Down	Unigene26365_All//gi|27261144|gb|AN87548.1|AF118783_1//0.00E+00//ribonucleotide reductase large subunit B [Glycine max]	Unigene26365_All//0.00E+00//AT2G21790| RNR1 (RIBONUCLEOTIDE REDUCTASE 1); ATP binding / protein binding / ribonucleoside-diphosphate reductase	Unigene26365_All//0.00E+00//TC167224		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism	GO:0006259//GO:0009142//GO:0010038//GO:0016728//GO:0032559//GO:0043234	nr +
Unigene26366_All	1532	8.67	4.10	4.73	29.65	26.14	12.94	13.08	9.66	16.93	-1.08E+00	1.53E-11	Down	-8.76E-01	5.67E-08		-1.82E-01	2.26E-02		-1.20E+00	8.85E-48	Down	-4.38E-01	6.51E-05		3.72E-01	6.79E-05		Unigene26366_All//gi|15222819|ref|NP_175400.1|//1.00E-150//PUB26 (PLANT U-BOX 26); binding / ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75173046|sp|Q9FXA4.1|PUB26_ARATH RecName: Full=U-box domain-containing protein 26; AltName: Full=Plant U-box protein 26 >gi|10120432|gb|AAG13057.1|AC011807_16 Hypothetical protein [Arabidopsis thaliana] >gi|115311483|gb|ABI93922.1| At1g49780 [Arabidopsis thaliana]	Unigene26366_All//4.00E-146//AT1G49780| PUB26 (PLANT U-BOX 26); binding / ubiquitin-protein ligase	Unigene26366_All//0.00E+00//TC168751		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene26370_All	1111	5.51	15.05	6.76	3.95	6.54	8.25	2.32	2.56	5.99	1.45E+00	4.11E-22	Up	2.95E-01	2.11E-01		7.29E-01	4.10E-04		1.06E+00	2.30E-08	Up	1.40E-01	6.95E-01		1.37E+00	1.25E-10	Up	Unigene26370_All//gi|147854975|emb|CAN80266.1|//1.00E-21//hypothetical protein [Vitis vinifera]		Unigene26370_All//0.00E+00//gi|78323949|gb|DT544223.1|DT544223				nr -
Unigene26374_All	1965	0.08	0.10	0.08	0.81	0.33	3.13	4.09	4.83	7.01	3.68E-01	8.16E-01		2.51E-02	1.00E+00		-1.28E+00	1.01E-02		1.95E+00	2.64E-13	Up	2.40E-01	1.85E-01		7.79E-01	5.78E-09		Unigene26374_All//gi|224126509|ref|XP_002329572.1|//1.00E-114//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222870281|gb|EEF07412.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene26374_All//1.00E-86//AT4G17980| anac071 (Arabidopsis NAC domain containing protein 71); transcription factor	Unigene26374_All//0.00E+00//ES796423	NAC		GO:0001071//GO:0005488//GO:0010468//GO:0032501	nr +
Unigene26376_All	1339	1.84	1.17	1.35	2.72	2.55	1.92	3.19	1.62	1.40	-6.47E-01	1.11E-01		-4.42E-01	3.09E-01		-9.31E-02	8.20E-01		-4.98E-01	1.34E-01		-9.74E-01	2.19E-04		-1.19E+00	5.69E-06	Down	Unigene26376_All//gi|115470825|ref|NP_001059011.1|//1.00E-144//Os07g0175100 [Oryza sativa Japonica Group] >gi|113610547|dbj|BAF20925.1| Os07g0175100 [Oryza sativa Japonica Group]	Unigene26376_All//4.00E-151//AT3G63270| unknown protein	Unigene26376_All//0.00E+00//TC169525				nr -
Unigene26377_All	1054	46.17	82.93	22.99	75.67	141.60	74.69	7.86	36.88	5.14	8.45E-01	1.16E-47		-1.01E+00	1.47E-34	Down	9.04E-01	4.02E-108		-1.88E-02	7.93E-01		2.23E+00	2.07E-111	Up	-6.13E-01	4.24E-04		Unigene26377_All//gi|186531069|ref|NP_001119410.1|//3.00E-62//metal ion binding [Arabidopsis thaliana]	Unigene26377_All//2.00E-41//AT5G50740| metal ion binding	Unigene26377_All//1.00E-163//TC147646				nr +
Unigene26378_All	1167	4.44	10.59	6.25	2.86	5.55	7.04	2.28	9.92	10.72	1.26E+00	2.01E-13	Up	4.94E-01	2.98E-02		9.56E-01	1.56E-05		1.30E+00	3.86E-10	Up	2.12E+00	1.23E-31	Up	2.23E+00	4.23E-37	Up	Unigene26378_All//gi|179743220|dbj|BAB79529.1|//2.00E-86//glycerol-3-phosphate acyltransferase [Citrus unshiu]	Unigene26378_All//1.00E-80//AT1G32200| ATS1; glycerol-3-phosphate O-acyltransferase	Unigene26378_All//0.00E+00//CO131582		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0003006//GO:0004497//GO:0006633//GO:0006650//GO:0006996//GO:0008374//GO:0009532//GO:0009725//GO:0016705//GO:0031224//GO:0046471//GO:0046872	nr +
Unigene26379_All	623	6.21	7.73	2.39	1.28	2.60	1.45	2.31	7.38	8.50	3.14E-01	2.72E-01		-1.38E+00	4.46E-05	Down	1.02E+00	5.05E-02		1.81E-01	8.07E-01		1.68E+00	1.05E-09	Up	1.88E+00	3.77E-13	Up	Unigene26379_All//gi|179743220|dbj|BAB79529.1|//6.00E-91//glycerol-3-phosphate acyltransferase [Citrus unshiu]	Unigene26379_All//1.00E-81//AT1G32200| ATS1; glycerol-3-phosphate O-acyltransferase	Unigene26379_All//0.00E+00//CO131582		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0003006//GO:0004497//GO:0006633//GO:0006650//GO:0006996//GO:0008374//GO:0009532//GO:0009725//GO:0016705//GO:0031224//GO:0046471//GO:0046872	nr -
Unigene2638_All	705	0.30	0.43	1.74	2.33	3.37	1.86	0.54	1.96	2.94	5.38E-01	6.71E-01		2.55E+00	8.25E-04	Up	5.32E-01	2.22E-01		-3.28E-01	5.64E-01		1.86E+00	7.81E-04	Up	2.44E+00	1.83E-07	Up	Unigene2638_All//gi|114050551|gb|AB149425.1|//2.00E-14//At1g68585 [Arabidopsis thaliana]	Unigene2638_All//9.00E-16//AT1G68585| unknown protein	Unigene2638_All//0.00E+00//AJ514138				nr +
Unigene26380_All	1323	1.27	0.38	0.00	2.75	1.74	1.19	2.27	1.36	1.29	-1.72E+00	1.56E-03		-1.03E+01	3.83E-09	Down	-6.56E-01	3.33E-02		-1.20E+00	1.96E-04	Down	-7.40E-01	2.14E-02		-8.09E-01	8.91E-03		Unigene26380_All//gi|297831842|ref|XP_002883803.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329643|gb|EFH60062.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene26380_All//0.00E+00//AT2G13600| pentatricopeptide (PPR) repeat-containing protein	Unigene26380_All//0.00E+00//TC175218				nr -
Unigene26381_All	985	6.48	6.58	5.14	7.18	8.15	9.03	3.35	6.83	6.88	2.30E-02	9.41E-01		-3.36E-01	1.86E-01		1.82E-01	4.53E-01		3.31E-01	1.07E-01		1.03E+00	5.74E-07	Up	1.04E+00	2.60E-07	Up			Unigene26381_All//0.00E+00//TC175112				
Unigene26385_All	1161	0.45	0.92	1.15	2.40	3.06	1.56	2.00	0.83	0.58	1.02E+00	1.27E-01		1.35E+00	3.17E-02		3.47E-01	3.24E-01		-6.27E-01	1.02E-01		-1.27E+00	8.52E-04	Down	-1.78E+00	6.55E-06	Down	Unigene26385_All//gi|7767672|gb|AAF69169.1|AC007915_21//1.00E-52//P27F5.21 [Arabidopsis thaliana]	Unigene26385_All//6.00E-21//ATMG00310| hypothetical protein	Unigene26385_All//5.00E-28//gi|73944223|gb|DT527531.1|DT527531				nr +
Unigene26386_All	1513	0.59	1.54	1.13	2.44	1.23	0.96	0.73	1.52	3.21	1.39E+00	1.41E-03		9.38E-01	7.67E-02		-9.87E-01	9.53E-04		-1.35E+00	3.06E-05	Down	1.06E+00	5.00E-03		2.14E+00	3.26E-14	Up							
Unigene26387_All	1005	16.97	1.87	7.10	16.85	10.24	3.86	6.98	1.41	5.23	-3.19E+00	1.06E-59	Down	-1.26E+00	1.35E-17	Down	-7.18E-01	6.38E-09		-2.12E+00	4.87E-41	Down	-2.30E+00	1.46E-21	Down	-4.17E-01	3.12E-02		Unigene26387_All//gi|89111876|gb|AB060710.1|//6.00E-24//At5g67390 [Arabidopsis thaliana]	Unigene26387_All//2.00E-20//AT5G67390| unknown protein	Unigene26387_All//0.00E+00//GE653735				nr +
Unigene26390_All	555	27.24	95.68	26.96	27.91	59.19	46.63	49.06	71.17	96.55	1.81E+00	1.53E-94	Up	-1.51E-02	9.41E-01		1.08E+00	3.69E-32	Up	7.40E-01	1.72E-12		5.37E-01	1.67E-12		9.77E-01	6.78E-47				Unigene26390_All//5.00E-168//TC173542				

Unigene26393_All	1353	0.23	0.15	0.31	2.98	3.41	3.10	3.37	0.74	1.59	-6.31E-01	6.22E-01		4.41E-01	6.77E-01		1.94E-01	5.57E-01		5.79E-02	8.72E-01		-2.19E+00	1.96E-13	Down	-1.09E+00	1.38E-05	Down	Unigene26393_All//gi|224065527|ref|XP_002301841.1|//1.00E-132//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222843567|gb|EEE81114.1|multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene26393_All//9.00E-89//AT1G04120| ATMRP5; ATPase, coupled to transmembrane movement of substances / sulfonylurea receptor	Unigene26393_All//0.00E+00//TC148823			GO:0004888//GO:0005773//GO:0006875//GO:0006970//GO:0031090	nr +
Unigene26394_All	2318	17.56	16.39	23.13	12.29	15.70	15.33	20.99	8.13	8.63	-9.92E-02	2.99E-01		3.98E-01	7.22E-08		3.53E-01	2.31E-05		3.19E-01	3.49E-04		-1.37E+00	5.25E-71	Down	-1.28E+00	3.13E-66	Down	Unigene26394_All//gi|297534856|ref|XP_002885310.1|//0.00E+00//ATNHD1 [Arabidopsis lyrata subsp. lyrata] >gi|297331150|gb|EFH61569.1|ATNHD1 [Arabidopsis lyrata subsp. lyrata]	Unigene26394_All//0.00E+00//AT3G19490| ATNHD1; potassium:hydrogen antiporter/ sodium:hydrogen antiporter	Unigene26394_All//0.00E+00//TC169847			GO:0005451//GO:0006812//GO:0015142//GO:0030001//GO:0031224//GO:0043231	nr -
Unigene26396_All	1360	1.69	2.98	0.94	2.38	2.13	3.22	5.04	19.85	18.04	8.16E-01	7.17E-03		-8.49E-01	5.44E-02		-1.63E-01	6.63E-01		4.36E-01	1.53E-01		1.98E+00	1.11E-66	Up	1.84E+00	2.83E-56	Up	Unigene26396_All//gi|82697961|gb|AB88901 5.1|//1.00E-129//CXE carboxylesterase [Actinidia deliciosa]	Unigene26396_All//3.00E-96//AT1G68620| hydrolase					nr +
Unigene26397_All	2104	0.75	0.72	0.56	0.97	0.79	24.80	7.73	16.28	-4.62E-02	9.40E-01		-4.22E-01	4.37E-01		-4.31E-01	3.48E-01		-2.90E-01	5.68E-01		-1.68E+00	6.04E-103	Down	-6.07E-01	1.13E-20		Unigene26397_All//gi|297821244|ref|XP_002878505.1|//1.00E-111//endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324343|gb|EFH54764.1|endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26397_All//3.00E-109//AT2G43240| endonuclease/exonuclease/phosphatase family protein	Unigene26397_All//0.00E+00//TC159707				nr +
Unigene26398_All	2069	0.25	0.10	0.36	0.58	0.52	0.70	6.99	1.88	4.33	-1.37E+00	1.97E-01		5.11E-01	5.47E-01		-1.64E-01	8.16E-01		2.74E-01	6.49E-01		-1.90E+00	3.74E-34	Down	-6.90E-01	8.68E-08		Unigene26398_All//gi|42569699|ref|NP_181280.3|//1.00E-163//endonuclease/exonuclease/phosphatase family protein [Arabidopsis thaliana]	Unigene26398_All//2.00E-162//AT2G37440| endonuclease/exonuclease/phosphatase family protein	Unigene26398_All//0.00E+00//TC159707				nr -
Unigene2640_All	564	5.94	2.43	4.25	4.42	4.58	1.84	2.17	0.96	4.17	-1.29E+00	2.14E-04	Down	-4.83E-01	1.79E-01		5.23E-02	9.16E-01		-1.26E+00	1.84E-03		-1.17E+00	3.41E-02		9.39E-01	9.21E-03		Unigene2640_All//gi|114050551|gb|AB149425.1|//4.00E-15//At1g68585 [Arabidopsis thaliana]	Unigene2640_All//2.00E-16//AT1G68585| unknown protein	Unigene2640_All//7.00E-158//AJ514138				nr -
Unigene26403_All	971	18.86	11.79	9.82	34.37	23.30	31.95	57.43	23.46	15.39	-6.77E-01	1.69E-07		-9.42E-01	4.80E-12		-5.61E-01	3.78E-11		-1.05E-01	3.49E-01		-1.29E+00	2.00E-74	Down	-1.90E+00	4.88E-134	Down	Unigene26403_All//gi|192910756|gb|ACF06486.1|//9.00E-96//60S ribosomal protein L11 [Elaeis guineensis] >gi|192910758|gb|ACF06487.1| 60S ribosomal protein L11 [Elaeis guineensis]	Unigene26403_All//6.00E-86//AT5G45775| 60S ribosomal protein L11 (RPL11D)	Unigene26403_All//0.00E+00//TC153800		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene26404_All	577	1.72	1.84	1.29	0.26	0.84	0.47	3.22	1.01	0.83	9.81E-02	8.80E-01		-4.15E-01	5.72E-01		1.69E+00	1.66E-01		8.59E-01	6.31E-01		-1.67E+00	2.33E-04	Down	-1.96E+00	1.89E-05	Down	Unigene26404_All//gi|297850802|ref|XP_002890282.1|//5.00E-54//UbiE/COQ5 methyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339124|gb|EFH69541.1|UbiE/COQ5 methyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26404_All//5.00E-45//AT1G23360| UbiE/COQ5 methyltransferase family protein			ko03010|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0016741//GO:0043231	nr -
Unigene2641_All	1368	30.75	17.41	19.89	42.28	31.67	30.21	3.12	1.37	1.72	-8.21E-01	2.72E-22		-6.29E-01	1.17E-13		-4.17E-01	3.52E-11		-4.85E-01	3.63E-13		-1.18E+00	1.05E-05	Down	-8.61E-01	7.03E-04		Unigene2641_All//gi|18424719|ref|NP_568974.1|//6.00E-94//ATFP3; metal ion binding / transition metal ion binding [Arabidopsis thaliana]	Unigene2641_All//1.00E-54//AT5G63530| ATFP3; metal ion binding / transition metal ion binding	Unigene2641_All//0.00E+00//TC136530				nr +
Unigene26412_All	1179	25.38	14.53	12.74	50.32	46.06	48.42	100.95	37.61	34.33	-8.05E-01	1.37E-15		-9.95E-01	4.46E-21		-1.28E-01	8.05E-02		-5.56E-02	5.27E-01		-1.42E+00	1.67E-183	Down	-1.56E+00	3.05E-215	Down	Unigene26412_All//gi|117165712|dbj|BAF36056.1|//1.00E-151//calreticulin-1 [Glycine max]	Unigene26412_All//2.00E-113//AT1G56340| CRT1 (CALRETICULIN 1); calcium ion binding / unfolded protein binding	Unigene26412_All//0.00E+00//TC149458		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr +
Unigene26413_All	1271	1.65	2.15	3.39	9.01	10.27	11.23	2.79	0.69	2.16	3.87E-01	3.28E-01		1.04E+00	6.82E-04	Up	1.88E-01	2.92E-01		3.17E-01	3.97E-02		-2.02E+00	1.20E-09	Down	-3.70E-01	2.03E-01		Unigene26413_All//gi|124360659|gb|ABN08648.1|//1.00E-155//Pectinesterase [Medicago truncatula]	Unigene26413_All//3.00E-139//AT1G05310| pectinesterase family protein			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0005618//GO:0016788	nr +
Unigene26417_All	1541	3.97	1.71	3.66	2.42	2.84	2.17	2.25	0.92	1.34	-1.22E+00	9.02E-07	Down	-1.17E-01	6.41E-01		2.27E-01	5.09E-01		-1.61E-01	6.52E-01		-1.29E+00	2.44E-05	Down	-7.43E-01	9.03E-03		Unigene26417_All//gi|115442163|ref|NP_001045361.1|//1.00E-141//Os01g0941800 [Oryza sativa Japonica Group] >gi|18814963|dbj|BAB85431.1|purple acid phosphatase-like [Oryza sativa Japonica Group] >gi|113534892|dbj|BAF07275.1|Os01g0941800 [Oryza sativa Japonica Group]	Unigene26417_All//5.00E-142//AT3G10150| PAP16 (PURPLE ACID PHOSPHATASE 16); acid phosphatase/ protein serine/threonine phosphatase	Unigene26417_All//0.00E+00//TC163876				nr -
Unigene26418_All	3183	0.00	1.53	0.20	3.98	0.51	1.05	16.96	28.43	9.81	1.06E+01	1.00E-27	Up	7.65E+00	1.16E-03		-2.97E+00	1.31E-52	Down	-1.92E+00	5.26E-27	Down	7.45E-01	9.22E-49		-7.90E-01	1.97E-33		Unigene26418_All//gi|148251494|gb|ABQ53598.1|//0.00E+00//stachyose synthase [Cucumis sativus]	Unigene26418_All//0.00E+00//AT4G01970| AtSTS (Arabidopsis thaliana stachyose synthase); galactinol-raffinose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene26418_All//0.00E+00//TC175973		ko00052|Galactose metabolism	GO:0008378//GO:0009311//GO:0044424	nr +
Unigene2642_All	1283	15.37	35.94	26.73	13.05	18.28	18.38	20.20	16.78	21.77	1.23E+00	2.64E-46	Up	7.98E-01	8.52E-17		4.87E-01	3.83E-06		4.94E-01	6.63E-06		-2.68E-01	6.21E-03		1.08E-01	2.93E-01		Unigene2642_All//gi|115394650|gb|AB197241.1|//1.00E-125//PHD2 [Glycine max]	Unigene2642_All//1.00E-86//AT5G20510| AL5 (ALFIN-LIKE 5); DNA binding / methylated histone residue binding	Unigene2642_All//0.00E+00//gi|78334389|gb|DT554663.1|DT554663	Alfin-like			nr +
Unigene26422_All	1055	6.05	3.79	3.28	6.09	2.77	7.79	7.41	9.98	7.21	-6.73E-01	3.86E-03		-8.83E-01	2.93E-04		-1.13E+00	1.80E-07	Down	3.55E-01	9.53E-02		4.29E-01	6.73E-03		-3.98E-02	8.48E-01		Unigene26422_All//gi|45477067|sp|P92552.1|M1220_ARATH//1.00E-24//RecName: Full=Uncharacterized mitochondrial protein AtMg01220; AltName: Full=ORF113	Unigene26422_All//2.00E-26//ATMG01220| hypothetical protein	Unigene26422_All//0.00E+00//gi|13350711|gb|BG441059.1|BG441059				nr -
Unigene26424_All	1006	1.20	1.11	1.16	3.81	1.81	3.14	2.86	1.83	1.27	-1.10E-01	8.45E-01		-3.87E-02	9.68E-01		-1.07E+00	2.44E-04	Down	-2.79E-01	4.20E-01		-6.45E-01	5.20E-02		-1.17E+00	3.14E-04	Down	Unigene26424_All//gi|225456953|ref|XP_002278337.1|//4.00E-91//PREDICTED: similar to transcription factor jumonji (jmjC) domain-containing protein [Vitis vinifera]	Unigene26424_All//3.00E-72//AT5G63080| transcription factor jumonji (jmjC) domain-containing protein	Unigene26424_All//0.00E+00//ES800020				nr +
Unigene26426_All	1059	2.03	4.69	4.07	10.68	7.74	22.13	105.60	521.72	311.79	1.21E+00	1.37E-05	Up	1.01E+00	1.02E-03		-4.64E-01	3.73E-03		1.05E+00	4.44E-20	Up	2.30E+00	0.00E+00	Up	1.56E+00	0.00E+00	Up	Unigene26426_All//gi|40218371|gb|AB83118.1|//7.00E-68//secretory laccase [Gossypium arboreum]	Unigene26426_All//3.00E-47//AT5G48100| TT10 (TRANSPARENT TESTA 10); copper ion binding / laccase	Unigene26426_All//0.00E+00//TC174717		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene26428_All	880	2.14	2.76	5.75	30.28	26.06	20.02	4.13	1.23	1.63	3.69E-01	3.73E-01		1.43E+00	9.55E-07	Up	-2.17E-01	4.29E-02		-5.98E-01	4.54E-09		-1.74E+00	3.07E-08	Down	-1.34E+00	4.14E-06	Down	Unigene26428_All//gi|29029102|gb|AA064930.1|//3.00E-34//At1g58070 [Arabidopsis thaliana]						nr +
Unigene26429_All	963	26.30	20.52	24.66	8.48	10.55	8.77	6.10	4.08	2.40	-3.58E-01	1.01E-03		-9.26E-02	4.70E-01		3.14E-01	8.98E-02		4.79E-02	8.43E-01		-5.81E-01	7.78E-03		-1.35E+00	2.19E-09	Down	Unigene26429_All//gi|79330574|ref|NP_001032057.1|//3.00E-46//LPA2 (low psii accumulation2) [Arabidopsis thaliana]	Unigene26429_All//4.00E-26//AT5G51545| LPA2 (low psii accumulation2)	Unigene26429_All//0.00E+00//TC147346			GO:0009536//GO:0034357	nr +
Unigene26430_All	1139	7.81	4.76	4.77	29.00	25.27	23.67	10.13	7.89	4.23	-7.14E-01	2.15E-04		-7.12E-01	3.91E-04		-1.98E-01	3.85E-02		-2.93E-01	1.78E-03		-3.61E-01	1.78E-02		-1.26E+00	6.01E-16	Down	Unigene26430_All//gi|40241231|emb|CAF02295.1|//6.00E-73//Rho GDP-dissociation inhibitor 1 [Medicago truncatula]	Unigene26430_All//3.00E-50//AT3G07880| Rho GDP-dissociation inhibitor family protein	Unigene26430_All//0.00E+00//TC136622			GO:0005092//GO:0043231	nr +
Unigene26431_All	1088	11.69	4.01	4.60	44.96	44.56	33.75	34.86	13.06	12.74	-1.54E+00	1.08E-18	Down	-1.34E+00	1.18E-14	Down	-1.28E-02	8.95E-01		-4.14E-01	1.50E-08		-1.42E+00	1.92E-58	Down	-1.45E+00	1.97E-62	Down	Unigene26431_All//gi|109946571|gb|ABG48464.1|//3.00E-33//At5g57000 [Arabidopsis thaliana]	Unigene26431_All//1.00E-34//AT5G57000| unknown protein	Unigene26431_All//0.00E+00//TC138179				nr +
Unigene26432_All	1283	2.28	2.25	0.29	1.48	0.83	0.81	2.70	1.99	0.71	-2.07E-02	9.74E-01		-2.97E+00	1.52E-09	Down	-8.27E-01	6.86E-02		-8.66E-01	7.02E-02		-4.43E-01	1.45E-01		-1.92E+00	3.20E-09	Down	Unigene26432_All//gi|159025733|emb|CAN88867.1|//1.00E-93//D6-type cyclin [Populus trichocarpa]	Unigene26432_All//2.00E-50//AT4G03270| CYCD6;1 (Cyclin D6;1); cyclin-dependent protein kinase	Unigene26432_All//3.00E-66//gi|48881083|gb|CO132105.1|CO132105			GO:0009987//GO:0043231	nr -
Unigene26433_All	952	10.00	5.70	5.20	7.12	9.33	7.69	10.44	3.60	6.49	-8.13E-01	1.37E-05		-9.43E-01	1.34E-06		3.91E-01	4.40E-02		1.11E-01	6.70E-01		-1.54E+00	8.02E-18	Down	-6.86E-01	1.38E-05		Unigene26433_All//gi|226508374|ref|NP_001147050.1|//9.00E-50//nicotiana lesion-inducing like [Zea mays] >gi|195606894|gb|ACG25277.1|nicotiana lesion-inducing like [Zea mays]	Unigene26433_All//2.00E-47//AT1G04340| lesion inducing protein-related	Unigene26433_All//0.00E+00//TC147688			GO:0043231	nr -
Unigene26434_All	1314	20.79	15.12	21.76	4.17	4.40	3.95	2.64	0.92	0.91	-4.60E-01	8.99E-06		6.63E-02	6.07E-01		7.83E-02	8.14E-01		-7.72E-02	7.83E-01		-1.52E+00	1.31E-06	Down	-1.54E+00	5.53E-07	Down	Unigene26434_All//gi|115450080|ref|NP_001048641.1|//1.00E-123//Os02g0834700 [Oryza sativa Japonica Group] >gi|50253330|dbj|BAD29598.1| cell division inhibitor-like [Oryza sativa Japonica Group] >gi|88193771|dbj|BAE79755.1| cell division inhibitor-like [Oryza sativa Japonica Group] >gi|113538172|dbj|BAF10555.1|Os02g0834700 [Oryza sativa Japonica Group]	Unigene26434_All//1.00E-112//AT2G21280| SUL4; binding / catalytic/ coenzyme binding	Unigene26434_All//0.00E+00//TC169512			GO:0003824//GO:0005488//GO:0008152	nr -
Unigene26435_All	1373	7.51	3.69	3.14	10.16	12.26	19.64	7.48	23.50	42.33	-1.02E+00	1.97E-08	Down	-1.26E+00	7.24E-11	Down	2.72E-01	4.98E-02		9.51E-01	1.39E-19		1.65E+00	3.82E-62	Up	2.50E+00	2.97E-194	Up	Unigene26435_All//gi|14285652|sp|O24035.3|PANC_LOTJA//1.00E-124//RecName: Full=Pantoate--beta-alanine ligase; AltName: Full=Pantothenate synthetase; AltName: Full=Pantoate-activating enzyme; Flags: Precursor >gi|2292921|emb|CAA71302.1|pantoate--beta-alanine ligase [Lotus japonicus]	Unigene26435_All//3.00E-108//AT5G48840| PANC (ARABIDOPSIS HOMOLOG OF BACTERIAL PANC); pantoate-beta-alanine ligase/ protein homodimerization	Unigene26435_All//0.00E+00//AI730340		ko00410|beta-Alanine metabolism//ko00770|Pantothenate and CoA biosynthesis	GO:0009058//GO:0016874	nr +
Unigene26438_All	1212	3.07	0.42	0.97	48.66	63.36	50.90	9.80	4.24	6.31	-2.87E+00	3.40E-12	Down	-1.66E+00	3.10E-06	Down	3.81E-01	2.99E-12		6.49E-02	4.45E-01		-1.21E+00	6.29E-15	Down	-6.35E-01	8.62E-06		Unigene26438_All//gi|225626267|gb|ACN97183.1|//1.00E-141//peroxidase [Populus trichocarpa]	Unigene26438_All//1.00E-129//AT5G42180| peroxidase 64 (PER64) (P64) (PEROX)	Unigene26438_All//1.00E-145//TC145326		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0046872	nr +
Unigene26439_All	1293	2.67	12.89	1.19	5.62	9.69	5.13	11.90	41.73	202.86	2.27E+00	3.79E-40	Up	-1.16E+00	1.01E-03		7.85E-01	1.63E-07		-1.32E-01	6.35E-01		1.81E+00	1.33E-117	Up	4.09E+00	0.00E+00	Up	Unigene26439_All//gi|206584337|gb|ACI15341.1|//1.00E-163//NAC domain protein NAC1 [Gossypium hirsutum] >gi|206584349|gb|ACI15347.1| NAC domain protein NAC1 [Gossypium hirsutum]	Unigene26439_All//2.00E-92//AT5G08790| ATAF2; transcription activator	Unigene26439_All//0.00E+00//TC137879	NAC			nr -
Unigene26440_All	624	19.37	13.15	18.26	27.62	21.03	24.68	49.19	26.06	23.56	-5.58E-01	5.90E-04		-8.49E-02	6.30E-01		-3.94E-01	1.90E-03		-1.62E-01	2.95E-01		-9.17E-01	4.79E-24		-1.06E+00	2.29E-31	Down	Unigene26440_All//gi|192910920|gb|ACF06568.1|//2.00E-81//disulfide-isomerase precursor-like protein [Elaeis guineensis]	Unigene26440_All//9.00E-70//AT2G47470| UNE5 (UNFERTILIZED EMBRYO SAC 5); protein disulfide isomerase	Unigene26440_All//0.00E+00//gi|164329217|gb|ES830879.1|ES830879		ko04141|Protein processing in endoplasmic reticulum	GO:0003006//GO:0005618//GO:0005783//GO:0009566//GO:0010038//GO:0016020//GO:0016862//GO:0019725//GO:0033554//GO:0048229	nr -
Unigene26441_All	632	0.00	0.48	0.00	30.82	22.94	14.01	129.05	87.49	22.82	8.91E+00	4.43E-02		null	null		-4.26E-01	2.62E-04		-1.14E+00	3.18E-19	Down	-5.61E-01	6.16E-27		-2.50E+00	1.94E-276	Down	Unigene26441_All//gi|153805698|gb|ABS52574.1|//7.00E-64//nodulin family protein [Gossypium hirsutum]	Unigene26441_All//2.00E-41//AT1G21890| nodulin MtN21 family protein	Unigene26441_All//0.00E+00//TC150784			GO:0044464	nr +
Unigene26442_All	1444	0.00	0.00	0.00	2.28	1.19	1.44	23.42	18.18	4.25	null	null		null	null		-9.33E-01	3.59E-03		-6.62E-01	5.44E-02		-3.66E-01	9.14E-06		-2.46E+00	4.88E-113	Down	Unigene26442_All//gi|153805698|gb|ABS52574.1|//2.00E-58//nodulin family protein [Gossypium hirsutum]	Unigene26442_All//3.00E-36//AT1G21890| nodulin MtN21 family protein	Unigene26442_All//0.00E+00//gi|109827183|gb|DW225881.1|DW225881			GO:0044464	nr -

Unigene26443_All	1182	0.58	0.47	0.00	1.31	1.02	1.03	3.26	1.70	1.65	-2.87E-01	7.10E-01		-9.17E+00	7.64E-04	Down	-3.58E-01	5.31E-01		-3.41E-01	5.61E-01		-9.40E-01	7.62E-04		-9.79E-01	3.16E-04		Unigene26443_All//gi|87162913|gb|AB028708.1|//2.00E-62//ELM2: AT-rich interaction region; Homeodomain-related [Medicago truncatula]	Unigene26443_All//0.00E+00//TC171375	Unigene26443_All//0.00E+00//gi|21097741|gb|BQ410054.1|BQ410054			GO:0043231//GO:0044444	nr -
Unigene26445_All	452	0.23	2.80	0.24	1.21	1.37	1.60	1.40	2.59	4.76	3.60E+00	2.27E-05	Up	2.53E-02	1.00E+00		1.78E-01	8.64E-01		3.99E-01	6.51E-01		8.84E-01	1.21E-01		1.76E+00	2.14E-05	Up	Unigene26445_All//gi|30682907|ref|NP_188012.2|//5.00E-20//AtGRF5 (GROWTH-REGULATING FACTOR 5); transcription activator [Arabidopsis thaliana] >gi|21539888|gb|AAM52880.1| transcription activator [Arabidopsis thaliana]	Unigene26445_All//3.00E-21//AT3G13960| AtGRF5 (GROWTH-REGULATING FACTOR 5); transcription activator	Unigene26445_All//2.00E-89//TC171375	GRF			nr +
Unigene26446_All	2165	0.44	0.80	0.30	0.32	1.72	0.71	0.90	1.87	2.74	8.71E-01	8.07E-02		-5.59E-01	4.39E-01		2.42E+00	2.77E-11	Up	1.14E+00	3.89E-02		1.06E+00	1.07E-04	Up	1.61E+00	5.99E-12	Up	Unigene26446_All//gi|30682907|ref|NP_188012.2|//7.00E-61//AtGRF5 (GROWTH-REGULATING FACTOR 5); transcription activator [Arabidopsis thaliana] >gi|21539888|gb|AAM52880.1| transcription activator [Arabidopsis thaliana]	Unigene26446_All//5.00E-50//AT3G13960| AtGRF5 (GROWTH-REGULATING FACTOR 5); transcription activator	Unigene26446_All//0.00E+00//TC171375	GRF	ko04140|Regulation of autophagy		nr +
Unigene26447_All	1889	0.80	0.89	0.70	9.92	7.11	3.68	4.90	1.53	1.31	1.40E-01	7.71E-01		-1.89E-01	7.21E-01		-4.80E-01	4.91E-05		-1.43E+00	3.37E-26	Down	-1.68E+00	6.67E-19	Down	-1.91E+00	4.89E-23	Down	Unigene26447_All//gi|297792079|ref|XP_002863924.1|//0.00E+00//phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309759|gb|EFH40183.1| phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26447_All//3.00E-172//AT5G48800| phototropic-responsive NPH3 family protein	Unigene26447_All//0.00E+00//DW226239			GO:0005488//GO:0009314//GO:0016020//GO:0060089	nr +
Unigene26448_All	848	21.59	10.46	16.33	32.49	32.85	22.21	10.02	6.95	5.17	-1.05E+00	7.54E-15	Down	-4.04E-01	2.86E-03		1.62E-02	9.05E-01		-5.49E-01	4.10E-08		-5.28E-01	2.87E-03		-9.56E-01	5.60E-08		Unigene26448_All//gi|50844675|gb|AT84459.1|//3.00E-57//cytochrome b5 isoform Cb5-B [Vernicia fordii]	Unigene26448_All//2.00E-54//AT2G32720| CB5-B (CYTOCHROME B5 ISOFORM B); heme binding	Unigene26448_All//0.00E+00//gi|13350731|gb|BG441079.1|BG441079		ko00910|Nitrogen metabolism	GO:0005506//GO:0006091//GO:0008940//GO:0031090//GO:0031224//GO:0042598//GO:0043231//GO:0051234	nr +
Unigene26449_All	931	6.69	14.64	6.75	18.30	17.13	17.61	8.90	11.76	6.50	1.13E+00	1.36E-12	Up	1.32E-02	9.79E-01		-9.57E-02	5.57E-01		-5.54E-02	7.20E-01		4.02E-01	9.82E-03		-4.53E-01	9.67E-03		Unigene26449_All//gi|15236885|ref|NP_194414.1|//7.00E-42//SUMO1 (SMALL UBIQUITIN-LIKE MODIFIER 1); protein binding / protein tag [Arabidopsis thaliana] >gi|21542462|sp|P55852.2|SMT3_ARATH RecName: Full=Ubiquitin-like protein SMT3 >gi|4455207|emb|CAB36530.1| ubiquitin-like protein [Arabidopsis thaliana] >gi|7269526|emb|CAB79539.1| ubiquitin-like protein [Arabidopsis thaliana] >gi|18252862|gb|AAL62360.1| ubiquitin-like protein [Arabidopsis thaliana] >gi|21592529|gb|AAM64478.1| ubiquitin-like protein [Arabidopsis thaliana] >gi|22652842|gb|AAN03845.1| small ubiquitin-like modifier 1 [Arabidopsis thaliana] >gi|30725548|gb|AAP37796.1| At4g26840 [Arabidopsis thaliana]	Unigene26449_All//3.00E-43//AT4G26840| SUMO1 (SMALL UBIQUITIN-LIKE MODIFIER 1); protein binding / protein tag	Unigene26449_All//0.00E+00//TC141880			GO:0005488//GO:0009408//GO:0032446//GO:0043231//GO:0043392	nr +
Unigene2645_All	1785	1.41	1.65	3.67	3.96	3.65	4.68	2.08	1.03	0.78	2.27E-01	5.61E-01		1.38E+00	3.43E-08	Up	-1.20E-01	6.22E-01		2.40E-01	2.90E-01		-1.02E+00	3.76E-04	Down	-1.42E+00	1.10E-06	Down	Unigene2645_All//gi|297807655|ref|XP_002871711.1|//1.00E-157//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317548|gb|EFH47970.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2645_All//3.00E-137//AT5G16260| RNA recognition motif (RRM)-containing protein	Unigene2645_All//0.00E+00//ES809717				nr +
Unigene26450_All	1211	1.69	1.26	1.67	7.08	5.09	2.61	6.42	3.31	1.05	-4.25E-01	3.64E-01		-1.21E-02	1.00E+00		-4.75E-01	1.20E-02		-1.44E+00	2.14E-12	Down	-9.55E-01	4.05E-07		-2.61E+00	2.38E-28	Down	Unigene26450_All//gi|140053517|gb|ABE79572.2|//1.00E-117//Protein kinase [Medicago truncatula]	Unigene26450_All//1.00E-61//AT4G20270| BAM3 (BARELY ANY MERISTEM 3); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene26450_All//0.00E+00//gi|109883049|gb|DW512019.1|DW512019		ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488//GO:0044464	nr +
Unigene26454_All	1303	8.03	7.19	8.62	4.59	5.97	3.50	5.13	2.44	2.45	-1.59E-01	3.98E-01		1.03E-01	6.22E-01		3.81E-01	7.36E-02		-3.90E-01	1.26E-01		-1.07E+00	2.32E-07	Down	-1.07E+00	1.40E-07	Down	Unigene26454_All//gi|115435874|ref|NP_001042695.1|//4.00E-51//Os01g0268900 [Oryza sativa Japonica Group] >gi|113532226|dbj|BAF04609.1| Os01g0268900 [Oryza sativa Japonica Group]	Unigene26454_All//4.00E-69//AT2G26840| unknown protein	Unigene26454_All//0.00E+00//TC148570			GO:0009536	nr -
Unigene2646_All	2181	0.55	0.26	0.61	0.75	1.04	0.75	1.57	0.77	0.58	-1.11E+00	7.50E-02		1.46E-01	7.93E-01		4.67E-01	3.10E-01		-1.58E-02	9.67E-01		-1.03E+00	5.63E-04	Down	-1.43E+00	2.83E-06	Down	Unigene2646_All//gi|297807655|ref|XP_002871711.1|//1.00E-178//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317548|gb|EFH47970.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2646_All//7.00E-158//AT5G16260| RNA recognition motif (RRM)-containing protein	Unigene2646_All//0.00E+00//TC170047				nr -
Unigene26460_All	1186	9.62	8.93	7.36	13.36	12.02	9.10	12.73	1.30	2.32	-1.07E-01	5.81E-01		-3.85E-01	3.12E-02		-1.52E-01	3.33E-01		-5.53E-01	4.97E-05		-3.29E+00	1.90E-66	Down	-2.46E+00	1.02E-50	Down	Unigene26460_All//gi|255545204|ref|XP_002513663.1|//2.00E-44//conserved hypothetical protein [Ricinus communis] >gi|223547571|gb|EEF49066.1| conserved hypothetical protein [Ricinus communis]	Unigene26460_All//2.00E-05//AT3G14190| unknown protein	Unigene26460_All//0.00E+00//TC168271				nr +
Unigene26462_All	1557	0.30	1.56	1.16	1.47	1.50	3.60	33.21	29.04	135.41	2.37E+00	1.02E-06	Up	1.94E+00	4.89E-04	Up	3.12E-02	9.54E-01		1.29E+00	5.10E-07	Up	-1.93E-01	4.52E-03		2.03E+00	0.00E+00	Up	Unigene26462_All//gi|42569681|ref|NP_181207.2|//1.00E-137//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	Unigene26462_All//2.00E-137//AT2G36690| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene26462_All//0.00E+00//DW498667		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr -
Unigene26463_All	932	200.86	198.71	114.27	84.88	131.83	109.56	71.77	49.78	32.27	-1.56E-02	7.26E-01		-8.14E-01	2.37E-92		6.35E-01	1.46E-48		3.68E-01	7.37E-14		-5.28E-01	5.01E-20		-1.15E+00	9.72E-77	Down	Unigene26463_All//gi|119351383|gb|ABL65518.1|//1.00E-96//chloroplast Cu/Zn superoxide dismutase [Gossypium arboreum]	Unigene26463_All//3.00E-79//AT2G28190| CSD2 (COPPER/ZINC SUPEROXIDE DISMUTASE 2); superoxide dismutase	Unigene26463_All//0.00E+00//BF272580		ko04146|Peroxisome	GO:0003824//GO:0005576//GO:0006801//GO:0006950//GO:0009314//GO:0009532//GO:0010038//GO:0016209//GO:0043169	nr -
Unigene26466_All	1096	7.07	2.77	4.37	10.18	3.96	5.65	6.60	0.65	1.53	-1.35E+00	1.13E-09	Down	-6.92E-01	1.43E-03		-1.36E+00	1.09E-16	Down	-8.51E-01	3.34E-07		-3.35E+00	1.20E-32	Down	-2.11E+00	1.18E-20	Down	Unigene26466_All//gi|18398011|ref|NP_028242.1|//7.00E-07//PDV2 (PLASTID DIVISION2) [Arabidopsis thaliana] >gi|4678204|gb|AAD26950.1| expressed protein [Arabidopsis thaliana] >gi|117413982|dbj|BAF36495.1| plastid division protein PDV2 [Arabidopsis thaliana] >gi|117413986|dbj|BAF36497.1| plastid division protein PDV2 [Arabidopsis thaliana]	Unigene26466_All//3.00E-08//AT2G16070| PDV2 (PLASTID DIVISION2)	Unigene26466_All//0.00E+00//TC174319			GO:0005488//GO:0006810//GO:0044464//GO:0048285	nr +
Unigene26467_All	898	7.05	7.28	6.64	18.03	15.49	19.56	16.43	14.01	7.99	4.61E-02	8.49E-01		-8.61E-02	7.29E-01		-2.19E-01	1.36E-01		1.18E-01	4.68E-01		-2.30E-01	9.85E-02		-1.04E+00	4.53E-15	Down			Unigene26467_All//1.00E-34//ES800361				
Unigene26468_All	1200	32.87	18.79	35.54	935.84	892.33	679.48	58.77	31.14	12.91	-8.07E-01	2.24E-20		1.13E-01	2.38E-01		-6.87E-02	8.08E-07		-4.62E-01	1.06E-224		-9.16E-01	3.76E-54		-2.19E+00	2.75E-203	Down	Unigene26468_All//gi|30841338|gb|AA92753.1|//1.00E-131//arabinogalactan protein [Gossypium hirsutum]	Unigene26468_All//5.00E-59//AT5G60490| FLA12	Unigene26468_All//0.00E+00//TC130000			GO:0016020	nr -
Unigene26470_All	913	39.03	29.30	23.85	47.41	32.74	54.71	43.95	17.76	19.02	-4.13E-01	3.91E-06		-7.10E-01	2.52E-14		-5.34E-01	3.81E-13		2.07E-01	7.37E-03		-1.31E+00	9.74E-55	Down	-1.21E+00	6.86E-50	Down	Unigene26470_All//gi|87240356|gb|AB032214.1|//2.00E-58//Ribosomal protein L34e [Medicago truncatula] >gi|124360947|gb|ABN08919.1| Ribosomal protein L34e [Medicago truncatula]	Unigene26470_All//2.00E-47//AT1G26880| 60S ribosomal protein L34 (RPL34A)	Unigene26470_All//0.00E+00//gi|21100019|gb|BQ412332.1|BQ412332		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0031981	nr +
Unigene26471_All	1124	3.40	1.94	3.93	4.30	4.87	4.38	4.21	1.12	1.24	-8.10E-01	9.66E-03		2.11E-01	5.11E-01		1.80E-01	5.44E-01		2.69E-02	9.45E-01		-1.92E+00	7.43E-12	Down	-1.76E+00	4.79E-11	Down	Unigene26471_All//gi|209171162|gb|AC142847.1|//7.00E-87//RING finger protein [Glycine max]	Unigene26471_All//1.00E-61//AT1G23980| zinc finger (C3HC4-type RING finger) family protein	Unigene26471_All//0.00E+00//TC176929			GO:0006464//GO:0016301//GO:0031224//GO:0032559//GO:0046914	nr -
Unigene26472_All	898	0.23	0.00	0.12	1.39	2.19	0.20	0.89	0.42	0.49	-7.86E+00	1.22E-01		-9.75E-01	6.21E-01		6.56E-01	1.66E-01		-2.79E+00	1.35E-04	Down	-1.09E+00	1.29E-01		-8.74E-01	1.96E-01		Unigene26472_All//gi|9369405|gb|AAF87153.1|AC002423_18//2.00E-77//T23E23.15 [Arabidopsis thaliana]	Unigene26472_All//3.00E-62//AT1G23980| zinc finger (C3HC4-type RING finger) family protein	Unigene26472_All//0.00E+00//TC176929			GO:0006464//GO:0016301//GO:0031224//GO:0032559//GO:0046914	nr +
Unigene26473_All	630	4.15	3.62	5.58	1.03	5.25	3.23	1.68	1.53	2.85	-1.98E-01	6.12E-01		4.26E-01	2.33E-01		2.35E+00	8.93E-10	Up	1.65E+00	5.82E-04	Up	-1.37E-01	8.15E-01		7.62E-01	6.98E-02				Unigene26473_All//7.00E-07//TC163127				
Unigene26477_All	967	34.63	73.57	53.97	14.11	25.46	18.03	9.66	15.39	17.63	1.09E+00	7.50E-59	Up	6.40E-01	2.35E-17		8.51E-01	2.44E-16		3.53E-01	8.65E-03		6.71E-01	2.18E-07		8.68E-01	6.71E-13		Unigene26477_All//gi|115450785|ref|NP_001048993.1|//1.00E-74//Os03g0152600 [Oryza sativa (japonica cultivar-group)] >gi|108706229|gb|ABF94024.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547464|dbj|BAF10907.1| Os03g0152600 [Oryza sativa Japonica Group]	Unigene26477_All//1.00E-80//AT2G36895| unknown protein	Unigene26477_All//0.00E+00//TC167371			GO:0009536	nr -
Unigene26478_All	488	0.21	0.00	0.00	1.12	0.49	0.56	1.73	0.17	1.31	-7.74E+00	3.72E-01		-7.74E+00	3.94E-01		-1.18E+00	2.25E-01		-1.02E+00	3.30E-01		-3.34E+00	2.51E-04	Down	-4.08E-01	5.49E-01		Unigene26478_All//gi|145340316|ref|NP_193430.3|//2.00E-45//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|110738029|dbj|BAF00949.1| kinase like protein [Arabidopsis thaliana]	Unigene26478_All//2.00E-46//AT4G16970| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene26478_All//8.00E-176//ES834303			GO:0004674//GO:0006464//GO:0031410//GO:0032559	nr +
Unigene26479_All	1769	3.49	0.54	0.48	5.86	5.94	1.56	5.40	0.85	1.53	-2.68E+00	1.68E-18	Down	-2.86E+00	7.30E-19	Down	1.95E-02	9.40E-01		-1.91E+00	4.65E-22	Down	-2.67E+00	2.45E-34	Down	-1.82E+00	2.54E-22	Down	Unigene26479_All//gi|145340316|ref|NP_193430.3|//1.00E-158//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|110738029|dbj|BAF00949.1| kinase like protein [Arabidopsis thaliana]	Unigene26479_All//5.00E-160//AT4G16970| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene26479_All//0.00E+00//gi|164261070|gb|ES794548.1|ES794548			GO:0004674//GO:0006464//GO:0032559	nr -
Unigene26480_All	2504	1.94	1.07	2.57	10.31	5.14	3.55	7.04	4.76	1.32	-8.58E-01	1.67E-03		4.05E-01	1.03E-01		-1.00E+00	2.43E-23	Down	-1.54E+00	6.16E-40	Down	-5.66E-01	1.45E-06		-2.41E+00	6.35E-58	Down	Unigene26480_All//gi|297596537|ref|NP_001042723.2|//0.00E+00//Os01g0275900 [Oryza sativa Japonica Group] >gi|255673109|dbj|BAF04637.2| Os01g0275900 [Oryza sativa Japonica Group]		Unigene26480_All//0.00E+00//TC147477				nr -

Unigene26481_All	994	37.27	15.04	28.88	57.63	54.36	54.70	50.53	21.40	26.69	-1.31E+00	1.55E-41	Down	-3.68E-01	5.31E-05		-8.45E-02	3.09E-01		-7.52E-02	3.92E-01		-1.24E+00	5.85E-63	Down	-9.21E-01	3.12E-40		Unigene26481_All//gi|297807241|ref|XP_002871504.1|//1.00E-81//eukaryotic translation initiation factor SUI1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317341|gb|EFH47763.1| eukaryotic translation initiation factor SUI1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26481_All//6.00E-60//AT5G11900| eukaryotic translation initiation factor SUI1 family protein	Unigene26481_All//0.00E+00//TC131589			GO:0006412//GO:0008135	nr -
Unigene26482_All	776	45.31	45.90	46.73	24.39	26.85	23.75	22.94	16.21	8.16	1.88E-02	8.57E-01		4.46E-02	6.63E-01		1.38E-01	3.20E-01		-3.88E-02	7.91E-01		-5.01E-01	1.81E-05		-1.49E+00	6.33E-31	Down	Unigene26482_All//gi|13605902|gb|AK32936.1|AF367350_1//6.00E-43//At1g04290/F19P19_27 [Arabidopsis thaliana] >gi|18491135|gb|AAL69536.1| At1g04290/F19P19_27 [Arabidopsis thaliana]	Unigene26482_All//2.00E-36//AT1G04290| thioesterase family protein	Unigene26482_All//0.00E+00//TC150242			GO:0016289//GO:0042579	nr -
Unigene26484_All	1033	4.91	3.68	2.84	22.52	16.13	9.44	1.68	0.20	0.35	-4.17E-01	1.23E-01		-7.93E-01	4.21E-03		-4.81E-01	3.94E-06		-1.25E+00	1.39E-26	Down	-3.05E+00	1.18E-07	Down	-2.27E+00	5.17E-06	Down	Unigene26484_All//gi|22327962|ref|NP_200709.2|//1.00E-130//protein kinase-related [Arabidopsis thaliana] >gi|9759232|dbj|BAB09644.1| protein kinase-like protein [Arabidopsis thaliana] >gi|19715586|gb|AAL91617.1| AT5g59010/k19m22_210 [Arabidopsis thaliana] >gi|11074228|gb|AB404487.1| At5g59010 [Arabidopsis thaliana]	Unigene26484_All//2.00E-122//AT5G59010| protein kinase-related	Unigene26484_All//0.00E+00//TC148078		ko04626|Plant-pathogen interaction		nr -
Unigene26486_All	2898	0.67	0.58	1.47	0.21	0.10	0.28	18.57	17.83	26.74	-2.11E-01	6.27E-01		1.14E+00	2.62E-04	Up	-1.12E+00	2.26E-01		4.43E-01	6.21E-01		-5.92E-02	4.56E-01		5.26E-01	1.76E-23		Unigene26486_All//gi|115460468|ref|NP_001053834.1|//1.00E-177//Os04g0610900 [Oryza sativa Japonica Group] >gi|38345798|emb|CAE03570.2| OSJNBa0085I10.15 [Oryza sativa (japonica cultivar-group)] >gi|113565405|dbj|BAF15748.1| Os04g0610900 [Oryza sativa Japonica Group]	Unigene26486_All//0.00E+00//AT4G24480| serine/threonine protein kinase, putative	Unigene26486_All//0.00E+00//C0131275		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0032559	nr +
Unigene26489_All	1136	0.88	0.27	0.23	0.00	0.09	0.00	94.94	9.82	43.31	-1.71E+00	2.09E-02		-1.90E+00	1.70E-02		6.51E+00	4.56E-01		null	null		-3.27E+00	0.00E+00	Down	-1.13E+00	9.80E-120	Down	Unigene26489_All//gi|171854669|dbj|BAG16524.1|//9.00E-64//C2 domain-containing protein [Capsicum chinense]	Unigene26489_All//5.00E-47//AT4G34150| C2 domain-containing protein	Unigene26489_All//3.00E-07//TC136856		ko04626|Plant-pathogen interaction//ko03040|Spliceosome//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr -
Unigene2649_All	1330	5.19	13.52	4.08	31.80	27.11	53.04	38.59	26.30	69.49	1.38E+00	4.11E-22	Up	-3.47E-01	1.48E-01		-2.30E-01	3.94E-03		7.38E-01	6.48E-33		-5.53E-01	7.27E-17		8.49E-01	1.55E-63		Unigene2649_All//gi|5902391|gb|AAD55493.1|AC008148_3//9.00E-47//Unknown protein [Arabidopsis thaliana] >gi|11762244|gb|AAG40399.1|AF325047_1 At1g70780 [Arabidopsis thaliana] >gi|15146214|gb|AAK83590.1| At1g70780/F5A18_4 [Arabidopsis thaliana] >gi|23506215|gb|AAN31119.1| At1g70780/F5A18_4 [Arabidopsis thaliana]	Unigene2649_All//4.00E-48//AT1G70780| unknown protein	Unigene2649_All//0.00E+00//TC154833				nr -
Unigene26490_All	736	25.02	38.97	31.18	31.68	24.05	40.01	30.62	28.68	13.37	6.39E-01	3.16E-10		3.18E-01	8.63E-03		-3.97E-01	1.71E-04		3.37E-01	6.66E-04		-9.45E-02	4.42E-01		-1.20E+00	5.81E-28	Down	Unigene26490_All//gi|225457632|ref|XP_002273197.1|//5.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene26490_All//0.00E+00//gi|13244072|gb|BE053162.2|BE053162				nr -
Unigene26493_All	799	24.29	18.90	11.60	22.07	19.61	28.32	216.22	320.82	742.67	-3.62E-01	4.11E-03		-1.07E+00	1.72E-15	Down	-1.71E-01	2.42E-01		3.60E-01	1.73E-03		5.69E-01	3.96E-85		1.78E+00	0.00E+00	Up	Unigene26493_All//gi|219547603|gb|ABR04092.2|//2.00E-53//cytochrome b5 [Malus x domestica]	Unigene26493_All//7.00E-42//AT5G53560| CB5-E (CYTOCHROME B5 ISOFORM E); heme binding	Unigene26493_All//3.00E-56//TC142244		ko00910|Nitrogen metabolism	GO:0005506//GO:0006091//GO:0008940//GO:0009534//GO:0031090//GO:0032424//GO:0042598//GO:0051234	nr -
Unigene26494_All	925	101.47	36.87	48.24	324.73	287.62	300.08	289.84	171.02	162.11	-1.46E+00	4.38E-123	Down	-1.07E+00	1.31E-73	Down	-1.75E-01	4.40E-11		-1.14E-01	9.54E-05		-7.61E-01	1.71E-148		-8.38E-01	5.07E-180		Unigene26494_All//gi|46318067|gb|AS87601.1|//5.00E-88//membrane-anchored endo-1,4-beta-glucanase [Gossypium hirsutum]	Unigene26494_All//3.00E-56//AT5G49720| ATGDA1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9A1); cellulase/hydrolase, hydrolyzing O-glycosyl compounds	Unigene26494_All//0.00E+00//TC161105		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0044238	nr +
Unigene26496_All	1656	0.85	1.16	1.77	3.82	3.10	2.51	2.63	1.51	1.23	4.47E-01	3.56E-01		1.05E+00	6.29E-03		-3.02E-01	2.22E-01		-6.07E-01	9.17E-03		-7.96E-01	2.07E-03		-1.10E+00	1.84E-05	Down	Unigene26496_All//gi|124360865|gb|ABN08837.1|//3.00E-99//Helix-hairpin-helix motif, class 2 [Medicago truncatula]	Unigene26496_All//4.00E-126//AT1G01880| DNA repair protein, putative	Unigene26496_All//0.00E+00//C0132374		ko03420|Nucleotide excision repair	GO:0004520//GO:0006259//GO:0043231//GO:0043566//GO:0048229	nr +
Unigene26499_All	896	1.40	10.18	1.25	9.23	8.72	9.93	9.06	21.64	25.17	2.86E+00	1.14E-28	Up	-1.67E-01	7.75E-01		-8.12E-02	7.51E-01		1.06E-01	6.47E-01		1.26E+00	2.87E-25	Up	1.47E+00	6.18E-38	Up	Unigene26499_All//gi|18414255|ref|NP_568121.1|//4.00E-84//RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding [Arabidopsis thaliana] >gi|2723477|dbj|BAA24074.1| GTP-binding protein [Arabidopsis thaliana] >gi|7378638|emb|CAB83314.1| AtRab GTP-binding protein [Arabidopsis thaliana]	Unigene26499_All//2.00E-84//AT5G03530| RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding	Unigene26499_All//0.00E+00//TC161080			GO:0004620//GO:0004721//GO:0006351//GO:0006464//GO:0006810//GO:0032029//GO:0032561//GO:0035556//GO:0042579//GO:0043169//GO:0043234	nr -
Unigene2650_All	623	2.86	1.30	4.19	3.68	4.48	5.94	3.94	1.68	2.43	-1.13E+00	2.21E-02		5.53E-01	1.80E-01		2.84E-01	5.18E-01		6.93E-01	3.17E-02		-1.23E+00	8.56E-04	Down	-6.96E-01	4.53E-02		Unigene2650_All//gi|1934972|emb|CAA69903.1|//3.00E-86//dihydropterin pyrophosphokinase /dihydropteroate synthase [Pisum sativum]	Unigene2650_All//2.00E-80//AT4G30000| dihydropterin pyrophosphokinase, putative / dihydropteroate synthase, putative / DHPS, putative	Unigene2650_All//2.00E-158//TC172771		ko00790|Folate biosynthesis		nr -
Unigene26501_All	1000	6.80	4.56	5.11	13.95	11.33	8.72	5.71	5.06	2.35	-5.77E-01	1.04E-02		-4.12E-01	8.59E-02		-3.00E-01	4.58E-02		-6.78E-01	3.49E-06		-1.75E-01	4.95E-01		-1.28E+00	1.62E-08	Down			Unigene26501_All//1.00E-46//TC132116				
Unigene26503_All	1138	1.33	7.79	3.28	3.94	2.94	2.98	8.10	23.32	13.37	2.55E+00	1.15E-24	Up	1.30E+00	1.44E-04	Up	-4.25E-01	1.40E-01		-4.04E-01	1.82E-01		1.53E+00	8.64E-46	Up	7.23E-01	9.86E-09		Unigene26503_All//gi|30017255|gb|AP12861.1|//3.00E-63//At2g40095 [Arabidopsis thaliana]	Unigene26503_All//8.00E-41//AT2G40095| unknown protein	Unigene26503_All//0.00E+00//gi|109825781|gb|DW224504.1|DW224504			GO:0003824//GO:0009267	nr -
Unigene26504_All	1015	2.17	2.85	2.15	3.78	2.95	3.03	7.33	5.02	3.30	3.94E-01	3.00E-01		-9.40E-03	1.00E+00		-3.57E-01	2.78E-01		-3.21E-01	3.52E-01		-5.45E-01	4.29E-03		-1.15E+00	2.51E-09	Down	Unigene26504_All//gi|90962940|gb|AB692394.1|//2.00E-21//At5g14105 [Arabidopsis thaliana]	Unigene26504_All//1.00E-12//AT5G14105| unknown protein	Unigene26504_All//0.00E+00//gi|164288583|gb|ES794856.1|ES794856			GO:0005746	nr +
Unigene26505_All	1052	13.23	7.66	6.38	23.96	18.04	30.95	13.91	7.79	8.67	-7.89E-01	1.94E-07		-1.05E+00	4.76E-11	Down	-4.10E-01	4.75E-05		3.70E-01	6.65E-05		-8.37E-01	2.68E-10		-6.81E-01	1.03E-07		Unigene26505_All//gi|18399930|ref|NP_566450.1|//3.00E-97//RNA binding [Arabidopsis thaliana] >gi|50897250|gb|AAT85764.1| At3g13230 [Arabidopsis thaliana]	Unigene26505_All//2.00E-91//AT3G13230| RNA binding	Unigene26505_All//0.00E+00//TC141079			GO:0003676	nr +
Unigene26506_All	986	12.63	8.27	11.61	22.68	16.94	18.23	13.94	9.07	4.93	-6.10E-01	1.32E-04		-1.21E-01	5.18E-01		-4.21E-01	9.19E-05		-3.15E-01	7.03E-03		-6.20E-01	4.35E-06		-1.50E+00	2.82E-24	Down	Unigene26506_All//gi|37051125|dbj|BAC81659.1|//3.00E-60//DNA binding with one finger 2 protein [Pisum sativum]	Unigene26506_All//6.00E-44//AT2G28510| Dof-type zinc finger domain-containing protein	Unigene26506_All//0.00E+00//TC148738	C2C2-Dof		GO:0005488	nr +
Unigene26507_All	391	0.00	0.26	0.00	0.00	0.00	1.39	0.87	1.18	5.50	8.02E+00	3.87E-01		null	null		null	null		1.04E+01	2.46E-03		4.43E-01	6.31E-01		2.67E+00	1.98E-08	Up	Unigene26507_All//gi|30690409|ref|NP_850456.1|//4.00E-06//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene26507_All//1.00E-06//AT2G46495| zinc finger (C3HC4-type RING finger) family protein	Unigene26507_All//1.00E-99//TC160583			GO:0016301	nr +
Unigene26508_All	1254	0.75	3.15	2.29	0.91	0.55	0.68	1.05	3.23	11.98	2.07E+00	5.33E-09	Up	1.61E+00	8.37E-05	Up	-7.34E-01	2.38E-01		-4.17E-01	5.42E-01		1.63E+00	2.50E-08	Up	3.52E+00	3.44E-71	Up	Unigene26508_All//gi|121489775|emb|CAK18859.1|//8.00E-16//Putative RING-H2 finger protein precursor [Phillyrea latifolia]	Unigene26508_All//5.00E-16//AT5G53110| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: zinc finger (C3HC4-type RING finger) family protein (TAIR:AT2G46495.1); Has 118 Blast hits to 116 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 118; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene26508_All//0.00E+00//TC160583				nr -
Unigene26509_All	843	0.12	0.72	0.32	0.35	0.29	0.43	0.35	1.04	4.40	2.54E+00	2.46E-02		1.35E+00	4.09E-01		-3.10E-01	8.20E-01		2.74E-01	8.33E-01		1.57E+00	2.54E-02		3.65E+00	1.54E-18	Up	Unigene26509_All//gi|30690409|ref|NP_850456.1|//9.00E-09//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene26509_All//5.00E-12//AT5G53110| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: zinc finger (C3HC4-type RING finger) family protein (TAIR:AT2G46495.1); Has 118 Blast hits to 116 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 118; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene26509_All//0.00E+00//TC160583				nr +
Unigene2651_All	1947	3.01	1.82	1.20	4.96	4.09	3.90	4.50	3.33	3.01	-7.24E-01	3.05E-03		-1.32E+00	6.20E-07	Down	-2.81E-01	1.45E-01		-3.49E-01	6.99E-02		-4.34E-01	1.38E-02		-5.80E-01	5.89E-04		Unigene2651_All//gi|1934972|emb|CAA69903.1|//0.00E+00//dihydropterin pyrophosphokinase /dihydropteroate synthase [Pisum sativum]	Unigene2651_All//0.00E+00//AT4G30000| dihydropterin pyrophosphokinase, putative / dihydropteroate synthase, putative / DHPS, putative	Unigene2651_All//0.00E+00//TC172771		ko00790|Folate biosynthesis		nr -
Unigene26511_All	1314	1.19	0.27	0.49	2.77	1.65	1.86	6.50	2.67	2.70	-2.15E+00	3.32E-04	Down	-1.30E+00	2.26E-02		-7.45E-01	1.45E-02		-5.76E-01	7.81E-02		-1.28E+00	6.01E-12	Down	-1.27E+00	3.79E-12	Down	Unigene26511_All//gi|115465898|ref|NP_001056548.1|//1.00E-110//Os06g0104100 [Oryza sativa Japonica Group] >gi|113594588|dbj|BAF18462.1| Os06g0104100 [Oryza sativa Japonica Group]	Unigene26511_All//7.00E-72//AT1G62730| transferase	Unigene26511_All//0.00E+00//TC174436			GO:0003824//GO:0008152	nr +

Unigene26513_All	973	3.12	2.71	3.28	5.22	4.11	5.06	1.65	0.99	0.41	-2.04E-01	6.01E-01		7.43E-02	8.34E-01		-3.47E-01	2.08E-01		-4.56E-02	8.88E-01		-7.41E-01	1.15E-01		-2.01E+00	5.95E-05	Down	Unigene26513_All//gi|115485799|ref|NP_001068043.1|//1.00E-20//Os11g0543300 [Oryza sativa Japonica Group] >gi|113645265|dbj|BAF28406.1|Os11g0543300 [Oryza sativa Japonica Group]	Unigene26513_All//2.00E-17//AT3G50170| unknown protein	Unigene26513_All//6.00E-27//ES800152				nr -
Unigene26514_All	1433	7.70	1.27	1.04	7.93	4.21	5.77	2.86	2.16	0.56	-2.60E+00	1.68E-31	Down	-2.89E+00	8.03E-34	Down	-9.14E-01	4.37E-09		-4.59E-01	6.30E-03		-4.07E-01	1.43E-01		-2.36E+00	9.63E-14	Down	Unigene26514_All//gi|297725701|ref|NP_001178214.1|//1.00E-17//Os07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1|Os07g0501200 [Oryza sativa Japonica Group]		Unigene26514_All//0.00E+00//gi|21097481|gb|BQ409794.1|BQ409794				nr +
Unigene26515_All	813	6.95	2.99	5.44	6.80	6.35	5.17	5.30	1.08	2.89	-1.22E+00	2.58E-06	Down	-3.55E-01	1.92E-01		-9.83E-02	7.54E-01		-3.97E-01	1.34E-01		-2.30E+00	1.80E-13	Down	-8.76E-01	5.42E-04		Unigene26515_All//gi|115485231|ref|NP_001067759.1|//1.00E-53//Os11g0312400 [Oryza sativa Japonica Group] >gi|585338|sp|Q08480.1|KAD2_ORYSJ RecName: Full=Adenylate kinase B; Short=AK B; AltName: Full=ATP-AMP transphosphorylase B >gi|391879|dbj|BAA01181.1| adenylate kinase-b [Oryza sativa] >gi|62734015|gb|AAX96124.1| adenylate kinase b (ec 2.7.4.3) (atp-amp transphosphorylase) [Oryza sativa Japonica Group] >gi|113644981|dbj|BAF28122.1|Os11g0312400 [Oryza sativa Japonica Group]	Unigene26515_All//4.00E-51//AT5G50370| adenylate kinase, putative	Unigene26515_All//0.00E+00//TC176332		ko00230|Purine metabolism	GO:0009117//GO:0016776//GO:0019205//GO:0032559//GO:0044424	nr -
Unigene26516_All	1040	4.18	4.82	2.25	3.16	2.55	3.26	6.67	2.73	2.15	2.08E-01	4.62E-01		-8.90E-01	3.45E-03		-3.10E-01	3.94E-01		4.30E-02	9.26E-01		-1.29E+00	6.81E-10	Down	-1.64E+00	2.81E-14	Down	Unigene26516_All//gi|115485231|ref|NP_001067759.1|//1.00E-116//Os11g0312400 [Oryza sativa Japonica Group] >gi|585338|sp|Q08480.1|KAD2_ORYSJ RecName: Full=Adenylate kinase B; Short=AK B; AltName: Full=ATP-AMP transphosphorylase B >gi|391879|dbj|BAA01181.1| adenylate kinase-b [Oryza sativa] >gi|62734015|gb|AAX96124.1| adenylate kinase b (ec 2.7.4.3) (atp-amp transphosphorylase) [Oryza sativa Japonica Group] >gi|113644981|dbj|BAF28122.1|Os11g0312400 [Oryza sativa Japonica Group]	Unigene26516_All//4.00E-107//AT5G63400| ADK1 (ADENYLATE KINASE 1); ATP binding / adenylate kinase/ nucleobase, nucleoside, nucleotide kinase/ nucleotide kinase/ phosphotransferase, phosphate group as acceptor	Unigene26516_All//0.00E+00//TC176332		ko00230|Purine metabolism		nr +
Unigene26517_All	785	1.93	2.84	5.02	2.22	1.80	3.39	0.75	0.96	0.51	5.55E-01	2.02E-01		1.38E+00	3.58E-05	Up	-3.04E-01	5.58E-01		6.12E-01	1.28E-01		3.46E-01	6.20E-01		-5.71E-01	4.78E-01		Unigene26517_All//gi|297796763|ref|XP_002866266.1|//4.00E-17//phox domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297312101|gb|EFH42525.1| phox domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene26517_All//7.00E-17//AT5G58440| SNX2a (SORTING NEXIN 2a); phosphoinositide binding	Unigene26517_All//2.00E-54//ES792635			GO:0006810//GO:0008289//GO:0044464	nr +
Unigene26519_All	962	9.19	37.50	14.72	28.95	77.86	76.62	22.77	119.39	95.87	2.03E+00	7.91E-75	Up	6.80E-01	1.01E-05		1.43E+00	8.77E-112	Up	1.40E+00	1.46E-97	Up	2.39E+00	0.00E+00	Up	2.07E+00	3.28E-245	Up	Unigene26519_All//gi|116874786|emb|CAL63739.1|//1.00E-104//beta-carotene hydroxylase [Citrus kinokuni]	Unigene26519_All//3.00E-89//AT5G52570| BETA-OHASE 2 (BETA-CAROTENE HYDROXYLASE 2); carotene beta-ring hydroxylase	Unigene26519_All//0.00E+00//TC147313		ko00906|Carotenoid biosynthesis		nr -
Unigene2652_All	1333	24.61	17.18	15.82	19.21	12.89	9.45	5.96	2.73	2.57	-5.18E-01	3.16E-08		-6.38E-01	4.67E-11		-5.75E-01	4.62E-09		-1.02E+00	3.43E-21	Down	-1.13E+00	2.82E-09	Down	-1.21E+00	1.13E-10	Down	Unigene2652_All//gi|5042435|gb|AAD38274.1|AC006193_30//1.00E-120//Unknown protein [Arabidopsis thaliana] >gi|34146814|gb|AAQ62415.1|At1g64980 [Arabidopsis thaliana]	Unigene2652_All//4.00E-121//AT1G64980| unknown protein	Unigene2652_All//0.00E+00//gi|164244033|gb|ES821447.1|ES821447				nr +
Unigene26520_All	785	30.59	3.68	9.16	23.67	26.32	80.32	2.64	18.69	1.73	-3.06E+00	1.44E-80	Down	-1.74E+00	1.76E-39	Down	1.53E-01	2.70E-01		1.76E+00	5.93E-116	Up	2.82E+00	1.74E-55	Up	-6.13E-01	1.11E-01		Unigene26520_All//gi|6562381|emb|CAB62537.1|//1.00E-81//pseudo-hevein [Hevea brasiliensis]	Unigene26520_All//2.00E-75//AT3G04720| PR4 (PATHOGENESIS-RELATED 4); chitin binding	Unigene26520_All//0.00E+00//TC173903		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0004553//GO:0006026//GO:0006970//GO:0009725//GO:0009814//GO:0030247//GO:0050832	nr +
Unigene26522_All	1036	2.12	3.08	1.13	15.87	10.47	6.76	72.40	10.49	13.38	5.39E-01	1.24E-01		-9.08E-01	4.56E-02		-6.00E-01	1.90E-06		-1.23E+00	1.96E-18	Down	-2.79E+00	1.68E-278	Down	-2.44E+00	1.15E-246	Down	Unigene26522_All//gi|157812633|gb|ABV80356.1|//1.00E-118//phosphoenolpyruvate carboxylase [Gossypium hirsutum]	Unigene26522_All//7.00E-112//AT3G14940| ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase	Unigene26522_All//0.00E+00//TC153428		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene26523_All	1676	1.25	0.63	0.83	5.65	4.40	3.42	3.20	0.62	0.62	-9.76E-01	2.85E-02		-5.96E-01	2.08E-01		-3.61E-01	5.12E-02		-7.23E-01	7.37E-05		-2.36E+00	3.88E-17	Down	-2.37E+00	7.73E-18	Down	Unigene26523_All//gi|297793657|ref|XP_002864713.1|//1.00E-115//nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310548|gb|EFH40972.1| nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26523_All//1.00E-107//AT5G60980| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene26523_All//0.00E+00//gi|5047437|gb|AI728585.1|AI728585		ko03040|Spliceosome	GO:0043231	nr -
Unigene26524_All	898	4.89	3.61	2.49	5.05	3.99	7.04	43.22	128.13	122.67	-4.39E-01	1.35E-01		-9.75E-01	1.30E-03		-3.40E-01	2.52E-01		4.80E-01	4.53E-02		1.57E+00	4.02E-204	Up	1.50E+00	7.92E-188	Up	Unigene26524_All//gi|15238163|ref|NP_198988.1|//1.00E-33//protein kinase family protein [Arabidopsis thaliana]	Unigene26524_All//2.00E-33//AT5G41730| protein kinase family protein				GO:0004672	nr +
Unigene26525_All	1304	74.71	72.90	80.94	63.53	66.97	51.36	22.44	17.18	10.88	-3.55E-02	5.92E-01		1.16E-01	4.11E-02		7.61E-02	2.42E-01		-3.07E-01	2.86E-08		-3.85E-01	1.58E-05		-1.04E+00	3.66E-29	Down	Unigene26525_All//gi|115486837|ref|NP_001068562.1|//3.00E-86//Os11g0708400 [Oryza sativa Japonica Group] >gi|75527236|gb|ABA95533.1| GDSL-like Lipase/Acylhydrolase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113645784|dbj|BAF28925.1|Os11g0708400 [Oryza sativa Japonica Group]	Unigene26525_All//2.00E-83//AT3G11210| GDSL-motif lipase/hydrolase family protein	Unigene26525_All//0.00E+00//gi|109883921|gb|DW512891.1|DW512891			GO:0016787//GO:0044238	nr +
Unigene26526_All	698	6.37	7.91	10.45	7.92	10.56	9.58	20.41	10.18	8.22	3.13E-01	2.32E-01		7.14E-01	1.46E-03		4.14E-01	5.63E-02		2.74E-01	2.81E-01		-1.00E+00	2.33E-13	Down	-1.31E+00	1.05E-20	Down	Unigene26526_All//gi|21536936|gb|AAM61277.1|//8.00E-38//protein phosphatase 2C-1ike [Arabidopsis thaliana]	Unigene26526_All//8.00E-33//AT5G06750| protein phosphatase 2C family protein / PP2C family protein	Unigene26526_All//0.00E+00//TC160266			GO:0004721//GO:0006464//GO:0043169//GO:0043231//GO:0043234	nr +
Unigene26527_All	1678	4.77	10.96	6.82	0.80	1.99	2.23	0.23	1.32	1.28	1.20E+00	2.52E-18	Up	5.16E-01	3.12E-03		1.31E+00	8.86E-05	Up	1.48E+00	6.96E-06	Up	2.54E+00	4.83E-08	Up	2.50E+00	6.75E-08	Up	Unigene26527_All//gi|162134187|gb|ABX82525.1|//2.00E-52//S-locus F-box-like protein b [Petunia integrifolia subsp. inflata]	Unigene26527_All//3.00E-30//AT4G12560| F-box family protein	Unigene26527_All//0.00E+00//gi|109862386|gb|DW491363.1|DW491363				nr +
Unigene26529_All	1030	56.28	17.41	24.35	63.50	90.94	83.75	362.71	106.07	236.25	-1.69E+00	2.21E-94	Down	-1.21E+00	3.87E-55	Down	5.18E-01	7.72E-26		3.99E-01	1.28E-13		-1.77E+00	0.00E+00	Down	-6.19E-01	2.12E-147		Unigene26529_All//gi|211906546|gb|ACJ11766.1|//1.00E-169//class III peroxidase [Gossypium hirsutum]	Unigene26529_All//2.00E-123//AT4G33420| peroxidase, putative	Unigene26529_All//0.00E+00//TC160803		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209//GO:0031410	nr +
Unigene26530_All	497	8.11	26.10	19.93	8.32	15.66	16.81	2.38	5.55	4.25	1.69E+00	2.10E-21	Up	1.30E+00	5.34E-11	Up	9.13E-01	4.17E-06		1.01E+00	3.73E-07	Up	1.22E+00	4.07E-04	Up	8.35E-01	2.91E-02		Unigene26530_All//gi|99455082|gb|AAG03119.1|AC004133_13//7.00E-06//F5J9.24 [Arabidopsis thaliana]		Unigene26530_All//1.00E-140//TC166793				nr +
Unigene26531_All	1175	4.10	16.95	10.11	5.85	14.98	10.80	1.80	4.73	5.63	2.05E+00	4.35E-42	Up	1.30E+00	3.87E-13	Up	1.36E+00	1.91E-24	Up	8.85E-01	1.63E-08		1.39E+00	5.00E-09	Up	1.65E+00	1.31E-13	Up	Unigene26531_All//gi|115473321|ref|NP_001060259.1|//3.00E-17//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene26531_All//1.00E-11//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene26531_All//0.00E+00//TC166793			GO:0044464	nr -
Unigene26535_All	3109	0.82	0.70	0.27	4.17	5.04	4.69	17.94	6.65	6.96	-2.35E-01	5.75E-01		-1.59E+00	2.80E-04	Down	2.75E-01	5.79E-02		1.72E-01	3.12E-01		-1.43E+00	6.85E-87	Down	-1.37E+00	1.98E-83	Down	Unigene26535_All//gi|15242342|ref|NP_197062.1|//9.00E-55//LNG1 (LONGIFOLIA1) [Arabidopsis thaliana]	Unigene26535_All//2.00E-46//AT1G74160| unknown protein	Unigene26535_All//0.00E+00//TC175671				nr -
Unigene26536_All	1249	3.31	1.34	1.49	3.51	3.89	4.34	6.26	6.39	3.09	-1.31E+00	2.62E-05	Down	-1.15E+00	3.03E-04	Down	1.48E-01	6.37E-01		3.06E-01	2.81E-01		2.94E-02	8.99E-01		-1.02E+00	3.97E-08	Down	Unigene26536_All//gi|110432095|gb|ABG73621.1|//1.00E-125//leucine-rich repeat receptor-1ike kinase [Populus tomentosa]	Unigene26536_All//2.00E-106//AT3G25560| NIK2 (NSP-INTERACTING KINASE 2); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene26536_All//6.00E-148//TC141331		ko04626|Plant-pathogen interaction		nr +
Unigene26539_All	2346	1.67	0.82	0.75	9.34	6.28	2.19	1.42	0.43	0.36	-1.03E+00	9.77E-04	Down	-1.16E+00	4.07E-04	Down	-5.73E-01	8.92E-08		-2.09E+00	6.90E-52	Down	-1.74E+00	1.37E-07	Down	-2.00E+00	2.40E-09	Down	Unigene26539_All//gi|115473321|ref|NP_001060259.1|//1.00E-32//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene26539_All//9.00E-09//AT2G17920| nucleic acid binding / zinc ion binding	Unigene26539_All//3.00E-37//ES823673				nr -
Unigene26543_All	1117	6.56	105.83	6.58	3.30	6.57	10.63	5.26	11.64	30.07	4.01E+00	0.00E+00	Up	4.60E-03	1.00E+00		9.93E-01	1.46E-06		1.69E+00	6.52E-21	Up	1.15E+00	5.75E-15	Up	2.51E+00	3.05E-113	Up	Unigene26543_All//gi|34550779|gb|AAQ74955.1|//1.00E-68//6b1aa-8e [Gossypium barbadense]	Unigene26543_All//3.00E-56//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene26543_All//0.00E+00//TC133678			GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr +
Unigene26546_All	1149	24.91	12.88	23.13	17.56	45.10	54.09	18.44	11.31	25.83	-9.52E-01	1.38E-19		-1.07E-01	3.85E-01		1.36E+00	4.96E-72	Up	1.62E+00	9.00E-102	Up	-7.05E-01	5.13E-11		4.87E-01	2.03E-08		Unigene26546_All//gi|23297181|gb|AAN12515.1|//2.00E-97//phosphoenolpyruvate carboxylase kinase [Glycine max] >gi|23297184|gb|AAN12516.1| phosphoenolpyruvate carboxylase kinase [Glycine max] >gi|34809054|gb|AAQ82624.1| phosphoenolpyruvate-carboxylase kinase [Glycine max] >gi|34809056|gb|AAQ82625.1| phosphoenolpyruvate-carboxylase kinase [Glycine max]	Unigene26546_All//gi|78326184|gb|DT546458.1|DT546458	Unigene26546_All//0.00E+00//gi|78326184|gb|DT546458.1|DT546458		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene26547_All	981	10.72	4.39	3.58	20.62	11.72	18.69	14.44	7.54	8.73	-1.29E+00	4.97E-12	Down	-1.58E+00	2.15E-15	Down	-8.14E-01	5.03E-13		-1.41E-01	3.25E-01		-9.37E-01	6.13E-12		-7.26E-01	2.84E-08		Unigene26547_All//gi|87162616|gb|AB028411.1|//1.00E-11//C3368.2 , related [Medicago truncatula]	Unigene26547_All//3.00E-13//AT5G60030| unknown protein	Unigene26547_All//0.00E+00//AI730380		ko03040|Spliceosome		nr -
Unigene2655_All	1248	4.15	1.30	5.67	3.75	2.90	3.44	5.05	3.18	3.96	-1.68E+00	5.80E-09	Down	4.51E-01	5.23E-02		-3.73E-01	1.91E-01		-1.26E-01	7.01E-01		-6.66E-01	1.45E-03		-3.51E-01	9.38E-02		Unigene2655_All//gi|18420226|ref|NP_568040.1|//3.00E-64//phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis thaliana]	Unigene2655_All//2.00E-65//AT4G38370| phosphoglycerate/bisphosphoglycerate mutase family protein	Unigene2655_All//0.00E+00//gi|109882987|gb|DW511957.1|DW511957				nr -

Unigene26550_All	683	48.49	25.30	22.38	25.67	26.07	34.39	1.86	3.37	2.27	-9.39E-01	4.80E-22		-1.12E+00	5.96E-28	Down	2.19E-02	8.99E-01		4.22E-01	1.42E-04		8.58E-01	2.27E-02		2.93E-01	5.53E-01		Unigene26550_All//gi|45183613|gb|AS55478.1|//4.00E-23//Tha8 [Zea mays]	Unigene26550_All//7.00E-55//AT3G27750| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: VPS9B (TAIR:AT5G09320.1); Has 54 Blast hits to 54 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene26550_All//0.00E+00//DW229368			GO:0009536	nr -
Unigene26551_All	984	18.72	20.13	19.70	37.31	38.18	18.59	13.71	18.77	16.88	1.05E-01	4.47E-01		7.38E-02	6.21E-01		3.32E-02	8.01E-01		-1.01E+00	2.67E-29	Down	4.54E-01	7.55E-05		3.01E-01	1.32E-02		Unigene26551_All//gi|297727877|ref|NP_001176302.1|//4.00E-13//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1|Os11g0106066 [Oryza sativa Japonica Group]	Unigene26551_All//9.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene26551_All//2.00E-159//BF270114				nr -
Unigene26553_All	925	5.09	12.33	6.27	9.75	4.50	6.49	30.12	65.97	25.67	1.28E+00	9.81E-13	Up	3.02E-01	2.59E-01		-1.11E+00	5.73E-10	Down	-5.86E-01	1.92E-03		1.13E+00	5.50E-66	Up	-2.31E-01	1.23E-02		Unigene26553_All//gi|113367188|gb|ABI34651.1|//1.00E-54//bZIP transcription factor bZIP73A [Glycine max]	Unigene26553_All//6.00E-35//AT3G30530| ATBZIP42 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 42); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene26553_All//0.00E+00//gi|109885741|gb|DW514711.1|DW514711	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0043231	nr +
Unigene26554_All	1482	11.16	4.65	6.40	11.16	9.90	14.45	8.22	3.75	2.74	-1.26E+00	6.10E-18	Down	-8.03E-01	1.69E-08		-1.73E-01	2.55E-01		3.72E-01	1.63E-03		-1.13E+00	7.78E-14	Down	-1.58E+00	2.43E-23	Down	Unigene26554_All//gi|115474161|ref|NP_001060679.1|//1.00E-101//Os07g0685800 [Oryza sativa Japonica Group] >gi|33146492|dbj|BAC79601.1|carbonyl reductase -like protein [Oryza sativa Japonica Group] >gi|50509139|dbj|BAD30279.1|carbonyl reductase -like protein [Oryza sativa Japonica Group] >gi|113612215|dbj|BAF22593.1|Os07g0685800 [Oryza sativa Japonica Group]	Unigene26554_All//3.00E-72//AT1G01800| short-chain dehydrogenase/reductase (SDR) family protein	Unigene26554_All//0.00E+00//gi|164370146|gb|ES804969.1|ES804969		ko04146|Peroxisome//ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0003824//GO:0008152//GO:0043231	nr -
Unigene26557_All	897	28.99	28.36	19.53	31.71	23.80	25.78	33.37	23.58	12.26	-3.18E-02	7.85E-01		-5.70E-01	2.07E-07		-4.14E-01	1.03E-05		-2.99E-01	3.43E-03		-5.01E-01	1.19E-08		-1.44E+00	4.11E-49	Down	Unigene26557_All//gi|29423617|gb|AA073433.1|//1.00E-88//vacuolar membrane ATPase subunit c'' [Citrus limon]	Unigene26557_All//2.00E-66//AT4G32530| vacuolar ATP synthase, putative / V-ATPase, putative	Unigene26557_All//0.00E+00//TC137529		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0005488//GO:0006754//GO:0006818//GO:0015077//GO:0017111//GO:0031224//GO:0033176//GO:0043231	nr -
Unigene26558_All	1508	16.58	28.19	33.12	57.25	26.83	68.43	62.30	496.98	58.12	7.65E-01	5.44E-20		9.98E-01	4.48E-35		-1.09E+00	2.42E-89	Down	2.58E-01	1.96E-07		3.00E+00	0.00E+00	Up	-1.00E-01	4.77E-02		Unigene26558_All//gi|62526573|gb|AA384672.1|//1.00E-174//aldo/keto reductase AKR [Manihot esculenta]	Unigene26558_All//2.00E-152//AT1G60710| ATB2; oxidoreductase	Unigene26558_All//0.00E+00//TC148226		ko00010|Glycolysis / Gluconeogenesis//ko00053|Ascorbate and aldarate metabolism//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene26561_All	1354	0.35	2.54	1.22	1.62	1.25	1.40	2.44	3.77	3.56	2.87E+00	3.10E-11	Up	1.81E+00	1.76E-03		-3.77E-01	4.06E-01		-2.09E-01	6.59E-01		6.29E-01	7.90E-03		5.48E-01	2.13E-02		Unigene26561_All//gi|297850668|ref|XP_002893215.1|//7.00E-90//SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339057|gb|EFH69474.1|SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26561_All//6.00E-90//AT4G08690| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene26561_All//0.00E+00//TC168930			GO:0051234	nr +
Unigene26563_All	718	18.22	8.12	8.31	26.36	15.64	8.87	41.87	19.85	45.39	-1.17E+00	9.31E-13	Down	-1.13E+00	1.17E-11	Down	-7.54E-01	9.63E-11		-1.57E+00	2.06E-30	Down	-1.08E+00	1.69E-30	Down	1.16E-01	2.04E-01			Unigene26563_All//6.00E-165//TC170189				
Unigene26564_All	911	22.92	51.84	43.08	37.07	42.37	45.41	50.40	61.48	42.94	1.18E+00	1.39E-44	Up	9.11E-01	8.03E-24		1.93E-01	2.89E-02		2.93E-01	3.80E-04		2.87E-01	5.55E-06		-2.31E-01	8.93E-04		Unigene26564_All//gi|15237703|ref|NP_201248.1|//2.00E-86//octicosapeptide/Phox/Bem1p (PB1) domain-containing protein [Arabidopsis thaliana] >gi|17064916|gb|AAL32612.1|Unknown protein [Arabidopsis thaliana] >gi|31711922|gb|AAP68317.1|At5g64430 [Arabidopsis thaliana]	Unigene26564_All//2.00E-76//AT5G64430| octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	Unigene26564_All//0.00E+00//gi|78337751|gb|DT558025.1|DT558025			GO:0009526	nr +
Unigene26567_All	602	21.90	13.47	23.53	94.58	71.67	42.39	51.41	32.70	27.66	-7.02E-01	6.13E-06		1.03E-01	5.65E-01		-4.00E-01	3.07E-10		-1.16E+00	9.31E-57	Down	-6.53E-01	7.75E-14		-8.94E-01	5.72E-24		Unigene26567_All//gi|20269031|emb|CAC84706.1|//2.00E-40//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene26567_All//2.00E-18//AT5G65670| IAA9 (INDOLE-3-ACETIC ACID INDUCIBLE 9); transcription factor	Unigene26567_All//0.00E+00//gi|164284672|gb|ES833126.1|ES833126			GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr -
Unigene26569_All	1950	16.07	5.66	10.68	4.01	3.44	1.92	0.17	0.21	0.25	-1.50E+00	2.37E-43	Down	-5.90E-01	2.60E-09		-2.20E-01	3.28E-01		-1.06E+00	2.74E-07	Down	3.05E-01	7.57E-01		4.99E-01	6.12E-01		Unigene26569_All//gi|224081184|ref|XP_002306325.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222855774|gb|EEE93321.1|cytochrome P450 [Populus trichocarpa]	Unigene26569_All//4.00E-176//AT1G61950| CYP89A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene26569_All//0.00E+00//TC145850		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016712	nr +
Unigene2657_All	1417	0.37	0.68	0.53	0.63	0.32	0.83	0.54	0.06	0.14	8.80E-01	2.13E-01		5.11E-01	5.47E-01		-1.00E+00	1.61E-01		3.89E-01	5.80E-01		-3.19E+00	7.92E-04	Down	-1.93E+00	1.14E-02		Unigene2657_All//gi|18420226|ref|NP_568040.1|//4.00E-64//phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis thaliana]	Unigene2657_All//2.00E-65//AT4G38370| phosphoglycerate/bisphosphoglycerate mutase family protein	Unigene2657_All//0.00E+00//gi|109882987|gb|DW511957.1|DW511957				nr -
Unigene26572_All	1221	7.80	7.22	4.80	16.20	26.26	8.06	26.28	15.92	27.64	-1.11E-01	6.10E-01		-7.01E-01	2.83E-04		6.97E-01	3.90E-15		-1.01E+00	4.54E-16	Down	-7.24E-01	5.38E-17		7.24E-02	4.52E-01		Unigene26572_All//gi|224136918|ref|XP_002322448.1|//1.00E-120//f-box family protein [Populus trichocarpa] >gi|222869444|gb|EEF06575.1| f-box family protein [Populus trichocarpa]	Unigene26572_All//1.00E-98//AT1G63090| AtPP2-A11 (Phloem protein 2-A11); carbohydrate binding	Unigene26572_All//0.00E+00//TC144403			GO:0005488	nr +
Unigene26574_All	1279	9.16	4.56	3.79	9.23	6.00	6.50	5.49	3.27	3.49	-1.01E+00	2.97E-09	Down	-1.27E+00	1.60E-12	Down	-6.21E-01	4.60E-05		-5.07E-01	1.84E-03		-7.48E-01	1.44E-04		-6.54E-01	6.18E-04		Unigene26574_All//gi|115440683|ref|NP_001044621.1|//2.00E-80//Os01g0817000 [Oryza sativa Japonica Group] >gi|113534152|dbj|BAF06535.1|Os01g0817000 [Oryza sativa Japonica Group]	Unigene26574_All//2.00E-92//AT1G09575| unknown protein	Unigene26574_All//0.00E+00//gi|78351053|gb|DT571327.1|DT571327			GO:0043231	nr +
Unigene26575_All	1239	5.19	9.28	11.91	11.18	10.73	10.72	14.23	16.73	19.00	8.38E-01	7.31E-07		1.20E+00	3.10E-14	Up	-5.92E-02	7.69E-01		-6.07E-02	7.25E-01		2.34E-01	3.98E-02		4.17E-01	2.15E-05		Unigene26575_All//gi|149939499|gb|ABR45956.1|//5.00E-94//coronitine insensitive 1 [Arabidopsis lyrata]	Unigene26575_All//5.00E-94//AT2G39940| COI1 (CORONATINE INSENSITIVE 1); protein binding / ubiquitin-protein ligase	Unigene26575_All//0.00E+00//ES843332		ko04626|Plant-pathogen interaction	GO:0005488//GO:0006952//GO:0009611//GO:0009639//GO:0009719//GO:0009908//GO:0019787//GO:0023033//GO:0031461//GO:0043161//GO:0051707	nr +
Unigene26576_All	776	186.16	92.46	78.43	100.91	102.64	65.36	107.99	34.79	40.04	-1.01E+00	9.06E-106	Down	-1.25E+00	8.02E-144	Down	2.45E-02	7.79E-01		-6.27E-01	1.11E-27		-1.63E+00	2.76E-158	Down	-1.43E+00	4.61E-134	Down	Unigene26576_All//gi|225435032|ref|XP_002284277.1|//3.00E-71//PREDICTED: similar to Histone H2B isoform 1 [Vitis vinifera]	Unigene26576_All//6.00E-45//AT5G59910| HTB4; DNA binding	Unigene26576_All//0.00E+00//TC146180			GO:0000785//GO:0003676//GO:0031981//GO:0034728	nr +
Unigene26579_All	819	31.24	12.62	14.04	8.70	7.06	6.67	16.06	6.02	9.34	-1.31E+00	7.66E-29	Down	-1.15E+00	7.26E-23	Down	-3.00E-01	1.89E-01		-3.82E-01	9.42E-02		-1.41E+00	9.60E-21	Down	-7.82E-01	1.09E-08		Unigene26579_All//gi|50253464|gb|AAT71934.1|//3.00E-26//At2g47485 [Arabidopsis thaliana] >gi|51972104|gb|AAU15156.1|At2g47485 [Arabidopsis thaliana]	Unigene26579_All//9.00E-24//AT2G47485| unknown protein	Unigene26579_All//0.00E+00//ES809351				nr +
Unigene26580_All	1193	22.94	9.47	10.13	7.72	7.85	6.25	4.11	3.19	2.27	-1.28E+00	1.12E-29	Down	-1.18E+00	2.94E-25	Down	2.34E-02	9.27E-01		-3.07E-01	1.31E-01		-3.67E-01	1.46E-01		-8.56E-01	2.74E-04		Unigene26580_All//gi|30690114|ref|NP_195199.2|//6.00E-76//ribosome-binding factor A family protein [Arabidopsis thaliana] >gi|78099793|sp|O65693.2|RBFA_ARATH RecName: Full=Probable ribosome-binding factor A, chloroplastic; Flags: Precursor >gi|30023650|gb|AAP13358.1|At4g34730 [Arabidopsis thaliana]	Unigene26580_All//5.00E-67//AT4G34730| ribosome-binding factor A family protein	Unigene26580_All//0.00E+00//TC156628			GO:0009536//GO:0042254	nr +
Unigene26584_All	909	15.25	91.36	34.86	15.45	8.75	11.48	83.72	83.55	176.32	2.58E+00	3.34E-230	Up	1.19E+00	9.08E-30	Up	-8.21E-01	2.57E-09		-4.29E-01	3.96E-03		-3.10E-03	9.98E-01		1.07E+00	6.07E-162	Up	Unigene26584_All//gi|7770334|gb|AAF69704.1|AC016041_9//5.00E-29//F27J15.21 [Arabidopsis thaliana] >gi|45476547|gb|AAS65939.1|At1g49000 [Arabidopsis thaliana] >gi|46338832|gb|AAS88762.1|At1g49000 [Arabidopsis thaliana]	Unigene26584_All//3.00E-26//AT1G49000| unknown protein	Unigene26584_All//0.00E+00//EX168841			GO:0043231	nr -
Unigene26585_All	1138	1.66	1.16	1.31	6.61	10.32	3.69	44.99	91.56	13.48	-5.16E-01	2.77E-01		-3.37E-01	5.04E-01		6.43E-01	3.72E-05		-8.41E-01	5.41E-05		1.03E+00	1.11E-95	Up	-1.74E+00	5.11E-109	Down	Unigene26585_All//gi|15241598|ref|NP_196452.1|//8.00E-62//GRAM domain-containing protein / ABA-responsive protein-related [Arabidopsis thaliana] >gi|75172412|sp|Q9FTA0.1|GEML4_ARATH RecName: Full=GEM-like protein 4	Unigene26585_All//4.00E-63//AT5G08350| GRAM domain-containing protein / ABA-responsive protein-related	Unigene26585_All//0.00E+00//TC176476				nr +
Unigene26588_All	702	37.41	26.85	25.49	42.65	41.30	27.47	44.57	33.52	19.41	-4.79E-01	5.95E-06		-5.54E-01	3.86E-07		-4.62E-02	7.25E-01		-6.35E-01	3.48E-11		-4.11E-01	1.68E-06		-1.20E+00	1.14E-38	Down	Unigene26588_All//gi|18401305|ref|NP_565633.1|//1.00E-66//AGO4 (ARGONAUTE 4); nucleic acid binding [Arabidopsis thaliana] >gi|20197419|gb|AAC77862.2|Argonaute (AGO4)-like protein [Arabidopsis thaliana]	Unigene26588_All//8.00E-68//AT2G27040| AGO4 (ARGONAUTE 4); nucleic acid binding	Unigene26588_All//0.00E+00//gi|73863130|gb|DT463869.1|DT463869			GO:0000790//GO:0006305//GO:0006342//GO:0008135//GO:0016246//GO:0016604//GO:0034968//GO:0042742	nr +
Unigene26589_All	808	5.83	8.28	11.53	10.85	6.78	4.64	1.41	3.41	1.43	5.06E-01	2.67E-02		9.85E-01	6.47E-07		-6.79E-01	1.67E-04		-1.23E+00	4.92E-10	Down	1.27E+00	2.43E-04	Up	1.74E-02	9.72E-01			Unigene26589_All//2.00E-60//DR457975				
Unigene2659_All	2111	13.68	7.15	8.90	19.28	20.08	15.81	9.07	3.27	6.36	-9.36E-01	3.19E-19		-6.20E-01	2.32E-09		5.88E-02	5.81E-01		-2.86E-01	5.75E-04		-1.47E+00	1.09E-31	Down	-5.13E-01	2.94E-06		Unigene2659_All//gi|18418038|ref|NP_567884.1|//1.00E-55//TIFY8 (TIFY DOMAIN PROTEIN 8) [Arabidopsis thaliana] >gi|75147164|sp|Q84MB2.1|TIF8_ARATH RecName: Full=Protein TIFY 8 >gi|30102642|gb|AAP21239.1|At4g32570 [Arabidopsis thaliana]	Unigene2659_All//9.00E-49//AT4G32570| TIFY8 (TIFY DOMAIN PROTEIN 8)	Unigene2659_All//0.00E+00//TC132422	Tify	ko04626|Plant-pathogen interaction//ko00904|Diterpenoid biosynthesis		nr -
Unigene26590_All	951	6.93	7.41	7.34	6.44	3.26	5.89	16.49	2.15	5.86	9.54E-02	6.78E-01		8.15E-02	7.29E-01		-9.83E-01	9.19E-06		-1.30E-01	6.37E-01		-2.94E+00	6.24E-62	Down	-1.49E+00	2.18E-27	Down	Unigene26590_All//gi|117650695|gb|ABK54297.1|//3.00E-28//glycine-rich protein [Gossypium hirsutum]		Unigene26590_All//0.00E+00//TC176421		ko03040|Spliceosome		nr +
Unigene26591_All	961	28.37	38.86	35.08	20.99	30.39	46.76	14.78	27.49	27.24	4.54E-01	2.01E-07		3.06E-01	1.63E-03		5.34E-01	8.74E-09		1.16E+00	3.70E-44	Up	8.95E-01	5.52E-20		8.82E-01	7.96E-20		Unigene26591_All//gi|225447533|ref|XP_002268473.1|//4.00E-13//PREDICTED: hypothetical protein [Vitis vinifera]					GO:0003677//GO:0006351//GO:0043231	nr +

Unigene26592_All	809	59.63	45.47	32.45	19.46	11.62	17.59	10.98	19.12	5.22	-3.91E-01	2.67E-07		-8.78E-01	2.18E-27		-7.44E-01	7.95E-09		-1.46E-01	3.88E-01		8.01E-01	4.22E-10		-1.07E+00	7.64E-10	Down	Unigene26592_All//gi|115440869|ref|NP_001044714.1|//2.00E-40//0s01g0833600 [Oryza sativa Japonica Group] >gi|113534245|dbj|BAF06628.1|Os01g0833600 [Oryza sativa Japonica Group]	Unigene26592_All//1.00E-05//AT1G68660| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: protein catabolic process; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Adaptor protein ClpS, core (InterPro:IPR003769), Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like (InterPro:IPR014719); Has 513 Blast hits to 513 proteins in 129 species: Archae - 0; Bacteria - 273; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 201 (source: NCBI BLink).	Unigene26592_All//0.00E+00//gi|109884051|gb|DW513021.1|DW513021			GO:0009057//GO:0043231	nr -
Unigene26595_All	832	13.90	13.46	10.37	40.00	28.60	37.51	85.48	95.70	15.23	-4.63E-02	7.93E-01		-4.23E-01	1.63E-02		-4.84E-01	1.31E-08		-9.26E-02	4.14E-01		1.63E-01	2.64E-03		-2.49E+00	6.59E-240	Down			Unigene26595_All//0.00E+00//TC159600					
Unigene26597_All	772	6.78	11.42	6.41	11.29	12.09	13.10	46.06	96.96	412.37	7.53E-01	1.10E-04		-7.93E-02	7.73E-01		9.83E-02	6.68E-01		2.15E-01	2.96E-01		1.07E+00	2.39E-74	Up	3.16E+00	0.00E+00	Up	Unigene26597_All//gi|198449163|gb|ACH88751.1|//3.00E-54//WRKY DNA binding protein [Fragaria x ananassa]	Unigene26597_All//1.00E-46//AT5G13080| WRKY75; transcription factor	Unigene26597_All//0.00E+00//gi|109868468|gb|DW497444.1|DW497444	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0010468//GO:0043231	nr -
Unigene26598_All	841	10.89	11.81	4.50	17.41	15.56	13.86	59.27	41.70	56.18	1.17E-01	5.73E-01		-1.28E+00	6.10E-10	Down	-1.63E-01	3.15E-01		-3.30E-01	2.81E-02		-5.07E-01	3.79E-14		-7.73E-02	3.13E-01		Unigene26598_All//gi|222423247|dbj|BAH19600.1|//7.00E-49//AT2G35610 [Arabidopsis thaliana]	Unigene26598_All//1.00E-50//AT2G35610| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: Golgi apparatus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Reticulon (InterPro:IPR003389); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G70630.1); Has 210 Blast hits to 209 proteins in 24 species: Archae - 0; Bacteria - 6; Metazoa - 3; Fungi - 0; Plants - 175; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink).	Unigene26598_All//0.00E+00//TC144544			GO:0043231	nr +
Unigene26599_All	518	7.27	5.09	6.37	60.49	40.68	40.63	4.82	1.69	0.00	-5.16E-01	1.05E-01		-1.90E-01	6.00E-01		-5.72E-01	7.26E-11		-5.74E-01	7.30E-10		-1.51E+00	6.17E-05	Down	-1.22E+01	2.32E-18	Down	Unigene26599_All//gi|115459422|ref|NP_001053311.1|//3.00E-37//0s04g0515400 [Oryza sativa Japonica Group] >gi|32482945|emb|CAE02349.1|OSJNBb0072M01.10 [Oryza sativa (japonica cultivar-group)] >gi|38345698|emb|CAE01918.2|OSJNBb0070J16.14 [Oryza sativa (japonica cultivar-group)] >gi|113564882|dbj|BAF15225.1|Os04g0515400 [Oryza sativa Japonica Group] >gi|116310843|emb|CAH67630.1|OSIGBa0140J09.11 [Oryza sativa (indica cultivar-group)]	Unigene26599_All//6.00E-28//AT3G25400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: NTP Pyrophosphohydrolase MazG-related, RS21-C6 (InterPro:IPR011294), EAR (InterPro:IPR009039), NTP pyrophosphohydrolase MazG, putative catalytic core (InterPro:IPR004518); Has 572 Blast hits to 572 proteins in 181 species: Archae - 11; Bacteria - 286; Metazoa - 71; Fungi - 1; Plants - 31; Viruses - 0; Other Eukaryotes - 172 (source: NCBI BLink).	Unigene26599_All//0.00E+00//CA993230				nr +
Unigene266_All	2072	16.01	5.26	13.16	35.68	39.29	22.65	16.47	5.83	6.35	-1.61E+00	2.11E-50	Down	-2.83E-01	4.21E-03		1.39E-01	1.91E-02		-6.56E-01	2.58E-28		-1.50E+00	3.25E-57	Down	-1.38E+00	6.30E-52	Down	Unigene266_All//gi|47498987|gb|AAT28309.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Pyrus pyrifolia]	Unigene266_All//0.00E+00//AT1G28440| HSL1 (HAESA-Like 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene266_All//0.00E+00//gi|78341271|gb|DT561545.1|DT561545		ko04626|Plant-pathogen interaction		nr +
Unigene26601_All	1166	5.83	2.82	2.19	5.90	5.29	2.44	5.11	0.07	3.38	-1.05E+00	5.10E-06	Down	-1.41E+00	1.06E-08	Down	-1.57E-01	5.63E-01		-1.27E+00	1.89E-08	Down	-6.16E+00	7.43E-39	Down	-5.96E-01	4.37E-03		Unigene26601_All//gi|15233971|ref|NP_195015.1|//8.00E-60//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|71189062|sp|Q82632.1|GATA9_ARATH RecName: Full=GATA transcription factor 9 >gi|30725358|gb|AAP37701.1|At4g32890 [Arabidopsis thaliana]	Unigene26601_All//4.00E-57//AT4G32890| zinc finger (GATA type) family protein	Unigene26601_All//0.00E+00//TC144325	C2C2-GATA		GO:0046872	nr -
Unigene26603_All	693	23.25	3.00	7.53	45.43	30.26	29.72	100.24	43.91	55.48	-2.96E+00	1.91E-52	Down	-1.63E+00	2.98E-24	Down	-5.86E-01	2.23E-11		-6.12E-01	4.81E-11		-1.19E+00	1.59E-81	Down	-8.54E-01	9.79E-49		Unigene26603_All//gi|30690755|ref|NP_174240.2|//2.00E-63//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|79318852|ref|NP_001031109.1|dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75223284|sp|Q6NPR7.1|PMT0_ARATH RecName: Full=Probable methyltransferase PMT24 >gi|38564284|gb|AAR23721.1|At1g29470 [Arabidopsis thaliana]	Unigene26603_All//8.00E-65//AT1G29470| dehydration-responsive protein-related	Unigene26603_All//0.00E+00//TC140843			GO:0043231	nr -
Unigene26604_All	1215	5.64	2.63	0.26	4.92	9.44	2.38	4.70	0.45	2.46	-1.10E+00	1.61E-06	Down	-4.42E+00	5.91E-30	Down	9.40E-01	3.59E-09		-1.05E+00	1.24E-05	Down	-3.39E+00	3.33E-26	Down	-9.34E-01	1.80E-05		Unigene26604_All//gi|115449017|ref|NP_001048288.1|//2.00E-62//0s02g0776900 [Oryza sativa Japonica Group] >gi|51039831|tpg|DAA05205.1|TPA_exp: growth-regulating factor 1 [Oryza sativa (japonica cultivar-group)] >gi|113537819|dbj|BAF10202.1|Os02g0776900 [Oryza sativa Japonica Group]	Unigene26604_All//1.00E-50//AT3G13960| AtGRF5 (GROWTH-REGULATING FACTOR 5); transcription activator	Unigene26604_All//0.00E+00//TC157130	GRF		GO:0043231	nr +
Unigene26607_All	1641	1.56	3.03	1.10	1.55	1.83	1.87	1.88	1.35	0.80	9.54E-01	4.54E-04		-5.02E-01	2.39E-01		2.38E-01	5.71E-01		2.74E-01	4.92E-01		-4.79E-01	1.40E-01		-1.23E+00	9.25E-05	Down	Unigene26607_All//gi|42563328|ref|NP_178012.2|//0.00E+00//pseudouridine synthase family protein [Arabidopsis thaliana] >gi|75110951|sp|Q5XET6.1|PUS3_ARATH RecName: Full=RNA pseudouridine synthase 3, mitochondrial; AltName: Full=RNA-uridine isomerase 3; AltName: Full=RNA pseudouridylate synthase 3; Flags: Precursor >gi|53850479|gb|AAU95416.1|At1g78910 [Arabidopsis thaliana] >gi|56790228|gb|AAW30031.1|At1g78910 [Arabidopsis thaliana]	Unigene26607_All//2.00E-179//AT1G78910| pseudouridine synthase family protein	Unigene26607_All//0.00E+00//CO091003			GO:0003676//GO:0009451//GO:0016866//GO:0043231	nr -
Unigene26608_All	1067	2.30	3.13	1.90	4.90	6.04	5.38	2.81	1.21	1.68	4.44E-01	2.01E-01		-2.81E-01	5.20E-01		3.00E-01	2.31E-01		1.33E-01	6.46E-01		-1.21E+00	2.22E-04	Down	-7.44E-01	1.61E-02				Unigene26608_All//1.00E-77//DT465448					ESTscan -
Unigene26609_All	1009	24.63	6.23	14.09	14.27	15.15	7.03	3.18	1.24	1.11	-1.98E+00	1.34E-50	Down	-8.06E-01	1.61E-12		8.68E-02	6.12E-01		-1.02E+00	3.80E-12	Down	-1.36E+00	2.29E-05	Down	-1.53E+00	1.77E-06	Down	Unigene26609_All//gi|297805064|ref|XP_002870416.1|//7.00E-98//peptidyl-prolyl cis-trans isomerase [Arabidopsis lyrata subsp. lyrata] >gi|297316252|gb|EFH46675.1|peptidyl-prolyl cis-trans isomerase [Arabidopsis lyrata subsp. lyrata]	Unigene26609_All//7.00E-43//AT5G35100| peptidyl-prolyl cis-trans isomerase	Unigene26609_All//0.00E+00//gi|48791841|gb|CO093155.1|CO093155			GO:0009536//GO:0016859//GO:0044267//GO:0044436	nr +
Unigene2661_All	1672	0.88	0.52	0.25	0.51	0.51	0.27	1.95	1.45	0.83	-7.66E-01	1.59E-01		-1.78E+00	4.08E-03		2.37E-02	9.92E-01		-9.07E-01	2.47E-01		-4.25E-01	1.83E-01		-1.22E+00	6.24E-05	Down	Unigene2661_All//gi|15230968|ref|NP_191375.1|//3.00E-25//XIJ; motor [Arabidopsis thaliana] >gi|6735328|emb|CAB68154.1| myosin heavy chain MYA3 [Arabidopsis thaliana]	Unigene2661_All//1.00E-36//AT3G58160| XIJ; motor			ko03040|Spliceosome		nr -
Unigene26612_All	842	23.49	23.05	3.48	55.32	77.50	55.35	6.58	11.42	5.25	-2.73E-02	8.44E-01		-2.76E+00	1.72E-57	Down	4.87E-01	3.36E-16		1.00E-03	9.91E-01		7.96E-01	1.60E-06		-3.25E-01	1.53E-01				Unigene26612_All//0.00E+00//TC146444					
Unigene26616_All	824	29.34	63.95	33.09	32.28	35.81	57.22	57.42	70.66	49.31	1.12E+00	3.57E-46	Up	1.74E-01	1.38E-01		1.50E-01	1.72E-01		8.26E-01	8.58E-27		2.99E-01	1.20E-06		-2.20E-01	1.39E-03		Unigene26616_All//gi|78191476|gb|ABB29959.1|//2.00E-26//ubiquitin fusion-degradation protein-like [Solanum tuberosum]	Unigene26616_All//1.00E-14//AT2G21270| ubiquitin fusion degradation UFD1 family protein	Unigene26616_All//0.00E+00//gi|164361392|gb|ES804845.1|ES804845			GO:0019941	nr -
Unigene26618_All	810	70.99	97.02	69.55	115.37	117.08	114.14	55.90	27.50	31.03	4.51E-01	1.55E-14		-2.95E-02	7.20E-01		2.12E-02	7.93E-01		-1.56E-02	8.21E-01		-1.02E+00	5.72E-42	Down	-8.49E-01	8.32E-32		Unigene26618_All//gi|284433762|gb|ADB85087.1|//2.00E-42//vacuolar ATP synthase subunit G1 [Jatropha curcas]	Unigene26618_All//2.00E-32//AT3G01390| VMA10 (VACUOLAR MEMBRANE ATPASE 10); hydrogen ion transporting ATP synthase, rotational mechanism	Unigene26618_All//0.00E+00//TC171899		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0005774//GO:0015078//GO:0015988//GO:0043234	nr -
Unigene26619_All	1219	0.00	0.00	0.48	31.02	17.23	328.93	40.10	159.74	143.28	null	null		8.91E+00	2.17E-03		-8.48E-01	1.09E-25		3.41E+00	0.00E+00	Up	1.99E+00	0.00E+00	Up	1.84E+00	0.00E+00	Up	Unigene26619_All//gi|110816009|gb|ABG91752.1|//1.00E-71//HyPRP2 [Gossypium hirsutum]	Unigene26619_All//4.00E-26//AT1G62510| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene26619_All//0.00E+00//TC133639			GO:0005488//GO:0006810//GO:0031224	nr +
Unigene26621_All	890	21.10	10.42	10.59	44.44	38.50	48.46	47.03	26.96	20.23	-1.02E+00	1.38E-14	Down	-9.95E-01	1.89E-13		-2.07E-01	1.46E-02		1.25E-01	1.80E-01		-8.03E-01	4.26E-26		-1.22E+00	1.30E-52	Down	Unigene26621_All//gi|15240154|ref|NP_200925.1|//7.00E-68//40S ribosomal protein S19 (RPS19C) [Arabidopsis thaliana] >gi|297793669|ref|XP_002864719.1|40S ribosomal protein S19 [Arabidopsis lyrata subsp. lyrata] >gi|27923837|sp|Q9FNF8.1|RS193_ARATH RecName: Full=40S ribosomal protein S19-3 >gi|9759463|dbj|BAB10379.1| 40S ribosomal protein S19 [Arabidopsis thaliana] >gi|34365671|gb|AAQ65147.1|At5g61170 [Arabidopsis thaliana] >gi|51970120|dbj|BAD43752.1| 40S ribosomal protein S19 - like [Arabidopsis thaliana] >gi|297310554|gb|EFH40978.1| 40S ribosomal protein S19 [Arabidopsis lyrata subsp. lyrata]	Unigene26621_All//3.00E-69//AT5G61170| 40S ribosomal protein S19 (RPS19C)	Unigene26621_All//0.00E+00//TC154956		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0031981	nr -

Unigene26622_A11	1417	0.00	0.43	0.45	3.34	5.86	12.40	1.49	1.03	3.35	8.75E+00	1.17E-03		8.82E+00	1.16E-03		8.10E-01	2.10E-05		1.89E+00	7.50E-36	Up	-5.31E-01	1.91E-01		1.17E+00	2.70E-06	Up	Unigene26622_A11//gi|18397682|ref|NP_564365.1|//1.00E-110//ATPUP4; purine transmembrane transporter [Arabidopsis thaliana] >gi|75213346|sp|Q9SY29.1|PUP4_ARATH RecName: Full=Probable purine permease 4; Short=AtPUP4 >gi|4926830|gb|AAD32940.1|AC004135_15 T17H7.15 [Arabidopsis thaliana]	Unigene26622_A11//3.00E-92//AT1G30840| ATPUP4; purine transmembrane transporter				GO:0043231	nr -
Unigene26624_A11	817	9.29	10.17	6.58	8.78	10.50	11.28	19.82	22.46	9.85	1.31E-01	5.64E-01		-4.96E-01	2.56E-02		2.57E-01	2.31E-01		3.61E-01	6.88E-02		1.80E-01	1.54E-01		-1.01E+00	1.15E-15	Down	Unigene26624_A11//gi|2582645|emb|CAA05352.1|//7.00E-30//RSZp22 protein [Arabidopsis thaliana]	Unigene26624_A11//2.00E-05//AT4G31580| SRZ-22; protein binding	Unigene26624_A11//0.00E+00//TC150335			GO:0000377//GO:0016604//GO:0046914	nr +
Unigene26625_A11	1249	0.67	2.03	0.64	2.47	3.23	2.50	2.64	1.10	1.75	1.60E+00	1.72E-04	Up	-6.76E-02	9.40E-01		3.84E-01	2.34E-01		1.29E-02	9.71E-01		-1.26E+00	5.73E-05	Down	-5.90E-01	4.46E-02		Unigene26625_A11//gi|297826461|ref|XP_002881113.1|//8.00E-08//hypothetical protein ARALYDRAFT_320802 [Arabidopsis lyrata subsp. lyrata] >gi|297326952|gb|EFH57372.1| hypothetical protein ARALYDRAFT_320802 [Arabidopsis lyrata subsp. lyrata]		Unigene26625_A11//0.00E+00//ES838429				nr -
Unigene26626_A11	716	7.23	9.27	9.00	8.97	12.31	10.22	39.98	17.80	24.31	3.58E-01	1.28E-01		3.15E-01	2.19E-01		4.56E-01	1.71E-02		1.87E-01	4.61E-01		-1.17E+00	5.38E-33	Down	-7.17E-01	1.69E-15				Unigene26626_A11//2.00E-121//gi|109852030|gb|DW481009.1|DW481009				
Unigene26627_A11	1266	2.44	0.88	0.84	5.47	4.54	2.75	2.37	2.21	1.07	-1.47E+00	8.07E-05	Down	-1.54E+00	8.48E-05	Down	-2.68E-01	2.63E-01		-9.94E-01	6.20E-06		-1.00E-01	7.70E-01		-1.15E+00	2.93E-04	Down	Unigene26627_A11//gi|124359163|gb|ABN05686.1|//1.00E-19//Zinc finger, CCHC-type [Medicago truncatula]	Unigene26627_A11//1.00E-06//AT3G31430| unknown protein	Unigene26627_A11//2.00E-24//DR454123			GO:0005488	nr -
Unigene26628_A11	816	3.46	2.98	2.22	4.33	3.92	3.82	10.93	10.76	4.78	-2.16E-01	5.90E-01		-6.42E-01	1.02E-01		-1.43E-01	6.98E-01		-1.83E-01	6.07E-01		-2.35E-02	9.20E-01		-1.19E+00	1.47E-11	Down	Unigene26628_A11//gi|115482538|ref|NP_001061862.1|//1.00E-18//Os10g0478400 [Oryza sativa Japonica Group] >gi|110289265|gb|AAP54285.2| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113639471|dbj|BAF26776.1| Os10g0478400 [Oryza sativa Japonica Group]	Unigene26628_A11//3.00E-26//AT2G37035| unknown protein	Unigene26628_A11//0.00E+00//ES849364				nr +
Unigene26632_A11	971	2.42	0.42	2.36	5.90	1.70	3.77	5.49	7.83	6.44	-2.54E+00	4.62E-07	Down	-4.02E-02	9.38E-01		-1.79E+00	5.62E-13	Down	-6.47E-01	8.53E-03		5.14E-01	6.60E-03		2.32E-01	2.98E-01				Unigene26632_A11//1.00E-24//TC178205				
Unigene26633_A11	834	2.01	0.49	0.77	1.73	1.16	0.81	0.96	1.65	3.49	-2.05E+00	3.19E-04	Down	-1.39E+00	1.16E-02		-5.83E-01	2.98E-01		-1.09E+00	5.14E-02		7.80E-01	1.32E-01		1.86E+00	1.85E-07	Up			Unigene26633_A11//2.00E-17//TC178205				
Unigene26634_A11	761	14.51	32.16	28.55	21.14	36.97	69.67	68.50	191.46	107.95	1.15E+00	1.48E-22	Up	9.77E-01	4.78E-15		8.06E-01	5.13E-17		1.72E+00	2.51E-94	Up	1.48E+00	5.33E-238	Up	6.56E-01	1.67E-36		Unigene26634_A11//gi|224136574|ref|XP_002326894.1|//9.00E-34//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222835209|gb|EEE73644.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene26634_A11//3.00E-11//AT1G65910| anac028 (Arabidopsis NAC domain containing protein 28); transcription factor	Unigene26634_A11//3.00E-65//DW487635	NAC			nr -
Unigene26636_A11	805	4.03	19.20	8.93	4.15	6.84	10.88	10.29	28.76	35.24	2.25E+00	6.94E-37	Up	1.15E+00	7.53E-07	Up	7.23E-01	3.08E-03		1.39E+00	6.89E-12	Up	1.48E+00	2.09E-38	Up	1.78E+00	8.67E-62	Up	Unigene26636_A11//gi|18391073|ref|NP_563854.1|//6.00E-30//POLD4 (POLYMERASE DELTA 4); DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|89861061|gb|ABF59014.1| At1g09815 [Arabidopsis thaliana]	Unigene26636_A11//2.00E-22//AT1G09815| POLD4 (POLYMERASE DELTA 4); DNA-directed DNA polymerase	Unigene26636_A11//0.00E+00//ES793545		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03020|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair	GO:0006259	nr +
Unigene26638_A11	877	31.26	81.23	50.40	54.36	74.33	97.23	24.06	29.12	26.26	1.38E+00	2.90E-85	Up	6.89E-01	9.17E-17		4.51E-01	3.59E-14		8.39E-01	2.48E-49		2.76E-01	5.19E-03		1.26E-01	2.56E-01		Unigene26638_A11//gi|297815946|ref|XP_002875856.1|//9.00E-52//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321694|gb|EFH52115.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26638_A11//4.00E-53//AT3G47640| basic helix-loop-helix (bHLH) family protein	Unigene26638_A11//0.00E+00//gi|164262628|gb|ES845166.1|ES845166	bHLH		GO:0010468//GO:0043231	nr +
Unigene2664_A11	1569	10.67	6.36	7.50	33.02	28.09	15.98	4.66	1.78	0.66	-7.46E-01	4.72E-08		-5.09E-01	3.04E-04		-2.33E-01	9.42E-04		-1.05E+00	5.46E-44	Down	-1.39E+00	1.53E-11	Down	-2.82E+00	5.48E-29	Down	Unigene2664_A11//gi|89357197|gb|ABD72481.1|//0.00E+00//TCP domain-like protein I [Gossypium barbadense]	Unigene2664_A11//1.00E-54//AT3G47620| AtTCP14 (TEOSINTE BRANCHED1, CYCLOIDEA and PCF (TCP) 14); transcription factor	Unigene2664_A11//0.00E+00//TC129644	TCP			nr +
Unigene26640_A11	1646	0.86	0.55	0.55	4.90	1.99	1.67	4.03	2.87	2.81	-6.31E-01	2.56E-01		-6.42E-01	2.75E-01		-1.30E+00	2.15E-11	Down	-1.55E+00	5.06E-13	Down	-4.91E-01	1.68E-02		-5.22E-01	8.12E-03		Unigene26640_A11//gi|18400116|ref|NP_565544.1|//1.00E-177//galactosyl transferase GMA12/MNN10 family protein [Arabidopsis thaliana] >gi|46576210|sp|081007.1|GT7_ARATH RecName: Full=Putative glycosyltransferase 7; Short=AtGT7 >gi|34452007|gb|AAC32437.1| Expressed protein [Arabidopsis thaliana]	Unigene26640_A11//4.00E-179//AT2G22900| galactosyl transferase GMA12/MNN10 family protein	Unigene26640_A11//0.00E+00//BF274289			GO:0031224//GO:0042285	nr +
Unigene26643_A11	1898	1.43	0.43	0.56	2.44	2.96	2.00	6.82	0.99	2.39	-1.75E+00	2.50E-05	Down	-1.35E+00	1.03E-03		2.77E-01	3.15E-01		-2.88E-01	3.57E-01		-2.78E+00	2.10E-48	Down	-1.51E+00	3.80E-23	Down	Unigene26643_A11//gi|15237300|ref|NP_200103.1|//1.00E-128//ATIM (TIMELESS) [Arabidopsis thaliana]	Unigene26643_A11//2.00E-128//AT5G52910| ATIM (TIMELESS)	Unigene26643_A11//0.00E+00//ES844996				nr +
Unigene26644_A11	978	68.85	18.55	32.18	27.00	17.96	14.82	1.69	1.11	1.43	-1.89E+00	8.33E-128	Down	-1.10E+00	7.15E-55	Down	-5.88E-01	1.11E-09		-8.65E-01	1.29E-16		-6.02E-01	2.00E-01		-2.42E-01	5.92E-01		Unigene26644_A11//gi|297799182|ref|XP_002867475.1|//2.00E-60//YGGT family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313311|gb|EFH43734.1| YGGT family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26644_A11//8.00E-62//AT4G27990| YGGT family protein	Unigene26644_A11//0.00E+00//gi|82756475|gb|DV850037.1|DV850037			GO:0044464	nr -
Unigene26646_A11	1446	3.62	23.37	4.60	6.72	14.22	9.15	37.16	106.08	156.02	2.69E+00	2.62E-98	Up	3.47E-01	1.56E-01		1.08E+00	3.75E-20	Up	4.46E-01	3.90E-03		1.51E+00	3.53E-258	Up	2.07E+00	0.00E+00	Up	Unigene26646_A11//gi|297803354|ref|XP_002869561.1|//6.00E-55//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315397|gb|EFH45820.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26646_A11//7.00E-47//AT4G27470| zinc finger (C3HC4-type RING finger) family protein	Unigene26646_A11//0.00E+00//TC170105		ko04146|Peroxisome	GO:0005488	nr -
Unigene26648_A11	671	2.18	0.60	0.40	5.20	4.26	3.84	2.71	1.74	2.32	-1.85E+00	1.97E-03		-2.46E+00	2.95E-04	Down	-2.87E-01	4.20E-01		-4.38E-01	2.10E-01		-6.36E-01	1.45E-01		-2.27E-01	5.99E-01		Unigene26648_A11//gi|38194913|gb|AB123301.1|//2.00E-46//anthocyanin acyltransferase [Phaseolus vulgaris]	Unigene26648_A11//4.00E-25//AT1G03940| transferase family protein	Unigene26648_A11//0.00E+00//TC174995		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016747	nr +
Unigene26649_A11	1305	1.64	0.97	1.63	3.17	2.59	2.87	3.43	2.37	1.62	-7.60E-01	8.11E-02		-1.02E-02	1.00E+00		-2.93E-01	3.58E-01		-1.41E-01	6.85E-01		-5.35E-01	3.77E-02		-1.09E+00	1.69E-05	Down	Unigene26649_A11//gi|225434959|ref|XP_002281079.1|//1.00E-160//PREDICTED: similar to GTP1/OBG family member [Vitis vinifera]	Unigene26649_A11//2.00E-127//AT1G07615| GTP binding	Unigene26649_A11//0.00E+00//DW500550			GO:0032561//GO:0043231	nr +
Unigene2665_A11	1327	15.97	22.91	13.96	45.76	101.57	60.96	46.45	49.80	105.26	5.21E-01	1.00E-07		-1.93E-01	1.46E-01		1.15E+00	1.63E-144	Up	4.14E-01	1.23E-13		1.00E-01	1.26E-01		1.18E+00	4.65E-164	Up	Unigene2665_A11//gi|224091544|ref|XP_002309282.1|//1.00E-130//f-box family protein [Populus trichocarpa] >gi|222855258|gb|EEE92805.1| f-box family protein [Populus trichocarpa]	Unigene2665_A11//3.00E-50//AT2G44130| kelch repeat-containing F-box family protein	Unigene2665_A11//0.00E+00//gi|109878646|gb|DW507616.1|DW507616				nr -
Unigene26651_A11	1081	113.26	32.20	91.23	62.26	64.51	40.82	2.86	1.74	1.55	-1.81E+00	4.56E-219	Down	-3.12E-01	4.46E-11		5.12E-02	5.40E-01		-6.09E-01	1.05E-22		-7.15E-01	2.38E-02		-8.83E-01	3.87E-03		Unigene26651_A11//gi|297797641|ref|XP_002866705.1|//3.00E-96//signal transducer [Arabidopsis lyrata subsp. lyrata] >gi|297312540|gb|EFH42964.1| signal transducer [Arabidopsis lyrata subsp. lyrata]	Unigene26651_A11//3.00E-93//AT5G67385| protein binding / signal transducer	Unigene26651_A11//0.00E+00//TC151135			GO:0009314//GO:0060089	nr -
Unigene26653_A11	795	8.36	9.69	17.28	2.57	2.90	6.76	6.81	4.94	1.80	2.13E-01	3.55E-01		1.05E+00	7.24E-11	Up	1.76E-01	7.34E-01		1.40E+00	1.51E-07	Up	-4.62E-01	4.72E-02		-1.92E+00	6.79E-14	Down			Unigene26653_A11//4.00E-160//TC134105				
Unigene26655_A11	699	12.20	12.61	10.28	23.45	17.00	13.25	9.13	9.51	3.31	4.79E-02	8.17E-01		-2.47E-01	2.60E-01		-4.64E-01	2.94E-04		-8.24E-01	9.35E-10		5.79E-02	8.01E-01		-1.47E+00	2.18E-11	Down			Unigene26655_A11//0.00E+00//TC175772				
Unigene26656_A11	1286	1114.48	723.00	1195.64	401.57	460.51	439.06	70.36	47.94	31.85	-6.24E-01	0.00E+00		1.01E-01	1.54E-15		1.98E-01	9.83E-27		1.29E-01	2.33E-10		-5.54E-01	3.95E-29		-1.14E+00	3.57E-102	Down	Unigene26656_A11//gi|224140038|ref|XP_002323394.1|//1.00E-117//2-cys peroxiredoxin [Populus trichocarpa] >gi|222868024|gb|EEF05155.1| 2-cys peroxiredoxin [Populus trichocarpa]	Unigene26656_A11//6.00E-108//AT5G06290| 2-Cys Prx B (2-Cysteine peroxiredoxin B); antioxidant/ peroxiredoxin	Unigene26656_A11//0.00E+00//gi|164292883|gb|ES797578.1|ES797578				nr -
Unigene26666_A11	1167	1.30	4.39	1.00	2.73	1.86	1.78	1.05	2.29	2.36	1.75E+00	2.46E-09	Up	-3.73E-01	5.09E-01		-5.55E-01	1.04E-01		-6.18E-01	7.96E-02		1.13E+00	1.24E-03		1.16E+00	5.25E-04	Up	Unigene26666_A11//gi|18408753|ref|NP_564896.1|//1.00E-101//ASY1 (ASYNAPTIC 1); DNA binding [Arabidopsis thaliana]	Unigene26666_A11//5.00E-103//AT1G67370| ASY1 (ASYNAPTIC 1); DNA binding				GO:0005694//GO:0007128//GO:0009553//GO:0009555//GO:0043231	nr +
Unigene26667_A11	590	0.00	0.34	0.18	1.44	0.41	5.28	24.58	80.05	55.30	8.42E+00	1.36E-01		7.50E+00	3.99E-01		-1.81E+00	1.78E-02		1.88E+00	9.91E-07	Up	1.70E+00	1.02E-94	Up	1.17E+00	1.89E-38	Up	Unigene26667_A11//gi|30683908|ref|NP_193436.2|//1.00E-28//ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1) [Arabidopsis thaliana] >gi|22095652|sp|Q23547.2|EXLB1_ARATH RecName: Full=Expansin-like B1; Short=AtEXLB1; Short=At-EXPR1; Short=AtEXPR1; AltName: Full=Ath-ExpBeta-3.1; Flags: Precursor >gi|29028846|gb|AAO64802.1| At4g17030 [Arabidopsis thaliana] >gi|110736418|dbj|BAF00176.1| Expansin-like protein [Arabidopsis thaliana]	Unigene26667_A11//8.00E-30//AT4G17030| ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1)	Unigene26667_A11//3.00E-129//DR458852				nr -
Unigene26668_A11	1049	0.00	3.19	1.88	14.01	3.87	90.93	105.12	613.95	342.33	1.16E+01	4.94E-19	Up	1.09E+01	7.46E-11	Up	-1.85E+00	2.79E-34	Down	2.70E+00	6.53E-298	Up	2.55E+00	0.00E+00	Up	1.70E+00	0.00E+00	Up	Unigene26668_A11//gi|30683908|ref|NP_193436.2|//8.00E-85//ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1) [Arabidopsis thaliana] >gi|22095652|sp|Q23547.2|EXLB1_ARATH RecName: Full=Expansin-like B1; Short=AtEXLB1; Short=At-EXPR1; Short=AtEXPR1; AltName: Full=Ath-ExpBeta-3.1; Flags: Precursor >gi|29028846|gb|AAO64802.1| At4g17030 [Arabidopsis thaliana] >gi|110736418|dbj|BAF00176.1| Expansin-like protein [Arabidopsis thaliana]	Unigene26668_A11//4.00E-86//AT4G17030| ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1)	Unigene26668_A11//0.00E+00//TC172733				nr -
Unigene26670_A11	1669	1.57	0.97	0.54	9.82	5.12	4.60	2.31	1.03	0.69	-6.90E-01	7.70E-02		-1.53E+00	3.62E-04	Down	-9.40E-01	1.71E-13		-1.09E+00	2.66E-15	Down	-1.17E+00	3.99E-05	Down	-1.74E+00	6.00E-09	Down	Unigene26670_A11//gi|79407941|ref|NP_188636.2|//0.00E+00//aspartic-type endopeptidase [Arabidopsis thaliana] >gi|11994777|dbj|BAB03167.1| nucleoid chloroplast DNA-binding protein-like [Arabidopsis thaliana]	Unigene26670_A11//7.00E-155//AT3G20015| aspartic-type endopeptidase	Unigene26670_A11//0.00E+00//DW510562			GO:0004175//GO:0019538//GO:0044464	nr +

Unigene26673_All	1137	3.41	2.18	1.41	2.72	3.85	2.78	0.41	0.33	0.60	-6.41E-01	3.90E-02			-1.28E+00	1.31E-04	Down	5.02E-01	8.65E-02			3.37E-02	9.45E-01		-3.06E-01	7.36E-01		5.43E-01	4.75E-01		Unigene26673_All//gi|115646816|gb|AB117128.1|//3.00E-40//At5g67020 [Arabidopsis thaliana]	Unigene26673_All//4.00E-45//AT2G22790| unknown protein	Unigene26673_All//6.00E-46//CO091549				nr +
Unigene26674_All	846	81.45	41.99	61.12	25.50	24.42	22.21	8.45	5.58	2.78	-9.56E-01	1.87E-46			-4.14E-01	1.23E-10		-6.21E-02	6.70E-01			-1.99E-01	1.24E-01		-5.97E-01	2.17E-03		-1.60E+00	2.67E-14	Down	Unigene26674_All//gi|122064924|sp|Q0JG75.2|PSB28_ORYSJ//7.00E-57//RecName: Full=Photosystem II reaction center PSB28 protein, chloroplastic; AltName: Full=Photosystem II protein W-like; Flags: Precursor	Unigene26674_All//2.00E-53//AT4G28660| PSB28 (PHOTOSYSTEM II REACTION CENTER PSB28 PROTEIN)	Unigene26674_All//0.00E+00//TC136812		ko00195|Photosynthesis	GO:0009523//GO:0009532//GO:0009534//GO:0044237	nr -
Unigene26676_All	795	6.52	5.67	7.64	6.64	4.85	3.07	7.50	6.52	3.91	-2.00E-01	4.74E-01			2.29E-01	3.90E-01		-4.53E-01	7.76E-02			-1.11E+00	1.63E-05	Down	-2.02E-01	3.97E-01		-9.40E-01	9.96E-06		Unigene26676_All//gi|28416763|gb|AA042912.1|//3.00E-37//At1g65000 [Arabidopsis thaliana]	Unigene26676_All//2.00E-38//AT1G65000| unknown protein	Unigene26676_All//0.00E+00//gi|109872835|gb|DW501810.1|DW501810				nr -
Unigene26677_All	731	2.15	4.99	5.46	10.02	9.09	5.75	8.62	8.35	7.96	1.22E+00	2.38E-04	Up	1.35E+00	4.36E-05	Up	-1.40E-01	5.83E-01			-8.02E-01	1.48E-04		-4.60E-02	8.49E-01		-1.15E-01	6.13E-01					Unigene26677_All//0.00E+00//DR460293				
Unigene26679_All	943	4.72	4.78	7.34	6.76	6.13	6.66	5.69	3.28	1.56	2.01E-02	9.66E-01			6.38E-01	5.90E-03		-1.40E-01	6.02E-01			-2.24E-02	9.43E-01		-7.96E-01	5.19E-04		-1.87E+00	2.48E-13	Down			Unigene26679_All//2.00E-39//DR460170				
Unigene26680_All	1760	0.59	0.89	1.42	12.43	13.29	11.29	8.53	3.87	11.27	5.86E-01	2.67E-01			1.26E+00	3.30E-03		9.65E-02	4.96E-01			-1.38E-01	3.15E-01		-1.14E+00	4.68E-17	Down	4.03E-01	1.93E-04		Unigene26680_All//gi|297798462|ref|XP_002867115.1|//1.00E-174//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312951|gb|EFH43374.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26680_All//1.00E-166//AT4G34500| protein kinase family protein	Unigene26680_All//0.00E+00//TC134074		ko04626|Plant-pathogen interaction		nr -
Unigene26681_All	2433	0.56	0.54	0.57	2.62	3.47	3.56	6.92	10.31	19.13	-4.61E-02	9.46E-01			2.56E-02	9.84E-01		4.04E-01	4.29E-02			4.44E-01	2.63E-02		5.76E-01	3.05E-09		1.47E+00	7.10E-77	Up	Unigene26681_All//gi|126143480|dbj|BAF47279.1|//0.00E+00//lectin-receptor like protein kinase 3 [Nicotiana tabacum]	Unigene26681_All//0.00E+00//AT4G04960| lectin protein kinase, putative	Unigene26681_All//0.00E+00//DN780966		ko04626|Plant-pathogen interaction	GO:0003676//GO:0004713//GO:0004871//GO:0006260//GO:0006464//GO:0016020//GO:0030246//GO:0032559//GO:0034061	nr -
Unigene26682_All	883	11.38	51.36	24.00	9.14	12.05	10.95	1.20	1.56	0.77	2.17E+00	1.33E-102	Up	1.08E+00	3.79E-17	Up	3.99E-01	2.11E-02				2.60E-01	2.00E-01		3.84E-01	4.75E-01		-6.42E-01	2.62E-01		Unigene26682_All//gi|114050563|gb|AB149431.1|//8.00E-18//At3g16120 [Arabidopsis thaliana]	Unigene26682_All//4.00E-19//AT3G16120| dynein light chain, putative	Unigene26682_All//0.00E+00//TC178235			GO:0003774//GO:0015630//GO:0042995//GO:0043231//GO:0048468//GO:0048513	nr -
Unigene26683_All	609	1.72	6.74	6.82	0.98	2.32	1.93	0.28	0.34	0.00	1.97E+00	8.40E-09	Up	1.99E+00	1.24E-08	Up	1.24E+00	3.03E-02				9.74E-01	1.34E-01		3.06E-01	8.36E-01		-8.12E+00	1.08E-01		Unigene26683_All//gi|114050563|gb|AB149431.1|//9.00E-37//At3g16120 [Arabidopsis thaliana]	Unigene26683_All//5.00E-38//AT3G16120| dynein light chain, putative	Unigene26683_All//0.00E+00//gi|109885722|gb|DW514692.1|DW514692			GO:0003774//GO:0015630//GO:0042995//GO:0043231//GO:0048468//GO:0048513	nr -
Unigene26684_All	973	5.05	4.48	7.66	19.45	23.07	16.11	13.21	3.95	4.38	-1.75E-01	5.55E-01			6.00E-01	7.04E-03		2.46E-01	3.71E-02			-2.73E-01	3.98E-02		-1.74E+00	3.59E-27	Down	-1.59E+00	8.75E-25	Down	Unigene26684_All//gi|297797135|ref|XP_002866452.1|//4.00E-58//cupin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312287|gb|EFH42711.1| cupin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26684_All//2.00E-57//AT5G61750| cupin family protein				GO:0003824//GO:0005576//GO:0031410//GO:0046914	nr -
Unigene26685_All	2337	0.00	0.00	0.00	51.69	25.15	13.18	175.09	41.56	29.17	null	null		null	null		-1.04E+00	5.97E-115	Down	-1.97E+00	1.19E-263	Down	-2.07E+00	0.00E+00	Down	-2.59E+00	0.00E+00	Down	Unigene26685_All//gi|15231918|ref|NP_187461.1|//0.00E+00//FRO3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter/ transporter [Arabidopsis thaliana] >gi|238479686|ref|NP_001154595.1| FRO3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter/ transporter [Arabidopsis thaliana] >gi|19310969|gb|AAL86700.1|AF448231_1 ferric reductase defective [Arabidopsis thaliana] >gi|15912323|gb|AAL08295.1| T8G24.8/T8G24.8 [Arabidopsis thaliana] >gi|15982820|gb|AAL09757.1| T8G24.8/T8G24.8 [Arabidopsis thaliana] >gi|22137274|gb|AAM91482.1| At3g08040/T8G24.8 [Arabidopsis thaliana] >gi|30102520|gb|AAP21178.1| At3g08040/T8G24.8 [Arabidopsis thaliana]	Unigene26685_All//8.00E-169//AT3G08040| FRO3 (FERRIC REDUCTASE DEFECTIVE 3); antiporter/ transporter	Unigene26685_All//0.00E+00//TC173080			GO:0015291//GO:0015893//GO:0016020//GO:0030005	nr -
Unigene26686_All	1288	1.30	0.67	1.53	1.70	1.58	2.10	0.56	2.37	3.65	-9.59E-01	5.93E-02			2.35E-01	6.29E-01		-1.09E-01	8.32E-01			3.06E-01	4.66E-01		2.09E+00	1.06E-08	Up	2.71E+00	7.81E-18	Up	Unigene26686_All//gi|6522592|emb|CAB61957.1|//7.00E-89//receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene26686_All//3.00E-90//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0016772	nr +
Unigene26688_All	1572	6.39	6.06	3.66	15.97	14.11	14.31	13.91	5.90	5.88	-7.66E-02	6.83E-01			-8.05E-01	1.82E-05		-1.79E-01	1.22E-01			-1.59E-01	1.97E-01		-1.24E+00	9.80E-28	Down	-1.24E+00	8.87E-29	Down	Unigene26688_All//gi|115447503|ref|NP_001047531.1|//2.00E-17//Os02g0638000 [Oryza sativa Japonica Group] >gi|113537062|dbj|BAF09445.1| Os02g0638000 [Oryza sativa Japonica Group]	Unigene26688_All//1.00E-14//AT5G58210| hydroxyproline-rich glycoprotein family protein	Unigene26688_All//0.00E+00//TC140713				nr -
Unigene2669_All	369	3.12	6.73	1.15	1.49	1.68	1.35	6.65	4.42	14.14	1.11E+00	6.72E-03			-1.43E+00	3.87E-02		1.78E-01	8.64E-01			-1.42E-01	8.85E-01		-5.89E-01	1.09E-01		1.09E+00	3.08E-06	Up	Unigene2669_All//gi|33111959|emb|CAE12163.1|//5.00E-15//expansin-like protein [Quercus robur]	Unigene2669_All//5.00E-09//AT3G45970| ATEXLA1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A1)	Unigene2669_All//2.00E-178//gi|164253154|gb|ES793367.1|ES793367				nr -
Unigene26691_All	1151	6.18	3.96	2.73	10.47	8.83	15.62	4.08	2.11	2.11	-6.42E-01	3.37E-03			-1.18E+00	4.88E-07	Down	-2.47E-01	1.51E-01			5.76E-01	6.11E-06		-9.53E-01	1.33E-04		-9.50E-01	9.26E-05		Unigene26691_All//gi|2462757|gb|AAB71976.1|//1.00E-14//Hypothetical protein [Arabidopsis thaliana]	Unigene26691_All//9.00E-15//AT1G60640| unknown protein	Unigene26691_All//0.00E+00//ES798780				nr -
Unigene26693_All	1221	17.05	23.20	16.53	9.87	9.34	9.17	4.02	9.48	12.07	4.44E-01	1.26E-05			-4.52E-02	7.41E-01		-8.09E-02	6.81E-01			-1.06E-01	6.15E-01		1.24E+00	4.29E-15	Up	1.59E+00	7.00E-28	Up	Unigene26693_All//gi|194579021|gb|ACF75544.1|//2.00E-34//At3g11690 [Arabidopsis thaliana]	Unigene26693_All//1.00E-13//AT3G11690| unknown protein	Unigene26693_All//0.00E+00//TC146993				nr -
Unigene26695_All	1557	1.48	8.92	0.21	1.50	4.91	3.10	8.58	13.18	46.11	2.59E+00	4.73E-39	Up	-2.85E+00	2.60E-07	Down	1.71E+00	6.52E-15	Up	1.05E+00	1.32E-04	Up	6.19E-01	1.13E-08		2.43E+00	1.52E-231	Up	Unigene26695_All//gi|7331156|gb|AAF60299.1|AF233640_1//3.00E-26//cytochrome b5 DIF-F [Petunia x hybrida]	Unigene26695_All//5.00E-12//AT5G48810| CB5-D (CYTOCHROME B5 ISOFORM D); heme binding	Unigene26695_All//0.00E+00//gi|73862727|gb|DT465466.1|DT465466			GO:0043231	nr -
Unigene26698_All	1086	0.34	1.45	0.93	1.42	1.08	1.62	1.99	1.65	0.99	2.10E+00	4.40E-04	Up	1.47E+00	4.95E-02		-3.99E-01	4.68E-01			1.90E-01	7.11E-01		-2.63E-01	5.45E-01		-1.00E+00	7.92E-03		Unigene26698_All//gi|30683798|ref|NP_849544.1|//5.00E-85//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|119360071|gb|ABL66764.1| At4g16765 [Arabidopsis thaliana]	Unigene26698_All//2.00E-80//AT4G16765| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene26698_All//0.00E+00//TC168767			GO:0008152//GO:0016706//GO:0046914	nr +
Unigene267_All	3861	13.73	4.96	7.38	19.33	13.04	5.67	26.16	8.40	6.35	-1.47E+00	2.61E-70	Down	-8.96E-01	4.62E-31		-5.68E-01	6.49E-25			-1.77E+00	2.03E-140	Down	-1.64E+00	1.68E-191	Down	-2.04E+00	8.24E-267	Down	Unigene267_All//gi|47498987|gb|AAT28309.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Pyrus pyrifolia]	Unigene267_All//0.00E+00//AT1G28440| HSL1 (HAESA-Like 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene267_All//0.00E+00//TC178063				nr +
Unigene2670_All	1017	25.88	38.71	9.27	3.62	5.28	10.17	25.36	97.93	65.65	5.81E-01	1.01E-11		-1.48E+00	2.35E-34	Down	5.43E-01	3.31E-02			1.49E+00	2.49E-15	Up	1.95E+00	1.68E-239	Up	1.37E+00	1.70E-99	Up	Unigene2670_All//gi|33111959|emb|CAE12163.1|//1.00E-115//expansin-like protein [Quercus robur]	Unigene2670_All//8.00E-92//AT4G38400| ATEXLA2 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A2)	Unigene2670_All//0.00E+00//TC153792				nr -
Unigene26700_All	1271	1.81	7.02	2.97	11.91	10.16	18.41	0.17	0.33	0.60	1.95E+00	4.27E-18	Up	7.16E-01	2.96E-02		-2.30E-01	1.28E-01			6.28E-01	1.19E-08		9.83E-01	3.73E-01		1.84E+00	1.64E-02		Unigene26700_All//gi|224106127|ref|XP_002314053.1|//5.00E-79//cinnamoyl CoA reductase-like protein [Populus trichocarpa] >gi|222850461|gb|EEE88008.1| cinnamoyl CoA reductase-like protein [Populus trichocarpa]	Unigene26700_All//9.00E-72//AT5G19440| cinnamyl-alcohol dehydrogenase, putative (CAD)	Unigene26700_All//0.00E+00//ES842564		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis	GO:0003824//GO:0005488//GO:0008152	nr +
Unigene26701_All	1507	1.94	4.81	1.17	1.52	0.53	1.29	1.15	7.93	2.22	1.31E+00	1.17E-08	Up	-7.38E-01	5.40E-02		-1.53E+00	1.64E-04	Down	-2.39E-01	6.35E-01		2.79E+00	1.10E-44	Up	9.49E-01	1.29E-03		Unigene26701_All//gi|28133041|gb|ADA60975.1|//2.00E-90//lateral root primordium 1 [Brassica rapa subsp. pekinensis]	Unigene26701_All//2.00E-62//AT5G12330| LRP1 (LATERAL ROOT PRIMORDIUM 1); protein homodimerization	Unigene26701_All//4.00E-103//gi|78331902|gb|DT552176.1|DT552176	SRS		GO:0009725//GO:0042802//GO:0048513	nr +
Unigene26703_All	1607	38.00	17.85	42.38	16.77	29.57	15.06	0.29	0.21	0.00	-1.09E+00	4.90E-51	Down	1.58E-01	2.40E-02		8.18E-01	3.08E-29			-1.55E-01	1.95E-01		-4.76E-01	6.60E-01		-8.18E+00	1.09E-03		Unigene26703_All//gi|30689221|ref|NP_173915.2|//2.00E-89//zinc finger (B-box type) family protein [Arabidopsis thaliana] >gi|52782786|sp|Q8RWD0.2|COL16_ARATH RecName: Full=Zinc finger protein CONSTANS-LIKE 16 >gi|53749166|gb|AAU90068.1| At1g25440 [Arabidopsis thaliana]	Unigene26703_All//1.00E-84//AT1G25440| zinc finger (B-box type) family protein	Unigene26703_All//0.00E+00//TC154795	C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0044464	nr -
Unigene26704_All	492	1.91	0.82	1.08	6.07	3.85	1.84	4.12	2.21	2.43	-1.22E+00	9.43E-02		-8.23E-01	2.71E-01		-6.58E-01	5.84E-02			-1.73E+00	5.70E-06	Down	-9.01E-01	2.61E-02		-7.64E-01	4.92E-02		Unigene26704_All//gi|115463389|ref|NP_001055294.1|//2.00E-15//Os05g0356800 [Oryza sativa Japonica Group] >gi|113578845|dbj|BAF17208.1| Os05g0356800 [Oryza sativa Japonica Group]	Unigene26704_All//2.00E-19//AT2G47480| unknown protein					nr +
Unigene26705_All	1196	1.66	1.27	1.07	2.58	1.73	1.51	4.70	2.62	2.03	-3.87E-01	3.88E-01		-6.38E-01	1.87E-01		-5.80E-01	9.32E-02			-7.74E-01	2.89E-02		-8.43E-01	1.65E-04		-1.21E+00	8.99E-08	Down	Unigene26705_All//gi|28416815|gb|AA042938.1|//2.00E-17//At3g62640 [Arabidopsis thaliana]	Unigene26705_All//2.00E-25//AT2G47480| unknown protein	Unigene26705_All//6.00E-09//TC169645				nr -
Unigene26706_All	662	18.34	14.39	5.47	26.71	45.98	75.45	51.92	99.12	73.54	-3.50E-01	3.53E-02		-1.75E+00	2.93E-20	Down	7.84E-01	1.58E-17			1.50E+00	6.82E-73	Up	9.33E-01	7.03E-52		5.02E-01	5.94E-14		Unigene26706_All//gi|4093155|gb|AAC99772.1|//1.00E-39//phytochrome-associated protein 1 [Arabidopsis thaliana]	Unigene26706_All//4.00E-36//AT3G16500| PAP1 (PHYTOCHROME-ASSOCIATED PROTEIN 1); transcription factor	Unigene26706_All//0.00E+00//gi|164247201|gb|ES821155.1|ES821155			GO:0001071//GO:0003676//GO:0005515//GO:0006351//GO:0006412//GO:0006801//GO:0006970//GO:0009718//GO:0009255//GO:0010182//GO:0010468//GO:0016021//GO:0016791//GO:0019637//GO:0043231	nr +
Unigene26707_All	1605	2.22	1.23	0.40	37.93	11.89	4.87	10.98	2.08	1.29	-8.48E-01	9.32E-03		-2.48E+00	1.49E-09	Down	-1.67E+00	2.94E-122	Down	-2.96E+00	1.26E-215	Down	-2.40E+00	1.07E-55	Down	-3.09E+00	1.65E-75	Down	Unigene26707_All//gi|257831443|gb|ACV71022.1|//6.00E-20//UPA23 [Capsicum annuum]	Unigene26707_All//2.00E-20//AT5G22930| unknown protein	Unigene26707_All//0.00E+00//TC175352		ko03040|Spliceosome		nr +
Unigene26708_All	1269	9.57	9.66	11.29	13.62	17.31	20.50	14.09	6.59	6.88	1.46E-02	9.52E-01		2.39E-01	1.45E-01		3.46E-01	2.20E-03			5.90E-01	1.29E-08		-1.10E+00	5.01E-19	Down	-1.04E+00	6.31E-18	Down	Unigene26708_All//gi|297849836|ref|XP_002892799.1|//1.00E-143//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297338641|gb|EFH69058.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene26708_All//2.00E-133//AT1G14300| binding	Unigene26708_All//0.00E+00//TC146472				nr -
Unigene26709_All	1155	1.09	1.84	1.84	2.16	1.61	1.88	3.26	1.23	3.07	7.61E-01	8.36E-02		7.62E-01	9.80E-02		-4.22E-01	3.14E-01			-2.00E-01	6.48E-01		-1.40E+00	1.96E-06	Down	-8.58E-02	7.63E-01		Unigene26709_All//gi|224092083|ref|XP_002309467.1|//6.00E-90//f-box family protein [Populus trichocarpa] >gi|222855443|gb|EEE92990.1| f-box family protein [Populus trichocarpa]	Unigene26709_All//7.00E-82//AT4G33210| F-box family protein (FBL15)	Unigene26709_All//0.00E+00//ES830058				nr -
Unigene26710_All	1885	80.16	34.60	61.13	63.93	57.62	48.66	25.19	18.71	10.38	-1.21E+00	1.54E-148	Down	-3.91E-01	2.58E-20		-1.50E-01	1.03E-03			-3.94E-01	2.13E-18		-4.29E-01	3.89E-10		-1.28E+00	2.30E-64	Down	Unigene26710_All//gi|15233455|ref|NP_194641.1|//1.00E-138//6-phosphogluconate dehydrogenase NAD-binding domain-containing protein [Arabidopsis thaliana]	Unigene26710_All//3.00E-129//AT4G29120| 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein	Unigene26710_All//0.00E+00//TC133711		ko00903|Limonene and pinene degradation//ko00280|Valine, leucine and isoleucine degradation	GO:0006007//GO:0016616//GO:0048037	nr -

Unigene26711_All	1657	2.65	1.56	1.54	14.07	11.85	9.65	6.74	1.82	3.10	-7.66E-01	7.84E-03		-7.82E-01	9.50E-03		-2.48E-01	2.88E-02		-5.44E-01	7.03E-07		-1.89E+00	1.87E-26	Down	-1.12E+00	5.94E-13	Down	Unigene26711_All//gi|297844322|ref|XP_002890042.1//1.00E-179//glucose-methanol-choline oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335884|gb|EFH66301.1| glucose-methanol-choline oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26711_All//8.00E-180//AT1G14190| glucose-methanol-choline (GMC) oxidoreductase family protein			ko00460|Cyanoamino acid metabolism	GO:0016491//GO:0016832//GO:0030554//GO:0044281	nr +
Unigene26712_All	1354	4.56	3.89	1.14	8.72	8.60	5.17	6.68	2.01	2.44	-2.29E-01	3.61E-01		-2.00E+00	1.38E-12	Down	-2.05E-02	9.14E-01		-7.54E-01	2.75E-06		-1.74E+00	2.82E-19	Down	-1.45E+00	1.45E-15	Down	Unigene26712_All//gi|297601699|ref|NP_001061288.2//1.00E-24//Os03g0750900 [Oryza sativa Japonica Group] >gi|255674903|dbj|BAF13202.2| Os03g0750900 [Oryza sativa Japonica Group]	Unigene26712_All//6.00E-58//AT4G17240| unknown protein	Unigene26712_All//0.00E+00//gi|78339596|gb|DT559870.1|DT559870				nr +
Unigene26714_All	1669	19.44	37.37	16.21	22.44	18.63	26.09	16.36	34.01	21.51	9.43E-01	4.75E-41		-2.62E-01	9.44E-03		-2.69E-01	1.34E-03		2.17E-01	9.02E-03		1.06E+00	5.48E-55	Up	3.94E-01	4.58E-07		Unigene26714_All//gi|15239078|ref|NP_196713.1|//0.00E+00//ASP3 (ASPARTATE AMINOTRANSFERASE 3); L-aspartate:2-oxoglutarate aminotransferase [Arabidopsis thaliana] >gi|1168258|sp|P46644.1|AAT3_ARATH RecName: Full=Aspartate aminotransferase, chloroplastic; AltName: Full=Transaminase A; Flags: Precursor >gi|693692|gb|AAA79371.1| aspartate aminotransferase [Arabidopsis thaliana] >gi|7573409|emb|CAB87712.1| aspartate aminotransferase (Asp3) [Arabidopsis thaliana]	Unigene26714_All//0.00E+00//AT5G11520| ASP3 (ASPARTATE AMINOTRANSFERASE 3); L-aspartate:2-oxoglutarate aminotransferase	Unigene26714_All//0.00E+00//TC130500		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism//ko00350|Tyrosine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0008483//GO:0009060//GO:0009064//GO:0009066//GO:0009078//GO:0010260//GO:0016020//GO:0042579//GO:0043648//GO:0046914//GO:0048037	nr -
Unigene26715_All	1580	6.26	41.56	23.36	1.73	7.17	6.15	0.11	0.16	0.53	2.73E+00	9.98E-194	Up	1.90E+00	1.92E-68	Up	2.05E+00	6.97E-28	Up	1.83E+00	4.34E-19	Up	5.69E-01	6.74E-01		2.31E+00	2.74E-03		Unigene26715_All//gi|15220875|ref|NP_173229.1|//0.00E+00//EGY3 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN-LIKE 3) [Arabidopsis thaliana] >gi|9665065|gb|AAF97267.1|AC034106_10 F2H15.10 [Arabidopsis thaliana]	Unigene26715_All//0.00E+00//AT1G17870| EGY3 (ETHYLENE-DEPENDENT GRAVITROPISM-DEFICIENT AND YELLOW-GREEN-LIKE 3)	Unigene26715_All//0.00E+00//TC170221			GO:0000302//GO:0009642//GO:0016787//GO:0043231	nr -
Unigene26717_All	1086	0.87	0.37	2.40	2.71	1.59	2.16	3.82	2.35	3.23	-1.22E+00	9.43E-02		1.47E+00	5.63E-04	Up	-7.72E-01	2.61E-02		-3.24E-01	4.16E-01		-7.01E-01	8.50E-03		-2.41E-01	3.83E-01		Unigene26717_All//gi|300260051|gb|EFJ14273.1|//5.00E-10//hypothetical protein VOLCADRAFT_121342 [Volvox carteri f. nagariensis]		Unigene26717_All//2.00E-67//TC144178			GO:0006810	nr +
Unigene26718_All	706	4.30	6.10	1.89	3.39	2.93	5.50	12.88	24.98	4.12	5.05E-01	8.66E-02		-1.19E+00	1.82E-03		-2.11E-01	6.15E-01		7.00E-01	2.51E-02		9.56E-01	4.03E-15		-1.64E+00	1.41E-18	Down	Unigene26718_All//gi|33391721|gb|AAQ17461.1|//2.00E-47//beta-D-glucosidase [Gossypium hirsutum]	Unigene26718_All//5.00E-35//AT5G20950| glycosyl hydrolase family 3 protein	Unigene26718_All//0.00E+00//gi|21097453|gb|BQ409766.1|BQ409766		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0005618//GO:0015926//GO:0044238	nr -
Unigene2672_All	1483	6.63	6.36	3.05	7.05	8.13	6.46	17.22	14.35	9.48	-6.17E-02	7.46E-01		-1.12E+00	8.97E-09	Down	2.04E-01	2.64E-01		-1.28E-01	5.53E-01		-2.64E-01	7.75E-03		-8.61E-01	9.67E-19		Unigene2672_All//gi|124360656|gb|AB008645.1|//1.00E-178//Tubulin binding cofactor C [Medicago truncatula]	Unigene2672_All//7.00E-175//AT3G57890| tubulin-specific chaperone C-related	Unigene2672_All//0.00E+00//gi|164261410|gb|ES822882.1|ES822882				nr -
Unigene26721_All	939	13.48	6.37	5.84	18.30	14.01	25.15	23.55	12.37	12.77	-1.08E+00	4.63E-11	Down	-1.21E+00	1.96E-12	Down	-3.86E-01	2.44E-03		4.59E-01	2.97E-05		-9.28E-01	6.57E-18		-8.83E-01	4.94E-17		Unigene26721_All//gi|295311704|ref|YP_003387364.1|//8.00E-27//ribosomal protein S19 [Cucurbita pepo] >gi|259156832|gb|ACV96693.1| ribosomal protein S19 [Cucurbita pepo]	Unigene26721_All//2.00E-23//AT5G47320| RPS19 (RIBOSOMAL PROTEIN S19); RNA binding	Unigene26721_All//0.00E+00//TC141522		ko03010|Ribosome	GO:0000314//GO:0003723//GO:0005198//GO:0009536//GO:0010467	nr +
Unigene26724_All	1559	9.03	2.50	2.84	19.43	14.27	19.58	12.39	5.20	6.01	-1.85E+00	2.05E-26	Down	-1.67E+00	4.67E-22	Down	-4.45E-01	7.66E-07		1.16E-02	9.39E-01		-1.25E+00	4.13E-25	Down	-1.05E+00	1.39E-19	Down	Unigene26724_All//gi|30689119|ref|NP_850375.1|//1.00E-132//ribosomal protein L1 family protein [Arabidopsis thaliana]	Unigene26724_All//3.00E-111//AT2G42710| ribosomal protein L1 family protein	Unigene26724_All//0.00E+00//TC133755		ko03010|Ribosome		nr -
Unigene26725_All	778	12.24	24.16	12.11	9.16	16.29	24.61	4.89	87.08	21.40	9.81E-01	1.01E-13		-1.48E-02	9.61E-01		8.31E-01	2.65E-08		1.43E+00	2.82E-26	Up	4.15E+00	0.00E+00	Up	2.13E+00	2.18E-46	Up	Unigene26725_All//gi|99723391|gb|AAG10641.1|AC022521|19//8.00E-09//Hypothetical protein [Arabidopsis thaliana]		Unigene26725_All//0.00E+00//TC160414				nr -
Unigene26727_All	1127	1.25	7.24	1.84	0.97	1.25	3.37	16.96	98.87	163.60	2.53E+00	1.43E-22	Up	5.56E-01	2.37E-01		3.65E-01	5.62E-01		1.79E+00	1.33E-07	Up	2.54E+00	0.00E+00	Up	3.27E+00	0.00E+00	Up	Unigene26727_All//gi|260600584|gb|ACX47024.1|//1.00E-107//NAP-like transcription factor [Vitis vinifera]	Unigene26727_All//1.00E-90//AT1G69490| NAP (NAC-like, activated by AP3/PI); transcription factor	Unigene26727_All//0.00E+00//gi|164347371|gb|EX164646.1|EX164646	NAC			nr -
Unigene26729_All	867	167.16	142.89	139.97	81.99	113.71	96.73	0.44	1.49	1.84	-2.26E-01	1.01E-07		-2.56E-01	3.92E-09		4.72E-01	5.42E-23		2.39E-01	1.98E-05		1.77E+00	1.84E-03		2.07E+00	5.52E-05	Up	Unigene26729_All//gi|297824527|ref|XP_002880146.1|//2.00E-80//thylakoid lumenal 15 kDa protein, chloroplast [Arabidopsis lyrata subsp. lyrata] >gi|297325985|gb|EFH56405.1| thylakoid lumenal 15 kDa protein, chloroplast [Arabidopsis lyrata subsp. lyrata]	Unigene26729_All//4.00E-75//AT2G49920| thylakoid lumenal 15 kDa protein, chloroplast	Unigene26729_All//0.00E+00//TC138213				nr +
Unigene26732_All	1020	4.21	5.12	3.34	5.23	6.99	5.62	6.05	3.20	2.38	2.83E-01	3.09E-01		-3.32E-01	3.01E-01		4.19E-01	5.80E-02		1.06E-01	6.98E-01		-9.21E-01	1.61E-05		-1.34E+00	8.55E-10	Down	Unigene26732_All//gi|15226108|ref|NP_180901.1|//4.00E-84//DAL1 (DIFFERENTIATION AND GREENING-LIKE 1) [Arabidopsis thaliana] >gi|79532285|gb|AAL48226.1|AF44635_1_1 At2g33430/F4P9.20 [Arabidopsis thaliana] >gi|24594425|gb|AABR0660.1| plastid protein [Arabidopsis thaliana] >gi|20453405|gb|AAM19941.1| At2g33430/F4P9.20 [Arabidopsis thaliana] >gi|110736869|dbj|BAF00392.1| plastid protein [Arabidopsis thaliana]	Unigene26732_All//2.00E-85//AT2G33430| DAL1 (DIFFERENTIATION AND GREENING-LIKE 1)	Unigene26732_All//5.00E-148//TC130033				nr +
Unigene26733_All	1364	13.62	2.71	6.29	14.17	10.25	17.98	4.09	14.37	7.24	-2.33E+00	2.27E-46	Down	-1.12E+00	6.57E-16	Down	-4.67E-01	5.90E-05		3.44E-01	1.80E-03		1.81E+00	2.94E-43	Up	8.24E-01	2.91E-07		Unigene26733_All//gi|115477851|ref|NP_001062521.1|//2.00E-68//Os08g0562600 [Oryza sativa Japonica Group] >gi|113624490|dbj|BAF24435.1| Os08g0562600 [Oryza sativa Japonica Group]	Unigene26733_All//8.00E-45//AT5G23950| C2 domain-containing protein	Unigene26733_All//0.00E+00//gi|164323654|gb|ES849478.1|ES849478				nr -
Unigene26735_All	953	7.30	5.00	2.07	6.12	8.82	4.41	5.81	1.75	1.88	-5.47E-01	1.38E-02		-1.82E+00	1.59E-12	Down	5.28E-01	6.35E-03		-4.73E-01	6.01E-02		-1.73E+00	5.01E-12	Down	-1.63E+00	1.70E-11	Down	Unigene26735_All//gi|15225495|ref|NP_182073.1|//1.00E-131//AtAUR3 (ATAURORA3); ATP binding / histone kinase(H3-S10 specific) / protein kinase [Arabidopsis thaliana] >gi|75318481|sp|Q64629.1|AUR3_ARATH RecName: Full=Serine/threonine-protein kinase Aurora-3; Short=AtAur3; AltName: Full=Aurora-like kinase 3 >gi|18491289|gb|AAL69469.1| At2g45490/F17K2.2 [Arabidopsis thaliana] >gi|55467122|emb|CAH69534.1| aurora-like kinase 3 [Arabidopsis thaliana] >gi|67845863|dbj|BAE00021.1| Aurora kinase [Arabidopsis thaliana]	Unigene26735_All//2.00E-132//AT2G45490| AtAUR3 (ATAURORA3); ATP binding / histone kinase(H3-S10 specific) / protein kinase	Unigene26735_All//0.00E+00//DW240002				nr -
Unigene26737_All	1094	152.28	94.76	131.47	31.33	39.44	39.14	6.18	14.48	15.48	-6.84E-01	5.93E-63		-2.12E-01	1.91E-07		3.32E-01	1.23E-05		3.21E-01	6.02E-05		1.23E+00	4.50E-20	Up	1.32E+00	1.59E-24	Up	Unigene26737_All//gi|15215606|gb|AAK91348.1|//1.00E-90//At1g67700/F12A21_30 [Arabidopsis thaliana] >gi|21435985|gb|AAM51570.1| At1g67700/F12A21_30 [Arabidopsis thaliana]	Unigene26737_All//3.00E-84//AT1G67700| unknown protein	Unigene26737_All//0.00E+00//TC140119				nr -
Unigene26740_All	730	24.51	15.55	13.42	39.24	36.89	17.57	5.33	1.66	1.58	-6.57E-01	5.33E-07		-8.69E-01	2.27E-10		-8.91E-02	4.70E-01		-1.16E+00	7.59E-29	Down	-1.68E+00	2.23E-08	Down	-1.75E+00	3.85E-09	Down	Unigene26740_All//gi|60116608|gb|AT11859.2|//2.00E-73//expansin 1 [Mangifera indica]	Unigene26740_All//2.00E-69//AT2G28950| ATEXPA6 (ARABIDOPSIS THALIANA EXPANSIN A6)	Unigene26740_All//0.00E+00//gi|78330458|gb|DT550732.1|DT550732				nr -
Unigene26741_All	633	18.10	26.66	36.17	19.60	16.70	17.62	13.36	12.28	5.92	5.58E-01	3.56E-05		9.99E-01	2.12E-16		-2.31E-01	1.74E-01		-1.53E-01	4.15E-01		-1.21E-01	5.76E-01		-1.18E+00	9.00E-11	Down		Unigene26741_All//3.00E-06//AT4G40030| histone H3.2	Unigene26741_All//0.00E+00//gi|78328970|gb|DT549244.1|DT549244				kegg -
Unigene26742_All	1440	3.02	1.55	0.81	63.51	42.49	32.40	0.18	0.00	0.00	-9.62E-01	1.02E-03		-1.89E+00	2.01E-08	Down	-5.80E-01	1.27E-31		-9.71E-01	2.90E-68		-7.46E+00	4.04E-02		-7.46E+00	3.04E-02		Unigene26742_All//gi|108706201|gb|ABF93996.1|//1.00E-120//Integral membrane protein DUF6 containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene26742_All//1.00E-78//AT4G08300| nodulin MtN21 family protein	Unigene26742_All//0.00E+00//TC147428				nr +
Unigene26743_All	942	5.72	4.68	3.79	11.95	12.17	10.64	10.95	8.25	4.61	-2.90E-01	2.81E-01		-5.95E-01	2.71E-02		2.65E-02	9.02E-01		-1.67E-01	3.93E-01		-4.08E-01	1.12E-02		-1.25E+00	3.71E-14	Down	Unigene26743_All//gi|124359162|gb|ABN05685.1|//4.00E-07//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene26743_All//4.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene26743_All//0.00E+00//ES836149				nr +
Unigene26745_All	971	12.29	5.17	4.33	23.14	16.67	16.14	5.14	5.47	4.10	-1.25E+00	5.84E-13	Down	-1.50E+00	3.39E-16	Down	-4.73E-01	8.88E-06		-5.20E-01	3.55E-06		8.94E-02	7.30E-01		-3.25E-01	1.80E-01				Unigene26745_All//0.00E+00//gi|164332210|gb|ES843579.1|ES843579				
Unigene26747_All	1184	22.76	36.20	25.14	39.13	34.93	30.52	17.10	37.03	13.06	6.70E-01	4.02E-16		1.44E-01	2.12E-01		-1.64E-01	4.18E-02		-3.59E-01	2.20E-06		1.11E+00	1.59E-46	Up	-3.90E-01	2.57E-04		Unigene26747_All//gi|3047092|gb|AAC13604.1|//6.00E-31//T26022.2 gene product [Arabidopsis thaliana]	Unigene26747_All//2.00E-28//AT5G35320| unknown protein	Unigene26747_All//0.00E+00//gi|78344863|gb|DT565137.1|DT565137				nr -
Unigene26752_All	3469	0.03	0.00	0.05	1.11	1.03	0.38	8.43	9.35	8.66	-4.92E+00	3.72E-01		6.10E-01	7.48E-01		-9.90E-02	8.04E-01		-1.55E+00	1.65E-06	Down	1.49E-01	1.12E-01		3.80E-02	7.06E-01		Unigene26752_All//gi|115477174|ref|NP_001062183.1|//1.00E-143//Os08g0505200 [Oryza sativa Japonica Group] >gi|113624152|dbj|BAF24097.1| Os08g0505200 [Oryza sativa Japonica Group]	Unigene26752_All//7.00E-142//AT5G43230| unknown protein	Unigene26752_All//2.00E-122//C0110165				nr -
Unigene26753_All	993	9.17	19.95	12.12	7.93	8.50	10.42	8.86	12.04	8.59	1.12E+00	9.42E-18	Up	4.03E-01	1.97E-02		1.00E-01	6.83E-01		3.94E-01	3.03E-02		4.43E-01	2.59E-03		-4.48E-02	8.08E-01		Unigene26753_All//gi|224103611|ref|XP_002313121.1|//4.00E-46//thioredoxin m [Populus trichocarpa] >gi|222849529|gb|EEE87076.1| thioredoxin m [Populus trichocarpa]	Unigene26753_All//9.00E-45//AT2G15570| thioredoxin M-type 3, chloroplast (TRX-M3)	Unigene26753_All//3.00E-72//TC142798				nr -
Unigene26754_All	740	1.91	1.51	2.37	4.24	2.42	1.53	2.40	2.32	0.22	-3.42E-01	5.48E-01		3.15E-01	5.52E-01		-8.10E-01	1.47E-02		-1.47E+00	4.15E-05	Down	-5.14E-02	9.23E-01		-3.48E+00	4.53E-09	Down	Unigene26754_All//gi|223452526|gb|ACM89590.1|//6.00E-40//disease resistance protein [Glycine max]	Unigene26754_All//9.00E-30//AT1G74170| AtRLP13 (Receptor Like Protein 13); protein binding			ko04626|Plant-pathogen interaction		nr -

Unigene26756_A11	1029	34.17	12.26	41.40	27.55	16.30	8.56	7.15	4.10	2.40	-1.48E+00	2.47E-47	Down	2.77E-01	1.24E-03		-7.57E-01	5.68E-16		-1.69E+00	4.13E-50	Down	-8.01E-01	3.03E-05		-1.57E+00	2.49E-14	Down	Unigene26756_A11//gi|3367524|gb|AAC28509.1|//1.00E-48//P8K4.12 [Arabidopsis thaliana] >gi|115311437|gb|ABI93899.1| At1g61930 [Arabidopsis thaliana]	Unigene26756_A11//3.00E-42//AT1G11700| unknown protein	Unigene26756_A11//0.00E+00//TC149272				nr +
Unigene26757_A11	909	15.94	27.26	18.69	18.14	18.68	20.87	15.21	9.56	5.79	7.74E-01	3.46E-12		2.29E-01	1.28E-01		4.21E-02	8.32E-01		2.02E-01	1.48E-01		-6.69E-01	6.71E-07		-1.39E+00	5.41E-22	Down	Unigene26757_A11//gi|226490910|ref|NP_001150369.1|//2.00E-70//LOC100283999 [Zea mays] >gi|195638716|gb|ACG38826.1| maf-like protein CV_0124 [Zea mays]	Unigene26757_A11//7.00E-76//AT5G42770| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytoplasm; CONTAINS InterPro DOMAIN/s: Maf-like protein (InterPro:IPR003697); BEST Arabidopsis thaliana protein match is: Maf family protein (TAIR:AT5G66550.1); Has 4061 Blast hits to 4057 proteins in 1128 species: Archae - 23; Bacteria - 2744; Metazoa - 45; Fungi - 50; Plants - 61; Viruses - 0; Other Eukaryotes - 1138 (source: NCBI BLink).	Unigene26757_A11//0.00E+00//TC139491				nr -
Unigene26761_A11	1863	4.33	1.82	1.57	19.44	11.72	7.64	7.83	1.73	2.31	-1.25E+00	5.64E-09	Down	-1.46E+00	1.11E-10	Down	-7.30E-01	4.64E-19		-1.35E+00	6.04E-46	Down	-2.18E+00	3.39E-41	Down	-1.76E+00	3.29E-32	Down	Unigene26761_A11//gi|297841763|ref|XP_002888763.1|//1.00E-171//NHL repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297334604|gb|EFH65022.1| NHL repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene26761_A11//7.00E-138//AT1G70280| NHL repeat-containing protein	Unigene26761_A11//0.00E+00//TC145519				nr +
Unigene26762_A11	1058	8.31	35.10	12.23	15.73	18.29	19.68	16.34	22.60	17.74	2.08E+00	1.71E-29	Up	5.58E-01	5.92E-04		2.18E-01	1.01E-01		3.24E-01	8.11E-03		4.67E-01	2.57E-06		1.18E-01	3.62E-01					Unigene26762_A11//0.00E+00//TC166028				
Unigene26763_A11	802	4.83	13.20	8.23	35.90	47.66	53.67	60.73	54.25	38.70	1.45E+00	2.66E-14	Up	7.70E-01	1.20E-03		4.09E-01	3.54E-07		5.80E-01	1.87E-13		-1.63E-01	2.38E-02		-6.50E-01	8.71E-22		Unigene26763_A11//gi|115449199|ref|NP_001048379.1|//1.00E-68//Os02g0794700 [Oryza sativa Japonica Group] >gi|113537910|dbj|BAF10293.1| Os02g0794700 [Oryza sativa Japonica Group]	Unigene26763_A11//3.00E-65//AT2G24200| cytosol aminopeptidase	Unigene26763_A11//0.00E+00//TC131714		ko00480|Glutathione metabolism		nr +
Unigene26767_A11	1066	13.40	4.47	9.29	30.00	18.38	28.81	28.40	11.41	13.19	-1.58E+00	1.14E-21	Down	-5.28E-01	6.00E-04		-7.07E-01	5.79E-16		-5.84E-02	6.17E-01		-1.32E+00	6.61E-42	Down	-1.11E+00	5.38E-33	Down	Unigene26767_A11//gi|18410318|ref|NP_567025.1|//2.00E-55//mitochondrial glycoprotein family protein / MAM33 family protein [Arabidopsis thaliana] >gi|30102600|gb|AAP21218.1| At3g55605 [Arabidopsis thaliana]	Unigene26767_A11//3.00E-45//AT5G02050| mitochondrial glycoprotein family protein / MAM33 family protein	Unigene26767_A11//0.00E+00//TC135128				nr -
Unigene26769_A11	1267	0.91	2.24	2.77	4.91	12.34	20.43	1.57	4.02	15.94	1.30E+00	7.29E-04	Up	1.61E+00	1.02E-05	Up	1.33E+00	4.37E-21	Up	2.06E+00	1.33E-58	Up	1.36E+00	4.67E-08	Up	3.35E+00	1.96E-91	Up	Unigene26769_A11//gi|20857962|gb|AC131101.1|//8.00E-16//At5g56880 [Arabidopsis thaliana]	Unigene26769_A11//9.00E-06//AT5G56880| unknown protein	Unigene26769_A11//1.00E-40//ES838897				nr -
Unigene26771_A11	916	3.60	3.32	1.92	3.97	5.41	4.19	11.35	4.15	4.04	-1.17E-01	7.25E-01		-9.08E-01	1.12E-02		4.47E-01	1.04E-01		7.82E-02	8.24E-01		-1.45E+00	3.44E-17	Down	-1.49E+00	2.09E-18	Down	Unigene26771_A11//gi|55819798|gb|AA66094.1|//1.00E-40//At5g63260 [Arabidopsis thaliana] >gi|56790210|gb|AAW30022.1| At5g63260 [Arabidopsis thaliana]	Unigene26771_A11//6.00E-42//AT5G63260| zinc finger (CCCH-type) family protein	Unigene26771_A11//0.00E+00//TC169737	C3H	ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene26773_A11	1286	35.68	12.41	32.67	2.63	1.77	2.77	0.20	0.20	0.00	-1.52E+00	2.41E-64	Down	-1.27E-01	1.56E-01		-5.76E-01	7.85E-02		7.49E-02	8.42E-01		-1.69E-02	1.02E+00		-7.62E+00	3.04E-02		Unigene26773_A11//gi|222875436|gb|ACM68924.1|//0.00E+00//gibberellin 20-oxidase [Gossypium hirsutum]	Unigene26773_A11//2.00E-107//AT5G51810| GA20OX2 (GIBBERELLIN 20 OXIDASE 2); gibberellin 20-oxidase	Unigene26773_A11//0.00E+00//TC155605		ko00904|Diterpenoid biosynthesis		nr +
Unigene26775_A11	3057	0.29	2.67	0.52	1.01	1.64	2.05	4.56	8.98	24.38	3.20E+00	1.29E-28	Up	8.45E-01	1.25E-01		7.03E-01	6.66E-03		1.02E+00	1.32E-05	Up	9.77E-01	6.89E-24		2.42E+00	2.03E-239	Up	Unigene26775_A11//gi|224106445|ref|XP_002314168.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222850576|gb|EEE88123.1| GRAS family transcription factor [Populus trichocarpa]	Unigene26775_A11//8.00E-150//AT2G29060| scarecrow transcription factor family protein	Unigene26775_A11//0.00E+00//gi|109874705|gb|DW503679.1|DW503679	GRAS			nr -
Unigene26776_A11	709	1.11	1.57	0.45	1.41	1.21	1.72	1.25	3.65	1.18	5.06E-01	4.22E-01		-1.30E+00	1.38E-01		-2.11E-01	7.79E-01		2.92E-01	6.61E-01		1.55E+00	3.03E-05	Up	-8.58E-02	8.98E-01									
Unigene26777_A11	1246	17.68	10.78	12.44	6.28	7.54	4.06	2.10	0.81	0.90	-7.14E-01	1.24E-09		-5.07E-01	2.54E-05		2.66E-01	1.88E-01		-6.29E-01	2.12E-03		-1.39E+00	1.23E-04	Down	-1.23E+00	3.51E-04	Down	Unigene26777_A11//gi|115458802|ref|NP_001053001.1|//9.00E-75//Os04g0462300 [Oryza sativa Japonica Group] >gi|38344973|emb|CAE01536.2| OSJNBa0072F16.18 [Oryza sativa (japonica cultivar-group)] >gi|113564572|dbj|BAF14915.1| Os04g0462300 [Oryza sativa Japonica Group]	Unigene26777_A11//8.00E-99//AT3G25805| unknown protein	Unigene26777_A11//0.00E+00//TC143839				nr +
Unigene2678_A11	1624	159.35	100.59	160.77	46.23	35.22	51.67	13.82	33.02	14.18	-6.64E-01	2.52E-92		1.28E-02	7.38E-01		-3.92E-01	7.05E-13		1.61E-01	6.24E-03		1.26E+00	1.85E-68	Up	3.65E-02	7.48E-01		Unigene2678_A11//gi|91694293|gb|AB041798.1|//0.00E+00//gamma-tocopherol methyltransferase [Gossypium hirsutum]	Unigene2678_A11//2.00E-125//AT1G64970| G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERASE); tocopherol O-methyltransferase	Unigene2678_A11//0.00E+00//TC138121		ko00564|Glycerophospholipid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00100|Steroid biosynthesis		nr -
Unigene26780_A11	1000	1.88	2.08	2.61	2.24	1.31	2.26	3.93	2.34	1.71	1.41E-01	7.39E-01		4.70E-01	2.53E-01		-7.77E-01	5.80E-02		1.06E-02	9.82E-01		-7.48E-01	6.34E-03		-1.20E+00	1.26E-05	Down	Unigene26780_A11//gi|41176619|gb|AA896599.1|//4.00E-81/4-alpha-glucanotransferase [Solanum tuberosum]	Unigene26780_A11//7.00E-79//AT2G40840| DPE2 (DISPROPORTIONATING ENZYME 2); 4-alpha-glucanotransferase/ heteroglycan binding	Unigene26780_A11//0.00E+00//DW501432		ko00500|Starch and sucrose metabolism		nr +
Unigene26781_A11	880	48.69	14.39	22.81	99.46	74.08	39.98	49.82	30.73	15.08	-1.76E+00	9.50E-74	Down	-1.09E+00	6.75E-35	Down	-4.25E-01	2.77E-17		-1.31E+00	2.72E-106	Down	-6.97E-01	1.58E-21		-1.72E+00	2.20E-92	Down	Unigene26781_A11//gi|223452472|gb|ACM89563.1|//7.00E-92//receptor-like protein kinase [Glycine max]	Unigene26781_A11//7.00E-86//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene26781_A11//0.00E+00//TC152381				nr +
Unigene26783_A11	1186	1.19	0.43	1.12	8.11	5.57	3.58	3.78	2.22	1.95	-1.48E+00	1.15E-02		-8.56E-02	8.81E-01		-5.40E-01	1.88E-03		-1.18E+00	2.49E-10	Down	-7.67E-01	2.55E-03		-9.56E-01	1.26E-04		Unigene26783_A11//gi|53370641|gb|AB389136.1|//2.00E-10//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene26783_A11//0.00E+00//ES800203				nr -
Unigene26785_A11	547	25.35	13.06	16.84	40.25	42.24	59.36	40.58	28.50	17.12	-9.57E-01	5.74E-10		-5.90E-01	1.58E-04		6.96E-02	6.14E-01		5.61E-01	1.00E-09		-5.10E-01	8.27E-07		-1.25E+00	2.44E-29	Down	Unigene26785_A11//gi|62287477|sp|Q9M5M1.1|RS11_ELPES//4.00E-50//RecName: Full=40S ribosomal protein S11 >gi|6984142|gb|AAF34771.1|AF227626_1 40S ribosomal protein S11 [Euphorbia esula]	Unigene26785_A11//1.00E-49//AT3G48930| EMB1080 (embryo defective 1080); structural constituent of ribosome	Unigene26785_A11//0.00E+00//TC150261		ko03010|Ribosome		nr -
Unigene26786_A11	527	72.18	66.05	39.20	159.08	124.35	131.55	408.52	218.65	153.38	-1.28E-01	1.82E-01		-8.81E-01	8.09E-22		-3.55E-01	5.56E-12		-2.74E-01	6.86E-07		-9.02E-01	2.03E-159		-1.41E+00	0.00E+00	Down	Unigene26786_A11//gi|158144895|gb|ABW21688.1|//5.00E-32//enolase [Gossypium hirsutum]	Unigene26786_A11//1.00E-29//AT2G36530| LOS2; copper ion binding / phosphopyruvate hydratase	Unigene26786_A11//0.00E+00//gi|21094022|gb|BQ406347.1|BQ406347		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation		nr -
Unigene26787_A11	1796	12.53	5.92	3.50	10.82	14.13	9.35	20.93	11.89	12.60	-1.08E+00	5.42E-19	Down	-1.84E+00	5.98E-40	Down	3.86E-01	1.64E-04		-2.10E-01	1.26E-01		-8.16E-01	3.97E-24		-7.32E-01	9.21E-21		Unigene26787_A11//gi|5080804|gb|AAD39313.1|AC007258_2//1.00E-116//Hypothetical protein [Arabidopsis thaliana] >gi|15010642|gb|AAK73980.1| At1g59710/T30E16_31 [Arabidopsis thaliana] >gi|22137290|gb|AAM91490.1| At1g59710/T30E16_31 [Arabidopsis thaliana]	Unigene26787_A11//2.00E-117//AT1G59710| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27100.1); Has 119 Blast hits to 107 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 119; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene26787_A11//0.00E+00//TC134757				nr +
Unigene2679_A11	1836	11.91	34.80	22.74	17.34	15.83	18.35	11.12	9.45	8.25	1.55E+00	7.45E-91	Up	9.33E-01	2.51E-26		-1.31E-01	2.23E-01		8.20E-02	4.72E-01		-2.36E-01	3.97E-02		-4.32E-01	4.54E-05		Unigene2679_A11//gi|6714278|gb|AAF25974.1|AC017118_11//1.00E-107//F6N18.17 [Arabidopsis thaliana]	Unigene2679_A11//7.00E-108//AT1G32790| RNA-binding protein, putative	Unigene2679_A11//0.00E+00//gi|109843907|gb|DW242465.1|DW242465		ko03040|Spliceosome		nr -
Unigene26790_A11	458	1.37	1.99	2.44	7.94	2.71	2.76	1.11	1.00	1.48	5.39E-01	4.49E-01		8.33E-01	2.23E-01		-1.55E+00	6.21E-07	Down	-1.52E+00	4.55E-06	Down	-1.42E-01	8.76E-01		4.17E-01	6.01E-01									
Unigene26791_A11	1259	1.29	0.40	1.23	2.10	1.37	1.51	1.98	0.90	0.76	-1.68E+00	2.36E-03		-7.08E-02	8.95E-01		-6.17E-01	1.03E-01		-4.77E-01	2.39E-01		-1.14E+00	1.62E-03		-1.38E+00	1.26E-04	Down								
Unigene26792_A11	1593	0.89	1.72	0.64	5.60	4.97	2.15	2.12	1.05	1.70	9.54E-01	1.28E-02		-4.82E-01	3.97E-01		-1.71E-01	4.39E-01		-1.38E+00	4.27E-12	Down	-1.02E+00	7.56E-04	Down	-3.20E-01	2.95E-01		Unigene26792_A11//gi|30692614|ref|NP_174471.2|//1.00E-141//BRX (BREVIS RADIX); identical protein binding / water channel [Arabidopsis thaliana] >gi|229621711|sp|Q1T7I5.2|BRX_ARATH RecName: Full=Protein BREVIS RADIX; Short=AtBRX	Unigene26792_A11//2.00E-131//AT1G31880| BRX (BREVIS RADIX); identical protein binding / water channel	Unigene26792_A11//0.00E+00//TC178261				nr -
Unigene26794_A11	1295	1.17	1.88	1.48	1.31	0.93	0.98	2.55	8.13	10.58	6.81E-01	9.55E-02		3.37E-01	4.97E-01		-4.91E-01	3.29E-01		-4.22E-01	4.36E-01		1.68E+00	3.23E-21	Up	2.06E+00	1.21E-36	Up	Unigene26794_A11//gi|115465926|ref|NP_001056562.1|//2.00E-12//Os06g0106100 [Oryza sativa Japonica Group] >gi|113594602|dbj|BAF18476.1| Os06g0106100 [Oryza sativa Japonica Group]	Unigene26794_A11//8.00E-13//AT3G13200| EMB2769 (EMBRYO DEFECTIVE 2769)	Unigene26794_A11//3.00E-29//ES832676		ko03040|Spliceosome		nr -
Unigene26798_A11	1293	11.45	33.23	36.41	30.71	65.22	57.46	0.00	0.13	0.00	1.54E+00	9.66E-61	Up	1.67E+00	6.78E-73	Up	1.09E+00	1.32E-82	Up	9.04E-01	8.63E-49		7.01E+00	1.39E-01		null	null		Unigene26798_A11//gi|9739011|gb|AAF97863.1|//4.00E-66//outward-rectifying potassium channel KCO1 [Eucalyptus camaldulensis]	Unigene26798_A11//6.00E-61//AT5G35630| ATKCO1; calcium-activated potassium channel/ ion channel/ outward rectifier potassium channel	Unigene26798_A11//0.00E+00//TC140124				nr +
Unigene268_A11	3672	28.30	11.38	19.08	38.98	44.54	26.28	11.19	9.87	7.15	-1.31E+00	6.08E-116	Down	-5.68E-01	1.51E-27		1.93E-01	2.19E-07		-5.68E-01	3.62E-42		-1.82E-01	2.07E-02		-6.47E-01	2.42E-18		Unigene268_A11//gi|134142350|gb|AB061511.1|//0.00E+00//LRR receptor-like protein kinase m1* [Malus x domestica]	Unigene268_A11//0.00E+00//AT1G28440| HSL1 (HAESA-Like 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene268_A11//0.00E+00//TC163187				nr -
Unigene26801_A11	1186	2.38	2.78	3.10	2.60	3.16	2.67	4.63	2.26	1.55	2.21E-01	5.43E-01		3.79E-01	2.70E-01		2.81E-01	4.28E-01		3.37E-02	9.45E-01		-1.04E+00	6.29E-06	Down	-1.58E+00	5.12E-11	Down	Unigene26801_A11//gi|76880168|dbj|BAE48857.1|//1.00E-77//MurB reductase [Physcomitrella patens subsp. patens]		Unigene26801_A11//0.00E+00//TC154290				nr -
Unigene26802_A11	1219	1.80	5.28	2.23	11.52	19.10	15.12	6.59	9.22	6.77	1.55E+00	8.14E-10	Up	3.06E-01	4.48E-01		7.29E-01	5.82E-12		3.92E-01	2.32E-03		4.85E-01	1.37E-03		3.78E-02	8.53E-01		Unigene26802_A11//gi|297838865|ref|XP_002887314.1|//1.00E-120//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333155|gb|EFH63573.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26802_A11//6.00E-115//AT1G70590| F-box family protein	Unigene26802_A11//0.00E+00//TC134722		ko04141|Protein processing in endoplasmic reticulum		nr -

Unigene26803_A11	879	33.09	40.29	26.53	33.49	38.31	32.52	25.35	59.82	29.87	2.84E-01	1.93E-03		-3.19E-01	2.52E-03		1.94E-01	4.26E-02		-4.24E-02	7.20E-01		1.24E+00	1.07E-65	Up	2.37E-01	1.30E-02		Unigene26803_A11//gi|297844182|ref|XP_002889972.1|//3.00E-37//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297335814|gb|EFH66231.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	Unigene26803_A11//0.00E+00//TC157002		ko03040|Spliceosome		nr +
Unigene26807_A11	1082	4.21	2.90	2.02	8.38	8.02	7.05	3.71	2.39	2.32	-5.35E-01	6.02E-02		-1.06E+00	3.89E-04	Down	-6.32E-02	8.03E-01		-2.48E-01	2.36E-01		-6.32E-01	2.02E-02		-6.78E-01	9.49E-03		Unigene26807_A11//gi|297845572|ref|XP_002890667.1|//4.00E-81//BSD domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297336509|gb|EFH66926.1| BSD domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene26807_A11//3.00E-56//AT1G69030| INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: BSD (InterPro:IPR005607); BEST Arabidopsis thaliana protein match is: BSD domain-containing protein (TAIR:AT1G26300.1); Has 173 Blast hits to 173 proteins in 34 species: Archae - 4; Bacteria - 4; Metazoa - 52; Fungi - 10; Plants - 92; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene26807_A11//0.00E+00//gi|164273376|gb|ES813809.1|ES813809				nr -
Unigene26808_A11	1308	18.80	18.87	31.55	449.20	179.84	168.98	36.79	28.63	19.16	5.00E-03	9.87E-01		7.47E-01	5.57E-18		-1.32E+00	0.00E+00	Down	-1.41E+00	0.00E+00	Down	-3.62E-01	1.07E-07		-9.41E-01	5.43E-40		Unigene26808_A11//gi|89243481|gb|AB064879.1|//1.00E-124//nicotianamine synthase [Malus xiaojinensis]	Unigene26808_A11//7.00E-110//AT1G09240| NAS3 (NICOTIANAMINE SYNTHASE 3); nicotianamine synthase	Unigene26808_A11//0.00E+00//TC169743				nr +
Unigene26809_A11	752	72.85	78.50	71.66	57.90	66.81	62.52	91.64	63.92	43.92	1.08E-01	1.53E-01		-2.37E-02	7.75E-01		2.07E-01	5.20E-03		1.11E-01	2.21E-01		-5.20E-01	4.52E-20		-1.06E+00	3.28E-69	Down	Unigene26809_A11//gi|192910730|gb|ACF06472.1|//2.00E-32//light-inducible protein ATLS1 [Elaeis guineensis]	Unigene26809_A11//1.00E-30//AT5G01650| macrophage migration inhibitory factor family protein / MIF family protein	Unigene26809_A11//0.00E+00//TC150640				nr -
Unigene26810_A11	735	12.03	13.51	10.07	18.23	16.21	22.43	10.41	5.06	8.94	1.68E-01	3.83E-01		-2.57E-01	2.40E-01		-1.70E-01	3.18E-01		2.99E-01	3.61E-02		-1.04E+00	5.84E-08	Down	-2.19E-01	2.64E-01				Unigene26810_A11//9.00E-118//BQ411106					
Unigene26811_A11	1058	6.78	7.28	4.93	142.00	109.16	66.12	33.89	10.03	7.08	1.04E-01	6.29E-01		-4.58E-01	4.77E-02		-3.79E-01	7.84E-24		-1.10E+00	7.74E-138	Down	-1.76E+00	2.44E-75	Down	-2.26E+00	5.32E-108	Down	Unigene26811_A11//gi|117950163|gb|ABK58465.1|//1.00E-100//LIM domain protein GLIMlb [Populus tremula x Populus alba]	Unigene26811_A11//9.00E-88//AT1G10200| WLIM1; transcription factor/ zinc ion binding	Unigene26811_A11//0.00E+00//TC139325	LIM			nr +
Unigene26813_A11	1190	2.68	8.43	6.13	4.60	5.09	5.35	6.32	10.26	6.46	1.65E+00	2.97E-16	Up	1.19E+00	2.46E-07	Up	1.45E-01	5.94E-01		2.17E-01	4.18E-01		6.98E-01	1.39E-06		3.09E-02	8.92E-01		Unigene26813_A11//gi|33186647|gb|AAP97493.1|//4.00E-32//UDP-Glc-4-epimerase [Solanum tuberosum]	Unigene26813_A11//3.00E-28//AT1G12780| UGE1 (UDP-D-glucose/UDP-D-galactose 4-epimerase 1); UDP-glucose 4-epimerase/ protein dimerization	Unigene26813_A11//1.00E-142//ES805135		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism		nr -
Unigene26815_A11	631	9.20	8.03	7.00	14.84	20.36	19.40	6.83	17.22	12.44	-1.97E-01	4.49E-01		-3.94E-01	1.41E-01		4.56E-01	2.61E-03		3.86E-01	1.90E-02		1.33E+00	7.89E-16	Up	8.64E-01	2.25E-06		Unigene26815_A11//gi|297598660|ref|NP_001046029.2|//1.00E-46//Os02g0170500 [Oryza sativa Japonica Group] >gi|148921420|dbj|BAF64449.1| HAP5 subunit of HAP complex [Oryza sativa Japonica Group] >gi|255670636|dbj|BAF07943.2| Os02g0170500 [Oryza sativa Japonica Group]	Unigene26815_A11//5.00E-33//AT1G56170| NF-YC2 (NUCLEAR FACTOR Y, SUBUNIT C2); DNA binding / transcription activator/ transcription factor	Unigene26815_A11//9.00E-133//ES848985	CCAAT			nr -
Unigene26816_A11	1421	3.68	7.95	4.38	5.89	8.82	9.76	5.83	14.47	9.92	1.11E+00	2.67E-10	Up	2.52E-01	3.46E-01		5.83E-01	1.08E-04		7.28E-01	8.17E-07		1.31E+00	1.59E-28	Up	7.67E-01	6.18E-09		Unigene26816_A11//gi|46250703|dbj|BAD15085.1|//7.00E-77//CCAAT-box binding factor HAP5 homolog [Daucus carota]	Unigene26816_A11//2.00E-60//AT1G56170| NF-YC2 (NUCLEAR FACTOR Y, SUBUNIT C2); DNA binding / transcription activator/ transcription factor	Unigene26816_A11//0.00E+00//TC136831	CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication		nr +
Unigene26817_A11	1424	32.63	22.24	23.75	49.18	58.88	70.19	19.45	10.42	8.67	-5.53E-01	1.29E-12		-4.58E-01	9.03E-09		2.60E-01	9.39E-07		5.13E-01	1.58E-24		-9.00E-01	3.81E-21		-1.17E+00	8.07E-33	Down	Unigene26817_A11//gi|15241404|ref|NP_196949.1|//1.00E-158//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75181027|sp|Q9LY84.1|GDL76_ARATH RecName: Full=GDSL esterase/lipase At5g14450; AltName: Full=Extracellular lipase At5g14450; Flags: Precursor >gi|7573470|emb|CAB87784.1| early nodule-specific protein-like [Arabidopsis thaliana] >gi|28950957|gb|AAO63402.1| At5g14450 [Arabidopsis thaliana]	Unigene26817_A11//3.00E-158//AT5G14450| GDSL-motif lipase/hydrolase family protein	Unigene26817_A11//0.00E+00//TC132204				nr -
Unigene26819_A11	1458	0.68	0.63	2.26	3.14	2.83	2.48	3.57	1.18	3.88	-1.24E-01	8.42E-01		1.73E+00	6.46E-06	Up	-1.49E-01	6.22E-01		-3.43E-01	2.60E-01		-1.60E+00	2.94E-10	Down	1.21E-01	6.18E-01		Unigene26819_A11//gi|42562804|ref|NP_564728.2|//7.00E-91//WD-40 repeat family protein / beige-related [Arabidopsis thaliana]	Unigene26819_A11//3.00E-92//AT1G58230| WD-40 repeat family protein / beige-related					nr -
Unigene2682_A11	2455	6.01	3.30	2.82	34.29	28.42	25.76	31.98	19.70	17.46	-8.64E-01	5.10E-09		-1.09E+00	2.37E-12	Down	-2.71E-01	2.08E-07		-4.13E-01	3.38E-14		-6.99E-01	4.35E-38		-8.73E-01	4.31E-57		Unigene2682_A11//gi|18398763|ref|NP_564419.1|//0.00E+00//dehydration-responsive family protein [Arabidopsis thaliana] >gi|75268396|sp|Q9C884.1|PMT1_ARATH RecName: Full=Probable methyltransferase PMT18 >gi|32306499|gb|AAP78933.1| At1g33170 [Arabidopsis thaliana]	Unigene2682_A11//0.00E+00//AT1G33170| dehydration-responsive family protein	Unigene2682_A11//0.00E+00//TC163481				nr -
Unigene26821_A11	1407	3.24	5.08	0.61	8.92	4.58	6.81	8.68	2.05	1.42	6.50E-01	2.96E-03		-2.42E+00	9.28E-12	Down	-9.63E-01	7.42E-11		-3.91E-01	1.53E-02		-2.08E+00	1.03E-32	Down	-2.62E+00	3.10E-44	Down	Unigene26821_A11//gi|255570408|ref|XP_002526163.1|//1.00E-169//stearoyl-ACP desaturase [Ricinus communis] >gi|195963829|gb|ACG59947.1| stearoyl-acyl-carrier protein desaturase [Ricinus communis] >gi|195963831|gb|ACG59948.1| stearoyl-acyl-carrier protein desaturase [Ricinus communis] >gi|223534540|gb|EEF36239.1| stearoyl-ACP desaturase [Ricinus communis]	Unigene26821_A11//1.00E-156//AT1G43800| acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative	Unigene26821_A11//0.00E+00//gi|78350795|gb|DT571069.1|DT571069		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis		nr -
Unigene26823_A11	1094	105.12	68.73	83.43	18.44	21.31	13.29	7.38	1.95	2.04	-6.13E-01	4.80E-36		-3.33E-01	9.51E-12		2.09E-01	8.03E-02		-4.72E-01	7.85E-05		-1.92E+00	9.43E-20	Down	-1.86E+00	1.66E-19	Down	Unigene26823_A11//gi|188036222|pdb|3BBN|U//4.00E-52//Chain U, Homology Model For The Spinach Chloroplast 30s Subunit Fitted To 9.4a Cryo-Em Map Of The 70s Chlororibosome. >gi|17154781|gb|AAL35983.1|AF104396_1 ribosome-like protein [Cucumis sativus]	Unigene26823_A11//8.00E-29//AT3G27160| GBS1 (GLUCOSE HYPERSENSITIVE 1); structural constituent of ribosome	Unigene26823_A11//0.00E+00//gi|109868871|gb|DW497847.1|DW497847				nr -
Unigene26824_A11	766	1.71	1.92	0.90	2.67	2.34	2.95	3.75	1.64	1.98	1.68E-01	7.42E-01		-9.18E-01	1.38E-01		-1.90E-01	6.96E-01		1.45E-01	7.46E-01		-1.20E+00	3.65E-04	Down	-9.25E-01	3.74E-03								
Unigene26825_A11	1497	0.42	0.00	0.07	7.05	3.27	3.77	1.33	1.09	1.46	-8.71E+00	7.92E-04	Down	-2.56E+00	2.72E-02		-1.11E+00	1.54E-11	Down	-9.04E-01	1.62E-07		-2.86E-01	5.28E-01		1.41E-01	7.15E-01		Unigene26825_A11//gi|224075800|ref|XP_002304773.1|//0.00E+00//cytokinin oxidase [Populus trichocarpa] >gi|222842205|gb|EEE79752.1| cytokinin oxidase [Populus trichocarpa]	Unigene26825_A11//4.00E-169//AT2G41510| CKX1 (CYTOKININ OXIDASE/DEHYDROGENASE 1); cytokinin dehydrogenase	Unigene26825_A11//0.00E+00//ES837714		ko00908|Zeatin biosynthesis		nr +
Unigene26828_A11	1033	1.52	0.93	2.68	7.14	8.00	24.09	16.70	51.43	52.30	-7.05E-01	1.80E-01		8.19E-01	3.85E-02		1.65E-01	4.98E-01		1.76E+00	1.05E-45	Up	1.62E+00	2.26E-99	Up	1.65E+00	2.49E-105	Up	Unigene26828_A11//gi|6688816|emb|CAB65283.1|//2.00E-28//Enod93 protein [Medicago sativa subsp. x varia]	Unigene26828_A11//2.00E-24//AT5G25940| early nodulin-related	Unigene26828_A11//0.00E+00//DR463532				nr -
Unigene26829_A11	1239	1.22	1.10	0.13	2.01	0.86	0.77	2.25	2.23	2.44	-1.49E-01	7.64E-01		-3.25E+00	1.40E-05	Down	-1.22E+00	1.28E-03		-1.39E+00	6.58E-04	Down	-1.66E-02	9.96E-01		1.18E-01	7.20E-01		Unigene26829_A11//gi|15239759|ref|NP_200294.1|//1.00E-177//DOMON domain-containing protein / dopamine beta-monooxygenase N-terminal domain-containing protein [Arabidopsis thaliana] >gi|19699059|gb|AAL90897.1| At5g54830/MDG8_9 [Arabidopsis thaliana] >gi|27363250|gb|AAO11544.1| At5g54830/MDG8_9 [Arabidopsis thaliana]	Unigene26829_A11//2.00E-178//AT5G54830| DOMON domain-containing protein / dopamine beta-monooxygenase N-terminal domain-containing protein	Unigene26829_A11//0.00E+00//TC178179				nr +
Unigene2683_A11	1897	1.13	4.51	0.76	1.18	5.65	11.78	5.97	2.14	2.69	2.00E+00	6.84E-18	Up	-5.77E-01	2.17E-01		2.26E+00	1.11E-29	Up	3.32E+00	7.05E-86	Up	-1.48E+00	3.07E-19	Down	-1.15E+00	1.02E-13	Down	Unigene2683_A11//gi|240256292|ref|NP_196927.4|//0.00E+00//protein binding [Arabidopsis thaliana]	Unigene2683_A11//0.00E+00//AT5G14230| protein binding	Unigene2683_A11//0.00E+00//gi|73859705|gb|DT462444.1|DT462444				nr +
Unigene26833_A11	795	51.93	27.09	29.81	355.34	218.57	424.99	245.38	188.42	88.70	-9.39E-01	2.70E-27		-8.01E-01	3.49E-20		-7.01E-01	1.33E-136		2.58E-01	5.04E-23		-3.81E-01	1.56E-31		-1.47E+00	0.00E+00	Down	Unigene26833_A11//gi|1150684|emb|CAA64425.1|//4.00E-60//cell wall-plasma membrane linker protein [Brassica napus]	Unigene26833_A11//4.00E-25//AT3G22142| structural constituent of cell wall	Unigene26833_A11//0.00E+00//gi|109840896|gb|DW239456.1|DW239456		ko03040|Spliceosome		nr -
Unigene26835_A11	1276	0.98	1.03	2.00	5.58	5.18	6.16	5.43	1.97	2.40	6.91E-02	9.12E-01		1.03E+00	1.37E-02		-1.08E-01	6.72E-01		1.42E-01	5.79E-01		-1.47E+00	6.67E-12	Down	-1.18E+00	5.22E-09	Down			Unigene26835_A11//5.00E-34//FL577570				
Unigene26837_A11	1134	3.23	1.92	3.05	4.13	5.65	5.81	8.84	2.29	3.37	-7.49E-01	1.94E-02		-8.16E-02	8.07E-01		4.52E-01	5.33E-02		4.94E-01	3.43E-02		-1.95E+00	8.24E-25	Down	-1.39E+00	4.26E-16	Down	Unigene26837_A11//gi|225440868|ref|XP_002276568.1|//2.00E-89//PREDICTED: similar to glutaredoxin family protein [Vitis vinifera]	Unigene26837_A11//6.00E-62//AT5G03870| glutaredoxin family protein	Unigene26837_A11//8.00E-153//gi|73944213|gb|DT527521.1|DT527521				nr +
Unigene26838_A11	1829	3.58	0.89	1.78	28.33	18.90	9.11	3.14	1.58	0.72	-2.01E+00	4.68E-14	Down	-1.01E+00	3.06E-05	Down	-5.84E-01	2.79E-18		-1.64E+00	2.06E-87	Down	-9.96E-01	8.39E-06		-2.13E+00	9.30E-17	Down	Unigene26838_A11//gi|113205243|gb|AAT39312.2|//1.00E-142//Major Facilitator Superfamily protein [Solanum demissum]	Unigene26838_A11//2.00E-146//AT3G54650| NAX1 (NITRATE EXCRETION TRANSPORTER1); nitrate efflux transmembrane transporter/ transporter	Unigene26838_A11//0.00E+00//DW517732				nr -
Unigene26839_A11	1022	15.05	11.85	13.49	29.68	26.69	27.31	24.28	10.96	10.88	-3.45E-01	1.72E-02		-1.58E-01	3.47E-01		-1.54E-01	1.51E-01		-1.20E-01	3.03E-01		-1.15E+00	5.53E-28	Down	-1.16E+00	2.89E-29	Down	Unigene26839_A11//gi|77556188|gb|AB98984.1|//5.00E-38//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene26839_A11//3.00E-37//AT3G17300| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Complex 1 LYR protein (InterPro:IPR008011); Has 28 Blast hits to 28 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene26839_A11//0.00E+00//TC150509				nr +
Unigene26843_A11	1843	3.41	2.36	3.73	12.84	8.71	6.69	26.29	11.13	8.47	-5.27E-01	2.55E-02		1.30E-01	6.30E-01		-5.60E-01	4.78E-08		-9.40E-01	3.88E-17		-1.24E+00	9.21E-61	Down	-1.63E+00	1.84E-94	Down	Unigene26843_A11//gi|209171162|gb|ACI42847.1|//1.00E-137//RING finger protein [Glycine max]	Unigene26843_A11//2.00E-106//AT5G40250| zinc finger (C3HC4-type RING finger) family protein	Unigene26843_A11//0.00E+00//TC145927				nr +
Unigene26844_A11	1119	1.78	0.77	1.28	5.12	3.29	3.59	5.63	2.91	2.35	-1.21E+00	9.79E-03		-4.68E-01	3.45E-01		-6.37E-01	6.50E-03		-5.11E-01	4.16E-02		-9.50E-01	7.09E-06		-1.26E+00	4.12E-09	Down	Unigene26844_A11//gi|51090585|dbj|BAD36037.1|//8.00E-86//natC N(alpha)-terminal acetyltransferase, Mak10 subunit-like [Oryza sativa (japonica Group)]	Unigene26844_A11//1.00E-79//AT2G11000| ATMAK10; acetyltransferase					nr -

Unigene26847_All	2657	0.04	0.08	0.00	0.00	0.26	2.57	1.26	5.52	25.68	9.54E-01	6.21E-01		-5.30E+00	3.94E-01		8.02E+00	3.05E-04	Up	1.13E+01	2.13E-41	Up	2.13E+00	2.96E-40	Up	4.35E+00	0.00E+00	Up	Unigene26847_All//gi|282927332|gb|ACF60504.2|//0.00E+00//respiratory burst oxidase-like protein [Citrullus colocynthis]	Unigene26847_All//0.00E+00//AT5G47910| RBOHD (RESPIRATORY BURST OXIDASE HOMOLOGUE D); NAD(P)H oxidase	Unigene26847_All//0.00E+00//gi|78334269|gb|DT554543.1|DT554543		ko04626|Plant-pathogen interaction		nr -
Unigene26849_All	1228	4.52	0.83	0.95	3.57	2.61	3.31	21.11	5.21	35.10	-2.45E+00	3.74E-15	Down	-2.24E+00	4.74E-13	Down	-4.53E-01	1.15E-01		-1.09E-01	7.24E-01		-2.02E+00	6.88E-66	Down	7.34E-01	1.18E-23		Unigene26849_All//gi|82697977|gb|AB88902.3.1|//1.00E-95//CXE carboxylesterase [Actinidia eriantha]	Unigene26849_All//2.00E-71//AT1G47480| hydrolase	Unigene26849_All//0.00E+00//CO099553				nr +
Unigene26850_All	667	5.65	18.23	10.78	3.51	6.40	4.67	3.42	4.07	7.70	1.69E+00	3.59E-20	Up	9.32E-01	4.36E-05		8.67E-01	2.25E-03		4.13E-01	2.81E-01		2.51E-01	5.09E-01		1.17E+00	8.54E-07	Up							
Unigene26851_All	868	4.58	12.67	4.91	9.53	11.11	9.16	9.45	10.30	10.33	1.47E+00	4.78E-15	Up	9.94E-02	7.46E-01		2.22E-01	2.88E-01		-5.70E-02	7.99E-01		1.25E-01	5.44E-01		1.28E-01	5.07E-01		Unigene26851_All//gi|18411133|ref|NP_567078.1|//1.00E-42//TXR1 (THAXTOMIN A RESISTANT 1) [Arabidopsis thaliana] >gi|141904872|gb|AAX55724.1|AF380643_1 AT3g59280/F25L23_140 [Arabidopsis thaliana] >gi|15809738|gb|AAL06797.1| AT3g59280/F25L23_140 [Arabidopsis thaliana] >gi|32306447|gb|AAM63549.1| thaxtomin resistance protein TXR1 [Arabidopsis thaliana]	Unigene26851_All//5.00E-44//AT3G59280| TXR1 (THAXTOMIN A RESISTANT 1)	Unigene26851_All//0.00E+00//TC164164				nr -
Unigene26852_All	1029	1.47	1.82	2.23	3.97	2.44	2.11	6.66	4.63	3.21	3.05E-01	5.31E-01		5.94E-01	1.81E-01		-7.00E-01	1.40E-02		-9.14E-01	2.15E-03		-5.24E-01	9.12E-03		-1.05E+00	1.43E-07	Down	Unigene26852_All//gi|225444429|ref|XP_002266411.1|//2.00E-10//PREDICTED: similar to UBA-like; HSC20, C-terminal oligomerisation [Vitis vinifera]		Unigene26852_All//0.00E+00//TC139697				nr +
Unigene26854_All	1056	7.13	12.57	4.49	3.16	3.65	7.70	13.09	20.07	60.85	8.17E-01	1.66E-07		-6.69E-01	2.44E-03		2.09E-01	5.68E-01		1.28E+00	7.40E-10	Up	6.16E-01	7.39E-09		2.22E+00	5.88E-186	Up	Unigene26854_All//gi|222139394|gb|ACM45716.1|//1.00E-101//class IV chitinase [Pyrus pyrifolia]	Unigene26854_All//1.00E-93//AT3G54420| ATEP3; chitinase	Unigene26854_All//0.00E+00//TC136057		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene26857_All	930	15.13	17.00	12.60	47.73	29.62	14.47	4.23	3.60	3.08	1.68E-01	2.74E-01		-2.65E-01	1.07E-01		-6.88E-01	5.44E-21		-1.72E+00	1.48E-80	Down	-2.34E-01	4.38E-01		-4.55E-01	9.17E-02		Unigene26857_All//gi|87116560|gb|ABD19644.1|//2.00E-64//At1g21050 [Arabidopsis thaliana]	Unigene26857_All//4.00E-58//AT1G21050| unknown protein	Unigene26857_All//0.00E+00//gi|109886278|gb|DW515248.1|DW515248				nr -
Unigene26858_All	1485	134.31	49.51	57.19	26.30	27.85	17.24	0.00	0.11	0.00	-1.44E+00	2.21E-255	Down	-1.23E+00	1.00E-194	Down	8.26E-02	4.18E-01		-6.09E-01	2.01E-13		6.82E+00	1.39E-01		null	null		Unigene26858_All//gi|18447767|gb|AAL67994.1|//0.00E+00//acyltransferase-like protein [Gossypium hirsutum]	Unigene26858_All//7.00E-143//AT5G23940| EMB3009 (embryo defective 3009); transferase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene26858_All//0.00E+00//TC130226		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene26859_All	1587	5.18	1.37	1.71	5.18	4.69	2.73	10.50	6.56	4.47	-1.91E+00	2.06E-16	Down	-1.60E+00	2.57E-12	Down	-1.44E-01	5.62E-01		-9.23E-01	3.40E-06		-6.79E-01	2.50E-08		-1.23E+00	6.97E-22	Down	Unigene26859_All//gi|297791015|ref|XP_002863392.1|//1.00E-65//ubiquitin-specific protease 21 [Arabidopsis lyrata subsp. lyrata] >gi|297309227|gb|EFH39651.1| ubiquitin-specific protease 21 [Arabidopsis lyrata subsp. lyrata]	Unigene26859_All//6.00E-67//AT5G46740| UBP21 (UBIQUITIN-SPECIFIC PROTEASE 21); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene26859_All//0.00E+00//DT458339		ko04144|Endocytosis		nr -
Unigene2686_All	1862	15.01	9.52	13.58	1.90	5.77	5.77	2.18	1.35	1.56	-6.56E-01	1.92E-10		-1.44E-01	2.32E-01		1.60E+00	4.11E-19	Up	1.60E+00	1.13E-17	Up	-6.95E-01	1.00E-02		-4.81E-01	6.75E-02		Unigene2686_All//gi|115440815|ref|NP_001044687.1|//1.00E-35//Os01g0829100 [Oryza sativa Japonica Group] >gi|15624058|dbj|BAB68111.1| protein kinase-like [Oryza sativa Japonica Group] >gi|20160634|dbj|BAB89579.1| protein kinase-like [Oryza sativa Japonica Group] >gi|113534218|dbj|BAF06601.1| Os01g0829100 [Oryza sativa Japonica Group]	Unigene2686_All//1.00E-10//AT4G27780| ACBP2 (ACYL-COA BINDING PROTEIN ACBP 2); acyl-CoA binding / lead ion binding	Unigene2686_All//0.00E+00//gi|78336626|gb|DT556900.1|DT556900				nr -
Unigene26860_All	1799	4.07	2.23	2.22	15.84	12.69	10.42	16.05	3.90	5.45	-8.72E-01	5.82E-05		-8.75E-01	1.03E-04		-3.20E-01	9.02E-04		-6.04E-01	7.76E-10		-2.04E+00	2.52E-74	Down	-1.56E+00	5.64E-53	Down	Unigene26860_All//gi|18396647|ref|NP_564298.1|//0.00E+00//SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|42571671|ref|NP_973926.1| SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75331738|sp|Q93Y09.1|SCP45_ARATH RecName: Full=Serine carboxypeptidase-like 45; Flags: Precursor >gi|31376397|gb|AAP49525.1| At1g28110 [Arabidopsis thaliana]	Unigene26860_All//0.00E+00//AT1G28110| SCPL45 (SERINE CARBOXYPEPTIDASE-LIKE 45 PRECURSOR); serine-type carboxypeptidase	Unigene26860_All//0.00E+00//DW225354				nr -
Unigene26861_All	1541	31.13	40.64	21.91	21.82	21.74	18.02	37.37	48.58	134.43	3.84E-01	5.93E-09		-5.07E-01	9.91E-11		-5.10E-03	9.61E-01		-2.76E-01	3.15E-03		3.78E-01	1.85E-12		1.85E+00	0.00E+00	Up	Unigene26861_All//gi|297832316|ref|XP_002884040.1|//5.00E-89//peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329880|gb|EFH60299.1| peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene26861_All//5.00E-77//AT2G17120| LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR)	Unigene26861_All//0.00E+00//TC132352		ko04626|Plant-pathogen interaction		nr -
Unigene26862_All	779	1.21	0.07	0.75	2.94	2.39	3.94	2.44	3.33	7.06	-4.22E+00	1.36E-04	Down	-6.85E-01	3.69E-01		-3.01E-01	5.15E-01		4.23E-01	2.71E-01		4.46E-01	2.25E-01		1.53E+00	2.08E-10	Up	Unigene26862_All//gi|224129878|ref|XP_002320693.1|//1.00E-08//predicted protein [Populus trichocarpa] >gi|222861466|gb|EEE99008.1| predicted protein [Populus trichocarpa]		Unigene26862_All//2.00E-128//gi|73858992|gb|DT461731.1|DT461731				nr +
Unigene26863_All	602	0.35	0.34	0.53	2.23	1.94	1.88	0.84	1.18	3.51	-4.60E-02	9.88E-01		6.11E-01	6.25E-01		-2.00E-01	7.50E-01		-2.52E-01	6.86E-01		4.86E-01	5.42E-01		2.06E+00	2.53E-06	Up			Unigene26863_All//3.00E-89//DT461731				
Unigene26866_All	1003	43.45	35.46	35.41	24.34	27.95	23.96	3.20	1.50	0.91	-2.93E-01	3.07E-04		-2.95E-01	4.61E-04		2.00E-01	6.21E-02		-2.28E-02	8.75E-01		-1.09E+00	4.62E-04	Down	-1.81E+00	5.15E-08	Down	Unigene26866_All//gi|15221033|ref|NP_173261.1|//1.00E-110//ATLP-1 [Arabidopsis thaliana] >gi|27735265|sp|P50699.2|TLPH_ARATH RecName: Full=Thaumatin-like protein; Flags: Precursor	Unigene26866_All//6.00E-108//AT1G18250| ATLP-1	Unigene26866_All//0.00E+00//TC132842				nr -
Unigene26870_All	1334	13.57	7.18	17.96	24.83	26.15	13.37	16.20	5.17	13.62	-9.19E-01	5.47E-12		4.05E-01	4.82E-04		7.45E-02	5.28E-01		-8.93E-01	7.97E-22		-1.65E+00	8.01E-42	Down	-2.50E-01	1.80E-02		Unigene26870_All//gi|224078846|ref|XP_002305651.1|//0.00E+00//f-box family protein [Populus trichocarpa] >gi|222848615|gb|EEE86162.1| f-box family protein [Populus trichocarpa]	Unigene26870_All//9.00E-137//AT3G62980| TIR1 (TRANSPORT INHIBITOR RESPONSE 1); auxin binding / protein binding / ubiquitin-protein ligase	Unigene26870_All//0.00E+00//TC171308		ko04626|Plant-pathogen interaction		nr -
Unigene26871_All	612	1.71	0.00	0.52	0.41	0.84	0.59	1.04	0.55	0.98	-1.07E+01	3.80E-06	Down	-1.71E+00	2.35E-02		1.05E+00	3.49E-01		5.37E-01	6.94E-01		-9.24E-01	2.63E-01		-8.59E-02	9.19E-01		Unigene26871_All//gi|15217226|gb|AAB92570.1|AC074354_4//2.00E-17//Hypothetical protein [Oryza sativa Japonica Group]	Unigene26871_All//9.00E-15//AT5G61190| zinc finger protein-related					nr +
Unigene26872_All	1499	3.00	0.47	1.07	3.52	3.24	3.50	2.88	0.95	1.54	-2.67E+00	1.44E-13	Down	-1.49E+00	1.92E-06	Down	-1.21E-01	6.86E-01		-1.13E-02	9.60E-01		-1.60E+00	1.22E-08	Down	-9.00E-01	3.83E-04		Unigene26872_All//gi|30697493|ref|NP_200927.2|//1.00E-20//zinc finger protein-related [Arabidopsis thaliana]	Unigene26872_All//2.00E-22//AT5G61190| zinc finger protein-related		C2H2			nr -
Unigene26873_All	1557	2.08	2.90	0.86	6.69	6.50	7.05	5.30	11.92	13.56	4.75E-01	9.94E-02		-1.28E+00	5.13E-04	Down	-4.04E-02	8.35E-01		7.60E-02	6.97E-01		1.17E+00	9.70E-22	Up	1.36E+00	1.66E-31	Up	Unigene26873_All//gi|224111734|ref|XP_002319958.1|//1.00E-125//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222864988|gb|EEF02129.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene26873_All//2.00E-104//AT1G25560| TEM1 (TEMPRANILLO 1); transcription factor	Unigene26873_All//0.00E+00//gi|78348903|gb|DT569177.1|DT569177		AP2-EREBP		nr -
Unigene26875_All	712	1.25	4.91	2.54	3.22	3.87	4.00	1.90	4.58	2.63	1.97E+00	1.28E-07	Up	1.03E+00	4.43E-02		2.66E-01	5.61E-01		3.12E-01	4.59E-01		1.27E+00	5.74E-05	Up	4.69E-01	2.63E-01				Unigene26875_All//3.00E-151//TC133866				
Unigene26877_All	771	6.45	1.31	0.69	1.49	1.47	1.35	1.65	1.30	1.86	-2.29E+00	1.15E-12	Down	-3.22E+00	4.08E-17	Down	-1.18E-02	9.64E-01		-1.41E-01	8.21E-01		-3.39E-01	5.58E-01		1.77E-01	7.13E-01		Unigene26877_All//gi|5091545|gb|AAD39574.1|AC007067_14//5.00E-56//T10024.14 [Arabidopsis thaliana] >gi|149944329|gb|ABR46207.1| At1g10522 [Arabidopsis thaliana]	Unigene26877_All//4.00E-56//AT1G10522| unknown protein	Unigene26877_All//0.00E+00//TC137072				nr -
Unigene26878_All	501	20.78	5.26	6.91	14.32	6.67	8.74	1.18	1.17	0.80	-1.98E+00	1.48E-21	Down	-1.59E+00	2.39E-15	Down	-1.10E+00	6.35E-08	Down	-7.11E-01	8.96E-04		-1.67E-02	1.02E+00		-5.71E-01	4.78E-01		Unigene26878_All//gi|5091545|gb|AAD39574.1|AC007067_14//3.00E-21//T10024.14 [Arabidopsis thaliana] >gi|149944329|gb|ABR46207.1| At1g10522 [Arabidopsis thaliana]	Unigene26878_All//3.00E-20//AT1G10522| unknown protein	Unigene26878_All//4.00E-122//TC137072				nr +
Unigene26879_All	1103	7.87	2.21	2.94	14.72	14.42	9.34	5.06	4.24	6.68	-1.84E+00	2.11E-16	Down	-1.42E+00	5.17E-11	Down	-2.97E-02	8.52E-01		-6.57E-01	9.74E-07		-2.54E-01	3.07E-01		4.01E-01	3.40E-02		Unigene26879_All//gi|224145434|ref|XP_002325641.1|//9.00E-82//predicted protein [Populus trichocarpa] >gi|222862516|gb|EEF00023.1| predicted protein [Populus trichocarpa]	Unigene26879_All//3.00E-06//AT2G23460| XLG1 (EXTRA-LARGE G-PROTEIN 1); guanyl nucleotide binding / signal transducer	Unigene26879_All//0.00E+00//gi|78335785|gb|DT556059.1|DT556059				nr +
Unigene2688_All	808	1.23	1.38	2.64	6.78	5.07	2.01	7.64	3.78	1.38	1.65E-01	7.79E-01		1.10E+00	1.82E-02		-4.19E-01	9.89E-02		-1.75E+00	1.21E-10	Down	-1.02E+00	2.34E-06	Down	-2.47E+00	2.61E-21	Down	Unigene2688_All//gi|15238519|ref|NP_200786.1|//4.00E-37//MYB59 (MYB DOMAIN PROTEIN 59); DNA binding / transcription factor [Arabidopsis thaliana] >gi|97179947|sp|Q4JLS4.2|MYB59_ARATH RecName: Full=Transcription factor MYB59; AltName: Full=Myb-related protein 59; Short=AtMYB59 >gi|9758843|dbj|BAB09515.1| Myb-related transcription factor-like protein [Arabidopsis thaliana] >gi|41619478|gb|AAS10111.1| MYB transcription factor [Arabidopsis thaliana]	Unigene2688_All//8.00E-38//AT5G59780| MYB59 (MYB DOMAIN PROTEIN 59); DNA binding / transcription factor	Unigene2688_All//3.00E-90//gi|78348549|gb|DT568823.1|DT568823		MYB		nr -
Unigene26880_All	1732	26.73	7.31	13.87	17.14	8.85	7.07	10.03	6.35	7.29	-1.87E+00	1.15E-86	Down	-9.47E-01	7.89E-30		-9.54E-01	1.09E-24		-1.28E+00	8.17E-35	Down	-6.61E-01	2.73E-08		-4.61E-01	6.83E-05		Unigene26880_All//gi|77416925|gb|AB481858.1|//1.00E-120//brittle 1 protein-like [Solanum tuberosum]	Unigene26880_All//1.00E-99//AT4G32400| SHS1 (SODIUM HYPERSENSITIVE 1); binding / nucleotide transmembrane transporter/ transporter	Unigene26880_All//0.00E+00//TC176370				nr -

Unigene26881_All	1719	1.80	7.81	2.39	3.39	4.51	5.83	0.20	0.27	0.76	2.12E+00	7.54E-30	Up	4.10E-01	2.08E-01		4.11E-01	5.08E-02		7.83E-01	1.06E-05		4.43E-01	6.31E-01		1.96E+00	5.04E-04	Up	Unigene26881_All//gi|297811489|ref|XP_002873628.1|//1.00E-58//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319465|gb|EFH49887.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26881_All//5.00E-57//AT5G13800| hydrolase, alpha/beta fold family protein	Unigene26881_All//0.00E+00//TC177999				nr -
Unigene26883_All	1055	10.12	3.17	8.33	17.47	12.83	13.31	9.26	4.91	4.30	-1.67E+00	1.15E-17	Down	-2.81E-01	1.42E-01		-4.46E-01	2.06E-04		-3.92E-01	2.18E-03		-9.14E-01	3.58E-08		-1.10E+00	3.15E-11	Down	Unigene26883_All//gi|87241311|gb|AB033169.1|//1.00E-36//C2 [Medicago truncatula]	Unigene26883_All//4.00E-24//AT3G16510| C2 domain-containing protein	Unigene26883_All//0.00E+00//gi|78329156|gb|DT549430.1|DT549430		ko03040|Spliceosome		nr +
Unigene26884_All	1043	21.02	14.53	13.17	13.66	18.55	6.76	0.28	0.08	0.38	-5.33E-01	4.94E-06		-6.74E-01	2.47E-08		4.42E-01	1.94E-04		-1.02E+00	6.40E-12	Down	-1.83E+00	2.11E-01		4.29E-01	6.61E-01		Unigene26884_All//9.00E-17//TC166882					
Unigene26885_All	1218	1.33	0.87	0.96	2.17	1.61	1.00	1.39	1.82	3.53	-6.08E-01	2.34E-01		-4.69E-01	3.87E-01		-4.28E-01	2.88E-01		-1.11E+00	4.11E-03		3.89E-01	3.46E-01		1.35E+00	4.90E-07	Up	Unigene26885_All//gi|6850900|emb|CAB71063.1|//2.00E-24//copia-type polyprotein [Arabidopsis thaliana]					nr -
Unigene26886_All	1723	0.12	0.18	0.19	12.17	6.08	12.06	4.93	3.35	1.64	5.38E-01	6.71E-01		6.10E-01	6.25E-01		-1.00E+00	4.89E-19	Down	-1.36E-02	9.39E-01		-5.59E-01	1.56E-03		-1.59E+00	1.33E-16	Down	Unigene26886_All//gi|7547009|gb|AAF63756.1|AF243475,1//0.00E-00//pectate lyase [Vitis vinifera]	Unigene26886_All//0.00E+00//AT5G63180| pectate lyase family protein	Unigene26886_All//0.00E+00//DW509693		ko00040|Pentose and glucuronate interconversions		nr -
Unigene26887_All	649	4.43	11.95	1.39	14.43	38.41	28.74	16.61	37.87	32.17	1.43E+00	1.91E-10	Up	-1.67E+00	5.32E-05	Down	1.41E+00	1.07E-36	Up	9.94E-01	1.01E-14		1.19E+00	3.21E-29	Up	9.53E-01	4.18E-18		Unigene26887_All//gi|187609561|gb|ACD13288.1|//2.00E-52//cold shock domain protein 1 [Oryza sativa Japonica Group]	Unigene26887_All//7.00E-25//AT2G17870| cold-shock DNA-binding family protein	Unigene26887_All//0.00E+00//gi|109884188|gb|DW513158.1|DW513158	CSD			nr +
Unigene26888_All	1047	4.90	82.27	5.65	10.09	27.73	19.20	27.66	43.67	109.89	4.07E+00	0.00E+00	Up	2.05E-01	4.41E-01		1.46E+00	9.02E-45	Up	9.28E-01	3.48E-14		6.59E-01	2.40E-20		1.99E+00	9.30E-290	Up	Unigene26888_All//gi|145049690|gb|ABP35526.1|//1.00E-118//CCR4-associated factor [Ipomoea batatas]	Unigene26888_All//2.00E-115//AT3G44260| CCR4-NOT transcription complex protein, putative	Unigene26888_All//0.00E+00//TC146581		ko03018|RNA degradation		nr -
Unigene26889_All	1327	2.60	14.97	4.82	1.16	1.01	2.14	0.00	0.00	0.00	2.52E+00	5.32E-54	Up	8.88E-01	2.63E-04		-2.02E-01	7.27E-01		8.82E-01	1.87E-02		null	null		null	null		Unigene26889_All//gi|18252325|gb|AL66194.1|AF386512_1//1.00E-128//cytochrome P450 [Pyrus communis]	Unigene26889_All//2.00E-71//AT3G48270| CYP71A26; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene26889_All//0.00E+00//TC167772		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene2689_All	706	6.52	3.44	6.86	28.79	22.29	13.82	16.53	10.00	3.22	-9.21E-01	1.12E-03		7.38E-02	7.96E-01		-3.69E-01	1.42E-03		-1.06E+00	6.79E-18	Down	-7.24E-01	1.03E-06		-2.36E+00	1.30E-37	Down	Unigene2689_All//gi|15231343|ref|NP_190199.1|//1.00E-64//MYB111 (MYB DOMAIN PROTEIN 111); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75335604|sp|Q9LX82.1|MYB48_ARATH RecName: Full=Transcription factor MYB48; AltName: Full=Myb-related protein 48; Short=AtMYB48 >gi|7799001|emb|CAB60940.1| Myb DNA binding protein-like [Arabidopsis thaliana] >gi|41619274|gb|AAS10064.1| MYB transcription factor [Arabidopsis thaliana]	Unigene2689_All//1.00E-57//AT5G59780| MYB59 (MYB DOMAIN PROTEIN 59); DNA binding / transcription factor	Unigene2689_All//6.00E-122//gi|78348549|gb|DT568823.1|DT568823	MYB			nr +
Unigene26890_All	966	7.10	1.05	2.76	13.20	11.09	11.45	2.58	2.64	1.65	-2.76E+00	4.37E-21	Down	-1.36E+00	2.36E-08	Down	-2.52E-01	1.26E-01		-2.05E-01	2.43E-01		3.15E-02	9.56E-01		-6.47E-01	6.07E-02		Unigene26890_All//gi|18402827|ref|NP_564557.1|//5.00E-68//Erv1/Alr family protein [Arabidopsis thaliana] >gi|28372928|gb|AAO39946.1| Atlg49880 [Arabidopsis thaliana] >gi|45571904|emb|CAD83013.1| mitochondrial sulfhydryl oxidase Erv1p [Arabidopsis thaliana]	Unigene26890_All//2.00E-69//AT1G49880| Erv1/Alr family protein	Unigene26890_All//0.00E+00//TC175765				nr -
Unigene26892_All	1332	6.76	35.23	52.65	2.69	7.96	16.04	0.35	0.13	0.66	2.38E+00	1.26E-118	Up	2.96E+00	9.09E-221	Up	1.56E+00	3.10E-18	Up	2.57E+00	1.83E-63	Up	-1.48E+00	1.53E-01		9.14E-01	1.59E-01		Unigene26892_All//gi|297829526|ref|XP_002882645.1|//6.00E-86//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328485|gb|EFH58904.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26892_All//6.00E-85//AT3G09930| GDSL-motif lipase/hydrolase family protein	Unigene26892_All//0.00E+00//TC173850				nr +
Unigene269_All	1505	0.94	1.08	1.95	10.26	11.74	9.57	5.25	2.11	3.41	1.99E-01	6.82E-01		1.05E+00	6.29E-03		1.94E-01	1.77E-01		-1.00E-01	5.75E-01		-1.32E+00	1.56E-11	Down	-6.22E-01	5.01E-04		Unigene269_All//gi|42565945|ref|NP_567014.2|//1.00E-134//RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	Unigene269_All//6.00E-121//AT3G55020| RabGAP/TBC domain-containing protein	Unigene269_All//0.00E+00//CK640461				nr -
Unigene2690_All	1259	2.58	2.13	6.89	15.47	9.60	5.35	13.84	8.76	2.72	-2.73E-01	4.37E-01		1.42E+00	4.74E-11	Up	-6.88E-01	1.75E-09		-1.53E+00	3.52E-30	Down	-6.59E-01	2.86E-08		-2.35E+00	2.54E-55	Down	Unigene2690_All//gi|225435070|ref|XP_002284400.1|//1.00E-89//PREDICTED: similar to MYB transcription factor MYB139 [Vitis vinifera]	Unigene2690_All//1.00E-72//AT5G59780| MYB59 (MYB DOMAIN PROTEIN 59); DNA binding / transcription factor	Unigene2690_All//0.00E+00//gi|78348549|gb|DT568823.1|DT568823	MYB			nr +
Unigene26900_All	1946	0.40	0.21	1.12	26.08	23.89	24.42	8.21	2.45	1.49	-9.53E-01	2.33E-01		1.48E+00	1.81E-03		-1.27E-01	1.14E-01		-9.54E-02	2.82E-01		-1.75E+00	9.80E-34	Down	-2.46E+00	1.11E-53	Down	Unigene26900_All//gi|1621467|gb|AAB17194.1|//0.00E-00//laccase [Liriodendron tulipifera]	Unigene26900_All//0.00E+00//AT5G60020| LAC17 (laccase 17); laccase	Unigene26900_All//0.00E+00//TC152487		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene26903_All	928	9.87	35.65	13.83	22.60	20.33	18.25	450.00	97.82	493.35	1.85E+00	5.85E-61	Up	4.87E-01	2.99E-03		-1.52E-01	2.58E-01		-3.08E-01	1.14E-02		-2.20E+00	0.00E+00	Down	1.33E-01	1.15E-10		Unigene26903_All//gi|18396047|ref|NP_566159.1|//3.00E-97//SRG3 (senescence-related gene 3); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase [Arabidopsis thaliana]	Unigene26903_All//3.00E-85//AT3G02040| SRG3 (senescence-related gene 3); glycerophosphodiester phosphodiesterase/ phosphoric diester hydrolase	Unigene26903_All//0.00E+00//TC141623				nr +
Unigene26905_All	688	19.62	120.05	56.97	45.69	61.01	91.18	85.79	156.01	91.90	2.61E+00	5.38E-232	Up	1.54E+00	5.41E-54	Up	4.17E-01	4.10E-08		9.97E-01	1.73E-48		8.63E-01	4.97E-74		9.92E-02	1.20E-01		Unigene26905_All//gi|145567026|gb|ABP81863.1|//3.00E-31//LATE BLOOMER 1 [Pisum sativum]	Unigene26905_All//1.00E-29//AT1G22770| GI (GIGANTEA)	Unigene26905_All//0.00E+00//gi|109888167|gb|DW517136.1|DW517136		ko04712|Circadian rhythm - plant		nr -
Unigene26906_All	999	15.35	16.84	25.75	159.32	151.01	120.75	9.18	2.80	6.38	1.34E-01	3.71E-01		7.47E-01	1.95E-11		-7.72E-02	8.13E-02		-4.00E-01	8.27E-25		-1.71E+00	3.53E-19	Down	-5.25E-01	1.39E-03		Unigene26906_All//gi|196122014|gb|ACG69481.1|//2.00E-79//germin-like protein 5 [Glycine max]	Unigene26906_All//7.00E-66//AT1G10460| GLP7 (GERMIN-LIKE PROTEIN 7); manganese ion binding / nutrient reservoir	Unigene26906_All//0.00E+00//TC152308				nr +
Unigene26907_All	1097	5.72	2.36	2.09	3.72	3.17	1.69	0.93	0.11	0.40	-1.28E+00	1.94E-07	Down	-1.46E+00	2.00E-08	Down	-2.32E-01	4.92E-01		-1.14E+00	1.44E-04	Down	-3.02E+00	1.08E-04	Down	-1.21E+00	4.17E-02		Unigene26907_All//gi|15233990|ref|NP_192705.1|//1.00E-125//oxidoreductase family protein [Arabidopsis thaliana] >gi|73921136|sp|Q9SZ83.1|Y4967_ARATH RecName: Full=Uncharacterized oxidoreductase At4g09670 >gi|4538897|emb|CAB39634.1| AX110P-like protein [Arabidopsis thaliana] >gi|7267662|emb|CAB78090.1| AX110P-like protein [Arabidopsis thaliana] >gi|21554042|gb|AAM63123.1| AX110P-like protein [Arabidopsis thaliana]	Unigene26907_All//2.00E-119//AT4G09670| oxidoreductase family protein	Unigene26907_All//0.00E+00//gi|78352743|gb|DT573017.1|DT573017				nr +
Unigene26908_All	690	2.58	9.25	2.55	4.84	4.39	2.95	27.21	24.84	16.80	1.84E+00	3.19E-12	Up	-1.77E-02	9.95E-01		-1.39E-01	7.21E-01		-7.16E-01	3.51E-02		-1.32E-01	3.23E-01		-6.95E-01	5.74E-10		Unigene26908_All//gi|224120972|ref|XP_002318465.1|//7.00E-50//SAUR family protein [Populus trichocarpa] >gi|22859138|gb|EEE96685.1| SAUR family protein [Populus trichocarpa]	Unigene26908_All//1.00E-29//AT2G46690| auxin-responsive family protein	Unigene26908_All//0.00E+00//TC156585				nr +
Unigene26912_All	1379	32.93	5.14	20.39	17.52	7.32	4.72	2.58	1.00	0.90	-2.68E+00	2.11E-132	Down	-6.92E-01	2.67E-17		-1.26E+00	1.35E-31	Down	-1.89E+00	3.48E-50	Down	-1.36E+00	6.91E-06	Down	-1.52E+00	4.66E-07	Down	Unigene26912_All//gi|297804354|ref|XP_002870061.1|//1.00E-122//ATPUP10 [Arabidopsis lyrata subsp. lyrata] >gi|297315897|gb|EFH46320.1| ATPUP10 [Arabidopsis lyrata subsp. lyrata]	Unigene26912_All//6.00E-98//AT4G18210| ATPUP10; purine transmembrane transporter	Unigene26912_All//0.00E+00//TC147519				nr -
Unigene26913_All	961	78.40	45.87	31.42	476.27	386.38	378.08	325.00	116.65	199.03	-7.73E-01	1.45E-35		-1.32E+00	5.42E-82	Down	-3.02E-01	9.09E-47		-3.33E-01	4.39E-50		-1.48E+00	0.00E+00	Down	-7.08E-01	2.49E-156		Unigene26913_All//gi|211906444|gb|ACJ11715.1|//1.00E-124//fructokinase [Gossypium hirsutum]	Unigene26913_All//8.00E-104//AT3G59480| pfkB-type carbohydrate kinase family protein	Unigene26913_All//0.00E+00//TC137418		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr +
Unigene26914_All	314	1.00	0.81	1.70	0.00	0.77	0.72	1.75	0.13	0.00	-3.09E-01	7.89E-01		7.62E-01	4.53E-01		9.58E+00	1.04E-01		9.49E+00	1.19E-01		-3.72E+00	3.23E-03		-1.08E+01	2.80E-04	Down	Unigene26914_All//gi|297604477|ref|NP_001055487.2|//1.00E-06//Os05g0401200 [Oryza sativa Japonica Group] >gi|255676350|dbj|BAF17401.2| Os05g0401200 [Oryza sativa Japonica Group]		Unigene26914_All//4.00E-121//TC173609				nr -
Unigene26916_All	943	7.60	3.01	6.27	9.51	6.61	7.85	7.80	3.59	5.03	-1.34E+00	6.69E-09	Down	-2.78E-01	2.42E-01		-5.25E-01	3.90E-03		-2.76E-01	1.91E-01		-1.12E+00	1.50E-08	Down	-6.34E-01	6.48E-04		Unigene26916_All//gi|297822433|ref|XP_002879099.1|//1.00E-88//sand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324938|gb|EFH55358.1| sand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26916_All//1.00E-87//AT2G28390| SAND family protein	Unigene26916_All//0.00E+00//gi|78350936|gb|DT571210.1|DT571210				nr -
Unigene26917_All	1320	3.61	0.54	2.06	10.38	11.79	15.53	12.04	9.09	9.08	-2.75E+00	8.97E-15	Down	-8.10E-01	4.87E-03		1.84E-01	2.43E-01		5.82E-01	8.80E-07		-4.06E-01	1.19E-03		-4.07E-01	8.37E-04		Unigene26917_All//gi|124359713|gb|ABD32380.2|//2.00E-72//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene26917_All//5.00E-69//AT1G22490| basic helix-loop-helix (bHLH) family protein	Unigene26917_All//0.00E+00//TC157801	bHLH			nr -
Unigene26918_All	1247	36.88	158.27	96.29	15.62	76.60	93.51	4.24	23.39	37.44	2.10E+00	0.00E+00	Up	1.38E+00	6.40E-141	Up	2.29E+00	3.45E-270	Up	2.58E+00	0.00E+00	Up	2.46E+00	1.98E-94	Up	3.14E+00	8.41E-199	Up	Unigene26918_All//gi|115311433|gb|AB193897.1|//9.00E-18//At1g65690 [Arabidopsis thaliana] >gi|222422971|dbj|BAH19470.1| AT4G01670 [Arabidopsis thaliana]	Unigene26918_All//5.00E-07//AT2G46940| unknown protein	Unigene26918_All//0.00E+00//gi|78350061|gb|DT570335.1|DT570335				nr +
Unigene26921_All	1278	0.94	1.67	0.58	1.83	0.84	2.40	1.89	2.78	4.99	8.23E-01	6.26E-02		-6.91E-01	2.86E-01		-1.13E+00	3.99E-03		3.92E-01	3.12E-01		5.60E-01	5.76E-02		1.40E+00	1.36E-10	Up	Unigene26921_All//gi|292630758|sp|C4B8C4.1|EPFL3_ARATH//1.00E-11//RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 3; Short=EPF-like protein 3; Flags: Precursor >gi|237512859|dbj|BAH58782.1| EPFL3 [Arabidopsis thaliana]	Unigene26921_All//9.00E-11//AT2G30370| allergen-related					nr +
Unigene26924_All	1838	2.51	0.77	0.75	2.30	2.66	2.21	8.12	15.85	16.26	-1.70E+00	3.45E-08	Down	-1.73E+00	5.61E-08	Down	2.08E-01	5.24E-01		-5.89E-02	8.60E-01		9.65E-01	8.50E-25		1.00E+00	1.26E-27	Up	Unigene26924_All//gi|38016017|gb|AA007515.1|//1.00E-105//At1g33340 [Arabidopsis thaliana]	Unigene26924_All//2.00E-102//AT1G33340| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related					nr +
Unigene26925_All	1225	1.20	5.79	3.43	2.11	1.57	4.98	6.90	5.73	3.64	2.28E+00	1.74E-17	Up	1.52E+00	3.11E-06	Up	-4.26E-01	2.98E-01		1.23E+00	3.86E-07	Up	-2.68E-01	1.57E-01		-9.22E-01	1.54E-07		Unigene26925_All//gi|82697963|gb|AB089016.1|//1.00E-139//CXE carboxylesterase [Actinidia deliciosa]	Unigene26925_All//1.00E-83//AT5G06570| hydrolase	Unigene26925_All//0.00E+00//gi|164282348|gb|ES809570.1|ES809570				nr +

Unigene26927_All	1163	1.21	13.11	6.55	4.03	1.92	1.83	8.62	34.86	3.77	3.43E+00	1.32E-56	Up	2.43E+00	1.49E-19	Up	-1.06E+00	4.18E-05	Down	-1.14E+00	3.91E-05	Down	2.02E+00	2.88E-102	Up	-1.19E+00	6.87E-13	Down	Unigene26927_All//gi|224062643|ref|XP_002300866.1|//8.00E-79//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842592|gb|EEE80139.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene26927_All//3.00E-71//AT2G43000| anac042 (Arabidopsis NAC domain containing protein 42); transcription factor	Unigene26927_All//9.00E-159//DW224083	NAC			nr +
Unigene26928_All	673	7.07	3.46	7.20	21.76	14.74	7.18	3.27	1.30	1.24	-1.03E+00	2.24E-04	Down	2.54E-02	9.45E-01		-5.62E-01	3.11E-05		-1.60E+00	3.02E-24	Down	-1.32E+00	8.35E-04	Down	-1.39E+00	3.22E-04	Down	Unigene26928_All//gi|53370641|gb|AU89136.1|//1.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene26928_All//6.00E-07//AT4G09490| RNase H domain-containing protein	Unigene26928_All//2.00E-56//ES8188849				nr +
Unigene2693_All	1465	21.18	14.11	16.97	15.00	13.28	9.80	5.45	1.83	2.67	-5.86E-01	1.48E-09		-3.19E-01	1.70E-03		-1.75E-01	1.67E-01		-6.13E-01	6.37E-08		-1.58E+00	4.74E-15	Down	-1.03E+00	1.77E-08	Down	Unigene2693_All//gi|224132502|ref|XP_002328301.1|//1.00E-59//GATA zinc finger protein regulating nitrogen assimilation [Populus trichocarpa] >gi|222837816|gb|EEE76181.1| GATA zinc finger protein regulating nitrogen assimilation [Populus trichocarpa]	Unigene2693_All//3.00E-47//AT1G08010| zinc finger (GATA type) family protein	Unigene2693_All//0.00E+00//TC161188	C2C2-GATA			nr -
Unigene26933_All	1646	9.54	7.88	12.36	13.68	12.22	11.22	8.40	3.81	5.47	-2.75E-01	5.98E-02		3.74E-01	3.48E-03		-1.63E-01	1.98E-01		-2.86E-01	1.56E-02		-1.14E+00	8.38E-16	Down	-6.19E-01	2.48E-06		Unigene26933_All//gi|224086998|ref|XP_002308026.1|//1.00E-128//predicted protein [Populus trichocarpa] >gi|222851002|gb|EEE91549.1| predicted protein [Populus trichocarpa]	Unigene26933_All//7.00E-89//AT3G57400| unknown protein					nr +
Unigene26934_All	1703	0.06	0.48	0.31	4.42	5.32	5.09	13.16	31.61	18.41	2.95E+00	3.29E-03		2.35E+00	5.87E-02		2.68E-01	1.94E-01		2.05E-01	3.71E-01		1.26E+00	1.99E-69	Up	4.85E-01	8.83E-09		Unigene26934_All//gi|224055771|ref|XP_002298645.1|//0.00E+00//hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase-like protein [Populus trichocarpa] >gi|222845903|gb|EEE83450.1| hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase-like protein [Populus trichocarpa]	Unigene26934_All//0.00E+00//AT5G41040| transferase family protein	Unigene26934_All//0.00E+00//TC133098		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene26937_All	1123	1.35	4.24	0.47	3.50	4.05	5.63	18.26	31.30	29.55	1.65E+00	4.33E-08	Up	-1.51E+00	1.05E-02		2.08E-01	5.45E-01		6.84E-01	3.31E-03		7.78E-01	7.06E-21		6.95E-01	8.32E-17		Unigene26937_All//gi|224127334|ref|XP_002320048.1|//4.00E-66//SAUR family protein [Populus trichocarpa] >gi|222860821|gb|EEE98363.1| SAUR family protein [Populus trichocarpa]	Unigene26937_All//1.00E-46//AT3G60690| auxin-responsive family protein	Unigene26937_All//8.00E-76//DW226405				nr -
Unigene26938_All	814	1.80	4.79	1.64	2.20	2.33	3.66	6.75	11.04	9.35	1.41E+00	1.46E-05	Up	-1.38E-01	7.97E-01		7.88E-02	8.89E-01		7.33E-01	4.57E-02		7.09E-01	3.44E-05		4.69E-01	1.08E-02		Unigene26938_All//gi|226494281|ref|NP_001151795.1|//2.00E-49//cysteine-type peptidase [Zea mays] >gi|195649729|gb|ACG44337.1| cysteine-type peptidase [Zea mays]	Unigene26938_All//3.00E-35//AT2G27350| OTU-like cysteine protease family protein	Unigene26938_All//3.00E-102//gi|73848919|gb|DT457939.1|DT457939				nr +
Unigene26939_All	955	17.59	11.73	23.14	5.37	6.27	8.42	2.08	3.19	6.72	-5.85E-01	1.52E-05		3.96E-01	1.13E-03		2.24E-01	4.19E-01		6.48E-01	1.37E-03		6.19E-01	5.41E-02		1.69E+00	1.05E-13	Up	Unigene26939_All//gi|226498094|ref|NP_001148441.1|//2.00E-59//cyclase/dehydrase [Zea mays] >gi|195619296|gb|ACG31478.1| cyclase/dehydrase [Zea mays]	Unigene26939_All//1.00E-61//AT1G02475| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Streptomyces cyclase/dehydrase (InterPro:IPR005031); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01883.1); Has 350 Blast hits to 350 proteins in 105 species: Archae - 0; Bacteria - 211; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 110 (source: NCBI BLink).	Unigene26939_All//0.00E+00//CO122228				nr -
Unigene2694_All	1323	1.86	1.46	2.46	1.54	1.85	1.09	0.67	0.28	0.09	-3.53E-01	3.76E-01		4.02E-01	2.75E-01		2.60E-01	5.83E-01		-4.99E-01	2.99E-01		-1.24E+00	6.79E-02		-2.89E+00	3.04E-04	Down	Unigene2694_All//gi|297849094|ref|XP_002892428.1|//2.00E-45//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338270|gb|EFH68687.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2694_All//1.00E-41//AT1G08010| zinc finger (GATA type) family protein	Unigene2694_All//0.00E+00//TC161188	C2C2-GATA			nr +
Unigene26940_All	1100	7.71	1.66	6.24	14.36	10.74	3.16	13.18	7.14	15.21	-2.22E+00	2.81E-20	Down	-3.03E-01	1.59E-01		-4.19E-01	1.57E-03		-2.18E+00	1.27E-39	Down	-8.84E-01	3.83E-11		2.06E-01	1.01E-01		Unigene26940_All//gi|297802268|ref|XP_002869018.1|//1.00E-107//GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314854|gb|EFH45277.1| GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene26940_All//1.00E-102//AT4G36830| GNS1/SUR4 membrane family protein	Unigene26940_All//5.00E-37//TC171527				nr +
Unigene26941_All	928	1.30	4.20	1.21	7.73	8.57	8.86	24.56	41.26	25.03	1.70E+00	5.30E-07	Up	-1.06E-01	8.62E-01		1.49E-01	5.40E-01		1.97E-01	3.98E-01		7.48E-01	2.86E-21		2.74E-02	8.11E-01		Unigene26941_All//gi|124361158|gb|ABN09130.1|//3.00E-43//DC1; C1-like [Medicago truncatula]	Unigene26941_All//2.00E-102//AT2G16050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: DC1 (InterPro:IPR004146); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G20990.1); Has 719 Blast hits to 448 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 717; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).						nr +
Unigene26942_All	949	2.10	1.17	2.13	4.20	3.63	2.05	2.63	1.23	1.09	-8.35E-01	6.77E-02		2.54E-02	9.75E-01		-2.11E-01	5.54E-01		-1.04E+00	6.23E-04	Down	-1.09E+00	2.53E-03		-1.27E+00	3.68E-04	Down	Unigene26942_All//gi|15224422|ref|NP_181336.1|//5.00E-97//chaperone protein dnaJ-related [Arabidopsis thaliana]	Unigene26942_All//3.00E-93//AT2G38000| chaperone protein dnaJ-related	Unigene26942_All//0.00E+00//gi|78324458|gb|DT544732.1|DT544732				nr -
Unigene26945_All	1047	18.74	9.92	11.09	7.14	7.40	5.00	3.84	13.21	24.69	-9.18E-01	6.65E-13		-7.57E-01	4.52E-09		5.23E-02	8.27E-01		-5.12E-01	1.65E-02		1.78E+00	4.17E-30	Up	2.69E+00	5.45E-94	Up	Unigene26945_All//gi|124359981|gb|ABN07997.1|//7.00E-06//contains similarity to reverse transcriptase, related [Medicago truncatula]		Unigene26945_All//0.00E+00//DR453735				nr +
Unigene26946_All	866	8.88	156.22	41.94	2.53	3.26	2.50	0.34	3.52	1.43	4.14E+00	0.00E+00	Up	2.24E+00	2.68E-83	Up	3.65E-01	3.73E-01		-1.59E-02	9.62E-01		3.37E+00	4.00E-14	Up	2.06E+00	5.00E-04	Up	Unigene26946_All//gi|297599774|ref|NP_001047798.2|//2.00E-75//Os02g0692700 [Oryza sativa Japonica Group] >gi|255671178|dbj|BAF09712.2| Os02g0692700 [Oryza sativa Japonica Group]	Unigene26946_All//1.00E-65//AT4G17900| zinc-binding family protein	Unigene26946_All//4.00E-151//TC158446	PLATZ			nr -
Unigene26947_All	1169	3.67	8.24	6.83	44.53	34.88	22.33	4.09	12.76	7.12	1.17E+00	1.52E-09	Up	8.97E-01	2.88E-05		-3.53E-01	1.55E-07		-9.96E-01	1.06E-40		1.64E+00	6.04E-29	Up	8.01E-01	5.20E-06		Unigene26947_All//gi|79456826|ref|NP_191763.3|//1.00E-100//catalytic/ hydrolase [Arabidopsis thaliana] >gi|38603864|gb|AAR24677.1| At3g62040 [Arabidopsis thaliana]	Unigene26947_All//3.00E-101//AT3G62040| catalytic/ hydrolase	Unigene26947_All//0.00E+00//TC146500				nr +
Unigene26948_All	761	25.30	76.10	67.45	24.61	21.77	16.62	10.11	13.40	7.96	1.59E+00	1.13E-85	Up	1.41E+00	2.12E-62	Up	-1.77E-01	2.04E-01		-5.67E-01	4.82E-06		4.06E-01	1.22E-02		-3.46E-01	6.32E-02		Unigene26948_All//gi|4803925|gb|AAD29798.1|//2.00E-31//expressed protein [Arabidopsis thaliana] >gi|15010702|gb|AAK74010.1| At2g21180/F26H11.6 [Arabidopsis thaliana] >gi|16974343|gb|AAL31156.1| At2g21180/F26H11.6 [Arabidopsis thaliana]	Unigene26948_All//6.00E-27//AT2G21180| unknown protein	Unigene26948_All//0.00E+00//gi|109835974|gb|DW234537.1|DW234537				nr -
Unigene26949_All	863	5.82	1.82	5.99	6.81	6.58	4.29	2.79	0.58	0.92	-1.68E+00	1.01E-08	Down	4.03E-02	8.91E-01		-4.90E-02	8.51E-01		-6.67E-01	5.82E-03		-2.26E+00	1.02E-07	Down	-1.60E+00	2.35E-05	Down	Unigene26949_All//gi|240255303|ref|NP_187469.4|//5.00E-81//protein binding / signal transducer [Arabidopsis thaliana]	Unigene26949_All//0.00E+00//gi|21102780|gb|BQ415093.1|BQ415093					nr +
Unigene26950_All	2106	0.87	0.79	1.16	3.38	2.34	1.33	1.08	0.34	0.51	-1.31E-01	7.72E-01		4.20E-01	3.39E-01		-5.33E-01	1.07E-02		-1.35E+00	1.77E-09	Down	-1.68E+00	3.10E-05	Down	-1.09E+00	3.16E-03		Unigene26950_All//gi|240255303|ref|NP_187469.4|//0.00E+00//protein binding / signal transducer [Arabidopsis thaliana]	Unigene26950_All//0.00E+00//AT3G08570| protein binding / signal transducer	Unigene26950_All//0.00E+00//gi|21094164|gb|BQ406477.1|BQ406477				nr +
Unigene26953_All	562	1.30	1.08	1.90	8.60	7.05	2.49	1.28	1.19	0.14	-2.69E-01	7.19E-01		5.40E-01	4.18E-01		-2.87E-01	3.17E-01		-1.79E+00	1.07E-09	Down	-1.04E-01	8.93E-01		-3.17E+00	8.09E-04	Down	Unigene26953_All//gi|225016152|gb|ACN78975.1|//3.00E-10//Rpp4 candidate 2 [Glycine max]		Unigene26953_All//6.00E-106//TC165695				nr -
Unigene26955_All	588	76.26	184.75	129.86	110.98	128.90	120.13	111.88	158.30	90.52	1.28E+00	2.04E-115	Up	7.68E-01	2.09E-34		2.16E-01	1.65E-04		1.14E-01	1.01E-01		5.01E-01	4.54E-25		-3.06E-01	6.25E-08		Unigene26955_All//gi|32488878|emb|CAE03550.1|//7.00E-18//OSJNBa0060006.16 [Oryza sativa (japonica cultivar-group)]	Unigene26955_All//3.00E-10//AT5G20900| JAZ12 (JASMONATE-ZIM-DOMAIN PROTEIN 12)	Unigene26955_All//0.00E+00//gi|11207950|gb|BF276880.1|BF276880	Tify	ko04626|Plant-pathogen interaction		nr +
Unigene26956_All	1114	78.06	42.39	58.84	16.41	17.74	10.38	0.11	0.15	0.89	-8.81E-01	5.33E-51		-4.08E-01	7.06E-13		1.13E-01	4.48E-01		-6.61E-01	1.43E-07		3.98E-01	8.14E-01		2.97E+00	1.11E-04	Up	Unigene26956_All//gi|297816988|ref|XP_002876377.1|//1.00E-103//thylakoid lumenal 20 kDa protein [Arabidopsis lyrata subsp. lyrata] >gi|297322215|gb|EFH52636.1| thylakoid lumenal 20 kDa protein [Arabidopsis lyrata subsp. lyrata]	Unigene26956_All//2.00E-95//AT3G56650| thylakoid lumenal 20 kDa protein	Unigene26956_All//0.00E+00//TC139844		ko00195|Photosynthesis		nr -

Unigene26958_A11	1558	2.32	1.14	0.31	20.56	13.55	6.09	45.73	7.70	13.99	-1.03E+00	1.69E-03		-2.91E+00	2.00E-11	Down	-6.02E-01	4.21E-12		-1.76E+00	7.13E-60	Down	-2.57E+00	6.18E-242	Down	-1.71E+00	1.01E-147	Down	Unigene26958_A11//gi|17979520|gb|AAL50095.1|/1.00E-140//At2g41800/T11A7.10 [Arabidopsis thaliana] >gi|20453311|gb|AAM19894.1| At2g41800/T11A7.10 [Arabidopsis thaliana]	Unigene26958_A11//5.00E-145//AT2G41810| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41800.1); Has 161 Blast hits to 157 proteins in 12 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 159; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene26958_A11//0.00E+00//TC135216				nr +
Unigene26959_A11	685	26.12	21.53	20.13	30.47	31.62	37.78	21.91	10.43	8.96	-2.79E-01	3.90E-02		-3.76E-01	6.45E-03		5.34E-02	7.41E-01		3.10E-01	4.03E-03		-1.07E+00	1.71E-15	Down	-1.29E+00	3.13E-21	Down	Unigene26959_A11//gi|115460474|ref|NP_001053837.1|//2.00E-21//Os04g0611300 [Oryza sativa Japonica Group] >gi|113565408|dbj|BAF15751.1| Os04g0611300 [Oryza sativa Japonica Group]		Unigene26959_A11//0.00E+00//TC153548				nr -
Unigene2696_A11	2480	0.91	1.02	1.85	2.41	2.11	2.17	2.47	1.20	1.03	1.71E-01	6.58E-01		1.03E+00	5.47E-04	Up	-1.92E-01	4.90E-01		-1.54E-01	6.08E-01		-1.05E+00	1.37E-06	Down	-1.22E+00	6.09E-09	Down	Unigene2696_A11//gi|224112050|ref|XP_002316067.1|//1.00E-158//DNA methyltransferase [Populus trichocarpa] >gi|222865107|gb|EEF02238.1| DNA methyltransferase [Populus trichocarpa]	Unigene2696_A11//9.00E-117//AT3G17310| methyltransferase family protein	Unigene2696_A11//0.00E+00//TC147043				nr -
Unigene26961_A11	608	27.54	19.08	13.75	43.01	36.25	34.84	92.49	56.23	37.48	-5.29E-01	9.33E-05		-1.00E+00	3.42E-12	Down	-2.47E-01	1.97E-02		-3.04E-01	4.51E-03		-7.18E-01	8.97E-29		-1.30E+00	2.94E-78	Down	Unigene26961_A11//gi|222424564|dbj|BAH20237.1|//1.00E-44//AT2G01970 [Arabidopsis thaliana]	Unigene26961_A11//2.00E-37//AT2G01970| endomembrane protein 70, putative	Unigene26961_A11//0.00E+00//TC172438				nr -
Unigene26962_A11	793	12.07	7.73	7.52	20.23	17.76	14.41	4.80	1.69	4.37	-6.43E-01	5.08E-04		-6.83E-01	3.86E-04		-1.88E-01	2.19E-01		-4.89E-01	3.30E-04		-1.51E+00	3.93E-07	Down	-1.35E-01	6.31E-01		Unigene26962_A11//gi|18404610|ref|NP_565878.1|//1.00E-28//ribosome biogenesis regulatory protein (RRS1) family protein [Arabidopsis thaliana] >gi|83305639|sp|Q9SU88.2|RRS1_ARATH RecName: Full=Ribosome biogenesis regulatory protein homolog	Unigene26962_A11//8.00E-30//AT2G37990| ribosome biogenesis regulatory protein (RRS1) family protein	Unigene26962_A11//0.00E+00//TC179226				nr +
Unigene26963_A11	1244	2.82	0.53	0.60	1.60	1.91	1.31	3.98	3.70	3.04	-2.41E+00	1.20E-09	Down	-2.23E+00	2.09E-08	Down	2.54E-01	5.87E-01		-2.93E-01	5.68E-01		-1.06E-01	6.93E-01		-3.86E-01	1.06E-01		Unigene26963_A11//gi|42567992|ref|NP_197554.2|//1.00E-134//ATBRXL4 (BREVIS RADIX-LIKE 4) [Arabidopsis thaliana] >gi|75151601|sp|Q8GZ92.1|BRXL4_ARATH RecName: Full=Protein Brevis radix-like 4; Short=AtBRXL4	Unigene26963_A11//2.00E-117//AT5G20540| ATBRXL4 (BREVIS RADIX-LIKE 4)	Unigene26963_A11//0.00E+00//TC161373				nr -
Unigene26964_A11	649	13.06	45.05	17.15	26.17	46.80	43.15	24.63	38.64	32.41	1.79E+00	2.66E-51	Up	3.93E-01	2.98E-02		8.38E-01	1.42E-19		7.21E-01	6.81E-13		6.50E-01	2.79E-11		3.96E-01	1.51E-04		Unigene26964_A11//gi|121309739|dbj|BAF44192.1|//7.00E-22//SNF1-related kinase [Solanum lycopersicum]	Unigene26964_A11//0.00E+00//gi|48803303|gb|CO104617.1|CO104617				nr +
Unigene26965_A11	1502	4.11	3.10	1.21	6.33	3.67	7.46	9.71	7.21	8.43	-4.05E-01	9.43E-02		-1.77E+00	8.91E-11	Down	-7.88E-01	4.29E-06		2.35E-01	2.14E-01		-4.30E-01	1.04E-03		-2.03E-01	1.35E-01		Unigene26965_A11//gi|18402211|ref|NP_566631.1|//4.00E-78//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75274079|sp|Q9LT81.1|C3H39_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 39; Short=AtC3H39 >gi|14335094|gb|AAK59826.1| AT3g19360/MLD14_8 [Arabidopsis thaliana] >gi|19548069|gb|AAL87398.1| AT3g19360/MLD14_8 [Arabidopsis thaliana]	Unigene26965_A11//5.00E-77//AT3G19360| zinc finger (CCCH-type) family protein	Unigene26965_A11//0.00E+00//gi|78346504|gb|DT566778.1|DT566778	C3H			nr -
Unigene26966_A11	916	8.51	25.28	8.78	7.07	13.98	12.28	1.52	0.78	1.09	1.57E+00	4.52E-34	Up	4.46E-02	8.42E-01		9.84E-01	5.91E-11		7.96E-01	1.76E-06		-9.74E-01	5.54E-02		-4.86E-01	3.29E-01		Unigene26966_A11//gi|14190507|gb|AAK55734.1|AF380653_1|/9.00E-37//At2g17240/T23A1.10 [Arabidopsis thaliana] >gi|4584347|gb|AAD25142.1| expressed protein [Arabidopsis thaliana] >gi|15899722|gb|AAL06814.1| At2g17240/T23A1.10 [Arabidopsis thaliana]	Unigene26966_A11//3.00E-23//AT3G24506| unknown protein	Unigene26966_A11//0.00E+00//BQ410197				nr -
Unigene26967_A11	1174	2.41	0.52	0.82	4.92	2.87	2.00	3.06	3.63	2.10	-2.22E+00	3.19E-07	Down	-1.56E+00	1.54E-04	Down	-7.76E-01	7.28E-04		-1.30E+00	2.04E-07	Down	2.46E-01	4.09E-01		-5.41E-01	5.43E-02		Unigene26967_A11//gi|9743345|gb|AAF97969.1|AC000103.19//1.00E-75//F21J9.30 [Arabidopsis thaliana]	Unigene26967_A11//3.00E-23//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene26967_A11//4.00E-19//gi|78341627|gb|DT561901.1|DT561901				nr -
Unigene26968_A11	812	8.44	18.10	10.43	12.94	19.97	18.35	13.02	11.48	12.36	1.10E+00	5.64E-13	Up	3.05E-01	1.57E-01		6.26E-01	1.27E-06		5.04E-01	4.12E-04		-1.82E-01	3.09E-01		-7.43E-02	6.61E-01		Unigene26968_A11//gi|224060241|ref|XP_002300101.1|//2.00E-86//Cl-channel clc-7 [Populus trichocarpa] >gi|222847359|gb|EEE84906.1| Cl-channel clc-7 [Populus trichocarpa]	Unigene26968_A11//6.00E-78//AT3G27170| CLC-B (CHLORIDE CHANNEL B); anion channel/ voltage-gated chloride channel					nr -
Unigene26969_A11	906	1.27	1.57	1.00	1.43	0.68	1.10	50.96	110.99	66.57	3.02E-01	6.11E-01		-3.47E-01	6.16E-01		-1.06E+00	6.06E-02		-3.82E-01	5.50E-01		1.12E+00	4.77E-107	Up	3.86E-01	7.71E-11		Unigene26969_A11//gi|19911587|dbj|BAB86897.1|//1.00E-124//syringolide-induced protein B13-1-1 [Glycine max]	Unigene26969_A11//8.00E-111//AT4G39830| L-ascorbate oxidase, putative	Unigene26969_A11//0.00E+00//TC136349		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene26970_A11	751	23.76	55.39	21.77	9.02	21.83	30.79	11.26	28.83	69.97	1.22E+00	1.20E-41	Up	-1.26E-01	3.95E-01		1.27E+00	8.96E-21	Up	1.77E+00	4.94E-43	Up	1.36E+00	1.50E-31	Up	2.64E+00	1.96E-186	Up	Unigene26970_A11//gi|18396963|ref|NP_566234.1|//2.00E-06//glycine-rich protein [Arabidopsis thaliana] >gi|145331966|ref|NP_001078105.1| glycine-rich protein [Arabidopsis thaliana] >gi|98960897|gb|ABF58932.1| At3g04640 [Arabidopsis thaliana]		Unigene26970_A11//0.00E+00//DW497022				nr +
Unigene26974_A11	906	25.70	60.01	25.16	31.01	40.21	36.54	5.41	11.26	2.81	1.22E+00	2.23E-54	Up	-3.08E-02	8.11E-01		3.75E-01	6.24E-06		2.37E-01	1.43E-02		1.06E+00	1.48E-10	Up	-9.44E-01	6.81E-05		Unigene26974_A11//gi|18424785|ref|NP_568984.1|//5.00E-48//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|75161488|sp|Q8VYT9.1|NLTL5_ARATH RecName: Full=Non-specific lipid-transfer protein-like protein At5g64080; Flags: Precursor >gi|17979494|gb|AAL50083.1| AT5g64080/MEJ24_6 [Arabidopsis thaliana] >gi|20147301|gb|AAM10364.1| AT5g64080/MEJ24_6 [Arabidopsis thaliana]	Unigene26974_A11//4.00E-41//AT5G64080| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene26974_A11//0.00E+00//TC142949				nr +
Unigene26979_A11	1000	2.25	1.87	2.88	3.99	3.00	2.39	4.48	4.76	2.15	-2.63E-01	5.55E-01		3.54E-01	3.85E-01		-4.12E-01	1.84E-01		-7.35E-01	1.56E-02		8.83E-02	7.42E-01		-1.06E+00	2.59E-05	Down	Unigene26979_A11//gi|108710756|gb|ABF98551.1|//1.00E-79//Eukaryotic membrane protein family protein, expressed {Oryza sativa (japonica cultivar-group)}	Unigene26979_A11//2.00E-90//AT1G67960| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Membrane protein,Tapt1/CMV receptor (InterPro:IPR008010); Has 243 Blast hits to 229 proteins in 123 species: Archae - 0; Bacteria - 0; Metazoa - 79; Fungi - 87; Plants - 18; Viruses - 0; Other Eukaryotes - 59 (source: NCBI BLink).	Unigene26979_A11//0.00E+00//CO122146				nr +
Unigene2698_A11	2380	24.31	16.20	13.85	41.57	34.15	25.69	35.58	19.63	16.50	-5.86E-01	3.97E-17		-8.12E-01	9.72E-29		-2.84E-01	2.43E-09		-6.94E-01	1.21E-41		-8.58E-01	4.30E-58		-1.11E+00	5.25E-91	Down	Unigene2698_A11//gi|290490570|dbj|BAI79272.1|//0.00E-00//LysM type receptor kinase [Lotus japonicus]	Unigene2698_A11//0.00E+00//AT1G51940| protein kinase family protein / peptidoglycan-binding LysM domain-containing protein	Unigene2698_A11//0.00E+00//TC169683		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006464//GO:0009056//GO:0032559	nr -
Unigene26980_A11	717	85.67	90.95	132.35	11.12	12.97	7.68	15.04	12.59	5.61	8.63E-02	2.37E-01		6.28E-01	4.99E-30		2.22E-01	2.98E-01		-5.33E-01	9.30E-03		-2.56E-01	1.24E-01		-1.42E+00	7.82E-18	Down	Unigene26980_A11//gi|195611218|gb|ACG27439.1|//7.00E-45//enzyme of the cupin superfamily [Zea mays] >gi|195617380|gb|ACG30520.1| enzyme of the cupin superfamily [Zea mays] >gi|195617482|gb|ACG30571.1| enzyme of the cupin superfamily [Zea mays] >gi|195617682|gb|ACG30671.1| enzyme of the cupin superfamily [Zea mays]	Unigene26980_A11//2.00E-45//AT4G10300| FUNCTIONS IN: molecular_function unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Cupin, RmlC-type (InterPro:IPR014051), Protein of unknown function DUF861, cupin-3 (InterPro:IPR008579), RmlC-like jelly roll fold (InterPro:IPR014710); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G04300.1); Has 356 Blast hits to 356 proteins in 93 species: Archae - 0; Bacteria - 181; Metazoa - 0; Fungi - 0; Plants - 80; Viruses - 0; Other Eukaryotes - 95 (source: NCBI BLink).	Unigene26980_A11//0.00E+00//gi|5046979|gb|AI728127.1|AI728127				nr +

Unigene26981_All	1362	4.11	1.49	1.02	3.55	3.89	2.98	2.92	0.77	1.02	-1.47E+00	4.58E-08	Down	-2.02E+00	1.41E-11	Down	1.34E-01	6.60E-01		-2.49E-01	4.15E-01		-1.93E+00	3.91E-10	Down	-1.51E+00	1.04E-07	Down	Unigene26981_All//gi|51316929|sp|Q9SF9.1|CR4_ARATH//5.00E-77//RecName: Full=Interactor of constitutive active ROPs 4 >gi|8052548|gb|AAF71812.1|AC013430_21 F3F9.6 [Arabidopsis thaliana]	Unigene26981_All//6.00E-62//AT1G78430| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 8 growth stages; BEST Arabidopsis thaliana protein match is: tropomyosin-related (TAIR:AT1G17140.2); Has 36552 Blast hits to 19717 proteins in 1278 species: Archae - 377; Bacteria - 3766; Metazoa - 19812; Fungi - 2701; Plants - 1105; Viruses - 197; Other Eukaryotes - 8594 (source: NCBI BLink).	Unigene26981_All//0.00E+00//ES851380				nr -
Unigene26982_All	465	8.33	18.52	13.28	14.78	14.22	20.78	19.09	40.90	46.18	1.15E+00	1.72E-08	Up	6.74E-01	6.47E-03		-5.62E-02	8.23E-01		4.92E-01	7.82E-03		1.10E+00	3.41E-20	Up	1.27E+00	3.73E-29	Up	Unigene26982_All//gi|115443701|ref|NP_001045630.1|//7.00E-30//Os02g0106800 [Oryza sativa Japonica Group] >gi|113535161|dbj|BAF07544.1|Os02g0106800 [Oryza sativa Japonica Group]	Unigene26982_All//4.00E-37//AT4G10430| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; CONTAINS InterPro DOMAIN/s: TMPIT-like (InterPro:IPR012926); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G33230.1); Has 192 Blast hits to 192 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 142; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink).	Unigene26982_All//0.00E+00//TC137318				nr -
Unigene26984_All	770	9.24	0.46	2.56	1.49	1.34	31.09	6.37	3.20	2.17	-4.33E+00	4.79E-32	Down	-1.85E+00	4.32E-13	Down	-1.49E-01	8.32E-01		4.38E+00	4.28E-114	Up	-9.92E-01	4.82E-05		-1.55E+00	1.20E-09	Down	Unigene26984_All//gi|224053406|ref|XP_002297803.1|//2.00E-59//AP2/EREBP domain-containing transcription factor [Populus trichocarpa] >gi|222845061|gb|EEE82608.1|AP2/EREBP domain-containing transcription factor [Populus trichocarpa]	Unigene26984_All//3.00E-38//AT5G25190| ethylene-responsive element-binding protein, putative	Unigene26984_All//2.00E-13//EX168096	AP2-EREBP			nr -
Unigene26985_All	710	50.40	37.75	32.63	42.31	37.88	51.46	115.53	65.93	38.83	-4.17E-01	3.06E-06		-6.28E-01	1.09E-11		-1.60E-01	1.35E-01		2.83E-01	1.48E-03		-8.09E-01	5.19E-51		-1.57E+00	6.41E-151	Down	Unigene26985_All//gi|1174867|sp|P46269.2|QCR8_SOLTU//6.00E-31//RecName: Full=Cytochrome b-c1 complex subunit 8; AltName: Full=Ubiquinol-cytochrome c reductase complex ubiquinone-binding protein QP-C; AltName: Full=Ubiquinol-cytochrome c reductase complex 8.2 kDa protein; AltName: Full=Complex III subunit VII; AltName: Full=Complex III subunit 8 >gi|633687|emb|CAA55862.1|ubiquinol--cytochrome c reductase [Solanum tuberosum] >gi|1094912|prf||2107179A cytochrome c oxidase:SUBUNIT-8,2kD	Unigene26985_All//9.00E-30//AT3G10860| ubiquinol-cytochrome C reductase complex ubiquinone-binding protein, putative / ubiquinol-cytochrome C reductase complex 8.2 kDa protein, putative	Unigene26985_All//0.00E+00//TC168820				nr -
Unigene26986_All	760	5.85	38.07	9.18	7.87	6.12	14.74	25.54	66.05	90.48	2.70E+00	1.40E-84	Up	6.49E-01	4.84E-03		-3.63E-01	1.43E-01		9.06E-01	7.10E-08		1.37E+00	2.61E-73	Up	1.83E+00	1.89E-154	Up	Unigene26986_All//gi|107987750|dbj|BAB16427.1|//1.00E-58//NtEIG-E80 [Nicotiana tabacum]	Unigene26986_All//3.00E-51//AT3G54040| photoassimilate-responsive protein-related	Unigene26986_All//0.00E+00//gi|73865761|gb|DT468499.1|DT468499				nr -
Unigene26989_All	510	3.18	3.18	0.42	3.52	3.44	2.04	0.91	0.57	1.25	-5.00E-04	9.97E-01		-2.93E+00	1.92E-05	Down	-3.02E-02	9.51E-01		-7.88E-01	1.13E-01		-6.69E-01	5.09E-01		4.55E-01	5.78E-01		Unigene26989_All//gi|255559621|ref|XP_002520830.1|//9.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223539961|gb|EEF41539.1|conserved hypothetical protein [Ricinus communis]		Unigene26989_All//0.00E+00//TC132296				nr +
Unigene2699_All	1332	3.14	3.42	3.04	2.99	2.66	2.92	4.38	3.23	1.73	1.24E-01	6.65E-01		-4.86E-02	8.81E-01		-1.68E-01	6.07E-01		-3.70E-02	9.27E-01		-4.39E-01	4.99E-02		-1.34E+00	3.18E-09	Down	Unigene2699_All//gi|115444695|ref|NP_001046127.1|//2.00E-48//Os02g0187200 [Oryza sativa Japonica Group] >gi|113535658|dbj|BAF08041.1|Os02g0187200 [Oryza sativa Japonica Group]	Unigene2699_All//8.00E-47//AT4G38040| exostosin family protein	Unigene2699_All//0.00E+00//TC149313				nr +
Unigene26991_All	1867	0.31	0.43	0.23	1.20	0.85	1.33	5.32	2.10	2.60	4.94E-01	5.26E-01		-4.34E-01	6.23E-01		-5.01E-01	2.44E-01		1.48E-01	7.27E-01		-1.34E+00	1.19E-14	Down	-1.03E+00	2.68E-10	Down	Unigene26991_All//gi|115451409|ref|NP_001049305.1|//1.00E-109//Os03g0203100 [Oryza sativa Japonica Group] >gi|108706728|gb|ABF94523.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547776|dbj|BAF11219.1|Os03g0203100 [Oryza sativa Japonica Group]	Unigene26991_All//6.00E-155//AT4G30150| EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Nucleolar 27S pre-rRNA processing, Urb2/Npa2 (InterPro:IPR018849); Has 31 Blast hits to 27 proteins in 14 species: Archae - 0; Bacteria - 2; Metazoa - 3; Fungi - 0; Plants - 19; Viruses - 3; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene26991_All//0.00E+00//TC132919				nr +
Unigene26993_All	857	1.28	2.72	1.49	6.63	7.19	5.43	2.81	1.07	1.49	1.08E+00	1.05E-02		2.18E-01	7.02E-01		1.18E-01	6.82E-01		-2.88E-01	2.98E-01		-1.39E+00	2.41E-04	Down	-9.19E-01	9.16E-03									
Unigene26994_All	623	38.88	13.66	18.29	78.92	66.88	82.86	74.72	25.83	36.58	-1.51E+00	8.42E-34	Down	-1.09E+00	8.76E-20	Down	-2.39E-01	9.84E-04		7.03E-02	4.52E-01		-1.53E+00	2.05E-80	Down	-1.03E+00	7.17E-45	Down	Unigene26994_All//gi|225433375|ref|XP_002285608.1|//1.00E-106//PREDICTED: similar to GroEL-like chaperone, ATPase [Vitis vinifera]	Unigene26994_All//8.00E-106//AT3G23990| HSP60 (HEAT SHOCK PROTEIN 60); ATP binding	Unigene26994_All//0.00E+00//gi|164312058|gb|ES818989.1|ES818989		ko03018|RNA degradation		nr +
Unigene26996_All	726	9.87	4.33	5.06	12.08	10.62	16.17	21.90	7.54	6.80	-1.19E+00	1.48E-07	Down	-9.64E-01	2.59E-05		-1.85E-01	4.03E-01		4.22E-01	1.16E-02		-1.54E+00	4.21E-28	Down	-1.69E+00	5.45E-33	Down	Unigene26996_All//gi|14423400|gb|AAK62382.1|AF386937_1//5.00E-22//Unknown protein [Arabidopsis thaliana] >gi|24899683|gb|AAN65056.1|Unknown protein [Arabidopsis thaliana]	Unigene26996_All//3.00E-23//AT1G27435| unknown protein	Unigene26996_All//0.00E+00//DW519607				nr -
Unigene26997_All	1167	0.90	0.91	0.59	0.94	1.39	1.86	1.09	1.25	2.56	2.41E-02	9.89E-01		-5.96E-01	3.93E-01		5.63E-01	3.15E-01		9.84E-01	2.63E-02		2.06E-01	6.81E-01		1.24E+00	1.30E-04	Up	Unigene26997_All//gi|145338580|ref|NP_188247.2|//1.00E-100//TRZ4 (TRNASE Z 4); 3'-tRNA processing endoribonuclease/ catalytic [Arabidopsis thaliana]	Unigene26997_All//1.00E-88//AT3G16260| TRZ4 (TRNASE Z 4); 3'-tRNA processing endoribonuclease/ catalytic	Unigene26997_All//2.00E-126//DW512273				nr -
Unigene26999_All	619	9.55	20.30	11.53	17.87	21.03	23.06	22.75	23.29	33.85	1.09E+00	5.13E-11	Up	2.71E-01	2.58E-01		2.35E-01	1.62E-01		3.68E-01	1.48E-02		3.45E-02	8.27E-01		5.74E-01	4.71E-08		Unigene26999_All//gi|156620978|gb|ABU88852.1|//5.00E-62//lammer-type protein kinase [Sorghum bicolor]	Unigene26999_All//4.00E-58//AT4G24740| APC2 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 2); kinase/ protein kinase	Unigene26999_All//2.00E-177//DT466017				nr -
Unigene270_All	2931	7.77	3.91	5.27	23.66	27.89	25.02	11.32	5.18	7.75	-9.91E-01	9.00E-17		-5.60E-01	2.19E-06		2.38E-01	1.18E-05		8.10E-02	2.69E-01		-1.13E+00	3.19E-36	Down	-5.48E-01	2.32E-11		Unigene270_All//0.00E+00//gi|42565945|ref|NP_567014.2|//0.00E-00//Rab5GAP/TBC domain-containing protein [Arabidopsis thaliana]	Unigene270_All//0.00E+00//AT3G55020| RabGAP/TBC domain-containing protein	Unigene270_All//0.00E+00//TC148356	ko04144|Endocytosis			nr -
Unigene2700_All	2242	24.88	8.16	13.06	39.33	36.17	26.33	19.61	5.97	5.35	-1.61E+00	1.78E-84	Down	-9.29E-01	1.02E-34		-1.21E-01	3.67E-02		-5.79E-01	4.77E-27		-1.72E+00	2.05E-89	Down	-1.87E+00	6.48E-104	Down	Unigene2700_All//gi|3157949|gb|AAC17632.1|//0.00E-00//Similar to glucan endo-1,3-beta-D-glucosidase precursor gb|Z28697 from Nicotiana tabacum. ESTs gb|Z18185 and gb|AA603362 come from this gene [Arabidopsis thaliana]	Unigene2700_All//6.00E-161//AT1G11820| catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene2700_All//0.00E+00//TC145272	ko00500|Starch and sucrose metabolism		GO:0008422//GO:0043167//GO:0044238	nr -
Unigene27006_All	660	66.04	51.36	32.27	109.14	67.20	97.72	196.60	122.41	117.89	-3.63E-01	6.58E-06		-1.03E+00	2.32E-32	Down	-7.00E-01	7.63E-35		-1.60E-01	1.32E-02		-6.84E-01	5.29E-60		-7.38E-01	2.21E-70		Unigene27006_All//gi|61651606|dbj|BAD91176.1|//2.00E-31//plastidic phosphate translocator-like protein1 [Mesembryanthemum crystallinum]	Unigene27006_All//2.00E-22//AT5G25400| phosphate translocator-related	Unigene27006_All//0.00E+00//TC141120				nr -
Unigene27007_All	702	9.69	20.57	8.80	8.94	13.05	13.90	40.35	61.50	35.53	1.09E+00	1.61E-12	Up	-1.39E-01	6.03E-01		5.45E-01	2.85E-03		6.36E-01	4.30E-04		6.08E-01	8.35E-17		-1.84E-01	4.95E-02		Unigene27007_All//gi|6653740|gb|AAF22842.1|AF209910_1//2.00E-48//vacuolar sorting receptor protein [Prunus dulcis]	Unigene27007_All//5.00E-49//AT2G14740| ATVSR3 (ARABIDOPSIS THALIANA VACUOLAR SORTING RECEPTOR 3); calcium ion binding	Unigene27007_All//0.00E+00//gi|48812064|gb|CO113377.1|CO113377				nr -
Unigene27008_All	812	9.99	5.55	9.57	21.72	16.28	12.40	6.09	2.73	2.06	-8.47E-01	3.52E-05		-6.09E-02	7.81E-01		-4.15E-01	8.25E-04		-8.08E-01	3.97E-10		-1.16E+00	2.65E-06	Down	-1.56E+00	7.92E-10	Down	Unigene27008_All//gi|218190326|gb|EEC72753.1|//5.00E-06//hypothetical protein Osl_06384 [Oryza sativa Indica Group]		Unigene27008_All//1.00E-67//ES796355				nr +
Unigene2701_All	2132	5.77	4.28	4.75	8.36	7.43	7.90	11.52	4.98	6.37	-4.31E-01	7.88E-03		-2.81E-01	1.12E-01		-1.71E-01	2.36E-01		-8.22E-02	6.36E-01		-1.21E+00	4.46E-30	Down	-8.55E-01	7.43E-18		Unigene2701_All//gi|115471649|ref|NP_001059423.1|//0.00E-00//Os07g0300900 [Oryza sativa Japonica Group] >gi|113610959|dbj|BAF21337.1|Os07g0300900 [Oryza sativa Japonica Group]	Unigene2701_All//0.00E+00//AT5G14060| ARAB-AK-LYS; amino acid binding / aspartate kinase	Unigene2701_All//0.00E+00//TC144550		ko00270|Cysteine and methionine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00300|Lysine biosynthesis	GO:0008652//GO:0016774//GO:0031406	nr -
Unigene27010_All	1383	1.82	1.50	1.27	12.89	8.89	4.44	20.21	12.33	8.27	-2.74E-01	5.06E-01		-5.15E-01	2.31E-01		-5.37E-01	8.82E-06		-1.54E+00	8.59E-28	Down	-7.13E-01	1.53E-14		-1.29E+00	1.04E-38	Down	Unigene27010_All//gi|15227200|ref|NP_179828.1|//1.00E-149//peroxidase 17 (PER17) (P17) [Arabidopsis thaliana] >gi|254532217|sp|Q96JZ2.1|PER17_ARATH RecName: Full=Peroxidase 17; Short=Atperox P17; AltName: Full=ATP25a; Flags: Precursor	Unigene27010_All//3.00E-150//AT2G22420| peroxidase 17 (PER17) (P17)	Unigene27010_All//0.00E+00//TC152203		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene27011_All	1173	5.00	1.34	2.91	3.48	1.94	2.19	1.62	1.00	0.48	-1.90E+00	8.61E-12	Down	-7.82E-01	2.17E-03		-8.46E-01	2.69E-03		-6.66E-01	2.72E-02		-7.01E-01	9.78E-02		-1.77E+00	5.92E-05	Down	Unigene27011_All//gi|115470299|ref|NP_001058748.1|//1.00E-119//Os07g0113500 [Oryza sativa Japonica Group] >gi|22831309|dbj|BAC16163.1|pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa Japonica Group] >gi|24414055|dbj|BAC22304.1|pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa Japonica Group] >gi|113610284|dbj|BAF20662.1|Os07g0113500 [Oryza sativa Japonica Group]	Unigene27011_All//7.00E-120//AT4G37380| pentatricopeptide (PPR) repeat-containing protein	Unigene27011_All//0.00E+00//CO120969				nr -

Unigene27012_All	1435	7.77	4.73	1.00	0.62	1.46	1.70	47.47	6.29	15.52	-7.15E-01	2.69E-05		-2.95E+00	6.23E-35	Down	1.23E+00	5.57E-03		1.44E+00	6.17E-04	Up	-2.92E+00	3.26E-265	Down	-1.61E+00	4.47E-130	Down	Unigene27012_All//gi|14423450|gb|AK62407.1|AF386962_1//1.00E-141//Unknown protein [Arabidopsis thaliana] >gi|30725566|gb|AAP37805.1|At5g25460 [Arabidopsis thaliana]	Unigene27012_All//1.00E-142//AT5G25460| unknown protein	Unigene27012_All//0.00E+00//TC138865				nr -
Unigene27013_All	617	17.98	7.39	5.52	34.96	25.06	38.94	123.96	66.11	83.94	-1.28E+00	1.44E-12	Down	-1.70E+00	6.05E-18	Down	-4.80E-01	1.03E-05		1.56E-01	2.24E-01		-9.07E-01	1.19E-57		-5.63E-01	3.43E-26				Unigene27013_All//0.00E+00//gi|109836801|gb|DW235362.1|DW235362				
Unigene27017_All	1198	7.42	3.47	14.67	8.52	8.57	11.42	1.62	0.38	0.47	-1.10E+00	3.57E-08	Down	9.82E-01	2.11E-12		7.00E-03	9.77E-01		4.22E-01	5.58E-03		-2.08E+00	8.32E-06	Down	-1.80E+00	3.77E-05	Down	Unigene27017_All//gi|82697939|gb|AB698004.1|//1.00E-100//CXE carboxylesterase [Malus pumila]	Unigene27017_All//1.00E-93//AT2G45600| hydrolase	Unigene27017_All//0.00E+00//TC148291				nr +
Unigene27018_All	1495	1.01	2.10	1.46	6.80	5.69	5.26	3.00	1.96	1.31	1.05E+00	3.15E-03		5.25E-01	2.47E-01		-2.57E-01	1.72E-01		-3.71E-01	4.40E-02		-6.15E-01	1.60E-02		-1.20E+00	2.72E-06	Down	Unigene27018_All//gi|224114113|ref|XP_002316671.1|//4.00E-37//NBS resistance protein [Populus trichocarpa] >gi|222859736|gb|EEE97283.1| NBS resistance protein [Populus trichocarpa]	Unigene27018_All//1.00E-24//AT5G45490| disease resistance protein-related			ko04626|Plant-pathogen interaction		nr -
Unigene2702_All	1530	1.81	2.32	3.48	1.30	2.81	2.45	4.12	3.28	5.34	3.55E-01	2.95E-01		9.41E-01	5.06E-04		1.11E+00	9.01E-05	Up	9.12E-01	4.00E-03		-3.29E-01	1.36E-01		3.75E-01	3.66E-02		Unigene2702_All//gi|15231744|ref|NP_190877.1|//1.00E-109//UPL7; ubiquitin-protein ligase [Arabidopsis thaliana] >gi|79314848|ref|NP_001030850.1|UPL7; ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75265625|sp|Q9SCQ2.1|UPL7_ARATH RecName: Full=E3 ubiquitin-protein ligase UPL7; Short=Ubiquitin-protein ligase 7	Unigene2702_All//1.00E-107//AT3G53090| UPL7; ubiquitin-protein ligase					nr +
Unigene27023_All	1417	2.70	9.05	3.16	3.69	3.23	5.45	5.61	12.51	21.09	1.75E+00	3.46E-22	Up	2.28E-01	4.64E-01		-1.92E-01	5.30E-01		5.62E-01	7.17E-03		1.16E+00	2.00E-20	Up	1.91E+00	8.57E-72	Up	Unigene27023_All//gi|51536446|gb|AL05461.1|//1.00E-50//At4g35070 [Arabidopsis thaliana] >gi|51972074|gb|AAU15141.1|At4g35070 [Arabidopsis thaliana]	Unigene27023_All//8.00E-40//AT4G35070| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 8 growth stages; CONTAINS InterPro DOMAIN/s: S-ribonuclease binding protein, SBP1, pollen (InterPro:IPR017066); BEST Arabidopsis thaliana protein match is: SBP1 (s-ribonuclease binding protein 1); protein binding / zinc ion binding (TAIR:AT1G45976.1); Has 762 Blast hits to 716 proteins in 103 species: Archae - 2; Bacteria - 18; Metazoa - 250; Fungi - 8; Plants - 213; Viruses - 21; Other Eukaryotes - 250 (source: NCBI BLink).	Unigene27023_All//0.00E+00//TC163531				nr +
Unigene27026_All	849	18.55	38.14	23.02	54.86	58.89	60.48	122.31	86.74	74.37	1.04E+00	2.59E-25	Up	3.11E-01	1.94E-02		1.02E-01	2.34E-01		1.41E-01	8.26E-02		-4.96E-01	2.08E-27		-7.18E-01	7.31E-54				Unigene27026_All//0.00E+00//TC168785				
Unigene27028_All	1027	8.10	4.24	4.15	25.80	21.76	16.93	1.61	0.37	0.47	-9.33E-01	4.39E-06		-9.66E-01	4.65E-06		-2.46E-01	1.94E-02		-6.08E-01	2.75E-09		-2.13E+00	3.64E-05	Down	-1.79E+00	1.90E-04	Down	Unigene27028_All//gi|122180229|sp|Q1PEY6.1|EPFL6_ARATH//5.00E-28//RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 6; Short=EPF-like protein 6; Flags: Precursor >gi|91806295|gb|ABE65875.1| allergen-like [Arabidopsis thaliana]	Unigene27028_All//4.00E-19//AT2G30370| allergen-related	Unigene27028_All//4.00E-167//gi|164330137|gb|EX163954.1|EX163954				nr -
Unigene27029_All	1214	4.35	82.43	24.61	47.11	68.10	98.81	7.24	17.28	13.06	4.24E+00	0.00E+00	Up	2.50E+00	3.58E-78	Up	5.32E-01	6.08E-24		1.07E+00	1.99E-103	Up	1.25E+00	3.28E-27	Up	8.50E-01	1.11E-11		Unigene27029_All//gi|89111818|gb|AB060681.1|//8.00E-13//At1g67920 [Arabidopsis thaliana]	Unigene27029_All//4.00E-14//AT1G67920| unknown protein	Unigene27029_All//0.00E+00//TC179120				nr -
Unigene2703_All	2155	3.45	9.88	8.99	9.50	20.81	18.38	0.04	0.04	0.00	1.52E+00	7.05E-30	Up	1.38E+00	4.64E-23	Up	1.13E+00	7.92E-47	Up	9.52E-01	1.43E-28		-1.48E-02	1.01E+00		-5.29E+00	3.58E-01		Unigene2703_All//gi|224054546|ref|XP_002298314.1|//0.00E+00//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222845572|gb|EEE83119.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene2703_All//2.00E-136//AT3G51860| CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	Unigene2703_All//0.00E+00//TC131691			GO:0006811//GO:0015075//GO:0031224	nr -
Unigene27031_All	1848	0.45	5.57	1.27	0.22	1.04	2.22	3.34	11.33	145.30	3.62E+00	4.72E-40	Up	1.48E+00	1.09E-03		2.28E+00	1.20E-05	Up	3.37E+00	3.36E-16	Up	1.76E+00	1.98E-44	Up	5.44E+00	0.00E+00	Up	Unigene27031_All//gi|84514169|gb|AB539093.1|//0.00E+00//cytochrome P450 monooxygenase CYP94C9 [Medicago truncatula]	Unigene27031_All//5.00E-170//AT2G27690| CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene27031_All//0.00E+00//gi|73860437|gb|DT463176.1|DT463176		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene27034_All	1101	19.29	16.02	18.09	8.73	12.17	9.64	1.42	0.15	0.72	-2.69E-01	2.87E-02		-9.30E-02	5.14E-01		4.79E-01	1.12E-03		1.43E-01	4.94E-01		-3.23E+00	2.68E-07	Down	-9.73E-01	3.21E-02		Unigene27034_All//gi|255529749|gb|ACU12849.1|//6.00E-44//cutin deficient 2 [Solanum lycopersicum]	Unigene27034_All//6.00E-16//AT4G00730| ANL2 (ANTHOCYANINLESS 2); transcription factor/ transcription regulator	Unigene27034_All//9.00E-119//TC157315	HB			nr -
Unigene27036_All	1341	0.66	2.30	0.56	1.26	0.85	1.58	0.88	0.22	0.68	1.80E+00	4.12E-06	Up	-2.55E-01	7.17E-01		-5.76E-01	2.53E-01		3.26E-01	5.02E-01		-2.02E+00	1.06E-03		-3.70E-01	5.03E-01		Unigene27036_All//gi|297827875|ref|XP_002881820.1|//5.00E-69//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327659|gb|EFH58079.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene27036_All//7.00E-62//AT2G42080| DNAJ heat shock N-terminal domain-containing protein	Unigene27036_All//0.00E+00//TC147468				nr +
Unigene27037_All	376	7.79	6.20	7.79	12.98	15.48	20.78	16.08	10.12	32.95	-3.30E-01	3.76E-01		-6.00E-04	9.99E-01		2.54E-01	3.55E-01		6.79E-01	9.56E-04		-6.69E-01	1.78E-03		1.04E+00	1.36E-12	Up			Unigene27037_All//0.00E+00//BE052932				
Unigene27039_All	1087	20.84	128.75	4.90	23.42	24.52	55.05	18.16	16.26	17.30	2.63E+00	0.00E+00	Up	-2.09E+00	1.61E-47	Down	6.63E-02	6.04E-01		1.23E+00	5.59E-65	Up	-1.59E-01	2.01E-01		-7.04E-02	6.01E-01		Unigene27039_All//gi|3759184|dbj|BAA33810.1|//1.00E-127//phi-1 [Nicotiana tabacum]	Unigene27039_All//4.00E-121//AT4G08950| EXO (EXORDIUM)	Unigene27039_All//0.00E+00//TC137639				nr -
Unigene27041_All	2003	0.60	0.76	1.17	1.74	1.41	1.35	1.98	1.69	6.34	3.37E-01	5.39E-01		9.61E-01	2.79E-02		-3.04E-01	3.89E-01		-3.64E-01	3.14E-01		-2.31E-01	4.41E-01		1.68E+00	4.70E-26	Up	Unigene27041_All//gi|297804352|ref|XP_002870060.1|//5.00E-76//purine permease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315896|gb|EFH46319.1| purine permease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27041_All//8.00E-70//AT4G18210| ATPUP10; purine transmembrane transporter	Unigene27041_All//6.00E-149//CA992609				nr +
Unigene27042_All	1111	31.22	31.29	34.51	60.89	66.61	85.45	27.90	39.76	13.45	2.90E-03	9.83E-01		1.44E-01	1.42E-01		1.30E-01	4.21E-02		4.89E-01	2.06E-21		5.12E-01	8.49E-13		-1.05E+00	3.25E-31	Down	Unigene27042_All//gi|79436765|ref|NP_190351.2|//8.00E-38//enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor [Arabidopsis thaliana]	Unigene27042_All//3.00E-38//AT3G47670| enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor	Unigene27042_All//0.00E+00//DW240334		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene27043_All	1860	1.74	5.78	0.60	0.00	0.00	0.00	6.73	24.97	27.69	1.73E+00	1.99E-18	Up	-1.54E+00	5.17E-05	Down	null	null		null	null		1.89E+00	1.51E-107	Up	2.04E+00	1.97E-134	Up	Unigene27043_All//gi|193878340|gb|ACF25910.1|//0.00E+00//MLO-like protein 3 [Vitis vinifera]	Unigene27043_All//1.00E-174//AT1G61560| MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding	Unigene27043_All//1.00E-75//DW225778				nr +
Unigene27046_All	1052	0.95	1.49	2.48	3.03	2.19	2.53	3.58	4.29	1.89	6.60E-01	2.16E-01		1.39E+00	9.95E-04	Up	-4.67E-01	1.81E-01		-2.59E-01	5.00E-01		2.63E-01	3.54E-01		-9.18E-01	8.08E-04		Unigene27046_All//gi|289540938|gb|AD009609.1|//3.00E-18//zinc-mediated transcriptional activator [Trifolium repens]	Unigene27046_All//7.00E-09//AT4G22140| DNA binding / protein binding / zinc ion binding	Unigene27046_All//0.00E+00//TC158236				nr +
Unigene27047_All	981	6.29	1.55	0.98	7.92	5.44	2.03	3.36	0.60	2.31	-2.02E+00	2.18E-13	Down	-2.69E+00	1.05E-17	Down	-5.42E-01	6.06E-03		-1.97E+00	2.62E-17	Down	-2.49E+00	1.85E-11	Down	-5.38E-01	6.78E-02		Unigene27047_All//gi|42572779|ref|NP_974485.1|//8.00E-89//phosphoinositide binding [Arabidopsis thaliana]	Unigene27047_All//2.00E-66//AT3G63300| phosphoinositide binding	Unigene27047_All//0.00E+00//ES842178				nr -
Unigene27048_All	1264	91.06	14.71	29.66	4.97	6.37	8.40	17.86	115.17	37.54	-2.63E+00	0.00E+00	Down	-1.62E+00	8.74E-170	Down	3.60E-01	8.46E-02		7.58E-01	1.04E-05		2.69E+00	0.00E+00	Up	1.07E+00	2.57E-48	Up	Unigene27048_All//gi|297835524|ref|XP_002885644.1|//1.00E-87//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331484|gb|EFH61903.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27048_All//2.00E-88//AT3G24420| hydrolase, alpha/beta fold family protein	Unigene27048_All//0.00E+00//TC136761				nr +
Unigene27049_All	1746	1.95	7.89	5.03	2.43	2.98	1.35	0.22	0.17	0.11	2.02E+00	8.85E-29	Up	1.37E+00	1.29E-10	Up	2.96E-01	3.10E-01		-8.50E-01	3.54E-03		-3.79E-01	7.23E-01		-9.33E-01	3.79E-01		Unigene27049_All//gi|15227253|ref|NP_179847.1|//0.00E+00//lyase [Arabidopsis thaliana]	Unigene27049_All//0.00E+00//AT2G22620| lyase	Unigene27049_All//0.00E+00//TC133372				nr +
Unigene27051_All	1347	9.94	12.30	9.76	10.91	9.59	11.74	10.83	6.33	5.21	3.07E-01	2.86E-02		-2.62E-02	8.85E-01		-1.87E-01	2.45E-01		1.05E-01	5.49E-01		-7.75E-01	4.20E-09		-1.06E+00	2.94E-15	Down	Unigene27051_All//gi|42562121|ref|NP_173178.3|//1.00E-104//auxin-induced-related / indole-3-acetic acid induced-related [Arabidopsis thaliana] >gi|209572597|sp|Q9LQ17.2|CIA30_ARATH RecName: Full=Probable complex I intermediate-associated protein 30 >gi|117168231|gb|ABK32198.1|At1g17350 [Arabidopsis thaliana]	Unigene27051_All//4.00E-105//AT1G17350| auxin-induced-related / indole-3-acetic acid induced-related	Unigene27051_All//0.00E+00//TC143157				nr -
Unigene27052_All	624	21.80	55.62	61.36	40.79	71.46	95.47	28.05	55.33	82.87	1.35E+00	1.14E-40	Up	1.49E+00	1.63E-50	Up	8.09E-01	6.35E-27		1.23E+00	3.75E-64	Up	9.80E-01	5.64E-30		1.56E+00	1.45E-93	Up	Unigene27052_All//gi|238479688|ref|NP_001154596.1|//5.00E-73//ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C [Arabidopsis thaliana]	Unigene27052_All//8.00E-66//AT3G08510| ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C	Unigene27052_All//0.00E+00//gi|109861011|gb|DW489990.1|DW489990		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene27053_All	1306	0.08	0.00	0.41	48.90	11.21	6.02	206.25	92.14	52.38	-6.32E+00	3.72E-01		2.35E+00	5.87E-02		-2.13E+00	1.27E-178	Down	-3.02E+00	6.05E-231	Down	-1.16E+00	1.75E-302	Down	-1.98E+00	0.00E+00	Down	Unigene27053_All//gi|224553206|sp|Q9FX85.1|PER10_ARATH//1.00E-119//RecName: Full=Peroxidase 10; Short=Atperox P10; AltName: Full=ATPsa; Flags: Precursor >gi|10120418|gb|AAG13043.1|AC011807_2 peroxidase ATP5a [Arabidopsis thaliana] >gi|30017315|gb|AAP12891.1|At1g49570 [Arabidopsis thaliana]	Unigene27053_All//7.00E-121//AT1G49570| peroxidase, putative	Unigene27053_All//0.00E+00//DW511623		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene27054_All	807	21.07	35.47	17.09	34.20	30.30	33.08	80.05	41.28	31.05	7.52E-01	2.58E-13		-3.02E-01	3.75E-02		-1.75E-01	1.11E-01		-4.81E-02	6.89E-01		-9.56E-01	3.14E-53		-1.37E+00	1.57E-96	Down	Unigene27054_All//gi|115451819|ref|NP_001049510.1|//6.00E-50//Os03g0240700 [Oryza sativa Japonica Group] >gi|108707094|gb|ABF94889.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547981|dbj|BAF11424.1|Os03g0240700 [Oryza sativa Japonica Group]	Unigene27054_All//1.00E-39//AT3G17780| unknown protein	Unigene27054_All//0.00E+00//TC153080				nr -
Unigene27055_All	642	3.99	4.18	4.56	4.97	5.79	8.72	0.20	1.37	0.93	6.70E-02	8.64E-01		1.92E-01	6.26E-01		2.22E-01	5.42E-01		8.13E-01	1.11E-03		2.79E+00	6.97E-04	Up	2.24E+00	1.67E-02		Unigene27055_All//gi|115441655|ref|NP_001045107.1|//1.00E-52//Os01g0900900 [Oryza sativa Japonica Group] >gi|113534638|dbj|BAF07021.1|Os01g0900900 [Oryza sativa Japonica Group]	Unigene27055_All//2.00E-52//AT3G57810| OTU-like cysteine protease family protein	Unigene27055_All//2.00E-84//CO096471				nr -

Unigene27057_All	764	13.63	53.92	35.41	3.59	23.48	24.59	1.33	15.65	16.58	1.98E+00	6.07E-83	Up	1.38E+00	8.84E-32	Up	2.71E+00	4.12E-61	Up	2.78E+00	1.18E-60	Up	3.56E+00	2.57E-56	Up	3.64E+00	6.91E-62	Up	Unigene27057_All//gi|46518383|gb|AAS99673.1|/3.00E-28//At3g62070 [Arabidopsis thaliana] >gi|48310405|gb|AAT41814.1| At3g62070 [Arabidopsis thaliana]	Unigene27057_All//2.00E-19//AT3G62070| unknown protein	Unigene27057_All//0.00E+00//TC159389				nr +
Unigene27058_All	1066	5.20	11.60	12.89	103.46	64.87	68.04	10.15	103.16	3.66	1.16E+00	6.83E-12	Up	1.31E+00	3.30E-15	Up	-6.74E-01	9.48E-50		-6.05E-01	2.16E-36		3.34E+00	0.00E+00	Up	-1.47E+00	8.64E-19	Down	Unigene27058_All//gi|224088816|ref|XP_002308552.1|/1.00E-45//glutaredoxin [Populus trichocarpa] >gi|222854528|gb|EEE92075.1| glutaredoxin [Populus trichocarpa]	Unigene27058_All//3.00E-43//AT4G33040| glutaredoxin family protein	Unigene27058_All//0.00E+00//TC154274				nr -
Unigene27059_All	1285	0.81	159.38	87.64	10.66	65.57	174.61	0.20	0.13	0.00	7.61E+00	0.00E+00	Up	6.75E+00	0.00E+00	Up	2.62E+00	1.93E-277	Up	4.03E+00	0.00E+00	Up	-6.02E-01	6.48E-01		-7.63E+00	3.04E-02		Unigene27059_All//gi|90265044|emb|CAH67640.1|//2.00E-12//H0102C09.1 [Oryza sativa (indica cultivar-group)]	Unigene27059_All//7.00E-21//gi|78329741|gb|DT550015.1|DT550015				nr +
Unigene27062_All	1348	16.61	32.06	17.62	4.69	6.36	7.67	2.76	0.62	0.62	9.49E-01	6.25E-29		8.48E-02	5.33E-01		4.39E-01	2.48E-02		7.09E-01	4.75E-05		-2.15E+00	6.89E-11	Down	-2.15E+00	2.83E-11	Down	Unigene27062_All//gi|15218937|ref|NP_176787.1|//1.00E-104//oxidoreductase N-terminal domain-containing protein [Arabidopsis thaliana]	Unigene27062_All//8.00E-106//AT1G66130| oxidoreductase N-terminal domain-containing protein	Unigene27062_All//0.00E+00//TC135580		ko00562|Inositol phosphate metabolism		nr +
Unigene27063_All	1187	1.06	7.47	1.39	18.80	25.67	16.17	1.03	2.64	17.59	2.82E+00	1.75E-27	Up	3.95E-01	4.55E-01		4.50E-01	7.65E-07		-2.17E-01	7.97E-02		1.35E+00	3.17E-05	Up	4.09E+00	5.05E-111	Up	Unigene27063_All//gi|209954711|dbj|BAG60546.1|//3.00E-79//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene27063_All//3.00E-53//AT1G24100| UGT74B1 (UDP-glucosyl transferase 74B1); UDP-glycosyltransferase/ thiohydroximate beta-D-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene27063_All//0.00E+00//gi|109877149|gb|DW506123.1|DW506123		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr +
Unigene27065_All	942	1.39	8.23	5.88	13.48	7.57	20.09	1.93	4.75	4.65	2.57E+00	7.87E-22	Up	2.08E+00	5.66E-12	Up	-8.34E-01	1.07E-08		5.75E-01	3.39E-06		1.30E+00	9.93E-07	Up	1.27E+00	1.33E-06	Up	Unigene27065_All//gi|20466362|gb|AAM20498.1|/8.00E-38//calmodulin-like protein [Arabidopsis thaliana] >gi|22136314|gb|AAM91235.1| calmodulin-like protein [Arabidopsis thaliana]	Unigene27065_All//7.00E-39//AT3G50770| calmodulin-related protein, putative			ko04626|Plant-pathogen interaction		nr +
Unigene27068_All	803	4.69	3.41	3.12	26.12	11.45	7.59	13.37	60.01	61.82	-4.61E-01	1.47E-01		-5.90E-01	7.72E-02		-1.19E+00	4.26E-25	Down	-1.78E+00	3.55E-40	Down	2.17E+00	4.35E-133	Up	2.21E+00	3.81E-143	Up	Unigene27068_All//gi|113367166|gb|ABI34640.1|/5.00E-70//bZIP transcription factor bZIP35 [Glycine max]	Unigene27068_All//2.00E-35//AT3G30530| AT8G18P42 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 42); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene27068_All//1.00E-06//gi|13352698|gb|BG443046.1|BG443046	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene2707_All	2225	0.63	0.27	1.20	51.45	43.69	34.26	14.19	2.29	2.49	-1.22E+00	3.33E-02		9.14E-01	2.41E-02		-2.36E-01	1.09E-07		-5.87E-01	8.99E-36		-2.63E+00	2.29E-110	Down	-2.51E+00	4.95E-108	Down	Unigene2707_All//gi|224090738|ref|XP_002309069.1|/0.00E+00//laccase 110c [Populus trichocarpa] >gi|222855045|gb|EEE92592.1| laccase 110c [Populus trichocarpa]	Unigene2707_All//0.00E+00//AT5G60020| LAC17 (laccase 17); laccase	Unigene2707_All//0.00E+00//TC134140		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr -
Unigene27070_All	1197	1.31	0.51	0.09	4.58	2.59	2.79	8.62	1.43	3.10	-1.37E+00	1.19E-02		-3.88E+00	1.55E-06	Down	-8.22E-01	5.08E-04		-7.13E-01	4.53E-03		-2.59E+00	7.46E-36	Down	-1.48E+00	4.65E-18	Down	Unigene27070_All//gi|222424922|dbj|BAH20412.1|//1.00E-126//AT3G13750 [Arabidopsis thaliana]	Unigene27070_All//4.00E-122//AT3G13750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene27070_All//0.00E+00//TC130564		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation		nr -
Unigene27073_All	1391	8.09	10.13	7.47	20.23	14.43	18.99	26.75	11.09	25.86	3.25E-01	3.46E-02		-1.16E-01	5.70E-01		-4.87E-01	1.83E-07		-9.12E-02	4.76E-01		-1.27E+00	1.16E-48	Down	-4.86E-02	5.98E-01		Unigene27073_All//gi|108864347|gb|ABA93307.2|//1.00E-98//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene27073_All//8.00E-114//AT3G15240| unknown protein	Unigene27073_All//0.00E+00//gi|78352267|gb|DT572541.1|DT572541				nr +
Unigene27076_All	818	2.49	0.87	0.72	4.20	3.24	3.31	3.67	2.15	2.78	-1.52E+00	1.32E-03		-1.80E+00	4.36E-04	Down	-3.74E-01	2.83E-01		-3.43E-01	3.46E-01		-7.74E-01	1.60E-02		-4.03E-01	2.05E-01		Unigene27076_All//5.00E-52//AT3G15750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene27076_All//5.00E-52//AT3G15750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene27076_All//0.00E+00//gi|13248734|gb|BF278228.2|BF278228		ko04626|Plant-pathogen interaction		nr -
Unigene27078_All	1059	0.59	6.12	1.26	1.60	3.64	2.43	2.56	7.14	11.06	3.37E+00	6.09E-24	Up	1.08E+00	7.97E-02		1.19E+00	9.62E-05	Up	6.04E-01	1.39E-01		1.48E+00	4.40E-13	Up	2.11E+00	1.47E-32	Up			Unigene27078_All//1.00E-18//TC158642				
Unigene2708_All	2122	22.51	22.52	25.22	10.94	10.69	11.13	1.49	6.34	1.26	4.00E-04	9.96E-01		1.64E-01	4.06E-02		-3.27E-02	8.11E-01		2.51E-02	8.63E-01		2.09E+00	6.42E-36	Up	-2.49E-01	4.38E-01		Unigene2708_All//gi|40781599|gb|AAR89809.1|//1.00E-116//reductase 1 [Hydrangea macrophylla] >gi|40781603|gb|AAR89811.1| reductase 1 [Hydrangea macrophylla]	Unigene2708_All//2.00E-104//AT1G59960| aldo/keto reductase, putative	Unigene2708_All//0.00E+00//ES799262		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr -
Unigene27080_All	578	2.26	2.37	5.99	1.29	1.91	0.94	0.29	0.51	0.69	6.48E-02	9.18E-01		1.40E+00	9.49E-05	Up	5.60E-01	4.27E-01		-4.64E-01	6.06E-01		7.91E-01	5.63E-01		1.24E+00	2.51E-01		Unigene27080_All//gi|115459040|ref|NP_001053120.1|//4.00E-22//Os04g0482900 [Oryza sativa Japonica Group] >gi|32488468|emb|CAE03139.1| OSJNBa0081L15.1 [Oryza sativa (japonica cultivar-group)] >gi|38345260|emb|CAD41104.2| OSJNBb0011N17.21 [Oryza sativa (japonica cultivar-group)] >gi|113564691|dbj|BAF15034.1| Os04g0482900 [Oryza sativa Japonica Group] >gi|116309940|emb|CAH66972.1| H0525D09.12 [Oryza sativa (indica cultivar-group)]	Unigene27080_All//2.00E-22//AT5G40500| unknown protein	Unigene27080_All//4.00E-70//TC148542				nr +
Unigene27082_All	1260	4.78	7.40	6.21	7.47	5.33	6.06	13.15	6.30	11.60	6.32E-01	7.86E-04		3.80E-01	8.77E-02		-4.88E-01	6.12E-03		-3.03E-01	1.31E-01		-1.06E+00	8.35E-17	Down	-1.81E-01	1.59E-01		Unigene27082_All//gi|115441175|ref|NP_001044867.1|//2.00E-86//Os01g0859400 [Oryza sativa Japonica Group] >gi|113534398|dbj|BAF06781.1| Os01g0859400 [Oryza sativa Japonica Group]	Unigene27082_All//7.00E-05//AT5G66610| dual specificity protein phosphatase family protein	Unigene27082_All//0.00E+00//TC139531				nr -
Unigene27083_All	1061	124.51	330.90	203.72	96.06	197.85	182.99	85.68	139.61	93.46	1.41E+00	0.00E+00	Up	7.10E-01	2.39E-84		1.04E+00	2.89E-192	Up	9.30E-01	5.92E-133		7.04E-01	5.49E-72		1.25E-01	8.53E-03		Unigene27083_All//gi|15224852|ref|NP_179571.1|//8.00E-27//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75220226|sp|Q82199.1|C3H20_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 20; Short=AtC3H20	Unigene27083_All//1.00E-24//AT2G19810| zinc finger (CCCH-type) family protein	Unigene27083_All//0.00E+00//TC154497	C3H			nr -
Unigene27084_All	835	2.51	2.18	3.32	16.88	8.41	16.93	3.19	6.21	10.74	-1.98E-01	6.36E-01		4.04E-01	3.22E-01		-1.00E+00	5.41E-13	Down	4.00E-03	9.81E-01		9.60E-01	4.83E-05		1.75E+00	1.00E-19	Up	Unigene27084_All//gi|45752744|gb|AAS76270.1|//5.00E-62//At4g26490 [Arabidopsis thaliana]	Unigene27084_All//4.00E-63//AT4G26490| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 4 anthesis, LP.04 four leaves visible, F mature embryo stage, petal differentiation and expansion stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G56050.1); Has 263 Blast hits to 263 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 263; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene27084_All//6.00E-08//BQ410731				nr +
Unigene27087_All	494	25.21	56.21	33.52	95.29	82.11	70.03	49.30	73.18	33.47	1.16E+00	8.81E-26	Up	4.11E-01	4.00E-03		-2.15E-01	4.56E-03		-4.44E-01	2.55E-09		5.70E-01	9.53E-13		-5.59E-01	7.27E-09		Unigene27087_All//gi|224069160|ref|XP_002326289.1|//3.00E-26//copper transporter [Populus trichocarpa] >gi|222833482|gb|EEE71969.1| copper transporter [Populus trichocarpa]	Unigene27087_All//1.00E-14//AT5G20650| COPT5; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter	Unigene27087_All//0.00E+00//TC156099				nr -
Unigene2709_All	2452	10.16	25.23	12.88	10.60	18.51	11.86	19.33	15.87	26.19	1.31E+00	6.95E-69	Up	3.43E-01	6.19E-04		8.04E-01	4.30E-27		1.62E-01	1.49E-01		-2.85E-01	3.91E-05		4.38E-01	2.58E-14		Unigene2709_All//gi|225470922|ref|XP_002264409.1|//0.00E+00//PREDICTED: Myc2 bHLH protein [Vitis vinifera]	Unigene2709_All//1.00E-157//AT1G01260| basic helix-loop-helix (bHLH) family protein	Unigene2709_All//0.00E+00//TC134094	bHLH	ko04626|Plant-pathogen interaction	GO:0010468//GO:0016628//GO:0043231	nr +
Unigene27091_All	2848	1.45	0.41	0.34	5.04	5.38	3.82	3.27	1.89	6.98	-1.83E+00	3.94E-08	Down	-2.11E+00	3.55E-09	Down	9.51E-02	5.87E-01		-3.98E-01	7.20E-03		-7.87E-01	3.05E-06		1.10E+00	1.71E-21	Up	Unigene27091_All//gi|188509938|gb|ACD56624.1|//1.00E-165//UNE1-like protein [Gossypium raimondii]	Unigene27091_All//2.00E-133//AT1G29300| UNE1 (unfertilized embryo sac 1)	Unigene27091_All//0.00E+00//TC167459				nr +
Unigene27095_All	833	8.04	9.85	7.80	16.03	7.28	8.89	16.04	15.05	13.06	2.94E-01	1.64E-01		-4.39E-02	8.61E-01		-1.14E+00	4.64E-15	Down	-8.50E-01	1.79E-08		-9.16E-02	6.02E-01		-2.97E-01	3.03E-02		Unigene27095_All//gi|110289587|gb|AB666263.1|//3.00E-49//ICE-like protease p20 domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene27095_All//4.00E-30//AT4G17080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MORN motif (InterPro:IPR003409); BEST Arabidopsis thaliana protein match is: MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein /phosphatidylinositol-4-phosphate 5-kinase-related (TAIR:AT2G35170.1); Has 18005 Blast hits to 5199 proteins in 343 species: Archae - 0; Bacteria - 1726; Metazoa - 3046; Fungi - 93; Plants - 653; Viruses - 0; Other Eukaryotes - 12487 (source: NCBI BLink).	Unigene27095_All//8.00E-97//gi|164367889|gb|ES802654.1|ES802654		ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +

Unigene27098_All	1074	1.22	0.90	0.10	3.71	2.34	0.88	2.24	1.32	1.56	-4.42E-01	4.41E-01		-3.62E+00	2.81E-05	Down	-6.65E-01	2.22E-02		-2.07E+00	9.92E-10	Down	-7.62E-01	3.75E-02		-5.26E-01	1.40E-01		Unigene27098_All//gi|15219798|ref|NP_171966.1|//1.00E-143//AAA-type ATPase family protein [Arabidopsis thaliana]	Unigene27098_All//5.00E-145//AT1G04730| AAA-type ATPase family protein	Unigene27098_All//0.00E+00//BF272568				nr +
Unigene2710_All	708	27.49	3.86	7.67	30.11	24.46	31.83	64.02	12.34	25.38	-2.83E+00	1.72E-60	Down	-1.84E+00	1.21E-34	Down	-3.00E-01	9.71E-03		8.00E-02	5.97E-01		-2.38E+00	1.42E-140	Down	-1.33E+00	1.30E-65	Down	Unigene2710_All//gi|297829086|ref|XP_002882425.1|//5.00E-46//60S ribosomal protein L22-2 [Arabidopsis lyrata subsp. lyrata] >gi|297328265|gb|EFH58684.1| 60S ribosomal protein L22-2 [Arabidopsis lyrata subsp. lyrata]	Unigene2710_All//2.00E-32//AT3G05560| 60S ribosomal protein L22-2 (RPL22B)	Unigene2710_All//0.00E+00//TC155207		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene27101_All	868	7.35	14.30	9.51	7.81	9.36	7.54	5.60	46.47	3.95	9.60E-01	5.12E-09		3.71E-01	8.58E-02		2.63E-01	2.35E-01		-4.90E-02	8.57E-01		3.05E+00	4.30E-164	Up	-5.05E-01	3.25E-02		Unigene27101_All//gi|4091842|gb|AA53845.1|AC011806_22//9.00E-06//Putative shock protein [Oryza sativa]	Unigene27101_All//2.00E-06//AT2G45760| BAP2 (BOX ASSOCIATION PROTEIN 2)	Unigene27101_All//0.00E+00//gi|109889255|gb|DW518223.1|DW518223				nr -
Unigene27102_All	1805	0.35	0.31	0.27	4.80	1.43	0.80	13.09	15.68	66.70	-1.72E-01	8.29E-01		-3.90E-01	6.46E-01		-1.75E+00	9.89E-19	Down	-2.58E+00	9.26E-27	Down	2.60E-01	5.46E-03		2.35E+00	0.00E+00	Up	Unigene27102_All//gi|115484967|ref|NP_001067627.1|//8.00E-12//Os11g0251400 [Oryza sativa Japonica Group] >gi|62733062|gb|AAX95179.1| expressed protein [Oryza sativa Japonica Group] >gi|77549628|gb|ABA92425.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108864196|gb|ABG22429.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108864197|gb|ABG22430.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113644849|dbj|BAF27990.1| Os11g0251400 [Oryza sativa Japonica Group]		Unigene27102_All//1.00E-131//gi|109890353|gb|DW519317.1|DW519317				nr +
Unigene27103_All	687	3.66	3.10	3.41	3.12	3.91	2.70	292.08	142.54	133.32	-2.39E-01	5.71E-01		-1.00E-01	8.05E-01		3.27E-01	4.52E-01		-2.10E-01	6.61E-01		-1.04E+00	8.03E-187	Down	-1.13E+00	7.37E-222	Down	Unigene27103_All//gi|297843598|ref|XP_002889680.1|//5.00E-38//calmodulin binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297335522|gb|EFH65939.1| calmodulin binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene27103_All//2.00E-38//AT1G08110| lactoylglutathione lyase, putative / glyoxalase I, putative	Unigene27103_All//0.00E+00//gi|164278017|gb|ES827984.1|ES827984		ko00620|Pyruvate metabolism		nr +
Unigene27106_All	262	0.80	0.00	0.00	3.61	1.71	0.34	13.23	2.71	3.19	-9.64E+00	1.22E-01		-9.64E+00	1.46E-01		-1.08E+00	1.16E-01		-3.39E+00	3.18E-04	Down	-2.29E+00	6.49E-11	Down	-2.05E+00	5.59E-10	Down	Unigene27106_All//gi|3860333|emb|CAA10134.1|//1.00E-13//basic blue copper protein [Cicer arietinum]	Unigene27106_All//1.00E-12//AT2G02850| AHPN (PLANTACYANIN); copper ion binding / electron carrier	Unigene27106_All//5.00E-89//TC160241				nr +
Unigene27107_All	539	7.67	3.38	2.96	65.34	49.38	33.10	15.69	3.18	6.28	-1.18E+00	1.18E-04	Down	-1.37E+00	2.41E-05	Down	-4.04E-01	1.18E-06		-9.81E-01	4.75E-27		-2.30E+00	8.14E-26	Down	-1.32E+00	9.42E-13	Down	Unigene27107_All//gi|195615404|gb|ACG29532.1|//2.00E-36//chemocyanin precursor [Zea mays]	Unigene27107_All//3.00E-37//AT2G02850| AHPN (PLANTACYANIN); copper ion binding / electron carrier	Unigene27107_All//0.00E+00//TC160241				nr +
Unigene27108_All	1001	31.83	25.46	48.41	3.43	4.75	5.68	0.51	2.25	0.72	-3.22E-01	8.12E-04		6.05E-01	1.15E-14		4.67E-01	9.69E-02		7.27E-01	3.29E-03		2.15E+00	7.34E-07	Up	4.99E-01	5.01E-01		Unigene27108_All//gi|297850564|ref|XP_002893163.1|//1.00E-101//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339005|gb|EFH69422.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27108_All//2.00E-101//AT1G21460| nodulin MtN3 family protein	Unigene27108_All//0.00E+00//TC159438				nr +
Unigene27109_All	629	67.29	30.69	29.04	147.30	98.87	105.69	228.74	133.23	89.94	-1.13E+00	8.17E-38	Down	-1.21E+00	1.45E-40	Down	-5.75E-01	1.42E-31		-4.79E-01	2.82E-20		-7.80E-01	1.93E-83		-1.35E+00	2.24E-209	Down	Unigene27109_All//gi|224117452|ref|XP_002331716.1|//1.00E-113//Sec61 transport protein [Populus trichocarpa] >gi|222874322|gb|EEF11453.1| Sec61 transport protein [Populus trichocarpa]	Unigene27109_All//1.00E-105//AT2G34250| protein transport protein sec61, putative	Unigene27109_All//0.00E+00//TC132607		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export		nr -
Unigene27110_All	530	11.16	8.70	6.23	5.26	7.67	8.18	7.58	2.52	3.76	-3.59E-01	1.50E-01		-8.41E-01	9.44E-04		5.43E-01	7.53E-02		6.36E-01	3.06E-02		-1.59E+00	5.36E-08	Down	-1.01E+00	1.44E-04	Down	Unigene27110_All//gi|115479725|ref|NP_001063456.1|//1.00E-83//Os09g0474300 [Oryza sativa Japonica Group] >gi|113631689|dbj|BAF25370.1| Os09g0474300 [Oryza sativa Japonica Group]	Unigene27110_All//4.00E-68//AT2G04030| CR88; ATP binding	Unigene27110_All//1.00E-119//DW237245		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene27111_All	910	5.92	12.25	7.08	4.65	4.92	4.37	5.76	8.82	7.09	1.05E+00	2.45E-09	Up	2.58E-01	3.21E-01		8.03E-02	8.11E-01		-9.14E-02	7.73E-01		6.14E-01	7.57E-04		3.00E-01	1.54E-01		Unigene27111_All//gi|15239457|ref|NP_197936.1|//2.00E-28//CID6 (CTC-Interacting Domain 6); protein binding [Arabidopsis thaliana] >gi|34365572|gb|AAQ65100.1| At5g25540 [Arabidopsis thaliana] >gi|222422897|dbj|BAH19435.1| AT5G25540 [Arabidopsis thaliana]	Unigene27111_All//7.00E-28//AT5G25540| CID6 (CTC-Interacting Domain 6); protein binding	Unigene27111_All//0.00E+00//BF270381				nr -
Unigene27112_All	932	83.76	82.04	109.07	32.39	27.38	22.97	11.21	8.03	4.70	-2.99E-02	6.56E-01		3.81E-01	2.93E-13		-2.43E-01	1.25E-02		-4.96E-01	1.87E-07		-4.81E-01	2.33E-03		-1.25E+00	2.14E-14	Down	Unigene27112_All//gi|156105710|gb|ABU49226.1|//4.00E-73//chloroplast methionine sulfoxide reductase B2 precursor [Nicotiana tabacum]	Unigene27112_All//2.00E-69//AT4G21860| MSRB2 (methionine sulfoxide reductase B 2); peptide-methionine-(S)-S-oxide reductase	Unigene27112_All//0.00E+00//gi|13354782|gb|BG445130.1|BG445130				nr -
Unigene27113_All	939	7.19	4.80	1.53	4.56	3.01	11.25	47.32	8.99	24.40	-5.82E-01	1.01E-02		-2.23E+00	1.14E-15	Down	-6.01E-01	3.25E-02		1.30E+00	6.57E-13	Up	-2.40E+00	2.96E-139	Down	-9.56E-01	5.89E-38		Unigene27113_All//gi|150416575|gb|ABR68795.1|//1.00E-133//aquaporin gamma-TIP [Gossypium hirsutum]	Unigene27113_All//1.00E-87//AT4G01470| TIP1;3 (TONOPLAST INTRINSIC PROTEIN 1;3); urea transmembrane transporter/ water channel	Unigene27113_All//0.00E+00//TC135494				nr +
Unigene27116_All	793	3.17	6.65	2.22	6.78	5.43	8.09	0.96	1.69	1.06	1.07E+00	5.65E-05	Up	-5.15E-01	2.31E-01		-3.22E-01	2.30E-01		2.54E-01	3.37E-01		8.14E-01	1.22E-01		1.37E-01	8.36E-01					Unigene27116_All//4.00E-111//TC160766				
Unigene27117_All	534	13.13	17.65	18.35	3.54	3.03	3.55	14.49	9.31	3.36	4.27E-01	2.44E-02		4.83E-01	1.19E-02		-2.26E-01	6.37E-01		3.00E-03	9.99E-01		-6.38E-01	6.07E-04		-2.11E+00	5.03E-22	Down				Unigene27117_All//0.00E+00//TC146744				
Unigene27118_All	1058	14.59	22.22	23.76	16.15	22.03	20.87	138.27	43.93	51.89	6.07E-01	7.37E-08		7.04E-01	3.75E-10		4.48E-01	2.43E-05		3.70E-01	1.43E-03		-1.65E+00	7.42E-281	Down	-1.41E+00	2.74E-229	Down	Unigene27118_All//gi|158512763|sp|A2IBF8.1|CFI_GOSHI//1.00E-123//RecName: Full=Chalcone--flavonone isomerase; Short=Chalcone isomerase >gi|121755801|gb|ABM64798.1| chalcone isomerase [Gossypium hirsutum]	Unigene27118_All//8.00E-82//AT3G55120| TT5 (TRANSPARENT TESTA 5); chalcone isomerase	Unigene27118_All//0.00E+00//TC167565		ko00941|Flavonoid biosynthesis		nr -
Unigene27121_All	1267	0.21	0.00	0.34	1.45	0.87	1.85	2.14	0.79	2.26	-7.69E+00	6.71E-02		7.03E-01	5.54E-01		-7.42E-01	1.09E-01		3.50E-01	4.53E-01		-1.43E+00	5.82E-05	Down	8.41E-02	8.03E-01		Unigene27121_All//gi|147823314|emb|CAN77450.1|//4.00E-10//hypothetical protein [Vitis vinifera]						nr -
Unigene27122_All	1078	6.12	3.67	2.62	7.67	8.47	6.62	5.49	2.25	4.92	-7.38E-01	1.24E-03		-1.22E+00	6.37E-07	Down	1.42E-01	5.54E-01		-2.13E-01	3.58E-01		-1.29E+00	1.42E-08	Down	-1.60E-01	5.00E-01		Unigene27122_All//gi|18404847|ref|NP_565895.1|//6.00E-93//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|15912257|gb|AAL08262.1| At2g38740/T6A23.6 [Arabidopsis thaliana] >gi|195417993|gb|AAL87360.1| At2g38740/T6A23.6 [Arabidopsis thaliana] >gi|20197393|gb|AAC67344.2| expressed protein [Arabidopsis thaliana]	Unigene27122_All//3.00E-94//AT2G38740| haloacid dehalogenase-like hydrolase family protein	Unigene27122_All//0.00E+00//ES839553		ko00740|Riboflavin metabolism		nr +
Unigene27123_All	1118	1.45	2.76	1.05	9.98	8.38	10.66	7.45	8.79	1.67	9.30E-01	9.03E-03		-4.69E-01	3.87E-01		-2.53E-01	1.59E-01		9.56E-02	6.23E-01		2.38E-01	1.80E-01		-2.15E+00	3.00E-24	Down	Unigene27123_All//gi|15231124|ref|NP_191431.1|//3.00E-36//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene27123_All//2.00E-37//AT3G58720| zinc finger (C3HC4-type RING finger) family protein	Unigene27123_All//0.00E+00//CD485575				nr -
Unigene27124_All	824	0.76	1.84	1.68	2.78	1.04	0.60	1.85	1.83	1.02	1.28E+00	2.09E-02		1.14E+00	5.84E-02		-1.41E+00	4.59E-04	Down	-2.21E+00	2.84E-06	Down	-1.67E-02	1.01E+00		-8.63E-01	6.03E-02					Unigene27124_All//1.00E-06//ES833895				
Unigene27126_All	897	1103.87	900.64	1052.12	145.61	206.61	128.79	4.62	3.08	1.73	-2.94E-01	1.26E-78		-6.93E-02	3.23E-05		5.05E-01	1.56E-48		-1.77E-01	7.36E-05		-5.87E-01	2.86E-02		-1.42E+00	2.44E-07	Down	Unigene27126_All//gi|73620643|sp|Q94587.1|CRD1_EUPES//1.00E-114//RecName: Full=Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic; Short=Mg-protoporphyrin IX monomethyl ester oxidative cyclase; Flags: Precursor >gi|16033631|gb|AAL13304.1|AF417577_1 leucine zipper-containing protein [Euphorbia esula]	Unigene27126_All//2.00E-113//AT3G56940| CRD1 (COPPER RESPONSE DEFECT 1); DNA binding / magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	Unigene27126_All//0.00E+00//TC138352		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene27127_All	1469	1.14	1.38	2.50	2.48	3.45	3.87	4.06	4.72	5.23	2.76E-01	5.62E-01		1.13E+00	8.24E-04	Up	4.77E-01	7.69E-02		6.46E-01	9.48E-03		2.19E-01	3.26E-01		3.67E-01	4.84E-02		Unigene27127_All//gi|18399985|ref|NP_565538.1|//1.00E-85//GEM (GL2-EXPRESSION MODULATOR) [Arabidopsis thaliana] >gi|75160436|sp|Q8SSF8.1|GEM_ARATH RecName: Full=GLABRA2 expression modulator >gi|20197888|gb|AAM15301.1| Expressed protein [Arabidopsis thaliana] >gi|145076288|gb|ABP35534.1| GL2 expression modulator [Arabidopsis thaliana]	Unigene27127_All//4.00E-87//AT2G22475| GEM (GL2-EXPRESSION MODULATOR)	Unigene27127_All//0.00E+00//TC148322				nr +
Unigene27129_All	557	11.55	8.73	15.30	20.93	21.02	9.16	3.04	2.25	2.29	-4.04E-01	8.73E-02		4.05E-01	5.47E-02		6.40E-03	9.78E-01		-1.19E+00	1.36E-12	Down	-4.32E-01	3.70E-01		-4.08E-01	3.58E-01		Unigene27129_All//gi|94807644|gb|ABF47119.1|//9.00E-19//At1g31335 [Arabidopsis thaliana]		Unigene27129_All//0.00E+00//gi|21098239|gb|BQ410552.1|BQ410552				nr -
Unigene2713_All	2911	4.04	1.78	3.16	9.19	5.91	6.13	10.66	9.65	6.99	-1.19E+00	7.20E-12	Down	-3.54E-01	4.52E-02		-6.36E-01	3.39E-11		-5.85E-01	8.95E-09		-1.44E-01	1.35E-01		-6.08E-01	1.02E-12		Unigene2713_All//gi|297793187|ref|XP_002864478.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310313|gb|EFH40737.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2713_All//0.00E+00//AT5G56790| protein kinase family protein	Unigene2713_All//0.00E+00//ES815443		ko04626|Plant-pathogen interaction	GO:0004672//GO:0043231	nr +
Unigene27130_All	1504	0.52	0.30	0.11	2.42	3.30	2.88	3.49	0.94	3.23	-7.83E-01	3.28E-01		-2.30E+00	1.79E-02		4.48E-01	1.04E-01		2.54E-01	4.47E-01		-1.88E+00	9.31E-13	Down	-1.09E-01	6.49E-01		Unigene27130_All//gi|297842307|ref|XP_002889035.1|//1.00E-138//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334876|gb|EFH65294.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27130_All//1.00E-146//AT4G36180| leucine-rich repeat family protein	Unigene27130_All//2.00E-166//gi|78330251|gb|DT550525.1|DT550525				nr -

Unigene27131_All	803	12.18	3.28	9.48	33.44	25.43	21.93	10.95	1.67	1.64	-1.89E+00	3.97E-19	Down	-3.62E-01	6.61E-02		-3.95E-01	5.03E-05		-6.08E-01	2.09E-09		-2.72E+00	2.72E-32	Down	-2.74E+00	1.07E-33	Down	Unigene27131_All//gi|13605511|gb|AK32749.1|AF361581_1/1.00E-32//AT4g35320/F23E12_120 [Arabidopsis thaliana] >gi|16323284|gb|AAL15397.1|AT4g35320/F23E12_120 [Arabidopsis thaliana]	Unigene27131_All//2.00E-25//AT4G35320| unknown protein	Unigene27131_All//0.00E+00//gi|109854753|gb|DW483732.1|DW483732				nr +
Unigene27132_All	961	5.77	1.90	2.33	6.53	5.23	4.42	1.50	1.00	1.12	-1.60E+00	5.16E-09	Down	-1.31E+00	1.63E-06	Down	-3.20E-01	1.90E-01		-5.64E-01	1.65E-02		-5.81E-01	2.52E-01		-4.18E-01	3.91E-01		Unigene27132_All//gi|115450943|ref|NP_001049072.1|//5.00E-71//Os03g0166000 [Oryza sativa Japonica Group] >gi|108706359|gb|ABF94154.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547543|dbj|BAF10986.1| Os03g0166000 [Oryza sativa Japonica Group]	Unigene27132_All//2.00E-39//AT3G07030| nucleic acid binding	Unigene27132_All//0.00E+00//gi|78325875|gb|DT546149.1|DT546149				nr -
Unigene27133_All	1236	3.05	2.75	4.78	2.34	2.95	3.18	6.81	0.68	0.74	-1.50E-01	6.26E-01		6.50E-01	1.05E-02		3.37E-01	3.32E-01		4.44E-01	1.76E-01		-3.33E+00	9.64E-38	Down	-3.20E+00	1.28E-37	Down	Unigene27133_All//gi|73761707|gb|AZ83353.1|//0.00E+00//TTG1-like protein [Gossypium hirsutum]	Unigene27133_All//8.00E-107//AT1G12910| ATAN11 (ANTHOCYANIN11); nucleotide binding	Unigene27133_All//0.00E+00//TC129665				nr +
Unigene27134_All	1358	4.43	3.10	0.90	3.41	2.54	2.56	5.57	7.79	4.84	-5.17E-01	3.32E-02		-2.30E+00	1.66E-14	Down	-4.28E-01	1.28E-01		-4.14E-01	1.60E-01		4.83E-01	2.11E-03		-2.03E-01	3.13E-01		Unigene27134_All//gi|162279930|ref|NP_064075.2|//1.00E-65//ribosomal protein S12 [Beta vulgaris subsp. vulgaris] >gi|87248036|gb|ABD36073.1| ribosomal protein S12 [Beta vulgaris subsp. vulgaris] >gi|148491434|dbj|BAA99468.2| ribosomal protein S12 [Beta vulgaris subsp. vulgaris]	Unigene27134_All//3.00E-59//ATMG00980| ribosomal protein L2	Unigene27134_All//0.00E+00//gi|164254745|gb|ES829629.1|ES829629		ko03010|Ribosome//ko00190|Oxidative phosphorylation		nr -
Unigene27135_All	1325	2.41	1.15	0.56	0.98	1.01	1.40	4.88	4.07	6.67	-1.07E+00	2.34E-03		-2.10E+00	3.53E-07	Down	5.23E-02	9.57E-01		5.16E-01	3.15E-01		-2.63E-01	2.41E-01		4.51E-01	7.67E-03		Unigene27135_All//gi|89000925|gb|AB059052.1|//1.00E-88//At2g41990 [Arabidopsis thaliana]	Unigene27135_All//1.00E-68//AT2G41990| unknown protein	Unigene27135_All//0.00E+00//TC145532				nr -
Unigene27138_All	478	20.91	5.51	7.69	29.60	24.49	27.02	33.97	23.00	22.25	-1.92E+00	6.29E-20	Down	-1.44E+00	6.78E-13	Down	-2.73E-01	7.27E-02		-1.31E-01	4.67E-01		-5.63E-01	4.65E-06		-6.10E-01	4.05E-07		Unigene27138_All//gi|5731257|gb|AAD48836.1|AF165924_1/3.00E-06//auxin-induced basic helix-loop-helix transcription factor [Gossypium hirsutum]		Unigene27138_All//7.00E-99//TC170177		ko03040|Spliceosome		nr +
Unigene27139_All	949	47.91	54.09	36.30	112.65	130.74	83.95	62.15	27.31	43.91	1.75E-01	2.42E-02		-4.00E-01	7.63E-07		2.15E-01	6.07E-07		-4.24E-01	9.56E-19		-1.19E+00	6.22E-69	Down	-5.01E-01	1.02E-16		Unigene27139_All//gi|166343829|gb|ABY88657.1|//1.00E-129//beta-tubulin 10 [Gossypium hirsutum]	Unigene27139_All//8.00E-120//AT5G12250| TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton	Unigene27139_All//0.00E+00//TC148779		ko04145|Phagosome		nr -
Unigene27140_All	1329	1.34	0.99	1.28	6.78	5.36	9.62	37.64	133.06	86.63	-4.33E-01	3.75E-01		-6.20E-02	9.06E-01		-3.39E-01	7.96E-02		5.03E-01	1.26E-03		1.82E+00	0.00E+00	Up	1.20E+00	1.67E-139	Up	Unigene27140_All//gi|297805118|ref|XP_002870443.1|//1.00E-124//auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316279|gb|EFH46702.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27140_All//4.00E-121//AT5G35735| auxin-responsive family protein	Unigene27140_All//0.00E+00//TC175130				nr -
Unigene27141_All	1068	7.25	6.40	8.43	2.71	5.35	5.29	3.29	15.61	2.95	-1.79E-01	4.19E-01		2.17E-01	3.20E-01		9.84E-01	3.62E-05		9.66E-01	1.03E-04		2.25E+00	1.13E-48	Up	-1.57E-01	6.09E-01		Unigene27141_All//gi|224053426|ref|XP_002297813.1|//6.00E-61//f-box family protein [Populus trichocarpa] >gi|222845071|gb|EEE82618.1| f-box family protein [Populus trichocarpa]	Unigene27141_All//2.00E-46//AT5G24560| AtPP2-B12 (Phloem protein 2-B12); carbohydrate binding	Unigene27141_All//1.00E-43//ES827311				nr +
Unigene27142_All	1357	1.70	4.33	1.77	3.01	3.20	3.66	3.58	3.85	4.46	1.35E+00	1.62E-07	Up	5.78E-02	8.94E-01		8.71E-02	8.28E-01		2.82E-01	3.52E-01		1.04E-01	6.90E-01		3.17E-01	1.44E-01		Unigene27142_All//gi|115464099|ref|NP_001055649.1|//9.00E-33//Os05g0436900 [Oryza sativa Japonica Group] >gi|113576200|dbj|BAF17563.1| Os05g0436900 [Oryza sativa Japonica Group]	Unigene27142_All//6.00E-34//AT5G41060| zinc finger (DHHC type) family protein	Unigene27142_All//0.00E+00//gi|13244602|gb|BE052085.2|BE052085				nr +
Unigene27143_All	731	5.15	25.16	6.85	13.77	21.53	13.22	1.74	9.55	32.54	2.29E+00	1.28E-44	Up	4.10E-01	1.50E-01		6.45E-01	9.10E-07		-5.81E-02	7.77E-01		2.46E+00	4.74E-23	Up	4.23E+00	2.12E-129	Up	Unigene27143_All//gi|75158446|sp|Q8RUN2.1|LOG1_ARATH//2.00E-26//RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1; AltName: Full=Protein LONELY GUY 1 >gi|20197602|gb|AAM15149.1| expressed protein [Arabidopsis thaliana] >gi|20197733|gb|AAM15229.1| expressed protein [Arabidopsis thaliana]	Unigene27143_All//8.00E-28//AT2G28305| unknown protein	Unigene27143_All//2.00E-69//TC178682				nr -
Unigene27144_All	904	30.91	11.10	7.07	18.90	18.06	19.63	31.10	14.84	14.72	-1.48E+00	1.03E-37	Down	-2.13E+00	6.05E-60	Down	-6.60E-02	6.95E-01		5.49E-02	7.22E-01		-1.07E+00	3.45E-28	Down	-1.08E+00	1.51E-29	Down	Unigene27144_All//gi|22329049|ref|NP_194864.2|//1.00E-36//selenium binding [Arabidopsis thaliana] >gi|17065486|gb|AAL32897.1| Unknown protein [Arabidopsis thaliana]	Unigene27144_All//3.00E-33//AT4G31360| selenium binding	Unigene27144_All//0.00E+00//TC138181				nr -
Unigene27145_All	1143	1.19	1.95	0.23	1.22	2.77	3.64	4.22	1.02	3.62	7.13E-01	9.64E-02		-2.35E+00	7.62E-04	Down	1.18E+00	5.52E-04	Up	1.57E+00	5.24E-07	Up	-2.04E+00	4.97E-13	Down	-2.18E-01	3.96E-01		Unigene27145_All//gi|57869094|gb|AAW57535.1|//3.00E-87//pollen-specific kinase partner protein [Solanum lycopersicum]	Unigene27145_All//3.00E-82//AT1G52240| ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor	Unigene27145_All//0.00E+00//TC175517				nr +
Unigene27146_All	885	0.95	1.60	2.29	2.48	2.41	1.94	2.58	0.90	2.07	7.61E-01	1.74E-01		1.27E+00	8.67E-03		-3.79E-02	9.29E-01		-3.53E-01	4.57E-01		-1.52E+00	1.21E-04	Down	-3.17E-01	3.98E-01		Unigene27146_All//gi|18422700|ref|NP_568665.1|//2.00E-81//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|223635755|sp|Q56XR6.2|PP421_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g46680	Unigene27146_All//1.00E-82//AT5G46680| pentatricopeptide (PPR) repeat-containing protein	Unigene27146_All//0.00E+00//DT464174				nr +
Unigene27147_All	1929	0.27	1.31	0.08	1.16	0.71	0.33	1.14	2.30	19.00	2.28E+00	1.11E-06	Up	-1.71E+00	1.40E-01		-7.03E-01	8.81E-02		-1.83E+00	5.88E-05	Down	1.01E+00	9.56E-05	Up	4.06E+00	1.38E-193	Up	Unigene27147_All//gi|12003396|gb|AAG43555.1|AF211537_1/8.00E-82//Avr9/Cf-9 rapidly elicited protein 137 [Nicotiana tabacum]	Unigene27147_All//1.00E-66//AT3G23160| unknown protein	Unigene27147_All//0.00E+00//TC143545				nr -
Unigene27148_All	965	1.41	3.52	2.76	23.33	21.62	10.39	215.30	71.20	96.89	1.32E+00	1.54E-04	Up	9.69E-01	1.68E-02		-1.10E-01	4.23E-01		-1.17E+00	4.85E-23	Down	-1.60E+00	0.00E+00	Down	-1.15E+00	2.33E-236	Down	Unigene27148_All//gi|15232289|ref|NP_191587.1|//1.00E-39//UCC3 (UCLACYANIN 3); copper ion binding / electron carrier [Arabidopsis thaliana] >gi|1518059|gb|AAB07009.1| blue-copper binging protein III [Arabidopsis thaliana] >gi|3395770|gb|AAC32461.1| uclacyanin 3 [Arabidopsis thaliana] >gi|75762004|emb|CAB87865.1| uclacyanin 3 [Arabidopsis thaliana] >gi|94442505|gb|ABF19040.1| At3g60280 [Arabidopsis thaliana]	Unigene27148_All//5.00E-27//AT3G60280| UCC3 (UCLACYANIN 3); copper ion binding / electron carrier	Unigene27148_All//0.00E+00//gi|13247733|gb|BF271992.2|BF271992				nr -
Unigene27149_All	2419	36.66	15.33	29.65	13.28	16.41	14.86	0.14	0.10	0.41	-1.26E+00	1.40E-92	Down	-3.06E-01	6.00E-08		3.05E-01	1.47E-04		1.62E-01	9.99E-02		-4.31E-01	7.03E-01		1.56E+00	1.33E-02		Unigene27149_All//gi|297811451|ref|XP_002873609.1|//0.00E+00//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319446|gb|EFH49868.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27149_All//0.00E+00//AT5G13400| proton-dependent oligopeptide transport (POT) family protein	Unigene27149_All//0.00E+00//TC140896				nr -
Unigene27150_All	1153	13.34	1.98	1.15	103.08	107.31	121.70	4.14	0.15	0.38	-2.75E+00	1.51E-46	Down	-3.53E+00	8.48E-57	Down	5.79E-02	3.06E-01		2.40E-01	1.11E-08		-4.84E+00	3.52E-28	Down	-3.45E+00	4.00E-23	Down	Unigene27150_All//gi|1008904|gb|AAB39950.1|//1.00E-162//xyloglucan endotransglycosylase [Tropaeolum majus]	Unigene27150_All//2.00E-145//AT5G13870| EXGT-A4 (ENDOXYLOGLUCAN TRANSFERASE A4); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase	Unigene27150_All//0.00E+00//TC139183				nr -
Unigene27151_All	1344	1.05	1.77	0.63	5.00	6.58	3.26	8.87	5.69	4.36	7.53E-01	6.78E-02		-7.30E-01	2.21E-01		3.96E-01	4.20E-02		-6.18E-01	5.79E-03		-6.41E-01	1.14E-05		-1.03E+00	4.50E-12	Down	Unigene27151_All//gi|5042406|gb|AAD38245.1|AC006193_1//3.00E-48//Hypothetical Protein [Arabidopsis thaliana] >gi|6633823|gb|AAF19682.1|AC009519_16 F1N19.26 [Arabidopsis thaliana]	Unigene27151_All//3.00E-36//AT1G64690| unknown protein	Unigene27151_All//0.00E+00//TC166656				nr +
Unigene27152_All	1031	0.36	3.24	2.84	13.24	18.30	17.08	9.35	4.58	2.67	3.19E+00	4.99E-12	Up	3.00E+00	1.14E-09	Up	4.67E-01	9.68E-05		3.68E-01	5.68E-03		-1.03E+00	1.17E-09	Down	-1.81E+00	2.24E-22	Down	Unigene27152_All//gi|224123262|ref|XP_002319035.1|//2.00E-58//histidine phosphotransfer protein [Populus trichocarpa] >gi|222857411|gb|EEE94958.1| histidine phosphotransfer protein [Populus trichocarpa]	Unigene27152_All//1.00E-44//AT3G21510| AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 1); histidine phosphotransfer kinase	Unigene27152_All//0.00E+00//DW505021				nr -
Unigene27153_All	2052	0.15	0.47	0.03	0.87	0.74	0.86	2.45	3.97	5.57	1.62E+00	3.15E-02		-2.56E+00	1.59E-01		-2.43E-01	6.16E-01		-2.58E-02	9.47E-01		6.96E-01	1.19E-04		1.18E+00	2.66E-14	Up	Unigene27153_All//gi|66792640|gb|AAV56422.1|//8.00E-57//At4g22860 [Arabidopsis thaliana]	Unigene27153_All//2.00E-45//AT4G22860| unknown protein	Unigene27153_All//0.00E+00//TC168929				nr -
Unigene27154_All	1327	0.75	2.98	2.05	8.07	6.28	4.32	2.36	2.20	2.01	1.99E+00	1.32E-08	Up	1.45E+00	4.85E-04	Up	-3.62E-01	3.50E-02		-9.01E-01	1.40E-07		-9.68E-02	7.73E-01		-2.29E-01	4.83E-01		Unigene27154_All//gi|1143711|gb|AAA84891.1|//2.00E-67//non-green plastid inner envelope membrane protein precursor [Brassica oleracea var. botrytis]	Unigene27154_All//1.00E-54//AT2G38550| unknown protein	Unigene27154_All//0.00E+00//TC175349				nr +
Unigene27155_All	1660	0.76	0.12	0.80	3.33	2.32	5.39	2.01	3.55	3.46	-2.63E+00	3.16E-04	Down	8.45E-02	8.85E-01		-5.20E-01	3.36E-02		6.94E-01	2.56E-04		8.19E-01	1.71E-04		7.80E-01	2.96E-04		Unigene27155_All//gi|35187439|gb|AAQ84311.1|//2.00E-40//fiber protein Fb17 [Gossypium barbadense]	Unigene27155_All//6.00E-13//AT4G34590| GBF6 (G-BOX BINDING FACTOR 6); DNA binding / protein heterodimerization/ transcription factor	Unigene27155_All//1.00E-56//gi|54123099|gb|CO498608.1|CO498608	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene27158_All	538	39.19	49.73	17.92	65.00	54.02	72.61	91.55	56.71	42.95	3.44E-01	1.17E-03		-1.13E+00	2.49E-18	Down	-2.67E-01	2.27E-03		1.60E-01	8.79E-02		-6.91E-01	1.02E-23		-1.09E+00	4.73E-52	Down			Unigene27158_All//0.00E+00//gi|164271200|gb|ES823028.1|ES823028				
Unigene27159_All	1137	0.18	42.16	0.28	0.61	0.48	0.95	3.94	3.86	34.06	7.84E+00	1.39E-267	Up	6.10E-01	6.25E-01		-3.40E-01	6.80E-01		6.36E-01	3.73E-01		-3.03E-02	9.30E-01		3.11E+00	2.44E-163	Up	Unigene27159_All//gi|2582800|emb|CAA72341.1|//6.00E-95//protein phosphatase 2C [Medicago sativa]	Unigene27159_All//9.00E-76//AT2G30020| protein phosphatase 2C, putative / PP2C, putative	Unigene27159_All//0.00E+00//gi|109836609|gb|DW235170.1|DW235170				nr -

Unigene27160_All	1441	0.44	42.12	0.74	0.10	0.19	0.09	1.67	4.26	21.01	6.60E+00	0.00E+00	Up	7.62E-01	2.69E-01		8.83E-01	5.95E-01		-1.42E-01	9.43E-01		1.35E+00	1.86E-09	Up	3.65E+00	1.84E-147	Up	Unigene27160_All//gi|75223238|sp|Q80871.1|P2C25_ARATH//1.00E-130//RecName: Full=Probable protein phosphatase 2C 25; Short=AtPP2C25; AltName: Full=Protein phosphatase AP2C1	Unigene27160_All//2.00E-112//AT2G30020| protein phosphatase 2C, putative / PP2C, putative	Unigene27160_All//0.00E+00//gi|109836609|gb|DW235170.1|DW235170				nr -
Unigene27161_All	1196	132.99	37.49	219.10	22.53	23.96	66.61	0.00	0.00	0.00	-1.83E+00	4.10E-287	Down	7.20E-01	9.70E-105		8.83E-02	4.86E-01		1.56E+00	1.38E-123	Up	null	null		null	null		Unigene27161_All//gi|224077338|ref|XP_002305292.1|//1.00E-91//cytochrome P450 [Populus trichocarpa] >gi|222848256|gb|EEE85803.1| cytochrome P450 [Populus trichocarpa]	Unigene27161_All//4.00E-66//AT3G25180| CYP82G1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene27161_All//0.00E+00//gi|48827534|gb|CO125924.1|CO125924		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene27162_All	1039	1.71	7.85	6.46	7.96	5.14	9.61	17.13	5.99	40.61	2.20E+00	3.40E-19	Up	1.92E+00	5.81E-13	Up	-6.32E-01	7.61E-04		2.72E-01	1.70E-01		-1.52E+00	1.03E-30	Down	1.25E+00	1.79E-54	Up	Unigene27162_All//gi|21592813|gb|AAM64762.1|//1.00E-100//ids4-like protein [Arabidopsis thaliana]	Unigene27162_All//1.00E-100//AT5G20150| SPX1 (SPX DOMAIN GENE 1)	Unigene27162_All//0.00E+00//gi|109852446|gb|DW481425.1|DW481425				nr +
Unigene27163_All	854	198.93	226.05	229.40	26.66	31.53	28.24	2.67	5.82	2.80	1.84E-01	5.19E-07		2.06E-01	3.47E-08		2.42E-01	2.16E-02		8.32E-02	5.58E-01		1.12E+00	4.71E-06	Up	6.62E-02	8.67E-01		Unigene27163_All//gi|297847890|ref|XP_002891826.1|//5.00E-38//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337668|gb|EFH68085.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27163_All//8.00E-36//AT2G44300| lipid transfer protein-related	Unigene27163_All//0.00E+00//TC143206				nr +
Unigene27164_All	1303	6.46	1.24	3.23	17.55	19.45	12.82	2.69	2.31	1.68	-2.38E+00	6.85E-22	Down	-1.00E+00	1.82E-06	Down	1.49E-01	2.25E-01		-4.52E-01	5.03E-05		-2.22E-01	5.03E-01		-6.80E-01	1.61E-02		Unigene27164_All//gi|15238328|ref|NP_199039.1|//1.00E-165//scp142 (serine carboxypeptidase-like 42); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75170531|sp|Q9FN05.1|SCP42_ARATH RecName: Full=Serine carboxypeptidase-like 42; Flags: Precursor >gi|136055557|gb|AAK32772.1|AF36160 4_1 AT5g42240/K5J14_4 [Arabidopsis thaliana] >gi|10177009|dbj|BAB10197.1| serine carboxypeptidase II-like [Arabidopsis thaliana] >gi|23505957|gb|AAN28838.1| At5g42240/K5J14_4 [Arabidopsis thaliana]	Unigene27164_All//4.00E-151//AT5G42240| scp142 (serine carboxypeptidase-like 42); serine-type carboxypeptidase	Unigene27164_All//0.00E+00//gi|78349492|gb|DT569766.1|DT569766				nr -
Unigene27165_All	728	57.06	55.54	69.71	6.98	16.22	10.61	4.53	4.13	6.57	-3.90E-02	6.74E-01		2.89E-01	1.92E-04		1.22E+00	4.75E-14	Up	6.04E-01	3.68E-03		-1.32E-01	6.87E-01		5.36E-01	2.50E-02		Unigene27165_All//gi|12003388|gb|AAG43551.1|AF211533_1/9.00E-29//Avr9/Cf-9 rapidly elicited protein 146 [Nicotiana tabacum]	Unigene27165_All//4.00E-26//AT1G32140| unknown protein	Unigene27165_All//0.00E+00//DW240057				nr -
Unigene27166_All	1076	26.55	28.40	38.01	2.82	9.92	5.12	4.87	3.77	4.89	9.70E-02	3.82E-01		5.18E-01	1.39E-09		1.81E+00	1.87E-22	Up	8.59E-01	6.47E-04		-3.71E-01	1.29E-01		4.40E-03	9.84E-01		Unigene27166_All//gi|12003388|gb|AAG43551.1|AF211533_1/9.00E-34//Avr9/Cf-9 rapidly elicited protein 146 [Nicotiana tabacum]	Unigene27166_All//5.00E-31//AT1G32140| unknown protein	Unigene27166_All//0.00E+00//DW240057				nr +
Unigene27169_All	1115	2.39	0.82	2.10	1.65	1.61	2.43	2.84	1.54	1.75	-1.55E+00	1.50E-04	Down	-1.88E-01	6.24E-01		-4.16E-02	9.26E-01		5.56E-01	1.65E-01		-8.88E-01	4.35E-03		-7.00E-01	1.95E-02		Unigene27169_All//gi|297800842|ref|XP_002868305.1|//3.00E-81//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297314141|gb|EFH44564.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene27169_All//1.00E-82//AT4G14190| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT3G42630.1); Has 7409 Blast hits to 2639 proteins in 94 species: Archae - 1; Bacteria - 0; Metazoa - 60; Fungi - 16; Plants - 7130; Viruses - 0; Other Eukaryotes - 202 (source: NCBI BLink).	Unigene27169_All//0.00E+00//gi|164323016|gb|ES801506.1|ES801506				nr -
Unigene2717_All	1139	10.75	10.72	9.96	17.14	12.94	17.76	38.09	23.45	17.94	-3.70E-03	9.79E-01		-1.10E-01	5.71E-01		-4.06E-01	5.30E-04		5.12E-02	7.21E-01		-7.00E-01	1.92E-21		-1.09E+00	1.56E-45	Down	Unigene2717_All//gi|30023682|gb|AAP13374.1|//3.00E-95//At3g51610 [Arabidopsis thaliana]	Unigene2717_All//3.00E-95//AT3G51610| unknown protein	Unigene2717_All//0.00E+00//TC139146			GO:0006950//GO:0031410	nr +
Unigene27171_All	836	3.63	1.70	0.38	2.80	2.35	2.38	5.77	3.35	2.81	-1.10E+00	2.49E-03		-3.25E+00	1.12E-10	Down	-2.54E-01	5.74E-01		-2.37E-01	6.34E-01		-7.83E-01	1.32E-03		-1.04E+00	1.76E-05	Down	Unigene27171_All//gi|225428412|ref|XP_002286254.1|//8.00E-49//PREDICTED: similar to Bifunctional dihydrofolate reductase-thymidylate synthase [Vitis vinifera]	Unigene27171_All//3.00E-38//AT2G16370| THY-1 (THYMIDYLATE SYNTHASE 1); dihydrofolate reductase/ thymidylate synthase	Unigene27171_All//0.00E+00//gi|11209970|gb|BF278900.1|BF278900		ko00240|Pyrimidine metabolism//ko00670|One carbon pool by folate//ko00790|Folate biosynthesis		nr +
Unigene27173_All	667	2.20	1.22	2.24	6.12	5.58	6.84	5.83	2.26	1.25	-8.54E-01	1.22E-01		2.54E-02	9.82E-01		-1.35E-01	6.93E-01		1.59E-01	6.18E-01		-1.37E+00	2.08E-06	Down	-2.22E+00	3.69E-12	Down	Unigene27173_All//gi|14190517|gb|AAK55739.1|AF380658_1/2.00E-45//At1g53031 [Arabidopsis thaliana] >gi|15809782|gb|AAL06819.1| At1g53031 [Arabidopsis thaliana]	Unigene27173_All//3.00E-46//AT1G53035| unknown protein	Unigene27173_All//0.00E+00//TC152566				nr -
Unigene27174_All	812	24.49	23.46	8.00	14.78	11.45	14.35	12.08	5.46	12.51	-6.15E-02	6.43E-01		-1.61E+00	1.76E-29	Down	-3.69E-01	2.07E-02		-4.31E-02	8.23E-01		-1.15E+00	1.56E-11	Down	5.06E-02	7.72E-01		Unigene27174_All//gi|28301674|emb|CAB62264.3|//4.00E-42//calcium-binding protein [Lotus japonicus]	Unigene27174_All//3.00E-40//AT3G07490| AGD11 (ARF-GAP domain 11); calcium ion binding	Unigene27174_All//0.00E+00//TC166626		ko04626|Plant-pathogen interaction		nr -
Unigene27176_All	782	82.50	31.36	58.29	11.78	16.07	20.62	8.43	17.58	7.90	-1.40E+00	3.68E-79	Down	-5.01E-01	6.53E-14		4.48E-01	3.59E-03		8.07E-01	3.34E-09		1.06E+00	5.00E-14	Up	-9.51E-02	6.58E-01		Unigene27176_All//gi|6056421|gb|AAF02885.1|AC009525_19/1.00E-44//Unknown protein [Arabidopsis thaliana] >gi|14423480|gb|AAK62422.1|AF38697 7_1 Unknown protein [Arabidopsis thaliana]	Unigene27176_All//8.00E-46//AT1G02816| unknown protein	Unigene27176_All//0.00E+00//gi|109875999|gb|DW504973.1|DW504973				nr -
Unigene2718_All	1131	20.54	22.22	17.70	30.57	26.88	22.52	25.61	18.74	11.87	1.14E-01	3.68E-01		-2.14E-01	8.69E-02		-1.85E-01	4.90E-02		-4.41E-01	6.31E-07		-4.51E-01	4.68E-07		-1.11E+00	9.60E-32	Down	Unigene2718_All//gi|115455313|ref|NP_001051257.1|//1.00E-101//Os03g0747300 [Oryza sativa Japonica Group] >gi|113549728|dbj|BAF13171.1| Os03g0747300 [Oryza sativa Japonica Group]	Unigene2718_All//7.00E-127//AT5G47420| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF124 (InterPro:IPR002838), Tryptophan RNA-binding attenuator protein-like (InterPro:IPR016031); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G17420.1); Has 568 Blast hits to 568 proteins in 252 species: Archae - 56; Bacteria - 410; Metazoa - 0; Fungi - 8; Plants - 37; Viruses - 0; Other Eukaryotes - 57 (source: NCBI BLink).	Unigene2718_All//0.00E+00//TC130367				nr +
Unigene27180_All	922	8.68	51.38	14.84	13.89	30.81	66.57	11.88	41.80	32.19	2.57E+00	1.74E-130	Up	7.74E-01	9.08E-07		1.15E+00	1.52E-30	Up	2.26E+00	2.83E-156	Up	1.82E+00	1.62E-84	Up	1.44E+00	6.38E-48	Up	Unigene27180_All//gi|224073168|ref|XP_002304005.1|//6.00E-41//f-box family protein [Populus trichocarpa] >gi|222841437|gb|EEE78984.1| f-box family protein [Populus trichocarpa]		Unigene27180_All//0.00E+00//TC173611				nr +
Unigene27183_All	934	4.03	6.51	6.33	3.89	5.75	9.04	7.33	12.04	36.30	6.91E-01	4.03E-03		6.50E-01	1.05E-02		5.63E-01	2.67E-02		1.22E+00	1.97E-09	Up	7.15E-01	2.30E-06		2.31E+00	2.37E-103	Up	Unigene27183_All//gi|4204289|gb|AAD10670.1|//2.00E-29//Unknown protein [Arabidopsis thaliana]	Unigene27183_All//9.00E-26//AT1G04000| unknown protein	Unigene27183_All//0.00E+00//TC178710				nr +
Unigene27184_All	1147	2.28	1.41	1.53	8.60	6.30	3.43	2.88	2.30	1.84	-6.90E-01	7.70E-02		-5.74E-01	1.61E-01		-4.48E-01	1.04E-02		-1.33E+00	1.27E-12	Down	-3.25E-01	3.25E-01		-6.43E-01	2.83E-02		Unigene27184_All//gi|9755452|gb|AAF98213.1|AC007152_9//7.00E-16//Hypothetical protein [Arabidopsis thaliana]	Unigene27184_All//6.00E-11//AT5G38300| unknown protein	Unigene27184_All//1.00E-09//DW500218				nr +
Unigene27186_All	909	12.84	14.49	5.98	20.06	18.07	24.15	11.77	13.06	10.30	1.75E-01	3.05E-01		-1.10E+00	4.70E-10	Down	-1.51E-01	3.12E-01		2.68E-01	2.79E-02		1.50E-01	3.84E-01		-1.92E-01	2.42E-01		Unigene27186_All//gi|8954043|gb|AAF82217.1|AC067971_25/1.00E-28//Strong similarity to a mitochondrial carrier protein from Ribes nigrum gb|AJ007380. It contains a mitochondrial carrier protein domain PF|00153. ESTs gb|T46775, gb|R90539, gb|AW029646 and gb|AA605443 come from this gene [Arabidopsis thaliana]	Unigene27186_All//1.00E-08//AT1G07020| unknown protein	Unigene27186_All//0.00E+00//gi|21102593|gb|BQ414906.1|BQ414906				nr +
Unigene27189_All	1207	51.63	14.15	13.37	166.61	133.20	54.07	26.90	5.26	5.22	-1.87E+00	3.13E-116	Down	-1.95E+00	5.04E-119	Down	-3.23E-01	1.58E-23		-1.62E+00	0.00E+00	Down	-2.35E+00	9.08E-100	Down	-2.37E+00	1.42E-103	Down	Unigene27189_All//gi|15221033|ref|NP_173261.1|//1.00E-115//ATLP-1 [Arabidopsis thaliana] >gi|27735265|sp|P50699.2|TLPH_ARATH RecName: Full=Thaumatin-like protein; Flags: Precursor	Unigene27189_All//3.00E-115//AT1G73620| thaumatin-like protein, putative / pathogenesis-related protein, putative	Unigene27189_All//0.00E+00//TC131991				nr +
Unigene27195_All	763	34.42	80.15	57.02	104.53	69.01	99.44	125.95	362.30	64.64	1.22E+00	9.09E-61	Up	7.28E-01	4.01E-18		-5.99E-01	2.81E-29		-7.19E-02	3.11E-01		1.52E+00	0.00E+00	Up	-9.62E-01	5.96E-82		Unigene27195_All//gi|297840523|ref|XP_002888143.1|//7.00E-52//DC1 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333984|gb|EFH64402.1| DC1 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene27195_All//1.00E-52//AT1G60420| DC1 domain-containing protein	Unigene27195_All//0.00E+00//TC145938				nr -
Unigene27196_All	719	20.59	52.64	28.00	33.32	47.85	56.47	42.22	67.37	71.92	1.35E+00	2.00E-44	Up	4.43E-01	5.06E-04		5.22E-01	7.07E-10		7.61E-01	3.52E-20		6.74E-01	2.29E-22		7.68E-01	1.85E-30		Unigene27196_All//gi|297841455|ref|XP_002888609.1|//3.00E-84//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334450|gb|EFH64868.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27196_All//6.00E-85//AT1G67580| protein kinase family protein	Unigene27196_All//0.00E+00//TC177473				nr -

Unigene27197_A11	1304	2.09	1.71	0.78	2.37	2.38	2.77	6.45	3.14	4.80	-2.87E-01	4.60E-01		-1.43E+00	5.90E-04	Down	5.00E-03	1.00E+00		2.26E-01	5.49E-01		-1.04E+00	1.20E-08	Down	-4.28E-01	1.39E-02		Unigene27197_A11//gi|224110992|ref|XP_002332999.1|//7.00E-56//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834484|gb|EEE72961.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene27197_A11//5.00E-13//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene27197_A11//2.00E-95//BG443054		ko04626|Plant-pathogen interaction		nr +
Unigene27198_A11	1642	1.05	1.54	0.29	3.73	1.87	1.87	3.12	2.09	1.19	5.53E-01	1.67E-01		-1.85E+00	1.14E-03		-9.99E-01	6.60E-06		-9.97E-01	2.36E-05		-5.78E-01	1.47E-02		-1.39E+00	1.20E-08	Down	Unigene27198_A11//gi|224134186|ref|XP_002327777.1|//7.00E-89//short internodes 2 [Populus trichocarpa] >gi|222836862|gb|EEE75255.1| short internodes 2 [Populus trichocarpa]	Unigene27198_A11//8.00E-68//AT1G75520| SRS5 (SHI-RELATED SEQUENCE 5)	Unigene27198_A11//3.00E-51//DT527409	SRS			nr -
Unigene27199_A11	946	3.98	1.98	3.66	4.00	3.46	2.63	6.35	3.23	2.61	-1.01E+00	1.56E-03		-1.22E-01	7.08E-01		-2.11E-01	5.41E-01		-6.08E-01	5.61E-02		-9.77E-01	7.36E-06		-1.28E+00	6.30E-09	Down	Unigene27199_A11//gi|18417725|ref|NP_567865.1|//1.00E-111//proton extrusion protein-related [Arabidopsis thaliana]	Unigene27199_A11//7.00E-113//AT4G31040| proton extrusion protein-related	Unigene27199_A11//0.00E+00//TC165568				nr +
Unigene2720_A11	1089	0.62	1.35	0.44	5.08	4.77	2.45	2.68	1.84	0.29	1.11E+00	4.53E-02		-5.05E-01	5.82E-01		-8.87E-02	7.86E-01		-1.05E+00	2.68E-05	Down	-5.40E-01	1.05E-01		-3.19E+00	1.79E-13	Down	Unigene2720_A11//gi|34146840|gb|AAQ62428.1|//8.00E-74//At5g23100 [Arabidopsis thaliana]	Unigene2720_A11//1.00E-71//AT5G23100| unknown protein	Unigene2720_A11//0.00E+00//gi|78331037|gb|DT551311.1|DT551311			GO:0043231	nr -
Unigene27200_A11	835	3.76	2.73	3.57	4.95	3.05	1.84	2.99	2.55	1.38	-4.61E-01	1.96E-01		-7.41E-02	8.38E-01		-6.98E-01	1.37E-02		-1.43E+00	2.99E-06	Down	-2.27E-01	5.78E-01		-1.11E+00	1.54E-03		Unigene27200_A11//gi|18397705|ref|NP_564367.1|//7.00E-12//integral membrane HRF1 family protein [Arabidopsis thaliana] >gi|145324088|ref|NP_001077633.1| integral membrane HRF1 family protein [Arabidopsis thaliana]	Unigene27200_A11//1.00E-13//AT1G30890| integral membrane HRF1 family protein					nr +
Unigene27203_A11	779	2.69	2.86	3.14	23.98	19.85	23.89	10.20	13.04	2.97	9.12E-02	8.27E-01		2.27E-01	6.19E-01		-2.73E-01	3.29E-02		-5.60E-03	9.64E-01		3.54E-01	3.19E-02		-1.78E+00	3.21E-18	Down	Unigene27203_A11//gi|195648500|gb|ACG43718.1|//2.00E-57//actin-depolymerizing factor 5 [Zea mays]	Unigene27203_A11//3.00E-43//AT2G31200| ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); actin binding	Unigene27203_A11//0.00E+00//gi|109870472|gb|DW499448.1|DW499448				nr +
Unigene27204_A11	1112	5.41	3.51	2.63	14.69	15.42	11.13	2.36	5.34	2.51	-6.25E-01	9.50E-03		-1.04E+00	4.47E-05	Down	6.98E-02	6.81E-01		-4.01E-01	3.45E-03		1.18E+00	1.43E-07	Up	8.93E-02	7.92E-01		Unigene27204_A11//gi|145322966|ref|NP_001030949.2|//8.00E-54//nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana]	Unigene27204_A11//1.00E-46//AT2G01940| nucleic acid binding / transcription factor/ zinc ion binding	Unigene27204_A11//0.00E+00//gi|109890213|gb|DW519177.1|DW519177	C2H2			nr -
Unigene27209_A11	811	1.29	3.25	2.30	3.38	2.21	2.39	1.30	1.24	0.54	1.33E+00	9.56E-04	Up	8.33E-01	9.48E-02		-6.14E-01	9.73E-02		-4.97E-01	2.14E-01		-7.54E-02	9.09E-01		-1.27E+00	2.97E-02		Unigene27209_A11//gi|297721647|ref|NP_001173186.1|//5.00E-39//Os02g0802800 (Oryza sativa Japonica Group) >gi|255671323|dbj|BAH91915.1| Os02g0802800 (Oryza sativa Japonica Group)		Unigene27209_A11//0.00E+00//DW489187				nr +
Unigene2721_A11	1065	2.90	1.90	0.95	17.03	11.90	9.50	1.39	3.69	1.38	-6.07E-01	8.64E-02		-1.61E+00	4.40E-05	Down	-5.17E-01	1.62E-05		-8.42E-01	4.16E-11		1.41E+00	1.08E-06	Up	-5.60E-03	9.85E-01		Unigene2721_A11//gi|34146840|gb|AAQ62428.1|//1.00E-78//At5g23100 [Arabidopsis thaliana]	Unigene2721_A11//6.00E-80//AT5G23100| unknown protein	Unigene2721_A11//0.00E+00//DW508843			GO:0043231	nr -
Unigene27211_A11	701	8.43	5.85	9.34	7.89	8.01	7.54	26.00	17.59	10.06	-5.27E-01	3.14E-02		1.48E-01	5.86E-01		2.17E-02	9.59E-01		-6.54E-02	8.15E-01		-5.64E-01	1.02E-06		-1.37E+00	5.89E-28	Down	Unigene27211_A11//gi|30102524|gb|AAP21180.1|//3.00E-23//At3g08610 [Arabidopsis thaliana]	Unigene27211_A11//7.00E-24//AT3G08610| unknown protein	Unigene27211_A11//0.00E+00//TC160649		ko00190|Oxidative phosphorylation		nr +
Unigene27212_A11	1312	1.36	0.39	0.73	7.48	2.83	4.58	137.89	95.51	146.91	-1.81E+00	6.59E-04	Down	-8.92E-01	8.34E-02		-1.40E+00	2.47E-15	Down	-7.08E-01	7.30E-05		-5.30E-01	4.05E-53		9.13E-02	7.13E-03		Unigene27212_A11//gi|224072526|ref|XP_002303770.1|//5.00E-53//SAUR family protein [Populus trichocarpa] >gi|222841202|gb|EEE78749.1| SAUR family protein [Populus trichocarpa]	Unigene27212_A11//2.00E-23//AT5G60760| auxin-responsive family protein	Unigene27212_A11//0.00E+00//TC152425				nr +
Unigene27213_A11	1022	9.37	2.13	3.80	17.55	12.67	11.18	8.03	1.39	1.60	-2.14E+00	8.10E-22	Down	-1.30E+00	1.17E-10	Down	-4.70E-01	1.09E-04		-6.50E-01	3.04E-07		-2.53E+00	6.69E-28	Down	-2.33E+00	3.12E-26	Down	Unigene27213_A11//gi|15242476|ref|NP_199382.1|//3.00E-58//NLI interacting factor (NIF) family protein [Arabidopsis thaliana]	Unigene27213_A11//9.00E-59//AT5G45700| NLI interacting factor (NIF) family protein	Unigene27213_A11//0.00E+00//gi|21098383|gb|BQ410696.1|BQ410696				nr -
Unigene27215_A11	980	0.91	0.78	0.54	4.22	2.60	1.20	1.68	1.75	1.91	-2.27E-01	7.27E-01		-7.40E-01	3.47E-01		-6.98E-01	1.36E-02		-1.82E+00	1.48E-08	Down	5.55E-02	9.18E-01		1.83E-01	6.60E-01									
Unigene27216_A11	1584	0.13	0.35	0.20	0.31	0.30	0.43	4.40	2.88	2.01	1.41E+00	1.69E-01		6.11E-01	6.25E-01		-4.71E-02	9.49E-01		4.44E-01	6.22E-01		-6.15E-01	1.84E-03		-1.13E+00	1.50E-08	Down			Unigene27216_A11//6.00E-93//TC150446					
Unigene27217_A11	874	37.30	30.78	32.78	61.73	52.24	40.00	11.80	6.12	4.19	-2.77E-01	3.98E-03		-1.86E-01	7.68E-02		-2.41E-01	4.43E-04		-6.26E-01	3.25E-19		-9.47E-01	4.58E-09		-1.49E+00	2.49E-18	Down	Unigene27217_A11//gi|297812467|ref|XP_002874117.1|//2.00E-80//isochorismatase hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319954|gb|EFH50376.1| isochorismatase hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27217_A11//2.00E-78//AT5G23230| NIC2 (NICOTINAMIDASE 2); catalytic/ nicotinamidase	Unigene27217_A11//0.00E+00//TC142337				nr +
Unigene27218_A11	658	7.32	14.55	8.09	93.34	82.95	71.79	53.65	16.32	23.79	9.92E-01	1.67E-07		1.46E-01	6.38E-01		-1.70E-01	1.12E-02		-3.79E-01	4.72E-09		-1.72E+00	6.67E-72	Down	-1.17E+00	4.82E-42	Down	Unigene27218_A11//gi|224053463|ref|XP_002297828.1|//1.00E-23//predicted protein [Populus trichocarpa] >gi|222845086|gb|EEE82633.1| predicted protein [Populus trichocarpa]	Unigene27218_A11//9.00E-05//AT3G24060| self-incompatibility protein-related	Unigene27218_A11//0.00E+00//DR456343				nr +
Unigene27221_A11	876	40.02	142.00	39.76	82.06	91.51	145.85	90.11	200.58	144.57	1.83E+00	2.52E-223	Up	-9.50E-03	9.45E-01		1.57E-01	7.03E-03		8.30E-01	2.34E-72		1.15E+00	5.58E-195	Up	6.82E-01	1.11E-59		Unigene27221_A11//gi|227206180|dbj|BAH57145.1|//6.00E-59//AT3G07090 [Arabidopsis thaliana]	Unigene27221_A11//1.00E-52//AT3G07090| unknown protein	Unigene27221_A11//0.00E+00//TC135183				nr -
Unigene27222_A11	1464	8.61	5.05	7.97	16.47	11.78	11.85	15.77	8.99	6.07	-7.69E-01	1.45E-06		-1.13E-01	5.52E-01		-4.83E-01	2.26E-06		-4.75E-01	1.08E-05		-8.10E-01	5.61E-15		-1.38E+00	1.75E-35	Down	Unigene27222_A11//gi|15237326|ref|NP_200111.1|//7.00E-54//vesicle-associated membrane protein-related [Arabidopsis thaliana]	Unigene27222_A11//7.00E-50//AT5G52990| vesicle-associated membrane protein-related	Unigene27222_A11//0.00E+00//gi|78323476|gb|DT543750.1|DT543750		ko04130|SNARE interactions in vesicular transport		nr -
Unigene27223_A11	617	2.63	16.42	10.79	3.47	7.14	13.76	3.91	13.41	13.30	2.64E+00	2.88E-29	Up	2.04E+00	6.70E-14	Up	1.04E+00	1.88E-04	Up	1.99E+00	1.08E-18	Up	1.78E+00	2.96E-18	Up	1.77E+00	2.31E-18	Up	Unigene27223_A11//gi|225458627|ref|XP_002284791.1|//8.00E-07//PREDICTED: ripening-related bZIP protein-like isoform 2 [Vitis vinifera] >gi|225458629|ref|XP_002284785.1| PREDICTED: ripening-related bZIP protein-like isoform 1 [Vitis vinifera]		Unigene27223_A11//3.00E-37//BQ412305				nr +
Unigene27225_A11	686	8.31	7.46	9.94	11.62	11.95	13.36	16.09	10.48	5.40	-1.56E-01	5.69E-01		2.57E-01	3.04E-01		4.02E-02	8.71E-01		2.02E-01	3.61E-01		-6.18E-01	4.89E-05		-1.57E+00	4.54E-21	Down	Unigene27225_A11//gi|30316393|sp|Q9SKC0.3|HIBDH_ARATH//4.00E-50//RecName: Full=Probable 3-hydroxyisobutyrate dehydrogenase, mitochondrial; Short=HIBADH; Flags: Precursor >gi|105830240|gb|ABF74718.1| At4g20930 [Arabidopsis thaliana] >gi|110737072|dbj|BAF00489.1| 3-hydroxyisobutyrate dehydrogenase -like protein [Arabidopsis thaliana]	Unigene27225_A11//6.00E-43//AT4G20930| 3-hydroxyisobutyrate dehydrogenase, putative	Unigene27225_A11//0.00E+00//TC144027		ko00903|Limonene and pinene degradation//ko00280|Valine, leucine and isoleucine degradation		nr +
Unigene27227_A11	1210	0.35	0.50	0.88	191.11	78.60	31.91	28.20	23.14	11.06	5.39E-01	5.63E-01		1.35E+00	6.01E-02		-1.28E+00	0.00E+00	Down	-2.58E+00	0.00E+00	Down	-2.85E-01	6.12E-04		-1.35E+00	1.86E-50	Down	Unigene27227_A11//gi|116871384|gb|ABK30788.1|//1.00E-139//xyloglucan endotransglycosylase 1 [Litchi chinensis]	Unigene27227_A11//7.00E-112//AT3G44990| XTR8 (XYLOGLUCAN ENDO-TRANSGLYCOSYLASE-RELATED 8); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene27227_A11//0.00E+00//TC152107				nr +
Unigene27228_A11	1306	11.06	31.04	12.84	19.45	35.09	43.05	14.50	46.15	37.92	1.49E+00	9.46E-55	Up	2.16E-01	1.50E-01		8.51E-01	3.83E-30		1.15E+00	1.89E-54	Up	1.67E+00	2.41E-117	Up	1.39E+00	3.83E-75	Up	Unigene27228_A11//gi|4510354|gb|AAD21443.1|//1.00E-52//expressed protein [Arabidopsis thaliana] >gi|15450733|gb|AAK96638.1| At2g36220/F2H17.17 [Arabidopsis thaliana] >gi|18491123|gb|AAL69530.1| At2g36220/F2H17.17 [Arabidopsis thaliana]	Unigene27228_A11//5.00E-39//AT2G36220| unknown protein	Unigene27228_A11//0.00E+00//TC151397				nr -
Unigene27229_A11	1242	1.56	3.35	1.33	13.68	14.97	12.58	1.09	1.38	0.22	1.10E+00	2.95E-04	Up	-2.30E-01	6.13E-01		1.31E-01	3.91E-01		-1.20E-01	4.62E-01		3.41E-01	4.76E-01		-2.28E+00	7.13E-05	Down	Unigene27229_A11//gi|225456020|ref|XP_002279587.1|//1.00E-105//PREDICTED: similar to inositol polyphosphate multikinase [Vitis vinifera]	Unigene27229_A11//2.00E-92//AT5G61760| ATIPK2BETA; inositol or phosphatidylinositol kinase/ inositol trisphosphate 6-kinase	Unigene27229_A11//0.00E+00//TC130598				nr +
Unigene27231_A11	1797	0.20	0.65	0.59	0.28	0.10	0.40	5.55	2.30	1.29	1.67E+00	1.33E-02		1.54E+00	3.53E-02		-1.53E+00	1.45E-01		5.37E-01	5.60E-01		-1.27E+00	1.27E-13	Down	-2.11E+00	3.53E-28	Down	Unigene27231_A11//gi|15234427|ref|NP_193869.1|//1.00E-157//ARK3 (A. THALIANA RECEPTOR KINASE 3); kinase/ transmembrane receptor protein serine/threonine kinase [Arabidopsis thaliana] >gi|3402757|emb|CAA20203.1| receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana] >gi|7268935|emb|CAB81245.1| receptor-like serine/threonine protein kinase ARK3 [Arabidopsis thaliana]	Unigene27231_A11//3.00E-163//AT4G27300| S-locus protein kinase, putative	Unigene27231_A11//8.00E-114//gi|109868712|gb|DW497688.1|DW497688		ko04626|Plant-pathogen interaction		nr -
Unigene27233_A11	854	41.91	288.35	112.36	48.24	174.11	162.62	28.62	57.95	74.73	2.78E+00	0.00E+00	Up	1.42E+00	2.04E-117	Up	1.85E+00	0.00E+00	Up	1.75E+00	2.81E-253	Up	1.02E+00	2.47E-45	Up	1.38E+00	1.86E-96	Up	Unigene27233_A11//gi|15223262|ref|NP_172333.1|//3.00E-29//ACHT4 (ATYPICAL CYS HIS RICH THIOREDOXIN 4); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor [Arabidopsis thaliana] >gi|51701910|sp|Q64654.1|TRL11_ARATH RecName: Full=Thioredoxin-like 1-1, chloroplastic; AltName: Full=Lilium-type thioredoxin 1-1; AltName: Full=Atypical cysteine/histidine-rich thioredoxin 4; Short=AtACHT4; Flags: Precursor >gi|4973256|gb|AAD35005.1|AF144387_1 thioredoxin-like 1 [Arabidopsis thaliana] >gi|9802552|gb|AAF99754.1|AC003981_4 F22O13.5 [Arabidopsis thaliana]	Unigene27233_A11//1.00E-30//AT1G08570| ACHT4 (ATYPICAL CYS HIS RICH THIOREDOXIN 4); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	Unigene27233_A11//0.00E+00//TC158664				nr -
Unigene27235_A11	636	2.80	8.60	3.27	2.43	1.46	1.28	1.79	2.17	3.13	1.62E+00	5.69E-09	Up	2.23E-01	6.07E-01		-7.32E-01	1.59E-01		-9.26E-01	8.58E-02		2.73E-01	6.39E-01		8.03E-01	4.22E-02				Unigene27235_A11//0.00E+00//gi|73861223|gb|DT463962.1|DT463962				
Unigene27239_A11	841	2.99	1.08	2.53	5.98	5.00	3.28	2.01	0.89	0.81	-1.46E+00	4.79E-04	Down	-2.38E-01	5.95E-01		-2.60E-01	3.70E-01		-8.69E-01	9.62E-04		-1.17E+00	1.05E-02		-1.32E+00	3.08E-03		Unigene27239_A11//gi|297600512|ref|NP_001049317.2|//8.00E-18//Os03g0206100 (Oryza sativa Japonica Group) >gi|255674297|dbj|BAF11231.2| Os03g0206100 (Oryza sativa Japonica Group)	Unigene27239_A11//3.00E-15//AT3G19570| unknown protein	Unigene27239_A11//0.00E+00//gi|78352155|gb|DT572429.1|DT572429				nr -

Unigene2724_All	3240	3.41	1.38	0.67	4.18	4.36	3.57	9.88	4.95	5.23	-1.31E+00	7.08E-13	Down	-2.34E+00	8.47E-27	Down	5.94E-02	7.79E-01		-2.29E-01	1.73E-01		-9.96E-01	1.28E-28		-9.19E-01	7.19E-26		Unigene2724_All//gi|40241245|emb|CAF02297.1|//1.00E-115//cysteine-rich polycomb-like protein [Lotus japonicus] >gi|40241253|emb|CAF02298.1| cysteine-rich polycomb-like protein [Lotus japonicus]	Unigene2724_All//2.00E-59//AT4G14770| TCX2 (TESMIN/TSO1-LIKE CXC 2); transcription factor	Unigene2724_All//0.00E+00//CO126859	CPP			nr -
Unigene27242_All	707	0.15	0.86	0.00	0.21	0.49	0.19	0.78	0.00	0.06	2.54E+00	2.46E-02		-7.21E+00	3.94E-01		1.20E+00	4.26E-01		-1.42E-01	9.43E-01		-9.60E+00	4.61E-04	Down	-3.79E+00	2.03E-03		Unigene27242_All//gi|857395|dbj|BAA09465.1|//2.00E-16//mitotic cyclin a2-type [Glycine max]	Unigene27242_All//2.00E-10//AT5G25380| CYCA2;1 (cyclin a2;1); cyclin-dependent protein kinase regulator	Unigene27242_All//0.00E+00//gi|164341510|gb|ES841224.1|ES841224				nr -
Unigene27245_All	2022	0.36	0.38	0.95	3.10	3.18	2.19	4.68	1.70	2.38	5.32E-02	9.63E-01		1.39E+00	6.13E-03		3.70E-02	9.00E-01		-5.04E-01	3.43E-02		-1.47E+00	5.92E-16	Down	-9.74E-01	4.74E-09		Unigene27245_All//gi|18423042|ref|NP_568712.1|//0.00E+00//amine oxidase-related [Arabidopsis thaliana]	Unigene27245_All//0.00E+00//AT5G49555| amine oxidase-related	Unigene27245_All//0.00E+00//gi|78351675|gb|DT571949.1|DT571949		ko00906|Carotenoid biosynthesis		nr +
Unigene27246_All	936	6.04	18.73	18.94	33.00	19.57	27.55	9.62	15.27	12.64	1.63E+00	1.99E-27	Up	1.65E+00	2.86E-27	Up	-7.54E-01	3.19E-17		-2.60E-01	8.61E-03		6.67E-01	4.73E-07		3.94E-01	6.40E-03		Unigene27246_All//gi|190897590|gb|ACE97308.1|//5.00E-58//pectinesterase inhibitor [Populus tremula]	Unigene27246_All//9.00E-55//AT1G14890| enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor	Unigene27246_All//0.00E+00//gi|109875180|gb|DW504154.1|DW504154		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene27247_All	1170	3.40	7.54	6.10	6.98	8.77	7.99	12.21	10.68	9.64	1.15E+00	1.27E-08	Up	8.44E-01	2.16E-04		3.29E-01	7.26E-02		1.95E-01	3.80E-01		-1.94E-01	1.86E-01		-3.42E-01	8.70E-03		Unigene27247_All//gi|115462381|ref|NP_001051790.1|//6.00E-10//Os03g0176500 (Oryza sativa Japonica Group) >gi|113578341|dbj|BAF16704.1| Os05g0176500 (Oryza sativa Japonica Group)	Unigene27247_All//3.00E-11//AT1G08220| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: mitochondrial proton-transporting ATP synthase complex assembly; LOCATED IN: mitochondrial inner membrane; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: ATPase assembly factor ATP10, mitochondria (InterPro:IPR007849); Has 100 Blast hits to 100 proteins in 48 species: Archae - 6; Bacteria - 0; Metazoa - 2; Fungi - 63; Plants - 15; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink).	Unigene27247_All//1.00E-154//gi|72270711|gb|DT047790.1|DT047790				nr -
Unigene27249_All	586	0.54	1.21	0.73	1.19	1.53	0.46	2.38	2.28	0.68	1.18E+00	1.75E-01		4.41E-01	6.77E-01		3.60E-01	6.55E-01		-1.36E+00	1.31E-01		-6.10E-02	9.18E-01		-1.81E+00	6.10E-04	Down	Unigene27249_All//gi|30689150|ref|NP_173900.2|//1.00E-06//ATRBL10 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 10) [Arabidopsis thaliana]	Unigene27249_All//7.00E-08//AT1G25290| ATRBL10 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 10)	Unigene27249_All//0.00E+00//CO119867				nr +
Unigene27250_All	539	21.26	24.35	18.28	31.70	32.45	25.39	34.28	19.15	16.78	1.96E-01	2.39E-01		-2.18E-01	2.42E-01		3.39E-02	8.29E-01		-3.20E-01	1.97E-02		-8.40E-01	7.16E-13		-1.03E+00	2.34E-18	Down	Unigene27250_All//gi|115439979|ref|NP_001044269.1|//7.00E-29//Os01g0752800 (Oryza sativa Japonica Group) >gi|113533800|dbj|BAF06183.1| Os01g0752800 (Oryza sativa Japonica Group)	Unigene27250_All//4.00E-15//AT5G46020| unknown protein	Unigene27250_All//9.00E-108//gi|21100169|gb|BQ412482.1|BQ412482				nr +
Unigene27252_All	751	8.50	8.16	9.93	11.61	10.45	13.29	35.86	28.88	16.34	-5.81E-02	8.09E-01		2.24E-01	3.62E-01		-1.51E-01	5.20E-01		1.95E-01	3.54E-01		-3.12E-01	9.56E-04		-1.13E+00	1.24E-30	Down	Unigene27252_All//gi|297725871|ref|NP_001175299.1|//3.00E-11//Os07g0620501 (Oryza sativa Japonica Group) >gi|255677975|dbj|BAH94027.1| Os07g0620501 (Oryza sativa Japonica Group)	Unigene27252_All//7.00E-12//AT3G12587| unknown protein	Unigene27252_All//7.00E-174//gi|164351730|gb|EX166116.1|EX166116				nr +
Unigene27253_All	735	37.80	86.17	26.08	40.60	44.93	29.68	61.90	74.89	92.96	1.19E+00	1.83E-60	Up	-5.35E-01	4.18E-07		1.46E-01	1.57E-01		-4.52E-01	2.49E-06		2.75E-01	1.65E-05		5.87E-01	3.58E-25		Unigene27253_All//gi|18400140|ref|NP_566461.1|//4.00E-57//PRA8 [Arabidopsis thaliana] >gi|75273356|sp|Q8LLG6.1|PRI3_ARATH RecName: Full=PRA1 family protein F3; Short=AtPRA1.F3	Unigene27253_All//9.00E-46//AT3G13720| PRA8	Unigene27253_All//0.00E+00//TC155127				nr -
Unigene27255_All	1504	14.92	7.18	13.52	3.54	3.21	2.34	0.25	0.39	0.77	-1.06E+00	2.66E-18	Down	-1.42E-01	2.91E-01		-1.45E-01	6.09E-01		-5.98E-01	2.10E-02		6.21E-01	4.78E-01		1.60E+00	5.68E-03		Unigene27255_All//gi|15239489|ref|NP_200965.1|//4.00E-54//TCP5 (TEOSINTE BRANCHED1, CYCLOIDEA AND PCF TRANSCRIPTION FACTOR 5); transcription factor [Arabidopsis thaliana] >gi|75171652|sp|Q9FMZ3.1|TCP5_ARATH RecName: Full=Transcription factor TCP5 >gi|119360035|gb|ABL66746.1| At5g60970 [Arabidopsis thaliana]	Unigene27255_All//3.00E-45//AT5G60970| TCP5 (TEOSINTE BRANCHED1, CYCLOIDEA AND PCF TRANSCRIPTION FACTOR 5); transcription factor	Unigene27255_All//0.00E+00//gi|164315775|gb|ES828171.1|ES828171	TCP			nr +
Unigene27256_All	935	4.14	6.88	6.61	2.66	5.34	2.99	0.86	0.04	0.68	7.33E-01	1.61E-03		6.74E-01	6.47E-03		1.00E+00	1.03E-04	Up	1.69E-01	6.98E-01		-4.26E+00	8.48E-05	Down	-3.34E-01	6.19E-01		Unigene27256_All//gi|15226289|ref|NP_180361.1|//3.00E-39//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565332|sp|Q9SJJ7.1|ATL2E_ARATH RecName: Full=RING-H2 finger protein ATL2E >gi|28950793|gb|AAO63320.1| At2g27940 [Arabidopsis thaliana]	Unigene27256_All//3.00E-32//AT2G27940| zinc finger (C3HC4-type RING finger) family protein	Unigene27256_All//9.00E-103//CK640441				nr +
Unigene27257_All	1615	4.96	3.23	3.17	14.84	9.04	11.02	15.89	4.81	7.97	-6.17E-01	2.58E-03		-6.47E-01	2.41E-03		-7.15E-01	2.64E-12		-4.29E-01	8.17E-05		-1.72E+00	9.67E-53	Down	-9.96E-01	8.15E-24		Unigene27257_All//gi|115456723|ref|NP_001051962.1|//1.00E-93//Os03g0858600 (Oryza sativa Japonica Group) >gi|108712208|gb|ABG00003.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550433|dbj|BAF13876.1| Os03g0858600 (Oryza sativa Japonica Group)	Unigene27257_All//2.00E-131//AT5G51670| unknown protein	Unigene27257_All//1.00E-47//TC178814				nr +
Unigene27258_All	866	259.31	85.66	318.52	370.10	385.27	319.85	691.62	216.12	215.75	-1.60E+00	0.00E+00	Down	2.97E-01	4.92E-22		5.80E-02	5.24E-02		-2.11E-01	5.17E-15		-1.68E+00	0.00E+00	Down	-1.68E+00	0.00E+00	Down	Unigene27258_All//gi|50313460|gb|AAT46600.1|//1.00E-165//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene27258_All//6.00E-108//AT3G23510| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene27258_All//0.00E+00//TC129559		ko00100|Steroid biosynthesis		nr +
Unigene27259_All	890	652.01	267.92	389.56	691.24	734.98	777.22	295.39	107.21	154.52	-1.28E+00	0.00E+00	Down	-7.43E-01	2.63E-244		8.85E-02	1.51E-06		1.69E-01	6.38E-21		-1.46E+00	0.00E+00	Down	-9.35E-01	2.90E-212		Unigene27259_All//gi|32401253|gb|AAP80800.1|//1.00E-136//class VII chitinase precursor [Gossypium hirsutum] >gi|32401255|gb|AAP80801.1| class VII chitinase precursor [Gossypium hirsutum]	Unigene27259_All//8.00E-95//AT1G05850| POM1 (POM-POM1); chitinase	Unigene27259_All//0.00E+00//gi|78325668|gb|DT545942.1|DT545942		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene27260_All	1883	0.28	7.08	0.51	0.21	0.31	1.08	3.57	12.63	101.49	4.67E+00	6.88E-62	Up	8.73E-01	2.38E-01		5.55E-01	5.99E-01		2.35E+00	7.25E-06	Up	1.82E+00	9.93E-53	Up	4.83E+00	0.00E+00	Up	Unigene27260_All//gi|66792674|gb|AY356439.1|//1.00E-90//At1g13480 [Arabidopsis thaliana]	Unigene27260_All//1.00E-80//AT1G13520| unknown protein	Unigene27260_All//0.00E+00//gi|78325059|gb|DT545333.1|DT545333				nr +
Unigene27261_All	591	13.28	7.97	7.03	15.68	18.47	16.05	12.16	10.25	5.86	-7.36E-01	3.83E-04		-9.18E-01	2.36E-05		2.37E-01	2.09E-01		3.37E-02	8.92E-01		-2.46E-01	2.43E-01		-1.05E+00	6.43E-08	Down	Unigene27261_All//gi|115462481|ref|NP_001051840.1|//3.00E-36//Os05g0188300 (Oryza sativa Japonica Group) >gi|54287454|gb|AAV31198.1| unknow protein [Oryza sativa Japonica Group] >gi|113578391|dbj|BAF16754.1| Os05g0188300 (Oryza sativa Japonica Group)	Unigene27261_All//8.00E-31//AT5G19570| unknown protein	Unigene27261_All//0.00E+00//TC173978				nr +
Unigene27263_All	464	8.23	15.51	9.07	4.51	9.50	5.35	49.84	48.10	23.53	9.14E-01	3.37E-05		1.39E-01	6.47E-01		1.08E+00	1.18E-04	Up	2.48E-01	6.05E-01		-5.13E-02	6.71E-01		-1.08E+00	1.33E-24	Down	Unigene27263_All//gi|226491776|ref|NP_001152474.1|//1.00E-06//brain protein 44-like protein [Zea mays] >gi|195656655|gb|ACG47795.1| brain protein 44-like protein [Zea mays]	Unigene27263_All//1.00E-08//AT5G20090| unknown protein	Unigene27263_All//0.00E+00//gi|21094997|gb|BQ407310.1|BQ407310				nr -
Unigene27264_All	1293	10.72	122.11	120.63	2.27	4.42	13.20	0.13	0.00	0.37	3.51E+00	0.00E+00	Up	3.49E+00	0.00E+00	Up	9.60E-01	5.55E-05		2.54E+00	5.58E-50	Up	-7.03E+00	1.34E-01		1.50E+00	1.27E-01		Unigene27264_All//gi|115462741|ref|NP_001051970.1|//1.00E-106//Os05g0228000 (Oryza sativa Japonica Group) >gi|113578521|dbj|BAF16884.1| Os05g0228000 (Oryza sativa Japonica Group)	Unigene27264_All//7.00E-102//AT4G28940| catalytic	Unigene27264_All//0.00E+00//TC176820				nr -
Unigene27266_All	603	1.13	2.77	1.06	0.99	1.48	1.05	2.80	0.49	1.92	1.30E+00	1.32E-02		-9.01E-02	9.22E-01		5.83E-01	4.72E-01		8.11E-02	9.45E-01		-2.53E+00	2.71E-06	Down	-5.50E-01	2.08E-01				Unigene27266_All//1.00E-51//TC178474				
Unigene27270_All	690	39.66	37.97	22.38	53.86	42.32	52.56	90.14	71.72	42.21	-6.29E-02	6.21E-01		-8.25E-01	2.84E-14		-3.48E-01	2.03E-05		-3.52E-02	7.39E-01		-3.30E-01	2.69E-08		-1.09E+00	9.63E-66	Down	Unigene27270_All//gi|115458588|ref|NP_001052894.1|//2.00E-59//Os04g0444600 (Oryza sativa Japonica Group) >gi|38344536|emb|CAE02442.2| OSJNBa0027P08.4 (Oryza sativa (japonica cultivar-group)] >gi|38344584|emb|CAE02431.2| OSJNBa0058G03.7 (Oryza sativa (japonica cultivar-group)] >gi|113564465|dbj|BAF14808.1| Os04g0444600 (Oryza sativa Japonica Group)	Unigene27270_All//2.00E-58//AT1G29150| ATS9 (ARABIDOPSIS NON-ATPASE SUBUNIT 9)	Unigene27270_All//0.00E+00//TC159288		ko03050|Proteasome		nr -
Unigene27272_All	871	0.00	1.86	0.00	0.51	1.23	2.54	0.83	3.84	7.00	1.09E+01	2.97E-09	Up	null	null		1.25E+00	6.99E-02		2.30E+00	3.32E-06	Up	2.22E+00	3.66E-10	Up	3.08E+00	4.78E-26	Up	Unigene27272_All//gi|28416677|gb|AA042869.1|//4.00E-51//At5g42860 [Arabidopsis thaliana]	Unigene27272_All//5.00E-43//AT5G42860| unknown protein	Unigene27272_All//1.00E-129//TC146950				nr +
Unigene27273_All	2697	0.04	1.03	0.38	0.55	0.60	1.79	0.53	1.89	5.64	4.74E+00	2.72E-13	Up	3.27E+00	5.93E-04	Up	1.15E-01	8.39E-01		1.69E+00	7.40E-09	Up	1.83E+00	6.30E-12	Up	3.40E+00	4.19E-70	Up	Unigene27273_All//gi|28416677|gb|AA042869.1|//2.00E-70//At5g42860 [Arabidopsis thaliana]	Unigene27273_All//2.00E-36//AT5G42860| unknown protein	Unigene27273_All//5.00E-82//TC146950				nr +
Unigene27274_All	869	22.94	11.49	17.28	15.59	10.07	8.26	4.04	0.91	2.80	-9.98E-01	6.02E-15		-4.09E-01	1.49E-03		-6.31E-01	6.94E-06		-9.16E-01	1.15E-09		-2.14E+00	2.98E-10	Down	-5.30E-01	6.27E-02		Unigene27274_All//gi|261889456|gb|ACY06328.1|//2.00E-55//S-adenosyl-L-methionine: caffeic acid 3-O-methyltransferase [Medicago sativa]	Unigene27274_All//8.00E-50//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene27274_All//0.00E+00//TC136969		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene27276_All	1023	4.40	1.49	2.45	24.30	5.86	7.81	28.93	55.20	11.88	-1.57E+00	3.14E-07	Down	-8.46E-01	4.46E-03		-2.05E+00	2.15E-66	Down	-1.64E+00	3.60E-42	Down	9.32E-01	1.09E-44		-1.28E+00	1.08E-40	Down	Unigene27276_All//gi|15231343|ref|NP_190199.1|//3.00E-72//MYB111 (MYB DOMAIN PROTEIN 111); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75335604|sp|Q9LX82.1|MYB48_ARATH RecName: Full=Transcription factor MYB48; AltName: Full=Myb-related protein 48; Short=AtMYB48 >gi|7799001|emb|CAB90940.1| Myb DNA binding protein-like [Arabidopsis thaliana] >gi|41619274|gb|AAS10064.1| MYB transcription factor [Arabidopsis thaliana]	Unigene27276_All//7.00E-68//AT3G46130| MYB111 (MYB DOMAIN PROTEIN 111); DNA binding / transcription factor	Unigene27276_All//3.00E-72//TC178283	MYB			nr +

Unigene27278_All	1557	8.20	19.75	9.47	14.27	17.63	18.10	11.41	9.96	10.34	1.27E+00	8.01E-33	Up	2.08E-01	2.06E-01		3.05E-01	2.40E-03		3.43E-01	7.15E-04		-1.96E-01	1.28E-01		-1.42E-01	2.65E-01		Unigene27278_All//gi|297597912|ref|NP_001044722.2|//1.00E-162//0s01g0834700 [Oryza sativa Japonica Group] >gi|205688775|sp|Q0JHZ2.2|C3H11_ORYSJ RecName: Full=Zinc finger CCCH domain-containing protein 11; Short=OsC3H11 >gi|255673848|dbj|BAF06636.2|0s01g0834700 [Oryza sativa Japonica Group]	Unigene27278_All//7.00E-141//AT2G20280| zinc finger (CCCH-type) family protein	Unigene27278_All//0.00E+00//C0105840	C3H			nr +
Unigene27279_All	1098	480.42	408.26	442.63	346.02	397.48	397.79	42.47	88.58	45.50	-2.35E-01	8.22E-28		-1.18E-01	1.46E-07		2.00E-01	2.89E-20		2.01E-01	1.52E-18		1.06E+00	2.02E-94	Up	9.93E-02	1.77E-01		Unigene27279_All//gi|197726026|gb|ACH73166.1|//1.00E-111//CONSTANS-like protein [Prunus persica]	Unigene27279_All//7.00E-102//AT5G24930| zinc finger (B-box type) family protein	Unigene27279_All//0.00E+00//TC139952	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene2728_All	1039	11.43	15.46	13.17	9.06	13.16	22.43	10.34	6.56	11.96	4.36E-01	1.81E-03		2.05E-01	2.38E-01		5.38E-01	1.79E-04		1.31E+00	5.56E-28	Up	-6.57E-01	2.19E-05		2.11E-01	1.58E-01		Unigene2728_All//gi|115485527|ref|NP_001067907.1|//1.00E-110//0s11g0483900 [Oryza sativa Japonica Group] >gi|113645129|dbj|BAF28270.1|0s11g0483900 [Oryza sativa Japonica Group]	Unigene2728_All//7.00E-108//AT1G67400| INVOLVED IN: phagocytosis; LOCATED IN: cytoskeleton; CONTAINS InterPro DOMAIN/s: Engulfment and cell motility, ELMO (InterPro:IPR006816); BEST Arabidopsis thaliana protein match is: phagocytosis and cell motility protein ELMO1-related (TAIR:AT3G43400.1); Has 660 Blast hits to 660 proteins in 104 species: Archae - 0; Bacteria - 0; Metazoa - 430; Fungi - 39; Plants - 109; Viruses - 0; Other Eukaryotes - 82 (source: NCBI BLink).	Unigene2728_All//0.00E+00//gi|164317722|gb|ES794609.1|ES794609			GO:0006897//GO:0043232	nr +
Unigene27280_All	1485	83.96	34.53	55.76	119.99	82.34	44.46	14.69	7.49	5.15	-1.28E+00	7.84E-134	Down	-5.91E-01	2.98E-35		-5.43E-01	1.63E-54		-1.43E+00	2.38E-246	Down	-9.73E-01	4.83E-19		-1.51E+00	1.69E-38	Down	Unigene27280_All//gi|124359162|gb|ABN05683.1|//1.00E-10//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene27280_All//0.00E+00//TC163047				nr -
Unigene27281_All	1183	15.48	12.29	12.96	19.20	16.39	20.54	9.69	32.89	9.50	-3.33E-01	1.14E-02		-2.56E-01	7.06E-02		-2.29E-01	5.09E-02		9.72E-02	4.69E-01		1.76E+00	4.86E-82	Up	-2.84E-02	8.72E-01		Unigene27281_All//gi|297811053|ref|XP_002873410.1|//2.00E-09//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319247|gb|EFH49669.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]		Unigene27281_All//0.00E+00//gi|78349274|gb|DT569548.1|DT569548				nr +
Unigene27282_All	432	0.97	1.41	0.00	3.00	1.59	3.24	7.83	3.39	4.06	5.39E-01	5.63E-01		-9.92E+00	1.56E-02		-9.11E-01	1.09E-01		1.12E-01	8.61E-01		-1.21E+00	8.02E-05	Down	-9.48E-01	1.14E-03		Unigene27282_All//gi|115477336|ref|NP_001062264.1|//2.00E-46//0s08g0520000 [Oryza sativa Japonica Group] >gi|113624233|dbj|BAF24178.1|0s08g0520000 [Oryza sativa Japonica Group]	Unigene27282_All//2.00E-46//AT3G20240| mitochondrial substrate carrier family protein	Unigene27282_All//0.00E+00//TC178838				nr -
Unigene27283_All	1482	2.19	1.09	0.36	3.46	2.97	2.77	8.19	4.46	5.99	-1.00E+00	3.93E-03		-2.61E+00	3.09E-09	Down	-2.19E-01	4.51E-01		-3.20E-01	2.66E-01		-8.78E-01	2.36E-09		-4.50E-01	1.44E-03		Unigene27283_All//gi|297830712|ref|XP_002883238.1|//1.00E-142//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329078|gb|EFH59497.1|mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27283_All//2.00E-129//AT3G20240| mitochondrial substrate carrier family protein	Unigene27283_All//0.00E+00//TC135592				nr -
Unigene27287_All	1383	104.68	175.86	131.57	52.34	42.83	45.65	22.96	40.13	8.12	7.48E-01	8.98E-107		3.30E-01	7.20E-18		-2.89E-01	3.17E-07		-1.97E-01	1.51E-03		8.06E-01	1.69E-34		-1.50E+00	6.25E-55	Down	Unigene27287_All//gi|29469000|gb|AA043182.1|//1.00E-122//peptide methionine sulfoxide reductase [Gossypium barbadense]	Unigene27287_All//1.00E-95//AT4G25130| peptide methionine sulfoxide reductase, putative	Unigene27287_All//0.00E+00//C0096720				nr +
Unigene27289_All	577	121.87	54.18	27.04	121.13	125.09	55.57	129.92	31.29	36.66	-1.17E+00	1.27E-65	Down	-2.17E+00	1.69E-154	Down	4.65E-02	5.62E-01		-1.12E+00	2.42E-66	Down	-2.05E+00	1.21E-193	Down	-1.83E+00	2.52E-170	Down	Unigene27289_All//gi|298712420|emb|CBJ133198.1|//2.00E-52//histone H4 [Ectocarpus siliculosus]	Unigene27289_All//8.00E-38//AT5G59970| histone H4	Unigene27289_All//0.00E+00//TC157368				nr +
Unigene27290_All	962	1.69	1.79	1.66	3.42	5.80	5.73	9.45	6.99	26.17	8.70E-02	8.59E-01		-2.19E-02	9.89E-01		7.63E-01	1.61E-03		7.45E-01	3.12E-03		-4.34E-01	1.18E-02		1.47E+00	4.36E-42	Up	Unigene27290_All//gi|87244449|gb|AB034616.1|//8.00E-93//green ripe-like 1 [Solanum lycopersicum]	Unigene27290_All//9.00E-94//AT2G26070| RTE1 (REVERSION-TO-ETHYLENE SENSITIVITY)	Unigene27290_All//0.00E+00//TC153199				nr +
Unigene27291_All	1473	1.74	4.68	2.21	2.16	3.25	2.88	7.78	14.67	13.71	1.43E+00	2.43E-09	Up	3.41E-01	3.69E-01		5.86E-01	3.10E-02		4.13E-01	1.92E-01		9.15E-01	4.20E-17		8.18E-01	9.40E-14				Unigene27291_All//0.00E+00//gi|21097295|gb|BQ409608.1|BQ409608				
Unigene27292_All	1520	0.17	0.43	0.18	11.37	10.51	13.97	5.23	3.88	0.29	1.33E+00	1.45E-01		2.58E-02	1.00E+00		-1.14E-01	4.78E-01		2.96E-01	1.54E-02		-4.32E-01	2.07E-02		-4.18E+00	3.60E-44	Down	Unigene27292_All//gi|224099345|ref|XP_002311447.1|//0.00E+00//lysine/histidine transporter [Populus trichocarpa] >gi|222851267|gb|EEE88814.1|lysine/histidine transporter [Populus trichocarpa]	Unigene27292_All//0.00E+00//AT1G25530| lysine and histidine specific transporter, putative	Unigene27292_All//0.00E+00//TC165186				nr -
Unigene27293_All	921	3.81	11.39	6.19	6.11	10.43	16.57	23.14	156.84	27.25	1.58E+00	5.76E-16	Up	7.01E-01	6.89E-03		7.71E-01	1.02E-05		1.44E+00	2.54E-21	Up	2.76E+00	0.00E+00	Up	2.36E-01	1.58E-02		Unigene27293_All//gi|111074300|gb|AB804523.1|//6.00E-40//At3g27880 [Arabidopsis thaliana]	Unigene27293_All//4.00E-26//AT3G27880| unknown protein	Unigene27293_All//0.00E+00//TC176589				nr +
Unigene27294_All	1799	0.12	0.59	0.59	9.05	7.73	6.50	3.85	3.51	38.91	2.35E+00	2.58E-03		2.35E+00	3.61E-03		-2.28E-01	1.14E-01		-4.78E-01	4.12E-04		-1.36E-01	5.70E-01		3.34E+00	0.00E+00	Up	Unigene27294_All//gi|115451515|ref|NP_001049358.1|//1.00E-176//0s03g0212800 [Oryza sativa Japonica Group] >gi|75301142|sp|Q8L7J2.1|BGLO6_ORYSJ RecName: Full=Beta-glucosidase 6; Short=Os3bglu6; Flags: Precursor >gi|22658440|gb|AAN01354.1| beta-glucosidase [Oryza sativa Japonica Group] >gi|108706820|gb|ABF94615.1|Glycosyl hydrolase family 1 protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547829|dbj|BAF11272.1|0s03g0212800 [Oryza sativa Japonica Group]	Unigene27294_All//4.00E-177//AT1G26560| BGLU40 (BETA GLUCOSIDASE 40); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene27294_All//0.00E+00//C0121149		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr +
Unigene27295_All	758	92.84	356.76	158.63	66.18	76.50	95.39	0.00	0.22	0.00	1.94E+00	0.00E+00	Up	7.73E-01	1.71E-54		2.09E-01	1.99E-03		5.28E-01	8.39E-19		7.79E+00	1.39E-01		null	null		Unigene27295_All//gi|4337175|gb|AAD18096.1|//2.00E-48//ESTs gb|T20589, gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428, gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457, gb|T20921, gb|AA042762 and gb|AA720210 come from this gene [Arabidopsis thaliana]	Unigene27295_All//5.00E-49//AT1G09310| unknown protein	Unigene27295_All//0.00E+00//TC154150				nr -
Unigene27298_All	666	115.25	191.72	159.91	96.79	209.25	172.24	17.01	17.70	28.65	7.34E-01	1.50E-54		4.73E-01	2.39E-20		1.11E+00	1.12E-141	Up	8.32E-01	3.06E-65		5.68E-02	7.36E-01		7.52E-01	2.08E-11		Unigene27298_All//gi|7768153|emb|CAB90634.1|//5.00E-16//protein phosphatase 2C (PP2C) [Fagus sylvatica]	Unigene27298_All//1.00E-15//AT4G38520| protein phosphatase 2C family protein / PP2C family protein	Unigene27298_All//0.00E+00//TC174839				nr +
Unigene2730_All	1686	29.02	119.04	57.86	1.30	1.43	2.81	0.33	3.97	0.28	2.04E+00	0.00E+00	Up	9.96E-01	7.25E-68		1.37E-01	8.05E-01		1.11E+00	6.09E-05	Up	3.60E+00	4.42E-32	Up	-2.02E-01	7.93E-01		Unigene2730_All//gi|15225317|ref|NP_180217.1|//1.00E-163//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|2739374|gb|AAC14498.1| En/Spm-like transposon protein [Arabidopsis thaliana] >gi|50253512|gb|AAT71958.1|At2g26490 [Arabidopsis thaliana] >gi|53850519|gb|AAU95436.1|At2g26490 [Arabidopsis thaliana]	Unigene2730_All//6.00E-165//AT2G26490| transducin family protein / WD-40 repeat family protein	Unigene2730_All//0.00E+00//C0125636		ko03040|Spliceosome		nr +
Unigene27300_All	1016	2.57	4.24	1.83	28.83	19.45	20.76	1.79	5.72	2.04	7.19E-01	1.38E-02		-4.89E-01	2.38E-01		-5.67E-01	4.80E-10		-4.74E-01	9.93E-07		1.68E+00	4.70E-12	Up	1.88E-01	6.28E-01		Unigene27300_All//gi|33285288|emb|CAD58040.1|//1.00E-57//homeodomain protein vaamana [Arabidopsis thaliana]	Unigene27300_All//2.00E-58//AT5G02030| RPL (REPLUMLESS); DNA binding / sequence-specific DNA binding / transcription factor	Unigene27300_All//0.00E+00//TC143603	HB			nr -
Unigene27301_All	862	3.10	3.59	1.48	12.37	8.31	6.13	9.71	4.51	2.50	2.12E-01	5.79E-01		-1.06E+00	9.11E-03		-5.74E-01	4.12E-04		-1.01E+00	4.97E-09	Down	-1.11E+00	1.87E-09	Down	-1.96E+00	1.14E-21	Down	Unigene27301_All//gi|117168149|gb|ABK32157.1|//2.00E-48//At1g61667 [Arabidopsis thaliana]	Unigene27301_All//1.00E-46//AT1G61667| unknown protein	Unigene27301_All//0.00E+00//TC130576				nr -
Unigene27302_All	664	31.60	42.12	30.63	32.78	38.84	41.69	89.02	74.84	39.96	4.15E-01	5.12E-05		-4.46E-02	7.44E-01		2.45E-01	2.38E-02		3.47E-01	7.03E-04		-2.50E-01	4.95E-05		-1.16E+00	3.74E-68	Down	Unigene27302_All//gi|242129052|gb|ACS83605.1|//1.00E-34//ATP synthase epsilon subunit 1 [Gossypium hirsutum]	Unigene27302_All//3.00E-30//AT1G51650| ATP synthase epsilon chain, mitochondrial	Unigene27302_All//0.00E+00//gi|13245061|gb|BE052162.2|BE052162		ko00190|Oxidative phosphorylation		nr -
Unigene27303_All	872	2.16	0.87	2.08	0.97	0.67	1.40	0.92	2.16	5.07	-1.31E+00	7.13E-03		-5.70E-02	9.13E-01		-5.33E-01	4.90E-01		5.26E-01	4.24E-01		1.23E+00	4.43E-03		2.46E+00	3.42E-15	Up								
Unigene27304_All	730	8.46	2.50	1.31	4.30	4.29	8.85	0.35	0.00	0.00	-1.76E+00	3.16E-11	Down	-2.69E+00	1.05E-17	Down	-2.10E-03	9.85E-01		1.04E+00	6.81E-06	Up	-8.44E+00	4.04E-02		-8.44E+00	3.04E-02		Unigene27304_All//gi|224103097|ref|XP_002312924.1|//3.00E-35//SAUR family protein [Populus trichocarpa] >gi|222849332|gb|EEE86879.1| SAUR family protein [Populus trichocarpa]	Unigene27304_All//2.00E-20//AT1G29430| auxin-responsive family protein	Unigene27304_All//8.00E-38//DN804344				nr -
Unigene27305_All	990	11.79	7.63	4.14	6.89	12.77	11.59	0.13	0.30	0.20	-6.28E-01	1.49E-04		-1.51E+00	6.27E-16	Down	8.89E-01	3.26E-09		7.49E-01	5.20E-06		1.21E+00	3.92E-01		6.51E-01	6.65E-01		Unigene27305_All//gi|224103097|ref|XP_002312924.1|//2.00E-46//SAUR family protein [Populus trichocarpa] >gi|222849332|gb|EEE86879.1| SAUR family protein [Populus trichocarpa]	Unigene27305_All//3.00E-33//AT1G29430| auxin-responsive family protein	Unigene27305_All//5.00E-49//TC159428				nr +
Unigene27307_All	604	9.96	7.63	4.94	8.25	11.74	11.29	21.56	28.92	13.19	-3.84E-01	1.22E-01		-1.01E+00	6.67E-05	Down	5.10E-01	1.82E-02		4.53E-01	4.91E-02		4.24E-01	3.51E-04		-7.09E-01	2.10E-07				Unigene27307_All//0.00E+00//TC133233				
Unigene27308_All	595	0.79	2.98	2.06	1.67	2.55	1.14	2.27	0.70	1.00	1.91E+00	4.26E-04	Up	1.38E+00	3.74E-02		6.03E-01	2.97E-01		-5.56E-01	4.47E-01		-1.69E+00	1.96E-03		-1.18E+00	1.86E-02				Unigene27308_All//0.00E+00//BP275236				

Unigene2731_All	561	0.56	1.08	1.04	3.02	3.93	3.94	15.90	81.36	15.84	9.54E-01	3.14E-01		9.00E-01	3.77E-01		3.80E-01	4.24E-01		3.86E-01	4.10E-01		2.36E+00	1.03E-139	Up	-6.00E-03	9.68E-01		Unigene2731_All//gi|195622338|gb|ACG32999.1|//3.00E-36//glutathione S-transferase, C-terminal-like [Zea mays]	Unigene2731_All//1.00E-37//AT4G19880| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cadmium ion; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Glutathione S-transferase, predicted (InterPro:IPR016639), Glutathione S-transferase, C-terminal (InterPro:IPR004046), Glutathione S-transferase, C-terminal-like (InterPro:IPR010987), Glutathione S-transferase/chloride channel, C-terminal (InterPro:IPR017933), Thioredoxin-like fold (InterPro:IPR012336); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G45020.1); Has 1635 Blast hits to 1635 proteins in 489 species: Archae - 12; Bacteria - 905; Metazoa - 23; Fungi - 158; Plants - 57; Viruses - 0; Other Eukaryotes - 480 (source: NCBI BLink).	Unigene2731_All//7.00E-161//TC167429			GO:0003824//GO:0009536//GO:0010038	nr +
Unigene27310_All	480	1.74	3.27	5.88	3.74	5.17	2.54	2.29	0.78	0.42	9.08E-01	8.56E-02		1.75E+00	3.10E-05	Up	4.67E-01	2.80E-01		-5.57E-01	2.76E-01		-1.55E+00	1.12E-02		-2.46E+00	2.04E-04	Down			Unigene27310_All//8.00E-145//BG444302				
Unigene27313_All	646	13.20	9.10	9.07	14.27	10.18	13.70	55.17	29.24	21.15	-5.37E-01	6.72E-03		-5.42E-01	8.74E-03		-4.87E-01	6.96E-03		-5.81E-02	7.90E-01		-9.16E-01	9.67E-28		-1.38E+00	1.25E-54	Down			Unigene27313_All//4.00E-144//gi|13245272|gb|BE053528.2|BE053528				
Unigene27315_All	546	27.41	31.27	18.43	33.57	28.13	40.20	136.91	66.75	93.91	1.91E-01	1.90E-01		-5.72E-01	1.30E-04		-2.55E-01	5.11E-02		2.60E-01	3.36E-02		-1.04E+00	3.50E-70	Down	-5.44E-01	3.67E-24		Unigene27315_All//gi|110559491|gb|ABG76000.1|//2.00E-34//GRP-like protein 2 [Gossypium hirsutum]	Unigene27315_All//5.00E-24//AT3G08960| RGP3 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 3); transferase, transferring hexosyl groups	Unigene27315_All//0.00E+00//gi|21090031|gb|BQ402344.1|BQ402344			nr +
Unigene27318_All	575	17.11	4.85	8.15	28.50	19.10	30.63	52.87	20.13	20.85	-1.82E+00	2.93E-18	Down	-1.07E+00	3.36E-08	Down	-5.77E-01	4.90E-06		1.04E-01	5.23E-01		-1.39E+00	7.61E-46	Down	-1.34E+00	1.18E-44	Down	Unigene27318_All//gi|149391097|gb|ABR25566.1|//1.00E-29//H/ACA ribonucleoprotein complex subunit 2 [Oryza sativa Indica Group]	Unigene27318_All//3.00E-27//AT5G08180| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	Unigene27318_All//0.00E+00//TC171116				nr -
Unigene27319_All	648	5.97	4.46	7.72	10.69	14.67	14.08	36.41	13.87	11.99	-4.23E-01	1.83E-01		3.71E-01	2.04E-01		4.57E-01	1.22E-02		3.98E-01	4.23E-02		-1.39E+00	9.53E-36	Down	-1.60E+00	3.48E-45	Down	Unigene27319_All//gi|75294330|sp|Q6ZL94.1|SUCA_ORYSJ//3.00E-21//RecName: Full=Probable succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial; AltName: Full=Succinyl-CoA synthetase subunit alpha; Short=SCS-alpha; Flags: Precursor	Unigene27319_All//2.00E-21//AT5G23250| succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative	Unigene27319_All//0.00E+00//gi|164331649|gb|ES795797.1|ES795797		ko00020|Citrate cycle (TCA cycle)//ko00640|Propanoate metabolism		nr +
Unigene2732_All	1639	7.28	13.60	7.28	18.21	26.66	60.90	89.28	390.42	81.86	9.02E-01	4.03E-14		-1.00E-04	1.00E+00		5.50E-01	1.25E-13		1.74E+00	1.83E-180	Up	2.13E+00	0.00E+00	Up	-1.25E-01	1.10E-03		Unigene2732_All//gi|124301261|gb|ABC75353.2|//1.00E-160//Intracellular chloride channel [Medicago truncatula]	Unigene2732_All//3.00E-164//AT4G19880| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cadmium ion; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Glutathione S-transferase, predicted (InterPro:IPR016639), Glutathione S-transferase, C-terminal (InterPro:IPR004046), Glutathione S-transferase, C-terminal-like (InterPro:IPR010987), Glutathione S-transferase/chloride channel, C-terminal (InterPro:IPR017933), Thioredoxin-like fold (InterPro:IPR012336); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G45020.1); Has 1635 Blast hits to 1635 proteins in 489 species: Archae - 12; Bacteria - 905; Metazoa - 23; Fungi - 158; Plants - 57; Viruses - 0; Other Eukaryotes - 480 (source: NCBI BLink).	Unigene2732_All//0.00E+00//TC173622			nr +
Unigene27320_All	475	62.34	60.48	57.29	44.57	66.77	143.38	70.50	39.42	58.54	-4.37E-02	6.89E-01		-1.22E-01	2.97E-01		5.83E-01	4.72E-11		1.69E+00	1.15E-117	Up	-8.39E-01	1.32E-22		-2.68E-01	1.10E-03		Unigene27320_All//gi|257219560|gb|ACV50433.1|//1.00E-45//chloroplast ferritin 2 precursor [Jatropha curcas]	Unigene27320_All//2.00E-34//AT3G11050| ATFER2 (ferritin 2); binding / ferric iron binding / oxidoreductase/ transition metal ion binding	Unigene27320_All//0.00E+00//gi|13354388|gb|BG444736.1|BG444736		ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene27321_All	1029	0.31	0.20	0.31	25.85	41.76	79.40	9.61	11.33	16.49	-6.31E-01	6.22E-01		2.53E-02	1.00E+00		6.92E-01	6.44E-20		1.62E+00	3.27E-133	Up	2.37E-01	1.38E-01		7.79E-01	8.03E-11		Unigene27321_All//gi|30698967|ref|NP_177524.2|//7.00E-57//BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75299562|sp|Q8GWK7.1|BEE3_ARATH RecName: Full=Transcription factor BEE 3; AltName: Full=Protein Brassinosteroid enhanced expression 3; AltName: Full=Transcription factor EN 76; AltName: Full=bHLH transcription factor bHLH050; AltName: Full=Basic helix-loop-helix protein 50; Short=bHLH 50; Short=AtbHLH50	Unigene27321_All//3.00E-51//AT1G73830| BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor	Unigene27321_All//3.00E-121//TC150221	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr +
Unigene27322_All	1184	0.00	0.00	0.00	2.52	3.32	6.71	0.75	0.78	1.28	null	null		null	null		3.93E-01	2.29E-01		1.41E+00	4.79E-11	Up	5.05E-02	9.61E-01		7.70E-01	9.92E-02		Unigene27322_All//gi|30698967|ref|NP_177524.2|//8.00E-53//BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75299562|sp|Q8GWK7.1|BEE3_ARATH RecName: Full=Transcription factor BEE 3; AltName: Full=Protein Brassinosteroid enhanced expression 3; AltName: Full=Transcription factor EN 76; AltName: Full=bHLH transcription factor bHLH050; AltName: Full=Basic helix-loop-helix protein 50; Short=bHLH 50; Short=AtbHLH50	Unigene27322_All//1.00E-47//AT1G73830| BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor	Unigene27322_All//1.00E-93//TC150221	bHLH	ko04712|Circadian rhythm - plant		nr +
Unigene27323_All	1376	12.74	29.50	3.79	1.74	0.20	0.20	7.19	7.17	10.92	1.21E+00	3.89E-40	Up	-1.75E+00	4.10E-29	Down	-3.12E+00	1.16E-10	Down	-3.14E+00	2.53E-09	Down	-4.30E-03	1.02E+00		6.02E-01	1.72E-06		Unigene27323_All//gi|227204229|dbj|BAH56966.1|//1.00E-133//AT4G36850 [Arabidopsis thaliana]	Unigene27323_All//2.00E-134//AT4G36850| INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Cystinosin/ERS1p repeat (InterPro:IPR006603); BEST Arabidopsis thaliana protein match is: PQ-loop repeat family protein / transmembrane family protein (TAIR:AT2G41050.1); Has 599 Blast hits to 441 proteins in 106 species: Archae - 0; Bacteria - 0; Metazoa - 197; Fungi - 311; Plants - 38; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink).	Unigene27323_All//0.00E+00//DN804070				nr -
Unigene27325_All	627	52.65	18.02	19.87	65.47	65.47	75.99	99.06	47.80	48.80	-1.55E+00	1.64E-47	Down	-1.41E+00	9.00E-40	Down	0.00E+00	9.98E-01		2.15E-01	6.30E-03		-1.05E+00	7.91E-60	Down	-1.02E+00	1.02E-58	Down	Unigene27325_All//gi|258406674|gb|ACV72060.1|//1.00E-106//RackK1 [Phaseolus vulgaris]	Unigene27325_All//1.00E-103//AT1G48630| RACK1B_AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding	Unigene27325_All//0.00E+00//gi|78323542|gb|DT543816.1|DT543816		ko03022|Basal transcription factors		nr +
Unigene27326_All	1013	48.76	38.97	42.16	7.67	8.46	4.99	0.08	0.12	1.26	-3.23E-01	1.78E-05		-2.10E-01	9.70E-03		1.42E-01	5.47E-01		-6.19E-01	2.59E-03		5.68E-01	7.82E-01		3.91E+00	4.24E-07	Up	Unigene27326_All//gi|226508540|ref|NP_001150384.1|//3.00E-42//FHA domain containing protein [Zea mays] >gi|195638808|gb|ACG38872.1| FHA domain containing protein [Zea mays]	Unigene27326_All//7.00E-40//AT2G21530| forkhead-associated domain-containing protein / FHA domain-containing protein	Unigene27326_All//0.00E+00//DW517846				nr +
Unigene27327_All	479	15.29	15.97	34.68	31.30	21.14	22.91	47.05	40.84	34.85	6.28E-02	7.76E-01		1.18E+00	1.19E-15	Up	-5.67E-01	2.08E-05		-4.50E-01	1.60E-03		-2.04E-01	6.37E-02		-4.33E-01	1.59E-05		Unigene27327_All//gi|159487004|ref|XP_001701526.1|//3.00E-06//glyoxal or galactose oxidase [Chlamydomonas reinhardtii] >gi|158271587|gb|ED097403.1| glyoxal or galactose oxidase [Chlamydomonas reinhardtii]		Unigene27327_All//9.00E-120//TC151198				nr +
Unigene27328_All	1177	0.13	2.58	1.09	2.03	1.55	4.22	0.93	3.52	8.02	4.28E+00	1.18E-13	Up	3.02E+00	1.48E-04	Up	-3.90E-01	3.59E-01		1.06E+00	8.95E-05	Up	1.91E+00	2.16E-10	Up	3.10E+00	3.35E-40	Up	Unigene27328_All//gi|124360510|gb|ABN08520.1|//1.00E-77//Protein kinase [Medicago truncatula]	Unigene27328_All//0.00E+00//AT5G35090| MAPKKK15; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene27328_All//0.00E+00//gi|78326107|gb|DT546381.1|DT546381		ko04626|Plant-pathogen interaction		nr -
Unigene27329_All	2286	1.42	0.84	1.37	27.46	18.72	13.59	0.26	0.18	0.12	-7.53E-01	2.83E-02		-4.62E-02	9.05E-01		-5.52E-01	5.26E-20		-1.01E+00	1.76E-50	Down	-5.02E-01	5.74E-01		-1.09E+00	1.86E-01		Unigene27329_All//gi|224093786|ref|XP_002369991.1|//0.00E+00//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222852894|gb|EEE90441.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene27329_All//0.00E+00//AT5G10180| AST68; sulfate transmembrane transporter	Unigene27329_All//8.00E-22//TC150451				nr +
Unigene27331_All	631	30.76	200.43	66.33	32.53	68.38	82.10	72.83	48.82	42.62	2.70E+00	0.00E+00	Up	1.11E+00	6.65E-35	Up	1.07E+00	2.13E-41	Up	1.34E+00	1.15E-63	Up	-5.77E-01	2.45E-16		-7.73E-01	1.33E-27		Unigene27331_All//gi|115466590|ref|NP_001056894.1|//1.00E-56//Os06g0163200 [Oryza sativa Japonica Group] >gi|113594934|dbj|BAF18808.1| Os06g0163200 [Oryza sativa Japonica Group]	Unigene27331_All//2.00E-52//AT5G25770| unknown protein	Unigene27331_All//0.00E+00//TC165103				nr -

Unigene27332_All	954	0.49	2.18	0.39	1.15	3.93	13.44	49.19	202.36	182.49	2.14E+00	2.88E-05	Up	-3.37E-01	7.34E-01		1.78E+00	6.61E-08	Up	3.55E+00	2.63E-52	Up	2.04E+00	0.00E+00	Up	1.89E+00	0.00E+00	Up	Unigene27332_All//gi|283136100|gb|ADB11369.1|//5.00E-77//tau class glutathione transferase GSTU43 [Populus trichocarpa]	Unigene27332_All//5.00E-51//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	Unigene27332_All//0.00E+00//DT464570		ko00480|Glutathione metabolism		nr -
Unigene27333_All	1272	7.69	16.13	9.42	10.53	10.61	14.70	13.73	14.46	12.15	1.07E+00	4.93E-17	Up	2.92E-01	1.01E-01		1.06E-02	9.57E-01		4.81E-01	1.26E-04		7.47E-02	6.19E-01		-1.76E-01	1.59E-01		Unigene27333_All//gi|18396813|ref|NP_564310.1|//5.00E-88//SYP61 (SYNTAXIN OF PLANTS 61); SNAP receptor [Arabidopsis thaliana] >gi|28380156|sp|Q94617.1|SYP61_ARATH RecName: Full=Syntaxin-61; Short=AtSYP61; AltName: Full=Osmotic stress-sensitive mutant 1 >gi|16041650|gb|AAK40222.2|AF355754_1 syntaxin of plants 61 [Arabidopsis thaliana]	Unigene27333_All//5.00E-70//AT1G28490| SYP61 (SYNTAXIN OF PLANTS 61); SNAP receptor	Unigene27333_All//0.00E+00//gi|109867418|gb|DW496394.1|DW496394		ko04130|SNARE interactions in vesicular transport		nr -
Unigene27335_All	699	3.07	3.41	3.66	6.98	5.17	2.97	4.60	3.83	4.10	1.51E-01	7.07E-01		2.53E-01	5.60E-01		-4.33E-01	1.10E-01		-1.23E+00	6.36E-06	Down	-2.65E-01	4.30E-01		-1.64E-01	6.11E-01		Unigene27335_All//gi|224092083|ref|XP_002309467.1|//5.00E-32//f-box family protein [Populus trichocarpa] >gi|222855443|gb|EEE92990.1| f-box family protein [Populus trichocarpa]	Unigene27335_All//3.00E-23//AT4G33210| F-box family protein (FBL15)	Unigene27335_All//0.00E+00//gi|21097628|gb|BQ409941.1|BQ409941				nr -
Unigene27336_All	1215	0.00	38.91	2.02	0.16	2.01	14.27	0.31	0.38	3.80	1.52E+01	4.78E-273	Up	1.10E+01	1.64E-13	Up	3.62E+00	6.72E-11	Up	6.44E+00	1.23E-98	Up	2.73E-01	7.69E-01		3.60E+00	9.24E-23	Up	Unigene27336_All//gi|226496133|ref|NP_001151589.1|//1.00E-76//protein phosphatase 2C ABI1 [Zea mays] >gi|195647972|gb|ACG43454.1| protein phosphatase 2C ABI1 [Zea mays]	Unigene27336_All//1.00E-54//AT3G11410| PP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA); protein binding / protein serine/threonine phosphatase	Unigene27336_All//1.00E-25//TC164924				nr +
Unigene27337_All	569	7.82	8.37	6.27	19.09	15.37	13.89	26.75	11.39	8.96	9.89E-02	7.28E-01		-3.18E-01	3.14E-01		-3.12E-01	7.42E-02		-4.58E-01	7.88E-03		-1.23E+00	1.82E-19	Down	-1.58E+00	8.21E-29	Down	Unigene27337_All//gi|20197808|gb|AAU15256.1|//2.00E-20//Expressed protein [Arabidopsis thaliana] >gi|109134131|gb|ABG25064.1| At2g18245 [Arabidopsis thaliana]	Unigene27337_All//1.00E-21//AT2G18245| unknown protein	Unigene27337_All//0.00E+00//DT049264				nr -
Unigene27338_All	834	198.43	195.69	212.74	175.31	253.93	171.88	26.41	21.55	12.66	-2.01E-02	6.65E-01		1.01E-01	1.81E-02		5.35E-01	1.81E-61		-2.85E-02	6.37E-01		-2.94E-01	5.92E-03		-1.06E+00	9.92E-23	Down	Unigene27338_All//gi|186615717|gb|ABQ96663.1|//2.00E-81//F-box protein [Gossypium hirsutum]	Unigene27338_All//3.00E-44//AT4G24210| SLY1 (SLEEPY1)	Unigene27338_All//0.00E+00//gi|21094035|gb|BQ406360.1|BQ406360				nr -
Unigene27340_All	1395	2.59	13.00	2.98	11.25	11.97	10.23	7.85	13.03	35.55	2.33E+00	5.76E-45	Up	2.02E-01	5.45E-01		9.00E-02	5.94E-01		-1.37E-01	4.09E-01		7.31E-01	3.74E-10		2.18E+00	1.12E-140	Up	Unigene27340_All//gi|259121427|gb|ACV92033.1|//3.00E-89//WRKY transcription factor 31 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene27340_All//1.00E-53//AT5G49520| WRKY48; transcription factor	Unigene27340_All//0.00E+00//TC140811	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene27341_All	630	96.67	64.42	70.58	267.34	207.60	146.39	71.88	34.83	15.87	-5.86E-01	5.66E-18		-4.54E-01	4.31E-11		-3.65E-01	8.26E-25		-8.69E-01	5.51E-104		-1.05E+00	2.03E-43	Down	-2.18E+00	3.15E-130	Down	Unigene27341_All//gi|38566582|gb|AAR24181.1|//9.00E-19//At4g09890 [Arabidopsis thaliana] >gi|108240010|gb|ABR92324.1| At4g09890 [Arabidopsis thaliana]	Unigene27341_All//5.00E-20//AT4G09890| unknown protein	Unigene27341_All//0.00E+00//gi|164344895|gb|ES827162.1|ES827162				nr +
Unigene27345_All	901	5.28	5.23	2.60	4.75	5.47	6.02	1.13	4.08	1.99	-1.49E-02	9.78E-01		-1.02E+00	4.28E-04	Down	2.01E-01	5.40E-01		3.39E-01	2.22E-01		1.86E+00	5.37E-09	Up	8.21E-01	5.13E-02					Unigene27345_All//2.00E-45//gi|109840790|gb|DW239350.1|DW239350				
Unigene27346_All	750	0.00	1.01	0.28	2.86	2.98	1.20	2.65	5.52	14.61	9.99E+00	1.77E-04	Up	8.15E+00	1.41E-01		6.34E-02	9.04E-01		-1.25E+00	4.94E-03		1.06E+00	9.04E-05	Up	2.46E+00	1.45E-36	Up	Unigene27346_All//gi|209970618|gb|ACJ03070.1|//5.00E-63//M18-53Bp [Malus floribunda]	Unigene27346_All//2.00E-34//AT2G34930| disease resistance family protein	Unigene27346_All//3.00E-114//ES811464		ko04626|Plant-pathogen interaction		nr +
Unigene27347_All	807	0.65	0.50	0.53	1.91	1.79	0.90	1.83	1.61	7.21	-3.68E-01	6.83E-01		-2.96E-01	7.50E-01		-9.46E-02	8.46E-01		-1.10E+00	4.18E-02		-1.92E-01	7.04E-01		1.97E+00	3.02E-15	Up	Unigene27347_All//gi|209970618|gb|ACJ03070.1|//3.00E-60//M18-53Bp [Malus floribunda]	Unigene27347_All//1.00E-36//AT2G34930| disease resistance family protein	Unigene27347_All//3.00E-108//ES811464		ko04626|Plant-pathogen interaction		nr +
Unigene27348_All	821	0.00	0.00	0.00	2.06	1.38	0.44	4.79	0.41	2.47	null	null		null	null		-5.76E-01	2.53E-01		-2.23E+00	7.57E-05	Down	-3.56E+00	5.95E-19	Down	-9.53E-01	3.78E-04		Unigene27348_All//gi|224065140|ref|XP_002301687.1|//1.00E-60//leucine-rich repeat transmembrane protein [Populus trichocarpa] >gi|222843413|gb|EEE80960.1| leucine-rich repeat transmembrane protein [Populus trichocarpa]	Unigene27348_All//2.00E-48//AT1G48480| RKL1; ATP binding / kinase/ protein serine/threonine kinase	Unigene27348_All//4.00E-154//TC175345				nr +
Unigene27349_All	1593	0.30	0.25	0.00	4.32	3.63	3.69	9.58	1.34	2.23	-2.16E-01	8.17E-01		-8.21E+00	8.65E-03		-2.49E-01	3.11E-01		-2.28E-01	3.78E-01		-2.84E+00	3.12E-58	Down	-2.11E+00	1.47E-42	Down	Unigene27349_All//gi|224065140|ref|XP_002301687.1|//1.00E-158//leucine-rich repeat transmembrane protein [Populus trichocarpa] >gi|222843413|gb|EEE80960.1| leucine-rich repeat transmembrane protein [Populus trichocarpa]	Unigene27349_All//3.00E-114//AT3G17840| RLK902; ATP binding / kinase/ protein serine/threonine kinase	Unigene27349_All//0.00E+00//TC175345				nr +
Unigene27350_All	758	25.75	23.06	15.67	34.90	32.39	34.97	62.08	32.53	20.02	-1.59E-01	2.40E-01		-7.17E-01	2.88E-08		-1.08E-01	3.91E-01		3.20E-03	9.77E-01		-9.32E-01	1.91E-37		-1.63E+00	1.12E-91	Down	Unigene27350_All//gi|162464278|ref|NP_001105143.1|//1.00E-50//VIP3 protein [Zea mays] >gi|13446646|emb|CAC35070.1| VIP3 protein [Zea mays]	Unigene27350_All//1.00E-40//AT1G08780| AIP3 (ABI3-INTERACTING PROTEIN 3); unfolded protein binding	Unigene27350_All//0.00E+00//gi|13244725|gb|BE054452.2|BE054452				nr -
Unigene27351_All	746	2.38	1.83	1.93	1.80	4.29	5.45	13.60	26.11	98.42	-3.79E-01	4.35E-01		-3.07E-01	5.62E-01		1.25E+00	2.50E-04	Up	1.60E+00	5.49E-07	Up	9.41E-01	3.47E-16		2.86E+00	1.05E-283	Up	Unigene27351_All//gi|50253464|gb|AAT71934.1|//1.00E-07//At2g47485 [Arabidopsis thaliana] >gi|51972104|gb|AAU15156.1| At2g47485 [Arabidopsis thaliana]	Unigene27351_All//1.00E-05//AT2G47485| unknown protein					nr +
Unigene27353_All	591	22.22	19.55	26.58	52.17	65.49	121.51	181.85	133.10	127.13	-1.85E-01	2.72E-01		2.58E-01	9.30E-02		3.28E-01	5.21E-05		1.22E+00	1.46E-76	Up	-4.50E-01	6.83E-24		-5.16E-01	2.49E-31		Unigene27353_All//gi|283136142|gb|ADB11390.1|//1.00E-26//tau class glutathione transferase GSTU24 [Populus trichocarpa]	Unigene27353_All//8.00E-12//AT3G09270| ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	Unigene27353_All//0.00E+00//gi|164283733|gb|ES851610.1|ES851610		ko00480|Glutathione metabolism		nr +
Unigene27354_All	723	3.26	28.66	5.16	6.41	9.48	7.93	11.58	27.69	11.63	3.14E+00	1.02E-70	Up	6.63E-01	4.60E-02		5.65E-01	9.47E-03		3.08E-01	2.57E-01		1.26E+00	4.16E-26	Up	5.90E-03	9.72E-01		Unigene27354_All//gi|94807642|gb|AB747118.1|//2.00E-20//At5g57123 [Arabidopsis thaliana]	Unigene27354_All//2.00E-25//AT5G10695| unknown protein	Unigene27354_All//0.00E+00//TC159655				nr -
Unigene27355_All	1127	0.51	1.39	0.52	1.90	5.62	5.05	5.59	4.56	9.12	1.45E+00	8.58E-03		2.52E-02	9.98E-01		1.56E+00	4.93E-11	Up	1.41E+00	4.61E-08	Up	-2.93E-01	1.93E-01		7.06E-01	5.72E-06		Unigene27355_All//gi|15232355|ref|NP_191612.1|//1.00E-65//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|62900345|sp|O49743.1|GATA4_ARATH RecName: Full=GATA transcription factor 4; Short=AtGATA-4 >gi|14190407|gb|AAK55684.1|AF378881_1 AT3g60530/T8B10_190 [Arabidopsis thaliana] >gi|2959736|emb|CAA74002.1| homologous to GATA-binding transcription factors [Arabidopsis thaliana] >gi|7288001|emb|CAB81839.1| GATA transcription factor 4 [Arabidopsis thaliana] >gi|45117395|gb|AAR62588.1| AT3g60530/T8B10_190 [Arabidopsis thaliana] >gi|15215891|gb|AAK91489.1| AT3g60530/T8B10_190 [Arabidopsis thaliana]	Unigene27355_All//5.00E-52//AT3G60530| zinc finger (GATA type) family protein	Unigene27355_All//0.00E+00//TC145610	C2C2-GATA			nr +
Unigene27357_All	1415	24.03	32.66	36.35	19.05	21.42	19.37	23.16	22.66	10.53	4.42E-01	1.32E-08		5.97E-01	3.48E-15		1.69E-01	1.08E-01		2.47E-02	8.57E-01		-3.16E-02	7.58E-01		-1.14E+00	3.20E-37	Down	Unigene27357_All//gi|116310462|emb|CAH67466.1|//8.00E-84//OS1GRa0159110.11 [Oryza sativa (indica cultivar-group)]	Unigene27357_All//5.00E-103//AT3G60590| unknown protein	Unigene27357_All//0.00E+00//TC162886				nr -
Unigene27359_All	796	109.70	126.86	120.82	26.35	37.38	50.33	14.98	22.21	62.66	2.10E-01	5.53E-05		1.39E-01	1.63E-02		5.05E-01	3.92E-08		9.34E-01	5.47E-28		5.68E-01	1.27E-06		2.06E+00	4.08E-132	Up	Unigene27359_All//gi|75338852|sp|Q9ZQE6.1|CML1_ARATH/8.00E-43//RecName: Full=Calmodulin-like protein 1 >gi|30102922|gb|AAP21379.1| At2g15680 [Arabidopsis thaliana]	Unigene27359_All//4.00E-44//AT2G15680| calmodulin-related protein, putative	Unigene27359_All//0.00E+00//TC145569		ko04626|Plant-pathogen interaction		nr -
Unigene2736_All	1150	15.06	13.53	13.15	99.20	74.83	77.80	39.71	23.26	13.61	-1.55E-01	2.93E-01		-1.96E-01	1.95E-01		-4.07E-01	1.17E-20		-3.51E-01	3.70E-14		-7.72E-01	1.48E-26		-1.54E+00	3.97E-82	Down	Unigene2736_All//gi|297810567|ref|XP_002873167.1|//1.00E-101//ACT domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319004|gb|EFH49426.1| ACT domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2736_All//7.00E-97//AT5G04740| ACT domain-containing protein	Unigene2736_All//0.00E+00//TC132202			GO:0006950//GO:0009526//GO:0009532//GO:0009534//GO:0031406	nr -
Unigene27360_All	676	13.85	20.31	10.95	9.36	19.51	16.37	21.39	25.16	32.77	5.52E-01	2.67E-04		-3.40E-01	9.37E-02		1.06E+00	1.19E-12	Up	8.07E-01	1.63E-06		2.34E-01	6.67E-02		6.15E-01	1.80E-09		Unigene27360_All//gi|186511712|ref|NP_001118974.1|//1.00E-103//MBK; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Unigene27360_All//2.00E-104//AT4G13020| MBK; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene27360_All//0.00E+00//TC176397		ko03420|Nucleotide excision repair		nr +
Unigene27361_All	777	1.95	6.78	6.17	0.71	1.73	1.22	1.58	2.69	0.97	1.80E+00	6.96E-10	Up	1.66E+00	7.48E-08	Up	1.29E+00	2.91E-02		7.92E-01	2.99E-01		7.69E-01	5.41E-02		-6.96E-01	1.86E-01					Unigene27361_All//0.00E+00//TC148517				
Unigene27362_All	1443	5.44	3.23	2.55	11.32	10.98	11.77	11.28	8.52	6.98	-7.52E-01	2.90E-04		-1.09E+00	6.61E-07	Down	-4.47E-02	8.19E-01		5.56E-02	7.23E-01		-4.06E-01	1.04E-03		-6.92E-01	1.09E-08		Unigene27362_All//gi|297815942|ref|XP_002873854.1|//1.00E-140//transcription regulator/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297321692|gb|EFH52113.1| transcription regulator/ zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene27362_All//4.00E-121//AT3G47610| transcription regulator/ zinc ion binding	Unigene27362_All//0.00E+00//TC139367				nr +
Unigene27364_All	999	0.63	1.52	1.39	4.64	4.83	3.48	3.51	2.80	1.24	1.28E+00	2.09E-02		1.14E+00	5.84E-02		5.75E-02	8.58E-01		-4.14E-01	1.60E-01		-3.26E-01	3.05E-01		-1.51E+00	6.97E-07	Down	Unigene27364_All//gi|15217445|ref|NP_177893.1|//1.00E-104//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|12323299|gb|AAG51631.1|AC012193_13 thaumatin-like protein; 12104-13574 [Arabidopsis thaliana]	Unigene27364_All//1.00E-104//AT1G77700| pathogenesis-related thaumatin family protein					nr -
Unigene27365_All	474	31.57	19.88	23.82	60.53	70.61	63.55	153.07	53.96	101.95	-6.67E-01	3.89E-06		-4.07E-01	7.41E-03		2.22E-01	1.79E-02		7.02E-02	5.88E-01		-1.50E+00	1.46E-121	Down	-5.86E-01	9.47E-27		Unigene27365_All//gi|3334115|sp|O22342.1|ADT1_GOSHI//7.00E-42//RecName: Full=ADP,ATP carrier protein 1, mitochondrial; AltName: Full=ADP/ATP translocase 1; AltName: Full=Adenine nucleotide translocator 1; Short=ANT 1; Flags: Precursor >gi|2463664|gb|AAB72047.1| adenine nucleotide translocator 1 [Gossypium hirsutum]	Unigene27365_All//2.00E-23//AT5G13490| AAC2 (ADP/ATP carrier 2); ATP:ADP antiporter/ binding	Unigene27365_All//0.00E+00//TC174802				nr +

Unigene27370_All	787	223.84	386.23	331.27	66.59	78.54	205.85	25.95	48.06	36.70	7.87E-01	2.26E-145		5.66E-01	6.91E-68		2.38E-01	1.90E-04		1.63E+00	3.81E-266	Up	8.89E-01	5.68E-28		5.00E-01	1.36E-08		Unigene27370_All//gi|115452497|ref|NP_001049849.1|//9.00E-39//0s03g0299600 [Oryza sativa Japonica Group] >gi|113548320|dbj|BAF11763.1| Os03g0299600 [Oryza sativa Japonica Group]	Unigene27370_All//5.00E-30//AT3G10985| SAG20 (SENESCENCE ASSOCIATED GENE 20)	Unigene27370_All//0.00E+00//TC156933				nr +
Unigene27371_All	2962	0.57	0.27	0.65	0.45	0.40	0.21	5.54	5.40	15.41	-1.05E+00	4.04E-02		1.96E-01	6.73E-01		-2.00E-01	7.50E-01		-1.09E+00	6.42E-02		-3.53E-02	8.10E-01		1.48E+00	3.81E-76	Up	Unigene27371_All//gi|223452339|gb|ACM89497.1|//0.00E+00//receptor-like protein kinase like protein [Glycine max]	Unigene27371_All//0.00E+00//AT5G35370| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding			ko04626|Plant-pathogen interaction		nr +
Unigene27372_All	996	5.67	61.40	48.38	6.30	8.06	5.76	0.13	0.04	0.08	3.44E+00	3.83E-226	Up	3.09E+00	2.46E-158	Up	3.54E-01	9.28E-02		-1.30E-01	6.29E-01		-1.60E+00	5.34E-01		-6.70E-01	7.20E-01		Unigene27372_All//gi|87241486|gb|AB033344.1|//8.00E-66//Pollen Ole e 1 allergen and extensin [Medicago truncatula]	Unigene27372_All//8.00E-39//AT5G15780| pollen Ole e 1 allergen and extensin family protein	Unigene27372_All//0.00E+00//gi|109875829|gb|DW504803.1|DW504803				nr -
Unigene27373_All	1010	1.71	4.57	3.37	4.34	2.90	1.43	5.44	10.59	8.84	1.42E+00	1.89E-06	Up	9.81E-01	5.16E-03		-5.83E-01	3.65E-02		-1.60E+00	1.15E-07	Down	9.61E-01	1.45E-09		6.99E-01	3.20E-05		Unigene27373_All//gi|75154211|sp|Q8L7R5.1|U497J_ARATH//3.00E-54//RecName: Full=UPF0497 membrane protein At3g23200 >gi|30102860|gb|AAP21348.1| At3g23220 [Arabidopsis thaliana]	Unigene27373_All//4.00E-46//AT3G23200| unknown protein	Unigene27373_All//0.00E+00//DW519577				nr +
Unigene27375_All	583	35.90	63.97	46.95	92.11	90.67	107.14	40.76	84.52	161.06	8.33E-01	2.72E-20		3.87E-01	3.25E-04		-2.28E-02	8.32E-01		2.18E-01	1.13E-03		1.05E+00	1.25E-47	Up	1.98E+00	2.11E-235	Up	Unigene27375_All//gi|259121417|gb|ACV92028.1|//3.00E-37//WRKY transcription factor 26 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene27375_All//1.00E-13//AT2G23320| WRKY15; calmodulin binding / transcription factor	Unigene27375_All//2.00E-69//DV849051	WRKY			nr +
Unigene27377_All	704	64.51	26.34	32.15	89.65	71.37	76.15	261.85	107.58	142.21	-1.29E+00	9.38E-50	Down	-1.00E+00	3.14E-32	Down	-3.29E-01	5.48E-08		-2.36E-01	3.44E-04		-1.28E+00	4.70E-242	Down	-8.81E-01	7.46E-135		Unigene27377_All//gi|224060325|ref|XP_002300143.1|//1.00E-129//mitochondrial phosphate carrier protein [Populus trichocarpa] >gi|222847401|gb|EEE84948.1| mitochondrial phosphate carrier protein [Populus trichocarpa]	Unigene27377_All//7.00E-117//AT5G14040| mitochondrial phosphate transporter	Unigene27377_All//0.00E+00//TC129860				nr -
Unigene27378_All	673	34.67	26.58	23.58	41.01	41.39	46.98	133.31	55.52	61.98	-3.84E-01	7.27E-04		-5.56E-01	1.80E-06		1.36E-02	9.24E-01		1.96E-01	5.63E-02		-1.26E+00	2.59E-115	Down	-1.11E+00	6.73E-96	Down	Unigene27378_All//gi|257219570|gb|ACV50438.1|//2.00E-47//ribosomal protein L37 [Jatropha curcas]	Unigene27378_All//1.00E-43//AT3G16080| 60S ribosomal protein L37 (RPL37C)	Unigene27378_All//0.00E+00//TC152630		ko03010|Ribosome		nr +
Unigene27380_All	670	1.87	2.50	1.11	8.18	6.12	5.93	1.01	3.18	1.43	4.13E-01	4.09E-01		-7.52E-01	2.32E-01		-4.19E-01	9.89E-02		-4.63E-01	7.55E-02		1.66E+00	7.87E-05	Up	4.99E-01	4.19E-01		Unigene27380_All//gi|170660047|gb|ACB28472.1|//4.00E-50//polyprotein [Ananas comosus]						nr +
Unigene27382_All	2110	0.57	0.31	0.20	1.91	0.78	1.16	3.99	8.44	7.57	-8.69E-01	1.56E-01		-1.50E+00	2.71E-02		-1.29E+00	7.14E-06	Down	-7.26E-01	1.61E-02		1.08E+00	1.70E-18	Up	9.25E-01	2.03E-13		Unigene27382_All//gi|41079288|gb|AB99490.1|//0.00E+00//PHO1-like protein [Arabidopsis thaliana]	Unigene27382_All//0.00E+00//AT2G03240| LOCATED IN: integral to membrane; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G14040.1); Has 764 Blast hits to 738 proteins in 146 species: Archae - 0; Bacteria - 0; Metazoa - 262; Fungi - 250; Plants - 154; Viruses - 0; Other Eukaryotes - 98 (source: NCBI BLink).	Unigene27382_All//0.00E+00//CO071120				nr -
Unigene27383_All	572	26.89	16.48	17.04	29.09	25.22	27.32	92.99	47.28	39.49	-7.07E-01	7.24E-07		-6.59E-01	7.58E-06		-2.06E-01	1.58E-01		-9.05E-02	6.12E-01		-9.76E-01	1.67E-45		-1.24E+00	3.28E-68	Down	Unigene27383_All//gi|75299406|sp|Q8GTE3.1|RS3A_CICAR//2.00E-51//RecName: Full=40S ribosomal protein S3a >gi|24817254|emb|CAD56219.1| ribosomal protein S3a [Cicer arietinum]	Unigene27383_All//6.00E-48//AT4G34670| 40S ribosomal protein S3A (RPS3aB)	Unigene27383_All//0.00E+00//gi|13244762|gb|BE054034.2|BE054034		ko03010|Ribosome		nr +
Unigene27384_All	645	7.63	6.28	7.27	2.32	14.90	7.91	14.03	15.16	17.29	-2.79E-01	3.34E-01		-6.98E-02	8.08E-01		2.68E+00	2.19E-32	Up	1.77E+00	6.88E-10	Up	1.12E-01	5.78E-01		3.02E-01	4.76E-02		Unigene27384_All//gi|297805770|ref|XP_002870769.1|//7.00E-33//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316605|gb|EFH47028.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27384_All//6.00E-26//AT5G39670| calcium-binding EF hand family protein	Unigene27384_All//3.00E-46//gi|109885980|gb|DW514950.1|DW514950		ko04626|Plant-pathogen interaction		nr -
Unigene27386_All	1047	33.83	22.02	24.72	47.44	37.30	42.23	37.11	15.29	13.85	-6.20E-01	7.53E-12		-4.53E-01	1.02E-06		-3.47E-01	5.13E-07		-1.68E-01	3.62E-02		-1.28E+00	2.52E-51	Down	-1.42E+00	5.40E-62	Down	Unigene27386_All//gi|18398140|ref|NP_564385.1|//3.00E-40//NFD3 (NUCLEAR FUSION DEFECTIVE 3); structural constituent of ribosome [Arabidopsis thaliana]	Unigene27386_All//2.00E-37//AT1G31817| NFD3 (NUCLEAR FUSION DEFECTIVE 3); structural constituent of ribosome	Unigene27386_All//0.00E+00//TC141944		ko03010|Ribosome		nr -
Unigene27387_All	970	6.10	21.73	18.61	20.08	12.07	12.71	76.76	135.13	46.37	1.83E+00	1.66E-38	Up	1.61E+00	8.08E-27	Up	-7.34E-01	1.45E-10		-6.60E-01	5.39E-08		8.16E-01	4.23E-82		-7.27E-01	9.10E-40		Unigene27387_All//gi|16848451|gb|AAB36543.1|//6.00E-41//DnaJ-like protein [Phaseolus vulgaris]	Unigene27387_All//1.00E-33//AT2G17880| DNAJ heat shock protein, putative	Unigene27387_All//0.00E+00//TC154838				nr +
Unigene27388_All	710	4.35	9.35	5.10	12.14	8.10	7.57	7.09	6.48	3.93	1.10E+00	2.49E-06	Up	2.30E-01	5.16E-01		-5.84E-01	1.52E-03		-6.81E-01	4.05E-04		-1.30E-01	6.33E-01		-8.51E-01	2.42E-04		Unigene27388_All//gi|15231204|ref|NP_187939.1|//6.00E-28//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|9294537|dbj|BAB02800.1| DnaJ-like protein [Arabidopsis thaliana] >gi|32816917|gb|AAP88343.1| At3g13310 [Arabidopsis thaliana]	Unigene27388_All//3.00E-23//AT3G13310| DNAJ heat shock N-terminal domain-containing protein	Unigene27388_All//0.00E+00//TC162697				nr +
Unigene27389_All	1987	0.79	3.90	4.98	3.01	6.33	6.59	0.04	0.00	0.08	2.30E+00	2.51E-19	Up	2.66E+00	5.64E-28	Up	1.07E+00	2.70E-12	Up	1.13E+00	7.79E-13	Up	-5.41E+00	4.04E-01		9.13E-01	6.24E-01		Unigene27389_All//gi|224123896|ref|XP_002319191.1|//0.00E+00//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222857567|gb|EEE95114.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene27389_All//1.00E-161//AT5G17860| CAX7 (calcium exchanger 7); calcium:sodium antiporter/ cation:cation antiporter	Unigene27389_All//0.00E+00//ES839743				nr -
Unigene27390_All	659	2.06	6.15	2.42	3.48	5.54	3.56	3.21	3.93	3.39	1.58E+00	1.34E-06	Up	2.32E-01	6.46E-01		6.72E-01	3.48E-02		3.54E-02	9.44E-01		2.94E-01	4.34E-01		7.77E-02	8.46E-01		Unigene27390_All//gi|18411983|ref|NP_567243.1|//6.00E-91//ATCUL1 (ARABIDOPSIS THALIANA CULLIN 1); protein binding [Arabidopsis thaliana] >gi|79324981|ref|NP_001031575.1| ATCUL1 (ARABIDOPSIS THALIANA CULLIN 1); protein binding [Arabidopsis thaliana] >gi|79324983|ref|NP_001031576.1| ATCUL1 (ARABIDOPSIS THALIANA CULLIN 1); protein binding [Arabidopsis thaliana] >gi|68052236|sp|Q94H96.1|CUL1_ARATH RecName: Full=Cullin-1 >gi|30524960|emb|CAC85264.1| cullin 1 [Arabidopsis thaliana] >gi|222423687|dbj|BAH10810.1| AT4G02570 [Arabidopsis thaliana]	Unigene27390_All//4.00E-71//AT4G02570| ATCUL1 (ARABIDOPSIS THALIANA CULLIN 1); protein binding	Unigene27390_All//0.00E+00//ES810516		ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair		nr -
Unigene27391_All	991	6.81	7.36	3.44	10.00	6.74	6.20	9.86	6.12	4.38	1.12E-01	6.08E-01		-9.86E-01	3.32E-05		-5.69E-01	7.93E-04		-6.91E-01	1.00E-04		-6.89E-01	2.47E-05		-1.17E+00	3.23E-12	Down	Unigene27391_All//gi|30687459|ref|NP_189078.2|//2.00E-89//SYP32 (SYNTAXIN OF PLANTS 32); SNAP receptor [Arabidopsis thaliana] >gi|28380163|sp|Q9LK09.1|SYP32_ARATH RecName: Full=Syntaxin-32; Short=AtSYP32 >gi|11994697|dbj|BAB02935.1| probable t-SNARE (soluble NSF attachment protein receptor) SED5; ER to Golgi transport [Arabidopsis thaliana]	Unigene27391_All//4.00E-63//AT3G24350| SYP32 (SYNTAXIN OF PLANTS 32); SNAP receptor	Unigene27391_All//0.00E+00//TC173651		ko04130|SNARE interactions in vesicular transport		nr +
Unigene27393_All	838	4.93	3.93	4.51	6.30	7.40	8.25	6.61	3.99	1.95	-3.28E-01	2.92E-01		-1.29E-01	6.81E-01		2.31E-01	3.93E-01		3.88E-01	9.73E-02		-7.28E-01	1.21E-03		-1.76E+00	9.33E-13	Down	Unigene27393_All//gi|30689328|ref|NP_181857.2|//7.00E-41//far-red impaired responsive family protein / FAR1 family protein [Arabidopsis thaliana]	Unigene27393_All//1.00E-40//AT2G43280| far-red impaired responsive family protein / FAR1 family protein					nr -
Unigene27397_All	790	41.46	42.78	52.10	75.79	93.89	71.52	93.44	49.57	34.75	4.53E-02	6.60E-01		3.30E-01	1.35E-04		3.09E-01	3.55E-08		-8.38E-02	3.12E-01		-9.15E-01	1.86E-56		-1.43E+00	1.06E-117	Down	Unigene27397_All//gi|211906514|gb|ACJ11750.1|//1.00E-121//lactoylglutathione lyase [Gossypium hirsutum]	Unigene27397_All//8.00E-102//AT1G11840| ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase/ metal ion binding	Unigene27397_All//0.00E+00//TC169962		ko00620|Pyruvate metabolism		nr +
Unigene27398_All	1547	0.88	0.88	0.28	4.12	10.93	7.33	1.72	1.03	3.63	8.20E-03	9.87E-01		-1.67E+00	8.96E-03		1.41E+00	8.17E-25	Up	8.30E-01	5.84E-07		-7.46E-01	3.09E-02		1.08E+00	1.55E-06	Up	Unigene27398_All//gi|210111348|gb|ACJ07153.1|//3.00E-76//R2R3 MYB transcription factor [Gossypium hirsutum]	Unigene27398_All//7.00E-68//AT5G15310| ATMYB16 (MYB DOMAIN PROTEIN 16); DNA binding / transcription factor	Unigene27398_All//0.00E+00//TC166092	MYB			nr +
Unigene274_All	3023	13.48	55.50	25.95	17.30	31.70	31.06	12.73	22.98	30.89	2.04E+00	0.00E+00	Up	9.45E-01	4.58E-50		8.74E-01	1.42E-65		8.44E-01	7.59E-55		8.52E-01	3.13E-47		1.28E+00	1.06E-124	Up	Unigene274_All//gi|4874274|gb|AAD31339.1|AC007354_12//0.00E+00//Similar to gb|X02844 lipase precursor from Staphylococcus hyicus. ESTs gb|AI239406 and gb|T76725 come from this gene [Arabidopsis thaliana] >gi|30387885|gb|AAP31958.1| At1g10740 [Arabidopsis thaliana]	Unigene274_All//0.00E+00//AT1G10740| unknown protein	Unigene274_All//0.00E+00//TC161440				nr +
Unigene2740_All	1702	5.32	12.41	6.60	15.42	12.08	14.17	4.42	6.38	3.72	1.22E+00	1.50E-21	Up	3.12E-01	8.92E-02		-3.53E-01	4.12E-04		-1.22E-01	3.33E-01		5.30E-01	5.74E-04		-2.49E-01	2.02E-01		Unigene2740_All//gi|297839263|ref|XP_002887513.1|//1.00E-157//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333354|gb|EFH63772.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2740_All//3.00E-150//AT1G73880| UGT89B1 (UDP-GLUCOSYL TRANSFERASE 89B1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl group	Unigene2740_All//0.00E+00//gi|78327915|gb|DT548189.1|DT548189		ko00908|Zeatin biosynthesis		nr +

Unigene27400_All	784	12.81	4.59	2.58	4.07	2.64	2.30	1.02	2.03	0.76	-1.48E+00	4.47E-14	Down	-2.31E+00	4.32E-24	Down	-6.26E-01	6.27E-02		-8.20E-01	1.80E-02		9.83E-01	3.70E-02		-4.27E-01	5.42E-01		Unigene27400_All//gi|15231568|ref|NP_189282.1|//2.00E-43//octicosapeptide/Phox/Bemlp (PB1) domain-containing protein [Arabidopsis thaliana] >gi|42570483|ref|NP_850632.2| octicosapeptide/Phox/Bemlp (PB1) domain-containing protein [Arabidopsis thaliana] >gi|42572541|ref|NP_974366.1| octicosapeptide/Phox/Bemlp (PB1) domain-containing protein [Arabidopsis thaliana] >gi|79607899|ref|NP_974365.2| octicosapeptide/Phox/Bemlp (PB1) domain-containing protein [Arabidopsis thaliana] >gi|88310174|gb|AAT41768.1| At3g26510 [Arabidopsis thaliana] >gi|50198888|gb|AAT70464.1| At3g26510 [Arabidopsis thaliana] >gi|222423305|dbj|BAH19828.1| AT3G26510 [Arabidopsis thaliana] >gi|222423555|dbj|BAH19747.1| AT3G26510 [Arabidopsis thaliana] >gi|222423780|dbj|BAH19856.1| AT3G26510 [Arabidopsis thaliana]	Unigene27400_All//9.00E-37//AT3G26510| octicosapeptide/Phox/Bemlp (PB1) domain-containing protein	Unigene27400_All//0.00E+00//TC153851				nr -
Unigene27405_All	2086	0.78	1.72	0.71	1.00	1.90	0.65	14.21	27.39	5.98	1.15E+00	5.31E-04	Up	-1.21E-01	8.10E-01		9.21E-01	1.95E-03		-6.27E-01	1.72E-01		9.47E-01	2.09E-46		-1.25E+00	4.74E-39	Down	Unigene27405_All//gi|209867508|gb|AC190292.1|//6.00E-86//WRKY transcription factor [Picrorhiza kurroa]	Unigene27405_All//7.00E-54//AT4G01720| WRKY47; transcription factor	Unigene27405_All//7.00E-50//AI730840	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene27406_All	447	14.63	7.71	9.53	22.29	19.11	17.58	10.40	5.14	2.67	-9.25E-01	6.69E-05		-6.19E-01	1.00E-02		-2.22E-01	2.61E-01		-3.42E-01	7.01E-02		-1.02E+00	5.46E-05	Down	-1.96E+00	2.10E-12	Down	Unigene27406_All//gi|122178675|sp|Q6J3M2.1|6631_ARATH//2.00E-29//RecName: Full=UPF0631 protein At3g19508	Unigene27406_All//2.00E-30//AT3G19508| unknown protein	Unigene27406_All//1.00E-158//DW509041				nr +
Unigene27407_All	1472	0.50	0.17	0.25	6.29	3.25	2.33	7.55	3.95	2.08	-1.53E+00	7.78E-02		-9.75E-01	2.64E-01		-9.53E-01	5.08E-08		-1.43E+00	2.78E-13	Down	-9.37E-01	1.54E-09		-1.86E+00	1.39E-26	Down	Unigene27407_All//gi|559921|emb|CAA56570.1|//1.00E-159//axi 1 [Nicotiana tabacum]	Unigene27407_All//9.00E-156//AT1G76270| unknown protein	Unigene27407_All//0.00E+00//DR456175				nr -
Unigene27408_All	1119	0.84	1.22	0.81	1.16	1.14	1.09	6.01	27.71	4.95	5.39E-01	3.59E-01		-5.70E-02	9.49E-01		-2.36E-02	9.50E-01		-8.70E-02	8.93E-01		2.21E+00	7.82E-88	Up	-2.80E-01	1.75E-01		Unigene27408_All//gi|38605517|sp|Q9SV60.1|XTH2_ARATH//3.00E-91//RecName: Full=Xyloglucan endotransglucosylase/hydrolase protein 2; Short=At-XTH2; Short=XTH-2; Flags: Precursor >gi|5123950|emb|CAB45508.1| endoxyloglucan transferase-like protein [Arabidopsis thaliana] >gi|7268011|emb|CAB78351.1| endoxyloglucan transferase-like protein [Arabidopsis thaliana]	Unigene27408_All//4.00E-90//AT4G13090| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene27408_All//0.00E+00//gi|164266375|gb|ES827892.1|ES827892				nr -
Unigene27409_All	1552	1.28	0.78	0.69	27.96	21.79	16.15	22.15	4.63	4.26	-7.09E-01	1.20E-01		-9.01E-01	6.17E-02		-3.60E-01	1.35E-06		-7.92E-01	3.19E-23		-2.26E+00	2.26E-100	Down	-2.38E+00	3.35E-110	Down	Unigene27409_All//gi|297598707|ref|NP_001046107.2|//1.00E-129//Os02g0184200 [Oryza sativa Japonica Group] >gi|255670659|dbj|BAF08021.2| Os02g0184200 [Oryza sativa Japonica Group]	Unigene27409_All//6.00E-113//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene27409_All//0.00E+00//TC137953		ko00190|Oxidative phosphorylation		nr -
Unigene27410_All	628	11.91	5.81	7.46	40.85	34.98	33.01	100.79	32.41	26.39	-1.04E+00	1.90E-06	Down	-6.75E-01	2.31E-03		-2.24E-01	4.05E-02		-3.08E-01	4.47E-03		-1.64E+00	5.52E-120	Down	-1.93E+00	1.41E-155	Down			Unigene27410_All//0.00E+00//TC139600				
Unigene27411_All	1108	11.62	38.46	5.38	13.67	24.86	17.77	11.33	14.49	16.94	1.73E+00	4.09E-71	Up	-1.11E+00	3.97E-11	Down	8.63E-01	1.13E-18		3.79E-01	2.25E-03		3.54E-01	4.95E-03		5.80E-01	2.02E-07		Unigene27411_All//gi|87241016|gb|AB032874.1|//8.00E-40//VQ [Medicago truncatula]	Unigene27411_All//2.00E-23//AT3G56880| VQ motif-containing protein	Unigene27411_All//0.00E+00//TC140785				nr +
Unigene27413_All	1127	0.42	0.36	0.14	1.46	3.02	1.84	2.29	0.37	1.73	-2.16E-01	8.17E-01		-1.56E+00	2.04E-01		1.05E+00	1.25E-03		3.38E-01	4.92E-01		-2.63E+00	1.34E-09	Down	-4.02E-01	2.48E-01		Unigene27413_All//gi|115450161|ref|NP_001048681.1|//9.00E-16//Os03g0105800 [Oryza sativa Japonica Group] >gi|113547152|dbj|BAF10595.1| Os03g0105800 [Oryza sativa Japonica Group]	Unigene27413_All//2.00E-48//AT4G11450| unknown protein	Unigene27413_All//0.00E+00//TC178197				nr -
Unigene27414_All	651	25.96	21.02	15.05	39.33	30.84	41.83	28.51	14.19	19.34	-3.05E-01	2.77E-02		-7.86E-01	2.14E-08		-3.51E-01	5.40E-04		8.90E-02	4.87E-01		-1.01E+00	3.10E-17	Down	-5.60E-01	5.35E-07		Unigene27414_All//gi|18402072|ref|NP_565682.1|//6.00E-34//mitochondrial import inner membrane translocase (TIM10) [Arabidopsis thaliana] >gi|145329981|ref|NP_001077976.1| mitochondrial import inner membrane translocase (TIM10) [Arabidopsis thaliana] >gi|12230205|sp|Q9ZR33.1|TIM10_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit Tim10 >gi|5107174|gb|AAD39999.1|AF150093_1 small zinc finger-like protein [Arabidopsis thaliana] >gi|3980383|gb|AAC95186.1| expressed protein [Arabidopsis thaliana] >gi|28466793|gb|AAO44005.1| At2g29530 [Arabidopsis thaliana]	Unigene27414_All//3.00E-35//AT2G29530| mitochondrial import inner membrane translocase (TIM10)	Unigene27414_All//0.00E+00//gi|13244647|gb|BE053536.2|BE053536				nr +
Unigene27415_All	863	3.15	3.70	1.79	23.84	20.99	8.32	3.28	1.89	2.77	2.31E-01	5.29E-01		-8.17E-01	4.17E-02		-1.84E-01	1.60E-01		-1.52E+00	2.10E-31	Down	-7.97E-01	1.65E-02		-2.45E-01	4.74E-01		Unigene27415_All//gi|281428053|gb|ADM69473.1|//1.00E-122//MYB transcription factor [Gossypium arboreum]	Unigene27415_All//1.00E-51//AT5G14750| ATMYB66 (MYB DOMAIN PROTEIN 66); DNA binding / protein binding / transcription factor/ transcription regulator	Unigene27415_All//0.00E+00//TC142972	MYB			nr -
Unigene27416_All	1028	1.88	0.35	1.45	1.89	1.78	1.71	0.70	1.46	1.12	-2.45E+00	1.00E-05	Down	-3.77E-01	4.36E-01		-9.01E-02	8.35E-01		-1.41E-01	7.62E-01		1.07E+00	2.90E-02		6.85E-01	2.12E-01		Unigene27416_All//gi|108864619|gb|ABA96093.2|//8.00E-82//oxidoreductase, aldo/keto reductase family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene27416_All//1.00E-38//AT1G04420| aldo/keto reductase family protein	Unigene27416_All//0.00E+00//gi|164267196|gb|ES807993.1|ES807993				nr -
Unigene27420_All	1272	7.90	6.21	6.45	9.16	6.17	6.50	13.59	5.65	6.20	-3.46E-01	6.21E-02		-2.93E-01	1.38E-01		-5.70E-01	2.16E-04		-4.96E-01	2.52E-03		-1.27E+00	6.31E-23	Down	-1.13E+00	6.10E-20	Down	Unigene27420_All//gi|222101943|gb|ACM44066.1|//1.00E-102//NADPH-dependent codeinone reductase-like protein [Papaver nudicaule]	Unigene27420_All//9.00E-110//AT1G59960| aldo/keto reductase, putative	Unigene27420_All//1.00E-74//gi|21090728|gb|BQ403041.1|BQ403041		ko00051|Fructose and mannose metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene27422_All	819	8.94	22.71	7.28	15.75	9.54	4.36	47.96	105.89	62.31	1.34E+00	6.10E-22	Up	-2.97E-01	2.15E-01		-7.23E-01	5.25E-07		-1.85E+00	2.84E-26	Down	1.14E+00	5.10E-95	Up	3.78E-01	5.40E-09		Unigene27422_All//gi|115482956|ref|NP_001065071.1|//7.00E-32//Os10g0518000 [Oryza sativa Japonica Group] >gi|113639680|dbj|BAF26985.1| Os10g0518000 [Oryza sativa Japonica Group]	Unigene27422_All//4.00E-56//AT4G24130| unknown protein	Unigene27422_All//0.00E+00//gi|109854540|gb|DW483519.1|DW483519				nr +
Unigene27423_All	1499	33.89	2.54	1.95	0.00	0.05	0.00	42.65	32.01	11.88	-3.74E+00	5.51E-204	Down	-4.12E+00	1.17E-211	Down	5.52E+00	6.10E-01		null	null		-4.14E-01	1.42E-12		-1.84E+00	2.15E-147	Down	Unigene27423_All//gi|62526573|gb|AX84672.1|//1.00E-164//aldo/keto reductase AKR [Manihot esculenta]	Unigene27423_All//2.00E-147//AT1G60710| ATR2; oxidoreductase	Unigene27423_All//0.00E+00//TC148226		ko00053|Ascorbate and aldarate metabolism//ko00051|Fructose and mannose metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr -
Unigene27426_All	1074	2.24	0.61	2.73	5.10	4.33	5.89	5.47	5.18	16.69	-1.87E+00	3.44E-05	Down	2.83E-01	4.68E-01		-2.37E-01	3.96E-01		2.07E-01	4.52E-01		-8.03E-02	7.38E-01		1.61E+00	2.28E-34	Up	Unigene27426_All//gi|18397921|ref|NP_566304.1|//9.00E-87//PUB9 (PLANT U-BOX 9); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75207393|sp|Q9SR70.1|PUB9_ARATH RecName: Full=U-box domain-containing protein 9; AltName: Full=Plant U-box protein 9 >gi|19715649|gb|AAL91644.1| AT3g07360/F21O3_7 [Arabidopsis thaliana]	Unigene27426_All//4.00E-88//AT3G07360| PUB9 (PLANT U-BOX 9); ubiquitin-protein ligase	Unigene27426_All//4.00E-105//TC160186				nr -
Unigene2743_All	1231	13.22	12.27	9.08	16.87	14.04	17.57	12.88	18.16	27.48	-1.08E-01	4.87E-01		-5.41E-01	1.51E-04		-2.65E-01	2.78E-02		5.86E-02	7.01E-01		4.96E-01	1.49E-06		1.09E+00	8.26E-36	Up	Unigene2743_All//gi|18398123|ref|NP_565388.1|//2.00E-90//metal ion binding [Arabidopsis thaliana] >gi|20198032|gb|AAD22294.2| expressed protein [Arabidopsis thaliana]	Unigene2743_All//8.00E-92//AT2G16460| metal ion binding	Unigene2743_All//0.00E+00//TC173363			GO:0016020//GO:0043169//GO:0043231	nr -
Unigene27430_All	1504	0.80	1.01	0.64	6.13	4.58	2.40	2.56	1.92	1.72	3.37E-01	5.39E-01		-3.28E-01	6.27E-01		-4.20E-01	2.22E-02		-1.35E+00	3.91E-12	Down	-4.16E-01	1.49E-01		-5.71E-01	3.38E-02		Unigene27430_All//gi|42567992|ref|NP_197554.2|//1.00E-128//ATBRXL4 (BREVIS RADIX-LIKE 4) [Arabidopsis thaliana] >gi|75151601|sp|Q8GZ92.1|BRXL4_ARATH RecName: Full=Protein Brevis radix-like 4; Short=AtBRXL4	Unigene27430_All//9.00E-125//AT5G20540| ATBRXL4 (BREVIS RADIX-LIKE 4)	Unigene27430_All//0.00E+00//TC161373				nr -
Unigene27433_All	632	10.18	12.19	11.46	62.19	70.83	67.24	24.89	10.58	16.77	2.59E-01	2.38E-01		1.70E-01	4.87E-01		1.88E-01	2.01E-02		1.13E-01	2.33E-01		-1.23E+00	3.99E-20	Down	-5.70E-01	3.15E-06		Unigene27433_All//gi|238909259|gb|ACR77748.1|//9.00E-43//plastocyanin-like domain-containing protein [Astragalus sinicus]	Unigene27433_All//1.00E-41//AT3G27200| plastocyanin-like domain-containing protein	Unigene27433_All//0.00E+00//DT527549				nr +
Unigene27436_All	855	8.75	4.09	6.73	5.07	6.44	6.34	1.68	1.08	0.89	-1.10E+00	5.32E-07	Down	-3.80E-01	9.70E-02		3.46E-01	1.99E-01		3.23E-01	2.47E-01		-6.45E-01	2.05E-01		-9.25E-01	5.24E-02		Unigene27436_All//gi|18401044|ref|NP_566539.1|//8.00E-74//isochorismatase hydrolase family protein [Arabidopsis thaliana] >gi|16648698|gb|AAL25541.1| AT3g16190/MYA6_2 [Arabidopsis thaliana] >gi|23505997|gb|AAN28858.1| At3g16190/MYA6_2 [Arabidopsis thaliana]	Unigene27436_All//4.00E-59//AT3G16190| isochorismatase hydrolase family protein	Unigene27436_All//6.00E-39//ES834461				nr -
Unigene27437_All	968	2.59	1.83	2.92	4.73	4.52	4.34	7.34	17.06	14.69	-5.02E-01	2.17E-01		1.68E-01	6.54E-01		-6.75E-02	8.26E-01		-1.26E-01	6.77E-01		1.22E+00	1.31E-20	Up	1.00E+00	1.28E-13	Up	Unigene27437_All//gi|297841079|ref|XP_002888421.1|//4.00E-70//enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334262|gb|EFH64680.1| enoyl-CoA hydratase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27437_All//5.00E-61//AT1G65520| ECI1 (DELTA(3), DELTA(2)-ENOYL COA ISOMERASE 1); carnitine racemase/ catalytic/ dodecenoyl-CoA delta-isomerase	Unigene27437_All//0.00E+00//gi|109859047|gb|DW488026.1|DW488026		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism		nr -
Unigene2744_All	946	6.91	19.50	9.79	11.22	9.32	9.69	18.68	44.67	8.93	1.50E+00	1.95E-25	Up	5.03E-01	1.11E-02		-2.67E-01	1.45E-01		-2.11E-01	2.90E-01		1.26E+00	3.31E-54	Up	-1.07E+00	1.60E-18	Down			Unigene2744_All//0.00E+00//DT466704				

Unigene27441_All	1863	2.53	0.60	0.60	9.06	10.35	7.01	13.19	5.70	13.15	-2.08E+00	9.95E-11	Down	-2.07E+00	3.56E-10	Down	1.92E-01	1.62E-01		-3.72E-01	6.09E-03		-1.21E+00	4.46E-30	Down	-3.80E-03	9.67E-01		Unigene27441_All//gi|115446441|ref|NP_001047000.1|//1.00E-46//0s02g0526700 [Oryza sativa Japonica Group] >gi|113536531|dbj|BAF08914.1| Os02g0526700 [Oryza sativa Japonica Group]	Unigene27441_All//5.00E-64//AT5G49100| unknown protein	Unigene27441_All//0.00E+00//TC176060				nr -
Unigene27442_All	1110	11.31	73.72	49.84	7.94	14.89	15.99	0.11	0.23	0.86	2.70E+00	1.02E-238	Up	2.14E+00	9.46E-120	Up	9.07E-01	2.70E-12		1.01E+00	2.22E-14	Up	9.83E-01	5.17E-01		2.91E+00	1.88E-04	Up	Unigene27442_All//gi|15146256|gb|AA83611.1|//4.00E-63//AT5g52420/K24M7_17 [Arabidopsis thaliana] >gi|19699160|gb|AAL90946.1| AT5g52420/K24M7_17 [Arabidopsis thaliana]	Unigene27442_All//2.00E-64//AT5G52420| unknown protein	Unigene27442_All//5.00E-111//DW230006				nr +
Unigene27443_All	533	15.02	22.06	11.79	20.19	17.57	22.88	54.81	45.72	25.79	5.54E-01	7.94E-04		-3.49E-01	1.17E-01		-2.00E-01	3.04E-01		1.81E-01	3.39E-01		-2.62E-01	4.26E-03		-1.09E+00	4.73E-31	Down	Unigene27443_All//gi|15220930|ref|NP_175778.1|//3.00E-61//RPT1A (REGULATORY PARTICLE TRIPLE-A 1A); ATPase [Arabidopsis thaliana] >gi|297853156|ref|XP_002894459.1| regulatory particle triple-a 1A [Arabidopsis lyrata subsp. lyrata] >gi|28558169|sp|Q9SS85.1|PRS7A_ARATH RecName: Full=26S protease regulatory subunit 7 homolog A; AltName: Full=26S proteasome subunit 7 homolog A; AltName: Full=26S proteasome AAA-ATPase subunit RPT1a; AltName: Full=Regulatory particle triple-A ATPase subunit 1a >gi|6056388|gb|AAF02852.1|AC009324_1 26S proteasome ATPase subunit [Arabidopsis thaliana] >gi|12324021|gb|AAG51970.1|AC022460_8 26S proteasome ATPase subunit; 3861-6264 [Arabidopsis thaliana] >gi|17065568|gb|AAL32938.1| 26S proteasome ATPase subunit [Arabidopsis thaliana] >gi|23197722|gb|AAN15388.1| 26S proteasome ATPase subunit [Arabidopsis thaliana] >gi|297340301|gb|EFH70718.1| regulatory particle triple-a 1A	Unigene27443_All//2.00E-62//AT1G53750| RPT1A (REGULATORY PARTICLE TRIPLE-A 1A); ATPase	Unigene27443_All//0.00E+00//CO076615		ko03050|Proteasome		nr -
Unigene27444_All	1031	7.76	4.77	6.09	1.45	1.64	1.66	5.33	1.70	2.74	-7.04E-01	5.91E-04		-3.49E-01	1.17E-01		1.75E-01	7.88E-01		2.00E-01	6.97E-01		-1.65E+00	3.32E-11	Down	-9.58E-01	1.70E-05		Unigene27444_All//gi|87214921|gb|ABD33279.1|//2.00E-31//Zinc finger, RING-type [Medicago truncatula]	Unigene27444_All//1.00E-22//AT4G24204| protein binding / zinc ion binding	Unigene27444_All//0.00E+00//TC154289				nr +
Unigene27445_All	796	10.71	6.17	8.76	22.34	18.17	25.02	18.64	11.45	6.31	-7.95E-01	6.10E-05		-2.90E-01	1.82E-01		-2.98E-01	2.14E-02		1.63E-01	2.45E-01		-7.04E-01	5.99E-08		-1.56E+00	9.13E-28	Down									
Unigene27447_All	1408	0.78	0.90	0.79	3.43	3.77	2.69	3.15	0.74	0.76	2.05E-01	7.16E-01		2.53E-02	9.88E-01		1.34E-01	6.60E-01		-3.49E-01	2.31E-01		-2.09E+00	2.23E-12	Down	-2.05E+00	1.66E-12	Down	Unigene27447_All//gi|15450719|gb|AAK96631.1|//1.00E-144//At1g79420/T8K14_16 [Arabidopsis thaliana] >gi|22654486|gb|AAM98335.1| At1g79420/T8K14_16 [Arabidopsis thaliana]	Unigene27447_All//2.00E-135//AT1G79420| unknown protein	Unigene27447_All//0.00E+00//TC170901				nr +
Unigene27448_All	633	31.08	65.48	22.29	28.09	26.28	20.55	11.96	54.74	21.52	1.08E+00	5.76E-34	Up	-4.79E-01	1.95E-04		-9.66E-02	5.39E-01		-4.51E-01	4.70E-04		2.19E+00	1.88E-97	Up	8.48E-01	4.00E-10		Unigene27448_All//gi|297832390|ref|XP_002884077.1|//3.00E-50//protein-methionine-s-oxide reductase [Arabidopsis lyrata subsp. lyrata] >gi|297329917|gb|EFH60336.1| protein-methionine-s-oxide reductase [Arabidopsis lyrata subsp. lyrata]	Unigene27448_All//3.00E-52//AT2G17705| unknown protein	Unigene27448_All//0.00E+00//TC168354				nr -
Unigene2745_All	2091	5.28	3.42	4.53	13.91	13.55	12.94	15.39	5.84	13.85	-6.28E-01	2.36E-04		-2.20E-01	2.47E-01		-3.77E-02	7.92E-01		-1.05E-01	3.99E-01		-1.40E+00	8.82E-49	Down	-1.52E-01	8.88E-02		Unigene2745_All//gi|34365761|gb|AAQ65192.1|//1.00E-144//At3g08670 [Arabidopsis thaliana]	Unigene2745_All//4.00E-60//AT3G08670| unknown protein	Unigene2745_All//0.00E+00//DW241422				nr +
Unigene27450_All	836	8.82	21.40	7.77	14.84	11.90	16.64	12.80	18.95	21.87	1.28E+00	1.34E-19	Up	-1.83E-01	4.40E-01		-3.18E-01	4.70E-02		1.65E-01	3.50E-01		5.66E-01	5.47E-06		7.74E-01	1.79E-11		Unigene27450_All//gi|18399399|ref|NP_565477.1|//5.00E-23//RPN1A (26S PROTEASOME REGULATORY SUBUNIT S2 1A); binding / enzyme regulator [Arabidopsis thaliana] >gi|20198043|gb|AAD21708.2| 26S proteasome regulatory subunit S2 (RPN1) [Arabidopsis thaliana] >gi|32700010|gb|AAP86655.1| 26S proteasome subunit RPN1a [Arabidopsis thaliana]	Unigene27450_All//2.00E-24//AT2G20580| RPN1A (26S PROTEASOME REGULATORY SUBUNIT S2 1A); binding / enzyme regulator	Unigene27450_All//2.00E-174//gi|21101171|gb|BQ413484.1|BQ413484		ko03050|Proteasome		nr -
Unigene27452_All	1310	0.40	2.55	0.20	1.67	2.18	2.03	3.42	4.66	3.04	2.68E+00	3.40E-10	Up	-9.75E-01	3.76E-01		3.83E-01	3.37E-01		2.82E-01	5.15E-01		4.45E-01	4.06E-02		-1.70E-01	5.44E-01		Unigene27452_All//gi|224122872|ref|XP_002318937.1|//3.00E-18//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222857313|gb|EEE94860.1| chromatin remodeling complex subunit [Populus trichocarpa]		Unigene27452_All//0.00E+00//ES835070				nr +
Unigene27456_All	979	7.32	3.16	4.90	3.71	4.82	3.60	0.00	0.09	0.00	-1.21E+00	9.05E-08	Down	-5.81E-01	1.10E-02		3.76E-01	2.01E-01		-4.58E-02	9.07E-01		6.42E+00	4.01E-01		null	null		Unigene27456_All//gi|30023666|gb|AAP13366.1|//3.00E-39//At1g21820 [Arabidopsis thaliana]	Unigene27456_All//2.00E-28//AT1G21830| unknown protein	Unigene27456_All//6.00E-61//gi|109877626|gb|DW506599.1|DW506599				nr -
Unigene27457_All	788	97.60	214.06	150.63	118.91	116.77	122.14	150.23	125.97	72.75	1.13E+00	3.17E-148	Up	6.26E-01	2.83E-37		-2.62E-02	7.23E-01		3.86E-02	5.94E-01		-2.54E-01	1.70E-09		-1.05E+00	1.44E-115	Down	Unigene27457_All//gi|297609877|ref|NP_001063805.2|//4.00E-27//Os09g0539500 [Oryza sativa Japonica Group] >gi|255679097|dbj|BAF25719.2| Os09g0539500 [Oryza sativa Japonica Group]	Unigene27457_All//2.00E-21//AT5G42190| ASK2 (ARABIDOPSIS SKP1-LIKE 2); protein binding / ubiquitin-protein ligase	Unigene27457_All//0.00E+00//TC140813		ko04141|Protein processing in endoplasmic reticulum/ko04120|Ubiquitin mediated proteolysis		nr +
Unigene27458_All	1040	2.52	1.07	0.36	2.44	1.79	1.82	3.37	2.53	1.57	-1.23E+00	2.07E-03		-2.81E+00	3.91E-08	Down	-4.50E-01	2.70E-01		-4.22E-01	3.23E-01		-4.14E-01	1.75E-01		-1.10E+00	1.38E-04	Down	Unigene27458_All//gi|226493972|ref|NP_001150073.1|//1.00E-101//LOC100284406 [Zea mays] >gi|195641730|gb|ACG40333.1| uracil-DNA glycosylase [Zea mays]	Unigene27458_All//5.00E-100//AT3G18630| uracil DNA glycosylase family protein	Unigene27458_All//0.00E+00//CO086349		ko03410|Base excision repair		nr +
Unigene27459_All	870	20.33	16.95	15.98	31.09	32.85	35.35	33.19	15.61	20.70	-2.62E-01	5.56E-02		-3.48E-01	1.30E-02		7.95E-02	5.49E-01		1.85E-01	7.84E-02		-1.09E+00	8.06E-30	Down	-6.81E-01	2.36E-14		Unigene27459_All//gi|124359813|gb|ABD33071.2|//3.00E-59//Thioredoxin domain 2; Thioredoxin fold [Medicago truncatula]	Unigene27459_All//1.00E-39//AT1G07960| ATPDIL5-1 (PDI-like 5-1)	Unigene27459_All//0.00E+00//TC134550		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene2746_All	1764	5.37	3.36	3.02	12.76	11.09	3.10	9.92	2.18	2.57	-6.76E-01	2.85E-04		-8.31E-01	1.92E-05		-2.03E-01	9.19E-02		-2.04E+00	9.60E-52	Down	-2.19E+00	1.82E-49	Down	-1.95E+00	5.44E-44	Down	Unigene2746_All//gi|17386118|gb|AAL38605.1|AF446872_1//0.00E+00//AT5g50150/MPF21_17 [Arabidopsis thaliana] >gi|15529145|gb|AAK97667.1| AT5g50150/MPF21_17 [Arabidopsis thaliana]	Unigene2746_All//1.00E-158//AT5G50150| unknown protein	Unigene2746_All//0.00E+00//TC151865				nr +
Unigene27460_All	934	0.67	0.49	0.34	1.44	1.03	1.40	4.30	1.70	2.18	-4.61E-01	6.19E-01		-9.75E-01	3.16E-01		-4.80E-01	4.15E-01		-3.83E-02	9.48E-01		-1.34E+00	2.17E-06	Down	-9.83E-01	2.13E-04		Unigene27460_All//gi|119935825|gb|ABM06005.1|//2.00E-07//At5g04320 [Arabidopsis thaliana]	Unigene27460_All//8.00E-09//AT5G04320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: meiotic chromosome segregation; LOCATED IN: chromosome, centromeric region, nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Shugoshin, C-terminal (InterPro:IPR011515); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G10440.1); Has 951 Blast hits to 743 proteins in 147 species: Archae - 0; Bacteria - 61; Metazoa - 474; Fungi - 60; Plants - 48; Viruses - 0; Other Eukaryotes - 308 (source: NCBI BLink).	Unigene27460_All//0.00E+00//CO101544				nr +
Unigene27462_All	2001	1.93	0.51	0.56	1.44	0.31	0.32	5.11	3.49	4.02	-1.93E+00	3.26E-08	Down	-1.79E+00	4.30E-07	Down	-2.22E+00	7.27E-09	Down	-2.19E+00	1.06E-07	Down	-5.52E-01	5.21E-04		-3.46E-01	2.82E-02		Unigene27462_All//gi|297812551|ref|XP_002874159.1|//1.00E-162//C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319996|gb|EFH50418.1| C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27462_All//1.00E-144//AT5G24030| SLAH3 (SLAC1 HOMOLOGUE 3); transporter	Unigene27462_All//0.00E+00//TC149205				nr +
Unigene27463_All	854	12.31	11.15	9.42	14.23	13.35	10.95	9.95	7.05	4.80	-1.43E-01	4.57E-01		-3.87E-01	3.92E-02		-9.27E-02	6.15E-01		-3.79E-01	2.16E-02		-4.98E-01	5.07E-03		-1.05E+00	3.54E-09	Down	Unigene27463_All//gi|17065491|gb|AAL32901.1|//3.00E-32//Unknown protein [Arabidopsis thaliana] >gi|30102802|gb|AAP21319.1| At5g22280 [Arabidopsis thaliana]	Unigene27463_All//2.00E-31//AT3G44280| unknown protein	Unigene27463_All//0.00E+00//TC139722				nr -
Unigene27465_All	366	4.86	4.43	4.36	11.71	15.34	8.88	9.13	3.54	2.94	-1.34E-01	7.71E-01		-1.55E-01	7.45E-01		3.90E-01	1.37E-01		-3.98E-01	2.01E-01		-1.37E+00	1.36E-05	Down	-1.63E+00	2.61E-07	Down			Unigene27465_All//1.00E-136//gi|109888907|gb|DW517876.1|DW517876				ESTscan +
Unigene27466_All	648	5.73	5.79	4.03	11.53	9.41	6.13	13.25	5.48	1.41	1.34E-02	9.86E-01		-5.10E-01	1.35E-01		-2.94E-01	1.87E-01		-9.11E-01	1.38E-05		-1.27E+00	7.22E-12	Down	-3.23E+00	1.12E-38	Down			Unigene27466_All//0.00E+00//TC167035				
Unigene27467_All	806	0.00	0.00	0.00	0.00	0.00	0.00	2.05	6.69	2.17	null	null		null	null		null	null		null	null		1.71E+00	1.56E-11	Up	8.82E-02	8.46E-01		Unigene27467_All//gi|294861496|gb|ADF45510.1|//2.00E-12//type 2 ribosome-inactivating protein precursor [Camellia sinensis] >gi|294861498|gb|ADF45511.1| type 2 ribosome-inactivating protein precursor [Camellia sinensis]		Unigene27467_All//2.00E-08//TC158682				nr +
Unigene27468_All	2151	0.10	0.05	0.00	0.23	0.16	0.63	27.77	100.46	36.52	-1.05E+00	5.65E-01		-6.60E+00	1.46E-01		-5.33E-01	5.94E-01		1.44E+00	1.69E-02		1.85E+00	0.00E+00	Up	3.95E-01	1.93E-14		Unigene27468_All//gi|294861496|gb|ADF45510.1|//2.00E-91//type 2 ribosome-inactivating protein precursor [Camellia sinensis] >gi|294861498|gb|ADF45511.1| type 2 ribosome-inactivating protein precursor [Camellia sinensis]		Unigene27468_All//1.00E-42//TC136011				nr +

Unigene27469_All	1550	0.78	0.00	0.21	2.06	0.93	1.92	13.58	22.38	84.10	-9.60E+00	5.01E-07	Down	-1.91E+00	7.10E-03		-1.14E+00	4.82E-04	Down	-9.70E-02	7.96E-01		7.20E-01	3.72E-18		2.63E+00	0.00E+00	Up	Unigene27469_All//gi|18423435|ref|NP_568777.1|//7.00E-68//WRKY27; transcription factor [Arabidopsis thaliana] >gi|29839628|sp|Q9FLX8.1|WRK27_ARATH RecName: Full=Probable WRKY transcription factor 27; AltName: Full=WRKY DNA-binding protein 27 >gi|15991728|gb|AAL13041.1|AF418310_1 WRKY transcription factor 27 [Arabidopsis thaliana] >gi|111074370|gb|ABH04558.1|At5g52830 [Arabidopsis thaliana]	Unigene27469_All//6.00E-52//AT5G52830| WRKY27; transcription factor	Unigene27469_All//8.00E-15//TC163461	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene27470_All	1016	3.19	9.28	10.69	4.31	6.78	7.07	0.75	1.93	1.53	1.54E+00	6.87E-14	Up	1.74E+00	3.15E-18	Up	6.52E-01	2.37E-03		7.12E-01	9.58E-04		1.37E+00	1.31E-03		1.03E+00	2.56E-02		Unigene27470_All//gi|194570021|gb|ACF75544.1|//9.00E-27//At3g11690 [Arabidopsis thaliana]	Unigene27470_All//4.00E-22//AT3G11690| unknown protein	Unigene27470_All//6.00E-21//TC146993				nr -
Unigene27472_All	1204	3.74	1.30	2.65	7.94	9.41	6.34	1.33	0.62	1.42	-1.52E+00	6.01E-07	Down	-4.94E-01	1.03E-01		2.44E-01	1.78E-01		-3.26E-01	9.57E-02		-1.09E+00	1.97E-02		9.25E-02	8.38E-01		Unigene27472_All//gi|28416695|gb|AA042878.1|//4.00E-68//At1g51540 [Arabidopsis thaliana] >gi|110743235|dbj|BAE99508.1|At1g51540 [Arabidopsis thaliana]	Unigene27472_All//1.00E-68//AT1G51540| INVOLVED IN: biological_process unknown; LOCATED IN: Golgi apparatus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Galactose oxidase/kelch, beta-propeller (InterPro:IPR011043), Kelch repeat type 1 (InterPro:IPR006652), Kelch repeat type 2 (InterPro:IPR011498), Kelch related (InterPro:IPR013089), Kelch-type beta propeller (InterPro:IPR015915); BEST Arabidopsis thaliana protein match is: kelch repeat-containing protein (TAIR:AT3G27220.1); Has 1571 Blast hits to 1365 proteins in 151 species: Archae - 11; Bacteria - 200; Metazoa - 1128; Fungi - 24; Plants - 53; Viruses - 41; Other Eukaryotes - 114 (source: NCBI BLink).	Unigene27472_All//0.00E+00//DF465748				nr -
Unigene27473_All	777	9.90	54.78	13.16	68.60	46.89	65.74	54.41	200.26	193.60	2.47E+00	3.20E-112	Up	4.11E-01	3.00E-02		-5.49E-01	7.19E-17		-6.14E-02	4.98E-01		1.88E+00	0.00E+00	Up	1.83E+00	0.00E+00	Up	Unigene27473_All//gi|87162616|gb|AB028411.1|//2.00E-26//C3363B.2 , related [Medicago truncatula]		Unigene27473_All//0.00E+00//TC146686		ko03040|Spliceosome		nr -
Unigene27475_All	1230	1057.73	628.26	1113.62	282.93	396.59	285.52	17.98	38.53	18.36	-7.52E-01	0.00E+00		7.43E-02	7.54E-08		4.87E-01	1.32E-119		1.32E-02	6.99E-01		1.10E+00	3.34E-49	Up	3.07E-02	7.92E-01		Unigene27475_All//gi|268612156|pdb|2WSC|N//2.00E-66//Chain N, Improved Model Of Plant Photosystem I >gi|268612174|pdb|2WSE|N Chain N, Improved Model Of Plant Photosystem I >gi|268612192|pdb|2WSF|N Chain N, Improved Model Of Plant Photosystem I >gi|28629385|gb|AAO49652.1|photosystem I-N subunit [Phaseolus vulgaris]	Unigene27475_All//1.00E-51//AT5G64040| PSAN; calmodulin binding	Unigene27475_All//0.00E+00//TC143213		ko00195|Photosynthesis		nr +
Unigene27477_All	1065	1.13	2.24	2.05	3.60	4.40	3.35	3.41	3.34	1.12	9.85E-01	1.78E-02		8.59E-01	5.86E-02		2.88E-01	3.47E-01		-1.04E-01	7.54E-01		-3.35E-02	9.30E-01		-1.61E+00	1.06E-07	Down	Unigene27477_All//gi|18086334|gb|AAL57630.1|//4.00E-16//AT5g61910/k22g18_30 [Arabidopsis thaliana]	Unigene27477_All//3.00E-23//AT2G32910| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61910.3); Has 954 Blast hits to 804 proteins in 137 species: Archae - 0; Bacteria - 69; Metazoa - 446; Fungi - 64; Plants - 191; Viruses - 0; Other Eukaryotes - 184 (source: NCBI BLink).	Unigene27477_All//0.00E+00//CO089363				nr +
Unigene2748_All	2440	2.68	1.47	1.66	6.80	5.26	9.61	12.25	4.59	6.17	-8.62E-01	1.88E-04		-6.93E-01	3.87E-03		-3.69E-01	4.80E-03		4.99E-01	5.80E-06		-1.42E+00	3.18E-46	Down	-9.89E-01	2.75E-27		Unigene2748_All//gi|115438873|ref|NP_001043716.1|//1.00E-62//Os01g0649000 [Oryza sativa Japonica Group] >gi|113533247|dbj|BAF05630.1|Os01g0649000 [Oryza sativa Japonica Group]	Unigene2748_All//5.00E-62//AT1G15420| unknown protein	Unigene2748_All//0.00E+00//TC139900				nr +
Unigene27481_All	830	1.83	0.49	0.51	1.80	0.50	1.09	3.06	4.99	1.97	-1.90E+00	1.25E-03		-1.83E+00	2.74E-03		-1.85E+00	5.94E-04	Down	-7.26E-01	1.93E-01		7.06E-01	8.12E-03		-6.35E-01	6.30E-02				Unigene27481_All//0.00E+00//TC168884				
Unigene27482_All	743	32.46	19.16	18.28	35.80	34.62	43.95	16.73	7.14	10.67	-7.61E-01	1.36E-11		-8.29E-01	9.59E-13		-4.84E-02	7.30E-01		2.96E-01	1.75E-03		-1.23E+00	5.97E-16	Down	-6.49E-01	3.26E-06		Unigene27482_All//gi|225442456|ref|XP_002283614.1|//6.00E-43//PREDICTED: similar to B5 #5 (cytochrome b5 family protein #5); heme binding / transition metal ion binding [Vitis vinifera]	Unigene27482_All//1.00E-34//AT1G60660| CB5LP (CYTOCHROME B5-LIKE PROTEIN); heme binding	Unigene27482_All//0.00E+00//TC150347		ko00910|Nitrogen metabolism		nr -
Unigene27483_All	873	1.62	1.33	0.37	2.11	3.00	2.74	2.91	2.01	1.10	-2.78E-01	6.08E-01		-2.14E+00	1.24E-03		5.06E-01	2.19E-01		3.77E-01	4.01E-01		-5.31E-01	1.42E-01		-1.41E+00	8.57E-05	Down			Unigene27483_All//2.00E-08//TC136631				
Unigene27484_All	908	1.50	1.45	1.06	1.76	2.39	2.29	3.59	2.76	1.62	-4.63E-02	9.46E-01		-5.05E-01	3.82E-01		4.45E-01	3.40E-01		3.82E-01	4.38E-01		-3.77E-01	2.40E-01		-1.14E+00	1.61E-04	Down	Unigene27484_All//gi|92870927|gb|ABE80127.1|//1.00E-22//Auxin responsive SAUR protein [Medicago truncatula]	Unigene27484_All//3.00E-16//AT4G34750| auxin-responsive protein, putative / small auxin up RNA (SAUR_E)	Unigene27484_All//0.00E+00//ES791469				nr +
Unigene27485_All	1227	11.77	8.26	9.03	8.57	7.77	5.37	5.13	1.87	6.14	-5.11E-01	5.17E-04		-3.83E-01	1.40E-02		-1.40E-01	5.07E-01		-6.73E-01	8.97E-05		-1.45E+00	9.41E-11	Down	2.57E-01	1.90E-01		Unigene27485_All//gi|5852184|emb|CAB55422.1|//8.00E-34//H0811D08.3 [Oryza sativa (indica cultivar-group)]	Unigene27485_All//7.00E-08//AT1G73320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: Expressed protein (TAIR:AT1G08125.1); Has 1043 Blast hits to 1041 proteins in 162 species: Archae - 0; Bacteria - 35; Metazoa - 424; Fungi - 344; Plants - 150; Viruses - 0; Other Eukaryotes - 90 (source: NCBI BLink).	Unigene27485_All//0.00E+00//TC137785				nr -
Unigene27486_All	705	5.05	1.01	1.36	8.76	6.69	7.37	2.82	1.30	7.29	-2.33E+00	2.10E-09	Down	-1.89E+00	5.07E-07	Down	-3.89E-01	1.03E-01		-2.50E-01	3.51E-01		-1.11E+00	7.17E-03		1.37E+00	1.95E-08	Up	Unigene27486_All//gi|5669656|gb|AAD46413.1|AF096263.1|//1.00E-33//ER33 protein [Solanum lycopersicum]	Unigene27486_All//7.00E-33//AT1G05710| ethylene-responsive protein, putative	Unigene27486_All//0.00E+00//TC142836	bHLH			nr +
Unigene2749_All	1573	13.30	17.07	6.40	16.85	23.82	15.82	20.75	28.22	45.08	3.60E-01	6.39E-04		-1.06E+00	2.16E-16	Down	5.00E-01	6.15E-10		-9.08E-02	4.80E-01		4.44E-01	4.35E-10		1.12E+00	5.60E-77	Up	Unigene2749_All//gi|15223723|ref|NP_172889.1|//1.00E-126//APK2A (PROTEIN KINASE 2A); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|75318424|sp|Q49839.1|APK2A_ARATH RecName: Full=Protein kinase 2A, chloroplastic; Flags: Precursor >gi|7262679|gb|AAF43937.1|AC012188_14 Strong similarity, practically identical, to APK2a protein from Arabidopsis thaliana gb|D88206 and contains a Eukaryotic protein kinase PF|00069 domain, ESTs gb|AA712684, gb|H76755, gb|AA651227 come from this gene >gi|2852447|dbj|BAA24694.1|protein kinase [Arabidopsis thaliana] >gi|16649049|gb|AAL24376.1| Strong similarity to APK2a protein [Arabidopsis thaliana]	Unigene2749_All//1.00E-123//AT1G14370| APK2A (PROTEIN KINASE 2A); ATP binding / kinase/ protein serine/threonine kinase	Unigene2749_All//0.00E+00//gi|164309554|gb|ES816041.1|ES816041		ko04626|Plant-pathogen interaction		nr -
Unigene27490_All	1160	20.75	7.86	14.64	12.58	10.54	11.56	10.61	3.57	4.74	-1.40E+00	4.32E-30	Down	-5.03E-01	1.17E-05		-2.56E-01	8.93E-02		-1.22E-01	4.86E-01		-1.57E+00	1.28E-22	Down	-1.16E+00	5.09E-15	Down	Unigene27490_All//gi|297803262|ref|XP_002869515.1|//1.00E-102//EMB1923 [Arabidopsis lyrata subsp. lyrata] >gi|297315351|gb|EFH45774.1|EMB1923 [Arabidopsis lyrata subsp. lyrata]	Unigene27490_All//1.00E-86//AT4G28210| emb1923 (embryo defective 1923)	Unigene27490_All//0.00E+00//TC155483				nr +
Unigene27495_All	612	21.71	146.21	19.84	54.94	96.72	74.61	28.88	51.22	88.73	2.75E+00	5.90E-266	Up	-1.30E-01	4.62E-01		8.16E-01	3.53E-36		4.41E-01	6.59E-09		8.27E-01	1.06E-20		1.62E+00	2.30E-103	Up	Unigene27495_All//gi|292668913|gb|ADE41111.1|//8.00E-49//AP2 domain class transcription factor [Malus x domestica]	Unigene27495_All//2.00E-22//AT5G44210| EKP9 (ERF DOMAIN PROTEIN 9); DNA binding / transcription factor/ transcription repressor	Unigene27495_All//0.00E+00//EX171752	AP2-EREBP			nr -
Unigene27496_All	818	15.29	7.12	8.85	2.25	2.65	2.10	0.00	0.00	0.00	-1.10E+00	3.17E-11	Down	-7.88E-01	2.05E-06		2.35E-01	6.20E-01		-1.03E-01	8.38E-01		null	null		null	null		Unigene27496_All//gi|4966370|gb|AAD34701.1|AC006341_29//8.00E-63//F3O9.30 [Arabidopsis thaliana] >gi|22655156|gb|AAM98168.1|expressed protein [Arabidopsis thaliana] >gi|30023742|gb|AAP13404.1|At1g16500 [Arabidopsis thaliana]	Unigene27496_All//3.00E-60//AT1G79160| unknown protein	Unigene27496_All//0.00E+00//TC151425				nr +

Unigene27500_All	613	83.13	42.73	31.27	96.54	101.34	129.96	231.89	96.48	120.69	-9.60E-01	8.90E-35		-1.41E+00	1.67E-61	Down	7.00E-02	3.95E-01		4.29E-01	2.51E-14		-1.27E+00	1.16E-182	Down	-9.42E-01	1.27E-116		Unigene27500_All//gi|76160947|gb|AB40437.1|//1.00E-53//40S ribosomal protein S7-like protein [Solanum tuberosum] >gi|77999315|gb|ABB17004.1| ribosomal protein S7-like protein [Solanum tuberosum] >gi|82623373|gb|ABB87101.1| 40S ribosomal protein S7-like protein-like [Solanum tuberosum]	Unigene27500_All//2.00E-54//AT1G48830| 40S ribosomal protein S7 (RPS7A)	Unigene27500_All//0.00E+00//TC141548		ko03010|Ribosome		nr +
Unigene27501_All	778	1.41	0.85	1.30	4.99	3.05	2.21	3.91	1.50	2.10	-7.38E-01	2.50E-01		-1.19E-01	8.50E-01		-7.10E-01	1.58E-02		-1.18E+00	1.43E-04	Down	-1.38E+00	3.15E-05	Down	-8.98E-01	3.59E-03		Unigene27501_All//gi|106337893|emb|CAC10555.1|//1.00E-96//ammonium transporter (AMT1.1) [Lotus japonicus]	Unigene27501_All//1.00E-91//AT4G13510| AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter	Unigene27501_All//0.00E+00//DW496501				nr -
Unigene27503_All	1091	13.72	6.55	4.69	12.83	17.86	13.12	10.58	3.03	1.21	-1.07E+00	1.22E-12	Down	-1.55E+00	4.64E-21	Down	4.78E-01	4.76E-05		3.25E-02	8.62E-01		-1.81E+00	1.04E-25	Down	-3.13E+00	2.29E-50	Down	Unigene27503_All//gi|22328908|ref|NP_680738.1|//1.00E-81//methyltransferase [Arabidopsis thaliana]	Unigene27503_All//6.00E-79//AT4G24805| methyltransferase	Unigene27503_All//0.00E+00//TC144286				nr +
Unigene27505_All	748	8.39	5.22	4.06	21.78	19.01	25.36	20.01	12.63	11.98	-6.86E-01	3.51E-03		-1.05E+00	2.45E-05	Down	-1.96E-01	1.88E-01		2.20E-01	1.12E-01		-6.64E-01	2.61E-07		-7.40E-01	5.91E-09		Unigene27505_All//gi|14596139|gb|AK68797.1|//2.00E-19//Unknown protein [Arabidopsis thaliana]	Unigene27505_All//2.00E-20//AT1G06720| INVOLVED IN: ribosome biogenesis; LOCATED IN: nucleus; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: AARP2CN (InterPro:IPR012948), Protein of unknown function DUF663 (InterPro:IPR007034); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G42440.1); Has 7944 Blast hits to 5342 proteins in 373 species: Archae - 33; Bacteria - 667; Metazoa - 2609; Fungi - 1045; Plants - 414; Viruses - 80; Other Eukaryotes - 3096 (source: NCBI BLink).	Unigene27505_All//0.00E+00//TC143064				nr +
Unigene27506_All	827	165.25	448.43	263.09	45.48	56.25	69.47	6.03	2.78	3.28	1.44E+00	0.00E+00	Up	6.71E-01	7.65E-77		3.07E-01	2.83E-05		6.11E-01	1.91E-19		-1.12E+00	4.86E-06	Down	-8.81E-01	1.61E-04		Unigene27506_All//gi|4337175|gb|AAD18096.1|//7.00E-46//ESTs gb|T20589, gb|T04618, gb|AA597906, gb|T04111, gb|884180, gb|R65428, gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457, gb|T20921, gb|AA042762 and gb|AA720210 come from this gene [Arabidopsis thaliana]	Unigene27506_All//5.00E-47//AT1G09310| unknown protein	Unigene27506_All//0.00E+00//TC177124				nr -
Unigene27507_All	860	9.55	8.01	19.26	12.74	18.30	16.96	36.82	23.08	9.64	-2.53E-01	2.31E-01		1.01E+00	2.83E-12	Up	5.22E-01	8.06E-05		4.13E-01	4.99E-03		-6.74E-01	6.66E-15		-1.93E+00	2.90E-78	Down	Unigene27507_All//gi|20466362|gb|AAM20498.1|//2.00E-54//calmodulin-like protein [Arabidopsis thaliana] >gi|22136314|gb|AAM91235.1| calmodulin-like protein [Arabidopsis thaliana]	Unigene27507_All//4.00E-46//AT3G50770| calmodulin-related protein, putative	Unigene27507_All//0.00E+00//TC167355		ko04626|Plant-pathogen interaction		nr -
Unigene27508_All	1046	3.15	3.44	2.85	2.19	1.84	1.51	0.00	0.60	0.38	1.26E-01	6.95E-01		-1.45E-01	6.81E-01		-2.49E-01	5.87E-01		-5.36E-01	2.24E-01		9.23E+00	1.47E-04	Up	8.57E+00	3.96E-03		Unigene27508_All//gi|297790792|ref|XP_002863281.1|//1.00E-125//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297309915|gb|EFH39540.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene27508_All//2.00E-125//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene27508_All//0.00E+00//TC147263				nr -
Unigene27510_All	905	49.72	12.60	16.24	81.13	46.61	73.46	63.12	19.17	20.03	-1.98E+00	6.02E-91	Down	-1.61E+00	2.98E-66	Down	-8.00E-01	7.97E-45		-1.43E-01	2.72E-02		-1.72E+00	3.51E-116	Down	-1.66E+00	2.09E-113	Down	Unigene27510_All//gi|15221798|ref|NP_173289.1|//1.00E-106//60S ribosomal protein L6 (RPL6A) [Arabidopsis thaliana] >gi|75173375|sp|Q9FZ76.1|RL61_ARATH RecName: Full=60S ribosomal protein L6-1 >gi|9795602|gb|AAF98420.1|AC026238_12 Putative 60S ribosomal protein L6 [Arabidopsis thaliana] >gi|15451190|gb|AAK96866.1| Putative 60S ribosomal protein L6 [Arabidopsis thaliana]	Unigene27510_All//1.00E-87//AT1G74050| 60S ribosomal protein L6 (RPL6C)	Unigene27510_All//0.00E+00//TC147093		ko03010|Ribosome		nr +
Unigene27512_All	684	0.15	2.00	0.70	2.04	1.61	2.18	1.85	2.38	2.04	3.71E+00	7.18E-06	Up	2.20E+00	9.15E-02		-3.40E-01	5.62E-01		9.56E-02	8.79E-01		3.62E-01	4.56E-01		1.37E-01	7.79E-01		Unigene27512_All//gi|4702692 3|gb|AT008882.1|//2.00E-61//ring zinc finger protein [Hyacinthus orientalis]	Unigene27512_All//1.00E-32//AT1G75560| zinc knuckle (CCHC-type) family protein	Unigene27512_All//0.00E+00//TC142591				nr -
Unigene27514_All	761	4.26	15.25	4.62	6.09	7.42	6.65	34.17	56.79	57.06	1.84E+00	1.44E-21	Up	1.16E-01	7.30E-01		2.86E-01	3.06E-01		1.27E-01	6.94E-01		7.33E-01	4.47E-23		7.40E-01	3.81E-24		Unigene27514_All//gi|16604322|gb|AL24167.1|//1.00E-08//At2g37940/T8P21.15 [Arabidopsis thaliana] >gi|196991984|gb|AL969958.1| At2g37940/T8P21.15 [Arabidopsis thaliana]	Unigene27514_All//7.00E-10//AT2G37940| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: phosphatidic acid phosphatase-related / PAP2-related (TAIR:AT3G54020.1); Has 316 Blast hits to 316 proteins in 75 species: Archae - 0; Bacteria - 0; Metazoa - 213; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 55 (source: NCBI BLink).	Unigene27514_All//0.00E+00//gi|164349273|gb|ES815700.1|ES815700				nr -
Unigene27515_All	585	19.68	41.57	11.29	28.10	21.60	27.87	31.87	50.44	73.82	1.08E+00	2.34E-20	Up	-8.02E-01	4.03E-06		-3.79E-01	3.80E-03		-1.19E-02	9.45E-01		6.62E-01	1.53E-13		1.21E+00	1.87E-53	Up	Unigene27515_All//gi|222424688|dbj|BAH20298.1|//1.00E-13//AT2G37940 [Arabidopsis thaliana]	Unigene27515_All//7.00E-15//AT2G37940| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: phosphatidic acid phosphatase-related / PAP2-related (TAIR:AT3G54020.1); Has 316 Blast hits to 316 proteins in 75 species: Archae - 0; Bacteria - 0; Metazoa - 213; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 55 (source: NCBI BLink).	Unigene27515_All//0.00E+00//gi|164349273|gb|ES815700.1|ES815700				nr -
Unigene27519_All	980	2.99	2.64	3.80	13.27	14.55	14.33	1.60	3.24	0.28	-1.81E-01	6.03E-01		3.47E-01	3.16E-01		1.33E-01	4.50E-01		1.12E-01	5.49E-01		1.02E+00	1.11E-03		-2.49E+00	5.08E-06	Down	Unigene27519_All//gi|159138941|gb|AB889470.1|//2.00E-55//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene27519_All//2.00E-50//AT2G29500| 17.6 kDa class I small heat shock protein (HSP17.6B-CI)	Unigene27519_All//0.00E+00//TC148519				nr +
Unigene27522_All	677	2.78	8.23	3.22	10.89	7.38	5.47	13.24	16.36	7.18	1.57E+00	1.03E-08	Up	2.13E-01	6.16E-01		-5.62E-01	5.62E-03		-9.93E-01	2.85E-06		3.05E-01	5.49E-02		-8.83E-01	1.94E-07		Unigene27522_All//gi|224129628|ref|XP_002320633.1|//6.00E-11//predicted protein [Populus trichocarpa] >gi|118484370|gb|ABK94062.1| unknown [Populus trichocarpa] >gi|222861406|gb|EEE98948.1| predicted protein [Populus trichocarpa]		Unigene27522_All//0.00E+00//TC159690				nr +
Unigene27526_All	1284	0.57	24.94	20.53	3.03	2.84	4.96	0.00	0.00	0.00	5.45E+00	1.09E-160	Up	5.17E+00	1.26E-126	Up	-9.01E-02	8.20E-01		7.13E-01	2.08E-03		null	null		null	null		Unigene27526_All//gi|297605040|ref|NP_001056573.2|//1.00E-110//Os06g0109000 [Oryza sativa Japonica Group] >gi|255676646|dbj|BAF18487.2| Os06g0109000 [Oryza sativa Japonica Group]	Unigene27526_All//5.00E-59//AT1G08940| phosphoglycerate/bisphosphoglycerate mutase family protein	Unigene27526_All//0.00E+00//TC170446				nr +
Unigene27528_All	954	2.52	3.82	6.14	2.25	0.94	0.95	0.22	0.18	0.00	6.00E-01	6.35E-02		1.28E+00	1.15E-06	Up	-1.26E+00	2.52E-03		-1.25E+00	4.94E-03		-3.39E-01	8.12E-01		-7.79E+00	5.80E-02		Unigene27528_All//gi|222837071|gb|EEE75450.1|//9.00E-36//predicted protein [Populus trichocarpa]		Unigene27528_All//9.00E-63//gi|109826980|gb|DW225688.1|DW225688				nr -
Unigene27530_All	1996	0.21	0.86	0.53	1.15	0.97	1.83	21.25	27.16	26.37	2.04E+00	2.81E-04	Up	1.35E+00	6.01E-02		-2.49E-01	5.87E-01		6.75E-01	3.84E-02		3.54E-01	2.84E-08		3.12E-01	1.03E-06		Unigene27530_All//gi|15221488|ref|NP_177038.1|//0.00E+00//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|12229673|sp|Q9SX33.1|ALA9_ARATH RecName: Full=Putative phospholipid-transporting ATPase 9; Short=AtALA9; AltName: Full=Aminophospholipid flippase 9 >gi|5734708|gb|AAD49973.1|AC008075_6 Similar to gb|AF067820 ATPase II from Homo sapiens and is a member of PF|00122 E1-E2 ATPases family [Arabidopsis thaliana]	Unigene27530_All//0.00E+00//AT1G68710| haloacid dehalogenase-like hydrolase family protein					nr +
Unigene27531_All	509	4.63	4.38	2.30	9.98	4.67	6.92	4.73	4.11	4.15	-7.87E-02	8.45E-01		-1.01E+00	2.16E-02		-1.10E+00	9.94E-06	Down	-5.28E-01	4.94E-02		-2.06E-01	6.32E-01		-1.91E-01	6.09E-01		Unigene27531_All//gi|108863967|gb|AB622350.1|//2.00E-17//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene27531_All//2.00E-13//AT5G09225| unknown protein					nr +
Unigene27532_All	821	29.12	22.16	16.54	74.81	73.32	66.73	21.01	13.95	9.03	-3.95E-01	4.20E-04		-8.16E-01	2.50E-12		-2.91E-02	7.60E-01		-1.65E-01	1.92E-02		-5.91E-01	6.71E-07		-1.22E+00	2.88E-22	Down	Unigene27532_All//gi|18401618|ref|NP_564498.1|//1.00E-34//WPP2 [Arabidopsis thaliana] >gi|75168866|sp|Q9C500.1|WPP2_ARATH RecName: Full=WPP domain-containing protein 2; AltName: Full=MFP1 attachment factor 2	Unigene27532_All//3.00E-23//AT1G47200| WPP2	Unigene27532_All//0.00E+00//TC139258				nr -
Unigene27533_All	745	59.27	296.33	78.34	107.99	123.97	194.72	60.89	147.21	107.43	2.32E+00	0.00E+00	Up	4.02E-01	1.13E-08		1.99E-01	1.13E-04		8.51E-01	1.33E-85		1.27E+00	2.77E-142	Up	8.19E-01	5.88E-52		Unigene27533_All//gi|18086435|gb|AAL57672.1|//3.00E-24//AT4g25690/L23G19_70 [Arabidopsis thaliana] >gi|53850545|gb|AAU95449.1| At4g25690 [Arabidopsis thaliana] >gi|222423850|dbj|BAH18890.1| AT4G25690 [Arabidopsis thaliana]	Unigene27533_All//2.00E-18//AT4G25690| unknown protein	Unigene27533_All//0.00E+00//TC147035				nr -
Unigene27534_All	839	19.52	2.29	6.98	15.08	11.62	4.84	0.66	0.05	0.14	-3.09E+00	1.16E-55	Down	-1.48E+00	1.34E-21	Down	-3.77E-01	1.44E-02		-1.64E+00	9.75E-22	Down	-3.72E+00	3.23E-03		-2.20E+00	2.24E-02		Unigene27534_All//gi|15235432|ref|NP_192172.1|//7.00E-59//protein kinase family protein [Arabidopsis thaliana]	Unigene27534_All//4.00E-56//AT4G02630| protein kinase family protein	Unigene27534_All//0.00E+00//DR462357		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism		nr +

Unigene27535_All	606	115.26	41.05	18.98	76.53	55.91	50.08	78.98	63.52	68.30	-1.49E+00	2.06E-94	Down	-2.60E+00	2.02E-190	Down	-4.53E-01	1.74E-10		-6.12E-01	5.95E-16		-3.14E-01	4.48E-06		-2.10E-01	2.19E-03		Unigene27535_All//gi|195617694|gb|ACG30677.1|//2.00E-52//histone H4 [Zea mays]	Unigene27535_All//1.00E-40//AT5G59970| histone H4	Unigene27535_All//0.00E+00//TC167771				nr -
Unigene27537_All	656	0.96	2.39	3.08	2.66	4.46	5.23	4.25	4.65	3.16	1.32E+00	1.50E-02		1.69E+00	8.47E-04	Up	7.47E-01	3.97E-02		9.77E-01	3.45E-03		1.29E-01	7.11E-01		-4.30E-01	1.96E-01		Unigene27537_All//gi|224077882|ref|XP_002305450.1|//1.00E-65//ebs-bah-phd domain-containing protein [Populus trichocarpa] >gi|222848414|gb|EEE85961.1| ebs-bah-phd domain-containing protein [Populus trichocarpa]	Unigene27537_All//2.00E-58//AT4G39100| SHL1 (short life); transcription factor/ zinc-mediated transcriptional activator	Unigene27537_All//9.00E-161//gi|84172094|gb|DR460742.1|DR460742				nr -
Unigene27538_All	1192	2.46	3.49	1.34	5.52	4.74	5.15	7.45	4.59	2.11	5.04E-01	9.48E-02		-8.75E-01	2.26E-02		-2.20E-01	3.88E-01		-9.83E-02	6.93E-01		-6.98E-01	5.11E-05		-1.82E+00	7.27E-21	Down	Unigene27538_All//gi|75181374|sp|Q9LZZ7.1|SKA1_ARATH//1.00E-105//RecName: Full=Spindle and kinetochore-associated protein 1 homolog	Unigene27538_All//3.00E-100//AT3G60060| unknown protein	Unigene27538_All//0.00E+00//DT047103				nr -
Unigene27540_All	862	1.70	18.63	4.02	3.58	3.32	8.75	91.62	63.47	483.47	3.45E+00	6.30E-60	Up	1.24E+00	4.59E-04	Up	-1.12E-01	8.00E-01		1.29E+00	3.15E-09	Up	-5.30E-01	1.23E-23		2.40E+00	0.00E+00	Up	Unigene27540_All//gi|297381026|gb|ADI39634.1|//4.00E-48//plastid jasmonates ZIM-domain protein [Hevea brasiliensis]	Unigene27540_All//5.00E-39//AT1G19180| JAZ1 (JASMONATE-ZIM-DOMAIN PROTEIN 1); protein binding	Unigene27540_All//0.00E+00//gi|78323663|gb|DT543937.1|DT543937	Tify	ko04626|Plant-pathogen interaction		nr -
Unigene27541_All	747	4.34	28.22	5.56	5.87	4.24	12.76	7.75	26.80	14.72	2.70E+00	1.04E-61	Up	3.57E-01	2.67E-01		-4.69E-01	1.02E-01		1.12E+00	2.34E-09	Up	1.79E+00	2.12E-43	Up	9.25E-01	1.65E-09		Unigene27541_All//gi|15228034|ref|NP_181216.1|//5.00E-66//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana]	Unigene27541_All//3.00E-67//AT2G36780| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene27541_All//0.00E+00//TC137499		ko00908|Zeatin biosynthesis		nr +
Unigene27542_All	653	71.71	71.85	34.74	163.48	118.55	161.22	129.82	111.37	67.35	2.90E-03	9.88E-01		-1.05E+00	1.99E-35	Down	-4.64E-01	1.36E-24		-2.01E-02	7.48E-01		-2.21E-01	1.39E-05		-9.47E-01	1.91E-70		Unigene27542_All//gi|224073851|ref|XP_002304187.1|//1.00E-15//predicted protein [Populus trichocarpa] >gi|222841619|gb|EEE79166.1| predicted protein [Populus trichocarpa]		Unigene27542_All//0.00E+00//TC174504				nr +
Unigene27545_All	1151	10.41	7.53	3.70	1.73	4.34	5.02	1.47	0.07	0.48	-4.68E-01	4.33E-03		-1.49E+00	4.39E-16	Down	1.33E+00	5.46E-07	Up	1.54E+00	3.30E-09	Up	-4.34E+00	1.16E-09	Down	-1.60E+00	5.13E-04	Down	Unigene27545_All//gi|15238111|ref|NP_199561.1|//1.00E-156//pectinesterase family protein [Arabidopsis thaliana] >gi|75301651|sp|Q8LFF3.1|PME68_ARATH RecName: Full=Probable pectinesterase 68; Short=PE 68; AltName: Full=Pectin methylesterase 68; Short=AtPME68; Flags: Precursor >gi|20856815|gb|AAM26686.1| At5g47500/MXJ7_9 [Arabidopsis thaliana] >gi|23308329|gb|AAN18134.1| At5g47500/MXJ7_9 [Arabidopsis thaliana]	Unigene27545_All//1.00E-150//AT5G47500| pectinesterase family protein	Unigene27545_All//0.00E+00//TC136602		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene27546_All	2562	0.94	1.05	2.06	4.88	7.20	14.70	25.86	15.47	25.84	1.58E-01	6.75E-01		1.13E+00	4.13E-05	Up	5.62E-01	2.95E-06		1.59E+00	4.47E-60	Up	-7.42E-01	1.10E-35		-9.00E-04	9.87E-01		Unigene27546_All//gi|31324528|gb|AAP47579.1|//0.00E+00//receptor kinase Lecrk [Gossypium hirsutum]	Unigene27546_All//0.00E+00//AT2G37710| RLK (receptor lectin kinase); kinase	Unigene27546_All//0.00E+00//TC134597		ko04626|Plant-pathogen interaction		nr +
Unigene27547_All	920	2.16	3.64	4.86	7.69	14.78	11.19	1.24	4.59	1.30	7.50E-01	2.65E-02		1.17E+00	1.19E-04	Up	9.43E-01	7.43E-11		5.42E-01	2.15E-03		1.89E+00	2.06E-10	Up	6.62E-02	9.19E-01		Unigene27547_All//gi|15235683|ref|NP_195487.1|//2.00E-38//AtbZIP7 (Arabidopsis thaliana basic leucine-zipper 7); DNA binding / transcription factor >gi|4490718|emb|CAB38921.1| bZIP transcription factor-like protein [Arabidopsis thaliana] >gi|7270756|emb|CAB80438.1| bZIP transcription factor-like protein [Arabidopsis thaliana]	Unigene27547_All//1.00E-33//AT4G37730| AtbZIP7 (Arabidopsis thaliana basic leucine-zipper 7); DNA binding / transcription factor	Unigene27547_All//7.00E-79//ES838565	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene27548_All	771	34.13	29.57	21.07	73.46	65.97	57.35	9.16	5.75	1.60	-2.07E-01	6.43E-02		-6.96E-01	2.08E-10		-1.55E-01	3.10E-02		-3.57E-01	1.33E-07		-6.72E-01	5.95E-04		-2.52E+00	8.80E-25	Down	Unigene27548_All//gi|15233117|ref|NP_191705.1|//1.00E-66//BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|297302998|ref|XP_002878382.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata] >gi|4689366|gb|AAD27870.1|AF134155_1 BRH1 RING finger protein [Arabidopsis thaliana] >gi|6850837|emb|CAB71076.1| RING finger protein [Arabidopsis thaliana] >gi|21554590|gb|AAM63625.1| RING finger protein [Arabidopsis thaliana] >gi|297324220|gb|EFH54641.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata]	Unigene27548_All//5.00E-68//AT3G61460| BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding	Unigene27548_All//6.00E-51//gi|109874868|gb|DW503842.1|DW503842				nr +
Unigene27549_All	762	15.38	23.67	24.88	23.99	20.43	18.85	40.01	27.75	15.32	6.22E-01	1.84E-06		6.94E-01	1.18E-07		-2.32E-01	8.29E-02		-3.48E-01	7.56E-03		-5.28E-01	1.43E-09		-1.38E+00	6.07E-47	Down	Unigene27549_All//gi|223019809|dbj|BAH22449.1|//3.00E-53//GmATG8d [Glycine max]	Unigene27549_All//7.00E-44//AT1G62040| ATG8C (autophagy 8c); microtubule binding	Unigene27549_All//0.00E+00//TC165614		ko04140|Regulation of autophagy		nr -
Unigene27550_All	1381	1.29	1.47	0.66	2.34	3.79	2.81	2.42	0.61	2.11	1.88E-01	6.66E-01		-9.75E-01	5.87E-02		6.93E-01	6.15E-03		2.63E-01	4.58E-01		-2.00E+00	5.10E-09	Down	-2.00E-01	5.41E-01		Unigene27550_All//gi|9757959|dbj|BAB08447.1|//0.00E+00//TMV resistance protein-like [Arabidopsis thaliana]	Unigene27550_All//0.00E+00//AT5G42140| zinc finger protein, putative / regulator of chromosome condensation (RCC1) family protein	Unigene27550_All//0.00E+00//ES837228		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene27551_All	945	1.11	1.29	0.45	2.53	2.51	2.72	1.83	0.09	1.26	2.17E-01	7.05E-01		-1.30E+00	7.47E-02		-9.10E-03	9.69E-01		1.07E-01	7.99E-01		-4.37E+00	6.16E-10	Down	-5.37E-01	2.13E-01		Unigene27551_All//gi|297827081|ref|XP_002881423.1|//4.00E-38//ATOFP15/OFP15 [Arabidopsis lyrata subsp. lyrata] >gi|297327262|gb|EFH57682.1| ATOFP15/OFP15 [Arabidopsis lyrata subsp. lyrata]	Unigene27551_All//2.00E-24//AT5G04820| OFP13 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 13)	Unigene27551_All//0.00E+00//TC168558				nr -
Unigene27553_All	686	3.13	2.81	7.61	21.93	8.23	8.76	7.33	12.25	13.42	-1.56E-01	7.11E-01		1.28E+00	5.18E-06	Up	-1.41E+00	1.20E-23	Down	-1.32E+00	6.93E-19	Down	7.40E-01	3.26E-05		8.71E-01	2.06E-07				Unigene27553_All//0.00E+00//gi|78330246|gb|DT550520.1|DT550520				
Unigene27554_All	701	1.04	3.76	2.58	6.04	16.90	12.95	1.51	4.71	4.09	1.85E+00	1.72E-05	Up	1.31E+00	1.21E-02		1.48E+00	7.13E-19	Up	1.10E+00	1.04E-08	Up	1.64E+00	5.35E-07	Up	1.44E+00	2.10E-05	Up	Unigene27554_All//gi|224131232|ref|XP_002321033.1|//5.00E-38//glutaredoxin [Populus trichocarpa] >gi|222861806|gb|EEE99348.1| glutaredoxin [Populus trichocarpa]	Unigene27554_All//4.00E-39//AT3G62930| glutaredoxin family protein	Unigene27554_All//0.00E+00//DW509205				nr -
Unigene27555_All	800	142.18	57.57	59.11	231.26	206.70	277.19	276.67	132.70	116.93	-1.30E+00	1.82E-125	Down	-1.27E+00	4.73E-116	Down	-1.62E-01	3.96E-06		2.61E-01	1.18E-15		-1.06E+00	3.35E-214	Down	-1.24E+00	6.51E-284	Down	Unigene27555_All//gi|559761891|sp|Q6UNT2.1|RL5_CUCSA//6.00E-47//RecName: Full=60S ribosomal protein L5 >gi|34484312|gb|AAQ72789.1| 60S ribosomal protein L5 [Cucumis sativus]	Unigene27555_All//4.00E-36//AT3G25520| ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); 5S rRNA binding / structural constituent of ribosome	Unigene27555_All//0.00E+00//TC133185		ko03010|Ribosome		nr +
Unigene27556_All	1248	8.59	3.69	3.16	3.91	3.39	3.69	0.24	0.13	0.06	-1.22E+00	2.70E-11	Down	-1.44E+00	8.26E-14	Down	-2.05E-01	5.13E-01		-8.37E-02	7.77E-01		-8.23E-01	5.40E-01		-1.89E+00	1.68E-01		Unigene27556_All//gi|224063126|ref|XP_002301003.1|//1.00E-140//flavonol synthase 2 [Populus trichocarpa] >gi|222842729|gb|EEE80276.1| flavonol synthase 2 [Populus trichocarpa]	Unigene27556_All//8.00E-118//AT5G08640| FLS (FLAVONOL SYNTHASE); flavonol synthase	Unigene27556_All//0.00E+00//TC137603		ko00941|Flavonoid biosynthesis		nr +
Unigene27557_All	255	0.00	0.20	1.67	4.49	5.00	3.54	3.48	3.11	0.31	7.63E+00	6.17E-01		1.07E+01	1.38E-02		1.53E-01	8.22E-01		-3.43E-01	6.37E-01		-1.61E-01	8.04E-01		-3.48E+00	7.33E-05	Down	Unigene27557_All//gi|255584162|ref|XP_002532821.1|//2.00E-30//conserved hypothetical protein [Ricinus communis] >gi|223527441|gb|EEF29578.1| conserved hypothetical protein [Ricinus communis]	Unigene27557_All//8.00E-06//AT5G62200| embryo-specific protein-related					nr +
Unigene27558_All	887	0.29	1.54	1.20	3.82	2.56	2.60	3.48	2.50	0.90	2.39E+00	4.04E-04	Up	2.03E+00	8.68E-03		-5.76E-01	7.85E-02		-5.56E-01	1.07E-01		-4.79E-01	1.40E-01		-1.95E+00	1.79E-08	Down	Unigene27558_All//gi|87162930|gb|ABD28725.1|//1.00E-15//Embryo-specific 3 [Medicago truncatula]	Unigene27558_All//7.00E-19//AT2G41475| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Lipase/lipooxygenase, PLAT/LH2 (InterPro:IPR008976), Embryo-specific 3 (InterPro:IPR010417); BEST Arabidopsis thaliana protein match is: embryo-specific protein-related (TAIR:AT5G62200.1); Has 60 Blast hits to 60 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 60; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr +
Unigene27559_All	1646	0.06	14.75	0.58	1.82	2.24	4.34	0.13	1.09	1.50	7.86E+00	2.41E-135	Up	3.19E+00	1.03E-03		3.02E-01	3.98E-01		1.26E+00	1.90E-08	Up	3.09E+00	5.77E-08	Up	3.55E+00	2.67E-12	Up	Unigene27559_All//gi|297822091|ref|XP_002878628.1|//3.00E-65//ATHSFA2 [Arabidopsis lyrata subsp. lyrata] >gi|297324767|gb|EFH55187.1| ATHSFA2 [Arabidopsis lyrata subsp. lyrata]	Unigene27559_All//5.00E-65//AT2G26150| ATHSFA2; DNA binding / transcription factor	Unigene27559_All//2.00E-58//TC158707	HSF			nr -
Unigene27561_All	418	15.02	15.52	10.32	13.59	9.64	10.91	35.50	31.30	14.87	4.68E-02	8.47E-01		-5.42E-01	2.84E-02		-4.95E-01	4.11E-02		-3.16E-01	2.39E-01		-1.82E-01	2.10E-01		-1.26E+00	3.72E-20	Down	Unigene27561_All//gi|226509830|ref|NP_001152314.1|//2.00E-19//mps one binder kinase activator-like 1A [Zea mays] >gi|195654991|gb|ACG46963.1| mps one binder kinase activator-like 1A [Zea mays]	Unigene27561_All//5.00E-20//AT5G45550| mob1/phocein family protein	Unigene27561_All//4.00E-97//gi|21095413|gb|BQ407726.1|BQ407726				nr +
Unigene27564_All	944	58.31	32.63	11.39	68.60	19.77	33.54	57.69	55.92	19.03	-8.37E-01	6.58E-30		-2.36E+00	1.32E-133	Down	-1.79E+00	9.08E-144	Down	-1.03E+00	1.36E-53	Down	-4.49E-02	6.03E-01		-1.60E+00	6.14E-103	Down	Unigene27564_All//gi|224075319|ref|XP_002304592.1|//6.00E-62//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222842024|gb|EEE79571.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene27564_All//3.00E-41//AT4G17500| ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene27564_All//0.00E+00//TC172997	AP2-EREBP			nr -
Unigene27565_All	397	5.93	3.96	7.24	7.03	9.02	7.51	6.50	3.05	2.01	-5.84E-01	1.58E-01		2.88E-01	4.63E-01		3.60E-01	3.14E-01		9.56E-02	8.06E-01		-1.09E+00	2.12E-03		-1.69E+00	4.27E-06	Down							
Unigene27566_All	304	0.17	0.00	0.53	1.80	2.72	2.53	0.70	6.46	1.57	-7.43E+00	6.12E-01		1.61E+00	5.11E-01		5.93E-01	4.93E-01		4.87E-01	5.91E-01		3.22E+00	5.87E-09	Up	1.18E+00	2.18E-01				Unigene27566_All//2.00E-98//DT049104				

Unigene27567_All	673	3.03	2.56	1.27	13.55	11.92	8.99	3.14	6.65	2.37	-2.44E-01	6.15E-01		-1.26E+00	9.17E-03		-1.84E-01	3.94E-01		-5.91E-01	1.62E-03		1.08E+00	3.06E-05	Up	-4.08E-01	3.01E-01		Unigene27567_All//gi|30696757|ref|NP_849837.1|//1.00E-14//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	Unigene27567_All//2.00E-12//AT1G62790| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene27567_All//5.00E-147//DT049104				nr -
Unigene27568_All	919	0.40	1.76	1.80	0.98	1.46	3.39	3.04	1.82	1.39	2.15E+00	2.79E-04	Up	2.17E+00	3.37E-04	Up	5.83E-01	3.42E-01		1.80E+00	2.25E-06	Up	-7.39E-01	2.78E-02		-1.13E+00	6.07E-04	Down										
Unigene27571_All	1189	14.26	1.45	7.84	6.62	4.92	2.01	0.11	0.14	0.23	-3.30E+00	2.71E-61	Down	-8.63E-01	9.32E-10		-4.27E-01	3.48E-02		-1.72E+00	1.23E-14	Down	3.98E-01	8.14E-01		1.14E+00	3.99E-01		Unigene27571_All//gi|224112158|ref|XP_002332820.1|//4.00E-22//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834208|gb|EEE72685.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene27571_All//2.00E-05//AT5G05400| disease resistance protein (CC-NBS-LRR class), putative			ko04626|Plant-pathogen interaction		nr +
Unigene27572_All	830	1.83	2.38	2.12	4.62	6.89	4.57	2.19	1.11	0.77	3.81E-01	4.03E-01		2.12E-01	6.61E-01		5.76E-01	1.82E-02		-1.59E-02	9.52E-01		-9.84E-01	2.32E-02		-1.51E+00	5.47E-04	Down	Unigene27572_All//gi|140053482|gb|AB080459.1|//1.00E-06//RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H [Medicago truncatula]		Unigene27572_All//1.00E-52//CO088279				nr +
Unigene27573_All	734	22.31	51.50	37.36	15.13	20.08	24.12	29.90	50.51	29.96	1.21E+00	3.32E-37	Up	7.44E-01	4.46E-12		4.08E-01	3.84E-03		6.72E-01	1.71E-07		7.57E-01	5.35E-21		3.10E-03	9.76E-01		Unigene27573_All//gi|1805617|dbj|BAA08552.1|//3.00E-41//OSH45 [Oryza sativa Japonica Group]	Unigene27573_All//4.00E-38//AT5G11060| KNAT4 (KNOTTED1-LIKE HOMEOBOX GENE 4); transcription activator/ transcription factor	Unigene27573_All//0.00E+00//gi|11207866|gb|BF276796.1|BF276796	HB			nr -
Unigene27575_All	540	3.58	2.63	4.93	1.48	2.30	1.67	3.29	1.47	0.74	-4.48E-01	3.48E-01		4.60E-01	2.59E-01		6.37E-01	3.15E-01		1.81E-01	8.07E-01		-1.16E+00	8.83E-03		-2.16E+00	8.30E-06	Down	Unigene27575_All//gi|224088154|ref|XP_002308346.1|//1.00E-14//SET domain protein [Populus trichocarpa] >gi|222854322|gb|EEE91869.1| SET domain protein [Populus trichocarpa]	Unigene27575_All//2.00E-15//AT5G06620| SDG38 (SET DOMAIN PROTEIN 38)	Unigene27575_All//0.00E+00//TC177901				nr +
Unigene27576_All	354	29.56	13.17	17.60	30.40	25.10	35.85	21.50	17.12	14.74	-1.17E+00	2.31E-10	Down	-7.48E-01	4.42E-05		-2.76E-01	1.24E-01		2.38E-01	1.73E-01		-3.29E-01	9.52E-02		-5.44E-01	2.86E-03		Unigene27576_All//gi|15226840|ref|NP_181030.1|//1.00E-32//coatomer protein epsilon subunit family protein / COPE family protein [Arabidopsis thaliana] >gi|6647445|sp|O64748.1|COPE2_ARATH RecName: Full=Coatomer subunit epsilon-2; AltName: Full=Epsilon-coat protein 2; Short=Epsilon-COP 2 >gi|19715634|gb|AAL91638.1| At2g34840/F19I3.7 [Arabidopsis thaliana] >gi|22655446|gb|AAM98315.1| At2g34840/F19I3.7 [Arabidopsis thaliana]	Unigene27576_All//5.00E-34//AT2G34840| coatomer protein epsilon subunit family protein / COPE family protein	Unigene27576_All//0.00E+00//gi|78334031|gb|DT554305.1|DT554305				nr -
Unigene27577_All	633	159.61	116.47	140.23	88.53	142.42	111.45	471.23	268.01	189.00	-4.55E-01	8.99E-19		-1.87E-01	6.11E-04		6.86E-01	8.32E-41		3.32E-01	3.71E-08		-8.14E-01	1.76E-185		-1.32E+00	0.00E+00	Down	Unigene27577_All//gi|225380880|gb|ACN88681.1|//2.00E-37//VTC2-like protein [Malus x domestica]	Unigene27577_All//9.00E-23//AT4G26850| VTC2 (vitamin c defective 2); GDP-D-glucose phosphorylase/ GDP-galactose:glucose-1-phosphate guanyltransferase/ GDP-galactose:mannose-1-phosphate guanyltransferase/ GDP-galactose:myoinositol-1-phosphate guanyltransferase/ galactose-1-phosphate guanylyltra	Unigene27577_All//0.00E+00//gi|84143936|gb|DN758178.1|DN758178				nr +
Unigene27579_All	315	46.84	19.30	14.88	51.08	60.02	57.78	92.21	26.67	41.86	-1.28E+00	2.11E-16	Down	-1.65E+00	8.71E-23	Down	2.33E-01	8.05E-02		1.78E-01	2.28E-01		-1.79E+00	8.40E-63	Down	-1.14E+00	3.35E-33	Down	Unigene27579_All//gi|15230312|ref|NP_191308.1|//6.00E-25//40S ribosomal protein S2 (RPS2D) [Arabidopsis thaliana] >gi|75313287|sp|Q9SCM3.1|RS24_ARATH RecName: Full=40S ribosomal protein S2-4 >gi|6706420|emb|CAB66106.1| 40S ribosomal protein S2 homolog [Arabidopsis thaliana] >gi|21536514|gb|AAM60846.1| 40S ribosomal protein S2 homolog [Arabidopsis thaliana] >gi|30017231|gb|AAP12849.1| At3g57490 [Arabidopsis thaliana] >gi|110736085|dbj|BAF00015.1| 40S ribosomal protein S2 homolog [Arabidopsis thaliana]	Unigene27579_All//9.00E-15//AT3G57490| 40S ribosomal protein S2 (RPS2D)	Unigene27579_All//4.00E-152//TC159706		ko03010|Ribosome		nr +
Unigene27580_All	454	20.97	8.04	14.31	44.88	36.41	48.05	90.15	31.48	37.73	-1.38E+00	3.72E-12	Down	-5.52E-01	4.43E-03		-3.02E-01	1.13E-02		9.85E-02	4.94E-01		-1.52E+00	8.67E-70	Down	-1.26E+00	4.46E-54	Down	Unigene27580_All//gi|224131666|ref|XP_002328078.1|//1.00E-35//histone deacetylase [Populus trichocarpa] >gi|222837593|gb|EEE75958.1| histone deacetylase [Populus trichocarpa]	Unigene27580_All//1.00E-29//AT3G44750| HDA3 (HISTONE DEACETYLASE 3); histone deacetylase/ nucleic acid binding / zinc ion binding	Unigene27580_All//0.00E+00//gi|11201686|gb|BF270691.1|BF270691	C2H2			nr -
Unigene27581_All	296	6.72	3.59	3.96	9.59	3.49	2.29	5.00	2.40	2.56	-9.02E-01	4.86E-02		-7.63E-01	1.14E-01		-1.46E+00	4.28E-05	Down	-2.07E+00	4.39E-07	Down	-1.06E+00	3.15E-02		-9.67E-01	3.93E-02				Unigene27581_All//1.00E-09//gi|48740336|gb|CO070855.1|CO070855				
Unigene27583_All	285	9.18	25.78	10.28	21.67	24.53	26.94	11.87	25.66	22.92	1.49E+00	1.62E-10	Up	1.63E-01	6.59E-01		1.79E-01	5.04E-01		3.14E-01	1.67E-01		1.11E+00	2.06E-08	Up	9.50E-01	3.06E-06				Unigene27583_All//3.00E-13//TC169701				
Unigene27584_All	288	66.85	20.94	31.06	105.51	77.12	110.87	103.06	38.46	54.50	-1.68E+00	2.58E-31	Down	-1.11E+00	2.99E-16	Down	-4.52E-01	4.78E-07		7.15E-02	5.63E-01		-1.42E+00	3.42E-46	Down	-9.19E-01	4.49E-24		Unigene27584_All//gi|77999275|gb|ABH69984.1|//6.00E-40//thaliana 60S ribosomal protein L7 (At2g44120) [Solanum tuberosum]	Unigene27584_All//6.00E-27//AT3G13580| 60S ribosomal protein L7 (RPL7D)	Unigene27584_All//9.00E-162//gi|21092206|gb|BQ404519.1|BQ404519		ko03010|Ribosome		nr +
Unigene27585_All	536	38.95	28.55	36.36	29.09	37.07	31.43	66.10	30.10	28.99	-4.48E-01	1.90E-04		-9.91E-02	4.87E-01		3.50E-01	3.55E-03		1.12E-01	4.99E-01		-1.14E+00	6.43E-39	Down	-1.19E+00	4.18E-43	Down	Unigene27585_All//gi|17065406|gb|AAL32857.1|//8.00E-07//Unknown protein [Arabidopsis thaliana]	Unigene27585_All//6.00E-13//AT1G42960| expressed protein localized to the inner membrane of the chloroplast.	Unigene27585_All//0.00E+00//gi|109875244|gb|DW504218.1|DW504218				nr +
Unigene27590_All	386	42.15	15.75	16.97	35.62	31.67	46.92	104.06	48.08	51.60	-1.42E+00	5.13E-21	Down	-1.31E+00	6.14E-18	Down	-1.70E-01	3.16E-01		3.98E-01	2.17E-03		-1.11E+00	9.85E-43	Down	-1.01E+00	1.04E-37	Down	Unigene27590_All//gi|297829496|ref|XP_002882630.1|//7.00E-60//60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata] >gi|297328470|gb|EFH58889.1| 60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata]	Unigene27590_All//5.00E-61//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)	Unigene27590_All//0.00E+00//TC153123		ko03010|Ribosome		nr -
Unigene27592_All	964	3.85	3.78	3.37	3.15	8.11	3.00	1.23	0.30	0.21	-2.61E-02	9.52E-01		-1.94E-01	5.94E-01		1.36E+00	3.96E-11	Up	-7.21E-02	8.59E-01		-2.02E+00	1.06E-03		-2.57E+00	6.97E-05	Down			Unigene27592_All//3.00E-87//ES793011				
Unigene27593_All	606	6.22	10.70	15.03	9.78	12.16	11.40	10.74	13.31	7.43	7.84E-01	7.16E-04		1.27E+00	6.93E-10	Up	3.14E-01	1.66E-01		2.21E-01	3.99E-01		3.09E-01	1.08E-01		-5.32E-01	7.61E-03		Unigene27593_All//gi|229335619|gb|ACQ57002.1|//8.00E-33//EDR1 [Glycine max]	Unigene27593_All//8.00E-25//AT1G08720| EDR1 (ENHANCED DISEASE RESISTANCE 1); MAP kinase kinase kinase/ kinase/ protein serine/threonine/tyrosine kinase	Unigene27593_All//1.00E-48//TC147601				nr +
Unigene27594_All	671	2.18	1.06	0.95	8.17	5.18	4.51	6.99	5.54	2.20	-1.05E+00	5.84E-02		-1.20E+00	4.21E-02		-6.56E-01	6.23E-03		-8.57E-01	6.22E-04		-3.35E-01	2.05E-01		-1.67E+00	3.24E-10	Down			Unigene27594_All//8.00E-44//gi|78345999|gb|DT566273.1|DT566273				
Unigene27595_All	668	0.86	0.76	0.00	2.61	1.55	1.42	2.15	0.44	1.37	-1.84E-01	8.25E-01		-9.75E+00	2.60E-03		-7.55E-01	1.15E-01		-8.78E-01	7.90E-02		-2.30E+00	5.89E-05	Down	-6.50E-01	1.74E-01		Unigene27595_All//gi|297834468|ref|XP_002885116.1|//5.00E-61//glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata] >gi|297330956|gb|EFH61375.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata]	Unigene27595_All//1.00E-61//AT3G15940| glycosyl transferase family 1 protein	Unigene27595_All//2.00E-78//gi|48749939|gb|CO080458.1|CO080458		ko00561|Glycerolipid metabolism		nr -
Unigene27596_All	1509	12.86	10.88	17.22	1.52	1.10	0.66	1.15	0.28	0.84	-2.42E-01	6.53E-02		4.21E-01	1.39E-04		-4.71E-01	2.74E-01		-1.21E+00	4.51E-03		-2.05E+00	3.55E-05	Down	-4.43E-01	3.13E-01		Unigene27596_All//gi|2194119|gb|AAB61094.1|//1.00E-136//F20P5.5 gene product [Arabidopsis thaliana]	Unigene27596_All//2.00E-132//AT1G70230| unknown protein	Unigene27596_All//0.00E+00//gi|73864691|gb|DT467430.1|DT467430				nr +
Unigene27597_All	650	9.74	14.58	9.83	9.04	8.32	10.77	13.01	9.97	4.60	5.82E-01	1.83E-03		1.34E-02	9.78E-01		-1.21E-01	6.63E-01		2.52E-01	3.11E-01		-3.84E-01	3.46E-02		-1.50E+00	2.72E-15	Down	Unigene27597_All//gi|114050695|gb|AB149492.1|//2.00E-32//At5g63135 [Arabidopsis thaliana]	Unigene27597_All//1.00E-18//AT5G63135| unknown protein	Unigene27597_All//0.00E+00//ES838723				nr -
Unigene27598_All	667	0.71	5.24	3.11	0.60	1.65	1.22	2.09	0.63	4.84	2.89E+00	1.80E-11	Up	2.14E+00	5.02E-05	Up	1.47E+00	3.09E-02		1.03E+00	2.17E-01		-1.74E+00	1.29E-03		1.21E+00	8.81E-05	Up	Unigene27598_All//gi|297789954|ref|XP_002862895.1|//2.00E-29//WRKY DNA-binding protein 49 [Arabidopsis lyrata subsp. lyrata] >gi|297308663|gb|EFH39154.1| WRKY DNA-binding protein 49 [Arabidopsis lyrata subsp. lyrata]	Unigene27598_All//1.00E-27//AT5G43290| WRKY49; transcription factor	Unigene27598_All//2.00E-106//TC136988	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene276_All	1173	1.12	6.00	4.36	1.78	2.70	2.77	1.01	2.35	2.62	2.43E+00	1.04E-18	Up	1.97E+00	2.40E-10	Up	5.99E-01	8.91E-02		6.36E-01	7.07E-02		1.22E+00	4.07E-04	Up	1.37E+00	2.17E-05	Up	Unigene276_All//gi|4874274|gb|AAD31339.1|AC007354_12//1.00E-141//Similar to gb|X02844 lipase precursor from Staphylococcus hyicus. ESTs gb|AI239406 and gb|T76725 come from this gene [Arabidopsis thaliana] >gi|30387585|gb|AAP31958.1| At1g10740 [Arabidopsis thaliana]	Unigene276_All//4.00E-142//AT1G10740| unknown protein	Unigene276_All//0.00E+00//TC161440				nr +
Unigene2760_All	1141	61.72	29.31	33.04	39.07	35.49	35.15	38.50	31.36	26.95	-1.07E+00	2.10E-57	Down	-9.02E-01	1.47E-41		-1.39E-01	1.04E-01		-1.53E-01	7.81E-02		-2.96E-01	3.92E-05		-5.14E-01	2.96E-13		Unigene2760_All//gi|15229349|ref|NP_187130.1|//1.00E-108//ribose 5-phosphate isomerase-related [Arabidopsis thaliana]	Unigene2760_All//1.00E-104//AT3G04790| ribose 5-phosphate isomerase-related	Unigene2760_All//0.00E+00//TC132446		ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway	GO:0006098//GO:0016861//GO:0043231	nr -
Unigene27601_All	362	11.85	13.02	12.06	27.38	25.49	22.71	30.25	18.36	14.86	1.35E-01	6.25E-01		2.54E-02	9.49E-01		-1.03E-01	6.20E-01		-2.70E-01	1.72E-01		-7.21E-01	2.66E-06		-1.03E+00	3.66E-11	Down			Unigene27601_All//0.00E+00//gi|21091768|gb|BQ404081.1|BQ404081				
Unigene27607_All	254	38.93	32.72	35.85	31.58	50.30	39.30	32.79	45.58	68.86	-2.51E-01	1.94E-01		-1.19E-01	5.89E-01		6.72E-01	5.80E-06		3.16E-01	1.02E-01		4.75E-01	1.44E-03		1.07E+00	2.46E-18	Up	Unigene27607_All//gi|30027167|gb|AAP06759.1|//3.00E-37//auxin response factor-like protein [Mangifera indica]	Unigene27607_All//4.00E-27//AT5G62000| ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Unigene27607_All//4.00E-139//gi|164248008|gb|ES801801.1|ES801801	ARF			nr +
Unigene27610_All	583	10.50	7.21	11.60	23.41	24.39	27.73	11.46	14.05	5.47	-5.42E-01	2.39E-02		1.44E-01	5.91E-01		5.93E-02	7.78E-01		2.44E-01	1.02E-01		2.94E-01	1.27E-01		-1.07E+00	1.40E-07	Down	Unigene27610_All//gi|35187452|gb|AAQ84317.1|//4.00E-68//fiber NTGP1-related protein [Gossypium barbadense]	Unigene27610_All//6.00E-67//AT5G58060| YKT61	Unigene27610_All//0.00E+00//DW224324		ko04130|SNARE interactions in vesicular transport		nr -
Unigene27611_All	667	4.24	24.16	2.95	2.91	2.94	2.23	16.48	29.89	297.21	2.51E+00	1.15E-43	Up	-5.20E-01	1.90E-01		1.48E-02	9.89E-01		-3.82E-01	4.51E-01		8.59E-01	2.60E-14		4.17E+00	0.00E+00	Up	Unigene27611_All//gi|224128742|ref|XP_002328955.1|//4.00E-08//predicted protein [Populus trichocarpa] >gi|222839189|gb|EEE77540.1| predicted protein [Populus trichocarpa]		Unigene27611_All//0.00E+00//TC145130				nr -
Unigene27613_All	386	81.60	69.70	80.43	44.14	47.28	55.46	63.75	29.13	32.72	-2.27E-01	2.27E-02		-2.09E-02	8.54E-01		9.93E-02	5.54E-01		3.30E-01	5.96E-03		-1.13E+00	4.34E-27	Down	-9.62E-01	1.18E-21		Unigene27613_All//gi|211906518|gb|ACJ11752.1|//7.00E-68//glyceraldehyde-3-phosphate dehydrogenase C subunit [Gossypium hirsutum]	Unigene27613_All//5.00E-56//AT1G13440| GAPC2 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene27613_All//0.00E+00//TC133856		ko00010|Glycolysis / Gluconeogenesis		nr -

Unigene27615_All	1327	0.75	2.60	1.61	2.70	3.40	1.50	0.57	1.54	0.81	1.79E+00	1.04E-06	Up	1.10E+00	1.82E-02		3.31E-01	2.92E-01		-8.52E-01	8.19E-03		1.43E+00	6.34E-04	Up	4.99E-01	3.90E-01		Unigene27615_All//gi|297796531|ref|XP_002856150.1|//1.00E-133//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311985|gb|EFH42409.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27615_All//1.00E-124//AT5G56450| mitochondrial substrate carrier family protein	Unigene27615_All//0.00E+00//TC174757				nr +
Unigene27616_All	668	14.57	60.99	38.90	33.41	29.90	43.88	21.65	27.78	13.48	2.07E+00	2.04E-86	Up	1.42E+00	7.26E-32	Up	-1.60E-01	2.12E-01		3.93E-01	5.97E-05		3.60E-01	1.87E-03		-6.84E-01	1.12E-07		Unigene27616_All//gi|148733635|gb|AB009296.1|//1.00E-20//ethphon-induced protein [Hevea brasiliensis] >gi|212960212|gb|ACJ38661.1| ethphon-induced protein [Hevea brasiliensis]	Unigene27616_All//3.00E-18//AT2G44670| senescence-associated protein-related	Unigene27616_All//8.00E-118//ES805431				nr +
Unigene27617_All	786	2.86	2.39	0.88	4.18	1.10	3.85	2.21	1.17	2.28	-2.63E-01	5.55E-01		-1.70E+00	3.72E-04	Down	-1.93E+00	1.94E-08	Down	-1.20E-01	7.39E-01		-9.15E-01	4.03E-02		4.84E-02	9.30E-01		Unigene27617_All//gi|18406257|ref|NP_564731.1|//3.00E-60//ZF14; antiporter/ drug transporter/ transporter [Arabidopsis thaliana] >gi|8979940|gb|AAF82254.1|AC008051_5 Identical to gene ZF14 from Arabidopsis thaliana gb|AB028198 and is a member of an uncharacterized integral membrane protein UPF PF|01554 family >gi|6520161|dbj|BAA87939.1| ZF14 [Arabidopsis thaliana]	Unigene27617_All//1.00E-52//AT1G58340| ZF14; antiporter/ drug transporter/ transporter					nr +
Unigene27623_All	595	6.07	2.13	3.22	3.52	5.04	2.28	1.71	0.42	0.27	-1.51E+00	1.07E-05	Down	-9.13E-01	7.14E-03		5.18E-01	1.66E-01		-6.27E-01	1.72E-01		-2.02E+00	2.83E-03		-2.67E+00	1.94E-04	Down	Unigene27623_All//gi|115460402|ref|NP_001053801.1|//2.00E-46//Os04g0606500 [Oryza sativa Japonica Group] >gi|383465458|emb|CAD41777.2| OSJNBa0035M09.9 [Oryza sativa (japonica cultivar-group)] >gi|113565372|dbj|BAF15715.1| Os04g0606500 [Oryza sativa Japonica Group] >gi|116309734|emb|CAH66778.1| OS1GRa0113113.4 [Oryza sativa (indica cultivar-group)]	Unigene27623_All//4.00E-47//AT4G22290| ubiquitin thiolesterase					nr +
Unigene27624_All	426	12.53	16.30	9.63	93.78	148.65	210.87	4.37	3.92	3.65	3.79E-01	9.60E-02		-3.80E-01	1.71E-01		6.65E-01	3.25E-27		1.17E+00	1.68E-89	Up	-1.54E-01	7.27E-01		-2.60E-01	5.59E-01		Unigene27624_All//gi|28416723|gb|AA042892.1|//2.00E-10//At5g50335 [Arabidopsis thaliana]		Unigene27624_All//5.00E-155//gi|164280988|gb|ES825495.1|ES825495				nr -
Unigene27625_All	298	15.98	50.67	23.77	38.28	33.16	39.71	24.40	42.08	29.14	1.67E+00	2.33E-24	Up	5.73E-01	1.27E-02		-2.07E-01	2.62E-01		5.28E-02	7.85E-01		7.86E-01	4.14E-08		2.56E-01	1.54E-01			Unigene27625_All//4.00E-07//AT1G75380| wound-responsive protein-related	Unigene27625_All//1.00E-160//gi|109882383|gb|DW511353.1|DW511353				
Unigene27628_All	309	24.04	20.66	13.61	13.22	16.72	10.96	22.71	56.67	46.93	-2.19E-01	3.48E-01		-8.21E-01	2.33E-04		3.39E-01	2.29E-01		-2.70E-01	4.20E-01		1.32E+00	1.25E-24	Up	1.05E+00	7.61E-15	Up	Unigene27628_All//gi|11611667|gb|AAG39002.1|AF213399_1//2.00E-27//SLT1 protein [Nicotiana tabacum]	Unigene27628_All//4.00E-22//AT2G37570| SLT1 (sodium- and lithium-tolerant 1)	Unigene27628_All//3.00E-143//TC177960				nr +
Unigene27633_All	234	66.85	39.19	84.88	76.85	72.99	45.74	30.17	15.00	25.20	-7.70E-01	5.80E-08		3.44E-01	8.36E-03		-7.43E-02	6.27E-01		-7.49E-01	4.09E-09		-1.01E+00	4.55E-07	Down	-2.60E-01	2.00E-01		Unigene27633_All//gi|115437550|ref|NP_001043322.1|//4.00E-10//Os01g0555600 [Oryza sativa Japonica Group] >gi|20146287|dbj|BAB89069.1| dynein light chain-like protein [Oryza sativa Japonica Group] >gi|20161709|dbj|BAB90626.1| dynein light chain-like protein [Oryza sativa Japonica Group] >gi|113532853|dbj|BAF05236.1| Os01g0555600 [Oryza sativa Japonica Group]	Unigene27633_All//1.00E-17//AT4G27360| dynein light chain, putative	Unigene27633_All//2.00E-113//EX166923				nr +
Unigene27635_All	280	42.79	8.69	10.84	46.97	33.57	39.84	99.06	29.11	39.27	-2.30E+00	1.07E-29	Down	-1.98E+00	1.17E-23	Down	-4.84E-01	8.76E-04		-2.37E-01	1.61E-01		-1.77E+00	5.97E-59	Down	-1.33E+00	1.73E-40	Down	Unigene27635_All//gi|226505142|ref|NP_001149258.1|//5.00E-39//ribosomal proteinS12 (homolog) [Zea mays] >gi|195625842|gb|ACG34751.1| 40S ribosomal protein S12 [Zea mays]	Unigene27635_All//3.00E-37//AT2G32060| 40S ribosomal protein S12 (RPS12C)	Unigene27635_All//5.00E-157//gi|13352990|gb|BG443338.1|BG443338		ko03010|Ribosome		nr +
Unigene2764_All	1516	34.82	40.11	44.82	51.26	47.18	49.90	32.60	19.85	12.59	2.04E-01	3.28E-03		3.64E-01	2.10E-08		-1.20E-01	5.57E-02		-3.88E-02	6.37E-01		-7.16E-01	2.87E-25		-1.37E+00	1.37E-74	Down	Unigene2764_All//gi|6056421|gb|AAF02885.1|AC009525_19//3.00E-45//Unknown protein [Arabidopsis thaliana] >gi|14423480|gb|AAK62422.1|AF38697_1 Unknown protein [Arabidopsis thaliana]	Unigene2764_All//1.00E-46//AT1G02816| unknown protein	Unigene2764_All//0.00E+00//TC146358		GO:0016020//GO:0043231		nr -
Unigene27640_All	541	16.92	8.52	13.58	14.46	11.84	8.93	4.14	1.93	1.10	-9.90E-01	3.29E-07		-3.17E-01	1.29E-01		-2.88E-01	1.84E-01		-6.95E-01	6.54E-04		-1.10E+00	4.26E-03		-1.91E+00	3.35E-06	Down			Unigene27640_All//2.00E-10//gi|109870876|gb|DW499852.1|DW499852				
Unigene27642_All	263	29.64	51.83	38.27	33.34	34.83	28.68	72.99	57.85	36.35	8.06E-01	1.59E-07		3.69E-01	5.60E-02		6.32E-02	8.18E-01		-2.17E-01	3.27E-01		-3.35E-01	3.27E-03		-1.01E+00	2.62E-18	Down	Unigene27642_All//gi|106879581|emb|CAJ38374.1|//1.00E-13//transcription initiation factor [Plantago major]	Unigene27642_All//2.00E-14//AT4G24440| transcription initiation factor IIA gamma chain / TFIIA-gamma (TFIIA-S)	Unigene27642_All//6.00E-101//ES826553		ko03022|Basal transcription factors		nr +
Unigene27643_All	467	55.01	58.05	57.58	52.05	49.04	53.87	79.76	60.23	31.65	7.75E-02	5.26E-01		6.60E-02	6.21E-01		-8.62E-02	5.40E-01		4.94E-02	7.01E-01		-4.05E-01	2.10E-07		-1.33E+00	5.41E-54	Down	Unigene27643_All//gi|115441727|ref|NP_001045143.1|//2.00E-21//Os01g0908400 [Oryza sativa Japonica Group] >gi|20804891|dbj|BAB92572.1| P0497A05.16 [Oryza sativa Japonica Group] >gi|113534674|dbj|BAF07057.1| Os01g0908400 [Oryza sativa Japonica Group]	Unigene27643_All//1.00E-09//AT1G67785| unknown protein	Unigene27643_All//3.00E-129//DR458202				nr -
Unigene27644_All	519	38.11	10.25	14.26	49.81	38.02	56.30	127.41	50.25	42.83	-1.89E+00	5.17E-38	Down	-1.42E+00	2.56E-24	Down	-3.90E-01	9.24E-05		1.77E-01	1.09E-01		-1.34E+00	1.87E-93	Down	-1.57E+00	8.82E-122	Down	Unigene27644_All//gi|226529688|ref|NP_001150716.1|//7.00E-39//60S ribosomal protein L15 [Zea mays] >gi|195641286|gb|ACG40111.1| 60S ribosomal protein L15 [Zea mays]	Unigene27644_All//2.00E-27//AT4G16720| 60S ribosomal protein L15 (RPL15A)	Unigene27644_All//3.00E-163//gi|21097292|gb|BQ409605.1|BQ409605		ko03010|Ribosome		nr -
Unigene27645_All	339	7.72	18.68	10.37	9.70	14.32	10.52	37.17	54.49	46.42	1.28E+00	2.03E-07	Up	4.26E-01	2.33E-01		5.63E-01	3.80E-02		1.18E-01	7.37E-01		5.52E-01	1.42E-06		3.21E-01	9.90E-03				Unigene27645_All//1.00E-87//TC178656				
Unigene27649_All	581	172.00	170.85	162.41	310.03	289.05	238.25	184.55	154.16	91.61	-9.70E-03	8.79E-01		-8.28E-02	1.74E-01		-1.01E-01	8.82E-03		-3.80E-01	1.66E-25		-2.60E-01	5.28E-09		-1.01E+00	5.73E-99	Down	Unigene27649_All//gi|284520994|gb|ADB93072.1|//6.00E-45//profilin-1 [Jatropha curcas]	Unigene27649_All//1.00E-28//AT5G56600| PRF3 (PROFILIN 3); actin binding	Unigene27649_All//0.00E+00//gi|21096317|gb|BQ408630.1|BQ408630				nr -
Unigene27651_All	567	9.78	13.58	21.79	12.74	28.54	38.63	1.86	2.80	2.67	4.74E-01	2.49E-02		1.16E+00	2.08E-11	Up	1.16E+00	7.38E-18	Up	1.60E+00	2.03E-35	Up	5.87E-01	2.24E-01		5.18E-01	2.74E-01		Unigene27651_All//gi|224130286|ref|XP_002328572.1|//3.00E-48//glutaredoxin [Populus trichocarpa] >gi|222838554|gb|EEE76919.1| glutaredoxin [Populus trichocarpa]	Unigene27651_All//3.00E-42//AT3G21460| electron carrier/ protein disulfide oxidoreductase	Unigene27651_All//1.00E-08//TC167129				nr +
Unigene27652_All	792	2.97	11.90	3.63	2.08	2.09	0.57	0.21	0.00	0.10	2.00E+00	1.14E-19	Up	2.88E-01	4.63E-01		7.90E-03	9.98E-01		-1.86E+00	6.76E-04	Down	-7.74E+00	1.34E-01		-1.09E+00	5.53E-01		Unigene27652_All//gi|19699290|gb|AAL91256.1|//8.00E-83//At1g15070/F9L1_1 [Arabidopsis thaliana] >gi|24111379|gb|AAN46813.1| At1g15070/F9L1_1 [Arabidopsis thaliana]	Unigene27652_All//9.00E-74//AT1G15060| LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031088, alpha/beta hydrolase, At1g15070 (InterPro:IPR016069); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73750.1); Has 120 Blast hits to 104 proteins in 29 species: Archae - 0; Bacteria - 61; Metazoa - 1; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene27652_All//2.00E-168//C0129534				nr -
Unigene27653_All	430	73.61	96.27	57.58	103.57	72.55	117.53	74.63	59.58	36.13	3.87E-01	2.85E-06		-3.54E-01	3.85E-04		-5.13E-01	1.36E-12		1.83E-01	1.95E-02		-3.25E-01	1.42E-04		-1.05E+00	5.53E-32	Down	Unigene27653_All//gi|115476070|ref|NP_001061631.1|//4.00E-34//Os08g0359500 [Oryza sativa Japonica Group] >gi|75132349|sp|Q6YYB0.1|Y8359_ORYSJ RecName: Full=Uncharacterized protein Os08g0359500 >gi|113623600|dbj|BAF23545.1| Os08g0359500 [Oryza sativa Japonica Group]	Unigene27653_All//2.00E-29//AT4G02450| glycine-rich protein	Unigene27653_All//0.00E+00//TC138182				nr -
Unigene27655_All	580	1.71	1.75	0.92	4.04	4.39	2.88	3.28	0.94	0.96	2.77E-02	9.86E-01		-9.01E-01	2.22E-01		1.22E-01	8.12E-01		-4.87E-01	2.69E-01		-1.81E+00	7.18E-05	Down	-1.77E+00	5.92E-05	Down	Unigene27655_All//gi|115452609|ref|NP_001049905.1|//2.00E-08//Os03g0308600 [Oryza sativa Japonica Group] >gi|108707755|gb|ABF95550.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548376|dbj|BAF11819.1| Os03g0308600 [Oryza sativa Japonica Group]	Unigene27655_All//9.00E-18//AT1G06320| unknown protein	Unigene27655_All//0.00E+00//gi|109884379|gb|DW513349.1|DW513349				nr +
Unigene27659_All	1088	2.02	5.91	1.27	4.30	1.93	1.33	3.30	3.23	0.59	1.55E+00	8.14E-10	Up	-6.67E-01	1.42E-01		-1.16E+00	9.38E-06	Down	-1.70E+00	8.54E-09	Down	-3.37E-02	9.30E-01		-2.50E+00	7.06E-13	Down			Unigene27659_All//9.00E-162//gi|21097585|gb|BQ409898.1|BQ409898				
Unigene27663_All	494	41.84	25.75	11.75	53.65	35.76	37.48	94.40	82.24	59.19	-7.00E-01	8.16E-09		-1.83E+00	1.63E-36	Down	-5.85E-01	1.24E-09		-5.17E-01	4.18E-07		-1.99E-01	5.75E-03		-6.73E-01	3.55E-22		Unigene27663_All//gi|255555073|ref|XP_002518574.1|//4.00E-11//transcription regulator, putative [Ricinus communis] >gi|223542419|gb|EEF43961.1| transcription regulator, putative [Ricinus communis]	Unigene27663_All//2.00E-05//AT4G25210| transcription regulator	Unigene27663_All//0.00E+00//gi|21099139|gb|BQ411452.1|BQ411452	GeBP			nr -
Unigene27666_All	727	4.68	1.60	1.98	10.55	8.24	6.46	3.08	2.53	1.59	-1.55E+00	1.45E-05	Down	-1.24E+00	5.32E-04	Down	-3.57E-01	9.16E-02		-7.08E-01	5.91E-04		-2.85E-01	4.95E-01		-9.56E-01	9.46E-03		Unigene27666_All//gi|3695380|gb|AAC62783.1|//6.00E-56//F1104.7 [Arabidopsis thaliana]	Unigene27666_All//3.00E-57//AT4G01570| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene27667_All	671	38.44	27.34	23.89	46.25	43.93	64.41	61.50	35.75	25.65	-4.92E-01	4.05E-06		-6.86E-01	5.65E-10		-7.43E-02	5.56E-01		4.78E-01	1.08E-09		-7.83E-01	1.19E-24		-1.26E+00	7.28E-55	Down	Unigene27667_All//gi|40287508|gb|AAR83868.1|//2.00E-60//60S ribosomal protein L12 [Capsicum annuum]	Unigene27667_All//6.00E-60//AT5G60670| 60S ribosomal protein L12 (RPL12C)	Unigene27667_All//0.00E+00//gi|164246272|gb|ES830800.1|ES830800		ko03010|Ribosome		nr -
Unigene2767_All	489	2.25	7.88	6.42	5.30	7.39	3.51	7.18	13.08	14.66	1.81E+00	1.73E-07	Up	1.52E+00	8.23E-05	Up	4.81E-01	1.52E-01		-5.94E-01	1.39E-01		8.66E-01	3.35E-05		1.03E+00	1.30E-07	Up	Unigene2767_All//gi|155967399|gb|AB041516.1|//2.00E-06//biotin carboxyl carrier protein subunit [Gossypium hirsutum]	Unigene2767_All//5.00E-07//AT5G16390| CAC1 (CHLOROPLASTIC ACETYLCOENZYME A CARBOXYLASE 1); acetyl-CoA carboxylase/ biotin binding	Unigene2767_All//4.00E-116//DR453962		ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis		nr -

Unigene27671_All	833	1.44	0.37	0.51	2.51	3.31	3.42	1.68	0.35	1.87	-1.98E+00	3.72E-03		-1.50E+00	2.71E-02		3.97E-01	3.26E-01		4.44E-01	2.67E-01		-2.25E+00	9.69E-05	Down	1.55E-01	7.40E-01		Unigene27671_All//gi|27476088|gb|AA017019.1|//1.00E-112//Hypothetical protein [Oryza sativa Japonica Group]	Unigene27671_All//8.00E-105//AT2G22610| kinesin motor protein-related	Unigene27671_All//4.00E-15//TC144773				nr +
Unigene27672_All	403	47.26	99.58	36.60	134.61	108.60	120.47	90.86	125.18	38.36	1.08E+00	6.44E-33	Up	-3.69E-01	5.63E-03		-3.10E-01	2.99E-06		-1.60E-01	3.64E-02		4.62E-01	3.42E-12		-1.24E+00	9.68E-48	Down	Unigene27672_All//gi|110737195|dbj|BAF00546.1|//1.00E-42//TPR-repeat protein [Arabidopsis thaliana]	Unigene27672_All//5.00E-25//AT1G62740| stress-inducible protein, putative	Unigene27672_All//5.00E-121//gi|11200690|gb|BF269695.1|BF269695				nr +
Unigene27673_All	479	44.89	95.10	43.02	120.84	86.34	77.41	72.20	72.34	50.73	1.08E+00	1.08E-37	Up	-6.14E-02	6.43E-01		-4.85E-01	1.16E-14		-6.43E-01	1.59E-21		2.60E-03	1.02E+00		-5.09E-01	1.89E-10					Unigene27673_All//2.00E-176//TC164390				
Unigene27678_All	543	116.69	99.47	61.00	191.46	162.28	166.51	299.39	234.15	133.09	-2.30E-01	5.86E-04		-9.36E-01	7.78E-40		-2.39E-01	3.55E-07		-2.01E-01	6.00E-05		-3.55E-01	3.45E-23		-1.17E+00	1.19E-189	Down	Unigene27678_All//gi|493725|emb|CAA55912.1|//1.00E-32//beta tubulin [Oryza sativa (japonica cultivar-group)]	Unigene27678_All//9.00E-28//AT5G44340| TUB4; structural constituent of cytoskeleton	Unigene27678_All//0.00E+00//gi|21100869|gb|BQ413182.1|BQ413182	ko04145|Phagosome			nr +
Unigene27679_All	1123	0.51	0.54	0.95	3.06	1.63	0.76	3.09	1.94	1.74	7.91E-02	9.41E-01		8.88E-01	2.06E-01		-9.13E-01	3.43E-03		-2.00E+00	3.93E-08	Down	-6.74E-01	2.28E-02		-8.29E-01	3.71E-03		Unigene27679_All//gi|115474625|ref|NP_001060909.1|//1.00E-80//Os08g0128200 [Oryza sativa Japonica Group] >gi|113622878|dbj|BAF22823.1|Os08g0128200 [Oryza sativa Japonica Group]	Unigene27679_All//7.00E-97//AT1G67570| unknown protein					nr +
Unigene2768_All	639	9.50	19.43	13.75	9.82	8.08	10.39	11.31	10.79	11.35	1.03E+00	4.54E-10	Up	5.34E-01	8.64E-03		-2.81E-01	2.65E-01		8.10E-02	7.52E-01		-6.82E-02	7.57E-01		4.10E-03	9.82E-01		Unigene2768_All//gi|255547536|ref|XP_002514825.1|//2.00E-18//Biotin carboxyl carrier protein subunit of of Het-ACCase (BCCP1) [Ricinus communis] >gi|223545876|gb|EEF47379.1|Biotin carboxyl carrier protein subunit of of Het-ACCase (BCCP1) [Ricinus communis]	Unigene2768_All//6.00E-18//AT5G15530| BCCP2 (BIOTIN CARBOXYL CARRIER PROTEIN 2); biotin binding	Unigene2768_All//2.00E-140//TC162510	ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis	GO:0006631//GO:0009536//GO:0016421//GO:0019842//GO:0043234	nr -
Unigene27680_All	1962	1.31	0.05	0.52	1.09	0.82	0.62	9.70	1.56	1.06	-4.66E+00	2.58E-12	Down	-1.34E+00	1.64E-03		-4.04E-01	3.75E-01		-8.13E-01	6.70E-02		-2.64E+00	5.38E-67	Down	-3.20E+00	3.24E-84	Down	Unigene27680_All//gi|15241158|ref|NP_197471.1|//1.00E-165//MATE efflux protein-related [Arabidopsis thaliana] >gi|676338058|gb|AAT38828.1| MATE efflux protein-related [Arabidopsis thaliana]	Unigene27680_All//5.00E-148//AT5G19700| MATE efflux protein-related	Unigene27680_All//0.00E+00//TC170491				nr +
Unigene27681_All	700	6.95	2.75	3.42	9.68	6.99	6.52	12.38	4.48	5.92	-1.34E+00	2.66E-06	Down	-1.02E+00	3.66E-04	Down	-4.70E-01	3.15E-02		-5.71E-01	1.10E-02		-1.47E+00	1.11E-14	Down	-1.06E+00	1.56E-09	Down	Unigene27681_All//gi|297804630|ref|XP_002870199.1|//1.00E-22//At4g15930 [Arabidopsis lyrata subsp. lyrata] >gi|297316035|gb|EFH46458.1|At4g15930 [Arabidopsis lyrata subsp. lyrata]	Unigene27681_All//1.00E-23//AT4G15930| microtubule motor	Unigene27681_All//1.00E-132//DR455272				nr +
Unigene27683_All	1066	0.00	0.38	0.60	1.96	1.49	2.16	0.95	88.34	3.29	8.57E+00	1.36E-02		9.23E+00	1.16E-03		-4.01E-01	3.84E-01		1.39E-01	7.56E-01		6.54E+00	0.00E+00	Up	1.79E+00	1.95E-08	Up	Unigene27683_All//gi|224138226|ref|XP_002322761.1|//1.00E-171//cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa] >gi|222867291|gb|EEF04522.1|cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa]	Unigene27683_All//2.00E-136//AT4G37990| ELI3-2 (ELICITOR-ACTIVATED GENE 3-2); aryl-alcohol dehydrogenase/ mannitol dehydrogenase	Unigene27683_All//0.00E+00//TC179502	ko00940|Phenylpropanoid biosynthesis			nr +
Unigene27684_All	586	4.64	4.41	1.09	10.29	7.82	7.48	6.93	4.28	5.64	-7.43E-02	8.43E-01		-2.09E+00	3.48E-06	Down	-3.96E-01	1.01E-01		-4.60E-01	6.23E-02		-6.95E-01	1.00E-02		-2.96E-01	2.85E-01		Unigene27684_All//gi|297792321|ref|XP_002864045.1|//1.00E-06//hypothetical protein ARALYDRAFT_918030 [Arabidopsis lyrata subsp. lyrata] >gi|297309880|gb|EFH40304.1|hypothetical protein ARALYDRAFT_918030 [Arabidopsis lyrata subsp. lyrata]		Unigene27684_All//1.00E-85//TC173113	ko00760|Nicotinate and nicotinamide metabolism			nr +
Unigene27685_All	265	0.59	0.38	0.20	1.88	1.56	0.68	6.54	2.68	1.65	-6.31E-01	7.27E-01		-1.56E+00	5.33E-01		-2.70E-01	8.02E-01		-1.46E+00	1.93E-01		-1.29E+00	4.58E-03		-1.98E+00	3.36E-05	Down				Unigene27685_All//3.00E-127//ES841831				
Unigene27686_All	768	5.72	5.94	3.88	10.05	9.15	5.88	14.31	7.40	5.55	5.33E-02	8.56E-01		-5.60E-01	6.63E-02		-1.36E-01	5.82E-01		-7.74E-01	1.60E-04		-9.52E-01	1.14E-09		-1.37E+00	3.71E-17	Down	Unigene27686_All//gi|38346560|emb|CAE04721.2|//2.00E-35//OSJNBa0043L24.9 [Oryza sativa (japonica cultivar-group)] >gi|116310322|emb|CAH67338.1|OSIGBa0157A06.7 [Oryza sativa (indica cultivar-group)]	Unigene27686_All//5.00E-36//AT2G20190| CLASP (CLIP-ASSOCIATED PROTEIN); binding	Unigene27686_All//0.00E+00//ES841831				nr -
Unigene27689_All	561	2.61	4.34	5.51	7.46	3.74	3.62	2.86	3.43	3.41	7.31E-01	7.31E-02		1.08E+00	4.00E-03		-9.94E-01	3.32E-04		-1.04E+00	4.05E-04	Down	2.59E-01	5.82E-01		2.51E-01	5.72E-01					Unigene27689_All//0.00E+00//TC151151				
Unigene2769_All	1265	3.60	13.26	4.50	7.92	15.35	12.85	9.73	14.74	13.51	1.88E+00	7.89E-32	Up	3.24E-01	2.39E-01		9.56E-01	1.18E-15		6.99E-01	2.21E-07		5.99E-01	1.50E-07		4.74E-01	5.02E-05		Unigene2769_All//gi|22330241|ref|NP_683431.1|//4.00E-25//proline-rich family protein [Arabidopsis thaliana]		Unigene2769_All//0.00E+00//gi|78334388|gb|DT554662.1|DT554662	ko03040|Spliceosome			nr -
Unigene27691_All	751	1.88	3.37	4.40	3.98	4.08	4.09	2.31	1.61	0.80	8.43E-01	3.48E-02		1.22E+00	7.48E-04	Up	3.62E-02	9.47E-01		3.92E-02	9.36E-01		-5.16E-01	2.59E-01		-1.54E+00	6.50E-04	Down	Unigene27691_All//gi|255561945|ref|XP_002521981.1|//3.00E-06//protein farnesyltransferase alpha subunit, putative [Ricinus communis] >gi|223538785|gb|EEF40385.1|protein farnesyltransferase alpha subunit, putative [Ricinus communis]	Unigene27691_All//2.00E-05//AT1G10095| protein prenyltransferase	Unigene27691_All//3.00E-68//TC141515				nr +
Unigene27694_All	674	0.08	0.23	0.00	3.33	2.71	2.28	5.52	2.79	1.77	1.54E+00	5.31E-01		-6.28E+00	6.24E-01		-2.97E-01	5.29E-01		-5.46E-01	2.22E-01		-9.84E-01	5.58E-04		-1.64E+00	4.54E-08	Down	Unigene27694_All//gi|15222372|ref|NP_172210.1|//7.00E-12//josephin protein-related [Arabidopsis thaliana] >gi|38454076|gb|AAR20732.1|At1g07300 [Arabidopsis thaliana] >gi|38603992|gb|AAR24739.1|At1g07300 [Arabidopsis thaliana]	Unigene27694_All//4.00E-13//AT1G07300| josephin protein-related	Unigene27694_All//2.00E-23//DR513418				nr +
Unigene27695_All	413	26.98	13.99	14.18	74.18	55.03	38.93	70.94	32.28	36.27	-9.48E-01	4.62E-08		-9.28E-01	2.02E-07		-4.31E-01	1.54E-06		-9.30E-01	1.25E-21		-1.14E+00	2.30E-32	Down	-9.68E-01	7.52E-26					Unigene27695_All//4.00E-137//gi|21100090|gb|BQ412403.1|BQ412403				
Unigene27698_All	783	50.65	18.77	22.10	64.64	44.29	65.70	72.95	23.81	22.84	-1.43E+00	7.33E-51	Down	-1.20E+00	3.03E-37	Down	-5.46E-01	7.31E-16		2.35E-02	7.94E-01		-1.62E+00	2.41E-106	Down	-1.68E+00	2.82E-115	Down	Unigene27698_All//gi|282848250|gb|AB802906.1|//5.00E-55//60S ribosomal protein L30 [Jatropha curcas]	Unigene27698_All//1.00E-53//AT1G36240| 60S ribosomal protein L30 (RPL30A)	Unigene27698_All//0.00E+00//gi|21089507|gb|BQ401820.1|BQ401820	ko03010|Ribosome			nr +
Unigene277_All	1165	2.34	0.52	1.83	5.00	2.54	2.71	2.83	1.94	2.70	-2.16E+00	8.60E-07	Down	-3.53E-01	3.87E-01		-9.77E-01	1.86E-05		-8.83E-01	2.58E-04		-5.47E-01	7.66E-02		-6.74E-02	8.28E-01		Unigene277_All//gi|297843666|ref|XP_002889714.1|//5.00E-25//prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335556|gb|EFH65973.1|prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene277_All//8.00E-13//AT1G55190| PRA7	Unigene277_All//0.00E+00//gi|78342006|gb|DT562280.1|DT562280				nr -
Unigene27700_All	690	15.24	26.51	20.07	18.92	22.01	21.47	10.48	3.39	5.14	7.99E-01	1.12E-09		3.97E-01	1.28E-02		2.19E-01	1.59E-01		1.83E-01	2.73E-01		-1.63E+00	2.90E-14	Down	-1.03E+00	1.08E-07	Down	Unigene27700_All//gi|8469220|sp|Q9SQI3.1|FATB_GOSHI//2.00E-40//RecName: Full=Myristoyl-acyl carrier protein thioesterase, chloroplastic; AltName: Full=16:0-acyl-carrier protein thioesterase; Short=16:0-ACP thioesterase; AltName: Full=Acyl-[acyl-carrier-protein] hydrolase; AltName: Full=PATE; Flags: Precursor >gi|6048397|gb|AAF02215.1|AF076535_1 palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]	Unigene27700_All//4.00E-13//AT1G08510| FATB (fatty acyl-ACP thioesterases B); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase	Unigene27700_All//0.00E+00//gi|78345892|gb|DT566166.1|DT566166	ko00061|Fatty acid biosynthesis			nr -
Unigene27701_All	522	20.15	32.03	12.14	31.21	26.19	36.42	73.06	42.04	32.21	6.69E-01	9.11E-07		-7.31E-01	6.23E-05		-2.53E-01	7.38E-02		2.23E-01	1.05E-01		-7.97E-01	1.41E-23		-1.18E+00	7.21E-46	Down	Unigene27701_All//gi|195615790|gb|ACG29725.1|//1.00E-42//transmembrane 9 superfamily protein member 4 [Zea mays]	Unigene27701_All//2.00E-35//AT5G10840| endomembrane protein 70, putative	Unigene27701_All//0.00E+00//TC160758				nr +
Unigene27704_All	844	15.87	9.61	12.81	7.02	7.96	6.05	1.30	0.10	0.00	-7.24E-01	2.56E-06		-3.09E-01	6.27E-02		1.80E-01	5.13E-01		-2.16E-01	4.38E-01		-3.72E+00	7.15E-06	Down	-1.03E+01	3.33E-08	Down	Unigene27704_All//gi|195636746|gb|ACG37841.1|//6.00E-31//DNA binding protein [Zea mays]	Unigene27704_All//3.00E-22//AT3G56220| transcription regulator	Unigene27704_All//0.00E+00//gi|109876677|gb|DW505651.1|DW505651				nr -
Unigene27705_All	1391	0.08	0.51	0.27	2.76	2.82	24.42	177.24	145.79	423.96	2.76E+00	9.14E-03		1.83E+00	2.13E-01		3.35E-02	9.41E-01		3.15E+00	3.87E-124	Up	-2.82E-01	8.62E-23		1.26E+00	0.00E+00	Up	Unigene27705_All//gi|295291568|gb|ADF87393.1|//1.00E-124//class II chitinase [Arachis hypogaea]	Unigene27705_All//4.00E-116//AT1G02360| chitinase, putative	Unigene27705_All//1.00E-28//gi|54120214|gb|CO495723.1|CO495723	ko00520|Amino sugar and nucleotide sugar metabolism			nr +
Unigene27709_All	481	11.53	35.61	13.06	9.42	9.02	21.69	17.05	32.32	16.07	1.63E+00	1.18E-26	Up	1.80E-01	4.97E-01		-6.32E-02	8.25E-01		1.20E+00	2.51E-11	Up	9.23E-01	1.07E-12		-8.58E-02	6.55E-01		Unigene27709_All//gi|1351365|sp|P48505.2|UCR11_SOLTU//1.00E-14//RecName: Full=Ubiquinol-cytochrome c reductase complex 6.7 kDa protein; Short=CR6 >gi|633683|emb|CAA57768.1|cytochrome c reductase subunit [Solanum tuberosum]	Unigene27709_All//3.00E-05//AT2G40765| unknown protein	Unigene27709_All//4.00E-119//gi|109885729|gb|DW514699.1|DW514699				nr +
Unigene2771_All	1598	2.52	1.24	1.43	2.90	2.39	2.15	3.94	3.61	3.57	-1.03E+00	8.10E-04	Down	-8.15E-01	1.03E-02		-2.77E-01	3.54E-01		-4.33E-01	1.38E-01		-1.27E-01	6.26E-01		-1.45E-01	5.36E-01		Unigene2771_All//gi|42570346|ref|NP_850177.2|//1.00E-157//CNX2 (COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 2); catalytic [Arabidopsis thaliana] >gi|79323865|ref|NP_001031461.1|CNX2 (COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 2); catalytic [Arabidopsis thaliana] >gi|30253535|sp|Q39055.1|CNX2_ARATH RecName: Full=Molybdopterin biosynthesis protein CNX2; AltName: Full=Molybdenum cofactor biosynthesis enzyme CNX2 >gi|662871|emb|CAA88107.1| Cnx2 [Arabidopsis thaliana]	Unigene2771_All//4.00E-158//AT2G31955| CNX2 (COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 2); catalytic	Unigene2771_All//5.00E-121//ES843237				nr +
Unigene27710_All	605	2.42	5.95	3.34	8.97	7.46	5.60	8.88	7.74	3.03	1.30E+00	1.18E-04	Up	4.66E-01	3.39E-01		-2.67E-01	3.23E-01		-6.81E-01	7.18E-03		-1.98E-01	4.40E-01		-1.55E+00	1.78E-10	Down				Unigene27710_All//2.00E-53//TC175844				
Unigene27712_All	670	1.25	0.98	3.89	2.16	3.44	3.10	2.33	1.43	1.96	-3.46E-01	6.12E-01		1.64E+00	1.60E-04	Up	6.76E-01	1.14E-01		5.24E-01	2.72E-01		-7.03E-01	1.40E-01		-2.51E-01	6.18E-01		Unigene27712_All//gi|297843258|ref|XP_002889510.1|//5.00E-83//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335352|gb|EFH65769.1|transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27712_All//5.00E-83//AT1G04510| transducin family protein / WD-40 repeat family protein	Unigene27712_All//0.00E+00//gi|48811048|gb|CO112361.1|CO112361	ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis			nr +
Unigene27717_All	570	217.45	148.54	164.14	267.77	292.58	240.87	72.62	52.13	35.44	-5.50E-01	4.99E-32		-4.06E-01	6.28E-18		1.28E-01	9.94E-04		-1.53E-01	2.37E-04		-4.78E-01	9.48E-11		-1.04E+00	2.76E-40	Down				Unigene27717_All//4.00E-156//TC132407				

Unigene27718_All	947	1.27	0.21	0.51	2.52	1.64	2.38	1.16	0.62	1.22	-2.57E+00	5.35E-04	Down	-1.33E+00	4.65E-02		-6.26E-01	1.19E-01		-8.25E-02	8.57E-01		-9.10E-01	1.24E-01		7.18E-02	9.11E-01		Unigene27718_All//gi|15225790|ref|NP_180247.1|//4.00E-35//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75100043|sp|081028.1|PP171_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g26790, mitochondrial; Flags: Precursor	Unigene27718_All//5.00E-28//AT2G26790| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene2772_All	361	6.09	2.95	3.69	5.38	7.73	7.51	5.74	2.43	2.21	-1.05E+00	1.61E-02		-7.23E-01	1.12E-01		5.22E-01	1.80E-01		4.80E-01	2.34E-01		-1.24E+00	2.35E-03		-1.38E+00	5.68E-04	Down	Unigene2772_All//gi|31711880|gb|AAP68296.1|//2.00E-07//At5g50840 [Arabidopsis thaliana]	Unigene2772_All//1.00E-08//AT5G50840| INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: LINC2 (LITTLE NUCLEI2) (TAIR:AT1G13220.2); Has 50047 Blast hits to 27335 proteins in 1173 species: Archae - 429; Bacteria - 3521; Metazoa - 26018; Fungi - 2663; Plants - 1200; Viruses - 162; Other Eukaryotes - 16054 (source: NCBI BLink).	Unigene2772_All//0.00E+00//C0079728				nr +
Unigene27720_All	706	4.08	5.96	11.54	10.94	14.93	12.92	36.41	33.33	21.50	5.47E-01	6.72E-02		1.50E+00	2.93E-11	Up	4.49E-01	8.89E-03		2.41E-01	2.58E-01		-1.28E-01	2.42E-01		-7.60E-01	2.10E-15		Unigene27720_All//gi|14533853|ref|NP_001076772.1|//3.00E-53//ZEU1 (ZEUS1); ATP binding / thymidylate kinase [Arabidopsis thaliana]	Unigene27720_All//1.00E-46//AT5G59410| ZEU1 (ZEUS1); ATP binding / thymidylate kinase	Unigene27720_All//0.00E+00//TC147805		ko00240|Pyrimidine metabolism		nr -
Unigene27722_All	462	76.78	50.45	42.88	167.66	117.47	133.73	305.94	208.98	101.67	-6.06E-01	1.95E-11		-8.41E-01	6.97E-19		-5.13E-01	1.44E-21		-3.26E-01	1.17E-08		-5.50E-01	1.63E-44		-1.59E+00	1.54E-263	Down	Unigene27722_All//gi|3334138|sp|Q39817.1|CALX_SOYBN//1.00E-57//RecName: Full=Calnexin homolog; Flags: Precursor >gi|6690003|gb|AAA80588.1| calnexin [Glycine max]	Unigene27722_All//3.00E-46//AT5G07340| calnexin, putative	Unigene27722_All//0.00E+00//gi|13248163|gb|BF274418.2|BF274418		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr +
Unigene27723_All	924	8.15	22.54	21.90	29.44	36.30	35.39	96.50	87.39	98.22	1.47E+00	7.83E-28	Up	1.43E+00	3.89E-25	Up	3.02E-01	6.86E-04		2.66E-01	5.54E-03		-1.43E-01	5.53E-03		2.54E-02	6.59E-01		Unigene27723_All//gi|225346675|gb|ACN86359.1|//3.00E-84//GID1-4 [Gossypium hirsutum]	Unigene27723_All//1.00E-73//AT5G27320| GID1C (GA INSENSITIVE DWARF1C); hydrolase	Unigene27723_All//0.00E+00//TC152798				nr -
Unigene27727_All	426	1.60	0.00	0.00	2.92	2.18	0.00	0.30	0.00	0.00	-1.06E+01	4.10E-04	Down	-1.06E+01	7.64E-04	Down	-4.22E-01	5.06E-01		-1.15E+01	8.64E-08	Down	-8.22E+00	2.35E-01		-8.22E+00	2.00E-01		Unigene27727_All//gi|224143524|ref|XP_002324985.1|//3.00E-16//predicted protein [Populus trichocarpa] >gi|222866419|gb|EEF03550.1| predicted protein [Populus trichocarpa]		Unigene27727_All//1.00E-69//CA993836				nr +
Unigene27729_All	582	60.77	11.75	18.94	88.93	104.43	77.06	59.13	40.00	73.72	-2.37E+00	1.04E-89	Down	-1.68E+00	2.78E-55	Down	2.32E-01	3.39E-04		-2.07E-01	5.98E-03		-5.64E-01	5.71E-12		3.18E-01	7.86E-06		Unigene27729_All//gi|15235668|ref|NP_193070.1|//9.00E-87//leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] >gi|75337952|sp|Q9T0K5.1|LRX3_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 3; Short=LRR/EXTENSIN3; Short=AtLRX3; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|4584539|emb|CAB40769.1| extensin-like protein [Arabidopsis thaliana] >gi|7268037|emb|CAB78376.1| extensin-like protein [Arabidopsis thaliana]	Unigene27729_All//7.00E-45//AT4G13340| leucine-rich repeat family protein / extensin family protein	Unigene27729_All//0.00E+00//TC135314		ko03040|Spliceosome		nr -
Unigene2773_All	1481	6.32	4.17	4.82	10.26	8.95	7.11	7.31	4.23	2.42	-5.99E-01	1.38E-03		-3.92E-01	4.95E-02		-1.97E-01	2.07E-01		-5.30E-01	1.53E-04		-7.88E-01	3.82E-07		-1.59E+00	4.88E-21	Down	Unigene2773_All//gi|31711880|gb|AAP68296.1|//1.00E-130//At5g50840 [Arabidopsis thaliana]	Unigene2773_All//2.00E-124//AT5G50840| INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: LINC2 (LITTLE NUCLEI2) (TAIR:AT1G13220.2); Has 50047 Blast hits to 27335 proteins in 1173 species: Archae - 429; Bacteria - 3521; Metazoa - 26018; Fungi - 2663; Plants - 1200; Viruses - 162; Other Eukaryotes - 16054 (source: NCBI BLink).	Unigene2773_All//0.00E+00//C0079728				nr +
Unigene27732_All	969	5.56	6.90	7.25	45.96	39.06	22.33	6.68	1.81	2.59	3.12E-01	1.90E-01		3.83E-01	1.06E-01		-2.35E-01	2.33E-03		-1.04E+00	1.50E-37	Down	-1.88E+00	1.52E-15	Down	-1.37E+00	1.91E-10	Down	Unigene27732_All//gi|7340688|emb|CAB82867.1|//1.00E-95//thaumatin-like protein [Arabidopsis thaliana]	Unigene27732_All//2.00E-81//AT5G02140| thaumatin-like protein, putative	Unigene27732_All//0.00E+00//gi|164351763|gb|ES810106.1|ES810106				nr -
Unigene27733_All	530	8.98	51.82	23.31	16.07	38.66	66.47	13.16	34.93	37.36	2.53E+00	1.34E-74	Up	1.38E+00	8.88E-15	Up	1.27E+00	1.24E-25	Up	2.05E+00	2.62E-79	Up	1.41E+00	1.22E-28	Up	1.51E+00	1.95E-34	Up	Unigene27733_All//gi|224073168|ref|XP_002304905.1|//5.00E-56//f-box family protein [Populus trichocarpa] >gi|222841437|gb|EEE78984.1| f-box family protein [Populus trichocarpa]	Unigene27733_All//7.00E-16//AT1G80440| kelch repeat-containing F-box family protein	Unigene27733_All//2.00E-136//gi|78345445|gb|DT565719.1|DT565719				nr +
Unigene27734_All	820	11.55	4.26	7.73	19.26	19.02	23.96	53.16	33.44	28.23	-1.44E+00	9.25E-13	Down	-5.80E-01	2.83E-03		-1.76E-02	9.16E-01		3.15E-01	1.31E-02		-6.69E-01	5.81E-20		-9.13E-01	1.44E-34		Unigene27734_All//gi|13430182|gb|AAK25758.1|AF334838_1//2.00E-60//ribosomal protein L17 [Castanea sativa]	Unigene27734_All//3.00E-61//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene27734_All//0.00E+00//BF275985		ko03010|Ribosome		nr -
Unigene27736_All	441	2.73	19.42	16.06	10.62	15.38	11.57	2.78	9.48	8.85	2.83E+00	1.15E-26	Up	2.56E+00	2.77E-19	Up	5.35E-01	1.53E-02		1.24E-01	6.96E-01		1.77E+00	1.61E-09	Up	1.67E+00	1.54E-08	Up	Unigene27736_All//gi|28466825|gb|AA044021.1|//2.00E-11//At1g29640 [Arabidopsis thaliana]	Unigene27736_All//1.00E-12//AT1G29640| unknown protein					nr +
Unigene27738_All	487	52.43	66.59	71.73	60.66	71.70	77.90	133.44	80.76	59.23	3.45E-01	2.83E-04		4.52E-01	1.26E-06		2.41E-01	7.35E-03		3.61E-01	2.18E-05		-7.25E-01	1.20E-33		-1.17E+00	1.61E-76	Down	Unigene27738_All//gi|297838469|ref|XP_002887116.1|//5.00E-40//F1N21.17 [Arabidopsis lyrata subsp. lyrata] >gi|297322957|gb|EFH63375.1| F1N21.17 [Arabidopsis lyrata subsp. lyrata]	Unigene27738_All//3.00E-06//AT1G67350| unknown protein	Unigene27738_All//0.00E+00//TC162368				nr +
Unigene27739_All	676	0.31	1.65	0.63	2.06	4.48	2.41	1.81	0.00	4.13	2.41E+00	1.59E-03		1.03E+00	3.96E-01		1.12E+00	1.43E-03		2.21E-01	6.77E-01		-1.08E+01	9.98E-09	Down	1.19E+00	3.83E-04	Up	Unigene27739_All//gi|297821244|ref|XP_002878505.1|//7.00E-34//endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324343|gb|EFH54764.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27739_All//3.00E-34//AT3G63240| endonuclease/exonuclease/phosphatase family protein	Unigene27739_All//2.00E-19//BQ406915				nr -
Unigene2774_All	1788	10.04	4.48	1.52	10.06	9.24	4.52	18.66	17.32	35.07	-1.16E+00	3.55E-17	Down	-2.72E+00	1.50E-51	Down	-1.22E-01	4.27E-01		-1.15E+00	3.54E-18	Down	-1.07E-01	2.67E-01		9.11E-01	8.84E-49		Unigene2774_All//gi|15237505|ref|NP_198901.1|//1.00E-140//UPM1 (UROPHORPHIRIN METHYLASE 1); uroporphyrin-III C-methyltransferase [Arabidopsis thaliana] >gi|18087581|gb|AAL58921.1|AF462833_1 AT5g40850/MTK7_8 [Arabidopsis thaliana] >gi|1146165|gb|AAB92676.1| urophorphyrin III methylase [Arabidopsis thaliana] >gi|10177964|dbj|BAB11347.1| urophorphyrin III methylase [Arabidopsis thaliana] >gi|16604390|gb|AAL24201.1| AT5g40850/MTK7_8 [Arabidopsis thaliana] >gi|19310499|gb|AAL84983.1| AT5g40850/MTK7_8 [Arabidopsis thaliana] >gi|22655404|gb|AAM98294.1| At5g40850/MTK7_8 [Arabidopsis thaliana]	Unigene2774_All//1.00E-141//AT5G40850| UPM1 (UROPHORPHIRIN METHYLASE 1); uroporphyrin-III C-methyltransferase	Unigene2774_All//0.00E+00//TC176887			GO:0008152//GO:0016740	nr -
Unigene27740_All	590	21.02	3.86	5.42	26.17	20.72	31.16	26.94	15.23	12.49	-2.44E+00	5.87E-33	Down	-1.96E+00	4.44E-24	Down	-3.37E-01	1.50E-02		2.51E-01	6.75E-02		-8.23E-01	7.72E-11		-1.11E+00	7.99E-18	Down	Unigene27740_All//gi|34365593|gb|AAQ65108.1|//4.00E-19//At1g70350 [Arabidopsis thaliana]	Unigene27740_All//2.00E-12//AT1G70350| unknown protein	Unigene27740_All//0.00E+00//gi|109877451|gb|DW506424.1|DW506424				nr -
Unigene27743_All	731	10.24	15.46	9.32	1.64	2.26	1.98	1.79	0.23	0.00	5.95E-01	4.27E-04		-1.35E-01	5.95E-01		4.67E-01	4.04E-01		2.74E-01	6.49E-01		-2.97E+00	8.34E-06	Down	-1.08E+01	9.85E-10	Down	Unigene27743_All//gi|18407486|ref|NP_566114.1|//3.00E-18//AGP26 (ARABINOGALACTAN PROTEIN 26) [Arabidopsis thaliana] >gi|119361080|sp|Q94F57.2|AGP26_ARATH RecName: Full=Classical arabinogalactan protein 26; Flags: Precursor >gi|3738305|gb|AAC63647.1| expressed protein [Arabidopsis thaliana] >gi|20197561|gb|AAM15130.1| expressed protein [Arabidopsis thaliana]		Unigene27743_All//0.00E+00//TC130045		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene27744_All	641	2.12	1.11	0.50	4.74	5.21	6.55	10.03	3.00	49.47	-9.39E-01	1.02E-01		-2.09E+00	1.95E-03		1.37E-01	7.52E-01		4.67E-01	1.31E-01		-1.74E+00	5.76E-14	Down	2.30E+00	1.72E-96	Up	Unigene27744_All//gi|296080964|emb|CBI18596.3|//5.00E-08//unnamed protein product [Vitis vinifera]		Unigene27744_All//0.00E+00//DT464746				nr -
Unigene27745_All	312	25.66	15.59	14.00	36.08	33.44	36.62	24.93	16.48	12.39	-7.19E-01	4.50E-04		-8.74E-01	4.46E-05		-1.10E-01	5.85E-01		2.14E-02	9.33E-01		-5.98E-01	1.28E-03		-1.01E+00	5.36E-08	Down	Unigene27745_All//gi|261351264|gb|ACX71299.1|//1.00E-27//RNA-binding protein RZ-1 [Capsicum annuum]	Unigene27745_All//2.00E-21//AT3G26420| ATRZ-1A; RNA binding / nucleotide binding	Unigene27745_All//4.00E-155//TC144606		ko03010|Ribosome//ko03040|Spliceosome		nr -
Unigene27747_All	530	0.10	0.10	0.00	9.77	5.52	5.20	1.04	1.42	3.53	-4.60E-02	9.85E-01		-6.63E+00	6.24E-01		-8.24E-01	7.57E-04		-9.11E-01	4.31E-04		4.53E-01	5.59E-01		1.77E+00	8.08E-05	Up	Unigene27747_All//gi|227204265|dbj|BAH56984.1|//5.00E-11//AT3G14280 [Arabidopsis thaliana]	Unigene27747_All//4.00E-12//AT3G14280| unknown protein	Unigene27747_All//2.00E-173//TC155778				nr -
Unigene2775_All	1125	24.42	17.97	19.31	158.96	136.73	124.73	31.31	21.85	12.15	-4.42E-01	1.83E-05		-3.38E-01	1.83E-03		-2.17E-01	4.46E-10		-3.50E-01	8.77E-22		-5.19E-01	1.22E-10		-1.37E+00	5.48E-53	Down	Unigene2775_All//gi|15224802|ref|NP_179548.1|//1.00E-120//TET2 (TETRASPANIN2) [Arabidopsis thaliana] >gi|40822966|gb|AAR92249.1| At2g19580 [Arabidopsis thaliana] >gi|46518389|gb|AAS99676.1| At2g19580 [Arabidopsis thaliana]	Unigene2775_All//2.00E-99//AT2G19580| TET2 (TETRASPANIN2)	Unigene2775_All//0.00E+00//gi|164347467|gb|ES822739.1|ES822739			GO:0016020//GO:0031410	nr +
Unigene27751_All	620	11.56	18.06	11.17	16.31	5.44	50.41	7.64	31.75	17.35	6.44E-01	1.50E-04		-5.03E-02	8.31E-01		-1.58E+00	6.15E-19	Down	1.63E+00	1.41E-51	Up	2.06E+00	2.94E-51	Up	1.18E+00	1.70E-13	Up			Unigene27751_All//4.00E-30//AW187099				

Unigene27752_All	1284	0.00	0.63	0.08	0.47	2.90	0.67	3.10	3.26	4.16	9.30E+00	9.38E-05	Up	6.37E+00	3.99E-01		2.64E+00	2.12E-12	Up	5.21E-01	5.23E-01		7.26E-02	8.04E-01		4.26E-01	6.09E-02		Unigene27752_All//gi|15235633|ref|NP_195474.1|//1.00E-109//HLS1 (HOOKLESS 1); N-acetyltransferase [Arabidopsis thaliana] >gi|4468983|emb|CAB38297.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|7270740|emb|CAB80423.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|51969462|dbj|BAD43423.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|51970376|dbj|BAD43880.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|11074338|gb|AB040542.1| At4g37580 [Arabidopsis thaliana]	Unigene27752_All//2.00E-103//AT4G37580| HLS1 (HOOKLESS 1); N-acetyltransferase					nr -
Unigene27755_All	548	0.29	0.09	0.10	1.09	0.38	1.15	4.17	3.58	1.67	-1.63E+00	4.89E-01		-1.56E+00	5.33E-01		-1.53E+00	1.01E-01		8.10E-02	9.43E-01		-2.17E-01	6.22E-01		-1.32E+00	4.63E-04	Down			Unigene27755_All//6.00E-07//TC135391				
Unigene27756_All	502	1.35	0.61	0.95	2.98	2.47	1.44	6.82	3.25	2.78	-1.16E+00	1.89E-01		-5.05E-01	5.82E-01		-2.70E-01	6.17E-01		-1.05E+00	5.67E-02		-1.07E+00	3.71E-04	Down	-1.30E+00	1.51E-05	Down			Unigene27756_All//3.00E-12//ES811102				
Unigene27757_All	2180	0.12	0.23	1.32	0.23	0.09	0.23	1.69	2.80	5.01	9.54E-01	3.73E-01		3.46E+00	9.44E-11	Up	-1.27E+00	2.22E-01		-3.80E-03	9.87E-01		7.30E-01	6.09E-04		1.57E+00	1.56E-20	Up	Unigene27757_All//gi|224101393|ref|XP_002312260.1|//0.00E+00//phol-like protein [Populus trichocarpa] >gi|222852080|gb|EEE89627.1| phol-like protein [Populus trichocarpa]	Unigene27757_All//0.00E+00//AT1G14040| LOCATED IN: integral to membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03240.1); Has 732 Blast hits to 696 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 238; Fungi - 246; Plants - 151; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink).	Unigene27757_All//1.00E-48//gi|78329839|gb|DT550113.1|DT550113				nr -
Unigene27758_All	335	3.59	4.24	3.02	11.15	8.43	9.98	32.31	18.22	11.54	2.38E-01	6.50E-01		-2.50E-01	6.75E-01		-4.04E-01	2.15E-01		-1.61E-01	6.52E-01		-8.27E-01	1.08E-07		-1.49E+00	4.64E-19	Down	Unigene27758_All//gi|145334189|ref|NP_001078475.1|//5.00E-07//RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome [Arabidopsis thaliana]		Unigene27758_All//3.00E-137//gi|21092702|gb|BQ405015.1|BQ405015		ko03010|Ribosome		nr +
Unigene2776_All	2257	17.08	10.30	8.07	0.93	2.03	1.38	2.21	0.54	2.29	-7.29E-01	7.40E-17		-1.08E+00	6.36E-31	Down	1.13E+00	3.66E-05	Up	5.75E-01	1.17E-01		-2.04E+00	1.88E-13	Down	5.39E-02	8.31E-01		Unigene2776_All//gi|30684447|ref|NP_193591.2|//1.00E-158//proline-rich family protein [Arabidopsis thaliana] >gi|22135814|gb|AAM91093.1| AT4g18560/F28J12_220 [Arabidopsis thaliana] >gi|28416477|gb|AAO42769.1| At4g18560/F28J12_220 [Arabidopsis thaliana]	Unigene2776_All//2.00E-125//AT4G18570| proline-rich family protein	Unigene2776_All//0.00E+00//TC178551		ko03040|Spliceosome		nr -
Unigene27760_All	783	20.71	41.67	17.75	29.39	39.62	61.37	36.02	79.37	46.40	1.01E+00	2.69E-24	Up	-2.23E-01	1.45E-01		4.31E-01	1.77E-06		1.06E+00	2.83E-41	Up	1.14E+00	4.79E-68	Up	3.66E-01	2.54E-06		Unigene27760_All//gi|297848396|ref|XP_002892079.1|//1.00E-07//ORMDL family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337921|gb|EFH68338.1| ORMDL family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27760_All//8.00E-09//AT1G01230| ORMDL family protein	Unigene27760_All//0.00E+00//gi|21100963|gb|BQ413276.1|BQ413276				nr -
Unigene27762_All	639	9.42	19.98	10.83	15.12	15.14	21.42	23.22	20.15	25.87	1.09E+00	3.79E-11	Up	2.02E-01	4.04E-01		1.80E-03	9.99E-01		5.02E-01	8.19E-04		-2.05E-01	1.45E-01		1.56E-01	2.37E-01		Unigene27762_All//gi|6653740|gb|AAF22842.1|AF209910_1//2.00E-44//vacuolar sorting receptor protein [Prunus dulcis]	Unigene27762_All//5.00E-37//AT2G14740| ATVSR3 (ARABIDOPSIS THALIANA VACULOLAR SORTING RECEPTOR 3); calcium ion binding	Unigene27762_All//0.00E+00//ES831687				nr -
Unigene27764_All	604	33.61	111.07	40.73	5.28	12.26	13.38	0.56	0.90	1.25	1.72E+00	2.19E-111	Up	2.77E-01	1.86E-02		1.22E+00	6.03E-09	Up	1.34E+00	1.88E-10	Up	6.84E-01	4.49E-01		1.16E+00	1.06E-01		Unigene27764_All//gi|16323184|gb|AAL15326.1|//2.00E-09//At1g30260/F12P21_9 [Arabidopsis thaliana] >gi|21436007|gb|AAM51581.1| At1g30260/F12P21_9 [Arabidopsis thaliana]	Unigene27764_All//1.00E-09//AT1G30260| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cytokinin stimulus; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: galactosyltransferase family protein (TAIR:AT4G21060.1); Has 16 Blast hits to 16 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene27764_All//0.00E+00//TC160907				nr -
Unigene27765_All	579	31.54	19.60	13.80	88.87	63.99	74.02	22.64	17.25	12.11	-6.86E-01	1.25E-07		-1.19E+00	2.36E-17	Down	-4.74E-01	1.49E-12		-2.64E-01	3.11E-04		-3.92E-01	5.27E-03		-9.03E-01	7.98E-11				Unigene27765_All//0.00E+00//gi|18101395|gb|BM360649.1|BM360649				
Unigene2768_All	338	1.55	8.39	9.93	0.74	1.12	2.14	4.63	1.85	1.65	2.44E+00	5.81E-08	Up	2.68E+00	7.30E-10	Up	6.05E-01	6.59E-01		1.54E+00	9.17E-02		-1.32E+00	6.35E-03		-1.49E+00	1.74E-03				Unigene2768_All//2.00E-154//ES804588				
Unigene2777_All	1686	28.49	5.05	9.06	37.08	14.69	4.23	6.22	0.12	1.61	-2.50E+00	2.72E-129	Down	-1.65E+00	4.38E-73	Down	-1.34E+00	2.63E-89	Down	-3.13E+00	3.73E-234	Down	-5.65E+00	4.24E-66	Down	-1.95E+00	8.54E-27	Down	Unigene2777_All//gi|144583293|gb|ABP01349.1|//0.00E+00//DB-sphingolipid desaturase [Jatropha curcas]	Unigene2777_All//0.00E+00//AT2G46210| delta-8 sphingolipid desaturase, putative	Unigene2777_All//0.00E+00//TC163699		ko00910|Nitrogen metabolism	GO:0005506//GO:0000631//GO:0016705	nr -
Unigene27773_All	387	7.57	14.14	6.88	6.82	2.67	5.84	9.40	18.36	84.72	9.01E-01	4.43E-04		-1.38E-01	7.11E-01		-1.35E+00	2.45E-04	Down	-2.26E-01	6.28E-01		9.67E-01	1.12E-06		3.17E+00	5.34E-141	Up	Unigene27773_All//gi|224133962|ref|XP_002327722.1|//4.00E-15//predicted protein [Populus trichocarpa] >gi|222836807|gb|EEE75200.1| predicted protein [Populus trichocarpa]		Unigene27773_All//5.00E-22//DR454610				nr -
Unigene27775_All	588	18.51	16.72	19.56	21.01	15.17	14.98	46.16	27.79	21.07	-1.47E-01	4.32E-01		7.98E-02	6.62E-01		-4.70E-01	1.94E-03		-4.88E-01	2.11E-03		-7.32E-01	8.71E-15		-1.13E+00	9.43E-31	Down	Unigene27775_All//gi|225216858|gb|ACN85156.1|//2.00E-21//26S protease regulatory subunit S10B [Oryza nivara]	Unigene27775_All//2.00E-21//AT5G43010| RPT4A; ATPase [Oryza nivara]	Unigene27775_All//0.00E+00//TC164859		ko03050|Proteasome		nr -
Unigene27778_All	976	1.07	0.00	0.22	2.40	1.13	1.34	2.43	1.33	1.06	-1.01E+01	3.80E-06	Down	-2.30E+00	4.70E-03		-1.09E+00	5.67E-03		-8.38E-01	4.48E-02		-8.70E-01	1.87E-02		-1.19E+00	1.05E-03		Unigene27778_All//gi|227462996|gb|ACF39950.1|//1.00E-156//pentatricopeptide repeat protein [Gossypium hirsutum] >gi|227462998|gb|ACF39951.1| pentatricopeptide repeat protein [Gossypium hirsutum]	Unigene27778_All//5.00E-66//AT5G66520| pentatricopeptide (PPR) repeat-containing protein	Unigene27778_All//0.00E+00//TC160744				nr +
Unigene27783_All	425	3.20	2.03	2.51	2.58	7.37	7.01	4.68	4.13	3.56	-6.59E-01	2.44E-01		-3.53E-01	5.65E-01		1.52E+00	1.89E-05	Up	1.44E+00	1.15E-04	Up	-1.79E-01	6.74E-01		-3.93E-01	3.41E-01				Unigene27783_All//8.00E-86//gi|13351069|gb|BG441417.1|BG441417				
Unigene27787_All	365	4.01	11.94	9.05	22.93	18.21	14.48	9.61	10.99	6.66	1.57E+00	5.07E-07	Up	1.17E+00	1.19E-03		-3.33E-01	1.01E-01		-6.63E-01	7.20E-04		1.93E-01	5.36E-01		-5.30E-01	6.27E-02		Unigene27787_All//gi|18106916|ref|NP_564765.1|//3.00E-09//MEE9 (maternal effect embryo arrest 9) [Arabidopsis thaliana]	Unigene27787_All//2.00E-06//AT1G60870| MEE9 (maternal effect embryo arrest 9)	Unigene27787_All//2.00E-12//TC156576				nr +
Unigene27788_All	660	0.16	11.06	1.86	5.66	1.57	1.57	8.33	28.24	15.81	6.12E+00	2.56E-38	Up	3.55E+00	6.10E-05	Up	-1.85E+00	5.08E-09	Down	-1.85E+00	5.91E-08	Down	1.76E+00	1.26E-39	Up	9.25E-01	4.44E-09		Unigene27788_All//gi|18403453|ref|NP_566712.1|//6.00E-43//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|15010698|gb|AAK74008.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] >gi|18958062|gb|AAL79604.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] >gi|84778474|dbj|BAE73264.1| xylogen like protein 8 [Arabidopsis thaliana]	Unigene27788_All//8.00E-40//AT3G22600| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene27788_All//0.00E+00//gi|54121950|gb|CO497459.1|CO497459				nr -
Unigene2779_All	1509	13.35	2.08	6.18	55.39	30.24	6.73	17.74	7.01	3.38	-2.68E+00	4.74E-59	Down	-1.11E+00	3.99E-17	Down	-8.73E-01	2.27E-59		-3.04E+00	4.57E-304	Down	-1.34E+00	3.59E-38	Down	-2.39E+00	1.47E-86	Down	Unigene2779_All//gi|15224291|ref|NP_181282.1|//1.00E-136//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|4056506|gb|AAC98072.1| nodulin-like protein [Arabidopsis thaliana] >gi|14994253|gb|AAK73261.1| nodulin-like protein [Arabidopsis thaliana]	Unigene2779_All//8.00E-126//AT2G37460| nodulin MtN21 family protein	Unigene2779_All//0.00E+00//gi|164260147|gb|ES795355.1|ES795355			GO:0044464	nr +
Unigene27790_All	410	10.97	20.39	14.55	4.98	8.73	6.72	38.36	23.14	13.89	8.94E-01	1.01E-05		4.07E-01	1.19E-01		8.10E-01	1.07E-02		4.32E-01	2.93E-01		-7.29E-01	7.32E-09		-1.47E+00	9.38E-27	Down	Unigene27790_All//gi|226499536|ref|NP_001148902.1|//2.00E-16//NADH-ubiquinone oxidoreductase 23 kDa subunit [Zea mays] >gi|195623106|gb|ACG33383.1| NADH-ubiquinone oxidoreductase 23 kDa subunit [Zea mays]	Unigene27790_All//2.00E-09//AT1G79010| NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial (TYKY)	Unigene27790_All//0.00E+00//TC163989		ko00190|Oxidative phosphorylation		nr +
Unigene27792_All	733	268.53	247.47	394.40	333.88	458.46	310.97	108.15	67.40	50.82	-1.18E-01	1.76E-03		5.55E-01	1.21E-72		4.58E-01	1.89E-73		-1.03E-01	2.13E-03		-6.82E-01	7.36E-37		-1.09E+00	6.00E-83	Down	Unigene27792_All//gi|15242041|ref|NP_197570.1|//2.00E-28//senescence-associated protein-related [Arabidopsis thaliana] >gi|30725354|gb|AAP37699.1| At5g20700 [Arabidopsis thaliana]	Unigene27792_All//4.00E-25//AT5G20700| senescence-associated protein-related	Unigene27792_All//0.00E+00//TC161071				nr +
Unigene27796_All	564	3.53	11.50	7.55	4.59	4.58	6.89	18.14	24.68	15.61	1.71E+00	3.19E-11	Up	1.10E+00	4.02E-04	Up	-4.30E-03	9.80E-01		5.84E-01	6.64E-02		4.44E-01	9.80E-04		-2.17E-01	1.95E-01		Unigene27796_All//gi|15229360|ref|NP_191839.1|//3.00E-36//NPL41 (NPL4-LIKE PROTEIN 1) [Arabidopsis thaliana] >gi|75181052|sp|Q9LYC2.1|NPL41_ARATH RecName: Full=NPL4-like protein 1 >gi|110735118|gb|ABG89129.1| NPL4a [synthetic construct]	Unigene27796_All//2.00E-37//AT3G63000| NPL41 (NPL4-LIKE PROTEIN 1)	Unigene27796_All//0.00E+00//TC159930				nr -
Unigene27799_All	913	0.23	1.11	0.52	3.11	2.23	0.89	2.59	1.19	0.61	2.28E+00	4.10E-03		1.20E+00	3.03E-01		-4.83E-01	1.96E-01		-1.80E+00	5.07E-06	Down	-1.12E+00	2.64E-03		-2.09E+00	3.31E-07	Down			Unigene27799_All//2.00E-85//TC152739				
Unigene2780_All	1321	1.82	1.46	0.65	2.22	2.55	0.85	4.58	5.09	6.06	-3.22E-01	4.35E-01		-1.50E+00	8.47E-04	Down	1.99E-01	6.16E-01		-1.38E+00	1.96E-04	Down	1.54E-01	5.17E-01		4.05E-01	2.44E-02		Unigene2780_All//gi|297802820|ref|XP_002869294.1|//2.00E-75//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315130|gb|EFH45553.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2780_All//1.00E-76//AT4G32060| calcium-binding EF hand family protein	Unigene2780_All//0.00E+00//TC162792			GO:0031410//GO:0043231	nr +
Unigene27800_All	564	72.82	76.63	61.18	88.50	85.60	103.14	140.56	93.52	66.89	7.36E-02	4.26E-01		-2.51E-01	4.50E-03		-4.81E-02	5.98E-01		2.21E-01	1.53E-03		-5.88E-01	1.84E-28		-1.07E+00	1.06E-80	Down	Unigene27800_All//gi|195626816|gb|ACG35238.1|//5.00E-57//NADH-ubiquinone oxidoreductase 20 kDa subunit [Zea mays]	Unigene27800_All//7.00E-47//AT5G11770| NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial	Unigene27800_All//0.00E+00//gi|21098902|gb|BQ411215.1|BQ411215		ko00190|Oxidative phosphorylation		nr -

Unigene27804_All	328	6.54	7.26	8.44	16.86	22.05	22.44	35.45	17.08	28.66	1.51E-01	7.07E-01		3.68E-01	3.75E-01		3.87E-01	8.16E-02		4.13E-01	6.45E-02		-1.05E+00	6.68E-12	Down	-3.07E-01	3.87E-02				Unigene27804_All//2.00E-116//gi|164285625|gb|ES818848.1|ES818848				
Unigene27805_All	386	2.30	8.01	2.76	4.77	4.55	3.04	3.94	2.49	3.51	1.80E+00	4.12E-06	Up	2.60E-01	6.82E-01		-6.97E-02	8.75E-01		-6.50E-01	1.92E-01		-6.63E-01	1.73E-01		-1.68E-01	7.13E-01				Unigene27805_All//7.00E-40//TC148936				
Unigene27806_All	752	1531.08	540.79	1362.12	444.42	524.91	280.11	0.96	1.39	1.17	-1.50E+00	0.00E+00	Down	-1.69E-01	7.62E-31		2.40E-01	6.35E-26		-6.66E-01	8.30E-130		5.40E-01	3.95E-01		2.86E-01	6.45E-01		Unigene27806_All//gi|224072580|ref|XP_002303791.1|/4.00E-54//light-harvesting complex I protein Lhca2 [Populus trichocarpa] >gi|222841223|gb|EEE78770.1| light-harvesting complex I protein Lhca2 [Populus trichocarpa]	Unigene27806_All//1.00E-41//AT3G61470| LHCA2; chlorophyll binding	Unigene27806_All//0.00E+00//gi|48750291|gb|CO080810.1|CO080810	ko00196|Photosynthesis - antenna proteins		nr -
Unigene27808_All	663	8.37	2.52	3.45	15.55	15.01	13.69	32.84	7.69	8.89	-1.73E+00	6.08E-10	Down	-1.28E+00	2.77E-06	Down	-5.12E-02	8.33E-01		-1.84E-01	3.79E-01		-2.09E+00	3.93E-58	Down	-1.88E+00	3.04E-52	Down				Unigene27808_All//0.00E+00//gi|21103696|gb|BQ416009.1|BQ416009				
Unigene27811_All	756	2.56	14.21	2.54	5.07	7.38	9.08	3.02	22.89	33.25	2.47E+00	8.88E-29	Up	-1.42E-02	9.99E-01		5.40E-01	3.01E-02		8.40E-01	1.46E-04		2.92E+00	1.13E-67	Up	3.46E+00	4.15E-117	Up	Unigene27811_All//gi|27808522|gb|AAO24541.1|/4.00E-50//At4g33985 [Arabidopsis thaliana]	Unigene27811_All//5.00E-39//AT4G33985| unknown protein	Unigene27811_All//0.00E+00//TC152383			nr +
Unigene27812_All	693	21.44	22.08	11.53	35.58	24.94	34.15	73.58	81.72	161.08	4.24E-02	7.81E-01		-8.96E-01	3.82E-09		-5.12E-01	3.45E-07		-5.93E-02	6.70E-01		1.51E-01	2.31E-02		1.13E+00	1.29E-122	Up	Unigene27812_All//gi|50844679|gb|AAT84461.1|/4.00E-59//cytochrome b5 isoform Cb5-D [Vernicia fordii]	Unigene27812_All//2.00E-43//AT1G26340| CB5-A (CYTOCHROME B5 ISOFORM A); heme binding	Unigene27812_All//0.00E+00//TC162993	ko00910|Nitrogen metabolism		nr +
Unigene27814_All	457	0.34	0.00	0.93	2.94	2.34	2.87	2.22	0.00	1.66	-8.42E+00	2.16E-01		1.44E+00	2.53E-01		-3.33E-01	5.81E-01		-3.83E-02	9.48E-01		-1.11E+01	2.97E-07	Down	-4.23E-01	4.77E-01		Unigene27814_All//gi|15227887|ref|NP_179365.1|//3.00E-10//DC1 domain-containing protein [Arabidopsis thaliana] >gi|34146812|gb|AAQ62414.1| At2g17740 [Arabidopsis thaliana]	Unigene27814_All//2.00E-11//AT2G17740| DC1 domain-containing protein	Unigene27814_All//6.00E-10//TC143949			nr -
Unigene27817_All	637	31.79	61.57	13.12	10.17	26.06	16.24	43.21	48.16	49.03	9.54E-01	1.52E-26		-1.28E+00	2.93E-21	Down	1.36E+00	4.03E-23	Up	6.75E-01	1.08E-04		1.57E-01	1.02E-01		1.82E-01	3.95E-02				Unigene27817_All//6.00E-26//ES804421				
Unigene27818_All	398	79.93	72.44	87.37	174.73	155.74	134.70	75.00	46.10	27.63	-1.42E-01	1.75E-01		1.28E-01	2.31E-01		-1.66E-01	8.00E-03		-3.75E-01	5.24E-10		-7.02E-01	4.28E-15		-1.44E+00	9.00E-49	Down	Unigene27818_All//gi|30841446|gb|AAP34361.1|/2.00E-31//fiber protein Fb14 [Gossypium barbadense] >gi|66271051|gb|AAY43803.1| Fb14 [Gossypium hirsutum]	Unigene27818_All//8.00E-27//AT2G47690| NADH-ubiquinone oxidoreductase-related	Unigene27818_All//0.00E+00//TC162934	ko00190|Oxidative phosphorylation		nr -
Unigene27819_All	731	8.88	8.94	6.99	8.65	12.77	12.54	12.72	6.92	5.83	1.08E-02	9.84E-01		-3.44E-01	1.69E-01		5.61E-01	1.86E-03		5.35E-01	4.71E-03		-8.79E-01	2.26E-07		-1.13E+00	4.87E-11	Down	Unigene27819_All//gi|225444227|ref|XP_002277069.1|/1.00E-19//PREDICTED: similar to OSJNBb0061C13.7 [Vitis vinifera]	Unigene27819_All//1.00E-19//AT2G30942| unknown protein	Unigene27819_All//0.00E+00//DW513042			nr +
Unigene27820_All	566	47.98	92.92	63.98	101.04	147.54	135.01	108.91	235.27	139.29	9.54E-01	2.33E-35		4.15E-01	5.97E-06		5.46E-01	2.39E-25		4.18E-01	3.63E-13		1.11E+00	3.87E-139	Up	3.55E-01	4.98E-12		Unigene27820_All//gi|289157792|gb|ADC84428.1|/1.00E-30//ZLW [Morus alba var. multiculis]	Unigene27820_All//4.00E-20//AT2G38410| VHS domain-containing protein / GAT domain-containing protein	Unigene27820_All//0.00E+00//TC155640			nr +
Unigene27822_All	461	6.36	5.94	5.20	12.75	5.23	10.48	6.79	4.62	3.28	-9.88E-02	7.78E-01		-2.90E-01	4.56E-01		-1.29E+00	2.77E-08	Down	-2.83E-01	2.99E-01		-5.54E-01	8.20E-02		-1.05E+00	6.42E-04	Down			Unigene27822_All//3.00E-08//DW239979				
Unigene27823_All	731	0.50	0.00	0.44	7.63	6.36	2.04	9.60	3.26	0.87	-8.97E+00	1.97E-02		-1.97E-01	8.66E-01		-2.63E-01	3.25E-01		-1.90E+00	4.62E-12	Down	-1.56E+00	4.39E-13	Down	-3.46E+00	8.85E-34	Down	Unigene27823_All//gi|75164334|sp|Q945M8.1|U497L_ARATH//1.00E-51//RecName: Full=UPF0497 membrane protein At3g53850 >gi|15724236|gb|AAL06511.1|AF412058_1 AT4g31460/F3L17_30 [Arabidopsis thaliana] >gi|21464571|gb|AAM52240.1| AT4g31460/F3L17_30 [Arabidopsis thaliana]	Unigene27823_All//4.00E-39//AT3G53850| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0497, trans-membrane plant (InterPro:IPR006702); BEST Arabidopsis thaliana protein match is: integral membrane protein, putative (TAIR:AT5G02060.1); Has 100 Blast hits to 100 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 100; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene27823_All//5.00E-30//TC162042			nr +
Unigene27824_All	1116	1.45	0.86	2.67	11.34	9.29	5.42	2.08	0.67	1.11	-7.53E-01	1.41E-01		8.79E-01	2.04E-02		-2.88E-01	7.47E-02		-1.06E+00	1.90E-11	Down	-1.63E+00	4.15E-05	Down	-9.13E-01	1.12E-02		Unigene27824_All//gi|124359162|gb|ABN05685.1|//2.00E-55//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene27824_All//1.00E-15//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene27824_All//1.00E-62//ES822996			nr -
Unigene27825_All	694	6.33	3.43	5.98	7.97	7.00	5.34	4.69	1.81	2.24	-8.84E-01	2.26E-03		-8.15E-02	7.86E-01		-1.88E-01	5.26E-01		-5.78E-01	2.26E-02		-1.38E+00	1.60E-05	Down	-1.07E+00	3.85E-04	Down	Unigene27825_All//gi|224083434|ref|XP_002307025.1|/6.00E-07//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222856474|gb|EEE94021.1| cc-nbs-lrr resistance protein [Populus trichocarpa]					nr +
Unigene27826_All	376	95.32	141.09	92.62	99.89	94.24	139.45	151.58	103.71	65.27	5.66E-01	7.83E-15		-4.14E-02	6.94E-01		-8.41E-02	4.25E-01		4.81E-01	9.06E-12		-5.48E-01	2.61E-18		-1.22E+00	3.35E-71	Down	Unigene27826_All//gi|42565125|ref|NP_188924.3|//1.00E-32//emp24/gp25L/p24 protein-related [Arabidopsis thaliana] >gi|11994713|dbj|BAB03029.1| coated vesicle membrane protein-like [Arabidopsis thaliana] >gi|17979492|gb|AAL50082.1| AT3g22845/MWI23_22 [Arabidopsis thaliana] >gi|20147305|gb|AAM10366.1| AT3g22845/MWI23_22 [Arabidopsis thaliana]	Unigene27826_All//2.00E-26//AT3G22845| emp24/gp25L/p24 protein-related	Unigene27826_All//0.00E+00//TC176696			nr -
Unigene27828_All	1948	0.30	3.30	0.22	0.13	0.21	0.53	1.41	8.97	16.10	3.48E+00	1.93E-24	Up	-4.34E-01	6.23E-01		7.30E-01	5.86E-01		2.06E+00	6.55E-03		2.67E+00	4.35E-62	Up	3.51E+00	8.53E-148	Up	Unigene27828_All//gi|15235354|ref|NP_195164.1|//1.00E-150//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|29028888|gb|AAO64823.1| At4g34380 [Arabidopsis thaliana]	Unigene27828_All//3.00E-152//AT4G34380| transducin family protein / WD-40 repeat family protein	Unigene27828_All//0.00E+00//TC139483			nr -
Unigene2783_All	1246	15.28	14.31	18.42	8.00	6.25	4.71	3.12	3.49	1.47	-9.46E-02	5.14E-01		2.69E-01	2.86E-02		-3.56E-01	4.73E-02		-7.63E-01	1.63E-05		1.60E-01	6.11E-01		-1.09E+00	6.94E-05	Down	Unigene2783_All//gi|18407205|ref|NP_566091.1|//8.00E-98//plastid-lipid associated protein PAP / fibrillin family protein [Arabidopsis thaliana] >gi|75162466|sp|Q8W4F1.1|PAP10_ARATH RecName: Full=Probable plastid-lipid-associated protein 10, chloroplastic; AltName: Full=Fibrillin-10; Flags: Precursor >gi|17065012|gb|AAL32675.1| Unknown protein [Arabidopsis thaliana] >gi|20197139|gb|AAC34229.2| Expressed protein [Arabidopsis thaliana]	Unigene2783_All//2.00E-92//AT2G46910| plastid-lipid associated protein PAP / fibrillin family protein	Unigene2783_All//0.00E+00//TC147432		GO:0009570	nr -
Unigene27831_All	417	62.11	24.30	29.37	91.51	66.23	108.31	198.73	81.59	66.78	-1.35E+00	9.48E-31	Down	-1.08E+00	7.01E-21	Down	-4.66E-01	3.48E-09		2.43E-01	2.35E-03		-1.28E+00	2.81E-109	Down	-1.57E+00	1.66E-152	Down	Unigene27831_All//gi|209967447|gb|ACJ02352.1|/4.00E-24//60S ribosomal protein L39 [Vernicia fordii] >gi|257219568|gb|ACV50437.1| 60S ribosomal protein L39 [Jatropha curcas]	Unigene27831_All//4.00E-24//AT4G31985| 60S ribosomal protein L39 (RPL39C)	Unigene27831_All//0.00E+00//TC170051	ko03010|Ribosome		nr -
Unigene27832_All	787	31.78	12.10	16.04	42.09	39.64	63.70	43.95	19.70	17.87	-1.39E+00	5.36E-31	Down	-9.87E-01	1.78E-17		-8.65E-02	4.50E-01		5.98E-01	2.12E-16		-1.16E+00	3.45E-39	Down	-1.30E+00	3.44E-48	Down	Unigene27832_All//gi|257219570|gb|ACV50438.1|/2.00E-37//ribosomal protein L37 [Jatropha curcas]	Unigene27832_All//9.00E-36//AT1G15250| 60S ribosomal protein L37 (RPL37A)	Unigene27832_All//0.00E+00//TC168393	ko03010|Ribosome		nr -
Unigene27833_All	736	1.56	4.47	1.09	1.83	4.12	2.82	4.48	3.52	6.12	1.52E+00	2.93E-05	Up	-5.27E-01	4.10E-01		1.17E+00	8.71E-04	Up	6.27E-01	1.82E-01		-3.48E-01	2.84E-01		4.49E-01	7.26E-02		Unigene27833_All//gi|3915165|sp|O50046.1|TRPB_CAMAC//2.00E-91//RecName: Full=Tryptophan synthase beta chain 2, chloroplastic; Flags: Precursor >gi|2792520|gb|AAB97087.1| tryptophan synthase beta subunit [Camptotheca acuminata] >gi|2801771|gb|AAB97526.1| tryptophan synthase beta [Camptotheca acuminata]	Unigene27833_All//3.00E-89//AT4G27070| TSB2 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT 2); tryptophan synthase	Unigene27833_All//4.00E-98//gi|48776191|gb|CO085557.1|CO085557	ko00260|Glycine, serine and threonine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene27834_All	536	8.98	11.63	16.49	13.38	11.82	10.87	36.84	45.30	11.67	3.73E-01	1.25E-01		8.77E-01	1.45E-05		-1.79E-01	4.72E-01		-3.00E-01	2.05E-01		2.99E-01	3.04E-03		-1.66E+00	7.81E-40	Down	Unigene27834_All//gi|18416384|ref|NP_568240.1|//5.00E-29//ATER [Arabidopsis thaliana] >gi|28427741|sp|Q9SG19.1|ERH_ARATH RecName: Full=Enhancer of rudimentary homolog >gi|1595812|gb|AAC49667.1| enhancer of rudimentary homolog ATER [Arabidopsis thaliana]	Unigene27834_All//3.00E-30//AT5G10810| ATER	Unigene27834_All//0.00E+00//TC160037			nr -
Unigene27836_All	396	23.52	11.52	13.18	29.31	21.83	37.52	99.51	43.80	35.31	-1.03E+00	9.23E-08	Down	-8.36E-01	2.06E-05		-4.25E-01	7.66E-03		3.56E-01	1.60E-02		-1.18E+00	3.77E-46	Down	-1.49E+00	1.12E-67	Down	Unigene27836_All//gi|15229631|ref|NP_190560.1|//5.00E-30//60S ribosomal protein L26 (RPL26A) [Arabidopsis thaliana] >gi|297816242|ref|XP_002876004.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|27735242|sp|P51414.2|RL261_ARATH RecName: Full=60S ribosomal protein L26-1 >gi|6723436|emb|CAB66929.1| 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana] >gi|297321842|gb|EFH52263.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene27836_All//1.00E-13//AT3G49910| 60S ribosomal protein L26 (RPL26A)	Unigene27836_All//0.00E+00//gi|21100482|gb|BQ412795.1|BQ412795	ko03010|Ribosome		nr +
Unigene27838_All	550	1.90	5.53	3.49	4.80	22.16	25.62	5.92	12.08	14.41	1.54E+00	5.28E-05	Up	8.73E-01	7.66E-02		2.21E+00	6.86E-33	Up	2.42E+00	4.72E-39	Up	1.03E+00	6.75E-07	Up	1.28E+00	1.94E-11	Up	Unigene27838_All//gi|224072560|ref|XP_002303782.1|/1.00E-07//predicted protein [Populus trichocarpa] >gi|222841214|gb|EEE78761.1| predicted protein [Populus trichocarpa]		Unigene27838_All//6.00E-180//gi|109834062|gb|DW232627.1|DW232627			nr +
Unigene27839_All	637	2.46	6.28	2.93	2.82	2.16	2.20	8.70	8.07	10.32	1.35E+00	2.31E-05	Up	2.48E-01	6.19E-01		-3.81E-01	4.47E-01		-3.57E-01	4.96E-01		-1.08E-01	6.65E-01		2.47E-01	2.46E-01				Unigene27839_All//8.00E-07//TC135620				
Unigene27841_All	580	20.93	9.78	12.76	26.37	21.97	19.00	9.77	9.51	2.88	-1.10E+00	7.52E-11	Down	-7.14E-01	2.23E-05		-2.63E-01	7.09E-02		-4.73E-01	7.62E-04		-3.83E-02	8.86E-01		-1.76E+00	5.22E-13	Down	Unigene27841_All//gi|124301040|gb|ABN04772.1|//2.00E-19//At4g21740 [Arabidopsis thaliana]	Unigene27841_All//5.00E-10//AT4G21740| unknown protein	Unigene27841_All//0.00E+00//TC160554			nr +
Unigene27842_All	1111	0.28	0.41	0.29	1.93	1.86	2.60	8.14	2.52	2.33	5.39E-01	6.02E-01		2.53E-02	1.00E+00		-5.20E-02	9.02E-01		4.32E-01	2.77E-01		-1.69E+00	1.26E-18	Down	-1.80E+00	5.68E-21	Down	Unigene27842_All//gi|18416049|ref|NP_567674.1|//1.00E-116//SPX (SYG1/Pho81/XPR1) domain-containing protein [Arabidopsis thaliana]	Unigene27842_All//5.00E-93//AT4G22990| SPX (SYG1/Pho81/XPR1) domain-containing protein	Unigene27842_All//0.00E+00//TC138350			nr +

Unigene27844_All	846	2.47	2.99	3.65	17.55	8.39	8.06	3.65	1.04	0.85	2.76E-01	5.02E-01		5.61E-01	1.37E-01		-1.07E+00	5.29E-15	Down	-1.12E+00	1.79E-14	Down	-1.81E+00	1.82E-07	Down	-2.11E+00	2.98E-09	Down	Unigene27844_All//gi|40823013|gb|AB92253.1|//2.00E-35//At2g15730 [Arabidopsis thaliana] >gi|45752690|gb|AAS76243.1|At2g15730 [Arabidopsis thaliana]	Unigene27844_All//1.00E-36//AT2G15730| unknown protein	Unigene27844_All//0.00E+00//CO121056				nr +
Unigene27847_All	362	14.45	21.42	22.51	21.05	22.83	30.32	43.21	52.53	107.08	5.67E-01	6.74E-03		6.39E-01	2.45E-03		1.17E-01	6.15E-01		5.26E-01	2.01E-03		2.82E-01	1.58E-02		1.31E+00	4.07E-54	Up	Unigene27847_All//gi|297811169|ref|XP_002873468.1|//7.00E-15//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319305|gb|EFH49727.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27847_All//1.00E-08//AT5G10650| zinc finger (C3HC4-type RING finger) family protein	Unigene27847_All//0.00E+00//CO079221				nr -
Unigene27848_All	397	2.24	5.36	6.17	2.89	3.56	4.10	3.51	3.37	1.81	1.26E+00	5.48E-03		1.46E+00	9.35E-04	Up	3.01E-01	6.16E-01		5.05E-01	3.72E-01		-6.10E-02	9.18E-01		-9.60E-01	4.80E-02					Unigene27848_All//5.00E-167//TC164608				
Unigene2785_All	1132	3.10	2.86	4.89	1.98	1.43	0.64	0.63	0.22	0.18	-1.12E-01	7.27E-01		6.60E-01	1.25E-02		-4.70E-01	2.84E-01		-1.63E+00	2.41E-04	Down	-1.52E+00	5.42E-02		-1.85E+00	1.78E-02		Unigene2785_All//gi|18407205|ref|NP_566091.1|//1.00E-102//plastid-lipid associated protein PAP / fibrillin family protein [Arabidopsis thaliana] >gi|75162466|sp|Q8W4F1.1|PAP10_ARATH RecName: Full=Probable plastid-lipid-associated protein 10, chloroplastic; AltName: Full=Fibrillin-10; Flags: Precursor >gi|17065042|gb|AAL32675.1|Unknown protein [Arabidopsis thaliana] >gi|20197139|gb|AAC34229.2|Expressed protein [Arabidopsis thaliana]	Unigene2785_All//2.00E-96//AT2G46910| plastid-lipid associated protein PAP / fibrillin family protein	Unigene2785_All//0.00E+00//TC147432		GO:0043231		nr -
Unigene27852_All	1431	0.18	0.46	0.30	0.94	2.67	5.84	0.44	1.75	4.51	1.33E+00	1.45E-01		7.04E-01	5.54E-01		1.51E+00	1.71E-06	Up	2.64E+00	1.13E-25	Up	1.98E+00	7.17E-07	Up	3.35E+00	1.17E-29	Up				Unigene27852_All//3.00E-125//gi|3325742|gb|AI054628.1|AI054628				
Unigene27854_All	392	8.14	13.18	11.95	12.83	10.80	12.33	30.74	13.86	8.64	6.95E-01	8.24E-03		5.54E-01	5.83E-02		-2.48E-01	3.95E-01		-5.81E-02	8.52E-01		-1.15E+00	5.02E-14	Down	-1.83E+00	3.45E-28	Down	Unigene27854_All//gi|297445546|emb|CBI40711.3|//3.00E-07//unnamed protein product [Vitis vinifera]		Unigene27854_All//3.00E-162//TC160610		ko03040|Spliceosome		nr -
Unigene27855_All	483	29.79	8.92	8.16	38.68	35.58	33.19	49.72	18.78	13.94	-1.74E+00	7.67E-25	Down	-1.87E+00	3.11E-26	Down	-1.21E-01	4.23E-01		-2.21E-01	1.12E-01		-1.40E+00	7.51E-37	Down	-1.83E+00	1.75E-55	Down	Unigene27855_All//gi|15231455|ref|NP_190240.1|//8.00E-33//TIM9; P-P-bond-hydrolysis-driven protein transmembrane transporter [Arabidopsis thaliana] >gi|126439856|sp|Q9XGX9.2|TIM9_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit Tim9; AltName: Full=Protein EMBRYO DEFECTIVE 2474 >gi|6523059|emb|CAB62326.1| small zinc finger-like protein TIM9 [Arabidopsis thaliana]	Unigene27855_All//5.00E-34//AT3G46560| TIM9; P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene27855_All//0.00E+00//TC153538				nr -
Unigene27860_All	411	34.50	19.97	33.95	58.42	53.20	52.75	39.91	18.00	10.47	-7.89E-01	1.47E-07		-2.33E-02	8.96E-01		-1.35E-01	2.94E-01		-1.47E-01	2.47E-01		-1.15E+00	8.41E-19	Down	-1.93E+00	7.58E-41	Down	Unigene27860_All//gi|162955861|gb|ABY25306.1|//9.00E-66//pyrophosphate-dependent phosphofructokinase beta subunit [Citrus sinensis x Poncirus trifoliata]	Unigene27860_All//3.00E-63//AT4G04040| MEE51 (maternal effect embryo arrest 51); diphosphate-fructose-6-phosphate 1-phosphotransferase	Unigene27860_All//0.00E+00//TC157104		ko00051|Fructose and mannose metabolism		nr +
Unigene27861_All	398	16.56	14.90	6.02	24.16	25.96	22.47	113.46	127.49	56.35	-1.53E-01	5.44E-01		-1.46E+00	7.48E-09	Down	1.04E-01	6.16E-01		-1.05E-01	6.30E-01		1.68E-01	1.64E-02		-1.01E+00	3.97E-42	Down		Unigene27861_All//1.00E-65//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene27861_All//0.00E+00//gi|13350351|gb|BG440699.1|BG440699		ko04145|Phagosome		kegg -
Unigene27862_All	558	4.88	1.73	2.86	1.96	4.13	2.51	1.89	0.75	0.93	-1.50E+00	1.89E-04	Down	-7.68E-01	5.47E-02		1.07E+00	9.83E-03		3.53E-01	5.79E-01		-1.34E+00	2.90E-02		-1.03E+00	7.30E-02		Unigene27862_All//gi|297823195|ref|XP_002879480.1|//4.00E-35//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297325319|gb|EFH35739.1|nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene27862_All//4.00E-36//AT1G29250| nucleic acid binding	Unigene27862_All//0.00E+00//TC168273				nr +
Unigene27864_All	2105	0.05	0.10	0.00	0.09	0.15	0.39	6.19	16.26	5.22	9.54E-01	6.21E-01		-5.64E+00	3.94E-01		6.36E-01	6.95E-01		2.03E+00	2.17E-02		1.39E+00	1.62E-51	Up	-2.44E-01	8.62E-02		Unigene27864_All//gi|297609225|ref|NP_001062856.2|//1.00E-161//Os09g0321200 [Oryza sativa Japonica Group] >gi|255678772|dbj|BAF24770.2|Os09g0321200 [Oryza sativa Japonica Group]	Unigene27864_All//2.00E-54//AT3G63520| CCD1 (CAROTENOID CLEAVAGE DIOXYGENASE 1); 9-cis-epoxycarotenoid dioxygenase	Unigene27864_All//0.00E+00//TC131394				nr +
Unigene27865_All	712	40.93	21.71	20.34	47.23	44.88	60.20	58.55	35.05	31.67	-9.15E-01	1.04E-18		-1.01E+00	5.37E-21	Down	-7.34E-02	5.37E-01		3.50E-01	1.06E-05		-7.41E-01	1.07E-22		-8.87E-01	1.59E-31		Unigene27865_All//gi|224995910|gb|ACN76858.1|//1.00E-73//seed ripening regulated protein [Camellia oleifera]	Unigene27865_All//6.00E-41//AT2G18110| elongation factor 1-beta, putative / EF-1-beta, putative	Unigene27865_All//0.00E+00//TC132139				nr +
Unigene27868_All	939	2.51	0.97	2.33	1.80	1.69	2.45	2.43	1.56	0.55	-1.37E+00	1.46E-03		-1.09E-01	7.94E-01		-9.66E-02	8.34E-01		4.44E-01	3.33E-01		-6.42E-01	9.17E-02		-2.14E+00	3.51E-07	Down	Unigene27868_All//gi|297852260|ref|XP_002894011.1|//9.00E-58//F27F5.25 [Arabidopsis lyrata subsp. lyrata] >gi|297339853|gb|EFH70270.1|F27F5.25 [Arabidopsis lyrata subsp. lyrata]	Unigene27868_All//9.00E-58//AT1G45170| unknown protein	Unigene27868_All//0.00E+00//DR456218				nr +
Unigene27869_All	259	0.40	2.15	0.41	0.19	0.80	0.87	3.10	0.32	0.92	2.41E+00	3.93E-02		2.55E-02	1.00E+00		2.05E+00	3.95E-01		2.18E+00	3.23E-01		-3.26E+00	4.48E-04	Down	-1.75E+00	1.55E-02		Unigene27869_All//gi|115455377|ref|NP_001051289.1|//1.00E-23//Os03g0751000 [Oryza sativa Japonica Group] >gi|40538985|gb|AAR87242.1|expressed protein [Oryza sativa Japonica Group] >gi|108711108|gb|ABF98903.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549760|dbj|BAF13203.1|Os03g0751000 [Oryza sativa Japonica Group]	Unigene27869_All//1.00E-22//AT2G04900| unknown protein	Unigene27869_All//3.00E-124//TC150054				nr -
Unigene2787_All	1809	11.45	7.73	3.62	4.24	4.21	2.80	17.55	13.52	23.21	-5.67E-01	2.50E-06		-1.66E+00	5.44E-32	Down	-1.15E-02	9.54E-01		-6.01E-01	3.79E-03		-3.77E-01	9.92E-06		4.03E-01	2.02E-08		Unigene2787_All//gi|15220732|ref|NP_173326.1|//1.00E-177//lipase class 3 family protein [Arabidopsis thaliana]	Unigene2787_All//2.00E-178//AT1G30370| lipase class 3 family protein	Unigene2787_All//0.00E+00//TC175119			GO:0004091//GO:0009536//GO:0044238	nr +
Unigene27870_All	685	34.75	36.84	42.76	26.69	27.80	21.36	22.78	19.71	9.83	8.40E-02	5.02E-01		2.99E-01	4.67E-03		5.88E-02	7.30E-01		-3.21E-01	1.48E-02		-2.09E-01	1.29E-01		-1.21E+00	4.70E-20	Down	Unigene27870_All//gi|115455377|ref|NP_001051289.1|//5.00E-45//Os03g0751000 [Oryza sativa Japonica Group] >gi|40538985|gb|AAR87242.1|expressed protein [Oryza sativa Japonica Group] >gi|108711108|gb|ABF98903.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549760|dbj|BAF13203.1|Os03g0751000 [Oryza sativa Japonica Group]	Unigene27870_All//4.00E-45//AT2G04900| unknown protein	Unigene27870_All//0.00E+00//TC150054				nr +
Unigene27871_All	1601	0.62	1.20	0.67	2.36	4.54	3.53	2.61	0.50	1.64	9.54E-01	4.27E-02		9.94E-02	8.79E-01		9.41E-01	5.31E-06		5.77E-01	2.24E-02		-2.40E+00	9.55E-14	Down	-6.71E-01	8.61E-03		Unigene27871_All//gi|29029014|gb|AA064886.1|//1.00E-123//At4g13370 [Arabidopsis thaliana]	Unigene27871_All//2.00E-119//AT4G13370| unknown protein	Unigene27871_All//0.00E+00//gi|109878919|gb|DW507889.1|DW507889				nr -
Unigene27872_All	588	49.92	218.10	69.91	44.65	61.49	87.95	16.90	48.05	19.85	2.13E+00	1.83E-281	Up	4.86E-01	1.17E-08		4.62E-01	2.13E-08		9.78E-01	7.93E-39		1.51E+00	7.29E-48	Up	2.32E-01	1.28E-01		Unigene27872_All//gi|124359217|gb|ABN05728.1|//2.00E-10//Octicosapeptide/Phox/Bem1p [Medicago truncatula]	Unigene27872_All//1.00E-07//AT5G64430| octicosapeptide/Phox/Bem1p (PB1) domain-containing protein	Unigene27872_All//0.00E+00//gi|109845200|gb|DW243758.1|DW243758				nr -
Unigene27875_All	788	1.66	0.58	0.47	2.21	1.57	0.57	1.61	0.90	0.46	-1.52E+00	1.35E-02		-1.81E+00	6.66E-03		-4.92E-01	3.18E-01		-1.95E+00	2.67E-04	Down	-8.36E-01	1.23E-01		-1.82E+00	1.09E-03		Unigene27875_All//gi|115445589|ref|NP_001046574.1|//1.00E-64//Os02g0286200 [Oryza sativa Japonica Group] >gi|47847721|dbj|BAD21500.1|lipase class 3-like [Oryza sativa Japonica Group] >gi|113536105|dbj|BAF08488.1|Os02g0286200 [Oryza sativa Japonica Group]	Unigene27875_All//1.00E-64//AT4G10955| lipase class 3 family protein	Unigene27875_All//0.00E+00//TC134615				nr +
Unigene27878_All	367	2.57	11.18	11.75	6.92	8.35	6.15	17.05	26.42	13.68	2.12E+00	1.32E-09	Up	2.20E+00	4.66E-10	Up	2.71E-01	5.19E-01		-1.70E-01	6.78E-01		6.32E-01	1.15E-04		-3.18E-01	1.34E-01					Unigene27878_All//0.00E+00//TC154422				
Unigene27879_All	589	1.42	1.81	0.36	1.52	1.11	1.76	4.45	4.40	9.33	3.46E-01	6.19E-01		-1.97E+00	2.71E-02		-4.55E-01	5.58E-01		2.12E-01	7.55E-01		-1.66E-02	9.98E-01		1.07E+00	2.38E-06	Up								
Unigene2788_All	1424	4.52	3.74	3.63	41.31	32.14	28.39	31.86	32.14	98.45	-2.75E-01	2.58E-01		-3.17E-01	2.16E-01		-3.62E-01	7.33E-09		-5.42E-01	3.15E-16		1.27E-02	8.94E-01		1.63E+00	9.93E-268	Up	Unigene2788_All//gi|223452391|gb|ACM89523.1|//1.00E-116//protein kinase family protein [Glycine max]	Unigene2788_All//4.00E-100//AT2G23200| protein kinase family protein	Unigene2788_All//0.00E+00//DW227487		ko04626|Plant-pathogen interaction		nr -
Unigene27881_All	466	10.67	19.57	13.14	8.98	7.39	10.18	7.35	5.74	3.33	8.76E-01	5.50E-06		3.01E-01	2.44E-01		-2.81E-01	3.83E-01		1.81E-01	5.91E-01		-3.57E-01	2.57E-01		-1.14E+00	1.08E-04	Down								
Unigene27882_All	659	1.11	0.31	2.10	3.63	2.19	2.67	0.71	3.04	1.33	-1.85E+00	4.08E-02		9.19E-01	1.27E-01		-7.25E-01	6.73E-02		-4.41E-01	3.15E-01		2.11E+00	4.88E-06	Up	9.14E-01	1.59E-01					Unigene27882_All//3.00E-102//FL577497				
Unigene27885_All	813	2.19	4.43	8.19	2.02	3.90	2.89	26.89	32.49	38.32	1.02E+00	1.97E-03		1.90E+00	9.14E-13	Up	9.47E-01	5.49E-03		5.15E-01	2.40E-01		2.73E-01	4.75E-03		5.11E-01	1.56E-09		Unigene27885_All//gi|122214588|sp|Q3EA54.1|U4970_ARATH//3.00E-28//RecName: Full=UPF0497 membrane protein At4g11655	Unigene27885_All//1.00E-16//AT4G11655| transmembrane protein, putative	Unigene27885_All//3.00E-68//TC177471				nr +
Unigene27887_All	720	32.63	7.25	17.90	14.94	9.28	5.33	1.23	1.34	0.28	-2.17E+00	1.10E-53	Down	-8.66E-01	2.37E-13		-6.88E-01	1.74E-05		-1.49E+00	3.53E-16	Down	1.15E-01	8.57E-01		-2.16E+00	2.68E-03		Unigene27887_All//gi|17386128|gb|AAL38610.1|AF446877_1//1.00E-24//AT3g52740/F3C22_140 [Arabidopsis thaliana] >gi|15450655|gb|AAU96599.1|AT3g52740/F3C22_140 [Arabidopsis thaliana]	Unigene27887_All//8.00E-26//AT3G52740| unknown protein	Unigene27887_All//0.00E+00//gi|109875992|gb|DW504966.1|DW504966				nr -
Unigene27888_All	397	13.84	31.14	11.80	16.94	34.00	27.64	49.95	95.59	163.67	1.17E+00	4.20E-12	Up	-2.29E-01	4.02E-01		1.01E+00	6.54E-12	Up	7.07E-01	2.74E-05		9.37E-01	1.54E-30		1.71E+00	1.12E-133	Up	Unigene27888_All//gi|219560134|gb|ACL27275.1|//1.00E-10//homeodomain leucine-zipper 1 [Capsicum annuum]		Unigene27888_All//0.00E+00//TC143756				nr +
Unigene27889_All	539	5.34	9.02	7.11	13.59	7.09	12.07	33.57	23.03	13.30	7.57E-01	5.51E-03		4.14E-01	2.22E-01		-9.38E-01	2.66E-06		-1.71E-01	4.95E-01		-5.44E-01	2.61E-06		-1.34E+00	9.64E-27	Down				Unigene27889_All//1.00E-143//DW501241				
Unigene2789_All	1811	8.26	3.27	5.15	6.22	4.75	3.09	2.45	1.68	2.57	-1.34E+00	9.96E-18	Down	-6.83E-01	4.89E-06		-3.87E-01	1.89E-02		-1.01E+00	1.99E-09	Down	-5.41E-01	3.66E-02		7.03E-02	7.87E-01		Unigene2789_All//gi|15240831|ref|NP_196379.1|//1.00E-113//protein kinase family protein [Arabidopsis thaliana]	Unigene2789_All//5.00E-108//AT5G07620| protein kinase family protein	Unigene2789_All//0.00E+00//TC144213			GO:0006464//GO:0016301//GO:0032559//GO:0043231	nr -
Unigene27890_All	1132	4.81	2.06	3.34	8.76	7.00	7.02	16.55	7.02	7.81	-1.22E+00	3.71E-06	Down	-5.25E-01	5.07E-02		-3.24E-01	7.81E-02		-3.19E-01	9.67E-02		-1.24E+00	6.26E-24	Down	-1.08E+00	4.48E-20	Down	Unigene27890_All//gi|297850978|ref|XP_002893370.1|//4.00E-96//peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339212|gb|EFH69629.1|peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27890_All//2.00E-97//AT1G26940| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	Unigene27890_All//0.00E+00//TC146834		ko03040|Spliceosome		nr +

Unigene27891_All	694	4.07	13.73	4.14	6.96	11.96	7.87	15.54	14.82	45.12	1.75E+00	9.42E-17	Up	2.54E-02	9.65E-01		7.80E-01	4.19E-05		1.78E-01	5.61E-01		-6.85E-02	7.07E-01		1.54E+00	1.07E-55	Up	Unigene27891_All//gi|6714272|gb|AAF25968.1|AC017118.5//3.00E-44//F6N18.8 [Arabidopsis thaliana]	Unigene27891_All//1.00E-42//AT1G32700| zinc-binding family protein	Unigene27891_All//0.00E+00//TC130530	PLATZ			nr -
Unigene27893_All	633	6.28	4.56	3.53	465.25	424.32	280.54	77.88	68.54	28.51	-4.61E-01	1.37E-01		-8.30E-01	9.42E-03		-1.33E-01	1.42E-06		-7.30E-01	2.13E-134		-1.84E-01	8.83E-03		-1.45E+00	9.85E-81	Down	Unigene27893_All//gi|18416160|ref|NP_567685.1|//3.00E-24//SP1L5 (SPIRAL1-LIKE5) [Arabidopsis thaliana]	Unigene27893_All//1.00E-25//AT4G23496| SP1L5 (SPIRAL1-LIKE5)	Unigene27893_All//0.00E+00//gi|109880833|gb|DW509803.1|DW509803				nr -
Unigene27894_All	625	56.67	31.94	38.25	95.17	87.22	58.03	40.25	5.75	6.37	-8.27E-01	3.87E-19		-5.67E-01	9.19E-10		-1.26E-01	8.36E-02		-7.14E-01	1.69E-26		-2.81E+00	1.96E-94	Down	-2.66E+00	6.86E-92	Down	Unigene27894_All//gi|18396079|ref|NP_566161.1|//2.00E-22//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	Unigene27894_All//1.00E-23//AT3G02120| hydroxyproline-rich glycoprotein family protein	Unigene27894_All//0.00E+00//TC155073				nr -
Unigene27895_All	966	0.76	1.05	2.48	6.34	6.88	8.09	5.56	9.43	11.09	4.68E-01	4.89E-01		1.71E+00	2.01E-04	Up	1.17E-01	6.68E-01		3.51E-01	1.12E-01		7.63E-01	7.55E-06		9.97E-01	2.09E-10		Unigene27895_All//gi|51536446|gb|AAU05461.1|//2.00E-36//At4g35070 [Arabidopsis thaliana] >gi|51972074|gb|AAU15141.1| At4g35070 [Arabidopsis thaliana]	Unigene27895_All//1.00E-27//AT4G35070| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 8 growth stages; CONTAINS InterPro DOMAIN/s: S-ribonuclease binding protein, SBP1, pollen (InterPro:IPR017066); BEST Arabidopsis thaliana protein match is: SBP1 (s-ribonuclease binding protein 1); protein binding / zinc ion binding (TAIR:AT1G45976.1); Has 762 Blast hits to 716 proteins in 103 species: Archae - 2; Bacteria - 18; Metazoa - 250; Fungi - 8; Plants - 213; Viruses - 21; Other Eukaryotes - 250 (source: NCBI BLink).	Unigene27895_All//3.00E-19//DW505027				nr -
Unigene27896_All	539	46.21	27.26	23.02	34.29	29.26	34.02	23.85	20.63	17.22	-7.61E-01	5.79E-12		-1.01E+00	6.29E-18	Down	-2.29E-01	8.46E-02		-1.13E-02	9.44E-01		-2.09E-01	1.73E-01		-4.70E-01	5.82E-04		Unigene27896_All//gi|154269428|gb|ABS72341.1|//7.00E-35//rapid alkalinization factor precursor [Litchi chinensis]	Unigene27896_All//9.00E-36//AT3G16570| RALFL23 (ralf-like 23); signal transducer	Unigene27896_All//0.00E+00//gi|21092925|gb|BQ405238.1|BQ405238				nr -
Unigene27901_All	813	4.83	60.77	7.79	9.13	7.96	39.83	23.87	42.72	26.85	3.65E+00	1.46E-192	Up	6.91E-01	4.53E-03		-1.97E-01	4.17E-01		2.13E+00	1.92E-76	Up	8.40E-01	1.94E-23		1.70E-01	1.23E-01		Unigene27901_All//gi|224101487|ref|XP_002312301.1|//1.00E-97//1-cys peroxiredoxin [Populus trichocarpa] >gi|222852121|gb|EEE89668.1| 1-cys peroxiredoxin [Populus trichocarpa]	Unigene27901_All//8.00E-89//AT1G48130| ATPER1: antioxidant/ thioredoxin peroxidase	Unigene27901_All//0.00E+00//gi|109871672|gb|DW500648.1|DW500648		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene27903_All	1267	6.36	2.20	3.70	5.11	5.16	3.64	1.30	1.22	0.82	-1.53E+00	5.64E-12	Down	-7.82E-01	2.35E-04		1.48E-02	9.62E-01		-4.91E-01	3.61E-02		-9.25E-02	8.46E-01		-6.71E-01	1.27E-01		Unigene27903_All//gi|297790937|ref|XP_002863353.1|//3.00E-76//vesicle-associated membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309188|gb|EFH39612.1| vesicle-associated membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27903_All//1.00E-71//AT5G47180| vesicle-associated membrane family protein / VAMP family protein	Unigene27903_All//0.00E+00//TC159185				nr +
Unigene27904_All	1151	8.77	6.65	10.69	14.28	9.21	8.32	2.28	0.94	1.04	-4.00E-01	2.81E-02		2.85E-01	1.06E-01		-6.32E-01	4.97E-07		-7.80E-01	5.87E-09		-1.27E+00	3.66E-04	Down	-1.13E+00	9.11E-04	Down	Unigene27904_All//gi|124359981|gb|ABN07997.1|//5.00E-06//contains similarity to reverse trancriptase, related [Medicago truncatula]		Unigene27904_All//3.00E-26//TC133829				nr -
Unigene27906_All	1071	2.78	4.16	1.04	6.51	5.56	4.22	1.42	0.31	0.26	5.80E-01	4.41E-02		-1.42E+00	3.22E-04	Down	-2.27E-01	3.46E-01		-6.27E-01	4.22E-03		-2.19E+00	5.96E-05	Down	-2.45E+00	8.71E-06	Down	Unigene27906_All//gi|297842911|ref|XP_002888887.1|//3.00E-44//IQ-domain 8 [Arabidopsis lyrata subsp. lyrata] >gi|297347228|gb|EFH65146.1| IQ-domain 8 [Arabidopsis lyrata subsp. lyrata]	Unigene27906_All//3.00E-39//AT1G72670| iqd8 (IQ-domain 8); calmodulin binding	Unigene27906_All//0.00E+00//TC177458				nr +
Unigene27909_All	798	2.23	1.59	0.53	2.12	2.89	0.57	2.44	2.15	1.15	-4.90E-01	3.25E-01		-2.06E+00	3.27E-04	Down	4.46E-01	3.15E-01		-1.91E+00	4.25E-04	Down	-1.83E-01	6.70E-01		-1.09E+00	7.10E-03		Unigene27909_All//gi|118482393|gb|ABR93119.1|//7.00E-08//unknown [Populus trichocarpa]		Unigene27909_All//0.00E+00//ES838729				nr -
Unigene27912_All	1191	5.10	2.21	5.50	7.07	9.34	8.34	7.85	7.58	12.18	-1.20E+00	1.25E-06	Down	1.10E-01	6.52E-01		4.02E-01	1.70E-02		2.39E-01	2.33E-01		-4.96E-02	7.96E-01		6.34E-01	8.10E-07		Unigene27912_All//gi|15223207|ref|NP_172318.1|//2.00E-79//kelch repeat-containing protein / serine/threonine phosphoesterase family protein [Arabidopsis thaliana] >gi|60359046|sp|Q9SJF0.2|BSL2_ARATH RecName: Full=Serine/threonine-protein phosphatase BSL2; AltName: Full=BSL1-like protein 2	Unigene27912_All//1.00E-65//AT1G08420| kelch repeat-containing protein / serine/threonine phosphoesterase family protein	Unigene27912_All//0.00E+00//DW498718				nr +
Unigene27913_All	797	14.90	27.27	13.36	54.31	51.29	66.41	14.75	65.55	8.50	8.72E-01	4.63E-13		-1.57E-01	3.88E-01		-8.28E-02	3.96E-01		2.90E-01	4.92E-05		2.15E+00	4.35E-143	Up	-7.95E-01	4.49E-08		Unigene27913_All//gi|159138945|gb|ABW89472.1|//2.00E-85//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene27913_All//1.00E-60//AT2G29500| 17.6 kDa class I small heat shock protein (HSP17.6B-CI)	Unigene27913_All//0.00E+00//TC168808				nr -
Unigene27914_All	1172	1.83	1.56	1.86	1.62	1.06	0.85	13.82	5.96	13.53	-2.34E-01	6.22E-01		2.54E-02	9.73E-01		-6.11E-01	1.90E-01		-9.30E-01	5.00E-02		-1.21E+00	3.38E-20	Down	-3.04E-02	8.27E-01		Unigene27914_All//gi|15220383|ref|NP_171993.1|//3.00E-82//tyrosine specific protein phosphatase family protein [Arabidopsis thaliana] >gi|73921030|sp|Q9ZVN4.1|Y1500_ARATH RecName: Full=Probable tyrosine-protein phosphatase At1g05000 >gi|4056425|gb|AAC97999.1| ESTs gb|H36249, gb|AA59732 and gb|AA651219 come from this gene [Arabidopsis thaliana] >gi|28950701|gb|AA063274.1| At1g05000 [Arabidopsis thaliana]	Unigene27914_All//1.00E-83//AT1G05000| tyrosine specific protein phosphatase family protein	Unigene27914_All//0.00E+00//DT461723				nr +
Unigene27915_All	836	11.39	9.27	6.62	177.51	135.89	61.80	12.29	13.80	4.24	-2.97E-01	1.25E-01		-7.82E-01	5.24E-05		-3.86E-01	3.05E-24		-1.52E+00	8.63E-225	Down	1.67E-01	3.30E-01		-1.53E+00	5.52E-19	Down	Unigene27915_All//gi|119366570|gb|ABL67522.1|//5.00E-11//CLAVATA3/ESR-related protein precursor [Zinnia violacea]	Unigene27915_All//3.00E-07//AT3G24770| CLE41 (CLAVATA3/ESR-RELATED 41); protein binding / receptor binding	Unigene27915_All//0.00E+00//TC143922				nr -
Unigene27916_All	683	13.02	8.53	11.07	107.87	68.42	53.89	19.99	22.15	9.33	-6.10E-01	1.56E-03		-2.34E-01	2.78E-01		-6.57E-01	6.96E-32		-1.00E+00	6.52E-58	Down	1.48E-01	3.19E-01		-1.10E+00	3.13E-15	Down	Unigene27916_All//gi|119366570|gb|ABL67522.1|//3.00E-12//CLAVATA3/ESR-related protein precursor [Zinnia violacea]	Unigene27916_All//7.00E-07//AT3G24770| CLE41 (CLAVATA3/ESR-RELATED 41); protein binding / receptor binding	Unigene27916_All//0.00E+00//DW507259				nr +
Unigene27917_All	1943	0.78	0.10	1.12	5.95	10.00	9.39	2.92	0.82	1.44	-2.90E+00	2.07E-05	Down	5.25E-01	2.46E-01		7.49E-01	1.62E-10		6.59E-01	1.88E-07		-1.83E+00	2.83E-13	Down	-1.02E+00	3.55E-06	Down	Unigene27917_All//gi|15226437|ref|NP_182199.1|//0.00E+00//FAD-binding domain-containing protein [Arabidopsis thaliana]	Unigene27917_All//0.00E+00//AT2G46760| FAD-binding domain-containing protein	Unigene27917_All//0.00E+00//TC166981		ko00053|Ascorbate and aldarate metabolism		nr -
Unigene27919_All	413	1.52	2.33	2.19	0.96	2.83	3.17	6.96	3.34	2.60	6.17E-01	3.76E-01		5.28E-01	4.79E-01		1.55E+00	1.81E-02		1.72E+00	6.55E-03		-1.06E+00	1.43E-03		-1.42E+00	2.27E-05	Down			Unigene27919_All//7.00E-145//TC169323				
Unigene2792_All	3649	11.46	48.21	30.40	0.67	2.20	1.24	0.00	0.01	0.00	2.07E+00	0.00E+00	Up	1.41E+00	1.62E-133	Up	1.72E+00	9.37E-16	Up	8.88E-01	1.72E-03		3.52E+00	6.35E-01		null	null		Unigene2792_All//gi|223452526|gb|ACM89590.1|//1.00E-157//disease resistance protein [Glycine max]	Unigene2792_All//2.00E-131//AT1G74170| AtRLP13 (Receptor Like Protein 13); protein binding	Unigene2792_All//3.00E-07//DT465312		ko04626|Plant-pathogen interaction		nr +
Unigene27921_All	254	121.33	46.28	42.56	124.34	108.32	168.38	142.65	56.77	87.52	-1.39E+00	5.93E-38	Down	-1.51E+00	2.36E-41	Down	-1.99E-01	4.23E-02		4.38E-01	2.94E-08		-1.33E+00	8.50E-51	Down	-7.05E-01	8.15E-19		Unigene27921_All//gi|7488934|pir||T14304//4.00E-23//ribosomal protein - carrot (fragment)	Unigene27921_All//6.00E-19//AT3G53740| 60S ribosomal protein L36 (RPL36B)	Unigene27921_All//6.00E-107//gi|109876929|gb|DW505903.1|DW505903		ko03010|Ribosome		nr -
Unigene27923_All	779	15.65	4.49	2.73	112.74	63.08	29.80	6.02	1.56	1.02	-1.80E+00	3.59E-22	Down	-2.52E+00	3.54E-32	Down	-8.38E-01	4.68E-58		-1.92E+00	5.63E-185	Down	-1.95E+00	4.96E-12	Down	-2.56E+00	4.87E-17	Down	Unigene27923_All//gi|15240191|ref|NP_201508.1|//2.00E-33//RALFL34 (ralf-like 34); signal transducer [Arabidopsis thaliana]	Unigene27923_All//8.00E-29//AT5G67070| RALFL34 (ralf-like 34); signal transducer	Unigene27923_All//0.00E+00//TC157920				nr -
Unigene27924_All	936	6.88	9.47	12.57	13.78	11.63	4.83	0.59	0.13	0.17	4.62E-01	1.79E-02		8.71E-01	4.33E-07		-2.46E-01	1.36E-01		-1.51E+00	8.27E-20	Down	-2.13E+00	3.31E-02		-1.79E+00	5.06E-02		Unigene27924_All//gi|8778340|gb|AAF29348.1|AC007887_7//1.00E-141//F15D4.13 [Arabidopsis thaliana]	Unigene27924_All//3.00E-22//ATMG00860| hypothetical protein	Unigene27924_All//5.00E-49//gi|195983364|gb|FL576858.1|FL576858				nr +
Unigene27925_All	1741	2.04	0.96	2.05	8.93	5.85	3.48	14.45	11.81	12.72	-1.09E+00	9.97E-04	Down	4.10E-03	9.97E-01		-6.09E-01	2.83E-06		-1.36E+00	2.70E-20	Down	-2.91E-01	3.25E-03		-1.84E-01	6.67E-02		Unigene27925_All//gi|18700103|gb|AAL77663.1|//1.00E-136//AT5g10770/T30N20_40 [Arabidopsis thaliana] >gi|24111269|gb|AAN46758.1| At5g10770/T30N20_40 [Arabidopsis thaliana]	Unigene27925_All//1.00E-116//AT5G10770| chloroplast nucleoid DNA-binding protein, putative	Unigene27925_All//1.00E-32//gi|109828526|gb|DW227149.1|DW227149				nr -
Unigene27928_All	630	3.24	7.40	2.28	11.39	16.23	8.10	103.55	231.34	634.32	1.19E+00	3.47E-05	Up	-5.05E-01	2.92E-01		5.12E-01	2.92E-03		-4.91E-01	2.56E-02		1.16E+00	5.43E-163	Up	2.61E+00	0.00E+00	Up	Unigene27928_All//gi|40457261|gb|AAR86686.1|//1.00E-39//proline dehydrogenase [Glycine max]	Unigene27928_All//5.00E-31//AT5G38710| proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative	Unigene27928_All//0.00E+00//gi|84166897|gb|DR455545.1|DR455545				nr -
Unigene27930_All	905	1.16	0.95	0.88	1.16	1.83	3.09	2.90	2.08	3.61	-2.81E-01	6.44E-01		-3.90E-01	5.89E-01		6.60E-01	2.18E-01		1.42E+00	2.46E-04	Up	-4.79E-01	1.83E-01		3.18E-01	3.14E-01		Unigene27930_All//gi|297811695|ref|XP_002873731.1|//1.00E-124//sister chromatid cohesion 2 [Arabidopsis lyrata subsp. lyrata] >gi|297319568|gb|EFH99990.1| sister chromatid cohesion 2 [Arabidopsis lyrata subsp. lyrata]	Unigene27930_All//1.00E-97//AT5G15540| EMB2773 (EMBRYO DEFECTIVE 2773); binding / protein binding / zinc ion binding					nr -
Unigene27932_All	1301	0.08	4.79	0.82	1.42	3.84	6.98	0.07	1.16	0.06	5.90E+00	2.49E-32	Up	3.35E+00	3.36E-04	Up	1.44E+00	7.92E-08	Up	2.30E+00	6.94E-24	Up	4.15E+00	2.17E-08	Up	-8.69E-02	9.72E-01		Unigene27932_All//gi|38346716|emb|CAE04866.2|//3.00E-31//OSJNBa0086006.14 [Oryza sativa (japonica cultivar-group)]	Unigene27932_All//8.00E-23//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative					nr +
Unigene27934_All	2346	0.00	0.00	0.00	0.00	0.03	0.08	15.93	6.93	51.42	null	null		null	null		4.88E+00	6.10E-01		6.27E+00	1.94E-01		-1.20E+00	8.39E-45	Down	1.69E+00	3.50E-243	Up	Unigene27934_All//gi|42568204|ref|NP_198813.3|//0.00E+00//catalytic [Arabidopsis thaliana]	Unigene27934_All//0.00E+00//AT5G39970| catalytic	Unigene27934_All//5.00E-08//gi|78334327|gb|DT554601.1|DT554601				nr +
Unigene27935_All	649	20.64	16.16	10.50	7.14	5.15	7.86	3.19	0.77	0.74	-3.53E-01	2.44E-02		-9.75E-01	1.81E-09		-4.72E-01	8.70E-02		1.40E-01	6.50E-01		-2.05E+00	5.02E-06	Down	-2.12E+00	1.66E-06	Down	Unigene27935_All//gi|62086403|dbj|BAD91804.1|//1.00E-71//cyclo-DOPA 5-O-glucosyltransferase [Celosia cristata]	Unigene27935_All//1.00E-52//AT5G12890| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene27935_All//0.00E+00//gi|48779575|gb|CO088941.1|CO088941		ko00940|Phenylpropanoid biosynthesis		nr -

Unigene27936_All	925	9.96	18.19	12.20	19.82	26.51	46.48	0.59	0.45	1.38	8.69E-01	3.09E-10		2.94E-01	1.12E-01		4.20E-01	5.16E-05		1.23E+00	1.30E-46	Up	-3.95E-01	6.34E-01		1.21E+00	2.09E-02		Unigene27936_All//gi|94549041|gb|ABF39005.1|/4.00E-40//plant cell wall protein S1IFR88 [Solanum lycopersicum]	Unigene27936_All//9.00E-34//AT2G46150| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54200.1); Has 137 Blast hits to 136 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 133; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene27936_All//0.00E+00//TC136055				nr +
Unigene27941_All	673	6.61	12.80	7.04	6.74	8.44	8.72	16.02	27.33	34.69	9.54E-01	1.91E-06		9.17E-02	7.50E-01		3.26E-01	2.25E-01		3.73E-01	1.51E-01		7.70E-01	3.76E-11		1.11E+00	9.22E-26	Up	Unigene27941_All//gi|17064766|gb|AAL32537.1|/4.00E-25//Unknown protein [Arabidopsis thaliana] >gi|23197816|gb|AAN15435.1| Unknown protein [Arabidopsis thaliana]	Unigene27941_All//2.00E-26//AT4G08500| MEKK1 (MAP KINASE KINASE KINASE 1); DNA binding / MAP kinase kinase kinase/ kinase/ kinase binding / protein binding	Unigene27941_All//0.00E+00//DT463421		ko04626|Plant-pathogen interaction		nr -
Unigene27943_All	1687	2.20	1.50	4.73	1.39	1.18	0.56	0.00	0.05	0.00	-5.52E-01	8.30E-02		1.10E+00	4.00E-07	Up	-2.29E-01	6.11E-01		-1.30E+00	1.98E-03		5.63E+00	4.01E-01		null	null		Unigene27943_All//gi|115480809|ref|NP_001063998.1|/9.00E-10//Os09g0572500 [Oryza sativa Japonica Group] >gi|113632231|dbj|BAF25912.1| Os09g0572500 [Oryza sativa Japonica Group]					nr +
Unigene27944_All	691	0.45	57.71	5.93	0.00	0.10	0.92	1.47	0.91	7.96	6.99E+00	1.64E-217	Up	3.71E+00	4.94E-16	Up	6.64E+00	6.10E-01		9.84E+00	7.60E-04	Up	-6.95E-01	2.63E-01		2.44E+00	1.64E-18	Up	Unigene27944_All//gi|297850166|ref|XP_002882964.1|/6.00E-44//phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297338806|gb|EFH69223.1| phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene27944_All//7.00E-44//AT1G17710| phosphatase	Unigene27944_All//9.00E-124//gi|73865272|gb|DT468010.1|DT468010				nr -
Unigene27945_All	977	1.93	374.39	24.85	0.10	0.39	2.31	8.05	5.22	29.03	7.60E+00	0.00E+00	Up	3.69E+00	1.66E-93	Up	1.93E+00	1.94E-01		4.50E+00	4.66E-11	Up	-6.25E-01	6.93E-04		1.85E+00	2.24E-65	Up	Unigene27945_All//gi|295646225|gb|ADG23055.1|/1.00E-110//haloacid dehalogenase [Phaseolus vulgaris]	Unigene27945_All//4.00E-107//AT1G73010| phosphatase	Unigene27945_All//0.00E+00//TC135239				nr +
Unigene27946_All	1083	0.87	7.30	1.38	1.61	1.49	10.88	1.37	5.06	14.49	3.07E+00	1.06E-26	Up	6.63E-01	2.44E-01		-1.07E-01	8.26E-01		2.76E+00	7.19E-38	Up	1.89E+00	2.71E-13	Up	3.41E+00	2.44E-72	Up	Unigene27946_All//gi|257831443|gb|ACV71022.1|//2.00E-51//UPA23 [Capsicum annuum]	Unigene27946_All//4.00E-44//AT2G28690| unknown protein	Unigene27946_All//0.00E+00//DR452606				nr +
Unigene27947_All	928	10.88	5.02	7.46	16.21	14.17	15.96	16.04	11.26	7.17	-1.12E+00	2.20E-09	Down	-5.45E-01	3.70E-03		-1.94E-01	2.20E-01		-2.23E-02	9.10E-01		-5.10E-01	7.61E-05		-1.16E+00	5.75E-18	Down	Unigene27947_All//gi|15242004|ref|NP_201100.1|/2.00E-37//catalytic/ nucleotide binding [Arabidopsis thaliana] >gi|32815911|gb|AAP88340.1| At5g62950 [Arabidopsis thaliana]	Unigene27947_All//3.00E-35//AT5G62950| catalytic/ nucleotide binding	Unigene27947_All//0.00E+00//DN762437				nr -
Unigene2795_All	1709	10.72	8.92	8.88	13.79	31.72	23.52	22.39	17.39	28.81	-2.64E-01	4.87E-02		-2.71E-01	5.33E-02		1.20E+00	2.91E-62	Up	7.71E-01	2.06E-20		-3.65E-01	2.22E-06		3.64E-01	3.49E-08		Unigene2795_All//gi|15219142|ref|NP_173610.1|/1.00E-155//MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein /phosphatidylinositol-4-phosphate 5-kinase-related [Arabidopsis thaliana] >gi|6552740|gb|AAF16539.1|AC013482_13 T26F17.15 [Arabidopsis thaliana]	Unigene2795_All//6.00E-122//AT1G21920| MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein /phosphatidylinositol-4-phosphate 5-kinase-related	Unigene2795_All//0.00E+00//CO104549		ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene27950_All	1079	4.46	1.41	1.97	3.65	2.90	3.35	5.33	1.74	2.44	-1.66E+00	2.67E-08	Down	-1.18E+00	5.65E-05	Down	-3.29E-01	3.18E-01		-1.23E-01	7.06E-01		-1.61E+00	2.31E-11	Down	-1.13E+00	3.44E-07	Down	Unigene27950_All//gi|18405190|ref|NP_564674.1|/8.00E-38//zinc finger (Ran-binding) family protein [Arabidopsis thaliana]		Unigene27950_All//0.00E+00//TC160783				nr -
Unigene27951_All	1549	0.00	0.72	0.21	0.96	0.89	2.30	22.74	85.10	25.33	9.49E+00	2.00E-06	Up	7.69E+00	4.52E-02		-1.18E-01	8.23E-01		1.26E+00	1.51E-04	Up	1.90E+00	0.00E+00	Up	1.56E-01	4.89E-02		Unigene27951_All//gi|297827243|ref|XP_002876254.1|/1.00E-118//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325093|gb|EFH55513.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27951_All//1.00E-119//AT2G30140| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene27951_All//0.00E+00//gi|164256279|gb|ES793880.1|ES793880		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism		nr -
Unigene27952_All	806	0.78	1.95	3.04	0.62	1.79	2.69	10.75	32.51	14.33	1.32E+00	1.50E-02		1.96E+00	2.81E-05	Up	1.54E+00	7.24E-03		2.12E+00	1.42E-05	Up	1.60E+00	3.00E-48	Up	4.15E-01	4.48E-03		Unigene27952_All//gi|83630933|gb|ABC26915.1|/3.00E-52//WRKY53 [Glycine max]	Unigene27952_All//1.00E-41//AT5G13080| WRKY75; transcription factor	Unigene27952_All//0.00E+00//DW505739	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene27953_All	1241	0.55	1.47	6.57	18.18	1.86	1.78	2.21	0.54	0.13	1.42E+00	4.69E-03		3.58E+00	1.01E-30	Up	-3.29E+00	3.92E-104	Down	-3.35E+00	3.58E-90	Down	-2.04E+00	1.00E-07	Down	-4.11E+00	1.85E-15	Down	Unigene27953_All//gi|2274915|emb|CAA03908.1|/1.00E-128//beta-1,3-glucanase [Citrus sinensis]	Unigene27953_All//1.00E-101//AT3G57240| BG3 (BETA-1,3-GLUCANASE 3); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene27953_All//0.00E+00//gi|3326349|gb|AI055235.1|AI055235		ko00500|Starch and sucrose metabolism		nr +
Unigene27954_All	455	10.23	8.24	8.54	8.32	8.48	8.44	30.20	21.95	12.17	-3.13E-01	2.82E-01		-2.61E-01	3.96E-01		2.68E-02	9.59E-01		2.01E-02	9.48E-01		-4.60E-01	6.75E-04		-1.31E+00	5.71E-20	Down	Unigene27954_All//gi|30685150|ref|NP_188529.2|/6.00E-08//VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor [Arabidopsis thaliana] >gi|75153628|sp|Q8L3Y1.1|VRN1_ARATH RecName: Full=B3 domain-containing transcription factor VRN1; AltName: Full=Protein VERNALIZATION 1 >gi|21734794|gb|AAW76972.1|AF289051_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|21734796|gb|AAW76973.1|AF289052_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|89000959|gb|ABD59069.1| At3g18990 [Arabidopsis thaliana]	Unigene27954_All//4.00E-09//AT3G18990| VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor	Unigene27954_All//0.00E+00//gi|18098729|gb|BM357983.1|BM357983	ABI3VP1			nr +
Unigene27956_All	950	5.40	3.73	3.76	9.44	8.81	7.70	6.19	4.22	2.77	-5.32E-01	4.46E-02		-5.23E-01	6.06E-02		-9.97E-02	6.54E-01		-2.93E-01	1.56E-01		-5.51E-01	1.19E-02		-1.16E+00	1.28E-07	Down	Unigene27956_All//gi|18147590|dbj|BAB83083.1|/1.00E-119//cycloartenol synthase [Betula platyphylla]	Unigene27956_All//5.00E-107//AT2G07050| CAS1 (cycloartenol synthase 1); cycloartenol synthase	Unigene27956_All//2.00E-131//gi|164289622|gb|ES791464.1|ES791464		ko00100|Steroid biosynthesis		nr +
Unigene27959_All	815	7.58	9.76	5.88	6.66	5.58	7.48	1.50	8.05	7.53	3.66E-01	8.25E-02		-3.65E-01	1.51E-01		-2.57E-01	3.52E-01		1.67E-01	5.63E-01		2.42E+00	2.58E-21	Up	2.32E+00	1.77E-19	Up	Unigene27959_All//gi|188509972|gb|ACD56656.1|/4.00E-11//putative MYB transcription factor [Gossypioides kirkii]		Unigene27959_All//6.00E-08//CO094216				nr +
Unigene27961_All	828	3.73	0.61	1.93	11.31	6.90	11.45	6.13	3.48	3.70	-2.61E+00	2.67E-09	Down	-9.50E-01	1.07E-02		-7.12E-01	3.98E-05		1.83E-02	9.48E-01		-8.15E-01	5.83E-04		-7.26E-01	1.55E-03		Unigene27961_All//gi|92856607|gb|ABE27407.1|/1.00E-77//At3g50850 [Arabidopsis thaliana]	Unigene27961_All//3.00E-74//AT5G49560| unknown protein	Unigene27961_All//0.00E+00//TC131321				nr +
Unigene27964_All	1145	2.60	12.08	14.42	9.01	12.66	24.69	0.11	0.07	0.66	2.21E+00	2.16E-32	Up	2.47E+00	1.07E-42	Up	4.92E-01	4.31E-04		1.46E+00	1.04E-39	Up	-6.02E-01	7.66E-01		2.58E+00	2.45E-03		Unigene27964_All//gi|297799074|ref|XP_002867421.1|/3.00E-91//zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313257|gb|EFH43680.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27964_All//3.00E-87//AT2G19810| zinc finger (CCCH-type) family protein	Unigene27964_All//0.00E+00//gi|78332580|gb|DT552854.1|DT552854	C3H			nr -
Unigene27966_All	890	1.82	2.16	5.15	2.41	2.75	1.12	2.95	2.58	2.37	2.48E-01	6.22E-01		1.50E+00	1.38E-06	Up	1.91E-01	6.89E-01		-1.11E+00	1.19E-02		-1.90E-01	6.51E-01		-3.12E-01	3.78E-01		Unigene27966_All//gi|18378607|gb|AAL68641.1|AF458763.1|/3.00E-09//polyprotein [Oryza sativa Japonica Group]		Unigene27966_All//7.00E-48//ES807842				nr -
Unigene27967_All	1061	1.92	7.35	4.22	6.48	6.07	5.87	10.32	11.94	10.06	1.94E+00	9.95E-16	Up	1.13E+00	1.85E-04	Up	-9.43E-02	7.31E-01		-1.41E-01	6.14E-01		2.10E-01	1.76E-01		-3.65E-02	8.30E-01				Unigene27967_All//0.00E+00//TC159803				
Unigene27968_All	679	28.59	34.85	34.66	23.11	31.49	48.95	5.92	2.46	2.88	2.86E-01	1.31E-02		2.78E-01	2.16E-02		4.47E-01	6.42E-05		1.08E+00	1.32E-29	Up	-1.26E+00	6.39E-06	Down	-1.04E+00	9.61E-05	Down	Unigene27968_All//gi|4544453|gb|AAD22361.1|/3.00E-74//expressed protein [Arabidopsis thaliana] >gi|117168219|gb|ABK32192.1| At2g22370 [Arabidopsis thaliana]	Unigene27968_All//3.00E-75//AT2G22370| unknown protein	Unigene27968_All//0.00E+00//TC143209				nr -
Unigene27970_All	435	15.28	24.11	19.95	7.79	4.75	6.13	96.71	383.56	104.86	6.59E-01	1.84E-04		3.85E-01	6.59E-02		-7.13E-01	2.56E-02		-3.46E-01	3.45E-01		1.99E+00	0.00E+00	Up	1.17E-01	1.21E-01		Unigene27970_All//gi|283136112|gb|ADB11375.1|/5.00E-19//tau class glutathione transferase GSTU51 [Populus trichocarpa]	Unigene27970_All//3.00E-17//AT1G10360| ATGSTU18 (GLUTATHIONE S-TRANSFERASE TAU 18); glutathione transferase	Unigene27970_All//0.00E+00//gi|109876015|gb|DW504989.1|DW504989		ko00480|Glutathione metabolism		nr -
Unigene27973_All	996	1.16	2.80	1.44	9.30	15.94	9.79	7.26	1.80	3.20	1.28E+00	1.02E-03		3.21E-01	5.92E-01		7.77E-01	3.24E-09		7.43E-02	7.20E-01		-2.01E+00	8.84E-19	Down	-1.18E+00	2.05E-09	Down	Unigene27973_All//gi|5926718|dbj|BAA84640.1|/6.00E-89//PRA2 [Pisum sativum]	Unigene27973_All//2.00E-77//AT1G01200| ATRABA3 (ARABIDOPSIS RAB GTPASE HOMOLOG A3); GTP binding	Unigene27973_All//0.00E+00//gi|109883751|gb|DW512721.1|DW512721				nr +
Unigene27974_All	1759	0.51	0.12	0.45	2.92	0.69	0.82	74.61	51.73	30.28	-2.13E+00	1.06E-02		-1.55E-01	8.24E-01		-2.09E+00	2.83E-14	Down	-1.83E+00	1.45E-10	Down	-5.28E-01	1.44E-38		-1.30E+00	4.01E-181	Down	Unigene27974_All//gi|224069144|ref|XP_002326285.1|/0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222833478|gb|EEE71955.1| cytochrome P450 [Populus trichocarpa]	Unigene27974_All//1.00E-107//AT5G07990| TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	Unigene27974_All//0.00E+00//FL684464		ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene27975_All	851	2.34	6.85	4.57	11.00	12.91	12.74	10.38	6.68	4.68	1.55E+00	5.71E-09	Up	9.67E-01	2.91E-03		2.30E-01	2.23E-01		2.11E-01	2.85E-01		-6.37E-01	2.24E-04		-1.15E+00	7.38E-11	Down	Unigene27975_All//gi|192910858|gb|ACF06537.1|/8.00E-38//24 kDa seed maturation protein [Elaeis guineensis]	Unigene27975_All//4.00E-64//AT3G18260| reticulon family protein (RTNLB9)					nr -
Unigene27976_All	867	2.29	13.85	7.68	3.62	3.34	6.30	11.31	15.67	33.08	2.59E+00	6.95E-34	Up	1.74E+00	2.19E-11	Up	-1.18E-01	7.85E-01		8.00E-01	1.55E-03		4.70E-01	5.62E-04		1.55E+00	1.46E-51	Up	Unigene27976_All//gi|255553937|ref|XP_002518009.1|/2.00E-17//conserved hypothetical protein [Ricinus communis] >gi|223542991|gb|EEF44527.1| conserved hypothetical protein [Ricinus communis]		Unigene27976_All//7.00E-125//DN817448				nr +
Unigene27977_All	1728	0.15	0.12	0.37	0.92	0.22	0.73	14.51	30.28	40.60	-3.68E-01	7.78E-01		1.29E+00	1.86E-01		-2.07E+00	9.66E-05	Down	-3.34E-01	5.63E-01		1.06E+00	3.07E-51	Up	1.48E+00	1.69E-117	Up	Unigene27977_All//gi|13161397|dbj|BAB33033.1|/1.00E-166//CPRD2 [Vigna unguiculata]	Unigene27977_All//1.00E-129//AT5G44400| FAD-binding domain-containing protein	Unigene27977_All//0.00E+00//TC170571		ko00620|Pyruvate metabolism//ko00908|Zeatin biosynthesis		nr +
Unigene27978_All	976	1.23	2.54	0.93	7.86	7.76	4.91	21.62	555.76	133.64	1.04E+00	1.03E-02		-4.11E-01	5.25E-01		-1.81E-02	9.45E-01		-6.80E-01	9.69E-04		4.68E+00	0.00E+00	Up	2.63E+00	0.00E+00	Up	Unigene27978_All//gi|297242517|gb|AD124922.1|/1.00E-109//pirin [Carica papaya]	Unigene27978_All//9.00E-82//AT1G50590| pirin, putative	Unigene27978_All//0.00E+00//TC130127				nr +
Unigene27979_All	879	8.21	5.25	3.88	9.63	7.44	4.01	0.87	0.43	0.82	-6.47E-01	2.88E-03		-1.08E+00	2.61E-06	Down	-3.72E-01	5.95E-02		-1.27E+00	3.53E-10	Down	-1.02E+00	1.69E-01		-8.58E-02	9.09E-01		Unigene27979_All//gi|256002927|gb|ACU52707.1|/1.00E-48//bHLH transcription factor PTF1 [Glycine max]	Unigene27979_All//7.00E-43//AT3G57800| basic helix-loop-helix (bHLH) family protein	Unigene27979_All//0.00E+00//gi|78344226|gb|DT564500.1|DT564500	bHLH			nr -

Unigene27980_All	987	12.19	4.06	5.56	3.48	2.65	0.41	0.17	0.08	0.00	-1.59E+00	1.98E-18	Down	-1.13E+00	8.71E-11	Down	-3.93E-01	2.52E-01		-3.08E+00	5.62E-13	Down	-1.02E+00	6.14E-01		-7.42E+00	1.08E-01		Unigene27980_All//gi|224101833|ref|XP_002334238.1|//3.00E-64//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|148372081|gb|ABQ62972.1| TINY-like protein [Populus trichocarpa] >gi|222870106|gb|EEF07237.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene27980_All//7.00E-47//AT2G44940| AP2 domain-containing transcription factor TINY, putative	Unigene27980_All//0.00E+00//TC145309	AP2-EREBP			nr +
Unigene27981_All	1124	2.79	0.23	0.28	1.60	4.56	0.88	6.88	5.61	6.63	-3.63E+00	9.98E-13	Down	-3.30E+00	3.58E-11	Down	1.52E+00	1.22E-08	Up	-8.52E-01	8.34E-02		-2.94E-01	1.38E-01		-5.46E-02	7.83E-01		Unigene27981_All//gi|157932074|gb|ABW05088.1|//6.00E-43//ovate-like protein [Nicotiana tabacum]	Unigene27981_All//6.00E-16//AT2G18500| OFP7 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 7)					nr -
Unigene27984_All	1405	0.22	0.29	0.00	0.64	0.49	0.13	116.01	44.80	17.41	3.69E-01	7.24E-01		-7.80E+00	4.91E-02		-3.81E-01	6.05E-01		-2.31E+00	5.79E-03		-1.37E+00	2.01E-237	Down	-2.74E+00	0.00E+00	Down	Unigene27984_All//gi|297829824|ref|XP_002882794.1|//1.00E-136//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328634|gb|EFH59053.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene27984_All//2.00E-137//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene27984_All//1.00E-96//TC134433		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene27985_All	830	3.53	12.39	5.33	24.79	4.85	18.56	82.83	245.03	90.33	1.81E+00	7.87E-19	Up	5.93E-01	4.90E-02		-2.35E+00	1.71E-65	Down	-4.18E-01	4.59E-04		1.56E+00	0.00E+00	Up	1.25E-01	2.54E-02		Unigene27985_All//gi|62241063|dbj|BAD93688.1|//3.00E-69//glucosyltransferase [Nicotiana tabacum]	Unigene27985_All//7.00E-69//AT2G36780| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene27985_All//0.00E+00//TC152589		ko00908|Zeatin biosynthesis		nr -
Unigene27986_All	1185	0.40	0.56	0.40	2.69	3.66	3.58	2.00	1.38	0.74	4.84E-01	5.90E-01		2.52E-02	1.00E+00		4.45E-01	1.41E-01		4.13E-01	1.92E-01		-5.39E-01	1.53E-01		-1.43E+00	1.25E-04	Down	Unigene27986_All//gi|255561064|ref|XP_002521544.1|//2.00E-39//conserved hypothetical protein [Ricinus communis] >gi|223539222|gb|EEF40815.1| conserved hypothetical protein [Ricinus communis]	Unigene27986_All//1.00E-19//AT5G66440| unknown protein	Unigene27986_All//0.00E+00//gi|164242073|gb|ES836689.1|ES836689				nr +
Unigene27989_All	753	13.48	10.43	13.93	20.57	20.26	17.51	21.39	12.10	7.72	-3.70E-01	4.35E-02		4.75E-02	8.07E-01		-2.23E-02	8.94E-01		-2.32E-01	1.33E-01		-8.22E-01	5.94E-11		-1.47E+00	1.68E-27	Down	Unigene27989_All//gi|297812923|ref|XP_002874345.1|//3.00E-46//ribosomal protein L18 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320182|gb|EFH50604.1| ribosomal protein L18 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene27989_All//8.00E-34//AT5G27820| ribosomal protein L18 family protein	Unigene27989_All//0.00E+00//TC151815		ko03010|Ribosome		nr -
Unigene27997_All	1133	6.05	2.19	3.15	0.92	1.09	1.20	33.77	31.28	47.19	-1.47E+00	1.08E-09	Down	-9.42E-01	6.01E-05		2.45E-01	7.39E-01		3.73E-01	5.63E-01		-1.11E-01	2.17E-01		4.83E-01	3.12E-14		Unigene27997_All//gi|42567704|ref|NP_196298.2|//6.00E-51//myb family transcription factor [Arabidopsis thaliana]	Unigene27997_All//3.00E-52//AT5G06800| myb family transcription factor		G2-like			nr +
Unigene27998_All	791	1.79	4.48	2.56	16.18	15.37	27.69	16.20	9.35	24.63	1.33E+00	9.56E-05	Up	5.19E-01	2.78E-01		-7.48E-02	7.02E-01		7.75E-01	1.71E-11		-7.92E-01	2.22E-08		6.05E-01	3.31E-08		Unigene27998_All//gi|10444366|gb|AAG17877.1|AF293404_1|/4.00E-10//suspensor-specific protein [Phaseolus coccineus] >gi|13173147|gb|AAK14318.1|AF32518 7_2 suspensor-specific protein [Phaseolus coccineus]	Unigene27998_All//7.00E-05//AT1G49310| unknown protein	Unigene27998_All//0.00E+00//gi|109870649|gb|DW499625.1|DW499625				nr -
Unigene2800_All	2111	2.43	2.02	0.88	4.77	4.93	2.97	5.67	3.35	2.15	-2.69E-01	3.41E-01		-1.46E+00	4.96E-07	Down	4.75E-02	8.26E-01		-6.81E-01	1.11E-04		-7.60E-01	2.14E-07		-1.40E+00	3.29E-19	Down	Unigene2800_All//gi|15240531|ref|NP_200365.1|//0.00E+00//TRN1 (TORNADO 1) [Arabidopsis thaliana]	Unigene2800_All//0.00E+00//AT5G55540| TRN1 (TORNADO 1)	Unigene2800_All//0.00E+00//C0082135			GO:0005635//GO:0006913//GO:0009887//GO:0010051//GO:0016049//GO:0022892//GO:0048507//GO:0060918	nr +
Unigene28001_All	1647	1.59	13.87	9.25	6.41	15.91	13.74	0.00	0.00	0.77	3.13E+00	1.13E-77	Up	2.54E+00	9.53E-41	Up	1.31E+00	1.67E-34	Up	1.10E+00	8.32E-21	Up	null	null		9.60E+00	3.29E-09	Up	Unigene28001_All//gi|32480324|emb|CAE02456.1|//4.00E-06//OSJNBa0042D13.9 [Oryza sativa (japonica cultivar-group)]		Unigene28001_All//0.00E+00//TC168547				nr -
Unigene28004_All	714	3.00	1.85	3.88	16.88	5.88	3.42	8.17	20.96	23.94	-7.03E-01	1.09E-01		3.68E-01	3.75E-01		-1.52E+00	3.26E-21	Down	-2.31E+00	1.91E-32	Down	1.36E+00	4.19E-22	Up	1.55E+00	3.92E-31	Up	Unigene28004_All//gi|224129002|ref|XP_002320476.1|//1.00E-06//predicted protein [Populus trichocarpa] >gi|118484421|gb|ABK94087.1| unknown [Populus trichocarpa] >gi|222861249|gb|EEE98791.1| predicted protein [Populus trichocarpa]		Unigene28004_All//0.00E+00//TC160268				nr -
Unigene28005_All	415	59.38	44.93	41.70	160.37	117.33	143.11	287.20	193.87	108.48	-4.02E-01	2.51E-04		-5.10E-01	6.61E-06		-4.51E-01	1.01E-14		-1.64E-01	1.45E-02		-5.67E-01	9.25E-40		-1.40E+00	4.55E-185	Down	Unigene28005_All//gi|56744207|dbj|BAD81043.1|//1.00E-75//calnexin [Glycine max]	Unigene28005_All//6.00E-64//AT5G61790| calnexin 1 (CNX1)	Unigene28005_All//0.00E+00//gi|21089362|gb|BQ401675.1|BQ401675		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr +
Unigene28006_All	746	12.69	11.00	19.42	71.98	37.57	30.94	8.73	4.59	3.31	-2.06E-01	3.09E-01		6.13E-01	5.53E-05		-9.38E-01	4.00E-43		-1.22E+00	4.79E-58	Down	-9.26E-01	8.02E-06		-1.40E+00	7.36E-11	Down	Unigene28006_All//gi|115467978|ref|NP_001057588.1|//1.00E-51//Os06g0352200 [Oryza sativa Japonica Group] >gi|113595628|dbj|BAF19502.1| Os06g0352200 [Oryza sativa Japonica Group]	Unigene28006_All//2.00E-73//AT4G18425| unknown protein	Unigene28006_All//7.00E-63//TC143181				nr +
Unigene28007_All	1350	0.74	2.40	1.34	2.47	2.75	6.19	11.93	14.49	11.72	1.71E+00	5.49E-06	Up	8.65E-01	8.81E-02		1.56E-01	6.78E-01		1.32E+00	1.44E-10	Up	2.80E-01	1.47E-02		-2.65E-02	8.54E-01		Unigene28007_All//gi|224119358|ref|XP_002318052.1|//1.00E-112//f-box family protein [Populus trichocarpa] >gi|222858725|gb|EEE96272.1| f-box family protein [Populus trichocarpa]	Unigene28007_All//1.00E-50//AT5G62940| Dof-type zinc finger domain-containing protein	Unigene28007_All//3.00E-20//TC170824	C2C2-Dof			nr -
Unigene28008_All	715	1.46	1.35	1.19	2.86	3.47	5.56	2.37	3.39	0.84	-1.20E-01	8.43E-01		-2.97E-01	6.42E-01		2.80E-01	5.65E-01		9.61E-01	1.69E-03		5.19E-01	1.64E-01		-1.50E+00	9.77E-04	Down	Unigene28008_All//gi|115460218|ref|NP_001053709.1|//4.00E-35//Os04g0590900 [Oryza sativa Japonica Group] >gi|38346723|emb|CAE04873.2| OSJNBa0086006.21 [Oryza sativa (japonica cultivar-group)] >gi|113565280|dbj|BAF15623.1| Os04g0590900 [Oryza sativa Japonica Group] >gi|116311028|emb|CAH67959.1| OSIGBa0142102-OSIGBa0101B20.2 [Oryza sativa (indica cultivar-group)]	Unigene28008_All//6.00E-33//AT1G72220| zinc finger (C3HC4-type RING finger) family protein	Unigene28008_All//0.00E+00//TC167855				nr +
Unigene28009_All	1264	0.00	0.00	0.08	113.50	81.92	72.53	5.22	5.26	1.80	null	null		6.40E+00	3.99E-01		-4.70E-01	8.19E-34		-6.46E-01	4.83E-53		1.09E-02	9.96E-01		-1.54E+00	1.56E-12	Down	Unigene28009_All//gi|15235279|ref|NP_194567.1|//1.00E-140//leucine-rich repeat family protein [Arabidopsis thaliana] >gi|2842481|emb|CAA16878.1| extensin-like protein [Arabidopsis thaliana] >gi|7269692|emb|CAB79640.1| extensin-like protein [Arabidopsis thaliana]	Unigene28009_All//5.00E-128//AT4G28380| leucine-rich repeat family protein	Unigene28009_All//0.00E+00//TC176772		ko04626|Plant-pathogen interaction		nr -
Unigene28011_All	1020	11.75	3.13	5.27	4.59	3.21	4.96	3.32	0.00	0.70	-1.91E+00	1.63E-23	Down	-1.16E+00	4.69E-11	Down	-5.17E-01	5.66E-02		1.11E-01	7.03E-01		-1.17E+01	6.37E-24	Down	-2.24E+00	8.64E-11	Down	Unigene28011_All//gi|14625943|emb|CAC44011.1|//1.00E-18//snakin2 [Solanum tuberosum] >gi|194475635|gb|ACF74550.1| snakin-2 [Solanum tuberosum] >gi|194475637|gb|ACF74551.1| snakin-2 [Solanum tuberosum] >gi|194475639|gb|ACF74552.1| snakin-2 [Solanum tuberosum]	Unigene28011_All//7.00E-16//AT1G22690| gibberellin-responsive protein, putative	Unigene28011_All//0.00E+00//TC172315				nr +
Unigene28012_All	998	3.77	0.66	1.12	1.00	0.62	2.04	1.36	0.00	0.24	-2.52E+00	8.53E-11	Down	-1.75E+00	9.90E-07	Down	-6.85E-01	3.11E-01		1.03E+00	2.56E-02		-1.04E+01	1.30E-09	Down	-2.50E+00	2.46E-05	Down	Unigene28012_All//gi|75249332|sp|Q93X17.1|SNAK2_SOLTU//1.00E-20//RecName: Full=Snakin-2; Flags: Precursor >gi|14625945|emb|CAC44012.1| snakin2 [Solanum tuberosum]	Unigene28012_All//9.00E-19//AT1G22690| gibberellin-responsive protein, putative	Unigene28012_All//0.00E+00//TC172315				nr +
Unigene28013_All	780	2.62	4.48	3.07	2.30	3.58	3.71	2.55	3.27	18.54	7.77E-01	1.86E-02		2.32E-01	6.18E-01		6.37E-01	9.33E-02		6.89E-01	6.79E-02		3.60E-01	3.48E-01		2.86E+00	1.53E-56	Up	Unigene28013_All//gi|157782958|gb|ABV72393.1|//2.00E-63//coronatine-insensitive 1 [Hevea brasiliensis]	Unigene28013_All//2.00E-48//AT2G39940| COI1 (CORONATINE INSENSITIVE 1); protein binding / ubiquitin-protein ligase	Unigene28013_All//3.00E-136//ES843332		ko04626|Plant-pathogen interaction		nr +
Unigene28015_All	806	10.97	9.87	9.25	8.53	7.73	4.15	1.94	4.51	3.86	-1.53E-01	4.70E-01		-2.46E-01	2.49E-01		-1.41E-01	5.83E-01		-1.04E+00	2.63E-06	Down	1.22E+00	3.71E-05	Up	9.90E-01	1.33E-03		Unigene28015_All//gi|98960857|gb|ABF58912.1|//4.00E-07//At1g75190 [Arabidopsis thaliana] >gi|222424457|dbj|BAH20184.1| AT1G75190 [Arabidopsis thaliana]						nr +
Unigene28016_All	857	30.65	9.70	18.52	57.49	49.70	55.91	29.01	13.41	16.04	-1.66E+00	5.89E-42	Down	-7.27E-01	3.79E-11		-2.10E-01	4.53E-03		-4.00E-02	6.88E-01		-1.11E+00	1.02E-26	Down	-8.55E-01	4.49E-18		Unigene28016_All//gi|154511684|gb|AAK96853.1|//2.00E-54//Unknown protein [Arabidopsis thaliana]	Unigene28016_All//1.00E-55//AT5G39600| unknown protein	Unigene28016_All//0.00E+00//TC150276				nr -
Unigene28017_All	669	282.41	157.16	202.02	52.87	64.75	35.71	6.32	1.94	2.98	-8.46E-01	1.10E-102		-4.83E-01	3.99E-37		2.93E-01	1.39E-04		-5.66E-01	8.73E-11		-1.71E+00	3.29E-09	Down	-1.09E+00	3.10E-05	Down	Unigene28017_All//gi|226528954|ref|NP_001150884.1|//3.00E-22//plastid-specific ribosomal protein 6 [Zea mays] >gi|195642604|gb|ACG40770.1| plastid-specific ribosomal protein 6 precursor [Zea mays]	Unigene28017_All//1.00E-16//AT5G17870| PSRP6 (PLASTID-SPECIFIC 50S RIBOSOMAL PROTEIN 6)	Unigene28017_All//0.00E+00//TC157407				nr +
Unigene28019_All	1251	0.50	1.05	0.34	1.00	2.95	1.44	7.27	4.51	14.49	1.07E+00	7.10E-02		-5.60E-01	5.54E-01		1.56E+00	1.35E-06	Up	5.37E-01	3.05E-01		-6.88E-01	5.12E-05		9.96E-01	5.86E-17		Unigene28019_All//gi|224127272|ref|XP_002320031.1|//3.00E-86//f-box family protein [Populus trichocarpa] >gi|222860804|gb|EEE98346.1| f-box family protein [Populus trichocarpa]	Unigene28019_All//1.00E-86//AT5G43190| F-box family protein (FBX6)	Unigene28019_All//5.00E-34//gi|54121977|gb|CO497486.1|CO497486				nr -
Unigene2802_All	1679	5.39	2.81	4.22	38.12	24.59	14.93	10.10	5.63	7.14	-9.42E-01	1.23E-06		-3.54E-01	8.51E-02		-6.33E-01	5.86E-26		-1.35E+00	2.66E-81	Down	-8.44E-01	5.67E-12		-5.00E-01	2.00E-05		Unigene2802_All//gi|111074178|gb|ABH04462.1|//2.00E-78//At5g22090 [Arabidopsis thaliana]	Unigene2802_All//5.00E-57//AT5G22090| unknown protein	Unigene2802_All//0.00E+00//DW239830				nr -
Unigene28024_All	563	6.51	7.47	5.49	13.36	12.29	18.93	7.06	2.97	7.78	2.00E-01	5.29E-01		-2.46E-01	4.82E-01		-1.20E-01	6.13E-01		5.03E-01	3.84E-03		-1.25E+00	8.98E-06	Down	1.41E-01	6.10E-01				Unigene28024_All//0.00E+00//gi|78348526|gb|DT568800.1|DT568800				
Unigene28025_All	1411	0.00	0.07	0.53	0.00	0.05	3.97	13.90	12.12	312.10	6.17E+00	3.87E-01		9.05E+00	3.27E-04	Up	5.61E+00	6.10E-01		1.20E+01	6.54E-34	Up	-1.99E-01	9.80E-02		4.49E+00	0.00E+00	Up	Unigene28025_All//gi|268638403|gb|ACJ17543.1|//1.00E-137//oxidoreductase [Capsicum annuum]	Unigene28025_All//5.00E-130//AT5G05600| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene28025_All//0.00E+00//CO120621		ko00941|Flavonoid biosynthesis		nr +
Unigene28028_All	825	2.85	2.09	2.32	3.02	3.63	1.97	1.03	2.13	3.72	-4.51E-01	2.83E-01		-2.97E-01	5.08E-01		2.67E-01	5.31E-01		-6.15E-01	1.34E-01		1.05E+00	1.79E-02		1.86E+00	7.74E-08	Up	Unigene28028_All//gi|224061867|ref|XP_002300638.1|//2.00E-32//bromodomain protein [Populus trichocarpa] >gi|222842364|gb|EEE79911.1| bromodomain protein [Populus trichocarpa]	Unigene28028_All//2.00E-13//AT1G20670| DNA-binding bromodomain-containing protein	Unigene28028_All//2.00E-134//DN803555				nr +

Unigene28029_All	446	2.11	7.50	5.25	6.81	9.19	5.06	4.55	2.81	3.13	1.83E+00	1.10E-06	Up	1.31E+00	3.27E-03		4.31E-01	1.66E-01		-4.28E-01	2.59E-01		-6.95E-01	8.83E-02		-5.42E-01	1.68E-01		Unigene28029_All//gi|297843040|ref|XP_002889401.1|//2.00E-16//cytochrome c oxidase assembly protein CtaG [Arabidopsis lyrata subsp. lyrata] >gi|297335243|gb|EFH65660.1| cytochrome c oxidase assembly protein CtaG [Arabidopsis lyrata subsp. lyrata]	Unigene28029_All//4.00E-17//AT1G02410| cytochrome c oxidase assembly protein CtaG / Cox11 family	Unigene28029_All//9.00E-126//gi|164277025|gb|ES796109.1|ES796109		ko00190|Oxidative phosphorylation		nr +
Unigene28031_All	706	2.82	5.17	1.89	3.39	2.83	1.34	5.15	4.74	1.69	8.76E-01	6.72E-03		-5.79E-01	2.40E-01		-2.60E-01	5.56E-01		-1.33E+00	1.38E-03		-1.21E-01	7.02E-01		-1.61E+00	1.06E-07	Down	Unigene28031_All//gi|224069756|ref|XP_002326406.1|//5.00E-65//f-box family protein [Populus trichocarpa] >gi|222833599|gb|EEE72076.1| f-box family protein [Populus trichocarpa]	Unigene28031_All//5.00E-57//AT3G53000| AtFP2-A15 (Phloem protein 2-A15); carbohydrate binding	Unigene28031_All//1.00E-116//TC168451				nr -
Unigene28032_All	1004	2.14	2.93	7.69	5.71	6.69	2.11	4.00	2.12	1.19	4.54E-01	2.21E-01		1.85E+00	3.68E-14	Up	2.29E-01	3.73E-01		-1.43E+00	1.94E-08	Down	-9.14E-01	7.76E-04		-1.75E+00	2.15E-09	Down	Unigene28032_All//gi|224120698|ref|XP_002318395.1|//1.00E-19//predicted protein [Populus trichocarpa] >gi|222859068|gb|EEE96615.1| predicted protein [Populus trichocarpa]	Unigene28032_All//2.00E-08//AT1G37113| unknown protein	Unigene28032_All//0.00E+00//TC148324				nr -
Unigene28033_All	720	34.81	144.34	35.72	24.49	22.67	36.38	63.24	290.65	134.79	2.05E+00	7.79E-218	Up	3.74E-02	7.61E-01		-1.12E-01	4.84E-01		5.71E-01	3.23E-08		2.20E+00	0.00E+00	Up	1.09E+00	6.41E-101	Up	Unigene28033_All//gi|5702231|gb|AAD47213.1|AF145386_1//2.00E-48//hypersensitive reaction associated Ca2+-binding protein [Phaseolus vulgaris]	Unigene28033_All//3.00E-42//AT5G49480| ATCP1 (Ca2+-binding protein 1); calcium ion binding	Unigene28033_All//0.00E+00//gi|73863826|gb|DT466565.1|DT466565		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene28034_All	837	4.44	1.15	1.02	11.13	24.52	17.43	9.19	9.64	22.89	-1.95E+00	5.58E-08	Down	-2.12E+00	2.22E-08	Down	1.14E+00	7.78E-22	Up	6.47E-01	6.31E-06		6.80E-02	7.40E-01		1.32E+00	2.04E-27	Up	Unigene28034_All//gi|11596186|gb|AAG38521.1|AF283536_1/8.00E-12//cystatin-like protein [Citrus x paradisi]	Unigene28034_All//2.00E-08//AT5G47550| cysteine protease inhibitor, putative / cystatin, putative	Unigene28034_All//1.00E-169//ES805154				nr -
Unigene28035_All	705	4.75	21.27	12.09	9.11	6.64	16.72	12.05	20.16	23.39	2.16E+00	4.28E-34	Up	1.35E+00	4.46E-10	Up	-4.56E-01	4.39E-02		8.75E-01	7.94E-08		7.42E-01	2.71E-08		9.57E-01	1.43E-14		Unigene28035_All//gi|18416509|ref|NP_568246.1|//1.00E-61//HY5 (ELONGATED HYPOCOTYL 5); DNA binding / double-stranded DNA binding / transcription factor [Arabidopsis thaliana] >gi|20138463|sp|Q24646.1|HY5_ARATH RecName: Full=Transcription factor HY5; AltName: Full=Protein LONG HYPOCOTYL 5; AltName: Full=bZIP transcription factor 56; Short=AtbZIP56 >gi|2244709|dbj|BAA21116.1| HY5 [Arabidopsis thaliana] >gi|2251085|dbj|BAA21327.1| HY5 [Arabidopsis thaliana] >gi|8953388|emb|CAB96661.1| HY5 [Arabidopsis thaliana] >gi|98960907|gb|ABF58937.1| At5g11260 [Arabidopsis thaliana] >gi|110738599|dbj|BAF01225.1| bZip transcription factor HY5 / AtbZip56 [Arabidopsis thaliana]	Unigene28035_All//6.00E-44//AT5G11260| HY5 (ELONGATED HYPOCOTYL 5); DNA binding / double-stranded DNA binding / transcription factor		bZIP			nr -
Unigene28036_All	935	1.57	1.73	1.42	3.04	2.03	7.25	12.25	6.57	7.24	1.46E-01	7.64E-01		-1.38E-01	7.97E-01		-5.84E-01	1.08E-01		1.25E+00	4.84E-08	Up	-8.99E-01	3.28E-09		-7.59E-01	2.42E-07		Unigene28036_All//gi|115461238|ref|NP_001054219.1|//8.00E-41//Os04g0671300 [Oryza sativa Japonica Group] >gi|90265249|emb|CAH67702.1| H0624F09.10 [Oryza sativa (indica cultivar-group)] >gi|113565790|dbj|BAF16133.1| Os04g0671300 [Oryza sativa Japonica Group]	Unigene28036_All//7.00E-39//AT1G65840| ATPAO4 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 4); amine oxidase/ polyamine oxidase	Unigene28036_All//0.00E+00//gi|78347122|gb|DT567396.1|DT567396				nr +
Unigene28037_All	798	1.18	2.35	0.67	5.49	7.59	4.75	6.52	3.61	2.55	9.93E-01	3.79E-02		-8.23E-01	2.71E-01		4.67E-01	5.23E-02		-2.09E-01	5.31E-01		-8.51E-01	2.78E-04		-1.36E+00	1.75E-08	Down	Unigene28037_All//gi|15209175|gb|AAK91893.1|AC091627_6/3.00E-14//Hsp20/alpha crystallin family protein [Solanum demissum]	Unigene28037_All//1.00E-16//AT1G54400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to heat; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: HSP20-like chaperone (InterPro:IPR008978); BEST Arabidopsis thaliana protein match is: heat shock family protein (TAIR:AT2G27140.1); Has 35 Blast hits to 35 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene28037_All//0.00E+00//TC144559				nr -
Unigene28038_All	733	35.62	29.38	29.57	134.08	283.89	254.53	1.15	1.03	0.98	-2.78E-01	1.07E-02		-2.69E-01	1.88E-02		1.08E+00	1.81E-202	Up	9.25E-01	1.30E-126		-1.69E-01	7.99E-01		-2.38E-01	7.02E-01		Unigene28038_All//gi|225698189|gb|ACO07292.1|//5.00E-34//expansin 10 [Cucumis sativus]	Unigene28038_All//7.00E-33//AT2G39700| ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	Unigene28038_All//7.00E-140//gi|78347821|gb|DT568095.1|DT568095				nr +
Unigene28039_All	593	23.73	44.35	31.97	44.86	61.38	47.30	115.79	167.46	409.20	9.02E-01	1.65E-16		4.30E-01	1.14E-03		4.52E-01	3.72E-08		7.63E-02	5.63E-01		5.32E-01	9.46E-30		1.82E+00	0.00E+00	Up	Unigene28039_All//gi|224551852|gb|ACN54324.1|//1.00E-108//NADPH:cytochrome P450 reductase [Gossypium hirsutum]	Unigene28039_All//3.00E-70//AT4G30210| ATR2 (ARABIDOPSIS P450 REDUCTASE 2); NADPH-hemoprotein reductase	Unigene28039_All//0.00E+00//gi|109825437|gb|DW224170.1|DW224170				nr +
Unigene2804_All	1902	14.55	5.73	10.30	14.35	18.59	11.83	1.98	1.82	2.20	-1.35E+00	1.66E-32	Down	-4.98E-01	2.66E-06		3.74E-01	9.74E-06		-2.79E-01	8.12E-03		-1.17E-01	7.06E-01		1.53E-01	6.15E-01		Unigene2804_All//gi|116248050|gb|ABJ90340.1|//0.00E+00//steroid 22-alpha-hydroxylase [Gossypium hirsutum]	Unigene2804_All//0.00E+00//AT3G5606 0| DWF4 (DWARF 4); steroid 22-alpha hydroxylase	Unigene2804_All//0.00E+00//TC137611		ko00905|Brassinosteroid biosynthesis	GO:0000902//GO:0005506//GO:0008395//GO:0009725//GO:0009965//GO:0016129//GO:0016709//GO:0023033//GO:0031410//GO:0043231	nr -
Unigene28043_All	935	1.06	1.90	3.13	2.82	3.35	1.50	2.03	1.16	1.24	8.35E-01	8.91E-02		1.56E+00	1.08E-04	Up	2.47E-01	5.62E-01		-9.15E-01	1.82E-02		-8.08E-01	5.51E-02		-7.20E-01	7.44E-02		Unigene28043_All//gi|116310937|emb|CAH67874.1|//2.00E-19//OS1GRa0153E02-OS1GRa0093I20.3 [Oryza sativa (indica cultivar-group)]	Unigene28043_All//3.00E-12//AT4G23160| protein kinase family protein	Unigene28043_All//0.00E+00//CO070620				nr +
Unigene28045_All	836	4.38	0.85	1.53	10.43	7.08	4.27	5.16	3.80	2.76	-2.37E+00	7.54E-10	Down	-1.52E+00	1.73E-05	Down	-5.58E-01	2.40E-03		-1.29E+00	9.54E-11	Down	-4.41E-01	9.99E-02		-9.00E-01	3.83E-04		Unigene28045_All//gi|27261142|gb|AAN87547.1|AF118784_1//2.00E-97//ribonucleotide reductase large subunit A [Glycine max]	Unigene28045_All//2.00E-80//AT2G21790| RNR1 (RIBONUCLEOTIDE REDUCTASE 1); ATP binding / protein binding / ribonucleoside-diphosphate reductase	Unigene28045_All//2.00E-180//TC156270		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism		nr +
Unigene28046_All	1317	1.35	6.00	3.32	0.08	0.24	0.31	15.28	14.19	4.72	2.15E+00	3.71E-18	Up	1.30E+00	3.23E-05	Up	1.64E+00	3.21E-01		2.03E+00	1.49E-01		-1.07E-01	4.00E-01		-1.70E+00	7.58E-42	Down	Unigene28046_All//gi|10764852|gb|AAG22832.1|AC007508_5/2.00E-93//F1K23.9 [Arabidopsis thaliana]	Unigene28046_All//5.00E-95//AT1G28710| unknown protein	Unigene28046_All//2.00E-126//DN818236				nr -
Unigene28047_All	998	9.49	5.18	7.95	10.23	8.01	3.80	1.61	0.46	0.28	-8.74E-01	3.49E-06		-2.55E-01	2.23E-01		-3.54E-01	4.53E-02		-1.43E+00	1.61E-14	Down	-1.81E+00	3.20E-04	Down	-2.53E+00	2.96E-06	Down	Unigene28047_All//gi|115480315|ref|NP_001063751.1|//1.00E-82//Os09g0530800 [Oryza sativa Japonica Group] >gi|113631984|dbj|BAF25665.1| Os09g0530800 [Oryza sativa Japonica Group]	Unigene28047_All//2.00E-79//AT5G11940| subtilase family protein					nr +
Unigene28048_All	1516	0.07	0.00	0.21	5.29	2.66	3.25	16.06	18.28	4.41	-6.11E+00	3.72E-01		1.61E+00	3.05E-01		-9.93E-01	1.75E-07		-7.04E-01	4.50E-04		1.86E-01	5.91E-02		-1.86E+00	1.91E-57	Down	Unigene28048_All//gi|87240777|gb|ABD32635.1|//1.00E-136//Leucine-rich repeat, plant specific [Medicago truncatula]	Unigene28048_All//3.00E-133//AT4G06744| leucine-rich repeat family protein / extensin family protein			ko04626|Plant-pathogen interaction		nr -
Unigene28049_All	731	0.79	0.90	0.44	30.87	30.05	23.97	21.98	3.09	5.61	1.95E-01	8.07E-01		-8.49E-01	3.97E-01		-3.86E-02	8.17E-01		-3.65E-01	1.43E-03		-2.83E+00	4.48E-61	Down	-1.97E+00	4.60E-41	Down	Unigene28049_All//gi|124502497|gb|ABN13629.1|//1.00E-90//blue copper-like protein [Gossypium hirsutum]	Unigene28049_All//2.00E-28//AT1G22480| plastocyanin-like domain-containing protein	Unigene28049_All//0.00E+00//gi|109880317|gb|DW509287.1|DW509287				nr +
Unigene28050_All	659	20.80	14.76	17.37	20.79	17.82	23.99	89.12	43.06	36.27	-4.95E-01	1.11E-03		-2.60E-01	1.22E-01		-2.22E-01	1.65E-01		2.07E-01	1.89E-01		-1.05E+00	2.03E-56	Down	-1.30E+00	4.39E-81	Down	Unigene28050_All//gi|115469972|ref|NP_001058585.1|//4.00E-68//Os06g0715500 [Oryza sativa Japonica Group] >gi|113596625|dbj|BAF20499.1| Os06g0715500 [Oryza sativa Japonica Group]	Unigene28050_All//3.00E-57//AT2G21160| translocon-associated protein alpha (TRAP alpha) family protein	Unigene28050_All//0.00E+00//TC160225		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene28051_All	715	13.46	12.26	10.43	21.74	21.00	14.53	38.79	29.75	16.16	-1.35E-01	5.09E-01		-3.69E-01	6.26E-02		-4.99E-02	8.02E-01		-5.81E-01	2.42E-05		-3.83E-01	3.13E-05		-1.26E+00	3.00E-37	Down	Unigene28051_All//gi|4098246|gb|AAD00253.1|//1.00E-25//homeobox 2 protein [Solanum lycopersicum]	Unigene28051_All//2.00E-22//AT1G62990| KNAT7 (KNOTTED-LIKE HOMEOBOX OF ARABIDOPSIS THALIANA 7); DNA binding / transcription activator/ transcription factor	Unigene28051_All//0.00E+00//TC170386	HB			nr -
Unigene28053_All	878	1.19	2.19	2.06	3.18	2.75	5.20	6.40	11.85	2.27	8.80E-01	6.09E-02		7.91E-01	1.21E-01		-2.11E-01	6.08E-01		7.10E-01	1.22E-02		8.88E-01	2.85E-08		-1.50E+00	2.01E-10	Down	Unigene28053_All//gi|111074162|gb|ABH04454.1|//4.00E-21//At3g52480 [Arabidopsis thaliana]	Unigene28053_All//6.00E-18//AT3G52480| unknown protein	Unigene28053_All//0.00E+00//TC135637				nr +
Unigene28054_All	1040	201.79	151.42	194.16	47.61	64.10	58.50	9.72	3.30	3.18	-4.14E-01	2.99E-32		-5.56E-02	1.86E-01		4.29E-01	3.12E-13		2.97E-01	6.59E-06		-1.56E+00	1.62E-18	Down	-1.61E+00	5.33E-20	Down	Unigene28054_All//gi|225432240|ref|XP_002270819.1|//2.00E-56//PREDICTED: similar to ribosomal protein S17 isoform 1 [Vitis vinifera] >gi|189096139|pdb|3BB0|Q Chain Q, Homology Model For The Spinach Chloroplast 50s Subunit Fitted To 9.4a Cryo-Em Map Of The 70s Chlororibosome	Unigene28054_All//2.00E-57//AT1G48350| ribosomal protein L18 family protein	Unigene28054_All//0.00E+00//TC135137		ko03010|Ribosome		nr -

Unigene28056_All	869	0.66	0.52	0.12	7.85	5.86	5.72	7.20	2.93	3.99	-3.36E-01	6.90E-01		-2.43E+00	4.40E-02		-4.21E-01	5.71E-02		-4.58E-01	4.49E-02		-1.30E+00	4.31E-09	Down	-8.52E-01	3.41E-05		Unigene28056_All//gi|18405401|ref|NP_565933.1|//7.00E-71//LBD15 (LOB DOMAIN-CONTAINING PROTEIN 15) [Arabidopsis thaliana] >gi|29427824|sp|Q8L5T5.2|LBD15_ARATH RecName: Full=LOB domain-containing protein 15; AltName: Full=ASYMMETRIC LEAVES 2-like protein 11; Short=AS2-like protein 11 >gi|17227160|gb|AAL38034.1|AF447889_1 LOB DOMAIN 15 [Arabidopsis thaliana] >gi|2651309|gb|AAB87589.1| expressed protein [Arabidopsis thaliana] >gi|91806339|gb|ABE65897.1| LOB domain protein 15/lateral organ boundaries domain protein 15 [Arabidopsis thaliana] >gi|94442507|gb|ABF19041.1| At2g40470 [Arabidopsis thaliana] >gi|219807098|dbj|BAH10555.1| ASYMMETRIC LEAVES2-like 11 protein [Arabidopsis thaliana]	Unigene28056_All//2.00E-50//AT2G40470| LBD15 (LOB DOMAIN-CONTAINING PROTEIN 15)	Unigene28056_All//7.00E-88//DW519375		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene28058_All	997	3847.23	854.32	2078.73	77.34	85.55	99.52	0.51	0.50	26.73	-2.17E+00	0.00E+00	Down	-8.88E-01	0.00E+00		1.46E-01	1.07E-02		3.64E-01	3.48E-13		-1.65E-02	1.02E+00		5.72E+00	2.53E-170	Up	Unigene28058_All//gi|226494771|ref|NP_001147005.1|//7.00E-30//jasmonate-induced protein [Zea mays] >gi|195606394|gb|ACG25027.1| jasmonate-induced protein [Zea mays]		Unigene28058_All//0.00E+00//TC163252				nr -
Unigene28059_All	360	0.00	2.53	0.00	2.77	1.34	2.01	0.47	0.12	2.21	1.13E+01	2.62E-05	Up	null	null		-1.05E+00	1.16E-01		-4.63E-01	5.26E-01		-2.02E+00	3.67E-01		2.24E+00	4.37E-03				Unigene28059_All//1.00E-84//DW502335				
Unigene28060_All	991	0.16	0.66	0.16	4.83	5.00	5.42	2.13	1.01	4.90	2.07E+00	3.93E-02		2.53E-02	1.00E+00		5.23E-02	8.72E-01		1.69E-01	5.93E-01		-1.08E+00	6.86E-03		1.20E+00	1.05E-06	Up	Unigene28060_All//gi|255570843|ref|XP_002526374.1|//6.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223534333|gb|EEF36045.1| conserved hypothetical protein [Ricinus communis]		Unigene28060_All//1.00E-132//DW502335				nr -
Unigene28061_All	269	17.70	11.87	6.53	21.67	22.02	29.21	62.40	23.46	29.92	-5.77E-01	3.67E-02		-1.44E+00	1.91E-06	Down	2.32E-02	9.52E-01		4.31E-01	4.24E-02		-1.41E+00	3.64E-26	Down	-1.06E+00	1.61E-17	Down	Unigene28061_All//gi|587562|emb|CAA56520.1|//7.00E-36//mitochondrial processing peptidase [Solanum tuberosum]	Unigene28061_All//4.00E-33//AT1G51980| mitochondrial processing peptidase alpha subunit, putative	Unigene28061_All//2.00E-150//TC142878				nr +
Unigene28062_All	462	8.38	9.43	10.60	7.22	3.50	7.92	1.01	1.63	1.47	1.71E-01	5.99E-01		3.40E-01	2.43E-01		-1.04E+00	9.94E-04	Down	1.32E-01	7.01E-01		6.94E-01	3.66E-01		5.42E-01	4.75E-01		Unigene28062_All//gi|224103963|ref|XP_002313263.1|//3.00E-08//predicted protein [Populus trichocarpa] >gi|222849671|gb|EEE87218.1| predicted protein [Populus trichocarpa]		Unigene28062_All//0.00E+00//gi|78340692|gb|DT560966.1|DT560966				nr +
Unigene28063_All	436	1.20	4.18	1.47	1.83	2.92	0.93	0.87	2.01	2.65	1.80E+00	6.20E-04	Up	2.89E-01	7.25E-01		6.77E-01	2.91E-01		-9.71E-01	2.30E-01		1.21E+00	7.78E-02		1.60E+00	5.68E-03		Unigene28063_All//gi|156618908|ref|YP_001430044.1|//3.00E-14//photosystem I assembly protein Ycf3 [Cuscuta gronovii] >gi|171769770|sp|A7W902.1|YCF3_CUSGR RecName: Full=Photosystem I assembly protein ycf3 >gi|156555946|emb|CAM98330.1| PSI assembly protein Ycf3 [Cuscuta gronovii]	Unigene28063_All//3.00E-13//AT1G00360| Encodes a protein required for photosystem I assembly and stability. In Chlamydomonas reinhardtii, this protein seems to act as a PSI specific chaperone facilitating the assembly of the complex by interacting with PsaA and PsaD. A loss of function mutation in tobacco leads to a loss of photosystem I.	Unigene28063_All//2.00E-58//TC167141				nr +
Unigene28065_All	1008	0.47	0.10	0.26	3.46	1.84	4.21	1.34	3.03	1.23	-2.22E+00	7.76E-02		-8.23E-01	4.57E-01		-9.07E-01	3.38E-03		2.84E-01	4.05E-01		1.17E+00	2.99E-04	Up	-1.32E-01	7.85E-01		Unigene28065_All//gi|224116922|ref|XP_002331847.1|//4.00E-63//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222875085|gb|EEF12216.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene28065_All//1.00E-51//AT4G27950| CKF4 (CYTOKININ RESPONSE FACTOR 4); DNA binding / transcription factor	Unigene28065_All//8.00E-48//gi|84169116|gb|DR457764.1|DR457764	AP2-EREBP			nr -
Unigene28066_All	517	24.39	11.47	19.16	27.65	35.90	89.37	83.09	29.91	70.82	-1.09E+00	4.08E-11	Down	-3.48E-01	4.12E-02		3.77E-01	2.35E-03		1.69E+00	2.34E-80	Up	-1.47E+00	3.90E-70	Down	-2.31E-01	1.40E-03		Unigene28066_All//gi|3818416|gb|AAD03487.1|//8.00E-40//proline-rich cell wall protein [Medicago sativa]		Unigene28066_All//1.00E-11//ES798127		ko03040|Spliceosome		nr -
Unigene28067_All	1166	0.45	0.74	0.50	2.14	3.75	2.52	1.38	0.14	1.06	7.19E-01	3.48E-01		1.63E-01	8.50E-01		8.12E-01	3.76E-03		2.37E-01	5.79E-01		-3.26E+00	1.49E-07	Down	-3.80E-01	4.03E-01		Unigene28067_All//gi|30697941|ref|NP_201208.2|//2.00E-72//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75245766|sp|Q8LJV3.1|PMTQ_ARATH RecName: Full=Probable methyltransferase PMT26 >gi|21928175|gb|AAM78114.1| At5g64030/MBM17_13 [Arabidopsis thaliana] >gi|27764914|gb|AAO23578.1| At5g64030/MBM17_13 [Arabidopsis thaliana]	Unigene28067_All//1.00E-73//AT3G51070| dehydration-responsive protein-related			ko03040|Spliceosome		nr -
Unigene28071_All	1053	12.22	9.05	13.00	399.89	289.90	274.71	8.79	18.42	6.58	-4.34E-01	6.01E-03		8.85E-02	6.18E-01		-4.64E-01	2.46E-96		-5.42E-01	6.09E-113		1.07E+00	1.21E-19	Up	-4.18E-01	1.14E-02		Unigene28071_All//gi|34733398|gb|AAQ81636.1|//6.00E-91//MADS-box protein GmNMH7 [Glycine max]	Unigene28071_All//3.00E-76//AT3G54340| AP3 (APETALA 3); DNA binding / transcription factor	Unigene28071_All//0.00E+00//TC154044	MADS			nr -
Unigene28072_All	411	7.13	6.90	15.16	8.61	9.13	6.81	1.54	1.63	2.62	-4.63E-02	9.07E-01		1.09E+00	1.34E-05	Up	8.58E-02	8.19E-01		-3.37E-01	3.48E-01		7.65E-02	9.37E-01		7.62E-01	1.85E-01				Unigene28072_All//8.00E-12//ES803332				
Unigene28073_All	454	18.09	16.18	12.78	37.74	28.82	36.11	115.57	74.29	48.79	-1.61E-01	4.61E-01		-5.01E-01	1.83E-02		-3.89E-01	2.25E-03		-6.38E-02	6.71E-01		-6.38E-01	5.65E-22		-1.24E+00	4.94E-68	Down			Unigene28073_All//0.00E+00//gi|21103280|gb|BQ415593.1|BQ415593				
Unigene28074_All	642	2.36	1.42	2.32	1.63	2.15	3.10	0.99	2.47	2.79	-7.34E-01	1.70E-01		-2.52E-02	9.84E-01		3.97E-01	5.49E-01		9.26E-01	4.76E-02		1.32E+00	5.83E-03		1.50E+00	7.33E-04	Up	Unigene28074_All//gi|255554298|ref|XP_002518189.1|//4.00E-23//conserved hypothetical protein [Ricinus communis] >gi|223542785|gb|EEF44322.1| conserved hypothetical protein [Ricinus communis]		Unigene28074_All//5.00E-14//TC132324				nr +
Unigene28075_All	536	50.86	158.06	61.99	31.78	34.37	36.15	83.77	97.55	64.81	1.64E+00	1.99E-130	Up	2.86E-01	3.83E-03		1.13E-01	4.72E-01		1.86E-01	1.90E-01		2.20E-01	1.00E-03		-3.70E-01	8.82E-08		Unigene28075_All//gi|161778780|gb|ABX79341.1|//3.00E-51//cysteine protease [Vitis vinifera]	Unigene28075_All//6.00E-47//AT4G39090| RD19 (RESPONSIVE TO DEHYDRATION 19); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene28075_All//0.00E+00//TC171904				nr +
Unigene28076_All	742	2.54	2.05	1.08	5.17	6.27	1.70	9.97	8.90	2.26	-3.09E-01	5.23E-01		-1.24E+00	1.45E-02		2.77E-01	3.77E-01		-1.60E+00	8.69E-07	Down	-1.64E-01	4.51E-01		-2.14E+00	1.58E-21	Down	Unigene28076_All//gi|88900376|gb|ABD57500.1|//3.00E-27//At5g40460 [Arabidopsis thaliana]	Unigene28076_All//6.00E-18//AT5G40460| unknown protein	Unigene28076_All//1.00E-36//DW511790				nr +
Unigene28078_All	1170	0.98	1.56	0.82	1.58	2.03	1.97	5.42	1.46	2.01	6.64E-01	1.69E-01		-2.64E-01	6.64E-01		3.66E-01	4.23E-01		3.22E-01	4.88E-01		-1.89E+00	2.55E-15	Down	-1.43E+00	5.92E-11	Down	Unigene28078_All//gi|462013|sp|P35016.1|ENPL_CATRO//0.00E+00//RecName: Full=Endoplasmin homolog; AltName: Full=Glucose-regulated protein 94 homolog; Short=GRP-94 homolog; Flags: Precursor >gi|348696|gb|AAA16785.1| heat shock protein 90 [Catharanthus roseus]	Unigene28078_All//1.00E-171//AT4G24190| SHD (SHEPHERD); ATP binding / unfolded protein binding	Unigene28078_All//0.00E+00//TC166008		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene28083_All	439	5.48	6.93	12.74	6.35	5.10	7.10	4.53	2.29	1.45	3.37E-01	3.73E-01		1.22E+00	6.12E-06	Up	-3.18E-01	4.26E-01		1.60E-01	6.98E-01		-9.86E-01	1.65E-02		-1.64E+00	1.05E-04	Down	Unigene28083_All//gi|224130518|ref|XP_002328629.1|//4.00E-14//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222838611|gb|EEE76976.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene28083_All//4.00E-13//AT4G12020| WRKY19; transcription factor	Unigene28083_All//6.00E-87//ES794927	WRKY			nr +
Unigene28085_All	531	2.56	2.19	6.32	0.84	0.39	0.94	7.01	6.53	3.90	-2.23E-01	6.76E-01		1.30E+00	3.27E-04	Up	-1.12E+00	3.15E-01		1.48E-01	9.06E-01		-1.01E-01	7.39E-01		-8.45E-01	2.09E-03				Unigene28085_All//2.00E-10//GE654118				ESTscan -
Unigene28087_All	1063	6.15	2.57	6.21	4.69	3.30	4.93	9.27	5.90	5.17	-1.26E+00	1.61E-07	Down	1.38E-02	9.76E-01		-5.04E-01	5.43E-02		7.27E-02	8.02E-01		-6.52E-01	5.88E-05		-8.42E-01	1.60E-07		Unigene28087_All//gi|115488000|ref|NP_001066487.1|//5.00E-37//Os12g0244200 [Oryza sativa Japonica Group] >gi|77554416|gb|ABA97212.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113648994|dbj|BAF29506.1| Os12g0244200 [Oryza sativa Japonica Group]	Unigene28087_All//5.00E-38//AT3G01740| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Ribosomal protein L37, mitochondrial (InterPro:IPR013870); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G14290.1); Has 117 Blast hits to 117 proteins in 58 species: Archae - 0; Bacteria - 0; Metazoa - 56; Fungi - 22; Plants - 27; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink).	Unigene28087_All//0.00E+00//gi|48778914|gb|CO088280.1|CO088280				nr -
Unigene28088_All	452	17.02	28.81	15.90	18.52	19.05	11.79	13.10	18.22	3.17	7.60E-01	1.32E-06		-9.75E-02	6.65E-01		4.08E-02	8.64E-01		-6.51E-01	9.08E-04		4.76E-01	8.71E-03		-2.05E+00	2.10E-16	Down	Unigene28088_All//gi|115473321|ref|NP_001060259.1|//2.00E-10//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene28088_All//3.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene28088_All//0.00E+00//BF271393				nr +
Unigene28090_All	257	7.13	23.66	9.32	14.92	7.37	11.07	33.40	46.02	75.49	1.73E+00	8.97E-11	Up	3.88E-01	3.90E-01		-1.02E+00	4.86E-04	Down	-4.31E-01	1.95E-01		4.63E-01	1.71E-03		1.18E+00	1.99E-23	Up			Unigene28090_All//2.00E-36//EX166516				
Unigene28091_All	707	1.55	2.44	1.66	2.75	1.56	0.77	2.45	1.30	2.08	6.49E-01	1.97E-01		9.25E-02	8.81E-01		-8.18E-01	6.69E-02		-1.84E+00	1.99E-04	Down	-9.15E-01	4.03E-02		-2.34E-01	5.96E-01		Unigene28091_All//gi|224129022|ref|XP_002320481.1|//1.00E-106//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222861254|gb|EEE98796.1| nucleobase ascorbate transporter [Populus trichocarpa]	Unigene28091_All//1.00E-100//AT2G05760| xanthine/uracil permease family protein	Unigene28091_All//4.00E-101//ES804248				nr -
Unigene28092_All	792	1.06	1.79	1.48	3.52	2.35	1.82	1.82	0.53	0.20	7.61E-01	1.74E-01		4.85E-01	4.47E-01		-5.85E-01	1.11E-01		-9.49E-01	1.13E-02		-1.78E+00	8.40E-04	Down	-3.17E+00	5.96E-07	Down	Unigene28092_All//gi|124359163|gb|ABN05686.1|//2.00E-25//Zinc finger, CCHC-type [Medicago truncatula]	Unigene28092_All//3.00E-08//AT2G01050| nucleic acid binding / zinc ion binding					nr -
Unigene28093_All	932	1.74	4.24	1.89	1.71	1.18	4.51	4.36	1.12	0.51	1.28E+00	5.56E-05	Up	1.16E-01	8.09E-01		-5.33E-01	3.18E-01		1.40E+00	4.78E-06	Up	-1.96E+00	1.56E-10	Down	-3.09E+00	6.67E-18	Down	Unigene28093_All//gi|62546193|gb|AAX85983.1|//3.00E-65//NAC6 protein [Glycine max] >gi|66394520|gb|AAY46126.1| NAC domain protein NAC6 [Glycine max]	Unigene28093_All//2.00E-64//AT2G17040| anac036 (Arabidopsis NAC domain containing protein 36); transcription factor	Unigene28093_All//0.00E+00//gi|31072445|gb|CA992724.1|CA992724	NAC			nr -

Unigene28096_All	905	1.68	1.85	1.53	11.23	6.32	6.69	14.11	12.15	6.25	1.40E-01	7.71E-01		-1.32E-01	8.01E-01		-8.30E-01	5.04E-07		-7.48E-01	1.93E-05		-2.16E-01	1.57E-01		-1.17E+00	8.38E-16	Down	Unigene28096_All//gi|1381676|gb|AA897114.1|//1.00E-104//small GTP-binding protein [Glycine max]	Unigene28096_All//3.00E-101//AT5G65270| AtRABA4a (Arabidopsis Rab GTPase homolog A4a); GTP binding	Unigene28096_All//0.00E+00//TC159394				nr +
Unigene28097_All	623	3.11	11.47	2.22	11.51	10.94	20.52	59.18	70.98	65.29	1.88E+00	5.64E-14	Up	-4.84E-01	3.33E-01		-7.32E-02	8.02E-01		8.33E-01	8.24E-08		2.62E-01	2.88E-04		1.42E-01	7.07E-02		Unigene28097_All//gi|1170746|sp|P46519.1|LEA14_SOYBN//5.00E-60//RecName: Full=Desiccation protectant protein Lea14 homolog	Unigene28097_All//1.00E-54//AT1G01470| LEA14 (LATE EMBRYOGENESIS ABUNDANT 14)	Unigene28097_All//0.00E+00//TC151511				nr -
Unigene28098_All	514	0.61	2.86	1.24	2.71	2.55	2.11	6.50	5.69	7.13	2.23E+00	4.29E-04	Up	1.03E+00	2.81E-01		-9.21E-02	8.58E-01		-3.64E-01	5.56E-01		-1.91E-01	5.89E-01		1.34E-01	6.45E-01		Unigene28098_All//gi|255557957|ref|XP_002520007.1|//2.00E-31//conserved hypothetical protein [Ricinus communis] >gi|223540771|gb|EEF42331.1| conserved hypothetical protein [Ricinus communis]	Unigene28098_All//2.00E-18//AT3G03140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: PWWP (InterPro:IPR000313); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G21295.1); Has 422 Blast hits to 270 proteins in 77 species: Archae - 0; Bacteria - 12; Metazoa - 232; Fungi - 62; Plants - 66; Viruses - 0; Other Eukaryotes - 50 (source: NCBI BLink).	Unigene28098_All//1.00E-51//TC153658				nr -
Unigene281_All	734	0.50	0.14	0.87	3.87	3.61	3.08	3.17	1.03	1.41	-1.85E+00	1.87E-01		8.03E-01	3.88E-01		-9.88E-02	8.25E-01		-3.30E-01	4.14E-01		-1.63E+00	4.15E-05	Down	-1.17E+00	1.46E-03		Unigene281_All//gi|30690809|ref|NP_182306.2|//2.00E-81//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|145331439|ref|NP_001078078.1| zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|62901446|sp|Q944921.2|CH32_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 32; Short=AtC3H32; AltName: Full=Zinc finger (CCCH domain-containing protein ZFN-like 1 >gi|134031914|gb|ABO45694.1| At2g47850 [Arabidopsis thaliana]	Unigene281_All//3.00E-77//AT2G47850| zinc finger (CCCH-type) family protein	Unigene281_All//0.00E+00//TC141469	C3H	ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene28100_All	212	15.80	12.67	18.59	38.07	34.44	33.23	77.78	23.66	27.62	-3.18E-01	3.74E-01		2.35E-01	4.85E-01		-1.45E-01	5.66E-01		-1.96E-01	4.02E-01		-1.72E+00	5.39E-34	Down	-1.49E+00	8.59E-29	Down	Unigene28100_All//gi|34098897|gb|AAQ56831.1|//4.00E-27//At3g03960 [Arabidopsis thaliana]	Unigene28100_All//1.00E-28//AT3G03960| chaperonin, putative	Unigene28100_All//1.00E-116//TC165581				nr -
Unigene28101_All	804	8.59	3.21	3.78	11.77	9.47	7.08	3.73	2.65	4.61	-1.42E+00	2.46E-09	Down	-1.19E+00	6.64E-07	Down	-3.15E-01	9.77E-02		-7.34E-01	5.65E-05		-4.94E-01	1.34E-01		3.04E-01	3.01E-01		Unigene28101_All//gi|56384580|gb|AA98851.1|//4.00E-76//AT-rich element binding factor 1 [Pisum sativum]	Unigene28101_All//1.00E-72//AT2G40620| bZIP transcription factor family protein	Unigene28101_All//0.00E+00//gi|48879886|gb|CO130908.1|CO130908	bZIP			nr +
Unigene28103_All	459	11.40	37.20	21.11	31.91	26.48	32.47	55.36	67.93	40.62	1.71E+00	2.12E-28	Up	8.89E-01	3.72E-06		-2.69E-01	7.17E-02		2.52E-02	9.00E-01		2.95E-01	7.27E-04		-4.47E-01	2.01E-06		Unigene28103_All//gi|145334237|ref|NP_001078499.1|//5.00E-14//ATGB2 (GTP-BINDING 2); GTP binding [Arabidopsis thaliana]	Unigene28103_All//4.00E-15//AT4G35860| ATGB2 (GTP-BINDING 2); GTP binding	Unigene28103_All//0.00E+00//gi|21100882|gb|BQ413195.1|BQ413195				nr -
Unigene28104_All	747	16.11	5.29	4.21	2.87	2.81	2.06	6.79	4.03	6.45	-1.61E+00	1.00E-18	Down	-1.94E+00	4.35E-23	Down	-2.82E-02	9.51E-01		-4.80E-01	3.06E-01		-7.54E-01	1.45E-03		-7.38E-02	7.62E-01		Unigene28104_All//gi|297805120|ref|XP_002870444.1|//8.00E-43//glycosyl hydrolase family protein 17 [Arabidopsis lyrata subsp. lyrata] >gi|297316280|gb|EFH46703.1| glycosyl hydrolase family protein 17 [Arabidopsis lyrata subsp. lyrata]	Unigene28104_All//2.00E-41//AT5G35740| glycosyl hydrolase family protein 17	Unigene28104_All//2.00E-13//TC175026				nr -
Unigene28106_All	715	1.24	1.13	1.04	3.41	2.60	2.34	2.78	1.05	1.39	-1.34E-01	8.41E-01		-2.55E-01	7.17E-01		-3.93E-01	3.47E-01		-5.47E-01	1.95E-01		-1.40E+00	9.38E-04	Down	-9.97E-01	1.18E-02		Unigene28106_All//gi|240256302|ref|NP_197227.4|//6.00E-95//catalytic/ transferase [Arabidopsis thaliana]	Unigene28106_All//3.00E-96//AT5G17250| catalytic/ transferase	Unigene28106_All//0.00E+00//DW478724		ko00563|Glycosylphosphatidylinositol(GPI)-anchor biosynthesis		nr +
Unigene28107_All	1215	0.34	2.67	1.10	0.53	0.45	0.74	1.39	3.96	4.79	2.95E+00	6.75E-11	Up	1.67E+00	9.89E-03		-2.33E-01	8.07E-01		4.80E-01	5.50E-01		1.51E+00	8.85E-09	Up	1.78E+00	2.16E-13	Up	Unigene28107_All//gi|85813774|emb|CAJ65923.1|//4.00E-09//xylan 1,4-beta-xylosidase [Populus alba x Populus tremula]	Unigene28107_All//7.00E-11//AT1G78060| glycosyl hydrolase family 3 protein					nr +
Unigene28108_All	627	17.02	17.05	16.22	21.53	24.28	28.52	293.67	1121.55	488.42	2.40E-03	9.89E-01		-6.96E-02	7.17E-01		1.73E-01	2.94E-01		4.06E-01	1.85E-03		1.93E+00	0.00E+00	Up	7.34E-01	1.26E-162		Unigene28108_All//gi|297610489|ref|NP_001064615.2|//1.00E-10//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene28108_All//8.00E-05//AT1G60680| aldo/keto reductase family protein	Unigene28108_All//0.00E+00//TC170896				nr +
Unigene28109_All	884	3.43	1.32	2.23	1.92	1.95	2.04	5.64	4.44	5.05	-1.38E+00	2.10E-04	Down	-6.23E-01	9.78E-02		2.37E-02	9.74E-01		9.31E-02	8.66E-01		-3.45E-01	1.72E-01		-1.61E-01	5.44E-01		Unigene28109_All//gi|18417421|ref|NP_568302.1|//5.00E-49//tRNA (adenine-N1-)-methyltransferase [Arabidopsis thaliana]	Unigene28109_All//3.00E-50//AT5G14600| tRNA (adenine-N1-)-methyltransferase	Unigene28109_All//0.00E+00//TC153904				nr -
Unigene2811_All	3032	21.26	11.82	17.42	14.67	13.08	12.54	24.91	21.97	10.88	-8.48E-01	1.27E-35		-2.87E-01	2.22E-05		-1.65E-01	4.48E-02		-2.26E-01	5.38E-03		-1.81E-01	1.06E-03		-1.19E+00	1.50E-91	Down	Unigene2811_All//gi|15239154|ref|NP_196733.1|//0.00E+00//alpha-glucosidase 1 (AGLU1) [Arabidopsis thaliana] >gi|7572386|emb|CAB87690.1| alpha-glucosidase 1 [Arabidopsis thaliana] >gi|15450745|gb|AAK96644.1| AT5g11720/T22P22_110 [Arabidopsis thaliana] >gi|25090119|gb|AAN72233.1| At5g11720/T22P22_110 [Arabidopsis thaliana]	Unigene2811_All//0.00E+00//AT5G11720| alpha-glucosidase 1 (AGLU1)	Unigene2811_All//0.00E+00//TC170860		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism	GO:0005488//GO:0005576//GO:0005618//GO:0015926//GO:0031410//GO:0043231//GO:0044238	nr +
Unigene28110_All	817	91.90	96.63	74.43	148.10	199.32	277.06	467.72	334.31	1140.01	7.24E-02	2.85E-01		-3.04E-01	9.23E-07		4.29E-01	1.07E-31		9.04E-01	1.02E-147		-4.84E-01	1.25E-94		1.29E+00	0.00E+00	Up	Unigene28110_All//gi|115338597|gb|AB194388.1|//1.00E-154//isopentyl diphosphate isomerase [Gossypium barbadense]	Unigene28110_All//7.00E-114//AT3G02780| IPP2 (ISOPENTENYL PYROPHOSPHATE:DIMETHYLALLYL PYROPHOSPHATE ISOMERASE 2); isopentenyl-diphosphate delta-isomerase	Unigene28110_All//0.00E+00//TC130918		ko00900|Terpenoid backbone biosynthesis		nr +
Unigene28112_All	1092	8.43	8.72	15.26	1.00	0.28	3.64	0.00	0.00	0.00	4.89E-02	8.04E-01		8.56E-01	1.70E-09		-1.82E+00	5.10E-03		1.86E+00	2.62E-08	Up	null	null		null	null		Unigene28112_All//gi|151655577|gb|ABS18382.1|//1.00E-146//3-ketoacyl-CoA synthase [Eranthis hyemalis]	Unigene28112_All//1.00E-147//AT1G19440| KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene28112_All//0.00E+00//TC157876		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr -
Unigene28113_All	765	3.08	9.74	4.11	7.03	8.01	7.97	6.19	7.70	8.18	1.66E+00	2.41E-12	Up	4.16E-01	2.64E-01		1.88E-01	5.15E-01		1.81E-01	5.20E-01		3.16E-01	1.73E-01		4.02E-01	5.41E-02		Unigene28113_All//gi|1370152|emb|CAA98182.1|//4.00E-84//RAB11F [Lotus japonicus]	Unigene28113_All//8.00E-83//AT1G18200| AtRAB46b (Arabidopsis Rab GTPase homolog A6b); GTP binding / GTPase/ protein binding	Unigene28113_All//0.00E+00//DW518651				nr -
Unigene28114_All	762	1.37	3.46	2.17	7.26	9.99	23.17	8.71	6.86	8.78	1.33E+00	9.56E-04	Up	6.58E-01	2.26E-01		4.61E-01	2.77E-02		1.68E+00	1.57E-30	Up	-3.46E-01	1.05E-01		1.19E-02	9.73E-01		Unigene28114_All//gi|55419650|gb|AAV51938.1|//2.00E-63//AP2/EREBP transcription factor ERF-1 [Gossypium hirsutum]	Unigene28114_All//3.00E-23//AT1G53170| EBF8; DNA binding / transcription factor/ transcription repressor	Unigene28114_All//2.00E-44//TC132542	AP2-EREBP			nr +
Unigene28115_All	640	81.67	24.62	42.35	161.74	156.14	112.56	75.51	30.96	34.05	-1.73E+00	8.25E-88	Down	-9.47E-01	1.29E-33		-5.08E-02	4.23E-01		-5.23E-01	1.95E-26		-1.29E+00	3.40E-64	Down	-1.15E+00	2.20E-55	Down	Unigene28115_All//gi|18700165|gb|AAL77694.1|//6.00E-80//AT3g13510/MRP15_15 [Arabidopsis thaliana] >gi|24797030|gb|AAN64527.1| At3g13510/MRP15_15 [Arabidopsis thaliana]	Unigene28115_All//2.00E-86//AT5G56530| unknown protein	Unigene28115_All//0.00E+00//gi|164341420|gb|ES821828.1|ES821828				nr -
Unigene28117_All	257	38.48	21.29	24.24	27.72	23.85	29.35	77.98	47.00	24.65	-8.54E-01	3.32E-06		-6.67E-01	4.19E-04		-2.17E-01	3.72E-01		8.24E-02	7.31E-01		-7.30E-01	4.26E-11		-1.66E+00	1.58E-40	Down	Unigene28117_All//gi|297849130|ref|XP_002892446.1|//5.00E-43//UDP-D-apiose/UDP-D-xylose synthase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297338288|gb|EFH68705.1| UDP-D-apiose/UDP-D-xylose synthase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene28117_All//2.00E-44//AT1G08200| AXS2 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 2); UDP-glucuronate decarboxylase	Unigene28117_All//6.00E-141//gi|78328458|gb|DT548732.1|DT548732		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene2812_All	1074	0.78	0.42	0.89	2.13	0.74	1.35	3.03	1.09	1.11	-8.76E-01	2.47E-01		1.95E-01	7.70E-01		-1.53E+00	1.64E-04	Down	-6.65E-01	1.24E-01		-1.48E+00	4.82E-06	Down	-1.45E+00	4.08E-06	Down	Unigene2812_All//gi|34098897|gb|AAQ56831.1|//2.00E-09//At3g03960 [Arabidopsis thaliana]	Unigene2812_All//1.00E-10//AT3G03960| chaperonin, putative	Unigene2812_All//5.00E-154//DT468337			GO:0005488//GO:0044464	nr +
Unigene28121_All	280	10.46	10.86	16.74	21.17	16.60	18.39	9.66	8.21	23.62	5.33E-02	8.89E-01		6.78E-01	1.99E-02		-3.51E-01	1.60E-01		-2.03E-01	4.74E-01		-2.35E-01	5.40E-01		1.29E+00	9.73E-10	Up	Unigene28121_All//gi|15227173|ref|NP_178816.1|//4.00E-22//ATRABH1D (ARABIDOPSIS RAB GTPASE HOMOLOG H1D); GTP binding [Arabidopsis thaliana]	Unigene28121_All//1.00E-23//AT5G10260| AtRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding	Unigene28121_All//3.00E-137//TC169246				nr -
Unigene28122_All	1204	0.61	1.39	0.97	3.85	4.12	3.15	4.78	1.91	3.47	1.19E+00	2.17E-02		6.77E-01	3.04E-01		9.81E-02	7.88E-01		-2.88E-01	3.57E-01		-1.32E+00	1.15E-08	Down	-4.59E-01	3.32E-02		Unigene28122_All//gi|224072881|ref|XP_002303925.1|//1.00E-145//RNA polymerase IV subunit [Populus trichocarpa] >gi|222841357|gb|EEE78904.1| RNA polymerase IV subunit [Populus trichocarpa]	Unigene28122_All//7.00E-126//AT2G40030| NRPD1B; DNA binding / DNA-directed RNA polymerase			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene28124_All	594	3.52	7.34	3.14	6.12	5.51	8.59	8.40	15.13	6.17	1.06E+00	3.36E-04	Up	-1.67E-01	7.06E-01		-1.53E-01	6.66E-01		4.89E-01	7.30E-02		8.49E-01	8.88E-07		-4.45E-01	5.79E-02		Unigene28124_All//gi|224082200|ref|XP_002306600.1|//2.00E-23//predicted protein [Populus trichocarpa] >gi|222856049|gb|EEE93596.1| predicted protein [Populus trichocarpa]		Unigene28124_All//5.00E-82//BE054702				nr +
Unigene28125_All	255	21.54	46.10	25.06	20.71	26.87	55.44	28.85	50.65	43.90	1.10E+00	1.71E-10	Up	2.18E-01	3.84E-01		3.76E-01	1.04E-01		1.42E+00	2.07E-19	Up	8.12E-01	9.24E-09		6.06E-01	4.16E-05		Unigene28125_All//gi|297617634|ref|XP_002876700.1|//6.00E-36//NPL4 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322538|gb|EFH52959.1| NPL4 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28125_All//4.00E-26//AT3G63000| NPL41 (NPL4-LIKE PROTEIN 1)	Unigene28125_All//4.00E-142//gi|21103184|gb|BQ415497.1|BQ415497				nr -

Unigene28127_All	2165	0.07	0.37	0.05	1.01	0.38	0.98	3.93	14.23	11.80	2.37E+00	1.01E-02		-5.59E-01	7.76E-01		-1.41E+00	6.73E-04	Down	-4.62E-02	9.33E-01		1.86E+00	7.33E-70	Up	1.59E+00	1.14E-47	Up	Unigene28127_All//gi|15218697|ref|NP_171804.1|//1.00E-176//epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related [Arabidopsis thaliana] >gi|463960222|sp|Q9S465.1|CAP4_ARATH RecName: Full=Putative clathrin assembly protein At1g03050 >gi|4587573|gb|AAD25804.1|AC006550_12 Similar to clathrin assembly protein gb|AF041374 (CALM) from Rattus norvegicus [Arabidopsis thaliana] >gi|91805731|gb|ABE65594.1| clathrin assembly protein-like [Arabidopsis thaliana]	Unigene28127_All//1.00E-141//AT1G03050| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	Unigene28127_All//2.00E-07//TC156852				nr +
Unigene28128_All	783	2.34	1.68	1.43	2.16	4.35	2.19	3.46	0.64	0.81	-4.75E-01	3.32E-01		-7.12E-01	1.56E-01		1.01E+00	1.96E-03		1.90E-02	9.70E-01		-2.43E+00	2.87E-09	Down	-2.09E+00	4.03E-08	Down	Unigene28128_All//gi|15236687|ref|NP_194942.1|//1.00E-63//ATVAMP711 (ARABIDOPSIS THALIANA VESICLE-ASSOCIATED MEMBRANE PROTEIN 711) [Arabidopsis thaliana] >gi|27805754|sp|Q49377.2|VA711_ARATH RecName: Full=Vesicle-associated membrane protein 711; Short=AtVAMP711; AltName: Full=v-SNARE synaptobrevin 7C; Short=AtVAMP7C >gi|16612292|gb|AAL27509.1|AF439840_1 AT4g32150/F10N7_40 [Arabidopsis thaliana] >gi|3858935|emb|CAA16574.1| synaptobrevin-like protein [Arabidopsis thaliana] >gi|4103357|gb|AAD01748.1| vesicle-associated membrane protein 7C [Arabidopsis thaliana] >gi|7270119|emb|CAB79933.1| synaptobrevin-like protein [Arabidopsis thaliana] >gi|21593706|gb|AAM65673.1| synaptobrevin-like protein [Arabidopsis thaliana] >gi|219280069|gb|AAK78063.1| AT4g32150/F10N7_40 [Arabidopsis thaliana] >gi|110740910|dbj|BAE98551.1|	Unigene28128_All//6.00E-57//AT4G32150| ATVAMP711 (ARABIDOPSIS THALIANA VESICLE-ASSOCIATED MEMBRANE PROTEIN 711)	Unigene28128_All//0.00E+00//TC174055		ko04130|SNARE interactions in vesicular transport		nr -
Unigene2813_All	1094	1.00	2.59	3.21	5.24	4.15	6.28	2.51	4.05	4.73	1.37E+00	4.19E-04	Up	1.68E+00	5.16E-06	Up	-3.34E-01	1.94E-01		2.61E-01	3.02E-01		6.89E-01	7.18E-03		9.14E-01	7.28E-05					Unigene2813_All//3.00E-155//DT468337				
Unigene28130_All	255	7.80	10.73	17.75	6.06	8.51	9.39	10.78	7.87	7.97	4.61E-01	2.35E-01		1.19E+00	8.65E-05	Up	4.90E-01	2.98E-01		6.32E-01	1.36E-01		-4.54E-01	1.98E-01		-4.36E-01	1.94E-01					Unigene28130_All//5.00E-120//gi|48742508|gb|CO073027.1|CO073027				
Unigene28132_All	760	2.27	0.27	2.87	1.31	1.40	0.83	2.06	1.70	1.78	-3.09E+00	2.13E-06	Down	3.39E-01	4.56E-01		9.96E-02	9.02E-01		-6.56E-01	3.71E-01		-2.72E-01	6.13E-01		-2.08E-01	6.41E-01		Unigene28132_All//gi|211906526|gb|ACJ11756.1|//1.00E-119//rhamnose synthase [Gossypium hirsutum]	Unigene28132_All//8.00E-117//AT3G14790| RHM3 (RHAMNOSE BIOSYNTHESIS 3); UDP-L-rhamnose synthase/ catalytic	Unigene28132_All//0.00E+00//gi|48823506|gb|CO124819.1|CO124819		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene28133_All	701	531.94	834.35	631.78	72.48	79.19	132.91	3.86	4.11	1.31	6.49E-01	1.34E-199		2.48E-01	4.34E-25		1.28E-01	9.61E-02		8.75E-01	8.47E-58		9.19E-02	7.92E-01		-1.56E+00	9.39E-06	Down	Unigene28133_All//gi|164449260|gb|ABY56089.1|//5.00E-43//proton gradient regulation 5 [Cucumis melo] >gi|164449273|gb|ABY56101.1| proton gradient regulation 5 [Cucumis sativus]	Unigene28133_All//4.00E-38//AT2G05620| PGR5 (proton gradient regulation 5); electron carrier	Unigene28133_All//0.00E+00//TC158376				nr +
Unigene28134_All	1250	0.33	0.32	0.55	1.87	3.39	3.29	2.50	1.20	0.89	-4.64E-02	9.80E-01		7.26E-01	3.97E-01		8.55E-01	2.72E-03		8.12E-01	6.80E-03		-1.06E+00	8.47E-04	Down	-1.49E+00	3.94E-06	Down	Unigene28134_All//gi|15240452|ref|NP_200316.1|//7.00E-77//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75170788|sp|Q9FIA1.1|GDLS7_ARATH RecName: Full=GDSL esterase/lipase At5g55050; AltName: Full=Extracellular lipase At5g55050; Flags: Precursor >gi|10177380|dbj|BAB10579.1| GDSL-motif lipase/hydrolase-like protein [Arabidopsis thaliana]	Unigene28134_All//1.00E-71//AT5G55050| GDSL-motif lipase/hydrolase family protein	Unigene28134_All//1.00E-155//TC149882				nr -
Unigene28135_All	648	15.42	0.00	1.07	4.61	1.43	3.28	6.46	0.45	1.91	-1.39E+01	4.32E-58	Down	-3.85E+00	1.26E-39	Down	-1.68E+00	1.84E-06	Down	-4.94E-01	1.95E-01		-3.84E+00	2.28E-21	Down	-1.76E+00	7.69E-10	Down	Unigene28135_All//gi|75164757|sp|Q94824.1|SNAK1_SOLTU//5.00E-33//RecName: Full=Snakin-1; Flags: Precursor >gi|14627134|emb|CAC44032.1| snakin-1 [Solanum tuberosum]	Unigene28135_All//5.00E-20//AT2G14900| gibberellin-regulated family protein	Unigene28135_All//0.00E+00//TC149811				nr -
Unigene28139_All	810	27.26	10.76	15.78	17.83	9.57	9.98	6.00	12.59	1.03	-1.34E+00	5.90E-26	Down	-7.89E-01	8.08E-11		-8.99E-01	4.24E-11		-8.38E-01	6.63E-09		1.07E+00	9.59E-11	Up	-2.54E+00	1.76E-17	Down	Unigene28139_All//gi|224119654|ref|XP_002331213.1|//3.00E-35//SAUR family protein [Populus trichocarpa] >gi|222873334|gb|EEF10465.1| SAUR family protein [Populus trichocarpa]	Unigene28139_All//3.00E-28//AT1G17345| auxin-responsive protein-related	Unigene28139_All//3.00E-176//gi|109885919|gb|DW514889.1|DW514889				nr +
Unigene2814_All	1881	13.85	19.61	17.41	20.18	25.12	18.58	20.75	31.82	123.07	5.02E-01	1.21E-08		3.30E-01	7.90E-04		3.16E-01	1.30E-05		-1.19E-01	2.35E-01		6.17E-01	1.46E-23		2.57E+00	0.00E+00	Up	Unigene2814_All//gi|18394385|ref|NP_564003.1|//1.00E-146//protein kinase family protein [Arabidopsis thaliana] >gi|16649103|gb|AAL24403.1| Unknown protein [Arabidopsis thaliana] >gi|23197888|gb|AAN15471.1| Unknown protein [Arabidopsis thaliana]	Unigene2814_All//6.00E-148//AT1G16670| protein kinase family protein	Unigene2814_All//0.00E+00//TC159973		ko04626|Plant-pathogen interaction		nr +
Unigene28142_All	943	62.81	24.07	30.66	126.89	147.78	91.00	110.97	21.58	43.64	-1.38E+00	8.45E-72	Down	-1.03E+00	6.40E-44	Down	2.20E-01	4.63E-08		-4.80E-01	4.33E-26		-2.36E+00	0.00E+00	Down	-1.35E+00	2.07E-152	Down	Unigene28142_All//gi|134035500|gb|AB047738.1|//1.00E-141//alpha-tubulin [Gossypium hirsutum]	Unigene28142_All//7.00E-118//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene28142_All//0.00E+00//gi|78329513|gb|DT549787.1|DT549787		ko04145|Phagosome		nr -
Unigene28144_All	1412	3.48	1.00	2.87	5.01	3.83	3.81	0.12	0.24	0.25	-1.79E+00	2.55E-09	Down	-2.81E-01	3.57E-01		-3.88E-01	7.74E-02		-3.96E-01	8.19E-02		9.83E-01	4.24E-01		1.08E+00	3.50E-01		Unigene28144_All//gi|295687237|gb|ADG27844.1|//1.00E-178//RNA helicase-like protein [Gossypium hirsutum]	Unigene28144_All//1.00E-138//AT3G53110| LOS4 (LOW EXPRESSION OF OSMOTICALLY RESPONSIVE GENES 4); ATP-dependent helicase/ RNA helicase/ RNA-dependent ATPase	Unigene28144_All//0.00E+00//BG441024				nr +
Unigene28145_All	460	38.79	132.73	64.71	27.07	71.57	76.68	41.64	57.88	58.55	1.77E+00	1.45E-105	Up	7.39E-01	6.68E-13		1.40E+00	6.91E-48	Up	1.50E+00	8.70E-52	Up	4.75E-01	3.94E-07		4.92E-01	7.49E-08					Unigene28145_All//0.00E+00//TC145649				
Unigene28146_All	1235	0.59	0.66	0.30	8.07	9.20	9.33	13.83	20.47	53.94	1.46E-01	8.39E-01		-9.75E-01	2.64E-01		1.90E-01	3.19E-01		2.09E-01	2.70E-01		5.66E-01	4.66E-09		1.96E+00	4.89E-165	Up	Unigene28146_All//gi|224054172|ref|XP_002298127.1|//1.00E-89//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845385|gb|EEE82932.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene28146_All//3.00E-81//AT1G52800| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene28146_All//0.00E+00//ES849745		ko00904|Diterpenoid biosynthesis		nr +
Unigene28147_All	844	395.44	101.88	101.14	467.51	362.22	267.77	436.68	113.75	154.73	-1.96E+00	0.00E+00	Down	-1.97E+00	0.00E+00	Down	-3.68E-01	1.11E-58		-8.04E-01	6.08E-213		-1.94E+00	0.00E+00	Down	-1.50E+00	0.00E+00	Down	Unigene28147_All//gi|166343823|gb|ABY86654.1|//1.00E-110//beta-tubulin 2 [Gossypium hirsutum]	Unigene28147_All//3.00E-101//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene28147_All//0.00E+00//TC131815		ko04145|Phagosome		nr +
Unigene28148_All	1106	0.19	0.60	0.00	5.18	3.99	3.92	2.60	1.93	1.15	1.65E+00	8.14E-02		-7.56E+00	1.46E-01		-3.78E-01	1.34E-01		-4.02E-01	1.22E-01		-4.32E-01	2.11E-01		-1.17E+00	3.14E-04	Down	Unigene28148_All//gi|9454546|gb|AAF87869.1|AC012561_2/2.00E-42//Unknown protein [Arabidopsis thaliana]	Unigene28148_All//1.00E-43//AT1G50660| unknown protein	Unigene28148_All//0.00E+00//gi|21095666|gb|BQ407979.1|BQ407979				nr +
Unigene28149_All	487	12.03	11.76	15.20	36.93	29.63	35.89	40.72	17.68	19.71	-3.34E-02	9.04E-01		3.37E-01	1.44E-01		-3.18E-01	1.26E-02		-4.11E-02	7.93E-01		-1.20E+00	3.18E-24	Down	-1.05E+00	4.19E-20	Down				Unigene28149_All//0.00E+00//TC173624				
Unigene28151_All	630	51.57	46.33	55.28	13.28	17.11	7.53	3.42	1.13	0.95	-1.55E-01	1.31E-01		1.00E-01	3.65E-01		3.65E-01	3.63E-02		-8.20E-01	2.83E-05		-1.60E+00	1.06E-04	Down	-1.85E+00	8.47E-06	Down	Unigene28151_All//gi|7484766|pir||T10190//2.00E-56//L-ascorbate peroxidase (EC 1.11.1.11) precursor - cucurbit >gi|1321627|dbj|BAA12029.1| thylakoid-bound ascorbate peroxidase [Cucurbita cv. Kurokawa Amakuri]	Unigene28151_All//3.00E-48//AT1G77490| TAPX (THYLAKOIDAL ASCORBATE PEROXIDASE); L-ascorbate peroxidase	Unigene28151_All//0.00E+00//TC164132		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene28152_All	457	7.10	7.76	6.76	12.10	12.06	14.03	72.81	27.16	21.88	1.29E-01	6.90E-01		-7.08E-02	8.43E-01		-5.20E-03	9.76E-01		2.14E-01	4.23E-01		-1.42E+00	1.03E-51	Down	-1.73E+00	7.31E-71	Down				Unigene28152_All//1.00E-137//TC158651				
Unigene28153_All	840	1.06	1.87	1.33	2.85	2.87	1.51	4.08	0.35	1.14	8.20E-01	1.23E-01		3.30E-01	6.40E-01		1.17E-02	9.88E-01		-9.19E-01	2.55E-02		-3.55E+00	1.50E-16	Down	-1.84E+00	1.16E-08	Down	Unigene28153_All//gi|297831754|ref|XP_002883759.1|//1.00E-31//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297329599|gb|EFH60018.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene28153_All//9.00E-32//AT2G07170| binding	Unigene28153_All//0.00E+00//ES795474				nr -
Unigene28155_All	889	0.59	1.71	0.96	2.75	5.66	6.05	13.46	12.51	102.04	1.54E+00	6.71E-03		7.04E-01	3.83E-01		1.04E+00	5.27E-05	Up	1.14E+00	1.09E-05	Up	-1.06E-01	5.52E-01		2.92E+00	0.00E+00	Up								
Unigene28157_All	701	103.00	23.13	68.82	84.07	57.97	65.07	3.08	0.30	1.93	-2.15E+00	2.05E-162	Down	-5.82E-01	4.14E-20		-5.36E-01	7.51E-18		-3.70E-01	2.37E-08		-3.37E+00	3.41E-10	Down	-6.71E-01	7.39E-02		Unigene28157_All//gi|15242049|ref|NP_197574.1|//1.00E-29//invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana] >gi|58331821|gb|AAW70408.1| At5g20740 [Arabidopsis thaliana]	Unigene28157_All//2.00E-40//AT5G20740| invertase/pectin methylesterase inhibitor family protein	Unigene28157_All//0.00E+00//TC148440		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene28158_All	679	3.39	1.49	1.88	3.74	2.79	3.86	10.46	5.17	5.46	-1.18E+00	5.68E-03		-8.49E-01	5.44E-02		-4.24E-01	3.05E-01		4.41E-02	9.35E-01		-1.02E+00	3.40E-07	Down	-9.39E-01	1.21E-06		Unigene28158_All//gi|114050677|gb|ABI49488.1|//7.00E-42//At2g37510 [Arabidopsis thaliana]	Unigene28158_All//7.00E-39//AT2G37510| RNA-binding protein, putative	Unigene28158_All//0.00E+00//ES822408		ko03010|Ribosome//ko03040|Spliceosome		nr -
Unigene28159_All	640	3.19	0.48	5.82	3.19	1.45	2.61	2.31	0.13	1.37	-2.75E+00	1.06E-06	Down	8.69E-01	8.74E-03		-1.14E+00	7.97E-03		-2.90E-01	5.68E-01		-4.15E+00	2.74E-08	Down	-7.56E-01	1.07E-01		Unigene28159_All//gi|15229587|ref|NP_188439.1|//2.00E-90//EMB1270 (embryo defective 1270) [Arabidopsis thaliana] >gi|75222187|sp|Q6G1S8.1|PP241_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g18110, chloroplastic; AltName: Full=Protein EMBRYO DEFECTIVE 1270; Flags: Precursor >gi|58013026|gb|AAW62966.1| chloroplast embryo-defective 1270 [Arabidopsis thaliana]	Unigene28159_All//9.00E-92//AT3G18110| EMB1270 (embryo defective 1270)				nr +
Unigene2816_All	2534	17.14	37.99	12.04	28.48	31.49	30.12	35.76	68.75	44.92	1.15E+00	1.05E-86	Up	-5.09E-01	7.63E-10		1.45E-01	1.52E-02		8.06E-02	2.59E-01		9.43E-01	5.30E-139		3.29E-01	7.89E-15		Unigene2816_All//gi|297796761|ref|XP_002866265.1|//0.00E+00//ATEX07OB1 [Arabidopsis lyrata subsp. lyrata] >gi|297312100|gb|EFH42524.1| ATEX07OB1 [Arabidopsis lyrata subsp. lyrata]	Unigene2816_All//0.00E+00//AT5G58430| ATEX07OB1 (exocyst subunit EX070 family protein B1); protein binding	Unigene2816_All//0.00E+00//TC154425			GO:0005488//GO:0016020//GO:0043234//GO:0048278	nr +
Unigene28160_All	606	4.92	11.62	5.18	11.18	11.59	11.18	24.77	29.93	19.52	1.24E+00	7.67E-08	Up	7.51E-02	8.33E-01		5.23E-02	8.38E-01		0.00E+00	9.98E-01		2.73E-01	2.32E-02		-3.43E-01	6.86E-03					Unigene28160_All//0.00E+00//DW232098				

Unigene28161_All	598	0.87	2.12	1.96	2.75	3.34	4.91	1.84	1.89	0.33	1.28E+00	3.83E-02		1.16E+00	8.16E-02		2.81E-01	5.83E-01		8.37E-01	2.31E-02		3.78E-02	9.76E-01		-2.46E+00	2.04E-04	Down	Unigene28161_All//gi|225441993|ref|XP_002271332.1|/4.00E-23//PREDICTED: similar to GTP binding / translation initiation factor [Vitis vinifera]	Unigene28161_All//2.00E-15//AT1G53900| GTP binding / translation initiation factor	Unigene28161_All//2.00E-176//DW479314				nr -
Unigene28162_All	1102	0.95	0.78	0.34	4.84	1.81	2.42	2.23	5.73	2.35	-2.81E-01	6.44E-01		-1.49E+00	4.42E-02		-1.42E+00	1.07E-08	Down	-1.00E+00	9.00E-05	Down	1.36E+00	7.87E-10	Up	7.85E-02	8.26E-01		Unigene28162_All//gi|297601677|ref|NP_001061246.2|/2.00E-74//Os03g0745600 [Oryza sativa Japonica Group] >gi|255674891|dbj|BAF13160.2|Os03g0745600 [Oryza sativa Japonica Group]	Unigene28162_All//1.00E-55//AT3G63310| glutamate binding	Unigene28162_All//8.00E-42//TC132000				nr -
Unigene28165_All	577	1.81	2.81	0.83	2.33	1.19	3.21	33.78	42.30	89.00	6.32E-01	2.23E-01		-1.13E+00	1.17E-01		-9.66E-01	8.22E-02		4.61E-01	3.82E-01		3.25E-01	1.13E-03		1.40E+00	7.79E-79	Up			Unigene28165_All//2.00E-68//gi|109868569|gb|DW497545.1|DW497545				
Unigene28166_All	834	4.14	1.22	1.66	2.99	2.11	2.49	3.40	5.11	1.00	-1.77E+00	1.18E-06	Down	-1.32E+00	2.29E-04	Down	-5.04E-01	2.13E-01		-2.62E-01	5.66E-01		5.90E-01	2.53E-02		-1.76E+00	6.35E-07	Down	Unigene28166_All//gi|15226168|ref|NP_178215.1|//1.00E-17//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene28166_All//3.00E-17//AT2G01050| nucleic acid binding / zinc ion binding	Unigene28166_All//0.00E+00//DW516140				nr -
Unigene28168_All	396	4.49	4.61	4.84	16.23	12.44	13.12	2.99	0.63	1.71	3.62E-02	9.58E-01		1.08E-01	8.14E-01		-3.84E-01	1.00E-01		-3.07E-01	2.23E-01		-2.24E+00	4.21E-04	Down	-8.06E-01	1.31E-01									
Unigene28169_All	508	1.65	3.59	0.94	3.63	2.98	3.20	3.33	4.69	6.90	1.12E+00	2.19E-02		-8.05E-01	3.22E-01		-2.83E-01	5.82E-01		-1.81E-01	7.08E-01		4.94E-01	1.95E-01		1.05E+00	2.84E-04	Up			Unigene28169_All//2.00E-133//C0127087				
Unigene28170_All	1008	0.47	1.41	0.32	3.11	3.11	2.06	1.89	3.98	1.38	1.59E+00	7.37E-03		-5.60E-01	6.28E-01		-2.20E-03	9.85E-01		-5.95E-01	9.66E-02		1.08E+00	9.30E-05	Up	-4.48E-01	2.80E-01		Unigene28170_All//gi|224074695|ref|XP_002304428.1|/2.00E-76//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222841860|gb|EEE79407.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene28170_All//1.00E-36//AT1G12260| NAC007 (ARABIDOPSIS NAC 007); transcription factor	Unigene28170_All//4.00E-148//TC152071	NAC			nr +
Unigene28172_All	1051	3.14	12.39	20.11	0.52	2.75	2.02	0.08	0.00	0.00	1.98E+00	1.35E-26	Up	2.68E+00	6.22E-60	Up	2.40E+00	8.67E-09	Up	1.95E+00	5.45E-05	Up	-6.33E+00	4.04E-01		-6.33E+00	3.58E-01		Unigene28172_All//gi|18412668|ref|NP_565230.1|/6.00E-58//binding [Arabidopsis thaliana] >gi|5902369|gb|AAD55471.1|AC009322_11 Unknown protein [Arabidopsis thaliana]	Unigene28172_All//8.00E-47//AT1G80130| binding	Unigene28172_All//0.00E+00//TC168081				nr -
Unigene28174_All	602	23.03	12.88	15.30	48.57	41.07	55.37	196.72	81.44	77.96	-8.39E-01	3.81E-08		-5.90E-01	1.58E-04		-2.42E-01	1.46E-02		1.89E-01	5.95E-02		-1.27E+00	1.24E-153	Down	-1.34E+00	3.06E-170	Down	Unigene28174_All//gi|225462164|ref|XP_002266780.1|/1.00E-108//PREDICTED: similar to elongation factor 2 [Vitis vinifera]	Unigene28174_All//6.00E-108//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene28174_All//0.00E+00//TC143657				nr +
Unigene28181_All	853	1.29	1.07	1.31	3.27	0.73	3.65	2.58	3.53	4.20	-2.69E-01	6.51E-01		2.54E-02	9.88E-01		-2.17E+00	2.42E-08	Down	1.60E-01	6.98E-01		4.53E-01	1.73E-01		7.06E-01	1.20E-02		Unigene28181_All//gi|18411286|ref|NP_567168.1|/6.00E-31//EDA8 (EMBRYO SAC DEVELOPMENT ARREST 8) [Arabidopsis thaliana] >gi|79324957|ref|NP_001031563.1|EDA8 (EMBRYO SAC DEVELOPMENT ARREST 8) [Arabidopsis thaliana] >gi|6049879|gb|AAF02794.1|AF195115_14 F5I10.17 gene product [Arabidopsis thaliana] >gi|2252837|gb|AAB62836.1|A_IG005I10.17 gene product [Arabidopsis thaliana] >gi|7267118|emb|CAB80789.1|AT4g00310 [Arabidopsis thaliana] >gi|15146200|gb|AAK83583.1|AT4g00310/A_IG005I10_17 [Arabidopsis thaliana] >gi|19699130|gb|AAL90931.1|AT4g00310/A_IG005I10_17 [Arabidopsis thaliana] >gi|222423695|dbj|BAH19814.1|AT4G00310 [Arabidopsis thaliana]	Unigene28181_All//7.00E-11//AT4G00310| EDA8 (EMBRYO SAC DEVELOPMENT ARREST 8)					nr +
Unigene28182_All	280	64.47	23.16	16.17	53.19	42.80	90.17	72.48	35.38	39.27	-1.48E+00	1.37E-24	Down	-2.00E+00	9.02E-36	Down	-3.14E-01	2.89E-02		7.61E-01	8.85E-13		-1.03E+00	1.34E-19	Down	-8.84E-01	9.61E-16		Unigene28182_All//gi|297794223|ref|XP_002864996.1|/6.00E-38//60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|297310831|gb|EFH41255.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene28182_All//4.00E-32//AT5G67510| 60S ribosomal protein L26 (RPL26B)	Unigene28182_All//5.00E-148//gi|109870431|gb|DW499407.1|DW499407		ko03010|Ribosome		nr -
Unigene28186_All	458	35.30	15.82	29.76	64.93	66.62	67.75	102.38	38.42	36.97	-1.16E+00	2.06E-15	Down	-2.46E-01	1.07E-01		3.69E-02	8.01E-01		6.12E-02	6.44E-01		-1.41E+00	6.56E-72	Down	-1.47E+00	2.20E-78	Down	Unigene28186_All//gi|195641082|gb|ACG40009.1|//3.00E-78//T-complex protein 1 subunit epsilon [Zea mays]	Unigene28186_All//1.00E-78//AT1G24510| T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative	Unigene28186_All//0.00E+00//gi|48800568|gb|C0101882.1|C0101882				nr +
Unigene28187_All	465	13.61	4.25	8.02	15.53	13.03	18.16	20.73	13.48	16.54	-1.68E+00	8.01E-11	Down	-7.64E-01	1.74E-03		-2.53E-01	2.85E-01		2.26E-01	3.20E-01		-6.21E-01	1.57E-04		-3.26E-01	4.68E-02		Unigene28187_All//gi|240846170|dbj|BAH79623.1|//2.00E-52//Rsdv1 resistance like protein [Glycine max]	Unigene28187_All//2.00E-48//AT3G20000| TOM40; P-P-bond-hydrolysis-driven protein transmembrane transporter/ voltage-gated anion channel	Unigene28187_All//0.00E+00//gi|109870748|gb|DW499724.1|DW499724				nr -
Unigene28189_All	1274	1.72	0.76	0.54	2.97	2.38	2.62	10.29	13.42	9.35	-1.19E+00	6.83E-03		-1.67E+00	5.54E-04	Down	-3.21E-01	3.27E-01		-1.80E-01	6.40E-01		3.83E-01	1.51E-03		-1.38E-01	3.64E-01		Unigene28189_All//gi|297853502|ref|XP_002894632.1|//2.00E-76//phloem protein 2-B13 [Arabidopsis lyrata subsp. lyrata] >gi|297340474|gb|EFH70891.1|phloem protein 2-B13 [Arabidopsis lyrata subsp. lyrata]	Unigene28189_All//3.00E-77//AT1G56240| AtPP2-B13 (Phloem protein 2-B13); carbohydrate binding	Unigene28189_All//0.00E+00//TC153333				nr -
Unigene2819_All	1733	34.57	105.61	44.06	46.13	38.55	49.23	29.54	94.11	29.40	1.61E+00	3.92E-275	Up	3.50E-01	9.63E-09		-2.59E-01	1.58E-06		9.36E-02	1.46E-01		1.67E+00	0.00E+00	Up	-7.00E-03	9.49E-01		Unigene2819_All//gi|124360726|gb|AB008703.1|//1.00E-166//Heat shock protein DnaJ [Medicago truncatula]	Unigene2819_All//7.00E-127//AT2G20560| DNAJ heat shock family protein	Unigene2819_All//0.00E+00//TC135168			GO:0005515//GO:0044267	nr +
Unigene28190_All	383	90.71	80.30	81.89	130.97	101.87	135.61	146.60	85.01	58.46	-1.76E-01	6.98E-02		-1.48E-01	1.53E-01		-3.63E-01	1.19E-07		5.02E-02	6.21E-01		-7.86E-01	1.63E-33		-1.33E+00	2.72E-80	Down	Unigene28190_All//gi|18423437|ref|NP_568778.1|//2.00E-44//NADH-ubiquinone oxidoreductase-related [Arabidopsis thaliana] >gi|250908853|sp|Q9FLX7.1|NDUA5_ARATH RecName: Full=Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial; Flags: Precursor >gi|15809966|gb|AAL06910.1|AT5g52840/MXC20_6 [Arabidopsis thaliana] >gi|18958052|gb|AAL79599.1|AT5g52840/MXC20_6 [Arabidopsis thaliana]	Unigene28190_All//1.00E-45//AT5G52840| NADH-ubiquinone oxidoreductase-related	Unigene28190_All//0.00E+00//gi|5047255|gb|AI728403.1|AI728403		ko00190|Oxidative phosphorylation		nr +
Unigene28191_All	1429	0.59	1.95	0.56	0.80	0.94	1.61	0.98	1.70	2.59	1.74E+00	2.33E-05	Up	-6.76E-02	9.40E-01		2.29E-01	7.47E-01		1.01E+00	1.82E-02		7.97E-01	2.91E-02		1.41E+00	1.51E-06	Up	Unigene28191_All//gi|18391081|ref|NP_563856.1|//1.00E-113//histidine acid phosphatase family protein [Arabidopsis thaliana] >gi|15456401|gb|AAN96494.1|At1g09870/F21M12_26 [Arabidopsis thaliana]	Unigene28191_All//3.00E-115//AT1G09870| histidine acid phosphatase family protein	Unigene28191_All//0.00E+00//gi|21098825|gb|BQ411138.1|BQ411138				nr -
Unigene28192_All	332	11.03	2.29	8.02	23.41	22.30	18.23	69.92	34.62	32.76	-2.27E+00	2.15E-09	Down	-4.60E-01	1.79E-01		-6.99E-02	8.04E-01		-3.61E-01	9.89E-02		-1.01E+00	1.37E-21	Down	-1.09E+00	4.58E-25	Down	Unigene28192_All//gi|151368158|gb|ABS10814.1|//4.00E-57//chloroplast transketolase precursor [Gossypium barbadense]	Unigene28192_All//1.00E-43//AT2G45290| transketolase, putative	Unigene28192_All//0.00E+00//gi|13350369|gb|BG440717.1|BG440717		ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway		nr +
Unigene28194_All	988	5.77	3.03	2.48	5.29	4.46	5.94	4.49	2.12	1.41	-9.32E-01	1.99E-04		-1.22E+00	4.76E-06	Down	-2.47E-01	3.88E-01		1.67E-01	5.72E-01		-1.09E+00	2.95E-05	Down	-1.67E+00	1.04E-09	Down	Unigene28194_All//gi|262263161|dbj|BA148083.1|//7.00E-62//MIS12 homologue [Nicotiana tabacum] >gi|262263171|dbj|BA148088.1|kinetochore protein [Nicotiana tomentosiformis]	Unigene28194_All//7.00E-53//AT5G35520| MIS12 (MINICHROMOSOME INSTABILITY 12 (MIS12)-LIKE)	Unigene28194_All//0.00E+00//gi|11207349|gb|BF276279.1|BF276279				nr +
Unigene28195_All	961	1.14	3.37	1.33	4.61	2.90	5.45	51.61	61.15	75.74	1.56E+00	2.24E-05	Up	2.18E-01	7.02E-01		-6.69E-01	1.41E-02		2.41E-01	4.16E-01		2.45E-01	7.82E-05		5.54E-01	3.52E-24				Unigene28195_All//0.00E+00//gi|109881752|gb|DW510722.1|DW510722				
Unigene28196_All	1237	4.57	2.50	2.11	2.13	2.81	1.57	0.55	0.54	0.55	-8.70E-01	5.21E-04		-1.11E+00	2.63E-05	Down	3.98E-01	2.64E-01		-4.43E-01	2.86E-01		-1.67E-02	1.02E+00		1.60E-03	9.97E-01		Unigene28196_All//gi|264664489|sp|C0LGP4.1|Y3475_ARATH//2.00E-87//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At3g47570; Flags: Precursor >gi|224589592|gb|ACN59329.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene28196_All//8.00E-89//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative	Unigene28196_All//2.00E-147//gi|109873265|gb|DW502240.1|DW502240		ko04626|Plant-pathogen interaction		nr +
Unigene2820_All	2268	1.20	5.27	2.14	1.60	1.96	1.25	5.11	9.49	8.22	2.14E+00	6.97E-27	Up	8.33E-01	3.45E-03		2.89E-01	3.66E-01		-3.54E-01	3.11E-01		8.94E-01	2.10E-16		6.87E-01	1.17E-09									
Unigene28201_All	474	4.97	38.06	7.08	5.68	8.57	16.20	1.34	2.03	10.59	2.94E+00	9.44E-58	Up	5.11E-01	1.50E-01		5.95E-01	4.77E-02		1.51E+00	8.70E-12	Up	6.00E-01	3.67E-01		2.98E+00	6.51E-21	Up	Unigene28201_All//gi|75223238|sp|Q80871.1|P2C25_ARATH//2.00E-21//RecName: Full=Probable protein phosphatase 2C 25; Short=AtPP2C25; AltName: Full=Protein phosphatase AP2C1		Unigene28201_All//2.00E-90//TC157217		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene28203_All	1142	0.50	0.67	0.28	1.27	0.57	0.71	30.21	6.66	0.84	4.01E-01	6.01E-01		-8.49E-01	3.97E-01		-1.14E+00	3.09E-02		-8.29E-01	1.41E-01		-2.18E+00	1.50E-96	Down	-5.17E+00	7.17E-216	Down	Unigene28203_All//gi|115438859|ref|NP_001043709.1|//2.00E-66//Os01g0647000 [Oryza sativa Japonica Group] >gi|113533240|dbj|BAF05623.1|Os01g0647000 [Oryza sativa Japonica Group]	Unigene28203_All//7.00E-85//AT5G19970| unknown protein					nr +
Unigene28205_All	478	22.99	65.40	27.40	64.82	125.78	80.22	116.14	142.44	74.26	1.51E+00	3.49E-43	Up	2.54E-01	1.39E-01		9.56E-01	7.05E-48		3.07E-01	3.31E-04		2.95E-01	2.00E-07		-6.45E-01	2.25E-24		Unigene28205_All//gi|146454608|gb|ABQ41970.1|//1.00E-37//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Sonneratia caseolaris]	Unigene28205_All//3.00E-38//AT3G53980| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene28205_All//4.00E-57//gi|48744779|gb|C0075298.1|C0075298				nr +
Unigene28207_All	877	0.06	0.35	0.49	2.95	3.14	1.80	57.85	42.08	15.13	2.54E+00	1.51E-01		3.02E+00	5.73E-02		8.88E-02	8.32E-01		-7.13E-01	7.29E-02		-4.59E-01	4.04E-12		-1.94E+00	4.98E-125	Down	Unigene28207_All//gi|151347477|gb|ABS01351.1|//8.00E-48//basic leucine zipper protein [Carica papaya]	Unigene28207_All//2.00E-31//AT1G08320| bZIP family transcription factor	Unigene28207_All//6.00E-42//C0126363	bZIP			nr -
Unigene28209_All	515	4.57	7.28	6.41	6.48	4.41	3.51	16.67	5.76	6.42	6.71E-01	3.45E-02		4.88E-01	1.77E-01		-5.54E-01	9.41E-02		-8.86E-01	8.46E-03		-1.53E+00	1.88E-15	Down	-1.38E+00	1.01E-13	Down	Unigene28209_All//gi|225440308|ref|XP_002262887.1|//1.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene28209_All//4.00E-05//AT5G59613| unknown protein	Unigene28209_All//7.00E-167//TC167479				nr -
Unigene2821_All	1502	25.19	52.66	41.52	4.01	4.91	3.76	5.69	5.57	6.87	1.06E+00	3.78E-63	Up	7.21E-01	2.61E-25		2.90E-01	2.13E-01		-9.45E-02	7.19E-01		-3.10E-02	8.87E-01		2.73E-01	9.14E-02		Unigene2821_All//gi|18402763|ref|NP_564553.1|//1.00E-151//phospholipase C/ phosphoric diester hydrolase [Arabidopsis thaliana] >gi|10120435|gb|AAG13060.1|AC011807_19 Unknown protein [Arabidopsis thaliana]	Unigene2821_All//6.00E-153//AT1G49740| phospholipase C/ phosphoric diester hydrolase	Unigene2821_All//0.00E+00//C0130997				nr +
Unigene28210_All	604	0.95	1.43	2.12	5.28	3.42	2.69	4.27	5.95	1.58	5.82E-01	4.27E-01		1.15E+00	6.95E-02		-6.26E-01	6.27E-02		-9.71E-01	4.94E-03		4.79E-01	1.07E-01		-1.43E+00	5.84E-05	Down			Unigene28210_All//4.00E-61//FL577353				
Unigene28211_All	1048	16.43	0.68	2.79	2.90	3.88	2.24	0.00	0.00	0.00	-4.60E+00	3.97E-80	Down	-2.56E+00	4.37E-46	Down	4.19E-01	1.86E-01		-3.72E-01	3.40E-01		null	null		null	null				Unigene28211_All//0.00E+00//DW501342				

Unigene28212_All	656	3.99	0.62	2.27	1.59	1.26	2.13	0.32	0.25	1.21	-2.69E+00	3.11E-08	Down	-8.11E-01	4.75E-02		-3.40E-01	5.96E-01		4.20E-01	4.92E-01		-3.39E-01	8.12E-01		1.91E+00	1.08E-02		Unigene28212_All//gi|15242850|ref|NP_200579.1|//5.00E-79//heat shock protein-related [Arabidopsis thaliana] >gi|9759268|dbj|BAB09589.1| 101 kDa heat shock protein; HSP101-like protein [Arabidopsis thaliana]	Unigene28212_All//3.00E-80//AT5G37710| heat shock protein-related					nr -
Unigene28213_All	627	17.19	55.44	46.20	34.56	63.65	68.72	19.02	29.53	34.18	1.69E+00	2.36E-56	Up	1.43E+00	8.08E-36	Up	8.81E-01	7.82E-28		9.92E-01	3.64E-33		6.35E-01	3.13E-08		8.46E-01	2.37E-15		Unigene28213_All//gi|115453347|ref|NP_001050274.1|//2.00E-73//Os03g0390200 [Oryza sativa Japonica Group] >gi|71153740|sp|Q7SLR7.1|SAPK1_ORYSJ RecName: Full=Serine/threonine-protein kinase SAPK1; AltName: Full=Osmotic stress/abscisic acid-activated protein kinase 1 >gi|37991924|gb|AAR06370.1| abscisic acid-inducible protein kinase [Oryza sativa Japonica Group] >gi|46917330|dbj|BAD17997.1| serine/threonine protein kinase SAPK1 [Oryza sativa Japonica Group] >gi|113548745|dbj|BAF12188.1| Os03g0390200 [Oryza sativa Japonica Group]	Unigene28213_All//6.00E-72//AT4G33950| OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase	Unigene28213_All//0.00E+00//gi|48794876|gb|C0096190.1|C0096190				nr -
Unigene28214_All	356	105.38	58.78	65.37	105.09	76.80	102.89	193.47	74.67	51.25	-8.42E-01	7.98E-21		-6.89E-01	2.67E-14		-4.52E-01	1.50E-08		-3.05E-02	7.73E-01		-1.37E+00	8.99E-101	Down	-1.92E+00	2.90E-167	Down	Unigene28214_All//gi|297806647|ref|XP_002871207.1|//1.00E-48//40S ribosomal protein S17 [Arabidopsis lyrata subsp. lyrata] >gi|297317044|gb|EFH47466.1| 40S ribosomal protein S17 [Arabidopsis lyrata subsp. lyrata]	Unigene28214_All//7.00E-50//AT5G04800| 40S ribosomal protein S17 (RPS17D)	Unigene28214_All//0.00E+00//gi|109882392|gb|DW511362.1|DW511362		ko03010|Ribosome		nr +
Unigene28216_All	415	186.97	165.07	308.85	248.11	256.31	206.34	392.54	152.88	140.54	-1.80E-01	3.26E-03		7.24E-01	6.93E-52		4.69E-02	4.61E-01		-2.66E-01	7.08E-08		-1.36E+00	4.35E-234	Down	-1.48E+00	6.98E-274	Down	Unigene28216_All//gi|300793598|tpg|DAA33865.1|//7.00E-49//TPA: TPA_inf: aquaporin PIP2;10 [Gossypium hirsutum]	Unigene28216_All//4.00E-23//AT2G37180| RD28 (RESPONSIVE TO DESICCATION 28); water channel	Unigene28216_All//0.00E+00//gi|164337053|gb|ES804671.1|ES804671				nr +
Unigene28217_All	1314	0.48	0.96	0.49	6.75	8.26	8.76	5.53	17.75	5.76	1.01E+00	9.38E-02		2.54E-02	9.97E-01		2.91E-01	1.07E-01		3.77E-01	2.78E-02		1.68E+00	2.75E-46	Up	5.78E-02	7.75E-01		Unigene28217_All//gi|15225326|ref|NP_180221.1|//1.00E-39//AR781 [Arabidopsis thaliana] >gi|2739378|gb|AAC14501.1| AR781, similar to yeast pheromone receptor [Arabidopsis thaliana] >gi|23297321|gb|AAN12941.1| AR781 [Arabidopsis thaliana]	Unigene28217_All//2.00E-25//AT2G26530| AR781	Unigene28217_All//0.00E+00//gi|78337281|gb|DT557555.1|DT557555				nr -
Unigene28219_All	1280	2.94	0.75	1.33	6.07	4.44	1.91	7.00	5.58	1.62	-1.97E+00	3.51E-08	Down	-1.14E+00	6.36E-04	Down	-4.52E-01	2.55E-02		-1.67E+00	6.09E-14	Down	-3.27E-01	6.83E-02		-2.11E+00	1.93E-25	Down	Unigene28219_All//gi|56550679|gb|AAY97793.1|//1.00E-118//At5g10750 [Arabidopsis thaliana] >gi|57222152|gb|AAW38983.1| At5g10750 [Arabidopsis thaliana]	Unigene28219_All//5.00E-119//AT5G10750| unknown protein	Unigene28219_All//0.00E+00//ES824945				nr -
Unigene28220_All	447	4.92	10.88	8.82	5.91	7.93	8.99	6.62	11.13	12.66	1.15E+00	4.19E-05	Up	8.43E-01	8.63E-03		4.26E-01	2.20E-01		6.06E-01	4.98E-02		7.49E-01	1.78E-03		9.35E-01	2.14E-05				Unigene28220_All//1.00E-174//gi|48811001|gb|C0112314.1|C0112314				
Unigene28221_All	480	1.42	1.16	2.33	2.39	2.37	2.35	3.44	1.13	3.40	-2.87E-01	7.10E-01		7.17E-01	2.87E-01		-1.18E-02	9.64E-01		-2.11E-02	9.62E-01		-1.60E+00	8.96E-04	Down	-1.37E-02	9.67E-01				Unigene28221_All//6.00E-07//ES793754				
Unigene28225_All	4640	0.01	0.00	0.00	0.15	0.03	0.30	7.46	0.76	3.02	-3.50E+00	6.12E-01		-3.50E+00	6.24E-01		-2.34E+00	1.01E-02		1.01E+00	8.41E-02		-3.30E+00	1.89E-152	Down	-1.30E+00	1.40E-48	Down	Unigene28225_All//gi|256538311|gb|ACU82515.1|//0.00E+00//pleiotropic drug resistance protein [Cucumis sativus]	Unigene28225_All//0.00E+00//AT2G26910| PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances	Unigene28225_All//9.00E-42//TC147767		ko02010|ABC transporters		nr +
Unigene28226_All	683	0.69	2.37	3.04	1.39	1.06	1.06	1.11	1.04	1.46	1.78E+00	1.52E-03		2.14E+00	5.02E-05	Up	-3.88E-01	5.85E-01		-3.89E-01	6.28E-01		-9.91E-02	8.96E-01		3.88E-01	5.38E-01		Unigene28226_All//gi|15236546|ref|NP_194913.1|//4.00E-86//PGR3 (PROTON GRADIENT REGULATION 3) [Arabidopsis thaliana] >gi|75213543|sp|Q9SZ52.1|PP344_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g31850, chloroplastic; AltName: Full=Protein PROTON GRADIENT REGULATION 3; Flags: Precursor	Unigene28226_All//1.00E-87//AT4G31850| PGR3 (PROTON GRADIENT REGULATION 3)					nr -
Unigene28228_All	357	35.47	23.56	17.60	78.42	54.11	81.22	48.68	25.41	17.07	-5.90E-01	1.90E-04		-1.01E+00	1.67E-09	Down	-5.35E-01	1.04E-08		5.06E-02	7.00E-01		-9.38E-01	1.75E-14		-1.51E+00	8.03E-31	Down			Unigene28228_All//9.00E-144//gi|109830584|gb|DW229143.1|DW229143				
Unigene28229_All	492	12.87	8.65	7.58	15.79	14.77	22.77	40.48	22.34	16.52	-5.73E-01	1.44E-02		-7.64E-01	1.74E-03		-9.70E-02	6.97E-01		5.27E-01	1.72E-03		-8.57E-01	2.85E-14		-1.29E+00	5.96E-28	Down	Unigene28229_All//gi|192913018|gb|ACF06617.1|//3.00E-37//40S ribosomal protein S8 [Elaeis guineensis]	Unigene28229_All//4.00E-30//AT5G20290| 40S ribosomal protein S8 (RPS8A)	Unigene28229_All//0.00E+00//gi|164248980|gb|ES797915.1|ES797915		ko03010|Ribosome		nr -
Unigene28231_All	755	0.69	0.00	0.14	2.64	2.60	3.95	2.97	0.44	2.27	-9.44E+00	2.93E-03		-2.30E+00	6.76E-02		-2.18E-02	9.48E-01		5.81E-01	1.23E-01		-2.74E+00	8.38E-09	Down	-3.87E-01	3.12E-01		Unigene28231_All//gi|116047943|gb|ABJ53197.1|//1.00E-111//myosin XI-2 [Nicotiana benthamiana]	Unigene28231_All//1.00E-108//AT5G43900| MYA2 (ARABIDOPSIS MYOSIN 2); GTP-dependent protein binding / Rab GTPase binding / motor	Unigene28231_All//0.00E+00//DT463172				nr +
Unigene28233_All	728	0.00	2.30	0.88	1.03	0.76	1.30	1.68	0.86	6.79	1.12E+01	1.54E-09	Up	9.78E+00	1.16E-03		-4.40E-01	5.85E-01		3.44E-01	6.49E-01		-9.68E-01	7.84E-02		2.01E+00	2.33E-13	Up			Unigene28233_All//0.00E+00//CO090130				
Unigene28234_All	490	2.67	6.51	2.50	3.15	2.67	2.03	0.52	1.02	1.06	1.29E+00	3.45E-04	Up	-9.49E-02	8.72E-01		-2.39E-01	6.59E-01		-6.36E-01	2.47E-01		9.84E-01	3.11E-01		1.03E+00	2.53E-01		Unigene28234_All//gi|225429774|ref|XP_002280589.1|//2.00E-144//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene28235_All	534	1.86	3.23	0.60	0.65	3.03	0.42	4.04	6.97	8.28	7.93E-01	1.14E-01		-1.64E+00	3.43E-02		2.21E+00	1.12E-04	Up	-6.27E-01	6.21E-01		7.87E-01	5.55E-03		1.04E+00	4.63E-05	Up			Unigene28235_All//2.00E-102//DW505396				
Unigene28236_All	790	0.73	0.19	0.27	2.33	0.65	1.89	1.71	1.38	0.40	-1.92E+00	7.01E-02		-1.43E+00	1.76E-01		-1.84E+00	1.14E-04	Down	-3.07E-01	5.67E-01		-3.16E-01	5.76E-01		-2.09E+00	1.85E-04	Down			Unigene28236_All//0.00E+00//CO098208				
Unigene28237_All	1620	1.91	0.19	0.56	13.47	7.21	3.51	1.02	0.67	0.27	-3.34E+00	1.01E-11	Down	-1.77E+00	1.05E-05	Down	-9.02E-01	1.24E-16		-1.94E+00	7.89E-47	Down	-6.02E-01	2.00E-01		-1.91E+00	8.63E-05	Down	Unigene28237_All//gi|145323770|ref|NP_001077474.1|//1.00E-102//ATP-dependent Clp protease ClpB protein-related [Arabidopsis thaliana]	Unigene28237_All//3.00E-84//AT1G07200| ATP-dependent Clp protease ClpB protein-related	Unigene28237_All//0.00E+00//ES801276				nr -
Unigene28238_All	329	14.47	12.01	5.02	13.63	12.66	17.30	71.07	39.13	26.03	-2.69E-01	3.66E-01		-1.53E+00	5.52E-07	Down	-1.06E-01	7.66E-01		3.44E-01	2.02E-01		-8.61E-01	9.92E-17		-1.45E+00	1.05E-38	Down	Unigene28238_All//gi|76161014|gb|AB440470.1|//2.00E-15//ribosomal protein S6-like protein [Solanum tuberosum]	Unigene28238_All//6.00E-14//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome	Unigene28238_All//4.00E-158//gi|72268831|gb|DT046902.1|DT046902		ko03010|Ribosome		nr -
Unigene28239_All	307	7.67	17.66	7.98	8.60	8.52	9.86	52.47	57.59	40.49	1.20E+00	5.65E-06	Up	5.71E-02	8.94E-01		-1.27E-02	9.66E-01		1.97E-01	6.19E-01		1.34E-01	3.29E-01		-3.74E-01	2.05E-03		Unigene28239_All//gi|115486533|ref|NP_001068410.1|//1.00E-09//Os11g0661400 [Oryza sativa Japonica Group] >gi|113645632|dbj|BAF28773.1| Os11g0661400 [Oryza sativa Japonica Group]	Unigene28239_All//4.00E-10//AT4G02480| AAA-type ATPase family protein	Unigene28239_All//2.00E-153//TC171734				nr +
Unigene2824_All	2869	1.73	0.79	0.67	5.21	6.39	4.22	2.89	1.57	1.49	-1.12E+00	4.35E-05	Down	-1.37E+00	2.65E-06	Down	2.94E-01	2.34E-02		-3.04E-01	4.24E-02		-8.77E-01	1.26E-06		-9.59E-01	7.61E-08		Unigene2824_All//gi|297816576|ref|XP_002876171.1|//0.00E+00//kcbp-interacting protein kinase [Arabidopsis lyrata subsp. lyrata] >gi|297322009|gb|EFH52430.1| kcbp-interacting protein kinase [Arabidopsis lyrata subsp. lyrata]	Unigene2824_All//0.00E+00//AT3G5280 90| KIPK (KCBP-interacting protein kinase); kinase/ protein binding / protein kinase	Unigene2824_All//0.00E+00//TC155939			GO:0004672//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene28240_All	306	63.43	22.35	30.45	95.23	82.49	116.60	161.25	129.21	105.98	-1.50E+00	4.11E-27	Down	-1.06E+00	2.66E-15	Down	-2.07E-01	4.24E-02		2.92E-01	1.15E-03		-3.20E-01	2.07E-06		-6.06E-01	1.57E-19		Unigene28240_All//gi|1710587|sp|P50346.1|RL40_SOYBN//2.00E-45//RecName: Full=60S acidic ribosomal protein P0 >gi|11968897|gb|AAB63814.1| acidic ribosomal protein P0 [Glycine max]	Unigene28240_All//4.00E-46//AT3G09200| 60S acidic ribosomal protein P0 (RPP0B)	Unigene28240_All//3.00E-165//TC158189		ko03010|Ribosome		nr -
Unigene28241_All	1454	0.61	0.38	0.37	6.34	7.18	7.11	3.98	0.26	1.32	-6.74E-01	3.69E-01		-7.40E-01	3.47E-01		1.79E-01	3.84E-01		1.66E-01	4.25E-01		-3.94E+00	5.69E-30	Down	-1.60E+00	1.05E-11	Down	Unigene28241_All//gi|5903103|gb|AAD55661.1|AC008017_34//1.00E-161//Hypothetical protein [Arabidopsis thaliana]	Unigene28241_All//3.00E-164//AT1G73140| unknown protein					nr -
Unigene28242_All	2607	0.44	0.21	0.16	1.01	0.94	0.81	2.95	0.27	6.28	-1.05E+00	1.01E-01		-1.43E+00	3.87E-02		-1.11E-01	8.17E-01		-3.15E-01	4.65E-01		-3.44E+00	1.59E-35	Down	1.09E+00	1.06E-17	Up	Unigene28242_All//gi|221441857|ref|XP_002324278.1|//0.00E+00//anion exchanger family protein [Populus trichocarpa] >gi|222865712|gb|EEF02843.1| anion exchanger family protein [Populus trichocarpa]	Unigene28242_All//0.00E+00//AT1G15460| BOR4 (REQUIRES HIGH BORON 4); anion exchanger	Unigene28242_All//0.00E+00//gi|13355573|gb|BG445921.1|BG445921				nr +
Unigene28245_All	485	1.29	4.81	2.09	2.05	3.83	3.45	4.88	2.84	0.90	1.89E+00	4.41E-05	Up	6.88E-01	3.42E-01		9.00E-01	6.06E-02		7.46E-01	1.57E-01		-7.80E-01	3.51E-02		-2.43E+00	1.60E-08	Down	Unigene28245_All//gi|297599090|ref|NP_001046657.2|//2.00E-38//Os02g0313500 [Oryza sativa Japonica Group] >gi|255670833|dbj|BAF08571.2| Os02g0313500 [Oryza sativa Japonica Group]	Unigene28245_All//2.00E-38//AT1G66590| cox19 family protein	Unigene28245_All//0.00E+00//TC170452				nr -
Unigene28248_All	624	67.50	20.79	35.50	2.24	4.36	1.59	2.57	0.00	1.02	-1.70E+00	4.02E-69	Down	-9.27E-01	3.09E-26		9.64E-01	1.02E-02		-4.89E-01	4.09E-01		-1.13E+01	2.16E-11	Down	-1.33E+00	3.75E-03		Unigene28248_All//gi|18404030|ref|NP_565833.1|//3.00E-29//OFP15 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 15) [Arabidopsis thaliana] >gi|4510364|gb|AAD21452.1| expressed protein [Arabidopsis thaliana] >gi|19942265|gb|AAK73267.1| Unknown protein [Arabidopsis thaliana]	Unigene28248_All//6.00E-27//AT5G04820| OFP13 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 13)	Unigene28248_All//8.00E-158//DW504876				nr +
Unigene28249_All	331	44.26	44.39	40.70	25.13	39.12	60.45	22.48	24.37	20.94	4.40E-03	9.84E-01		-1.21E-01	4.76E-01		6.38E-01	1.45E-05		1.27E+00	6.02E-23	Up	1.16E-01	6.12E-01		-1.02E-01	6.26E-01		Unigene28249_All//gi|30524687|emb|CAC85245.1|//3.00E-26//salt tolerance protein 4 [Beta vulgaris]	Unigene28249_All//9.00E-15//AT1G51510| Y14; RNA binding / protein binding	Unigene28249_All//7.00E-166//gi|5047786|gb|AT728934.1|AT728934		ko03040|Spliceosome		nr +
Unigene2825_All	1578	7.63	16.28	6.82	10.04	7.90	11.71	9.65	12.02	11.03	1.09E+00	6.37E-22	Up	-1.62E-01	3.86E-01		-3.46E-01	1.09E-02		2.22E-01	1.14E-01		3.18E-01	5.87E-03		1.94E-01	1.16E-01		Unigene2825_All//gi|297836026|ref|XP_002885895.1|//1.00E-158//PHP domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331735|gb|EFH62154.1| PHP domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2825_All//7.00E-136//AT2G13840| PHP domain-containing protein	Unigene2825_All//0.00E+00//TC143416			GO:0003676//GO:0006259//GO:0034061	nr +
Unigene28253_All	382	5.34	5.57	1.53	9.13	10.10	15.84	8.74	10.72	6.88	6.06E-02	8.97E-01		-1.80E+00	4.36E-04	Down	1.45E-01	7.00E-01		7.95E-01	8.34E-01		2.94E-01	3.15E-01		-3.45E-01	2.55E-01				Unigene28253_All//1.00E-155//DW502797				
Unigene28254_All	454	11.41	41.52	5.40	10.09	17.90	11.64	18.63	24.95	35.36	1.86E+00	3.02E-35	Up	-1.08E+00	1.02E-04	Down	8.26E-01	1.83E-05		2.05E-01	4.92E-01		4.22E-01	5.57E-03		9.25E-01	1.76E-13		Unigene28254_All//gi|224111470|ref|XP_002315866.1|//7.00E-06//predicted protein [Populus trichocarpa] >gi|222864906|gb|EEF02037.1| predicted protein [Populus trichocarpa]		Unigene28254_All//3.00E-101//TC174060				nr +
Unigene28259_All	768	1.77	1.12	2.50	0.84	1.61	0.88	0.22	0.16	1.35	-6.59E-01	2.44E-01		4.95E-01	3.22E-01		9.37E-01	1.36E-01		6.51E-02	9.50E-01		-4.31E-01	7.93E-01		2.61E+00	2.37E-04	Up	Unigene28259_All//gi|72384490|gb|AAZ67606.1|//2.00E-43//80A08_21 [Brassica rapa subsp. pekinensis]	Unigene28259_All//1.00E-44//AT5G10250| DOT3 (DEFECTIVELY ORGANIZED TRIBUTARIES 3); protein binding / signal transducer					nr -
Unigene28260_All	396	26.29	34.29	26.09	19.88	21.04	29.99	63.85	55.20	28.77	3.83E-01	1.33E-02		-1.13E-02	9.75E-01		8.24E-02	7.61E-01		5.94E-01	2.36E-04		-2.10E-01	4.06E-02		-1.15E+00	1.94E-29	Down			Unigene28260_All//0.00E+00//TC161174				

Unigene28264_All	381	1.10	6.12	2.52	4.31	3.98	4.62	1.44	2.30	1.05	2.48E+00	9.11E-07	Up	1.20E+00	1.15E-01		-1.18E-01	8.13E-01		9.96E-02	8.61E-01		6.75E-01	3.28E-01		-4.64E-01	5.97E-01				Unigene28264_All//2.00E-120//DW512033				
Unigene28265_All	1972	0.19	0.59	0.38	0.71	0.16	0.07	3.79	4.11	4.89	1.67E+00	1.33E-02		1.03E+00	2.37E-01		-2.17E+00	1.92E-04	Down	-3.36E+00	5.87E-06	Down	1.16E-01	6.13E-01		3.65E-01	2.50E-02		Unigene28265_All//gi|212552160|gb|AC331801.1|//2.00E-90//receptor-like protein kinase [Glycine max]	Unigene28265_All//2.00E-76//AT4G05200| protein kinase family protein	Unigene28265_All//7.00E-127//ES842258		ko04626|Plant-pathogen interaction		nr +
Unigene28267_All	389	30.13	15.11	26.97	18.57	19.74	7.31	2.17	1.93	0.72	-9.96E-01	4.42E-09		-1.60E-01	3.82E-01		8.83E-02	7.51E-01		-1.34E+00	1.43E-09	Down	-1.69E-01	7.99E-01		-1.60E+00	2.02E-02		Unigene28267_All//gi|224135335|ref|XP_002322044.1|//3.00E-18//f-box family protein [Populus trichocarpa] >gi|222869040|gb|EEF06171.1| f-box family protein [Populus trichocarpa]	Unigene28267_All//3.00E-09//AT5G60850| OBP4; DNA binding / transcription factor	Unigene28267_All//3.00E-122//TC161129	C2C2-Dof			nr +
Unigene2827_All	1610	0.59	9.88	2.48	1.21	1.65	1.82	6.70	31.10	7.82	4.08E+00	1.16E-67	Up	2.08E+00	8.37E-09	Up	4.49E-01	2.82E-01		5.96E-01	1.16E-01		2.22E+00	3.19E-142	Up	2.24E-01	1.28E-01		Unigene2827_All//gi|18650616|gb|AAL75907.1|//1.00E-119//AT4g03420/F9H3_4 [Arabidopsis thaliana] >gi|20453247|gb|AAM19862.1|AT4g03420/F9H3_4 [Arabidopsis thaliana]	Unigene2827_All//2.00E-115//AT4G03420| unknown protein	Unigene2827_All//5.00E-124//TC143805				nr -
Unigene28271_All	1249	1486.68	993.39	1629.05	68.24	78.85	49.25	82.06	88.54	40.16	-5.82E-01	0.00E+00		1.32E-01	1.01E-33		2.09E-01	2.41E-05		-4.71E-01	4.04E-18		1.10E-01	2.01E-02		-1.03E+00	8.58E-98	Down	Unigene28271_All//gi|231688|sp|P30567.1|CATA2_GOSHI//0.00E+00//RecName: Full=Catalase isozyme 2 >gi|184888|emb|CAA39998.1| subunit 2 of cotton catalase [Gossypium hirsutum]	Unigene28271_All//0.00E+00//AT4G35090| CAT2 (CATALASE 2); catalase	Unigene28271_All//0.00E+00//TC131978		ko04146|Peroxisome//ko00380|Tryptophan metabolism		nr +
Unigene28274_All	2060	0.20	0.10	0.16	0.19	0.00	1.29	52.71	14.16	61.63	-1.05E+00	3.66E-01		-3.90E-01	7.17E-01		-7.60E+00	4.38E-03		2.74E+00	8.11E-09	Up	-1.90E+00	4.01E-252	Down	2.26E-01	1.72E-08		Unigene28274_All//gi|115464983|ref|NP_001656091.1|//3.00E-70//Os05g0524500 [Oryza sativa Japonica Group] >gi|113579642|dbj|BAF18005.1|Os05g0524500 [Oryza sativa Japonica Group]	Unigene28274_All//3.00E-64//AT1G05700| leucine-rich repeat protein kinase, putative			ko04626|Plant-pathogen interaction		nr +
Unigene28275_All	715	1.39	2.41	0.15	2.79	5.11	3.03	1.42	0.12	1.45	7.93E-01	1.14E-01		-3.22E+00	7.83E-04	Down	8.73E-01	5.22E-03		1.22E-01	7.88E-01		-3.60E+00	2.38E-05	Down	2.97E-02	9.69E-01		Unigene28275_All//gi|115452307|ref|NP_001049754.1|//8.00E-20//Os03g0283400 [Oryza sativa Japonica Group] >gi|108707536|gb|ABF95331.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548225|dbj|BAF11668.1|Os03g0283400 [Oryza sativa Japonica Group]		Unigene28275_All//0.00E+00//CO112898				nr +
Unigene28277_All	628	7.08	7.50	7.80	6.50	5.32	6.11	10.84	5.19	4.82	8.35E-02	7.66E-01		1.40E-01	6.17E-01		-2.90E-01	3.69E-01		-8.96E-02	7.83E-01		-1.06E+00	2.21E-07	Down	-1.17E+00	8.92E-09	Down			Unigene28277_All//6.00E-103//gi|48828920|gb|CO127310.1|CO127310				
Unigene28279_All	1938	17.25	14.20	14.76	21.59	29.09	15.15	3.10	0.30	1.07	-2.81E-01	2.94E-03		-2.26E-01	2.53E-02		4.30E-01	2.70E-11		-5.11E-01	1.27E-10		-3.36E+00	2.72E-27	Down	-1.54E+00	1.87E-11	Down	Unigene28279_All//gi|14667837|gb|AB042350.1|//1.00E-116//trihelix transcription factor [Glycine max]	Unigene28279_All//1.00E-102//AT5G28300| trihelix DNA-binding protein, putative	Unigene28279_All//0.00E+00//TC147740	Trihelix	ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene2828_All	2117	31.29	152.13	35.44	8.85	10.33	17.92	0.36	0.53	0.23	2.28E+00	0.00E+00	Up	1.80E-01	5.55E-03		2.23E-01	6.83E-02		1.02E+00	1.52E-30	Up	5.68E-01	3.44E-01		-6.71E-01	3.42E-01		Unigene2828_All//gi|30696940|ref|NP_200588.2|//0.00E+00//CER3 (ECERIFERUM 3); binding / catalytic/ iron ion binding / oxidoreductase [Arabidopsis thaliana] >gi|75151993|sp|Q8H1Z0.1|WAX2_ARATH RecName: Full=Protein WAX2; AltName: Full=Protein YORE-YORE; AltName: Full=Protein FACELESS POLLEN 1 >gi|22900949|gb|AAN06975.1|cuticle protein [Arabidopsis thaliana] >gi|37051339|dbj|BAC81644.1| YORE-YORE protein [Arabidopsis thaliana] >gi|40714041|dbj|BAD06945.1|faceless pollen-1 [Arabidopsis thaliana]	Unigene2828_All//0.00E+00//AT5G57800| CER3 (ECERIFERUM 3); binding / catalytic/ iron ion binding / oxidoreductase	Unigene2828_All//0.00E+00//TC139747			GO:0003006//GO:0003824//GO:0006633//GO:0007275//GO:0031224//GO:0043231//GO:0046914	nr -
Unigene28280_All	472	17.51	142.78	39.94	40.21	23.20	48.32	86.35	206.15	238.69	3.03E+00	3.23E-221	Up	1.19E+00	7.45E-18	Up	-7.93E-01	9.91E-12		2.65E-01	2.60E-02		1.26E+00	1.62E-123	Up	1.47E+00	5.83E-185	Up	Unigene28280_All//gi|297825155|ref|XP_002880460.1|//4.00E-36//homeobox-leucine zipper protein 9 [Arabidopsis lyrata subsp. lyrata] >gi|297326299|gb|EFH56719.1|homeobox-leucine zipper protein 9 [Arabidopsis lyrata subsp. lyrata]	Unigene28280_All//8.00E-13//AT4G37790| HAT22; transcription factor	Unigene28280_All//0.00E+00//DR453682	HB			nr +
Unigene28281_All	402	61.17	28.86	29.54	102.60	91.83	101.22	52.80	24.95	15.66	-1.08E+00	8.69E-21	Down	-1.05E+00	5.51E-19	Down	-1.60E-01	6.64E-02		-1.95E-02	8.60E-01		-1.08E+00	6.44E-22	Down	-1.75E+00	3.37E-46	Down	Unigene28281_All//gi|12585316|sp|Q9M4G4.1|PGMC_SOLTU//9.00E-23//RecName: Full=Phosphoglucomutase, cytoplasmic; Short=PGM; AltName: Full=Glucose phosphomutase >gi|8250624|emb|CAB93681.1|cytosolic phosphoglucomutase [Solanum tuberosum]	Unigene28281_All//2.00E-23//AT1G70730| phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative	Unigene28281_All//0.00E+00//gi|21102309|gb|BQ414622.1|BQ414622		ko00500|Starch and sucrose metabolism//ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene28286_All	1046	0.35	0.24	0.66	1.24	4.64	1.30	1.78	1.64	3.58	-5.32E-01	6.27E-01		9.19E-01	3.11E-01		1.91E+00	4.62E-11	Up	6.50E-02	9.33E-01		-1.19E-01	7.87E-01		1.01E+00	2.86E-04	Up	Unigene28286_All//gi|60327196|gb|AAX19021.1|//3.00E-52//Cf-2.3 [Solanum pimpinellifolium]	Unigene28286_All//5.00E-45//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative	Unigene28286_All//1.00E-31//ES834884		ko04626|Plant-pathogen interaction		nr +
Unigene28287_All	553	150.53	48.84	66.83	585.34	498.41	354.53	49.24	39.83	34.58	-1.62E+00	1.50E-127	Down	-1.17E+00	3.21E-75	Down	-2.32E-01	3.44E-20		-7.23E-01	2.01E-145		-3.06E-01	1.15E-03		-5.10E-01	1.93E-08		Unigene28287_All//gi|10945615|gb|AG24616.1|AF298594_1//5.00E-40//arabinogalactan protein [Nicotiana alata]		Unigene28287_All//0.00E+00//TC145216		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene28288_All	431	0.49	6.35	0.25	9.02	7.59	4.40	9.91	6.69	12.94	3.71E+00	3.29E-11	Up	-9.75E-01	6.21E-01		-2.48E-01	4.64E-01		-1.03E+00	7.71E-04	Down	-5.66E-01	3.20E-02		3.85E-01	8.48E-02		Unigene28288_All//gi|300157045|gb|EFJ23672.1|//5.00E-18//ubiquitin-conjugating enzyme 5, E2 [Selaginella moellendorffii] >gi|300167774|gb|EFJ34378.1|ubiquitin-conjugating enzyme 5, E2 [Selaginella moellendorffii]	Unigene28288_All//1.00E-07//AT2G46030| UBC6 (ubiquitin-conjugating enzyme 6); ubiquitin-protein ligase	Unigene28288_All//0.00E+00//TC161092		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene2829_All	1568	95.67	34.12	69.55	25.26	32.83	26.21	2.75	1.68	1.40	-1.49E+00	9.99E-202	Down	-4.60E-01	4.67E-27		3.78E-01	2.73E-08		5.35E-02	6.39E-01		-7.12E-01	6.18E-03		-9.77E-01	1.29E-04		Unigene2829_All//gi|3335350|gb|AAC27152.1|//1.00E-164//Similar to gb|284386 anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus [Arabidopsis thaliana]	Unigene2829_All//7.00E-104//AT1G65450| transferase family protein	Unigene2829_All//0.00E+00//TC141124		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016746	nr +
Unigene28291_All	586	17.41	15.30	15.08	17.26	14.46	9.02	2.45	3.78	0.68	-1.86E-01	3.47E-01		-2.07E-01	3.09E-01		-2.56E-01	1.76E-01		-9.36E-01	1.24E-07		6.24E-01	1.10E-01		-1.85E+00	3.87E-04	Down	Unigene28291_All//gi|79470575|ref|NP_192968.3|//1.00E-07//CYP706A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|5281042|emb|CAB45978.1|flavonoid 3', 5'-hydroxylase-like protein [Arabidopsis thaliana] >gi|7267932|emb|CAB78274.1|flavonoid 3', 5'-hydroxylase-like protein [Arabidopsis thaliana] >gi|45773944|gb|AAS76776.1|At4g12310 [Arabidopsis thaliana] >gi|110741730|dbj|BAE98811.1|flavonoid 3',5'-hydroxylase -like protein [Arabidopsis thaliana]		Unigene28291_All//0.00E+00//TC163775				nr +
Unigene28292_All	404	21.37	15.93	25.57	40.57	47.31	44.83	47.72	26.48	21.99	-4.24E-01	3.33E-02		2.59E-01	1.88E-01		2.22E-01	9.61E-02		1.44E-01	3.51E-01		-8.50E-01	1.21E-13		-1.12E+00	1.08E-21	Down			Unigene28292_All//0.00E+00//EV497569				
Unigene28293_All	1616	2.27	3.23	1.35	0.31	0.15	0.25	4.84	5.41	1.23	5.11E-01	5.28E-02		-7.46E-01	2.61E-02		-1.05E+00	3.15E-01		-2.94E-01	7.57E-01		1.59E-01	4.22E-01		-1.97E+00	1.80E-20	Down	Unigene28293_All//gi|260177086|gb|ACX33886.1|//1.00E-148//flavin monooxygenase-like protein [Solanum lycopersicum var. cerasiforme]	Unigene28293_All//3.00E-147//AT5G25620| YUC6 (YUCCA6); FAD binding / NADP or NADPH binding / flavin-containing monooxygenase/ monooxygenase/ oxidoreductase	Unigene28293_All//1.00E-137//ES848043		ko00380|Tryptophan metabolism		nr -
Unigene28294_All	1254	21.61	14.83	20.81	9.06	14.22	8.54	1.31	0.03	0.13	-5.43E-01	1.73E-07		-5.48E-02	6.42E-01		6.51E-01	1.01E-07		-8.55E-02	6.80E-01		-5.30E+00	2.16E-10	Down	-3.37E+00	2.89E-08	Down	Unigene28294_All//gi|75185987|sp|Q9M7N6.1|MAF1_SOLLC//1.00E-28//RecName: Full=MFP1 attachment factor 1 >gi|7546725|gb|AAF63657.1|AF118113_1 MFP1 attachment factor 1 [Solanum lycopersicum]	Unigene28294_All//3.00E-26//AT1G47200| WPP2	Unigene28294_All//0.00E+00//gi|13353799|gb|BG444147.1|BG444147				nr +
Unigene28295_All	1825	0.46	0.11	0.12	0.79	2.87	0.72	9.13	12.69	190.55	-2.05E+00	1.68E-02		-1.97E+00	2.71E-02		1.86E+00	1.65E-11	Up	-1.41E-01	7.93E-01		4.75E-01	2.62E-06		4.38E+00	0.00E+00	Up	Unigene28295_All//gi|297821122|ref|XP_002878444.1|//1.00E-132//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324282|gb|EFH54703.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28295_All//2.00E-124//AT3G62240| zinc finger (C2H2 type) family protein	Unigene28295_All//2.00E-102//gi|78345390|gb|DT565664.1|DT565664	C2H2			nr +
Unigene28296_All	2216	0.19	0.09	0.00	0.27	0.95	0.37	0.97	1.74	31.51	-1.05E+00	3.66E-01		-7.56E+00	1.56E-02		1.81E+00	9.78E-05	Up	4.44E-01	6.21E-01		8.34E-01	2.72E-03		5.02E+00	0.00E+00	Up	Unigene28296_All//gi|297821122|ref|XP_002878444.1|//1.00E-120//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324282|gb|EFH54703.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28296_All//9.00E-121//AT3G62240| zinc finger (C2H2 type) family protein	Unigene28296_All//7.00E-121//gi|78345390|gb|DT565664.1|DT565664	C2H2			nr +
Unigene28299_All	250	25.32	69.92	33.02	26.30	33.06	77.32	28.75	38.95	26.77	1.47E+00	1.91E-23	Up	3.83E-01	7.74E-02		3.30E-01	1.15E-01		1.56E+00	4.58E-30	Up	4.38E-01	8.12E-03		-1.03E-01	6.31E-01		Unigene28299_All//gi|227204473|dbj|BAH57088.1|//5.00E-34//AT2G25280 [Arabidopsis thaliana]	Unigene28299_All//2.00E-35//AT2G25280| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Mediator of ErbB2-driven cell motility (Memo), related (InterPro:IPR002737); Has 742 Blast hits to 742 proteins in 323 species: Archae - 138; Bacteria - 240; Metazoa - 132; Fungi - 82; Plants - 26; Viruses - 0; Other Eukaryotes - 124 (source: NCBI BLink).	Unigene28299_All//9.00E-137//gi|21101399|gb|BQ413712.1|BQ413712				nr +

Unigene283_All	903	0.35	0.51	1.42	3.42	4.23	2.60	6.88	3.24	2.47	5.39E-01	6.02E-01		2.03E+00	3.44E-03		3.08E-01	3.79E-01		-3.95E-01	3.04E-01		-1.09E+00	4.87E-07	Down	-1.48E+00	3.12E-11	Down	Unigene283_All//gi|145331437|ref|NP_001078077.1|//5.00E-60//zinc finger (CCCH-type) family protein [Arabidopsis thaliana]	Unigene283_All//9.00E-46//AT2G47850| zinc finger (CCCH-type) family protein	Unigene283_All//0.00E+00//TC141469	C3H	ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene2830_All	1999	4.34	11.66	4.34	8.12	8.39	8.20	17.64	31.43	19.13	1.42E+00	9.29E-30	Up	-9.00E-04	9.96E-01		4.64E-02	8.16E-01		1.37E-02	9.49E-01		8.33E-01	3.48E-41		1.17E-01	1.62E-01		Unigene2830_All//gi|115478350|ref|NP_001062770.1|//1.00E-95//0s09g0281800 [Oryza sativa Japonica Group] >gi|113631003|dbj|BAF24684.1|Os09g0281800 [Oryza sativa Japonica Group]	Unigene2830_All//1.00E-157//AT4G12070| unknown protein	Unigene2830_All//0.00E+00//TC168405				nr +
Unigene28300_All	858	0.98	1.36	0.00	3.02	1.65	0.84	1.97	1.46	0.88	4.77E-01	4.39E-01		-9.93E+00	1.19E-04	Down	-8.76E-01	1.86E-02		-1.84E+00	1.09E-05	Down	-4.32E-01	3.70E-01		-1.16E+00	8.24E-03		Unigene28300_All//gi|224138410|ref|XP_002322807.1|//3.00E-65//nitrilase 3 [Populus trichocarpa] >gi|222867437|gb|EEF04568.1|nitrilase 3 [Populus trichocarpa]	Unigene28300_All//3.00E-48//AT3G44300| NIT2 (nitrilase 2); indole-3-acetonitrile nitrilase/ indole-3-acetonitrile nitrile hydratase/ nitrilase	Unigene28300_All//4.00E-123//gi|78334257|gb|DT554531.1|DT554531		ko00380|Tryptophan metabolism//ko00910|Nitrogen metabolism//ko00460|Cyanoamino acid metabolism		nr -
Unigene28303_All	1461	0.32	1.39	0.58	0.17	0.31	0.96	4.17	5.66	7.31	2.11E+00	4.59E-05	Up	8.56E-01	2.80E-01		8.46E-01	5.14E-01		2.49E+00	1.86E-04	Up	4.43E-01	1.49E-02		8.10E-01	1.39E-07		Unigene28303_All//gi|224140975|ref|XP_002323852.1|//1.00E-114//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222866854|gb|EEF03985.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene28303_All//3.00E-84//AT1G26870| FEZ (FEZ); transcription factor	Unigene28303_All//1.00E-07//C0124002	NAC			nr +
Unigene28304_All	286	2.38	3.19	2.79	2.96	2.05	2.53	18.04	7.45	6.96	4.23E-01	5.64E-01		2.32E-01	7.49E-01		-5.33E-01	4.90E-01		-2.29E-01	7.51E-01		-1.27E+00	1.83E-07	Down	-1.37E+00	1.46E-08	Down			Unigene28304_All//1.00E-62//gi|164264591|gb|ES851944.1|ES851944				
Unigene28305_All	441	2.14	1.38	1.21	22.59	16.40	16.49	33.36	12.13	17.62	-6.31E-01	3.66E-01		-8.23E-01	2.71E-01		-4.62E-01	7.58E-03		-4.54E-01	1.25E-02		-1.46E+00	3.46E-24	Down	-9.21E-01	1.95E-12		Unigene28305_All//gi|297842739|ref|XP_002889251.1|//1.00E-22//GAPCP-1 [Arabidopsis lyrata subsp. lyrata] >gi|297335092|gb|EFH65510.1|GAPCP-1 [Arabidopsis lyrata subsp. lyrata]	Unigene28305_All//2.00E-16//AT1G79530| GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene28305_All//0.00E+00//TC130847		ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene28307_All	1018	0.82	3.73	1.99	6.26	5.07	4.92	12.96	8.54	7.01	2.18E+00	3.13E-09	Up	1.27E+00	8.67E-03		-3.04E-01	2.16E-01		-3.47E-01	1.62E-01		-6.02E-01	1.28E-05		-8.87E-01	1.32E-10		Unigene28307_All//gi|297841421|ref|XP_002888592.1|//8.00E-61//rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334433|gb|EFH64851.1|rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28307_All//9.00E-59//AT1G67360| rubber elongation factor (REF) family protein	Unigene28307_All//0.00E+00//TC162268				nr -
Unigene28308_All	264	11.69	13.63	17.35	23.21	16.70	32.33	72.55	36.10	23.09	2.21E-01	5.23E-01		5.69E-01	5.48E-02		-4.75E-01	4.11E-02		4.78E-01	1.67E-02		-1.01E+00	9.08E-18	Down	-1.65E+00	1.90E-38	Down			Unigene28308_All//2.00E-135//TC174141				
Unigene2831_All	1680	10.78	36.13	20.82	9.87	7.28	10.38	11.93	25.28	11.31	1.75E+00	1.49E-102	Up	9.51E-01	7.68E-23		-4.40E-01	5.78E-04		7.17E-02	6.67E-01		1.08E+00	4.13E-43	Up	-7.67E-02	5.58E-01		Unigene2831_All//gi|16648766|gb|AAL25574.1|//1.00E-166//AT5g47860/MCA23_20 [Arabidopsis thaliana] >gi|22655374|gb|AAM98279.1|At5g47860/MCA23_20 [Arabidopsis thaliana]	Unigene2831_All//1.00E-167//AT5G47860| unknown protein	Unigene2831_All//0.00E+00//TC147669				nr +
Unigene28310_All	438	44.68	34.59	20.30	87.00	78.93	73.31	104.83	57.35	50.12	-3.69E-01	3.33E-03		-1.14E+00	2.98E-17	Down	-1.40E-01	1.36E-01		-2.47E-01	5.01E-03		-8.70E-01	1.24E-32		-1.06E+00	1.18E-46	Down			Unigene28310_All//0.00E+00//TC129604				
Unigene28311_All	672	129.95	142.06	118.15	116.83	61.85	280.93	13.46	28.67	10.43	1.29E-01	2.25E-02		-1.37E-01	2.54E-02		-9.18E-01	1.19E-60		1.27E+00	8.45E-213	Up	1.09E+00	3.29E-20	Up	-3.68E-01	2.92E-02		Unigene28311_All//gi|67937775|gb|AA983346.1|//4.00E-32//non-specific lipid transfer protein precursor [Fragaria x ananassa]	Unigene28311_All//1.00E-25//AT5G59310| LTP4 (LIPID TRANSFER PROTEIN 4); lipid binding	Unigene28311_All//0.00E+00//TC149452				nr +
Unigene28312_All	435	6.50	15.38	8.08	10.65	13.06	8.41	20.51	22.48	26.10	1.24E+00	1.62E-07	Up	3.15E-01	3.91E-01		2.95E-01	2.86E-01		-3.41E-01	2.60E-01		1.33E-01	4.94E-01		3.48E-01	1.96E-02		Unigene28312_All//gi|7211773|gb|AAF40430.1|//5.00E-34//protein kinase MK5 [Mesembryanthemum crystallinum]	Unigene28312_All//1.00E-31//AT3G53570| AFC1 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene28312_All//0.00E+00//gi|84166719|gb|DR455367.1|DR455367				nr +
Unigene28314_All	498	132.38	48.13	73.03	169.35	131.31	138.76	145.94	119.85	53.12	-1.46E+00	1.55E-86	Down	-8.58E-01	7.51E-36		-3.67E-01	9.04E-13		-2.88E-01	1.63E-07		-2.84E-01	2.06E-07		-1.46E+00	1.15E-119	Down	Unigene28314_All//gi|211906474|gb|ACJ11730.1|//5.00E-28//glycine-rich RNA-binding protein [Gossypium hirsutum]	Unigene28314_All//2.00E-17//AT2G21660| CCR2 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	Unigene28314_All//0.00E+00//ES805426		ko03040|Spliceosome		nr -
Unigene28315_All	446	14.43	29.31	21.61	28.03	22.70	28.25	49.77	59.04	39.21	1.02E+00	2.08E-10	Up	5.83E-01	2.39E-03		-3.05E-01	5.79E-02		1.12E-02	9.46E-01		2.46E-01	1.19E-02		-3.44E-01	7.30E-04				Unigene28315_All//0.00E+00//gi|11200609|gb|BF269614.1|BF269614				
Unigene28316_All	464	22.78	18.02	21.12	19.97	20.11	15.96	58.04	29.91	23.10	-3.38E-01	6.06E-02		-1.09E-01	6.10E-01		1.03E-02	9.64E-01		-3.23E-01	1.06E-01		-9.57E-01	1.05E-22		-1.33E+00	4.18E-39	Down	Unigene28316_All//gi|296082567|emb|CBI21572.3|//1.00E-17//unnamed protein product [Vitis vinifera]	Unigene28316_All//3.00E-17//AT1G42960| expressed protein localized to the inner membrane of the chloroplast.	Unigene28316_All//0.00E+00//gi|21090702|gb|BQ403015.1|BQ403015				nr +
Unigene2832_All	1699	21.99	12.85	14.01	29.03	28.11	21.45	12.32	5.73	6.10	-7.75E-01	4.58E-18		-6.50E-01	6.34E-13		-4.62E-02	6.19E-01		-4.36E-01	1.98E-09		-1.10E+00	2.51E-22	Down	-1.01E+00	3.59E-20	Down	Unigene2832_All//gi|115471617|ref|NP_001059407.1|//1.00E-146//Os07g0295400 [Oryza sativa Japonica Group] >gi|113610943|dbj|BAF21321.1|Os07g0295400 [Oryza sativa Japonica Group]	Unigene2832_All//9.00E-142//AT1G24310| unknown protein	Unigene2832_All//0.00E+00//TC159042			GO:0043231	nr -
Unigene28320_All	986	4.03	7.50	10.91	3.54	3.74	5.82	0.17	0.38	3.35	8.96E-01	3.57E-05		1.44E+00	9.12E-14	Up	7.95E-02	8.21E-01		7.18E-01	3.56E-03		1.15E+00	3.27E-01		4.29E+00	1.36E-18	Up	Unigene28320_All//gi|18650620|gb|AAL75909.1|//2.00E-82//AT3g50440/T20E23_40 [Arabidopsis thaliana] >gi|22655406|gb|AAM98295.1|At3g50440/T20E23_40 [Arabidopsis thaliana]	Unigene28320_All//2.00E-82//AT3G50440| MES10 (METHYL ESTERASE 10); hydrolase/ hydrolase, acting on ester bonds / methyl jasmonate esterase	Unigene28320_All//0.00E+00//TC167437		ko00901|Indole alkaloid biosynthesis		nr -
Unigene28325_All	450	40.23	102.80	87.09	17.16	46.22	21.78	51.49	121.30	67.99	1.35E+00	3.98E-54	Up	1.11E+00	5.48E-33	Up	1.43E+00	3.40E-31	Up	3.44E-01	7.34E-02		1.24E+00	5.64E-68	Up	4.01E-01	2.50E-06				Unigene28325_All//3.00E-08//TC168329				ESTscan -
Unigene28326_All	359	15.30	8.33	4.60	16.37	10.74	12.83	44.87	15.60	16.09	-8.78E-01	5.77E-04		-1.73E+00	2.10E-09	Down	-6.08E-01	8.62E-03		-3.52E-01	1.79E-01		-1.52E+00	4.17E-28	Down	-1.48E+00	9.03E-28	Down			Unigene28326_All//3.00E-150//TC138329				
Unigene28327_All	772	0.00	1.18	0.14	4.07	2.01	1.40	1.59	1.95	2.68	1.02E+01	2.62E-05	Up	7.11E+00	3.99E-01		-1.02E+00	1.99E-03		-1.53E+00	2.26E-05	Down	2.95E-01	5.82E-01		7.57E-01	5.04E-02		Unigene28327_All//gi|297821461|ref|XP_002876613.1|//1.00E-107//DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324452|gb|EFH54872.1| DNAJ heat shock family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28327_All//3.00E-107//AT2G22360| DNAJ heat shock family protein	Unigene28327_All//0.00E+00//C0131948				nr +
Unigene28331_All	2126	0.42	0.24	0.30	0.94	0.58	0.64	3.28	0.79	4.61	-8.12E-01	2.68E-01		-4.77E-01	5.33E-01		-6.85E-01	1.25E-01		-5.56E-01	2.41E-01		-2.06E+00	9.62E-19	Down	4.90E-01	2.07E-03		Unigene28331_All//gi|30684540|ref|NP_193617.2|//1.00E-127//ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene28331_All//6.00E-72//AT4G18820| ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding	Unigene28331_All//8.00E-130//ES816108				nr +
Unigene28332_All	1671	1.19	0.67	1.50	5.78	1.98	1.78	13.23	5.95	0.88	-8.35E-01	6.77E-02		3.32E-01	4.26E-01		-1.55E+00	1.59E-17	Down	-1.70E+00	1.46E-17	Down	-1.15E+00	3.52E-25	Down	-3.91E+00	4.74E-116	Down	Unigene28332_All//gi|224114037|ref|XP_002332458.1|//1.00E-152//cytochrome P450 [Populus trichocarpa] >gi|222832529|gb|EEE71006.1|cytochrome P450 [Populus trichocarpa]	Unigene28332_All//7.00E-97//AT1G13080| CYP71B2 (CYTOCHROME P450 71B2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene28332_All//1.00E-07//EX169678		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene28333_All	548	94.90	513.07	187.06	90.08	63.40	69.31	261.71	261.91	168.88	2.43E+00	0.00E+00	Up	9.79E-01	2.57E-69		-5.07E-01	1.38E-13		-3.78E-01	2.16E-07		1.10E-03	1.02E+00		-6.32E-01	2.56E-59		Unigene28333_All//gi|91208941|ref|YP_538976.1|//8.00E-79//ribosomal protein L2 [Gossypium hirsutum] >gi|91208966|ref|YP_538999.1|ribosomal protein L2 [Gossypium hirsutum] >gi|118597127|sp|Q2L944.1|RK2_GOSHI RecName: Full=50S ribosomal protein L2, chloroplastic >gi|85687455|gb|ABC73667.1|ribosomal protein L2 [Gossypium hirsutum] >gi|85687480|gb|ABC73692.1|ribosomal protein L2 [Gossypium hirsutum]	Unigene28333_All//8.00E-61//ATCG01310| encodes a chloroplast ribosomal protein L2, a constituent of the large subunit of the ribosomal complex	Unigene28333_All//0.00E+00//TC163622		ko03010|Ribosome		nr +
Unigene28334_All	1300	2.25	0.08	0.98	11.42	3.50	11.05	4.65	0.55	1.50	-4.85E+00	2.57E-14	Down	-1.20E+00	2.12E-03		-1.71E+00	8.02E-31	Down	-4.77E-02	7.78E-01		-3.09E+00	1.84E-25	Down	-1.63E+00	1.66E-12	Down	Unigene28334_All//gi|224131344|ref|XP_002321061.1|//1.00E-107//cytokinin biosynthetic isopentenyltransferase [Populus trichocarpa] >gi|222861834|gb|EEE99376.1|cytokinin biosynthetic isopentenyltransferase [Populus trichocarpa]	Unigene28334_All//1.00E-99//AT3G63110| ATIPT3 (ARABIDOPSIS THALIANA ISOPENTENYLTRANSFERASE 3); ATP binding / tRNA isopentenyltransferase/ transferase, transferring alkyl or aryl (other than methyl) groups	Unigene28334_All//0.00E+00//gi|109891097|gb|DW520060.1|DW520060		ko00908|Zeatin biosynthesis		nr +
Unigene28335_All	382	14.93	5.97	10.87	22.43	19.11	18.33	5.64	1.75	1.88	-1.32E+00	3.88E-07	Down	-4.57E-01	8.40E-02		-2.31E-01	2.87E-01		-2.92E-01	1.72E-01		-1.69E+00	5.26E-05	Down	-1.59E+00	7.54E-05	Down	Unigene28335_All//gi|147790859|emb|CAN61730.1|//2.00E-06//hypothetical protein [Vitis vinifera]		Unigene28335_All//9.00E-135//ES822595				nr -
Unigene28337_All	1076	45.95	21.61	32.27	24.54	25.83	24.68	14.81	8.97	9.33	-1.09E+00	2.49E-41	Down	-5.10E-01	3.79E-11		7.39E-02	5.72E-01		8.40E-03	9.56E-01		-7.23E-01	7.45E-09		-6.67E-01	4.70E-08		Unigene28337_All//gi|297789604|ref|XP_002862749.1|//1.00E-84//myb family transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297308457|gb|EFH39007.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene28337_All//7.00E-59//AT5G45420| myb family transcription factor	Unigene28337_All//0.00E+00//TC143540	MYB-related			nr +
Unigene28339_All	550	2.28	0.83	2.13	6.25	5.70	3.28	5.53	1.90	2.68	-1.46E+00	1.95E-02		-1.00E-01	8.66E-01		-1.33E-01	7.32E-01		-9.28E-01	4.95E-03		-1.54E+00	4.98E-06	Down	-1.05E+00	7.86E-04	Down	Unigene28339_All//gi|18416416|ref|NP_568242.1|//5.00E-23//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene28339_All//3.00E-24//AT5G10940| transducin family protein / WD-40 repeat family protein	Unigene28339_All//0.00E+00//DW481597				nr -
Unigene28344_All	389	26.90	14.07	12.46	40.21	28.33	39.47	150.32	64.90	50.28	-9.35E-01	1.82E-07		-1.11E+00	3.54E-09	Down	-5.05E-01	1.12E-04		-2.66E-02	8.85E-01		-1.21E+00	1.22E-70	Down	-1.58E+00	1.75E-108	Down	Unigene28344_All//gi|7340791|emb|CAA63107.1|//2.00E-16//ribosomal protein L23 [Spinacia oleracea]	Unigene28344_All//3.00E-17//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene28344_All//0.00E+00//TC147207		ko03010|Ribosome		nr -
Unigene28346_All	1137	1.33	0.58	0.61	6.70	2.54	3.57	28.08	9.01	6.80	-1.20E+00	2.75E-02		-1.13E+00	4.79E-02		-1.40E+00	5.53E-12	Down	-9.07E-01	1.20E-05		-1.64E+00	4.73E-61	Down	-2.05E+00	6.20E-85	Down	Unigene28346_All//gi|211906538|gb|ACJ11762.1|//1.00E-172//class III peroxidase [Gossypium hirsutum]	Unigene28346_All//1.00E-100//AT5G05340| peroxidase, putative	Unigene28346_All//0.00E+00//TC155897		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene28348_All	272	65.21	69.48	71.07	56.41	49.75	44.33	70.88	40.87	29.59	9.16E-02	5.31E-01		1.24E-01	3.98E-01		-1.81E-01	2.50E-01		-3.48E-01	1.64E-02		-7.94E-01	3.00E-12		-1.26E+00	4.53E-26	Down	Unigene28348_All//gi|145910320|gb|ABP98813.1|//7.00E-47//chloroplast biotin carboxylase [Gossypium hirsutum]	Unigene28348_All//2.00E-45//AT5G35360| CAC2; acetyl-CoA carboxylase/ biotin carboxylase	Unigene28348_All//3.00E-152//TC129969		ko00280|Valine, leucine and isoleucine degradation		nr -
Unigene28349_All	529	16.22	18.58	19.03	27.03	25.39	17.59	26.69	16.04	6.70	1.96E-01	3.28E-01		2.30E-01	2.49E-01		-9.02E-02	5.96E-01		-6.20E-01	1.72E-05		-7.35E-01	3.87E-08		-1.99E+00	8.83E-37	Down	Unigene28349_All//gi|225470816|ref|XP_002264634.1|//2.00E-18//PREDICTED: similar to Wound-induced basic protein [Vitis vinifera]		Unigene28349_All//7.00E-161//gi|11209680|gb|BF278610.1|BF278610				nr -

Unigene2835_All	2150	11.46	4.38	11.81	3.64	2.77	1.64	0.55	0.10	1.20	-1.39E+00	2.31E-30	Down	4.37E-02	7.20E-01		-3.93E-01	5.65E-02		-1.15E+00	3.22E-08	Down	-2.50E+00	1.47E-04	Down	1.13E+00	1.10E-03		Unigene2835_All//gi|225439540|ref|XP_002264433.1|//0.00E+00//PREDICTED: similar to MATE efflux family protein [Vitis vinifera]	Unigene2835_All//3.00E-140//AT2G38330| MATE efflux family protein	Unigene2835_All//0.00E+00//gi|78346396|gb|DT566670.1|DT566670			GO:0015291//GO:0015893//GO:0044464	nr -
Unigene28351_All	390	12.34	2.21	13.24	36.28	27.99	40.99	17.02	6.00	8.78	-2.48E+00	2.04E-13	Down	1.02E-01	7.14E-01		-3.74E-01	9.36E-03		1.77E-01	2.70E-01		-1.50E+00	8.01E-12	Down	-9.54E-01	2.05E-06		Unigene28351_All//gi|124359308|gb|AB029456.2|//1.00E-32//Ribosomal protein S21e [Medicago truncatula]	Unigene28351_All//1.00E-32//AT5G27700| structural constituent of ribosome	Unigene28351_All//0.00E+00//gi|13245377|gb|BE055806.2|BE055806		ko03010|Ribosome		nr +
Unigene28352_All	398	42.07	21.26	23.55	117.78	72.59	92.26	316.36	329.75	90.39	-9.85E-01	2.05E-12		-8.37E-01	3.46E-09		-6.98E-01	1.02E-22		-3.52E-01	2.90E-06		5.98E-02	2.11E-01		-1.81E+00	8.25E-282	Down	Unigene28352_All//gi|211906506|gb|ACJ11746.1|//8.00E-64//luminal binding protein [Gossypium hirsutum]	Unigene28352_All//4.00E-46//AT5G28540| BIP1; ATP binding	Unigene28352_All//0.00E+00//gi|109826447|gb|DW225161.1|DW225161		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr +
Unigene28355_All	398	2.23	11.71	4.82	0.63	0.43	0.57	0.00	0.00	0.00	2.39E+00	2.24E-12	Up	1.11E+00	2.53E-02		-5.33E-01	7.12E-01		-1.41E-01	9.29E-01		null	null		null	null		Unigene28355_All//gi|213053812|gb|ACJ39211.1|//6.00E-32//inducer of CBF expression 1 [Glycine max]	Unigene28355_All//4.00E-31//AT1G12860| SCRM2 (SCREAM 2); DNA binding / transcription factor	Unigene28355_All//6.00E-65//TC154950	bHLH			nr +
Unigene28357_All	569	8.55	6.95	6.08	17.33	16.82	17.22	84.49	40.40	34.52	-3.00E-01	2.93E-01		-4.91E-01	8.84E-02		-4.31E-02	8.26E-01		-9.20E-03	9.56E-01		-1.06E+00	2.07E-47	Down	-1.29E+00	4.23E-66	Down	Unigene28357_All//gi|82623435|gb|AB887132.1|//5.00E-34//translocon-associated protein beta family protein-like [Solanum tuberosum]	Unigene28357_All//7.00E-28//AT5G14030| translocon-associated protein beta (TRAPB) family protein	Unigene28357_All//0.00E+00//TC145111		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene28359_All	774	3.65	0.65	0.41	3.54	4.76	3.09	2.40	0.16	0.88	-2.48E+00	3.88E-08	Down	-3.14E+00	1.08E-09	Down	4.27E-01	2.06E-01		-1.95E-01	6.39E-01		-3.89E+00	7.06E-10	Down	-1.46E+00	6.77E-04	Down	Unigene28359_All//gi|42564100|ref|NP_187868.2|//1.00E-73//protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|79313205|ref|NP_001030682.1| protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|75273276|sp|Q9LHJ9.1|P2C38_ARATH RecName: Full=Probable protein phosphatase 2C 38; Short=AtPP2C38 >gi|9294356|dbj|BAB02253.1| protein phosphatase 2C [Arabidopsis thaliana] >gi|28466963|gb|AAO44090.1| At3g12620 [Arabidopsis thaliana] >gi|222424096|dbj|BAH20008.1| AT3G12620 [Arabidopsis thaliana] >gi|222424228|dbj|BAH20072.1| AT3G12620 [Arabidopsis thaliana]	Unigene28359_All//1.00E-66//AT3G12620| protein phosphatase 2C family protein / PP2C family protein	Unigene28359_All//0.00E+00//CO127480				nr +
Unigene28360_All	498	3.26	0.41	4.92	5.90	4.91	5.80	1.53	1.18	1.04	-3.00E+00	6.72E-06	Down	5.95E-01	1.60E-01		-2.66E-01	5.14E-01		-2.41E-02	9.54E-01		-3.79E-01	6.35E-01		-5.55E-01	4.23E-01		Unigene28360_All//gi|3377822|gb|AAC28195.1|//2.00E-25//contains similarity to Caenorhabditis elegans MEL-26 (GB:U67737) [Arabidopsis thaliana]	Unigene28360_All//2.00E-08//AT4G08455| BTB/POZ domain-containing protein	Unigene28360_All//4.00E-51//TC137021				nr +
Unigene28361_All	534	32.82	63.67	37.89	89.65	76.22	75.10	122.17	187.14	448.15	9.56E-01	3.37E-23		2.07E-01	1.33E-01		-2.34E-01	1.53E-03		-2.55E-01	8.49E-04		6.15E-01	1.34E-38		1.88E+00	0.00E+00	Up			Unigene28361_All//0.00E+00//gi|21095628|gb|BQ407941.1|BQ407941				
Unigene28362_All	770	1.36	3.82	2.21	2.59	2.28	3.40	1.21	1.14	0.78	1.49E+00	1.12E-04	Up	7.04E-01	1.81E-01		-1.82E-01	7.16E-01		3.95E-01	3.59E-01		-8.37E-02	9.05E-01		-6.38E-01	3.08E-01								
Unigene28363_All	441	1.78	3.79	4.59	1.02	1.64	1.02	3.64	0.38	1.08	1.09E+00	3.43E-02		1.37E+00	5.21E-03		6.90E-01	4.47E-01		1.06E-02	1.00E+00		-3.26E+00	1.49E-07	Down	-1.75E+00	2.96E-04	Down	Unigene28363_All//gi|88010848|gb|ABD38862.1|//8.00E-09//At3g22210 [Arabidopsis thaliana]	Unigene28363_All//2.00E-06//AT3G22210| unknown protein	Unigene28363_All//1.00E-149//gi|164327832|gb|ES824217.1|ES824217				nr -
Unigene28364_All	466	23.69	11.20	17.14	9.19	6.58	5.33	1.00	0.18	0.51	-1.08E+00	1.01E-09	Down	-4.67E-01	9.27E-03		-4.83E-01	9.47E-02		-7.86E-01	6.71E-03		-2.48E+00	3.38E-02		-9.60E-01	3.13E-01		Unigene28364_All//gi|17266309|gb|AAL5744.1|//4.00E-14//fortune-1 [Cycas edentata]	Unigene28364_All//2.00E-11//AT3G22210| unknown protein	Unigene28364_All//0.00E+00//gi|164327832|gb|ES824217.1|ES824217				nr -
Unigene28365_All	1110	23.47	14.11	8.20	16.65	16.13	9.85	0.00	0.00	0.00	-7.35E-01	8.74E-12		-1.52E+00	3.29E-35	Down	-4.56E-02	8.04E-01		-7.58E-01	1.54E-09		null	null		null	null		Unigene28365_All//gi|297820490|ref|XP_002878128.1|//2.00E-76//strictosidine synthase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323966|gb|EFH54387.1| strictosidine synthase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28365_All//9.00E-78//AT3G57030| strictosidine synthase family protein	Unigene28365_All//0.00E+00//gi|13355393|gb|BG445741.1|BG445741		ko00901|Indole alkaloid biosynthesis		nr +
Unigene28367_All	892	4.63	1.08	2.81	5.92	4.67	3.39	1.52	0.52	0.27	-2.10E+00	1.25E-09	Down	-7.24E-01	2.08E-02		-3.42E-01	2.05E-01		-8.03E-01	1.70E-03		-1.56E+00	3.85E-03		-2.50E+00	2.46E-05	Down	Unigene28367_All//gi|2865427|gb|AAC02666.1|//9.00E-12//polyprotein [Arabidopsis thaliana]		Unigene28367_All//1.00E-34//gi|78334096|gb|DT554370.1|DT554370				nr +
Unigene2837_All	2348	3.79	1.19	1.56	2.93	2.29	3.12	2.34	1.57	6.23	-1.67E+00	7.65E-15	Down	-1.28E+00	1.14E-09	Down	-3.56E-01	1.16E-01		8.99E-02	7.12E-01		-5.80E-01	1.08E-02		1.41E+00	2.15E-23	Up	Unigene2837_All//gi|79342966|ref|NP_172737.2|//0.00E+00//EMB1586 (embryo defective 1586); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana] >gi|108861896|sp|Q8W4E1.2|RH47_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 47, mitochondrial; AltName: Full=Protein INCREASED SIZE EXCLUSION LIMIT 1; AltName: Full=Protein EMBRYO DEFECTIVE 1586; Flags: Precursor >gi|12056979|gb|AAF58089.2|AC025417_17 T12C24.30 [Arabidopsis thaliana] >gi|51969316|dbj|BAD43350.1| similar to ATP-dependent RNA helicase [Arabidopsis thaliana] >gi|51969564|dbj|BAD43474.1| similar to ATP-dependent RNA helicase [Arabidopsis thaliana] >gi|51969644|dbj|BAD43514.1| similar to ATP-dependent RNA helicase [Arabidopsis thaliana] >gi|51969728|dbj|BAD43556.1| similar to ATP-dependent RNA helicase [Arabidopsis thaliana] >gi|51970230|dbj|BAD43807.1|	Unigene2837_All//0.00E+00//AT1G12770| EMB1586 (embryo defective 1586); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene2837_All//0.00E+00//TC166625		ko03040|Spliceosome	GO:0004386//GO:0010196//GO:0032559//GO:0042623//GO:0043231//GO:0044216	nr +
Unigene28370_All	1635	0.13	0.00	0.00	0.37	0.00	0.47	1.68	3.73	6.07	-7.00E+00	1.22E-01		-7.00E+00	1.46E-01		-8.51E+00	1.78E-04	Down	3.61E-01	6.80E-01		1.15E+00	1.68E-07	Up	1.85E+00	2.05E-23	Up	Unigene28370_All//gi|10177485|dbj|BAB10876.1|//1.00E-103//polyprotein [Arabidopsis thaliana]	Unigene28370_All//1.00E-67//AT4G23160| protein kinase family protein	Unigene28370_All//6.00E-16//ES830408				nr +
Unigene28372_All	852	1197.73	268.93	549.37	92.85	68.06	38.86	0.45	3.38	0.98	-2.16E+00	0.00E+00	Down	-1.12E+00	0.00E+00	Down	-4.48E-01	3.20E-17		-1.26E+00	1.43E-89	Down	2.92E+00	8.43E-12	Up	1.14E+00	9.20E-02		Unigene28372_All//gi|8745402|gb|AAF78903.1|AF248055_1//1.00E-45//proline-rich protein [Glycine max]	Unigene28372_All//2.00E-30//AT2G45180| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene28372_All//0.00E+00//TC148134				nr -
Unigene28374_All	387	80.31	26.84	39.90	70.54	61.93	93.13	75.71	45.04	45.40	-1.58E+00	3.36E-46	Down	-1.01E+00	2.28E-22	Down	-1.88E-01	8.46E-02		4.01E-01	4.10E-06		-7.49E-01	1.59E-16		-7.38E-01	1.34E-16		Unigene28374_All//gi|1173209|sp|P46293.1|RS16_GOSHI//4.00E-61//RecName: Full=40S ribosomal protein S16 >gi|439654|emb|CAA53567.1| RS16 protein, 40S subunit [Gossypium hirsutum]	Unigene28374_All//1.00E-55//AT2G09990| 40S ribosomal protein S16 (RPS16A)	Unigene28374_All//0.00E+00//gi|13248789|gb|BF278459.2|BF278459		ko03010|Ribosome		nr +
Unigene28375_All	408	69.38	51.66	32.37	47.25	43.21	31.33	82.90	44.56	28.51	-4.25E-01	2.82E-05		-1.10E+00	2.00E-23	Down	-1.29E-01	3.81E-01		-5.93E-01	1.15E-06		-8.96E-01	2.01E-25		-1.54E+00	8.44E-61	Down			Unigene28375_All//0.00E+00//gi|164300042|gb|ES819869.1|ES819869				kegg -
Unigene28376_All	699	7.34	5.51	11.81	64.78	55.96	22.48	0.73	1.02	0.11	-4.13E-01	1.25E-01		6.87E-01	1.03E-03		-2.11E-01	6.65E-03		-1.53E+00	4.15E-69	Down	4.86E-01	5.42E-01		-2.67E+00	1.37E-02				Unigene28376_All//2.00E-35//DW501308				
Unigene28378_All	582	9.08	4.70	11.89	9.24	9.05	8.23	1.60	1.65	3.90	-9.50E-01	2.87E-04		3.90E-01	1.03E-01		-3.02E-02	9.11E-01		-1.68E-01	5.87E-01		4.75E-02	9.64E-01		1.29E+00	6.77E-04	Up	Unigene28378_All//gi|9454543|gb|AAF87866.1|AC022520_10//3.00E-62//unknown protein [Arabidopsis thaliana]	Unigene28378_All//7.00E-63//AT1G53120| RNA-binding S4 domain-containing protein	Unigene28378_All//0.00E+00//gi|109876178|gb|DW505152.1|DW505152				nr -
Unigene28379_All	1224	75.06	10.93	79.70	3.70	2.03	1.81	0.03	0.24	0.07	-2.78E+00	1.50E-278	Down	8.65E-02	1.56E-01		-8.71E-01	9.95E-04		-1.03E+00	2.32E-04	Down	2.79E+00	9.47E-02		9.16E-01	7.50E-01		Unigene28379_All//gi|257831431|gb|ACY71016.1|//9.00E-59//LTA16 [Capsicum annuum]	Unigene28379_All//3.00E-58//AT5G50790| nodulin MtN3 family protein	Unigene28379_All//0.00E+00//CA992742				nr +
Unigene28381_All	602	2.52	2.36	2.30	1.74	3.20	1.28	3.23	2.43	0.73	-9.69E-02	8.47E-01		-1.32E-01	8.01E-01		8.82E-01	6.00E-02		-4.46E-01	5.32E-01		-4.11E-01	3.55E-01		-2.15E+00	2.89E-06	Down			Unigene28381_All//2.00E-72//TC147753				
Unigene28382_All	640	6.21	6.18	9.07	10.12	12.59	12.98	26.29	12.02	6.16	-8.80E-03	9.90E-01		5.46E-01	3.51E-02		3.15E-01	1.45E-01		3.60E-01	8.79E-02		-1.13E+00	8.99E-19	Down	-2.09E+00	1.78E-46	Down	Unigene28382_All//gi|25992541|gb|AAN77150.1|//3.00E-24//fiber protein Fb11 [Gossypium barbadense]	Unigene28382_All//2.00E-19//AT2G46540| unknown protein	Unigene28382_All//0.00E+00//TC165971				nr +
Unigene28384_All	634	8.25	3.92	4.79	15.01	14.28	14.89	15.27	9.03	9.61	-1.08E+00	5.26E-05	Down	-7.86E-01	3.97E-03		-7.12E-02	7.69E-01		-1.15E-02	9.48E-01		-7.58E-01	4.14E-06		-6.68E-01	2.99E-05		Unigene28384_All//gi|90654201|gb|ABD95975.1|//1.00E-52//mitochondrial import receptor-like protein [Nicotiana tabacum]	Unigene28384_All//3.00E-47//AT3G20000| TOM40; P-P-bond-hydrolysis-driven protein transmembrane transporter/ voltage-gated anion channel	Unigene28384_All//0.00E+00//gi|78352273|gb|DT572547.1|DT572547				nr +
Unigene28385_All	742	1.55	93.62	0.79	1.01	3.25	4.63	3.25	46.64	27.17	5.92E+00	0.00E+00	Up	-9.75E-01	1.46E-01		1.69E+00	6.31E-05	Up	2.20E+00	7.40E-09	Up	3.84E+00	1.09E-172	Up	3.06E+00	4.58E-84	Up	Unigene28385_All//gi|222822697|gb|ACM68461.1|//9.00E-70//stress-associated protein 11 [Solanum pennellii]	Unigene28385_All//6.00E-55//AT3G28210| PMZ; zinc ion binding	Unigene28385_All//0.00E+00//TC149651	C2H2			nr +
Unigene28386_All	604	12.65	32.47	20.45	9.57	12.14	13.76	7.56	19.86	15.04	1.36E+00	1.67E-23	Up	6.94E-01	3.06E-05		3.44E-01	1.26E-01		5.24E-01	9.21E-03		1.39E+00	1.52E-18	Up	9.92E-01	6.84E-09		Unigene28386_All//gi|30695366|ref|NP_564615.3|//2.00E-28//peroxisomal membrane protein-related [Arabidopsis thaliana] >gi|14326545|gb|AAK60317.1|AF385726_1 At1g52870/F14G24_14 [Arabidopsis thaliana] >gi|259900145|gb|ANV72239.1| At1g52870/F14G24_14 [Arabidopsis thaliana]	Unigene28386_All//9.00E-30//AT1G52870| peroxisomal membrane protein-related	Unigene28386_All//2.00E-16//CO070993		ko04146|Peroxisome		nr +
Unigene28389_All	758	1.73	0.27	1.26	5.45	6.91	4.47	5.24	2.70	4.94	-2.69E+00	1.84E-04	Down	-4.49E-01	4.58E-01		3.40E-01	2.26E-01		-2.88E-01	3.98E-01		-9.57E-01	4.86E-04		-8.58E-02	7.54E-01		Unigene28389_All//gi|224144595|ref|XP_002325344.1|//2.00E-26//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222862219|gb|EEE99725.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]		Unigene28389_All//4.00E-120//CO080430				nr -
Unigene2839_All	2118	16.60	8.90	11.44	21.17	18.60	16.29	25.65	5.76	10.76	-8.99E-01	8.63E-22		-5.37E-01	7.40E-09		-1.87E-01	1.99E-02		-3.78E-01	9.18E-07		-2.15E+00	2.33E-149	Down	-1.25E+00	3.10E-71	Down	Unigene2839_All//gi|15239712|ref|NP_197433.1|//0.00E+00//RANGAP2 (RAN GTPASE ACTIVATING PROTEIN 2); RAN GTPase activator [Arabidopsis thaliana] >gi|20582946|sp|Q9M651.2|RAGP2_ARATH RecName: Full=RAN GTPase-activating protein 2; Short=Ran6AP2; Short=AtRan6AP2	Unigene2839_All//0.00E+00//AT5G19320| RANGAP2 (RAN GTPASE ACTIVATING PROTEIN 2); RAN GTPase activator	Unigene2839_All//0.00E+00//TC166791			GO:0005488//GO:0006970//GO:0007186//GO:0009536//GO:0012505//GO:0016020//GO:0016301//GO:0051169	nr +

Unigene28390_All	1088	1.64	3.35	1.27	1.88	4.02	1.70	2.06	0.31	0.66	1.04E+00	1.48E-03		-3.62E-01	4.82E-01		1.10E+00	9.22E-05	Up	-1.41E-01	7.57E-01		-2.74E+00	8.38E-09	Down	-1.64E+00	3.26E-05	Down	Unigene28390_All//gi|54261721|gb|AAX31164.1|/6.00E-35//At1g80060 [Arabidopsis thaliana] >gi|58331795|gb|AAW70395.1| At1g80060 [Arabidopsis thaliana]	Unigene28390_All//8.00E-34//AT1G80060| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: protein modification process; LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin (InterPro:IPR000626); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32270.1); Has 97 Blast hits to 97 proteins in 32 species: Archae - 0; Bacteria - 0; Metazoa - 56; Fungi - 0; Plants - 38; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink).	Unigene28390_All//0.00E+00//gi|78332302|gb|DT552576.1|DT552576				nr -
Unigene28391_All	789	33.42	9.25	15.19	5.18	4.54	34.46	0.21	0.48	0.00	-1.85E+00	5.01E-49	Down	-1.14E+00	4.60E-23	Down	-1.90E-01	5.77E-01		2.73E+00	3.14E-86	Up	1.15E+00	3.27E-01		-7.74E+00	1.08E-01		Unigene28391_All//gi|38344885|emb|CAD41908.2|//4.00E-06//OSJNBa0033G05.9 [Oryza sativa (japonica cultivar-group)] >gi|90399283|emb|CAH68244.1| H0306F03.11 [Oryza sativa (indica cultivar-group)]							nr -
Unigene28392_All	1090	0.14	0.37	0.44	1.69	2.05	2.32	6.94	1.84	2.05	1.37E+00	2.74E-01		1.61E+00	1.82E-01		2.80E-01	5.67E-01		4.57E-01	2.88E-01		-1.92E+00	1.76E-18	Down	-1.76E+00	3.94E-17	Down	Unigene28392_All//gi|30680599|ref|NP_563810.2|//1.00E-117//bZIP family transcription factor [Arabidopsis thaliana] >gi|79317351|ref|NP_001030999.1| bZIP family transcription factor [Arabidopsis thaliana] >gi|42272369|emb|CAC40022.1| bZIP transcription factor [Arabidopsis thaliana]	Unigene28392_All//1.00E-114//AT1G08320| bZIP family transcription factor	Unigene28392_All//4.00E-62//gi|48827973|gb|CO126363.1|CO126363	bZIP			nr +
Unigene28393_All	1228	0.64	0.91	0.43	1.01	0.28	1.47	1.24	2.42	3.15	5.06E-01	4.22E-01		-5.60E-01	4.96E-01		-1.85E+00	2.11E-03		5.37E-01	3.05E-01		9.63E-01	3.04E-03		1.34E+00	2.19E-06	Up	Unigene28393_All//gi|297796091|ref|XP_002865930.1|/6.00E-95//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297311765|gb|EFH42189.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene28393_All//4.00E-94//AT5G52850| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene28394_All	607	1.47	16.28	0.53	5.50	5.39	6.77	14.98	37.25	91.36	3.47E+00	3.38E-37	Up	-1.48E+00	6.99E-02		-2.89E-02	9.37E-01		3.00E-01	3.79E-01		1.31E+00	2.06E-31	Up	2.61E+00	1.63E-194	Up	Unigene28394_All//gi|69111473|gb|AZ03389.1|/3.00E-36//C2H2 transcription factor [Glycine max]	Unigene28394_All//0.00E+00//gi|109827624|gb|DW226299.1|DW226299	C2H2			nr +
Unigene28395_All	533	9.82	22.15	6.19	6.26	6.78	30.00	6.27	3.61	37.22	1.17E+00	1.20E-11	Up	-6.64E-01	1.49E-02		1.16E-01	7.89E-01		2.26E+00	6.74E-41	Up	-7.97E-01	8.25E-03		2.57E+00	7.42E-69	Up	Unigene28395_All//gi|18411926|ref|NP_567231.1|//5.00E-18//SAG21 (SENESCENCE-ASSOCIATED GENE 21) [Arabidopsis thaliana] >gi|152942220|gb|AAU95287.1|AF410301_1 AT4g02380/T14P8_2 [Arabidopsis thaliana] >gi|14517508|gb|AAK62644.1| AT4g02380/T14P8_2 [Arabidopsis thaliana] >gi|15450609|gb|AAK96576.1| AT4g02380/T14P8_2 [Arabidopsis thaliana] >gi|15809760|gb|AAL06808.1| AT4g02380/T14P8_2 [Arabidopsis thaliana] >gi|21592389|gb|AAM64340.1| late embryogenis abundant protein [Arabidopsis thaliana] >gi|88396780|gb|AAW72736.1| late embryogenesis abundant-like protein [Arabidopsis thaliana]	Unigene28395_All//2.00E-09//AT4G02380| SAG21 (SENESCENCE-ASSOCIATED GENE 21)	Unigene28395_All//1.00E-63//DN799918				nr +
Unigene28396_All	835	1.00	1.40	0.96	4.12	3.63	2.49	3.65	0.85	1.15	4.77E-01	4.39E-01		-6.78E-02	9.40E-01		-1.82E-01	6.06E-01		-7.26E-01	2.91E-02		-2.10E+00	8.98E-09	Down	-1.67E+00	6.36E-07	Down	Unigene28396_All//gi|186510818|ref|NP_190459.2|//3.00E-56//DNA binding / catalytic/ chromatin binding / nuclease [Arabidopsis thaliana]	Unigene28396_All//2.00E-51//AT3G48900| DNA binding / catalytic/ chromatin binding / nuclease					nr +
Unigene28398_All	1691	0.31	0.78	0.31	2.24	5.60	4.99	2.70	0.72	1.65	1.33E+00	2.73E-02		2.54E-02	9.99E-01		1.32E+00	7.93E-13	Up	1.16E+00	8.88E-09	Up	-1.91E+00	1.97E-11	Down	-7.11E-01	3.47E-03		Unigene28398_All//gi|224131672|ref|XP_002321149.1|//0.00E+00//glycosyl hydrolase family 9 [Populus trichocarpa] >gi|222861922|gb|EEE99464.1| glycosyl hydrolase family 9 [Populus trichocarpa]	Unigene28398_All//0.00E+00//AT2G32990| AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene28398_All//2.00E-34//C0108799		ko00500|Starch and sucrose metabolism		nr +
Unigene2840_All	1415	2.03	5.19	3.84	2.04	2.99	3.77	5.38	5.82	5.15	1.35E+00	3.35E-09	Up	9.16E-01	6.09E-04		5.52E-01	6.22E-02		8.83E-01	5.82E-04		1.14E-01	6.14E-01		-6.20E-02	7.56E-01		Unigene2840_All//gi|18411319|ref|NP_565147.1|//1.00E-156//SKP2B; ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75318353|sp|Q49286.1|FBL5_ARATH RecName: Full=F-box/LRR-repeat protein 5 >gi|2829911|gb|AAC00619.1| Unknown protein [Arabidopsis thaliana] >gi|21593038|gb|AAM64987.1| F-box protein family, AtFBL5 [Arabidopsis thaliana] >gi|89000991|gb|ABD59085.1| At1g77000 [Arabidopsis thaliana]	Unigene2840_All//2.00E-157//AT1G77000| SKP2B; ubiquitin-protein ligase	Unigene2840_All//0.00E+00//gi|109879816|gb|DN508786.1|DN508786		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene28401_All	1152	0.32	0.18	0.18	8.22	6.07	3.92	2.46	1.89	2.52	-8.54E-01	4.89E-01		-7.82E-01	5.53E-01		-4.37E-01	1.51E-02		-1.07E+00	9.16E-09	Down	-3.82E-01	2.76E-01		3.79E-02	9.29E-01		Unigene28401_All//gi|145335995|ref|NP_173629.2|//1.00E-105//ATP binding / inositol pentakisphosphate 2-kinase [Arabidopsis thaliana]	Unigene28401_All//3.00E-97//AT1G22100| ATP binding / inositol pentakisphosphate 2-kinase	Unigene28401_All//0.00E+00//TC138769				nr +
Unigene28404_All	1010	5.28	1.00	2.58	1.73	1.84	0.94	0.00	0.17	2.76	-2.40E+00	3.07E-14	Down	-1.03E+00	1.51E-04	Down	9.30E-02	8.66E-01		-8.78E-01	7.90E-02		7.37E+00	1.39E-01		1.14E+01	5.84E-20	Up	Unigene28404_All//gi|124359339|gb|ABD28498.2|//3.00E-09//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene28404_All//9.00E-06//AT3G26855| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: reverse transcriptase-related (TAIR:AT2G02650.1); Has 97 Blast hits to 97 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 97; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr +
Unigene28406_All	617	16.62	97.48	61.28	44.65	65.52	70.64	4.66	5.83	2.26	2.55E+00	1.31E-164	Up	1.88E+00	3.00E-69	Up	5.53E-01	9.24E-13		6.62E-01	4.59E-17		3.22E-01	3.04E-01		-1.04E+00	1.17E-03		Unigene28406_All//gi|76262500|gb|AB441400.1|/4.00E-17//pherophorin-C2 protein precursor [Chlamydomonas reinhardtii]	Unigene28406_All//1.00E-128//gi|164303399|gb|ES797686.1|ES797686	ko03040|Spliceosome			nr +
Unigene28407_All	454	19.13	11.05	12.20	13.61	14.11	16.71	24.21	23.48	11.41	-7.92E-01	5.47E-05		-6.49E-01	1.41E-03		5.23E-02	8.49E-01		2.97E-01	1.98E-01		-4.46E-02	8.02E-01		-1.09E+00	3.32E-12	Down			Unigene28407_All//8.00E-145//gi|164334866|gb|ES816912.1|ES816912				
Unigene28409_All	2241	13.38	6.10	12.62	13.16	18.33	15.96	0.32	0.54	0.36	-1.13E+00	5.86E-27	Down	-8.44E-02	4.72E-01		4.78E-01	4.63E-10		2.79E-01	2.02E-03		7.54E-01	1.77E-01		1.49E-01	8.23E-01		Unigene28409_All//gi|33391721|gb|AAQ17461.1|//0.00E+00//beta-D-glucosidase [Gossypium hirsutum]	Unigene28409_All//0.00E+00//AT5G20950| glycosyl hydrolase family 3 protein	Unigene28409_All//0.00E+00//TC159075		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr +
Unigene28411_All	868	0.24	2.22	0.98	0.40	0.79	1.93	1.75	2.12	3.58	3.20E+00	3.42E-07	Up	2.03E+00	2.24E-02		9.82E-01	2.98E-01		2.26E+00	9.88E-05	Up	2.73E-01	5.68E-01		1.03E+00	8.80E-04	Up	Unigene28411_All//gi|187941007|gb|ACD39775.1|//7.00E-12//seed imbibition protein 1 [Vitis vinifera]	Unigene28411_All//1.00E-11//AT3G57520| AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase, hydrolyzing O-glycosyl compounds	Unigene28411_All//5.00E-61//gi|164293552|gb|ES810015.1|ES810015				nr -
Unigene28412_All	1594	0.26	0.57	0.00	4.22	1.47	1.13	1.14	4.12	17.15	1.12E+00	1.30E-01		-8.04E+00	1.56E-02		-1.52E+00	4.93E-12	Down	-1.90E+00	2.38E-14	Down	1.85E+00	2.12E-15	Up	3.91E+00	1.63E-140	Up	Unigene28412_All//gi|115444363|ref|NP_001045961.1|//4.00E-53//Os02g0159200 [Oryza sativa Japonica Group] >gi|113535492|dbj|BAF07875.1| Os02g0159200 [Oryza sativa Japonica Group]	Unigene28412_All//3.00E-61//AT1G79910| unknown protein	Unigene28412_All//1.00E-60//DT463696				nr -
Unigene28413_All	608	28.74	69.92	7.44	17.78	25.03	7.95	22.81	2.41	33.68	1.28E+00	7.12E-46	Up	-1.95E+00	1.38E-33	Down	4.94E-01	2.71E-04		-1.16E+00	2.81E-11	Down	-3.24E+00	2.24E-60	Down	5.62E-01	1.22E-07		Unigene28413_All//gi|98961017|gb|ABF58992.1|//6.00E-17//At3g57450 [Arabidopsis thaliana]	Unigene28413_All//3.00E-18//AT3G57450| unknown protein	Unigene28413_All//0.00E+00//gi|164288126|gb|ES798766.1|ES798766				nr -
Unigene28416_All	758	2.55	5.82	3.65	1.31	2.00	2.74	4.69	6.62	8.57	1.19E+00	6.34E-05	Up	5.16E-01	1.99E-01		6.05E-01	2.97E-01		1.06E+00	1.98E-02		4.98E-01	4.01E-02		8.71E-01	1.75E-05									
Unigene28417_All	691	6.28	1.98	7.09	4.97	6.48	3.20	0.73	1.27	0.46	-1.67E+00	1.39E-07	Down	1.74E-01	5.79E-01		3.81E-01	2.10E-01		-6.35E-01	5.92E-02		7.91E-01	2.41E-01		-6.71E-01	4.48E-01				Unigene28417_All//4.00E-24//gi|164250506|gb|ES830147.1|ES830147				
Unigene28418_All	348	1.05	4.95	1.53	3.01	1.19	3.37	4.01	1.08	0.92	2.23E+00	1.09E-04	Up	5.40E-01	6.10E-01		-1.34E+00	3.95E-02		1.67E-01	7.91E-01		-1.89E+00	5.91E-04	Down	-2.13E+00	1.13E-04	Down			Unigene28418_All//7.00E-09//gi|78325723|gb|DT545997.1|DT545997				
Unigene28419_All	676	13.78	3.52	6.30	17.98	13.60	16.30	27.89	12.43	10.61	-1.97E+00	3.60E-19	Down	-1.13E+00	1.95E-08	Down	-4.03E-01	9.89E-03		-1.41E-01	4.69E-01		-1.17E+00	5.36E-22	Down	-1.39E+00	1.10E-29	Down	Unigene28419_All//gi|18421913|ref|NP_568574.1|//3.00E-36//60S ribosomal protein-related [Arabidopsis thaliana]	Unigene28419_All//1.00E-35//AT5G39800| 60S ribosomal protein-related	Unigene28419_All//0.00E+00//TC154453				nr +
Unigene2842_All	2077	21.66	19.39	29.46	35.86	32.68	46.19	29.23	42.00	61.97	-1.60E-01	5.91E-02		4.43E-01	1.04E-10		-1.34E-01	3.26E-02		3.65E-01	7.34E-13		5.23E-01	2.09E-25		1.08E+00	4.19E-132	Up	Unigene2842_All//gi|9279693|dbj|BAB01250.1|//1.00E-174//kinase-like protein [Arabidopsis thaliana]	Unigene2842_All//4.00E-174//AT3G22750| protein kinase, putative	Unigene2842_All//0.00E+00//TC142361			GO:0004713//GO:0006464//GO:0032559	nr -

Unigene28420_All	659	37.79	394.13	43.15	117.24	363.90	277.56	179.07	400.58	777.85	3.38E+00	0.00E+00	Up	1.91E-01	9.05E-02		1.63E+00	0.00E+00	Up	1.24E+00	1.68E-200	Up	1.16E+00	1.28E-295	Up	2.12E+00	0.00E+00	Up	Unigene28420_All//gi|1850968|gb|AA848305.1|//4.00E-75//Hs1pro-1 [Beta procumbens]	Unigene28420_All//3.00E-65//AT3G55840| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Hs1pro-1, C-terminal (InterPro:IPR009743), Hs1pro-1, N-terminal (InterPro:IPR009869); BEST Arabidopsis thaliana protein match is: HSPRO2 (ARABIDOPSIS ORTHOLOG OF SUGAR BEET HS1 PRO-1 2) (TAIR:AT2G40000.1); Has 43 Blast hits to 43 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene28420_All//0.00E+00//TC136188				nr +
Unigene28421_All	233	38.62	15.44	42.28	38.48	31.92	21.52	2.72	2.33	1.20	-1.32E+00	8.21E-11	Down	1.31E-01	5.40E-01		-2.70E-01	1.81E-01		-8.39E-01	8.46E-06		-2.23E-01	7.73E-01		-1.19E+00	1.33E-01		Unigene28421_All//gi|159463554|ref|XP_001690007.1|//1.00E-07//SR protein factor [Chlamydomonas reinhardtii] >gi|158283995|gb|EDP09745.1| SR protein factor [Chlamydomonas reinhardtii]		Unigene28421_All//2.00E-112//gi|109870908|gb|DW499884.1|DW499884		ko03040|Spliceosome		nr +
Unigene28422_All	629	13.31	5.72	6.60	22.10	10.35	12.71	12.10	6.25	6.90	-1.22E+00	5.43E-09	Down	-1.01E+00	1.62E-06	Down	-1.09E+00	1.08E-14	Down	-7.98E-01	5.84E-08		-9.54E-01	5.74E-07		-8.10E-01	1.10E-05		Unigene28422_All//gi|297722477|ref|NP_001173602.1|//2.00E-20//Os03g0701550 [Oryza sativa Japonica Group] >gi|255674814|dbj|BAH92330.1|Os03g0701550 [Oryza sativa Japonica Group]	Unigene28422_All//3.00E-65//AT5G11760| unknown protein	Unigene28422_All//0.00E+00//TC158459				nr -
Unigene28423_All	652	156.72	160.63	145.46	440.46	360.67	468.54	443.49	301.99	142.49	3.56E-02	5.71E-01		-1.08E-01	6.39E-02		-2.88E-01	4.86E-27		8.92E-02	2.98E-03		-5.54E-01	1.49E-91		-1.64E+00	0.00E+00	Down	Unigene28423_All//gi|462013|sp|P35016.1|ENPL_CATRO//1.00E-108//RecName: Full=Endoplasmin homolog; AltName: Full=Glucose-regulated protein 94 homolog; Short=GRP-94 homolog; Flags: Precursor >gi|348696|gb|AAA16785.1| heat shock protein 90 [Catharanthus roseus]	Unigene28423_All//1.00E-106//AT4G24190| SHD (SHEPHERD); ATP binding / unfolded protein binding	Unigene28423_All//0.00E+00//gi|164302774|gb|ES850511.1|ES850511		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene28424_All	889	3.47	6.95	1.38	1.23	1.78	0.15	2.90	0.28	1.03	1.00E+00	3.35E-05	Up	-1.33E+00	4.86E-04	Down	5.32E-01	3.40E-01		-3.02E+00	2.14E-04	Down	-3.36E+00	4.57E-12	Down	-1.49E+00	3.19E-05	Down	Unigene28424_All//gi|15233710|ref|NP_194146.1|//8.00E-38//AtGRF8 (GROWTH-REGULATING FACTOR 8); transcription activator [Arabidopsis thaliana]	Unigene28424_All//4.00E-20//AT4G24150| AtGRF8 (GROWTH-REGULATING FACTOR 8); transcription activator	Unigene28424_All//0.00E+00//TC141570	GRF			nr -
Unigene28425_All	656	77.44	288.95	57.88	78.75	214.91	121.72	70.19	78.05	575.66	1.90E+00	0.00E+00	Up	-4.20E-01	3.24E-08		1.45E+00	4.43E-215	Up	6.28E-01	3.88E-28		1.53E-01	3.04E-02		3.04E+00	0.00E+00	Up	Unigene28425_All//gi|224112801|ref|XP_002332694.1|//9.00E-49//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222832948|gb|EEE71425.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene28425_All//2.00E-36//AT5G51190| AP2 domain-containing transcription factor, putative	Unigene28425_All//0.00E+00//gi|109850121|gb|DW479100.1|DW479100	AP2-EREBP			nr +
Unigene28426_All	684	1.91	3.19	0.08	1.89	2.92	1.45	3.21	1.34	3.20	7.36E-01	9.04E-02		-4.62E+00	4.46E-06	Down	6.25E-01	1.87E-01		-3.82E-01	5.50E-01		-1.26E+00	1.42E-03		-4.90E-03	9.85E-01					Unigene28426_All//2.00E-22//DR460845				
Unigene28427_All	1281	7.72	4.19	4.61	1.13	2.55	1.59	0.00	0.07	0.06	-8.81E-01	1.70E-06		-7.42E-01	8.64E-05		1.18E+00	4.49E-04	Up	4.93E-01	3.11E-01		6.03E+00	4.01E-01		5.96E+00	4.04E-01		Unigene28427_All//gi|297849156|ref|XP_002892459.1|//1.00E-160//strictosidine synthase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338301|gb|EFH68718.1| strictosidine synthase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28427_All//6.00E-161//AT1G08470| strictosidine synthase family protein	Unigene28427_All//0.00E+00//TC175912		ko00901|Indole alkaloid biosynthesis		nr -
Unigene28431_All	1207	1.08	0.88	0.66	1.86	1.71	0.97	2.73	1.77	5.88	-2.98E-01	5.95E-01		-7.12E-01	2.42E-01		-1.18E-01	8.19E-01		-9.33E-01	2.93E-02		-6.30E-01	3.98E-02		1.10E+00	2.52E-08	Up	Unigene28431_All//gi|168274274|dbj|BAG09557.1|//1.00E-110//acetylcholinesterase [Mascroptilium atropurpureum]	Unigene28431_All//1.00E-101//AT5G14450| GDSL-motif lipase/hydrolase family protein	Unigene28431_All//0.00E+00//TC149445				nr +
Unigene28432_All	416	9.06	9.14	11.39	13.29	11.01	13.57	5.59	5.53	11.49	1.26E-02	9.88E-01		3.31E-01	2.69E-01		-2.72E-01	3.13E-01		3.00E-02	9.34E-01		-1.66E-02	1.00E+00		1.04E+00	1.99E-05	Up			Unigene28432_All//2.00E-148//BG444898				
Unigene28433_All	727	28.93	9.90	26.37	14.46	20.18	10.13	0.35	0.12	0.05	-1.55E+00	1.57E-30	Down	-1.34E-01	3.48E-01		4.81E-01	5.34E-04		-5.14E-01	3.16E-03		-1.60E+00	3.10E-01		-2.67E+00	1.15E-01		Unigene28433_All//gi|18403387|ref|NP_565771.1|//1.00E-45//SPL3 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3); DNA binding / transcription factor [Arabidopsis thaliana] >gi|67461216|sp|P93015.2|SPL3_ARATH RecName: Full=Squamosa promoter-binding-like protein 3 >gi|2462081|emb|CAA70578.1| squamosa-promoter binding protein like 3 [Arabidopsis thaliana] >gi|5931651|emb|CAB56579.1| squamosa promoter binding protein-like 3 [Arabidopsis thaliana] >gi|5931663|emb|CAB56585.1| squamosa promoter binding protein-like 3 [Arabidopsis thaliana]	Unigene28433_All//8.00E-37//AT2G33810| SPL3 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3); DNA binding / transcription factor	Unigene28433_All//0.00E+00//TC164023	SBP			nr -
Unigene28434_All	608	8.61	9.58	9.81	13.68	10.65	12.33	10.36	5.77	4.46	1.55E-01	5.69E-01		1.89E-01	4.85E-01		-3.62E-01	7.18E-02		-1.50E-01	5.30E-01		-8.44E-01	5.90E-05		-1.22E+00	1.13E-08	Down			Unigene28434_All//0.00E+00//gi|21098115|gb|BQ410428.1|BQ410428				
Unigene28435_All	780	6.71	32.81	10.10	9.77	10.99	10.25	31.60	55.46	20.43	2.29E+00	6.16E-62	Up	5.91E-01	6.12E-03		1.70E-01	4.64E-01		6.88E-02	7.67E-01		8.11E-01	2.19E-27		-6.29E-01	7.07E-11		Unigene28435_All//gi|18421893|ref|NP_568568.1|//8.00E-33//calcium-binding EF hand family protein [Arabidopsis thaliana] >gi|75331780|sp|Q93227.1|CML45_ARATH RecName: Full=Probable calcium-binding protein CML45; AltName: Full=Calmodulin-like protein 45 >gi|16648830|gb|AAL25605.1| AT5g39670/MIJ24_140 [Arabidopsis thaliana] >gi|20466131|gb|AAM19987.1| AT5g39670/MIJ24_140 [Arabidopsis thaliana]	Unigene28435_All//4.00E-34//AT5G39670| calcium-binding EF hand family protein	Unigene28435_All//0.00E+00//TC152396		ko04626|Plant-pathogen interaction		nr -
Unigene28436_All	690	1.67	0.22	0.46	2.09	3.39	3.40	1.16	0.36	0.81	-2.92E+00	2.75E-04	Down	-1.85E+00	1.07E-02		6.97E-01	9.87E-02		7.01E-01	1.02E-01		-1.68E+00	2.46E-02		-5.26E-01	4.35E-01		Unigene28436_All//gi|30681147|ref|NP_172416.2|//4.00E-41//haspin-related [Arabidopsis thaliana] >gi|3482920|gb|AAC33205.1| Hypothetical protein [Arabidopsis thaliana]	Unigene28436_All//2.00E-32//AT1G09450| haspin-related					nr +
Unigene28437_All	1164	4.54	2.18	3.52	18.10	9.23	7.88	1.24	0.61	1.57	-1.06E+00	5.92E-05	Down	-3.66E-01	1.95E-01		-9.72E-01	3.56E-18		-1.20E+00	1.44E-22	Down	-1.02E+00	4.18E-02		3.50E-01	4.15E-01		Unigene28437_All//gi|38194907|gb|AR12295.1|//5.00E-20//retrovirus-related pol polyprotein [Phaseolus vulgaris]		Unigene28437_All//0.00E+00//TC153347				nr +
Unigene28439_All	887	6.49	3.71	3.96	1.40	3.46	0.51	0.00	0.00	0.00	-8.05E-01	1.15E-03		-7.12E-01	5.79E-03		1.30E+00	2.25E-04	Up	-1.46E+00	1.95E-02		null	null		null	null		Unigene28439_All//gi|19911211|dbj|BAB86932.1|//2.00E-76//glucosyltransferase-14 [Vigna angularis]	Unigene28439_All//3.00E-63//AT2G36780| UDP-glucoronosyl/UDP-glucosyl transferase family protein			ko00908|Zeatin biosynthesis		nr -
Unigene2844_All	1654	2.15	2.21	1.22	1.60	3.93	2.81	3.66	5.26	5.25	3.62E-02	9.25E-01		-8.14E-01	1.70E-02		1.30E+00	9.63E-09	Up	8.17E-01	3.33E-03		5.24E-01	2.76E-03		5.23E-01	2.14E-03		Unigene2844_All//gi|13367212|gb|AB134663.1|//1.00E-124//bZIP transcription factor bZIP117 [Glycine max]	Unigene2844_All//5.00E-71//AT4G36730| GBF1; sequence-specific DNA binding / transcription factor	Unigene2844_All//0.00E+00//gi|78341616|gb|DT561890.1|DT561890	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0003677//GO:0007569//GO:0010467//GO:0042743//GO:0044424	nr -
Unigene28440_All	969	1.08	0.78	0.33	2.11	3.16	1.31	3.49	0.73	1.81	-4.61E-01	4.86E-01		-1.71E+00	2.35E-02		5.86E-01	1.05E-01		-6.92E-01	1.32E-01		-2.25E+00	1.77E-10	Down	-9.48E-01	1.14E-03		Unigene28440_All//gi|22331190|ref|NP_188642.2|//3.00E-58//TTN9 (TITAN9) [Arabidopsis thaliana] >gi|42572493|ref|NP_974342.1| TTN9 (TITAN9) [Arabidopsis thaliana]	Unigene28440_All//3.00E-50//AT3G20070| TTN9 (TITAN9)	Unigene28440_All//0.00E+00//gi|193218966|gb|EY197238.1|EY197238				nr -
Unigene28442_All	832	2.58	2.50	0.83	4.73	4.55	2.88	4.07	0.10	1.44	-4.63E-02	9.25E-01		-1.63E+00	8.10E-04	Down	-5.51E-02	8.62E-01		-7.17E-01	1.94E-02		-5.34E+00	5.10E-21	Down	-1.50E+00	1.24E-06	Down	Unigene28442_All//gi|297724275|ref|NP_001174501.1|//1.00E-17//Os05g0532500 [Oryza sativa Japonica Group] >gi|255676518|dbj|BAH93229.1| Os05g0532500 [Oryza sativa Japonica Group]	Unigene28442_All//4.00E-34//AT4G12540| unknown protein	Unigene28442_All//0.00E+00//TC139698				nr +
Unigene28443_All	786	4.73	2.77	3.05	2.79	5.83	4.08	10.70	1.01	0.86	-7.70E-01	1.53E-02		-6.33E-01	5.83E-02		1.06E+00	9.72E-05	Up	5.49E-01	1.29E-01		-3.41E+00	1.76E-38	Down	-3.64E+00	4.62E-42	Down	Unigene28443_All//gi|49944295|gb|ABR46190.1|//6.00E-38//At5g20670 [Arabidopsis thaliana]	Unigene28443_All//1.00E-29//AT5G20670| unknown protein	Unigene28443_All//0.00E+00//TC149698				nr +
Unigene28444_All	280	47.84	46.33	40.13	40.03	35.05	32.74	14.65	20.30	33.29	-4.63E-02	7.79E-01		-2.54E-01	1.40E-01		-1.92E-01	3.16E-01		-2.90E-01	1.09E-01		4.71E-01	3.73E-02		1.18E+00	7.94E-12	Up	Unigene28444_All//gi|224053040|ref|XP_002297677.1|//1.00E-09//predicted protein [Populus trichocarpa] >gi|222844935|gb|EEE82482.1| predicted protein [Populus trichocarpa]		Unigene28444_All//2.00E-141//gi|78347300|gb|DT567574.1|DT567574				nr +
Unigene28445_All	650	0.32	16.92	1.31	0.92	2.33	4.86	23.48	41.47	49.28	5.72E+00	2.62E-56	Up	2.03E+00	2.24E-02		1.34E+00	1.45E-02		2.40E+00	4.81E-09	Up	8.21E-01	1.05E-17		1.07E+00	8.36E-33	Up	Unigene28445_All//gi|115483026|ref|NP_001065106.1|//9.00E-25//Os10g0524300 [Oryza sativa Japonica Group] >gi|62733656|gb|AA000717.2| expressed protein [Oryza sativa Japonica Group] >gi|78708937|gb|ABB47912.1| LysM domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639715|dbj|BAF27020.1| Os10g0524300 [Oryza sativa Japonica Group]	Unigene28445_All//4.00E-22//AT5G62150| peptidoglycan-binding LysM domain-containing protein	Unigene28445_All//0.00E+00//TC165000				nr +

Unigene28447_All	638	16.81	3.18	4.34	7.65	4.91	2.76	31.88	4.13	9.30	-2.40E+00	4.67E-28	Down	-1.95E+00	7.48E-21	Down	-6.40E-01	1.31E-02		-1.47E+00	1.49E-07	Down	-2.95E+00	1.88E-80	Down	-1.78E+00	4.24E-45	Down	Unigene28447_All//gi|22001640|sp|Q93192.1|HBL2_GOSHI//7.00E-86//RecName: Full=Non-symbiotic hemoglobin 2; AltName: Full=GOShi GLB2; Short=Hb2 >gi|15809418|gb|AAK21604.1| non-symbiotic hemoglobin class 2 [Gossypium hirsutum]	Unigene28447_All//5.00E-64//AT2G10520| HHB2 (ARABIDOPSIS HAEMOGLOBIN 2); oxygen transporter	Unigene28447_All//0.00E+00//TC161350				nr +
Unigene28448_All	1650	0.06	11.15	0.94	0.42	1.63	2.68	0.18	0.20	1.38	7.46E+00	1.41E-101	Up	3.88E+00	1.75E-06	Up	1.95E+00	1.89E-06	Up	2.67E+00	5.93E-14	Up	1.76E-01	8.80E-01		2.94E+00	1.06E-09	Up	Unigene28448_All//gi|30684088|ref|NP_193188.2|//0.00E+00//transporter-related [Arabidopsis thaliana]	Unigene28448_All//3.00E-180//AT4G17550| transporter-related					nr -
Unigene28449_All	287	4.74	2.30	6.31	4.69	4.92	4.56	19.74	10.19	7.22	-1.05E+00	6.97E-02		4.12E-01	4.05E-01		7.00E-02	9.24E-01		-3.83E-02	9.48E-01		-9.53E-01	2.17E-05		-1.45E+00	4.61E-10	Down			Unigene28449_All//3.00E-149//gi|21092911|gb|BQ405224.1|BQ405224				
Unigene28845_All	1951	31.48	82.30	19.92	86.40	84.84	95.70	80.40	126.07	160.19	1.39E+00	2.63E-193	Up	-6.60E-01	2.14E-21		-2.63E-02	5.96E-01		1.47E-01	7.46E-05		6.49E-01	4.14E-103		9.95E-01	9.67E-278		Unigene28845_All//gi|116265950|gb|AB191223.1|//1.00E-175//CBL-interacting protein kinase 16 [Populus trichocarpa]	Unigene28845_All//2.00E-143//AT2G30360| SIP4 (SOS3-INTERACTING PROTEIN 4); kinase/protein kinase	Unigene28845_All//0.00E+00//TC155761		ko04140|Regulation of autophagy		nr +
Unigene28451_All	430	0.85	4.83	1.49	3.01	1.76	2.94	4.03	0.00	13.06	2.50E+00	3.59E-06	Up	8.03E-01	3.88E-01		-7.74E-01	1.77E-01		-3.45E-02	9.56E-01		-1.20E+01	2.79E-12	Down	1.70E+00	3.68E-12	Up									
Unigene28452_All	357	4.25	10.22	5.67	9.77	9.36	9.49	18.48	25.05	22.65	1.27E+00	1.43E-04	Up	4.15E-01	3.85E-01		-6.20E-02	8.53E-01		-4.19E-02	9.20E-01		4.39E-01	1.16E-02		2.94E-01	1.10E-01		Unigene28452_All//gi|297842143|ref|XP_002888953.1|//1.00E-16//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334794|gb|EFH65212.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28452_All//4.00E-22//AT1G68820| membrane protein, putative	Unigene28452_All//8.00E-169//TC159216				nr -
Unigene28456_All	1825	0.26	0.28	0.18	0.00	0.09	0.89	5.93	2.40	3.54	1.06E-01	9.23E-01		-5.59E-01	6.28E-01		6.56E+00	2.27E-01		9.80E+00	1.09E-09	Up	-1.30E+00	2.89E-15	Down	-7.46E-01	8.21E-07		Unigene28456_All//gi|224149387|ref|XP_002336800.1|//0.00E+00//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222836925|gb|EEE75318.1| oligopeptide transporter OPT family [Populus trichocarpa]	Unigene28456_All//0.00E+00//AT1G48370| YSL8 (YELLOW STRIPE LIKE 8); oligopeptide transporter	Unigene28456_All//0.00E+00//TC151019				nr -
Unigene28459_All	1045	1.05	0.87	0.76	2.15	4.35	2.16	0.81	0.20	0.38	-2.69E-01	6.51E-01		-4.60E-01	4.97E-01		1.02E+00	1.92E-04	Up	1.06E-02	9.82E-01		-2.02E+00	7.45E-03		-1.09E+00	9.98E-02		Unigene28459_All//gi|124360970|gb|ABN08942.1|//3.00E-51//Quinonprotein alcohol dehydrogenase-like [Medicago truncatula]		Unigene28459_All//4.00E-59//TC173444				nr -
Unigene28846_All	1711	27.31	15.04	14.07	72.81	57.76	31.81	11.02	8.04	6.03	-8.60E-01	1.16E-26		-9.57E-01	1.32E-30		-3.34E-01	1.08E-15		-1.19E+00	4.39E-130	Down	-4.56E-01	5.78E-05		-8.70E-01	2.57E-14		Unigene28846_All//gi|119360031|gb|ABL66744.1|//5.00E-77//At1g54200 [Arabidopsis thaliana]	Unigene28846_All//1.00E-52//AT1G54200| unknown protein	Unigene28846_All//0.00E+00//TC146965				nr +
Unigene28460_All	438	4.30	1.27	2.31	10.01	4.56	10.31	4.92	1.15	2.36	-1.76E+00	5.92E-04	Down	-8.97E-01	7.25E-02		-1.13E+00	2.83E-05	Down	4.30E-02	9.08E-01		-2.10E+00	1.94E-06	Down	-1.06E+00	5.27E-03		Unigene28460_All//gi|75116543|sp|Q67XX3.1|FB252_ARATH//1.00E-27//RecName: Full=F-box protein At5g06550	Unigene28460_All//7.00E-20//AT5G06550| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: cell surface receptor linked signal transduction; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Cyclin-like F-box (InterPro:IPR001810), Transcription factor jumonji/aspartyl beta-hydroxylase (InterPro:IPR003347), Transcription factor jumonji (InterPro:IPR013129); BEST Arabidopsis thaliana protein match is: transferase, transferring glycosyl groups (TAIR:AT1G78280.1); Has 1299 Blast hits to 1289 proteins in 204 species: Archae - 0; Bacteria - 195; Metazoa - 777; Fungi - 106; Plants - 94; Viruses - 0; Other Eukaryotes - 127 (source: NCBI BLink).	Unigene28460_All//3.00E-156//ES830069				nr -
Unigene28464_All	839	2.99	2.78	1.02	10.15	8.04	5.38	3.07	1.64	1.38	-1.08E-01	7.80E-01		-1.56E+00	4.06E-04	Down	-3.36E-01	9.34E-02		-9.15E-01	2.57E-06		-9.03E-01	1.03E-02		-1.16E+00	8.00E-04	Down	Unigene28464_All//gi|20197354|gb|AAM15039.1|//1.00E-09//Expressed protein [Arabidopsis thaliana] >gi|89111870|gb|ABD60707.1| At2g35585 [Arabidopsis thaliana]	Unigene28464_All//7.00E-11//AT2G35585| unknown protein	Unigene28464_All//0.00E+00//ES850995				nr +
Unigene28468_All	634	0.58	2.08	1.85	4.09	3.48	3.21	3.80	0.73	1.70	1.85E+00	3.97E-03		1.68E+00	1.64E-02		-2.33E-01	5.89E-01		-3.50E-01	4.08E-01		-2.39E+00	3.53E-08	Down	-1.16E+00	1.19E-03		Unigene28468_All//gi|56461774|gb|AAV91343.1|//2.00E-37//At2g01990 [Arabidopsis thaliana]	Unigene28468_All//2.00E-38//AT1G14630| unknown protein	Unigene28468_All//1.00E-101//DR459344				nr -
Unigene28469_All	372	35.44	16.75	15.03	46.87	36.47	59.85	54.10	25.06	19.49	-1.08E+00	1.84E-11	Down	-1.24E+00	2.03E-13	Down	-3.62E-01	4.47E-03		3.53E-01	2.39E-03		-1.11E+00	1.04E-21	Down	-1.47E+00	2.99E-34	Down	Unigene28469_All//gi|37625525|gb|AAQ86376.1|//2.00E-15//ribosomal protein L11-like protein [Solanum palustre]	Unigene28469_All//3.00E-16//AT5G45175| 60S ribosomal protein L11 (RPL11D)	Unigene28469_All//0.00E+00//gi|164284723|gb|ES850921.1|ES850921		ko03010|Ribosome		nr -
Unigene2847_All	1008	3.79	21.97	4.17	3.81	8.03	22.98	27.26	81.27	191.33	2.54E+00	1.91E-60	Up	1.39E-01	6.47E-01		1.08E+00	3.94E-08	Up	2.59E+00	2.04E-69	Up	1.58E+00	1.47E-146	Up	2.81E+00	0.00E+00	Up	Unigene2847_All//gi|9795618|gb|AAF98436.1|AC021044_15//1.00E-39//Hypothetical protein [Arabidopsis thaliana]	Unigene2847_All//8.00E-36//AT1G28190| unknown protein	Unigene2847_All//0.00E+00//TC140437				nr +
Unigene28472_All	1038	0.30	3.81	0.62	1.39	1.96	1.57	22.85	85.56	146.38	3.65E+00	8.54E-16	Up	1.03E+00	2.81E-01		4.92E-01	3.16E-01		1.71E-01	7.50E-01		1.90E+00	4.08E-207	Up	2.68E+00	0.00E+00	Up	Unigene28472_All//gi|4914316|gb|AAD32864.1|AC005489_2//2.00E-26//F14N23.2 [Arabidopsis thaliana] >gi|107738163|gb|ABF83653.1| At1g10140 [Arabidopsis thaliana]	Unigene28472_All//6.00E-23//AT1G10140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031279 (InterPro:IPR016972); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G58420.1); Has 38 Blast hits to 38 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene28472_All//1.00E-09//gi|109856645|gb|DW485624.1|DW485624				nr -
Unigene28473_All	508	1.34	1.60	0.84	1.47	2.58	1.96	3.00	8.56	10.35	2.53E-01	7.26E-01		-6.75E-01	4.41E-01		8.08E-01	1.84E-01		4.11E-01	6.02E-01		1.51E+00	4.63E-08	Up	1.79E+00	3.03E-12	Up	Unigene28473_All//gi|13506745|gb|AK28315.1|AF224705_1//2.00E-36//receptor-like protein kinase 4 [Arabidopsis thaliana]	Unigene28473_All//9.00E-32//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene28473_All//1.00E-131//TC137716				nr +
Unigene28474_All	1183	0.40	1.54	1.44	0.29	1.14	1.15	0.64	0.85	2.26	1.95E+00	2.77E-04	Up	1.86E+00	1.15E-03		1.95E+00	1.81E-03		1.96E+00	2.03E-03		3.98E-01	5.45E-01		1.81E+00	1.04E-06	Up	Unigene28474_All//gi|115469600|ref|NP_001058399.1|//3.00E-71//Os06g0685700 [Oryza sativa Japonica Group] >gi|75253259|sp|Q653H7.1|ARFR_ORYSJ RecName: Full=Auxin response factor 18; AltName: Full=OsARF10 >gi|113596439|dbj|BAF20313.1| Os06g0685700 [Oryza sativa Japonica Group]	Unigene28474_All//4.00E-65//AT4G30080| ARF16 (AUXIN RESPONSE FACTOR 16); miRNA binding / transcription factor	Unigene28474_All//0.00E+00//gi|13353479|gb|BG443827.1|BG443827	ARF			nr +
Unigene28477_All	636	53.88	88.83	100.39	0.78	5.25	5.97	0.00	0.00	0.25	7.21E-01	8.36E-24		8.98E-01	1.59E-37		2.75E+00	1.27E-11	Up	2.93E+00	3.33E-13	Up	null	null		7.97E+00	1.40E-01		Unigene28477_All//gi|16323184|gb|AAL15326.1|//9.00E-09//At1g30260/F12P21_9 [Arabidopsis thaliana] >gi|21436007|gb|AAM51581.1| At1g30260/F12P21_9 [Arabidopsis thaliana]	Unigene28477_All//2.00E-09//AT1G30260| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cytokinin stimulus; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: galactosyltransferase family protein (TAIR:AT4G21060.1); Has 16 Blast hits to 16 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene28477_All//1.00E-27//TC161131				nr -
Unigene28478_All	357	79.14	26.40	32.52	84.98	73.21	90.45	195.77	76.45	90.28	-1.58E+00	3.62E-42	Down	-1.28E+00	1.02E-29	Down	-2.15E-01	3.01E-02		9.01E-02	4.45E-01		-1.36E+00	2.45E-100	Down	-1.12E+00	3.68E-76	Down	Unigene28478_All//gi|226528613|ref|NP_001148602.1|//2.00E-23//60S ribosomal protein L15 [Zea mays] >gi|195620698|gb|ACG32179.1| 60S ribosomal protein L15 [Zea mays] >gi|195637452|gb|ACG38194.1| 60S ribosomal protein L15 [Zea mays]	Unigene28478_All//3.00E-12//AT4G16720| 60S ribosomal protein L15 (RPL15A)	Unigene28478_All//0.00E+00//TC155951		ko03010|Ribosome		nr +
Unigene2848_All	2346	5.13	1.99	3.25	8.64	7.60	7.07	3.93	3.42	3.67	-1.37E+00	6.50E-15	Down	-6.60E-01	9.32E-05		-1.85E-01	1.61E-01		-2.91E-01	2.08E-02		-2.00E-01	2.91E-01		-9.91E-02	5.94E-01		Unigene2848_All//gi|297850950|ref|XP_002893356.1|//0.00E+00//galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339198|gb|EFH69615.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2848_All//0.00E+00//AT1G27120| galactosyltransferase family protein	Unigene2848_All//0.00E+00//ES796580			GO:0006464//GO:0009536//GO:0030246//GO:0031224//GO:0035250	nr -
Unigene28480_All	1536	1.16	0.96	0.59	7.33	8.21	5.32	2.01	0.90	0.47	-2.76E-01	5.91E-01		-9.74E-01	5.87E-02		1.63E-01	3.82E-01		-4.62E-01	6.17E-03		-1.16E+00	3.02E-04	Down	-2.11E+00	2.98E-09	Down	Unigene28480_All//gi|22328630|ref|NP_193210.2|//1.00E-170//phosphoinositide binding [Arabidopsis thaliana] >gi|42572905|ref|NP_974549.1| phosphoinositide binding [Arabidopsis thaliana]	Unigene28480_All//3.00E-111//AT3G22810| phosphoinositide binding	Unigene28480_All//0.00E+00//gi|78324923|gb|DT545197.1|DT545197				nr +
Unigene28482_All	1409	2.79	5.43	1.21	6.89	4.59	3.97	0.03	0.09	0.00	9.63E-01	6.69E-06		-1.20E+00	2.56E-04	Down	-5.85E-01	6.35E-04		-7.95E-01	9.85E-06		1.57E+00	5.45E-01		-4.91E+00	6.13E-01		Unigene28482_All//gi|157267438|gb|ABV26441.1|//3.00E-29//cycloidea-like 1b protein [Helianthus annuus]	Unigene28482_All//4.00E-22//AT3G18550| BRC1 (BRANCHED 1); transcription factor	Unigene28482_All//3.00E-26//TC173365	TCP			nr +
Unigene28484_All	588	0.89	0.00	0.36	6.27	13.00	13.06	0.22	2.56	4.20	-9.80E+00	2.93E-03		-1.30E+00	2.42E-01		1.05E+00	1.90E-07	Up	1.06E+00	4.76E-07	Up	3.57E+00	1.40E-07	Up	4.28E+00	5.22E-14	Up	Unigene28484_All//gi|29423270|gb|AAO73521.1|//2.00E-08//gag-pol polyprotein [Glycine max]		Unigene28484_All//3.00E-12//TC172325				nr -
Unigene28485_All	820	0.83	0.87	0.78	3.22	1.97	4.52	23.00	13.97	4.96	6.06E-02	9.57E-01		-9.01E-02	9.22E-01		-7.06E-01	5.83E-02		4.88E-01	1.43E-01		-7.20E-01	3.09E-10		-2.21E+00	8.99E-56	Down	Unigene28485_All//gi|15238913|ref|NP_196658.1|//3.00E-42//zinc finger (C2H2 type) family protein [Arabidopsis thaliana] >gi|8979731|emb|CAB96852.1| zinc finger-like protein [Arabidopsis thaliana]	Unigene28485_All//2.00E-43//AT5G10970| zinc finger (C2H2 type) family protein	Unigene28485_All//6.00E-36//TC163558	C2H2			nr +

Unigene28486_All	297	6.52	3.07	1.97	54.01	67.71	46.38	46.41	23.08	13.41	-1.09E+00	2.08E-02		-1.72E+00	9.79E-04	Down	3.26E-01	6.68E-03		-2.20E-01	1.48E-01		-1.01E+00	4.97E-13	Down	-1.79E+00	3.60E-31	Down	Unigene28486_All//gi|153799903|gb|ABS50670.1|//2.00E-47//alpha-tubulin [Eucalyptus grandis]	Unigene28486_All//5.00E-37//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene28486_All//8.00E-153//EV494150		ko04145|Phagosome		nr +
Unigene28487_All	327	1.76	0.31	0.98	6.25	4.53	4.28	3.49	1.15	0.37	-2.51E+00	2.94E-02		-8.49E-01	3.97E-01		-4.64E-01	3.07E-01		-5.45E-01	2.45E-01		-1.60E+00	7.50E-03		-3.26E+00	8.94E-06	Down	Unigene28487_All//gi|224120040|ref|XP_002318227.1|//9.00E-09//predicted protein [Populus trichocarpa] >gi|222858900|gb|EEE96447.1|predicted protein [Populus trichocarpa]	Unigene28487_All//3.00E-06//AT2G43380| DC1 domain-containing protein					nr +
Unigene28488_All	865	0.00	0.88	0.31	2.48	3.54	3.92	3.18	2.22	5.76	9.78E+00	1.77E-04	Up	8.27E+00	8.02E-02		5.17E-01	1.61E-01		6.61E-01	5.28E-02		-5.15E-01	1.37E-01		8.58E-01	2.55E-04		Unigene28488_All//gi|224054390|ref|XP_002298236.1|//6.00E-66//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|134038600|gb|ABO48368.1| TINY-like protein 1 [Populus trichocarpa] >gi|222845494|gb|EEE83041.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene28488_All//9.00E-48//AT5G25810| tny (TINY); DNA binding / transcription factor	Unigene28488_All//0.00E+00//TC140914	AP2-EREBP			nr +
Unigene28489_All	484	1.73	1.26	1.98	1.54	1.85	3.36	2.53	1.55	0.58	-4.61E-01	5.43E-01		1.95E-01	7.70E-01		2.61E-01	7.79E-01		1.12E+00	3.47E-02		-7.05E-01	2.06E-01		-2.14E+00	3.24E-04	Down	Unigene28489_All//gi|30683442|ref|NP_850805.1|//1.00E-53//pre-mRNA cleavage complex-related [Arabidopsis thaliana] >gi|42573337|ref|NP_974765.1| pre-mRNA cleavage complex-related [Arabidopsis thaliana]	Unigene28489_All//9.00E-55//AT5G11010| pre-mRNA cleavage complex-related	Unigene28489_All//2.00E-105//DR461669				nr -
Unigene2849_All	1448	55.61	161.98	31.30	144.66	215.15	108.20	119.83	136.44	301.71	1.54E+00	0.00E+00	Up	-8.29E-01	3.01E-41		5.73E-01	2.91E-102		-4.19E-01	2.21E-35		1.87E-01	7.24E-09		1.33E+00	0.00E+00	Up	Unigene2849_All//gi|171452362|dbj|BAG15872.1|//1.00E-147//transcription factor [Bruguiera gymnorhiza]	Unigene2849_All//4.00E-63//AT2G40140| CZF1; transcription factor	Unigene2849_All//0.00E+00//TC170402	C3H		GO:0006952//GO:0009743	nr +
Unigene28490_All	584	0.90	1.48	0.55	1.45	1.24	1.08	1.38	3.01	3.89	7.19E-01	3.48E-01		-7.12E-01	4.97E-01		-2.28E-01	7.79E-01		-4.22E-01	6.18E-01		1.13E+00	1.16E-02		1.50E+00	1.14E-04	Up								
Unigene28491_All	844	0.50	0.78	0.69	6.96	6.81	3.48	1.75	2.03	0.80	6.54E-01	4.48E-01		4.85E-01	6.30E-01		-3.16E-02	9.05E-01		-1.00E+00	3.34E-05	Down	2.12E-01	6.38E-01		-1.13E+00	1.72E-02		Unigene28491_All//gi|224090677|ref|XP_002309054.1|//7.00E-11//predicted protein [Populus trichocarpa] >gi|222855030|gb|EEE92577.1|predicted protein [Populus trichocarpa]		Unigene28491_All//0.00E+00//gi|21098685|gb|BQ410998.1|BQ410998				nr -
Unigene28492_All	559	3.00	5.17	4.48	1.60	5.98	1.45	0.00	0.00	0.00	7.87E-01	3.32E-02		5.80E-01	1.67E-01		1.90E+00	1.10E-07	Up	-1.41E-01	8.48E-01		null	null		null	null				Unigene28492_All//7.00E-07//EX168199				
Unigene28493_All	1067	2.11	0.76	1.20	4.30	7.20	1.99	1.03	0.43	0.37	-1.47E+00	9.69E-04	Down	-8.16E-01	6.86E-02		7.45E-01	1.89E-04		-1.11E+00	7.52E-05	Down	-1.26E+00	3.46E-02		-1.46E+00	1.18E-02		Unigene28493_All//gi|30689405|ref|NP_197820.2|//1.00E-55//WD-40 repeat family protein [Arabidopsis thaliana]	Unigene28493_All//3.00E-54//AT5G24320| WD-40 repeat family protein					nr -
Unigene28496_All	971	1.62	1.88	1.48	12.98	4.75	14.79	12.67	22.60	14.11	2.17E-01	6.34E-01		-1.27E-01	8.07E-01		-1.45E+00	1.23E-20	Down	1.89E-01	2.63E-01		8.35E-01	5.78E-15		1.56E-01	2.92E-01		Unigene28496_All//gi|15221679|ref|NP_174417.1|//5.00E-60//LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4) [Arabidopsis thaliana] >gi|29428037|sp|Q9SHE9.1|LBD4_ARATH RecName: Full=LOB domain-containing protein 4; AltName: Full=ASYMMETRIC LEAVES 2-like protein 6; Short=AS2-like protein 6 >gi|6692123|gb|AAF24588.1|AC007654_4 T19E23.11 [Arabidopsis thaliana] >gi|50253474|gb|AAT71939.1|At1g31320 [Arabidopsis thaliana] >gi|51972120|gb|AAU15164.1|At1g31320 [Arabidopsis thaliana] >gi|219807088|dbj|BAH10550.1|ASYMMETRIC LEAVES2-like 6 protein [Arabidopsis thaliana]	Unigene28496_All//2.00E-61//AT1G31320| LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4)	Unigene28496_All//0.00E+00//gi|109873715|gb|DW502690.1|DW502690		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene28497_All	513	13.97	49.88	23.87	4.66	11.95	7.57	0.66	0.65	3.18	1.84E+00	1.13E-46	Up	7.73E-01	3.99E-06		1.36E+00	8.96E-09	Up	7.00E-01	2.51E-02		-1.65E-02	1.02E+00		2.27E+00	1.29E-05	Up			Unigene28497_All//6.00E-07//TC140954				
Unigene28498_All	801	1.63	1.71	2.79	4.35	5.03	5.07	1.90	0.47	0.65	6.48E-02	9.18E-01		7.74E-01	8.44E-02		2.08E-01	5.56E-01		2.21E-01	5.26E-01		-2.02E+00	1.51E-04	Down	-1.56E+00	1.38E-03		Unigene28498_All//gi|15228789|ref|NP_191158.1|//3.00E-94//ESK1 (ESKIMO 1) [Arabidopsis thaliana]	Unigene28498_All//1.00E-95//AT3G55990| ESK1 (ESKIMO 1)	Unigene28498_All//4.00E-89//TC170083				nr -
Unigene28501_All	376	3.62	14.15	9.06	2.38	4.76	11.89	12.82	7.78	5.72	1.97E+00	3.59E-11	Up	1.33E+00	2.34E-04	Up	9.98E-01	4.19E-02		2.32E+00	4.28E-12	Up	-7.20E-01	3.14E-03		-1.16E+00	1.97E-06	Down	Unigene28501_All//gi|297800436|ref|XP_002868102.1|//8.00E-09//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297313938|gb|EFH84361.1|oxidoreductase [Arabidopsis lyrata subsp. lyrata]		Unigene28501_All//1.00E-112//gi|3326436|gb|AI055322.1|AI055322				nr -
Unigene28502_All	802	0.00	0.00	0.00	0.25	0.34	0.34	80.45	8.91	22.70	null	null		null	null		4.68E-01	8.17E-01		4.44E-01	7.63E-01		-3.17E+00	1.97E-273	Down	-1.83E+00	1.07E-146	Down	Unigene28502_All//gi|297820136|ref|XP_002877951.1|//2.00E-59//universal stress protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323789|gb|EFH54210.1|universal stress protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28502_All//7.00E-60//AT3G53990| universal stress protein (USP) family protein	Unigene28502_All//0.00E+00//DR460631				nr +
Unigene28503_All	641	8.33	8.93	5.23	7.85	8.11	6.13	45.38	25.36	16.78	1.02E-01	6.88E-01		-6.70E-01	1.32E-02		4.75E-02	8.80E-01		-3.57E-01	2.15E-01		-8.39E-01	9.01E-20		-1.44E+00	2.79E-47	Down	Unigene28503_All//gi|297851424|ref|XP_002893593.1|//3.00E-13//60S ribosomal protein L18A-1 [Arabidopsis lyrata subsp. lyrata] >gi|297339435|gb|EFH09852.1| 60S ribosomal protein L18A-1 [Arabidopsis lyrata subsp. lyrata]	Unigene28503_All//2.00E-14//AT2G34480| 60S ribosomal protein L18A (RPL18aB)	Unigene28503_All//0.00E+00//TC175347		ko03010|Ribosome		nr -
Unigene28504_All	692	0.30	0.00	0.31	2.30	2.19	2.68	0.79	1.39	2.42	-8.24E+00	1.22E-01		2.55E-02	1.00E+00		-7.32E-02	8.77E-01		2.16E-01	6.91E-01		8.07E-01	2.12E-01		1.61E+00	5.97E-04	Up	Unigene28504_All//gi|255544956|ref|XP_002513539.1|//2.00E-09//leucine-rich repeat containing protein, putative [Ricinus communis] >gi|223547447|gb|EEF48942.1|leucine-rich repeat containing protein, putative [Ricinus communis]		Unigene28504_All//2.00E-81//DN800146				nr +
Unigene28506_All	550	28.82	11.33	30.59	7.16	6.45	11.09	0.00	0.00	0.00	-1.35E+00	5.72E-19	Down	8.60E-02	6.11E-01		-1.50E-01	6.57E-01		6.32E-01	8.27E-03		null	null		null	null				Unigene28506_All//3.00E-92//ES795123				
Unigene28507_All	482	28.22	46.57	34.03	35.24	43.22	80.68	24.21	131.11	42.81	7.23E-01	5.84E-10		2.70E-01	7.20E-02		2.95E-01	1.38E-02		1.19E+00	2.38E-40	Up	2.44E+00	2.85E-201	Up	8.23E-01	3.70E-14				Unigene28507_All//2.00E-121//gi|82755680|gb|DV849242.1|DV849242				
Unigene28510_All	544	33.18	28.78	28.88	38.18	31.40	42.01	76.40	40.72	24.83	-2.05E-01	1.36E-01		-2.01E-01	1.69E-01		-2.82E-01	1.78E-02		1.38E-01	3.10E-01		-9.08E-01	9.42E-32		-1.62E+00	2.65E-80	Down	Unigene28510_All//gi|282848248|gb|ADB02905.1|//8.00E-31//cytochrome b-c1 complex subunit 8 [Jatropha curcas]	Unigene28510_All//1.00E-30//AT3G10860| ubiquinol-cytochrome C reductase complex ubiquinone-binding protein, putative / ubiquinol-cytochrome C reductase complex 8.2 kDa protein, putative	Unigene28510_All//0.00E+00//TC170400				nr -
Unigene28511_All	810	28.68	12.14	14.99	1.66	3.49	2.12	0.00	0.10	0.00	-1.24E+00	2.98E-24	Down	-9.36E-01	5.80E-15		1.07E+00	3.51E-03		3.52E-01	5.25E-01		6.69E+00	4.01E-01		null	null		Unigene28511_All//gi|41745624|gb|AAS10177.1|//7.00E-90//YABBY-like transcription factor GRAMINIFOLIA [Antirrhinum majus]	Unigene28511_All//1.00E-67//AT2G45190| AFO (ABNORMAL FLORAL ORGANS); protein binding / transcription factor/ transcription regulator	Unigene28511_All//0.00E+00//gi|164271143|gb|ES818051.1|ES818051	C2C2-YABBY			nr -
Unigene28515_All	332	176.50	88.06	108.42	210.36	234.72	222.55	87.23	47.71	66.72	-1.00E+00	7.58E-43	Down	-7.03E-01	9.00E-23		1.58E-01	7.75E-03		8.13E-02	2.64E-01		-8.71E-01	6.69E-21		-3.87E-01	1.01E-05		Unigene28515_All//gi|6015064|sp|P93447.3|EFID_PIMBR//1.00E-27//RecName: Full=Elongation factor 1-delta; Short=EF-1-delta; AltName: Full=Elongation factor 1B-beta; AltName: Full=eEF-1B beta >gi|18418870|gb|AAB68395.1|elongation factor 1-beta [Pimpinella brachycarpa]	Unigene28515_All//1.00E-25//AT2G18110| elongation factor 1-beta, putative / EF-1-beta, putative	Unigene28515_All//3.00E-177//gi|13356382|gb|BG446730.1|BG446730				nr +
Unigene28516_All	504	12.98	5.83	10.25	155.67	118.00	99.65	238.08	190.90	78.57	-1.15E+00	1.13E-06	Down	-3.41E-01	1.72E-01		-4.00E-01	6.64E-14		-6.44E-01	4.68E-29		-3.19E-01	2.52E-14		-1.60E+00	7.29E-226	Down			Unigene28516_All//3.00E-123//gi|164353858|gb|EX166932.1|EX166932				
Unigene28517_All	759	2.76	3.81	4.07	40.63	32.03	14.82	4.01	0.28	0.94	4.65E-01	2.14E-01		5.61E-01	1.37E-01		-3.43E-01	1.67E-04		-1.46E+00	5.71E-44	Down	-3.86E+00	9.31E-16	Down	-2.09E+00	4.90E-09	Down	Unigene28517_All//gi|297811791|ref|XP_002873779.1|//1.00E-26//rop-interactive crib motif-containing protein 4 [Arabidopsis lyrata subsp. lyrata] >gi|297319616|gb|EFH50038.1| rop-interactive crib motif-containing protein 4 [Arabidopsis lyrata subsp. lyrata]	Unigene28517_All//1.00E-17//AT5G16190| RIC4 (ROP-INTERACTIVE CRIB MOTIF-CONTAINING PROTEIN 4); protein binding					nr -
Unigene28518_All	552	9.76	8.26	4.53	6.86	10.79	3.68	1.84	1.14	0.79	-2.41E-01	3.72E-01		-1.11E+00	4.83E-05	Down	6.54E-01	5.26E-03		-8.98E-01	3.98E-03		-6.95E-01	2.63E-01		-1.21E+00	4.17E-02		Unigene28518_All//gi|155967399|gb|ABU41516.1|//1.00E-62//biotin carboxyl carrier protein subunit [Gossypium hirsutum]	Unigene28518_All//4.00E-33//AT5G16390| CAC1 (CHLOROPLASTIC ACETYLCOENZYME A CARBOXYLASE 1); acetyl-CoA carboxylase/ biotin binding	Unigene28518_All//0.00E+00//gi|78347647|gb|DT567921.1|DT567921		ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis		nr +
Unigene28519_All	680	2.85	6.33	4.70	2.49	1.82	2.39	1.06	0.86	0.41	1.15E+00	1.18E-04	Up	7.23E-01	4.65E-02		-4.50E-01	3.87E-01		-5.89E-02	9.21E-01		-2.97E-01	6.85E-01		-1.37E+00	6.51E-02									
Unigene2852_All	1576	1.59	2.67	3.41	0.41	0.13	0.66	0.27	0.58	0.20	7.44E-01	1.21E-02		1.10E+00	5.35E-05	Up	-1.65E+00	6.52E-02		6.82E-01	3.45E-01		1.12E+00	8.95E-02		-4.08E-01	6.54E-01		Unigene2852_All//gi|21700765|gb|AAG38144.1|//1.00E-120//phosphoglycerate mutase-like protein [Glycine max]	Unigene2852_All//1.00E-112//AT5G64460| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G58280.3); Has 385 Blast hits to 382 proteins in 84 species: Archae - 0; Bacteria - 19; Metazoa - 2; Fungi - 201; Plants - 67; Viruses - 0; Other Eukaryotes - 96 (source: NCBI BLink).	Unigene2852_All//0.00E+00//TC162224				nr +
Unigene28520_All	545	0.29	8.37	0.59	5.12	5.94	8.62	10.16	11.89	16.52	4.86E+00	7.93E-22	Up	1.03E+00	4.71E-01		2.15E-01	5.88E-01		7.52E-01	6.72E-03		2.26E-01	3.28E-01		7.01E-01	2.80E-05		Unigene28520_All//gi|99646724|emb|CAK22419.1|//7.00E-35//B12D-like protein [Beta vulgaris]	Unigene28520_All//9.00E-33//AT3G48140| senescence-associated protein, putative	Unigene28520_All//0.00E+00//TC168410				nr +
Unigene28522_All	514	1.73	4.04	3.11	9.59	10.59	59.84	23.85	24.64	59.99	1.22E+00	7.47E-03		8.45E-01	1.25E-01		1.42E-01	6.27E-01		2.64E+00	6.87E-94	Up	4.66E-02	7.80E-01		1.33E+00	2.70E-44	Up	Unigene28522_All//gi|40218371|gb|AB83118.1|//1.00E-46//secretory laccase [Gossypium arboreum]	Unigene28522_All//3.00E-40//AT5G09360| LAC14 (laccase 14); laccase	Unigene28522_All//0.00E+00//TC134603		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +

Unigene28523_All	706	16.38	42.49	25.87	45.37	67.90	106.64	12.70	25.63	46.16	1.38E+00	3.52E-36	Up	6.60E-01	7.92E-07		5.82E-01	2.06E-16		1.23E+00	1.26E-81	Up	1.01E+00	5.56E-17	Up	1.86E+00	1.29E-75	Up	Unigene28523_All//gi|40218371|gb|AAR83118.1|//1.00E-61//secretory laccase [Gossypium arboreum]	Unigene28523_All//3.00E-44//AT5G09360| LAC14 (laccase 14); laccase	Unigene28523_All//0.00E+00//gi|164343933|gb|ES810495.1|ES810495		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene28525_All	1036	2.32	0.68	1.03	8.99	8.94	3.10	0.41	0.16	0.23	-1.76E+00	7.43E-05	Down	-1.18E+00	7.06E-03		-8.10E-03	9.66E-01		-1.54E+00	8.81E-15	Down	-1.34E+00	2.24E-01		-8.23E-01	3.99E-01		Unigene28525_All//gi|225463464|ref|XP_002272948.1|//4.00E-64//PREDICTED: similar to cytochrome B561-related [Vitis vinifera]	Unigene28525_All//8.00E-54//AT2G30890| membrane protein, putative					nr +
Unigene28526_All	623	2.60	1.46	3.50	2.64	4.15	4.20	3.12	1.34	0.77	-8.31E-01	1.08E-01		4.29E-01	3.62E-01		6.52E-01	1.02E-01		6.72E-01	9.36E-02		-1.22E+00	3.87E-03		-2.02E+00	7.23E-06	Down	Unigene28526_All//gi|124359162|gb|AB005685.1|//7.00E-16//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene28526_All//8.00E-10//TC161815					nr -
Unigene28527_All	857	0.61	0.35	0.75	2.67	0.88	0.79	74.00	13.80	3.30	-7.83E-01	4.22E-01		2.88E-01	7.25E-01		-1.60E+00	9.43E-05	Down	-1.76E+00	7.84E-05	Down	-2.42E+00	3.66E-201	Down	-4.49E+00	0.00E+00	Down	Unigene28527_All//gi|9294177|dbj|BAB02079.1|//1.00E-66//nodulin-1ile protein [Arabidopsis thaliana]	Unigene28527_All//3.00E-37//AT3G25190| nodulin, putative	Unigene28527_All//2.00E-38//gi|109885344|gb|DW514314.1|DW514314		ko03040|Spliceosome		nr +
Unigene28528_All	409	118.46	37.79	47.65	237.99	202.74	229.46	125.08	78.07	97.02	-1.65E+00	4.33E-76	Down	-1.31E+00	1.66E-52	Down	-2.31E-01	2.13E-06		-5.26E-02	4.28E-01		-6.80E-01	6.10E-24		-3.67E-01	1.34E-08		Unigene28528_All//gi|15225613|ref|NP_181530.1|//4.00E-89//60S acidic ribosomal protein P0 (RPP0A) [Arabidopsis thaliana] >gi|12229886|sp|O04204.1|RLA01_ARATH RecName: Full=60S acidic ribosomal protein P0-1 >gi|2088654|gb|AAB95286.1| 60S acidic ribosomal protein P0 [Arabidopsis thaliana]	Unigene28528_All//3.00E-50//AT2G40010| 60S acidic ribosomal protein P0 (RPP0A)	Unigene28528_All//0.00E+00//gi|78337086|gb|DT557360.1|DT557360		ko03010|Ribosome		nr -
Unigene28530_All	899	9.84	2.37	1.24	1.11	1.76	0.25	7.38	8.51	8.91	-2.05E+00	2.92E-19	Down	-2.98E+00	4.72E-28	Down	6.69E-01	2.24E-01		-2.14E+00	5.32E-03		2.05E-01	3.37E-01		2.71E-01	1.48E-01		Unigene28530_All//gi|19309913|emb|CAC41010.2|//1.00E-116//Mobl-like protein [Medicago sativa subsp. falcata] >gi|47846249|emb|CAG25781.1| Mobl-like protein [Medicago sativa subsp. falcata]	Unigene28530_All//4.00E-107//AT5G45550| mobl/phocein family protein	Unigene28530_All//0.00E+00//TC138642				nr -
Unigene28532_All	866	0.00	0.23	0.00	2.36	2.27	8.55	2.98	5.98	1.06	7.87E+00	1.36E-01		null	null		-5.73E-02	8.94E-01		1.86E+00	5.03E-15	Up	1.01E+00	2.19E-05	Up	-1.49E+00	3.19E-05	Down	Unigene28532_All//gi|15221679|ref|NP_174417.1|//1.00E-36//LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4) [Arabidopsis thaliana] >gi|29428037|sp|Q9SHE9.1|LBD4_ARATH RecName: Full=LOB domain-containing protein 4; AltName: Full=ASYMMETRIC LEAVES 2-like protein 6; Short=AS2-like protein 6 >gi|6692123|gb|AAF24588.1|AC007654_4 T19E23.11 [Arabidopsis thaliana] >gi|50253474|gb|AAT71939.1| At1g31320 [Arabidopsis thaliana] >gi|51972120|gb|AAU15164.1| At1g31320 [Arabidopsis thaliana] >gi|219807088|dbj|BAH10550.1| ASYMMETRIC LEAVES2-like 6 protein [Arabidopsis thaliana]	Unigene28532_All//4.00E-31//AT1G31320| LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4)	Unigene28532_All//0.00E+00//TC144603		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene28533_All	510	2.46	0.99	2.40	22.86	11.34	8.41	4.56	2.38	2.03	-1.31E+00	3.41E-02		-3.60E-02	9.71E-01		-1.01E+00	6.29E-11	Down	-1.44E+00	1.02E-16	Down	-9.40E-01	1.20E-02		-1.17E+00	1.46E-03		Unigene28533_All//gi|15218382|ref|NP_177360.1|//9.00E-23//PATL1 (PATELLIN 1); transporter [Arabidopsis thaliana] >gi|78099065|sp|Q56WK6.2|PATL1_ARATH RecName: Full=Patellin-1	Unigene28533_All//5.00E-24//AT1G72150| PATL1 (PATELLIN 1); transporter	Unigene28533_All//2.00E-13//TC172129				nr +
Unigene28534_All	293	8.04	23.86	10.54	16.66	13.28	12.18	58.87	57.91	42.29	1.57E+00	8.66E-11	Up	3.92E-01	3.05E-01		-3.27E-01	2.51E-01		-4.52E-01	1.09E-01		-2.37E-02	8.74E-01		-4.78E-01	3.88E-05		Unigene28534_All//gi|297613088|ref|NP_001066671.2|//3.00E-45//Os12g0428600 [Oryza sativa Japonica Group] >gi|255670264|dbj|BAF29690.2| Os12g0428600 [Oryza sativa Japonica Group]	Unigene28534_All//9.00E-42//AT1G70320| UPL2 (UBIQUITIN-PROTEIN LIGASE 2); ubiquitin-protein ligase	Unigene28534_All//1.00E-164//TC177303		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene28535_All	397	62.47	29.99	65.32	45.17	48.66	39.25	4.58	4.53	10.74	-1.06E+00	3.35E-20	Down	6.44E-02	6.42E-01		1.07E-01	4.91E-01		-2.03E-01	1.59E-01		-1.66E-02	1.01E+00		1.23E+00	3.55E-06	Up	Unigene28535_All//gi|242199346|gb|ACS87994.1|//4.00E-27//UDP-glucosyltransferase family 1 protein [Citrus sinensis]	Unigene28535_All//2.00E-17//AT1G22370| AtUGT85A5 (UDP-glucosyl transferase 85A5); glucuronosyltransferase/ transferase, transferring glycosyl groups	Unigene28535_All//0.00E+00//TC136268		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis		nr +
Unigene28539_All	315	5.48	5.95	4.56	14.87	16.84	6.45	5.91	3.18	3.16	1.19E-01	7.92E-01		-2.64E-01	6.37E-01		1.80E-01	5.57E-01		-1.20E+00	1.58E-05	Down	-8.91E-01	3.70E-02		-9.01E-01	2.77E-02									
Unigene2854_All	2409	9.27	312.51	16.87	7.07	8.83	16.84	12.20	70.25	67.46	5.07E+00	0.00E+00	Up	8.63E-01	1.53E-22		3.21E-01	5.83E-03		1.25E+00	3.47E-45	Up	2.53E+00	0.00E+00	Up	2.47E+00	0.00E+00	Up	Unigene2854_All//gi|18405495|ref|NP_565940.1|//1.00E-171//rhodanese-like domin-containing protein [Arabidopsis thaliana] >gi|95147288|gb|ABF57279.1| At2g40760 [Arabidopsis thaliana]	Unigene2854_All//3.00E-157//AT2G40760| rhodanese-like domain-containing protein	Unigene2854_All//0.00E+00//TC170195			GO:0043231	nr -
Unigene28541_All	1155	367.42	620.49	459.15	18.85	61.69	45.55	0.00	0.22	0.10	7.56E-01	0.00E+00		3.22E-01	1.12E-48		1.71E+00	6.88E-138	Up	1.27E+00	4.42E-60	Up	7.76E+00	4.31E-02		6.69E+00	2.43E-01		Unigene28541_All//gi|18405191|gb|AAM22683.1|AF482951_1//1.00E-127//carbonic anhydrase [Gossypium hirsutum]	Unigene28541_All//3.00E-95//AT3G01500| CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	Unigene28541_All//0.00E+00//TC145204		ko00910|Nitrogen metabolism		nr +
Unigene28542_All	815	0.26	0.62	0.52	47.92	41.79	38.51	0.88	3.69	0.54	1.28E+00	2.31E-01		1.03E+00	3.96E-01		-1.98E-01	2.18E-02		-3.15E-01	1.84E-04		2.07E+00	1.69E-08	Up	-7.14E-01	3.27E-01		Unigene28542_All//gi|30682417|ref|NP_850793.1|//2.00E-19//VQ motif-containing protein [Arabidopsis thaliana] >gi|91806832|gb|ABE66143.1| VQ motif-containing protein [Arabidopsis thaliana] >gi|109946555|gb|ADG48456.1| At5g08480 [Arabidopsis thaliana]	Unigene28542_All//4.00E-16//AT5G08480| VQ motif-containing protein	Unigene28542_All//2.00E-29//gi|109876547|gb|DW505521.1|DW505521				nr +
Unigene28543_All	427	1.35	2.02	1.12	4.43	4.84	4.87	4.36	5.38	11.29	5.82E-01	4.27E-01		-2.64E-01	7.67E-01		1.26E-01	8.36E-01		1.34E-01	7.76E-01		3.05E-01	4.47E-01		1.37E+00	5.50E-08	Up	Unigene28543_All//gi|18700163|gb|AAL77693.1|//3.00E-07//AT4g02720/T10P11_1 [Arabidopsis thaliana] >gi|20857302|gb|AAM26710.1| AT4g02720/T10P11_1 [Arabidopsis thaliana]		Unigene28543_All//3.00E-36//C0129412				nr -
Unigene28546_All	610	400.38	380.19	466.85	31.69	46.06	71.74	19.06	98.94	100.90	-7.47E-02	3.40E-02		2.22E-01	2.79E-13		5.40E-01	1.20E-08		1.18E+00	2.07E-44	Up	2.38E+00	1.50E-186	Up	2.40E+00	1.59E-196	Up	Unigene28546_All//gi|16848851|gb|AAB36543.1|//1.00E-37//DnaJ-like protein [Phaseolus vulgaris]	Unigene28546_All//9.00E-30//AT4G36040| DNAJ heat shock N-terminal domain-containing protein (J11)	Unigene28546_All//0.00E+00//TC156737				nr -
Unigene28547_All	605	240.42	141.46	141.44	16.22	15.25	2.69	0.00	0.00	0.00	-7.65E-01	8.58E-67		-7.65E-01	1.21E-64		-8.86E-02	6.87E-01		-2.59E+00	2.31E-30	Down	null	null		null	null		Unigene28547_All//gi|22328170|ref|NP_680546.1|//8.00E-36//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|14533294|ref|NP_001078336.1| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|20147360|gb|AAM10392.1| AT4g00170/F6N15_21 [Arabidopsis thaliana] >gi|62236106|gb|AAV84509.1| At4g00165 [Arabidopsis thaliana]	Unigene28547_All//5.00E-35//AT4G00165| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene28547_All//0.00E+00//TC159236				nr +
Unigene28548_All	493	0.85	5.86	2.38	2.73	2.65	2.20	2.40	1.61	1.05	2.79E+00	2.99E-09	Up	1.48E+00	3.04E-02		-3.97E-02	9.41E-01		-3.11E-01	6.37E-01		-5.76E-01	3.18E-01		-1.19E+00	2.80E-02									
Unigene28551_All	1107	14.65	5.77	3.22	8.59	9.49	3.67	2.18	0.15	1.51	-1.35E+00	2.38E-19	Down	-2.18E+00	4.33E-36	Down	1.43E-01	5.12E-01		-1.23E+00	7.45E-11	Down	-3.85E+00	1.50E-12	Down	-5.26E-01	1.40E-01		Unigene28551_All//gi|257831433|gb|ACV71017.1|//2.00E-73//UPA17 [Capsicum annuum]	Unigene28551_All//4.00E-28//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene28551_All//0.00E+00//TC132104	GRF			nr +
Unigene28554_All	348	7.67	20.24	15.76	8.87	8.02	7.53	31.35	28.10	18.55	1.40E+00	2.74E-09	Up	1.04E+00	1.04E-04	Up	-1.47E-01	7.14E-01		-2.38E-01	5.58E-01		-1.58E-01	3.82E-01		-7.57E-01	5.15E-07		Unigene28554_All//gi|71040677|gb|AAZ20287.1|//2.00E-13//ubiquitin-conjugating enzyme 2 [Arachis hypogaea]	Unigene28554_All//2.00E-11//AT1G70660| UBC22 (UBC ZWEI HOMOLOGE 2); protein binding / ubiquitin-protein ligase	Unigene28554_All//4.00E-78//gi|109826967|gb|DW225675.1|DW225675				nr +
Unigene28557_All	411	3.95	1.73	0.52	2.67	3.35	4.84	10.39	2.75	2.42	-1.19E+00	2.32E-02		-2.93E+00	1.92E-05	Down	3.30E-01	6.09E-01		8.59E-01	6.81E-02		-1.92E+00	8.79E-11	Down	-2.10E+00	1.89E-12	Down			Unigene28557_All//5.00E-13//TC140743				
Unigene28559_All	559	14.23	10.06	9.34	3.48	4.87	7.27	1.74	3.22	0.50	-5.00E-01	1.55E-02		-6.08E-01	4.59E-03		4.86E-01	2.25E-01		1.07E+00	4.39E-04	Up	8.86E-01	4.22E-02		-1.80E+00	5.53E-03		Unigene28559_All//gi|30102908|gb|AAP21372.1|//1.00E-48//At5g02710 [Arabidopsis thaliana]	Unigene28559_All//7.00E-50//AT5G02710| unknown protein	Unigene28559_All//0.00E+00//TC158040				nr -
Unigene2856_All	1398	3.18	1.38	3.54	3.28	2.86	2.91	3.66	2.84	2.19	-1.21E+00	4.26E-05	Down	1.55E-01	6.26E-01		-1.98E-01	5.47E-01		-1.73E-01	6.16E-01		-3.66E-01	1.39E-01		-7.38E-01	1.23E-03		Unigene2856_All//gi|30688712|ref|NP_194780.2|//1.00E-130//AtATG18b [Arabidopsis thaliana]	Unigene2856_All//2.00E-123//AT4G30510| AtATG18b	Unigene2856_All//2.00E-55//TC165352				nr -
Unigene28560_All	484	33.51	13.82	19.58	46.93	50.73	85.66	18.26	19.08	17.86	-1.28E+00	6.16E-18	Down	-7.75E-01	6.64E-08		1.12E-01	3.94E-01		8.68E-01	1.14E-25		6.39E-02	7.38E-01		-3.16E-02	8.76E-01				Unigene28560_All//2.00E-161//gi|81167987|gb|DR456635.1|DR456635				
Unigene28562_All	522	11.63	24.66	9.49	20.99	24.08	27.25	11.58	13.61	21.52	1.08E+00	3.26E-11	Up	-2.93E-01	2.63E-01		1.98E-01	2.72E-01		3.76E-01	1.25E-02		2.33E-01	2.81E-01		8.94E-01	3.29E-09				Unigene28562_All//4.00E-128//BF270264				
Unigene28564_All	412	0.38	3.57	0.52	4.23	4.26	4.38	5.03	2.64	7.35	3.23E+00	1.15E-05	Up	4.40E-01	7.75E-01		1.05E-02	9.97E-01		5.12E-02	9.37E-01		-9.31E-01	2.02E-02		5.47E-01	7.91E-02				Unigene28564_All//5.00E-07//TC178533				
Unigene28567_All	618	0.85	0.74	0.95	5.08	7.80	4.24	11.56	16.50	35.00	-1.98E-01	8.20E-01		1.63E-01	8.50E-01		6.19E-01	2.11E-02		-2.61E-01	5.01E-01		5.13E-01	1.32E-03		1.60E+00	6.68E-41	Up			Unigene28567_All//0.00E+00//TC179289				
Unigene28568_All	499	3.04	11.88	1.92	18.97	2.14	14.12	124.55	360.41	122.63	1.97E+00	2.34E-12	Up	-6.63E-01	2.41E-01		-3.15E+00	7.72E-42	Down	-4.26E-01	2.42E-02		1.53E+00	0.00E+00	Up	-2.25E-02	7.51E-01		Unigene28568_All//gi|297827173|ref|XP_002881469.1|//2.00E-10//don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297327308|gb|EFH57728.1| don-glucosyltransferase [Arabidopsis lyrata subsp. lyrata]		Unigene28568_All//0.00E+00//gi|164309302|gb|ES850990.1|ES850990		ko00908|Zeatin biosynthesis		nr +
Unigene28569_All	536	4.59	17.11	40.93	38.75	8.48	19.89	318.28	369.61	134.83	1.90E+00	6.30E-18	Up	3.16E+00	1.39E-73	Up	-2.19E+00	1.67E-60	Down	-9.63E-01	1.07E-15		2.16E-01	2.05E-11		-1.24E+00	4.73E-218	Down	Unigene28569_All//gi|225433078|ref|XP_002285104.1|//6.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene28569_All//0.00E+00//TC153431				nr -
Unigene28573_All	1717	0.03	0.41	0.37	0.29	1.34	1.50	3.62	13.07	25.59	3.76E+00	2.36E-03		3.61E+00	6.97E-03		2.21E+00	1.77E-06	Up	2.37E+00	2.39E-07	Up	1.85E+00	6.70E-51	Up	2.82E+00	6.59E-168	Up	Unigene28573_All//gi|15235905|ref|NP_194034.1|//0.00E+00//MATE efflux protein-related [Arabidopsis thaliana]	Unigene28573_All//4.00E-158//AT4G23030| MATE efflux protein-related	Unigene28573_All//0.00E+00//DN780885				nr -
Unigene28574_All	2458	0.21	0.37	0.04	0.24	0.17	0.51	2.34	1.58	15.27	8.02E-01	2.71E-01		-2.30E+00	6.76E-02		-5.33E-01	5.62E-01		1.08E+00	8.18E-02		-5.65E-01	1.08E-02		2.71E+00	3.12E-137	Up	Unigene28574_All//gi|87162555|gb|ABD28350.1|//1.00E-100//Protein phosphatase 2C-1ike [Medicago truncatula]	Unigene28574_All//7.00E-97//AT3G16800| protein phosphatase 2C, putative / PP2C, putative	Unigene28574_All//1.00E-39//TC134595				nr +

Unigene28578_All	1072	0.54	0.57	0.65	8.46	4.37	2.99	6.67	5.07	4.76	7.92E-02	9.41E-01		2.66E-01	7.36E-01		-9.53E-01	7.31E-08		-1.50E+00	6.92E-14	Down	-3.95E-01	4.85E-02		-4.87E-01	1.03E-02		Unigene28578_All//gi|15221679|ref|NP_174417.1|//2.00E-73//LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4) [Arabidopsis thaliana] >gi|29428037|sp|Q9SHE9.1|LBD4_ARATH RecName: Full=LOB domain-containing protein 4; AltName: Full=ASYMMETRIC LEAVES 2-like protein 6; Short=AS2-like protein 6 >gi|6692123|gb|AAF24588.1|AC007654_4 T19E23.11 [Arabidopsis thaliana] >gi|50253474|gb|AAT71939.1|At1g31320 [Arabidopsis thaliana] >gi|51972120|gb|AAU15164.1|At1g31320 [Arabidopsis thaliana] >gi|219807088|dbj|BAH10550.1|ASYMMETRIC LEAVES2-like 6 protein [Arabidopsis thaliana]	Unigene28578_All//2.00E-55//AT1G31320| LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4)	Unigene28578_All//7.00E-107//TC144603		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene28579_All	707	0.00	0.07	0.23	0.56	1.32	0.19	2.03	2.84	0.17	6.16E+00	6.16E-01		7.82E+00	2.39E-01		1.22E+00	1.05E-01		-1.56E+00	2.31E-01		4.81E-01	2.53E-01		-3.59E+00	1.22E-07	Down	Unigene28579_All//gi|224090875|ref|XP_002309107.1|//5.00E-86//cytochrome P450 [Populus trichocarpa] >gi|222855083|gb|EEE92630.1|cytochrome P450 [Populus trichocarpa]	Unigene28579_All//5.00E-45//AT3G52970| CYP76G1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene2858_All	1761	2.35	1.90	1.48	5.71	5.49	2.59	2.35	1.02	1.95	-3.06E-01	3.32E-01		-6.64E-01	3.45E-02		-5.65E-02	8.19E-01		-1.14E+00	2.88E-10	Down	-1.21E+00	1.06E-05	Down	-2.74E-01	3.21E-01		Unigene2858_All//gi|15226341|ref|NF_178281.1|//1.00E-170//ribophorin I family protein [Arabidopsis thaliana] >gi|63003800|gb|AAY25429.1|At2g01720 [Arabidopsis thaliana]	Unigene2858_All//8.00E-144//AT2G01720| ribophorin I family protein	Unigene2858_All//0.00E+00//C0125979		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0006464//GO:0031224//GO:0043231	nr -
Unigene28582_All	1227	0.17	0.00	0.00	2.31	3.23	3.17	116.33	15.09	8.12	-7.41E+00	1.22E-01		-7.41E+00	1.46E-01		4.80E-01	1.29E-01		4.52E-01	1.69E-01		-2.95E+00	0.00E+00	Down	-3.84E+00	0.00E+00	Down	Unigene28582_All//gi|224054176|ref|XP_002298129.1|//3.00E-96//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE92934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene28582_All//1.00E-90//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene28582_All//0.00E+00//TC131966		ko00904|Diterpenoid biosynthesis		nr -
Unigene28584_All	670	1.80	1.51	0.32	2.53	2.42	1.55	2.21	2.25	0.65	-2.48E-01	6.62E-01		-2.50E+00	1.15E-03		-6.56E-02	8.89E-01		-7.05E-01	1.74E-01		2.40E-02	9.95E-01		-1.76E+00	5.33E-04	Down		Unigene28584_All//8.00E-07//ES815948				
Unigene28585_All	689	2.66	3.75	2.94	3.62	3.70	3.41	19.27	15.95	5.32	4.97E-01	2.16E-01		1.44E-01	7.45E-01		3.29E-02	9.61E-01		-8.48E-02	8.47E-01		-2.72E-01	6.01E-02		-1.86E+00	1.51E-31	Down	Unigene28585_All//gi|297830204|ref|XP_002882984.1|//3.00E-22//thioesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328824|gb|EFH59243.1|thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28585_All//2.00E-23//AT3G16175| thioesterase family protein	Unigene28585_All//0.00E+00//TC142768				nr -
Unigene28588_All	464	90.55	25.33	37.18	116.70	86.24	151.75	129.30	59.36	51.17	-1.84E+00	7.67E-77	Down	-1.28E+00	5.21E-44	Down	-4.36E-01	2.18E-11		3.79E-01	3.05E-10		-1.12E+00	2.85E-64	Down	-1.34E+00	8.16E-87	Down	Unigene28588_All//gi|40287508|gb|AA883868.1|//7.00E-33//60S ribosomal protein L12 [Capsicum annuum]	Unigene28588_All//2.00E-32//AT5G60670| 60S ribosomal protein L12 (RPL12C)	Unigene28588_All//0.00E+00//gi|21094552|gb|BQ406865.1|BQ406865		ko03010|Ribosome		nr -
Unigene28589_All	526	2.98	1.35	6.68	7.58	4.58	7.13	1.04	0.95	0.68	-1.15E+00	3.18E-02		1.16E+00	8.51E-04	Up	-7.25E-01	1.20E-02		-8.83E-02	7.91E-01		-1.32E-01	8.80E-01		-6.16E-01	4.68E-01		Unigene28589_All//gi|222136863|gb|ACM45081.1|//1.00E-21//3-dehydroquinate synthase [Vitis vinifera]	Unigene28589_All//3.00E-16//AT5G66120| 3-dehydroquinate synthase, putative	Unigene28589_All//3.00E-89//TC159258		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr +
Unigene28590_All	413	101.09	45.64	60.73	158.49	145.91	166.77	206.79	93.31	118.65	-1.15E+00	4.46E-38	Down	-7.35E-01	1.11E-17		-1.19E-01	8.56E-02		7.34E-02	3.45E-01		-1.15E+00	1.98E-94	Down	-8.02E-01	1.08E-53		Unigene28590_All//gi|99014568|emb|CAK22271.1|//2.00E-50//40S ribosomal protein S11 [Chenopodium rubrum]	Unigene28590_All//4.00E-41//AT5G23740| RPS11-BETA (RIBOSOMAL PROTEIN S11-BETA); structural constituent of ribosome	Unigene28590_All//0.00E+00//gi|13351026|gb|BG441278.1|BG441278		ko03010|Ribosome		nr -
Unigene28591_All	1231	4.72	3.70	4.67	8.58	6.52	6.38	11.61	10.53	5.37	-3.49E-01	1.69E-01		-1.41E-02	9.79E-01		-3.96E-01	2.01E-02		-4.26E-01	1.60E-02		-1.41E-01	3.68E-01		-1.11E+00	3.59E-16	Down	Unigene28591_All//gi|15228202|ref|NP_190343.1|//6.00E-96//esterase/lipase/thioesterase family protein [Arabidopsis thaliana] >gi|34146868|gb|AAQ62442.1|At3g47590 [Arabidopsis thaliana]	Unigene28591_All//3.00E-89//AT3G47590| esterase/lipase/thioesterase family protein	Unigene28591_All//0.00E+00//TC133507				nr -
Unigene28592_All	212	29.12	25.33	27.38	76.13	70.33	77.12	35.50	17.35	28.38	-2.01E-01	4.20E-01		-8.91E-02	7.22E-01		-1.14E-01	4.98E-01		1.86E-02	9.28E-01		-1.03E+00	9.39E-08	Down	-3.23E-01	8.92E-02		Unigene28592_All//gi|226501960|ref|NP_001151315.1|//6.00E-32//transmembrane 9 superfamily protein member 1 [Zea mays]	Unigene28592_All//6.00E-32//AT5G37310| LOCATED IN: integral to membrane, Golgi apparatus, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nonaspanin (TM9SF) (InterPro:IPR004240); BEST Arabidopsis thaliana protein match is: endomembrane protein 70, putative (TAIR:AT1G14670.1); Has 1019 Blast hits to 986 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 444; Fungi - 148; Plants - 242; Viruses - 0; Other Eukaryotes - 185 (source: NCBI BLink).	Unigene28592_All//4.00E-114//TC148949				nr +
Unigene28593_All	2085	0.00	0.00	0.00	0.00	0.10	0.37	3.02	4.21	6.96	null	null		null	null		6.63E+00	1.57E-01		8.52E+00	1.27E-04	Up	4.78E-01	6.19E-03		1.20E+00	2.51E-18	Up	Unigene28593_All//gi|300157379|gb|EFJ24005.1|//1.00E-148//ubiquitin-protein ligase, PUB17 [Selaginella moellendorffii]	Unigene28593_All//5.00E-101//AT1G29340| PUB17 (PLANT U-BOX 17); ubiquitin-protein ligase			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene28594_All	645	0.49	0.55	1.32	0.46	1.28	2.31	2.23	2.66	2.78	1.76E-01	8.83E-01		1.44E+00	8.23E-02		1.47E+00	7.56E-02		2.32E+00	2.17E-04	Up	2.54E-01	6.22E-01		3.19E-01	4.73E-01							
Unigene28598_All	236	42.57	48.74	43.77	30.40	31.66	51.86	63.24	47.46	29.20	1.95E-01	2.81E-01		4.03E-02	8.37E-01		5.90E-02	8.21E-01		7.71E-01	1.19E-06		-4.14E-01	1.43E-03		-1.11E+00	6.40E-17	Down		Unigene28598_All//4.00E-83//TC143297				
Unigene286_All	578	8.24	7.01	4.42	11.12	10.31	15.47	28.82	12.87	16.06	-2.32E-01	4.15E-01		-8.98E-01	1.87E-03		-1.09E-01	6.87E-01		4.77E-01	1.41E-02		-1.16E+00	1.94E-19	Down	-8.44E-01	3.76E-12		Unigene286_All//gi|115477084|ref|NP_001062138.1|//3.00E-96//Os08g0496900 [Oryza sativa Japonica Group] >gi|113624107|dbj|BAF24052.1|Os08g0496900 [Oryza sativa Japonica Group]	Unigene286_All//1.00E-97//AT4G12650| LOCATED IN: integral to membrane, Golgi apparatus, plasma membrane, vacuole; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nonaspanin (TM9SF) (InterPro:IPR004240); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35160.1); Has 983 Blast hits to 980 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 434; Fungi - 144; Plants - 228; Viruses - 0; Other Eukaryotes - 177 (source: NCBI BLink).	Unigene286_All//0.00E+00//gi|78345055|gb|DT565329.1|DT565329				nr +
Unigene2860_All	1702	3.01	9.38	4.94	6.82	6.80	9.37	9.27	9.21	6.02	1.64E+00	3.90E-25	Up	7.15E-01	5.57E-04		-4.60E-03	9.74E-01		4.58E-01	9.08E-04		-8.90E-03	9.82E-01		-6.23E-01	3.56E-07		Unigene2860_All//gi|297825503|ref|XP_002880634.1|//1.00E-167//zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326473|gb|EFH56893.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2860_All//5.00E-108//AT2G24830| zinc finger (CCCH-type) family protein / D111/G-patch domain-containing protein	Unigene2860_All//0.00E+00//TC168212	C3H		GO:0044464//GO:0046914	nr -
Unigene28601_All	604	0.35	0.17	0.18	0.66	1.82	2.54	2.10	1.38	3.30	-1.05E+00	5.65E-01		-9.75E-01	6.21E-01		1.47E+00	3.09E-02		1.95E+00	9.15E-04	Up	-6.02E-01	2.72E-01		6.51E-01	1.01E-01		Unigene28601_All//gi|255548600|ref|XP_002515356.1|//3.00E-47//conserved hypothetical protein [Ricinus communis] >gi|223545300|gb|EEF46805.1|conserved hypothetical protein [Ricinus communis]	Unigene28601_All//9.00E-29//AT4G31570| unknown protein					nr +
Unigene28602_All	1812	0.00	0.00	0.03	0.16	0.40	0.95	6.37	10.61	14.84	null	null		4.88E+00	6.36E-01		1.28E+00	1.56E-01		2.52E+00	2.09E-05	Up	7.36E-01	8.44E-11		1.22E+00	5.61E-34	Up	Unigene28602_All//gi|18396577|ref|NP_566206.1|//1.00E-166//NPC4 (NONSPECIFIC PHOSPHOLIPASE C4); hydrolase, acting on ester bonds / phospholipase C [Arabidopsis thaliana] >gi|14335156|gb|AAK59858.1|AT3g03530/T21P5_5 [Arabidopsis thaliana] >gi|23506053|gb|AAN28886.1|At3g03530/T21P5_5 [Arabidopsis thaliana] >gi|24417131|dbj|BAC22508.1|phosphatidylglycerol specific phospholipase C [Arabidopsis thaliana]	Unigene28602_All//2.00E-167//AT3G03530| NPC4 (NONSPECIFIC PHOSPHOLIPASE C4); hydrolase, acting on ester bonds / phospholipase C	Unigene28602_All//8.00E-34//TC176393		ko00564|Glycerophospholipid metabolism//ko00562|Inositol phosphate metabolism//ko00565|Ether lipid metabolism		nr +
Unigene28603_All	1033	1.22	1.28	1.19	2.46	3.77	1.27	2.17	1.17	0.89	6.92E-02	9.12E-01		-3.61E-02	9.71E-01		6.15E-01	4.54E-02		-9.56E-01	1.59E-02		-8.87E-01	2.04E-02		-1.29E+00	6.63E-04	Down	Unigene28603_All//gi|13605521|gb|AAK32754.1|AF361586_1|//5.00E-63//AT3g17900/MEB5_12 [Arabidopsis thaliana] >gi|23506057|gb|AAN28888.1|At3g17900/MEB5_12 [Arabidopsis thaliana]	Unigene28603_All//2.00E-64//AT3G17900| unknown protein	Unigene28603_All//6.00E-21//ES800091				nr +
Unigene28604_All	723	18.74	12.47	7.22	251.76	105.59	104.51	2000.09	431.89	863.23	-5.87E-01	1.14E-04		-1.38E+00	3.97E-16	Down	-1.25E+00	5.04E-235	Down	-1.27E+00	9.80E-209	Down	-2.21E+00	0.00E+00	Down	-1.21E+00	0.00E+00	Down	Unigene28604_All//gi|791148|emb|CAA60021.1|//1.00E-48//extensin-like protein [Vigna unguiculata]		Unigene28604_All//4.00E-175//TC147309		ko03040|Spliceosome		nr +
Unigene28607_All	960	0.11	0.11	0.89	2.96	2.91	3.86	1.94	0.52	0.62	-4.57E-02	9.89E-01		3.03E+00	3.01E-03		-2.57E-02	9.51E-01		3.83E-01	2.68E-01		-1.89E+00	5.01E-05	Down	-1.64E+00	1.88E-04	Down	Unigene28607_All//gi|30689066|ref|NP_194882.2|//3.00E-68//ATEXO70G1 (exocyst subunit EXO70 family protein G1); protein binding [Arabidopsis thaliana] >gi|32347268|gb|AAP31853.1| EXO70-G1 protein [Arabidopsis thaliana]	Unigene28607_All//2.00E-69//AT4G31540| ATEXO70G1 (exocyst subunit EXO70 family protein G1); protein binding					nr +
Unigene28608_All	703	438.14	299.48	456.98	116.00	131.67	140.89	36.99	17.84	19.32	-5.49E-01	2.54E-78		6.07E-02	6.07E-02		1.83E-01	4.53E-04		2.80E-01	2.62E-08		-1.05E+00	1.52E-25	Down	-9.37E-01	7.38E-22				Unigene28608_All//0.00E+00//gi|109886478|gb|DW515448.1|DW515448				ESTscan -
Unigene28611_All	368	3.84	3.72	1.74	6.23	9.45	9.70	57.10	8.06	1.19	-4.63E-02	9.45E-01		-1.14E+00	5.55E-02		6.02E-01	7.01E-02		6.39E-01	5.41E-02		-2.82E+00	1.80E-79	Down	-5.58E+00	2.96E-136	Down	Unigene28611_All//gi|224083767|ref|XP_002307116.1|//1.00E-08//predicted protein [Populus trichocarpa] >gi|222856565|gb|EEE94112.1|predicted protein [Populus trichocarpa]						nr +

Unigene28612_All	638	7.95	3.10	7.51	8.12	12.52	13.66	1.39	1.05	0.56	-1.36E+00	1.09E-06	Down	-8.26E-02	7.70E-01		6.25E-01	1.46E-03		7.51E-01	9.57E-05		-4.09E-01	5.62E-01		-1.31E+00	4.40E-02		Unigene28612_All//gi|297797389|ref|XP_002866579.1|//8.00E-69//UVB-resistance 8 [Arabidopsis lyrata subsp. lyrata] >gi|297312414|gb|EFH42838.1| UVB-resistance 8 [Arabidopsis lyrata subsp. lyrata]	Unigene28612_All//4.00E-70//AT5G63860| UVR8 (UVB-RESISTANCE 8); chromatin binding / guanyl-nucleotide exchange factor	Unigene28612_All//0.00E+00//TC141996		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene28614_All	1197	0.09	0.59	1.16	1.91	2.19	2.15	6.61	23.22	15.28	2.76E+00	9.14E-03		3.73E+00	1.05E-05	Up	1.92E-01	6.70E-01		1.68E-01	6.80E-01		1.81E+00	4.37E-61	Up	1.21E+00	4.42E-23	Up	Unigene28614_All//gi|298201176|gb|AD160290.1|//6.00E-12//PALMATE-LIKE PENTAFOLIATA2 [Glycine max]	Unigene28614_All//5.00E-13//AT3G23140| zinc finger (C2H2 type) family protein		C2H2			nr -
Unigene28615_All	656	10.45	6.64	11.69	6.23	3.15	2.55	0.52	0.00	0.00	-6.53E-01	3.48E-03		1.62E-01	4.99E-01		-9.83E-01	4.68E-04		-1.29E+00	2.19E-05	Down	-9.01E+00	1.17E-02		-9.01E+00	8.14E-03		Unigene28615_All//gi|115468306|ref|NP_001057752.1|//3.00E-20//Os06g0523300 [Oryza sativa Japonica Group] >gi|113595792|dbj|BAF19666.1| Os06g0523300 [Oryza sativa Japonica Group]	Unigene28615_All//8.00E-21//AT5G41761| unknown protein	Unigene28615_All//0.00E+00//TC170294				nr +
Unigene28618_All	642	10.84	0.32	0.25	30.18	8.69	1.27	33.26	3.39	2.05	-5.10E+00	2.08E-34	Down	-5.45E+00	6.78E-34	Down	-1.80E+00	3.76E-43	Down	-4.58E+00	2.47E-98	Down	-3.30E+00	5.05E-94	Down	-4.02E+00	1.58E-114	Down	Unigene28618_All//gi|75164757|sp|Q94874.1|SNAK1_SOLTU//3.00E-27//RecName: Full=Snakin-1; Flags: Precursor >gi|14627134|emb|CAC44032.1| snakin-1 [Solanum tuberosum]	Unigene28618_All//9.00E-25//AT2G14900| gibberellin-regulated family protein	Unigene28618_All//2.00E-171//TC153629				nr -
Unigene2862_All	1362	41.10	149.07	87.15	23.59	46.27	39.16	31.42	49.31	52.83	1.86E+00	0.00E+00	Up	1.08E+00	8.15E-95	Up	9.72E-01	1.66E-51		7.31E-01	1.28E-24		6.51E-01	7.34E-29		7.50E-01	2.60E-40		Unigene2862_All//gi|16648816|gb|AAL25598.1|//4.00E-36//AT5g54540/MRB17_4 [Arabidopsis thaliana] >gi|20466129|gb|AAM19986.1| AT5g54540/MRB17_4 [Arabidopsis thaliana]	Unigene2862_All//1.00E-31//AT5G54540| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP012943 (InterPro:IPR016006); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25170.1); Has 60 Blast hits to 60 proteins in 11 species: Archae - 0; Bacteria - 2; Metazoa - 2; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene2862_All//0.00E+00//TC171361				nr +
Unigene28624_All	405	8.40	3.63	10.39	16.60	13.52	12.82	52.93	25.28	14.36	-1.21E+00	4.18E-04	Down	3.07E-01	3.53E-01		-2.97E-01	2.14E-01		-3.73E-01	1.19E-01		-1.07E+00	1.24E-21	Down	-1.88E+00	2.45E-51	Down	Unigene28624_All//gi|4206124|gb|AAD11431.1|//7.00E-18//T-complex protein 1 epsilon subunit [Mesembryanthemum crystallinum]	Unigene28624_All//9.00E-19//AT1G24510| T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative	Unigene28624_All//0.00E+00//gi|109889739|gb|DW518707.1|DW518707				nr -
Unigene28625_All	1819	0.00	0.08	0.00	0.05	0.04	0.00	98.41	18.63	10.27	6.39E+00	2.35E-01		null	null		-5.32E-01	8.16E-01		-5.78E+00	4.00E-01		-2.40E+00	0.00E+00	Down	-3.26E+00	0.00E+00	Down	Unigene28625_All//gi|38636547|dbj|BAD02939.1|//0.00E+00//high-affinity nitrate transporter [Prunus persica] >gi|48675347|dbj|BAD22821.1| nitrate transporter [Prunus persica]	Unigene28625_All//0.00E+00//AT1G08090| ATNRT2:1 (NITRATE TRANSPORTER 2:1); nitrate transmembrane transporter	Unigene28625_All//9.00E-46//CB074791				nr +
Unigene28626_All	480	5.89	2.43	5.21	11.93	5.95	11.48	19.29	11.67	7.80	-1.28E+00	8.71E-04	Down	-1.75E-01	6.41E-01		-1.00E+00	1.37E-05	Down	-5.62E-02	8.46E-01		-7.25E-01	1.66E-05		-1.31E+00	1.15E-13	Down			Unigene28626_All//1.00E-177//gi|78333272|gb|DT553546.1|DT553546				
Unigene28628_All	789	1.79	0.77	0.27	0.76	6.76	2.80	1.77	3.55	7.07	-1.22E+00	3.33E-02		-2.73E+00	1.57E-04	Down	3.16E+00	3.83E-21	Up	1.89E+00	5.58E-05	Up	1.01E+00	2.85E-03		2.00E+00	7.09E-15	Up	Unigene28628_All//gi|92886073|gb|ABE88083.1|//2.00E-73//Protein kinase [Medicago truncatula]	Unigene28628_All//6.00E-73//AT4G03230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene28628_All//5.00E-101//DT469086		ko04626|Plant-pathogen interaction		nr -
Unigene28630_All	407	1.29	1.99	1.70	3.67	3.47	4.55	122.79	117.58	284.35	6.32E-01	4.02E-01		4.04E-01	6.09E-01		-8.20E-02	8.70E-01		3.09E-01	5.68E-01		-6.25E-02	4.47E-01		1.21E+00	8.10E-142	Up	Unigene28630_All//gi|44681326|gb|AAS47603.1|//4.00E-18//At3g20340 [Arabidopsis thaliana] >gi|45773836|gb|AAS76722.1| At3g20340 [Arabidopsis thaliana]	Unigene28630_All//6.00E-13//AT3G20340| Expression of the gene is downregulated in the presence of paraquat, an inducer of photooxidative stress.					nr +
Unigene28631_All	440	0.59	3.80	0.85	1.36	0.63	0.72	1.35	1.61	1.54	2.68E+00	1.99E-05	Up	5.11E-01	6.54E-01		-1.12E+00	2.26E-01		-9.19E-01	3.51E-01		2.63E-01	7.21E-01		1.94E-01	7.87E-01		Unigene28631_All//gi|225466723|ref|XP_002266876.1|//2.00E-53//PREDICTED: similar to transcription factor, partial [Vitis vinifera]	Unigene28631_All//3.00E-48//AT2G38695| unknown protein	Unigene28631_All//4.00E-26//gi|78338093|gb|DT558367.1|DT558367				nr -
Unigene28633_All	556	0.38	1.73	1.15	3.49	6.57	7.72	39.24	77.35	60.40	2.20E+00	6.58E-03		1.61E+00	1.11E-01		9.10E-01	3.59E-03		1.14E+00	1.06E-04	Up	9.79E-01	4.21E-37		6.22E-01	3.70E-14		Unigene28633_All//gi|224084233|ref|XP_002307238.1|//5.00E-11//predicted protein [Populus trichocarpa] >gi|222856687|gb|EEE94234.1| predicted protein [Populus trichocarpa]	Unigene28633_All//2.00E-06//AT5G66985| unknown protein	Unigene28633_All//0.00E+00//TC168014				nr +
Unigene28634_All	1540	0.20	0.66	0.14	0.55	0.09	0.59	14.50	32.05	73.99	1.69E+00	2.14E-02		-5.59E-01	6.63E-01		-2.62E+00	1.65E-03		9.30E-02	9.20E-01		1.14E+00	1.46E-54	Up	2.35E+00	0.00E+00	Up	Unigene28634_All//gi|229558122|gb|ACQ76811.1|//2.00E-86//WRKY transcription factor 72 [Brassica napus]	Unigene28634_All//4.00E-69//AT5G15130| WRKY72; transcription factor	Unigene28634_All//5.00E-16//DT467483	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene28635_All	444	9.55	31.95	13.91	23.90	44.52	52.69	34.95	78.98	70.26	1.74E+00	2.07E-24	Up	5.44E-01	2.92E-02		8.98E-01	2.18E-14		1.14E+00	9.00E-23	Up	1.18E+00	1.10E-40	Up	1.01E+00	4.43E-29	Up	Unigene28635_All//gi|225458627|ref|XP_002284791.1|//4.00E-44//PREDICTED: ripening-related bZIP protein-like isoform 2 [Vitis vinifera] >gi|225458629|ref|XP_002284785.1| PREDICTED: ripening-related bZIP protein-like isoform 1 [Vitis vinifera]	Unigene28635_All//5.00E-27//AT4G34000| ABF3 (ABSCISIC ACID RESPONSIVE ELEMENTS-BINDING FACTOR 3); DNA binding / protein binding / transcription activator/ transcription factor	Unigene28635_All//0.00E+00//TC167225	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene28636_All	297	17.97	15.70	18.47	11.74	9.74	6.84	37.01	23.92	18.38	-1.95E-01	4.79E-01		3.95E-02	8.90E-01		-2.70E-01	4.58E-01		-7.79E-01	1.78E-02		-6.30E-01	3.69E-05		-1.01E+00	6.05E-11	Down			Unigene28636_All//4.00E-167//TC146324				
Unigene28637_All	993	0.21	0.00	0.05	13.59	7.56	12.60	0.64	5.39	0.76	-7.72E+00	1.22E-01		-1.98E+00	3.81E-01		-8.47E-01	1.91E-09		-1.10E-01	5.65E-01		3.08E+00	1.95E-22	Up	2.55E-01	7.07E-01		Unigene28637_All//gi|87240457|gb|AB032315.1|//2.00E-38//CCT [Medicago truncatula]	Unigene28637_All//2.00E-29//AT5G39990| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot apex, stem, leaf whorl, flower; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: CCT domain (InterPro:IPR010402); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41380.1); Has 918 Blast hits to 918 proteins in 64 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 885; Viruses - 0; Other Eukaryotes - 32 (source: NCBI BLink).	Unigene28637_All//0.00E+00//gi|109890176|gb|DW519140.1|DW519140	C2C2-CO-like			nr +
Unigene28639_All	2633	0.00	0.12	0.00	0.00	0.01	0.02	12.59	3.05	1.89	6.85E+00	4.43E-02		null	null		3.71E+00	8.30E-01		4.10E+00	6.96E-01		-2.05E+00	1.48E-85	Down	-2.73E+00	1.16E-124	Down	Unigene28639_All//gi|49240345|gb|AAT58045.1|//0.00E+00//high-affinity K+ transporter [Capsicum annuum]	Unigene28639_All//0.00E+00//AT4G13420| HAK5 (HIGH AFFINITY K+ TRANSPORTER 5); potassium ion transmembrane transporter/ potassium:sodium symporter	Unigene28639_All//0.00E+00//DT461379				nr -
Unigene28640_All	450	66.85	33.22	35.50	143.69	146.39	149.64	47.35	43.10	41.79	-1.01E+00	1.45E-22	Down	-9.13E-01	1.93E-18		2.69E-02	7.79E-01		5.86E-02	4.79E-01		-1.36E-01	2.62E-01		-1.81E-01	1.04E-01		Unigene28640_All//gi|15230291|ref|NP_188544.1|//1.00E-19//ATRBP47B (RNA-binding protein 47B); RNA binding [Arabidopsis thaliana] >gi|111074446|gb|ABH04596.1| At3g19130 [Arabidopsis thaliana]		Unigene28640_All//5.00E-180//gi|78329425|gb|DT549699.1|DT549699				nr +
Unigene28641_All	521	2.91	7.10	4.19	2.58	2.18	2.34	1.70	1.12	0.84	1.29E+00	1.03E-04	Up	5.25E-01	2.46E-01		-2.43E-01	6.80E-01		-1.41E-01	8.01E-01		-6.02E-01	3.85E-01		-1.02E+00	1.09E-01				Unigene28641_All//6.00E-07//ES813989				
Unigene28648_All	616	17.75	7.98	14.78	5.98	5.53	4.91	1.51	1.36	0.13	-1.15E+00	1.28E-10	Down	-2.64E-01	1.61E-01		-1.13E-01	7.73E-01		-2.85E-01	4.20E-01		-1.54E-01	8.08E-01		-3.55E+00	3.97E-05	Down			Unigene28648_All//2.00E-22//FL577754				
Unigene28649_All	556	8.28	5.83	10.92	7.44	6.63	2.84	0.91	0.38	0.86	-5.06E-01	7.45E-02		3.99E-01	1.24E-01		-1.66E-01	6.04E-01		-1.39E+00	5.25E-06	Down	-1.28E+00	1.86E-01		-8.58E-02	9.30E-01		Unigene28649_All//gi|3915687|sp|P22418.2|F16P1_SPIOL//9.00E-27//RecName: Full=Fructose-1,6-bisphosphatase, chloroplastic; Short=FBPase; AltName: Full=D-fructose-1,6-bisphosphate 1-phosphohydrolase; Flags: Precursor >gi|2529374|gb|AAD10207.1| fructose 1,6-bisphosphatase [Spinacia oleracea]	Unigene28649_All//1.00E-27//AT3G54050| fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	Unigene28649_All//0.00E+00//TC148258		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene2865_All	685	60.57	122.79	105.49	104.36	136.53	116.37	128.57	103.24	99.80	1.02E+00	1.30E-62	Up	8.00E-01	5.87E-35		3.88E-01	2.53E-15		1.57E-01	9.78E-03		-3.17E-01	1.28E-10		-3.65E-01	4.63E-14		Unigene2865_All//gi|192910708|gb|ACF06462.1|//9.00E-90//24 kDa seed maturation protein [Elaeis guineensis]	Unigene2865_All//6.00E-61//ATIG64090| reticulon family protein (RTNLB3)	Unigene2865_All//0.00E+00//TC133376			GO:0043231	nr +
Unigene28650_All	919	14.23	10.81	14.37	7.64	6.11	8.99	2.53	2.68	0.82	-3.97E-01	1.16E-02		1.38E-02	9.54E-01		-3.24E-01	1.56E-01		2.35E-01	3.07E-01		8.46E-02	8.26E-01		-1.62E+00	2.77E-05	Down	Unigene28650_All//gi|20466362|gb|AAM20498.1|//2.00E-37//calmodulin-like protein [Arabidopsis thaliana] >gi|22136314|gb|AAM91235.1| calmodulin-like protein [Arabidopsis thaliana]	Unigene28650_All//2.00E-35//AT3G50770| calmodulin-related protein, putative			ko04626|Plant-pathogen interaction		nr +
Unigene28652_All	805	0.26	0.38	0.00	44.86	18.52	7.57	1.79	0.52	0.74	5.39E-01	6.71E-01		-8.02E+00	1.46E-01		-1.28E+00	4.52E-48	Down	-2.57E+00	1.55E-109	Down	-1.78E+00	8.40E-04	Down	-1.27E+00	9.34E-03		Unigene28652_All//gi|87240796|gb|AB032654.1|//6.00E-33//Zinc finger, RING-type [Medicago truncatula]	Unigene28652_All//6.00E-27//AT4G03965| protein binding / zinc ion binding	Unigene28652_All//0.00E+00//TC154064		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene28653_All	436	3.48	0.46	0.85	4.23	7.98	6.22	5.24	6.42	7.68	-2.90E+00	2.07E-05	Down	-2.03E+00	1.23E-03		9.16E-01	4.42E-03		5.56E-01	1.65E-01		2.95E-01	4.10E-01		5.52E-01	6.04E-02				Unigene28653_All//8.00E-46//TC163705				
Unigene28654_All	1158	18.07	13.13	24.37	28.31	28.37	20.28	22.89	8.34	11.66	-4.61E-01	1.19E-04		4.31E-01	4.20E-05		3.20E-03	9.79E-01		-4.81E-01	1.23E-07		-1.46E+00	7.47E-43	Down	-9.73E-01	1.14E-23		Unigene28654_All//gi|79314149|ref|NP_001030808.1|//4.00E-20//CEF (clone eighty-four); protein binding / transporter/ zinc ion binding [Arabidopsis thaliana]	Unigene28654_All//1.00E-15//AT4G32640| protein binding / zinc ion binding	Unigene28654_All//7.00E-101//gi|164282512|gb|ES828064.1|ES828064		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis		nr -
Unigene28655_All	247	3.60	22.16	1.94	22.59	68.59	43.52	21.40	72.93	80.32	2.62E+00	6.11E-16	Up	-8.92E-01	2.46E-01		1.60E+00	5.52E-30	Up	9.46E-01	4.20E-08		1.77E+00	1.57E-38	Up	1.91E+00	7.03E-48	Up	Unigene28655_All//gi|224079209|ref|XP_002305794.1|//5.00E-10//predicted protein [Populus trichocarpa] >gi|222848758|gb|EEE86305.1| predicted protein [Populus trichocarpa]		Unigene28655_All//7.00E-116//TC149668				nr +
Unigene28658_All	1448	0.00	0.00	0.00	0.21	0.64	0.16	11.53	7.85	3.00	null	null		null	null		1.64E+00	3.35E-02		-4.04E-01	7.51E-01		-5.55E-01	4.48E-06		-1.94E+00	6.35E-42	Down	Unigene28658_All//gi|151347477|gb|ABS01351.1|//2.00E-17//basic leucine zipper protein [Carica papaya]	Unigene28658_All//3.00E-10//AT1G08320| bZIP family transcription factor	Unigene28658_All//2.00E-27//CO085603	bZIP			nr -

Unigene28659_All	1192	0.61	0.26	0.18	1.21	0.66	0.83	1.53	3.02	3.18	-1.27E+00	1.36E-01			-1.78E+00	6.00E-02		-8.67E-01	1.04E-01		-5.40E-01	3.59E-01		9.83E-01	7.33E-04		1.06E+00	1.41E-04	Up	Unigene28659_All//gi|224144888|ref|XP_002336183.1|//1.00E-123//phol-like protein [Populus trichocarpa] >gi|222831897|gb|EEE70374.1| phol-like protein [Populus trichocarpa]	Unigene28659_All//9.00E-112//AT1G14040| LOCATED IN: integral to membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: SPX, N-terminal (InterPro:IPR004331), EXS, C-terminal (InterPro:IPR004342); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03240.1); Has 732 Blast hits to 696 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 238; Fungi - 246; Plants - 151; Viruses - 0; Other Eukaryotes - 97 (source: NCBI BLink).	Unigene28659_All//0.00E+00//CO071120				nr +
Unigene28660_All	523	22.71	46.89	40.22	33.53	41.22	40.50	51.33	66.65	51.80	1.05E+00	1.54E-19	Up	8.25E-01	4.02E-11		2.98E-01	1.08E-02		2.73E-01	2.80E-02		3.77E-01	3.39E-06		1.30E-02	9.23E-01		Unigene28660_All//gi|297729283|ref|NP_001177005.1|//2.00E-19//Os12g0553900 [Oryza sativa Japonica Group] >gi|255670386|dbj|BAH95733.1|Os12g0553900 [Oryza sativa Japonica Group]	Unigene28660_All//2.00E-09//AT5G27860| unknown protein	Unigene28660_All//0.00E+00//gi|164302268|gb|ES828665.1|ES828665				nr +
Unigene28661_All	522	0.00	2.43	0.61	2.29	0.40	0.35	5.67	4.88	1.30	1.12E+01	2.86E-07	Up	9.26E+00	4.52E-02		-2.53E+00	1.46E-04	Down	-2.73E+00	2.36E-04	Down	-2.15E-01	5.60E-01		-2.13E+00	5.20E-09	Down	Unigene28661_All//gi|297849514|ref|XP_002892638.1|//6.00E-52//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338480|gb|EFH68897.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28661_All//8.00E-52//AT1G11300| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene28661_All//1.00E-72//CO081718		ko04626|Plant-pathogen interaction		nr +
Unigene28663_All	1720	0.52	1.27	2.07	7.04	6.47	5.25	1.13	0.73	0.95	1.29E+00	3.97E-03		2.00E+00	1.43E-07	Up	-1.22E-01	5.42E-01		-4.22E-01	9.62E-03		-6.33E-01	1.35E-01		-2.52E-01	5.59E-01		Unigene28663_All//gi|15230158|ref|NP_188497.1|//2.00E-41//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene28663_All//5.00E-36//AT3G18670| ankyrin repeat family protein				nr -
Unigene28664_All	782	84.64	32.53	43.17	55.36	50.38	22.93	0.00	0.00	0.00	-1.38E+00	8.03E-80	Down	-9.71E-01	3.20E-44		-1.36E-01	1.20E-01		-1.27E+00	4.04E-50	Down	null	null		null	null		Unigene28664_All//gi|18397934|ref|NP_565380.1|//1.00E-34//glycine-rich protein [Arabidopsis thaliana] >gi|15294186|gb|AAK95270.1|AF410284_1 At2g15780/F19G14.22 [Arabidopsis thaliana] >gi|5306253|gb|AAD41986.1| expressed protein [Arabidopsis thaliana] >gi|20147265|gb|AAM10346.1| At2g15780/F19G14.22 [Arabidopsis thaliana]	Unigene28664_All//3.00E-34//AT2G15780| glycine-rich protein	Unigene28664_All//0.00E+00//TC145831				nr +
Unigene28665_All	652	0.24	5.13	0.82	0.23	1.27	1.04	2.53	3.65	5.07	4.41E+00	2.87E-15	Up	1.76E+00	1.29E-01		2.47E+00	6.72E-03		2.18E+00	3.14E-02		5.31E-01	1.58E-01		1.00E+00	7.62E-04	Up									
Unigene28666_All	720	5.89	2.82	2.44	17.71	10.76	13.74	0.59	0.70	0.28	-1.06E+00	3.72E-04	Down	-1.27E+00	6.10E-05	Down	-7.19E-01	7.21E-07		-3.67E-01	2.27E-02		2.47E-01	7.84E-01		-1.09E+00	2.82E-01		Unigene28666_All//gi|62945915|gb|AAY22200.1|//8.00E-52//squalene monooxygenase [Datura inoxia]	Unigene28666_All//1.00E-46//AT1G58440| XF1: squalene monooxygenase	Unigene28666_All//0.00E+00//TC143054		ko00100|Steroid biosynthesis		nr -
Unigene28667_All	755	1.87	1.34	0.71	2.51	0.82	0.24	7.22	8.47	2.85	-4.79E-01	3.92E-01		-1.41E+00	2.12E-02		-1.61E+00	4.43E-04	Down	-3.39E+00	5.72E-08	Down	2.30E-01	3.24E-01		-1.34E+00	9.90E-09	Down									
Unigene28668_All	1679	0.12	0.39	0.22	7.09	9.97	3.28	0.35	0.40	0.45	1.65E+00	8.14E-02		8.33E-01	5.16E-01		4.91E-01	1.27E-04		-1.11E+00	1.47E-11	Down	1.76E-01	8.15E-01		3.55E-01	6.16E-01		Unigene28668_All//gi|240255739|ref|NP_192257.4|//1.00E-22//protein binding [Arabidopsis thaliana]	Unigene28668_All//2.00E-23//AT4G03480| protein binding	Unigene28668_All//3.00E-101//gi|78341071|gb|DT561345.1|DT561345				nr +
Unigene28670_All	919	2.45	3.58	2.55	6.78	6.97	4.96	2.16	1.50	0.61	5.50E-01	1.11E-01		5.86E-02	8.94E-01		4.07E-02	8.88E-01		-4.49E-01	6.47E-02		-5.27E-01	2.14E-01		-1.83E+00	2.39E-05	Down					Unigene28670_All//8.00E-14//TC142602				
Unigene28672_All	597	0.96	3.14	1.07	6.51	9.52	2.12	12.25	6.23	5.87	1.70E+00	8.73E-04	Up	1.51E-01	8.56E-01		5.48E-01	2.58E-02		-1.62E+00	5.69E-07	Down	-9.76E-01	5.94E-07		-1.06E+00	3.86E-08	Down					Unigene28672_All//6.00E-32//gi|78345879|gb|DT566153.1|DT566153				
Unigene28674_All	1093	13.55	1.85	3.02	0.36	0.22	0.33	1.70	9.98	2.62	-2.87E+00	8.68E-47	Down	-2.17E+00	1.29E-32	Down	-7.26E-01	5.46E-01		-1.41E-01	9.04E-01		2.55E+00	3.80E-37	Up	6.25E-01	5.13E-02		Unigene28674_All//gi|30024600|dbj|BAC75672.1|//6.00E-85//transcription factor MYB102 [Lotus japonicus]	Unigene28674_All//7.00E-78//AT1G34670| AtMYB93 (myb domain protein 93); DNA binding / transcription factor	Unigene28674_All//9.00E-17//TC139493	MYB			nr -
Unigene28675_All	344	19.16	88.52	39.78	52.13	69.17	60.00	46.21	74.24	61.96	2.21E+00	2.20E-70	Up	1.05E+00	6.42E-11	Up	4.08E-01	1.13E-04		2.03E-01	1.28E-01		6.84E-01	1.80E-12		4.23E-01	4.53E-05		Unigene28675_All//gi|14572048|gb|AK67355.1|AF387795_1//5.00E-63//transcription factor [Cucumis melo]	Unigene28675_All//1.00E-50//AT2G27050| EIL1 (ETHYLENE-INSENSITIVE3-LIKE 1); transcription factor/ transcription regulator	Unigene28675_All//0.00E+00//gi|78348296|gb|DT568570.1|DT568570	EIL			nr +
Unigene28677_All	739	3.82	1.30	0.86	4.99	3.03	4.22	0.74	1.41	1.89	-1.55E+00	8.71E-05	Down	-2.14E+00	1.39E-06	Down	-7.20E-01	1.77E-02		-2.42E-01	5.00E-01		9.27E-01	1.30E-01		1.34E+00	7.75E-03		Unigene28677_All//gi|224142601|ref|XP_002324643.1|//6.00E-67//actin related protein [Populus trichocarpa] >gi|222860077|gb|EEF03208.1| actin related protein [Populus trichocarpa]	Unigene28677_All//6.00E-50//AT3G33520| ATARP6; structural constituent of cytoskeleton	Unigene28677_All//1.00E-178//CO119753				nr -
Unigene28680_All	720	22.45	12.95	27.36	2.49	6.12	8.91	0.00	0.12	0.00	-7.94E-01	1.33E-08		2.85E-01	3.30E-02		1.30E+00	4.80E-06	Up	1.84E+00	6.78E-13	Up	6.86E+00	4.01E-01		null	null		Unigene28680_All//gi|57545995|gb|AW51884.1|//1.00E-79//nitrate and chloride transporter [Glycine max]	Unigene28680_All//8.00E-79//AT2G39210| nodulin family protein	Unigene28680_All//0.00E+00//gi|109857571|gb|DW486550.1|DW486550				nr -
Unigene28686_All	251	47.53	20.19	25.88	70.65	65.30	90.33	70.07	29.31	38.89	-1.24E+00	9.73E-13	Down	-8.77E-01	3.07E-07		-1.14E-01	4.69E-01		3.54E-01	2.03E-03		-1.26E+00	4.60E-23	Down	-8.50E-01	6.39E-13		Unigene28686_All//gi|54039313|sp|P62302.1|RS13_SOYBN//8.00E-40//RecName: Full=40S ribosomal protein S13 >gi|44662862|gb|AAS47510.1| ribosomal protein S13 [Glycine max] >gi|161367348|gb|ABX71080.1| ribosomal protein S13 [Glycine max]	Unigene28686_All//2.00E-39//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene28686_All//9.00E-140//gi|11202936|gb|BF271941.1|BF271941		ko03010|Ribosome		nr -
Unigene28687_All	853	129.24	94.86	160.81	21.78	31.53	16.63	0.69	3.58	2.15	-4.46E-01	9.71E-20		3.15E-01	1.41E-12		5.34E-01	3.93E-08		-3.90E-01	2.22E-03		2.37E+00	4.99E-10	Up	1.63E+00	2.55E-04	Up	Unigene28687_All//gi|5305145|emb|CAB46084.1|//1.00E-115//fructose-1,6-bisphosphatase [Pisum sativum]	Unigene28687_All//1.00E-106//AT1G43670| fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	Unigene28687_All//0.00E+00//TC167262		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene28688_All	788	1.46	0.45	1.15	1.20	1.88	1.43	1.02	3.08	1.92	-1.70E+00	1.21E-02		-3.47E-01	6.16E-01		6.46E-01	2.65E-01		2.55E-01	6.91E-01		1.59E+00	3.82E-05	Up	9.14E-01	5.00E-02		Unigene28688_All//gi|224115768|ref|XP_002332052.1|//1.00E-91//magnesium transporter [Populus trichocarpa] >gi|222831938|gb|EEE70415.1| magnesium transporter [Populus trichocarpa]	Unigene28688_All//3.00E-71//AT1G16010| magnesium transporter CorA-like family protein (MRS2-1)	Unigene28688_All//4.00E-77//gi|21089462|gb|BQ401775.1|BQ401775				nr +
Unigene2869_All	1586	23.36	22.30	26.52	5.69	5.71	5.18	1.79	0.53	2.16	-6.68E-02	5.20E-01		1.84E-01	4.34E-02		6.40E-03	9.82E-01		-1.34E-01	5.66E-01		-1.76E+00	1.15E-06	Down	2.74E-01	3.74E-01		Unigene2869_All//gi|30683693|ref|NP_563943.2|//1.00E-112//CAAX amino terminal protease family protein [Arabidopsis thaliana]	Unigene2869_All//1.00E-96//AT1G14270| CAAX amino terminal protease family protein	Unigene2869_All//0.00E+00//TC168717			GO:0016787//GO:0043231	nr -
Unigene28690_All	365	3.30	3.05	7.88	7.37	6.04	2.47	4.05	0.34	2.07	-1.10E-01	8.45E-01		1.26E+00	1.44E-03		-2.88E-01	4.93E-01		-1.57E+00	7.46E-05	Down	-3.56E+00	1.75E-07	Down	-9.67E-01	3.93E-02		Unigene28690_All//gi|28951019|gb|AA063433.1|//3.00E-08//At2g46710 [Arabidopsis thaliana]	Unigene28690_All//8.00E-06//AT2G46710| rac GTPase activating protein, putative	Unigene28690_All//3.00E-122//TC160147				nr +
Unigene28695_All	451	1.04	2.13	2.13	1.99	1.53	2.00	1.88	1.85	0.18	1.03E+00	1.45E-01		1.03E+00	1.68E-01		-3.81E-01	6.05E-01		1.06E-02	9.93E-01		-1.66E-02	1.02E+00		-3.41E+00	1.35E-04	Down									
Unigene28696_All	1111	0.61	0.14	0.19	2.11	2.91	1.63	1.48	0.30	0.29	-2.16E+00	2.84E-02		-1.68E+00	8.70E-02		4.67E-01	1.95E-01		-3.74E-01	4.05E-01		-2.30E+00	1.36E-05	Down	-2.37E+00	5.20E-06	Down	Unigene28696_All//gi|225426767|ref|XP_002276100.1|//8.00E-39//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene28696_All//4.00E-19//AT4G11780| unknown protein	Unigene28696_All//0.00E+00//gi|21089804|gb|BQ402117.1|BQ402117				nr -
Unigene28699_All	704	3.12	0.65	1.97	0.85	1.66	1.28	1.08	2.61	1.87	-2.27E+00	6.39E-06	Down	-6.67E-01	1.42E-01		9.70E-01	1.37E-01		5.96E-01	4.56E-01		1.27E+00	3.69E-03		7.89E-01	1.19E-01		Unigene28699_All//gi|224146383|ref|XP_002325988.1|//9.00E-91//calcium dependent protein kinase 11 [Populus trichocarpa] >gi|222862863|gb|EEF00370.1| calcium dependent protein kinase 11 [Populus trichocarpa]	Unigene28699_All//2.00E-89//AT1G35670| ATCDPK2 (CALCIUM-DEPENDENT PROTEIN KINASE 2); calmodulin-dependent protein kinase/ kinase	Unigene28699_All//1.00E-141//TC141830		ko04626|Plant-pathogen interaction		nr -
Unigene287_All	2637	14.96	9.26	9.25	28.35	25.46	24.70	40.15	15.52	25.61	-6.92E-01	9.07E-16		-6.94E-01	3.48E-15		-1.55E-01	1.05E-02		-1.99E-01	1.05E-03		-1.37E+00	3.28E-154	Down	-6.49E-01	4.32E-46		Unigene287_All//gi|115477084|ref|NP_001062138.1|//0.00E+00//Os08g0196900 [Oryza sativa Japonica Group] >gi|113624107|dbj|BAF24052.1|Os08g0196900 [Oryza sativa Japonica Group]	Unigene287_All//0.00E+00//AT4G12650| LOCATED IN: integral to membrane, Golgi apparatus, plasma membrane, vacuole; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nonaspanin (TM9SF) (InterPro:IPR004240); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35160.1); Has 983 Blast hits to 980 proteins in 161 species: Archae - 0; Bacteria - 0; Metazoa - 434; Fungi - 144; Plants - 228; Viruses - 0; Other Eukaryotes - 177 (source: NCBI BLink).	Unigene287_All//0.00E+00//TC158340				nr -
Unigene2870_All	1557	11.79	35.34	13.82	19.26	19.86	14.16	21.43	23.62	16.35	1.58E+00	5.08E-81	Up	2.28E-01	7.92E-02		4.43E-02	7.43E-01		-4.44E-01	3.48E-06		1.41E-01	1.07E-01		-3.90E-01	1.55E-06		Unigene2870_All//gi|297849772|ref|XP_002892767.1|//1.00E-105//glucosamine/galactosamine-6-phosphate isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338609|gb|EFH69026.1| glucosamine/galactosamine-6-phosphate isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2870_All//2.00E-104//AT1G13700| glucosamine/galactosamine-6-phosphate isomerase family protein	Unigene2870_All//0.00E+00//TC139342		ko00030|Pentose phosphate pathway	GO:0004091//GO:0006007	nr +
Unigene28700_All	691	4.77	1.61	2.00	6.49	6.63	5.10	0.00	0.00	0.00	-1.56E+00	1.68E-05	Down	-1.25E+00	6.16E-04	Down	3.08E-02	9.41E-01		-3.48E-01	2.58E-01		null	null		null	null		Unigene28700_All//gi|224061202|ref|XP_002300368.1|//2.00E-69//cytochrome P450 [Populus trichocarpa] >gi|222847626|gb|EEE85173.1| cytochrome P450 [Populus trichocarpa]	Unigene28700_All//2.00E-30//AT3G48310| CYP71A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene28700_All//0.00E+00//ES824538		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +

Unigene28701_All	1719	1.92	1.24	1.24	1.28	0.92	0.97	1.16	0.92	4.82	-6.31E-01	6.46E-02		-6.30E-01	7.86E-02		-4.69E-01	2.94E-01		-3.91E-01	3.98E-01		-3.23E-01	4.58E-01		2.06E+00	1.53E-22	Up	Unigene28701_All//gi|30693150|ref|NP_190486.2|//0.00E+00//EMB2261 (embryo defective 2261) [Arabidopsis thaliana] >gi|75222188|sp|Q5G1T1.1|PP272_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g49170, chloroplastic; AltName: Full=Protein EMBRYO DEFECTIVE 2261; Flags: Precursor >gi|88013018|gb|AAW62962.1| embryo-defective 2261 [Arabidopsis thaliana] >gi|88013020|gb|AAW62963.1| embryo-defective 2261 [Arabidopsis thaliana]	Unigene28701_All//0.00E+00//AT3G49170| EMB2261 (embryo defective 2261)				nr +
Unigene28702_All	1274	0.08	0.00	0.00	0.23	0.11	0.89	36.61	11.02	11.54	-6.36E+00	3.72E-01		-6.36E+00	3.94E-01		-1.12E+00	4.24E-01		1.92E+00	6.72E-03		-1.73E+00	6.57E-96	Down	-1.67E+00	1.68E-93	Down	Unigene28702_All//gi|197090699|gb|ACH41750.1|//3.00E-80//ST5a [Brassica rapa subsp. chinensis] >gi|197090701|gb|ACH41751.1| ST5a [Brassica rapa subsp. rapa] >gi|197090703|gb|ACH41752.1| ST5a [Brassica rapa subsp. rapa]	Unigene28702_All//1.00E-80//AT1G74100| SOT16 (SULFOTRANSFERASE 16); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene28702_All//0.00E+00//C0097446		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism		nr -
Unigene28706_All	558	0.47	1.18	0.38	2.77	2.10	3.48	2.05	0.45	2.43	1.33E+00	1.45E-01		-2.97E-01	8.32E-01		-3.99E-01	4.68E-01		3.31E-01	5.22E-01		-2.19E+00	6.83E-04	Down	2.47E-01	6.33E-01		Unigene28706_All//gi|225438627|ref|XP_002276798.1|//4.00E-44//PREDICTED: similar to binding [Vitis vinifera]	Unigene28706_All//4.00E-36//AT2G22125| binding	Unigene28706_All//0.00E+00//gi|109855219|gb|DW484198.1|DW484198				nr -
Unigene28707_All	1223	0.68	0.25	0.26	1.83	2.98	1.26	3.11	0.55	1.47	-1.46E+00	6.69E-02		-1.39E+00	9.66E-02		7.03E-01	2.65E-02		-5.46E-01	2.22E-01		-2.51E+00	3.42E-13	Down	-1.09E+00	8.46E-05	Down	Unigene28707_All//gi|297601509|ref|XP_001650955.2|//5.00E-69//Os03g0691500 [Oryza sativa Japonica Group] >gi|255674803|dbj|BAF12869.2| Os03g0691500 [Oryza sativa Japonica Group]	Unigene28707_All//4.00E-64//AT4G38070| bHLH family protein		bHLH			nr -
Unigene28708_All	816	0.77	0.75	1.70	0.85	1.14	1.27	1.30	0.82	3.17	-4.63E-02	9.72E-01		1.14E+00	5.84E-02		4.15E-01	6.06E-01		5.75E-01	4.27E-01		-6.61E-01	2.78E-01		1.29E+00	2.41E-04	Up	Unigene28708_All//gi|297805766|ref|XP_002870767.1|//2.00E-34//EMB2745 [Arabidopsis lyrata subsp. lyrata] >gi|297316603|gb|EFH47026.1| EMB2745 [Arabidopsis lyrata subsp. lyrata]	Unigene28708_All//1.00E-34//AT5G39710| EMB2745 (EMBRYO DEFECTIVE 2745)					nr +
Unigene28709_All	545	49.06	142.71	82.46	123.21	200.36	347.63	144.92	402.31	219.73	1.54E+00	7.83E-110	Up	7.49E-01	1.23E-19		7.01E-01	2.37E-51		1.50E+00	2.81E-275	Up	1.47E+00	0.00E+00	Up	6.01E-01	3.03E-45		Unigene28709_All//gi|224136574|ref|XP_002326894.1|//5.00E-19//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222835209|gb|EEE73644.1| NAC domain protein, IPR003441 [Populus trichocarpa]		Unigene28709_All//2.00E-07//DT048855				nr +
Unigene28710_All	335	41.08	25.41	26.07	151.82	121.19	92.48	247.62	127.13	90.97	-6.93E-01	4.78E-06		-6.56E-01	2.81E-05		-3.25E-01	2.08E-06		-7.15E-01	8.16E-23		-9.62E-01	7.50E-69		-1.44E+00	1.39E-134	Down	Unigene28710_All//gi|211906466|gb|ACJ11726.1|//1.00E-60//serine hydroxymethyltransferase [Gossypium hirsutum]	Unigene28710_All//3.00E-48//AT4G13930| SHM4 (serine hydroxymethyltransferase 4); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene28710_All//0.00E+00//TC175310		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr -
Unigene28711_All	535	9.39	2.94	6.97	19.09	18.41	5.66	1.66	0.78	1.04	-1.68E+00	1.01E-08	Down	-4.30E-01	1.37E-01		-5.23E-02	8.29E-01		-1.75E+00	2.13E-19	Down	-1.09E+00	1.07E-01		-6.71E-01	2.94E-01		Unigene28711_All//gi|297835194|ref|XP_002885479.1|//1.00E-31//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297331319|gb|EFH61738.1| expressed protein [Arabidopsis lyrata subsp. lyrata]				ko03040|Spliceosome		nr -
Unigene28712_All	1793	0.00	0.00	0.00	0.36	0.00	0.05	36.64	43.64	16.29	null	null		null	null		-8.50E+00	7.85E-05	Down	-2.84E+00	1.02E-02		2.52E-01	1.84E-06		-1.17E+00	3.75E-77	Down	Unigene28712_All//gi|224071585|ref|XP_002303528.1|//1.00E-125//cytochrome P450 [Populus trichocarpa] >gi|222840960|gb|EEE78507.1| cytochrome P450 [Populus trichocarpa]	Unigene28712_All//2.00E-106//AT4G12300| CYP706A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene28712_All//0.00E+00//DN779367		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene28713_All	313	10.36	32.86	16.16	5.57	10.12	11.11	44.04	94.27	58.93	1.66E+00	8.09E-17	Up	6.41E-01	2.14E-02		8.62E-01	1.18E-02		9.96E-01	2.68E-03		1.10E+00	7.42E-31	Up	4.20E-01	1.82E-04					Unigene28713_All//2.00E-141//TC144658				
Unigene28714_All	402	1.69	1.13	1.59	2.73	1.71	0.34	1.47	0.42	0.40	-5.77E-01	4.94E-01		-9.01E-02	9.22E-01		-6.70E-01	3.06E-01		-3.02E+00	2.14E-04	Down	-1.82E+00	4.71E-02		-1.89E+00	3.22E-02									
Unigene28716_All	590	0.71	0.86	0.36	1.10	0.53	0.77	2.51	2.48	8.51	2.76E-01	7.64E-01		-9.75E-01	4.12E-01		-1.06E+00	2.26E-01		-5.20E-01	5.88E-01		-1.66E-02	1.01E+00		1.76E+00	1.66E-11	Up	Unigene28716_All//gi|369957198|gb|AQ87021.1|//1.00E-55//VDAC1.3 [Lotus japonicus]	Unigene28716_All//3.00E-37//AT3G01280| VDAC1 (VOLTAGE DEPENDENT ANION CHANNEL 1); voltage-gated anion channel	Unigene28716_All//0.00E+00//TC148502				nr +
Unigene28718_All	358	10.52	4.67	6.25	11.97	10.58	17.66	5.08	4.55	6.68	-1.17E+00	2.82E-04	Down	-7.52E-01	2.30E-02		-1.78E-01	5.84E-01		5.62E-01	1.74E-02		-1.58E-01	7.23E-01		3.95E-01	2.86E-01			Unigene28718_All//7.00E-05//AT2G06530| VPS2.1	Unigene28718_All//1.00E-93//TC169830		ko04144|Endocytosis		kegg +
Unigene28719_All	1172	0.27	0.13	0.09	1.45	1.44	0.31	4.00	4.14	3.81	-1.05E+00	4.43E-01		-1.56E+00	3.30E-01		-5.40E-03	9.76E-01		-2.23E+00	7.57E-05	Down	4.69E-02	8.68E-01		-7.29E-02	7.74E-01		Unigene28719_All//gi|79570100|ref|NP_181364.2|//1.00E-32//DNA binding / transcription factor [Arabidopsis thaliana]	Unigene28719_All//7.00E-31//AT2G38300| DNA binding / transcription factor	Unigene28719_All//0.00E+00//TC130273	G2-like			nr -
Unigene28721_All	337	0.31	3.31	1.74	0.30	1.23	1.61	24.46	34.23	17.26	3.41E+00	1.24E-04	Up	2.48E+00	3.75E-02		2.05E+00	1.47E-01		2.44E+00	4.41E-02		4.85E-01	1.17E-03		-5.03E-01	3.98E-03					Unigene28721_All//1.00E-127//TC170686				
Unigene28722_All	993	4.27	2.81	0.54	3.66	2.77	3.05	5.83	1.77	1.00	-6.05E-01	4.04E-02		-2.99E+00	1.10E-13	Down	-4.01E-01	2.27E-01		-2.65E-01	4.67E-01		-1.72E+00	1.73E-12	Down	-2.54E+00	1.09E-20	Down	Unigene28722_All//gi|18400719|ref|NP_565584.1|//1.00E-116//ribonuclease HII family protein [Arabidopsis thaliana] >gi|49066054|sp|Q9SE76.2|RNH2A_ARATH RecName: Full=Ribonuclease H2 subunit A; Short=RNase H2 subunit A; AltName: Full=Ribonuclease HI subunit A; AltName: Full=Ribonuclease HI large subunit; Short=RNase HI large subunit	Unigene28722_All//4.00E-118//AT2G25100| ribonuclease HII family protein	Unigene28722_All//0.00E+00//TC152575		ko03030|DNA replication	GO:0003676//GO:0016891//GO:0044260	nr +
Unigene28724_All	976	2.31	0.42	1.25	1.58	1.13	0.56	5.85	4.45	4.00	-2.47E+00	1.33E-06	Down	-8.77E-01	4.95E-02		-4.87E-01	3.67E-01		-1.51E+00	6.01E-03		-3.93E-01	8.70E-02		-5.48E-01	1.08E-02		Unigene28724_All//gi|297728401|ref|NP_001176564.1|//4.00E-08//Os11g0521000 [Oryza sativa Japonica Group] >gi|77551166|gb|ABA93963.1| GDSL-like Lipase/Acylhydrolase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255680130|dbj|BAH95292.1| Os11g0521000 [Oryza sativa Japonica Group]		Unigene28724_All//5.00E-120//TC153347			GO:0016787//GO:0044238	nr -
Unigene28725_All	851	1.17	64.13	1.94	9.01	9.51	13.48	1.14	10.66	0.19	5.78E+00	1.27E-280	Up	7.32E-01	1.71E-01		7.71E-02	7.83E-01		5.81E-01	4.33E-04		3.22E+00	2.80E-39	Up	-2.61E+00	3.35E-04	Down	Unigene28725_All//gi|15081660|gb|AA82485.1|//2.00E-36//AT3g10020/T22K18_16 [Arabidopsis thaliana] >gi|15529276|gb|AAX97732.1| AT3g10020/T22K18_16 [Arabidopsis thaliana] >gi|15809812|gb|AAL06834.1| AT3g10020/T22K18_16 [Arabidopsis thaliana] >gi|20147181|gb|AAM10307.1| AT3g10020/T22K18_16 [Arabidopsis thaliana]	Unigene28725_All//7.00E-29//AT3G10020| unknown protein	Unigene28725_All//0.00E+00//TC155923			GO:0006950//GO:0045333	nr -
Unigene28727_All	803	0.52	0.44	0.73	8.87	5.45	4.44	2.42	2.97	0.69	-2.39E-01	8.10E-01		4.85E-01	6.30E-01		-7.04E-01	5.47E-04		-9.98E-01	4.03E-06		2.93E-01	4.61E-01		-1.80E+00	3.77E-05	Down	Unigene28727_All//gi|260619528|gb|ACX47456.1|//2.00E-48//LIM1 [Hevea brasiliensis]	Unigene28727_All//3.00E-46//AT3G55770| LIM domain-containing protein	Unigene28727_All//1.00E-67//TC162109	LIM			nr +
Unigene28728_All	551	1.42	0.92	2.13	1.81	3.31	2.38	5.52	3.11	52.64	-6.31E-01	4.08E-01		5.78E-01	3.90E-01		8.73E-01	7.31E-02		3.95E-01	5.45E-01		-8.29E-01	9.27E-03		3.25E+00	1.05E-127	Up				Unigene28728_All//0.00E+00//TC141760				
Unigene28729_All	784	1.20	0.06	1.56	2.35	1.98	2.02	2.70	1.28	1.73	-4.22E+00	1.36E-04	Down	3.79E-01	5.55E-01		-2.50E-01	6.04E-01		-2.22E-01	6.73E-01		-1.08E+00	6.86E-03		-6.42E-01	9.20E-02		Unigene28729_All//gi|223635640|sp|Q6NQ81.2|PP304_ARATH//2.00E-54//RecName: Full=Pentatricopeptide repeat-containing protein At4g04790, mitochondrial; Flags: Precursor	Unigene28729_All//2.00E-56//AT4G04790| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G21880.1); Has 8701 Blast hits to 4047 proteins in 142 species: Archae - 4; Bacteria - 18; Metazoa - 161; Fungi - 114; Plants - 8118; Viruses - 0; Other Eukaryotes - 286 (source: NCBI BLink).				GO:0043231	nr +
Unigene28732_All	213	4.91	5.00	0.50	6.08	3.23	4.45	30.37	16.88	19.83	2.41E-02	9.89E-01		-3.30E+00	4.58E-04	Down	-9.11E-01	1.09E-01		-4.50E-01	4.84E-01		-8.48E-01	4.20E-05		-6.15E-01	2.07E-03					Unigene28732_All//8.00E-106//TC167454				
Unigene28734_All	816	7.44	1.86	0.98	11.66	6.37	4.04	1.45	0.31	1.22	-2.00E+00	5.64E-13	Down	-2.93E+00	5.41E-19	Down	-8.72E-01	3.83E-07		-1.53E+00	5.92E-15	Down	-2.24E+00	4.21E-04	Down	-2.49E-01	6.27E-01		Unigene28734_All//gi|22331920|ref|NP_191889.2|//7.00E-69//phosphoinositide binding [Arabidopsis thaliana]	Unigene28734_All//1.00E-47//AT3G63300| phosphoinositide binding	Unigene28734_All//2.00E-152//TC132277				nr +
Unigene28736_All	560	130.90	55.65	46.59	158.87	190.75	220.25	276.56	124.49	127.98	-1.23E+00	2.09E-74	Down	-1.49E+00	6.85E-96	Down	2.64E-01	1.07E-08		4.71E-01	6.75E-26		-1.15E+00	1.67E-171	Down	-1.11E+00	1.43E-166	Down	Unigene28736_All//gi|297827841|ref|XP_002881803.1|//1.00E-97//40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata] >gi|297327642|gb|EFH58062.1| 40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata]	Unigene28736_All//2.00E-98//AT1G58684| 40S ribosomal protein S2, putative	Unigene28736_All//0.00E+00//TC129809		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr -
Unigene28738_All	774	1.49	0.26	0.62	5.34	3.96	0.99	1.75	0.65	1.65	-2.51E+00	8.99E-04	Down	-1.26E+00	6.41E-02		-4.32E-01	1.54E-01		-2.43E+00	3.88E-12	Down	-1.43E+00	7.15E-03		-8.58E-02	8.66E-01		Unigene28738_All//gi|225348641|gb|ACN87282.1|//4.00E-69//with no lysine kinase [Glycine max]	Unigene28738_All//4.00E-41//AT3G18750| WNK8 (WITH NO K (=LYSINE) 6); kinase/ protein kinase	Unigene28738_All//2.00E-177//DR457515		ko04712|Circadian rhythm - plant	GO:0004674	nr -
Unigene28742_All	1755	0.18	0.29	0.12	1.73	1.35	1.39	2.12	4.36	4.43	6.90E-01	4.99E-01		-5.59E-01	6.63E-01		-3.55E-01	3.38E-01		-3.17E-01	4.17E-01		1.04E+00	6.24E-08	Up	1.06E+00	1.55E-08	Up	Unigene28742_All//gi|157399680|gb|ABV53464.1|//1.00E-128//pseudo-response regulator 5 [Castanea sativa]	Unigene28742_All//7.00E-33//AT5G24470| APRR5 (ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator	Unigene28742_All//0.00E+00//TC138768		ko04712|Circadian rhythm - plant		nr +

Unigene28743_All	372	18.99	32.55	23.19	51.15	36.56	40.19	47.05	43.03	21.63	7.78E-01	2.00E-06		2.88E-01	1.81E-01		-4.84E-01	3.50E-05		-3.48E-01	6.18E-03		-1.29E-01	3.59E-01		-1.12E+00	7.28E-20	Down	Unigene28743_All//gi|125991251|sp|A0Z278.1|YCF2_GOSBA//4.00E-06//RecName: Full=Protein ycf2 >gi|119224904|dbj|BAF41290.1| Hypothetical protein [Gossypium barbadense] >gi|119224922|dbj|BAF41308.1| Hypothetical protein [Gossypium barbadense]		Unigene28743_All//0.00E+00//gi|21094095|gb|BQ406408.1|BQ406408				nr -
Unigene28744_All	1087	2.94	1.82	2.20	1.28	3.01	2.04	0.31	0.00	0.00	-6.92E-01	4.56E-02		-4.13E-01	2.64E-01		1.23E+00	2.62E-04	Up	6.66E-01	1.34E-01		-8.28E+00	1.17E-02		-8.28E+00	8.14E-03		Unigene28744_All//gi|161562211|gb|ABV61020.1|//3.00E-85//zinc finger-homeodomain protein 1 [Eschscholzia californica]	Unigene28744_All//2.00E-61//AT4G24660| ATHB22 (HOMEOBOX PROTEIN 22); DNA binding / transcription factor	Unigene28744_All//0.00E+00//gi|78349454|gb|DT569728.1|DT569728	zf-HD			nr -
Unigene28745_All	502	21.37	9.49	11.99	20.94	11.94	12.24	19.54	11.82	14.76	-1.17E+00	1.15E-10	Down	-8.34E-01	4.22E-06		-8.11E-01	5.58E-07		-7.75E-01	6.44E-06		-7.25E-01	8.82E-06		-4.05E-01	1.14E-02					Unigene28745_All//1.00E-57//TC155687				
Unigene28746_All	298	44.07	11.05	7.86	40.29	18.03	14.70	13.05	0.14	0.40	-2.00E+00	3.09E-27	Down	-2.49E+00	3.66E-34	Down	-1.16E+00	5.57E-14	Down	-1.45E+00	2.02E-17	Down	-6.54E+00	7.34E-26	Down	-5.02E+00	2.40E-24	Down	Unigene28746_All//gi|297724413|ref|NP_001174570.1|//6.00E-16//Os06g0115700 [Oryza sativa Japonica Group] >gi|255676660|dbj|BAH93298.1| Os06g0115700 [Oryza sativa Japonica Group]	Unigene28746_All//2.00E-09//AT4G28310| unknown protein	Unigene28746_All//1.00E-157//gi|164286116|gb|ES818852.1|ES818852			GO:0043231	nr -
Unigene28747_All	619	2.11	8.68	2.67	9.25	5.45	15.10	3.07	19.45	16.99	2.04E+00	9.20E-12	Up	3.36E-01	5.35E-01		-7.64E-01	9.48E-04		7.07E-01	1.32E-04		2.66E+00	7.40E-43	Up	2.47E+00	3.39E-35	Up	Unigene28747_All//gi|21322711|emb|CAD22154.1|//5.00E-62//pherophorin-dz1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome	GO:0009888//GO:0010051//GO:0031410//GO:0048827	nr +
Unigene28749_All	1690	1.08	0.66	1.48	0.35	0.14	0.27	10.11	4.06	10.18	-7.16E-01	1.36E-01		4.51E-01	2.91E-01		-1.31E+00	1.56E-01		-4.05E-01	6.73E-01		-1.32E+00	4.92E-24	Down	1.09E-02	9.57E-01		Unigene28749_All//gi|4160280|emb|CAA06921.1|//0.00E+00//purple acid phosphatase [Ipomoea batatas]	Unigene28749_All//0.00E+00//AT2G16430| PAP10 (PURPLE ACID PHOSPHATASE 10); acid phosphatase/ protein serine/threonine phosphatase	Unigene28749_All//0.00E+00//TC142660			GO:0005618//GO:0016791//GO:0044421//GO:0046914	nr -
Unigene2875_All	1199	17.72	36.30	23.41	20.40	20.76	20.34	14.49	24.30	10.47	1.03E+00	1.58E-33	Up	4.02E-01	1.51E-04		2.56E-02	8.50E-01		-4.20E-03	9.69E-01		7.45E-01	2.85E-16		-4.70E-01	4.86E-05		Unigene2875_All//gi|196196276|gb|ACG76109.1|//5.00E-75//pathogenesis-induced protein [Arachis hypogaea]	Unigene2875_All//1.00E-71//AT1G01360| unknown protein	Unigene2875_All//0.00E+00//gi|109825716|gb|DW224439.1|DW224439			GO:0004871//GO:0005488//GO:0009755	nr -
Unigene28752_All	562	0.28	1.53	0.38	2.13	0.37	3.46	42.58	133.27	61.32	2.46E+00	6.27E-03		4.40E-01	7.75E-01		-2.53E+00	1.46E-04	Down	7.00E-01	1.45E-01		1.65E+00	9.69E-143	Up	5.26E-01	5.85E-11		Unigene28752_All//gi|217033861|gb|ACJ76787.1|//6.00E-21//S-norcoclaurine synthase 2 [Argemone mexicana]		Unigene28752_All//3.00E-157//FF403697				nr -
Unigene28753_All	699	0.75	0.58	0.53	6.27	7.19	2.39	0.79	0.00	1.60	-3.68E-01	6.83E-01		-4.89E-01	6.32E-01		1.98E-01	5.44E-01		-1.39E+00	2.36E-06	Down	-9.62E+00	4.61E-04	Down	1.02E+00	6.87E-02		Unigene28753_All//gi|44681394|gb|AS47637.1|//1.00E-09//At5g51850 [Arabidopsis thaliana] >gi|53828599|gb|AAU94409.1| At5g51850 [Arabidopsis thaliana]	Unigene28753_All//8.00E-15//AT5G62170| unknown protein	Unigene28753_All//1.00E-11//ES837236				nr -
Unigene28755_All	748	178.93	132.63	159.25	3.66	8.33	5.13	0.23	0.06	0.05	-4.32E-01	1.84E-22		-1.68E-01	3.39E-04		1.19E+00	2.44E-07	Up	4.87E-01	1.35E-01		-2.02E+00	3.67E-01		-2.08E+00	3.13E-01		Unigene28755_All//gi|30683176|ref|NP_850080.1|//1.00E-67//YABBY5 (YABBY5); transcription factor [Arabidopsis thaliana] >gi|30683179|ref|NP_850081.1| YABBY5 (YABBY5); transcription factor [Arabidopsis thaliana] >gi|75244351|sp|Q8GW46.1|YAB5_ARATH RecName: Full=Axial regulator YABBY 5 >gi|28372960|gb|AAO39962.1| At2g26580 [Arabidopsis thaliana]	Unigene28755_All//6.00E-69//AT2G26580| YAB5 (YABBY5); transcription factor	Unigene28755_All//0.00E+00//TC139496	C2C2-YABBY		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene28756_All	750	1.05	1.89	1.99	4.72	4.18	3.31	2.82	1.17	0.90	8.54E-01	1.28E-01		9.26E-01	1.05E-01		-1.75E-01	6.16E-01		-5.10E-01	1.34E-01		-1.27E+00	1.68E-03		-1.64E+00	5.85E-05	Down				Unigene28756_All//2.00E-20//TC177101				
Unigene28759_All	324	0.97	10.17	4.93	1.54	1.17	2.09	0.13	1.94	1.48	3.39E+00	1.75E-12	Up	2.35E+00	2.09E-04	Up	-3.95E-01	6.89E-01		4.44E-01	6.22E-01		3.89E+00	1.15E-03		3.50E+00	7.29E-03		Unigene28759_All//gi|255581277|ref|XP_002531450.1|//4.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223528943|gb|EEF30937.1| conserved hypothetical protein [Ricinus communis]		Unigene28759_All//5.00E-105//gi|73860085|gb|DT462824.1|DT462824				nr -
Unigene28760_All	418	4.13	11.03	4.59	6.08	5.11	3.46	0.71	1.60	0.76	1.42E+00	1.89E-06	Up	1.51E-01	7.44E-01		-2.51E-01	5.58E-01		-8.14E-01	4.09E-02		1.18E+00	1.44E-01		1.07E-01	9.45E-01		Unigene28760_All//gi|24461857|gb|AN62344.1|AF506028-11//2.00E-13//CTV.15 [Citrus trifoliata]	Unigene28760_All//1.00E-10//AT5G11090| serine-rich protein-related	Unigene28760_All//2.00E-55//TC174550				nr +
Unigene28762_All	465	0.00	10.13	2.75	0.43	2.15	2.62	22.37	97.16	57.66	1.33E+01	7.47E-27	Up	1.14E+01	4.69E-07	Up	2.33E+00	3.22E-03		2.61E+00	3.93E-04	Up	2.12E+00	2.09E-121	Up	1.37E+00	3.46E-40	Up	Unigene28762_All//gi|54310818|gb|AY33646.1|//5.00E-16//phytosulfokine precursor [Avicennia marina]	Unigene28762_All//1.00E-14//AT3G49780| ATPSK4 (PHYTOSULFOKINE 4 PRECURSOR); growth factor	Unigene28762_All//2.00E-12//TC156906			GO:0032502//GO:0044421	nr +
Unigene28763_All	475	118.19	51.74	89.46	1914.44	1234.09	1098.75	207.04	97.49	86.55	-1.19E+00	4.09E-54	Down	-4.02E-01	2.42E-08		-6.34E-01	0.00E+00		-8.01E-01	0.00E+00		-1.09E+00	1.97E-99	Down	-1.26E+00	4.87E-129	Down	Unigene28763_All//gi|232024|sp|Q01197.1|E6_GOSHI//5.00E-44//RecName: Full=Protein E6 >gi|1000084|gb|AAB03079.1| E6 [Gossypium hirsutum] >gi|209361537|gb|ACI43385.1| E6-1 protein kinase [Gossypium hirsutum]	Unigene28763_All//3.00E-07//AT2G33850| unknown protein	Unigene28763_All//0.00E+00//gi|21094921|gb|BQ407234.1|BQ407234				nr +
Unigene28764_All	688	166.70	427.60	237.61	111.65	86.14	201.46	85.17	124.23	43.89	1.36E+00	0.00E+00	Up	5.11E-01	1.13E-35		-3.74E-01	4.32E-12		8.52E-01	5.66E-82		5.45E-01	9.16E-27		-9.57E-01	8.23E-50		Unigene28764_All//gi|15236885|ref|NP_194414.1|//4.00E-42//SUM01 (SMALL UBIQUITIN-LIKE MODIFIER 1); protein binding / protein tag [Arabidopsis thaliana] >gi|21542462|sp|P55852.2|SMT3_ARATH RecName: Full=Ubiquitin-like protein SMT3 >gi|4452207|emb|CAB36530.1| ubiquitin-like protein [Arabidopsis thaliana] >gi|7269526|emb|CAB75539.1| ubiquitin-like protein [Arabidopsis thaliana] >gi|18252867|gb|AAL62360.1| ubiquitin-like protein [Arabidopsis thaliana] >gi|21592529|gb|AAM64478.1| ubiquitin-like protein [Arabidopsis thaliana] >gi|22652842|gb|AAN03845.1| small ubiquitin-like modifier 1 [Arabidopsis thaliana] >gi|30725548|gb|AAP37796.1| At4g26840 [Arabidopsis thaliana]	Unigene28764_All//2.00E-43//AT4G26840| SUM01 (SMALL UBIQUITIN-LIKE MODIFIER 1); protein binding / protein tag	Unigene28764_All//0.00E+00//TC154277			GO:0005488//GO:0009408//GO:0032446//GO:0043231//GO:0043392	nr -
Unigene28765_All	644	6.82	4.56	6.70	45.41	46.89	22.37	1.58	7.20	2.54	-5.81E-01	4.42E-02		-2.71E-02	9.45E-01		4.65E-02	7.30E-01		-1.02E+00	4.68E-24	Down	2.19E+00	1.21E-13	Up	6.87E-01	1.23E-01		Unigene28765_All//gi|224068654|ref|XP_002302792.1|//4.00E-16//predicted protein [Populus trichocarpa] >gi|222844518|gb|EEE82065.1| predicted protein [Populus trichocarpa]		Unigene28765_All//0.00E+00//gi|109834839|gb|DW233404.1|DW233404				nr +
Unigene28766_All	1440	0.22	0.60	0.22	1.04	1.20	0.50	16.62	7.20	3.68	1.46E+00	6.59E-02		2.56E-02	1.00E+00		2.04E-01	7.38E-01		-1.05E+00	5.67E-02		-1.21E+00	3.35E-29	Down	-2.18E+00	5.08E-69	Down	Unigene28766_All//gi|225424442|ref|XP_002285121.1|//6.00E-57//PREDICTED: similar to ZFP4 (ZINC FINGER PROTEIN 4); nucleic acid binding / transcription factor/ zinc ion binding [Vitis vinifera]	Unigene28766_All//4.00E-52//AT1G66140| ZFP4 (ZINC FINGER PROTEIN 4); nucleic acid binding / transcription factor/ zinc ion binding		C2H2		GO:0005488	nr +
Unigene28767_All	1267	0.70	1.24	0.50	0.39	0.33	0.57	14.25	1.25	6.57	8.20E-01	1.23E-01		-4.77E-01	5.33E-01		-2.70E-01	8.02E-01		5.37E-01	5.60E-01		-3.51E+00	4.57E-84	Down	-1.12E+00	2.48E-20	Down	Unigene28767_All//gi|8778991|gb|AAF79906.1|AC022472_15//2.00E-13//Contains similarity to nuclear protein ZAP from Mus musculus gb|AB033168. ESTs gb|AV521697, gb|AV440130 come from this gene [Arabidopsis thaliana]		Unigene28767_All//0.00E+00//ES829923				nr -
Unigene28768_All	1209	0.48	1.93	2.16	12.32	9.23	11.84	9.23	4.25	1.29	2.02E+00	1.87E-05	Up	2.18E+00	2.86E-06	Up	-4.17E-01	2.41E-03		-5.71E-02	7.33E-01		-1.12E+00	1.55E-12	Down	-2.84E+00	3.00E-44	Down	Unigene28768_All//gi|71905457|gb|AAZ52706.1|//2.00E-50//expressed protein [Arabidopsis thaliana]	Unigene28768_All//4.00E-51//AT1G52330| unknown protein	Unigene28768_All//1.00E-34//TC153618				nr +
Unigene28769_All	608	32.70	21.08	23.73	17.70	12.52	24.88	15.37	7.29	6.75	-6.33E-01	2.96E-07		-4.62E-01	3.10E-04		-5.00E-01	2.26E-03		4.92E-01	5.17E-04		-1.08E+00	4.89E-10	Down	-1.19E+00	5.44E-12	Down	Unigene28769_All//gi|75265972|sp|Q9SJU8.1|RT31_ARATH//1.00E-26//RecName: Full=30S ribosomal protein S31, mitochondrial; Flags: Precursor >gi|11692890|gb|AAG40048.1|AF324697_1 At2g21290 [Arabidopsis thaliana] >gi|4567264|gb|AAD23677.1| expressed protein [Arabidopsis thaliana]	Unigene28769_All//2.00E-08//AT2G21290| unknown protein	Unigene28769_All//0.00E+00//TC173428			GO:0030529//GO:0043231	nr +
Unigene28770_All	565	74.08	40.54	35.06	36.50	37.36	22.22	0.00	0.00	0.00	-8.70E-01	2.02E-24		-1.08E+00	2.26E-33	Down	3.36E-02	8.25E-01		-7.16E-01	1.25E-09		null	null		null	null		Unigene28770_All//gi|85001697|gb|ABC68403.1|//2.00E-63//cytochrome P450 monooxygenase CYP86A24 [Glycine max]	Unigene28770_All//5.00E-58//AT4G00360| CYP86A2 (CYTOCHROME P450 86 A2); fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene28770_All//0.00E+00//TC164843		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016712//GO:0044464	nr +
Unigene28771_All	695	1.36	0.80	1.07	2.01	0.40	1.82	1.46	4.99	1.38	-7.57E-01	2.86E-01		-3.37E-01	6.16E-01		-2.34E+00	8.15E-05	Down	-1.41E-01	7.97E-01		1.77E+00	4.74E-08	Up	-8.58E-02	8.88E-01		Unigene28771_All//gi|7267528|emb|CAB78010.1|//7.00E-72//receptor protein kinase-like protein [Arabidopsis thaliana] >gi|7321074|emb|CAB82121.1| receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene28771_All//4.00E-73//AT4G08850| kinase	Unigene28771_All//2.00E-07//gi|73860367|gb|DT463106.1|DT463106		ko03410|Base excision repair	GO:0004672//GO:0006464//GO:0031224//GO:0032559	nr +
Unigene28772_All	497	20.42	13.97	10.18	29.87	23.42	34.80	60.57	29.43	27.98	-5.48E-01	2.23E-03		-1.00E+00	1.11E-07	Down	-3.51E-01	1.28E-02		2.21E-01	1.32E-01		-1.04E+00	5.91E-29	Down	-1.11E+00	3.30E-33	Down	Unigene28772_All//gi|335990374|gb|AAQ22726.1|//2.00E-22//40S ribosomal protein S25 [Glycine max]	Unigene28772_All//5.00E-22//AT2G21580| 40S ribosomal protein S25 (RPS25B)	Unigene28772_All//0.00E+00//gi|21090748|gb|BQ403061.1|BQ403061		ko03010|Ribosome	GO:0010467//GO:0015935//GO:0016020	nr +
Unigene28773_All	1143	1.28	0.84	0.37	7.58	3.34	2.05	3.03	0.40	0.98	-6.06E-01	2.68E-01		-1.78E+00	4.08E-03		-1.18E+00	1.64E-10	Down	-1.88E+00	3.45E-18	Down	-2.91E+00	4.51E-14	Down	-1.64E+00	1.46E-07	Down	Unigene28773_All//gi|115438735|ref|NP_001043647.1|//3.00E-40//Os01g0631500 [Oryza sativa Japonica Group] >gi|20161490|dbj|BAB90413.1| beta 1,3-glucanase-like [Oryza sativa Japonica Group] >gi|113533178|dbj|BAF05561.1| Os01g0631500 [Oryza sativa Japonica Group]	Unigene28773_All//3.00E-32//AT2G30933| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: X8 (InterPro:IPR012946); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G29380.1); Has 799 Blast hits to 763 proteins in 42 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 23; Plants - 773; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink).	Unigene28773_All//0.00E+00//TC176256			GO:0031410	nr -
Unigene28775_All	804	0.00	0.88	0.00	0.06	0.00	0.73	0.63	1.82	4.46	9.79E+00	3.33E-04	Up	null	null		-5.95E+00	5.55E-01		3.56E+00	8.48E-03		1.53E+00	2.96E-03		2.82E+00	2.45E-14	Up				Unigene28775_All//3.00E-50//ES821058				

Unigene28776_All	602	4.00	2.53	4.25	3.89	4.58	3.98	18.75	9.65	3.97	-6.63E-01	1.06E-01		8.68E-02	8.28E-01		2.35E-01	5.86E-01		3.20E-02	9.50E-01		-9.58E-01	5.10E-10		-2.24E+00	3.51E-34	Down			Unigene28776_All//7.00E-121//gi|21099960|gb|BQ412273.1|BQ412273				
Unigene28778_All	1100	0.24	1.80	1.26	0.77	1.35	1.19	1.81	0.53	2.17	2.92E+00	8.36E-07	Up	2.40E+00	5.37E-04	Up	8.06E-01	1.54E-01		6.29E-01	3.15E-01		-1.76E+00	6.52E-05	Down	2.67E-01	4.83E-01		Unigene28778_All//gi|145337595|ref|NP_177713.3|//1.00E-130//VPS35B (VPS35 HOMOLOG B) [Arabidopsis thaliana]	Unigene28778_All//1.00E-131//AT1G75850| VPS35B (VPS35 HOMOLOG B)	Unigene28778_All//9.00E-14//gi|48790469|gb|CO091783.1|CO091783				nr -
Unigene28779_All	682	18.64	8.77	20.85	5.41	2.27	3.05	0.25	0.67	1.05	-1.09E+00	3.40E-11	Down	1.61E-01	3.57E-01		-1.25E+00	3.39E-05	Down	-8.27E-01	9.08E-03		1.44E+00	1.67E-01		2.08E+00	1.09E-02		Unigene28779_All//gi|15238322|ref|NP_201309.1|//4.00E-13//senescence-associated protein-related [Arabidopsis thaliana]	Unigene28779_All//2.00E-14//AT5G65010| senescence-associated protein-related	Unigene28779_All//6.00E-20//TC165014				nr -
Unigene28781_All	459	109.32	74.85	61.95	123.40	119.21	155.27	283.99	192.04	134.10	-5.47E-01	2.71E-13		-8.19E-01	2.30E-25		-4.98E-02	5.85E-01		3.32E-01	3.30E-08		-5.64E-01	4.63E-43		-1.08E+00	1.97E-134	Down	Unigene28781_All//gi|297819344|ref|XP_002877555.1|//7.00E-14//40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata] >gi|297323393|gb|EFH53814.1| 40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata]	Unigene28781_All//5.00E-15//AT5G62300| 40S ribosomal protein S20 (RPS20C)	Unigene28781_All//0.00E+00//TC142651		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0031981	nr -
Unigene28782_All	456	3.56	6.33	8.52	7.21	10.12	8.72	10.85	8.16	9.26	8.32E-01	2.43E-02		1.26E+00	1.46E-04	Up	4.89E-01	8.48E-02		2.74E-01	4.28E-01		-4.11E-01	9.80E-02		-2.28E-01	3.64E-01				Unigene28782_All//6.00E-84//TC147585				
Unigene28783_All	370	25.03	34.65	33.82	34.06	42.63	37.35	43.65	57.05	92.60	4.69E-01	3.01E-03		4.34E-01	9.54E-03		3.24E-01	2.08E-02		1.33E-01	4.70E-01		3.86E-01	3.11E-04		1.09E+00	7.74E-36	Up	Unigene28783_All//gi|297829912|ref|XP_002882838.1|//9.00E-61//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328678|gb|EFH59097.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28783_All//4.00E-62//AT3G13670| protein kinase family protein	Unigene28783_All//0.00E+00//gi|48812865|gb|CO114178.1|CO114178			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene28785_All	411	4.58	1.23	2.20	3.51	3.85	3.63	0.41	0.00	0.68	-1.89E+00	2.73E-04	Down	-1.06E+00	3.51E-02		1.33E-01	8.25E-01		4.50E-02	9.43E-01		-8.68E+00	1.34E-01		7.22E-01	5.97E-01		Unigene28785_All//gi|18406843|ref|NP_566049.1|//7.00E-23//oxidoreductase family protein [Arabidopsis thaliana] >gi|15724346|gb|AAL06566.1|AF412113_1 At2g45630/F17K2.16 [Arabidopsis thaliana] >gi|18700248|gb|AAL77734.1| At2g45630/F17K2.16 [Arabidopsis thaliana]	Unigene28785_All//4.00E-24//AT2G45630| oxidoreductase family protein	Unigene28785_All//0.00E+00//TC133975			GO:0005488//GO:0016614	nr -
Unigene28786_All	480	2.94	6.76	4.22	3.53	4.09	3.67	2.47	2.35	2.66	1.20E+00	6.93E-04	Up	5.19E-01	2.78E-01		2.13E-01	6.94E-01		5.65E-02	9.33E-01		-6.91E-02	9.13E-01		1.07E-01	8.40E-01		Unigene28786_All//gi|297829856|ref|XP_002882810.1|//4.00E-25//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328650|gb|EFH59069.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene28786_All//3.00E-26//AT3G13224| RNA recognition motif (RRM)-containing protein	Unigene28786_All//5.00E-106//gi|21091481|gb|BQ403794.1|BQ403794		ko03040|Spliceosome	GO:0003676//GO:0032991	nr +
Unigene28789_All	1351	0.19	0.08	0.32	0.44	0.71	1.10	16.43	18.41	55.03	-1.37E+00	3.83E-01		7.04E-01	5.54E-01		6.90E-01	3.61E-01		1.32E+00	1.96E-02		1.64E-01	1.30E-01		1.74E+00	9.08E-157	Up	Unigene28789_All//gi|79344495|ref|NP_172900.2|//2.00E-51//protein binding [Arabidopsis thaliana]	Unigene28789_All//4.00E-47//AT4G10720| ankyrin repeat family protein	Unigene28789_All//0.00E+00//TC136712			GO:0010033	nr +
Unigene2879_All	1495	10.11	13.90	9.58	3.80	3.98	4.35	2.29	4.98	5.30	4.58E-01	1.44E-04		-7.81E-02	6.20E-01		6.91E-02	8.11E-01		1.96E-01	4.73E-01		1.12E+00	1.28E-08	Up	1.21E+00	1.63E-10	Up	Unigene2879_All//gi|21592861|gb|AAM64811.1|//5.00E-97//uroporphyrinogen III synthase [Arabidopsis thaliana]	Unigene2879_All//2.00E-88//AT2G26540| HEMD; uroporphyrinogen-III synthase	Unigene2879_All//0.00E+00//ES810135	ko00860|Porphyrin and chlorophyll metabolism	GO:0006779//GO:0009536//GO:0016836	nr -
Unigene28791_All	788	0.20	0.00	0.00	5.06	3.80	2.81	6.92	1.27	1.82	-7.64E+00	2.16E-01		-7.64E+00	2.45E-01		-4.12E-01	1.84E-01		-8.49E-01	5.02E-03		-2.44E+00	4.47E-18	Down	-1.93E+00	4.24E-14	Down	Unigene28791_All//gi|2739377|gb|AAC14500.1|//1.00E-09//expressed protein [Arabidopsis thaliana]	Unigene28791_All//2.00E-09//AT3G57500| unknown protein			GO:0005488	nr +
Unigene28794_All	912	0.11	63.84	12.85	0.22	1.21	4.16	0.00	0.55	1.27	9.12E+00	0.00E+00	Up	6.81E+00	4.35E-62	Up	2.47E+00	1.07E-03		4.25E+00	8.13E-18	Up	9.10E+00	1.02E-03		1.03E+01	2.28E-08	Up	Unigene28794_All//gi|46931316|gb|AT06462.1|//6.00E-09//At3g27250 [Arabidopsis thaliana]	Unigene28794_All//5.00E-11//AT5G40790| unknown protein	Unigene28794_All//7.00E-150//TC174265				nr +
Unigene28795_All	1008	1.14	0.50	0.90	2.13	2.05	2.20	2.94	1.82	1.23	-1.18E+00	6.62E-02		-3.47E-01	6.16E-01		-5.21E-02	9.02E-01		4.70E-02	9.34E-01		-6.87E-01	3.47E-02		-1.26E+00	9.67E-05	Down	Unigene28795_All//gi|297827241|ref|XP_002881503.1|//2.00E-97//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327342|gb|EFH57762.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene28795_All//2.00E-91//AT2G37310| pentatricopeptide (PPR) repeat-containing protein	Unigene28795_All//0.00E+00//gi|164247957|gb|ES800745.1|ES800745				nr -
Unigene28796_All	395	3.18	0.00	4.58	3.91	3.57	4.92	1.28	1.48	1.21	-1.16E+01	2.54E-07	Down	5.28E-01	3.04E-01		-1.29E-01	8.32E-01		3.31E-01	5.22E-01		2.06E-01	8.00E-01		-8.58E-02	9.30E-01				Unigene28796_All//0.00E+00//TC147317				
Unigene28797_All	844	1.86	0.96	2.21	2.42	4.86	2.09	0.40	0.00	0.09	-9.53E-01	7.08E-02		2.48E-01	6.19E-01		1.00E+00	5.56E-04	Up	-2.14E-01	6.65E-01		-8.65E+00	1.17E-02		-2.09E+00	1.07E-01		Unigene28797_All//gi|3600054|gb|AAC35541.1|//1.00E-46//P2P3.4 gene product [Arabidopsis thaliana] >gi|71140356|gb|AAZ23919.1| At4g11090 [Arabidopsis thaliana]	Unigene28797_All//3.00E-42//AT4G23790| unknown protein	Unigene28797_All//2.00E-63//gi|48799810|gb|CO101124.1|CO101124				nr +
Unigene28799_All	580	10.46	7.86	10.83	1.98	1.84	0.93	1.60	1.37	0.14	-4.12E-01	9.13E-02		5.01E-02	8.43E-01		-1.02E-01	8.56E-01		-1.08E+00	9.66E-02		-2.28E-01	7.18E-01		-3.55E+00	3.97E-05	Down	Unigene28799_All//gi|124360157|gb|ABN08173.1|//5.00E-24//Peptidase, cysteine peptidase active site [Medicago truncatula]	Unigene28799_All//4.00E-18//AT5G27290| unknown protein	Unigene28799_All//4.00E-116//gi|109984536|gb|DW513506.1|DW513506			GO:0043231	nr +
Unigene28801_All	362	34.98	20.58	23.09	66.33	90.75	106.67	64.94	17.90	50.18	-7.66E-01	1.54E-06		-5.99E-01	2.68E-04		4.52E-01	2.06E-07		6.86E-01	4.06E-16		-1.86E+00	1.13E-53	Down	-3.72E-01	1.56E-04		Unigene28801_All//gi|224089205|ref|XP_002308657.1|//1.00E-60//cellulose synthase [Populus trichocarpa] >gi|222854633|gb|EEE92180.1| cellulose synthase [Populus trichocarpa]	Unigene28801_All//3.00E-36//AT4G32410| CESA1 (CELLULOSE SYNTHASE 1); cellulose synthase/transferase, transferring glycosyl groups	Unigene28801_All//0.00E+00//TC159461			GO:0006972//GO:0009250//GO:0009832//GO:0016759//GO:0031224//GO:0043231//GO:0045229//GO:0046914	nr +
Unigene28802_All	538	2.53	6.50	0.49	1.76	2.24	3.11	2.28	1.71	0.37	1.36E+00	7.74E-05	Up	-2.35E+00	7.62E-04	Down	3.49E-01	5.95E-01		8.20E-01	1.19E-01		-4.15E-01	4.66E-01		-2.62E+00	4.02E-05	Down	Unigene28802_All//gi|8096269|dbj|BAA95789.1|//8.00E-17//KED [Nicotiana tabacum]				ko03040|Spliceosome		nr +
Unigene28805_All	877	0.24	1.73	0.67	5.06	3.73	5.36	3.81	1.67	2.04	2.86E+00	2.69E-05	Up	1.49E+00	1.53E-01		-4.39E-01	1.28E-01		8.33E-02	7.91E-01		-1.19E+00	1.12E-04	Down	-8.98E-01	2.15E-03		Unigene28805_All//gi|75338852|sp|Q92QE6.1|CML1_ARATH//7.00E-60//RecName: Full=Calmodulin-like protein 1 >gi|30102922|gb|AAP21379.1| At2g15680 [Arabidopsis thaliana]	Unigene28805_All//3.00E-61//AT2G15680| calmodulin-related protein, putative	Unigene28805_All//0.00E+00//gi|164287246|gb|ES844824.1|ES844824		ko04626|Plant-pathogen interaction	GO:0008152//GO:0016628//GO:0046872	nr +
Unigene28808_All	636	0.99	0.96	1.84	1.25	2.11	1.85	1.40	2.43	3.95	-4.63E-02	9.72E-01		9.00E-01	1.70E-01		7.53E-01	2.15E-01		5.59E-01	4.04E-01		8.01E-01	9.44E-02		1.50E+00	4.49E-05	Up			Unigene28808_All//1.00E-08//gi|5047225|gb|AT2G37373.1|AT2G37373				
Unigene28810_All	1493	0.56	0.17	0.39	0.20	0.14	0.24	8.13	4.93	31.01	-1.72E+00	3.63E-02		-5.15E-01	5.15E-01		-5.33E-01	6.79E-01		2.74E-01	8.33E-01		-7.22E-01	6.45E-07		1.93E+00	1.82E-112	Up	Unigene28810_All//gi|3399777|gb|AAC32828.1|//5.00E-58//symbiotic ammonium transporter [Glycine max]	Unigene28810_All//5.00E-53//AT4G37850| basic helix-loop-helix (bHLH) family protein	Unigene28810_All//3.00E-79//TC134717	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene28811_All	604	6.41	5.20	5.91	21.69	16.99	16.30	52.29	37.85	21.63	-3.02E-01	3.63E-01		-1.18E-01	7.15E-01		-3.52E-01	2.05E-02		-4.12E-01	8.23E-03		-4.66E-01	4.68E-08		-1.27E+00	8.54E-43	Down	Unigene28811_All//gi|20453062|gb|AAM19776.1|//1.00E-102//AT3g08530/T8G24_1 [Arabidopsis thaliana] >gi|21928019|gb|AAM28038.1| AT3g08530/T8G24_1 [Arabidopsis thaliana]	Unigene28811_All//7.00E-96//AT3G08530| clathrin heavy chain, putative	Unigene28811_All//0.00E+00//gi|48817694|gb|CO119007.1|CO119007		ko04144|Endocytosis		nr -
Unigene28812_All	347	74.49	32.56	21.94	76.95	59.44	97.36	127.21	44.57	52.58	-1.19E+00	2.37E-25	Down	-1.76E+00	3.06E-43	Down	-3.72E-01	1.52E-04		3.39E-01	2.02E-04		-1.51E+00	6.94E-75	Down	-1.27E+00	1.51E-59	Down	Unigene28812_All//gi|15238999|ref|NP_198867.1|//2.00E-52//40S ribosomal protein S10 (RPS10B) [Arabidopsis thaliana] >gi|20139725|sp|Q9FF58.1|RS10_ARATH RecName: Full=40S ribosomal protein S10-2 >gi|14030699|gb|AAK53024.1|AF37544_1 AT5g41520/MBK23_4 [Arabidopsis thaliana] >gi|14335122|gb|AAK59840.1| AT5g41520/MBK23_4 [Arabidopsis thaliana] >gi|16974521|gb|AAL31170.1| AT5g41520/MBK23_4 [Arabidopsis thaliana]	Unigene28812_All//9.00E-26//AT5G41520| 40S ribosomal protein S10 (RPS10B)	Unigene28812_All//0.00E+00//gi|13350214|gb|BG440563.1|BG440563		ko03010|Ribosome	GO:0009536//GO:0010467//GO:0015935//GO:0030312	nr +
Unigene28814_All	1199	0.26	0.00	0.00	3.32	1.98	1.66	12.55	23.01	8.31	-8.03E+00	3.66E-02		-8.03E+00	4.91E-02		-7.46E-01	9.58E-03		-1.00E+00	9.11E-04	Down	8.74E-01	4.74E-20		-5.96E-01	2.00E-06		Unigene28814_All//gi|110931814|gb|ABH02906.1|//3.00E-77//MYB transcription factor MYB161 [Glycine max]	Unigene28814_All//1.00E-63//AT3G49690| MYB84 (MYB DOMAIN PROTEIN 84); DNA binding / transcription factor	Unigene28814_All//4.00E-56//TC137837	MYB		GO:0003676//GO:0009725//GO:0010468//GO:0043231	nr +
Unigene28815_All	299	7.52	7.46	6.23	5.83	5.53	6.65	46.81	24.46	16.12	-1.31E-02	9.90E-01		-2.72E-01	5.60E-01		-7.70E-02	8.69E-01		1.89E-01	6.88E-01		-9.36E-01	8.68E-12		-1.54E+00	1.30E-25	Down			Unigene28815_All//9.00E-88//TC168297				
Unigene28817_All	679	0.00	0.00	0.00	62.65	37.12	30.26	11.02	12.62	9.09	null	null		null	null		-7.55E-01	1.18E-23		-1.05E+00	2.39E-36	Down	1.95E-01	3.28E-01		-2.77E-01	1.52E-01				Unigene28817_All//0.00E+00//DW224477				
Unigene28818_All	748	180.33	93.28	83.01	9.86	12.94	33.87	0.34	0.11	0.16	-9.51E-01	1.67E-89		-1.12E+00	3.76E-113	Down	3.92E-01	3.33E-02		1.78E+00	1.80E-47	Up	-1.60E+00	3.10E-01		-1.09E+00	4.28E-01		Unigene28818_All//gi|59042581|gb|AW83819.1|//1.00E-47//GASA2-like protein [Pelargonium zonale]	Unigene28818_All//3.00E-35//AT3G10185| Encodes a Gibberellin-regulated GASA/GAST/Snakin family protein	Unigene28818_All//0.00E+00//TC147876				nr +
Unigene2882_All	1327	853.42	35.70	119.50	126.96	63.63	143.59	5.48	4.44	2.58	-4.58E+00	0.00E+00	Down	-2.84E+00	0.00E+00	Down	-9.97E-01	1.71E-149		1.78E-01	8.73E-07		-3.03E-01	1.39E-01		-1.09E+00	2.25E-08	Down	Unigene2882_All//gi|81230696|gb|AB89694.1|//1.00E-141//alpha-expansin 2 [Gossypium hirsutum]	Unigene2882_All//5.00E-106//AT2G40610| ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	Unigene2882_All//0.00E+00//TC129679				nr +
Unigene28820_All	870	0.72	0.82	0.55	21.82	30.71	20.51	2.43	1.20	0.92	1.76E-01	8.17E-01		-3.90E-01	6.46E-01		4.94E-01	4.29E-07		-8.93E-02	5.80E-01		-1.02E+00	1.04E-02		-1.41E+00	3.88E-04	Down	Unigene28820_All//gi|15451058|gb|AA96800.1|//6.00E-10//Unknown protein [Arabidopsis thaliana]	Unigene28820_All//2.00E-12//AT5G10695| unknown protein	Unigene28820_All//0.00E+00//TC153581				nr +
Unigene28821_All	356	1.62	5.27	1.05	1.26	3.29	2.16	10.45	15.03	16.00	1.70E+00	8.73E-04	Up	-6.27E-01	5.27E-01		1.38E+00	3.33E-02		7.76E-01	3.78E-01		5.24E-01	2.40E-02		6.15E-01	4.32E-03		Unigene28821_All//gi|7769853|gb|AAF69531.1|AC008007_6//1.00E-14//F12M16.10 [Arabidopsis thaliana]	Unigene28821_All//5.00E-16//AT1G53190| zinc finger (C3HC4-type RING finger) family protein	Unigene28821_All//0.00E+00//CO094619			GO:0046914	nr -
Unigene28823_All	1149	0.59	0.09	0.23	0.82	0.84	0.28	2.24	0.29	1.73	-2.75E+00	1.06E-02		-1.35E+00	1.50E-01		2.69E-02	9.88E-01		-1.58E+00	3.51E-02		-2.95E+00	9.63E-11	Down	-3.73E-01	2.91E-01		Unigene28823_All//gi|188509938|gb|ACD56624.1|//0.00E+00//UNE1-like protein [Gossypium raimondii]	Unigene28823_All//3.00E-65//AT1G29300| UNE1 (unfertilized embryo sac 1)	Unigene28823_All//2.00E-30//gi|164245981|gb|ES802474.1|ES802474				nr +
Unigene28825_All	600	0.35	2.28	1.51	1.91	1.03	2.18	1.90	2.37	1.99	2.71E+00	1.29E-04	Up	2.11E+00	1.42E-02		-8.86E-01	1.53E-01		1.93E-01	7.47E-01		3.16E-01	5.63E-01		6.62E-02	9.19E-01		Unigene28825_All//gi|115461783|ref|NP_001054491.1|//1.00E-16//Os05g0120300 [Oryza sativa Japonica Group] >gi|113578042|dbj|BAF16405.1| Os05g0120300 [Oryza sativa Japonica Group]	Unigene28825_All//9.00E-26//AT5G02640| unknown protein	Unigene28825_All//0.00E+00//gi|109869315|gb|DW498291.1|DW498291				nr -
Unigene28826_All	530	174.53	56.41	60.99	27.44	37.75	32.55	0.08	0.63	5.49	-1.63E+00	2.14E-142	Down	-1.52E+00	3.63E-124	Down	4.60E-01	7.29E-05		2.46E-01	8.48E-02		2.98E+00	5.73E-02		6.10E+00	2.88E-19	Up			Unigene28826_All//5.00E-168//gi|109876232|gb|DW505206.1|DW505206				
Unigene28827_All	708	18.77	7.09	17.45	34.97	25.63	35.98	53.57	32.23	34.16	-1.41E+00	4.78E-17	Down	-1.05E-01	5.73E-01		-4.48E-01	9.26E-06		4.10E-02	7.51E-01		-7.33E-01	2.28E-20		-6.49E-01	4.04E-17		Unigene28827_All//gi|29119027|emb|CBET07387.1|//5.00E-76//NAP-related protein [Medicago sativa subsp. x varia]	Unigene28827_All//1.00E-70//AT1G74560| NRP1 (NAP1-RELATED PROTEIN 1); DNA binding / chromatin binding / histone binding	Unigene28827_All//0.00E+00//gi|13353123|gb|BG443471.1|BG443471			GO:0003676//GO:0005515//GO:0006950//GO:0009755//GO:0010038//GO:0010102//GO:0034728//GO:0043231//GO:0048869//GO:0051707	nr -
Unigene28829_All	860	0.49	0.59	0.00	3.65	2.36	1.73	0.88	3.06	0.46	2.76E-01	7.64E-01		-8.93E+00	1.56E-02		-6.27E-01	6.48E-02		-1.07E+00	2.12E-03		1.79E+00	2.31E-06	Up	-9.34E-01	1.82E-01		Unigene28829_All//gi|42566276|ref|NP_192255.2|//4.00E-27//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene28829_All//3.00E-17//AT1G03670| ankyrin repeat family protein					nr +
Unigene28830_All	1074	45.55	18.02	18.05	13.13	11.73	16.74	0.00	0.00	0.00	-1.34E+00	1.85E-56	Down	-1.34E+00	2.30E-54	Down	-1.62E-01	3.32E-01		3.51E-01	7.97E-03		null	null		null	null		Unigene28830_All//gi|20149046|gb|AAM12778.1|//2.00E-20//auxin-induced SAUR-like protein [Capsicum annuum]	Unigene28830_All//6.00E-21//AT4G38840| auxin-responsive protein, putative	Unigene28830_All//0.00E+00//DW512758			GO:0006950//GO:0009725//GO:0016020	nr -

Unigene28831_All	473	62.39	28.92	50.55	77.62	68.22	60.15	604.26	327.12	234.15	-1.11E+00	1.03E-25	Down	-3.04E-01	3.92E-03		-1.86E-01	4.03E-02		-3.68E-01	2.01E-05		-8.85E-01	5.48E-205		-1.37E+00	0.00E+00	Down	Unigene28831_All//gi|30687535|ref|NP_194457.2|//8.00E-29//quinone reductase family protein [Arabidopsis thaliana] >gi|34365651|gb|AAQ65137.1|At4g27270 [Arabidopsis thaliana]	Unigene28831_All//5.00E-30//AT4G27270| quinone reductase family protein	Unigene28831_All//0.00E+00//TC131108			GO:0000166//GO:0006350//GO:0016020//GO:0016655//GO:0043231	nr +
Unigene28833_All	415	20.80	9.28	41.83	14.04	5.97	1.85	0.61	0.50	0.38	-1.16E+00	1.15E-08	Down	1.01E+00	9.22E-13	Up	-1.23E+00	9.97E-08	Down	-2.92E+00	1.19E-20	Down	-2.80E-01	8.29E-01		-6.71E-01	6.05E-01				Unigene28833_All//6.00E-56//TC172737				
Unigene28834_All	503	1.77	1.21	1.16	3.37	1.10	1.44	10.93	15.37	2.06	-5.49E-01	4.42E-01		-6.03E-01	4.18E-01		-1.62E+00	9.57E-04	Down	-1.23E+00	1.61E-02		4.92E-01	8.78E-03		-2.41E+00	1.56E-18	Down	Unigene28834_All//gi|108711605|gb|ABF99400.1|//1.00E-33//F-box domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]		Unigene28834_All//0.00E+00//gi|164345604|gb|EX168412.1|EX168412				nr -
Unigene28835_All	701	1.72	0.87	0.15	5.61	2.36	2.77	1.33	2.44	3.18	-9.85E-01	1.13E-01		-3.50E+00	8.78E-05	Down	-1.25E+00	1.63E-05	Down	-1.02E+00	8.38E-04	Down	8.82E-01	4.98E-02		1.26E+00	9.46E-04	Up	Unigene28835_All//gi|255569418|ref|XP_002525676.1|//3.00E-08//transcription initiation factor brf1, putative [Ricinus communis] >gi|223534976|gb|EEF36659.1|transcription initiation factor brf1, putative [Ricinus communis]						nr +
Unigene28839_All	1271	0.08	0.00	0.00	2.51	1.73	1.35	0.93	0.89	3.60	-6.36E+00	3.72E-01		-6.36E+00	3.94E-01		-5.33E-01	1.20E-01		-8.93E-01	9.76E-03		-6.90E-02	9.13E-01		1.95E+00	5.18E-12	Up	Unigene28839_All//gi|35187439|gb|AAQ84311.1|//4.00E-14//fiber protein Fb17 [Gossypium barbadense]		Unigene28839_All//1.00E-13//TC149899				nr +
Unigene28842_All	587	3.12	1.38	1.72	9.33	7.51	3.69	5.26	1.78	3.39	-1.18E+00	1.60E-02		-8.56E-01	9.04E-02		-3.14E-01	2.38E-01		-1.34E+00	2.30E-07	Down	-1.56E+00	3.35E-06	Down	-6.32E-01	3.83E-02				Unigene28842_All//0.00E+00//ES810726				
Unigene28844_All	2009	0.16	0.91	0.03	0.15	0.36	0.16	10.90	7.14	9.97	2.54E+00	1.40E-05	Up	-2.56E+00	1.59E-01		1.27E+00	1.56E-01		8.11E-02	9.50E-01		-6.11E-01	5.05E-09		-1.28E-01	2.61E-01		Unigene28844_All//gi|15238089|ref|NP_196581.1|//0.00E+00//transporter-related [Arabidopsis thaliana]	Unigene28844_All//0.00E+00//AT5G10190| transporter-related	Unigene28844_All//0.00E+00//gi|78348752|gb|DT569026.1|DT569026			GO:0006810//GO:0009566//GO:0022891//GO:0044464	nr +
Unigene28847_All	501	4.91	2.73	6.16	4.97	1.92	2.88	0.34	0.33	0.00	-8.46E-01	3.66E-02		3.29E-01	3.88E-01		-1.37E+00	3.43E-04	Down	-7.85E-01	5.15E-02		-1.68E-02	1.02E+00		-8.40E+00	1.08E-01				Unigene28847_All//6.00E-10//gi|11200850|gb|BF269855.1|BF269855				
Unigene28848_All	508	3.30	18.15	7.76	4.31	6.30	4.89	50.10	56.03	39.52	2.46E+00	1.14E-24	Up	1.23E+00	1.72E-04	Up	5.47E-01	1.23E-01		1.81E-01	6.97E-01		1.61E-01	1.05E-01		-3.42E-01	2.89E-04		Unigene28848_All//gi|225348627|gb|ACN87275.1|//2.00E-37//short chain dehydrogenase/reductase [Nandina domestica]	Unigene28848_All//4.00E-34//AT3G61220| short-chain dehydrogenase/reductase (SDR) family protein	Unigene28848_All//0.00E+00//TC177921		ko04146|Peroxisome//ko01040|Biosynthesis of unsaturated fatty acids//ko00906|Carotenoid biosynthesis//ko00061|Fatty acid biosynthesis	GO:0008152//GO:0016616	nr -
Unigene28849_All	872	642.37	190.18	303.68	1237.76	1126.25	669.27	43.73	16.15	12.66	-1.76E+00	0.00E+00	Down	-1.08E+00	0.00E+00	Down	-1.36E-01	7.17E-24		-8.87E-01	0.00E+00		-1.44E+00	4.69E-60	Down	-1.79E+00	1.17E-84	Down	Unigene28849_All//gi|300793604|tpg|DAA33868.1|//1.00E-140//TPA: TPA_inf: aquaporin TIP1;5 [Gossypium hirsutum]	Unigene28849_All//6.00E-116//AT2G36830| GAMMA-TIP (GAMMA TONOPLAST INTRINSIC PROTEIN); water channel	Unigene28849_All//0.00E+00//gi|78326141|gb|DT546415.1|DT546415				nr -
Unigene28851_All	1491	13.93	0.34	2.86	0.47	0.51	0.30	0.94	0.78	0.75	-5.36E+00	9.40E-105	Down	-2.29E+00	9.31E-49	Down	1.20E-01	9.05E-01		-6.27E-01	4.76E-01		-2.54E-01	6.33E-01		-3.23E-01	5.30E-01		Unigene28851_All//gi|224074159|ref|XP_002304279.1|//1.00E-129//mtn21-like protein [Populus trichocarpa] >gi|222841711|gb|EEE79258.1|mtn21-like protein [Populus trichocarpa]	Unigene28851_All//6.00E-94//AT5G47470| nodulin MtN21 family protein	Unigene28851_All//0.00E+00//TC149456			GO:0043231	nr +
Unigene28852_All	727	0.00	0.70	0.15	0.96	0.57	0.87	4.89	0.86	3.62	9.45E+00	4.04E-03		7.19E+00	3.99E-01		-7.55E-01	3.69E-01		-1.42E-01	8.66E-01		-2.50E+00	2.52E-12	Down	-4.34E-01	1.31E-01		Unigene28852_All//gi|115487410|ref|NP_001066192.1|//9.00E-22//Os12g0155100 [Oryza sativa Japonica Group] >gi|77553688|gb|ABA96484.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113648699|dbj|BAF29211.1|Os12g0155100 [Oryza sativa Japonica Group]	Unigene28852_All//3.00E-17//AT5G22390| unknown protein	Unigene28852_All//7.00E-26//TC159078				nr +
Unigene28854_All	729	0.14	0.42	1.68	1.37	1.28	1.24	0.64	1.38	2.68	1.54E+00	3.23E-01		3.55E+00	6.10E-05	Up	-9.96E-02	8.68E-01		-1.41E-01	8.36E-01		1.11E+00	7.67E-02		2.07E+00	6.08E-06	Up	Unigene28854_All//gi|22327387|ref|NP_198442.2|//2.00E-75//AMP-dependent synthetase and ligase family protein [Arabidopsis thaliana]	Unigene28854_All//1.00E-76//AT5G35930| AMP-dependent synthetase and ligase family protein				GO:0005488//GO:0016853//GO:0043231	nr +
Unigene28855_All	564	2.32	3.05	5.66	2.65	3.24	2.40	0.75	1.41	0.92	3.97E-01	4.22E-01		1.29E+00	5.42E-04	Up	2.88E-01	5.96E-01		-1.41E-01	7.88E-01		9.10E-01	2.11E-01		2.93E-01	7.27E-01		Unigene28855_All//gi|15226168|ref|NP_178215.1|//3.00E-13//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene28855_All//2.00E-14//AT2G01050| nucleic acid binding / zinc ion binding					nr +
Unigene28857_All	1037	20.89	7.38	9.35	0.14	0.46	0.00	0.00	0.00	0.00	-1.50E+00	4.46E-30	Down	-1.16E+00	1.27E-19	Down	1.69E+00	1.66E-01		-7.17E+00	2.33E-01		null	null		null	null		Unigene28857_All//gi|298201168|gb|ADI60286.1|//3.00E-52//PALMATE-LIKE PENTAFOLIATA1 [Medicago truncatula]	Unigene28857_All//4.00E-37//AT4G17810| nucleic acid binding / transcription factor/ zinc ion binding		C2H2		GO:0005488	nr -
Unigene28859_All	696	0.00	0.15	0.31	3.01	2.87	6.75	1.64	0.78	0.69	7.19E+00	3.87E-01		8.26E+00	1.41E-01		-6.70E-02	8.77E-01		1.17E+00	3.16E-05	Up	-1.07E+00	6.31E-02		-1.26E+00	2.42E-02		Unigene28859_All//gi|255563792|ref|XP_002522897.1|//1.00E-35//conserved hypothetical protein [Ricinus communis] >gi|223537882|gb|EEF39497.1|conserved hypothetical protein [Ricinus communis]	Unigene28859_All//8.00E-06//AT3G13130| unknown protein	Unigene28859_All//0.00E+00//DW498633				nr +
Unigene2886_All	1819	6.30	6.91	7.90	3.64	7.78	5.11	3.42	1.31	1.29	1.33E-01	4.46E-01		3.27E-01	3.91E-02		1.10E+00	2.96E-14	Up	4.90E-01	9.64E-03		-1.38E+00	6.61E-10	Down	-1.40E+00	1.89E-10	Down			Unigene2886_All//4.00E-128//ES816926				
Unigene28860_All	454	130.69	639.73	344.60	99.96	308.55	370.96	78.60	107.44	171.55	2.29E+00	0.00E+00	Up	1.40E+00	1.77E-186	Up	1.63E+00	1.19E-252	Up	1.89E+00	0.00E+00	Up	4.51E-01	2.56E-11		1.13E+00	2.89E-85	Up	Unigene28860_All//gi|115462479|ref|NP_001051839.1|//1.00E-07//Os05g0188100 [Oryza sativa Japonica Group] >gi|113578390|dbj|BAF16753.1|Os05g0188100 [Oryza sativa Japonica Group]		Unigene28860_All//2.00E-164//TC155600				nr -
Unigene28861_All	416	3.77	1.34	0.77	13.65	10.02	5.10	6.40	0.60	1.72	-1.49E+00	6.73E-03		-2.30E+00	3.17E-04	Down	-4.47E-01	7.01E-02		-1.42E+00	2.87E-08	Down	-3.41E+00	1.39E-12	Down	-1.89E+00	3.72E-07	Down			Unigene28861_All//2.00E-179//gi|78347266|gb|DT567540.1|DT567540				
Unigene28862_All	578	28.42	11.05	13.36	29.73	20.38	35.40	103.21	52.64	32.74	-1.36E+00	5.49E-20	Down	-1.09E+00	1.23E-13	Down	-5.45E-01	9.72E-06		2.52E-01	4.96E-02		-9.71E-01	1.51E-50		-1.66E+00	1.79E-118	Down	Unigene28862_All//gi|209967449|gb|ACJ02353.1|//1.00E-28//60S ribosomal protein L27A [Vernicia fordii]	Unigene28862_All//1.00E-25//AT1G23290| RPL27AB; structural constituent of ribosome	Unigene28862_All//5.00E-165//TC166255		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene28863_All	256	9.20	12.47	14.77	16.35	6.99	16.41	18.17	11.43	4.05	4.39E-01	2.15E-01		6.83E-01	3.85E-02		-1.22E+00	1.20E-05	Down	5.40E-03	9.87E-01		-6.69E-01	7.25E-03		-2.17E+00	5.36E-14	Down	Unigene28863_All//gi|297725871|ref|NP_001175299.1|//2.00E-12//Os07g0620501 [Oryza sativa Japonica Group] >gi|255677975|dbj|BAH94027.1|Os07g0620501 [Oryza sativa Japonica Group]	Unigene28863_All//4.00E-12//AT5G02502| unknown protein	Unigene28863_All//6.00E-104//gi|164261738|gb|EV493637.1|EV493637			GO:0031410	nr -
Unigene28864_All	628	29.33	29.05	16.28	31.17	34.87	31.86	30.77	8.79	17.45	-1.38E-02	9.38E-01		-8.49E-01	2.86E-10		1.62E-01	2.19E-01		3.14E-02	8.39E-01		-1.81E+00	1.29E-42	Down	-8.19E-01	2.73E-13		Unigene28864_All//gi|195618310|gb|ACG30985.1|//2.00E-38//60S acidic ribosomal protein P1 [Zea mays] >gi|195625300|gb|ACG34480.1|60S acidic ribosomal protein P1 [Zea mays]	Unigene28864_All//6.00E-18//AT5G47700| 60S acidic ribosomal protein P1 (RPP1C)	Unigene28864_All//1.00E-141//TC154577		ko03010|Ribosome	GO:0005198//GO:0005840//GO:0006412//GO:0016020//GO:0043231	nr -
Unigene28865_All	639	42.99	37.43	61.25	7.09	7.38	2.83	0.00	0.13	0.81	-2.00E-01	6.75E-02		5.11E-01	5.34E-09		5.76E-02	8.60E-01		-1.33E+00	3.85E-06	Down	7.03E+00	4.01E-01		9.66E+00	6.13E-04	Up	Unigene28865_All//gi|124300960|gb|ABN04732.1|//1.00E-35//At5g62140 [Arabidopsis thaliana]	Unigene28865_All//7.00E-30//AT5G62140| unknown protein	Unigene28865_All//0.00E+00//gi|109879951|gb|DW508921.1|DW508921			GO:0009536	nr -
Unigene28867_All	1262	0.00	0.00	0.00	0.00	0.00	0.00	5.96	3.08	1.89	null	null		null	null		null	null		null	null		-9.53E-01	6.83E-07		-1.65E+00	1.16E-15	Down	Unigene28867_All//gi|297827389|ref|XP_002881577.1|//1.00E-32//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297327416|gb|EFH57836.1|DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene28867_All//6.00E-34//AT2G38300| DNA binding / transcription factor		G2-like		GO:0001071//GO:0010468//GO:0043231	nr +
Unigene28869_All	1247	0.00	0.12	0.51	0.36	0.39	0.36	2.51	3.52	6.01	6.93E+00	2.35E-01		9.00E+00	1.16E-03		1.05E-01	9.55E-01		1.08E-02	1.00E+00		4.88E-01	6.35E-02		1.26E+00	1.48E-10	Up	Unigene28869_All//gi|124365513|gb|ABN09747.1|//4.00E-33//Cyclin-like F-box; F-box protein interaction domain; Four-helical cytokine [Medicago truncatula]	Unigene28869_All//7.00E-13//AT4G12560| F-box family protein	Unigene28869_All//0.00E+00//gi|78325190|gb|DT545464.1|DT545464				nr -
Unigene28870_All	1078	0.19	1.69	0.59	1.62	2.24	1.93	6.55	20.82	4.84	3.12E+00	1.05E-06	Up	1.61E+00	1.11E-01		4.67E-01	2.92E-01		2.53E-01	6.37E-01		1.67E+00	4.23E-44	Up	-4.36E-01	2.33E-02		Unigene28870_All//gi|4510354|gb|AAD21443.1|//9.00E-47//expressed protein [Arabidopsis thaliana] >gi|15450733|gb|AAK96638.1|At2g36220/F2H17.17 [Arabidopsis thaliana] >gi|18491123|gb|AAL69530.1|At2g36220/F2H17.17 [Arabidopsis thaliana]	Unigene28870_All//2.00E-30//AT3G52710| unknown protein	Unigene28870_All//0.00E+00//TC179407			GO:0016020//GO:0045333	nr -
Unigene28871_All	1039	37.47	13.12	13.38	165.02	92.77	117.19	192.80	92.00	72.81	-1.51E+00	3.48E-54	Down	-1.49E+00	7.58E-51	Down	-8.31E-01	1.20E-111		-4.94E-01	3.69E-39		-1.07E+00	3.80E-196	Down	-1.40E+00	0.00E+00	Down			Unigene28871_All//3.00E-155//gi|21089819|gb|BQ402132.1|BQ402132				
Unigene28875_All	259	1.01	9.19	1.03	20.77	19.28	37.14	13.39	3.71	4.46	3.19E+00	1.01E-08	Up	2.53E-02	1.00E+00		-1.08E-01	7.29E-01		8.38E-01	4.23E-06		-1.85E+00	1.67E-08	Down	-1.59E+00	2.87E-07	Down			Unigene28875_All//1.00E-105//TC157818				
Unigene28878_All	395	2.65	9.36	6.34	1.77	1.13	2.52	0.00	1.38	2.02	1.82E+00	2.79E-07	Up	1.26E+00	3.30E-03		-6.40E-01	4.54E-01		5.11E-01	4.92E-01		1.04E+01	5.36E-04	Up	1.10E+01	7.36E-06	Up							
Unigene28880_All	271	64.48	21.69	19.65	89.89	85.90	114.16	162.10	55.21	66.74	-1.57E+00	4.68E-26	Down	-1.71E+00	2.90E-28	Down	-6.55E-02	6.16E-01		3.45E-01	3.27E-04		-1.55E+00	1.82E-77	Down	-1.28E+00	1.12E-59	Down	Unigene28880_All//gi|1173256|sp|P46299.1|RS4_GOSHI//5.00E-46//RecName: Full=40S ribosomal protein S4 >gi|488739|emb|CAA55882.1|ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene28880_All//1.00E-32//AT5G58420| 40S ribosomal protein S4 (RPS4D)	Unigene28880_All//3.00E-149//TC147248		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene28882_All	498	12.19	110.50	31.65	15.90	12.45	13.60	39.82	51.28	31.04	3.18E+00	1.35E-189	Up	1.38E+00	1.02E-18	Up	-3.54E-01	8.78E-02		-2.26E-01	3.37E-01		3.65E-01	1.55E-04		-3.59E-01	8.98E-04		Unigene28882_All//gi|225348627|gb|ACN87275.1|//6.00E-28//short chain dehydrogenase/reductase [Nandina domestica]	Unigene28882_All//1.00E-23//AT1G01800| short-chain dehydrogenase/reductase (SDR) family protein	Unigene28882_All//1.00E-128//TC154214			GO:0008152//GO:0016616	nr +
Unigene28883_All	1164	0.67	0.61	0.18	1.03	2.25	1.40	6.25	3.12	1.57	-1.46E-01	8.37E-01		-1.88E+00	4.13E-02		1.13E+00	3.31E-03		4.44E-01	4.29E-01		-1.00E+00	3.59E-07	Down	-1.99E+00	2.82E-19	Down	Unigene28883_All//gi|33465891|gb|AAQ19327.1|//3.00E-23//bZIP-like protein [Oryza sativa Japonica Group]	Unigene28883_All//7.00E-07//ATMG00310| hypothetical protein	Unigene28883_All//2.00E-21//DW511580				nr +
Unigene28885_All	818	0.00	0.25	0.46	1.46	0.59	1.27	3.05	1.79	22.45	7.95E+00	1.36E-01		8.83E+00	2.50E-02		-1.31E+00	2.84E-02		-2.03E-01	7.36E-01		-7.70E-01	3.19E-02		2.88E+00	4.77E-72	Up			Unigene28885_All//9.00E-05//AT1G58225| unknown protein				
Unigene28886_All	1374	0.00	0.11	0.16	3.99	2.61	2.47	0.58	1.16	2.29	6.79E+00	2.35E-01		7.28E+00	1.41E-01		-6.14E-01	1.10E-02		-6.94E-01	5.80E-03		9.83E-01	3.70E-02		1.97E+00	1.36E-08	Up	Unigene28886_All//gi|297804542|ref|XP_002870155.1|//1.00E-180//ATIN4 [Arabidopsis lyrata subsp. lyrata] >gi|297315991|gb|EFH46414.1|ATIN4 [Arabidopsis lyrata subsp. lyrata]	Unigene28886_All//3.00E-180//AT4G14480| INT4 (INOSITOL TRANSPORTER 4); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen symporter	Unigene28886_All//1.00E-07//CO097454				nr -
Unigene28888_All	797	1.12	6.99	2.20	3.38	2.51	1.76	7.53	7.29	4.10	2.65E+00	2.14E-16	Up	9.82E-01	5.82E-02		-4.30E-01	2.79E-01		-9.42E-01	1.39E-02		-4.74E-02	8.48E-01		-8.78E-01	3.11E-05		Unigene28888_All//gi|157427568|gb|ABP02014.1|//8.00E-22//acetyl-CoA carboxylase [Jatropha curcas]	Unigene28888_All//6.00E-16//AT1G36160| ACC1 (ACETYL-COENZYME A CARBOXYLASE 1); acetyl-CoA carboxylase	Unigene28888_All//0.00E+00//DW232659		ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis	GO:0006631//GO:0016421//GO:0019842//GO:0032559	nr +

Unigene28889_All	443	10.63	2.97	8.05	1.80	1.32	2.04	2.20	1.42	2.25	-1.84E+00	3.12E-09	Down	-4.00E-01	1.80E-01		-4.45E-01	5.73E-01		1.81E-01	8.07E-01		-6.33E-01	3.28E-01		3.45E-02	9.70E-01		Unigene28889_All//gi|18397936|ref|NP_565381.1|//5.00E-32//SQN (SQUINT); peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi|75333353|sp|Q9C566.1|CYP40_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase CYP40; Short=PPIase CYP40; AltName: Full=Cyclophilin of 40 kDa; Short=Cyclophilin-40; AltName: Full=Rotamase CYP40; AltName: Full=Protein SQUINT >gi|13412983|gb|AAK02067.1|cyclophilin-40 [Arabidopsis thaliana] >gi|20197802|gb|AAD41985.2|expressed protein [Arabidopsis thaliana] >gi|115311455|gb|ABI93908.1|At2g15790 [Arabidopsis thaliana]	Unigene28889_All//3.00E-33//AT2G15790| SQN (SQUINT); peptidyl-prolyl cis-trans isomerase	Unigene28889_All//1.00E-75//TC179340			GO:0003006//GO:0009791//GO:0016859//GO:0044267//GO:0044424	nr -
Unigene2889_All	879	10.54	25.65	22.35	15.07	32.99	45.21	22.56	63.57	47.72	1.28E+00	1.08E-24	Up	1.09E+00	3.92E-16	Up	1.13E+00	2.59E-30	Up	1.58E+00	5.22E-63	Up	1.49E+00	9.52E-93	Up	1.08E+00	1.97E-43	Up	Unigene2889_All//gi|225458627|ref|XP_002284791.1|//3.00E-60//PREDICTED: ripening-related bZIP protein-like isoform 2 [Vitis vinifera] >gi|225458629|ref|XP_002284785.1|PREDICTED: ripening-related bZIP protein-like isoform 1 [Vitis vinifera]	Unigene2889_All//1.00E-42//AT3G19290| ABF4 (ABRE BINDING FACTOR 4); DNA binding / protein binding / transcription activator/ transcription factor	Unigene2889_All//0.00E+00//TC167225	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0006970//GO:0009755//GO:0030528//GO:0043231	nr +
Unigene28890_All	702	0.15	2.31	1.14	1.35	1.42	0.90	1.45	1.07	0.91	3.95E+00	3.77E-07	Up	2.93E+00	5.06E-03		7.74E-02	9.37E-01		-5.82E-01	4.37E-01		-4.32E-01	5.03E-01		-6.71E-01	2.53E-01				Unigene28890_All//0.00E+00//TC138337				
Unigene28891_All	968	0.32	0.10	0.00	2.01	0.89	0.56	2.80	0.43	2.80	-1.63E+00	2.76E-01		-8.34E+00	4.91E-02		-1.17E+00	7.80E-03		-1.84E+00	1.99E-04	Down	-2.69E+00	2.64E-10	Down	1.70E-03	9.98E-01		Unigene28891_All//gi|115435356|ref|XP_001042436.1|//5.00E-41//Os01g0222300 (Oryza sativa Japonica Group) >gi|113531967|dbj|BAF04350.1|Os01g0222300 (Oryza sativa Japonica Group)	Unigene28891_All//1.00E-55//AT5G52950| unknown protein					nr +
Unigene28892_All	426	4.18	4.28	6.00	4.91	4.20	1.38	0.20	0.29	0.19	3.62E-02	9.58E-01		5.23E-01	2.16E-01		-2.25E-01	6.16E-01		-1.83E+00	1.08E-04	Down	5.68E-01	7.82E-01		-8.61E-02	9.72E-01		Unigene28892_All//gi|297839431|ref|XP_002887597.1|//2.00E-18//ATP-dependent protease La domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333438|gb|EFH63856.1| ATP-dependent protease La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene28892_All//2.00E-17//AT1G75460| ATP-dependent protease La (LON) domain-containing protein	Unigene28892_All//2.00E-170//TC153960			GO:0009536//GO:0019538	nr +
Unigene28893_All	1075	4.04	0.33	0.94	4.03	3.30	1.81	3.62	0.31	0.74	-3.61E+00	2.39E-17	Down	-2.10E+00	1.42E-09	Down	-2.89E-01	3.50E-01		-1.16E+00	6.73E-05	Down	-3.54E+00	1.09E-18	Down	-2.29E+00	1.34E-12	Down	Unigene28893_All//gi|297845494|ref|XP_002890628.1|//2.00E-82//ATORC6/ORC6 [Arabidopsis lyrata subsp. lyrata] >gi|297336470|gb|EFH66887.1|ATORC6/ORC6 [Arabidopsis lyrata subsp. lyrata]	Unigene28893_All//3.00E-83//AT1G26840| ORC6 (ORIGIN RECOGNITION COMPLEX PROTEIN 6); DNA binding	Unigene28893_All//0.00E+00//TC148761			GO:0000808//GO:0003676//GO:0005515//GO:0006259	nr -
Unigene28894_All	407	5.14	11.08	5.10	3.06	3.47	2.33	0.31	0.62	1.08	1.11E+00	1.40E-04	Up	-1.11E-02	1.00E+00		1.81E-01	8.02E-01		-3.93E-01	5.49E-01		9.84E-01	5.17E-01		1.79E+00	9.60E-02				Unigene28894_All//0.00E+00//gi|48746392|gb|C0076911.1|C0076911				
Unigene28895_All	354	1.92	5.58	4.51	1.69	0.29	0.64	10.63	28.69	11.14	1.54E+00	1.57E-03		1.23E+00	2.70E-02		-2.53E+00	1.36E-02		-1.40E+00	1.58E-01		1.43E+00	1.84E-16	Up	6.78E-02	8.10E-01		Unigene28895_All//gi|211905343|gb|ACJ11251.1|//2.00E-11//Ted2 [Gossypium hirsutum]	Unigene28895_All//8.00E-09//AT5G61510| NADP-dependent oxidoreductase, putative	Unigene28895_All//2.00E-132//gi|48780180|gb|C0089546.1|C0089546			GO:0004022//GO:0008152//GO:0016655//GO:0046914	nr +
Unigene28896_All	293	394.10	88.20	217.36	172.22	117.17	94.33	25.11	30.81	29.78	-2.16E+00	2.99E-260	Down	-8.59E-01	1.59E-62		-5.56E-01	2.44E-16		-8.68E-01	1.83E-31		2.95E-01	1.02E-01		2.46E-01	1.73E-01				Unigene28896_All//2.00E-20//TC149797				
Unigene28898_All	900	1.45	0.96	1.66	6.97	7.88	6.07	2.72	0.74	0.58	-6.03E-01	3.07E-01		1.89E-01	7.21E-01		1.77E-01	5.06E-01		-2.00E-01	4.65E-01		-1.87E+00	2.52E-06	Down	-2.24E+00	4.62E-08	Down	Unigene28898_All//gi|115463853|ref|NP_001055526.1|//1.00E-97//Os05g0409100 (Oryza sativa Japonica Group) >gi|113579077|dbj|BAF17440.1|Os05g0409100 (Oryza sativa Japonica Group)	Unigene28898_All//1.00E-114//AT5G50290| unknown protein				GO:0031410	nr -
Unigene28899_All	569	17.29	15.67	14.23	6.65	10.83	42.31	50.97	59.94	138.49	-1.41E-01	4.83E-01		-2.81E-01	1.58E-01		7.03E-01	2.08E-03		2.67E+00	2.22E-74	Up	2.34E-01	5.86E-03		1.44E+00	2.53E-126	Up	Unigene28899_All//gi|83316226|gb|ABC02397.1|//2.00E-51//1-aminocyclopropane-1-carboxylate oxidase [Gossypium hirsutum]	Unigene28899_All//4.00E-37//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene28899_All//6.00E-180//gi|78348134|gb|DT568408.1|DT568408		ko00270|Cysteine and methionine metabolism	GO:0003006//GO:0006555//GO:0006950//GO:0016641//GO:0019842//GO:0043169	nr -
Unigene289_All	272	0.38	0.37	0.20	3.48	0.25	0.50	10.10	9.68	1.61	-4.61E-02	9.89E-01		-9.74E-01	7.21E-01		-3.78E+00	3.40E-05	Down	-2.80E+00	1.18E-03		-6.17E-02	8.69E-01		-2.65E+00	1.15E-10	Down			Unigene289_All//3.00E-13//C0119670				
Unigene2890_All	3047	0.79	0.47	0.12	4.81	3.56	3.19	8.58	2.11	2.55	-7.63E-01	6.23E-02		-2.69E+00	3.25E-07	Down	-4.33E-01	1.71E-03		-5.93E-01	3.11E-05		-2.02E+00	1.61E-66	Down	-1.75E+00	1.62E-56	Down	Unigene2890_All//gi|212717139|gb|ACJ37411.1|//0.00E+00//receptor-like protein kinase [Glycine max]	Unigene2890_All//0.00E+00//AT4G36180| leucine-rich repeat family protein	Unigene2890_All//0.00E+00//TC146511		ko04626|Plant-pathogen interaction	GO:0016020//GO:0016772	nr +
Unigene28900_All	821	1.15	1.48	1.17	0.12	0.08	0.99	1.80	7.43	5.48	3.69E-01	5.56E-01		2.54E-02	9.91E-01		-5.33E-01	8.16E-01		3.03E+00	2.68E-03		2.04E+00	2.83E-16	Up	1.61E+00	3.14E-09	Up	Unigene28900_All//gi|297804080|ref|XP_002869924.1|//4.00E-86//FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315760|gb|EFH46183.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene28900_All//3.00E-87//AT4G20830| FAD-binding domain-containing protein	Unigene28900_All//2.00E-14//TC163182			GO:0003824//GO:0005576//GO:0005618//GO:0006950//GO:0016020//GO:0043231	nr -
Unigene28903_All	279	10.31	8.54	20.04	7.68	11.97	10.36	0.15	0.60	2.28	-2.73E-01	4.72E-01		9.58E-01	2.77E-04		6.41E-01	5.80E-02		4.32E-01	2.77E-01		1.98E+00	3.79E-01		3.91E+00	7.65E-04	Up	Unigene28903_All//gi|255537774|ref|XP_002510452.1|//2.00E-06//pentatricopeptide repeat-containing protein, putative [Ricinus communis] >gi|223551153|gb|EEF52639.1|pentatricopeptide repeat-containing protein, putative [Ricinus communis]						nr +
Unigene28904_All	984	1621.63	1777.55	1787.01	116.89	180.79	78.30	3.05	11.00	4.82	1.32E-01	2.58E-30		1.40E-01	8.56E-33		6.29E-01	4.81E-69		-5.78E-01	4.96E-35		1.85E+00	6.76E-25	Up	6.59E-01	5.85E-03		Unigene28904_All//gi|493636|dbj|BAA06153.1|//2.00E-36//CR9 [Cucumis sativus] >gi|76601|prf|2015094A cytokinin-repressed protein CR9	Unigene28904_All//1.00E-24//AT3G26740| CCL (CCR-LIKE)	Unigene28904_All//0.00E+00//TC138499				nr +
Unigene28905_All	257	5.50	7.29	3.11	14.92	9.38	16.17	11.35	7.16	5.12	4.08E-01	3.81E-01		-8.23E-01	1.60E-01		-6.70E-01	2.44E-02		1.15E-01	7.20E-01		-6.66E-01	4.24E-02		-1.15E+00	3.57E-04	Down			Unigene28905_All//9.00E-97//TC174977				
Unigene28906_All	1108	0.57	0.27	0.10	12.27	3.11	5.05	3.40	0.87	1.62	-1.05E+00	2.50E-01		-2.56E+00	2.72E-02		-1.98E+00	9.60E-35	Down	-1.28E+00	2.88E-16	Down	-1.97E+00	6.91E-10	Down	-1.07E+00	1.16E-04	Down	Unigene28906_All//gi|222875434|gb|ACM68923.1|//1.00E-144//gibberellin 20-oxidase [Gossypium hirsutum]	Unigene28906_All//1.00E-108//AT5G51810| GA20OX2 (GIBBERELLIN 20 OXIDASE 2); gibberellin 20-oxidase	Unigene28906_All//0.00E+00//TC168612		ko00904|Diterpenoid biosynthesis		nr +
Unigene28908_All	359	7.72	4.38	4.45	7.08	6.52	5.41	9.78	3.84	6.33	-8.20E-01	2.93E-02		-7.96E-01	4.51E-02		-1.18E-01	8.03E-01		-3.88E-01	3.74E-01		-1.35E+00	9.92E-06	Down	-6.28E-01	2.65E-02		Unigene28908_All//gi|18417421|ref|NP_568302.1|//5.00E-27//tRNA (adenine-N1-)-methyltransferase [Arabidopsis thaliana]	Unigene28908_All//2.00E-28//AT5G14600| tRNA (adenine-N1-)-methyltransferase	Unigene28908_All//0.00E+00//gi|5045566|gb|AI726714.1|AI726714			GO:0001510//GO:0016020//GO:0016426	nr +
Unigene28910_All	298	10.53	1.02	3.22	4.85	3.93	0.91	12.77	59.47	3.48	-3.37E+00	5.52E-12	Down	-1.71E+00	1.46E-05	Down	-3.03E-01	5.95E-01		-2.41E+00	1.41E-04	Down	2.22E+00	7.32E-51	Up	-1.88E+00	9.08E-10	Down			Unigene28910_All//2.00E-141//gi|18100803|gb|BM360069.1|BM360069				
Unigene28911_All	1325	1.22	0.80	0.24	19.93	10.86	3.85	1.18	2.33	2.19	-6.08E-01	2.34E-01		-2.34E+00	1.96E-04	Down	-8.75E-01	4.84E-19		-2.37E+00	4.85E-73	Down	9.83E-01	1.96E-03		8.95E-01	4.93E-03		Unigene28911_All//gi|297810749|ref|XP_002873258.1|//2.00E-53//glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319095|gb|EFH49517.1|glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene28911_All//7.00E-54//AT5G06470| glutaredoxin family protein	Unigene28911_All//0.00E+00//TC167604			GO:0015036//GO:0019725	nr -
Unigene28912_All	1840	16.27	12.50	23.67	0.11	0.21	0.10	0.14	1.00	0.43	-3.80E-01	1.22E-04		5.42E-01	5.67E-11		9.27E-01	5.23E-01		-1.41E-01	9.35E-01		2.86E+00	1.36E-07	Up	1.65E+00	2.32E-02		Unigene28912_All//gi|242199344|gb|ACS87993.1|//1.00E-157//UDP-glucosyltransferase family 1 protein [Citrus sinensis]	Unigene28912_All//3.00E-118//AT1G05680| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene28912_All//4.00E-119//TC144746		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr -
Unigene28913_All	357	49.54	24.55	21.18	75.07	86.62	91.09	104.69	80.43	57.81	-1.01E+00	1.18E-13	Down	-1.23E+00	1.55E-17	Down	2.06E-01	3.92E-02		2.79E-01	3.45E-03		-3.80E-01	1.08E-06		-8.57E-01	8.14E-27		Unigene28913_All//gi|79321519|ref|NP_001031305.1|//2.00E-46//HSP91; ATP binding [Arabidopsis thaliana]	Unigene28913_All//8.00E-48//AT1G79930| HSP91; ATP binding	Unigene28913_All//0.00E+00//D8454906			GO:0000950//GO:0008152//GO:0010038//GO:0016020//GO:0016628//GO:0032559//GO:0043231	nr +
Unigene28914_All	360	1.16	3.38	3.85	0.00	1.15	0.00	3.41	1.39	0.89	1.54E+00	1.75E-02		1.73E+00	6.71E-03		1.02E+01	1.25E-02		null	null		-1.29E+00	2.09E-02		-1.94E+00	7.80E-04	Down			Unigene28914_All//5.00E-87//gi|73859610|gb|DT462349.1|DT462349				
Unigene28922_All	334	15.20	5.61	19.29	3.13	1.96	1.08	1.77	1.00	0.48	-1.44E+00	3.43E-07	Down	3.44E-01	1.69E-01		-6.77E-01	3.14E-01		-1.53E+00	2.88E-02		-8.24E-01	3.48E-01		-1.89E+00	3.22E-02				Unigene28922_All//5.00E-65//TC158220				
Unigene28923_All	1075	4.04	5.80	3.22	4.26	4.93	5.88	4.21	6.38	13.01	5.21E-01	2.83E-02		-3.27E-01	3.03E-01		2.11E-01	4.91E-01		4.64E-01	5.39E-02		5.99E-01	2.69E-03		1.63E+00	1.94E-27	Up	Unigene28923_All//gi|292668913|gb|ADE41111.1|//1.00E-60//AP2 domain class transcription factor [Malus x domestica]	Unigene28923_All//5.00E-21//AT1G28370| ERF11 (ERF DOMAIN PROTEIN 11); DNA binding / transcription factor/ transcription repressor	Unigene28923_All//1.00E-46//gi|78322782|gb|DT543056.1|DT543056	AP2-EREBP		GO:0006350	nr +
Unigene28924_All	371	59.65	24.58	61.57	2.42	3.06	2.07	0.23	0.68	0.43	-1.28E+00	3.15E-24	Down	4.57E-02	7.22E-01		3.42E-01	6.20E-01		-2.24E-01	7.50E-01		1.57E+00	3.26E-01		9.14E-01	6.24E-01		Unigene28924_All//gi|88011082|gb|AB038900.1|//2.00E-27//At5g20935 [Arabidopsis thaliana]	Unigene28924_All//1.00E-28//AT5G20935| unknown protein				GO:0043231	nr -
Unigene28927_All	739	0.00	0.00	0.00	2.97	1.82	2.26	0.11	2.83	0.81	null	null		null	null		-7.07E-01	9.08E-02		-3.91E-01	3.98E-01		4.63E+00	3.28E-12	Up	2.82E+00	5.65E-03		Unigene28927_All//gi|575404|emb|CAA52343.1|//2.00E-84//cellulase [Sambucus nigra]	Unigene28927_All//3.00E-69//AT4G09740| AtGH9B14 (Arabidopsis thaliana glycosyl hydrolase 9B14); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene28927_All//0.00E+00//C0120758		ko00500|Starch and sucrose metabolism	GO:0003006//GO:0004553//GO:0009251//GO:0009827//GO:0031410	nr +
Unigene28928_All	1867	1.12	1.03	1.34	3.98	6.20	9.39	1.49	0.22	0.64	-1.20E-01	7.77E-01		2.58E-01	5.55E-01		6.41E-01	4.61E-05		1.24E+00	1.60E-19	Up	-2.74E+00	8.81E-11	Down	-1.22E+00	2.37E-04	Down	Unigene28928_All//gi|224068797|ref|XP_002326202.1|//0.00E+00//s-adenosylmethionine synthetase 6 [Populus trichocarpa] >gi|223635286|sp|A9P9K5.1|METK4_POPTR RecName: Full=S-adenosylmethionine synthase 4; Short=AdoMet synthase 4; AltName: Full=Methionine adenosyltransferase 4; Short=MAT 4 >gi|222833395|gb|EEE71872.1| s-adenosylmethionine synthetase 6 [Populus trichocarpa]	Unigene28928_All//0.00E+00//AT2G36880| MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase	Unigene28928_All//0.00E+00//TC159160		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0000097//GO:0016020//GO:0016765//GO:0032559//GO:0044424//GO:0016914	nr +
Unigene2893_All	1308	8.76	3.45	6.31	6.09	5.34	4.94	3.14	0.93	1.52	-1.35E+00	6.81E-14	Down	-4.73E-01	7.08E-03		-1.89E-01	4.16E-01		-3.04E-01	1.71E-01		-1.76E+00	2.63E-09	Down	-1.04E+00	7.86E-05	Down	Unigene2893_All//gi|297826669|ref|XP_002881217.1|//1.00E-129//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327056|gb|EFH57476.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene2893_All//6.00E-119//AT2G32230| pentatricopeptide (PPR) repeat-containing protein	Unigene2893_All//1.00E-37//gi|164315909|gb|ES846957.1|ES846957			GO:0043231	nr -
Unigene28930_All	374	21.26	17.21	11.53	39.56	30.11	21.49	44.54	30.51	20.35	-3.06E-01	1.51E-01		-8.83E-01	4.07E-05		-3.94E-01	4.59E-03		-8.80E-01	7.56E-10		-5.46E-01	6.55E-06		-1.13E+00	3.44E-19	Down	Unigene28930_All//gi|297796593|ref|XP_002866181.1|//2.00E-15//coatomer subunit beta-1 [Arabidopsis lyrata subsp. lyrata] >gi|297312016|gb|EFH42440.1|coatomer subunit beta-1 [Arabidopsis lyrata subsp. lyrata]	Unigene28930_All//2.00E-16//AT4G31480| coatomer beta subunit, putative / beta-coat protein, putative / beta-COP, putative	Unigene28930_All//9.00E-104//TC148728			GO:0005515//GO:0015031//GO:0030120	nr +

Unigene28932_All	631	1.33	0.00	1.35	1.50	1.20	1.07	0.94	2.52	0.76	-1.04E+01	5.57E-05	Down	2.53E-02	9.93E-01		-3.21E-01	6.38E-01		-4.83E-01	5.19E-01		1.42E+00	3.29E-03		-3.08E-01	6.79E-01		Unigene28932_All//gi|18404252|ref|NP_030235.1|//1.00E-37//ACT domain-containing protein [Arabidopsis thaliana] >gi|4883601|gb|AAD31570.1| expressed protein [Arabidopsis thaliana]	Unigene28932_All//2.00E-33//AT2G36840| ACT domain-containing protein	Unigene28932_All//0.00E+00//gi|109868365|gb|DW497341.1|DW497341			GO:0031406	nr -
Unigene28936_All	301	50.41	92.25	59.62	42.86	75.39	91.83	74.31	76.79	37.06	8.72E-01	1.83E-16		2.42E-01	9.17E-02		8.15E-01	4.82E-14		1.10E+00	2.72E-25	Up	4.74E-02	7.02E-01		-1.00E+00	3.98E-21	Down	Unigene28936_All//gi|15225213|ref|NP_180161.1|//2.00E-16//ATCTH; transcription factor [Arabidopsis thaliana] >gi|75220235|sp|Q82307.1|C3H23_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 23; Short=AtC3H23; AltName: Full=Protein ATCTH >gi|14030625|gb|AAK52987.1|AF375403.1 At2g25900/F17H15.7 [Arabidopsis thaliana] >gi|22136536|gb|AAM91054.1| At2g25900/F17H15.7 [Arabidopsis thaliana]	Unigene28936_All//2.00E-14//AT2G25900| ATCTH; transcription factor	Unigene28936_All//6.00E-160//gi|109835977|gb|DW234540.1|DW234540	C3H		GO:0003676//GO:0010468//GO:0044424//GO:0046872	nr -
Unigene28938_All	572	0.55	1.24	2.61	0.52	1.44	1.66	0.74	0.88	1.39	1.18E+00	1.75E-01		2.25E+00	5.49E-04	Up	1.47E+00	7.56E-02		1.67E+00	3.07E-02		2.46E-01	7.84E-01		9.14E-01	1.85E-01		Unigene28938_All//gi|170660047|gb|ACB28472.1|//8.00E-31//polyprotein [Ananas comosus]		Unigene28938_All//7.00E-10//TC153780			GO:0003676//GO:0003824//GO:0009987//GO:0043170//GO:0044238	nr -
Unigene28939_All	461	6.13	3.74	3.12	8.54	8.96	7.25	23.48	11.15	10.63	-7.14E-01	5.52E-02		-9.75E-01	1.32E-02		7.04E-02	8.35E-01		-2.36E-01	4.96E-01		-1.07E+00	1.84E-11	Down	-1.14E+00	5.35E-13	Down			Unigene28939_All//2.00E-139//gi|84166644|gb|DR455292.1|DR455292				
Unigene28942_All	479	55.27	42.21	55.81	68.22	75.20	76.37	259.33	100.17	109.62	-3.89E-01	2.33E-04		1.39E-02	9.20E-01		1.40E-01	1.55E-01		1.63E-01	9.42E-02		-1.37E+00	5.17E-181	Down	-1.24E+00	1.40E-159	Down	Unigene28942_All//gi|211906470|gb|AC111728.1|//4.00E-56//glyceraldehyde-3-phosphate dehydrogenase [Gossypium hirsutum]	Unigene28942_All//2.00E-54//AT1G13440| GAPC2 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene28942_All//0.00E+00//gi|164304902|gb|EV495200.1|EV495200		ko00010|Glycolysis / Gluconeogenesis	GO:0000166//GO:0006007//GO:0008943//GO:0044424	nr -
Unigene28944_All	764	0.41	0.27	0.00	1.24	1.58	4.43	0.89	2.79	4.22	-6.31E-01	6.22E-01		-8.68E+00	4.91E-02		3.49E-01	5.95E-01		1.84E+00	4.47E-07	Up	1.66E+00	7.87E-05	Up	2.25E+00	2.92E-10	Up							
Unigene28945_All	466	7.07	3.70	2.63	3.85	3.62	3.59	0.27	0.54	0.34	-9.36E-01	6.25E-03		-1.43E+00	1.22E-04	Down	-8.79E-02	8.47E-01		-1.02E-01	8.43E-01		9.83E-01	5.17E-01		3.29E-01	8.51E-01		Unigene28945_All//gi|297725027|ref|NP_001174877.1|//5.00E-41//Os06g0587900 (Oryza sativa Japonica Group) >gi|255677187|dbj|BAH93605.1| Os06g0587900 (Oryza sativa Japonica Group)	Unigene28945_All//3.00E-28//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0003676//GO:0003824//GO:0044238//GO:0044260//GO:0046872	nr +
Unigene28947_All	415	34.92	10.26	49.53	9.36	11.37	10.77	0.31	0.40	0.29	-1.77E+00	1.48E-25	Down	5.04E-01	5.67E-05		2.80E-01	3.64E-01		2.03E-01	5.49E-01		3.99E-01	8.14E-01		-8.56E-02	9.69E-01				Unigene28947_All//9.00E-129//TC143356				
Unigene28948_All	1656	0.00	0.18	0.00	1.71	0.58	0.38	1.35	1.03	5.36	7.52E+00	4.43E-02		null	null		-1.56E+00	1.46E-05	Down	-2.17E+00	1.76E-07	Down	-3.87E-01	3.45E-01		1.99E+00	4.77E-23	Up	Unigene28948_All//gi|15237876|ref|NP_197791.1|//1.00E-173//SLAH3 (SLAC1 HOMOLOGUE 3); transporter [Arabidopsis thaliana] >gi|51536498|gb|AAU05487.1| At5g24030 [Arabidopsis thaliana] >gi|52421299|gb|AAU45219.1| At5g24030 [Arabidopsis thaliana]	Unigene28948_All//2.00E-153//AT5G24030| SLAH3 (SLAC1 HOMOLOGUE 3); transporter	Unigene28948_All//2.00E-120//gi|11206590|gb|BF275520.1|BF275520				nr +
Unigene28949_All	542	1.45	0.75	1.38	2.85	2.48	2.17	3.82	2.54	0.51	-9.53E-01	2.33E-01		-7.41E-02	9.35E-01		-2.02E-01	7.27E-01		-3.95E-01	4.84E-01		-5.87E-01	1.48E-01		-2.89E+00	6.04E-09	Down			Unigene28949_All//3.00E-61//CO108933				
Unigene28895_All	1373	1.14	5.72	0.78	4.57	17.48	11.09	17.52	54.43	63.89	2.32E+00	9.36E-20	Up	-5.60E-01	3.18E-01		1.94E+00	8.22E-55	Up	1.28E+00	7.88E-18	Up	1.64E+00	4.39E-141	Up	1.87E+00	5.75E-203	Up	Unigene2895_All//gi|224127502|ref|XP_002320090.1|//1.00E-121//f-box family protein [Populus trichocarpa] >gi|222860863|gb|EEE98405.1| f-box family protein [Populus trichocarpa]	Unigene2895_All//5.00E-111//AT3G61060| AtPP2-A13 (Arabidopsis thaliana phloem protein 2-A13); carbohydrate binding	Unigene2895_All//0.00E+00//TC163286				nr +
Unigene28950_All	1314	0.08	0.23	0.04	1.44	1.00	1.24	3.15	1.40	2.73	1.54E+00	3.23E-01		-9.75E-01	7.21E-01		-5.33E-01	2.63E-01		-2.19E-01	6.71E-01		-1.17E+00	1.72E-05	Down	-2.09E-01	4.59E-01		Unigene28950_All//gi|297724159|ref|NP_001174443.1|//7.00E-25//Os05g0134000 (Oryza sativa Japonica Group) >gi|255676397|dbj|BAH93171.1| Os05g0134000 (Oryza sativa Japonica Group)					GO:0043231//GO:0044444	nr -
Unigene28951_All	742	20.87	6.21	19.23	56.59	30.77	8.22	0.91	0.45	0.27	-1.75E+00	7.58E-27	Down	-1.18E-01	4.74E-01		-8.79E-01	2.67E-30		-2.78E+00	2.27E-139	Down	-1.02E+00	2.04E-01		-1.76E+00	2.80E-02		Unigene28951_All//gi|259121397|gb|ACV92018.1|//1.00E-23//WRKY transcription factor 16 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene28951_All//2.00E-18//AT5G64810| WRKY51; transcription factor	Unigene28951_All//3.00E-40//DW496555	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0010468//GO:0043231	nr -
Unigene28954_All	811	10.32	4.81	6.04	7.99	10.36	5.46	0.00	0.00	0.00	-1.10E+00	8.93E-08	Down	-7.73E-01	2.22E-04		3.76E-01	6.43E-02		-5.49E-01	1.77E-02		null	null		null	null				Unigene28954_All//2.00E-07//TC156540				
Unigene28955_All	590	1.42	0.00	0.36	1.01	0.70	0.92	3.94	2.55	1.08	-1.05E+01	5.57E-05	Down	-1.97E+00	2.71E-02		-5.33E-01	5.62E-01		-1.41E-01	8.79E-01		-6.28E-01	9.58E-02		-1.87E+00	2.99E-06	Down							
Unigene28956_All	689	0.61	3.38	0.85	0.58	0.65	0.72	1.84	2.18	3.82	2.48E+00	9.11E-07	Up	4.85E-01	6.30E-01		1.68E-01	9.04E-01		3.18E-01	7.58E-01		2.46E-01	6.67E-01		1.05E+00	2.03E-03		Unigene28956_All//gi|15237702|ref|NP_200664.1|//1.00E-06//phosphatidate cytidylyltransferase family protein [Arabidopsis thaliana] >gi|92039771|sp|Q67ZN7.2|PHYK2_ARATH RecName: Full=Probable phytol kinase 2, chloroplastic; Flags: Precursor	Unigene28956_All//7.00E-08//AT5G58560| phosphatidate cytidylyltransferase family protein	Unigene28956_All//3.00E-34//DR454473				nr -
Unigene28957_All	870	1.26	0.47	0.06	0.63	0.16	0.31	2.58	2.69	9.80	-1.44E+00	3.36E-02		-4.37E+00	4.94E-05	Down	-1.99E+00	5.12E-02		-1.02E+00	3.30E-01		6.28E-02	8.81E-01		1.93E+00	2.59E-21	Up							
Unigene28958_All	327	5.60	6.51	4.07	28.33	24.33	17.13	71.50	133.06	18.40	2.17E-01	6.23E-01		-4.60E-01	3.79E-01		-2.20E-01	2.93E-01		-7.26E-01	8.25E-05		8.96E-01	1.87E-32		-1.96E+00	5.82E-59	Down			Unigene28958_All//2.00E-117//gi|84144386|gb|DN758628.1|DN758628				
Unigene2896_All	1641	35.93	23.25	31.22	6.41	9.53	6.47	3.56	1.20	2.18	-6.28E-01	1.19E-19		-2.03E-01	5.76E-03		5.73E-01	1.50E-05		1.40E-02	9.53E-01		-1.57E+00	4.03E-11	Down	-7.03E-01	9.20E-04		Unigene2896_All//gi|297843242|ref|XP_002889502.1|//1.00E-164//aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335344|gb|EFH65761.1| aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2896_All//3.00E-163//AT1G04420| aldo/keto reductase family protein	Unigene2896_All//0.00E+00//TC137112		ko00053|Ascorbate and aldarate metabolism	GO:0004672//GO:0008152	nr -
Unigene28960_All	813	0.58	0.44	0.46	0.86	0.47	0.78	1.09	2.06	2.70	-4.09E-01	6.69E-01		-3.37E-01	7.34E-01		-8.81E-01	3.00E-01		-1.41E-01	8.66E-01		9.13E-01	4.52E-02		1.30E+00	7.65E-04	Up							
Unigene28961_All	1798	0.00	0.39	0.00	0.86	1.05	0.60	3.22	6.72	8.62	8.62E+00	3.33E-04	Up	null	null		2.95E-01	5.87E-01		-5.11E-01	3.72E-01		1.06E+00	1.98E-12	Up	1.42E+00	5.88E-25	Up	Unigene28961_All//gi|15238607|ref|NP_198426.1|//1.00E-143//SAP (STERILE APETALA); transcription factor/ transcription regulator [Arabidopsis thaliana] >gi|305805503|sp|Q8FKH1.1|SAP_ARATH RecName: Full=Transcriptional regulator STERILE APETALA >gi|9758652|dbj|BAB09276.1| sterile apetala [Arabidopsis thaliana]	Unigene28961_All//1.00E-144//AT5G35770| SAP (STERILE APETALA); transcription factor/ transcription regulator		SAP			nr -
Unigene28962_All	668	0.78	0.61	0.72	1.86	0.77	0.41	1.14	2.57	3.70	-3.68E-01	6.83E-01		-1.27E-01	8.98E-01		-1.27E+00	2.92E-02		-2.20E+00	1.10E-03		1.17E+00	9.92E-03		1.70E+00	8.13E-06	Up			Unigene28962_All//0.00E+00//gi|164333360|gb|ES846363.1|ES846363				
Unigene28964_All	890	0.35	0.00	0.84	2.07	0.66	3.50	5.18	1.27	1.16	-8.46E+00	3.66E-02		1.25E+00	1.54E-01		-1.65E+00	4.01E-04	Down	7.58E-01	3.37E-02		-2.03E+00	2.12E-12	Down	-2.15E+00	8.88E-14	Down	Unigene28964_All//gi|115447329|ref|NP_001047444.1|//3.00E-18//Os02g0617700 (Oryza sativa Japonica Group) >gi|113536975|dbj|BAF09358.1| Os02g0617700 (Oryza sativa Japonica Group)	Unigene28964_All//3.00E-17//AT5G14580| polyribonucleotide nucleotidyltransferase, putative	Unigene28964_All//0.00E+00//TC156773		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03018|RNA degradation	GO:0003676//GO:0006401//GO:0008408//GO:0010467//GO:0016779//GO:0043231	nr -
Unigene28965_All	405	11.50	11.64	8.55	13.04	15.98	14.05	62.64	23.01	20.26	1.72E-02	9.73E-01		-4.28E-01	1.49E-01		2.94E-01	2.40E-01		1.08E-01	6.92E-01		-1.44E+00	1.61E-10	Down	-1.63E+00	1.27E-19	Down			Unigene28965_All//1.00E-180//TC141846				
Unigene28967_All	474	5.96	6.63	1.24	21.96	24.48	21.82	9.19	6.97	9.08	1.53E-01	6.58E-01		-2.27E+00	5.16E-07	Down	1.57E-01	4.24E-01		-9.60E-03	9.54E-01		-3.99E-01	1.38E-01		-1.74E-02	9.65E-01				Unigene28967_All//9.00E-49//DW508327				
Unigene28968_All	745	0.56	1.36	1.29	1.34	0.69	1.33	2.44	1.63	5.78	1.28E+00	6.99E-02		1.20E+00	1.15E-01		-9.48E-01	1.58E-01		-3.90E-03	9.88E-01		-5.85E-01	1.85E-01		1.24E+00	2.56E-06	Up							
Unigene2897_All	1718	1.83	1.95	1.64	3.28	1.48	3.36	18.41	26.59	23.86	9.12E-02	7.83E-01		-1.54E-01	6.68E-01		-1.14E+00	1.09E-06	Down	3.84E-02	9.06E-01		5.31E-01	4.69E-14		3.74E-01	2.71E-07		Unigene2897_All//gi|186495165|ref|NP_565074.2|//1.00E-103//calmodulin binding [Arabidopsis thaliana]	Unigene2897_All//9.00E-105//AT1G73805| calmodulin binding	Unigene2897_All//0.00E+00//DT462584		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005515	nr +
Unigene28970_All	498	0.00	0.41	0.00	3.20	4.29	7.35	2.55	1.18	1.60	8.67E+00	1.36E-01		null	null		4.22E-01	3.82E-01		1.20E+00	2.27E-04	Up	-1.12E+00	3.93E-02		-6.71E-01	1.95E-01		Unigene28970_All//gi|15236188|ref|NP_195203.1|//1.00E-33//auxin-responsive family protein [Arabidopsis thaliana]	Unigene28970_All//6.00E-35//AT4G34770| auxin-responsive family protein	Unigene28970_All//2.00E-13//CO102462				nr -
Unigene28971_All	711	0.00	2.35	0.00	4.76	2.28	3.94	11.71	6.53	11.88	1.12E+01	1.54E-09	Up	null	null		-1.07E+00	7.04E-04	Down	-2.75E-01	4.68E-01		-8.44E-01	2.68E-06		2.00E-02	9.38E-01		Unigene28971_All//gi|44681326|gb|AAS47603.1|//4.00E-68//At3g20340 [Arabidopsis thaliana] >gi|45773836|gb|AAS76722.1| At3g20340 [Arabidopsis thaliana]	Unigene28971_All//6.00E-10//AT4G21920| unknown protein	Unigene28971_All//0.00E+00//gi|109877650|gb|DW506623.1|DW506623				nr -
Unigene28972_All	958	0.55	0.21	0.22	10.87	4.39	7.26	11.21	3.27	0.75	-1.37E+00	1.97E-01		-1.30E+00	2.42E-01		-1.31E+00	1.11E-14	Down	-5.82E-01	7.98E-04		-1.78E+00	1.87E-23	Down	-3.90E+00	1.29E-56	Down							
Unigene28973_All	363	0.58	2.09	3.37	2.06	3.13	1.99	3.96	1.61	1.65	1.86E+00	3.73E-02		2.55E+00	8.25E-04	Up	6.05E-01	3.84E-01		-4.82E-02	9.50E-01		-1.30E+00	1.07E-02		-1.27E+00	9.34E-03				Unigene28973_All//3.00E-122//gi|78325650|gb|DT545924.1|DT545924				
Unigene28975_All	1624	0.00	0.06	0.00	0.00	0.04	0.17	25.20	45.48	114.46	5.96E+00	3.87E-01		null	null		5.41E+00	6.10E-01		7.38E+00	7.03E-02		8.52E-01	4.37E-50		2.18E+00	0.00E+00	Up	Unigene28975_All//gi|240256381|ref|NP_568561.4|//2.00E-99//transferase/ transferase, transferring acyl groups other than amino-acyl groups [Arabidopsis thaliana] >gi|15450169|gb|AAK96528.1| AT5g39050/MXF12_60 [Arabidopsis thaliana] >gi|25090341|gb|AAN72280.1| At5g39050/MXF12_60 [Arabidopsis thaliana]	Unigene28975_All//2.00E-92//AT5G39050| transferase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene28975_All//9.00E-18//gi|164368157|gb|ES850671.1|ES850671		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0008374//GO:0009813	nr -
Unigene28980_All	468	1.34	2.27	2.39	4.79	1.47	2.99	0.00	0.36	1.11	7.61E-01	2.48E-01		8.33E-01	2.23E-01		-1.70E+00	4.70E-05	Down	-6.79E-01	1.20E-01		8.48E+00	1.39E-01		1.01E+01	6.13E-04	Up							
Unigene28984_All	614	1.19	0.99	1.91	1.95	2.08	1.62	3.58	3.61	7.79	-2.69E-01	7.19E-01		6.78E-01	3.04E-01		9.19E-02	9.00E-01		-2.67E-01	6.88E-01		1.09E-02	1.02E+00		1.12E+00	5.17E-06	Up	Unigene28984_All//gi|158937162|dbj|BAF91636.1|//2.00E-06//CLE family 0sCLE801 protein (Oryza sativa Japonica Group)		Unigene28984_All//0.00E+00//DW505741				nr -
Unigene28985_All	466	15.83	6.74	14.51	0.32	1.63	0.87	2.45	0.00	0.94	-1.23E+00	3.86E-08	Down	-1.26E-01	6.30E-01		2.34E+00	1.37E-02		1.44E+00	2.82E-01		-1.13E+01	3.88E-08	Down	-1.38E+00	1.42E-02				Unigene28985_All//1.00E-171//TC136853				
Unigene28987_All	693	0.98	1.75	1.61	0.93	3.98	1.76	1.83	0.90	1.15	8.38E-01	1.73E-01		7.17E-01	2.87E-01		2.09E+00	3.52E-02	Up	9.13E-01	1.52E-01		-1.02E+00	5.93E-02		-6.71E-01	1.95E-01				Unigene28987_All//8.00E-07//TC163653				
Unigene28988_All	1130	0.19	0.00	0.00	6.08	3.02	1.96	0.15	0.00	0.00	-7.53E+00	1.22E-01		-7.53E+00	1.46E-01		-1.01E+00	1.11E-06	Down	-1.64E+00	5.00E-12	Down	-7.23E+00	1.34E-01		-7.23E+00	1.08E-01								
Unigene28989_All	470	1.22	0.11	0.45	7.53	7.91	5.86	4.32	9.87	1.70	-3.51E+00	9.03E-03		-1.43E+00	1.76E-01		7.25E-02	8.41E-01		-3.60E-01	3.08E-01		1.19E+00	3.44E-06	Up	-1.35E+00	8.26E-04	Down			Unigene28989_All//3.00E-129//TC168403				
Unigene2899_All	601	5.14	2.19	5.67	6.22	5.44	6.61	9.22	8.76	4.97	-1.23E+00	7.17E-04	Down	1.43E-01	6.78E-01		-1.92E-01	5.85E-01		8.92E-02	7.96E-01		-7.28E-02	7.72E-01		-8.90E-01	5.42E-05		Unigene2899_All//gi|22328041|ref|NP_201202.2|//6.00E-66//copine-related [Arabidopsis thaliana] >gi|79332056|ref|NP_001032132.1| copine-related [Arabidopsis thaliana]	Unigene2899_All//1.00E-66//AT5G63970| copine-related	Unigene2899_All//0.00E+00//BG447439			GO:0043231//GO:0046914	nr +
Unigene28990_All	688	4.79	0.15	0.77	1.52	1.20	0.79	0.25	0.00	0.00	-5.02E+00	2.47E-16	Down	-2.63E+00	1.84E-09	Down	-3.40E-01	5.96E-01		-9.49E-01	1.69E-01		-7.94E+00	1.34E-01		-7.94E+00	1.08E-01		Unigene28990_All//gi|6635236|dbj|BAA88636.1|//6.00E-46//elicitor-inducible LRR receptor-like protein EILP [Nicotiana tabacum]	Unigene28990_All//4.00E-35//AT1G71390| AtRLP11 (Receptor Like Protein 11); protein binding					nr -

Unigene28991_All	845	0.37	0.60	1.26	1.24	1.02	1.55	1.95	0.30	1.23	6.91E-01	4.99E-01		1.76E+00	1.85E-02		-2.81E-01	6.74E-01		3.24E-01	6.37E-01		-2.72E+00	1.39E-06	Down	-6.71E-01	1.27E-01		Unigene28991_All//gi|124359343|gb|ABQ28505.2|//7.00E-43//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene28991_All//2.00E-18//AT3G24255| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G23910.1); Has 2302 Blast hits to 2235 proteins in 74 species: Archae - 4; Bacteria - 15; Metazoa - 871; Fungi - 12; Plants - 1295; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).	Unigene28991_All//7.00E-11//ES819977			GO:0003824	nr +
Unigene28992_All	486	4.41	6.57	5.26	1.44	1.42	0.74	0.00	0.00	1.15	5.74E-01	1.01E-01		2.53E-01	5.60E-01		-1.81E-02	9.61E-01		-9.49E-01	2.88E-01		null	null		1.02E+01	3.28E-04	Up	Unigene28992_All//gi|297817582|ref|XP_002876674.1|//4.00E-34//CP12-2 [Arabidopsis lyrata subsp. lyrata] >gi|297322512|gb|EFH52933.1| CP12-2 [Arabidopsis lyrata subsp. lyrata]	Unigene28992_All//9.00E-28//AT3G62410| CP12-2; protein binding	Unigene28992_All//0.00E+00//gi|164314593|gb|EX168960.1|EX168960			GO:0005488//GO:0009314//GO:0009532//GO:0015977//GO:0018149//GO:0034285	nr +
Unigene28994_All	658	0.64	1.46	1.70	2.04	1.05	2.75	5.65	2.79	1.82	1.20E+00	9.57E-02		1.42E+00	4.40E-02		-9.66E-01	8.22E-02		4.26E-01	4.19E-01		-1.02E+00	3.76E-04	Down	-1.64E+00	4.54E-08	Down	Unigene28994_All//gi|22331732|ref|NP_190655.2|//4.00E-71//clathrin adaptor complex small chain family protein [Arabidopsis thaliana]	Unigene28994_All//2.00E-72//AT3G60860| clathrin adaptor complex small chain family protein	Unigene28994_All//0.00E+00//gi|109872952|gb|DW501927.1|DW501927			GO:0005488//GO:0015031//GO:0022892//GO:0030118	nr -
Unigene28996_All	299	12.25	2.37	13.89	8.66	4.72	6.65	0.00	0.00	0.00	-2.37E+00	7.54E-10	Down	1.82E-01	5.96E-01		-8.76E-01	1.86E-02		-3.82E-01	3.76E-01		null	null		null	null										
Unigene28997_All	2168	0.10	0.56	0.44	0.14	0.22	0.27	3.32	10.28	10.38	2.54E+00	5.98E-04	Up	2.20E+00	9.10E-03		6.90E-01	5.67E-01		9.74E-01	3.46E-01		1.63E+00	1.94E-42	Up	1.65E+00	2.31E-44	Up	Unigene28997_All//gi|4530126|gb|AAD21872.1|//0.00E+00//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene28997_All//2.00E-169//AT4G38830| protein kinase family protein	Unigene28997_All//1.00E-32//TC153623		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene28998_All	424	3.46	3.59	5.53	2.70	7.07	9.16	0.20	0.79	0.09	5.33E-02	9.33E-01		6.78E-01	1.23E-01		1.39E+00	1.15E-04	Up	1.76E+00	1.32E-07	Up	1.98E+00	1.44E-01		-1.08E+00	6.76E-01				Unigene28998_All//5.00E-07//gi|73865257|gb|DT467995.1|DT467995				
Unigene28999_All	536	1.85	43.01	4.87	2.14	2.83	9.61	0.79	1.09	0.07	4.54E+00	4.68E-105	Up	1.39E+00	9.95E-04	Up	4.03E-01	5.14E-01		2.17E+00	8.14E-13	Up	4.69E-01	6.13E-01		-3.41E+00	1.24E-02		Unigene28999_All//gi|22330903|ref|NP_187381.2|//2.00E-26//nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	Unigene28999_All//1.00E-24//AT3G07250| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene28999_All//2.00E-133//gi|78326627|gb|DT546901.1|DT546901			GO:0005488	nr +
Unigene29_All	485	2.80	3.03	2.42	4.93	3.62	1.12	6.80	7.33	9.61	1.11E-01	8.31E-01		-2.16E-01	7.04E-01		-4.45E-01	2.97E-01		-2.14E+00	2.62E-06	Down	1.07E-01	7.28E-01		4.99E-01	4.03E-02		Unigene29_All//gi|224122778|ref|XP_002330477.1|//1.00E-90//histone acetyltransferase [Populus trichocarpa] >gi|222871889|gb|EEF09020.1| histone acetyltransferase [Populus trichocarpa]	Unigene29_All//2.00E-79//AT1G79000| HAC1 (HISTONE ACETYLTRANSFERASE OF THE CBP FAMILY 1); H3/H4 histone acetyltransferase/ histone acetyltransferase/ transcription cofactor	Unigene29_All//0.00E+00//TC162741				nr -
Unigene290_All	3106	2.12	2.79	2.21	24.23	12.03	11.87	34.03	18.18	11.62	3.94E-01	4.81E-02		5.93E-02	8.05E-01		-1.01E+00	2.16E-68	Down	-1.03E+00	5.25E-62	Down	-9.05E-01	4.95E-79		-1.55E+00	3.60E-190	Down	Unigene290_All//gi|15234620|ref|NP_194740.1|//0.00E+00//HMA2; cadmium-transporting ATPase [Arabidopsis thaliana] >gi|12229675|sp|Q9SZW4.1|AHM3_ARATH RecName: Full=Putative cadmium/zinc-transporting ATPase 3 >gi|4938487|emb|CAB43846.1| cadmium-transporting ATPase-like protein [Arabidopsis thaliana] >gi|7269911|emb|CAB81004.1| cadmium-transporting ATPase-like protein [Arabidopsis thaliana]	Unigene290_All//0.00E+00//AT4G30110| HMA2; cadmium-transporting ATPase	Unigene290_All//0.00E+00//C0119671				nr +
Unigene29001_All	728	1.22	13.71	1.76	1.23	2.79	1.43	0.29	0.80	0.44	3.49E+00	1.04E-37	Up	5.23E-01	3.99E-01		1.18E+00	9.07E-03		2.12E-01	7.55E-01		1.47E+00	1.02E-01		5.92E-01	6.13E-01				Unigene29001_All//3.00E-176//ES831359				
Unigene29004_All	442	11.01	3.55	7.59	35.61	23.06	19.72	63.23	26.48	28.75	-1.63E+00	3.55E-08	Down	-5.37E-01	6.18E-02		-6.27E-01	1.15E-06		-8.53E-01	6.31E-10		-1.26E+00	4.22E-36	Down	-1.14E+00	7.12E-32	Down	Unigene29004_All//gi|211906474|gb|ACJ11730.1|//2.00E-11//glycine-rich RNA-binding protein [Gossypium hirsutum]	Unigene29004_All//1.00E-11//AT2G21660| CCR2 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	Unigene29004_All//0.00E+00//gi|78324076|gb|DT544350.1|DT544350			GO:0003006//GO:0004672//GO:0004871//GO:0006405//GO:0006464//GO:0006952//GO:0006970//GO:0009536//GO:0009699//GO:0010038//GO:0010118//GO:0016070//GO:0016620//GO:0032392//GO:0032559//GO:0042579//GO:0042802//GO:0043566//GO:0048511	nr +
Unigene29005_All	299	12.60	8.47	3.92	8.66	7.95	4.98	34.08	8.39	9.19	-5.72E-01	7.05E-02		-1.69E+00	2.07E-06	Down	-1.25E-01	7.92E-01		-7.97E-01	4.26E-02		-2.02E+00	2.10E-26	Down	-1.89E+00	5.49E-25	Down			Unigene29005_All//1.00E-142//TC155591				
Unigene2901_All	1071	5.18	6.34	11.98	15.49	11.38	11.01	25.50	17.01	15.07	2.92E-01	2.16E-01		1.21E+00	1.11E-12	Up	-4.44E-01	5.07E-04		-4.93E-01	2.24E-04		-5.84E-01	3.08E-10		-7.59E-01	2.75E-16		Unigene2901_All//gi|23328041|ref|NP_201202.2|//1.00E-122//copine-related [Arabidopsis thaliana] >gi|79332056|ref|NP_001032132.1| copine-related [Arabidopsis thaliana]	Unigene2901_All//4.00E-123//AT5G63970| copine-related	Unigene2901_All//0.00E+00//TC174595				nr -
Unigene29010_All	225	11.63	15.31	11.12	20.81	18.21	23.89	49.61	44.40	17.35	3.97E-01	2.39E-01		-6.39E-02	8.77E-01		-1.92E-01	5.59E-01		1.99E-01	5.02E-01		-1.60E-01	3.66E-01		-1.52E+00	3.48E-20	Down			Unigene29010_All//3.00E-96//gi|78333701|gb|DT553975.1|DT553975				
Unigene29011_All	1606	0.03	0.03	0.07	0.78	0.81	0.65	81.01	28.45	41.70	-4.49E-02	9.85E-01		1.02E+00	7.03E-01		7.15E-02	9.26E-01		-2.62E-01	6.88E-01		-1.51E+00	9.49E-219	Down	-9.58E-01	8.24E-110		Unigene29011_All//gi|225470869|ref|XP_002269732.1|//1.00E-168//PREDICTED: (-)-a-terpineol synthase [Vitis vinifera]	Unigene29011_All//4.00E-120//AT3G25830| ATTPS-CIN (terpene synthase-like sequence-1,8-cineole); (E)-beta-ocimene synthase/ myrcene synthase	Unigene29011_All//0.00E+00//TC149686		ko00902|Monoterpenoid biosynthesis		nr +
Unigene29014_All	548	1.24	1.85	1.65	0.45	2.64	3.38	2.62	0.46	1.45	5.75E-01	3.83E-01		4.12E-01	5.94E-01		2.54E+00	7.72E-05	Up	2.89E+00	1.35E-06	Up	-2.52E+00	2.00E-05	Down	-8.51E-01	7.34E-02		Unigene29014_All//gi|44917575|gb|AAS49112.1|//8.00E-39//At5g10320 [Arabidopsis thaliana]	Unigene29014_All//3.00E-40//AT5G10320| unknown protein	Unigene29014_All//0.00E+00//C0126207				nr -
Unigene29015_All	782	2.34	0.39	0.14	2.36	0.48	0.92	1.03	0.32	0.51	-2.59E+00	9.26E-06	Down	-4.10E+00	7.79E-08	Down	-2.28E+00	5.07E-06	Down	-1.35E+00	5.69E-03		-1.68E+00	2.46E-02		-1.01E+00	1.35E-01		Unigene29015_All//gi|224072103|ref|XP_002303625.1|//2.00E-62//AP2/EREBP domain-containing transcription factor [Populus trichocarpa] >gi|222841057|gb|EEE78604.1| AP2/EREBP domain-containing transcription factor [Populus trichocarpa]	Unigene29015_All//2.00E-35//AT4G23750| CRF2 (CYTOKININ RESPONSE FACTOR 2); DNA binding / transcription factor	Unigene29015_All//5.00E-141//gi|78350658|gb|DT570332.1|DT570332	AP2-EREBP		GO:0005488//GO:0006350//GO:0006606//GO:0009793//GO:0043231//GO:0048513	nr -
Unigene29016_All	493	0.42	5.14	1.40	2.83	3.91	2.47	1.97	1.10	2.75	3.60E+00	3.49E-10	Up	1.73E+00	7.67E-02		4.67E-01	3.50E-01		-1.94E-01	7.27E-01		-8.40E-01	1.87E-01		4.78E-01	3.55E-01									
Unigene29017_All	676	0.00	0.45	0.00	6.26	1.83	0.40	3.19	1.67	1.24	8.81E+00	4.43E-02		null	null		-1.77E+00	1.47E-09	Down	-3.97E+00	1.21E-19	Down	-9.34E-01	1.70E-02		-1.37E+00	4.70E-04	Down	Unigene29017_All//gi|15219811|ref|NP_176873.1|//3.00E-26//ZFP6 (ZINC FINGER PROTEIN 6); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|27923892|sp|Q39265.1|ZFP6_ARATH RecName: Full=Zinc finger protein 6 >gi|9755451|gb|AAF98212.1|AC007152_8 zinc finger protein zep6 [Arabidopsis thaliana] >gi|790683|gb|AAA87302.1| zinc finger protein [Arabidopsis thaliana] >gi|15215717|gb|AAK91404.1| At1g67030/F1019_5 [Arabidopsis thaliana] >gi|20147413|gb|AAM10416.1| At1g67030/F1019_5 [Arabidopsis thaliana]	Unigene29017_All//6.00E-22//AT1G67030| ZFP6 (ZINC FINGER PROTEIN 6); nucleic acid binding / transcription factor/ zinc ion binding		C2H2		GO:0043229	nr -
Unigene29018_All	519	13.11	38.95	13.24	20.83	17.25	19.75	11.00	12.00	14.81	1.57E+00	7.43E-30	Up	1.43E-02	9.73E-01		-2.72E-01	1.32E-01		-7.64E-02	6.94E-01		1.26E-01	6.33E-01		4.30E-01	1.94E-02				Unigene29018_All//0.00E+00//gi|13351077|gb|BG441425.1|BG441425				
Unigene29019_All	472	0.55	0.32	0.11	1.06	1.68	1.05	1.88	3.10	6.33	-7.83E-01	6.20E-01		-2.30E+00	2.43E-01		6.69E-01	4.42E-01		-4.00E-03	9.87E-01		7.20E-01	1.46E-01		1.75E+00	4.02E-07	Up	Unigene29019_All//gi|115474867|ref|NP_001061030.1|//4.00E-13//Os08g0157400 [Oryza sativa Japonica Group] >gi|113622999|dbj|BAF22944.1| Os08g0157400 [Oryza sativa Japonica Group] >gi|149392499|gb|ABR26052.1| ring zinc finger protein-like [Oryza sativa Indica Group]	Unigene29019_All//1.00E-10//AT5G14430| zinc finger (C3HC4-type RING finger) family protein	Unigene29019_All//3.00E-92//TC130093		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0031410	nr +
Unigene2902_All	1995	45.87	24.81	25.62	83.45	68.91	85.19	113.76	46.53	37.72	-8.86E-01	3.31E-54		-8.40E-01	7.71E-48		-2.76E-01	1.22E-14		2.98E-02	5.78E-01		-1.29E+00	3.13E-300	Down	-1.59E+00	0.00E+00	Down	Unigene2902_All//0.00E+00//gi|115445301|ref|NP_001046430.1|//0.00E+00//Os02g0247200 [Oryza sativa Japonica Group] >gi|113535961|dbj|BAF08344.1| Os02g0247200 [Oryza sativa Japonica Group]	Unigene2902_All//0.00E+00//AT5G26360| chaperonin, putative	Unigene2902_All//0.00E+00//TC155641			GO:0005515//GO:0032559//GO:0044267//GO:0044424	nr +
Unigene29020_All	627	0.50	1.45	1.61	0.95	2.20	0.65	2.43	0.13	1.21	1.54E+00	4.51E-02		1.69E+00	2.74E-02		1.20E+00	3.86E-02		-5.56E-01	5.76E-01		-4.19E+00	1.46E-08	Down	-1.01E+00	2.94E-02		Unigene29020_All//gi|70568824|dbj|BAE06272.1|//6.00E-44//cyclin D [Scutellaria baicalensis]	Unigene29020_All//4.00E-43//AT5G67260| CYCD3;2 (CYCLIN D3;2); cyclin-dependent protein kinase	Unigene29020_All//0.00E+00//C0070032			GO:0005488//GO:0007049//GO:0008283//GO:0043231	nr -
Unigene29022_All	435	1.80	5.24	1.59	0.11	2.30	1.45	1.46	0.10	4.58	1.54E+00	6.01E-04	Up	-1.81E-01	8.07E-01		4.33E+00	4.31E-05	Up	3.67E+00	5.05E-03		-3.92E+00	9.81E-04	Down	1.65E+00	1.08E-04	Up			Unigene29022_All//0.00E+00//DW500155				
Unigene29024_All	510	1.33	2.98	2.09	2.64	2.03	1.42	3.65	1.88	1.17	1.16E+00	3.43E-02		6.47E-01	3.62E-01		-3.81E-01	5.36E-01		-8.96E-01	1.30E-01		-9.53E-01	2.57E-02		-1.64E+00	1.88E-04	Down								
Unigene29026_All	884	0.53	0.06	0.42	0.62	0.47	0.31	2.68	2.22	1.13	-3.22E+00	2.73E-02		-3.37E-01	7.34E-01		-4.07E-01	6.58E-01		-1.02E+00	3.30E-01		-2.69E-01	5.09E-01		-1.25E+00	6.37E-04	Down	Unigene29026_All//gi|15239738|ref|NP_197442.1|//1.00E-102//ABC transporter family protein [Arabidopsis thaliana] >gi|109896159|sp|Q3E9B8.1|AB23G_ARATH RecName: Full=ABC transporter G family member 23; Short=ABC transporter ABCG.23; Short=AtABCG23; AltName: Full=Probable white-brown complex homolog protein 24; Short=AtWBC24	Unigene29026_All//5.00E-96//AT5G19410| ABC transporter family protein	Unigene29026_All//0.00E+00//gi|109881302|gb|DW510272.1|DW510272		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015405//GO:0017111//GO:0032559//GO:0044464	nr -
Unigene29028_All	700	0.00	0.00	0.00	0.00	0.00	0.00	1.15	1.85	3.59	null	null		null	null		null	null		null	null		6.90E-01	2.02E-01		1.64E+00	1.14E-05	Up	Unigene29028_All//gi|110816488|sp|Q3BAI2.1|YC91_PHAAO//5.00E-09//RecName: Full=Uncharacterized protein 08F91		Unigene29028_All//2.00E-54//TC141618				nr +
Unigene2903_All	715	2.71	5.67	5.36	2.44	1.69	2.65	4.02	4.73	2.79	1.07E+00	5.32E-04	Up	9.86E-01	2.63E-03		-5.33E-01	2.92E-01		1.22E-01	8.06E-01		2.36E-01	4.78E-01		-5.29E-01	9.93E-02				Unigene2903_All//1.00E-55//DR460129				
Unigene29030_All	338	10.53	13.94	10.24	28.00	13.65	11.89	32.77	22.88	16.50	4.05E-01	1.51E-01		-3.97E-02	9.17E-01		-1.04E+00	2.48E-09	Down	-1.24E+00	6.51E-11	Down	-5.19E-01	6.58E-04		-9.90E-01	1.09E-10		Unigene29030_All//gi|224136077|ref|XP_002322234.1|//1.00E-29//acyl:coa ligase [Populus trichocarpa] >gi|222869230|gb|EEF06361.1| acyl:coa ligase [Populus trichocarpa]	Unigene29030_All//5.00E-26//AT5G63380| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene29030_All//0.00E+00//gi|109873608|gb|DW502583.1|DW502583		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0009694//GO:0009850//GO:0016408//GO:0016703//GO:0042579	nr +

Unigene29031_All	591	473.99	163.33	290.31	35.15	35.66	23.08	0.00	0.00	1.35	-1.54E+00	0.00E+00	Down	-7.07E-01	2.81E-108		2.08E-02	8.95E-01		-6.07E-01	2.11E-07		null	null		1.04E+01	7.36E-06	Up	Unigene29031_All//gi|162461856|ref|NP_001105414.1|//5.00E-83//glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic precursor [Zea mays] >gi|120657|sp|P09315.1|G3PA_MAIZE RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase A, chloroplastic; AltName: Full=NADP-dependent glyceraldehydephosphate dehydrogenase subunit A; Flags: Precursor >gi|168479|gb|AAA33464.1| glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi|763035|emb|CAA33455.1| glyceraldehyde-3-phosphate dehydrogenase [Zea mays]	Unigene29031_All//7.00E-80//AT1G12900| GAPA-2 (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT 2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene29031_All//0.00E+00//gi|109867648|gb|DW496624.1|DW496624		ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0005576//GO:0006007//GO:0008943//GO:0009526//GO:0009532//GO:0015977	nr -
Unigene29032_All	1205	0.17	0.93	0.00	0.00	0.54	3.41	0.84	4.30	4.40	2.41E+00	1.59E-03		-7.44E+00	1.46E-01		9.08E+00	4.92E-04	Up	1.17E+01	8.86E-25	Up	2.35E+00	1.91E-16	Up	2.38E+00	1.96E-17	Up	Unigene29032_All//gi|6850900|emb|CAB71063.1|//8.00E-80//copia-type polyprotein [Arabidopsis thaliana]	Unigene29032_All//4.00E-09//ATMG00300| hypothetical protein	Unigene29032_All//9.00E-42//DT468735			GO:0003676//GO:0006259	nr -
Unigene29036_All	387	28.26	29.07	39.22	8.37	19.66	8.52	0.00	0.43	0.21	4.08E-02	8.22E-01		4.73E-01	1.52E-03		1.23E+00	2.25E-09	Up	2.61E-02	9.53E-01		8.75E+00	1.39E-01		7.69E+00	4.01E-01					Unigene29036_All//4.00E-07//TC164767				
Unigene29037_All	352	0.30	0.00	1.51	1.84	1.76	2.57	7.33	2.49	3.17	-8.22E+00	3.72E-01		2.35E+00	5.87E-02		-6.32E-02	9.25E-01		4.80E-01	5.50E-01		-1.56E+00	2.82E-05	Down	-1.21E+00	4.99E-04	Down				Unigene29037_All//1.00E-07//CO123662				
Unigene29038_All	436	12.48	13.83	17.22	5.26	2.92	1.24	0.58	0.38	0.55	1.48E-01	5.85E-01		4.65E-01	3.91E-02		-8.47E-01	3.50E-02		-2.08E+00	7.11E-06	Down	-6.02E-01	6.48E-01		-8.58E-02	9.57E-01									
Unigene2904_All	1043	4.06	5.25	4.80	5.87	5.78	5.46	4.13	3.05	1.99	3.69E-01	1.58E-01		2.40E-01	4.03E-01		-2.40E-02	9.29E-01		-1.07E-01	6.74E-01		-4.41E-01	9.99E-02		-1.06E+00	3.87E-05	Down				Unigene2904_All//4.00E-105//gi|78327960|gb|DT548234.1|DT548234				kegg +
Unigene29041_All	1435	0.84	1.20	1.93	0.07	0.00	0.00	3.36	0.61	5.25	5.18E-01	3.08E-01		1.20E+00	2.76E-03		-6.12E+00	3.13E-01		-6.12E+00	4.00E-01		-2.46E+00	3.71E-16	Down	6.44E-01	4.78E-04		Unigene29041_All//gi|118430824|gb|ABK91948.1|//1.00E-150//proline dehydrogenase [Actinidia deliciosa]	Unigene29041_All//3.00E-98//AT5G38710| proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative	Unigene29041_All//6.00E-99//TC136050				nr -
Unigene29044_All	704	0.15	0.79	1.66	1.84	1.03	0.71	3.54	4.10	1.30	2.41E+00	3.93E-02		3.49E+00	1.09E-04	Up	-8.41E-01	1.44E-01		-1.38E+00	2.30E-02		2.09E-01	5.82E-01		-1.45E+00	7.03E-05	Down	Unigene29044_All//gi|32396098|gb|AAP43916.1|//1.00E-39//integrase [Gossypium herbaceum]		Unigene29044_All//4.00E-129//DR461345			GO:0003676//GO:0004175//GO:0006260//GO:0006325//GO:0019538//GO:0034061//GO:0043231//GO:0044427//GO:0046914	nr +
Unigene29045_All	527	3.38	7.98	16.77	1.80	0.13	1.11	47.90	17.77	18.90	1.24E+00	5.11E-05	Up	2.31E+00	2.33E-21	Up	-3.78E+00	3.40E-05	Down	-6.89E-01	3.58E-01		-1.43E+00	9.29E-40	Down	-1.34E+00	3.28E-37	Down	Unigene29045_All//gi|255558380|ref|XP_002520217.1|//1.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223540709|gb|EEF42272.1| conserved hypothetical protein [Ricinus communis]		Unigene29045_All//3.00E-160//gi|109828397|gb|DW227020.1|DW227020				nr -
Unigene29046_All	342	29.53	19.11	16.04	25.05	20.14	22.45	189.89	134.19	59.64	-6.28E-01	4.73E-04		-8.81E-01	2.83E-06		-3.15E-01	1.18E-01		-1.58E-01	4.93E-01		-5.01E-01	8.91E-18		-1.67E+00	1.75E-130	Down				Unigene29046_All//0.00E+00//gi|21096914|gb|BQ409227.1|BQ409227				
Unigene29050_All	630	4.90	1.61	0.68	3.56	2.95	3.08	1.54	0.86	0.82	-1.61E+00	2.25E-05	Down	-2.86E+00	1.18E-09	Down	-2.70E-01	5.54E-01		-2.07E-01	6.58E-01		-8.40E-01	1.87E-01		-9.09E-01	1.31E-01		Unigene29050_All//gi|115446175|ref|NP_001046867.1|//8.00E-31//Os02g0489500 [Oryza sativa Japonica Group] >gi|113536398|dbj|BAF08781.1| Os02g0489500 [Oryza sativa Japonica Group]	Unigene29050_All//1.00E-53//AT5G63100| unknown protein	Unigene29050_All//0.00E+00//gi|78347158|gb|DT567432.1|DT567432			GO:0003824//GO:0009536	nr +
Unigene29051_All	617	30.27	15.85	22.09	360.81	321.02	311.39	928.59	656.27	297.92	-9.34E-01	1.16E-12		-4.54E-01	6.21E-04		-1.69E-01	8.48E-08		-2.13E-01	8.37E-11		-5.01E-01	2.51E-150		-1.64E+00	0.00E+00	Down	Unigene29051_All//gi|258489633|gb|ACV72640.1|//1.00E-119//sucrose synthase 1 [Gossypium hirsutum]	Unigene29051_All//2.00E-108//AT5G20830| SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase	Unigene29051_All//0.00E+00//gi|109827559|gb|DW226235.1|DW226235		ko00500|Starch and sucrose metabolism		nr -
Unigene29053_All	282	0.56	0.18	1.13	3.36	2.93	4.48	1.80	4.59	7.77	-1.63E+00	4.89E-01		1.03E+00	4.71E-01		-1.96E-01	8.04E-01		4.18E-01	5.23E-01		1.35E+00	1.28E-02		2.11E+00	1.02E-06	Up								ESTscan +
Unigene29054_All	601	0.00	0.08	0.18	0.66	0.63	1.58	0.63	2.02	3.51	6.40E+00	6.16E-01		7.47E+00	3.99E-01		-7.32E-02	9.25E-01		1.25E+00	9.60E-02		1.67E+00	4.19E-03		2.47E+00	1.11E-07	Up				Unigene29054_All//3.00E-12//TC151712				
Unigene29055_All	593	0.00	4.70	0.00	0.00	0.23	1.52	7.63	14.17	25.73	1.22E+01	7.43E-16	Up	null	null		7.86E+00	3.18E-01		1.06E+01	2.07E-05	Up	8.93E-01	6.90E-07		1.75E+00	4.47E-33	Up	Unigene29055_All//gi|115476680|ref|NP_001061936.1|//5.00E-09//Os08g0448100 [Oryza sativa Japonica Group] >gi|113623905|dbj|BAF23850.1| Os08g0448100 [Oryza sativa Japonica Group]	Unigene29055_All//3.00E-25//AT5G57510| unknown protein	Unigene29055_All//0.00E+00//TC172618				nr +
Unigene29056_All	454	1.84	1.34	0.00	1.32	2.20	1.29	14.43	9.94	9.39	-4.61E-01	5.43E-01		-1.08E+01	1.19E-04	Down	7.40E-01	3.10E-01		-2.60E-02	9.64E-01		-5.38E-01	8.94E-03		-6.21E-01	1.76E-03					Unigene29056_All//3.00E-169//TC172050				
Unigene29057_All	443	0.71	4.12	3.25	4.84	5.29	5.61	6.49	20.00	7.19	2.54E+00	1.40E-05	Up	2.20E+00	8.73E-04	Up	1.29E-01	8.20E-01		2.14E-01	6.29E-01		1.62E+00	3.18E-17	Up	1.49E-01	6.33E-01		Unigene29057_All//gi|30315017|gb|AAP30740.1|//7.00E-21//glutathione-S-transferase [Vitis vinifera]	Unigene29057_All//2.00E-21//AT1G17170| ATGSTU24 (GLUTATHIONE S-TRANSFERASE TAU 24); glutathione binding / glutathione transferase	Unigene29057_All//3.00E-79//gi|31407290|gb|CD486325.1|CD486325		ko00480|Glutathione metabolism	GO:0009404//GO:0016765//GO:0042277//GO:0044424	nr -
Unigene29058_All	671	1.40	15.33	4.13	0.59	3.18	2.96	0.32	0.12	1.07	3.45E+00	1.79E-38	Up	1.56E+00	1.81E-04	Up	2.42E+00	1.23E-06	Up	2.32E+00	1.15E-05	Up	-1.34E+00	4.30E-01		1.76E+00	2.48E-02		Unigene29058_All//gi|224092264|ref|XP_002309533.1|//1.00E-52//histidine phosphotransfer protein [Populus trichocarpa] >gi|222855509|gb|EEE93056.1| histidine phosphotransfer protein [Populus trichocarpa]	Unigene29058_All//5.00E-42//AT3G16360| AHP4 (HPT PHOSPHOTRANSMITTER 4); histidine phosphotransfer kinase/ transferase, transferring phosphorus-containing groups	Unigene29058_All//9.00E-90//TC164475			GO:0004871//GO:0008152//GO:0009736//GO:0016628//GO:0023060//GO:0043231	nr -
Unigene29059_All	428	7.95	20.24	15.55	9.43	17.70	12.24	0.00	0.00	0.00	1.35E+00	1.11E-10	Up	9.69E-01	4.94E-05		9.09E-01	6.39E-06		3.77E-01	1.80E-01		null	null		null	null										
Unigene2906_All	1137	31.38	133.60	45.24	18.05	72.69	64.55	16.18	38.19	56.94	2.09E+00	0.00E+00	Up	5.28E-01	2.78E-12		2.01E+00	2.18E-198	Up	1.84E+00	6.20E-143	Up	1.24E+00	1.87E-54	Up	1.82E+00	2.03E-144	Up	Unigene2906_All//gi|115459466|ref|NP_001053333.1|//1.00E-25//Os04g0520700 [Oryza sativa Japonica Group] >gi|21741857|emb|CAD41447.1| OSJNBa0019011.12 [Oryza sativa (japonica cultivar-group)] >gi|113564904|dbj|BAF15247.1| Os04g0520700 [Oryza sativa Japonica Group] >gi|116310726|emb|CAH67522.1| OSIGBa0131L05.3 [Oryza sativa (indica cultivar-group)]	Unigene2906_All//5.00E-29//AT5G03230| unknown protein	Unigene2906_All//0.00E+00//TC161346			GO:0005488	nr -
Unigene29063_All	669	0.16	0.15	0.40	4.24	2.06	2.43	2.91	17.49	2.26	-4.59E-02	9.89E-01		1.35E+00	4.09E-01		-1.04E+00	2.85E-03		-8.04E-01	3.06E-02		2.59E+00	1.90E-40	Up	-3.62E-01	3.81E-01					Unigene29063_All//1.00E-11//DT465163				
Unigene29064_All	723	8.68	6.38	4.86	6.48	9.95	5.87	1.23	0.00	0.11	-4.45E-01	6.21E-02		-8.37E-01	6.48E-04		6.20E-01	3.08E-03		-1.41E-01	6.58E-01		-1.03E+01	2.24E-06	Down	-3.48E+00	7.33E-05	Down	Unigene29064_All//gi|297852508|ref|XP_002894135.1|//3.00E-47//EMB1144 [Arabidopsis lyrata subsp. lyrata] >gi|297339977|gb|EFH70394.1| EMB1144 [Arabidopsis lyrata subsp. lyrata]	Unigene29064_All//1.00E-48//AT1G48850| EMB1144 (embryo defective 1144); chorismate synthase	Unigene29064_All//0.00E+00//TC161190		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0003006//GO:0008652//GO:0009536//GO:0016838//GO:0031981	nr -
Unigene29065_All	492	0.43	1.96	0.22	2.84	1.12	1.47	3.78	7.73	131.99	2.20E+00	6.58E-03		-9.75E-01	6.21E-01		-1.34E+00	1.36E-02		-9.49E-01	9.91E-02		1.03E+00	2.65E-04	Up	5.13E+00	0.00E+00	Up								
Unigene29069_All	688	1.29	0.52	0.31	2.46	1.65	2.82	0.00	0.24	2.20	-1.33E+00	7.96E-02		-2.06E+00	1.78E-02		-5.76E-01	2.53E-01		1.97E-01	6.75E-01		7.92E+00	1.39E-01		1.11E+01	6.77E-11	Up	Unigene29069_All//gi|89179406|gb|ABD63142.1|//2.00E-17//Retrotransposon gag protein [Asparagus officinalis]		Unigene29069_All//2.00E-103//DN801339			GO:0003676//GO:0003824//GO:0006259	nr -
Unigene2907_All	2138	1.76	3.89	2.22	7.60	7.76	5.96	9.81	4.09	5.96	1.14E+00	4.28E-08	Up	3.31E-01	2.69E-01		3.15E-02	8.51E-01		-3.51E-01	1.21E-02		-1.26E+00	1.54E-27	Down	-7.18E-01	1.29E-11		Unigene2907_All//gi|24661856|gb|AAN62343.1|AF506028_10//0.00E+00//nodulin-like protein [Citrus trifoliata]	Unigene2907_All//3.00E-169//AT1G80530| nodulin family protein	Unigene2907_All//0.00E+00//TC148335			GO:0006810	nr +
Unigene29070_All	423	7.30	3.23	2.90	7.30	3.26	8.97	0.50	0.00	0.85	-1.17E+00	1.17E-03		-1.33E+00	4.86E-04	Down	-1.16E+00	4.72E-04	Down	2.97E-01	3.94E-01		-8.97E+00	7.44E-02		7.62E-01	4.99E-01		Unigene29070_All//gi|225463468|ref|XP_002276545.1|//1.00E-16//PREDICTED: similar to RPL18AA (60S RIBOSOMAL PROTEIN L18A-1); structural constituent of ribosome isoform 2 [Vitis vinifera]		Unigene29070_All//2.00E-34//TC175406		ko04144|Endocytosis		nr -
Unigene29072_All	655	1.20	4.41	1.14	1.83	3.58	1.72	12.78	9.76	9.31	1.88E+00	4.54E-06	Up	-7.41E-02	9.35E-01		9.70E-01	1.89E-02		-8.25E-02	9.06E-01		-3.89E-01	3.36E-02		-4.58E-01	8.41E-03		Unigene29072_All//gi|186522071|ref|NP_850807.2|//2.00E-14//ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana]	Unigene29072_All//4.00E-15//AT5G11170| ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene29072_All//6.00E-91//TC146447		ko03040|Spliceosome	GO:0010038//GO:0030312//GO:0031981//GO:0032559//GO:0042623	nr +
Unigene29074_All	1149	5.24	17.11	12.00	5.77	11.99	17.37	0.07	0.00	0.07	1.71E+00	1.21E-32	Up	1.20E+00	2.36E-13	Up	1.06E+00	4.05E-13	Up	1.59E+00	4.75E-32	Up	-6.20E+00	4.04E-01		-8.69E-02	9.72E-01		Unigene29074_All//gi|15241261|ref|NP_199890.1|//2.00E-75//AtHSD6 (hydroxysteroid dehydrogenase 6); binding / catalytic/ oxidoreductase [Arabidopsis thaliana] >gi|57291844|gb|AAW49294.1| At5g50770 [Arabidopsis thaliana]	Unigene29074_All//1.00E-69//AT5G50700| short-chain dehydrogenase/reductase (SDR) family protein	Unigene29074_All//0.00E+00//TC132379		ko00903|Limonene and pinene degradation//ko01040|Biosynthesis of unsaturated fatty acids//ko00906|Carotenoid biosynthesis//ko00061|Fatty acid biosynthesis	GO:0008152//GO:0016491//GO:0044464	nr -
Unigene29075_All	579	1.54	1.23	1.38	3.96	2.32	1.64	1.31	0.14	0.41	-3.26E-01	6.22E-01		-1.55E-01	8.24E-01		-7.71E-01	5.66E-02		-1.27E+00	2.82E-03		-3.19E+00	7.92E-04	Down	-1.67E+00	2.39E-02					Unigene29075_All//7.00E-07//AW187376				
Unigene29076_All	343	15.86	16.99	18.01	20.62	15.46	22.78	135.72	56.30	34.15	9.88E-02	6.94E-01		1.83E-01	4.94E-01		-4.16E-01	5.55E-02		1.44E-01	5.73E-01		-1.27E+00	1.31E-60	Down	-1.99E+00	3.72E-119	Down				Unigene29076_All//3.00E-29//TC165550				
Unigene29077_All	458	36.21	70.80	34.53	53.19	66.62	58.97	12.28	35.59	18.09	9.67E-01	1.37E-22		-6.86E-02	6.52E-01		3.25E-01	5.06E-04		1.49E-01	2.15E-01		1.54E+00	1.13E-28	Up	5.59E-01	1.35E-03		Unigene29077_All//gi|18423010|ref|NP_568708.1|//3.00E-14//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|215534492|gb|AAM62585.1| extensin like protein [Arabidopsis thaliana] >gi|194708810|gb|ACF88489.1| At5g49280 [Arabidopsis thaliana]		Unigene29077_All//3.00E-70//TC151767			GO:0031224	nr -
Unigene29078_All	484	0.65	1.47	2.42	3.50	3.70	0.65	1.92	0.52	2.22	1.18E+00	1.75E-01		1.90E+00	8.12E-03		8.03E-02	8.91E-01		-2.42E+00	2.78E-05	Down	-1.89E+00	6.92E-03		2.10E-01	7.09E-01					Unigene29078_All//6.00E-07//EX164332				
Unigene29079_All	542	2.12	8.04	1.57	5.88	2.67	10.92	4.37	5.01	115.47	1.92E+00	5.20E-09	Up	-4.34E-01	5.10E-01		-1.14E+00	4.82E-04	Down	8.92E-01	2.21E-04		1.98E-01	6.23E-01		4.72E+00	0.00E+00	Up	Unigene29079_All//gi|115448987|ref|NP_001048273.1|//4.00E-13//Os02g0774200 [Oryza sativa Japonica Group] >gi|113537804|dbj|BAF10187.1| Os02g0774200 [Oryza sativa Japonica Group]	Unigene29079_All//4.00E-05//AT1G05575| unknown protein				GO:0045333	nr +

Unigene2908_All	1612	88.28	436.03	133.03	31.98	60.35	79.96	62.74	393.09	219.90	2.30E+00	0.00E+00	Up	5.92E-01	1.42E-60		9.16E-01	4.91E-72		1.32E+00	1.97E-155	Up	2.65E+00	0.00E+00	Up	1.81E+00	0.00E+00	Up	Unigene2908_All//gi|3334223|sp|P93836.2|HPPD_ARATH//0.00E+00//RecName: Full=4-hydroxyphenylpyruvate dioxygenase; AltName: Full=4-hydroxyphenylpyruvic acid oxidase; Short=HPPDase; Short=HPPD; Short=HPD >gi|55669757|pdb|1SP9|A Chain A, 4-Hydroxyphenylpyruvate Dioxygenase >gi|55669758|pdb|1SP9|B Chain B, 4-Hydroxyphenylpyruvate Dioxygenase >gi|16226618|gb|AAL16215.1|AF428446_1 At1g06570/F12H11_12 [Arabidopsis thaliana] >gi|2145039|gb|AAB58404.1| p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi|2392518|gb|AAB70025.1| p-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi|30988559|gb|AAC15697.1| 4-hydroxyphenylpyruvate dioxygenase [Arabidopsis thaliana] >gi|18252207|gb|AAL61936.1| 4-hydroxyphenylpyruvate dioxygenase (HPD) [Arabidopsis thaliana] >gi|22136134|gb|AAM91145.1| 4-hydroxyphenylpyruvate dioxygenase (HPD) [Arabidopsis thaliana]	Unigene2908_All//0.00E+00//AT1G06570| PDS1 (PHYTOENE DESATURATION 1); 4-hydroxyphenylpyruvate dioxygenase	Unigene2908_All//0.00E+00//TC158993		ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0005515//GO:0006558//GO:0006570//GO:0009536//GO:0016109//GO:0016102//GO:0042360//GO:0043169//GO:0045426	nr +
Unigene29080_All	260	54.53	29.62	30.52	69.74	88.21	109.09	171.40	80.22	94.69	-8.81E-01	5.84E-09		-8.38E-01	6.79E-08		3.39E-01	2.13E-03		6.45E-01	7.52E-11		-1.10E+00	4.49E-46	Down	-8.56E-01	9.66E-32		Unigene29080_All//gi|242129046|gb|ACS83602.1|//3.00E-42//ATP synthase beta subunit 1 [Gossypium hirsutum]	Unigene29080_All//5.00E-21//AT5G08690| ATP synthase beta chain 2, mitochondrial	Unigene29080_All//4.00E-145//TC140191		ko00190|Oxidative phosphorylation	GO:0000275//GO:0015078//GO:0015662//GO:0019586//GO:0019829//GO:0032359	nr +
Unigene29081_All	540	8.14	11.92	8.28	32.66	32.90	13.30	0.55	0.00	0.00	5.50E-01	1.83E-02		2.54E-02	9.48E-01		1.09E-02	9.62E-01		-1.30E+00	2.47E-21	Down	-9.10E+00	2.18E-02		-9.10E+00	1.58E-02		Unigene29081_All//gi|224088816|ref|XP_002308552.1|//2.00E-43//glutaredoxin [Populus trichocarpa] >gi|222854528|gb|EEE92075.1| glutaredoxin [Populus trichocarpa]	Unigene29081_All//5.00E-39//AT4G33040| glutaredoxin family protein	Unigene29081_All//3.00E-138//TC174585				nr +
Unigene29082_All	375	3.91	6.22	3.27	4.65	5.69	5.06	22.10	15.83	9.88	6.70E-01	1.11E-01		-2.58E-01	6.23E-01		2.92E-01	5.58E-01		1.22E-01	8.06E-01		-4.82E-01	7.64E-03		-1.16E+00	2.15E-10	Down	Unigene29082_All//gi|78814561|gb|AB829948.1|//3.00E-17//vesicle transport v-SNARE 11-like [Solanum tuberosum]	Unigene29082_All//2.00E-10//AT5G39510| SGR4 (SHOOT GRAVITROPISM 4); receptor	Unigene29082_All//3.00E-91//TC135191		ko04130|SNARE interactions in vesicular transport	GO:0004871//GO:0005515//GO:0015031//GO:0016041//GO:0044464//GO:0048193	nr -
Unigene29084_All	459	1.71	0.00	0.70	1.52	2.03	0.59	1.57	1.55	1.04	-1.07E+01	1.09E-04	Down	-1.30E+00	1.38E-01		4.15E-01	6.06E-01		-1.36E+00	1.31E-01		-1.66E-02	1.02E+00		-5.88E-01	4.09E-01		Unigene29084_All//gi|225441323|ref|XP_002274379.1|//6.00E-48//PREDICTED: similar to mature-like protein [Vitis vinifera]	Unigene29084_All//2.00E-62//AT5G04050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: RNA splicing; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Intron maturase, type II (InterPro:IPR000442); BEST Arabidopsis thaliana protein match is: intron maturase, type II family protein (TAIR:AT1G74350.1); Has 2089 Blast hits to 2073 proteins in 800 species: Archae - 3; Bacteria - 1302; Metazoa - 5; Fungi - 34; Plants - 655; Viruses - 0; Other Eukaryotes - 90 (source: NCBI BLink).				GO:0003676//GO:0006260//GO:0006396//GO:0034061	nr +
Unigene29085_All	1778	0.41	0.46	0.24	33.87	21.81	16.71	0.90	24.17	0.45	1.46E-01	8.39E-01		-7.82E-01	3.80E-01		-6.35E-01	1.24E-24		-1.02E+00	7.98E-49	Down	4.74E+00	5.25E-247	Up	-1.01E+00	2.40E-02		Unigene29085_All//gi|15220954|ref|NP_174363.1|//0.00E+00//FAD-binding domain-containing protein [Arabidopsis thaliana] >gi|16323167|gb|AAL15318.1| At1g30760/T518_22 [Arabidopsis thaliana] >gi|28416457|gb|AAO42759.1| At1g30760/T518_22 [Arabidopsis thaliana]	Unigene29085_All//0.00E+00//AT1G30760| FAD-binding domain-containing protein	Unigene29085_All//3.00E-61//gi|48829334|gb|CO127724.1|CO127724			GO:0008152//GO:0030554//GO:0044464//GO:0046993	nr +
Unigene29086_All	1210	0.74	0.50	0.00	10.29	7.94	2.65	10.06	8.05	4.18	-5.49E-01	4.42E-01		-9.52E+00	6.30E-05	Down	-3.74E-01	1.62E-02		-1.96E+00	2.92E-27	Down	-3.22E-01	3.11E-02		-1.27E+00	6.40E-17	Down	Unigene29086_All//gi|15225833|ref|NP_180889.1|//5.00E-63//IAA13; transcription factor [Arabidopsis thaliana] >gi|186504957|ref|NP_001118434.1| IAA13; transcription factor [Arabidopsis thaliana] >gi|12083208|gb|AAG48763.1|AF332399_1 auxin-regulated protein IAA13 [Arabidopsis thaliana] >gi|972929|gb|AAC49054.1| IAA13 [Arabidopsis thaliana] >gi|24594114|gb|AAR80649.1| auxin regulated protein (IAA13) [Arabidopsis thaliana] >gi|21537404|gb|AAM61745.1| auxin regulated protein IAA13 [Arabidopsis thaliana]	Unigene29086_All//5.00E-49//AT2G33310| IAA13; transcription factor	Unigene29086_All//0.00E+00//AI725624			GO:0003002//GO:0005488//GO:0009725//GO:0009790//GO:0009987//GO:0030528//GO:0048513	nr -
Unigene29089_All	357	0.00	0.00	1.79	0.56	0.87	0.25	0.00	2.11	0.89	null	null		1.08E+01	1.16E-03		6.37E-01	6.95E-01		-1.14E+00	5.69E-01		1.10E+01	2.07E-05	Up	9.80E+00	1.34E-02				Unigene29089_All//1.00E-133//DW516431				
Unigene2909_All	1562	41.10	24.10	42.41	52.94	48.39	64.62	44.96	30.61	18.95	-7.70E-01	3.45E-30		4.52E-02	5.89E-01		-1.30E-01	2.85E-02		2.88E-01	7.70E-09		-5.55E-01	7.14E-23		-1.25E+00	4.93E-91	Down	Unigene2909_All//gi|15223991|ref|NP_172953.1|//1.00E-148//scp150 (serine carboxypeptidase-like 50; serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75336113|sp|Q9SEQ6.1|SCP50_ARATH RecName: Full=Serine carboxypeptidase-like 50; Flags: Precursor >gi|6899645|gb|AAF31022.1|AC012189_4 Contains similarity to serine-type carboxypeptidase like protein from Arabidopsis thaliana gi|4678929 and contains two Serine carboxypeptidase domains PF|00450 >gi|19715607|gb|AAL91626.1| At1g15000/T15D22_7 [Arabidopsis thaliana] >gi|27363234|gb|AAO11536.1| At1g15000/T15D22_7 [Arabidopsis thaliana]	Unigene2909_All//8.00E-150//AT1G15000| scp150 (serine carboxypeptidase-like 50); serine-type carboxypeptidase	Unigene2909_All//0.00E+00//TC142344		ko00940|Phenylpropanoid biosynthesis	GO:0004180//GO:0019538	nr +
Unigene29090_All	435	0.00	1.40	0.73	1.26	3.17	3.32	0.19	2.21	2.20	1.04E+01	1.17E-03		9.52E+00	4.52E-02		1.33E+00	2.25E-02		1.40E+00	1.56E-02		3.51E+00	5.50E-05	Up	3.50E+00	4.29E-05	Up	Unigene29090_All//gi|297813749|ref|XP_002874758.1|//3.00E-09//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326595|gb|EFH51017.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29090_All//6.00E-09//AT4G12140| zinc finger (C3HC4-type RING finger) family protein	Unigene29090_All//0.00E+00//DW516431			GO:0009743//GO:0010038//GO:0019787//GO:0032446//GO:0046872	nr -
Unigene29091_All	670	1.87	3.93	1.91	2.23	5.09	1.48	0.69	0.12	0.18	1.07E+00	6.69E-03		2.54E-02	9.86E-01		1.19E+00	2.84E-04	Up	-5.89E-01	3.05E-01		-2.48E+00	3.38E-02		-1.96E+00	5.82E-02		Unigene29091_All//gi|124359163|gb|ABN05686.1|//4.00E-08//Zinc finger, CCHC-type [Medicago truncatula]						nr +
Unigene29092_All	400	6.54	7.09	4.66	7.22	4.91	6.77	51.26	21.52	19.22	1.17E-01	7.46E-01		-4.89E-01	2.38E-01		-5.58E-01	1.24E-01		-9.25E-02	8.10E-01		-1.25E+00	1.42E-26	Down	-1.42E+00	6.72E-33	Down	Unigene29092_All//gi|192910904|gb|ACF06560.1|//6.00E-08//ribosomal protein L35A [Elaeis guineensis]	Unigene29092_All//1.00E-08//AT1G74270| 60S ribosomal protein L35a (RPL35aC)	Unigene29092_All//2.00E-126//gi|11204507|gb|BF273437.1|BF273437		ko03010|Ribosome	nr -
Unigene29093_All	442	3.08	5.04	3.61	4.73	2.96	3.37	4.50	2.74	0.81	7.13E-01	9.64E-02		2.32E-01	6.46E-01		-6.77E-01	1.17E-01		-4.89E-01	3.03E-01		-7.13E-01	8.37E-02		-2.47E+00	2.18E-07	Down			Unigene29093_All//3.00E-42//ES808780				
Unigene29095_All	398	0.39	0.25	0.40	5.63	3.81	9.87	3.82	7.88	14.71	-6.31E-01	7.27E-01		2.54E-02	1.00E+00		-5.65E-01	1.81E-01		8.10E-01	8.64E-03		1.04E+00	9.81E-04	Up	1.94E+00	4.76E-15	Up			Unigene29095_All//2.00E-71//DW234218				
Unigene29096_All	622	9.08	4.15	10.96	2.64	2.71	1.09	0.00	1.08	0.13	-1.13E+00	1.06E-05	Down	2.71E-01	2.75E-01		3.76E-02	9.55E-01		-1.28E+00	1.42E-02		1.01E+01	7.64E-05	Up	7.00E+00	4.04E-01		Unigene29096_All//gi|1360725|emb|CAA87068.1|//1.00E-51//non-photosynthetic ferredoxin [Citrus sinensis]	Unigene29096_All//3.00E-37//AT2G27510| ATFD3 (ferredoxin 3); 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding	Unigene29096_All//5.00E-116//gi|164252574|gb|ES826438.1|ES826438		ko00195|Photosynthesis	GO:0006091//GO:0043169//GO:0051536	nr +
Unigene29098_All	472	68.84	38.32	28.88	899.72	522.15	540.43	241.59	139.02	95.88	-8.45E-01	3.06E-18		-1.25E+00	7.08E-33	Down	-7.85E-01	1.86E-250		-7.35E-01	2.80E-196		-7.97E-01	7.75E-69		-1.33E+00	1.58E-163	Down	Unigene29098_All//gi|66271029|gb|AY443792.1|//3.00E-37//E6-3 [Gossypium hirsutum]	Unigene29098_All//6.00E-07//AT2G33850| unknown protein	Unigene29098_All//6.00E-164//TC136014			GO:0016772//GO:0030312	nr +
Unigene291_All	2866	19.73	5.41	5.76	56.94	23.50	17.48	107.54	114.01	46.97	-1.87E+00	1.67E-105	Down	-1.78E+00	2.89E-95	Down	-1.28E+00	6.48E-217	Down	-1.70E+00	3.04E-291	Down	8.43E-02	1.28E-03		-1.20E+00	0.00E+00	Down	Unigene291_All//gi|38050296|gb|AAR10767.1|//0.00E+00//potential Zn/Cd heavy metal transporter [Arabidopsis thaliana]	Unigene291_All//0.00E+00//AT4G30110| HMA2; cadmium-transporting ATPase	Unigene291_All//0.00E+00//C0092545				nr -
Unigene2910_All	1892	1.38	1.23	1.35	3.16	2.93	2.22	5.48	2.85	2.21	-1.67E-01	6.59E-01		-3.35E-02	9.49E-01		-1.09E-01	7.04E-01		-5.09E-01	3.80E-02		-9.42E-01	5.06E-09		-1.31E+00	3.21E-15	Down	Unigene2910_All//gi|297808335|ref|XP_002872051.1|//2.00E-68//prenylcysteine alpha-carboxyl methyltransferase 14A [Arabidopsis lyrata subsp. lyrata] >gi|297317888|gb|EFH48310.1| prenylcysteine alpha-carboxyl methyltransferase 14A [Arabidopsis lyrata subsp. lyrata]	Unigene2910_All//2.00E-62//AT5G23320| ATSTE14A (ARABIDOPSIS HOMOLOG OF YEAST STE14 A); carboxyl-O-methyltransferase/ protein-S-isoprenylcysteine O-methyltransferase	Unigene2910_All//0.00E+00//TC163487			GO:0003880//GO:0006479//GO:0009738//GO:0009791//GO:0031224//GO:0031410//GO:0043231//GO:0048513	nr +
Unigene29100_All	636	1.48	0.16	1.00	3.21	1.30	0.64	20.61	4.67	8.46	-3.22E+00	6.77E-04	Down	-5.60E-01	4.39E-01		-1.31E+00	2.38E-03		-2.33E+00	5.35E-06	Down	-2.14E+00	2.64E-36	Down	-1.29E+00	1.57E-18	Down			Unigene29100_All//0.00E+00//TC150182				
Unigene29101_All	225	15.35	9.68	12.31	23.69	17.91	14.25	43.78	28.42	13.81	-6.64E-01	4.45E-02		-3.19E-01	3.91E-01		-4.04E-01	1.20E-01		-7.33E-01	4.07E-03		-6.23E-01	1.22E-04		-1.66E+00	2.09E-20	Down			Unigene29101_All//9.00E-112//TC154688				
Unigene29102_All	290	1.80	6.29	1.84	2.06	2.26	2.02	0.73	1.01	0.55	1.80E+00	6.20E-04	Up	2.54E-02	9.99E-01		1.30E-01	9.05E-01		-2.59E-02	9.64E-01		4.69E-01	7.06E-01		-4.08E-01	7.55E-01								
Unigene29104_All	390	61.04	33.91	31.54	191.21	192.66	159.35	21.79	6.97	10.11	-8.48E-01	1.18E-13		-9.53E-01	9.41E-16		1.09E-02	8.94E-01		-2.63E-01	8.73E-06		-1.65E+00	6.94E-17	Down	-1.11E+00	6.37E-10	Down	Unigene29104_All//gi|242129044|gb|ACS83601.1|//7.00E-47//ATP synthase delta subunit 1 [Gossypium hirsutum]	Unigene29104_All//1.00E-18//AT5G47030| ATP synthase delta' chain, mitochondrial	Unigene29104_All//0.00E+00//gi|11204580|gb|BF273510.1|BF273510		ko00190|Oxidative phosphorylation	GO:0000275//GO:0006970//GO:0015078//GO:0015986//GO:0019829//GO:0032359//GO:0046914	nr +
Unigene29106_All	654	62.16	126.75	114.48	54.84	107.68	66.36	13.19	21.15	17.30	1.03E+00	1.52E-62	Up	8.81E-01	1.44E-42		9.73E-01	1.07E-57		2.75E-01	6.43E-04		6.82E-01	4.28E-07		3.92E-01	8.15E-03		Unigene29106_All//gi|21552998|gb|AAM62421.1|AF515799_1//3.00E-13//Drm3 [Pisum sativum]	Unigene29106_All//1.00E-12//AT1G56220| dormancy/auxin associated family protein	Unigene29106_All//1.00E-175//gi|164339000|gb|ES814447.1|ES814447				nr +

Unigene2911_All	1528	5.48	3.02	10.52	40.20	35.34	10.17	29.94	110.51	11.50	-8.60E-01	1.92E-05		9.42E-01	1.12E-10		-1.86E-01	4.90E-03		-1.98E+00	3.48E-135	Down	1.88E+00	0.00E+00	Up	-1.38E+00	1.10E-69	Down	Unigene2911_All//gi|15236455|ref|NP_192569.1|//1.00E-128//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|5262202|emb|CAB45799.1|nodulin-like protein [Arabidopsis thaliana] >gi|7267470|emb|CAB77954.1|nodulin-like protein [Arabidopsis thaliana]	Unigene2911_All//3.00E-116//AT4G08290| nodulin MtN21 family protein	Unigene2911_All//0.00E+00//TC178624				nr -
Unigene29111_All	284	3.68	1.25	6.00	3.86	6.18	6.84	7.89	7.21	3.09	-1.56E+00	2.67E-02		7.04E-01	1.81E-01		6.80E-01	1.81E-01		8.25E-01	8.28E-02		-1.30E-01	7.42E-01		-1.35E+00	3.87E-04	Down				Unigene29111_All//7.00E-70//ES829746				
Unigene29112_All	638	0.90	0.71	1.50	5.86	3.83	1.20	0.53	0.00	0.12	-3.36E-01	6.90E-01		7.36E-01	3.23E-01		-6.12E-01	4.49E-02		-2.28E+00	2.87E-10	Down	-9.05E+00	1.17E-02		-2.09E+00	1.07E-01		Unigene29112_All//gi|3513745|gb|AAC33961.1|//7.00E-42//contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]	Unigene29112_All//5.00E-24//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene29112_All//0.00E+00//TC145217				nr +
Unigene29113_All	291	5.03	4.70	3.66	0.86	1.42	1.71	2.76	8.62	2.60	-9.87E-02	8.47E-01		-4.60E-01	4.10E-01		7.30E-01	5.86E-01		9.96E-01	3.94E-01		1.64E+00	1.71E-05	Up	-8.59E-02	9.05E-01		Unigene29113_All//gi|255561616|ref|XP_002521818.1|//2.00E-14//conserved hypothetical protein [Ricinus communis] >gi|223539031|gb|EEF40628.1|conserved hypothetical protein [Ricinus communis]		Unigene29113_All//5.00E-09//CA994077				nr -
Unigene29114_All	401	0.52	3.92	1.99	2.24	1.29	2.03	2.64	0.83	1.89	2.91E+00	1.58E-05	Up	1.93E+00	3.42E-02		-7.96E-01	2.75E-01		-1.41E-01	8.48E-01		-1.66E+00	8.55E-03		-4.82E-01	3.98E-01									
Unigene29117_All	300	104.64	253.85	139.69	53.30	109.85	136.85	25.93	37.89	45.28	1.28E+00	2.81E-81	Up	4.17E-01	8.19E-07		1.04E+00	2.49E-30	Up	1.36E+00	5.87E-52	Up	5.47E-01	2.62E-04		8.04E-01	2.68E-09		Unigene29117_All//gi|1732363|gb|AAC06385.1|//4.00E-27//early fruit mRNA [Malus x domestica]	Unigene29117_All//2.00E-07//AT2G25670| unknown protein	Unigene29117_All//2.00E-61//gi|84173969|gb|DR462617.1|DR462617			GO:0046914	nr +
Unigene29118_All	429	1.95	5.79	4.22	2.90	3.61	2.84	1.87	1.17	0.56	1.57E+00	2.52E-04	Up	1.11E+00	3.00E-02		3.15E-01	5.97E-01		-3.03E-02	9.47E-01		-6.80E-01	3.53E-01		-1.75E+00	1.55E-02					Unigene29118_All//0.00E+00//ES806016				
Unigene29119_All	731	1.22	0.42	0.80	8.52	4.24	2.53	1.56	1.20	0.05	-1.55E+00	4.56E-02		-6.03E-01	4.18E-01		-1.01E+00	4.65E-06	Down	-1.75E+00	5.44E-12	Down	-3.79E-01	5.32E-01		-4.84E+00	2.34E-07	Down				Unigene29119_All//0.00E+00//DW498663				
Unigene2912_All	370	6.36	0.82	2.59	3.50	2.98	6.59	10.51	10.39	21.00	-2.95E+00	3.71E-08	Down	-1.30E+00	3.68E-03		-2.33E-01	7.05E-01		9.13E-01	2.67E-02		-1.66E-02	9.87E-01		9.98E-01	8.52E-08		Unigene2912_All//gi|115445459|ref|NP_001046509.1|//2.00E-10//Os02g0267000 [Oryza sativa Japonica Group] >gi|113536040|dbj|BAF08423.1|Os02g0267000 [Oryza sativa Japonica Group]	Unigene2912_All//4.00E-11//AT3G24590| PLSP1 (plastidic type I signal peptidase 1); peptidase	Unigene2912_All//8.00E-166//gi|73865305|gb|DT468043.1|DT468043		ko03060|Protein export	GO:0019538//GO:0031224//GO:0070011	nr +
Unigene29121_All	818	0.00	0.00	0.00	4.14	0.00	0.61	61.40	49.00	55.91	null	null		null	null		-1.20E+01	1.66E-25	Down	-2.77E+00	1.56E-11	Down	-3.26E-01	1.03E-06		-1.35E-01	5.30E-02		Unigene29121_All//gi|297832496|ref|XP_002884130.1|//2.00E-29//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329970|gb|EFH60389.1|protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29121_All//9.00E-19//AT2G18370| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene29121_All//0.00E+00//gi|109826977|gb|DR225685.1|DR225685			GO:0005488//GO:0006810	nr -
Unigene29125_All	579	1.17	2.45	1.29	2.58	2.14	3.74	2.63	0.51	1.03	1.06E+00	6.14E-02		1.32E-01	8.64E-01		-2.70E-01	6.17E-01		5.37E-01	2.42E-01		-2.38E+00	2.15E-05	Down	-1.35E+00	4.52E-03		Unigene29125_All//gi|297807463|ref|XP_002871615.1|//1.00E-33//ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317452|gb|EFH47674.1|ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29125_All//4.00E-34//AT5G14360| ubiquitin family protein	Unigene29125_All//1.00E-66//gi|109877833|gb|DW506806.1|DW506806			GO:0043231//GO:0043412	nr -
Unigene29126_All	422	2.11	0.00	0.50	3.66	4.65	1.50	1.50	0.89	1.79	-1.10E+01	2.86E-05	Down	-2.06E+00	1.78E-02		3.46E-01	5.18E-01		-1.29E+00	1.75E-02		-7.54E-01	3.73E-01		2.55E-01	7.07E-01		Unigene29126_All//gi|186510389|ref|NP_189115.3|//1.00E-12//ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene29126_All//9.00E-14//AT3G24715| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase				GO:0016301	nr -
Unigene29128_All	1035	0.51	1.08	0.51	2.74	1.43	1.96	1.47	1.13	3.16	1.09E+00	9.57E-02		2.55E-02	9.99E-01		-9.39E-01	7.35E-03		-4.83E-01	2.20E-01		-3.79E-01	4.49E-01		1.10E+00	2.76E-04	Up	Unigene29128_All//gi|186511352|ref|NP_191849.2|//8.00E-08//zinc ion binding [Arabidopsis thaliana]		Unigene29128_All//3.00E-50//ES850162				nr -
Unigene29129_All	310	101.27	30.73	33.84	286.19	232.83	419.58	82.79	72.00	79.42	-1.72E+00	1.39E-52	Down	-1.58E+00	5.60E-45	Down	-2.98E-01	3.44E-09		5.52E-01	3.43E-36		-2.02E-01	4.84E-02		-5.99E-02	6.17E-01		Unigene29129_All//gi|7340791|emb|CAA63107.1|//6.00E-28//ribosomal protein L23 [Spinacia oleracea]	Unigene29129_All//1.00E-17//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene29129_All//7.00E-169//TC143192		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene2913_All	1131	1.99	0.72	0.71	2.51	2.16	2.88	5.46	7.50	13.35	-1.47E+00	9.69E-04	Down	-1.49E+00	1.37E-03		-2.16E-01	5.92E-01		1.96E-01	6.43E-01		4.59E-01	1.03E-02		1.29E+00	3.72E-21	Up	Unigene2913_All//gi|226501412|ref|NP_001149530.1|//5.00E-26//LOC100283156 [Zea mays] >gi|195627824|gb|ACG35742.1|peptidase/ serine-type peptidase [Zea mays]	Unigene2913_All//1.00E-25//AT3G24590| PLSP1 (plastidic type I signal peptidase 1); peptidase	Unigene2913_All//0.00E+00//TC133800		ko03060|Protein export	GO:0003676//GO:0009534//GO:0009668//GO:0010467//GO:0019538//GO:0030124//GO:0031967//GO:0070011	nr +
Unigene29130_All	483	136.27	105.12	119.73	144.39	130.90	209.36	151.26	75.80	58.89	-3.75E-01	5.67E-09		-1.87E-01	7.42E-03		-1.42E-01	2.84E-02		5.36E-01	8.04E-27		-9.97E-01	2.16E-64		-1.36E+00	2.10E-108	Down	Unigene29130_All//gi|56311398|emb|CAI29267.1|//2.00E-52//coatomer zeta2 subunit [Medicago truncatula]	Unigene29130_All//8.00E-45//AT3G09800| protein binding	Unigene29130_All//0.00E+00//TC148180			GO:0051234	nr +
Unigene29131_All	959	0.44	0.42	0.28	2.70	2.80	7.35	18.08	24.36	24.01	-4.63E-02	9.80E-01		-6.53E-01	5.94E-01		5.23E-02	9.12E-01		1.44E+00	3.57E-10	Up	4.31E-01	1.92E-05		4.10E-01	3.80E-05		Unigene29131_All//gi|224075846|ref|XP_002304794.1|//4.00E-64//type-a response regulator [Populus trichocarpa] >gi|222842226|gb|EEE79773.1|type-a response regulator [Populus trichocarpa]	Unigene29131_All//4.00E-54//AT2G41310| ATRR3 (RESPONSE REGULATOR 3); transcription regulator/ two-component response regulator	Unigene29131_All//0.00E+00//gi|3326361|gb|AI055247.1|AI055247	ARR-B	ko04712|Circadian rhythm - plant	GO:0004871//GO:0006351//GO:0023060	nr +
Unigene29132_All	1175	1.78	0.26	0.32	0.51	0.35	1.11	2.27	4.16	0.95	-2.78E+00	6.12E-07	Down	-2.49E+00	6.97E-06	Down	-5.33E-01	5.62E-01		1.13E+00	6.33E-02		8.77E-01	3.08E-04		-1.26E+00	2.49E-04	Down	Unigene29132_All//gi|281185490|sp|C0LGG6.2|Y5189_ARATH//1.00E-108//RecName: Full=Probable LRR receptor-like protein kinase At1g51890; Flags: Precursor >gi|9802790|gb|AAF99859.1|AC015448_9 Putative protein kinase [Arabidopsis thaliana]	Unigene29132_All//1.00E-105//AT1G51890| leucine-rich repeat protein kinase, putative			ko04626|Plant-pathogen interaction		nr +
Unigene29133_All	817	34.26	30.39	50.64	7.13	9.86	2.32	0.10	0.10	0.68	-1.73E-01	1.18E-01		5.64E-01	3.39E-11		4.67E-01	2.02E-02		-1.62E+00	3.77E-10	Down	-1.68E-02	1.01E+00		2.72E+00	9.38E-03		Unigene29133_All//gi|15222665|ref|NP_173946.1|//3.00E-66//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|28950717|gb|AAO63282.1|At1g26220 [Arabidopsis thaliana]	Unigene29133_All//5.00E-65//AT1G26220| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene29133_All//0.00E+00//TC172591			GO:0009536//GO:0016407	nr -
Unigene29135_All	3652	0.09	0.03	0.00	0.03	0.04	0.25	10.45	3.54	5.56	-1.63E+00	2.76E-01		-6.43E+00	4.91E-02		4.66E-01	8.77E-01		3.18E+00	9.74E-04	Up	-1.56E+00	4.75E-68	Down	-9.10E-01	3.25E-30		Unigene29135_All//gi|263505419|sp|C0LGV1.1|RCH1_ARATH//0.00E+00//RecName: Full=LRR receptor-like serine/threonine-protein kinase RCH1; AltName: Full=Protein ROOT CLAVATA-HOMOLOG1 1; Flags: Precursor >gi|224589709|gb|ACN59386.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene29135_All//0.00E+00//AT5G48940| leucine-rich repeat transmembrane protein kinase, putative	Unigene29135_All//9.00E-63//ES792979			GO:0004672//GO:0005488	nr -
Unigene29136_All	3980	0.00	0.00	0.00	0.05	0.02	0.00	2.34	0.86	0.73	null	null		null	null		-1.53E+00	4.16E-01		-5.65E+00	1.34E-01		-1.44E+00	2.73E-15	Down	-1.68E+00	1.62E-19	Down	Unigene29136_All//gi|263505419|sp|C0LGV1.1|RCH1_ARATH//0.00E+00//RecName: Full=LRR receptor-like serine/threonine-protein kinase RCH1; AltName: Full=Protein ROOT CLAVATA-HOMOLOG1 1; Flags: Precursor >gi|224589709|gb|ACN59386.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene29136_All//0.00E+00//AT5G48940| leucine-rich repeat transmembrane protein kinase, putative	Unigene29136_All//7.00E-33//ES792979			GO:0004713//GO:0004871//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0032559	nr -
Unigene29138_All	684	10.86	8.07	10.43	8.96	9.41	1.52	0.00	0.00	0.47	-4.28E-01	4.79E-02		-5.83E-02	8.01E-01		7.17E-02	8.23E-01		-2.56E+00	7.59E-19	Down	null	null		8.86E+00	1.34E-02		Unigene29138_All//gi|225425630|ref|XP_002271277.1|//6.00E-11//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296086343|emb|CBI31932.3|unnamed protein product [Vitis vinifera]						nr -
Unigene29139_All	633	0.00	0.00	1.18	1.81	0.76	0.86	1.07	0.26	1.70	null	null		1.02E+01	3.27E-04	Up	-1.25E+00	4.15E-02		-1.08E+00	9.66E-02		-2.02E+00	1.98E-02		6.69E-01	2.44E-01		Unigene29139_All//gi|15238761|ref|NP_200163.1|//9.00E-57//AT0PT9 (ARABIDOPSIS THALIANA OLIGOPEPTIDE TRANSPORTER 9); oligopeptide transporter [Arabidopsis thaliana] >gi|67460973|sp|Q9FJ82.1|OPT9_ARATH RecName: Full=Oligopeptide transporter 9; Short=AtOPT9 >gi|9759190|dbj|BAB09727.1|isp4 protein [Arabidopsis thaliana]	Unigene29139_All//4.00E-57//AT5G53510| AT0PT9 (ARABIDOPSIS THALIANA OLIGOPEPTIDE TRANSPORTER 9); oligopeptide transporter				GO:0015197//GO:0015833//GO:0016020	nr +
Unigene2914_All	1382	25.86	26.54	61.46	33.49	25.47	34.67	73.42	8.11	18.07	3.78E-02	7.02E-01		1.25E+00	4.32E-85	Up	-3.95E-01	3.08E-08		5.03E-02	6.40E-01		-3.18E+00	0.00E+00	Down	-2.02E+00	2.15E-264	Down	Unigene2914_All//gi|121755805|gb|ABM64800.1|//0.00E+00//dihydroflavonol 4-reductase [Gossypium hirsutum]	Unigene2914_All//1.00E-146//AT5G42800| DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase	Unigene2914_All//0.00E+00//TC147298		ko00941|Flavonoid biosynthesis	GO:0008152//GO:0048037	nr +
Unigene29141_All	330	106.07	51.44	50.51	192.92	154.44	197.49	251.25	129.95	121.57	-1.04E+00	1.36E-27	Down	-1.07E+00	1.25E-27	Down	-3.21E-01	1.05E-07		3.38E-02	6.98E-01		-9.51E-01	1.44E-67		-1.05E+00	2.47E-81	Down	Unigene29141_All//gi|2104681|emb|CAA66481.1|//7.00E-41//transcription factor [Vicia faba var. minor]	Unigene29141_All//1.00E-25//AT4G17520| nuclear RNA-binding protein, putative	Unigene29141_All//0.00E+00//TC141608				nr +
Unigene29143_All	760	1.17	4.87	0.28	2.75	2.31	2.61	1.11	1.43	1.73	2.06E+00	2.09E-08	Up	-2.06E+00	1.78E-02		-2.53E-01	5.92E-01		-7.43E-02	8.82E-01		3.62E-01	5.69E-01		6.37E-01	2.11E-01		Unigene29143_All//gi|15229447|ref|NP_188986.1|//3.00E-14//EDA6 (EMBRYO SAC DEVELOPMENT ARREST 6) [Arabidopsis thaliana]	Unigene29143_All//7.00E-16//AT5G44060| unknown protein	Unigene29143_All//0.00E+00//TC177753			GO:0003006//GO:0009553	nr -
Unigene29144_All	767	0.82	1.12	0.14	32.60	19.57	18.90	5.18	0.60	0.99	4.56E-01	5.46E-01		-2.56E+00	2.72E-02		-7.36E-01	1.76E-13		-7.87E-01	1.73E-13		-3.11E+00	4.60E-17	Down	-2.39E+00	1.60E-13	Down	Unigene29144_All//gi|225450273|ref|XP_002267267.1|//5.00E-19//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene29144_All//1.00E-10//AT2G31930| unknown protein	Unigene29144_All//0.00E+00//gi|164302382|gb|EV492011.1|EV492011				nr -

Unigene29145_All	669	0.47	2.95	0.48	1.49	6.28	1.89	4.11	1.37	1.07	2.65E+00	3.05E-06	Up	2.56E-02	1.00E+00		2.08E+00	1.12E-10	Up	3.44E-01	6.24E-01		-1.58E+00	1.11E-05	Down	-1.94E+00	1.45E-07	Down	Unigene29145_All//gi|15234987|ref|NP_192765.1|//9.00E-20//wound-responsive family protein [Arabidopsis thaliana] >gi|3695408|gb|AAC62808.1| contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi|4538956|emb|CAB39780.1| probable wound-induced protein [Arabidopsis thaliana] >gi|7267724|emb|CAB78150.1| probable wound-induced protein [Arabidopsis thaliana] >gi|21553934|gb|AAM63015.1| probable wound-induced protein [Arabidopsis thaliana] >gi|90962948|gb|ABE02398.1| At4g10270 [Arabidopsis thaliana]	Unigene29145_All//2.00E-16//AT4G10270| wound-responsive family protein	Unigene29145_All//1.00E-110//gi|109881310|gb|DW510280.1|DW510280			GO:0006950	nr -
Unigene29146_All	662	5.06	5.74	11.02	1.43	1.20	0.89	0.00	0.00	0.12	1.83E-01	6.01E-01		1.12E+00	9.92E-07	Up	-2.57E-01	7.27E-01		-6.89E-01	3.58E-01		null	null		6.91E+00	4.04E-01		Unigene29146_All//gi|30687365|ref|NP_189056.2|//8.00E-14//FMA (FAMA); DNA binding / transcription activator/ transcription factor [Arabidopsis thaliana] >gi|75283553|sp|Q56YJ8.1|FAMA_ARATH RecName: Full=Transcription factor FAMA; AltName: Full=Transcription factor EN 14; AltName: Full=bHLH transcription factor bHLH097; AltName: Full=Basic helix-loop-helix protein 97; Short=bHLH 97; Short=AtbHLH97 >gi|114213507|gb|ABI54336.1| At3g24140 [Arabidopsis thaliana]	Unigene29146_All//4.00E-15//AT3G24140| FMA (FAMA); DNA binding / transcription activator/ transcription factor		bHLH		GO:0009913//GO:0010468//GO:0010557//GO:0030528//GO:0043231//GO:0045595//GO:0048523	nr -
Unigene29147_All	717	0.44	0.42	0.00	1.81	1.39	0.50	0.77	0.64	3.06	-4.62E-02	9.85E-01		-8.77E+00	4.91E-02		-3.75E-01	5.57E-01		-1.84E+00	3.54E-03		-2.58E-01	7.60E-01		2.00E+00	2.59E-06	Up			Unigene29147_All//6.00E-11//gi|3326269|gb|AI055155.1|AI055155				
Unigene29148_All	852	1.23	0.59	0.25	1.70	1.74	1.96	2.38	0.98	0.42	-1.05E+00	1.20E-01		-2.30E+00	4.70E-03		3.55E-02	9.64E-01		2.10E-01	6.82E-01		-1.28E+00	1.98E-03		-2.50E+00	1.27E-07	Down			Unigene29148_All//7.00E-91//gi|3325955|gb|AI054841.1|AI054841				
Unigene29150_All	428	37.28	103.71	47.90	93.81	171.53	120.72	0.00	0.20	0.74	1.48E+00	4.13E-59	Up	3.61E-01	4.65E-03		8.71E-01	5.39E-50		3.64E-01	3.52E-07		7.61E+00	4.01E-01		9.54E+00	1.34E-02				Unigene29150_All//0.00E+00//gi|109878558|gb|DW507528.1|DW507528				
Unigene29154_All	474	12.36	3.63	5.39	3.15	2.18	0.38	0.18	0.18	0.42	-1.77E+00	9.47E-11	Down	-1.20E+00	4.86E-06	Down	-5.33E-01	3.21E-01		-3.05E+00	7.42E-06	Down	-1.63E-02	1.01E+00		1.24E+00	4.69E-01		Unigene29154_All//gi|11544985|ref|NP_001046272.1|//1.00E-42//Os02g0211200 [Oryza sativa Japonica Group] >gi|113538803|dbj|BAF08186.1| Os02g0211200 [Oryza sativa Japonica Group]	Unigene29154_All//6.00E-42//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative	Unigene29154_All//2.00E-120//TC143249		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006464//GO:0016628//GO:0031224//GO:0032559	nr -
Unigene29156_All	373	6.31	6.52	3.28	6.41	6.46	7.75	18.82	11.32	8.01	4.68E-02	9.20E-01		-9.43E-01	3.08E-02		1.17E-02	9.88E-01		2.74E-01	5.07E-01		-7.34E-01	1.92E-04		-1.23E+00	9.95E-10	Down			Unigene29156_All//4.00E-106//gi|164284664|gb|ES833118.1|ES833118				
Unigene29157_All	559	3.56	5.98	7.72	3.12	4.99	8.97	0.00	0.00	0.00	7.50E-01	2.65E-02		1.12E+00	3.00E-04	Up	6.78E-01	7.29E-02		1.52E+00	5.67E-08	Up	null	null		null	null									
Unigene29159_All	580	2.62	1.05	2.48	2.40	2.67	0.93	5.03	2.52	2.27	-1.32E+00	1.68E-02		-7.77E-02	8.89E-01		1.52E-01	8.29E-01		-1.36E+00	1.87E-02		-9.96E-01	2.42E-03		-1.15E+00	3.57E-04	Down	Unigene29159_All//gi|15419985|gb|AAK97227.1|AF302013_1/6.00E-25//CDK-activating kinase [Medicago sativa subsp. x varia]	Unigene29159_All//1.00E-13//AT1G73690| CDKD1;1 (CYCLIN-DEPENDENT KINASE D1;1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene29159_All//0.00E+00//ES833709		ko03420|Nucleotide excision repair	GO:0004674//GO:0006464//GO:0007049//GO:0032559//GO:0043231//GO:0048869	nr +
Unigene2916_All	2194	2.34	1.78	3.16	8.79	8.63	5.85	18.42	27.01	231.04	-3.94E-01	1.42E-01		4.33E-01	6.76E-02		-2.56E-02	8.62E-01		-5.88E-01	1.42E-06		5.52E-01	2.84E-19		3.65E+00	0.00E+00	Up	Unigene2916_All//gi|224067296|ref|XP_002302453.1|//0.00E+00//cytochrome P450 allene oxide synthase [Populus trichocarpa] >gi|222844179|gb|EEE81726.1| cytochrome P450 allene oxide synthase [Populus trichocarpa]	Unigene2916_All//0.00E+00//AT5G42650| AOS (ALLENE OXIDE SYNTHASE); allene oxide synthase/ hydro-lyase/ oxygen binding	Unigene2916_All//0.00E+00//TC142912		ko00592|alpha-Linolenic acid metabolism	GO:0005506//GO:0016491//GO:0016836	nr +
Unigene29161_All	311	3.03	64.68	31.68	2.88	0.66	0.87	6.66	25.00	8.07	4.42E+00	3.48E-90	Up	3.39E+00	2.38E-35	Up	-2.12E+00	5.22E-03		-1.73E+00	2.81E-02		1.91E+00	8.07E-19	Up	2.77E-01	4.53E-01				Unigene29161_All//4.00E-07//gi|13354866|gb|BG445214.1|BG445214				
Unigene29162_All	515	5.18	1.97	5.17	6.48	5.22	5.61	7.55	5.44	6.11	-1.40E+00	5.02E-04	Down	-3.20E-03	9.93E-01		-3.13E-01	3.85E-01		-2.08E-01	6.08E-01		-4.74E-01	9.39E-02		-3.06E-01	2.79E-01		Unigene29162_All//gi|296932945|gb|ADH89593.1|//2.00E-12//SNF5-type chromatin-remodeling complex protein [Glycine max] >gi|297179845|gb|ADI23919.1| SNF5 [Glycine max]	Unigene29162_All//6.00E-12//AT3G17590| BSH (BUSHY GROWTH); chromatin binding / protein binding	Unigene29162_All//0.00E+00//ES835094			GO:0005488//GO:0005694//GO:0016568//GO:0043231	nr +
Unigene29163_All	721	2.69	0.14	1.18	1.66	1.05	0.81	1.47	1.10	0.61	-4.26E+00	6.09E-09	Down	-1.18E+00	1.70E-02		-6.58E-01	2.90E-01		-1.03E+00	1.06E-01		-4.13E-01	5.15E-01		-1.27E+00	2.97E-02		Unigene29163_All//gi|229609827|gb|ACQ83529.1|//1.00E-36//CBL-interacting protein kinase 13 [Vitis vinifera]	Unigene29163_All//5.00E-34//AT5G45820| CIPK20 (CBL-INTERACTING PROTEIN KINASE 20); kinase/ protein serine/threonine kinase	Unigene29163_All//5.00E-42//gi|13351954|gb|BG442302.1|BG442302		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0023060//GO:0032559	nr +
Unigene29165_All	600	3.49	1.86	2.84	11.54	8.72	4.89	1.97	0.63	0.66	-9.09E-01	4.11E-02		-2.97E-01	5.35E-01		-4.04E-01	6.82E-02		-1.24E+00	3.57E-08	Down	-1.65E+00	5.03E-03		-1.57E+00	5.26E-03		Unigene29165_All//gi|22330712|ref|NP_177940.2|//5.00E-70//APUM7 (Arabidopsis Pumilio 7); RNA binding / binding [Arabidopsis thaliana]	Unigene29165_All//3.00E-71//AT1G78160| APUM7 (Arabidopsis Pumilio 7); RNA binding / binding	Unigene29165_All//0.00E+00//TC156951			GO:0003676//GO:0044424	nr -
Unigene29166_All	567	3.41	5.36	8.26	12.65	9.35	4.38	0.15	0.37	0.14	6.51E-01	6.92E-02		1.28E+00	1.97E-05	Up	-4.36E-01	4.14E-02		-1.53E+00	2.01E-11	Down	1.31E+00	4.47E-01		-8.57E-02	9.72E-01		Unigene29166_All//gi|2865437|gb|AAC02672.1|//1.00E-08//polyprotein [Arabidopsis arenosa]						nr -
Unigene29168_All	942	1.39	0.54	1.58	0.53	0.29	2.49	3.41	1.11	5.29	-1.37E+00	2.40E-02		1.89E-01	7.21E-01		-8.55E-01	4.07E-01		2.24E+00	2.39E-06	Up	-1.62E+00	9.96E-07	Down	6.32E-01	6.61E-03				Unigene29168_All//2.00E-100//DW498164				ESTscan +
Unigene29171_All	1116	5.06	3.59	3.48	5.40	7.47	6.35	0.11	0.90	0.29	-4.97E-01	4.76E-02		-5.40E-01	4.09E-02		4.67E-01	1.79E-02		2.34E-01	3.51E-01		2.98E+00	1.37E-04	Up	1.33E+00	2.93E-01		Unigene29171_All//gi|7076798|emb|CAB75913.1|//1.00E-105//probable serine/threonine-specific protein kinase [Arabidopsis thaliana]	Unigene29171_All//3.00E-106//AT3G55550| lectin protein kinase, putative	Unigene29171_All//0.00E+00//TC142188		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0030246//GO:0031410//GO:0032559	nr -
Unigene29174_All	847	0.00	0.36	0.19	0.12	0.57	0.00	30.50	13.03	32.74	8.49E+00	4.43E-02		7.56E+00	2.39E-01		2.28E+00	7.83E-02		-6.88E+00	4.00E-01		-1.23E+00	2.84E-32	Down	1.02E-01	3.27E-01		Unigene29174_All//gi|288559172|sp|B9HBX2.1|U4978_POPTR/|5.00E-58//RecName: Full=UPF0497 membrane protein 8	Unigene29174_All//4.00E-49//AT5G06200| integral membrane family protein				GO:0016020	nr -
Unigene29175_All	980	0.11	0.00	0.54	1.37	0.32	0.14	2.16	2.56	1.34	-6.74E+00	3.72E-01		2.35E+00	5.87E-02		-2.12E+00	3.41E-04	Down	-3.31E+00	1.08E-05	Down	2.46E-01	5.38E-01		-6.85E-01	7.07E-02		Unigene29175_All//gi|222612692|gb|EEE50824.1|//6.00E-07//hypothetical protein OsJ_31232 [Oryza sativa Japonica Group]	Unigene29175_All//6.00E-05//AT3G31430| unknown protein					nr +
Unigene29176_All	387	25.28	10.34	12.93	42.09	28.83	44.58	49.49	30.13	27.59	-1.29E+00	2.90E-11	Down	-9.67E-01	5.12E-07		-5.46E-01	1.75E-05		8.29E-02	6.41E-01		-7.16E-01	2.67E-10		-8.43E-01	8.08E-14		Unigene29176_All//gi|25091502|sp|Q9LKA5.1|UMP1_ARATH/|1.00E-55//RecName: Full=Uncharacterized protein At3g15000, mitochondrial >gi|16226543|gb|AAL16196.1|AF42842 7_1 AT3g15000/K13M2_14 [Arabidopsis thaliana] >gi|53828613|gb|AAU94431.1| At3g15000 [Arabidopsis thaliana]	Unigene29176_All//5.00E-57//AT3G15000| LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: plastid developmental protein DAG, putative (TAIR:AT3G06790.2); Has 50779 Blast hits to 24732 proteins in 941 species: Archae - 10; Bacteria - 4862; Metazoa - 25623; Fungi - 7071; Plants - 6957; Viruses - 900; Other Eukaryotes - 5356 (source: NCBI BLink).	Unigene29176_All//0.00E+00//ES809586			GO:0046914	nr +
Unigene29177_All	486	821.20	396.81	555.29	290.17	195.77	243.01	366.60	223.51	71.15	-1.05E+00	0.00E+00	Down	-5.65E-01	2.74E-103		-5.68E-01	8.62E-47		-2.56E-01	7.75E-10		-7.14E-01	1.54E-88		-2.37E+00	0.00E+00	Down	Unigene29177_All//gi|974782|emb|CAA88019.1|//1.00E-26//cobalamin-independent methionine synthase [Solenostemon scutellarioides]	Unigene29177_All//1.00E-24//AT5G17920| ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase	Unigene29177_All//0.00E+00//TC171115		ko00270|Cysteine and methionine metabolism	GO:0000097//GO:0008172//GO:0044424//GO:0046914	nr +
Unigene29178_All	646	0.65	1.80	0.08	0.85	2.19	0.70	1.24	2.59	3.64	1.48E+00	2.49E-02		-2.98E+00	6.46E-02		1.37E+00	1.78E-02		-2.79E-01	7.57E-01		1.06E+00	2.09E-02		1.55E+00	5.38E-05	Up			Unigene29178_All//2.00E-32//gi|109868718|gb|DW497694.1|DW497694				
Unigene29180_All	1359	0.00	0.00	0.00	0.00	0.00	0.00	12.04	6.98	47.64	null	null		null	null		null	null		null	null		-7.86E-01	2.36E-10		1.98E+00	1.15E-162	Up			Unigene29180_All//4.00E-75//DT462210				
Unigene29183_All	606	10.79	7.02	4.31	9.04	7.05	3.28	0.56	0.62	0.46	-6.20E-01	7.02E-03		-1.33E+00	1.09E-07	Down	-3.60E-01	1.64E-01		-1.46E+00	2.42E-08	Down	1.53E-01	8.90E-01		-2.79E-01	7.81E-01				Unigene29183_All//0.00E+00//TC168750				
Unigene29187_All	448	2.10	0.23	0.59	2.22	2.77	1.81	1.79	0.84	2.05	-3.22E+00	6.77E-04	Down	-1.82E+00	2.53E-02		3.15E-01	6.29E-01		-2.93E-01	6.89E-01		-1.09E+00	1.29E-01		1.90E-01	7.54E-01		Unigene29187_All//gi|297852834|ref|XP_002894298.1|//3.00E-37//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340140|gb|EFH70557.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29187_All//2.00E-38//AT1G51170| protein kinase family protein				GO:0000166//GO:0004672	nr -
Unigene29188_All	716	0.44	2.26	0.60	2.16	4.71	1.83	1.30	3.44	1.06	2.37E+00	1.02E-04	Up	4.41E-01	6.77E-01		1.13E+00	6.03E-04	Up	-2.38E-01	6.81E-01		1.41E+00	1.76E-04	Up	-2.97E-01	6.31E-01								
Unigene29190_All	258	171.36	69.92	112.07	77.81	66.74	86.65	73.58	39.04	30.42	-1.29E+00	1.59E-48	Down	-6.13E-01	1.03E-13		-2.22E-01	8.22E-02		1.55E-01	2.40E-01		-9.14E-01	4.06E-15		-1.27E+00	4.12E-26	Down	Unigene29190_All//gi|1762130|gb|AAB39827.1|//1.00E-39//chaperonin-60 beta subunit [Solanum tuberosum]	Unigene29190_All//1.00E-39//AT3G13470| chaperonin, putative	Unigene29190_All//2.00E-131//gi|164348799|gb|ES791522.1|ES791522		ko03018|RNA degradation	GO:0005515//GO:0005840//GO:0006457//GO:0009526//GO:0009532//GO:0031981//GO:0032559	nr +
Unigene29193_All	419	10.24	3.99	9.15	3.21	2.05	4.31	0.50	0.20	0.19	-1.36E+00	8.99E-06	Down	-1.62E-01	6.41E-01		-6.44E-01	2.63E-01		4.26E-01	4.19E-01		-1.34E+00	4.30E-01		-1.41E+00	3.80E-01		Unigene29193_All//gi|297849508|ref|XP_002892635.1|//2.00E-29//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297338477|gb|EFH68894.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene29193_All//1.00E-26//AT1G11290| CRR22 (CHLORORESPIRATORY REDUCTION22); endonuclease				GO:0009451//GO:0009536	nr -
Unigene29194_All	964	0.22	0.21	0.22	0.26	0.89	1.50	2.76	4.12	8.76	-4.66E-02	9.88E-01		2.57E-02	1.00E+00		1.79E+00	2.95E-02		2.54E+00	1.16E-04	Up	5.76E-01	3.68E-02		1.66E+00	2.01E-17	Up	Unigene29194_All//gi|115451173|ref|NP_001049187.1|//5.00E-12//Os03g0184100 [Oryza sativa Japonica Group] >gi|108706546|gb|ABF94341.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108706547|gb|ABF94342.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108706548|gb|ABF94343.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547658|dbj|BAF11101.1| Os03g0184100 [Oryza sativa Japonica Group]	Unigene29194_All//3.00E-21//AT5G42900| unknown protein	Unigene29194_All//0.00E+00//TC162745				nr +
Unigene29195_All	811	1.55	0.62	1.18	3.07	2.68	4.23	1.67	0.46	0.59	-1.31E+00	3.41E-02		-3.90E-01	5.38E-01		-1.99E-01	6.31E-01		4.63E-01	1.94E-01		-1.85E+00	9.22E-04	Down	-1.50E+00	3.72E-03		Unigene29195_All//gi|75206826|sp|Q9SM14.1|U496N_ARATH/|1.00E-36//RecName: Full=UPF0496 protein At3g49070	Unigene29195_All//4.00E-38//AT3G49070| unknown protein					nr -

Unigene29196_All	1156	0.36	3.46	0.09	1.55	3.72	7.03	3.58	6.87	13.79	3.26E+00	1.49E-14	Up	-1.98E+00	1.51E-01		1.26E+00	1.06E-05	Up	2.18E+00	4.15E-20	Up	9.39E-01	4.71E-07		1.94E+00	1.53E-39	Up	Unigene29196_All//gi|145333037|ref|NP_001078384.1|//4.00E-14//RTFL12 (ROTUNDIFOLIA LIKE 12) [Arabidopsis thaliana] >gi|42822053|tpg|DAA02281.1| TPA_exp: DVL10 [Arabidopsis thaliana]	Unigene29196_All//2.00E-15//AT4G13395| RTFL12 (ROTUNDIFOLIA LIKE 12)	Unigene29196_All//0.00E+00//DW506251			GO:0043231//GO:0048513	nr +
Unigene29198_All	543	0.67	0.75	0.20	3.49	1.97	5.99	23.05	9.24	8.80	1.46E-01	8.98E-01		-1.78E+00	2.34E-01		-8.26E-01	6.86E-02		7.81E-01	2.43E-02		-1.32E+00	7.31E-18	Down	-1.39E+00	7.33E-20	Down	Unigene29198_All//gi|44681326|gb|AAS47603.1|//2.00E-11//At3g20340 [Arabidopsis thaliana] >gi|45773836|gb|AAS76722.1| At3g20340 [Arabidopsis thaliana]	Unigene29198_All//1.00E-12//AT3G20340| Expression of the gene is downregulated in the presence of paraquat, an inducer of photoxidative stress.	Unigene29198_All//0.00E+00//DW510819				nr +
Unigene29199_All	480	24.42	6.54	11.09	15.88	19.15	20.42	2.55	1.13	0.42	-1.90E+00	7.05E-23	Down	-1.14E+00	1.39E-10	Down	2.71E-01	1.83E-01		3.63E-01	5.68E-02		-1.17E+00	3.41E-02		-2.62E+00	4.02E-05	Down								
Unigene2920_All	1667	3.74	1.12	4.28	3.32	2.11	2.68	3.75	0.80	1.58	-1.73E+00	4.35E-11	Down	1.97E-01	4.10E-01		-6.55E-01	6.03E-03		-3.07E-01	2.68E-01		-2.23E+00	1.55E-18	Down	-1.25E+00	5.86E-09	Down	Unigene2920_All//gi|1708191|sp|Q07423.1|HEX6_RICCO//0.00E+00//RecName: Full=Hexose carrier protein HEX6 >gi|467319|gb|AAA79857.1| hexose carrier protein [Ricinus communis]	Unigene2920_All//7.00E-156//AT5G61520| hexose transporter, putative	Unigene2920_All//0.00E+00//TC166881			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224	nr -
Unigene29200_All	927	0.40	0.11	0.11	0.27	0.45	1.46	1.82	2.84	3.40	-1.85E+00	1.87E-01		-1.78E+00	2.34E-01		7.30E-01	5.86E-01		2.44E+00	2.97E-04	Up	6.39E-01	6.88E-02		8.96E-01	3.24E-03		Unigene29200_All//gi|9665118|gb|AAF97302.1|AC007843_5//4.00E-08//hypothetical protein [Arabidopsis thaliana]		Unigene29200_All//1.00E-138//ES830634			GO:0005488	nr +
Unigene29201_All	559	1.03	0.54	1.14	3.56	2.40	2.02	7.49	4.64	15.32	-9.21E-01	3.43E-01		1.51E-01	8.56E-01		-5.69E-01	2.13E-01		-8.20E-01	7.58E-02		-6.92E-01	8.98E-03		1.03E+00	5.97E-09	Up	Unigene29201_All//gi|75127082|sp|Q6NN02.1|Y4445_ARATH//6.00E-19//RecName: Full=Uncharacterized protein At4g14450, chloroplastic; Flags: Precursor >gi|38603896|gb|AAR24693.1| At4g14450 [Arabidopsis thaliana] >gi|41349908|gb|AAS00339.1| At4g14450 [Arabidopsis thaliana]	Unigene29201_All//4.00E-14//AT4G14450| unknown protein	Unigene29201_All//0.00E+00//TC160850				nr +
Unigene29203_All	727	346.17	166.09	433.84	126.49	86.63	76.60	0.00	0.17	0.00	-1.06E+00	5.53E-199	Down	3.26E-01	7.40E-30		-5.46E-01	1.53E-28		-7.24E-01	1.17E-41		7.43E+00	2.40E-01		null	null		Unigene29203_All//gi|211906510|gb|ACJ11748.1|//3.00E-72//major latex-like protein [Gossypium hirsutum]	Unigene29203_All//2.00E-47//AT1G24020| MLP423 (MLP-LIKE PROTEIN 423)	Unigene29203_All//0.00E+00//gi|164365930|gb|ES812558.1|ES812558			GO:0006950//GO:0044464	nr +
Unigene29205_All	593	45.62	74.51	57.74	98.37	155.05	288.65	686.75	1086.76	1148.94	7.08E-01	3.30E-18		3.40E-01	3.77E-04		6.56E-01	1.50E-38		1.55E+00	1.21E-262	Up	6.62E-01	7.24E-279		7.42E-01	0.00E+00		Unigene29205_All//gi|89274062|dbj|BAE80740.1|//3.00E-85//cysteine proteinase [Platycodon grandiflorus]	Unigene29205_All//1.00E-73//AT1G47128| RD21 (responsive to dehydration 21); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene29205_All//0.00E+00//TC133010			GO:0004175//GO:0016628//GO:0019538	nr -
Unigene29206_All	1586	0.46	0.06	0.47	1.19	0.17	0.68	2.21	3.74	9.17	-2.85E+00	6.26E-03		2.57E-02	9.95E-01		-2.78E+00	1.25E-07	Down	-8.04E-01	9.25E-02		7.58E-01	4.64E-04		2.05E+00	9.81E-39	Up	Unigene29206_All//gi|115448007|ref|NP_001047783.1|//1.00E-118//Os02g0689200 [Oryza sativa Japonica Group] >gi|113537314|dbj|BAF09697.1| Os02g0689200 [Oryza sativa Japonica Group]	Unigene29206_All//4.00E-111//AT1G44750| ATPUP11; purine transmembrane transporter	Unigene29206_All//0.00E+00//TC165168				nr +
Unigene29208_All	780	1.48	6.04	5.46	79.06	33.60	40.53	4511.35	2334.18	2191.38	2.03E+00	2.22E-10	Up	1.89E+00	2.70E-08	Up	-1.23E+00	9.35E-78	Down	-9.64E-01	1.27E-45		-9.51E-01	0.00E+00		-1.04E+00	0.00E+00	Down	Unigene29208_All//gi|48426429|emb|CAA66109.3|//2.00E-18//specific tissue protein 2 [Cicer arietinum]		Unigene29208_All//0.00E+00//TC147395				nr +
Unigene29212_All	361	2.17	0.28	1.18	2.76	1.43	1.50	1.76	0.00	0.00	-2.95E+00	3.66E-03		-8.81E-01	2.95E-01		-9.48E-01	1.58E-01		-8.78E-01	2.20E-01		-1.08E+01	1.23E-04	Down	-1.08E+01	7.11E-05	Down			Unigene29212_All//4.00E-10//gi|78325606|gb|DT545880.1|DT545880				
Unigene29213_All	1568	1.27	0.36	0.34	15.98	8.76	1.81	0.97	0.35	0.84	-1.83E+00	2.47E-04	Down	-1.90E+00	3.07E-04	Down	-8.67E-01	8.34E-18		-3.14E+00	3.93E-94	Down	-1.49E+00	2.91E-03		-2.11E-01	6.41E-01		Unigene29213_All//gi|15226011|ref|NP_182180.1|//0.00E+00//LAC6 (laccase 6); laccase [Arabidopsis thaliana] >gi|75338836|sp|Q9ZPY2.1|LAC6_ARATH RecName: Full=Laccase-6; AltName: Full=Benzenediol:oxygen oxidoreductase 6; AltName: Full=Urishiol oxidase 6; AltName: Full=Diphenol oxidase 6; Flags: Precursor	Unigene29213_All//0.00E+00//AT2G46570| LAC6 (laccase 6); laccase	Unigene29213_All//2.00E-111//TC131302		ko00910|Nitrogen metabolism/ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr +
Unigene29215_All	200	212.68	74.99	106.50	34.62	40.81	58.04	10.36	7.94	6.18	-1.50E+00	1.41E-58	Down	-9.98E-01	7.00E-30		2.37E-01	3.00E-01		7.45E-01	5.04E-06		-3.83E-01	3.73E-01		-7.46E-01	5.19E-02		Unigene29215_All//gi|154354069|gb|ABS76144.1|//1.00E-32//chloroplast omega-3 fatty acid desaturase [Elaeis oleifera]	Unigene29215_All//8.00E-33//AT5G05580| FAD8 (FATTY ACID DESATURASE 8); omega-3 fatty acid desaturase	Unigene29215_All//4.00E-86//TC146456		ko01040|Biosynthesis of unsaturated fatty acids	GO:0003824//GO:0006631//GO:0009941	nr +
Unigene29216_All	638	196.74	76.32	103.24	45.05	61.85	55.57	20.61	11.46	8.68	-1.37E+00	1.32E-148	Down	-9.30E-01	9.44E-78		4.57E-01	5.77E-09		3.03E-01	7.49E-04		-8.46E-01	1.65E-09		-1.25E+00	8.70E-18	Down	Unigene29216_All//gi|1694625|dbj|BAA11475.1|//9.00E-51//omega-3 fatty acid desaturase [Nicotiana tabacum] >gi|21668486|dbj|BAC01274.1| plastid omega-3 fatty acid desaturase [Nicotiana tabacum]	Unigene29216_All//3.00E-48//AT5G05580| FAD8 (FATTY ACID DESATURASE 8); omega-3 fatty acid desaturase	Unigene29216_All//0.00E+00//gi|48804622|gb|CO105936.1|CO105936		ko01040|Biosynthesis of unsaturated fatty acids	GO:0006631//GO:0009941//GO:0016705	nr +
Unigene29218_All	639	0.33	0.40	1.17	1.56	1.89	0.92	1.52	0.00	1.43	2.76E-01	8.43E-01		1.83E+00	5.05E-02		2.75E-01	7.00E-01		-7.63E-01	2.89E-01		-1.06E+01	5.83E-07	Down	-8.58E-02	8.91E-01		Unigene29218_All//gi|22796151|emb|CAD42234.1|//1.00E-97//kinesin-like protein [Arabidopsis thaliana]	Unigene29218_All//7.00E-99//AT3G43210| TES (TETRASPORE); microtubule motor				GO:0000226//GO:0003774//GO:0007349//GO:0009536//GO:0015630//GO:0032559//GO:0033206//GO:0048229	nr -
Unigene29220_All	693	0.08	0.58	0.61	0.72	0.60	0.52	7.99	20.93	53.12	2.95E+00	5.91E-02		3.03E+00	5.73E-02		-2.70E-01	8.02E-01		-4.63E-01	6.59E-01		1.39E+00	3.78E-22	Up	2.73E+00	5.01E-136	Up			Unigene29220_All//8.00E-07//TC174042				
Unigene29222_All	493	3.18	2.06	7.13	4.24	6.71	3.21	0.60	0.42	0.48	-6.31E-01	2.31E-01		1.16E+00	8.51E-04	Up	6.60E-01	5.16E-02		-4.04E-01	3.93E-01		-5.02E-01	6.78E-01		-3.08E-01	7.75E-01		Unigene29222_All//gi|12323763|gb|AAG51843.1|AC010926_6//7.00E-40//DAG-like protein; 97518-96580 [Arabidopsis thaliana] >gi|124301130|gb|ABN04817.1| At1g72530 [Arabidopsis thaliana]	Unigene29222_All//4.00E-41//AT1G72530| plastid developmental protein DAG, putative	Unigene29222_All//0.00E+00//TC132433			GO:0046914	nr -
Unigene29223_All	1241	0.00	0.08	0.00	0.00	0.06	0.44	28.58	13.77	25.20	6.35E+00	3.87E-01		null	null		5.79E+00	6.10E-01		8.77E+00	2.45E-03		-1.05E+00	1.32E-34	Down	-1.82E-01	2.71E-02		Unigene29223_All//gi|225426040|ref|XP_002274274.1|//9.00E-57//PREDICTED: similar to AT4g27960 [Vitis vinifera] >gi|225462705|ref|XP_002267153.1| PREDICTED: similar to AT4g27960 [Vitis vinifera] >gi|224812550|gb|ACN64930.1| ubiquitin-conjugating enzyme E2 [Vigna radiata]	Unigene29223_All//2.00E-57//AT5G41700| UBC8 (UBIQUITIN CONJUGATING ENZYME 8); protein binding / ubiquitin-protein ligase	Unigene29223_All//8.00E-64//gi|13244249|gb|BE052968.2|BE052968		ko04141|Protein processing in endoplasmic reticulum/ko04120|Ubiquitin mediated proteolysis	GO:0006464//GO:0016020//GO:0019787//GO:0019941//GO:0032559//GO:0043231//GO:0060255	nr -
Unigene29224_All	1224	0.09	0.00	0.00	0.00	0.00	4.21	13.20	8.91	4.91	-6.42E+00	3.72E-01		-6.42E+00	3.94E-01		null	null		1.20E+01	3.87E-31	Up	-5.66E-01	4.33E-06		-1.42E+00	2.33E-26	Down	Unigene29224_All//gi|19698452|gb|AAL93154.1|AF485268_1//0.00E+00//bacterial-induced class III peroxidase [Gossypium hirsutum]	Unigene29224_All//1.00E-114//AT2G41480| electron carrier/ heme binding / peroxidase	Unigene29224_All//0.00E+00//TC175162		ko00940|Phenylpropanoid biosynthesis/ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209	nr +
Unigene29225_All	1336	0.00	0.00	0.00	0.00	0.00	0.24	1.33	0.50	0.30	null	null		null	null		null	null		7.89E+00	4.07E-02		-1.41E+00	1.85E-03		-2.16E+00	8.30E-06	Down	Unigene29225_All//gi|225626273|gb|ACN97188.1|//1.00E-140//peroxidase [Populus trichocarpa]	Unigene29225_All//3.00E-112//AT2G41480| electron carrier/ heme binding / peroxidase	Unigene29225_All//0.00E+00//TC175162		ko00940|Phenylpropanoid biosynthesis/ko00360|Phenylalanine metabolism		nr -
Unigene29226_All	907	2.19	1.51	0.65	15.60	8.01	2.89	3.68	0.74	1.05	-5.39E-01	2.35E-01		-1.76E+00	6.51E-04	Down	-9.61E-01	3.89E-12		-2.43E+00	1.57E-40	Down	-2.32E+00	1.03E-10	Down	-1.80E+00	2.88E-08	Down	Unigene29226_All//gi|297727877|ref|NP_001176302.1|//6.00E-06//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1| Os11g0106066 [Oryza sativa Japonica Group]	Unigene29226_All//3.00E-05//AT3G25270| nucleic acid binding	Unigene29226_All//0.00E+00//TC166752				nr +
Unigene29228_All	1129	7.92	4.94	3.07	0.22	0.79	0.12	0.00	0.00	0.00	-6.83E-01	3.83E-04		-1.37E+00	8.90E-11	Down	1.85E+00	2.15E-02		-8.78E-01	6.16E-01		null	null		null	null		Unigene29228_All//gi|169667041|gb|ACA64093.1|//5.00E-94//MAEWEST protein [Petunia x hybrida]	Unigene29228_All//2.00E-51//AT3G18010| WOX1 (WUSCHEL related homeobox 1); transcription factor	Unigene29228_All//0.00E+00//gi|78345635|gb|DT565909.1|DT565909	HB		GO:0001071//GO:0003677//GO:0005634//GO:0006351//GO:0010468//GO:0040007//GO:0048444//GO:0048598//GO:0048827	nr +
Unigene29229_All	598	6.82	2.29	2.94	0.42	0.98	3.10	0.35	0.00	2.66	-1.58E+00	1.09E-06	Down	-1.22E+00	1.61E-04	Down	1.23E+00	2.33E-01		2.89E+00	1.35E-06	Up	-8.47E+00	7.44E-02		2.91E+00	5.82E-07	Up	Unigene29229_All//gi|297596936|ref|NP_001043247.2|//1.00E-09//Os01g0532300 [Oryza sativa Japonica Group] >gi|255673318|dbj|BAF05161.2| Os01g0532300 [Oryza sativa Japonica Group]		Unigene29229_All//6.00E-63//gi|164239671|gb|ES806989.1|ES806989				nr +
Unigene2923_All	1887	0.89	0.59	0.82	2.35	3.27	4.67	20.82	16.68	146.27	-5.87E-01	2.42E-01		-1.17E-01	8.14E-01		4.75E-01	4.54E-02		9.90E-01	3.11E-07		-3.20E-01	2.82E-05		2.81E+00	0.00E+00	Up	Unigene2923_All//gi|297817536|ref|XP_002876651.1|//0.00E+00//metal ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322489|gb|EFH52910.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene2923_All//0.00E+00//AT3G62010| unknown protein	Unigene2923_All//0.00E+00//TC149976				nr -
Unigene29230_All	654	6.40	0.16	3.91	1.52	3.00	0.83	0.00	0.13	0.00	-5.37E+00	2.75E-21	Down	-7.12E-01	2.22E-02		9.78E-01	3.42E-02		-8.78E-01	2.20E-01		7.00E+00	4.01E-01		null	null									
Unigene29231_All	1877	0.22	1.89	0.23	6.53	12.15	10.23	0.34	0.11	0.13	3.08E+00	2.43E-12	Up	2.56E-02	1.00E+00		8.96E-01	1.80E-16		6.47E-01	1.37E-07		-1.60E+00	6.27E-02		-1.41E+00	7.94E-02		Unigene29231_All//gi|224056879|ref|XP_002299069.1|//1.00E-144//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222846327|gb|EEE83874.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene29231_All//1.00E-121//AT1G55730| ATCAX5; calcium:cation antiporter/ cation:cation antiporter	Unigene29231_All//2.00E-25//ES827544				nr +
Unigene29232_All	634	3.14	1.28	4.20	2.28	2.44	2.28	2.73	0.99	0.50	-1.29E+00	5.96E-03		4.21E-01	3.10E-01		1.01E-01	8.69E-01		6.00E-04	9.96E-01		-1.47E+00	1.48E-03		-2.44E+00	1.80E-06	Down			Unigene29232_All//6.00E-26//gi|164306032|gb|ES833200.1|ES833200				
Unigene29233_All	1202	0.00	0.13	0.09	15.79	14.64	19.20	3.34	1.04	2.15	6.98E+00	2.35E-01		6.47E+00	3.98E-01		-1.09E-01	4.73E-01		2.82E-01	1.60E-02		-1.68E+00	1.31E-08	Down	-6.33E-01	1.56E-02		Unigene29233_All//gi|15219751|ref|NP_176853.1|//1.00E-61//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75262243|sp|Q9C9N3.1|C3H14_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 14; Short=At C3H14	Unigene29233_All//1.00E-56//AT1G66810| zinc finger (CCCH-type) family protein	Unigene29233_All//0.00E+00//gi|54116423|gb|CO491932.1|CO491932	C3H		GO:0046914	nr -
Unigene29236_All	437	2.04	2.90	1.46	1.48	1.18	3.20	5.32	3.92	1.37	5.10E-01	3.79E-01		-4.77E-01	5.33E-01		-3.26E-01	7.10E-01		1.11E+00	5.66E-02		-4.40E-01	2.56E-01		-1.96E+00	1.31E-06	Down			Unigene29236_All//0.00E+00//TC132888				
Unigene29237_All	554	45.05	12.16	14.99	81.02	71.79	49.40	105.09	31.84	41.78	-1.89E+00	1.28E-47	Down	-1.59E+00	5.04E-36	Down	-1.74E-01	3.16E-02		-7.14E-01	3.96E-20		-1.72E+00	9.91E-119	Down	-1.33E+00	1.22E-83	Down	Unigene29237_All//gi|134035500|gb|AB047738.1|//1.00E-41//alpha-tubulin [Gossypium hirsutum]	Unigene29237_All//7.00E-31//AT1G64740| TUA1 (ALPHA-1 TUBULIN); structural constituent of cytoskeleton	Unigene29237_All//0.00E+00//gi|21090042|gb|BQ402355.1|BQ402355		ko04145|Phagosome	GO:0006970//GO:0007010//GO:0007017//GO:0009536//GO:0009629//GO:0010038//GO:0015630//GO:0016020//GO:0017111//GO:0030312//GO:0031981//GO:0032561//GO:0043234//GO:0043623	nr +
Unigene29238_All	865	2.42	4.86	3.57	1.21	2.55	1.88	0.00	0.00	0.00	1.01E+00	7.90E-04	Up	5.61E-01	1.37E-01		1.08E+00	1.21E-02		6.36E-01	2.39E-01		null	null		null	null		Unigene29238_All//gi|158578531|gb|ABW74556.1|//6.00E-31//copia-like pol polyprotein [Boechera divaricarpa]					GO:0005488//GO:0008152	nr +
Unigene29239_All	517	4.25	173.08	2.68	11.85	44.83	69.45	166.42	891.29	525.22	5.35E+00	0.00E+00	Up	-6.67E-01	1.42E-01		1.92E+00	2.30E-52	Up	2.55E+00	2.01E-105	Up	2.42E+00	0.00E+00	Up	1.66E+00	0.00E+00	Up	Unigene29239_All//gi|19699035|gb|AAL91002.1|//5.00E-37//asparagine synthetase [Securigera parviflora]	Unigene29239_All//6.00E-36//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene29239_All//0.00E+00//CO128870		ko00910|Nitrogen metabolism/ko00250|Alanine, aspartate and glutamate metabolism	GO:0005528//GO:0009064//GO:0009267//GO:0009612//GO:0009746//GO:0016884//GO:0032559//GO:0034285	nr +
Unigene2924_All	1053	16.55	35.46	21.95	29.05	37.05	86.90	62.08	96.25	96.82	1.10E+00	8.51E-32	Up	4.08E-01	5.71E-04		3.51E-01	1.19E-05		1.58E+00	3.77E-144	Up	6.33E-01	4.14E-41		6.41E-01	2.49E-43		Unigene2924_All//gi|88196765|gb|ABD43025.1|//2.00E-85//At4g24380 [Arabidopsis thaliana]	Unigene2924_All//8.00E-87//AT4G24380| unknown protein	Unigene2924_All//0.00E+00//gi|109835354|gb|DW233918.1|DW233918			GO:0000166//GO:0008614//GO:0016641//GO:0042579	nr -

Unigene29240_All	548	0.29	2.40	1.46	2.27	2.39	1.57	0.93	0.76	1.89	3.07E+00	5.92E-05	Up	2.35E+00	1.46E-02		7.14E-02	9.26E-01		-5.37E-01	3.94E-01		-2.80E-01	7.49E-01		1.03E+00	7.96E-02		Unigene29240_All//gi|22327146|ref|NP_198205.2|//5.00E-71//FRS10 (FAR1-related sequence 10); zinc ion binding [Arabidopsis thaliana] >gi|257051024|sp|Q9LKR4.2|FRS10_ARATH RecName: Full=Putative protein FAR1-RELATED SEQUENCE 10	Unigene29240_All//3.00E-72//AT5G28530| FRS10 (FAR1-related sequence 10); zinc ion binding				GO:0046914	nr +
Unigene29243_All	603	0.17	2.69	1.24	12.56	11.31	12.43	78.32	69.17	143.70	3.95E+00	3.77E-07	Up	2.83E+00	8.52E-03		-1.51E-01	5.57E-01		-1.43E-02	9.42E-01		-1.79E-01	1.34E-02		8.76E-01	7.82E-63				Unigene29243_All//0.00E+00//DW487885					
Unigene29244_All	785	0.33	0.84	1.49	22.91	17.46	15.82	6.25	0.53	1.27	1.33E+00	1.45E-01		2.16E+00	3.59E-03		-3.92E-01	1.51E-03		-5.34E-01	2.62E-05		-3.55E+00	1.75E-23	Down	-2.30E+00	8.83E-16	Down	Unigene29244_All//gi|297826449|ref|XP_002881107.1|//1.00E-20//ATOFP17/OFP17 [Arabidopsis lyrata subsp. lyrata] >gi|297326946|gb|EFH57366.1|ATOFP17/OFP17 [Arabidopsis lyrata subsp. lyrata]	Unigene29244_All//7.00E-19//AT2G30395| OFP17 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 17)	Unigene29244_All//0.00E+00//gi|109884745|gb|DW513715.1|DW513715			GO:0043231	nr +
Unigene29245_All	711	0.29	1.07	0.75	1.54	1.89	0.83	3.57	1.18	4.15	1.86E+00	3.73E-02		1.35E+00	2.25E-01		2.93E-01	6.42E-01		-9.00E-01	1.81E-01		-1.60E+00	2.15E-05	Down	2.17E-01	5.36E-01				Unigene29245_All//0.00E+00//CO100352					
Unigene29247_All	1319	0.00	0.00	0.00	0.11	0.16	0.00	6.28	2.50	1.81	null	null		null	null		4.67E-01	8.25E-01		-6.82E+00	2.33E-01		-1.33E+00	3.30E-12	Down	-1.79E+00	4.06E-19	Down	Unigene29247_All//gi|115450439|ref|NP_001048820.1|//1.00E-103//Os03g0125800 [Oryza sativa Japonica Group] >gi|113547291|dbj|BAF10734.1|Os03g0125800 [Oryza sativa Japonica Group]	Unigene29247_All//2.00E-96//AT5G52790| CBS domain-containing protein-related					nr +
Unigene29249_All	229	0.00	0.00	0.00	0.44	0.00	0.00	2.95	0.91	0.00	null	null		null	null		-8.77E+00	3.13E-01		-8.77E+00	4.00E-01		-1.69E+00	4.19E-02		-1.15E+01	3.56E-05	Down								
Unigene29250_All	816	0.00	0.00	0.00	3.97	0.84	0.00	3.37	3.53	4.00	null	null		null	null		-2.23E+00	6.06E-10	Down	-1.20E+01	2.26E-20	Down	6.95E-02	8.47E-01		2.49E-01	4.31E-01		Unigene29250_All//gi|224121254|ref|XP_002318537.1|//3.00E-15//predicted protein [Populus trichocarpa] >gi|222859210|gb|EEE96757.1|predicted protein [Populus trichocarpa]						nr -
Unigene29251_All	1401	0.22	0.58	0.00	0.25	3.12	19.02	0.18	13.31	6.20	1.37E+00	9.21E-02		-7.81E+00	4.91E-02		3.65E+00	1.44E-19	Up	6.26E+00	2.20E-150	Up	6.20E+00	6.94E-121	Up	5.10E+00	5.88E-53	Up	Unigene29251_All//gi|224082932|ref|XP_002306897.1|//6.00E-79//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222856346|gb|EEE93893.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene29251_All//5.00E-45//AT1G75490| DNA binding / transcription factor	Unigene29251_All//1.00E-72//TC178922	AP2-EREBP		GO:0006350//GO:0009743//GO:0010468	nr +
Unigene29252_All	908	0.58	0.56	0.12	1.48	1.10	0.55	6.71	2.81	3.03	-4.63E-02	9.76E-01		-2.30E+00	6.76E-02		-4.30E-01	4.68E-01		-1.44E+00	1.59E-02		-1.26E+00	1.73E-08	Down	-1.15E+00	9.80E-08	Down	Unigene29252_All//gi|30725614|gb|AP37829.1|//1.00E-107//At5g12470 [Arabidopsis thaliana]	Unigene29252_All//8.00E-109//AT5G12470| unknown protein	Unigene29252_All//0.00E+00//TC177423				nr -
Unigene29253_All	651	2.41	0.39	1.55	1.99	2.27	1.87	0.97	0.90	1.47	-2.63E+00	4.14E-05	Down	-6.34E-01	2.47E-01		1.93E-01	7.84E-01		-8.70E-02	8.93E-01		-1.16E-01	8.88E-01		5.92E-01	3.46E-01									
Unigene29254_All	315	4.48	2.09	3.72	3.00	1.97	3.30	7.52	2.79	2.40	-1.10E+00	5.16E-02		-2.70E-01	6.16E-01		-6.11E-01	3.90E-01		1.34E-01	8.58E-01		-1.43E+00	1.94E-04	Down	-1.65E+00	1.81E-05	Down	Unigene29254_All//gi|22326997|ref|NP_197656.2|//1.00E-18//emb1211 (embryo defective 1211) [Arabidopsis thaliana] >gi|20453116|gb|AAM19800.1|AT5g22640/MDJ22_6 [Arabidopsis thaliana]		Unigene29254_All//4.00E-47//gi|48777690|gb|CO087056.1|CO087056			GO:0003006//GO:0009526//GO:0009534	nr +
Unigene29255_All	677	0.00	0.00	0.00	2.35	1.07	4.74	9.12	4.07	9.59	null	null		null	null		-1.14E+00	2.19E-02		1.01E+00	3.80E-03		-1.16E+00	1.07E-07	Down	7.31E-02	7.43E-01				Unigene29255_All//5.00E-08//A1055471					
Unigene29258_All	546	0.77	0.28	0.59	1.28	2.40	1.24	3.87	3.14	1.53	-1.46E+00	2.34E-01		-3.90E-01	7.17E-01		9.08E-01	1.35E-01		-4.18E-02	9.44E-01		-3.03E-01	4.78E-01		-1.34E+00	6.80E-04	Down								
Unigene29259_All	478	2.85	4.45	3.34	3.96	5.98	3.12	2.39	0.52	1.50	6.46E-01	1.41E-01		2.32E-01	6.46E-01		5.94E-01	1.15E-01		-3.45E-01	4.99E-01		-2.19E+00	6.83E-04	Down	-6.71E-01	2.20E-01		Unigene29359_All//gi|115437600|ref|NP_001043335.1|//1.00E-10//Os01g0558500 [Oryza sativa Japonica Group] >gi|113532866|dbj|BAF05249.1|Os01g0558500 [Oryza sativa Japonica Group]	Unigene29259_All//2.00E-14//AT3G21295| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: PWWP (InterPro:IPR000313); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G51745.1); Has 428 Blast hits to 314 proteins in 77 species: Archae - 0; Bacteria - 111; Metazoa - 87; Fungi - 55; Plants - 63; Viruses - 0; Other Eukaryotes - 112 (source: NCBI BLink).	Unigene29259_All//0.00E+00//ES793017				nr +
Unigene29260_All	308	1.87	0.66	5.36	1.78	3.24	3.08	4.39	3.80	1.16	-1.51E+00	1.36E-01		1.52E+00	6.71E-03		8.66E-01	2.34E-01		7.92E-01	2.99E-01		-2.09E-01	6.89E-01		-1.92E+00	4.37E-04	Down			Unigene29260_All//2.00E-107//gi|21100442|gb|BQ412755.1|BQ412755					
Unigene29261_All	843	25.88	21.22	19.58	2.01	2.37	5.84	0.50	0.50	0.57	-2.87E-01	1.72E-02		-4.02E-01	1.01E-03		2.38E-01	6.37E-01		1.54E+00	6.01E-08	Up	-1.65E-02	1.02E+00		1.77E-01	8.46E-01		Unigene29261_All//gi|149944295|gb|ABR46190.1|//3.00E-33//At5g20670 [Arabidopsis thaliana]	Unigene29261_All//9.00E-27//AT5G20670| unknown protein	Unigene29261_All//0.00E+00//TC151833				nr +
Unigene29262_All	976	0.00	0.31	0.38	78.29	24.38	12.91	290.42	259.08	108.13	8.28E+00	4.43E-02		8.58E+00	2.50E-02		-1.68E+00	1.09E-154	Down	-2.60E+00	4.51E-235	Down	-1.65E-01	8.04E-10		-1.43E+00	0.00E+00	Down	Unigene29262_All//gi|18415051|ref|NP_568160.1|//8.00E-39//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|88011017|gb|ABD38889.1|At5g05960 [Arabidopsis thaliana]	Unigene29262_All//4.00E-40//AT5G05960| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene29262_All//0.00E+00//gi|109828455|gb|DW227078.1|DW227078			GO:0005488//GO:0006810//GO:0016787//GO:0044464	nr -
Unigene29263_All	386	72.92	21.53	33.80	114.73	120.79	139.23	146.23	68.22	81.74	-1.76E+00	9.91E-49	Down	-1.11E+00	1.28E-23	Down	7.43E-02	4.43E-01		2.79E-01	8.53E-05		-1.10E+00	1.54E-58	Down	-8.39E-01	1.19E-38		Unigene29263_All//gi|195620934|gb|ACG32292.1|//3.00E-49//60S ribosomal protein L23 [Zea mays]	Unigene29263_All//2.00E-49//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene29263_All//2.00E-172//gi|109873572|gb|DW502547.1|DW502547		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene29264_All	470	0.11	11.00	0.45	0.53	0.73	1.73	0.90	2.58	5.85	6.63E+00	8.92E-28	Up	2.03E+00	3.61E-01		4.68E-01	7.79E-01		1.71E+00	4.57E-02		1.52E+00	8.16E-03		2.70E+00	1.08E-10	Up			Unigene29264_All//0.00E+00//gi|73861383|gb|DT464122.1|DT464122					
Unigene29265_All	853	0.74	0.24	0.75	0.76	1.70	1.85	4.76	1.37	1.63	-1.63E+00	9.23E-02		2.55E-02	9.97E-01		1.16E+00	3.97E-02		1.29E+00	1.78E-02		-1.79E+00	1.87E-09	Down	-1.54E+00	4.60E-08	Down	Unigene29265_All//gi|115479681|ref|NP_001063434.1|//3.00E-84//Os09g0469900 [Oryza sativa Japonica Group] >gi|113631667|dbj|BAF25348.1|Os09g0469900 [Oryza sativa Japonica Group]		Unigene29265_All//0.00E+00//ES843951			GO:0006400//GO:0016763//GO:0043231//GO:0044249	nr +
Unigene29267_All	623	8.06	2.20	6.58	4.56	5.31	3.19	0.88	0.40	1.02	-1.88E+00	4.69E-10	Down	-2.93E-01	3.25E-01		2.19E-01	5.85E-01		-5.15E-01	1.87E-01		-1.13E+00	2.18E-01		2.14E-01	7.73E-01				Unigene29267_All//8.00E-10//ES835959					
Unigene2927_All	2094	12.99	4.77	10.40	16.91	16.23	15.46	2.12	5.79	2.30	-1.45E+00	1.29E-35	Down	-3.21E-01	3.43E-03		-5.95E-02	6.00E-01		-1.29E-01	2.15E-01		1.45E+00	8.05E-20	Up	1.19E-01	6.37E-01		Unigene2927_All//gi|297843348|ref|XP_002889555.1|//0.00E+00//glycosyl hydrolase family 20 protein [Arabidopsis lyrata subsp. lyrata] >gi|297335397|gb|EFH65814.1|glycosyl hydrolase family 20 protein [Arabidopsis lyrata subsp. lyrata]	Unigene2927_All//0.00E+00//AT1G05590| HEXO2 (BETA-HEXOSAMINIDASE 2); beta-N-acetylhexosaminidase/ hexosaminidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene2927_All//0.00E+00//TC157097		ko00520|Amino sugar and nucleotide sugar metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series//ko00603|Glycosphingolipid biosynthesis - globo series	GO:0008194//GO:0015929//GO:0016020//GO:0031410//GO:0043167//GO:0044238	nr +
Unigene29270_All	768	5.45	2.31	1.94	2.21	1.79	1.82	0.28	0.60	0.42	-1.24E+00	5.19E-05	Down	-1.49E+00	5.14E-06	Down	-2.98E-01	5.76E-01		-2.75E-01	6.38E-01		1.12E+00	2.74E-01		5.92E-01	6.13E-01				Unigene29270_All//0.00E+00//TC162645					
Unigene29271_All	754	7.91	1.88	0.28	7.40	8.04	4.07	2.36	0.33	0.74	-2.07E+00	2.39E-13	Down	-4.81E+00	2.26E-27	Down	1.19E-01	6.81E-01		-8.61E-01	5.07E-04		-2.82E+00	2.67E-07	Down	-1.67E+00	2.20E-04	Down	Unigene29271_All//gi|125568905|gb|EAZ10420.1|//3.00E-06//hypothetical protein Os_00252 [Oryza sativa Japonica Group]		Unigene29271_All//0.00E+00//gi|18099821|gb|BM339075.1|BM339075				nr +
Unigene29273_All	817	21.13	23.63	19.23	39.63	23.39	18.74	12.83	7.78	7.90	1.61E-01	2.36E-01		-1.36E-01	3.96E-01		-7.61E-01	2.51E-18		-1.08E+00	4.16E-29	Down	-7.23E-01	4.25E-06		-7.00E-01	5.01E-06				Unigene29273_All//0.00E+00//BQ403348					
Unigene29274_All	818	6.72	6.63	5.14	11.63	6.23	5.52	4.55	0.77	2.19	-1.91E-02	9.60E-01		-3.85E-01	1.56E-01		-9.01E-01	1.60E-07		-1.08E+00	6.70E-09	Down	-2.57E+00	3.01E-13	Down	-1.05E+00	1.58E-04	Down			Unigene29274_All//0.00E+00//BQ403348					
Unigene29277_All	628	8.16	50.59	4.92	2.46	1.10	3.67	0.94	0.07	0.51	2.63E+00	3.52E-90	Up	-7.31E-01	7.99E-03		-1.16E+00	2.17E-02		5.77E-01	1.96E-01		-3.82E+00	1.78E-03		-8.93E-01	2.71E-01		Unigene29277_All//gi|226529630|ref|NP_001152607.1|//2.00E-23//growth-regulating factor [Zea mays] >gi|195638087|gb|ACG48511.1|growth-regulating factor [Zea mays]	Unigene29277_All//1.00E-20//AT4G37740| AtGRF2 (GROWTHREGULATING FACTOR 2); transcription activator	Unigene29277_All//0.00E+00//gi|109870684|gb|DW499660.1|DW499660	GRF			nr -
Unigene29278_All	293	6.25	12.62	8.54	5.27	14.57	10.79	0.72	0.71	0.00	1.01E+00	1.69E-03		4.51E-01	2.91E-01		1.47E+00	6.01E-07	Up	1.03E+00	3.28E-03		-1.67E-02	1.02E+00		-9.49E+00	5.80E-02				Unigene29278_All//3.00E-07//CO131853					
Unigene2928_All	914	54.95	17.24	14.86	83.66	75.80	99.22	107.92	56.47	48.21	-1.67E+00	1.72E-80	Down	-1.89E+00	6.68E-92	Down	-1.42E-01	1.95E-02		2.46E-01	3.97E-06		-9.34E-01	6.85E-78		-1.16E+00	2.78E-114	Down	Unigene2928_All//gi|3023847|sp|O24076.1|GBLP_MEDSA//1.00E-134//RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein >gi|2385376|emb|CAA69934.1| G protein beta subunit-like [Medicago sativa subsp. x varia]	Unigene2928_All//9.00E-134//AT1G48630| RACK1B_AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding	Unigene2928_All//0.00E+00//TC153942		ko03040|Spliceosome//ko03022|Basal transcription factors		nr +
Unigene29281_All	712	73.41	412.19	162.52	88.08	156.60	143.61	174.82	686.58	342.10	2.49E+00	0.00E+00	Up	1.15E+00	3.74E-101	Up	8.30E-01	5.37E-70		7.05E-01	7.10E-44		1.97E+00	0.00E+00	Up	9.69E-01	2.56E-207		Unigene29281_All//gi|297808579|ref|XP_002872173.1|//8.00E-12//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318010|gb|EFH48432.1|zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29281_All//1.00E-12//AT5G25560| zinc finger (C3HC4-type RING finger) family protein	Unigene29281_All//0.00E+00//TC167466		ko04120|Ubiquitin mediated proteolysis	GO:0031410//GO:0043231//GO:0046914	nr +
Unigene29284_All	488	2.79	31.88	16.37	30.32	60.12	64.23	0.00	0.17	0.16	3.52E+00	6.39E-59	Up	2.55E+00	1.15E-21	Up	9.88E-01	9.34E-25		1.08E+00	5.97E-28	Up	7.42E+00	4.01E-01		7.35E+00	4.04E-01		Unigene29284_All//gi|167375990|gb|ABZ79407.1|//2.00E-27//pyrroline-5-carboxylate synthetase [Gossypium arboreum]	Unigene29284_All//1.00E-25//AT3G55610| P5CS2 (DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHASE 2); catalytic/ glutamate 5-kinase/ glutamate-5-semialdehyde dehydrogenase/ oxidoreductase	Unigene29284_All//2.00E-86//TC177130		ko00330|Arginine and proline metabolism	GO:0003006//GO:0006560//GO:0006972//GO:0009536//GO:0009725//GO:0016620//GO:0016646//GO:0016774//GO:0032559	nr -
Unigene29285_All	478	321.92	438.85	376.98	122.76	148.11	183.49	35.29	76.60	72.09	4.47E-01	5.94E-37		2.28E-01	4.36E-09		2.71E-01	3.16E-06		5.80E-01	8.43E-27		1.12E+00	3.49E-39	Up	1.03E+00	3.26E-33	Up			Unigene29285_All//0.00E+00//TC148063					ESTscan +
Unigene29286_All	426	25.91	48.41	27.25	36.72	34.03	39.23	120.98	82.90	54.99	9.02E-01	4.19E-13		7.25E-02	6.97E-01		-1.10E-01	5.31E-01		9.54E-02	5.84E-01		-5.45E-01	1.60E-16		-1.14E+00	4.40E-58	Down	Unigene29286_All//gi|224072049|ref|XP_002303615.1|//5.00E-06//predicted protein [Populus trichocarpa] >gi|222841047|gb|EEE78594.1|predicted protein [Populus trichocarpa]	Unigene29286_All//7.00E-06//AT4G23630| BTI1 (VIRB2-INTERACTING PROTEIN 1)	Unigene29286_All//0.00E+00//gi|109869226|gb|DW498202.1|DW498202				nr -
Unigene29287_All	1577	0.13	0.06	0.00	0.00	0.09	0.06	40.99	3.31	20.29	-1.05E+00	5.65E-01		-7.05E+00	1.46E-01		6.45E+00	3.18E-01		5.84E+00	4.76E-01		-3.63E+00	0.00E+00	Down	-1.01E+00	1.91E-60	Down	Unigene29287_All//gi|240256390|ref|NP_199107.5|//1.00E-118//triacylglycerol lipase [Arabidopsis thaliana]	Unigene29287_All//1.00E-114//AT5G42930| triacylglycerol lipase	Unigene29287_All//2.00E-80//TC151789				nr +
Unigene29289_All	653	1.12	0.00	0.41	6.41	3.48	1.45	0.71	0.51	0.37	-1.01E+01	2.11E-04	Down	-1.46E+00	1.12E-01		-8.81E-01	1.50E-03		-2.14E+00	1.31E-10	Down	-4.76E-01	6.60E-01		-9.60E-01	3.13E-01				Unigene29289_All//4.00E-24//ES807753					ESTscan +
Unigene29290_All	923	0.00	0.05	0.00	3.62	2.87	0.78	2.52	1.36	0.09	5.78E+00	6.16E-01		null	null		-3.32E-01	3.49E-01		-2.21E+00	7.00E-09	Down	-8.91E-01	1.72E-02		-4.87E+00	1.64E-14	Down	Unigene29290_All//gi|42565945|ref|NP_567014.2|//4.00E-42//RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	Unigene29290_All//4.00E-42//AT3G55020| RabGAP/TBC domain-containing protein	Unigene29290_All//7.00E-113//TC152064			GO:0005099//GO:0032318//GO:0044464	nr +
Unigene29291_All	1282	0.37	0.28	0.08	0.23	0.16	0.42	21.50	8.90	3.51	-4.09E-01	6.69E-01		-2.14E+00	1.03E-01		-5.32E-01	6.79E-01		8.59E-01	4.23E-01		-1.27E+00	2.39E-36	Down	-2.61E+00	9.20E-99	Down	Unigene29291_All//gi|211906540|gb|ACJ11763.1|//1.00E-113//class III peroxidase [Gossypium hirsutum]	Unigene29291_All//1.00E-100//AT4G37530| peroxidase, putative	Unigene29291_All//0.00E+00//gi|109863533|gb|DW492510.1|DW492510		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene29293_All	1004	0.63	0.66	0.37	0.00	0.07	0.18	3.20	5.04	12.30	6.94E-02	9.50E-01		-7.52E-01	4.11E-01		6.10E+00	6.10E-01		7.49E+00	1.94E-01		6.54E-01	5.90E-03		1.94E+00	8.29E-31	Up			Unigene29293_All//1.00E-173//TC136870					

Unigene29295_All	483	0.00	2.52	0.00	1.13	1.28	2.15	0.96	0.35	0.91	1.13E+01	5.47E-07	Up	null	null		1.78E-01	8.64E-01		9.23E-01	1.96E-01		-1.48E+00	1.53E-01		-8.58E-02	9.34E-01		Unigene29295_All//gi|255585234|ref|XP_002533319.1|//7.00E-19//phosphatidylinositol-4-phosphate 5-kinase, putative [Ricinus communis] >gi|223526863|gb|EEF29076.1|phosphatidylinositol-4-phosphate 5-kinase, putative [Ricinus communis]	Unigene29295_All//1.00E-54//TC139787			GO:0016740	nr -
Unigene29296_All	1318	0.00	0.00	0.00	0.08	0.00	0.00	5.23	5.11	11.12	null	null		null	null		-6.24E+00	3.13E-01		-6.24E+00	4.00E-01		-3.45E-02	8.87E-01		1.09E+00	6.24E-16	Up	Unigene29296_All//gi|24461861|gb|AAN62348.1|AF506028.15//1.00E-104//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene29296_All//2.00E-79//AT1G15890| disease resistance protein (CC-NBS-LRR class), putative	Unigene29296_All//0.00E+00//NP831324		ko04626|Plant-pathogen interaction	GO:0006950//GO:0012501//GO:0016787//GO:0032559	nr +
Unigene29297_All	612	0.77	1.90	0.87	5.29	2.25	2.14	5.53	10.38	4.75	1.31E+00	4.44E-02		1.77E-01	8.45E-01		-1.23E+00	1.48E-04	Down	-1.31E+00	1.75E-04	Down	9.09E-01	1.51E-05		-2.18E-01	4.89E-01		Unigene29297_All//gi|15221451|ref|NP_172122.1|//4.00E-34//copper-binding family protein [Arabidopsis thaliana]	Unigene29297_All//2.00E-35//AT1G06330| copper-binding family protein	Unigene29297_All//0.00E+00//DT464878			GO:0030001	nr +
Unigene29298_All	350	1.20	4.63	4.41	2.13	4.62	2.58	4.35	5.61	6.26	1.95E+00	6.79E-04	Up	1.88E+00	1.93E-03		1.12E+00	3.29E-02		2.74E-01	7.10E-01		3.68E-01	4.00E-01		5.26E-01	1.66E-01								
Unigene29299_All	1297	0.08	0.63	0.00	0.08	0.11	0.07	1.56	1.64	48.93	2.95E+00	3.29E-03		-6.33E+00	3.94E-01		4.68E-01	8.77E-01		-1.42E-01	9.50E-01		7.09E-02	8.69E-01		4.97E+00	0.00E+00	Up	Unigene29299_All//gi|297797667|ref|XP_002866718.1|//1.00E-94//MAPKKK19 [Arabidopsis lyrata subsp. lyrata] >gi|297312553|gb|EFH42977.1|MAPKKK19 [Arabidopsis lyrata subsp. lyrata]	Unigene29299_All//8.00E-92//AT5G67080| MAPKKK19; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene29299_All//0.00E+00//TC153624		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene29302_All	509	2.78	0.80	0.00	8.32	2.23	9.76	1.50	0.99	0.63	-1.80E+00	3.03E-03		-1.14E+01	1.01E-07	Down	-1.90E+00	1.82E-10	Down	2.31E-01	4.58E-01		-6.02E-01	4.12E-01		-1.26E+00	7.70E-02		Unigene29302_All//gi|149728087|gb|ABR28346.1|//3.00E-28//MYB transcription factor MYB114 [Medicago truncatula]	Unigene29302_All//2.00E-26//AT2G21650| MEE3 (MATERNAL EFFECT EMBRYO ARREST 3); DNA binding / transcription factor	Unigene29302_All//0.00E+00//gi|109885546|gb|DW514516.1|DW514516	MYB-related		GO:0003006//GO:0003676//GO:0006350//GO:0010468	nr -
Unigene29303_All	322	0.00	2.52	0.99	1.70	1.71	0.42	13.52	15.19	37.98	1.13E+01	9.38E-05	Up	9.95E+00	4.52E-02		7.90E-03	9.83E-01		-2.02E+00	7.05E-02		1.67E-01	5.55E-01		1.49E+00	2.73E-21	Up			Unigene29303_All//3.00E-137//TC145788				
Unigene29305_All	361	0.87	3.93	2.51	1.52	3.15	1.25	1.41	0.93	7.84	2.18E+00	6.84E-04	Up	1.53E+00	5.77E-02		1.05E+00	1.10E-01		-2.79E-01	7.57E-01		-6.02E-01	5.31E-01		2.48E+00	4.58E-10	Up			Unigene29305_All//3.00E-100//gi|50484538|gb|AI729586.1|AI729586				
Unigene29308_All	286	2.93	0.35	5.96	7.66	9.99	20.53	0.00	0.88	0.28	-3.05E+00	2.11E-03		1.03E+00	5.24E-02		3.83E-01	3.37E-01		1.42E+00	2.14E-08	Up	9.78E+00	4.31E-02		8.12E+00	4.04E-01				Unigene29308_All//3.00E-07//TC153265				
Unigene29309_All	925	0.34	0.22	0.23	0.75	0.89	1.56	0.87	0.59	2.58	-6.31E-01	6.22E-01		-5.60E-01	6.63E-01		2.45E-01	8.03E-01		1.05E+00	6.64E-02		-5.64E-01	4.30E-01		1.57E+00	3.67E-05	Up	Unigene29309_All//gi|22329400|ref|NP_172231.2|//1.00E-111//ftsh10 (FtsH protease 10; ATP binding / ATPase/ metalloendopeptidase/ nucleoside-triphosphatase/ nucleotide binding / zinc ion binding [Arabidopsis thaliana] >gi|75331189|sp|Q8VZI8.1|FTSH8_ARATH RecName: Full=Cell division protease ftsH homolog 10, mitochondrial; Short=AtFtsH10; Flags: Precursor >gi|17381253|gb|AAL36045.1|At1g07510/F22G5_9 [Arabidopsis thaliana] >gi|21700787|gb|AAM70517.1|At1g07510/F22G5_9 [Arabidopsis thaliana]	Unigene29309_All//1.00E-112//AT1G07510| ftsh10 (FtsH protease 10; ATP binding / ATPase/ metalloendopeptidase/ nucleoside-triphosphatase/ nucleotide binding / zinc ion binding	Unigene29309_All//0.00E+00//ES820255			GO:0004175//GO:0009057//GO:0016462//GO:0019538//GO:0031224//GO:0032559//GO:0046914	nr -
Unigene29313_All	317	3.80	0.32	4.87	4.40	7.50	1.14	0.00	0.00	0.38	-3.57E+00	3.63E-05	Down	3.60E-01	5.20E-01		7.69E-01	6.35E-02		-1.95E+00	1.43E-03		null	null		8.56E+00	2.43E-01		Unigene29313_All//gi|224082332|ref|XP_002306650.1|//2.00E-35//amino acid permease [Populus trichocarpa] >gi|222856099|gb|EEE93646.1| amino acid permease [Populus trichocarpa]	Unigene29313_All//1.00E-33//AT1G77380| AAP3; amino acid transmembrane transporter	Unigene29313_All//3.00E-106//gi|78353568|gb|DT573842.1|DT573842			GO:0031224	nr +
Unigene29314_All	233	3.82	4.57	6.63	6.84	9.61	6.40	3.45	2.33	0.34	2.59E-01	6.75E-01		7.96E-01	1.50E-01		4.90E-01	2.88E-01		-9.70E-02	8.59E-01		-5.64E-01	4.30E-01		-3.33E+00	2.47E-04	Down			Unigene29314_All//1.00E-12//CO077070				
Unigene29316_All	1748	0.00	0.00	0.37	0.43	0.20	19.25	5.03	1.32	29.45	null	null		8.51E+00	1.16E-03		-1.12E+00	1.62E-01		5.49E+00	5.35E-181	Up	-1.94E+00	1.21E-21	Down	2.55E+00	6.11E-176	Up	Unigene29316_All//gi|224060245|ref|XP_002300103.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222847361|gb|EEE84908.1|cytochrome P450 [Populus trichocarpa]	Unigene29316_All//1.00E-175//AT3G48520| CYP94B3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene29316_All//0.00E+00//gi|78339905|gb|DT560179.1|DT560179		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016712	nr +
Unigene29318_All	430	0.97	0.24	1.86	1.27	1.76	1.26	1.57	0.10	0.83	-2.05E+00	1.21E-01		9.32E-01	2.56E-01		4.67E-01	6.07E-01		-1.58E-02	9.75E-01		-4.02E+00	5.36E-04	Down	-9.16E-01	2.21E-01		Unigene29318_All//gi|297849104|ref|XP_002892433.1|//2.00E-31//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297338275|gb|EFH68692.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene29318_All//3.00E-26//AT1G08070| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene29319_All	543	1.45	4.67	4.81	2.75	0.82	0.17	0.08	0.00	0.15	1.69E+00	8.51E-05	Up	1.73E+00	7.95E-05	Up	-1.74E+00	1.14E-03		-4.05E+00	3.05E-07	Down	-6.28E+00	6.57E-01		9.13E-01	7.50E-01		Unigene29319_All//gi|115485949|ref|NP_001068118.1|//4.00E-33//Os11g0569600 [Oryza sativa Japonica Group] >gi|113645340|dbj|BAF28481.1|Os11g0569600 [Oryza sativa Japonica Group]	Unigene29319_All//1.00E-33//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674//GO:0008152//GO:0016020//GO:0016491	nr -
Unigene29320_All	460	0.46	0.66	2.32	1.41	3.14	3.14	2.76	0.73	1.21	5.39E-01	6.71E-01		2.35E+00	3.61E-03		1.16E+00	3.97E-02		1.16E+00	4.25E-02		-1.92E+00	9.98E-04	Down	-1.19E+00	2.28E-02				Unigene29320_All//9.00E-09//EV483286				
Unigene29322_All	1467	0.00	0.14	0.07	0.00	0.00	0.00	2.05	3.65	18.47	7.11E+00	1.36E-01		6.18E+00	3.98E-01		null	null		null	null		8.34E-01	2.95E-04		3.17E+00	1.23E-116	Up	Unigene29322_All//gi|14586969|gb|AK70407.1|AF369930_2/2.00E-72//pol polyprotein [Citrus x paradisi]	Unigene29322_All//5.00E-65//AT4G00980| zinc knuckle (CCHC-type) family protein				GO:0003676//GO:0043170//GO:0044238	nr -
Unigene29323_All	695	0.08	0.00	0.00	0.72	0.40	0.84	7.91	0.60	6.88	-6.23E+00	6.12E-01		-6.23E+00	6.24E-01		-8.55E-01	4.07E-01		2.37E-01	7.98E-01		-3.72E+00	3.22E-27	Down	-2.01E-01	4.03E-01		Unigene29323_All//gi|269854726|gb|ACZ51393.1|//7.00E-51//NBS-LRR resistance protein-like protein [Gossypium hirsutum]	Unigene29323_All//6.00E-22//AT5G36930| disease resistance protein (TIR-NBS-LRR class), putative	Unigene29323_All//5.00E-156//gi|48779754|gb|CO089120.1|CO089120		ko04626|Plant-pathogen interaction	GO:0006950//GO:0012501//GO:0032559	nr -
Unigene29324_All	467	268.21	416.86	268.64	559.16	830.87	800.27	27.61	58.80	31.56	6.36E-01	1.80E-64		2.30E-03	9.90E-01		5.71E-01	7.28E-127		5.17E-01	1.08E-91		1.09E+00	1.87E-28	Up	1.93E-01	1.58E-01		Unigene29324_All//gi|18423010|ref|NP_568708.1|//2.00E-18//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|21553492|gb|AAM62585.1|extensin like protein [Arabidopsis thaliana] >gi|194708810|gb|ACF88489.1|At5g49280 [Arabidopsis thaliana]		Unigene29324_All//0.00E+00//TC151767		ko03040|Spliceosome//ko00270|Cysteine and methionine metabolism	GO:0031224	nr +
Unigene29325_All	1910	0.00	0.00	0.00	0.00	0.00	0.00	1.79	2.19	9.09	null	null		null	null		null	null		null	null		2.87E-01	3.23E-01		2.34E+00	2.83E-54	Up	Unigene29325_All//gi|297820152|ref|XP_002877959.1|//0.00E+00//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323797|gb|EFH54218.1|proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29325_All//0.00E+00//AT5G01180| PTR5 (PEPTIDE TRANSPORTER 5); dipeptide transporter/ transporter	Unigene29325_All//4.00E-79//TC158352			GO:0000904//GO:0006857//GO:0008152//GO:0015198//GO:0031224	nr -
Unigene29326_All	394	0.66	1.29	0.95	4.55	1.14	4.24	1.82	0.85	1.21	9.54E-01	3.73E-01		5.11E-01	6.54E-01		-2.00E+00	4.72E-05	Down	-1.02E-01	8.43E-01		-1.10E+00	1.49E-01		-5.88E-01	4.09E-01				Unigene29326_All//0.00E+00//CO129081				
Unigene29329_All	983	0.43	0.10	0.00	0.86	0.95	1.29	0.13	0.30	1.78	-2.05E+00	1.21E-01		-8.73E+00	1.56E-02		1.35E-01	8.71E-01		5.78E-01	3.77E-01		1.21E+00	3.92E-01		3.79E+00	2.44E-09	Up	Unigene29329_All//gi|297831842|ref|XP_002883803.1|//1.00E-51//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329643|gb|EFH60062.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene29329_All//9.00E-53//AT2G13600| pentatricopeptide (PPR) repeat-containing protein	Unigene29329_All//9.00E-97//TC153612				nr -
Unigene29330_All	566	6.93	3.76	2.16	21.74	15.51	13.64	5.53	2.66	1.34	-8.83E-01	4.21E-03		-1.68E+00	1.27E-06	Down	-4.87E-01	1.30E-03		-6.72E-01	1.85E-05		-1.06E+00	8.47E-04	Down	-2.05E+00	4.58E-09	Down			Unigene29330_All//4.00E-70//gi|84166287|gb|DR454935.1|DR454935				
Unigene29331_All	252	4.15	47.25	4.01	8.50	14.62	17.21	17.62	23.39	26.72	3.51E+00	4.04E-45	Up	-4.86E-02	9.57E-01		7.83E-01	1.23E-02		1.02E+00	4.74E-04	Up	4.09E-01	6.89E-02		6.01E-01	2.17E-03				Unigene29331_All//4.00E-62//gi|73859048|gb|DT461787.1|DT461787				
Unigene29332_All	394	0.00	1.54	0.00	1.01	4.37	2.29	4.08	16.02	8.49	1.06E+01	1.17E-03		null	null		2.11E+00	1.06E-04	Up	1.18E+00	1.29E-01		1.97E+00	4.30E-16	Up	1.06E+00	3.75E-04	Up			Unigene29332_All//5.00E-07//CO112920				
Unigene29333_All	720	2.11	0.84	1.41	5.74	6.79	4.20	2.82	0.81	0.83	-1.32E+00	1.68E-02		-5.85E-01	3.05E-01		2.42E-01	4.35E-01		-4.50E-01	1.48E-01		-1.79E+00	4.24E-05	Down	-1.76E+00	3.30E-05	Down	Unigene29333_All//gi|224118022|ref|XP_002331538.1|//1.00E-113//acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa] >gi|222873762|gb|EEF10893.1|acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]	Unigene29333_All//4.00E-106//AT5G16370| AAE5 (ACYL ACTIVATING ENZYME 5); catalytic	Unigene29333_All//0.00E+00//gi|48812387|gb|CO113700.1|CO113700		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene29336_All	327	0.00	0.93	0.00	3.20	2.32	5.66	111.84	141.88	435.91	9.86E+00	4.43E-02		null	null		-4.66E-01	5.02E-01		8.24E-01	9.38E-02		3.43E-01	7.89E-07		1.96E+00	0.00E+00	Up	Unigene29336_All//gi|225442485|ref|XP_002278313.1|//2.00E-43//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene29336_All//2.00E-35//AT1G59870| PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	Unigene29336_All//2.00E-147//gi|78354132|gb|DT574406.1|DT574406		ko02010|ABC transporters	GO:0000041//GO:0009526//GO:0009814//GO:0015082//GO:0015604//GO:0015893//GO:0016020//GO:0019762//GO:0032559//GO:0042626//GO:0050832//GO:0052482//GO:0071365	nr +
Unigene29337_All	444	0.94	4.34	2.64	3.14	3.41	6.41	0.00	0.47	0.63	2.20E+00	4.47E-05	Up	1.48E+00	3.04E-02		1.19E-01	8.39E-01		1.03E+00	6.02E-03		8.88E+00	7.85E-02		9.29E+00	2.43E-02				Unigene29337_All//1.00E-07//TC136172				
Unigene29338_All	530	0.49	0.38	1.11	1.88	1.17	0.77	5.98	3.63	2.10	-3.68E-01	7.78E-01		1.16E+00	2.47E-01		-6.85E-01	3.11E-01		-1.29E+00	7.06E-02		-7.22E-01	2.05E-02		-1.51E+00	2.64E-06	Down			Unigene29338_All//4.00E-08//TC133723				
Unigene29341_All	585	0.00	0.00	0.00	1.11	1.18	2.62	0.07	0.36	2.59	null	null		null	null		8.88E-02	9.49E-01		1.25E+00	2.40E-02		2.30E+00	2.40E-01		5.16E+00	1.25E-09	Up	Unigene29341_All//gi|297804542|ref|XP_002870155.1|//4.00E-80//ATINT4 [Arabidopsis lyrata subsp. lyrata] >gi|297315991|gb|EFH46414.1|ATINT4 [Arabidopsis lyrata subsp. lyrata]	Unigene29341_All//4.00E-74//AT4G16480| INT4 (INOSITOL TRANSPORTER 4); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen symporter	Unigene29341_All//3.00E-12//gi|78323715|gb|DT543989.1|DT543989			GO:0005365//GO:0006810//GO:0008152//GO:0016628//GO:0031224	nr -
Unigene29342_All	871	0.42	1.16	0.86	2.00	2.89	3.89	1.84	0.38	0.59	1.47E+00	4.06E-02		1.03E+00	2.37E-01		5.28E-01	2.07E-01		9.58E-01	4.44E-03		-2.26E+00	2.23E-05	Down	-1.63E+00	6.02E-04	Down	Unigene29342_All//gi|18401489|ref|NP_566576.1|//2.00E-54//meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana]	Unigene29342_All//2.00E-56//AT3G17380| meprin and TRAF homology domain-containing protein / MATH domain-containing protein					nr -
Unigene29344_All	1021	1.02	0.10	0.52	4.54	2.77	1.28	0.75	0.53	0.66	-3.37E+00	2.13E-04	Down	-9.75E-01	1.67E-01		-7.14E-01	6.76E-03		-1.82E+00	1.47E-09	Down	-4.86E-01	5.25E-01		-1.68E-01	7.94E-01		Unigene29344_All//gi|224126161|ref|XP_002319770.1|//1.00E-124//cytochrome P450 [Populus trichocarpa] >gi|222858146|gb|EEE95693.1|cytochrome P450 [Populus trichocarpa]	Unigene29344_All//6.00E-97//AT2G37690| CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene29344_All//4.00E-133//TC171887		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0016491	nr +
Unigene29345_All	314	0.00	2.42	0.34	4.28	2.63	0.29	1.48	1.46	1.02	1.12E+01	1.77E-04	Up	8.41E+00	3.98E-01		-7.03E-01	2.18E-01		-3.90E+00	2.12E-06	Down	-1.67E-02	1.02E+00		-5.45E-01	5.66E-01				Unigene29345_All//1.00E-16//gi|48817141|gb|CO118454.1|CO118454				

Unigene29346_All	222	217.53	52.72	179.42	72.03	75.23	36.21	0.00	0.00	0.54	-2.04E+00	1.03E-101	Down	-2.78E-01	5.07E-04		6.27E-02	7.32E-01		-9.92E-01	8.10E-13		null	null		9.07E+00	2.43E-01		Unigene29346_All//gi|15240938|ref|NP_198667.1|//4.00E-07//rhomboid family protein [Arabidopsis thaliana] >gi|145334671|ref|NP_001078681.1| rhomboid family protein [Arabidopsis thaliana] >gi|46518449|gb|AAS99706.1| At5g38510 [Arabidopsis thaliana]		Unigene29346_All//2.00E-122//TC154843			GO:0016020	nr +
Unigene29349_All	552	0.00	0.18	0.19	0.63	1.06	1.72	3.22	0.38	1.73	7.52E+00	3.87E-01		7.59E+00	3.98E-01		7.47E-01	4.81E-01		1.44E+00	5.71E-02		-3.09E+00	6.63E-08	Down	-8.93E-01	3.36E-02		Unigene29349_All//gi|15220004|ref|NP_178104.1|//5.00E-72//ROPGEF12 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 12); Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana] >gi|190610066|gb|ACE79744.1| At1g79860 [Arabidopsis thaliana]	Unigene29349_All//3.00E-73//AT1G79860| ROPGEF12 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 12); Rho guanyl-nucleotide exchange factor	Unigene29349_All//2.00E-99//TC136788			GO:0000904//GO:0003006//GO:0005088//GO:0016020//GO:0016772//GO:0043231	nr +
Unigene29351_All	482	3.15	7.78	7.51	18.40	11.36	13.77	1.93	3.38	1.74	1.31E+00	7.33E-05	Up	1.25E+00	2.82E-04	Up	-6.96E-01	1.03E-04		-4.18E-01	3.44E-02		8.09E-01	8.07E-02		-1.53E-01	7.93E-01								
Unigene29352_All	594	22.90	14.16	56.39	3.52	11.48	6.08	0.00	0.00	0.13	-6.94E-01	5.37E-06		1.30E+00	6.17E-36	Up	1.70E+00	2.64E-13	Up	7.88E-01	1.53E-02		null	null		7.07E+00	4.04E-01								
Unigene29354_All	622	1.26	0.90	1.28	2.40	3.82	1.02	1.50	0.20	0.51	-4.94E-01	5.30E-01		2.54E-02	9.94E-01		6.69E-01	1.10E-01		-1.24E+00	2.45E-02		-2.89E+00	3.28E-04	Down	-1.55E+00	1.68E-02			Unigene29354_All//2.00E-180//TC155287				
Unigene29355_All	593	0.79	2.05	0.90	5.12	8.77	3.88	6.56	6.98	37.49	1.37E+00	3.15E-02		1.77E-01	8.45E-01		7.75E-01	2.13E-03		-4.00E-01	3.02E-01		8.92E-02	7.62E-01		2.51E+00	3.44E-75	Up	Unigene29355_All//gi|115338597|gb|AB194388.1|//2.00E-35//isopentyl diphosphate isomerase [Gossypium barbadense]	Unigene29355_All//6.00E-31//AT3G02780| IPP2 (ISOPENTENYL PYROPHOSPHATE:DIMETHYLALLYL PYROPHOSPHATE ISOMERASE 2); isopentenyl-diphosphate delta-isomerase	Unigene29355_All//2.00E-118//CD809327		ko00900|Terpenoid backbone biosynthesis	GO:0006720//GO:0006779//GO:0016863//GO:0043169	nr -
Unigene29356_All	346	20.26	22.26	19.85	24.62	31.85	27.93	36.29	18.12	21.42	1.36E-01	5.65E-01		-2.95E-02	9.12E-01		3.71E-01	3.02E-02		1.82E-01	3.92E-01		-1.00E+00	7.69E-12	Down	-7.61E-01	5.33E-08		Unigene29356_All//gi|126512826|gb|AB015583.1|//1.00E-10//LLP-Rop1 [Lilium longiflorum]	Unigene29356_All//4.00E-12//AT1G75840| ARAC5 (RAC-LIKE GTP BINDING PROTEIN 5); GTP binding / GTPase	Unigene29356_All//4.00E-87//TC168845		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene29361_All	542	65.74	115.17	73.00	13.51	30.94	19.42	0.00	0.00	0.22	8.09E-01	7.83E-32		1.51E-01	1.18E-01		1.20E+00	2.87E-19	Up	5.23E-01	2.76E-03		null	null		7.78E+00	2.43E-01		Unigene29361_All//gi|87138093|gb|AB028283.1|//3.00E-50//zinc finger protein CONSTANS-LIKE 2 [Glycine max]	Unigene29361_All//6.00E-35//AT3G02380| COL2 (constans-like 2); transcription factor/ zinc ion binding	Unigene29361_All//0.00E+00//TC141709	C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0044464//GO:0046914	nr -
Unigene29363_All	476	0.22	1.49	0.67	3.45	2.53	0.76	2.84	0.70	1.51	2.76E+00	9.14E-03		1.61E+00	3.05E-01		-4.48E-01	3.94E-01		-2.19E+00	1.26E-04	Down	-2.02E+00	4.01E-04	Down	-9.16E-01	6.35E-02			Unigene29363_All//1.00E-20//TC163694				
Unigene29366_All	284	0.55	5.17	0.94	1.05	0.97	1.43	0.74	1.47	2.10	3.23E+00	1.15E-05	Up	7.62E-01	6.44E-01		-1.18E-01	9.00E-01		4.44E-01	7.01E-01		9.83E-01	3.73E-01		1.50E+00	7.88E-02			Unigene29366_All//5.00E-83//TC143711				
Unigene29367_All	413	0.00	1.72	0.00	1.81	1.08	0.55	4.09	4.66	4.53	1.02E+01	3.33E-04	Up	null	null		-7.39E-01	3.57E-01		-1.73E+00	5.00E-02		1.83E-01	6.68E-01		1.47E-01	7.25E-01								
Unigene29369_All	446	93.97	98.16	77.01	54.17	94.12	60.05	32.99	14.24	62.17	6.30E-02	5.06E-01		-2.87E-01	8.89E-04		7.97E-01	9.69E-25		1.49E-01	2.19E-01		-1.21E+00	2.28E-18	Down	9.14E-01	3.25E-22			Unigene29369_All//0.00E+00//TC175160				
Unigene29370_All	667	252.19	315.72	343.69	472.53	343.99	459.42	479.09	172.45	131.40	3.24E-01	1.08E-20		4.47E-01	5.73E-39		-4.58E-01	2.03E-70		-4.06E-02	2.37E-01		-1.47E+00	0.00E+00	Down	-1.87E+00	0.00E+00	Down	Unigene29370_All//gi|211905341|gb|ACJ11250.1|//9.00E-55//S-adenosyl-L-homocystein hydrolase [Gossypium hirsutum]	Unigene29370_All//3.00E-42//AT4G13940| MEES8 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding	Unigene29370_All//0.00E+00//TC177368		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0003006//GO:0006342//GO:0010608//GO:0016020//GO:0016802//GO:0043231//GO:0046914	nr -
Unigene29372_All	427	4.90	16.26	4.36	5.83	8.23	13.54	28.22	45.61	26.68	1.73E+00	3.50E-12	Up	-1.67E-01	7.06E-01		4.96E-01	1.45E-01		1.21E+00	1.20E-06	Up	6.93E-01	6.53E-10		-8.08E-02	6.25E-01			Unigene29372_All//7.00E-176//TC140320				
Unigene29373_All	664	1.10	1.53	1.12	5.48	6.22	3.95	2.36	0.31	0.66	4.68E-01	4.89E-01		2.54E-02	9.95E-01		1.84E-01	5.99E-01		-4.73E-01	1.58E-01		-2.90E+00	1.13E-06	Down	-1.84E+00	2.17E-04	Down	Unigene29373_All//gi|78128515|gb|AB822752.1|//2.00E-31//ferritin [Chorispora bungeana]	Unigene29373_All//2.00E-19//AT2G40300| ATFER4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal ion binding	Unigene29373_All//0.00E+00//TC132347		ko00860|Porphyrin and chlorophyll metabolism	GO:0000041//GO:0005506//GO:0008152//GO:0009536//GO:0016724//GO:0030005	nr -
Unigene29374_All	371	2.68	6.28	11.91	8.86	8.26	8.40	1.14	0.45	1.29	1.23E+00	4.09E-03		2.15E+00	4.66E-10	Up	-1.01E-01	8.11E-01		-7.73E-02	8.37E-01		-1.34E+00	2.24E-01		1.77E-01	8.46E-01			Unigene29374_All//3.00E-159//DR458674				
Unigene29376_All	637	1.15	0.48	0.59	2.66	1.62	1.84	2.19	0.79	0.31	-1.27E+00	1.36E-01		-9.75E-01	2.64E-01		-7.13E-01	1.48E-01		-5.28E-01	3.21E-01		-1.48E+00	4.92E-03		-2.81E+00	4.25E-06	Down							
Unigene29379_All	976	0.96	0.05	0.33	3.98	2.33	0.83	1.08	0.39	0.41	-4.22E+00	1.36E-04	Down	-1.56E+00	4.90E-02		-7.74E-01	8.05E-03		-2.26E+00	1.61E-10	Down	-1.49E+00	1.64E-02		-1.41E+00	1.72E-02		Unigene29379_All//gi|10177143|dbj|BAB10503.1|//1.00E-41//retroelement pol polyprotein-like [Arabidopsis thaliana]	Unigene29379_All//2.00E-24//AT4G23160| protein kinase family protein			GO:0005488	nr +
Unigene29381_All	446	7.51	0.68	0.00	71.26	34.98	65.31	0.66	1.22	0.80	-3.46E+00	4.89E-13	Down	-1.29E+01	2.27E-18	Down	-1.03E+00	8.28E-30	Down	-1.26E-01	2.58E-01		8.77E-01	3.46E-01		2.77E-01	7.87E-01		Unigene29381_All//gi|7025493|gb|AAF35901.1|AF230332_1//2.00E-33//expansin 2 [Zinnia violacea]	Unigene29381_All//7.00E-23//AT1G26770| ATEXPA10 (ARABIDOPSIS THALIANA EXPANSIN A 10); structural constituent of cell wall	Unigene29381_All//9.00E-160//gi|78335807|gb|DT556081.1|DT556081			GO:0007047//GO:0044464	nr -
Unigene29383_All	500	0.00	3.85	1.70	1.00	1.10	5.60	0.51	0.42	3.43	1.19E+01	5.73E-11	Up	1.07E+01	9.03E-05	Up	1.45E-01	9.05E-01		2.49E+00	2.21E-08	Up	-2.80E-01	8.29E-01		2.76E+00	4.59E-07	Up	Unigene29383_All//gi|18395843|ref|NP_566139.1|//1.00E-42//5'-AMP-activated protein kinase beta-1 subunit-related [Arabidopsis thaliana]	Unigene29383_All//3.00E-43//AT3G01510| 5'-AMP-activated protein kinase beta-1 subunit-related	Unigene29383_All//0.00E+00//TC140851			GO:0004721//GO:0005488//GO:0006464//GO:0043231	nr +
Unigene29385_All	690	0.15	0.95	0.31	8.88	6.04	4.45	1.78	0.24	0.29	2.65E+00	1.50E-02		1.03E+00	5.91E-01		-5.56E-01	1.46E-02		-9.96E-01	2.36E-05		-2.87E+00	2.54E-05	Down	-2.62E+00	4.02E-05	Down	Unigene29385_All//gi|115452921|ref|NP_001650061.1|//1.00E-17//Os03g0339700 (Oryza sativa Japonica Group) >gi|108708050|gb|ABF95845.1| expressed protein (Oryza sativa (japonica cultivar-group)) >gi|113548532|dbj|BAF11975.1| Os03g0339700 (Oryza sativa Japonica Group)	Unigene29385_All//1.00E-54//AT2G40480| unknown protein	Unigene29385_All//1.00E-82//TC143717			GO:0005488	nr -
Unigene29389_All	296	74.95	51.01	35.80	152.81	130.88	187.52	142.84	104.91	65.41	-5.55E-01	1.72E-06		-1.07E+00	1.37E-17	Down	-2.24E-01	3.72E-03		2.95E-01	2.12E-05		-4.45E-01	1.02E-09		-1.13E+00	4.31E-47	Down	Unigene29389_All//gi|164652934|gb|ABV65000.1|//1.00E-49//14-3-3a protein [Gossypium hirsutum]	Unigene29389_All//2.00E-43//AT1G22300| GRF10 (GENERAL REGULATORY FACTOR 10); ATP binding / protein binding / protein phosphorylated amino acid binding	Unigene29389_All//2.00E-159//gi|21090223|gb|BQ402536.1|BQ402536			GO:0005515	nr -
Unigene2939_All	1029	1.83	17.14	6.78	30.89	41.23	43.50	2.05	7.55	6.43	3.23E+00	7.69E-62	Up	1.89E+00	3.22E-13	Up	4.17E-01	3.57E-08		4.94E-01	1.34E-10		1.88E+00	1.89E-18	Up	1.65E+00	1.31E-13	Up	Unigene2939_All//gi|195638024|gb|AC538480.1|//2.00E-82//cytochrome c oxidoreductase [Zea mays]	Unigene2939_All//6.00E-58//AT4G15920| INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPR018169), RAG1-activating protein 1 homologue (InterPro:IPR018179), MtN3 and saliva related transmembrane protein (InterPro:IPR004316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene2939_All//0.00E+00//TC173244			GO:0031224	nr -
Unigene29391_All	472	113.84	72.78	85.52	152.93	175.09	142.19	155.86	70.40	123.82	-6.45E-01	7.83E-19		-4.13E-01	2.17E-08		1.95E-01	4.04E-04		-1.05E-01	1.34E-01		-1.15E+00	2.83E-81	Down	-3.32E-01	4.36E-10		Unigene29391_All//gi|195658081|gb|ACG48508.1|//1.00E-23//60S ribosomal protein L21 [Zea mays]	Unigene29391_All//8.00E-24//AT1G57860| 60S ribosomal protein L21	Unigene29391_All//5.00E-152//BG444561		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr -
Unigene29393_All	296	2.47	15.41	23.57	11.78	22.34	35.09	0.29	0.56	1.62	2.64E+00	1.78E-13	Up	3.25E+00	3.29E-24	Up	9.23E-01	2.34E-05		1.57E+00	1.14E-16	Up	9.83E-01	6.33E-01		2.50E+00	2.51E-02		Unigene29393_All//gi|167962545|dbj|BAG09377.1|//2.00E-06//peroxisomal betaine-aldehyde dehydrogenase [Glycine max]	Unigene29393_All//7.00E-07//AT3G48170| ALDH10A9; 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Unigene29393_All//4.00E-164//CA993845		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene29395_All	563	0.65	3.51	4.63	3.72	2.57	1.60	0.00	0.00	0.07	2.43E+00	9.73E-06	Up	2.83E+00	3.22E-08	Up	-5.33E-01	2.31E-01		-1.21E+00	6.91E-03		null	null		6.15E+00	6.45E-01		Unigene29395_All//gi|225637998|gb|ACN97419.1|//8.00E-55//thaumatin-like protein [Pyrus pyrifolia]	Unigene29395_All//7.00E-44//AT1G75800| pathogenesis-related thaumatin family protein	Unigene29395_All//0.00E+00//TC163905			GO:0006952//GO:0016787	nr +
Unigene29398_All	558	2.72	3.90	8.02	0.71	1.48	0.89	0.00	0.00	0.14	5.22E-01	2.36E-01		1.56E+00	8.41E-07	Up	1.05E+00	1.99E-01		3.18E-01	7.58E-01		null	null		7.16E+00	4.04E-01		Unigene29398_All//gi|124339162|gb|ABN05685.1|//4.00E-08//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene29398_All//1.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative					nr -
Unigene29399_All	745	3.09	0.61	0.29	5.22	4.90	2.61	0.96	1.29	0.11	-2.34E+00	2.32E-06	Down	-3.43E+00	1.38E-08	Down	-9.01E-02	8.20E-01		-1.00E+00	1.13E-03		4.19E-01	5.31E-01		-3.17E+00	8.09E-04	Down	Unigene29399_All//gi|159025703|emb|CAN88852.1|//2.00E-74//D1-type cyclin [Populus trichocarpa]	Unigene29399_All//9.00E-30//AT2G22490| CYCD2;1 (Cyclin D2;1); cyclin-dependent protein kinase regulator/ protein binding	Unigene29399_All//0.00E+00//gi|78344701|gb|DT564975.1|DT564975			GO:0009987//GO:0043231	nr -
Unigene294_All	412	2.16	0.25	0.26	4.96	5.35	12.72	65.47	112.30	65.66	-3.13E+00	1.19E-03		-3.06E+00	2.25E-03		1.10E-01	8.25E-01		1.36E+00	4.17E-07	Up	7.78E-01	2.86E-27		4.00E-03	9.65E-01		Unigene294_All//gi|41052474|dbj|BAD07484.1|//9.00E-47//PDR-type ABC transporter 2 [Nicotiana tabacum]	Unigene294_All//6.00E-47//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene294_All//4.00E-168//TC147767		ko02010|ABC transporters		nr +
Unigene2940_All	703	9.01	11.60	9.92	8.15	7.05	7.65	1.80	4.58	1.70	3.66E-01	7.79E-02		1.40E-01	5.92E-01		-2.08E-01	4.47E-01		-9.21E-02	7.32E-01		1.34E+00	2.74E-05	Up	-8.58E-02	8.72E-01			Unigene2940_All//1.00E-42//TC165396				
Unigene29404_All	359	0.58	0.85	1.19	6.38	3.07	1.26	1.77	2.21	1.44	5.39E-01	6.71E-01		1.03E+00	3.96E-01		-1.06E+00	8.04E-03		-2.34E+00	1.06E-06	Down	3.24E-01	6.33E-01		-2.92E-01	6.84E-01								
Unigene29406_All	360	0.15	3.38	1.48	3.32	1.91	1.25	1.29	1.39	1.33	4.54E+00	6.47E-06	Up	3.35E+00	2.06E-02		-7.96E-01	1.87E-01		-1.40E+00	2.82E-02		1.09E-01	9.14E-01		3.98E-02	9.76E-01		Unigene29406_All//gi|146552062|gb|ABQ42205.1|//2.00E-28//dehydration-responsive element binding protein 6 [Glycine max]	Unigene29406_All//1.00E-23//AT2G44940| AP2 domain-containing transcription factor TINY, putative	Unigene29406_All//4.00E-81//DR512859	AP2-EREBP		GO:0001071//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene29408_All	805	0.71	1.45	0.26	3.77	1.63	3.82	2.10	0.83	1.88	1.02E+00	1.10E-01		-1.43E+00	1.75E-01		-1.22E+00	3.11E-04	Down	1.53E-02	9.66E-01		-1.34E+00	3.80E-03		-1.60E-01	7.13E-01		Unigene29408_All//gi|226494694|ref|NP_001151344.1|//1.00E-114//arsenical pump-driving ATPase [Zea mays] >gi|195645964|gb|ACG42450.1| arsenical pump-driving ATPase [Zea mays]	Unigene29408_All//1.00E-104//AT3G10350| anion-transporting ATPase family protein	Unigene29408_All//5.00E-27//TC168472			GO:0003824//GO:0030003//GO:0032559	nr -
Unigene29411_All	518	2.02	0.10	1.03	1.44	1.33	1.66	1.88	1.05	0.31	-4.37E+00	3.91E-05	Down	-9.75E-01	1.67E-01		-1.18E-01	8.62E-01		2.00E-01	7.89E-01		-8.40E-01	1.87E-01		-2.61E+00	3.35E-04	Down	Unigene29411_All//gi|223452550|gb|ACM89602.1|//2.00E-22//receptor protein kinase-like protein [Glycine max]	Unigene29411_All//1.00E-17//AT4G08850| kinase	Unigene29411_All//2.00E-142//gi|109874656|gb|DW503630.1|DW503630		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr -
Unigene29413_All	1648	0.13	0.06	0.78	4.72	10.55	7.76	0.05	0.43	0.00	-1.05E+00	5.65E-01		2.61E+00	5.01E-04	Up	1.16E+00	4.07E-19	Up	7.18E-01	3.40E-06		3.07E+00	1.67E-03		-5.68E+00	3.58E-01		Unigene29413_All//gi|224096498|ref|XP_002310634.1|//1.00E-154//cytochrome P450 [Populus trichocarpa] >gi|222853537|gb|EEE91084.1| cytochrome P450 [Populus trichocarpa]	Unigene29413_All//4.00E-99//AT3G26310| CYP71B35; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene29413_All//0.00E+00//TC157205		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene29414_All	400	6.93	0.38	3.59	3.11	1.46	0.79	1.59	0.10	1.00	-4.19E+00	1.74E-12	Down	-9.48E-01	1.68E-02		-1.09E+00	6.06E-02		-1.98E+00	2.61E-03		-3.92E+00	9.81E-04	Down	-6.71E-01	3.86E-01		Unigene29414_All//gi|225451804|ref|XP_002281338.1|//2.00E-62//PREDICTED: brassinosteroid-6-oxidase [Vitis vinifera]	Unigene29414_All//2.00E-55//AT5G38970| BR6OX1 (BRASSINOSTEROID-6-OXIDASE 1); monooxygenase/ oxygen binding	Unigene29414_All//3.00E-94//TC166913		ko00905|Brassinosteroid biosynthesis	GO:0000226//GO:0005506//GO:0006091//GO:0009646//GO:0016129//GO:0016491//GO:0031224//GO:0032501//GO:0048878	nr -
Unigene29416_All	341	122.90	59.14	58.56	125.05	112.09	198.14	154.86	91.07	71.38	-1.06E+00	1.83E-33	Down	-1.07E+00	6.24E-33	Down	-1.58E-01	6.54E-02		6.64E-01	2.69E-26		-7.66E-01	3.28E-30		-1.12E+00	8.15E-58	Down	Unigene29416_All//1.00E-CAC20221.1|//2.00E-59//ribosomal protein L2 [Glycine max]	Unigene29416_All//1.00E-60//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene29416_All//0.00E+00//gi|132456608|gb|BE053920.2|BE053920		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene29417_All	533	1.18	25.10	1.50	0.93	4.91	2.03	6.43	11.68	22.27	4.41E+00	5.00E-60	Up	3.47E-01	6.35E-01		2.39E+00	5.83E-08	Up	1.12E+00	1.03E-01		8.63E-01	4.62E-05		1.79E+00	1.05E-26	Up							
Unigene29418_All	468	25.38	6.93	18.66	11.81	11.77	9.46	0.27	0.18	0.43	-1.87E+00	9.45E-23	Down	-4.44E-01	1.02E-02		-5.20E-03	9.76E-01		-3.21E-01	2.38E-01		-6.02E-01	7.66E-01		6.51E-01	6.65E-01		Unigene29418_All//gi|30690642|ref|NP_195357.2|//2.00E-18//radical SAM domain-containing protein / TRAM domain-containing protein [Arabidopsis thaliana] >gi|32129440|sp|Q8H0V1.1|CKSP1_ARATH RecName: Full=CDK5RAP1-like protein >gi|30725464|gb|AAP37754.1| At4g36390 [Arabidopsis thaliana]	Unigene29418_All//1.00E-19//AT4G36390| radical SAM domain-containing protein / TRAM domain-containing protein				GO:0016070//GO:0051536	nr -

Unigene29419_All	439	0.48	0.23	1.94	1.48	1.10	1.03	2.22	0.00	0.09	-1.05E+00	5.65E-01		2.03E+00	2.24E-02		-4.26E-01	6.08E-01		-5.20E-01	5.88E-01		-1.11E+01	5.83E-07	Down	-4.61E+00	3.32E-06	Down	Unigene29419_All//gi|57283317|emb|CAG26717.1|//2.00E-38//nitrate transporter [Populus tremula x Populus tremuloides]	Unigene29419_All//8.00E-30//AT1G12940| ATNRT2.5 (nitrate transporter2.5); nitrate transmembrane transporter	Unigene29419_All//8.00E-151//DN816839			GO:0006810//GO:0016020	nr +
Unigene2942_All	1639	6.10	7.98	7.99	8.42	8.49	5.95	5.96	5.53	2.77	3.88E-01	1.40E-02		3.91E-01	1.76E-02		1.18E-02	9.50E-01		-5.00E-01	7.60E-04		-1.07E-01	6.05E-01		-1.10E+00	3.15E-11	Down	Unigene2942_All//gi|297816094|ref|XP_002875930.1|//1.00E-111//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321768|gb|EFH52189.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2942_All//4.00E-104//AT3G48880| F-box family protein	Unigene2942_All//0.00E+00//gi|133543390|gb|BG444738.1|BG444738				nr -
Unigene29420_All	579	1.90	4.38	5.15	0.00	0.48	0.47	2.19	8.95	10.60	1.21E+00	3.11E-03		1.44E+00	2.51E-04	Up	8.89E+00	7.02E-02		8.87E+00	7.03E-02		2.03E+00	8.04E-14	Up	2.27E+00	5.26E-19	Up	Unigene29420_All//gi|115479571|ref|NP_001063379.1|//1.00E-12//Os09g0458900 [Oryza sativa Japonica Group] >gi|113631612|dbj|BAF25293.1|Os09g0458900 [Oryza sativa Japonica Group]	Unigene29420_All//4.00E-09//AT2G43290| MSS3 (multicopy suppressors of snf4 deficiency in yeast 3); calcium ion binding	Unigene29420_All//1.00E-119//DN801022		ko04626|Plant-pathogen interaction		nr -
Unigene29422_All	361	1.74	0.56	0.89	2.35	1.53	2.63	1.41	2.08	6.18	-1.63E+00	9.23E-02		-9.75E-01	3.16E-01		-6.20E-01	4.13E-01		1.63E-01	8.25E-01		5.68E-01	4.47E-01		2.14E+00	6.41E-07	Up	Unigene29422_All//gi|297808313|ref|XP_002872040.1|//6.00E-06//enhancer of ag-4 2 [Arabidopsis lyrata subsp. lyrata] >gi|297317877|gb|EFH48299.1| enhancer of ag-4 2 [Arabidopsis lyrata subsp. lyrata]		Unigene29422_All//2.00E-24//TC157199			GO:0009908//GO:0048496//GO:0048506	nr -
Unigene29423_All	728	4.24	1.18	0.95	0.55	0.28	0.56	2.73	4.19	7.72	-1.84E+00	2.51E-06	Down	-2.16E+00	3.48E-07	Down	-9.48E-01	4.21E-01		2.84E-02	9.85E-01		6.19E-01	5.41E-02		1.50E+00	2.53E-10	Up	Unigene29423_All//gi|224142613|ref|XP_002324649.1|//3.00E-27//equilibrative nucleoside transporter [Populus trichocarpa] >gi|222866083|gb|EEF03214.1| equilibrative nucleoside transporter [Populus trichocarpa]	Unigene29423_All//4.00E-14//AT1G02630| equilibrative nucleoside transporter, putative (ENT8)	Unigene29423_All//2.00E-23//TC176124				nr +
Unigene29424_All	736	0.57	4.41	2.68	1.90	2.29	5.52	6.32	10.17	3.90	2.95E+00	6.75E-11	Up	2.23E+00	5.06E-05	Up	2.75E-01	6.18E-01		1.54E+00	1.09E-06	Up	6.86E-01	2.99E-04		-6.97E-01	3.79E-03		Unigene29424_All//gi|30102564|gb|AAP21200.1|//2.00E-14//At3g19660 [Arabidopsis thaliana]	Unigene29424_All//1.00E-15//AT3G19660| unknown protein	Unigene29424_All//6.00E-17//DW504286			GO:0031410	nr +
Unigene29426_All	2424	0.00	5.04	4.85	0.00	0.04	0.02	0.00	0.00	0.02	1.23E+01	4.70E-70	Up	1.22E+01	3.66E-66	Up	5.41E+00	4.56E-01		4.22E+00	6.96E-01		null	null		4.04E+00	6.45E-01		Unigene29426_All//gi|29539334|dbj|BAC67668.1|//0.00E+00//elongation factor-2 [Cyanidioschyzon merolae]	Unigene29426_All//0.00E+00//AT1G56070| LGS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding				GO:0000166//GO:0006950//GO:0008135//GO:0009536//GO:0016020//GO:0016787//GO:0031981//GO:0046914	nr +
Unigene29427_All	525	0.90	0.58	3.35	0.47	0.92	0.52	0.81	3.18	0.76	-6.31E-01	5.54E-01		1.90E+00	7.52E-04	Up	9.53E-01	4.24E-01		1.22E-01	9.44E-01		1.98E+00	7.99E-05	Up	-8.58E-02	9.39E-01		Unigene29427_All//gi|224112158|ref|XP_002332820.1|//2.00E-15//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834208|gb|EEE72685.1| cc-nbs-lrr resistance protein [Populus trichocarpa]						nr +
Unigene29428_All	340	1.23	1.19	0.31	4.69	1.62	0.80	2.24	3.32	2.81	-4.63E-02	9.80E-01		-1.97E+00	1.51E-01		-1.53E+00	2.44E-03		-2.56E+00	2.78E-05	Down	5.68E-01	3.44E-01		3.29E-01	5.93E-01					Unigene29428_All//4.00E-07//ES826490					
Unigene29430_All	604	0.69	1.51	0.71	4.70	6.39	1.27	1.54	0.28	0.79	1.12E+00	1.30E-01		2.54E-02	1.00E+00		4.42E-01	1.71E-01		-1.89E+00	2.34E-06	Down	-2.48E+00	1.07E-03		-9.60E-01	1.20E-01		Unigene29430_All//gi|30684136|ref|NP_850130.1|//1.00E-30//RTFL2 (ROTUNDIFOLIA LIKE 2) [Arabidopsis thaliana] >gi|42822059|tpg|DAA02284.1| TPA_exp: DWL13 [Arabidopsis thaliana]	Unigene29430_All//2.00E-14//AT3G29125| RTFL2 (ROTUNDIFOLIA LIKE 2)	Unigene29430_All//0.00E+00//gi|109889877|gb|DW518845.1|DW518845			GO:0009536//GO:0048513	nr -
Unigene29432_All	2260	0.12	0.04	0.16	0.11	0.08	0.00	2.53	1.89	11.76	-1.37E+00	3.83E-01		5.10E-01	6.54E-01		-5.32E-01	7.12E-01		-6.78E+00	7.34E-02		-4.21E-01	6.46E-02		2.22E+00	2.15E-77	Up	Unigene29432_All//gi|256538311|gb|ACU82515.1|//0.00E+00//pleiotropic drug resistance protein [Cucumis sativus]	Unigene29432_All//0.00E+00//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene29432_All//0.00E+00//TC147767		ko03040|Spliceosome//ko02010|ABC transporters	GO:0016887	nr +
Unigene29437_All	370	1.70	2.33	1.30	3.23	4.56	1.59	1.83	1.58	0.11	4.56E-01	5.46E-01		-3.90E-01	6.46E-01		4.97E-01	3.60E-01		-1.03E+00	1.06E-01		-2.09E-01	7.82E-01		-4.09E+00	3.10E-04	Down				Unigene29437_All//3.00E-97//gi|13352472|gb|BG442820.1|BG442820				
Unigene29438_All	207	27.80	64.62	31.13	22.38	31.11	16.58	70.67	103.58	110.47	1.22E+00	8.19E-14	Up	1.63E-01	5.38E-01		4.75E-01	4.04E-02		-4.33E-01	1.38E-01		5.52E-01	1.74E-07		6.45E-01	1.66E-10		Unigene29438_All//gi|297831216|ref|XP_002883490.1|//2.00E-26//transaminase [Arabidopsis lyrata subsp. lyrata] >gi|297326330|gb|EFH59749.1| transaminase [Arabidopsis lyrata subsp. lyrata]	Unigene29438_All//1.00E-27//AT3G24090| glutamine-fructose-6-phosphate transaminase (isomerizing)/ sugar binding / transaminase	Unigene29438_All//1.00E-113//TC164771		ko00520|Amino sugar and nucleotide sugar metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0005975//GO:0008483//GO:0030246//GO:0043231	nr -
Unigene29439_All	1208	0.61	25.96	3.57	0.00	1.68	3.96	0.11	0.00	0.00	5.42E+00	5.31E-157	Up	2.56E+00	6.19E-12	Up	1.07E+01	1.10E-12	Up	1.20E+01	6.33E-29	Up	-6.71E+00	2.35E-01		-6.71E+00	2.00E-01		Unigene29439_All//gi|224129384|ref|XP_002326573.1|//1.00E-143//bile acid:Na+ symporter family protein [Populus trichocarpa] >gi|222861346|gb|EEE98888.1| bile acid:Na+ symporter family protein [Populus trichocarpa]	Unigene29439_All//3.00E-123//AT3G25410| bile acid:sodium symporter family protein	Unigene29439_All//0.00E+00//CO120157				nr -
Unigene29440_All	679	1.70	0.22	0.63	2.49	3.14	1.33	2.62	0.62	0.76	-2.92E+00	2.75E-04	Down	-1.43E+00	3.87E-02		3.34E-01	5.11E-01		-9.07E-01	7.45E-02		-2.09E+00	2.21E-05	Down	-1.78E+00	1.06E-04	Down	Unigene29440_All//gi|30688490|ref|NP_194720.2|//7.00E-48//ORC5 (ORIGIN RECOGNITION COMPLEX PROTEIN 5); protein binding [Arabidopsis thaliana] >gi|49659272|emb|CAE01429.1| origin recognition complex 5 subunit [Arabidopsis thaliana]	Unigene29440_All//4.00E-49//AT4G29910| ORC5 (ORIGIN RECOGNITION COMPLEX PROTEIN 5); protein binding				GO:0005515//GO:0006259//GO:0043229	nr +
Unigene29443_All	304	3.10	4.17	1.75	7.37	4.42	4.90	11.68	4.81	1.83	4.28E-01	4.74E-01		-8.23E-01	2.71E-01		-7.39E-01	7.26E-02		-5.89E-01	1.85E-01		-1.28E+00	2.07E-05	Down	-2.67E+00	1.11E-13	Down	Unigene29443_All//gi|255548810|ref|XP_002515461.1|//5.00E-07//Aberrant root formation protein, putative [Ricinus communis] >gi|223545405|gb|EEF46910.1| Aberrant root formation protein, putative [Ricinus communis]	Unigene29443_All//3.00E-05//AT5G11030| ALF4 (ABERRANT LATERAL ROOT FORMATION 4)	Unigene29443_All//1.00E-108//gi|21096022|gb|BQ408335.1|BQ408335				nr -
Unigene29444_All	393	24.23	23.85	15.04	27.00	25.59	32.52	75.63	38.18	27.07	-2.27E-02	9.22E-01		-6.88E-01	3.64E-04		-7.76E-02	7.25E-01		2.69E-01	1.15E-01		-9.86E-01	3.19E-26		-1.48E+00	1.18E-50	Down				Unigene29444_All//0.00E+00//TC178745				
Unigene29445_All	1926	0.87	0.26	0.50	0.78	0.68	1.20	1.58	1.37	4.22	-1.72E+00	1.56E-03		-8.05E-01	1.35E-01		-1.92E-01	7.47E-01		6.24E-01	1.53E-01		-2.09E-01	5.66E-01		1.42E+00	1.88E-13	Up									
Unigene29446_All	881	0.00	0.92	0.36	0.17	0.16	1.69	25.72	210.07	46.80	9.85E+00	9.38E-05	Up	8.50E+00	4.52E-02		-1.18E-01	9.11E-01		3.32E+00	4.73E-06	Up	3.03E+00	0.00E+00	Up	8.64E-01	1.10E-29		Unigene29446_All//gi|18397934|ref|NP_565380.1|//5.00E-35//glycine-rich protein [Arabidopsis thaliana] >gi|15294186|gb|AAK95270.1|AF410284_1 At2g15780/F19G14.22 [Arabidopsis thaliana] >gi|5306253|gb|AAD41986.1| expressed protein [Arabidopsis thaliana] >gi|20147265|gb|AAM10346.1| At2g15780/F19G14.22 [Arabidopsis thaliana]	Unigene29446_All//8.00E-35//AT2G15780| glycine-rich protein	Unigene29446_All//1.00E-09//TC145831				nr +
Unigene29447_All	669	1.09	0.15	0.32	1.56	2.47	1.62	2.02	5.31	0.36	-2.85E+00	6.26E-03		-1.78E+00	6.00E-02		6.60E-01	2.18E-01		5.12E-02	9.47E-01		1.39E+00	4.89E-06	Up	-2.50E+00	2.46E-05	Down				Unigene29447_All//3.00E-151//gi|198883973|gb|DW512943.1|DW512943				
Unigene29449_All	405	133.97	131.37	146.73	309.09	270.38	255.15	468.74	342.93	228.31	-2.83E-02	7.25E-01		1.31E-01	8.91E-02		-1.93E-01	7.38E-06		-2.77E-01	4.06E-10		-4.51E-01	1.19E-41		-1.04E+00	1.91E-182	Down	Unigene29449_All//gi|211906462|gb|ACJ11724.1|//1.00E-79//glutamine synthase [Gossypium hirsutum]	Unigene29449_All//1.00E-73//AT5G37600| ATGSR1; copper ion binding / glutamate-ammonia ligase	Unigene29449_All//0.00E+00//ES827183		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006541//GO:0016211//GO:0032559//GO:0044424//GO:0071941	nr -
Unigene29450_All	228	17.67	18.22	10.98	31.90	29.90	27.93	25.41	19.80	10.31	4.45E-02	8.92E-01		-6.87E-01	3.07E-02		-9.31E-02	7.27E-01		-1.92E-01	4.48E-01		-3.60E-01	1.19E-01		-1.30E+00	7.88E-09	Down				Unigene29450_All//3.00E-121//gi|18101034|gb|BM360288.1|BM360288				
Unigene29453_All	314	64.82	143.78	113.11	66.47	128.97	179.79	50.09	113.81	128.40	1.15E+00	4.67E-41	Up	8.03E-01	1.44E-17		9.56E-01	2.61E-32		1.44E+00	2.67E-77	Up	1.18E+00	7.19E-42	Up	1.36E+00	1.85E-59	Up	Unigene29453_All//gi|15233475|ref|NP_193190.1|//5.00E-38//NF-YB3 (NUCLEAR FACTOR Y, SUBUNIT B3); transcription factor [Arabidopsis thaliana] >gi|75219213|sp|Q23310.1|NFYB3_ARATH RecName: Full=Nuclear transcription factor Y subunit B-3; Short=AtNF-YB-3; AltName: Full=Transcriptional activator HAP3C >gi|2248810|emb|CAB10233.1| CCAAT-binding transcription factor subunit A(CBF-A) [Arabidopsis thaliana] >gi|7268160|emb|CAB78496.1| CCAAT-binding transcription factor subunit A(CBF-A) [Arabidopsis thaliana] >gi|28372860|gb|AAO39912.1| At4g14540 [Arabidopsis thaliana]	Unigene29453_All//7.00E-33//AT4G14540| NF-YB3 (NUCLEAR FACTOR Y, SUBUNIT B3); transcription factor	Unigene29453_All//1.00E-167//TC152354	CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication	GO:0001071//GO:0003677//GO:0006351//GO:0043231	nr -
Unigene29455_All	1722	2.37	0.47	1.58	0.64	0.04	0.34	20.97	5.78	6.71	-2.33E+00	1.03E-10	Down	-5.88E-01	6.42E-02		-3.99E+00	3.49E-06	Down	-9.00E-01	1.81E-01		-1.86E+00	4.40E-82	Down	-1.64E+00	3.04E-71	Down	Unigene29455_All//gi|10953887|gb|AAG25643.1|AF303396_1/1.00E-108//UDP-glucosyltransferase HRA25 [Phaseolus vulgaris]	Unigene29455_All//1.00E-99//AT3G02100| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene29455_All//2.00E-25//CO121894		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene29458_All	496	1.48	2.15	0.54	5.12	4.51	16.94	1.53	0.59	0.56	5.39E-01	4.03E-01		-1.46E+00	1.12E-01		-1.83E-01	6.66E-01		1.73E+00	2.21E-15	Up	-1.38E+00	6.73E-02		-1.45E+00	4.46E-02									
Unigene29461_All	579	46.18	20.30	17.93	63.06	48.59	71.45	160.14	76.01	68.67	-1.19E+00	6.43E-26	Down	-1.36E+00	6.90E-31	Down	-3.76E-01	4.32E-06		1.80E-01	4.14E-02		-1.08E+00	3.42E-92	Down	-1.22E+00	3.29E-116	Down	Unigene29461_All//gi|3023858|sp|Q39836.1|GBLP_SOYBN//3.00E-38//RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein >gi|1256608|gb|AAB05941.1| G beta-like protein [Glycine max]	Unigene29461_All//1.00E-38//AT1G48630| RACK1B,AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding	Unigene29461_All//0.00E+00//TC142556			GO:0004683//GO:0004871//GO:0005840//GO:0009536//GO:0010038//GO:0019897//GO:0031981//GO:0048513	nr +
Unigene29464_All	585	0.18	0.69	0.36	0.94	1.77	3.32	1.16	2.50	1.63	1.95E+00	1.44E-01		1.03E+00	5.91E-01		9.15E-01	1.97E-01		1.83E+00	2.80E-04	Up	1.11E+00	2.51E-02		4.99E-01	4.19E-01		Unigene29464_All//gi|119260031|gb|ABL66744.1|//4.00E-36//At1g54200 [Arabidopsis thaliana]	Unigene29464_All//1.00E-24//AT3G13980| unknown protein	Unigene29464_All//0.00E+00//gi|73848774|gb|DT457794.1|DT457794				nr +
Unigene29467_All	871	0.90	0.06	0.98	2.97	2.57	1.81	1.65	1.58	1.05	-3.95E+00	8.54E-04	Down	1.19E-01	8.69E-01		-2.11E-01	6.04E-01		-7.13E-01	7.29E-02		-5.97E-02	9.19E-01		-6.50E-01	1.74E-01		Unigene29467_All//gi|115451891|ref|NP_001049546.1|//5.00E-66//Os02g0246900 [Oryza sativa Japonica Group] >gi|113548017|dbj|BAF11460.1|Os03g0246900 [Oryza sativa Japonica Group]	Unigene29467_All//3.00E-57//AT2G45420| LBD18 (LOB DOMAIN-CONTAINING PROTEIN 18)			ko00250|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0010087//GO:0010160	nr +
Unigene29469_All	366	6.15	5.68	10.91	2.45	6.49	1.85	0.23	0.23	0.00	-1.15E-01	7.78E-01		8.28E-01	9.30E-03		1.41E+00	6.97E-04	Up	-4.04E-01	6.23E-01		-1.63E-02	1.01E+00		-7.85E+00	3.58E-01										
Unigene29470_All	619	2.28	6.55	3.61	2.98	5.34	2.48	0.48	0.47	0.58	1.52E+00	2.60E-06	Up	6.63E-01	1.39E-01		8.43E-01	1.14E-02		-2.63E-01	6.37E-01		-1.67E-02	1.02E+00		2.77E-01	7.87E-01					Unigene29470_All//5.00E-79//DR457022				
Unigene29473_All	484	1.41	0.00	0.99	1.96	0.85	0.56	5.59	4.75	2.47	-1.05E+01	4.10E-04	Down	-5.05E-01	5.82E-01		-1.20E+00	8.32E-02		-1.80E+00	1.83E-02		-2.35E-01	5.40E-01		-1.18E+00	4.69E-04	Down		Unigene29473_All//6.00E-05//AT1G13180| DIS1 (DISTORTED TRICHOMES 1); ATP binding / actin binding / protein binding / structural constituent of cytoskeleton	Unigene29473_All//8.00E-34//DW506841				

Unigene29476_All	1008	6.96	1.86	3.43	0.89	0.79	0.45	0.92	0.95	0.95	-1.90E+00	5.32E-14	Down	-1.02E+00	1.24E-05	Down	-1.79E-01	8.15E-01		-9.90E-01	1.96E-01		4.75E-02	9.64E-01		3.96E-02	9.67E-01		Unigene29476_All//gi|15223284|ref|NP_171611.1|//5.00E-49//NGA3 (NGATHA3); transcription factor [Arabidopsis thaliana] >gi|75192354|sp|Q9MAN1.1|NGA3_ARATH RecName: Full=B3 domain-containing transcription factor NGA3; AltName: Full=Protein NGATHA3 >gi|6715649|gb|AAF26476.1|AC007323_17 T25K16.3 [Arabidopsis thaliana] >gi|227060706|gb|ACF18973.1|NGATHA3 [Arabidopsis thaliana]	Unigene29476_All//4.00E-46//AT1G01030| NGA3 (NGATHA3); transcription factor	Unigene29476_All//0.00E+00//gi|109869303|gb|DW498279.1|DW498279	AB13VP1		GO:0006350//GO:0009791//GO:0010468//GO:0048827	nr -
Unigene2948_All	2101	57.75	48.98	47.85	35.87	33.91	38.24	31.78	63.90	69.13	-2.38E-01	3.63E-07		-2.71E-01	1.41E-08		-8.11E-02	2.45E-01		9.22E-02	1.72E-01		1.01E+00	1.06E-119	Up	1.12E+00	2.59E-157	Up	Unigene2948_All//gi|224133228|ref|XP_002321515.1|//0.00E+00//glutathione reductase [Populus trichocarpa] >gi|222868511|gb|EEF05642.1|glutathione reductase [Populus trichocarpa]	Unigene2948_All//0.00E+00//AT3G54660| GR (GLUTATHIONE REDUCTASE); ATP binding / glutathione-disulfide reductase	Unigene2948_All//0.00E+00//TC168797		ko00480|Glutathione metabolism	GO:0006091//GO:0006790//GO:0009532//GO:0015038//GO:0019725//GO:0032559//GO:0046914	nr +
Unigene29481_All	711	9.79	12.83	20.75	7.92	8.38	3.81	0.00	0.59	0.22	3.90E-01	4.39E-02		1.08E+00	3.06E-12	Up	8.18E-02	8.08E-01		-1.05E+00	2.16E-05	Down	9.20E+00	3.65E-03		7.81E+00	1.40E-01		Unigene29481_All//gi|124360931|gb|ABN08903.1|//9.00E-08//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene29481_All//1.00E-07//AT2G20180| PIL5 (PHYTOCHROME INTERACTING FACTOR 3-LIKE 5); DNA binding / phytochrome binding / transcription factor	Unigene29481_All//4.00E-52//gi|48797306|gb|CO098620.1|CO098620	bHLH		GO:0003676//GO:0005515//GO:0006779//GO:0009630//GO:0009640//GO:0010017//GO:0010029//GO:0010468//GO:0010476//GO:0043231	nr +
Unigene29482_All	517	5.57	5.00	5.77	2.51	4.20	2.27	0.00	0.40	1.16	-1.55E-01	6.67E-01		5.14E-02	8.95E-01		7.44E-01	9.04E-02		-1.41E-01	8.06E-01		8.66E+00	7.85E-02		1.02E+01	1.75E-04	Up	Unigene29482_All//gi|195642942|gb|ACG40939.1|//4.00E-09//CP5 [Zea mays]	Unigene29482_All//3.00E-10//AT1G64720| CP5	Unigene29482_All//2.00E-47//ES830234				nr +
Unigene29484_All	538	123.70	169.53	152.72	185.00	183.06	197.61	227.28	72.64	95.30	4.55E-01	5.35E-17		3.04E-01	2.46E-07		-1.52E-02	8.22E-01		9.52E-02	9.04E-02		-1.65E+00	4.38E-233	Down	-1.25E+00	2.18E-159	Down	Unigene29484_All//gi|283135906|gb|ADB11344.1|//2.00E-63//DRAR class glutathione transferase DHAR2 [Populus trichocarpa]	Unigene29484_All//4.00E-63//AT1G75270| DHAR2 (DEHYDROASCORBATE REDUCTASE 2); glutathione binding / glutathione dehydrogenase (ascorbate)	Unigene29484_All//0.00E+00//gi|109835577|gb|DW234140.1|DW234140			GO:0005576//GO:0006464//GO:0009532//GO:0009608//GO:0009719//GO:0010038//GO:0015038//GO:0016020//GO:0042277//GO:0042579//GO:0043900//GO:0046914	nr +
Unigene29486_All	733	0.14	1.52	0.87	1.16	0.28	1.48	0.58	0.74	2.12	3.41E+00	1.24E-04	Up	2.61E+00	2.33E-02		-2.04E+00	9.05E-03		3.56E-01	6.40E-01		3.62E-01	6.73E-01		1.88E+00	2.07E-04	Up	Unigene29486_All//gi|152405801|ref|NP_199803.1|//1.00E-23//octicosapeptide/Phox/Bemlp (PB1) domain-containing protein [Arabidopsis thaliana] >gi|56381921|gb|AAV85679.1|At5g49920 [Arabidopsis thaliana] >gi|58331811|gb|AAW70403.1|At5g49920 [Arabidopsis thaliana]	Unigene29486_All//3.00E-22//AT5G49920| octicosapeptide/Phox/Bemlp (PB1) domain-containing protein	Unigene29486_All//0.00E+00//gi|78325714|gb|DT545988.1|DT545988			nr +
Unigene29489_All	1352	0.00	0.00	0.00	1.14	0.15	0.07	30.46	13.17	7.96	null	null		null	null		-2.90E+00	1.43E-06	Down	-4.10E+00	1.58E-07	Down	-1.21E+00	7.63E-50	Down	-1.94E+00	9.89E-102	Down	Unigene29489_All//gi|297610489|ref|NP_001064615.2|//1.00E-133//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2|Os10g0419100 [Oryza sativa Japonica Group]	Unigene29489_All//4.00E-101//AT1G60690| aldo/keto reductase family protein	Unigene29489_All//3.00E-17//TC142702		ko00010|Glycolysis / Gluconeogenesis//ko00053|Ascorbate and aldarate metabolism//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene29490_All	777	0.00	0.52	0.00	3.78	7.09	6.86	0.60	0.59	2.05	9.03E+00	1.36E-02		null	null		9.07E-01	1.90E-04		8.59E-01	8.20E-04		-1.67E-02	1.02E+00		1.78E+00	3.04E-04	Up	Unigene29490_All//gi|297809277|ref|XP_002872522.1|//2.00E-83//subtilase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318359|gb|EFH48781.1|subtilase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29490_All//2.00E-83//AT1G32960| SBT3.3; identical protein binding / serine-type endopeptidase				GO:0005576//GO:0005618//GO:0019538//GO:0070011	nr -
Unigene29499_All	218	2.64	11.85	4.64	8.23	10.90	5.39	0.00	1.92	0.55	2.17E+00	1.89E-06	Up	8.14E-01	2.51E-01		4.06E-01	3.67E-01		-6.11E-01	2.28E-01		1.09E+01	3.65E-03		9.10E+00	2.43E-01					Unigene29499_All//2.00E-07//gi|3325770|gb|AI054656.1|AI054656				
Unigene2950_All	1658	1.96	1.16	0.84	2.07	1.99	1.39	3.06	2.97	6.01	-7.53E-01	2.83E-02		-1.23E+00	8.40E-04	Down	-5.63E-02	8.69E-01		-5.78E-01	8.88E-02		-4.09E-02	8.84E-01		9.73E-01	2.18E-09		Unigene2950_All//6.00E-29//AT1G64625| transcription factor	Unigene2950_All//8.00E-43//TC168429			GO:0043231	nr +
Unigene29501_All	294	4.81	3.96	0.36	3.73	3.28	3.84	2.16	3.84	0.95	-2.78E-01	6.08E-01		-3.73E+00	8.90E-06	Down	-1.85E-01	8.01E-01		4.30E-02	9.42E-01		8.31E-01	1.51E-01		-1.19E+00	1.33E-01					Unigene29501_All//2.00E-08//gi|78342857|gb|DT563131.1|DT563131				
Unigene29507_All	358	14.18	15.14	38.38	5.43	5.10	2.14	2.60	0.47	0.67	9.53E-02	7.19E-01		1.44E+00	1.94E-17	Up	-9.01E-02	8.35E-01		-1.34E+00	4.60E-03		-2.48E+00	1.07E-03		-1.96E+00	3.98E-03					Unigene29507_All//3.00E-26//gi|109873038|gb|DW502013.1|DW502013				
Unigene29510_All	282	115.59	44.20	48.15	213.74	169.12	206.76	285.32	101.97	127.00	-1.39E+00	5.96E-40	Down	-1.26E+00	2.14E-33	Down	-3.38E-01	5.19E-08		-4.79E-02	6.03E-01		-1.48E+00	3.78E-132	Down	-1.17E+00	5.18E-94	Down	Unigene29510_All//gi|297824403|ref|XP_002880084.1|//2.00E-46//60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata] >gi|297325923|gb|EFH56343.1| 60S ribosomal protein L7 [Arabidopsis lyrata subsp. lyrata]	Unigene29510_All//5.00E-40//AT2G44120| 60S ribosomal protein L7 (RPL7C)	Unigene29510_All//3.00E-158//gi|13349892|gb|BG440241.1|BG440241		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr +
Unigene29511_All	284	2.76	6.78	14.06	2.46	2.43	1.75	0.60	8.68	2.10	1.29E+00	7.23E-03		2.35E+00	4.27E-10	Up	-1.81E-02	9.61E-01		-4.89E-01	5.98E-01		3.87E+00	8.16E-13	Up	1.82E+00	3.94E-02									
Unigene29517_All	1298	0.00	0.00	0.00	0.15	0.00	0.00	29.48	1.19	9.64	null	null		null	null		-7.26E+00	8.43E-02		-7.26E+00	1.34E-01		-4.63E+00	7.73E-218	Down	-1.61E+00	2.00E-73	Down	Unigene29517_All//gi|224101327|ref|XP_002312234.1|//5.00E-69//metal tolerance protein [Populus trichocarpa] >gi|222852054|gb|EEE89601.1| metal tolerance protein [Populus trichocarpa]	Unigene29517_All//4.00E-43//AT1G79520| cation efflux family protein				GO:0006811//GO:0015075//GO:0044464	nr -
Unigene29518_All	417	0.63	0.97	2.43	1.19	0.74	1.30	3.45	0.90	0.76	6.32E-01	6.01E-01		1.95E+00	1.37E-02		-6.85E-01	5.15E-01		1.22E-01	9.21E-01		-1.93E+00	3.78E-04	Down	-2.17E+00	6.88E-05	Down				Unigene29518_All//8.00E-15//TC173678				
Unigene29519_All	540	1.45	0.38	0.79	2.77	1.08	1.92	0.47	0.70	25.75	-1.95E+00	2.62E-02		-8.82E-01	2.95E-01		-1.35E+00	9.45E-03		-5.25E-01	3.66E-01		5.68E-01	6.37E-01		5.78E+00	2.59E-89	Up				Unigene29519_All//9.00E-37//gi|109878926|gb|DW507896.1|DW507896				
Unigene29521_All	380	125.85	71.47	62.36	381.47	313.00	329.34	177.02	124.07	71.40	-8.16E-01	5.29E-25		-1.01E+00	2.33E-34	Down	-2.85E-01	1.34E-13		-2.12E-01	3.09E-07		-5.13E-01	3.78E-19		-1.31E+00	3.24E-94	Down				Unigene29521_All//0.00E+00//TC130750				
Unigene29524_All	516	132.12	733.92	178.53	171.74	392.67	260.04	225.74	348.14	442.63	2.47E+00	0.00E+00	Up	4.34E-01	3.14E-15		1.19E+00	4.11E-230	Up	5.99E-01	4.52E-43		6.25E-01	1.16E-70		9.71E-01	2.10E-195		Unigene29524_All//gi|9294810|gb|AAF86687.1|//4.00E-26//MTD1 [Medicago truncatula]	Unigene29524_All//4.00E-09//AT5G21940| unknown protein	Unigene29524_All//0.00E+00//gi|164247015|gb|EX168050.1|EX168050			GO:0005488	nr +
Unigene2953_All	468	46.06	5.09	21.62	17.14	5.30	2.70	8.58	10.63	3.32	-3.18E+00	3.63E-75	Down	-1.09E+00	9.50E-18	Down	-1.69E+00	1.27E-16	Down	-2.67E+00	1.21E-25	Down	3.08E-01	2.36E-01		-1.37E+00	7.63E-07	Down	Unigene2953_All//gi|212717149|gb|AC357416.1|//1.00E-39//stress-induced receptor-like kinase [Glycine max]	Unigene2953_All//8.00E-21//AT4G18250| receptor serine/threonine kinase, putative	Unigene2953_All//4.00E-48//ES826968		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene29533_All	615	2.30	15.08	4.59	0.97	0.67	0.88	0.48	2.31	7.06	2.71E+00	1.34E-27	Up	9.98E-01	1.10E-02		-5.33E-01	5.62E-01		-1.42E-01	8.79E-01		2.26E+00	8.04E-05	Up	3.88E+00	1.21E-22	Up	Unigene29533_All//gi|12003390|gb|AAG43552.1|AF211534_1/6.00E-12//Avr9/Cf-9 rapidly elicited protein 169 [Nicotiana tabacum]	Unigene29533_All//4.00E-09//AT1G17147| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: VQ (InterPro:IPR008889); BEST Arabidopsis thaliana protein match is: VQ motif-containing protein (TAIR:AT1G78410.1); Has 18 Blast hits to 18 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene29533_All//5.00E-20//gi|21101273|gb|BQ413586.1|BQ413586				nr -
Unigene29535_All	583	3.05	0.70	2.01	1.20	3.01	2.01	0.36	0.00	0.00	-2.13E+00	1.23E-04	Down	-6.03E-01	2.42E-01		1.33E+00	7.60E-03		7.52E-01	2.53E-01		-8.50E+00	7.44E-02		-8.50E+00	5.80E-02		Unigene29535_All//gi|92886081|gb|AB038091.1|//3.00E-30//Transferase family [Medicago truncatula]	Unigene29535_All//2.00E-26//AT5G67150| transferase family protein	Unigene29535_All//0.00E+00//TC150605			GO:0016747	nr +
Unigene29536_All	374	5.88	1.35	0.85	9.19	8.75	8.94	1.47	0.45	0.21	-2.12E+00	1.67E-05	Down	-2.78E+00	7.59E-07	Down	-7.13E-02	8.27E-01		-4.05E-02	9.25E-01		-1.72E+00	7.23E-02		-2.79E+00	7.96E-03		Unigene29536_All//gi|15021748|gb|AK77901.1|AF397029_1/8.00E-09//root nodule extensin [Pisum sativum]		Unigene29536_All//4.00E-41//gi|78338470|gb|DT558744.1|DT558744				nr +
Unigene29537_All	227	58.54	25.00	28.38	75.49	50.97	83.16	124.05	61.31	63.53	-1.23E+00	5.63E-14	Down	-1.04E+00	1.87E-10	Down	-5.67E-01	4.26E-06		1.40E-01	3.57E-01		-1.02E+00	3.98E-26	Down	-9.65E-01	9.02E-25		Unigene29537_All//gi|192910760|gb|ACF06488.1|//7.00E-36//ribosomal protein L13a [Elaeis guineensis]	Unigene29537_All//1.00E-36//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene29537_All//2.00E-125//gi|13247718|gb|BF271909.2|BF271909		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0010467//GO:0015934	nr -
Unigene29538_All	412	11.18	13.16	16.03	19.10	18.89	19.62	33.56	15.93	18.66	2.36E-01	3.85E-01		5.20E-01	3.05E-02		-1.63E-02	9.51E-01		3.86E-02	8.83E-01		-1.08E+00	1.96E-14	Down	-8.47E-01	2.72E-10		Unigene29538_All//gi|12229923|sp|Q9M4T8.1|PSA5_SOYBN//1.00E-32//RecName: Full=Proteasome subunit alpha type-5; AltName: Full=20S proteasome alpha subunit E; AltName: Full=20S proteasome subunit alpha-5 >gi|7839485|gb|AAF70292.1|AF255338_1 20S proteasome subunit [Glycine max]	Unigene29538_All//4.00E-33//AT3G14290| PAE2; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene29538_All//2.00E-172//TC157674		ko03050|Proteasome	GO:0004175//GO:0005839//GO:0005840//GO:0010038//GO:0016020//GO:0019941//GO:0043231	nr -
Unigene2954_All	1237	0.21	1.02	1.16	0.89	0.75	1.64	11.18	11.72	4.73	2.28E+00	1.06E-03		2.46E+00	3.26E-04	Up	-2.37E-01	7.30E-01		8.91E-01	5.35E-02		6.90E-02	6.48E-01		-1.24E+00	1.81E-18	Down	Unigene2954_All//gi|212717129|gb|AC357406.1|//2.00E-26//stress-induced receptor-like kinase [Glycine max]	Unigene2954_All//6.00E-13//AT4G18250| receptor serine/threonine kinase, putative	Unigene2954_All//3.00E-26//ES826968		ko04626|Plant-pathogen interaction	GO:0016301	nr -
Unigene29540_All	484	0.65	4.61	1.21	16.36	19.35	7.84	22.10	17.01	15.15	2.83E+00	2.19E-07	Up	9.00E-01	3.77E-01		2.42E-01	2.39E-01		-1.06E+00	2.20E-07	Down	-3.78E-01	1.73E-02		-5.45E-01	3.03E-04					Unigene29540_All//6.00E-158//FL577058				
Unigene29541_All	1342	0.00	0.08	0.71	0.74	0.05	4.44	8.32	11.65	22.12	6.24E+00	3.87E-01		9.48E+00	2.46E-05	Up	-3.86E+00	1.61E-05	Down	2.58E+00	5.09E-18	Up	4.86E-01	1.11E-04		1.41E+00	1.43E-46	Up	Unigene29541_All//gi|75264365|sp|Q9LY29.1|EF115_ARATH//5.00E-53//RecName: Full=Ethylene-responsive transcription factor ERF115 >gi|106879181|gb|ABF82620.1|At5g07310 [Arabidopsis thaliana]	Unigene29541_All//2.00E-36//AT5G61890| AP2 domain-containing transcription factor family protein	Unigene29541_All//2.00E-12//TC174950	AP2-EREBP		GO:0006350//GO:0006952	nr -
Unigene29542_All	811	0.32	0.25	0.00	1.47	1.19	1.95	1.41	0.62	0.20	-3.68E-01	7.78E-01		-8.33E+00	8.57E-02		-3.10E-01	6.07E-01		4.03E-01	4.77E-01		-1.19E+00	4.02E-02		-2.84E+00	3.60E-05	Down	Unigene29542_All//gi|15217508|ref|NP_172412.1|//3.00E-47//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|193806401|sp|Q56XI1.2|PPR25_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g09410 >gi|3482916|gb|AAC33201.1|Hypothetical protein [Arabidopsis thaliana] >gi|91805759|gb|ABE65608.1|pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	Unigene29542_All//2.00E-44//AT1G56690| pentatricopeptide (PPR) repeat-containing protein	Unigene29542_All//0.00E+00//TC158727				nr -
Unigene29544_All	997	0.00	0.00	1.12	2.25	3.14	2.27	0.13	0.25	0.08	null	null		1.01E+01	3.43E-06	Up	4.83E-01	1.87E-01		1.06E-02	9.82E-01		9.84E-01	5.17E-01		-6.71E-01	7.20E-01		Unigene29544_All//gi|53370641|gb|AAU89136.1|//4.00E-09//F-box domain containing protein [Oryza sativa Japonica Group]						nr -
Unigene29546_All	455	210.78	1317.18	654.92	179.11	188.68	309.20	1.95	2.66	1.40	2.64E+00	0.00E+00	Up	1.64E+00	0.00E+00	Up	7.50E-02	2.58E-01		7.88E-01	7.52E-73		4.49E-01	4.29E-01		-4.78E-01	4.57E-01		Unigene29546_All//gi|225428877|ref|XP_002282482.1|//3.00E-24//PREDICTED: similar to leucine-rich repeat family protein [Vitis vinifera]		Unigene29546_All//0.00E+00//TC163057			GO:0005488//GO:0005618	nr +

Unigene29547_All	383	0.82	5.56	1.11	2.34	3.60	0.59	2.10	1.64	3.64	2.76E+00	6.33E-07	Up	4.41E-01	6.77E-01		6.19E-01	3.14E-01		-1.99E+00	1.36E-02		-3.58E-01	6.49E-01		7.96E-01	1.05E-01		Unigene29547_All//gi|18418498|ref|NP_567970.1|//2.00E-11//complex 1 family protein / LVR family protein [Arabidopsis thaliana] >gi|15724258|gb|AAL06522.1|AF412069_1 AT4g34700/T4L20_280 [Arabidopsis thaliana] >gi|24111283|gb|AAN46765.1|At4g34700/T4L20_280 [Arabidopsis thaliana]	Unigene29547_All//2.00E-12//AT4G34700| complex 1 family protein / LVR family protein	Unigene29547_All//1.00E-28//BE051924		ko00190|Oxidative phosphorylation	GO:0005740//GO:0030964//GO:0043094	nr -
Unigene29548_All	1996	0.45	0.10	0.00	8.81	5.28	4.64	1.91	0.67	0.24	-2.13E+00	1.06E-02		-8.80E+00	6.30E-05	Down	-7.39E-01	1.09E-09		-9.26E-01	1.46E-12		-1.51E+00	3.93E-07	Down	-2.99E+00	2.37E-16	Down	Unigene29548_All//gi|224068322|ref|XP_002302704.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222844430|gb|EEE81977.1| GH3 family protein [Populus trichocarpa]	Unigene29548_All//0.00E+00//AT2G47750| GH3.9 (PUTATIVE INDOLE-3-ACETIC ACID-AMIDO SYNTHETASE GH3.9)	Unigene29548_All//0.00E+00//gi|3325970|gb|A10548856.1|A10548856			GO:0009314//GO:0009526//GO:0009725//GO:0016881//GO:0048878	nr +
Unigene2955_All	2984	7.61	18.25	14.10	17.23	18.37	21.17	18.75	13.45	10.17	1.26E+00	3.53E-57	Up	8.90E-01	1.59E-24		9.27E-02	2.70E-01		2.98E-01	3.98E-06		-4.79E-01	2.69E-14		-8.82E-01	1.30E-41		Unigene2955_All//gi|223452363|gb|ACM89509.1|//0.00E+00//protein kinase family protein [Glycine max]	Unigene2955_All//4.00E-154//AT5G63940| protein kinase family protein	Unigene2955_All//0.00E+00//TC173269		ko04626|Plant-pathogen interaction	GO:0004683//GO:0006464//GO:0032559//GO:0050896	nr +
Unigene29550_All	653	0.48	0.00	0.16	3.05	1.85	2.49	2.01	0.51	1.40	-8.91E+00	3.66E-02		-1.56E+00	3.30E-01		-7.25E-01	1.02E-01		-2.93E-01	5.68E-01		-1.97E+00	6.34E-04	Down	-5.17E-01	3.14E-01		Unigene29550_All//gi|288559202|sp|B9RH17.1|U497D_RICCO//2.00E-32//RecName: Full=UPF0497 membrane protein 13	Unigene29550_All//9.00E-20//AT4G25010| integral membrane family protein	Unigene29550_All//0.00E+00//TC150458				nr +
Unigene29555_All	1844	0.06	167.45	64.48	0.05	0.11	0.00	0.00	0.00	0.00	1.15E+01	0.00E+00	Up	1.02E+01	0.00E+00	Up	1.05E+00	6.12E-01		-5.75E+00	4.00E-01		null	null		null	null		Unigene29555_All//sp|Q24388|LSP2_DROME//0.00E+00//Larval serum protein 2 OS=Drosophila melanogaster GN=Lsp2 PE=1 SV=2							swissprot +
Unigene29556_All	590	4.43	1.46	2.89	3.80	7.24	6.12	0.72	0.14	1.22	-1.60E+00	1.16E-04	Down	-6.19E-01	1.37E-01		9.30E-01	1.04E-03		6.89E-01	3.56E-02		-2.34E+00	5.46E-02		7.62E-01	3.02E-01									
Unigene29557_All	348	22.25	12.09	12.55	9.59	8.41	4.41	0.97	0.24	0.34	-8.81E-01	2.85E-05		-8.27E-01	1.48E-04		-1.89E-01	6.18E-01		-1.12E+00	9.10E-04	Down	-2.02E+00	1.36E-01		-1.50E+00	2.11E-01		Unigene29557_All//gi|108711605|gb|ABF99400.1|//1.00E-28//F-box domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]		Unigene29557_All//0.00E+00//gi|109870541|gb|DW499517.1|DW499517				nr -
Unigene2956_All	1815	2.10	1.09	0.65	7.38	2.68	1.97	23.36	22.18	34.00	-9.51E-01	2.52E-03		-1.70E+00	1.38E-06	Down	-1.46E+00	2.93E-22	Down	-1.91E+00	2.40E-28	Down	-7.53E-02	3.95E-01		5.41E-01	7.42E-20		Unigene2956_All//gi|40457261|gb|AAR86686.1|//1.00E-165//proline dehydrogenase [Glycine max]	Unigene2956_All//8.00E-135//AT5G38710| proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative	Unigene2956_All//0.00E+00//TC136050				nr -
Unigene29560_All	331	80.30	182.32	151.22	106.25	130.77	210.67	38.32	37.88	95.68	1.18E+00	3.39E-57	Up	9.13E-01	2.20E-30		3.00E-01	9.25E-05		9.88E-01	5.11E-53		-1.66E-02	9.38E-01		1.32E+00	6.04E-45	Up			Unigene29560_All//4.00E-118//gi|21095992|gb|BQ408305.1|BQ408305				
Unigene29561_All	317	0.66	1.92	1.68	3.77	4.02	3.28	1.87	0.00	0.50	1.54E+00	1.22E-01		1.35E+00	2.25E-01		9.18E-02	9.00E-01		-2.03E-01	7.36E-01		-1.09E+01	2.39E-04	Down	-1.89E+00	3.22E-02				Unigene29561_All//1.00E-53//ES839853				
Unigene29562_All	409	16.50	56.24	19.40	31.06	50.52	32.69	0.10	0.00	0.29	1.77E+00	5.76E-40	Up	2.33E-01	3.15E-01		7.02E-01	5.03E-10		7.37E-02	6.78E-01		-6.69E+00	6.57E-01		1.50E+00	5.58E-01				Unigene29562_All//2.00E-173//TC158552				
Unigene29563_All	849	641.90	307.42	786.52	635.09	502.74	244.81	79.48	57.65	23.88	-1.06E+00	0.00E+00	Down	2.93E-01	2.00E-51		-3.37E-01	6.74E-68		-1.38E+00	0.00E+00	Down	-4.63E-01	4.30E-16		-1.73E+00	6.49E-143	Down	Unigene29563_All//gi|18411783|ref|NP_565167.1|//2.00E-36//senescence-associated protein-related [Arabidopsis thaliana] >gi|6573767|gb|AAF17687.1|AC009243_14 F28K19.24 [Arabidopsis thaliana]	Unigene29563_All//1.00E-26//AT1G78020| senescence-associated protein-related	Unigene29563_All//0.00E+00//TC162101				nr +
Unigene29565_All	608	0.00	34.50	0.09	0.00	0.68	5.27	0.21	3.51	6.09	1.51E+01	1.02E-120	Up	6.45E+00	6.36E-01		9.41E+00	1.25E-02		1.24E+01	2.90E-19	Up	4.07E+00	1.54E-11	Up	4.87E+00	2.55E-22	Up	Unigene29565_All//gi|255548822|ref|XP_002515467.1|//1.00E-15//conserved hypothetical protein [Ricinus communis] >gi|223545411|gb|EEF46916.1| conserved hypothetical protein [Ricinus communis]	Unigene29565_All//8.00E-10//AT5G11070| unknown protein	Unigene29565_All//0.00E+00//TC133837				nr -
Unigene29567_All	471	0.56	0.65	3.28	1.06	0.88	0.86	2.06	0.98	1.86	2.17E-01	8.65E-01		2.56E+00	1.20E-04	Up	-2.70E-01	8.02E-01		-2.93E-01	7.57E-01		-1.08E+00	8.88E-02		-1.50E-01	7.92E-01				Unigene29567_All//1.00E-07//gi|78347225|gb|DT567499.1|DT567499				
Unigene29569_All	753	0.00	3.77	0.14	6.75	6.04	11.28	2.92	0.56	14.76	1.19E+01	3.83E-16	Up	7.14E+00	3.98E-01		-1.61E-01	5.92E-01		7.41E-01	1.49E-04		-2.40E+00	1.55E-07	Down	2.34E+00	6.30E-35	Up	Unigene29569_All//gi|5902368|gb|AAD55470.1|AC009322_10//4.00E-64//unknown protein [Arabidopsis thaliana]	Unigene29569_All//3.00E-70//AT3G15810| unknown protein	Unigene29569_All//4.00E-61//gi|109876934|gb|DW505908.1|DW505908			GO:0005488	nr -
Unigene29571_All	1342	0.00	0.00	0.00	0.00	0.00	0.00	17.01	16.85	48.63	null	null		null	null		null	null		null	null		-1.40E-02	9.26E-01		1.52E+00	1.13E-112	Up	Unigene29571_All//gi|15236657|ref|NP_193515.1|//1.00E-104//DNA-binding protein-related [Arabidopsis thaliana] >gi|17933299|gb|AAL48232.1|AF446359_1 AT4g17800/d14935c [Arabidopsis thaliana] >gi|20453387|gb|AAM19932.1|AT4g17800/d14935c [Arabidopsis thaliana] >gi|119657390|tpd|FAA00294.1| TPA: AT-hook motif nuclear localized protein 23 [Arabidopsis thaliana]	Unigene29571_All//4.00E-70//AT4G17800| DNA-binding protein-related	Unigene29571_All//1.00E-127//gi|78329872|gb|DT550146.1|DT550146				nr +
Unigene29573_All	740	0.42	0.27	0.65	33.25	13.68	7.69	6.86	3.05	2.96	-6.31E-01	6.22E-01		6.10E-01	5.87E-01		-1.28E+00	4.75E-33	Down	-2.11E+00	5.14E-59	Down	-1.17E+00	1.62E-06	Down	-1.21E+00	4.17E-07	Down	Unigene29573_All//gi|92122701|gb|AABE73781.1|//1.00E-44//dirigent-related protein [Tamarix androssowii]	Unigene29573_All//7.00E-25//AT2G21100| disease resistance-responsive protein-related / dirigent protein-related	Unigene29573_All//0.00E+00//DW503592			GO:0031410	nr -
Unigene29574_All	538	0.39	0.38	2.57	4.35	4.99	3.86	5.50	15.85	2.30	-4.64E-02	9.88E-01		2.73E+00	1.78E-04	Up	1.98E-01	6.47E-01		-1.72E-01	6.79E-01		1.53E+00	3.03E-15	Up	-1.26E+00	9.67E-05	Down	Unigene29574_All//gi|8778315|gb|AAF79324.1|AC002304_17//2.00E-15//F14J16.29 [Arabidopsis thaliana]		Unigene29574_All//1.00E-08//TC148715		ko03040|Spliceosome		nr +
Unigene29575_All	429	70.74	51.14	34.26	94.64	65.34	62.22	43.76	36.34	23.68	-4.68E-01	1.66E-06		-1.05E+00	3.77E-23	Down	-5.34E-01	2.31E-12		-6.05E-01	8.89E-14		-2.68E-01	2.33E-02		-8.86E-01	1.13E-14		Unigene29575_All//gi|30682547|ref|NP_849375.1|//8.00E-06//four F5 protein-related / 4F5 protein-related [Arabidopsis thaliana] >gi|28416731|gb|AAO42896.1|At4g13612 [Arabidopsis thaliana]		Unigene29575_All//0.00E+00//TC159377				nr -
Unigene29577_All	430	0.49	2.12	1.24	1.85	1.68	2.00	1.38	4.67	2.41	2.12E+00	1.04E-02		1.35E+00	2.25E-01		-1.40E-01	8.29E-01		1.07E-01	9.05E-01		1.76E+00	6.27E-05	Up	8.07E-01	1.68E-01		Unigene29577_All//gi|115480479|ref|NP_001063833.1|//8.00E-08//Os09g0544900 [Oryza sativa Japonica Group] >gi|113632066|dbj|BAF25747.1|Os09g0544900 [Oryza sativa Japonica Group]	Unigene29577_All//2.00E-07//AT1G76150| maoC-like dehydratase domain-containing protein	Unigene29577_All//3.00E-36//TC135341				nr -
Unigene29578_All	990	0.85	0.15	0.38	1.01	0.59	0.14	3.50	2.24	1.77	-2.46E+00	6.70E-03		-1.17E+00	1.52E-01		-7.67E-01	2.60E-01		-2.88E+00	6.76E-04	Down	-6.46E-01	2.94E-02		-9.84E-01	6.39E-04		Unigene29578_All//gi|297848736|ref|XP_002892249.1|//4.00E-52//high mobility group family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338091|gb|EFH68508.1| high mobility group family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29578_All//7.00E-42//AT1G04880| high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein	Unigene29578_All//1.00E-46//TC179102			GO:0001071//GO:0003676//GO:0010468//GO:0043231	nr -
Unigene29579_All	381	101.76	43.22	69.74	224.49	264.73	240.16	64.70	48.82	82.92	-1.24E+00	9.94E-40	Down	-5.45E-01	6.15E-10		2.38E-01	7.30E-07		9.73E-02	1.14E-01		-4.06E-01	3.33E-05		3.58E-01	1.96E-05		Unigene29579_All//gi|211906500|gb|ACJ11743.1|//2.00E-27//pyruvate dehydrogenase alpha subunit [Gossypium hirsutum]	Unigene29579_All//2.00E-18//AT1G24180| IAR4; oxidoreductase, acting on the aldehyde or oxo group of donors, disulfide as acceptor / pyruvate dehydrogenase (acetyl-transferring)	Unigene29579_All//1.00E-170//gi|78328160|gb|DT548434.1|DT548434		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)//ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis	GO:0004738//GO:0006007//GO:0006970//GO:0031980//GO:0046914	nr +
Unigene29580_All	529	0.79	1.72	2.62	3.11	3.97	0.43	1.04	0.79	0.68	1.12E+00	1.30E-01		1.73E+00	6.71E-03		3.54E-01	4.78E-01		-2.86E+00	4.80E-06	Down	-3.95E-01	6.34E-01		-6.16E-01	4.68E-01				Unigene29580_All//6.00E-07//EX169758				
Unigene29583_All	900	64.47	7.94	35.20	108.54	114.63	83.85	1.17	6.87	2.66	-3.02E+00	5.84E-192	Down	-8.73E-01	1.56E-32		7.88E-02	1.73E-01		-3.72E-01	1.34E-13		2.55E+00	2.51E-21	Up	1.18E+00	1.21E-03		Unigene29583_All//gi|255557613|ref|XP_002519836.1|//5.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223540882|gb|EEF42440.1| conserved hypothetical protein [Ricinus communis]		Unigene29583_All//0.00E+00//TC170960				nr +
Unigene29585_All	354	20.10	806.70	183.97	12.95	51.07	102.57	28.31	52.78	44.57	5.33E+00	0.00E+00	Up	3.19E+00	7.50E-221	Up	1.98E+00	1.52E-42	Up	2.99E+00	4.20E-126	Up	8.99E-01	1.79E-14		6.55E-01	1.03E-07		Unigene29585_All//gi|76446335|gb|ABA42952.1|//2.00E-11//RING-H2 finger protein [Citrus trifoliata]	Unigene29585_All//1.00E-09//AT2G04240| XERICO; protein binding / zinc ion binding	Unigene29585_All//3.00E-162//TC158612			GO:0006714//GO:0006970//GO:0009725//GO:0009743//GO:0046914	nr +
Unigene29587_All	345	0.61	0.15	1.08	4.04	1.40	1.44	8.33	4.24	3.81	-2.05E+00	3.34E-01		8.33E-01	5.16E-01		-1.53E+00	5.22E-03		-1.49E+00	1.09E-02		-9.75E-01	3.22E-03		-1.13E+00	4.98E-04	Down			Unigene29587_All//0.00E+00//BQ414561				
Unigene29589_All	306	2.05	0.00	0.87	7.81	5.63	4.58	1.80	0.55	0.00	-1.10E+01	7.92E-04	Down	-1.24E+00	2.13E-01		-4.74E-01	2.57E-01		-7.72E-01	6.29E-02		-1.72E+00	7.23E-02		-1.08E+01	2.80E-04	Down	Unigene29589_All//gi|297824545|ref|XP_002880155.1|//4.00E-23//CYCP3_1 [Arabidopsis lyrata subsp. lyrata] >gi|297325994|gb|EFH56414.1|CYCP3_1 [Arabidopsis lyrata subsp. lyrata]	Unigene29589_All//5.00E-24//AT2G45080| cycp3;1 (cyclin p3;1); cyclin-dependent protein kinase	Unigene29589_All//5.00E-151//TC162153			GO:0005488//GO:0007049	nr -
Unigene29594_All	359	21.42	12.70	12.31	24.28	15.73	28.31	127.43	59.49	41.17	-7.54E-01	3.25E-04		-7.99E-01	2.54E-04		-6.26E-01	5.74E-04		2.21E-01	2.76E-01		-1.10E+00	1.60E-47	Down	-1.63E+00	5.84E-89	Down	Unigene29594_All//gi|1173209|sp|P46293.1|RS16_GOSHI//1.00E-17//RecName: Full=40S ribosomal protein S16 >gi|439654|emb|CAA53567.1| RS16 protein, 40S subunit [Gossypium hirsutum]	Unigene29594_All//2.00E-17//AT5G18380| 40S ribosomal protein S16 (RPS16C)	Unigene29594_All//0.00E+00//TC148235		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0030312	nr +
Unigene29598_All	302	14.03	6.71	14.63	47.01	58.38	38.43	0.70	0.00	0.00	-1.06E+00	3.72E-04	Down	6.06E-02	8.41E-01		3.13E-01	1.75E-02		-2.91E-01	6.29E-02		-9.45E+00	7.44E-02		-9.45E+00	5.80E-02		Unigene29598_All//gi|297825869|ref|XP_002880817.1|//3.00E-25//nitrate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326656|gb|EFH57076.1| nitrate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene29598_All//1.00E-26//AT2G26690| nitrate transporter (NTP2)	Unigene29598_All//4.00E-158//gi|48809901|gb|CO111215.1|CO111215			GO:0006950//GO:0009719//GO:0015833//GO:0031224	nr +
Unigene29599_All	1207	0.39	0.08	0.13	0.91	1.51	1.61	2.52	0.97	2.24	-2.22E+00	7.76E-02		-1.56E+00	2.04E-01		7.36E-01	1.37E-01		8.25E-01	8.28E-02		-1.38E+00	3.15E-05	Down	-1.68E-01	6.11E-01		Unigene29599_All//gi|297828291|ref|XP_002882028.1|//1.00E-125//sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327867|gb|EFH58287.1| sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene29599_All//6.00E-126//AT2G45700| sterile alpha motif (SAM) domain-containing protein	Unigene29599_All//0.00E+00//TC179553			GO:0006259//GO:0050896	nr +
Unigene2960_All	821	404.36	124.05	176.94	4.67	5.33	1.71	0.00	0.00	0.10	-1.70E+00	0.00E+00	Down	-1.19E+00	0.00E+00	Down	1.89E-01	5.85E-01		-1.45E+00	5.55E-06	Down	null	null		6.60E+00	4.04E-01		Unigene2960_All//gi|77540212|gb|ABA86964.1|//1.00E-148//glyceraldehyde-3-phosphate dehydrogenase B subunit [Glycine max]	Unigene2960_All//3.00E-122//AT1G42970| GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase (NADP+)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene2960_All//0.00E+00//TC165205		ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene29600_All	507	88.96	52.57	43.90	123.01	97.40	144.04	177.63	103.29	67.73	-7.59E-01	6.35E-21		-1.02E+00	9.80E-33	Down	-3.37E-01	3.15E-08		2.28E-01	1.81E-04		-7.82E-01	8.74E-53		-1.39E+00	6.14E-138	Down	Unigene29600_All//gi|297804766|ref|XP_002870267.1|//2.00E-41//60S ribosomal protein L27 [Arabidopsis lyrata subsp. lyrata] >gi|297316103|gb|EFH46526.1| 60S ribosomal protein L27 [Arabidopsis lyrata subsp. lyrata]	Unigene29600_All//3.00E-33//AT4G15000| 60S ribosomal protein L27 (RPL27C)	Unigene29600_All//0.00E+00//TC148424		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +

Unigene29601_All	554	1.89	0.37	0.77	2.52	2.80	1.63	3.13	0.75	0.36	-2.37E+00	2.49E-03			-1.30E+00	7.46E-02			1.52E-01	8.29E-01			-6.27E-01	2.89E-01			-2.05E+00	3.55E-05	Down	-3.12E+00	3.99E-08	Down						
Unigene29604_All	514	3.77	6.01	8.81	9.40	8.24	5.45	2.96	4.88	5.81	6.75E-01	5.73E-02			1.23E+00	5.33E-05	Up	-1.90E-01	5.57E-01				-7.87E-01	3.54E-03			7.20E-01	4.44E-02		9.73E-01	2.02E-03		Unigene29604_All//gi|124360485|gb|ABN08493.1|//2.00E-21//Disease resistance protein [Medicago truncatula]	Unigene29604_All//2.00E-05//AT1G50180| disease resistance protein (CC-NBS-LRR class), putative	Unigene29604_All//6.00E-118//TC136213			GO:0005488	nr +
Unigene29605_All	408	38.86	15.15	28.45	130.27	87.61	89.66	192.54	126.62	59.95	-1.36E+00	3.26E-19	Down	-4.50E-01	2.09E-03			-5.72E-01	4.05E-18			-5.39E-01	1.33E-14			-6.05E-01	1.23E-29		-1.68E+00	2.32E-159	Down	Unigene29605_All//gi|57639078|gb|AK65475.1|//3.00E-49//ER-binding protein [Malus pumila]	Unigene29605_All//2.00E-43//AT5G42020| BIP2; ATP binding	Unigene29605_All//0.00E+00//gi|78343253|gb|DT563527.1|DT563527		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0008152//GO:0016628//GO:0032559//GO:0044432//GO:0050896	nr +
Unigene29606_All	784	536.02	217.28	276.17	686.28	706.41	659.02	308.10	216.55	167.48	-1.30E+00	0.00E+00	Down	-9.57E-01	2.39E-272			4.17E-02	7.71E-02			-5.85E-02	1.12E-02			-5.09E-01	1.21E-65		-8.79E-01	5.30E-176		Unigene29606_All//gi|4339609|gb|AAB04557.1|//5.00E-91//delta-tonoplast intrinsic protein [Gossypium hirsutum]	Unigene29606_All//2.00E-78//AT3G16240| DELTA-TIP; ammonia transporter/ methylammonium transmembrane transporter/ water channel	Unigene29606_All//0.00E+00//gi|84152789|gb|DN802144.1|DN802144			GO:0000322//GO:0000325//GO:0005275//GO:0005372//GO:0005618//GO:0009526//GO:0031224//GO:0042044//GO:0042886//GO:0042887	nr -
Unigene29607_All	286	4.57	4.25	12.85	14.46	11.20	5.84	1.33	0.00	2.51	-1.05E-01	8.46E-01			1.49E+00	2.18E-05	Up	-3.69E-01	2.32E-01			-1.31E+00	1.52E-05	Down	-1.04E+01	6.18E-03		9.14E-01	2.12E-01								ESTscan +
Unigene29608_All	1069	0.00	0.05	0.35	1.03	0.39	1.10	107.66	392.97	159.09	5.57E+00	6.16E-01			8.45E+00	2.50E-02		-1.41E+00	2.62E-02			9.96E-02	8.93E-01			1.87E+00	0.00E+00	Up	5.63E-01	4.71E-57		Unigene29608_All//gi|18395880|ref|NP_564244.1|//5.00E-98//FAD-binding domain-containing protein [Arabidopsis thaliana] >gi|9797760|gb|AAF98578.1|AC013427_21 Contains weak similarity to berberine bridge enzyme (bbe1) from Berberis stolonifera gb|AF019347 and contains a FAD binding PF|01565 domain. ESTs gb|AI995621, gb|AV440363 come from this gene [Arabidopsis thaliana]	Unigene29608_All//2.00E-99//AT1G26380| FAD-binding domain-containing protein	Unigene29608_All//0.00E+00//gi|164314564|gb|EX167881.1|EX167881				nr +
Unigene29609_All	1062	0.99	1.24	1.91	3.00	3.37	1.23	0.00	0.16	0.26	3.32E-01	5.83E-01			9.52E-01	4.57E-02		1.68E-01	6.54E-01			-1.28E+00	2.50E-04	Down	7.30E+00	1.39E-01		8.04E+00	2.43E-02		Unigene29609_All//gi|224106565|ref|XP_002314209.1|//1.00E-158//endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa] >gi|222850617|gb|EEE88164.1|endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa]	Unigene29609_All//2.00E-159//AT1G07810| ECA1 (ER-TYPE CA2+-ATPASE 1); calcium-transporting ATPase	Unigene29609_All//4.00E-142//TC158686				nr +
Unigene2961_All	1976	161.30	81.08	94.53	36.98	31.19	26.22	1.95	0.89	0.26	-9.92E-01	3.59E-226			-7.71E-01	4.54E-143		-2.46E-01	1.75E-05			-4.96E-01	3.60E-17			-1.13E+00	6.35E-05	Down	-2.89E+00	5.39E-16	Down	Unigene2961_All//gi|77540212|gb|AB486964.1|//0.00E+00//glyceraldehyde-3-phosphate dehydrogenase B subunit [Glycine max]	Unigene2961_All//0.00E+00//AT1G42970| GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase (NADP+)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene2961_All//0.00E+00//TC133576		ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0005576//GO:0006950//GO:0008943//GO:0009314//GO:0009526//GO:0009532//GO:0009534//GO:0010038//GO:0015977//GO:0019318//GO:0034285	nr +
Unigene29612_All	740	0.49	7.87	2.88	0.54	2.37	0.31	2.29	0.51	2.96	3.99E+00	1.24E-24	Up	2.54E+00	3.97E-06	Up	2.14E+00	7.45E-05	Up	-8.19E-01	5.06E-01		-2.17E+00	2.25E-05	Down	3.74E-01	3.43E-01		Unigene29612_All//gi|297789954|ref|XP_002862895.1|//3.00E-35//WRKY DNA-binding protein 49 [Arabidopsis lyrata subsp. lyrata] >gi|297308663|gb|EFH39154.1| WRKY DNA-binding protein 49 [Arabidopsis lyrata subsp. lyrata]	Unigene29612_All//1.00E-32//AT5G43290| WRKY49; transcription factor	Unigene29612_All//0.00E+00//TC136988	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0006350//GO:0010468//GO:0043231	nr +
Unigene29613_All	322	97.00	356.10	102.86	53.37	116.35	168.45	47.01	114.74	283.32	1.88E+00	1.95E-213	Up	8.46E-02	4.42E-01		1.12E+00	8.33E-39	Up	1.66E+00	1.30E-91	Up	1.29E+00	3.09E-49	Up	2.59E+00	0.00E+00	Up	2.59E+00	0.00E+00	Up	Unigene29613_All//gi|206584339|gb|ACI15342.1|//3.00E-57//NAC domain protein NAC2 [Gossypium hirsutum] >gi|206584351|gb|ACI15348.1| NAC domain protein NAC2 [Gossypium hirsutum]	Unigene29613_All//3.00E-28//AT1G01720| ATAF1; transcription activator/ transcription factor	Unigene29613_All//1.00E-179//gi|73864025|gb|DT466764.1|DT466764	NAC		GO:0001071//GO:0003676//GO:0006950//GO:0009738//GO:0010468//GO:0030528//GO:0032501	nr -
Unigene29614_All	588	0.00	0.00	0.00	2.20	1.29	0.69	10.28	3.91	1.49	null	null		null	null		-7.74E-01	1.77E-01		-1.67E+00	7.13E-03		-1.40E+00	9.00E-10	Down	-2.79E+00	8.57E-24	Down	-2.79E+00	8.57E-24	Down	Unigene29614_All//gi|297802294|ref|XP_002869031.1|//8.00E-24//At4g36570 [Arabidopsis lyrata subsp. lyrata] >gi|38566494|gb|AAR24137.1|At4g36570 [Arabidopsis thaliana] >gi|40823588|gb|AAR92291.1|At4g36570 [Arabidopsis thaliana] >gi|297314867|gb|EFH45290.1|At4g36570 [Arabidopsis lyrata subsp. lyrata]	Unigene29614_All//3.00E-23//AT2G21650| MEE3 (MATERNAL EFFECT EMBRYO ARREST 3); DNA binding / transcription factor	Unigene29614_All//0.00E+00//TC170129	MYB-related		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene29616_All	1041	0.85	0.00	0.31	1.24	1.16	1.61	1.62	0.08	0.46	-9.74E+00	2.86E-05	Down	-1.48E+00	6.99E-02		-1.04E-01	8.43E-01		3.68E-01	5.07E-01		-4.34E+00	1.16E-09	Down	-1.82E+00	1.21E-04	Down	-1.82E+00	1.21E-04	Down	Unigene29616_All//gi|297808759|ref|XP_002872263.1|//1.00E-95//serine-type peptidase/ trypsin [Arabidopsis lyrata subsp. lyrata] >gi|297318100|gb|EFH48522.1|serine-type peptidase/ trypsin [Arabidopsis lyrata subsp. lyrata]	Unigene29616_All//1.00E-88//AT5G27660| catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase	Unigene29616_All//0.00E+00//TC170550			GO:0004175//GO:0005488//GO:0019538//GO:0044424	nr -
Unigene29618_All	1447	0.43	0.67	0.66	3.96	3.86	2.87	0.76	0.29	0.11	6.17E-01	3.76E-01			6.10E-01	3.86E-01		-3.83E-02	8.86E-01			-4.63E-01	6.94E-02			-1.40E+00	2.04E-02		-2.79E+00	6.37E-05	Down	Unigene29618_All//gi|56409840|emb|CAI30145.1|//1.00E-164//glycosyltransferase [Medicago truncatula]	Unigene29618_All//5.00E-152//AT2G41640| transferase, transferring glycosyl groups	Unigene29618_All//0.00E+00//TC163595				nr +
Unigene29619_All	732	0.93	2.08	2.55	1.97	0.66	2.22	4.74	5.94	1.36	1.16E+00	3.43E-02			1.45E+00	4.96E-03		-1.58E+00	3.30E-03			1.71E-01	7.50E-01			3.26E-01	2.38E-01		-1.80E+00	1.61E-08	Down	Unigene29619_All//gi|5230728|gb|AAD40979.1|AF089851_1//2.00E-08//peroxisomal copper-containing amine oxidase [Glycine max]	Unigene29619_All//3.00E-08//AT2G42490| copper amine oxidase, putative	Unigene29619_All//7.00E-94//CO084306		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene2962_All	551	9.59	7.63	17.98	3.89	4.25	3.85	1.07	3.03	3.40	-3.29E-01	2.21E-01			9.06E-01	1.87E-06		1.29E-01	8.20E-01			-1.31E-02	9.68E-01			1.50E+00	1.58E-03		1.66E+00	1.72E-04	Up	Unigene2962_All//gi|15149819|emb|CAC50874.1|//2.00E-29//S-like RNAse 28 [Antirrhinum hispanicum subsp. mollissimum]	Unigene2962_All//2.00E-29//AT2G39780| RNS2 (RIBONUCLEASE 2); RNA binding / endoribonuclease/ ribonuclease T2	Unigene2962_All//2.00E-161//gi|78325334|gb|DT545608.1|DT545608			GO:0004521//GO:0031410//GO:0032502//GO:0043231	nr -
Unigene29620_All	797	0.00	0.00	0.00	0.00	0.00	0.00	47.69	101.05	13.50	null	null		null	null		null	null		null	null		1.08E+00	4.61E-81	Up	-1.82E+00	1.83E-86	Down									ESTscan -
Unigene29621_All	593	0.35	0.94	1.53	3.70	2.61	5.10	24.38	49.34	34.40	1.41E+00	1.69E-01			2.11E+00	1.42E-02		-5.00E-01	2.53E-01			4.65E-01	2.23E-01			1.02E+00	4.42E-27	Up	4.96E-01	2.95E-06		Unigene29621_All//gi|224151719|ref|XP_002337145.1|//2.00E-47//cytochrome P450 [Populus trichocarpa] >gi|222838355|gb|EEE76720.1|cytochrome P450 [Populus trichocarpa]	Unigene29621_All//8.00E-25//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene29621_All//0.00E+00//TC131128		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00941|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr +
Unigene29622_All	881	3.21	1.67	4.05	0.23	0.08	0.10	9.02	7.50	1.22	-9.43E-01	1.17E-02			3.37E-01	3.50E-01		-1.53E+00	4.16E-01			-1.14E+00	5.69E-01			-2.67E-01	1.76E-01		-2.89E+00	3.48E-32	Down	Unigene29622_All//gi|549977|gb|AAA50235.1|//1.00E-23//cDNA-5-encoded protein [Arabidopsis thaliana]	Unigene29622_All//4.00E-15//AT4G26130| unknown protein					nr +
Unigene29623_All	1223	12.02	1.16	2.79	0.69	0.82	0.66	0.66	0.41	1.34	-3.37E+00	2.64E-54	Down	-2.11E+00	2.41E-31	Down	2.38E-01	7.85E-01		-5.89E-02	9.44E-01		-6.80E-01	3.53E-01		1.02E+00	2.23E-02					Unigene29623_All//gi|56550681|gb|AAV97794.1|//5.00E-17//At5g67350 [Arabidopsis thaliana] >gi|59658292|gb|AAX12856.1|At5g67350 [Arabidopsis thaliana]		Unigene29623_All//0.00E+00//DN802261				nr +
Unigene29624_All	800	1.11	0.06	0.33	5.29	3.01	2.65	1.00	0.21	0.15	-4.13E+00	2.52E-04	Down	-1.74E+00	3.79E-02		-8.13E-01	3.26E-03		-9.96E-01	6.48E-04		-2.26E+00	4.82E-03		-2.75E+00	9.43E-04	Down	-2.75E+00	9.43E-04	Down	Unigene29624_All//gi|145105398|gb|ABP35583.1|//9.00E-95//CBL-interacting protein kinase [Gossypium hirsutum]	Unigene29624_All//9.00E-79//AT5G25110| CIPK25 (CBL-INTERACTING PROTEIN KINASE 25); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene29624_All//0.00E+00//CO094917		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0006952//GO:0023060//GO:0032559	nr +
Unigene29625_All	394	0.27	3.09	2.30	0.63	2.10	0.46	0.86	1.80	2.02	3.54E+00	4.02E-05	Up	3.11E+00	1.76E-03		1.73E+00	3.97E-02		-4.64E-01	7.44E-01		1.07E+00	1.67E-01		1.24E+00	7.69E-02										
Unigene29627_All	554	0.28	31.74	3.36	0.18	0.12	1.79	1.07	2.87	4.82	6.81E+00	3.58E-95	Up	3.57E+00	2.70E-07	Up	-5.33E-01	8.16E-01		3.32E+00	3.47E-04	Up	1.42E+00	3.29E-03		2.17E+00	2.81E-08	Up	2.17E+00	2.81E-08	Up	Unigene29627_All//gi|20197247|gb|AAM14995.1|//6.00E-12//Expressed protein [Arabidopsis thaliana]	Unigene29627_All//4.00E-11//AT2G38465| unknown protein				GO:0016020	nr +
Unigene29628_All	284	30.03	14.27	13.69	30.70	30.19	32.92	134.73	81.09	49.66	-1.07E+00	1.30E-07	Down	-1.13E+00	7.79E-08	Down	-2.39E-02	9.13E-01		1.01E-01	6.56E-01		-7.33E-01	1.58E-20		-1.44E+00	3.22E-62	Down	-1.44E+00	3.22E-62	Down	Unigene29628_All//gi|297833728|ref|XP_002884746.1|//6.00E-08//40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata] >gi|297330586|gb|EFH61005.1| 40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata]	Unigene29628_All//3.00E-09//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene29628_All//2.00E-159//gi|21103232|gb|BQ415545.1|BQ415545		ko03010|Ribosome		nr +
Unigene29631_All	1017	0.72	4.58	0.10	3.33	1.66	1.47	2.20	17.47	0.59	2.67E+00	6.20E-14	Up	-2.78E+00	1.04E-02		-1.01E+00	1.38E-03		-1.18E+00	4.22E-04	Down	2.99E+00	5.27E-71	Up	-1.91E+00	3.35E-06	Down	-1.91E+00	3.35E-06	Down	Unigene29631_All//gi|15234969|ref|NP_194250.1|//4.00E-63//ATHSP23.6-MITO (MITOCHONDRION-LOCALIZED SMALL HEAT SHOCK PROTEIN 23.6) [Arabidopsis thaliana] >gi|3122232|sp|Q96331.1|HS23M_ARATH RecName: Full=23.6 kDa heat shock protein, mitochondrial; Short=AtHsp23.6; Flags: Precursor >gi|1669866|gb|AAB38795.1|AtHSP23.6-mito [Arabidopsis thaliana] >gi|4454008|emb|CAA23061.1|Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana] >gi|7269370|emb|CAB79429.1|Arabidopsis mitochondrion-localized small heat shock protein (AtHSP23.6-mito) [Arabidopsis thaliana] >gi|28950739|gb|AAO63293.1|At4g25200 [Arabidopsis thaliana] >gi|222424012|dbj|BAH19967.1|AT4G25200 [Arabidopsis thaliana]	Unigene29631_All//9.00E-59//AT4G25200| ATHSP23.6-MITO (MITOCHONDRION-LOCALIZED SMALL HEAT SHOCK PROTEIN 23.6)	Unigene29631_All//0.00E+00//gi|78325083|gb|DT545357.1|DT545357			GO:0006950//GO:0009536//GO:0010038	nr -
Unigene29633_All	412	0.64	3.57	1.42	0.97	1.34	1.21	0.10	0.91	1.35	2.49E+00	1.51E-04	Up	1.16E+00	2.47E-01		4.67E-01	6.68E-01		3.18E-01	7.57E-01		3.15E+00	3.41E-02		3.72E+00	2.38E-03						Unigene29633_All//5.00E-07//BG445509				
Unigene29634_All	778	0.20	1.76	0.68	0.26	0.40	0.75	2.50	0.64	1.54	3.12E+00	3.45E-05	Up	1.76E+00	1.29E-01		6.38E-01	6.95E-01		1.56E+00	1.36E-01		-1.96E+00	2.03E-05	Down	-7.03E-01	7.80E-02					Unigene29634_All//gi|4928399|gb|AAD33582.1|AF132014_1//7.00E-28//RING-H2 zinc finger protein ATL4 [Arabidopsis thaliana]	Unigene29634_All//4.00E-19//AT3G60220| ATL4; protein binding / zinc ion binding	Unigene29634_All//5.00E-36//gi|78339148|gb|DT559422.1|DT559422				nr -
Unigene29637_All	1923	0.22	0.00	0.00	0.26	0.29	1.06	22.98	14.63	26.04	-7.77E+00	1.05E-02		-7.77E+00	1.56E-02		1.46E-01	9.05E-01		2.03E+00	5.23E-05	Up	-6.52E-01	2.46E-19		1.81E-01	7.62E-03					Unigene29637_All//gi|297848456|ref|XP_002892109.1|//0.00E+00//glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] >gi|297337951|gb|EFH68368.1|glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	Unigene29637_All//0.00E+00//AT1G02460| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene29637_All//0.00E+00//ES833865		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553//GO:0044238//GO:0045229	nr +
Unigene29638_All	1002	0.73	0.71	0.85	4.42	2.41	1.76	0.97	0.17	0.40	-4.61E-02	9.68E-01		2.18E-01	7.57E-01		-8.79E-01	1.03E-03		-1.33E+00	4.77E-06	Down	-2.54E+00	6.41E-04	Down	-1.29E+00	3.62E-02					Unigene29638_All//gi|63259081|gb|AAV40250.1|//1.00E-41//Cys2/His2 zinc-finger transcription factor [Silene latifolia]	Unigene29638_All//3.00E-31//AT2G45120| zinc finger (C2H2 type) family protein	Unigene29638_All//0.00E+00//gi|78324535|gb|DT548809.1|DT548809	C2H2		GO:0044464	nr -

Unigene29639_All	392	5.07	3.62	8.42	9.53	7.99	7.26	5.29	0.11	0.71	-4.87E-01	2.93E-01		7.32E-01	4.06E-02		-2.54E-01	4.63E-01		-3.93E-01	2.42E-01		-5.63E+00	2.86E-13	Down	-2.89E+00	6.04E-09	Down	Unigene29639_All//gi|229597364|gb|ACQ52802.1|//3.00E-41//vacuolar invertase [Gossypium hirsutum]		Unigene29639_All//0.00E+00//TC158013			GO:0016798//GO:0044238	nr -
Unigene2964_All	1446	2.97	4.06	1.66	8.44	6.12	3.90	4.91	2.54	2.26	4.54E-01	6.68E-02		-8.40E-01	6.05E-03		-4.64E-01	2.43E-03		-1.11E+00	7.62E-12	Down	-9.50E-01	1.64E-06		-1.12E+00	1.39E-08	Down	Unigene2964_All//gi|15240744|ref|NP_196342.1|//1.00E-130//ATRBL3 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 3) [Arabidopsis thaliana] >gi|7546703|emb|CAB87281.1| membrane protein [Arabidopsis thaliana] >gi|16648762|gb|AAL25572.1| AT5g07250/T28J14_190 [Arabidopsis thaliana] >gi|20466143|gb|AAM19993.1| AT5g07250/T28J14_190 [Arabidopsis thaliana]	Unigene2964_All//4.00E-75//AT5G07250| ATRBL3 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 3)	Unigene2964_All//0.00E+00//TC161511				nr +
Unigene29640_All	356	9.85	4.84	3.74	14.69	7.45	4.06	1.19	0.94	0.11	-1.02E+00	2.04E-03		-1.40E+00	9.37E-05	Down	-9.80E-01	5.51E-05		-1.86E+00	5.67E-11	Down	-3.39E-01	7.30E-01		-3.41E+00	1.24E-02				Unigene29640_All//1.00E-41//TC157512				
Unigene29641_All	884	1944.33	780.39	1260.05	212.27	251.64	142.39	4.35	3.26	2.03	-1.32E+00	0.00E+00	Down	-6.26E-01	0.00E+00		2.45E-01	2.16E-15		-5.76E-01	1.75E-56		-4.16E-01	1.49E-01		-1.10E+00	6.17E-05	Down	Unigene29641_All//gi|3023752|sp|Q43517.1|FER1_SOLLC//2.00E-47//RecName: Full=Ferredoxin-1, chloroplastic; AltName: Full=Ferredoxin 1; Flags: Precursor >gi|1418982|emb|CAA99756.1| ferredoxin-1 [Solanum lycopersicum]	Unigene29641_All//2.00E-29//AT1G10960| ATFD1 (FERREDOXIN 1); 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding	Unigene29641_All//0.00E+00//gi|164270307|gb|ES813748.1|ES813748		ko00195|Photosynthesis	GO:0006091//GO:0009532//GO:0043169//GO:0051234//GO:0051536	nr +
Unigene29643_All	378	11.21	23.46	41.84	11.73	12.03	20.67	2.80	2.32	1.58	1.07E+00	9.15E-08	Up	1.90E+00	1.52E-29	Up	3.60E-02	9.23E-01		8.18E-01	6.73E-05		-2.68E-01	6.46E-01		-8.23E-01	1.50E-01				Unigene29643_All//4.00E-26//DR463450				
Unigene29646_All	712	0.00	0.71	0.60	1.96	0.97	0.82	5.40	2.70	2.18	9.47E+00	4.04E-03		9.22E+00	1.38E-02		-1.02E+00	6.01E-02		-1.25E+00	3.03E-02		-1.00E+00	3.53E-04	Down	-1.31E+00	3.35E-06	Down			Unigene29646_All//3.00E-34//CO097312				
Unigene29649_All	813	1.42	0.75	0.66	4.78	2.75	3.89	1.30	0.82	0.29	-9.21E-01	1.43E-01		-1.11E+00	9.93E-02		-7.96E-01	6.32E-03		-2.98E-01	3.97E-01		-6.61E-01	2.78E-01		-2.14E+00	9.36E-04	Down			Unigene29649_All//2.00E-63//DT327030				
Unigene2965_All	1086	19.13	42.60	33.88	26.65	33.93	44.50	9.46	19.90	19.77	1.16E+00	2.18E-42	Up	8.25E-01	5.34E-19		3.48E-01	2.68E-05		7.40E-01	8.62E-23		1.07E+00	5.48E-22	Up	1.06E+00	4.27E-22	Up	Unigene2965_All//1.00E-39//AT5G67620| unknown protein	Unigene2965_All//0.00E+00//TC166181			GO:0015630	nr -
Unigene29650_All	668	0.24	4.17	2.15	0.45	0.77	0.20	0.06	1.00	4.35	4.15E+00	2.54E-12	Up	3.20E+00	2.79E-05	Up	7.89E-01	4.98E-01		-1.14E+00	4.57E-01		3.98E+00	6.38E-04	Up	6.10E+00	2.88E-19	Up							
Unigene29651_All	460	0.00	0.00	0.12	9.42	4.19	3.63	23.90	38.52	14.98	null	null		6.86E+00	6.36E-01		-1.17E+00	1.89E-05	Down	-1.37E+00	3.44E-06	Down	6.89E-01	5.16E-09		-6.74E-01	6.40E-06		Unigene29651_All//gi|15242391|ref|NP_197082.1|//1.00E-17//pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] >gi|9755623|emb|CAC01777.1| proline-rich protein [Arabidopsis thaliana] >gi|27311645|gb|AAO00788.1| proline-rich protein [Arabidopsis thaliana] >gi|53828649|gb|AAL94434.1| At5g15780 [Arabidopsis thaliana]	Unigene29651_All//6.00E-93//gi|132455569|gb|BE053369.2|BE053369			ko03040|Spliceosome		nr +
Unigene29653_All	653	0.88	0.39	0.65	0.31	2.74	1.87	2.98	0.32	1.65	-1.18E+00	2.26E-01		-4.34E-01	6.23E-01		3.17E+00	3.11E-07	Up	2.61E+00	3.93E-04	Up	-3.22E+00	6.50E-09	Down	-8.55E-01	3.19E-02		Unigene29653_All//gi|240255315|ref|NP_187642.4|//3.00E-32//ATP binding / microtubule motor [Arabidopsis thaliana]	Unigene29653_All//6.00E-34//AT3G10310| ATP binding / microtubule motor	Unigene29653_All//1.00E-67//DW482370			GO:0000166//GO:0003774	nr -
Unigene29654_All	625	0.75	7.38	1.28	0.40	0.22	0.72	2.71	3.34	2.68	3.29E+00	7.82E-17	Up	7.62E-01	3.62E-01		-8.55E-01	5.73E-01		8.59E-01	4.69E-01		3.05E-01	4.77E-01		-1.54E-02	9.62E-01		Unigene29654_All//gi|3914376|sp|Q42870.1|PLSC_LIMDO//1.00E-52//RecName: Full=1-acyl-sn-glycerol-3-phosphate acyltransferase; Short=1-AGP acyltransferase; Short=1-AGPAT; AltName: Full=Lysophosphatidic acid acyltransferase; Short=LPAAT >gi|1197334|emb|CAA58239.1| 1-acylglycerol-3-phosphate O-acyltransferase [Limnanthes douglasii] >gi|89147818|gb|ABD62751.1| acyl-CoA:sn-1-acylglycerol-3-phosphate acyltransferase [Limnanthes douglasii]	Unigene29654_All//3.00E-08//AT4G30580| ATS2; 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase	Unigene29654_All//0.00E+00//gi|13350435|gb|BG440783.1|BG440783		ko00564|Glycerophospholipid metabolism/ko00561|Glycerolipid metabolism	GO:0003006//GO:0009526//GO:0016411//GO:0031224//GO:0016471	nr -
Unigene29655_All	1061	0.64	0.29	0.00	0.94	1.33	0.34	4.66	4.25	22.49	-1.16E+00	1.89E-01		-9.32E+00	7.64E-04	Down	5.03E-01	4.15E-01		-1.46E+00	4.18E-02		-1.32E-01	6.67E-01		2.27E+00	1.52E-71	Up	Unigene29655_All//gi|121501706|gb|ABM65247.1|//2.00E-87//calmodulin-binding protein [Beta vulgaris]	Unigene29655_All//7.00E-67//AT2G26190| calmodulin-binding family protein	Unigene29655_All//2.00E-58//DN817850			GO:0000741//GO:0009743//GO:0043231	nr -
Unigene29656_All	1105	1.56	1.56	1.20	8.48	5.45	3.35	0.08	0.08	0.11	-3.10E-03	9.92E-01		-3.75E-01	4.71E-01		-6.36E-01	2.60E-04		-1.34E+00	3.72E-12	Down	-1.71E-02	1.01E+00		5.00E-01	8.08E-01		Unigene29656_All//gi|122162768|sp|Q01JD1.1|SPL7_ORYSI//3.00E-25//RecName: Full=Squamosa promoter-binding-like protein 7 >gi|116310136|emb|CAH67152.1| OSIGBa0123F23.9 [Oryza sativa (indica cultivar-group)]	Unigene29656_All//4.00E-23//AT2G42200| SPL9 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9); transcription factor	Unigene29656_All//1.00E-53//gi|164264486|gb|ES847235.1|ES847235	SBP		GO:0003676//GO:0043231	nr +
Unigene29657_All	1383	0.00	0.00	0.00	0.07	0.00	0.00	14.58	7.25	14.89	null	null		null	null		-6.17E+00	3.13E-01		-6.17E+00	4.00E-01		-1.01E+00	1.11E-18	Down	3.04E-02	8.06E-01		Unigene29657_All//gi|73624747|gb|AAZ79231.1|//1.00E-159//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene29657_All//2.00E-144//AT4G23990| ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	Unigene29657_All//3.00E-26//ES825844				nr +
Unigene29658_All	453	142.53	38.59	121.43	67.19	68.49	27.32	0.37	0.00	0.53	-1.88E+00	6.34E-122	Down	-2.31E-01	7.84E-04		2.77E-02	8.24E-01		-1.30E+00	1.54E-36	Down	-8.54E+00	1.34E-01		4.99E-01	7.07E-01		Unigene29658_All//gi|82468803|gb|ABB76766.1|//2.70E-72//lupeol synthase [Ricinus communis]	Unigene29658_All//6.00E-68//AT1G78955| CAMS1 (Camelliol C synthase 1); beta-amyrin synthase	Unigene29658_All//0.00E+00//TC144206		ko00100|Steroid biosynthesis	GO:0031559	nr +
Unigene2966_All	970	31.88	37.66	24.87	54.49	56.41	47.96	22.14	50.54	46.78	2.41E-01	8.31E-03		-3.58E-01	3.92E-04		5.00E-02	5.82E-01		-1.84E-01	1.50E-02		1.19E+00	1.19E-57	Up	1.08E+00	9.04E-47	Up	Unigene2966_All//gi|11762168|gb|AAG40362.1|AF325010_1//3.00E-48//AT5g16110 [Arabidopsis thaliana] >gi|15809952|gb|AAL06903.1| AT5g16110/T21H19_30 [Arabidopsis thaliana]	Unigene2966_All//6.00E-33//AT5G16110| unknown protein	Unigene2966_All//0.00E+00//TC154713				nr +
Unigene29661_All	351	10.43	4.91	11.23	4.97	3.83	2.96	0.12	0.24	0.00	-1.09E+00	8.27E-04	Down	1.06E-01	7.39E-01		-3.77E-01	4.65E-01		-7.47E-01	1.38E-01		9.83E-01	7.31E-01		-6.91E+00	6.13E-01		Unigene29661_All//gi|1770305|emb|CAA92278.1|//2.00E-29//1,3-beta-glucanase [Gossypium hirsutum]	Unigene29661_All//2.00E-16//AT3G57240| BG3 (BETA-1,3-GLUCANASE 3); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene29661_All//9.00E-110//TC170841		ko00500|Starch and sucrose metabolism	GO:0016798//GO:0043167//GO:0044238	nr -
Unigene29662_All	679	1.23	0.00	0.78	6.24	6.09	6.72	0.31	0.25	1.70	-1.03E+01	5.57E-05	Down	-6.53E-01	3.96E-01		-3.52E-02	9.10E-01		1.07E-01	7.29E-01		-3.39E-01	8.12E-01		2.45E+00	1.69E-04	Up							
Unigene29664_All	561	12.59	13.37	27.34	25.22	38.24	34.21	61.72	82.47	80.67	8.64E-02	6.95E-01		1.12E+00	2.48E-13	Up	6.01E-01	5.00E-08		4.40E-01	3.94E-04		4.18E-01	1.75E-09		3.86E-01	2.21E-08		Unigene29664_All//gi|297804388|ref|XP_002870078.1|//2.00E-57//zinc-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315914|gb|EFH46337.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29664_All//2.00E-58//AT4G17900| zinc-binding family protein	Unigene29664_All//0.00E+00//TC162774	PLATZ			nr -
Unigene29665_All	453	1.04	1.57	0.00	0.22	0.15	2.99	37.52	113.76	168.15	5.91E-01	4.78E-01		-1.00E+01	8.65E-03		-5.33E-01	8.16E-01		3.77E+00	4.57E-06	Up	1.60E+00	1.61E-94	Up	2.16E+00	8.01E-214	Up	Unigene29665_All//gi|300680026|gb|ADK27717.1|//1.00E-70//GH3 [Dimocarpus longan]	Unigene29665_All//5.00E-61//AT2G23170| GH3.3; indole-3-acetic acid amido synthetase	Unigene29665_All//0.00E+00//gi|73863321|gb|DT466060.1|DT466060			GO:0009314//GO:0009725//GO:0016881//GO:0048878	nr +
Unigene29667_All	1229	0.34	0.70	0.17	0.81	0.76	0.11	4.37	5.65	9.50	1.04E+00	1.72E-01		-9.75E-01	4.12E-01		-9.97E-02	8.68E-01		-2.88E+00	6.76E-04	Down	3.70E-01	7.30E-02		1.12E+00	2.02E-13	Up	Unigene29667_All//gi|50844679|gb|AAT84461.1|//2.00E-06//cytochrome b5 isoform Cb5-D [Vernicia fordii]	Unigene29667_All//1.00E-07//AT5G48810| CB5-D (CYTOCHROME B5 ISOFORM D); heme binding	Unigene29667_All//0.00E+00//DT466809			GO:0005506	nr -
Unigene2967_All	1673	4.50	3.51	2.48	3.90	4.78	3.32	1.52	1.07	0.64	-3.58E-01	1.00E-01		-8.59E-01	1.05E-04		2.92E-01	1.83E-01		-2.32E-01	3.82E-01		-4.97E-01	1.73E-01		-1.24E+00	4.29E-04	Down	Unigene2967_All//gi|297840101|ref|XP_002887932.1|//1.00E-155//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333773|gb|EFH64191.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2967_All//2.00E-130//AT1G63900| zinc finger (C3HC4-type RING finger) family protein	Unigene2967_All//0.00E+00//TC172303				nr -
Unigene29670_All	330	0.00	0.00	0.00	58.12	37.15	24.50	1.15	4.18	0.85	null	null		null	null		-6.46E-01	2.13E-08		-1.25E+00	8.28E-22	Down	1.86E+00	7.81E-04	Up	-4.48E-01	6.41E-01		Unigene29670_All//gi|42572555|ref|NP_974373.1|//2.00E-38//MIF2 (MINI ZINC FINGER 2); DNA binding [Arabidopsis thaliana] >gi|88960352|gb|AB057488.1| At3g28917 [Arabidopsis thaliana]	Unigene29670_All//1.00E-16//AT3G28917| MIF2 (MINI ZINC FINGER 2); DNA binding	Unigene29670_All//1.00E-179//ES795028	zf-HD		GO:0003676//GO:0009639//GO:0009725//GO:0032501	nr -
Unigene29673_All	517	0.00	0.49	1.65	0.87	0.67	0.96	1.55	4.77	2.31	8.94E+00	7.86E-02		1.07E+01	9.03E-05	Up	-3.81E-01	7.22E-01		1.48E-01	9.06E-01		1.62E+00	2.56E-05	Up	5.73E-01	2.93E-01				Unigene29673_All//6.00E-07//ES793074				
Unigene29675_All	497	3.79	1.33	0.86	4.51	2.01	2.00	1.96	3.36	0.80	-1.52E+00	2.28E-03		-2.14E+00	1.32E-04	Down	-1.17E+00	3.91E-03		-1.17E+00	6.25E-03		7.82E-01	8.76E-02		-1.29E+00	3.62E-02				Unigene29675_All//0.00E+00//TC166448				
Unigene29676_All	766	7.86	1.92	5.63	2.73	2.70	1.36	0.33	0.16	0.31	-2.03E+00	3.69E-13	Down	-4.80E-01	5.99E-02		-1.81E-02	9.56E-01		-1.01E+00	2.37E-02		-1.02E+00	4.95E-01		-8.57E-02	9.57E-01		Unigene29676_All//gi|115475531|ref|NP_001061362.1|//5.00E-55//Os08g0248100 [Oryza sativa Japonica Group] >gi|113623331|dbj|BAF23276.1| Os08g0248100 [Oryza sativa Japonica Group]	Unigene29676_All//2.00E-52//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0016301	nr -
Unigene29677_All	470	1.89	1.72	2.49	6.25	2.93	2.21	0.99	0.00	0.25	-1.34E-01	8.41E-01		3.97E-01	5.45E-01		-1.09E+00	1.41E-03		-1.50E+00	6.21E-05	Down	-9.95E+00	1.71E-03		-1.96E+00	5.82E-02								
Unigene29678_All	430	64.85	65.40	70.96	122.91	105.79	95.47	143.16	78.54	59.39	1.21E-02	9.32E-01		1.30E-01	2.48E-01		-2.17E-01	2.13E-03		-3.65E-01	2.19E-07		-8.66E-01	3.85E-43		-1.27E+00	3.37E-82	Down			Unigene29678_All//0.00E+00//TC162479				
Unigene2968_All	2057	2.03	1.35	1.37	5.98	4.15	3.51	4.40	1.40	1.84	-5.87E-01	4.80E-02		-5.69E-01	6.97E-02		-5.27E-01	4.53E-04		-7.68E-01	1.04E-06		-1.65E+00	5.42E-18	Down	-1.26E+00	1.17E-12	Down	Unigene2968_All//gi|115441427|ref|NP_001044993.1|//1.00E-114//Os01g0880400 [Oryza sativa Japonica Group] >gi|56784629|dbj|BAD81676.1| leaf senescence related protein-like [Oryza sativa Japonica Group] >gi|113534524|dbj|BAF06907.1| Os01g0880400 [Oryza sativa Japonica Group]	Unigene2968_All//5.00E-153//AT1G48880| unknown protein	Unigene2968_All//0.00E+00//TC148030				nr -
Unigene29683_All	908	0.75	1.40	0.35	1.26	2.39	2.19	1.40	0.37	1.45	8.97E-01	1.36E-01		-1.09E+00	2.39E-01		9.21E-01	3.38E-02		7.95E-01	9.16E-02		-1.92E+00	9.98E-04	Down	5.17E-02	9.40E-01		Unigene29683_All//gi|145359470|ref|NP_200812.2|//2.00E-83//NRPC1; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding / zinc ion binding [Arabidopsis thaliana]	Unigene29683_All//3.00E-78//AT5G60040| NRPC1; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding / zinc ion binding			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0001882//GO:0003676//GO:0010467//GO:0034062//GO:0043231//GO:0046914	nr +
Unigene29684_All	964	0.65	2.68	1.82	9.66	11.00	9.14	0.09	0.13	0.08	2.04E+00	4.81E-06	Up	1.48E+00	5.78E-03		1.87E-01	3.46E-01		-8.10E-02	7.00E-01		5.69E-01	7.82E-01		-8.47E-02	9.72E-01		Unigene29684_All//gi|15242318|ref|NP_197054.1|//7.00E-37//ankyrin repeat family protein [Arabidopsis thaliana] >gi|28961039|gb|AAO63443.1| At5g15500 [Arabidopsis thaliana]	Unigene29684_All//9.00E-34//AT5G15500| ankyrin repeat family protein					nr +
Unigene29687_All	353	114.42	87.70	133.20	228.47	218.71	202.92	37.61	123.37	66.25	-3.84E-01	4.61E-06		2.19E-01	8.27E-03		-6.30E-02	3.74E-01		-1.71E-01	4.02E-03		1.71E+00	3.80E-88	Up	8.17E-01	9.50E-16		Unigene29687_All//gi|255542418|ref|XP_002512272.1|//6.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223548233|gb|EEF49724.1| conserved hypothetical protein [Ricinus communis]		Unigene29687_All//0.00E+00//gi|109848789|gb|DW477769.1|DW477769				nr +

Unigene29688_All	363	6.34	8.93	5.72	29.92	19.73	8.46	1.16	0.00	0.77	4.94E-01	1.54E-01		-1.49E-01	7.21E-01		-6.00E-01	1.78E-04		-1.82E+00	1.13E-21	Down	-1.02E+01	3.25E-03		-6.00E-01	5.53E-01		Unigene29688_All//gi|297822697|ref|XP_002879231.1|//3.00E-06//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325070|gb|EFH55490.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29688_All//1.00E-07//AT2G29730| UGT71D1 (UDP-GLUCOSYL TRANSFERASE 71D1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene29688_All//4.00E-103//TC171383			GO:0035251	nr -
Unigene29689_All	980	0.21	1.03	1.20	0.41	0.70	0.46	3.06	1.36	8.62	2.28E+00	4.10E-03		2.48E+00	1.36E-03		7.90E-01	4.04E-01		1.81E-01	8.83E-01		-1.17E+00	3.59E-04	Down	1.49E+00	5.33E-15	Up	Unigene29689_All//gi|283136110|gb|ADB11374.1|//7.00E-83//tau class glutathione transferase GSTU50 [Populus trichocarpa]	Unigene29689_All//2.00E-48//AT3G09270| ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	Unigene29689_All//0.00E+00//TC140417		ko00480|Glutathione metabolism	GO:0016740//GO:0016846	nr -
Unigene29693_All	243	29.93	12.51	15.12	20.70	23.95	20.07	89.78	41.11	34.76	-1.26E+00	2.77E-08	Down	-9.85E-01	1.51E-05		2.10E-01	4.58E-01		-4.47E-02	8.92E-01		-1.13E+00	5.25E-24	Down	-1.37E+00	2.84E-33	Down				Unigene29693_All//5.00E-135//TC141168				
Unigene29697_All	812	42.59	82.31	56.00	80.73	46.14	109.29	16.40	35.72	29.34	9.51E-01	1.73E-44		3.95E-01	1.05E-06		-8.07E-01	1.06E-40		4.37E-01	2.00E-16		1.12E+00	1.98E-31	Up	8.39E-01	9.80E-17		Unigene29697_All//gi|6478218|gb|AAF13743.1|AF109921|//1.00E-42//caleosin [Sesamum indicum]	Unigene29697_All//5.00E-41//AT4G26740| ATS1 (ARABIDOPSIS THALIANA SEED GENE 1); calcium ion binding	Unigene29697_All//0.00E+00//TC165247			GO:0003006//GO:0004497//GO:0006633//GO:0006950//GO:0006996//GO:0008374//GO:0009532//GO:0016705//GO:0031224//GO:0016471//GO:0016872	nr -
Unigene29698_All	244	16.73	3.95	10.04	13.27	20.46	23.69	42.28	15.25	26.45	-2.08E+00	2.03E-09	Down	-7.36E-01	1.95E-02		6.25E-01	1.76E-02		8.36E-01	6.30E-04		-1.47E+00	2.13E-17	Down	-6.77E-01	1.19E-05		Unigene29698_All//gi|1173256|sp|P46299.1|RS4_GOSHI//9.00E-26//RecName: Full=40S ribosomal protein S4 >gi|488739|emb|CAA55882.1| ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene29698_All//2.00E-26//AT5G07090| 40S ribosomal protein S4 (RPS4B)	Unigene29698_All//3.00E-133//gi|109863236|gb|DW492213.1|DW492213		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr -
Unigene297_All	2595	4.60	10.58	6.24	10.08	10.19	9.33	10.51	11.55	10.99	1.20E+00	4.32E-27	Up	4.40E-01	2.26E-03		1.61E-02	9.09E-01		-1.12E-01	3.94E-01		1.36E-01	1.70E-01		6.49E-02	5.53E-01		Unigene297_All//gi|236172202|dbj|BAC20873.1|//1.00E-174//VP1/AB13 family regulatory protein-like protein [Oryza sativa Japonica Group]	Unigene297_All//5.00E-135//AT4G32010| HSL1 (HST2-LIKE 1); transcription factor	Unigene297_All//0.00E+00//TC161066	ABI3VP1	ko00310|Lysine degradation		nr +
Unigene2970_All	1049	2.64	12.90	2.13	3.99	5.35	9.82	6.93	6.69	30.95	2.29E+00	5.91E-33	Up	-3.10E-01	4.36E-01		4.24E-01	9.96E-02		1.30E+00	1.53E-12	Up	-5.06E-02	8.17E-01		2.16E+00	3.06E-91	Up	Unigene2970_All//gi|18415709|ref|NP_567629.1|//4.00E-34//F-box family protein [Arabidopsis thaliana] >gi|142989915|sp|Q65416.2|SK127_ARATH RecName: Full=F-box protein SKIP27; AltName: Full=SKP1-interacting partner 27 >gi|171168229|gb|ABK32197.1| At4g21510 [Arabidopsis thaliana]	Unigene2970_All//1.00E-35//AT4G21510| F-box family protein	Unigene2970_All//0.00E+00//TC150059			GO:0043231	nr +
Unigene29700_All	233	0.00	0.87	0.46	0.64	4.73	1.55	2.18	4.48	10.77	9.76E+00	1.36E-01		8.84E+00	3.98E-01		2.88E+00	3.08E-04	Up	1.27E+00	3.82E-01		1.04E+00	8.74E-02		2.31E+00	2.35E-08	Up				Unigene29700_All//3.00E-07//DW503655				
Unigene29701_All	1035	0.30	1.66	0.72	0.43	0.43	0.61	2.74	5.73	20.17	2.46E+00	3.84E-05	Up	1.25E+00	1.54E-01		-2.30E-03	9.69E-01		4.96E-01	6.37E-01		1.07E+00	1.43E-06	Up	2.88E+00	7.61E-82	Up				Unigene29701_All//3.00E-106//DW508969				
Unigene29702_All	824	0.32	0.49	0.13	0.24	0.25	0.16	2.51	1.57	1.02	6.32E-01	6.01E-01		-1.30E+00	4.36E-01		5.21E-02	9.89E-01		-5.57E-01	7.33E-01		-6.77E-01	9.28E-02		-1.31E+00	9.85E-04	Down								
Unigene29704_All	385	5.57	2.37	8.85	6.34	6.44	2.70	3.40	1.95	0.72	-1.23E+00	5.86E-03		6.68E-01	5.67E-02		2.25E-02	9.65E-01		-1.23E+00	2.60E-03		-8.01E-01	1.33E-01		-2.23E+00	1.19E-04	Down				Unigene29704_All//4.00E-07//DW223992				
Unigene29706_All	617	0.25	10.51	4.49	0.16	0.67	1.68	0.07	2.17	2.78	5.37E+00	1.99E-32	Up	4.14E+00	8.12E-12	Up	2.05E+00	1.47E-01		3.38E+00	2.04E-04	Up	4.98E+00	3.03E-08	Up	5.34E+00	5.50E-11	Up				Unigene29706_All//1.00E-51//FL576813				
Unigene2971_All	959	0.33	0.53	0.44	13.66	13.47	11.11	3.88	0.52	1.12	6.91E-01	4.99E-01		4.41E-01	6.77E-01		-2.08E-02	9.09E-01		-2.98E-01	6.92E-02		-2.89E+00	6.16E-15	Down	-1.79E+00	5.03E-09	Down	Unigene2971_All//gi|238481047|ref|NP_001154284.1|//2.00E-75//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene2971_All//1.00E-76//AT4G33330| transferase, transferring glycosyl groups	Unigene2971_All//2.00E-48//TC135116			GO:0035251	nr +
Unigene29710_All	285	114.19	45.16	31.58	137.91	109.83	209.34	218.23	73.91	84.99	-1.34E+00	8.22E-38	Down	-1.85E+00	3.02E-58	Down	-3.28E-01	3.56E-05		6.02E-01	1.17E-19		-1.56E+00	3.19E-110	Down	-1.36E+00	2.35E-92	Down	Unigene29710_All//gi|226505142|ref|NP_001149258.1|//2.00E-38//ribosomal proteinS12 (homolog) [Zea mays] >gi|195625842|gb|ACG34751.1| 40S ribosomal protein S12 [Zea mays]	Unigene29710_All//3.00E-39//AT2G32060| 40S ribosomal protein S12 (RPS12C)	Unigene29710_All//1.00E-157//gi|13353155|gb|BG443503.1|BG443503		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279//GO:0043231	nr -
Unigene29713_All	483	0.54	0.84	0.33	3.92	2.50	0.94	2.28	2.77	0.41	6.32E-01	6.01E-01		-7.12E-01	6.22E-01		-6.51E-01	1.60E-01		-2.07E+00	6.30E-05	Down	2.83E-01	6.34E-01		-2.46E+00	2.04E-04	Down				Unigene29713_All//1.00E-78//TC140706				
Unigene29715_All	549	0.76	2.22	2.72	0.54	1.07	2.63	0.69	0.30	1.31	1.54E+00	1.75E-02		1.83E+00	2.94E-03		9.70E-01	3.47E-01		2.27E+00	3.41E-04	Up	-1.19E+00	3.09E-01		9.14E-01	2.12E-01		Unigene29715_All//gi|18411126|ref|NP_565133.1|//1.00E-96//auxin efflux carrier family protein [Arabidopsis thaliana] >gi|30699180|ref|NP_849892.1| auxin efflux carrier family protein [Arabidopsis thaliana]	Unigene29715_All//1.00E-37//AT1G76520| auxin efflux carrier family protein	Unigene29715_All//0.00E+00//EX165837			GO:0044464//GO:0060918	nr -
Unigene29716_All	430	206.24	579.99	476.28	47.73	92.17	71.32	50.15	38.98	19.46	1.49E+00	0.00E+00	Up	1.21E+00	2.84E-194	Up	9.50E-01	2.88E-31		5.79E-01	9.58E-10		-3.64E-01	6.12E-04		-1.37E+00	8.80E-33	Down	Unigene29716_All//gi|37724583|gb|AAO12870.1|//3.00E-17//wound induced protein-like [Vitis vinifera]	Unigene29716_All//3.00E-08//AT4G10270| wound-responsive family protein	Unigene29716_All//3.00E-116//TC170814				nr -
Unigene29717_All	235	7.12	1.51	1.81	7.84	3.08	4.61	1.98	2.31	1.53	-2.24E+00	1.26E-04	Down	-1.97E+00	7.74E-04	Down	-1.35E+00	3.21E-03		-7.66E-01	1.18E-01		2.24E-01	7.92E-01		-3.75E-01	6.65E-01					Unigene29717_All//3.00E-07//DR463273				
Unigene2972_All	1742	0.66	0.52	0.31	18.70	18.92	14.67	5.05	2.11	0.89	-3.36E-01	6.09E-01		-1.11E+00	9.93E-02		1.66E-02	8.94E-01		-3.50E-01	1.60E-04		-1.26E+00	6.20E-12	Down	-2.50E+00	1.78E-30	Down	Unigene2972_All//gi|238481047|ref|NP_001154284.1|//0.00E+00//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene2972_All//0.00E+00//AT4G33330| transferase, transferring glycosyl groups	Unigene2972_All//0.00E+00//TC135116			GO:0035251//GO:0044464	nr +
Unigene29721_All	400	207.32	71.57	158.82	1453.58	1473.14	1041.35	104.33	41.27	67.63	-1.53E+00	5.10E-117	Down	-3.85E-01	4.17E-11		1.93E-02	4.79E-01		-4.81E-01	1.41E-125		-1.34E+00	5.92E-59	Down	-6.26E-01	1.34E-17		Unigene29721_All//gi|32440933|dbj|BAC78827.1|//3.00E-54//caffeic acid O-methyltransferase [Rosa chinensis var. spontanea]	Unigene29721_All//2.00E-41//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene29721_All//0.00E+00//gi|13349702|gb|BG440052.1|BG440052		ko00940|Phenylpropanoid biosynthesis/ko00944|Flavone and flavonol biosynthesis	GO:0005515//GO:0008171//GO:0009699	nr -
Unigene29727_All	639	0.41	0.32	1.17	2.42	3.34	4.03	0.46	0.78	1.93	-3.68E-01	7.78E-01		1.51E+00	9.50E-02		4.67E-01	3.20E-01		7.37E-01	6.76E-02		7.61E-01	4.22E-01		2.06E+00	5.00E-04	Up	Unigene29727_All//gi|14030679|gb|AAK53014.1|AF375430_1//6.00E-27//AT5g45310/K9E15_9 [Arabidopsis thaliana] >gi|16974513|gb|AAL31166.1| AT5g45310/K9E15_9 [Arabidopsis thaliana]	Unigene29727_All//3.00E-28//AT5G45310| unknown protein	Unigene29727_All//0.00E+00//TC178829				nr -
Unigene29728_All	549	1.43	1.11	0.00	4.26	3.70	3.62	99.27	103.31	73.65	-3.68E-01	6.23E-01		-1.05E+01	2.22E-04	Down	-2.05E-01	6.33E-01		-2.37E-01	6.34E-01		5.75E-02	4.58E-01		-4.31E-01	5.84E-12		Unigene29728_All//gi|224076976|ref|XP_002305076.1|//3.00E-19//predicted protein [Populus trichocarpa] >gi|222848040|gb|EEE85587.1| predicted protein [Populus trichocarpa]		Unigene29728_All//0.00E+00//TC177786				nr -
Unigene29729_All	426	3.07	1.31	4.38	1.29	0.97	0.85	1.89	1.47	0.28	-1.23E+00	3.96E-02		5.11E-01	3.12E-01		-4.07E-01	6.58E-01		-6.01E-01	5.66E-01		-3.58E-01	6.49E-01		-2.75E+00	9.43E-04	Down				Unigene29729_All//1.00E-07//DW518704				
Unigene2973_All	2149	4.21	1.11	1.91	13.70	8.52	13.81	10.17	5.15	5.04	-1.93E+00	3.73E-18	Down	-1.14E+00	2.27E-08	Down	-6.84E-01	6.12E-14		1.13E-02	9.43E-01		-9.81E-01	2.46E-19		-1.01E+00	5.94E-21	Down	Unigene2973_All//gi|115440647|ref|NP_001044603.1|//9.00E-45//Os01g0814000 [Oryza sativa Japonica Group] >gi|113534134|dbj|BAF06517.1| Os01g0814000 [Oryza sativa Japonica Group]	Unigene2973_All//7.00E-48//AT5G18440| unknown protein	Unigene2973_All//0.00E+00//gi|13351221|gb|BG441569.1|BG441569				nr -
Unigene29730_All	405	0.39	0.00	2.24	3.69	1.79	1.45	12.84	68.21	18.98	-8.60E+00	2.16E-01		2.53E+00	5.63E-03		-1.05E+00	4.30E-02		-1.35E+00	1.52E-02		2.41E+00	4.08E-87	Up	5.64E-01	1.95E-03		Unigene29730_All//gi|110931840|gb|ABH02919.1|//4.00E-44//MYB transcription factor MYB117 [Glycine max]	Unigene29730_All//5.00E-43//AT1G79180| MYB63 (MYB DOMAIN PROTEIN 63); DNA binding / transcription activator/ transcription factor	Unigene29730_All//2.00E-61//TC167316	MYB			nr +
Unigene29732_All	663	0.08	0.15	0.16	0.75	0.16	0.41	6.89	21.56	23.92	9.54E-01	7.26E-01		1.03E+00	7.03E-01		-2.27E+00	4.22E-02		-8.78E-01	4.20E-01		1.65E+00	7.70E-28	Up	1.80E+00	1.87E-35	Up	Unigene29732_All//gi|302143298|emb|CBI21859.3|//5.00E-19//unnamed protein product [Vitis vinifera]		Unigene29732_All//4.00E-24//gi|73861561|gb|DT464300.1|DT464300				nr -
Unigene29733_All	483	1.19	0.42	1.54	4.33	2.71	1.31	1.14	0.87	1.07	-1.51E+00	1.36E-01		3.73E-01	6.23E-01		-6.77E-01	1.17E-01		-1.73E+00	2.25E-04	Down	-3.95E-01	6.34E-01		-8.58E-02	9.27E-01					Unigene29733_All//7.00E-19//ES800203				
Unigene29737_All	667	1.02	0.46	0.32	11.80	4.08	2.71	5.13	2.82	2.39	-1.16E+00	1.89E-01		-1.68E+00	8.70E-02		-1.53E+00	3.76E-14	Down	-2.12E+00	2.67E-19	Down	-8.65E-01	3.65E-03		-1.10E+00	1.68E-04	Down	Unigene29737_All//gi|225430575|ref|XP_002263122.1|//9.00E-31//PREDICTED: similar to GDU1 [Vitis vinifera]	Unigene29737_All//3.00E-12//AT5G24920| AtGDU5 (Arabidopsis thaliana GLUTAMINE DUMPER 5)	Unigene29737_All//0.00E+00//gi|109886016|gb|DR514986.1|DR514986				nr -
Unigene29738_All	749	0.21	0.68	0.28	1.33	2.62	1.03	2.48	0.11	1.65	1.69E+00	1.34E-01		4.40E-01	7.75E-01		9.78E-01	3.42E-02		-3.76E-01	6.32E-01		-4.48E+00	9.04E-11	Down	-5.91E-01	1.51E-01		Unigene29738_All//gi|15218418|ref|NP_177370.1|//6.00E-21//kinesin motor protein-related [Arabidopsis thaliana]	Unigene29738_All//3.00E-22//AT1G72250| kinesin motor protein-related					nr +
Unigene29739_All	276	2.09	9.73	5.79	1.44	3.74	4.75	0.00	0.00	0.00	2.22E+00	7.31E-07	Up	1.47E+00	9.57E-03		1.37E+00	5.14E-02		1.72E+00	6.55E-03		null	null		null	null		Unigene29739_All//gi|15081799|gb|AAB82554.1|//4.00E-23//At1g05070/T7A14_6 [Arabidopsis thaliana] >gi|22655016|gb|AAM88099.1| At1g05070/T7A14_6 [Arabidopsis thaliana]	Unigene29739_All//6.00E-14//AT1G05070| unknown protein	Unigene29739_All//3.00E-75//DR463407				nr +
Unigene2974_All	1126	41.59	66.10	47.20	45.26	51.84	51.26	46.52	24.42	18.65	6.69E-01	2.46E-27		1.83E-01	2.11E-02		1.96E-01	4.04E-03		1.80E-01	1.29E-02		-9.30E-01	2.12E-41		-1.32E+00	2.46E-74	Down	Unigene2974_All//gi|10177953|dbj|BAB11312.1|//2.00E-98//aluminum-induced protein-like [Arabidopsis thaliana] >gi|21537246|gb|AAM61587.1| aluminum-induced protein-like [Arabidopsis thaliana]	Unigene2974_All//5.00E-97//AT3G22850| unknown protein	Unigene2974_All//0.00E+00//TC138052			GO:0043231//GO:0044444	nr -
Unigene29743_All	818	0.00	0.06	0.00	7.06	5.39	2.98	0.00	0.00	0.00	5.95E+00	6.16E-01		null	null		-3.91E-01	1.15E-01		-1.24E+00	5.56E-07	Down	null	null		null	null		Unigene29743_All//gi|9049359|dbj|BAA99394.1|//5.00E-09//vacuolar calcium binding protein [Raphanus sativus]		Unigene29743_All//0.00E+00//TC135237				nr +
Unigene29744_All	561	0.00	5.33	14.81	0.00	2.27	1.13	0.00	0.00	0.00	1.24E+01	5.19E-17	Up	1.39E+01	1.64E-46	Up	1.11E+01	7.21E-08	Up	1.01E+01	7.60E-04	Up	null	null		null	null		Unigene29744_All//gi|260766526|gb|ACX50285.1|//6.00E-50//cytochrome oxidase subunit 1 [Guillardia theta]	Unigene29744_All//7.00E-49//ATMG01360| cytochrome c oxidase subunit 1			ko00190|Oxidative phosphorylation		nr -
Unigene29745_All	917	0.74	0.72	2.21	0.38	0.15	1.13	1.43	4.42	0.22	-4.62E-02	9.69E-01		1.57E+00	1.64E-03		-1.34E+00	3.08E-01		1.57E+00	2.92E-02		1.63E+00	2.50E-08	Up	-2.72E+00	1.32E-05	Down	Unigene29745_All//gi|12003402|gb|AAG43558.1|AF211540_1/1.00E-11//Avr9/Cf-9 rapidly elicited protein 75 [Nicotiana tabacum]	Unigene29745_All//6.00E-05//AT1G22470| unknown protein	Unigene29745_All//3.00E-118//DV849227				nr +
Unigene29746_All	1264	0.25	0.16	0.08	0.43	0.00	0.00	6.69	5.89	6.68	-6.32E-01	6.22E-01		-1.56E+00	3.30E-01		-8.76E+00	4.01E-04	Down	-8.76E+00	1.52E-03		-1.85E-01	3.66E-01		-1.70E-03	9.90E-01		Unigene29746_All//gi|297799102|ref|XP_002867435.1|//4.00E-81//ring-H2 finger protein ATL4J precursor [Arabidopsis lyrata subsp. lyrata] >gi|297313271|gb|EFH43694.1| ring-H2 finger protein ATL4J precursor [Arabidopsis lyrata subsp. lyrata]	Unigene29746_All//6.00E-81//AT4G28890| protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene29746_All//6.00E-12//TC132917				nr +
Unigene29747_All	637	1.81	0.72	0.25	2.89	2.87	3.12	0.86	0.33	0.50	-1.34E+00	4.03E-02		-2.85E+00	6.02E-04	Down	-1.42E-02	9.65E-01		1.09E-01	8.28E-01		-1.40E+00	1.34E-01		-7.86E-01	3.62E-01		Unigene29747_All//gi|242075750|ref|XP_002447811.1|//7.00E-06//hypothetical protein SORBIDRAFT_06g016240 [Sorghum bicolor] >gi|241938994|gb|EES12139.1| hypothetical protein SORBIDRAFT_06g016240 [Sorghum bicolor]		Unigene29747_All//0.00E+00//gi|21094767|gb|BQ407080.1|BQ407080				nr -
Unigene29748_All	337	1.40	3.61	3.95	10.20	6.23	2.28	1.13	0.25	0.12	1.37E+00	3.15E-02		1.50E+00	1.84E-02		-7.10E-01	2.49E-02		-2.16E+00	6.50E-09	Down	-2.19E+00	8.75E-02		-3.26E+00	2.22E-02		Unigene29748_All//gi|40233067|gb|AAR83340.1|//3.00E-14//homeodomain protein HB1 [Populus tomentosa] >gi|40233103|gb|AAR83342.1| homeodomain protein HB1 [Populus tomentosa]	Unigene29748_All//2.00E-69//AT1G20700| WOX14 (WUSCHEL RELATED HOMEOBOX 14); DNA binding / transcription factor	Unigene29748_All//2.00E-154//ES800482	HB			nr +
Unigene29749_All	790	4.83	1.35	4.04	3.91	2.44	0.57	0.91	0.00	0.25	-1.84E+00	1.17E-07	Down	-2.58E-01	4.43E-01		-6.80E-01	4.52E-02		-2.77E+00	1.42E-10	Down	-9.83E+00	3.26E-05	Down	-1.85E+00	1.78E-02		Unigene29749_All//gi|297738811|emb|CBI28056.3|//9.00E-24//unnamed protein product [Vitis vinifera]						nr +

Unigene29751_All	1685	0.34	0.00	0.06	12.00	7.30	3.54	0.85	0.15	0.14	-8.42E+00	1.52E-03		-2.43E+00	4.40E-02		-7.18E-01	1.50E-10		-1.76E+00	3.66E-38	Down	-2.52E+00	2.00E-05	Down	-2.59E+00	8.29E-06	Down	Unigene29751_All//gi|1087017|gb|AAB35284.1|//7.00E-26//arabinogalactan-protein [Nicotiana alata]		Unigene29751_All//0.00E+00//DR453249				nr -
Unigene29752_All	278	1.88	9.30	4.60	2.51	0.99	0.65	1.67	1.95	4.16	2.30E+00	6.83E-07	Up	1.29E+00	4.48E-02		-1.34E+00	1.09E-01		-1.95E+00	3.91E-02		2.24E-01	7.92E-01		1.31E+00	1.95E-02				Unigene29752_All//3.00E-07//gi|73849952|gb|DT458972.1|DT458972				
Unigene29753_All	1334	0.59	0.11	0.80	0.41	0.10	1.15	5.32	13.22	21.80	-2.37E+00	1.09E-02		4.41E-01	5.22E-01		-1.99E+00	5.12E-02		1.49E+00	8.00E-03		1.31E+00	1.32E-24	Up	2.03E+00	7.59E-76	Up	Unigene29753_All//gi|224052970|ref|XP_002297642.1|//1.00E-145//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222844900|gb|EEE82447.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene29753_All//8.00E-133//AT3G13610| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene29753_All//0.00E+00//TC178591		ko00941|Flavonoid biosynthesis		nr +
Unigene29754_All	310	8.44	8.01	19.58	9.80	17.11	4.66	0.00	0.00	0.00	-7.54E-02	8.43E-01		1.21E+00	2.24E-06	Up	8.03E-01	1.25E-03		-1.07E+00	2.63E-03		null	null		null	null		Unigene29754_All//gi|115438903|ref|NP_001043731.1|//3.00E-16//Os01g0651300 [Oryza sativa Japonica Group] >gi|113533262|dbj|BAF05645.1| Os01g0651300 [Oryza sativa Japonica Group]	Unigene29754_All//2.00E-16//AT1G28600| lipase, putative	Unigene29754_All//3.00E-165//TC152013				nr +
Unigene29756_All	269	0.00	6.22	6.93	0.74	3.84	6.21	3.30	1.86	1.93	1.26E+01	1.54E-09	Up	1.28E+01	2.89E-10	Up	2.37E+00	2.24E-03		3.07E+00	2.60E-06	Up	-8.24E-01	2.24E-01		-7.78E-01	2.20E-01								
Unigene29757_All	261	18.24	46.59	32.64	12.79	24.94	22.32	24.78	33.63	12.67	1.35E+00	9.63E-15	Up	8.40E-01	4.66E-05		9.64E-01	1.26E-05		8.04E-01	9.62E-04		4.40E-01	1.23E-02		-9.68E-01	2.10E-06		Unigene29757_All//gi|15219078|ref|NP_175683.1|//8.00E-11//HTA9 (HISTONE H2A PROTEIN 9); DNA binding [Arabidopsis thaliana] >gi|75308904|sp|Q9XI44.1|H2AV3_ARATH RecName: Full=Probable histone H2A variant 3; AltName: Full=HTA9 >gi|16648742|gb|AAL25563.1| At1g52740/F14G24_1 [Arabidopsis thaliana]		Unigene29757_All//1.00E-98//TC152142				nr -
Unigene29758_All	486	1.40	0.21	4.38	5.33	5.95	6.97	0.44	0.60	0.49	-2.75E+00	1.06E-02		1.65E+00	7.53E-04	Up	1.59E-01	7.26E-01		3.87E-01	2.91E-01		4.69E-01	7.06E-01		1.77E-01	9.08E-01		Unigene29758_All//gi|297849270|ref|XP_002892516.1|//4.00E-17//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297338358|gb|EFH68775.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]						nr -
Unigene2976_All	1551	3.10	1.93	1.79	5.33	4.97	4.31	6.24	2.88	5.78	-6.87E-01	1.20E-02		-7.98E-01	5.27E-03		-1.00E-01	6.70E-01		-3.07E-01	1.54E-01		-1.11E+00	6.40E-11	Down	-1.11E-01	5.56E-01		Unigene2976_All//gi|227202670|dbj|BAH56808.1|//1.00E-122//AT1G79090 [Arabidopsis thaliana]	Unigene2976_All//2.00E-93//AT1G79090| unknown protein	Unigene2976_All//7.00E-148//TC158831		ko03018|RNA degradation		nr +
Unigene29760_All	520	2.11	0.10	0.00	3.54	2.38	1.39	1.63	0.72	0.69	-4.44E+00	2.09E-05	Down	-1.10E+01	4.94E-06	Down	-5.72E-01	2.29E-01		-1.35E+00	5.69E-03		-1.17E+00	9.29E-02		-1.24E+00	6.26E-02		Unigene29760_All//gi|195620462|gb|ACG32061.1|//3.00E-21//ubiquitin ligase protein FANCL [Zea mays]	Unigene29760_All//5.00E-22//AT5G65740| protein binding / zinc ion binding			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene29765_All	442	28.53	2.75	2.17	28.06	46.90	26.36	0.00	0.00	0.00	-3.37E+00	1.21E-46	Down	-3.72E+00	1.31E-48	Down	7.41E-01	5.30E-11		-9.02E-02	6.38E-01		null	null		null	null		Unigene29765_All//gi|2565429|gb|AAB82000.1|//1.00E-23//glycine-rich protein [Onobrychis viciifolia]		Unigene29765_All//0.00E+00//TC151682		ko03040|Spliceosome		nr +
Unigene29766_All	729	0.43	0.21	0.22	3.69	1.89	1.36	0.99	0.46	0.55	-1.05E+00	4.43E-01		-9.75E-01	5.06E-01		-9.66E-01	7.63E-03		-1.44E+00	2.48E-04	Down	-1.10E+00	1.49E-01		-8.51E-01	2.39E-01		Unigene29766_All//gi|16226216|gb|AAL16105.1|AF428273_1//1.00E-56//AT4g20040/F18F4_140 [Arabidopsis thaliana] >gi|22137222|gb|AAM91456.1| AT4g20040/F18F4_140 [Arabidopsis thaliana]	Unigene29766_All//2.00E-58//AT4G20040| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Pectin lyase fold/virulence factor (InterPro:IPR011050), Parallel beta-helix repeat (InterPro:IPR006626); BEST Arabidopsis thaliana protein match is: QRT3 (QUARTET 3); polygalacturonase (TAIR:AT4G20050.2); Has 90 Blast hits to 90 proteins in 38 species: Archae - 0; Bacteria - 51; Metazoa - 0; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene29766_All//0.00E+00//gi|164293127|gb|ES833480.1|ES833480				nr +
Unigene29768_All	483	90.99	65.67	86.43	97.46	103.38	653.05	118.35	167.96	271.78	-4.71E-01	3.94E-09		-7.41E-02	4.35E-01		8.50E-02	3.40E-01		2.74E+00	0.00E+00	Up	5.05E-01	2.66E-22		1.20E+00	3.09E-158	Up	Unigene29768_All//gi|300793588|tpg|DAA33860.1|//2.00E-09//TPA: TPA_inf: aquaporin PIP1:6 [Gossypium hirsutum]	Unigene29768_All//1.00E-10//AT4G00430| PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel	Unigene29768_All//0.00E+00//gi|164297463|gb|ES840953.1|ES840953				nr -
Unigene29769_All	552	0.00	3.21	0.77	1.62	1.93	1.72	1.53	1.51	2.02	1.16E+01	4.14E-10	Up	9.59E+00	1.38E-02		2.52E-01	7.58E-01		8.10E-02	9.31E-01		-1.67E-02	1.02E+00		4.00E-01	4.88E-01				Unigene29769_All//7.00E-07//TC173134				
Unigene2977_All	1747	5.84	67.84	26.09	7.78	21.86	28.39	10.33	16.36	23.42	3.54E+00	0.00E+00	Up	2.16E+00	7.19E-100	Up	1.49E+00	1.08E-60	Up	1.87E+00	1.12E-98	Up	6.63E-01	3.56E-13		1.18E+00	1.16E-48	Up	Unigene2977_All//gi|51870705|dbj|BAD42432.1|//1.00E-123//bZip transcription factor [Psophocarpus tetragonolobus]	Unigene2977_All//1.00E-90//AT2G46270| GBF3 (G-BOX BINDING FACTOR 3); sequence-specific DNA binding / transcription factor	Unigene2977_All//0.00E+00//gi|13247698|gb|BF271790.2|BF271790	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0005488//GO:0006350	nr +
Unigene29773_All	536	1.17	3.59	0.50	3.44	1.28	0.84	1.58	0.39	2.75	1.62E+00	1.18E-03		-1.24E+00	2.13E-01		-1.42E+00	2.01E-03		-2.03E+00	1.02E-04	Down	-2.02E+00	7.45E-03		8.02E-01	9.06E-02				Unigene29773_All//8.00E-173//DW243256				
Unigene29774_All	1007	0.21	1.36	0.69	0.30	0.07	0.09	4.91	6.85	7.99	2.71E+00	1.29E-04	Up	1.73E+00	7.67E-02		-2.12E+00	1.65E-01		-1.73E+00	2.89E-01		4.79E-01	1.73E-02		7.02E-01	8.00E-05		Unigene29774_All//gi|6683479|dbj|BAA89230.1|//2.00E-92//wts2L [Citrullus lanatus]	Unigene29774_All//1.00E-52//AT3G51680| short-chain dehydrogenase/reductase (SDR) family protein			ko00906|Carotenoid biosynthesis		nr +
Unigene29777_All	573	3.38	6.37	9.85	1.74	2.28	1.97	0.52	0.36	0.14	9.14E-01	4.70E-03		1.54E+00	2.67E-08	Up	3.93E-01	5.44E-01		1.81E-01	7.84E-01		-5.02E-01	6.78E-01		-1.89E+00	1.68E-01		Unigene29777_All//gi|10956148|ref|NP_052129.1|//9.00E-99//beta-lactamase [Staphylococcus aureus] >gi|10956150|ref|NP_052130.1| beta-lactamase [Staphylococcus aureus] >gi|1126199|pir||T51301 beta-lactamase (EC 3.5.2.6) - fission yeast (Schizosaccharomyces pombe) >gi|67464382|pdb|1ZG4|A Chain A, Tem1 Beta Lactamase >gi|4704644|gb|AAD28190.1|AF110459_3 beta-lactamase [Cloning vector pBBR1-GFP] >gi|4733039|gb|AAD28564.1|AF118921_1 beta-lactamase [alk-system cloning vector pSPZ2Not] >gi|4959728|gb|AAD34468.1|AF136443_1 beta-lactamase [Cloning vector pUC-TP] >gi|5006905|gb|AAD37723.1|AF146395_1 beta-lactamase [Cloning vector pCLZip] >gi|5702092|gb|AAD47138.1|AF061181_2 beta-lactamase [Mammalian expression vector pCI-nGL1-HEGO] >gi|5733495|gb|AAD49607.1|AF147464_1 beta-lactamase [Expression vector pViet] >gi|5802284|gb|AAD51639.1|AF170481_2 beta-lactamase [Cloning vector		Unigene29777_All//1.00E-48//gi|48807266|gb|CO108580.1|CO108580				nr +
Unigene29779_All	1154	0.00	0.00	0.00	0.00	0.00	0.00	182.64	10.07	2.45	null	null		null	null		null	null		null	null		-4.18E+00	0.00E+00	Down	-6.22E+00	0.00E+00	Down	Unigene29779_All//gi|89243481|gb|ABD64879.1|//4.00E-81//nicotianamine synthase [Malus xiaojinensis]	Unigene29779_All//1.00E-76//AT1G56430| NAS4 (NICOTIANAMINE SYNTHASE 4); nicotianamine synthase					nr +
Unigene29780_All	296	1.94	1.37	3.42	1.35	2.09	5.34	1.86	1.13	0.94	-5.06E-01	6.00E-01		8.14E-01	2.51E-01		6.37E-01	5.49E-01		1.99E+00	6.07E-04	Up	-7.17E-01	4.22E-01		-9.79E-01	2.50E-01		Unigene29780_All//gi|20043011|gb|AAM08819.1|AC090486_29//4.00E-12//Putative retroelement [Oryza sativa Japonica Group]	Unigene29780_All//2.00E-06//ATMG01250| hypothetical protein					nr -
Unigene29781_All	490	2.78	4.55	2.93	0.51	2.67	2.49	0.00	0.00	0.00	7.13E-01	9.64E-02		7.99E-02	8.87E-01		2.39E+00	3.51E-04	Up	2.29E+00	1.17E-03		null	null		null	null		Unigene29781_All//gi|224077908|ref|XP_002305459.1|//5.00E-30//coniferylaldehyde 5-hydroxylase [Populus trichocarpa] >gi|222848423|gb|EEE85970.1| coniferylaldehyde 5- hydroxylase [Populus trichocarpa]	Unigene29781_All//5.00E-18//AT4G36220| FAH1 (FERULIC ACID 5-HYDROXYLASE 1); ferulate 5-hydroxylase/ monooxygenase	Unigene29781_All//1.00E-07//TC152108		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene29785_All	554	0.00	0.00	0.00	0.54	0.06	0.24	2.29	2.11	0.29	null	null		null	null		-3.12E+00	7.56E-02		-1.14E+00	4.57E-01		-1.16E-01	8.30E-01		-2.99E+00	6.36E-06	Down	Unigene29785_All//gi|32489125|emb|CAE04792.1|//2.00E-17//OSJNB0018J12.5 [Oryza sativa (japonica cultivar-group)]	Unigene29785_All//3.00E-12//AT4G23160| protein kinase family protein					nr -
Unigene29789_All	361	2.90	2.67	0.89	1.10	2.96	1.00	2.81	1.74	0.11	-1.20E-01	8.43E-01		-1.71E+00	2.35E-02		1.42E+00	4.05E-02		-1.41E-01	9.04E-01		-6.95E-01	2.63E-01		-4.67E+00	1.72E-06	Down							
Unigene2979_All	1687	4.12	0.69	4.48	9.57	10.06	6.93	2.58	1.36	1.77	-2.58E+00	6.43E-20	Down	1.20E-01	6.18E-01		7.29E-02	6.63E-01		-4.65E-01	6.55E-04		-9.22E-01	3.88E-04		-5.44E-01	3.06E-02		Unigene2979_All//gi|15233452|ref|NP_194639.1|//3.00E-90//ethylene-responsive family protein [Arabidopsis thaliana] >gi|75159400|sp|Q8S3D1.2|BH068_ARATH RecName: Full=Transcription factor bHLH068; AltName: Full=Transcription factor EN 60; AltName: Full=bHLH transcription factor bHLH068; AltName: Full=Basic helix-loop-helix protein 68; Short=bHLH 68; Short=AtbHLH68	Unigene2979_All//7.00E-78//AT4G29100| ethylene-responsive family protein	Unigene2979_All//0.00E+00//gi|164309143|gb|ES818883.1|ES818883	bHLH		GO:0010468//GO:0043231	nr +
Unigene29790_All	2098	0.00	0.00	0.00	0.00	0.00	0.00	5.60	8.55	11.98	null	null		null	null		null	null		null	null		6.09E-01	1.74E-07		1.10E+00	5.53E-27	Up	Unigene29790_All//gi|224100679|ref|XP_002311971.1|//1.00E-175//cytochrome P450 [Populus trichocarpa] >gi|222851791|gb|EEE89338.1| cytochrome P450 [Populus trichocarpa]	Unigene29790_All//6.00E-111//AT5G24910| CYP714A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00966|Glucosinolate biosynthesis		nr -
Unigene29792_All	428	0.00	0.00	0.00	1.05	1.21	1.27	0.30	0.98	2.33	null	null		null	null		2.04E-01	8.59E-01		2.74E-01	7.83E-01		1.72E+00	1.35E-01		2.97E+00	1.11E-04	Up	Unigene29792_All//gi|15240194|ref|NP_201509.1|//1.00E-07//MAPKKK19; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|10177595|dbj|BAB10942.1| protein kinase-like protein [Arabidopsis thaliana]	Unigene29792_All//9.00E-09//AT5G67080| MAPKKK19; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene29792_All//6.00E-16//TC141370				nr +

Unigene29793_All	519	2.52	1.95	0.62	3.84	3.18	2.78	1.87	1.21	0.38	-3.68E-01	5.31E-01		-2.03E+00	3.02E-03		-2.70E-01	5.86E-01		-4.63E-01	3.46E-01		-6.33E-01	3.28E-01		-2.29E+00	9.84E-04	Down	Unigene29793_All//gi|15240177|ref|NP_196299.1|//4.00E-44//mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana]	Unigene29793_All//2.00E-45//AT5G06810| mitochondrial transcription termination factor-related / mTERF-related					nr -
Unigene29795_All	254	0.82	4.79	2.94	0.20	0.95	1.60	1.00	0.16	0.16	2.54E+00	5.98E-04	Up	1.83E+00	5.05E-02		2.27E+00	3.05E-01		3.03E+00	6.03E-02		-2.60E+00	1.44E-01		-2.67E+00	1.15E-01										
Unigene29796_All	317	4.95	0.48	3.02	3.30	2.72	4.70	0.40	0.66	0.75	-3.37E+00	2.77E-06	Down	-7.12E-01	2.02E-01		-2.81E-01	6.74E-01		5.11E-01	3.95E-01		7.20E-01	6.32E-01		9.14E-01	5.42E-01		Unigene29796_All//gi|224126363|ref|XP_002329535.1|//8.00E-14//predicted protein [Populus trichocarpa] >gi|222870244|gb|EEF07375.1| predicted protein [Populus trichocarpa]						nr -
Unigene298_All	3004	0.44	1.30	0.39	0.63	1.42	0.93	1.69	1.15	1.70	1.58E+00	2.17E-06	Up	-1.59E-01	7.76E-01		1.17E+00	4.14E-05	Up	5.65E-01	1.48E-01		-5.49E-01	2.17E-02		7.20E-03	9.73E-01		Unigene298_All//gi|23617202|dbj|BAC20873.1|//0.00E+00//VP1/ABI3 family regulatory protein-like protein [Oryza sativa Japonica Group]	Unigene298_All//7.00E-154//AT4G32010| HSL1 (HSI2-LIKE 1); transcription factor	Unigene298_All//0.00E+00//TC161066	ABI3VP1	ko00310|Lysine degradation		nr -
Unigene2980_All	1896	2.37	1.10	1.24	4.20	4.89	2.67	13.69	3.33	6.32	-1.12E+00	1.23E-04	Down	-9.41E-01	1.62E-03		2.17E-01	3.14E-01		-6.56E-01	1.16E-03		-2.04E+00	6.74E-67	Down	-1.11E+00	9.39E-29	Down	Unigene2980_All//gi|224125422|ref|XP_002319582.1|//0.00E+00//dehydroquinate dehydratase/ shikimate dehydrogenase [Populus trichocarpa] >gi|222857958|gb|EEE95505.1| dehydroquinate dehydratase/ shikimate dehydrogenase [Populus trichocarpa]	Unigene2980_All//0.00E+00//AT3G06350| MEE32 (MATERNAL EFFECT EMBRYO ARREST 32); 3-dehydroquinate dehydratase/ NADP or NADPH binding / binding / catalytic/ shikimate 5-dehydrogenase	Unigene2980_All//0.00E+00//TC149525		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0000166//GO:0003006//GO:0008652//GO:0009532//GO:0016616//GO:0016836	nr +
Unigene29801_All	432	1.82	0.70	0.12	5.19	2.95	0.63	4.21	0.39	2.40	-1.37E+00	9.60E-02		-3.88E+00	1.60E-03		-8.15E-01	4.54E-02		-3.05E+00	1.55E-08	Down	-3.44E+00	7.71E-09	Down	-8.12E-01	5.01E-02				Unigene29801_All//5.00E-50//TC171513					
Unigene29802_All	612	0.34	9.52	8.00	0.98	1.29	6.64	0.00	0.14	0.13	4.80E+00	1.29E-27	Up	4.55E+00	5.83E-22	Up	4.06E-01	6.32E-01		2.77E+00	2.43E-13	Up	7.09E+00	4.01E-01		7.02E+00	4.04E-01		Unigene29802_All//gi|48310140|gb|AAT41761.1|//5.00E-11//At5g57790 [Arabidopsis thaliana] >gi|52218790|gb|AAU29465.1| At5g57790 [Arabidopsis thaliana]						nr +
Unigene29807_All	368	1.42	4.68	0.43	1.90	2.06	2.33	14.25	2.61	2.38	1.72E+00	1.41E-03		-1.71E+00	1.40E-01		1.19E-01	9.05E-01		2.99E-01	6.87E-01		-2.45E+00	1.95E-17	Down	-2.58E+00	4.02E-19	Down	Unigene29807_All//gi|283837097|emb|CBH19893.1|//6.00E-17//cell division control 20 [Solanum lycopersicum var. cerasiforme]	Unigene29807_All//4.00E-18//AT4G33260| CDC20.2; signal transducer	Unigene29807_All//7.00E-157//DW232567		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene2981_All	1329	20.67	23.03	23.72	25.08	20.55	28.04	29.20	19.59	11.78	1.56E-01	1.38E-01		1.99E-01	6.06E-02		-2.87E-01	1.25E-03		1.61E-01	9.48E-02		-5.76E-01	7.16E-14		-1.31E+00	1.05E-54	Down	Unigene2981_All//gi|15233282|ref|NP_190965.1|//6.00E-96//proteasome inhibitor-related [Arabidopsis thaliana] >gi|18203248|sp|Q9M330.1|PSMF1_ARATH RecName: Full=Probable proteasome inhibitor	Unigene2981_All//7.00E-75//AT3G53970| proteasome inhibitor-related	Unigene2981_All//0.00E+00//TC150493		ko03050|Proteasome		nr -
Unigene29811_All	868	589.94	860.45	945.68	223.59	327.97	404.65	240.43	268.49	109.01	5.45E-01	6.30E-186		6.81E-01	7.41E-297		5.53E-01	1.08E-87		8.56E-01	5.27E-209		1.59E-01	9.42E-08		-1.14E+00	6.66E-234	Down	Unigene29811_All//gi|124484383|dbj|BAF46302.1|//1.00E-102//cysteine proteinase precursor [Ipomoea nil]	Unigene29811_All//4.00E-88//AT4G39090| RD19 (RESPONSIVE TO DEHYDRATION 19); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene29811_All//0.00E+00//gi|78323339|gb|DT543613.1|DT543613				nr +
Unigene29812_All	386	0.14	0.53	0.97	1.94	4.55	2.93	16.32	9.10	37.16	1.95E+00	3.75E-01		2.83E+00	9.31E-02		1.23E+00	1.31E-02		5.96E-01	3.98E-01		-8.44E-01	5.89E-05		1.19E+00	8.94E-18	Up	Unigene29812_All//gi|14194099|gb|AAK56244.1|AF367258_1//3.00E-24//AT3g52990/F8J2_160 [Arabidopsis thaliana] >gi|21537185|gb|AAM61526.1| pyruvate kinase-like protein [Arabidopsis thaliana] >gi|24111299|gb|AAN46773.1| At3g52990/F8J2_160 [Arabidopsis thaliana]	Unigene29812_All//1.00E-25//AT3G52990| pyruvate kinase, putative	Unigene29812_All//5.00E-93//TC177746		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene29814_All	577	3.17	1.76	2.77	2.50	0.66	0.70	2.13	2.03	0.69	-8.54E-01	7.59E-02		-1.97E-01	6.80E-01		-1.93E+00	5.06E-04	Down	-1.83E+00	1.94E-03		-6.73E-02	9.14E-01		-1.62E+00	3.49E-03				Unigene29814_All//7.00E-07//TC137698					
Unigene2982_All	2015	2.96	1.08	1.37	4.85	4.63	4.12	6.13	3.13	3.54	-1.45E+00	1.93E-08	Down	-1.11E+00	1.66E-05	Down	-6.53E-02	7.89E-01		-2.33E-01	2.53E-01		-9.68E-01	4.73E-11		-7.92E-01	2.23E-08		Unigene2982_All//gi|30102514|gb|AAP21175.1|//0.00E+00//AT3g14120/MAG2_7 [Arabidopsis thaliana]	Unigene2982_All//0.00E+00//AT3G14120| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: transport; LOCATED IN: nuclear pore; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nuclear pore protein 84/107 (InterPro:IPR007252); Has 207 Blast hits to 206 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 123; Fungi - 57; Plants - 22; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene2982_All//3.00E-49//gi|48801163|gb|CO102477.1|CO102477				nr +
Unigene29820_All	717	0.58	0.92	0.52	1.04	1.34	1.51	2.24	1.40	0.61	6.54E-01	4.48E-01		-1.67E-01	8.79E-01		3.68E-01	6.24E-01		5.37E-01	4.55E-01		-6.80E-01	1.47E-01		-1.87E+00	1.38E-04	Down			Unigene29820_All//2.00E-07//ES826553					
Unigene29821_All	325	4.35	4.05	0.33	6.13	4.98	0.56	0.65	0.77	0.61	-1.01E-01	8.47E-01		-3.73E+00	8.90E-06	Down	-3.00E-01	5.56E-01		-3.46E+00	1.64E-08	Down	2.46E-01	8.53E-01		-8.59E-02	9.61E-01									
Unigene29822_All	378	1.38	4.16	1.41	2.37	2.37	1.67	0.00	0.00	1.37	1.59E+00	4.56E-03		2.54E-02	9.99E-01		-2.10E-03	9.78E-01		-5.04E-01	5.11E-01		null	null		1.04E+01	6.13E-04	Up	Unigene29822_All//gi|15227610|ref|NP_180534.1|//2.00E-21//UGT71D1 (UDP-GLUCOSYL TRANSFERASE 71D1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|30387555|gb|AAP31943.1| At2g29730 [Arabidopsis thaliana]	Unigene29822_All//1.00E-14//AT2G29730| UGT71D1 (UDP-GLUCOSYL TRANSFERASE 71D1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups					nr +
Unigene29824_All	595	0.00	0.00	0.00	4.69	2.03	3.72	0.21	0.00	0.00	null	null		null	null		-1.21E+00	6.40E-04	Down	-3.34E-01	4.13E-01		-7.74E+00	2.35E-01		-7.74E+00	2.00E-01		Unigene29824_All//gi|15227652|ref|NP_181181.1|//1.00E-15//AtGRF3 (GROWTH-REGULATING FACTOR 3); transcription activator [Arabidopsis thaliana] >gi|21539884|gb|AAM52878.1| transcription activator [Arabidopsis thaliana] >gi|11074412|gb|AB004579.1| At2g36400 [Arabidopsis thaliana]	Unigene29824_All//1.00E-15//AT2G36400| AtGRF3 (GROWTH-REGULATING FACTOR 3); transcription activator	Unigene29824_All//8.00E-16//AI055588	GRF			nr +
Unigene29825_All	790	0.00	0.00	0.00	0.00	0.00	0.00	38.05	37.56	4.29	null	null		null	null		null	null		null	null		-1.87E-02	8.68E-01		-3.15E+00	9.23E-131	Down	Unigene29825_All//gi|253760977|ref|XP_002489033.1|//2.00E-07//hypothetical protein SORBIDRAFT_03S1s002020 [Sorghum bicolor] >gi|241947330|gb|EES20475.1| hypothetical protein SORBIDRAFT_03S1s002020 [Sorghum bicolor]		Unigene29825_All//7.00E-23//ES839149				nr +
Unigene29826_All	626	0.00	0.00	0.00	0.00	0.00	0.00	10.13	1.94	2.29	null	null		null	null		null	null		null	null		-2.39E+00	2.28E-20	Down	-2.14E+00	1.45E-18	Down	Unigene29826_All//gi|1545805|dbj|BAA10929.1|//9.00E-17//cytochrome P450 like_TBP [Nicotiana tabacum]		Unigene29826_All//2.00E-32//ES794483				nr -
Unigene29827_All	712	0.00	0.14	0.07	0.28	0.58	1.52	162.11	23.95	37.94	7.15E+00	3.87E-01		6.23E+00	6.36E-01		1.05E+00	4.26E-01		2.44E+00	1.61E-03		-2.76E+00	0.00E+00	Down	-2.10E+00	0.00E+00	Down	Unigene29827_All//gi|224139378|ref|XP_002323083.1|//9.00E-56//cytochrome P450 [Populus trichocarpa] >gi|222867713|gb|EEF04844.1| cytochrome P450 [Populus trichocarpa]	Unigene29827_All//1.00E-35//AT3G48310| CYP71A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene29827_All//3.00E-102//C0115886		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism		nr +
Unigene29828_All	583	0.72	0.17	0.27	1.54	1.54	0.08	1.67	0.14	0.34	-2.05E+00	1.20E-01		-1.39E+00	2.80E-01		-2.20E-03	9.78E-01		-4.31E+00	1.14E-04	Down	-3.54E+00	4.32E-05	Down	-2.29E+00	9.84E-04	Down	Unigene29828_All//gi|255538598|ref|XP_002510364.1|//6.00E-22//hypothetical protein RCOM_1593930 [Ricinus communis] >gi|223551065|gb|EEF52551.1| hypothetical protein RCOM_1593930 [Ricinus communis]	Unigene29828_All//6.00E-09//AT3G56870| unknown protein	Unigene29828_All//0.00E+00//TC157963				nr +
Unigene29829_All	341	0.92	0.89	0.47	1.02	2.12	1.72	0.99	1.72	5.61	-4.63E-02	9.85E-01		-9.75E-01	5.06E-01		1.05E+00	2.40E-01		7.52E-01	4.67E-01		7.91E-01	3.74E-01		2.50E+00	4.21E-07	Up			Unigene29829_All//3.00E-91//ES793337					
Unigene29830_All	1023	0.97	0.89	0.99	0.10	0.10	0.00	1.07	2.53	0.04	-1.24E-01	8.42E-01		2.55E-02	9.90E-01		5.24E-02	9.67E-01		-6.61E+00	4.00E-01		1.24E+00	5.53E-04	Up	-4.79E+00	4.55E-07	Down								
Unigene29835_All	556	42.06	19.05	20.59	52.14	45.09	51.34	48.06	20.30	15.76	-1.14E+00	1.60E-21	Down	-1.03E+00	1.50E-17	Down	-2.10E-01	4.08E-02		-2.25E-02	8.61E-01		-1.24E+00	4.88E-34	Down	-1.61E+00	2.56E-51	Down	Unigene29835_All//gi|115449229|ref|NP_001048394.1|//2.00E-24//Os02g0797200 [Oryza sativa Japonica Group] >gi|162459376|ref|NP_001105473.1| 60S ribosomal protein L39 [Zea mays] >gi|1710551|sp|P51425.1|RL39_MAIZE RecName: Full=60S ribosomal protein L39 >gi|55977802|sp|P51426.2|RL39_ORYSJ RecName: Full=60S ribosomal protein L39 >gi|1177369|emb|CAA64728.1| ribosomal protein L39 [Zea mays] >gi|47497037|dbj|BAD19090.1| 60S RIBOSOMAL PROTEIN L39 [Oryza sativa Japonica Group] >gi|113537925|dbj|BAF10308.1| Os02g0797200 [Oryza sativa Japonica Group] >gi|149390885|gb|ABR25460.1| 60S ribosomal protein L39 [Oryza sativa Indica Group] >gi|195609506|gb|ACG26583.1| 60S ribosomal protein L39 [Zea mays] >gi|195609702|gb|ACG26681.1| 60S ribosomal protein L39 [Zea mays] >gi|195609876|gb|ACG26768.1| 60S ribosomal protein L39 [Zea mays]	Unigene29835_All//4.00E-23//AT4G31985| 60S ribosomal protein L39 (RPL39C)	Unigene29835_All//0.00E+00//TC158710		ko03010|Ribosome		nr -
Unigene29838_All	659	0.08	0.69	0.48	0.00	0.00	0.41	10.01	16.17	36.09	3.12E+00	3.58E-02		2.61E+00	1.46E-01		null	null		8.68E+00	7.03E-02		6.92E-01	8.67E-06		1.85E+00	6.23E-55	Up	Unigene29838_All//gi|283136076|gb|ADB11357.1|//7.00E-30//tau class glutathione transferase GSTU25 [Populus trichocarpa]	Unigene29838_All//6.00E-11//AT3G09270| ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	Unigene29838_All//1.00E-08//ES799293		ko00480|Glutathione metabolism		nr +
Unigene29842_All	312	0.84	1.79	0.00	3.67	4.30	3.76	0.68	3.35	0.38	1.09E+00	2.74E-01		-9.71E+00	8.57E-02		2.29E-01	7.47E-01		3.55E-02	9.52E-01		2.31E+00	8.56E-04	Up	-8.23E-01	5.99E-01									

Unigene29844_All	857	0.00	0.59	0.00	0.00	0.00	0.00	55.55	9.90	18.13	9.21E+00	4.04E-03		null	null		null	null		null	null		-2.49E+00	6.48E-156	Down	-1.62E+00	2.30E-91	Down	Unigene29844_All//gi|145442272|gb|AB988856.1|//1.00E-104//endonuclease [Glycine max]	Unigene29844_All//2.00E-100//AT1G11190| BFN1 (BIFUNCTIONAL NUCLEASE 1); T/G mismatch-specific endonuclease/ endoribonuclease, producing 5'-phosphomonoesters / nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease	Unigene29844_All//0.00E+00//DW495821				nr +
Unigene29845_All	368	1.99	1.10	0.29	5.28	4.30	9.20	20.45	5.22	7.79	-8.54E-01	3.05E-01		-2.78E+00	1.04E-02		-2.95E-01	5.46E-01		8.02E-01	1.76E-02		-1.97E+00	4.89E-19	Down	-1.39E+00	2.48E-12	Down	Unigene29845_All//gi|225433375|ref|XP_002285608.1|//9.00E-26//PREDICTED: similar to GroEL-like chaperone, ATPase [Vitis vinifera]	Unigene29845_All//2.00E-16//AT3G23990| HSP60 (HEAT SHOCK PROTEIN 60); ATP binding	Unigene29845_All//7.00E-157//TC133542		ko03018|RNA degradation		nr -
Unigene29846_All	434	2.53	2.69	5.28	6.08	9.92	11.66	10.23	7.80	25.79	8.49E-02	8.94E-01		1.06E+00	1.72E-02		7.05E-01	1.35E-02		9.38E-01	4.02E-04		-3.91E-01	1.42E-01		1.33E+00	1.05E-16	Up				Unigene29846_All//4.00E-54//TC156709				
Unigene2985_All	555	19.42	21.91	17.94	6.01	6.95	6.10	1.30	4.82	0.93	1.74E-01	3.32E-01		-1.14E-01	5.87E-01		2.09E-01	5.68E-01		2.13E-02	9.48E-01		1.90E+00	6.62E-07	Up	-4.73E-01	5.20E-01		Unigene2985_All//gi|225440476|ref|XP_002272736.1|//9.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene2985_All//1.00E-65//AT3G53880| aldo/keto reductase family protein	Unigene2985_All//5.00E-131//BM358142				nr +
Unigene29853_All	912	0.00	0.89	0.00	0.00	0.00	0.10	13.68	31.53	4.32	9.80E+00	9.38E-05	Up	null	null		null	null		6.63E+00	4.76E-01		1.21E+00	8.78E-35	Up	-1.66E+00	1.56E-25	Down	Unigene29853_All//gi|15241674|ref|NP_195827.1|//1.00E-36//protein kinase-related [Arabidopsis thaliana] >gi|75335716|sp|Q9LZM4.1|WAKLQ_ARATH RecName: Full=Wall-associated receptor kinase-like 20; Flags: Precursor	Unigene29853_All//2.00E-36//AT5G02070| protein kinase-related					nr -
Unigene29854_All	265	4.15	12.05	7.23	11.28	12.08	9.20	4.79	5.52	1.65	1.54E+00	3.26E-05	Up	8.03E-01	1.02E-01		9.96E-02	8.35E-01		-2.93E-01	4.68E-01		2.06E-01	6.81E-01		-1.53E+00	4.40E-03				Unigene29854_All//1.00E-95//gi|11200670|gb|BF269675.1|BF269675				
Unigene29858_All	498	0.11	0.61	0.21	0.00	0.55	1.09	62.40	193.70	366.31	2.54E+00	1.51E-01		1.03E+00	7.03E-01		9.11E+00	7.02E-02		1.01E+01	2.45E-03		1.63E+00	8.72E-182	Up	2.55E+00	0.00E+00	Up	Unigene29858_All//gi|167962017|dbj|BAG09366.1|//2.00E-66//peroxisomal short-chain dehydrogenase/reductase family protein [Glycine max]	Unigene29858_All//5.00E-42//AT4G05530| IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase	Unigene29858_All//7.00E-99//DW512254		ko04146|Peroxisome		nr +
Unigene29859_All	573	0.37	1.86	0.28	0.78	1.32	0.47	6.27	39.17	8.69	2.35E+00	2.58E-03		-3.90E-01	8.07E-01		7.57E-01	3.95E-01		-7.26E-01	5.32E-01		2.64E+00	9.44E-79	Up	4.71E-01	4.51E-02		Unigene29859_All//gi|283135850|gb|ADB11316.1|//4.00E-28//tau class glutathione transferase GSTU12 [Populus trichocarpa]	Unigene29859_All//2.00E-13//AT3G09270| ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	Unigene29859_All//0.00E+00//gi|109843891|gb|DW242449.1|DW242449		ko00480|Glutathione metabolism		nr -
Unigene2986_All	1467	52.46	94.15	73.29	35.15	34.72	53.04	4.64	9.49	3.83	8.44E-01	9.72E-75		4.82E-01	2.70E-21		-1.77E-02	8.43E-01		5.94E-01	7.28E-25		1.03E+00	1.29E-13	Up	-2.77E-01	1.77E-01		Unigene2986_All//gi|297823651|ref|XP_002879708.1|//1.00E-145//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297325547|gb|EFH55967.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene2986_All//3.00E-131//AT2G37770| aldo/keto reductase family protein	Unigene2986_All//0.00E+00//TC132440		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr -
Unigene29860_All	215	0.00	0.00	0.00	0.00	1.68	18.09	202.37	9.26	null	null			null	null		null	null		1.07E+01	2.37E-02		3.48E+00	3.95E-200	Up	-9.66E-01	3.45E-04		Unigene29860_All//gi|283135850|gb|ADB11316.1|//3.00E-10//tau class glutathione transferase GSTU12 [Populus trichocarpa]		Unigene29860_All//5.00E-73//TC171132				nr +
Unigene29866_All	458	4.23	2.43	8.95	1.63	1.65	1.48	0.09	0.46	0.09	-7.96E-01	8.57E-02		1.08E+00	6.37E-04	Up	1.98E-02	1.00E+00		-1.41E-01	8.60E-01		2.31E+00	2.40E-01		-8.53E-02	9.72E-01									
Unigene29869_All	610	0.43	0.83	0.96	2.04	0.96	1.33	2.63	0.48	2.42	9.54E-01	3.73E-01		1.16E+00	2.47E-01		-1.09E+00	6.06E-02		-6.15E-01	3.33E-01		-2.46E+00	7.71E-06	Down	-1.24E-01	7.77E-01		Unigene29869_All//gi|240256168|ref|NP_195277.4|//4.00E-30//MLH3 (MUTL PROTEIN HOMOLOG 3); ATP binding / mismatched DNA binding [Arabidopsis thaliana]	Unigene29869_All//2.00E-31//AT4G35520| MLH3 (MUTL PROTEIN HOMOLOG 3); ATP binding / mismatched DNA binding			ko03430|Mismatch repair		nr -
Unigene29870_All	327	6.40	15.81	6.35	2.89	3.26	3.31	14.87	24.80	17.30	1.30E+00	2.17E-06	Up	-1.11E-02	1.00E+00		1.74E-01	8.16E-01		1.96E-01	7.67E-01		7.38E-01	4.81E-05		2.18E-01	3.50E-01		Unigene29870_All//gi|195619554|gb|ACG31607.1|//3.00E-10//ubiquitin-conjugating enzyme E2-17 kDa [Zea mays]	Unigene29870_All//1.00E-11//AT1G64230| ubiquitin-conjugating enzyme, putative	Unigene29870_All//3.00E-131//TC162585		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene29872_All	521	3.01	2.43	7.26	0.96	2.58	1.73	0.24	0.24	0.23	-3.09E-01	5.67E-01		1.27E+00	1.72E-04	Up	1.43E+00	1.64E-02		8.59E-01	2.70E-01		-1.67E-02	1.02E+00		-8.61E-02	9.69E-01		Unigene29872_All//gi|224059590|ref|XP_002299922.1|//9.00E-44//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222847180|gb|EEE84727.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene29872_All//1.00E-28//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene29872_All//7.00E-53//gi|84153379|gb|DN802734.1|DN802734		ko04626|Plant-pathogen interaction		nr +
Unigene29873_All	287	0.18	0.71	1.86	0.17	0.96	1.10	2.06	2.77	16.93	1.95E+00	3.75E-01		3.35E+00	2.06E-02		2.47E+00	2.23E-01		2.67E+00	1.44E-01		4.24E-01	5.77E-01		3.04E+00	1.30E-20	Up			Unigene29873_All//3.00E-07//ES837816				
Unigene29875_All	651	22.74	3.27	8.26	1.22	1.22	0.35	0.00	0.00	0.06	-2.80E+00	1.36E-45	Down	-1.46E+00	3.71E-19	Down	-9.10E-03	9.67E-01		-1.82E+00	3.32E-02		null	null		5.94E+00	6.45E-01		Unigene29875_All//gi|296149181|gb|ADG96405.1|//3.00E-42//S-locus receptor kinase [Olea europaea]	Unigene29875_All//6.00E-40//AT4G27300| S-locus protein kinase, putative	Unigene29875_All//5.00E-11//DT469086		ko04626|Plant-pathogen interaction		nr -
Unigene29876_All	601	1.92	2.36	0.35	0.33	1.66	1.20	1.27	2.16	3.98	3.02E-01	6.11E-01		-2.43E+00	1.85E-03		2.33E+00	3.22E-03		1.86E+00	4.71E-02		7.68E-01	1.50E-01		1.65E+00	1.81E-05	Up			Unigene29876_All//2.00E-167//gi|48797641|gb|CO098955.1|CO098955				
Unigene29877_All	584	0.00	0.00	0.27	1.36	1.42	0.08	0.87	0.21	1.84	null	null		8.10E+00	2.39E-01		5.22E-02	9.65E-01		-4.14E+00	4.13E-04	Down	-2.02E+00	5.20E-02		1.08E+00	5.98E-02		Unigene29877_All//gi|224113567|ref|XP_002332557.1|//1.00E-50//nbs-lrr resistance protein [Populus trichocarpa] >gi|222833033|gb|EEE71510.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene29877_All//1.00E-23//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene29877_All//2.00E-07//TC130356		ko04626|Plant-pathogen interaction		nr -
Unigene29878_All	455	10.12	68.93	33.12	1.75	1.36	1.89	0.56	1.47	0.88	2.77E+00	4.52E-94	Up	1.71E+00	1.93E-24	Up	-3.63E-01	6.23E-01		1.07E-01	9.05E-01		1.40E+00	8.81E-02		6.51E-01	5.44E-01		Unigene29878_All//gi|7635498|emb|CAB88668.1|//3.00E-56//histone H2B [Cicer arietinum]	Unigene29878_All//8.00E-36//AT5G59910| HTB4; DNA binding	Unigene29878_All//2.00E-71//TC149523				nr +
Unigene2988_All	2063	10.55	7.25	7.12	19.32	15.69	13.57	27.91	12.58	9.40	-5.42E-01	3.74E-06		-5.67E-01	2.93E-06		-3.00E-01	1.63E-04		-5.09E-01	4.51E-10		-1.15E+00	4.74E-64	Down	-1.57E+00	7.64E-106	Down	Unigene2988_All//gi|18424534|ref|NP_568947.1|//0.00E+00//signal recognition particle-related / SRP-related [Arabidopsis thaliana] >gi|9758397|dbj|BAB08884.1| signal recognition particle 68kD protein-like [Arabidopsis thaliana]	Unigene2988_All//0.00E+00//AT5G61970| signal recognition particle-related / SRP-related	Unigene2988_All//0.00E+00//TC134474		ko03060|Protein export		nr -
Unigene29880_All	297	6.17	1.54	2.15	6.37	7.65	12.01	0.71	0.00	0.27	-2.01E+00	1.86E-04	Down	-1.52E+00	4.00E-03		2.64E-01	5.84E-01		9.15E-01	5.07E-03		-9.48E+00	7.44E-02		-1.41E+00	3.80E-01				Unigene29880_All//4.00E-59//DW509807				
Unigene29882_All	361	1.01	1.54	0.74	4.28	4.77	9.38	0.00	0.12	0.44	6.06E-01	5.31E-01		-4.60E-01	6.97E-01		1.57E-01	8.13E-01		1.13E+00	8.21E-04	Up	6.86E+00	6.34E-01		8.79E+00	1.40E-01				Unigene29882_All//4.00E-10//FL577411				
Unigene29883_All	284	3.50	4.28	0.19	1.23	1.70	2.23	4.76	3.68	1.54	2.91E-01	6.04E-01		-4.22E+00	1.62E-04	Down	4.67E-01	7.04E-01		8.59E-01	3.90E-01		-3.73E-01	4.95E-01		-1.63E+00	1.95E-03				Unigene29883_All//4.00E-59//DT054133				
Unigene29884_All	642	0.82	24.31	0.91	1.40	2.09	1.83	1.12	0.39	0.50	4.90E+00	2.19E-74	Up	1.63E-01	8.50E-01		5.83E-01	3.42E-01		3.89E-01	5.80E-01		-1.52E+00	5.42E-02		-1.17E+00	1.09E-01		Unigene29884_All//gi|37202082|gb|AAQ89656.1|//9.00E-25//At5g38700 [Arabidopsis thaliana]	Unigene29884_All//4.00E-30//AT5G38700| unknown protein	Unigene29884_All//0.00E+00//gi|109872126|gb|DW501102.1|DW501102				nr +
Unigene29886_All	650	2.25	0.62	1.15	3.76	3.34	1.67	4.55	0.64	1.29	-1.85E+00	1.97E-03		-9.75E-01	9.25E-02		-1.70E-01	7.04E-01		-1.17E+00	4.10E-03		-2.82E+00	9.57E-12	Down	-1.82E+00	1.65E-07	Down	Unigene29886_All//gi|224069605|ref|XP_002303010.1|//7.00E-07//predicted protein [Populus trichocarpa] >gi|222844736|gb|EEE82283.1| predicted protein [Populus trichocarpa]		Unigene29886_All//1.00E-08//ES795053				nr -
Unigene29888_All	697	1.58	0.87	0.00	1.43	1.09	1.62	2.06	4.62	1.94	-8.54E-01	1.90E-01		-1.06E+01	4.93E-06	Down	-3.95E-01	5.73E-01		1.81E-01	7.84E-01		1.16E+00	2.18E-04	Up	-8.58E-02	8.60E-01		Unigene29888_All//gi|22327990|ref|NP_200888.2|//2.00E-34//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|28416657|gb|AA042859.1| At5g60800 [Arabidopsis thaliana]	Unigene29888_All//1.00E-25//AT5G60800| heavy-metal-associated domain-containing protein	Unigene29888_All//2.00E-164//gi|78345487|gb|DT565761.1|DT565761				nr -
Unigene29890_All	815	0.06	0.56	0.20	2.75	6.30	3.10	0.47	0.87	1.08	3.12E+00	3.58E-02		1.61E+00	5.11E-01		1.19E+00	3.43E-06	Up	1.74E-01	6.78E-01		9.01E-01	2.40E-01		1.20E+00	6.68E-02		Unigene29890_All//gi|24461867|gb|AAN62354.1|AF556028_23//2.00E-25//CTV.22 [Citrus trifoliata]	Unigene29890_All//4.00E-22//AT1G15780| unknown protein					nr +
Unigene29892_All	322	32.33	47.52	43.66	80.60	84.48	107.02	276.66	482.86	589.41	5.56E-01	9.72E-05		4.33E-01	5.71E-03		6.79E-02	6.10E-01		4.09E-01	4.50E-06		8.04E-01	9.65E-95		1.09E+00	1.75E-196	Up	Unigene29892_All//gi|15553478|gb|AAL01887.1|AF401403_1//3.00E-40//acyl-CoA oxidase [Glycine max]	Unigene29892_All//4.00E-38//AT4G16760| ACX1 (ACYL-COA OXIDASE 1); acyl-CoA oxidase	Unigene29892_All//3.00E-177//TC137718		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene29895_All	420	125.07	360.12	149.10	22.65	26.40	45.27	2.21	0.00	0.00	1.53E+00	4.19E-210	Up	2.54E-01	2.63E-04		2.21E-01	2.41E-01		9.99E-01	4.12E-15		-1.11E+01	1.14E-06	Down	-1.11E+01	5.47E-07	Down	Unigene29895_All//gi|25090250|gb|AAN72262.1|//3.00E-34//At1g44575/T18F15 [Arabidopsis thaliana]	Unigene29895_All//2.00E-30//AT1G44575| NPQ4 (NONPHOTOCHEMICAL QUENCHING); chlorophyll binding / xanthophyll binding	Unigene29895_All//6.00E-176//TC131107		ko00195|Photosynthesis		nr -
Unigene29899_All	1051	372.72	129.93	262.96	892.86	1301.73	1131.41	0.36	2.07	0.42	-1.52E+00	0.00E+00	Down	-5.03E-01	2.27E-82		5.44E-01	0.00E+00		3.42E-01	3.40E-135		2.51E+00	8.14E-08	Up	2.04E-01	8.26E-01		Unigene29899_All//gi|14423450|gb|AAK62407.1|AF386962_1//1.00E-155//Unknown protein [Arabidopsis thaliana] >gi|30725566|gb|AAP37805.1| At5g25460 [Arabidopsis thaliana]	Unigene29899_All//5.00E-158//AT5G11420| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cell wall, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25460.1); Has 185 Blast hits to 157 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 185; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene29899_All//0.00E+00//gi|164360372|gb|ES816407.1|ES816407				nr +
Unigene299_All	4661	6.68	17.61	9.95	14.66	18.31	16.74	24.27	34.05	27.47	1.40E+00	2.03E-100	Up	5.75E-01	6.58E-13		3.20E-01	6.05E-10		1.91E-01	1.36E-03		4.88E-01	2.70E-40		1.79E-01	9.08E-06		Unigene299_All//gi|23617202|dbj|BAC20873.1|//0.00E+00//VP1/ABI3 family regulatory protein-like protein [Oryza sativa Japonica Group]	Unigene299_All//2.00E-140//AT4G32010| HSL1 (HSI2-LIKE 1); transcription factor	Unigene299_All//0.00E+00//TC175806	ABI3VP1	ko04144|Endocytosis		nr -
Unigene29900_All	479	0.87	1.48	0.89	0.00	1.08	1.79	0.44	1.75	1.75	7.61E-01	3.62E-01		2.55E-02	1.00E+00		1.01E+01	3.21E-03		1.08E+01	3.79E-05	Up	1.98E+00	8.88E-03		1.98E+00	7.05E-03				Unigene29900_All//6.00E-07//TC152247				
Unigene29902_All	550	0.10	0.46	0.00	2.54	1.50	0.49	2.00	1.06	1.01	2.28E+00	2.34E-01		-6.57E+00	6.24E-01		-7.55E-01	1.67E-01		-2.36E+00	2.38E-04	Down	-9.10E-01	1.24E-01		-9.79E-01	8.01E-02		Unigene29902_All//gi|297828041|ref|XP_002881903.1|//3.00E-40//3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327742|gb|EFH58162.1| 3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29902_All//7.00E-36//AT2G43420| 3-beta hydroxysteroid dehydrogenase/isomerase family protein	Unigene29902_All//1.00E-20//DN802081				nr +
Unigene29904_All	278	0.38	0.00	0.00	1.79	1.73	0.97	5.93	2.41	1.43	-8.56E+00	3.72E-01		-8.56E+00	3.94E-01		-4.72E-02	9.49E-01		-8.79E-01	4.20E-01		-1.30E+00	5.42E-03		-2.05E+00	3.66E-05	Down								

Unigene29905_All	1199	0.00	13.90	3.38	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	8.25E-96	Up	1.17E+01	1.92E-22	Up	null	null		null	null		null	null		null	null		Unigene29905_All//gi|260516654|gb|ACX43954.1|//1.00E-65//cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516656|gb|ACX43955.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516658|gb|ACX43956.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516660|gb|ACX43957.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516662|gb|ACX43958.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516664|gb|ACX43959.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516666|gb|ACX43960.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516668|gb|ACX43961.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516670|gb|ACX43962.1| cysteine protease 2 [Brachiaria hybrid cultivar]	Unigene29905_All//6.00E-63//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase					nr -
Unigene29906_All	755	0.42	0.67	0.14	5.87	3.15	3.47	0.67	0.39	0.00	6.91E-01	4.99E-01		-1.56E+00	3.30E-01		-9.00E-01	7.79E-04		-7.59E-01	7.64E-03		-7.94E-01	4.02E-01		-9.39E+00	5.54E-04	Down	Unigene29906_All//gi|214011869|gb|ACJ61689.1|//1.00E-60//WOX4 [Solanum lycopersicum] >gi|214011873|gb|ACJ61691.1| WOX4 [Solanum lycopersicum]	Unigene29906_All//2.00E-42//AT1G46480| WOX4 (WUSCHEL RELATED HOMEOBOX 4); transcription factor	Unigene29906_All//6.00E-125//ES801433	HB			nr -
Unigene29908_All	1458	0.00	0.00	0.00	0.00	0.00	0.00	36.10	55.84	99.95	null	null		null	null		null	null		null	null		6.29E-01	7.39E-33		1.47E+00	1.34E-239	Up	Unigene29908_All//gi|297851852|ref|XP_002893807.1|//1.00E-145//alliinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339649|gb|EFH70066.1| alliinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene29908_All//3.00E-144//AT1G31060| alliinase family protein					nr +
Unigene2991_All	1074	9.30	4.43	8.83	11.46	15.45	13.33	7.99	11.09	10.72	-1.07E+00	9.81E-09	Down	-7.63E-02	6.99E-01		4.32E-01	9.19E-04		2.19E-01	1.86E-01		4.73E-01	1.27E-03		4.24E-01	3.74E-03		Unigene2991_All//gi|115479757|ref|NP_001063472.1|//3.00E-122//Os09g0478500 [Oryza sativa Japonica Group] >gi|113631705|dbj|BAF25386.1| Os09g0478500 [Oryza sativa Japonica Group]	Unigene2991_All//1.00E-07//AT5G17750| DG6PL2 (D6 PROTEIN KINASE LIKE 2); kinase	Unigene2991_All//0.00E+00//ES814369			GO:0004672//GO:0005488//GO:0005634	nr -
Unigene29910_All	1737	0.24	0.79	0.61	1.15	0.63	0.10	11.98	7.03	5.00	1.71E+00	5.54E-03		1.35E+00	6.01E-02		-8.55E-01	5.06E-02		-3.46E+00	1.64E-08	Down	-7.69E-01	1.72E-12		-1.26E+00	4.79E-28	Down	Unigene29910_All//gi|224106295|ref|XP_002314117.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222850525|gb|EEE88072.1| cytochrome P450 [Populus trichocarpa]	Unigene29910_All//0.00E+00//AT5G58860| CYP86A1 (CYTOCHROME P450 86 A1); fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene29910_All//0.00E+00//TC134417		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene29915_All	385	0.00	0.26	0.97	0.65	0.63	0.35	2.09	1.19	0.31	8.04E+00	3.87E-01		9.92E+00	2.50E-02		-4.71E-02	9.51E-01		-8.78E-01	6.16E-01		-8.05E-01	2.58E-01		-2.75E+00	9.43E-04	Down		Unigene29915_All//6.00E-34//ES825629					ESTscan +
Unigene29916_All	322	66.78	103.07	82.69	60.33	58.60	81.21	71.30	88.78	35.01	6.26E-01	2.54E-11		3.08E-01	5.64E-03		-4.20E-02	8.14E-01		4.29E-01	3.78E-05		3.16E-01	5.29E-04		-1.03E+00	1.98E-22	Down	Unigene29916_All//gi|254030287|gb|ACT53874.1|//2.00E-14//zinc finger protein [Saccharum officinarum]	Unigene29916_All//5.00E-13//AT1G51200| zinc finger (AN1-like) family protein	Unigene29916_All//1.00E-127//TC136378				nr -
Unigene29918_All	633	0.50	0.00	0.00	2.52	1.36	1.21	0.13	0.46	4.47	-8.95E+00	3.66E-02		-8.95E+00	4.91E-02		-8.89E-01	7.64E-02		-1.05E+00	4.57E-02		1.79E+00	2.24E-01		5.06E+00	1.81E-17	Up	Unigene29918_All//gi|297851458|ref|XP_002893610.1|//4.00E-44//heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297339452|gb|EFH69869.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene29918_All//7.00E-36//AT1G30280| heat shock protein binding	Unigene29918_All//7.00E-78//gi|109879481|gb|DW508451.1|DW508451				nr -
Unigene29921_All	232	61.79	87.58	62.66	95.55	117.26	150.67	125.75	262.48	214.82	5.03E-01	3.65E-05		2.01E-02	9.12E-01		2.95E-01	3.60E-03		6.57E-01	1.23E-13		1.06E+00	1.61E-59	Up	7.73E-01	1.17E-29		Unigene29921_All//gi|224131746|ref|XP_002328098.1|//7.00E-23//ethylene-insensitive 3b [Populus trichocarpa] >gi|222837613|gb|EEE75978.1| ethylene-insensitive 3b [Populus trichocarpa]	Unigene29921_All//1.00E-07//AT3G20770| EIN3 (ETHYLENE-INSENSITIVE3); transcription factor	Unigene29921_All//5.00E-126//gi|11201804|gb|BF270809.1|BF270809	EIL			nr -
Unigene29923_All	654	1.68	21.69	4.40	0.23	0.42	0.28	0.00	0.00	0.12	3.69E+00	5.57E-56	Up	1.39E+00	5.14E-04	Up	8.82E-01	5.95E-01		2.74E-01	9.05E-01		null	null		6.93E+00	4.04E-01		Unigene29923_All//gi|84314120|gb|ABC55672.1|//1.00E-28//dehydrin DH22a [Coffea canephora]						nr -
Unigene29926_All	552	1.23	1.10	2.22	0.00	0.00	0.00	48.48	59.06	118.87	-1.62E-01	8.32E-01		8.49E-01	1.85E-01		null	null		null	null		2.85E-01	8.63E-04		1.29E+00	2.16E-89	Up	Unigene29926_All//gi|300498294|gb|ADK23849.1|//9.00E-38//WRKY72 [Solanum lycopersicum]	Unigene29926_All//1.00E-21//AT5G15130| WRKY72; transcription factor	Unigene29926_All//3.00E-09//DT467483	WRKY			nr +
Unigene29933_All	554	5.48	0.37	0.00	4.32	3.67	1.63	2.21	0.30	0.58	-3.90E+00	5.41E-13	Down	-1.24E+01	1.24E-16	Down	-2.35E-01	5.94E-01		-1.40E+00	8.07E-04	Down	-2.87E+00	2.54E-05	Down	-1.94E+00	7.80E-04	Down	Unigene29933_All//gi|117168079|gb|ABK32122.1|//1.00E-10//At5g54970 [Arabidopsis thaliana]	Unigene29933_All//7.00E-12//AT5G54970| unknown protein	Unigene29933_All//0.00E+00//DR456345				nr +
Unigene29934_All	1391	0.00	0.18	0.08	0.97	0.25	0.26	1.67	1.62	4.15	7.51E+00	7.86E-02		6.26E+00	3.98E-01		-1.97E+00	7.30E-04	Down	-1.90E+00	2.26E-03		-4.31E-02	9.28E-01		1.31E+00	7.82E-09	Up	Unigene29934_All//gi|145534915|ref|NP_001078803.1|//1.00E-95//ACR1 (ACT Domain Repeat 1); amino acid binding [Arabidopsis thaliana]	Unigene29934_All//4.00E-95//AT5G65890| ACR1 (ACT Domain Repeat 1); amino acid binding	Unigene29934_All//0.00E+00//C0126686				nr +
Unigene29935_All	350	5.38	0.43	2.43	6.55	6.20	4.13	0.60	0.48	0.68	-3.63E+00	7.52E-08	Down	-1.14E+00	2.33E-02		-7.89E-02	8.45E-01		-6.65E-01	1.24E-01		-3.38E-01	8.12E-01		1.77E-01	9.08E-01								
Unigene29939_All	258	3.24	2.95	0.00	1.16	0.93	2.98	0.98	0.97	1.85	-1.39E-01	8.39E-01		-1.17E+01	1.19E-04	Down	-3.10E-01	8.20E-01		1.36E+00	1.18E-01		-1.67E-02	1.02E+00		9.14E-01	3.38E-01			Unigene29939_All//6.00E-144//DW499806					
Unigene2994_All	1791	6.98	6.05	4.70	5.81	5.56	7.26	12.49	27.00	22.60	-2.06E-01	2.32E-01		-5.72E-01	5.59E-04		-6.51E-02	7.85E-01		3.21E-01	4.83E-02		1.11E+00	4.29E-51	Up	8.56E-01	9.96E-29		Unigene2994_All//gi|15221420|ref|NP_179409.1|//0.00E+00//ATMPK7 (ARABIDOPSIS THALIANA MAP KINASE 7); MAP kinase/ kinase [Arabidopsis thaliana] >gi|21431797|sp|Q39027.2|MPK7_ARATH RecName: Full=Mitogen-activated protein kinase 7; Short=MAP kinase 7; Short=AtMPK7 >gi|4874286|gb|AAD31349.1| MAP kinase (ATMPK7) [Arabidopsis thaliana] >gi|110739420|dbj|BAF01620.1| MAP kinase [Arabidopsis thaliana]	Unigene2994_All//0.00E+00//AT2G18170| ATMPK7 (ARABIDOPSIS THALIANA MAP KINASE 7); MAP kinase/ kinase	Unigene2994_All//0.00E+00//TC156132		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0032559	nr +
Unigene29941_All	332	1.10	1.53	0.00	1.20	4.05	4.63	4.33	1.64	0.84	4.68E-01	6.11E-01		-1.01E+01	2.78E-02		1.75E+00	4.15E-03		1.95E+00	9.15E-04	Up	-1.40E+00	6.15E-03		-2.37E+00	2.52E-05	Down							
Unigene29944_All	688	0.00	0.07	0.00	1.30	0.65	1.12	1.11	0.06	2.03	6.20E+00	6.16E-01		null	null		-1.00E+00	1.61E-01		-2.24E-01	7.50E-01		-4.19E+00	1.57E-04	Down	8.74E-01	7.41E-02		Unigene29944_All//gi|18412659|ref|NP_567142.1|//5.00E-38//PLP9 (PATATIN-LIKE PROTEIN 9); nutrient reservoir [Arabidopsis thaliana] >gi|15912227|gb|AAL08247.1| AT3g63200/F16M2_50 [Arabidopsis thaliana] >gi|24111291|gb|AAN46769.1| At3g63200/F16M2_50 [Arabidopsis thaliana]	Unigene29944_All//3.00E-39//AT3G63200| PLP9 (PATATIN-LIKE PROTEIN 9); nutrient reservoir	Unigene29944_All//0.00E+00//gi|78354216|gb|DT574490.1|DT574490				nr +
Unigene29947_All	894	1.23	0.51	0.60	0.67	1.16	1.11	1.18	0.79	3.61	-1.27E+00	5.68E-02		-1.05E+00	1.35E-01		7.89E-01	2.74E-01		7.33E-01	3.21E-01		-5.73E-01	3.60E-01		1.61E+00	7.06E-07	Up	Unigene29947_All//gi|15221424|ref|NP_172113.1|//1.00E-17//GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding [Arabidopsis thaliana] >gi|30679613|ref|NP_849601.1| GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding [Arabidopsis thaliana] >gi|8844128|gb|AAF80220.1|AC025290_9 Contains similarity to a Ring3 protein from Homo sapiens gi|133157 and contains a bromodomain PF|00439. EST gb|F14211 comes from this gene [Arabidopsis thaliana]	Unigene29947_All//6.00E-19//AT1G06230| GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding					nr +
Unigene29949_All	1075	0.00	0.09	0.00	0.37	0.38	0.25	12.82	3.23	1.52	6.56E+00	3.87E-01		null	null		5.24E-02	9.89E-01		-5.56E-01	6.38E-01		-1.99E+00	9.82E-35	Down	-3.08E+00	5.98E-59	Down	Unigene29949_All//gi|30683485|ref|NP_172838.2|//2.00E-60//beta-1,3-glucanase-related [Arabidopsis thaliana]	Unigene29949_All//2.00E-32//AT1G18650| PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding	Unigene29949_All//8.00E-82//TC153735				nr -
Unigene2995_All	2892	11.31	18.08	9.92	16.91	19.81	15.41	18.90	45.41	61.18	6.77E-01	7.32E-20		-1.88E-01	7.25E-02		2.28E-01	6.81E-04		-1.34E-01	1.13E-01		1.26E+00	2.37E-168	Up	1.69E+00	0.00E+00	Up	Unigene2995_All//gi|297836714|ref|XP_002886239.1|//0.00E+00//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332079|gb|EFH62498.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene2995_All//0.00E+00//AT2G19130| S-locus lectin protein kinase family protein	Unigene2995_All//0.00E+00//TC173435		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0008037//GO:0030246//GO:0031410//GO:0032559//GO:0043231	nr +
Unigene29950_All	681	0.00	7.37	1.41	0.00	0.10	0.00	17.14	27.07	14.10	1.28E+01	1.34E-28	Up	1.05E+01	2.46E-05	Up	6.66E+00	6.10E-01		null	null		6.60E-01	1.04E-08		-2.82E-01	5.89E-02								
Unigene29951_All	556	291.53	1432.41	497.26	258.75	300.26	487.54	131.25	416.30	625.38	2.30E+00	0.00E+00	Up	7.70E-01	3.53E-124		2.15E-01	3.88E-09		9.14E-01	2.83E-180		1.67E+00	0.00E+00	Up	2.25E+00	0.00E+00	Up	Unigene29951_All//gi|284433802|gb|ADB85107.1|//2.00E-45//translation initiation factor-like protein [Jatropha curcas]	Unigene29951_All//3.00E-46//AT5G54940| eukaryotic translation initiation factor SUI1, putative	Unigene29951_All//0.00E+00//TC158412				nr +
Unigene29952_All	747	0.21	1.09	0.21	0.73	2.07	1.57	0.68	0.78	2.29	2.37E+00	1.01E-02		2.59E-02	1.00E+00		1.50E+00	6.01E-03		1.10E+00	9.17E-02		2.06E-01	8.00E-01		1.76E+00	1.93E-04	Up	Unigene29952_All//gi|193806505|sp|Q9LN69.2|PP250_ARATH//3.00E-69//RecName: Full=Putative pentatricopeptide repeat-containing protein At1g19290	Unigene29952_All//3.00E-64//AT1G19290| LOCATED IN: mitochondrion; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT5G55840.1); Has 31003 Blast hits to 6161 proteins in 194 species: Archae - 6; Bacteria - 22; Metazoa - 935; Fungi - 736; Plants - 27904; Viruses - 0; Other Eukaryotes - 1400 (source: NCBI BLink).					nr +
Unigene29954_All	333	0.16	3.65	0.64	52.21	0.00	0.00	4.82	0.25	5.14	4.54E+00	6.47E-06	Up	2.03E+00	3.61E-01		-1.57E+01	6.54E-134	Down	-1.57E+01	2.34E-111	Down	-4.26E+00	4.13E-09	Down	9.25E-02	8.38E-01		Unigene29954_All//gi|87162542|gb|ABD28337.1|//2.00E-19//Cyclin-like F-box [Medicago truncatula]	Unigene29954_All//8.00E-14//AT2G02240| MEE66 (maternal effect embryo arrest 66)	Unigene29954_All//3.00E-146//C0107905				nr -

Unigene29956_All	433	0.60	3.28	1.48	0.35	1.91	2.40	1.95	3.86	5.52	2.44E+00	2.47E-04	Up	1.29E+00	1.86E-01		2.47E+00	6.72E-03		2.80E+00	8.13E-04	Up	9.83E-01	3.14E-02		1.50E+00	7.16E-05	Up	Unigene29956_All//gi|32700038|gb|AAP86669.1|//1.00E-61//26S proteasome subunit RPN9| [Arabidopsis thaliana]	Unigene29956_All//1.00E-52//AT4G19006| 26S proteasome regulatory subunit, putative (RPN9)	Unigene29956_All//0.00E+00//gi|109870670|gb|DW199646.1|DW199646		ko03050|Proteasome		nr +
Unigene29957_All	413	47.63	44.29	34.68	48.85	36.10	22.64	63.37	29.65	21.03	-1.05E-01	4.49E-01		-4.58E-01	3.85E-04		-4.36E-01	1.31E-04		-1.11E+00	3.96E-19	Down	-1.10E+00	2.12E-27	Down	-1.59E+00	1.56E-49	Down	Unigene29957_All//gi|217426823|gb|ACK44531.1|//3.00E-16//AT5G09960-like protein [Arabidopsis arenosa]	Unigene29957_All//2.00E-17//AT5G09960| unknown protein	Unigene29957_All//1.00E-112//TC144801				nr -
Unigene29959_All	668	0.00	11.68	0.64	0.30	0.36	2.50	0.63	11.20	6.32	1.35E+01	1.26E-44	Up	9.32E+00	1.38E-02		2.74E-01	8.95E-01		3.07E+00	2.60E-06	Up	4.15E+00	8.65E-40	Up	3.32E+00	1.72E-19	Up	Unigene29959_All//gi|255565105|ref|XP_002523345.1|//3.00E-33//conserved hypothetical protein [Ricinus communis] >gi|223537252|gb|EEF38884.1| conserved hypothetical protein [Ricinus communis]	Unigene29959_All//9.00E-18//AT2G46190| unknown protein	Unigene29959_All//0.00E+00//TC150415				nr -
Unigene2996_All	1680	74.99	72.60	61.71	107.49	100.52	139.58	417.01	401.76	885.79	-4.69E-02	3.88E-01		-2.81E-01	1.84E-09		-9.67E-02	1.28E-02		3.77E-01	2.05E-32		-5.38E-02	2.72E-03		1.09E+00	0.00E+00	Up	Unigene2996_All//gi|164604962|dbj|BAF98277.1|//0.00E+00//acetyl-CoA C-acetyltransferase [Hevea brasiliensis]	Unigene2996_All//0.00E+00//AT5G48230| ACAT2 (ACETOACETYL-COA THIOLASE 2); acetyl-CoA C-acetyltransferase/ catalytic	Unigene2996_All//0.00E+00//TC149814		ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00900|Terpenoid backbone biosynthesis//ko00072|Synthesis and degradation of ketone bodies	GO:0003006//GO:0016020//GO:0016453//GO:0042579	nr +
Unigene29961_All	212	91.56	91.78	63.05	128.77	114.03	150.62	211.80	108.43	98.28	3.40E-03	9.87E-01		-5.38E-01	3.11E-05		-1.75E-01	1.12E-01		2.26E-01	2.31E-02		-9.66E-01	6.72E-38		-1.11E+00	1.28E-48	Down	Unigene29961_All//gi|195605472|gb|ACG24566.1|//1.00E-31//40S ribosomal protein S5 [Zea mays]	Unigene29961_All//3.00E-32//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	Unigene29961_All//4.00E-114//TC178745		ko03010|Ribosome		nr -
Unigene29964_All	494	0.00	0.00	0.00	0.00	0.00	0.00	1.97	2.79	7.66	null	null		null	null		null	null		null	null		5.04E-01	3.48E-01		1.96E+00	4.11E-10	Up										
Unigene29966_All	851	1.11	2.14	3.38	0.70	0.85	0.96	1.29	0.74	0.42	9.54E-01	4.89E-02		1.61E+00	8.37E-05	Up	2.75E-01	8.01E-01		4.44E-01	6.21E-01		-8.10E-01	1.69E-01		-1.62E+00	6.27E-03		Unigene29966_All//gi|115473321|ref|NP_001060259.1|//4.00E-34//Os07g0613900 (Oryza sativa Japonica Group) >gi|113611795|dbj|BAF22173.1| Os07g0613900 (Oryza sativa Japonica Group)								nr +
Unigene29967_All	336	0.00	0.60	0.00	0.00	0.51	2.42	2.77	8.71	28.93	9.24E+00	1.36E-01		null	null		9.00E+00	2.27E-01		1.12E+01	6.95E-05	Up	1.65E+00	2.47E-06	Up	3.39E+00	8.59E-45	Up	Unigene29967_All//gi|19715905|emb|CAC84140.1|//2.00E-46//NADPH oxidase [Nicotiana tabacum]	Unigene29967_All//1.00E-43//AT5G47910| RBOHD (RESPIRATORY BURST OXIDASE HOMOLOGUE D); NAD(P)H oxidase	Unigene29967_All//9.00E-79//CO101724		ko04626|Plant-pathogen interaction		nr -
Unigene2997_All	1524	2.51	3.13	3.98	16.25	20.90	15.08	3.58	1.01	2.04	3.19E-01	2.67E-01		6.69E-01	7.43E-03		3.64E-01	5.34E-05		-1.07E-01	4.18E-01		-1.82E+00	1.16E-12	Down	-8.12E-01	2.43E-04		Unigene2997_All//gi|301073323|gb|AD656449.1|//4.00E-35//acyl-CoA-binding protein [Vitis vinifera]	Unigene2997_All//7.00E-29//AT4G24230| ACBP3 (ACYL-COA-BINDING DOMAIN 3); acyl-CoA binding	Unigene2997_All//6.00E-59//TC154976			GO:0005504//GO:0044421	nr +
Unigene29975_All	377	0.14	1.34	2.54	2.11	1.46	1.20	1.12	0.33	0.63	3.28E+00	2.11E-02		4.20E+00	2.16E-04	Up	-5.33E-01	5.10E-01		-8.19E-01	3.20E-01		-1.75E+00	1.24E-01		-8.23E-01	3.99E-01				Unigene29975_All//5.00E-19//ES842308					
Unigene29976_All	490	7.15	31.64	12.50	3.66	4.78	7.47	0.95	0.94	1.14	2.15E+00	7.31E-35	Up	8.05E-01	1.19E-03		3.85E-01	4.03E-01		1.03E+00	1.41E-03		-1.65E-02	1.02E+00		2.62E-01	7.66E-01				Unigene29976_All//1.00E-26//TC172046					
Unigene2998_All	700	1.42	1.16	1.37	0.85	1.08	0.90	0.97	0.90	0.00	-2.94E-01	6.37E-01		-5.26E-02	9.54E-01		3.42E-01	7.20E-01		8.10E-02	9.45E-01		-1.10E-01	8.90E-01		-9.92E+00	3.56E-05	Down								
Unigene29981_All	3229	0.06	0.03	0.00	0.00	0.00	0.00	3.77	6.77	15.30	-1.05E+00	5.65E-01		-6.02E+00	1.46E-01		null	null		null	null		8.44E-01	3.49E-15		2.02E+00	3.02E-127	Up	Unigene29981_All//gi|209970607|gb|ACJ03066.1|//0.00E+00//M18S-3Xp [Malus floribunda]	Unigene29981_All//3.00E-126//AT2G34930| disease resistance family protein			ko04626|Plant-pathogen interaction		nr +
Unigene29982_All	1268	0.12	0.00	0.00	0.00	0.05	0.11	6.67	3.86	1.73	-6.95E+00	2.16E-01		-6.95E+00	2.45E-01		5.76E+00	6.10E-01		6.74E+00	3.11E-01		-7.90E-01	8.73E-06		-1.95E+00	1.04E-21	Down	Unigene29982_All//gi|15242536|ref|NP_198817.1|//1.00E-134//AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene29982_All//2.00E-134//AT5G40010| AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene29982_All//5.00E-31//TC152212				nr -
Unigene29984_All	643	2.36	0.63	1.66	0.77	1.23	2.81	0.72	0.78	0.50	-1.90E+00	1.25E-03		-5.11E-01	3.80E-01		6.69E-01	4.42E-01		1.86E+00	4.17E-04	Up	1.09E-01	9.14E-01		-5.45E-01	5.66E-01		Unigene29984_All//gi|255573995|ref|XP_002527915.1|//2.00E-88//anthranilate phosphoribosyltransferase, putative [Ricinus communis] >gi|223532690|gb|EEF34472.1| anthranilate phosphoribosyltransferase, putative [Ricinus communis]	Unigene29984_All//8.00E-89//AT1G70570| anthranilate phosphoribosyltransferase, putative	Unigene29984_All//0.00E+00//CO121028				nr -
Unigene29985_All	812	0.13	0.00	0.00	0.43	0.85	1.67	0.89	3.40	15.90	-7.01E+00	3.72E-01		-7.01E+00	3.93E-01		9.82E-01	2.98E-01		1.96E+00	2.03E-03		1.94E+00	2.70E-07	Up	4.17E+00	1.00E-69	Up									
Unigene29986_All	219	0.00	0.00	0.00	10.46	3.62	2.06	2.12	0.38	0.18	null	null		null	null		-1.53E+00	1.64E-04	Down	-2.34E+00	1.06E-06	Down	-2.48E+00	3.38E-02		-3.55E+00	6.85E-03				Unigene29986_All//2.00E-07//DW223966					
Unigene29987_All	855	0.00	0.00	0.00	0.00	0.00	0.00	5.69	1.86	3.26	null	null		null	null		null	null		null	null		-1.61E+00	9.66E-10	Down	-8.02E-01	6.64E-04		Unigene29987_All//gi|224112361|ref|XP_002316163.1|//1.00E-117//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222865203|gb|EEF02334.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene29987_All//1.00E-94//AT3G45850| kinesin motor protein-related	Unigene29987_All//0.00E+00//DW501235	XAC			nr -
Unigene29994_All	730	0.00	0.00	0.00	0.00	0.00	0.12	12.51	21.36	28.81	null	null		null	null		null	null		6.95E+00	4.76E-01		7.72E-01	1.34E-09		1.20E+00	3.21E-26	Up	Unigene29994_All//gi|19911575|dbj|BAB86891.1|//4.00E-14//syringolide-induced protein 14-1-1 [Glycine max]								nr -
Unigene29996_All	298	5.44	0.68	6.08	5.35	2.77	3.03	5.82	2.38	8.02	-3.00E+00	6.72E-06	Down	1.59E-01	7.37E-01		-9.48E-01	5.80E-02		-8.20E-01	1.25E-01		-1.29E+00	4.58E-03		4.64E-01	2.00E-01				Unigene29996_All//8.00E-79//CO091281					ESTscan +
Unigene3_All	751	3.14	0.81	2.69	8.76	9.72	2.83	3.72	1.67	1.22	-1.95E+00	2.39E-05	Down	-2.19E-01	6.21E-01		1.51E-01	5.60E-01		-1.63E+00	1.72E-11	Down	-1.15E+00	6.98E-04	Down	-1.61E+00	4.09E-06	Down	Unigene3_All//gi|15231259|ref|NP_190171.1|//1.00E-104//kinesin motor protein-related [Arabidopsis thaliana] >gi|7339486|emb|CAB82809.1| kinesin-related protein-like [Arabidopsis thaliana]	Unigene3_All//4.00E-90//AT3G45850| kinesin motor protein-related	Unigene3_All//0.00E+00//ES793376				nr -
Unigene30_All	435	2.29	4.89	1.35	5.84	4.59	4.05	4.08	6.15	10.44	1.10E+00	1.39E-02		-7.63E-01	2.94E-01		-3.47E-01	4.10E-01		-5.28E-01	2.02E-01		5.91E-01	8.97E-02		1.35E+00	1.96E-07	Up	Unigene30_All//gi|224097301|ref|XP_002310900.1|//7.00E-76//histone acetyltransferase [Populus trichocarpa] >gi|222853803|gb|EEE91350.1| histone acetyltransferase [Populus trichocarpa]	Unigene30_All//2.00E-72//AT1G79000| HAC1 (HISTONE ACETYLTRANSFERASE OF THE CBP FAMILY 1); H3/H4 histone acetyltransferase/ histone acetyltransferase/ transcription cofactor		TAZ			nr +
Unigene30001_All	256	10.01	6.73	11.23	5.64	4.17	0.71	1.32	0.00	1.71	-5.74E-01	1.45E-01		1.66E-01	6.57E-01		-4.36E-01	4.44E-01		-3.00E+00	1.34E-05	Down	-1.04E-01	1.17E-02		3.74E-01	6.82E-01									
Unigene30002_All	555	27.53	7.30	18.71	0.99	1.05	0.49	0.00	0.00	0.00	-1.91E+00	6.44E-30	Down	-5.57E-01	1.66E-04		9.54E-02	9.51E-01		-1.02E+00	3.30E-01		null	null		null	null		Unigene30002_All//gi|6729550|emb|CAB67635.1|//1.00E-13//zinc finger-like protein [Arabidopsis thaliana]	Unigene30002_All//5.00E-10//AT2G41940| ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding	Unigene30002_All//0.00E+00//TC159851	C2H2			nr -
Unigene30005_All	587	0.00	1.12	0.73	1.87	2.82	3.08	0.07	0.14	0.00	1.01E+01	6.25E-04	Up	9.50E+00	1.38E-02		5.93E-01	2.77E-01		7.21E-01	1.51E-01		9.84E-01	7.31E-01		-6.17E+00	6.13E-01				Unigene30005_All//0.00E+00//TC177041					
Unigene30007_All	295	0.00	1.37	0.90	2.70	0.23	1.53	2.87	1.42	1.49	1.04E+01	1.36E-02		9.82E+00	8.02E-02		-3.53E+00	3.03E-04	Down	-8.19E-01	3.20E-01		-1.02E+00	1.41E-01		-9.48E-01	1.47E-01										
Unigene30008_All	479	0.00	1.59	0.00	0.21	0.14	0.38	7.24	3.66	62.46	1.06E+01	1.77E-04	Up	null	null		-5.33E-01	8.16E-01		8.58E-01	6.95E-01		-9.82E-01	9.45E-04		3.11E+00	2.96E-126	Up	Unigene30008_All//gi|224086894|ref|XP_002307998.1|//7.00E-07//predicted protein [Populus trichocarpa] >gi|118486037|gb|ABK94862.1| unknown [Populus trichocarpa] >gi|222853974|gb|EEE91521.1| predicted protein [Populus trichocarpa]		Unigene30008_All//0.00E+00//gi|109884200|gb|DW513170.1|DW513170				nr -
Unigene3001_All	947	3.09	2.46	3.15	4.31	4.18	3.96	1.92	2.21	0.46	-3.30E-01	3.76E-01		2.54E-02	9.63E-01		-4.47E-02	8.86E-01		-1.24E-01	6.98E-01		2.01E-01	6.41E-01		-2.05E+00	1.27E-05	Down			Unigene3001_All//1.00E-37//gi|78342688|gb|DT562962.1|DT562962					
Unigene30010_All	400	2.75	0.00	1.20	2.49	3.87	3.84	0.53	0.00	0.50	-1.14E+01	1.95E-06	Down	-1.20E+00	8.57E-02		6.37E-01	2.56E-01		6.24E-01	2.70E-01		-9.05E+00	7.44E-02		-8.58E-02	9.61E-01		Unigene30010_All//gi|66792640|gb|AAY56422.1|//7.00E-10//At4g22860 [Arabidopsis thaliana]	Unigene30010_All//9.00E-05//AT4G11990| unknown protein					nr +
Unigene30012_All	569	5.79	1.78	4.30	4.03	4.66	3.10	0.37	0.44	1.19	-1.70E+00	4.26E-06	Down	-4.28E-01	2.41E-01		2.11E-01	6.21E-01		-3.80E-01	4.02E-01		2.46E-01	8.53E-01		1.68E+00	3.70E-02		Unigene30012_All//gi|18405476|ref|NP_565939.1|//2.00E-39//GLY1; glycerol-3-phosphate dehydrogenase (NAD+) [Arabidopsis thaliana]	Unigene30012_All//8.00E-40//AT2G40690| GLY1; glycerol-3-phosphate dehydrogenase (NAD+)	Unigene30012_All//0.00E+00//CO113710				nr -
Unigene30015_All	465	1.80	1.63	3.09	5.14	2.52	1.46	2.46	1.62	1.54	-1.39E-01	8.39E-01		7.80E-01	1.80E-01		-1.03E+00	8.02E-03		-1.82E+00	3.18E-05	Down	-6.02E-01	3.08E-01		-6.71E-01	2.20E-01				Unigene30015_All//0.00E+00//TC149179					
Unigene30016_All	348	240.41	63.48	130.83	462.07	417.48	391.16	169.97	61.13	103.49	-1.92E+00	6.07E-162	Down	-8.78E-01	3.85E-47		-1.46E-01	1.50E-04		-2.40E-01	6.11E-10		-1.48E+00	1.95E-96	Down	-7.16E-01	6.10E-31		Unigene30016_All//gi|3122703|sp|O22644.1|RL23A_FRIAG//2.00E-30//RecName: Full=60S ribosomal protein L23A >gi|2641201|gb|AAB86852.1| ribosomal protein L23a [Fritillaria agrestis]	Unigene30016_All//6.00E-14//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene30016_All//4.00E-146//gi|11203379|gb|BF272384.1|BF272384		ko03010|Ribosome		nr +
Unigene30017_All	280	2.43	0.00	0.38	3.74	3.57	2.42	0.60	0.00	0.00	-1.12E+01	4.10E-04	Down	-2.67E+00	1.69E-02		-6.70E-02	9.06E-01		-6.27E-01	3.81E-01		-9.24E+00	1.34E-01		-9.24E+00	1.08E-01										
Unigene30019_All	1551	0.00	0.00	0.00	0.00	0.00	0.00	5.83	6.63	0.05	null	null		null	null		null	null		null	null		1.84E-01	3.08E-01		-6.83E+00	7.60E-63	Down	Unigene30019_All//gi|4139170|gb|AAD03711.1|//0.00E+00//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene30019_All//0.00E+00//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene30019_All//1.00E-72//CD809343				nr -
Unigene3002_All	1572	5.03	2.10	2.57	7.51	6.70	4.42	7.64	2.23	4.18	-1.26E+00	5.70E-09	Down	-9.65E-01	8.66E-06		-1.64E-01	3.87E-01		-7.63E-01	2.08E-06		-1.77E+00	4.34E-26	Down	-8.69E-01	1.97E-09		Unigene3002_All//gi|42571181|ref|NP_973664.1|//0.00E+00//POLD2 (DNA POLYMERASE DELTA SMALL SUBUNIT); DNA binding / DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|31376377|gb|AAP49515.1| At2g42120 [Arabidopsis thaliana] >gi|62320658|dbj|BAD95325.1| DNA polymerase delta small subunit like protein [Arabidopsis thaliana]	Unigene3002_All//0.00E+00//AT2G42120| POLD2 (DNA POLYMERASE DELTA SMALL SUBUNIT); DNA binding / DNA-directed DNA polymerase	Unigene3002_All//0.00E+00//TC156175		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair	GO:0003676//GO:0006259//GO:0034061//GO:0043231	nr +
Unigene30021_All	558	0.09	0.18	0.00	2.32	1.54	0.81	1.82	0.37	0.36	9.53E-01	7.26E-01		-6.55E+00	6.24E-01		-5.89E-01	3.13E-01		-1.52E+00	1.32E-02		-2.28E+00	1.11E-03		-2.35E+00	5.84E-04	Down	Unigene30021_All//gi|115456465|ref|NP_001051833.1|//3.00E-29//Os03g0837800 (Oryza sativa Japonica Group) >gi|28376715|gb|AAO41145.1| myosin-like protein (Oryza sativa Japonica Group) >gi|108711985|gb|ABF99780.1| expressed protein (Oryza sativa (japonica cultivar-group)) >gi|113550304|dbj|BAF13747.1| Os03g0837800 (Oryza sativa Japonica Group)	Unigene30021_All//6.00E-45//AT2G33793| unknown protein					nr -
Unigene30022_All	271	1.16	0.56	0.98	0.18	1.02	1.83	0.78	4.32	1.76	-1.05E+00	4.43E-01		-2.38E-01	8.50E-01		2.47E+00	2.23E-01		3.32E+00	2.31E-02		2.47E+00	1.92E-04	Up	1.18E+00	2.18E-01		Unigene30022_All//gi|146261314|gb|ABQ14926.1|//3.00E-16//Ycf2 (Ribes americanum)	Unigene30022_All//3.00E-16//ATCG01280| hypothetical protein	Unigene30022_All//1.00E-34//TC129552				nr +

Unigene30023_All	1278	0.00	0.16	0.00	0.04	0.00	0.74	38.21	21.49	4.21	7.31E+00	1.36E-01		null	null		-5.29E+00	5.55E-01		4.25E+00	1.11E-04	Up	-8.31E-01	4.55E-32		-3.18E+00	3.38E-214	Down	Unigene30023_All//gi|75297894|sp|Q84MB3.1|ACCH1_ARATH//1.00E-104//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene30023_All//1.00E-101//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative			ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene30025_All	1758	0.00	0.43	0.24	0.06	0.00	0.51	1.61	8.27	18.38	8.76E+00	1.77E-04	Up	7.92E+00	1.38E-02		-5.83E+00	3.13E-01		3.18E+00	9.74E-04	Up	2.36E+00	4.46E-45	Up	3.51E+00	2.83E-152	Up	Unigene30025_All//gi|297727443|ref|NP_001176085.1|//1.00E-101//Os10g0331700 [Oryza sativa Japonica Group] >gi|22655755|gb|AAN04172.1| Putative glucosyltransferase [Oryza sativa Japonica Group] >gi|31431229|gb|AAP53037.1| UDP-glucoronosyl and UDP-glucosyl transferase family protein [Oryza sativa (japonica cultivar-group)] >gi|255676305|dbj|BAH94813.1| Os10g0331700 [Oryza sativa Japonica Group]	Unigene30025_All//5.00E-93//AT3G02100| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene30025_All//0.00E+00//CO121894		ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr +
Unigene30027_All	383	3.14	0.00	0.28	1.95	4.05	2.36	0.99	0.11	0.21	-1.16E+01	5.01E-07	Down	-3.50E+00	8.78E-05	Down	1.05E+00	5.02E-02		2.74E-01	7.10E-01		-3.19E+00	3.12E-02		-2.26E+00	6.49E-02		Unigene30027_All//gi|297834340|ref|XP_002885062.1|//1.00E-10//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297330892|gb|EFH61311.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene30027_All//1.00E-09//AT3G14730| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene30030_All	591	0.00	4.12	1.08	2.36	2.97	2.98	1.43	0.50	0.67	1.20E+01	7.73E-14	Up	1.01E+01	1.16E-03		3.32E-01	5.46E-01		3.37E-01	5.42E-01		-1.53E+00	3.21E-02		-1.09E+00	9.98E-02		Unigene30030_All//gi|15218566|ref|NP_174686.1|//3.00E-21//phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] >gi|5091620|gb|AAD39608.1|AC007454_7 Contains similarity to gi|836774 PAB1 protein from Saccharomyces cerevisiae genome gb|D50617 [Arabidopsis thaliana]	Unigene30030_All//3.00E-19//AT1G34260| phosphatidylinositol-4-phosphate 5-kinase family protein	Unigene30030_All//4.00E-33//gi|109865748|gb|DW494724.1|DW494724		ko04145|Phagosome//ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene30032_All	517	153.32	20.29	69.01	485.13	389.91	159.95	246.89	370.58	117.36	-2.92E+00	6.00E-253	Down	-1.15E+00	1.01E-69	Down	-3.15E-01	5.62E-28		-1.60E+00	0.00E+00	Down	5.86E-01	3.52E-67		-1.07E+00	8.96E-130	Down	Unigene30032_All//gi|89759711|emb|CAB96832.1|//1.00E-50//nucleoid DNA-binding protein cnd41-like protein [Arabidopsis thaliana]	Unigene30032_All//1.00E-37//AT5G10770| chloroplast nucleoid DNA-binding protein, putative	Unigene30032_All//0.00E+00//TC174453				nr +
Unigene30036_All	266	58.22	24.00	24.62	79.40	72.75	100.51	135.74	61.44	62.90	-1.28E+00	3.59E-17	Down	-1.24E+00	9.88E-16	Down	-1.26E-01	3.61E-01		3.40E-01	1.15E-03		-1.14E+00	3.98E-40	Down	-1.11E+00	2.20E-39	Down			Unigene30036_All//2.00E-141//gi|21095861|gb|BQ408174.1|BQ408174				
Unigene30037_All	1240	0.00	8.09	6.48	0.00	0.00	0.00	0.07	0.00	0.00	1.30E+01	1.76E-57	Up	1.27E+01	5.31E-45	Up	null	null		null	null		-6.09E+00	4.04E-01		-6.09E+00	3.58E-01		Unigene30037_All//gi|17367847|sp|Q9XF97.1|RL4_PRUAR//1.00E-122//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32206.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene30037_All//9.00E-106//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)	Unigene30037_All//1.00E-22//BQ405438		ko03010|Ribosome		nr +
Unigene30040_All	672	6.00	2.04	4.04	1.48	1.84	0.60	0.13	0.00	0.24	-1.56E+00	1.64E-06	Down	-5.69E-01	7.68E-02		3.15E-01	6.29E-01		-1.29E+00	7.06E-02		-6.98E+00	4.04E-01		9.14E-01	6.24E-01		Unigene30040_All//gi|3582436|dbj|BAA33065.1|//4.00E-87//beta-D-glucan exohydrolase [Nicotiana tabacum]	Unigene30040_All//6.00E-84//AT5G20950| glycosyl hydrolase family 3 protein	Unigene30040_All//0.00E+00//TC150940		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr +
Unigene30045_All	617	93.70	29.81	69.22	1.61	2.29	0.59	0.00	0.00	0.00	-1.65E+00	5.61E-91	Down	-4.37E-01	6.77E-10		5.03E-01	4.15E-01		-1.46E+00	4.18E-02		null	null		null	null		Unigene30045_All//gi|14030737|gb|AAK53043.1|AF375459_1//3.00E-31//At2g26500 [Arabidopsis thaliana] >gi|16974525|gb|AAL31172.1| At2g26500/T9J22.17 [Arabidopsis thaliana] >gi|20196942|gb|AAM14841.1| expressed protein [Arabidopsis thaliana]	Unigene30045_All//2.00E-21//AT2G26500| cytochrome b6f complex subunit (petM), putative	Unigene30045_All//0.00E+00//TC157388				nr -
Unigene30046_All	236	27.71	69.99	34.30	41.58	59.24	75.21	8.60	39.85	42.03	1.34E+00	2.06E-19	Up	3.08E-01	1.65E-01		5.11E-01	3.30E-04		8.55E-01	4.81E-11		2.21E+00	3.27E-27	Up	2.29E+00	1.72E-30	Up			Unigene30046_All//4.00E-49//gi|109855959|gb|DW484938.1|DW484938				
Unigene30048_All	1219	0.09	10.43	6.20	0.00	0.00	0.07	0.00	0.00	0.00	6.93E+00	4.16E-69	Up	6.18E+00	6.82E-39	Up	null	null		6.21E+00	4.76E-01		null	null		null	null		Unigene30048_All//gi|298705474|emb|CBJ28749.1|//2.00E-19//Hypothetical leucine rich repeat protein [Ectocarpus siliculosus]	Unigene30048_All//3.00E-09//AT1G35710| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction		nr +
Unigene3005_All	1535	8.52	6.93	5.55	38.29	32.73	13.42	6.28	7.62	7.34	-2.98E-01	6.49E-02		-6.19E-01	1.25E-04		-2.27E-01	5.61E-04		-1.51E+00	2.00E-88	Down	2.80E-01	7.33E-02		2.26E-01	1.49E-01		Unigene3005_All//gi|15232059|ref|NP_189337.1|//4.00E-83//AT-TCP20; transcription factor [Arabidopsis thaliana] >gi|75272954|sp|Q9LSD5.1|TCP20_ARATH RecName: Full=Transcription factor TCP20	Unigene3005_All//6.00E-66//AT3G27010| AT-TCP20; transcription factor	Unigene3005_All//0.00E+00//TC171470	TCP			nr +
Unigene30050_All	336	0.00	2.11	0.00	0.30	0.21	0.54	3.65	2.74	2.85	1.10E+01	3.33E-04	Up	null	null		-5.32E-01	8.16E-01		8.59E-01	6.95E-01		-4.15E-01	4.66E-01		-3.59E-01	5.10E-01				Unigene30050_All//3.00E-137//TC144926				
Unigene30051_All	476	3.41	0.00	0.22	1.88	1.52	2.28	2.22	0.18	1.00	-1.17E+01	2.11E-09	Down	-3.93E+00	8.58E-07	Down	-3.10E-01	6.65E-01		2.74E-01	6.70E-01		-3.66E+00	1.31E-05	Down	-1.14E+00	4.77E-02		Unigene30051_All//gi|297810127|ref|XP_002887945.1|//1.00E-55//PDE316 [Arabidopsis lyrata subsp. lyrata] >gi|297333786|gb|EFH64204.1| PDE316 [Arabidopsis lyrata subsp. lyrata]	Unigene30051_All//6.00E-50//AT1G63680| MURE; ATP binding / acid-amino acid ligase/ ligase	Unigene30051_All//2.00E-93//gi|78347965|gb|DT568239.1|DT568239				nr -
Unigene30052_All	223	28.39	22.95	28.42	34.40	29.80	43.54	35.45	23.05	12.33	-3.07E-01	2.13E-01		1.40E-03	9.94E-01		-2.07E-01	3.78E-01		3.40E-01	7.81E-02		-6.21E-01	7.25E-04		-1.52E+00	1.15E-14	Down			Unigene30052_All//3.00E-68//TC139553				
Unigene30053_All	308	31.26	78.97	30.08	75.85	61.16	58.36	46.26	53.87	47.73	1.34E+00	2.99E-28	Up	-5.52E-02	7.83E-01		-3.11E-01	4.36E-03		-3.78E-01	7.10E-04		2.20E-01	9.28E-02		4.51E-02	7.54E-01				Unigene30053_All//2.00E-126//gi|57901459|gb|CB066519.1|CB066519				
Unigene30055_All	692	0.00	0.00	0.46	33.47	10.65	3.13	1.96	0.36	0.12	null	null		8.85E+00	4.52E-02		-1.65E+00	1.01E-45	Down	-3.42E+00	3.03E-94	Down	-2.43E+00	5.63E-05	Down	-4.09E+00	7.07E-08	Down	Unigene30055_All//gi|18404328|ref|NP_566754.1|//2.00E-07//CLE41 (CLAVATA3/ESR-RELATED 41); protein binding / receptor binding [Arabidopsis thaliana] >gi|58331817|gb|AAW70406.1| At3g24770 [Arabidopsis thaliana]		Unigene30055_All//0.00E+00//gi|109869095|gb|DW498071.1|DW498071				nr +
Unigene30057_All	652	0.32	0.16	1.23	0.46	3.59	5.89	1.49	0.19	2.14	-1.05E+00	5.65E-01		1.93E+00	3.42E-02		2.97E+00	7.31E-09	Up	3.68E+00	2.70E-16	Up	-2.96E+00	1.89E-04	Down	5.20E-01	2.99E-01		Unigene30057_All//gi|297849954|ref|XP_002892858.1|//2.00E-56//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297338700|gb|EFH69117.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene30057_All//4.00E-55//AT1G15290| binding	Unigene30057_All//6.00E-54//gi|109851526|gb|DW480505.1|DW480505				nr -
Unigene30058_All	897	0.00	0.00	0.00	7.33	2.73	0.91	0.00	0.00	0.00	null	null		null	null		-1.43E+00	9.95E-11	Down	-3.02E+00	5.64E-24	Down	null	null		null	null								
Unigene30059_All	445	2.94	7.29	4.19	2.91	2.24	2.13	0.10	0.09	0.00	1.31E+00	2.47E-04	Up	5.11E-01	3.12E-01		-3.75E-01	5.57E-01		-4.50E-01	4.84E-01		-1.68E-02	1.00E+00		-6.57E+00	6.12E-01				Unigene30059_All//0.00E+00//TC135224				
Unigene3006_All	1612	12.95	7.36	7.53	21.85	16.00	13.95	13.27	5.70	6.80	-8.16E-01	2.36E-11		-7.82E-01	4.04E-10		-4.49E-01	5.41E-08		-6.47E-01	1.75E-13		-1.22E+00	1.46E-26	Down	-9.66E-01	4.85E-19		Unigene3006_All//gi|115486791|ref|NP_001068539.1|//1.00E-32//Os11g0703600 [Oryza sativa Japonica Group] >gi|77552699|gb|ABA95496.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|77552700|gb|ABA95497.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113645761|dbj|BAF28902.1| Os11g0703600 [Oryza sativa Japonica Group]	Unigene3006_All//9.00E-38//AT5G39350| unknown protein	Unigene3006_All//0.00E+00//TC155723			GO:0044464	nr +
Unigene30064_All	1259	0.00	0.00	0.00	0.28	0.16	0.04	7.56	5.98	2.12	null	null		null	null		-7.55E-01	5.67E-01		-2.95E+00	8.30E-02		-3.39E-01	4.89E-02		-1.83E+00	1.81E-22	Down	Unigene30064_All//gi|37780214|gb|AAP55487.1|//1.00E-08//resistance protein RGC2 [Lactuca sativa]	Unigene30064_All//1.00E-07//AT3G25510| disease resistance protein (TIR-NBS-LRR class), putative	Unigene30064_All//1.00E-22//TC160592				nr +
Unigene30065_All	603	0.52	4.45	2.65	2.56	3.14	6.52	0.70	0.28	0.26	3.10E+00	1.60E-09	Up	2.35E+00	2.09E-04	Up	2.95E-01	5.87E-01		1.35E+00	1.99E-05	Up	-1.34E+00	2.24E-01		-1.41E+00	1.74E-01		Unigene30065_All//gi|297835708|ref|XP_002885236.1|//1.00E-46//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331576|gb|EFH61995.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene30065_All//2.00E-47//AT2G04100| MATE efflux family protein					nr -
Unigene30068_All	623	0.34	11.63	2.31	0.00	0.22	0.00	6.45	1.27	0.64	5.11E+00	2.09E-35	Up	2.78E+00	1.05E-04	Up	7.79E+00	3.18E-01		null	null		-2.34E+00	7.44E-13	Down	-3.33E+00	5.36E-19	Down	Unigene30068_All//gi|6714297|gb|AAF25993.1|AC013354_12//2.00E-24//F15H18.19 [Arabidopsis thaliana] >gi|8671771|gb|AAF78377.1|AC069551_10 T10O22.26 [Arabidopsis thaliana]	Unigene30068_All//9.00E-20//AT1G18290| unknown protein	Unigene30068_All//0.00E+00//DW512422				nr -
Unigene3007_All	1327	6.55	1.26	2.73	20.50	10.51	21.68	32.75	10.61	13.75	-2.38E+00	1.51E-22	Down	-1.26E+00	2.59E-09	Down	-9.64E-01	5.04E-23		8.10E-02	5.23E-01		-1.63E+00	8.28E-82	Down	-1.25E+00	4.48E-57	Down	Unigene3007_All//gi|224054176|ref|XP_002298129.1|//3.00E-86//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene3007_All//6.00E-82//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene3007_All//0.00E+00//TC133026		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis	GO:0008152//GO:0016491//GO:0044464	nr -
Unigene30072_All	335	0.00	0.61	0.00	4.76	2.98	3.91	0.00	1.75	0.83	9.24E+00	1.36E-01		null	null		-6.75E-01	1.88E-01		-2.83E-01	6.38E-01		1.08E+01	2.81E-04	Up	9.70E+00	2.43E-02		Unigene30072_All//gi|224118624|ref|XP_002331408.1|//2.00E-14//trans-cinnamate 4-monooxygenase [Populus trichocarpa] >gi|183585161|gb|ACC63872.1| trans-cinnamate 4-hydroxylase [Populus trichocarpa] >gi|222873622|gb|EEF10753.1| trans-cinnamate 4-monooxygenase [Populus trichocarpa]				ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene30073_All	758	0.28	1.67	0.14	0.72	0.82	1.79	1.39	4.63	7.20	2.60E+00	3.59E-04	Up	-9.75E-01	6.21E-01		1.78E-01	8.64E-01		1.31E+00	2.93E-02		1.73E+00	6.71E-08	Up	2.37E+00	8.46E-18	Up							
Unigene30074_All	689	0.15	0.74	0.08	0.65	0.60	0.13	0.68	1.82	3.12	2.28E+00	6.23E-02		-9.75E-01	7.21E-01		-1.18E-01	8.86E-01		-2.31E+00	7.81E-02		1.43E+00	1.04E-02		2.21E+00	6.01E-07	Up							
Unigene30075_All	780	0.40	1.36	0.82	1.72	1.72	1.80	0.81	2.79	2.66	1.76E+00	1.43E-02		1.03E+00	2.81E-01		-2.10E-03	9.81E-01		5.80E-02	9.39E-01		1.78E+00	2.47E-05	Up	1.71E+00	4.86E-05	Up			Unigene30075_All//0.00E+00//gi|73850528|gb|DT459548.1|DT459548				
Unigene30076_All	752	0.83	1.89	1.42	0.00	0.18	0.42	17.88	2.50	0.90	1.18E+00	3.93E-02		7.62E-01	2.69E-01		7.52E+00	3.18E-01		8.72E+00	4.07E-02		-2.84E+00	2.52E-51	Down	-4.31E+00	6.73E-76	Down	Unigene30076_All//gi|115452497|ref|NP_001049849.1|//1.00E-42//Os03g0299600 [Oryza sativa Japonica Group] >gi|113548320|dbj|BAF11763.1| Os03g0299600 [Oryza sativa Japonica Group]	Unigene30076_All//6.00E-24//AT3G10985| SAG20 (SENESCENCE ASSOCIATED GENE 20)	Unigene30076_All//0.00E+00//gi|109834164|gb|DW232729.1|DW232729				nr +

Unigene30077_All	977	0.00	0.57	2.23	0.00	0.00	0.09	19.21	1.71	1.35	9.16E+00	2.18E-03		1.11E+01	4.95E-12	Up	null	null		6.53E+00	4.76E-01		-3.49E+00	5.13E-87	Down	-3.84E+00	3.27E-97	Down	Unigene30077_All//gi|297820478|ref|XP_002878122.1|//4.00E-36//OBP3-responsive gene 3 [Arabidopsis lyrata subsp. lyrata] >gi|297323960|gb|EFH54381.1| OBP3-responsive gene 3 [Arabidopsis lyrata subsp. lyrata]	Unigene30077_All//2.00E-34//AT3G56970| BHLH038; DNA binding / transcription factor		bHLH			nr -
Unigene30078_All	405	0.78	0.75	0.66	1.35	4.85	2.12	1.88	2.58	1.67	-4.61E-02	9.85E-01		-2.38E-01	8.50E-01		1.84E+00	1.54E-04	Up	6.47E-01	4.23E-01		4.57E-01	4.63E-01		-1.68E-01	7.94E-01									
Unigene3008_All	2378	1.30	0.72	0.92	3.16	3.55	2.36	5.00	2.72	2.46	-8.41E-01	1.74E-02		-5.00E-01	1.85E-01		1.66E-01	4.88E-01		-4.26E-01	5.00E-02		-8.75E-01	3.96E-09		-1.02E+00	6.09E-12	Down	Unigene3008_All//gi|56748564|sp|Q9M3G7.1|ATM_ARATH//0.00E+00//RecName: Full=Serine/threonine-protein kinase ATM; AltName: Full=Ataxia telangiectasia mutated homolog; Short=AtATM >gi|7960715|emb|CAB92122.1| AtATM [Arabidopsis thaliana]	Unigene3008_All//0.00E+00//AT3G48190| ATM (ATAXIA-TELANGIECTASIA MUTATED); 1-phosphatidylinositol-3-phosphate 5-kinase	Unigene3008_All//0.00E+00//C0074268			GO:0016772//GO:0032559	nr -
Unigene30083_All	353	0.30	1.15	0.75	1.98	1.07	0.26	3.59	1.89	0.00	1.95E+00	1.44E-01		1.35E+00	4.09E-01		-8.81E-01	2.99E-01		-2.95E+00	5.84E-03		-9.24E-01	8.68E-02		-1.18E+01	1.99E-09	Down		Unigene30083_All//1.00E-127//TC165493					
Unigene30087_All	741	0.00	0.00	0.29	0.40	1.25	0.00	0.80	2.54	5.43	null	null		8.17E+00	1.41E-01		1.64E+00	3.35E-02		-8.66E+00	4.00E-02		1.67E+00	2.19E-04	Up	2.77E+00	1.09E-15	Up		Unigene30087_All//6.00E-45//gi|195982824|gb|FL577081.1|FL577081					
Unigene30088_All	485	1.29	1.25	1.32	8.32	8.45	3.72	11.59	0.00	3.78	-4.62E-02	9.72E-01		2.54E-02	9.97E-01		2.23E-02	9.54E-01		-1.16E+00	1.29E-04	Down	-1.35E+01	7.71E-40	Down	-1.62E+00	1.45E-11	Down	Unigene30088_All//gi|1706740|sp|P52837.1|FST_FLACH//5.00E-45//RecName: Full=Flavonol 4'-sulfotransferase; Short=F4-ST >gi|168169|gb|AAA33343.1| flavonol 4'-sulfotransferase [Flaveria chloraefolia]	Unigene30088_All//5.00E-39//AT1G74100| SOT16 (SULFOTRANSFERASE 16); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene30088_All//7.00E-167//TC170106		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr -
Unigene3009_All	1572	13.45	5.00	8.91	38.50	26.59	10.52	42.87	12.02	20.05	-1.43E+00	2.61E-27	Down	-5.94E-01	1.41E-06		-5.34E-01	3.59E-18		-1.87E+00	2.55E-123	Down	-1.83E+00	7.12E-150	Down	-1.10E+00	2.22E-71	Down	Unigene3009_All//gi|17747106|gb|AAK68745.2|//6.00E-74//Unknown protein [Arabidopsis thaliana]	Unigene3009_All//3.00E-58//AT5G61340| unknown protein	Unigene3009_All//0.00E+00//TC149846				nr -
Unigene30092_All	424	1.23	0.24	0.00	0.00	1.79	3.62	1.79	0.69	2.26	-2.37E+00	4.76E-02		-1.03E+01	4.75E-03		1.08E+01	1.17E-04	Up	1.18E+01	3.78E-09	Up	-1.38E+00	6.73E-02		3.29E-01	5.93E-01		Unigene30092_All//gi|145344920|ref|XP_001416972.1|//7.00E-12//NCS1 family transporter: cytosine/purines/uracil/thiamine/allantoin [Ostreococcus lucimarinus CCE9901] >gi|144577198|gb|AB095265.1| NCS1 family transporter: cytosine/purines/uracil/thiamine/allantoin [Ostreococcus lucimarinus CCE9901]				ko03040|Spliceosome		nr -
Unigene30093_All	1618	0.00	10.68	4.25	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.52E-99	Up	1.21E+01	2.29E-38	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene30096_All	858	0.24	1.18	0.25	0.00	0.36	0.21	1.08	4.24	10.26	2.28E+00	4.10E-03		2.58E-02	1.00E+00		8.50E+00	4.54E-02		7.72E+00	1.94E-01		1.97E+00	1.53E-09	Up	3.24E+00	4.21E-39	Up		Unigene30096_All//2.00E-38//TC139392					
Unigene30097_All	822	4.90	1800.98	1030.73	1.09	0.17	7.36	2.98	2.90	3.00	8.52E+00	0.00E+00	Up	7.72E+00	0.00E+00	Up	-2.70E+00	8.77E-04	Down	2.75E+00	1.36E-19	Up	-4.18E-02	9.28E-01		1.04E-02	9.74E-01		Unigene30097_All//gi|55168340|gb|AV442205.1|//8.00E-40//unknow protein [Oryza sativa Japonica Group]		Unigene30097_All//2.00E-128//TC149394				nr +
Unigene30098_All	476	1.21	4.05	1.23	29.30	1.66	0.38	5.24	0.00	4.52	1.74E+00	5.85E-04	Up	2.54E-02	9.98E-01		-4.14E+00	2.98E-78	Down	-6.27E+00	6.64E-82	Down	-1.24E+01	1.21E-17	Down	-2.14E-01	5.78E-01			Unigene30098_All//1.00E-84//C0070687					
Unigene30099_All	318	0.33	0.16	1.51	8.30	3.14	3.55	0.00	2.10	0.38	-1.05E+00	6.84E-01		2.20E+00	9.15E-02		-1.40E+00	1.52E-04	Down	-1.23E+00	1.69E-03		1.10E+01	7.64E-05	Up	8.55E+00	2.43E-01			Unigene30099_All//1.00E-84//TC145587					
Unigene3010_All	1148	10.21	10.06	9.51	17.31	13.95	12.75	15.73	6.84	8.50	-2.07E-02	9.20E-01		-1.03E-01	6.16E-01		-3.12E-01	9.46E-03		-4.42E-01	2.66E-04		-1.20E+00	4.94E-22	Down	-8.87E-01	3.50E-14		Unigene3010_All//gi|6685428|sp|Q9ZTN2.1|ERD2_PETHY//1.00E-109//RecName: Full=ER lumen protein retaining receptor; AltName: Full=HDEL receptor; AltName: Full=PGP169-12 >gi|4105782|gb|AAD02548.1| PGPS/D6 [Petunia x hybrida]	Unigene3010_All//7.00E-100//AT3G25040| ER lumen protein retaining receptor, putative / HDEL receptor, putative	Unigene3010_All//0.00E+00//TC131790				nr -
Unigene30102_All	294	0.18	2.76	0.00	0.00	0.70	0.00	1.44	1.56	1.63	3.95E+00	7.52E-04	Up	-7.48E+00	6.24E-01		9.46E+00	1.57E-01		null	null		1.21E-01	9.07E-01		1.77E-01	8.46E-01									
Unigene30103_All	220	0.24	4.15	1.69	0.68	0.47	1.64	11.53	23.56	18.65	4.12E+00	2.34E-04	Up	2.83E+00	9.31E-02		-5.33E-01	7.85E-01		1.27E+00	3.82E-01		1.03E+00	1.45E-05	Up	6.94E-01	7.57E-03			Unigene30103_All//7.00E-57//DW509229					
Unigene30105_All	537	0.68	1.04	1.88	0.93	0.06	1.35	1.89	2.41	5.34	6.06E-01	5.31E-01		1.47E+00	4.95E-02		-3.86E+00	5.31E-03		5.37E-01	5.60E-01		3.53E-01	5.36E-01		1.50E+00	1.11E-05	Up		Unigene30105_All//3.00E-24//TC152706					
Unigene30107_All	1010	0.16	0.10	0.00	7.74	4.71	0.54	5.32	0.08	1.66	-6.32E-01	7.27E-01		-7.28E+00	2.45E-01		-7.19E-01	1.89E-04		-3.85E+00	2.73E-35	Down	-6.00E+00	9.84E-35	Down	-1.68E+00	1.14E-11	Down	Unigene30107_All//gi|18411885|ref|NP_565175.1|//1.00E-46//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|21537200|gb|AAM61541.1| RNA recognition motif-containing protein SEB-4 [Arabidopsis thaliana] >gi|124300976|gb|ABN04740.1| Atlg78260 [Arabidopsis thaliana]	Unigene30107_All//4.00E-29//AT1G22330| RNA binding / nucleic acid binding / nucleotide binding	Unigene30107_All//0.00E+00//TC162867				nr +
Unigene30110_All	1279	0.00	9.67	4.12	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	6.25E-71	Up	1.20E+01	2.42E-29	Up	null	null		null	null		null	null		null	null									
Unigene30111_All	434	15.43	137.76	59.63	9.53	18.80	28.51	0.00	0.19	0.09	3.16E+00	1.34E-204	Up	1.95E+00	8.51E-50	Up	9.81E-01	4.05E-07		1.58E+00	6.99E-20	Up	7.59E+00	4.01E-01		6.52E+00	6.45E-01		Unigene30111_All//gi|117957141|gb|ABK59039.1|//9.00E-47//MYB96-like protein [Citrus macrophylla]	Unigene30111_All//2.00E-47//AT5G62470| MYB96 (myb domain protein 96); DNA binding / transcription factor	Unigene30111_All//8.00E-80//TC133949	MYB			nr -
Unigene30117_All	399	27.93	10.29	30.56	2.25	2.07	1.92	0.00	0.00	0.00	-1.44E+00	6.15E-15	Down	1.30E-01	4.89E-01		-1.18E-01	8.51E-01		-2.24E-01	7.50E-01		null	null		null	null		Unigene30117_All//gi|145356202|ref|NP_195636.2|//5.00E-32//ATRL1 (ARABIDOPSIS RAD-LIKE 1); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene30117_All//7.00E-28//AT4G38250| ATRL1 (ARABIDOPSIS RAD-LIKE 1); DNA binding / transcription factor	Unigene30117_All//0.00E+00//DW503354	MYB-related			nr +
Unigene30118_All	516	0.00	0.59	0.62	0.68	1.87	2.98	5.16	3.89	3.63	9.20E+00	4.43E-02		9.27E+00	4.52E-02		1.47E+00	4.80E-02		2.14E+00	3.75E-04	Up	-4.09E-01	2.56E-01		-5.09E-01	1.30E-01		Unigene30118_All//gi|297604909|ref|NP_001056321.2|//2.00E-10//Os05g0562400 [Oryza sativa Japonica Group] >gi|255676572|dbj|BAF18235.2| Os05g0562400 [Oryza sativa Japonica Group]	Unigene30118_All//6.00E-14//AT5G44180| homeobox transcription factor, putative	Unigene30118_All//3.00E-52//gi|78325734|gb|DT546008.1|DT546008				nr -
Unigene30119_All	412	1.52	0.74	2.46	1.93	2.01	0.99	1.54	0.00	0.58	-1.05E+00	2.50E-01		6.88E-01	3.42E-01		5.23E-02	9.65E-01		-9.71E-01	2.30E-01		-1.06E+01	1.23E-04	Down	-1.41E+00	7.94E-02		Unigene30119_All//gi|224127987|ref|XP_002320213.1|//5.00E-58//endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa] >gi|222860986|gb|EEE98528.1| endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa]	Unigene30119_All//6.00E-41//AT4G00900| ECA2 (ER-TYPE CA2+-ATPASE 2); calcium-transporting ATPase	Unigene30119_All//1.00E-109//TC157977				nr +
Unigene30120_All	268	4.49	3.21	4.37	7.06	6.81	8.26	36.60	17.93	17.99	-4.82E-01	4.20E-01		-3.87E-02	9.68E-01		-5.27E-02	9.05E-01		2.25E-01	6.34E-01		-1.03E+00	8.26E-10	Down	-1.02E+00	4.43E-10	Down		Unigene30120_All//2.00E-100//DW235906					
Unigene30123_All	254	3.30	0.00	0.84	3.33	1.90	3.20	3.00	0.66	0.31	-1.17E+01	5.57E-05	Down	-1.97E+00	2.71E-02		-8.13E-01	2.80E-01		-5.89E-02	9.44E-01		-2.19E+00	7.77E-03		-3.26E+00	4.48E-04	Down		Unigene30123_All//5.00E-95//DW502584					
Unigene30127_All	1145	0.14	0.00	0.28	0.39	0.51	0.16	3.06	3.18	15.07	-7.10E+00	2.16E-01		1.03E+00	4.71E-01		3.85E-01	7.32E-01		-1.31E+00	2.73E-01		5.12E-02	8.77E-01		2.30E+00	1.12E-52	Up	Unigene30127_All//gi|121501706|gb|ABM55247.1|//1.00E-128//calmodulin-binding protein [Beta vulgaris]	Unigene30127_All//1.00E-100//AT5G57010| calmodulin-binding family protein	Unigene30127_All//0.00E+00//gi|73862889|gb|DT465628.1|DT465628				nr -
Unigene30128_All	324	0.48	0.31	0.33	4.77	1.49	1.53	2.61	0.26	0.12	-6.31E-01	7.27E-01		-5.60E-01	7.76E-01		-1.68E+00	1.27E-03		-1.64E+00	3.26E-03		-3.34E+00	2.51E-04	Down	-4.41E+00	2.37E-05	Down		Unigene30128_All//4.00E-07//DW226904					
Unigene30130_All	518	0.61	0.00	0.93	2.98	2.33	3.23	1.63	0.48	0.23	-9.24E+00	3.66E-02		6.10E-01	5.87E-01		-3.58E-01	5.31E-01		1.14E-01	8.38E-01		-1.75E+00	1.64E-02		-2.82E+00	5.38E-04	Down	Unigene30130_All//gi|115480009|ref|NP_001063598.1|//5.00E-23//Os09g0504900 [Oryza sativa Japonica Group] >gi|113631831|dbj|BAF25512.1| Os09g0504900 [Oryza sativa Japonica Group]	Unigene30130_All//4.00E-32//AT1G50910| unknown protein	Unigene30130_All//0.00E+00//TC143681				nr -
Unigene30132_All	654	2.72	1.01	0.24	1.60	1.63	1.31	0.84	0.45	2.38	-1.43E+00	4.85E-03		-3.48E+00	8.41E-07	Down	2.93E-02	9.80E-01		-2.86E-01	6.89E-01		-9.10E-01	3.19E-01		1.50E+00	1.87E-03		Unigene30132_All//gi|297805766|ref|XP_002870767.1|//1.00E-78//EMB2745 [Arabidopsis lyrata subsp. lyrata] >gi|297316603|gb|EFH47026.1| EMB2745 [Arabidopsis lyrata subsp. lyrata]	Unigene30132_All//8.00E-80//AT5G39710| EMB2745 (EMBRYO DEFECTIVE 2745)					nr +
Unigene30136_All	518	0.30	0.00	0.72	2.12	0.27	0.44	1.63	1.45	1.77	-8.24E+00	2.16E-01		1.25E+00	3.66E-01		-2.99E+00	6.16E-05	Down	-2.28E+00	1.97E-03		-1.69E-01	7.99E-01		1.16E-01	8.57E-01		Unigene30136_All//gi|222137860|gb|ACM45449.1|//3.00E-45//DUO pollen 3 [Arabidopsis thaliana]	Unigene30136_All//5.00E-20//AT1G64570| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Homeodomain-like (InterPro:IPR009057); Has 1675 Blast hits to 1424 proteins in 225 species: Archae - 2; Bacteria - 192; Metazoa - 559; Fungi - 257; Plants - 67; Viruses - 46; Other Eukaryotes - 552 (source: NCBI BLink).						nr +
Unigene30137_All	837	0.00	0.48	0.00	0.95	0.91	0.32	14.09	4.09	4.57	8.92E+00	1.36E-02		null	null		-7.32E-02	9.08E-01		-1.56E+00	6.27E-02		-1.78E+00	8.05E-26	Down	-1.63E+00	1.80E-23	Down	Unigene30137_All//gi|196122040|gb|ACG69194.1|//5.00E-75//germin-like protein 18 [Glycine max]	Unigene30137_All//4.00E-61//AT3G10080| germin-like protein, putative					nr -
Unigene30139_All	582	0.18	0.09	0.46	1.28	0.95	0.85	10.75	5.24	11.16	-1.05E+00	6.84E-01		1.35E+00	4.09E-01		-4.40E-01	5.85E-01		-5.89E-01	4.87E-01		-1.04E+00	1.30E-06	Down	5.35E-02	8.06E-01			Unigene30139_All//5.00E-05//AT4G36910| LEJ2 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 2)	Unigene30139_All//2.00E-81//TC173916				
Unigene30142_All	581	0.18	7.67	0.00	0.09	1.01	0.86	1.02	1.29	1.23	5.41E+00	1.93E-22	Up	-7.49E+00	3.93E-01		3.56E+00	8.14E-03		3.32E+00	2.31E-02		3.46E-01	6.20E-01		2.77E-01	6.90E-01		Unigene30142_All//gi|30680158|ref|NP_172229.2|//1.00E-09//RTFL3 (ROTUNDIFOLIA LIKE 3) [Arabidopsis thaliana] >gi|42822051|tpg|DAA02280.1| TPA_exp: DVL9 [Arabidopsis thaliana] >gi|88900362|gb|ABD57493.1| Atlg07490 [Arabidopsis thaliana]	Unigene30142_All//2.00E-09//AT4G13395| RTFL12 (ROTUNDIFOLIA LIKE 12)	Unigene30142_All//0.00E+00//TC175851				nr +
Unigene30143_All	1947	0.00	13.61	6.95	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.07E-152	Up	1.28E+01	3.69E-76	Up	null	null		null	null		null	null		null	null		Unigene30143_All//gi|110739133|dbj|BAF01483.1|//1.00E-110//pyruvate kinase [Arabidopsis thaliana]	Unigene30143_All//5.00E-110//AT5G63680| pyruvate kinase, putative			ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene30144_All	589	2.84	0.52	0.54	8.63	6.49	3.76	0.86	0.14	0.00	-2.46E+00	4.49E-05	Down	-2.39E+00	1.21E-04	Down	-4.11E-01	1.24E-01		-1.20E+00	6.62E-06	Down	-2.60E+00	2.05E-02		-9.75E+00	5.54E-04	Down		Unigene30144_All//0.00E+00//ES796462					
Unigene30146_All	382	3.29	1.86	1.95	1.83	2.07	0.59	1.33	0.00	0.31	-8.24E-01	1.69E-01		-7.52E-01	2.32E-01		1.84E-01	8.27E-01		-1.63E+00	7.45E-02		-1.04E+01	8.89E-04	Down	-2.09E+00	3.64E-02		Unigene30146_All//gi|75319077|sp|P93008.1|RH21_ARATH//5.00E-06//RecName: Full=DEAD-box ATP-dependent RNA helicase 21	Unigene30146_All//2.00E-07//AT2G33730| DEAD box RNA helicase, putative	Unigene30146_All//2.00E-33//gi|78337290|gb|DT557564.1|DT557564		ko03040|Spliceosome		nr +
Unigene30147_All	449	1.86	0.56	0.00	0.78	1.84	1.91	2.64	2.33	1.33	-1.72E+00	3.63E-02		-1.09E+01	1.19E-04	Down	1.24E+00	1.29E-01		1.30E+00	1.07E-01		-1.80E-01	7.44E-01		-9.86E-01	6.53E-02			Unigene30147_All//5.00E-07//TC178295					
Unigene30150_All	294	2.67	2.07	1.09	2.03	1.76	0.00	3.02	1.42	1.63	-3.68E-01	6.23E-01		-1.30E+00	1.38E-01		-2.11E-01	8.23E-01		-1.10E+01	7.70E-04	Down	-1.09E+00	1.07E-01		-8.93E-01	1.60E-01		Unigene30150_All//gi|22331387|ref|NP_683600.1|//6.00E-11//CLE25 (CLAVATA3/ESR-RELATED 25); protein binding / receptor binding [Arabidopsis thaliana]	Unigene30150_All//6.00E-08//AT3G28455| CLE25 (CLAVATA3/ESR-RELATED 25); protein binding / receptor binding	Unigene30150_All//3.00E-07//TC167055				nr +

Unigene30154_All	319	2.62	1.91	0.17	5.62	5.07	3.68	1.46	0.92	1.25	-4.61E-01	5.43E-01		-3.97E+00	9.08E-04	Down	-1.48E-01	7.95E-01		-6.11E-01	2.28E-01		-6.69E-01	5.09E-01		-2.23E-01	7.90E-01		Unigene30154_All//gi|53749477|gb|AU90330.1|/4.00E-18//Putative receptor kinase-like protein, identical [Solanum demissum]	Unigene30154_All//3.00E-16//AT2G25790| leucine-rich repeat transmembrane protein kinase, putative	Unigene30154_All//4.00E-56//TC179552				nr -
Unigene30157_All	310	9.11	1.14	6.87	3.05	4.67	3.21	0.00	0.00	0.00	-2.99E+00	8.69E-10	Down	-4.08E-01	3.12E-01		6.12E-01	3.04E-01		7.01E-02	9.38E-01		null	null		null	null			Unigene30157_All//8.00E-05//AT3G52720| ACA1 (ALPHA CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	Unigene30157_All//3.00E-38//TC149389		ko00910|Nitrogen metabolism		kegg +
Unigene30161_All	1087	0.05	1.12	0.10	0.00	0.25	0.25	117.08	23.80	91.15	4.54E+00	6.47E-06	Up	1.03E+00	7.03E-01		7.99E+00	7.02E-02		7.96E+00	7.03E-02		-2.30E+00	0.00E+00	Down	-3.61E-01	1.69E-19		Unigene30161_All//gi|15239359|ref|NP_200860.1|//1.00E-141//late embryogenesis abundant protein-related / LEA protein-related [Arabidopsis thaliana] >gi|40823110|gb|AAR92259.1|At5g60520 [Arabidopsis thaliana]	Unigene30161_All//1.00E-137//AT5G60520| late embryogenesis abundant protein-related / LEA protein-related	Unigene30161_All//3.00E-118//TC177555				nr -
Unigene30162_All	272	6.54	0.37	1.57	10.99	8.48	8.97	3.26	0.46	1.03	-4.13E+00	4.10E-08	Down	-2.06E+00	3.27E-04	Down	-3.74E-01	3.17E-01		-2.93E-01	4.68E-01		-2.82E+00	5.65E-04	Down	-1.67E+00	1.33E-02											
Unigene30168_All	572	0.00	0.27	2.05	0.26	0.78	1.90	2.22	1.75	2.86	8.05E+00	2.35E-01		1.10E+01	1.77E-06	Up	1.58E+00	2.17E-01		2.86E+00	4.98E-04	Up	-3.39E-01	5.58E-01		3.65E-01	4.27E-01		Unigene30168_All//gi|297613455|ref|NP_001067177.2|/9.00E-15//Os12g0594200 [Oryza sativa Japonica Group] >gi|255670145|dbj|BAF30196.2|Os12g0594200 [Oryza sativa Japonica Group]	Unigene30168_All//3.00E-56//AT3G50880| INVOLVED IN: protein localization; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Vacuolar protein sorting-associated protein (InterPro:IPR009543); Has 239 Blast hits to 235 proteins in 73 species: Archae - 0; Bacteria - 0; Metazoa - 130; Fungi - 71; Plants - 23; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink).					nr -
Unigene30171_All	489	0.96	0.00	0.44	5.40	2.18	0.55	1.82	0.26	1.22	-9.91E+00	5.55E-03		-1.14E+00	3.32E-01		-1.31E+00	3.87E-04	Down	-3.28E+00	1.17E-10	Down	-2.82E+00	5.65E-04	Down	-5.71E-01	3.71E-01		Unigene30171_All//gi|255579724|ref|XP_002530701.1|/1.00E-06//cyclin d, putative [Ricinus communis] >gi|223529757|gb|EEF31696.1|cyclin d, putative [Ricinus communis]		Unigene30171_All//2.00E-161//DT457600				nr -
Unigene30173_All	838	0.44	0.60	0.32	1.19	0.99	1.62	2.67	8.23	32.99	4.68E-01	6.11E-01		-4.60E-01	6.97E-01		-2.70E-01	7.00E-01		4.44E-01	4.72E-01		1.62E+00	1.50E-13	Up	3.63E+00	6.61E-134	Up	Unigene30173_All//gi|115502172|sp|Q8S0K7.2|EXLB1_ORYSJ//2.00E-88//RecName: Full=Expansin-like B1; AltName: Full=OsEXLB1; AltName: Full=Expensin-related 1; AltName: Full=OsEXPR1; AltName: Full=OsaEXPb3.1; Flags: Precursor	Unigene30173_All//5.00E-48//AT4G17030| ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1)	Unigene30173_All//0.00E+00//TC130252				nr +
Unigene30175_All	296	0.53	1.71	2.88	18.51	16.52	6.10	1.29	0.42	4.17	1.69E+00	1.34E-01		2.44E+00	9.09E-03		-1.64E-01	5.74E-01		-1.60E+00	1.98E-09	Down	-1.60E+00	1.81E-01		1.70E+00	2.59E-03				Unigene30175_All//3.00E-07//TC149341					
Unigene30176_All	518	33.74	33.55	23.23	46.74	33.90	40.54	64.24	47.28	30.69	-7.90E-03	9.77E-01		-5.38E-01	8.75E-05		-4.63E-01	5.79E-06		-2.05E-01	8.57E-02		-4.42E-01	9.85E-08		-1.07E+00	4.11E-34	Down	Unigene30176_All//gi|29826242|gb|AA091861.1|/1.00E-09//TGB12K interacting protein 2 [Nicotiana tabacum]	Unigene30176_All//1.00E-08//AT4G35450| ANK2 (ANKYRIN REPEAT-CONTAINING PROTEIN 2); protein binding	Unigene30176_All//4.00E-165//gi|109880407|gb|DW509377.1|DW509377				nr -
Unigene30177_All	2465	0.28	0.41	0.15	0.10	0.13	0.18	1.01	2.68	8.84	5.75E-01	3.83E-01		-8.68E-01	3.51E-01		3.16E-01	8.38E-01		8.59E-01	4.69E-01		1.40E+00	1.11E-10	Up	3.13E+00	1.27E-92	Up	Unigene30177_All//gi|56561617|emb|CAG28412.1|/1.00E-154//S-receptor kinase-like protein 1 [Senecio squalidus]	Unigene30177_All//7.00E-125//AT1G65790| ARK1 (A. THALIANA RECEPTOR KINASE 1); kinase/ protein kinase/ protein serine/threonine kinase/ transmembrane receptor protein kinase	Unigene30177_All//3.00E-12//BG441915		ko04626|Plant-pathogen interaction		nr +
Unigene30181_All	621	0.00	0.33	0.26	1.76	1.33	11.42	5.38	10.30	21.23	8.35E+00	1.36E-01		8.01E+00	2.39E-01		-4.07E-01	5.61E-01		2.69E+00	2.32E-22	Up	9.37E-01	8.00E-06		1.98E+00	1.10E-33	Up	Unigene30181_All//gi|270271278|gb|ACZ67169.1|//6.00E-75//plant disease resistance response protein [Populus balsamifera]	Unigene30181_All//1.00E-45//AT1G64160| disease resistance-responsive family protein / dirigent family protein	Unigene30181_All//0.00E+00//TC145242				nr -
Unigene30182_All	1103	1.42	0.83	0.82	0.77	1.50	0.57	0.00	0.00	1.19	-7.83E-01	1.36E-01		-7.94E-01	1.48E-01		9.65E-01	6.19E-02		-4.22E-01	6.18E-01		null	null		1.02E+01	1.73E-09	Up	Unigene30182_All//gi|224061845|ref|XP_002300627.1|/7.00E-76//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842353|gb|EEE79900.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene30182_All//1.00E-60//AT1G76420| CUC3 (CUP SHAPED COTYLEDON3); transcription factor	Unigene30182_All//2.00E-116//gi|78348936|gb|DT569210.1|DT569210	NAC			nr -
Unigene30184_All	543	2.12	3.55	1.86	3.12	0.89	0.17	0.39	0.00	0.00	7.42E-01	1.14E-01		-1.86E-01	7.59E-01		-1.81E+00	2.80E-04	Down	-4.23E+00	2.19E-08	Down	-8.60E+00	7.44E-02		-8.60E+00	5.80E-02		Unigene30184_All//gi|224084498|ref|XP_002307317.1|/2.00E-39//f-box family protein [Populus trichocarpa] >gi|222856766|gb|EEE94313.1| f-box family protein [Populus trichocarpa]	Unigene30184_All//1.00E-11//AT5G65590| Dof-type zinc finger domain-containing protein		C2C2-Dof			nr -
Unigene30185_All	517	5.46	0.29	3.19	3.66	3.73	1.92	1.23	1.05	0.54	-4.22E+00	9.18E-13	Down	-7.75E-01	4.74E-02		2.67E-02	9.64E-01		-9.30E-01	5.00E-02		-2.23E-01	7.73E-01		-1.19E+00	1.33E-01				Unigene30185_All//0.00E+00//ES845775					
Unigene30191_All	723	0.72	0.70	1.91	23.56	22.34	12.37	8.60	0.12	0.88	-4.64E-02	9.76E-01		1.40E+00	2.28E-02		-7.71E-02	6.23E-01		-9.30E-01	2.78E-12		-6.22E+00	1.26E-40	Down	-3.29E+00	1.18E-28	Down	Unigene30191_All//gi|15239533|ref|NP_197370.1|/3.00E-12//AGP25 (ARABINOGALACTAN PROTEINS 25) [Arabidopsis thaliana] >gi|75127081|sp|Q6NN00.1|AGP25_ARATH RecName: Full=Classical arabinogalactan protein 25; Flags: Precursor >gi|38454062|gb|AAR20725.1|At5g18690 [Arabidopsis thaliana] >gi|41349912|gb|AAS00341.1|At5g18690 [Arabidopsis thaliana]		Unigene30191_All//0.00E+00//TC168069				nr +
Unigene30195_All	1763	1.01	0.57	0.12	14.47	7.32	6.53	1.01	0.33	1.20	-8.12E-01	9.59E-02		-3.06E+00	3.81E-06	Down	-9.82E-01	2.68E-22		-1.15E+00	2.51E-25	Down	-1.60E+00	5.26E-04	Down	2.50E-01	5.50E-01		Unigene30195_All//gi|15242143|ref|NP_200556.1|/0.00E+00//AAA-type ATPase family protein [Arabidopsis thaliana]	Unigene30195_All//0.00E+00//AT5G57480| AAA-type ATPase family protein	Unigene30195_All//0.00E+00//TC139256				nr +
Unigene30198_All	619	2.20	0.33	1.03	1.69	2.00	1.31	0.41	0.27	0.32	-2.75E+00	1.08E-04	Down	-1.09E+00	7.48E-02		2.45E-01	7.39E-01		-3.64E-01	6.33E-01		-6.01E-01	6.48E-01		-3.49E-01	7.66E-01		Unigene30198_All//gi|600118|emb|CAA84230.1|/3.00E-14//extensin-like protein [Zea mays] >gi|1096557|prf|2111476A extensin-like domain		Unigene30198_All//3.00E-09//TC167127		ko00040|Spliceosome//ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene3020_All	1368	12.47	28.56	28.03	55.53	33.03	37.64	223.86	114.85	98.08	1.20E+00	7.00E-38	Up	1.17E+00	8.46E-35	Up	-7.50E-01	1.87E-41		-5.61E-01	3.87E-22		-9.63E-01	8.48E-253		-1.19E+00	0.00E+00	Down	Unigene3020_All//gi|33411520|dbj|BAC81420.1|/1.00E-173//nitrate transporter [Prunus persica]	Unigene3020_All//1.00E-122//AT1G12110| NRT1.1; nitrate transmembrane transporter/ transporter	Unigene3020_All//0.00E+00//TC165574				nr -
Unigene30204_All	440	6.18	1.15	1.45	8.94	3.76	2.05	4.52	0.48	0.91	-2.42E+00	1.10E-07	Down	-2.09E+00	3.48E-06	Down	-1.25E+00	1.63E-05	Down	-2.12E+00	6.60E-10	Down	-3.25E+00	3.61E-09	Down	-2.32E+00	6.40E-07	Down	Unigene30204_All//gi|224080516|ref|XP_002306147.1|/5.00E-42//SAUR family protein [Populus trichocarpa] >gi|222849111|gb|EEE86658.1| SAUR family protein [Populus trichocarpa]	Unigene30204_All//5.00E-39//AT4G34760| auxin-responsive family protein	Unigene30204_All//1.00E-29//DW503189				nr -
Unigene30205_All	933	0.00	0.00	0.00	0.00	0.00	0.00	1.77	1.97	3.54	null	null		null	null		null	null		null	null		1.58E-01	7.24E-01		1.00E+00	7.62E-04	Up	Unigene30205_All//gi|45593281|gb|AA568190.1|/7.00E-68//Myb transcription factor [Vitis vinifera]	Unigene30205_All//2.00E-56//AT3G13540| ATMYB5 (MYB DOMAIN PROTEIN 5); DNA binding / transcription factor	Unigene30205_All//0.00E+00//gi|78354131|gb|DT574405.1|DT574405	MYB			nr +
Unigene30207_All	387	0.54	2.23	4.40	2.83	1.78	1.05	1.09	1.30	0.72	2.04E+00	1.59E-02		3.03E+00	6.93E-06	Up	-6.70E-01	3.06E-01		-1.43E+00	3.46E-02		2.46E-01	7.84E-01		-6.00E-01	5.53E-01		Unigene30207_All//gi|145337595|ref|NP_177713.3|/3.00E-62//VPS35B (VPS35 HOMOLOG B) [Arabidopsis thaliana]	Unigene30207_All//1.00E-63//AT1G75850| VPS35B (VPS35 HOMOLOG B)	Unigene30207_All//4.00E-07//TC140280				nr -
Unigene30208_All	407	3.86	0.50	0.79	5.14	2.54	3.44	0.21	0.82	0.59	-2.95E+00	1.18E-05	Down	-2.30E+00	3.17E-04	Down	-1.02E+00	1.57E-02		-5.80E-01	2.11E-01		1.98E+00	1.44E-01		1.50E+00	3.39E-01				Unigene30208_All//4.00E-137//TC154327					
Unigene30211_All	303	0.00	0.00	0.00	2.14	3.07	1.34	3.49	0.41	0.26	null	null		null	null		5.22E-01	5.25E-01		-6.72E-01	4.78E-01		-3.08E+00	6.12E-05	Down	-3.73E+00	6.13E-06	Down			Unigene30211_All//8.00E-107//gi|78333297|gb|DT553571.1|DT553571					
Unigene30212_All	467	2.80	3.47	1.60	3.84	0.81	1.64	1.27	1.79	2.39	3.10E-01	5.64E-01		-8.11E-01	1.90E-01		-2.24E+00	9.32E-06	Down	-1.22E+00	1.31E-02		4.98E-01	4.86E-01		9.14E-01	1.03E-01				Unigene30212_All//9.00E-09//TC131237					
Unigene30213_All	504	6.12	1.01	1.06	16.31	15.10	7.44	0.00	0.00	0.16	-2.61E+00	2.67E-09	Down	-2.54E+00	1.45E-08	Down	-1.11E-01	6.23E-01		-1.13E+00	2.09E-08	Down	null	null		7.30E+00	4.04E-01				Unigene30213_All//0.00E+00//DW506989					
Unigene30215_All	606	3.45	2.34	2.81	2.14	2.56	2.98	2.23	0.69	0.33	-5.61E-01	2.13E-01		-2.97E-01	5.35E-01		2.59E-01	6.64E-01		4.80E-01	3.66E-01		-1.69E+00	1.96E-03		-2.76E+00	7.51E-06	Down	Unigene30215_All//gi|18424254|ref|NP_568910.1|/2.00E-16//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|15450687|gb|AAK96615.1|AT5g59550/f2o15_210 [Arabidopsis thaliana] >gi|17380612|gb|AAL36069.1|AT5g59550/f2o15_210 [Arabidopsis thaliana] >gi|110735082|gb|ABG89111.1|ubiquitin-interacting factor 1b [synthetic construct]	Unigene30215_All//9.00E-14//AT1G55530| zinc finger (C3HC4-type RING finger) family protein	Unigene30215_All//0.00E+00//AI725476				nr +
Unigene30221_All	617	0.00	0.33	2.24	1.05	1.34	1.46	2.19	2.51	1.55	8.36E+00	1.36E-01		1.11E+01	1.23E-07	Up	3.52E-01	6.87E-01		4.80E-01	5.50E-01		1.93E-01	6.95E-01		-5.01E-01	3.22E-01		Unigene30221_All//gi|224073090|ref|XP_002303967.1|/1.00E-75//SET domain protein [Populus trichocarpa] >gi|222841399|gb|EEE78946.1| SET domain protein [Populus trichocarpa]	Unigene30221_All//6.00E-69//AT1G73100| SUVH3 (SU(VAR)3-9 HOMOLOG 3); histone methyltransferase	Unigene30221_All//0.00E+00//TC171813		ko00310|Lysine degradation		nr +
Unigene30224_All	916	0.00	5.03	2.27	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.84E-26	Up	1.11E+01	1.92E-11	Up	null	null		null	null		null	null		null	null											
Unigene30225_All	254	3.09	0.20	6.92	3.14	4.07	2.67	0.50	1.81	0.78	-3.95E+00	8.54E-04	Down	1.16E+00	2.63E-02		3.74E-01	6.04E-01		-2.35E-01	7.54E-01		1.86E+00	8.80E-02		6.51E-01	6.65E-01				Unigene30225_All//1.00E-43//TC145852					
Unigene3023_All	1850	5.77	5.48	3.45	11.61	12.29	11.84	7.18	4.68	3.04	-7.48E-02	6.81E-01		-7.40E-01	4.36E-05		8.21E-02	5.73E-01		2.89E-02	8.48E-01		-6.18E-01	6.95E-06		-1.24E+00	8.34E-18	Down	Unigene3023_All//gi|75168878|sp|Q9C518.1|TCP8_ARATH//2.00E-66//RecName: Full=Transcription factor TCP8 >gi|30725660|gb|AAP37852.1|At1g58100 [Arabidopsis thaliana]	Unigene3023_All//1.00E-67//AT1G58100| TCP family transcription factor, putative	Unigene3023_All//0.00E+00//TC135656	TCP			nr +
Unigene30231_All	820	1.15	0.00	1.82	3.89	2.18	4.08	0.15	0.00	0.05	-1.02E+01	1.46E-05	Down	6.63E-01	2.44E-01		-8.32E-01	1.12E-02		6.81E-02	8.64E-01		-7.27E+00	2.35E-01		-1.67E+00	4.77E-01		Unigene30231_All//gi|115476382|ref|NP_001061787.1|/8.00E-15//Os08g0411300 [Oryza sativa Japonica Group] >gi|113623756|dbj|BAF23701.1|Os08g0411300 [Oryza sativa Japonica Group]	Unigene30231_All//1.00E-38//AT4G39840| unknown protein	Unigene30231_All//5.00E-178//CO121393				nr +
Unigene30233_All	643	1.22	0.00	0.58	1.01	1.71	1.69	1.64	1.69	0.99	-1.03E+01	1.09E-04	Down	-1.07E+00	2.10E-01		7.67E-01	2.69E-01		7.43E-01	2.89E-01		3.99E-02	9.73E-01		-7.30E-01	2.01E-01		Unigene30233_All//gi|115482418|ref|NP_001061802.1|/4.00E-22//Os10g0466100 [Oryza sativa Japonica Group] >gi|113639411|dbj|BAF26716.1|Os10g0466100 [Oryza sativa Japonica Group]	Unigene30233_All//6.00E-32//AT3G23235| unknown protein	Unigene30233_All//0.00E+00//DW497526				nr -
Unigene30235_All	313	268.79	198.15	228.65	76.87	73.27	41.84	1.76	0.27	0.00	-4.40E-01	6.92E-15		-2.33E-01	8.11E-05		-6.92E-02	5.99E-01		-8.77E-01	1.48E-15		-2.72E+00	1.22E-02		-1.08E+01	2.80E-04	Down	Unigene30235_All//gi|13676400|dbj|BAB41189.1|/3.00E-55//NADPH-protochlorophyllide oxidoreductase 1 [Amaranthus tricolor]	Unigene30235_All//5.00E-45//AT4G27440| PORB (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE B); oxidoreductase/ protochlorophyllide reductase	Unigene30235_All//7.00E-175//gi|164370317|gb|ES841485.1|ES841485		ko00860|Porphyrin and chlorophyll metabolism		nr +

Unigene30236_All	500	6.70	2.23	4.90	4.28	2.82	0.81	0.00	0.00	0.00	-1.59E+00	1.13E-05	Down	-4.51E-01	2.16E-01		-6.01E-01	1.65E-01		-2.40E+00	1.86E-06	Down	null	null		null	null		Unigene30236_All//gi|255587680|ref|XP_002534354.1|//8.00E-13//Transcription factor ICE1, putative [Ricinus communis] >gi|223525438|gb|EEF28027.1| Transcription factor ICE1, putative [Ricinus communis]		Unigene30236_All//3.00E-15//ES803422				nr -
Unigene30237_All	803	0.00	0.50	0.00	0.87	1.72	0.90	7.95	0.62	3.72	8.98E+00	1.36E-02		null	null		9.82E-01	9.11E-02		5.12E-02	9.48E-01		-3.67E+00	3.24E-31	Down	-1.10E+00	1.49E-07	Down	Unigene30237_All//gi|297598701|ref|XP_001646103.2|//1.00E-56//Os02g0183000 [Oryza sativa Japonica Group] >gi|255670656|dbj|BAF08017.2| Os02g0183000 [Oryza sativa Japonica Group]	Unigene30237_All//1.00E-61//AT2G12646| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF597 (InterPro:IPR006734); BEST Arabidopsis thaliana protein match is: zinc-binding protein, putative (TAIR:AT3G60670.1); Has 191 Blast hits to 191 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 191; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene30237_All//6.00E-76//gi|3325907|gb|AI054793.1|AI054793	PLATZ			nr -
Unigene30238_All	341	1.38	1.04	0.94	1.02	2.12	2.38	2.85	2.21	23.95	-4.09E-01	6.69E-01		-5.60E-01	6.28E-01		1.05E+00	2.40E-01		1.22E+00	1.40E-01		-3.70E-01	5.87E-01		3.07E+00	1.61E-34	Up	Unigene30238_All//gi|79312708|ref|NP_001030628.1|//9.00E-19//NADH:ubiquinone oxidoreductase family protein [Arabidopsis thaliana]	Unigene30238_All//5.00E-20//AT3G03100| NADH:ubiquinone oxidoreductase family protein	Unigene30238_All//1.00E-59//BG441770		ko00190|Oxidative phosphorylation		nr -
Unigene30239_All	396	0.92	3.33	1.88	0.63	1.30	2.28	2.24	1.90	0.30	1.85E+00	3.97E-03		1.03E+00	2.37E-01		1.05E+00	3.49E-01		1.86E+00	2.18E-02		-2.39E-01	7.21E-01		-2.89E+00	3.04E-04	Down	Unigene30239_All//gi|211906462|gb|ACJ11724.1|//1.00E-58//glutamine synthase [Gossypium hirsutum]	Unigene30239_All//6.00E-56//AT3G17820| ATG5KB6: copper ion binding / glutamate-ammonia ligase	Unigene30239_All//0.00E+00//TC177144		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene3024_All	2140	4.50	1.75	3.06	4.96	4.94	5.07	5.53	2.64	2.55	-1.36E+00	5.55E-12	Down	-5.56E-01	3.95E-03		-5.30E-03	9.71E-01		3.08E-02	8.95E-01		-1.07E+00	2.27E-12	Down	-1.12E+00	1.20E-13	Down	Unigene3024_All//gi|87241379|gb|ABD33237.1|//1.00E-122//Pentatricopeptide repeat [Medicago truncatula]	Unigene3024_All//1.00E-113//AT2G30780| pentatricopeptide (PPR) repeat-containing protein	Unigene3024_All//0.00E+00//gi|21093586|gb|BQ405899.1|BQ405899			GO:0043231	nr +
Unigene30242_All	684	16.29	34.22	10.90	23.67	23.36	24.56	58.29	90.99	121.67	1.07E+00	2.21E-19	Up	-5.80E-01	1.04E-03		-1.90E-02	9.09E-01		5.35E-02	7.36E-01		6.42E-01	3.15E-26		1.06E+00	7.38E-83	Up	Unigene30242_All//gi|15232394|ref|NP_190970.1|//1.00E-113//phosphatidic acid phosphatase-related / PAP2-related [Arabidopsis thaliana] >gi|226550034|gb|AAM98108.1| At3g54020/F5K20_320 [Arabidopsis thaliana]	Unigene30242_All//5.00E-105//AT3G54020| phosphatidic acid phosphatase-related / PAP2-related	Unigene30242_All//0.00E+00//TC132955				nr +
Unigene30245_All	413	0.51	2.45	2.71	0.60	2.33	1.42	0.82	2.33	7.52	2.28E+00	4.09E-03		2.42E+00	2.21E-03		1.95E+00	1.16E-02		1.24E+00	2.31E-01		1.51E+00	2.24E-02		3.20E+00	4.65E-14	Up			Unigene30245_All//5.00E-84//DT464140				
Unigene30246_All	365	0.57	0.00	0.29	4.09	2.17	0.99	2.55	0.80	1.64	-9.16E+00	1.22E-01		-9.75E-01	6.21E-01		-9.16E-01	7.91E-02		-2.05E+00	5.54E-04	Down	-1.67E+00	1.45E-02		-6.38E-01	3.08E-01		Unigene30246_All//gi|297598338|ref|NP_001045419.2|//2.00E-16//Os01g0952300 [Oryza sativa Japonica Group] >gi|255674079|dbj|BAF07333.2| Os01g0952300 [Oryza sativa Japonica Group]	Unigene30246_All//8.00E-17//AT5G19420| Ran GTPase binding / chromatin binding / zinc ion binding				nr +
Unigene30248_All	530	1.48	0.38	0.00	1.60	0.52	0.34	1.99	0.47	1.13	-1.95E+00	2.62E-02		-1.05E+01	2.22E-04	Down	-1.62E+00	3.13E-02		-2.23E+00	9.52E-03		-2.08E+00	1.78E-03		-8.23E-01	1.50E-01									
Unigene3025_All	2867	1.90	0.69	0.58	17.27	10.59	8.93	14.07	7.70	3.61	-1.46E+00	7.89E-08	Down	-1.72E+00	3.17E-09	Down	-7.05E-01	2.15E-24		-9.51E-01	6.14E-36		-8.70E-01	9.29E-29		-1.96E+00	2.45E-101	Down	Unigene3025_All//gi|193870826|gb|ACF23000.1|//1.00E-154//heat shock-like protein [Arabidopsis thaliana]	Unigene3025_All//1.00E-132//AT4G29920| heat shock protein-related					nr -
Unigene30252_All	529	1.19	0.19	0.00	1.70	2.28	2.13	1.84	0.24	0.75	-2.63E+00	1.78E-02		-1.02E+01	1.41E-03		4.27E-01	5.52E-01		3.33E-01	6.22E-01		-2.96E+00	1.89E-04	Down	-1.29E+00	3.62E-02		Unigene30252_All//gi|297817792|ref|XP_002876779.1|//5.00E-21//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322617|gb|EFH53038.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene30252_All//3.00E-16//AT2G01818| zinc ion binding	Unigene30252_All//0.00E+00//ES832355				nr -
Unigene30257_All	405	10.72	26.40	22.09	12.30	21.34	24.76	9.50	15.27	29.31	1.30E+00	2.55E-12	Up	1.04E+00	2.95E-07	Up	7.95E-01	1.91E-05		1.01E+00	2.20E-08	Up	6.85E-01	1.19E-03		1.63E+00	2.25E-23	Up	Unigene30257_All//gi|78059502|gb|AB118115.1|//8.00E-11//RPN9 [Nicotiana benthamiana]	Unigene30257_All//5.00E-11//AT5G45620| 26S proteasome regulatory subunit, putative (RPN9)	Unigene30257_All//9.00E-55//TC152997		ko03050|Proteasome		nr +
Unigene30258_All	257	32.57	16.36	17.40	25.59	27.33	32.16	96.73	48.30	33.79	-9.93E-01	1.07E-06		-9.04E-01	1.54E-05		9.54E-02	7.41E-01		3.30E-01	1.26E-01		-1.00E+00	1.24E-22	Down	-1.52E+00	5.71E-44	Down			Unigene30258_All//5.00E-129//TC152190				
Unigene30260_All	2181	0.00	0.05	0.00	0.11	0.24	0.08	5.84	5.63	22.47	5.54E+00	3.87E-01		null	null		1.05E+00	3.49E-01		-4.64E-01	7.44E-01		-5.06E-02	7.60E-01		1.95E+00	4.26E-120	Up	Unigene30260_All//gi|38112427|gb|AR11299.1|//1.00E-125//lectin-like receptor kinase 7;2 [Medicago truncatula]	Unigene30260_All//6.00E-110//AT5G60280| lectin protein kinase family protein			ko04626|Plant-pathogen interaction		nr -
Unigene30261_All	646	0.00	0.78	0.00	0.08	0.00	0.14	0.85	3.36	1.42	9.62E+00	4.04E-03		null	null		-6.27E+00	5.55E-01		8.59E-01	7.94E-01		1.98E+00	4.73E-06	Up	7.37E-01	2.43E-01		Unigene30261_All//gi|224075299|ref|XP_002304589.1|//8.00E-28//nbs-lrr resistance protein [Populus trichocarpa] >gi|222842021|gb|EEE79568.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene30261_All//2.00E-08//AT5G48620| disease resistance protein (CC-NBS-LRR class), putative			ko04626|Plant-pathogen interaction		nr -
Unigene30262_All	574	0.46	0.97	1.21	1.04	3.90	3.07	1.84	0.58	3.19	1.09E+00	2.74E-01		1.40E+00	1.39E-01		1.90E+00	2.60E-05	Up	1.56E+00	2.61E-03		-1.66E+00	8.55E-03		7.94E-01	5.61E-02									
Unigene30263_All	355	9.14	1.71	5.40	4.49	3.30	1.78	0.00	0.00	0.00	-2.42E+00	5.43E-09	Down	-7.59E-01	3.56E-02		-4.45E-01	4.08E-01		-1.33E+00	1.23E-02		null	null		null	null				Unigene30263_All//4.00E-07//TC154804				
Unigene30266_All	538	0.58	3.58	1.39	2.59	1.34	1.43	0.63	0.31	0.30	2.62E+00	5.09E-06	Up	1.25E+00	1.54E-01		-9.48E-01	8.16E-02		-8.61E-01	1.34E-01		-1.02E+00	4.00E-01		-1.09E+00	3.55E-01									
Unigene30267_All	573	1.10	1.06	2.23	1.48	7.39	4.89	0.81	0.44	1.04	-4.63E-02	9.72E-01		1.03E+00	1.03E-01		2.32E+00	2.86E-12	Up	1.73E+00	1.64E-05	Up	-8.91E-01	3.84E-01		3.62E-01	6.37E-01				Unigene30267_All//3.00E-46//CO128436				
Unigene30268_All	366	0.00	0.00	0.15	0.54	0.75	0.12	23.80	11.99	5.77	null	null		7.18E+00	6.36E-01		4.67E-01	8.17E-01		-2.14E+00	3.47E-01		-9.89E-01	2.71E-08		-2.04E+00	9.63E-24	Down			Unigene30268_All//5.00E-127//TC151599				
Unigene30270_All	459	0.46	2.54	0.12	0.87	0.75	0.39	0.92	0.46	0.17	2.48E+00	9.79E-04	Up	-1.97E+00	3.81E-01		-2.11E-01	8.25E-01		-1.14E+00	3.79E-01		-1.02E+00	3.50E-01		-2.41E+00	3.94E-02		Unigene30270_All//gi|224082468|ref|XP_002306703.1|//6.00E-32//SET domain protein [Populus trichocarpa] >gi|222856152|gb|EEE93699.1| SET domain protein [Populus trichocarpa]	Unigene30270_All//3.00E-13//AT1G43245| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; CONTAINS InterPro DOMAIN/s: SET (InterPro:IPR001214); Has 432 Blast hits to 430 proteins in 119 species: Archae - 0; Bacteria - 0; Metazoa - 212; Fungi - 80; Plants - 47; Viruses - 3; Other Eukaryotes - 90 (source: NCBI BLink).	Unigene30270_All//2.00E-127//gi|21091568|gb|BQ403881.1|BQ403881				nr -
Unigene30271_All	731	0.00	0.83	0.00	0.00	0.09	0.00	1.45	2.69	4.03	9.70E+00	1.17E-03		null	null		6.56E+00	6.10E-01		null	null		8.94E-01	3.10E-02		1.48E+00	1.01E-05	Up	Unigene30271_All//gi|255585638|ref|XP_002533505.1|//1.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223526629|gb|EEF28874.1| conserved hypothetical protein [Ricinus communis]		Unigene30271_All//1.00E-138//TC137735				nr -
Unigene30272_All	719	0.00	0.00	0.00	0.00	0.00	0.00	8.41	2.03	5.04	null	null		null	null		null	null		null	null		-2.05E+00	3.32E-16	Down	-7.38E-01	3.89E-04		Unigene30272_All//gi|224126143|ref|XP_002319765.1|//1.00E-47//hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase-like protein [Populus trichocarpa] >gi|222858141|gb|EEE95688.1| hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase-like protein [Populus trichocarpa]	Unigene30272_All//2.00E-39//AT5G17540| transferase family protein	Unigene30272_All//4.00E-12//ES842370		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene30273_All	380	1.65	1.07	2.52	5.90	4.08	1.07	2.23	0.33	1.15	-6.31E-01	4.75E-01		6.10E-01	3.86E-01		-5.33E-01	2.14E-01		-2.46E+00	6.31E-07	Down	-2.75E+00	9.73E-04	Down	-9.48E-01	1.47E-01									
Unigene30274_All	614	0.00	0.83	0.00	0.97	0.73	0.59	0.41	3.00	1.88	9.69E+00	4.04E-03		null	null		-4.17E-01	6.27E-01		-7.27E-01	4.60E-01		2.86E+00	1.36E-07	Up	2.19E+00	4.81E-04	Up	Unigene30274_All//gi|87240761|gb|AB032619.1|//2.00E-08//Cyclin-like F-box [Medicago truncatula]	Unigene30274_All//3.00E-08//AT1G47056| VFB1 (VIER F-BOX PROTEINE 1); ubiquitin-protein ligase	Unigene30274_All//8.00E-19//TC158328				nr -
Unigene30276_All	1026	2.45	0.79	1.51	6.21	5.03	1.89	0.33	0.20	0.35	-1.63E+00	1.33E-04	Down	-7.02E-01	9.42E-02		-3.04E-01	2.16E-01		-1.72E+00	6.08E-12	Down	-6.95E-01	5.77E-01		8.41E-02	9.57E-01		Unigene30276_All//gi|87247485|gb|AB035825.1|//2.00E-72//shattering protein [Oryza nivara] >gi|87247487|gb|AB035826.1| shattering protein [Oryza nivara]	Unigene30276_All//1.00E-51//AT2G35640| hydroxyproline-rich glycoprotein family protein	Unigene30276_All//0.00E+00//gi|78328358|gb|DT548632.1|DT548632				nr -
Unigene30279_All	585	0.00	0.00	0.00	1.53	0.29	0.00	5.64	4.57	3.88	null	null		null	null		-2.38E+00	2.29E-03		-1.06E+01	1.21E-05	Down	-3.02E-01	3.68E-01		-5.38E-01	6.78E-02									
Unigene30281_All	584	66.74	16.57	24.98	106.62	79.43	131.47	146.97	47.88	49.18	-2.01E+00	2.15E-80	Down	-1.42E+00	1.76E-47	Down	-4.25E-01	2.05E-12		3.02E-01	1.72E-07		-1.62E+00	7.75E-160	Down	-1.58E+00	8.56E-159	Down	Unigene30281_All//gi|209967443|gb|ACJ02350.1|//9.00E-89//60S ribosomal protein L13A [Vernicia fordii]	Unigene30281_All//1.00E-82//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene30281_All//0.00E+00//gi|21095060|gb|BQ407373.1|BQ407373		ko03010|Ribosome		nr -
Unigene30283_All	485	0.43	0.10	0.00	3.70	2.91	2.42	1.92	0.69	0.25	-2.05E+00	3.34E-01		-8.75E+00	1.46E-01		-3.45E-01	5.12E-01		-6.11E-01	2.28E-01		-1.48E+00	2.77E-02		-2.96E+00	1.72E-04	Down			Unigene30283_All//6.00E-07//TC176438				
Unigene30284_All	344	268.60	248.78	264.39	366.08	294.00	380.87	193.21	91.00	53.16	-1.11E-01	5.88E-02		-2.28E-02	7.21E-01		-3.16E-01	2.42E-14		5.72E-02	3.05E-01		-1.09E+00	2.07E-67	Down	-1.86E+00	2.99E-155	Down	Unigene30284_All//gi|255677281|dbj|BAF20135.2| Os06g0650100 [Oryza sativa Japonica Group]	Unigene30284_All//1.00E-49//AT1G31340| RUB1 (RELATED TO UBIQUITIN 1); protein binding	Unigene30284_All//0.00E+00//TC166692				nr +
Unigene30286_All	442	3.55	0.23	0.96	1.69	1.87	1.63	0.86	0.76	0.90	-3.95E+00	5.06E-07	Down	-1.88E+00	1.82E-03		1.45E-01	8.70E-01		-4.82E-02	9.50E-01		-1.87E-01	8.57E-01		6.62E-02	9.66E-01		Unigene30286_All//gi|225445386|ref|XP_002281711.1|//5.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene30286_All//6.00E-06//AT2G29760| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene30287_All	821	5.74	0.25	0.00	1.70	2.64	1.32	0.00	0.00	0.00	-4.54E+00	5.77E-22	Down	-1.25E+01	5.92E-26	Down	6.37E-01	1.55E-01		-3.64E-01	5.56E-01		null	null		null	null		Unigene30287_All//gi|37051131|dbj|BAC81662.1|//2.00E-59//DNA binding with one finger 5 protein [Pisum sativum]	Unigene30287_All//7.00E-42//AT3G50410| OBP1 (OBF BINDING PROTEIN 1); DNA binding / protein binding / transcription factor	Unigene30287_All//9.00E-41//gi|109876744|gb|DW505718.1|DW505718	C2C2-Dof	ko03040|Spliceosome		nr -
Unigene30288_All	307	0.00	0.00	4.16	1.46	0.90	1.62	1.10	0.00	1.95	null	null		1.20E+01	4.69E-07	Up	-7.03E-01	5.30E-01		1.48E-01	9.06E-01		-1.01E+01	1.17E-02		8.21E-01	3.20E-01		Unigene30288_All//gi|124359893|gb|ABN07919.1|//6.00E-24//Zinc finger, N-recognin; WD40-like [Medicago truncatula]	Unigene30288_All//7.00E-13//AT3G02260| BIG (BIG); binding / ubiquitin-protein ligase/ zinc ion binding	Unigene30288_All//7.00E-58//TC160407				nr -
Unigene30289_All	405	0.52	0.00	0.00	0.98	1.45	1.56	2.09	0.00	0.20	-9.01E+00	1.22E-01		-9.01E+00	1.46E-01		5.55E-01	5.99E-01		6.66E-01	4.92E-01		-1.10E+01	4.39E-06	Down	-3.41E+00	1.35E-04	Down	Unigene30289_All//gi|15239612|ref|NP_197394.1|//2.00E-54//BUD2 (BUSHY AND DWARF 2); adenosylmethionine decarboxylase [Arabidopsis thaliana] >gi|78098576|gb|ABB20589.1| S-adenosylmethionine decarboxylase [Arabidopsis thaliana]	Unigene30289_All//1.00E-55//AT5G18930| BUD2 (BUSHY AND DWARF 2); adenosylmethionine decarboxylase	Unigene30289_All//2.00E-120//TC160079		ko00270|Cysteine and methionine metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene3029_All	1717	22.85	15.67	10.98	23.01	23.59	28.54	20.29	9.15	9.49	-5.44E-01	1.67E-10		-1.06E+00	2.51E-30	Down	3.58E-02	7.70E-01		3.11E-01	2.83E-05		-1.15E+00	5.29E-39	Down	-1.10E+00	2.59E-37	Down	Unigene3029_All//gi|8648949|emb|CAA51273.2|//1.00E-177//dihydrodipicolinate synthase [Populus trichocarpa x Populus deltoides]	Unigene3029_All//3.00E-178//AT2G45440| DHDPS2 (DIHYDRODIPICOLINATE SYNTHASE); catalytic/ dihydrodipicolinate synthase/ lyase	Unigene3029_All//0.00E+00//TC133968		ko00300|Lysine biosynthesis	GO:0009089//GO:0016836	nr -
Unigene30290_All	445	1.06	3.87	3.35	2.13	2.40	1.42	0.10	0.38	0.36	1.87E+00	6.55E-04	Up	1.66E+00	5.94E-03		1.74E-01	8.16E-01		-5.82E-01	4.37E-01		1.98E+00	3.79E-01		1.91E+00	3.77E-01									

Unigene30291_All	710	1.03	0.00	1.65	1.54	0.92	0.06	2.56	0.88	1.29	-1.00E+01	2.11E-04	Down	6.77E-01	3.04E-01		-7.44E-01	2.45E-01		-4.60E+00	8.28E-06	Down	-1.54E+00	6.84E-04	Down	-9.89E-01	1.76E-02		Unigene30291_All//gi|66841323|dbj|BAD99219.1|//1.00E-15//polypeptide with a gag-like domain [Petunia x hybrida]	Unigene30291_All//6.00E-05//AT1G21280| unknown protein					nr -
Unigene30292_All	440	0.00	1.84	0.73	0.45	1.49	0.51	1.73	2.56	3.17	1.08E+01	9.38E-05	Up	9.50E+00	4.52E-02		1.72E+00	8.16E-02		1.80E-01	9.35E-01		5.68E-01	3.44E-01		8.74E-01	7.41E-02		Unigene30292_All//gi|240254272|ref|NP_564685.4|//3.00E-38//SR33; RNA binding / protein binding [Arabidopsis thaliana] >gi|6572475|gb|AAF17288.1|AF099940_1 Serine/arginine-rich protein [Arabidopsis thaliana] >gi|9843659|emb|CAC03603.1| SC35-like splicing factor SCL33, 33 kD [Arabidopsis thaliana] >gi|56744214|gb|AAW28547.1|At1g55310 [Arabidopsis thaliana]	Unigene30292_All//2.00E-39//AT1G55310| SR33; RNA binding / protein binding	Unigene30292_All//0.00E+00//D8462398				nr +
Unigene30294_All	267	3.72	0.38	1.60	7.46	3.10	7.95	4.12	1.57	3.28	-3.29E+00	3.81E-04	Down	-1.22E+00	1.00E-01		-1.27E+00	3.55E-03		9.13E-02	8.58E-01		-1.40E+00	2.04E-02		-3.27E-01	5.82E-01		Unigene30294_All//gi|115481106|ref|NP_001064146.1|//7.00E-12//Os10g0141900 [Oryza sativa Japonica Group] >gi|16519465|gb|AAL25174.1|AC079852_7 Putative tRNA-guanine transglycosylase [Oryza sativa] >gi|19919982|gb|AAM08430.1|AC112513_16 Putative tRNA-guanine transglycosylase [Oryza sativa] >gi|31430120|gb|AAP52078.1| tRNA-guanine transglycosylases, various specificities family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|10288598|gb|AB065910.1| tRNA-guanine transglycosylases, various specificities family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113638755|dbj|BAF26060.1|Os10g0141900 [Oryza sativa Japonica Group]		Unigene30294_All//2.00E-137//gi|78322814|gb|DT543088.1|DT543088				nr -
Unigene30295_All	574	2.37	3.88	7.70	0.52	0.00	0.00	0.00	0.00	0.00	7.13E-01	9.64E-02		1.70E+00	1.60E-07	Up	-9.02E+00	2.01E-02		-9.02E+00	4.00E-02		null	null		null	null		Unigene30295_All//gi|3893085|emb|CAA10192.1|//2.00E-11//glycine-rich protein 2 [Cicer arietinum]				ko03040|Spliceosome		nr +
Unigene30296_All	880	1.25	1.27	0.18	6.45	5.09	2.93	0.72	0.29	0.27	2.08E-02	9.87E-01		-2.78E+00	1.00E-03		-3.43E-01	1.80E-01		-1.14E+00	4.43E-06	Down	-1.34E+00	1.13E-01		-1.41E+00	7.94E-02		Unigene30296_All//gi|16649129|gb|AAL24416.1|//4.00E-31//Unknown protein [Arabidopsis thaliana] >gi|20198107|gb|AAD25563.2| expressed protein [Arabidopsis thaliana]	Unigene30296_All//8.00E-34//AT2G38820| unknown protein	Unigene30296_All//0.00E+00//gi|109847140|gb|DW476120.1|DW476120				nr +
Unigene30297_All	376	0.97	0.67	4.39	1.85	0.18	2.04	1.24	0.44	0.64	-5.32E-01	6.27E-01		2.17E+00	3.37E-04	Up	-3.34E+00	1.25E-03		1.39E-01	8.78E-01		-1.48E+00	1.53E-01		-9.60E-01	3.13E-01		Unigene30297_All//gi|6579196|gb|AAF18239.1|AC011438_1//1.00E-16//T23G18.5 [Arabidopsis thaliana]		Unigene30297_All//1.00E-22//CO098816				nr +
Unigene30298_All	699	1.65	0.43	0.38	2.42	0.34	1.29	1.15	0.96	1.65	-1.92E+00	5.78E-03		-2.11E+00	4.75E-03		-2.81E+00	5.97E-07	Down	-9.07E-01	7.45E-02		-2.65E-01	7.04E-01		5.24E-01	3.53E-01		Unigene30298_All//gi|15240153|ref|NP_201497.1|//3.00E-84//prolyl oligopeptidase family protein [Arabidopsis thaliana] >gi|9758541|dbj|BAB08935.1|protease-like [Arabidopsis thaliana]	Unigene30298_All//2.00E-85//AT5G66960| prolyl oligopeptidase family protein	Unigene30298_All//6.00E-131//ES828640				nr +
Unigene30299_All	508	0.10	0.90	0.63	1.37	1.90	1.51	1.17	0.41	3.76	3.12E+00	3.58E-02		2.61E+00	1.46E-01		4.67E-01	5.47E-01		1.39E-01	8.78E-01		-1.50E+00	9.13E-02		1.69E+00	1.15E-04	Up	Unigene30299_All//gi|9454546|gb|AAF87869.1|AC012561_2//6.00E-10//Unknown protein [Arabidopsis thaliana]		Unigene30299_All//5.00E-23//ES792479				nr +
Unigene3030_All	1401	28.05	11.39	12.96	9.49	6.98	9.06	3.29	1.10	1.25	-1.30E+00	1.58E-43	Down	-1.11E+00	5.79E-33	Down	-4.44E-01	2.37E-03		-6.77E-02	7.00E-01		-1.58E+00	5.56E-09	Down	-1.39E+00	6.58E-08	Down	Unigene3030_All//gi|30686476|ref|NP_850840.1|//5.00E-93//EMB1241 (embryo defective 1241); adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization [Arabidopsis thaliana] >gi|4583546|emb|CAB40281.1| GrpE protein [Arabidopsis thaliana] >gi|9759048|dbj|BAB09570.1| GrpE protein [Arabidopsis thaliana]	Unigene3030_All//6.00E-85//AT5G17710| EMB1241 (embryo defective 1241); adenyl-nucleotide exchange factor/ chaperone binding / protein homodimerization	Unigene3030_All//0.00E+00//TC178849			GO:0003006//GO:0000626//GO:0009532//GO:0030554//GO:0031980//GO:0042802//GO:0044267//GO:0046914	nr -
Unigene30300_All	1263	0.54	0.40	0.00	0.39	0.38	0.00	0.97	0.93	4.29	-4.25E-01	5.97E-01		-9.07E+00	7.64E-04	Down	-4.72E-02	9.49E-01		-8.62E+00	2.97E-03		-6.72E-02	9.14E-01		2.14E+00	9.52E-16	Up	Unigene30300_All//gi|40822853|gb|AA892244.1|//5.00E-24//At5g20110 [Arabidopsis thaliana] >gi|45752676|gb|AAS76236.1|At5g20110 [Arabidopsis thaliana]	Unigene30300_All//6.00E-25//AT5G20110| dynein light chain, putative	Unigene30300_All//0.00E+00//gi|72272608|gb|DT048737.1|DT048737				nr +
Unigene30302_All	1593	0.00	0.00	0.00	0.00	0.00	0.00	2.68	3.23	0.10	null	null		null	null		null	null		null	null		2.68E-01	3.01E-01		-4.74E+00	6.72E-26	Down	Unigene30302_All//gi|18401040|ref|NP_565616.1|//1.00E-116//ftsh4 (FtsH protease 4); ATP-dependent peptidase/ ATPase/ metallopeptidase [Arabidopsis thaliana] >gi|75100022|sp|O80983.2|FTSH4_ARATH RecName: Full=Cell division protease ftsH homolog 4, mitochondrial; Short=AtFtsH4; Flags: Precursor	Unigene30302_All//2.00E-111//AT2G26140| ftsh4 (FtsH protease 4); ATP-dependent peptidase/ ATPase/ metallopeptidase					nr -
Unigene30305_All	460	2.84	0.55	0.69	2.06	1.27	1.47	1.47	0.91	0.61	-2.37E+00	5.60E-04	Down	-2.03E+00	3.01E-03		-6.93E-01	3.15E-01		-4.82E-01	5.18E-01		-6.95E-01	3.94E-01		-1.28E+00	9.48E-02		Unigene30305_All//gi|75265624|sp|Q9SCP4.1|PP279_ARATH//2.00E-37//RecName: Full=Pentatricopeptide repeat-containing protein At3g53170 >gi|6630737|emb|CAB64220.1| nodulin / glutamate-ammonia ligase-like protein [Arabidopsis thaliana]	Unigene30305_All//1.00E-38//AT3G53170| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: glutamine biosynthetic process; LOCATED IN: nucleolus; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT5G48730.1); Has 17188 Blast hits to 5538 proteins in 167 species: Archae - 1; Bacteria - 16; Metazoa - 307; Fungi - 211; Plants - 16025; Viruses - 0; Other Eukaryotes - 628 (source: NCBI BLink).					nr +
Unigene30308_All	468	0.89	1.95	4.89	2.77	4.12	4.25	0.00	0.00	0.00	1.12E+00	1.30E-01		2.45E+00	2.61E-06	Up	5.74E-01	2.41E-01		6.18E-01	2.00E-01		null	null		null	null		Unigene30308_All//gi|60459560|gb|AAX18166.2|//2.00E-32//CNGC2 [Gossypium hirsutum]	Unigene30308_All//2.00E-23//AT5G15410| DND1 (DEFENSE NO DEATH 1); calcium channel/ calmodulin binding / cation channel/ cyclic nucleotide binding / intracellular cAMP activated cation channel/ intracellular cyclic nucleotide activated cation channel/ inward rectifier potassium channel	Unigene30308_All//4.00E-26//TC139161		ko04626|Plant-pathogen interaction		nr +
Unigene30309_All	539	0.39	0.47	2.37	1.48	0.77	2.01	7.53	8.68	4.51	2.76E-01	8.43E-01		2.61E+00	5.01E-04	Up	-9.48E-01	2.21E-01		4.44E-01	5.39E-01		2.06E-01	4.59E-01		-7.40E-01	4.44E-03			Unigene30309_All//1.00E-137//DW478659					
Unigene30310_All	392	0.00	6.85	0.27	0.38	2.20	2.07	0.86	1.17	1.02	1.27E+01	2.81E-15	Up	8.09E+00	3.98E-01		2.53E+00	4.66E-03		2.44E+00	8.58E-03		4.43E-01	6.31E-01		2.36E-01	8.04E-01		Unigene30310_All//gi|17221648|dbj|BAB78478.1|//2.00E-21//preproMP73 [Cucurbita maxima]	Unigene30310_All//9.00E-18//AT2G18540| cupin family protein					nr -
Unigene30313_All	710	0.22	1.28	0.00	0.35	0.39	0.57	1.85	3.18	8.64	2.54E+00	3.88E-03		-7.79E+00	2.45E-01		1.45E-01	9.61E-01		7.07E-01	5.97E-01		7.84E-01	3.99E-02		2.23E+00	1.52E-18	Up		Unigene30313_All//1.00E-45//TC131396					
Unigene30314_All	1153	0.23	0.00	0.00	0.13	0.00	0.08	4.84	1.12	3.01	-7.83E+00	6.70E-02		-7.83E+00	8.57E-02		-7.02E+00	1.66E-01		-7.27E-01	7.15E-01		-2.11E+00	1.51E-15	Down	-6.87E-01	1.55E-03		Unigene30314_All//gi|168274274|dbj|BAG09557.1|//1.00E-119//acetylcholinesterase [Macropitilium atropurpureum]	Unigene30314_All//3.00E-107//AT5G14450| GDSL-motif lipase/hydrolase family protein	Unigene30314_All//0.00E+00//TC147741				nr +
Unigene30315_All	632	0.25	0.00	0.51	0.00	0.44	0.14	8.70	5.09	1.89	-7.96E+00	2.16E-01		1.03E+00	4.71E-01		8.77E+00	7.02E-02		7.16E+00	4.76E-01		-7.72E-01	6.38E-04		-2.20E+00	1.04E-16	Down							
Unigene3032_All	2103	6.27	22.58	16.81	2.13	3.90	3.24	0.08	0.00	0.00	1.85E+00	6.83E-87	Up	1.42E+00	1.76E-43	Up	8.70E-01	5.89E-06		6.05E-01	6.94E-03		-6.33E+00	1.34E-01		-6.33E+00	1.08E-01		Unigene3032_All//gi|224127132|ref|XP_002329408.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222870458|gb|EEF07589.1| GH3 family protein [Populus trichocarpa]	Unigene3032_All//0.00E+00//AT4G03400| DFL2 (DWARF IN LIGHT 2)	Unigene3032_All//0.00E+00//TC167574			GO:0009314//GO:0009536//GO:0009725	nr -
Unigene30321_All	474	30.69	44.36	56.06	34.79	13.15	8.48	2.23	0.88	0.50	5.32E-01	8.70E-06		8.69E-01	3.93E-15		-1.40E+00	1.33E-25	Down	-2.04E+00	7.46E-38	Down	-1.34E+00	2.90E-02		-2.14E+00	9.36E-04	Down	Unigene30321_All//gi|28565534|gb|AAO43000.1|//9.00E-18//early tobacco anther 1 [Nicotiana tabacum]		Unigene30321_All//0.00E+00//gi|109876829|gb|DW505803.1|DW505803				nr -
Unigene30327_All	284	0.74	1.43	0.38	4.39	0.97	0.00	5.36	0.00	1.96	9.54E-01	4.14E-01		-9.75E-01	6.21E-01		-2.18E+00	4.83E-04	Down	-1.21E+01	8.64E-08	Down	-1.24E+01	8.51E-11	Down	-1.45E+00	2.57E-03		Unigene30327_All//gi|255630260|gb|ACU15483.1|//7.00E-12//unknown [Glycine max]		Unigene30327_All//3.00E-143//gi|109874854|gb|DW503828.1|DW503828				nr +
Unigene30329_All	688	0.15	0.00	0.15	0.58	1.20	1.44	4.18	1.34	1.74	-7.25E+00	3.72E-01		2.54E-02	1.00E+00		1.05E+00	1.99E-01		1.32E+00	7.15E-02		-1.64E+00	3.27E-06	Down	-1.27E+00	1.18E-04	Down	Unigene30329_All//gi|79482708|ref|NP_194028.2|//2.00E-53//AESP (ARABIDOPSIS HOMOLOG OF SEPARASE); peptidase [Arabidopsis thaliana] >gi|57019012|gb|AAW32909.1|separase [Arabidopsis thaliana]	Unigene30329_All//3.00E-44//AT4G22970| AESP (ARABIDOPSIS HOMOLOG OF SEPARASE); peptidase					nr +
Unigene30333_All	1308	0.00	5.46	5.66	0.08	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.81E-41	Up	1.25E+01	2.22E-41	Up	-6.25E+00	3.13E-01		-6.25E+00	4.00E-01		null	null		null	null		Unigene30333_All//gi|51209923|ref|YP_063587.1|//8.00E-38//ribosomal protein S11 [Gracilaria tenuistipitata var. liui] >gi|62287422|sp|Q08833.1|RR11_GRATL RecName: Full=30S ribosomal protein S11, chloroplastic >gi|50657677|gb|AAT79662.1| 30S ribosomal protein S11 [Gracilaria tenuistipitata var. liui]	Unigene30333_All//2.00E-29//ATCG00750| 30S chloroplast ribosomal protein S11			ko03010|Ribosome		nr +
Unigene30335_All	388	3.64	1.70	0.27	4.75	1.51	2.79	0.00	0.00	0.00	-1.10E+00	5.16E-02		-3.73E+00	8.89E-06	Down	-1.65E+00	4.01E-04	Down	-7.66E-01	1.18E-01		null	null		null	null		Unigene30335_All//gi|6523547|emb|CAB62280.1|//2.00E-26//hydroxyproline-rich glycoprotein DZ-HRGP [Volvox carteri f. nagariensis]		Unigene30335_All//5.00E-81//TC177700				nr -

Unigene30336_All	827	0.51	0.18	0.13	4.34	3.83	1.26	0.00	0.00	0.00	-1.46E+00	2.34E-01		-1.97E+00	1.51E-01		-1.79E-01	6.03E-01		-1.79E+00	2.35E-07	Down	null	null		null	null		Unigene30336_All//gi|48310189|gb|AAT41771.1|//3.00E-62//At5g42680 [Arabidopsis thaliana] >gi|52218794|gb|AAU29467.1| At5g42680 [Arabidopsis thaliana]	Unigene30336_All//1.00E-63//AT5G42680| unknown protein	Unigene30336_All//9.00E-69//TC157321				nr +
Unigene3034_All	1625	24.66	53.94	30.57	29.98	26.49	32.32	32.47	82.05	24.83	1.13E+00	6.91E-77	Up	3.10E-01	7.04E-05		-1.79E-01	2.00E-02		1.09E-01	2.00E-01		1.34E+00	2.14E-186	Up	-3.87E-01	1.12E-09		Unigene3034_All//gi|297829464|ref|XP_002882614.1|//1.00E-156//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328454|gb|EFH58873.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3034_All//1.00E-144//AT3G09350| armadillo/beta-catenin repeat family protein	Unigene3034_All//0.00E+00//TC131995		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene30340_All	582	0.00	20.11	0.18	0.60	0.71	3.03	1.24	0.65	0.82	1.43E+01	3.96E-67	Up	7.52E+00	3.98E-01		2.45E-01	8.53E-01		2.34E+00	3.97E-05	Up	-9.34E-01	2.26E-01		-5.88E-01	4.09E-01		Unigene30340_All//gi|17221648|dbj|BAB78478.1|//9.00E-26//preproMP73 [Cucurbita maxima]		Unigene30340_All//1.00E-125//TC170410		ko03040|Spliceosome		nr +
Unigene30343_All	568	0.83	2.14	3.09	1.40	1.33	0.56	0.45	1.03	0.42	1.37E+00	3.15E-02		1.90E+00	7.52E-04	Up	-7.32E-02	9.08E-01		-1.33E+00	1.06E-01		1.21E+00	1.71E-01		-8.58E-02	9.57E-01		Unigene30343_All//gi|224081252|ref|XP_002306353.1|//5.00E-07//ABC transporter family protein [Populus trichocarpa] >gi|222855802|gb|EEE93349.1| ABC transporter family protein [Populus trichocarpa]	Unigene30343_All//3.00E-08//AT5G09930| ATGCN2; transporter	Unigene30343_All//9.00E-34//TC149541				nr +
Unigene30345_All	941	0.00	0.00	0.00	0.00	0.00	0.00	2.92	0.76	9.99	null	null		null	null		null	null		null	null		-1.95E+00	2.44E-07	Down	1.77E+00	5.05E-21	Up	Unigene30345_All//gi|4972075|emb|CAB43882.1|//3.00E-12//proton pump interactor [Arabidopsis thaliana] >gi|7269604|emb|CAB81400.1| proton pump interactor [Arabidopsis thaliana]	Unigene30345_All//2.00E-17//AT1G10880| unknown protein	Unigene30345_All//0.00E+00//TC141923				nr -
Unigene30346_All	366	8.43	36.27	12.51	31.71	51.09	104.52	52.45	97.18	315.33	2.10E+00	3.11E-29	Up	5.69E-01	5.48E-02		6.88E-01	7.95E-09		1.72E+00	3.71E-68	Up	8.90E-01	2.22E-26		2.59E+00	0.00E+00	Up	Unigene30346_All//gi|47824991|gb|AAT38764.1|//2.00E-11//Putative ATPase protein, identical [Solanum demissum]		Unigene30346_All//1.00E-50//TC133425		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene30348_All	669	4.15	7.65	15.68	0.45	0.46	3.71	0.00	0.00	0.00	8.84E-01	8.99E-04		1.92E+00	5.07E-20	Up	5.23E-02	9.98E-01		3.05E+00	3.93E-09	Up	null	null		null	null		Unigene30348_All//gi|228480462|gb|ACQ41892.1|//8.00E-78//3-ketoacyl-CoA synthase [Camellia oleifera]	Unigene30348_All//1.00E-68//AT1G19440| KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene30348_All//2.00E-56//AI730004				nr +
Unigene30351_All	292	10.57	6.25	8.39	15.87	14.39	13.92	130.89	34.50	46.25	-7.59E-01	3.18E-02		-3.34E-01	4.00E-01		-1.41E-01	6.46E-01		-1.89E-01	5.68E-01		-1.92E+00	6.95E-91	Down	-1.50E+00	4.53E-66	Down	Unigene30351_All//gi|115460394|ref|NP_001053797.1|//1.00E-09//Os04g0605900 [Oryza sativa Japonica Group] >gi|113565368|dbj|BAF15711.1| Os04g0605900 [Oryza sativa Japonica Group]	Unigene30351_All//1.00E-10//AT2G01250| 60S ribosomal protein L7 (RPL7B)	Unigene30351_All//3.00E-75//gi|21092694|gb|BQ405007.1|BQ405007		ko03010|Ribosome		nr +
Unigene30353_All	304	0.86	0.00	0.18	4.26	0.79	1.63	2.92	1.37	2.88	-9.75E+00	6.70E-02		-2.30E+00	2.43E-01		-2.43E+00	1.10E-04	Down	-1.38E+00	2.30E-02		-1.09E+00	1.07E-01		-1.87E-02	9.66E-01					Unigene30353_All//4.00E-164//TC164322				
Unigene30354_All	819	3.00	0.31	2.02	2.80	1.98	1.10	1.65	0.92	0.88	-3.28E+00	2.66E-09	Down	-5.75E-01	1.78E-01		-5.02E-01	2.35E-01		-1.34E+00	1.70E-03		-8.47E-01	1.03E-01		-9.16E-01	6.35E-02		Unigene30354_All//gi|15229025|ref|NP_190449.1|//2.00E-31//sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	Unigene30354_All//1.00E-32//AT3G48800| sterile alpha motif (SAM) domain-containing protein	Unigene30354_All//0.00E+00//gi|78333611|gb|DT553885.1|DT553885				nr +
Unigene30358_All	412	0.89	2.09	0.13	4.23	3.09	1.21	0.62	0.00	0.00	1.23E+00	1.12E-01		-2.78E+00	1.03E-01		-4.53E-01	3.73E-01		-1.81E+00	5.79E-04	Down	-9.27E+00	4.04E-02		-9.27E+00	3.04E-02					Unigene30358_All//0.00E+00//CO089214				
Unigene30359_All	643	0.00	0.00	0.00	0.00	0.00	0.00	1.97	2.08	17.78	null	null		null	null		null	null		null	null		7.65E-02	8.93E-01		3.17E+00	1.44E-49	Up	Unigene30359_All//gi|224137170|ref|XP_002327053.1|//2.00E-40//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222835368|gb|EEE73803.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene30359_All//2.00E-32//AT2G44840| EERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	Unigene30359_All//0.00E+00//BF275652	AP2-EREBP			nr -
Unigene30362_All	539	0.78	3.76	0.99	3.33	3.00	2.26	0.08	0.39	0.52	2.28E+00	1.73E-05	Up	3.47E-01	7.06E-01		-1.48E-01	7.95E-01		-5.56E-01	2.76E-01		2.31E+00	2.40E-01		2.72E+00	9.93E-02		Unigene30362_All//gi|89111882|gb|ABD60713.1|//2.00E-06//At1g58420 [Arabidopsis thaliana]	Unigene30362_All//1.00E-07//AT1G58420| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031279 (InterPro:IPR016972); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10140.1); Has 28 Blast hits to 28 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene30362_All//7.00E-127//gi|109856645|gb|DW485624.1|DW485624				nr -
Unigene30364_All	654	0.00	0.16	0.00	0.30	0.74	1.10	4.46	7.22	46.90	7.28E+00	3.87E-01		null	null		1.27E+00	2.92E-01		1.86E+00	4.71E-02		6.95E-01	4.89E-03		3.39E+00	2.19E-140	Up	Unigene30364_All//gi|224072526|ref|XP_002303770.1|//1.00E-37//SAUR family protein [Populus trichocarpa] >gi|222841202|gb|EEE78749.1| SAUR family protein [Populus trichocarpa]	Unigene30364_All//8.00E-29//AT5G50760| auxin-responsive family protein	Unigene30364_All//0.00E+00//DT048318				nr +
Unigene30365_All	347	1.81	0.88	3.07	1.29	0.00	0.26	4.63	3.25	44.78	-1.05E+00	2.50E-01		7.62E-01	2.69E-01		-1.03E+01	2.00E-03		-2.31E+00	7.81E-02		-5.10E-01	2.90E-01		3.27E+00	4.21E-69	Up	Unigene30365_All//gi|115445545|ref|NP_001046552.1|//5.00E-06//Os02g0279800 [Oryza sativa Japonica Group] >gi|113536083|dbj|BAF08466.1| Os02g0279800 [Oryza sativa Japonica Group]	Unigene30365_All//2.00E-11//AT2G35736| unknown protein					nr -
Unigene30367_All	1536	1.40	0.89	0.76	3.47	3.56	1.68	2.01	0.63	0.60	-6.49E-01	1.35E-01		-8.73E-01	5.80E-02		3.88E-02	9.04E-01		-1.05E+00	4.13E-05	Down	-1.68E+00	8.33E-07	Down	-1.75E+00	1.98E-07	Down	Unigene30367_All//gi|115473321|ref|NP_001060259.1|//1.00E-19//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]		Unigene30367_All//2.00E-31//ES811125				nr -
Unigene30368_All	709	0.00	1.00	0.00	3.51	2.14	1.15	12.28	7.96	5.28	9.97E+00	3.33E-04	Up	null	null		-7.17E-01	6.35E-02		-1.62E+00	1.09E-04	Down	-6.26E-01	3.16E-04		-1.22E+00	1.16E-11	Down	Unigene30368_All//gi|226531011|ref|NP_001147668.1|//6.00E-21//lipid binding protein [Zea mays] >gi|195612468|gb|ACG28064.1| lipid binding protein [Zea mays]	Unigene30368_All//3.00E-20//AT1G70250| receptor serine/threonine kinase, putative	Unigene30368_All//0.00E+00//TC174945				nr -
Unigene30369_All	534	7.45	1.71	12.66	4.01	1.68	2.62	0.00	3.29	0.00	-2.12E+00	2.10E-09	Down	7.66E-01	1.10E-03		-1.26E+00	2.52E-03		-6.14E-01	1.77E-01		1.17E+01	2.29E-12	Up	null	null					Unigene30369_All//6.00E-07//TC138106				
Unigene3037_All	2370	3.97	1.30	2.49	8.66	5.43	2.63	4.26	0.76	1.40	-1.61E+00	7.93E-15	Down	-6.72E-01	5.43E-04		-6.72E-01	1.42E-09		-1.72E+00	2.06E-37	Down	-2.49E+00	1.21E-33	Down	-1.61E+00	5.33E-20	Down	Unigene3037_All//gi|9758198|dbj|BAB08672.1|//0.00E+00//receptor-like protein kinase [Arabidopsis thaliana] >gi|224589719|gb|ACN59391.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene3037_All//0.00E+00//AT5G51560| leucine-rich repeat transmembrane protein kinase, putative	Unigene3037_All//0.00E+00//CO085660			GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene30370_All	264	47.76	210.55	68.38	71.51	161.61	121.63	37.64	77.10	84.81	2.14E+00	3.68E-123	Up	5.18E-01	1.21E-04		1.18E+00	2.04E-47	Up	7.66E-01	2.88E-16		1.03E+00	1.27E-19	Up	1.17E+00	9.67E-27	Up				Unigene30370_All//2.00E-33//EX167695				
Unigene30373_All	649	1.13	0.31	0.41	5.99	4.35	2.78	0.46	0.13	0.68	-1.85E+00	4.08E-02		-1.46E+00	1.12E-01		-4.61E-01	1.38E-01		-1.10E+00	3.44E-04	Down	-1.82E+00	2.11E-01		5.66E-01	5.78E-01		Unigene30373_All//gi|272725401|gb|ACH97123.2|//2.00E-86//GDH2 [Camellia sinensis]	Unigene30373_All//2.00E-85//AT5G07440| GDH2 (GLUTAMATE DEHYDROGENASE 2); ATP binding / glutamate dehydrogenase [NAD(P)+]/ glutamate dehydrogenase/ oxidoreductase	Unigene30373_All//0.00E+00//TC178475		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr +
Unigene30375_All	704	0.15	0.65	0.00	2.41	1.17	1.92	7.45	2.02	4.47	2.12E+00	9.59E-02		-7.22E+00	3.93E-01		-1.04E+00	3.10E-02		-3.22E-01	5.65E-01		-1.88E+00	9.31E-13	Down	-7.36E-01	1.09E-03		Unigene30375_All//gi|8778581|gb|AAF79589.1|AC007945.9//4.00E-14//F28C11.16 [Arabidopsis thaliana] >gi|4056436|gb|AAC98009.1| EST gb|AA650912 comes from this gene [Arabidopsis thaliana] >gi|34365603|gb|AAQ65113.1| At1g23530 [Arabidopsis thaliana]		Unigene30375_All//5.00E-08//DW503150				nr -
Unigene30377_All	937	0.50	1.30	0.23	0.53	0.66	0.58	0.77	2.32	4.93	1.37E+00	3.15E-02		-1.14E+00	3.32E-01		3.15E-01	7.84E-01		1.22E-01	9.21E-01		1.60E+00	1.06E-04	Up	2.68E+00	2.22E-17	Up	Unigene30377_All//gi|37993655|gb|AAR06913.1|//5.00E-98//UDP-glycosyltransferase 85A8 [Stevia rebaudiana]	Unigene30377_All//2.00E-83//AT1G22380| AtUGT85A3 (UDP-glucosyl transferase 85A3); glucuronosyltransferase/ transcription factor/ transferase, transferring glycosyl groups	Unigene30377_All//0.00E+00//TC135725		ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene30378_All	576	0.45	1.32	3.24	12.11	13.33	8.70	0.37	1.23	0.21	1.54E+00	7.40E-02		2.83E+00	5.06E-06	Up	1.39E-01	5.88E-01		-4.76E-01	3.41E-02		1.75E+00	3.21E-02		-8.23E-01	5.99E-01		Unigene30378_All//gi|9758954|dbj|BAB09341.1|//9.00E-12//ankyrin-repeat-containing protein-like [Arabidopsis thaliana]	Unigene30378_All//9.00E-13//AT5G54620| ankyrin repeat family protein					nr +
Unigene3038_All	2349	6.79	87.99	37.83	27.21	121.79	90.50	12.22	24.59	35.95	3.70E+00	0.00E+00	Up	2.48E+00	4.55E-230	Up	2.16E+00	0.00E+00	Up	1.73E+00	0.00E+00	Up	1.01E+00	5.29E-52	Up	1.56E+00	1.72E-151	Up	Unigene3038_All//gi|9294810|gb|AAF86687.1|//2.00E-40//MTD1 [Medicago truncatula]	Unigene3038_All//4.00E-25//AT5G21940| unknown protein	Unigene3038_All//0.00E+00//DW482106			GO:0005488//GO:0043231	nr +
Unigene30380_All	400	1.05	0.76	1.86	0.50	0.95	0.56	1.48	2.09	4.38	-4.61E-01	6.50E-01		8.33E-01	3.39E-01		9.27E-01	5.23E-01		1.81E-01	9.35E-01		4.98E-01	4.86E-01		1.57E+00	5.53E-04	Up				Unigene30380_All//5.00E-07//EX172147				
Unigene30381_All	595	0.18	1.02	0.63	2.18	0.58	0.30	1.28	2.32	3.01	2.54E+00	2.46E-02		1.83E+00	2.13E-01		-1.91E+00	1.25E-03		-2.84E+00	7.63E-05	Down	8.58E-01	9.44E-02		1.24E+00	4.17E-03					Unigene30381_All//0.00E+00//TC144926				
Unigene30382_All	598	6.65	10.17	13.98	0.67	1.90	0.00	0.00	0.00	0.00	6.13E-01	1.07E-02		1.07E+00	4.15E-07	Up	1.51E+00	2.36E-02		-9.38E+00	1.11E-02		null	null		null	null		Unigene30382_All//gi|48309996|gb|AAT41734.1|//1.00E-16//At1g67910 [Arabidopsis thaliana] >gi|56121922|gb|AAV74242.1| At1g67910 [Arabidopsis thaliana] >gi|222423710|dbj|BAH19821.1| AT1G67910 [Arabidopsis thaliana]	Unigene30382_All//2.00E-16//AT1G67910| unknown protein					nr +
Unigene30383_All	341	0.00	1.93	0.00	4.38	1.01	1.06	3.35	2.21	2.34	1.09E+01	6.23E-04	Up	null	null		-2.12E+00	1.37E-04	Down	-2.05E+00	5.54E-04	Down	-6.02E-01	3.08E-01		-5.19E-01	3.56E-01					Unigene30383_All//4.00E-07//DW238277				
Unigene30385_All	493	1.17	0.41	1.30	3.03	1.47	0.64	3.43	4.58	2.02	-1.51E+00	1.36E-01		1.51E-01	8.56E-01		-1.05E+00	4.30E-02		-2.24E+00	2.25E-04	Down	4.16E-01	3.00E-01		-7.64E-01	7.73E-02									
Unigene30386_All	455	0.23	0.00	0.35	23.10	9.31	8.54	1.12	2.48	1.84	-7.85E+00	3.72E-01		6.10E-01	7.48E-01		-1.31E+00	7.51E-15	Down	-1.44E+00	4.80E-15	Down	1.15E+00	4.79E-02		7.22E-01	2.82E-01		Unigene30386_All//gi|255575155|ref|XP_002528482.1|//1.00E-09//conserved hypothetical protein [Ricinus communis] >gi|223532091|gb|EEF33899.1| conserved hypothetical protein [Ricinus communis]						nr +

Unigene30387_All	273	1.34	0.19	0.98	0.73	1.51	0.66	0.00	0.61	1.90	-2.85E+00	7.80E-02		-4.60E-01	6.97E-01		1.05E+00	4.26E-01		-1.42E-01	9.35E-01		9.26E+00	1.39E-01		1.09E+01	6.13E-04	Up	Unigene30387_All//gi|12322008|gb|AAG51046.1|AC069473.8/|2.00E-21//gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] >gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]						nr +
Unigene30389_All	415	1.26	0.73	0.51	1.92	1.66	1.41	1.73	0.30	0.00	-7.83E-01	4.22E-01		-1.30E+00	2.42E-01		-2.11E-01	8.06E-01		-4.41E-01	6.14E-01		-2.52E+00	4.69E-03		-1.08E+01	1.78E-05	Down	Unigene30389_All//gi|30678566|ref|NP_563685.2|//3.00E-28//leucine-rich repeat family protein [Arabidopsis thaliana]	Unigene30389_All//2.00E-29//AT1G03440| leucine-rich repeat family protein	Unigene30389_All//4.00E-60//gi|164357636|gb|ES811296.1|ES811296				nr +
Unigene30391_All	762	0.48	26.73	2.45	0.20	0.54	1.54	0.00	0.33	0.89	5.80E+00	7.84E-105	Up	2.35E+00	4.96E-05	Up	1.47E+00	2.80E-01		2.97E+00	1.83E-04	Up	8.36E+00	4.31E-02		9.80E+00	4.96E-05	Up	Unigene30391_All//gi|75170815|sp|Q9FIF5.1|P2C78_ARATH//8.00E-37//RecName: Full=Probable protein phosphatase 2C 78; Short=AtPP2C78 >gi|15809792|gb|AAL06824.1| AT5g59220/mnc17_110 [Arabidopsis thaliana] >gi|18377817|gb|AAL67095.1| AT5g59220/mnc17_110 [Arabidopsis thaliana]	Unigene30391_All//4.00E-38//AT5G59220| protein phosphatase 2C, putative / PP2C, putative	Unigene30391_All//4.00E-80//TC141499				nr -
Unigene30392_All	376	0.83	1.08	0.57	3.44	3.39	1.44	1.69	0.67	0.11	3.69E-01	7.24E-01		-5.60E-01	6.63E-01		-2.36E-02	9.50E-01		-1.26E+00	3.78E-02		-1.34E+00	1.13E-01		-3.99E+00	5.82E-04	Down	Unigene30392_All//gi|28200786|emb|CAD45374.1|//1.00E-20//potyviral helper component protease-interacting protein 1 [Solanum tuberosum subsp. andigena]	Unigene30392_All//8.00E-20//AT4G01270| zinc finger (C3HC4-type RING finger) family protein	Unigene30392_All//3.00E-113//DT463419				nr +
Unigene30397_All	221	45.69	27.05	27.47	77.76	66.69	63.15	68.30	51.06	30.28	-7.56E-01	2.72E-05		-7.34E-01	8.52E-05		-2.22E-01	1.14E-01		-3.00E-01	2.96E-02		-4.20E-01	1.13E-03		-1.17E+00	1.73E-18	Down	Unigene30397_All//gi|297829762|ref|XP_002882763.1|//2.00E-15//Aha1 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328603|gb|EFH59022.1| Aha1 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene30397_All//8.00E-09//AT3G12050| Aha1 domain-containing protein	Unigene30397_All//4.00E-40//TC143262				nr -
Unigene30398_All	287	0.55	1.94	0.74	7.12	2.76	2.52	8.40	18.35	13.60	1.83E+00	9.02E-02		4.41E-01	7.75E-01		-1.37E+00	1.51E-03		-1.50E+00	1.24E-03		1.13E+00	2.13E-06	Up	6.96E-01	9.19E-03				Unigene30398_All//4.00E-59//DW501838				
Unigene304_All	1109	1.32	0.27	1.34	4.76	5.22	5.01	1.26	1.62	4.20	-2.27E+00	3.39E-04	Down	2.54E-02	9.82E-01		1.32E-01	6.48E-01		7.32E-02	7.93E-01		3.65E-01	4.23E-01		1.74E+00	1.43E-10	Up	Unigene304_All//gi|302035373|gb|ADK92393.1|//1.00E-105//auxin response factor 8-1 [Solanum lycopersicum]	Unigene304_All//8.00E-103//AT5G37020| ARF8 (AUXIN RESPONSE FACTOR 8); transcription factor	Unigene304_All//2.00E-55//DW483532	ARF			nr +
Unigene3040_All	1734	6.13	2.48	1.66	35.59	22.88	17.35	43.30	8.39	13.26	-1.30E+00	2.44E-12	Down	-1.89E+00	1.02E-19	Down	-6.38E-01	2.11E-25		-1.04E+00	1.80E-51	Down	-2.37E+00	9.90E-232	Down	-1.71E+00	1.63E-155	Down	Unigene3040_All//gi|27311797|gb|AAO00864.1|//1.00E-147//Unknown protein [Arabidopsis thaliana] >gi|30725618|gb|AAP37831.1| At4g31350 [Arabidopsis thaliana]	Unigene3040_All//1.00E-142//AT4G31350| unknown protein	Unigene3040_All//0.00E+00//TC166951				nr -
Unigene30400_All	1146	0.00	0.00	0.00	0.00	0.00	0.00	100.68	28.08	26.84	null	null		null	null		null	null		null	null		-1.84E+00	1.33E-257	Down	-1.91E+00	4.73E-278	Down	Unigene30400_All//gi|224054172|ref|XP_002298127.1|//1.00E-133//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845385|gb|EEE82932.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene30400_All//5.00E-119//AT1G52790| oxidoreductase, 2OG-Fe(II) oxygenase family protein			ko00904|Diterpenoid biosynthesis		nr +
Unigene30402_All	431	0.61	0.24	1.73	1.96	1.28	0.63	5.30	3.59	1.11	-1.37E+00	3.83E-01		1.51E+00	9.50E-02		-6.20E-01	4.13E-01		-1.64E+00	4.18E-02		-5.62E-01	1.43E-01		-2.26E+00	1.32E-07	Down	Unigene30402_All//gi|83319215|dbj|BAE53712.1|//2.00E-28//At3g21480 [Arabidopsis thaliana]	Unigene30402_All//1.00E-29//AT3G21480| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: intracellular; CONTAINS InterPro DOMAIN/s: BRCT (InterPro:IPR001357); BEST Arabidopsis thaliana protein match is: transcription coactivator (TAIR:AT4G03130.1); Has 489 Blast hits to 455 proteins in 115 species: Archae - 2; Bacteria - 37; Metazoa - 270; Fungi - 30; Plants - 45; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).	Unigene30402_All//8.00E-154//gi|13353411|gb|BG443759.1|BG443759				nr -
Unigene30404_All	686	0.53	1.03	0.23	2.40	0.80	0.59	2.53	0.73	0.87	9.54E-01	2.62E-01		-1.20E+00	3.96E-01		-1.58E+00	1.53E-03		-2.02E+00	3.04E-04	Down	-1.79E+00	1.89E-04	Down	-1.54E+00	6.50E-04	Down	Unigene30404_All//gi|18421273|ref|NP_568509.1|//2.00E-21//calcium-binding EF hand family protein [Arabidopsis thaliana] >gi|42740922|gb|AAS44557.1| protein phosphatase 2A beta [Arabidopsis thaliana]	Unigene30404_All//9.00E-18//AT5G28850| calcium-binding EF hand family protein	Unigene30404_All//0.00E+00//TC170971				nr +
Unigene30405_All	462	0.00	0.55	0.23	0.22	0.15	0.39	0.55	1.36	2.93	9.10E+00	7.86E-02		7.85E+00	3.98E-01		-5.32E-01	8.16E-01		8.59E-01	6.95E-01		1.31E+00	1.26E-01		2.42E+00	4.42E-05	Up	Unigene30405_All//gi|147770960|emb|CAN69709.1|//3.00E-07//hypothetical protein [Vitis vinifera]						nr +
Unigene30408_All	976	0.00	0.00	0.00	0.61	0.56	0.46	2.60	0.69	27.02	null	null		null	null		-1.18E-01	8.76E-01		-4.05E-01	6.73E-01		-1.92E+00	1.02E-06	Down	3.38E+00	2.98E-120	Up	Unigene30408_All//gi|224137172|ref|XP_002327054.1|//7.00E-56//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222835369|gb|EEE73804.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene30408_All//5.00E-51//AT2G44840| ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	Unigene30408_All//2.00E-26//TC173432	AP2-EREBP			nr -
Unigene30410_All	743	0.14	0.27	0.72	1.27	1.07	0.18	16.16	7.99	4.34	9.54E-01	6.21E-01		2.35E+00	5.87E-02		-2.57E-01	7.27E-01		-2.80E+00	1.18E-03		-1.02E+00	1.31E-11	Down	-1.90E+00	2.09E-29	Down	Unigene30410_All//gi|288558966|sp|B9SY63.1|U497F_RICCO//7.00E-60//RecName: Full=UPF0497 membrane protein 15	Unigene30410_All//3.00E-50//AT5G44550| integral membrane family protein	Unigene30410_All//0.00E+00//gi|109857887|gb|DW486866.1|DW486866				nr +
Unigene30412_All	306	1.71	0.33	1.04	1.63	2.03	1.77	1.24	1.09	9.11	-2.37E+00	4.76E-02		-7.12E-01	4.97E-01		3.15E-01	7.84E-01		1.22E-01	9.21E-01		-1.87E-01	8.57E-01		2.87E+00	1.65E-11	Up			Unigene30412_All//4.00E-07//DT047208				
Unigene30413_All	1743	0.00	45.81	21.42	0.00	0.00	0.00	0.00	0.00	0.00	1.55E+01	0.00E+00	Up	1.44E+01	6.38E-212	Up	null	null		null	null		null	null		null	null		Unigene30413_All//gi|9858781|gb|AAG01128.1|AF273333.13//2.00E-09//BAC19.13 [Solanum lycopersicum]						nr -
Unigene30415_All	551	0.00	0.64	0.00	0.54	0.00	0.08	0.61	2.50	1.95	9.33E+00	2.46E-02		null	null		-9.08E+00	2.01E-02		-2.73E+00	1.37E-01		2.03E+00	3.35E-04	Up	1.67E+00	6.16E-03				Unigene30415_All//1.00E-08//C0126079				
Unigene30416_All	626	0.00	0.00	0.00	4.38	1.93	0.72	6.75	0.67	0.95	null	null		null	null		-1.18E+00	9.38E-04	Down	-2.60E+00	7.76E-09	Down	-3.34E+00	2.73E-19	Down	-2.82E+00	4.40E-17	Down	Unigene30416_All//gi|255586543|ref|XP_002533908.1|//3.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223526129|gb|EEF28473.1| conserved hypothetical protein [Ricinus communis]	Unigene30416_All//6.00E-11//AT3G61660| unknown protein					nr +
Unigene30418_All	240	6.10	6.76	5.55	7.06	3.59	8.66	92.49	28.04	21.25	1.46E-01	7.64E-01		-1.38E-01	7.97E-01		-9.76E-01	4.19E-02		2.95E-01	5.64E-01		-1.72E+00	1.12E-45	Down	-2.12E+00	4.09E-62	Down			Unigene30418_All//6.00E-101//TC139069				
Unigene30419_All	357	2.64	0.28	1.49	2.23	1.45	2.28	1.18	1.76	1.00	-3.22E+00	6.77E-04	Down	-8.23E-01	2.71E-01		-6.26E-01	4.24E-01		2.85E-02	9.71E-01		5.68E-01	5.04E-01		-2.38E-01	7.88E-01		Unigene30419_All//gi|224075299|ref|XP_002304589.1|//2.00E-37//nbs-lrr resistance protein [Populus trichocarpa] >gi|222842021|gb|EEE79568.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene30419_All//2.00E-09//AT5G46730| disease resistance protein (CC-NBS class), putative	Unigene30419_All//6.00E-148//TC136593		ko04626|Plant-pathogen interaction		nr -
Unigene30423_All	297	0.00	0.68	0.00	11.41	15.54	22.20	0.00	3.38	0.54	9.41E+00	1.36E-01		null	null		4.46E-01	1.23E-01		9.61E-01	2.39E-05		1.17E+01	3.93E-07	Up	9.07E+00	1.40E-01		Unigene30423_All//gi|17016987|gb|AAL33553.1|AF436852_1/|3.00E-22//pyruvate decarboxylase [Cucumis melo]	Unigene30423_All//7.00E-23//AT4G33070| pyruvate decarboxylase, putative	Unigene30423_All//2.00E-147//TC160373		ko00010|Glycolysis / Gluconeogenesis//ko00380|Tryptophan metabolism		nr -
Unigene30427_All	364	2.44	0.00	0.88	2.05	0.57	1.36	0.35	0.23	2.96	-1.13E+01	2.86E-05	Down	-1.48E+00	6.99E-02		-1.85E+00	2.53E-02		-5.89E-01	4.87E-01		-6.02E-01	7.66E-01		3.08E+00	3.77E-05	Up			Unigene30427_All//4.00E-10//TC157829				
Unigene30428_All	1702	0.00	0.00	0.00	0.06	0.02	0.05	20.39	7.24	6.91	null	null		null	null		-1.53E+00	5.86E-01		-1.40E-01	9.50E-01		-1.49E+00	6.41E-58	Down	-1.56E+00	1.05E-63	Down	Unigene30428_All//gi|55375996|gb|AAV50009.1|//1.00E-114//anthranilate N-hydroxycinnamoyl/benzoyltransferase [Malus x domestica]	Unigene30428_All//1.00E-74//AT5G67150| transferase family protein	Unigene30428_All//2.00E-117//TC140818		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene30431_All	453	0.00	0.22	0.00	13.75	3.88	8.87	0.00	0.00	0.00	7.81E+00	3.87E-01		null	null		-1.83E+00	2.02E-14	Down	-6.31E-01	7.04E-03		null	null		null	null		Unigene30431_All//gi|224079043|ref|XP_002365727.1|//3.00E-09//predicted protein [Populus trichocarpa] >gi|222848691|gb|EEE86238.1| predicted protein [Populus trichocarpa]						nr -
Unigene3044_All	1553	120.78	69.20	125.08	30.06	40.20	37.89	0.52	1.94	1.03	-8.04E-01	1.84E-93		5.05E-02	2.51E-01		4.20E-01	6.18E-12		3.34E-01	5.36E-07		1.91E+00	1.01E-07	Up	9.88E-01	2.95E-02		Unigene3044_All//gi|39598908|gb|AAR28998.1|//1.00E-137//CMI 1a interacting protein 1 [Nicotiana tabacum]		Unigene3044_All//0.00E+00//TC138047			GO:0005488//GO:0006325//GO:0016192//GO:0016741//GO:0043231//GO:0044427	nr -
Unigene30440_All	574	1.00	1.24	0.65	8.24	4.80	3.38	1.55	0.15	0.76	3.02E-01	6.93E-01		-6.27E-01	5.27E-01		-7.81E-01	2.56E-03		-1.29E+00	4.20E-06	Down	-3.41E+00	1.40E-04	Down	-1.02E+00	1.09E-01		Unigene30440_All//gi|2346988|dbj|BAA21928.1|//1.00E-36//ZPT4-4 [Petunia x hybrida]	Unigene30440_All//9.00E-23//AT2G45120| zinc finger (C2H2 type) family protein		C2H2			nr +
Unigene30442_All	375	0.00	0.00	0.00	0.00	0.00	0.00	5.98	2.67	1.81	null	null		null	null		null	null		null	null		-1.16E+00	2.72E-03		-1.73E+00	1.59E-05	Down							
Unigene30443_All	714	0.07	0.14	0.45	0.42	0.24	1.52	0.36	2.05	4.24	9.53E-01	7.26E-01		2.61E+00	1.46E-01		-7.96E-01	5.57E-01		1.86E+00	1.00E-02		2.53E+00	1.65E-05	Up	3.58E+00	4.87E-15	Up	Unigene30443_All//gi|29836575|gb|AAM92562.1|//1.00E-104//protein kinase GhCLK1 [Gossypium herbaceum] >gi|29836577|gb|AAM92563.1| protein kinase GhCLK1 [Gossypium raimondii]	Unigene30443_All//1.00E-69//AT2G19400| protein kinase, putative	Unigene30443_All//0.00E+00//TC155182				nr +
Unigene30452_All	364	0.00	0.00	0.00	0.00	0.19	0.00	6.39	2.30	12.70	null	null		null	null		7.56E+00	6.09E-01		null	null		-1.48E+00	1.54E-04	Down	9.91E-01	6.11E-05								
Unigene30453_All	355	1.03	3.28	4.35	2.67	2.62	1.91	1.79	0.24	0.56	1.67E+00	1.33E-02		2.08E+00	8.49E-04	Up	-2.57E-02	9.56E-01		-4.82E-01	5.18E-01		-2.92E+00	4.19E-03		-1.67E+00	4.29E-02								
Unigene30454_All	648	0.40	0.70	0.00	1.31	3.19	9.34	0.00	0.45	0.80	8.02E-01	4.60E-01		-8.66E+00	8.57E-02		1.29E+00	4.17E-03		2.84E+00	3.42E-20	Up	8.82E+00	2.35E-02		9.64E+00	6.13E-04	Up	Unigene30454_All//gi|224131232|ref|XP_002321033.1|//7.00E-39//glutaredoxin [Populus trichocarpa] >gi|222861806|gb|EEE99348.1| glutaredoxin [Populus trichocarpa]	Unigene30454_All//4.00E-38//AT1G03020| glutaredoxin family protein	Unigene30454_All//0.00E+00//TC155902				nr +
Unigene30455_All	850	0.00	0.00	0.00	0.12	0.00	0.00	3.53	0.93	1.08	null	null		null	null		-6.87E+00	3.13E-01		-6.87E+00	4.00E-01		-1.92E+00	8.65E-08	Down	-1.71E+00	4.79E-07	Down	Unigene30455_All//gi|183229550|gb|ACG60273.1|//2.00E-69//aluminum-activated malate transporter [Glycine max]	Unigene30455_All//1.00E-52//AT3G11680| unknown protein					nr +
Unigene30456_All	382	11.78	4.64	1.67	10.43	6.94	1.54	0.00	1.53	1.15	-1.34E+00	6.42E-06	Down	-2.82E+00	1.15E-13	Down	-5.88E-01	4.56E-02		-2.76E+00	1.86E-13	Down	1.06E+01	2.81E-04	Up	1.02E+01	2.13E-03				Unigene30456_All//6.00E-136//ES821663				
Unigene30457_All	785	0.00	0.00	0.00	0.00	0.00	0.00	28.92	62.13	10.56	null	null		null	null		null	null		null	null		1.10E+00	7.53E-51	Up	-1.45E+00	8.14E-38	Down	Unigene30457_All//gi|224127144|ref|XP_002329411.1|//1.00E-101//alkaloid o-methyltransferase related [Populus trichocarpa] >gi|222870461|gb|EEF07592.1| alkaloid o-methyltransferase related [Populus trichocarpa]	Unigene30457_All//3.00E-46//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene30457_All//0.00E+00//TC157783		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene3046_All	2213	1.73	3.00	3.18	30.41	26.81	25.22	15.23	9.39	5.83	7.97E-01	4.93E-04		8.80E-01	1.33E-04		-1.82E-01	3.79E-03		-2.70E-01	1.61E-05		-6.98E-01	9.06E-17		-1.38E+00	9.04E-52	Down	Unigene3046_All//gi|30725324|gb|AAP37684.1|//3.00E-42//At3g01680 [Arabidopsis thaliana]	Unigene3046_All//2.00E-43//AT3G01680| unknown protein					nr -
Unigene30463_All	434	2.53	0.35	0.98	3.44	1.98	1.67	0.88	0.67	0.37	-2.85E+00	4.77E-04	Down	-1.37E+00	5.32E-02		-7.96E-01	1.31E-01		-1.05E+00	5.67E-02		-3.79E-01	7.23E-01		-1.26E+00	2.48E-01				Unigene30463_All//5.00E-07//TC156393				

Unigene30466_All	271	5.99	1.68	1.38	4.96	6.35	7.67	25.90	11.72	7.79	-1.83E+00	1.15E-03		-2.12E+00	5.11E-04	Down	3.56E-01	5.38E-01		6.27E-01	1.82E-01		-1.14E+00	1.90E-08	Down	-1.73E+00	1.35E-15	Down			Unigene30466_All//5.00E-77//gi|21095337|gb|BQ407650.1|BQ407650				
Unigene3047_All	2035	55.79	17.65	33.91	36.03	36.13	37.77	26.72	13.56	15.33	-1.66E+00	2.25E-179	Down	-7.18E-01	2.69E-45		3.80E-03	9.64E-01		6.80E-02	3.59E-01		-9.79E-01	9.73E-47		-8.02E-01	1.60E-34		Unigene3047_All//gi|15233723|ref|NP_194713.1|//0.00E+00//MTO2 (METHIONINE OVER-ACCUMULATOR 2); threonine synthase [Arabidopsis thaliana] >gi|20140904|sp|Q9SZB5.1|THRC1_ARATH RecName: Full=Threonine synthase 1, chloroplastic; AltName: Full=Protein METHIONINE OVER-ACCUMULATOR 2; Flags: Precursor >gi|4856369|dbj|BAA77707.1| threonine synthase [Arabidopsis thaliana] >gi|4914408|emb|CAB43659.1| threonine synthase [Arabidopsis thaliana] >gi|7269883|emb|CAB79742.1| threonine synthase [Arabidopsis thaliana]	Unigene3047_All//0.00E+00//AT4G29840| MTO2 (METHIONINE OVER-ACCUMULATOR 2); threonine synthase	Unigene3047_All//0.00E+00//TC152704		ko00260|Glycine, serine and threonine metabolism//ko00750|Vitamin B6 metabolism	GO:0006566//GO:0009536//GO:0016838//GO:0048037	nr +
Unigene30474_All	490	0.21	0.62	0.76	0.00	0.46	21.92	102.19	188.14	1.54E+00	3.23E-01		1.83E+00	2.13E-01		null	null		8.85E+00	1.19E-01		2.22E+00	1.13E-142	Up	3.10E+00	0.00E+00	Up	Unigene30474_All//gi|225434046|ref|XP_002273068.1|//5.00E-22//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene30474_All//3.00E-06//AT4G28460| unknown protein	Unigene30474_All//9.00E-09//DW505792				nr -
Unigene30475_All	325	82.91	43.97	25.07	55.79	60.39	44.89	150.39	54.66	77.47	-9.15E-01	2.34E-17		-1.73E+00	9.64E-44	Down	1.14E-01	4.52E-01		-3.14E-01	1.82E-02		-1.46E+00	1.32E-78	Down	-9.57E-01	9.91E-42		Unigene30475_All//gi|195606516|gb|ACG25088.1|//1.00E-16//histone H3 [Zea mays]	Unigene30475_All//7.00E-18//AT5G10980| histone H3	Unigene30475_All//7.00E-172//TC149940				nr -
Unigene30476_All	446	0.70	0.57	0.24	1.56	2.08	0.91	3.98	2.44	0.54	-3.10E-01	7.89E-01		-1.56E+00	3.30E-01		4.15E-01	6.06E-01		-7.79E-01	3.93E-01		-7.09E-01	1.09E-01		-2.89E+00	9.05E-08	Down								
Unigene30478_All	568	0.74	5.71	2.44	1.49	1.09	0.32	2.01	1.25	2.10	2.95E+00	6.74E-11	Up	1.73E+00	6.71E-03		-4.50E-01	5.52E-01		-2.23E+00	9.52E-03		-6.84E-01	2.37E-01		6.62E-02	9.19E-01									
Unigene30479_All	263	0.00	0.96	0.00	5.68	16.37	9.27	0.00	0.48	0.15	9.91E+00	7.86E-02		null	null		1.53E+00	2.21E-07	Up	7.07E-01	9.04E-02		8.90E+00	2.40E-01		7.24E+00	6.45E-01									
Unigene3048_All	2183	18.41	46.58	22.86	31.72	24.58	19.26	5.29	1.53	1.28	1.34E+00	2.23E-116	Up	3.12E-01	5.86E-05		-3.68E-01	1.26E-10		-7.20E-01	3.38E-31		-1.79E+00	2.31E-25	Down	-2.05E+00	2.74E-31	Down	Unigene3048_All//gi|224145241|ref|XP_002325575.1|//1.00E-166//multicopper oxidase [Populus trichocarpa] >gi|222862450|gb|EEE99956.1| multicopper oxidase [Populus trichocarpa]	Unigene3048_All//1.00E-136//AT5G09360| LACI4 (laccase 14); laccase	Unigene3048_All//0.00E+00//TC130768		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0008152//GO:0016682//GO:0046872	nr +
Unigene30480_All	1053	0.10	0.00	0.00	0.00	0.00	0.00	2.33	0.67	2.23	-6.64E+00	3.72E-01		-6.64E+00	3.93E-01		null	null		null	null		-1.79E+00	5.61E-06	Down	-6.11E-02	8.73E-01		Unigene30480_All//gi|15227274|ref|NP_179257.1|//1.00E-116//nodulin family protein [Arabidopsis thaliana] >gi|4581109|gb|AAD24599.1| nodulin-like protein [Arabidopsis thaliana] >gi|20165250|gb|AAM19945.1| At2g16660/T24I21.7 [Arabidopsis thaliana] >gi|23463081|gb|AAN33210.1| At2g16660/T24I21.7 [Arabidopsis thaliana]	Unigene30480_All//3.00E-78//AT2G16660| nodulin family protein					nr -
Unigene30482_All	721	0.00	0.21	0.00	0.00	0.86	0.38	2.05	3.07	4.70	7.72E+00	2.35E-01		null	null		9.75E+00	7.90E-04	Up	8.55E+00	7.03E-02		5.82E-01	1.37E-01		1.19E+00	6.82E-05	Up	Unigene30482_All//gi|116310937|emb|CAH67874.1|//3.00E-41//OSIGBa0153E02-OSIGBa0093I20.3 [Oryza sativa (indica cultivar-group)]	Unigene30482_All//7.00E-27//AT4G23160| protein kinase family protein					nr +
Unigene30486_All	576	3.45	6.33	6.38	15.13	12.08	29.09	415.17	536.67	910.55	8.76E-01	6.72E-03		8.86E-01	8.12E-03		-3.26E-01	1.01E-01		9.43E-01	3.24E-12		3.70E-01	6.32E-47		1.13E+00	0.00E+00	Up	Unigene30486_All//gi|38016531|gb|AB07601.1|//7.00E-65//fiber quinone-oxidoreductase [Gossypium barbadense]	Unigene30486_All//3.00E-48//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene30486_All//0.00E+00//gi|73861156|gb|DT463895.1|DT463895				nr -
Unigene30489_All	276	0.38	0.92	0.77	0.18	0.25	0.16	6.74	3.63	15.30	1.28E+00	4.35E-01		1.03E+00	5.91E-01		4.67E-01	9.58E-01		-1.42E-01	9.52E-01		-8.91E-01	3.70E-02		1.18E+00	8.12E-06	Up			Unigene30489_All//1.00E-120//DW508199				
Unigene3049_All	1905	13.10	14.47	10.40	2.43	3.40	0.90	0.22	0.18	0.00	1.43E-01	2.12E-01		-3.33E-01	3.74E-03		4.83E-01	3.61E-02		-1.43E+00	6.00E-07	Down	-3.38E-01	7.30E-01		-7.79E+00	2.14E-03		Unigene3049_All//gi|18412203|ref|NP_567121.1|//4.00E-80//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75294405|sp|Q70064.1|BH067_ARATH RecName: Full=Transcription factor bHLH67; AltName: Full=Transcription factor EN 11; AltName: Full=bHLH transcription factor bHLH067; AltName: Full=Basic helix-loop-helix protein 67; Short=bHLH 67; Short=AtbHLH67 >gi|45935017|gb|AAS79543.1| At3g61950 [Arabidopsis thaliana]	Unigene3049_All//2.00E-55//AT3G61950| basic helix-loop-helix (bHLH) family protein	Unigene3049_All//0.00E+00//TC168875	bHLH	ko04626|Plant-pathogen interaction	GO:0010468	nr +
Unigene30492_All	488	0.86	6.65	2.84	1.43	6.35	6.11	0.26	0.34	13.39	2.95E+00	6.74E-11	Up	1.73E+00	6.71E-03		2.15E+00	2.61E-08	Up	2.10E+00	2.41E-07	Up	3.99E-01	8.14E-01		5.69E+00	7.12E-42	Up	Unigene30492_All//gi|122703622|gb|ABM66381.1|//4.00E-14//pollen coat-like protein [Camellia sinensis]	Unigene30492_All//2.00E-07//AT5G38760| unknown protein	Unigene30492_All//0.00E+00//TC159468				nr +
Unigene30494_All	530	0.99	0.00	0.00	1.79	0.91	1.19	3.35	0.71	1.50	-9.95E+00	2.92E-03		-9.95E+00	4.75E-03		-9.73E-01	1.60E-01		-5.82E-01	4.37E-01		-2.24E+00	8.44E-06	Down	-1.16E+00	6.84E-03		Unigene30494_All//gi|297811869|ref|XP_002873818.1|//1.00E-41//phosphatidylinositolglycan class O (PIG-O) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319655|gb|EFH50077.1| phosphatidylinositolglycan class O (PIG-O) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene30494_All//4.00E-41//AT5G17250| catalytic/transferase					nr +
Unigene30498_All	257	0.20	1.77	4.97	2.52	2.01	0.53	0.16	0.81	0.16	3.12E+00	3.58E-02		4.61E+00	5.51E-06	Up	-3.26E-01	7.10E-01		-2.26E+00	2.76E-02		2.31E+00	2.40E-01		-8.58E-02	9.72E-01									
Unigene30499_All	295	5.14	0.34	0.00	4.39	2.45	0.92	2.29	0.00	0.68	-3.90E+00	9.44E-07	Down	-1.23E+01	2.73E-08	Down	-8.41E-01	1.44E-01		-2.26E+00	6.70E-04	Down	-1.12E+01	6.34E-05	Down	-1.76E+00	2.80E-02		Unigene30499_All//gi|18056482|emb|CAC83650.1|//7.00E-10//CDC6b protein [Arabidopsis thaliana]	Unigene30499_All//3.00E-11//AT1G07270| cell division control protein CDC6b, putative (CDC6b)					nr -
Unigene30500_All	329	0.95	0.62	0.00	3.03	0.63	1.37	2.18	1.02	0.12	-6.31E-01	6.22E-01		-9.90E+00	4.91E-02		-2.27E+00	1.67E-03		-1.14E+00	1.09E-01		-1.10E+00	1.49E-01		-4.17E+00	1.64E-04	Down	Unigene30500_All//gi|158578541|gb|ABW74566.1|//9.00E-12//integrase [Boechera divaricarpa]						nr -
Unigene30503_All	592	1.15	0.51	0.54	7.07	5.93	4.12	3.86	2.19	1.28	-1.16E+00	1.89E-01		-1.09E+00	2.39E-01		-2.53E-01	4.37E-01		-7.79E-01	8.15E-03		-8.17E-01	3.07E-02		-1.59E+00	4.22E-05	Down	Unigene30503_All//gi|255563929|ref|XP_002522964.1|//4.00E-15//Disease resistance protein RGA2, putative [Ricinus communis] >gi|223537776|gb|EEF39394.1| Disease resistance protein RGA2, putative [Ricinus communis]		Unigene30503_All//0.00E+00//DT457825				nr +
Unigene30504_All	430	2.56	1.65	1.98	3.94	2.24	1.16	0.98	0.97	0.46	-6.31E-01	3.35E-01		-3.67E-01	6.01E-01		-8.13E-01	9.38E-02		-1.77E+00	9.00E-04	Down	-1.67E-02	1.02E+00		-1.09E+00	2.82E-01		Unigene30504_All//gi|195605628|gb|ACG24644.1|//1.00E-28//protein SYS1 [Zea mays]	Unigene30504_All//6.00E-27//AT1G79990| LOCATED IN: endomembrane system, COPI vesicle coat, Golgi membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SYS1 homologue (InterPro:IPR016972); Has 55556 Blast hits to 24059 proteins in 620 species: Archae - 38; Bacteria - 5697; Metazoa - 25539; Fungi - 10898; Plants - 5309; Viruses - 0; Other Eukaryotes - 8075 (source: NCBI BLink).	Unigene30504_All//4.00E-69//DW519727				nr +
Unigene30506_All	471	0.00	0.00	0.00	0.00	0.00	0.00	2.15	2.75	0.00	null	null		null	null		null	null		null	null		3.53E-01	5.36E-01		-1.11E+01	1.35E-07	Down								
Unigene30508_All	407	2261.11	1464.31	1545.43	71.36	63.29	31.51	2.60	1.23	1.47	-6.27E-01	2.34E-295		-5.49E-01	2.79E-226		-1.73E-01	1.04E-01		-1.18E+00	4.91E-30	Down	-1.08E+00	7.50E-02		-8.23E-01	1.50E-01		Unigene30508_All//gi|4754913|gb|AAD29049.1|AF132854_1//2.00E-33//carbonic anhydrase isoform 1 [Gossypium hirsutum]	Unigene30508_All//2.00E-15//AT3G01500| CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	Unigene30508_All//0.00E+00//gi|109878430|gb|DW507400.1|DW507400		ko00910|Nitrogen metabolism		nr +
Unigene30509_All	551	0.10	0.00	0.00	1.81	2.06	0.16	1.38	0.68	0.94	-6.57E+00	6.12E-01		-6.57E+00	6.24E-01		1.90E-01	8.14E-01		-3.46E+00	1.73E-04	Down	-1.02E+00	1.69E-01		-5.55E-01	4.23E-01		Unigene30509_All//gi|240254041|ref|NP_172303.4|//3.00E-49//TIL1 (TILTED 1); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding / zinc ion binding [Arabidopsis thaliana]	Unigene30509_All//2.00E-50//AT1G08260| TIL1 (TILTED 1); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding / zinc ion binding			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication		nr -
Unigene3051_All	1952	26.00	17.60	34.62	14.04	16.19	8.51	2.40	0.92	1.47	-5.63E-01	3.92E-14		4.13E-01	2.14E-10		2.06E-01	3.64E-02		-7.21E-01	9.67E-13		-1.38E+00	1.11E-07	Down	-7.10E-01	3.02E-03		Unigene3051_All//gi|18398119|ref|NP_564384.1|//0.00E+00//CYP97A3 (CYTOCHROME P450-TYPE MONOOXYGENASE 97A3); carotene beta-ring hydroxylase/ oxygen binding [Arabidopsis thaliana] >gi|15912337|gb|AAL08302.1| At1g31800/68069_m00159 [Arabidopsis thaliana] >gi|16648793|gb|AAL25587.1| At1g31800/68069_m00159 [Arabidopsis thaliana] >gi|22655378|gb|AAM98281.1| At1g31800/68069_m00159 [Arabidopsis thaliana]	Unigene3051_All//0.00E+00//AT1G31800| CYP97A3 (CYTOCHROME P450-TYPE MONOOXYGENASE 97A3); carotene beta-ring hydroxylase/ oxygen binding	Unigene3051_All//0.00E+00//TC172389		ko00906|Carotenoid biosynthesis//ko00590|Arachidonic acid metabolism	GO:0005506//GO:0009536//GO:0016117//GO:0016712	nr +
Unigene30510_All	460	0.46	0.66	1.16	2.49	1.42	1.47	5.42	3.73	1.91	5.39E-01	6.71E-01		1.35E+00	2.25E-01		-8.08E-01	1.92E-01		-7.58E-01	2.45E-01		-5.42E-01	1.39E-01		-1.51E+00	3.80E-05	Down	Unigene30510_AllI//gi|40809691|dbj|BAD07265.1|//5.00E-72//alpha-tubulin [Cepedea sp. BrS]	Unigene30510_All//2.00E-40//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene30510_All//5.00E-81//TC152174		ko04145|Phagosome		nr +
Unigene30515_All	452	1.16	1.01	0.24	0.33	1.83	0.40	1.87	0.28	0.79	-1.98E-01	8.20E-01		-2.30E+00	6.76E-02		2.47E+00	6.72E-03		2.74E-01	9.05E-01		-2.75E+00	9.73E-04	Down	-1.24E+00	6.26E-02		Unigene30515_All//gi|224106015|ref|XP_002314014.1|//3.00E-21//tubulin, beta chain [Populus trichocarpa] >gi|222850422|gb|EEE87969.1| tubulin, beta chain [Populus trichocarpa]	Unigene30515_All//4.00E-22//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene30515_All//2.00E-74//ES846230		ko04145|Phagosome		nr -
Unigene30518_All	439	10.49	3.69	10.43	3.86	1.80	3.09	0.00	0.19	0.00	-1.51E+00	5.16E-07	Down	-7.80E-03	1.00E+00		-1.10E+00	2.21E-02		-3.22E-01	5.65E-01		7.57E+00	4.01E-01		null	null		Unigene30518_All//gi|77540212|gb|AB386964.1|//9.00E-24//glyceraldehyde-3-phosphate dehydrogenase B subunit [Glycine max]	Unigene30518_All//2.00E-17//AT1G42970| GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase (NAD(P+))/ glyceraldehyde-3-phosphate dehydrogenase	Unigene30518_All//2.00E-133//TC138490		ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene30520_All	239	11.16	2.97	10.47	9.80	9.80	6.61	0.53	0.00	1.33	-1.91E+00	8.10E-06	Down	-9.24E-02	8.12E-01		2.00E-04	9.89E-01		-5.67E-01	1.93E-01		-9.05E+00	2.35E-01		1.33E+00	2.93E-01				Unigene30520_All//4.00E-111//CO491965				

Unigene30524_All	479	0.22	0.42	1.56	3.54	1.22	1.23	79.35	139.61	272.30	9.53E-01	6.21E-01		2.83E+00	8.52E-03		-1.53E+00	1.66E-03		-1.53E+00	3.33E-03		8.15E-01	3.30E-42		1.78E+00	2.69E-282	Up	Unigene30524_All//gi|297828435|ref|XP_002882100.1|//7.00E-77//P-glycoprotein 4, P-glycoprotein4 [Arabidopsis lyrata subsp. lyrata] >gi|297327939|gb|EFH58359.1| P-glycoprotein 4, P-glycoprotein4 [Arabidopsis lyrata subsp. lyrata]	Unigene30524_All//2.00E-72//AT2G47000| ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase	Unigene30524_All//0.00E+00//DT462038		ko02010|ABC transporters		nr +
Unigene30525_All	263	1.59	1.54	2.02	10.61	17.55	1.20	0.32	0.00	2.27	-4.62E-02	9.80E-01		3.47E-01	7.06E-01		7.26E-01	7.78E-03		-3.14E+00	8.36E-11	Down	-8.33E+00	4.04E-01		2.82E+00	5.65E-03					Unigene30525_All//3.00E-109//C0497323				
Unigene30534_All	265	0.99	0.38	1.61	6.39	2.73	1.19	0.48	0.79	1.50	-1.37E+00	3.83E-01		7.03E-01	5.54E-01		-1.23E+00	1.06E-02		-2.42E+00	2.78E-05	Down	7.21E-01	6.32E-01		1.65E+00	1.40E-01									
Unigene30535_All	275	0.38	5.16	1.36	4.17	2.00	0.66	1.08	0.00	0.00	3.76E+00	3.98E-06	Up	1.83E+00	2.13E-01		-1.06E+00	8.45E-02		-2.67E+00	4.12E-04	Down	-1.01E+01	2.18E-02		-1.01E+01	1.58E-02					Unigene30535_All//2.00E-101//ES835500				
Unigene30537_All	262	0.00	3.09	0.00	1.33	0.79	0.52	1.45	1.91	1.06	1.16E+01	9.38E-05	Up	null	null		-7.55E-01	5.67E-01		-1.36E+00	3.57E-01		3.98E-01	6.52E-01		-4.48E-01	6.41E-01									
Unigene30538_All	369	1618.83	1463.65	2506.93	962.13	823.74	691.77	28.19	1.47	2.81	-1.45E-01	6.81E-13		6.31E-01	2.31E-292		-2.24E-01	1.06E-20		-4.76E-01	2.58E-75		-4.26E+00	2.16E-56	Down	-3.33E+00	4.73E-48	Down	Unigene30538_All//sp|P03276|PEN3_ADE02//6.00E-57//Penton protein OS=Human adenovirus C serotype 2 GN=PIII PE=1 SV=1						swissprot +
Unigene3054_All	1721	10.58	20.64	14.29	36.50	38.98	13.12	6.61	4.13	3.38	9.64E-01	1.55E-24		4.34E-01	1.36E-04		9.48E-02	1.94E-01		-1.48E+00	4.75E-91	Down	-6.79E-01	6.04E-06		-9.67E-01	1.42E-10		Unigene3054_All//0.00E+00//AT1G70710| ATGH9B1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9B1); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene3054_All//0.00E+00//TC159092		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0009536//GO:0009825//GO:0044238	nr +
Unigene30544_All	298	4.74	15.81	6.61	5.52	2.20	2.58	17.45	12.06	23.53	1.74E+00	1.48E-08	Up	4.80E-01	3.31E-01		-1.33E+00	6.77E-03		-1.10E+00	3.43E-02		-5.33E-01	2.36E-02		4.31E-01	2.61E-02					Unigene30544_All//3.00E-134//gi|109841680|gb|DW240240.1|DW240240				
Unigene30545_All	301	1.74	2.02	6.72	2.48	0.46	0.00	0.42	0.00	0.26	2.17E-01	7.93E-01		1.95E+00	1.89E-04	Up	-2.44E+00	5.60E-03		-1.13E+01	9.81E-05	Down	-8.72E+00	2.35E-01		-6.71E-01	7.20E-01					Unigene30545_All//2.00E-67//DW505512				
Unigene30548_All	234	3.13	8.01	5.92	2.55	7.80	15.44	0.36	0.54	1.02	1.36E+00	5.88E-03		9.19E-01	1.27E-01		1.61E+00	1.19E-03		2.60E+00	3.73E-11	Up	5.68E-01	7.82E-01		1.50E+00	3.39E-01					Unigene30548_All//4.00E-120//TC174608				
Unigene3055_All	1491	34.04	14.10	31.39	4.71	4.06	7.09	0.91	0.64	1.07	-1.27E+00	3.82E-54	Down	-1.17E-01	1.74E-01		-2.13E-01	3.86E-01		5.89E-01	6.57E-04		-4.93E-01	3.67E-01		2.36E-01	6.16E-01		Unigene3055_All//gi|18395855|ref|NP_566142.1|//1.00E-137//PPT2 (PHOSPHOENOLPYRUVATE (PEP)/PHOSPHATE TRANSLOCATOR 2); antiporter/ triose-phosphate transmembrane transporter [Arabidopsis thaliana] >gi|30725606|gb|AAP37825.1| At3g01550 [Arabidopsis thaliana]	Unigene3055_All//2.00E-138//AT3G01550| PPT2 (PHOSPHOENOLPYRUVATE (PEP)/PHOSPHATE TRANSLOCATOR 2); antiporter/ triose-phosphate transmembrane transporter	Unigene3055_All//0.00E+00//gi|109880844|gb|DW509814.1|DW509814				nr +
Unigene30551_All	2987	0.00	0.00	0.00	0.00	0.00	0.00	6.09	0.43	7.76	null	null		null	null		null	null		null	null		-3.81E+00	1.25E-90	Down	3.51E-01	4.21E-04		Unigene30551_All//gi|297719681|ref|NP_001172202.1|//1.00E-105//0s01g0176800 [Oryza sativa Japonica Group] >gi|255672929|dbj|BAH90932.1| Os01g0176800 [Oryza sativa Japonica Group]	Unigene30551_All//1.00E-110//AT1G52780| unknown protein					nr +
Unigene30553_All	262	9.39	20.11	19.11	9.70	11.83	16.55	36.31	46.10	26.15	1.10E+00	3.66E-05	Up	1.03E+00	2.76E-04	Up	2.87E-01	4.76E-01		7.71E-01	8.03E-03		3.45E-01	2.09E-02		-4.73E-01	3.39E-03					Unigene30553_All//2.00E-122//gi|164253436|gb|ES806362.1|ES806362				
Unigene30554_All	337	0.47	0.30	0.47	0.00	0.00	0.00	2.38	3.47	0.00	-6.31E-01	7.27E-01		2.52E-02	1.00E+00		null	null		null	null		5.43E-01	3.59E-01		-1.12E+01	4.43E-06	Down								
Unigene30556_All	341	0.00	1.04	1.72	2.05	0.00	0.93	1.36	0.00	0.47	1.00E+01	2.46E-02		1.07E+01	2.17E-03		-1.10E+01	3.44E-05	Down	-1.14E+00	2.01E-01		-1.04E+01	1.71E-03		-1.55E+00	1.16E-01		Unigene30556_All//gi|115473321|ref|NP_001060259.1|//3.00E-17//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene30556_All//9.00E-05//AT1G43760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706), Endonuclease/exonuclease/phosphatase (InterPro:IPR005135); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40390.1); Has 2614 Blast hits to 2551 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 1517; Fungi - 2; Plants - 1086; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).					nr +
Unigene3056_All	1429	3.11	1.45	1.98	2.54	2.02	2.37	3.67	2.02	2.26	-1.10E+00	1.69E-04	Down	-6.56E-01	2.88E-02		-3.30E-01	3.22E-01		-1.02E-01	7.63E-01		-8.62E-01	2.17E-04		-7.00E-01	1.87E-03		Unigene3056_All//gi|30695792|ref|NP_173866.2|//1.00E-106//methyltransferase [Arabidopsis thaliana] >gi|56550685|gb|AAV97796.1| At1g51650 [Arabidopsis thaliana]	Unigene3056_All//9.00E-108//AT1G51650| methyltransferase	Unigene3056_All//0.00E+00//TC138738		ko00350|Tyrosine metabolism//ko00450|Selenoamino acid metabolism//ko00340|Histidine metabolism		nr -
Unigene30566_All	2121	0.00	0.14	0.00	0.47	0.52	0.49	30.46	12.45	7.55	7.16E+00	4.43E-02		null	null		1.45E-01	8.37E-01		6.02E-02	9.47E-01		-1.29E+00	5.96E-86	Down	-2.01E+00	1.92E-167	Down	Unigene30566_All//gi|156447779|gb|ABU63668.1|//1.00E-150//CYCLOPS [Lotus japonicus]						nr +
Unigene30567_All	560	0.09	3.71	1.24	0.36	1.29	2.34	0.23	0.00	0.00	5.31E+00	1.58E-10	Up	3.73E+00	3.99E-03		1.86E+00	4.52E-02		2.72E+00	1.49E-04	Up	-7.82E+00	2.35E-01		-7.82E+00	2.00E-01									
Unigene3057_All	1474	4.37	5.53	3.03	15.38	12.97	5.52	9.35	0.74	3.95	3.42E-01	1.03E-01		-5.25E-01	3.17E-02		-2.46E-01	3.35E-02		-1.48E+00	3.02E-33	Down	-3.67E+00	1.03E-66	Down	-1.24E+00	1.55E-18	Down	Unigene3057_All//gi|18412659|ref|NP_567142.1|//1.00E-157//PLP9 (PATATIN-LIKE PROTEIN 9); nutrient reservoir [Arabidopsis thaliana] >gi|15912227|gb|AAL08247.1| AT3g63200/F16M2_50 [Arabidopsis thaliana] >gi|24111291|gb|AAN46769.1| At3g63200/F16M2_50 [Arabidopsis thaliana]	Unigene3057_All//1.00E-151//AT3G63200| PLP9 (PATATIN-LIKE PROTEIN 9); nutrient reservoir	Unigene3057_All//0.00E+00//TC155243				nr -
Unigene30571_All	422	0.00	0.00	0.00	0.71	0.33	2.14	5.31	0.00	0.57	null	null		null	null		-1.12E+00	4.24E-01		1.60E+00	4.34E-02		-1.24E+01	7.52E-16	Down	-3.23E+00	1.32E-10	Down				Unigene30571_All//4.00E-174//TC162786				
Unigene30573_All	433	11.36	17.79	16.60	260.92	90.26	337.84	1430.01	1901.66	863.85	6.47E-01	2.04E-03		5.48E-01	1.63E-02		-1.53E+00	6.65E-199	Down	3.73E-01	5.06E-20		4.11E-01	3.30E-150		-7.27E-01	0.00E+00		Unigene30573_All//gi|170442|gb|AAA34163.1|//3.00E-18//extensin (class I) [Solanum lycopersicum]		Unigene30573_All//0.00E+00//gi|164330959|gb|ES822453.1|ES822453		ko03040|Spliceosome//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr +
Unigene30574_All	740	0.00	0.00	0.00	0.00	0.00	0.00	1.43	3.61	1.83	null	null		null	null		null	null		null	null		1.34E+00	1.64E-04	Up	3.58E-01	4.90E-01									
Unigene30576_All	275	0.38	0.37	0.77	2.17	1.25	1.97	19.06	5.78	26.08	-4.62E-02	9.89E-01		1.03E+00	5.91E-01		-7.96E-01	3.88E-01		-1.41E-01	8.79E-01		-1.72E+00	2.22E-11	Down	4.52E-01	1.78E-02					Unigene30576_All//2.00E-76//DR455269				
Unigene30579_All	262	0.80	5.61	2.24	2.47	6.31	2.59	0.65	0.00	0.00	2.81E+00	4.58E-05	Up	1.48E+00	1.53E-01		1.35E+00	9.24E-03		6.51E-02	9.50E-01		-9.33E+00	1.34E-01		-9.33E+00	1.08E-01									
Unigene3058_All	660	1.98	1.31	5.97	2.87	6.26	3.90	3.33	2.03	1.03	-6.03E-01	3.07E-01		1.59E+00	3.16E-06	Up	1.13E+00	1.09E-04	Up	4.44E-01	3.01E-01		-7.17E-01	6.46E-02		-1.70E+00	2.47E-05	Down	Unigene3058_All//gi|7769863|gb|AAF69541.1|AC008807_16//6.00E-37//F12M16.29 [Arabidopsis thaliana]	Unigene3058_All//1.00E-37//AT1G53400| unknown protein	Unigene3058_All//2.00E-127//TC141948			GO:0005488	nr -
Unigene30582_All	255	29.14	11.13	10.23	27.35	15.26	44.81	63.17	31.80	30.46	-1.39E+00	1.07E-09	Down	-1.51E+00	2.29E-10	Down	-8.42E-01	4.11E-05		7.12E-01	1.52E-05		-9.90E-01	1.10E-14		-1.05E+00	1.22E-16	Down	Unigene30582_All//gi|226503021|ref|NP_001149705.1|//6.00E-30//40S ribosomal protein S9 [Zea mays] >gi|195629612|gb|ACG36447.1| 40S ribosomal protein S9 [Zea mays]	Unigene30582_All//8.00E-30//AT5G39850| 40S ribosomal protein S9 (RPS9C)	Unigene30582_All//4.00E-142//gi|84149076|gb|DN780376.1|DN780376		ko03010|Ribosome		nr +
Unigene30584_All	721	0.00	0.70	0.00	0.21	0.19	0.69	2.40	0.52	1.16	9.46E+00	4.04E-03		null	null		-1.18E-01	9.11E-01		1.73E+00	1.45E-01		-2.20E+00	1.38E-05	Down	-1.05E+00	1.45E-02		Unigene30584_All//gi|226500662|ref|NP_001147306.1|//1.00E-37//flavoprotein wrbA [Zea mays] >gi|195609730|gb|ACG26695.1| flavoprotein wrbA [Zea mays]	Unigene30584_All//3.00E-40//AT4G36750| quinone reductase family protein	Unigene30584_All//4.00E-52//gi|78347943|gb|DT568217.1|DT568217				nr +
Unigene30586_All	458	1.03	1.77	1.05	4.79	1.35	1.08	0.00	0.00	0.35	7.84E-01	3.23E-01		2.55E-02	1.00E+00		-1.82E+00	2.16E-05	Down	-2.14E+00	7.83E-06	Down	null	null		8.44E+00	1.40E-01		Unigene30586_All//gi|229609893|gb|ACQ83562.1|//4.00E-19//calcineurin B-like protein 08 [Vitis vinifera]	Unigene30586_All//1.00E-19//AT5G24270| SOS3 (SALT OVERLY SENSITIVE 3); calcium ion binding / calcium-dependent protein serine/threonine phosphatase	Unigene30586_All//2.00E-15//TC156917		ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene3059_All	851	23.24	7.50	16.02	26.17	28.65	18.89	6.01	4.96	4.26	-1.63E+00	5.61E-31	Down	-5.37E-01	2.69E-05		1.31E-01	3.15E-01		-4.70E-01	3.24E-05		-2.77E-01	2.79E-01		-4.97E-01	3.03E-02		Unigene3059_All//gi|7769863|gb|AAF69541.1|AC008807_16//3.00E-44//F12M16.29 [Arabidopsis thaliana]	Unigene3059_All//4.00E-45//AT1G53400| unknown protein	Unigene3059_All//0.00E+00//TC141948			GO:0005488	nr +
Unigene30593_All	540	0.00	3.38	4.34	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.14E-10	Up	1.21E+01	6.41E-13	Up	null	null		null	null		null	null		null	null		Unigene30593_All//gi|297846544|ref|XP_002891153.1|//3.00E-56//At1g31330/T19E23_1 [Arabidopsis lyrata subsp. lyrata] >gi|297336995|gb|EFH67412.1| At1g31330/T19E23_1 [Arabidopsis lyrata subsp. lyrata]	Unigene30593_All//2.00E-66//AT1G31330| PSAF (photosystem I subunit F)	Unigene30593_All//3.00E-30//TC136116		ko00195|Photosynthesis		nr -
Unigene30608_All	256	4.70	0.20	2.08	5.25	3.23	4.23	6.11	1.96	2.02	-4.57E+00	5.88E-06	Down	-1.18E+00	7.58E-02		-7.03E-01	2.18E-01		-3.11E-01	6.37E-01		-1.64E+00	1.02E-03		-1.59E+00	9.20E-04	Down								
Unigene30609_All	233	43.79	124.17	42.97	56.87	62.22	77.15	226.46	447.20	317.17	1.50E+00	7.94E-40	Up	-2.73E-02	8.97E-01		1.30E-01	4.61E-01		4.40E-01	6.54E-04		9.82E-01	3.97E-89		4.86E-01	1.45E-19		Unigene30609_All//gi|241740196|gb|ACS68205.1|//1.00E-36//ubiquitin 10.2 [Brassica napus]	Unigene30609_All//4.00E-38//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene30609_All//5.00E-129//gi|109837424|gb|DW235985.1|DW235985				nr -
Unigene30613_All	338	3.25	0.90	0.32	3.68	2.45	4.54	2.25	0.37	0.35	-1.85E+00	8.99E-03		-3.37E+00	2.67E-04	Down	-5.92E-01	3.18E-01		3.02E-01	6.35E-01		-2.60E+00	2.81E-03		-2.67E+00	1.64E-03		Unigene30613_All//gi|15220076|ref|NP_178136.1|//1.00E-24//PSF1 (PARTNER OF SLD FIVE 1) [Arabidopsis thaliana] >gi|5902373|gb|AAD55475.1|AC009322_15 [unknown protein [Arabidopsis thaliana] >gi|34365591|gb|AAQ65107.1| At1g80190 [Arabidopsis thaliana] >gi|51969246|dbj|BAD43315.1| At1g80190 [Arabidopsis thaliana]	Unigene30613_All//2.00E-25//AT1G80190| PSF1 (PARTNER OF SLD FIVE 1)	Unigene30613_All//9.00E-70//ES850894				nr +
Unigene30614_All	431	478.66	826.23	1921.82	1.27	0.00	0.00	0.00	0.00	0.18	7.88E-01	1.97E-170		2.01E+00	0.00E+00	Up	-1.03E+01	4.01E-04	Down	-1.03E+01	1.52E-03		null	null		7.53E+00	4.04E-01		Unigene30614_All//gi|110816009|gb|ABG91752.1|//1.00E-13//HyPRP2 [Gossypium hirsutum]		Unigene30614_All//6.00E-99//gi|109884747|gb|DW513717.1|DW513717				nr -
Unigene30616_All	411	0.38	0.37	0.39	0.61	0.50	0.77	4.22	1.42	1.74	-4.64E-02	9.89E-01		2.55E-02	1.00E+00		-2.70E-01	8.23E-01		3.44E-01	7.97E-01		-1.57E+00	7.85E-04	Down	-1.27E+00	3.64E-03					Unigene30616_All//9.00E-18//CO119622				ESTscan -
Unigene30619_All	260	3.82	0.39	5.33	10.73	3.97	5.73	1.30	0.32	0.00	-3.29E+00	3.81E-04	Down	4.78E-01	4.06E-01		-1.43E+00	6.68E-05	Down	-9.04E-01	1.58E-02		-2.02E+00	1.36E-01		-1.03E+01	8.14E-03					Unigene30619_All//5.00E-09//BQ408176				
Unigene30620_All	329	5.25	8.62	15.05	48.45	60.29	39.26	1.93	4.57	5.09	7.17E-01	5.45E-02		1.52E+00	3.27E-07	Up	3.15E-01	9.68E-03		-3.04E-01	3.58E-02		1.25E+00	1.16E-02		1.40E+00	2.16E-03		Unigene30620_All//gi|224119134|ref|XP_002331333.1|//2.00E-13//cytochrome P450 [Populus trichocarpa] >gi|222873916|gb|EEF11047.1| cytochrome P450 [Populus trichocarpa]	Unigene30620_All//3.00E-11//AT1G17060| CYP72C1 (CYTOCHROME P450 72C1); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene30620_All//4.00E-84//TC139184				nr -
Unigene30625_All	348	0.00	0.00	0.00	2.43	0.10	0.26	0.85	1.32	1.95	null	null		null	null		-4.62E+00	2.79E-05	Down	-3.23E+00	1.04E-03		6.35E-01	5.36E-01		1.19E+00	1.20E-01		Unigene30625_All//gi|224106451|ref|XP_002314170.1|//1.00E-32//GRAS family transcription factor [Populus trichocarpa] >gi|222856578|gb|EEE88125.1| GRAS family transcription factor [Populus trichocarpa]	Unigene30625_All//3.00E-29//AT2G29060| scarecrow transcription factor family protein		GRAS			nr +
Unigene30634_All	482	0.00	0.00	0.00	0.10	0.29	0.19	44.47	91.48	107.45	null	null		null	null		1.47E+00	6.19E-01		8.59E-01	7.94E-01		1.04E+00	6.07E-42	Up	1.27E+00	5.72E-69	Up	Unigene30634_All//gi|75267717|sp|Q9ZP41.1|EGC_CITJA//1.00E-12//RecName: Full=EG45-like domain containing protein; AltName: Full=Blight-associated protein p12; AltName: Full=Plant natriuretic peptide; Short=PNP; Flags: Precursor >gi|4102727|gb|AAD03398.1| blight-associated protein p12 precursor [Citrus jambhiri]	Unigene30634_All//5.00E-12//AT2G18660| EXLB3 (EXPANSIN-LIKE B3 PRECURSOR)					nr -

Unigene30640_All	657	0.08	0.00	0.32	0.91	0.84	11.89	2.25	0.00	0.00	-6.31E+00	6.12E-01		2.03E+00	3.61E-01		-1.18E-01	8.76E-01		3.71E+00	4.26E-33	Up	-1.11E+01	1.68E-10	Down	-1.11E+01	5.85E-11	Down	Unigene30640_All//gi|85069285|gb|ABC69714.1|//2.00E-26//ARF2-like protein [Nicotiana tabacum]	Unigene30640_All//2.00E-21//AT5G62000| ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Unigene30640_All//0.00E+00//ES830051	ARF			nr -
Unigene30641_All	564	0.00	12.40	3.68	0.00	0.00	0.00	0.00	0.00	1.36E+01	5.86E-40	Up	1.18E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene30641_All//gi|301113542|ref|XP_002998541.1|//3.00E-32//heat shock protein 90 [Phytophthora infestans T30-4] >gi|262111842|gb|EEY69894.1| heat shock protein 90 [Phytophthora infestans T30-4]	Unigene30641_All//2.00E-29//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene30642_All	308	0.34	0.82	0.00	1.13	0.56	0.44	2.75	5.29	7.63	1.28E+00	4.35E-01		-8.41E+00	3.93E-01		-1.02E+00	4.23E-01		-1.36E+00	3.37E-01		9.47E-01	4.07E-02		1.47E+00	1.04E-04	Up								
Unigene30647_All	724	0.14	0.00	0.00	0.48	0.10	0.69	0.76	1.39	2.37	-7.17E+00	3.72E-01		-7.17E+00	3.93E-01		-2.34E+00	1.01E-01		5.11E-01	6.41E-01		8.68E-01	1.64E-01		1.64E+00	4.04E-04	Up	Unigene30647_All//gi|4249381|gb|AAD14478.1|//3.00E-09//Strong similarity to gb|AF039376 Evelknievel retrotransposon polyprotein from Arabidopsis arenosa [Arabidopsis thaliana]		Unigene30647_All//1.00E-11//gi|78324799|gb|DT545073.1|DT545073				nr -
Unigene30650_All	307	0.00	0.00	0.00	12.17	1.23	4.71	1.10	0.00	0.26	null	null		null	null		-3.30E+00	2.07E-17	Down	-1.37E+00	2.10E-05	Down	-1.01E+01	1.17E-02		-2.09E+00	1.07E-01				Unigene30650_All//2.00E-163//DR460393					
Unigene30656_All	468	1.12	3.03	1.93	2.02	0.88	0.19	0.00	0.00	0.17	1.44E+00	1.37E-02		7.91E-01	3.04E-01		-1.20E+00	8.31E-02		-3.39E+00	3.18E-04	Down	null	null		7.41E+00	4.04E-01				Unigene30656_All//5.00E-07//TC179257					
Unigene30662_All	592	11.67	6.08	10.16	10.35	8.84	6.56	0.43	0.28	1.95	-9.41E-01	2.95E-05		-1.99E-01	4.14E-01		-2.27E-01	3.89E-01		-6.58E-01	5.34E-03		-6.02E-01	6.48E-01		2.19E+00	4.81E-04	Up	Unigene30662_All//gi|240255348|ref|NP_188102.4|//2.00E-07//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana]	Unigene30662_All//1.00E-08//AT3G14840| leucine-rich repeat family protein / protein kinase family protein					nr -
Unigene30663_All	443	0.24	0.46	0.12	1.91	0.62	0.61	0.38	2.36	1.71	9.54E-01	6.21E-01		-9.75E-01	7.21E-01		-1.62E+00	3.13E-02		-1.64E+00	4.18E-02		2.63E+00	2.86E-04	Up	2.16E+00	6.98E-03									
Unigene30664_All	490	1.28	0.21	0.00	0.20	1.05	1.47	2.42	0.51	3.41	-2.63E+00	1.78E-02		-1.03E+01	1.41E-03		2.37E+00	5.64E-02		2.86E+00	7.12E-03		-2.24E+00	4.21E-04	Down	4.99E-01	2.63E-01				Unigene30664_All//2.00E-49//ES808398					
Unigene30667_All	236	5.10	1.29	0.68	1.90	2.19	1.34	0.00	0.18	0.00	-1.98E+00	3.72E-03		-2.91E+00	3.56E-04	Down	2.04E-01	8.59E-01		-5.04E-01	6.49E-01		7.47E+00	6.34E-01		null	null				Unigene30667_All//3.00E-07//TC151127					
Unigene30668_All	635	777.89	430.25	881.18	104.88	95.71	56.69	3.80	1.12	1.76	-8.54E-01	2.25E-272		1.80E-01	3.06E-17		-1.32E-01	4.98E-02		-8.88E-01	6.47E-43		-1.76E+00	8.64E-06	Down	-1.11E+00	1.88E-03		Unigene30668_All//gi|159895667|gb|ABX10444.1|//1.00E-55//phosphoethanolamine N-methyltransferase [Gossypium hirsutum]	Unigene30668_All//1.00E-49//AT1G48600| phosphoethanolamine N-methyltransferase 2, putative (NMT2)	Unigene30668_All//1.00E-175//gi|84172382|gb|DR461030.1|DR461030		ko00564|Glycerophospholipid metabolism//ko00100|Steroid biosynthesis		nr -
Unigene30669_All	437	1.68	1.39	0.73	0.46	0.39	1.45	1.06	2.49	3.56	-2.69E-01	7.19E-01		-1.20E+00	1.80E-01		-2.11E-01	8.59E-01		1.67E+00	9.79E-02		1.22E+00	4.08E-02		1.74E+00	4.59E-04	Up								
Unigene30670_All	647	0.49	2.04	0.49	1.54	2.18	1.75	0.46	0.65	1.91	2.07E+00	1.71E-03		2.53E-02	1.00E+00		5.03E-01	4.15E-01		1.81E-01	7.84E-01		4.98E-01	6.33E-01		2.06E+00	5.00E-04	Up			Unigene30670_All//4.00E-67//DR459403					
Unigene30673_All	543	3.57	0.93	1.18	0.83	0.19	0.75	0.16	0.00	0.51	-1.93E+00	1.74E-04	Down	-1.60E+00	1.93E-03		-2.12E+00	7.28E-02		-1.41E-01	9.00E-01		-7.28E+00	4.04E-01		1.72E+00	2.30E-01		Unigene30673_All//gi|124360612|gb|ABN08611.1|//1.00E-53//CBS [Medicago truncatula]	Unigene30673_All//3.00E-33//AT4G27460| CBS domain-containing protein	Unigene30673_All//2.00E-22//gi|48815122|gb|C0116435.1|C0116435				nr -
Unigene30674_All	1713	0.00	0.00	0.00	0.00	0.00	0.00	15.72	5.15	5.86	null	null		null	null		null	null		null	null		-1.61E+00	2.62E-50	Down	-1.42E+00	2.56E-43	Down	Unigene30674_All//gi|15225475|ref|NP_182067.1|//1.00E-106//DNA-binding protein-related [Arabidopsis thaliana] >gi|50198795|gb|AAT70431.1| At2g45430 [Arabidopsis thaliana] >gi|56121926|gb|AAV74244.1| At2g45430 [Arabidopsis thaliana] >gi|119657388|tpd|FAA00293.1| TPA: AT-hook motif nuclear localized protein 22 [Arabidopsis thaliana]	Unigene30674_All//6.00E-64//AT2G45430| DNA-binding protein-related	Unigene30674_All//2.00E-12//TC131035				nr +
Unigene30675_All	511	0.00	0.00	0.00	6.34	3.84	1.94	0.50	0.33	0.00	null	null		null	null		-7.22E-01	2.79E-02		-1.70E+00	2.60E-06	Down	-6.01E-01	6.48E-01		-8.96E+00	3.04E-02									
Unigene30679_All	541	0.58	1.31	0.69	5.16	12.09	3.67	0.70	0.15	0.22	1.18E+00	1.75E-01		2.48E-01	8.23E-01		1.23E+00	4.27E-08	Up	-4.89E-01	2.17E-01		-2.19E+00	8.75E-02		-1.67E+00	1.40E-01		Unigene30679_All//gi|134035510|gb|AB047743.1|//3.00E-31//homeobox protein [Gossypium hirsutum]	Unigene30679_All//6.00E-24//AT5G15150| ATHB-3 (ARABIDOPSIS THALIANA HOMEOBOX 3); DNA binding / sequence-specific DNA binding / transcription factor	Unigene30679_All//0.00E+00//gi|109859877|gb|DR488856.1|DR488856	HB			nr +
Unigene30682_All	288	0.00	2.11	1.85	9.86	4.42	14.27	1.17	0.00	0.28	1.10E+01	1.17E-03		1.09E+01	4.04E-03		-1.16E+00	9.64E-04	Down	5.34E-01	8.44E-02		-1.02E+01	1.17E-02		-2.09E+00	1.07E-01									ESTscan +
Unigene30683_All	1626	0.00	0.37	0.00	0.06	0.13	0.33	12.85	53.18	66.40	8.55E+00	1.17E-03		null	null		1.05E+00	6.12E-01		2.44E+00	4.41E-02		2.05E+00	3.40E-222	Up	2.37E+00	0.00E+00	Up	Unigene30683_All//gi|9279609|dbj|BAB01067.1|//1.00E-66//acetyltranferase-like protein [Arabidopsis thaliana]	Unigene30683_All//9.00E-62//AT3G26040| transferase family protein			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene30689_All	264	2.77	0.00	0.00	2.83	2.22	3.59	0.00	0.16	0.00	-1.14E+01	2.11E-04	Down	-1.14E+01	4.13E-04	Down	-3.52E-01	6.51E-01		3.44E-01	6.49E-01		7.31E+00	6.34E-01		null	null		Unigene30689_All//gi|297740201|emb|CBI30383.3|//1.00E-07//unnamed protein product [Vitis vinifera]		Unigene30689_All//2.00E-76//TC179432				nr -
Unigene30690_All	462	0.23	0.00	0.35	0.22	0.45	0.10	36.61	20.08	15.09	-7.82E+00	3.72E-01		6.10E-01	7.48E-01		1.05E+00	6.12E-01		-1.14E+00	6.77E-01		-8.66E-01	1.91E-12		-1.28E+00	1.80E-23	Down	Unigene30690_All//gi|112383512|gb|AB117893.1|//6.00E-40//cell-wall invertase [Coffea canephora]	Unigene30690_All//1.00E-34//AT3G13790| ATBFRUCT1; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene30690_All//7.00E-173//ES796097		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene30693_All	1467	0.25	0.07	0.00	0.03	0.40	0.00	0.92	1.11	14.28	-1.85E+00	1.87E-01		-7.96E+00	2.78E-02		3.55E+00	8.14E-03		-5.09E+00	6.35E-01		2.69E-01	6.10E-01		3.95E+00	9.80E-109	Up	Unigene30693_All//gi|12003384|gb|AG43549.1|AF211531_1|4.00E-66//Avr9/Cf-9 rapidly elicited protein 111B [Nicotiana tabacum]	Unigene30693_All//3.00E-53//AT4G25480| DREB1A (DEHYDRATION RESPONSE ELEMENT B1A); DNA binding / transcription activator/ transcription factor	Unigene30693_All//0.00E+00//gi|164256215|gb|ES791635.1|ES791635	AP2-EREBP			nr +
Unigene30694_All	939	0.00	0.00	0.00	0.32	0.07	0.00	4.50	1.07	0.89	null	null		null	null		-2.12E+00	1.65E-01		-8.31E+00	4.00E-02		-2.08E+00	9.54E-12	Down	-2.34E+00	5.77E-14	Down	Unigene30694_All//gi|297806327|ref|XP_002871047.1|//2.00E-74//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316884|gb|EFH47306.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene30694_All//2.00E-70//AT5G03610| GDSL-motif lipase/hydrolase family protein					nr -
Unigene30695_All	333	0.31	3.50	0.64	0.90	1.96	0.68	0.63	1.26	1.20	3.48E+00	7.08E-05	Up	1.03E+00	5.91E-01		1.13E+00	2.38E-01		-4.05E-01	7.51E-01		9.83E-01	3.73E-01		9.14E-01	3.86E-01									
Unigene30699_All	227	16.36	24.78	9.85	13.83	16.38	18.30	227.23	386.47	107.41	5.98E-01	1.72E-02		-7.32E-01	2.77E-02		2.45E-01	5.16E-01		4.05E-01	2.06E-01		7.66E-01	1.27E-49		-1.08E+00	1.35E-53	Down	Unigene30699_All//gi|192910686|gb|ACF06451.1|//3.00E-21//QM-like protein [Elaeis guineensis]	Unigene30699_All//8.00E-19//AT1G26910| 60S ribosomal protein L10 (RPL10B)	Unigene30699_All//4.00E-123//gi|109826234|gb|DW224955.1|DW224955		ko03010|Ribosome		nr +
Unigene30703_All	466	0.90	0.00	0.34	2.03	0.89	0.48	1.72	0.63	0.17	-9.81E+00	1.05E-02		-1.39E+00	2.80E-01		-1.20E+00	8.31E-02		-2.07E+00	8.57E-03		-1.46E+00	4.65E-02		-3.33E+00	2.47E-04	Down	Unigene30703_All//gi|224125708|ref|XP_002329698.1|//6.00E-14//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222870606|gb|EEF07737.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene30703_All//4.00E-08//AT3G17730| anac057 (Arabidopsis NAC domain containing protein 57); transcription factor		NAC			nr +
Unigene30707_All	3590	0.00	0.06	0.00	0.22	0.07	0.08	5.94	8.15	13.46	5.82E+00	1.36E-01		null	null		-1.73E+00	2.86E-02		-1.56E+00	6.27E-02		4.57E-01	2.77E-07		1.18E+00	2.17E-57	Up	Unigene30707_All//gi|115435462|ref|NP_001042489.1|//0.00E+00//Os01g0229700 [Oryza sativa Japonica Group] >gi|113532020|dbj|BAF04403.1| Os01g0229700 [Oryza sativa Japonica Group]	Unigene30707_All//7.00E-50//AT3G06880| nucleotide binding	Unigene30707_All//0.00E+00//gi|164312745|gb|ES848791.1|ES848791		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene30708_All	583	0.00	0.17	0.73	0.34	0.00	0.46	22.92	66.82	148.01	7.44E+00	3.87E-01		9.51E+00	1.38E-02		-8.42E+00	8.43E-02		4.44E-01	7.63E-01		1.54E+00	5.32E-68	Up	2.69E+00	0.00E+00	Up	Unigene30708_All//gi|167962017|dbj|BAG09366.1|//1.00E-13//peroxisomal short-chain dehydrogenase/reductase family protein [Glycine max]	Unigene30708_All//1.00E-05//AT4G05530| IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase	Unigene30708_All//2.00E-146//DW512254		ko04146|Peroxisome		nr +
Unigene30711_All	297	5.11	1.88	0.00	4.03	3.01	1.98	3.70	0.28	0.27	-1.44E+00	9.80E-03		-1.23E+01	2.73E-08	Down	-4.17E-01	5.22E-01		-1.03E+00	1.06E-01		-3.72E+00	7.15E-06	Down	-3.79E+00	3.27E-06	Down			Unigene30711_All//2.00E-58//TC162854					
Unigene30712_All	494	14.93	88.31	20.80	28.23	28.44	46.63	186.50	460.43	419.27	2.56E+00	3.94E-120	Up	4.78E-01	1.05E-02		1.05E-02	9.57E-01		7.24E-01	8.90E-11		1.30E+00	1.77E-305	Up	1.17E+00	2.73E-239	Up	Unigene30712_All//gi|270300599|gb|ACZ69386.1|//1.00E-32//polyubiquitin UBQ14 [Cucumis sativus]	Unigene30712_All//7.00E-34//AT4G05050| UBQ11 (UBIQUITIN 11); protein binding	Unigene30712_All//0.00E+00//gi|164300495|gb|ES814990.1|ES814990				nr -
Unigene30717_All	828	0.00	0.00	0.00	0.00	0.00	0.00	53.36	9.14	0.38	null	null		null	null		null	null		null	null		-2.55E+00	1.33E-148	Down	-7.12E+00	0.00E+00	Down			Unigene30717_All//2.00E-14//TC154839					
Unigene30718_All	1068	0.59	0.00	0.00	0.42	0.06	0.42	4.91	0.78	4.85	-9.20E+00	7.91E-04	Down	-9.20E+00	1.41E-03		-2.70E+00	3.24E-02		1.06E-02	1.00E+00		-2.65E+00	5.29E-19	Down	-1.76E-02	9.61E-01		Unigene30718_All//gi|224146520|ref|XP_002326036.1|//1.00E-116//flavonoid o-methyltransferase related [Populus trichocarpa] >gi|222862911|gb|EEF00418.1| flavonoid o-methyltransferase related [Populus trichocarpa]	Unigene30718_All//1.00E-52//AT4G35160| O-methyltransferase family 2 protein			ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene30719_All	443	0.00	1.03	0.00	0.00	0.00	0.51	0.57	2.45	3.06	1.00E+01	7.44E-03		null	null		null	null		8.99E+00	1.19E-01		2.10E+00	1.40E-03		2.42E+00	4.42E-05	Up			Unigene30719_All//5.00E-07//TC155040					
Unigene3072_All	1384	3.63	2.56	0.88	6.12	5.47	2.48	4.55	1.27	1.81	-5.02E-01	6.27E-02		-2.04E+00	1.42E-10	Down	-1.61E-01	4.89E-01		-1.30E+00	1.27E-10	Down	-1.84E+00	9.14E-15	Down	-1.33E+00	8.44E-10	Down	Unigene3072_All//gi|223452506|gb|ACM89580.1|//0.00E+00//serine/threonine protein kinase-like protein [Glycine max]	Unigene3072_All//5.00E-167//AT5G15080| protein kinase, putative	Unigene3072_All//0.00E+00//TC161177		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0032559	nr +
Unigene30721_All	401	1.57	3.29	5.18	0.37	1.80	1.13	0.63	0.21	0.00	1.07E+00	7.10E-02		1.73E+00	5.70E-04	Up	2.27E+00	1.95E-02		1.60E+00	2.05E-01		-1.60E+00	3.10E-01		-9.31E+00	3.04E-02		Unigene30721_All//gi|255556946|ref|XP_002519506.1|//6.00E-09//phosphoglycerate kinase, putative [Ricinus communis] >gi|223541369|gb|EEF02920.1| phosphoglycerate kinase, putative [Ricinus communis]						nr -
Unigene30722_All	232	22.33	40.40	37.64	36.29	35.92	17.91	29.52	22.52	49.45	8.56E-01	6.32E-06		7.54E-01	2.00E-04		-1.47E-02	9.55E-01		-1.02E+00	2.46E-07	Down	-3.91E-01	5.74E-02		7.44E-01	4.22E-07				Unigene30722_All//3.00E-84//TC155447					
Unigene30723_All	389	203.10	132.21	246.81	428.99	257.07	375.70	127.60	88.10	63.29	-6.19E-01	1.91E-25		2.81E-01	2.19E-07		-7.39E-01	1.62E-88		-1.91E-01	7.14E-07		-5.34E-01	2.13E-15		-1.01E+00	2.27E-46	Down	Unigene30723_All//gi|74273619|gb|AB01477.1|//1.00E-50//cytochrome P450 DDWF1 [Gossypium hirsutum]	Unigene30723_All//6.00E-21//AT3G26330| CYP71B37; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene30723_All//0.00E+00//gi|11205416|gb|BF274346.1|BF274346		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016701//GO:0016709	nr +
Unigene30726_All	260	96.79	40.54	42.40	124.15	111.65	173.01	121.64	47.74	51.79	-1.26E+00	1.08E-26	Down	-1.19E+00	1.19E-23	Down	-1.53E-01	1.37E-01		4.79E-01	4.30E-10		-1.35E+00	1.91E-45	Down	-1.23E+00	9.97E-41	Down	Unigene30726_All//gi|195617898|gb|ACG30779.1|//8.00E-27//60S acidic ribosomal protein P1 [Zea mays]	Unigene30726_All//8.00E-16//AT5G24510| 60s acidic ribosomal protein P1, putative	Unigene30726_All//4.00E-145//TC168471		ko03010|Ribosome	GO:0005198//GO:0006412//GO:0030529	nr -
Unigene30727_All	246	4.04	2.06	3.46	8.50	5.32	2.20	1.20	0.34	0.00	-9.72E-01	1.58E-01		-2.23E-01	7.34E-01		-6.77E-01	1.17E-01		-1.95E+00	4.94E-05	Down	-1.82E+00	2.11E-01		-1.02E+01	1.58E-02		Unigene30727_All//gi|2865437|gb|AAC02672.1|//2.00E-16//polyprotein [Arabidopsis arenosa]	Unigene30727_All//6.00E-08//AT4G23160| protein kinase family protein	Unigene30727_All//3.00E-47//gi|13247337|gb|BF269918.2|BF269918			GO:0003676//GO:0008152//GO:0046914	nr -
Unigene30729_All	421	147.39	3248.02	1603.32	65.31	78.36	149.87	1.91	1.49	0.57	4.46E+00	0.00E+00	Up	3.44E+00	0.00E+00	Up	2.63E-01	4.25E-03		1.20E+00	1.79E-65	Up	-3.58E-01	6.48E-01		-1.75E+00	1.55E-02		Unigene30729_All//gi|222160332|gb|ACM47360.1|//3.00E-47//BURP domain protein [Glycine max]	Unigene30729_All//6.00E-40//AT5G25610| RD22; nutrient reservoir	Unigene30729_All//0.00E+00//TC129623				nr -
Unigene3073_All	1406	3.94	6.63	4.51	10.81	13.52	16.00	42.01	27.05	16.21	7.49E-01	7.16E-05		1.92E-01	4.58E-01		3.23E-01	9.51E-03		5.66E-01	4.77E-07		-6.35E-01	1.82E-24		-1.37E+00	4.40E-89	Down	Unigene3073_All//gi|297835378|ref|XP_002885571.1|//9.00E-83//dienelactone hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331411|gb|EFH61830.1| dienelactone hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3073_All//3.00E-83//AT3G23570| dienelactone hydrolase family protein	Unigene3073_All//0.00E+00//TC179001			GO:0005576//GO:0006970//GO:0016020//GO:0016787//GO:0043231	nr -
Unigene30731_All	302	2.43	2.01	4.41	14.85	7.30	2.99	0.28	0.42	0.53	-2.69E-01	7.19E-01		8.62E-01	1.54E-01		-1.02E+00	1.19E-04	Down	-2.31E+00	2.14E-12	Down	5.68E-01	7.82E-01		9.14E-01	6.24E-01				Unigene30731_All//9.00E-08//DR455039					ESTscan -
Unigene30734_All	324	62.33	33.94	23.67	27.37	15.41	33.18	9.40	0.90	20.53	-8.77E-01	2.39E-12		-1.40E+00	2.75E-24	Down	-8.29E-01	3.49E-06		2.78E-01	1.37E-01		-3.38E+00	3.41E-14	Down	1.13E+00	4.20E-08	Up			Unigene30734_All//4.00E-90//DR512552					
Unigene30735_All	299	0.18	0.00	0.00	7.16	2.65	2.42	0.00	0.00	0.00	-7.45E+00	6.12E-01		-7.45E+00	6.24E-01		-1.44E+00	6.37E-04	Down	-1.57E+00	5.56E-04	Down	null	null		null	null				Unigene30735_All//1.00E-56//DR513765					
Unigene30737_All	278	0.19	1.09	1.53	0.18	0.12	0.81	3.50	0.60	4.16	2.54E+00	1.51E-01		3.03E+00	5.73E-02		-5.32E-01	8.25E-01		2.18E+00	3.23E-01		-2.54E+00	6.41E-04	Down	2.49E-01	6.41E-01									

Unigene30740_All	688	0.00	6.19	3.72	0.00	0.10	0.00	0.00	0.00	0.12	1.26E+01	3.04E-24	Up	1.19E+01	4.20E-14	Up	6.65E+00	6.09E-01		null	null		null	null		6.86E+00	4.04E-01		Unigene30740_All//gi|159488620|ref|XP_001702303.1|//7.00E-72//ribosomal protein S9, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii]>gi|158271208|gb|EDO97033.1|ribosomal protein S9, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii]	Unigene30740_All//3.00E-71//AT5G15200| 40S ribosomal protein S9 (RPS9B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0003312//GO:0031981	nr +
Unigene30742_All	247	374.51	2100.22	1497.04	434.82	272.00	310.11	102.88	114.05	42.74	2.49E+00	0.00E+00	Up	2.00E+00	0.00E+00	Up	-6.77E-01	7.25E-49		-4.88E-01	3.53E-24		1.49E-01	1.41E-01		-1.27E+00	2.36E-34	Down			Unigene30742_All//3.00E-90//gi|11204491|gb|BF273421.1|BF273421				
Unigene30753_All	441	0.36	0.92	1.69	0.23	0.86	2.15	0.29	1.14	2.71	1.37E+00	2.74E-01		2.25E+00	2.35E-02		1.93E+00	1.94E-01		3.25E+00	5.84E-04	Up	1.98E+00	5.74E-02		3.24E+00	7.29E-06	Up							
Unigene30755_All	268	0.00	0.00	0.00	7.44	1.93	2.02	0.00	0.00	0.00	null	null		null	null		-1.95E+00	2.27E-05	Down	-1.88E+00	1.26E-04	Down	null	null		null	null									
Unigene30756_All	247	0.21	2.26	1.29	3.03	0.14	3.11	0.86	0.17	0.65	3.41E+00	1.24E-02		2.61E+00	1.46E-01		-4.44E+00	1.31E-04	Down	3.91E-02	9.59E-01		-2.34E+00	2.37E-01		-4.08E-01	7.55E-01		Unigene30756_All//gi|31433131|gb|AAP54684.1|//3.00E-22//armadillo/beta-catenin-like repeat family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene30756_All//8.00E-15//AT1G01830| armadillo/beta-catenin repeat family protein	Unigene30756_All//2.00E-91//BF272959			GO:0003824	nr +
Unigene30757_All	601	0.09	1.01	1.68	0.99	0.00	0.00	0.00	0.00	0.00	3.54E+00	7.24E-03		4.27E+00	1.19E-04	Up	-9.96E+00	1.78E-04	Down	-9.96E+00	7.70E-04	Down	null	null		null	null									ESTscan -
Unigene30758_All	477	0.00	0.00	0.00	1.04	0.00	0.57	1.42	1.75	2.17	null	null		null	null		-1.00E+01	8.98E-04	Down	-8.78E-01	4.20E-01		3.05E-01	6.47E-01		6.15E-01	3.01E-01		Unigene30758_All//gi|222424697|dbj|BAH20302.1|//2.00E-40//AT3G26890 [Arabidopsis thaliana]	Unigene30758_All//1.00E-41//AT3G26890| unknown protein	Unigene30758_All//0.00E+00//ES827937				nr +
Unigene30759_All	413	2864.34	1228.46	2410.69	395.38	497.85	310.13	1.54	1.52	1.64	-1.22E+00	0.00E+00	Down	-2.49E-01	1.80E-66		3.33E-01	4.92E-25		-3.50E-01	5.43E-20		-1.66E-02	1.02E+00		9.47E-02	9.12E-01		Unigene30759_All//gi|224124190|ref|XP_002330127.1|//1.00E-76//light-harvesting complex I protein Lhca4 [Populus trichocarpa]>gi|22287126|gb|EEF08392.1|light-harvesting complex I protein Lhca4 [Populus trichocarpa]	Unigene30759_All//3.00E-72//AT3G47470| LHCA4 (LIGHT-HARVESTING CHLOROPHYLL-PROTEIN COMPLEX I SUBUNIT A4); chlorophyll binding	Unigene30759_All//0.00E+00//gi|164256539|gb|ES813408.1|ES813408		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009536	nr +
Unigene3076_All	1782	5.23	3.81	4.75	11.07	8.62	10.29	10.06	2.65	8.23	-4.56E-01	1.61E-02		-1.37E-01	5.31E-01		-3.61E-01	2.24E-03		-1.05E-01	4.80E-01		-1.92E+00	5.08E-43	Down	-2.90E-01	1.25E-02		Unigene3076_All//gi|297822747|ref|XP_002881756.1|//1.00E-100//PQ-loop repeat family protein [Arabidopsis lyrata subsp. lyrata]>gi|297327595|gb|EFH58015.1| PQ-loop repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3076_All//2.00E-89//AT2G41050| PQ-loop repeat family protein / transmembrane family protein	Unigene3076_All//0.00E+00//ES798401			GO:0044464	nr -
Unigene30761_All	535	0.29	0.19	0.50	1.21	2.00	0.42	0.55	0.39	2.38	-6.31E-01	7.27E-01		7.62E-01	6.44E-01		7.21E-01	3.14E-01		-1.52E+00	1.12E-01		-5.02E-01	6.78E-01		2.11E+00	3.17E-04	Up							
Unigene30762_All	301	1.04	0.51	5.13	2.15	1.14	0.00	1.83	0.97	1.19	-1.05E+00	4.43E-01		2.30E+00	3.37E-04	Up	-9.11E-01	3.04E-01		-1.11E-01	3.90E-04	Down	-9.10E-01	3.19E-01		-6.16E-01	4.68E-01				Unigene30762_All//3.00E-07//CO101027				
Unigene30763_All	335	5.78	1.21	2.38	3.27	5.86	4.45	1.39	1.37	2.62	-2.26E+00	2.83E-05	Down	-1.28E+00	1.07E-02		8.41E-01	7.10E-02		4.44E-01	4.57E-01		-1.66E-02	1.02E+00		9.14E-01	1.59E-01		Unigene30763_All//gi|297744125|emb|CBI37095.3|//4.00E-14//unnamed protein product [Vitis vinifera]						nr -
Unigene30764_All	893	0.00	0.00	0.00	0.00	0.00	0.00	2.89	4.26	0.00	null	null		null	null		null	null		null	null		5.60E-01	4.78E-02		-1.15E+01	5.57E-19	Down	Unigene30764_All//gi|30112263|ref|XP_002909042.1|//3.00E-82//40S ribosomal protein S6 [Phytophthora infestans T30-4]>gi|262099804|gb|EEY57856.1| 40S ribosomal protein S6 [Phytophthora infestans T30-4]	Unigene30764_All//3.00E-60//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome	Unigene30764_All//2.00E-17//BF268962		ko03010|Ribosome	GO:0030529	nr +
Unigene30766_All	736	0.00	0.00	0.00	0.41	0.37	0.18	0.11	0.11	2.06	null	null		null	null		-1.18E-01	9.00E-01		-1.14E+00	4.57E-01		-1.64E-02	1.01E+00		4.16E+00	1.20E-08	Up	Unigene30766_All//gi|297834560|ref|XP_002885162.1|//8.00E-37//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]>gi|297331002|gb|EFH61421.1|nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene30766_All//9.00E-36//AT4G15920| INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPR018169), RAG1-activating protein 1 homologue (InterPro:IPR018179), MtN3 and saliva related transmembrane protein (InterPro:IPR004316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene30766_All//1.00E-11//TC153405			GO:0044464	nr +
Unigene30767_All	265	8.09	0.38	4.02	2.82	1.30	1.36	0.00	0.00	0.00	-4.40E+00	4.70E-10	Down	-1.01E+00	2.88E-02		-1.12E+00	1.62E-01		-1.05E+00	2.21E-01		null	null		null	null				Unigene30767_All//2.00E-11//TC154843				
Unigene30769_All	749	50.23	16.37	25.10	90.25	85.10	118.91	211.12	76.28	108.19	-1.62E+00	1.25E-57	Down	-1.00E+00	1.28E-26	Down	-8.48E-02	2.53E-01		3.98E-01	5.97E-14		-1.47E+00	4.42E-255	Down	-9.65E-01	8.32E-135		Unigene30769_All//gi|38327504|gb|AAR17783.1|//1.00E-105//ribosomal protein L3 [Solanum lycopersicum]	Unigene30769_All//8.00E-96//AT1G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	Unigene30769_All//0.00E+00//gi|109862574|gb|DW491551.1|DW491551		ko03010|Ribosome		nr -
Unigene3077_All	2158	3.69	8.64	9.43	3.97	8.51	10.97	20.10	11.81	7.18	1.23E+00	2.96E-19	Up	1.35E+00	1.96E-23	Up	1.10E+00	1.74E-18	Up	1.47E+00	1.13E-33	Up	-7.67E-01	5.23E-25		-1.49E+00	1.03E-73	Down	Unigene3077_All//gi|222424455|dbj|BAH20183.1|//1.00E-157//AT4G34860 [Arabidopsis thaliana]	Unigene3077_All//4.00E-151//AT4G34860| beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative	Unigene3077_All//0.00E+00//TC168427				nr -
Unigene30770_All	520	0.00	0.29	0.00	1.34	1.26	1.39	3.41	0.80	5.52	8.19E+00	2.35E-01		null	null		-9.22E-02	8.95E-01		5.11E-02	9.48E-01		-2.09E+00	2.21E-05	Down	6.92E-01	3.06E-02		Unigene30770_All//gi|15226012|ref|NP_179689.1|//4.00E-59//NPY2 (NAKED PINS IN YUC MUTANTS 2); protein binding / signal transducer [Arabidopsis thaliana]	Unigene30770_All//2.00E-60//AT2G14820| NPY2 (NAKED PINS IN YUC MUTANTS 2); protein binding / signal transducer	Unigene30770_All//6.00E-146//DR463593			GO:0005488//GO:0009314//GO:0060089	nr -
Unigene30771_All	442	51.49	23.84	57.71	7.10	5.84	7.66	0.10	0.00	0.09	-1.11E+00	4.71E-20	Down	1.64E-01	1.80E-01		-2.81E-01	4.54E-01		1.10E-01	7.60E-01		-6.58E+00	6.57E-01		-8.70E-02	9.72E-01		Unigene30771_All//gi|159895667|gb|ABX10444.1|//2.00E-14//phosphoethanolamine N-methyltransferase [Gossypium hirsutum]	Unigene30771_All//4.00E-09//AT1G48600| phosphoethanolamine N-methyltransferase 2, putative (NMT2)	Unigene30771_All//0.00E+00//BE052405		ko00564|Glycerophospholipid metabolism	GO:0000902//GO:0008168//GO:0042439//GO:0048868	nr +
Unigene3078_All	1980	0.32	1.05	1.05	0.33	1.01	1.57	5.06	1.35	0.87	1.73E+00	3.59E-04	Up	1.73E+00	5.70E-04	Up	1.62E+00	5.51E-04	Up	2.27E+00	2.28E-08	Up	-1.91E+00	4.65E-24	Down	-2.55E+00	2.34E-35	Down	Unigene3078_All//gi|5123703|emb|CAB45447.1|//0.00E+00//invertase-like protein [Arabidopsis thaliana]>gi|7270437|emb|CAB80203.1|invertase-like protein [Arabidopsis thaliana]>gi|15215776|gb|AAK91433.1|AT4g34860/F11111_100 [Arabidopsis thaliana]>gi|27363384|gb|AAO11611.1|At4g34860/F11111_100 [Arabidopsis thaliana]	Unigene3078_All//0.00E+00//AT4G34860| beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative	Unigene3078_All//0.00E+00//TC168427			GO:0004553//GO:0044444	nr -
Unigene30783_All	247	0.42	0.41	0.65	0.00	0.56	0.73	2.05	1.52	0.00	-4.64E-02	9.89E-01		6.10E-01	7.48E-01		9.12E+00	3.18E-01		9.51E+00	1.94E-01		-4.32E-01	6.18E-01		-1.10E+01	5.54E-04	Down							
Unigene30785_All	203	13.40	5.49	10.75	11.29	3.39	2.45	6.25	12.35	5.89	-1.29E+00	1.04E-03		-3.18E-01	4.28E-01		-1.73E+00	2.83E-05	Down	-2.21E+00	2.84E-06	Down	9.83E-01	6.15E-03		-8.58E-02	8.72E-01								
Unigene30795_All	448	1.28	0.34	0.24	2.78	2.84	0.20	0.47	0.00	0.00	-1.92E+00	7.01E-02		-2.43E+00	4.40E-02		3.29E-02	9.68E-01		-3.79E+00	7.61E-06	Down	-8.88E+00	7.44E-02		-8.88E+00	5.80E-02				Unigene30795_All//4.00E-14//gi|3325634|gb|AI054520.1|AI054520				
Unigene30798_All	324	4.04	0.00	0.82	2.00	0.32	2.23	2.22	0.77	0.37	-1.20E+01	1.28E-07	Down	-2.30E+00	1.21E-03		-2.65E+00	7.46E-03		1.58E-01	8.59E-01		-1.52E+00	5.42E-02		-2.59E+00	2.81E-03		Unigene30798_All//gi|30694644|ref|NP_191302.2|//2.00E-25//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]>gi|218525905|sp|Q7Y211.2|PP285_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g57430, chloroplastic; Flags: Precursor	Unigene30798_All//1.00E-23//AT3G57430| pentatricopeptide (PPR) repeat-containing protein	Unigene30798_All//1.00E-28//CO096036			GO:0043231	nr +
Unigene3080_All	1975	9.70	6.88	8.52	12.96	12.38	6.40	5.29	1.84	1.78	-4.96E-01	8.07E-05		-1.87E-01	1.92E-01		-6.66E-02	6.03E-01		-1.02E+00	5.10E-21	Down	-1.52E+00	1.84E-18	Down	-1.57E+00	5.48E-20	Down	Unigene3080_All//gi|225445059|ref|XP_002283473.1|//0.00E+00//PREDICTED: similar to beta-1,3-glucanase [Vitis vinifera]	Unigene3080_All//0.00E+00//AT5G56590| glycosyl hydrolase family 17 protein	Unigene3080_All//0.00E+00//ES806261		ko00500|Starch and sucrose metabolism	GO:0005618//GO:0008422//GO:0031225//GO:0031410//GO:0043167//GO:0044438	nr +
Unigene30800_All	266	3.34	4.95	5.20	33.90	23.69	35.99	277.05	155.08	58.41	5.67E-01	3.41E-01		6.38E-01	2.82E-01		-5.17E-01	4.37E-03		8.67E-02	6.71E-01		-8.37E-01	1.29E-48		-2.25E+00	1.11E-219	Down			Unigene30800_All//7.00E-110//gi|109869265|gb|DW498241.1|DW498241				
Unigene30801_All	372	0.98	0.82	0.14	4.29	2.31	1.09	0.45	0.34	0.54	-2.69E-01	8.01E-01		-2.78E+00	1.03E-01		-8.89E-01	7.64E-02		-1.97E+00	4.88E-04	Down	-4.31E-01	7.93E-01		2.36E-01	8.83E-01				Unigene30801_All//2.00E-12//DR457757				
Unigene30803_All	665	3.07	5.49	6.41	0.22	0.16	0.14	0.00	0.00	0.12	8.38E-01	9.35E-03		1.06E+00	6.13E-04	Up	-5.33E-01	7.85E-01		-7.27E-01	7.15E-01		null	null		6.90E+00	4.04E-01		Unigene30803_All//gi|30725678|gb|AAP37861.1|//5.00E-52//At2g21080 [Arabidopsis thaliana]	Unigene30803_All//5.00E-51//AT2G21080| unknown protein				GO:0043231	nr +
Unigene30805_All	1172	0.09	0.00	0.00	0.68	0.12	0.15	25.72	22.32	12.37	-6.48E+00	3.72E-01		-6.48E+00	3.93E-01		-2.53E+00	3.08E-03		-2.14E+00	1.54E-02		-2.04E-01	2.74E-02		-1.06E+00	1.58E-30	Down	Unigene30805_All//gi|15221260|ref|NP_177586.1|//1.00E-150//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana]>gi|75169843|sp|Q9CA68.1|GDL31_ARATH RecName: Full=GDSL esterase/lipase At1g74460; AltName: Full=Extracellular lipase At1g74460; Flags: Precursor	Unigene30805_All//2.00E-151//AT1G74460| GDSL-motif lipase/hydrolase family protein	Unigene30805_All//0.00E+00//TC162868			GO:0016787	nr -
Unigene30806_All	212	22.71	19.60	18.08	15.74	16.08	11.50	22.74	25.43	49.61	-2.12E-01	4.61E-01		-3.28E-01	2.70E-01		3.06E-02	9.55E-01		-4.53E-01	2.05E-01		1.62E-01	5.45E-01		1.13E+00	2.88E-12	Up	Unigene30806_All//gi|297795893|ref|XP_002868831.1|//1.00E-30//heat shock protein 93-V [Arabidopsis lyrata subsp. lyrata]>gi|297311666|gb|EFH42090.1| heat shock protein 93-V [Arabidopsis lyrata subsp. lyrata]	Unigene30806_All//3.00E-24//AT5G50920| CLPC1; ATP binding / ATP-dependent peptidase/ ATPase	Unigene30806_All//4.00E-114//gi|84170099|gb|DR458747.1|DR458747			GO:0003676//GO:0006281//GO:0006605//GO:0009532//GO:0009534//GO:0009657//GO:0009706//GO:0015995//GO:0016788//GO:0017038//GO:0030312//GO:0032559//GO:0042623	nr -
Unigene30807_All	719	0.29	1168.57	26.37	0.35	0.57	11.24	0.00	0.35	2.66	1.20E+01	0.00E+00	Up	6.50E+00	1.81E-99	Up	7.30E-01	5.86E-01		5.02E+00	1.30E-41	Up	8.45E+00	4.31E-02		1.14E+01	1.02E-13	Up	Unigene30807_All//gi|126075|sp|P09441.2|LEA13_GOSHI//9.00E-94//RecName: Full=Late embryogenesis abundant protein D-113; Short=LEA D-113>gi|18492|emb|CAA31590.1| D-113 Lea protein [Gossypium hirsutum]>gi|226553|prf||1601521C Lea D-113 gene		Unigene30807_All//1.00E-175//TC165354		ko03040|Spliceosome	GO:0007275	nr +
Unigene30808_All	411	3.44	0.12	0.00	3.03	1.34	0.33	0.00	0.00	0.00	-4.80E+00	4.49E-07	Down	-1.17E+01	1.01E-07	Down	-1.18E+00	4.23E-02		-3.20E+00	3.61E-05	Down	null	null		null	null		Unigene30808_All//gi|224057042|ref|XP_002299116.1|//3.00E-51//neutral amino acid transport protein [Populus trichocarpa]>gi|222846374|gb|EEE83921.1|neutral amino acid transport protein [Populus trichocarpa]	Unigene30808_All//2.00E-23//AT3G13620| amino acid permease family protein	Unigene30808_All//0.00E+00//gi|13246732|gb|BE054055.2|BE054055			GO:0015171//GO:0015837//GO:0031224	nr +

Unigene3081_All	1448	5.96	3.85	3.86	8.94	6.21	6.99	6.04	2.14	4.04	-6.31E-01	1.28E-03		-6.27E-01	2.15E-03		-5.27E-01	2.97E-04		-3.56E-01	2.59E-02		-1.50E+00	2.73E-15	Down	-5.80E-01	5.89E-04		Unigene3081_All//gi|45825145|gb|AAS77480.1|//1.00E-127//At5g19300 [Arabidopsis thaliana]	Unigene3081_All//2.00E-118//AT5G19300| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nucleic acid-binding, OB-fold-like (InterPro:IPR016027), Protein of unknown function DUF171 (InterPro:IPR003750); Has 4766 Blast hits to 2044 proteins in 217 species: Archae - 72; Bacteria - 102; Metazoa - 2264; Fungi - 372; Plants - 195; Viruses - 4; Other Eukaryotes - 1757 (source: NCBI BLink).	Unigene3081_All//0.00E+00//gi|109858106|gb|DW487085.1|DW487085					nr -
Unigene30812_All	351	3.73	1.73	3.19	2.27	1.77	3.86	9.03	5.00	3.41	-1.11E+00	6.24E-02		-2.26E-01	6.96E-01		-3.63E-01	6.23E-01		7.66E-01	2.05E-01		-8.53E-01	6.12E-03		-1.41E+00	8.85E-06	Down	Unigene30812_All//gi|297843714|ref|XP_002889738.1|//7.00E-07//20S proteasome beta subunit PBG1 [Arabidopsis lyrata subsp. lyrata] >gi|297335580|gb|EFH65997.1| 20S proteasome beta subunit PBG1 [Arabidopsis lyrata subsp. lyrata]	Unigene30812_All//2.00E-07//AT1G56450| PBG1; peptidase/ threonine-type endopeptidase	Unigene30812_All//1.00E-62//gi|84168317|gb|DR456965.1|DR456965		ko03050|Proteasome	GO:0000502//GO:0004175	nr -
Unigene30816_All	487	0.75	0.62	2.41	7.98	7.42	1.85	0.78	0.60	0.82	-2.69E-01	8.01E-01		1.68E+00	1.64E-02		-1.04E-01	7.86E-01		-2.10E+00	1.09E-09	Down	-3.79E-01	7.23E-01		6.60E-02	9.66E-01		Unigene30816_All//gi|225016141|gb|ACN78965.1|//3.00E-07//Rpp4 candidate 1 [Glycine max]		Unigene30816_All//9.00E-40//TC165695				nr -
Unigene30818_All	494	0.95	1.44	0.00	3.53	1.60	0.73	5.14	3.38	0.48	5.91E-01	4.78E-01		-9.90E+00	8.64E-03		-1.14E+00	1.57E-02		-2.27E+00	4.52E-05	Down	-6.02E-01	9.38E-02		-3.41E+00	1.81E-12	Down								
Unigene30819_All	248	0.42	0.61	0.00	6.63	1.94	1.09	2.05	1.35	2.57	5.39E-01	7.79E-01		-8.72E+00	3.93E-01		-1.77E+00	4.68E-04	Down	-2.60E+00	1.60E-05	Down	-6.02E-01	5.31E-01		3.29E-01	6.60E-01				Unigene30819_All//8.00E-91//gi|78337672|gb|DT557946.1|DT557946				
Unigene30821_All	251	0.00	1.41	0.21	2.38	3.16	0.36	0.67	1.00	7.30	1.05E+01	2.46E-02		7.73E+00	6.36E-01		4.06E-01	6.32E-01		-2.73E+00	1.74E-02		5.68E-01	6.74E-01		3.44E+00	4.55E-09	Up			Unigene30821_All//1.00E-132//TC155960				
Unigene30822_All	403	1.17	0.75	0.00	8.90	2.14	5.72	3.15	0.52	1.09	-6.31E-01	5.54E-01		-1.02E+01	8.64E-03		-2.06E+00	6.41E-10	Down	-6.39E-01	5.07E-02		-2.60E+00	5.14E-05	Down	-1.53E+00	4.40E-03		Unigene30822_All//gi|15232315|ref|NP_188700.1|//5.00E-34//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|75299591|sp|Q8GXT3.1|BHI23_ARATH RecName: Full=Transcription factor bHLH123; AltName: Full=Transcription factor EN 63; AltName: Full=bHLH transcription factor bHLH123; AltName: Full=Basic helix-loop-helix protein 123; Short=bHLH 123; Short=AtbHLH123	Unigene30822_All//8.00E-33//AT3G20640| ethylene-responsive protein -related	Unigene30822_All//4.00E-149//TC154675	bHLH		GO:0001071//GO:0009536//GO:0010468	nr -
Unigene30823_All	416	6.92	23.75	11.14	32.33	41.14	53.20	125.82	211.69	227.54	1.78E+00	1.07E-17	Up	6.87E-01	1.89E-02		3.48E-01	8.26E-03		7.18E-01	2.96E-10		7.51E-01	4.36E-48		8.55E-01	7.60E-66				Unigene30823_All//0.00E+00//TC155875				
Unigene30826_All	758	0.00	13.64	5.55	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	3.12E-59	Up	1.24E+01	2.43E-23	Up	null	null		null	null		null	null		null	null							GO:0003824	nr -
Unigene30827_All	420	11.96	6.64	3.55	36.65	21.89	49.36	22.55	3.98	0.95	-8.50E-01	1.51E-03		-1.75E+00	9.14E-09	Down	-7.43E-01	1.22E-08		4.30E-01	3.06E-04		-2.50E+00	9.98E-32	Down	-4.57E+00	1.24E-55	Down	Unigene30827_All//gi|118484615|gb|ABR94181.1|//9.00E-10//unknown [Populus trichocarpa]		Unigene30827_All//3.00E-119//BP276211				nr +
Unigene30828_All	473	0.88	0.86	0.00	0.32	1.75	2.20	1.34	0.88	1.94	-4.62E-02	9.80E-01		-9.79E+00	1.56E-02		2.47E+00	6.72E-03		2.80E+00	8.12E-04	Up	-6.02E-01	4.67E-01		5.31E-01	4.07E-01				Unigene30828_All//6.00E-07//TC155772				
Unigene30829_All	313	0.33	0.32	0.00	0.16	0.00	0.00	22.83	52.34	49.51	-4.60E-02	9.89E-01		-8.39E+00	3.93E-01		-7.31E+00	5.55E-01		-7.31E+00	6.35E-01		1.20E+00	5.78E-20	Up	1.12E+00	1.88E-17	Up			Unigene30829_All//5.00E-151//TC137326				
Unigene3083_All	1065	35.67	87.87	30.75	52.53	95.68	81.21	388.42	376.83	202.49	1.30E+00	1.94E-102	Up	-2.14E-01	2.34E-02		8.65E-01	1.41E-68		6.29E-01	1.87E-30		-4.37E-02	8.36E-02		-9.40E-01	0.00E+00		Unigene3083_All//gi|87201358|gb|AAX07458.2|//3.00E-86//ethylene-responsive element binding protein EBP2 [Gossypium hirsutum]	Unigene3083_All//2.00E-22//AT1G53910| RAP2.12; DNA binding / transcription factor	Unigene3083_All//0.00E+00//TC149098	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene30834_All	307	2.56	0.00	0.00	3.08	2.58	1.18	1.65	0.41	0.91	-1.13E+01	1.09E-04	Down	-1.13E+01	2.22E-04	Down	-2.57E-01	7.27E-01		-1.39E+00	6.08E-02		-2.02E+00	5.20E-02		-8.63E-01	3.39E-01		Unigene30834_All//gi|115483464|ref|NP_001065402.1|//9.00E-23//Os10g0563500 [Oryza sativa Japonica Group] >gi|113639934|dbj|BAF27239.1|Os10g0563500 [Oryza sativa Japonica Group]	Unigene30834_All//4.00E-22//AT4G16970| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase				GO:0004672//GO:0006464//GO:0032559	nr -
Unigene30835_All	559	0.94	0.36	0.38	0.62	2.34	3.39	1.06	0.67	0.00	-1.37E+00	1.97E-01		-1.30E+00	2.42E-01		1.91E+00	2.51E-03		2.44E+00	9.81E-06	Up	-6.54E-01	4.45E-01		-1.00E+01	1.41E-04	Down	Unigene30835_All//gi|35401180|gb|AAC34320.1|//2.00E-86//Unknown protein [Arabidopsis thaliana]	Unigene30835_All//1.00E-47//AT1G09980| INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF676, hydrolase-like (InterPro:IPR000751); BEST Arabidopsis thaliana protein match is: ZW18 (TAIR:AT1G58350.2); Has 342 Blast hits to 275 proteins in 70 species: Archae - 0; Bacteria - 0; Metazoa - 214; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 83 (source: NCBI BLink).	Unigene30835_All//6.00E-72//TC153779				nr +
Unigene30836_All	1219	0.00	0.00	0.00	0.00	0.00	0.00	6.76	2.57	3.53	null	null		null	null		null	null		null	null		-1.40E+00	4.85E-13	Down	-9.38E-01	1.46E-07		Unigene30836_All//gi|224054180|ref|XP_002298131.1|//7.00E-72//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845389|gb|EEE82936.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene30836_All//2.00E-66//AT1G52800| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene30836_All//8.00E-30//ES849745		ko00904|Diterpenoid biosynthesis	GO:0016491	nr +
Unigene30837_All	316	0.66	0.00	1.52	0.47	1.31	0.57	0.54	3.84	1.51	-9.37E+00	1.22E-01		1.20E+00	3.02E-01		1.47E+00	2.80E-01		2.74E-01	9.05E-01		2.84E+00	3.39E-05	Up	1.50E+00	1.27E-01										
Unigene30839_All	546	0.00	0.00	0.00	0.00	0.06	0.00	6.12	2.07	3.72	null	null		null	null		5.98E+00	8.30E-01		null	null		-1.57E+00	1.15E-06	Down	-7.17E-01	1.36E-02		Unigene30839_All//gi|269854726|gb|ACZ51393.1|//7.00E-59//NBS-LRR resistance protein-like protein [Gossypium hirsutum]	Unigene30839_All//1.00E-33//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene30839_All//0.00E+00//gi|48776229|gb|CO085595.1|CO085595		ko04626|Plant-pathogen interaction	GO:0006950//GO:0012501//GO:0032559	nr -
Unigene30843_All	904	0.00	0.34	0.12	0.17	0.46	0.15	1.26	3.61	4.76	8.39E+00	4.43E-02		6.88E+00	3.98E-01		1.47E+00	2.80E-01		-1.41E-01	9.43E-01		1.51E+00	3.09E-06	Up	1.91E+00	4.65E-11	Up	Unigene30843_All//gi|29423276|gb|AA073525.1|//2.00E-36//gag-pol polyprotein [Glycine max]					GO:0005488	nr +
Unigene30845_All	1085	0.10	0.09	0.29	0.37	0.13	2.83	8.88	3.78	23.65	-4.56E-02	9.89E-01		1.61E+00	3.05E-01		-1.53E+00	2.05E-01		2.95E+00	7.99E-11	Up	-1.23E+00	1.17E-12	Down	1.41E+00	1.97E-40	Up	Unigene30845_All//gi|224075092|ref|XP_002304554.1|//2.00E-86//AP2/EREBP domain-containing transcription factor [Populus trichocarpa] >gi|222841986|gb|EEE79533.1| AP2/EREBP domain-containing transcription factor [Populus trichocarpa]	Unigene30845_All//2.00E-42//AT1G64380| AP2 domain-containing transcription factor, putative	Unigene30845_All//0.00E+00//TC154225	AP2-EREBP		GO:0000160//GO:0001071//GO:0003676//GO:0006350//GO:0009314//GO:0009651//GO:0009743//GO:0023033//GO:0043231	nr -
Unigene30846_All	507	0.21	1.00	0.00	1.28	4.96	5.61	0.00	0.74	0.24	2.28E+00	6.23E-02		-7.69E+00	3.93E-01		1.96E+00	4.19E-06	Up	2.14E+00	3.45E-07	Up	9.54E+00	6.85E-03		7.88E+00	2.43E-01		Unigene30846_All//gi|207693265|gb|ACI25287.1|//9.00E-49//ARM repeat containing protein [Populus trichocarpa]	Unigene30846_All//8.00E-44//AT4G34940| ARO1 (ARMADILLO REPEAT ONLY 1); binding				GO:0000904//GO:0007010//GO:0016020//GO:0043231	nr -
Unigene30847_All	470	0.00	0.00	0.00	0.00	0.00	0.00	26.72	3.73	7.12	null	null		null	null		null	null		null	null		-2.84E+00	5.36E-48	Down	-1.91E+00	5.68E-31	Down									
Unigene30848_All	618	1.61	0.98	2.33	4.51	3.73	2.05	1.37	0.00	0.06	-7.09E-01	3.05E-01		5.32E-01	3.71E-01		-2.74E-01	5.12E-01		-1.14E+00	2.41E-03		-1.04E+01	4.39E-06	Down	-4.41E+00	2.37E-05	Down	Unigene30848_All//gi|124359941|gb|ABN07957.1|//3.00E-19//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene30848_All//6.00E-15//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene30848_All//0.00E+00//gi|13352305|gb|BG442653.1|BG442653			GO:0043231	nr +
Unigene3085_All	1679	0.65	3.26	0.79	4.09	3.47	3.12	6.65	2.32	3.63	2.32E+00	6.46E-14	Up	2.77E-01	6.16E-01		-2.40E-01	3.14E-01		-3.92E-01	9.18E-02		-1.52E+00	1.13E-19	Down	-8.73E-01	6.92E-09		Unigene3085_All//gi|297797517|ref|XP_002866643.1|//1.00E-148//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312478|gb|EFH42902.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3085_All//9.00E-140//AT5G64970| mitochondrial substrate carrier family protein	Unigene3085_All//0.00E+00//DW506754				nr -
Unigene30852_All	265	457.46	233.08	114.34	355.84	311.22	260.41	175.98	79.18	87.80	-9.73E-01	1.35E-83		-2.00E+00	1.44E-239	Down	-1.93E-01	1.41E-04		-4.50E-01	1.74E-18		-1.15E+00	3.31E-52	Down	-1.00E+00	4.86E-43	Down	Unigene30852_All//gi|195628612|gb|ACG36136.1|//8.00E-43//histone H4 [Zea mays]	Unigene30852_All//1.00E-31//AT5G59970| histone H4	Unigene30852_All//4.00E-148//gi|21091617|gb|BQ403930.1|BQ403930			GO:0000785//GO:0003676//GO:0006950//GO:0009536//GO:0016020//GO:0031981//GO:0034728	nr -
Unigene30856_All	483	0.00	0.00	0.00	2.78	0.00	0.00	1.84	1.04	0.08	null	null		null	null		-1.14E+01	5.66E-10	Down	-1.14E+01	2.08E-08	Down	-8.24E-01	2.24E-01		-4.48E+00	1.23E-05	Down	Unigene30856_All//gi|38346024|emb|CAE01955.2|//4.00E-26//OSJNB0071D01.1 [Oryza sativa (japonica cultivar-group)] >gi|38346892|emb|CAE03917.2| OSJNB0015G09.11 [Oryza sativa (japonica cultivar-group)]	Unigene30856_All//3.00E-22//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative	Unigene30856_All//1.00E-41//DR460632		ko04626|Plant-pathogen interaction	GO:0016740	nr +
Unigene3086_All	1029	3.56	3.10	4.30	6.29	5.96	2.81	3.16	3.37	2.56	-1.98E-01	5.65E-01		2.71E-01	3.89E-01		-7.93E-02	7.92E-01		-1.16E+00	4.95E-07	Down	9.16E-02	7.75E-01		-3.08E-01	3.28E-01		Unigene3086_All//gi|115454535|ref|NP_001050868.1|//5.00E-45//Os03g0670100 [Oryza sativa Japonica Group] >gi|108710316|gb|ABF98111.1| ABC transporter family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549339|dbj|BAF12782.1| Os03g0670100 [Oryza sativa Japonica Group]	Unigene3086_All//3.00E-46//AT1G65410| ATNAP11 (ARABIDOPSIS THALIANA NON-INTRINSIC ABC PROTEIN 11); transporter	Unigene3086_All//5.00E-151//ES848625			GO:0006810//GO:0009536//GO:0015116//GO:0017111//GO:0032559	nr +
Unigene30863_All	1633	0.00	0.00	0.00	0.00	0.00	0.00	3.50	0.41	4.37	null	null		null	null		null	null		null	null		-3.09E+00	4.19E-24	Down	3.21E-01	1.03E-01		Unigene30863_All//gi|183229550|gb|ACC60273.1|//1.00E-160//aluminum-activated malate transporter [Glycine max]	Unigene30863_All//4.00E-135//AT3G11680| unknown protein					nr -
Unigene30864_All	212	143.64	70.51	95.70	277.27	215.06	365.99	174.51	87.73	121.58	-1.03E+00	1.83E-23	Down	-5.86E-01	5.84E-09		-3.67E-01	4.89E-09		4.01E-01	2.23E-12		-9.92E-01	9.32E-33		-5.21E-01	1.44E-11		Unigene30864_All//gi|29419231|gb|AA061852.1|//9.00E-34//translation elongation factor-1 alpha [Malva pusilla]	Unigene30864_All//7.00E-34//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene30864_All//9.00E-112//TC152746			GO:0004779//GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene30866_All	424	0.62	3.23	1.13	1.76	1.22	0.43	0.30	0.49	0.75	2.39E+00	4.04E-04	Up	8.73E-01	4.17E-01		-5.33E-01	5.26E-01		-2.05E+00	2.45E-02		7.20E-01	6.32E-01		1.33E+00	2.93E-01				Unigene30866_All//2.00E-98//TC174612				
Unigene30867_All	651	0.00	0.00	0.00	0.00	0.05	0.00	1.23	3.27	0.00	null	null		null	null		5.73E+00	8.30E-01		null	null		1.41E+00	5.52E-04	Up	-1.03E+01	4.43E-06	Down	Unigene30867_All//gi|297812211|ref|XP_002873989.1|//5.00E-72//ribosomal protein S8 [Arabidopsis lyrata subsp. lyrata] >gi|297319826|gb|EFH50248.1| ribosomal protein S8 [Arabidopsis lyrata subsp. lyrata]	Unigene30867_All//2.00E-55//AT5G59240| 40S ribosomal protein S8 (RPS8B)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0030312//GO:0031981	nr +
Unigene30868_All	265	1.38	3.63	1.81	0.94	2.60	6.82	4.63	9.94	3.46	1.39E+00	5.77E-02		3.88E-01	6.97E-01		1.47E+00	1.16E-01		2.86E+00	2.24E-06	Up	1.10E+00	1.70E-03		-4.20E-01	4.28E-01				Unigene30868_All//3.00E-72//TC176364				

Unigene30873_All	393	0.00	0.52	0.00	0.00	0.00	0.00	173.21	102.31	78.46	9.01E+00	1.36E-01		null	null		null	null		null	null		-7.60E-01	3.68E-38		-1.14E+00	5.97E-77	Down	Unigene30873_All//gi|255558488|ref|XP_002520269.1|/8.00E-11//Desacetoxyvindoline 4-hydroxylase, putative [Ricinus communis] >gi|223540488|gb|EEF42055.1| Desacetoxyvindoline 4-hydroxylase, putative [Ricinus communis]					GO:0016491	nr +
Unigene30874_All	1083	0.68	1.50	0.25	0.64	1.62	0.75	3.71	7.83	14.49	1.15E+00	2.93E-02		-1.46E+00	1.12E-01		1.33E+00	7.60E-03		2.21E-01	7.78E-01		1.08E+00	3.33E-09	Up	1.97E+00	1.46E-39	Up	Unigene30874_All//gi|115482912|ref|NP_001065049.1|/9.00E-07//Os10g0513300 [Oryza sativa Japonica Group] >gi|113639658|dbj|BAF26963.1| Os10g0513300 [Oryza sativa Japonica Group]		Unigene30874_All//4.00E-28//TC131129				nr +
Unigene30876_All	432	2.79	1.52	0.99	1.38	1.99	1.15	0.10	0.19	2.03	-8.69E-01	1.56E-01		-1.50E+00	2.71E-02		5.26E-01	5.45E-01		-2.67E-01	7.57E-01		9.83E-01	7.31E-01		4.37E+00	2.26E-05	Up	Unigene30876_All//gi|15225457|ref|NP_182060.1|/5.00E-52//CRR4 (CHLOROREPIRATORY REDUCTION 4) [Arabidopsis thaliana]	Unigene30876_All//4.00E-53//AT2G45350| CRR4 (CHLOROREPIRATORY REDUCTION 4)	Unigene30876_All//0.00E+00//CO093317			GO:0009451//GO:0043231	nr -
Unigene30878_All	731	0.00	0.28	0.00	0.00	0.42	0.00	18.45	7.09	8.01	8.12E+00	1.36E-01		null	null		8.73E+00	4.54E-02		null	null		-1.38E+00	1.69E-20	Down	-1.20E+00	2.88E-17	Down	Unigene30878_All//gi|224065844|ref|XP_002301972.1|/4.00E-17//predicted protein [Populus trichocarpa] >gi|222843698|gb|EEE81245.1| predicted protein [Populus trichocarpa]	Unigene30878_All//1.00E-06//AT1G30750| unknown protein					nr -
Unigene30880_All	450	2.33	1.35	3.20	5.87	4.29	4.11	5.26	1.49	3.19	-7.83E-01	2.34E-01		4.58E-01	4.15E-01		-4.53E-01	2.52E-01		-5.12E-01	2.08E-01		-1.82E+00	6.14E-06	Down	-7.23E-01	4.14E-02		Unigene30880_All//gi|42566201|ref|NP_191968.3|/7.00E-08//asparaginase 2 family protein [Arabidopsis thaliana]	Unigene30880_All//5.00E-09//AT4G00590| asparaginase 2 family protein	Unigene30880_All//1.00E-81//DW229212			GO:0016811	nr -
Unigene30881_All	514	0.00	53.33	20.62	0.00	0.00	0.00	0.00	0.00	0.00	1.57E+01	5.58E-158	Up	1.43E+01	1.66E-59	Up	null	null		null	null		null	null		null	null		Unigene30881_All//gi|297794223|ref|XP_002864996.1|/4.00E-45//60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|297310831|gb|EFH41255.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene30881_All//1.00E-44//AT3G49910| 60S ribosomal protein L26 (RPL26A)			ko03010|Ribosome	GO:0005198//GO:0006950//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene30886_All	1116	0.00	19.39	17.89	0.00	0.03	0.08	0.00	0.00	0.07	1.42E+01	1.57E-124	Up	1.41E+01	7.46E-113	Up	4.95E+00	8.30E-01		6.34E+00	4.76E-01		null	null		6.16E+00	4.04E-01		Unigene30886_All//gi|195618110|gb|ACG30885.1|/2.00E-26//translationally-controlled tumor protein [Zea mays] >gi|195618316|gb|ACG30988.1| translationally-controlled tumor protein [Zea mays]	Unigene30886_All//1.00E-23//AT3G16640| TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN)					nr +
Unigene30888_All	487	0.54	4.27	3.06	0.61	0.99	0.37	0.09	0.77	0.33	2.99E+00	2.82E-07	Up	2.51E+00	1.98E-04	Up	6.90E-01	5.67E-01		-7.26E-01	6.39E-01		3.15E+00	3.41E-02		1.91E+00	3.77E-01				Unigene30888_All//0.00E+00//DW233277				
Unigene3089_All	955	1.37	1.33	0.56	3.55	1.73	2.84	1.73	1.62	0.88	-4.63E-02	9.48E-01		-1.30E+00	4.12E-02		-1.04E+00	9.92E-04	Down	-3.22E-01	3.94E-01		-9.26E-02	8.46E-01		-9.79E-01	2.63E-02		Unigene3089_All//gi|115454535|ref|NP_001050868.1|/4.00E-45//Os03g0670100 [Oryza sativa Japonica Group] >gi|108710316|gb|ABF98111.1| ABC transporter family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549339|dbj|BAF12782.1| Os03g0670100 [Oryza sativa Japonica Group]	Unigene3089_All//3.00E-46//AT1G65410| ATNAP11 (ARABIDOPSIS THALIANA NON-INTRINSIC ABC PROTEIN 11); transporter	Unigene3089_All//4.00E-151//ES848625			GO:0006810//GO:0009536//GO:0015116//GO:0017111//GO:0032559	nr -
Unigene30891_All	351	2.24	105.81	15.78	2.13	15.89	24.58	11.80	60.49	166.16	5.56E+00	4.70E-188	Up	2.82E+00	8.01E-17	Up	2.90E+00	2.18E-20	Up	3.53E+00	4.41E-35	Up	2.36E+00	2.14E-65	Up	3.82E+00	7.16E-294	Up	Unigene30891_All//gi|206584345|gb|ACI15345.1|/3.00E-23//NAC domain protein NAC4 [Gossypium hirsutum] >gi|206584355|gb|ACI15350.1| NAC domain protein NAC4 [Gossypium hirsutum]		Unigene30891_All//3.00E-156//gi|164247972|gb|EX164108.1|EX164108			GO:0003676//GO:0010468	nr -
Unigene30893_All	482	0.43	0.00	0.22	0.21	2.71	1.03	0.53	5.03	0.25	-8.76E+00	1.22E-01		-9.74E-01	6.21E-01		3.72E+00	4.93E-06	Up	2.32E+00	6.88E-02		3.26E+00	4.93E-11	Up	-1.09E+00	4.28E-01				Unigene30893_All//1.00E-47//TC154059				
Unigene30895_All	955	0.00	8.12	2.56	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	2.47E-44	Up	1.13E+01	1.64E-13	Up	null	null		null	null		null	null		null	null		Unigene30895_All//gi|4586590|dbj|BAA76427.1|/2.00E-06//aspartic proteinase [Cicer arietinum]	Unigene30895_All//5.00E-06//AT1G62290| aspartyl protease family protein					nr +
Unigene30897_All	828	0.00	0.00	0.00	0.00	0.00	0.00	2.25	1.56	0.43	null	null		null	null		null	null		null	null		-5.22E-01	2.33E-01		-2.38E+00	1.08E-06	Down								ESTscan -
Unigene30900_All	459	0.11	0.77	4.41	0.00	0.83	1.57	0.09	1.73	0.87	2.76E+00	9.59E-02		5.27E+00	7.03E-10	Up	9.69E+00	1.96E-02		1.06E+01	2.31E-04	Up	4.23E+00	1.05E-04	Up	3.24E+00	2.14E-02									
Unigene30903_All	451	2.67	1.12	2.01	0.88	1.68	1.80	2.62	0.19	1.06	-1.25E+00	4.69E-02		-4.11E-01	5.25E-01		9.27E-01	2.97E-01		1.03E+00	2.17E-01		-3.82E+00	2.12E-06	Down	-1.31E+00	1.69E-02		Unigene30903_All//gi|240255306|ref|NP_187508.5|/1.00E-66//binding / protein transporter [Arabidopsis thaliana]	Unigene30903_All//1.00E-67//AT3G08960| binding / protein transporter				GO:0015031//GO:0022892//GO:0031410	nr +
Unigene30905_All	278	0.94	0.18	2.30	2.87	2.85	0.16	0.61	0.45	1.58	-2.37E+00	2.14E-01		1.29E+00	1.86E-01		-9.10E-03	9.67E-01		-4.14E+00	4.13E-04	Down	-4.32E-01	7.93E-01		1.37E+00	1.82E-01									
Unigene30906_All	736	138.20	111.80	86.31	78.11	70.04	67.99	121.84	90.18	51.48	-3.06E-01	2.03E-09		-6.79E-01	7.44E-37		-1.57E-01	2.71E-02		-2.00E-01	4.86E-03		-4.34E-01	8.06E-19		-1.24E+00	1.59E-115	Down	Unigene30906_All//gi|164652940|gb|ABY65003.1|/2.00E-27//14-3-3d protein [Gossypium hirsutum]	Unigene30906_All//6.00E-24//AT1G78300| GRF2 (GENERAL REGULATORY FACTOR 2); protein binding / protein phosphorylated amino acid binding	Unigene30906_All//0.00E+00//TC144288			GO:0005515	nr +
Unigene30907_All	299	10.67	50.67	19.41	23.16	20.85	17.07	0.14	42.63	0.13	2.25E+00	4.52E-36	Up	8.63E-01	7.73E-04		-1.52E-01	5.54E-01		-4.40E-01	5.31E-02		8.24E+00	5.29E-88	Up	-8.62E-02	9.72E-01		Unigene30907_All//gi|159138935|gb|ABW89467.1|/4.00E-13//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene30907_All//3.00E-09//AT3G46230| ATHSP17.4	Unigene30907_All//1.00E-99//gi|13353133|gb|BG443481.1|BG443481				nr +
Unigene30910_All	358	1.61	1.13	0.30	4.59	0.19	0.76	5.91	8.06	3.00	-5.06E-01	6.00E-01		-2.43E+00	4.40E-02		-4.58E+00	6.03E-10	Down	-2.60E+00	1.60E-05	Down	4.48E-01	1.91E-01		-9.75E-01	1.06E-02				Unigene30910_All//2.00E-154//DW510603				
Unigene30911_All	405	0.26	0.00	0.00	10.70	5.53	2.01	1.15	0.93	0.10	-8.01E+00	3.72E-01		-8.01E+00	3.93E-01		-9.53E-01	4.43E-04		-2.41E+00	1.30E-12	Down	-3.06E-01	7.36E-01		-3.54E+00	6.85E-03									
Unigene30913_All	1140	0.18	0.00	0.37	0.22	0.27	0.36	9.20	17.82	22.72	-7.52E+00	1.22E-01		1.03E+00	3.96E-01		3.15E-01	8.38E-01		7.07E-01	5.97E-01		9.54E-01	3.16E-17		1.30E+00	3.07E-36	Up	Unigene30913_All//gi|145839451|gb|ABP96804.1|/1.00E-126//receptor-like protein kinase [Capsicum annuum]	Unigene30913_All//3.00E-111//AT5G38280| PBS8; kinase/ transmembrane receptor protein serine/threonine kinase	Unigene30913_All//0.00E+00//DW511405		ko04626|Plant-pathogen interaction		nr +
Unigene30915_All	1136	0.09	0.00	0.00	0.00	0.00	0.16	34.13	14.16	14.59	-6.53E+00	3.72E-01		-6.53E+00	3.93E-01		null	null		7.31E+00	1.94E-01		-1.27E+00	1.47E-50	Down	-1.23E+00	2.25E-49	Down	Unigene30915_All//gi|13752458|gb|AK38665.1|/1.00E-104//stem secoisolariciresinol dehydrogenase [Forsythia x intermedia]	Unigene30915_All//1.00E-66//AT1G52340| ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase	Unigene30915_All//0.00E+00//TC133162		ko00906|Carotenoid biosynthesis	GO:0033764//GO:0046246	nr -
Unigene30919_All	275	3.23	0.00	1.55	1.27	1.25	1.15	0.00	0.00	0.00	-1.17E+01	2.86E-05	Down	-1.06E+00	1.76E-01		-1.81E-02	9.58E-01		-1.41E-01	9.12E-01		null	null		null	null				Unigene30919_All//3.00E-07//TC162759				
Unigene3092_All	1087	12.76	35.10	17.68	9.26	6.91	14.50	27.42	37.60	62.42	1.46E+00	4.08E-50	Up	4.71E-01	3.02E-04		-4.23E-01	1.52E-02		6.48E-01	2.36E-06		4.56E-01	8.66E-10		1.19E+00	8.58E-81	Up	Unigene3092_All//gi|75297894|sp|Q84MB3.1|ACCH1_ARATH//1.00E-124//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene3092_All//2.00E-111//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene3092_All//4.00E-102//gi|189098380|gb|FG551532.1|FG551532		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene30920_All	442	0.00	0.69	0.00	0.00	0.00	0.00	26.21	62.79	13.52	9.43E+00	4.43E-02		null	null		null	null		null	null		1.26E+00	5.40E-36	Up	-9.55E-01	1.52E-10		Unigene30920_All//gi|224074401|ref|XP_002304364.1|/2.00E-28//4-coumarate-coa ligase [Populus trichocarpa] >gi|222841796|gb|EEE79343.1| 4-coumarate-coa ligase [Populus trichocarpa]	Unigene30920_All//2.00E-26//AT4G19010| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene30920_All//9.00E-163//CO101209		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0006575//GO:0006950//GO:0009694//GO:0016405//GO:0016703//GO:0042579	nr -
Unigene30921_All	391	0.00	0.00	0.00	72.11	36.90	19.98	0.43	0.53	0.00	null	null		null	null		-9.67E-01	5.69E-24		-1.85E+00	9.52E-57	Down	3.06E-01	8.36E-01		-8.76E+00	1.08E-01		Unigene30921_All//gi|186510343|ref|NP_001078202.2|/6.00E-11//LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4) [Arabidopsis thaliana]	Unigene30921_All//7.00E-05//AT3G23290| LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4)	Unigene30921_All//0.00E+00//TC146825				nr +
Unigene30922_All	552	0.38	0.18	0.00	0.72	0.12	0.16	1.46	4.39	9.67	-1.05E+00	5.65E-01		-8.57E+00	1.46E-01		-2.53E+00	5.79E-02		-2.14E+00	1.26E-01		1.59E+00	3.82E-05	Up	2.73E+00	2.48E-20	Up	Unigene30922_All//gi|148533991|gb|ABQ85120.1|/1.00E-12//ARG05 [Arabidopsis thaliana]		Unigene30922_All//2.00E-16//TC165715			GO:0008283//GO:0043231//GO:0043401//GO:0045927	nr -
Unigene30925_All	1170	0.00	0.00	0.00	0.00	0.00	0.00	4.63	1.11	3.98	null	null		null	null		null	null		null	null		-2.06E+00	1.03E-14	Down	-2.15E-01	3.71E-01		Unigene30925_All//gi|224127790|ref|XP_002329178.1|/1.00E-135//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222870959|gb|EEF08090.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene30925_All//7.00E-109//AT4G10350| ANAC070 (Arabidopsis NAC domain containing protein 70); transcription factor	Unigene30925_All//2.00E-08//TC145375	NAC		GO:0009832//GO:0010557	nr -
Unigene30926_All	326	63.56	238.12	59.13	81.75	221.29	135.91	77.43	151.80	213.37	1.91E+00	1.07E-147	Up	-1.04E-01	4.61E-01		1.44E+00	1.06E-108	Up	7.33E-01	1.22E-20		9.71E-01	5.22E-42		1.46E+00	5.86E-114	Up	Unigene30926_All//gi|29294065|gb|AAO73902.1|/8.00E-11//expressed protein [Arabidopsis thaliana] >gi|30023750|gb|AAP13408.1| At5g21940 [Arabidopsis thaliana]	Unigene30926_All//9.00E-10//AT5G21940| unknown protein	Unigene30926_All//2.00E-129//DR454692			GO:0005488//GO:0043231	nr -
Unigene30929_All	387	0.41	0.65	0.41	2.32	2.31	8.29	0.00	0.00	0.21	6.91E-01	6.27E-01		2.54E-02	1.00E+00		-2.10E-03	9.78E-01		1.84E+00	1.00E-06	Up	null	null		7.69E+00	4.04E-01				Unigene30929_All//5.00E-19//DR461639				
Unigene3093_All	1312	1.83	2.47	2.44	40.78	39.19	31.19	6.80	2.33	1.43	4.30E-01	2.21E-01		4.09E-01	2.70E-01		-5.74E-02	5.45E-01		-3.87E-01	2.88E-08		-1.55E+00	2.93E-16	Down	-2.25E+00	2.30E-27	Down	Unigene3093_All//gi|60657592|gb|AAX33317.1|/0.00E+00//secondary cell wall-related glycosyltransferase family 8 [Populus tremula x Populus tremuloides]	Unigene3093_All//0.00E+00//AT3G18660| PGSIP1 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 1); transferase, transferring glycosyl groups	Unigene3093_All//0.00E+00//TC169088			GO:0035251	nr -
Unigene30931_All	515	0.00	14.76	7.24	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	1.86E-43	Up	1.28E+01	1.20E-20	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene30933_All	415	0.13	0.24	0.77	1.32	0.58	1.74	2.75	0.50	0.67	9.54E-01	7.26E-01		2.61E+00	1.46E-01		-1.18E+00	2.25E-01		3.99E-01	6.51E-01		-2.45E+00	2.46E-04	Down	-2.03E+00	8.64E-04	Down								
Unigene30937_All	1510	0.00	138.12	52.69	0.00	0.14	0.03	0.00	0.00	0.00	1.71E+01	0.00E+00	Up	1.57E+01	0.00E+00	Up	7.10E+00	1.57E-01		4.90E+00	6.96E-01		null	null		null	null		Unigene30937_All//sp|P11997|LSP1G_DROME//0.00E+00//Larval serum protein 1 gamma chain OS=Drosophila melanogaster GN=Lsp1gamma PE=2 SV=2						swissprot +
Unigene30938_All	910	0.00	0.00	0.00	0.00	0.00	0.00	3.58	5.74	0.04	null	null		null	null		null	null		null	null		6.82E-01	3.39E-03		-6.35E+00	2.39E-22	Down	Unigene30938_All//gi|297827841|ref|XP_002881803.1|/1.00E-105//40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata] >gi|297327642|gb|EFH58062.1| 40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata]	Unigene30938_All//1.00E-85//AT3G57490| 40S ribosomal protein S2 (RPS2D)	Unigene30938_All//2.00E-08//DW519163		ko03010|Ribosome		nr -
Unigene3094_All	999	20.22	166.82	97.12	20.19	77.90	146.11	22.64	85.64	115.09	3.04E+00	0.00E+00	Up	2.26E+00	1.95E-225	Up	1.95E+00	2.23E-179	Up	2.86E+00	0.00E+00	Up	1.92E+00	1.41E-201	Up	2.35E+00	0.00E+00	Up	Unigene3094_All//gi|225458627|ref|XP_002284791.1|/8.00E-73//PREDICTED: ripening-related bZIP protein-like isoform 2 [Vitis vinifera] >gi|225458629|ref|XP_002284785.1| PREDICTED: ripening-related bZIP protein-like isoform 1 [Vitis vinifera]	Unigene3094_All//3.00E-45//AT3G19290| ABF4 (ABRE BINDING FACTOR 4); DNA binding / protein binding / transcription activator/ transcription factor	Unigene3094_All//0.00E+00//TC156582	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0006970//GO:0009755//GO:0030528//GO:0043231	nr -
Unigene30941_All	373	81.64	104.74	146.47	26.98	51.51	143.36	31.74	36.64	105.20	3.59E-01	2.63E-05		8.43E-01	5.32E-29		9.33E-01	6.61E-15		2.41E+00	5.90E-147	Up	2.07E-01	1.61E-01		1.73E+00	4.01E-82	Up	Unigene30941_All//gi|118132690|gb|ABK60196.1|/2.00E-24//PIP2 protein [Gossypium hirsutum]	Unigene30941_All//7.00E-22//AT2G45960| PIP1B (NAMED PLASMA MEMBRANE INTRINSIC PROTEIN 1B); water channel	Unigene30941_All//6.00E-74//ES828342			GO:0016020	nr +

Unigene30943_All	1985	0.00	0.15	0.27	0.00	0.00	0.05	0.47	1.43	7.55	7.26E+00	4.43E-02		8.07E+00	4.04E-03		null	null		5.51E+00	4.76E-01		1.61E+00	5.54E-06	Up	4.01E+00	1.13E-78	Up	Unigene30943_All//gi|297822769|ref|XP_002879267.1|//0.00E+00//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325106|gb|EFH55526.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene30943_All//2.00E-178//AT1G06800| lipase class 3 family protein	Unigene30943_All//0.00E+00//TC168797			GO:0004091//GO:0009536//GO:0044238	nr -
Unigene30945_All	366	0.14	0.14	0.00	1.09	0.94	0.12	1.39	1.03	4.68	-4.72E-02	9.85E-01		-7.16E+00	6.24E-01		-2.11E-01	8.25E-01		-3.14E+00	4.88E-02		-4.32E-01	6.18E-01		1.76E+00	1.93E-04	Up	Unigene30945_All//gi|115474339|ref|NP_001060766.1|//2.00E-21//Os08g0102100 [Oryza sativa Japonica Group] >gi|113622735|dbj|BAF22680.1| Os08g0102100 [Oryza sativa Japonica Group]	Unigene30945_All//4.00E-24//AT3G44330| INVOLVED IN: protein processing; LOCATED IN: mitochondrion, endoplasmic reticulum, plasma membrane, vacuole; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nicalin (InterPro:IPR016574), EF-HAND 1 (InterPro:IPR018247), Nicastrin (InterPro:IPR008710); Has 192 Blast hits to 192 proteins in 79 species: Archae - 6; Bacteria - 5; Metazoa - 124; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink).	Unigene30945_All//8.00E-95//gi|48821612|gb|CO122925.1|CO122925			GO:0016787//GO:0031224//GO:0031410//GO:0043231//GO:0051604	nr -
Unigene30946_All	487	3.98	2.08	0.98	7.47	4.60	3.34	1.22	1.20	0.82	-9.34E-01	4.45E-02		-2.01E+00	2.05E-04	Down	-7.00E-01	2.22E-02		-1.16E+00	3.09E-04	Down	-1.66E-02	1.02E+00		-5.71E-01	4.78E-01		Unigene30946_All//gi|115462287|ref|NP_001051743.1|//2.00E-33//Os05g0164900 [Oryza sativa Japonica Group] >gi|113578294|dbj|BAF16657.1| Os05g0164900 [Oryza sativa Japonica Group]	Unigene30946_All//3.00E-48//AT5G01660| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Kelch repeat type 1 (InterPro:IPR006652), Galactose oxidase/kelch, beta-propeller (InterPro:IPR011043), Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089), Kelch-type beta propeller (InterPro:IPR015915); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11000.2); Has 12390 Blast hits to 5423 proteins in 323 species: Archae - 22; Bacteria - 787; Metazoa - 5729; Fungi - 223; Plants - 966; Viruses - 639; Other Eukaryotes - 1024 (source: NCBI BLink).					nr +
Unigene30947_All	216	3.15	0.00	0.99	1.15	0.80	0.21	0.78	0.00	0.37	-1.16E+01	4.10E-04	Down	-1.68E+00	8.70E-02		-5.33E-01	7.12E-01		-2.46E+00	2.23E-01		-9.61E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene30947_All//gi|224092091|ref|XP_002309468.1|//7.00E-25//cytokinin oxidase [Populus trichocarpa] >gi|222855444|gb|EEE92991.1| cytokinin oxidase [Populus trichocarpa]	Unigene30947_All//3.00E-25//AT5G21482| CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase	Unigene30947_All//2.00E-69//TC164612	ko00908|Zeatin biosynthesis	GO:0009690//GO:0016645//GO:0030554	nr +
Unigene30948_All	925	0.34	3.62	0.12	0.54	0.74	6.35	0.00	0.00	0.26	3.41E+00	9.83E-13	Up	-1.56E+00	3.30E-01		4.67E-01	6.12E-01		3.56E+00	4.04E-24	Up	null	null		8.01E+00	4.39E-02		Unigene30948_All//gi|6226510|sp|Q9ZSK5.1|2OG_PHALU//2.00E-98//RecName: Full=Zeatin O-glucosyltransferase; AltName: Full=Trans-zeatin O-beta-D-glucosyltransferase >gi|4140691|gb|AAD04166.1| zeatin O-glucosyltransferase [Phaseolus lunatus]	Unigene30948_All//7.00E-36//AT3G46660| UGT76E12 (UDP-GLUCOSYL TRANSFERASE 76E12); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene30948_All//0.00E+00//TC164996	ko00908|Zeatin biosynthesis	GO:0008194//GO:0016758	nr -
Unigene30949_All	266	3.93	0.00	1.60	4.87	0.26	1.87	1.11	0.31	0.30	-1.19E+01	3.80E-06	Down	-1.30E+00	7.46E-02		-4.23E+00	1.56E-07	Down	-1.38E+00	2.30E-02		-1.82E+00	2.11E-01		-1.89E+00	1.68E-01				Unigene30949_All//2.00E-85//BF278242				
Unigene3095_All	1266	7.69	3.56	5.38	3.34	5.03	2.64	2.14	0.76	1.23	-1.11E+00	5.25E-09	Down	-5.14E-01	7.44E-03		5.89E-01	9.43E-03		-3.41E-01	2.88E-01		-1.49E+00	3.15E-05	Down	-8.00E-01	1.49E-02		Unigene3095_All//gi|18405476|ref|NP_565939.1|//3.00E-68//GLY1; glycerol-3-phosphate dehydrogenase (NAD+) [Arabidopsis thaliana]	Unigene3095_All//1.00E-69//AT2G40690| GLY1; glycerol-3-phosphate dehydrogenase (NAD+)	Unigene3095_All//0.00E+00//TC170511	ko00564|Glycerophospholipid metabolism	GO:0000166//GO:0006072//GO:0006644//GO:0008610//GO:0009814//GO:0016616//GO:0043231//GO:0043234//GO:0048037	nr -
Unigene30950_All	578	0.00	0.00	0.00	0.00	0.00	0.00	12.29	2.10	2.48	null	null		null	null		null	null		null	null		-2.55E+00	1.75E-24	Down	-2.31E+00	1.35E-22	Down	Unigene30950_All//gi|8569094|gb|AAF76439.1|AC015445_6//5.00E-20//Contains similarity to PR1a protein precursor from Nicotiana tabacum gb|D90196 and contains an SCP domain PF|00188. EST gb|R64931 comes from this gene [Arabidopsis thaliana]	Unigene30950_All//2.00E-17//AT1G50060| pathogenesis-related protein, putative		ko04626|Plant-pathogen interaction		nr -
Unigene30951_All	478	1.64	0.42	0.00	0.21	1.37	1.42	0.00	0.17	1.42	-1.95E+00	2.62E-02		-1.07E+01	2.22E-04	Down	2.72E+00	1.37E-02		2.77E+00	1.14E-02		7.45E+00	4.01E-01		1.05E+01	4.96E-05	Up								ESTscan -
Unigene30952_All	454	0.23	1.45	0.23	0.11	0.38	1.69	6.61	4.79	17.29	2.65E+00	1.49E-02		2.54E-02	1.00E+00		1.79E+00	5.20E-01		3.95E+00	1.02E-03		-4.66E-01	1.59E-01		1.39E+00	1.24E-12	Up			Unigene30952_All//3.00E-144//gi|48779846|gb|CO089212.1|CO089212				
Unigene30957_All	690	1.67	0.51	0.00	3.54	2.15	1.44	0.67	0.00	0.29	-1.70E+00	1.21E-02		-1.07E+01	2.60E-06	Down	-7.21E-01	6.54E-02		-1.30E+00	1.60E-03		-9.40E+00	1.71E-03		-1.22E+00	2.00E-01		Unigene30957_All//gi|297605262|ref|NP_001056943.2|//2.00E-08//Os06g0173000 [Oryza sativa Japonica Group] >gi|255676762|dbj|BAF18857.2| Os06g0173000 [Oryza sativa Japonica Group]						nr +
Unigene30958_All	838	0.00	13.00	4.83	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.89E-62	Up	1.22E+01	1.92E-22	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene30959_All	290	0.00	0.00	0.00	0.00	0.00	0.00	1.46	6.05	13.05	null	null		null	null		null	null		null	null		2.05E+00	3.20E-05	Up	3.16E+00	8.37E-17	Up								
Unigene3096_All	2022	6.42	19.90	9.85	7.07	7.54	11.10	7.72	11.12	9.00	1.63E+00	4.64E-62	Up	6.18E-01	1.18E-06		9.36E-02	5.97E-01		6.51E-01	7.73E-09		5.27E-01	2.89E-07		2.23E-01	5.98E-02		Unigene3096_All//gi|5815235|gb|AAD52609.1|AF173640_1//5.00E-93//splicing factor SR1 [Arabidopsis thaliana]	Unigene3096_All//9.00E-76//AT1G09140| SF2/ASF-like splicing modulator (SRP30)	Unigene3096_All//0.00E+00//TC137542	ko03040|Spliceosome	GO:0003676//GO:0005515//GO:0016604//GO:0050896	nr +
Unigene30960_All	498	0.32	0.10	0.00	0.40	0.41	1.09	0.51	3.19	3.44	-1.63E+00	4.89E-01		-8.30E+00	2.45E-01		5.24E-02	9.89E-01		1.44E+00	1.93E-01		2.65E+00	3.44E-06	Up	2.76E+00	4.59E-07	Up			Unigene30960_All//6.00E-07//ES817133				
Unigene30965_All	413	15.84	0.00	6.32	0.72	0.17	0.00	0.00	0.00	0.00	-1.40E+01	6.57E-38	Down	-1.33E+00	1.09E-07	Down	-2.12E+00	1.65E-01		-9.50E+00	4.00E-02		null	null		null	null		Unigene30965_All//gi|225447396|ref|XP_002281293.1|//5.00E-07//PREDICTED: hypothetical protein [Vitis vinifera] >gi|147789234|emb|CAN78011.1| hypothetical protein [Vitis vinifera] >gi|297739334|emb|CBI28985.3| unnamed protein product [Vitis vinifera]		Unigene30965_All//2.00E-154//FL576398			nr +
Unigene30966_All	642	2.53	0.47	0.83	6.52	4.67	2.67	0.20	0.65	0.19	-2.42E+00	7.51E-05	Down	-1.61E+00	5.02E-03		-4.82E-01	1.01E-01		-1.29E+00	1.76E-05	Down	1.72E+00	1.35E-01		-8.57E-02	9.69E-01								
Unigene30968_All	701	0.00	0.00	0.00	0.00	0.00	0.00	2.71	2.92	0.00	null	null		null	null		null	null		null	null		1.06E-01	8.00E-01		-1.14E+01	4.91E-14	Down	Unigene30968_All//gi|15221798|ref|NP_173289.1|//4.00E-26//60S ribosomal protein L6 (RPL6A) [Arabidopsis thaliana] >gi|75173375|sp|Q9FZ76.1|RL61_ARATH RecName: Full=60S ribosomal protein L6-1 >gi|9795602|gb|AAF98420.1|AC026238_12 Putative 60S ribosomal protein L6 [Arabidopsis thaliana] >gi|15451190|gb|AAK96866.1| Putative 60S ribosomal protein L6 [Arabidopsis thaliana]	Unigene30968_All//8.00E-22//AT1G74060| 60S ribosomal protein L6 (RPL6B)		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene30973_All	474	4.86	6.84	2.36	30.06	29.93	14.77	0.71	0.71	0.00	4.94E-01	1.54E-01		-1.04E+00	1.91E-02		-6.00E-03	9.64E-01		-1.03E+00	4.32E-12	Down	-1.67E-02	1.02E+00		-9.48E+00	8.14E-03		Unigene30973_All//gi|171452356|dbj|BAG15869.1|//8.00E-27//ankyrin repeat protein [Bruguiera gymnorhiza]	Unigene30973_All//1.00E-27//AT4G10720| ankyrin repeat family protein	Unigene30973_All//4.00E-128//TC130834		GO:0010033	nr -
Unigene30974_All	952	0.11	34.44	12.47	0.00	0.00	0.00	0.00	0.00	0.00	8.29E+00	2.18E-184	Up	6.83E+00	5.55E-63	Up	null	null		null	null		null	null		null	null		Unigene30974_All//gi|297852652|ref|XP_002894207.1|//1.00E-13//ARP protein [Arabidopsis lyrata subsp. lyrata] >gi|297340049|gb|EFH70466.1| ARP protein [Arabidopsis lyrata subsp. lyrata]	Unigene30974_All//2.00E-10//AT1G49670| NQR; binding / catalytic/ oxidoreductase/ zinc ion binding			GO:0006950//GO:0043231//GO:0044444	nr -
Unigene30977_All	576	3.00	0.26	2.22	2.85	1.49	1.02	0.37	0.00	0.00	-3.51E+00	4.63E-07	Down	-4.34E-01	3.93E-01		-9.33E-01	5.72E-02		-1.49E+00	4.95E-03		-8.52E+00	7.44E-02		-8.52E+00	5.80E-02		Unigene30977_All//gi|225451974|ref|XP_002279826.1|//5.00E-49//PREDICTED: hypothetical protein [Vitis vinifera] >gi|298204374|emb|CBI16854.3| unnamed protein product [Vitis vinifera]	Unigene30977_All//3.00E-31//AT5G16030| unknown protein	Unigene30977_All//0.00E+00//gi|48740706|gb|CO071225.1|CO071225			nr +
Unigene30978_All	828	0.06	0.61	0.26	5.23	3.49	1.09	0.46	0.61	0.91	3.28E+00	2.11E-02		2.02E+00	3.61E-01		-5.83E-01	3.77E-02		-2.26E+00	1.05E-11	Down	3.98E-01	6.52E-01		9.92E-01	1.63E-01		Unigene30978_All//gi|297742227|emb|CBI34376.3|//9.00E-22//unnamed protein product [Vitis vinifera]	Unigene30978_All//7.00E-05//AT4G23493| unknown protein	Unigene30978_All//0.00E+00//gi|13246216|gb|BE052216.2|BE052216			nr +
Unigene30979_All	234	1.57	1.73	2.28	1.92	5.74	2.32	7.41	4.11	2.38	1.46E-01	8.98E-01		5.40E-01	6.10E-01		1.58E+00	8.62E-03		2.74E-01	7.83E-01		-8.51E-01	5.62E-02		-1.64E+00	3.35E-04	Down			Unigene30979_All//1.00E-12//ES850878				
Unigene30980_All	1476	0.00	53.90	22.37	0.14	0.00	0.00	0.00	0.00	0.00	1.57E+01	0.00E+00	Up	1.44E+01	2.68E-187	Up	-7.08E+00	8.43E-02		-7.08E+00	1.33E-01		null	null		null	null		Unigene30980_All//gi|254558248|gb|ACT67906.1|//0.00E+00//heat shock protein 70 [Ulva prolifera]	Unigene30980_All//2.00E-164//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene30980_All//9.00E-27//TC133087	ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0016887//GO:0032559//GO:0050896	nr -
Unigene30987_All	426	0.00	0.48	0.00	2.46	2.83	0.74	1.49	0.10	0.65	8.89E+00	1.36E-01		null	null		2.04E-01	8.01E-01		-1.73E+00	1.55E-02		-3.92E+00	9.81E-04	Down	-1.19E+00	1.33E-01				Unigene30987_All//5.00E-07//gi|78331403|gb|DT551677.1|DT551677				
Unigene30989_All	779	0.40	0.00	0.00	2.43	1.19	0.35	0.16	0.00	0.00	-8.65E+00	3.65E-02		-8.65E+00	4.91E-02		-1.03E+00	2.20E-02		-2.80E+00	9.57E-07	Down	-7.35E+00	2.35E-01		-7.35E+00	2.00E-01		Unigene30989_All//gi|115464761|ref|NP_001055980.1|//3.00E-36//Os05g0506000 [Oryza sativa Japonica Group] >gi|113579531|dbj|BAF17894.1| Os05g0506000 [Oryza sativa Japonica Group]	Unigene30989_All//8.00E-37//AT5G48850| ATSDI1 (SULPHUR DEFICIENCY-INDUCED 1); binding	Unigene30989_All//0.00E+00//TC178041			nr -
Unigene30990_All	380	1.24	0.40	0.84	0.26	0.54	0.71	2.56	1.21	0.42	-1.63E+00	1.58E-01		-5.60E-01	6.28E-01		1.05E+00	6.12E-01		1.44E+00	4.09E-01		-1.08E+00	8.88E-02		-2.61E+00	3.35E-04	Down			Unigene30990_All//9.00E-67//gi|48879239|gb|CO130261.1|CO130261				
Unigene30993_All	641	0.33	0.00	0.00	0.70	1.61	0.56	2.24	0.00	0.62	-8.35E+00	1.22E-01		-8.35E+00	1.46E-01		1.20E+00	8.56E-02		-3.11E-01	7.57E-01		-1.11E+01	3.33E-10	Down	-1.85E+00	3.87E-04	Down	Unigene30993_All//gi|224110480|ref|XP_002315532.1|//5.00E-98//sodium proton exchanger [Populus trichocarpa] >gi|222864572|gb|EEF01703.1| sodium proton exchanger [Populus trichocarpa]	Unigene30993_All//7.00E-91//AT3G06370| NHX4 (SODIUM HYDROGEN EXCHANGER 4); sodium ion transmembrane transporter/ sodium:hydrogen antiporter	Unigene30993_All//6.00E-171//TC154409		GO:0005451//GO:0030001//GO:0031224//GO:0055067	nr -
Unigene30996_All	276	1.52	3.67	0.39	1.08	1.00	0.00	2.76	0.30	0.14	1.28E+00	6.99E-02		-1.97E+00	1.51E-01		-1.18E-01	9.00E-01		-1.01E+01	4.00E-02		-3.19E+00	7.92E-04	Down	-4.26E+00	8.65E-05	Down								

Unigene30998_All	493	0.00	0.00	0.22	0.00	0.00	0.00	3.69	10.17	3.64	null	null		7.75E+00	3.98E-01		null	null		null	null		1.46E+00	8.85E-09	Up	-2.02E-02	9.66E-01		Unigene30998_All//gi|224062151|ref|XP_002300780.1|//2.00E-39//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222842506|gb|EEE90053.1|AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene30998_All//3.00E-23//AT3G23230| ethylene-responsive factor, putative	Unigene30998_All//0.00E+00//TC157083	AP2-EREBP		GO:0000160//GO:0001071//GO:0006351//GO:0009743//GO:0010468//GO:0043231	nr -
Unigene310_All	2574	10.12	6.99	4.41	24.09	17.47	25.65	31.41	15.26	16.10	-5.35E-01	4.83E-07		-1.20E+00	9.49E-25	Down	-4.64E-01	1.84E-14		9.04E-02	2.31E-01		-1.04E+00	2.18E-76	Down	-9.64E-01	2.68E-69		Unigene310_All//gi|6685536|sp|P56821.1|EIF3B_TOBAC//0.00E+00//RecName: Full=Eukaryotic translation initiation factor 3 subunit B; Short=eIF3b; AltName: Full=eIF-3-eta; AltName: Full=eIF3 p110 >gi|5911685|emb|CAA72721.1| PRT1 protein [Nicotiana tabacum]	Unigene310_All//0.00E+00//AT5G27640| TIF3B1 (TRANSLATION INITIATION FACTOR 3B1); nucleic acid binding / translation initiation factor	Unigene310_All//0.00E+00//TC174426				nr -
Unigene31002_All	423	2.35	0.72	0.63	2.71	0.98	0.43	3.30	4.25	2.26	-1.71E+00	2.08E-02		-1.90E+00	1.70E-02		-1.47E+00	1.73E-02		-2.66E+00	4.12E-04	Down	3.65E-01	4.23E-01		-5.45E-01	2.66E-01								
Unigene31003_All	842	0.00	3.55	3.79	0.00	0.04	0.00	0.00	0.00	0.00	1.18E+01	5.19E-17	Up	1.19E+01	1.15E-17	Up	5.35E+00	8.30E-01		null	null		null	null		null	null		Unigene31003_All//sp|P17661|DESM_HUMAN//2.00E-37//Desmin OS=Homo sapiens GN=DES PE=1 SV=3						swissprot -
Unigene31007_All	711	0.96	0.78	0.37	1.19	0.63	0.64	2.79	0.82	2.69	-2.87E-01	7.10E-01		-1.35E+00	1.50E-01		-9.20E-01	2.17E-01		-9.07E-01	2.47E-01		-1.76E+00	6.52E-05	Down	-5.55E-02	9.02E-01				Unigene31007_All//0.00E+00//ES805591				
Unigene31009_All	1154	0.00	0.00	0.00	0.00	0.00	0.00	10.41	2.21	3.14	null	null		null	null		null	null		null	null		-2.24E+00	4.30E-35	Down	-1.73E+00	5.60E-26	Down	Unigene31009_All//gi|15226598|ref|NP_179755.1|//1.00E-103//pectinesterase family protein [Arabidopsis thaliana] >gi|75206124|sp|Q9SLJ9.1|PME11_ARATH RecName: Full=Putative pectinesterase 11; Short=PE 11; AltName: Full=Pectin methylesterase 11; Short=AtPME11	Unigene31009_All//3.00E-104//AT2G21610| pectinesterase family protein	Unigene31009_All//4.00E-62//TC179074		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0030312//GO:0044424	nr -
Unigene3101_All	1293	41.92	23.36	27.18	18.26	17.20	15.05	7.10	2.72	1.48	-8.44E-01	7.43E-30		-6.25E-01	2.93E-17		-8.60E-02	5.50E-01		-2.79E-01	1.56E-02		-1.39E+00	2.77E-14	Down	-2.26E+00	2.86E-28	Down	Unigene3101_All//gi|15234935|ref|NP_195615.1|//1.00E-53//RNA binding [Arabidopsis thaliana] >gi|28950859|gb|AAO63353.1|At4g39040 [Arabidopsis thaliana]	Unigene3101_All//4.00E-43//AT4G39040| RNA binding	Unigene3101_All//0.00E+00//CO132389			GO:0003676//GO:0009536	nr +
Unigene31010_All	1274	0.00	0.00	0.00	0.00	0.00	0.00	0.53	0.62	3.28	null	null		null	null		null	null		null	null		2.31E-01	7.34E-01		2.63E+00	1.85E-15	Up	Unigene31010_All//gi|284029888|gb|ADB66335.1|//2.00E-76//CC-NBS-LRR protein [Quercus suber]	Unigene31010_All//3.00E-54//AT3G14470| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction		nr -
Unigene31011_All	245	4.91	1.24	0.43	1.02	1.41	0.37	0.00	0.00	0.00	-1.98E+00	3.72E-03		-3.50E+00	8.78E-05	Down	4.67E-01	7.29E-01		-1.46E+00	4.07E-01		null	null		null	null									
Unigene31013_All	548	0.48	0.74	0.00	0.64	0.38	0.41	1.16	0.92	4.14	6.32E-01	6.01E-01		-8.90E+00	8.57E-02		-7.55E-01	5.67E-01		-6.27E-01	6.21E-01		-3.39E-01	6.63E-01		1.84E+00	6.10E-06	Up			Unigene31013_All//2.00E-07//DT465324				
Unigene31015_All	588	187.39	967.03	369.76	207.81	144.53	142.71	10630.09	6428.01	5806.48	2.37E+00	0.00E+00	Up	9.81E-01	4.34E-147		-5.24E-01	4.32E-35		-5.42E-01	3.57E-33		-7.26E-01	0.00E+00		-8.72E-01	0.00E+00		Unigene31015_All//gi|62856977|gb|AAY16439.1|//7.00E-23//metallothionein-like protein [Betula platyphylla]	Unigene31015_All//2.00E-09//AT3G09390| MT2A (METALLOTHIONEIN 2A); copper ion binding	Unigene31015_All//0.00E+00//TC158845			GO:0043169	nr -
Unigene31016_All	990	0.00	0.10	0.54	1.61	5.01	1.87	1.11	1.27	1.61	6.68E+00	3.87E-01		9.07E+00	4.04E-03		1.64E+00	2.87E-09	Up	2.16E-01	6.91E-01		1.90E-01	7.28E-01		5.36E-01	2.42E-01		Unigene31016_All//gi|39725413|emb|CAE09057.1|//4.00E-43//MYB transcription factor [Eucalyptus gunnii]	Unigene31016_All//2.00E-43//AT5G12870| MYB46 (MYB DOMAIN PROTEIN 46); DNA binding / transcription factor	Unigene31016_All//2.00E-23//DN802716	MYB		GO:0001071//GO:0003676//GO:0006351//GO:0009832//GO:0010033//GO:0010168//GO:0043231	nr -
Unigene31017_All	293	7.32	17.47	12.90	1.02	2.23	0.92	0.29	0.29	2.31	1.25E+00	5.19E-06	Up	8.18E-01	1.31E-02		1.13E+00	2.38E-01		-1.42E-01	9.21E-01		-1.66E-02	1.01E+00		3.00E+00	2.00E-03		Unigene31017_All//gi|297850684|ref|XP_002893223.1|//2.00E-33//transcription factor/ transferase, transferring glycosyl groups [Arabidopsis lyrata subsp. lyrata] >gi|297339065|gb|EFH69482.1|transcription factor/ transferase, transferring glycosyl groups [Arabidopsis lyrata subsp. lyrata]	Unigene31017_All//2.00E-34//AT1G22380| AtUGT85A3 (UDP-glucosyl transferase 85A3); glucuronosyltransferase/ transcription factor/ transferase, transferring glycosyl groups	Unigene31017_All//8.00E-150//DT465722		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis	GO:0035251	nr +
Unigene31020_All	716	0.00	0.00	0.00	0.00	0.00	0.00	7.09	15.47	25.93	null	null		null	null		null	null		null	null		1.13E+00	1.48E-12	Up	1.87E+00	1.03E-43	Up			Unigene31020_All//1.00E-11//CO086373				
Unigene31022_All	591	1.95	1.20	0.90	2.53	4.66	1.68	3.51	2.33	0.40	-6.98E-01	2.66E-01		-1.11E+00	9.93E-02		8.82E-01	1.82E-02		-5.89E-01	3.04E-01		-5.87E-01	1.48E-01		-3.12E+00	1.46E-09	Down	Unigene31022_All//gi|89276301|gb|ABO66507.1|//2.00E-71//actin depolymerizing factor 5 [Gossypium hirsutum]	Unigene31022_All//3.00E-60//AT2G16700| ADF5 (ACTIN DEPOLYMERIZING FACTOR 5); actin binding	Unigene31022_All//0.00E+00//AI727184			GO:0008092//GO:0044464	nr +
Unigene31023_All	727	0.43	0.14	0.00	0.69	0.57	0.12	10.24	5.23	1.15	-1.63E+00	2.76E-01		-8.75E+00	4.91E-02		-2.70E-01	8.02E-01		-2.46E+00	4.83E-02		-9.68E-01	5.55E-07		-3.15E+00	6.69E-33	Down	Unigene31023_All//gi|15218784|ref|NP_174195.1|//1.00E-69//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|10764865|gb|AAF24557.2|AC007508_20 F18C23.4 [Arabidopsis thaliana]	Unigene31023_All//3.00E-51//AT1G29000| heavy-metal-associated domain-containing protein					nr -
Unigene31024_All	961	0.00	0.00	0.00	0.00	0.00	1.97	0.00	3.78	16.50	null	null		null	null		null	null		1.09E+01	2.55E-11	Up	1.19E+01	1.39E-25	Up	1.40E+01	6.82E-114	Up	Unigene31024_All//gi|6686397|gb|AAF23831.1|AC007234_3//3.00E-13//F1E22.12 [Arabidopsis thaliana]	Unigene31024_All//1.00E-07//AT5G42905| nucleic acid binding / ribonuclease H					nr +
Unigene31026_All	623	0.00	30.01	25.47	0.00	0.00	0.00	0.14	0.00	0.38	1.49E+01	1.57E-107	Up	1.46E+01	1.71E-89	Up	null	null		null	null		-7.08E+00	4.04E-01		1.50E+00	3.39E-01									
Unigene31028_All	872	0.12	0.29	1.47	0.40	0.24	0.62	2.67	3.88	2.97	1.28E+00	4.35E-01		3.61E+00	3.41E-05	Up	-7.55E-01	5.67E-01		6.36E-01	5.61E-01		5.42E-01	7.53E-02		1.55E-01	6.59E-01		Unigene31028_All//gi|301070456|gb|ADK55590.1|//7.00E-94//plastid NEP-interaction protein [Nicotiana benthamiana]	Unigene31028_All//8.00E-90//AT4G35840| zinc finger (C3HC4-type RING finger) family protein	Unigene31028_All//0.00E+00//TC140428			GO:0009743//GO:0046914	nr +
Unigene31029_All	753	0.00	0.00	0.00	0.00	0.00	0.00	4.60	30.36	6.35	null	null		null	null		null	null		null	null		2.72E+00	8.38E-83	Up	4.64E-01	5.48E-02		Unigene31029_All//gi|111379984|gb|AAQ63185.2|//6.00E-91//germin-like protein 3 [Vitis vinifera]	Unigene31029_All//4.00E-76//AT5G39110| germin-like protein, putative	Unigene31029_All//0.00E+00//gi|109873402|gb|DW502377.1|DW502377			GO:0004871//GO:0005576//GO:0008152//GO:0016623//GO:0046914	nr +
Unigene31030_All	544	74.54	372.66	161.22	582.94	743.27	701.69	94.35	160.58	134.53	2.32E+00	0.00E+00	Up	1.11E+00	3.61E-73	Up	3.51E-01	5.02E-54		2.68E-01	1.05E-27		7.67E-01	1.63E-49		5.12E-01	3.27E-21		Unigene31030_All//gi|115456333|ref|NP_001051767.1|//2.00E-06//Os03g0826800 [Oryza sativa Japonica Group] >gi|108711857|gb|ABF99652.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550238|dbj|BAF13681.1|Os03g0826800 [Oryza sativa Japonica Group]	Unigene31030_All//3.00E-06//AT1G19530| unknown protein	Unigene31030_All//0.00E+00//gi|109828662|gb|DW227283.1|DW227283				nr -
Unigene31031_All	259	1.82	0.20	1.23	3.27	1.06	1.05	2.12	9.52	4.15	-3.22E+00	2.73E-02		-5.60E-01	6.28E-01		-1.62E+00	3.13E-02		-1.64E+00	4.18E-02		2.17E+00	1.77E-07	Up	9.69E-01	9.17E-02								
Unigene31035_All	1182	0.04	0.13	0.32	0.51	0.29	0.19	2.43	4.00	1.04	1.54E+00	5.31E-01		2.83E+00	9.31E-02		-7.96E-01	3.88E-01		-1.40E+00	1.58E-01		7.16E-01	3.71E-03		-1.22E+00	1.94E-04	Down			Unigene31035_All//0.00E+00//TC135842				
Unigene31036_All	714	0.15	1.14	0.60	0.14	0.19	0.63	4.09	11.94	8.09	2.95E+00	3.29E-03		2.02E+00	1.39E-01		4.68E-01	8.77E-01		2.18E+00	1.03E-01		1.55E+00	1.56E-15	Up	9.86E-01	6.44E-06								
Unigene31037_All	551	0.00	0.74	0.19	0.18	1.19	1.89	1.84	0.83	0.29	9.52E+00	1.36E-02		7.59E+00	3.98E-01		2.72E+00	1.37E-02		3.38E+00	2.04E-04	Up	-1.14E+00	6.62E-02		-2.67E+00	1.94E-04	Down							
Unigene31039_All	439	0.00	0.00	0.00	0.00	0.16	0.00	62.51	30.94	19.69	null	null		null	null		7.29E+00	6.09E-01		null	null		-1.01E+00	2.17E-25	Down	-1.67E+00	2.16E-55	Down	Unigene31039_All//gi|224111864|ref|XP_002316007.1|//8.00E-43//cytochrome P450 [Populus trichocarpa] >gi|222865047|gb|EEF02178.1|cytochrome P450 [Populus trichocarpa]	Unigene31039_All//1.00E-29//AT2G46960| CYP706B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene31039_All//0.00E+00//TC142380		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0016491	nr -
Unigene31041_All	521	13.86	103.38	57.54	11.38	15.60	20.46	0.73	0.64	0.23	2.90E+00	2.64E-169	Up	2.05E+00	1.11E-61	Up	4.55E-01	2.36E-02		8.46E-01	8.79E-07		-1.87E-01	8.57E-01		-1.67E+00	1.40E-01		Unigene31041_All//gi|49615301|gb|AAT66912.1|//6.00E-59//dehydration-induced protein RD22-like protein 1 [Gossypium arboreum]	Unigene31041_All//3.00E-09//AT5G25610| RD22; nutrient reservoir	Unigene31041_All//0.00E+00//gi|164348367|gb|EV494757.1|EV494757				nr +
Unigene31044_All	241	42.33	171.77	69.16	187.48	341.50	495.49	91.58	216.44	436.74	2.02E+00	2.41E-85	Up	7.08E-01	4.88E-07		8.65E-01	1.97E-55		1.40E+00	1.66E-157	Up	1.24E+00	2.30E-65	Up	2.25E+00	0.00E+00	Up			Unigene31044_All//2.00E-119//TC178596				
Unigene31045_All	654	11322.34	15144.12	14906.82	4188.05	4066.21	4054.42	20.75	18.85	8.16	4.20E-01	0.00E+00		3.97E-01	0.00E+00		-4.26E-02	1.76E-06		-4.68E-02	4.62E-07		-1.39E-01	3.91E-01		-1.35E+00	1.62E-20	Down	Unigene31045_All//gi|11095210|gb|AAG29777.1|//2.00E-61//lipid transfer protein 3 precursor [Gossypium hirsutum] >gi|208427031|gb|ACI26697.1| lipid transfer protein [Gossypium hirsutum]	Unigene31045_All//8.00E-32//AT2G38540| LP1; calmodulin binding	Unigene31045_All//0.00E+00//gi|13244858|gb|BE052440.2|BE052440			GO:0005488//GO:0006810	nr -
Unigene31046_All	213	5.65	0.24	5.00	9.59	6.79	6.57	0.20	0.20	0.00	-4.57E+00	5.88E-06	Down	-1.76E-01	7.67E-01		-4.98E-01	2.80E-01		-5.45E-01	2.45E-01		-1.68E-02	1.00E+00		-7.63E+00	6.12E-01				Unigene31046_All//3.00E-74//CO086972				
Unigene31047_All	468	4.47	10.07	12.52	10.54	14.94	18.63	1.45	1.07	0.43	1.17E+00	4.12E-05	Up	1.48E+00	3.78E-08	Up	5.03E-01	2.09E-02		8.22E-01	2.00E-05		-4.32E-01	6.12E-01		-1.76E+00	2.80E-02				Unigene31047_All//5.00E-07//ES811799				
Unigene3105_All	1522	4.57	10.69	5.39	7.92	8.78	6.80	6.44	4.01	6.62	1.22E+00	8.44E-17	Up	2.37E-01	2.97E-01		1.48E-01	4.15E-01		-2.21E-01	2.23E-01		-6.85E-01	2.60E-05		3.92E-02	8.26E-01		Unigene3105_All//gi|28416689|gb|AAO42875.1|//1.00E-172//At3g50340 [Arabidopsis thaliana]	Unigene3105_All//5.00E-149//AT3G50340| unknown protein	Unigene3105_All//0.00E+00//TC140023				nr +
Unigene31050_All	996	0.00	36.78	14.06	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	2.18E-211	Up	1.38E+01	6.82E-79	Up	null	null		null	null		null	null		null	null		Unigene31050_All//gi|29839253|sp|Q9FYZ.1|FRI_MALXI//2.00E-15//RecName: Full=Ferritin, chloroplastic; AltName: Full=Apf1; Flags: Precursor >gi|150869913|gb|AAK83702.1|AF331550_5_1 ferritin [Malus xiaojinensis]	Unigene31050_All//1.00E-122//AT3G11050| ATFER2 (ferritin 2); binding / ferric iron binding / oxidoreductase/ transition metal ion binding					nr +
Unigene31051_All	377	0.69	2.02	0.71	1.06	1.46	0.72	32.30	19.62	2.11	1.54E+00	7.40E-02		2.53E-02	1.00E+00		4.67E-01	6.68E-01		-5.56E-01	6.38E-01		-7.19E-01	6.84E-07		-3.93E+00	1.78E-64	Down	Unigene31051_All//gi|297813757|ref|XP_002874762.1|//4.00E-35//At4g12320 [Arabidopsis lyrata subsp. lyrata] >gi|297320599|gb|EFH51021.1|At4g12320 [Arabidopsis lyrata subsp. lyrata]	Unigene31051_All//4.00E-56//AT4G12300| CYP706A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene31051_All//2.00E-157//TC141023		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506//GO:0016020	nr -
Unigene31052_All	424	0.25	0.48	0.00	0.00	1.54	0.43	0.90	1.77	2.35	9.54E-01	6.21E-01		-7.95E+00	3.93E-01		1.06E+01	4.92E-04	Up	8.74E+00	1.94E-01		9.83E-01	1.89E-01		1.39E+00	2.47E-02								
Unigene31053_All	522	0.90	0.49	0.00	5.73	5.61	1.99	0.57	0.08	0.46	-8.94E-01	3.89E-01		-9.82E+00	8.64E-03		-3.02E-02	9.37E-01		-1.52E+00	4.15E-05	Down	-2.82E+00	8.85E-02		-3.08E-01	7.75E-01				Unigene31053_All//2.00E-37//FL576717				
Unigene31056_All	887	0.00	0.23	0.06	4.66	0.39	0.81	40.14	202.33	490.24	7.84E+00	1.36E-01		5.91E+00	6.36E-01		-3.59E+00	1.02E-20	Down	-2.52E+00	1.27E-12	Down	2.33E+00	0.00E+00	Up	3.61E+00	0.00E+00	Up	Unigene31056_All//gi|40218371|gb|AAR83118.1|//1.00E-116//secretory laccase [Gossypium arboreum]	Unigene31056_All//4.00E-59//AT5G09360| LAC14 (laccase 14); laccase	Unigene31056_All//0.00E+00//FF403648		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0016491	nr +
Unigene31058_All	443	1.42	0.23	0.84	3.37	0.86	0.92	0.10	0.00	0.00	-2.63E+00	1.78E-02		-7.52E-01	4.11E-01		-1.98E+00	2.94E-04	Down	-1.88E+00	1.24E-03		-6.58E+00	6.57E-01		-6.58E+00	6.12E-01								
Unigene31060_All	326	1.12	0.00	1.31	1.53	3.91	0.83	2.72	0.90	0.24	-1.01E+01	1.97E-02		2.18E-01	8.31E-01		1.35E+00	2.76E-02		-8.78E-01	4.20E-01		-1.60E+00	2.18E-02		-3.48E+00	7.33E-05	Down			Unigene31060_All//2.00E-157//TC174360				
Unigene31063_All	354	0.00	0.00	0.00	0.99	0.00	0.26	5.97	4.37	2.25	null	null		null	null		-9.94E+00	9.45E-03		-1.95E+00	1.96E-01		-4.51E-01	2.73E-01		-1.41E+00	3.88E-04	Down	Unigene31063_All//gi|115444985|ref|NP_001046272.1|//1.00E-30//Os02g0211200 [Oryza sativa Japonica Group] >gi|113535803|dbj|BAF08186.1|Os02g0211200 [Oryza sativa Japonica Group]	Unigene31063_All//3.00E-30//AT3G47580| leucine-rich repeat transmembrane protein kinase, putative	Unigene31063_All//1.00E-170//TC143249		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006464//GO:0016628//GO:0031224//GO:0032559	nr -
Unigene31064_All	457	0.00	3.44	1.17	2.18	0.75	1.48	0.00	0.82	0.61	1.17E+01	5.70E-09	Up	1.02E+01	4.04E-03		-1.53E+00	2.33E-02		-5.57E-01	4.47E-01		9.68E+00	6.85E-03		9.25E+00	2.43E-02								
Unigene31065_All	568	0.00	0.36	0.00	0.00	0.12	0.00	91.63	19.87	30.30	8.48E+00	1.36E-01		null	null		6.92E+00	6.09E-01		null	null		-2.21E+00	2.24E-147	Down	-1.60E+00	3.94E-98	Down	Unigene31065_All//gi|115480809|ref|NP_001063998.1|//3.00E-06//Os09g0572500 [Oryza sativa Japonica Group] >gi|113632231|dbj|BAF25912.1|Os09g0572500 [Oryza sativa Japonica Group]				ko00270|Cysteine and methionine metabolism	GO:0003824//GO:0005488//GO:0016020//GO:0043231	nr -
Unigene31066_All	394	0.00	0.00	0.00	0.00	0.00	0.00	27.04	22.70	3.44	null	null		null	null		null	null		null	null		-2.52E-01	1.34E-01		-2.98E+00	3.02E-44	Down							

Unigene31067_All	1556	0.00	0.00	0.00	0.06	0.04	0.00	27.20	4.38	1.46	null	null		null	null		-5.31E-01	8.16E-01		-6.00E+00	4.00E-01		-2.64E+00	5.45E-148	Down	-4.22E+00	1.44E-234	Down	Unigene31067_All//gi|15240534|ref|NP_199780.1|//1.00E-111//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|8978266|dbj|BAB98157.1| anthocyanidin-3-glucoside rhamnosyltransferase-like [Arabidopsis thaliana] >gi|28931061|gb|AAO63454.1| At5g49690 [Arabidopsis thaliana]	Unigene31067_All//8.00E-113//AT5G49690| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene31067_All//0.00E+00//TC159852		ko00908|Zeatin biosynthesis		nr -
Unigene31070_All	507	0.93	0.80	0.00	3.73	1.49	0.98	2.42	0.00	0.94	-2.16E-01	8.17E-01		-9.86E+00	8.64E-03		-1.32E+00	3.34E-03		-1.93E+00	1.45E-04	Down	-1.12E+01	9.98E-09	Down	-1.36E+00	1.18E-02		Unigene31070_All//gi|71480741|gb|AAB85402.2|//2.00E-64//beta-1,3-glucanase [Camellia sinensis]	Unigene31070_All//1.00E-64//AT2G01630| glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative	Unigene31070_All//8.00E-142//TC145789		ko00500|Starch and sucrose metabolism	GO:0008422//GO:0031225//GO:0031410//GO:0043167//GO:0044238	nr +
Unigene31076_All	570	0.00	0.18	0.19	0.17	0.00	0.00	4.75	29.70	2.45	7.47E+00	3.87E-01		7.55E+00	3.98E-01		-7.45E+00	3.13E-01		-7.45E+00	4.00E-01		2.65E+00	1.32E-59	Up	-9.57E-01	3.85E-03		Unigene31076_All//gi|42570080|ref|NP_683294.2|//2.00E-30//phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis thaliana]	Unigene31076_All//1.00E-31//AT1G09935| phosphoglycerate/bisphosphoglycerate mutase family protein					nr -
Unigene31082_All	455	2.87	0.45	2.69	2.85	1.82	0.60	0.00	0.00	0.18	-2.69E+00	1.84E-04	Down	-9.49E-02	8.72E-01		-6.48E-01	2.72E-01		-2.26E+00	6.70E-04	Down	null	null		7.45E+00	4.04E-01		Unigene31082_All//gi|224057042|ref|XP_002299116.1|//9.00E-33//neutral amino acid transport protein [Populus trichocarpa] >gi|222846374|gb|EEE83921.1| neutral amino acid transport protein [Populus trichocarpa]	Unigene31082_All//3.00E-24//AT3G13620| amino acid permease family protein	Unigene31082_All//2.00E-52//gi|13246732|gb|BE054055.2|BE054055			GO:0015171//GO:0015837//GO:0031224	nr +
Unigene31084_All	1554	0.20	0.00	0.21	0.71	0.71	0.64	27.32	5.97	1.15	-7.66E+00	3.65E-02		2.55E-02	1.00E+00		8.00E-03	9.92E-01		-1.41E-01	8.26E-01		-2.19E+00	1.67E-119	Down	-4.57E+00	1.02E-247	Down	Unigene31084_All//gi|18390599|ref|NP_563756.1|//1.00E-114//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|8816462|gb|AAF80123.1|AC024174_5 Contains similarity to UDPG glucosyltransferase from Solanum berthaultii gi|2232354 and contains UDP-glycoronosyl and UDP-glucosyl transferases PF|00201 domain. ESTs gb|AV551176, gb|Z46581, gb|AV439781, gb|AV542338, gb|AV525326, gb|AV538963, gb|Z46580, gb|AV547292, gb|AV532314, gb|AV565317, gb|AV542340 come from this gene [Arabidopsis thaliana] >gi|30387515|gb|AAP31923.1| At1g06000 [Arabidopsis thaliana]	Unigene31084_All//4.00E-115//AT1G06000| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene31084_All//3.00E-08//gi|78349510|gb|DT569784.1|DT569784		ko00908|Zeatin biosynthesis	GO:0016740	nr +
Unigene31085_All	543	0.00	0.00	0.00	0.83	0.25	0.17	229.54	148.86	35.66	null	null		null	null		-1.70E+00	1.35E-01		-2.31E+00	7.81E-02		-6.25E-01	2.74E-49		-2.69E+00	0.00E+00	Down								
Unigene31087_All	447	13.34	11.68	14.41	25.63	21.88	20.71	22.42	11.87	8.82	-1.93E-01	4.53E-01		1.11E-01	6.50E-01		-2.28E-01	2.04E-01		-3.07E-01	8.08E-02		-9.17E-01	2.12E-08		-1.35E+00	2.32E-15	Down			Unigene31087_All//6.00E-96//TC169673				
Unigene31088_All	635	0.08	0.80	0.00	0.39	0.81	0.00	0.00	4.08	2.32	3.28E+00	2.11E-02		-6.36E+00	6.24E-01		1.05E+00	3.49E-01		-8.62E+00	7.33E-02		1.20E+01	3.15E-18	Up	1.12E+01	1.30E-10	Up			Unigene31088_All//5.00E-45//BF268767				
Unigene31094_All	555	0.09	0.09	0.00	1.08	0.93	0.16	6.17	3.77	56.56	-4.66E-02	9.85E-01		-6.56E+00	6.24E-01		-2.11E-01	8.23E-01		-2.73E+00	1.74E-02		-7.13E-01	1.67E-02		3.20E+00	5.59E-136	Up	Unigene31094_All//gi|224087611|ref|XP_002308196.1|//2.00E-80//laccase 110a [Populus trichocarpa] >gi|222854172|gb|EEE91719.1| laccase 110a [Populus trichocarpa]	Unigene31094_All//3.00E-74//AT3G09220| LAC7 (laccase 7); laccase			ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0031410//GO:0046914	nr +
Unigene31096_All	524	2.80	0.00	0.41	0.86	2.04	2.24	0.73	0.88	0.30	-1.14E+01	1.65E-08	Down	-2.78E+00	9.28E-05	Down	1.25E+00	6.99E-02		1.39E+00	3.52E-02		2.73E-01	7.69E-01		-1.26E+00	2.48E-01		Unigene31096_All//gi|15227199|ref|NP_179827.1|//4.00E-17//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75206347|sp|Q9SJZ3.1|PP169_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g22410, mitochondrial; Flags: Precursor >gi|18086349|gb|AAL57637.1| At2g22410/F14M13.19 [Arabidopsis thaliana]	Unigene31096_All//4.00E-16//AT2G22410| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene31098_All	807	0.19	9.67	1.06	0.37	1.28	2.41	0.68	0.57	0.69	5.64E+00	9.00E-40	Up	2.44E+00	9.09E-03		1.79E+00	1.39E-02		2.70E+00	1.84E-06	Up	-2.58E-01	7.60E-01		2.10E-02	9.79E-01		Unigene31098_All//gi|255580545|ref|XP_002531097.1|//2.00E-15//hypothetical protein RCOM_1417730 [Ricinus communis] >gi|223529943|gb|EEF31311.1| hypothetical protein RCOM_1417730 [Ricinus communis]		Unigene31098_All//0.00E+00//gi|78326627|gb|DT546901.1|DT546901				nr +
Unigene31099_All	331	20.23	49.14	21.40	18.36	20.18	27.70	9.84	14.65	9.63	1.28E+00	6.06E-18	Up	8.07E-02	7.30E-01		1.37E-01	6.00E-01		5.93E-01	1.60E-03		5.75E-01	1.90E-02		-3.07E-02	9.40E-01				Unigene31099_All//3.00E-162//gi|164272864|gb|EV487092.1|EV487092				
Unigene3110_All	1020	2.26	18.73	5.43	6.20	13.84	31.26	25.91	67.24	110.49	3.05E+00	1.65E-63	Up	1.27E+00	3.16E-06	Up	1.16E+00	1.67E-15	Up	2.33E+00	1.98E-84	Up	1.38E+00	1.87E-100	Up	2.09E+00	6.11E-303	Up	Unigene3110_All//gi|6688529|emb|CAB65169.1|//1.00E-54//I-box binding factor [Solanum lycopersicum]	Unigene3110_All//2.00E-49//AT5G04760| myb family transcription factor	Unigene3110_All//0.00E+00//TC147041	MYB		GO:0001071//GO:0010468	nr +
Unigene31100_All	329	1.91	0.00	0.49	1.51	1.26	0.00	0.26	0.00	0.12	-1.09E+01	7.91E-04	Down	-1.97E+00	6.50E-02		-2.70E-01	8.02E-01		-1.06E+01	2.97E-03		-8.01E+00	4.03E-01		-1.09E+00	6.76E-01		Unigene31100_All//gi|297829220|ref|XP_002882542.1|//2.00E-10//SET domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328382|gb|EFH58801.1| SET domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene31100_All//1.00E-11//AT3G07670| SET domain-containing protein	Unigene31100_All//6.00E-49//DR463152			GO:0008757//GO:0009536	nr +
Unigene31101_All	683	1.00	0.74	1.33	0.51	0.61	0.53	4.83	2.39	6.30	-4.25E-01	5.97E-01		4.12E-01	5.94E-01		2.45E-01	8.53E-01		5.14E-02	9.69E-01		-1.02E+00	9.01E-04	Down	3.84E-01	1.40E-01				Unigene31101_All//7.00E-35//TC169453				
Unigene31102_All	291	16.72	5.92	9.88	41.94	32.78	31.66	56.08	17.09	21.22	-1.50E+00	2.56E-07	Down	-7.59E-01	7.54E-03		-3.56E-01	2.52E-02		-4.06E-01	1.29E-02		-1.71E+00	1.41E-33	Down	-1.40E+00	5.22E-26	Down	Unigene31102_All//gi|261280336|gb|ACM67308.2|//3.00E-19//triosphosphate isomerase-like protein type I [Dimocarpus longan]	Unigene31102_All//6.00E-11//AT3G55440| TPI (TR10SEPHOSPHATE ISOMERASE); triose-phosphate isomerase	Unigene31102_All//7.00E-107//gi|5049163|gb|AIT30311.1|AI730311		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00562|Inositol phosphate metabolism//ko00051|Fructose and mannose metabolism	GO:0005576//GO:0006007//GO:0006631//GO:0006970//GO:0009532//GO:0010038//GO:0016020//GO:0016747//GO:0016861//GO:0030312//GO:0046914	nr -
Unigene31104_All	1310	0.00	7.50	2.89	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.60E-56	Up	1.15E+01	6.02E-21	Up	null	null		null	null		null	null		null	null		Unigene31104_All//gi|56121721|gb|AAV74197.1|//2.00E-62//glutamate dehydrogenase 1 [Lupinus luteus]	Unigene31104_All//5.00E-63//AT5G18170| GDH1 (GLUTAMATE DEHYDROGENASE 1); ATP binding / glutamate dehydrogenase [NAD(P)+]/ oxidoreductase	Unigene31104_All//1.00E-13//DW493862		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006970//GO:0009642//GO:0010038//GO:0016639//GO:0019222//GO:0032559//GO:0043231//GO:0046914	nr -
Unigene31106_All	626	0.00	0.00	0.00	0.00	0.00	0.00	13.44	7.88	3.37	null	null		null	null		null	null		null	null		-7.71E-01	1.50E-05		-1.99E+00	2.93E-22	Down	Unigene31106_All//gi|29772735|ref|NP_001172729.1|//7.00E-33//Os01g0935200 [Oryza sativa Japonica Group] >gi|148921414|dbj|BAF64446.1| HAP3 subunit of HAP complex [Oryza sativa Japonica Group] >gi|255674039|dbj|BAH91459.1| Os01g0935200 [Oryza sativa Japonica Group]	Unigene31106_All//4.00E-33//AT2G47810| NF-YB5 (NUCLEAR FACTOR Y, SUBUNIT B5); transcription factor		CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication	GO:0001071//GO:0003677//GO:0006351//GO:0043231	nr +
Unigene31107_All	459	114.10	108.40	164.51	238.87	149.67	150.45	157.15	108.36	69.61	-7.39E-02	3.80E-01		5.28E-01	9.79E-18		-6.74E-01	1.42E-49		-6.67E-01	5.31E-43		-5.36E-01	3.89E-22		-1.17E+00	3.57E-85	Down	Unigene31107_All//gi|257219554|gb|ACV50430.1|//1.00E-19//copper chaperone [Jatropha curcas]	Unigene31107_All//1.00E-14//AT1G66240| ATX1 (ARABIDOPSIS HOMOLOG OF ANTI-OXIDANT 1); metal ion binding	Unigene31107_All//0.00E+00//gi|82755318|gb|DV848880.1|DV848880			GO:0005507//GO:0006970//GO:0009536//GO:0010038//GO:0030005//GO:0032302//GO:0034755	nr -
Unigene31108_All	298	0.35	7.99	3.57	0.17	0.23	0.00	0.43	0.14	1.20	4.51E+00	4.03E-11	Up	3.35E+00	3.36E-04	Up	4.67E-01	9.58E-01		-7.39E+00	6.35E-01		-1.60E+00	5.34E-01		1.50E+00	2.04E-01				Unigene31108_All//2.00E-58//BE055490				
Unigene31109_All	359	15.01	22.72	41.09	3.75	8.92	2.77	0.35	0.23	0.89	5.98E-01	3.24E-03		1.45E+00	5.53E-19	Up	1.25E+00	2.50E-04	Up	-4.37E-01	4.70E-01		-6.02E-01	7.66E-01		1.33E+00	2.93E-01		Unigene31109_All//gi|6635344|gb|AAF19790.1|AF162206_1|//4.00E-08//cytosolic fructose-1,6-bisphosphate [Lactuca sativa]	Unigene31109_All//3.00E-08//AT1G43670| fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	Unigene31109_All//6.00E-77//CO083855		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene31113_All	379	0.41	0.53	3.79	1.05	0.73	1.91	0.00	0.00	0.53	3.69E-01	8.16E-01		3.20E+00	2.79E-05	Up	-5.33E-01	6.16E-01		8.59E-01	3.42E-01		null	null		9.04E+00	7.89E-02		Unigene31113_All//gi|145324006|ref|NP_001077592.1|//9.00E-23//protein kinase family protein [Arabidopsis thaliana]	Unigene31113_All//4.00E-24//AT1G24030| protein kinase family protein	Unigene31113_All//1.00E-16//TC149479			GO:0004702//GO:0006464//GO:0032559	nr +
Unigene31116_All	319	23.62	25.73	24.04	37.01	45.77	33.70	87.61	44.29	34.47	1.24E-01	5.96E-01		2.54E-02	9.22E-01		3.07E-01	3.92E-02		-1.35E-01	4.88E-01		-9.84E-01	1.26E-24		-1.35E+00	2.69E-41	Down			Unigene31116_All//8.00E-144//TC145040				
Unigene31117_All	290	4.15	0.52	1.29	6.53	3.92	4.36	3.06	2.45	0.96	-2.98E+00	1.58E-04	Down	-1.69E+00	1.44E-02		-7.36E-01	1.06E-01		-5.82E-01	2.31E-01		-3.22E-01	6.33E-01		-1.67E+00	1.33E-02		Unigene31117_All//gi|297834808|ref|XP_002885286.1|//3.00E-30//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331126|gb|EFH61545.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene31117_All//5.00E-30//AT3G18970| pentatricopeptide (PPR) repeat-containing protein	Unigene31117_All//1.00E-123//DW507394			GO:0043231	nr -
Unigene31119_All	634	0.17	4.32	2.10	0.55	0.65	0.28	0.07	0.46	0.63	4.71E+00	5.11E-13	Up	3.67E+00	1.90E-05	Up	2.45E-01	8.53E-01		-9.49E-01	4.81E-01		2.79E+00	9.47E-02		3.24E+00	2.14E-02								
Unigene31120_All	242	0.43	6.28	1.32	0.00	1.00	0.00	0.00	4.15	4.28	3.86E+00	1.23E-06	Up	1.61E+00	3.05E-01		9.96E+00	1.04E-01		null	null		1.20E+01	3.93E-07	Up	1.21E+01	1.58E-07	Up							
Unigene31121_All	320	0.65	0.63	0.33	0.31	0.65	0.71	3.70	2.87	0.75	-4.62E-02	9.88E-01		-9.75E-01	6.21E-01		1.05E+00	6.12E-01		1.18E+00	5.49E-01		-3.65E-01	5.42E-01		-2.31E+00	2.04E-04	Down							
Unigene31122_All	417	3.51	3.04	3.06	4.78	2.06	0.32	0.00	0.00	0.00	-2.10E-01	6.84E-01		-1.97E-01	7.14E-01		-1.21E+00	5.33E-03		-3.88E+00	2.91E-09	Down	null	null		null	null		Unigene31122_All//gi|224053945|ref|XP_002298051.1|//1.00E-12//predicted protein [Populus trichocarpa] >gi|222845309|gb|EEE82856.1| predicted protein [Populus trichocarpa]		Unigene31122_All//2.00E-135//ES790396				nr -
Unigene31124_All	325	4.19	0.31	3.60	1.53	1.80	2.64	0.26	0.39	0.25	-3.75E+00	5.95E-06	Down	-2.16E-01	7.04E-01		2.33E-01	8.26E-01		7.85E-01	3.33E-01		5.68E-01	7.82E-01		-8.57E-02	9.72E-01								
Unigene31125_All	344	102.06	81.90	63.16	199.69	194.10	184.20	234.02	160.62	116.85	-3.18E-01	4.99E-04		-6.92E-01	1.55E-13		-4.10E-02	5.98E-01		-1.17E-01	9.80E-02		-5.43E-01	3.82E-25		-1.00E+00	1.73E-73	Down			Unigene31125_All//0.00E+00//gi|11201640|gb|BF270549.1|BF270549				
Unigene3113_All	890	71.19	151.61	115.53	42.20	60.44	53.89	17.34	12.49	8.42	1.09E+00	1.27E-111	Up	6.99E-01	3.44E-39		5.18E-01	5.33E-15		3.53E-01	2.24E-06		-4.73E-01	1.87E-04		-1.04E+00	9.13E-16	Down	Unigene3113_All//gi|154721452|gb|ABS84825.1|//1.00E-54//thioredoxin [Limonium bicolor]	Unigene3113_All//2.00E-45//AT3G15360| TRX-M4 (ARABIDOPSIS THIOREDOXIN M-TYPE 4); enzyme activator	Unigene3113_All//0.00E+00//TC138886			GO:0005975//GO:0009526//GO:0009534//GO:0015036//GO:0018904//GO:0019725//GO:0030234//GO:0030312//GO:0044092//GO:0044093	nr +
Unigene31130_All	503	0.00	0.10	1.48	1.19	1.51	1.80	0.25	0.17	0.55	6.65E+00	6.16E-01		1.05E+01	3.27E-04	Up	3.42E-01	7.20E-01		5.96E-01	4.55E-01		-6.02E-01	7.66E-01		1.14E+00	3.99E-01		Unigene31130_All//gi|15222150|ref|NP_172763.1|//2.00E-48//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75200670|sp|Q9SAD9.1|PPR40_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g13040, mitochondrial; Flags: Precursor >gi|6850387|gb|AAD31057.1|AC007357_6 F3F19.6 [Arabidopsis thaliana]	Unigene31130_All//9.00E-50//AT1G13040| pentatricopeptide (PPR) repeat-containing protein	Unigene31130_All//2.00E-37//CO112612			GO:0044464	nr -

Unigene31131_All	400	0.00	0.00	0.00	0.25	0.43	0.23	0.42	2.19	5.88	null	null		null	null		7.89E-01	7.71E-01		-1.42E-01	9.50E-01		2.38E+00	2.18E-03		3.80E+00	2.43E-12	Up	Unigene31131_All//gi|22266675|dbj|BAC07544.1|//4.00E-07//myb-related transcription factor VIMIBBI-2 [Vitis labrusca x Vitis vinifera]						nr +
Unigene31132_All	520	1.61	3.22	5.22	4.41	8.61	9.99	5.61	3.46	4.21	9.98E-01	5.09E-02		1.70E+00	7.10E-05	Up	9.66E-01	4.56E-04		1.18E+00	8.39E-06	Up	-6.99E-01	3.31E-02		-4.13E-01	2.00E-01		Unigene31132_All//gi|18422747|ref|NP_568675.1|//2.00E-09//LON2 (LON PROTEASE 2); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase [Arabidopsis thaliana] >gi|3914002|sp|O64948.1|LONP2_ARATH RecName: Full=Lon protease homolog 2, peroxisomal >gi|2935279|gb|AAC05085.1| Lon protease [Arabidopsis thaliana] >gi|9759446|dbj|BAB10243.1| mitochondrial Lon protease homolog 1 precursor [Arabidopsis thaliana]	Unigene31132_All//8.00E-11//AT5G47040| LON2 (LON PROTEASE 2); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase					nr +
Unigene31134_All	1013	0.15	0.05	0.00	0.84	0.51	1.87	5.68	0.91	1.81	-1.63E+00	4.89E-01		-7.28E+00	2.45E-01		-7.13E-01	3.36E-01		1.16E+00	1.59E-02		-2.64E+00	9.66E-21	Down	-1.65E+00	4.04E-12	Down	Unigene31134_All//gi|115436456|ref|NP_001042986.1|//2.00E-68//Os01g0351800 [Oryza sativa Japonica Group] >gi|113532517|dbj|BAF04900.1| Os01g0351800 [Oryza sativa Japonica Group]	Unigene31134_All//8.00E-49//AT2G38240| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene31134_All//0.00E+00//gi|109872645|gb|DW501620.1|DW501620		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis	GO:0008152//GO:0016706	nr -
Unigene31142_All	328	12.92	64.88	56.66	2.28	3.88	16.39	0.00	1.53	0.49	2.33E+00	1.24E-52	Up	2.13E+00	3.07E-40	Up	7.70E-01	2.20E-01		2.85E+00	4.95E-18	Up	1.06E+01	1.02E-03		8.92E+00	1.40E-01		Unigene31142_All//gi|1209703|gb|AAB87721.1|//4.00E-35//maize g11 homolog [Arabidopsis thaliana]	Unigene31142_All//1.00E-36//AT1G02205| CER1 (ECERIFERUM 1); octadecanal decarbonylase	Unigene31142_All//8.00E-101//gi|48801471|gb|C0102785.1|C0102785			GO:0003676//GO:0006260//GO:0006631//GO:0031224//GO:0034061//GO:0043231//GO:0046914	nr +
Unigene31145_All	495	0.00	0.00	0.11	0.00	0.42	0.00	2.73	12.67	4.27	null	null		6.75E+00	6.36E-01		8.71E+00	1.57E-01		null	null		2.21E+00	2.22E-18	Up	6.42E-01	9.48E-02				Unigene31145_All//1.00E-32//EX167366					
Unigene31146_All	326	22.31	25.65	20.42	17.73	23.03	48.21	1035.73	772.45	2150.80	2.01E-01	3.65E-01		-1.28E-01	6.25E-01		3.78E-01	8.33E-02		1.44E+00	4.95E-22	Up	-4.23E-01	2.10E-65		1.05E+00	0.00E+00	Up	Unigene31146_All//gi|61354279|gb|AX44033.1|//4.00E-58//(+)-delta-cadinene synthase [Gossypium hirsutum]	Unigene31146_All//2.00E-23//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene31146_All//3.00E-165//gi|164271302|gb|ES831177.1|ES831177		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0010334//GO:0046872	nr -
Unigene3115_All	857	78.45	66.46	75.31	67.43	58.87	43.79	118.90	261.11	133.37	-2.39E-01	2.09E-04		-5.90E-02	4.43E-01		-1.96E-01	3.94E-03		-6.23E-01	2.41E-20		1.14E+00	1.62E-241	Up	1.66E-01	1.17E-04		Unigene3115_All//gi|15242741|ref|NP_195958.1|//3.00E-61//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|7376619|emb|CAB83295.1| farnesylated protein-like [Arabidopsis thaliana] >gi|16604513|gb|AAL32262.1| At5g03380/C160EPL23M [Arabidopsis thaliana] >gi|21591780|gb|AAM64219.1| cadmium induced protein CdI19 [Arabidopsis thaliana] >gi|21655291|gb|AAM65357.1| At5g03380/C160EPL23M [Arabidopsis thaliana]	Unigene3115_All//1.00E-40//AT2G36950| heavy-metal-associated domain-containing protein	Unigene3115_All//0.00E+00//gi|109888532|gb|DW517501.1|DW517501			GO:0046872	nr +
Unigene31151_All	267	3.72	3.61	4.79	3.92	2.06	2.71	9.66	3.76	1.94	-4.63E-02	9.58E-01		3.62E-01	5.67E-01		-9.25E-01	1.55E-01		-5.34E-01	4.56E-01		-1.36E+00	1.76E-04	Down	-2.32E+00	9.74E-09	Down			Unigene31151_All//1.00E-129//TC170071					
Unigene31152_All	605	0.26	0.08	1.32	1.24	1.76	1.12	1.05	0.83	0.00	-1.63E+00	4.89E-01		2.35E+00	1.46E-02		5.15E-01	4.86E-01		-1.41E-01	8.60E-01		-3.39E-01	6.63E-01		-1.00E+01	7.11E-05	Down	Unigene31152_All//gi|1039355|emb|CAA63093.1|//4.00E-57//alcohol dehydrogenase [Solanum tuberosum]	Unigene31152_All//1.00E-32//AT1G32780| alcohol dehydrogenase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism	GO:0008152//GO:0016616//GO:0046872	nr -
Unigene31153_All	220	0.95	6.22	1.45	2.72	4.07	4.11	1.92	3.80	1.63	2.71E+00	1.29E-04	Up	6.10E-01	6.24E-01		5.83E-01	4.72E-01		5.96E-01	4.55E-01		9.83E-01	1.58E-01		-2.38E-01	7.88E-01									
Unigene31156_All	692	0.00	0.00	0.00	0.00	0.05	0.00	11.91	2.84	4.20	null	null		null	null		5.64E+00	8.30E-01		null	null		-2.07E+00	3.97E-22	Down	-1.50E+00	5.76E-15	Down	Unigene31156_All//gi|115451023|ref|NP_001049112.1|//6.00E-31//Os03g0171300 [Oryza sativa Japonica Group] >gi|113547583|dbj|BAF11026.1| Os03g0171300 [Oryza sativa Japonica Group]	Unigene31156_All//1.00E-26//AT1G26945| KDR (KIDARI); transcription regulator	Unigene31156_All//2.00E-13//TC158578	bHLH		GO:0009314//GO:0009536//GO:0010468	nr -
Unigene31157_All	219	1.91	3.24	1.46	0.00	0.63	2.89	0.39	1.34	0.36	7.61E-01	3.62E-01		-3.90E-01	7.17E-01		9.30E+00	3.18E-01		1.15E+01	7.60E-04	Up	1.79E+00	2.24E-01		-8.58E-02	9.72E-01									
Unigene31158_All	455	2.18	0.00	0.00	4.82	2.27	1.69	0.19	0.00	0.00	-1.11E+01	7.45E-06	Down	-1.11E+01	1.77E-05	Down	-1.09E+00	8.04E-03		-1.51E+00	6.85E-04	Down	-7.54E+00	4.03E-01		-7.54E+00	3.58E-01		Unigene31158_All//gi|19911201|dbj|BAB88927.1|//6.00E-40//glucosyltransferase-9 [Vigna angularis]	Unigene31158_All//2.00E-37//AT3G53150| UGT73D1 (UDP-glucosyl transferase 73D1); UDP-glycosyltransferase/ transferase, transferring hexosyl groups			ko00908|Zeatin biosynthesis	GO:0016757	nr +
Unigene31160_All	724	0.00	0.00	0.00	0.00	0.00	0.06	4.32	2.77	1.10	null	null		null	null		null	null		5.96E+00	6.96E-01		-6.41E-01	4.19E-02		-1.97E+00	1.11E-08	Down	Unigene31160_All//gi|16924043|gb|AL31655.1|AC079179_10//4.00E-10//Unknown protein [Oryza sativa] >gi|20042881|gb|AAM08709.1|AC11660 1_2 Unknown protein [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr +
Unigene31162_All	1400	0.04	0.18	0.30	0.43	0.05	0.90	0.63	3.08	2.28	2.27E+00	2.34E-01		3.02E+00	5.73E-02		-3.12E+00	4.87E-03		1.08E+00	8.18E-02		2.28E+00	2.79E-13	Up	1.84E+00	4.95E-08	Up	Unigene31162_All//gi|4530126|gb|AAD21872.1|//1.00E-152//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene31162_All//3.00E-118//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene31162_All//4.00E-152//gi|78336821|gb|DT557095.1|DT557095		ko04626|Plant-pathogen interaction		nr -
Unigene31164_All	759	0.00	0.00	0.21	5.64	1.77	3.87	2.06	0.33	0.00	null	null		7.72E+00	2.39E-01		-1.67E+00	6.00E-09	Down	-5.45E-01	6.84E-02		-2.64E+00	4.08E-06	Down	-1.10E+01	1.42E-11	Down	Unigene31164_All//gi|9802596|gb|AAF99798.1|AC012463_15//2.00E-84//T22E6_19 [Arabidopsis thaliana]	Unigene31164_All//2.00E-88//AT1G47740| unknown protein	Unigene31164_All//5.00E-147//TC156499			GO:0043231	nr -
Unigene31167_All	842	0.00	9.51	6.83	0.00	0.00	0.05	0.10	0.00	0.00	1.32E+01	8.57E-46	Up	1.27E+01	4.80E-32	Up	null	null		5.74E+00	6.96E-01		-6.65E+00	4.03E-01		-6.65E+00	3.58E-01		Unigene31167_All//gi|301098633|ref|XP_002898409.1|//5.00E-10//lamin-like protein [Phytophthora infestans T30-4] >gi|262105180|gb|EEY63232.1| lamin-like protein [Phytophthora infestans T30-4]	Unigene31167_All//4.00E-05//AT5G41790| CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding					nr +
Unigene31168_All	603	1.39	0.08	0.44	0.74	0.29	0.37	0.28	0.62	0.33	-4.05E+00	4.65E-04	Down	-1.65E+00	5.45E-02		-1.38E+00	2.16E-01		-9.89E-01	3.94E-01		1.15E+00	3.27E-01		2.36E-01	8.83E-01		Unigene31168_All//gi|8778812|gb|AAF79817.1|AC007396_17//2.00E-18//T4O12.27 [Arabidopsis thaliana]	Unigene31168_All//4.00E-19//AT1G76065| CONTAINS InterPro DOMAIN/s: Complex 1 LYR protein (InterPro:IPR008011); Has 53 Blast hits to 53 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 32; Fungi - 9; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene31168_All//2.00E-146//TC161712			GO:0043231	nr +
Unigene3117_All	2451	0.51	1.36	0.78	7.95	4.72	5.16	4.78	4.95	2.28	1.41E+00	6.99E-05	Up	6.10E-01	2.20E-01		-7.51E-01	5.56E-11		-6.23E-01	2.74E-07		4.95E-02	7.69E-01		-1.07E+00	1.15E-12	Down	Unigene3117_All//gi|223452393|gb|ACM89524.1|//1.00E-133//PERONIA receptor-like kinase [Glycine max]	Unigene3117_All//6.00E-118//AT5G28680| protein kinase family protein	Unigene3117_All//0.00E+00//TC167288				nr +
Unigene31170_All	490	0.11	0.00	0.00	0.00	0.00	0.28	75.16	12.45	10.00	-6.74E+00	6.12E-01		-6.74E+00	6.24E-01		null	null		8.11E+00	3.11E-01		-2.59E+00	1.50E-126	Down	-2.91E+00	7.72E-148	Down	Unigene31170_All//gi|211906536|gb|ACJ11761.1|//8.00E-20//class III peroxidase [Gossypium hirsutum]	Unigene31170_All//1.00E-14//AT1G05260| RC13 (RARE COLD INDUCIBLE GENE 3); peroxidase	Unigene31170_All//4.00E-08//TC166713		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006972//GO:0008152//GO:0009414//GO:0016209//GO:0031410//GO:0043231	nr +
Unigene31171_All	389	2.42	5.08	6.30	2.31	3.98	6.27	5.00	3.98	10.04	1.07E+00	2.17E-02		1.38E+00	1.64E-03		7.89E-01	1.51E-01		1.44E+00	6.17E-04	Up	-3.31E-01	4.51E-01		1.01E+00	2.16E-04	Up			Unigene31171_All//0.00E+00//gi|78325128|gb|DT545402.1|DT545402					
Unigene31173_All	583	0.00	0.00	0.18	1.28	0.35	0.00	7.47	3.94	2.26	null	null		7.51E+00	3.98E-01		-1.85E+00	2.53E-02		-1.03E+01	9.80E-05	Down	-9.22E-01	3.88E-04		-1.73E+00	5.83E-10	Down	Unigene31173_All//gi|15238604|ref|NP_200815.1|//9.00E-10//ankyrin repeat family protein [Arabidopsis thaliana] >gi|8777346|dbj|BAA96936.1| ankyrin-like protein [Arabidopsis thaliana] >gi|67633894|gb|AAY78871.1| ankyrin repeat family protein [Arabidopsis thaliana]	Unigene31173_All//5.00E-11//AT5G60070| ankyrin repeat family protein	Unigene31173_All//5.00E-88//AI729861				nr +
Unigene31174_All	447	0.23	0.11	2.62	0.67	0.77	1.21	0.57	0.28	2.67	-1.05E+00	6.84E-01		3.48E+00	1.09E-04	Up	2.05E-01	9.01E-01		8.59E-01	4.23E-01		-1.02E+00	4.95E-01		2.24E+00	3.02E-04	Up			Unigene31174_All//8.00E-46//DW227700					
Unigene31176_All	273	0.96	1.30	2.15	2.92	2.02	1.16	4.49	1.22	0.58	4.39E-01	7.01E-01		1.16E+00	2.47E-01		-5.33E-01	5.10E-01		-1.33E+00	1.06E-01		-1.87E+00	1.57E-03		-2.94E+00	1.14E-05	Down								
Unigene31177_All	416	0.75	0.97	0.51	2.87	1.49	3.15	3.96	0.40	1.92	3.69E-01	7.24E-01		-5.60E-01	6.63E-01		-9.48E-01	1.12E-01		1.32E-01	8.34E-01		-3.30E+00	8.30E-08	Down	-1.05E+00	1.76E-02		Unigene31177_All//gi|13877126|gb|AAK43709.1|AF358865_1//1.00E-07//ribosomal protein L32 [Mercurialis annua] >gi|13899053|gb|AAK48948.1|AF370436_1 ribosomal protein L32 [Mercurialis annua] >gi|13899055|gb|AAK48949.1|AF370437_1 ribosomal protein L32 [Mercurialis annua] >gi|13899057|gb|AAK48950.1|AF370438_1 ribosomal protein L32 [Mercurialis annua]		Unigene31177_All//7.00E-114//TC144900		ko03010|Ribosome		nr -
Unigene31179_All	437	0.00	0.00	0.24	0.68	0.00	0.21	16.06	6.98	9.30	null	null		7.93E+00	3.98E-01		-9.42E+00	2.01E-02		-1.73E+00	2.89E-01		-1.20E+00	4.49E-09	Down	-7.88E-01	4.08E-05		Unigene31179_All//gi|53127612|emb|CAD49079.1|//7.00E-16//fructan 1-exohydrolase [Campanula rapunculoides]	Unigene31179_All//2.00E-14//AT3G13790| ATBFRUCT1; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene31179_All//3.00E-11//gi|84155251|gb|DN804606.1|DN804606		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism	GO:0004553//GO:0006950//GO:0030312//GO:0043231//GO:0044238	nr +
Unigene3118_All	1418	1.44	2.82	0.53	4.29	3.84	4.11	3.76	3.54	9.07	9.72E-01	1.59E-03		-1.45E+00	3.17E-03		-1.60E-01	5.62E-01		-6.09E-02	8.21E-01		-8.70E-02	7.29E-01		1.27E+00	8.79E-18	Up	Unigene3118_All//gi|18398633|ref|NP_566356.1|//2.00E-75//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene3118_All//3.00E-63//AT5G09770| zinc finger (C3HC4-type RING finger) family protein	Unigene3118_All//0.00E+00//TC155126			GO:0016020//GO:0046872	nr +
Unigene31181_All	1053	0.00	0.00	0.00	0.00	0.00	0.00	2.77	4.76	0.04	null	null		null	null		null	null		null	null		7.82E-01	1.05E-03		-6.20E+00	6.52E-20	Down	Unigene31181_All//gi|115463079|ref|NP_001055139.1|//1.00E-138//Os05g0302700 [Oryza sativa Japonica Group] >gi|113578690|dbj|BAF17053.1| Os05g0302700 [Oryza sativa Japonica Group]	Unigene31181_All//4.00E-126//AT4G28390| AAC3 (ADP/ATP CARRIER 3); ATP:ADP antiporter/ binding	Unigene31181_All//2.00E-17//EV483520				nr +
Unigene31188_All	1149	0.00	146.06	57.00	0.00	0.06	0.00	0.00	0.00	0.00	1.72E+01	0.00E+00	Up	1.58E+01	0.00E+00	Up	5.90E+00	6.09E-01		null	null		null	null		null	null		Unigene31188_All//gi|226458915|gb|EEH56211.1|//2.00E-06//predicted protein [Micromonas pusilla CCMP1545]						nr +
Unigene31189_All	688	0.68	0.29	0.31	3.40	2.20	0.13	0.18	0.00	0.12	-1.22E+00	2.72E-01		-1.14E+00	3.32E-01		-6.28E-01	1.23E-01		-4.70E+00	3.40E-12	Down	-7.53E+00	2.35E-01		-6.71E-01	7.20E-01		Unigene31189_All//gi|30684865|ref|NP_180679.2|//7.00E-34//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75299570|sp|Q8GX46.1|BH091_ARATH RecName: Full=Transcription factor bHLH91; AltName: Full=Transcription factor EN 25; AltName: Full=bHLH transcription factor bHLH091; AltName: Full=Basic helix-loop-helix protein 91; Short=bHLH 91; Short=AtbHLH91 >gi|32362297|gb|AAP80176.1| At2g31210 [Arabidopsis thaliana]	Unigene31189_All//9.00E-35//AT2G31210| basic helix-loop-helix (bHLH) family protein	Unigene31189_All//0.00E+00//TC171098	bHLH	ko04626|Plant-pathogen interaction		nr +

Unigene3119_All	1164	20.99	7.18	10.11	30.30	24.82	28.05	46.28	19.10	23.00	-1.55E+00	2.38E-35	Down	-1.05E+00	5.65E-19	Down	-2.88E-01	8.24E-04		-1.11E-01	3.04E-01		-1.28E+00	1.31E-70	Down	-1.01E+00	5.22E-50	Down	Unigene3119_All//gi|1778374|gb|AAB71417.1|//3.00E-44//glycine-rich RNA-binding protein PsGRBP [Pisum sativum] >gi|206586422|gb|ACI15745.1| glycine-rich RNA-binding protein [Pisum sativum]	Unigene3119_All//3.00E-33//AT4G13850| GR-RBP2 (GLYCINE-RICH RNA-BINDING PROTEIN 2); ATP binding / RNA binding / double-stranded DNA binding / single-stranded DNA binding	Unigene3119_All//0.00E+00//TC154081		ko03010|Ribosome//ko03040|Spliceosome	GO:0006950//GO:0032501//GO:0032559//GO:0043231//GO:0043566//GO:0046914	nr -
Unigene31190_All	398	2.23	2.42	3.48	8.89	4.24	3.40	2.44	2.21	4.80	1.14E-01	8.65E-01		6.38E-01	2.82E-01		-1.07E+00	4.95E-04	Down	-1.38E+00	3.20E-05	Down	-1.48E-01	8.13E-01		9.76E-01	1.65E-02		Unigene31190_All//gi|115444617|ref|NP_001046088.1|//2.00E-14//Os02g0180000 [Oryza sativa Japonica Group] >gi|75290241|sp|Q6ETK3.1|P2C11_ORYSJ RecName: Full=Probable protein phosphatase 2C 11; Short=OsPP2C11 >gi|113535619|dbj|BAF08002.1| Os02g0180000 [Oryza sativa Japonica Group]	Unigene31190_All//3.00E-15//AT4G31860| protein phosphatase 2C, putative / PP2C, putative	Unigene31190_All//0.00E+00//DW511843			GO:0004721//GO:0006464//GO:0016020//GO:0043169//GO:0043234	nr +
Unigene31191_All	231	13.59	5.70	11.06	3.67	2.53	0.59	0.37	0.54	0.34	-1.25E+00	5.13E-04	Down	-2.97E-01	4.23E-01		-5.33E-01	4.90E-01		-2.64E+00	3.54E-03		5.68E-01	7.82E-01		-8.61E-02	9.72E-01				Unigene31191_All//5.00E-89//TC135394				
Unigene31198_All	720	0.44	0.07	0.00	1.11	0.48	0.63	10.69	58.40	16.54	-2.63E+00	1.31E-01		-8.77E+00	4.91E-02		-1.21E+00	1.14E-01		-8.19E-01	3.20E-01		2.45E+00	6.56E-135	Up	6.30E-01	1.04E-05		Unigene31198_All//gi|115490848|gb|AB197958.1|//1.00E-15//alpha-crystalline heat shock protein [Gossypium arboreum] >gi|115490850|gb|AB197959.1| alpha-crystalline heat shock protein [Gossypium arboreum]	Unigene31198_All//5.00E-12//AT4G27670| HSP21 (HEAT SHOCK PROTEIN 21)	Unigene31198_All//1.00E-153//NP12958050			GO:0000302//GO:0009536//GO:0009642	nr +
Unigene31199_All	398	3.29	0.51	2.01	1.75	0.95	1.13	1.27	1.05	0.80	-2.69E+00	1.84E-04	Down	-7.12E-01	2.42E-01		-8.81E-01	2.99E-01		-6.27E-01	4.76E-01		-2.80E-01	7.49E-01		-6.71E-01	4.48E-01		Unigene31199_All//gi|15221382|ref|NP_177616.1|//7.00E-29//nodulin family protein [Arabidopsis thaliana] >gi|5882744|gb|AAD55297.1|AC008263_28 Strong similarity to gb|AF031243 nodule-specific protein (NLJ70) from Lotus Japonicus and is a member of the PF|00083 Sugar (and other) transporter family. EST gb|Z37715 comes from this gene [Arabidopsis thaliana]	Unigene31199_All//4.00E-30//AT1G74780| nodulin family protein	Unigene31199_All//3.00E-17//gi|78349229|gb|DT569503.1|DT569503				nr -
Unigene3120_All	1346	10.26	59.03	29.20	16.65	31.95	40.94	57.45	81.98	64.29	2.52E+00	1.36E-214	Up	1.51E+00	1.22E-52	Up	9.40E-01	2.33E-33		1.30E+00	9.40E-65	Up	5.13E-01	7.42E-31		1.62E-01	1.25E-03		Unigene3120_All//gi|145567026|gb|AB981863.1|//1.00E-170//LATE BLOOMER 1 [Pisum sativum]	Unigene3120_All//4.00E-150//AT1G22770| GI (GIGANTEA)	Unigene3120_All//0.00E+00//TC152646		ko04712|Circadian rhythm - plant		nr -
Unigene31200_All	1504	0.00	0.07	0.00	8.48	17.72	9.31	0.00	0.06	0.00	6.07E+00	3.87E-01		null	null		1.06E+00	2.39E-25	Up	1.35E-01	4.57E-01		5.80E+00	4.01E-01		null	null		Unigene31200_All//gi|285804235|gb|ADC35598.1|//2.00E-99//class I KNOX homeobox transcription factor KNOPE6 [Prunus persica]	Unigene31200_All//9.00E-64//AT1G23380| KNAT6; DNA binding / transcription activator/ transcription factor	Unigene31200_All//0.00E+00//TC160887	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene31201_All	763	0.00	0.00	0.00	0.00	0.00	0.00	2.55	0.44	57.49	null	null		null	null		null	null		null	null		-2.54E+00	3.67E-07	Down	4.50E+00	4.88E-248	Up	Unigene31201_All//gi|224137170|ref|XP_002327053.1|//3.00E-38//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222835368|gb|EEE73803.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene31201_All//3.00E-33//AT2G44840| ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	Unigene31201_All//0.00E+00//TC173432	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231//GO:0050896	nr -
Unigene31202_All	452	0.93	0.22	0.71	2.31	1.60	0.30	1.12	1.29	1.06	-2.05E+00	1.20E-01		-3.90E-01	7.17E-01		-5.33E-01	4.27E-01		-2.95E+00	3.82E-04	Down	2.06E-01	8.00E-01		-8.58E-02	9.30E-01		Unigene31202_All//gi|15222081|ref|NP_175353.1|//7.00E-16//protein kinase family protein [Arabidopsis thaliana] >gi|5430769|gb|AAD43169.1|AC007504_24 Similar to somatic embryogenesis receptor-like kinase [Arabidopsis thaliana] >gi|91805953|gb|ABE65705.1| protein kinase family protein [Arabidopsis thaliana]				ko00270|Cysteine and methionine metabolism		nr +
Unigene31203_All	322	8.94	2.52	2.98	32.49	16.79	7.99	1.44	0.52	0.25	-1.83E+00	6.76E-06	Down	-1.59E+00	1.05E-04	Down	-9.52E-01	5.65E-09		-2.02E+00	5.66E-24	Down	-1.48E+00	1.53E-01		-2.55E+00	2.35E-02		Unigene31203_All//gi|63259081|gb|AY40250.1|//4.00E-12//Cys2/His2 zinc-finger transcription factor [Silene latifolia]	Unigene31203_All//1.00E-09//AT1G02030| zinc finger (C2H2 type) family protein	Unigene31203_All//3.00E-134//ES824934	C2H2		GO:0010468//GO:0044464//GO:0046914	nr +
Unigene31204_All	328	29.67	29.81	38.96	36.91	42.62	38.97	65.48	39.37	21.62	7.00E-03	9.88E-01		3.93E-01	1.85E-02		2.08E-01	2.09E-01		7.84E-02	6.96E-01		-7.34E-01	6.36E-12		-1.60E+00	4.52E-41	Down			Unigene31204_All//0.00E+00//gi|13245001|gb|BE053257.2|BE053257				
Unigene31205_All	941	0.00	0.48	0.00	10.16	7.61	4.70	1.21	0.44	0.72	8.92E+00	7.44E-03		null	null		-4.17E-01	2.03E-02		-1.11E+00	2.08E-09	Down	-1.45E+00	1.40E-02		-7.53E-01	1.68E-01		Unigene31205_All//gi|30683971|ref|NP_193455.2|//2.00E-43//ATMAP70-5 (microtubule-associated proteins 70-5); microtubule binding [Arabidopsis thaliana] >gi|29028914|gb|AAO64836.1| At4g17220 [Arabidopsis thaliana] >gi|76058020|emb|CAJ31082.1| 70 kDa microtubule associated protein Type 5 [Arabidopsis thaliana]	Unigene31205_All//1.00E-42//AT4G17220| ATMAP70-5 (microtubule-associated proteins 70-5); microtubule binding	Unigene31205_All//1.00E-40//DW500608			GO:0003002//GO:0042546//GO:0044464	nr -
Unigene31207_All	1143	0.00	0.00	0.00	0.00	0.00	0.00	23.86	54.89	0.28	null	null		null	null		null	null		null	null		1.20E+00	1.19E-74	Up	-6.42E+00	5.65E-186	Down	Unigene31207_All//gi|145408595|ref|YP_001152219.1|//4.00E-06//ORF58f [Pinus koraiensis] >gi|145048844|gb|ABP35460.1| ORF58f [Pinus koraiensis]		Unigene31207_All//3.00E-26//TC165658			GO:0009536	nr -
Unigene31208_All	1184	0.09	0.00	0.00	0.46	0.58	0.38	1.07	1.77	2.46	-6.47E+00	3.72E-01		-6.47E+00	3.93E-01		3.30E-01	7.52E-01		-2.79E-01	7.57E-01		7.20E-01	7.28E-02		1.20E+00	2.46E-04	Up	Unigene31208_All//gi|30683133|ref|NP_196599.2|//5.00E-92//helicase domain-containing protein / IBR domain-containing protein / zinc finger protein-related [Arabidopsis thaliana]	Unigene31208_All//7.00E-88//AT4G01020| helicase domain-containing protein / IBR domain-containing protein / zinc finger protein-related	Unigene31208_All//3.00E-106//TC153718			GO:0005488//GO:0016787//GO:0043231	nr +
Unigene31210_All	814	0.39	0.00	0.07	1.77	0.47	1.05	1.82	0.72	1.52	-8.59E+00	3.65E-02		-2.56E+00	1.59E-01		-1.93E+00	5.06E-04	Down	-7.51E-01	1.90E-01		-1.34E+00	7.48E-03		-2.61E-01	6.13E-01		Unigene31210_All//gi|297746159|emb|CBI16215.3|//7.00E-06//unnamed protein product [Vitis vinifera]		Unigene31210_All//0.00E+00//TC152353				nr +
Unigene31211_All	815	1.28	5.41	0.78	0.73	0.51	1.55	1.04	13.59	0.10	2.07E+00	5.46E-10	Up	-7.12E-01	3.15E-01		-5.33E-01	5.62E-01		1.08E+00	8.18E-02		3.71E+00	4.77E-54	Up	-3.41E+00	1.35E-04	Down	Unigene31211_All//gi|2326354|emb|CAA67022.1|//4.00E-44//LMW heat shock protein [Arabidopsis thaliana]	Unigene31211_All//5.00E-38//AT4G25200| ATHSP23.6-MITO (MITOCHONDRION-LOCALIZED SMALL HEAT SHOCK PROTEIN 23.6)	Unigene31211_All//0.00E+00//gi|78325083|gb|DT545357.1|DT545357			GO:0010038//GO:0043231	nr +
Unigene31215_All	306	3.25	0.99	6.61	14.65	6.75	6.35	1.80	1.37	0.78	-1.71E+00	2.08E-02		1.03E+00	3.20E-02		-1.12E+00	2.87E-05	Down	-1.21E+00	2.43E-05	Down	-3.95E-01	6.34E-01		-1.20E+00	1.64E-01		Unigene31215_All//gi|115434700|ref|NP_001042108.1|//2.00E-14//Os01g0165100 [Oryza sativa Japonica Group] >gi|113531639|dbj|BAF04022.1| Os01g0165100 [Oryza sativa Japonica Group]	Unigene31215_All//3.00E-16//AT2G40390| unknown protein				GO:0043231	nr +
Unigene31217_All	277	29.28	47.01	41.52	29.85	22.87	24.46	76.93	65.94	32.94	6.83E-01	1.25E-05		5.04E-01	3.87E-03		-3.84E-01	5.41E-02		-2.88E-01	1.91E-01		-2.22E-01	4.78E-02		-1.22E+00	1.84E-27	Down			Unigene31217_All//1.00E-123//TC132744				
Unigene31218_All	373	0.84	5.30	0.57	2.54	1.75	2.42	0.23	0.22	0.00	2.65E+00	3.05E-06	Up	-5.60E-01	6.63E-01		-5.33E-01	4.51E-01		-6.74E-02	9.34E-01		-1.66E-02	1.01E+00		-7.82E+00	3.58E-01		Unigene31218_All//gi|225435311|ref|XP_002285132.1|//2.00E-19//PREDICTED: similar to hydroxyproline-rich glycoprotein family protein [Vitis vinifera]	Unigene31218_All//7.00E-06//AT3G45230| hydroxyproline-rich glycoprotein family protein	Unigene31218_All//0.00E+00//TC165188				nr +
Unigene31219_All	1399	0.07	0.29	0.08	0.78	0.15	0.19	26.38	12.91	15.46	1.95E+00	1.44E-01		2.49E-02	1.00E+00		-2.41E+00	5.06E-04	Down	-2.02E+00	4.74E-03		-1.03E+00	8.40E-35	Down	-7.71E-01	3.09E-22		Unigene31219_All//gi|297538227|ref|XP_002886995.1|//1.00E-145//carboxylic ester hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297332836|gb|EFH63254.1| carboxylic ester hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene31219_All//2.00E-145//AT3G62280| carboxylesterase/ hydrolase, acting on ester bonds					nr -
Unigene31220_All	538	5.25	12.43	3.76	1.85	1.98	3.61	3.14	4.04	11.85	1.24E+00	1.62E-07	Up	-4.82E-01	2.32E-01		9.96E-02	9.02E-01		9.63E-01	4.20E-02		3.62E-01	3.92E-01		1.91E+00	5.38E-16	Up			Unigene31220_All//1.00E-60//TC175109				
Unigene31222_All	323	0.00	0.00	0.00	0.00	0.00	0.00	5.11	10.48	40.83	null	null		null	null		null	null		null	null		1.04E+00	6.00E-04	Up	3.00E+00	4.65E-54	Up			Unigene31222_All//1.00E-47//DW505792				
Unigene31224_All	583	0.00	72.57	30.60	0.00	0.00	0.00	0.00	0.00	0.00	1.61E+01	2.89E-244	Up	1.49E+01	1.02E-100	Up	null	null		null	null		null	null		null	null		Unigene31224_All//gi|226348824|gb|ACO50728.1|//7.00E-25//ATPase subunit 6 [Micromonas pusilla CCMP1545]	Unigene31224_All//4.00E-07//ATMG00410| ATPase subunit 6			ko00190|Oxidative phosphorylation	GO:0006811//GO:0016020	nr +
Unigene31226_All	857	1.65	2.42	0.93	1.05	1.77	0.79	2.86	0.24	0.60	5.56E-01	2.16E-01		-8.23E-01	1.60E-01		7.57E-01	1.71E-01		-4.05E-01	6.23E-01		-3.55E+00	5.08E-12	Down	-2.24E+00	4.62E-08	Down	Unigene31226_All//gi|18417879|ref|NP_567883.1|//1.00E-27//WRKY family transcription factor [Arabidopsis thaliana] >gi|34365741|gb|AAQ65182.1| At4g31805 [Arabidopsis thaliana]	Unigene31226_All//2.00E-26//AT4G31805| WRKY family transcription factor	Unigene31226_All//2.00E-20//TC162344			GO:0005515	nr -
Unigene31229_All	649	0.16	2.11	0.25	0.46	0.53	0.49	3.58	3.22	1.53	3.71E+00	7.18E-06	Up	6.10E-01	7.48E-01		2.04E-01	9.01E-01		8.10E-02	9.50E-01		-1.54E-01	6.98E-01		-1.22E+00	9.07E-04	Down			Unigene31229_All//2.00E-140//gi|164283179|gb|ES834639.1|ES834639				
Unigene3123_All	2108	69.55	48.19	72.50	25.76	24.67	26.37	10.21	8.66	4.50	-5.29E-01	2.92E-35		6.00E-02	2.36E-01		-6.25E-02	4.93E-01		3.41E-02	6.89E-01		-2.37E-01	3.29E-02		-1.18E+00	2.67E-26	Down	Unigene3123_All//gi|30268668|dbj|BAC76005.1|//0.00E+00//RelA-SpoT like protein RSH4 [Nicotiana tabacum]	Unigene3123_All//0.00E+00//AT3G17470| RelA/SpoT domain-containing protein / calcium-binding EF-hand family protein	Unigene3123_All//0.00E+00//TC143298		ko04626|Plant-pathogen interaction	GO:0009617//GO:0016794//GO:0043231//GO:0046872	nr +
Unigene31230_All	1455	0.00	0.00	0.00	0.00	0.00	0.00	6.33	13.36	5.97	null	null		null	null		null	null		null	null		1.08E+00	5.77E-20	Up	-8.58E-02	6.31E-01		Unigene31230_All//gi|15241250|ref|NP_197505.1|//1.00E-147//protein kinase family protein [Arabidopsis thaliana] >gi|75332090|sp|Q94C25.1|Y5005_ARATH RecName: Full=Probable receptor-like protein kinase At5g20050; Flags: Precursor >gi|14335072|gb|AAK59800.1| AT5g20050/F28I16_200 [Arabidopsis thaliana] >gi|27363358|gb|AAO11598.1| At5g20050/F28I16_200 [Arabidopsis thaliana]	Unigene31230_All//2.00E-143//AT5G20050| protein kinase family protein	Unigene31230_All//6.00E-139//TC176962		ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006468//GO:0016020//GO:0032559	nr -
Unigene31233_All	699	17.89	22.18	15.16	33.49	19.85	20.22	14.34	8.79	5.07	3.10E-01	3.34E-02		-2.39E-01	1.78E-01		-7.55E-01	3.40E-13		-7.28E-01	3.78E-11		-7.06E-01	1.18E-05		-1.50E+00	6.30E-18	Down			Unigene31233_All//2.00E-94//BF270197				
Unigene31236_All	1690	0.06	0.12	0.00	0.18	0.12	0.08	13.21	4.48	6.86	9.54E-01	6.21E-01		-5.95E+00	3.93E-01		-5.33E-01	6.79E-01		-1.14E+00	4.57E-01		-1.56E+00	5.19E-40	Down	-9.45E-01	3.58E-19		Unigene31236_All//gi|15229439|ref|NP_191906.1|//0.00E+00//scp40 (serine carboxypeptidase-like 40; serine-type carboxypeptidase [Arabidopsis thaliana] >gi|129987782|sp|Q0WRX3.2|SCP40_ARATH RecName: Full=Serine carboxypeptidase-like 40; Flags: Precursor >gi|75733330|emb|CAB87800.1| serin carboxypeptidase-like protein [Arabidopsis thaliana] >gi|21593182|gb|AAM65131.1| serin carboxypeptidase-like protein [Arabidopsis thaliana]	Unigene31236_All//6.00E-179//AT3G63470| scp40 (serine carboxypeptidase-like 40); serine-type carboxypeptidase	Unigene31236_All//0.00E+00//TC173402			GO:0004180//GO:0019538	nr -

Unigene31242_All	489	0.21	0.21	0.76	0.41	0.85	0.37	26.28	82.14	93.77	-4.66E-02	9.89E-01		1.83E+00	2.13E-01		1.05E+00	4.26E-01		-1.42E-01	9.35E-01		1.64E+00	1.05E-76	Up	1.83E+00	5.35E-104	Up	Unigene31242_All//gi|15233513|ref|NP_193200.1|//5.00E-25//CAM8 (CALMODULIN 8); calcium ion binding [Arabidopsis thaliana] >gi|75318109|sp|Q23320.1|CML8_ARATH RecName: Full=Calmodulin-like protein 8; Short=AtCaM-8 >gi|5825600|gb|AAD53314.1|AF178074_1 calmodulin 8 [Arabidopsis thaliana] >gi|2244820|emb|CAB10243.1| calmodulin [Arabidopsis thaliana] >gi|7268170|emb|CAB78506.1| calmodulin [Arabidopsis thaliana] >gi|88900402|gb|ABD57513.1| At4g14640 [Arabidopsis thaliana]	Unigene31242_All//3.00E-26//AT4G14640| CAM8 (CALMODULIN 8); calcium ion binding	Unigene31242_All//1.00E-23//DR462870		ko04626|Plant-pathogen interaction	GO:0009593//GO:0016491//GO:0019932//GO:0046872	nr +
Unigene31244_All	1117	0.00	0.00	0.00	0.00	0.00	0.00	4.54	2.36	0.21	null	null		null	null		null	null		null	null		-9.46E-01	7.35E-05		-4.41E+00	2.21E-29	Down	Unigene31244_All//gi|301119055|ref|XP_002907255.1|//5.00E-15//conserved hypothetical protein [Phytophthora infestans T30-4] >gi|262105767|gb|EEY63819.1| conserved hypothetical protein [Phytophthora infestans T30-4]						nr -
Unigene31245_All	304	1.89	1.50	1.40	2.62	1.93	1.49	5.84	3.30	1.57	-3.36E-01	6.90E-01		-4.34E-01	6.23E-01		-4.45E-01	5.73E-01		-8.20E-01	3.20E-01		-8.24E-01	6.07E-02		-1.89E+00	4.84E-05	Down			Unigene31245_All//5.00E-71//ES814069				
Unigene31246_All	521	0.00	0.00	0.00	0.00	0.00	0.00	19.31	1.93	4.28	null	null		null	null		null	null		null	null		-3.33E+00	5.71E-45	Down	-2.17E+00	1.85E-29	Down	Unigene31246_All//gi|15221264|ref|NP_177590.1|//6.00E-29//bHLH family protein [Arabidopsis thaliana] >gi|75308937|sp|Q9C464.1|BHI35_ARATH RecName: Full=Transcription factor bHLH135; AltName: Full=Transcription factor EN 67; AltName: Full=bHLH transcription factor bHLH135; AltName: Full=Basic helix-loop-helix protein 135; Short=bHLH 135; Short=AtbHLH135 >gi|27764980|gb|AAO23611.1| At1g74500 [Arabidopsis thaliana]	Unigene31246_All//1.00E-23//AT1G74500| bHLH family protein	Unigene31246_All//1.00E-11//DW501889	bHLH		GO:0009314//GO:0009536//GO:0010468	nr -
Unigene31247_All	1506	0.00	17.06	9.51	0.00	0.02	0.00	0.00	0.00	1.41E+01	5.28E-148	Up	1.32E+01	1.05E-80	Up	4.52E+00	8.30E-01		null	null		null	null		null	null		Unigene31247_All//gi|159466892|ref|XP_001691632.1|//0.00E+00//beta subunit of mitochondrial ATP synthase [Chlamydomonas reinhardtii] >gi|384796|sp|P38482.1|ATPBM_CHLREREC RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Precursor >gi|18123|emb|CAA43808.1| H(+)-transporting ATP synthase; beta subunit of mitochondrial ATP synthase [Chlamydomonas reinhardtii] >gi|158278978|gb|EDP04740.1| beta subunit of mitochondrial ATP synthase [Chlamydomonas reinhardtii]	Unigene31247_All//0.00E+00//AT5G08680| ATP synthase beta chain, mitochondrial, putative	Unigene31247_All//3.00E-45//ES804359		ko00190|Oxidative phosphorylation	GO:0000275//GO:0015078//GO:0015662//GO:0015986//GO:0019829//GO:0032559	nr -
Unigene31248_All	628	0.42	0.56	0.08	0.63	0.33	0.29	5.12	15.44	6.53	4.39E-01	7.01E-01		-2.30E+00	2.43E-01		-9.48E-01	4.21E-01		-1.14E+00	3.79E-01		1.59E+00	2.71E-18	Up	3.53E-01	1.94E-01		Unigene31248_All//gi|15229901|ref|NP_190005.1|//2.00E-07//pyridine nucleotide-disulphide oxidoreductase family protein [Arabidopsis thaliana] >gi|30725576|gb|AAP37810.1| At3g44190 [Arabidopsis thaliana]	Unigene31248_All//1.00E-08//AT3G44190| pyridine nucleotide-disulphide oxidoreductase family protein	Unigene31248_All//2.00E-41//TC168988				nr +
Unigene3125_All	1956	2.70	3.24	5.88	10.26	9.81	9.49	11.31	4.64	11.18	2.61E-01	2.94E-01		1.12E+00	3.33E-10	Up	-6.58E-02	6.59E-01		-1.13E-01	4.53E-01		-1.29E+00	9.00E-30	Down	-1.58E-02	9.08E-01		Unigene3125_All//gi|22326581|ref|NP_195946.2|//0.00E+00//LAC11 (laccase 11); laccase [Arabidopsis thaliana] >gi|75331174|sp|Q8VZA1.1|LAC11_ARATH RecName: Full=Laccase-11; AltName: Full=Benzenediol:oxygen oxidoreductase 11; AltName: Full=Urishiol oxidase 11; AltName: Full=Diphenol oxidase 11; Flags: Precursor >gi|17473695|gb|AAL38304.1| laccase (diphenol oxidase)-like protein [Arabidopsis thaliana] >gi|20148527|gb|AAM10154.1| laccase (diphenol oxidase)-like protein [Arabidopsis thaliana]	Unigene3125_All//0.00E+00//AT5G03260| LAC11 (laccase 11); laccase	Unigene3125_All//2.00E-10//TC152487		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0031410//GO:0046914	nr +
Unigene31250_All	415	0.50	1.47	0.13	7.08	2.41	4.24	1.83	2.22	1.15	1.54E+00	1.22E-01		-1.97E+00	3.81E-01		-1.56E+00	9.86E-06	Down	-7.39E-01	4.33E-02		2.73E-01	6.70E-01		-6.71E-01	3.42E-01		Unigene31250_All//gi|225436341|ref|XP_002268902.1|//3.00E-07//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297734849|emb|CBI17083.3| unnamed protein product [Vitis vinifera]	Unigene31250_All//3.00E-05//AT3G44735| PSK1; growth factor	Unigene31250_All//8.00E-15//DW512026				nr +
Unigene31252_All	450	44.65	15.88	25.44	61.77	43.24	59.62	38.05	28.42	33.20	-1.49E+00	1.09E-27	Down	-8.11E-01	2.31E-10		-5.15E-01	4.31E-08		-5.12E-02	7.01E-01		-4.21E-01	4.48E-04		-1.97E-01	1.13E-01		Unigene31252_All//gi|112443176|gb|AB118976.1|//5.00E-08//nuclear-localized RNA binding protein [Capsicum annuum]		Unigene31252_All//2.00E-179//gi|78343680|gb|DT563954.1|DT563954				nr -
Unigene31255_All	746	0.00	27.10	10.92	0.00	0.00	0.00	0.00	0.00	0.00	1.47E+01	2.55E-116	Up	1.34E+01	1.32E-45	Up	null	null		null	null		null	null		null	null		Unigene31255_All//sp|P02516|HSP23_DROME//3.00E-53//Heat shock protein 23 OS=Drosophila melanogaster GN=Hsp23 PE=1 SV=2						swissprot -
Unigene31256_All	364	0.14	2.37	0.00	0.41	3.22	4.71	1.28	1.15	1.64	4.04E+00	4.20E-04	Up	-7.17E+00	6.24E-01		2.97E+00	1.37E-04	Up	3.52E+00	3.17E-07	Up	-1.54E-01	8.70E-01		3.62E-01	6.37E-01				Unigene31256_All//4.00E-07//TC169686				
Unigene31263_All	478	0.77	0.00	0.56	5.84	3.96	1.80	0.27	0.00	0.92	-9.58E+00	1.97E-02		-4.60E-01	6.97E-01		-5.59E-01	1.33E-01		-1.70E+00	1.63E-05	Down	-8.05E+00	2.35E-01		1.79E+00	9.60E-02		Unigene31263_All//gi|15228781|ref|NP_191154.1|//6.00E-16//CCR3 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 3); kinase [Arabidopsis thaliana] >gi|75335634|sp|Q9LY50.1|ACCR3_ARATH RecName: Full=Putative serine/threonine-protein kinase-like protein CCR3; AltName: Full=Protein CRINKLY 4 RELATED 3; Short=AtCCR3; Flags: Precursor >gi|7573490|emb|CAB87849.1| receptor kinase-like protein [Arabidopsis thaliana]	Unigene31263_All//3.00E-16//AT3G55950| CCR3 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 3); kinase	Unigene31263_All//9.00E-09//DN759978			GO:0016772//GO:0042802	nr +
Unigene31264_All	1196	0.09	0.00	0.00	0.17	0.06	0.38	17.46	27.96	8.43	-6.45E+00	3.72E-01		-6.45E+00	3.93E-01		-1.53E+00	4.15E-01		1.18E+00	3.38E-01		6.79E-01	7.08E-16		-1.05E+00	2.78E-21	Down	Unigene31264_All//gi|15231093|ref|NP_190765.1|//8.00E-89//AtSAT1 (Arabidopsis thaliana sterol O-acyltransferase 1); acyltransferase >gi|34365695|gb|AAQ65159.1| At3g51970 [Arabidopsis thaliana] >gi|51968422|dbj|BAD42903.1| wax synthase-like protein [Arabidopsis thaliana]	Unigene31264_All//4.00E-90//AT3G51970| AtSAT1 (Arabidopsis thaliana sterol O-acyltransferase 1); acyltransferase					nr +
Unigene31271_All	361	0.00	0.00	0.00	0.00	0.00	0.00	33.38	3.59	4.86	null	null		null	null		null	null		null	null		-3.22E+00	4.05E-52	Down	-2.78E+00	1.35E-46	Down							
Unigene31275_All	943	0.00	14.83	0.00	0.05	0.26	0.24	0.09	1.24	4.99	1.39E+01	2.69E-80	Up	null	null		2.28E+00	3.05E-01		2.18E+00	3.23E-01		3.79E+00	2.86E-06	Up	5.80E+00	1.97E-30	Up	Unigene31275_All//gi|224088649|ref|XP_002308508.1|//2.00E-61//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372132|gb|ABQ62997.1| RAP2-like protein [Populus trichocarpa] >gi|222854484|gb|EEE92031.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene31275_All//4.00E-33//AT1G19210| AP2 domain-containing transcription factor, putative	Unigene31275_All//0.00E+00//DW505344	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231//GO:0050896	nr +
Unigene31276_All	412	0.00	1.72	0.00	0.00	0.00	0.44	3.59	8.12	4.06	1.07E+01	3.33E-04	Up	null	null		null	null		8.78E+00	1.94E-01		1.18E+00	1.35E-04	Up	1.77E-01	6.86E-01								
Unigene31279_All	471	2.89	1.51	2.49	4.12	6.14	5.75	2.51	0.36	0.68	-9.39E-01	1.02E-01		-2.16E-01	7.04E-01		5.74E-01	1.28E-01		4.80E-01	2.34E-01		-2.82E+00	4.41E-05	Down	-1.89E+00	1.24E-03		Unigene31279_All//gi|224060331|ref|XP_002300146.1|//6.00E-12//predicted protein [Populus trichocarpa] >gi|222847404|gb|EEE84951.1| predicted protein [Populus trichocarpa]		Unigene31279_All//0.00E+00//TC158491				nr +
Unigene31282_All	895	4.91	1.36	4.22	11.41	9.20	3.84	20.69	19.43	20.83	-1.85E+00	9.28E-09	Down	-2.17E-01	4.98E-01		-3.11E-01	8.51E-02		-1.57E+00	1.15E-16	Down	-9.10E-02	5.22E-01		9.80E-03	9.60E-01		Unigene31282_All//gi|28557342|dbj|BAC57589.1|//2.00E-16//membrane located receptor-like protein [Nicotiana tabacum]	Unigene31282_All//3.00E-07//AT2G46495| zinc finger (C3HC4-type RING finger) family protein	Unigene31282_All//0.00E+00//TC150336			GO:0016740	nr -
Unigene31285_All	570	0.18	0.36	0.00	0.17	0.36	0.16	3.34	5.06	14.75	9.54E-01	6.21E-01		-7.52E+00	3.93E-01		1.05E+00	6.12E-01		-1.41E-01	9.50E-01		6.00E-01	7.23E-02		2.14E+00	5.38E-24	Up	Unigene31285_All//gi|297603944|ref|NP_001054803.2|//1.00E-09//Os05g0179100 [Oryza sativa Japonica Group] >gi|255676079|dbj|BAF16717.2| Os05g0179100 [Oryza sativa Japonica Group]	Unigene31285_All//1.00E-10//AT4G13395| RTFL12 (ROTUNDIFOLIA LIKE 12)	Unigene31285_All//9.00E-142//DW499877			GO:0043231//GO:0048513	nr +
Unigene31286_All	261	3.41	3.30	0.00	0.95	0.00	0.69	0.32	1.28	1.68	-4.63E-02	9.62E-01		-1.17E+01	6.30E-05	Down	-9.90E+00	4.18E-02		-4.63E-01	7.44E-01		1.98E+00	1.44E-01		2.37E+00	4.04E-02								
Unigene31287_All	211	142.83	159.93	203.91	62.56	55.81	31.04	94.78	53.48	24.36	1.63E-01	1.01E-01		5.14E-01	6.44E-10		-1.65E-01	3.42E-01		-1.01E+00	5.16E-11	Down	-8.26E-01	1.74E-13		-1.96E+00	1.30E-50	Down			Unigene31287_All//3.00E-111//gi|84151773|gb|DN801128.1|DN801128				
Unigene31288_All	1693	0.00	13.05	4.18	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	3.60E-127	Up	1.20E+01	1.43E-39	Up	null	null		null	null		null	null		null	null		Unigene31288_All//gi|186528371|ref|NP_198994.2|//2.00E-18//CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding [Arabidopsis thaliana]	Unigene31288_All//3.00E-11//AT5G41790| CIP1 (COP1-INTERACTIVE PROTEIN 1); protein binding					nr +
Unigene31289_All	680	0.00	0.00	0.00	1.10	0.10	0.00	7.90	6.88	2.70	null	null		null	null		-3.44E+00	6.19E-04	Down	-1.01E+01	9.80E-05	Down	-1.98E-01	4.40E-01		-1.55E+00	1.77E-10	Down	Unigene31289_All//gi|256010124|gb|ACU55135.1|//7.00E-52//dirigent-like protein 1 [Gossypium hirsutum]	Unigene31289_All//2.00E-42//AT1G58170| disease resistance-responsive protein-related / dirigent protein-related	Unigene31289_All//5.00E-110//ES824103				nr -

Unigene31290_All	395	0.66	0.64	0.54	1.39	0.44	0.46	4.07	10.48	4.14	-4.63E-02	9.86E-01			-2.97E-01	8.32E-01		-1.67E+00	9.26E-02		-1.60E+00	1.32E-01		1.36E+00	1.02E-06	Up	2.38E-02	9.67E-01		Unigene31290_All//gi|224071451|ref|XP_002303466.1|//9.00E-11//predicted protein [Populus trichocarpa] >gi|222840898|gb|EEE78445.1| predicted protein [Populus trichocarpa]		Unigene31290_All//8.00E-49//DW501483				nr -
Unigene31292_All	1767	0.00	0.00	0.00	0.00	0.00	0.00	2.08	6.50	0.00	null	null			null	null		null	null		null	null		1.64E+00	1.74E-22	Up	-1.10E+01	4.79E-27	Down	Unigene31292_All//gi|297803438|ref|XP_002869603.1|//0.00E+00//early-responsive to dehydration 8 [Arabidopsis lyrata subsp. lyrata] >gi|297315439|gb|EFH45862.1| early-responsive to dehydration 8 [Arabidopsis lyrata subsp. lyrata]	Unigene31292_All//0.00E+00//AT5G56030|HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Unigene31292_All//2.00E-25//TC153364		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0006970//GO:0009408//GO:0009791//GO:0030312//GO:0031647//GO:0032559//GO:0043231//GO:0044267//GO:0044444//GO:0048827	nr +
Unigene31294_All	1001	0.00	34.07	17.40	0.00	0.00	0.00	0.00	0.00	0.00	1.51E+01	1.03E-196	Up	1.41E+01	2.72E-98	Up	null	null		null	null		null	null		null	null		Unigene31294_All//gi|836950|gb|AAC49006.1|//1.00E-12//CIP1 [Arabidopsis thaliana] >gi|1096881|prf|2112355A CIP1 protein	Unigene31294_All//7.00E-08//AT3G16000| MFP1 (MAR BINDING FILAMENT-LIKE PROTEIN 1); DNA binding				nr +
Unigene31296_All	517	0.00	0.59	0.62	1.83	0.67	1.22	2.04	4.45	6.01	9.20E+00	4.43E-02		9.27E+00	4.52E-02		-1.46E+00	3.60E-02		-5.82E-01	4.37E-01		1.12E+00	3.23E-03		1.56E+00	2.25E-06	Up	Unigene31296_All//gi|115479833|ref|NP_001063510.1|//1.00E-41//Os09g0483500 (Oryza sativa Japonica Group) >gi|113631743|dbj|BAF25424.1| Os09g0483500 (Oryza sativa Japonica Group)	Unigene31296_All//2.00E-32//AT2G44310| calcium-binding EF hand family protein	Unigene31296_All//6.00E-121//TC162100			GO:0046872	nr +
Unigene31297_All	544	0.00	0.28	0.00	0.00	0.13	0.00	184.51	146.82	89.42	8.13E+00	2.35E-01		null	null		6.98E+00	6.09E-01		null	null		-3.30E-01	7.19E-13		-1.05E+00	6.06E-98	Down	Unigene31297_All//gi|21554334|gb|AAM63441.1|//7.00E-13//latex-abundant protein-like [Arabidopsis thaliana]	Unigene31297_All//4.00E-14//AT5G04200| AtMC9 (metacaspase 9); cysteine-type peptidase	Unigene31297_All//6.00E-118//TC153373			GO:0005576//GO:0044238//GO:0070011	nr -
Unigene31302_All	560	0.37	0.36	0.19	0.89	1.41	0.81	3.25	7.31	3.41	-4.63E-02	9.88E-01		-9.74E-01	6.21E-01		6.69E-01	4.42E-01		-1.41E-01	8.93E-01		1.17E+00	2.00E-05	Up	7.29E-02	8.71E-01		Unigene31302_All//gi|112253907|ref|YP_717162.1|//3.00E-87//NADH dehydrogenase subunit 6 [Brassica napus] >gi|37591109|dbj|BAC98911.1| NADH dehydrogenase subunit 6 [Brassica napus]	Unigene31302_All//2.00E-73//ATMG00270| NADH dehydrogenase subunit 6	Unigene31302_All//0.00E+00//TC143345		ko00190|Oxidative phosphorylation	GO:0005746//GO:0015980//GO:0030964//GO:0031224//GO:0031410//GO:0050136//GO:0051234	nr -
Unigene31303_All	724	8.74	2.66	7.58	0.00	0.43	0.44	0.00	0.00	0.00	-1.72E+00	3.86E-11	Down	-2.07E-01	4.17E-01		8.74E+00	4.54E-02		8.77E+00	4.07E-02		null	null		null	null		Unigene31303_All//gi|115464331|ref|NP_001055765.1|//2.00E-27//Os05g0462000 (Oryza sativa Japonica Group) >gi|113579316|dbj|BAF17679.1| Os05g0462000 (Oryza sativa Japonica Group)	Unigene31303_All//3.00E-29//AT3G55240| Overexpression leads to PEL (Pseudo-Etiolation in Light) phenotype.	Unigene31303_All//1.00E-15//EX172273			GO:0044464	nr -
Unigene31304_All	510	0.00	0.89	0.21	27.35	11.28	13.37	1.08	0.66	0.08	9.80E+00	7.44E-03		7.71E+00	3.98E-01		-1.28E+00	8.11E-19	Down	-1.03E+00	5.59E-12	Down	-7.17E-01	4.22E-01		-3.79E+00	2.03E-03					Unigene31304_All//2.00E-130//DR459941				
Unigene31307_All	772	0.27	0.26	0.41	0.39	0.27	0.00	2.63	2.00	5.73	-4.65E-02	9.88E-01		6.11E-01	6.24E-01		-5.33E-01	6.79E-01		-8.60E+00	4.00E-02		-3.92E-01	3.68E-01		1.12E+00	1.20E-05	Up	Unigene31307_All//gi|224139090|ref|XP_002326765.1|//7.00E-15//predicted protein [Populus trichocarpa] >gi|222834087|gb|EEE72564.1| predicted protein [Populus trichocarpa]		Unigene31307_All//1.00E-79//DN817187				nr +
Unigene3131_All	1188	3.44	3.67	3.36	9.35	8.26	5.78	6.90	5.17	3.25	9.46E-02	7.44E-01		-3.12E-02	9.35E-01		-1.79E-01	3.47E-01		-6.94E-01	2.98E-05		-4.17E-01	2.32E-02		-1.09E+00	2.47E-09	Down	Unigene3131_All//gi|3415134|gb|AAC31614.1|//6.00E-93//Phyb1 [Pimpinella brachycarpa]	Unigene3131_All//1.00E-76//AT4G15030| unknown protein	Unigene3131_All//2.00E-58//ES820143				nr -
Unigene31311_All	491	0.75	1.24	0.65	1.62	2.74	0.74	1.03	1.62	3.49	7.31E-01	4.16E-01		-1.97E-01	8.66E-01		7.53E-01	2.15E-01		-1.14E+00	1.63E-01		6.46E-01	3.83E-01		1.76E+00	1.93E-04	Up	Unigene31311_All//gi|20260474|gb|AAM13135.1|//1.00E-61//26S proteasome subunit-like protein [Arabidopsis thaliana] >gi|28059321|gb|AAO30047.1| 26S proteasome subunit-like protein [Arabidopsis thaliana] >gi|32700036|gb|AAF86668.1| 26S proteasome subunit RPN9a [Arabidopsis thaliana]	Unigene31311_All//9.00E-63//AT5G45620| 26S proteasome regulatory subunit, putative (RPN9)	Unigene31311_All//3.00E-144//gi|73864995|gb|DT467734.1|DT467734		ko03050|Proteasome	GO:0005838//GO:0019941//GO:0043231	nr -
Unigene31312_All	650	3.62	0.00	0.74	4.52	2.60	0.69	0.13	0.26	0.00	-1.18E+01	1.33E-13	Down	-2.30E+00	5.12E-06	Down	-8.01E-31	2.04E-02		-2.70E+00	8.04E-10	Down	9.83E-01	6.33E-01		-7.02E+00	3.58E-01		Unigene31312_All//gi|226713179|sp|A7PNN8.1||4978_VITVI//1.00E-53//RecName: Full=UPF0497 membrane protein 8	Unigene31312_All//2.00E-20//AT4G25040| integral membrane family protein	Unigene31312_All//0.00E+00//gi|164349690|gb|ES847870.1|ES847870			GO:0016020	nr -
Unigene31316_All	506	0.72	1.30	1.05	4.13	3.33	2.77	4.18	2.40	1.50	8.47E-01	3.48E-01		5.40E-01	6.10E-01		-3.10E-01	5.23E-01		-5.80E-01	2.11E-01		-8.03E-01	4.24E-02		-1.48E+00	2.15E-04	Down							
Unigene31317_All	677	0.15	0.15	1.42	0.00	0.00	0.00	4.93	1.30	1.71	-4.65E-02	9.89E-01		3.20E+00	1.02E-03		null	null		null	null		-1.93E+00	1.22E-08	Down	-1.53E+00	9.89E-07	Down	Unigene31317_All//gi|42571383|ref|NP_973782.1|//2.00E-21//disease resistance-responsive family protein [Arabidopsis thaliana] >gi|8438894|gb|AAF75080.1|AC007583_16 Contains similarity to disease resistance response protein from Pisum sativum gb|M18250. EST gb|F13940 comes from this gene [Arabidopsis thaliana]	Unigene31317_All//1.00E-22//AT1G07730| disease resistance-responsive family protein					nr -
Unigene31318_All	320	6.05	12.03	12.98	5.76	8.39	8.33	3.96	5.36	2.74	9.92E-01	1.64E-03		1.10E+00	4.78E-04	Up	5.43E-01	1.69E-01		5.32E-01	1.95E-01		4.34E-01	3.66E-01		-5.33E-01	3.10E-01					Unigene31318_All//7.00E-61//gi|109880030|gb|DW509000.1|DW509000				
Unigene31319_All	310	0.00	3.43	0.69	3.05	1.67	1.89	0.82	2.29	2.06	1.17E+01	3.81E-06	Up	9.42E+00	1.41E-01		-8.74E-01	2.10E-01		-6.89E-01	3.58E-01		1.49E+00	6.15E-02		1.33E+00	1.00E-01								
Unigene3132_All	1056	24.87	41.79	27.03	62.74	38.87	37.98	31.63	21.49	14.79	7.49E-01	5.63E-20		1.20E-01	3.18E-01		-6.91E-01	2.32E-31		-7.24E-01	3.35E-30		-5.58E-01	2.03E-11		-1.10E+00	7.83E-36	Down	Unigene3132_All//gi|124359660|gb|AB006032.1|//2.00E-53//Galactose-binding like [Medicago truncatula]	Unigene3132_All//3.00E-48//AT4G19840| ATPP2-A1; carbohydrate binding	Unigene3132_All//0.00E+00//TC141013			GO:0043231	nr -
Unigene31320_All	272	1.15	0.56	3.13	3.66	2.53	6.31	2.64	1.54	0.15	-1.05E+00	4.43E-01		1.44E+00	8.23E-02		-5.33E-01	4.45E-01		7.85E-01	1.31E-01		-7.82E-01	3.10E-01		-4.17E+00	1.64E-04	Down				Unigene31320_All//4.00E-31//TC176768				
Unigene31321_All	365	0.14	0.00	0.00	0.14	0.00	0.37	3.36	1.37	61.45	-7.16E+00	6.12E-01		-7.16E+00	6.24E-01		-7.09E+00	5.55E-01		1.44E+00	6.38E-01		-1.29E+00	2.09E-02		4.19E+00	2.37E-121	Up	Unigene31321_All//gi|212717149|gb|ACJ37416.1|//7.00E-13//stress-induced receptor-like kinase [Glycine max]	Unigene31321_All//1.00E-10//AT1G70250| receptor serine/threonine kinase, putative	Unigene31321_All//2.00E-40//TC165373			GO:0000166//GO:0004672	nr -
Unigene31324_All	286	2.20	0.00	0.37	2.44	0.24	0.95	3.10	0.88	0.84	-1.11E+01	7.91E-04	Down	-2.56E+00	2.72E-02		-3.34E+00	1.25E-03		-1.36E+00	1.31E-01		-1.82E+00	1.08E-02		-1.89E+00	6.34E-03		Unigene31324_All//gi|15228363|ref|NP_190408.1|//2.00E-20//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75207690|sp|Q9SIK5.1|PP269_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g48250, chloroplastic; Flags: Precursor	Unigene31324_All//8.00E-22//AT3G48250| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene31325_All	222	4.24	20.77	5.52	3.59	2.79	5.70	1.71	0.56	0.72	2.29E+00	1.10E-11	Up	3.79E-01	5.55E-01		-3.63E-01	6.23E-01		6.66E-01	2.99E-01		-1.60E+00	1.81E-01		-1.26E+00	2.48E-01					Unigene31325_All//5.00E-33//FL577698				
Unigene31328_All	449	226.65	178.98	183.23	472.85	428.64	253.78	622.06	258.97	228.03	-3.41E-01	2.26E-11		-3.07E-01	4.76E-09		-1.42E-01	1.78E-05		-8.98E-01	1.87E-138		-1.26E+00	0.00E+00	Down	-1.45E+00	0.00E+00	Down	Unigene31328_All//gi|951427|gb|AAA74692.1|//9.00E-64//stearoyl-acyl-carrier protein desaturase [Ricinus communis]	Unigene31328_All//2.00E-54//AT2G43710| SSI2; acyl-[acyl-carrier-protein] desaturase/ stearoyl-CoA 9-desaturase	Unigene31328_All//0.00E+00//TC142123		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0006631//GO:0009536//GO:0016717//GO:0046872	nr +
Unigene31329_All	412	2.41	0.00	1.29	1.69	0.25	1.43	0.82	0.30	0.48	-1.12E+01	7.45E-06	Down	-9.01E-01	2.22E-01		-2.76E+00	3.99E-03		-2.48E-01	7.56E-01		-1.43E+00	2.58E-01		-7.64E-01	5.01E-01					Unigene31329_All//3.00E-05//AT5G66520| pentatricopeptide (PPR) repeat-containing protein					
Unigene3133_All	2452	6.89	7.83	14.09	5.87	5.98	4.57	0.14	0.07	0.39	1.84E-01	1.75E-01		1.03E+00	8.69E-26	Up	2.71E-02	8.83E-01		-3.62E-01	1.56E-02		-1.02E+00	3.99E-01		1.50E+00	1.93E-02		Unigene3133_All//gi|4530126|gb|AAD21872.1|//1.00E-180//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene3133_All//5.00E-144//AT4G05200| protein kinase family protein	Unigene3133_All//0.00E+00//TC139931		ko04626|Plant-pathogen interaction	GO:0016301	nr +
Unigene31332_All	483	75.61	77.74	158.76	10.11	10.41	4.86	0.61	0.00	0.00	4.00E-02	6.85E-01		1.07E+00	4.36E-60	Up	4.24E-02	9.00E-01		-1.06E+00	8.96E-05	Down	-9.26E+00	2.18E-02		-9.26E+00	1.58E-02		Unigene31332_All//gi|225442509|ref|XP_002284032.1|//1.00E-18//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297743214|emb|CBI36081.3| unnamed protein product [Vitis vinifera]						nr +
Unigene31333_All	437	0.00	0.23	0.00	1.94	3.47	1.76	2.71	0.00	0.46	7.86E+00	3.87E-01		null	null		8.39E-01	1.29E-01		-1.42E-01	8.54E-01		-1.14E+01	1.97E-08	Down	-2.57E+00	6.97E-05	Down	Unigene31333_All//gi|44917559|gb|AAS49104.1|//1.00E-11//At3g42800 [Arabidopsis thaliana]	Unigene31333_All//2.00E-09//AT3G42800| unknown protein	Unigene31333_All//4.00E-20//TC153674			GO:0005488	nr +
Unigene31335_All	1222	0.00	0.00	0.00	0.00	0.00	0.00	1.80	2.29	0.00	null	null		null	null		null	null		null	null		3.49E-01	3.34E-01		-1.08E+01	3.38E-16	Down	Unigene31335_All//gi|298714497|emb|CBJ27519.1|//2.00E-78//eukaryotic elongation factor-1 B gamma [Ectocarpus siliculosus]	Unigene31335_All//2.00E-30//AT1G57720| elongation factor 1B-gamma, putative / eEF-1B gamma, putative				GO:0006412	nr +
Unigene31336_All	425	7.14	6.80	3.26	9.03	6.32	8.93	3.58	6.69	8.62	-7.14E-02	8.41E-01		-1.13E+00	2.86E-03		-5.14E-01	9.40E-02		-1.59E-02	9.52E-01		9.01E-01	6.73E-03		1.27E+00	1.18E-05	Up	Unigene31336_All//gi|147777618|emb|CAN73688.1|//8.00E-11//hypothetical protein [Vitis vinifera]		Unigene31336_All//0.00E+00//TC146687				nr +
Unigene31337_All	818	1.09	0.31	0.20	2.31	1.18	0.66	2.89	0.72	0.63	-1.81E+00	2.38E-02		-2.48E+00	7.18E-03		-9.73E-01	3.01E-02		-1.80E+00	3.14E-04	Down	-2.02E+00	1.14E-06	Down	-2.19E+00	1.28E-07	Down	Unigene31337_All//gi|124359163|gb|ABN05686.1|//2.00E-17//Zinc finger, CCHC-type [Medicago truncatula]	Unigene31337_All//5.00E-05//AT3G31430| unknown protein					nr +
Unigene31345_All	588	0.00	0.69	0.36	0.76	0.35	0.54	0.79	1.63	2.57	9.43E+00	1.36E-02		8.50E+00	1.41E-01		-1.12E+00	3.15E-01		-5.04E-01	6.49E-01		1.05E+00	1.03E-01		1.70E+00	6.86E-04	Up							
Unigene31347_All	452	0.12	0.00	0.00	0.00	0.08	0.00	13.28	2.87	18.77	-6.86E+00	6.12E-01		-6.86E+00	6.24E-01		6.25E+00	8.30E-01		null	null		-2.21E+00	1.11E-17	Down	4.99E-01	3.84E-03		Unigene31347_All//gi|73624747|gb|AAZ79231.1|//1.00E-35//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene31347_All//2.00E-35//AT4G24010| ATCSLG1; cellulose synthase/ transferase/ transferase, transferring glycosyl groups				GO:0009987//GO:0016020//GO:0016757	nr +
Unigene31350_All	346	9.83	0.59	0.92	8.93	5.18	3.39	0.00	0.00	0.00	-4.07E+00	6.35E-15	Down	-3.41E+00	2.00E-12	Down	-7.86E-01	1.93E-02		-1.40E+00	1.08E-04	Down	null	null		null	null					Unigene31350_All//2.00E-27//TC177189				
Unigene31351_All	816	5.96	1.12	9.14	2.87	0.97	1.11	0.26	0.26	0.59	-2.42E+00	3.74E-13	Down	6.16E-01	5.62E-03		-1.56E+00	1.03E-04	Down	-1.37E+00	1.18E-03		-1.68E-02	1.02E+00		1.18E+00	2.18E-01					Unigene31351_All//1.00E-06//BG441208				
Unigene31353_All	357	14.80	1.14	0.75	0.84	0.77	3.16	0.12	0.82	2.90	-3.70E+00	2.05E-21	Down	-4.31E+00	9.37E-23	Down	-1.18E-01	9.00E-01		1.92E+00	6.72E-03		2.79E+00	9.47E-02		4.62E+00	2.03E-06	Up							
Unigene31354_All	386	11.93	5.12	5.93	9.94	8.83	16.26	25.63	19.60	9.29	-1.22E+00	2.56E-05	Down	-1.01E+00	6.54E-04	Down	-1.70E-01	6.11E-01		7.11E-01	2.34E-03		-3.87E-01	1.95E-02		-1.46E+00	3.87E-17	Down	Unigene31354_All//gi|5706704|gb|AAD47346.1|AF112440_1//5.00E-35//ribosomal protein S26 [Pisum sativum]	Unigene31354_All//5.00E-21//AT3G56340| 40S ribosomal protein S26 (RPS26C)	Unigene31354_All//5.00E-87//gi|164274156|gb|ES817745.1|ES817745		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene31355_All	507	0.31	0.40	0.74	9.43	6.18	2.85	3.67	0.00	0.79	3.69E-01	8.16E-01		1.25E+00	3.66E-01		-6.10E-01	2.00E-02		-1.73E+00	3.52E-09	Down	-1.18E+01	3.59E-13	Down	-2.22E+00	3.02E-06	Down				Unigene31355_All//2.00E-44//DW501685				
Unigene31356_All	265	5.92	0.76	3.82	6.20	3.12	1.36	1.44	0.95	1.65	-2.95E+00	1.18E-05	Down	-6.34E-01	2.47E-01		-9.92E-01	4.23E-02		-2.19E+00	1.26E-04	Down	-6.02E-01	6.12E-01		2.04E-01	8.26E-01					Unigene31356_All//4.00E-133//TC144363				
Unigene31359_All	304	1.38	6.00	1.93	7.05	9.52	11.74	9.32	10.17	5.90	2.12E+00	1.13E-04	Up	4.85E-01	6.30E-01		4.33E-01	2.75E-01		7.36E-01	2.50E-02		1.27E-01	7.15E-01		-6.60E-01	3.92E-02		Unigene31359_All//gi|42573463|ref|NP_974828.1|//5.00E-10//AGP41 (ARABINOGALACTAN-PROTEIN 41) [Arabidopsis thaliana] >gi|105829394|gb|ABF74692.1| At5g24105 [Arabidopsis thaliana]	Unigene31359_All//3.00E-11//AT5G24105| AGP41 (ARABINOGALACTAN-PROTEIN 41)				GO:0031224	nr -
Unigene31360_All	1302	0.00	44.48	20.37	0.08	0.00	0.00	0.00	0.00	0.00	1.54E+01	0.00E+00	Up	1.43E+01	3.42E-150	Up	-6.26E+00	3.13E-01		-6.26E+00	4.00E-01		null	null		null	null		Unigene31360_All//gi|301122113|ref|XP_002908783.1|//0.00E+00//beta-tubulin [Phytophthora infestans T30-4] >gi|262099545|gb|EEY57597.1| beta-tubulin [Phytophthora infestans T30-4]	Unigene31360_All//0.00E+00//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene31360_All//9.00E-113//TC141009		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene31362_All	304	2.41	2.33	2.45	14.26	25.26	16.64	6.81	21.45	7.21	-4.62E-02	9.68E-01		2.54E-02	9.95E-01		8.25E-01	3.48E-05		2.23E-01	4.74E-01		1.65E+00	3.37E-13	Up	8.08E-02	8.39E-01		Unigene31362_All//gi|225455521|ref|XP_002267233.1|//3.00E-09//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene31362_All//1.00E-16//TC179067			GO:0016491//GO:0046872	nr -
Unigene31363_All	535	0.00	1.23	0.40	0.65	0.71	0.25	6.40	0.16	0.45	1.03E+01	6.25E-04	Up	8.64E+00	1.41E-01		1.19E-01	9.58E-01		-1.36E+00	3.37E-01		-5.36E+00	2.62E-21	Down	-3.84E+00	3.07E-18	Down				Unigene31363_All//0.00E+00//gi|84157904|gb|DN826951.1|DN826951				

Unigene31364_All	790	0.00	0.00	0.00	0.00	0.00	0.00	2.57	3.23	0.00	null	null		null	null		null	null		null	null		3.29E-01	3.98E-01		-1.13E+01	5.82E-15	Down	Unigene31364_All//gi|115475908|ref|NP_001061550.1|//3.00E-51//Os08g0326400 [Oryza sativa Japonica Group] >gi|115480049|ref|NP_001063618.1|Os09g0507800 [Oryza sativa Japonica Group] >gi|548774|sp|P35685.1|RL7A_ORYSJ RecName: Full=60S ribosomal protein L7a >gi|303855|dbj|BAA02156.1| ribosomal protein L7A [Oryza sativa Japonica Group] >gi|38423963|dbj|BAD01672.1| 60S ribosomal protein L7A [Oryza sativa Japonica Group] >gi|38637005|dbj|BAD03264.1| 60S ribosomal protein L7A [Oryza sativa Japonica Group] >gi|113623519|dbj|BAF23464.1| Os08g0326400 [Oryza sativa Japonica Group] >gi|113631851|dbj|BAF25532.1| Os09g0507800 [Oryza sativa Japonica Group]	Unigene31364_All//3.00E-36//AT3G62870| 60S ribosomal protein L7A (RPL7aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene31366_All	621	0.08	0.16	0.69	0.80	0.78	0.65	1.02	2.89	0.26	9.53E-01	7.26E-01		3.02E+00	5.73E-02		-4.73E-02	9.49E-01		-2.94E-01	7.57E-01		1.50E+00	9.45E-04	Up	-1.99E+00	2.04E-02		Unigene31366_All//gi|13877617|gb|AK43886.1|AF370509_1/2.00E-12//protein kinase-like protein [Arabidopsis thaliana] >gi|30725492|gb|AAV37768.1| At3g24600 [Arabidopsis thaliana]				ko03040|Spliceosome//ko04144|Endocytosis//ko00270|Cysteine and methionine metabolism	GO:0003824	nr +
Unigene31367_All	295	5.32	0.00	0.18	0.34	1.17	1.07	0.14	0.14	0.00	-1.24E+01	4.20E-09	Down	-4.88E+00	2.04E-07	Down	1.79E+00	2.58E-01		1.67E+00	3.09E-01		-1.62E-02	1.00E+00		-7.16E+00	6.12E-01		Unigene31367_All//gi|118487366|gb|AB835511.1|//6.00E-12//unknown [Populus trichocarpa]		Unigene31367_All//6.00E-166//gi|21102104|gb|BQ414417.1|BQ414417				nr -
Unigene3137_All	1105	21.07	9.58	5.93	37.37	33.03	16.06	4.97	3.44	9.23	-1.14E+00	3.05E-21	Down	-1.83E+00	5.13E-41	Down	-1.78E-01	3.65E-02		-1.22E+00	9.72E-45	Down	-5.31E-01	2.00E-02		8.92E-01	2.06E-08		Unigene3137_All//gi|124359162|gb|AB605685.1|//1.00E-06//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene3137_All//8.00E-07//AT3G09510| nucleic acid binding	Unigene3137_All//0.00E+00//gi|164289850|gb|ES826067.1|ES826067				nr -
Unigene31371_All	538	0.00	0.19	0.00	0.37	0.38	0.59	3.77	19.34	14.00	7.56E+00	3.87E-01		null	null		5.20E-02	9.89E-01		6.66E-01	6.48E-01		2.36E+00	2.03E-32	Up	1.89E+00	1.83E-18	Up	Unigene31371_All//gi|144954332|gb|ABP04242.1|//9.00E-35//calmodulin binding protein-like [Elaeis guineensis]	Unigene31371_All//2.00E-20//AT3G50770| calmodulin-related protein, putative	Unigene31371_All//2.00E-13//gi|109868242|gb|DW497218.1|DW497218		ko04626|Plant-pathogen interaction	GO:0046872	nr +
Unigene31372_All	457	0.00	0.00	0.00	0.22	0.00	0.00	4.35	9.60	9.33	null	null		null	null		-7.77E+00	3.13E-01		-7.77E+00	4.00E-01		1.14E+00	1.45E-05	Up	1.10E+00	2.51E-05	Up								
Unigene31373_All	761	0.41	0.00	0.14	3.14	1.45	1.31	5.72	0.38	1.10	-8.69E+00	3.65E-02		-1.56E+00	3.30E-01		-1.12E+00	4.01E-03		-1.27E+00	2.28E-03		-3.90E+00	1.88E-22	Down	-2.38E+00	1.18E-14	Down	Unigene31373_All//gi|224077988|ref|XP_002305471.1|//4.00E-49//SAUR family protein [Populus trichocarpa] >gi|222848435|gb|EEE85982.1| SAUR family protein [Populus trichocarpa]	Unigene31373_All//1.00E-38//AT1G75590| auxin-responsive family protein	Unigene31373_All//0.00E+00//TC152621			GO:0005515//GO:0009725	nr -
Unigene31375_All	1179	0.44	0.21	0.72	0.17	0.29	0.08	1.40	3.05	0.07	-1.05E+00	3.11E-01		7.03E-01	3.83E-01		7.89E-01	5.96E-01		-1.14E+00	5.69E-01		1.12E+00	1.34E-04	Up	-4.37E+00	7.28E-10	Down	Unigene31375_All//gi|224111952|ref|XP_002316034.1|//4.00E-64//GRAS family transcription factor [Populus trichocarpa] >gi|222865074|gb|EEF02205.1| GRAS family transcription factor [Populus trichocarpa]	Unigene31375_All//1.00E-11//AT3G50650| scarecrow-like transcription factor 7 (SCL7)	Unigene31375_All//7.00E-64//TC152674	GRAS			nr -
Unigene3138_All	2202	6.80	0.46	0.77	21.02	7.85	2.05	2.42	0.36	0.09	-3.88E+00	4.21E-62	Down	-3.13E+00	1.27E-49	Down	-1.42E+00	1.04E-72	Down	-3.36E+00	3.51E-185	Down	-2.75E+00	4.86E-20	Down	-4.74E+00	3.54E-32	Down	Unigene3138_All//gi|124360549|gb|AB353126.2|//5.00E-70//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene3138_All//6.00E-27//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene3138_All//0.00E+00//gi|18099285|gb|BM358539.1|BM358539				nr -
Unigene31381_All	571	0.82	0.71	0.65	0.35	0.30	0.32	2.00	1.46	0.42	-2.16E-01	8.17E-01		-3.37E-01	7.34E-01		-2.11E-01	8.59E-01		-1.42E-01	9.35E-01		-4.50E-01	4.44E-01		-2.26E+00	3.40E-04	Down	Unigene31381_All//gi|7406455|emb|CAB85557.1|//4.00E-26//3-phosphoinositide-dependent protein kinase-1 PDK1 [Arabidopsis thaliana]	Unigene31381_All//2.00E-27//AT5G04510| PDK1 (3'-PHOSPHOINOSITIDE-DEPENDENT PROTEIN KINASE 1); 3-phosphoinositide-dependent protein kinase/ kinase/ phosphoinositide binding / protein binding / protein kinase	Unigene31381_All//4.00E-30//TC148500			GO:0004674//GO:0005543//GO:0033674	nr -
Unigene31389_All	257	0.00	0.00	0.00	0.19	0.00	0.00	27.97	114.49	333.28	null	null		null	null		-7.60E+00	5.55E-01		-7.60E+00	6.35E-01		2.03E+00	3.27E-75	Up	3.57E+00	0.00E+00	Up	Unigene31389_All//gi|40218371|gb|AB83118.1|//6.00E-38//secretory laccase [Gossypium arboreum]	Unigene31389_All//1.00E-15//AT3G09220| LAC7 (laccase 7); laccase	Unigene31389_All//1.00E-83//TC137114		ko00910|Nitrogen metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr -
Unigene3139_All	454	0.00	0.22	0.23	0.88	0.76	0.20	7.92	4.23	3.86	7.80E+00	3.87E-01		7.87E+00	3.98E-01		-2.11E-01	8.25E-01		-2.14E+00	1.26E-01		-9.03E-01	1.84E-03		-1.04E+00	2.62E-04	Down	Unigene3139_All//gi|224129814|ref|XP_002328809.1|//4.00E-30//methionine s-methyltransferase [Populus trichocarpa] >gi|222839107|gb|EEE77458.1| methionine s-methyltransferase [Populus trichocarpa]	Unigene3139_All//1.00E-29//AT5G48810| MMT; S-adenosylmethionine-dependent methyltransferase	Unigene3139_All//2.00E-151//TC138718		ko00450|Selenoamino acid metabolism	GO:0006790//GO:0008757//GO:0048037	nr +
Unigene31392_All	364	3.16	0.00	2.05	0.00	0.19	0.37	0.00	0.00	0.00	-1.16E+01	9.91E-07	Down	-6.27E-01	3.56E-01		7.56E+00	6.09E-01		8.54E+00	3.11E-01		null	null		null	null									ESTscan +
Unigene31393_All	389	0.00	0.00	0.00	0.00	0.00	0.00	1.63	2.79	0.00	null	null		null	null		null	null		null	null		7.77E-01	1.94E-01		-1.07E+01	7.11E-05	Down	Unigene31393_All//gi|213959111|gb|ACJ54890.1|//2.00E-44//heat shock protein 70 [Oryza sativa Japonica Group]	Unigene31393_All//4.00E-45//AT5G02490| heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0000302//GO:0009642//GO:0010038//GO:0016020//GO:0019899//GO:0030312//GO:0032446//GO:0032559//GO:0043231//GO:0051707	nr -
Unigene31394_All	240	0.00	0.42	0.00	1.04	0.00	0.00	0.18	1.74	3.49	8.72E+00	3.87E-01		null	null		-1.00E+01	4.18E-02		-1.00E+01	7.33E-02		3.31E+00	2.00E-02		4.31E+00	4.10E-05	Up	Unigene31394_All//gi|147843354|emb|CAN82657.1|//6.00E-08//hypothetical protein [Vitis vinifera]		Unigene31394_All//3.00E-07//TC145278				nr +
Unigene3140_All	1108	3.78	3.75	5.24	8.86	11.22	8.93	18.28	6.15	13.91	-1.07E-02	9.87E-01		4.72E-01	7.12E-02		3.41E-01	3.42E-02		1.13E-02	9.51E-01		-1.57E+00	1.01E-36	Down	-3.94E-01	2.23E-04		Unigene3140_All//gi|224129814|ref|XP_002328809.1|//1.00E-147//methionine s-methyltransferase [Populus trichocarpa] >gi|222839107|gb|EEE77458.1| methionine s-methyltransferase [Populus trichocarpa]	Unigene3140_All//1.00E-146//AT5G48810| MMT; S-adenosylmethionine-dependent methyltransferase	Unigene3140_All//0.00E+00//TC138718		ko00450|Selenoamino acid metabolism		nr +
Unigene31402_All	237	1.32	9.41	3.15	0.63	1.45	1.33	8.03	17.81	17.99	2.83E+00	2.19E-07	Up	1.25E+00	1.54E-01		1.20E+00	4.26E-01		1.08E+00	4.76E-01		1.15E+00	2.00E-05	Up	1.16E+00	9.71E-06	Up								
Unigene31408_All	425	3.57	1.55	2.76	2.34	0.49	3.40	1.49	5.61	3.00	-1.20E+00	2.75E-02		-3.73E-01	5.08E-01		-2.27E+00	1.67E-03		5.37E-01	3.76E-01		1.91E+00	2.78E-06	Up	1.01E+00	5.22E-02		Unigene31408_All//gi|225434496|ref|XP_002278283.1|//5.00E-11//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene31408_All//3.00E-141//DW231746				nr -
Unigene31410_All	207	10.36	1.96	4.63	13.96	13.14	12.87	35.13	28.87	22.52	-2.40E+00	3.76E-06	Down	-1.16E+00	1.29E-02		-8.69E-02	8.21E-01		-1.17E-01	7.58E-01		-2.83E-01	1.71E-01		-6.42E-01	6.04E-04		Unigene31410_All//gi|3334320|sp|O22518.1|RSSA_SOYBN//1.00E-12//RecName: Full=40S ribosomal protein SA; AltName: Full=p40 >gi|2444420|gb|AAB82659.1| ribosome-associated protein p40 [Glycine max]	Unigene31410_All//2.00E-13//AT3G04770| RPSAb (40S ribosomal protein SA B); structural constituent of ribosome	Unigene31410_All//3.00E-111//TC171428		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935	nr -
Unigene31411_All	284	0.37	0.00	0.00	3.33	0.61	0.32	0.89	1.47	1.12	-8.53E+00	3.72E-01		-8.53E+00	3.93E-01		-2.46E+00	1.25E-03		-3.39E+00	3.17E-04	Down	7.20E-01	5.07E-01		3.29E-01	7.63E-01				Unigene31411_All//8.00E-08//TC148619				
Unigene31416_All	212	3.21	1.43	4.77	4.70	4.87	3.83	19.54	19.52	8.64	-1.16E+00	1.89E-01		5.73E-01	4.04E-01		5.23E-02	9.54E-01		-2.93E-01	6.89E-01		-2.00E-03	9.92E-01		-1.18E+00	9.73E-06	Down			Unigene31416_All//4.00E-92//TC179164				
Unigene31420_All	297	7.22	0.00	0.72	5.70	7.54	7.60	1.28	1.13	1.21	-1.28E-01	2.13E-12	Down	-3.33E+00	7.63E-08	Down	4.02E-01	3.92E-01		4.15E-01	3.80E-01		-1.87E-01	8.57E-01		-8.58E-02	9.43E-01								
Unigene31422_All	346	166.94	114.23	106.81	88.25	101.22	206.89	138.82	155.47	184.57	-5.48E-01	3.14E-15		-6.44E-01	2.46E-19		1.98E-01	3.40E-02		1.23E+00	2.96E-77	Up	1.63E-01	1.63E-02		4.11E-01	9.52E-13		Unigene31422_All//gi|222424262|dbj|BAH20088.1|//1.00E-55//AT3G58610 [Arabidopsis thaliana]	Unigene31422_All//4.00E-57//AT3G58610| ketol-acid reductoisomerase	Unigene31422_All//0.00E+00//gi|189092476|gb|FG548011.1|FG548011		ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis	GO:0005576//GO:0008652//GO:0009526//GO:0009532//GO:0010038//GO:0016616//GO:0030312//GO:0042802//GO:0046914//GO:0050661	nr +
Unigene31429_All	519	0.00	0.20	0.10	0.10	0.13	0.35	2.61	2.82	0.23	7.61E+00	3.87E-01		6.68E+00	6.36E-01		4.67E-01	9.58E-01		1.86E+00	4.58E-01		1.13E-01	8.23E-01		-3.50E+00	4.24E-07	Down	Unigene31429_All//gi|242048142|ref|XP_002461817.1|//6.00E-08//hypothetical protein SORBIDRAFT_02g008730 [Sorghum bicolor] >gi|241925194|gb|EER98338.1| hypothetical protein SORBIDRAFT_02g008730 [Sorghum bicolor]	Unigene31429_All//1.00E-05//AT3G25270| nucleic acid binding	Unigene31429_All//7.00E-90//DW498997				nr -
Unigene3143_All	2288	5.03	1.42	1.40	9.43	11.05	9.00	39.79	3.85	11.47	-1.83E+00	2.26E-21	Down	-1.85E+00	8.64E-21	Down	2.29E-01	3.98E-02		-6.67E-02	6.47E-01		-3.37E+00	0.00E+00	Down	-1.79E+00	8.56E-202	Down	Unigene3143_All//gi|133778842|gb|AB038761.1|//2.00E-36//At5g17160 [Arabidopsis thaliana]	Unigene3143_All//2.00E-35//AT5G17160| unknown protein	Unigene3143_All//0.00E+00//ES818024				nr -
Unigene31432_All	494	0.00	0.00	0.00	0.00	0.00	0.00	1.97	2.37	0.00	null	null		null	null		null	null		null	null		2.67E-01	6.28E-01		-1.09E+01	2.72E-07	Down	Unigene31432_All//gi|12580855|emb|CAC27136.1|//3.00E-77//40S ribosomal protein S2 [Picea abies]	Unigene31432_All//3.00E-77//AT3G57490| 40S ribosomal protein S2 (RPS2D)	Unigene31432_All//2.00E-16//TC156363		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015935	nr -
Unigene31437_All	778	0.07	0.65	0.14	0.19	0.58	0.00	2.88	0.48	0.15	3.27E+00	2.11E-02		1.02E+00	7.03E-01		1.58E+00	2.17E-01		-7.59E+00	2.33E-01		-2.57E+00	2.90E-08	Down	-4.23E+00	6.02E-13	Down	Unigene31437_All//gi|186511765|ref|NP_193161.2|//9.00E-07//structural constituent of ribosome [Arabidopsis thaliana]	Unigene31437_All//2.00E-08//AT4G14250| structural constituent of ribosome	Unigene31437_All//1.00E-27//gi|11204002|gb|BF272932.1|BF272932				nr -
Unigene3144_All	1875	1.56	0.62	1.14	3.32	2.44	2.14	2.25	3.63	4.31	-1.33E+00	4.32E-04	Down	-4.60E-01	2.37E-01		-4.43E-01	5.68E-02		-6.31E-01	7.04E-03		6.88E-01	5.79E-04		9.36E-01	2.37E-07		Unigene3144_All//gi|297794391|ref|XP_002865080.1|//3.00E-24//zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310915|gb|EFH41339.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3144_All//4.00E-23//AT5G66270| zinc finger (CCCH-type) family protein	Unigene3144_All//0.00E+00//TC151012	C3H			nr +
Unigene31440_All	208	0.00	3.17	1.54	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.25E-04	Up	1.06E+01	4.52E-02		null	null		null	null		null	null		null	null									
Unigene31441_All	254	14.42	22.34	20.75	15.10	11.66	14.94	15.31	19.25	6.90	6.32E-01	1.14E-02		5.26E-01	5.52E-02		-3.73E-01	2.48E-01		-1.59E-02	9.52E-01		3.30E-01	2.02E-01		-1.15E+00	2.84E-05	Down		Unigene31441_All//4.00E-05//AT5G47200| ATRAB1A; GTP binding	Unigene31441_All//1.00E-98//EX172329				ESTscan +
Unigene31444_All	480	0.00	3.48	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.54E-09	Up	1.10E+01	2.46E-05	Up	null	null		null	null		null	null		null	null		Unigene31444_All//sp|P13527|CP6A1_MUSDO//1.00E-15//Cytochrome P450 6A1 OS=Musca domestica GN=CYP6A1 PE=2 SV=1						swissprot +
Unigene31445_All	352	0.89	0.14	0.91	3.40	3.72	0.90	4.68	0.95	3.17	-2.63E+00	1.31E-01		2.55E-02	1.00E+00		1.30E-01	8.39E-01		-1.92E+00	4.14E-03		-2.30E+00	1.36E-05	Down	-5.64E-01	2.02E-01				Unigene31445_All//5.00E-136//TC155351				
Unigene31450_All	392	1.33	2.07	6.52	0.00	0.26	0.00	0.00	0.00	0.00	6.32E-01	4.02E-01		2.29E+00	1.74E-06	Up	8.04E+00	4.56E-01		null	null		null	null		null	null		Unigene31450_All//gi|30725678|gb|AF37861.1|//3.00E-41//At2g21080 [Arabidopsis thaliana]	Unigene31450_All//1.00E-42//AT2G21080| unknown protein				GO:0043231	nr +
Unigene31451_All	372	0.00	4.09	1.86	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.10E-08	Up	1.09E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene31451_All//sp|P62870|ELOB_RAT//3.00E-07//Transcription elongation factor B polypeptide 2 OS=Rattus norvegicus GN=Tceb2 PE=1 SV=1						swissprot -
Unigene31453_All	262	0.00	0.97	0.00	3.42	0.39	2.59	0.16	0.32	0.46	9.92E+00	7.86E-02		null	null		-3.12E+00	2.80E-04	Down	-4.05E-01	6.23E-01		9.83E-01	7.31E-01		1.50E+00	5.58E-01				Unigene31453_All//1.00E-98//gi|11200755|gb|BF269760.1|BF269760				
Unigene31454_All	434	0.00	33.86	11.66	0.23	0.00	0.00	0.00	0.00	0.00	1.50E+01	2.14E-84	Up	1.35E+01	3.83E-28	Up	-7.84E+00	3.13E-01		-7.84E+00	4.00E-01		null	null		null	null		Unigene31454_All//gi|195617898|gb|ACG30779.1|//7.00E-29//60S acidic ribosomal protein P1 [Zea mays]	Unigene31454_All//4.00E-17//AT4G00810| 60S acidic ribosomal protein P1 (RPP1B)	Unigene31454_All//1.00E-19//DW502089		ko03010|Ribosome	GO:0006412//GO:0030529	nr +
Unigene31456_All	363	0.00	2.23	3.08	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	9.38E-05	Up	1.16E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene31456_All//sp|O43639|NCK2_HUMAN//7.00E-20//Cytoplasmic protein NCK2 OS=Homo sapiens GN=NCK2 PE=1 SV=2						swissprot +
Unigene31458_All	279	0.00	0.00	0.00	0.18	0.25	3.24	0.00	0.90	1.00	null	null		null	null		4.67E-01	9.58E-01		4.18E+00	1.95E-04	Up	9.81E+00	4.31E-02		9.97E+00	2.43E-02								

Unigene31463_All	399	0.00	0.00	0.00	0.00	0.00	0.00	2.44	1.99	0.10	null	null		null	null		null	null		null	null		-2.92E-01	6.31E-01		-4.61E+00	3.32E-06	Down	Unigene31463_All//gi|297838641|ref|XP_002887202.1|//6.00E-11//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297333043|gb|EFH63461.1| expressed protein [Arabidopsis lyrata subsp. lyrata]				ko03040|Spliceosome		nr -
Unigene31464_All	349	0.00	0.00	0.15	110.76	53.97	28.99	3.76	1.68	0.00	null	null		7.25E+00	6.36E-01		-1.04E+00	8.47E-37	Down	-1.93E+00	2.18E-82	Down	-1.16E+00	2.87E-02		-1.19E+01	9.85E-10	Down			Unigene31464_All//6.00E-148//TC153771				
Unigene31467_All	348	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.46	null	null		null	null		null	null		null	null		1.10E+01	3.98E-05	Up	8.84E+00	1.40E-01		Unigene31467_All//gi|87280654|gb|AB036512.1|//9.00E-23//bacterial blight resistance protein XA26 [Oryza sativa Indica Group] >gi|90018761|gb|ABD84046.1| bacterial blight resistance protein XA26 [Oryza sativa Indica Group] >gi|90018763|gb|ABD84047.1| bacterial blight resistance protein XA26 [Oryza sativa Japonica Group]	Unigene31467_All//3.00E-23//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0016628//GO:0031224//GO:0032559	nr -
Unigene31468_All	347	0.45	0.00	0.77	0.14	1.09	0.00	0.37	1.81	2.99	-8.82E+00	2.16E-01		7.63E-01	6.44E-01		2.93E+00	8.16E-02		-7.17E+00	6.35E-01		2.31E+00	1.46E-02		3.03E+00	6.50E-05	Up	Unigene31468_All//gi|225450776|ref|XP_002283736.1|//5.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene31468_All//6.00E-06//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase					nr -
Unigene31469_All	286	0.37	3.54	0.00	0.35	0.00	0.16	0.89	0.73	1.67	3.28E+00	3.79E-04	Up	-8.52E+00	3.93E-01		-8.44E+00	3.13E-01		-1.14E+00	6.76E-01		-2.80E-01	8.29E-01		9.14E-01	3.38E-01			Unigene31469_All//3.00E-26//TC160818				
Unigene31470_All	544	0.00	0.00	0.00	0.00	0.00	0.00	3.11	0.38	0.00	null	null		null	null		null	null		null	null		-3.02E+00	2.08E-07	Down	-1.16E+01	1.70E-12	Down	Unigene31470_All//gi|145344436|ref|XP_001416738.1|//1.00E-59//Peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Ostreococcus lucimarinus CCE9901] >gi|144576964|gb|ABO95031.1| Peptidyl-prolyl cis-trans isomerase, cyclophilin-type [Ostreococcus lucimarinus CCE9901]	Unigene31470_All//7.00E-57//AT2G29960| CYP5 (CYCLOPHILIN 5); peptidyl-prolyl cis-trans isomerase	Unigene31470_All//4.00E-11//DW502183			GO:0016859//GO:0044267	nr -
Unigene31476_All	303	3.11	1.00	0.18	9.54	8.41	2.83	2.23	1.52	0.92	-1.63E+00	3.13E-02		-4.14E+00	2.90E-04	Down	-1.81E-01	6.41E-01		-1.75E+00	6.75E-06	Down	-5.57E-01	4.89E-01		-1.28E+00	9.48E-02								
Unigene31479_All	242	0.00	0.00	0.00	0.00	0.00	0.00	2.80	2.76	0.00	null	null		null	null		null	null		null	null		-1.66E-02	1.02E+00		-1.14E+01	3.56E-05	Down	Unigene31479_All//gi|226507767|ref|NP_001147360.1|//1.00E-28//40S ribosomal protein S4 [Zea mays] >gi|195610502|gb|ACG27081.1| 40S ribosomal protein S4 [Zea mays]	Unigene31479_All//7.00E-29//AT5G07090| 40S ribosomal protein S4 (RPS4B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0031981//GO:0042221	nr -
Unigene3148_All	3248	0.68	2.23	0.52	1.99	2.77	5.44	7.71	28.58	38.96	1.72E+00	1.33E-12	Up	-3.67E-01	4.12E-01		4.73E-01	1.18E-02		1.45E+00	8.78E-25	Up	1.89E+00	2.45E-214	Up	2.34E+00	0.00E+00	Up	Unigene3148_All//gi|297596153|ref|NP_001042093.2|//1.00E-152//Os01g0161300 [Oryza sativa Japonica Group] >gi|255672898|dbj|BAF04007.2| Os01g0161300 [Oryza sativa Japonica Group]	Unigene3148_All//3.00E-134//AT2G15080| AtRLP19 (Receptor Like Protein 19); kinase/ protein binding			ko04626|Plant-pathogen interaction	GO:0003824	nr +
Unigene31483_All	334	0.31	0.46	0.00	2.54	3.20	0.14	0.00	0.00	0.00	5.39E-01	7.79E-01		-8.29E+00	3.93E-01		3.34E-01	6.42E-01		-4.23E+00	2.18E-04	Down	null	null		null	null		Unigene31483_All//gi|15231538|ref|NP_189261.1|//8.00E-21//CYP71B34; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|13878379|sp|Q9LIP6.1|C71BV_ARATH RecName: Full=Cytochrome P450 71B34 >gi|9294288|dbj|BAB02190.1| cytochrome P450 [Arabidopsis thaliana]	Unigene31483_All//4.00E-20//AT3G26300| CYP71B34; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506	nr +
Unigene31487_All	394	0.53	0.77	0.27	0.25	0.00	0.00	0.75	3.50	2.53	5.39E-01	6.71E-01		-9.75E-01	6.21E-01		-7.98E+00	3.13E-01		-7.98E+00	4.00E-01		2.22E+00	1.31E-04	Up	1.75E+00	6.57E-03		Unigene31487_All//gi|15233416|ref|NP_193816.1|//4.00E-56//FAD-binding domain-containing protein [Arabidopsis thaliana] >gi|5262224|emb|CAB45850.1| reticuline oxidase-like protein [Arabidopsis thaliana] >gi|7268880|emb|CAB79084.1| reticuline oxidase-like protein [Arabidopsis thaliana] >gi|222424693|dbj|BAH20300.1| AT4G20840 [Arabidopsis thaliana]	Unigene31487_All//2.00E-37//AT4G20840| FAD-binding domain-containing protein	Unigene31487_All//2.00E-37//C0108368			GO:0005576//GO:0005618//GO:0006950//GO:0008152//GO:0016020//GO:0030054//GO:0043231//GO:0046993	nr -
Unigene31492_All	228	0.00	12.89	3.50	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.01E-16	Up	1.18E+01	1.72E-04	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene315_All	2304	0.93	2.90	2.13	2.38	2.15	1.74	3.87	2.10	1.26	1.64E+00	5.68E-11	Up	1.19E+00	3.77E-05	Up	-1.44E-01	6.04E-01		-4.47E-01	8.84E-02		-8.80E-01	4.11E-07		-1.62E+00	7.72E-18	Down	Unigene315_All//gi|18398260|ref|NP_565399.1|//1.00E-148//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|133778824|gb|ABO38752.1| At2g16940 [Arabidopsis thaliana]	Unigene315_All//5.00E-142//AT2G16940| RNA recognition motif (RRM)-containing protein	Unigene315_All//0.00E+00//gi|78342818|gb|DT563092.1|DT563092				nr +
Unigene3150_All	1481	7.10	10.54	1.80	2.76	3.58	6.31	2.91	2.85	3.44	5.70E-01	5.36E-05		-1.98E+00	7.78E-21	Down	3.77E-01	1.63E-01		1.19E+00	4.13E-10	Up	-3.08E-02	9.30E-01		2.42E-01	3.35E-01		Unigene3150_All//gi|297789410|ref|XP_002862675.1|//1.00E-156//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308337|gb|EFH38933.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3150_All//6.00E-139//AT1G66780| MATE efflux family protein	Unigene3150_All//0.00E+00//TC140612				nr +
Unigene31502_All	453	0.00	2.80	0.94	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.86E-07	Up	9.88E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene31502_All//gi|188496900|dbj|BAG32349.1|//7.00E-06//glucan binding protein-1 [Actinophrys sol]						nr -
Unigene31507_All	285	0.37	0.00	1.87	2.45	2.42	0.00	0.15	0.15	1.54	-8.52E+00	3.72E-01		2.35E+00	5.87E-02		-1.81E-02	9.61E-01		-1.13E+01	1.96E-04	Down	-1.66E-02	1.00E+00		3.37E+00	1.26E-02		Unigene31507_All//gi|224112233|ref|XP_002332812.1|//4.00E-13//leucine rich repeat family protein with ABC domain [Populus trichocarpa] >gi|222833206|gb|EEE71683.1| leucine rich repeat family protein with ABC domain [Populus trichocarpa]	Unigene31507_All//2.00E-65//AT2G25470| AtRLP21 (Receptor Like Protein 21); protein binding					nr -
Unigene3151_All	987	39.92	35.37	38.90	47.59	37.58	42.37	24.63	14.99	8.44	-1.74E-01	5.31E-02		-3.73E-02	7.06E-01		-3.41E-01	1.80E-06		-1.68E-01	4.23E-02		-7.16E-01	7.18E-13		-1.55E+00	3.42E-44	Down			Unigene3151_All//5.00E-43//TC174859				
Unigene31511_All	285	0.37	2.84	4.11	7.69	21.39	3.49	5.49	4.55	1.96	2.95E+00	3.29E-03		3.48E+00	1.09E-04	Up	1.48E+00	8.39E-10	Up	-1.14E+00	8.68E-03		-2.72E-01	6.13E-01		-1.49E+00	1.74E-03		Unigene31511_All//gi|15234987|ref|NP_192765.1|//2.00E-12//wound-responsive family protein [Arabidopsis thaliana] >gi|3695408|gb|AAC62808.1| contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi|4538956|emb|CAB39780.1| probable wound-induced protein [Arabidopsis thaliana] >gi|7267724|emb|CAB78150.1| probable wound-induced protein [Arabidopsis thaliana] >gi|21553934|gb|AAM63015.1| probable wound-induced protein [Arabidopsis thaliana] >gi|90962948|gb|ABE02398.1| At4g10270 [Arabidopsis thaliana]	Unigene31511_All//8.00E-14//AT4G10270| wound-responsive family protein	Unigene31511_All//1.00E-123//TC145255				nr +
Unigene31515_All	347	0.00	0.29	0.31	0.43	0.50	0.78	3.53	1.32	0.69	8.19E+00	3.86E-01		8.26E+00	3.98E-01		2.04E-01	9.50E-01		8.59E-01	6.31E-01		-1.42E+00	1.21E-02		-2.36E+00	1.22E-04	Down							
Unigene31519_All	560	0.00	0.00	0.00	0.00	0.00	0.00	1.89	3.58	0.00	null	null		null	null		null	null		null	null		9.25E-01	2.36E-02		-1.09E+01	6.72E-08	Down	Unigene31519_All//gi|92870918|gb|ABE80118.1|//6.00E-35//Ribosomal protein L24E [Medicago truncatula]	Unigene31519_All//1.00E-25//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome			ko03010|Ribosome	GO:0009536//GO:0009755//GO:0015934//GO:0016020//GO:0031981//GO:0048438	nr -
Unigene3152_All	1777	30.59	15.83	16.99	24.70	22.30	25.82	64.60	26.88	24.66	-9.51E-01	1.79E-36		-8.48E-01	4.26E-29		-1.47E-01	8.34E-02		6.43E-02	5.19E-01		-1.26E+00	1.49E-147	Down	-1.39E+00	2.59E-175	Down	Unigene3152_All//gi|18418270|ref|NP_567934.1|//0.00E+00//AGD2 (ABERRANT GROWTH AND DEATH 2); L,L-diaminopimelate aminotransferase/ transaminase [Arabidopsis thaliana] >gi|75163801|sp|Q93ZN9.1|DAPAT_ARATH RecName: Full=LL-diaminopimelate aminotransferase, chloroplastic; Short=LL-DAP-aminotransferase; Short=DAP-aminotransferase; Short=DAP-AT; Short=AtDAP-AT; AltName: Full=Protein ABERRANT GROWTH AND DEATH 2; Flags: Precursor >gi|15912291|gb|AAL08279.1| AT4g33680/T16L1_170 [Arabidopsis thaliana] >gi|41323503|gb|AAR99909.1| aminotransferase AGD2 [Arabidopsis thaliana]	Unigene3152_All//0.00E+00//AT4G33680| AGD2 (ABERRANT GROWTH AND DEATH 2); L,L-diaminopimelate aminotransferase/ transaminase	Unigene3152_All//0.00E+00//TC134605		ko00300|Lysine biosynthesis	GO:0005083//GO:0008483//GO:0009085//GO:0009532//GO:0009627//GO:0032012//GO:0046914//GO:0048037	nr +
Unigene31521_All	455	0.00	0.00	0.12	0.55	0.91	0.00	910.09	331.15	149.64	null	null		6.87E+00	6.36E-01		7.30E-01	5.86E-01		-9.10E+00	7.33E-02		-1.46E+00	0.00E+00	Down	-2.60E+00	0.00E+00	Down	Unigene31521_All//gi|71534908|gb|AAZ32858.1|//3.00E-37//BURP domain-containing protein [Medicago sativa]	Unigene31521_All//5.00E-25//AT1G49320| BURP domain-containing protein	Unigene31521_All//1.00E-07//gi|78329288|gb|DT549562.1|DT549562				nr +
Unigene31522_All	238	0.00	3.41	0.90	0.42	1.30	0.19	1.60	1.40	0.84	1.17E+01	9.38E-05	Up	9.81E+00	1.41E-01		1.64E+00	3.21E-01		-1.14E+00	6.76E-01		-1.87E-01	8.57E-01		-9.34E-01	3.79E-01			Unigene31522_All//1.00E-92//C0091785				
Unigene31528_All	482	0.00	6.20	6.19	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	5.19E-17	Up	1.26E+01	1.77E-16	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene31529_All	244	13.51	2.70	4.58	2.04	2.12	2.04	0.00	0.34	0.00	-2.32E+00	9.48E-09	Down	-1.56E+00	3.55E-05	Down	5.23E-02	9.80E-01		-3.90E-03	9.87E-01		8.42E+00	4.01E-01		null	null			Unigene31529_All//3.00E-07//TC141372				
Unigene3153_All	1552	19.05	11.39	16.61	5.68	6.39	7.16	5.09	1.89	2.49	-7.41E-01	1.86E-13		-1.98E-01	7.33E-02		1.70E-01	4.24E-01		3.34E-01	6.19E-02		-1.43E+00	4.89E-13	Down	-1.03E+00	2.17E-08	Down	Unigene3153_All//gi|89000921|gb|AB059050.1|//1.00E-109//At2g04360 [Arabidopsis thaliana]	Unigene3153_All//1.00E-102//AT2G04360| unknown protein	Unigene3153_All//0.00E+00//TC173461			GO:0043231	nr +
Unigene31533_All	299	0.35	0.00	0.00	2.33	0.12	0.76	0.85	0.28	0.40	-8.45E+00	3.72E-01		-8.45E+00	3.93E-01		-4.34E+00	2.80E-04	Down	-1.63E+00	7.45E-02		-1.60E+00	3.10E-01		-1.09E+00	4.28E-01								
Unigene31534_All	386	0.00	2.49	1.79	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.38E-05	Up	1.08E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene31534_All//sp|Q28GH3|SAE2_XENTR//5.00E-07//SUMO-activating enzyme subunit 2 OS=Xenopus tropicalis GN=uba2 PE=2 SV=1						swissprot +
Unigene31540_All	874	0.00	41.63	19.44	0.00	0.00	0.00	0.00	0.00	0.00	1.53E+01	6.40E-210	Up	1.42E+01	7.28E-96	Up	null	null		null	null		null	null		null	null		Unigene31540_All//gi|74325193|ref|YP_316613.1|//2.00E-22//ATPase subunit 9 [Thalassiosira pseudonana] >gi|74100259|gb|AAZ99420.1| ATPase subunit 9 [Thalassiosira pseudonana]		Unigene31540_All//1.00E-18//TC166849		ko00190|Oxidative phosphorylation	GO:0003824//GO:0005740//GO:0006754//GO:0006818//GO:0015078//GO:0031224//GO:0032559//GO:0033177	nr +

Unigene31542_All	384	0.00	0.00	0.00	0.00	0.09	0.00	0.66	8.82	1.04	null	null		null	null		6.49E+00	8.30E-01		null	null		3.74E+00	5.65E-17	Up	6.51E-01	5.44E-01		Unigene31542_All//gi|71534999|gb|AZ32897.1|/.3.00E-28//monooxygenase [Medicago sativa]	Unigene31542_All//4.00E-28//AT4G38540| monooxygenase, putative (MO2)	Unigene31542_All//8.00E-58//DW488507				nr +
Unigene31544_All	291	0.00	0.35	1.65	3.77	0.36	0.78	0.00	0.00	0.00	8.44E+00	3.86E-01		1.07E+01	7.48E-03		-3.41E+00	1.67E-05	Down	-2.28E+00	1.97E-03		null	null		null	null					Unigene31544_All//7.00E-27//FL576983				
Unigene31545_All	330	0.16	1.38	0.32	0.45	1.04	0.41	1.41	0.89	4.83	3.12E+00	3.58E-02		1.03E+00	7.03E-01		1.20E+00	4.26E-01		-1.42E-01	9.43E-01		-6.69E-01	5.09E-01		1.78E+00	3.04E-04	Up			Unigene31545_All//4.00E-07//gi|13248156|gb|BF276042.2|BF276042				
Unigene31550_All	459	0.34	0.22	0.23	0.11	2.25	0.98	0.00	0.00	0.00	-6.31E-01	7.27E-01		-5.60E-01	7.76E-01		4.37E+00	2.73E-05	Up	3.18E+00	3.79E-02		null	null		null	null		Unigene31550_All//gi|22331699|ref|NP_190436.2|//6.00E-50//XH/XS domain-containing protein / XS zinc finger domain-containing protein [Arabidopsis thaliana] >gi|42572615|ref|NP_974403.1| XH/XS domain-containing protein / XS zinc finger domain-containing protein [Arabidopsis thaliana]	Unigene31550_All//1.00E-47//AT3G48670| XH/XS domain-containing protein / XS zinc finger domain-containing protein	Unigene31550_All//0.00E+00//gi|78344398|gb|DT564672.1|DT564672			GO:0043231	nr -
Unigene31553_All	368	0.14	0.00	3.04	0.41	1.03	0.00	0.00	0.00	0.00	-7.15E+00	6.12E-01		4.42E+00	3.51E-05	Up	1.34E+00	3.40E-01		-8.67E+00	2.33E-01		null	null		null	null		Unigene31553_All//sp|P0A0V9|CTRA_NEISE//2.00E-12//Capsule polysaccharide export outer membrane protein ctrA OS=Neisseria meningitidis GN=ctrA PE=3 SV=1							swissprot +
Unigene31561_All	332	0.00	290.59	192.63	0.00	0.00	2.58	0.00	0.00	0.00	1.81E+01	0.00E+00	Up	1.76E+01	0.00E+00	Up	null	null		1.13E+01	3.79E-05	Up	null	null		null	null									
Unigene31562_All	257	0.00	0.00	0.00	0.00	0.27	0.18	33.73	12.69	4.03	null	null		null	null		8.07E+00	6.09E-01		7.46E+00	6.96E-01		-1.41E+00	6.94E-14	Down	-3.06E+00	3.44E-37	Down	Unigene31562_All//gi|37359170|gb|AAL05954.1|//6.00E-06//agglutinin [Amaranthus caudatus]							nr +
Unigene31574_All	466	0.11	0.76	0.00	0.75	0.74	0.48	1.45	2.33	7.10	2.76E+00	9.59E-02		-6.81E+00	6.24E-01		-1.80E-02	9.58E-01		-6.27E-01	6.21E-01		6.84E-01	2.51E-01		2.29E+00	1.12E-10	Up			Unigene31574_All//0.00E+00//TC138158				
Unigene31576_All	282	0.00	3.23	1.70	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.62E-05	Up	1.07E+01	7.48E-03		null	null		null	null		null	null		null	null									
Unigene31579_All	1466	0.00	0.00	0.00	0.07	0.00	0.15	0.72	0.88	5.76	null	null		null	null		-6.09E+00	3.13E-01		1.18E+00	5.49E-01		2.94E-01	6.23E-01		3.00E+00	7.17E-35	Up	Unigene31579_All//gi|75326590|sp|Q76312.1|PDR1_TOBAC//1.00E-159//RecName: Full=Pleiotropic drug resistance protein 1; AltName: Full=NtPDR1 >gi|41052472|dbj|BAD07483.1| PDR-type ABC transporter 1 [Nicotiana tabacum]	Unigene31579_All//1.00E-135//AT1G59870| PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	Unigene31579_All//8.00E-55//DF464626		ko02010|ABC transporters	GO:0017111//GO:0032559//GO:0044464	nr -
Unigene31582_All	353	0.00	0.00	0.00	0.00	0.00	0.00	1.44	0.00	3.61	null	null		null	null		null	null		null	null		-1.05E+01	8.89E-04	Down	1.33E+00	1.23E-02		Unigene31582_All//gi|224123518|ref|XP_002319099.1|//1.00E-22//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222857475|gb|EEE95022.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene31582_All//1.00E-10//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene31582_All//1.00E-13//CO091061	AP2-EREBP		GO:0000160//GO:0003676//GO:0006350//GO:0006950//GO:0010468//GO:0023033	nr -
Unigene31583_All	288	2.36	1.06	1.85	3.29	2.15	1.88	2.79	0.29	2.49	-1.16E+00	1.89E-01		-3.53E-01	6.64E-01		-6.11E-01	3.90E-01		-8.04E-01	2.77E-01		-3.26E+00	4.48E-04	Down	-1.64E-01	7.94E-01				Unigene31583_All//3.00E-07//TC133555				
Unigene31589_All	262	4.59	7.93	4.06	1.90	1.84	0.52	6.46	24.57	1.06	7.88E-01	7.72E-02		-1.76E-01	7.67E-01		-4.72E-02	9.49E-01		-1.88E+00	1.08E-01		1.93E+00	6.38E-16	Up	-2.60E+00	9.91E-07	Down			Unigene31589_All//1.00E-80//TC135423				
Unigene3159_All	2233	113.59	180.80	160.11	42.68	42.41	59.18	24.77	36.44	55.31	6.71E-01	5.54E-146		4.95E-01	4.18E-73		-9.10E-03	8.96E-01		4.72E-01	9.53E-28		5.57E-01	1.42E-26		1.16E+00	4.35E-141	Up	Unigene3159_All//gi|15234447|ref|NP_192386.1|//0.00E+00//ATABC1 (ATP BINDING CASSETTE PROTEIN 1); ATPase, coupled to transmembrane movement of substances / protein binding / transporter [Arabidopsis thaliana] >gi|75216473|sp|Q9ZS97.1|AB81_ARATH RecName: Full=UPF0051 protein ABC18, chloroplastic; AltName: Full=ABC transporter I family member 8; Short=ABC transporter ABC1.8; Short=AtABC18; AltName: Full=Non-intrinsic ABC protein 1; Short=Protein ABC1; AltName: Full=Protein LONG AFTER FAR-RED 6; AltName: Full=Plastid sufB-like protein; Flags: Precursor >gi|4115931|gb|AAD03441.1| contains similarity to Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana] >gi|15529143|gb|AAK97666.1| AT4g04770/T4B21_16 [Arabidopsis thaliana] >gi|15912265|gb|AAL08266.1| AT4g04770/T4B21_16 [Arabidopsis thaliana] >gi|22655482|gb|AAM98333.1|	Unigene3159_All//0.00E+00//AT4G04770| ATABC1 (ATP BINDING CASSETTE PROTEIN 1); ATPase, coupled to transmembrane movement of substances / protein binding / transporter	Unigene3159_All//0.00E+00//TC138009			GO:0005743//GO:0009536//GO:0009639//GO:0015405//GO:0030005//GO:0031163//GO:0032559//GO:0043623	nr -
Unigene31590_All	598	1.57	0.17	3.38	0.50	1.44	0.30	0.07	0.00	0.00	-3.22E+00	6.77E-04	Down	1.10E+00	2.17E-02		1.53E+00	5.80E-02		-7.26E-01	6.39E-01		-6.14E+00	6.57E-01		-6.14E+00	6.12E-01									
Unigene31593_All	349	8.40	79.85	8.39	15.56	20.03	18.12	29.92	46.71	110.50	3.25E+00	3.90E-98	Up	-6.00E-04	9.99E-01		3.65E-01	1.11E-01		2.20E-01	4.11E-01		6.42E-01	1.77E-07		1.88E+00	8.61E-91	Up			Unigene31593_All//0.00E+00//gi|109837944|gb|DW236505.1|DW236505				
Unigene31595_All	744	0.00	0.00	0.00	0.20	0.56	0.30	7.96	2.02	0.43	null	null		null	null		1.47E+00	2.79E-01		5.95E-01	7.21E-01		-1.98E+00	3.38E-15	Down	-4.22E+00	3.24E-33	Down	Unigene31595_All//gi|297835708|ref|XP_002885736.1|//1.00E-49//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331576|gb|EFH61995.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene31595_All//6.00E-42//AT2G04100| MATE efflux family protein	Unigene31595_All//0.00E+00//TC162411			GO:0006810//GO:0015291//GO:0044464	nr +
Unigene31596_All	217	0.00	4.67	2.45	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.26E-06	Up	1.13E+01	4.04E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene31597_All	216	0.73	0.00	5.18	1.38	0.32	0.42	0.00	0.00	0.00	-9.51E+00	2.16E-01		2.83E+00	7.34E-04	Up	-2.12E+00	1.65E-01		-1.73E+00	2.89E-01		null	null		null	null									
Unigene31598_All	242	0.00	3.14	1.98	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.77E-04	Up	1.10E+01	7.48E-03		null	null		null	null		null	null		null	null		Unigene31598_All//gi|2417401 96|gb|AC58620.1|//1.00E-38//ubiquitin 10.2 [Brassica napus]	Unigene31598_All//5.00E-40//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene31598_All//3.00E-41//BF277514			GO:0044424	nr +
Unigene3160_All	2383	3.14	2.30	2.06	9.62	6.49	6.75	11.67	6.44	4.31	-4.51E-01	3.64E-02		-6.11E-01	5.97E-03		-5.68E-01	5.53E-08		-5.11E-01	4.03E-06		-8.59E-01	1.12E-19		-1.44E+00	2.57E-45	Down	Unigene3160_All//0.00E+00//AT1G16970| KU70 (ARABIDOPSIS THALIANA KU70 HOMOLOGO); double-stranded DNA binding / protein binding	Unigene3160_All//0.00E+00//TC154188		ko03450|Non-homologous end-joining	GO:0000726//GO:0003678//GO:0043566//GO:0044428	nr -
Unigene31600_All	338	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.85	1.53	null	null		null	null		null	null		null	null		1.09E+01	1.47E-04	Up	1.06E+01	6.13E-04	Up			Unigene31600_All//2.00E-18//TC149394				
Unigene31605_All	340	0.00	0.00	0.00	1.90	0.81	0.00	1.24	2.58	3.75	null	null		null	null		-1.23E+00	1.60E-01		-1.09E+01	3.90E-04	Down	1.05E+00	1.23E-01		1.59E+00	3.57E-03									
Unigene3161_All	1521	3.89	4.36	6.27	3.60	1.83	6.35	11.56	32.18	20.01	1.67E-01	5.01E-01		6.89E-01	3.47E-04		-9.74E-01	3.80E-05		8.19E-01	6.56E-06		1.48E+00	7.36E-80	Up	7.91E-01	3.38E-19		Unigene3161_All//gi|407057|emb|CAA81443.1|//1.00E-159//protein kinase [Mesembryanthemum crystallinum]	Unigene3161_All//6.00E-140//AT1G78290| serine/threonine protein kinase, putative	Unigene3161_All//3.00E-79//TC159504				nr +
Unigene31611_All	414	0.13	0.98	2.32	0.00	0.83	0.22	0.00	0.00	0.00	2.95E+00	5.91E-02		4.20E+00	2.16E-04	Up	9.70E+00	3.01E-02		7.77E+00	4.76E-01		null	null		null	null		Unigene31611_All//gi|194476714|ref|YP_002048893.1|//5.00E-18//DNA polymerase III subunit alpha [Paulinella chromatophora] >gi|171191721|gb|ACB42683.1| DNA polymerase III subunit alpha [Paulinella chromatophora]							nr -
Unigene31612_All	233	323.81	207.90	136.21	415.19	302.08	466.56	970.99	622.27	311.01	-6.39E-01	1.06E-25		-1.25E+00	1.85E-75	Down	-4.59E-01	6.69E-22		1.68E-01	7.75E-04		-6.42E-01	3.66E-93		-1.64E+00	0.00E+00	Down	Unigene31612_All//gi|25992539|gb|AAN77149.1|//1.00E-37//fiber protein Fb9 [Gossypium barbadense]	Unigene31612_All//4.00E-38//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Unigene31612_All//5.00E-129//BP272339		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0006970//GO:0009408//GO:0009791//GO:0016020//GO:0030312//GO:0031647//GO:0031981//GO:0032559//GO:0044267//GO:0044444//GO:0048827//GO:0051592	nr +
Unigene31613_All	759	0.14	0.40	0.00	0.39	0.32	0.24	0.72	0.39	18.69	1.54E+00	3.23E-01		-7.11E+00	3.93E-01		-3.10E-01	8.20E-01		-7.27E-01	6.39E-01		-9.10E-01	3.19E-01		4.69E+00	1.74E-82	Up	Unigene31613_All//gi|23328857|ref|NP_680734.1|//2.00E-08//END04 (endonuclease 4); T/G mismatch-specific endonuclease/ endonuclease/ nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease [Arabidopsis thaliana]	Unigene31613_All//9.00E-10//AT4G21585| END04 (endonuclease 4); T/G mismatch-specific endonuclease/ endonuclease/ nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease	Unigene31613_All//1.00E-45//ES816027				nr -
Unigene31614_All	983	0.11	0.62	0.33	0.46	0.46	0.96	0.43	0.21	2.67	2.54E+00	2.46E-02		1.61E+00	3.05E-01		-2.20E-03	9.69E-01		1.08E+00	1.48E-01		-1.02E+00	3.50E-01		2.64E+00	5.10E-10	Up	Unigene31614_All//gi|18265373|dbj|BAB84015.1|//3.00E-43//polyprotein [Arabidopsis thaliana]	Unigene31614_All//6.00E-15//AT4G23160| protein kinase family protein	Unigene31614_All//7.00E-36//AI726870				nr -
Unigene31619_All	289	0.18	7.54	2.21	0.00	1.31	0.47	0.00	0.14	0.00	5.38E+00	4.42E-11	Up	3.61E+00	6.97E-03		1.04E+01	1.96E-02		8.87E+00	3.11E-01		7.18E+00	6.34E-01		null	null									
Unigene31621_All	348	170.19	372.89	231.21	100.92	107.86	218.16	231.57	248.13	150.65	1.13E+00	6.44E-114	Up	4.42E-01	8.38E-14		9.60E-02	3.56E-01		1.11E+00	6.06E-70	Up	9.97E-02	7.35E-02		-6.20E-01	1.19E-32		Unigene31621_All//gi|11602749|emb|CAC18557.1|//6.00E-12//early nodulin END18 [Vicia faba]	Unigene31621_All//2.00E-12//AT3G03270| universal stress protein (USP) family protein / early nodulin END18 family protein	Unigene31621_All//0.00E+00//gi|21101255|gb|BQ413568.1|BQ413568			GO:0050896	nr -
Unigene31623_All	593	0.00	48.88	14.91	0.00	0.12	0.00	0.00	0.00	0.00	1.56E+01	4.44E-167	Up	1.39E+01	1.56E-49	Up	6.86E+00	6.09E-01		null	null		null	null		null	null		Unigene31623_All//gi|255593650|ref|XP_002535920.1|//2.00E-08//alpha-amylase, putative [Ricinus communis] >gi|223521525|gb|EEF26463.1| alpha-amylase, putative [Ricinus communis]							nr -
Unigene31624_All	325	0.00	2.81	6.39	0.00	3.71	0.42	0.00	0.00	0.00	1.15E+01	2.62E-05	Up	1.26E+01	1.92E-11	Up	1.19E+01	1.95E-07	Up	8.70E+00	3.11E-01		null	null		null	null		Unigene31624_All//gi|49147195|ref|YP_025788.1|//9.00E-18//ATP synthase F0 subunit 6 [Pseudendoclonium akinetum] >gi|33439210|gb|AAQ18747.1| ATP synthase F0 subunit 6 [Pseudendoclonium akinetum]	Unigene31624_All//4.00E-05//ATMG00410| ATPase subunit 6			ko00190|Oxidative phosphorylation	GO:0006754//GO:0015992//GO:0016020//GO:0044424	nr +
Unigene31625_All	298	0.88	1.19	0.00	0.33	0.35	0.76	0.43	3.79	2.41	4.39E-01	7.01E-01		-9.78E+00	8.57E-02		5.25E-02	9.67E-01		1.18E+00	5.49E-01		3.15E+00	2.58E-05	Up	2.50E+00	4.03E-03				Unigene31625_All//2.00E-79//TC158360				
Unigene3163_All	1915	3.91	8.41	4.34	7.80	7.14	4.48	7.53	10.08	10.94	1.11E+00	2.78E-14	Up	1.51E-01	5.11E-01		-1.29E-01	4.55E-01		-8.00E-01	1.50E-08		4.22E-01	1.71E-04		5.40E-01	2.66E-07		Unigene3163_All//gi|30682162|ref|NP_192993.2|//1.00E-106//F-box family protein [Arabidopsis thaliana] >gi|145333023|ref|NP_001078377.1| F-box family protein [Arabidopsis thaliana] >gi|142989747|sp|Q9SU30.2|FB233_ARATH RecName: Full=F-box protein At4g12560	Unigene3163_All//2.00E-107//AT4G12560| F-box family protein	Unigene3163_All//0.00E+00//TC149560				nr +
Unigene31630_All	274	42.01	89.50	30.90	47.81	64.72	98.73	21.76	30.81	19.19	1.09E+00	7.07E-21	Up	-4.43E-01	1.19E-02		4.37E-01	4.79E-04		1.05E+00	6.74E-23	Up	5.02E-01	4.88E-03		-1.81E-01	4.31E-01				Unigene31630_All//5.00E-77//ES823143				
Unigene31633_All	274	0.00	0.00	0.00	0.00	1.38	0.66	0.15	0.46	2.91	null	null		null	null		1.04E+01	1.96E-02		9.36E+00	1.94E-01		1.57E+00	5.45E-01		4.24E+00	7.42E-05	Up			Unigene31633_All//3.00E-07//ES848643				
Unigene31637_All	409	0.00	0.00	0.00	0.00	0.00	0.00	2.79	1.64	0.00	null	null		null	null		null	null		null	null		-7.72E-01	1.81E-01		-1.14E+01	1.65E-08	Down	Unigene31637_All//gi|48596903|dbj|BAD22764.1|//3.00E-54//ribosomal protein [Bromus inermis]	Unigene31637_All//3.00E-28//AT4G16720| 60S ribosomal protein L15 (RPL15A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene3164_All	1098	138.57	66.54	103.69	99.36	111.96	93.99	109.71	49.33	50.65	-1.06E+00	2.90E-120	Down	-4.18E-01	4.06E-23		1.72E-01	1.05E-04		-8.01E-02	1.62E-01		-1.15E+00	8.37E-134	Down	-1.12E+00	2.39E-130	Down	Unigene3164_All//gi|1360725|emb|CAA87068.1|//2.00E-45//non-photosynthetic ferredoxin [Citrus sinensis]	Unigene3164_All//5.00E-42//AT2G27510| ATFD3 (ferredoxin 3); 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding	Unigene3164_All//0.00E+00//TC134013		ko00195|Photosynthesis	GO:0006091//GO:0043169//GO:0051536	nr +
Unigene31644_All	386	0.00	0.26	0.00	0.26	0.27	0.70	1.97	0.22	2.27	8.04E+00	3.86E-01		null	null		5.21E-02	9.67E-01		1.44E+00	4.09E-01		-3.19E+00	7.92E-04	Down	2.04E-01	7.47E-01									

Unigene31646_All	296	0.35	3.42	3.78	2.02	4.54	1.68	0.86	0.28	0.81	3.28E+00	3.79E-04	Up	3.42E+00	1.92E-04	Up	1.17E+00	4.76E-02		-2.67E-01	7.57E-01		-1.60E+00	3.10E-01		-8.58E-02	9.57E-01		Unigene31646_All//gi|255542580|ref|XP_002512353.1|//8.00E-06//hypothetical protein RCOM_1431030 [Ricinus communis] >gi|223548314|gb|EEF49805.1| hypothetical protein RCOM_1431030 [Ricinus communis]		Unigene31646_All//5.00E-117//ES835962				nr +
Unigene31648_All	363	0.72	0.00	3.81	0.55	0.76	0.50	0.00	0.00	0.00	-9.49E+00	6.70E-02		2.40E+00	5.37E-04	Up	4.67E-01	8.17E-01		-1.41E-01	9.35E-01		null	null		null	null										ESTscan -
Unigene3165_All	964	75.33	37.53	68.83	151.10	136.31	136.66	95.31	47.09	40.67	-1.01E+00	4.04E-53	Down	-1.30E-01	5.86E-02		-1.49E-01	2.76E-04		-1.45E-01	7.58E-04		-1.02E+00	1.61E-83	Down	-1.23E+00	3.23E-116	Down	Unigene3165_All|gi|115472937|ref|NP_001060067.1|//1.00E-120//0s07g0573400 (Oryza sativa Japonica Group) >gi|113611603|dbj|BAF21981.1| 0s07g0573400 (Oryza sativa Japonica Group)	Unigene3165_All//4.00E-120//AT1G55360| unknown protein	Unigene3165_All//0.00E+00//TC162778				nr +
Unigene31654_All	215	0.49	0.24	3.22	8.34	15.54	27.31	0.20	0.19	1.30	-1.05E+00	6.84E-01		2.73E+00	1.40E-02		8.97E-01	6.59E-03		1.71E+00	8.64E-11	Up	-1.70E-02	1.00E+00		2.72E+00	9.93E-02				Unigene31654_All//2.00E-07//TC169895				
Unigene31662_All	213	7.37	4.04	5.25	5.61	5.01	5.51	39.90	15.31	8.98	-8.66E-01	9.97E-02		-4.89E-01	3.92E-01		-1.63E-01	8.16E-01		-2.59E-02	9.54E-01		-1.38E+00	3.05E-13	Down	-2.15E+00	1.05E-24	Down			Unigene31662_All//4.00E-117//gi|164256472|gb|ES807112.1|ES807112				
Unigene31663_All	347	2.41	0.29	0.00	1.72	2.18	0.26	1.83	2.05	1.72	-3.05E+00	2.11E-03		-1.12E+01	1.19E-04	Down	3.42E-01	7.20E-01		-2.73E+00	1.74E-02		1.64E-01	8.24E-01		-8.59E-02	9.19E-01									
Unigene31666_All	570	0.00	2.76	1.59	0.00	0.00	0.08	0.00	0.00	0.00	1.14E+01	5.70E-09	Up	1.06E+01	4.71E-05	Up	null	null		6.31E+00	6.96E-01		null	null		null	null		Unigene31666_All//gi|21554405|gb|AAM63510.1|//3.00E-16//Actin-depolymerizing factor ADF-6 [Arabidopsis thaliana]	Unigene31666_All//3.00E-16//AT2G31200| ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); actin binding				nr +
Unigene31669_All	688	0.00	0.00	0.00	0.00	0.00	0.00	2.03	1.34	0.00	null	null		null	null		null	null		null	null		-6.02E-01	2.40E-01		-1.10E+01	2.40E-10	Down	Unigene31669_All//gi|18087585|gb|AL58923.1|AF462833_1//2.00E-22//At1g02780/T14P4_3 [Arabidopsis thaliana]	Unigene31669_All//2.00E-13//AT4G02230| 60S ribosomal protein L19 (RPL19C)		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene31670_All	762	0.00	6.72	2.38	0.00	0.09	0.00	0.00	0.00	0.00	1.27E+01	3.53E-29	Up	1.12E+01	5.69E-10	Up	6.50E+00	6.09E-01		null	null		null	null		null	null		Unigene31670_All//gi|301122201|ref|XP_002908827.1|//7.00E-84//mitochondrial-processing peptidase subunit beta [Phytophthora infestans T30-4] >gi|262099589|gb|EEY57641.1| mitochondrial-processing peptidase subunit beta [Phytophthora infestans T30-4]	Unigene31670_All//2.00E-72//AT3G02090| mitochondrial processing peptidase beta subunit, putative			GO:0003824//GO:0005515//GO:0005746//GO:0010033//GO:0022904//GO:0046872	nr +
Unigene31671_All	430	0.00	0.00	0.00	0.23	0.00	2.31	0.20	0.39	3.52	null	null		null	null		-7.86E+00	3.13E-01		3.32E+00	3.47E-04	Up	9.83E-01	6.33E-01		4.16E+00	1.20E-08	Up	Unigene31671_All//gi|10178101|dbj|BAB11488.1|//6.00E-17//receptor-like protein kinase [Arabidopsis thaliana]				GO:0016301	nr +
Unigene31673_All	230	183.81	96.93	76.40	196.66	157.20	221.10	164.71	118.48	84.53	-9.23E-01	3.56E-27		-1.27E+00	2.37E-43	Down	-3.23E-01	1.06E-05		1.69E-01	3.22E-02		-4.75E-01	8.25E-10		-9.62E-01	7.53E-33		Unigene31673_All|gi|225440831|ref|XP_002282071.1|//5.00E-39//PREDICTED: similar to ubiquitin fusion protein [Vitis vinifera] >gi|71040673|gb|AAZ20285.1| ubiquitin fusion protein [Arachis hypogaea] >gi|192910738|gb|ACF06477.1| ubiquitin fusion protein [Elaeis guineensis] >gi|284433784|gb|ADB85098.1| ubiquitin C variant [Jatropha curcas]	Unigene31673_All//8.00E-UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene31673_All//3.00E-127//TC158943		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0031981//GO:0032446	nr -
Unigene31675_All	657	0.00	0.00	0.00	0.00	0.00	0.00	2.38	1.15	0.00	null	null		null	null		null	null		null	null		-1.06E+00	2.63E-02		-1.12E+01	1.42E-11	Down	Unigene31675_All|gi|1706586|sp|P50256.1|EF1AC_POPPU//2.00E-37//RecName: Full=Elongation factor 1-alpha C; Short=EF-1-alpha C >gi|476155|gb|AAA61793.1| EF1-alpha [Porphyra purpurea]	Unigene31675_All//6.00E-30//AT5G60390| elongation factor 1-alpha / EF-1-alpha			GO:0000166//GO:0006412	nr -
Unigene31676_All	314	0.00	0.00	0.00	0.00	0.00	0.43	0.94	2.13	10.28	null	null		null	null		null	null		8.75E+00	3.11E-01		1.18E+00	1.44E-01		3.45E+00	1.60E-15	Up									
Unigene31677_All	506	37.33	112.05	45.99	71.77	56.21	97.47	381.27	600.92	718.28	1.59E+00	1.15E-83	Up	3.01E-01	1.27E-02		-3.52E-01	1.98E-05		4.42E-01	1.42E-09		6.56E-01	7.55E-130		9.14E-01	2.02E-280		Unigene31677_All|gi|38016531|gb|AAR07601.1|//1.00E-76//fiber quinone-oxidoreductase [Gossypium barbadense]	Unigene31677_All//2.00E-65//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene31677_All//0.00E+00//TC153773			GO:0008152//GO:0009534//GO:0016020//GO:0016655//GO:0046914	nr -
Unigene31678_All	227	2.07	0.00	0.00	1.76	0.91	0.40	2.42	0.00	1.23	-1.10E+01	5.55E-03		-1.10E+01	8.64E-03		-9.48E-01	4.21E-01		-2.14E+00	1.26E-01		-1.12E+01	4.61E-04	Down	-9.79E-01	2.50E-01				Unigene31678_All//3.00E-84//TC150125				
Unigene31681_All	357	0.00	0.00	0.00	0.00	0.00	0.00	7.70	1.17	1.23	null	null		null	null		null	null		null	null		-2.72E+00	1.53E-10	Down	-2.65E+00	1.15E-10	Down			Unigene31681_All//8.00E-06//AT2G28160| FRU (FER-LIKE REGULATOR OF IRON UPTAKE); DNA binding / transcription factor		b4LH			
Unigene31682_All	246	0.64	11.95	0.65	1.82	1.68	1.29	1.20	5.78	0.97	4.23E+00	4.04E-13	Up	2.53E-02	1.00E+00		-1.18E-01	8.86E-01		-5.04E-01	6.49E-01		2.26E+00	8.04E-05	Up	-3.08E-01	7.75E-01				Unigene31682_All//1.00E-61//gi|78327977|gb|DT548251.1|DT548251				
Unigene31684_All	588	0.00	0.00	0.00	0.00	0.00	0.00	1.65	0.07	0.00	null	null		null	null		null	null		null	null		-4.54E+00	6.92E-06	Down	-1.07E+01	2.72E-07	Down	Unigene31684_All|gi|224054176|ref|XP_002298129.1|//4.00E-71//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene31684_All//2.00E-68//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene31684_All//4.00E-150//CD486481		ko00904|Diterpenoid biosynthesis	GO:0008152//GO:0016701//GO:0016706//GO:0044464//GO:0046914	nr +
Unigene31687_All	260	1.21	2.73	0.61	0.19	0.53	3.82	0.16	1.45	0.31	1.18E+00	1.75E-01		-9.75E-01	5.06E-01		1.47E+00	6.19E-01		4.32E+00	6.32E-05	Up	3.15E+00	3.41E-02		9.15E-01	7.50E-01				Unigene31687_All//3.00E-07//DT466704				
Unigene31691_All	269	2.72	0.94	0.00	0.56	1.66	1.01	0.31	0.00	0.00	-1.53E+00	7.78E-02		-1.14E+01	4.13E-04	Down	1.58E+00	2.17E-01		8.59E-01	6.31E-01		-8.30E+00	4.03E-01		-8.30E+00	3.58E-01				Unigene31691_All//8.00E-11//gi|109858205|gb|DW487184.1|DW487184				
Unigene31692_All	218	130.32	80.19	69.86	192.40	118.94	215.46	190.07	102.96	82.05	-7.01E-01	8.07E-12		-9.00E-01	4.99E-17		-6.94E-01	3.78E-20		1.63E-01	4.96E-02		-8.85E-01	2.49E-30		-1.21E+00	9.35E-52	Down	Unigene31692_All//gi|209967443|gb|ACJ02350.1|//8.00E-30//60S ribosomal protein L13A [Vernicia fordii]	Unigene31692_All//5.00E-30//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene31692_All//4.00E-120//gi|13246994|gb|BF268165.2|BF268165		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934	nr +
Unigene3170_All	371	0.00	0.00	0.57	0.54	0.00	0.24	4.22	1.69	1.18	null	null		9.17E+00	1.41E-01		-9.07E+00	8.43E-02		-1.14E+00	5.69E-01		-1.32E+00	6.35E-03		-1.84E+00	2.17E-04	Down								
Unigene31701_All	351	0.00	6.64	1.67	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.91E-13	Up	1.07E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene31701_All//sp|Q5RFH0|ATP5L_PONAB//2.00E-17//ATP synthase subunit g, mitochondrial OS=Pongo abelii GN=ATP5L PE=3 SV=1						swissprot -
Unigene31705_All	404	0.39	2.63	0.00	0.12	0.60	0.45	0.10	0.21	0.99	2.76E+00	8.45E-04	Up	-8.60E+00	2.45E-01		2.27E+00	3.05E-01		1.86E+00	4.58E-01		9.83E-01	7.31E-01		3.24E+00	2.14E-02				Unigene31705_All//2.00E-37//TC132071				
Unigene31707_All	382	0.00	0.00	0.00	0.00	0.00	0.00	18.48	28.23	0.42	null	null		null	null		null	null		null	null		6.11E-01	7.54E-05		-5.47E+00	1.33E-45	Down	Unigene31707_All//gi|116222125|gb|ABJ80933.1|//7.00E-66//actin [Leucocryptos marina]	Unigene31707_All//6.00E-64//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene31707_All//1.00E-35//TC153744		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008015//GO:0008092//GO:0012501//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0048747//GO:0051707//GO:0060415	nr -
Unigene3171_All	833	1.01	0.97	0.70	1.26	1.07	0.81	20.81	8.13	7.27	-4.64E-02	9.64E-01		-5.15E-01	5.15E-01		-2.25E-01	7.53E-01		-6.27E-01	3.81E-01		-1.36E+00	1.85E-25	Down	-1.52E+00	6.36E-31	Down	Unigene3171_All//gi|171854589|dbj|BAG16485.1|//3.00E-62//succinic semialdehyde reductase isoform1 [Solanum lycopersicum]	Unigene3171_All//2.00E-54//AT3G25530| GLYR1 (GLYOXYLATE REDUCTASE 1); 3-hydroxybutyrate dehydrogenase/ phosphogluconate dehydrogenase (decarboxylating)	Unigene3171_All//3.00E-81//gi|48803105|gb|CO104419.1|CO104419		ko00903|Limonene and pinene degradation//ko00280|Valine, leucine and isoleucine degradation	GO:0006007//GO:0006950//GO:0009081//GO:0016616//GO:0044444//GO:0048037	nr +
Unigene31711_All	265	0.00	2.49	0.00	1.32	0.39	0.00	0.32	0.16	1.80	1.13E+01	6.25E-04	Up	null	null		-1.76E+00	1.90E-01		-1.04E+01	2.12E-02		-1.02E+00	7.24E-01		2.50E+00	2.51E-02		Unigene31711_All|gi|297824921|ref|XP_002880343.1|//2.00E-38//structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata] >gi|297326182|gb|EFH56602.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	Unigene31711_All//8.00E-40//AT2G48110| REP4 (REDUCED EPIDERMAL FLUORESCENCE 4)	Unigene31711_All//6.00E-67//ES813254				nr -
Unigene31712_All	265	0.00	3.82	2.41	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.26E-06	Up	1.12E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene31712_All|gi|224011487|ref|XP_002295518.1|//7.00E-08//ASSY [Thalassiosira pseudonana CCMP1335] >gi|209583549|gb|ACI64235.1| ASSY [Thalassiosira pseudonana CCMP1335]				ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene31713_All	312	0.00	3.90	2.05	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.47E-07	Up	1.10E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene3713_All//sp|Q24523|BUN2_DROME//3.00E-08//Protein bunched, class 2/F isoform OS=Drosophila melanogaster GN=bun PE=1 SV=3						swissprot -
Unigene31714_All	391	0.00	2.59	0.27	4.71	1.59	1.39	3.35	2.57	4.38	1.13E+01	7.26E-06	Up	8.09E+00	3.98E-01		-1.57E+00	7.12E-04	Down	-1.77E+00	4.90E-04	Down	-3.86E-01	4.87E-01		3.86E-01	3.88E-01				Unigene31714_All//4.00E-149//TC173284				
Unigene31716_All	412	0.00	2.09	3.88	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	4.95E-05	Up	1.19E+01	8.44E-09	Up	null	null		null	null		null	null		null	null										
Unigene31717_All	379	0.28	0.80	0.28	4.73	4.63	0.95	0.00	0.00	0.00	1.54E+00	3.23E-01		2.54E-02	1.00E+00		-3.02E-02	9.51E-01		-2.31E+00	2.69E-05	Down	null	null		null	null				Unigene31717_All//3.00E-20//TC176784				
Unigene3172_All	848	2.34	5.38	3.20	1.94	3.45	1.76	39.94	13.55	8.50	1.20E+00	4.01E-05	Up	4.50E-01	2.65E-01		8.32E-01	2.07E-02		-1.41E-01	7.85E-01		-1.56E+00	3.51E-60	Down	-2.23E+00	1.59E-100	Down	Unigene3172_All|gi|15375068|gb|AAK94781.1|//1.00E-123//gamma hydroxybutyrate dehydrogenase [Arabidopsis thaliana]	Unigene3172_All//1.00E-117//AT3G25530| GLYR1 (GLYOXYLATE REDUCTASE 1); 3-hydroxybutyrate dehydrogenase/ phosphogluconate dehydrogenase (decarboxylating)	Unigene3172_All//2.00E-165//TC137136		ko00903|Limonene and pinene degradation//ko00280|Valine, leucine and isoleucine degradation	GO:0006007//GO:0009081//GO:0016616//GO:0048037	nr +
Unigene31720_All	323	0.65	0.16	0.00	0.31	0.00	0.42	5.24	1.16	0.49	-2.05E+00	3.34E-01		-9.34E+00	1.46E-01		-8.27E+00	3.13E-01		4.44E-01	8.61E-01		-2.17E+00	2.25E-05	Down	-3.41E+00	1.56E-08	Down								
Unigene31721_All	584	0.00	15.53	6.20	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	6.32E-52	Up	1.26E+01	4.74E-20	Up	null	null		null	null		null	null		null	null		Unigene31721_All|gi|195604208|gb|ACG23934.1|//9.00E-36//40S ribosomal protein S12 [Zea mays] >gi|195616250|gb|ACG29955.1| 40S ribosomal protein S12 [Zea mays]	Unigene31721_All//1.00E-33//AT2G32060| 40S ribosomal protein S12 (RPS12C)			ko03010|Ribosome	GO:0005840	nr -
Unigene31725_All	276	737.42	715.06	850.26	563.12	615.34	392.56	128.99	310.74	60.05	-4.44E-02	2.91E-01		2.05E-01	1.20E-09		1.28E-01	8.63E-04		-5.21E-01	4.44E-39		1.27E+00	9.90E-111	Up	-1.10E+00	1.78E-38	Down	Unigene31725_All|gi|224111864|ref|XP_002316007.1|//6.00E-30//cytochrome P450 [Populus trichocarpa] >gi|222865047|gb|EEF02178.1| cytochrome P450 [Populus trichocarpa]	Unigene31725_All//2.00E-26//AT3G14630| CYP72A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene31725_All//7.00E-150//gi|5047096|gb|AI728244.1|AI728244		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0008152//GO:0016634	nr -
Unigene31726_All	359	0.00	0.42	0.00	0.56	0.38	1.51	1.88	1.16	9.65	8.73E+00	2.35E-01		null	null		-5.33E-01	7.48E-01		1.44E+00	1.93E-01		-6.95E-01	3.94E-01		2.36E+00	1.60E-11	Up			Unigene31726_All//0.00E+00//gi|78340908|gb|DT561182.1|DT561182				
Unigene31727_All	220	0.00	0.00	0.24	0.00	0.47	0.21	0.38	2.47	9.60	null	null		7.92E+00	6.36E-01		8.88E+00	4.56E-01		7.68E+00	6.96E-01		2.68E+00	1.38E-02		4.64E+00	1.32E-12	Up								
Unigene31728_All	526	2.09	0.10	2.02	1.33	2.16	2.92	0.16	0.16	0.23	-4.44E+00	2.09E-05	Down	-4.50E-02	9.61E-01		7.04E-01	3.06E-01		1.14E+00	3.89E-02		-1.71E-02	1.01E+00		4.99E-01	8.07E-01									
Unigene31739_All	250	7.74	10.34	16.19	4.78	4.41	5.42	3.04	2.67	2.07	4.17E-01	3.03E-01		1.06E+00	8.56E-04	Up	-1.18E-01	8.27E-01		1.81E-01	7.57E-01		-1.87E-01	7.91E-01		-5.55E-01	4.23E-01			Unigene31739_All//5.00E-07//AT1G06210| NHS domain-containing protein / GAT domain-containing protein	Unigene31739_All//1.00E-61//CO125906				
Unigene31740_All	370	0.28	3.97	2.01	3.23	1.77	3.66	0.23	1.24	0.65	3.81E+00	2.22E-06	Up	2.83E+00	8.52E-03		-8.70E-01	1.50E-01		1.81E-01	7.57E-01		2.44E+00	3.74E-02		1.50E+00	3.39E-01		Unigene31740_All|gi|225425912|ref|XP_002267341.1|//2.00E-28//PREDICTED: similar to P21J9.9 [Vitis vinifera]	Unigene31740_All//3.00E-26//AT3G26040| transferase family protein			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016413	nr -
Unigene31747_All	726	0.36	0.70	1.83	0.27	0.43	0.37	0.52	1.73	2.96	9.54E-01	3.73E-01		2.35E+00	8.68E-04	Up	6.37E-01	6.95E-01		4.44E-01	7.63E-01		1.72E+00	2.80E-03		2.50E+00	6.75E-08	Up	Unigene31747_All|gi|255537763|ref|XP_002509948.1|//1.00E-22//conserved hypothetical protein [Ricinus communis] >gi|223549847|gb|EEF51335.1| conserved hypothetical protein [Ricinus communis]	Unigene31747_All//3.00E-05//AT5G41860| unknown protein					nr +

Unigene31748_All	219	17.20	41.65	21.40	26.16	33.96	32.58	25.68	35.12	36.02	1.28E+00	2.43E-10	Up	3.15E-01	3.03E-01		3.77E-01	8.42E-02		3.17E-01	1.84E-01		4.52E-01	1.73E-02		4.88E-01	6.71E-03				Unigene31748_All//5.00E-101//gi|164339779|gb|ES841143.1|ES841143				
Unigene31751_All	260	0.00	3.12	2.46	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.38E-05	Up	1.13E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene31751_All//gi|301106937|ref|XP_002902551.1|//1.00E-15//glutamate-rich WD repeat-containing protein [Phytophthora infestans T30-4] >gi|262098425|gb|EEY56477.1| glutamate-rich WD repeat-containing protein [Phytophthora infestans T30-4]	Unigene31751_All//2.00E-11//AT2G19540| transducin family protein / WD-40 repeat family protein				nr -
Unigene31753_All	543	0.00	0.00	0.20	0.00	0.00	0.00	1.56	6.39	2.13	null	null		7.62E+00	3.98E-01		null	null		null	null		2.04E+00	1.59E-09	Up	4.50E-01	4.17E-01		Unigene31753_All//gi|29839623|sp|Q9FJB5.1|RPS1_ARATH//1.00E-17//RecName: Full=Disease resistance RPP8-like protein 3 >gi|9758146|dbj|BAB08703.1| disease resistance protein [Arabidopsis thaliana] >gi|110742305|dbj|BAE99077.1| disease resistance protein [Arabidopsis thaliana]	Unigene31753_All//5.00E-15//AT5G35450| disease resistance protein (CC-NBS-LRR class), putative		ko04626|Plant-pathogen interaction	GO:0000166//GO:0002252//GO:0009314//GO:0009607//GO:0012501//GO:0016020//GO:0033554	nr -
Unigene31754_All	367	0.86	0.97	0.15	15.34	0.09	0.00	47.00	1.48	2.28	1.76E-01	8.83E-01		-2.56E+00	1.59E-01		-7.35E+00	6.15E-41	Down	-1.39E+01	1.16E-35	Down	-4.99E+00	1.58E-102	Down	-4.37E+00	4.63E-98	Down	Unigene31754_All//gi|89243481|gb|ABD64879.1|//4.00E-42//nicotianamine synthase [Malus xiaojinensis]	Unigene31754_All//5.00E-36//AT1G09240| NAS3 (NICOTIANAMINE SYNTHASE 3); nicotianamine synthase	Unigene31754_All//0.00E+00//gi|109882514|gb|DW511484.1|DW511484			GO:0016765//GO:0018130	nr -
Unigene31755_All	442	0.00	0.23	0.00	0.00	0.78	0.51	1.24	0.66	5.50	7.84E+00	3.86E-01		null	null		9.61E+00	3.01E-02		9.00E+00	1.19E-01		-9.10E-01	3.19E-01		2.14E+00	1.70E-07	Up								
Unigene31756_All	656	0.08	0.39	0.00	0.23	0.42	0.00	2.06	3.38	0.43	2.27E+00	2.34E-01		-6.32E+00	6.24E-01		8.82E-01	5.95E-01		-7.83E+00	2.33E-01		7.11E-01	6.62E-02		-2.28E+00	7.13E-05	Down			Unigene31756_All//8.00E-07//ES842405					
Unigene31758_All	324	2.42	0.16	0.00	1.23	0.53	0.00	0.00	0.00	0.00	-3.95E+00	8.54E-04	Down	-1.12E+01	2.22E-04	Down	-1.21E+00	3.14E-01		-1.03E+01	1.11E-02		null	null		null	null		Unigene31758_All//COG3206//2.00E-12//Uncharacterized protein involved in exopolysaccharide biosynthesis						cog -
Unigene31760_All	296	101.99	58.20	55.59	124.37	102.61	115.50	162.41	59.87	57.07	-8.09E-01	7.52E-16		-8.76E-01	2.82E-17		-2.78E-01	9.93E-04		-1.07E-01	3.10E-01		-1.44E+00	1.02E-75	Down	-1.51E+00	1.53E-83	Down	Unigene31760_All//gi|82623403|gb|AB88716.1|//1.00E-47//40S ribosomal protein S19-like [Solanum tuberosum]	Unigene31760_All//3.00E-48//AT5G61170| 40S ribosomal protein S19 (RPS19C)	Unigene31760_All//2.00E-166//TC154681	ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0031981	nr +
Unigene31761_All	397	0.00	0.13	2.55	0.00	0.95	0.23	0.00	0.00	0.00	7.00E+00	6.16E-01		1.13E+01	1.27E-05	Up	9.90E+00	1.96E-02		7.83E+00	4.76E-01		null	null		null	null									
Unigene31762_All	380	0.41	0.53	0.00	1.31	1.63	1.43	2.11	3.74	7.86	3.69E-01	8.16E-01		-8.69E+00	2.45E-01		3.15E-01	7.84E-01		1.22E-01	9.21E-01		8.23E-01	1.03E-01		1.90E+00	7.85E-08	Up	Unigene31762_All//gi|297843736|ref|XP_002889749.1|//6.00E-14//ATP-citrate lyase A-3 [Arabidopsis lyrata subsp. lyrata] >gi|297335591|gb|EFH66008.1| ATP-citrate lyase A-3 [Arabidopsis lyrata subsp. lyrata]	Unigene31762_All//8.00E-15//AT1G09430| ACLA-3; ATP citrate synthase	Unigene31762_All//3.00E-60//ES836404	ko00020|Citrate cycle (TCA cycle)	GO:0004774//GO:0032559	nr -
Unigene31769_All	254	0.21	4.79	0.42	0.00	0.00	0.18	0.00	0.00	1.88	4.54E+00	6.47E-06	Up	1.03E+00	7.03E-01		null	null		7.47E+00	6.96E-01		null	null		1.09E+01	1.14E-03									
Unigene3177_All	1250	1.97	1.58	1.41	2.95	2.81	2.75	2.81	2.57	1.08	-3.16E-01	4.38E-01		-4.85E-01	2.55E-01		-6.97E-02	8.25E-01		-1.03E-01	7.59E-01		-1.25E-01	6.97E-01		-1.37E+00	4.17E-06	Down	Unigene3177_All//gi|15222202|ref|NP_172164.1|//8.00E-72//RNA polymerase Rpb7 N-terminal domain-containing protein [Arabidopsis thaliana]	Unigene3177_All//9.00E-67//AT1G06790| RNA polymerase Rpb7 N-terminal domain-containing protein	Unigene3177_All//0.00E+00//TC138702	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0010467//GO:0034062	nr +
Unigene31777_All	246	0.21	5.56	0.00	2.43	0.56	0.37	0.00	0.68	0.32	4.71E+00	1.03E-06	Up	-7.73E+00	6.24E-01		-2.12E+00	3.06E-02		-2.73E+00	1.74E-02		9.41E+00	1.39E-01		8.34E+00	4.04E-01									
Unigene31779_All	319	0.00	0.00	0.00	0.00	0.00	0.00	45.99	16.12	14.86	null	null		null	null		null	null		null	null		-1.51E+00	2.14E-25	Down	-1.63E+00	4.21E-29	Down	Unigene31779_All//gi|124360970|gb|ABN08942.1|//7.00E-18//Quinonprotein alcohol dehydrogenase-like [Medicago truncatula]						nr +
Unigene3178_All	1044	13.18	5.24	5.66	15.70	15.87	17.52	24.46	12.69	10.80	-1.33E+00	2.90E-16	Down	-1.22E+00	1.15E-13	Down	1.53E-02	9.41E-01		1.58E-01	2.94E-01		-9.47E-01	3.27E-21		-1.18E+00	6.38E-31	Down	Unigene3178_All//gi|297806647|ref|XP_002871207.1|//3.00E-59//40S ribosomal protein S17 [Arabidopsis lyrata subsp. lyrata] >gi|297317044|gb|EFH47466.1| 40S ribosomal protein S17 [Arabidopsis lyrata subsp. lyrata]	Unigene3178_All//2.00E-55//AT5G04800| 40S ribosomal protein S17 (RPS17D)	Unigene3178_All//0.00E+00//gi|21102555|gb|BQ414868.1|BQ414868	ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene31780_All	244	0.00	4.57	6.33	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.00E-06	Up	1.26E+01	1.65E-08	Up	null	null		null	null		null	null		null	null									
Unigene31781_All	244	7.72	9.97	20.95	85.13	59.27	92.92	1937.61	1303.20	1806.78	3.69E-01	3.73E-01		1.44E+00	6.61E-07	Up	-5.22E-01	2.41E-06		1.26E-01	3.63E-01		-5.72E-01	5.48E-158		-1.01E-01	8.39E-07		Unigene31781_All//gi|52632335|gb|AAU85528.1|//4.00E-18//pathogenesis-related protein 10 [Gossypium herbaceum]		Unigene31781_All//9.00E-103//NP959318		GO:0006950	nr -
Unigene31782_All	480	0.00	5.59	2.88	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.80E-15	Up	1.15E+01	1.23E-07	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene31783_All	684	0.46	1.26	2.57	0.44	0.76	0.73	0.00	0.00	0.00	1.46E+00	6.59E-02		2.48E+00	4.72E-05	Up	7.89E-01	4.98E-01		7.33E-01	5.16E-01		null	null		null	null		Unigene31783_All//sp|P20370|DC4C_ACIAD//1.00E-11//4-carboxymuconolactone decarboxylase OS=Acinetobacter sp. (strain ADP1) GN=pcaC PE=4 SV=2						swissprot +
Unigene31785_All	218	4.32	0.93	2.44	2.29	0.00	2.49	0.00	1.34	0.73	-2.22E+00	6.65E-03		-8.23E-01	2.71E-01		-1.12E+01	8.98E-04	Down	1.22E-01	9.21E-01		1.04E-01	2.35E-02		9.51E+00	1.40E-01									
Unigene31787_All	262	1.80	8.51	0.00	0.38	0.13	2.07	0.32	1.28	3.65	2.24E+00	7.09E-06	Up	-1.08E+01	8.64E-03		-1.53E+00	5.86E-01		2.44E+00	4.41E-02		1.98E+00	1.44E-01		3.50E+00	4.29E-05	Up			Unigene31787_All//9.00E-131//TC177302					
Unigene31788_All	469	1.45	5.40	4.88	0.96	1.03	1.16	0.09	0.45	1.02	1.90E+00	1.79E-05	Up	1.75E+00	2.24E-04	Up	1.05E-01	9.54E-01		2.74E-01	7.83E-01		2.31E+00	2.40E-01		3.50E+00	7.29E-03		Unigene31788_All//gi|222142535|gb|ACM45954.1|//9.00E-17//serine hydroxymethyltransferase 4 [Glycine max]	Unigene31788_All//2.00E-17//AT4G32520| SHM3 (SERINE HYDROXYMETHYLTRANSFERASE 3); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene31788_All//2.00E-62//TC138673	ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate	GO:0009069//GO:0009536//GO:0016742//GO:0048037	nr +
Unigene31789_All	668	0.24	1.44	3.19	0.30	0.26	0.20	0.00	0.00	0.00	2.62E+00	2.34E-03		3.76E+00	1.35E-08	Up	-2.11E-01	8.59E-01		-5.57E-01	7.33E-01		null	null		null	null		Unigene31789_All//gi|159471892|ref|XP_001694090.1|//2.00E-12//xanthine dehydrogenase/oxidase [Chlamydomonas reinhardtii] >gi|158277257|gb|EDP03026.1| xanthine dehydrogenase/oxidase [Chlamydomonas reinhardtii]	Unigene31789_All//2.00E-13//AT4G34890| XDH1 (XANTHINE DEHYDROGENASE 1); xanthine dehydrogenase		ko00230|Purine metabolism//ko04146|Peroxisome//ko00232|Caffeine metabolism	GO:0005488//GO:0006144//GO:0006950//GO:0006975//GO:0042221	nr -
Unigene31795_All	904	0.12	0.11	0.00	0.39	0.65	0.30	0.47	3.05	7.62	-4.68E-02	9.89E-01		-6.86E+00	3.93E-01		7.48E-01	4.81E-01		-3.64E-01	7.55E-01		2.71E+00	1.68E-10	Up	4.03E+00	1.32E-36	Up								
Unigene31797_All	247	0.00	9.44	2.80	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	2.91E-13	Up	1.15E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene31797_All//gi|300078545|gb|ADJ67180.1|//2.00E-13//F9L1.21 protein [Jatropha curcas]				GO:0016020	nr +
Unigene31799_All	811	0.19	0.00	0.00	0.06	0.00	0.00	0.52	0.62	5.80	-7.60E+00	2.15E-01		-7.60E+00	2.45E-01		-5.94E+00	5.55E-01		-5.94E+00	6.35E-01		2.46E-01	7.84E-01		3.48E+00	1.77E-22	Up	Unigene31799_All//gi|63003792|gb|AAY25425.1|//3.00E-92//At3g19990 [Arabidopsis thaliana] >gi|111074436|gb|AB406591.1| At3g19990 [Arabidopsis thaliana]	Unigene31799_All//4.00E-89//AT3G19990| unknown protein	Unigene31799_All//5.00E-27//gi|109882824|gb|DW511794.1|DW511794			GO:0009532	nr +
Unigene318_All	3558	4.07	4.86	4.40	10.35	9.97	6.49	6.02	2.01	7.20	2.54E-01	6.89E-02		1.11E-01	5.04E-01		-5.37E-02	6.17E-01		-6.74E-01	4.57E-15		-1.58E+00	2.81E-39	Down	2.57E-01	7.36E-03		Unigene318_All//gi|31711766|gb|AAP68239.1|//2.00E-78//At2g29510 [Arabidopsis thaliana]	Unigene318_All//2.00E-39//AT2G29510| unknown protein	Unigene318_All//0.00E+00//TC159488				nr +
Unigene31810_All	396	3.30	0.51	4.84	7.80	2.61	5.13	0.21	0.00	0.50	-2.69E+00	1.84E-04	Down	5.52E-01	2.59E-01		-1.58E+00	4.09E-06	Down	-6.04E-01	9.44E-02		-7.74E+00	4.03E-01		1.24E+00	4.69E-01		Unigene31810_All//gi|15227619|ref|NP_180537.1|//2.00E-09//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75100656|sp|Q82380.1|PP175_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g29760, chloroplastic; Flags: Precursor	Unigene31810_All//2.00E-08//AT3G05240| pentatricopeptide (PPR) repeat-containing protein				nr +
Unigene31812_All	537	0.78	2.36	0.50	0.56	2.37	0.84	1.02	8.17	10.39	1.60E+00	1.20E-02		-6.53E-01	5.94E-01		2.09E+00	1.41E-03		5.96E-01	6.40E-01		3.00E+00	4.59E-18	Up	3.34E+00	1.08E-25	Up	Unigene31812_All//gi|225454888|ref|XP_002278945.1|//2.00E-23//PREDICTED: similar to NADH glutamate dehydrogenase [Vitis vinifera] >gi|11691872|emb|CAC18730.1| NADH glutamate dehydrogenase [Vitis vinifera]	Unigene31812_All//6.00E-24//AT5G07440| GDH2 (GLUTAMATE DEHYDROGENASE 2); ATP binding / glutamate dehydrogenase [NAD(P)+]/ glutamate dehydrogenase/ oxidoreductase	Unigene31812_All//1.00E-85//TC161202	ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006519//GO:0006970//GO:0010038//GO:0016020//GO:0016639//GO:0032559//GO:0043231//GO:0046914	nr +
Unigene3182_All	1506	6.08	4.71	5.06	10.15	7.71	3.96	1.80	1.80	4.50	-3.68E-01	5.84E-02		-2.66E-01	2.10E-01		-3.98E-01	3.42E-03		-1.36E+00	6.07E-20	Down	5.70E-03	1.02E+00		1.32E+00	2.51E-10	Up	Unigene3182_All//gi|224057256|ref|XP_002299197.1|//1.00E-120//chalcone synthase-like protein [Populus trichocarpa] >gi|222846455|gb|EEE84002.1| chalcone synthase-like protein [Populus trichocarpa]	Unigene3182_All//9.00E-112//AT5G13930| TT4 (TRANSPARENT TESTA 4); naringenin-chalcone synthase	Unigene3182_All//0.00E+00//DW506069	ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr -
Unigene31828_All	273	22.04	15.22	9.75	27.01	25.23	28.79	45.38	49.14	29.77	-5.34E-01	2.71E-02		-1.18E+00	4.93E-06	Down	-9.83E-02	7.03E-01		9.21E-02	6.89E-01		1.15E-01	4.82E-01		-6.08E-01	1.28E-05		Unigene31828_All//gi|18410687|ref|NP_567047.1|//4.00E-24//EIF3E (EUKARYOTIC TRANSLATION INITIATION FACTOR 3E); translation initiation factor [Arabidopsis thaliana] >gi|12407658|gb|AAG53613.1|AF285832_1 eukaryotic initiation factor 3E subunit [Arabidopsis thaliana]	Unigene31828_All//2.00E-25//AT3G57290| EIF3E (EUKARYOTIC TRANSLATION INITIATION FACTOR 3E); translation initiation factor	Unigene31828_All//1.00E-114//gi|84155328|gb|DN804683.1|DN804683		GO:0006351//GO:0006970//GO:0008135//GO:0009639//GO:0009791//GO:0016020//GO:0043231//GO:0043234	nr -
Unigene31830_All	459	0.46	0.00	0.70	8.90	3.38	5.71	1.20	0.73	1.22	-8.83E+00	1.22E-01		6.10E-01	6.24E-01		-1.40E+00	1.13E-06	Down	-6.41E-01	3.41E-02		-7.17E-01	4.22E-01		2.10E-02	9.79E-01		Unigene31830_All//gi|39777536|gb|AB231108.1|//4.00E-26//peroxidase precursor [Quercus suber]	Unigene31830_All//2.00E-15//AT5G58390| peroxidase, putative	Unigene31830_All//8.00E-151//gi|11210200|gb|BF279130.1|BF279130	ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0006950//GO:0008152//GO:0046872	nr -
Unigene31833_All	326	0.80	0.16	2.29	0.92	0.74	0.14	1.95	0.13	0.73	-2.37E+00	2.14E-01		1.51E+00	9.50E-02		-3.10E-01	8.20E-01		-2.73E+00	1.37E-01		-3.92E+00	9.81E-04	Down	-1.41E+00	7.94E-02		Unigene31833_All//gi|223452530|gb|ACM89592.1|//1.00E-20//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene31833_All//1.00E-14//AT3G56370| leucine-rich repeat transmembrane protein kinase, putative	Unigene31833_All//8.00E-175//gi|78342627|gb|DT562901.1|DT562901	ko04626|Plant-pathogen interaction	GO:0005488//GO:0016020//GO:0016772	nr -
Unigene31836_All	431	9.10	1.88	7.17	0.23	0.16	0.42	0.69	0.29	0.00	-2.28E+00	4.78E-10	Down	-3.45E-01	3.04E-01		-5.33E-01	8.16E-01		8.58E-01	6.95E-01		-1.24E+00	3.73E-01		-9.42E+00	1.58E-02									
Unigene31841_All	403	0.00	1.26	1.72	0.00	1.11	0.22	0.00	0.00	0.00	1.03E+01	4.04E-03		1.07E+01	6.16E-04	Up	1.01E+01	8.01E-03		7.81E+00	4.76E-01		null	null		null	null		Unigene31841_All//gi|226458331|gb|EEH55628.1|//3.00E-09//Multidrug/Oligosaccharidyl-lipid/Polysaccharide flippase superfamily [Micromonas pusilla CCMP1545]	Unigene31841_All//7.00E-05//AT2G04100| MATE efflux family protein				nr +
Unigene31844_All	234	22.36	22.74	18.21	30.65	13.54	11.77	43.55	29.47	40.18	2.41E-02	9.46E-01		-2.97E-01	3.05E-01		-1.18E+00	9.07E-09	Down	-1.38E+00	7.01E-10	Down	-5.63E-01	4.09E-04		-1.16E-01	5.24E-01				Unigene31844_All//1.00E-89//gi|84164138|gb|DR452786.1|DR452786				
Unigene31846_All	216	0.24	0.00	3.45	5.07	0.96	0.21	0.00	0.00	0.00	-7.92E+00	6.12E-01		3.83E+00	2.23E-03		-2.41E+00	5.06E-04	Down	-4.60E+00	8.28E-06	Down	null	null		null	null									
Unigene31849_All	269	0.00	0.00	0.99	3.33	0.51	1.34	2.36	0.47	0.59	null	null		9.95E+00	8.02E-02		-2.70E+00	8.77E-04	Down	-1.31E+00	8.52E-02		-2.34E+00	1.27E-02		-1.99E+00	2.04E-02									
Unigene3185_All	1691	1.02	1.53	0.44	21.53	10.98	8.31	4.63	2.22	1.74	5.82E-01	1.38E-01		-1.21E+00	2.32E-02		-9.72E-01	3.67E-31		-1.37E+00	1.42E-47	Down	-1.06E+00	2.69E-08	Down	-1.41E+00	5.43E-13	Down	Unigene3185_All//gi|671868|emb|CAA87080.1|//1.00E-121//heat shock transcription factor 5 [Glycine max]	Unigene3185_All//4.00E-87//AT1G46264| AT-HSFB4; DNA binding / transcription factor	Unigene3185_All//0.00E+00//gi|78340237|gb|DT560511.1|DT560511	HSF		GO:0001071//GO:0003677//GO:0006351//GO:0043231//GO:0050896	nr -
Unigene31850_All	216	3.15	1.41	3.94	4.38	0.32	2.51	1.96	0.58	0.00	-1.16E+00	1.89E-01		3.25E-01	6.47E-01		-3.78E+00	3.39E-05	Down	-8.04E-01	2.77E-01		-1.75E+00	1.24E-01		-1.09E+01	2.14E-03				Unigene31850_All//6.00E-08//TC132101				
Unigene31854_All	245	0.00	1.24	3.48	1.42	0.98	0.55	0.00	0.68	0.33	1.03E+01	4.43E-02		1.18E+01	9.03E-05	Up	-5.33E-01	6.46E-01		-1.36E+00	3.37E-01		9.41E+00	1.39E-01		8.33E+00	4.04E-01				Unigene31854_All//5.00E-120//ES813391				
Unigene31857_All	425	0.00	8.58	2.51	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	9.10E-21	Up	1.13E+01	6.62E-06	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene31859_All	301	26.25	26.77	30.43	21.35	21.62	8.25	62.79	25.55	60.62	2.82E-02	9.08E-01		2.13E-01	3.25E-01		1.84E-02	9.48E-01		-1.37E+00	7.85E-09	Down	-1.30E+00	6.62E-26	Down	-5.07E-02	6.85E-01				Unigene31859_All//3.00E-140//gi|164265240|gb|ES809143.1|ES809143				
Unigene31860_All	251	0.00	2.62	3.39	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.25E-04	Up	1.17E+01	9.03E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene31863_All	206	24.89	8.36	16.29	5.32	3.84	4.38	0.00	0.00	0.00	-1.57E+00	3.51E-08	Down	-6.12E-01	2.71E-02		-4.69E-01	4.82E-01		-2.79E-01	6.89E-01		null	null		null	null		Unigene31863_All//gi|118582586|gb|ABL07607.1|//2.00E-11//beta-amyrin synthase [Polygala tenuifolia]	Unigene31863_All//4.00E-12//AT1G78955| CAMS1 (Camelliol C synthase 1); beta-amyrin synthase	Unigene31863_All//6.00E-14//gi|164302226|gb|ES807570.1|ES807570		ko00100|Steroid biosynthesis	GO:0016866	nr +

Unigene31864_All	627	0.00	0.00	0.00	0.00	0.00	0.00	0.67	2.60	0.00	null	null		null	null		null	null		null	null		1.95E+00	1.26E-04	Up	-9.40E+00	2.14E-03		Unigene31864_All//gi|27923848|sp|O65059.1|RS15_PICMA//5.00E-46//RecName: Full=40S ribosomal protein S15 >gi|2982268|gb|AAC32121.1| probable 40S ribosomal protein S15 [Picea mariana]	Unigene31864_All//4.00E-34//AT5G09500| 40S ribosomal protein S15 (RPS15C)	Unigene31864_All//2.00E-10//gi|109830543|gb|DW229102.1|DW229102		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene31865_All	510	0.00	0.30	0.00	0.00	0.14	2.57	0.08	0.16	1.48	8.22E+00	2.35E-01		null	null		7.08E+00	6.09E-01		1.13E+01	8.37E-08	Up	9.83E-01	7.31E-01		4.16E+00	1.34E-04	Up	Unigene31865_All//gi|34539778|gb|AAQ74768.1|//5.00E-31//dehydrin [Brassica napus] >gi|37547533|gb|AAN08718.1| dehydrin [Brassica juncea] >gi|37547535|gb|AAN08719.1| dehydrin [Brassica juncea]	Unigene31865_All//4.00E-12//AT2G21490| LEA (DEHYDRIN LEA)					nr -
Unigene31868_All	398	0.00	0.25	0.00	0.13	0.00	0.79	0.00	0.53	2.80	7.99E+00	3.86E-01		null	null		-6.97E+00	5.55E-01		2.67E+00	1.44E-01		9.04E+00	7.85E-02		1.15E+01	4.36E-08	Up				Unigene31868_All//5.00E-07//ES827115				
Unigene3187_All	221	0.71	0.00	0.48	3.38	1.09	0.41	3.06	0.38	0.18	-9.47E+00	2.15E-01		-5.60E-01	7.76E-01		-1.63E+00	4.48E-02		-3.05E+00	3.33E-03		-3.02E+00	2.43E-03		-4.09E+00	3.10E-04	Down				Unigene3187_All//7.00E-122//TC148073				
Unigene31872_All	323	44.87	23.53	17.48	148.36	173.78	89.77	87.57	17.73	18.25	-9.31E-01	5.82E-10		-1.36E+00	6.55E-17	Down	2.28E-01	7.97E-04		-7.25E-01	4.92E-22		-2.30E+00	8.36E-85	Down	-2.26E+00	1.69E-85	Down	Unigene31872_All//gi|118481921|gb|ABK92885.1|//2.00E-09//unknown [Populus trichocarpa] >gi|118485176|gb|ABK94449.1| unknown [Populus trichocarpa]		Unigene31872_All//1.00E-127//TC173688				nr -
Unigene3188_All	1553	2.19	2.35	1.78	13.76	11.53	5.47	6.29	5.76	4.23	1.01E-01	7.51E-01		-2.97E-01	4.00E-01		-2.55E-01	3.23E-02		-1.33E+00	8.12E-27	Down	-1.27E-01	5.17E-01		-5.71E-01	3.19E-04		Unigene3188_All//gi|53370641|gb|AAU89136.1|//2.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene3188_All//2.00E-08//AT5G65005| nucleic acid binding	Unigene3188_All//0.00E+00//TC148073				nr -
Unigene31884_All	232	0.23	0.00	0.46	3.01	1.19	0.00	0.00	0.00	0.00	-7.82E+00	6.12E-01		1.03E+00	7.03E-01		-1.34E+00	1.09E-01		-1.16E+01	1.96E-04	Down	null	null		null	null									
Unigene31886_All	282	13.92	28.21	16.99	8.48	14.04	21.46	43.63	54.39	161.33	1.02E+00	1.27E-06	Up	2.88E-01	3.48E-01		7.28E-01	1.53E-02		1.34E+00	5.94E-08	Up	3.18E-01	1.49E-02		1.89E+00	3.97E-107	Up	Unigene31886_All//gi|85542670|gb|AB671315.1|//1.00E-21//3-hydroxy-3-methylglutaryl-coenzyme A reductase [Gossypium barbadense]	Unigene31886_All//2.00E-20//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene31886_All//2.00E-76//ES826160		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene31889_All	256	0.41	0.00	4.16	0.00	0.13	0.71	2.31	3.59	0.93	-8.68E+00	3.72E-01		3.35E+00	3.36E-04	Up	7.07E+00	8.30E-01		9.46E+00	1.94E-01		6.35E-01	3.48E-01		-1.31E+00	1.15E-01									
Unigene31891_All	626	0.00	0.00	0.00	0.00	0.00	0.00	0.81	1.07	3.37	null	null		null	null		null	null		null	null		3.98E-01	6.48E-01		2.06E+00	2.53E-06	Up								
Unigene31896_All	255	0.00	0.60	2.71	1.76	1.76	2.48	2.65	2.13	1.72	9.22E+00	2.35E-01		1.14E+01	6.16E-04	Up	-2.10E-03	9.69E-01		4.96E-01	6.37E-01		-3.16E-01	6.74E-01		-6.26E-01	4.03E-01									
Unigene3190_All	1554	4.48	2.48	2.88	2.05	3.50	2.88	2.50	0.70	0.97	-8.54E-01	1.28E-04		-6.38E-01	5.88E-03		7.71E-01	1.68E-03		4.88E-01	1.01E-01		-1.84E+00	2.22E-09	Down	-1.36E+00	1.34E-06	Down	Unigene3190_All//gi|20197808|gb|AAM15256.1|//2.00E-92//Expressed protein [Arabidopsis thaliana] >gi|109134131|gb|ABG25064.1| At2g18245 [Arabidopsis thaliana]	Unigene3190_All//1.00E-93//AT2G18245| unknown protein	Unigene3190_All//0.00E+00//ES812552		GO:0043231	nr +
Unigene3191_All	1810	1.53	1.93	1.47	5.34	5.52	5.26	13.48	14.73	35.68	3.34E-01	3.34E-01		-5.86E-02	8.85E-01		4.73E-02	8.19E-01		-2.02E-02	9.38E-01		1.28E-01	2.36E-01		1.40E+00	1.16E-99	Up	Unigene3191_All//gi|9755446|gb|AAF98207.1|AC007152_3/1.00E-27//Putative protein kinase [Arabidopsis thaliana]	Unigene3191_All//8.00E-27//AT5G38260| serine/threonine protein kinase, putative	Unigene3191_All//2.00E-59//TC129826		GO:0016301	nr +
Unigene31911_All	556	0.00	0.00	0.00	0.00	0.00	0.00	0.99	0.00	2.08	null	null		null	null		null	null		null	null		-9.95E+00	4.61E-04	Down	1.07E+00	5.22E-02		Unigene31911_All//gi|224058587|ref|XP_002299554.1|//3.00E-49//mtn21-like protein [Populus trichocarpa] >gi|222846812|gb|EEE84359.1| mtn21-like protein [Populus trichocarpa]	Unigene31911_All//1.00E-31//AT1G68170| nodulin MtN21 family protein	Unigene31911_All//0.00E+00//ES817270				nr -
Unigene31912_All	328	2.87	0.00	0.00	0.61	0.32	0.55	0.64	1.40	1.46	-1.15E+01	1.46E-05	Down	-1.15E+01	3.35E-05	Down	-9.48E-01	5.88E-01		-1.41E-01	9.35E-01		1.12E+00	2.74E-01		1.18E+00	2.18E-01		Unigene31912_All//gi|2832408|emb|CAA74605.1|//2.00E-37//R2R3-MYB transcription factor [Arabidopsis thaliana]	Unigene31912_All//6.00E-35//AT3G49690| MYB84 (MYB DOMAIN PROTEIN 84); DNA binding / transcription factor	Unigene31912_All//1.00E-19//NP524476	MYB	GO:0001071//GO:0003676//GO:0006351//GO:0009725//GO:0010468//GO:0043231	nr +
Unigene31914_All	232	0.68	0.00	0.00	4.94	1.63	0.78	1.28	0.00	1.03	-9.40E+00	2.15E-01		-9.40E+00	2.45E-01		-1.60E+00	1.02E-02		-2.66E+00	4.12E-04	Down	-1.03E+01	2.18E-02		-3.08E-01	7.75E-01		Unigene31914_All//gi|42565162|ref|NP_189089.3|//2.00E-21//TMS membrane family protein / tumour differentially expressed (TDE) family protein [Arabidopsis thaliana] >gi|17381270|gb|AAL36053.1| AT3g24470/MXP5_4 [Arabidopsis thaliana] >gi|37201996|gb|AAQ89613.1| At3g24470/MXP5_4 [Arabidopsis thaliana]	Unigene31914_All//7.00E-23//AT3G24460| TMS membrane family protein / tumour differentially expressed (TDE) family protein			GO:0003006//GO:0044464	nr -
Unigene31916_All	247	1.06	1.23	5.82	2.62	3.49	1.83	1.03	0.68	0.00	2.17E-01	8.65E-01		2.46E+00	3.26E-04	Up	4.11E-01	6.11E-01		-5.20E-01	5.88E-01		-6.01E-01	6.48E-01		-1.00E+01	3.04E-02					Unigene31916_All//3.00E-10//TC178633				
Unigene31922_All	399	0.26	0.38	0.00	1.25	0.00	0.11	0.74	0.63	1.50	5.39E-01	7.79E-01		-8.04E+00	3.93E-01		-1.03E+01	8.98E-04	Down	-3.46E+00	1.61E-02		-2.39E-01	8.39E-01		1.01E+00	2.18E-01		Unigene31922_All//gi|27764548|gb|AAO23078.1|//1.00E-07//polyprotein [Glycine max]				GO:0003676//GO:0006259//GO:0043231	nr -
Unigene31924_All	561	1.12	0.00	0.95	0.36	0.25	0.00	0.38	0.82	0.14	-1.01E+01	7.91E-04	Down	-2.38E-01	7.75E-01		-5.33E-01	7.48E-01		-8.47E+00	1.33E-01		1.12E+00	2.74E-01		-1.41E+00	3.80E-01		Unigene31924_All//gi|56561617|emb|CAG28412.1|//1.00E-35//S-receptor kinase-like protein 1 [Senecio squalidus]	Unigene31924_All//7.00E-26//AT1G67520| lectin protein kinase family protein			GO:0016301	nr -
Unigene31927_All	285	1.84	0.36	0.37	5.94	2.05	1.11	0.74	0.15	0.00	-2.37E+00	4.75E-02		-2.30E+00	6.76E-02		-1.53E+00	1.66E-03		-2.42E+00	2.78E-05	Down	-2.34E+00	2.37E-01		-9.53E+00	5.80E-02					Unigene31927_All//7.00E-67//TC142253				ESTscan -
Unigene31928_All	292	30.82	79.65	29.73	22.69	66.39	18.41	17.23	117.23	46.11	1.37E+00	4.89E-28	Up	-5.21E-02	8.04E-01		1.55E+00	1.13E-32	Up	-3.02E-01	2.24E-01		2.77E+00	6.51E-126	Up	1.42E+00	8.28E-22	Up	Unigene31928_All//gi|224116328|ref|XP_002331955.1|//1.00E-16//glutaredoxin C9 [Populus trichocarpa] >gi|222874732|gb|EEF11863.1| glutaredoxin C9 [Populus trichocarpa]	Unigene31928_All//2.00E-08//AT1G28480| GRX480; electron carrier/ protein disulfide oxidoreductase	Unigene31928_All//4.00E-136//TC151442		GO:0009987//GO:0010033//GO:0023033	nr +
Unigene3193_All	1250	0.33	0.16	0.17	2.79	1.54	0.65	1.08	2.24	2.10	-1.05E+00	3.66E-01		-9.75E-01	4.11E-01		-8.55E-01	5.83E-03		-2.10E+00	9.85E-09	Down	1.05E+00	1.88E-03		9.59E-01	4.61E-03		Unigene3193_All//gi|297796181|ref|XP_002865975.1|//5.00E-88//WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311810|gb|EFH42234.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3193_All//3.00E-79//AT5G24320| WD-40 repeat family protein	Unigene3193_All//2.00E-30//CO120903		ko03022|Basal transcription factors	GO:0019897//GO:0023060	nr +
Unigene31930_All	486	0.00	0.00	0.00	0.00	0.00	0.00	0.35	3.44	11.31	null	null		null	null		null	null		null	null		3.31E+00	6.97E-08	Up	5.02E+00	1.98E-33	Up	Unigene31930_All//gi|224116020|ref|XP_002332028.1|//9.00E-16//predicted protein [Populus trichocarpa] >gi|222875253|gb|EEF12384.1| predicted protein [Populus trichocarpa]						nr -
Unigene31937_All	688	0.00	0.00	0.00	0.00	0.00	0.00	2.03	1.28	0.00	null	null		null	null		null	null		null	null		-6.69E-01	1.94E-01		-1.10E+01	2.40E-10	Down								
Unigene31938_All	518	0.00	0.00	0.00	0.00	0.00	0.00	15.92	1.94	0.85	null	null		null	null		null	null		null	null		-3.04E+00	5.78E-34	Down	-4.23E+00	3.47E-46	Down	Unigene31938_All//sp|Q5T9S5|CCD18_HUMAN//3.00E-06//Coiled-coil domain-containing protein 18 OS=Homo sapiens GN=CCDC18 PE=1 SV=1		Unigene31938_All//4.00E-125//TC161176				swissprot +
Unigene31939_All	586	0.45	2.85	0.82	0.51	0.82	1.16	3.10	2.14	4.89	2.68E+00	1.99E-05	Up	8.73E-01	4.17E-01		6.90E-01	5.66E-01		1.18E+00	2.08E-01		-5.36E-01	2.32E-01		6.58E-01	3.95E-02					Unigene31939_All//4.00E-30//TC140792				
Unigene3194_All	1594	0.23	0.45	1.37	5.50	3.28	1.81	2.65	0.94	1.97	9.53E-01	2.62E-01		2.58E+00	2.37E-06	Up	-7.44E-01	3.53E-05		-1.60E+00	9.62E-15	Down	-1.49E+00	1.02E-07	Down	-4.26E-01	1.01E-01		Unigene3194_All//gi|30689400|ref|NP_851068.1|//1.00E-138//WD-40 repeat family protein [Arabidopsis thaliana]	Unigene3194_All//2.00E-138//AT5G24320| WD-40 repeat family protein	Unigene3194_All//2.00E-31//DR453715		ko03022|Basal transcription factors		nr -
Unigene31946_All	336	0.00	0.00	0.00	0.00	0.00	0.00	0.50	1.24	8.06	null	null		null	null		null	null		null	null		1.31E+00	2.34E-01		4.00E+00	1.17E-14	Up								
Unigene31947_All	283	1.85	0.72	0.00	4.22	2.07	0.80	0.75	0.00	0.14	-1.37E+00	1.97E-01		-1.09E+01	4.75E-03		-1.03E+00	8.42E-02		-2.40E+00	7.07E-04	Down	-9.55E+00	7.44E-02		-2.41E+00	1.95E-01		Unigene31947_All//gi|19310401|gb|AAL84940.1|//2.00E-09//At2g46980/F14M4.19 [Arabidopsis thaliana]	Unigene31947_All//2.00E-11//AT2G46980| unknown protein					nr +
Unigene31949_All	266	0.00	0.00	0.00	3.18	2.85	0.00	0.16	0.00	0.00	null	null		null	null		-1.61E-01	8.14E-01		-1.16E+01	2.43E-05	Down	-7.31E+00	6.57E-01		-7.31E+00	6.12E-01			Unigene31949_All//5.00E-05//AT4G34540| isoflavone reductase family protein	Unigene31949_All//1.00E-12//TC144170				
Unigene3195_All	1518	22.61	5.61	15.47	16.05	11.75	14.49	2.87	1.32	2.20	-2.01E+00	6.26E-71	Down	-5.48E-01	6.07E-09		-4.50E-01	1.04E-05		-1.47E-01	2.43E-01		-1.12E+00	2.25E-05	Down	-3.80E-01	1.40E-01		Unigene3195_All//gi|226533172|ref|NP_001149252.1|//1.00E-99//LOC100282874 [Zea mays] >gi|195625782|gb|ACG34721.1| thioredoxin family protein [Zea mays]	Unigene3195_All//7.00E-103//AT4G28590| unknown protein	Unigene3195_All//6.00E-65//gi|109834478|gb|DW233043.1|DW233043				nr +
Unigene31954_All	359	0.00	0.00	0.00	0.83	0.00	0.13	2.47	0.00	0.00	null	null		null	null		-9.70E+00	2.01E-02		-2.73E+00	1.37E-01		-1.13E+01	2.24E-06	Down	-1.13E+01	1.10E-06	Down			Unigene31954_All//3.00E-66//DW517200				
Unigene31955_All	244	0.00	2.70	1.96	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.25E-04	Up	1.09E+01	7.48E-03		null	null		null	null		null	null		null	null		Unigene31955_All//sp|Q2LZ58|CHRB_DROPS//5.00E-16//Protein charybde OS=Drosophila pseudoobscura pseudoobscura GN=chrb PE=2 SV=1						swissprot +
Unigene31956_All	211	76.13	54.51	57.29	85.23	54.84	30.82	42.08	32.49	27.19	-4.82E-01	5.20E-04		-4.10E-01	4.86E-03		-6.36E-01	1.01E-07		-1.47E+00	3.60E-26	Down	-3.73E-01	3.52E-02		-6.30E-01	1.69E-04				Unigene31956_All//2.00E-91//gi|164311976|gb|EX164435.1|EX164435				ESTscan -
Unigene31957_All	573	0.09	3.54	4.00	0.00	0.00	0.32	0.00	0.00	0.00	5.28E+00	2.99E-10	Up	5.45E+00	2.66E-11	Up	null	null		8.30E+00	1.94E-01		null	null		null	null		Unigene31957_All//gi|226500248|ref|NP_001147705.1|//9.00E-33//nascent polypeptide-associated complex alpha subunit-like protein [Zea mays] >gi|195613184|gb|ACG28422.1| nascent polypeptide-associated complex alpha subunit-like protein [Zea mays]	Unigene31957_All//3.00E-31//AT3G12390| nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative	Unigene31957_All//2.00E-07//EX171181		GO:0005840//GO:0006970	nr -
Unigene3196_All	1599	39.89	29.72	35.73	74.33	91.20	87.64	45.16	45.22	18.11	-4.24E-01	8.66E-11		-1.59E-01	2.82E-02		2.95E-01	2.37E-14		2.38E-01	1.50E-08		1.80E-03	1.02E+00		-1.32E+00	4.78E-102	Down	Unigene3196_All//gi|297798950|ref|XP_002867359.1|//1.00E-134//integral membrane Yip1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313195|gb|EFH43618.1| integral membrane Yip1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3196_All//4.00E-104//AT2G18840| integral membrane Yip1 family protein	Unigene3196_All//0.00E+00//TC163573		ko03040|Spliceosome		nr -
Unigene31962_All	371	0.00	25.40	6.60	0.00	0.09	0.00	0.00	0.00	0.00	1.46E+01	5.67E-54	Up	1.27E+01	1.64E-13	Up	6.54E+00	8.30E-01		null	null		null	null		null	null									ESTscan -
Unigene31965_All	421	0.00	0.96	0.00	0.47	3.03	1.07	0.40	0.99	2.46	9.91E+00	1.36E-02		null	null		2.68E+00	1.57E-04	Up	1.18E+00	3.38E-01		1.31E+00	2.34E-01		2.61E+00	2.37E-04	Up								
Unigene31966_All	513	18.87	39.90	20.24	38.84	36.52	37.94	11.79	12.14	8.08	1.08E+00	2.74E-17	Up	1.01E-01	6.20E-01		-8.91E-02	5.54E-01		-3.37E-02	8.21E-01		4.27E-02	8.63E-01		-5.45E-01	8.68E-03				Unigene31966_All//0.00E+00//gi|11199373|gb|BF268378.1|BF268378				
Unigene31967_All	332	0.32	0.00	0.00	0.60	0.83	4.08	0.00	0.00	0.24	-8.30E+00	3.72E-01		-8.30E+00	3.93E-01		4.67E-01	8.17E-01		2.77E+00	9.12E-05	Up	null	null		7.91E+00	4.04E-01		Unigene31967_All//gi|224146504|ref|XP_002326030.1|//1.00E-37//beta-ketoacyl-coa synthase family protein [Populus trichocarpa] >gi|222862905|gb|EEF00412.1| beta-ketoacyl-coa synthase family protein [Populus trichocarpa]	Unigene31967_All//7.00E-36//AT5G04530| KCS19 (3-KETOACYL-COA SYNTHASE 19); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene31967_All//0.00E+00//TC135401		GO:0006631//GO:0006950//GO:0009314//GO:0016747//GO:0043231	nr +
Unigene31969_All	348	0.00	0.00	0.00	0.00	0.00	0.26	0.00	0.84	2.63	null	null		null	null		null	null		8.02E+00	4.76E-01		9.72E+00	2.35E-02		1.14E+01	1.08E-06	Up								
Unigene31973_All	273	0.00	0.00	0.00	0.00	0.00	0.00	8.52	0.92	1.90	null	null		null	null		null	null		null	null		-3.21E+00	1.59E-10	Down	-2.17E+00	2.13E-07	Down	Unigene31973_All//gi|225703022|dbj|BAH30233.1|//9.00E-09//cytochrome c oxidase subunit II [Haptoglossa sp. SZ03]				ko00190|Oxidative phosphorylation	GO:0016491//GO:0022900//GO:0043231//GO:0044425//GO:0046914	nr +
Unigene31975_All	338	0.00	5.70	1.42	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.73E-11	Up	1.05E+01	7.48E-03		null	null		null	null		null	null		null	null		Unigene31975_All//sp|Q9VH95|YC17_DROME//2.00E-20//Uncharacterized protein CG16817 OS=Drosophila melanogaster GN=CG16817 PE=1 SV=1						swissprot +
Unigene31979_All	263	0.80	0.00	1.21	3.22	4.98	1.55	5.95	0.48	3.33	-9.64E+00	1.22E-01		6.10E-01	6.24E-01		6.28E-01	3.11E-01		-1.06E+00	1.81E-01		-3.64E+00	5.20E-08	Down	-8.36E-01	6.46E-02				Unigene31979_All//1.00E-52//CO091564				

Unigene31983_All	269	0.00	9.04	4.75	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	7.73E-14	Up	1.22E+01	4.69E-07	Up	null	null		null	null		null	null		null	null		Unigene31983_All//gi|1703376|sp|P51824.2|ARF1_SOLTU//4.00E-42//RecName: Full=ADP-ribosylation factor 1 >gi|396808|emb|CAA52468.1| ADP-ribosylation factor 1 [Solanum tuberosum]	Unigene31983_All//3.00E-41//AT5G14670| ATARFA1B (ADP-ribosylation factor A1B); GTP binding / phospholipase activator/ protein binding	Unigene31983_All//2.00E-11//ES827280			GO:0006464//GO:0015031//GO:0032561//GO:0035556//GO:0043231	nr -
Unigene31988_All	456	0.80	0.22	0.35	1.86	1.28	0.30	5.47	1.01	0.52	-1.85E+00	1.87E-01		-1.20E+00	3.96E-01		-5.33E-01	4.90E-01		-2.64E+00	3.54E-03		-2.44E+00	1.25E-08	Down	-3.38E+00	3.35E-12	Down	Unigene31988_All//gi|294769202|gb|ADF36482.1|/3.00E-81//high-affinity potassium transporter protein 2 [Gossypium hirsutum]	Unigene31988_All//1.00E-64//AT1G70300| KUP6; potassium ion transmembrane transporter	Unigene31988_All//0.00E+00//TC159801			GO:0016020//GO:0030001//GO:0046873	nr +
Unigene31989_All	310	0.00	6.37	3.26	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.97E-11	Up	1.17E+01	1.27E-05	Up	null	null		null	null		null	null		null	null											ESTscan -
Unigene3199_All	811	10.84	6.12	8.01	20.45	12.44	10.19	7.46	4.38	3.19	-8.24E-01	2.50E-05		-4.36E-01	3.46E-02		-7.17E-01	9.83E-09		-1.01E+00	1.50E-13	Down	-7.67E-01	3.41E-04		-1.22E+00	2.04E-08	Down	Unigene3199_All//gi|116309014|emb|CAH66131.1|/3.00E-07//OSIGBa0133L04.5 [Oryza sativa (indica cultivar-group)]	Unigene3199_All//6.00E-06//AT5G65005| nucleic acid binding	Unigene3199_All//0.00E+00//TC176721				nr -
Unigene31993_All	610	0.00	0.00	0.17	0.16	0.00	0.30	1.11	4.25	12.67	null	null		7.45E+00	3.98E-01		-7.35E+00	3.13E-01		8.59E-01	6.95E-01		1.94E+00	6.92E-07	Up	3.51E+00	6.79E-37	Up	Unigene31993_All//gi|255538156|ref|XP_002510143.1|/1.00E-09//conserved hypothetical protein [Ricinus communis] >gi|223550844|gb|EEF52330.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene31998_All	230	0.00	3.08	1.85	0.00	0.30	0.00	0.00	0.00	0.00	1.16E+01	3.33E-04	Up	1.09E+01	1.38E-02		8.23E+00	6.09E-01		null	null		null	null		null	null		Unigene31998_All//gi|15233606|ref|NP_191680.1|//9.00E-18//PRMT11 (ARGININE METHYLTRANSFERASE 11); protein-arginine N-methyltransferase [Arabidopsis thaliana] >gi|75208030|sp|Q9SU94.1|ANM11_ARATH RecName: Full=Probable protein arginine N-methyltransferase 1.1; AltName: Full=Arginine methyltransferase pam1 >gi|5123545|emb|CAB45311.1| arginine methyltransferase (pam1) [Arabidopsis thaliana] >gi|7269850|emb|CAB79709.1| arginine methyltransferase (pam1) [Arabidopsis thaliana] >gi|21593404|gb|AAM65371.1| arginine methyltransferase pam1 [Arabidopsis thaliana] >gi|23297369|gb|AAN12952.1| arginine methyltransferase pam1 [Arabidopsis thaliana]	Unigene31998_All//4.00E-19//AT4G29510| PRMT11 (ARGININE METHYLTRANSFERASE 11); protein-arginine N-methyltransferase				GO:0005515//GO:0008276//GO:0043231	nr -
Unigene31999_All	244	1.50	0.83	0.44	4.08	0.28	0.37	1.21	0.34	0.33	-8.54E-01	4.89E-01		-1.78E+00	2.34E-01		-3.85E+00	1.61E-05	Down	-3.46E+00	1.73E-04	Down	-1.82E+00	2.11E-01		-1.89E+00	1.68E-01										
Unigene320_All	3424	1.67	0.77	1.84	2.52	2.20	2.14	2.67	0.99	2.86	-1.11E+00	1.21E-05	Down	1.40E-01	6.20E-01		-1.93E-01	3.87E-01		-2.36E-01	2.86E-01		-1.43E+00	6.75E-15	Down	1.02E-01	5.99E-01		Unigene320_All//gi|31711766|gb|AAP68239.1|//1.00E-117//At2g29510 [Arabidopsis thaliana]	Unigene320_All//1.00E-78//AT2G29510| unknown protein	Unigene320_All//0.00E+00//TC164552				nr -
Unigene3200_All	274	24.82	5.36	11.08	11.09	15.46	10.71	1.39	3.66	0.87	-2.21E+00	2.34E-16	Down	-1.16E+00	1.25E-06	Down	4.79E-01	1.12E-01		-4.98E-02	9.08E-01		1.40E+00	2.82E-02		-6.71E-01	5.31E-01		Unigene3200_All//gi|42568893|ref|NP_178403.2|/2.00E-12//mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana]	Unigene3200_All//3.00E-09//AT2G03050| mitochondrial transcription termination factor-related / mTERF-related	Unigene3200_All//8.00E-153//TC164849				nr +
Unigene32001_All	309	0.17	2.62	0.34	0.48	0.00	0.00	1.78	1.89	1.16	3.95E+00	7.52E-04	Up	1.03E+00	7.03E-01		-8.92E+00	1.66E-01		-8.92E+00	2.33E-01		9.03E-02	9.27E-01		-6.16E-01	4.68E-01				Unigene32001_All//6.00E-123//TC132192					
Unigene32006_All	451	0.00	0.00	0.00	0.22	0.00	0.00	4.59	1.76	1.06	null	null		null	null		-7.79E+00	3.13E-01		-7.79E+00	4.00E-01		-1.38E+00	8.02E-04	Down	-2.12E+00	1.66E-06	Down	Unigene32006_All//gi|115485951|ref|NP_001068119.1|/6.00E-28//Os11g0569800 [Oryza sativa Japonica Group] >gi|113645341|dbj|BAF28482.1| Os11g0569800 [Oryza sativa Japonica Group]	Unigene32006_All//8.00E-25//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0004871//GO:0008152//GO:0016020//GO:0016491	nr -
Unigene32007_All	489	0.00	0.00	0.00	0.20	0.00	0.09	2.59	6.07	0.73	null	null		null	null		-7.67E+00	3.13E-01		-1.14E+00	6.76E-01		1.23E+00	2.14E-04	Up	-1.82E+00	1.09E-03										
Unigene32009_All	409	1.02	1.24	0.52	2.07	0.84	2.10	2.07	0.10	0.88	2.76E-01	7.64E-01		-9.75E-01	4.11E-01		-1.30E+00	8.00E-02		1.91E-02	9.82E-01		-4.34E+00	4.55E-05	Down	-1.24E+00	6.26E-02				Unigene32009_All//5.00E-07//ES814122					
Unigene32011_All	534	0.00	14.80	10.47	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	3.29E-45	Up	1.34E+01	3.82E-31	Up	null	null		null	null		null	null		null	null		Unigene32011_All//gi|301122631|ref|XP_002909042.1|/6.00E-49//40S ribosomal protein S6 [Phytophthora infestans T30-4] >gi|262099804|gb|EEY57856.1| 40S ribosomal protein S6 [Phytophthora infestans T30-4]	Unigene32011_All//1.00E-39//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome			ko03010|Ribosome	GO:0030529	nr +
Unigene32012_All	439	0.00	2.08	1.46	0.11	0.55	0.31	0.00	0.19	0.00	1.10E+01	2.62E-05	Up	1.05E+01	1.16E-03		2.27E+00	3.05E-01		1.44E+00	6.38E-01		7.57E+00	4.01E-01		null	null										
Unigene32014_All	471	0.00	0.00	0.00	0.00	0.00	0.00	6.28	1.42	0.93	null	null		null	null		null	null		null	null		-2.15E+00	9.07E-09	Down	-2.76E+00	6.83E-12	Down	Unigene32014_All//gi|8569094|gb|AAF76439.1|AC015445_6//6.00E-16//Contains similarity to PR1a protein precursor from Nicotiana tabacum gb|D90196 and contains an SCP domain PF|00188. EST gb|R64931 comes from this gene [Arabidopsis thaliana]	Unigene32014_All//7.00E-12//AT1G50060| pathogenesis-related protein, putative			ko04626|Plant-pathogen interaction		nr +
Unigene32017_All	397	0.00	31.14	12.88	0.00	0.00	0.00	0.00	0.00	0.00	1.49E+01	6.25E-71	Up	1.37E+01	1.92E-28	Up	null	null		null	null		null	null		null	null		Unigene32017_All//gi|157011451|gb|ABV00887.1|//2.00E-66//actin [Rhodomonas sp. CCMP768]	Unigene32017_All//6.00E-65//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene32017_All//5.00E-84//TC153744		ko04145|Phagosome	GO:0032559//GO:0043232	nr +
Unigene32019_All	466	0.22	1.96	0.00	0.00	1.03	0.78	0.18	0.45	9.83	3.12E+00	1.14E-03		-7.81E+00	3.93E-01		1.00E+01	5.07E-03		9.60E+00	2.37E-02		1.31E+00	4.47E-01		5.76E+00	1.34E-29	Up									
Unigene3202_All	875	13.33	10.89	11.02	28.98	29.44	21.63	39.72	44.18	18.35	-2.93E-01	8.92E-02		-2.76E-01	1.34E-01		2.27E-02	8.68E-01		-4.22E-01	6.40E-05		1.54E-01	6.57E-02		-1.11E+00	3.47E-38	Down	Unigene3202_All//gi|195652255|gb|ACG45595.1|/6.00E-26//WDL1 [Zea mays]	Unigene3202_All//5.00E-23//AT4G32330| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009657); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G25480.1); Has 4728 Blast hits to 3313 proteins in 331 species: Archae - 4; Bacteria - 347; Metazoa - 2216; Fungi - 461; Plants - 233; Viruses - 22; Other Eukaryotes - 1445 (source: NCBI BLink).	Unigene3202_All//0.00E+00//TC138293				nr +
Unigene32020_All	709	0.00	5.86	2.33	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.16E-23	Up	1.12E+01	4.30E-09	Up	null	null		null	null		null	null		null	null											ESTscan -
Unigene32025_All	498	0.00	5.90	5.35	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.01E-16	Up	1.24E+01	1.07E-14	Up	null	null		null	null		null	null		null	null		Unigene32025_All//sp|P28750|EXU_DROME//3.00E-34//Maternal protein exuperantia OS=Drosophila melanogaster GN=exu PE=1 SV=2						swissprot -
Unigene32029_All	716	0.00	0.00	0.00	0.00	0.00	0.00	2.72	0.41	0.28	null	null		null	null		null	null		null	null		-2.73E+00	1.08E-07	Down	-3.29E+00	1.95E-09	Down	Unigene32029_All//gi|34501378|ref|NP_904166.1|//1.00E-14//NADH dehydrogenase subunit 2 [Physcomitrella patens subsp. patens] >gi|75325320|sp|Q6YX89.1|NU2C_PHYPA RecName: Full=NAD(P)H-quinone oxidoreductase subunit 2, chloroplastic; AltName: Full=NAD(P)H dehydrogenase, subunit 2; AltName: Full=NADH-plastoquinone oxidoreductase subunit 2 >gi|34494748|dbj|BAC85015.1| NADH dehydrogenase ND2 subunit [Physcomitrella patens subsp. patens]				ko00190|Oxidative phosphorylation	GO:0044464	nr -
Unigene32031_All	1095	0.00	10.37	2.43	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	4.44E-65	Up	1.12E+01	1.07E-14	Up	null	null		null	null		null	null		null	null		Unigene32031_All//gi|224089583|ref|XP_002308766.1|//3.00E-25//cytochrome P450 [Populus trichocarpa] >gi|222854742|gb|EEE92289.1| cytochrome P450 [Populus trichocarpa]	Unigene32031_All//4.00E-25//AT5G38450| CYP735A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00908|Zeatin biosynthesis//ko00591|Linoleic acid metabolism//ko00100|Steroid biosynthesis//ko00590|Arachidonic acid metabolism	GO:0005488//GO:0008152//GO:0065007	nr +
Unigene32033_All	599	0.00	5.24	4.36	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.08E-18	Up	1.21E+01	2.12E-14	Up	null	null		null	null		null	null		null	null		Unigene32033_All//gi|219117691|ref|XP_002179636.1|//1.00E-11//long chain acyl-coa synthetase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217408689|gb|EEC48622.1| long chain acyl-coa synthetase [Phaeodactylum tricornutum CCAP 1055/1]						nr -
Unigene32036_All	379	0.00	0.00	0.00	0.00	0.00	0.00	1.34	5.29	0.21	null	null		null	null		null	null		null	null		1.98E+00	1.22E-05	Up	-2.67E+00	1.37E-02										
Unigene32037_All	469	0.22	0.65	0.00	0.96	1.10	0.87	0.54	1.69	2.80	1.54E+00	3.23E-01		-7.80E+00	3.93E-01		2.01E-01	8.59E-01		-1.41E-01	9.00E-01		1.63E+00	2.88E-02		2.37E+00	7.20E-05	Up									
Unigene3204_All	1403	2.80	7.80	2.58	22.30	45.09	80.96	54.88	155.15	116.76	1.48E+00	3.68E-15	Up	-1.16E-01	7.18E-01		1.02E+00	1.39E-55	Up	1.86E+00	9.65E-225	Up	1.50E+00	0.00E+00	Up	1.09E+00	3.21E-169	Up	Unigene3204_All//gi|224122012|ref|XP_002318728.1|//1.00E-134//f-box family protein [Populus trichocarpa] >gi|222859401|gb|EEE96948.1| f-box family protein [Populus trichocarpa]	Unigene3204_All//1.00E-127//AT1G67340| zinc finger (MYND type) family protein / F-box family protein	Unigene3204_All//1.00E-164//TC174303				nr +
Unigene32042_All	389	4.98	0.65	0.27	0.26	0.18	0.00	3.04	0.86	0.61	-2.93E+00	8.83E-07	Down	-4.18E+00	2.33E-08	Down	-5.33E-01	8.16E-01		-8.00E+00	4.00E-01		-1.82E+00	2.43E-03		-2.31E+00	2.04E-04	Down	Unigene32042_All//gi|115479213|ref|NP_001063200.1|//6.00E-32//Os09g0420900 [Oryza sativa Japonica Group] >gi|113631433|dbj|BAF25114.1| Os09g0420900 [Oryza sativa Japonica Group]	Unigene32042_All//4.00E-19//AT4G31820| ENP (ENHANCER OF PINOID); protein binding / signal transducer	Unigene32042_All//2.00E-24//AI731519			GO:0005488//GO:0005768//GO:0008105//GO:0009314//GO:0009793//GO:0009908//GO:0009926//GO:0016020//GO:0060089	nr -

Unigene32043_All	402	0.00	34.79	13.91	0.00	0.00	0.00	0.00	0.00	0.00	1.51E+01	2.69E-80	Up	1.38E+01	3.82E-31	Up	null	null		null	null		null	null		null	null		Unigene32043_All//gi|15228895|ref|NP_191193.1|//1.00E-39//40S ribosomal protein S26 (RPS26C) [Arabidopsis thaliana] >gi|75264413|sp|Q9LYK9.1|RS263_ARATH RecName: Full=40S ribosomal protein S26-3 >gi|7572932|emb|CAB87433.1| 40S ribosomal protein S26 homolog [Arabidopsis thaliana] >gi|14532524|gb|AAK63990.1| AT3g56340/F18021_300 [Arabidopsis thaliana] >gi|22137298|gb|AAM91494.1| AT3g56340/F18021_300 [Arabidopsis thaliana]	Unigene32043_All//8.00E-41//AT3G56340| 40S ribosomal protein S26 (RPS26C)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0022613	nr -
Unigene32044_All	387	0.00	24.61	6.88	0.00	0.00	0.00	0.00	0.00	0.00	1.46E+01	1.48E-54	Up	1.27E+01	1.07E-14	Up	null	null		null	null		null	null		null	null		Unigene32044_All//gi|298711489|emb|CBJ26577.1|//1.00E-60//40S ribosomal protein S17 [Ectocarpus siliculosus]	Unigene32044_All//7.00E-31//AT2G05220| 40S ribosomal protein S17 (RPS17B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene32047_All	514	0.00	0.00	0.00	0.00	0.00	0.26	0.00	0.00	1.09	null	null		null	null		null	null		8.04E+00	3.11E-01		null	null		1.01E+01	3.28E-04	Up	Unigene32047_All//gi|218764874|gb|ACL11801.1|//8.00E-58//WOX9-like protein [Phaseolus coccineus]	Unigene32047_All//4.00E-35//AT2G33880| HB-3; transcription factor	Unigene32047_All//3.00E-49//CO490788	HB		GO:0001071//GO:0003006//GO:0003677//GO:0006351//GO:0008283//GO:0009725//GO:0010073//GO:0010468//GO:0043231	nr +
Unigene32049_All	1293	7.20	2.78	5.68	1.77	0.83	0.21	0.07	0.13	0.00	-1.37E+00	9.22E-12	Down	-3.42E-01	9.26E-02		-1.10E+00	5.65E-03		-3.08E+00	8.48E-09	Down	9.83E-01	6.33E-01		-6.03E+00	3.58E-01		Unigene32049_All//gi|242085688|ref|XP_002443269.1|/6.00E-09//hypothetical protein SORBIDRAFT_08g016660 [Sorghum bicolor] >gi|241943962|gb|EES17107.1| hypothetical protein SORBIDRAFT_08g016660 [Sorghum bicolor]	Unigene32049_All//6.00E-05//AT4G09490| RNase H domain-containing protein					nr -
Unigene3205_All	841	40.25	17.77	45.08	18.24	17.44	11.65	2.71	2.39	0.85	-1.18E+00	2.31E-32	Down	1.64E-01	9.31E-02		-6.48E-02	7.23E-01		-6.47E-01	3.04E-06		-1.87E-01	6.29E-01		-1.67E+00	2.12E-05	Down	Unigene3205_All//gi|15238184|ref|NP_196069.1|//9.00E-54//VTE5 (vitamin E pathway gene5); phosphatidate cytidylyltransferase/ phytol kinase [Arabidopsis thaliana] >gi|75181203|sp|Q9LZ76.1|PHTK1_ARATH RecName: Full=Phytol kinase 1, chloroplastic; AltName: Full=Vitamin E pathway gene 5 protein; Flags: Precursor >gi|60543321|gb|AAX22258.1| At5g04490 [Arabidopsis thaliana]	Unigene3205_All//1.00E-53//AT5G04490| VTE5 (vitamin E pathway gene5); phosphatidate cytidylyltransferase/ phytol kinase	Unigene3205_All//0.00E+00//gi|164264589|gb|ES851942.1|ES851942			GO:0006644//GO:0009941//GO:0016301//GO:0031224//GO:0042360	nr +
Unigene32050_All	351	0.00	12.70	9.56	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	2.11E-25	Up	1.32E+01	1.47E-18	Up	null	null		null	null		null	null		null	null		Unigene32050_All//sp|Q6VQ62|NPC2_DROME//6.00E-46//Protein NPC2 homolog OS=Drosophila melanogaster GN=Npc2a PE=1 SV=1						swissprot +
Unigene32051_All	441	0.47	0.00	0.00	0.11	0.16	0.00	1.92	10.14	2.89	-8.89E+00	1.22E-01		-8.89E+00	1.46E-01		4.67E-01	9.58E-01		-6.82E+00	6.35E-01		2.40E+00	1.25E-14	Up	5.92E-01	2.55E-01			Unigene32051_All//1.00E-07//TC171132				
Unigene32052_All	278	2.07	3.28	1.72	3.05	0.74	0.16	0.46	0.00	0.57	6.64E-01	3.75E-01		-2.64E-01	7.67E-01		-2.04E+00	9.05E-03		-4.23E+00	2.18E-04	Down	-8.83E+00	2.35E-01		3.29E-01	8.51E-01		Unigene32052_All//gi|5802244|gb|AAD51625.1|AF169022_1//2.00E-13//seed maturation protein PM37 [Glycine max]	Unigene32052_All//2.00E-10//AT3G44110| ATJ3; protein binding	Unigene32052_All//7.00E-36//gi|78352242|gb|DT572516.1|DT572516		ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0006950//GO:0032559//GO:0043169//GO:0044267//GO:0044424	nr -
Unigene32055_All	487	0.00	5.51	6.89	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.80E-15	Up	1.28E+01	1.47E-18	Up	null	null		null	null		null	null		null	null		Unigene32055_All//gi|298704860|emb|CBJ28377.1|//7.00E-16//DNA repair protein RAD52 homolog [Ectocarpus siliculosus]				ko03018|RNA degradation	GO:0044464	nr +
Unigene32056_All	832	0.00	32.22	12.74	0.12	0.00	0.00	0.00	0.00	0.00	1.50E+01	1.86E-154	Up	1.36E+01	1.65E-59	Up	-6.90E+00	3.13E-01		-6.90E+00	4.00E-01		null	null		null	null		Unigene32056_All//gi|6094086|sp|O65353.1|RL5_HELAN//1.00E-120//RecName: Full=60S ribosomal protein L5 >gi|3153904|gb|AAC17448.1| RPL5A-related protein [Helianthus annnuus]	Unigene32056_All//2.00E-87//AT5G39740| 60S ribosomal protein L5 (RPL5B)			ko03010|Ribosome	GO:0019843//GO:0030529	nr +
Unigene32058_All	422	1.12	0.00	1.77	2.12	0.33	2.35	0.90	0.99	2.08	-1.01E+01	5.55E-03		6.63E-01	4.19E-01		-2.70E+00	8.76E-04	Down	1.48E-01	8.42E-01		1.35E-01	8.99E-01		1.20E+00	6.68E-02		Unigene32058_All//gi|75191658|sp|Q9MX9.1|PPR18_ARATH//6.00E-52//RecName: Full=Pentatricopeptide repeat-containing protein At1g06710, mitochondrial; Flags: Precursor >gi|7523709|gb|AAF63148.1|AC011001_18 Hypothetical protein [Arabidopsis thaliana]	Unigene32058_All//3.00E-53//AT1G06710| pentatricopeptide (PPR) repeat-containing protein	Unigene32058_All//8.00E-151//DT462833			nr -
Unigene32065_All	422	0.25	1.20	0.00	3.42	0.33	1.28	2.50	1.78	0.09	2.28E+00	6.23E-02		-7.95E+00	3.93E-01		-3.39E+00	4.23E-07	Down	-1.41E+00	1.29E-02		-4.91E-01	4.22E-01		-4.73E+00	8.85E-07	Down	Unigene32065_All//gi|8778443|gb|AAF79451.1|AC025808_33//7.00E-28//F18014.11 [Arabidopsis thaliana]	Unigene32065_All//5.00E-17//AT1G16260| protein kinase family protein	Unigene32065_All//4.00E-100//CO118136			GO:0016772//GO:0051707	nr +
Unigene32073_All	450	0.00	9.57	5.56	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.56E-24	Up	1.24E+01	8.32E-14	Up	null	null		null	null		null	null		null	null							ESTscan -
Unigene32074_All	655	0.00	0.39	0.00	8.67	2.47	1.03	0.13	0.06	0.30	8.60E+00	7.86E-02		null	null		-1.81E+00	4.84E-13	Down	-3.07E+00	4.21E-21	Down	-1.02E+00	7.24E-01		1.24E+00	4.69E-01		Unigene32074_All//gi|60476420|gb|AX21349.1|//8.00E-50//lateral organ boundaries-like 3 [Lotus japonicus]	Unigene32074_All//6.00E-48//AT3G27650| LBD25 (LOB DOMAIN-CONTAINING PROTEIN 25)	Unigene32074_All//4.00E-169//DW505234		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0043231	nr -
Unigene32075_All	252	0.00	1.61	4.65	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	1.36E-02		1.22E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene32075_All//gi|116000710|emb|CAL50390.1|//2.00E-07//Predicted RNA-binding protein (1SS) [Ostreococcus tauri]					GO:0003824//GO:0005488//GO:0008152	nr -
Unigene32078_All	466	0.00	10.87	4.80	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	6.88E-29	Up	1.22E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene32078_All//gi|115468998|ref|NP_001058098.1|//1.00E-16//Os06g0622400 (Oryza sativa Japonica Group) >gi|113596138|dbj|BAF20012.1| Os06g0622400 (Oryza sativa Japonica Group)				ko03040|Spliceosome		nr +
Unigene3208_All	1201	18.86	28.69	22.12	38.78	56.51	54.26	2.18	4.80	2.55	6.05E-01	4.51E-11		2.30E-01	4.52E-02		5.43E-01	1.80E-20		4.85E-01	1.18E-14		1.14E+00	5.11E-07	Up	2.27E-01	4.99E-01		Unigene3208_All//gi|53370641|gb|AAU89136.1|//1.00E-19//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene3208_All//6.00E-09//AT3G09510| nucleic acid binding	Unigene3208_All//2.00E-64//TC146428				nr -
Unigene32080_All	430	0.00	0.00	0.00	0.00	0.00	0.00	3.24	4.37	0.00	null	null		null	null		null	null		null	null		4.31E-01	3.38E-01		-1.17E+01	2.40E-10	Down	Unigene32080_All//gi|112253311|gb|AB114243.1|//7.00E-29//60S ribosomal protein L32 [Pfiesteria piscicida]	Unigene32080_All//4.00E-27//AT4G18100| 60S ribosomal protein L32 (RPL32A)			ko03010|Ribosome	GO:0043231	nr -
Unigene32082_All	684	0.00	277.87	100.27	0.15	0.15	0.00	0.00	0.00	0.00	1.81E+01	0.00E+00	Up	1.66E+01	0.00E+00	Up	5.15E-02	9.67E-01		-7.19E+00	4.00E-01		null	null		null	null		Unigene32082_All//sp|P11996|LSP1B_DROME//4.00E-91//Larval serum protein 1 beta chain OS=Drosophila melanogaster GN=Lsp1beta PE=2 SV=3						swissprot +
Unigene32084_All	273	3.07	0.00	1.95	1.82	0.88	0.17	0.46	0.00	1.17	-1.16E+01	5.57E-05	Down	-6.53E-01	3.96E-01		-1.05E+00	3.15E-01		-3.46E+00	1.61E-02		-8.86E+00	2.35E-01		1.33E+00	2.93E-01				Unigene32084_All//4.00E-71//gi|78324778|gb|DT545052.1|DT545052				
Unigene32085_All	427	0.00	0.00	0.00	0.00	0.00	0.00	1.29	2.64	0.00	null	null		null	null		null	null		null	null		1.04E+00	7.39E-02		-1.03E+01	2.80E-04	Down	Unigene32085_All//gi|162606004|ref|XP_001713517.1|//1.00E-122//translation initiation factor eIF-5A.2 [Guillardia theta] >gi|13794437|gb|AAK39812.1|AF16581_8_20 translation initiation factor eIF-5A.2 [Guillardia theta]	Unigene32085_All//2.00E-09//AT1G69410| ELF5A-3 (EUKARYOTIC ELONGATION FACTOR 5A-3); translation initiation factor				GO:0003723//GO:0006417	nr -
Unigene32086_All	313	0.00	0.00	0.34	8.44	3.96	4.76	37.69	28.84	104.24	null	null		8.41E+00	3.98E-01		-1.09E+00	2.85E-03		-8.25E-01	3.39E-02		-3.86E-01	9.88E-03		1.47E+00	3.54E-54	Up	Unigene32086_All//gi|224111864|ref|XP_002316007.1|//3.00E-16//cytochrome P450 [Populus trichocarpa] >gi|222865047|gb|EEF02178.1| cytochrome P450 [Populus trichocarpa]	Unigene32086_All//5.00E-10//AT1G75130| CYP721A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene32086_All//2.00E-89//TC153451		ko00591|Linoleic acid metabolism	GO:0016491//GO:0046872	nr +
Unigene32091_All	548	0.00	0.00	0.00	0.00	0.00	0.00	9.34	9.84	0.80	null	null		null	null		null	null		null	null		7.57E-02	7.65E-01		-3.55E+00	2.64E-25	Down							
Unigene32094_All	364	0.14	1.25	2.34	0.27	0.66	0.74	0.00	0.00	0.00	3.12E+00	3.58E-02		4.03E+00	7.02E-04	Up	1.27E+00	5.32E-01		1.44E+00	4.09E-01		null	null		null	null							ESTscan -
Unigene32096_All	558	0.00	4.09	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.64E-13	Up	1.10E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene32096_All//gi|300264442|gb|EFJ48638.1|//9.00E-06//hypothetical protein VOLCADRAFT_104692 [Volvox carteri f. nagariensis]						nr +
Unigene32101_All	466	3.82	1.09	0.11	0.00	0.15	0.39	0.45	1.26	0.34	-1.81E+00	6.59E-04	Down	-5.06E+00	1.67E-08	Down	7.21E+00	6.09E-01		8.60E+00	1.94E-01		1.47E+00	1.02E-01		-4.08E-01	7.55E-01		Unigene32101_All//gi|119368546|ref|YP_913233.1|//9.00E-86//NADH dehydrogenase ND5 subunit [Gossypium barbadense] >gi|221272286|sp|A0ZZ82.1|NU5C_GOSBA RecName: Full=NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic; AltName: Full=NAD(P)H dehydrogenase subunit 5; AltName: Full=NADH-plastoquinone oxidoreductase subunit 5 >gi|119224908|dbj|BAF41294.1| NADH dehydrogenase ND5 subunit [Gossypium barbadense]	Unigene32101_All//6.00E-76//ATCG01010| Chloroplast encoded NADH dehydrogenase unit.	Unigene32101_All//0.00E+00//TC176110		ko00190|Oxidative phosphorylation	GO:0009534//GO:0022904//GO:0031224//GO:0048037//GO:0050136//GO:0051234	nr -
Unigene32102_All	392	3.20	0.00	1.49	1.14	0.79	0.46	1.19	0.00	0.51	-1.16E+01	2.54E-07	Down	-1.10E+00	8.60E-02		-5.33E-01	5.96E-01		-1.31E+00	2.73E-01		-1.02E+01	1.71E-03		-1.22E+00	2.00E-01		Unigene32102_All//gi|224160373|ref|XP_002338201.1|//3.00E-32//predicted protein [Populus trichocarpa] >gi|222871214|gb|EEF08345.1| predicted protein [Populus trichocarpa]	Unigene32102_All//3.00E-23//AT3G02060| DEAD/DEAH box helicase, putative	Unigene32102_All//0.00E+00//TC140721			GO:0001071//GO:0006351//GO:0009536//GO:0032559//GO:0042623	nr +
Unigene32107_All	546	6.90	0.46	1.85	0.00	0.00	0.00	0.00	0.00	0.00	-3.89E+00	5.49E-16	Down	-1.90E+00	2.03E-07	Down	null	null		null	null		null	null		null	null							
Unigene32108_All	660	5.95	3.61	4.52	1.06	0.31	0.07	0.13	0.00	2.17	-7.21E-01	1.93E-02		-3.96E-01	2.39E-01		-1.76E+00	4.11E-02		-3.95E+00	1.46E-03		-7.00E+00	4.03E-01		4.08E+00	3.98E-08	Up	Unigene32108_All//gi|115437336|ref|NP_001043270.1|//2.00E-67//Os01g0541800 (Oryza sativa Japonica Group) >gi|113532801|dbj|BAF05184.1| Os01g0541800 (Oryza sativa Japonica Group)	Unigene32108_All//4.00E-51//AT3G14770| nodulin MtN3 family protein	Unigene32108_All//2.00E-16//TC176376			GO:0031224//GO:0031410	nr +
Unigene32109_All	487	0.00	9.68	0.98	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	7.47E-27	Up	9.94E+00	7.48E-03		null	null		null	null		null	null		null	null							ESTscan -
Unigene3211_All	1224	5.56	9.69	3.13	14.85	15.08	13.43	11.88	51.02	59.53	8.02E-01	1.34E-06		-8.27E-01	4.20E-04		2.17E-02	8.98E-01		-1.45E-01	3.43E-01		2.10E+00	7.04E-166	Up	2.32E+00	2.04E-223	Up	Unigene3211_All//gi|297835206|ref|XP_002885485.1|//9.00E-20//VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331325|gb|EFH61744.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]		Unigene3211_All//0.00E+00//gi|109852036|gb|DW481015.1|DW481015				nr -

Unigene32114_All	223	13.84	5.91	7.88	17.42	14.05	17.82	109.97	63.72	33.23	-1.23E+00	7.17E-04	Down	-8.13E-01	2.83E-02		-3.10E-01	3.41E-01		3.26E-02	9.40E-01		-7.87E-01	3.95E-15		-1.73E+00	4.09E-52	Down			Unigene32114_All//9.00E-106//gi|21103527|gb|BQ415840.1|BQ415840				
Unigene32115_All	477	0.00	9.99	7.14	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	3.83E-27	Up	1.28E+01	7.39E-19	Up	null	null		null	null		null	null		null	null		Unigene32115_All//5.00E-34//60S ribosomal protein L21-1 [Phytophthora infestans T30-4] >gi|262100243|gb|EEY58295.1| 60S ribosomal protein L21-1 [Phytophthora infestans T30-4]	Unigene32115_All//2.00E-31//AT1G57860| 60S ribosomal protein L21			ko03010|Ribosome		nr -
Unigene32117_All	246	3.40	0.00	0.00	1.42	3.50	0.92	0.00	0.00	0.00	-1.17E+01	5.57E-05	Down	-1.17E+01	1.19E-04	Down	1.30E+00	1.02E-01		-6.27E-01	6.21E-01		null	null		null	null				Unigene32117_All//2.00E-134//TC168899				
Unigene32118_All	507	0.00	6.40	4.73	0.00	0.00	0.27	0.00	0.00	0.00	1.26E+01	1.87E-18	Up	1.22E+01	3.24E-13	Up	null	null		8.06E+00	3.11E-01		null	null		null	null		Unigene32118_All//gi|254033594|gb|ACT52263.1|//2.00E-06//formin 2B [Physcomitrella patens]	Unigene32118_All//5.00E-05//AT4G18670| protein binding / structural constituent of cell wall				GO:0005488	nr -
Unigene32119_All	1442	0.00	0.00	0.00	0.00	0.00	0.00	37.18	0.00	1.35	null	null		null	null		null	null		null	null		-1.52E+01	0.00E+00	Down	-4.78E+00	0.00E+00	Down							
Unigene32120_All	427	0.61	0.00	0.50	4.43	2.26	1.38	0.69	0.00	0.47	-9.26E+00	6.70E-02		-2.97E-01	8.32E-01		-9.73E-01	3.01E-02		-1.69E+00	6.39E-04	Down	-9.44E+00	2.18E-02		-5.71E-01	6.28E-01				Unigene32120_All//5.00E-07//TC145839				
Unigene32123_All	682	0.31	0.07	0.55	2.48	0.35	0.26	2.36	1.10	0.23	-2.05E+00	3.34E-01		8.33E-01	5.16E-01		-2.81E+00	5.97E-07	Down	-3.23E+00	6.72E-07	Down	-1.09E+00	1.97E-02		-3.33E+00	5.33E-08	Down	Unigene32123_All//gi|224127510|ref|XP_002320092.1|//4.00E-30//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|224130132|ref|XP_002320760.1| NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222860865|gb|EEE98407.1| NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222861533|gb|EEE99075.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene32123_All//2.00E-28//AT5G24590| TIP (TCV-INTERACTING PROTEIN); transcription coactivator/ transcription factor	Unigene32123_All//1.00E-33//gi|73862499|gb|DT465238.1|DT465238	NAC		GO:0001071//GO:0002252//GO:0003712//GO:0043231	nr +
Unigene32134_All	957	0.00	0.00	0.00	0.00	0.00	0.00	4.51	2.49	0.29	null	null		null	null		null	null		null	null		-8.56E-01	1.01E-03		-3.95E+00	2.72E-23	Down	Unigene32134_All//gi|6094086|sp|O65353.1|RL5_HELAN//1.00E-105//RecName: Full=60S ribosomal protein L5 >gi|3153904|gb|AAC17448.1| RPL5A-related protein [Helianthus annuus]	Unigene32134_All//5.00E-87//AT3G25520| ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); 5S rRNA binding / structural constituent of ribosome	Unigene32134_All//8.00E-11//gi|11203676|gb|BF272606.1|BF272606		ko03010|Ribosome	GO:0003002//GO:0005198//GO:0009536//GO:0009887//GO:0010467//GO:0015934//GO:0016020//GO:0019843//GO:0022613//GO:0031981//GO:0046914//GO:0051169//GO:0065003	nr +
Unigene32135_All	350	0.00	3.76	2.28	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.50E-07	Up	1.12E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene32135_All//sp|Q5XIA8|GHITM_RAT//1.00E-32//Growth hormone-inducible transmembrane protein OS=Rattus norvegicus GN=Ghitm PE=2 SV=1						swissprot +
Unigene32136_All	606	0.00	4.77	3.34	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.97E-16	Up	1.17E+01	3.79E-11	Up	null	null		null	null		null	null		null	null		Unigene32136_All//gi|498789|emb|CAA56109.1|//2.00E-40//cytochrome c1 [Solanum tuberosum]	Unigene32136_All//4.00E-24//AT3G27240| cytochrome c1, putative			ko00190|Oxidative phosphorylation	GO:0004721//GO:0005506//GO:0005746//GO:0006464//GO:0009055//GO:0022904//GO:0043234//GO:0043434	nr +
Unigene32138_All	356	0.00	0.00	0.00	0.00	0.00	0.00	3.56	3.05	0.00	null	null		null	null		null	null		null	null		-2.23E-01	6.77E-01		-1.18E+01	1.99E-09	Down	Unigene32138_All//gi|11502825|sp|Q8GYL5.2|RS25_ARATH//8.00E-30//RecName: Full=40S ribosomal protein S25-3 >gi|21617899|gb|AAM66949.1| ribosomal protein S25 [Arabidopsis thaliana] >gi|51970302|dbj|BAD43843.1| 40S ribosomal 25S subunit [Arabidopsis thaliana] >gi|98961037|gb|ABF59002.1| At4g34555 [Arabidopsis thaliana]	Unigene32138_All//6.00E-22//AT4G34555| 40S ribosomal protein S25, putative			ko03010|Ribosome	GO:0010467//GO:0015935//GO:0016020	nr +
Unigene32139_All	307	1.19	0.00	0.00	0.32	0.79	0.74	2.20	0.14	0.78	-1.02E+01	1.97E-02		-1.02E+01	2.78E-02		1.27E+00	5.32E-01		1.18E+00	5.49E-01		-4.02E+00	5.36E-04	Down	-1.50E+00	5.44E-02		Unigene32139_All//gi|124365519|gb|ABN09753.1|//4.00E-25//Tetratricopeptide-like helical [Medicago truncatula]	Unigene32139_All//6.00E-25//AT5G19020| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene32214_All	1627	11.54	16.51	11.03	16.47	14.79	22.62	18.32	34.86	44.12	5.16E-01	8.18E-07		-6.58E-02	6.43E-01		-1.55E-01	1.75E-01		4.58E-01	9.05E-08		9.28E-01	1.41E-44		1.27E+00	9.26E-95	Up	Unigene32214_All//gi|18149189|dbj|BAB83610.1|//7.00E-79//6b-interacting protein 1 [Nicotiana tabacum]	Unigene32214_All//1.00E-34//AT3G58630| transcription factor	Unigene32214_All//0.00E+00//TC141519	Trihelix		GO:0010468	nr +
Unigene32140_All	218	0.48	0.00	0.24	0.69	0.47	0.21	0.19	3.07	0.91	-8.91E+00	3.72E-01		-9.74E-01	7.21E-01		-5.33E-01	7.85E-01		-1.73E+00	5.01E-01		3.98E+00	6.38E-04	Up	2.24E+00	2.49E-01								
Unigene32141_All	488	0.21	28.76	13.20	0.00	0.07	0.00	0.00	0.00	0.00	7.07E+00	1.25E-76	Up	5.94E+00	1.05E-32	Up	6.14E+00	8.30E-01		null	null		null	null		null	null		Unigene32141_All//gi|14423905|sp|Q9XGL4.1|RL31_CYAPA//2.00E-40//RecName: Full=60S ribosomal protein L31 >gi|5123727|emb|CAB45375.1| ribosomal protein L31 [Cyanophora paradoxa]	Unigene32141_All//3.00E-27//AT4G26230| 60S ribosomal protein L31 (RPL31B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0044267	nr -
Unigene32147_All	379	0.00	0.00	0.00	0.00	0.36	0.00	1.90	1.32	0.21	null	null		null	null		8.51E+00	3.18E-01		null	null		-5.19E-01	5.07E-01		-3.17E+00	8.09E-04	Down			Unigene32147_All//1.00E-19//gi|13243624|gb|BE054754.2|BE054754				
Unigene32149_All	526	2.19	0.67	6.07	6.53	3.40	1.55	0.72	0.40	1.06	-1.70E+00	1.21E-02		1.47E+00	1.04E-04	Up	-9.41E-01	2.56E-03		-2.08E+00	1.63E-08	Down	-8.65E-01	4.41E-01		5.52E-01	5.27E-01				Unigene32149_All//1.00E-177//DW519466				
Unigene32150_All	565	0.00	0.00	0.09	0.26	0.00	0.08	2.47	0.30	2.47	null	null		6.56E+00	6.36E-01		-8.05E+00	1.65E-01		-1.73E+00	5.01E-01		-3.06E+00	2.69E-06	Down	-9.00E-04	9.95E-01		Unigene32150_All//gi|15226025|ref|NP_179096.1|//4.00E-27//gibberellin-regulated family protein [Arabidopsis thaliana] >gi|3650032|gb|AAC61287.1| similar to gibberellin-regulated proteins [Arabidopsis thaliana]	Unigene32150_All//4.00E-27//AT2G14900| gibberellin-regulated family protein	Unigene32150_All//9.00E-34//DW505454			GO:0050896	nr +
Unigene32154_All	446	0.23	95.09	40.36	0.00	0.00	0.00	0.00	0.00	0.00	8.66E+00	6.29E-240	Up	7.43E+00	1.77E-97	Up	null	null		null	null		null	null		null	null		Unigene32154_All//gi|159490006|ref|XP_001702980.1|//4.00E-51//ribosomal protein S11, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158270887|gb|EDO96718.1| ribosomal protein S11 [Chlamydomonas reinhardtii]	Unigene32154_All//2.00E-47//AT4G30800| 40S ribosomal protein S11 (RPS11B)	Unigene32154_All//4.00E-14//TC151907		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0003312	nr +
Unigene32155_All	423	0.00	0.00	0.00	0.00	0.00	0.00	5.00	9.09	0.00	null	null		null	null		null	null		null	null		8.63E-01	1.94E-03		-1.23E+01	1.40E-15	Down							
Unigene32158_All	423	0.00	0.00	0.00	0.00	0.00	0.00	21.79	15.71	4.24	null	null		null	null		null	null		null	null		-4.72E-01	5.51E-03		-2.36E+00	6.98E-30	Down							
Unigene32159_All	612	0.00	0.00	0.00	0.00	0.00	0.00	4.21	0.68	0.85	null	null		null	null		null	null		null	null		-2.63E+00	1.34E-09	Down	-2.32E+00	9.74E-09	Down	Unigene32159_All//gi|262186741|ref|YP_003276000.1|//5.00E-46//NADH dehydrogenase subunit 1 [Pleurozia purpurea] >gi|237780738|gb|ACR19384.1| NADH dehydrogenase subunit 1 [Pleurozia purpurea]	Unigene32159_All//2.00E-37//ATMG01275| Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C.			ko00190|Oxidative phosphorylation	GO:0016020	nr -
Unigene3216_All	1370	67.22	8.10	55.04	2.00	3.97	3.23	0.00	0.00	0.00	-3.05E+00	0.00E+00	Down	-2.88E-01	2.03E-07		9.90E-01	5.52E-05		6.92E-01	1.66E-02		null	null		null	null		Unigene3216_All//gi|5915821|sp|O48928.1|CT7A3_SOYBN//1.00E-176//RecName: Full=Cytochrome P450 77A3 >gi|2739010|gb|AAB94593.1| CYP77A3p [Glycine max]	Unigene3216_All//4.00E-165//AT5G04660| CYP77A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene3216_All//0.00E+00//DR462241		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene32160_All	321	0.00	0.00	0.00	0.00	0.00	0.00	52.42	186.45	0.62	null	null		null	null		null	null		null	null		1.83E+00	1.96E-132	Up	-6.40E+00	1.08E-114	Down							
Unigene32163_All	468	0.00	7.25	1.93	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.55E-19	Up	1.09E+01	4.71E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene3217_All	1225	0.90	1.28	0.65	3.01	1.43	3.47	11.60	27.23	33.66	5.16E-01	3.38E-01		-4.60E-01	4.97E-01		-1.07E+00	3.47E-04	Down	2.04E-01	5.59E-01		1.23E+00	1.40E-41	Up	1.54E+00	5.20E-73	Up	Unigene3217_All//gi|21618121|gb|AAM67171.1|//1.00E-100//RNA-binding protein-like protein [Arabidopsis thaliana]	Unigene3217_All//4.00E-100//AT3G47160| protein binding / zinc ion binding	Unigene3217_All//0.00E+00//gi|109874513|gb|DW503487.1|DW503487			GO:0004659//GO:0046914	nr -
Unigene32175_All	371	0.14	0.00	0.00	0.13	0.19	0.00	33.16	10.48	8.38	-7.14E+00	6.12E-01		-7.14E+00	6.24E-01		4.67E-01	9.58E-01		-7.07E+00	6.35E-01		-1.66E+00	1.91E-24	Down	-1.99E+00	5.64E-32	Down	Unigene32175_All//gi|221272207|sp|A2A1A0.1|NCS1_COPJA//5.00E-113//RecName: Full=S-norcoclaurine synthase 1; Short=CjNCS1 >gi|123720767|dbj|BAF45337.1| norcoclaurine synthase [Coptis japonica var. dissecta] >gi|301072256|gb|ADK56103.1| 2OG/Fe(II)-dependent dioxygenase-like protein [synthetic construct]	Unigene32175_All//1.00E-06//AT4G25300| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene32175_All//3.00E-08//TC164207			GO:0008152//GO:0016491//GO:0016829	nr -
Unigene32176_All	227	1.15	0.45	0.70	5.05	4.10	2.19	6.71	1.29	1.76	-1.37E+00	3.83E-01		-7.12E-01	6.22E-01		-3.01E-01	6.23E-01		-1.21E+00	6.46E-02		-2.38E+00	2.15E-05	Down	-1.93E+00	1.54E-04	Down			Unigene32176_All//2.00E-116//gi|21103050|gb|BQ415363.1|BQ415363				
Unigene32177_All	402	0.00	11.34	7.42	0.00	0.17	0.00	0.11	0.00	0.00	1.35E+01	5.54E-26	Up	1.29E+01	1.77E-16	Up	7.42E+00	6.09E-01		null	null		-6.72E+00	6.57E-01		-6.72E+00	6.12E-01		Unigene32177_All//gi|89513312|gb|AB074515.1|//2.00E-47//ribosomal protein [Pteris vittata]	Unigene32177_All//2.00E-43//AT1G36240| 60S ribosomal protein L30 (RPL30A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene32179_All	278	12.99	4.19	4.60	10.75	9.04	9.10	56.88	24.51	22.36	-1.63E+00	2.89E-06	Down	-1.50E+00	2.50E-05	Down	-2.50E-01	5.40E-01		-2.41E-01	5.60E-01		-1.21E+00	9.27E-20	Down	-1.35E+00	8.66E-24	Down			Unigene32179_All//2.00E-104//TC153230				
Unigene32182_All	257	0.00	3.55	4.35	0.39	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.62E-05	Up	1.21E+01	3.43E-06	Up	-8.60E+00	3.13E-01		-8.60E+00	4.00E-01		null	null		null	null		Unigene32182_All//sp|Q5NVN0|KPYM_PONAB//2.00E-18//Pyruvate kinase isozyme M1 OS=Pongo abelii GN=PKM2 PE=2 SV=3						swissprot +
Unigene32183_All	437	0.00	4.41	3.17	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.73E-11	Up	1.16E+01	1.23E-07	Up	null	null		null	null		null	null		null	null									
Unigene32188_All	668	0.39	0.08	0.48	0.15	0.10	0.14	0.57	0.56	2.86	-2.37E+00	2.14E-01		2.89E-01	8.10E-01		-5.32E-01	8.16E-01		-1.41E-01	9.50E-01		-1.66E-02	1.02E+00		2.33E+00	1.30E-06	Up	Unigene32188_All//gi|75170629|sp|Q9FHK4.1|Y5S19_ARATH//2.00E-12//RecName: Full=Uncharacterized protein At5g05190 >gi|30725434|gb|AAP37739.1| At5g05190 [Arabidopsis thaliana]	Unigene32188_All//2.00E-14//AT5G05190| unknown protein	Unigene32188_All//5.00E-14//TC140516				nr -
Unigene32189_All	1430	0.00	0.00	0.00	0.00	0.00	0.00	4.97	6.17	0.00	null	null		null	null		null	null		null	null		3.12E-01	8.64E-02		-1.23E+01	2.88E-52	Down	Unigene32189_All//gi|41391170|gb|AAD03711.1|//0.00E+00//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene32189_All//0.00E+00//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene32189_All//2.00E-46//gi|78338038|gb|DT558312.1|DT558312			GO:0006412//GO:0008135//GO:0016772//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene32190_All	348	0.00	7.57	3.67	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	5.45E-15	Up	1.18E+01	4.69E-07	Up	null	null		null	null		null	null		null	null		Unigene32190_All//gi|301103448|ref|XP_002900810.1|//2.00E-30//50S ribosomal protein L1 [Phytophthora infestans T30-4] >gi|262101565|gb|EEY59617.1| 50S ribosomal protein L1 [Phytophthora infestans T30-4]	Unigene32190_All//7.00E-25//AT3G63490| ribosomal protein L1 family protein			ko03010|Ribosome	GO:0003676//GO:0005840//GO:0010467//GO:0043231	nr -
Unigene32191_All	293	26.07	31.13	50.52	5.95	8.23	15.26	476.63	185.44	217.01	2.56E-01	2.08E-01		9.55E-01	4.36E-10		4.67E-01	2.92E-01		1.36E+00	3.71E-06	Up	-1.36E+00	4.51E-201	Down	-1.14E+00	2.09E-155	Down			Unigene32191_All//8.00E-116//TC145780				

Unigene32194_All	483	0.33	0.52	2.87	0.00	0.36	0.19	0.00	0.17	0.00	6.91E-01	6.26E-01		3.14E+00	4.89E-05	Up	8.48E+00	2.27E-01		7.55E+00	4.76E-01		7.44E+00	4.01E-01		null	null		Unigene32194_All//gi|15240003|ref|NP_196252.1|//2.00E-24//ATNUDX27 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 27); bis(5'-adenosyl)-pentaphosphatase/bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) [Arabidopsis thaliana] >gi|75309234|sp|Q9FNH4.1|NUD27_ARATH RecName: Full=Nudix hydrolase 27, chloroplastic; Short=AtNUDT27; Flags: Precursor >gi|13937175|gb|AAK50081.1|AF372941_1_1 AT5g06340/MBF15_14 [Arabidopsis thaliana] >gi|9758414|dbj|BAB08956.1| diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase-like protein [Arabidopsis thaliana] >gi|21360539|gb|AAM47466.1|At1g79500/T8K14_8 [Arabidopsis thaliana]	Unigene32194_All//1.00E-25//AT5G06340| ATNUDX27 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 27); bis(5'-adenosyl)-pentaphosphatase/bis(5'-nucleosyl)-tetraphosphatase (asymmetrical)				GO:0004551//GO:0009536	nr -
Unigene32196_All	354	0.00	0.00	0.00	0.00	0.00	0.00	2.75	1.89	0.00	null	null		null	null		null	null		null	null		-5.40E-01	4.02E-01		-1.14E+01	2.72E-07	Down	Unigene32196_All//gi|225685853|dbj|BAH30213.1|//4.00E-47//methionine S-adenosyl transferase [Cylindrotheca closterium]	Unigene32196_All//3.00E-32//AT4G01850| SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase	Unigene32196_All//1.00E-13//BG445760		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0016765//GO:0032559//GO:0044237//GO:0044424//GO:0046872	nr -
Unigene32197_All	463	2.37	0.00	7.94	0.43	0.00	1.85	0.00	0.00	0.00	-1.12E+01	1.95E-06	Down	1.74E+00	1.48E-06	Up	-8.75E+00	8.43E-02		2.11E+00	1.44E-02		null	null		null	null		Unigene32197_All//gi|22854880|gb|AAN09798.1|//5.00E-41//benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Nicotiana tabacum]	Unigene32197_All//9.00E-25//AT3G03480| CHAT (acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase); acetyl CoA:(Z)-3-hexen-1-ol acetyltransferase	Unigene32197_All//0.00E+00//gi|164348961|gb|ES835608.1|ES835608			GO:0016747	nr -
Unigene32199_All	473	0.00	0.21	0.23	0.00	0.00	0.00	3.75	1.59	0.67	7.74E+00	3.86E-01		7.82E+00	3.98E-01		null	null		null	null		-1.24E+00	5.46E-03		-2.48E+00	1.05E-06	Down	Unigene32199_All//gi|224120746|ref|XP_002318407.1|//2.00E-15//predicted protein [Populus trichocarpa] >gi|222859080|gb|EEE96627.1| predicted protein [Populus trichocarpa]		Unigene32199_All//1.00E-10//TC153177			GO:0006350//GO:0010468	nr +
Unigene322_All	617	1.87	2.87	6.39	5.09	5.02	4.76	1.92	2.37	1.94	6.24E-01	2.09E-01		1.78E+00	3.73E-07	Up	-1.81E-02	9.49E-01		-9.63E-02	7.90E-01		3.05E-01	5.74E-01		1.37E-02	9.78E-01		Unigene322_All//gi|113205376|gb|AAU93592.2|//1.00E-58//uncharacterized plant-specific domain TIGR01589 family protein [Solanum demissum]	Unigene322_All//2.00E-42//AT2G46420| unknown protein	Unigene322_All//0.00E+00//TC161829			nr +
Unigene3220_All	513	2.75	3.85	2.28	2.43	2.42	2.02	4.04	3.50	1.63	4.84E-01	3.02E-01		-2.70E-01	6.16E-01		-6.60E-03	9.73E-01		-2.62E-01	6.88E-01		-2.05E-01	6.32E-01		-1.31E+00	9.85E-04	Down			Unigene3220_All//2.00E-158//TC172853				
Unigene32204_All	693	0.00	0.00	0.00	0.00	0.00	0.00	1.53	2.35	5.06	null	null		null	null		null	null		null	null		6.25E-01	1.84E-01		1.73E+00	4.30E-08	Up	Unigene32204_All//gi|209970603|gb|ACJ03064.1|//7.00E-48//AM19-5p [Malus floribunda]	Unigene32204_All//1.00E-19//AT1G07390| protein binding				nr +
Unigene32205_All	553	0.00	6.23	3.18	0.00	0.12	0.00	0.00	0.00	0.00	1.26E+01	1.31E-19	Up	1.16E+01	1.12E-09	Up	6.96E+00	6.09E-01		null	null		null	null		null	null		Unigene32205_All//gi|20805287|gb|AAM28648.1|AF430645_1//7.00E-06//protein disulfide isomerase-like PDI-M [Physcomitrella patens]	Unigene32205_All//2.00E-05//AT3G54960| ATPDIL1-3 (PDI-LIKE 1-3); protein disulfide isomerase			ko04141|Protein processing in endoplasmic reticulum	GO:0043229//GO:0044444	nr -
Unigene32206_All	737	0.00	0.00	0.00	0.00	0.00	0.00	2.18	0.45	1.62	null	null		null	null		null	null		null	null		-2.26E+00	2.23E-05	Down	-4.27E-01	3.59E-01								ESTscan -
Unigene32207_All	485	0.00	3.76	2.64	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.14E-10	Up	1.14E+01	4.69E-07	Up	null	null		null	null		null	null		null	null									
Unigene32208_All	592	0.00	0.00	0.00	5.89	4.83	0.92	0.00	0.00	0.00	null	null		null	null		-2.87E-01	4.20E-01		-2.69E+00	1.72E-11	Down	null	null		null	null		Unigene32208_All//gi|115479419|ref|NP_001063303.1|//2.00E-17//Os09g0445500 [Oryza sativa Japonica Group] >gi|113631536|dbj|BAF25217.1| Os09g0445500 [Oryza sativa Japonica Group]	Unigene32208_All//8.00E-12//AT1G67030| ZFP6 (ZINC FINGER PROTEIN 6); nucleic acid binding / transcription factor/ zinc ion binding		C2H2			nr -
Unigene32211_All	365	0.00	0.00	0.00	0.00	0.00	0.00	2.20	2.86	0.00	null	null		null	null		null	null		null	null		3.79E-01	5.56E-01		-1.11E+01	4.43E-06	Down	Unigene32211_All//gi|41323492|gb|AAR99906.1|//9.00E-15//60S ribosomal protein L14 [Chara globularis]	Unigene32211_All//1.00E-12//AT4G27090| 60S ribosomal protein L14 (RPL14B)			ko03010|Ribosome	GO:0005622	nr +
Unigene32214_All	437	0.00	0.00	0.00	0.00	0.00	0.00	2.71	1.72	0.18	null	null		null	null		null	null		null	null		-6.54E-01	2.47E-01		-3.89E+00	9.21E-07	Down	Unigene32214_All//gi|6094040|sp|O65743.1|RL24_CICAR//4.00E-15//RecName: Full=60S ribosomal protein L24 >gi|2961300|emb|CAA12358.1| ribosomal protein L24 [Cicer arietinum]	Unigene32214_All//1.00E-10//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome			ko03010|Ribosome	GO:0043229	nr +
Unigene32215_All	434	0.00	0.00	0.00	0.00	0.00	0.00	2.14	2.41	0.09	null	null		null	null		null	null		null	null		1.68E-01	7.81E-01		-4.55E+00	6.41E-06	Down	Unigene32215_All//gi|192913032|gb|ACF06624.1|//5.00E-53//40S ribosomal protein S11 [Elaeis guineensis]	Unigene32215_All//3.00E-11//DR453672			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0043231	nr +
Unigene3222_All	1325	29.54	14.72	16.04	76.21	59.18	50.00	22.59	7.89	8.99	-1.00E+00	6.53E-29	Down	-8.81E-01	1.83E-22		-3.65E-01	4.89E-15		-6.08E-01	1.10E-33		-1.52E+00	2.76E-51	Down	-1.33E+00	2.31E-43	Down	Unigene3222_All//gi|124360377|gb|AB08390.1|//1.00E-61//Harpin-induced 1 [Medicago truncatula]	Unigene3222_All//5.00E-38//AT5G11890| FUNCTIONS IN: molecular_function unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17620.1); Has 455 Blast hits to 454 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 453; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene3222_All//0.00E+00//TC158911			GO:0016020	nr +
Unigene32221_All	301	0.00	0.00	0.35	1.99	0.00	1.65	0.70	0.56	0.79	null	null		8.47E+00	3.98E-01		-1.10E+01	1.78E-04	Down	-2.67E-01	7.57E-01		-3.39E-01	8.12E-01		1.77E-01	9.08E-01								
Unigene32229_All	314	0.00	2.90	2.37	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.62E-05	Up	1.12E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene32229_All//sp|P10145|IL8_HUMAN//2.00E-34//Interleukin-8 OS=Homo sapiens GN=IL8 PE=1 SV=1						swissprot +
Unigene3223_All	1170	14.76	7.36	14.47	26.78	40.12	21.11	6.76	7.57	3.44	-1.00E+00	3.69E-13	Down	-2.80E-02	8.55E-01		5.83E-01	3.81E-16		-3.43E-01	3.07E-04		1.64E-01	3.98E-01		-9.75E-01	1.05E-07		Unigene3223_All//gi|124359981|gb|AB07997.1|//7.00E-08//contains similarity to reverse transcriptase, related [Medicago truncatula]	Unigene3223_All//3.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene3223_All//9.00E-122//gi|73850054|gb|DT459074.1|DT459074			GO:0005488//GO:0016740	nr -
Unigene32230_All	302	0.87	10.23	1.59	0.99	0.34	0.60	1.54	0.55	0.13	3.56E+00	3.22E-12	Up	8.73E-01	4.17E-01		-1.53E+00	2.98E-01		-7.26E-01	6.39E-01		-1.48E+00	1.53E-01		-3.55E+00	6.85E-03				Unigene32230_All//2.00E-11//DW515941				
Unigene32231_All	864	9.33	1.82	5.36	0.23	0.40	0.31	0.00	0.00	0.00	-2.36E+00	8.84E-21	Down	-7.98E-01	1.74E-04		7.90E-01	5.96E-01		4.44E-01	7.63E-01		null	null		null	null		Unigene32231_All//gi|224118954|ref|XP_002317948.1|//3.00E-48//f-box family protein [Populus trichocarpa] >gi|222858621|gb|EEE96168.1| f-box family protein [Populus trichocarpa]	Unigene32231_All//7.00E-32//AT5G60850| OBP4; DNA binding / transcription factor	Unigene32231_All//0.00E+00//ES807004	C2C2-Dof			nr +
Unigene32232_All	589	7.20	1.46	5.51	0.51	0.00	0.08	0.00	0.00	0.00	-2.30E+00	6.35E-11	Down	-3.84E-01	2.35E-01		-8.99E+00	2.01E-02		-2.73E+00	1.37E-01		null	null		null	null		Unigene32232_All//gi|224112233|ref|XP_002332812.1|//2.00E-25//leucine rich repeat family protein with ABC domain [Populus trichocarpa] >gi|222833206|gb|EEE71683.1| leucine rich repeat family protein with ABC domain [Populus trichocarpa]	Unigene32232_All//1.00E-19//AT1G74190| AtRLP15 (Receptor Like Protein 15); protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene32233_All	416	0.25	33.25	16.90	0.48	0.00	0.00	0.00	0.00	0.00	7.05E+00	1.80E-75	Up	6.07E+00	6.10E-36	Up	-8.90E+00	8.43E-02		-8.90E+00	1.33E-01		null	null		null	null		Unigene32233_All//gi|159486879|ref|XP_001701464.1|//3.00E-20//ribosomal protein S30, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158271646|gb|EDO97461.1| ribosomal protein S30 [Chlamydomonas reinhardtii] >gi|300255282|gb|EFJ39611.1| component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene32233_All//2.00E-14//AT5G56670| 40S ribosomal protein S30 (RPS30C)			ko03010|Ribosome		nr -
Unigene32235_All	1215	0.00	12.26	3.02	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	1.45E-85	Up	1.16E+01	2.39E-20	Up	null	null		null	null		null	null		null	null		Unigene32235_All//sp|Q9V496|APLP_DROME//2.00E-84//Apolipophorins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2						swissprot +
Unigene32236_All	543	0.00	0.00	0.00	0.00	0.00	0.00	3.58	1.62	0.00	null	null		null	null		null	null		null	null		-1.15E+00	6.23E-03		-1.18E+01	2.41E-14	Down	Unigene32236_All//gi|226502919|ref|NP_001149726.1|//3.00E-47//60S ribosomal protein L5-1 [Zea mays] >gi|195629822|gb|ACG36552.1| 60S ribosomal protein L5-1 [Zea mays]	Unigene32236_All//5.00E-33//AT5G39740| 60S ribosomal protein L5 (RPL5B)			ko03010|Ribosome		nr +
Unigene32238_All	349	0.00	4.94	5.34	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.99E-10	Up	1.24E+01	2.89E-10	Up	null	null		null	null		null	null		null	null									
Unigene32239_All	659	0.79	0.15	1.13	2.42	2.77	0.41	0.83	0.38	0.12	-2.37E+00	4.75E-02		5.11E-01	5.47E-01		1.95E-01	7.43E-01		-2.56E+00	2.78E-05	Down	-1.13E+00	2.18E-01		-2.79E+00	7.96E-03				Unigene32239_All//0.00E+00//TC172033				
Unigene32240_All	422	0.00	6.84	4.29	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.97E-16	Up	1.21E+01	5.69E-10	Up	null	null		null	null		null	null		null	null		Unigene32240_All//gi|115462177|ref|NP_001054688.1|//2.00E-41//Os05g0155100 [Oryza sativa Japonica Group] >gi|54291850|gb|AAV32218.1| cytoplasmic ribosomal protein L18 [Oryza sativa Japonica Group] >gi|113578239|dbj|BAF16602.1| Os05g0155100 [Oryza sativa Japonica Group] >gi|149392184|gb|ABR25945.1| 60S ribosomal protein L18 [Oryza sativa Indica Group]	Unigene32240_All//1.00E-41//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome	Unigene32240_All//5.00E-07//gi|78337576|gb|DT557850.1|DT557850		ko03010|Ribosome		nr -
Unigene32242_All	715	0.00	0.00	0.00	0.00	0.00	0.00	4.73	1.75	0.11	null	null		null	null		null	null		null	null		-1.43E+00	5.24E-06	Down	-5.41E+00	6.05E-22	Down	Unigene32242_All//gi|1173256|sp|P46299.1|RS4_GOSHI//3.00E-90//RecName: Full=40S ribosomal protein S4 >gi|488739|emb|CAA55882.1| ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene32242_All//2.00E-88//AT5G58420| 40S ribosomal protein S4 (RPS4D)			ko03010|Ribosome		nr -

Unigene32243_All	298	0.00	0.00	0.00	0.00	0.00	0.00	2.13	4.35	0.00	null	null		null	null		null	null		null	null		1.03E+00	5.33E-02		-1.11E+01	7.11E-05	Down	Unigene32243_All//gi|301107834|ref|XP_002902999.1|//7.00E-28//40S ribosomal protein S3-3 [Phytophthora infestans T30-4] >gi|262098117|gb|EEY56169.1| 40S ribosomal protein S3-3 [Phytophthora infestans T30-4]	Unigene32243_All//4.00E-28//AT2G31610| 40S ribosomal protein S3 (RPS3A)			ko03010|Ribosome		nr +
Unigene32244_All	406	0.00	0.00	0.00	0.00	0.00	0.00	3.54	2.88	0.49	null	null		null	null		null	null		null	null		-2.97E-01	5.92E-01		-2.85E+00	2.40E-06	Down	Unigene32244_All//gi|157092851|gb|ABV22080.1|//1.00E-21//60S ribosomal protein L26 [Amphidinium carterae] >gi|157092853|gb|ABV22081.1| 60S ribosomal protein L26 [Amphidinium carterae]	Unigene32244_All//5.00E-11//AT3G49910| 60S ribosomal protein L26 (RPL26A)			ko03010|Ribosome		nr +
Unigene32245_All	332	3.78	0.31	3.69	0.00	0.00	0.00	0.89	0.38	0.24	-3.63E+00	2.00E-05	Down	-3.60E-02	9.71E-01		null	null		null	null		-1.24E+00	3.73E-01		-1.89E+00	1.68E-01		Unigene32245_All//gi|224060381|ref|XP_002300171.1|//8.00E-33//high mobility group family [Populus trichocarpa] >gi|222847429|gb|EEE84976.1| high mobility group family [Populus trichocarpa]	Unigene32245_All//7.00E-31//AT1G04880| high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein	Unigene32245_All//0.00E+00//TC179102				nr -
Unigene32251_All	314	8.33	20.66	25.44	55.84	31.58	55.38	3866.62	4092.12	2855.82	1.31E+00	7.36E-08	Up	1.61E+00	3.57E-12	Up	-8.22E-01	1.55E-11		-1.21E-02	9.53E-01		8.18E-02	3.61E-11		-4.37E-01	3.65E-254		Unigene32251_All//gi|10505374|gb|AAG18453.1|AF305066_1//2.00E-35//PR protein class 10 [Gossypium hirsutum]		Unigene32251_All//7.00E-175//EV496241				nr -
Unigene32252_All	485	0.00	2.09	0.44	0.41	0.28	0.00	0.78	1.47	2.38	1.10E+01	7.26E-06	Up	8.78E+00	1.41E-01		-5.33E-01	7.48E-01		-8.68E+00	1.33E-01		9.01E-01	2.40E-01		1.60E+00	5.68E-03									
Unigene32253_All	367	0.00	0.00	0.00	0.00	0.00	0.00	3.34	6.26	0.00	null	null		null	null		null	null		null	null		9.07E-01	1.62E-02		-1.17E+01	4.03E-09	Down	Unigene32253_All//gi|146454508|gb|ABQ41920.1|//3.00E-36//60S ribosomal protein large subunit 9 [Sonneratia alba] >gi|156633690|gb|ABU90844.1| ribosomal protein L9 [Sonneratia alba] >gi|156633692|gb|ABU90845.1| ribosomal protein L9 [Sonneratia alba] >gi|156633696|gb|ABU90847.1| ribosomal protein L9 [Sonneratia alba] >gi|156633694|gb|ABU90846.1| ribosomal protein L9 [Sonneratia alba] >gi|156633698|gb|ABU90848.1| ribosomal protein L9 [Sonneratia alba] >gi|156633700|gb|ABU90849.1| ribosomal protein L9 [Sonneratia alba] >gi|156633702|gb|ABU90850.1| ribosomal protein L9 [Sonneratia alba] >gi|156633704|gb|ABU90851.1| ribosomal protein L9 [Sonneratia alba] >gi|156633706|gb|ABU90852.1| ribosomal protein L9 [Sonneratia alba] >gi|156633708|gb|ABU90853.1| ribosomal protein L9 [Sonneratia alba] >gi|156633710|gb|ABU90854.1| ribosomal protein L9 [Sonneratia alba] >gi|156633712|gb|ABU90855.1| ribosomal protein L9 [Sonneratia alba] >gi|156633714|gb|ABU90856.1| ribosomal protein L9 [Sonneratia	Unigene32253_All//8.00E-36//AT4G10450| 60S ribosomal protein L9 (RPL90D)			ko03010|Ribosome		nr +
Unigene32255_All	489	0.00	0.00	0.00	1.53	2.04	0.37	0.00	0.00	1.06	null	null		null	null		4.19E-01	5.85E-01		-2.05E+00	2.45E-02		null	null		1.00E+01	6.13E-04	Up	Unigene32255_All//gi|226490392|dbj|BAH56489.1|//3.00E-55//pectin methylesterase 1 [Prunus persica]	Unigene32255_All//5.00E-53//AT2G26440| pectinesterase family protein	Unigene32255_All//3.00E-55//CO106074		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene32256_All	374	10.21	0.14	6.26	0.80	0.37	1.21	1.47	0.89	0.64	-6.24E+00	1.65E-20	Down	-7.05E-01	3.16E-02		-1.12E+00	4.24E-01		5.96E-01	6.40E-01		-7.17E-01	4.22E-01		-1.20E+00	1.64E-01									
Unigene3226_All	1546	1.29	15.11	3.58	9.34	22.25	17.00	12.33	34.33	15.49	3.55E+00	4.09E-89	Up	1.48E+00	1.09E-07	Up	1.25E+00	3.90E-42	Up	8.64E-01	2.46E-16		1.48E+00	1.35E-86	Up	3.28E-01	8.07E-04		Unigene3226_All//gi|116310760|emb|CAH67554.1|//4.00E-30//H0311C03.8 [Oryza sativa (indica cultivar-group)]	Unigene3226_All//1.00E-24//AT2G24290| unknown protein	Unigene3226_All//4.00E-177//CO096352				nr +
Unigene32263_All	510	0.00	0.00	0.00	0.59	0.00	0.27	3.73	1.23	0.47	null	null		null	null		-9.19E+00	2.01E-02		-1.14E+00	4.57E-01		-1.60E+00	3.09E-04	Down	-2.99E+00	1.57E-08	Down	Unigene32263_All//gi|115470775|ref|NP_001058986.1|//5.00E-34//Os07g0169600 [Oryza sativa Japonica Group] >gi|113610522|dbj|BAF20900.1| Os07g0169600 [Oryza sativa Japonica Group]	Unigene32263_All//3.00E-28//AT4G10500| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene32263_All//6.00E-121//gi|78328382|gb|DT548656.1|DT548656		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis		nr +
Unigene32265_All	1036	0.00	6.99	3.55	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.04E-41	Up	1.18E+01	2.39E-20	Up	null	null		null	null		null	null		null	null		Unigene32265_All//gi|7523675|gb|AAF63115.1|AC006423_16//6.00E-06//Hypothetical protein [Arabidopsis thaliana]						nr +
Unigene32267_All	495	0.21	31.22	12.16	0.00	0.00	0.00	0.00	0.00	0.00	7.21E+00	9.58E-85	Up	5.85E+00	2.33E-30	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene32269_All	488	0.43	0.00	0.87	0.00	0.00	0.00	0.26	3.68	2.20	-8.74E+00	1.22E-01		1.03E+00	3.96E-01		null	null		null	null		3.82E+00	2.08E-09	Up	3.08E+00	3.77E-05	Up								
Unigene3227_All	1230	13.70	3.91	6.88	11.83	2.49	4.96	3.68	4.89	4.37	-1.81E+00	1.69E-30	Down	-9.93E-01	4.37E-12		-2.25E+00	9.27E-44	Down	-1.25E+00	7.75E-17	Down	4.12E-01	6.27E-02		2.50E-01	3.01E-01		Unigene3227_All//gi|115502172|sp|Q850K7.2|EXLB1_ORYSJ//1.00E-44//RecName: Full=Expansin-like B1; AltName: Full=OsEXLB1; AltName: Full=Expensin-related 1; AltName: Full=OsEXPR1; AltName: Full=OsaEXPb3.1; Flags: Precursor	Unigene3227_All//4.00E-36//AT3G45970| ATEXLA1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A1)	Unigene3227_All//0.00E+00//gi|164259503|gb|ES822845.1|ES822845			GO:0031410	nr +
Unigene32270_All	345	0.00	0.00	0.00	0.00	0.00	0.00	1.72	0.97	0.00	null	null		null	null		null	null		null	null		-8.24E-01	3.48E-01		-1.07E+01	1.41E-04	Down	Unigene32270_All//gi|226532299|ref|NP_001147655.1|//2.00E-06//extensin [Zea mays] >gi|195612880|gb|ACG28270.1| extensin precursor [Zea mays]						nr +
Unigene32277_All	465	0.00	0.44	0.69	0.86	0.22	0.10	2.82	6.56	2.23	8.77E+00	1.36E-01		9.42E+00	4.52E-02		-1.95E+00	1.19E-01		-3.14E+00	4.88E-02		1.22E+00	1.83E-04	Up	-3.40E-01	5.21E-01									
Unigene32279_All	660	0.00	0.00	0.00	0.00	0.00	0.00	3.01	9.82	1.03	null	null		null	null		null	null		null	null		1.70E+00	1.17E-13	Up	-1.55E+00	2.04E-04	Down			Unigene32279_All//9.00E-16//FL577607				
Unigene32283_All	326	29.37	12.43	14.70	37.90	23.56	19.40	10.63	5.38	1.96	-1.24E+00	1.96E-10	Down	-9.99E-01	3.22E-07		-6.86E-01	3.46E-06		-9.66E-01	1.22E-09		-9.82E-01	9.45E-04		-2.44E+00	3.58E-12	Down	Unigene32283_All//gi|1439609|gb|AAB04557.1|//7.00E-17//delta-tonoplast intrinsic protein [Gossypium hirsutum]	Unigene32283_All//5.00E-145//AT1G16260| DELTA-TIP; ammonia transporter/ methylammonium transmembrane transporter/ water channel	Unigene32283_All//5.00E-145//TC179202				nr -
Unigene32285_All	291	0.00	0.00	0.00	0.00	0.00	0.00	3.20	3.45	0.14	null	null		null	null		null	null		null	null		1.09E-01	8.63E-01		-4.55E+00	6.41E-06	Down	Unigene32285_All//gi|1173198|sp|P46298.1|RS13_PEA//4.00E-32//RecName: Full=40S ribosomal protein S13 >gi|396639|emb|CAA80974.1| ribosomal protein S13 [Pisum sativum]	Unigene32285_All//2.00E-29//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome			ko03010|Ribosome		nr -
Unigene32288_All	483	0.00	10.81	2.43	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	9.24E-30	Up	1.12E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene32288_All//gi|159468321|ref|XP_001692331.1|//2.00E-50//pepsin-type aspartyl protease [Chlamydomonas reinhardtii] >gi|158278517|gb|EDP04281.1| pepsin-type aspartyl protease [Chlamydomonas reinhardtii]	Unigene32288_All//2.00E-40//AT1G11910| aspartyl protease family protein					nr -
Unigene32289_All	679	0.00	0.00	0.00	0.00	0.00	0.00	2.68	4.49	0.00	null	null		null	null		null	null		null	null		7.47E-01	1.92E-02		-1.14E+01	2.03E-13	Down	Unigene32289_All//gi|300268380|gb|EFJ52561.1|//1.00E-80//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene32289_All//2.00E-07//gi|84144231|gb|DN758473.1|DN758473	Unigene32289_All//2.00E-07//gi|84144231|gb|DN758473.1|DN758473		ko03010|Ribosome		nr -
Unigene32290_All	454	0.00	3.79	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.99E-10	Up	1.10E+01	4.71E-05	Up	null	null		null	null		null	null		null	null		Unigene32290_All//sp|P10909|CLUS_HUMAN//3.00E-85//Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1						swissprot -
Unigene32293_All	821	0.64	4.07	2.72	0.00	0.00	0.00	0.62	0.41	19.46	2.68E+00	3.40E-10	Up	2.10E+00	3.08E-05	Up	null	null		null	null		-6.02E-01	5.31E-01		4.98E+00	6.19E-96	Up	Unigene32293_All//gi|297837039|ref|XP_002886401.1|//1.00E-38//F2K11.21 [Arabidopsis lyrata subsp. lyrata] >gi|297332242|gb|EFH62660.1| F2K11.21 [Arabidopsis lyrata subsp. lyrata]	Unigene32293_All//1.00E-37//AT1G63410| unknown protein	Unigene32293_All//8.00E-32//FL576529				nr -
Unigene32300_All	224	0.00	0.45	3.09	0.89	1.23	2.22	0.19	0.75	0.71	8.82E+00	3.86E-01		1.16E+01	6.16E-04	Up	4.67E-01	8.17E-01		1.32E+00	2.52E-01		1.98E+00	3.79E-01		1.91E+00	3.77E-01									
Unigene32301_All	656	0.00	0.00	0.49	11.39	1.05	0.55	0.13	0.00	0.00	null	null		8.93E+00	4.52E-02		-3.44E+00	5.76E-36	Down	-4.37E-00	6.93E-37	Down	-7.01E+00	4.03E-01		-7.01E+00	3.58E-01									
Unigene32304_All	449	0.00	2.48	2.85	0.00	0.08	0.00	5.46	1.21	1.15	1.13E+01	2.00E-06	Up	1.15E+01	4.69E-07	Up	6.26E+00	8.30E-01		null	null		-2.17E+00	1.71E-07	Down	-2.24E+00	4.62E-08	Down	Unigene32304_All//gi|301110228|ref|XP_002904194.1|//2.00E-70//alpha-tubulin [Phytophthora infestans T30-4] >gi|262096320|gb|EEY54372.1| alpha-tubulin [Phytophthora infestans T30-4]	Unigene32304_All//4.00E-49//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene32304_All//2.00E-49//EV486359		ko04145|Phagosome		nr +
Unigene32308_All	325	0.00	1.09	4.42	0.00	0.00	0.14	0.00	0.00	0.00	1.01E+01	2.46E-02		1.21E+01	6.30E-08	Up	null	null		7.12E+00	6.96E-01		null	null		null	null		Unigene32308_All//sp|P01857|IGHG1_HUMAN//4.00E-59//Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1						swissprot +
Unigene32309_All	446	0.00	93.61	36.42	0.00	0.00	0.00	0.00	0.00	0.00	1.65E+01	4.90E-241	Up	1.52E+01	1.28E-91	Up	null	null		null	null		null	null		null	null		Unigene32309_All//sp|P0C1J6|FKBP4_RHIOR//5.00E-06//FK506-binding protein 4 OS=Rhizopus oryzae GN=FKBP4 PE=3 SV=1						swissprot -
Unigene3231_All	1432	4.35	12.28	6.95	5.71	5.89	7.66	11.57	17.72	18.14	1.50E+00	2.49E-24	Up	6.78E-01	3.15E-04		4.64E-02	8.43E-01		4.26E-01	1.43E-02		6.14E-01	2.17E-10		6.48E-01	6.34E-12		Unigene3231_All//gi|297830520|ref|XP_002883142.1|//1.00E-122//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328982|gb|EFH59401.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3231_All//2.00E-121//AT3G18820| zinc finger (DHHC type) family protein	Unigene3231_All//0.00E+00//gi|164355572|gb|ES794067.1|ES794067			GO:0031410//GO:0046914	nr +
Unigene32310_All	793	8.84	11.31	12.62	5.47	10.99	8.88	4.53	5.53	7.08	3.55E-01	7.23E-02		5.14E-01	6.52E-03		1.01E+00	7.02E-08	Up	7.01E-01	1.31E-03		2.88E-01	3.07E-01		6.44E-01	3.01E-03				Unigene32310_All//9.00E-07//EX167234				
Unigene32312_All	560	0.00	0.00	0.00	0.62	0.49	0.56	5.36	1.72	5.62	null	null		null	null		-3.40E-01	7.86E-01		-1.42E-01	9.12E-01		-1.64E+00	1.92E-06	Down	6.82E-02	8.36E-01		Unigene32312_All//gi|105923279|gb|ABF81468.1|//3.00E-41//TIR-NBS-LRR type disease resistance protein [Populus trichocarpa]	Unigene32312_All//3.00E-33//AT1G27170| ATP binding / protein binding / transmembrane receptor	Unigene32312_All//8.00E-136//TC145918				nr +
Unigene32314_All	653	0.00	35.31	16.96	0.15	0.00	0.00	0.00	0.00	0.00	1.51E+01	9.65E-133	Up	1.41E+01	3.13E-62	Up	-7.25E+00	3.13E-01		-7.25E+00	4.00E-01		null	null		null	null		Unigene32314_All//gi|6831610|sp|O48513.1|RL13_CHLSW//1.00E-58//RecName: Full=60S ribosomal protein L13; AltName: Full=BBC1 protein homolog >gi|2662188|dbj|BAA23724.1| BBC1 protein [Chlamydomonas sp. 880]	Unigene32314_All//2.00E-56//AT3G49010| ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene32315_All	420	0.50	0.24	3.42	0.95	1.56	1.61	0.70	0.70	0.09	-1.05E+00	5.64E-01		2.78E+00	1.05E-04	Up	7.15E-01	4.65E-01		7.66E-01	4.10E-01		-1.67E-02	1.02E+00		-2.89E+00	6.76E-02				Unigene32315_All//1.00E-121//DW496929				
Unigene32317_All	842	0.00	3.13	4.11	0.00	0.00	0.05	0.00	0.00	0.09	1.16E+01	5.45E-15	Up	1.20E+01	3.72E-19	Up	null	null		5.74E+00	6.96E-01		null	null		6.56E+00	4.04E-01		Unigene32317_All//gi|240254284|ref|NP_176000.4|//1.00E-06//binding / protein binding / ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene32317_All//7.00E-08//AT1G56010| binding / protein binding / ubiquitin-protein ligase					nr +

Unigene3232_All	1065	28.25	25.22	24.80	35.50	39.25	36.22	28.23	16.52	10.81	-1.64E-01	1.22E-01			-1.88E-01	8.62E-02		1.45E-01	1.04E-01		2.87E-02	7.88E-01			-7.73E-01	8.25E-18		-1.38E+00	2.74E-46	Down	Unigene3232_All//gi|242129050|gb|AC583604.1|//1.00E-105//ATP synthase delta subunit 3 [Gossypium hirsutum]	Unigene3232_All//2.00E-76//AT5G47030| ATP synthase delta' chain, mitochondrial	Unigene3232_All//0.00E+00//TC137183		ko00190|Oxidative phosphorylation	GO:0000275//GO:0006970//GO:0015078//GO:0015986//GO:0019829//GO:0032559//GO:0046914	nr +
Unigene32321_All	348	0.30	0.00	0.00	0.14	0.79	4.02	0.24	0.12	0.00	-8.23E+00	3.72E-01			-8.23E+00	3.93E-01		2.47E+00	2.23E-01		4.81E+00	3.50E-07	Up		-1.02E+00	7.24E-01		-7.92E+00	3.58E-01				Unigene32321_All//0.00E+00//gi|164278622|gb|ES812002.1|ES812002				
Unigene32323_All	452	0.00	0.00	0.00	0.00	0.00	0.00	2.62	3.33	0.00	null	null			null	null		null	null		null	null			3.46E-01	5.07E-01		-1.14E+01	8.15E-09	Down	Unigene32323_All//gi|226460767|gb|EEH58061.1|//2.00E-27//profilin [Micromonas pusilla CCMP1545]	Unigene32323_All//2.00E-22//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding				nr +
Unigene32324_All	564	0.00	9.16	4.53	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.81E-29	Up		1.21E+01	4.20E-14	Up	null	null		null	null			null	null		null	null		Unigene32324_All//gi|226460767|gb|EEH58061.1|//5.00E-15//profilin [Micromonas pusilla CCMP1545]	Unigene32324_All//3.00E-13//AT5G56600| PRF3 (PROFILIN 3); actin binding					nr +
Unigene32325_All	972	9.20	1.15	6.79	0.15	0.07	0.00	1.13	1.03	0.66	-3.00E+00	7.95E-30	Down		-4.38E-01	3.16E-02		-1.12E+00	5.83E-01		-7.26E+00	2.33E-01			-1.32E-01	8.19E-01		-7.86E-01	1.59E-01		Unigene32325_All//gi|15391731|emb|CAA93316.2|//1.00E-147//nitrite transporter [Cucumis sativus]	Unigene32325_All//2.00E-109//AT1G68570| proton-dependent oligopeptide transport (POT) family protein				nr -
Unigene32327_All	864	0.00	0.00	0.00	0.35	0.00	0.16	2.30	2.56	8.62	null	null			null	null		-8.43E+00	2.01E-02		-1.14E+00	4.57E-01			1.57E-01	7.02E-01		1.91E+00	1.84E-18	Up	Unigene32327_All//gi|301016726|dbj|BAJ11784.1|//5.00E-35//dehydration responsive protein [Corchorus olitorius]		Unigene32327_All//1.00E-46//TC171825			nr -
Unigene3233_All	233	0.90	7.39	2.06	1.28	1.03	0.58	2.00	5.38	3.25	3.04E+00	3.13E-06	Up		1.20E+00	3.02E-01		-3.10E-01	8.20E-01		-1.14E+00	4.57E-01			1.43E+00	1.04E-02		7.03E-01	3.27E-01		Unigene3233_All//gi|209573263|gb|AC162779.1|//1.00E-35//lipase [Jatropha curcas]	Unigene3233_All//1.00E-32//AT5G18640| lipase class 3 family protein	Unigene3233_All//3.00E-81//gi|164251319|gb|ES806339.1|ES806339			GO:0004091//GO:0031410//GO:0043231//GO:0044238	nr +
Unigene32332_All	1955	0.00	0.05	0.00	0.00	0.00	0.85	0.06	0.26	7.03	5.69E+00	3.86E-01			null	null		null	null		9.74E+00	5.83E-10	Up		1.98E+00	5.74E-02		6.76E+00	8.58E-93	Up	Unigene32332_All//gi|225440644|ref|XP_002274143.1|//8.00E-39//PREDICTED: similar to proton-dependent oligopeptide transport (POT) family protein [Vitis vinifera]	Unigene32332_All//5.00E-24//AT1G22540| proton-dependent oligopeptide transport (POT) family protein	Unigene32332_All//0.00E+00//gi|73859757|gb|DT462496.1|DT462496				nr -
Unigene32333_All	433	0.24	0.00	0.25	0.92	0.48	1.04	1.56	0.10	1.01	-7.92E+00	3.72E-01			2.54E-02	1.00E+00		-9.48E-01	4.21E-01		1.80E-01	8.83E-01			-4.02E+00	5.36E-04	Down	-6.26E-01	4.03E-01		Unigene32333_All//gi|30690436|ref|NP_182179.2|//4.00E-22//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene32333_All//2.00E-23//AT2G46560| transducin family protein / WD-40 repeat family protein					nr -
Unigene32334_All	518	0.00	2.15	0.31	0.29	0.27	0.61	1.06	1.21	1.69	1.11E+01	2.00E-06	Up		8.27E+00	2.39E-01		-1.18E-01	9.11E-01		1.08E+00	4.76E-01			1.90E-01	8.11E-01		6.73E-01	3.05E-01				Unigene32334_All//1.00E-29//AT1G29003				
Unigene32335_All	296	0.00	5.82	2.70	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.99E-10	Up		1.14E+01	1.72E-04	Up	null	null		null	null			null	null		null	null		Unigene32335_All//gi|159468754|ref|XP_001692539.1|//7.00E-18//dihydrolipoamide succinyltransferase, oxoglutarate dehydrogenase E2 component [Chlamydomonas reinhardtii] >gi|158278252|gb|EDP04017.1| dihydrolipoamide succinyltransferase, oxoglutarate dehydrogenase E2 component [Chlamydomonas reinhardtii]	Unigene32335_All//8.00E-09//AT4G26910| 2-oxoacid dehydrogenase family protein			ko00020|Citrate cycle (TCA cycle)//ko00310|Lysine degradation		nr +
Unigene32338_All	744	0.00	0.00	0.00	0.00	0.00	0.00	0.57	3.65	1.55	null	null			null	null		null	null		null	null			2.68E+00	2.87E-10	Up	1.45E+00	1.09E-02		Unigene32338_All//gi|222423859|dbj|BAH19894.1|//5.00E-77//AT5G14420| Arabidopsis thaliana]	Unigene32338_All//2.00E-78//AT5G14420| RGLG2 (RING domain Ligase2); ubiquitin-protein ligase	Unigene32338_All//7.00E-26//TC159525				nr +
Unigene3234_All	1502	2.09	11.94	4.64	2.65	1.67	1.38	3.32	7.51	5.44	2.51E+00	1.32E-48	Up		1.15E+00	1.06E-06	Up	-6.65E-01	2.22E-02		-9.40E-01	1.88E-03			1.18E+00	1.17E-13	Up	7.11E-01	5.70E-05		Unigene3234_All//gi|209573263|gb|AC162779.1|//1.00E-153//lipase [Jatropha curcas]	Unigene3234_All//5.00E-129//AT5G18640| lipase class 3 family protein	Unigene3234_All//0.00E+00//CO497433				nr -
Unigene32340_All	489	0.00	0.00	0.00	0.00	0.00	0.00	4.58	1.97	0.73	null	null			null	null		null	null		null	null			-1.22E+00	1.68E-03		-2.64E+00	8.10E-09	Down							ESTscan +
Unigene32342_All	978	0.00	0.00	0.00	0.00	0.00	0.00	1.38	3.50	0.20	null	null			null	null		null	null		null	null			1.34E+00	1.44E-05	Up	-2.76E+00	7.51E-06	Down	Unigene32342_All//gi|255083831|ref|XP_002508490.1|//1.00E-28//ATP-binding cassette superfamily [Micromonas sp. RCC299] >gi|226523767|gb|ACO69748.1| ATP-binding cassette superfamily [Micromonas sp. RCC299]	Unigene32342_All//4.00E-21//AT5G06530| ABC transporter family protein			ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene32343_All	401	0.00	1.01	2.12	0.00	0.00	0.00	0.00	0.00	0.10	9.98E+00	1.36E-02			1.11E+01	9.03E-05	Up	null	null		null	null			null	null		6.63E+00	6.45E-01		Unigene32343_All//gi|255077010|ref|XP_002502160.1|//5.00E-07//U1 small nuclear ribonucleoprotein [Micromonas sp. RCC299] >gi|226517425|gb|ACO63418.1| U1 small nuclear ribonucleoprotein [Micromonas sp. RCC299]				ko03040|Spliceosome		nr -
Unigene32345_All	818	0.00	22.55	94.20	0.12	0.25	0.28	0.41	0.15	0.00	1.45E+01	4.58E-106	Up		1.65E+01	0.00E+00	Up	1.05E+00	6.12E-01		1.18E+00	5.49E-01			-1.43E+00	2.58E-01		-8.69E+00	8.14E-03		Unigene32345_All//gi|149392583|gb|ABR26094.1|//3.00E-15//retrotransposon protein [Oryza sativa Indica Group]		Unigene32345_All//1.00E-73//TC165761			nr -
Unigene32346_All	359	0.29	0.42	1.04	1.25	3.17	0.88	4.48	1.98	1.22	5.39E-01	7.79E-01			1.83E+00	2.13E-01		1.34E+00	4.23E-02		-5.04E-01	6.49E-01			-1.18E+00	1.24E-02		-1.87E+00	1.38E-04	Down			Unigene32346_All//4.00E-07//TC179529				
Unigene32347_All	1467	0.00	0.00	0.00	0.00	0.00	0.00	1.21	1.68	8.15	null	null			null	null		null	null		null	null			4.74E-01	2.08E-01		2.75E+00	6.10E-45	Up	Unigene32347_All//gi|297608755|ref|NP_001062061.2|//2.00E-43//Os08g0481100 [Oryza sativa Japonica Group] >gi|255678535|dbj|BAF23975.2| Os08g0481100 [Oryza sativa Japonica Group]	Unigene32347_All//9.00E-58//AT4G40020| unknown protein					nr -
Unigene32348_All	777	0.00	42.65	16.79	0.00	0.00	0.00	0.00	0.00	0.00	1.54E+01	3.89E-191	Up		1.40E+01	1.96E-73	Up	null	null		null	null			null	null		null	null		Unigene32348_All//gi|42569129|ref|NP_179444.2|//8.00E-08//cupin family protein [Arabidopsis thaliana]						nr -
Unigene32349_All	334	0.16	0.15	0.00	3.13	9.90	1.49	0.89	1.75	10.97	-4.59E-02	9.83E-01			-7.29E+00	6.24E-01		1.66E+00	1.95E-06	Up	-1.07E+00	1.19E-01			9.83E-01	2.59E-01		3.63E+00	2.76E-18	Up			Unigene32349_All//7.00E-21//TC147469				
Unigene32351_All	702	0.00	0.00	0.00	0.14	0.83	0.90	0.24	5.18	4.82	null	null			null	null		2.56E+00	2.84E-02		2.67E+00	1.83E-02			4.43E+00	2.09E-20	Up	4.32E+00	4.01E-19	Up	Unigene32351_All//gi|226491243|ref|NP_001146854.1|//3.00E-12//RING zinc finger protein-like [Zea mays] >gi|195604260|gb|ACG23960.1| RING zinc finger protein-like [Zea mays]	Unigene32351_All//2.00E-12//AT5G20885| zinc finger (C3HC4-type RING finger) family protein	Unigene32351_All//0.00E+00//ES825947				nr -
Unigene32354_All	617	0.00	3.20	1.73	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.97E-11	Up		1.08E+01	6.62E-06	Up	null	null		null	null			null	null		null	null		Unigene32354_All//gi|168000925|ref|XP_001753166.1|//8.00E-18//HD2 type histone deacetylase [Physcomitrella patens subsp. patens] >gi|162695865|gb|EDQ82207.1| HD2 type histone deacetylase [Physcomitrella patens subsp. patens]						nr +
Unigene32355_All	421	30.32	17.21	27.83	32.54	31.49	28.11	110.47	50.53	38.51	-8.17E-01	2.85E-07			-1.24E-01	5.03E-01		-4.72E-02	8.17E-01		-2.11E-01	2.13E-01			-1.13E+00	2.28E-50	Down	-1.52E+00	9.74E-82	Down			Unigene32355_All//2.00E-179//gi|109836017|gb|DW234580.1|DW234580				
Unigene3236_All	1063	12.01	11.58	7.01	19.87	21.54	23.33	31.30	21.70	72.22	-5.22E-02	7.56E-01			-7.76E-01	2.21E-06		1.17E-01	3.95E-01		2.31E-01	4.53E-02			-5.28E-01	2.13E-10		1.21E+00	1.11E-93	Up	Unigene3236_All//gi|61651608|dbj|BAD91177.1|//1.00E-121//plastidic phosphate translocator-like protein2 [Mesembryanthemum crystallinum]	Unigene3236_All//7.00E-119//AT3G11320| organic anion transmembrane transporter	Unigene3236_All//0.00E+00//TC155027				nr +
Unigene32362_All	543	0.00	7.28	10.30	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.66E-22	Up		1.33E+01	3.82E-31	Up	null	null		null	null			null	null		null	null		Unigene32362_All//gi|298707969|emb|CBJ30340.1|//3.00E-43//triosephosphate isomerase/glyceraldehyde-3-phosphate dehydrogenase [Ectocarpus siliculosus]	Unigene32362_All//1.00E-43//AT1G79530| GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase			ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene32363_All	496	0.00	0.00	0.00	0.00	0.00	0.00	20.03	49.21	0.48	null	null			null	null		null	null		null	null			1.30E+00	3.77E-33	Up	-5.38E+00	1.55E-63	Down							
Unigene32364_All	630	0.00	0.00	0.00	0.00	0.00	0.00	8.52	4.11	0.00	null	null			null	null		null	null		null	null			-1.05E+00	6.63E-06	Down	-1.31E+01	1.73E-39	Down							ESTscan -
Unigene32369_All	813	0.71	0.00	0.46	0.61	0.89	0.61	4.37	5.81	1.52	-9.47E+00	1.52E-03			-6.27E-01	5.27E-01		5.38E-01	5.64E-01		-3.80E-03	9.87E-01			4.11E-01	1.09E-01		-1.52E+00	4.66E-07	Down	Unigene32369_All//gi|168485|gb|AAB36543.1|//5.00E-35//DnaJ-like protein [Phaseolus vulgaris]	Unigene32369_All//8.00E-27//AT2G17880| DNAJ heat shock protein, putative	Unigene32369_All//0.00E+00//TC152180				nr -
Unigene3237_All	1175	74.94	53.39	50.30	146.56	81.21	90.40	180.60	105.93	81.41	-4.89E-01	9.91E-19			-5.75E-01	6.47E-24		-8.52E-01	5.07E-117		-6.97E-01	1.11E-72			-7.70E-01	5.51E-120		-1.15E+00	1.28E-240	Down	Unigene3237_All//gi|74273619|gb|AB401477.1|//0.00E+00//cytochrome P450 DDWF1 [Gossypium hirsutum]	Unigene3237_All//8.00E-83//AT5G07990| TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	Unigene3237_All//0.00E+00//TC129591		ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr -
Unigene32370_All	359	1.31	0.85	0.30	3.89	1.92	0.63	0.71	1.28	0.67	-6.31E-01	5.54E-01			-2.14E+00	1.03E-01		-1.02E+00	6.01E-02		-2.63E+00	8.15E-05	Down		8.58E-01	3.96E-01		-8.58E-02	9.57E-01				Unigene32370_All//9.00E-73//gi|78328462|gb|DT548736.1|DT548736				
Unigene32372_All	675	0.00	41.14	15.30	0.00	0.00	0.00	0.00	0.00	0.00	1.53E+01	4.91E-160	Up		1.39E+01	5.37E-58	Up	null	null		null	null			null	null		null	null		Unigene32372_All//gi|6012952|emb|CAB57309.1|//1.00E-35//60S ribosomal protein L6 (YL 16 like) [Cyanophora paradoxa]	Unigene32372_All//4.00E-26//AT1G18540| 60S ribosomal protein L6 (RPL6A)			ko03010|Ribosome		nr +
Unigene32374_All	312	0.00	0.00	0.00	0.00	0.00	0.00	2.17	1.61	0.00	null	null			null	null		null	null		null	null			-4.32E-01	6.12E-01		-1.11E+01	3.56E-05	Down	Unigene32374_All//gi|260516678|gb|ACX43965.1|//2.00E-18//cysteine protease 1 [Brachiaria hybrid cultivar]	Unigene32374_All//4.00E-15//AT4G26880| CP1 (CYSTEINE PROTEINASE1); cysteine-type endopeptidase/ cysteine-type peptidase					nr -
Unigene32375_All	616	0.00	6.66	5.71	0.00	0.00	0.00	0.00	0.00	0.13	1.27E+01	2.25E-23	Up		1.25E+01	1.87E-19	Up	null	null		null	null			null	null		7.01E+00	4.04E-01		Unigene32375_All//gi|226505998|ref|NP_001146929.1|//4.00E-86//60S ribosomal protein L7a [Zea mays] >gi|195605318|gb|ACG24489.1| 60S ribosomal protein L7a [Zea mays]	Unigene32375_All//8.00E-68//AT3G62870| 60S ribosomal protein L7A (RPL7aB)			ko03010|Ribosome		nr +
Unigene32379_All	594	1.06	1.02	5.56	3.35	2.55	1.60	0.85	0.77	0.40	-4.63E-02	9.72E-01			2.39E+00	1.26E-08	Up	-3.95E-01	4.08E-01		-1.07E+00	2.00E-02			-1.42E-01	8.76E-01		-1.09E+00	2.28E-01		Unigene32379_All//gi|145338292|ref|NP_187547.2|//4.00E-26//RNA polymerase II transcription factor/ protein binding / transcription activator/ transcription regulator/ translation initiation factor/ zinc ion binding [Arabidopsis thaliana]	Unigene32379_All//2.00E-27//AT3G09360| RNA polymerase II transcription factor/ protein binding / transcription activator/ transcription regulator/ translation initiation factor/ zinc ion binding	Unigene32379_All//0.00E+00//TC147373				nr +
Unigene32380_All	288	0.00	0.00	0.00	0.00	0.00	0.00	3.23	2.90	0.00	null	null			null	null		null	null		null	null			-1.54E-01	8.08E-01		-1.17E+01	5.47E-07	Down	Unigene32380_All//gi|115470525|ref|NP_001058861.1|//1.00E-06//Os07g0139600 [Oryza sativa Japonica Group] >gi|113610397|dbj|BAF20775.1| Os07g0139600 [Oryza sativa Japonica Group]				ko03010|Ribosome		nr -
Unigene32383_All	766	0.00	4.76	3.41	0.00	0.00	0.12	0.00	0.00	0.00	1.22E+01	9.10E-21	Up		1.17E+01	2.12E-14	Up	null	null		6.88E+00	4.76E-01			null	null		null	null		Unigene32383_All//gi|160900504|ref|XP_001566086.1|//7.00E-78//alkyl hydroperoxide reductase subunit C [Delftia acidovorans SPH-1] >gi|160366088|gb|ABX37701.1| peroxiredoxin [Delftia acidovorans SPH-1] >gi|222871594|gb|EEF08725.1| 2-cys prx, alkyl hydroperoxide reductase-like protein [Populus trichocarpa]	Unigene32383_All//7.00E-31//AT5G06290| 2-Cys Prx B (2-Cysteine peroxiredoxin B); antioxidant/ peroxiredoxin					nr +
Unigene32387_All	253	0.21	4.01	1.26	1.58	2.72	0.71	0.50	0.50	1.89	4.28E+00	7.16E-05	Up		2.61E+00	1.46E-01		7.89E-01	4.04E-01		-1.14E+00	3.79E-01			-1.65E-02	1.02E+00		1.91E+00	6.30E-02								

Unigene32391_All	705	0.00	0.00	0.00	0.00	0.00	0.00	7.32	8.66	0.34	null	null		null	null		null	null		null	null		2.43E-01	3.07E-01		-4.43E+00	5.80E-30	Down							ESTscan -
Unigene32392_All	402	8.33	4.29	3.05	6.44	2.91	7.86	8.20	7.38	6.64	-9.59E-01	4.72E-03		-1.45E+00	8.55E-05	Down	-1.15E+00	1.97E-03		2.88E-01	4.71E-01		-1.52E-01	6.32E-01		-3.05E-01	3.30E-01				Unigene32392_All//2.00E-80//DW501456				
Unigene32393_All	626	0.00	71.31	32.49	0.00	0.00	0.00	0.00	0.00	0.00	1.61E+01	9.01E-258	Up	1.50E+01	5.66E-115	Up	null	null		null	null		null	null		null	null		Unigene32393_All//gi|192910686|gb|ACF06451.1|//7.00E-70//QM-like protein [Elaeis guineensis]	Unigene32393_All//5.00E-69//AT1G66580| 60S ribosomal protein L10 (RPL10C)	Unigene32393_All//4.00E-39//TC140923		ko03010|Ribosome		nr -
Unigene32394_All	446	0.00	1.59	2.51	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	3.33E-04	Up	1.13E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene32394_All//gi|194477305|ref|YP_002049484.1|//4.00E-33//ATPase [Paulinella chromatophora] >gi|171192312|gb|ACB43274.1| ATPase [Paulinella chromatophora]	Unigene32394_All//2.00E-30//AT5G15450| CLPR3 (CASEIN LYTIC PROTEINASE B3); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding					nr +
Unigene32395_All	517	0.00	1.76	0.41	0.39	2.26	1.83	0.33	0.08	0.15	1.08E+01	2.62E-05	Up	8.69E+00	1.41E-01		2.55E+00	5.02E-04	Up	2.25E+00	6.12E-03		-2.02E+00	3.67E-01		-1.09E+00	5.52E-01		Unigene32395_All//gi|22329577|ref|NP_172967.2|//2.00E-52//MATE efflux family protein [Arabidopsis thaliana]	Unigene32395_All//1.00E-53//AT1G15150| MATE efflux family protein					nr -
Unigene32397_All	674	0.16	11.05	5.93	0.00	0.20	0.00	0.19	0.00	0.00	6.15E+00	3.57E-39	Up	5.25E+00	2.62E-19	Up	7.68E+00	3.18E-01		null	null		-7.56E+00	2.35E-01		-7.56E+00	2.00E-01		Unigene32397_All//gi|159469668|ref|XP_001692985.1|//7.00E-89//ribosomal protein L8, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|158277787|gb|EDP00554.1| ribosomal protein L8 [Chlamydomonas reinhardtii]	Unigene32397_All//9.00E-82//AT4G36130| 60S ribosomal protein L8 (RPL8C)			ko03010|Ribosome		nr +
Unigene32399_All	379	0.00	4.68	5.90	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.14E-10	Up	1.25E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene32399_All//gi|255081756|ref|XP_002508100.1|//2.00E-13//DEAD/DEAH box helicase [Micromonas sp. RCC299] >gi|226523376|gb|ACO69358.1| DEAD/DEAH box helicase [Micromonas sp. RCC299]	Unigene32399_All//5.00E-13//AT2G45810| DEAD/DEAH box helicase, putative			ko03018|RNA degradation		nr +
Unigene32401_All	857	0.00	0.00	0.00	0.00	0.00	0.00	0.20	1.85	14.69	null	null		null	null		null	null		null	null		3.23E+00	2.21E-07	Up	6.22E+00	5.36E-83	Up			Unigene32401_All//4.00E-09//CO112306				
Unigene32405_All	653	0.16	72.47	47.46	0.00	0.00	0.00	0.00	0.00	0.00	8.82E+00	2.53E-268	Up	8.21E+00	4.11E-171	Up	null	null		null	null		null	null		null	null		Unigene32405_All//gi|15150747|ref|NP_150413.1|//8.00E-24//NADH dehydrogenase subunit 5 [Pylaiella littoralis] >gi|15147753|emb|CAC50854.1| NADH dehydrogenase subunit 5 [Pylaiella littoralis]	Unigene32405_All//6.00E-09//ATMG00665| Mitochondrial NADH dehydrogenase subunit 5. The gene is trans-spliced from three different pre-cursors, NAD5a, NAD5b and NAD5c.			ko00190|Oxidative phosphorylation		nr -
Unigene32406_All	438	0.12	14.92	0.73	0.68	0.31	0.52	0.00	0.19	0.00	6.96E+00	1.54E-35	Up	2.61E+00	1.46E-01		-1.12E+00	4.24E-01		-4.04E-01	7.51E-01		7.58E+00	4.01E-01		null	null				Unigene32406_All//1.00E-07//TC164284				
Unigene32409_All	448	0.00	10.07	4.40	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	1.08E-25	Up	1.21E+01	7.46E-11	Up	null	null		null	null		null	null		null	null		Unigene32409_All//sp|P82147|L2EFL_DROME//3.00E-53//Protein lethal(2)essential for life OS=Drosophila melanogaster GN=l(2)efl PE=1 SV=1						swissprot -
Unigene3241_All	1094	76.14	20.47	33.68	23.09	22.10	5.57	14.72	3.06	15.80	-1.90E+00	2.66E-158	Down	-1.18E+00	8.75E-76	Down	-6.32E-02	6.24E-01		-2.05E+00	2.83E-58	Down	-2.27E+00	1.13E-47	Down	1.02E-01	4.50E-01		Unigene3241_All//gi|297793861|ref|XP_002864815.1|//3.00E-79//integral membrane HPP family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310650|gb|EFH41074.1| integral membrane HPP family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3241_All//1.00E-68//AT5G62720| integral membrane HPP family protein	Unigene3241_All//0.00E+00//gi|109871291|gb|DW500267.1|DW500267			GO:0009528//GO:0031224	nr +
Unigene32410_All	806	0.00	0.00	0.00	3.21	0.85	0.62	0.58	0.41	0.30	null	null		null	null		-1.91E+00	1.16E-06	Down	-2.38E+00	1.23E-07	Down	-4.76E-01	6.59E-01		-9.60E-01	3.13E-01		Unigene32410_All//gi|30685150|ref|NP_188529.2|//2.00E-09//VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor [Arabidopsis thaliana] >gi|75153628|sp|Q8LLW1.1|VRN1_ARATH RecName: Full=B3 domain-containing transcription factor VRN1; AltName: Full=Protein VERNALIZATION 1 >gi|21734794|gb|AAM76972.1|AF28905 1_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|21734796|gb|AAM76973.1|AF28905 2_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|89000959|gb|ABD59069.1| At3g18990 [Arabidopsis thaliana]	Unigene32410_All//1.00E-10//AT3G18990| VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor		ABI3VP1			nr +
Unigene32411_All	439	0.00	0.00	0.00	0.00	0.00	0.00	2.22	2.00	0.00	null	null		null	null		null	null		null	null		-1.48E-01	8.12E-01		-1.11E+01	2.72E-07	Down	Unigene32411_All//gi|195605506|gb|ACG24583.1|//3.00E-50//60S ribosomal protein L10a-1 [Zea mays] >gi|195620954|gb|ACG32307.1| 60S ribosomal protein L10a-1 [Zea mays] >gi|195622848|gb|ACG33254.1| 60S ribosomal protein L10a-1 [Zea mays] >gi|195624806|gb|ACG34233.1| 60S ribosomal protein L10a-1 [Zea mays]	Unigene32411_All//1.00E-41//AT1G08360| 60S ribosomal protein L10A (RPL10aA)	Unigene32411_All//1.00E-16//CD486329		ko03010|Ribosome		nr -
Unigene32414_All	348	1.20	3.06	0.31	2.43	0.49	0.00	0.24	0.60	0.57	1.35E+00	5.00E-02		-1.97E+00	1.51E-01		-2.30E+00	4.14E-03		-1.12E+01	2.43E-05	Down	1.31E+00	4.47E-01		1.24E+00	4.68E-01		Unigene32414_All//gi|124360022|gb|ABN08038.1|//3.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene32414_All//1.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene32414_All//2.00E-24//TC163202				nr -
Unigene32417_All	361	0.00	3.51	4.57	0.00	0.00	0.00	0.23	0.00	0.00	1.18E+01	2.86E-07	Up	1.22E+01	4.30E-09	Up	null	null		null	null		-7.87E+00	4.03E-01		-7.87E+00	3.58E-01		Unigene32417_All//gi|4501883|ref|NP_001604.1|//3.00E-65//actin, aortic smooth muscle [Homo sapiens] >gi|6671507|ref|NP_031418.1| actin, aortic smooth muscle [Mus musculus] >gi|78045238|ref|NP_001029674.1| actin, aortic smooth muscle [Bos taurus] >gi|110625958|ref|NP_112266.1| actin, aortic smooth muscle [Rattus norvegicus] >gi|156119362|ref|NP_001095152.1| actin, aortic smooth muscle [Oryctolagus cuniculus] >gi|197097944|ref|NP_001126814.1| actin, aortic smooth muscle [Pongo abelii] >gi|213688375|ref|NP_001135417.1| actin, aortic smooth muscle [Homo sapiens] >gi|257470979|ref|NP_001158122.1| actin, aortic smooth muscle [Sus scrofa] >gi|73996085|ref|XP_534781.2| PREDICTED: similar to Actin, aortic smooth muscle (Alpha-actin 2) (Canis familiaris] >gi|114631685|ref|XP_521550.2|	Unigene32417_All//1.00E-63//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene32417_All//4.00E-72//TC153744		ko04145|Phagosome		nr +
Unigene32418_All	600	0.52	0.93	3.02	0.25	0.98	0.15	0.00	0.00	0.07	8.28E-01	3.81E-01		2.53E+00	2.82E-05	Up	1.97E+00	7.03E-02		-7.27E-01	7.15E-01		null	null		6.05E+00	6.45E-01		Unigene32418_All//gi|222871727|gb|EEF08858.1|//5.00E-48//predicted protein [Populus trichocarpa]						nr +
Unigene32419_All	304	0.00	4.17	0.00	1.97	0.68	1.78	0.42	0.82	2.36	1.20E+01	2.86E-07	Up	null	null		-1.53E+00	1.01E-01		-1.41E-01	8.79E-01		9.84E-01	5.17E-01		2.50E+00	4.03E-03								
Unigene3242_All	931	7.42	4.84	5.43	7.97	10.06	9.17	22.80	15.71	9.37	-6.15E-01	5.75E-03		-4.49E-01	5.77E-02		3.36E-01	8.27E-02		2.02E-01	3.87E-01		-5.37E-01	4.11E-07		-1.28E+00	2.26E-29	Down	Unigene3242_All//gi|16604501|gb|AAL24256.1|//1.00E-146//At2g01970/F14H20.4 [Arabidopsis thaliana]	Unigene3242_All//2.00E-65//AT2G01970| endomembrane protein 70, putative	Unigene3242_All//0.00E+00//DR455670				nr +
Unigene32423_All	1120	0.00	11.17	6.04	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	8.30E-72	Up	1.26E+01	9.22E-38	Up	null	null		null	null		null	null		null	null		Unigene32423_All//gi|55978000|gb|AAV68600.1|//2.00E-52//cyclin B [Ostreococcus tauri]	Unigene32423_All//7.00E-44//AT1G76310| CYCB2;4 (CYCLIN B2;4); cyclin-dependent protein kinase regulator					nr -
Unigene32424_All	453	0.00	0.00	0.00	0.00	0.00	0.00	4.01	0.00	0.79	null	null		null	null		null	null		null	null		-1.20E+01	7.10E-13	Down	-2.34E+00	1.83E-06	Down							
Unigene32427_All	431	0.00	8.58	5.07	0.00	0.00	0.10	0.00	0.00	0.00	1.31E+01	4.67E-21	Up	1.23E+01	4.95E-12	Up	null	null		6.71E+00	6.96E-01		null	null		null	null		Unigene32427_All//gi|15718887|ref|NP_000996.2|//5.00E-64//40S ribosomal protein S3 [Homo sapiens] >gi|77404290|ref|NP_001029219.1| 40S ribosomal protein S3 [Bos taurus] >gi|113205854|ref|NP_001038066.1| 40S ribosomal protein S3 [Sus scrofa] >gi|109107963|ref|XP_001086020.1| PREDICTED: 40S ribosomal protein S3 [Macaca mulatta] >gi|417719|sp|P23396.2|RS3_HUMAN RecName: Full=40S ribosomal protein S3 >gi|91207641|sp|Q3T169.1|RS3_BOVIN RecName: Full=40S ribosomal protein S3 >gi|115502828|sp|Q0280|2.1|RS3_PIG RecName: Full=40S ribosomal protein S3 >gi|187609257|pdb|2ZKQ|CC Chain c, Structure Of A Mammalian Ribosomal 40s Subunit Within An 80s Complex Obtained By Docking Homology Models Of The Rna And Proteins Into An 8.7 A Cryo-Em Map >gi|555941|gb|AAB60336.1| ribosomal protein S3 [Homo	Unigene32427_All//4.00E-41//AT2G31610| 40S ribosomal protein S3 (RPS3A)	Unigene32427_All//5.00E-10//ESS30182		ko03010|Ribosome		nr +
Unigene32431_All	871	0.00	1.75	0.00	0.06	0.08	0.31	4.37	7.39	8.19	1.08E+01	1.10E-08	Up	null	null		4.68E-01	9.58E-01		2.44E+00	2.22E-01		7.58E-01	2.46E-04		9.06E-01	2.73E-06				Unigene32431_All//6.00E-39//EX166648				
Unigene32438_All	814	0.64	1.00	1.44	1.47	1.02	1.66	0.93	2.46	1.86	6.32E-01	4.02E-01		1.16E+00	8.16E-02		-5.33E-01	3.93E-01		1.81E-01	7.57E-01		1.40E+00	9.14E-04	Up	9.92E-01	3.38E-02								ESTscan +
Unigene32440_All	244	7.08	2.91	15.49	0.00	0.28	0.00	0.35	0.17	0.00	-1.28E+00	1.19E-02		1.13E+00	6.96E-04	Up	8.14E+00	6.09E-01		null	null		-1.02E+00	7.24E-01		-8.44E+00	3.58E-01				Unigene32440_All//2.00E-14//DW514575				
Unigene32445_All	1583	0.00	0.00	0.00	0.00	0.00	0.00	0.53	1.27	8.28	null	null		null	null		null	null		null	null		1.25E+00	2.74E-03		3.95E+00	3.28E-68	Up	Unigene32445_All//gi|149392583|gb|ABR26094.1|//2.00E-09//retrotransposon protein [Oryza sativa Indica Group]		Unigene32445_All//6.00E-25//BF276577				nr -

Unigene32446_All	212	0.00	1.20	1.26	0.70	0.49	0.85	176.10	515.74	343.89	1.02E+01	7.86E-02		1.03E+01	8.02E-02		-5.33E-01	7.85E-01		2.74E-01	9.05E-01		1.55E+00	7.77E-191	Up	9.66E-01	2.64E-62				Unigene32446_All//7.00E-60//gi|109862765|gb|DW491742.1|DW491742				
Unigene32450_All	218	51.36	14.64	23.21	21.48	11.53	14.92	3.30	0.96	1.64	-1.81E+00	1.50E-20	Down	-1.15E+00	3.01E-10	Down	-8.97E-01	5.36E-04		-5.26E-01	6.39E-02		-1.78E+00	2.79E-02		-1.00E+00	1.66E-01				Unigene32450_All//6.00E-119//TC136919				
Unigene32454_All	528	0.00	8.06	2.62	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	3.04E-24	Up	1.14E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene32454_All//gi|301101616|ref|XP_002899896.1|//3.00E-20//alpha-actinin-1, putative [Phytophthora infestans T30-4] >gi|262102471|gb|EEY60523.1|alpha-actinin-1, putative [Phytophthora infestans T30-4]						nr +
Unigene32456_All	488	0.00	0.00	2.73	2.86	1.83	0.93	0.00	0.09	0.00	null	null		1.14E+01	2.40E-07	Up	-6.40E-01	2.55E-01		-1.63E+00	5.90E-03		6.42E+00	6.34E-01		null	null									
Unigene32458_All	627	0.00	13.74	5.44	0.00	0.05	0.00	0.00	0.00	0.00	1.37E+01	2.70E-49	Up	1.24E+01	7.39E-19	Up	5.78E+00	8.30E-01		null	null		null	null		null	null									ESTscan +
Unigene32459_All	271	2.32	0.00	1.18	2.57	1.02	2.83	0.62	1.08	0.29	-1.12E+01	7.91E-04	Down	-9.75E-01	3.16E-01		-1.34E+00	1.09E-01		1.39E-01	8.78E-01		7.91E-01	5.63E-01		-1.09E+00	5.52E-01		Unigene32459_All|gi|297609253|ref|NP_001062888.2|//1.00E-17//Os09g0327200 [Oryza sativa Japonica Group] >gi|255678787|dbj|BAF24802.2|Os09g0327200 [Oryza sativa Japonica Group]	Unigene32459_All//5.00E-19//AT2G22070| pentatricopeptide (PPR) repeat-containing protein	Unigene32459_All//2.00E-98//CO090875				nr +
Unigene3246_All	1748	20.98	13.19	22.60	15.22	18.05	16.98	1.55	3.08	0.71	-6.70E-01	6.06E-14		1.07E-01	2.84E-01		2.46E-01	1.00E-02		1.58E-01	1.57E-01		9.95E-01	1.78E-05		-1.13E+00	7.43E-04	Down	Unigene3246_All//gi|224133724|ref|XP_002321645.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222868641|gb|EEF05772.1|cytochrome P450 [Populus trichocarpa]	Unigene3246_All//3.00E-108//AT3G26310| CYP71B35; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene3246_All//0.00E+00//TC139031	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016491	nr -
Unigene32460_All	411	0.38	3.70	0.26	1.94	1.51	0.55	2.26	1.42	0.48	3.28E+00	6.57E-06	Up	-5.60E-01	7.76E-01		-3.63E-01	6.23E-01		-1.82E+00	3.32E-02		-6.69E-01	3.12E-01		-2.22E+00	1.63E-03		Unigene32460_All//gi|462013|sp|P35016.1|ENPL_CATRO//3.00E-09//RecName: Full=Endoplasmin homolog; AltName: Full=Glucose-regulated protein 94 homolog; Short=GRP-94 homolog; Flags: Precursor >gi|348696|gb|AAA16785.1| heat shock protein 90 [Catharanthus roseus]	Unigene32460_All//2.00E-08//AT4G24190| SHD (SHEPHERD); ATP binding / unfolded protein binding	Unigene32460_All//8.00E-46//TC169586	ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene32462_All	483	0.11	1.36	0.11	0.00	0.00	0.00	0.70	3.37	2.89	3.65E+00	4.10E-03		2.51E-02	9.95E-01		null	null		null	null		2.27E+00	1.94E-05	Up	2.04E+00	2.08E-04	Up								
Unigene32465_All	848	0.00	0.00	0.00	0.00	0.00	0.00	14.86	0.39	4.89	null	null		null	null		null	null		null	null		-5.24E+00	8.84E-77	Down	-1.60E+00	1.42E-24	Down	Unigene32465_All|gi|7770345|gb|AAF69715.1|AC016041_20//5.00E-34//F27J15.18 [Arabidopsis thaliana] >gi|38602922|gb|AAR24706.1|At1g49030 [Arabidopsis thaliana] >gi|44681424|gb|AAS47652.1|At1g49030 [Arabidopsis thaliana]	Unigene32465_All//2.00E-35//AT1G49030| unknown protein					nr +
Unigene32467_All	655	683.05	274.00	620.95	219.64	251.40	140.66	0.00	0.19	0.43	-1.32E+00	0.00E+00	Down	-1.38E-01	1.60E-08		1.95E-01	1.39E-07		-6.43E-01	9.62E-53		7.58E+00	2.40E-01		8.73E+00	2.43E-02		Unigene32467_All|gi|115485049|ref|NP_001067668.1|//3.00E-38//Os11g0267000 [Oryza sativa Japonica Group] >gi|77549790|gb|ABA92587.1| GUN4-like family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113644890|dbj|BAF28031.1|Os11g0267000 [Oryza sativa Japonica Group]	Unigene32467_All//2.00E-32//AT3G59400| GUN4; enzyme binding / tetrapyrrole binding	Unigene32467_All//9.00E-53//TC151181				nr -
Unigene32468_All	267	0.00	0.76	2.59	0.19	1.29	1.01	0.63	0.00	0.00	9.57E+00	1.36E-01		1.13E+01	6.16E-04	Up	2.79E+00	1.14E-01		2.44E+00	2.22E-01		-9.31E+00	1.34E-01		-9.31E+00	1.08E-01				Unigene32468_All//3.00E-44//TC160223				
Unigene32469_All	321	0.00	0.00	0.00	0.00	0.00	0.00	4.61	3.78	0.00	null	null		null	null		null	null		null	null		-2.88E-01	6.00E-01		-1.22E+01	5.85E-11	Down	Unigene32469_All|gi|115457852|ref|NP_001052526.1|//2.00E-30//Os04g0349500 [Oryza sativa Japonica Group] >gi|32489919|emb|CAE05511.1|OSJNBa0038P21.4 [Oryza sativa (japonica cultivar-group)] >gi|113564097|dbj|BAF14440.1|Os04g0349500 [Oryza sativa Japonica Group]	Unigene32469_All//3.00E-28//AT5G20290| 40S ribosomal protein S8 (RPS8A)		ko03010|Ribosome		nr +
Unigene3247_All	1656	17.28	28.27	27.30	47.95	62.45	55.75	18.56	7.47	13.45	7.10E-01	2.40E-19		6.60E-01	6.53E-16		3.81E-01	2.25E-16		2.17E-01	4.71E-05		-1.31E+00	2.07E-42	Down	-4.65E-01	4.33E-08		Unigene3247_All|gi|211906528|gb|ACJ11757.1|//0.00E+00//alpha-1,4 glucan phosphorylase [Gossypium hirsutum]	Unigene3247_All//0.00E+00//AT3G29320| glucan phosphorylase, putative	Unigene3247_All//0.00E+00//gi|78342620|gb|DT562894.1|DT562894	ko00500|Starch and sucrose metabolism	GO:0005515//GO:0006950//GO:0009532//GO:0009628//GO:0016758//GO:0048038//GO:0048037	nr -
Unigene32472_All	376	0.00	0.00	0.00	0.00	0.00	0.00	0.34	2.89	3.71	null	null		null	null		null	null		null	null		3.10E+00	4.52E-05	Up	3.46E+00	4.41E-07	Up			Unigene32472_All//8.00E-18//DT047714				
Unigene32473_All	323	0.00	2.04	0.00	0.93	0.85	0.14	0.39	0.52	0.37	1.10E+01	6.25E-04	Up	null	null		-1.18E-01	9.00E-01		-2.73E+00	1.37E-01		3.98E-01	8.14E-01		-8.59E-02	9.69E-01				Unigene32473_All//4.00E-07//DW234443				
Unigene32474_All	472	0.00	0.43	0.00	0.00	0.00	0.00	200.20	37.46	133.61	8.75E+00	1.36E-01		null	null		null	null		null	null		-2.42E+00	6.98E-299	Down	-5.83E-01	2.88E-34		Unigene32474_All|gi|16648951|gb|AAL24327.1|//2.00E-20//Unknown protein [Arabidopsis thaliana] >gi|31711760|gb|AAP68236.1|At3g01670 [Arabidopsis thaliana]	Unigene32474_All//2.00E-21//AT3G01670| unknown protein	Unigene32474_All//2.00E-99//ES831165			nr -
Unigene32477_All	535	0.00	0.00	0.00	0.93	0.26	0.00	4.82	7.97	1.19	null	null		null	null		-1.85E+00	8.43E-02		-9.86E+00	2.97E-03		7.25E-01	5.67E-03		-2.02E+00	1.75E-07	Down								
Unigene32484_All	381	0.00	3.86	1.40	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.11E-08	Up	1.04E+01	4.04E-03		null	null		null	null		null	null		null	null		Unigene32484_All|gi|297802832|ref|XP_002869300.1|//3.00E-17//60S ribosomal protein L39 [Arabidopsis lyrata subsp. lyrata] >gi|297821901|ref|XP_002878833.1|60S ribosomal protein L39 [Arabidopsis lyrata subsp. lyrata] >gi|297315136|gb|EFH45559.1| 60S ribosomal protein L39 [Arabidopsis lyrata subsp. lyrata] >gi|297324672|gb|EFH55092.1| 60S ribosomal protein L39 [Arabidopsis lyrata subsp. lyrata]	Unigene32484_All//4.00E-18//AT4G31985| 60S ribosomal protein L39 (RPL39C)		ko03010|Ribosome		nr -
Unigene32486_All	1018	0.00	0.00	0.00	0.00	0.07	0.18	11.09	3.98	0.08	null	null		null	null		6.08E+00	6.09E-01		7.47E+00	1.94E-01		-1.48E+00	4.53E-19	Down	-7.15E+00	3.27E-79	Down			Unigene32486_All//2.00E-08//FL576798				
Unigene32488_All	445	0.47	0.23	0.48	0.00	1.01	0.20	0.57	1.78	2.60	-1.05E+00	5.64E-01		2.55E-02	1.00E+00		9.97E+00	8.01E-03		7.67E+00	4.76E-01		1.65E+00	2.88E-02		2.19E+00	4.81E-04	Up								
Unigene3249_All	580	0.63	0.00	0.00	2.06	1.54	0.47	2.55	0.43	1.24	-9.30E+00	1.96E-02		-9.30E+00	2.78E-02		-4.17E-01	5.22E-01		-2.14E+00	1.81E-03		-2.56E+00	1.18E-05	Down	-1.05E+00	2.65E-02		Unigene3249_All|gi|224090869|ref|XP_002309106.1|//9.00E-50//predicted protein [Populus trichocarpa] >gi|222855082|gb|EEE92629.1|predicted protein [Populus trichocarpa]	Unigene3249_All//3.00E-27//AT2G37960| unknown protein	Unigene3249_All//4.00E-64//TC148258			nr +
Unigene32491_All	697	0.00	0.00	0.31	0.57	0.20	0.00	1.46	2.94	39.61	null	null		8.26E+00	1.41E-01		-1.53E+00	2.05E-01		-9.16E+00	1.11E-02		1.01E+00	1.23E-02		4.77E+00	1.01E-161	Up	Unigene32491_All|gi|297720115|ref|NP_001172419.1|//4.00E-08//Os01g0538700 [Oryza sativa Japonica Group] >gi|255673363|dbj|BAH91149.1|Os01g0538700 [Oryza sativa Japonica Group]		Unigene32491_All//2.00E-19//CO102469			nr +
Unigene32492_All	402	2.08	4.03	4.90	5.70	6.94	2.25	5.68	4.05	2.18	9.54E-01	6.65E-02		1.23E+00	1.21E-02		2.84E-01	5.18E-01		-1.34E+00	1.70E-03		-4.86E-01	2.16E-01		-1.38E+00	2.68E-04	Down	Unigene32492_All|gi|257196367|gb|ACV49920.1|//2.00E-09//ubiquitin-conjugating enzyme variant [Citrus sinensis]	Unigene32492_All//6.00E-10//AT3G52560| UEV1D-4 (UBIQUITIN E2 VARIANT 1D-4); protein binding / ubiquitin-protein ligase	Unigene32492_All//7.00E-111//CO111376			nr -
Unigene32495_All	490	0.00	0.00	0.00	0.00	0.00	0.00	2.93	5.80	0.00	null	null		null	null		null	null		null	null		9.83E-01	3.20E-03		-1.15E+01	1.19E-10	Down								
Unigene32499_All	608	0.09	0.00	0.70	0.08	0.11	0.00	2.50	1.24	0.46	-6.43E+00	6.12E-01		3.02E+00	5.73E-02		4.68E-01	9.58E-01		-6.36E+00	6.35E-01		-1.02E+00	3.53E-02		-2.45E+00	8.71E-06	Down	Unigene32499_All|gi|115447285|ref|NP_001047422.1|//5.00E-43//Os02g0614100 [Oryza sativa Japonica Group] >gi|113536953|dbj|BAF09336.1|Os02g0614100 [Oryza sativa Japonica Group]	Unigene32499_All//1.00E-39//AT4G22272| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter-related (TAIR:AT4G31600.1); Has 1302 Blast hits to 1300 proteins in 174 species: Archae - 0; Bacteria - 4; Metazoa - 376; Fungi - 239; Plants - 567; Viruses - 0; Other Eukaryotes - 116 (source: NCBI BLink).	Unigene32499_All//0.00E+00//TC175087				nr -
Unigene3250_All	841	11.94	6.27	14.06	3.97	7.62	4.30	0.20	0.20	1.14	-9.31E-01	3.77E-07		2.35E-01	2.04E-01		9.40E-01	2.37E-05		1.14E-01	7.43E-01		-1.66E-02	1.02E+00		2.50E+00	6.42E-04	Up	Unigene3250_All|gi|158427470|gb|AB938330.1|//4.00E-44//chloroplast fructose-1,6-bisphosphatase I [Fragaria x ananassa]	Unigene3250_All//4.00E-39//AT3G54050| fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	Unigene3250_All//0.00E+00//TC148258	ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway	GO:0005975//GO:0016491//GO:0019203//GO:0043231	nr -
Unigene32501_All	451	0.00	0.00	0.00	0.00	0.00	0.00	5.06	3.24	0.62	null	null		null	null		null	null		null	null		-6.42E-01	9.17E-02		-3.03E+00	3.22E-10	Down			Unigene32501_All//1.00E-13//TC149074				
Unigene32504_All	445	0.47	0.46	0.12	0.78	0.00	0.00	0.10	1.13	1.70	-4.61E-02	9.88E-01		-1.97E+00	3.81E-01		-9.61E+00	9.45E-03		-9.61E+00	2.12E-02		3.57E+00	6.53E-03		4.16E+00	1.34E-04	Up								
Unigene32506_All	580	0.00	0.00	0.00	0.00	0.00	0.00	3.79	6.63	0.27	null	null		null	null		null	null		null	null		8.07E-01	3.73E-03		-3.79E+00	8.31E-12	Down	Unigene32506_All|gi|192910906|gb|ACF06561.1|//5.00E-45//ribosomal protein L18a [Elaeis guineensis]	Unigene32506_All//8.00E-46//AT2G34480| 60S ribosomal protein L18A (RPL18aB)		ko03010|Ribosome		nr +
Unigene3251_All	1893	3.51	1.79	3.12	2.29	2.29	0.24	0.47	0.22	0.82	-9.69E-01	2.67E-05		-1.69E-01	5.14E-01		1.60E-03	9.96E-01		-3.26E+00	3.82E-17	Down	-1.09E+00	1.07E-01		8.07E-01	7.83E-02		Unigene3251_All|gi|4585576|gb|AAD25541.1|AF134051_1//1.00E-120//fructose-1,6-bisphosphatase precursor [Solanum tuberosum]	Unigene3251_All//7.00E-114//AT3G54050| fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	Unigene3251_All//0.00E+00//TC148258	ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene32512_All	644	0.00	7.47	3.14	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.96E-27	Up	1.16E+01	3.79E-11	Up	null	null		null	null		null	null		null	null		Unigene32512_All|sp|P34257|TC3A_CAEEL//2.00E-06//Transposable element Tc3 transposase OS=Caenorhabditis elegans GN=tc3a PE=1 SV=1						swissprot -
Unigene32515_All	535	4.40	1.04	0.90	8.38	7.27	7.85	2.37	4.53	3.28	-2.08E+00	9.93E-06	Down	-2.30E+00	5.12E-06	Down	-2.04E-01	5.35E-01		-9.41E-02	7.56E-01		9.34E-01	1.06E-02		4.67E-01	2.88E-01				Unigene32515_All//1.00E-119//gi|13248088|gb|BF274059.2|BF274059				

Unigene3252_All	903	22.13	17.11	21.05	15.17	14.49	15.75	21.44	12.73	8.56	-3.71E-01	2.81E-03		-7.23E-02	6.23E-01		-6.61E-02	7.36E-01		5.45E-02	7.54E-01		-7.53E-01	2.81E-11		-1.33E+00	3.18E-28	Down	Unigene3252_All//gi|116057142|emb|CAL51569.1|//3.00E-09//CNPV141 HAL3-like domain protein (ISS) [Ostreococcus tauri]	Unigene3252_All//3.00E-35//AT4G21192| FUNCTIONS IN: molecular function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Cytochrome c oxidase biogenesis protein Cmc1-like (InterPro:IPR013892); Has 111 Blast hits to 111 proteins in 53 species: Archae - 0; Bacteria - 0; Metazoa - 71; Fungi - 29; Plants - 9; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene3252_All//0.00E+00//gi|11207221|gb|BF276151.1|BF276151			GO:0005515//GO:0043234//GO:0044267	nr -
Unigene32520_All	606	0.00	0.00	0.00	0.00	0.00	0.00	8.79	7.79	0.53	null	null		null	null		null	null		null	null		-1.74E-01	5.18E-01		-4.06E+00	3.30E-29	Down		Unigene32520_All//8.00E-16//TC142721				
Unigene32522_All	357	0.00	8.23	1.64	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.01E-16	Up	1.07E+01	2.17E-03		null	null		null	null		null	null		null	null								ESTscan -
Unigene32524_All	502	0.00	0.00	0.00	4.07	1.51	0.90	0.00	0.00	0.00	null	null		null	null		-1.43E+00	9.35E-04	Down	-2.18E+00	1.41E-05	Down	null	null		null	null		Unigene32524_All//gi|225423491|ref|XP_002269100.1|//8.00E-69//PREDICTED: similar to 14-3-3 protein L11 1433-3 [Vitis vinifera]	Unigene32524_All//2.00E-67//AT1G26480| GRF12 (GENERAL REGULATORY FACTOR 12); protein binding / protein phosphorylated amino acid binding	Unigene32524_All//1.00E-26//EE593039				nr +
Unigene32529_All	460	2.62	0.00	1.62	4.55	2.10	0.39	1.38	0.09	0.00	-1.14E+01	5.01E-07	Down	-6.91E-01	2.86E-01		-1.12E+00	8.02E-03		-3.53E+00	4.65E-09	Down	-3.92E+00	9.80E-04	Down	-1.04E+01	7.11E-05	Down		Unigene32529_All//5.00E-07//EV487029				
Unigene3253_All	904	5.79	6.05	5.18	7.99	6.82	5.50	8.61	4.95	4.01	6.48E-02	8.04E-01		-1.59E-01	6.04E-01		-2.29E-01	3.29E-01		-5.40E-01	1.28E-02		-7.99E-01	1.79E-05		-1.10E+00	4.36E-09	Down	Unigene3253_All//gi|116057142|emb|CAL51569.1|//3.00E-09//CNPV141 HAL3-like domain protein (ISS) [Ostreococcus tauri]	Unigene3253_All//3.00E-35//AT4G21192| FUNCTIONS IN: molecular function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Cytochrome c oxidase biogenesis protein Cmc1-like (InterPro:IPR013892); Has 111 Blast hits to 111 proteins in 53 species: Archae - 0; Bacteria - 0; Metazoa - 71; Fungi - 29; Plants - 9; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene3253_All//0.00E+00//TC174227				nr -
Unigene32530_All	2266	0.00	9.57	3.24	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	7.99E-125	Up	1.17E+01	4.45E-41	Up	null	null		null	null		null	null		null	null		Unigene32530_All//gi|226457635|gb|EEH51934.1|//5.00E-12//JmjN/JmjC protein [Micromonas pusilla CCMP1545]						nr +
Unigene32533_All	629	0.17	0.00	0.00	0.48	0.11	0.00	0.81	2.66	5.76	-7.38E+00	3.72E-01		-7.38E+00	3.93E-01		-2.12E+00	1.65E-01		-8.89E+00	3.99E-02		1.72E+00	4.01E-04	Up	2.84E+00	1.44E-14	Up	Unigene32533_All//gi|224069222|ref|XP_002302930.1|//7.00E-14//nbs-lrr resistance protein [Populus trichocarpa] >gi|222844656|gb|EEE82203.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene32533_All//7.00E-06//AT5G43470| RPP8 (RECOGNITION OF PERONOSPORA PARASITICA 8); nucleotide binding	Unigene32533_All//6.00E-60//TC135463				nr +
Unigene32537_All	667	0.24	0.61	0.48	0.97	1.70	0.81	0.57	0.13	2.21	1.37E+00	2.74E-01		1.03E+00	4.71E-01		8.11E-01	2.24E-01		-2.57E-01	7.57E-01		-2.19E+00	8.75E-02		1.95E+00	2.09E-04	Up	Unigene32537_All//gi|300142885|gb|EFJ09581.1|//4.00E-28//ubiquitin-protein ligase, UPL1 [Selaginella moellendorffii]	Unigene32537_All//8.00E-27//AT1G70320| UPL2 (UBIQUITIN-PROTEIN LIGASE 2); ubiquitin-protein ligase	Unigene32537_All//2.00E-131//TC137410		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene32539_All	1555	0.00	5.25	2.36	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.14E-46	Up	1.12E+01	2.38E-20	Up	null	null		null	null		null	null		null	null		Unigene32539_All//gi|195604856|gb|ACG24258.1|//6.00E-13//plasminogen activator inhibitor 1 RNA-binding protein [Zea mays]						nr +
Unigene32540_All	804	0.26	0.13	0.53	0.00	0.09	0.06	13.36	3.12	3.27	-1.05E+00	5.64E-01		1.03E+00	3.96E-01		6.42E+00	6.09E-01		5.81E+00	6.96E-01		-2.10E+00	4.18E-29	Down	-2.03E+00	7.99E-29	Down	Unigene32540_All//gi|51091463|dbj|BAD36203.1|//9.00E-11//ankyrin-like protein [Oryza sativa Japonica Group] >gi|51091614|dbj|BAD36375.1| ankyrin-like protein [Oryza sativa Japonica Group]		Unigene32540_All//3.00E-47//CO091282				nr -
Unigene32542_All	443	0.00	0.00	0.00	0.79	0.23	0.61	4.29	1.42	3.24	null	null		null	null		-1.76E+00	1.90E-01		-3.64E-01	7.55E-01		-1.60E+00	3.09E-04	Down	-4.08E-01	3.33E-01		Unigene32542_All//gi|224135191|ref|XP_002327588.1|//7.00E-16//cc-nbs resistance protein [Populus trichocarpa] >gi|222836142|gb|EEE74563.1| cc-nbs resistance protein [Populus trichocarpa]	Unigene32542_All//9.00E-11//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene32542_All//1.00E-13//TC143926		ko04626|Plant-pathogen interaction		nr +
Unigene32544_All	810	0.00	7.32	5.00	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	7.74E-34	Up	1.23E+01	1.92E-22	Up	null	null		null	null		null	null		null	null		Unigene32544_All//sp|Q92482|AQP3_HUMAN//2.00E-15//Aquaporin-3 OS=Homo sapiens GN=AQP3 PE=2 SV=2						swissprot +
Unigene32545_All	957	0.00	0.00	0.00	0.05	0.76	0.14	0.35	0.13	2.96	null	null		null	null		3.86E+00	1.51E-03		1.44E+00	6.38E-01		-1.43E+00	2.58E-01		3.06E+00	2.24E-12	Up	Unigene32545_All//gi|3482933|gb|AAC33218.1|//2.00E-96//Similar to cdc2 protein kinases [Arabidopsis thaliana]	Unigene32545_All//3.00E-98//AT1G09600| protein kinase family protein	Unigene32545_All//1.00E-86//DN780253				nr +
Unigene32546_All	737	6.25	0.96	3.40	0.68	0.56	0.80	0.00	0.00	0.00	-2.70E+00	4.76E-14	Down	-8.79E-01	2.78E-03		-2.70E-01	8.02E-01		2.37E-01	7.98E-01		null	null		null	null		Unigene32546_All//gi|224124584|ref|XP_002319368.1|//1.00E-102//GH3 family protein [Populus trichocarpa] >gi|222857744|gb|EEE95291.1| GH3 family protein [Populus trichocarpa]	Unigene32546_All//9.00E-97//AT4G03400| DFL2 (DWARF IN LIGHT 2)	Unigene32546_All//0.00E+00//TC134400				nr -
Unigene32548_All	768	4.02	1.85	1.25	9.08	9.06	5.12	1.60	0.22	0.93	-1.12E+00	1.83E-03		-1.69E+00	2.20E-05	Down	-3.70E-03	9.80E-01		-8.28E-01	1.41E-04		-2.87E+00	2.54E-05	Down	-7.74E-01	1.40E-01		Unigene32548_All//gi|15217654|ref|NP_176626.1|//9.00E-55//proline-rich family protein [Arabidopsis thaliana] >gi|6633834|gb|AAF19693.1|AC009519_27 F1N19.3 [Arabidopsis thaliana] >gi|34365707|gb|AAQ65165.1| At1g64450 [Arabidopsis thaliana]	Unigene32548_All//1.00E-42//AT1G64450| proline-rich family protein	Unigene32548_All//3.00E-173//ES803922				nr -
Unigene3255_All	1237	3.09	4.51	3.31	3.34	6.29	5.62	6.43	13.11	11.40	5.45E-01	3.14E-02		1.02E-01	7.43E-01		9.13E-01	4.17E-06		7.50E-01	6.31E-04		1.03E+00	1.18E-15	Up	8.27E-01	4.77E-10		Unigene3255_All//gi|224086052|ref|XP_002307796.1|//4.00E-65//bromodomain protein [Populus trichocarpa] >gi|222857245|gb|EEE94792.1| bromodomain protein [Populus trichocarpa]	Unigene3255_All//2.00E-45//AT1G20670| DNA-binding bromodomain-containing protein	Unigene3255_All//9.00E-150//TC176210				nr +
Unigene32550_All	611	0.51	1.16	0.00	2.36	2.82	1.26	1.66	0.89	0.20	1.18E+00	1.75E-01		-9.01E+00	4.91E-02		2.53E-01	6.46E-01		-9.12E-01	1.06E-01		-9.01E-01	1.44E-01		-3.09E+00	5.36E-05	Down	Unigene32550_All//gi|297842683|ref|XP_002889223.1|//6.00E-87//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297335064|gb|EFH65482.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene32550_All//4.00E-88//AT1G78980| SRF5 (STRUBBELIG-RECEPTOR FAMILY 5); ATP binding / kinase/ protein serine/threonine kinase	Unigene32550_All//0.00E+00//TC166091		ko04626|Plant-pathogen interaction		nr +
Unigene32553_All	237	2.87	0.00	1.57	6.52	3.34	4.00	1.25	1.06	0.00	-1.15E+01	4.10E-04	Down	-8.68E-01	3.51E-01		-9.63E-01	5.85E-02		-7.03E-01	2.00E-01		-2.39E-01	8.39E-01		-1.03E+01	1.58E-02			Unigene32553_All//3.00E-07//DT049317				
Unigene32555_All	713	0.73	0.14	0.00	0.00	0.00	0.63	0.83	3.05	81.97	-2.37E+00	4.75E-02		-9.52E+00	4.75E-03		null	null		9.31E+00	7.75E-03		1.88E+00	1.11E-05	Up	6.63E+00	0.00E+00	Up	Unigene32555_All//gi|224146274|ref|XP_002325945.1|//3.00E-41//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372126|gb|ABQ62994.1| RAP2-like protein [Populus trichocarpa] >gi|222862820|gb|EEF00327.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene32555_All//2.00E-30//AT1G71520| AP2 domain-containing transcription factor, putative	Unigene32555_All//1.00E-51//TC167996	AP2-EREBP			nr -
Unigene32557_All	487	0.00	58.99	22.09	0.00	0.35	0.00	0.00	0.00	0.00	1.58E+01	1.30E-165	Up	1.44E+01	2.06E-60	Up	8.47E+00	2.27E-01		null	null		null	null		null	null		Unigene32557_All//sp|Q9VAJ4|OB99A_DROME//2.00E-16//General odorant-binding protein 99a OS=Drosophila melanogaster GN=Obp99a PE=1 SV=2						swissprot +
Unigene32558_All	426	0.00	12.73	9.75	0.00	0.32	0.00	0.00	0.00	0.00	1.36E+01	6.35E-31	Up	1.33E+01	4.83E-23	Up	8.34E+00	3.18E-01		null	null		null	null		null	null		Unigene32558_All//gi|24173796|gb|AAL91663.1|//2.00E-32//60s acidic ribosomal protein [Prunus dulcis] >gi|110013714|gb|ABR03379.1| 60S acidic ribosomal protein [Prunus dulcis]	Unigene32558_All//2.00E-10//AT2G27710| 60S acidic ribosomal protein P2 (RPP2B)			ko03010|Ribosome		nr -
Unigene32559_All	529	0.20	0.00	0.40	0.09	2.54	0.85	3.52	0.87	1.28	-7.63E+00	3.72E-01		1.03E+00	5.91E-01		4.75E+00	4.00E-07	Up	3.18E+00	3.79E-02		-2.02E+00	2.13E-05	Down	-1.46E+00	6.77E-04	Down	Unigene32559_All//gi|240256033|ref|NP_193913.4|//2.00E-55//binding / calmodulin binding [Arabidopsis thaliana]	Unigene32559_All//2.00E-56//AT4G21820| binding / calmodulin binding					nr +
Unigene32562_All	295	0.71	0.69	0.00	0.51	1.05	0.00	2.01	0.00	0.14	-4.63E-02	9.88E-01		-9.47E+00	1.46E-01		1.05E+00	5.31E-01		-8.98E+00	2.33E-01		-1.10E+01	2.39E-04	Down	-3.89E+00	1.09E-03		Unigene32562_All//gi|115476868|ref|NP_001062030.1|//4.00E-42//Os08g0474700 [Oryza sativa Japonica Group] >gi|113623999|dbj|BAF23944.1| Os08g0474700 [Oryza sativa Japonica Group]	Unigene32562_All//7.00E-42//AT2G21630| transport protein, putative	Unigene32562_All//4.00E-62//TC172267				nr -
Unigene32564_All	424	0.00	4.90	4.52	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.95E-12	Up	1.21E+01	1.47E-10	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene32565_All	445	2.47	0.91	0.84	0.56	2.63	2.84	0.00	0.00	0.36	-1.44E+00	3.36E-02		-1.56E+00	3.05E-02		2.23E+00	1.51E-03		2.34E+00	7.45E-04	Up	null	null		8.48E+00	1.40E-01		Unigene32565_All//gi|301154108|emb|CBR30202.1|//1.00E-00//Protein kinase APK1B [Musa balbisiana]	Unigene32565_All//2.00E-48//AT2G07180| protein kinase, putative	Unigene32565_All//5.00E-121//gi|73863623|gb|DT466362.1|DT466362		ko04626|Plant-pathogen interaction		nr -
Unigene32566_All	514	0.00	0.00	0.10	0.00	0.00	0.09	0.49	0.98	24.57	null	null		6.69E+00	6.36E-01		null	null		6.46E+00	6.96E-01		9.84E-01	3.11E-01		5.64E+00	2.24E-80	Up		Unigene32566_All//8.00E-68//TC146917				
Unigene32570_All	1056	0.00	0.00	0.00	0.00	0.03	0.04	0.88	2.85	5.85	null	null		null	null		5.03E+00	8.30E-01		5.42E+00	6.96E-01		1.69E+00	1.08E-06	Up	2.73E+00	2.16E-23	Up							
Unigene32571_All	544	0.00	48.53	15.37	0.00	0.00	0.00	0.00	0.00	0.00	1.56E+01	4.13E-152	Up	1.39E+01	8.19E-47	Up	null	null		null	null		null	null		null	null		Unigene32571_All//gi|301099993|ref|XP_002899087.1|//7.00E-58//40S ribosomal protein S16 [Phytophthora infestans T30-4] >gi|262104399|gb|EEY62451.1| 40S ribosomal protein S16 [Phytophthora infestans T30-4]	Unigene32571_All//9.00E-49//AT5G18380| 40S ribosomal protein S16 (RPS16C)			ko03010|Ribosome		nr -
Unigene32572_All	476	0.00	8.41	6.26	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	8.55E-23	Up	1.26E+01	1.77E-16	Up	null	null		null	null		null	null		null	null		Unigene32572_All//sp|P20439|CCNB_DROME//7.00E-16//G2/mitotic-specific cyclin-B OS=Drosophila melanogaster GN=CycB PE=1 SV=2						swissprot +
Unigene32573_All	1068	1.22	1.99	0.70	3.96	3.87	1.95	2.18	1.13	1.57	7.02E-01	1.13E-01		-8.11E-01	1.90E-01		-3.52E-02	9.10E-01		-1.03E+00	4.41E-04	Down	-9.40E-01	1.20E-02		-4.75E-01	1.96E-01		Unigene32573_All//gi|224133542|ref|XP_002321600.1|//1.00E-104//f-box family protein [Populus trichocarpa] >gi|222868596|gb|EEF05727.1| f-box family protein [Populus trichocarpa]	Unigene32573_All//7.00E-49//AT5G62940| Dof-type zinc finger domain-containing protein	Unigene32573_All//1.00E-22//TC170824	C2C2-Dof			nr +
Unigene32575_All	294	0.00	3.45	1.81	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.26E-06	Up	1.08E+01	4.04E-03		null	null		null	null		null	null		null	null		Unigene32575_All//sp|Q14094|CCNI_HUMAN//4.00E-50//Cyclin-I OS=Homo sapiens GN=CCNI PE=1 SV=1						swissprot -
Unigene32577_All	790	0.00	0.38	0.00	0.69	0.78	0.34	3.26	1.75	0.25	8.59E+00	4.43E-02		null	null		1.78E-01	8.64E-01		-1.02E+00	3.29E-01		-9.03E-01	1.03E-02		-3.69E+00	1.70E-13	Down		Unigene32577_All//7.00E-23//FL576934				

Unigene32578_A11	484	0.00	1.88	1.87	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	2.62E-05	Up	1.09E+01	4.71E-05	Up	null	null		null	null		null	null		null	null	Unigene32578_A11//gi|59976204|sp|Q9SM50.1|HY5_SOLLC//4.00E-06//RecName: Full=Transcription factor HY5; AltName: Full=LeHY5; AltName: Full=tHY5 >gi|6018699|emb|CAB57979.1| THY5 protein [Solanum lycopersicum]	Unigene32578_A11//2.00E-65//AT5G11260| HY5 (ELONGATED HYPOCOTYL 5); DNA binding / double-stranded DNA binding / transcription factor		bZIP			nr +
Unigene32579_A11	525	0.00	0.00	0.00	0.00	0.00	0.00	3.95	2.95	0.00	null	null		null	null		null	null		null	null		-4.22E-01	3.18E-01		-1.19E+01	2.86E-15	Down	Unigene32579_A11//gi|15236171|ref|NP_195193.1|//1.00E-65//40S ribosomal protein S3A (RPS3aB) [Arabidopsis thaliana] >gi|19884297|sp|Q42262.3|RS3A2_ARATH RecName: Full=40S ribosomal protein S3a-2 >gi|2661422|emb|CAA04689.1| Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi|3096936|emb|CAA18846.1| Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi|7270417|emb|CAB80184.1| Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi|17064848|gb|AAL32578.1| Putative S-phase-specific ribosomal protein [Arabidopsis thaliana]	Unigene32579_A11//9.00E-67//AT4G34670| 40S ribosomal protein S3A (RPS3aB)			ko03010|Ribosome		nr -
Unigene32583_A11	222	9.43	25.56	15.59	13.24	12.72	17.70	51.61	104.49	74.11	1.44E+00	6.40E-08	Up	7.26E-01	3.66E-02		-5.78E-02	8.76E-01		4.19E-01	2.04E-01		1.02E+00	1.14E-21	Up	5.22E-01	1.23E-05				Unigene32583_A11//3.00E-90//TC153285				
Unigene32585_A11	304	0.00	7.67	6.48	0.00	0.00	0.00	0.14	0.00	0.00	1.29E+01	2.91E-13	Up	1.27E+01	7.46E-11	Up	null	null		null	null		-7.12E+00	6.57E-01		-7.12E+00	6.12E-01		Unigene32585_A11//gi|300261322|gb|EFJ45536.1|//2.00E-26//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene32585_A11//7.00E-26//AT2G37600| 60S ribosomal protein L36 (RPL36A)			ko03010|Ribosome		nr -
Unigene32586_A11	309	0.00	13.61	5.51	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	5.92E-24	Up	1.24E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene32586_A11//gi|301112246|ref|XP_002905202.1|//5.00E-18//60S ribosomal protein L7 [Phytophthora infestans T30-4] >gi|262095532|gb|EEY53584.1| 60S ribosomal protein L7 [Phytophthora infestans T30-4]	Unigene32586_A11//1.00E-12//AT3G13580| 60S ribosomal protein L7 (RPL7D)			ko03010|Ribosome		nr -
Unigene32587_A11	415	0.00	9.77	3.34	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	4.39E-23	Up	1.17E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene32587_A11//gi|149071971|ref|XP_001293478.1|//6.00E-24//ribosomal protein L12 [Rhodomonas salina] >gi|134302922|gb|ABO70726.1| ribosomal protein L12 [Rhodomonas salina]	Unigene32587_A11//9.00E-12//AT4G36420| ribosomal protein L12 family protein			ko03010|Ribosome		nr -
Unigene3259_A11	1123	1.35	2.71	0.81	2.44	6.68	2.05	3.43	1.45	3.19	1.00E+00	5.51E-03		-7.45E-01	1.88E-01		1.45E+00	9.79E-12	Up	-2.50E-01	5.63E-01		-1.24E+00	1.49E-05	Down	-1.02E-01	7.18E-01		Unigene3259_A11//gi|257831433|gb|ACV71017.1|//2.00E-53//UPA17 [Capsicum annuum]	Unigene3259_A11//4.00E-39//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene3259_A11//0.00E+00//gi|78342358|gb|DT562632.1|DT562632	GRF		GO:0005488	nr -
Unigene32592_A11	374	0.42	0.00	0.00	1.60	0.37	0.85	4.41	0.00	0.64	-8.71E+00	2.15E-01		-8.71E+00	2.44E-01		-2.12E+00	3.06E-02		-9.19E-01	3.51E-01		-1.21E+01	1.09E-11	Down	-2.79E+00	5.06E-07	Down			Unigene32592_A11//4.00E-149//gi|84174866|gb|DR463514.1|DR463514				
Unigene32594_A11	460	0.00	0.11	0.00	2.60	2.02	0.79	2.30	0.45	0.87	6.78E+00	6.16E-01		null	null		-3.63E-01	5.70E-01		-1.73E+00	8.52E-03		-2.34E+00	6.78E-04	Down	-1.41E+00	1.72E-02									
Unigene32596_A11	306	16.41	0.00	4.18	0.00	0.00	0.00	0.00	0.00	0.00	-1.40E+01	4.63E-29	Down	-1.97E+00	3.47E-10	Down	null	null		null	null		null	null		null	null				Unigene32596_A11//5.00E-139//TC147272				
Unigene3597_A11	414	0.00	5.75	1.54	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.50E-13	Up	1.06E+01	1.16E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene32598_A11	289	0.00	13.15	5.90	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.23E-21	Up	1.25E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene32598_A11//sp|Q9V496|APLP_DROME//3.00E-06//Apolipoprotein OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2								swissprot +
Unigene326_A11	1153	1.45	3.43	0.09	1.60	2.06	3.06	1.69	2.43	2.52	1.24E+00	9.39E-05	Up	-3.97E+00	4.71E-07	Down	3.66E-01	4.23E-01		9.35E-01	4.49E-03		5.26E-01	1.27E-01		5.81E-01	6.80E-02		Unigene326_A11//gi|108710016|gb|ABF97811.1|//9.00E-98//DIRP family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene326_A11//1.00E-82//AT3G21430| DNA binding	Unigene326_A11//1.00E-22//ES833305				nr +
Unigene3260_A11	1492	7.89	5.50	5.46	5.31	4.64	5.69	3.17	1.43	1.23	-5.20E-01	1.62E-03		-5.31E-01	2.01E-03		-1.95E-01	4.03E-01		1.00E-01	6.80E-01		-1.15E+00	5.16E-06	Down	-1.37E+00	6.59E-08	Down	Unigene3260_A11//gi|115456073|ref|NP_001051637.1|//1.00E-115//0s03g0806700 [Oryza sativa Japonica Group] >gi|108711652|gb|ABF99447.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550108|dbj|BAF13851.1| Os03g0806700 [Oryza sativa Japonica Group]	Unigene3260_A11//6.00E-92//AT3G04860| unknown protein	Unigene3260_A11//0.00E+00//TC162910				nr +
Unigene32601_A11	1017	0.00	0.00	0.00	0.00	0.00	0.00	1.54	3.12	0.00	null	null		null	null		null	null		null	null		1.02E+00	1.11E-03		-1.06E+01	1.42E-11	Down	Unigene32601_A11//gi|160330969|ref|XP_001712192.1|//1.00E-132//ef2 [Hemiselmis andersenii] >gi|159765639|gb|ABW97867.1| ef2 [Hemiselmis andersenii]	Unigene32601_A11//5.00E-115//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding					nr +
Unigene32605_A11	327	0.00	0.00	0.16	0.00	0.00	0.00	5.17	3.58	1.34	null	null		7.35E+00	6.36E-01		null	null		null	null		-5.31E-01	2.50E-01		-1.95E+00	5.40E-05	Down	Unigene32605_A11//gi|224085806|ref|XP_002307703.1|//7.00E-26//cytochrome P450 [Populus trichocarpa] >gi|222857152|gb|EEE94699.1| cytochrome P450 [Populus trichocarpa]	Unigene32605_A11//4.00E-17//AT2G02580| CYP71B9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene32605_A11//7.00E-52//ES805212		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr +
Unigene32611_A11	298	0.00	0.00	0.00	8.36	3.47	0.76	0.00	0.00	0.00	null	null		null	null		-1.27E+00	8.49E-04	Down	-3.46E+00	1.55E-10	Down	null	null		null	null		Unigene32611_A11//gi|225454540|ref|XP_002278384.1|//4.00E-11//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene32611_A11//2.00E-126//gi|109871180|gb|DW500156.1|DW500156				nr +
Unigene32612_A11	446	129.16	87.71	134.80	88.24	104.31	638.16	132.05	220.97	374.27	-5.58E-01	1.03E-15		6.16E-02	4.51E-01		2.41E-01	1.38E-03		2.85E+00	0.00E+00	Up	7.43E-01	9.23E-53		1.50E+00	9.18E-284	Up	Unigene32612_A11//gi|300793588|tpg|DAA33860.1|//3.00E-79//TPA: TPA_inf: aquaporin PIP1;6 [Gossypium hirsutum]	Unigene32612_A11//4.00E-73//AT4G00430| PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel	Unigene32612_A11//0.00E+00//TC138431				nr -
Unigene32613_A11	494	0.00	9.85	2.26	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	1.00E-27	Up	1.11E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene32613_A11//gi|300122978|emb|CBK23985.2|//1.00E-09//unnamed protein product [Blastocystis hominis]						nr -
Unigene3262_A11	766	5.46	4.70	2.02	9.82	7.51	8.55	6.02	4.09	4.32	-2.19E-01	4.87E-01		-1.44E+00	9.41E-06	Down	-3.87E-01	6.72E-02		-2.00E-01	4.08E-01		-5.56E-01	2.77E-02		-4.79E-01	5.03E-02				Unigene3262_A11//1.00E-110//TC165454				
Unigene32625_A11	409	0.00	2.97	2.99	0.00	0.34	0.00	0.21	0.00	0.00	1.15E+01	5.47E-07	Up	1.15E+01	9.12E-07	Up	8.40E+00	3.18E-01		null	null		-7.69E+00	4.03E-01		-7.69E+00	3.58E-01		Unigene32625_A11//gi|288311314|gb|ADC45396.1|//2.00E-51//HSP90-2 [Glycine max]	Unigene32625_A11//2.00E-38//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene32625_A11//8.00E-09//TC151700		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene32627_A11	272	149.08	356.55	236.10	94.50	297.38	284.43	67.62	125.69	77.63	1.26E+00	8.89E-101	Up	6.63E-01	1.44E-22		1.65E+00	2.22E-149	Up	1.59E+00	6.55E-123	Up	8.95E-01	1.32E-25		1.99E-01	7.02E-02		Unigene32627_A11//gi|115435036|ref|NP_001042276.1|//8.00E-30//0s01g0192000 [Oryza sativa Japonica Group] >gi|75262988|sp|Q9FU27.1|C3H2_ORYSJ RecName: Full=Zinc finger CCCH domain-containing protein 2; Short=OsC3H2; AltName: Full=Protein DELAY OF THE ONSET OF SENESCENCE; Short=OsDOS >gi|9988428|dbj|BAB12694.1| CCCH-type zinc finger protein -like [Oryza sativa Japonica Group] >gi|113531807|dbj|BAF04190.1| Os01g0192000 [Oryza sativa Japonica Group]	Unigene32627_A11//2.00E-27//AT2G19810| zinc finger (CCCH-type) family protein	Unigene32627_A11//7.00E-150//gi|18099902|gb|BM359156.1|BM359156	C3H			nr +
Unigene32629_A11	437	0.00	0.00	0.00	0.23	0.00	0.00	1.94	4.30	49.68	null	null		null	null		-7.83E+00	3.13E-01		-7.83E+00	3.99E-01		1.15E+00	7.17E-03		4.68E+00	5.68E-126	Up								
Unigene3263_A11	727	16.34	10.66	6.96	14.59	13.12	21.12	6.57	5.92	4.88	-6.15E-01	1.74E-04		-1.23E+00	4.69E-12	Down	-1.54E-01	4.52E-01		5.33E-01	1.36E-01		-1.50E-01	6.13E-01		-4.30E-01	7.45E-02	Up			Unigene3263_A11//8.00E-180//TC165454				
Unigene32630_A11	252	2.49	7.24	3.59	0.99	2.87	2.51	11.74	13.60	35.25	1.54E+00	2.55E-03		5.28E-01	4.79E-01		1.54E+00	8.92E-02		1.34E+00	1.74E-01		2.12E-01	5.31E-01		1.59E+00	4.10E-17	Up			Unigene32630_A11//3.00E-84//TC130571				
Unigene32631_A11	468	0.00	1.41	0.68	1.49	0.22	1.06	0.72	0.71	1.36	1.05E+01	6.25E-04	Up	9.42E+00	4.52E-02		-2.76E+00	3.99E-03		-4.89E-01	5.98E-01		-1.65E-02	1.02E+00		9.14E-01	2.47E-01									ESTscan +
Unigene32635_A11	282	0.00	5.03	3.97	0.00	0.00	0.00	0.15	0.00	0.00	1.23E+01	4.06E-08	Up	1.20E+01	3.43E-06	Up	null	null		null	null		-7.23E+00	6.57E-01		-7.23E+00	6.12E-01		Unigene32635_A11//gi|297820930|ref|XP_002878348.1|//2.00E-35//40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata] >gi|297324186|gb|EFH54607.1| 40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata]	Unigene32635_A11//9.00E-37//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene32635_A11//3.00E-07//TC158660		ko03010|Ribosome		nr +
Unigene32636_A11	388	0.00	2.35	3.43	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.62E-05	Up	1.17E+01	2.40E-07	Up	null	null		null	null		null	null		null	null		Unigene32636_A11//sp|A5A6L1|CVR61_PANTR//1.00E-74//Protein CVR61 OS=Pan troglodytes GN=CVR61 PE=2 SV=1								swissprot +
Unigene32637_A11	261	0.00	0.78	0.41	4.39	0.53	1.21	0.00	0.00	0.00	9.60E+00	1.36E-01		8.67E+00	3.98E-01		-3.06E+00	3.10E-05	Down	-1.86E+00	6.47E-03		null	null		null	null				Unigene32637_A11//3.00E-16//DR176738				
Unigene32638_A11	450	0.00	0.00	0.00	0.00	0.00	0.00	6.58	3.34	0.89	null	null		null	null		null	null		null	null		-9.76E-01	2.70E-03		-2.89E+00	1.81E-12	Down	Unigene32638_A11//gi|90399361|emb|CAJ86180.1|//2.00E-29//H0212B02.7 [Oryza sativa (indica cultivar-group)]	Unigene32638_A11//1.00E-26//AT4G35350| XCP1 (XYLEM CYSTEINE PEPTIDASE 1); cysteine-type endopeptidase/ cysteine-type peptidase					nr -
Unigene3264_A11	2348	9.05	24.60	13.56	15.78	23.54	24.33	18.13	33.64	24.81	1.44E+00	3.08E-74	Up	5.84E-01	2.65E-09		5.77E-01	1.40E-18		6.24E-01	4.53E-20		8.92E-01	8.49E-58		4.52E-01	8.75E-14		Unigene3264_A11//gi|30696120|ref|NP_176041.2|//1.00E-124//PAPA-1-like family protein / zinc finger (HIT type) family protein [Arabidopsis thaliana]	Unigene3264_A11//1.00E-74//AT1G56460| PAPA-1-like family protein / zinc finger (HIT type) family protein	Unigene3264_A11//0.00E+00//gi|164252421|gb|ES809784.1|ES809784				nr +
Unigene32640_A11	415	0.88	5.01	2.44	0.24	0.58	0.87	0.00	0.91	0.19	2.50E+00	3.59E-06	Up	1.47E+00	4.95E-02		1.27E+00	5.32E-01		1.86E+00	2.19E-01		9.82E+00	6.85E-03		7.59E+00	4.04E-01				Unigene32640_A11//3.00E-141//C0087301				
Unigene32643_A11	284	0.00	0.00	0.00	4.56	1.82	0.48	0.00	0.00	0.00	null	null		null	null		-1.33E+00	1.98E-02		-3.26E+00	1.98E-05	Down	null	null		null	null									
Unigene32644_A11	550	0.48	0.00	0.19	3.26	2.07	0.57	0.92	0.23	0.58	-8.89E+00	6.70E-02		-1.30E+00	4.36E-01		-6.58E-01	1.66E-01		-2.50E+00	9.48E-06	Down	-2.02E+00	5.20E-02		-6.71E-01	4.48E-01									
Unigene32649_A11	507	0.62	33.98	4.83	0.39	1.90	2.94	0.42	0.66	0.00	5.78E+00	1.49E-88	Up	2.96E+00	4.43E-08	Up	2.27E+00	4.58E-03		2.90E+00	2.02E-05	Up	6.61E-01	6.09E-01		-8.70E+00	5.80E-02		Unigene32649_A11//gi|56512451|gb|AAV82890.1|//4.00E-31//Avr9/Cf-9 rapidly elicited protein 20 [Nicotiana tabacum]	Unigene32649_A11//7.00E-31//AT4G27280| calcium-binding EF hand family protein	Unigene32649_A11//5.00E-26//DW519149		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene3265_A11	2261	19.35	7.89	12.62	12.27	10.87	9.49	11.58	5.82	5.29	-1.29E+00	4.62E-48	Down	-6.16E-01	1.07E-13		-1.74E-01	1.10E-01		-3.71E-01	2.45E-04		-9.91E-01	2.24E-23		-1.13E+00	1.18E-29	Down	Unigene3265_A11//gi|11078533|gb|AAG29095.1|AF224745_1//0.00E+00//Glu-tRNA(Gln) amidotransferase subunit A [Arabidopsis thaliana]	Unigene3265_A11//0.00E+00//AT3G25660| glutamyl-tRNA(Gln) amidotransferase, putative	Unigene3265_A11//0.00E+00//TC139128		ko00970|Aminoacyl-tRNA biosynthesis	GO:0009532//GO:0010467//GO:0016811//GO:0016884	nr +
Unigene32650_A11	960	0.00	0.00	0.00	0.00	0.00	0.00	1.15	11.97	1.54	null	null		null	null		null	null		null	null		3.39E+00	6.51E-52	Up	4.23E-01	3.83E-01		Unigene32650_A11//gi|42570080|ref|NP_683294.2|//3.00E-73//phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis thaliana]	Unigene32650_A11//1.00E-74//AT1G09935| phosphoglycerate/bisphosphoglycerate mutase family protein					nr +
Unigene32651_A11	384	28.75	12.27	16.22	21.53	13.54	17.64	19.49	13.50	7.57	-1.23E+00	9.54E-12	Down	-8.25E-01	3.66E-06		-6.69E-01	3.41E-04		-2.88E-01	1.91E-01		-5.30E-01	5.43E-03		-1.36E+00	6.40E-12	Down			Unigene32651_A11//2.00E-37//TC152336				

Unigene32653_All	249	43.08	42.73	98.80	1257.76	427.88	1864.58	873.28	1524.79	620.14	-1.15E-02	9.71E-01		1.20E+00	2.17E-23	Up	-1.56E+00	0.00E+00	Down	5.68E-01	9.42E-135		8.04E-01	1.04E-230		-4.94E-01	1.28E-57		Unigene32653_All//gi|119711|sp|P06599.1|EXTN_DAUCA//3.00E-22//RecName: Full=Extensin; Flags: Precursor >gi|224686|prf||1111211A extensin		Unigene32653_All//5.00E-46//FF403806		ko03040|Spliceosome		nr +
Unigene32654_All	710	0.00	2.78	3.08	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.97E-11	Up	1.16E+01	4.95E-12	Up	null	null		null	null		null	null		null	null		Unigene32654_All//gi|197320662|gb|ACH68459.1|//1.00E-23//calcium-dependent protein 1 [Phytophthora sojae]	Unigene32654_All//7.00E-22//AT1G09640| elongation factor 1B-gamma, putative / eEF-1B gamma, putative				nr +
Unigene32655_All	406	0.00	0.00	0.00	0.00	0.00	0.00	2.60	2.47	0.00	null	null		null	null		null	null		null	null		-7.55E-02	9.09E-01		-1.13E+01	6.72E-08	Down	Unigene32655_All//gi|247421835|gb|ACS96445.1|//4.00E-60//S18.A ribosomal protein [Jatropha curcas]	Unigene32655_All//6.00E-52//AT4G28800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome	Unigene32655_All//5.00E-10//EV488285		ko03010|Ribosome		nr -
Unigene32656_All	316	0.00	5.61	2.36	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	4.14E-10	Up	1.12E+01	3.27E-04	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene32669_All	989	0.05	0.77	0.70	0.40	0.45	0.55	0.73	0.59	2.58	3.86E+00	1.33E-03		3.73E+00	3.99E-03		1.68E-01	9.04E-01		4.44E-01	6.78E-01		-2.97E-01	6.85E-01		1.83E+00	1.63E-06	Up	Unigene32669_All//gi|42563023|ref|NP_176917.2|//9.00E-24//ATREV3 (ARABIDOPSIS THALIANA RECOVERY PROTEIN 3); DNA binding / DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|343301129|dbj|BAC82450.1| catalytic subunit of polymerase zeta [Arabidopsis thaliana]	Unigene32669_All//5.00E-25//AT1G67500| ATREV3 (ARABIDOPSIS THALIANA RECOVERY PROTEIN 3); DNA binding / DNA-directed DNA polymerase				nr -
Unigene3267_All	1114	68.24	33.48	58.75	78.66	107.23	98.27	99.17	99.87	114.55	-1.03E+00	1.34E-57	Down	-2.16E-01	6.11E-04		4.47E-01	3.33E-25		3.21E-01	1.35E-11		1.02E-02	8.59E-01		2.08E-01	2.06E-07		Unigene3267_All//gi|226503369|ref|NP_001150346.1|//2.00E-67//xyloglucan endotransglucosylase/hydrolase protein 5 [Zea mays] >gi|195638572|gb|ACG38754.1| xyloglucan endotransglucosylase/hydrolase protein 5 precursor [Zea mays]	Unigene3267_All//7.00E-22//AT2G18800| XTH21 (XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 21); hydrolase, acting on glycosyl bonds / xyloglucan endotransglucosylase	Unigene3267_All//0.00E+00//TC137369		GO:0016787//GO:0044238	nr -
Unigene32671_All	457	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.18	4.88	null	null		null	null		null	null		null	null		-3.48E+00	7.79E-05	Down	1.26E+00	9.46E-04	Up	Unigene32671_All//gi|124360291|gb|ABN08304.1|//1.00E-32//Integral membrane protein DUF6 containing protein [Medicago truncatula]	Unigene32671_All//1.00E-26//AT1G68170| nodulin MtN21 family protein	Unigene32671_All//8.00E-77//ES817270				nr -
Unigene32675_All	296	7.95	12.33	5.94	13.63	14.89	5.19	2.71	1.13	2.29	6.32E-01	4.97E-02		-4.22E-01	3.51E-01		1.28E-01	7.25E-01		-1.39E+00	6.47E-06	Down	-1.26E+00	7.98E-02		-2.46E-01	7.00E-01					Unigene32675_All//9.00E-51//DW513049				
Unigene32677_All	403	0.78	0.00	0.00	0.00	0.26	0.22	0.00	0.21	2.17	-9.61E+00	3.65E-02		-9.61E+00	4.91E-02		8.00E+00	4.56E-01		7.81E+00	4.76E-01		7.70E+00	4.01E-01		1.11E+01	2.05E-06	Up	Unigene32677_All//gi|224106101|ref||XP_002314043.1|//1.00E-43//cation proton exchanger [Populus trichocarpa] >gi|222850451|gb|EEE87998.1| cation proton exchanger [Populus trichocarpa]	Unigene32677_All//4.00E-39//AT3G52080| chx28 (cation/hydrogen exchanger 28); monovalent cation:proton antiporter	Unigene32677_All//8.00E-09//ES842939				nr -
Unigene32678_All	283	0.55	2.15	3.95	0.35	0.00	0.00	0.00	0.00	0.00	1.95E+00	6.04E-02		2.83E+00	7.34E-04	Up	-8.46E+00	3.13E-01		-8.46E+00	3.99E-01		null	null		null	null								ESTscan +
Unigene3268_All	1728	0.85	2.93	0.99	11.39	13.31	7.03	9.52	11.25	5.60	1.79E+00	1.71E-09	Up	2.18E-01	6.56E-01		2.25E-01	5.68E-02		-6.96E-01	8.48E-09		2.41E-01	4.01E-02		-7.65E-01	2.81E-10		Unigene3268_All//gi|70609692|gb|AAZ05071.1|//0.00E+00//cytochrome P450 [Citrus sinensis]	Unigene3268_All//0.00E+00//AT5G05690| CYP (CONSTITUTIVE PHOTOMORPHOGENIC DWARF); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene3268_All//0.00E+00//gi|78333762|gb|DT554036.1|DT554036		ko00905|Brassinosteroid biosynthesis	GO:0000902//GO:0005506//GO:0009411//GO:0009908//GO:0010208//GO:0016129//GO:0016491//GO:0048878	nr -
Unigene32683_All	285	1.29	0.71	0.19	1.57	2.42	0.63	0.15	0.15	4.33	-8.54E-01	4.89E-01		-2.78E+00	1.03E-01		6.19E-01	5.30E-01		-1.31E+00	2.73E-01		-1.66E-02	1.00E+00		4.87E+00	9.59E-08	Up							
Unigene32689_All	211	22.56	9.61	28.01	8.03	5.39	6.85	9.22	2.58	4.15	-1.23E+00	1.51E-05	Down	3.12E-01	2.41E-01		-5.76E-01	2.53E-01		-2.29E-01	6.78E-01		-1.84E+00	4.63E-05	Down	-1.15E+00	4.53E-03					Unigene32689_All//3.00E-96//TC133253				
Unigene3269_All	1309	22.54	25.74	24.61	30.25	31.78	67.38	103.81	39.40	120.37	1.91E-01	5.00E-02		1.27E-01	2.47E-01		7.09E-02	5.06E-01		1.16E+00	2.91E-86	Up	-1.40E+00	1.57E-203	Down	2.14E-01	2.32E-09		Unigene3269_All//gi|118132686|gb|ABK60194.1|//1.00E-155//PIP1 protein [Gossypium hirsutum]	Unigene3269_All//1.00E-133//AT4G00430| PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel	Unigene3269_All//0.00E+00//gi|164258237|gb|ES795321.1|ES795321				nr +
Unigene32693_All	438	0.96	0.12	0.00	3.18	0.24	0.00	1.35	0.00	0.73	-3.05E+00	4.65E-02		-9.90E+00	1.56E-02		-3.75E+00	1.91E-07	Down	-1.16E+01	1.01E-08	Down	-1.04E+01	2.39E-04	Down	-8.93E-01	2.71E-01		Unigene32693_All//gi|115464887|ref||NP_001056043.1|//9.00E-08//Os05g0516100 [Oryza sativa Japonica Group] >gi|113579594|dbj|BAF17957.1| Os05g0516100 [Oryza sativa Japonica Group]		Unigene32693_All//2.00E-68//ES837555				nr +
Unigene327_All	1243	0.34	1.39	0.30	1.56	2.02	2.47	1.63	2.42	2.92	2.04E+00	2.81E-04	Up	-1.67E-01	8.79E-01		3.72E-01	3.99E-01		6.61E-01	7.00E-02		5.68E-01	8.08E-02		8.37E-01	2.79E-03		Unigene327_All//gi|108710016|gb|AB197811.1|//1.00E-68//DUF DNA family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene327_All//5.00E-60//AT3G21430| DNA binding				nr +
Unigene32700_All	336	2.34	0.15	0.32	3.71	0.00	0.00	0.88	0.00	0.47	-3.95E+00	8.54E-04	Down	-2.88E+00	6.35E-03		-1.19E+01	3.15E-09	Down	-1.19E+01	8.64E-08	Down	-9.78E+00	2.18E-02		-8.93E-01	4.71E-01								
Unigene32703_All	325	0.00	8.26	5.41	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	2.80E-15	Up	1.24E+01	1.12E-09	Up	null	null		null	null		null	null		null	null									
Unigene32704_All	270	0.00	0.00	0.00	1.48	0.13	0.50	3.45	0.93	0.00	null	null		null	null		-3.53E+00	2.09E-02		-1.56E+00	2.31E-01		-1.89E+00	6.92E-03		-1.18E+01	5.47E-07	Down				Unigene32704_All//2.00E-08//TC133431				
Unigene32706_All	392	2.94	0.00	3.67	3.05	2.46	1.15	0.22	0.00	0.20	-1.15E+01	9.91E-07	Down	3.21E-01	5.92E-01		-3.10E-01	6.07E-01		-1.40E+00	2.82E-02		-7.75E+00	4.03E-01		-8.54E-02	9.72E-01		Unigene32706_All//gi|224096788|ref||XP_002334669.1|//2.00E-16//nbs-lrr resistance protein [Populus trichocarpa] >gi|222874080|gb|EEF11211.1| nbs-lrr resistance protein [Populus trichocarpa]		Unigene32706_All//2.00E-49//ES837684				nr +
Unigene32709_All	412	0.00	6.52	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.80E-15	Up	1.07E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene32709_All//gi|22330139|ref|NP_175390.2|//7.00E-07//NQR; binding / catalytic/ oxidoreductase/ zinc ion binding [Arabidopsis thaliana] >gi|10120437|gb|AAG13062.1|AC011807_21 ARP protein [Arabidopsis thaliana] >gi|17065304|gb|AAL32806.1| ARP protein [Arabidopsis thaliana] >gi|18252161|gb|AAL61913.1| ARP protein [Arabidopsis thaliana] >gi|20259988|gb|AAM13341.1| ARP protein [Arabidopsis thaliana] >gi|30725460|gb|AAP37752.1| Atlg49670 [Arabidopsis thaliana]	Unigene32709_All//4.00E-08//AT1G49670| NQR; binding / catalytic/ oxidoreductase/ zinc ion binding		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis		nr -
Unigene3271_All	2034	5.66	3.84	3.72	12.86	13.58	10.86	10.27	3.80	4.72	-5.61E-01	7.78E-04		-6.06E-01	4.73E-04		7.86E-02	5.39E-01		-2.44E-01	2.76E-02		-1.43E+00	3.98E-33	Down	-1.12E+00	1.54E-23	Down	Unigene3271_All//gi|15231273|ref|NP_187965.1|//0.00E+00//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|42572413|ref|NP_974302.1| glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|42572415|ref|NP_974303.1| glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|38257734|sp|Q94CH8.1|E134_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 4; AltName: Full=(1->3)-beta-glucan endohydrolase 4; Short=(1->3)-beta-glucanase 4; AltName: Full=Beta-1,3-endoglucanase 4; Short=Beta-1,3-glucanase 4; Flags: Precursor >gi|222423996|dbj|BAH19959.1| AT3G13560 [Arabidopsis thaliana]	Unigene3271_All//0.00E+00//AT3G13560| glycosyl hydrolase family 17 protein	Unigene3271_All//0.00E+00//DW490948		ko00500|Starch and sucrose metabolism	GO:0016798//GO:0031225//GO:0043167//GO:0044238	nr +
Unigene32710_All	354	0.00	13.74	7.22	0.00	0.00	0.00	0.24	0.00	0.23	1.37E+01	1.00E-27	Up	1.28E+01	4.20E-14	Up	null	null		null	null		-7.90E+00	4.03E-01		-8.58E-02	9.72E-01		Unigene32710_All//gi|298709870|emb||CBJ26210.1|//4.00E-33//Ribosomal protein S27 [Ectocarpus siliculosus]	Unigene32710_All//1.00E-27//AT5G47930| 40S ribosomal protein S27 (RPS27D)			ko03010|Ribosome		nr -
Unigene32712_All	453	0.00	5.26	3.76	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.50E-13	Up	1.19E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene32712_All//gi|82623403|gb|AB88711 6.1|//3.00E-43//40S ribosomal protein S19-like [Solanum tuberosum]	Unigene32712_All//2.00E-43//AT5G41170| 40S ribosomal protein S19 (RPS19C)			ko03010|Ribosome		nr -
Unigene32713_All	715	0.00	0.00	0.00	0.00	0.00	0.00	1.48	2.69	0.00	null	null		null	null		null	null		null	null		8.63E-01	3.97E-02		-1.05E+01	6.72E-08	Down	Unigene32713_All//gi|300257738|gb|EFJ41983.1|//9.00E-24//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene32713_All//4.00E-14//AT5G27770| 60S ribosomal protein L22 (RPL22C)			ko03010|Ribosome		nr -
Unigene32714_All	414	0.00	0.00	0.00	1.32	0.17	0.00	0.61	19.59	0.29	null	null		null	null		-2.99E+00	9.38E-03		-1.04E+01	1.52E-03		5.00E+00	3.47E-48	Up	-1.09E+00	4.28E-01					Unigene32714_All//0.00E+00//gi|13244098|gb|BE053719.2|BE053719				
Unigene3272_All	1164	41.53	15.50	22.78	26.02	21.21	20.02	9.19	5.42	3.05	-1.42E+00	3.29E-61	Down	-8.66E-01	7.44E-27		-2.95E-01	1.70E-03		-3.78E-01	8.31E-05		-7.61E-01	1.04E-06		-1.59E+00	8.74E-21	Down	Unigene3272_All//gi|225431203|ref|XP_002271764.1|//1.00E-102//PREDICTED: similar to heat shock protein binding [Vitis vinifera]	Unigene3272_All//1.00E-88//AT3G51140| INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast inner membrane, chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: CDF1 (CELL GROWTH DEFECT FACTOR 1) (TAIR:AT5G23040.1); Has 133 Blast hits to 133 proteins in 42 species: Archae - 0; Bacteria - 60; Metazoa - 0; Fungi - 0; Plants - 57; Viruses - 0; Other Eukaryotes - 16 (source: NCBI BLink).	Unigene3272_All//0.00E+00//TC147889			GO:0005515//GO:0009528	nr -
Unigene32722_All	378	0.69	0.00	0.00	0.66	1.64	0.72	2.80	0.55	1.58	-9.43E+00	6.70E-02		-9.43E+00	8.57E-02		1.32E+00	1.88E-01		1.22E-01	9.44E-01		-2.34E+00	6.78E-04	Down	-8.23E-01	1.50E-01					Unigene32722_All//3.00E-76//DT468230				
Unigene32723_All	859	0.30	0.47	0.25	0.87	0.64	0.63	4.33	4.82	1.48	6.32E-01	6.01E-01		-2.96E-01	8.32E-01		-4.40E-01	5.85E-01		-4.63E-01	6.06E-01		1.53E-01	6.38E-01		-1.55E+00	1.74E-07	Down	Unigene32723_All//gi|297726953|ref||XP_001175840.1|//1.00E-08//Os09g0417400 [Oryza sativa Japonica Group] >gi|50253024|dbj|BAD29274.1| bHLH transcription factor PTF1-like protein [Oryza sativa Japonica Group] >gi|255678901|dbj|BAH94568.1| Os09g0417400 [Oryza sativa Japonica Group]	Unigene32723_All//4.00E-05//AT4G30980| basic helix-loop-helix (bHLH) family protein	Unigene32723_All//2.00E-29//TC179230	bHLH			nr +
Unigene32725_All	373	0.00	1.22	1.43	3.34	3.05	4.12	9.86	4.03	9.29	1.03E+01	7.43E-03		1.05E+01	4.04E-03		-1.32E-01	8.17E-01		3.02E-01	6.35E-01		-1.29E+00	1.24E-05	Down	-8.58E-02	7.65E-01					Unigene32725_All//5.00E-50//gi|84146027|gb|DN760269.1|DN760269				ESTscan +
Unigene32726_All	277	0.00	2.74	0.00	1.08	0.37	0.49	1.22	0.75	0.29	1.14E+01	1.77E-04	Up	null	null		-1.53E+00	2.98E-01		-1.14E+00	4.57E-01		-6.95E-01	5.77E-01		-2.09E+00	1.07E-01		Unigene32726_All//gi|224113671|ref||XP_002316539.1|//5.00E-18//nbs-lrr resistance protein [Populus trichocarpa] >gi|222859604|gb|EEE97151.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene32726_All//6.00E-09//AT5G11250| disease resistance protein (TIR-NBS-LRR class), putative				GO:0000166	nr -

Unigene32727_All	543	0.29	1.59	0.00	0.73	0.13	0.75	1.95	0.23	0.81	2.46E+00	6.27E-03		-8.18E+00	2.44E-01		-2.53E+00	5.79E-02		2.86E-02	9.85E-01		-3.08E+00	6.12E-05	Down	-1.27E+00	2.97E-02		Unigene32727_All//gi|115446443|ref|NP_001047001.1|//6.00E-41//AT5G43530| SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein [Oryza sativa Japonica Group] >gi|113536532|dbj|BAF08915.1| Os02g0527100 [Oryza sativa Japonica Group]	Unigene32727_All//5.00E-41//AT5G43530| SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein				GO:0003676//GO:0009526//GO:0032559//GO:0042623//GO:0046914	nr -
Unigene32729_All	326	0.00	6.37	2.12	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	7.94E-12	Up	1.11E+01	6.16E-04	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene3273_All	2518	7.81	3.84	7.32	17.03	16.08	4.86	0.39	0.30	0.19	-1.02E+00	2.34E-15	Down	-9.46E-02	5.26E-01		-8.29E-02	3.99E-01		-1.81E+00	1.93E-83	Down	-3.70E-01	5.87E-01		-1.02E+00	9.02E-02		Unigene3273_All//gi|224589671|gb|AC N39367.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene3273_All//6.00E-163//AT5G14210| leucine-rich repeat transmembrane protein kinase, putative	Unigene3273_All//0.00E+00//C0118945			GO:0004672//GO:0005488//GO:0008152//GO:0043231	nr +
Unigene32734_All	838	0.81	0.24	0.25	0.36	0.25	0.00	0.25	0.20	2.85	-1.75E+00	6.23E-02		-1.68E+00	8.70E-02		-5.33E-01	6.79E-01		-8.48E+00	3.99E-02		-3.39E-01	8.12E-01		3.50E+00	8.44E-12	Up							
Unigene32745_All	264	0.00	8.64	0.00	0.00	0.39	0.00	0.64	0.63	5.43	1.31E+01	5.64E-13	Up	null	null		8.61E+00	4.56E-01		null	null		-1.65E-02	1.02E+00		3.08E+00	1.21E-06	Up			Unigene32745_All//3.00E-07//gi|78337883|gb|DT558157.1|DT558157				
Unigene32748_All	370	0.00	0.00	0.00	0.67	0.37	0.37	1.60	0.79	5.17	null	null		null	null		-8.55E-01	5.73E-01		-8.78E-01	6.16E-01		-1.02E+00	2.40E-01		1.69E+00	1.15E-04	Up			Unigene32748_All//9.00E-107//gi|48742592|gb|C0073111.1|C0073111				
Unigene32749_All	474	0.00	1.92	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	2.62E-05	Up	9.40E+00	4.52E-02		null	null		null	null		null	null		null	null		Unigene32749_All//sp|Q8VHR5|P66B_MOUSE//5.00E-14//Transcriptional repressor p66-beta OS=Mus musculus GN=Gatad2b PE=1 SV=1						swissprot +
Unigene3275_All	1371	4.69	5.77	5.86	4.87	6.86	5.30	9.53	7.93	4.71	2.97E-01	1.69E-01		3.21E-01	1.46E-01		4.94E-01	6.56E-03		1.23E-01	6.23E-01		-2.66E-01	7.10E-02		-1.02E+00	5.56E-13	Down	Unigene3275_All//gi|89001001|gb|AB D59090.1|//1.00E-43//At1g76185 [Arabidopsis thaliana]	Unigene3275_All//7.00E-31//AT1G20460| unknown protein	Unigene3275_All//0.00E+00//TC157649				nr +
Unigene32753_All	325	0.48	0.00	2.29	4.45	1.06	2.08	0.13	1.03	0.12	-8.92E+00	2.15E-01		2.25E+00	2.35E-02		-2.07E+00	2.41E-04	Down	-1.09E+00	5.14E-02		2.98E+00	5.73E-02		-8.57E-02	9.71E-01									
Unigene32755_All	393	0.00	0.90	0.95	0.63	3.33	1.15	0.65	0.53	0.71	9.82E+00	2.46E-02		9.89E+00	2.50E-02		2.39E+00	3.51E-04	Up	8.59E-01	4.69E-01		-2.80E-01	8.28E-01		1.37E-01	9.29E-01		Unigene32755_All//gi|42566780|ref|NP_193159.3|//2.00E-31//CBS domain-containing protein-related [Arabidopsis thaliana] >gi|66792636|gb|AA156420.1| At4g14230 [Arabidopsis thaliana]	Unigene32755_All//5.00E-23//AT4G14230| CBS domain-containing protein-related	Unigene32755_All//5.00E-161//gi|48814367|gb|C0115680.1|C0115680			GO:0043231	nr -
Unigene32756_All	450	0.00	7.09	2.01	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	3.64E-18	Up	1.10E+01	4.71E-05	Up	null	null		null	null		null	null		null	null									
Unigene32757_All	492	0.00	6.49	1.73	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	3.64E-18	Up	1.08E+01	9.03E-05	Up	null	null		null	null		null	null		null	null		Unigene32757_All//sp|Q9VYR4|BGBP2_DROME//2.00E-07//Gram-negative bacteria-binding protein 2 OS=Drosophila melanogaster GN=GNBP2 PE=2 SV=3						swissprot +
Unigene32759_All	274	0.38	0.00	0.58	0.55	0.38	0.49	3.55	4.27	0.73	-8.58E+00	3.72E-01		6.10E-01	7.48E-01		-5.33E-01	7.85E-01		-1.41E-01	9.43E-01		2.67E-01	6.28E-01		-2.29E+00	9.84E-04	Down			Unigene32759_All//3.00E-07//EV499324				
Unigene3276_All	1618	32.14	26.46	37.88	2.00	1.98	1.23	3.89	0.31	1.28	-2.81E-01	1.42E-04		2.37E-01	8.02E-04		-1.59E-02	9.55E-01		-7.04E-01	4.15E-02		-3.65E+00	1.11E-30	Down	-1.60E+00	1.03E-12	Down	Unigene3276_All//gi|224103669|ref|XP_002313147.1|//1.00E-167//UDP-glucoronosyl/UDP-glucosyltransferase [Populus trichocarpa] >gi|222849555|gb|EEE87102.1| UDP-glucoronosyl/UDP-glucosyltransferase [Populus trichocarpa]	Unigene3276_All//4.00E-100//AT2G32360| UGT84B1 (UDP-glucosyl transferase 84B1); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ indole-3-acetate beta-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis	GO:0035251	nr -
Unigene32761_All	249	0.00	86.28	29.73	0.00	0.00	0.00	0.00	0.00	0.00	1.64E+01	1.19E-123	Up	1.49E+01	2.22E-41	Up	null	null		null	null		null	null		null	null					Unigene32761_All//2.00E-14//gi|109847166|gb|DW476146.1|DW476146				
Unigene32763_All	278	0.38	1.09	0.19	0.36	0.25	0.00	29.35	69.01	33.25	1.54E+00	3.23E-01		-9.75E-01	7.21E-01		-5.33E-01	8.16E-01		-8.49E+00	3.99E-01		1.23E+00	2.60E-24	Up	1.80E-01	3.26E-01				Unigene32763_All//2.00E-54//TC131580				
Unigene32764_All	617	0.68	0.16	0.00	0.00	0.11	0.00	3.22	0.27	0.77	-2.05E+00	1.20E-01		-9.41E+00	1.56E-02		6.80E+00	6.09E-01		null	null		-3.57E+00	6.95E-10	Down	-2.06E+00	4.43E-06	Down	Unigene32764_All//gi|8843803|dbj|BAB97351.1|//1.00E-72//protein kinase [Arabidopsis thaliana]	Unigene32764_All//5.00E-70//AT5G40030| protein kinase, putative	Unigene32764_All//2.00E-173//TC171959			GO:0004674//GO:0006464//GO:0009536//GO:0009926//GO:0016323//GO:0031981//GO:0032559	nr +
Unigene32767_All	976	0.00	8.36	2.51	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.14E-46	Up	1.13E+01	1.64E-13	Up	null	null		null	null		null	null		null	null		Unigene32767_All//gi|239819394|gb|ACS28251.1|//1.00E-140//cell division control protein [Nicotiana glutinosa]	Unigene32767_All//1.00E-125//AT3G53230| cell division cycle protein 48, putative / CDC48, putative	Unigene32767_All//9.00E-20//TC169574		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene32768_All	261	22.25	165.99	53.86	148.11	337.89	157.12	376.15	398.26	279.63	2.90E+00	3.14E-136	Up	1.28E+00	5.81E-15	Up	1.19E+00	1.03E-99	Up	8.52E-02	4.04E-01		8.24E-02	1.09E-01		-4.28E-01	1.44E-20				Unigene32768_All//1.00E-49//BG444278				
Unigene3277_All	1154	9.97	14.31	14.12	17.70	20.53	27.24	23.85	30.68	66.04	5.21E-01	1.37E-04		5.01E-01	4.49E-04		2.14E-01	6.84E-02		6.22E-01	3.06E-11		3.63E-01	6.43E-06		1.47E+00	1.18E-125	Up	Unigene3277_All//gi|223452416|gb|AC B89535.1|//1.00E-115//protein kinase [Glycine max]	Unigene3277_All//5.00E-106//AT2G28930| APK1B; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene3277_All//0.00E+00//gi|78352507|gb|DT572781.1|DT572781		ko04626|Plant-pathogen interaction		nr +
Unigene32770_All	263	0.00	5.78	0.40	4.92	0.92	0.00	0.96	0.32	0.15	1.25E+01	1.10E-08	Up	8.66E+00	3.98E-01		-2.43E+00	1.10E-04	Down	-1.23E+01	4.24E-08	Down	-1.60E+00	3.10E-01		-2.67E+00	1.15E-01									
Unigene32771_All	1267	0.21	0.12	0.08	0.83	0.95	0.32	5.57	0.33	0.47	-7.83E-01	6.20E-01		-1.30E+00	4.36E-01		2.05E-01	8.01E-01		-1.36E+00	4.89E-02		-4.08E+00	2.61E-37	Down	-3.56E+00	8.06E-35	Down	Unigene32771_All//gi|115464943|ref|NP_001056071.1|//1.00E-57//Os05g0520300 [Oryza sativa Japonica Group] >gi|113579622|dbj|BAF17985.1| Os05g0520300 [Oryza sativa Japonica Group]	Unigene32771_All//4.00E-36//AT5G25830| zinc finger (GATA type) family protein	Unigene32771_All//0.00E+00//gi|78327825|gb|DT548099.1|DT548099	C2C2-GATA		GO:0005488	nr -
Unigene32774_All	313	0.00	3.24	3.74	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.26E-06	Up	1.19E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene32774_All//gi|46810472|gb|AAT01617.1|//4.00E-10//omega gliadin [Triticum aestivum]					GO:0044464	nr +
Unigene32775_All	259	0.00	9.78	5.14	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	2.05E-14	Up	1.23E+01	2.40E-07	Up	null	null		null	null		null	null		null	null		Unigene32775_All//sp|P69780|LPP_SHIFL//2.00E-35//Major outer membrane lipoprotein OS=Shigella flexneri GN=lpp PE=3 SV=1						swissprot -
Unigene32777_All	551	0.00	4.97	2.71	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.44E-15	Up	1.14E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene32777_All//gi|255070161|ref|XP_002507162.1|//3.00E-84//cell division cycle protein 48-like protein, expessed [Micromonas sp. RCC299] >gi|226522437|gb|ACO68420.1| cell division cycle protein 48-like protein, expessed [Micromonas sp. RCC299]	Unigene32777_All//2.00E-77//AT3G53230| cell division cycle protein 48, putative / CDC48, putative	Unigene32777_All//6.00E-07//TC136558		ko04141|Protein processing in endoplasmic reticulum	GO:0009987//GO:0010038//GO:0016020//GO:0031981//GO:0032559//GO:0042623//GO:0044444	nr +
Unigene32778_All	518	0.00	0.00	0.00	0.19	0.00	0.00	0.57	1.37	3.15	null	null		null	null		-7.59E+00	3.13E-01		-7.59E+00	3.99E-01		1.26E+00	1.07E-01		2.46E+00	4.32E-06	Up	Unigene32778_All//gi|297850036|ref|XP_002892899.1|//3.00E-17//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338741|gb|EFH69158.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene32778_All//3.00E-17//AT1G16090| WAKL7 (wall associated kinase-like 7); protein serine/threonine kinase				GO:0016740	nr +
Unigene32780_All	352	0.00	12.52	4.69	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	4.10E-25	Up	1.22E+01	4.30E-09	Up	null	null		null	null		null	null		null	null		Unigene32780_All//gi|253759874|ref|XP_002488951.1|//1.00E-11//hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor] >gi|241947058|gb|EES20203.1| hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor]		Unigene32780_All//4.00E-38//TC148521				nr +
Unigene32782_All	348	50.67	20.68	54.17	63.41	42.55	27.25	21.14	11.05	17.74	-1.29E+00	8.91E-20	Down	9.64E-02	5.27E-01		-5.76E-01	6.77E-08		-1.22E+00	3.77E-24	Down	-9.36E-01	1.41E-06		-2.53E-01	2.00E-01				Unigene32782_All//3.00E-57//TC151803				
Unigene32783_All	416	1.64	0.00	4.86	0.36	0.00	0.43	0.00	0.00	0.00	-1.07E+01	4.10E-04	Down	1.57E+00	1.64E-03		-8.49E+00	1.65E-01		2.74E-01	9.05E-01		null	null		null	null									ESTscan +
Unigene32784_All	466	6.18	2.07	5.83	10.80	11.60	8.14	33.03	19.19	14.70	-1.58E+00	5.79E-05	Down	-8.35E-02	8.25E-01		1.04E-01	7.60E-01		-4.07E-01	1.45E-01		-7.83E-01	1.01E-09		-1.17E+00	1.09E-18	Down	Unigene32784_All//gi|211906502|gb|ACJ11744.1|//2.00E-22//Isocitrate dehydrogenase [Gossypium hirsutum]	Unigene32784_All//1.00E-22//AT1G65930| isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	Unigene32784_All//8.00E-74//EV481956		ko04146|Peroxisome//ko00480|Glutathione metabolism//ko00020|Citrate cycle (TCA cycle)	GO:0000166//GO:0004448//GO:0009060//GO:0009536//GO:0019752//GO:0044262//GO:0046872	nr -
Unigene32785_All	353	0.00	0.00	3.02	0.28	0.78	1.41	0.24	0.47	0.00	null	null		1.16E+01	6.62E-06	Up	1.47E+00	4.20E-01		2.32E+00	6.88E-02		9.84E-01	6.33E-01		-7.90E+00	3.58E-01									
Unigene32787_All	359	0.44	0.71	0.59	0.42	0.00	0.25	0.24	1.28	2.77	6.91E-01	6.26E-01		4.41E-01	7.75E-01		-8.70E+00	1.65E-01		-7.27E-01	7.15E-01		2.44E+00	3.74E-02		3.56E+00	2.43E-05	Up			Unigene32787_All//1.00E-133//ES808398				
Unigene32789_All	392	2.27	0.13	2.58	0.25	0.70	0.23	0.54	0.00	0.20	-4.13E+00	2.52E-04	Down	1.86E-01	7.75E-01		1.47E+00	4.20E-01		-1.42E-01	9.50E-01		-9.07E+00	7.44E-02		-1.41E+00	3.80E-01		Unigene32789_All//gi|224091126|ref|XP_002309188.1|//1.00E-16//predicted protein [Populus trichocarpa] >gi|222855164|gb|EEE92711.1| predicted protein [Populus trichocarpa]	Unigene32789_All//4.00E-14//AT5G01910| unknown protein	Unigene32789_All//7.00E-117//DW510148				nr -
Unigene32791_All	288	0.00	3.17	1.29	0.00	0.36	0.63	0.00	0.00	0.00	1.16E+01	2.62E-05	Up	1.03E+01	2.50E-02		8.49E+00	4.56E-01		9.29E+00	1.94E-01		null	null		null	null				Unigene32791_All//3.00E-134//gi|78329163|gb|DT549437.1|DT549437				
Unigene32795_All	534	2.45	1.90	1.40	0.56	0.19	0.00	2.30	0.55	0.30	-3.68E-01	5.31E-01		-8.11E-01	1.90E-01		-1.53E+00	2.98E-01		-9.13E+00	3.99E-02		-2.07E+00	6.67E-04	Down	-2.94E+00	1.14E-05	Down	Unigene32795_All//gi|224085728|ref|XP_002307681.1|//1.00E-44//cytokinin oxidase [Populus trichocarpa] >gi|222857130|gb|EEE94677.1| cytokinin oxidase [Populus trichocarpa]	Unigene32795_All//3.00E-38//AT1G75450| CKX5 (CYTOKININ OXIDASE 5); cytokinin dehydrogenase	Unigene32795_All//0.00E+00//TC167647		ko00908|Zeatin biosynthesis	GO:0006091//GO:0009690//GO:0009888//GO:0016645//GO:0030554//GO:0031410//GO:0043231	nr -
Unigene328_All	3476	0.53	1.40	0.32	1.56	1.67	2.44	1.25	1.68	2.92	1.41E+00	1.03E-06	Up	-7.12E-01	1.56E-01		1.00E-01	7.59E-01		6.45E-01	9.96E-04		4.26E-01	5.73E-02		1.22E+00	2.08E-13	Up	Unigene328_All//gi|50540713|gb|AAT77870.1|//0.00E+00//expressed protein [Oryza sativa Japonica Group]	Unigene328_All//8.00E-176//AT3G21430| DNA binding	Unigene328_All//3.00E-19//ES833305				nr -
Unigene3280_All	1462	3.04	2.29	1.97	4.53	2.28	3.00	4.71	2.32	2.21	-4.11E-01	1.58E-01		-6.29E-01	3.68E-02		-9.88E-01	3.13E-06		-5.97E-01	8.48E-03		-1.03E+00	4.30E-07	Down	-1.09E+00	4.47E-08	Down	Unigene3280_All//gi|224067238|ref|XP_002302424.1|//1.00E-145//nramp transporter [Populus trichocarpa] >gi|222844150|gb|EEE81697.1| nramp transporter [Populus trichocarpa]	Unigene3280_All//2.00E-151//AT1G47240| NRAMP2; inorganic anion transmembrane transporter/ metal ion transmembrane transporter	Unigene3280_All//0.00E+00//TC171679				nr +
Unigene32802_All	340	0.77	0.89	0.00	1.90	0.71	0.80	1.24	1.11	4.57	2.17E-01	8.65E-01		-9.59E+00	8.57E-02		-1.43E+00	1.05E-01		-1.26E+00	1.83E-01		-1.69E-01	8.65E-01		1.88E+00	2.07E-04	Up	Unigene32802_All//gi|219291116|gb|ACL13991.1|//1.00E-10//At2g33360 [Arabidopsis thaliana]	Unigene32802_All//6.00E-12//AT2G33360| unknown protein	Unigene32802_All//8.00E-27//gi|78345075|gb|DT565349.1|DT565349			GO:0043231	nr +
Unigene32805_All	374	0.00	0.81	0.28	1.86	0.46	0.00	1.13	1.56	0.53	9.67E+00	4.43E-02		8.15E+00	3.98E-01		-2.02E+00	2.15E-02		-1.09E+01	1.96E-04	Down	4.69E-01	6.13E-01		-1.09E+00	2.82E-01									ESTscan +
Unigene32806_All	253	0.83	3.00	1.68	3.54	2.18	0.00	0.17	0.66	0.00	1.86E+00	3.73E-02		1.03E+00	3.96E-01		-7.03E-01	3.25E-01		-1.18E+01	1.21E-05	Down	1.98E+00	3.79E-01		-7.38E+00	6.12E-01		Unigene32806_All//gi|297833916|ref|XP_002884840.1|//5.00E-32//organic anion transporter [Arabidopsis lyrata subsp. lyrata] >gi|297330680|gb|EFH61099.1| organic anion transporter [Arabidopsis lyrata subsp. lyrata]	Unigene32806_All//2.00E-33//AT3G11320| organic anion transmembrane transporter	Unigene32806_All//8.00E-128//gi|48821661|gb|C0122974.1|C0122974			GO:0031224	nr -
Unigene32810_All	321	0.00	3.63	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.05E-06	Up	1.10E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene32810_All//gi|300262824|gb|EFJ47028.1|//2.00E-07//transcription factor jumonji domain-containing protein [Volvox carteri f. nagariensis]						nr -
Unigene32811_All	259	0.61	2.54	4.73	0.19	1.60	2.44	1.63	1.13	0.92	2.07E+00	3.93E-02		2.96E+00	2.55E-04	Up	3.05E+00	5.67E-02		3.67E+00	5.05E-03		-5.31E-01	6.34E-01		-8.23E-01	3.99E-01				Unigene32811_All//3.00E-07//C0078971				
Unigene32815_All	281	0.00	4.33	1.71	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.47E-07	Up	1.07E+01	7.48E-03		null	null		null	null		null	null		null	null									
Unigene32817_All	298	0.00	33.67	19.66	0.00	0.00	0.00	0.00	0.00	0.00	1.50E+01	1.76E-57	Up	1.43E+01	1.20E-32	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene32819_All	285	8.08	19.02	6.54	10.84	12.45	17.91	45.25	128.47	105.12	1.24E+00	3.42E-06	Up	-3.05E-01	5.00E-01		2.00E-01	6.00E-01		7.25E-01	6.07E-03		1.51E+00	1.16E-61	Up	1.22E+00	1.46E-37	Up	Unigene32819_All//gi|226502817|ref|NP_001148792.1|//2.00E-46//vesicle-associated membrane protein 725 [Zea mays] >gi|195622198|gb|ACG32929.1| vesicle-associated membrane protein 725 [Zea mays]	Unigene32819_All//1.00E-46//AT2G32670| ATVAMP725	Unigene32819_All//8.00E-156//TC170076		ko04130|SNARE interactions in vesicular transport	GO:0006810//GO:0031224	nr +
Unigene3282_All	531	2.86	3.15	4.91	2.63	5.58	7.82	15.13	34.79	13.73	1.40E-01	7.71E-01		7.82E-01	5.59E-02		1.09E+00	2.27E-03		1.57E+00	5.24E-07	Up	1.20E+00	1.59E-22	Up	-1.40E-01	4.86E-01		Unigene3282_All//gi|297807887|ref|XP_002871827.1|//2.00E-17//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317664|gb|EFH48086.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3282_All//5.00E-18//AT5G18650| zinc finger (C3HC4-type RING finger) family protein	Unigene3282_All//0.00E+00//DW506473		ko04120|Ubiquitin mediated proteolysis	GO:0046914	nr +

Unigene32820_All	532	0.10	0.38	0.10	0.66	0.71	0.93	2.30	0.31	1.87	1.95E+00	3.75E-01		2.62E-02	9.95E-01		1.19E-01	9.58E-01		5.11E-01	6.41E-01		-2.87E+00	2.54E-05	Down	-3.00E-01	5.97E-01		Unigene32820_All//gi|297843100|ref|XP_002889431.1|//3.00E-37//phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335273|gb|EFH65690.1|phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene32820_All//9.00E-38//AT1G03010| phototropic-responsive NPH3 family protein	Unigene32820_All//4.00E-51//ES818787			GO:0000904//GO:0009314//GO:0016020//GO:0046872//GO:0060089	nr +
Unigene32822_All	321	4.89	1.89	12.61	0.93	2.15	1.97	0.66	0.78	0.25	-1.37E+00	1.19E-02		1.37E+00	3.06E-05	Up	1.20E+00	1.94E-01		1.08E+00	2.69E-01		2.46E-01	8.53E-01		-1.41E+00	3.80E-01									
Unigene32823_All	316	0.33	0.00	0.00	0.00	0.00	0.00	1.20	2.51	4.41	-8.37E+00	3.72E-01		-8.37E+00	3.93E-01		null	null		null	null		1.06E+00	1.41E-01		1.87E+00	4.97E-04	Up		Unigene32823_All//4.00E-06//AT1G69840| band 7 family protein	Unigene32823_All//9.00E-39//gi|48746682|gb|CO077201.1|CO077201				
Unigene32824_All	264	0.20	10.75	4.64	0.00	0.13	0.34	10.25	3.01	0.91	5.76E+00	1.04E-14	Up	4.55E+00	1.02E-05	Up	7.03E+00	8.30E-01		8.42E+00	4.76E-01		-1.77E+00	1.95E-06	Down	-3.50E+00	1.50E-13	Down	Unigene32824_All//gi|242039819|ref|XP_002467304.1|//2.00E-10//hypothetical protein SORBIDRAFT_01g024221 [Sorghum bicolor] >gi|241921158|gb|EER94302.1|hypothetical protein SORBIDRAFT_01g024221 [Sorghum bicolor]	Unigene32824_All//3.00E-13//TC176575				nr +
Unigene32828_All	695	0.00	8.82	6.67	0.00	0.00	0.26	0.00	0.00	0.00	1.31E+01	5.27E-35	Up	1.27E+01	9.74E-26	Up	null	null		8.02E+00	1.94E-01		null	null		null	null		Unigene32828_All//gi|74474915|dbj|BAE44441.1|//1.00E-16//dual specificity protein tyrosine phosphatase 1 [Solanum tuberosum]	Unigene32828_All//2.00E-16//AT3G23610| dual specificity protein phosphatase (DsPTP1)				GO:0004721	nr -
Unigene3283_All	1093	19.34	18.64	20.32	21.83	33.99	48.84	49.59	84.74	69.80	-5.34E-02	6.84E-01		7.11E-02	6.32E-01		6.39E-01	4.59E-15		1.16E+00	7.85E-53	Up	7.73E-01	3.94E-53		4.93E-01	1.09E-20		Unigene3283_All//gi|297807887|ref|XP_002871827.1|//1.00E-131//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317664|gb|EFH48086.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3283_All//2.00E-132//AT5G18650| zinc finger (C3HC4-type RING finger) family protein	Unigene3283_All//0.00E+00//TC135860		ko04120|Ubiquitin mediated proteolysis	GO:0046872	nr -
Unigene32830_All	379	0.97	1.60	0.00	1.05	0.91	1.67	2.01	0.22	0.21	7.31E-01	4.16E-01		-9.92E+00	2.78E-02		-2.11E-01	8.25E-01		6.66E-01	4.92E-01		-3.19E+00	7.92E-04	Down	-3.26E+00	4.48E-04	Down		Unigene32830_All//2.00E-52//gi|54115177|gb|CO490686.1|CO490686					
Unigene32832_All	464	0.45	1.97	3.33	0.75	0.67	0.68	0.00	0.00	0.00	2.12E+00	1.04E-02		2.88E+00	3.60E-05	Up	-1.70E-01	8.58E-01		-1.42E-01	9.12E-01		null	null		null	null									ESTscan -
Unigene32834_All	533	0.00	0.67	0.00	0.09	0.06	0.42	19.59	37.72	107.33	9.38E+00	2.46E-02		null	null		-5.33E-01	8.25E-01		2.18E+00	3.23E-01		9.45E-01	8.44E-17		2.45E+00	4.23E-187	Up								
Unigene32835_All	390	0.80	0.26	1.37	3.96	1.59	1.04	2.60	1.18	1.02	-1.63E+00	2.76E-01		7.62E-01	4.53E-01		-1.32E+00	9.76E-03		-1.93E+00	7.77E-04	Down	-1.14E+00	6.62E-02		-1.35E+00	2.51E-02		Unigene32835_All//gi|24461861|gb|AAN62348.1|AF506028_15//4.00E-09//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene32835_All//4.00E-09//AT4G26090| RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding	Unigene32835_All//2.00E-126//CO097771		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene32839_All	274	0.00	0.37	0.39	0.36	0.00	0.00	3.24	3.20	13.23	8.53E+00	3.86E-01		8.60E+00	3.98E-01		-8.51E+00	3.13E-01		-8.51E+00	3.99E-01		-1.67E-02	1.02E+00		2.03E+00	3.95E-10	Up								
Unigene3284_All	1415	4.36	7.48	6.62	6.86	8.03	9.58	5.05	2.16	2.48	7.78E-01	9.95E-06		6.02E-01	2.01E-03		2.26E-01	2.23E-01		4.80E-01	1.51E-03		-1.23E+00	1.65E-09	Down	-1.03E+00	1.31E-07	Down	Unigene3284_All//gi|15229892|ref|NP_187796.1|//1.00E-158//ANT1 (AROMATIC AND NEUTRAL TRANSPORTER 1); amino acid transmembrane transporter/ aromatic amino acid transmembrane transporter/ neutral amino acid transmembrane transporter [Arabidopsis thaliana] >gi|30725278|gb|AAP37661.1|At3g11900 [Arabidopsis thaliana]	Unigene3284_All//6.00E-152//AT3G11900| ANT1 (AROMATIC AND NEUTRAL TRANSPORTER 1); amino acid transmembrane transporter/ aromatic amino acid transmembrane transporter/ neutral amino acid transmembrane transporter	Unigene3284_All//1.00E-93//AI731913			GO:0031224	nr -
Unigene32844_All	398	73.49	22.92	28.50	196.00	140.77	120.97	18.17	15.65	19.32	-1.68E+00	1.79E-47	Down	-1.37E+00	8.09E-34	Down	-4.78E-01	4.57E-19		-6.96E-01	3.90E-33		-2.15E-01	3.23E-01		8.88E-02	6.58E-01			Unigene32844_All//5.00E-161//BG444270					
Unigene32847_All	258	3.65	0.79	0.00	0.39	0.40	0.70	2.79	1.13	0.46	-2.22E+00	6.65E-03		-1.18E+01	3.35E-05	Down	5.21E-02	9.66E-01		8.58E-01	6.95E-01		-1.30E+00	9.45E-02		-2.59E+00	2.81E-03		Unigene32847_All//gi|298569786|gb|ADI87421.1|//1.00E-12//fructokinase-like protein 1 [Nicotiana tabacum]	Unigene32847_All//1.00E-13//AT3G54090| pfkB-type carbohydrate kinase family protein	Unigene32847_All//8.00E-128//TC139950				nr -
Unigene32849_All	299	0.00	0.00	0.00	0.67	0.00	0.00	21.35	4.05	15.72	null	null		null	null		-9.38E+00	8.43E-02		-9.38E+00	1.33E-01		-2.40E+00	1.36E-20	Down	-4.42E-01	3.02E-02		Unigene32849_All//gi|73624747|gb|AAZ79231.1|//2.00E-11//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene32849_All//2.00E-06//AT4G23990| ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups				GO:0016740	nr -
Unigene32853_All	456	0.00	1.78	1.52	1.09	0.60	0.30	0.00	0.00	0.00	1.08E+01	9.38E-05	Up	1.06E+01	6.16E-04	Up	-8.55E-01	4.07E-01		-1.88E+00	1.08E-01		null	null		null	null		Unigene32853_All//COG2801//3.00E-39//Transposase and inactivated derivatives						cog -
Unigene32854_All	259	0.20	3.52	0.00	0.58	2.53	0.87	0.16	0.65	0.15	4.12E+00	2.34E-04	Up	-7.66E+00	6.24E-01		2.13E+00	3.78E-02		5.96E-01	7.21E-01		1.98E+00	3.79E-01		-8.56E-02	9.71E-01			Unigene32854_All//4.00E-37//TC159920					
Unigene32858_All	272	0.19	0.00	0.00	0.18	0.13	1.00	2.49	0.61	0.15	-7.59E+00	6.12E-01		-7.59E+00	6.24E-01		-5.32E-01	8.25E-01		2.44E+00	2.22E-01		-2.02E+00	1.98E-02		-4.09E+00	3.10E-04	Down								
Unigene3286_All	1660	17.68	20.82	17.51	12.21	19.11	12.90	19.87	8.41	10.97	2.36E-01	1.25E-02		-1.37E-02	9.17E-01		6.46E-01	3.79E-13		7.85E-02	6.22E-01		-1.24E+00	1.19E-41	Down	-8.57E-01	8.91E-24		Unigene3286_All//gi|27435851|gb|AAO13248.1|AF181993_1//1.00E-124//cyclin D [Populus tremula x Populus tremuloides]	Unigene3286_All//2.00E-83//AT4G34160| CYCD3;1 (CYCLIN D3;1); cyclin-dependent protein kinase regulator/ protein binding	Unigene3286_All//0.00E+00//ES807220				nr +
Unigene32862_All	266	5.70	0.19	3.40	1.50	0.39	0.85	0.00	0.16	0.00	-4.90E+00	1.23E-07	Down	-7.45E-01	1.88E-01		-1.95E+00	1.19E-01		-8.20E-01	5.06E-01		7.30E+00	6.34E-01		null	null			Unigene32862_All//8.00E-51//TC138510					
Unigene32864_All	353	0.00	3.16	2.26	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.00E-06	Up	1.11E+01	1.72E-04	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene32865_All	232	0.00	0.00	0.00	0.00	3.86	7.01	0.00	0.00	0.00	null	null		null	null		1.19E+01	1.69E-05	Up	1.28E+01	1.09E-09	Up	null	null		null	null		Unigene32865_All//gi|55442027|gb|AAV52268.1|//2.00E-18//methyl transferase [Brassica juncea]	Unigene32865_All//1.00E-18//AT1G19640| JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate O-methyltransferase			ko00592|alpha-Linolenic acid metabolism	GO:0006633//GO:0006950//GO:0008757//GO:0023033//GO:0031407//GO:0044124	nr -
Unigene32866_All	593	0.18	0.60	2.16	0.25	0.29	0.08	0.00	0.00	0.00	1.76E+00	2.18E-01		3.61E+00	3.41E-05	Up	2.04E-01	9.50E-01		-1.73E+00	5.01E-01		null	null		null	null									ESTscan +
Unigene3287_All	2266	2.33	0.87	0.54	4.13	4.13	2.37	6.46	1.88	2.80	-1.42E+00	2.48E-07	Down	-2.11E+00	1.40E-11	Down	2.00E-04	9.95E-01		-8.01E-01	1.27E-05		-1.78E+00	9.80E-32	Down	-1.21E+00	9.57E-19	Down	Unigene3287_All//gi|29028930|gb|AAO64844.1|//8.00E-51//At3g53320 [Arabidopsis thaliana]	Unigene3287_All//3.00E-17//AT3G53320| unknown protein	Unigene3287_All//0.00E+00//ES806424				nr -
Unigene32873_All	311	0.67	0.00	0.51	0.16	0.55	1.02	2.45	0.54	0.13	-9.39E+00	1.22E-01		-3.90E-01	8.07E-01		1.79E+00	5.20E-01		2.67E+00	1.44E-01		-2.19E+00	7.77E-03		-4.26E+00	8.65E-05	Down	Unigene32873_All//gi|75169169|sp|Q9C6S6.1|PPR67_ARATH//1.00E-19//RecName: Full=Putative pentatricopeptide repeat-containing protein At1g31840	Unigene32873_All//8.00E-21//AT1G31840| LOCATED IN: endomembrane system; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT3G22470.1); Has 23098 Blast hits to 5773 proteins in 180 species: Archae - 3; Bacteria - 16; Metazoa - 407; Fungi - 450; Plants - 21304; Viruses - 0; Other Eukaryotes - 918 (source: NCBI BLink).					nr -
Unigene32875_All	397	0.00	27.95	6.57	0.00	0.00	0.00	0.00	0.00	0.00	1.48E+01	1.28E-63	Up	1.27E+01	2.12E-14	Up	null	null		null	null		null	null		null	null		Unigene32875_All//gi|68449762|gb|AAY87868.1|//1.00E-47//cytoplasmic ribosomal protein S13 [Solanum lycopersicum]	Unigene32875_All//3.00E-48//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene32875_All//1.00E-10//TC176312		ko03010|Ribosome	GO:0000904//GO:0005198//GO:0009536//GO:0009887//GO:0010467//GO:0015935//GO:0003012//GO:0031981//GO:0033205	nr +
Unigene32878_All	268	0.00	4.92	5.17	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.50E-07	Up	1.23E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene32878_All//sp|P35044|TRYA4_LUCCU//3.00E-12//Trypsin alpha-4 OS=Lucilia cuprina PE=3 SV=1						swissprot -
Unigene3288_All	1230	3.57	7.83	4.46	4.09	6.05	8.15	7.91	11.83	8.29	1.13E+00	3.92E-09	Up	3.20E-01	2.44E-01		5.64E-01	6.44E-03		9.95E-01	3.33E-08		5.81E-01	8.74E-06		6.87E-02	6.91E-01		Unigene3288_All//gi|23304837|emb|CAD48198.1|//7.00E-54//RNA-binding protein [Medicago truncatula]	Unigene3288_All//1.00E-39//AT1G21320| nucleic acid binding / nucleotide binding	Unigene3288_All//0.00E+00//TC177206			GO:0005488	nr +
Unigene32881_All	283	1.66	1.25	0.75	2.99	2.80	2.55	9.41	3.99	3.80	-4.09E-01	6.69E-01		-1.14E+00	3.32E-01		-9.66E-02	8.77E-01		-2.29E-01	7.51E-01		-1.24E+00	4.36E-04	Down	-1.31E+00	1.48E-04	Down		Unigene32881_All//4.00E-139//TC175847					
Unigene32883_All	459	0.00	0.22	0.12	2.71	0.30	0.89	0.28	0.00	0.00	7.79E+00	3.86E-01		6.86E+00	6.36E-01		-3.18E+00	7.60E-06	Down	-1.62E+00	1.08E-02		-8.11E+00	2.35E-01		-8.11E+00	2.00E-01		Unigene32883_All//gi|124359529|gb|ABD32574.2|//4.00E-09//Endonuclease/exonuclease/phosphatase [Medicago truncatula]						nr +
Unigene32885_All	423	0.12	0.00	0.00	0.00	0.00	0.00	1.10	2.37	5.18	-6.95E+00	6.12E-01		-6.95E+00	6.24E-01		null	null		null	null		1.11E+00	7.67E-02		2.24E+00	3.75E-07	Up								
Unigene32886_All	414	0.00	0.00	0.00	0.00	0.00	0.00	3.98	2.12	0.00	null	null		null	null		null	null		null	null		-9.10E-01	4.74E-02		-1.20E+01	3.45E-12	Down	Unigene32886_All//gi|112253642|gb|ABI114406.1|//6.00E-53//40S ribosomal S14 [Prorocentrum minimum]	Unigene32886_All//5.00E-42//AT3G11510| 40S ribosomal protein S14 (RPS14B)	Unigene32886_All//9.00E-24//CD485874		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0031981	nr -
Unigene32888_All	630	4.24	0.72	0.00	2.13	2.73	0.36	1.95	0.13	0.82	-2.55E+00	6.04E-08	Down	-1.20E+01	1.32E-14	Down	3.56E-01	5.38E-01		-2.57E+00	1.41E-04	Down	-3.87E+00	1.15E-06	Down	-1.24E+00	1.98E-02		Unigene32888_All//gi|18397703|ref|NP_566290.1|//1.00E-37//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|71660789|sp|Q8LG10.2|GAT15_ARATH RecName: Full=GATA transcription factor 15	Unigene32888_All//2.00E-26//AT3G06740| zinc finger (GATA type) family protein	Unigene32888_All//1.00E-36//ES804921	C2C2-GATA		GO:0001071//GO:0003677//GO:0006351//GO:0046914	nr -
Unigene32890_All	353	0.00	55.69	21.27	0.00	0.00	0.00	0.00	0.00	0.00	1.58E+01	4.24E-113	Up	1.44E+01	5.53E-42	Up	null	null		null	null		null	null		null	null		Unigene32890_All//gi|115480759|ref|NP_001063973.1|//1.00E-30//Os09g0568800 [Oryza sativa Japonica Group] >gi|113632206|dbj|BAF25887.1|Os09g0568800 [Oryza sativa Japonica Group]	Unigene32890_All//4.00E-20//AT4G34555| 40S ribosomal protein S25, putative			ko03010|Ribosome	GO:0010467//GO:0015935	nr +
Unigene32893_All	420	0.50	0.36	0.00	0.00	2.05	10.11	0.20	0.50	0.00	-4.61E-01	7.58E-01		-8.96E+00	1.46E-01		1.10E+01	2.76E-05	Up	1.33E+01	1.31E-25	Up	1.31E+00	4.47E-01		-7.65E+00	3.58E-01		Unigene32893_All//gi|113029|sp|P17069.1|ACEA_GOSHI//2.00E-74//RecName: Full=Isocitrate lyase; Short=ICL; Short=Isocitratase; Short=Isocitrase	Unigene32893_All//4.00E-65//AT3G21720| ICL (ISOCITRATE LYASE); catalytic/ isocitrate lyase	Unigene32893_All//0.00E+00//TC146124		ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005488//GO:0005777//GO:0009060//GO:0016833//GO:0043436//GO:0044262	nr -
Unigene32895_All	404	0.39	1.25	1.98	0.86	0.85	0.78	3.56	5.07	0.79	1.69E+00	1.34E-01		2.35E+00	1.46E-02		-1.80E-02	9.58E-01		-1.41E-01	9.12E-01		5.11E-01	2.23E-01		-2.17E+00	6.88E-05	Down		Unigene32895_All//2.00E-40//ES838136					
Unigene32896_All	788	0.00	0.00	0.00	1.77	1.66	0.23	0.64	1.27	0.05	null	null		null	null		-9.20E-02	8.58E-01		-2.95E+00	2.40E-05	Down	9.83E-01	1.16E-01		-3.67E+00	3.75E-03		Unigene32896_All//gi|9759561|dbj|BAB11163.1|//4.00E-56//MtN21 nodulin protein-like [Arabidopsis thaliana]	Unigene32896_All//2.00E-57//AT5G07050| LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF6, transmembrane (InterPro:IPR000620); BEST Arabidopsis thaliana protein match is: nodulin MtN21 family protein (TAIR:AT2G40900.1); Has 2288 Blast hits to 2270 proteins in 280 species: Archae - 23; Bacteria - 774; Metazoa - 5; Fungi - 0; Plants - 641; Viruses - 0; Other Eukaryotes - 845 (source: NCBI BLink).	Unigene32896_All//0.00E+00//TC159804			GO:0044464	nr +
Unigene329_All	3686	1.31	2.86	1.75	3.77	4.90	5.01	6.06	7.06	10.74	1.13E+00	6.48E-10	Up	4.21E-01	8.86E-02		3.79E-01	2.54E-03		4.10E-01	1.32E-03		2.22E-01	2.62E-02		8.27E-01	1.40E-26		Unigene329_All//gi|186510286|ref|NP_001078197.2|//0.00E+00//DNA binding [Arabidopsis thaliana] >gi|75323048|sp|Q6A332.1|ALY3_ARATH RecName: Full=Protein ALWAYS EARLY 3; Short=AtALY3 >gi|50539422|emb|CAE47462.1|always early protein 3 [Arabidopsis thaliana]	Unigene329_All//0.00E+00//AT3G05380| DNA binding / transcription factor	Unigene329_All//1.00E-27//ES800310	MYB-related			nr -

Unigene3290_All	1312	14.16	7.18	5.03	23.58	25.49	14.35	12.99	3.12	2.88	-9.79E-01	1.45E-13		-1.49E+00	1.22E-24	Down	1.12E-01	3.09E-01		-7.16E-01	3.90E-14		-2.06E+00	1.33E-44	Down	-2.17E+00	3.03E-49	Down	Unigene3290_All//gi|77416931|gb|AB181861.1|//0.00E-00//UDP-glucose:protein transglucosylase-like [Solanum tuberosum]	Unigene3290_All//0.00E+00//TC167777			GO:0005618//GO:0005911//GO:0009250//GO:0035251//GO:0043231//GO:0045229	nr +
Unigene32902_All	294	0.36	0.86	0.00	2.20	0.82	0.00	0.29	1.14	0.54	1.28E+00	4.35E-01		-8.48E+00	3.93E-01		-1.43E+00	1.05E-01		-1.11E+01	3.90E-04	Down	1.98E+00	1.44E-01		9.14E-01	6.24E-01		Unigene32902_All//gi|225469228|ref|XP_002264243.1|//4.00E-07//PREDICTED: DNA binding protein WRKY2 [Vitis vinifera]		Unigene32902_All//2.00E-30//gi|48791512|gb|CO092826.1|CO092826			GO:0003677//GO:0010467	nr +
Unigene32904_All	318	12.18	5.26	14.90	2.66	0.65	0.85	0.00	0.00	0.00	-1.21E+00	1.46E-04	Down	2.92E-01	3.45E-01		-2.04E+00	9.05E-03		-1.64E+00	4.18E-02		null	null		null	null				Unigene32904_All//4.00E-07//TC149354				
Unigene32905_All	426	0.00	0.24	0.00	0.00	0.00	0.00	8.34	7.26	2.81	7.89E+00	3.86E-01		null	null		null	null		null	null		-2.00E-01	5.49E-01		-1.57E+00	2.44E-07	Down			Unigene32905_All//9.00E-21//TC149074				
Unigene32906_All	411	3.31	0.74	2.07	1.82	1.51	0.33	0.51	1.02	0.00	-2.16E+00	9.03E-04	Down	-6.75E-01	2.58E-01		-2.70E-01	7.48E-01		-2.46E+00	1.02E-02		9.83E-01	3.73E-01		-9.01E+00	5.80E-02		Unigene32906_All//gi|195611854|gb|ACG27757.1|//7.00E-52//pentatricopeptide repeat protein PPR868-14 [Zea mays]	Unigene32906_All//9.00E-48//AT4G37380| pentatricopeptide (PPR) repeat-containing protein	Unigene32906_All//2.00E-64//CO120970			nr +
Unigene32908_All	958	0.00	0.00	0.00	0.16	0.00	0.09	8.87	0.17	1.75	null	null		null	null		-7.29E+00	1.65E-01		-7.26E-01	7.15E-01		-5.67E+00	1.09E-53	Down	-2.34E+00	2.25E-27	Down	Unigene32908_All//gi|115435526|ref|NP_001042521.1|//1.00E-41//Os01g0235300 [Oryza sativa Japonica Group] >gi|113532052|dbj|BAF04435.1|Os01g0235300 [Oryza sativa Japonica Group]	Unigene32908_All//1.00E-23//AT1G17100| SOUL heme-binding family protein				nr +
Unigene3291_All	1252	5.01	4.78	3.15	28.57	30.97	36.51	57.95	24.80	23.58	-7.05E-02	7.70E-01		-6.72E-01	6.18E-03		1.17E-01	2.34E-01		3.54E-01	3.87E-06		-1.22E+00	7.03E-89	Down	-1.30E+00	4.84E-100	Down	Unigene3291_All//gi|6692816|dbj|BAA89423.1|//1.00E-148//allyl alcohol dehydrogenase [Nicotiana tabacum]	Unigene3291_All//2.00E-138//AT5G16990| NADP-dependent oxidoreductase, putative	Unigene3291_All//0.00E+00//TC131782			nr -
Unigene32910_All	322	0.00	3.46	3.47	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.00E-06	Up	1.18E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene32910_All//sp|P54611|VATE_DROME//5.00E-25//V-type proton ATPase subunit E OS=Drosophila melanogaster GN=Vha26 PE=1 SV=1					swissprot -
Unigene32911_All	340	0.15	0.30	0.47	1.32	0.20	0.53	0.37	2.34	2.81	9.54E-01	7.26E-01		1.61E+00	5.11E-01		-2.70E+00	3.24E-02		-1.31E+00	2.73E-01		2.65E+00	1.99E-03		2.91E+00	1.88E-04	Up	Unigene32911_All//gi|224133870|ref|XP_002321681.1|//4.00E-34//lysine/histidine transporter [Populus trichocarpa] >gi|222868677|gb|EEF05808.1|lysine/histidine transporter [Populus trichocarpa]	Unigene32911_All//1.00E-34//AT1G24400| LHT2 (LYSINE HISTIDINE TRANSPORTER 2); acidic amino acid transmembrane transporter/ amino acid transmembrane transporter/ neutral amino acid transmembrane transporter	Unigene32911_All//1.00E-115//TC162603			GO:0015171//GO:0015837//GO:0031224	nr -
Unigene32912_All	260	0.40	0.58	0.00	0.00	0.40	0.35	0.00	0.48	2.45	5.39E-01	7.79E-01		-8.65E+00	3.93E-01		8.63E+00	4.56E-01		8.44E+00	4.76E-01		8.91E+00	2.40E-01		1.13E+01	9.33E-05	Up			Unigene32912_All//4.00E-77//TC169327				
Unigene32913_All	514	0.00	0.00	0.00	0.00	0.00	0.00	3.70	3.17	0.00	null	null		null	null		null	null		null	null		-2.23E-01	6.53E-01		-1.19E+01	4.91E-14	Down	Unigene32913_All//gi|238014838|gb|ACR38454.1|//1.00E-14//unknown [Zea mays]		Unigene32913_All//2.00E-62//TC133518			nr -
Unigene32916_All	367	2.57	0.14	1.45	0.14	0.84	0.25	0.46	0.34	1.63	-4.22E+00	1.36E-04	Down	-8.23E-01	2.71E-01		2.64E+00	1.61E-01		8.59E-01	7.94E-01		-4.31E-01	7.93E-01		1.82E+00	3.94E-02								
Unigene32917_All	361	15.22	0.84	9.74	0.00	0.38	0.00	0.00	0.00	0.44	-4.18E+00	2.94E-24	Down	-6.45E-01	1.52E-02		8.58E+00	3.18E-01		null	null		null	null		8.79E+00	1.40E-01								
Unigene32918_All	388	1.08	4.83	1.78	1.03	0.44	1.51	0.76	13.25	0.10	2.16E+00	7.11E-05	Up	7.26E-01	3.96E-01		-1.21E+00	3.14E-01		5.59E-01	6.01E-01		4.12E+00	2.31E-27	Up	-2.89E+00	6.76E-02		Unigene32918_All//gi|30689834|ref|NP_182007.2|//6.00E-08//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]					nr +
Unigene3292_All	1358	85.15	58.09	47.13	58.51	59.03	72.43	212.02	105.97	151.26	-5.52E-01	4.32E-30		-8.53E-01	5.78E-62		1.29E-02	8.65E-01		3.08E-01	9.84E-10		-1.00E+00	2.32E-253	Down	-4.87E-01	3.66E-74		Unigene3292_All//gi|19913109|emb|CAC84547.1|//1.00E-155//dicarboxylate/tricarboxylate carrier [Nicotiana tabacum]	Unigene3292_All//3.00E-148//AT5G19760| dicarboxylate/tricarboxylate carrier (DTC)	Unigene3292_All//0.00E+00//TC138408			nr -
Unigene32920_All	484	0.32	0.00	0.99	0.62	1.14	0.65	3.14	0.35	0.91	-8.34E+00	2.15E-01		1.61E+00	1.82E-01		8.83E-01	4.21E-01		8.11E-02	9.50E-01		-3.19E+00	4.80E-07	Down	-1.80E+00	3.39E-04	Down	Unigene32920_All//gi|42567122|ref|NP_194227.2|//4.00E-67//ATP-binding region, ATPase-like domain-containing protein [Arabidopsis thaliana]	Unigene32920_All//2.00E-68//AT4G24970| ATP-binding region, ATPase-like domain-containing protein	Unigene32920_All//9.00E-46//CA994248			GO:0032559	nr +
Unigene32923_All	391	0.00	5.70	3.54	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.09E-12	Up	1.18E+01	1.23E-07	Up	null	null		null	null		null	null		null	null								
Unigene32924_All	414	0.38	168.16	130.42	0.24	0.17	0.76	0.20	0.00	0.10	8.79E+00	0.00E+00	Up	8.43E+00	8.08E-300	Up	-5.32E-01	8.16E-01		1.67E+00	3.09E-01		-7.67E+00	4.03E-01		-1.09E+00	6.76E-01		Unigene32924_All//gi|22550332|ref|NP_689371.1|//6.00E-08//ATP synthase F0 subunit 6 [Chaetosphaeridium globosum] >gi|22416998|gb|AAM96597.1|AF194279_2 ATP synthase F0 subunit 6 [Chaetosphaeridium globosum]			ko00190|Oxidative phosphorylation	GO:0006811//GO:0016020	nr -
Unigene32925_All	444	0.00	3.77	2.04	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.54E-09	Up	1.10E+01	4.71E-05	Up	null	null		null	null		null	null		null	null		Unigene32925_All//gi|68638026|emb|CAI99406.1|//1.00E-18//P-type ATPase [Flabellia petiolata]				GO:0006811//GO:0009206//GO:0031224//GO:0032559//GO:0042625	nr -
Unigene32928_All	575	0.00	8.81	1.76	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	6.88E-29	Up	1.08E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene32928_All//gi|10178920|emb|CAC08458.1|//8.00E-11//1-D-desoxyxylulose 5-phosphate synthase (DXS) [Narcissus pseudonarcissus]	Unigene32928_All//1.00E-11//AT4G15560| CLA1 (CLOROPLASTOS ALTERADOS 1); 1-deoxy-D-xylulose-5-phosphate synthase			ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway//ko00900|Terpenoid backbone biosynthesis	GO:0003824//GO:0009536//GO:0044249	nr +
Unigene32929_All	1049	0.00	0.00	0.00	0.05	0.07	0.00	0.36	1.55	2.54	null	null		null	null		4.68E-01	9.58E-01		-5.57E+00	6.35E-01		2.10E+00	5.14E-05	Up	2.81E+00	8.16E-11	Up	Unigene32929_All//gi|13605531|gb|AK32759.1|AF361591_1|//1.00E-106//AT5g06230|MBL20_11 [Arabidopsis thaliana] >gi|22137086|gb|AAM91388.1|At5g06230|MBL20_11 [Arabidopsis thaliana]	Unigene32929_All//2.00E-113//AT3G11570| unknown protein				nr -
Unigene3293_All	1484	2.89	4.85	2.87	7.28	9.31	6.45	8.35	3.01	3.87	7.46E-01	6.28E-04		-1.02E-02	9.97E-01		3.53E-01	1.86E-02		-1.75E-01	3.95E-01		-1.47E+00	1.07E-20	Down	-1.11E+00	4.07E-14	Down	Unigene3293_All//gi|115460218|ref|NP_001053709.1|//3.00E-68//Os04g0590900 [Oryza sativa Japonica Group] >gi|38346723|emb|CAE04873.2|OSJNBa0086006.21 [Oryza sativa (japonica cultivar-group)] >gi|113565280|dbj|BAF15623.1|Os04g0590900 [Oryza sativa Japonica Group] >gi|116311028|emb|CAH67959.1|OSIGBa0142102-OSIGBa0101820.2 [Oryza sativa (indica cultivar-group)]	Unigene3293_All//3.00E-55//AT3G03550| zinc finger (C3HC4-type RING finger) family protein	Unigene3293_All//0.00E+00//TC133182			GO:0005488	nr +
Unigene32930_All	384	0.00	0.00	0.00	0.00	0.00	0.00	0.00	10.56	3.94	null	null		null	null		null	null		null	null		1.34E+01	1.55E-28	Up	1.19E+01	6.77E-11	Up	Unigene32930_All//gi|224139556|ref|XP_002323167.1|//4.00E-08//ABC transporter family protein [Populus trichocarpa] >gi|222867797|gb|EEF04928.1| ABC transporter family protein [Populus trichocarpa]	Unigene32930_All//1.00E-08//AT2G23270| unknown protein				nr -
Unigene32933_All	611	0.34	0.08	0.00	0.33	0.00	0.00	2.98	2.80	0.20	-2.05E+00	3.34E-01		-8.42E+00	1.46E-01		-8.35E+00	8.43E-02		-8.35E+00	1.33E-01		-8.53E-02	8.51E-01		-3.93E+00	4.04E-10	Down	Unigene32933_All//gi|223452309|gb|ACM89482.1|//1.00E-26//receptor-like kinase [Glycine max]	Unigene32933_All//1.00E-26//AT5G28680| protein kinase family protein				GO:0000166//GO:0004672//GO:0006468//GO:0007275//GO:0009856//GO:0016020//GO:0044426	nr +
Unigene32934_All	384	0.00	16.10	9.01	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	2.70E-35	Up	1.31E+01	3.72E-19	Up	null	null		null	null		null	null		null	null		Unigene32934_All//gi|250448815|gb|ACM28278.1|//7.00E-10//ATP synthase epsilon subunit [Ananas comosus]	Unigene32934_All//8.00E-11//AT1G51650| ATP synthase epsilon chain, mitochondrial			ko00190|Oxidative phosphorylation	GO:0000275//GO:0006810//GO:0009206//GO:0015078	nr -
Unigene32940_All	311	0.00	0.00	0.00	0.00	0.00	0.00	2.45	1.34	0.13	null	null		null	null		null	null		null	null		-8.65E-01	2.39E-01		-4.26E+00	8.65E-05	Down	Unigene32940_All//gi|30697195|ref|NP_200732.2|//1.00E-18//40S ribosomal protein S8 (RPS8B) [Arabidopsis thaliana] >gi|17367670|sp|Q9FIF3.1|RS82_ARATH RecName: Full=40S ribosomal protein S8-2 >gi|9759245|dbj|BAB09769.1| 40S ribosomal protein S8 [Arabidopsis thaliana] >gi|28416637|gb|AAO42849.1|At5g59240 [Arabidopsis thaliana] >gi|110735841|dbj|BAE99897.1| 40S ribosomal protein S8 - like [Arabidopsis thaliana]	Unigene32940_All//1.00E-16//AT5G59240| 40S ribosomal protein S8 (RPS8B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0022613	nr -
Unigene32942_All	296	0.18	0.51	0.90	0.00	0.00	3.66	0.00	0.99	0.54	1.54E+00	5.31E-01		2.35E+00	2.39E-01		null	null		1.18E+01	1.82E-06	Up	9.95E+00	2.35E-02		9.07E+00	1.40E-01								
Unigene32946_All	232	1.35	9.17	2.98	0.64	0.45	0.19	0.18	0.36	2.40	2.76E+00	6.33E-07	Up	1.14E+00	2.18E-01		-5.33E-01	7.85E-01		-1.73E+00	5.01E-01		9.84E-01	7.31E-01		3.72E+00	2.38E-03								
Unigene32947_All	332	0.00	4.12	4.97	0.00	0.00	0.00	0.00	0.00	0.24	1.20E+01	7.80E-08	Up	1.23E+01	4.30E-09	Up	null	null		null	null		null	null		7.91E+00	4.04E-01								
Unigene32948_All	852	0.00	9.16	2.38	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.26E-44	Up	1.12E+01	3.79E-11	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene32949_All	396	0.00	4.09	2.96	0.00	0.00	0.23	0.00	0.00	0.00	1.20E+01	2.97E-09	Up	1.15E+01	1.77E-06	Up	null	null		7.83E+00	4.76E-01		null	null		null	null		Unigene32949_All//gi|159478619|ref|XP_001697100.1|//1.00E-08//hydroxyproline-rich glycoprotein, stress-induced [Chlamydomonas reinhardtii] >gi|158274558|gb|EDP00340.1|hydroxyproline-rich glycoprotein, stress-induced [Chlamydomonas reinhardtii]				GO:0016787	nr +
Unigene32953_All	972	0.00	0.00	0.00	0.00	0.00	0.00	1.52	7.70	0.00	null	null		null	null		null	null		null	null		2.34E+00	2.92E-23	Up	-1.06E+01	5.85E-11	Down							
Unigene3296_All	1431	10.64	5.03	11.09	8.70	9.14	6.28	1.83	1.05	0.72	-1.08E+00	4.02E-13	Down	5.97E-02	7.02E-01		7.14E-02	7.30E-01		-4.71E-01	3.00E-03		-8.01E-01	2.14E-02		-1.34E+00	1.25E-04	Down	Unigene3296_All//gi|22325471|ref|NP_178532.2|//1.00E-132//CPZ; 3'-tRNA processing endoribonuclease [Arabidopsis thaliana] >gi|11017757|sp|Q8LG33.1|RNZC_ARATH RecName: Full=Ribonuclease Z, chloroplastic; Short=RNase Z; AltName: Full=tRNase Z; AltName: Full=tRNA 3 endonuclease; AltName: Full=Zinc phosphodiesterase CPZ; Flags: Precursor	Unigene3296_All//1.00E-133//AT2G04530| CPZ; 3'-tRNA processing endoribonuclease	Unigene3296_All//0.00E+00//TC133280			GO:0008033//GO:0016891	nr +
Unigene32961_All	643	0.16	0.00	0.00	0.08	0.05	0.07	2.76	0.72	1.92	-7.35E+00	3.72E-01		-7.35E+00	3.93E-01		-5.32E-01	8.25E-01		-1.43E-01	9.52E-01		-1.95E+00	5.37E-05	Down	-5.24E-01	2.18E-01		Unigene32961_All//gi|225446948|ref|XP_002267468.1|//2.00E-30//PREDICTED: similar to RAP2-like protein [Vitis vinifera]	Unigene32961_All//1.00E-11//AT4G28140| AP2 domain-containing transcription factor, putative	Unigene32961_All//0.00E+00//CO128086	AP2-EREBP		GO:0006350//GO:0009743//GO:0010468//GO:0043231	nr -
Unigene32962_All	388	0.27	3.66	0.00	2.82	5.15	4.77	0.87	0.32	0.92	3.76E+00	3.98E-06	Up	-8.08E+00	3.93E-01		8.66E-01	5.93E-02		7.57E-01	1.27E-01		-1.43E+00	2.58E-01		8.41E-02	9.57E-01		Unigene32962_All//gi|75168952|sp|Q9C5H4.1|Y3627_ARATH//4.00E-20//RecName: Full=VHS domain-containing protein At3g16270	Unigene32962_All//6.00E-19//AT3G16270| INVOLVED IN: intracellular protein transport; LOCATED IN: membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: VHS (InterPro:IPR002014), ENTH/VHS (InterPro:IPR008942); Has 113 Blast hits to 112 proteins in 49 species: Archae - 0; Bacteria - 3; Metazoa - 48; Fungi - 1; Plants - 23; Viruses - 0; Other Eukaryotes - 38 (source: NCBI BLink).	Unigene32962_All//3.00E-70//gi|163449896|gb|EX170726.1|EX170726			GO:0005488//GO:0044464	nr -
Unigene32964_All	441	0.24	0.00	0.24	7.91	2.26	1.02	0.00	0.00	0.00	-7.89E+00	3.71E-01		2.53E-02	1.00E+00		-1.80E+00	3.75E-08	Down	-2.95E+00	1.27E-12	Down	null	null		null	null								

Unigene32965_All	433	0.00	36.16	15.62	0.00	0.00	0.00	0.00	0.00	0.00	1.51E+01	5.92E-90	Up	1.39E+01	9.22E-38	Up	null	null		null	null		null	null		null	null		Unigene32965_All//sp|Q9U8W7|TL5B_TACTR/|3.00E-24//Techylectin-5B OS=Tachypleus tridentatus PE=1 SV=1						swissprot -
Unigene3297_All	1864	13.98	5.22	6.88	6.87	3.86	3.90	2.79	2.58	2.29	-1.42E+00	2.92E-33	Down	-1.02E+00	3.19E-19	Down	-8.31E-01	1.02E-08		-8.16E-01	1.19E-07		-1.14E-01	6.55E-01		-2.87E-01	2.30E-01		Unigene3297_All//gi|240256121|ref|NP_194990.4|//0.00E+00//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|240256123|ref|NP_001119101.4| protein binding / zinc ion binding [Arabidopsis thaliana] >gi|259016138|sp|Q9M081.2|SC24B_ARATH RecName: Full=Protein transport protein Sec24-like At4g32640	Unigene3297_All//0.00E+00//AT4G32640| protein binding / zinc ion binding	Unigene3297_All//5.00E-75//TC172944			GO:0006950//GO:0009536//GO:0012507//GO:0015031//GO:0046914//GO:0048193	nr +
Unigene32970_All	420	0.00	4.83	2.54	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.54E-11	Up	1.13E+01	6.62E-06	Up	null	null		null	null		null	null		null	null		Unigene32970_All//gi|255593650|ref|XP_002535920.1|//7.00E-21//alpha-amylase, putative [Ricinus communis] >gi|223521525|gb|EEF26463.1| alpha-amylase, putative [Ricinus communis]					GO:0003824	nr +
Unigene32974_All	364	0.00	5.43	3.80	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.97E-11	Up	1.19E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene32974_All//gi|18422605|ref|NP_568651.1|//2.00E-53//SAG12 (SENESCENCE-ASSOCIATED GENE 12); cysteine-type peptidase [Arabidopsis thaliana] >gi|9758936|dbj|BAB09317.1| senescence-specific cysteine protease [Arabidopsis thaliana]	Unigene32974_All//4.00E-45//AT5G45890| SAG12 (SENESCENCE-ASSOCIATED GENE 12); cysteine-type peptidase				GO:0000323//GO:0004175//GO:0009725//GO:0010260//GO:0016628//GO:0019538//GO:0031410//GO:0050832	nr -
Unigene32976_All	487	0.21	0.21	0.00	9.10	2.19	2.23	1.22	0.43	0.08	-4.64E-02	9.89E-01		-7.75E+00	3.93E-01		-2.05E+00	4.02E-12	Down	-2.03E+00	1.62E-10	Down	-1.50E+00	9.13E-02		-3.89E+00	1.09E-03		Unigene32976_All//gi|297806791|ref|XP_002871279.1|//2.00E-13//F box protein family [Arabidopsis lyrata subsp. lyrata] >gi|34013883|gb|AAQ56109.1| F box protein family [Arabidopsis lyrata subsp. lyrata] >gi|297317116|gb|EFH47538.1| F box protein family [Arabidopsis lyrata subsp. lyrata]	Unigene32976_All//3.00E-13//AT5G07610| F-box family protein					nr -
Unigene3298_All	1399	1.38	8.26	2.32	0.64	0.84	1.42	10.18	17.99	26.17	2.58E+00	2.23E-32	Up	7.47E-01	3.82E-02		3.85E-01	5.89E-01		1.15E+00	1.42E-02		8.20E-01	1.44E-16		1.36E+00	2.78E-54	Up			Unigene3298_All//0.00E+00//gi|48749000|gb|C0079519.1|C0079519				ESTscan +
Unigene32980_All	617	0.00	0.33	0.00	0.16	0.17	0.00	2.19	6.30	4.00	8.36E+00	1.36E-01		null	null		5.18E-02	9.66E-01		-7.34E+00	3.99E-01		1.52E+00	2.43E-07	Up	8.68E-01	1.30E-02		Unigene32980_All//gi|79565313|ref|NP_180417.2|//5.00E-25//LBD11 (LOB DOMAIN-CONTAINING PROTEIN 11) [Arabidopsis thaliana]	Unigene32980_All//3.00E-26//AT2G28500| LBD11 (LOB DOMAIN-CONTAINING PROTEIN 11)	Unigene32980_All//2.00E-56//DT461920		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0043231	nr -
Unigene32981_All	2401	0.00	15.24	4.39	0.00	0.01	0.00	0.00	0.00	0.00	1.39E+01	4.28E-211	Up	1.21E+01	3.32E-59	Up	3.84E+00	8.29E-01		null	null		null	null		null	null		Unigene32981_All//gi|301108545|ref|XP_002903354.1|//9.00E-06//mucin-like protein [Phytophthora infestans T30-4] >gi|262097726|gb|EEY55778.1| mucin-like protein [Phytophthora infestans T30-4]						nr -
Unigene32982_All	358	22.36	18.54	33.91	23.65	31.36	13.25	15.12	164.38	13.35	-2.70E-01	2.14E-01		6.01E-01	3.49E-04		4.07E-01	1.49E-02		-8.37E-01	1.71E-05		3.44E+00	8.03E-268	Up	-1.79E-01	4.68E-01		Unigene32982_All//gi|226509426|ref|NP_001149968.1|//2.00E-34//LOC100283595 [Zea mays] >gi|195635793|gb|ACG37365.1| auxin-induced protein PCNT115 [Zea mays]	Unigene32982_All//5.00E-27//AT1G60690| aldo/keto reductase family protein	Unigene32982_All//2.00E-80//gi|78331636|gb|DT551910.1|DT551910		ko00053|Ascorbate and aldarate metabolism	GO:0004033//GO:0008152	nr +
Unigene32983_All	355	0.00	0.00	0.00	0.00	0.00	0.00	12.03	10.36	2.02	null	null		null	null		null	null		null	null		-2.15E-01	4.59E-01		-2.57E+00	1.13E-15	Down	Unigene32983_All//gi|238014838|gb|ACR38454.1|//1.00E-07//unknown [Zea mays]		Unigene32983_All//2.00E-12//DW234221				nr +
Unigene32984_All	325	0.00	13.25	4.59	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.56E-24	Up	1.22E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene32984_All//gi|226498630|ref|NP_001147418.1|//7.00E-12//LOC100281027 [Zea mays] >gi|195611236|gb|ACG27448.1| acyl-CoA-binding protein [Zea mays]	Unigene32984_All//4.00E-10//AT1G31812| ACBP6 (acyl-CoA-binding protein 6); acyl-CoA binding / phosphatidylcholine binding					nr -
Unigene3299_All	215	4.62	1.89	1.49	3.01	2.08	3.57	1.77	4.67	11.67	-1.29E+00	6.74E-02		-1.64E+00	3.43E-02		-5.33E-01	5.38E-01		2.46E-01	7.57E-01		1.40E+00	2.82E-02		2.72E+00	6.70E-10	Up	Unigene3299_All//gi|195637712|gb|ACG38324.1|//6.00E-28//inositol-tetrakisphosphate 1-kinase 3 [Zea mays]	Unigene3299_All//1.00E-27//AT4G08170| inositol 1,3,4-trisphosphate 5/6-kinase family protein	Unigene3299_All//3.00E-13//TC178329		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0006950//GO:0032559//GO:0043231//GO:0043647//GO:0046872//GO:0051765//GO:0051766	nr -
Unigene32991_All	487	0.00	8.53	3.72	0.00	0.00	0.00	0.00	0.00	0.08	1.31E+01	1.16E-23	Up	1.19E+01	5.69E-10	Up	null	null		null	null		null	null		6.35E+00	6.45E-01		Unigene32991_All//gi|57999636|dbj|BAD88438.1|//2.00E-44//60S ribosomal protein L6 CgRPL6 [Chara globularis]	Unigene32991_All//6.00E-35//AT1G74060| 60S ribosomal protein L6 (RPL6B)			ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene32992_All	332	0.00	0.00	0.00	2.55	0.62	0.00	0.00	0.25	0.00	null	null		null	null		-2.04E+00	9.04E-03		-1.13E+01	2.43E-05	Down	7.98E+00	4.01E-01		null	null			Unigene32992_All//3.00E-05//AT1G07476| unknown protein	Unigene32992_All//1.00E-114//DW517956				
Unigene32993_All	745	0.07	0.48	0.00	0.13	0.23	0.18	2.04	1.74	6.15	2.76E+00	9.59E-02		-6.13E+00	6.23E-01		7.90E-01	7.71E-01		4.44E-01	8.61E-01		-2.32E-01	6.26E-01		1.59E+00	2.92E-09	Up	Unigene32993_All//gi|227206124|dbj|BAH57117.1|//1.00E-90//AT5G47720 [Arabidopsis thaliana]	Unigene32993_All//5.00E-12//AT5G47720| acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative	Unigene32993_All//2.00E-57//BE055424		ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00900|Terpenoid backbone biosynthesis//ko00072|Synthesis and degradation of ketone bodies	GO:0016453	nr -
Unigene32995_All	540	0.00	0.00	0.00	0.55	2.55	1.25	0.00	0.08	0.00	null	null		null	null		2.20E+00	4.94E-04	Up	1.18E+00	2.08E-01		6.27E+00	6.34E-01		null	null		Unigene32995_All//gi|145360286|ref|NP_180032.2|//2.00E-51//carboxylesterase/ hydrolase, acting on ester bonds [Arabidopsis thaliana] >gi|229890094|sp|Q9SJA9.2|GDL39_ARATH RecName: Full=GDSL esterase/lipase At2g24560; AltName: Full=Extracellular lipase At2g24560; Flags: Precursor	Unigene32995_All//1.00E-52//AT2G24560| carboxylesterase/ hydrolase, acting on ester bonds	Unigene32995_All//0.00E+00//TC159824			GO:0016787//GO:0044238	nr +
Unigene32998_All	538	0.00	9.51	4.16	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	3.53E-29	Up	1.20E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene32998_All//sp|B4GX43|MAEL2_DROPE/|2.00E-33//Protein maelstrom 2 OS=Drosophila persimilis GN=mael2 PE=3 SV=2						swissprot +
Unigene32999_All	851	0.00	7.26	3.00	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.70E-35	Up	1.16E+01	4.20E-14	Up	null	null		null	null		null	null		null	null								
Unigene33_All	2242	3.94	8.11	4.58	6.73	6.42	6.69	11.47	12.84	15.65	1.04E+00	1.42E-14	Up	2.17E-01	2.78E-01		-6.85E-02	7.04E-01		-9.50E-03	9.46E-01		1.64E-01	9.58E-02		4.49E-01	1.41E-08		Unigene33_All//gi|224122778|ref|XP_002330477.1|//0.00E+00//histone acetyltransferase [Populus trichocarpa] >gi|222871889|gb|EEF09020.1| histone acetyltransferase [Populus trichocarpa]	Unigene33_All//0.00E+00//AT1G79000| HAC1 (HISTONE ACETYLTRANSFERASE OF THE CBP FAMILY 1); H3/H4 histone acetyltransferase/ histone acetyltransferase/ transcription cofactor	Unigene33_All//0.00E+00//TC162741				nr -
Unigene330_All	1140	0.50	0.00	0.00	0.44	0.94	0.48	4.23	1.91	2.06	-8.98E+00	1.52E-03		-8.98E+00	2.60E-03		1.10E+00	1.09E-01		1.22E-01	9.21E-01		-1.15E+00	4.35E-06	Down	-1.04E+00	1.76E-05	Down	Unigene330_All//gi|38260678|gb|AAR15492.1|//1.00E-111//glycosyl hydrolase [Arabidopsis arenosa]	Unigene330_All//5.00E-103//AT5G14950| GMI1 (GOLGI ALPHA-MANNOSIDASE II); alpha-mannosidase	Unigene330_All//6.00E-92//DW237521		ko00510|N-Glycan biosynthesis//ko00511|Other glycan degradation		nr -
Unigene3300_All	1524	2.61	1.06	0.70	1.27	2.37	1.42	1.94	4.96	9.75	-1.29E+00	4.46E-05	Down	-1.90E+00	8.11E-08	Down	8.96E-01	4.38E-03		1.58E-01	7.29E-01		1.35E+00	1.64E-11	Up	2.33E+00	3.34E-46	Up	Unigene3300_All//gi|156752167|gb|ABU93834.1|//1.00E-121//inositol phosphate kinase [Glycine max]	Unigene3300_All//2.00E-84//AT4G33770| inositol 1,3,4-trisphosphate 5/6-kinase family protein	Unigene3300_All//4.00E-180//gi|78335460|gb|DT555734.1|DT555734		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene33002_All	652	0.24	0.54	0.33	0.46	0.32	0.14	0.19	3.97	1.83	1.18E+00	3.72E-01		4.41E-01	7.75E-01		-5.33E-01	6.79E-01		-1.73E+00	2.89E-01		4.35E+00	1.60E-14	Up	3.24E+00	7.29E-06	Up	Unigene33002_All//gi|115479725|ref|NP_001063456.1|//2.00E-10//Os09g0474300 [Oryza sativa Japonica Group] >gi|113631689|dbj|BAF25370.1| Os09g0474300 [Oryza sativa Japonica Group]	Unigene33002_All//3.00E-11//AT2G04030| CR88; ATP binding	Unigene33002_All//1.00E-54//ES837739		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0006970//GO:0009416//GO:0009526//GO:0009532//GO:0010035//GO:0016020//GO:0032559	nr -
Unigene33006_All	521	0.00	0.00	0.00	0.00	0.00	0.00	3.41	3.37	0.15	null	null		null	null		null	null		null	null		-1.66E-02	1.01E+00		-4.48E+00	1.00E-10	Down	Unigene33006_All//gi|159466042|ref|XP_001691218.1|//1.00E-57//ribosomal protein S4, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158279190|gb|EDP04951.1| ribosomal protein S4, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii]	Unigene33006_All//3.00E-55//AT5G38420| 40S ribosomal protein S4 (RPS4D)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0031981//GO:0042221	nr -
Unigene33009_All	1378	0.08	35.74	15.30	0.07	0.00	0.00	0.00	0.00	0.00	8.88E+00	1.90E-279	Up	7.66E+00	6.18E-115	Up	-6.18E+00	3.13E-01		-6.18E+00	3.99E-01		null	null		null	null		Unigene33009_All//gi|226497070|ref|NP_001147047.1|//1.00E-112//60S ribosomal protein L4 [Zea mays] >gi|195606864|gb|ACG25262.1| 60S ribosomal protein L4 [Zea mays]	Unigene33009_All//2.00E-102//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)	Unigene33009_All//9.00E-33//BQ405438		ko03010|Ribosome		nr -
Unigene33011_All	603	0.00	0.00	0.00	0.33	0.34	0.75	5.75	1.59	2.64	null	null		null	null		5.23E-02	9.88E-01		1.18E+00	3.38E-01		-1.85E+00	1.67E-08	Down	-1.12E+00	1.22E-04	Down	Unigene33011_All//gi|297720735|ref|NP_001172729.1|//4.00E-41//Os01g0935200 [Oryza sativa Japonica Group] >gi|148921414|dbj|BAF64446.1| HAP3 subunit of HAP complex [Oryza sativa Japonica Group] >gi|255674039|dbj|BAH91459.1| Os01g0935200 [Oryza sativa Japonica Group]	Unigene33011_All//6.00E-39//AT1G08030| NF-YB4 (NUCLEAR FACTOR Y, SUBUNIT B4); transcription factor		CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication	GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene33012_All	513	0.31	0.69	0.00	0.49	0.20	0.09	7.50	2.04	3.18	1.18E+00	3.72E-01		-8.26E+00	2.44E-01		-1.27E+00	4.24E-01		-2.46E+00	2.23E-01		-1.88E+00	1.53E-09	Down	-1.24E+00	9.41E-06	Down							
Unigene33015_All	517	1.42	1.67	0.00	0.87	0.47	0.52	5.97	8.65	5.32	2.34E-01	7.28E-01		-1.05E+01	4.13E-04	Down	-8.95E-01	4.13E-01		-7.27E-01	5.32E-01		5.35E-01	3.82E-02		-1.67E-01	6.11E-01		Unigene33015_All//gi|297810771|ref|XP_002873269.1|//9.00E-10//ubiquitin-specific protease 12 [Arabidopsis lyrata subsp. lyrata] >gi|297319106|gb|EFH49528.1| ubiquitin-specific protease 12 [Arabidopsis lyrata subsp. lyrata]	Unigene33015_All//5.00E-11//AT5G06600| UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene33015_All//1.00E-38//TC174664				nr -
Unigene33016_All	407	0.00	0.12	0.00	0.61	0.00	0.00	4.36	0.00	12.33	6.96E+00	6.16E-01		null	null		-9.26E+00	4.18E-02		-9.26E+00	7.33E-02		-1.21E+01	1.41E-12	Down	1.50E+00	2.58E-09	Up	Unigene33016_All//gi|30684705|ref|NP_173061.2|//2.00E-10//WAKL7 (wall associated kinase-like 7); protein serine/threonine kinase [Arabidopsis thaliana]	Unigene33016_All//1.00E-11//AT1G16090| WAKL7 (wall associated kinase-like 7); protein serine/threonine kinase	Unigene33016_All//1.00E-81//TC134682			GO:0016301	nr -
Unigene33017_All	479	0.00	5.50	2.22	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.45E-15	Up	1.11E+01	6.62E-06	Up	null	null		null	null		null	null		null	null		Unigene33017_All//sp|O76217|PE1_ANOGA//1.00E-09//Peritrophin-1 OS=Anopheles gambiae GN=Aper1 PE=2 SV=2						swissprot -

Unigene33019_All	281	0.00	36.60	10.80	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	6.12E-59	Up	1.34E+01	8.92E-17	Up	null	null		null	null		null	null		null	null		Unigene33019_All//gi|149391425|gb|ABR25730.1|//7.00E-31//ubiquitin fusion protein [Oryza sativa Indica Group]	Unigene33019_All//3.00E-32//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene33019_All//2.00E-14//TC140719		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0003981//GO:0003246	nr +
Unigene33025_All	501	2.09	2.83	0.74	2.09	2.61	2.97	50.21	162.26	93.91	4.39E-01	4.25E-01		-1.49E+00	4.42E-02		3.23E-01	6.11E-01		5.11E-01	3.95E-01		1.69E+00	4.49E-161	Up	9.03E-01	2.42E-36		Unigene33025_All//gi|457744|emb|CAA54869.1|//9.00E-33//inorganic pyrophosphatase [Nicotiana tabacum]	Unigene33025_All//3.00E-33//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene33025_All//0.00E+00//EV492930		ko00190|Oxidative phosphorylation	GO:0006570//GO:0006818//GO:0015405//GO:0016462//GO:0016628//GO:0031410	nr -
Unigene33029_All	535	0.00	0.00	0.00	0.00	0.26	0.42	12.96	1.17	1.49	null	null		null	null		8.01E+00	3.18E-01		8.72E+00	1.19E-01		-3.47E+00	2.62E-32	Down	-3.12E+00	2.04E-30	Down	Unigene33029_All//gi|224062117|ref|XP_002300763.1|//4.00E-11//predicted protein [Populus trichocarpa] >gi|222842889|gb|EEE80036.1| predicted protein [Populus trichocarpa]	Unigene33029_All//2.00E-09//AT5G42785| unknown protein	Unigene33029_All//6.00E-07//CO123727				nr -
Unigene33030_All	401	0.00	4.17	1.06	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.54E-09	Up	1.01E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene33030_All//gi|33327349|gb|AAQ09007.1|//1.00E-36//superoxidase dismutase [Solanum lycopersicum]	Unigene33030_All//4.00E-36//AT3G28190| CSD2 (COPPER/ZINC SUPEROXIDE DISMUTASE 2); superoxide dismutase			ko04146|Peroxisome	GO:0003824//GO:0005576//GO:0006801//GO:0006950//GO:0009314//GO:0009532//GO:0010038//GO:0016209	nr -
Unigene33031_All	276	0.00	6.24	3.09	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	7.99E-10	Up	1.16E+01	9.02E-05	Up	null	null		null	null		null	null		null	null		Unigene33031_All//gi|225685855|dbj|BAH30214.1|//1.00E-28//methionine S-adenosyl transferase [Ditylum brightwellii]	Unigene33031_All//9.00E-26//AT3G17390| MTO3 (METHIONINE OVER-ACCUMULATOR 3); methionine adenosyltransferase			ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0016765//GO:0032559//GO:0044237//GO:0044424//GO:0046872	nr -
Unigene33036_All	309	0.00	0.00	2.59	0.16	0.22	0.15	1.78	4.73	0.26	null	null		1.13E+01	1.72E-04	Up	4.68E-01	9.58E-01		-1.41E-01	9.52E-01		1.41E-00	5.47E-03		-2.79E+00	7.96E-03									
Unigene33038_All	439	0.00	0.00	0.00	0.00	0.00	0.00	3.76	2.76	0.36	null	null		null	null		null	null		null	null		-4.44E-01	3.61E-01		-3.37E+00	2.88E-08	Down								ESTscan +
Unigene33039_All	320	0.00	2.53	1.16	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	9.38E-05	Up	1.02E+01	2.50E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene33040_All	343	0.61	0.15	1.24	11.91	6.73	3.03	0.37	0.85	0.81	-2.05E+00	3.34E-01		1.03E+00	3.96E-01		-8.24E-01	3.50E-03		-1.98E+00	2.12E-09	Down	1.21E+00	3.92E-01		1.14E+00	3.99E-01		Unigene33040_All//gi|28466875|gb|AAO44046.1|//2.00E-11//At1g77400 [Arabidopsis thaliana] >gi|51971947|dbj|BAD14638.1| At1g77400 [Arabidopsis thaliana]	Unigene33040_All//2.00E-05//AT1G21695| hydroxyproline-rich glycoprotein family protein	Unigene33040_All//4.00E-87//DW500061				nr +
Unigene33041_All	399	0.52	1.78	1.60	1.50	0.95	1.25	0.00	0.63	1.30	1.76E+00	5.60E-02		1.61E+00	1.11E-01		-6.58E-01	4.78E-01		-2.67E-01	7.57E-01		9.30E+00	4.31E-02		1.03E+01	6.13E-04	Up	Unigene33041_All//gi|30694992|ref|NP_191500.2|//2.00E-10//protein kinase family protein [Arabidopsis thaliana] >gi|680052253|sp|Q9LX30.2|GCN2_ARATH RecName: Full=Probable serine/threonine-protein kinase GCN2 >gi|24940154|emb|CAD30860.1| GCN2 homologue [Arabidopsis thaliana]	Unigene33041_All//4.00E-08//AT3G59410| protein kinase family protein					nr +
Unigene33042_All	565	0.28	0.36	0.38	0.18	0.30	0.00	0.15	1.04	3.95	3.69E-01	8.16E-01		4.41E-01	7.75E-01		7.89E-01	7.71E-01		-7.46E+00	3.99E-01		2.79E+00	8.26E-03		4.72E+00	2.07E-13	Up	Unigene33042_All//gi|18379277|ref|NP_565274.1|//2.00E-18//ankyrin repeat family protein [Arabidopsis thaliana] >gi|75315914|sp|Q9ZU96.1|Y2168_ARATH RecName: Full=Ankyrin repeat-containing protein At2g01680 >gi|4220480|gb|AAD12703.1| expressed protein [Arabidopsis thaliana]	Unigene33042_All//9.00E-20//AT2G01680| ankyrin repeat family protein	Unigene33042_All//2.00E-10//TC171065		GO:0016020	nr -
Unigene33045_All	339	0.31	3.14	0.47	5.29	6.91	4.80	0.25	0.00	0.47	3.35E+00	2.17E-04	Up	6.10E-01	7.48E-01		3.85E-01	4.03E-01		-1.41E-01	7.72E-01		-7.96E+00	4.03E-01		9.15E-01	6.24E-01									
Unigene33049_All	385	2.45	0.26	0.00	1.29	0.36	1.64	1.10	0.33	0.72	-3.22E+00	6.77E-04	Down	-1.13E+01	3.34E-05	Down	-1.85E+00	8.43E-02		3.44E-01	6.99E-01		-1.75E+00	1.24E-01		-6.01E-01	5.53E-01		Unigene33049_All//gi|115489008|ref|NP_001066991.1|//7.00E-58//0s12g0554400 [Oryza sativa Japonica Group] >gi|77556742|gb|ABA99538.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649498|db|BAF30010.1| Os12g0554400 [Oryza sativa Japonica Group]	Unigene33049_All//1.00E-60//AT5G54440| unknown protein	Unigene33049_All//7.00E-117//TC172864				nr +
Unigene33051_All	343	5.80	1.48	4.50	1.16	1.00	0.40	0.00	0.00	0.00	-1.97E+00	1.10E-04	Down	-3.65E-01	4.45E-01		-2.11E-01	8.25E-01		-1.56E+00	2.31E-01		null	null		null	null				Unigene33051_All//3.00E-66//gi|48798885|gb|CO100199.1|CO100199				
Unigene33053_All	617	0.85	1.23	0.60	0.32	0.50	0.15	0.82	2.10	2.71	5.39E-01	5.02E-01		-4.89E-01	6.32E-01		6.38E-01	6.95E-01		-1.14E+00	5.69E-01		1.35E+00	1.27E-02		1.72E+00	2.90E-04	Up	Unigene33053_All//gi|297826341|ref|XP_002881053.1|//3.00E-35//glutathione S-transferase 19 [Arabidopsis lyrata subsp. lyrata] >gi|297326892|gb|EFH57312.1| glutathione S-transferase 19 [Arabidopsis lyrata subsp. lyrata]	Unigene33053_All//1.00E-36//AT2G29490| ATGSTU1 (GLUTATHIONE S-TRANSFERASE TAU 1); glutathione transferase			ko00480|Glutathione metabolism	GO:0016846	nr -
Unigene33054_All	345	0.00	4.26	2.01	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.11E-08	Up	1.10E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene33054_All//gi|15225026|ref|NP_178969.1|//1.00E-53//AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE); alanine-glyoxylate transaminase/ serine-glyoxylate transaminase/ serine-pyruvate transaminase [Arabidopsis thaliana] >gi|30678921|ref|NP_849951.1| AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE); alanine-glyoxylate transaminase/ serine-glyoxylate transaminase/ serine-pyruvate transaminase [Arabidopsis thaliana] >gi|90185106|sp|Q56YA5.2|SGAT_ARATH RecName: Full=Serine--glyoxylate aminotransferase; AltName: Full=Alanine--glyoxylate aminotransferase; Short=AGT; AltName: Full=Serine--pyruvate aminotransferase >gi|3288821|gb|AAC26854.1| alanine:glyoxylate aminotransferase [Arabidopsis thaliana] >gi|4733989|gb|AAD28669.1| alanine-glyoxylate aminotransferase [Arabidopsis thaliana]	Unigene33054_All//5.00E-55//AT2G13360| AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE); alanine-glyoxylate transaminase/ serine-glyoxylate transaminase/ serine-pyruvate transaminase	Unigene33054_All//9.00E-39//TC139658		ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism	GO:0005576//GO:0008483//GO:0009532//GO:0016020//GO:0042579//GO:0043094//GO:0048037	nr -
Unigene33056_All	493	0.00	6.17	2.38	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.67E-17	Up	1.12E+01	1.77E-06	Up	null	null		null	null		null	null		null	null									
Unigene33057_All	356	0.00	1.14	0.75	0.00	0.00	0.76	52.97	73.38	274.84	1.02E+01	1.38E-02		9.55E+00	8.01E-02		null	null		9.57E+00	7.03E-02		4.70E-01	6.79E-07		2.38E+00	0.00E+00	Up	Unigene33057_All//gi|224054180|ref|XP_002298131.1|//1.00E-17//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845389|gb|EEE82936.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene33057_All//7.00E-15//AT4G03070| AOP1; oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene33057_All//1.00E-93//gi|73860785|gb|DT463524.1|DT463524			GO:0016491	nr +
Unigene33058_All	644	0.00	0.00	0.00	0.00	0.00	0.00	3.22	2.01	0.87	null	null		null	null		null	null		null	null		-6.77E-01	9.28E-02		-1.89E+00	9.50E-06	Down	Unigene33058_All//gi|115475257|ref|NP_001061225.1|//2.00E-24//0s08g0203700 [Oryza sativa Japonica Group] >gi|113623194|dbj|BAF23139.1| Os08g0203700 [Oryza sativa Japonica Group]	Unigene33058_All//4.00E-25//AT1G56130| leucine-rich repeat family protein / protein kinase family protein	Unigene33058_All//4.00E-30//gi|48740646|gb|CO071165.1|CO071165			GO:0000166//GO:0004713//GO:0008152//GO:0016020//GO:0016491//GO:0043140	nr +
Unigene33059_All	288	0.00	0.00	0.00	0.00	0.00	0.00	11.74	2.76	3.04	null	null		null	null		null	null		null	null		-2.09E+00	1.27E-09	Down	-1.95E+00	3.54E-09	Down								
Unigene33066_All	773	0.07	0.00	0.00	1.29	0.36	0.00	0.27	0.16	2.37	-6.08E+00	6.12E-01		-6.08E+00	6.23E-01		-1.85E+00	7.41E-03		-1.03E+01	2.97E-06	Down	-7.54E-01	6.32E-01		3.12E+00	2.25E-08	Up	Unigene33066_All//gi|297719939|ref|NP_001172331.1|//3.00E-61//0s01g0355000 [Oryza sativa Japonica Group] >gi|53791352|dbj|BAD52598.1| pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa Japonica Group] >gi|255673214|dbj|BAH91061.1| Os01g0355000 [Oryza sativa Japonica Group]	Unigene33066_All//3.00E-44//AT2G03880| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene33070_All	217	0.00	0.00	1.23	1.84	1.11	1.25	2.73	9.05	4.41	null	null		1.03E+01	8.01E-02		-7.25E-01	5.46E-01		-5.56E-01	6.38E-01		1.73E+00	9.55E-05	Up	6.92E-01	2.60E-01				Unigene33070_All//4.00E-52//TC165946				
Unigene33071_All	293	0.00	5.02	3.27	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.11E-08	Up	1.17E+01	2.46E-05	Up	null	null		null	null		null	null		null	null									
Unigene33073_All	334	0.00	0.00	0.64	0.15	0.31	0.00	0.51	1.25	3.10	null	null		9.32E+00	1.41E-01		1.05E+00	8.08E-01		-7.22E+00	6.35E-01		1.31E+00	2.34E-01		2.61E+00	2.37E-04	Up			Unigene33073_All//7.00E-21//TC176389				
Unigene33075_All	459	0.00	0.00	0.00	0.00	0.00	0.00	9.03	1.82	1.22	null	null		null	null		null	null		null	null		-2.31E+00	4.72E-13	Down	-2.89E+00	3.61E-17	Down	Unigene33075_All//gi|11466466|ref|NP_038169.1|//9.00E-41//apocytochrome b [Chrysodidymus synuroideus] >gi|7110463|gb|AAF36935.1|AF222718_9 apocytochrome b [Chrysodidymus synuroideus]	Unigene33075_All//6.00E-31//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.			ko00190|Oxidative phosphorylation	GO:0003824//GO:0022900//GO:0043231//GO:0044425	nr +
Unigene33079_All	357	0.00	6.10	5.97	0.00	0.00	0.00	0.24	0.00	0.00	1.26E+01	2.11E-12	Up	1.25E+01	9.78E-12	Up	null	null		null	null		-7.89E+00	4.03E-01		-7.89E+00	3.58E-01		Unigene33079_All//gi|226531828|ref|NP_001148017.1|//3.00E-30//40S ribosomal protein S25-1 [Zea mays] >gi|195615172|gb|ACG29416.1| 40S ribosomal protein S25-1 [Zea mays] >gi|195658723|gb|ACG48829.1| 40S ribosomal protein S25-1 [Zea mays]	Unigene33079_All//1.00E-21//AT4G34555| 40S ribosomal protein S25, putative			ko03010|Ribosome	GO:0010467//GO:0015935//GO:0016020	nr +
Unigene33081_All	354	0.00	2.43	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.95E-05	Up	1.04E+01	7.48E-03		null	null		null	null		null	null		null	null									
Unigene33082_All	312	0.84	0.49	0.17	4.79	2.21	0.29	0.14	0.00	0.26	-7.83E-01	6.20E-01		-2.30E+00	2.43E-01		-1.12E+00	3.10E-02		-4.05E+00	3.05E-07	Down	-7.08E+00	6.57E-01		9.15E-01	7.50E-01		Unigene33082_All//gi|224128266|ref|XP_002320284.1|//4.00E-07//predicted protein [Populus trichocarpa] >gi|222861057|gb|EEE98599.1| predicted protein [Populus trichocarpa]	Unigene33082_All//7.00E-05//AT3G62370| unknown protein				GO:0005506//GO:0008152	nr +
Unigene33083_All	702	0.00	0.00	0.00	0.00	0.00	0.00	3.01	1.96	0.28	null	null		null	null		null	null		null	null		-6.16E-01	1.26E-01		-3.41E+00	1.68E-10	Down	Unigene33083_All//gi|116222231|gb|ABJ80979.1|//1.00E-107//alpha tubulin [Porphyra yezoensis]	Unigene33083_All//2.00E-98//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene33083_All//2.00E-38//DR460752		ko04145|Phagosome		nr -

Unigene3309_All	1331	2.28	5.67	3.88	3.71	5.87	2.71	9.59	12.00	19.40	1.31E+00	4.53E-09	Up	7.67E-01	5.09E-03		6.65E-01	8.03E-04		-4.49E-01	1.10E-01		3.22E-01	1.15E-02		1.02E+00	1.56E-24	Up	Unigene3309_All//gi|18391484|ref|NP_563922.1|//1.00E-77//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|4850408|gb|AAD31078.1|AC007357_27 Contains PF|00097 Zinc finger (C3HC4) ring finger motif [Arabidopsis thaliana] >gi|87116602|gb|ABD19665.1|At1g13195 [Arabidopsis thaliana]	Unigene3309_All//1.00E-76//AT1G13195| zinc finger (C3HC4-type RING finger) family protein	Unigene3309_All//0.00E+00//TC175551			GO:0046914	nr -
Unigene33094_All	227	12.68	331.92	173.82	2.63	6.37	6.57	0.00	0.00	0.00	4.71E+00	0.00E+00	Up	3.78E+00	6.34E-155	Up	1.27E+00	2.38E-02		1.32E+00	1.96E-02		null	null		null	null			Unigene33094_All//6.00E-110//gi|13244864|gb|BE053296.2|BE053296				
Unigene33095_All	269	0.00	0.19	0.00	0.37	0.00	0.00	2.51	1.09	0.15	7.56E+00	6.16E-01		null	null		-8.53E+00	3.13E-01		-8.53E+00	3.99E-01		-1.21E+00	1.34E-01		-4.09E+00	3.10E-04	Down	Unigene33095_All//gi|297833634|ref|XP_002884699.1|//2.00E-23//D-alanine--D-alanine ligase family [Arabidopsis lyrata subsp. lyrata] >gi|297330539|gb|EFH60958.1| D-alanine--D-alanine ligase family [Arabidopsis lyrata subsp. lyrata]	Unigene33095_All//3.00E-23//AT3G08840| D-alanine--D-alanine ligase family	Unigene33095_All//3.00E-121//gi|78347707|gb|DT567981.1|DT567981			GO:0000270//GO:0009536//GO:0016881//GO:0030312//GO:0032559	nr -
Unigene33097_All	411	0.00	2.59	1.17	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.81E-06	Up	1.02E+01	7.48E-03		null	null		null	null		null	null		null	null		Unigene33097_All//sp|Q11174|CHIT_CAEEL//3.00E-08//Probable endochitinase OS=Caenorhabditis elegans GN=cht-1 PE=1 SV=1						swissprot -
Unigene33100_All	693	0.76	10.89	1.69	1.15	1.74	0.72	0.37	0.66	0.52	3.85E+00	5.71E-31	Up	1.16E+00	8.16E-02		5.97E-01	3.69E-01		-6.82E-01	4.05E-01		8.58E-01	3.96E-01		4.99E-01	6.27E-01		Unigene33100_All//gi|21536613|gb|AAM60945.1|//4.00E-10//contains similarity to protein disulfide isomerase-related protein [Arabidopsis thaliana]	Unigene33100_All//2.00E-11//AT5G18120| ATAPRLJ (APR-like 7)	Unigene33100_All//0.00E+00//gi|78330515|gb|DT550789.1|DT550789			GO:0019725//GO:0031410	nr -
Unigene33103_All	467	0.11	0.00	0.00	1.28	0.59	0.00	1.54	2.24	1.88	-6.81E+00	6.12E-01		-6.81E+00	6.23E-01		-1.12E+00	2.26E-01		-1.03E+01	7.70E-04	Down	5.40E-01	3.95E-01		2.86E-01	6.45E-01								
Unigene33106_All	680	0.77	0.37	1.88	1.17	1.32	0.00	0.50	0.49	0.35	-1.05E+00	3.11E-01		1.29E+00	4.48E-02		1.68E-01	8.32E-01		-1.02E+01	4.90E-05	Down	-1.66E-02	1.02E+00		-5.01E-01	6.49E-01		Unigene33106_All//gi|15222660|ref|NP_173944.1|//6.00E-33//phosphoribulokinase/uridine kinase family protein [Arabidopsis thaliana]	Unigene33106_All//3.00E-34//AT1G26190| phosphoribulokinase/uridine kinase family protein				GO:0006164//GO:0006397//GO:0009975//GO:0019204//GO:0019206//GO:0032559//GO:0034708	nr -
Unigene33107_All	319	0.00	0.00	0.00	0.00	0.22	0.71	24.78	47.43	250.15	null	null		null	null		7.75E+00	6.09E-01		9.47E+00	1.19E-01		9.36E-01	1.15E-12		3.34E+00	0.00E+00	Up	Unigene33107_All//gi|224092400|ref|XP_002309592.1|//2.00E-16//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222855568|gb|EEE93115.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene33107_All//5.00E-13//AT1G52810| 2-oxoglutarate-dependent dioxygenase-related	Unigene33107_All//6.00E-154//gi|31407058|gb|CD486093.1|CD486093			GO:0016491	nr +
Unigene33110_All	297	0.00	0.00	0.00	0.67	3.13	5.32	0.43	0.42	0.40	null	null		null	null		2.22E+00	6.50E-03		2.99E+00	7.30E-06	Up	-1.66E-02	1.02E+00		-8.59E-02	9.69E-01				Unigene33110_All//2.00E-58//EV497559				
Unigene33112_All	349	0.00	0.00	0.00	0.00	0.00	0.00	8.00	7.90	2.05	null	null		null	null		null	null		null	null		-1.66E-02	9.96E-01		-1.96E+00	9.05E-08	Down								
Unigene33113_All	303	2.76	2.84	5.10	0.49	3.75	0.89	0.00	0.00	0.00	4.12E-02	9.74E-01		8.83E-01	1.15E-01		2.93E+00	2.06E-04	Up	8.59E-01	6.31E-01		null	null		null	null		Unigene33113_All//gi|297843724|ref|XP_002889743.1|//9.00E-09//catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297335585|gb|EFH66002.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene33113_All//4.00E-10//AT1G09340| CRB (CHLOROPLAST RNA BINDING); binding / catalytic/ coenzyme binding	Unigene33113_All//2.00E-116//C0079467			GO:0008152//GO:0043231//GO:0048037	nr +
Unigene33115_All	639	0.25	0.08	0.08	5.15	5.34	2.12	0.00	0.13	0.00	-1.63E+00	4.89E-01		-1.56E+00	5.33E-01		5.23E-02	9.00E-01		-1.28E+00	2.02E-04	Down	7.03E+00	4.01E-01		null	null		Unigene33115_All//gi|166203230|gb|ABY84655.1|//4.00E-21//transcription factor [Glycine max]	Unigene33115_All//7.00E-14//AT2G44745| WRKY family transcription factor	Unigene33115_All//1.00E-23//TC154919	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene33116_All	460	6.60	6.39	2.55	0.97	0.97	1.47	2.48	2.45	4.68	-4.63E-02	9.05E-01		-1.37E+00	3.96E-04	Down	-2.10E-03	9.69E-01		5.96E-01	5.26E-01		-1.67E-02	1.01E+00		9.14E-01	1.58E-02				Unigene33116_All//9.00E-120//ES846306				
Unigene33119_All	494	0.00	0.10	0.75	0.40	0.21	0.09	3.17	0.85	2.10	6.68E+00	6.16E-01		9.56E+00	2.50E-02		-9.48E-01	5.88E-01		-2.14E+00	3.47E-01		-1.90E+00	2.25E-04	Down	-5.95E-01	1.95E-01								
Unigene33121_All	422	5.95	4.56	4.80	12.39	9.38	8.03	0.80	0.20	5.00	-3.83E-01	3.58E-01		-3.12E-01	4.62E-01		-4.01E-01	1.28E-01		-6.27E-01	1.61E-02		-2.02E+00	1.36E-01		2.64E+00	3.33E-08	Up	Unigene33121_All//gi|118486324|gb|ABX85003.1|//4.00E-09//unknown [Populus trichocarpa]	Unigene33121_All//4.00E-06//AT1G01090| PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-transferring)	Unigene33121_All//1.00E-140//gi|78338539|gb|DT558813.1|DT558813		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)//ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis		nr +
Unigene33122_All	349	0.00	3.34	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.05E-06	Up	1.07E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene33122_All//sp|P10124|SRGN_HUMAN//1.00E-49//Serglycin OS=Homo sapiens GN=SRGN PE=1 SV=3						swissprot +
Unigene33124_All	297	0.00	0.00	2.33	0.00	0.70	0.00	0.00	0.00	0.00	null	null		1.12E+01	6.16E-04	Up	9.44E+00	1.57E-01		null	null		null	null		null	null								ESTscan -
Unigene33129_All	348	0.00	0.00	0.31	0.72	2.08	2.73	2.07	0.60	0.23	null	null		8.26E+00	3.98E-01		1.54E+00	8.92E-02		1.93E+00	1.48E-02		-1.78E+00	2.79E-02		-3.17E+00	8.09E-04	Down	Unigene33129_All//gi|224107585|ref|XP_002314526.1|//9.00E-18//flavine-containing monoxygenase [Populus trichocarpa] >gi|222863566|gb|EEF00697.1| flavine-containing monoxygenase [Populus trichocarpa]	Unigene33129_All//1.00E-18//AT5G43890| YUCCA5; monooxygenase			ko00380|Tryptophan metabolism	GO:0009850//GO:0016709//GO:0030554	nr -
Unigene3313_All	1991	1.84	1.58	0.43	5.10	5.97	4.31	7.48	2.83	3.40	-2.21E-01	5.13E-01		-2.10E+00	3.53E-08	Down	2.25E-01	2.12E-01		-2.44E-01	2.20E-01		-1.40E+00	5.32E-23	Down	-1.14E+00	2.29E-17	Down	Unigene3313_All//gi|145324891|ref|NP_001077692.1|//0.00E+00//FU (FUSED); protein serine/threonine kinase [Arabidopsis thaliana] >gi|72004129|gb|AAZ66048.1| fused [Arabidopsis thaliana]	Unigene3313_All//0.00E+00//AT1G50240| FU (FUSED); protein serine/threonine kinase	Unigene3313_All//0.00E+00//TC156460			GO:0004672//GO:0005488//GO:0007349//GO:0033205//GO:0044444	nr +
Unigene33138_All	385	0.00	0.00	0.00	0.00	0.00	0.00	4.50	1.41	4.14	null	null		null	null		null	null		null	null		-1.67E+00	3.96E-04	Down	-1.21E-01	7.74E-01								
Unigene33139_All	295	0.00	18.55	5.23	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	3.25E-31	Up	1.24E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene33139_All//gi|195654217|gb|ACG46576.1|//2.00E-08//acyl-CoA-binding / phosphatidylcholine binding [Zea mays]	Unigene33139_All//1.00E-07//AT1G31812| ACBP6 (acyl-CoA-binding protein 6); acyl-CoA binding / phosphatidylcholine binding					nr +
Unigene3314_All	1100	39.48	16.77	21.59	85.91	69.87	93.53	241.54	97.65	95.43	-1.24E+00	2.00E-44	Down	-8.71E-01	2.26E-24		-2.98E-01	8.99E-10		1.23E-01	2.44E-02		-1.31E+00	0.00E+00	Down	-1.34E+00	0.00E+00	Down	Unigene3314_All//gi|225462164|ref|XP_002266780.1|//0.00E+00//PREDICTED: similar to elongation factor 2 [Vitis vinifera]	Unigene3314_All//0.00E+00//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene3314_All//0.00E+00//TC161459			GO:0006950//GO:0008135//GO:0009536//GO:0010467//GO:0016020//GO:0017111//GO:0031981//GO:0032561//GO:0046914	nr -
Unigene33143_All	439	0.00	2.19	1.46	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.38E-05	Up	1.05E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene33143_All//gi|224004780|ref|XP_002296041.1|//5.00E-56//F-type H-ATPase beta subunit [Thalassiosira pseudonana CCMP1335] >gi|209586073|gb|ACI64758.1| F-type H-ATPase beta subunit [Thalassiosira pseudonana CCMP1335]	Unigene33143_All//9.00E-56//AT5G08680| ATP synthase beta chain, mitochondrial, putative	Unigene33143_All//4.00E-14//EX166995		ko00190|Oxidative phosphorylation	GO:0000275//GO:0015078//GO:0015662//GO:0015986//GO:0019829//GO:0032559	nr -
Unigene33144_All	293	0.00	0.00	0.00	0.00	0.00	0.00	2.16	1.14	0.14	null	null		null	null		null	null		null	null		-9.24E-01	2.63E-01		-3.99E+00	5.82E-04	Down	Unigene33144_All//gi|75174963|sp|Q9LNG5.1|PPP7L_ARATH//7.00E-10//RecName: Full=Serine/threonine-protein phosphatase 7 long form homolog >gi|8778513|gb|AAF79521.1|AC023673_9 F21D18.16 [Arabidopsis thaliana]	Unigene33144_All//3.00E-11//AT1G48120| calcineurin-like phosphoesterase family protein	Unigene33144_All//2.00E-11//gi|78334205|gb|DT554479.1|DT554479				nr +
Unigene33146_All	391	0.00	0.00	0.54	0.25	0.09	0.23	1.19	3.74	6.11	null	null		9.09E+00	1.41E-01		-1.53E+00	5.86E-01		-1.42E-01	9.50E-01		1.65E+00	1.52E-03		2.36E+00	3.39E-08	Up	Unigene33146_All//gi|224055675|ref|XP_002298597.1|//1.00E-25//lysine/histidine transporter [Populus trichocarpa] >gi|222845855|gb|EEE83402.1| lysine/histidine transporter [Populus trichocarpa]	Unigene33146_All//7.00E-12//AT5G40780| LHT1; amino acid transmembrane transporter	Unigene33146_All//2.00E-40//TC158865				nr -
Unigene33147_All	658	0.32	0.00	0.08	4.32	1.62	0.48	0.19	0.13	0.00	-8.31E+00	1.22E-01		-1.98E+00	3.81E-01		-1.41E+00	7.06E-05	Down	-3.17E+00	4.53E-11	Down	-6.02E-01	7.66E-01		-7.59E+00	2.00E-01		Unigene33147_All//gi|226492298|ref|NP_001149113.1|//8.00E-59//ubiquitin-conjugating enzyme E2 I [Zea mays] >gi|195624824|gb|ACG34242.1| ubiquitin-conjugating enzyme E2 I [Zea mays]	Unigene33147_All//3.00E-57//AT3G57870| SCE1 (SUMO CONJUGATION ENZYME 1); SUMO ligase	Unigene33147_All//0.00E+00//EE592623		ko04120|Ubiquitin mediated proteolysis	GO:0006464//GO:0016881//GO:0060255	nr +
Unigene33148_All	287	0.00	0.00	0.00	0.00	0.00	0.00	4.12	1.89	0.00	null	null		null	null		null	null		null	null		-1.12E+00	4.65E-02		-1.20E+01	8.15E-09	Down	Unigene33148_All//gi|301093682|ref|XP_002997686.1|//2.00E-32//60S ribosomal protein L3 [Phytophthora infestans T30-4] >gi|262109935|gb|EEY67987.1| 60S ribosomal protein L3 [Phytophthora infestans T30-4]	Unigene33148_All//2.00E-24//AT1G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene3315_All	2027	12.54	10.32	12.56	63.77	74.37	59.07	21.48	13.67	8.47	-2.81E-01	1.09E-02		1.40E-03	9.89E-01		2.22E-01	8.20E-09		-1.11E-01	2.20E-02		-6.52E-01	4.17E-19		-1.34E+00	1.24E-63	Down	Unigene3315_All//gi|82592920|sp|P92990.2|JP650_ARATH//0.00E+00//RecName: Full=Probable polygalacturonase non-catalytic subunit JP650; AltName: Full=Aromatic-rich glycoprotein JP650; Flags: Precursor >gi|31766860|gb|AAC18803.1| Identical to polygalacuronase isoenzyme 1 beta subunit homolog mRNA gb|U63373. EST gb|AA404878 comes from this gene [Arabidopsis thaliana]	Unigene3315_All//0.00E+00//AT1G70370| BURP domain-containing protein / polygalacturonase, putative	Unigene3315_All//0.00E+00//TC130181			GO:0005576	nr +
Unigene33150_All	503	0.00	0.00	0.21	2.67	3.29	0.54	0.92	0.33	0.00	null	null		7.73E+00	3.98E-01		2.97E-01	6.09E-01		-2.31E+00	4.01E-04	Down	-1.48E+00	1.53E-01		-9.85E+00	1.09E-03		Unigene33150_All//gi|77552695|gb|ABX95492.1|//2.00E-19//Zinc finger, C3HC4 type family protein [Oryza sativa (japonica cultivar-group)]	Unigene33150_All//2.00E-16//AT3G03550| zinc finger (C3HC4-type RING finger) family protein					nr +
Unigene33153_All	339	0.00	2.69	0.16	0.88	1.22	0.27	0.62	0.00	0.47	1.14E+01	2.62E-05	Up	7.30E+00	6.35E-01		4.67E-01	7.41E-01		-1.73E+00	2.89E-01		-9.28E+00	7.44E-02		-4.08E-01	7.55E-01				Unigene33153_All//6.00E-80//gi|78347707|gb|DT567981.1|DT567981				ESTscan +
Unigene33161_All	846	0.19	1.08	0.13	0.24	0.12	0.48	1.25	1.14	4.52	2.54E+00	3.88E-03		-5.59E-01	7.76E-01		-9.48E-01	5.88E-01		1.03E+00	4.28E-01		-1.37E-01	8.15E-01		1.86E+00	1.50E-09	Up			Unigene33161_All//1.00E-104//C0110770				
Unigene33162_All	262	0.00	3.87	1.63	0.19	0.53	0.52	0.48	0.48	0.15	1.19E+01	7.26E-06	Up	1.07E+01	1.38E-02		1.47E+00	6.19E-01		1.44E+00	6.38E-01		-1.65E-02	1.02E+00		-1.67E+00	4.77E-01				Unigene33162_All//2.00E-79//ES852319				
Unigene33163_All	1024	0.31	1.14	1.35	3.89	3.63	1.23	0.95	1.06	0.54	1.89E+00	6.32E-03		2.14E+00	1.38E-03		-9.97E-02	7.96E-01		-1.66E+00	2.41E-07	Down	1.60E-01	7.82E-01		-8.02E-01	1.83E-01		Unigene33163_All//gi|115483462|ref|NP_001065401.1|//1.00E-44//Os10g0563400 [Oryza sativa Japonica Group] >gi|31433537|gb|AAP55035.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113639933|dbj|BAF27238.1| Os10g0563400 [Oryza sativa Japonica Group]	Unigene33163_All//4.00E-34//AT4G17540| unknown protein	Unigene33163_All//0.00E+00//ES817740				nr -
Unigene33172_All	743	0.35	0.75	0.86	0.74	1.99	1.64	1.99	1.63	4.29	1.09E+00	2.74E-01		1.29E+00	1.86E-01		1.43E+00	1.04E-02		1.15E+00	7.02E-02		-2.88E-01	6.00E-01		1.11E+00	3.16E-04	Up	Unigene33172_All//gi|240255973|ref|NP_193464.5|//3.00E-56//AT4G2484-1; RNA binding [Arabidopsis thaliana]	Unigene33172_All//1.00E-44//AT4G17330| AtG2484-1; RNA binding	Unigene33172_All//9.00E-118//TC152481			GO:0003676	nr -

Unigene33173_All	822	0.95	2.28	4.15	3.03	4.27	5.11	1.34	0.86	1.31	1.26E+00	1.00E-02		2.12E+00	9.57E-08	Up	4.96E-01	1.45E-01		7.54E-01	1.10E-02		-6.30E-01	2.93E-01		-3.13E-02	9.69E-01		Unigene33173_All//gi|240255973|ref|XP_193464.5//1.00E-51//ATG2484-1; RNA binding [Arabidopsis thaliana]	Unigene33173_All//5.00E-53//AT4G17330| ATG2484-1; RNA binding	Unigene33173_All//3.00E-118//TC152481			GO:0003676	nr -
Unigene33177_All	7239	4.09	9.02	5.87	9.46	10.09	10.89	18.64	17.71	21.77	1.14E+00	2.00E-58	Up	5.21E-01	4.85E-10		9.37E-02	1.75E-01		2.04E-01	5.26E-04		-7.38E-02	9.98E-02		2.24E-01	3.67E-10		Unigene33177_All|gi|240255973|ref|XP_193464.5//0.00E+00//ATG2484-1; RNA binding [Arabidopsis thaliana]	Unigene33177_All//0.00E+00//AT4G17330| ATG2484-1; RNA binding	Unigene33177_All//0.00E+00//TC147835				nr -
Unigene33178_All	568	5.16	4.64	1.78	10.26	6.91	7.47	16.30	7.28	6.24	-1.53E-01	6.68E-01		-1.53E+00	1.38E-04	Down	-5.70E-01	1.49E-02		-4.57E-01	7.05E-02		-1.16E+00	3.77E-11	Down	-1.38E+00	7.23E-15	Down	Unigene33178_All//gi|122235033|sp|Q0JNX5.1|COPB2_ORYSJ//2.00E-42//RecName: Full=Coatomer subunit beta-2; AltName: Full=Beta-coat protein 2; Short=Beta-COP 2	Unigene33178_All//2.00E-40//AT4G31480| coatomer beta subunit, putative / beta-coat protein, putative / beta-COP, putative	Unigene33178_All//0.00E+00//TC155285			GO:0005515//GO:0015031//GO:0030120	nr +
Unigene33182_All	5044	14.15	24.24	10.48	27.08	26.96	34.57	47.49	113.67	115.12	7.77E-01	1.50E-57		-4.33E-01	7.56E-12		-6.40E-03	9.11E-01		3.52E-01	1.93E-21		1.26E+00	0.00E+00	Up	1.28E+00	0.00E+00	Up	Unigene33182_All//gi|297611333|ref|NP_001065875.2//0.00E+00//Os11g0174000 [Oryza sativa Japonica Group] >gi|75283240|sp|Q53PC7.1|COPB1_ORYSJ RecName: Full=Coatomer subunit beta-1; AltName: Full=Beta-coat protein 1; Short=Beta-COP 1 >gi|77548943|gb|AB491740.1| Adaptin N terminal region family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255670838|dbj|BAF27720.2| Os11g0174000 [Oryza sativa Japonica Group]	Unigene33182_All//0.00E+00//AT4G31480| coatomer beta subunit, putative / beta-coat protein, putative / beta-COP, putative	Unigene33182_All//0.00E+00//TC161202		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0005515//GO:0015031//GO:0030120	nr +
Unigene33188_All	1036	1.31	2.01	1.64	1.73	2.03	2.48	4.29	2.02	1.65	6.11E-01	1.73E-01		3.25E-01	5.44E-01		2.28E-01	6.44E-01		5.22E-01	2.12E-01		-1.09E+00	2.95E-05	Down	-1.37E+00	1.69E-07	Down	Unigene33188_All|gi|18379230|ref|NP_563700.1//2.00E-76//PRP39; binding [Arabidopsis thaliana]	Unigene33188_All//9.00E-78//AT1G04080| PRP39; binding	Unigene33188_All//0.00E+00//TC164738			GO:0006396//GO:0043231//GO:0048506	nr -
Unigene33190_All	1975	1.70	1.26	2.94	4.34	4.34	3.48	3.25	1.44	1.65	-4.32E-01	2.14E-01		7.94E-01	1.96E-03		1.10E-03	9.98E-01		-3.20E-01	1.29E-01		-1.18E+00	3.95E-08	Down	-9.76E-01	1.92E-06		Unigene33190_All|gi|18379230|ref|NP_563700.1//2.00E-56//PRP39; binding [Arabidopsis thaliana]	Unigene33190_All//8.00E-58//AT1G04080| PRP39; binding	Unigene33190_All//0.00E+00//DR509436			GO:0005622//GO:0006396//GO:0048506	nr +
Unigene33198_All	326	1.93	2.49	1.31	2.90	3.17	1.66	7.65	2.82	3.67	3.69E-01	6.22E-01		-5.60E-01	5.53E-01		1.26E-01	8.71E-01		-8.04E-01	2.77E-01		-1.44E+00	1.15E-04	Down	-1.06E+00	2.35E-03		Unigene33198_All|gi|115466360|ref|NP_001056779.1|//3.00E-48//Os06g0143900 [Oryza sativa Japonica Group] >gi|75109943|sp|Q5VQ78.1|COB21_ORYSJ RecName: Full=Coatomer subunit beta'-1; AltName: Full=Beta'-coat protein 1; Short=Beta'-COP 1 >gi|113594819|dbj|BAF18693.1| Os06g0143900 [Oryza sativa Japonica Group]	Unigene33198_All//2.00E-46//AT1G52360| coatomer protein complex, subunit beta 2 (beta prime), putative	Unigene33198_All//1.00E-151//TC169380			GO:0006683//GO:0005488//GO:0015031//GO:0030120	nr -
Unigene332_All	4032	2.67	1.83	2.15	7.01	6.37	8.45	13.16	7.29	4.99	-5.43E-01	1.74E-03		-3.12E-01	9.69E-02		-1.37E-01	2.30E-01		2.70E-01	3.81E-03		-8.53E-01	2.46E-36		-1.40E+00	2.50E-82	Down	Unigene332_All|gi|297811631|ref|XP_002873699.1|//0.00E+00//golgi alpha-mannosidase ii [Arabidopsis lyrata subsp. lyrata] >gi|297319536|gb|EFH49958.1| golgi alpha-mannosidase ii [Arabidopsis lyrata subsp. lyrata]	Unigene332_All//0.00E+00//AT5G14950| GMII (GOLGI ALPHA-MANNOSIDASE II); alpha-mannosidase	Unigene332_All//0.00E+00//TC145843		ko00510|N-Glycan biosynthesis//ko00511|Other glycan degradation		nr +
Unigene33201_All	2341	10.91	5.87	6.92	21.24	16.33	17.75	28.27	16.87	13.87	-8.95E-01	6.62E-16		-6.57E-01	3.32E-09		-3.79E-01	3.36E-08		-2.59E-01	5.39E-04		-7.44E-01	7.27E-36		-1.03E+00	4.68E-63	Down	Unigene33201_All//gi|75169434|sp|Q9C827.1|COB22_ARATH//0.00E+00//RecName: Full=Coatomer subunit beta'-2; AltName: Full=Beta'-coat protein 2; Short=Beta'-COP 2	Unigene33201_All//0.00E+00//AT1G52360| coatomer protein complex, subunit beta 2 (beta prime), putative	Unigene33201_All//0.00E+00//TC133683			GO:0006683//GO:0005488//GO:0015031//GO:0030120	nr -
Unigene33204_All	1724	1.18	2.23	3.49	4.77	5.55	4.64	3.65	2.67	4.69	9.16E-01	3.51E-03		1.56E+00	6.24E-09	Up	2.20E-01	2.96E-01		-4.01E-02	8.71E-01		-4.54E-01	3.31E-02		3.60E-01	4.62E-02		Unigene33204_All|gi|145358042|ref|NP_197006.2|//0.00E+00//SNL2 (SIN3-LIKE 2) [Arabidopsis thaliana] >gi|296439819|sp|Q9LFQ3.2|SNL2_ARATH RecName: Full=Paired amphipathic helix protein Sin3-like 2	Unigene33204_All//0.00E+00//AT5G15020| SNL2 (SIN3-LIKE 2)	Unigene33204_All//2.00E-157//EX164980			GO:0006351//GO:0043231	nr +
Unigene33213_All	1867	2.83	4.83	5.42	3.04	7.25	7.62	2.40	3.98	6.72	7.71E-01	6.12E-05		9.37E-01	6.49E-07		1.25E+00	9.17E-17	Up	1.32E+00	1.26E-17	Up	7.31E-01	1.24E-04		1.49E+00	9.84E-22	Up	Unigene33213_All//gi|15230753|ref|NP_187314.1|//1.00E-136//protein kinase family protein [Arabidopsis thaliana]	Unigene33213_All//6.00E-119//AT3G06620| protein kinase family protein	Unigene33213_All//0.00E+00//gi|78346824|gb|DT567098.1|DT567098		ko04626|Plant-pathogen interaction		nr +
Unigene33214_All	550	2.76	3.22	2.81	2.99	5.51	3.28	1.92	6.69	5.94	2.25E-01	6.26E-01		2.54E-02	9.82E-01		8.82E-01	1.20E-02		1.36E-01	7.93E-01		1.80E+00	1.21E-08	Up	1.63E+00	4.78E-07	Up	Unigene33214_All|gi|297838539|ref|XP_002887151.1|//5.00E-33//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332992|gb|EFH63410.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene33214_All//6.00E-34//AT1G67890| protein kinase family protein	Unigene33214_All//6.00E-115//gi|84151137|gb|DN800492.1|DN800492			GO:0004702//GO:0006351//GO:0006464//GO:0023060//GO:0032559	nr -
Unigene33215_All	408	2.05	2.73	1.31	1.95	0.76	3.76	7.36	7.68	1.86	4.13E-01	5.26E-01		-6.53E-01	3.96E-01		-1.36E+00	7.74E-02		9.46E-01	8.51E-02		6.24E-02	8.57E-01		-1.99E+00	1.96E-08	Down	Unigene33215_All|gi|10177613|dbj|BAB10760.1|/1.00E-68//protein kinase [Arabidopsis thaliana]	Unigene33215_All//6.00E-70//AT5G49470| protein kinase family protein	Unigene33215_All//1.00E-161//TC167926			GO:0004702//GO:0006351//GO:0006464//GO:0023060//GO:0032559	nr -
Unigene33216_All	1277	6.68	1.94	3.59	6.59	8.44	4.49	12.18	6.45	10.95	-1.78E+00	1.78E-15	Down	-8.97E-01	1.45E-05		3.57E-01	4.17E-02		-5.54E-01	5.06E-03		-9.18E-01	1.27E-12		-1.54E-01	2.56E-01		Unigene33216_All|gi|124359937|gb|ABN07953.1|/5.00E-96//Protein kinase [Medicago truncatula]	Unigene33216_All//3.00E-95//AT5G49470| protein kinase family protein	Unigene33216_All//0.00E+00//TC135644			GO:0004672//GO:0006351//GO:0006464//GO:0023060//GO:0032559//GO:0060089	nr +
Unigene33218_All	2810	5.90	2.69	5.08	13.74	14.94	14.11	20.12	16.88	13.54	-1.14E+00	2.50E-15	Down	-2.17E-01	1.51E-01		1.21E-01	1.93E-01		3.86E-02	7.07E-01		-2.53E-01	6.24E-05		-5.71E-01	4.01E-20		Unigene33218_All|gi|15230753|ref|NP_187314.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana]	Unigene33218_All//0.00E+00//AT3G06620| protein kinase family protein	Unigene33218_All//0.00E+00//TC167926			GO:0004702//GO:0006351//GO:0006464//GO:0023060//GO:0032559	nr -
Unigene3322_All	1744	8.25	5.26	7.63	14.91	14.57	11.16	12.00	4.15	3.20	-6.50E-01	1.06E-05		-1.12E-01	5.20E-01		-3.31E-02	8.28E-01		-4.18E-01	6.04E-05		-1.53E+00	1.34E-36	Down	-1.91E+00	4.58E-51	Down	Unigene3322_All|gi|297798462|ref|XP_002867115.1|//1.00E-158//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312961|gb|EFH43374.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3322_All//3.00E-139//AT4G34500| protein kinase family protein	Unigene3322_All//0.00E+00//TC178668		ko04626|Plant-pathogen interaction		nr -
Unigene33221_All	2969	1.96	1.35	1.11	21.54	16.60	11.48	23.27	6.19	8.40	-5.37E-01	2.96E-02		-8.15E-01	1.49E-03		-3.76E-01	2.99E-10		-9.08E-01	8.81E-43		-1.91E+00	3.85E-162	Down	-1.47E+00	3.64E-115	Down	Unigene33221_All|gi|30690286|ref|NP_849565.1|//0.00E+00//TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2): carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|20453189|gb|AAM19835.1| AT4g35300/F23E12_140 [Arabidopsis thaliana]	Unigene33221_All//0.00E+00//AT4G35300| TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter	Unigene33221_All//0.00E+00//TC167066			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr -
Unigene33222_All	2662	4.95	2.63	3.78	16.54	9.73	7.06	28.95	8.32	9.62	-9.15E-01	6.78E-09		-3.90E-01	1.76E-02		-7.66E-01	4.37E-25		-1.23E+00	2.50E-48	Down	-1.80E+00	1.01E-166	Down	-1.59E+00	5.42E-144	Down	Unigene33222_All|gi|30690286|ref|NP_849565.1|//0.00E+00//TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2): carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|20453189|gb|AAM19835.1| AT4g35300/F23E12_140 [Arabidopsis thaliana]	Unigene33222_All//0.00E+00//AT4G35300| TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter	Unigene33222_All//0.00E+00//TC166889				nr +
Unigene33223_All	3171	10.18	3.39	5.76	8.37	6.69	5.24	9.03	2.82	4.86	-1.59E+00	3.06E-48	Down	-8.22E-01	1.32E-16		-3.24E-01	1.24E-03		-6.76E-01	4.24E-11		-1.68E+00	1.30E-56	Down	-8.93E-01	3.55E-22		Unigene33223_All|gi|224104813|ref|XP_002313575.1|//0.00E+00//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222849983|gb|EEE87530.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene33223_All//0.00E+00//AT4G35290| GLUR2 (GLUTAMATE RECEPTOR 2); intracellular ligand-gated ion channel	Unigene33223_All//1.00E-166//C0086122				nr -
Unigene33224_All	5767	0.80	0.84	1.03	2.60	2.56	2.42	8.63	3.89	5.66	7.93E-02	7.76E-01		3.73E-01	1.50E-01		-2.15E-02	9.01E-01		-1.04E-01	5.67E-01		-1.15E+00	2.19E-55	Down	-6.07E-01	8.70E-20		Unigene33224_All|gi|224104813|ref|XP_002313575.1|//0.00E+00//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222849983|gb|EEE87530.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene33224_All//0.00E+00//AT4G35290| GLUR2 (GLUTAMATE RECEPTOR 2); intracellular ligand-gated ion channel	Unigene33224_All//0.00E+00//TC167066				nr +
Unigene33226_All	1434	1.09	0.92	1.86	2.74	3.70	2.68	3.89	1.66	3.06	-2.53E-01	6.23E-01		7.62E-01	5.90E-02		4.30E-01	1.05E-01		-3.58E-02	9.30E-01		-1.23E+00	1.33E-07	Down	-3.49E-01	1.19E-01		Unigene33226_All|gi|42561615|ref|NP_171710.3|//1.00E-158//transcriptional regulator-related [Arabidopsis thaliana]	Unigene33226_All//5.00E-149//AT1G02080| transcriptional regulator-related	Unigene33226_All//3.00E-11//DW231681		ko03018|RNA degradation		nr -
Unigene3323_All	855	33.84	35.44	16.57	46.84	47.44	61.22	56.18	66.73	62.53	6.66E-02	5.71E-01		-1.03E+00	1.41E-21	Down	1.84E-02	8.63E-01		3.86E-01	4.84E-08		2.48E-01	7.97E-05		1.55E-01	1.98E-02		Unigene3323_All|gi|3024504|sp|Q40521.1|RB11B_TOBAC//1.00E-110//RecName: Full=Ras-related protein Rab11B	Unigene3323_All//5.00E-103//AT5G60860| AtRABA1f (Arabidopsis Rab GTPase homolog A1f); GTP binding	Unigene3323_All//0.00E+00//gi|48776479|gb|CO085845.1|CO085845				nr +
Unigene33230_All	459	0.68	0.00	0.81	0.00	1.80	0.49	1.84	2.82	2.69	-9.42E+00	3.65E-02		2.48E-01	8.23E-01		1.08E+01	4.48E-05	Up	8.94E+00	1.19E-01		6.16E-01	2.53E-01		5.46E-01	3.11E-01		Unigene33230_All|gi|224078860|ref|XP_002305657.1|//2.00E-47//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222848621|gb|EEE86168.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene33230_All//4.00E-44//AT1G30410| ATMRP13; ATPase, coupled to transmembrane movement of substances					nr +
Unigene33231_All	670	0.39	0.08	0.00	0.07	0.00	0.07	2.08	4.99	2.08	-2.37E+00	2.14E-01		-8.61E+00	8.57E-02		-6.22E+00	5.55E-01		-1.41E-01	9.52E-01		1.26E+00	4.93E-05	Up	-1.00E-03	9.95E-01		Unigene33231_All|gi|224144381|ref|XP_002336141.1|//9.00E-15//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222873976|gb|EEF11107.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene33231_All//2.00E-14//AT1G30400| MRP1 (ARABIDOPSIS THALIANA MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 1); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase	Unigene33231_All//0.00E+00//gi|31073578|gb|CA993857.1|CA993857				nr -
Unigene33236_All	2326	5.89	5.14	4.28	6.96	5.57	4.87	62.73	127.94	38.42	-1.97E-01	2.29E-01		-4.61E-01	3.65E-03		-3.22E-01	1.76E-02		-5.14E-01	1.42E-04		1.03E+00	1.77E-273	Up	-7.07E-01	1.82E-73		Unigene33236_All|gi|224116630|ref|XP_002317351.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222860416|gb|EEE97963.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene33236_All//0.00E+00//AT2G34660| ATMRP2 (ARABIDOPSIS THALIANA MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2); ATPase, coupled to transmembrane movement of substances	Unigene33236_All//0.00E+00//TC150803		ko02010|ABC transporters		nr +

Unigene33238_All	506	1.86	1.20	1.79	3.45	2.59	3.93	0.67	2.81	5.20	-6.31E-01	3.66E-01			-5.71E-02	9.49E-01			-4.14E-01	4.20E-01			1.89E-01	6.88E-01			2.07E+00	2.12E-04	Up	2.96E+00	3.43E-11	Up	Unigene33238_All//gi|297843622|ref|XP_002889692.1|//2.00E-26//kelch repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335534|gb|EFH65951.1| kelch repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene33238_All//4.00E-13//AT2G27210| kelch repeat-containing serine/threonine phosphoesterase family protein	Unigene33238_All//6.00E-47//DW498718				nr -
Unigene3324_All	1541	30.08	10.69	10.92	27.83	20.54	23.83	6.89	1.87	1.68	-1.49E+00	4.16E-63	Down	-1.46E+00	4.73E-59	Down	-4.39E-01	3.27E-09			-2.24E-01	7.03E-03		-1.88E+00	5.46E-25	Down	-2.04E+00	1.40E-28	Down	Unigene3324_All//gi|18404409|ref|NP_565860.1|//4.00E-59//chloroplast lumen common family protein [Arabidopsis thaliana] >gi|4056493|gb|AAC98059.1| chloroplast lumen common protein family [Arabidopsis thaliana] >gi|114050659|gb|ABI49479.1| At2g37400 [Arabidopsis thaliana]	Unigene3324_All//8.00E-95//AT3G53560| chloroplast lumen common family protein	Unigene3324_All//0.00E+00//gi|78333882|gb|DT554156.1|DT554156			GO:0009526//GO:0009534	nr -
Unigene3325_All	1966	2.55	7.19	3.11	11.81	13.85	7.53	0.71	0.53	0.99	1.49E+00	1.30E-19	Up	2.86E-01	2.75E-01		2.31E-01	2.94E-02			-6.48E-01	3.96E-09		-4.17E-01	4.25E-01		4.84E-01	2.37E-01		Unigene3325_All//gi|115461987|ref|NP_001054593.1|//1.00E-35//Os05g0139100 [Oryza sativa Japonica Group] >gi|113578144|dbj|BAF16507.1| Os05g0139100 [Oryza sativa Japonica Group]	Unigene3325_All//2.00E-34//AT1G09530| PIF3 (PHYTOCHROME INTERACTING FACTOR 3); DNA binding / protein binding / transcription factor/ transcription regulator	Unigene3325_All//0.00E+00//ES807419	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0010468//GO:0043231	nr -
Unigene33250_All	744	5.70	2.79	2.22	11.05	8.10	5.46	7.84	5.84	9.21	-1.03E+00	5.64E-04	Down	-1.36E+00	2.10E-05	Down	-4.48E-01	2.19E-02			-1.02E+00	3.77E-07	Down	-4.25E-01	5.83E-02		2.32E-01	2.68E-01		Unigene33250_All//gi|297607496|ref|NP_001060077.2|//1.00E-103//Os07g0575100 [Oryza sativa Japonica Group] >gi|255677906|dbj|BAF21991.2| Os07g0575100 [Oryza sativa Japonica Group]	Unigene33250_All//7.00E-88//AT5G19820| emb2734 (embryo defective 2734); binding / lyase	Unigene33250_All//0.00E+00//gi|109850687|gb|DW479666.1|DW479666				nr -
Unigene33251_All	1985	8.65	3.47	3.30	19.75	18.93	19.02	30.25	20.57	17.24	-1.32E+00	8.72E-20	Down	-1.39E+00	1.49E-20	Down	-6.15E-02	5.71E-01			-5.43E-02	6.42E-01		-5.56E-01	9.04E-20		-8.11E-01	8.94E-39		Unigene33251_All//gi|297812163|ref|XP_002873965.1|//0.00E+00//EMB2734 [Arabidopsis lyrata subsp. lyrata] >gi|297319802|gb|EFH50224.1| EMB2734 [Arabidopsis lyrata subsp. lyrata]	Unigene33251_All//0.00E+00//AT5G19820| emb2734 (embryo defective 2734); binding / lyase	Unigene33251_All//0.00E+00//TC166816				nr +
Unigene33254_All	504	0.52	0.00	0.85	3.56	1.02	2.96	2.18	2.74	3.72	-9.02E+00	6.70E-02		7.03E-01	5.54E-01		-1.80E+00	1.91E-04	Down	-2.67E-01	6.38E-01		3.27E-01	5.53E-01		7.68E-01	6.08E-02		Unigene33254_All//gi|289540935|gb|ADD09606.1|//1.00E-50//kinesin-related protein [Trifolium repens]	Unigene33254_All//2.00E-33//AT4G39050| kinesin-related protein (MKRP2)	Unigene33254_All//0.00E+00//TC161242				nr +
Unigene33256_All	3810	2.60	1.30	1.58	8.52	8.99	4.20	7.26	1.81	4.00	-9.94E-01	9.10E-08		-7.17E-01	1.50E-04		7.72E-02	5.15E-01			-1.02E+00	1.03E-26	Down	-2.00E+00	1.51E-69	Down	-8.58E-01	4.17E-20		Unigene33256_All//gi|30692169|ref|NP_195616.2|//0.00E+00//kinesin-related protein (MKRP2) [Arabidopsis thaliana] >gi|16902294|dbj|BAB71852.1| kinesin-related protein [Arabidopsis thaliana]	Unigene33256_All//0.00E+00//AT4G39050| kinesin-related protein (MKRP2)	Unigene33256_All//0.00E+00//TC132482				nr -
Unigene33257_All	3610	8.65	6.16	6.51	14.06	14.16	10.97	19.11	7.21	9.98	-4.90E-01	3.51E-07		-4.12E-01	3.67E-05		9.70E-03	9.26E-01			-3.58E-01	6.63E-07		-1.41E+00	1.39E-104	Down	-9.38E-01	1.20E-56		Unigene33257_All//gi|289540935|gb|ADD09606.1|//0.00E+00//kinesin-related protein [Trifolium repens]	Unigene33257_All//0.00E+00//AT4G39050| kinesin-related protein (MKRP2)	Unigene33257_All//0.00E+00//TC173673				nr -
Unigene33259_All	718	6.34	6.07	2.30	7.84	6.00	6.04	8.77	11.99	11.04	-6.30E-02	8.25E-01		-1.46E+00	2.47E-06	Down	-3.87E-01	1.26E-01			-3.77E-01	1.54E-01		4.51E-01	1.12E-02		3.32E-01	7.17E-02		Unigene33259_All//gi|115458106|ref|NP_001052653.1|//3.00E-22//Os04g0394300 [Oryza sativa Japonica Group] >gi|113564224|dbj|BAF14567.1| Os04g0394300 [Oryza sativa Japonica Group]	Unigene33259_All//4.00E-09//AT3G27700| RNA recognition motif (RRM)-containing protein	Unigene33259_All//9.00E-155//C0126681	C3H			nr -
Unigene3326_All	1549	1.93	1.41	0.96	23.25	14.03	11.49	14.22	7.29	7.64	-4.53E-01	2.16E-01		-1.00E+00	8.59E-03		-7.29E-01	6.60E-19			-1.02E+00	2.57E-29	Down	-9.65E-01	5.58E-19		-8.97E-01	2.13E-17		Unigene3326_All//gi|18412073|ref|NP_565187.1|//1.00E-126//brassinosteroid signalling positive regulator-related [Arabidopsis thaliana] >gi|61211694|sp|Q9ZV88.1|BEH4_ARATH RecName: Full=BES1/BZR1 homolog protein 4 >gi|3834322|gb|AAC83038.1| EST gb|R30300 comes from this gene [Arabidopsis thaliana] >gi|15215802|gb|AAK91446.1| At1g78700/F9K20_26 [Arabidopsis thaliana] >gi|19699252|gb|AAL90992.1| At1g78700/F9K20_26 [Arabidopsis thaliana]	Unigene3326_All//5.00E-88//AT1G78700| brassinosteroid signalling positive regulator-related	Unigene3326_All//0.00E+00//TC147242	BES1			nr +
Unigene33267_All	878	12.63	6.06	6.55	25.53	19.53	22.53	73.05	37.99	36.48	-1.06E+00	1.74E-09	Down	-9.48E-01	1.25E-07		-3.87E-01	3.69E-04			-1.80E-01	1.60E-01		-9.43E-01	9.64E-52		-1.00E+00	1.02E-58	Down	Unigene33267_All//gi|3559814|emb|CAA75777.1|//3.00E-87//transketolase 1 [Capsicum annuum]	Unigene33267_All//3.00E-82//AT2G45290| transketolase, putative	Unigene33267_All//0.00E+00//gi|164275700|gb|ES818146.1|ES818146		ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway		nr +
Unigene33268_All	1131	15.08	6.59	8.80	36.16	34.07	41.53	36.60	14.60	20.18	-1.20E+00	5.05E-17	Down	-7.76E-01	2.68E-08		-8.59E-02	3.94E-01			2.00E-01	1.30E-02		-1.33E+00	1.05E-57	Down	-8.59E-01	1.08E-29		Unigene33268_All//gi|7329685|emb|CAB82679.1|//1.00E-110//transketolase-like protein [Arabidopsis thaliana]	Unigene33268_All//5.00E-104//AT2G45290| transketolase, putative	Unigene33268_All//0.00E+00//gi|109842253|gb|DW240813.1|DW240813		ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway		nr -
Unigene33269_All	2877	555.38	278.97	429.33	119.45	131.12	101.19	23.10	11.53	11.11	-9.93E-01	0.00E+00		-3.71E-01	3.06E-191		1.35E-01	2.15E-08			-2.39E-01	2.17E-20		-1.00E+00	3.69E-59	Down	-1.06E+00	2.53E-66	Down	Unigene33269_All//gi|2501354|sp|Q42677.1|TKT7_CRAPL//0.00E+00//RecName: Full=Transketolase 7; Short=TK >gi|6649003|emb|CAA86609.1| transketolase [Craterostigma plantagineum]	Unigene33269_All//0.00E+00//AT2G45290| transketolase, putative	Unigene33269_All//0.00E+00//TC139125		ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway		nr -
Unigene33272_All	1486	0.81	1.64	2.15	2.15	3.08	3.19	4.92	2.81	8.28	1.02E+00	1.34E-02		1.41E+00	1.85E-04	Up	5.23E-01	6.57E-02			5.73E-01	4.13E-02		-8.07E-01	2.82E-05		7.51E-01	1.17E-07		Unigene33272_All//gi|225454244|ref|XP_002274479.1|//1.00E-166//PREDICTED: similar to 2-oxo acid dehydrogenase, lipoyl-binding site [Vitis vinifera]	Unigene33272_All//1.00E-128//AT4G00450| CRP (CRYPTIC PRECOCIOUS)	Unigene33272_All//2.00E-95//TC148979				nr +
Unigene33273_All	1272	0.04	0.24	0.42	1.02	1.35	0.99	0.80	0.43	2.29	2.54E+00	1.51E-01		3.35E+00	2.06E-02		4.11E-01	4.52E-01			-3.44E-02	9.56E-01		-9.01E-01	1.44E-01		1.52E+00	7.64E-06	Up	Unigene33273_All//gi|225454244|ref|XP_002274479.1|//1.00E-131//PREDICTED: similar to 2-oxo acid dehydrogenase, lipoyl-binding site [Vitis vinifera]	Unigene33273_All//5.00E-81//AT4G00450| CRP (CRYPTIC PRECOCIOUS)					nr -
Unigene33274_All	5704	1.29	2.66	1.48	4.49	4.40	4.03	12.17	13.04	13.41	1.04E+00	3.20E-12	Up	1.99E-01	3.90E-01		-2.85E-02	8.27E-01			-1.56E-01	2.03E-01		9.98E-02	1.00E-01		1.40E-01	1.05E-02		Unigene33274_All//gi|225454244|ref|XP_002274479.1|//0.00E+00//PREDICTED: similar to 2-oxo acid dehydrogenase, lipoyl-binding site [Vitis vinifera]	Unigene33274_All//0.00E+00//AT4G00450| CRP (CRYPTIC PRECOCIOUS)	Unigene33274_All//0.00E+00//TC145576				nr +
Unigene33275_All	7224	2.59	5.70	3.73	5.84	6.01	6.05	13.42	13.92	18.09	1.14E+00	5.82E-37	Up	5.29E-01	8.84E-07		4.03E-02	7.12E-01			5.12E-02	6.46E-01		5.28E-02	3.63E-01		4.31E-01	2.56E-27		Unigene33275_All//gi|225454244|ref|XP_002274479.1|//0.00E+00//PREDICTED: similar to 2-oxo acid dehydrogenase, lipoyl-binding site [Vitis vinifera]	Unigene33275_All//0.00E+00//AT4G00450| CRP (CRYPTIC PRECOCIOUS)	Unigene33275_All//0.00E+00//ES817985				nr +
Unigene33282_All	3132	1.35	0.58	2.19	1.02	0.88	1.11	1.84	1.77	1.62	-1.22E+00	6.08E-05	Down	6.97E-01	2.72E-03		-2.11E-01	5.86E-01			1.25E-01	7.24E-01		-4.87E-02	8.47E-01		-1.85E-01	4.31E-01		Unigene33282_All//gi|157863710|gb|ABV90876.1|//0.00E+00//inositol-1,4,5-triphosphate-5-phosphatase [Solanum lycopersicum]	Unigene33282_All//0.00E+00//AT1G71710| inositol polyphosphate 5-phosphatase, putative	Unigene33282_All//0.00E+00//TC178307				nr -
Unigene33285_All	997	1.00	0.30	0.05	1.35	1.38	1.86	3.56	2.81	9.79	-1.71E+00	2.08E-02		-4.22E+00	1.62E-04	Down	3.44E-02	9.63E-01			4.61E-01	3.82E-01		-3.43E-01	2.68E-01		1.46E+00	1.17E-16	Up	Unigene33285_All//gi|2444180|gb|AA871529.1|//1.00E-135//unconventional myosin [Helianthus annuus]	Unigene33285_All//2.00E-123//AT5G20490| XIK; motor/ protein binding	Unigene33285_All//0.00E+00//TC157777				nr +
Unigene33286_All	970	0.54	0.42	0.49	2.57	3.73	3.31	4.45	2.33	10.43	-3.68E-01	6.83E-01		-1.27E-01	8.98E-01		5.38E-01	1.02E-01			3.65E-01	3.42E-01		-9.34E-01	3.52E-04		1.23E+00	1.71E-13	Up	Unigene33286_All//gi|116047947|gb|ABJ53199.1|//1.00E-152//myosin XI-K [Nicotiana benthamiana]	Unigene33286_All//1.00E-135//AT5G20490| XIK; motor/ protein binding	Unigene33286_All//9.00E-57//ES812572				nr -
Unigene33287_All	2565	3.69	1.28	2.45	7.46	7.50	7.11	10.32	9.21	6.83	-1.52E+00	7.62E-14	Down	-5.92E-01	2.27E-03		9.10E-03	9.56E-01			-6.82E-02	6.65E-01		-1.65E-01	1.13E-01		-5.95E-01	1.42E-10		Unigene33287_All//gi|56201391|dbj|BAD72949.1|//0.00E+00//myosin XI [Nicotiana tabacum]	Unigene33287_All//0.00E+00//AT5G20490| XIK; motor/ protein binding	Unigene33287_All//0.00E+00//TC153197				nr -
Unigene33288_All	3631	1.05	0.29	0.26	5.61	4.11	4.89	15.64	14.90	54.57	-1.84E+00	1.17E-07	Down	-1.99E+00	5.54E-08	Down	-4.50E-01	6.85E-05			-1.99E-01	1.36E-01		-7.02E-02	3.65E-01		1.80E+00	0.00E+00	Up	Unigene33288_All//gi|56201391|dbj|BAD72949.1|//0.00E+00//myosin XI [Nicotiana tabacum]	Unigene33288_All//0.00E+00//AT5G20490| XIK; motor/ protein binding	Unigene33288_All//0.00E+00//TC175504				nr -
Unigene33289_All	3754	1.05	1.12	0.65	7.91	7.27	6.20	6.67	2.81	4.89	1.00E-01	7.33E-01		-6.80E-01	3.55E-02		-1.23E-01	2.86E-01			-3.52E-01	3.17E-04		-1.25E+00	3.87E-32	Down	-4.47E-01	2.44E-06		Unigene33289_All//gi|56201391|dbj|BAD72949.1|//0.00E+00//myosin XI [Nicotiana tabacum]	Unigene33289_All//0.00E+00//AT5G20490| XIK; motor/ protein binding	Unigene33289_All//0.00E+00//TC157152				nr +
Unigene3329_All	1507	22.74	10.89	14.45	60.06	64.05	52.06	11.05	12.59	11.16	-1.06E+00	9.21E-28	Down	-6.54E-01	5.04E-12		9.27E-02	1.11E-01			-2.06E-01	1.40E-04		1.88E-01	1.31E-01		1.32E-02	9.44E-01		Unigene3329_All//gi|30725596|gb|AAP37820.1|//1.00E-126//At1g29790 [Arabidopsis thaliana]	Unigene3329_All//4.00E-113//AT1G29790| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: Golgi apparatus, plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: methyltransferase (TAIR:AT5G40830.2); Has 127 Blast hits to 127 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 127; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene3329_All//0.00E+00//TC158506				nr +
Unigene33290_All	486	2.15	5.00	1.10	4.41	2.98	2.14	6.35	1.29	1.23	1.22E+00	3.60E-03		-9.75E-01	1.67E-01		-5.67E-01	1.93E-01			-1.04E+00	1.77E-02		-2.30E+00	7.46E-10	Down	-2.37E+00	1.47E-10	Down	Unigene33290_All//gi|164605535|dbj|BAF98601.1|//2.00E-66//CM0545.290.nc [Lotus japonicus]	Unigene33290_All//6.00E-59//AT3G11910| UBP13 (UBIQUITIN-SPECIFIC PROTEASE 13); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene33290_All//0.00E+00//TC148913				nr -
Unigene33292_All	912	2.81	3.56	3.62	7.76	5.70	6.04	6.07	2.98	3.93	3.39E-01	3.50E-01		3.65E-01	3.27E-01		-4.44E-01	3.91E-02			-3.60E-01	1.20E-01		-1.03E+00	7.09E-06	Down	-6.27E-01	4.01E-03		Unigene33292_All//gi|186520708|ref|NP_001119179.1|//1.00E-147//UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ubiquitin thiolesterase/ ubiquitin-specific protease [Arabidopsis thaliana]	Unigene33292_All//7.00E-137//AT5G06600| UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene33292_All//2.00E-107//TC174664				nr -
Unigene33293_All	1276	5.00	3.49	5.84	8.39	6.53	6.19	11.17	4.62	4.71	-5.18E-01	2.69E-02		2.24E-01	3.62E-01		-3.62E-01	3.50E-02			-4.38E-01	1.21E-02		-1.27E+00	3.37E-19	Down	-1.24E+00	4.07E-19	Down	Unigene33293_All//gi|164605535|dbj|BAF98601.1|//1.00E-171//CM0545.290.nc [Lotus japonicus]	Unigene33293_All//8.00E-166//AT5G06600| UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene33293_All//0.00E+00//TC148913				nr -
Unigene33294_All	2723	2.48	1.92	3.19	5.45	5.27	3.93	3.66	1.24	1.54	-3.71E-01	1.10E-01		3.63E-01	8.50E-02		-4.79E-02	8.14E-01			-4.72E-01	9.62E-04		-1.56E+00	2.77E-18	Down	-1.25E+00	8.14E-14	Down	Unigene33294_All//gi|30681531|ref|NP_850783.1|//0.00E+00//UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); double-stranded DNA binding / ubiquitin thiolesterase/ ubiquitin-specific protease [Arabidopsis thaliana]	Unigene33294_All//0.00E+00//AT5G06600| UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene33294_All//0.00E+00//TC148913				nr -

Unigene33297_All	552	1.99	0.18	1.35	1.26	0.62	1.64	1.99	1.44	1.37	-3.44E+00	1.19E-04	Down	-5.60E-01	3.93E-01		-1.02E+00	2.25E-01		3.73E-01	6.26E-01		-4.69E-01	4.31E-01		-5.38E-01	3.47E-01		Unigene33297_All//gi|78099801|sp|Q9SFU0.2|SC24A_ARATH//1.00E-73//RecName: Full=Protein transport protein Sec24-like At3g07100	Unigene33297_All//5.00E-75//AT3G07100| protein transport protein Sec24, putative	Unigene33297_All//3.00E-120//TC149264				nr -
Unigene33298_All	420	4.73	0.00	0.76	1.54	1.80	1.18	3.93	1.19	2.28	-1.22E+01	1.70E-11	Down	-2.64E+00	6.10E-06	Down	2.26E-01	8.32E-01		-3.82E-01	6.78E-01		-1.72E+00	4.45E-04	Down	-7.86E-01	7.29E-02		Unigene33298_All//gi|78099801|sp|Q9SFU0.2|SC24A_ARATH//7.00E-47//RecName: Full=Protein transport protein Sec24-like At3g07100	Unigene33298_All//4.00E-48//AT3G07100| protein transport protein Sec24, putative	Unigene33298_All//5.00E-149//gi|164335961|gb|ES797503.1|ES797503				nr +
Unigene33299_All	1796	2.01	1.41	0.80	3.91	3.51	4.27	4.17	3.30	3.26	-5.11E-01	1.19E-01		-1.33E+00	1.43E-04	Down	-1.57E-01	5.60E-01		1.28E-01	6.38E-01		-3.35E-01	9.22E-02		-3.54E-01	6.07E-02		Unigene33299_All//gi|78099801|sp|Q9SFU0.2|SC24A_ARATH//1.00E-173//RecName: Full=Protein transport protein Sec24-like At3g07100	Unigene33299_All//2.00E-142//AT3G07100| protein transport protein Sec24, putative	Unigene33299_All//0.00E+00//gi|109860346|gb|DW489325.1|DW489325		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene333_All	357	4.84	4.12	3.88	9.49	8.87	10.12	7.34	3.16	6.36	-2.33E-01	6.14E-01		-3.19E-01	5.53E-01		-9.66E-02	8.20E-01		9.31E-02	7.88E-01		-1.22E+00	6.08E-04	Down	-2.07E-01	5.80E-01		Unigene333_All//gi|87162600|gb|ABD28395.1|//9.00E-34//Nucleoporin interacting component: Protein prenyltransferase [Medicago truncatula]	Unigene333_All//3.00E-34//AT2G41620| nucleoporin interacting component family protein	Unigene333_All//6.00E-114//TC141240				nr +
Unigene33303_All	623	3.36	1.71	2.05	6.08	7.96	5.94	4.61	1.68	2.62	-9.76E-01	2.85E-02		-7.12E-01	1.32E-01		3.89E-01	1.65E-01		-3.18E-02	9.38E-01		-1.46E+00	2.35E-05	Down	-8.16E-01	1.02E-02		Unigene33303_All//gi|7019653|emb|CAB75754.1|//3.00E-61//spliceosomal-like protein [Arabidopsis thaliana] >gi|7019655|emb|CAB75756.1| spliceosomal-like protein [Arabidopsis thaliana]	Unigene33303_All//2.00E-62//AT3G55200| splicing factor, putative	Unigene33303_All//2.00E-28//DW482071		ko03040|Spliceosome		nr +
Unigene33304_All	2272	6.13	6.16	2.98	12.48	11.52	10.42	11.04	10.34	6.79	7.00E-03	9.86E-01		-1.04E+00	7.24E-11	Down	-1.15E-01	3.21E-01		-2.60E-01	1.25E-02		-9.41E-02	4.13E-01		-7.02E-01	3.39E-13		Unigene33304_All//gi|7019653|emb|CAB75754.1|//0.00E+00//spliceosomal-like protein [Arabidopsis thaliana] >gi|7019655|emb|CAB75756.1| spliceosomal-like protein [Arabidopsis thaliana]	Unigene33304_All//0.00E+00//AT3G55200| splicing factor, putative	Unigene33304_All//0.00E+00//TC134031		ko03040|Spliceosome		nr +
Unigene33307_All	1688	19.99	13.09	9.81	32.96	34.09	26.01	32.74	21.12	26.06	-6.11E-01	4.46E-11		-1.03E+00	6.12E-25	Down	4.84E-02	5.86E-01		-3.42E-01	6.05E-07		-6.32E-01	8.96E-23		-3.29E-01	1.07E-07		Unigene33307_All//gi|225453835|ref|XP_002272447.1|//0.00E+00//PREDICTED: similar to GAUT1/LGT1 (Galacturonosyltransferase 1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups [Vitis vinifera]	Unigene33307_All//0.00E+00//AT3G61130| GAUT1 (GALACTURONOSYLTRANSFERASE 1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups	Unigene33307_All//0.00E+00//EX170176				nr +
Unigene33308_All	2770	4.27	4.55	3.81	19.93	17.95	9.91	11.59	3.79	5.80	9.36E-02	6.20E-01		-1.65E-01	3.97E-01		-1.51E-01	4.09E-02		-1.01E+00	6.16E-44	Down	-1.61E+00	6.32E-60	Down	-9.99E-01	1.06E-29		Unigene33308_All//gi|225453835|ref|XP_002272447.1|//0.00E+00//PREDICTED: similar to GAUT1/LGT1 (Galacturonosyltransferase 1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups [Vitis vinifera]	Unigene33308_All//0.00E+00//AT3G61130| GAUT1 (GALACTURONOSYLTRANSFERASE 1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups	Unigene33308_All//0.00E+00//gi|73860701|gb|DT463440.1|DT463440				nr -
Unigene3331_All	757	52.60	30.39	36.72	75.41	84.38	101.60	62.67	19.60	38.47	-7.92E-01	6.63E-20		-5.19E-01	2.31E-09		1.62E-01	1.51E-02		4.30E-01	6.41E-14		-1.68E+00	3.02E-93	Down	-7.04E-01	2.67E-24		Unigene3331_All//gi|224121558|ref|XP_002318614.1|//1.00E-87//autoinhibited H+ ATPase [Populus trichocarpa] >gi|222859287|gb|EEE96834.1| autoinhibited H+ ATPase [Populus trichocarpa]	Unigene3331_All//2.00E-59//AT5G62670| AHA11 (Arabidopsis H(+)-ATPase 11); ATPase	Unigene3331_All//0.00E+00//TC142277		ko00190|Oxidative phosphorylation	GO:0006811//GO:0006818//GO:0006970//GO:0009206//GO:0015662//GO:0031224//GO:0032559//GO:0043169	nr -
Unigene33310_All	1581	9.60	3.62	5.05	19.09	14.96	8.74	8.85	4.57	3.70	-1.41E+00	2.31E-19	Down	-9.26E-01	8.07E-10		-3.52E-01	1.32E-04		-1.13E+00	4.61E-29	Down	-9.53E-01	4.10E-12		-1.26E+00	4.41E-19	Down	Unigene33310_All//gi|297820890|ref|XP_002878328.1|//0.00E+00//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324166|gb|EFH54587.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene33310_All//7.00E-149//AT3G60320| DNA binding	Unigene33310_All//0.00E+00//TC176868				nr -
Unigene33311_All	2758	1.56	0.57	0.46	12.28	7.08	6.76	11.65	5.83	5.92	-1.45E+00	2.84E-06	Down	-1.75E+00	1.50E-07	Down	-7.95E-01	1.18E-20		-8.61E-01	5.42E-21		-9.98E-01	8.07E-29		-9.76E-01	1.19E-28		Unigene33311_All//gi|297820890|ref|XP_002878328.1|//0.00E+00//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324166|gb|EFH54587.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene33311_All//0.00E+00//AT3G60320| DNA binding	Unigene33311_All//0.00E+00//TC176868				nr +
Unigene33312_All	2737	13.76	3.17	5.56	32.49	24.14	14.45	9.15	6.87	3.83	-2.12E+00	2.95E-83	Down	-1.31E+00	1.43E-40	Down	-4.28E-01	8.69E-18		-1.17E+00	1.12E-89	Down	-4.12E-01	2.15E-05		-1.26E+00	2.06E-33	Down	Unigene33312_All//gi|297820890|ref|XP_002878328.1|//0.00E+00//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324166|gb|EFH54587.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene33312_All//0.00E+00//AT3G60320| DNA binding	Unigene33312_All//0.00E+00//TC176868				nr -
Unigene33313_All	3020	5.11	2.32	3.81	6.61	3.61	2.81	4.52	1.45	1.73	-1.14E+00	1.89E-14	Down	-4.24E-01	4.34E-03		-8.72E-01	2.02E-14		-1.23E+00	2.34E-22	Down	-1.64E+00	1.70E-26	Down	-1.39E+00	1.40E-21	Down	Unigene33313_All//gi|30695172|ref|NP_191591.2|//0.00E+00//DNA binding [Arabidopsis thaliana]	Unigene33313_All//0.00E+00//AT3G60320| DNA binding	Unigene33313_All//0.00E+00//TC135352		ko03040|Spliceosome//ko04144|Endocytosis		nr +
Unigene33320_All	1644	0.83	1.97	1.39	2.97	3.10	2.50	2.65	1.83	2.74	1.25E+00	4.20E-04	Up	7.51E-01	8.86E-02		6.20E-02	8.38E-01		-2.48E-01	4.14E-01		-5.33E-01	4.16E-02		4.79E-02	8.67E-01		Unigene33320_All//gi|18394611|ref|NP_564052.1|//1.00E-167//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|134031898|gb|ABO45686.1| At1g18470 [Arabidopsis thaliana]	Unigene33320_All//6.00E-162//AT1G68820| membrane protein, putative	Unigene33320_All//0.00E+00//TC159216				nr -
Unigene33321_All	1776	0.85	0.71	1.14	5.55	4.75	3.69	7.57	5.01	2.69	-2.60E-01	6.19E-01		4.16E-01	3.85E-01		-2.25E-01	2.56E-01		-5.91E-01	9.64E-04		-5.95E-01	1.30E-05		-1.49E+00	1.34E-23	Down	Unigene33321_All//gi|115454857|ref|NP_001051029.1|//0.00E+00//Os03g0706900 [Oryza sativa Japonica Group] >gi|113549500|dbj|BAF12943.1| Os03g0706900 [Oryza sativa Japonica Group]	Unigene33321_All//0.00E+00//AT1G68820| membrane protein, putative	Unigene33321_All//0.00E+00//TC172368				nr +
Unigene33324_All	3262	0.45	0.93	0.28	2.92	2.80	4.21	4.69	11.71	10.86	1.05E+00	3.68E-03		-6.95E-01	2.36E-01		-6.02E-02	8.11E-01		5.29E-01	3.92E-04		1.32E+00	7.92E-53	Up	1.21E+00	6.37E-44	Up	Unigene33324_All//gi|297804588|ref|XP_002870178.1|//0.00E+00//calmodulin-binding transcription activator 5 [Arabidopsis lyrata subsp. lyrata] >gi|297316014|gb|EFH46437.1| calmodulin-binding transcription activator 5 [Arabidopsis lyrata subsp. lyrata]	Unigene33324_All//0.00E+00//AT4G16150| calmodulin binding / transcription regulator	Unigene33324_All//0.00E+00//TC134758	CAMTA			nr -
Unigene33329_All	2766	70.16	33.14	59.97	39.35	33.41	27.56	9.43	5.58	4.74	-1.08E+00	6.46E-159	Down	-2.26E-01	1.28E-09		-2.36E-01	2.42E-07		-5.14E-01	6.87E-27		-7.58E-01	4.33E-15		-9.93E-01	4.45E-24		Unigene33329_All//gi|124361190|gb|ABN09162.1|//0.00E+00//Deoxyribodipyrimidine photolyase, class 1 [Medicago truncatula]	Unigene33329_All//0.00E+00//AT4G08920| CRY1 (CRYPTOCHROME 1); ATP binding / blue light photoreceptor/ protein homodimerization/ protein kinase	Unigene33329_All//0.00E+00//TC158591		ko04712|Circadian rhythm - plant		nr -
Unigene3333_All	2414	3.97	1.85	2.82	6.52	6.89	7.11	7.67	6.20	11.39	-1.10E+00	8.62E-09	Down	-4.90E-01	1.18E-02		7.94E-02	6.27E-01		1.25E-01	4.44E-01		-3.08E-01	8.79E-03		5.70E-01	3.59E-10		Unigene3333_All//gi|2462134|emb|CAA73798.1|//1.00E-099//reverse transcriptase [Beta vulgaris subsp. vulgaris]						nr -
Unigene33337_All	2640	2.97	2.17	1.03	17.93	11.27	6.84	12.65	8.87	13.54	-4.55E-01	2.96E-02		-1.53E+00	3.94E-11	Down	-6.70E-01	2.59E-21		-1.39E+00	1.02E-62	Down	-5.13E-01	6.17E-10		9.74E-02	2.78E-01		Unigene33337_All//gi|115444965|ref|NP_001046262.1|//1.00E-125//Os02g0208900 [Oryza sativa Japonica Group] >gi|49387899|dbj|BAD25002.1| ZIGA2 protein-like [Oryza sativa Japonica Group] >gi|49387911|dbj|BAD25011.1| ZIGA2 protein-like [Oryza sativa Japonica Group] >gi|113535793|dbj|BAF08176.1| Os02g0208900 [Oryza sativa Japonica Group]	Unigene33337_All//9.00E-84//AT4G13350| NIG (NSP (NUCLEAR SHUTTLE PROTEIN)-INTERACTING GTPASE); GTP binding / GTPase	Unigene33337_All//0.00E+00//TC131877		ko04144|Endocytosis		nr -
Unigene33338_All	2577	0.22	0.14	0.00	0.91	0.76	0.30	0.87	0.45	0.79	-6.99E-01	4.50E-01		-7.80E+00	2.60E-03		-2.54E-01	5.74E-01		-1.61E+00	2.00E-04	Down	-9.37E-01	1.42E-02		-1.41E-01	7.07E-01		Unigene33338_All//gi|115444965|ref|NP_001046262.1|//1.00E-115//Os02g0208900 [Oryza sativa Japonica Group] >gi|49387899|dbj|BAD25002.1| ZIGA2 protein-like [Oryza sativa Japonica Group] >gi|49387911|dbj|BAD25011.1| ZIGA2 protein-like [Oryza sativa Japonica Group] >gi|113535793|dbj|BAF08176.1| Os02g0208900 [Oryza sativa Japonica Group]	Unigene33338_All//1.00E-111//AT4G13350| NIG (NSP (NUCLEAR SHUTTLE PROTEIN)-INTERACTING GTPASE); GTP binding / GTPase	Unigene33338_All//0.00E+00//gi|73860724|gb|DT463463.1|DT463463		ko04144|Endocytosis		nr +
Unigene33340_All	3452	7.70	9.98	9.33	24.24	25.30	26.06	19.39	32.10	39.87	3.74E-01	4.32E-05		2.78E-01	5.89E-03		6.14E-02	3.69E-01		1.04E-01	8.74E-02		7.27E-01	4.16E-57		1.04E+00	4.60E-132	Up	Unigene33340_All//gi|115444965|ref|NP_001046262.1|//1.00E-140//Os02g0208900 [Oryza sativa Japonica Group] >gi|49387899|dbj|BAD25002.1| ZIGA2 protein-like [Oryza sativa Japonica Group] >gi|49387911|dbj|BAD25011.1| ZIGA2 protein-like [Oryza sativa Japonica Group] >gi|113535793|dbj|BAF08176.1| Os02g0208900 [Oryza sativa Japonica Group]	Unigene33340_All//1.00E-118//AT4G13350| NIG (NSP (NUCLEAR SHUTTLE PROTEIN)-INTERACTING GTPASE); GTP binding / GTPase	Unigene33340_All//0.00E+00//gi|164270968|gb|ES800011.1|ES800011		ko04144|Endocytosis		nr +
Unigene33353_All	1393	1.28	2.69	2.45	2.50	5.91	3.18	2.19	1.65	6.12	1.08E+00	8.32E-04	Up	9.38E-01	7.50E-03		1.24E+00	3.56E-10	Up	3.44E-01	2.75E-01		-4.05E-01	2.29E-01		1.49E+00	4.86E-15	Up	Unigene33353_All//gi|224073274|ref|XP_002304055.1|//1.00E-107//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222841487|gb|EEE79034.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene33353_All//4.00E-55//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene33353_All//0.00E+00//gi|109860888|gb|DW489867.1|DW489867		ko04626|Plant-pathogen interaction		nr -
Unigene33355_All	2488	2.84	2.91	3.25	13.21	16.64	14.70	7.27	4.55	15.93	3.68E-02	8.78E-01		1.97E-01	3.92E-01		3.32E-01	1.98E-05		1.54E-01	1.18E-01		-6.76E-01	6.41E-09		1.13E+00	3.82E-44	Up	Unigene33355_All//gi|224073274|ref|XP_002304055.1|//1.00E-166//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222841487|gb|EEE79034.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene33355_All//9.00E-81//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene33355_All//0.00E+00//TC135010		ko04626|Plant-pathogen interaction		nr -

Unigene33361_All	3823	5.20	2.17	3.26	8.00	7.03	5.13	9.18	6.55	5.56	-1.26E+00	2.56E-21	Down	-6.74E-01	1.27E-07		-1.87E-01	6.48E-02		-6.42E-01	1.23E-11		-4.87E-01	1.55E-09		-7.22E-01	5.30E-19		Unigene33361_All//gi|300827400|gb|ADK36642.1|//0.00E+00//MAPKKKe [Solanum lycopersicum]	Unigene33361_All//0.00E+00//AT3G13530| MAPKKK7; ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene33361_All//0.00E+00//TC148034				nr -
Unigene33365_All	3096	2.28	0.25	1.43	2.59	2.57	1.84	11.13	5.32	4.85	-3.22E+00	3.13E-25	Down	-6.76E-01	3.16E-03		-1.19E-02	9.52E-01		-4.95E-01	1.60E-02		-1.07E+00	2.96E-34	Down	-1.20E+00	1.99E-42	Down	Unigene33365_All//gi|223452412|gb|ACM89533.1|//0.00E+00//protein kinase [Glycine max]	Unigene33365_All//0.00E+00//AT3G46290| protein kinase, putative	Unigene33365_All//0.00E+00//gi|109829136|gb|DW227730.1|DW227730				nr +
Unigene33366_All	2938	4.74	3.41	1.67	5.39	4.04	3.41	11.08	7.13	4.61	-4.72E-01	1.72E-03		-1.51E+00	7.53E-19	Down	-4.15E-01	1.72E-03		-6.60E-01	1.24E-06		-6.37E-01	6.41E-14		-1.27E+00	1.17E-43	Down	Unigene33366_All//gi|223452398|gb|ACM89526.1|//0.00E+00//protein kinase [Glycine max]	Unigene33366_All//0.00E+00//AT3G46290| protein kinase, putative	Unigene33366_All//0.00E+00//TC137028				nr +
Unigene33367_All	3156	3.56	4.98	3.64	10.05	15.04	14.40	3.38	7.44	4.61	4.82E-01	6.22E-04		3.21E-02	8.66E-01		5.81E-01	3.36E-16		5.18E-01	1.17E-11		1.14E+00	3.14E-26	Up	4.49E-01	4.53E-04		Unigene33367_All//gi|223452412|gb|ACM89533.1|//0.00E+00//protein kinase [Glycine max]	Unigene33367_All//0.00E+00//AT3G46290| protein kinase, putative	Unigene33367_All//0.00E+00//TC159391				nr +
Unigene3337_All	1659	1.32	0.64	0.74	4.44	3.72	3.27	5.45	2.34	3.36	-1.05E+00	1.61E-02		-8.44E-01	6.32E-02		-2.58E-01	2.65E-01		-4.44E-01	4.23E-02		-1.22E+00	1.04E-11	Down	-6.98E-01	2.68E-05		Unigene3337_All//gi|186524238|ref|NP_197443.3|//1.00E-137//Ran GTPase binding / chromatin binding / zinc ion binding [Arabidopsis thaliana]	Unigene3337_All//7.00E-94//AT5G19420| Ran GTPase binding / chromatin binding / zinc ion binding	Unigene3337_All//0.00E+00//TC145090		GO:0046872		nr +
Unigene33377_All	680	2.00	3.28	2.51	5.27	7.65	7.51	6.03	5.65	12.95	7.13E-01	9.64E-02		3.25E-01	5.44E-01		5.36E-01	4.02E-02		5.09E-01	6.19E-02		-9.30E-02	7.50E-01		1.10E+00	4.28E-10	Up	Unigene33377_All//gi|145359475|ref|NP_200825.2|//4.00E-74//RNA binding / nucleic acid binding / nucleotide binding / protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene33377_All//2.00E-75//AT5G60170| RNA binding / nucleic acid binding / nucleotide binding / protein binding / zinc ion binding	Unigene33377_All//2.00E-171//TC133790		ko03018|RNA degradation		nr -
Unigene3338_All	1550	5.23	6.18	6.91	8.84	6.95	4.66	8.84	6.20	3.78	2.40E-01	2.24E-01		4.00E-01	3.02E-02		-3.46E-01	2.00E-02		-9.23E-01	7.06E-10		-5.11E-01	1.55E-04		-1.23E+00	5.15E-18	Down	Unigene3338_All//gi|18415647|ref|NP_568185.1|//4.00E-57//mitochondrial transcription termination factor family protein / mTERF family protein [Arabidopsis thaliana]	Unigene3338_All//3.00E-58//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene3338_All//0.00E+00//TC137461				nr +
Unigene33384_All	2950	3.53	8.30	4.96	6.96	8.08	8.73	11.71	17.64	18.81	1.23E+00	3.76E-25	Up	4.92E-01	1.20E-03		2.16E-01	6.50E-02		3.27E-01	2.36E-03		5.91E-01	3.87E-19		6.84E-01	8.60E-27		Unigene33384_All//gi|115483835|ref|NP_001065579.1|//1.00E-124//Os11g0114700 [Oryza sativa Japonica Group] >gi|113644283|dbj|BAF27424.1|Os11g0114700 [Oryza sativa Japonica Group]	Unigene33384_All//0.00E+00//AT3G51620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: nucleotidyltransferase family protein (TAIR:AT3G56320.1); Has 160 Blast hits to 133 proteins in 36 species: Archae - 0; Bacteria - 0; Metazoa - 19; Fungi - 21; Plants - 98; Viruses - 0; Other Eukaryotes - 22 (source: NCBI BLink).	Unigene33384_All//0.00E+00//TC171312				nr +
Unigene33387_All	1948	1.45	0.75	0.49	1.69	1.41	1.58	2.73	2.60	2.19	-9.43E-01	1.17E-02		-1.56E+00	1.54E-04	Down	-2.55E-01	5.03E-01		-9.84E-02	7.88E-01		-7.51E-02	7.69E-01		-3.22E-01	1.68E-01		Unigene33387_All//gi|297837655|ref|XP_002886709.1|//2.00E-23//EMB1674 [Arabidopsis lyrata subsp. lyrata] >gi|297332550|gb|EFH62968.1|EMB1674 [Arabidopsis lyrata subsp. lyrata]	Unigene33387_All//1.00E-19//AT1G58210| EMB1674 (EMBRYO DEFECTIVE 1674)	Unigene33387_All//0.00E+00//CO071792				nr -
Unigene3339_All	1954	0.56	1.58	1.36	11.22	14.96	12.80	5.73	0.75	2.41	1.49E+00	6.91E-05	Up	1.28E+00	2.02E-03		4.16E-01	8.93E-06		1.91E-01	1.10E-01		-2.94E+00	2.06E-44	Down	-1.25E+00	2.20E-15	Down	Unigene3339_All//gi|22326581|ref|NP_195946.2|//0.00E+00//LAC11 (laccase 11); laccase [Arabidopsis thaliana] >gi|75331174|sp|Q8VZA1.1|LAC11_ARATH RecName: Full=Laccase-11; AltName: Full=Benzenediol:oxygen oxidoreductase 11; AltName: Full=Urishiol oxidase 11; AltName: Full=Diphenol oxidase 11; Flags: Precursor >gi|17473695|gb|AAL38304.1|laccase (diphenol oxidase)-like protein [Arabidopsis thaliana] >gi|20148527|gb|AAM10154.1|laccase (diphenol oxidase)-like protein [Arabidopsis thaliana]	Unigene3339_All//0.00E+00//AT5G03260| LAC11 (laccase 11); laccase	Unigene3339_All//4.00E-20//CA994018		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0031410//GO:0046914	nr +
Unigene334_All	2942	2.45	1.67	1.30	4.91	3.25	3.70	7.73	3.51	4.59	-5.55E-01	1.07E-02		-9.13E-01	5.99E-05		-5.94E-01	1.22E-05		-4.08E-01	5.56E-03		-1.14E+00	1.95E-25	Down	-7.52E-01	1.68E-13		Unigene334_All//gi|297813873|ref|XP_002874820.1|//0.00E+00//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320657|gb|EFH51079.1|transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene334_All//0.00E+00//AT4G04940| transducin family protein / WD-40 repeat family protein	Unigene334_All//0.00E+00//CO099399		ko03040|Spliceosome//ko03022|Basal transcription factors		nr +
Unigene33400_All	913	1.26	0.44	1.05	3.27	1.92	2.47	4.58	1.92	3.53	-1.51E+00	2.31E-02		-2.64E-01	6.64E-01		-7.67E-01	2.54E-02		-4.04E-01	3.00E-01		-1.25E+00	4.57E-06	Down	-3.75E-01	1.55E-01		Unigene33400_All//gi|47847642|dbj|BAD22128.1|//3.00E-13//myosin-like protein [Oryza sativa Japonica Group]	Unigene33400_All//3.00E-46//AT4G31570| unknown protein					nr +
Unigene3341_All	1621	6.78	5.72	2.30	9.19	14.30	8.75	14.84	4.13	8.77	-2.45E-01	1.78E-01		-1.56E+00	9.42E-16	Down	6.38E-01	1.55E-09		-7.08E-02	6.97E-01		-1.85E+00	2.04E-54	Down	-7.58E-01	2.03E-14		Unigene3341_All//gi|30685695|ref|NP_188661.2|//1.00E-146//structural constituent of ribosome [Arabidopsis thaliana]	Unigene3341_All//3.00E-122//AT3G20260| structural constituent of ribosome	Unigene3341_All//0.00E+00//gi|164283630|gb|ES821636.1|ES821636				nr -
Unigene33410_All	3098	9.25	4.17	6.17	14.99	15.02	12.03	13.24	6.45	6.26	-1.15E+00	1.84E-26	Down	-5.85E-01	1.88E-08		3.00E-03	9.77E-01		-3.17E-01	3.16E-05		-1.04E+00	6.09E-39	Down	-1.08E+00	1.01E-42	Down	Unigene33410_All//gi|22326894|ref|NP_197440.2|//0.00E+00//pleckstrin homology (PH) domain-containing protein / RhoGAP domain-containing protein [Arabidopsis thaliana] >gi|79598819|ref|NP_851042.2|pleckstrin homology (PH) domain-containing protein / RhoGAP domain-containing protein [Arabidopsis thaliana] >gi|20147217|gb|AAM10224.1|At5g19390/F7K24_140 [Arabidopsis thaliana] >gi|25090125|gb|AAN72235.1|At5g19390/F7K24_140 [Arabidopsis thaliana] >gi|222424276|dbj|BAH20095.1|AT5G19390 [Arabidopsis thaliana]	Unigene33410_All//0.00E+00//AT5G19390| pleckstrin homology (PH) domain-containing protein / RhoGAP domain-containing protein	Unigene33410_All//0.00E+00//TC165343				nr +
Unigene33412_All	7644	7.82	48.30	13.71	52.04	59.42	101.46	79.06	152.82	135.60	2.63E+00	0.00E+00	Up	8.09E-01	1.87E-51		1.91E-01	2.16E-19		9.63E-01	0.00E+00		9.51E-01	0.00E+00		7.78E-01	0.00E+00		Unigene33412_All//gi|225455692|ref|XP_002267865.1|//0.00E+00//PREDICTED: similar to GLT1 (NADH-dependent glutamate synthase 1 gene) [Vitis vinifera]	Unigene33412_All//0.00E+00//AT5G53460| GLT1; glutamate synthase (NADH)	Unigene33412_All//0.00E+00//TC151252		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene33413_All	1152	4.86	6.82	7.90	3.03	2.24	1.25	0.37	0.15	0.14	4.88E-01	1.95E-02		7.02E-01	3.88E-04		-4.33E-01	1.95E-01		-1.27E+00	1.32E-04	Down	-1.34E+00	2.24E-01		-1.41E+00	1.74E-01		Unigene33413_All//gi|42561588|ref|NP_171639.3|//1.00E-156//tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	Unigene33413_All//4.00E-152//AT1G01320| tetratricopeptide repeat (TPR)-containing protein	Unigene33413_All//6.00E-46//gi|48828089|gb|CO126479.1|CO126479				nr +
Unigene33419_All	2219	8.04	9.25	7.37	12.12	11.89	20.05	19.40	26.54	46.93	2.02E-01	1.21E-01		-1.26E-01	3.95E-01		-2.83E-02	8.24E-01		7.26E-01	2.31E-20		4.52E-01	1.45E-13		1.27E+00	3.23E-138	Up	Unigene33419_All//gi|115471691|ref|NP_001059444.1|//0.00E+00//Os07g0409900 [Oryza sativa Japonica Group] >gi|125592069|gb|AAF23901.2|AF194414_1 calcium-dependent protein kinase [Oryza sativa] >gi|113610980|dbj|BAF21358.1|Os07g0409900 [Oryza sativa Japonica Group]	Unigene33419_All//0.00E+00//AT4G36070| CPK18; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ protein kinase/ protein serine/threonine kinase	Unigene33419_All//0.00E+00//TC133012		ko04626|Plant-pathogen interaction		nr -
Unigene33423_All	4180	7.76	17.32	8.18	16.05	19.83	21.02	42.52	65.81	64.48	1.16E+00	2.93E-66	Up	7.57E-02	4.97E-01		3.05E-01	7.31E-09		3.89E-01	3.32E-13		6.30E-01	2.19E-109		6.01E-01	1.05E-100		Unigene33423_All//gi|15220369|ref|NP_176892.1|//0.00E+00//LINC1 (LITTLE NUCLEI) [Arabidopsis thaliana]	Unigene33423_All//0.00E+00//AT1G67230| LINC1 (LITTLE NUCLEI)	Unigene33423_All//0.00E+00//gi|73865032|gb|DT467771.1|DT467771		ko03040|Spliceosome		nr -
Unigene33426_All	6171	14.40	99.51	28.42	18.69	36.92	42.82	48.68	128.38	153.70	2.79E+00	0.00E+00	Up	9.81E-01	9.21E-119		9.83E-01	1.69E-189		1.20E+00	1.56E-272	Up	1.40E+00	0.00E+00	Up	1.66E+00	0.00E+00	Up	Unigene33426_All//gi|19699067|gb|AAL90901.1|//0.00E+00//AT5g20250/F5O24_140 [Arabidopsis thaliana] >gi|23308457|gb|AAN15198.1|At5g20250/F5O24_140 [Arabidopsis thaliana] >gi|110742681|dbj|BAE99252.1| seed imbitition protein-like [Arabidopsis thaliana]	Unigene33426_All//0.00E+00//AT5G20250| DIN10 (DARK INDUCIBLE 10); hydrolase, hydrolyzing O-glycosyl compounds	Unigene33426_All//0.00E+00//TC132686		ko00052|Galactose metabolism		nr -
Unigene33428_All	837	4.69	6.05	10.12	13.75	10.86	12.57	6.62	4.84	7.85	3.69E-01	1.79E-01		1.11E+00	1.46E-07	Up	-3.40E-01	4.06E-02		-1.29E-01	5.20E-01		-4.50E-01	5.06E-02		2.47E-01	2.46E-01		Unigene33428_All//gi|75146761|sp|Q84K11.1|PPP5_SOLLC//4.00E-90//RecName: Full=Serine/threonine-protein phosphatase 5; AltName: Full=LePP5 >gi|28141004|gb|AAO26213.1| type 5 protein serine/threonine phosphatase 62 kDa isoform [Solanum lycopersicum] >gi|28141085|gb|AAO26215.1| type 5 protein serine/threonine phosphatase 62 kDa isoform [Solanum lycopersicum]	Unigene33428_All//6.00E-76//AT2G42810| PP5.2 (PROTEIN PHOSPHATASE 5.2); phosphoprotein phosphatase/ protein binding / protein serine/threonine phosphatase	Unigene33428_All//0.00E+00//gi|78348159|gb|DT568433.1|DT568433				nr +
Unigene3343_All	1287	2.48	1.06	1.66	2.44	3.21	2.81	1.08	1.69	1.45	-1.22E+00	6.03E-04	Down	-5.84E-01	1.13E-01		3.97E-01	2.12E-01		2.03E-01	6.05E-01		6.39E-01	1.05E-01		4.24E-01	3.19E-01		Unigene3343_All//gi|158828302|gb|ABW81177.1|//9.00E-20//gag non-LTR retrotransposase [Arabidopsis cebennensis]	Unigene3343_All//9.00E-21//AT2G01050| nucleic acid binding / zinc ion binding	Unigene3343_All//4.00E-38//gi|78340235|gb|DT560509.1|DT560509				nr -
Unigene33430_All	1392	2.74	2.66	1.15	3.51	2.72	3.28	7.14	4.92	4.18	-4.63E-02	8.90E-01		-1.26E+00	1.80E-04	Down	-3.66E-01	1.90E-01		-9.79E-02	7.39E-01		-5.36E-01	9.35E-04		-7.73E-01	1.15E-06		Unigene33430_All//gi|75146761|sp|Q84K11.1|PPP5_SOLLC//3.00E-80//RecName: Full=Serine/threonine-protein phosphatase 5; AltName: Full=LePP5 >gi|28141004|gb|AAO26213.1| type 5 protein serine/threonine phosphatase 62 kDa isoform [Solanum lycopersicum] >gi|28141085|gb|AAO26215.1| type 5 protein serine/threonine phosphatase 62 kDa isoform [Solanum lycopersicum]	Unigene33430_All//5.00E-81//AT2G42810| PP5.2 (PROTEIN PHOSPHATASE 5.2); phosphoprotein phosphatase/ protein binding / protein serine/threonine phosphatase	Unigene33430_All//0.00E+00//TC176392				nr +

Unigene33440_All	597	0.96	3.48	0.00	2.00	0.81	1.21	2.83	2.38	2.54	1.85E+00	1.67E-04	Up	-9.91E+00	2.60E-03		-1.31E+00	2.84E-02		-7.26E-01	2.56E-01		-2.51E-01	6.29E-01		-1.60E-01	7.13E-01		Unigene33440_All//gi|222424288|dbj|BAH20101.1|//2.00E-44//AT3G54750|Arabidopsis thaliana]	Unigene33440_All//3.00E-45//AT3G54750| unknown protein	Unigene33440_All//2.00E-139//DV849382				nr +
Unigene33441_All	1054	0.79	0.14	0.66	1.61	1.83	1.63	3.45	1.43	2.19	-2.46E+00	6.70E-03		-2.74E-01	7.05E-01		1.87E-01	7.48E-01		1.91E-02	9.70E-01		-1.27E+00	1.75E-05	Down	-6.54E-01	1.82E-02		Unigene33441_All//gi|222424288|dbj|BAH20101.1|//1.00E-63//AT3G54750|Arabidopsis thaliana]	Unigene33441_All//9.00E-65//AT3G54750| unknown protein					nr +
Unigene33442_All	1321	2.69	1.84	0.97	4.90	2.14	2.60	6.85	3.01	3.59	-5.49E-01	9.40E-02		-1.48E+00	3.63E-05	Down	-1.20E+00	3.72E-08	Down	-9.16E-01	5.67E-05		-1.19E+00	2.81E-11	Down	-9.33E-01	3.90E-08		Unigene33442_All//gi|222424288|dbj|BAH20101.1|//1.00E-122//AT3G54750|Arabidopsis thaliana]	Unigene33442_All//4.00E-123//AT3G54750| unknown protein	Unigene33442_All//0.00E+00//DV849382				nr -
Unigene33444_All	2209	0.95	0.64	0.43	1.15	1.45	1.35	3.37	0.91	1.39	-5.61E-01	2.13E-01		-1.13E+00	1.70E-02		3.34E-01	3.84E-01		2.31E-01	5.91E-01		-1.89E+00	6.91E-18	Down	-1.28E+00	8.07E-11	Down	Unigene33444_All//gi|222424288|dbj|BAH20101.1|//1.00E-164//AT3G54750|Arabidopsis thaliana]	Unigene33444_All//2.00E-165//AT3G54750| unknown protein	Unigene33444_All//0.00E+00//DV849382				nr -
Unigene33445_All	3732	2.52	1.81	1.11	4.16	2.35	3.62	5.49	2.91	3.30	-4.83E-01	1.02E-02		-1.18E+00	4.09E-09	Down	-8.24E-01	2.57E-10		-2.03E-01	1.98E-01		-9.16E-01	2.57E-16		-7.36E-01	7.60E-12		Unigene33445_All//gi|75116543|sp|Q67XX3.1|FB252_ARATH//1.00E-160//RecName: Full=F-box protein At5g06550	Unigene33445_All//2.00E-161//AT5G06550| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: cell surface receptor linked signal transduction; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Cyclin-like F-box (InterPro:IPR001810), Transcription factor jumonji/aspartyl beta-hydroxylase (InterPro:IPR003347), Transcription factor jumonji (InterPro:IPR013129); BEST Arabidopsis thaliana protein match is: transferase, transferring glycosyl groups (TAIR:AT1G78280.1); Has 1299 Blast hits to 1289 proteins in 204 species: Archae - 0; Bacteria - 195; Metazoa - 777; Fungi - 106; Plants - 94; Viruses - 0; Other Eukaryotes - 127 (source: NCBI BLink).	Unigene33445_All//0.00E+00//ESS30069				nr -
Unigene33448_All	2320	1.47	2.14	1.51	3.29	5.51	4.83	2.92	1.44	2.11	5.46E-01	4.42E-02		4.74E-02	8.95E-01		7.45E-01	4.90E-07		5.55E-01	9.24E-04		-1.02E+00	6.85E-07	Down	-4.65E-01	1.77E-02		Unigene33448_All//gi|12229655|sp|Q9LK90.1|ALA8_ARATH//0.00E+00//RecName: Full=Putative phospholipid-transporting ATPase 8; Short=AtALA8; AltName: Full=Aminophospholipid flippase 8 >gi|11994492|dbj|BAB02533.1| P-type transporting ATPase-like protein [Arabidopsis thaliana]	Unigene33448_All//0.00E+00//AT3G27870| haloacid dehalogenase-like hydrolase family protein	Unigene33448_All//1.00E-76//TC142434				nr -
Unigene33449_All	3914	1.08	2.37	1.06	6.61	5.82	5.00	5.28	4.72	4.02	1.13E+00	8.31E-09	Up	-2.91E-02	9.40E-01		-1.82E-01	1.09E-01		-4.03E-01	1.21E-04		-1.62E-01	1.77E-01		-3.94E-01	1.86E-04		Unigene33449_All//gi|12229655|sp|Q9LK90.1|ALA8_ARATH//0.00E+00//RecName: Full=Putative phospholipid-transporting ATPase 8; Short=AtALA8; AltName: Full=Aminophospholipid flippase 8 >gi|11994492|dbj|BAB02533.1| P-type transporting ATPase-like protein [Arabidopsis thaliana]	Unigene33449_All//0.00E+00//AT3G27870| haloacid dehalogenase-like hydrolase family protein	Unigene33449_All//0.00E+00//TC142434				nr -
Unigene3345_All	857	39.13	28.68	23.55	55.69	66.30	71.30	79.73	14.00	19.66	-4.49E-01	1.24E-06		-7.33E-01	3.04E-14		2.52E-01	1.58E-04		3.57E-01	4.36E-08		-2.51E+00	8.04E-226	Down	-2.02E+00	6.72E-178	Down	Unigene3345_All//gi|297834946|ref|XP_002885355.1|//4.00E-88//ubiquitin-conjugating enzyme 19 [Arabidopsis lyrata subsp. lyrata] >gi|297331195|gb|EFH61614.1| ubiquitin-conjugating enzyme 19 [Arabidopsis lyrata subsp. lyrata]	Unigene3345_All//3.00E-89//AT1G50490| UBC20 (ubiquitin-conjugating enzyme 20); ubiquitin-protein ligase	Unigene3345_All//0.00E+00//gi|109859740|gb|DW488719.1|DW488719		ko04120|Ubiquitin mediated proteolysis	GO:0019787//GO:0019941//GO:0032446//GO:0032559//GO:0043231//GO:0060255//GO:0070646	nr +
Unigene33451_All	2170	1.49	3.55	1.52	2.75	3.41	3.25	6.27	3.97	10.96	1.25E+00	1.41E-08	Up	2.54E-02	9.60E-01		3.09E-01	1.74E-01		2.37E-01	3.45E-01		-6.61E-01	1.12E-06		8.05E-01	1.26E-15		Unigene33451_All//gi|62857012|dbj|BAD95891.1|//0.00E+00//Ser/Thr protein kinase [Lotus japonicus]	Unigene33451_All//0.00E+00//AT4G00720| ATSK32 (SHAGGY-LIKE PROTEIN KINASE 32); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene33451_All//0.00E+00//gi|73861298|gb|DT464037.1|DT464037				nr -
Unigene33453_All	1271	1.93	1.48	1.30	3.72	2.68	3.06	3.03	6.31	3.01	-3.92E-01	3.51E-01		-5.75E-01	1.78E-01		-4.73E-01	8.34E-02		-2.85E-01	3.57E-01		1.06E+00	1.57E-08	Up	-8.60E-03	9.69E-01		Unigene33453_All//gi|33591210|gb|AAQ23109.1|//1.00E-143//shaggy-related protein kinase 4 [Physcomitrella patens]	Unigene33453_All//2.00E-138//AT4G00720| ATSK32 (SHAGGY-LIKE PROTEIN KINASE 32); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene33453_All//0.00E+00//CO108942				nr +
Unigene33455_All	2006	6.10	12.00	5.34	12.24	15.11	14.66	13.49	17.84	38.75	9.75E-01	3.49E-17		-1.94E-01	2.92E-01		3.03E-01	1.35E-03		2.60E-01	1.11E-02		4.03E-01	4.48E-07		1.52E+00	5.46E-135	Up	Unigene33455_All//gi|15236918|ref|NP_191981.1|//0.00E+00//ATSK32 (SHAGGY-LIKE PROTEIN KINASE 32); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|12643793|sp|Q96287.3|KSG8_ARATH RecName: Full=Shaggy-related protein kinase theta; AltName: Full=ASK-theta >gi|1944518|emb|CAA69156.1| Shaggy-like kinase tetha [Arabidopsis thaliana] >gi|3047105|gb|AC13616.1| protein kinase [Arabidopsis thaliana] >gi|7267411|emb|CAB80881.1| Shaggy related protein kinase tetha [Arabidopsis thaliana] >gi|17063158|gb|AAL32976.1| AT4g00720/F6N23_11 [Arabidopsis thaliana] >gi|21700933|gb|AAM70590.1| AT4g00720/F6N23_11 [Arabidopsis thaliana] >gi|110740517|dbj|BAE98364.1| Shaggy related protein kinase theta [Arabidopsis thaliana]	Unigene33455_All//0.00E+00//AT4G00720| ATSK32 (SHAGGY-LIKE PROTEIN KINASE 32); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene33455_All//0.00E+00//gi|73848910|gb|DT457930.1|DT457930				nr +
Unigene33457_All	1120	7.89	4.34	7.84	16.37	18.14	10.52	9.32	1.79	6.01	-8.62E-01	1.02E-05		-9.10E-03	9.89E-01		1.48E-01	2.97E-01		-6.37E-01	3.77E-07		-2.38E+00	5.70E-33	Down	-6.33E-01	3.56E-05		Unigene33457_All//gi|22327641|ref|NP_199593.2|//1.00E-156//FRA1 (FRAGILE FIBER 1); microtubule motor [Arabidopsis thaliana] >gi|30695202|ref|NP_851151.1| FRA1 (FRAGILE FIBER 1); microtubule motor [Arabidopsis thaliana] >gi|27260890|gb|AAN86114.1| kinesin-like protein [Arabidopsis thaliana] >gi|27260892|gb|AAN86115.1| kinesin-like protein [Arabidopsis thaliana]	Unigene33457_All//4.00E-157//AT5G47820| FRA1 (FRAGILE FIBER 1); microtubule motor	Unigene33457_All//0.00E+00//TC170749				nr +
Unigene33462_All	868	2.95	4.20	4.11	5.57	3.05	2.03	2.29	0.63	1.24	5.09E-01	1.20E-01		4.77E-01	1.66E-01		-8.66E-01	6.72E-04		-1.46E+00	2.22E-07	Down	-1.87E+00	2.98E-05	Down	-8.86E-01	2.45E-02		Unigene33462_All//gi|15241663|ref|NP_195821.1|//1.00E-134//ROPGEF7; Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana] >gi|53828569|gb|AAU94394.1| At5g02010 [Arabidopsis thaliana] >gi|55733765|gb|AAV59279.1| At5g02010 [Arabidopsis thaliana]	Unigene33462_All//1.00E-128//AT5G02010| ROPGEF7; Rho guanyl-nucleotide exchange factor	Unigene33462_All//0.00E+00//gi|84150016|gb|DN781316.1|DN781316				nr +
Unigene33463_All	275	0.00	1.84	1.16	0.91	0.38	3.28	1.23	8.66	2.46	1.08E+01	4.04E-03		1.02E+01	4.52E-02		-1.27E+00	4.24E-01		1.86E+00	2.18E-02		2.82E+00	1.61E-09	Up	1.00E+00	1.91E-01					Unigene33463_All//3.00E-81//BG446496				
Unigene33464_All	1038	1.81	0.54	0.41	2.69	2.99	2.78	2.93	3.22	2.15	-1.76E+00	5.92E-04	Down	-2.14E+00	1.32E-04	Down	1.52E-01	7.30E-01		5.12E-02	9.16E-01		1.35E-01	6.77E-01		-4.48E-01	1.53E-01		Unigene33464_All//gi|115441057|ref|NP_001044808.1|//6.00E-74//Os01g0849100 [Oryza sativa Japonica Group] >gi|113534339|dbj|BAF06722.1| Os01g0849100 [Oryza sativa Japonica Group]	Unigene33464_All//1.00E-66//AT5G02010| ROPGEF7; Rho guanyl-nucleotide exchange factor	Unigene33464_All//0.00E+00//TC135122				nr -
Unigene33465_All	493	0.32	4.01	1.94	2.12	2.44	1.56	1.54	0.34	0.08	3.65E+00	3.76E-08	Up	2.61E+00	3.45E-03		2.04E-01	8.01E-01		-4.46E-01	5.32E-01		-2.19E+00	7.77E-03		-4.26E+00	8.65E-05	Down	Unigene33465_All//gi|15241663|ref|NP_195821.1|//2.00E-55//ROPGEF7; Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana] >gi|53828569|gb|AAU94394.1| At5g02010 [Arabidopsis thaliana] >gi|55733765|gb|AAV59279.1| At5g02010 [Arabidopsis thaliana]	Unigene33465_All//5.00E-54//AT5G02010| ROPGEF7; Rho guanyl-nucleotide exchange factor	Unigene33465_All//0.00E+00//gi|109848503|gb|DW477483.1|DW477483				nr -
Unigene33467_All	4277	0.62	3.92	1.41	1.50	1.96	7.21	8.01	40.82	27.86	2.65E+00	2.96E-48	Up	1.17E+00	4.99E-06	Up	3.81E-01	6.04E-02		2.26E+00	9.97E-79	Up	2.35E+00	0.00E+00	Up	1.80E+00	5.95E-262	Up	Unigene33467_All//gi|115441057|ref|NP_001044808.1|//1.00E-156//Os01g0849100 [Oryza sativa Japonica Group] >gi|113534339|dbj|BAF06722.1| Os01g0849100 [Oryza sativa Japonica Group]	Unigene33467_All//1.00E-148//AT5G05940| ROPGEF5 (ROP GUANINE NUCLEOTIDE EXCHANGE FACTOR 5); Rho guanyl-nucleotide exchange factor	Unigene33467_All//0.00E+00//TC135122				nr +
Unigene33468_All	1911	1.83	2.65	1.53	5.34	6.92	4.35	2.94	1.66	1.17	5.32E-01	4.69E-02		-2.59E-01	4.65E-01		3.73E-01	1.47E-02		-2.97E-01	1.19E-01		-8.24E-01	2.30E-04		-1.33E+00	6.75E-09	Down	Unigene33468_All//gi|15241663|ref|NP_195821.1|//1.00E-172//ROPGEF7; Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana] >gi|53828569|gb|AAU94394.1| At5g02010 [Arabidopsis thaliana] >gi|55733765|gb|AAV59279.1| At5g02010 [Arabidopsis thaliana]	Unigene33468_All//2.00E-172//AT5G02010| ROPGEF7; Rho guanyl-nucleotide exchange factor	Unigene33468_All//0.00E+00//ES818273				nr -
Unigene33469_All	1479	3.33	5.72	6.80	5.22	5.63	4.28	2.29	0.57	0.94	7.83E-01	8.78E-05		1.03E+00	5.77E-08	Up	1.10E-01	6.42E-01		-2.88E-01	2.06E-01		-2.02E+00	3.19E-09	Down	-1.28E+00	2.16E-05	Down	Unigene33469_All//gi|15241663|ref|NP_195821.1|//0.00E+00//ROPGEF7; Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana] >gi|53828569|gb|AAU94394.1| At5g02010 [Arabidopsis thaliana] >gi|55733765|gb|AAV59279.1| At5g02010 [Arabidopsis thaliana]	Unigene33469_All//4.00E-172//AT5G02010| ROPGEF7; Rho guanyl-nucleotide exchange factor	Unigene33469_All//0.00E+00//TC150559				nr +
Unigene33471_All	901	13.01	12.26	3.66	16.42	15.06	24.61	23.09	27.37	30.20	-8.54E-02	6.20E-01		-1.83E+00	7.78E-21	Down	-1.25E-01	4.67E-01		5.84E-01	2.55E-07		2.45E-01	1.60E-02		3.87E-01	2.00E-05		Unigene33471_All//gi|52207936|emb|CAE47068.1|//1.00E-111//ABC transporter [Populus tremula x Populus tremuloides]	Unigene33471_All//1.00E-111//AT3G54540| ATGCN4; transporter	Unigene33471_All//0.00E+00//TC172131				nr -

Unigene33472_All	2694	7.59	5.74	3.78	11.85	8.74	9.69	17.69	8.66	7.08	-4.05E-01	9.07E-04		-1.01E+00	6.62E-15	Down	-4.39E-01	5.18E-07		-2.91E-01	2.38E-03		-1.03E+00	1.23E-44	Down	-1.32E+00	8.85E-68	Down	Unigene33472_All//gi|52207936|emb|CAE47098.1|//0.00E+00//ABC transporter [Populus tremula x Populus tremuloides]	Unigene33472_All//0.00E+00//AT3G54540| ATGCM4; transporter	Unigene33472_All//0.00E+00//TC163283				nr +
Unigene33474_All	1486	29.22	18.11	27.92	36.84	32.21	16.59	6.69	6.75	3.89	-6.91E-01	3.12E-17		-6.61E-02	5.06E-01		-1.94E-01	5.85E-03		-1.15E+00	4.79E-54	Down	1.37E-02	9.68E-01		-7.82E-01	8.55E-07		Unigene33474_All//gi|6996308|emb|CAB75469.1|//1.00E-22//copia-type reverse transcriptase-like protein [Arabidopsis thaliana]	Unigene33474_All//1.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene33474_All//0.00E+00//TC177548				nr -
Unigene33480_All	2774	4.47	6.32	5.59	5.44	4.89	5.76	24.77	31.31	11.99	5.00E-01	1.59E-04		3.22E-01	3.45E-02		-1.54E-01	3.42E-01		8.30E-02	6.20E-01		3.38E-01	9.32E-12		-1.05E+00	1.90E-67	Down	Unigene33480_All//gi|30678834|ref|NP_566204.2|//0.00E+00//DegP7 (DegP protease 7): catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase [Arabidopsis thaliana] >gi|75330785|sp|Q8RY22.1|DEGP7_ARATH RecName: Full=Protease Do-like 7 >gi|19310429|gb|AAL84951.1| AT3g03380/T21F5_20 [Arabidopsis thaliana] >gi|27363448|gb|AAO11643.1| At3g03380/T21F5_20 [Arabidopsis thaliana]	Unigene33480_All//0.00E+00//AT3G03380| DegP7 (DegP protease 7); catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase	Unigene33480_All//0.00E+00//TC143107				nr +
Unigene33483_All	2371	1.08	2.52	1.21	3.40	4.05	4.13	5.60	5.46	6.00	1.22E+00	1.21E-06	Up	1.66E-01	6.57E-01		2.52E-01	2.13E-01		2.80E-01	1.58E-01		-3.51E-02	8.30E-01		9.94E-02	5.17E-01		Unigene33483_All//gi|15232498|ref|NP_188130.1|//1.00E-130//AAA-type ATPase family protein [Arabidopsis thaliana]	Unigene33483_All//1.00E-114//AT3G15120| AAA-type ATPase family protein	Unigene33483_All//6.00E-137//TC142926		ko03050|Proteasome		nr +
Unigene33485_All	1184	3.84	0.68	1.98	5.68	4.97	3.20	5.61	3.88	4.64	-2.49E+00	9.27E-13	Down	-9.58E-01	1.25E-03		-1.92E-01	4.48E-01		-8.26E-01	2.00E-04		-5.30E-01	9.54E-03		-2.72E-01	1.94E-01		Unigene33485_All//gi|108864075|gb|ABA91813.2|//1.00E-141//Armadillo/beta-catenin-like repeat family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene33485_All//9.00E-135//AT1G77460| binding	Unigene33485_All//0.00E+00//ES819726				nr -
Unigene33488_All	3795	1.25	1.39	1.64	2.85	3.59	2.77	4.12	1.77	3.83	1.46E-01	6.21E-01		3.88E-01	1.30E-01		3.35E-01	2.81E-02		-3.88E-02	8.57E-01		-1.22E+00	1.30E-19	Down	-1.06E-01	4.59E-01		Unigene33488_All//gi|297839607|ref|XP_002887685.1|//0.00E+00//C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333526|gb|EFH63944.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene33488_All//0.00E+00//AT1G77460| binding	Unigene33488_All//0.00E+00//ES819726				nr -
Unigene33491_All	1630	4.59	2.36	3.14	3.48	3.11	2.96	13.54	19.33	6.62	-9.58E-01	9.04E-06		-5.50E-01	1.37E-02		-1.66E-01	5.60E-01		-2.33E-01	4.06E-01		5.14E-01	1.93E-09		-1.03E+00	8.78E-22	Down	Unigene33491_All//gi|224065529|ref|XP_002301842.1|//1.00E-146//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222843568|gb|EEE81115.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene33491_All//1.00E-139//AT1G04120| ATMRP5: ATPase, coupled to transmembrane movement of substances / sulfonylurea receptor	Unigene33491_All//0.00E+00//TC141629		ko02010|ABC transporters		nr +
Unigene33492_All	3871	3.57	1.60	2.09	14.46	9.67	8.46	10.68	6.78	5.31	-1.16E+00	2.58E-13	Down	-7.71E-01	8.88E-07		-5.81E-01	1.42E-19		-7.74E-01	1.09E-28		-6.56E-01	2.39E-18		-1.01E+00	1.41E-38	Down	Unigene33492_All//gi|224132268|ref|XP_002321297.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222862070|gb|EEE99612.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene33492_All//1.00E-00//AT1G04120| ATMRP5; ATPase, coupled to transmembrane movement of substances / sulfonylurea receptor	Unigene33492_All//0.00E+00//gi|78342922|gb|DT563196.1|DT563196		ko02010|ABC transporters		nr +
Unigene33493_All	2620	1.92	3.23	1.44	4.16	2.71	11.70	5.70	5.62	2.40	7.53E-01	1.59E-04		-4.10E-01	1.50E-01		-6.21E-01	9.85E-05		1.49E+00	1.34E-44	Up	-2.07E-02	9.03E-01		-1.25E+00	5.09E-20	Down	Unigene33493_All//gi|28268678|dbj|BAC58864.1|//0.00E+00//respiratory burst oxidase homolog [Nicotiana benthamiana]	Unigene33493_All//0.00E+00//AT1G64060| ATRBOH F (ARABIDOPSIS THALIANA RESPIRATORY BURST OXIDASE PROTEIN F); NAD(P)H oxidase	Unigene33493_All//0.00E+00//TC173562		ko04626|Plant-pathogen interaction		nr +
Unigene33495_All	2111	19.36	60.03	45.25	12.74	29.02	29.95	10.03	18.57	8.08	1.63E+00	2.48E-194	Up	1.23E+00	7.90E-93	Up	1.19E+00	4.94E-69	Up	1.23E+00	1.28E-68	Up	8.88E-01	6.66E-29		-3.13E-01	2.88E-03		Unigene33495_All//gi|297816858|ref|XP_002876312.1|//0.00E+00//regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322150|gb|EFH52571.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	Unigene33495_All//1.00E-157//AT3G55580| regulator of chromosome condensation (RCC1) family protein	Unigene33495_All//0.00E+00//gi|78338723|gb|DT558997.1|DT558997		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene33496_All	2272	17.55	47.17	31.38	16.97	28.75	31.39	8.75	15.93	10.47	1.43E+00	7.29E-135	Up	8.39E-01	2.44E-37		7.61E-01	2.04E-35		8.87E-01	2.09E-45		8.65E-01	1.29E-25		2.59E-01	9.48E-03		Unigene33496_All//gi|15233306|ref|NP_191117.1|//1.00E-136//regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana] >gi|7076801|emb|CAB75916.1| Regulator of chromosome condensation-like protein [Arabidopsis thaliana]	Unigene33496_All//1.00E-98//AT3G55580| regulator of chromosome condensation (RCC1) family protein	Unigene33496_All//0.00E+00//TC139073		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene33498_All	633	7.36	4.40	1.35	4.01	6.80	4.64	13.29	12.48	5.98	-7.41E-01	7.86E-03		-2.45E+00	3.35E-12	Down	7.61E-01	7.41E-03		2.09E-01	6.38E-01		-9.10E-02	6.47E-01		-1.15E+00	2.01E-10	Down	Unigene33498_All//gi|115646710|gb|AB117069.1|//3.00E-20//At3g48710 [Arabidopsis thaliana]	Unigene33498_All//1.00E-05//AT3G48710| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: DEX, C-terminal (InterPro:IPR014876); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G63550.2); Has 48226 Blast hits to 25734 proteins in 1103 species: Archae - 54; Bacteria - 6881; Metazoa - 21026; Fungi - 4604; Plants - 1514; Viruses - 306; Other Eukaryotes - 13841 (source: NCBI BLink).	Unigene33498_All//3.00E-114//TC157812				nr +
Unigene3350_All	1120	4.30	1.90	3.00	7.52	7.07	5.00	12.27	5.34	4.94	-1.18E+00	2.86E-05	Down	-5.21E-01	7.30E-02		-8.81E-02	7.20E-01		-5.88E-01	2.79E-03		-1.20E+00	5.57E-17	Down	-1.31E+00	5.71E-20	Down	Unigene3350_All//gi|16323093|gb|AAL15281.1|//2.00E-42//At1g73940/F2P9_19 [Arabidopsis thaliana] >gi|21360419|gb|AAM47325.1| At1g73940/F2P9_19 [Arabidopsis thaliana]	Unigene3350_All//3.00E-40//AT1G73940| unknown protein	Unigene3350_All//0.00E+00//TC149823			GO:0043231	nr -
Unigene33502_All	361	4.49	1.97	3.69	4.00	2.48	9.51	4.22	9.38	2.10	-1.19E+00	2.32E-02		-2.85E-01	6.21E-01		-6.90E-01	2.06E-01		1.25E+00	2.28E-04	Up	1.15E+00	1.58E-04	Up	-1.01E+00	2.94E-02		Unigene33502_All//gi|116309951|emb|CAH66982.1|//3.00E-40//H0714H04.9 [Oryza sativa (indica cultivar-group)]	Unigene33502_All//1.00E-33//AT1G48920| ATNUC-L1; nucleic acid binding / nucleotide binding	Unigene33502_All//2.00E-151//gi|13351841|gb|BG442189.1|BG442189				nr +
Unigene33505_All	2379	28.85	10.44	11.68	49.06	47.94	63.75	126.68	67.89	92.92	-1.47E+00	9.24E-91	Down	-1.30E+00	1.98E-73	Down	-3.33E-02	5.91E-01		3.78E-01	2.94E-21		-9.00E-01	3.32E-222		-4.47E-01	2.28E-66		Unigene33505_All//gi|21700195|dbj|BAC02896.1|//1.00E-162//tobacco nucleolin [Nicotiana tabacum]	Unigene33505_All//7.00E-53//AT1G48920| ATNUC-L1; nucleic acid binding / nucleotide binding	Unigene33505_All//0.00E+00//gi|164250348|gb|ES814502.1|ES814502				nr -
Unigene33506_All	1109	2.97	2.10	2.59	4.04	3.60	5.29	6.10	1.88	5.07	-5.00E-01	1.44E-01		-1.97E-01	6.17E-01		-1.67E-01	6.06E-01		3.89E-01	1.31E-01		-1.69E+00	3.80E-14	Down	-2.68E-01	1.95E-01		Unigene33506_All//gi|49533766|gb|AT66765.1|//1.00E-18//Putative selenium-binding protein, related [Solanum demissum]	Unigene33506_All//1.00E-10//AT2G25580| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT4G32450.1); Has 7881 Blast hits to 3723 proteins in 97 species: Archae - 0; Bacteria - 6; Metazoa - 6; Fungi - 16; Plants - 7829; Viruses - 0; Other Eukaryotes - 24 (source: NCBI BLink).	Unigene33506_All//3.00E-115//gi|164344121|gb|ES843928.1|ES843928				nr -
Unigene3351_All	1815	3.34	1.54	2.46	3.51	1.50	0.77	12.67	3.32	7.90	-1.12E+00	5.08E-06	Down	-4.40E-01	8.54E-02		-1.23E+00	2.34E-08	Down	-2.19E+00	2.61E-16	Down	-1.93E+00	2.33E-55	Down	-6.81E-01	1.28E-11		Unigene3351_All//gi|186520611|ref|NP_001119177.1|//2.00E-52//transcription factor [Arabidopsis thaliana] >gi|75171862|sp|Q9FN73.1|Y5625_ARATH RecName: Full=B3 domain-containing protein At5g06250	Unigene3351_All//6.00E-48//AT2G36080| DNA-binding protein, putative	Unigene3351_All//0.00E+00//gi|78341852|gb|DT562126.1|DT562126	ABI3VP1		GO:0001071//GO:0006351//GO:0010468//GO:0030528	nr +
Unigene33512_All	1691	3.03	18.22	6.20	29.69	34.39	40.78	4.75	7.34	18.00	2.59E+00	8.00E-86	Up	1.03E+00	2.86E-08	Up	2.12E-01	1.64E-03		4.58E-01	5.31E-14		6.28E-01	1.09E-05		1.92E+00	1.06E-73	Up	Unigene33512_All//gi|2104685|emb|CAA66483.1|//3.00E-69//transcripteion factor [Vicia faba var. minor]	Unigene33512_All//4.00E-70//AT5G56780| unknown protein	Unigene33512_All//0.00E+00//gi|13245885|gb|BE054698.2|BE054698	HRT			nr +
Unigene33513_All	1357	3.43	9.00	6.51	16.56	25.43	24.06	5.70	6.50	13.71	1.39E+00	2.09E-15	Up	9.25E-01	5.18E-06		6.19E-01	2.79E-13		5.40E-01	3.63E-09		1.89E-01	3.41E-01		1.27E+00	3.95E-25	Up	Unigene33513_All//gi|2104685|emb|CAA66483.1|//3.00E-40//transcripteion factor [Vicia faba var. minor]	Unigene33513_All//3.00E-46//AT5G56780| unknown protein	Unigene33513_All//0.00E+00//gi|48826810|gb|CO125200.1|CO125200	HRT			nr -
Unigene33514_All	2376	8.32	5.89	6.70	49.58	42.28	25.30	28.13	7.37	10.98	-5.00E-01	5.15E-05		-3.13E-01	1.80E-02		-2.30E-01	1.49E-07		-9.71E-01	9.46E-88		-1.93E+00	1.96E-159	Down	-1.36E+00	7.97E-99	Down	Unigene33514_All//gi|115438729|ref|NP_001043644.1|//0.00E+00//Os01g0631100 [Oryza sativa Japonica Group] >gi|54291551|dbj|BAD61411.1| O-acetyltransferase-like [Oryza sativa Japonica Group] >gi|55297065|dbj|BAD68634.1| O-acetyltransferase-like [Oryza sativa Japonica Group] >gi|113533175|dbj|BAF05558.1| Os01g0631100 [Oryza sativa Japonica Group]	Unigene33514_All//0.00E+00//AT3G06550| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: CasIp-like (InterPro:IPR012419); BEST Arabidopsis thaliana protein match is: O-acetyltransferase family protein (TAIR:AT2G34410.2); Has 185 Blast hits to 183 proteins in 57 species: Archae - 0; Bacteria - 0; Metazoa - 97; Fungi - 25; Plants - 56; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	Unigene33514_All//0.00E+00//TC161301				nr +
Unigene33518_All	3870	6.15	8.94	5.28	9.07	8.74	8.30	12.76	13.09	28.62	5.40E-01	3.30E-09		-2.19E-01	7.67E-02		-5.46E-02	6.15E-01		-1.29E-01	2.18E-01		3.67E-02	6.47E-01		1.17E+00	1.14E-127	Up	Unigene33518_All//gi|225433442|ref|XP_002285674.1|//0.00E+00//PREDICTED: similar to catalytic [Vitis vinifera]	Unigene33518_All//0.00E+00//AT3G24180| catalytic/ glucosylceramidase	Unigene33518_All//0.00E+00//gi|84173932|gb|DR462580.1|DR462580				nr -

Unigene33352_All	1658	10.41	6.20	6.74	20.49	17.11	20.70	14.84	5.87	7.02	-7.47E-01	2.68E-08		-6.27E-01	5.50E-06		-2.60E-01	3.66E-03		1.48E-02	9.12E-01		-1.34E+00	4.58E-35	Down	-1.08E+00	4.97E-26	Down	Unigene3352_All//gi|18406875|ref|NP_566054.1|//1.00E-164//eukaryotic initiation factor 3 gamma subunit family protein [Arabidopsis thaliana] >gi|3386622|gb|AAC28552.1| expressed protein [Arabidopsis thaliana]	Unigene3352_All//1.00E-152//AT2G45730| eukaryotic initiation factor 3 gamma subunit family protein	Unigene3352_All//0.00E+00//TC142804				nr +
Unigene33520_All	2790	1.56	4.45	2.50	2.70	2.14	4.73	5.32	5.57	6.24	1.82E+00	1.11E-17	Up	6.84E-01	3.01E-03		-3.36E-01	1.20E-01		8.10E-01	1.09E-07		6.72E-02	6.44E-01		2.30E-01	5.77E-02		Unigene33520_All//gi|15232679|ref|NP_190276.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana]	Unigene33520_All//8.00E-176//AT3G46920| protein kinase family protein	Unigene33520_All//0.00E+00//D8454789				nr -
Unigene33521_All	4850	1.99	1.57	0.61	1.60	1.68	2.37	10.18	11.90	18.21	-3.41E-01	7.27E-02		-1.69E+00	1.67E-15	Down	7.06E-02	8.10E-01		5.62E-01	6.75E-04		2.25E-01	3.55E-04		8.39E-01	1.39E-59		Unigene33521_All//gi|15232679|ref|NP_190276.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana]	Unigene33521_All//0.00E+00//AT3G46920| protein kinase family protein	Unigene33521_All//0.00E+00//TC171578				nr +
Unigene33523_All	1714	10.20	4.29	6.71	14.47	12.60	15.86	11.52	8.73	9.39	-1.25E+00	1.22E-18	Down	-6.03E-01	1.05E-05		-2.00E-01	7.90E-02		1.32E-01	2.79E-01		-4.00E-01	3.10E-04		-2.95E-01	7.25E-03		Unigene33523_All//gi|15220233|ref|NP_175180.1|//1.00E-143//ATRBP47C (ARABIDOPSIS THALIANA RNA-BINDING PROTEIN 47C); RNA binding [Arabidopsis thaliana] >gi|5668812|gb|AAD46038.1|AC007519_23 Contains 3 PF|00076 RNA recognition motif domains. ESTs gb|R30092, gb|R30093, gb|AA394338, gb|N65719 and gb|AA591577 come from this gene [Arabidopsis thaliana]	Unigene33523_All//9.00E-112//AT1G47490| ATRBP47C (ARABIDOPSIS THALIANA RNA-BINDING PROTEIN 47C); RNA binding	Unigene33523_All//0.00E+00//TC158842		ko03040|Spliceosome		nr -
Unigene33524_All	512	6.13	1.39	3.54	8.56	7.60	7.23	2.23	1.47	2.10	-2.15E+00	1.16E-07	Down	-7.94E-01	3.07E-02		-1.72E-01	5.96E-01		-2.43E-01	4.59E-01		-6.02E-01	3.08E-01		-8.58E-02	8.81E-01		Unigene33524_All//gi|15594035|emb|CAC69852.1|//3.00E-19//nucleic acid binding protein [Nicotiana tabacum]		Unigene33524_All//3.00E-49//C0113927				nr -
Unigene33525_All	1398	8.38	3.95	1.22	13.86	13.52	18.93	6.38	4.22	5.78	-1.09E+00	2.44E-10	Down	-2.78E+00	1.61E-34	Down	-3.56E-02	8.12E-01		4.50E-01	1.29E-05		-5.98E-01	4.91E-04		-1.42E-01	4.54E-01		Unigene33525_All//gi|15594035|emb|CAC69852.1|//1.00E-157//nucleic acid binding protein [Nicotiana tabacum]	Unigene33525_All//6.00E-120//AT1G47490| ATRBP47C (ARABIDOPSIS THALIANA RNA-BINDING PROTEIN 47C); RNA binding	Unigene33525_All//0.00E+00//C0113927		ko03040|Spliceosome		nr -
Unigene33526_All	1818	7.68	3.40	4.92	10.99	11.14	13.22	10.35	7.43	7.36	-1.18E+00	9.63E-14	Down	-6.43E-01	3.47E-05		1.95E-02	9.03E-01		2.66E-01	2.09E-02		-4.79E-01	2.38E-05		-4.91E-01	9.05E-06		Unigene33526_All//gi|15594035|emb|CAC69852.1|//1.00E-175//nucleic acid binding protein [Nicotiana tabacum]	Unigene33526_All//1.00E-118//AT1G47490| ATRBP47C (ARABIDOPSIS THALIANA RNA-BINDING PROTEIN 47C); RNA binding	Unigene33526_All//0.00E+00//TC158842		ko03040|Spliceosome		nr +
Unigene33527_All	305	1.03	0.33	2.79	1.63	0.45	0.44	0.28	3.29	1.44	-1.63E+00	2.76E-01		1.44E+00	8.23E-02		-1.85E+00	8.43E-02		-1.88E+00	1.08E-01		3.57E+00	3.08E-05	Up	2.37E+00	4.04E-02										
Unigene33531_All	1535	6.82	2.94	3.95	19.08	14.92	18.24	72.11	52.44	60.68	-1.21E+00	5.44E-11	Down	-7.86E-01	1.83E-05		-3.55E-01	1.47E-04		-6.49E-02	6.34E-01		-4.60E-01	1.77E-25		-2.49E-01	6.69E-09		Unigene33531_All//gi|297792941|ref|XP_002864355.1|//1.00E-168//glucose-6-phosphate transporter 1 [Arabidopsis lyrata subsp. lyrata] >gi|297310190|gb|EFH40614.1| glucose-6-phosphate transporter 1 [Arabidopsis lyrata subsp. lyrata]	Unigene33531_All//4.00E-143//AT5G54800| GPT1; antiporter/ glucose-6-phosphate transmembrane transporter	Unigene33531_All//0.00E+00//gi|164353934|gb|ES808195.1|ES808195				nr -
Unigene33533_All	2211	27.97	20.17	22.09	89.92	96.50	85.59	36.64	17.64	21.06	-4.72E-01	1.39E-12		-3.41E-01	6.86E-07		1.02E-01	3.48E-03		-7.12E-02	7.89E-02		-1.05E+00	3.37E-78	Down	-7.99E-01	1.14E-50		Unigene33533_All//gi|297793001|ref|XP_002864385.1|//0.00E+00//atmap65-1 [Arabidopsis lyrata subsp. lyrata] >gi|297310220|gb|EFH40644.1| atmap65-1 [Arabidopsis lyrata subsp. lyrata]	Unigene33533_All//0.00E+00//AT5G55230| ATMAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1); microtubule binding	Unigene33533_All//0.00E+00//gi|78343713|gb|DT563987.1|DT563987				nr -
Unigene33534_All	2203	20.54	13.92	15.23	24.56	27.59	21.07	21.05	4.50	11.12	-5.62E-01	1.18E-12		-4.32E-01	9.57E-08		1.68E-01	1.40E-02		-2.21E-01	2.38E-03		-2.23E+00	5.23E-133	Down	-9.21E-01	3.22E-37		Unigene33534_All//gi|297793001|ref|XP_002864385.1|//0.00E+00//atmap65-1 [Arabidopsis lyrata subsp. lyrata] >gi|297310220|gb|EFH40644.1| atmap65-1 [Arabidopsis lyrata subsp. lyrata]	Unigene33534_All//0.00E+00//AT5G55230| ATMAP65-1 (MICROTUBULE-ASSOCIATED PROTEINS 65-1); microtubule binding	Unigene33534_All//0.00E+00//C0072875				nr +
Unigene33536_All	2343	8.40	21.84	17.18	10.65	10.49	15.75	5.59	4.30	5.87	1.38E+00	1.57E-61	Up	1.03E+00	5.30E-30	Up	-2.16E-02	8.70E-01		5.64E-01	4.37E-11		-3.80E-01	6.95E-03		6.85E-02	6.42E-01		Unigene33536_All//gi|224062475|ref|XP_002300839.1|//0.00E+00//f-box family protein [Populus trichocarpa] >gi|222842565|gb|EEE80112.1| f-box family protein [Populus trichocarpa]	Unigene33536_All//1.00E-69//AT4G02760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Cyclin-like F-box (InterPro:IPR001810); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02740.1); Has 3231 Blast hits to 948 proteins in 145 species: Archae - 0; Bacteria - 50; Metazoa - 1253; Fungi - 344; Plants - 69; Viruses - 27; Other Eukaryotes - 1488 (source: NCBI BLink).	Unigene33536_All//0.00E+00//TC177563				nr -
Unigene33540_All	1489	1.86	0.68	0.93	4.72	3.28	3.55	5.08	3.20	8.35	-1.45E+00	2.37E-04	Down	-1.00E+00	1.17E-02		-5.22E-01	1.33E-02		-4.11E-01	7.20E-02		-6.68E-01	3.92E-04		7.16E-01	3.54E-07		Unigene33540_All//gi|255547790|ref|XP_002514952.1|//2.00E-26//conserved hypothetical protein [Ricinus communis] >gi|223546003|gb|EEF47506.1| conserved hypothetical protein [Ricinus communis]		Unigene33540_All//0.00E+00//TC141326				nr +
Unigene33544_All	2410	9.01	6.18	7.14	32.99	38.58	32.83	14.93	5.62	6.91	-5.44E-01	3.63E-06		-3.36E-01	6.94E-03		2.26E-01	8.03E-06		-6.90E-03	9.41E-01		-1.41E+00	4.11E-55	Down	-1.11E+00	2.38E-39	Down	Unigene33544_All//gi|297842213|ref|XP_002888988.1|//7.00E-89//IQ-domain 31 [Arabidopsis lyrata subsp. lyrata] >gi|297334829|gb|EFH65247.1| IQ-domain 31 [Arabidopsis lyrata subsp. lyrata]	Unigene33544_All//2.00E-116//AT1G74690| IQD31 (IQ-domain 31); calmodulin binding	Unigene33544_All//0.00E+00//TC133339				nr -
Unigene33545_All	2310	2.36	1.73	1.54	12.18	16.55	7.92	2.21	0.89	0.91	-4.43E-01	8.68E-02		-6.09E-01	2.31E-02		4.42E-01	3.43E-08		-6.22E-01	3.38E-10		-1.32E+00	8.84E-08	Down	-1.28E+00	1.07E-07	Down	Unigene33545_All//gi|297842213|ref|XP_002888988.1|//2.00E-84//IQ-domain 31 [Arabidopsis lyrata subsp. lyrata] >gi|297334829|gb|EFH65247.1| IQ-domain 31 [Arabidopsis lyrata subsp. lyrata]	Unigene33545_All//9.00E-77//AT1G74690| IQD31 (IQ-domain 31); calmodulin binding	Unigene33545_All//0.00E+00//TC168175				nr +
Unigene33546_All	2708	19.05	14.07	18.62	74.34	76.36	68.51	30.07	12.05	12.56	-4.37E-01	2.44E-09		-3.28E-02	7.03E-01		3.88E-02	3.86E-01		-1.18E-01	1.34E-03		-1.32E+00	7.27E-112	Down	-1.26E+00	4.19E-107	Down	Unigene33546_All//gi|297842213|ref|XP_002888988.1|//7.00E-93//IQ-domain 31 [Arabidopsis lyrata subsp. lyrata] >gi|297334829|gb|EFH65247.1| IQ-domain 31 [Arabidopsis lyrata subsp. lyrata]	Unigene33546_All//1.00E-87//AT1G74690| IQD31 (IQ-domain 31); calmodulin binding	Unigene33546_All//0.00E+00//TC176137				nr -
Unigene33547_All	483	0.00	3.88	12.90	0.10	0.21	1.40	1.40	0.69	0.58	1.19E+01	1.11E-10	Up	1.37E+01	9.46E-35	Up	1.05E+00	8.08E-01		3.77E+00	2.97E-03		-1.02E+00	2.04E-01		-1.28E+00	9.48E-02		Unigene33547_All//gi|145408595|ref|YP_001152219.1|//2.00E-24//O8F58f [Pinus koraiensis] >gi|145048844|gb|ABP35460.1| O8F58f [Pinus koraiensis]		Unigene33547_All//4.00E-168//TC150009				nr -
Unigene33552_All	1590	6.52	9.78	7.60	7.61	7.34	3.35	23.99	26.68	13.20	5.87E-01	3.31E-05		2.23E-01	2.28E-01		-5.23E-02	8.16E-01		-1.18E+00	6.37E-13	Down	1.54E-01	5.18E-02		-8.61E-01	1.45E-27		Unigene33552_All//gi|15231598|ref|NP_189303.1|//1.00E-07//ATNUDX13 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 13); bis(5'-adenosyl)-pentaphosphatase/ hydrolase [Arabidopsis thaliana] >gi|30688456|ref|NP_850636.1| ATNUDX13 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 13); bis(5'-adenosyl)-pentaphosphatase/ hydrolase [Arabidopsis thaliana] >gi|68565871|sp|Q5Z888.1|NUD13_ARATH RecName: Full=Nudix hydrolase 13, mitochondrial; Short=AtNUDT13; Flags: Precursor >gi|62867627|gb|AAY17417.1| At3g26690 [Arabidopsis thaliana] >gi|89001031|gb|ABD59105.1| At3g26690 [Arabidopsis thaliana]	Unigene33552_All//1.00E-08//AT3G26690| ATNUDX13 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 13); bis(5'-adenosyl)-pentaphosphatase/ hydrolase	Unigene33552_All//2.00E-135//gi|31073635|gb|CA993914.1|CA993914				nr -
Unigene33553_All	1510	20.24	33.82	17.42	16.69	17.10	10.32	134.82	163.64	62.48	7.41E-01	1.31E-22		-2.16E-01	4.40E-02		3.51E-02	8.22E-01		-6.94E-01	4.81E-11		2.80E-01	1.72E-22		-1.11E+00	4.10E-218	Down	Unigene33553_All//gi|15231598|ref|NP_189303.1|//3.00E-56//ATNUDX13 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 13); bis(5'-adenosyl)-pentaphosphatase/ hydrolase [Arabidopsis thaliana] >gi|30688456|ref|NP_850636.1| ATNUDX13 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 13); bis(5'-adenosyl)-pentaphosphatase/ hydrolase [Arabidopsis thaliana] >gi|68565871|sp|Q5Z888.1|NUD13_ARATH RecName: Full=Nudix hydrolase 13, mitochondrial; Short=AtNUDT13; Flags: Precursor >gi|62867627|gb|AAY17417.1| At3g26690 [Arabidopsis thaliana] >gi|89001031|gb|ABD59105.1| At3g26690 [Arabidopsis thaliana]	Unigene33553_All//2.00E-57//AT3G26690| ATNUDX13 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 13); bis(5'-adenosyl)-pentaphosphatase/ hydrolase	Unigene33553_All//0.00E+00//DW227433				nr +
Unigene33554_All	2187	17.46	58.32	26.78	22.66	35.02	26.93	17.81	8.81	11.68	1.74E+00	6.85E-214	Up	6.17E-01	3.29E-18		6.28E-01	9.67E-30		2.49E-01	2.66E-04		-1.02E+00	9.89E-36	Down	-6.09E-01	9.56E-16		Unigene33554_All//gi|115449257|ref|NP_001048408.1|//0.00E+00//Os02g0799300 [Oryza sativa Japonica Group] >gi|113537939|dh|BAF10322.1| Os02g0799300 [Oryza sativa Japonica Group]	Unigene33554_All//4.00E-180//AT2G12400| unknown protein	Unigene33554_All//0.00E+00//TC137805				nr +
Unigene33556_All	3264	5.88	15.77	7.78	8.26	10.67	8.34	10.76	11.32	13.74	1.42E+00	7.73E-65	Up	4.04E-01	3.22E-04		3.69E-01	1.49E-05		1.51E-02	9.23E-01		7.26E-02	4.48E-01		3.53E-01	3.75E-07		Unigene33556_All//gi|297597754|ref|NP_001044475.2|//0.00E+00//Os01g0786900 [Oryza sativa Japonica Group] >gi|255673762|dh|BAF06389.2| Os01g0786900 [Oryza sativa Japonica Group]	Unigene33556_All//3.00E-117//AT1G03380| AtATG18g	Unigene33556_All//0.00E+00//C0082533				nr +

Unigene33559_All	2423	6.52	12.21	13.45	9.09	11.71	15.32	10.85	11.90	9.68	9.05E-01	1.38E-18		1.04E+00	8.20E-25	Up	3.66E-01	1.43E-04		7.54E-01	3.30E-18		1.33E-01	1.93E-01		-1.65E-01	9.78E-02		Unigene33559_All//gi|33329192|gb|AAQ09996.1|//0.00E+00//S3 self-incompatibility locus-linked pollen 3.15 protein [Petunia integrifolia subsp. inflata]	Unigene33559_All//0.00E+00//AT1G60995| unknown protein	Unigene33559_All//0.00E+00//gi|78332997|gb|DT553271.1|DT553271				nr -
Unigene3356_All	2134	4.49	1.52	2.05	7.26	7.16	12.34	25.32	11.50	11.59	-1.56E+00	1.77E-14	Down	-1.13E+00	1.05E-08	Down	-1.90E-02	9.11E-01		7.65E-01	2.05E-13		-1.14E+00	2.84E-59	Down	-1.13E+00	5.91E-60	Down	Unigene3356_All//gi|266567|sp|P29677.1|MPPA_SOLTU//0.00E+00//RecName: Full=Mitochondrial-processing peptidase subunit alpha; AltName: Full=Alpha-MPP; AltName: Full=Ubiquinol-cytochrome-c reductase subunit II; Flags: Precursor >gi|214993|emb|CAA46990.1| mitochondrial processing peptidase [Solanum tuberosum]	Unigene3356_All//2.00E-158//AT1G51980| mitochondrial processing peptidase alpha subunit, putative	Unigene3356_All//0.00E+00//TC175588			GO:0004175//GO:0006091//GO:0015078//GO:0019538//GO:0019866//GO:0043231//GO:0044425//GO:0046914//GO:0051234	nr +
Unigene33561_All	2312	5.32	2.59	4.35	18.06	18.16	11.00	13.79	5.24	5.00	-1.04E+00	3.91E-10	Down	-2.89E-01	1.01E-01		8.00E-03	9.53E-01		-7.15E-01	7.80E-19		-1.40E+00	3.65E-48	Down	-1.46E+00	2.74E-53	Down	Unigene33561_All//gi|115475401|ref|NP_001061297.1|//0.00E+00//Os08g0230200 [Oryza sativa Japonica Group] >gi|113623266|dbj|BAF23211.1| Os08g0230200 [Oryza sativa Japonica Group]	Unigene33561_All//0.00E+00//AT1G16860| merozoite surface protein-related	Unigene33561_All//0.00E+00//gi|164280206|gb|ES825115.1|ES825115				nr -
Unigene33562_All	2536	12.52	5.81	7.37	24.06	22.77	14.94	13.90	4.83	5.09	-1.11E+00	1.55E-27	Down	-7.65E-01	1.61E-14		-7.96E-02	3.15E-01		-6.87E-01	1.80E-25		-1.53E+00	1.05E-60	Down	-1.45E+00	5.42E-58	Down	Unigene33562_All//gi|115475401|ref|NP_001061297.1|//1.00E-159//Os08g0230200 [Oryza sativa Japonica Group] >gi|113623266|dbj|BAF23211.1| Os08g0230200 [Oryza sativa Japonica Group]	Unigene33562_All//1.00E-150//AT1G16860| merozoite surface protein-related	Unigene33562_All//0.00E+00//TC139929				nr +
Unigene33564_All	3994	7.22	16.06	7.64	9.28	8.20	10.19	14.91	13.35	17.30	1.15E+00	2.05E-58	Up	8.19E-02	4.85E-01		-1.79E-01	4.93E-02		1.35E-01	1.54E-01		-1.59E-01	1.36E-02		2.15E-01	1.20E-04		Unigene33564_All//gi|8480758|sp|Q9ZPV5.1|NOC2L_ARATH//0.00E+00//RecName: Full=Nucleolar complex protein 2 homolog; Short=Protein NOC2 homolog	Unigene33564_All//1.00E-167//AT2G18220| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0120 (InterPro:IPR005343); BEST Arabidopsis thaliana protein match is: RBL (REBELOTE) (TAIR:AT3G55510.1); Has 4846 Blast hits to 3236 proteins in 249 species: Archae - 2; Bacteria - 127; Metazoa - 2049; Fungi - 594; Plants - 200; Viruses - 69; Other Eukaryotes - 1805 (source: NCBI BLink).	Unigene33564_All//0.00E+00//TC139155				nr -
Unigene33565_All	271	53.29	33.09	30.85	47.79	43.46	47.66	14.04	6.01	6.03	-6.87E-01	3.18E-06		-7.89E-01	2.62E-07		-1.37E-01	4.48E-01		-3.90E-03	9.78E-01		-1.22E+00	2.09E-05	Down	-1.22E+00	1.34E-05	Down	Unigene33565_All//gi|110739370|dbj|BAF01597.1|//1.00E-42//heat shock like protein [Arabidopsis thaliana]	Unigene33565_All//5.00E-44//AT2G04030| CR88; ATP binding	Unigene33565_All//3.00E-149//gi|198417559|gb|DW476539.1|DW476539		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene33566_All	528	4.86	3.26	4.03	1.98	2.15	3.68	3.92	1.42	1.43	-5.74E-01	1.45E-01		-2.67E-01	5.32E-01		1.19E-01	8.71E-01		8.93E-01	6.06E-02		-1.46E+00	4.45E-04	Down	-1.45E+00	3.18E-04	Down	Unigene33566_All//gi|20453106|gb|AAM19795.1|//4.00E-91//At2g04030/F3C11.14 [Arabidopsis thaliana]	Unigene33566_All//2.00E-92//AT2G04030| CR88; ATP binding	Unigene33566_All//0.00E+00//TC140062		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene33568_All	1082	36.85	30.35	24.71	37.43	32.08	28.47	26.88	10.35	9.83	-2.80E-01	1.08E-03		-5.77E-01	3.20E-11		-2.23E-01	6.98E-03		-3.95E-01	1.19E-06		-1.38E+00	3.74E-43	Down	-1.45E+00	4.57E-48	Down	Unigene33568_All//gi|260505494|gb|ACX42226.1|//1.00E-110//heat shock protein 90 [Ipomoea nil]	Unigene33568_All//7.00E-105//AT2G04030| CR88; ATP binding	Unigene33568_All//0.00E+00//gi|164262225|gb|ES811962.1|ES811962		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene33569_All	2751	28.74	23.32	22.12	26.75	24.56	27.88	18.23	6.43	8.10	-3.02E-01	2.48E-07		-3.77E-01	2.84E-10		-1.23E-01	5.59E-02		5.98E-02	4.25E-01		-1.50E+00	3.23E-84	Down	-1.17E+00	3.55E-59	Down	Unigene33569_All//gi|15228059|ref|NP_178487.1|//0.00E+00//CR88; ATP binding [Arabidopsis thaliana] >gi|16930685|gb|AAL32008.1|AF436826_1 At2g04030/F3C11.14 [Arabidopsis thaliana] >gi|15450723|gb|AAK96633.1| At2g04030/F3C11.14 [Arabidopsis thaliana] >gi|25090168|gb|AAN72245.1| At2g04030/F3C11.14 [Arabidopsis thaliana]	Unigene33569_All//0.00E+00//AT2G04030| CR88; ATP binding	Unigene33569_All//0.00E+00//TC140062		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene33570_All	1957	4.65	4.32	3.65	3.36	3.41	2.63	3.52	1.32	1.28	-1.06E-01	6.07E-01		-3.52E-01	8.67E-02		2.28E-02	9.49E-01		-3.53E-01	1.45E-01		-1.41E+00	3.30E-11	Down	-1.46E+00	4.04E-12	Down	Unigene33570_All//gi|15228059|ref|NP_178487.1|//0.00E+00//CR88; ATP binding [Arabidopsis thaliana] >gi|16930685|gb|AAL32008.1|AF436826_1 At2g04030/F3C11.14 [Arabidopsis thaliana] >gi|15450723|gb|AAK96633.1| At2g04030/F3C11.14 [Arabidopsis thaliana] >gi|25090168|gb|AAN72245.1| At2g04030/F3C11.14 [Arabidopsis thaliana]	Unigene33570_All//0.00E+00//AT2G04030| CR88; ATP binding	Unigene33570_All//0.00E+00//TC140062		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene33572_All	3601	5.09	4.84	5.28	7.14	7.64	8.44	8.22	7.83	17.97	-7.12E-02	6.23E-01		5.40E-02	7.05E-01		9.81E-02	4.36E-01		2.42E-01	1.72E-02		-6.91E-02	5.38E-01		1.13E+00	3.37E-71	Up	Unigene33572_All//gi|3152572|gb|AAC17053.1|//0.00E+00//Contains homology to DNAJ heatshock protein gb|U32803 from Haemophilus influenzae [Arabidopsis thaliana]	Unigene33572_All//3.00E-179//AT1G16680| DNAJ heat shock N-terminal domain-containing protein / S-locus protein, putative	Unigene33572_All//6.00E-73//TC171510				nr +
Unigene33575_All	2502	3.81	3.26	4.00	6.95	7.12	5.25	1.79	4.33	9.74	-2.23E-01	2.60E-01		7.22E-02	7.16E-01		3.43E-02	8.24E-01		-4.04E-01	2.24E-03		1.27E+00	1.00E-14	Up	2.44E+00	9.81E-80	Up	Unigene33575_All//gi|225447735|ref|XP_002262698.1|//0.00E+00//PREDICTED: similar to somatic embryogenesis receptor-like kinase 3 [Vitis vinifera]	Unigene33575_All//0.00E+00//AT4G33430| BAK1 (BRI1-ASSOCIATED RECEPTOR KINASE); kinase/ protein binding / protein heterodimerization/ protein serine/threonine kinase	Unigene33575_All//0.00E+00//ES802219		ko04626|Plant-pathogen interaction		nr +
Unigene33577_All	1447	5.64	12.12	7.69	5.27	7.50	6.84	10.14	9.73	8.12	1.10E+00	2.16E-15	Up	4.47E-01	1.26E-02		5.09E-01	2.14E-03		3.76E-01	4.55E-02		-5.88E-02	7.05E-01		-3.20E-01	1.33E-02		Unigene33577_All//gi|148595724|emb|CAM12541.1|//2.00E-48//YA3 (Antirrhinum majus]	Unigene33577_All//1.00E-42//AT5G12840| NF-YA1 (NUCLEAR FACTOR Y, SUBUNIT A1); transcription factor	Unigene33577_All//0.00E+00//TC133249	CCAAT			nr +
Unigene3358_All	654	12.88	7.44	9.12	9.22	6.84	8.43	7.95	6.33	2.01	-7.92E-01	7.27E-05		-4.98E-01	1.73E-02		-4.29E-01	7.22E-02		-1.30E-01	6.41E-01		-3.30E-01	1.84E-01		-1.98E+00	5.60E-14	Down	Unigene3358_All//gi|18415425|ref|NP_567594.1|//1.00E-34//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|107738041|gb|ABF83619.1| At4g20030 [Arabidopsis thaliana]	Unigene3358_All//6.00E-36//AT4G20030| RNA recognition motif (RRM)-containing protein	Unigene3358_All//0.00E+00//gi|13246836|gb|BE055468.2|BE055468			GO:0003676//GO:0043231	nr +
Unigene33580_All	2232	2.98	6.42	4.13	4.33	4.23	3.72	6.86	7.02	12.85	1.11E+00	7.60E-13	Up	4.71E-01	1.80E-02		-3.45E-02	8.68E-01		-2.18E-01	2.99E-01		3.43E-02	8.18E-01		9.06E-01	1.26E-22		Unigene33580_All//gi|29028892|gb|AAO64825.1|//1.00E-157//At3g60680 [Arabidopsis thaliana]	Unigene33580_All//6.00E-134//AT3G60680| unknown protein	Unigene33580_All//0.00E+00//gi|54121293|gb|CO496802.1|CO496802				nr +
Unigene33582_All	1333	1.65	2.13	1.92	4.11	4.11	4.85	14.05	18.88	52.00	3.69E-01	3.43E-01		2.18E-01	6.28E-01		-1.20E-03	9.87E-01		2.37E-01	3.78E-01		4.26E-01	1.07E-05		1.89E+00	5.36E-163	Up	Unigene33582_All//gi|224131906|ref|XP_002328137.1|//1.00E-128//calcium dependent protein kinase 6 [Populus trichocarpa] >gi|222837652|gb|EEE76017.1| calcium dependent protein kinase 6 [Populus trichocarpa]	Unigene33582_All//8.00E-122//AT4G35310| CPK5 (calmodulin-domain protein kinase 5); ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene33582_All//0.00E+00//TC137022		ko04626|Plant-pathogen interaction		nr +
Unigene33583_All	1341	3.59	1.70	1.39	5.01	3.93	4.92	19.61	30.17	59.18	-1.08E+00	1.10E-04	Down	-1.37E+00	4.29E-06	Down	-3.52E-01	1.27E-01		-2.84E-02	9.28E-01		6.22E-01	2.13E-16		1.59E+00	2.93E-147	Up	Unigene33583_All//gi|164430467|gb|ABY55551.1|//0.00E+00//calcium-dependent protein kinase [Swainsona canescens]	Unigene33583_All//0.00E+00//AT2G17290| CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene33583_All//0.00E+00//TC164611		ko04626|Plant-pathogen interaction		nr -
Unigene33585_All	2188	9.85	2.71	3.67	59.56	40.83	66.86	48.41	20.29	18.28	-1.86E+00	1.90E-40	Down	-1.42E+00	1.33E-26	Down	-5.45E-01	3.70E-40		1.67E-01	7.74E-05		-1.25E+00	1.69E-134	Down	-1.40E+00	1.46E-164	Down	Unigene33585_All//gi|211906486|gb|ACJ11736.1|//0.00E+00//phosphoglycerate dehydrogenase [Gossypium hirsutum]	Unigene33585_All//0.00E+00//AT4G34200| EDM9 (embryo sac development arrest 9); ATP binding	Unigene33585_All//0.00E+00//TC147449		ko00260|Glycine, serine and threonine metabolism		nr -
Unigene33586_All	2142	8.62	4.42	4.77	28.37	24.02	21.86	10.24	2.52	2.81	-9.63E-01	3.76E-13		-8.53E-01	2.24E-10		-2.40E-01	1.67E-04		-3.76E-01	7.54E-09		-2.03E+00	4.16E-56	Down	-1.87E+00	5.61E-52	Down	Unigene33586_All//gi|211906486|gb|ACJ11736.1|//0.00E+00//phosphoglycerate dehydrogenase [Gossypium hirsutum]	Unigene33586_All//0.00E+00//AT4G34200| EDM9 (embryo sac development arrest 9); ATP binding	Unigene33586_All//0.00E+00//TC142613		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene33587_All	2375	1.89	0.87	1.46	2.98	2.39	2.42	5.41	2.73	8.27	-1.12E+00	1.23E-04	Down	-3.79E-01	2.25E-01		-3.16E-01	1.65E-01		-3.03E-01	2.05E-01		-9.89E-01	7.58E-12		6.12E-01	2.02E-08		Unigene33587_All//gi|224094296|ref|XP_002310129.1|//0.00E+00//SET domain protein [Populus trichocarpa] >gi|222853032|gb|EEE90579.1| SET domain protein [Populus trichocarpa]	Unigene33587_All//4.00E-149//AT2G33380| CLF (CURLY LEAF); transcription factor	Unigene33587_All//0.00E+00//ES832352				nr -
Unigene3359_All	949	4.85	4.70	5.67	5.04	3.66	4.09	4.59	2.55	1.81	-4.63E-02	8.76E-01		2.24E-01	4.19E-01		-4.59E-01	9.11E-02		-3.00E-01	3.23E-01		-8.45E-01	1.09E-03		-1.35E+00	3.57E-07	Down	Unigene3359_All//gi|18415425|ref|NP_567594.1|//3.00E-26//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|107738041|gb|ABF83619.1| At4g20030 [Arabidopsis thaliana]	Unigene3359_All//2.00E-27//AT4G20030| RNA recognition motif (RRM)-containing protein	Unigene3359_All//0.00E+00//CO121252		ko03040|Spliceosome	GO:0003676//GO:0043231	nr +
Unigene33594_All	1026	0.00	0.00	0.00	0.00	0.27	0.00	2.80	1.22	2.83	null	null		null	null		8.07E+00	7.01E-02		null	null		-1.20E+00	3.65E-04	Down	1.65E-02	9.70E-01		Unigene33594_All//gi|212717127|gb|ACJ37405.1|//4.00E-51//receptor-like protein kinase [Glycine max]	Unigene33594_All//3.00E-50//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene33594_All//2.00E-113//TC167179				nr -
Unigene33595_All	693	1.89	1.17	3.00	7.48	6.31	3.78	7.87	1.81	1.26	-6.90E-01	2.32E-01		6.67E-01	1.51E-01		-2.44E-01	3.96E-01		-9.84E-01	1.49E-04		-2.12E+00	2.46E-15	Down	-2.64E+00	2.46E-20	Down	Unigene33595_All//gi|223452296|gb|ACH89476.1|//1.00E-62//leucine-rich repeat family protein / protein kinase family protein [Glycine max]	Unigene33595_All//9.00E-61//AT1G53440| leucine-rich repeat family protein / protein kinase family protein	Unigene33595_All//0.00E+00//TC167179		ko04626|Plant-pathogen interaction		nr +
Unigene3360_All	678	1.08	0.97	1.34	2.94	1.07	2.60	1.62	1.11	0.35	-1.53E-01	8.35E-01		3.06E-01	6.57E-01		-1.46E+00	8.85E-04	Down	-1.78E-01	7.00E-01		-5.47E-01	3.72E-01		-2.20E+00	5.65E-04	Down	Unigene3360_All//gi|18415425|ref|NP_567594.1|//2.00E-38//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|107738041|gb|ABF83619.1| At4g20030 [Arabidopsis thaliana]	Unigene3360_All//9.00E-40//AT4G20030| RNA recognition motif (RRM)-containing protein	Unigene3360_All//0.00E+00//gi|13246836|gb|BE055468.2|BE055468		ko03040|Spliceosome	GO:0003676//GO:0043231	nr -
Unigene33600_All	2677	3.26	1.34	1.89	9.58	8.19	6.93	8.80	1.75	1.28	-1.28E+00	4.87E-10	Down	-7.88E-01	1.03E-04		-2.26E-01	3.83E-02		-4.67E-01	7.70E-06		-2.33E+00	1.09E-71	Down	-2.78E+00	2.24E-90	Down	Unigene33600_All//gi|224589567|gb|ACN59317.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene33600_All//0.00E+00//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene33600_All//0.00E+00//TC167179		ko04626|Plant-pathogen interaction		nr +

Unigene33601_All	405	1.16	0.25	1.05	4.67	2.81	4.24	1.57	0.83	0.00	-2.22E+00	7.76E-02		-1.45E-01	8.90E-01		-7.36E-01	1.06E-01		-1.41E-01	7.64E-01		-9.24E-01	2.63E-01		-1.06E+01	7.11E-05	Down	Unigene33601_All//gi|224104691|ref|XP_002313530.1|//1.00E-36//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222849938|gb|EEE87485.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene33601_All//3.00E-33//AT2G28070| ABC transporter family protein					nr -
Unigene33602_All	2992	1.71	2.10	2.33	7.86	7.77	3.85	6.08	2.04	1.64	2.93E-01	2.37E-01		4.44E-01	5.87E-02		-1.66E-02	9.04E-01		-1.03E+00	1.03E-19	Down	-1.58E+00	3.85E-33	Down	-1.89E+00	5.76E-44	Down	Unigene33602_All//gi|30683745|ref|NP_850111.1|//0.00E+00//ABC transporter family protein [Arabidopsis thaliana]	Unigene33602_All//0.00E+00//AT2G28070| ABC transporter family protein	Unigene33602_All//5.00E-76//D#515845		ko02010|ABC transporters		nr +
Unigene33603_All	2855	3.28	2.77	2.63	16.85	12.28	6.58	10.44	3.45	3.00	-2.45E-01	2.18E-01		-3.19E-01	1.20E-01		-4.57E-01	4.83E-11		-1.36E+00	1.64E-61	Down	-1.60E+00	7.49E-55	Down	-1.80E+00	7.42E-67	Down	Unigene33603_All//gi|30683745|ref|NP_850111.1|//0.00E+00//ABC transporter family protein [Arabidopsis thaliana]	Unigene33603_All//0.00E+00//AT2G28070| ABC transporter family protein	Unigene33603_All//8.00E-112//ES803516		ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene33604_All	2646	5.58	11.39	6.58	12.58	10.52	9.71	23.81	24.74	19.27	1.03E+00	2.65E-23	Up	2.39E-01	1.03E-01		-2.58E-01	4.37E-03		-3.73E-01	4.29E-05		5.51E-02	4.41E-01		-3.05E-01	1.33E-07		Unigene33604_All//gi|225439753|ref|XP_002273203.1|//0.00E+00//PREDICTED: similar to UPL4 (ubiquitin-protein ligase 4) [Vitis vinifera]	Unigene33604_All//0.00E+00//AT5G02880| UPL4; ubiquitin-protein ligase	Unigene33604_All//0.00E+00//TC154315		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene33605_All	5380	1.32	3.13	2.71	4.00	5.33	4.57	5.52	3.92	6.24	1.24E+00	1.06E-17	Up	1.04E+00	2.68E-11	Up	4.13E-01	1.31E-05		1.91E-01	1.14E-01		-4.94E-01	2.17E-08		1.76E-01	3.91E-02		Unigene33605_All//gi|225439753|ref|XP_002273203.1|//0.00E+00//PREDICTED: similar to UPL4 (ubiquitin-protein ligase 4) [Vitis vinifera]	Unigene33605_All//0.00E+00//AT5G02880| UPL4; ubiquitin-protein ligase	Unigene33605_All//0.00E+00//TC154315				nr -
Unigene3361_All	1012	12.72	30.64	12.79	11.37	12.08	12.94	38.94	59.68	45.27	1.27E+00	4.33E-33	Up	7.70E-03	9.87E-01		8.73E-02	6.59E-01		1.87E-01	3.00E-01		6.16E-01	1.05E-23		2.17E-01	1.91E-03		Unigene3361_All//gi|115474751|ref|NP_001060972.1|//3.00E-73//Os08g0141300 [Oryza sativa Japonica Group] >gi|42761338|dbj|BAD11591.1| 27k vesicle-associated membrane protein-associated protein-like [Oryza sativa Japonica Group] >gi|65736132|dbj|BAD13178.1| 27k vesicle-associated membrane protein-associated protein-like [Oryza sativa Japonica Group] >gi|113622941|dbj|BAF22886.1| Os08g0141300 [Oryza sativa Japonica Group]	Unigene3361_All//1.00E-72//AT4G21450| vesicle-associated membrane family protein / VAMP family protein	Unigene3361_All//0.00E+00//TC152558			GO:0009725//GO:0016020//GO:0043231	nr -
Unigene33610_All	1066	1.91	0.95	0.40	3.04	1.91	3.60	2.26	1.25	2.47	-1.01E+00	2.58E-02		-2.26E+00	3.27E-05	Down	-6.72E-01	4.14E-02		2.46E-01	4.86E-01		-8.50E-01	2.03E-02		1.26E-01	7.18E-01		Unigene33610_All//gi|124359529|gb|ABD22574.2|//4.00E-16//Endonuclease/exonuclease/phosphatase [Medicago truncatula]						nr -
Unigene33613_All	1595	5.28	3.34	2.87	32.57	25.99	11.75	8.88	2.49	4.50	-6.63E-01	8.55E-04		-8.79E-01	2.41E-05		-3.26E-01	1.50E-06		-1.47E+00	5.43E-75	Down	-1.83E+00	4.66E-32	Down	-9.82E-01	2.98E-13		Unigene33613_All//gi|224082931|ref|XP_002306554.1|//1.00E-136//f-box family protein [Populus trichocarpa] >gi|222856003|gb|EEE93550.1| f-box family protein [Populus trichocarpa]	Unigene33613_All//8.00E-129//AT5G49980| AFB5 (Auxin F-Box protein 5); ubiquitin-protein ligase	Unigene33613_All//0.00E+00//TC162794		ko04626|Plant-pathogen interaction		nr +
Unigene33615_All	374	4.20	2.57	1.85	4.80	5.62	1.09	2.94	1.01	2.13	-7.05E-01	1.80E-01		-1.18E+00	3.61E-02		2.28E-01	6.44E-01		-2.14E+00	6.96E-05	Down	-1.55E+00	1.12E-02		-4.64E-01	4.07E-01				Unigene33615_All//1.00E-28//gi|78337638|gb|DT557912.1|DT557912				
Unigene33617_All	2130	5.11	4.83	2.13	6.83	5.97	6.00	6.71	9.54	5.37	-8.14E-02	6.53E-01		-1.27E+00	1.48E-11	Down	-1.95E-01	2.25E-01		-1.87E-01	2.62E-01		5.07E-01	3.01E-06		-3.22E-01	1.41E-02		Unigene33617_All//gi|82697975|gb|AB889022.1|//1.00E-178//CXE carboxylesterase [Actinidia deliciosa]	Unigene33617_All//4.00E-178//AT3G27320| hydrolase	Unigene33617_All//0.00E+00//gi|78335094|gb|DT555368.1|DT555368				nr -
Unigene33620_All	468	3.13	0.00	6.03	0.75	0.74	0.39	1.08	0.98	0.94	-1.16E+01	1.65E-08	Down	9.46E-01	1.56E-02		-1.81E-02	9.58E-01		-9.49E-01	4.81E-01		-1.42E-01	8.76E-01		-2.11E-01	7.92E-01		Unigene33620_All//gi|226507753|ref|NP_001151897.1|//4.00E-22//ATP binding protein [Zea mays] >gi|195650743|gb|ACG44839.1| ATP binding protein [Zea mays]	Unigene33620_All//8.00E-23//AT5G50000| protein kinase, putative	Unigene33620_All//7.00E-96//gi|48814304|gb|CO115617.1|CO115617				nr -
Unigene33624_All	1667	132.89	128.06	143.71	31.56	42.62	34.81	0.76	2.53	8.75	-5.34E-02	1.70E-01		1.13E-01	1.32E-03		4.34E-01	2.49E-14		1.42E-01	5.99E-02		1.73E+00	2.28E-09	Up	3.52E+00	3.31E-69	Up	Unigene33624_All//gi|10720315|sp|O49939.1|TLP40_SPIOL//0.00E+00//Rec Name: Full=Peptidyl-prolyl cis-trans isomerase, chloroplastic; AltName: Full=40 kDa thylakoid lumen PPIase; AltName: Full=40 kDa thylakoid lumen rotamase; Flags: Precursor >gi|2864602|emb|CAA72792.1| thylakoid lumen rotamase [Spinacia oleracea]	Unigene33624_All//0.00E+00//AT3G01480| CYP38 (cyclophilin 38); peptidyl-prolyl cis-trans isomerase	Unigene33624_All//0.00E+00//TC157308				nr -
Unigene33625_All	1444	40.29	29.41	57.09	159.86	148.19	60.24	6.32	3.59	4.52	-4.54E-01	3.85E-11		5.03E-01	1.03E-17		-1.09E-01	8.15E-04		-1.41E+00	0.00E+00	Down	-8.17E-01	1.67E-06		-4.83E-01	3.46E-03		Unigene33625_All//gi|124360746|gb|ABN08723.1|//2.00E-06//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]		Unigene33625_All//1.00E-81//ES831629				nr +
Unigene33626_All	1410	12.62	12.22	23.79	42.04	39.37	16.27	2.28	2.05	1.38	-4.63E-02	7.43E-01		9.15E-01	1.30E-20		-9.48E-02	2.28E-01		-1.37E+00	9.25E-77	Down	-1.56E-01	6.29E-01		-7.19E-01	1.56E-02		Unigene33626_All//gi|30683745|ref|NP_850111.1|//0.00E+00//ABC transporter family protein [Arabidopsis thaliana]	Unigene33626_All//3.00E-15//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene33626_All//1.00E-127//ES831629				nr +
Unigene33628_All	1726	7.76	6.63	7.40	42.60	31.12	18.79	8.72	8.45	3.32	-2.26E-01	1.65E-01		-6.77E-02	6.96E-01		-4.53E-01	2.39E-16		-1.18E+00	1.64E-75	Down	-4.53E-02	7.63E-01		-1.39E+00	8.61E-24	Down	Unigene33628_All//gi|33465891|gb|AAQ19327.1|//6.00E-42//bZIP-like protein [Oryza sativa Japonica Group]	Unigene33628_All//5.00E-30//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene33628_All//0.00E+00//gi|11203987|gb|BF272917.1|BF272917				nr -
Unigene33629_All	1044	0.30	0.39	0.31	1.00	5.57	1.69	1.17	4.08	1.79	3.69E-01	7.24E-01		2.52E-02	1.00E+00		2.48E+00	5.10E-18	Up	7.52E-01	1.39E-01		1.80E+00	6.82E-10	Up	6.11E-01	1.40E-01		Unigene33629_All//gi|115472533|ref|NP_001059865.1|//1.00E-63//Os07g0534700 [Oryza sativa Japonica Group] >gi|113611401|dbj|BAF21779.1| Os07g0534700 [Oryza sativa Japonica Group]	Unigene33629_All//2.00E-54//AT4G11490| protein kinase family protein	Unigene33629_All//0.00E+00//DT464066		ko04626|Plant-pathogen interaction		nr +
Unigene3363_All	1353	5.68	3.71	4.33	1.66	1.53	2.44	3.22	1.11	1.44	-6.17E-01	3.26E-03		-3.93E-01	8.01E-02		-1.18E-01	8.19E-01		5.57E-01	1.17E-01		-1.53E+00	3.14E-08	Down	-1.16E+00	7.47E-06	Down	Unigene3363_All//gi|161598361|gb|AB374942.1|//1.00E-146//pyruvate orthophosphate dikinase regulatory protein [Glycine max]	Unigene3363_All//1.00E-134//AT4G21210| ATRP1 (PPDK REGULATORY PROTEIN); phosphoprotein phosphatase/ protein kinase	Unigene3363_All//0.00E+00//TC171574				nr -
Unigene33630_All	1284	0.49	0.28	0.75	2.79	6.25	2.81	1.25	2.38	2.92	-8.24E-01	3.75E-01		6.10E-01	3.86E-01		1.16E+00	4.98E-09	Up	1.06E-02	9.75E-01		9.25E-01	3.74E-03		1.22E+00	1.77E-05	Up	Unigene33630_All//gi|115472685|ref|NP_001059941.1|//7.00E-76//Os07g0550900 [Oryza sativa Japonica Group] >gi|113611477|dbj|BAF21855.1| Os07g0550900 [Oryza sativa Japonica Group]	Unigene33630_All//3.00E-72//AT1G67520| lectin protein kinase family protein	Unigene33630_All//0.00E+00//DT464066		ko04626|Plant-pathogen interaction		nr +
Unigene33631_All	1617	1.10	0.75	1.19	2.99	6.18	3.66	3.40	5.92	9.90	-5.49E-01	2.61E-01		1.08E-01	8.14E-01		1.05E+00	1.65E-09	Up	2.92E-01	2.81E-01		8.00E-01	1.48E-06		1.54E+00	5.03E-29	Up	Unigene33631_All//gi|223452430|gb|ACM89542.1|//4.00E-78//S-locus lectin protein kinase family protein [Glycine max] >gi|223452558|gb|ACM89606.1| S-locus lectin protein kinase family protein [Glycine max]	Unigene33631_All//1.00E-66//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene33631_All//1.00E-29//D#453099				nr +
Unigene33632_All	2841	1.71	1.75	1.29	2.30	2.65	2.43	14.88	22.77	40.33	2.93E-02	9.31E-01		-4.05E-01	1.63E-01		2.09E-01	3.92E-01		8.25E-02	7.43E-01		6.14E-01	3.55E-25		1.44E+00	1.19E-182	Up	Unigene33632_All//gi|115440355|ref|NP_001044457.1|//1.00E-169//Os01g0783800 [Oryza sativa Japonica Group] >gi|113533988|dbj|BAF06371.1| Os01g0783800 [Oryza sativa Japonica Group]	Unigene33632_All//1.00E-157//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene33632_All//0.00E+00//DT462243		ko04626|Plant-pathogen interaction		nr +
Unigene33633_All	1861	0.00	0.11	0.03	0.05	0.06	0.05	1.00	1.12	2.03	6.77E+00	1.36E-01		4.84E+00	6.35E-01		5.29E-02	9.66E-01		-1.42E-01	9.50E-01		1.68E-01	6.87E-01		1.02E+00	2.16E-04	Up	Unigene33633_All//gi|115440355|ref|NP_001044457.1|//1.00E-128//Os01g0783800 [Oryza sativa Japonica Group] >gi|113533988|dbj|BAF06371.1| Os01g0783800 [Oryza sativa Japonica Group]	Unigene33633_All//2.00E-112//AT4G21390| B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding	Unigene33633_All//0.00E+00//DT462243		ko04626|Plant-pathogen interaction		nr -
Unigene33635_All	1744	8.37	2.85	1.86	17.42	24.19	21.86	11.27	4.53	11.10	-1.56E+00	1.44E-21	Down	-2.17E+00	3.26E-32	Down	4.73E-01	3.95E-10		3.27E-01	1.29E-04		-1.32E+00	1.73E-27	Down	-2.21E-02	8.69E-01		Unigene33635_All//gi|18396241|ref|NP_564273.1|//1.00E-111//binding [Arabidopsis thaliana] >gi|15982866|gb|AAL09780.1| At1g27210/T7N9_27 [Arabidopsis thaliana] >gi|22655276|gb|AAM98228.1| expressed protein [Arabidopsis thaliana] >gi|30725456|gb|AAP37750.1| At1g27210 [Arabidopsis thaliana]	Unigene33635_All//2.00E-80//AT1G27210| binding	Unigene33635_All//0.00E+00//TC131346				nr +
Unigene33637_All	2772	5.74	2.32	2.44	11.66	14.35	9.60	16.34	5.35	10.13	-1.31E+00	3.60E-18	Down	-1.23E+00	5.46E-16	Down	2.99E-01	2.06E-04		-2.81E-01	3.16E-03		-1.61E+00	5.26E-84	Down	-6.89E-01	2.05E-22		Unigene33637_All//gi|8778871|gb|AAF79870.1|AC000348_23//1.00E-156//T7N9.27 [Arabidopsis thaliana]	Unigene33637_All//7.00E-119//AT1G27210| binding	Unigene33637_All//0.00E+00//TC131346				nr +
Unigene33639_All	1331	6.21	3.88	2.48	6.62	4.73	3.80	5.56	3.86	3.29	-6.78E-01	7.48E-04		-1.32E+00	1.58E-09	Down	-4.85E-01	8.96E-03		-8.02E-01	2.43E-05		-5.25E-01	6.18E-03		-7.56E-01	4.98E-05		Unigene33639_All//gi|115472185|ref|NP_001059691.1|//6.00E-49//Os07g0494900 [Oryza sativa Japonica Group] >gi|113611227|dbj|BAF21605.1| Os07g0494900 [Oryza sativa Japonica Group]	Unigene33639_All//1.00E-94//AT5G51150| unknown protein	Unigene33639_All//0.00E+00//TC147325				nr -
Unigene3364_All	1449	26.21	10.18	14.88	26.95	28.04	23.19	13.74	7.99	15.26	-1.37E+00	2.32E-45	Down	-8.17E-01	3.11E-19		5.72E-02	5.93E-01		-2.17E-01	1.41E-02		-7.83E-01	2.51E-12		1.51E-01	1.76E-01		Unigene3364_All//gi|15081622|gb|AAK82466.1|//2.00E-39//AT3g07470/F2I03_18 [Arabidopsis thaliana] >gi|27363316|gb|AAO11577.1| At3g07470/F2I03_18 [Arabidopsis thaliana]	Unigene3364_All//4.00E-40//AT3G07470| unknown protein	Unigene3364_All//0.00E+00//TC143477			GO:0031410//GO:0043231	nr -
Unigene33645_All	2041	1.51	0.37	0.83	3.44	2.63	3.54	7.04	1.84	3.01	-2.02E+00	4.70E-07	Down	-8.57E-01	2.11E-02		-3.87E-01	7.98E-02		4.10E-02	8.83E-01		-1.93E+00	7.11E-35	Down	-1.23E+00	6.44E-19	Down	Unigene33645_All//gi|79522090|ref|NP_568490.2|//0.00E+00//LON1 (LON PROTEASE 1); ATP binding / ATP-dependent peptidase/ serine-type peptidase [Arabidopsis thaliana]	Unigene33645_All//0.00E+00//AT5G26860| LON1 (LON PROTEASE 1); ATP binding / ATP-dependent peptidase/ serine-type peptidase	Unigene33645_All//0.00E+00//gi|78352734|gb|DT573008.1|DT573008				nr +
Unigene33647_All	1822	3.93	1.36	3.51	6.15	6.33	5.43	8.59	5.48	5.47	-1.53E+00	1.02E-10	Down	-1.66E-01	5.06E-01		4.16E-02	8.32E-01		-1.80E-01	3.63E-01		-6.47E-01	2.67E-07		-6.51E-01	1.24E-07		Unigene33647_All//gi|297725961|ref|NP_001175344.1|//0.00E+00//Os07g0689300 [Oryza sativa Japonica Group] >gi|255678077|dbj|BAH94072.1| Os07g0689300 [Oryza sativa Japonica Group]	Unigene33647_All//0.00E+00//AT5G26860| LON1 (LON PROTEASE 1); ATP binding / ATP-dependent peptidase/ serine-type peptidase	Unigene33647_All//0.00E+00//TC148269				nr -

Unigene33648_All	1085	182.71	325.17	315.77	95.08	118.22	99.82	119.36	472.27	217.88	8.32E-01	2.30E-185		7.89E-01	1.93E-160		3.14E-01	3.22E-14		7.01E-02	2.33E-01		1.98E+00	0.00E+00	Up	8.68E-01	1.31E-167		Unigene33648_All//gi|5263319|gb|AAD41421.1|AC007727_10//6.00E-70//ESTs gb|N96028, gb|F14286, gb|T20680, gb|F14443, gb|AA657300 and gb|N65244 come from this gene [Arabidopsis thaliana]	Unigene33648_All//2.00E-64//AT1G21680| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40-like Beta Propeller (InterPro:IPR011659), Six-bladed beta-propeller, TolB-like (InterPro:IPR011042); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21670.1); Has 6869 Blast hits to 3873 proteins in 790 species: Archae - 41; Bacteria - 3697; Metazoa - 41; Fungi - 39; Plants - 64; Viruses - 0; Other Eukaryotes - 2987 (source: NCBI BLink).	Unigene33648_All//0.00E+00//gi|109843799|gb|DW242357.1|DW242357				nr +
Unigene3365_All	1006	8.27	3.58	7.46	17.08	15.44	13.15	8.28	3.16	3.25	-1.21E+00	7.58E-09	Down	-1.48E-01	5.22E-01		-1.46E-01	3.32E-01		-3.77E-01	4.89E-03		-1.39E+00	4.16E-13	Down	-1.35E+00	5.51E-13	Down	Unigene3365_All//gi|73761693|gb|AAZ83346.1|//1.00E-118//steroid 5-alpha-reductase [Gossypium hirsutum]	Unigene3365_All//2.00E-81//AT2G38050| DET2 (DE-ETIOLATED 2); sterol 5-alpha reductase	Unigene3365_All//0.00E+00//TC135250		ko00905|Brassinosteroid biosynthesis	GO:0009314//GO:0016020//GO:0016129//GO:0016627//GO:0048878	nr +
Unigene33651_All	2966	8.98	13.21	5.80	33.91	28.29	27.23	41.27	37.26	16.59	5.57E-01	7.43E-11		-6.31E-01	6.07E-09		-2.61E-01	3.53E-08		-3.17E-01	1.77E-10		-1.48E-01	5.79E-04		-1.31E+00	8.89E-172	Down	Unigene33651_All//gi|297792281|ref|XP_002864025.1|//3.00E-31//transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata] >gi|297309860|gb|EFH40284.1| transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata]	Unigene33651_All//6.00E-23//AT5G50010| transcription factor/ transcription regulator	Unigene33651_All//0.00E+00//TC158838	bHLH			nr +
Unigene33652_All	2389	13.38	16.18	14.58	42.81	41.79	33.63	45.20	112.65	62.45	2.74E-01	1.69E-03		1.24E-01	2.44E-01		-3.48E-02	6.02E-01		-3.48E-01	1.35E-12		1.32E+00	0.00E+00	Up	4.66E-01	7.88E-36		Unigene33652_All//gi|15240599|ref|NP_199812.1|//1.00E-33//transcription factor/ transcription regulator [Arabidopsis thaliana] >gi|75170387|sp|Q9FG80.1|BH145_ARATH RecName: Full=Transcription factor bHLH145; AltName: Full=Transcription factor EN 131; AltName: Full=bHLH transcription factor bHLH145; AltName: Full=Basic helix-loop-helix protein 145; Short=bHLH 145; Short=AtbHLH145 >gi|28950883|gb|AAO63365.1|At5g50010 [Arabidopsis thaliana]	Unigene33652_All//5.00E-28//AT5G50010| transcription factor/ transcription regulator	Unigene33652_All//0.00E+00//gi|164288851|gb|ES844147.1|ES844147				nr -
Unigene33669_All	2624	6.98	3.78	3.67	19.12	17.30	15.92	13.53	5.67	9.76	-8.83E-01	2.21E-11		-9.26E-01	1.01E-11		-1.44E-01	6.75E-02		-2.64E-01	3.77E-04		-1.26E+00	1.27E-45	Down	-4.71E-01	2.02E-09		Unigene33669_All//gi|297827583|ref|XP_002881674.1|//0.00E+00//dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327513|gb|EFH57933.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene33669_All//0.00E+00//AT2G39750| dehydration-responsive family protein	Unigene33669_All//0.00E+00//TC137578				nr -
Unigene33670_All	2648	13.65	7.54	10.40	32.92	32.42	32.64	9.92	4.45	5.67	-8.57E-01	1.13E-20		-3.93E-01	1.94E-05		-2.21E-02	7.87E-01		-1.22E-02	8.73E-01		-1.16E+00	7.18E-30	Down	-8.06E-01	2.74E-17		Unigene33670_All//gi|297827583|ref|XP_002881674.1|//0.00E+00//dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327513|gb|EFH57933.1| dehydration-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene33670_All//0.00E+00//AT2G39750| dehydration-responsive family protein	Unigene33670_All//0.00E+00//TC130040				nr +
Unigene33678_All	795	4.87	3.95	2.95	11.15	14.38	13.75	8.51	3.26	4.46	-3.02E-01	3.63E-01		-7.25E-01	2.57E-02		3.67E-01	2.90E-02		3.02E-01	9.99E-02		-1.38E+00	1.01E-10	Down	-9.32E-01	2.65E-06		Unigene33678_All//gi|145362223|ref|NP_973754.2|//1.00E-116//targeting protein-related [Arabidopsis thaliana]	Unigene33678_All//3.00E-88//AT1G03780| targeting protein-related	Unigene33678_All//0.00E+00//gi|161432321|gb|ES843164.1|ES843164				nr -
Unigene33679_All	2834	1.85	1.07	1.07	4.59	7.36	4.16	5.80	1.50	3.12	-7.83E-01	2.70E-03		-7.86E-01	3.97E-03		6.83E-01	1.15E-09		-1.41E-01	4.51E-01		-1.95E+00	3.66E-40	Down	-8.95E-01	3.52E-13		Unigene33679_All//gi|145362223|ref|NP_973754.2|//1.00E-153//targeting protein-related [Arabidopsis thaliana]	Unigene33679_All//5.00E-148//AT1G03780| targeting protein-related	Unigene33679_All//0.00E+00//TC152590				nr -
Unigene33680_All	2577	1.97	1.69	0.95	6.38	7.22	6.05	14.26	1.96	4.85	-2.20E-01	4.27E-01		-1.05E+00	1.80E-04	Down	1.78E-01	2.14E-01		-7.73E-02	6.44E-01		-2.86E+00	1.82E-140	Down	-1.55E+00	7.05E-67	Down	Unigene33680_All//gi|145362223|ref|NP_973754.2|//0.00E+00//targeting protein-related [Arabidopsis thaliana]	Unigene33680_All//0.00E+00//AT1G03780| targeting protein-related	Unigene33680_All//0.00E+00//TC177145				nr -
Unigene33681_All	2040	0.62	0.55	0.39	2.27	1.42	1.26	2.47	0.51	1.04	-1.72E-01	7.55E-01		-6.53E-01	3.04E-01		-6.80E-01	1.02E-02		-8.48E-01	2.16E-03		-2.27E+00	2.28E-15	Down	-1.25E+00	2.18E-07	Down	Unigene33681_All//gi|145362223|ref|NP_973754.2|//0.00E+00//targeting protein-related [Arabidopsis thaliana]	Unigene33681_All//2.00E-177//AT1G03780| targeting protein-related	Unigene33681_All//0.00E+00//TC152590				nr -
Unigene33686_All	928	2.93	1.42	1.38	3.81	1.48	2.34	1.46	2.57	4.16	-1.05E+00	6.56E-03		-1.09E+00	6.96E-03		-1.36E+00	1.24E-05	Down	-7.06E-01	3.12E-02		8.16E-01	2.69E-02		1.51E+00	1.85E-07	Up	Unigene33686_All//gi|15218579|ref|NP_175058.1|//5.00E-82//AAA-type ATPase family protein [Arabidopsis thaliana] >gi|8778680|gb|AAF79688.1|AC022314_29 F9C16.7 [Arabidopsis thaliana]	Unigene33686_All//2.00E-78//AT4G05380| AAA-type ATPase family protein	Unigene33686_All//2.00E-177//TC133241				nr +
Unigene33687_All	3735	3.00	13.96	2.54	5.25	7.17	5.14	7.57	7.80	22.15	2.22E+00	6.44E-121	Up	-2.40E-01	2.08E-01		4.49E-01	4.55E-06		-3.21E-02	8.33E-01		4.25E-02	6.98E-01		1.55E+00	2.65E-147	Up	Unigene33687_All//gi|15218579|ref|NP_175058.1|//1.00E-134//AAA-type ATPase family protein [Arabidopsis thaliana] >gi|8778680|gb|AAF79688.1|AC022314_29 F9C16.7 [Arabidopsis thaliana]	Unigene33687_All//3.00E-133//AT1G43910| AAA-type ATPase family protein	Unigene33687_All//0.00E+00//gi|164304755|gb|ES824526.1|ES824526				nr +
Unigene33689_All	2851	1.98	1.81	2.09	7.74	5.69	4.77	4.67	1.23	1.69	-1.29E-01	6.04E-01		7.79E-02	7.63E-01		-4.44E-01	3.97E-05		-6.99E-01	7.31E-10		-1.92E+00	3.93E-32	Down	-1.47E+00	8.21E-23	Down	Unigene33689_All//gi|297836780|ref|XP_002886272.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332112|gb|EFH62531.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene33689_All//0.00E+00//AT2G20300| ALE2 (Abnormal Leaf Shape 2); kinase	Unigene33689_All//0.00E+00//TC167405		ko04626|Plant-pathogen interaction		nr +
Unigene3369_All	1416	10.72	25.59	9.74	13.05	18.12	19.97	13.76	33.06	34.49	1.26E+00	6.09E-38	Up	-1.38E-01	3.93E-01		4.73E-01	2.29E-06		6.13E-01	6.20E-10		1.26E+00	1.92E-60	Up	1.33E+00	3.00E-69	Up	Unigene3369_All//gi|297812519|ref|XP_002874143.1|//4.00E-20//sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319980|gb|EFH50402.1| sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene3369_All//1.00E-16//AT5G23680| sterile alpha motif (SAM) domain-containing protein	Unigene3369_All//0.00E+00//TC170218				nr -
Unigene33690_All	2987	2.96	2.17	1.53	12.12	9.50	7.62	7.57	1.58	2.33	-4.47E-01	2.23E-02		-9.49E-01	3.10E-06		-3.52E-01	2.10E-05		-6.70E-01	1.08E-14		-2.26E+00	2.33E-66	Down	-1.70E+00	4.92E-47	Down	Unigene33690_All//gi|30680947|ref|NP_849998.1|//0.00E+00//ALE2 (Abnormal Leaf Shape 2); kinase [Arabidopsis thaliana] >gi|110742054|dbj|BAE98959.1| protein kinase like protein [Arabidopsis thaliana]	Unigene33690_All//0.00E+00//AT2G20300| ALE2 (Abnormal Leaf Shape 2); kinase	Unigene33690_All//0.00E+00//TC171575		ko04626|Plant-pathogen interaction		nr +
Unigene33691_All	637	2.71	0.88	0.08	9.46	6.38	3.55	6.90	2.49	3.69	-1.63E+00	2.08E-03		-5.02E+00	3.13E-08	Down	-5.69E-01	1.31E-02		-1.42E+00	1.04E-08	Down	-1.47E+00	7.65E-08	Down	-9.04E-01	3.16E-04		Unigene33691_All//gi|2737926|gb|AAC49919.1|//3.00E-54//fimbrin-like protein AtFim2 [Arabidopsis thaliana]	Unigene33691_All//7.00E-54//AT5G48460| fimbrin-like protein, putative	Unigene33691_All//0.00E+00//TC173734				nr -
Unigene33692_All	1732	3.63	1.76	2.37	12.34	10.99	8.29	6.91	2.22	3.29	-1.05E+00	1.28E-05	Down	-6.15E-01	1.26E-02		-1.66E-01	2.02E-01		-5.73E-01	6.32E-07		-1.64E+00	2.61E-23	Down	-1.07E+00	6.30E-13	Down	Unigene33692_All//gi|226503007|ref|NP_001147889.1|//0.00E+00//fimbrin 1 [Zea mays] >gi|195614416|gb|ACG29038.1| fimbrin 1 [Zea mays]	Unigene33692_All//0.00E+00//AT5G48460| fimbrin-like protein, putative	Unigene33692_All//0.00E+00//TC173734				nr +
Unigene33693_All	2402	7.69	1.81	4.08	9.35	9.25	7.77	3.85	1.51	2.42	-2.08E+00	3.24E-40	Down	-9.15E-01	1.38E-11		-1.65E-02	9.07E-01		-2.68E-01	2.45E-02		-1.35E+00	7.46E-14	Down	-6.71E-01	4.27E-05		Unigene33693_All//gi|51971889|dbj|BAD41609.1|//0.00E+00//fimbrin 2 [Arabidopsis thaliana]	Unigene33693_All//0.00E+00//AT5G48460| fimbrin-like protein, putative	Unigene33693_All//0.00E+00//TC174350				nr +
Unigene33694_All	1254	3.50	7.15	5.35	6.79	6.76	6.16	6.00	4.57	6.39	1.03E+00	1.84E-07	Up	6.10E-01	9.82E-03		-8.00E-03	9.68E-01		-1.41E-01	5.55E-01		-3.94E-01	4.23E-02		8.95E-02	6.46E-01		Unigene33694_All//gi|33860243|gb|AAQ54906.1|//1.00E-154//cell cycle switch protein CCS52a [Lupinus luteus]	Unigene33694_All//1.00E-139//AT4G22910| FZR2 (FIZZY-RELATED 2); signal transducer	Unigene33694_All//0.00E+00//TC153890		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene33697_All	4120	10.02	4.58	7.72	27.98	35.66	39.35	83.97	49.67	62.96	-1.13E+00	8.21E-37	Down	-3.77E-01	1.07E-05		3.50E-01	8.64E-20		4.92E-01	1.26E-36		-7.58E-01	7.11E-190		-4.15E-01	1.76E-66		Unigene33697_All//gi|56157408|gb|AY880420.1|//1.00E-106//Prf interactor 30137 [Solanum lycopersicum]	Unigene33697_All//8.00E-74//AT5G06060| tropinone reductase, putative / tropine dehydrogenase, putative	Unigene33697_All//0.00E+00//TC150417		ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis		nr -
Unigene33700_All	444	0.12	0.00	0.24	1.68	2.25	3.05	18.57	5.65	8.79	-6.88E+00	6.11E-01		1.03E+00	7.03E-01		4.19E-01	5.85E-01		8.59E-01	1.50E-01		-1.72E+00	2.23E-17	Down	-1.08E+00	2.77E-09	Down			Unigene33700_All//7.00E-62//TC140227				ESTscan -
Unigene33701_All	661	0.08	0.38	0.08	0.60	0.63	1.43	10.11	8.92	3.13	2.27E+00	2.34E-01		2.53E-02	9.95E-01		5.22E-02	9.89E-01		1.23E+00	9.60E-02		-1.81E-01	4.28E-01		-1.69E+00	2.17E-14	Down			Unigene33701_All//4.00E-95//TC140227				
Unigene33702_All	5246	2.85	1.75	1.62	6.99	5.96	5.84	28.64	11.23	21.10	-7.06E-01	1.07E-06		-8.13E-01	6.56E-08		-2.30E-01	8.41E-03		-2.60E-01	3.66E-03		-1.35E+00	1.32E-213	Down	-4.40E-01	1.24E-32		Unigene33702_All//gi|292668967|gb|ADE41138.1|//1.00E-53//AP2 domain class transcription factor [Malus x domestica]	Unigene33702_All//2.00E-38//AT5G67190| AP2 domain-containing transcription factor, putative	Unigene33702_All//0.00E+00//gi|78353150|gb|DT573424.1|DT573424	AP2-EREBP			nr -
Unigene33707_All	2109	4.22	1.99	2.27	4.30	2.99	5.05	8.58	6.48	8.48	-1.08E+00	5.51E-08	Down	-8.92E-01	1.00E-05		-5.25E-01	3.65E-03		2.33E-01	2.32E-01		-4.05E-01	5.08E-04		-1.67E-02	9.14E-01		Unigene33707_All//gi|9392607|gb|AAF87216.1|AF231351_1//0.00E+00//plastidic glucose 6-phosphate dehydrogenase [Nicotiana tabacum]	Unigene33707_All//0.00E+00//AT5G13110| G6PD2 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 2); glucose-6-phosphate dehydrogenase	Unigene33707_All//0.00E+00//TC139918		ko00480|Glutathione metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene33708_All	2307	10.25	6.96	5.96	16.06	12.08	8.36	11.44	4.19	8.05	-5.58E-01	6.31E-07		-7.84E-01	2.04E-11		-4.12E-01	3.29E-07		-9.43E-01	1.28E-26		-1.45E+00	2.35E-42	Down	-5.07E-01	3.92E-08		Unigene33708_All//gi|9392607|gb|AAF87216.1|AF231351_1//0.00E+00//plastidic glucose 6-phosphate dehydrogenase [Nicotiana tabacum]	Unigene33708_All//0.00E+00//AT5G13110| G6PD2 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 2); glucose-6-phosphate dehydrogenase	Unigene33708_All//0.00E+00//TC139918		ko00480|Glutathione metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene33709_All	511	1.95	8.13	5.00	0.49	0.20	0.27	3.81	2.29	0.70	2.06E+00	2.15E-09	Up	1.36E+00	1.40E-03		-1.27E+00	4.24E-01		-8.79E-01	6.16E-01		-7.33E-01	7.89E-02		-2.44E+00	3.73E-07	Down	Unigene33709_All//gi|16648836|gb|AAL25608.1|//9.00E-41//At5g03355/C415EPL23M [Arabidopsis thaliana] >gi|21618291|gb|AAM67341.1| uracil transporter-like protein [Arabidopsis thaliana]	Unigene33709_All//4.00E-39//AT5G03555| permease, cytosine/purines, uracil, thiamine, allantoin family protein				nr +
Unigene3371_All	1102	7.41	11.63	9.76	5.88	6.12	6.11	3.07	3.11	1.16	6.51E-01	3.55E-05		3.98E-01	3.07E-02		5.97E-02	8.26E-01		5.54E-02	8.36E-01		1.90E-02	9.84E-01		-1.41E+00	4.15E-06	Down	Unigene3371_All//gi|194708822|gb|ACF88495.1|//4.00E-24//At5g55210 [Arabidopsis thaliana]	Unigene3371_All//1.00E-18//AT5G55210| unknown protein	Unigene3371_All//0.00E+00//TC135345				nr +

Unigene33710_All	630	11.05	46.41	23.92	1.74	1.69	2.22	0.20	0.00	0.25	2.07E+00	2.23E-62	Up	1.11E+00	4.81E-13	Up	-3.79E-02	9.49E-01		3.53E-01	5.79E-01		-7.65E+00	2.35E-01		3.29E-01	8.51E-01		Unigene33710_All//gi|42567620|ref|NP_568122.2|//2.00E-33//permease, cytosine/purines, uracil, thiamine, allantoin family protein [Arabidopsis thaliana] >gi|7378642|emb|CAB83318.1| uracil transporter-like protein [Arabidopsis thaliana]	Unigene33710_All//5.00E-34//AT5G03555| permease, cytosine/purines, uracil, thiamine, allantoin family protein					nr +
Unigene33711_All	1327	8.71	19.17	19.78	2.63	2.05	2.52	2.80	1.61	0.42	1.14E+00	4.59E-23	Up	1.18E+00	1.91E-24	Up	-3.58E-01	3.05E-01		-6.12E-02	8.71E-01		-8.04E-01	4.55E-03		-2.74E+00	1.16E-14	Down	Unigene33711_All//gi|16648836|gb|AAL25608.1|//1.00E-162//At5g03555/C415EPL23M [Arabidopsis thaliana] >gi|21618291|gb|AAM67341.1| uracil transporter-like protein [Arabidopsis thaliana]	Unigene33711_All//1.00E-142//AT5G03555| permease, cytosine/purines, uracil, thiamine, allantoin family protein	Unigene33711_All//4.00E-118//C0081242				nr +
Unigene33719_All	690	5.76	7.64	4.40	8.66	8.73	6.74	11.70	4.85	15.94	4.06E-01	1.27E-01		-3.90E-01	2.37E-01		1.17E-02	9.70E-01		-3.62E-01	1.58E-01		-1.27E+00	3.30E-11	Down	4.45E-01	2.92E-03		Unigene33719_All//gi|15225994|ref|NP_179079.1|//2.00E-71//VSR-2; calcium ion binding [Arabidopsis thaliana] >gi|30679216|ref|NP_849954.1| VSR-2; calcium ion binding [Arabidopsis thaliana] >gi|7115404|sp|Q56ZQ3.2|VSR4_ARATH RecName: Full=Vacuolar-sorting receptor 4; Short=AtVSR4; AltName: Full=Epidermal growth factor receptor-like protein 2b; Short=AtELP2b; AltName: Full=BPS0-like protein a; Short=AtBPS0a; Flags: Precursor >gi|30725454|gb|AAP37749.1|At2g14720 [Arabidopsis thaliana]	Unigene33719_All//4.00E-72//AT2G14720| VSR-2; calcium ion binding	Unigene33719_All//2.00E-161//ES808273				nr -
Unigene3372_All	1603	0.59	15.43	2.66	5.03	8.46	18.62	42.17	2121.96	320.03	4.71E+00	2.79E-115	Up	2.18E+00	7.58E-10	Up	7.50E-01	1.64E-07		1.89E+00	2.03E-60	Up	5.65E+00	0.00E+00	Up	2.92E+00	0.00E+00	Up	Unigene3372_All//gi|224062179|ref|XP_002300790.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222842516|gb|EEE80063.1| cytochrome P450 [Populus trichocarpa]	Unigene3372_All//2.00E-122//AT5G63450| CYP94B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene3372_All//0.00E+00//TC137283		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016712//GO:0043231//GO:0044425	nr +
Unigene33725_All	1475	7.38	3.37	7.11	14.35	14.31	17.36	13.21	12.21	7.00	-1.13E+00	2.81E-10	Down	-5.30E-02	7.78E-01		-4.20E-03	9.69E-01		2.75E-01	1.29E-02		-1.14E-01	4.00E-01		-9.18E-01	4.45E-16		Unigene33725_All//gi|57335420|emb|CAH10188.1|//1.00E-166//START domain-containing protein [Poa pratensis]	Unigene33725_All//0.00E+00//AT5G45560| pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein	Unigene33725_All//0.00E+00//gi|164338923|gb|ES798230.1|ES798230			GO:0043231	nr +
Unigene33729_All	488	0.11	1.97	1.75	2.25	1.76	0.46	2.08	0.94	0.73	4.20E+00	1.29E-04	Up	4.03E+00	7.02E-04	Up	-3.48E-01	5.97E-01		-2.28E+00	1.97E-03		-1.14E+00	6.62E-02		-1.50E+00	1.41E-02		Unigene33729_All//gi|296088117|emb|CBI35506.3|//4.00E-10//unnamed protein product [Vitis vinifera]		Unigene33729_All//7.00E-99//C0079407			GO:0004672//GO:0005488//GO:0008152	nr -
Unigene3373_All	1097	6.25	13.49	5.05	20.16	19.68	16.43	12.33	18.78	9.12	1.11E+00	3.08E-13	Up	-3.08E-01	2.14E-01		-3.48E-02	8.36E-01		-2.96E-01	1.29E-02		6.07E-01	1.98E-08		-4.36E-01	1.04E-03		Unigene3373_All//gi|269999990|gb|ACZ57923.1|//1.00E-58//DnaJ-like protein [Glycine max]	Unigene3373_All//5.00E-56//AT1G56300| DNAJ heat shock N-terminal domain-containing protein	Unigene3373_All//0.00E+00//TC155244			GO:0005515//GO:0044267//GO:0050896	nr +
Unigene33737_All	2062	5.79	7.15	3.56	3.09	1.90	2.15	8.35	8.72	22.97	3.06E-01	4.19E-02		-6.99E-01	3.88E-05		-7.00E-01	1.30E-03		-5.27E-01	2.47E-02		6.27E-02	6.42E-01		1.46E+00	9.96E-78	Up	Unigene33737_All//gi|297824839|ref|XP_002880302.1|//0.00E+00//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297326141|gb|EFH56561.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene33737_All//0.00E+00//AT2G47440| DNAJ heat shock N-terminal domain-containing protein	Unigene33737_All//0.00E+00//TC146165			GO:0005515//GO:0043231//GO:0044267//GO:0050896	nr -
Unigene33738_All	2381	4.48	5.00	3.09	5.25	5.55	4.42	10.71	2.74	8.73	1.58E-01	3.80E-01		-5.39E-01	3.04E-03		8.07E-02	6.76E-01		-2.49E-01	1.50E-01		-1.97E+00	1.14E-62	Down	-2.94E-01	2.00E-03		Unigene33738_All//gi|15226607|ref|NP_182266.1|//0.00E+00//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]	Unigene33738_All//2.00E-179//AT2G47440| DNAJ heat shock N-terminal domain-containing protein	Unigene33738_All//0.00E+00//TC141906			GO:0005515//GO:0043231//GO:0044267//GO:0050896	nr -
Unigene3374_All	1155	6.84	3.82	6.82	5.61	4.26	5.01	2.42	1.74	1.07	-8.42E-01	4.98E-05		-3.50E-03	9.95E-01		-3.95E-01	8.61E-02		-1.64E-01	5.51E-01		-4.76E-01	1.68E-01		-1.18E+00	3.83E-04	Down	Unigene3374_All//gi|295815790|gb|ADG36380.1|//4.00E-63//promoter-binding protein SPL9 [Vitis vinifera]	Unigene3374_All//1.00E-17//AT2G42200| SPL9 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 9); transcription factor	Unigene3374_All//0.00E+00//TC172221	SBP		GO:0007275//GO:0048856	nr +
Unigene33740_All	1586	10.09	5.62	9.17	7.63	6.04	5.01	1.92	0.69	0.90	-8.44E-01	2.24E-09		-1.39E-01	3.88E-01		-3.39E-01	3.56E-02		-6.07E-01	1.32E-04		-1.49E+00	9.46E-06	Down	-1.09E+00	5.17E-04	Down	Unigene33740_All//gi|6685070|gb|AAF23771.1|AF205859_1//1.00E-162//FtsZ protein [Gentiana lutea]	Unigene33740_All//2.00E-128//AT2G36250| FTSZ2-1; protein binding / structural molecule	Unigene33740_All//0.00E+00//TC167361				nr -
Unigene33741_All	1905	13.71	8.75	16.21	12.05	14.06	10.31	5.86	1.76	3.10	-6.47E-01	1.32E-09		2.42E-01	2.08E-02		2.22E-01	3.94E-02		-2.25E-01	6.42E-02		-1.74E+00	1.16E-23	Down	-9.21E-01	1.22E-09		Unigene33741_All//gi|6685070|gb|AAF23771.1|AF205859_1//0.00E+00//FtsZ protein [Gentiana lutea]	Unigene33741_All//2.00E-174//AT2G36250| FTSZ2-1; protein binding / structural molecule	Unigene33741_All//0.00E+00//TC167361			GO:0005515//GO:0009532//GO:0009658//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene33744_All	2420	5.62	14.11	7.92	12.10	15.27	16.57	12.79	20.60	27.46	1.33E+00	5.45E-39	Up	4.95E-01	1.47E-04		3.35E-01	5.54E-05		4.53E-01	2.87E-08		6.88E-01	8.32E-24		1.10E+00	1.89E-70	Up	Unigene33744_All//gi|169218920|gb|ACA50283.1|//0.00E+00//cytokinin hypersensitive 1 [Arabidopsis thaliana]	Unigene33744_All//2.00E-65//AT1G37140| ERF4 (ENHANCED ETHYLENE RESPONSE 4); DNA binding / transcription initiation factor	Unigene33744_All//0.00E+00//DT468517		ko03022|Basal transcription factors	GO:0005634//GO:0009873	nr +
Unigene33745_All	903	2.09	3.09	1.89	5.24	3.78	4.75	4.49	1.85	2.82	5.65E-01	1.36E-01		-1.45E-01	7.57E-01		-4.73E-01	8.33E-02		-1.41E-01	6.56E-01		-1.28E+00	4.51E-06	Down	-6.71E-01	9.89E-03		Unigene33745_All//gi|22330273|ref|NP_175986.2|//1.00E-100//TIM50 [Arabidopsis thaliana] >gi|75161466|sp|Q8VYE2.1|TIM50_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit TIM50; AltName: Full=Protein EMBRYO DEFECTIVE 1860; Flags: Precursor	Unigene33745_All//4.00E-94//AT1G15900| TIM50	Unigene33745_All//0.00E+00//TC156300			GO:0043231	nr -
Unigene33746_All	1349	4.62	3.00	4.03	9.23	6.02	6.19	9.00	4.43	5.37	-6.19E-01	8.79E-03		-1.97E-01	4.50E-01		-6.16E-01	3.05E-05		-5.76E-01	2.32E-04		-1.02E+00	8.19E-12	Down	-7.43E-01	1.76E-07		Unigene33746_All//gi|22330273|ref|NP_175986.2|//1.00E-122//TIM50 [Arabidopsis thaliana] >gi|75161466|sp|Q8VYE2.1|TIM50_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit TIM50; AltName: Full=Protein EMBRYO DEFECTIVE 1860; Flags: Precursor	Unigene33746_All//9.00E-113//AT1G15900| TIM50	Unigene33746_All//0.00E+00//TC156475				nr +
Unigene33747_All	1618	5.37	5.48	7.11	12.28	9.94	10.83	5.28	2.38	3.69	2.99E-02	8.94E-01		4.05E-01	2.23E-02		-3.06E-01	1.13E-02		-1.82E-01	1.93E-01		-1.15E+00	3.32E-10	Down	-5.15E-01	2.62E-03		Unigene33747_All//gi|22330273|ref|NP_175986.2|//1.00E-130//TIM50 [Arabidopsis thaliana] >gi|75161466|sp|Q8VYE2.1|TIM50_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit TIM50; AltName: Full=Protein EMBRYO DEFECTIVE 1860; Flags: Precursor	Unigene33747_All//2.00E-116//AT1G15900| TIM50	Unigene33747_All//0.00E+00//TC148283				nr -
Unigene33754_All	1965	2.50	1.32	1.76	9.89	6.99	6.27	1.74	0.94	0.75	-9.28E-01	6.46E-04		-5.07E-01	7.83E-02		-5.00E-01	1.49E-05		-6.56E-01	6.66E-08		-8.97E-01	2.61E-03		-1.22E+00	4.18E-05	Down	Unigene33754_All//gi|194595409|gb|ACF77017.1|//0.00E+00//ADP-glucose pyrophosphorylase large subunit [Citrus sinensis]	Unigene33754_All//0.00E+00//AT4G39210| APL3; glucose-1-phosphate adenylyltransferase	Unigene33754_All//0.00E+00//C0093068		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0009536//GO:0070566	nr +
Unigene33755_All	3147	16.26	14.68	21.12	27.56	38.67	41.93	7.89	4.33	2.23	-1.47E-01	6.38E-02		3.77E-01	9.57E-09		4.89E-01	3.77E-30		6.06E-01	2.87E-43		-8.65E-01	7.57E-18		-1.82E+00	7.65E-57	Down	Unigene33755_All//gi|2642640|gb|AAB91468.1|//0.00E+00//ADP-glucose pyrophosphorylase large subunit 2 [Citrullus lanatus subsp. vulgaris]	Unigene33755_All//5.00E-179//AT5G19220| APL1 (ADP GLUCOSE PYROPHOSPHORYLASE LARGE SUBUNIT 1); glucose-1-phosphate adenylyltransferase	Unigene33755_All//0.00E+00//TC156937		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0016798//GO:0032559//GO:0043167//GO:0070566	nr +
Unigene33757_All	1529	6.71	4.18	3.83	10.00	11.89	10.60	10.09	4.89	6.49	-6.84E-01	1.24E-04		-8.08E-01	1.34E-05		2.50E-01	6.32E-02		8.43E-02	6.08E-01		-1.04E+00	2.57E-15	Down	-6.38E-01	2.71E-07		Unigene33757_All//gi|111154399|gb|AB807428.1|//0.00E+00//vacuolar H+-ATPase subunit C [Gossypium hirsutum]	Unigene33757_All//2.00E-173//AT1G12840| DET3 (DE-ETIOLATED 3); proton-transporting ATPase, rotational mechanism	Unigene33757_All//0.00E+00//TC136419		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0000902//GO:0005773//GO:0006109//GO:0006754//GO:0009536//GO:0009699//GO:0019829//GO:0031090//GO:0033176	nr -
Unigene33758_All	1807	31.07	22.46	23.90	38.29	31.21	32.77	59.36	43.72	28.26	-4.68E-01	2.46E-11		-3.79E-01	1.54E-07		-2.95E-01	3.65E-07		-2.25E-01	3.38E-04		-4.41E-01	5.22E-23		-1.07E+00	8.76E-109	Down	Unigene33758_All//gi|111154399|gb|AB807428.1|//0.00E+00//vacuolar H+-ATPase subunit C [Gossypium hirsutum]	Unigene33758_All//1.00E-180//AT1G12840| DET3 (DE-ETIOLATED 3); proton-transporting ATPase, rotational mechanism	Unigene33758_All//0.00E+00//TC146772		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0000902//GO:0005773//GO:0006109//GO:0006754//GO:0009536//GO:0009699//GO:0019829//GO:0031090//GO:0033176	nr -
Unigene33761_All	577	1.81	0.97	1.48	1.90	1.49	1.17	1.83	2.54	5.80	-9.09E-01	1.75E-01		-2.97E-01	6.42E-01		-3.48E-01	5.97E-01		-6.94E-01	3.11E-01		4.69E-01	3.70E-01		1.66E+00	2.16E-07	Up	Unigene33761_All//gi|57281695|dbj|BAB86587.1|//3.00E-72//sphingosine kinase [Lotus japonicus]	Unigene33761_All//2.00E-67//AT5G23450| ATLCBK1 (A. THALIANA LONG-CHAIN BASE (LCB) KINASE 1); D-erythro-sphingosine kinase/ diacylglycerol kinase	Unigene33761_All//0.00E+00//TC158992			GO:0001727//GO:0003676//GO:0006260//GO:0006665//GO:0007186//GO:0016020//GO:0034061//GO:0043231	nr -
Unigene33762_All	1479	3.25	1.47	1.55	4.14	3.56	1.25	3.74	4.69	10.37	-1.14E+00	4.57E-05	Down	-1.07E+00	2.15E-04	Down	-2.18E-01	4.16E-01		-1.73E+00	1.34E-11	Down	3.25E-01	1.22E-01		1.47E+00	5.76E-26	Up	Unigene33762_All//gi|115482946|ref|NP_001065066.1|//1.00E-101//Os10g0516800 [Oryza sativa Japonica Group] >gi|113639675|dbj|BAF26980.1| Os10g0516800 [Oryza sativa Japonica Group]	Unigene33762_All//2.00E-90//AT5G23450| ATLCBK1 (A. THALIANA LONG-CHAIN BASE (LCB) KINASE 1); D-erythro-sphingosine kinase/ diacylglycerol kinase	Unigene33762_All//0.00E+00//TC158992		ko00600|Sphingolipid metabolism	GO:0006665//GO:0007186//GO:0016020//GO:0016301//GO:0043231	nr +
Unigene33764_All	1969	23.22	20.74	18.25	44.58	40.70	32.09	25.38	10.30	9.33	-1.63E-01	5.03E-02		-3.47E-01	1.87E-05		-1.31E-01	2.07E-02		-4.74E-01	6.64E-19		-1.30E+00	1.42E-67	Down	-1.44E+00	2.33E-81	Down	Unigene33764_All//gi|115468854|ref|NP_001058026.1|//1.00E-60//Os06g0606800 [Oryza sativa Japonica Group] >gi|113596066|dbj|BAF19940.1| Os06g0606800 [Oryza sativa Japonica Group]	Unigene33764_All//7.00E-69//AT4G32330| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G25480.1); Has 4728 Blast hits to 3313 proteins in 331 species: Archae - 4; Bacteria - 347; Metazoa - 2216; Fungi - 461; Plants - 233; Viruses - 22; Other Eukaryotes - 1445 (source: NCBI BLink).	Unigene33764_All//0.00E+00//TC140978				nr +

Unigene33765_All	1847	134.53	95.41	130.43	135.23	148.22	100.43	44.16	21.14	26.10	-4.96E-01	1.10E-52		-4.46E-02	2.51E-01		1.32E-01	4.54E-06		-4.29E-01	5.38E-44		-1.06E+00	1.02E-79	Down	-7.59E-01	9.66E-47		Unigene33765_All//gi|226533114|ref|NP_001148491.1|//1.00E-58//LOC100282106 [Zea mays] >gi|195619766|gb|ACG31713.1| seed specific protein Bn15D14A [Zea mays]	Unigene33765_All//3.00E-75//AT4G32330| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G25480.1); Has 4728 Blast hits to 3313 proteins in 331 species: Archae - 4; Bacteria - 347; Metazoa - 2216; Fungi - 461; Plants - 233; Viruses - 22; Other Eukaryotes - 1445 (source: NCBI BLink).	Unigene33765_All//0.00E+00//TC157612				nr +
Unigene33767_All	681	0.15	2.46	0.70	2.05	2.02	1.79	4.22	3.50	5.44	4.00E+00	2.08E-07	Up	2.19E+00	9.15E-02		-1.81E-02	9.59E-01		-1.94E-01	7.27E-01		-2.71E-01	4.47E-01		3.66E-01	1.99E-01		Unigene33767_All//gi|77556192|gb|AB498988.1|//1.00E-07//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene33767_All//8.00E-06//AT2G39580| unknown protein			GO:0043231	nr -
Unigene33769_All	1191	0.26	0.00	0.94	0.88	0.49	0.83	0.99	6.39	0.43	-8.04E+00	3.65E-02		1.83E+00	1.24E-02		-8.38E-01	2.01E-01		-7.41E-02	9.22E-01		2.68E+00	1.44E-27	Up	-1.19E+00	2.80E-02		Unigene33769_All//gi|42567319|ref|NP_194929.2|//2.00E-59//HSL1 (HSI2-LIKE 1); transcription factor [Arabidopsis thaliana] >gi|75320503|sp|Q5CC04.1|VAL2_ARATH RecName: Full=B3 domain-containing transcription repressor VAL2; AltName: Full=Protein VP1/ABI3-LIKE 2; AltName: Full=Protein HIGH-LEVEL EXPRESSION OF SUGAR-INDUCIBLE-LIKE 1 >gi|60677679|dbj|BAD90971.1| transcription factor B3-EAR motif family [Arabidopsis thaliana]	Unigene33769_All//5.00E-61//AT4G32010| HSL1 (HSI2-LIKE 1); transcription factor	Unigene33769_All//0.00E+00//CO093948	ABI3VP1		GO:0005488//GO:0006350//GO:0009725//GO:0009815//GO:0010431//GO:0010468//GO:0030528//GO:0034285//GO:0043231	nr +
Unigene33771_All	3192	1.15	0.75	0.72	4.65	3.06	3.83	7.43	23.43	5.88	-6.21E-01	5.28E-02		-6.78E-01	4.48E-02		-6.02E-01	6.49E-06		-2.78E-01	6.96E-02		1.66E+00	8.74E-144	Up	-3.38E-01	5.75E-04		Unigene33771_All//gi|297826459|ref|XP_002881112.1|//0.00E+00//high-level expression of sugar-inducible gene 2 [Arabidopsis lyrata subsp. lyrata] >gi|297326951|gb|EFH57371.1| high-level expression of sugar-inducible gene 2 [Arabidopsis lyrata subsp. lyrata]	Unigene33771_All//0.00E+00//AT2G30470| HSI2 (HIGH-LEVEL EXPRESSION OF SUGAR-INDUCIBLE GENE 2); transcription factor/ transcription repressor	Unigene33771_All//0.00E+00//TC148288	ABI3VP1		GO:0003676//GO:0006351//GO:0009845//GO:0010033//GO:0010431//GO:0010468//GO:0030528//GO:0043231//GO:0046914	nr +
Unigene33773_All	2053	5.12	4.62	6.43	12.40	11.29	9.37	8.09	3.50	3.84	-1.50E-01	4.28E-01		3.29E-01	4.83E-02		-1.35E-01	2.72E-01		-4.04E-01	1.32E-04		-1.21E+00	1.45E-20	Down	-1.07E+00	1.03E-17	Down	Unigene33773_All//gi|75162430|sp|Q8W486.1|Y1491_ARATH//0.00E+00//RecName: Full=DUF246 domain-containing protein At1g04910 >gi|17065372|gb|AAL32840.1| Similar to auxin-independent growth promoter (axi 1) [Arabidopsis thaliana] >gi|31711926|gb|AAP68319.1| At1g04910 [Arabidopsis thaliana]	Unigene33773_All//0.00E+00//AT1G04910| unknown protein	Unigene33773_All//0.00E+00//TC150426			GO:0043231	nr -
Unigene33778_All	848	13.57	43.26	18.40	8.58	21.28	19.17	3.29	12.17	14.28	1.67E+00	1.35E-58	Up	4.39E-01	2.92E-03		1.31E+00	7.96E-24	Up	1.16E+00	2.02E-16	Up	1.89E+00	2.12E-24	Up	2.12E+00	1.02E-33	Up	Unigene33778_All//gi|224138238|ref|XP_002322764.1|//1.00E-108//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222867394|gb|EEF04525.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene33778_All//2.00E-102//AT5G06530| ABC transporter family protein	Unigene33778_All//0.00E+00//TC160077		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015405//GO:0016020//GO:0017111//GO:0032559	nr -
Unigene33779_All	813	8.43	43.56	27.97	8.39	29.61	29.11	1.66	6.58	12.74	2.37E+00	4.33E-89	Up	1.73E+00	3.14E-37	Up	1.82E+00	1.26E-50	Up	1.79E+00	8.29E-45	Up	1.98E+00	7.77E-14	Up	2.94E+00	9.60E-42	Up	Unigene33779_All//gi|224138238|ref|XP_002322764.1|//5.00E-49//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222867394|gb|EEF04525.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene33779_All//5.00E-29//AT5G06530| ABC transporter family protein	Unigene33779_All//0.00E+00//TC153935			GO:0015098//GO:0016020//GO:0017111//GO:0032559	nr -
Unigene33780_All	2741	19.51	88.81	35.12	16.83	34.94	32.23	5.85	19.08	29.87	2.19E+00	0.00E+00	Up	8.48E-01	2.98E-51		1.05E+00	3.00E-89	Up	9.37E-01	1.57E-61		1.71E+00	5.03E-105	Up	2.35E+00	1.25E-254	Up	Unigene33780_All//gi|224138238|ref|XP_002322764.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222867394|gb|EEF04525.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene33780_All//0.00E+00//AT5G06530| ABC transporter family protein	Unigene33780_All//0.00E+00//TC160077		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015098//GO:0016020//GO:0032559//GO:0042626	nr +
Unigene33783_All	1851	2.29	0.88	1.41	2.75	2.05	1.05	2.47	2.15	2.00	-1.39E+00	7.36E-06	Down	-7.00E-01	2.35E-02		-4.24E-01	1.10E-01		-1.39E+00	3.12E-07	Down	-2.02E-01	4.78E-01		-3.02E-01	2.42E-01		Unigene33783_All//gi|261876465|dbj|BAI47558.1|//0.00E+00//cryptochrome2 [Glycine max]	Unigene33783_All//7.00E-172//AT1G04400| CRY2 (CRYPTOCHROME 2); blue light photoreceptor/ protein homodimerization	Unigene33783_All//0.00E+00//TC169697		ko04712|Circadian rhythm - plant	GO:0003913//GO:0006259	nr -
Unigene33785_All	849	3.33	2.57	3.89	5.40	7.06	5.43	5.38	2.66	1.88	-3.75E-01	3.34E-01		2.25E-01	5.53E-01		3.87E-01	1.22E-01		7.50E-03	9.80E-01		-1.02E+00	6.50E-05	Down	-1.52E+00	8.61E-09	Down	Unigene33785_All//gi|297842213|ref|XP_002888988.1|//2.00E-26//IQ-domain 31 [Arabidopsis lyrata subsp. lyrata] >gi|297334829|gb|EFH65247.1| IQ-domain 31 [Arabidopsis lyrata subsp. lyrata]	Unigene33785_All//3.00E-17//AT1G14350| IQD28 (IQ67 DOMAIN PROTEIN 28); calmodulin binding	Unigene33785_All//0.00E+00//TC145816			GO:0016020//GO:0044444	nr -
Unigene33786_All	2623	12.67	13.66	12.53	17.13	17.82	19.80	22.24	13.10	9.43	1.09E-01	2.82E-01		-1.61E-02	8.90E-01		5.66E-02	5.74E-01		2.09E-01	5.43E-03		-7.64E-01	3.72E-33		-1.24E+00	5.87E-75	Down	Unigene33786_All//gi|115465121|ref|NP_001056160.1|//1.00E-86//Os05g0535900 [Oryza sativa (japonica Group)] >gi|113579711|dbj|BAF18074.1| Os05g0535900 [Oryza sativa (japonica Group)]	Unigene33786_All//3.00E-51//AT1G14350| IQD28 (IQ67 DOMAIN PROTEIN 28); calmodulin binding	Unigene33786_All//0.00E+00//CO118151			GO:0044444	nr -
Unigene33787_All	1396	11.81	8.09	9.00	12.52	7.50	6.44	13.72	20.09	40.01	-5.45E-01	6.68E-05		-3.91E-01	6.68E-03		-7.40E-01	1.16E-09		-9.60E-01	2.99E-13		5.50E-01	1.68E-09		1.54E+00	2.96E-99	Up	Unigene33787_All//gi|2582800|emb|CAA72341.1|//2.00E-95//protein phosphatase 2C [Medicago sativa]	Unigene33787_All//1.00E-95//AT2G40180| ATHPP2C5; catalytic/ protein serine/threonine phosphatase	Unigene33787_All//0.00E+00//gi|164302153|gb|EX166660.1|EX166660			GO:0004721//GO:0006464//GO:0006952//GO:0009755//GO:0043169//GO:0043231//GO:0043234//GO:0051707	nr +
Unigene33788_All	1885	4.77	5.03	3.73	1.90	1.57	1.87	10.52	16.81	49.45	7.44E-02	7.06E-01		-3.57E-01	8.48E-02		-2.76E-01	4.30E-01		-2.59E-02	9.44E-01		6.76E-01	5.58E-15		2.23E+00	5.31E-272	Up	Unigene33788_All//gi|2582800|emb|CAA72341.1|//1.00E-110//protein phosphatase 2C [Medicago sativa]	Unigene33788_All//1.00E-98//AT2G40180| ATHPP2C5; catalytic/ protein serine/threonine phosphatase	Unigene33788_All//0.00E+00//gi|109853445|gb|DW482424.1|DW482424				nr -
Unigene33789_All	2001	5.67	7.17	6.04	8.54	5.70	5.26	5.83	5.24	12.90	3.37E-01	2.58E-02		9.04E-02	6.05E-01		-5.84E-01	2.16E-06		-6.99E-01	8.61E-08		-1.54E-01	3.77E-01		1.15E+00	1.26E-29	Up	Unigene33789_All//gi|30013681|gb|AAP03883.1|//1.00E-106//Avr9/Cf-9 rapidly elicited protein 284 [Nicotiana tabacum]	Unigene33789_All//8.00E-97//AT2G40180| ATHPP2C5; catalytic/ protein serine/threonine phosphatase	Unigene33789_All//0.00E+00//gi|78339431|gb|DT559705.1|DT559705				nr +
Unigene3379_All	1945	8.72	1.30	3.09	2.92	1.61	0.74	2.41	3.09	0.37	-2.74E+00	5.21E-51	Down	-1.49E+00	1.40E-22	Down	-8.58E-01	2.09E-04		-1.97E+00	7.59E-13	Down	3.59E-01	1.11E-01		-2.71E+00	4.13E-18	Down	Unigene3379_All//gi|297596562|ref|NP_001042775.2|//6.00E-40//Os01g0286100 [Oryza sativa (japonica Group)] >gi|255673123|dbj|BAF04689.2| Os01g0286100 [Oryza sativa (japonica Group)]	Unigene3379_All//2.00E-30//AT1G09530| PIF3 (PHYTOCHROME INTERACTING FACTOR 3); DNA binding / protein binding / transcription factor/ transcription regulator	Unigene3379_All//0.00E+00//TC172920	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0005515//GO:0009416//GO:0023033//GO:0031323//GO:0043231//GO:0051716	nr +
Unigene33793_All	2285	5.70	12.48	6.83	7.59	9.69	10.20	9.46	10.65	6.90	1.13E+00	1.53E-25	Up	2.60E-01	9.22E-02		3.53E-01	1.64E-03		4.27E-01	1.24E-04		1.71E-01	1.15E-01		-4.54E-01	9.86E-06		Unigene33793_All//gi|24459977|dbj|BAC22616.1|//0.00E+00//UDP-glucose:sterol 3-O-glucosyltransferase [Panax ginseng]	Unigene33793_All//0.00E+00//AT3G07020| UDP-glucose:sterol glucosyltransferase (UGT80A2)	Unigene33793_All//0.00E+00//TC168384			GO:0016020//GO:0030258//GO:0035251	nr +
Unigene33795_All	1611	8.57	18.62	15.07	15.80	18.58	16.09	13.02	11.91	10.98	1.12E+00	2.24E-26	Up	8.14E-01	1.80E-12		2.33E-01	1.93E-02		2.63E-02	8.49E-01		-1.29E-01	3.04E-01		-2.46E-01	2.27E-02		Unigene33795_All//gi|24459977|dbj|BAC22616.1|//0.00E+00//UDP-glucose:sterol 3-O-glucosyltransferase [Panax ginseng]	Unigene33795_All//0.00E+00//AT3G07020| UDP-glucose:sterol glucosyltransferase (UGT80A2)	Unigene33795_All//0.00E+00//TC168384			GO:0016020//GO:0030258//GO:0035251	nr +
Unigene3380_All	2467	7.95	5.05	3.19	4.18	2.97	2.11	0.34	0.47	0.32	-6.55E-01	1.49E-07		-1.32E+00	1.36E-21	Down	-4.92E-01	3.48E-03		-9.89E-01	1.88E-08		4.69E-01	4.16E-01		-8.58E-02	9.02E-01		Unigene3380_All//gi|224120186|ref|XP_002318267.1|//0.00E+00//leucine-rich repeat protein kinase [Populus trichocarpa] >gi|222858940|gb|EEE96487.1| leucine-rich repeat protein kinase [Populus trichocarpa]	Unigene3380_All//0.00E+00//AT5G07180| ERL2 (ERECTA-LIKE 2); kinase	Unigene3380_All//0.00E+00//CO131670			GO:0003006//GO:0004672//GO:0004871//GO:0006464//GO:0009886//GO:0016020//GO:0031410//GO:0032559//GO:0048229	nr +
Unigene33806_All	844	18.04	6.54	8.20	31.99	25.50	15.04	9.27	3.07	5.81	-1.46E+00	1.41E-20	Down	-1.14E+00	1.52E-13	Down	-3.27E-01	9.72E-04		-1.09E+00	1.14E-24	Down	-1.59E+00	6.11E-15	Down	-6.75E-01	1.76E-04		Unigene33806_All//gi|2232764|ref|NP_199593.2|//1.00E-116//FRA1 (FRAGILE FIBER 1); microtubule motor [Arabidopsis thaliana] >gi|30695302|ref|NP_851151.1| FRA1 (FRAGILE FIBER 1); microtubule motor [Arabidopsis thaliana] >gi|27260890|gb|AAN86114.1| kinesin-like protein [Arabidopsis thaliana] >gi|27260892|gb|AAN86115.1| kinesin-like protein [Arabidopsis thaliana]	Unigene33806_All//1.00E-110//AT5G47820| FRA1 (FRAGILE FIBER 1); microtubule motor	Unigene33806_All//0.00E+00//TC170749			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr -
Unigene33808_All	636	2.80	0.32	1.67	3.37	2.60	1.70	2.93	1.18	0.75	-3.13E+00	1.20E-06	Down	-7.40E-01	1.46E-01		-3.74E-01	4.16E-01		-9.83E-01	2.55E-02		-1.31E+00	2.76E-03		-1.96E+00	1.89E-05	Down		Unigene33808_All//0.00E+00//gi|109883771|gb|DW512741.1|DW512741				
Unigene33809_All	2162	9.49	2.74	4.56	12.35	11.56	6.50	4.30	0.91	2.60	-1.79E+00	1.59E-36	Down	-1.06E+00	4.06E-16	Down	-9.49E-02	4.50E-01		-9.27E-01	8.22E-19		-2.24E+00	1.86E-27	Down	-7.28E-01	9.15E-06		Unigene33809_All//gi|115477970|ref|NP_001062580.1|//1.00E-108//Os09g0114500 [Oryza sativa (japonica Group)] >gi|113630813|dbj|BAF24494.1| Os09g0114500 [Oryza sativa (japonica Group)]	Unigene33809_All//4.00E-80//AT5G47820| FRA1 (FRAGILE FIBER 1); microtubule motor	Unigene33809_All//0.00E+00//TC170749			GO:0003774//GO:0007017//GO:0015630//GO:0030198//GO:0032559	nr +
Unigene33811_All	659	4.68	2.54	2.42	7.86	5.80	3.15	4.04	2.03	2.42	-8.85E-01	1.26E-02		-9.50E-01	1.07E-02		-4.39E-01	9.23E-02		-1.32E+00	7.39E-07	Down	-9.94E-01	4.08E-03		-7.41E-01	2.52E-02		Unigene33811_All//gi|87241133|gb|ABD32991.1|//5.00E-66//Protein kinase [Medicago truncatula]	Unigene33811_All//2.00E-65//AT1G14370| APK2A (PROTEIN KINASE 2A); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene33811_All//4.00E-175//ES843997		ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0009536//GO:0016020//GO:0032559	nr +
Unigene33812_All	771	2.04	3.42	2.21	2.71	4.02	5.15	6.96	15.45	11.52	7.47E-01	5.48E-02		1.19E-01	8.07E-01		5.67E-01	1.15E-01		9.26E-01	2.47E-03		1.15E+00	7.35E-14	Up	7.26E-01	1.69E-05		Unigene33812_All//gi|87241133|gb|ABD32991.1|//4.00E-68//Protein kinase [Medicago truncatula]	Unigene33812_All//3.00E-62//AT2G02800| APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene33812_All//0.00E+00//TC168051			GO:0004713//GO:0006464//GO:0009536//GO:0016020//GO:0032559	nr -

Unigene33813_All	1729	2.06	2.49	1.57	3.03	1.85	1.46	3.84	1.89	1.80	2.76E-01	3.64E-01			-3.90E-01	2.65E-01		-7.08E-01	3.90E-03		-1.05E+00	5.13E-05	Down	-1.03E+00	7.26E-07	Down	-1.10E+00	8.16E-08	Down	Unigene33813_All//gi|15227042|ref|NP_178383.1|//1.00E-180//APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|42570659|ref|NP_973403.1|APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|75318425|sp|Q49840.1|APK2B_ARATH RecName: Full=Protein kinase 2B, chloroplastic; Flags: Precursor >gi|16226563|gb|AAL16201.1|AF428432_1 At2g02800/T20F6.6 [Arabidopsis thaliana] >gi|2852449|dbj|BAA24695.1|protein kinase [Arabidopsis thaliana] >gi|21928081|gb|AAM78069.1|At2g02800/T20F6.6 [Arabidopsis thaliana]	Unigene33813_All//9.00E-169//AT2G02800| APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene33813_All//0.00E+00//gi|164275658|gb|ES815989.1|ES815989			GO:0004713//GO:0006464//GO:0032559	nr +
Unigene33814_All	2091	13.36	26.49	9.52	13.67	16.45	16.74	16.94	38.96	31.21	9.87E-01	2.43E-39			-4.88E-01	3.72E-06		2.67E-01	2.82E-03		2.92E-01	1.32E-03		1.20E+00	1.31E-96	Up	8.81E-01	4.84E-48		Unigene33814_All//gi|87241133|gb|AB032991.1|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene33814_All//1.00E-173//AT2G02800| APK2B (PROTEIN KINASE 2B); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene33814_All//0.00E+00//gi|78343944|gb|DT564218.1|DT564218		ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0016020//GO:0032559//GO:0043231	nr -
Unigene33816_All	1160	2.44	5.50	4.50	5.41	4.19	5.72	2.70	5.76	5.63	1.18E+00	1.12E-06	Up	8.85E-01	1.18E-03		-3.70E-01	1.19E-01		8.10E-02	7.52E-01		1.10E+00	1.37E-07	Up	1.06E+00	2.55E-07	Up	Unigene33816_All//gi|30696301|ref|NP_849827.1|//5.00E-89//CW7 [Arabidopsis thaliana]	Unigene33816_All//2.00E-90//AT1G39520| CW7	Unigene33816_All//0.00E+00//TC176925			GO:0043231	nr -
Unigene33819_All	1792	1.69	4.95	2.35	5.48	2.69	4.16	2.74	4.73	5.09	1.55E+00	3.29E-13	Up	4.71E-01	1.39E-01		-1.03E+00	1.70E-09	Down	-3.97E-01	3.34E-02		7.91E-01	8.42E-06		8.95E-01	1.16E-07		Unigene33819_All//gi|30696301|ref|NP_849827.1|//4.00E-88//CW7 [Arabidopsis thaliana]	Unigene33819_All//2.00E-89//AT1G39520| CW7	Unigene33819_All//0.00E+00//TC167389			GO:0043231	nr -
Unigene33820_All	680	4.31	8.72	3.29	7.77	7.55	8.90	10.45	13.89	15.58	1.02E+00	4.00E-05	Up	-3.90E-01	3.27E-01		-4.14E-02	8.80E-01		1.97E-01	4.76E-01		4.11E-01	1.52E-02		5.77E-01	1.50E-04		Unigene33820_All//gi|147801049|emb|CAN77845.1|//7.00E-35//hypothetical protein [Vitis vinifera]	Unigene33820_All//2.00E-09//AT3G03140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: PWWP (InterPro:IPR000313); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G21295.1); Has 422 Blast hits to 270 proteins in 77 species: Archae - 0; Bacteria - 12; Metazoa - 232; Fungi - 62; Plants - 66; Viruses - 0; Other Eukaryotes - 50 (source: NCBI BLink).	Unigene33820_All//0.00E+00//ES823680				nr +
Unigene33821_All	4394	12.41	5.44	6.81	13.54	8.72	8.78	12.79	11.53	11.54	-1.19E+00	2.35E-52	Down	-8.65E-01	3.70E-30		-6.34E-01	3.02E-24		-6.25E-01	4.66E-21		-1.50E-01	2.57E-02		-1.48E-01	2.22E-02		Unigene33821_All//gi|115448113|ref|NP_001047836.1|//1.00E-105//Os02g07000000 [Oryza sativa Japonica Group] >gi|113537367|dbj|BAF09750.1|Os02g0700000 [Oryza sativa Japonica Group]	Unigene33821_All//2.00E-116//AT3G03140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: PWWP (InterPro:IPR000313); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G21295.1); Has 422 Blast hits to 270 proteins in 77 species: Archae - 0; Bacteria - 12; Metazoa - 232; Fungi - 62; Plants - 66; Viruses - 0; Other Eukaryotes - 50 (source: NCBI BLink).	Unigene33821_All//0.00E+00//TC145184		ko00230|Purine metabolism	GO:0016763//GO:0043096//GO:0044444	nr +
Unigene33822_All	1071	6.50	3.03	10.54	3.58	2.28	3.37	6.32	4.14	4.84	-1.10E+00	1.33E-06	Down	6.98E-01	6.67E-05		-6.50E-01	2.98E-02		-8.63E-02	7.92E-01		-6.11E-01	2.38E-03		-3.85E-01	5.27E-02		Unigene33822_All//gi|13346180|gb|AK19612.1|AF336279_1/2.00E-93//GHDEL61 [Gossypium hirsutum]	Unigene33822_All//5.00E-67//AT1G63650| EGL3 (ENHANCER OF GLABRA 3); DNA binding / transcription factor	Unigene33822_All//0.00E+00//TC132616	bHLH	ko04626|Plant-pathogen interaction	GO:0010468//GO:0043231	nr +
Unigene33823_All	1983	18.42	10.89	19.87	6.18	5.52	2.92	14.37	17.43	10.37	-7.59E-01	4.39E-17		1.10E-01	2.72E-01		-1.62E-01	3.81E-01		-1.08E+00	1.99E-11	Down	2.79E-01	7.66E-04		-4.71E-01	9.86E-08		Unigene33823_All//gi|13346182|gb|AK19613.1|AF336280_1/0.00E+00//GHDEL65 [Gossypium hirsutum]	Unigene33823_All//1.00E-128//AT5G41315| GL3 (GLABROUS 3); protein binding / transcription factor	Unigene33823_All//0.00E+00//TC131705	bHLH	ko04626|Plant-pathogen interaction	GO:0010468//GO:0043231	nr +
Unigene33824_All	2771	3.53	1.74	2.96	1.20	0.68	0.68	2.29	2.76	1.44	-1.02E+00	4.94E-08	Down	-2.55E-01	2.14E-01		-8.17E-01	1.04E-02		-8.15E-01	1.56E-02		2.70E-01	1.81E-01		-6.71E-01	9.06E-04		Unigene33824_All//gi|13346182|gb|AK19613.1|AF336280_1/0.00E+00//GHDEL65 [Gossypium hirsutum]	Unigene33824_All//1.00E-166//AT5G41315| GL3 (GLABROUS 3); protein binding / transcription factor	Unigene33824_All//0.00E+00//TC131705	bHLH	ko04626|Plant-pathogen interaction	GO:0010468//GO:0043231	nr +
Unigene33825_All	2335	4.01	3.02	3.90	15.94	8.73	14.26	21.89	5.71	13.60	-4.11E-01	3.06E-02		-4.06E-02	8.46E-01		-8.68E-01	2.56E-26		-1.61E-01	9.44E-02		-1.94E+00	1.37E-122	Down	-6.87E-01	4.70E-25		Unigene33825_All//gi|13346180|gb|AK19612.1|AF336279_1/0.00E+00//GHDEL61 [Gossypium hirsutum]	Unigene33825_All//5.00E-143//AT5G41315| GL3 (GLABROUS 3); protein binding / transcription factor	Unigene33825_All//0.00E+00//TC132616	bHLH	ko04626|Plant-pathogen interaction	GO:0010468//GO:0043231	nr +
Unigene33826_All	884	2.13	11.86	2.95	47.90	48.54	75.15	49.07	90.59	39.70	2.48E+00	3.54E-28	Up	4.70E-01	2.53E-01		1.91E-02	8.53E-01		6.50E-01	6.43E-25		8.84E-01	8.66E-58		-3.06E-01	1.55E-05		Unigene33826_All//gi|289166842|gb|ADC83471.1|//9.00E-49//caffeic acid O-methyltransferase [Salix miyabeana]	Unigene33826_All//2.00E-47//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene33826_All//8.00E-168//TC143440		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005515//GO:0008171//GO:0009699	nr +
Unigene33827_All	2718	10.97	33.89	16.65	148.05	160.25	289.28	70.92	118.25	87.64	1.63E+00	1.13E-140	Up	6.02E-01	1.26E-13		1.14E-01	3.84E-07		9.66E-01	0.00E+00		7.38E-01	2.38E-168		3.05E-01	3.34E-26		Unigene33827_All//gi|297808467|ref|XP_002872117.1|//1.00E-147//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297317954|gb|EFH48376.1|oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene33827_All//1.00E-143//AT5G24530| DMR6 (DOWNY MILDEW RESISTANT 6); oxidoreductase/ oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene33827_All//0.00E+00//TC177955		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene33828_All	1234	7.12	2.30	4.92	9.28	10.86	11.57	6.99	1.90	2.45	-1.63E+00	3.62E-14	Down	-5.34E-01	8.60E-03		2.26E-01	1.73E-01		3.17E-01	3.97E-02		-1.88E+00	1.76E-20	Down	-1.51E+00	1.02E-15	Down	Unigene33828_All//gi|42567736|ref|NP_196400.2|//1.00E-134//AtGUS2 (Arabidopsis thaliana glucuronidase 2); beta-glucuronidase >gi|75170142|sp|Q9FF10.1|HPSE1_ARATH RecName: Full=Heparanase-like protein 1; Flags: Precursor >gi|51536460|gb|AAU05468.1|At5g07830 [Arabidopsis thaliana] >gi|53793651|gb|AAU93572.1|At5g07830 [Arabidopsis thaliana]	Unigene33828_All//3.00E-135//AT5G07830| AtGUS2 (Arabidopsis thaliana glucuronidase 2); beta-glucuronidase	Unigene33828_All//0.00E+00//gi|164240662|gb|EX164821.1|EX164821				nr +
Unigene33829_All	1410	1.34	2.44	2.11	4.49	6.52	5.99	2.64	1.66	0.62	8.71E-01	9.04E-03		6.63E-01	8.02E-02		5.39E-01	3.13E-03		4.17E-01	4.12E-02		-6.69E-01	1.86E-02		-2.09E+00	7.28E-11	Down	Unigene33829_All//gi|42567736|ref|NP_196400.2|//1.00E-175//AtGUS2 (Arabidopsis thaliana glucuronidase 2); beta-glucuronidase >gi|75170142|sp|Q9FF10.1|HPSE1_ARATH RecName: Full=Heparanase-like protein 1; Flags: Precursor >gi|51536460|gb|AAU05468.1|At5g07830 [Arabidopsis thaliana] >gi|53793651|gb|AAU93572.1|At5g07830 [Arabidopsis thaliana]	Unigene33829_All//1.00E-176//AT5G07830| AtGUS2 (Arabidopsis thaliana glucuronidase 2); beta-glucuronidase	Unigene33829_All//0.00E+00//ES832462			GO:0016787//GO:0044464	nr -
Unigene33830_All	1962	23.92	9.22	15.88	32.55	32.21	23.99	11.94	4.43	6.86	-1.38E+00	1.58E-56	Down	-5.91E-01	1.15E-13		-1.53E-02	8.51E-01		-4.40E-01	3.18E-12		-1.43E+00	6.48E-37	Down	-7.99E-01	2.68E-15		Unigene33830_All//gi|42567736|ref|NP_196400.2|//0.00E+00//AtGUS2 (Arabidopsis thaliana glucuronidase 2); beta-glucuronidase >gi|75170142|sp|Q9FF10.1|HPSE1_ARATH RecName: Full=Heparanase-like protein 1; Flags: Precursor >gi|51536460|gb|AAU05468.1|At5g07830 [Arabidopsis thaliana] >gi|53793651|gb|AAU93572.1|At5g07830 [Arabidopsis thaliana]	Unigene33830_All//0.00E+00//AT5G07830| AtGUS2 (Arabidopsis thaliana glucuronidase 2); beta-glucuronidase	Unigene33830_All//0.00E+00//TC144052			GO:0005618//GO:0016787//GO:0031410	nr +
Unigene33832_All	697	4.73	9.60	9.32	2.79	4.10	1.68	0.73	0.42	0.46	1.02E+00	1.05E-05	Up	9.79E-01	5.30E-05		5.57E-01	1.45E-01		-7.26E-01	1.27E-01		-7.94E-01	4.02E-01		-6.71E-01	4.48E-01		Unigene33832_All//gi|50313464|gb|AT74602.1|//9.00E-85//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene33832_All//8.00E-70//AT3G23530| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene33832_All//0.00E+00//gi|109890498|gb|DW519462.1|DW519462			GO:0006629//GO:0008757//GO:0044464	nr +
Unigene33833_All	969	2.75	5.33	4.84	0.98	2.56	1.07	0.61	0.17	1.23	9.54E-01	3.34E-04		8.12E-01	5.08E-03		1.39E+00	5.73E-04	Up	1.34E-01	8.58E-01		-1.82E+00	4.71E-02		1.01E+00	5.98E-02		Unigene33833_All//gi|50313464|gb|AT74602.1|//1.00E-106//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene33833_All//5.00E-85//AT3G23530| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene33833_All//0.00E+00//TC129558			GO:0006629//GO:0008757//GO:0044464	nr +
Unigene33836_All	1594	5.32	2.92	5.78	8.09	8.40	7.96	8.70	3.99	4.02	-8.63E-01	1.60E-05		1.20E-01	5.97E-01		5.42E-02	8.04E-01		-2.38E-02	9.12E-01		-1.13E+00	1.54E-15	Down	-1.11E+00	9.76E-16	Down	Unigene33836_All//gi|269980527|gb|ACZ56438.1|//1.00E-165//IAA-amino acid hydrolase [Populus tomentosa]	Unigene33836_All//1.00E-146//AT5G56660| ILL2; IAA-Ala conjugate hydrolase/ IAA-amino acid conjugate hydrolase/ metallopeptidase	Unigene33836_All//0.00E+00//TC143221				nr -
Unigene33837_All	1905	11.48	7.71	8.47	18.25	18.76	12.83	26.46	13.78	10.60	-5.74E-01	9.40E-07		-4.39E-01	3.12E-04		3.98E-02	7.53E-01		-5.09E-01	7.21E-09		-9.41E-01	1.12E-40		-1.32E+00	1.50E-71	Down	Unigene33837_All//gi|224070738|ref|XP_002303219.1|//1.00E-171//iaa-amino acid hydrolase 11 [Populus trichocarpa] >gi|222840651|gb|EEE78198.1| iaa-amino acid hydrolase 11 [Populus trichocarpa]	Unigene33837_All//3.00E-164//AT1G51760| IAR3 (IAA-ALANINE RESISTANT 3); IAA-Ala conjugate hydrolase/ metallopeptidase	Unigene33837_All//0.00E+00//TC143221				nr +
Unigene33844_All	846	10.58	3.47	8.06	14.25	6.72	9.98	12.14	17.00	4.90	-1.61E+00	4.16E-14	Down	-3.93E-01	5.63E-02		-1.09E+00	1.23E-12	Down	-5.13E-01	1.38E-03		4.85E-01	2.34E-04		-1.31E+00	3.89E-15	Down	Unigene33844_All//gi|15226687|ref|NP_181578.1|//4.00E-89//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|20453068|gb|AAM19779.1|At2g40460/T2P4.19 [Arabidopsis thaliana] >gi|25090213|gb|AAN72253.1|At2g40460/T2P4.19 [Arabidopsis thaliana]	Unigene33844_All//2.00E-75//AT2G40460| proton-dependent oligopeptide transport (POT) family protein	Unigene33844_All//0.00E+00//CO080983			GO:0015833//GO:0031410//GO:0051707	nr +

Unigene33846_All	1991	14.27	9.98	20.11	3.70	5.48	10.05	12.13	3.55	3.60	-5.16E-01	3.43E-07		4.95E-01	1.01E-08		5.66E-01	5.43E-04		1.44E+00	8.11E-28	Up	-1.77E+00	1.18E-51	Down	-1.75E+00	2.44E-52	Down	Unigene33846_All//gi|15226687|ref|NP_181578.1|//0.00E+00//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|20453068|gb|AAM19779.1| At2g40460/T2P4.19 [Arabidopsis thaliana] >gi|25090213|gb|AAN72253.1| At2g40460/T2P4.19 [Arabidopsis thaliana]	Unigene33846_All//0.00E+00//AT2G40460| proton-dependent oligopeptide transport (POT) family protein	Unigene33846_All//0.00E+00//ES839651			GO:0015833//GO:0044464//GO:0051707	nr +
Unigene33847_All	515	26.41	14.17	17.68	43.43	39.52	36.04	74.46	47.31	35.35	-8.99E-01	6.66E-09		-5.79E-01	2.44E-04		-1.36E-01	3.09E-01		-2.69E-01	2.46E-02		-6.54E-01	5.18E-17		-1.07E+00	1.06E-39	Down	Unigene33847_All|gi|75319500|sp|Q39828.1|SDL5A_SOYBN//7.00E-81//RecName: Full=Dynamin-related protein 5A; AltName: Full=Soybean dynamin-like protein 5A; Short=SDL5A >gi|1218004|gb|AAC49183.1| SDL5A [Glycine max]	Unigene33847_All//5.00E-78//AT5G42080| ADL1 (ARABIDOPSIS DYNAMIN-LIKE PROTEIN); GTP binding / GTPase/ protein binding	Unigene33847_All//0.00E+00//gi|164302614|gb|ES815547.1|ES815547			GO:0000904//GO:0000919//GO:0003002//GO:0003006//GO:0006897//GO:0009534//GO:0015630//GO:0016020//GO:0017111//GO:0019901//GO:0032561	nr -
Unigene33849_All	1789	3.42	8.44	2.89	7.71	5.77	8.38	18.43	23.36	20.22	1.30E+00	3.80E-17	Up	-2.45E-01	3.67E-01		-4.18E-01	3.70E-03		1.20E-01	4.92E-01		3.42E-01	3.40E-06		1.33E-01	1.15E-01		Unigene33849_All|gi|75319500|sp|Q39828.1|SDL5A_SOYBN//0.00E+00//RecName: Full=Dynamin-related protein 5A; AltName: Full=Soybean dynamin-like protein 5A; Short=SDL5A >gi|1218004|gb|AAC49183.1| SDL5A [Glycine max]	Unigene33849_All//0.00E+00//AT5G42080| ADL1 (ARABIDOPSIS DYNAMIN-LIKE PROTEIN); GTP binding / GTPase/ protein binding	Unigene33849_All//0.00E+00//TC134519		ko04144|Endocytosis	GO:0000904//GO:0000919//GO:0003002//GO:0003006//GO:0006897//GO:0009534//GO:0015630//GO:0016020//GO:0017111//GO:0019901//GO:0032561	nr +
Unigene33853_All	2629	22.77	30.95	20.28	25.96	26.08	34.56	27.84	60.30	121.24	4.43E-01	1.39E-14		-1.67E-01	2.48E-02		6.60E-03	9.49E-01		4.13E-01	3.34E-15		1.12E+00	1.76E-166	Up	2.12E+00	0.00E+00	Up	Unigene33853_All|gi|113129056|gb|ABI30334.1|//0.00E+00//Cys-3-His zinc finger protein [Capsicum annuum]	Unigene33853_All//1.00E-171//AT5G58620| zinc finger (CCCH-type) family protein	Unigene33853_All//0.00E+00//TC171216	C3H		GO:0010468//GO:0046914	nr -
Unigene33857_All	4254	5.20	2.80	4.31	8.03	10.30	7.20	6.72	3.18	3.65	-8.94E-01	7.09E-14		-2.73E-01	2.98E-02		3.59E-01	1.57E-06		-1.58E-01	1.20E-01		-1.08E+00	4.45E-29	Down	-8.79E-01	1.30E-21		Unigene33857_All|gi|270269270|gb|ACZ66259.1|//0.00E+00//glucan/water dikinase [Solanum tuberosum]	Unigene33857_All//0.00E+00//AT5G26570| ATGWD3; carbohydrate kinase/ catalytic/ phosphoglucan, water dikinase	Unigene33857_All//0.00E+00//TC136131		ko00500|Starch and sucrose metabolism//ko00620|Pyruvate metabolism	GO:0005982//GO:0006468//GO:0009532//GO:0016301//GO:0032559	nr +
Unigene3386_All	1177	17.83	9.69	12.98	33.94	27.06	27.05	25.47	7.53	7.65	-8.80E-01	7.34E-13		-4.57E-01	2.36E-04		-3.27E-01	3.32E-05		-3.27E-01	7.83E-05		-1.76E+00	3.12E-63	Down	-1.74E+00	5.83E-64	Down	Unigene3386_All//gi|224086851|ref|XP_002307984.1|//1.00E-112//tubulin folding cofactor [Populus trichocarpa] >gi|222853960|gb|EEE91507.1| tubulin folding cofactor [Populus trichocarpa]	Unigene3386_All//4.00E-109//AT3G10220| tubulin folding cofactor B	Unigene3386_All//0.00E+00//TC160566			GO:0043231	nr -
Unigene33861_All	716	9.35	11.39	8.78	21.50	19.91	23.09	28.11	80.38	51.30	2.85E-01	1.82E-01		-9.20E-02	7.05E-01		-1.11E-01	5.30E-01		1.03E-01	5.50E-01		1.52E+00	1.71E-97	Up	8.68E-01	9.03E-27		Unigene33861_All|gi|15242532|ref|NP_198815.1|//4.00E-74//glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein [Arabidopsis thaliana] >gi|10176091|dbj|BAB10223.1| glycosylation enzyme-like protein [Arabidopsis thaliana] >gi|30102766|gb|AAP21301.1| At5g39990 [Arabidopsis thaliana]	Unigene33861_All//2.00E-75//AT5G39990| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	Unigene33861_All//0.00E+00//gi|18099791|gb|BM359045.1|BM359045			GO:0005975//GO:0035252//GO:0044464	nr +
Unigene33862_All	1847	3.68	3.13	3.40	6.99	6.79	6.46	11.35	24.82	23.36	-2.36E-01	3.32E-01		-1.14E-01	6.28E-01		-4.17E-02	8.22E-01		-1.14E-01	5.58E-01		1.13E+00	1.33E-49	Up	1.04E+00	5.03E-42	Up	Unigene33862_All|gi|297805704|ref|XP_002870736.1|//0.00E+00//glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata] >gi|297316572|gb|EFH46995.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata]	Unigene33862_All//0.00E+00//AT5G15650| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	Unigene33862_All//0.00E+00//gi|78334221|gb|DT554495.1|DT554495			GO:0005975//GO:0035252//GO:0044464	nr -
Unigene33865_All	1143	2.11	1.77	4.57	2.66	2.50	1.78	1.18	0.55	1.29	-2.48E-01	5.63E-01		1.12E+00	5.58E-05	Up	-8.84E-02	8.11E-01		-5.80E-01	1.15E-01		-1.11E+00	3.31E-02		1.24E-01	7.94E-01		Unigene33865_All|gi|7327818|emb|CAB82275.1|//1.00E-120//hypothetical protein [Arabidopsis thaliana]	Unigene33865_All//2.00E-112//AT5G01590| unknown protein	Unigene33865_All//0.00E+00//TC178837				nr -
Unigene33866_All	1498	5.76	2.13	4.05	7.95	7.68	5.43	1.30	0.73	0.64	-1.44E+00	1.13E-11	Down	-5.08E-01	1.36E-02		-4.98E-02	8.21E-01		-5.50E-01	6.29E-04		-8.40E-01	4.31E-02		-1.02E+00	1.07E-02		Unigene33866_All|gi|225439462|ref|XP_002268305.1|//0.00E+00//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297735626|emb|CBI18120.3| unnamed protein product [Vitis vinifera]	Unigene33866_All//0.00E+00//AT5G01590| unknown protein	Unigene33866_All//0.00E+00//TC178837			GO:0009526	nr -
Unigene33867_All	2164	16.13	7.49	7.95	12.50	11.39	11.48	6.08	2.47	3.31	-1.11E+00	3.86E-30	Down	-1.02E+00	1.60E-25	Down	-1.34E-01	2.59E-01		-1.23E-01	3.21E-01		-1.30E+00	2.85E-18	Down	-8.75E-01	2.41E-10		Unigene33867_All|gi|225439462|ref|XP_002268305.1|//0.00E+00//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297735626|emb|CBI18120.3| unnamed protein product [Vitis vinifera]	Unigene33867_All//0.00E+00//AT5G01590| unknown protein	Unigene33867_All//0.00E+00//TC154801			GO:0009526	nr -
Unigene33876_All	1547	5.68	14.61	7.78	10.37	11.04	10.77	11.10	9.54	8.68	1.36E+00	4.85E-27	Up	4.53E-01	8.01E-03		9.06E-02	5.82E-01		5.51E-02	7.30E-01		-2.18E-01	8.85E-02		-3.55E-01	2.52E-03		Unigene33876_All|gi|75338884|sp|Q9ZR40.1|U2A2B_NICPL//0.00E+00//RecName: Full=Splicing factor U2af large subunit B; AltName: Full=U2 small nuclear ribonucleoprotein auxiliary factor large subunit B; Short=U2 snRNP auxiliary factor large subunit B; AltName: Full=U2 auxiliary factor 65 kDa subunit B; AltName: Full=NpU2AF65b >gi|3850821|emb|CAA77135.1| U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]	Unigene33876_All//3.00E-174//AT1G60900| U2 snRNP auxiliary factor large subunit, putative	Unigene33876_All//0.00E+00//gi|78343603|gb|DT563877.1|DT563877		ko03040|Spliceosome	GO:0003676//GO:0006396//GO:0043231	nr -
Unigene33877_All	705	0.45	1.44	2.19	0.99	1.81	1.86	1.32	0.42	0.96	1.69E+00	2.14E-02		2.30E+00	3.37E-04	Up	8.69E-01	1.60E-01		9.09E-01	1.35E-01		-1.67E+00	1.45E-02		-4.58E-01	4.67E-01		Unigene33877_All|gi|222423510|dbj|BAH19725.1|//2.00E-73//AT4G36690 [Arabidopsis thaliana]	Unigene33877_All//1.00E-74//AT4G36690| ATU2AF65A; RNA binding / nucleic acid binding / nucleotide binding	Unigene33877_All//0.00E+00//gi|78353706|gb|DT573980.1|DT573980		ko03040|Spliceosome	GO:0000377//GO:0003676//GO:0006952//GO:0043231	nr -
Unigene33879_All	2209	0.38	1.19	1.59	0.99	1.01	0.67	1.82	1.19	0.83	1.65E+00	7.80E-05	Up	2.07E+00	9.34E-08	Up	3.04E-02	9.58E-01		-5.56E-01	2.19E-01		-6.09E-01	2.53E-02		-1.13E+00	2.63E-05	Down	Unigene33879_All|gi|75338884|sp|Q9ZR40.1|U2A2B_NICPL//0.00E+00//RecName: Full=Splicing factor U2af large subunit B; AltName: Full=U2 small nuclear ribonucleoprotein auxiliary factor large subunit B; Short=U2 snRNP auxiliary factor large subunit B; AltName: Full=U2 auxiliary factor 65 kDa subunit B; AltName: Full=NpU2AF65b >gi|3850821|emb|CAA77135.1| U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]	Unigene33879_All//2.00E-173//AT1G60900| U2 snRNP auxiliary factor large subunit, putative	Unigene33879_All//0.00E+00//gi|78343603|gb|DT563877.1|DT563877		ko03040|Spliceosome	GO:0000377//GO:0003676//GO:0006952//GO:0043231	nr +
Unigene3388_All	1142	18.97	5.95	8.44	42.62	37.90	52.16	58.90	21.34	19.71	-1.67E+00	4.12E-35	Down	-1.17E+00	7.88E-20	Down	-1.69E-01	2.96E-02		2.92E-01	1.26E-05		-1.47E+00	1.91E-108	Down	-1.58E+00	1.22E-124	Down	Unigene3388_All|gi|15239505|ref|NP_200911.1|//4.00E-70//GR-RBP3 (glycine-rich RNA-binding protein 3); ATP binding / RNA binding [Arabidopsis thaliana] >gi|16974556|gb|AAL31194.1| AT5g61030/maf19_30 [Arabidopsis thaliana] >gi|21928059|gb|AAM78058.1| AT5g61030/maf19_30 [Arabidopsis thaliana]	Unigene3388_All//4.00E-42//AT5G61030| GR-RBP3 (glycine-rich RNA-binding protein 3); ATP binding / RNA binding	Unigene3388_All//0.00E+00//DR458895		ko03040|Spliceosome	GO:0032559//GO:0043231//GO:0046914	nr -
Unigene33882_All	1766	3.26	6.89	6.72	6.32	7.37	11.61	9.84	14.89	14.51	1.08E+00	1.46E-10	Up	1.05E+00	1.94E-09	Up	2.22E-01	1.91E-01		8.78E-01	3.24E-13		5.97E-01	2.97E-10		5.60E-01	2.86E-09		Unigene33882_All|gi|224053527|ref|XP_002297857.1|//0.00E+00//serine/threonine protein kinase PBS1 [Populus trichocarpa] >gi|222845115|gb|EEE82662.1| serine/threonine protein kinase PBS1 [Populus trichocarpa]	Unigene33882_All//0.00E+00//AT5G13160| PBS1 (avrPphB susceptible 1); kinase/ protein serine/threonine kinase	Unigene33882_All//0.00E+00//TC159611		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006468//GO:0032559//GO:0042742	nr -
Unigene33883_All	1216	4.13	9.88	6.61	8.60	8.01	9.92	16.55	27.46	17.30	1.26E+00	4.26E-13	Up	6.79E-01	1.39E-03		-1.02E-01	6.13E-01		2.05E-01	2.68E-01		7.31E-01	6.31E-18		6.38E-02	6.06E-01		Unigene33883_All|gi|224053527|ref|XP_002297857.1|//1.00E-129//serine/threonine protein kinase PBS1 [Populus trichocarpa] >gi|222845115|gb|EEE82662.1| serine/threonine protein kinase PBS1 [Populus trichocarpa]	Unigene33883_All//1.00E-112//AT5G13160| PBS1 (avrPphB susceptible 1); kinase/ protein serine/threonine kinase	Unigene33883_All//0.00E+00//ES805533		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene33884_All	1917	0.71	2.33	2.50	1.77	2.78	2.62	5.18	5.45	6.75	1.71E+00	5.49E-08	Up	1.82E+00	8.08E-09	Up	6.56E-01	8.98E-03		5.66E-01	3.79E-02		7.27E-02	6.91E-01		3.82E-01	5.44E-03		Unigene33884_All|gi|224053527|ref|XP_002297857.1|//0.00E+00//serine/threonine protein kinase PBS1 [Populus trichocarpa] >gi|222845115|gb|EEE82662.1| serine/threonine protein kinase PBS1 [Populus trichocarpa]	Unigene33884_All//0.00E+00//AT5G13160| PBS1 (avrPphB susceptible 1); kinase/ protein serine/threonine kinase	Unigene33884_All//0.00E+00//TC159611		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006468//GO:0032559//GO:0042742	nr -
Unigene33885_All	508	1.44	9.28	1.05	5.49	9.83	8.00	8.91	77.50	50.74	2.69E+00	3.65E-14	Up	-4.60E-01	6.02E-01		8.40E-01	1.13E-03		5.43E-01	8.03E-02		3.12E+00	9.59E-164	Up	2.51E+00	6.72E-87	Up	Unigene33885_All|gi|108711675|gb|ABF99470.1|//4.00E-16//Raffinose synthase or seed imbibition protein Sip1 containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene33885_All//7.00E-16//AT5G20250| DIN10 (DARK INDUCIBLE 10); hydrolase, hydrolyzing O-glycosyl compounds	Unigene33885_All//0.00E+00//TC145745		ko00052|Galactose metabolism	GO:0005488//GO:0008378	nr +
Unigene33886_All	1594	6.89	31.31	4.24	13.31	37.81	36.21	25.68	139.55	134.29	2.18E+00	1.88E-113	Up	-7.00E-01	8.39E-05		1.51E+00	2.83E-97	Up	1.44E+00	1.09E-79	Up	2.44E+00	0.00E+00	Up	2.39E+00	0.00E+00	Up	Unigene33886_All|gi|90265053|emb|CAH67678.1|//1.00E-180//B0610A06.3 [Oryza sativa (indica cultivar-group)] >gi|116309847|emb|CAH66883.1| OSIGBa0158F13.14 [Oryza sativa (indica cultivar-group)]	Unigene33886_All//3.00E-158//AT3G57520| AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase, hydrolyzing O-glycosyl compounds	Unigene33886_All//0.00E+00//TC174764		ko00052|Galactose metabolism	GO:0005488	nr -
Unigene33887_All	2048	3.47	14.72	2.47	7.15	22.38	24.72	8.94	47.27	58.26	2.08E+00	8.70E-65	Up	-4.92E-01	3.35E-02		1.65E+00	4.95E-84	Up	1.79E+00	3.98E-95	Up	2.40E+00	5.83E-303	Up	2.70E+00	0.00E+00	Up	Unigene33887_All|gi|38345247|emb|CAD41091.2|//1.00E-177//OSJNBb0011N17.8 [Oryza sativa (japonica cultivar-group)]	Unigene33887_All//2.00E-155//AT3G57520| AtSIP2 (Arabidopsis thaliana seed imbibition 2); hydrolase, hydrolyzing O-glycosyl compounds	Unigene33887_All//0.00E+00//TC174764		ko00052|Galactose metabolism	GO:0005488	nr +

Unigene33888_All	3267	30.73	12.83	19.62	38.62	38.94	56.80	32.56	18.87	25.03	-1.26E+00	3.97E-105	Down	-6.47E-01	1.87E-33		1.17E-02	8.40E-01		5.57E-01	3.55E-52		-7.87E-01	7.05E-63		-3.79E-01	6.22E-18		Unigene33888_All//gi|42563316|ref|NP_177948.3|//0.00E+00//TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase [Arabidopsis thaliana] >gi|238479105|ref|NP_001154475.1|TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase [Arabidopsis thaliana] >gi|292630946|sp|Q9C9Q8.2|PMTT_ARATH RecName: Full=Probable pectin methyltransferase QUA2; AltName: Full=Protein QUASIMODO 2; AltName: Full=Protein OVERSENSITIVE TO SUGAR 1; AltName: Full=Protein TUMOROUS SHOOT DEVELOPMENT 2	Unigene33888_All//0.00E+00//AT1G78240| TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase	Unigene33888_All//0.00E+00//TC170284			GO:0016741//GO:0043231//GO:0045489//GO:0048513	nr +
Unigene3389_All	1041	0.90	0.10	0.51	4.31	2.88	2.39	7.47	0.96	2.41	-3.22E+00	6.76E-04	Down	-8.23E-01	2.71E-01		-5.82E-01	3.42E-02		-8.52E-01	2.51E-03		-2.96E+00	3.24E-31	Down	-1.63E+00	7.28E-16	Down	Unigene3389_All//gi|42567433|ref|NP_195313.2|//2.00E-70//aspartyl protease family protein [Arabidopsis thaliana] >gi|190576481|gb|ACE79041.1|At4g35880 [Arabidopsis thaliana] >gi|222423134|dbj|BAH19546.1|AT4G35880 [Arabidopsis thaliana]	Unigene3389_All//9.00E-67//AT4G35880| aspartyl protease family protein	Unigene3389_All//0.00E+00//TC148831			GO:0004175//GO:0019538//GO:0031224//GO:0031410	nr +
Unigene33890_All	714	9.01	2.06	3.73	12.42	9.26	18.15	31.15	11.01	12.83	-2.13E+00	7.60E-15	Down	-1.27E+00	3.69E-07	Down	-4.23E-01	2.44E-02		5.48E-01	3.77E-04		-1.50E+00	1.15E-37	Down	-1.28E+00	1.30E-30	Down	Unigene33890_All//gi|18416588|ref|NP_567724.1|//1.00E-108//FIB2 (FIBRILLARIN 2); snoRNA binding [Arabidopsis thaliana] >gi|67461067|sp|Q94A89.2|FBRL2_ARATH RecName: Full=rRNA 2'-O-methyltransferase fibrillarin 2; AltName: Full=Fibrillarin-like protein 2 >gi|9965655|gb|AAG10104.1|AF233444_1 fibrillarin 2 [Arabidopsis thaliana] >gi|4914455|emb|CAB43694.1|fibrillarin-like protein [Arabidopsis thaliana] >gi|7269413|emb|CAB81373.1|fibrillarin-like protein [Arabidopsis thaliana] >gi|9965796|gb|AAG10153.1|fibrillarin 2 [Arabidopsis thaliana] >gi|21536840|gb|AAM61172.1|fibrillarin 2 (AtFib2) [Arabidopsis thaliana] >gi|23297150|gb|AAN13105.1|fibrillarin 2 (AtFib2) [Arabidopsis thaliana]	Unigene33890_All//8.00E-110//AT4G25630| FIB2 (FIBRILLARIN 2); snoRNA binding	Unigene33890_All//0.00E+00//TC150919				nr +
Unigene33891_All	1236	6.94	2.71	4.05	19.18	16.24	22.69	21.04	9.30	9.73	-1.36E+00	9.40E-11	Down	-7.78E-01	1.51E-04		-2.40E-01	3.36E-02		2.42E-01	2.30E-02		-1.18E+00	1.77E-30	Down	-1.11E+00	1.06E-28	Down	Unigene33891_All//gi|30696189|ref|NP_568772.3|//1.00E-147//FIB1 (FIBRILLARIN 1); snoRNA binding [Arabidopsis thaliana] >gi|67461076|sp|Q9FEF8.1|FBRL1_ARATH RecName: Full=rRNA 2'-O-methyltransferase fibrillarin 1; AltName: Full=SKP1-interacting partner 7 >gi|9965653|gb|AAG10103.1|AF233443_1 fibrillarin 1 [Arabidopsis thaliana] >gi|9965751|gb|AAG10152.1|fibrillarin 1 [Arabidopsis thaliana] >gi|10177413|dbj|BAB10544.1|fibrillarin-like [Arabidopsis thaliana] >gi|22654993|gb|AAM98088.1|AT5g52470/K24M7_22 [Arabidopsis thaliana] >gi|28416513|gb|AAO42787.1|AT5g52470/K24M7_22 [Arabidopsis thaliana] >gi|110740295|dbj|BAF02044.1|fibrillarin homolog [Arabidopsis thaliana]	Unigene33891_All//2.00E-125//AT4G25630| FIB2 (FIBRILLARIN 2); snoRNA binding	Unigene33891_All//0.00E+00//TC150919				nr +
Unigene33892_All	1247	15.94	2.76	6.06	27.56	20.13	34.95	34.72	14.61	19.14	-2.53E+00	1.28E-54	Down	-1.39E+00	7.38E-24	Down	-4.53E-01	6.21E-08		3.43E-01	1.40E-05		-1.25E+00	5.46E-55	Down	-8.59E-01	4.58E-31		Unigene33892_All//gi|18416588|ref|NP_567724.1|//1.00E-149//FIB2 (FIBRILLARIN 2); snoRNA binding [Arabidopsis thaliana] >gi|67461067|sp|Q94A89.2|FBRL2_ARATH RecName: Full=rRNA 2'-O-methyltransferase fibrillarin 2; AltName: Full=Fibrillarin-like protein 2 >gi|9965655|gb|AAG10104.1|AF233444_1 fibrillarin 2 [Arabidopsis thaliana] >gi|4914455|emb|CAB43694.1|fibrillarin-like protein [Arabidopsis thaliana] >gi|7269413|emb|CAB81373.1|fibrillarin-like protein [Arabidopsis thaliana] >gi|9965796|gb|AAG10153.1|fibrillarin 2 [Arabidopsis thaliana] >gi|21536840|gb|AAM61172.1|fibrillarin 2 (AtFib2) [Arabidopsis thaliana] >gi|23297150|gb|AAN13105.1|fibrillarin 2 (AtFib2) [Arabidopsis thaliana]	Unigene33892_All//5.00E-128//AT4G25630| FIB2 (FIBRILLARIN 2); snoRNA binding	Unigene33892_All//0.00E+00//TC155352				nr -
Unigene33895_All	2112	5.33	4.29	4.59	5.42	5.84	4.77	2.94	1.11	1.15	-3.11E-01	7.64E-02		-2.15E-01	2.55E-01		1.06E-01	5.91E-01		-1.86E-01	3.37E-01		-1.41E+00	3.67E-10	Down	-1.35E+00	5.88E-10	Down	Unigene33895_All//gi|145338292|ref|NP_187547.2|//1.00E-150//RNA polymerase II transcription factor/ protein binding / transcription activator/ transcription regulator/ translation initiation factor/ zinc ion binding [Arabidopsis thaliana]	Unigene33895_All//3.00E-137//AT3G09360| RNA polymerase II transcription factor/ protein binding / transcription activator/ transcription regulator/ translation initiation factor/ zinc ion binding	Unigene33895_All//0.00E+00//gi|78349296|gb|DT569570.1|DT569570				nr -
Unigene33896_All	1371	2.63	1.26	1.48	23.33	18.31	13.80	15.76	6.07	3.89	-1.07E+00	1.13E-03		-8.35E-01	1.39E-02		-3.49E-01	8.71E-05		-7.57E-01	5.03E-16		-1.38E+00	2.88E-32	Down	-2.02E+00	1.12E-56	Down	Unigene33896_All//gi|224127204|ref|XP_002320013.1|//0.00E+00//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222860786|gb|EEE98328.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene33896_All//4.00E-107//AT4G37750| ANT (AINTEGUMENTA); DNA binding / transcription factor	Unigene33896_All//0.00E+00//TC166545	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene33897_All	2861	1.59	0.94	0.78	12.28	8.23	6.09	5.72	2.80	1.55	-7.61E-01	7.10E-03		-1.03E+00	5.87E-04	Down	-5.76E-01	2.85E-12		-1.01E+00	2.71E-28	Down	-1.03E+00	8.63E-16	Down	-1.89E+00	1.52E-39	Down	Unigene33897_All//gi|224127204|ref|XP_002320013.1|//0.00E+00//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222860786|gb|EEE98328.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene33897_All//3.00E-107//AT4G37750| ANT (AINTEGUMENTA); DNA binding / transcription factor	Unigene33897_All//0.00E+00//TC166545	AP2-EREBP		GO:0001071//GO:0003676//GO:0003824//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene33898_All	2496	3.14	1.83	1.11	19.58	18.47	11.69	11.55	5.11	2.73	-7.83E-01	1.62E-04		-1.50E+00	7.51E-11	Down	-8.38E-02	3.49E-01		-7.44E-01	1.75E-23		-1.18E+00	1.05E-33	Down	-2.08E+00	1.66E-78	Down	Unigene33898_All//gi|224127204|ref|XP_002320013.1|//0.00E+00//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222860786|gb|EEE98328.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene33898_All//2.00E-105//AT4G37750| ANT (AINTEGUMENTA); DNA binding / transcription factor	Unigene33898_All//0.00E+00//TC168860	AP2-EREBP		GO:0001071//GO:0003676//GO:0003824//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene3390_All	1919	1.01	0.21	0.44	6.02	3.62	3.04	3.02	0.59	1.56	-2.26E+00	2.83E-05	Down	-1.18E+00	1.70E-02		-7.32E-01	1.80E-06		-9.88E-01	2.23E-09		-2.36E+00	2.04E-18	Down	-9.55E-01	1.02E-05		Unigene3390_All//gi|42567433|ref|NP_195313.2|//0.00E+00//aspartyl protease family protein [Arabidopsis thaliana] >gi|190576481|gb|ACE79041.1|At4g35880 [Arabidopsis thaliana] >gi|222423134|dbj|BAH19546.1|AT4G35880 [Arabidopsis thaliana]	Unigene3390_All//0.00E+00//AT4G35880| aspartyl protease family protein	Unigene3390_All//0.00E+00//TC148831			GO:0004175//GO:0019538//GO:0031224	nr -
Unigene33902_All	960	0.38	0.16	0.39	10.59	5.20	11.24	3.04	3.09	2.57	-1.27E+00	3.36E-01		2.55E-02	1.00E+00		-1.03E+00	8.25E-10	Down	8.70E-02	6.88E-01		2.46E-02	9.71E-01		-2.40E-01	4.77E-01		Unigene33902_All//gi|224127726|ref|XP_002329162.1|//1.00E-62//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene33902_All//1.00E-28//AT4G12010| disease resistance protein (TIR-NBS-LRR class), putative	Unigene33902_All//2.00E-165//TC163532		ko04626|Plant-pathogen interaction		nr +
Unigene33904_All	791	0.26	1.28	0.81	9.32	4.27	6.17	2.89	1.80	1.61	2.28E+00	4.09E-03		1.61E+00	1.11E-01		-1.13E+00	2.09E-08	Down	-5.96E-01	5.06E-03		-6.84E-01	7.25E-02		-8.41E-01	2.05E-02		Unigene33904_All//gi|296081003|emb|CBI18507.3|//8.00E-09//unnamed protein product [Vitis vinifera]		Unigene33904_All//0.00E+00//ES835726				nr +
Unigene33906_All	2938	61.65	77.87	60.34	34.22	49.78	43.78	45.66	93.17	252.51	3.37E-01	4.80E-24		-3.11E-02	5.20E-01		5.41E-01	2.10E-43		3.56E-01	3.09E-16		1.03E+00	8.06E-252	Up	2.47E+00	0.00E+00	Up	Unigene33906_All//gi|68144100|gb|AY86086.1|//1.00E-103//stearoyl-ACP desaturase [Jatropha curcas]	Unigene33906_All//2.00E-101//AT2G43710| SSI2; acyl-[acyl-carrier-protein] desaturase/ stearoyl-CoA 9-desaturase	Unigene33906_All//0.00E+00//TC174500		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis		nr -
Unigene33907_All	992	2.53	12.67	4.13	4.62	14.02	8.92	12.36	26.42	23.81	2.32E+00	3.14E-31	Up	7.07E-01	2.45E-02		1.60E+00	1.19E-24	Up	9.50E-01	7.92E-07		1.10E+00	2.12E-27	Up	9.46E-01	3.92E-20		Unigene33907_All//gi|21554156|gb|AAM63235.1|//7.00E-22//alcohol dehydrogenase-like protein [Arabidopsis thaliana]	Unigene33907_All//3.00E-23//AT5G63620| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene33907_All//0.00E+00//gi|164239470|gb|ES795875.1|ES795875			GO:0008152//GO:0016616//GO:0046914	nr -
Unigene33908_All	1386	4.34	13.27	9.22	11.47	19.70	18.48	15.50	26.11	24.75	1.61E+00	3.23E-28	Up	1.09E+00	9.81E-11	Up	7.81E-01	1.11E-15		6.88E-01	5.73E-11		7.53E-01	2.35E-20		6.75E-01	1.49E-16		Unigene33908_All//gi|21554156|gb|AAM63235.1|//1.00E-48//alcohol dehydrogenase-like protein [Arabidopsis thaliana]	Unigene33908_All//7.00E-50//AT5G63620| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene33908_All//0.00E+00//CK640439		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00051|Fructose and mannose metabolism//ko00350|Tyrosine metabolism	GO:0008152//GO:0016616//GO:0046914	nr +

Unigene33909_All	1653	22.60	56.37	37.63	33.39	58.56	58.39	55.02	93.81	102.62	1.32E+00	3.79E-104	Up	7.35E-01	4.08E-26		8.11E-01	2.28E-58		8.06E-01	3.80E-52		7.70E-01	8.39E-88		8.99E-01	7.92E-128		Unigene33909_All//gi|297797361|ref|XP_002866565.1|//0.00E+00//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297312400|gb|EFH42824.1|oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene33909_All//0.00E+00//AT5G63620| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene33909_All//0.00E+00//TC171048		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism	GO:0008152//GO:0016616//GO:0046914	nr -
Unigene33913_All	3049	0.93	0.86	1.55	1.72	1.50	2.07	1.55	0.77	1.39	-1.01E-01	7.77E-01		7.46E-01	9.59E-03		-1.92E-01	5.30E-01		2.74E-01	2.99E-01		-1.02E+00	4.58E-05	Down	-1.65E-01	5.45E-01		Unigene33913_All//gi|38345908|emb|CAE04506.2|//0.00E+00//OSJNBa0059K02.16 [Oryza sativa (japonica cultivar-group)]	Unigene33913_All//0.00E+00//AT5G13690| alpha-N-acetylglucosaminidase family / NAGLU family			ko00531|Glycosaminoglycan degradation	GO:0015929//GO:0031410	nr +
Unigene33915_All	1398	10.78	6.31	7.54	25.23	18.57	20.77	13.88	11.60	6.21	-7.73E-01	9.58E-08		-5.15E-01	5.65E-04		-4.42E-01	8.95E-08		-2.80E-01	1.97E-03		-2.59E-01	2.60E-02		-1.16E+00	4.11E-23	Down	Unigene33915_All//gi|152926156|gb|ABS32230.1|//1.00E-156//transducin family protein [Carica papaya] >gi|164522082|gb|ABV60781.1|transducin family protein [Carica papaya]	Unigene33915_All//3.00E-131//AT1G71840| transducin family protein / WD-40 repeat family protein	Unigene33915_All//0.00E+00//gi|164242661|gb|ES795926.1|ES795926				nr -
Unigene33920_All	1662	43.38	32.29	40.27	40.01	39.49	37.39	19.74	9.41	10.57	-4.26E-01	3.52E-12		-1.07E-01	1.36E-01		-1.90E-02	8.18E-01		-9.78E-02	1.94E-01		-1.07E+00	7.19E-33	Down	-9.01E-01	1.12E-25		Unigene33920_All//gi|94449066|gb|ABF19057.1|//1.00E-146//plastid Tic40 [Ricinus communis]	Unigene33920_All//4.00E-115//AT5G16620| TIC40	Unigene33920_All//0.00E+00//TC152738			GO:0043231	nr -
Unigene33929_All	1609	9.01	3.34	4.17	8.02	6.40	7.58	11.06	6.00	6.76	-1.43E+00	4.97E-19	Down	-1.11E+00	1.79E-12	Down	-3.26E-01	3.69E-02		-8.14E-02	6.74E-01		-8.83E-01	1.88E-13		-7.11E-01	7.80E-10		Unigene33929_All//gi|225469131|ref|XP_002270366.1|//0.00E+00//PREDICTED: similar to octicosapeptide/Phox/Bemlp (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein [Vitis vinifera]	Unigene33929_All//1.00E-148//AT1G62390| octicosapeptide/Phox/Bemlp (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein	Unigene33929_All//0.00E+00//ES824443			GO:0050896	nr +
Unigene33931_All	2608	2.75	0.89	1.25	2.71	2.79	2.48	4.90	1.65	3.21	-1.62E+00	1.38E-11	Down	-1.14E+00	9.16E-07	Down	3.87E-02	8.85E-01		-1.31E-01	6.37E-01		-1.57E+00	2.28E-23	Down	-6.10E-01	8.65E-06		Unigene33931_All//gi|18407574|ref|NP_564794.1|//0.00E+00//octicosapeptide/Phox/Bemlp (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana] >gi|7940289|gb|AAF70848.1|AC003113_15 F2401.12 [Arabidopsis thaliana]	Unigene33931_All//0.00E+00//AT1G62390| octicosapeptide/Phox/Bemlp (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein	Unigene33931_All//0.00E+00//ES824443			GO:0050896	nr +
Unigene33934_All	2656	13.75	14.98	17.94	22.41	20.39	11.87	17.81	47.98	17.02	1.23E-01	1.90E-01		3.84E-01	1.13E-06		-1.36E-01	5.78E-02		-9.17E-01	1.46E-40		1.43E+00	3.79E-197	Up	-6.53E-02	4.09E-01		Unigene33934_All//gi|224071337|ref|XP_002303411.1|//1.00E-178//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222840843|gb|EEE78390.1|oligopeptide transporter OPT family [Populus trichocarpa]	Unigene33934_All//1.00E-164//AT4G10770| OPT7 (OLIGOPEPTIDE TRANSPORTER 7); oligopeptide transporter	Unigene33934_All//0.00E+00//gi|109876947|gb|DW505921.1|DW505921				nr +
Unigene33935_All	3593	13.06	8.83	15.19	23.15	31.20	20.60	5.71	7.90	2.56	-5.65E-01	3.22E-13		2.18E-01	4.24E-03		4.30E-01	4.48E-22		-1.68E-01	4.01E-03		4.69E-01	2.21E-07		-1.16E+00	3.07E-24	Down	Unigene33935_All//gi|224128410|ref|XP_002329155.1|//1.00E-153//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222869824|gb|EEF06955.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene33935_All//3.00E-79//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene33935_All//0.00E+00//ES818502		ko04626|Plant-pathogen interaction		nr +
Unigene33936_All	4215	9.87	12.12	12.03	33.56	37.56	67.28	19.19	36.23	24.96	2.96E-01	6.77E-05		2.85E-01	2.33E-04		1.62E-01	2.72E-05		1.00E+00	3.65E-220	Up	9.17E-01	2.31E-116		3.79E-01	1.02E-17		Unigene33936_All//gi|87240323|gb|AB032181.1|//0.00E+00//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene33936_All//2.00E-97//AT2G27230| LHW (LONESOME HIGHWAY); protein homodimerization/ transcription activator/ transcription factor	Unigene33936_All//0.00E+00//TC172328	bHLH			nr -
Unigene3394_All	1165	2.69	2.91	3.52	7.74	5.44	4.03	2.18	4.41	2.70	1.13E-01	7.29E-01		3.85E-01	2.32E-01		-5.09E-01	5.09E-03		-9.41E-01	6.30E-07		1.02E+00	1.94E-05	Up	3.11E-01	3.38E-01		Unigene3394_All//gi|18394842|ref|NP_564109.1|//1.00E-123//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|9558598|gb|AAP88361.1|AC026234_12 Contains similarity to a prolyl 4-hydroxylase alpha subunit protein from Gallus gallus gi|212530 [Arabidopsis thaliana] >gi|90962978|gb|ABE02413.1|At1g20270 [Arabidopsis thaliana]	Unigene3394_All//4.00E-109//AT1G20270| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene3394_All//0.00E+00//TC156311		ko00330|Arginine and proline metabolism		nr -
Unigene33948_All	1656	2.59	1.25	1.54	3.49	3.04	3.14	5.34	5.07	2.57	-1.05E+00	4.18E-04	Down	-7.47E-01	1.45E-02		-2.01E-01	4.69E-01		-1.54E-01	6.15E-01		-7.29E-02	7.20E-01		-1.05E+00	1.59E-09	Down	Unigene33948_All//gi|61889368|emb|CAI72505.1|//0.00E+00//beta 1,2 N-acetylglucosaminyltransferase [Populus alba x Populus tremula]	Unigene33948_All//4.00E-168//AT2G05320| beta-1,2-N-acetylglucosaminyltransferase II	Unigene33948_All//0.00E+00//TC170866		ko00510|N-Glycan biosynthesis	GO:0008375//GO:0009311//GO:0031224//GO:0044431	nr +
Unigene33949_All	1938	2.83	5.99	1.65	4.83	5.79	7.27	12.65	20.85	20.91	1.08E+00	4.18E-10	Up	-7.82E-01	3.16E-03		2.62E-01	1.50E-01		5.89E-01	5.63E-05		7.21E-01	4.86E-21		7.24E-01	8.34E-22		Unigene33949_All//gi|61889368|emb|CAI72505.1|//0.00E+00//beta 1,2 N-acetylglucosaminyltransferase [Populus alba x Populus tremula]	Unigene33949_All//5.00E-158//AT2G05320| beta-1,2-N-acetylglucosaminyltransferase II	Unigene33949_All//0.00E+00//gi|109877323|gb|DW506296.1|DW506296		ko00510|N-Glycan biosynthesis	GO:0008375//GO:0009311//GO:0031224//GO:0044431	nr +
Unigene3395_All	1619	11.05	7.92	4.83	16.06	14.42	11.10	12.17	8.85	9.06	-4.81E-01	2.31E-04		-1.19E+00	5.13E-17	Down	-1.55E-01	1.82E-01		-5.33E-01	2.49E-07		-4.59E-01	3.32E-05		-4.26E-01	7.88E-05		Unigene3395_All//gi|15224909|ref|NP_181395.1|//1.00E-137//KH domain-containing protein [Arabidopsis thaliana] >gi|30687577|ref|NP_850296.1| KH domain-containing protein [Arabidopsis thaliana] >gi|297827443|ref|XP_002881604.1|KH domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|75268069|sp|Q9ZV13.1|QKIL3_ARATH RecName: Full=KH domain-containing protein At2g38610; AltName: Full=Quaking-like protein 3 >gi|297327443|gb|EFH57863.1| KH domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene3395_All//2.00E-123//AT2G38610| KH domain-containing protein	Unigene3395_All//0.00E+00//TC131885				nr -
Unigene33951_All	1969	2.07	1.16	2.62	4.88	5.72	3.95	2.19	0.83	2.41	-8.40E-01	5.35E-03		3.40E-01	2.33E-01		2.28E-01	2.22E-01		-3.08E-01	1.18E-01		-1.40E+00	2.99E-07	Down	1.37E-01	6.06E-01		Unigene33951_All//gi|21322711|emb|CAD22154.1|//7.00E-63//phenophorin-dcl protein [Volvox carteri f. nagariensis]	Unigene33951_All//2.00E-30//AT1G31810| actin binding					nr +
Unigene33958_All	1583	26.44	3.55	12.45	103.53	77.01	37.75	41.99	45.57	19.00	-2.90E+00	1.12E-132	Down	-1.09E+00	9.34E-34	Down	-4.27E-01	2.71E-32		-1.46E+00	3.18E-232	Down	1.18E-01	4.89E-02		-1.14E+00	2.66E-75	Down	Unigene33958_All//gi|224142001|ref|XP_002323349.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222865783|gb|EEF02914.1|predicted protein [Populus trichocarpa]		Unigene33958_All//2.00E-52//gi|78346044|gb|DT566318.1|DT566318				nr -
Unigene33959_All	1761	7.70	6.30	13.34	57.88	19.50	16.39	46.15	62.06	19.75	-2.88E-01	6.83E-02		7.93E-01	1.38E-11		-1.57E+00	3.25E-186	Down	-1.82E+00	1.31E-199	Down	4.28E-01	3.96E-22		-1.22E+00	2.59E-102	Down	Unigene33959_All//gi|18700103|gb|AAL77663.1|//1.00E-152//AT5g10770/T30N20_40 [Arabidopsis thaliana] >gi|24111269|gb|AAN46758.1|At5g10770/T30N20_40 [Arabidopsis thaliana]	Unigene33959_All//7.00E-142//AT5G10770| chloroplast nucleoid DNA-binding protein, putative	Unigene33959_All//0.00E+00//TC135688				nr -
Unigene3396_All	1708	2.08	1.13	1.43	5.63	4.56	3.54	8.61	1.64	3.57	-8.86E-01	6.72E-03		-5.39E-01	1.21E-01		-3.05E-01	1.06E-01		-6.68E-01	2.22E-04		-2.39E+00	1.77E-46	Down	-1.27E+00	2.30E-20	Down	Unigene3396_All//gi|159025707|emb|CAN88854.1|//1.00E-115//D2/4-type cyclin [Populus trichocarpa]	Unigene3396_All//2.00E-61//AT2G22490| CYCD2;1 (Cyclin D2;1); cyclin-dependent protein kinase regulator/ protein binding	Unigene3396_All//0.00E+00//gi|11203368|gb|BF272373.1|BF272373			GO:0009987	nr +
Unigene33960_All	1995	11.78	7.34	9.82	24.15	21.58	26.92	16.59	6.73	16.61	-6.82E-01	1.72E-09		-2.62E-01	3.19E-02		-1.62E-01	3.98E-02		1.57E-01	4.24E-02		-1.30E+00	4.29E-45	Down	1.80E-03	9.83E-01		Unigene33960_All//gi|297614182|gb|AD148429.1|//1.00E-123//trichome birefringence [Arabidopsis thaliana]	Unigene33960_All//8.00E-121//AT5G06700| unknown protein	Unigene33960_All//0.00E+00//TC173837				nr -
Unigene33962_All	2543	1.83	1.55	0.82	9.48	8.53	4.40	3.18	0.53	1.25	-2.37E-01	4.11E-01		-1.16E+00	9.00E-05	Down	-1.52E-01	2.18E-01		-1.11E+00	1.23E-22	Down	-2.59E+00	2.93E-28	Down	-1.34E+00	1.70E-12	Down	Unigene33962_All//gi|224589547|gb|ACN59307.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene33962_All//0.00E+00//AT2G41820| leucine-rich repeat transmembrane protein kinase, putative	Unigene33962_All//3.00E-111//ES832883		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016020//GO:0016301	nr -
Unigene33963_All	3556	2.40	0.78	0.90	13.91	7.77	5.46	7.16	3.47	2.70	-1.61E+00	1.45E-13	Down	-1.42E+00	8.44E-11	Down	-8.41E-01	5.00E-33		-1.35E+00	1.19E-62	Down	-1.05E+00	8.92E-25	Down	-1.41E+00	2.94E-40	Down	Unigene33963_All//gi|224589547|gb|ACN59307.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene33963_All//0.00E+00//AT2G41820| leucine-rich repeat transmembrane protein kinase, putative	Unigene33963_All//0.00E+00//TC144309			GO:0005488//GO:0016020//GO:0016301	nr +
Unigene33964_All	340	0.00	2.68	1.25	3.96	4.25	2.52	3.36	5.90	5.74	1.14E+01	2.62E-05	Up	1.03E+01	1.38E-02		1.05E-01	8.70E-01		-6.48E-01	2.83E-01		8.14E-01	4.65E-02		7.74E-01	5.34E-02		Unigene33964_All//gi|212549818|gb|ACJ26769.1|//2.00E-43//AO2 [Arachis hypogaea]	Unigene33964_All//2.00E-37//AT2G27150| AO03 (Abscisic ALDEHYDE OXIDASE 3); abscisic aldehyde oxidase/ aldehyde oxidase/ indole-3-acetaldehyde oxidase		ko00230|Purine metabolism//ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00906|Carotenoid biosynthesis//ko00232|Caffeine metabolism	GO:0009850//GO:0016726//GO:0018488//GO:0030554//GO:0046914//GO:0051536	nr +
Unigene33965_All	933	2.58	11.19	5.65	6.14	7.20	5.62	6.84	10.44	8.03	2.12E+00	2.73E-23	Up	1.13E+00	4.13E-05	Up	2.29E-01	3.73E-01		-1.29E-01	6.53E-01		6.09E-01	1.94E-04		2.30E-01	2.47E-01		Unigene33965_All//gi|94467212|dbj|BAE93767.1|//1.00E-24//aldehyde oxidase [Brassica rapa subsp. pekinensis]	Unigene33965_All//1.00E-25//AT5G20960| AO01 (ARABIDOPSIS ALDEHYDE OXIDASE 1); aldehyde oxidase/ indole-3-acetaldehyde oxidase	Unigene33965_All//3.00E-10//DW233729		ko00380|Tryptophan metabolism//ko00906|Carotenoid biosynthesis	GO:0008152//GO:0016623//GO:0030554//GO:0046914//GO:0051536	nr +
Unigene33967_All	612	19.24	5.88	12.36	27.27	35.73	30.77	35.10	26.29	21.35	-1.71E+00	5.57E-20	Down	-6.39E-01	1.90E-04		3.90E-01	4.78E-04		1.75E-01	2.29E-01		-4.17E-01	8.01E-05		-7.17E-01	7.60E-12		Unigene33967_All//gi|154816302|gb|ABS87384.1|//1.00E-108//pyruvate kinase [Lactuca sativa]	Unigene33967_All//3.00E-103//AT3G22960| PKP-ALPHA; pyruvate kinase	Unigene33967_All//0.00E+00//gi|164303208|gb|ES852311.1|ES852311		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene3397_All	2103	3.91	0.34	0.68	8.20	4.63	8.29	15.20	7.59	6.93	-3.53E+00	8.82E-32	Down	-2.51E+00	8.80E-22	Down	-8.23E-01	2.33E-11		1.64E-02	9.36E-01		-1.00E+00	7.67E-29	Down	-1.13E+00	4.25E-36	Down	Unigene3397_All//gi|37983539|gb|AAR06289.1|//0.00E+00//5-phosphoribosyl-1-pyrophosphate amidotransferase [Nicotiana tabacum]	Unigene3397_All//0.00E+00//AT2G16570| ATASH1 (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 1); amidophosphoribosyltransferase	Unigene3397_All//0.00E+00//TC177290		ko00230|Purine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0006144//GO:0006163//GO:0009064//GO:0009887//GO:0016763//GO:0030012//GO:0043169//GO:0044435//GO:0051536	nr +
Unigene33974_All	1874	0.64	2.14	1.08	1.28	1.69	1.30	1.62	1.83	1.32	1.73E+00	2.33E-07	Up	7.50E-01	1.16E-01		4.06E-01	2.83E-01		2.85E-02	9.58E-01		1.71E-01	6.33E-01		-3.02E-01	3.61E-01		Unigene33974_All//gi|271278821|emb|CAY85529.1|//0.00E+00//Cop11 protein [Carica papaya]	Unigene33974_All//0.00E+00//AT3G61140| FUS6 (FUSCA 6)	Unigene33974_All//0.00E+00//gi|164247149|gb|ES814218.1|ES814218			GO:0000338//GO:0003006//GO:0005488//GO:0006970//GO:0009639//GO:0009642//GO:0043231//GO:0043234//GO:0065003	nr +
Unigene33976_All	877	2.51	3.99	3.34	2.33	1.96	2.32	5.06	1.76	3.18	6.70E-01	4.27E-02		4.14E-01	2.90E-01		-2.46E-01	6.10E-01		-7.10E-03	9.81E-01		-1.52E+00	2.74E-08	Down	-6.71E-01	6.67E-03		Unigene33976_All//gi|297799760|ref|XP_002867764.1|//1.00E-100//oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313600|gb|EFH44023.1|oxysterol-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene33976_All//2.00E-101//AT4G22540| ORP2A (OSBP(OXYSTEROL BINDING PROTEIN)-RELATED PROTEIN 2A); oxysterol binding / phosphoinositide binding	Unigene33976_All//2.00E-110//TC150365			GO:0006629//GO:0032934	nr -
Unigene33977_All	1564	4.25	3.50	4.43	9.62	9.14	8.43	14.76	5.48	9.83	-2.80E-01	2.36E-01		5.90E-02	8.05E-01		-7.41E-02	6.71E-01		-1.90E-01	2.39E-01		-1.43E+00	2.16E-36	Down	-5.86E-01	3.96E-09		Unigene33977_All//gi|225426979|ref|XP_002265557.1|//0.00E+00//PREDICTED: similar to oxysterol-binding family protein [Vitis vinifera]	Unigene33977_All//0.00E+00//AT4G22540| ORP2A (OSBP(OXYSTEROL BINDING PROTEIN)-RELATED PROTEIN 2A); oxysterol binding / phosphoinositide binding	Unigene33977_All//0.00E+00//TC150365			GO:0005543//GO:0006629//GO:0023060//GO:0032934//GO:0043231	nr +

Unigene33979_All	2759	2.37	1.51	2.35	4.73	5.85	5.73	5.55	0.91	4.19	-6.55E-01	4.32E-03		-9.60E-03	9.93E-01		3.07E-01	2.73E-02		2.76E-01	6.22E-02		-2.61E+00	2.54E-53	Down	-4.06E-01	1.10E-03		Unigene33979_All//gi|225426979|ref|XP_002265557.1|//0.00E+00//PREDICTED: similar to oxysterol-binding family protein [Vitis vinifera]	Unigene33979_All//0.00E+00//AT4G22540| OSP2A (OSBP(OXYSTEROL BINDING PROTEIN)-RELATED PROTEIN 2A); oxysterol binding / phosphoinositide binding	Unigene33979_All//0.00E+00//TC150365			GO:0005543//GO:0000629//GO:0023060//GO:0032934//GO:0043231	nr -
Unigene33980_All	479	5.02	2.54	4.89	7.28	5.46	7.35	6.27	1.31	1.75	-9.85E-01	1.66E-02		-3.87E-02	9.40E-01		-4.14E-01	2.22E-01		1.47E-02	9.64E-01		-2.26E+00	2.04E-09	Down	-1.84E+00	1.04E-07	Down	Unigene33980_All//gi|297850070|ref|XP_002892916.1|//7.00E-23//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297338758|gb|EFH69175.1|expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene33980_All//3.00E-104//gi|78353616|gb|DT573890.1|DT573890		ko03040|Spliceosome	GO:0000377//GO:0005488//GO:0009756//GO:0016604	nr +
Unigene33981_All	746	4.14	4.21	4.21	4.54	4.48	4.12	6.18	3.25	2.19	2.53E-02	9.63E-01		2.54E-02	9.61E-01		-2.02E-02	9.59E-01		-1.41E-01	6.83E-01		-9.27E-01	2.31E-04		-1.50E+00	1.08E-08	Down	Unigene33981_All//gi|15219287|ref|NP_173107.1|//1.00E-78//SR45; RNA binding / protein binding [Arabidopsis thaliana] >gi|6601502|gb|AAF19004.1|AF151366_1 arginine/serine-rich protein [Arabidopsis thaliana] >gi|9989058|gb|AAG10821.1|AC011808_9 arginine/serine-rich protein [Arabidopsis thaliana] >gi|56382017|gb|AAV85727.1|At1g16610 [Arabidopsis thaliana]	Unigene33981_All//6.00E-06//AT1G16610| SR45; RNA binding / protein binding	Unigene33981_All//0.00E+00//TC148096			GO:0000377//GO:0005488//GO:0009756//GO:0016604	nr +
Unigene33982_All	1441	3.20	2.18	1.07	3.32	3.56	2.66	3.40	1.02	1.27	-5.52E-01	5.02E-02		-1.58E+00	4.69E-07	Down	1.02E-01	7.75E-01		-3.17E-01	2.94E-01		-1.75E+00	7.11E-11	Down	-1.42E+00	1.43E-08	Down	Unigene33982_All//gi|15219287|ref|NP_173107.1|//1.00E-137//SR45; RNA binding / protein binding [Arabidopsis thaliana] >gi|6601502|gb|AAF19004.1|AF151366_1 arginine/serine-rich protein [Arabidopsis thaliana] >gi|9989058|gb|AAG10821.1|AC011808_9 arginine/serine-rich protein [Arabidopsis thaliana] >gi|56382017|gb|AAV85727.1|At1g16610 [Arabidopsis thaliana]	Unigene33982_All//7.00E-37//AT1G16610| SR45; RNA binding / protein binding	Unigene33982_All//0.00E+00//TC148096			GO:0043231	nr +
Unigene33983_All	1084	25.20	24.45	16.11	53.86	48.76	56.66	60.61	52.28	26.98	-4.35E-02	7.04E-01		-6.45E-01	1.70E-09		-1.43E-01	4.52E-02		7.32E-02	3.88E-01		-2.13E-01	2.89E-04		-1.17E+00	6.00E-77	Down	Unigene33983_All//gi|15219287|ref|NP_173107.1|//1.00E-105//SR45; RNA binding / protein binding [Arabidopsis thaliana] >gi|6601502|gb|AAF19004.1|AF151366_1 arginine/serine-rich protein [Arabidopsis thaliana] >gi|9989058|gb|AAG10821.1|AC011808_9 arginine/serine-rich protein [Arabidopsis thaliana] >gi|56382017|gb|AAV85727.1|At1g16610 [Arabidopsis thaliana]	Unigene33983_All//9.00E-14//AT1G16610| SR45; RNA binding / protein binding	Unigene33983_All//0.00E+00//TC133550			GO:0005488//GO:0043231	nr -
Unigene33988_All	3604	10.70	21.24	11.52	25.89	35.73	59.35	135.05	297.78	461.99	9.90E-01	2.44E-54		1.07E-01	2.69E-01		4.65E-01	4.25E-29		1.20E+00	7.87E-221	Up	1.14E+00	0.00E+00	Up	1.77E+00	0.00E+00	Up	Unigene33988_All//gi|124365601|gb|AAK50778.4|AF361893_1//0.00E+00//bacterial-induced lipoxygenase [Gossypium hirsutum]	Unigene33988_All//0.00E+00//TC130168		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0006633//GO:0016702//GO:0046914	nr +
Unigene33989_All	1671	2.66	1.00	2.74	3.34	3.92	5.62	4.63	13.68	40.94	-1.41E+00	2.98E-06	Down	4.23E-02	8.92E-01		2.30E-01	3.81E-01		7.52E-01	4.52E-05		1.56E+00	6.02E-41	Up	3.14E+00	3.83E-291	Up	Unigene33989_All//gi|297849514|ref|XP_002892638.1|//1.00E-119//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338480|gb|EFH68897.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene33989_All//2.00E-113//AT1G11330| S-locus lectin protein kinase family protein	Unigene33989_All//2.00E-71//CO081718		ko04626|Plant-pathogen interaction		nr -
Unigene33990_All	2252	4.25	1.69	2.25	5.02	4.71	6.42	4.94	11.21	36.99	-1.33E+00	1.40E-11	Down	-9.21E-01	2.15E-06		-9.24E-02	6.34E-01		3.54E-01	1.87E-02		1.18E+00	9.15E-30	Up	2.91E+00	0.00E+00	Up	Unigene33990_All//gi|6554204|gb|AAF16650.1|AC011661_28//1.00E-162//T23J18.2 [Arabidopsis thaliana]	Unigene33990_All//1.00E-141//AT1G11330| S-locus lectin protein kinase family protein	Unigene33990_All//1.00E-125//DT468630				nr +
Unigene33991_All	650	10.22	7.80	7.54	9.58	12.40	11.33	6.89	3.79	3.13	-3.91E-01	9.27E-02		-4.40E-01	7.03E-02		3.72E-01	7.52E-02		2.42E-01	3.23E-01		-8.62E-01	7.18E-04		-1.14E+00	6.96E-06	Down	Unigene33991_All//gi|585452|sp|P37225.1|MAON_SOLTU//7.00E-76//RecName: Full=NAD-dependent malic enzyme 59 kDa isoform, mitochondrial; Short=NAD-ME; Flags: Precursor >gi|438131|emb|CAA80547.1|precursor of the 59kDa subunit of the mitochondrial NAD+-dependent malic enzyme [Solanum tuberosum]	Unigene33991_All//3.00E-59//AT4G00570| malate oxidoreductase, putative	Unigene33991_All//0.00E+00//gi|48830151|gb|CO128541.1|CO128541		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0004470//GO:0031980//GO:0043169//GO:0043648	nr +
Unigene33992_All	1012	13.91	11.42	11.89	22.30	17.69	17.23	18.38	10.41	8.07	-2.85E-01	6.67E-02		-2.26E-01	1.75E-01		-3.34E-01	2.46E-03		-3.72E-01	1.11E-03		-8.21E-01	1.73E-12		-1.19E+00	5.20E-23	Down	Unigene33992_All//gi|6382043|gb|AAC13636.2|//7.00E-83//F6N23.16 gene product [Arabidopsis thaliana]	Unigene33992_All//2.00E-77//AT4G00570| malate oxidoreductase, putative	Unigene33992_All//0.00E+00//TC165997		ko000620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0004470//GO:0031980//GO:0043169//GO:0043648	nr +
Unigene33994_All	916	1.14	0.33	1.45	1.36	1.54	0.30	7.02	15.65	1.00	-1.78E+00	1.36E-02		3.47E-01	5.78E-01		1.81E-01	8.02E-01		-2.20E+00	1.10E-03		1.16E+00	1.08E-16	Up	-2.81E+00	1.81E-25	Down	Unigene33994_All//gi|224073568|ref|XP_002304113.1|//2.00E-39//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222841545|gb|EEE78692.1|white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene33994_All//3.00E-30//AT1G31770| ABC transporter family protein	Unigene33994_All//2.00E-39//CO117160			GO:0015405//GO:0015604//GO:0017111//GO:0032559//GO:0044464	nr -
Unigene33995_All	2486	1.52	0.04	0.75	6.09	5.25	5.96	8.61	2.93	3.78	-5.21E+00	5.98E-19	Down	-1.02E+00	2.23E-03		-2.15E-01	1.61E-01		-3.18E-02	8.63E-01		-1.56E+00	3.22E-38	Down	-1.19E+00	2.83E-26	Down	Unigene33995_All//gi|224129984|ref|XP_002328852.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222839150|gb|EEE77501.1|white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene33995_All//0.00E+00//AT1G31770| ABC transporter family protein	Unigene33995_All//0.00E+00//gi|48815847|gb|CO117160.1|CO117160		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015604//GO:0017111//GO:0032559//GO:0044464	nr +
Unigene33996_All	2610	7.84	1.63	6.16	16.49	8.40	5.12	20.31	50.20	4.58	-2.27E+00	2.39E-49	Down	-3.47E-01	6.91E-03		-9.72E-01	8.79E-37		-1.69E+00	6.54E-76	Down	1.31E+00	1.72E-176	Up	-2.15E+00	9.63E-150	Down	Unigene33996_All//gi|224129984|ref|XP_002328852.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222839150|gb|EEE77501.1|white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene33996_All//0.00E+00//AT1G31770| ABC transporter family protein	Unigene33996_All//0.00E+00//gi|164344908|gb|ES827175.1|ES827175		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015604//GO:0032559//GO:0042626//GO:0044464	nr -
Unigene33997_All	305	7.72	3.82	8.03	2.78	8.58	4.29	0.00	0.00	0.39	-1.01E+00	1.50E-02		5.71E-02	8.94E-01		1.63E+00	4.57E-05	Up	6.29E-01	3.15E-01		null	null		8.61E+00	2.43E-01		Unigene33997_All//gi|15242536|ref|NP_198817.1|//5.00E-14//AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene33997_All//2.00E-15//AT5G40010| AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene33997_All//1.00E-105//gi|109882511|gb|DW511481.1|DW511481			GO:0009725//GO:0017111//GO:0032559//GO:0043231	nr +
Unigene340_All	629	1.66	6.04	1.86	2.38	1.42	2.87	7.19	3.32	11.84	1.86E+00	1.18E-07	Up	1.63E-01	7.82E-01		-7.39E-01	1.63E-01		2.74E-01	6.40E-01		-1.11E+00	1.59E-05	Down	7.20E-01	1.09E-04		Unigene340_All//gi|240256041|ref|NP_194031.5|//3.00E-45//hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana]	Unigene340_All//2.00E-46//AT4G23000| hydrolase/ protein serine/threonine phosphatase	Unigene340_All//4.00E-172//DW492635				nr -
Unigene3400_All	2777	4.48	9.05	4.85	6.82	8.17	7.50	10.28	10.23	7.88	1.01E+00	5.04E-19	Up	1.14E-01	5.31E-01		2.62E-01	2.39E-02		1.37E-01	3.37E-01		-6.00E-03	9.89E-01		-3.84E-01	1.39E-05		Unigene3400_All//gi|115455663|ref|NP_001051432.1|//5.00E-88//Os03g0775600 [Oryza sativa Japonica Group] >gi|113549903|dbj|BAF13346.1|Os03g0775600 [Oryza sativa Japonica Group]	Unigene3400_All//2.00E-72//AT1G75180| unknown protein	Unigene3400_All//0.00E+00//gi|109878976|gb|DW507946.1|DW507946				nr -
Unigene34001_All	2338	2.33	1.54	1.96	5.05	4.51	4.06	8.81	3.47	3.99	-5.97E-01	1.96E-02		-2.49E-01	3.95E-01		-1.64E-01	3.87E-01		-3.16E-01	6.77E-02		-1.34E+00	1.05E-29	Down	-1.14E+00	6.34E-24	Down	Unigene34001_All//gi|62533251|dbj|BAD95575.1|//1.00E-148//chromosome associate protein submit H [Arabidopsis thaliana]	Unigene34001_All//1.00E-133//AT2G32590| INVOLVED IN: mitosis, mitotic cell cycle; LOCATED IN: nucleus, chloroplast; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Barren (InterPro:IPR008418); Has 340 Blast hits to 330 proteins in 142 species: Archae - 0; Bacteria - 0; Metazoa - 135; Fungi - 102; Plants - 21; Viruses - 1; Other Eukaryotes - 81 (source: NCBI BLink).	Unigene34001_All//0.00E+00//gi|78345782|gb|DT566056.1|DT566056			GO:0000278	nr +
Unigene34002_All	404	0.00	0.00	0.00	0.12	0.17	0.00	3.87	7.45	8.09	null	null		null	null		4.68E-01	9.58E-01		-6.95E+00	6.35E-01		9.44E-01	3.37E-03		1.06E+00	4.31E-04	Up	Unigene34002_All//gi|162463793|ref|NP_001105046.1|//5.00E-21//cytosolic aldehyde dehydrogenase RF2C [Zea mays] >gi|19850243|gb|AAL99609.1|AF348413_1 cytosolic aldehyde dehydrogenase RF2C [Zea mays]	Unigene34002_All//18//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene34002_All//2.00E-18//TC157786		ko00940|Phenylpropanoid biosynthesis	GO:0004030//GO:0009698	nr -
Unigene34003_All	1104	0.00	0.00	0.00	0.00	0.00	0.20	4.33	7.23	15.59	null	null		null	null		null	null		7.68E+00	1.19E-01		7.41E-01	5.25E-05		1.85E+00	6.19E-40	Up	Unigene34003_All//gi|197312909|gb|ACH63233.1|//4.00E-32//alcohol dehydrogenase [Rheum australe]	Unigene34003_All//7.00E-20//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene34003_All//1.00E-37//TC157786		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0004030//GO:0009698//GO:0043231	nr +

Unigene34004_All	2543	4.57	20.64	5.13	9.07	11.02	12.91	74.10	190.44	276.24	2.18E+01	8.50E-119	Up	1.68E-01	3.61E-01		2.81E-01	5.07E-03		5.10E-01	2.26E-08		1.36E+00	0.00E+00	Up	1.90E+00	0.00E+00	Up	Unigene34004_All//gi|197312909|gb|ACH63235.1|//0.00E+00//alcohol dehydrogenase [Rheum australe]	Unigene34004_All//0.00E+00//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene34004_All//0.00E+00//gi|73861174|gb|DT463913.1|DT463913		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0004030//GO:0009698	nr +
Unigene34006_All	604	1.73	1.26	0.18	2.06	1.31	1.79	1.89	1.73	0.73	-4.61E-01	4.86E-01		-3.30E+00	4.58E-04	Down	-6.53E-01	2.80E-01		-2.00E-01	7.33E-01		-1.28E-01	8.22E-01		-1.38E+00	1.42E-02								
Unigene34010_All	4543	6.82	19.95	9.47	13.29	16.98	16.76	25.62	48.48	57.11	1.55E+00	5.77E-129	Up	4.74E-01	1.16E-08		3.53E-01	9.00E-11		3.35E-01	7.05E-09		9.20E-01	1.64E-168		1.16E+00	1.71E-294	Up	Unigene34010_All//gi|186510319|ref|NP_001118676.1|//1.00E-118//TIC (TIME FOR COFFEE) [Arabidopsis thaliana]	Unigene34010_All//1.00E-53//AT3G22380| TIC (TIME FOR COFFEE)	Unigene34010_All//0.00E+00//TC130463		ko03040|Spliceosome		nr -
Unigene34014_All	2479	4.92	3.74	2.19	8.16	8.70	8.23	10.57	9.17	10.04	-3.95E-01	1.59E-02		-1.17E+00	2.14E-11	Down	9.20E-02	5.48E-01		1.34E-02	9.41E-01		-2.05E-01	4.10E-02		-7.42E-02	5.03E-01		Unigene34014_All//gi|42563113|ref|NP_177219.2|//1.00E-82//cyclin-related [Arabidopsis thaliana]	Unigene34014_All//8.00E-46//AT1G70620| cyclin-related	Unigene34014_All//0.00E+00//gi|21091211|gb|BQ403536.1|BQ403536		ko03040|Spliceosome		nr -
Unigene34015_All	1164	1.80	3.87	2.38	5.65	6.15	5.59	9.66	9.62	7.77	1.11E+00	1.40E-04	Up	4.04E-01	3.22E-01		1.23E-01	6.25E-01		-1.59E-02	9.56E-01		-5.80E-03	1.01E+00		-3.15E-01	3.68E-02		Unigene34015_All//gi|255574021|ref|XP_002527928.1|//2.00E-06//hydrolase, acting on ester bonds, putative [Ricinus communis] >gi|223532703|gb|EEF34485.1| hydrolase, acting on ester bonds, putative [Ricinus communis]		Unigene34015_All//0.00E+00//ES842851			GO:0003824	nr -
Unigene34017_All	5485	7.54	8.17	7.24	11.61	10.22	11.91	44.48	100.09	64.66	1.16E-01	1.90E-01		-5.73E-02	5.91E-01		-1.84E-01	4.64E-03		3.78E-02	6.53E-01		1.17E+00	0.00E+00	Up	5.40E-01	2.91E-109		Unigene34017_All//gi|224116630|ref|XP_002317351.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222860416|gb|EEE97963.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene34017_All//0.00E+00//AT2G34660| ATMRP2 (ARABIDOPSIS THALIANA MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 2); ATPase, coupled to transmembrane movement of substances	Unigene34017_All//0.00E+00//TC172273		ko02010|ABC transporters	GO:0005773//GO:0006810//GO:0016491//GO:0031090//GO:0031224//GO:0032559//GO:0042626	nr +
Unigene34018_All	1077	0.97	0.89	0.49	1.94	1.63	1.51	3.69	2.33	1.74	-1.20E-01	8.43E-01		-9.75E-01	1.67E-01		-2.53E-01	5.92E-01		-3.64E-01	4.57E-01		-6.64E-01	1.50E-02		-1.09E+00	5.67E-05	Down	Unigene34018_All//gi|79334443|ref|NP_171714.2|//1.00E-42//VAD1 (VASCULAR ASSOCIATED DEATH1) [Arabidopsis thaliana]	Unigene34018_All//5.00E-44//AT1G02120| VAD1 (VASCULAR ASSOCIATED DEATH1)	Unigene34018_All//2.00E-79//TC173463			GO:0043231	nr -
Unigene34021_All	917	25.45	6.80	13.65	33.35	29.07	22.26	11.90	8.84	6.39	-1.90E+00	4.60E-45	Down	-8.99E-01	4.41E-14		-1.99E-01	4.71E-02		-5.83E-01	6.64E-10		-4.28E-01	5.82E-03		-8.97E-01	4.43E-09		Unigene34021_All//gi|15231090|ref|NP_190763.1|//8.00E-06//zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|79314761|ref|NP_001030840.1| zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|75337705|sp|Q9SV09.1|C3H46_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 46; Short=AtC3H46 >gi|222422911|dbj|BAH19442.1| AT3G51950 [Arabidopsis thaliana]	Unigene34021_All//4.00E-07//AT3G51950| zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein	Unigene34021_All//0.00E+00//ES812703	C3H		GO:0003676//GO:0046872	nr +
Unigene34022_All	2740	23.35	7.10	14.15	30.82	36.47	26.21	11.65	7.52	9.04	-1.72E+00	2.67E-106	Down	-7.23E-01	4.85E-26		2.43E-01	4.51E-07		-2.34E-01	2.71E-05		-6.32E-01	1.76E-13		-3.65E-01	1.12E-05		Unigene34022_All//gi|15231090|ref|NP_190763.1|//1.00E-121//zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|79314761|ref|NP_001030840.1| zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|75337705|sp|Q9SV09.1|C3H46_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 46; Short=AtC3H46 >gi|222422911|dbj|BAH19442.1| AT3G51950 [Arabidopsis thaliana]	Unigene34022_All//2.00E-119//AT3G51950| zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein	Unigene34022_All//0.00E+00//TC172467	C3H		GO:0005488	nr +
Unigene34023_All	1587	1.12	0.77	0.64	4.77	3.41	3.10	3.46	1.42	3.29	-5.49E-01	2.61E-01		-8.14E-01	1.15E-01		-4.86E-01	1.70E-02		-6.21E-01	2.93E-03		-1.28E+00	5.54E-08	Down	-7.48E-02	7.48E-01		Unigene34023_All//gi|225442633|ref|XP_002284593.1|//0.00E+00//PREDICTED: similar to BY-2 kinesin-like protein 10 [Vitis vinifera]	Unigene34023_All//0.00E+00//AT3G16060| kinesin motor family protein	Unigene34023_All//0.00E+00//TC163744			GO:0003774//GO:0007017//GO:0015630//GO:0016020//GO:0032559//GO:0043231	nr +
Unigene34024_All	2819	14.81	4.49	8.07	13.50	13.06	9.55	10.87	1.60	5.10	-1.72E+00	9.46E-70	Down	-8.77E-01	9.99E-24		-4.81E-02	6.58E-01		-5.00E-01	2.40E-09		-2.76E+00	4.81E-113	Down	-1.09E+00	1.01E-32	Down	Unigene34024_All//gi|225442633|ref|XP_002284593.1|//0.00E+00//PREDICTED: similar to BY-2 kinesin-like protein 10 [Vitis vinifera]	Unigene34024_All//0.00E+00//AT3G16060| kinesin motor family protein	Unigene34024_All//0.00E+00//TC163744			GO:0000904//GO:0003774//GO:0007017//GO:0015630//GO:0016020//GO:0032559//GO:0044431	nr -
Unigene34028_All	978	7.28	13.88	7.08	7.84	8.24	11.45	9.34	18.80	18.33	9.32E-01	2.28E-09		-3.97E-02	8.72E-01		7.09E-02	8.03E-01		5.46E-01	1.14E-03		1.01E+00	3.84E-17	Up	9.73E-01	3.45E-16		Unigene34028_All//gi|18391117|ref|NP_563862.1|//3.00E-81//carbohydrate binding [Arabidopsis thaliana] >gi|75213370|sp|Q9SY57.1|P2A10_ARATH RecName: Full=Protein PHLOEM PROTEIN 2-LIKE A10; Short=AtPP2-A10 >gi|4914317|gb|AAD32865.1|AC005489_3 F14N23.3 [Arabidopsis thaliana] >gi|91807671|gb|ABF47131.1| At1g10150 [Arabidopsis thaliana]	Unigene34028_All//4.00E-72//AT1G10150| carbohydrate binding	Unigene34028_All//0.00E+00//gi|84165665|gb|DR454313.1|DR454313			GO:0005488	nr +
Unigene3404_All	933	7.18	4.45	5.65	5.45	4.91	4.89	4.35	1.79	2.22	-6.89E-01	2.36E-03		-3.45E-01	1.58E-01		-1.50E-01	6.04E-01		-1.56E-01	6.37E-01		-1.28E+00	4.51E-06	Down	-9.70E-01	2.34E-04		Unigene3404_All//gi|145332811|ref|NP_001078271.1|//1.00E-124//5'-3' exonuclease family protein [Arabidopsis thaliana]	Unigene3404_All//3.00E-125//AT3G52050| 5'-3' exonuclease family protein	Unigene3404_All//0.00E+00//DW239999		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination	GO:0004527//GO:0043231	nr -
Unigene34041_All	2482	6.16	14.05	6.84	12.40	13.31	16.78	19.52	25.43	24.64	1.19E+00	1.22E-33	Up	1.53E-01	3.32E-01		1.01E-01	3.65E-01		4.36E-01	5.26E-08		3.81E-01	8.93E-11		3.36E-01	1.11E-08		Unigene34041_All//gi|240254548|ref|NP_180365.5|//1.00E-135//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene34041_All//6.00E-111//AT2G27980| protein binding / zinc ion binding	Unigene34041_All//0.00E+00//gi|78353906|gb|DT574180.1|DT574180				nr -
Unigene34043_All	3196	10.71	28.73	17.88	10.58	12.64	13.33	18.27	23.59	24.02	1.42E+00	2.64E-115	Up	7.40E-01	2.88E-24		2.56E-01	1.68E-03		3.32E-01	3.28E-05		3.69E-01	5.36E-12		3.95E-01	4.07E-14		Unigene34043_All//gi|15229615|ref|NP_188457.1|//0.00E+00//EMB2454 (embryo defective 2454); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|20453199|gb|AAM19839.1| AT3g18290/MIE15_8 [Arabidopsis thaliana] >gi|29028750|gb|AAO64754.1| At3g18290/MIE15_8 [Arabidopsis thaliana]	Unigene34043_All//0.00E+00//AT3G18290| EMB2454 (embryo defective 2454); protein binding / zinc ion binding	Unigene34043_All//0.00E+00//TC141365		ko04120|Ubiquitin mediated proteolysis	GO:0003006//GO:0046914	nr +
Unigene34045_All	3983	18.35	8.77	15.32	23.69	19.93	20.68	58.75	46.99	38.67	-1.07E+00	8.37E-59	Down	-2.60E-01	4.18E-05		-2.49E-01	4.25E-07		-1.96E-01	2.36E-04		-3.22E-01	1.00E-27		-6.04E-01	1.04E-88		Unigene34045_All//gi|224133676|ref|XP_002327653.1|//0.00E+00//histidine kinase osmosensor protein [Populus trichocarpa] >gi|222836738|gb|EEE75131.1| histidine kinase osmosensor protein [Populus trichocarpa]	Unigene34045_All//0.00E+00//AT2G17820| ATHK1 (histidine kinase 1); histidine phosphotransfer kinase/ osmosensor/ protein histidine kinase	Unigene34045_All//0.00E+00//DW512893	Orphans	ko04712|Circadian rhythm - plant	GO:0004673//GO:0004888//GO:0006351//GO:0006468//GO:0006950//GO:0023060//GO:0032559//GO:0044464//GO:0048316	nr -
Unigene3405_All	1679	5.36	1.54	3.27	3.95	3.32	2.50	2.39	1.57	0.90	-1.80E+00	1.57E-16	Down	-7.14E-01	3.37E-04		-2.48E-01	3.12E-01		-6.58E-01	3.50E-03		-6.09E-01	2.53E-02		-1.41E+00	4.31E-07	Down	Unigene3405_All//gi|145332809|ref|NP_001078270.1|//1.00E-151//5'-3' exonuclease family protein [Arabidopsis thaliana]	Unigene3405_All//9.00E-153//AT3G52050| 5'-3' exonuclease family protein	Unigene3405_All//0.00E+00//TC174663		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination		nr +
Unigene34051_All	517	2.53	2.65	2.58	8.77	6.06	4.02	9.73	7.03	5.47	6.48E-02	9.17E-01		2.54E-02	9.85E-01		-5.33E-01	5.32E-02		-1.13E+00	6.75E-05	Down	-4.69E-01	5.37E-02		-8.31E-01	3.33E-04				Unigene34051_All//8.00E-99//gi|18101225|gb|BM360479.1|BM360479				
Unigene34054_All	2979	8.31	7.30	8.26	16.99	15.99	13.66	29.80	10.17	12.91	-1.87E-01	1.11E-01		-8.60E-03	9.66E-01		-8.78E-02	3.12E-01		-3.15E-01	1.48E-05		-1.55E+00	1.75E-155	Down	-1.21E+00	2.58E-109	Down	Unigene34054_All//gi|124360049|gb|ABN08065.1|//0.00E+00//BTB/POZ; Superoxide dismutase, copper/zinc binding; NPH3 [Medicago truncatula]	Unigene34054_All//0.00E+00//AT1G30440| phototropic-responsive NPH3 family protein	Unigene34054_All//0.00E+00//gi|48878288|gb|CO129310.1|CO129310			GO:0004871//GO:0005488//GO:0009314//GO:0016020	nr +
Unigene34057_All	4772	10.23	10.09	4.85	34.80	28.88	42.23	63.10	42.66	79.44	-2.02E-02	8.17E-01		-1.08E+00	1.27E-38	Down	-2.69E-01	6.35E-14		2.79E-01	4.26E-16		-5.65E-01	1.63E-98		3.32E-01	4.62E-48		Unigene34057_All//gi|89357137|gb|AB072304.1|//1.00E-27//apple fruit acidity-related protein [Malus x domestica]	Unigene34057_All//8.00E-32//AT5G40450| unknown protein	Unigene34057_All//0.00E+00//TC143011		ko03040|Spliceosome		nr -
Unigene34062_All	803	47.04	25.11	26.33	64.95	58.54	104.84	173.60	93.64	80.92	-9.06E-01	1.30E-23		-8.38E-01	6.00E-20		-1.50E-01	4.89E-02		6.91E-01	6.06E-35		-8.91E-01	2.59E-101		-1.10E+00	9.78E-148	Down	Unigene34062_All//gi|12580855|emb|CAC27136.1|//8.00E-94//40S ribosomal protein S2 [Picea abies]	Unigene34062_All//8.00E-89//AT2G41840| 40S ribosomal protein S2 (RPS2C)	Unigene34062_All//0.00E+00//TC156363		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene34063_All	1226	28.42	5.87	6.52	37.62	31.57	57.03	46.69	18.24	21.87	-2.28E+00	3.66E-84	Down	-2.13E+00	1.47E-74	Down	-2.53E-01	6.96E-04		6.00E-01	8.57E-23		-1.36E+00	2.75E-82	Down	-1.09E+00	1.48E-60	Down	Unigene34063_All//gi|297827841|ref|XP_002881803.1|//1.00E-125//40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata] >gi|297327642|gb|EFH58062.1| 40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata]	Unigene34063_All//2.00E-115//AT3G57490| 40S ribosomal protein S2 (RPS2D)	Unigene34063_All//0.00E+00//TC143947		ko03010|Ribosome		nr -
Unigene34066_All	441	3.20	7.81	4.35	2.94	5.86	3.89	11.79	15.45	13.46	1.29E+00	1.88E-04	Up	4.40E-01	3.86E-01		9.96E-01	1.02E-02		4.06E-01	4.62E-01		3.90E-01	5.93E-02		1.91E-01	4.05E-01				Unigene34066_All//1.00E-07//TC164510				
Unigene34067_All	3823	1.40	4.57	2.45	2.40	2.08	2.66	9.84	10.60	13.40	1.71E+00	3.50E-29	Up	8.12E-01	3.12E-05		-2.05E-01	3.22E-01		1.49E-01	4.81E-01		1.08E-01	2.16E-01		4.45E-01	6.40E-12		Unigene34067_All//gi|253971327|gb|ACT37432.1|//1.00E-122//type-1 phosphatidic acid phosphohydrolase 2 [Arabidopsis thaliana]	Unigene34067_All//3.00E-121//AT5G42870| lipin family protein	Unigene34067_All//0.00E+00//TC148394				nr -
Unigene3407_All	508	3.50	1.50	3.56	2.45	6.03	3.65	1.41	1.32	0.31	-1.23E+00	1.38E-02		2.54E-02	9.78E-01		1.30E+00	2.25E-04	Up	5.72E-01	2.58E-01		-1.04E-01	8.93E-01		-2.17E+00	7.75E-03		Unigene3407_All//gi|222635925|gb|EE66057.1|//2.00E-08//hypothetical protein OsJ_22054 [Oryza sativa Japonica Group]		Unigene3407_All//9.00E-37//DW225182				nr -
Unigene34073_All	867	0.48	1.23	0.92	1.15	1.47	0.68	1.22	2.56	4.32	1.35E+00	5.00E-02		9.32E-01	2.56E-01		3.55E-01	5.94E-01		-7.63E-01	2.89E-01		1.07E+00	5.89E-03		1.82E+00	3.52E-09	Up			Unigene34073_All//0.00E+00//TC159925				

Unigene34079_All	847	46.58	26.56	23.20	61.87	53.01	81.90	203.76	157.41	250.41	-8.10E-01	1.64E-20		-1.01E+00	4.24E-28	Down	-2.23E-01	1.57E-03		4.05E-01	2.47E-11		-3.72E-01	7.69E-27		2.97E-01	2.45E-22		Unigene34079_All//gi|46850204|gb|AAT02535.1|/1.00E-100//NADP-dependent malic enzyme 3 [Hydrilla verticillata]	Unigene34079_All//7.00E-88//AT5G25880| ATNADP-ME3 (NADP-malic enzyme 3); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor	Unigene34079_All//0.00E+00//TC152653		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0004470//GO:0043169//GO:0043648//GO:0044424	nr +
Unigene34080_All	2262	12.93	11.22	6.10	10.79	13.64	12.96	8.00	27.03	35.15	-2.04E-01	5.20E-02		-1.08E+00	1.19E-23	Down	3.38E-01	2.51E-04		2.64E-01	9.89E-03		1.76E+00	8.12E-128	Up	2.14E+00	1.64E-219	Up	Unigene34080_All//gi|81185071|gb|AAF73006.1|AF262997_1|/0.00E+00//NADP-dependent malic protein [Ricinus communis]	Unigene34080_All//0.00E+00//AT5G11670| ATNADP-ME2 (NADP-malic enzyme 2); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor	Unigene34080_All//0.00E+00//TC133072		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0004470//GO:0043169//GO:0043648//GO:0044424	nr -
Unigene34083_All	3655	10.51	36.22	27.19	34.17	35.63	52.18	29.36	9.35	17.73	1.79E+00	2.97E-230	Up	1.37E+00	5.61E-115	Up	6.05E-02	2.60E-01		6.11E-01	2.77E-63		-1.65E+00	2.10E-205	Down	-7.27E-01	6.30E-57		Unigene34083_All//gi|10086489|gb|AAG12549.1|AC007797_9|/0.00E+00//Unknown Protein [Arabidopsis thaliana]	Unigene34083_All//0.00E+00//AT1G19835| unknown protein	Unigene34083_All//0.00E+00//TC150429			GO:0016020	nr -
Unigene34084_All	3409	19.14	5.02	12.43	45.37	33.73	17.82	36.61	21.28	16.66	-1.93E+00	3.80E-127	Down	-6.22E-01	1.73E-20		-4.28E-01	1.32E-30		-1.35E+00	4.53E-195	Down	-7.83E-01	6.41E-73		-1.14E+00	4.72E-139	Down	Unigene34084_All//gi|20805911|gb|AAM28891.1|/0.00E+00//NADPH oxidase [Nicotiana tabacum] >gi|125971776|gb|ABN58915.1| rbohD [Nicotiana tabacum]	Unigene34084_All//0.00E+00//AT5G51060| RHD2 (ROOT HAIR DEFECTIVE 2); NAD(P)H oxidase	Unigene34084_All//0.00E+00//CO112621		ko04626|Plant-pathogen interaction	GO:0006950//GO:0008152//GO:0009913//GO:0010033//GO:0016021//GO:0016209//GO:0030554//GO:0046914//GO:0050664	nr +
Unigene34086_All	1836	1.31	0.69	1.60	2.79	5.33	3.79	9.28	2.37	6.77	-9.26E-01	2.42E-02		2.83E-01	4.68E-01		9.31E-01	8.91E-08		4.39E-01	5.52E-02		-1.97E+00	3.18E-42	Down	-4.55E-01	9.89E-05		Unigene34086_All//gi|4559292|gb|AAD22970.1|AF124148_1|/0.00E+00//trehalase 1 GMTRE1 [Glycine max]	Unigene34086_All//0.00E+00//AT4G24040| TRE1 (TREHALASE 1); alpha,alpha-trehalase/ trehalase	Unigene34086_All//0.00E+00//gi|109832479|gb|DW231038.1|DW231038		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0015927	nr +
Unigene34087_All	2183	11.91	10.61	7.93	10.34	9.80	24.50	53.49	100.73	109.41	-1.67E-01	1.44E-01		-5.87E-01	8.67E-08		-7.76E-02	5.83E-01		1.24E+00	5.98E-59	Up	9.13E-01	4.94E-166		1.03E+00	9.05E-226	Up	Unigene34087_All//gi|4559292|gb|AAD22970.1|AF124148_1|/0.00E+00//trehalase 1 GMTRE1 [Glycine max]	Unigene34087_All//0.00E+00//AT4G24040| TRE1 (TREHALASE 1); alpha,alpha-trehalase/ trehalase	Unigene34087_All//0.00E+00//TC146289		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0015927	nr -
Unigene3409_All	1506	3.72	0.77	0.53	2.88	1.88	1.92	21.70	3.66	13.25	-2.26E+00	5.75E-14	Down	-2.81E+00	7.45E-17	Down	-6.18E-01	2.65E-02		-5.84E-01	4.66E-02		-2.57E+00	4.62E-111	Down	-7.12E-01	2.50E-17											
Unigene34090_All	3683	1.32	1.77	2.07	3.22	3.32	2.78	3.09	2.26	1.37	4.26E-01	6.89E-02		6.46E-01	3.22E-03		4.42E-02	8.24E-01		-2.10E-01	2.55E-01		-4.52E-01	2.79E-03		-1.17E+00	4.58E-14	Down	Unigene34090_All//gi|224102795|ref|XP_002312804.1|/0.00E+00//cholesterol transport protein [Populus trichocarpa] >gi|222849212|gb|EEE86759.1| cholesterol transport protein [Populus trichocarpa]	Unigene34090_All//0.00E+00//AT4G38350| hedgehog receptor	Unigene34090_All//0.00E+00//CO120437			GO:0004888//GO:0015918//GO:0031224//GO:0043231	nr +
Unigene34091_All	3363	3.83	2.91	4.09	21.72	17.36	12.56	7.69	1.48	1.74	-3.96E-01	1.26E-02		9.41E-02	6.18E-01		-3.23E-01	7.25E-09		-7.90E-01	1.33E-38		-2.38E+00	1.17E-80	Down	-2.14E+00	3.31E-73	Down	Unigene34091_All//gi|15240762|ref|NP_201548.1|//0.00E+00//formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] >gi|75171125|sp|Q9FJX6.1|FH6_ARATH RecName: Full=Formin-like protein 6; Short=AtFH6; Short=AtFORMIN-6; Flags: Precursor >gi|9757868|dbj|BAB08455.1| formin-like protein [Arabidopsis thaliana] >gi|37694426|gb|AAQ99143.1| formin-like protein AtFH6 [Arabidopsis thaliana]	Unigene34091_All//0.00E+00//AT5G67470| formin homology 2 domain-containing protein / FH2 domain-containing protein	Unigene34091_All//0.00E+00//gi|164286427|gb|ES793847.1|ES793847		ko03040|Spliceosome	GO:0016043	nr +
Unigene34093_All	582	0.36	0.87	0.64	0.68	0.47	0.93	2.54	6.25	2.05	1.28E+00	2.31E-01		8.33E-01	5.16E-01		-5.33E-01	6.16E-01		4.44E-01	6.78E-01		1.30E+00	1.31E-05	Up	-3.08E-01	5.38E-01		Unigene34093_All//gi|115482938|ref|NP_001065062.1|/5.00E-111//Os10g0516300|Oryza sativa Japonica Group] >gi|113639671|dbj|BAF26976.1| Os10g0516300 [Oryza sativa Japonica Group]	Unigene34093_All//1.00E-11//AT2G43400| ETFQO (electron-transfer flavoprotein:ubiquinone oxidoreductase); catalytic/ electron carrier/ electron-transferring-flavoprotein dehydrogenase	Unigene34093_All//4.00E-110//gi|48811100|gb|CO112413.1|CO112413				nr -
Unigene34094_All	1730	3.45	12.33	5.69	5.27	6.41	7.00	13.22	22.15	19.94	1.84E+00	4.32E-39	Up	7.24E-01	1.30E-04		2.83E-01	1.14E-01		4.09E-01	1.29E-02		7.45E-01	4.10E-21		5.93E-01	2.16E-13		Unigene34094_All//gi|15224277|ref|NP_181868.1|//0.00E+00//ETFQO (electron-transfer flavoprotein:ubiquinone oxidoreductase); catalytic/ electron carrier/ electron-transferring-flavoprotein dehydrogenase [Arabidopsis thaliana]	Unigene34094_All//0.00E+00//AT2G43400| ETFQO (electron-transfer flavoprotein:ubiquinone oxidoreductase); catalytic/ electron carrier/ electron-transferring-flavoprotein dehydrogenase	Unigene34094_All//0.00E+00//TC140211			GO:0006551//GO:0009642//GO:0016649//GO:0031967//GO:0043231	nr -
Unigene34095_All	1135	0.60	2.95	0.70	2.11	2.09	2.03	5.07	9.35	7.72	2.30E+00	1.09E-08	Up	2.32E-01	7.49E-01		-9.10E-03	9.69E-01		-5.39E-02	9.13E-01		8.85E-01	2.26E-08		6.08E-01	3.25E-04		Unigene34095_All//gi|297824323|ref|NP_002880044.1|/3.00E-31//electron-transfer flavoprotein:ubiquinone oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297325883|gb|EFH56303.1| electron-transfer flavoprotein:ubiquinone oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene34095_All//5.00E-32//AT2G43400| ETFQO (electron-transfer flavoprotein:ubiquinone oxidoreductase); catalytic/ electron carrier/ electron-transferring-flavoprotein dehydrogenase	Unigene34095_All//0.00E+00//CO123954			GO:0006551//GO:0009642//GO:0016649//GO:0043231	nr -
Unigene34099_All	2383	7.16	19.60	12.74	7.50	10.38	17.93	14.42	28.90	44.79	1.45E+00	8.34E-61	Up	8.32E-01	5.50E-16		4.67E-01	4.97E-06		1.26E+00	7.04E-48	Up	1.00E+00	2.84E-61	Up	1.63E+00	3.46E-205	Up	Unigene34099_All//gi|30682074|ref|NP_179923.2|/0.00E+00//NAPRT2 (NICOTINATE PHOSPHORIBOSYLTRANSFERASE 2); nicotinate phosphoribosyltransferase [Arabidopsis thaliana]	Unigene34099_All//0.00E+00//AT2G23420| NAPRT2 (NICOTINATE PHOSPHORIBOSYLTRANSFERASE 2); nicotinate phosphoribosyltransferase	Unigene34099_All//0.00E+00//TC150024		ko00760|Nicotinate and nicotinamide metabolism	GO:0016763//GO:0019357//GO:0019359	nr +
Unigene341_All	758	5.52	8.76	7.31	7.29	8.59	7.69	16.68	20.62	35.90	6.65E-01	3.58E-03		4.04E-01	1.41E-01		2.35E-01	3.67E-01		7.54E-02	7.87E-01		3.06E-01	1.83E-02		1.11E+00	1.62E-29	Up	Unigene341_All//gi|186511674|ref|NP_192917.2|//1.00E-71//hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana]	Unigene341_All//1.00E-68//AT4G11800| hydrolase/ protein serine/threonine phosphatase	Unigene341_All//0.00E+00//TC156896		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene3410_All	1816	13.94	33.93	20.53	22.63	22.81	25.64	52.94	87.96	135.07	1.28E+00	3.24E-66	Up	5.58E-01	5.69E-10		1.15E-02	9.19E-01		1.80E-01	2.86E-02		7.33E-01	5.29E-83		1.35E+00	0.00E+00	Up	Unigene3410_All//gi|18000072|gb|AAL54887.1|AF092916_1|/0.00E+00//cytochrome P450-dependent fatty acid hydroxylase [Nicotiana tabacum]	Unigene3410_All//1.00E-125//AT5G63450| CYP94B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene3410_All//0.00E+00//TC134800		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506//GO:0008152	nr +
Unigene34100_All	355	0.00	2.71	0.00	0.42	0.58	0.25	3.33	4.12	2.58	1.14E+01	1.38E-05	Up	null	null		4.67E-01	8.25E-01		-7.27E-01	7.15E-01		3.05E-01	5.74E-01		-3.70E-01	5.03E-01		Unigene34100_All//gi|225436486|ref|XP_002275903.1|/2.00E-51//PREDICTED: similar to VPS24.1 [Vitis vinifera]	Unigene34100_All//5.00E-52//AT5G22950| VPS24.1	Unigene34100_All//5.00E-170//TC166165		ko04144|Endocytosis	GO:0006810//GO:0010008	nr -
Unigene34101_All	1012	0.83	1.50	2.42	5.41	4.97	5.36	3.47	3.72	2.09	8.61E-01	1.12E-01		1.55E+00	5.13E-04	Up	-1.24E-01	6.66E-01		-1.59E-02	9.45E-01		1.00E-01	7.41E-01		-7.33E-01	9.49E-03		Unigene34101_All//gi|297808285|ref|XP_002872026.1|/3.00E-29//SNF7 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317863|gb|EFH48285.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34101_All//3.00E-11//AT5G22950| VPS24.1	Unigene34101_All//0.00E+00//TC172992		ko04144|Endocytosis	GO:0006810//GO:0010008	nr -
Unigene34102_All	920	1.31	2.09	0.58	4.49	3.26	6.19	5.24	3.00	2.21	6.78E-01	1.45E-01		-1.18E+00	7.58E-02		-4.65E-01	1.18E-01		4.61E-01	7.27E-02		-8.05E-01	9.66E-04		-1.25E+00	4.59E-07	Down	Unigene34102_All//gi|297808285|ref|XP_002872026.1|/1.00E-102//SNF7 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317863|gb|EFH48285.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34102_All//4.00E-80//AT5G22950| VPS24.1	Unigene34102_All//0.00E+00//TC172992		ko04144|Endocytosis	GO:0006810	nr -
Unigene34103_All	1321	4.16	11.93	4.76	11.54	13.27	12.48	12.71	13.04	12.97	1.52E+00	2.37E-22	Up	1.94E-01	4.56E-01		2.02E-01	1.61E-01		1.13E-01	4.98E-01		3.69E-02	7.93E-01		2.94E-02	8.31E-01		Unigene34103_All//gi|297808285|ref|XP_002872026.1|/1.00E-103//SNF7 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317863|gb|EFH48285.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34103_All//4.00E-86//AT5G22950| VPS24.1	Unigene34103_All//0.00E+00//TC166165		ko04144|Endocytosis	GO:0006810	nr +
Unigene34104_All	763	6.65	2.79	4.33	7.83	9.61	7.87	10.14	8.76	6.32	-1.25E+00	5.39E-06	Down	-6.20E-01	2.58E-02		2.95E-01	2.03E-01		7.00E-03	9.78E-01		-2.10E-01	3.15E-01		-6.83E-01	1.63E-04		Unigene34104_All//gi|297816818|ref|XP_002876292.1|/4.00E-24//map kinase phosphatase [Arabidopsis lyrata subsp. lyrata] >gi|297322130|gb|EFH52551.1| map kinase phosphatase [Arabidopsis lyrata subsp. lyrata]	Unigene34104_All//8.00E-24//AT3G55270| MKP1 (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 1); MAP kinase tyrosine/serine/threonine phosphatase	Unigene34104_All//2.00E-112//ES847422			GO:0006796//GO:0006970//GO:0008138//GO:0009411	nr -
Unigene34109_All	2316	4.25	4.42	3.75	8.56	8.22	6.34	6.37	2.54	4.16	5.74E-02	7.61E-01		-1.81E-01	4.03E-01		-5.82E-02	7.14E-01		-4.34E-01	3.57E-04		-1.32E+00	4.92E-21	Down	-6.14E-01	1.28E-06		Unigene34109_All//gi|224088846|ref|XP_002308566.1|/0.00E+00//potassium efflux antiporter [Populus trichocarpa] >gi|222854542|gb|EEE92089.1| potassium efflux antiporter [Populus trichocarpa]	Unigene34109_All//0.00E+00//AT2G19600| ATKEA4; potassium ion transmembrane transporter/ potassium:hydrogen antiporter	Unigene34109_All//0.00E+00//TC176577			GO:0005451//GO:0030001//GO:0031224//GO:0043231//GO:0046873	nr +
Unigene34112_All	253	2.27	3.40	1.47	0.59	0.27	1.25	2.84	19.66	5.20	5.82E-01	4.27E-01		-6.27E-01	5.27E-01		-1.12E+00	5.83E-01		1.08E+00	4.76E-01		2.79E+00	5.29E-19	Up	8.71E-01	8.59E-02		Unigene34112_All//gi|145357530|ref|NP_195815.3|/3.00E-36//ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Unigene34112_All//1.00E-37//AT5G01950| ATP binding / kinase/ protein serine/threonine kinase	Unigene34112_All//6.00E-141//gi|31072574|gb|CA992853.1|CA992853		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0032559	nr -
Unigene34113_All	3406	13.92	30.02	26.94	5.79	5.16	5.44	31.06	83.24	97.78	1.11E+00	4.73E-87	Up	9.53E-01	2.37E-59		-1.68E-01	2.23E-01		-9.13E-02	5.61E-01		1.42E+00	0.00E+00	Up	1.65E+00	0.00E+00	Up	Unigene34113_All//gi|145357530|ref|NP_195815.3|/0.00E+00//ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Unigene34113_All//0.00E+00//AT5G01950| ATP binding / kinase/ protein serine/threonine kinase	Unigene34113_All//0.00E+00//gi|31072574|gb|CA992853.1|CA992853		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene34116_All	2125	4.73	1.29	3.71	20.77	17.02	19.21	25.05	28.44	10.44	-1.88E+00	2.13E-19	Down	-3.50E-01	7.20E-02		-2.88E-01	1.34E-04		-1.12E-01	2.29E-01		1.83E-01	3.45E-03		-1.26E+00	1.41E-70	Down	Unigene34116_All//gi|149938954|gb|ABR45722.1|/0.00E+00//G6PD1 [Actinidia chinensis]	Unigene34116_All//0.00E+00//AT5G40760| G6PD6 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 6); glucose-6-phosphate dehydrogenase	Unigene34116_All//0.00E+00//TC159471		ko00480|Glutathione metabolism//ko00030|Pentose phosphate pathway	GO:0006098//GO:0016616//GO:0044444	nr +
Unigene34118_All	3954	5.27	4.59	2.42	13.46	16.36	13.31	19.51	3.85	6.30	-1.99E-01	1.20E-01		-1.12E+00	7.33E-18	Down	2.82E-01	3.64E-06		-1.60E-02	8.68E-01		-2.34E+00	5.02E-235	Down	-1.63E+00	9.47E-150	Down	Unigene34118_All//gi|15217853|ref|NP_171773.1|/0.00E+00//ATCSLD5; 1,4-beta-D-xylan synthase/ cellulose synthase [Arabidopsis thaliana] >gi|75207418|sp|Q9SR99.1|CSLD5_ARATH RecName: Full=Cellulose synthase-like protein D5; Short=AtCslD5 >gi|6056428|gb|AAF02892.1|AC009525_26 Very similar to cellulose synthase catalytic subunit [Arabidopsis thaliana]	Unigene34118_All//0.00E+00//AT1G02730| ATCSLD5; 1,4-beta-D-xylan synthase/ cellulose synthase	Unigene34118_All//0.00E+00//gi|78349123|gb|DT569397.1|DT569397		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0006970//GO:0009250//GO:0016759//GO:0031224//GO:0042546//GO:0043231//GO:0045229//GO:0048513	nr -
Unigene3412_All	2239	18.25	9.28	10.01	11.97	14.72	9.70	15.88	2.56	7.54	-9.76E-01	8.73E-29		-8.66E-01	9.09E-23		2.98E-01	9.40E-04		-3.03E-01	4.11E-03		-2.63E+00	2.21E-124	Down	-1.07E+00	7.87E-37	Down	Unigene3412_All//gi|29029998|gb|AAO64878.1|/9.00E-96//At5g37010 [Arabidopsis thaliana]	Unigene3412_All//2.00E-61//AT5G37010| unknown protein	Unigene3412_All//0.00E+00//TC153218		ko03040|Spliceosome		nr -

Unigene34121_All	499	0.31	0.00	0.11	3.49	2.07	0.91	12.29	4.77	10.30	-8.30E+00	2.15E-01		-1.56E+00	5.33E-01		-7.55E-01	1.15E-01		-1.95E+00	2.67E-04	Down	-1.36E+00	1.37E-09	Down	-2.55E-01	2.47E-01		Unigene34121_All//gi|224056655|ref|XP_002298957.1|//5.00E-31//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222846215|gb|EEE83762.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene34121_All//1.00E-13//AT4G27190| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction	GO:0006950//GO:0012501//GO:0016787//GO:0032559	nr +
Unigene34124_All	5675	49.21	42.12	50.17	10.56	10.90	9.84	13.84	6.77	8.84	-2.25E-01	6.09E-14		2.78E-02	4.58E-01		4.63E-02	5.92E-01		-1.01E-01	2.00E-01		-1.03E+00	3.05E-73	Down	-6.47E-01	2.66E-34		Unigene34124_All//gi|18414469|ref|NP_568134.1|//0.00E+00//GLU1 (GLUTAMATE SYNTHASE 1); glutamate synthase (ferredoxin) [Arabidopsis thaliana]	Unigene34124_All//0.00E+00//AT5G04140| GLU1 (GLUTAMATE SYNTHASE 1); glutamate synthase (ferredoxin)	Unigene34124_All//0.00E+00//TC138643		ko00910|Nitrogen metabolism	GO:0005576//GO:0006536//GO:0009314//GO:0009526//GO:0009532//GO:0015930//GO:0031323//GO:0043094//GO:0043169//GO:0051536	nr +
Unigene34125_All	743	0.49	0.61	0.86	1.34	0.56	0.24	3.30	6.41	7.29	3.17E-01	7.44E-01		8.03E-01	3.88E-01		-1.27E+00	5.75E-02		-2.46E+00	2.07E-03		9.58E-01	1.10E-04		1.14E+00	6.83E-07	Up			Unigene34125_All//2.00E-180//TC179380				ESTscan +
Unigene34126_All	434	4.46	4.79	5.15	8.61	6.66	9.47	2.34	6.26	7.53	1.02E-01	8.15E-01		2.08E-01	6.21E-01		-3.69E-01	2.65E-01		1.38E-01	7.00E-01		1.42E+00	6.39E-05	Up	1.69E+00	2.30E-07	Up			Unigene34126_All//2.00E-86//gi|164254594|gb|ES814336.1|ES814336				ESTscan +
Unigene3413_All	1496	2.27	3.73	1.07	5.26	5.57	7.82	1.41	11.87	5.41	7.13E-01	4.69E-03		-1.09E+00	2.10E-03		8.24E-02	7.61E-01		5.72E-01	4.61E-04		3.07E+00	5.62E-73	Up	1.94E+00	2.30E-20	Up	Unigene3413_All//gi|297835206|ref|XP_002885485.1|//4.00E-24//VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331325|gb|EFH61744.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene3413_All//0.00E+00//TC175987				nr -
Unigene34130_All	2584	11.32	25.43	19.89	26.28	32.90	25.33	9.72	9.59	9.31	1.17E+00	5.48E-61	Up	8.13E-01	1.12E-25		3.25E-01	3.81E-10		-5.31E-02	5.12E-01		-1.91E-02	8.79E-01		-6.17E-02	6.07E-01		Unigene34130_All//gi|219291103|gb|ACL13986.1|//0.00E+00//At1g22460 [Arabidopsis thaliana]	Unigene34130_All//0.00E+00//AT1G22460| unknown protein	Unigene34130_All//0.00E+00//TC168347			GO:0043231	nr +
Unigene34132_All	1056	3.37	7.29	5.65	4.01	11.77	12.75	15.53	22.16	15.69	1.11E+00	2.64E-07	Up	7.45E-01	3.12E-03		1.55E+00	3.98E-21	Up	1.67E+00	3.00E-23	Up	5.13E-01	3.39E-07		1.47E-02	9.35E-01		Unigene34132_All//gi|224138778|ref|XP_002322899.1|//1.00E-102//serine/threonine protein kinase 2, CTR2 [Populus trichocarpa] >gi|222867529|gb|EEF04660.1| serine/threonine protein kinase 2, CTR2 [Populus trichocarpa]	Unigene34132_All//2.00E-98//AT5G03730| CTR1 (CONSTITUTIVE TRIPLE RESPONSE 1); kinase/ protein binding / protein serine/threonine kinase/ protein serine/threonine/tyrosine kinase	Unigene34132_All//0.00E+00//TC167850			GO:0004672//GO:0006464//GO:0032559	nr +
Unigene34133_All	2662	8.00	16.81	14.28	15.14	32.79	48.85	15.12	19.80	20.61	1.07E+00	2.15E-36	Up	8.36E-01	4.62E-20		1.12E+00	4.50E-89	Up	1.69E+00	2.99E-225	Up	3.89E-01	1.90E-09		4.47E-01	9.02E-13		Unigene34133_All//gi|237857405|gb|ACR23642.1|//0.00E+00//serine/threonine protein kinase [Prunus persica]	Unigene34133_All//0.00E+00//AT5G03730| CTR1 (CONSTITUTIVE TRIPLE RESPONSE 1); kinase/ protein binding / protein serine/threonine kinase/ protein serine/threonine/tyrosine kinase	Unigene34133_All//0.00E+00//TC149380			GO:0000166//GO:0004674//GO:0009685//GO:0009756//GO:0009873//GO:0017145//GO:0031090//GO:0034285//GO:0048506	nr -
Unigene34136_All	524	19.37	15.96	23.27	9.70	9.33	26.55	1.13	0.32	0.91	-2.80E-01	1.36E-01		2.65E-01	1.37E-01		-5.54E-02	8.40E-01		1.45E+00	9.64E-20	Up	-1.82E+00	4.71E-02		-3.08E-01	6.78E-01				Unigene34136_All//7.00E-124//TC148006				
Unigene34138_All	1634	31.73	22.23	20.43	13.29	15.34	17.27	2.56	1.07	1.02	-5.13E-01	2.57E-12		-6.35E-01	5.44E-17		2.07E-01	7.02E-02		3.78E-01	1.66E-04		-1.25E+00	4.57E-06	Down	-1.32E+00	9.06E-07	Down	Unigene34138_All//gi|280967729|gb|ACZ98535.1|//1.00E-180//transmembrane domain protein [Malus x domestica]	Unigene34138_All//2.00E-163//AT2G26900| bile acid:sodium symporter family protein	Unigene34138_All//0.00E+00//TC135824			GO:0005343//GO:0006820//GO:0030001//GO:0031224	nr -
Unigene3414_All	1878	9.95	24.12	12.65	11.11	20.28	17.00	12.09	13.53	23.67	1.28E+00	1.41E-48	Up	3.47E-01	3.26E-03		8.68E-01	6.67E-26		6.13E-01	3.85E-11		1.63E-01	1.28E-01		9.70E-01	1.33E-38		Unigene3414_All//gi|117958758|gb|AB539684.1|//3.00E-38//At4g32030 [Arabidopsis thaliana]	Unigene3414_All//4.00E-16//AT4G32030| unknown protein	Unigene3414_All//0.00E+00//TC177193				nr +
Unigene34142_All	2012	3.20	2.92	2.99	5.74	5.68	5.34	7.27	3.32	4.69	-1.31E-01	6.23E-01		-9.69E-02	7.01E-01		-1.56E-02	9.42E-01		-1.05E-01	6.31E-01		-1.13E+00	2.04E-16	Down	-6.32E-01	7.29E-07		Unigene34142_All//gi|51536496|gb|AAU05486.1|//1.00E-160//At1g33360 [Arabidopsis thaliana] >gi|53850505|gb|AAU95429.1| At1g33360 [Arabidopsis thaliana]	Unigene34142_All//5.00E-155//AT1G33360| ATP-dependent Clp protease ATP-binding subunit ClpX, putative	Unigene34142_All//0.00E+00//gi|78328780|gb|DT549054.1|DT549054			GO:0000166//GO:0016787	nr +
Unigene34145_All	1510	23.63	64.73	41.65	28.90	40.57	53.45	59.02	102.44	99.65	1.45E+00	1.42E-126	Up	8.18E-01	1.33E-31		4.89E-01	2.15E-15		8.87E-01	2.54E-51		7.95E-01	1.19E-92		7.56E-01	1.95E-84		Unigene34145_All//gi|112005099|gb|ABH85388.1|//0.00E+00//isovaleryl-CoA dehydrogenase [Beta vulgaris]	Unigene34145_All//0.00E+00//AT3G45300| IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase	Unigene34145_All//0.00E+00//TC134737	ko00280|Valine, leucine and isoleucine degradation	GO:0003995//GO:0008152//GO:0031980//GO:0032559	nr +
Unigene34146_All	1596	0.85	3.24	1.10	1.06	2.57	2.21	4.37	9.06	10.93	1.93E+00	1.37E-10	Up	3.69E-01	4.72E-01		1.27E+00	1.62E-05	Up	1.06E+00	1.36E-03		1.05E+00	1.55E-14	Up	1.32E+00	3.18E-25	Up	Unigene34146_All//gi|15230664|ref|NP_190116.1|//1.00E-19//IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase [Arabidopsis thaliana] >gi|110816334|sp|Q9SWG0.2|IVD_ARATH RecName: Full=Isovaleryl-CoA dehydrogenase, mitochondrial; Short=IVD; Flags: Precursor >gi|4995051|emb|CAA73227.1| Isovaleryl-CoA Dehydrogenase [Arabidopsis thaliana] >gi|6967096|emb|CAB72479.1| isovaleryl-CoA-dehydrogenase precursor (IVD) [Arabidopsis thaliana] >gi|110738147|dbj|BAF01005.1| isovaleryl-CoA-dehydrogenase precursor [Arabidopsis thaliana]	Unigene34146_All//8.00E-20//AT3G45300| IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase	Unigene34146_All//2.00E-105//ES822782	ko00280|Valine, leucine and isoleucine degradation	GO:0003995//GO:0008152//GO:0031980//GO:0032559	nr +
Unigene34151_All	3011	7.21	2.96	5.16	12.06	11.09	15.01	18.51	9.12	11.11	-1.28E+00	6.40E-24	Down	-4.82E-01	7.54E-05		-1.21E-01	2.29E-01		3.16E-01	4.72E-05		-1.02E+00	2.88E-51	Down	-7.36E-01	1.36E-30		Unigene34151_All//gi|13605690|gb|AK32838.1|AF361826_1|0.00E+00//At1g42440/F7F22_7 [Arabidopsis thaliana] >gi|22137072|gb|AAM91381.1| At1g42440/F7F22_7 [Arabidopsis thaliana]	Unigene34151_All//2.00E-176//AT1G42440| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ribosome biogenesis; LOCATED IN: nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: AARP2CN (InterPro:IPR012948), Protein of unknown function DUF663 (InterPro:IPR007034); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06720.1); Has 2447 Blast hits to 1812 proteins in 205 species: Archae - 0; Bacteria - 115; Metazoa - 903; Fungi - 423; Plants - 100; Viruses - 53; Other Eukaryotes - 853 (source: NCBI BLink).	Unigene34151_All//0.00E+00//ES810231			GO:0022613//GO:0043231	nr +
Unigene34153_All	3127	2.63	1.17	1.74	3.65	4.15	4.03	2.11	1.76	1.90	-1.17E+00	2.38E-08	Down	-5.97E-01	4.59E-03		1.87E-01	2.98E-01		1.44E-01	4.56E-01		-2.58E-01	2.43E-01		-1.52E-01	4.97E-01		Unigene34153_All//gi|13605690|gb|AK32838.1|AF361826_1|0.00E+00//At1g42440/F7F22_7 [Arabidopsis thaliana] >gi|22137072|gb|AAM91381.1| At1g42440/F7F22_7 [Arabidopsis thaliana]	Unigene34153_All//0.00E+00//AT1G42440| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ribosome biogenesis; LOCATED IN: nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: AARP2CN (InterPro:IPR012948), Protein of unknown function DUF663 (InterPro:IPR007034); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06720.1); Has 2447 Blast hits to 1812 proteins in 205 species: Archae - 0; Bacteria - 115; Metazoa - 903; Fungi - 423; Plants - 100; Viruses - 53; Other Eukaryotes - 853 (source: NCBI BLink).	Unigene34153_All//0.00E+00//ES810231			GO:0022613//GO:0043231	nr +
Unigene34155_All	2369	10.51	9.71	8.88	37.32	37.76	23.91	34.03	14.71	17.79	-1.15E-01	3.64E-01		-2.44E-01	4.07E-02		1.69E-02	8.14E-01		-6.43E-01	1.34E-32		-1.21E+00	7.11E-97	Down	-9.36E-01	8.94E-66		Unigene34155_All//gi|115475401|ref|NP_001061297.1|//0.00E+00//Os08g0230200 [Oryza sativa Japonica Group] >gi|113623266|dbj|BAF23211.1| Os08g0230200 [Oryza sativa Japonica Group]	Unigene34155_All//0.00E+00//AT1G16860| merozoite surface protein-related	Unigene34155_All//0.00E+00//TC175438			GO:0016020	nr -
Unigene34156_All	892	0.70	0.00	0.60	4.69	2.55	0.51	17.16	53.23	11.03	-9.46E+00	7.91E-04	Down	-2.38E-01	7.75E-01		-8.81E-01	1.50E-03		-3.21E+00	2.48E-16	Down	1.63E+00	1.02E-89	Up	-6.37E-01	3.08E-07		Unigene34156_All//gi|225452634|ref|XP_002276408.1|//1.00E-137//PREDICTED: similar to ABC transporter family protein [Vitis vinifera]	Unigene34156_All//1.00E-116//AT3G28345| ABC transporter family protein		ko02010|ABC transporters		nr -
Unigene34157_All	1155	1.13	0.26	0.41	5.56	2.00	0.63	3.66	0.83	0.21	-2.11E+00	1.46E-03		-1.45E+00	2.42E-02		-1.48E+00	4.86E-11	Down	-3.15E+00	1.84E-24	Down	-2.14E+00	3.68E-12	Down	-4.14E+00	1.28E-23	Down	Unigene34157_All//gi|225452634|ref|XP_002276408.1|//1.00E-148//PREDICTED: similar to ABC transporter family protein [Vitis vinifera]	Unigene34157_All//3.00E-126//AT3G28380| PGP17 (P-GLYCOPROTEIN 17); ATP binding / ATPase/ ATPase, coupled to transmembrane movement of substances / nucleoside-triphosphatase/ nucleotide binding	Unigene34157_All//0.00E+00//TC154840	ko02010|ABC transporters		nr -
Unigene34158_All	3841	0.59	0.11	0.06	5.65	3.04	0.82	52.44	178.58	34.73	-2.47E+00	1.32E-06	Down	-3.40E+00	2.44E-08	Down	-8.96E-01	2.34E-16		-2.78E+00	4.31E-72	Down	1.77E+00	0.00E+00	Up	-5.95E-01	1.73E-74		Unigene34158_All//gi|225452634|ref|XP_002276408.1|//0.00E+00//PREDICTED: similar to ABC transporter family protein [Vitis vinifera]	Unigene34158_All//0.00E+00//AT3G28345| ABC transporter family protein	Unigene34158_All//5.00E-123//gi|109884293|gb|DW513263.1|DW513263	ko02010|ABC transporters	GO:0006810//GO:0015405//GO:0017111//GO:0031224//GO:0032559	nr -
Unigene34159_All	688	3.50	1.69	2.24	2.39	2.95	0.20	1.78	1.28	1.10	-1.05E+00	1.13E-02		-6.40E-01	1.37E-01		3.06E-01	5.48E-01		-3.60E+00	2.61E-07	Down	-4.82E-01	4.08E-01		-6.96E-01	1.86E-01		Unigene34159_All//gi|77553129|gb|AB95925.1|//2.00E-88//Amidase family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene34159_All//6.00E-57//AT5G64440| AtFAAH (Arabidopsis thaliana fatty acid amide hydrolase); N-(long-chain-acyl)ethanolamine deacylase/ amidase	Unigene34159_All//0.00E+00//TC159857	ko00970|Aminoacyl-tRNA biosynthesis	GO:0016879	nr -
Unigene34160_All	1459	14.09	6.32	11.28	6.93	7.01	4.43	8.66	6.47	8.22	-1.16E+00	2.28E-19	Down	-3.22E-01	1.28E-02		1.63E-02	9.56E-01		-6.47E-01	2.33E-04		-4.20E-01	3.22E-03		-7.62E-02	6.37E-01		Unigene34160_All//gi|77553129|gb|AB95925.1|//1.00E-132//Amidase family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene34160_All//6.00E-78//AT5G64440| AtFAAH (Arabidopsis thaliana fatty acid amide hydrolase); N-(long-chain-acyl)ethanolamine deacylase/ amidase	Unigene34160_All//0.00E+00//TC169022	ko00970|Aminoacyl-tRNA biosynthesis		nr +
Unigene34161_All	2195	5.84	2.08	4.25	1.77	2.53	1.89	4.45	2.48	3.39	-1.49E+00	6.39E-18	Down	-4.60E-01	5.23E-03		5.13E-01	4.18E-02		9.68E-02	7.65E-01		-8.46E-01	2.88E-07		-3.91E-01	1.51E-02		Unigene34161_All//gi|77553129|gb|AB95925.1|//0.00E+00//Amidase family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene34161_All//2.00E-72//AT5G64440| AtFAAH (Arabidopsis thaliana fatty acid amide hydrolase); N-(long-chain-acyl)ethanolamine deacylase/ amidase	Unigene34161_All//0.00E+00//TC169022	ko00970|Aminoacyl-tRNA biosynthesis	GO:0016879	nr +
Unigene34162_All	1503	8.49	2.53	2.27	12.10	8.09	6.31	28.16	4.25	6.89	-1.75E+00	2.93E-22	Down	-1.91E+00	6.18E-24	Down	-5.81E-01	1.06E-06		-9.39E-01	2.84E-13		-2.73E+00	1.23E-153	Down	-2.03E+00	2.96E-111	Down	Unigene34162_All//gi|269791618|gb|ACN78877.2|//1.00E-177//minichromosome maintenance 2 protein [Pisum sativum]	Unigene34162_All//1.00E-158//AT1G44900| ATP binding / DNA binding / DNA-dependent ATPase	Unigene34162_All//0.00E+00//TC151386	ko03030|DNA replication		nr +
Unigene34163_All	495	2.85	0.10	0.86	3.32	4.31	2.55	1.28	0.00	1.77	-4.80E+00	4.49E-07	Down	-1.73E+00	6.13E-03		3.77E-01	4.40E-01		-3.78E-01	4.90E-01		-1.03E+01	1.23E-04	Down	4.67E-01	4.76E-01		Unigene34163_All//gi|27529848|dbj|BAC53939.1|//2.00E-74//MCM protein-like protein [Nicotiana tabacum]	Unigene34163_All//2.00E-72//AT1G44900| ATP binding / DNA binding / DNA-dependent ATPase	Unigene34163_All//1.00E-174//C0071013	ko03030|DNA replication	GO:0003676//GO:0006259//GO:0016462//GO:0032559//GO:0043231	nr -
Unigene34164_All	3291	3.72	0.79	0.97	5.80	5.43	3.35	10.18	1.27	4.15	-2.24E+00	1.92E-29	Down	-1.94E+00	1.72E-23	Down	-9.43E-02	5.61E-01		-7.92E-01	1.49E-10		-3.00E+00	1.56E-134	Down	-1.29E+00	2.10E-46	Down	Unigene34164_All//gi|269791618|gb|ACN78877.2|//0.00E+00//minichromosome maintenance 2 protein [Pisum sativum]	Unigene34164_All//0.00E+00//AT1G44900| ATP binding / DNA binding / DNA-dependent ATPase	Unigene34164_All//0.00E+00//TC151386	ko03030|DNA replication	GO:0003676//GO:0006259//GO:0016462//GO:0032559//GO:0043231	nr +

Unigene34165_All	2792	55.53	33.03	40.68	71.31	80.67	144.48	21.34	10.90	15.11	-7.49E-01	1.23E-68		-4.49E-01	9.84E-27		1.78E-01	1.27E-08		1.02E+00	0.00E+00	Up	-9.69E-01	2.65E-50		-4.98E-01	1.11E-16		Unigene34165_All//gi|67003905|gb|AA04496.2|//0.00E+00//endo-1,4-beta-glucanase [Gossypium hirsutum]	Unigene34165_All//0.00E+00//AT1G64390| AtGH9C2 (Arabidopsis thaliana glycosyl hydrolase 9C2); carbohydrate binding / catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene34165_All//0.00E+00//TC129567		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0005488//GO:0044238//GO:0044464	nr +
Unigene34166_All	519	4.03	5.37	5.95	5.18	7.70	7.05	1.87	1.37	0.38	4.13E-01	2.83E-01		5.62E-01	1.37E-01		5.70E-01	6.22E-02		4.44E-01	1.93E-01		-4.53E-01	4.90E-01		-2.29E+00	9.84E-04	Down	Unigene34166_All//gi|18404989|ref|NP_564662.1|//2.00E-23//esterase/lipase/thioesterase family protein [Arabidopsis thaliana] >gi|75339094|sp|Q9ZVN2.1|Y1457_ARATH RecName: Full=Acyltransferase-like protein At1g54570, chloroplastic; Flags: Precursor >gi|29029028|gb|AAO64893.1| At1g54570 [Arabidopsis thaliana]	Unigene34166_All//1.00E-24//AT1G54570| esterase/lipase/thioesterase family protein	Unigene34166_All//3.00E-104//EX165488			GO:0009570//GO:0016747	nr +
Unigene34169_All	3173	48.00	22.50	35.19	24.77	26.10	20.43	25.86	17.11	27.37	-1.09E+00	6.79E-127	Down	-4.48E-01	3.61E-26		7.53E-02	2.69E-01		-2.79E-01	1.12E-06		-5.96E-01	3.73E-30		8.17E-02	1.35E-01		Unigene34169_All//gi|45080975|gb|AAD21419.1|//1.00E-140//Unknown protein [Arabidopsis thaliana] >gi|11074464|gb|AH014605.1| At1g61740 [Arabidopsis thaliana]	Unigene34169_All//2.00E-115//AT4G21250| unknown protein	Unigene34169_All//0.00E+00//TC138402		ko04626|Plant-pathogen interaction	GO:0031410	nr -
Unigene3417_All	1729	1.79	7.21	2.46	1.24	1.71	1.85	4.48	10.47	15.78	2.01E+00	5.29E-26	Up	4.65E-01	1.37E-01		4.67E-01	2.24E-01		5.82E-01	1.05E-01		1.23E+00	9.02E-23	Up	1.82E+00	1.88E-61	Up	Unigene3417_All//gi|1708191|sp|Q07423.1|HEX6_RICCO//0.00E+00//RecName: Full=Hexose carrier protein HEX6 >gi|467319|gb|AAA78857.1| hexose carrier protein [Ricinus communis]	Unigene3417_All//4.00E-142//AT5G61520| hexose transporter, putative	Unigene3417_All//5.00E-72//TC166881			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224	nr +
Unigene34170_All	384	1.91	1.06	2.50	7.39	3.05	5.53	6.72	4.46	6.95	-8.54E-01	3.05E-01		3.88E-01	6.08E-01		-1.28E+00	2.82E-04	Down	-4.20E-01	2.93E-01		-5.90E-01	9.75E-02		4.95E-02	9.03E-01		Unigene34170_All//gi|297849662|ref|XP_002892712.1|//9.00E-27//UDP-D-glucose/UDP-D-galactose 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297338554|gb|EFH68971.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene34170_All//2.00E-26//AT1G12780| UGE1 (UDP-D-glucose/UDP-D-galactose 4-epimerase 1); UDP-glucose 4-epimerase/ protein dimerization	Unigene34170_All//2.00E-142//gi|164297013|gb|ES840943.1|ES840943		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism	GO:0005515//GO:0006012//GO:0016020//GO:0016857//GO:0044444//GO:0048037//GO:0048229//GO:0050896	nr +
Unigene34172_All	1762	13.66	6.73	6.13	35.11	25.88	26.91	29.47	39.33	54.31	-1.02E+00	1.48E-18	Down	-1.15E+00	1.40E-21	Down	-4.40E-01	3.69E-13		-3.84E-01	2.53E-09		4.17E-01	1.07E-13		8.82E-01	3.63E-70		Unigene34172_All//gi|297849662|ref|XP_002892712.1|//0.00E+00//UDP-D-glucose/UDP-D-galactose 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297338554|gb|EFH68971.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene34172_All//3.00E-175//AT1G12780| UGE1 (UDP-D-glucose/UDP-D-galactose 4-epimerase 1); UDP-glucose 4-epimerase/ protein dimerization	Unigene34172_All//0.00E+00//TC146297		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism	GO:0005515//GO:0006012//GO:0016020//GO:0016857//GO:0044444//GO:0048037//GO:0050896	nr -
Unigene34173_All	2224	16.73	26.79	20.66	19.60	21.60	17.34	12.21	8.08	5.82	6.80E-01	1.15E-22		3.05E-01	1.85E-04		1.40E-01	8.72E-02		-1.77E-01	4.01E-02		-5.95E-01	1.69E-10		-1.07E+00	4.41E-28	Down	Unigene34173_All//gi|240255387|ref|NP_188858.4|//1.00E-129//IQD5 (IQ-domain 5); calmodulin binding [Arabidopsis thaliana]	Unigene34173_All//5.00E-95//AT3G22190| IQD5 (IQ-domain 5); calmodulin binding	Unigene34173_All//0.00E+00//TC162617				nr +
Unigene34174_All	2060	12.27	6.40	8.92	14.17	16.62	16.09	17.24	8.34	7.04	-9.40E-01	4.88E-17		-4.60E-01	3.92E-05		2.30E-01	1.24E-02		1.84E-01	7.02E-02		-1.05E+00	2.28E-34	Down	-1.29E+00	4.09E-49	Down	Unigene34174_All//gi|240255387|ref|NP_188858.4|//1.00E-126//IQD5 (IQ-domain 5); calmodulin binding [Arabidopsis thaliana]	Unigene34174_All//3.00E-76//AT3G22190| IQD5 (IQ-domain 5); calmodulin binding	Unigene34174_All//0.00E+00//TC160535				nr -
Unigene34179_All	1066	0.98	2.71	2.10	6.50	6.82	6.27	1.15	1.53	1.61	1.46E+00	1.63E-04	Up	1.10E+00	1.53E-02		6.95E-02	8.14E-01		-5.09E-02	8.46E-01		4.11E-01	3.95E-01		4.83E-01	2.76E-01		Unigene34179_All//gi|224122608|ref|XP_002330524.1|//3.00E-82//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222872458|gb|EEF09589.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene34179_All//4.00E-52//AT4G29230| anac075 (Arabidopsis NAC domain containing protein 75); transcription factor	Unigene34179_All//0.00E+00//gi|78339049|gb|DT559323.1|DT559323	NAC	ko03022|Basal transcription factors	GO:0003676//GO:0010468//GO:0031410	nr -
Unigene3418_All	1948	15.98	41.38	45.60	4.35	7.92	8.56	0.00	0.00	0.00	1.37E+00	7.21E-96	Up	1.51E+00	4.52E-119	Up	8.65E-01	1.13E-10		9.77E-01	7.44E-13		null	null		null	null		Unigene3418_All//gi|18378959|ref|NP_563651.1|//1.00E-140//GPAT2 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 2); acyltransferase [Arabidopsis thaliana] >gi|83288232|sp|Q9FZ22.1|GPAT2_ARATH RecName: Full=Probable glycerol-3-phosphate acyltransferase 2; Short=AtGPAT2 >gi|9857535|gb|AAG00890.1|AC064879_8 Unknown protein [Arabidopsis thaliana] >gi|16930413|gb|AAL31892.1|AF419560_1 At1g02390/T6A9_17 [Arabidopsis thaliana] >gi|20453233|gb|AAM19855.1| At1g02390/T6A9_17 [Arabidopsis thaliana]	Unigene3418_All//1.00E-138//AT1G02390| GPAT2 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 2); acyltransferase	Unigene3418_All//0.00E+00//TC155816		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr +
Unigene34180_All	1805	1.65	3.20	2.36	9.30	12.19	11.58	1.08	1.00	2.16	9.54E-01	1.34E-04		5.15E-01	9.77E-02		3.90E-01	4.47E-04		3.17E-01	9.53E-03		-1.14E-01	7.91E-01		1.01E+00	2.16E-04	Up	Unigene34180_All//gi|224088037|ref|XP_002308301.1|//1.00E-170//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222854277|gb|EEE91824.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene34180_All//7.00E-121//AT4G29230| anac075 (Arabidopsis NAC domain containing protein 75); transcription factor	Unigene34180_All//0.00E+00//ES822387	NAC			nr +
Unigene34185_All	3177	4.36	7.77	2.16	6.24	8.22	10.38	20.27	20.18	76.71	8.32E-01	1.21E-13		-1.01E+00	2.20E-10	Down	3.97E-01	7.68E-05		7.34E-01	1.60E-15		-6.20E-03	9.55E-01		1.92E+00	0.00E+00	Up	Unigene34185_All//gi|282927332|gb|ACF05504.2|//0.00E+00//respiratory burst oxidase-like protein [Citrullus colocynthis]	Unigene34185_All//0.00E+00//AT5G47910| RBOHD (RESPIRATORY BURST OXIDASE HOMOLOGUE D); NAD(P)H oxidase	Unigene34185_All//0.00E+00//gi|78334269|gb|DT554543.1|DT554543		ko04626|Plant-pathogen interaction	GO:0006952//GO:0012501//GO:0016209//GO:0030554//GO:0031224//GO:0044237//GO:0046914//GO:0050664	nr +
Unigene34187_All	966	0.76	3.36	1.76	1.86	1.78	2.10	2.32	3.85	1.03	2.15E+00	7.84E-08	Up	1.22E+00	2.32E-02		-5.87E-02	8.99E-01		1.81E-01	7.01E-01		7.31E-01	1.00E-02		-1.17E+00	1.79E-03		Unigene34187_All//gi|290490572|dbj|BAI79273.1|//1.00E-134//LysM type receptor kinase [Lotus japonicus]	Unigene34187_All//2.00E-113//AT3G21630| CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase	Unigene34187_All//0.00E+00//TC167531		ko04626|Plant-pathogen interaction		nr -
Unigene34188_All	986	2.71	5.76	2.92	2.73	3.35	4.49	21.35	27.51	33.98	1.09E+00	2.01E-05	Up	1.08E-01	7.75E-01		2.97E-01	4.38E-01		7.18E-01	1.27E-02		3.65E-01	8.89E-05		6.70E-01	5.56E-16		Unigene34188_All//gi|290490572|dbj|BAI79273.1|//1.00E-133//LysM type receptor kinase [Lotus japonicus]	Unigene34188_All//2.00E-112//AT3G21630| CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase	Unigene34188_All//0.00E+00//gi|5050353|gb|AI731501.1|AI731501		ko04626|Plant-pathogen interaction		nr +
Unigene34189_All	2269	6.41	12.66	6.03	4.74	6.57	9.38	35.83	56.16	78.83	9.82E-01	1.37E-20		-8.79E-02	6.34E-01		4.71E-01	6.37E-04		9.83E-01	2.01E-16		6.48E-01	1.05E-53		1.14E+00	5.10E-198	Up	Unigene34189_All//gi|290490572|dbj|BAI79273.1|//0.00E+00//LysM type receptor kinase [Lotus japonicus]	Unigene34189_All//0.00E+00//AT3G21630| CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase	Unigene34189_All//0.00E+00//TC167531		ko04626|Plant-pathogen interaction	GO:0002238//GO:0004713//GO:0004871//GO:0006464//GO:0009743//GO:0016020//GO:0032559//GO:0050832	nr -
Unigene3419_All	2444	9.95	8.83	8.95	13.49	15.12	13.27	16.14	7.73	9.21	-1.73E-01	1.45E-01		-1.53E-01	2.37E-01		1.64E-01	8.06E-02		-2.42E-02	8.38E-01		-1.06E+00	6.41E-39	Down	-8.09E-01	1.04E-25		Unigene3419_All//gi|297829264|ref|XP_002882514.1|//0.00E+00//GPI transamidase component Gpi16 subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328354|gb|EFH58773.1| GPI transamidase component Gpi16 subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3419_All//0.00E+00//AT3G07140| GPI transamidase component Gpi16 subunit family protein	Unigene3419_All//0.00E+00//TC174283		ko00563|Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	GO:0030176//GO:0031410	nr -
Unigene34194_All	1897	0.39	3.45	1.18	0.95	0.82	1.69	7.71	16.28	1.64	3.16E+00	9.04E-23	Up	1.61E+00	6.62E-04	Up	-2.11E-01	6.80E-01		8.39E-01	1.62E-02		1.08E+00	2.44E-31	Up	-2.24E+00	6.01E-44	Down	Unigene34194_All//gi|37992755|gb|AR06584.1|//0.00E+00//glycinamide ribonucleotide synthetase [Nicotiana tabacum]	Unigene34194_All//0.00E+00//AT1G09830| phosphoribosylamine--glycine ligase (PUR2)	Unigene34194_All//0.00E+00//gi|78350016|gb|DT570290.1|DT570290		ko00230|Purine metabolism	GO:0006144//GO:0006163//GO:0009536//GO:0016879//GO:0032559	nr +
Unigene34196_All	1865	0.00	0.49	0.09	0.05	0.06	0.17	1.00	1.19	0.13	8.93E+00	2.62E-05	Up	6.42E+00	2.39E-01		5.30E-02	9.66E-01		1.67E+00	3.09E-01		2.52E-01	5.58E-01		-2.96E+00	2.82E-08	Down	Unigene34196_All//gi|37992755|gb|AR06584.1|//0.00E+00//glycinamide ribonucleotide synthetase [Nicotiana tabacum]	Unigene34196_All//0.00E+00//AT1G09830| phosphoribosylamine--glycine ligase (PUR2)	Unigene34196_All//0.00E+00//gi|78350016|gb|DT570290.1|DT570290		ko00230|Purine metabolism	GO:0006144//GO:0006163//GO:0009536//GO:0016879//GO:0032559	nr -
Unigene34197_All	2056	6.03	3.03	5.10	7.24	6.40	7.80	5.72	3.09	2.15	-9.93E-01	1.62E-09		-2.41E-01	1.75E-01		-1.79E-01	2.67E-01		1.06E-01	5.39E-01		-8.88E-01	3.04E-09		-1.41E+00	3.90E-19	Down	Unigene34197_All//gi|37992755|gb|AR06584.1|//0.00E+00//glycinamide ribonucleotide synthetase [Nicotiana tabacum]	Unigene34197_All//0.00E+00//AT1G09830| phosphoribosylamine--glycine ligase (PUR2)	Unigene34197_All//0.00E+00//TC137007		ko00230|Purine metabolism	GO:0006144//GO:0006163//GO:0009536//GO:0016879//GO:0032559	nr -
Unigene34199_All	1400	1.68	2.82	0.95	1.21	3.15	1.45	2.57	2.00	1.91	7.47E-01	1.49E-02		-8.23E-01	5.87E-02		1.38E+00	1.40E-06	Up	2.63E-01	6.30E-01		-3.60E-01	2.39E-01		-4.29E-01	1.33E-01		Unigene34199_All//gi|15232194|ref|NP_188991.1|//1.00E-151//glycosyl transferase family 17 protein [Arabidopsis thaliana]	Unigene34199_All//9.00E-153//AT3G27540| glycosyl transferase family 17 protein	Unigene34199_All//0.00E+00//TC160005				nr +
Unigene342_All	851	21.89	12.03	15.83	33.83	35.20	30.99	21.07	11.10	9.18	-8.64E-01	3.56E-11		-4.67E-01	4.36E-04		5.73E-02	6.39E-01		-1.27E-01	2.87E-01		-9.24E-01	1.42E-14		-1.20E+00	1.57E-22	Down	Unigene342_All//gi|20197808|gb|AAM15256.1|//2.00E-33//Expressed protein [Arabidopsis thaliana] >gi|109134131|gb|ABG25064.1| At2g18245 [Arabidopsis thaliana]	Unigene342_All//4.00E-34//AT2G18245| unknown protein	Unigene342_All//0.00E+00//gi|164352554|gb|EX171433.1|EX171433				nr +
Unigene3420_All	1052	14.82	8.04	11.39	13.87	12.90	10.99	5.75	4.69	2.80	-8.82E-01	8.60E-10		-3.80E-01	1.09E-02		-1.05E-01	5.46E-01		-3.36E-01	2.50E-02		-2.94E-01	2.04E-01		-1.04E+00	1.18E-06	Down	Unigene3420_All//gi|22087556|gb|AAW90961.1|AF516366_1/4.00E-47//5-formyltetrahydrofolate cycloligase [Solanum lycopersicum]	Unigene3420_All//1.00E-46//AT5G13050| 5-FCL (5-FORMYLTETRAHYDROFOLATE CYCLOLIGASE); 5-formyltetrahydrofolate cyclo-ligase			ko00670|One carbon pool by folate	GO:0006760//GO:0016882//GO:0032559//GO:0043231//GO:0046872	nr -
Unigene34200_All	1385	5.36	6.29	4.69	2.59	3.80	3.52	0.73	0.88	3.48	2.30E-01	2.70E-01		-1.94E-01	4.08E-01		5.55E-01	3.11E-02		4.44E-01	1.21E-01		2.56E-01	6.35E-01		2.25E+00	6.70E-15	Up	Unigene34200_All//gi|15232194|ref|NP_188991.1|//0.00E+00//glycosyl transferase family 17 protein [Arabidopsis thaliana]	Unigene34200_All//0.00E+00//AT3G27540| glycosyl transferase family 17 protein	Unigene34200_All//0.00E+00//TC160005			GO:0006486//GO:0008375//GO:0044464	nr -
Unigene34201_All	2977	33.15	142.63	73.09	29.95	59.59	64.52	11.55	14.08	24.89	2.11E+00	0.00E+00	Up	1.14E+00	1.63E-188	Up	9.93E-01	5.26E-150		1.11E+00	3.81E-175	Up	2.86E-01	1.11E-04		1.11E+00	4.04E-79	Up	Unigene34201_All//gi|18397470|ref|NP_564354.1|//0.00E+00//ERD4 (early-responsive to dehydration 4) [Arabidopsis thaliana]	Unigene34201_All//0.00E+00//AT1G30360| ERD4 (early-responsive to dehydration 4)	Unigene34201_All//0.00E+00//TC142948			GO:0009536//GO:0016020//GO:0031410	nr +
Unigene34205_All	440	2.14	2.30	1.69	3.62	3.29	0.82	4.04	4.94	2.72	1.06E-01	8.72E-01		-3.37E-01	6.16E-01		-1.40E-01	8.18E-01		-2.14E+00	2.07E-04	Down	2.92E-01	4.93E-01		-5.71E-01	1.79E-01		Unigene34205_All//gi|297610489|ref|NP_001061615.2|//9.00E-28//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene34205_All//3.00E-18//AT1G60750| oxidoreductase	Unigene34205_All//0.00E+00//gi|78331636|gb|DT551910.1|DT551910			GO:0004033//GO:0008152	nr -
Unigene34207_All	2933	0.25	0.60	0.18	1.04	0.68	0.23	1.25	3.43	0.57	1.28E+00	1.15E-02		-4.59E-01	6.02E-01		-6.05E-01	8.19E-02		-2.17E+00	5.86E-08	Down	1.45E+00	1.13E-16	Up	-1.14E+00	5.90E-05	Down	Unigene34207_All//gi|297610489|ref|NP_001061615.2|//1.00E-91//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene34207_All//5.00E-75//AT1G60690| aldo/keto reductase family protein	Unigene34207_All//0.00E+00//gi|78340622|gb|DT560896.1|DT560896		ko00010|Glycolysis / Gluconeogenesis//ko00053|Ascorbate and aldarate metabolism//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism	GO:0016491	nr +

Unigene34208_All	726	0.14	0.98	0.29	1.03	0.57	2.43	1.40	7.14	4.94	2.76E+00	9.14E-03		1.03E+00	5.91E-01		-8.55E-01	2.95E-01		1.24E+00	1.46E-02		2.35E+00	1.91E-16	Up	1.82E+00	8.42E-09	Up	Unigene34208_All//gi|87138101|gb|AB028287.1|//1.00E-107//circadian clock-associated FKF1 [Glycine max]	Unigene34208_All//4.00E-86//AT1G68050| FKF1 (FLAVIN-BINDING, KELCH REPEAT, F BOX 1); signal transducer/ two-component sensor/ ubiquitin-protein ligase	Unigene34208_All//0.00E+00//TC142237		ko04712|Circadian rhythm - plant		nr +
Unigene34209_All	2199	0.67	2.77	1.11	1.99	2.22	3.16	4.50	8.69	9.24	2.05E+00	2.39E-13	Up	7.42E-01	8.07E-02		1.58E-01	6.11E-01		6.66E-01	2.51E-03		9.49E-01	4.10E-16		1.04E+00	3.53E-20	Up	Unigene34209_All//gi|87138101|gb|AB028287.1|//0.00E+00//circadian clock-associated FKF1 [Glycine max]	Unigene34209_All//0.00E+00//AT1G68050| FKF1 (FLAVIN-BINDING, KELCH REPEAT, F BOX 1); signal transducer/ two-component sensor/ ubiquitin-protein ligase	Unigene34209_All//0.00E+00//TC131576		ko04712|Circadian rhythm - plant	GO:0005488//GO:0006351//GO:0009416//GO:0009908//GO:0010468//GO:0019787//GO:0019941//GO:0023060//GO:0048511//GO:0060089	nr -
Unigene34210_All	2198	0.36	1.06	0.05	1.16	1.07	1.64	2.89	6.66	7.14	1.57E+00	4.09E-04	Up	-2.88E+00	6.35E-03		-1.18E-01	8.03E-01		5.08E-01	1.31E-01		1.21E+00	4.19E-18	Up	1.31E+00	2.17E-22	Up	Unigene34210_All//gi|87138101|gb|AB028287.1|//0.00E+00//circadian clock-associated FKF1 [Glycine max]	Unigene34210_All//0.00E+00//AT1G68050| FKF1 (FLAVIN-BINDING, KELCH REPEAT, F BOX 1); signal transducer/ two-component sensor/ ubiquitin-protein ligase	Unigene34210_All//0.00E+00//TC142237		ko04712|Circadian rhythm - plant	GO:0005488//GO:0006351//GO:0009416//GO:0009908//GO:0010468//GO:0019787//GO:0019941//GO:0023060//GO:0048511//GO:0060089	nr +
Unigene34214_All	3825	5.49	2.19	2.77	12.85	12.00	10.02	8.83	1.29	3.15	-1.33E+00	2.51E-24	Down	-9.85E-01	9.96E-15		-9.91E-02	2.56E-01		-3.59E-01	9.82E-07		-2.78E+00	3.91E-125	Down	-1.49E+00	7.58E-58	Down	Unigene34214_All//gi|6446577|gb|AAD39534.2|//0.00E+00//cellulose synthase catalytic subunit [Gossypium hirsutum]	Unigene34214_All//0.00E+00//AT5G05170| CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene34214_All//0.00E+00//TC146243			GO:0006950//GO:0009250//GO:0009832//GO:0016759//GO:0031224//GO:0043231//GO:0045229//GO:0046914	nr -
Unigene34217_All	2346	5.29	2.40	4.29	9.11	6.43	6.80	6.31	8.30	8.63	-1.14E+00	9.84E-12	Down	-3.01E-01	8.43E-02		-5.03E-01	4.14E-06		-4.23E-01	2.87E-04		3.96E-01	3.98E-04		4.52E-01	2.27E-05		Unigene34217_All//gi|297816558|ref|XP_002876162.1|//1.00E-166//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297322000|gb|EFH52421.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene34217_All//8.00E-113//AT3G52660| RNA recognition motif (RRM)-containing protein	Unigene34217_All//0.00E+00//gi|78333354|gb|DT553628.1|DT553628		ko03040|Spliceosome	GO:0005488	nr +
Unigene34225_All	777	1.75	23.61	1.17	0.45	2.39	1.16	3.37	9.79	12.36	3.75E+00	3.07E-73	Up	-5.88E-01	3.37E-01		2.41E+00	8.22E-06	Up	1.37E+00	7.76E-02		1.54E+00	8.16E-14	Up	1.87E+00	5.02E-23	Up	Unigene34225_All//gi|124360185|gb|ABN08198.1|//7.00E-39//Glutamine amidotransferase, class I, active site [Medicago truncatula]	Unigene34225_All//3.00E-38//AT3G12670| emb2742 (embryo defective 2742); CTP synthase/ catalytic	Unigene34225_All//4.00E-40//TC173942		ko00240|Pyrimidine metabolism		nr -
Unigene34226_All	2361	45.81	320.50	31.69	28.80	73.98	67.75	37.36	152.15	173.61	2.81E+00	0.00E+00	Up	-5.32E-01	1.92E-25		1.36E+00	7.30E-243	Up	1.23E+00	2.20E-173	Up	2.03E+00	0.00E+00	Up	2.22E+00	0.00E+00	Up	Unigene34226_All//gi|222423455|dbj|BAH19698.1|//0.00E+00//AT1G30820 [Arabidopsis thaliana]	Unigene34226_All//0.00E+00//AT1G30820| CTP synthase, putative / UTP--ammonia ligase, putative	Unigene34226_All//0.00E+00//TC173942		ko00240|Pyrimidine metabolism		nr -
Unigene34227_All	2073	3.36	1.25	1.16	16.89	17.79	9.19	11.83	5.87	7.74	-1.43E+00	1.68E-09	Down	-1.54E+00	5.33E-10	Down	7.47E-02	5.12E-01		-8.78E-01	2.15E-22		-1.01E+00	1.11E-22	Down	-6.11E-01	2.56E-10		Unigene34227_All//gi|195628114|gb|ACG35887.1|//0.00E+00//auxin transporter-like protein 3 [Zea mays]	Unigene34227_All//0.00E+00//AT2G38120| AUX1 (AUXIN RESISTANT 1); amino acid transmembrane transporter/ auxin binding / auxin influx transmembrane transporter/ transporter	Unigene34227_All//0.00E+00//gi|164276637|gb|ES839983.1|ES839983				nr +
Unigene34228_All	1728	3.94	0.50	0.46	12.80	11.90	6.19	7.66	0.92	2.84	-2.98E+00	1.23E-22	Down	-3.09E+00	2.12E-22	Down	-1.06E-01	4.54E-01		-1.05E+00	4.44E-19	Down	-3.06E+00	1.71E-54	Down	-1.43E+00	6.05E-22	Down	Unigene34228_All//gi|224103225|ref|XP_002312973.1|//0.00E+00//auxin influx carrier component [Populus trichocarpa] >gi|222849381|gb|EEE86928.1| auxin influx carrier component [Populus trichocarpa]	Unigene34228_All//0.00E+00//AT2G21650| amino acid permease, putative	Unigene34228_All//0.00E+00//gi|78325852|gb|DT546126.1|DT546126				nr -
Unigene34229_All	1625	1.67	0.59	0.49	5.27	6.46	3.72	2.81	1.00	1.47	-1.50E+00	1.89E-04	Down	-1.77E+00	4.22E-05	Down	2.94E-01	1.10E-01		-5.02E-01	1.10E-02		-1.49E+00	3.05E-08	Down	-9.34E-01	1.49E-04		Unigene34229_All//gi|115464187|ref|NP_001055693.1|//0.00E+00//Os05g0447200 [Oryza sativa Japonica Group] >gi|75254071|sp|Q688J2.1|LAX2_ORYSJ RecName: Full=Auxin transporter-like protein 2 >gi|113579244|dbj|BAF17607.1| Os05g0447200 [Oryza sativa Japonica Group]	Unigene34229_All//4.00E-146//AT2G21050| amino acid permease, putative	Unigene34229_All//0.00E+00//gi|164276637|gb|ES839983.1|ES839983				nr +
Unigene34232_All	1354	13.56	14.26	18.72	10.52	6.31	7.84	12.27	10.22	3.41	7.21E-02	6.08E-01		4.65E-01	3.08E-05		-7.38E-01	6.00E-08		-4.25E-01	4.07E-03		-2.64E-01	3.79E-02		-1.85E+00	5.63E-39	Down	Unigene34232_All//gi|224126169|ref|XP_002319773.1|//1.00E-151//cytochrome P450 [Populus trichocarpa] >gi|222858149|gb|EEE95696.1| cytochrome P450 [Populus trichocarpa]	Unigene34232_All//5.00E-139//AT1G61950| CYP89A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene34232_All//6.00E-148//gi|54121731|gb|CO497240.1|CO497240		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene34233_All	1348	12.34	15.45	12.13	11.05	5.95	8.24	9.44	9.36	2.75	3.24E-01	8.21E-03		-2.54E-02	8.75E-01		-8.93E-01	2.69E-11		-4.23E-01	3.33E-03		-1.18E-02	9.70E-01		-1.78E+00	1.28E-28	Down	Unigene34233_All//gi|224081184|ref|XP_002306325.1|//1.00E-150//cytochrome P450 [Populus trichocarpa] >gi|222855774|gb|EEE93321.1| cytochrome P450 [Populus trichocarpa]	Unigene34233_All//2.00E-135//AT1G61950| CYP89A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene34233_All//4.00E-158//TC153079		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene34236_All	662	0.32	0.15	1.37	5.57	6.71	4.50	5.43	6.57	21.91	-1.05E+00	5.64E-01		2.11E+00	1.42E-02		2.69E-01	4.08E-01		-3.07E-01	3.96E-01		2.74E-01	3.39E-01		2.01E+00	1.02E-37	Up	Unigene34236_All//gi|13774348|gb|AAK38843.1|AF346308_1/6.00E-17//histidine-containing phosphotransfer protein [Catharanthus roseus]	Unigene34236_All//3.00E-14//AT3G21510| AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 1); histidine phosphotransfer kinase	Unigene34236_All//1.00E-150//TC159867				nr +
Unigene34237_All	376	0.14	2.70	0.57	1.19	1.28	2.40	47.12	43.91	157.24	4.28E+00	7.16E-05	Up	2.02E+00	3.61E-01		1.05E-01	9.54E-01		1.01E+00	1.96E-01		-1.02E-01	4.70E-01		1.74E+00	2.56E-124	Up	Unigene34237_All//gi|15239586|ref|NP_197387.1|//2.00E-36//inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis thaliana] >gi|19310427|gb|AAL84950.1| AT5g18860/F17K4_110 [Arabidopsis thaliana] >gi|22137232|gb|AAM91461.1| AT5g18860/F17K4_110 [Arabidopsis thaliana]	Unigene34237_All//9.00E-38//AT5G18860| inosine-uridine preferring nucleoside hydrolase family protein	Unigene34237_All//5.00E-13//TC160849				nr +
Unigene34238_All	863	0.00	0.47	0.06	1.21	0.40	0.94	47.47	43.25	142.74	8.88E+00	1.36E-02		5.95E+00	6.35E-01		-1.60E+00	1.49E-02		-3.64E-01	6.33E-01		-1.35E-01	1.03E-01		1.59E+00	3.93E-227	Up	Unigene34238_All//gi|15239586|ref|NP_197387.1|//1.00E-119//inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis thaliana] >gi|19310427|gb|AAL84950.1| AT5g18860/F17K4_110 [Arabidopsis thaliana] >gi|22137232|gb|AAM91461.1| AT5g18860/F17K4_110 [Arabidopsis thaliana]	Unigene34238_All//2.00E-120//AT5G18860| inosine-uridine preferring nucleoside hydrolase family protein	Unigene34238_All//2.00E-57//TC160849				nr -
Unigene34239_All	2808	3.45	3.61	4.34	10.84	14.18	16.60	14.67	14.27	32.80	6.62E-02	7.25E-01		3.33E-01	5.55E-02		3.87E-01	8.55E-07		6.15E-01	4.76E-16		-3.90E-02	6.64E-01		1.16E+00	9.48E-106	Up	Unigene34239_All//gi|297604490|ref|NP_001055513.2|//1.00E-108//Os05g0406200 [Oryza sativa Japonica Group] >gi|255676357|dbj|BAF17427.2| Os05g0406200 [Oryza sativa Japonica Group]	Unigene34239_All//1.00E-79//AT5G18860| inosine-uridine preferring nucleoside hydrolase family protein	Unigene34239_All//0.00E+00//TC159867				nr -
Unigene34243_All	1528	5.62	5.70	5.44	8.28	10.66	6.41	6.36	1.64	4.25	2.24E-02	9.29E-01		-4.68E-02	8.30E-01		3.64E-01	6.85E-03		-3.69E-01	2.25E-02		-1.96E+00	3.65E-24	Down	-5.83E-01	2.51E-04		Unigene34243_All//gi|42567317|ref|NP_194928.3|//1.00E-108//protein kinase family protein [Arabidopsis thaliana]	Unigene34243_All//3.00E-94//AT2G25220| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene34243_All//0.00E+00//TC175486		ko04626|Plant-pathogen interaction		nr +
Unigene34245_All	2121	4.17	4.92	6.43	9.35	9.51	7.81	5.18	1.42	2.33	2.39E-01	2.06E-01		6.25E-01	7.21E-05		2.55E-02	8.70E-01		-2.58E-01	4.61E-02		-1.87E+00	1.15E-25	Down	-1.15E+00	2.26E-13	Down	Unigene34245_All//gi|42567317|ref|NP_194928.3|//1.00E-145//protein kinase family protein [Arabidopsis thaliana]	Unigene34245_All//6.00E-132//AT2G25220| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene34245_All//0.00E+00//TC175486		ko04626|Plant-pathogen interaction		nr +
Unigene3425_All	908	78.48	28.40	84.86	25.57	21.24	6.96	1.16	0.46	0.26	-1.47E+00	4.14E-94	Down	1.13E-01	9.66E-02		-2.68E-01	1.73E-02		-1.88E+00	1.19E-47	Down	-1.34E+00	2.90E-02		-2.14E+00	9.36E-04	Down	Unigene3425_All//gi|224058595|ref|XP_002299557.1|//1.00E-48//cytochrome P450 [Populus trichocarpa] >gi|222846815|gb|EEE84362.1| cytochrome P450 [Populus trichocarpa]	Unigene3425_All//2.00E-46//AT1G12740| CYP87A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene3425_All//0.00E+00//TC171272		ko00905|Brassinosteroid biosynthesis	GO:0005506//GO:0008152//GO:0016709//GO:0031410	nr +
Unigene34250_All	445	0.00	0.80	0.48	0.56	3.87	0.71	5.51	8.83	2.24	9.64E+00	2.46E-02		8.90E+00	1.41E-01		2.79E+00	3.17E-06	Up	3.44E-01	7.97E-01		6.80E-01	1.34E-02		-1.30E+00	3.13E-04	Down			Unigene34250_All//1.00E-97//gi|109868422|gb|DW497398.1|DW497398				
Unigene34253_All	1572	12.78	37.23	17.31	14.93	15.07	23.44	12.51	24.25	19.21	1.54E+00	6.15E-83	Up	4.38E-01	4.64E-05		1.40E-02	9.29E-01		6.51E-01	3.89E-14		9.55E-01	1.13E-31		6.19E-01	1.03E-12		Unigene34253_All//gi|297839709|ref|XP_002887736.1|//1.00E-107//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297333577|gb|EFH63995.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene34253_All//8.00E-92//AT1G78420| protein binding / zinc ion binding	Unigene34253_All//0.00E+00//TC178878				nr +
Unigene34254_All	1620	3.20	7.32	5.65	6.43	5.21	5.46	4.20	3.77	3.69	1.19E+00	5.32E-12	Up	8.22E-01	3.20E-05		-3.03E-01	9.17E-02		-2.34E-01	2.28E-01		-1.58E-01	5.00E-01		-1.88E-01	3.80E-01		Unigene34254_All//gi|297839709|ref|XP_002887736.1|//1.00E-101//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297333577|gb|EFH63995.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene34254_All//1.00E-89//AT1G78420| protein binding / zinc ion binding	Unigene34254_All//0.00E+00//TC178878				nr +
Unigene34255_All	982	9.70	22.39	5.64	30.59	27.07	19.18	35.74	41.03	77.00	1.21E+00	5.76E-22	Up	-7.82E-01	5.24E-05		-1.76E-01	8.91E-02		-6.74E-01	2.11E-12		1.99E-01	1.11E-02		1.11E+00	1.22E-80	Up	Unigene34255_All//gi|16226874|gb|AAL16287.1|AF425357_1//5.00E-96//At1g74450/F1M20_13 [Arabidopsis thaliana]	Unigene34255_All//6.00E-86//AT1G74450| unknown protein	Unigene34255_All//0.00E+00//TC134335				nr +
Unigene34261_All	2637	1.35	3.88	3.72	10.82	19.90	17.54	8.00	28.13	26.98	1.52E+00	7.89E-15	Up	1.46E+00	6.42E-13	Up	8.79E-01	2.44E-36		6.96E-01	1.05E-19		1.81E+00	5.33E-162	Up	1.75E+00	2.80E-151	Up	Unigene34261_All//gi|224145173|ref|XP_002325552.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222862427|gb|EEE99933.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene34261_All//0.00E+00//AT1G71960| ABC transporter family protein	Unigene34261_All//0.00E+00//TC140272		ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene34262_All	898	10.14	4.74	7.23	2.61	3.14	2.11	0.24	0.33	1.06	-1.10E+00	2.46E-08	Down	-4.87E-01	1.51E-02		2.70E-01	5.41E-01		-3.04E-01	5.02E-01		4.69E-01	7.06E-01		2.18E+00	1.83E-03		Unigene34262_All//gi|224132258|ref|XP_002328224.1|//7.00E-12//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837739|gb|EEE76104.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene34262_All//5.00E-09//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene34262_All//0.00E+00//gi|48777038|gb|CO086404.1|CO086404				nr -

Unigene34263_All	3251	15.74	6.23	11.09	14.83	15.22	9.14	6.92	2.47	5.74	-1.34E+00	6.43E-59	Down	-5.05E-01	2.49E-11		3.73E-02	7.17E-01		-6.98E-01	8.47E-21		-1.49E+00	1.43E-37	Down	-2.71E-01	8.27E-03		Unigene34263_All//gi|15229439|ref|NP_191906.1|//0.00E+00//scpl40 (serine carboxypeptidase-like 40; serine-type carboxypeptidase [Arabidopsis thaliana] >gi|125987782|sp|Q0WKX3.2|SCP40_ARATH RecName: Full=Serine carboxypeptidase-like 40; Flags: Precursor >gi|7573330|emb|CAB87800.1| serin carboxypeptidase-like protein [Arabidopsis thaliana] >gi|21593182|gb|AAM65131.1| serin carboxypeptidase-like protein [Arabidopsis thaliana]	Unigene34263_All//0.00E+00//AT3G63470| scpl40 (serine carboxypeptidase-like 40); serine-type carboxypeptidase	Unigene34263_All//0.00E+00//TC173402				nr +
Unigene34264_All	376	2.37	1.08	0.00	2.91	0.92	0.72	3.37	2.00	0.64	-1.13E+00	1.30E-01		-1.12E+01	6.30E-05	Down	-1.67E+00	9.38E-03		-2.02E+00	4.74E-03		-7.54E-01	1.63E-01		-2.41E+00	7.19E-05	Down	Unigene34264_All//gi|15224645|ref|NP_180685.1|//2.00E-34//CDT1A (ARABIDOPSIS HOMOLOG OF YEAST CDT1 A); cyclin-dependent protein kinase/ protein binding [Arabidopsis thaliana]	Unigene34264_All//1.00E-35//AT2G31270| CDT1A (ARABIDOPSIS HOMOLOG OF YEAST CDT1 A); cyclin-dependent protein kinase/ protein binding	Unigene34264_All//1.00E-161//DW509567				nr +
Unigene34265_All	2207	3.70	1.47	1.25	7.63	6.48	3.85	4.27	0.47	0.88	-1.33E+00	5.70E-10	Down	-1.56E+00	7.53E-12	Down	-2.37E-01	9.09E-02		-9.88E-01	2.27E-13		-3.17E+00	2.16E-40	Down	-2.27E+00	3.54E-29	Down	Unigene34265_All//gi|15224645|ref|NP_180685.1|//8.00E-62//CDT1A (ARABIDOPSIS HOMOLOG OF YEAST CDT1 A); cyclin-dependent protein kinase/ protein binding [Arabidopsis thaliana]	Unigene34265_All//2.00E-50//AT2G31270| CDT1A (ARABIDOPSIS HOMOLOG OF YEAST CDT1 A); cyclin-dependent protein kinase/ protein binding	Unigene34265_All//0.00E+00//TC149933				nr +
Unigene34266_All	2075	6.35	3.74	2.77	14.12	10.90	8.84	10.17	3.95	4.30	-7.66E-01	8.78E-07		-1.20E+00	9.17E-13	Down	-3.73E-01	6.29E-05		-6.76E-01	3.55E-12		-1.36E+00	4.17E-31	Down	-1.24E+00	8.63E-28	Down	Unigene34266_All//gi|15224645|ref|NP_180685.1|//1.00E-107//CDT1A (ARABIDOPSIS HOMOLOG OF YEAST CDT1 A); cyclin-dependent protein kinase/ protein binding [Arabidopsis thaliana]	Unigene34266_All//2.00E-99//AT2G31270| CDT1A (ARABIDOPSIS HOMOLOG OF YEAST CDT1 A); cyclin-dependent protein kinase/ protein binding	Unigene34266_All//0.00E+00//gi|78338408|gb|DT558682.1|DT558682				nr +
Unigene34267_All	3509	7.51	8.48	8.09	27.48	50.97	69.44	17.28	9.41	16.97	1.74E-01	1.03E-01		1.06E-01	3.94E-01		8.91E-01	1.66E-126		1.34E+00	7.67E-299	Up	-8.77E-01	2.29E-43		-2.57E-02	7.18E-01		Unigene34267_All//gi|297807421|ref|XP_002871594.1|//0.00E+00//glycosyl hydrolase family 38 protein [Arabidopsis lyrata subsp. lyrata] >gi|297317431|gb|EFH47853.1| glycosyl hydrolase family 38 protein [Arabidopsis lyrata subsp. lyrata]	Unigene34267_All//0.00E+00//AT5G13980| glycosyl hydrolase family 38 protein	Unigene34267_All//0.00E+00//TC137413		ko00511|Other glycan degradation		nr +
Unigene34268_All	4061	5.08	3.38	2.33	10.38	8.67	12.03	7.11	6.14	22.25	-5.86E-01	1.23E-06		-1.12E+00	1.00E-17	Down	-2.60E-01	9.20E-04		2.14E-01	5.95E-03		-2.11E-01	2.58E-02		1.65E+00	1.69E-175	Up	Unigene34268_All//gi|2827550|emb|CAA16558.1|//0.00E+00//leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] >gi|7269119|emb|CAB79228.1| leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] >gi|38564276|gb|AAR23717.1| At4g22730 [Arabidopsis thaliana] >gi|51971929|dbj|BAD44629.1| leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] >gi|224589626|gb|ACN59346.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene34268_All//0.00E+00//AT4G22730| leucine-rich repeat transmembrane protein kinase, putative	Unigene34268_All//0.00E+00//TC135774				nr -
Unigene3427_All	1291	7.34	5.81	5.61	18.83	17.15	17.25	15.33	6.35	8.79	-3.37E-01	7.82E-02		-3.87E-01	5.16E-02		-1.35E-01	2.91E-01		-1.27E-01	3.36E-01		-1.27E+00	2.64E-26	Down	-8.01E-01	3.91E-13		Unigene3427_All//gi|18401087|ref|NP_566542.1|//1.00E-138//mitotic phosphoprotein N' end (MPPN) family protein [Arabidopsis thaliana]	Unigene3427_All//2.00E-139//AT3G16310| mitotic phosphoprotein N' end (MPPN) family protein	Unigene3427_All//0.00E+00//TC148279				nr +
Unigene34275_All	3311	2.05	0.96	0.69	6.20	7.31	5.54	7.52	4.53	4.93	-1.09E+00	2.18E-06	Down	-1.57E+00	4.51E-10	Down	2.38E-01	3.55E-02		-1.63E-01	2.36E-01		-7.31E-01	1.34E-13		-6.09E-01	2.17E-10		Unigene34275_All//gi|227206460|dbj|BAH57285.1|//0.00E+00//AT5G26850 [Arabidopsis thaliana]	Unigene34275_All//0.00E+00//AT5G26850| INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: cyclin-related (TAIR:AT2G41830.1); Has 199 Blast hits to 197 proteins in 66 species: Archae - 0; Bacteria - 0; Metazoa - 113; Fungi - 19; Plants - 59; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink).	Unigene34275_All//0.00E+00//TC150427				nr -
Unigene34278_All	1457	0.43	0.80	0.37	7.52	5.79	1.67	1.04	0.49	0.25	8.93E-01	1.56E-01		-2.38E-01	7.75E-01		-3.77E-01	2.48E-02		-2.17E+00	2.16E-27	Down	-1.10E+00	2.32E-02		-2.09E+00	6.46E-05	Down	Unigene34278_All//gi|30694036|ref|NP_175160.2|//2.00E-34//AtTLP6 (TUBBY LIKE PROTEIN 6); phosphoric diester hydrolase/ transcription factor [Arabidopsis thaliana] >gi|122236191|sp|Q0WPY0.1|TLP6_ARATH RecName: Full=Tubby-like F-box protein 6; Short=AtTLP6	Unigene34278_All//2.00E-34//AT1G47270| AtTLP6 (TUBBY LIKE PROTEIN 6); phosphoric diester hydrolase/ transcription factor	Unigene34278_All//5.00E-87//DR462383	TUB			nr -
Unigene34279_All	1578	0.36	0.22	0.44	12.66	10.39	2.29	2.30	1.80	1.41	-6.98E-01	4.49E-01		2.67E-01	7.36E-01		-2.85E-01	1.92E-02		-2.47E+00	5.36E-58	Down	-3.55E-01	2.39E-01		-7.05E-01	1.09E-02		Unigene34279_All//gi|224085682|ref|XP_002307662.1|//1.00E-142//f-box family protein [Populus trichocarpa] >gi|222857111|gb|EEE94658.1| f-box family protein [Populus trichocarpa]	Unigene34279_All//4.00E-134//AT1G47270| AtTLP6 (TUBBY LIKE PROTEIN 6); phosphoric diester hydrolase/ transcription factor	Unigene34279_All//0.00E+00//TC155861	TUB			nr +
Unigene3428_All	1168	3.05	3.95	3.51	18.55	15.42	9.28	8.14	5.94	3.21	3.74E-01	1.99E-01		2.05E-01	5.42E-01		-2.67E-01	2.26E-02		-9.99E-01	2.31E-17		-4.55E-01	6.47E-03		-1.35E+00	1.27E-14	Down	Unigene3428_All//gi|297827719|ref|XP_002881742.1|//3.00E-66//proline-rich family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327581|gb|EFH58001.1| proline-rich family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3428_All//5.00E-55//AT2G40815| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: C2 calcium-dependent membrane targeting (InterPro:IPR000008).	Unigene3428_All//0.00E+00//TC138822				nr -
Unigene34280_All	2124	0.94	1.55	1.05	7.76	9.01	3.57	1.83	1.00	1.88	7.28E-01	3.32E-02		1.70E-01	6.95E-01		2.16E-01	1.07E-01		-1.12E+00	5.81E-16	Down	-8.68E-01	1.70E-03		3.45E-02	9.22E-01		Unigene34280_All//gi|224085682|ref|XP_002307662.1|//1.00E-132//f-box family protein [Populus trichocarpa] >gi|222857111|gb|EEE94658.1| f-box family protein [Populus trichocarpa]	Unigene34280_All//3.00E-126//AT1G47270| AtTLP6 (TUBBY LIKE PROTEIN 6); phosphoric diester hydrolase/ transcription factor	Unigene34280_All//0.00E+00//CO122938	TUB			nr +
Unigene34281_All	722	12.39	10.18	8.85	18.77	14.17	14.76	14.05	10.36	4.86	-2.84E-01	1.56E-01		-4.86E-01	1.64E-02		-4.06E-01	5.42E-03		-3.46E-01	2.68E-02		-4.40E-01	6.47E-03		-1.53E+00	9.87E-19	Down	Unigene34281_All//gi|18418838|ref|NP_568364.1|//6.00E-39//FASS (FASS 1); protein phosphatase type 2B regulator [Arabidopsis thaliana] >gi|11494362|gb|AAG35778.1|AF28005_7_1 tonneau 2 [Arabidopsis thaliana] >gi|11494385|gb|AAG35792.1|AF290025_1 tonneau 2 [Arabidopsis thaliana]	Unigene34281_All//5.00E-36//AT5G18580| FASS (FASS 1); protein phosphatase type 2B regulator	Unigene34281_All//1.00E-175//DW499618				nr +
Unigene34283_All	3229	1.22	1.11	1.10	1.70	1.09	1.23	2.57	1.13	1.01	-1.25E-01	6.85E-01		-1.37E-01	6.66E-01		-6.42E-01	7.59E-03		-4.63E-01	7.55E-02		-1.19E+00	2.13E-10	Down	-1.34E+00	7.99E-13	Down	Unigene34283_All//gi|18418838|ref|NP_568364.1|//0.00E+00//FASS (FASS 1); protein phosphatase type 2B regulator [Arabidopsis thaliana] >gi|11494362|gb|AAG35778.1|AF28005_7_1 tonneau 2 [Arabidopsis thaliana] >gi|11494385|gb|AAG35792.1|AF290025_1 tonneau 2 [Arabidopsis thaliana]	Unigene34283_All//0.00E+00//AT5G18580| FASS (FASS 1); protein phosphatase type 2B regulator	Unigene34283_All//0.00E+00//TC171613				nr -
Unigene3429_All	1620	6.04	13.39	8.48	9.47	15.86	13.58	13.62	18.50	21.32	1.15E+00	4.56E-20	Up	4.90E-01	1.90E-03		7.44E-01	1.31E-13		5.20E-01	5.09E-06		4.41E-01	5.08E-07		6.46E-01	1.77E-15		Unigene3429_All//gi|226492856|ref|NP_001149901.1|//2.00E-96//LOC100283529 [Zea mays] >gi|195635353|gb|ACG37145.1| TLD family protein [Zea mays]	Unigene3429_All//4.00E-112//AT4G38870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TLDc (InterPro:IPR006571); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G05590.2); Has 2018 Blast hits to 1865 proteins in 220 species: Archae - 0; Bacteria - 39; Metazoa - 1002; Fungi - 279; Plants - 129; Viruses - 34; Other Eukaryotes - 535 (source: NCBI BLink).	Unigene3429_All//0.00E+00//C0084623				nr -
Unigene34291_All	1672	18.15	43.37	34.87	16.57	22.90	24.31	11.40	10.17	11.53	1.26E+00	2.27E-75	Up	9.42E-01	3.50E-37		4.67E-01	4.80E-09		5.53E-01	9.31E-12		-1.65E-01	1.92E-01		1.61E-02	9.17E-01		Unigene34291_All//gi|222136867|gb|ACM45083.1|//7.00E-92//shikimate kinase [Vitis vinifera]	Unigene34291_All//2.00E-89//AT2G21940| shikimate kinase, putative	Unigene34291_All//0.00E+00//TC130248		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene34296_All	875	15.13	15.81	9.98	21.69	12.24	8.21	5.22	4.92	2.55	6.35E-02	6.94E-01		-6.00E-01	1.79E-04		-8.26E-01	1.55E-12		-1.40E+00	8.48E-26	Down	-8.50E-02	7.60E-01		-1.03E+00	3.21E-05	Down	Unigene34296_All//gi|224122284|ref|XP_002330585.1|//6.00E-96//amino acid permease [Populus trichocarpa] >gi|222872143|gb|EEF09274.1| amino acid permease [Populus trichocarpa]	Unigene34296_All//3.00E-90//AT5G23810| AAP7; amino acid transmembrane transporter	Unigene34296_All//2.00E-131//C0108113				nr -
Unigene34297_All	1747	14.79	18.56	16.12	33.48	19.26	7.94	9.17	4.83	2.05	3.27E-01	5.96E-04		1.24E-01	3.03E-01		-7.98E-01	1.30E-35		-2.08E+00	9.43E-137	Down	-9.25E-01	4.07E-13		-2.16E+00	4.43E-46	Down	Unigene34297_All//gi|224122284|ref|XP_002330585.1|//0.00E+00//amino acid permease [Populus trichocarpa] >gi|222872143|gb|EEF09274.1| amino acid permease [Populus trichocarpa]	Unigene34297_All//2.00E-173//AT5G23810| AAP7; amino acid transmembrane transporter	Unigene34297_All//8.00E-154//gi|109834753|gb|DW233318.1|DW233318				nr +

Unigene34298_All	2205	3.68	7.28	7.39	4.70	3.62	4.77	4.79	26.35	10.66	9.86E-01	6.36E-12		1.01E+00	5.37E-12	Up	-3.75E-01	3.12E-02		2.24E-02	9.33E-01		2.46E+00	5.70E-187	Up	1.15E+00	2.50E-27	Up	Unigene34298_All//gi|209954711|dbj|BAG80546.1|//1.00E-139//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene34298_All//3.00E-107//AT1G24100| UGT74B1 (UDP-glucosyl transferase 74B1); UDP-glycosyltransferase/ thiohydroximate beta-D-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene34298_All//0.00E+00//TC155405		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr -
Unigene34299_All	1765	1.07	2.07	2.17	2.03	2.99	3.25	4.60	4.81	14.45	9.54E-01	3.28E-03		1.03E+00	1.80E-03		5.55E-01	3.11E-02		6.77E-01	6.08E-03		6.38E-02	7.53E-01		1.65E+00	2.53E-50	Up	Unigene34299_All//gi|75162429|sp|Q8W485.1|Y5010_ARATH//4.00E-14//RecName: Full=Uncharacterized protein At5g50100, mitochondrial; Flags: Precursor >gi|17065380|gb|AAL32844.1| Unknown protein [Arabidopsis thaliana]	Unigene34299_All//4.00E-13//AT5G50100| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Thioredoxin-like fold (InterPro:IPR012336), Putative thiol-disulphide oxidoreductase DCC (InterPro:IPR007263); Has 598 Blast hits to 598 proteins in 152 species: Archae - 0; Bacteria - 266; Metazoa - 3; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 302 (source: NCBI BLink).	Unigene34299_All//0.00E+00//gi|11206721|gb|BF275651.1|BF275651					nr -
Unigene343_All	2795	2.30	3.99	2.50	3.62	3.09	3.47	13.04	11.53	29.48	7.93E-01	3.80E-06		1.16E-01	6.18E-01		-2.27E-01	2.43E-01		-5.86E-02	7.75E-01		-1.78E-01	3.56E-02		1.18E+00	1.18E-96	Up	Unigene343_All//gi|240256041|ref|NP_194031.5|//0.00E+00//hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana]	Unigene343_All//0.00E+00//AT4G23000| hydrolase/ protein serine/threonine phosphatase	Unigene343_All//0.00E+00//C0132057					nr +
Unigene3430_All	1629	0.77	2.74	1.57	3.15	4.08	2.63	1.51	3.21	3.42	1.83E+00	1.15E-08	Up	1.03E+00	1.37E-02		3.73E-01	1.13E-01		-2.58E-01	3.95E-01		1.09E+00	4.56E-06	Up	1.19E+00	1.98E-07	Up	Unigene3430_All//gi|226492856|ref|NP_001149901.1|//7.00E-98//LOC100283529 [Zea mays] >gi|195635353|gb|ACG37145.1| TLD family protein [Zea mays]	Unigene3430_All//2.00E-113//AT4G38870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TLDc (InterPro:IPR006571); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G05590.2); Has 2018 Blast hits to 1865 proteins in 220 species: Archae - 0; Bacteria - 39; Metazoa - 1002; Fungi - 279; Plants - 129; Viruses - 34; Other Eukaryotes - 535 (source: NCBI BLink).	Unigene3430_All//0.00E+00//C0084623					nr +
Unigene34300_All	2730	4.94	8.83	9.52	1.95	2.23	3.08	1.53	3.11	2.70	8.37E-01	1.69E-13		9.45E-01	5.94E-17		1.94E-01	4.98E-01		6.56E-01	8.67E-04		1.02E+00	1.84E-08	Up	8.16E-01	1.45E-05		Unigene34300_All//gi|209954711|dbj|BAG80546.1|//1.00E-144//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene34300_All//1.00E-113//AT2G43840| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene34300_All//0.00E+00//TC155405		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr +
Unigene34302_All	1355	9.34	31.67	14.30	9.63	12.61	27.06	17.01	36.00	39.46	1.76E+00	1.42E-73	Up	6.14E-01	1.96E-06		3.88E-01	2.78E-03		1.49E+00	3.20E-53	Up	1.08E+00	2.72E-49	Up	1.21E+00	3.49E-66	Up	Unigene34302_All//gi|226499086|ref|NP_001148943.1|//1.00E-104//metabolite transport protein csbC [Zea mays] >gi|195623490|gb|ACG33575.1| metabolite transport protein csbC [Zea mays]	Unigene34302_All//1.00E-86//AT1G67300| hexose transporter, putative	Unigene34302_All//0.00E+00//TC137637					nr -
Unigene34303_All	1925	1.71	7.21	4.37	5.72	6.96	7.41	2.57	2.84	2.96	2.07E+00	5.33E-30	Up	1.35E+00	5.24E-10	Up	2.83E-01	7.54E-02		3.75E-01	1.29E-02		1.46E-01	5.95E-01		2.04E-01	3.88E-01		Unigene34303_All//gi|226499086|ref|NP_001148943.1|//1.00E-180//metabolite transport protein csbC [Zea mays] >gi|195623490|gb|ACG33575.1| metabolite transport protein csbC [Zea mays]	Unigene34303_All//6.00E-89//AT1G67300| hexose transporter, putative	Unigene34303_All//0.00E+00//TC137637					nr -
Unigene34310_All	915	13.55	33.89	23.16	14.92	17.01	14.26	23.01	26.27	18.33	1.32E+00	3.05E-35	Up	7.73E-01	4.25E-10		1.90E-01	2.26E-01		-6.45E-02	7.13E-01		1.91E-01	7.49E-02		-3.28E-01	1.80E-03		Unigene34310_All//gi|115489038|ref|NP_001067006.1|//8.00E-80//Os12g0557400 [Oryza sativa Japonica Group] >gi|77556776|gb|ABA99572.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649513|dbj|BAF30025.1| Os12g0557400 [Oryza sativa Japonica Group]	Unigene34310_All//3.00E-85//AT3G62580| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: late embryogenesis abundant domain-containing protein / LEA domain-containing protein (TAIR:AT1G72100.1); Has 237 Blast hits to 236 proteins in 85 species: Archae - 0; Bacteria - 4; Metazoa - 103; Fungi - 69; Plants - 61; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene34310_All//0.00E+00//gi|13247139|gb|BF268772.2|BF268772					nr -
Unigene34318_All	5263	0.93	0.23	0.38	3.92	2.82	4.00	7.20	4.96	5.22	-2.02E+00	9.05E-11	Down	-1.28E+00	1.10E-05	Down	-4.75E-01	2.22E-05		2.93E-02	8.49E-01		-5.39E-01	4.12E-12		-4.65E-01	9.35E-10		Unigene34318_All//gi|225442190|ref|XP_002274489.1|//0.00E+00//PREDICTED: similar to midasin-related [Vitis vinifera]	Unigene34318_All//0.00E+00//AT1G67120| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / transcription factor binding	Unigene34318_All//0.00E+00//TC142574					nr +
Unigene3432_All	1182	3.28	20.79	8.33	30.09	22.02	23.88	14.49	8.17	5.43	2.67E+00	6.98E-71	Up	1.35E+00	1.49E-11	Up	-4.50E-01	4.33E-08		-3.34E-01	1.64E-04		-8.27E-01	1.08E-11		-1.42E+00	1.17E-27	Down	Unigene3432_All//gi|225580053|gb|ACN94264.1|//1.00E-110//expansin [Rehmannia glutinosa] >gi|225580055|gb|ACN94265.1| expansin [Rehmannia glutinosa]	Unigene3432_All//9.00E-109//AT2G39700| ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	Unigene3432_All//0.00E+00//gi|109879722|gb|DW508692.1|DW508692					nr +
Unigene34321_All	238	9.01	2.77	5.82	35.79	34.72	25.62	5.68	2.28	3.18	-1.70E+00	3.02E-04	Down	-6.32E-01	1.70E-01		-4.36E-02	8.38E-01		-4.82E-01	1.52E-02		-1.32E+00	1.25E-02		-8.38E-01	8.98E-02					Unigene34321_All//9.00E-29//gi|78343038|gb|DT563312.1|DT563312					
Unigene34322_All	1472	24.63	11.26	22.90	56.41	56.47	44.21	65.46	40.63	25.06	-1.13E+00	2.30E-32	Down	-1.05E-01	3.24E-01		1.50E-03	9.86E-01		-3.52E-01	1.56E-10		-6.88E-01	2.84E-45		-1.39E+00	1.32E-146	Down	Unigene34322_All//gi|15239123|ref|NP_201371.1|//0.00E+00//BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|2827715|emb|CAA16688.1| receptor protein kinase - like protein [Arabidopsis thaliana] >gi|10177328|dbj|BAB10677.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|20466696|gb|AAM20665.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|31711786|gb|AAP68249.1| At5g65700 [Arabidopsis thaliana] >gi|110741066|dbj|BAE98627.1| receptor protein kinase like protein [Arabidopsis thaliana] >gi|224589751|gb|ACN59407.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene34322_All//0.00E+00//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene34322_All//0.00E+00//TC157537					nr -
Unigene34323_All	1898	10.06	5.07	9.31	36.38	41.93	29.58	28.91	14.95	14.40	-9.88E-01	3.91E-14		-1.11E-01	4.46E-01		2.05E-01	2.58E-04		-2.99E-01	1.09E-06		-9.51E-01	5.15E-45		-1.01E+00	1.06E-50	Down	Unigene34323_All//gi|15239123|ref|NP_201371.1|//0.00E+00//BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|2827715|emb|CAA16688.1| receptor protein kinase - like protein [Arabidopsis thaliana] >gi|10177328|dbj|BAB10677.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|20466696|gb|AAM20665.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|31711786|gb|AAP68249.1| At5g65700 [Arabidopsis thaliana] >gi|110741066|dbj|BAE98627.1| receptor protein kinase like protein [Arabidopsis thaliana] >gi|224589751|gb|ACN59407.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene34323_All//0.00E+00//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene34323_All//0.00E+00//ES803113					nr -
Unigene34324_All	3445	15.55	76.14	31.59	8.14	15.26	27.79	2.32	14.51	5.64	2.29E+00	0.00E+00	Up	1.02E+00	4.58E-79	Up	9.07E-01	2.24E-38		1.77E+00	3.39E-177	Up	2.65E+00	6.50E-175	Up	1.28E+00	9.50E-27	Up	Unigene34324_All//gi|224589477|gb|ACN59272.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene34324_All//0.00E+00//AT1G72180| leucine-rich repeat transmembrane protein kinase, putative	Unigene34324_All//0.00E+00//TC159027					nr -
Unigene34327_All	2586	1.15	2.37	1.75	2.23	2.42	2.48	2.70	3.17	2.76	1.04E+00	1.95E-05	Up	6.02E-01	4.40E-02		1.17E-01	6.82E-01		1.50E-01	6.06E-01		2.32E-01	2.40E-01		3.17E-02	8.94E-01		Unigene34327_All//gi|8843792|dbj|BAA97340.1|//1.00E-81//PRL1 associated protein-like [Arabidopsis thaliana] >gi|17065352|gb|AAL32830.1| PRL1 associated protein-like [Arabidopsis thaliana] >gi|21387179|gb|AAM47993.1| PRL1-associated protein-like protein [Arabidopsis thaliana]	Unigene34327_All//6.00E-80//AT5G58720| PRL1-interacting factor, putative	Unigene34327_All//0.00E+00//TC154524					nr -

Unigene34328_All	499	14.36	35.13	16.65	27.85	25.74	37.02	15.08	30.82	28.02	1.29E+00	1.64E-19	Up	2.13E-01	3.58E-01		-1.14E-01	5.43E-01		4.10E-01	1.32E-03		1.03E+00	6.03E-15	Up	8.94E-01	3.04E-11		Unigene34328_All//gi|108707100|gb|ABF94895.1|//6.00E-07//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene34328_All//9.00E-07//AT1G20100| unknown protein	Unigene34328_All//1.00E-97//gi|164326688|gb|ES838503.1|ES838503				nr -
Unigene34330_All	1515	1.11	6.76	1.23	3.78	5.50	4.74	3.85	7.03	5.39	2.61E+00	3.57E-29	Up	1.55E-01	7.41E-01		5.41E-01	5.27E-03		3.26E-01	1.65E-01		8.69E-01	3.53E-08		4.85E-01	6.01E-03		Unigene34330_All|gi|8778818|gb|AAF26770.2|AC007396_19//2.00E-06//T10I2.10 [Arabidopsis thaliana]	Unigene34330_All//1.00E-06//AT2G17787| unknown protein	Unigene34330_All//0.00E+00//TC144189				nr +
Unigene34331_All	2150	7.08	2.95	2.15	33.97	29.71	26.70	46.27	9.68	19.33	-1.27E+00	1.23E-16	Down	-1.72E+00	1.01E-24	Down	-1.93E-01	1.09E-03		-3.47E-01	3.82E-09		-2.26E+00	1.86E-289	Down	-1.26E+00	9.54E-131	Down	Unigene34331_All|gi|2499489|sp|Q41141.1|PFFB_RICCO//0.00E+00//RecName: Full=Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta; Short=PFP; AltName: Full=6-phosphofructokinase, pyrophosphate dependent; AltName: Full=Pyrophosphate-dependent 6-phosphofructose-1-kinase; AltName: Full=PP1-PFK >gi|483536|emb|CAA83683.1| pyrophosphate-dependent phosphofructokinase beta subunit [Ricinus communis]	Unigene34331_All//0.00E+00//AT1G12000| pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative	Unigene34331_All//0.00E+00//TC173428		ko00051|Fructose and mannose metabolism		nr +
Unigene34333_All	2011	10.38	16.58	13.98	17.07	19.16	41.82	28.49	17.52	23.10	6.75E-01	6.85E-13		4.30E-01	4.69E-05		1.67E-01	6.68E-02		1.29E+00	4.24E-98	Up	-7.01E-01	3.72E-28		-3.03E-01	6.63E-07		Unigene34333_All|gi|124558720|gb|ABN13969.1|//0.00E+00//1-deoxy-D-xylulose 5-phosphate reductoisomerase [Gossypium barbadense]	Unigene34333_All//0.00E+00//AT5G62790| DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE); 1-deoxy-D-xylulose-5-phosphate reductoisomerase	Unigene34333_All//0.00E+00//ES797674		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene34335_All	2607	8.75	9.64	33.07	12.96	11.23	28.13	2.74	4.92	2.61	1.40E-01	2.40E-01		1.92E+00	1.06E-161	Up	-2.07E-01	2.73E-02		1.12E+00	3.18E-68	Up	8.45E-01	2.92E-09		-6.88E-02	7.44E-01		Unigene34335_All|gi|297840451|ref|XP_002888107.1|//0.00E+00//terpene synthase/cyclase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333948|gb|EFH64366.1| terpene synthase/cyclase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34335_All//0.00E+00//AT1G61120| TPS04 (TERPENE SYNTHASE 04); (E,E)-geranyllinalool synthase	Unigene34335_All//0.00E+00//gi|48829907|gb|CO128297.1|CO128297		ko00904|Diterpenoid biosynthesis		nr -
Unigene34336_All	844	2.85	4.50	3.60	8.09	9.42	6.85	1.25	1.88	2.97	6.59E-01	3.66E-02		3.35E-01	4.02E-01		2.21E-01	3.36E-01		-2.39E-01	3.45E-01		5.87E-01	2.24E-01		1.25E+00	4.67E-04	Up	Unigene34336_All|gi|242038447|ref|XP_002466618.1|//5.00E-06//hypothetical protein SORBIDRAFT_01g011130 [Sorghum bicolor] >gi|241920472|gb|EER93616.1| hypothetical protein SORBIDRAFT_01g011130 [Sorghum bicolor]	Unigene34336_All//2.00E-05//AT1G33710| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G60720.1); Has 337 Blast hits to 335 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 337; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene34336_All//8.00E-168//ES846791				nr +
Unigene34338_All	1359	5.51	4.25	7.25	16.16	17.21	19.11	5.13	7.47	1.93	-3.73E-01	8.64E-02		3.97E-01	4.14E-02		9.00E-02	5.35E-01		2.41E-01	3.07E-02		5.42E-01	7.00E-04		-1.41E+00	1.11E-11	Down	Unigene34338_All|gi|115473321|ref|NP_001060259.1|//1.00E-16//Os07g0613900 [Oryza sativa (japonica Group)] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa (japonica Group)]	Unigene34338_All//6.00E-13//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene34338_All//0.00E+00//gi|164297041|gb|ES846791.1|ES846791				nr +
Unigene34339_All	1615	4.92	4.67	4.29	7.87	7.29	7.08	10.29	5.67	4.81	-7.50E-02	7.24E-01		-2.00E-01	3.87E-01		-1.09E-01	5.67E-01		-1.53E-01	4.09E-01		-8.60E-01	4.11E-12		-1.10E+00	2.82E-18	Down	Unigene34339_All|gi|283520942|gb|ADB25213.1|//0.00E+00//ethylene response 1 [Citrus sinensis] >gi|283520950|gb|ADB25217.1| ethylene response 1 [Citrus hybrid cultivar]	Unigene34339_All//0.00E+00//AT1G66340| ETR1 (ETHYLENE RESPONSE 1); ethylene binding / protein histidine kinase/ two-component response regulator	Unigene34339_All//0.00E+00//gi|78339504|gb|DT559778.1|DT559778	Orphans	ko04712|Circadian rhythm - plant		nr -
Unigene3434_All	552	4.83	2.29	1.35	4.69	2.99	2.45	0.31	0.15	0.36	-1.07E+00	5.82E-03		-1.84E+00	2.96E-05	Down	-6.48E-01	8.79E-02		-9.35E-01	1.71E-02		-1.02E+00	6.14E-01		2.36E-01	8.83E-01		Unigene3434_All|gi|71143481|gb|AAZ23955.1|//6.00E-34//GDSL-lipase 1 [Capsicum annuum]	Unigene3434_All//3.00E-32//AT1G29670| GDSL-motif lipase/hydrolase family protein	Unigene3434_All//0.00E+00//TC150214			GO:0005576//GO:0009536//GO:0016787//GO:0030312//GO:0044238	nr +
Unigene34340_All	2794	8.80	7.60	5.97	17.24	14.53	12.11	15.60	11.76	7.77	-2.12E-01	6.69E-02		-5.61E-01	7.14E-07		-2.47E-01	7.27E-04		-5.10E-01	4.46E-12		-4.08E-01	1.25E-08		-1.01E+00	1.94E-40	Down	Unigene34340_All|gi|227072259|gb|ACL81480.3|//0.00E+00//ethylene receptor [Dimocarpus longan]	Unigene34340_All//0.00E+00//AT1G66340| ETR1 (ETHYLENE RESPONSE 1); ethylene binding / protein histidine kinase/ two-component response regulator	Unigene34340_All//0.00E+00//gi|164269243|gb|ES811472.1|ES811472	Orphans	ko04712|Circadian rhythm - plant		nr +
Unigene34343_All	1835	10.41	7.54	11.14	28.21	23.27	28.13	49.38	20.64	15.74	-4.65E-01	2.24E-04		9.86E-02	4.96E-01		-2.78E-01	5.65E-05		-3.80E-03	9.60E-01		-1.26E+00	1.00E-115	Down	-1.65E+00	1.86E-178	Down	Unigene34343_All|gi|11133775|sp|Q43116.1|PDI_RICCO//0.00E+00//RecName: Full=Protein disulfide-isomerase; Short=PDI; Flags: Precursor >gi|1134968|gb|AAB05641.1| protein disulphide isomerase PDI [Ricinus communis] >gi|1587210|prf||2206331A protein disulfide isomerase	Unigene34343_All//0.00E+00//AT1G21750| ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase	Unigene34343_All//0.00E+00//TC129621		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene34344_All	1773	3.42	2.00	3.96	8.99	7.67	4.56	19.65	8.93	6.00	-7.75E-01	1.23E-03		2.12E-01	3.91E-01		-2.29E-01	1.16E-01		-9.80E-01	1.60E-12		-1.14E+00	2.15E-38	Down	-1.71E+00	8.56E-73	Down	Unigene34344_All|gi|49257109|dbj|BAD24712.1|//0.00E+00//protein disulfide isomerase-like protein [Glycine max]	Unigene34344_All//1.00E-178//AT1G21750| ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase	Unigene34344_All//0.00E+00//TC129621		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene34347_All	480	3.82	2.11	3.33	9.65	11.77	17.12	29.60	16.46	8.80	-8.54E-01	7.59E-02		-1.97E-01	6.80E-01		2.86E-01	3.06E-01		8.27E-01	3.30E-05		-8.47E-01	3.24E-10		-1.75E+00	4.04E-31	Down	Unigene34347_All|gi|115462827|ref|NP_001055013.1|//8.00E-22//Os05g0244700 [Oryza sativa (japonica Group)] >gi|113578564|dbj|BAF16927.1| Os05g0244700 [Oryza sativa (japonica Group)]	Unigene34347_All//4.00E-13//AT5G57850| aminotransferase class IV family protein	Unigene34347_All//1.00E-162//gi|109874391|gb|DW503365.1|DW503365		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene34348_All	1852	8.81	5.88	6.90	18.08	22.63	23.85	46.44	15.30	19.55	-5.84E-01	2.16E-05		-3.53E-01	1.56E-02		3.24E-01	2.86E-05		4.00E-01	2.61E-07		-1.60E+00	8.26E-158	Down	-1.25E+00	1.76E-111	Down	Unigene34348_All|gi|115435558|ref|NP_001042537.1|//1.00E-123//Os01g0238500 [Oryza sativa (japonica Group)] >gi|56784110|dbj|BAD81481.1| branched-chain amino acid aminotransferase -like [Oryza sativa (japonica Group)] >gi|113532068|dbj|BAF04451.1| Os01g0238500 [Oryza sativa (japonica Group)]	Unigene34348_All//7.00E-103//AT5G57850| aminotransferase class IV family protein	Unigene34348_All//0.00E+00//TC141006		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene3435_All	1365	20.81	8.35	8.08	34.71	24.67	27.66	0.19	0.25	0.53	-1.32E+00	2.60E-32	Down	-1.37E+00	7.64E-33	Down	-4.92E-01	2.09E-12		-3.27E-01	1.35E-05		3.99E-01	7.24E-01		1.50E+00	4.94E-02		Unigene3435_All|gi|164519779|gb|AB559947.1|//1.00E-164//nectar protein 1 [Jacaranda mimosifolia]	Unigene3435_All//4.00E-156//AT1G29670| GDSL-motif lipase/hydrolase family protein	Unigene3435_All//0.00E+00//TC151876				nr -
Unigene34353_All	1858	3.38	1.94	2.87	5.28	8.77	6.15	8.99	3.37	5.83	-8.04E-01	6.47E-04		-2.38E-01	3.78E-01		7.31E-01	1.47E-08		2.20E-01	2.41E-01		-1.41E+00	4.23E-26	Down	-6.24E-01	1.46E-07		Unigene34353_All|gi|18404252|ref|NP_030235.1|//1.00E-158//ACT domain-containing protein [Arabidopsis thaliana] >gi|4883601|gb|AAD31570.1| expressed protein [Arabidopsis thaliana]	Unigene34353_All//3.00E-159//AT2G36840| ACT domain-containing protein	Unigene34353_All//0.00E+00//gi|109863327|gb|DW492304.1|DW492304				nr -
Unigene34356_All	2306	5.49	15.71	11.25	8.17	10.14	11.22	8.18	9.61	12.28	1.52E+00	2.50E-50	Up	1.03E+00	1.49E-19	Up	3.12E-01	4.65E-03		4.59E-01	1.10E-05		2.32E-01	3.36E-02		5.87E-01	5.65E-11		Unigene34356_All|gi|18422940|ref|NP_568701.1|//4.00E-49//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|30695512|ref|NP_851156.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|42573624|ref|NP_974908.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene34356_All//2.00E-35//AT5G48655| zinc finger (C3HC4-type RING finger) family protein	Unigene34356_All//0.00E+00//TC166144		ko04120|Ubiquitin mediated proteolysis//ko04146|Peroxisome		nr +
Unigene34357_All	1368	28.46	9.19	19.54	30.95	26.33	32.52	21.42	12.83	5.74	-1.63E+00	2.39E-60	Down	-5.42E-01	6.89E-10		-2.33E-01	3.38E-03		7.13E-02	4.71E-01		-7.39E-01	3.77E-16		-1.90E+00	8.57E-71	Down	Unigene34357_All|gi|38344244|emb|CAD41337.2|//2.00E-21//OJ991113_30.21 [Oryza sativa (japonica cultivar-group)]	Unigene34357_All//3.00E-20//AT3G09510| nucleic acid binding	Unigene34357_All//0.00E+00//ES841553				nr +
Unigene34358_All	2034	7.64	2.67	4.66	10.38	8.38	9.50	5.74	4.05	0.96	-1.52E+00	3.77E-22	Down	-7.13E-01	1.13E-06		-3.09E-01	7.71E-03		-1.28E-01	3.77E-01		-5.03E-01	6.74E-04		-2.58E+00	1.30E-41	Down	Unigene34358_All|gi|38344244|emb|CAD41337.2|//1.00E-28//OJ991113_30.21 [Oryza sativa (japonica cultivar-group)]	Unigene34358_All//5.00E-22//AT3G09510| nucleic acid binding	Unigene34358_All//0.00E+00//ES841553				nr -
Unigene34361_All	1940	57.74	30.51	36.56	71.87	70.88	42.46	11.40	3.43	2.28	-9.21E-01	1.60E-70		-6.59E-01	1.66E-38		-2.01E-02	7.49E-01		-7.59E-01	2.25E-68		-1.73E+00	5.78E-46	Down	-2.32E+00	3.69E-69	Down	Unigene34361_All|gi|75171749|sp|Q9FMX2.1|TCP7_ARATH//5.00E-74//RecName: Full=Transcription factor TCP7	Unigene34361_All//1.00E-51//AT5G23280| TCP family transcription factor, putative	Unigene34361_All//0.00E+00//TC138187	TCP			nr +
Unigene34364_All	2177	13.65	10.24	11.77	23.75	22.87	19.67	27.13	20.12	13.40	-4.15E-01	2.78E-05		-2.15E-01	4.86E-02		-5.44E-02	5.61E-01		-2.72E-01	1.80E-04		-4.31E-01	1.54E-12		-1.02E+00	1.35E-55	Down	Unigene34364_All|gi|195636088|gb|ACG37512.1|//1.00E-180//aspartate aminotransferase [Zea mays]	Unigene34364_All//6.00E-152//AT2G22250| aminotransferase class I and II family protein	Unigene34364_All//0.00E+00//TC140602				nr -
Unigene34365_All	4172	11.21	2.91	7.01	10.54	7.21	3.49	11.06	3.39	4.62	-1.94E+00	3.51E-92	Down	-6.78E-01	3.32E-17		-5.47E-01	6.21E-14		-1.60E+00	1.07E-71	Down	-1.71E+00	5.19E-93	Down	-1.26E+00	5.58E-61	Down	Unigene34365_All|gi|223452516|gb|ACM89585.1|//0.00E+00//receptor-like protein kinase [Glycine max]	Unigene34365_All//0.00E+00//AT5G56040| leucine-rich repeat protein kinase, putative	Unigene34365_All//0.00E+00//ES831508				nr +
Unigene34370_All	2826	1.80	3.14	1.39	2.47	2.27	1.25	14.84	18.75	5.13	8.05E-01	3.55E-05		-3.65E-01	2.09E-01		-1.23E-01	6.15E-01		-9.85E-01	6.72E-06		3.38E-01	1.79E-07		-1.53E+00	1.21E-74	Down	Unigene34370_All|gi|295311650|ref|YP_003387253.1|//1.00E-70//NADH dehydrogenase subunit 5 [Citrullus lanatus] >gi|259156778|gb|ACV96640.1| NADH dehydrogenase subunit 5 [Citrullus lanatus]	Unigene34370_All//4.00E-63//ATMG00665| Mitochondrial NADH dehydrogenase subunit 5. The gene is trans-spliced from three different pre-cursors, NAD5a, NAD5b and NAD5c.	Unigene34370_All//0.00E+00//TC151014		ko00190|Oxidative phosphorylation		nr -
Unigene34373_All	2779	2.77	3.30	4.66	5.04	4.24	4.49	5.96	3.19	1.76	2.54E-01	2.11E-01		7.51E-01	3.78E-06		-2.49E-01	1.09E-01		-1.67E-01	3.39E-01		-9.03E-01	4.68E-13		-1.76E+00	2.19E-36	Down	Unigene34373_All|gi|297802822|ref|XP_002869295.1|//0.00E+00//neurochondrin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315131|gb|EFH45554.1| neurochondrin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34373_All//0.00E+00//AT4G32050| neurochondrin family protein					nr +
Unigene34374_All	635	12.03	11.81	7.38	21.97	21.85	20.91	20.37	9.74	10.41	-2.66E-02	9.16E-01		-7.05E-01	1.28E-03		-7.30E-03	9.63E-01		-7.10E-02	6.70E-01		-1.06E+00	2.35E-13	Down	-9.68E-01	6.40E-12		Unigene34374_All|gi|145357905|ref|NP_196717.3|//2.00E-85//catalytic [Arabidopsis thaliana]	Unigene34374_All//8.00E-87//AT5G11560| catalytic	Unigene34374_All//0.00E+00//TC176793				nr +
Unigene34375_All	2656	11.52	9.82	9.30	19.64	16.80	17.62	23.94	11.47	11.35	-2.30E-01	2.31E-02		-3.09E-01	2.65E-03		-2.25E-01	1.44E-03		-1.57E-01	4.59E-02		-1.06E+00	3.53E-62	Down	-1.08E+00	2.16E-65	Down	Unigene34375_All|gi|145357905|ref|NP_196717.3|//0.00E+00//catalytic [Arabidopsis thaliana]	Unigene34375_All//0.00E+00//AT5G11560| catalytic	Unigene34375_All//0.00E+00//TC176793				nr +

Unigene34376_All	3408	5.16	10.15	6.83	4.06	3.08	2.58	7.33	7.68	15.50	9.77E-01	1.88E-24		4.05E-01	6.00E-04		-3.99E-01	5.71E-03		-6.53E-01	8.62E-06		6.64E-02	5.91E-01		1.08E+00	2.21E-54	Up	Unigene34376_All//gi|297798762|ref|XP_002867265.1|//0.00E+00//octicosapeptide/Phox/Bemip domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297313101|gb|EFH43524.1|octicosapeptide/Phox/Bemip domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene34376_All//4.00E-158//AT2G25290| binding	Unigene34376_All//2.00E-76//C0079568				nr +
Unigene34377_All	1241	0.72	1.55	1.24	1.65	0.89	1.06	3.13	1.35	2.38	1.11E+00	1.89E-02		7.96E-01	1.50E-01		-8.90E-01	3.87E-02		-6.41E-01	1.68E-01		-1.22E+00	1.77E-05	Down	-4.00E-01	1.44E-01		Unigene34377_All//gi|115435884|ref|NP_001042700.1|//1.00E-114//Os01g0269900 [Oryza sativa Japonica Group] >gi|75285838|sp|Q5NB12.1|ARP6_ORYSJ RecName: Full=Actin-related protein 6 >gi|190356066|sp|A2WNB0.1|ARP6_ORYSI RecName: Full=Actin-related protein 6 >gi|113532231|dbj|BAF04614.1|Os01g0269900 [Oryza sativa Japonica Group]	Unigene34377_All//6.00E-105//AT3G33520| ATARP6; structural constituent of cytoskeleton	Unigene34377_All//0.00E+00//C0119753				nr +
Unigene34383_All	3158	11.93	4.38	7.49	15.74	10.81	6.98	11.31	9.26	15.87	-1.45E+00	5.39E-49	Down	-6.72E-01	9.05E-14		-5.43E-01	1.88E-15		-1.17E+00	1.10E-50	Down	-2.88E-01	3.73E-04		4.88E-01	1.14E-13		Unigene34383_All//gi|79346260|ref|NP_173302.2|//0.00E+00//IBS1 (IMPAIRED IN BABA-INDUCED STERILITY 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene34383_All//0.00E+00//AT1G18670| IBS1 (IMPAIRED IN BABA-INDUCED STERILITY 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene34383_All//0.00E+00//TC150220				nr +
Unigene34386_All	3189	5.73	18.43	2.82	5.31	10.51	6.47	27.39	93.07	193.90	1.69E+00	1.18E-94	Up	-1.02E+00	1.24E-13	Down	9.84E-01	4.56E-28		2.85E-01	2.26E-02		1.76E+00	0.00E+00	Up	2.82E+00	0.00E+00	Up	Unigene34386_All//gi|14589309|emb|CAC43237.1|//0.00E+00//lipoxygenase [Sesbania rostrata]	Unigene34386_All//0.00E+00//AT1G72520| lipoxygenase, putative	Unigene34386_All//0.00E+00//TC163056		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr -
Unigene34387_All	582	2.97	4.70	1.46	5.48	4.26	1.86	3.12	1.29	1.03	6.64E-01	8.03E-02		-1.02E+00	5.26E-02		-3.63E-01	3.13E-01		-1.56E+00	1.50E-05	Down	-1.27E+00	3.87E-03		-1.61E+00	2.86E-04	Down			Unigene34387_All//0.00E+00//gi|164239785|gb|ES821053.1|ES821053				
Unigene34388_All	1989	38.72	39.54	37.83	101.91	115.72	66.08	43.79	18.45	25.30	3.01E-02	6.53E-01		-3.36E-02	6.26E-01		1.83E-01	2.72E-09		-6.25E-01	1.61E-70		-1.25E+00	1.15E-109	Down	-7.92E-01	1.35E-53		Unigene34388_All//gi|30678225|ref|NP_178637.2|//0.00E+00//glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Unigene34388_All//0.00E+00//AT2G05790| glycosyl hydrolase family 17 protein	Unigene34388_All//0.00E+00//TC179267		ko00500|Starch and sucrose metabolism		nr +
Unigene34389_All	653	3.53	3.18	4.24	15.87	10.60	7.54	13.60	1.15	2.56	-1.48E-01	7.16E-01		2.66E-01	5.14E-01		-5.82E-01	4.19E-04		-1.07E+00	1.28E-09	Down	-3.56E+00	3.73E-42	Down	-2.41E+00	1.84E-29	Down	Unigene34389_All//gi|211906544|gb|AC111765.1|//1.00E-97//class III peroxidase [Gossypium hirsutum]	Unigene34389_All//2.00E-74//AT5G40150| peroxidase, putative	Unigene34389_All//0.00E+00//TC137932		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene34390_All	1409	4.49	2.52	3.44	15.41	9.14	5.77	8.22	0.92	1.78	-8.36E-01	3.71E-04		-3.86E-01	1.29E-01		-7.54E-01	2.93E-12		-1.42E+00	6.19E-30	Down	-3.16E+00	2.66E-49	Down	-2.21E+00	1.99E-34	Down	Unigene34390_All//gi|211906544|gb|AC111765.1|//1.00E-156//class III peroxidase [Gossypium hirsutum]	Unigene34390_All//2.00E-124//AT3G28200| peroxidase, putative	Unigene34390_All//0.00E+00//gi|78329881|gb|DT550155.1|DT550155		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene34391_All	1177	40.32	13.60	22.08	120.49	92.83	65.16	20.37	2.88	6.36	-1.57E+00	2.44E-69	Down	-8.69E-01	1.70E-26		-3.76E-01	3.56E-22		-8.87E-01	9.67E-91		-2.82E+00	1.39E-90	Down	-1.68E+00	5.38E-49	Down	Unigene34391_All//gi|211906544|gb|AC111765.1|//1.00E-180//class III peroxidase [Gossypium hirsutum]	Unigene34391_All//2.00E-126//AT3G28200| peroxidase, putative	Unigene34391_All//0.00E+00//TC137932		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene34392_All	2185	9.46	8.42	9.29	16.55	15.60	10.96	24.28	16.79	11.25	-1.68E-01	2.04E-01		-2.67E-02	8.49E-01		-8.52E-02	4.28E-01		-5.95E-01	5.24E-12		-5.32E-01	2.79E-16		-1.11E+00	1.70E-57	Down	Unigene34392_All//gi|145335796|ref|NP_173134.2|//0.00E+00//sugar binding / transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|9802774|gb|AAF99843.1|AC051629_10 Hypothetical protein [Arabidopsis thaliana] >gi|34098911|gb|AAQ56838.1|At1g16900 [Arabidopsis thaliana]	Unigene34392_All//0.00E+00//AT1G16900| sugar binding / transferase, transferring glycosyl groups	Unigene34392_All//0.00E+00//TC169562		ko00510|N-Glycan biosynthesis		nr +
Unigene34396_All	1302	7.39	8.72	5.24	12.55	11.82	9.82	23.87	49.47	19.61	2.38E-01	1.86E-01		-4.98E-01	1.01E-02		-8.61E-02	6.10E-01		-3.54E-01	1.09E-02		1.05E+00	6.31E-62	Up	-2.83E-01	9.00E-04		Unigene34396_All//gi|18403920|ref|NP_565816.1|//7.00E-55//dual specificity protein phosphatase family protein [Arabidopsis thaliana] >gi|20197531|gb|AAD15447.2|expressed protein [Arabidopsis thaliana]	Unigene34396_All//2.00E-51//AT2G35680| dual specificity protein phosphatase family protein	Unigene34396_All//0.00E+00//TC140299				nr -
Unigene34398_All	4175	1.99	1.69	0.61	3.96	3.90	2.91	6.51	2.66	3.73	-2.40E-01	2.58E-01		-1.70E+00	1.34E-13	Down	-2.20E-02	8.94E-01		-4.45E-01	9.61E-04		-1.29E+00	1.31E-36	Down	-8.04E-01	8.79E-18		Unigene34398_All//gi|297804636|ref|XP_002870202.1|//0.00E+00//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297316038|gb|EFH46461.1|binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene34398_All//0.00E+00//AT4G15890| binding	Unigene34398_All//0.00E+00//gi|78336188|gb|DT556462.1|DT556462				nr +
Unigene34399_All	3497	3.23	1.06	2.36	8.75	5.10	7.77	12.05	4.73	5.59	-1.61E+00	1.03E-17	Down	-4.53E-01	1.07E-02		-7.78E-01	5.17E-18		-1.70E-01	1.15E-01		-1.35E+00	2.79E-60	Down	-1.11E+00	1.07E-45	Down	Unigene34399_All//gi|150421697|sp|Q9ZQW4.2|UPO2B_ARATH//0.00E+00//RecName: Full=UPF0202 protein At3g57940	Unigene34399_All//0.00E+00//AT1G10490| unknown protein	Unigene34399_All//0.00E+00//ES851887				nr +
Unigene34400_All	592	8.48	8.30	9.44	15.15	12.80	15.41	14.00	6.85	9.62	-3.13E-02	9.21E-01		1.55E-01	5.99E-01		-2.43E-01	2.38E-01		2.50E-02	9.28E-01		-1.03E+00	1.93E-08	Down	-5.41E-01	1.89E-03		Unigene34400_All//gi|46931208|gb|AT06408.1|//4.00E-42//At5g59410 [Arabidopsis thaliana]	Unigene34400_All//2.00E-43//AT5G59410| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Rab5-interacting (InterPro:IPR010742); BEST Arabidopsis thaliana protein match is: Rab5-interacting family protein (TAIR:AT3G29020.1); Has 154 Blast hits to 154 proteins in 67 species: Archae - 0; Bacteria - 0; Metazoa - 108; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink).	Unigene34400_All//0.00E+00//TC134024				nr -
Unigene34401_All	875	5.62	5.50	3.29	7.80	6.30	6.97	18.60	12.47	7.38	-3.10E-02	9.23E-01		-7.74E-01	6.13E-03		-3.09E-01	1.86E-01		-1.63E-01	5.42E-01		-5.77E-01	2.53E-06		-1.33E+00	4.01E-24	Down	Unigene34401_All//gi|46931208|gb|AT06408.1|//4.00E-57//At5g59410 [Arabidopsis thaliana]	Unigene34401_All//2.00E-58//AT5G59410| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Rab5-interacting (InterPro:IPR010742); BEST Arabidopsis thaliana protein match is: Rab5-interacting family protein (TAIR:AT3G29020.1); Has 154 Blast hits to 154 proteins in 67 species: Archae - 0; Bacteria - 0; Metazoa - 108; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink).	Unigene34401_All//0.00E+00//TC139054				nr +
Unigene34402_All	1117	3.79	4.99	3.58	7.18	4.29	3.68	12.15	5.95	7.63	3.95E-01	1.26E-01		-8.57E-02	7.78E-01		-7.45E-01	8.51E-05		-9.65E-01	1.80E-06		-1.03E+00	2.77E-13	Down	-6.71E-01	4.71E-07		Unigene34402_All//gi|46931208|gb|AT06408.1|//3.00E-55//At5g59410 [Arabidopsis thaliana]	Unigene34402_All//2.00E-56//AT5G59410| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Rab5-interacting (InterPro:IPR010742); BEST Arabidopsis thaliana protein match is: Rab5-interacting family protein (TAIR:AT3G29020.1); Has 154 Blast hits to 154 proteins in 67 species: Archae - 0; Bacteria - 0; Metazoa - 108; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink).	Unigene34402_All//0.00E+00//TC134024				nr +
Unigene34407_All	3682	4.18	4.32	1.65	5.49	4.40	4.66	9.37	6.48	5.15	4.87E-02	7.45E-01		-1.34E+00	1.53E-17	Down	-3.22E-01	6.62E-03		-2.37E-01	6.95E-02		-5.32E-01	7.22E-11		-8.63E-01	3.91E-25		Unigene34407_All//gi|42568712|ref|NP_201066.2|//0.00E+00//transportin-SR-related [Arabidopsis thaliana] >gi|34365727|gb|AAQ65175.1|At5g62590 [Arabidopsis thaliana]	Unigene34407_All//0.00E+00//AT5G62600| transportin-SR-related	Unigene34407_All//0.00E+00//TC136696				nr +
Unigene34409_All	695	19.50	15.31	12.57	42.29	29.43	31.52	36.26	29.83	15.42	-3.49E-01	2.47E-02		-6.34E-01	6.03E-05		-5.23E-01	9.27E-09		-4.24E-01	1.24E-05		-2.82E-01	4.47E-03		-1.23E+00	1.06E-32	Down	Unigene34409_All//gi|297829762|ref|XP_002882763.1|//8.00E-44//Ahal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328603|gb|EFH59022.1| Ahal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene34409_All//4.00E-45//AT3G12050| Ahal domain-containing protein	Unigene34409_All//0.00E+00//gi|13351710|gb|BG442058.1|BG442058				nr -
Unigene3441_All	1395	4.58	7.81	5.12	1.54	3.80	4.95	12.00	23.94	9.71	7.71E-01	8.65E-06		1.61E-01	5.19E-01		1.31E+00	2.94E-07	Up	1.69E+00	2.15E-12	Up	9.96E-01	8.50E-30		-3.06E-01	1.10E-02		Unigene3441_All//gi|15229731|ref|NP_187742.1|//1.00E-138//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|111074382|gb|AB604564.1|At3g11340 [Arabidopsis thaliana]	Unigene3441_All//5.00E-135//AT3G11340| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene3441_All//0.00E+00//gi|78336207|gb|DT556481.1|DT556481		ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene34410_All	1737	22.56	13.74	10.73	41.24	34.69	30.45	40.48	32.39	15.64	-7.16E-01	1.41E-16		-1.07E+00	5.94E-31	Down	-2.49E-01	1.58E-05		-4.38E-01	1.73E-13		-3.22E-01	6.88E-09		-1.37E+00	1.26E-105	Down	Unigene34410_All//gi|297829762|ref|XP_002882763.1|//1.00E-149//Ahal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328603|gb|EFH59022.1| Ahal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene34410_All//5.00E-132//AT3G12050| Ahal domain-containing protein	Unigene34410_All//0.00E+00//gi|78340688|gb|DT560962.1|DT560962				nr -

Unigene34411_All	2894	4.21	1.65	2.76	8.55	8.70	9.19	6.53	8.09	6.19	-1.36E+00	6.68E-15	Down	-6.10E-01	2.80E-04		2.40E-02	8.59E-01		1.04E-01	4.18E-01		3.09E-01	2.63E-03		-7.62E-02	5.74E-01		Unigene34411_All//gi|297830396|ref|XP_002883080.1|//0.00E+00//cyclic nucleotide-binding transporter 1 [Arabidopsis lyrata subsp. lyrata] >gi|297328920|gb|EFH59339.1| cyclic nucleotide-binding transporter 1 [Arabidopsis lyrata subsp. lyrata]	Unigene34411_All//0.00E+00//AT3G17700| CNBT1 (CYCLIC NUCLEOTIDE-BINDING TRANSPORTER 1); calmodulin binding / cyclic nucleotide binding / ion channel	Unigene34411_All//0.00E+00//DF464890		ko04626|Plant-pathogen interaction		nr +
Unigene34413_All	2526	2.51	1.97	2.93	3.67	3.64	2.81	5.88	4.25	2.10	-3.50E-01	1.44E-01		2.25E-01	3.60E-01		-1.11E-02	9.52E-01		-3.86E-01	4.65E-02		-4.66E-01	3.17E-04		-1.49E+00	8.22E-26	Down	Unigene34413_All//gi|15809982|gb|AAL06918.1|//2.00E-62//AT3g10250/F14P13_15 [Arabidopsis thaliana] >gi|18958054|gb|AAL79600.1| AT3g10250/F14P13_15 [Arabidopsis thaliana] >gi|22242363|dbj|BAH19784.1| AT3G10250 [Arabidopsis thaliana]	Unigene34413_All//3.00E-63//AT3G10250| unknown protein	Unigene34413_All//0.00E+00//gi|164248448|gb|ES834173.1|ES834173				nr -
Unigene34415_All	636	9.30	21.27	5.44	10.42	9.37	15.55	22.67	29.24	25.18	1.19E+00	1.41E-13	Up	-7.72E-01	2.33E-03		-1.53E-01	5.61E-01		5.78E-01	1.32E-03		3.67E-01	1.46E-03		1.52E-01	2.58E-01		Unigene34415_All//gi|195652519|gb|ACG45727.1|//2.00E-50//PRA1 family protein [Zea mays]	Unigene34415_All//6.00E-38//AT5G02040| PRA1.A1 (PRENYLATED RAB ACCEPTOR 1.A1)	Unigene34415_All//0.00E+00//gi|78349703|gb|DT569977.1|DT569977				nr -
Unigene34416_All	701	11.72	28.84	12.08	16.20	16.31	26.80	57.90	79.84	56.09	1.30E+00	1.27E-22	Up	4.37E-02	8.41E-01		9.50E-03	9.69E-01		7.26E-01	5.90E-09		4.63E-01	1.74E-13		-4.58E-02	6.06E-01		Unigene34416_All//gi|195652519|gb|ACG45727.1|//9.00E-32//PRA1 family protein [Zea mays]	Unigene34416_All//1.00E-20//AT5G02040| PRA1.A1 (PRENYLATED RAB ACCEPTOR 1.A1)	Unigene34416_All//0.00E+00//DR463879				nr +
Unigene34419_All	741	2.26	0.96	0.86	6.25	6.92	3.11	3.71	2.59	3.12	-1.24E+00	1.66E-02		-1.39E+00	1.16E-02		1.47E-01	6.24E-01		-1.01E+00	2.76E-04	Down	-5.15E-01	1.37E-01		-2.50E-01	4.76E-01		Unigene34419_All//gi|124359479|gb|ABN05917.1|//6.00E-50//Engulfment and cell motility, ELM [Medicago truncatula]	Unigene34419_All//7.00E-49//AT2G14770| phagocytosis and cell motility protein ELMO1-related	Unigene34419_All//6.00E-165//TC137387				nr +
Unigene3442_All	1246	27.00	20.21	21.80	45.70	44.77	46.07	85.07	88.59	38.27	-4.18E-01	6.16E-06		-3.09E-01	1.50E-03		-2.95E-02	7.71E-01		1.17E-02	9.08E-01		5.85E-02	2.67E-01		-1.15E+00	5.10E-121	Down	Unigene3442_All//gi|15231451|ref|NP_190238.1|//1.00E-82//epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related [Arabidopsis thaliana]	Unigene3442_All//2.00E-74//AT3G46540| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	Unigene3442_All//0.00E+00//TC170912				nr -
Unigene34423_All	1978	1.08	1.18	0.89	3.53	2.18	2.17	8.12	33.47	3.26	1.20E-01	7.67E-01		-2.88E-01	5.45E-01		-6.96E-01	7.42E-04		-7.01E-01	1.30E-03		2.04E+00	1.74E-169	Up	-1.32E+00	2.52E-23	Down	Unigene34423_All//gi|8778289|gb|AAF79298.1|AC068602_21//2.00E-64//F14D16.29 [Arabidopsis thaliana]	Unigene34423_All//4.00E-68//AT1G19130| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF985 (InterPro:IPR009327), RmlC-like jelly roll fold (InterPro:IPR014710); Has 778 Blast hits to 778 proteins in 280 species: Archae - 8; Bacteria - 513; Metazoa - 2; Fungi - 16; Plants - 22; Viruses - 0; Other Eukaryotes - 217 (source: NCBI BLink).	Unigene34423_All//0.00E+00//gi|164369567|gb|EX170160.1|EX170160		ko03018|RNA degradation		nr +
Unigene34424_All	1716	12.41	5.17	9.34	26.42	14.87	13.63	8.06	8.67	3.71	-1.26E+00	6.29E-23	Down	-4.10E-01	9.44E-04		-8.29E-01	1.43E-29		-9.54E-01	4.07E-33		1.06E-01	4.99E-01		-1.12E+00	8.64E-16	Down	Unigene34424_All//gi|18379261|ref|NP_565267.1|//1.00E-151//epsin N-terminal homology (ENTH) domain-containing protein [Arabidopsis thaliana] >gi|46395897|sp|Q8LBH2.2|CAP8_ARATH RecName: Full=Putative clathrin assembly protein At2g01600 >gi|15983438|gb|AAL11587.1|AF424593_1 At2g01600/F219.22 [Arabidopsis thaliana] >gi|20197399|gb|AAM15059.1| expressed protein [Arabidopsis thaliana]	Unigene34424_All//1.00E-137//AT2G01600| epsin N-terminal homology (ENTH) domain-containing protein	Unigene34424_All//0.00E+00//TC163661				nr +
Unigene34425_All	2261	2.38	1.61	2.12	5.86	4.10	3.00	4.13	3.31	1.37	-5.63E-01	2.86E-02		-1.69E-01	5.68E-01		-5.17E-01	3.34E-04		-9.68E-01	2.56E-10		-3.21E-01	6.72E-02		-1.59E+00	3.46E-18	Down	Unigene34425_All//gi|18379261|ref|NP_565267.1|//0.00E+00//epsin N-terminal homology (ENTH) domain-containing protein [Arabidopsis thaliana] >gi|46395897|sp|Q8LBH2.2|CAP8_ARATH RecName: Full=Putative clathrin assembly protein At2g01600 >gi|15983438|gb|AAL11587.1|AF424593_1 At2g01600/F219.22 [Arabidopsis thaliana] >gi|20197399|gb|AAM15059.1| expressed protein [Arabidopsis thaliana]	Unigene34425_All//0.00E+00//AT2G01600| epsin N-terminal homology (ENTH) domain-containing protein	Unigene34425_All//0.00E+00//TC163661				nr +
Unigene34430_All	3576	3.01	1.39	1.19	7.10	5.13	5.39	10.95	4.63	6.19	-1.12E+00	5.32E-10	Down	-1.34E+00	1.94E-12	Down	-4.69E-01	2.30E-06		-3.98E-01	1.74E-04		-1.24E+00	2.06E-49	Down	-8.22E-01	3.61E-26		Unigene34430_All//gi|30699531|ref|NP_178183.2|//0.00E+00//SAR3 (SUPPRESSOR OF AUXIN RESISTANCE 3); porin [Arabidopsis thaliana]	Unigene34430_All//0.00E+00//AT1G80680| SAR3 (SUPPRESSOR OF AUXIN RESISTANCE 3); porin	Unigene34430_All//0.00E+00//TC178130				nr +
Unigene34432_All	2062	28.98	22.53	27.22	35.32	25.72	41.66	19.13	27.91	81.84	-3.63E-01	8.49E-08		-9.03E-02	2.61E-01		-4.58E-01	1.64E-16		2.38E-01	1.58E-05		5.45E-01	2.55E-18		2.10E+00	0.00E+00	Up	Unigene34432_All//gi|30694690|ref|NP_851134.1|//4.00E-68//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|16604442|gb|AAL24227.1| AT5g45100/K17022_9 [Arabidopsis thaliana] >gi|23505847|gb|AAN28783.1| At5g45100/K17022_9 [Arabidopsis thaliana]	Unigene34432_All//4.00E-55//AT5G45100| protein binding / zinc ion binding	Unigene34432_All//0.00E+00//TC136333				nr +
Unigene34434_All	5182	6.91	4.37	4.31	17.85	17.72	11.65	11.13	4.27	6.94	-6.60E-01	2.71E-13		-6.82E-01	1.97E-13		-1.04E-02	8.79E-01		-6.15E-01	1.41E-31		-1.38E+00	3.89E-85	Down	-6.81E-01	1.01E-27		Unigene34434_All//gi|42563167|ref|NP_177385.2|//0.00E+00//COP1-interacting protein-related [Arabidopsis thaliana]	Unigene34434_All//0.00E+00//AT3G14172| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: COP1-interacting protein-related (TAIR:AT1G72410.1); Has 2665 Blast hits to 1956 proteins in 215 species: Archae - 2; Bacteria - 189; Metazoa - 878; Fungi - 141; Plants - 132; Viruses - 5; Other Eukaryotes - 1318 (source: NCBI BLink).	Unigene34434_All//0.00E+00//TC178937				nr +
Unigene34437_All	4457	0.93	1.69	0.56	2.06	2.59	3.07	12.05	13.80	24.71	8.69E-01	4.81E-05		-7.24E-01	2.08E-02		3.32E-01	5.03E-02		5.78E-01	1.03E-04		1.96E-01	1.43E-03		1.04E+00	2.93E-105	Up	Unigene34437_All//gi|224100571|ref|XP_002311928.1|//0.00E+00//aminophospholipid ATPase [Populus trichocarpa] >gi|222851748|gb|EEE89295.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene34437_All//0.00E+00//AT5G04930| ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	Unigene34437_All//0.00E+00//DF462428				nr +
Unigene34443_All	3742	52.80	25.98	35.38	20.25	24.59	18.78	7.10	6.43	7.39	-1.02E+00	1.49E-147	Down	-5.78E-01	1.85E-53		2.80E-01	2.02E-08		-1.09E-01	1.07E-01		-1.41E-01	1.83E-01		5.84E-02	6.12E-01		Unigene34443_All//gi|225445166|ref|XP_002280712.1|//0.00E+00//PREDICTED: similar to Os12g0541500 [Vitis vinifera]	Unigene34443_All//0.00E+00//AT4G29060| emb2726 (embryo defective 2726); RNA binding / translation elongation factor	Unigene34443_All//0.00E+00//TC143864		ko03010|Ribosome//ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03018|RNA degradation		nr -
Unigene34445_All	927	0.79	0.27	0.80	14.94	14.23	12.57	15.83	1.76	5.29	-1.53E+00	7.78E-02		2.53E-02	9.95E-01		-7.04E-02	7.11E-01		-2.49E-01	1.27E-01		-3.17E+00	1.85E-62	Down	-1.58E+00	6.50E-28	Down	Unigene34445_All//gi|195653459|gb|ACG46197.1|//1.00E-106//integral membrane protein 1ike [Zea mays]	Unigene34445_All//2.00E-117//AT2G28315| LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: transporter-related (TAIR:AT1G06890.2); Has 1852 Blast hits to 1847 proteins in 207 species: Archae - 0; Bacteria - 58; Metazoa - 582; Fungi - 250; Plants - 685; Viruses - 0; Other Eukaryotes - 277 (source: NCBI BLink).	Unigene34445_All//0.00E+00//TC150441				nr -
Unigene34446_All	1432	0.40	0.74	0.37	11.31	10.53	8.58	18.19	1.11	5.37	8.87E-01	1.85E-01		-1.12E-01	9.07E-01		-1.02E-01	5.62E-01		-3.98E-01	3.89E-03		-4.04E+00	2.03E-135	Down	-1.76E+00	8.66E-57	Down	Unigene34446_All//gi|195653459|gb|ACG46197.1|//1.00E-138//integral membrane protein 1ike [Zea mays]	Unigene34446_All//6.00E-149//AT2G28315| LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: transporter-related (TAIR:AT1G06890.2); Has 1852 Blast hits to 1847 proteins in 207 species: Archae - 0; Bacteria - 58; Metazoa - 582; Fungi - 250; Plants - 685; Viruses - 0; Other Eukaryotes - 277 (source: NCBI BLink).	Unigene34446_All//0.00E+00//TC150441				nr -
Unigene34447_All	1474	0.53	1.20	2.57	69.35	47.99	35.42	11.73	9.05	4.16	1.18E+00	1.88E-02		2.27E+00	3.18E-09	Up	-5.31E-01	3.67E-30		-9.69E-01	5.27E-76		-3.75E-01	1.78E-03		-1.50E+00	3.38E-30	Down	Unigene34447_All//gi|195653459|gb|ACG46197.1|//1.00E-138//integral membrane protein 1ike [Zea mays]	Unigene34447_All//1.00E-150//AT2G28315| LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: transporter-related (TAIR:AT1G06890.2); Has 1852 Blast hits to 1847 proteins in 207 species: Archae - 0; Bacteria - 58; Metazoa - 582; Fungi - 250; Plants - 685; Viruses - 0; Other Eukaryotes - 277 (source: NCBI BLink).	Unigene34447_All//0.00E+00//TC150441				nr +
Unigene34448_All	964	1.74	2.52	1.88	3.05	1.50	0.98	45.13	123.96	37.86	5.39E-01	1.92E-01		1.13E-01	8.10E-01		-1.02E+00	2.82E-03		-1.63E+00	1.75E-05	Down	1.46E+00	2.24E-190	Up	-2.54E-01	3.68E-04		Unigene34448_All//gi|25044823|gb|AM28575.1|//2.00E-69//germin-1ike protein [Ananas comosus]	Unigene34448_All//2.00E-66//AT1G18980| germin-1ike protein, putative	Unigene34448_All//0.00E+00//TC154306				nr -

Unigene34449_All	1885	8.44	4.01	5.00	10.33	11.71	17.25	11.17	7.41	6.64	-1.08E+00	1.50E-13	Down	-7.55E-01	1.89E-07		1.81E-01	1.56E-01		7.39E-01	1.62E-15		-5.93E-01	2.76E-08		-7.51E-01	1.54E-12		Unigene34449_All//gi|224121584|ref|XP_002318620.1|//4.00E-68//5-formyltetrahydrofolate cyclo-ligase [Populus trichocarpa] >gi|222859293|gb|EEE96840.1| 5-formyltetrahydrofolate cyclo-ligase [Populus trichocarpa]	Unigene34449_All//2.00E-58//AT5G13050| 5-FCL (5-FORMYLTETRAHYDROFOLATE CYCLOLIGASE); 5-formyltetrahydrofolate cyclo-ligase	Unigene34449_All//0.00E+00//gi|48796337|gb|C0097651.1|C0097651		ko00670|One carbon pool by folate		nr +
Unigene34451_All	309	0.00	0.00	0.00	1.29	1.45	1.17	67.32	131.07	168.77	null	null		null	null		1.68E-01	9.04E-01		-1.41E-01	9.04E-01		9.61E-01	5.98E-34		1.33E+00	6.22E-74	Up	Unigene34451_All//gi|47026921|gb|AAT08681.1|//7.00E-39//aldo/keto reductase [Hyacinthus orientalis]	Unigene34451_All//4.00E-32//AT1G60710| ATB2; oxidoreductase	Unigene34451_All//5.00E-114//TC172706		ko00053|Ascorbate and aldarate metabolism		nr +
Unigene34452_All	584	3.49	1.82	5.38	3.75	5.31	4.95	35.33	46.45	79.95	-9.39E-01	3.76E-02		6.23E-01	9.08E-02		5.00E-01	1.71E-01		3.99E-01	3.21E-01		3.95E-01	2.18E-05		1.18E+00	2.96E-55	Up	Unigene34452_All//gi|185621058|gb|ACG32359.1|//6.00E-71//auxin-induced protein PCNT115 [Zea mays]	Unigene34452_All//1.00E-60//AT1G60690| aldo/keto reductase family protein	Unigene34452_All//9.00E-136//TC172706		ko00053|Ascorbate and aldarate metabolism		nr +
Unigene34453_All	1580	8.38	9.56	8.19	12.80	9.81	17.92	135.97	361.35	60.39	1.90E-01	2.22E-01		-3.28E-02	8.52E-01		-3.84E-01	8.78E-04		4.86E-01	9.35E-07		1.41E+00	0.00E+00	Up	-1.17E+00	7.55E-251	Down	Unigene34453_All//gi|297610489|ref|NP_001061615.2|//1.00E-133//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene34453_All//5.00E-106//AT1G60690| aldo/keto reductase family protein	Unigene34453_All//0.00E+00//TC164061		ko00010|Glycolysis / Gluconeogenesis//ko00053|Ascorbate and aldarate metabolism/ko00561|Glycerolipid metabolism		nr -
Unigene34459_All	627	1.34	2.51	1.87	3.81	2.47	4.32	2.29	3.80	5.21	9.08E-01	8.56E-02		4.85E-01	4.47E-01		-6.26E-01	1.19E-01		1.81E-01	6.83E-01		7.29E-01	4.86E-02		1.18E+00	1.06E-04	Up	Unigene34459_All//gi|15240208|ref|NP_188554.1|//3.00E-50//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|30693076|ref|NP_851102.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|145334655|ref|NP_001078673.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|186527150|ref|NP_001119323.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|186527153|ref|NP_001119324.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|15450067|gb|AAK96477.1| AT5g37380/MXJ8_170 [Arabidopsis thaliana] >gi|27363370|gb|AAO11604.1| At5g37380/MXJ8_170 [Arabidopsis thaliana]	Unigene34459_All//2.00E-51//AT5G37380| DNAJ heat shock N-terminal domain-containing protein	Unigene34459_All//0.00E+00//TC152894		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene34466_All	1995	7.45	5.33	8.25	8.99	8.91	6.27	9.43	4.40	3.75	-4.82E-01	8.95E-04		1.47E-01	3.65E-01		-1.33E-02	9.38E-01		-5.20E-01	4.52E-05		-1.10E+00	4.73E-20	Down	-1.33E+00	1.45E-27	Down	Unigene34466_All//gi|15229721|ref|NP_189945.1|//4.00E-84//zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana]	Unigene34466_All//2.00E-45//AT3G43590| zinc knuckle (CCHC-type) family protein	Unigene34466_All//0.00E+00//gi|164265493|gb|ES848936.1|ES848936				nr -
Unigene3447_All	1131	3.15	4.26	7.02	26.43	28.83	30.03	14.02	9.16	8.17	4.36E-01	1.21E-01		1.16E+00	1.41E-07	Up	1.26E-01	2.43E-01		1.84E-01	6.41E-02		-6.13E-01	8.67E-07		-7.79E-01	3.15E-10		Unigene3447_All//gi|192910808|gb|ACF06512.1|//1.00E-112//peroxisome type ascorbate peroxidase [Elaeis guineensis]	Unigene3447_All//1.00E-108//AT4G35000| APX3 (ASCORBATE PEROXIDASE 3); L-ascorbate peroxidase	Unigene3447_All//0.00E+00//TC147674		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene34471_All	1545	21.50	6.03	9.37	15.96	10.12	5.58	5.39	8.14	12.04	-1.83E+00	1.06E-60	Down	-1.20E+00	2.46E-31	Down	-6.57E-01	5.66E-11		-1.52E+00	2.00E-37	Down	5.95E-01	2.65E-05		1.16E+00	5.32E-22	Up	Unigene34471_All//gi|13785467|dbj|BAB43907.1|//0.00E+00//phosphoenol pyruvate carboxykinase [Flaveria trinervia]	Unigene34471_All//0.00E+00//AT4G37870| PCK1 (PHOSPHOENOLPYRUVATE CARBOXYKINASE 1); ATP binding / phosphoenolpyruvate carboxykinase (ATP)/ phosphoenolpyruvate carboxykinase/ purine nucleotide binding	Unigene34471_All//0.00E+00//TC143225		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism/ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)		nr +
Unigene34474_All	2451	3.67	5.29	3.35	9.51	7.61	5.91	7.33	3.31	4.91	5.28E-01	7.49E-04		-1.34E-01	5.52E-01		-3.21E-01	3.15E-03		-6.85E-01	4.74E-10		-1.15E+00	1.71E-20	Down	-5.79E-01	3.67E-07		Unigene34474_All//gi|42562765|ref|NP_175971.3|//0.00E+00//transcription factor-related [Arabidopsis thaliana]	Unigene34474_All//0.00E+00//AT1G55750| transcription factor-related	Unigene34474_All//0.00E+00//ES811187		ko03420|Nucleotide excision repair//ko03022|Basal transcription factors		nr +
Unigene34476_All	1316	13.00	6.85	11.17	25.40	23.99	16.64	5.94	1.46	2.36	-9.24E-01	1.80E-11		-2.19E-01	1.42E-01		-8.21E-02	4.72E-01		-6.10E-01	1.33E-11		-2.02E+00	1.83E-20	Down	-1.33E+00	5.21E-12	Down	Unigene34476_All//gi|224126287|ref|XP_002319802.1|//1.00E-154//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222858178|gb|EEE95725.1| glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene34476_All//5.00E-143//AT5G54690| GAUT12 (GALACTURONOSYLTRANSFERASE 12); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene34476_All//0.00E+00//D9518171				nr -
Unigene34477_All	2002	2.51	1.90	2.93	17.92	18.11	15.95	6.72	1.90	2.27	-4.02E-01	1.38E-01		2.22E-01	4.01E-01		1.58E-02	8.94E-01		-1.68E-01	8.52E-02		-1.82E+00	3.53E-30	Down	-1.57E+00	2.78E-25	Down	Unigene34477_All//gi|224126287|ref|XP_002319802.1|//0.00E+00//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222858178|gb|EEE95725.1| glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene34477_All//0.00E+00//AT5G54690| GAUT12 (GALACTURONOSYLTRANSFERASE 12); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene34477_All//0.00E+00//TC133176				nr +
Unigene34481_All	3043	2.44	0.70	3.66	12.36	8.87	6.04	6.09	1.84	1.52	-1.80E+00	8.28E-14	Down	5.83E-01	9.74E-04		-4.78E-01	1.82E-09		-1.03E+00	2.33E-31	Down	-1.73E+00	2.44E-38	Down	-2.00E+00	2.99E-48	Down	Unigene34481_All//gi|9759281|dbj|BAB09746.1|//0.00E+00//receptor protein kinase-like [Arabidopsis thaliana] >gi|224589717|gb|ACN59390.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene34481_All//0.00E+00//AT5G51350| leucine-rich repeat transmembrane protein kinase, putative	Unigene34481_All//0.00E+00//C0097615				nr -
Unigene34485_All	2076	1.54	1.00	1.39	3.89	6.30	8.05	4.15	6.38	8.69	-6.20E-01	7.51E-02		-1.51E-01	6.73E-01		6.97E-01	1.80E-06		1.05E+00	1.93E-14	Up	6.19E-01	6.85E-06		1.07E+00	9.42E-19	Up	Unigene34485_All//gi|224120592|ref|XP_002318368.1|//1.00E-146//nbs-lrr resistance protein [Populus trichocarpa] >gi|222859041|gb|EEE96588.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene34485_All//7.00E-69//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene34485_All//0.00E+00//TC147040		ko04626|Plant-pathogen interaction		nr -
Unigene34486_All	1764	3.03	0.95	2.02	7.29	5.33	5.12	5.85	7.82	12.83	-1.67E+00	3.35E-09	Down	-5.81E-01	3.23E-02		-4.51E-01	2.42E-03		-5.09E-01	1.00E-03		4.19E-01	2.03E-03		1.13E+00	1.20E-25	Up	Unigene34486_All//gi|224120592|ref|XP_002318368.1|//1.00E-147//nbs-lrr resistance protein [Populus trichocarpa] >gi|222859041|gb|EEE96588.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene34486_All//1.00E-82//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene34486_All//0.00E+00//TC131733		ko04626|Plant-pathogen interaction		nr +
Unigene34487_All	2471	7.26	2.05	3.19	19.86	13.46	8.79	23.54	5.55	6.43	-1.82E+00	7.31E-33	Down	-1.19E+00	6.08E-17	Down	-5.61E-01	3.68E-16		-1.18E+00	3.65E-50	Down	-2.09E+00	2.13E-153	Down	-1.87E+00	5.65E-137	Down	Unigene34487_All//gi|67003905|gb|AAN04496.2|//0.00E+00//endo-1,4-beta-glucanase [Gossypium hirsutum]	Unigene34487_All//0.00E+00//AT1G64390| AtGH9C2 (Arabidopsis thaliana glycosyl hydrolase 9C2); carbohydrate binding / catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene34487_All//0.00E+00//TC132254		ko00500|Starch and sucrose metabolism		nr -
Unigene3449_All	2239	1.26	0.95	1.14	3.32	4.37	3.17	2.98	1.19	3.06	-4.09E-01	2.82E-01		-1.45E-01	7.02E-01		3.98E-01	2.95E-02		-6.59E-02	7.85E-01		-1.32E+00	6.45E-10	Down	3.67E-02	8.76E-01		Unigene3449_All//gi|19715622|gb|AAL91632.1|//0.00E+00//AT4g37080/CTA10_280 [Arabidopsis thaliana] >gi|23463049|gb|AAN33194.1| At4g37080/CTA10_280 [Arabidopsis thaliana]	Unigene3449_All//4.00E-159//AT4G37080| unknown protein	Unigene3449_All//0.00E+00//TC138226				nr +
Unigene34491_All	1597	1.57	1.52	3.30	4.90	6.06	6.73	3.10	1.39	2.69	-4.63E-02	9.17E-01		1.07E+00	9.71E-05	Up	3.07E-01	1.10E-01		4.59E-01	8.58E-03		-1.16E+00	2.65E-06	Down	-2.01E-01	4.27E-01		Unigene34491_All//gi|145336060|ref|NP_173760.2|//0.00E+00//polygalacturonase [Arabidopsis thaliana]	Unigene34491_All//0.00E+00//AT1G23460| polygalacturonase	Unigene34491_All//4.00E-131//C0097869		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene34493_All	3364	7.00	6.19	4.24	5.46	4.51	5.67	8.60	13.34	17.68	-1.77E-01	1.42E-01		-7.22E-01	5.88E-10		-2.76E-01	3.26E-02		5.22E-02	7.25E-01		6.34E-01	9.61E-19		1.04E+00	1.49E-57	Up	Unigene34493_All//gi|297817774|ref|XP_002877270.1|//0.00E+00//phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323108|gb|EFH53529.1| phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34493_All//0.00E+00//AT3G43220| phosphoinositide phosphatase family protein	Unigene34493_All//0.00E+00//gi|3325746|gb|AI054632.1|AI054632				nr -
Unigene34495_All	962	0.38	0.42	0.33	2.80	4.58	6.15	16.92	11.38	121.75	1.47E-01	8.98E-01		-1.97E-01	8.66E-01		7.12E-01	1.12E-02		1.14E+00	3.50E-06	Up	-5.72E-01	3.14E-06		2.85E+00	0.00E+00	Up	Unigene34495_All//gi|297817536|ref|XP_002876651.1|//1.00E-150//metal ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322489|gb|EFH52910.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene34495_All//5.00E-146//AT3G62010| unknown protein					nr +
Unigene345_All	2465	15.11	12.79	15.47	46.22	45.26	47.20	36.91	17.55	14.98	-2.41E-01	7.45E-03		3.35E-02	7.39E-01		-3.01E-02	6.17E-01		3.03E-02	6.21E-01		-1.07E+00	3.67E-90	Down	-1.30E+00	8.77E-126	Down	Unigene345_All//gi|14486705|gb|AAK63247.1|AF367433_1|//0.00E+00//phosphatidylinositol transfer-like protein III [Lotus japonicus]	Unigene345_All//0.00E+00//AT2G21520| transporter	Unigene345_All//0.00E+00//ES809688				nr -
Unigene3450_All	967	10.12	5.14	6.50	4.33	4.67	2.15	2.49	2.33	2.22	-9.78E-01	1.61E-07		-6.39E-01	7.76E-04		1.08E-01	7.76E-01		-1.01E+00	5.97E-04	Down	-9.46E-02	8.07E-01		-1.64E-01	6.47E-01		Unigene3450_All//gi|164604998|dbj|BAF98295.1|//7.00E-36//2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Hevea brasiliensis]	Unigene3450_All//2.00E-33//AT1G63970| ISPF; 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Unigene3450_All//0.00E+00//DW499963		ko00900|Terpenoid backbone biosynthesis	GO:0006090//GO:0006779//GO:0009532//GO:0016109//GO:0016849	nr +
Unigene34501_All	2441	16.40	28.85	14.09	18.98	18.35	26.35	30.90	18.89	15.03	8.15E-01	2.69E-36		-2.19E-01	1.65E-02		-4.83E-02	6.11E-01		4.73E-01	7.01E-14		-7.10E-01	1.26E-37		-1.04E+00	3.44E-73	Down	Unigene34501_All//gi|18400838|ref|NP_566519.1|//1.00E-167//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|11994333|dbj|BAB02292.1| WD-40 repeat protein-like [Arabidopsis thaliana] >gi|25083282|gb|AAN72058.1| expressed protein [Arabidopsis thaliana] >gi|28059687|gb|AAO30083.1| Unknown protein [Arabidopsis thaliana]	Unigene34501_All//5.00E-162//AT3G15610| transducin family protein / WD-40 repeat family protein	Unigene34501_All//0.00E+00//TC156326				nr +
Unigene34503_All	1209	18.39	8.59	12.20	30.08	29.25	42.62	48.40	20.78	19.64	-1.10E+00	2.88E-19	Down	-5.92E-01	7.54E-07		-4.02E-02	7.41E-01		5.03E-01	1.71E-12		-1.22E+00	1.93E-71	Down	-1.30E+00	3.19E-81	Down	Unigene34503_All//gi|18418072|ref|NP_567904.1|//1.00E-112//AtLa1 (Arabidopsis thaliana La protein 1); RNA binding	Unigene34503_All//3.00E-97//AT4G32720| AtLa1 (Arabidopsis thaliana La protein 1); RNA binding	Unigene34503_All//0.00E+00//TC169179				nr +
Unigene34504_All	1686	5.00	2.10	2.97	3.99	4.96	5.36	7.90	2.58	4.58	-1.25E+00	2.33E-09	Down	-7.51E-01	2.90E-04		3.15E-01	1.35E-01		4.26E-01	2.96E-02		-1.62E+00	2.28E-25	Down	-7.85E-01	7.53E-09		Unigene34504_All//gi|297802732|ref|XP_002869250.1|//1.00E-115//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315086|gb|EFH45509.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene34504_All//3.00E-102//AT4G32720| AtLa1 (Arabidopsis thaliana La protein 1); RNA binding	Unigene34504_All//0.00E+00//TC157467				nr +

Unigene34507_All	4100	0.97	2.95	1.91	7.06	7.30	8.60	1.94	1.88	2.10	1.61E+00	9.81E-19	Up	9.77E-01	7.36E-06		4.82E-02	7.17E-01		2.85E-01	1.64E-03		-4.77E-02	8.21E-01		1.15E-01	5.73E-01		Unigene34507_All//gi|297815706|ref|XP_002875736.1|//1.00E-157//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321574|gb|EFH51995.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34507_All//8.00E-154//AT3G45620| transducin family protein / WD-40 repeat family protein	Unigene34507_All//0.00E+00//CO081449				nr +
Unigene34510_All	2120	6.27	4.35	5.15	7.03	6.92	4.20	2.37	4.46	8.06	-5.27E-01	6.21E-04		-2.84E-01	9.15E-02		-2.20E-02	8.99E-01		-7.43E-01	1.40E-07		9.09E-01	7.56E-08		1.76E+00	3.03E-37	Up	Unigene34510_All//gi|45271576|gb|AAS57526.1|//1.00E-163//serine/threonine protein kinase [Pisum sativum]	Unigene34510_All//3.00E-146//AT2G34650| PID (PINOID); kinase/ protein kinase/ protein serine/threonine kinase	Unigene34510_All//0.00E+00//TC158547				nr +
Unigene34512_All	1252	0.33	0.40	0.51	0.28	0.50	2.27	1.35	2.94	1.56	2.76E-01	7.64E-01		6.11E-01	5.09E-01		8.30E-01	4.15E-01		3.03E+00	2.56E-10	Up	1.12E+00	1.14E-04	Up	2.07E-01	6.25E-01		Unigene34512_All//gi|224129054|ref|XP_002320489.1|//3.00E-64//argonaute protein group [Populus trichocarpa] >gi|222861262|gb|EEE98804.1| argonaute protein group [Populus trichocarpa]	Unigene34512_All//4.00E-56//AT2G32940| AGO6 (ARGONAUTE 6); nucleic acid binding	Unigene34512_All//9.00E-73//DN804161				nr +
Unigene34513_All	2435	0.92	1.48	0.28	1.27	1.43	2.39	2.45	3.31	1.72	6.77E-01	3.69E-02		-1.70E+00	3.72E-04	Down	1.71E-01	6.51E-01		9.16E-01	1.74E-04		4.36E-01	1.84E-02		-5.11E-01	1.50E-02		Unigene34513_All//gi|268376309|gb|ACZ04920.1|//0.00E+00//argonaute 4-like protein [Pelargonium x hortorum]	Unigene34513_All//0.00E+00//AT2G32940| AGO6 (ARGONAUTE 6); nucleic acid binding	Unigene34513_All//0.00E+00//DN804161				nr +
Unigene34517_All	493	0.00	0.62	0.65	10.31	8.17	2.20	7.80	3.65	18.75	9.27E+00	4.43E-02		9.34E+00	4.52E-02		-3.35E-01	2.24E-01		-2.23E+00	2.13E-13	Down	-1.10E+00	9.99E-05	Down	1.26E+00	6.72E-13	Up	Unigene34517_All//gi|2341043|gb|AAB70448.1|//6.00E-15//Strong similarity to Arabidopsis REV3C (gb|X62461) [Arabidopsis thaliana] >gi|111074216|gb|ABH04481.1| Atlg04280 [Arabidopsis thaliana]	Unigene34517_All//4.00E-16//AT1G04280| unknown protein	Unigene34517_All//8.00E-68//TC161488				nr -
Unigene34518_All	1862	6.38	6.69	7.52	61.51	59.36	31.17	49.30	25.10	254.46	6.97E-02	6.86E-01		2.38E-01	1.49E-01		-5.11E-02	3.94E-01		-9.81E-01	9.19E-87		-9.74E-01	1.04E-77		2.37E+00	0.00E+00	Up	Unigene34518_All//gi|16482|emb|CAA44318.1|//0.00E+00//H1f1k [Arabidopsis thaliana]	Unigene34518_All//4.00E-168//AT1G01280| unknown protein	Unigene34518_All//0.00E+00//TC161488				nr -
Unigene34519_All	1051	3.58	5.01	4.26	5.59	6.03	4.38	2.49	5.73	1.93	4.84E-01	6.64E-02		2.48E-01	4.17E-01		1.08E-01	7.13E-01		-3.52E-01	1.79E-01		1.20E+00	7.46E-08	Up	-3.68E-01	2.94E-01		Unigene34519_All//gi|108709971|gb|ABF97766.1|//1.00E-49//Zinc finger, C3HC4 type family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene34519_All//1.00E-39//AT1G06770| DRIP1 (DREB2A-INTERACTING PROTEIN 1); protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene34519_All//0.00E+00//gi|164343023|gb|ES807852.1|ES807852				nr -
Unigene3452_All	2686	5.40	4.85	6.28	8.81	7.92	3.99	0.55	0.08	0.22	-1.54E-01	3.50E-01		2.20E-01	1.43E-01		-1.53E-01	2.22E-01		-1.14E+00	1.88E-23	Down	-2.82E+00	3.44E-06	Down	-1.31E+00	6.57E-03		Unigene3452_All//gi|56744299|gb|AAW28578.1|//1.00E-104//Putative gag-pol polyprotein, identical [Solanum demissum]		Unigene3452_All//8.00E-152//FL576926			GO:0003676//GO:0006260//GO:0034061//GO:0043231	nr -
Unigene34521_All	875	2.57	2.90	2.62	2.85	4.05	1.03	6.91	3.92	2.50	1.71E-01	6.58E-01		2.54E-02	9.71E-01		5.10E-01	1.29E-01		-1.46E+00	3.75E-04	Down	-8.19E-01	1.36E-04		-1.46E+00	8.26E-11	Down	Unigene34521_All//gi|15241031|ref|NP_198126.1|//2.00E-93//EMB2775 (EMBRYO DEFECTIVE 2775); DNA binding / nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene34521_All//2.00E-81//AT5G27740| EMB2775 (EMBRYO DEFECTIVE 2775); DNA binding / nucleoside-triphosphatase/ nucleotide binding	Unigene34521_All//0.00E+00//gi|164369693|gb|ES836972.1|ES836972		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03430|Mismatch repair		nr +
Unigene34522_All	1469	10.22	8.42	4.17	17.16	13.74	12.27	14.05	6.83	5.83	-2.80E-01	6.10E-02		-1.29E+00	3.02E-16	Down	-3.21E-01	1.97E-03		-4.84E-01	4.23E-06		-1.04E+00	4.40E-20	Down	-1.27E+00	4.23E-28	Down	Unigene34522_All//gi|15241031|ref|NP_198126.1|//1.00E-175//EMB2775 (EMBRYO DEFECTIVE 2775); DNA binding / nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene34522_All//3.00E-165//AT5G27740| EMB2775 (EMBRYO DEFECTIVE 2775); DNA binding / nucleoside-triphosphatase/ nucleotide binding	Unigene34522_All//0.00E+00//TC164911		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03430|Mismatch repair		nr +
Unigene34524_All	758	0.00	0.00	0.00	1.97	2.86	0.48	114.85	14.28	22.81	null	null		null	null		5.38E-01	2.39E-01		-2.05E+00	5.54E-04	Down	-3.01E+00	0.00E+00	Down	-2.33E+00	1.11E-271	Down	Unigene34524_All//gi|27463662|gb|AAO15899.1|//1.00E-43//secreted glycoprotein [Linum usitatissimum]	Unigene34524_All//5.00E-40//AT1G78850| curculin-like (mannose-binding) lectin family protein					nr -
Unigene34525_All	749	0.42	0.14	0.00	16.43	11.54	9.11	97.71	22.15	14.20	-1.63E+00	2.76E-01		-8.71E+00	4.91E-02		-5.10E-01	7.20E-04		-8.51E-01	6.98E-08		-2.14E+00	1.91E-199	Down	-2.78E+00	9.42E-280	Down	Unigene34525_All//gi|1107526|emb|CAA61158.1|//3.00E-85//SIEP1L protein [Beta vulgaris subsp. vulgaris]	Unigene34525_All//1.00E-73//AT1G78850| curculin-like (mannose-binding) lectin family protein	Unigene34525_All//2.00E-29//gi|31406661|gb|CD485696.1|CD485696				nr -
Unigene34526_All	1455	0.47	0.00	0.00	10.65	9.42	2.14	161.16	26.31	29.32	-8.87E+00	4.10E-04	Down	-8.87E+00	7.64E-04	Down	-1.77E-01	2.62E-01		-2.31E+00	9.28E-42	Down	-2.61E+00	0.00E+00	Down	-2.46E+00	0.00E+00	Down	Unigene34526_All//gi|15219200|ref|NP_178006.1|//1.00E-136//curculin-like (mannose-binding) lectin family protein [Arabidopsis thaliana] >gi|3834309|gb|AAC83025.1| Strong similarity to glycoprotein EP1 gb|L16983 Daucus carota and a member of S locus glycoprotein family PF|00954. ESTs gb|F13813, gb|T21052, gb|R30218 and gb|W43262 come from this gene [Arabidopsis thaliana] >gi|15450842|gb|AAK96692.1| Strong similarity to glycoprotein EP1 [Arabidopsis thaliana]	Unigene34526_All//3.00E-137//AT1G78850| curculin-like (mannose-binding) lectin family protein	Unigene34526_All//2.00E-24//gi|31406661|gb|CD485696.1|CD485696				nr +
Unigene34529_All	986	1.65	0.51	2.92	0.91	2.44	1.47	2.32	2.80	2.02	-1.68E+00	2.36E-03		8.26E-01	3.26E-02		1.43E+00	5.29E-04	Up	6.89E-01	2.32E-01		2.73E-01	4.56E-01		-1.97E-01	6.07E-01		Unigene34529_All//gi|115479213|ref|NP_001063200.1|//2.00E-70//Os09g0420900 (Oryza sativa Japonica Group) >gi|113631433|dbj|BAF25114.1| Os09g0420900 (Oryza sativa Japonica Group)	Unigene34529_All//3.00E-65//AT4G31820| ENP (ENHANCER OF PINOID); protein binding / signal transducer	Unigene34529_All//0.00E+00//TC141180				nr +
Unigene34530_All	321	9.94	1.26	2.32	0.31	0.75	0.00	1.84	0.13	0.62	-2.98E+00	6.39E-11	Down	-2.10E+00	3.53E-07	Down	1.27E+00	5.32E-01		-8.28E+00	3.99E-01		-3.82E+00	1.78E-03		-1.57E+00	6.49E-02		Unigene34530_All//gi|22329064|ref|NP_194910.2|//5.00E-38//ENP (ENHANCER OF PINOID); protein binding / signal transducer [Arabidopsis thaliana]	Unigene34530_All//2.00E-39//AT4G31820| ENP (ENHANCER OF PINOID); protein binding / signal transducer	Unigene34530_All//6.00E-86//AT731519				nr +
Unigene34534_All	3205	0.91	1.08	0.88	1.90	1.47	1.85	1.70	0.50	1.68	2.34E-01	5.03E-01		-5.40E-02	8.92E-01		-3.65E-01	1.35E-01		-3.87E-02	9.00E-01		-1.78E+00	2.56E-12	Down	-2.02E-02	9.52E-01		Unigene34534_All//gi|297796717|ref|XP_002866243.1|//1.00E-154//ubiquitin-specific protease 23 [Arabidopsis lyrata subsp. lyrata] >gi|297312078|gb|EFH42502.1| ubiquitin-specific protease 23 [Arabidopsis lyrata subsp. lyrata]	Unigene34534_All//6.00E-129//AT5G57990| UBP23 (UBIQUITIN-SPECIFIC PROTEASE 23); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene34534_All//0.00E+00//TC148048				nr -
Unigene34538_All	820	3.96	4.57	5.39	3.64	8.23	4.02	1.29	1.68	1.21	2.09E-01	5.37E-01		4.46E-01	1.46E-01		1.18E+00	8.36E-08	Up	1.42E-01	6.97E-01		3.84E-01	4.75E-01		-8.58E-02	8.85E-01		Unigene34538_All//gi|33391721|gb|AAQ17461.1|//1.00E-78//beta-D-glucosidase [Gossypium hirsutum]	Unigene34538_All//1.00E-66//AT5G20950| glycosyl hydrolase family 3 protein	Unigene34538_All//8.00E-100//gi|109850528|gb|DW479507.1|DW479507		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr -
Unigene3454_All	1042	25.06	17.51	15.18	7.79	8.43	12.40	9.49	2.89	2.98	-5.17E-01	1.07E-06		-7.23E-01	5.44E-11		1.13E-01	6.15E-01		6.70E-01	1.29E-05		-1.72E+00	1.06E-20	Down	-1.67E+00	1.36E-20	Down	Unigene3454_All//gi|224136057|ref|XP_002327370.1|//1.00E-50//phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa] >gi|222835740|gb|EEE74175.1| phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa]	Unigene3454_All//8.00E-44//AT5G09650| AtPPa6 (Arabidopsis thaliana pyrophosphorylase 6); inorganic diphosphatase/ pyrophosphatase	Unigene3454_All//0.00E+00//TC134407		ko00190|Oxidative phosphorylation	GO:0006793//GO:0016462//GO:0016491//GO:0044424//GO:0046872	nr +
Unigene34542_All	2074	28.28	33.59	36.77	31.13	33.69	37.24	54.39	100.14	158.13	2.48E-01	8.54E-05		3.79E-01	5.29E-10		1.14E-01	9.36E-02		2.59E-01	8.90E-06		8.81E-01	1.35E-147		1.54E+00	0.00E+00	Up	Unigene34542_All//gi|12043533|emb|CAC19789.1|//1.00E-153//MYB-like DNA-binding protein [Catharanthus roseus]	Unigene34542_All//1.00E-111//AT3G12560| TRFL9 (TRF-LIKE 9); DNA bending/ DNA binding / telomeric DNA binding	Unigene34542_All//0.00E+00//TC173929	MYB-related			nr -
Unigene34543_All	2809	3.35	3.57	1.80	8.09	7.50	6.00	8.67	1.16	2.89	9.12E-02	6.26E-01		-8.97E-01	4.62E-06		-1.08E-01	4.26E-01		-4.31E-01	1.24E-04		-2.90E+00	1.24E-94	Down	-1.58E+00	8.15E-46	Down	Unigene34543_All//gi|115474639|ref|NP_001060916.1|//0.00E+00//Os08g0129600 (Oryza sativa Japonica Group) >gi|29467527|dbj|BAC66716.1| proline-rich protein family-like [Oryza sativa Japonica Group] >gi|113622885|dbj|BAF22830.1| Os08g0129600 (Oryza sativa Japonica Group)	Unigene34543_All//6.00E-85//AT3G25690| CHUP1 (CHLOROPLAST UNUSUAL POSITIONING 1)	Unigene34543_All//0.00E+00//TC132881				nr +
Unigene34547_All	634	12.30	18.94	13.35	13.36	11.13	12.54	24.61	25.91	11.75	6.23E-01	1.34E-04		1.19E-01	6.20E-01		-2.63E-01	2.15E-01		-9.14E-02	6.70E-01		7.43E-02	6.49E-01		-1.07E+00	1.74E-16	Down			Unigene34547_All//2.00E-152//gi|21093801|gb|BQ406114.1|BQ406114				
Unigene3455_All	1758	78.06	37.93	48.89	25.81	26.35	25.10	9.88	3.21	3.33	-1.04E+00	9.94E-106	Down	-6.75E-01	4.42E-49		2.94E-02	8.05E-01		-4.05E-02	6.96E-01		-1.62E+00	4.44E-33	Down	-1.57E+00	1.61E-32	Down	Unigene3455_All//gi|15242465|ref|NP_196527.1|//1.00E-127//AtPPa6 (Arabidopsis thaliana pyrophosphorylase 6); inorganic diphosphatase/ pyrophosphatase >gi|75264322|sp|Q9LXC9.1|IPYR1_ARATH RecName: Full=Soluble inorganic pyrophosphatase 1, chloroplastic; AltName: Full=Pyrophosphate phospho-hydrolase 1; Short=PPase 1; AltName: Full=Inorganic pyrophosphatase 1; Flags: Precursor >gi|7671424|emb|CAB89365.1| inorganic pyrophosphatase-like protein [Arabidopsis thaliana] >gi|9758993|dbj|BAB09520.1| inorganic pyrophosphatase-like protein [Arabidopsis thaliana] >gi|12057177|emb|CAC19853.1| inorganic pyrophosphatase [Arabidopsis thaliana] >gi|45331391|gb|AAS57950.1| chloroplast inorganic pyrophosphatase [Arabidopsis thaliana]	Unigene3455_All//3.00E-126//AT5G09650| AtPPa6 (Arabidopsis thaliana pyrophosphorylase 6); inorganic diphosphatase/ pyrophosphatase	Unigene3455_All//0.00E+00//TC134407		ko00190|Oxidative phosphorylation	GO:0006793//GO:0016462//GO:0044424	nr +
Unigene34550_All	4528	4.97	3.83	2.56	9.54	11.08	9.06	21.52	10.19	14.61	-3.77E-01	1.16E-03		-9.55E-01	5.69E-15		2.16E-01	3.23E-03		-7.47E-02	4.64E-01		-1.08E+00	2.16E-97	Down	-5.59E-01	1.04E-32		Unigene34550_All//gi|224085131|ref|XP_002307505.1|//2.00E-09//predicted protein [Populus trichocarpa] >gi|222856954|gb|EEE94501.1| predicted protein [Populus trichocarpa]		Unigene34550_All//0.00E+00//gi|164275574|gb|ES805885.1|ES805885				nr -

Unigene34551_All	800	1.18	3.93	3.26	3.42	4.43	5.42	4.39	8.72	5.48	1.74E+00	5.91E-06	Up	1.47E+00	5.63E-04	Up	3.73E-01	2.98E-01		6.62E-01	2.39E-02		9.92E-01	7.95E-07		3.21E-01	2.22E-01		Unigene34551_All//gi|115489600|ref|NP_001067287.1|//3.00E-11//Os12g0617100 [Oryza sativa Japonica Group] >gi|77557071|gb|ABA99867.1|Initiation factor 2 subunit family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|77557072|gb|ABA99868.1|Initiation factor 2 subunit family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113649794|dbj|BAF30306.1|Os12g0617100 [Oryza sativa Japonica Group]	Unigene34551_All//1.00E-11//AT5G38610| eukaryotic translation initiation factor 2B family protein / eIF-2B family protein	Unigene34551_All//0.00E+00//gi|164368610|gb|ES842852.1|ES842852				nr -
Unigene34556_All	2746	9.45	5.42	5.91	40.82	33.80	21.99	26.73	9.70	11.66	-8.01E-11	1.68E-13		-6.76E-01	8.73E-10		-2.72E-01	9.32E-10		-8.92E-01	1.58E-72		-1.46E+00	4.97E-118	Down	-1.20E+00	3.51E-89	Down	Unigene34556_All//gi|280967730|gb|ACZ98536.1|//0.00E+00//protein kinase [Malus x domestica]	Unigene34556_All//0.00E+00//AT2G26730| leucine-rich repeat transmembrane protein kinase, putative	Unigene34556_All//0.00E+00//TC154496				nr -
Unigene34559_All	572	15.00	3.45	22.99	4.62	3.67	2.53	0.30	0.80	0.07	-2.12E+00	1.99E-19	Down	6.16E-01	1.24E-04		-3.30E-01	4.24E-01		-8.69E-01	2.50E-02		1.44E+00	1.67E-01		-2.09E+00	3.13E-01		Unigene34559_All//gi|3850570|gb|AAC72110.1|//4.00E-06//F15K9.6 [Arabidopsis thaliana]		Unigene34559_All//9.00E-71//TC153902				nr +
Unigene34456_All	1774	8.14	16.39	10.93	8.70	10.54	13.37	32.06	30.37	114.51	1.01E+00	8.59E-22	Up	4.25E-01	1.14E-03		2.76E-01	3.30E-02		6.19E-01	1.48E-08		-7.80E-02	2.98E-01		1.84E+00	0.00E+00	Up	Unigene34456_All//gi|225457017|ref|XP_002279079.1|//1.00E-155//PREDICTED: similar to ATPANK2 (PANTOTHENATE KINASE 2); pantothenate kinase [Vitis vinifera]	Unigene34456_All//1.00E-149//AT4G32180| ATPANK2 (PANTOTHENATE KINASE 2); pantothenate kinase	Unigene34456_All//0.00E+00//gi|164249216|gb|ES806660.1|ES806660		ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene34560_All	2274	325.38	154.79	300.72	83.92	81.21	72.67	21.10	19.26	18.08	-1.07E+00	0.00E+00	Down	-1.14E-01	1.27E-09		-4.74E-02	2.93E-01		-2.08E-01	5.64E-09		-1.32E-01	7.97E-02		-2.23E-01	1.04E-03		Unigene34560_All//gi|115462031|ref|NP_001054615.1|//3.00E-62//Os05g0143300 [Oryza sativa Japonica Group] >gi|113578166|dbj|BAF16529.1|Os05g0143300 [Oryza sativa Japonica Group]	Unigene34560_All//4.00E-62//AT4G02920| unknown protein	Unigene34560_All//0.00E+00//TC135711				nr +
Unigene34563_All	1766	0.83	1.23	1.42	4.40	2.81	2.17	1.68	2.04	1.83	5.73E-01	1.92E-01		7.73E-01	6.55E-02		-6.48E-01	8.54E-04		-1.02E+00	8.23E-07	Down	2.80E-01	3.84E-01		1.25E-01	6.89E-01		Unigene34563_All//gi|124359162|gb|ABN05683.1|//1.00E-61//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene34563_All//1.00E-42//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative					nr -
Unigene34566_All	497	0.42	1.63	3.43	1.70	2.22	3.00	3.66	3.53	2.97	1.95E+00	2.43E-02		3.03E+00	6.93E-06	Up	3.80E-01	6.01E-01		8.16E-01	1.48E-01		-5.06E-02	9.24E-01		-3.03E-01	4.88E-01									
Unigene34568_All	1782	0.35	0.31	1.23	0.70	0.64	0.46	2.47	1.31	0.83	-1.72E-01	8.29E-01		1.80E+00	2.49E-04	Up	-1.32E-01	8.17E-01		-6.15E-01	3.33E-01		-9.10E-01	4.26E-04		-1.58E+00	6.31E-09	Down	Unigene34568_All//gi|30684527|ref|NP_180586.2|//2.00E-06//unknown protein [Arabidopsis thaliana] >gi|26452565|db|BAC43367.1|unknown protein [Arabidopsis thaliana] >gi|28973165|gb|AAO63907.1|unknown protein [Arabidopsis thaliana]	Unigene34568_All//8.00E-08//AT2G30270| unknown protein	Unigene34568_All//0.00E+00//gi|78346137|gb|DT566411.1|DT566411				nr -
Unigene34571_All	2156	13.03	5.33	8.20	29.09	28.91	23.08	22.79	7.72	11.07	-1.29E+00	6.58E-31	Down	-6.68E-01	2.43E-10		-9.00E-03	9.17E-01		-3.34E-01	2.05E-07		-1.56E+00	2.99E-87	Down	-1.04E+00	3.84E-48	Down	Unigene34571_All//gi|18396159|ref|NP_566170.1|//0.00E+00//GAUT9 (Galacturonosyltransferase 9); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|26394254|sp|Q9FWA4.1|GAUT9_ARATH RecName: Full=Probable galacturonosyltransferase 9 >gi|19310441|gb|AAL84957.1|AT3g02350/F11A12_103 [Arabidopsis thaliana] >gi|28416491|gb|AAO42776.1|At3g02350/F11A12_103 [Arabidopsis thaliana]	Unigene34571_All//0.00E+00//AT3G02350| GAUT9 (Galacturonosyltransferase 9); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene34571_All//0.00E+00//TC155157				nr +
Unigene34572_All	3605	5.63	4.01	4.20	8.13	5.61	8.47	14.85	6.45	7.68	-4.91E-01	5.44E-05		-4.25E-01	8.31E-04		-5.35E-01	4.40E-09		5.98E-02	6.20E-01		-1.20E+00	4.66E-64	Down	-9.51E-01	3.76E-45		Unigene34572_All//gi|186489959|ref|NP_001117460.1|//0.00E+00//ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene34572_All//0.00E+00//AT1G50140| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene34572_All//0.00E+00//TC157079		ko00230|Purine metabolism		nr +
Unigene34573_All	3663	0.63	0.50	0.36	0.92	0.38	0.99	2.19	0.62	0.74	-3.36E-01	4.24E-01		-7.90E-01	7.45E-02		-1.30E+00	4.41E-05	Down	9.30E-02	7.88E-01		-1.83E+00	1.82E-18	Down	-1.57E+00	1.75E-15	Down	Unigene34573_All//gi|186510248|ref|NP_188608.3|//0.00E+00//ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene34573_All//0.00E+00//AT3G19740| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene34573_All//0.00E+00//TC157079		ko00230|Purine metabolism		nr +
Unigene34576_All	860	20.75	5.95	14.06	16.86	11.25	6.83	6.74	14.19	3.66	-1.80E+00	4.01E-32	Down	-5.62E-01	3.36E-05		-5.83E-01	1.70E-05		-1.30E+00	8.57E-18	Down	1.08E+00	8.09E-13	Up	-8.80E-01	4.26E-05		Unigene34576_All//gi|15148922|gb|AB84888.1|AF402607_1/6.00E-85//TGA-type basic leucine zipper protein TGA1.1 [Phaseolus vulgaris]	Unigene34576_All//3.00E-72//AT1G22070| TGA3; DNA binding / calmodulin binding / protein binding / transcription factor	Unigene34576_All//0.00E+00//gi|78354230|gb|DT574504.1|DT574504	bZIP			nr -
Unigene34577_All	1255	5.96	2.83	4.92	8.45	6.04	1.80	2.36	3.43	1.56	-1.08E+00	8.22E-07	Down	-2.77E-01	2.40E-01		-4.86E-01	3.32E-03		-2.23E+00	1.64E-27	Down	5.41E-01	4.01E-02		-6.00E-01	5.54E-02		Unigene34577_All//gi|15148922|gb|AB84888.1|AF402607_1/4.00E-77//TGA-type basic leucine zipper protein TGA1.1 [Phaseolus vulgaris]	Unigene34577_All//6.00E-60//AT1G22070| TGA3; DNA binding / calmodulin binding / protein binding / transcription factor	Unigene34577_All//0.00E+00//gi|78354230|gb|DT574504.1|DT574504	bZIP			nr +
Unigene34578_All	1571	18.02	5.71	10.68	16.90	12.52	6.38	4.98	12.29	3.17	-1.66E+00	4.38E-45	Down	-7.55E-01	9.87E-13		-4.33E-01	8.46E-06		-1.41E+00	5.37E-36	Down	1.30E+00	1.32E-26	Up	-6.51E-01	2.90E-04		Unigene34578_All//gi|156901569|gb|ABU96774.1|//1.00E-120//bZIP transcription factor [Brassica juncea]	Unigene34578_All//3.00E-104//AT1G77920| bZIP family transcription factor	Unigene34578_All//0.00E+00//gi|78354230|gb|DT574504.1|DT574504	bZIP			nr +
Unigene34580_All	527	1.39	2.12	1.72	6.14	3.40	3.09	14.20	13.09	6.58	6.06E-01	3.59E-01		3.06E-01	6.57E-01		-8.55E-01	8.46E-03		-9.94E-01	3.70E-03		-1.18E-01	6.20E-01		-1.11E+00	7.06E-09	Down			Unigene34580_All//2.00E-118//TC178208				
Unigene34582_All	3694	5.44	27.82	4.63	21.74	19.05	11.60	17.70	4.24	4.66	2.35E+00	9.85E-256	Up	-2.33E-01	8.50E-02		-1.90E-01	6.85E-04		-9.06E-01	2.06E-53		-2.06E+00	1.31E-169	Down	-1.93E+00	9.24E-160	Down	Unigene34582_All//gi|15242952|ref|NP_200041.1|//0.00E+00//protein transport protein-related [Arabidopsis thaliana] >gi|10177394|dbj|BAB10525.1|hyaluronan mediated motility receptor-like protein [Arabidopsis thaliana] >gi|47550677|gb|AAT35237.1|At5g52280 [Arabidopsis thaliana] >gi|51970830|dbj|BAD44107.1|hyaluronan mediated motility receptor-like protein [Arabidopsis thaliana]	Unigene34582_All//0.00E+00//AT1G63300| unknown protein	Unigene34582_All//0.00E+00//ES797179				nr +
Unigene34583_All	2619	5.63	9.11	4.47	11.07	11.73	12.90	7.64	1.24	5.25	6.94E-01	7.19E-10		-3.33E-01	3.29E-02		8.34E-02	5.01E-01		2.21E-01	2.24E-02		-2.62E+00	1.09E-69	Down	-5.41E-01	4.52E-07		Unigene34583_All//gi|15235900|ref|NP_192536.1|//0.00E+00//ATCSLC12 (CELLULOSE-SYNTHASE LIKE C12); cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75216205|sp|Q9ZQB9.1|CSLC2_ARATH RecName: Full=Probable xyloglucan glycosyltransferase 12; AltName: Full=Cellulose synthase-like protein C12; Short=AtCslC12 >gi|31711706|gb|AAP68209.1|At4g07960 [Arabidopsis thaliana]	Unigene34583_All//0.00E+00//AT4G07960| ATCSLC12 (CELLULOSE-SYNTHASE LIKE C12); cellulose synthase/ transferase, transferring glycosyl groups	Unigene34583_All//0.00E+00//TC166442				nr +
Unigene34586_All	2225	20.01	7.83	4.45	39.54	25.12	28.21	109.74	109.70	66.52	-1.35E+00	2.43E-52	Down	-2.17E+00	1.13E-97	Down	-6.55E-01	9.17E-38		-4.87E-01	7.52E-20		-5.00E-04	1.02E+00		-7.22E-01	6.88E-127		Unigene34586_All//gi|211906496|gb|ACJ11741.1|//0.00E+00//heat shock protein 70 [Gossypium hirsutum]	Unigene34586_All//0.00E+00//AT5G02500| HSC70-1 (HEAT SHOCK COGNATE PROTEIN 70-1); ATP binding	Unigene34586_All//0.00E+00//gi|164241519|gb|ES793553.1|ES793553		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -
Unigene34587_All	651	1.77	1.87	2.13	4.06	4.60	5.41	14.35	30.05	8.02	7.93E-02	9.00E-01		2.66E-01	6.23E-01		1.82E-01	6.59E-01		4.16E-01	2.33E-01		1.07E+00	8.72E-20	Up	-8.40E-01	3.63E-07				Unigene34587_All//0.00E+00//TC156048				
Unigene34590_All	978	0.32	0.21	0.65	0.10	0.28	0.00	6.31	3.80	1.51	-6.32E-01	6.22E-01		1.03E+00	2.81E-01		1.47E+00	4.20E-01		-6.67E+00	3.99E-01		-7.31E-01	5.49E-04		-2.07E+00	2.74E-17	Down	Unigene34590_All//gi|9294121|dbj|BAB01972.1|//4.00E-34//copia-like retrotransposable element [Arabidopsis thaliana]	Unigene34590_All//3.00E-08//AT4G23160| protein kinase family protein	Unigene34590_All//8.00E-54//TC177530				nr -
Unigene34594_All	2275	1.89	2.49	0.91	2.96	2.60	2.48	5.04	2.92	4.17	4.04E-01	1.16E-01		-1.05E+00	6.99E-04	Down	-1.83E-01	4.79E-01		-2.52E-01	3.20E-01		-7.86E-01	1.73E-07		-2.73E-01	7.05E-02		Unigene34594_All//gi|134031922|gb|AB045698.1|//1.00E-161//At2g02910 [Arabidopsis thaliana]	Unigene34594_All//1.00E-156//AT2G02910| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF616 (InterPro:IPR006852); BEST Arabidopsis thaliana protein match is: EMB2756 (EMBRYO DEFECTIVE 2756) (TAIR:AT1G34550.1); Has 191 Blast hits to 191 proteins in 22 species: Archae - 6; Bacteria - 21; Metazoa - 0; Fungi - 0; Plants - 106; Viruses - 0; Other Eukaryotes - 58 (source: NCBI BLink).	Unigene34594_All//0.00E+00//TC166816				nr +
Unigene34596_All	1749	0.27	0.23	0.06	0.17	0.55	0.46	10.66	3.11	4.05	-2.16E-01	8.17E-01		-2.14E+00	1.03E-01		1.69E+00	2.52E-02		1.44E+00	8.45E-02		-1.78E+00	3.02E-40	Down	-1.39E+00	2.34E-29	Down	Unigene34596_All//gi|224114037|ref|XP_002332458.1|//1.00E-159//cytochrome P450 [Populus trichocarpa] >gi|222832529|gb|EEE71006.1|cytochrome P450 [Populus trichocarpa]	Unigene34596_All//2.00E-109//AT3G26210| CYP71B23; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene34596_All//0.00E+00//TC149256		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene34597_All	1799	1.69	1.89	0.65	3.07	3.33	3.46	5.10	5.65	11.83	1.62E-01	6.21E-01		-1.37E+00	3.96E-04	Down	1.16E-01	6.98E-01		1.73E-01	5.41E-01		1.47E-01	4.25E-01		1.21E+00	7.83E-27	Up	Unigene34597_All//gi|224096502|ref|XP_002310636.1|//1.00E-121//cytochrome P450 [Populus trichocarpa] >gi|222853539|gb|EEE91086.1|cytochrome P450 [Populus trichocarpa]	Unigene34597_All//1.00E-89//AT1G13080| CYP71B2 (CYTOCHROME P450 71B2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene34597_All//0.00E+00//TC146608		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00966|Glucosinolate biosynthesis		nr +
Unigene34598_All	3310	7.92	3.44	4.67	12.31	10.92	12.84	13.85	7.13	6.88	-1.20E+00	6.03E-26	Down	-7.63E-01	4.68E-12		-1.73E-01	4.55E-02		6.07E-02	5.70E-01		-9.57E-01	4.57E-38		-1.01E+00	1.20E-42	Down	Unigene34598_All//gi|225465333|ref|XP_002271674.1|//0.00E+00//PREDICTED: similar to DNA gyrase subunit A, chloroplastic/mitochondrial [Vitis vinifera]	Unigene34598_All//0.00E+00//AT3G10690| DNA gyrase subunit A family protein	Unigene34598_All//0.00E+00//TC159853				nr +
Unigene3460_All	2967	10.21	7.69	8.76	22.41	20.11	20.02	20.59	13.06	9.68	-4.10E-01	2.84E-05		-2.21E-01	3.93E-02		-1.56E-01	1.64E-02		-1.63E-01	1.53E-02		-6.57E-01	8.35E-27		-1.09E+00	4.84E-64	Down	Unigene3460_All//gi|108707778|gb|ABF95573.1|//0.00E+00//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene3460_All//0.00E+00//AT4G16170| unknown protein	Unigene3460_All//0.00E+00//gi|164277281|gb|ES828441.1|ES828441			GO:0031410	nr +

Unigene34600_All	567	5.54	13.94	6.67	11.25	11.36	11.23	10.66	12.24	10.40	1.33E+00	1.23E-09	Up	2.68E-01	4.22E-01		1.42E-02	9.65E-01		-1.80E-03	9.91E-01		1.99E-01	3.84E-01		-3.62E-02	8.83E-01		Unigene34600_All|gi|224136238|ref|XP_002322279.1||/3.00E-26//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222869275|gb|EEF06406.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene34600_All//2.00E-15//AT2G47620| ATSWI3A (SWITCH/SUCROSE NONFERMENTING 3A); DNA binding	Unigene34600_All//0.00E+00//gi|48800653|gb|CO101967.1|CO101967				nr +
Unigene34602_All	2528	4.02	11.67	14.51	156.81	10.46	4.22	20.19	3.77	19.37	1.54E+00	5.93E-42	Up	1.85E+00	7.85E-66	Up	-3.91E+00	0.00E+00	Down	-5.22E+00	0.00E+00	Down	-2.42E+00	8.02E-162	Down	-5.98E-02	4.40E-01		Unigene34602_All|gi|79382269|ref|NP_177741.3||0.00E+00//serine-type endopeptidase/ serine-type peptidase [Arabidopsis thaliana]	Unigene34602_All//0.00E+00//AT1G76140| serine-type endopeptidase/ serine-type peptidase	Unigene34602_All//0.00E+00//TC143911				nr +
Unigene34603_All	2693	0.70	2.77	2.10	34.94	3.38	0.69	4.29	0.50	3.14	1.98E+00	1.61E-15	Up	1.58E+00	1.39E-08	Up	-3.37E+00	0.00E+00	Down	-5.67E+00	0.00E+00	Down	-3.11E+00	2.28E-48	Down	-4.51E-01	1.91E-03		Unigene34603_All|gi|186495710|ref|NP_001117606.1||0.00E+00//serine-type endopeptidase/ serine-type peptidase [Arabidopsis thaliana]	Unigene34603_All//0.00E+00//AT1G76140| serine-type endopeptidase/ serine-type peptidase	Unigene34603_All//0.00E+00//TC143911				nr -
Unigene34604_All	900	3.78	4.90	5.92	2.27	1.95	1.05	2.40	4.27	6.20	3.74E-01	2.12E-01		6.47E-01	1.65E-02		-2.18E-01	6.36E-01		-1.11E+00	1.47E-02		8.35E-01	2.72E-03		1.37E+00	4.38E-09	Up	Unigene34604_All|gi|297811169|ref|XP_002873468.1||4.00E-14//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319305|gb|EFH49727.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34604_All//4.00E-12//AT5G10650| zinc finger (C3HC4-type RING finger) family protein	Unigene34604_All//0.00E+00//TC140095				nr -
Unigene34605_All	2118	25.86	16.77	22.48	13.05	12.70	11.28	14.27	18.73	37.07	-6.25E-01	3.63E-18		-2.03E-01	8.30E-03		-3.98E-02	7.82E-01		-2.11E-01	5.47E-02		3.92E-01	2.10E-07		1.38E+00	1.76E-117	Up	Unigene34605_All|gi|297812691|ref|XP_002874229.1||1.00E-115//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320066|gb|EFH50488.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34605_All//2.00E-103//AT5G24870| zinc finger (C3HC4-type RING finger) family protein	Unigene34605_All//0.00E+00//TC165128				nr -
Unigene34606_All	470	2.12	1.29	2.49	2.97	0.73	3.56	2.25	1.33	1.02	-7.09E-01	3.05E-01		2.37E-01	6.97E-01		-2.02E+00	4.22E-04	Down	2.61E-01	6.36E-01		-7.54E-01	2.17E-01		-1.14E+00	4.77E-02		Unigene34606_All|gi|297803560|ref|XP_002869664.1||2.00E-52//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315500|gb|EFH45923.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34606_All//3.00E-43//AT4G25610| zinc finger (C2H2 type) family protein	Unigene34606_All//1.00E-134//C0096983	C2H2			nr -
Unigene3461_All	1073	5.80	2.36	4.67	4.32	4.36	5.47	4.41	1.52	2.93	-1.30E+00	1.62E-07	Down	-3.15E-01	2.30E-01		1.57E-02	9.63E-01		3.42E-01	1.95E-01		-1.54E+00	6.36E-09	Down	-5.89E-01	1.35E-02		Unigene3461_All|gi|15238461|ref|NP_200764.1||/5.00E-75//SRR1 (SENSITIVITY TO RED LIGHT REDUCED 1) [Arabidopsis thaliana] >gi|30697247|ref|NP_851224.1| SRR1 (SENSITIVITY TO RED LIGHT REDUCED 1) [Arabidopsis thaliana] >gi|31340430|sp|Q6GW26.2|SRR1_ARATH RecName: Full=Protein SENSITIVITY TO RED LIGHT REDUCED 1 >gi|25527089|gb|AAM97478.1| sensitivity to red light reduced protein [Arabidopsis thaliana] >gi|90186242|gb|ABD91497.1| At5g59560 [Arabidopsis thaliana]	Unigene3461_All//2.00E-76//AT5G59560| SRR1 (SENSITIVITY TO RED LIGHT REDUCED 1)	Unigene3461_All//0.00E+00//TC130952		GO:0007602//GO:0023033//GO:0043231//GO:0048511		nr +
Unigene34611_All	3442	1.81	0.57	2.29	4.56	3.63	2.89	4.41	3.44	1.92	-1.66E+00	1.87E-10	Down	3.40E-01	1.33E-01		-3.28E-01	1.75E-02		-6.59E-01	1.45E-06		-3.60E-01	5.61E-03		-1.20E+00	3.36E-19	Down	Unigene34611_All|gi|15232241|ref|NP_191562.1||/0.00E+00//SPL12 (squamosa promoter-binding protein-like 12); transcription factor [Arabidopsis thaliana] >gi|67461584|sp|Q9S7P5.1|SPL12_ARATH RecName: Full=Squamosa promoter-binding-like protein 12 >gi|6006395|emb|CAB56768.1| squamosa promoter binding protein-like 12 [Arabidopsis thaliana] >gi|6006403|emb|CAB56769.1| squamosa promoter binding protein-like 12 [Arabidopsis thaliana] >gi|7076756|emb|CAB75918.1| squamosa promoter binding protein-like 12 [Arabidopsis thaliana]	Unigene34611_All//0.00E+00//AT2G47070| SPL1 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 1); DNA binding / transcription factor	Unigene34611_All//3.00E-149//gi|84166641|gb|DR455289.1|DR455289	SBP			nr +
Unigene34613_All	2130	15.87	7.28	17.18	11.60	11.25	13.80	5.56	7.10	5.69	-1.12E+00	5.54E-30	Down	1.14E-01	2.70E-01		-4.39E-02	7.73E-01		2.51E-01	1.48E-02		3.54E-01	6.61E-03		3.28E-02	8.45E-01		Unigene34613_All|gi|224097462|ref|XP_002310944.1||/1.00E-178//autoinhibited calcium ATPase [Populus trichocarpa] >gi|222850764|gb|EEE88311.1| autoinhibited calcium ATPase [Populus trichocarpa]	Unigene34613_All//6.00E-152//AT3G21180| ACA9 (AUTOINHIBITED CA(2+)-ATPASE 9); calcium-transporting ATPase/ calmodulin binding	Unigene34613_All//0.00E+00//gi|109853438|gb|DW482417.1|DW482417				nr -
Unigene34614_All	3460	4.39	2.87	1.11	5.95	7.20	5.00	12.06	4.18	5.29	-6.12E-01	1.93E-05		-1.98E+00	6.39E-30	Down	2.75E-01	1.11E-02		-2.50E-01	4.92E-02		-1.53E+00	6.45E-72	Down	-1.19E+00	1.10E-50	Down	Unigene34614_All|gi|297801288|ref|XP_002868528.1||/0.00E+00//EMB2656 [Arabidopsis lyrata subsp. lyrata] >gi|297314364|gb|EFH44787.1| EMB2656 [Arabidopsis lyrata subsp. lyrata]	Unigene34614_All//0.00E+00//AT5G37630| EMB2656 (EMBRYO DEFECTIVE 2656); binding	Unigene34614_All//0.00E+00//TC157787				nr +
Unigene34616_All	390	0.40	0.00	0.00	0.38	0.00	0.35	2.60	1.18	0.41	-8.65E+00	2.15E-01		-8.65E+00	2.44E-01		-8.58E+00	1.65E-01		-1.42E-01	9.43E-01		-1.14E+00	6.62E-02		-2.67E+00	1.94E-04	Down	Unigene34616_All|gi|294769202|gb|ADF36482.1||2.00E-41//high-affinity potassium transporter protein 2 [Gossypium hirsutum]	Unigene34616_All//6.00E-35//AT1G70300| KUP6; potassium ion transmembrane transporter	Unigene34616_All//6.00E-62//TC142099				nr -
Unigene34617_All	2814	6.54	12.39	9.06	10.52	4.87	9.05	4.34	4.25	1.42	9.21E-01	2.30E-22		4.70E-01	2.36E-05		-1.11E+00	1.44E-31	Down	-2.16E-01	3.94E-02		-3.17E-02	8.54E-01		-1.62E+00	4.10E-24	Down	Unigene34617_All|gi|281485781|gb|ADA71305.1||/0.00E+00//potassium transporter [Gossypium hirsutum]	Unigene34617_All//0.00E+00//AT5G14880| potassium transporter, putative	Unigene34617_All//0.00E+00//TC146505				nr +
Unigene34618_All	3120	1.32	0.88	1.19	15.15	14.22	11.94	2.76	1.84	1.07	-5.95E-01	4.64E-02		-1.49E-01	6.25E-01		-9.20E-02	3.16E-01		-3.43E-01	4.77E-06		-5.91E-01	7.31E-04		-1.37E+00	1.23E-13	Down	Unigene34618_All|gi|127519339|gb|ABQ28522.1||/0.00E+00//kinesin-related protein [Gossypium hirsutum]	Unigene34618_All//0.00E+00//AT2G47500| ATP binding / microtubule motor	Unigene34618_All//0.00E+00//TC167954				nr -
Unigene3462_All	1306	2.12	1.90	2.16	4.54	3.11	2.94	2.56	1.18	2.01	-1.60E-01	6.64E-01		2.54E-02	9.65E-01		-5.45E-01	1.95E-02		-6.27E-01	9.46E-03		-1.11E+00	2.84E-04	Down	-3.45E-01	2.55E-01				Unigene3462_All//4.00E-13//DT049892				
Unigene34621_All	632	3.31	6.09	2.27	4.26	5.67	3.00	8.63	2.98	3.97	8.80E-01	4.96E-03		-5.42E-01	2.44E-01		4.13E-01	2.30E-01		-5.04E-01	2.11E-01		-1.54E+00	3.89E-10	Down	-1.12E+00	8.69E-07	Down	Unigene34621_All|gi|255538254|ref|XP_002510192.1||7.00E-14//Serine/threonine-protein kinase PBS1, putative [Ricinus communis] >gi|223550893|gb|EEF52379.1| Serine/threonine-protein kinase PBS1, putative [Ricinus communis]		Unigene34621_All//7.00E-149//TC148109				nr +
Unigene34622_All	2197	16.24	20.39	10.83	22.04	24.65	21.91	12.61	4.53	9.27	3.28E-01	3.76E-05		-5.84E-01	2.48E-10		1.62E-01	2.88E-02		-8.20E-03	9.44E-01		-1.48E+00	1.24E-45	Down	-4.44E-01	7.48E-07		Unigene34622_All|gi|15235432|ref|NP_192172.1||/0.00E+00//protein kinase family protein [Arabidopsis thaliana]	Unigene34622_All//2.00E-174//AT4G02630| protein kinase family protein	Unigene34622_All//0.00E+00//gi|78329502|gb|DT549776.1|DT549776		ko04626|Plant-pathogen interaction		nr -
Unigene34627_All	617	7.12	24.31	2.85	7.10	12.67	7.91	30.49	20.86	87.17	1.77E+00	2.56E-26	Up	-1.32E+00	2.24E-05	Down	8.34E-01	2.36E-05		1.54E-01	6.17E-01		-5.48E-01	1.34E-06		1.52E+00	5.15E-93	Up	Unigene34627_All|gi|122894104|gb|ABM67698.1||/2.00E-22//mitogen-activated protein kinase [Citrus sinensis]	Unigene34627_All//8.00E-20//AT3G45640| ATMPK3 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP kinase/ kinase/ protein binding / protein kinase	Unigene34627_All//0.00E+00//TC151662		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene34628_All	1575	15.91	30.11	8.49	14.83	24.44	23.54	49.56	29.54	152.40	9.20E-01	3.89E-30		-9.07E-01	2.72E-15		7.21E-01	3.72E-19		6.66E-01	8.92E-15		-7.47E-01	2.29E-42		1.62E+00	0.00E+00	Up	Unigene34628_All|gi|122894104|gb|ABM67698.1||/0.00E+00//mitogen-activated protein kinase [Citrus sinensis]	Unigene34628_All//0.00E+00//AT3G45640| ATMPK3 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE 3); MAP kinase/ kinase/ protein binding / protein kinase	Unigene34628_All//0.00E+00//TC133465		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene3463_All	870	39.27	37.27	35.99	24.22	23.27	21.80	12.25	2.79	4.17	-7.53E-02	4.80E-01		-1.26E-01	2.39E-01		-5.75E-02	7.08E-01		-1.52E-01	2.73E-01		-2.14E+00	1.59E-29	Down	-1.56E+00	5.05E-20	Down	Unigene3463_All|gi|87241159|gb|AB033017.1||/7.00E-46//Blue (type 1) copper domain [Medicago truncatula]	Unigene3463_All//8.00E-12//AT4G27520| plastocyanin-like domain-containing protein	Unigene3463_All//0.00E+00//gi|164287236|gb|ES844109.1|ES844109				nr +
Unigene34631_All	812	18.49	9.98	10.82	30.61	27.48	12.24	8.85	7.41	14.33	-8.89E-01	1.39E-09		-7.73E-01	2.42E-07		-1.56E-01	1.95E-01		-1.32E+00	8.46E-31	Down	-2.56E-01	2.30E-01		6.95E-01	1.79E-06		Unigene34631_All|gi|124359162|gb|ABN05685.1||2.00E-14//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene34631_All//4.00E-07//AT3G09510| nucleic acid binding	Unigene34631_All//2.00E-103//DR462197				nr -
Unigene34632_All	1359	1.16	0.89	1.33	3.23	2.13	0.80	1.43	2.52	2.93	-3.68E-01	4.87E-01		2.06E-01	6.64E-01		-6.00E-01	3.06E-02		-2.02E+00	2.66E-10	Down	8.17E-01	6.02E-03		1.03E+00	1.24E-04	Up	Unigene34632_All|gi|124359163|gb|ABN05686.1||/4.00E-19//Zinc finger, CCHC-type [Medicago truncatula]	Unigene34632_All//3.00E-09//AT3G31430| unknown protein	Unigene34632_All//1.00E-38//DR457757				nr +
Unigene34633_All	1211	3.97	2.68	3.91	9.05	7.79	3.69	4.61	3.93	5.92	-5.70E-01	3.79E-02		-2.24E-02	9.56E-01		-2.16E-01	2.47E-01		-1.29E+00	1.99E-13	Down	-2.28E-01	3.70E-01		3.62E-01	6.21E-02		Unigene34633_All|gi|124359162|gb|ABN05685.1||/2.00E-37//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene34633_All//2.00E-22//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene34633_All//5.00E-108//TC150448				nr -
Unigene34635_All	1989	23.07	72.71	27.41	10.44	17.57	37.49	31.14	62.07	23.98	1.66E+00	3.24E-226	Up	2.49E-01	9.38E-04		7.51E-01	1.12E-18		1.84E+00	8.27E-146	Up	9.95E-01	7.11E-108		-3.77E-01	9.89E-11		Unigene34635_All|gi|15485720|emb|CAC67501.1||0.00E+00//selenium binding protein [Medicago sativa]	Unigene34635_All//0.00E+00//AT4G14030| SBP1 (selenium-binding protein 1); selenium binding	Unigene34635_All//0.00E+00//TC166412				nr -
Unigene34638_All	2505	1.80	2.14	1.06	4.93	4.63	4.42	6.16	1.62	2.72	2.55E-01	3.60E-01		-7.57E-01	1.10E-02		-9.03E-02	6.25E-01		-1.59E-01	3.94E-01		-1.93E+00	3.06E-37	Down	-1.18E+00	4.84E-19	Down	Unigene34638_All|gi|30679610|ref|NP_195857.2||/4.00E-73//kinesin motor protein-related [Arabidopsis thaliana] >gi|59938334|gb|AAX12877.1| At5g02370 [Arabidopsis thaliana]	Unigene34638_All//1.00E-72//AT5G02370| kinesin motor protein-related	Unigene34638_All//0.00E+00//gi|164355692|gb|EX172568.1|EX172568				nr -
Unigene3464_All	711	1.47	9.19	1.35	4.06	3.20	4.51	58.28	13.76	112.34	2.64E+00	4.35E-19	Up	-1.27E-01	8.44E-01		-3.46E-01	3.72E-01		1.50E-01	6.78E-01		-2.08E+00	2.99E-109	Down	9.47E-01	4.94E-66		Unigene3464_All|gi|222424367|dbj|BAH20139.1||/5.00E-14//AT5G41080 [Arabidopsis thaliana]	Unigene3464_All//3.00E-15//AT5G41080| glycerophosphoryl diester phosphodiesterase family protein	Unigene3464_All//1.00E-113//TC152643			GO:0008081//GO:0019400//GO:0031410	nr +
Unigene34645_All	2705	26.89	10.12	12.68	38.58	32.45	22.29	35.47	50.22	41.66	-1.41E+00	1.33E-90	Down	-1.08E+00	3.98E-58	Down	-2.50E-01	8.19E-08		-7.92E-01	4.22E-55		5.02E-01	2.38E-36		2.32E-01	5.03E-08		Unigene34645_All|gi|15239414|ref|NP_200879.1||/0.00E+00//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|9759335|dbj|BAB09844.1| retroelement pol polyprotein-like [Arabidopsis thaliana]	Unigene34645_All//0.00E+00//AT5G60710| zinc finger (C3HC4-type RING finger) family protein	Unigene34645_All//0.00E+00//TC152829				nr +
Unigene34649_All	1387	8.86	6.14	3.80	13.50	10.43	11.98	15.58	8.26	7.09	-5.31E-01	9.85E-04		-1.22E+00	2.57E-12	Down	-3.73E-01	2.12E-03		-1.72E-01	2.29E-01		-9.16E-01	3.87E-17		-1.13E+00	9.09E-25	Down	Unigene34649_All|gi|115450015|ref|NP_001048609.1||7.00E-53//0s02g0829800 (Oryza sativa Japonica Group) >gi|48716331|dbj|BAD22943.1| membrane-associated salt-inducible protein-like [Oryza sativa Japonica Group] >gi|113538140|dbj|BAF10523.1| 0s02g0829800 [Oryza sativa Japonica Group]	Unigene34649_All//6.00E-35//AT1G61870| PPR336 (pentatricopeptide repeat 336)	Unigene34649_All//0.00E+00//gi|78333138|gb|DT553412.1|DT553412				nr +

Unigene3465_All	492	4.47	6.18	4.65	6.28	6.65	6.88	156.32	23.45	188.59	4.68E-01	2.00E-01		5.94E-02	8.94E-01		8.30E-02	8.26E-01		1.33E-01	7.14E-01		-2.74E+00	4.90E-280	Down	2.71E-01	9.41E-09		Unigene3465_All//gi|297805540|ref|XP_002870654.1|//5.00E-23//glycerophosphoryl diester phosphodiesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316490|gb|EFH46913.1| glycerophosphoryl diester phosphodiesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3465_All//4.00E-19//AT5G41080| glycerophosphoryl diester phosphodiesterase family protein	Unigene3465_All//0.00E+00//gi|73861301|gb|DT464040.1|DT464040			GO:0008081//GO:0019400	nr -
Unigene34655_All	2403	12.32	3.94	6.43	11.73	8.90	10.15	6.53	7.58	9.30	-1.64E+00	1.43E-46	Down	-9.39E-01	5.17E-19		-3.99E-01	2.49E-05		-2.09E-01	5.35E-02		2.16E-01	8.08E-02		5.11E-01	4.39E-07		Unigene34655_All//gi|10880466|gb|AG24263.1|AF106957.1|/1.00E-172//dual-specific kinase DSK1 [Nicotiana tabacum]	Unigene34655_All//1.00E-128//AT5G56790| protein kinase family protein	Unigene34655_All//0.00E+00//TC168857		ko04626|Plant-pathogen interaction		nr -
Unigene34657_All	1793	105.98	40.55	54.38	74.29	63.38	48.29	4.86	2.77	1.76	-1.39E+00	9.95E-230	Down	-9.63E-01	1.72E-124		-2.29E-01	2.07E-08		-6.22E-01	4.84E-46		-8.08E-01	3.88E-06		-1.47E+00	2.98E-15	Down	Unigene34657_All//gi|18408809|ref|NP_566917.1|//1.00E-110//iqd21 (IQ-domain 21); calmodulin binding [Arabidopsis thaliana] >gi|42572619|ref|NP_974405.1| iqd21 (IQ-domain 21); calmodulin binding [Arabidopsis thaliana] >gi|13605619|gb|AAK32803.1|AF36163 5.1 AT3g49260/F2K15_120 [Arabidopsis thaliana] >gi|21593446|gb|AAM65413.1| SF16-like protein [Arabidopsis thaliana] >gi|23308403|gb|AAN18171.1| At3g49260/F2K15_120 [Arabidopsis thaliana] >gi|39980284|gb|AAR32943.1| guard cell associated protein [Arabidopsis thaliana]	Unigene34657_All//4.00E-53//AT3G49260| iqd21 (IQ-domain 21); calmodulin binding	Unigene34657_All//0.00E+00//TC136359				nr +
Unigene34658_All	1368	4.90	3.67	5.88	1.42	1.94	1.06	3.15	2.51	1.08	-4.17E-01	7.06E-02		2.64E-01	2.44E-01		4.49E-01	2.82E-01		-4.27E-01	4.05E-01		-3.32E-01	2.38E-01		-1.55E+00	1.44E-08	Down	Unigene34658_All//gi|30688506|ref|NP_181637.2|//1.00E-126//methyltransferase-related [Arabidopsis thaliana] >gi|122223742|sp|Q09PT7.1|Y2104_ARATH RecName: Full=Uncharacterized methyltransferase At2g41040, chloroplastic; Flags: Precursor	Unigene34658_All//4.00E-127//AT2G41040| methyltransferase-related	Unigene34658_All//0.00E+00//CO070182		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00100|Steroid biosynthesis		nr -
Unigene34659_All	1536	9.20	7.55	12.55	3.50	4.93	5.38	12.22	9.20	3.99	-2.84E-01	6.72E-02		4.48E-01	5.91E-04		4.94E-01	1.77E-02		6.19E-01	1.90E-03		-4.10E-01	3.21E-04		-1.61E+00	1.78E-36	Down	Unigene34659_All//gi|30688506|ref|NP_181637.2|//1.00E-123//methyltransferase-related [Arabidopsis thaliana] >gi|122223742|sp|Q09PT7.1|Y2104_ARATH RecName: Full=Uncharacterized methyltransferase At2g41040, chloroplastic; Flags: Precursor	Unigene34659_All//3.00E-115//AT2G41040| methyltransferase-related	Unigene34659_All//0.00E+00//TC146890		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene3466_All	1223	6.03	3.11	2.74	11.49	10.14	7.13	5.57	2.60	3.52	-9.57E-01	1.09E-05		-1.14E+00	6.76E-07	Down	-1.80E-01	2.82E-01		-6.89E-01	2.27E-06		-1.10E+00	9.21E-08	Down	-6.62E-01	6.54E-04		Unigene3466_All//gi|115473777|ref|NP_001060487.1|//1.00E-08//Os07g0652800 [Oryza sativa Japonica Group] >gi|113612023|dbj|BAF22401.1| Os07g0652800 [Oryza sativa Japonica Group]		Unigene3466_All//0.00E+00//ES803332				nr +
Unigene34660_All	824	4.83	4.30	4.59	14.81	6.81	5.59	4.46	3.40	3.09	-1.65E-01	5.98E-01		-7.28E-02	8.19E-01		-1.12E+00	1.89E-13	Down	-1.41E+00	7.71E-17	Down	-3.94E-01	1.89E-01		-5.29E-01	5.70E-02		Unigene34660_All//gi|124359162|gb|ABN05685.1|//6.00E-17//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene34660_All//2.00E-09//AT3G09510| nucleic acid binding	Unigene34660_All//0.00E+00//gi|21101406|gb|BQ413719.1|BQ413719				nr -
Unigene34661_All	1680	13.67	8.08	14.55	21.20	16.05	15.67	5.81	4.03	2.18	-7.58E-01	5.00E-11		8.97E-02	4.98E-01		-4.02E-01	1.17E-06		-4.36E-01	5.50E-07		-5.29E-01	1.23E-03		-1.41E+00	4.15E-16	Down	Unigene34661_All//gi|297725701|ref|NP_001175214.1|//2.00E-19//Os02g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1| Os02g0501200 [Oryza sativa Japonica Group]	Unigene34661_All//2.00E-10//AT3G09510| nucleic acid binding	Unigene34661_All//0.00E+00//ES832366				nr +
Unigene34662_All	2568	9.82	10.67	10.55	8.38	10.23	12.86	4.49	7.62	10.11	1.20E-01	3.05E-01		1.04E-01	4.00E-01		2.88E-01	5.62E-03		6.17E-01	1.26E-11		7.61E-01	1.41E-11		1.17E+00	8.41E-31	Up	Unigene34662_All//gi|223452424|gb|ACM89539.1|//0.00E+00//protein kinase family protein [Glycine max]	Unigene34662_All//1.00E-169//AT2G28250| NCRK; kinase	Unigene34662_All//0.00E+00//TC155924		ko04626|Plant-pathogen interaction		nr +
Unigene34664_All	2119	0.74	0.77	0.55	0.33	0.57	0.98	0.32	0.20	0.56	4.69E-02	9.41E-01		-4.22E-01	4.37E-01		7.89E-01	2.24E-01		1.57E+00	7.98E-04	Up	-6.95E-01	3.94E-01		8.21E-01	1.26E-01		Unigene34664_All//gi|223452424|gb|ACM89539.1|//1.00E-148//protein kinase family protein [Glycine max]	Unigene34664_All//2.00E-127//AT2G28250| NCRK; kinase	Unigene34664_All//0.00E+00//TC158289		ko04626|Plant-pathogen interaction		nr +
Unigene34666_All	461	0.34	0.00	0.00	0.54	1.34	1.08	2.20	6.62	0.95	-8.41E+00	2.15E-01		-8.41E+00	2.44E-01		1.32E+00	1.88E-01		9.96E-01	3.94E-01		1.59E+00	2.98E-06	Up	-1.21E+00	4.17E-02		Unigene34666_All//gi|28951043|gb|AA063445.1|//3.00E-17//At2g25737 [Arabidopsis thaliana]	Unigene34666_All//2.00E-18//AT2G25737| unknown protein	Unigene34666_All//2.00E-49//TC154090				nr +
Unigene3467_All	1452	0.61	0.56	0.55	2.98	3.94	3.11	2.71	2.07	1.02	-1.34E-01	8.41E-01		-1.55E-01	8.24E-01		3.99E-01	1.19E-01		5.95E-02	8.59E-01		-3.86E-01	1.81E-01		-1.42E+00	5.19E-07	Down	Unigene3467_All//gi|45825141|gb|AAS77478.1|//7.00E-45//At5g22540 [Arabidopsis thaliana]	Unigene3467_All//8.00E-47//AT2G36430| unknown protein					nr -
Unigene34671_All	1041	72.73	47.75	46.45	87.09	81.34	87.07	53.61	22.85	26.64	-6.07E-01	1.40E-23		-6.47E-01	2.43E-25		-9.85E-02	9.70E-02		-3.00E-04	9.95E-01		-1.23E+00	4.21E-69	Down	-1.01E+00	7.92E-52	Down	Unigene34671_All//gi|211906520|gb|ACJ11753.1|//1.00E-152//UDP-D-apiose/UPD-D-xylose synthetase [Gossypium hirsutum]	Unigene34671_All//1.00E-150//AT1G08200| AXS2 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 2); UDP-glucuronate decarboxylase	Unigene34671_All//0.00E+00//TC141249		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene34672_All	1404	13.60	5.92	6.30	27.32	21.88	18.40	25.63	12.12	13.34	-1.20E+00	4.31E-19	Down	-1.11E+00	3.01E-16	Down	-3.21E-01	7.27E-05		-5.70E-01	8.57E-12		-1.08E+00	1.45E-36	Down	-9.42E-01	3.41E-30		Unigene34672_All//gi|211906520|gb|ACJ11753.1|//0.00E+00//UDP-D-apiose/UPD-D-xylose synthetase [Gossypium hirsutum]	Unigene34672_All//0.00E+00//AT1G08200| AXS2 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 2); UDP-glucuronate decarboxylase	Unigene34672_All//0.00E+00//TC136293		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene34673_All	3657	0.47	0.44	0.64	3.27	1.56	2.33	43.36	43.85	29.98	-9.05E-02	8.47E-01		4.41E-01	3.25E-01		-1.06E+00	3.70E-12	Down	-4.86E-01	2.70E-03		1.65E-02	7.20E-01		-5.32E-01	2.63E-48		Unigene34673_All//gi|62946489|gb|AAY22388.1|//0.00E+00//symbiosis receptor-like kinase [Tropaeolum majus]	Unigene34673_All//4.00E-120//AT2G37050| kinase	Unigene34673_All//0.00E+00//TC135238		ko04626|Plant-pathogen interaction		nr +
Unigene34674_All	1124	48.08	42.06	51.31	13.96	21.87	20.65	1.32	4.24	10.42	-1.93E-01	9.47E-03		9.36E-02	2.50E-01		6.48E-01	2.34E-10		5.65E-01	3.11E-07		1.69E+00	4.17E-10	Up	2.98E+00	7.09E-48	Up	Unigene34674_All//gi|15236930|ref|NP_195251.1|//1.00E-166//vestitone reductase-related [Arabidopsis thaliana] >gi|18087583|gb|AAL58922.1|AF46283 4_1 AT4g35250/F23E12_190 [Arabidopsis thaliana] >gi|22137054|gb|AAM91372.1| At4g35250/F23E12_190 [Arabidopsis thaliana]	Unigene34674_All//3.00E-164//AT4G35250| vestitone reductase-related	Unigene34674_All//0.00E+00//TC136137		ko00190|Oxidative phosphorylation//ko00100|Steroid biosynthesis		nr -
Unigene34675_All	1171	18.50	26.01	25.78	8.13	11.06	8.41	0.54	1.43	4.69	4.92E-01	4.80E-07		4.79E-01	2.14E-06		4.45E-01	3.26E-03		4.94E-02	8.18E-01		1.40E+00	2.88E-03		3.12E+00	8.74E-24	Up	Unigene34675_All//gi|115477733|ref|NP_001062462.1|//2.00E-81//Os08g0553800 [Oryza sativa Japonica Group] >gi|113624431|dbj|BAF24376.1| Os08g0553800 [Oryza sativa Japonica Group]	Unigene34675_All//2.00E-82//AT4G35250| vestitone reductase-related	Unigene34675_All//0.00E+00//gi|48740490|gb|CO071009.1|CO071009				nr +
Unigene34677_All	2362	12.98	6.59	9.02	5.99	5.35	6.31	4.19	4.30	1.91	-9.79E-01	6.80E-22		-5.26E-01	1.55E-07		-1.63E-01	3.26E-01		7.52E-02	6.81E-01		3.78E-02	8.40E-01		-1.14E+00	7.61E-12	Down	Unigene34677_All//gi|42565990|ref|NP_191277.3|//0.00E+00//GTP binding [Arabidopsis thaliana]	Unigene34677_All//0.00E+00//AT3G57180| GTP binding	Unigene34677_All//0.00E+00//TC179344		ko04626|Plant-pathogen interaction//ko00330|Arginine and proline metabolism		nr -
Unigene34682_All	860	4.14	5.72	4.83	11.30	11.57	12.03	27.92	39.12	58.23	4.66E-01	8.95E-02		2.23E-01	4.97E-01		3.49E-02	8.73E-01		9.05E-02	6.81E-01		4.87E-01	3.78E-09		1.06E+00	4.28E-50	Up	Unigene34682_All//gi|9858780|gb|AAG01127.1|AF273333_12//2.00E-30//BAC19_12 [Solanum lycopersicum]	Unigene34682_All//4.00E-19//AT5G66730| zinc finger (C2H2 type) family protein	Unigene34682_All//0.00E+00//TC155229	C2H2			nr +
Unigene34684_All	2560	15.16	57.18	15.85	28.02	43.78	50.19	26.05	34.56	101.96	1.91E+00	6.02E-280	Up	6.38E-02	5.38E-01		6.44E-01	2.16E-45		8.41E-01	2.00E-74		4.08E-01	1.18E-16		1.97E+00	0.00E+00	Up	Unigene34684_All//gi|115434224|ref|NP_001041870.1|//5.00E-54//Os01g0120700 [Oryza sativa Japonica Group] >gi|113331401|dbj|BAF03784.1| Os01g0120700 [Oryza sativa Japonica Group]		Unigene34684_All//0.00E+00//TC175217		ko03040|Spliceosome		nr +
Unigene34685_All	2198	18.00	4.98	6.11	52.60	45.70	23.14	21.54	3.80	5.60	-1.85E+00	3.07E-73	Down	-1.56E+00	1.89E-55	Down	-2.03E-01	6.00E-06		-1.18E+00	3.71E-119	Down	-2.50E+00	4.44E-156	Down	-1.94E+00	2.05E-117	Down	Unigene34685_All//gi|42569805|ref|NP_181587.2|//0.00E+00//ETG1 (E2F TARGET GENE 1) [Arabidopsis thaliana] >gi|63003830|gb|AAY25444.1| At2g40550 [Arabidopsis thaliana]	Unigene34685_All//7.00E-130//AT2G40550| ETG1 (E2F TARGET GENE 1)	Unigene34685_All//0.00E+00//TC132015				nr -
Unigene34689_All	1674	80.61	53.82	46.00	116.77	123.12	139.89	241.36	143.04	106.76	-5.83E-01	1.39E-38		-8.09E-01	4.85E-66		7.64E-02	4.35E-02		2.61E-01	2.07E-16		-7.55E-01	2.80E-220		-1.18E+00	0.00E+00	Down	Unigene34689_All//gi|13826392|sp|Q9FUM1.1|EF1G_PRUAV//1.00E-101//RecName: Full=Elongation factor 1-gamma; Short=EF-1-gamma; AltName: Full=eEF-1B gamma >gi|10444415|gb|AAG17901.1|AF297712_1 translation elongation factor 1-gamma [Prunus avium]	Unigene34689_All//2.00E-81//AT1G57720| elongation factor 1B-gamma, putative / eEF-1B gamma, putative	Unigene34689_All//0.00E+00//gi|164284946|gb|ES796409.1|ES796409				nr +
Unigene34691_All	3833	7.66	2.10	4.93	12.58	10.58	9.61	21.61	17.64	10.34	-1.87E+00	5.76E-55	Down	-6.35E-01	6.84E-10		-2.49E-01	6.17E-04		-3.88E-01	1.49E-07		-2.93E-01	9.28E-09		-1.06E+00	2.99E-83	Down	Unigene34691_All//gi|134142350|gb|ABO61511.1|//0.00E+00//LRR receptor-like protein kinase m1' [Malus x domestica]	Unigene34691_All//0.00E+00//AT4G28490| HAE (HAESA); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene34691_All//0.00E+00//TC164244				nr +
Unigene34693_All	758	0.14	0.13	0.00	1.97	2.86	1.25	9.76	5.46	3.84	-4.57E-02	9.88E-01		-7.11E+00	3.93E-01		5.38E-01	2.39E-01		-6.56E-01	2.40E-01		-8.39E-01	1.25E-05		-1.35E+00	1.35E-11	Down	Unigene34693_All//gi|240256160|ref|NP_195174.6|//1.00E-92//catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|259016223|sp|Q9M069.2|E137_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 7; AltName: Full=(1->3)-beta-glucan endohydrolase 7; Short=(1->3)-beta-glucanase 7; AltName: Full=Beta-1,3-endoglucanase 7; Short=Beta-1,3-glucanase 7; Flags: Precursor	Unigene34693_All//7.00E-94//AT4G34480| catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene34693_All//0.00E+00//TC137300		ko00500|Starch and sucrose metabolism		nr -

Unigene34694_All	1881	90.34	48.11	83.97	196.87	195.44	166.75	26.91	22.75	10.02	-9.09E-01	1.92E-104		-1.06E-01	1.46E-02		-1.05E-02	7.96E-01		-2.40E-01	5.89E-22		-2.42E-01	3.36E-04		-1.43E+00	8.88E-81	Down	Unigene34694_All//gi|240256160|ref|NP_195174.6|//0.00E+00//catalytic / cation binding / hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|259016223|sp|Q9M069.2|E137_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 7; AltName: Full=(1->3)-beta-glucan endohydrolase 7; Short=(1->3)-beta-glucanase 7; AltName: Full=Beta-1,3-endoglucanase 7; Short=Beta-1,3-glucanase 7; Flags: Precursor	Unigene34694_All//0.00E+00//AT4G34480| catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene34694_All//0.00E+00//TC137300		ko00500|Starch and sucrose metabolism		nr +
Unigene34697_All	512	6.64	24.05	1.87	12.75	28.85	17.02	11.56	19.59	35.25	1.86E+00	3.94E-23	Up	-1.83E+00	1.84E-06	Down	1.18E+00	1.19E-16	Up	4.18E-01	3.77E-02		7.61E-01	2.47E-06		1.61E+00	1.43E-34	Up	Unigene34697_All//gi|41057633|gb|AB98818.1|//1.00E-72//transcription factor WRKY1 [Gossypium arboreum]	Unigene34697_All//2.00E-24//AT1G80840| WRKY40; transcription factor	Unigene34697_All//0.00E+00//CO079369	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene34698_All	1563	26.21	111.81	10.05	45.35	99.96	62.41	27.73	52.25	95.89	2.09E+00	0.00E+00	Up	-1.38E+00	4.67E-48	Down	1.14E+00	3.56E-165	Up	4.61E-01	8.82E-20		9.14E-01	2.95E-62		1.79E+00	0.00E+00	Up	Unigene34698_All//gi|41057633|gb|AB98818.1|//1.00E-179//transcription factor WRKY1 [Gossypium arboreum]	Unigene34698_All//1.00E-57//AT1G80840| WRKY40; transcription factor	Unigene34698_All//0.00E+00//TC131065	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene3470_All	397	28.60	21.06	13.14	30.24	26.98	45.73	38.55	26.64	28.90	-4.42E-01	9.24E-03		-1.12E+00	4.77E-10	Down	-1.65E-01	3.77E-01		5.97E-01	2.47E-06		-5.34E-01	2.63E-05		-4.16E-01	8.23E-04		Unigene3470_All//gi|124360667|gb|AB008656.1|//2.00E-38//Ribosomal protein S10, eukaryotic and archaeal form [Medicago truncatula]	Unigene3470_All//1.00E-36//AT3G47370| 40S ribosomal protein S20 (RPS20B)	Unigene3470_All//0.00E+00//TC149574		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0031981	nr -
Unigene34703_All	762	6.04	6.58	7.48	3.66	5.69	1.54	0.50	1.10	1.25	1.24E-01	6.47E-01		3.07E-01	2.54E-01		6.37E-01	2.62E-02		-1.25E+00	9.65E-04	Down	1.14E+00	1.06E-01		1.33E+00	3.49E-02		Unigene34703_All//gi|151176133|gb|ABV42185.2|//6.00E-67//phototropin-1 [Solanum lycopersicum]	Unigene34703_All//5.00E-61//AT3G45780| PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase	Unigene34703_All//2.00E-81//TC149729				nr +
Unigene34704_All	776	138.96	66.86	121.46	92.05	96.12	57.91	2.94	0.43	0.82	-1.06E+00	4.74E-85	Down	-1.94E-01	2.04E-04		6.23E-02	4.09E-01		-6.69E-01	2.50E-28		-2.77E+00	4.83E-09	Down	-1.84E+00	4.73E-06	Down	Unigene34704_All//gi|151176133|gb|ABV42185.2|//5.00E-82//phototropin-1 [Solanum lycopersicum]	Unigene34704_All//5.00E-79//AT3G45780| PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase	Unigene34704_All//0.00E+00//TC149729				nr -
Unigene34706_All	1898	7.75	1.68	3.06	8.77	5.90	3.97	4.41	2.09	2.90	-2.20E+00	1.86E-34	Down	-1.34E+00	8.77E-17	Down	-5.72E-01	4.96E-06		-1.14E+00	1.38E-16	Down	-1.08E+00	4.52E-09	Down	-6.07E-01	4.52E-04		Unigene34706_All//gi|42569545|ref|NP_180761.2|//0.00E+00//endonuclease/exonuclease/phosphatase family protein [Arabidopsis thaliana]	Unigene34706_All//0.00E+00//AT2G32010| endonuclease/exonuclease/phosphatase family protein	Unigene34706_All//0.00E+00//TC137011				nr +
Unigene34707_All	1244	1.81	1.18	0.81	5.61	2.60	1.02	1.53	0.34	1.18	-6.15E-01	1.47E-01		-1.15E+00	1.10E-02		-1.11E+00	9.05E-08	Down	-2.46E+00	1.77E-20	Down	-2.19E+00	5.20E-06	Down	-3.68E-01	3.80E-01		Unigene34707_All//gi|149727871|gb|ABR28335.1|//2.00E-69//MYB transcription factor MYB40 [Medicago truncatula]	Unigene34707_All//1.00E-56//AT5G52660| myb family transcription factor	Unigene34707_All//2.00E-61//TC134560	MYB-related	ko04712|Circadian rhythm - plant		nr -
Unigene3471_All	1083	9.18	6.88	4.82	11.22	10.33	7.21	23.74	10.96	9.64	-4.16E-01	2.35E-02		-9.30E-01	1.03E-06		-1.19E-01	5.57E-01		-6.38E-01	5.55E-05		-1.11E+00	1.14E-27	Down	-1.30E+00	3.93E-36	Down	Unigene3471_All//gi|124360667|gb|AB008656.1|//1.00E-60//Ribosomal protein S10, eukaryotic and archaeal form [Medicago truncatula]	Unigene3471_All//1.00E-59//AT3G47370| 40S ribosomal protein S20 (RPS20B)	Unigene3471_All//0.00E+00//DT467449		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0031981	nr +
Unigene34715_All	653	8.41	23.82	29.11	6.33	21.36	29.33	8.35	22.53	11.84	1.50E+00	1.09E-21	Up	1.79E+00	1.02E-32	Up	1.75E+00	5.31E-28	Up	2.21E+00	1.24E-47	Up	1.43E+00	1.80E-23	Up	5.03E-01	5.71E-03				Unigene34715_All//2.00E-173//TC157893					
Unigene34716_All	2022	51.26	238.59	190.88	46.39	153.24	248.22	43.37	79.29	60.09	2.22E+00	0.00E+00	Up	1.90E+00	0.00E+00	Up	1.72E+00	0.00E+00	Up	2.42E+00	0.00E+00	Up	8.71E-01	6.51E-112		4.71E-01	8.05E-30		Unigene34716_All//gi|115480653|ref|NP_001063920.1|//4.00E-48//Os09g0539800 (Oryza sativa Japonica Group) >gi|113632153|dbj|BAF25834.1|Os09g0539800 (Oryza sativa Japonica Group)	Unigene34716_All//2.00E-37//AT3G13050| transporter-related	Unigene34716_All//0.00E+00//TC157893				nr +
Unigene34717_All	1705	2.30	4.93	1.16	6.37	1.45	12.48	5.21	34.91	67.18	1.10E+00	9.27E-08	Up	-9.94E-01	2.15E-03		-2.13E+00	1.37E-30	Down	9.70E-01	4.52E-16		2.74E+00	8.88E-217	Up	3.69E+00	0.00E+00	Up	Unigene34717_All//gi|225456495|ref|XP_002280924.1|//7.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene34717_All//6.00E-164//TC134807				nr +
Unigene34718_All	1686	6.67	4.30	3.25	14.12	1.59	13.61	26.33	58.21	57.35	-6.35E-01	1.74E-04		-1.04E+00	7.63E-09	Down	-3.15E+00	3.21E-105	Down	-5.36E-02	6.75E-01		1.14E+00	1.12E-107	Up	1.12E+00	3.35E-105	Up	Unigene34718_All//gi|224075453|ref|XP_002304640.1|//9.00E-69//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222842072|gb|EEE79619.1|AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene34718_All//2.00E-37//AT5G13330| Rap2.6L (related to AP2 6L); DNA binding / transcription factor	Unigene34718_All//0.00E+00//TC134807	AP2-EREBP			nr +
Unigene34719_All	2153	35.41	8.05	8.63	60.80	29.64	63.52	84.03	23.10	35.68	-2.14E+00	1.10E-169	Down	-2.04E+00	3.49E-154	Down	-1.04E+00	4.31E-124	Down	6.30E-02	2.33E-01		-1.86E+00	0.00E+00	Down	-1.24E+00	2.95E-230	Down	Unigene34719_All//gi|15230232|ref|NP_191274.1|//0.00E+00//NAP57 (Arabidopsis thaliana homologue of NAP57); pseudouridine synthase >gi|674604028|sp|Q8LE90.1|DKC1_ARATH RecName: Full=H/ACA ribonucleoprotein complex subunit 4; AltName: Full=Nucleolar protein NAP57 homolog; AltName: Full=Nopp-140-associated protein of 57 kDa homolog; Short=AtNAP57	Unigene34719_All//0.00E+00//AT3G57150| NAP57 (Arabidopsis thaliana homologue of NAP57); pseudouridine synthase	Unigene34719_All//0.00E+00//TC163642				nr -
Unigene34721_All	2631	29.09	18.20	24.17	88.42	94.59	67.55	40.48	16.60	22.38	-6.77E-01	9.25E-29		-2.68E-01	1.46E-05		9.73E-02	2.40E-03		-3.89E-01	3.79E-34		-1.29E+00	1.57E-140	Down	-8.55E-01	1.87E-74		Unigene34721_All//gi|297814432|ref|XP_002875099.1|//0.00E+00//atmap65-6 [Arabidopsis lyrata subsp. lyrata] >gi|297320937|gb|EFH51358.1|atmap65-6 [Arabidopsis lyrata subsp. lyrata]	Unigene34721_All//0.00E+00//AT2G01910| ATMAP65-6; microtubule binding	Unigene34721_All//0.00E+00//TC144771				nr +
Unigene34722_All	2580	3.73	3.02	3.78	16.55	13.56	10.03	7.96	2.01	4.32	-3.03E-01	1.16E-01		1.75E-02	9.47E-01		-2.87E-01	1.86E-04		-7.22E-01	1.44E-19		-1.99E+00	2.55E-51	Down	-8.81E-01	7.57E-16		Unigene34722_All//gi|297814432|ref|XP_002875099.1|//0.00E+00//atmap65-6 [Arabidopsis lyrata subsp. lyrata] >gi|297320937|gb|EFH51358.1|atmap65-6 [Arabidopsis lyrata subsp. lyrata]	Unigene34722_All//0.00E+00//AT2G01910| ATMAP65-6; microtubule binding	Unigene34722_All//0.00E+00//TC144771				nr +
Unigene34724_All	3389	0.56	1.32	1.96	1.68	1.83	3.46	3.18	3.37	3.73	1.24E+00	2.79E-05	Up	1.82E+00	4.68E-12	Up	1.26E-01	6.51E-01		1.05E+00	2.73E-10	Up	8.18E-02	6.29E-01		2.28E-01	1.18E-01		Unigene34724_All//gi|297830454|ref|XP_002883109.1|//3.00E-96//MYB4R1 [Arabidopsis lyrata subsp. lyrata] >gi|297328949|gb|EFH59368.1|MYB4R1 [Arabidopsis lyrata subsp. lyrata]	Unigene34724_All//9.00E-91//AT3G18100| MYB4R1 (myb domain protein 4R1); transcription factor	Unigene34724_All//9.00E-69//TC155353	MYB			nr -
Unigene34726_All	1055	33.13	12.15	15.65	62.09	51.24	67.00	80.55	24.72	34.51	-1.45E+00	1.40E-45	Down	-1.08E+00	4.50E-28	Down	-2.77E-01	4.09E-06		1.10E-01	1.19E-01		-1.70E+00	2.05E-170	Down	-1.22E+00	9.79E-107	Down	Unigene34726_All//gi|76160947|gb|AB404037.1|//1.00E-88//40S ribosomal protein S7-like protein [Solanum tuberosum] >gi|77999315|gb|ABB17004.1|ribosomal protein S7-like protein [Solanum tuberosum] >gi|82623373|gb|ABB87101.1| 40S ribosomal protein S7-like protein-like [Solanum tuberosum]	Unigene34726_All//1.00E-83//AT1G48830| 40S ribosomal protein S7 (RPS7A)	Unigene34726_All//0.00E+00//TC149215		ko03010|Ribosome		nr +
Unigene34728_All	1518	5.27	10.01	11.33	10.53	14.86	13.30	12.56	13.66	19.08	9.25E-01	2.87E-10		1.10E+00	1.45E-14	Up	4.96E-01	3.98E-06		3.36E-01	6.61E-03		1.21E-01	3.47E-01		6.03E-01	1.04E-11		Unigene34728_All//gi|226495213|ref|NP_001151563.1|//1.00E-141//CBS domain containing protein [Zea mays] >gi|195647750|gb|ACG43343.1|CBS domain containing protein [Zea mays]	Unigene34728_All//1.00E-125//AT5G50530| CBS domain-containing protein / octicosapeptide/Phox/Bem1 (PB1) domain-containing protein	Unigene34728_All//0.00E+00//gi|109857770|gb|DW486749.1|DW486749				nr -
Unigene34729_All	753	0.21	0.81	0.28	1.39	1.92	2.22	0.00	0.00	2.65	1.95E+00	6.04E-02		4.41E-01	7.75E-01		4.67E-01	4.44E-01		6.76E-01	2.05E-01		null	null		1.14E+01	2.77E-14	Up	Unigene34729_All//gi|297825869|ref|XP_002880817.1|//8.00E-08//nitrate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326656|gb|EFH57076.1|nitrate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene34729_All//4.00E-09//AT2G26690| nitrate transporter (NTP2)					nr -
Unigene34731_All	2127	4.26	3.14	3.05	9.30	5.10	5.92	5.05	2.20	3.45	-4.37E-01	2.41E-02		-4.79E-01	1.74E-02		-8.67E-01	3.88E-14		-6.50E-01	6.41E-08		-1.20E+00	2.14E-13	Down	-5.51E-01	2.54E-04		Unigene34731_All//gi|15225665|ref|NP_181553.1|//2.00E-72//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75263550|sp|Q9SZ33.1|PP196_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g40240, mitochondrial; Flags: Precursor	Unigene34731_All//2.00E-73//AT2G40240| pentatricopeptide (PPR) repeat-containing protein	Unigene34731_All//0.00E+00//gi|73860160|gb|DT462899.1|DT462899		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene34736_All	1337	127.22	58.21	91.72	23.96	32.86	27.73	4.08	3.06	4.80	-1.13E+00	5.19E-149	Down	-4.72E-01	4.54E-32		4.56E-01	7.06E-10		2.11E-01	2.16E-02		-4.13E-01	7.84E-02		2.34E-01	2.84E-01		Unigene34736_All//gi|297826847|ref|XP_002881306.1|//1.00E-109//ribosomal protein S5 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327145|gb|EFH57565.1|ribosomal protein S5 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34736_All//9.00E-73//AT2G33800| ribosomal protein S5 family protein	Unigene34736_All//0.00E+00//TC140893		ko03010|Ribosome		nr +
Unigene3474_All	1306	0.52	1.24	1.06	1.30	1.66	1.07	4.34	2.40	1.80	1.25E+00	1.82E-02		1.03E+00	8.63E-02		3.57E-01	4.60E-01		-2.75E-01	6.38E-01		-8.54E-01	1.29E-04		-1.27E+00	2.31E-08	Down	Unigene3474_All//gi|79594437|ref|NP_850262.2|//1.00E-112//FACE2 (FARNESYLATED PROTEIN-CONVERTING ENZYME 2); endopeptidase [Arabidopsis thaliana] >gi|398374415|emb|CAD59227.1|farnesylated-proteins converting enzyme-2 [Arabidopsis thaliana]	Unigene3474_All//6.00E-114//AT2G36305| FACE2 (FARNESYLATED PROTEIN-CONVERTING ENZYME 2); endopeptidase	Unigene3474_All//0.00E+00//gi|195983480|gb|FL576454.1|FL576454			GO:0004464	nr +
Unigene34741_All	2165	9.26	7.84	6.32	12.65	13.92	9.87	11.05	3.98	4.29	-2.39E-01	6.29E-02		-5.50E-01	1.45E-05		1.37E-01	2.20E-01		-3.59E-01	4.47E-04		-1.47E+00	1.91E-39	Down	-1.37E+00	2.67E-36	Down	Unigene34741_All//gi|195647788|gb|ACG43362.1|//1.00E-139//pollen-specific kinase partner protein [Zea mays]	Unigene34741_All//1.00E-127//AT3G55660| ROPGEF6; Rho guanyl-nucleotide exchange factor	Unigene34741_All//0.00E+00//TC134539				nr -
Unigene34744_All	2701	6.14	5.29	7.43	13.61	11.27	11.81	17.14	8.46	9.20	-2.15E-01	1.35E-01		2.76E-01	3.83E-02		-2.72E-01	1.28E-03		-2.05E-01	2.66E-02		-1.02E+00	1.60E-42	Down	-8.97E-01	1.34E-35		Unigene34744_All//gi|13605659|gb|AK32823.1|AF361810_1//1.00E-160//AT4g39690/T19P19_80 [Arabidopsis thaliana] >gi|21700889|gb|AAM70568.1|AT4g39690/T19P19_80 [Arabidopsis thaliana]	Unigene34744_All//4.00E-113//AT4G39690| unknown protein	Unigene34744_All//0.00E+00//TC139529		ko03022|Basal transcription factors		nr -
Unigene34745_All	2459	17.72	8.10	11.37	29.94	30.35	34.35	49.86	28.35	34.31	-1.13E+00	8.94E-39	Down	-6.41E-01	1.35E-14		1.94E-02	8.37E-01		1.98E-01	4.92E-04		-8.15E-01	1.02E-76		-5.39E-01	1.94E-38		Unigene34745_All//gi|110737396|dbj|BAF00642.1|//0.00E+00//dihydrolipoamide S-acetyltransferase precursor [Arabidopsis thaliana]	Unigene34745_All//0.00E+00//AT3G52200| LTA3; ATP binding / dihydrolipoyllysine-residue acetyltransferase	Unigene34745_All//0.00E+00//TC137995		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)		nr -

Unigene34746_All	3671	2.49	6.17	3.50	5.66	6.78	7.00	5.13	6.43	7.10	1.31E+00	1.82E-25	Up	4.87E-01	2.99E-03		2.61E-01	1.70E-02		3.07E-01	4.65E-03			3.28E-01	1.24E-03		4.70E-01	4.38E-07		Unigene34746_All//gi|38344202|emb|CAE05767.2|//1.00E-179//OSJNBa0064G10.18 [Oryza sativa (japonica cultivar-group)]	Unigene34746_All//4.00E-177//AT1G11160| nucleotide binding	Unigene34746_All//0.00E+00//DW492604		ko03040|Spliceosome		nr +
Unigene34747_All	667	0.16	5.77	0.48	1.42	0.36	7.18	23.90	57.09	48.86	5.20E+00	4.34E-19	Up	1.61E+00	3.05E-01		-1.97E+00	6.32E-03		2.34E+00	4.76E-13	Up	1.26E+00	7.63E-49	Up	1.03E+00	1.63E-31	Up			Unigene34747_All//5.00E-159//TC159088				
Unigene34748_All	2082	1.18	24.78	7.03	6.82	7.84	38.16	80.76	191.13	215.73	4.39E+00	3.96E-230	Up	2.57E+00	9.25E-40	Up	2.01E-01	1.79E-01		2.48E+00	3.67E-226	Up	1.24E+00	0.00E+00	Up	1.42E+00	0.00E+00	Up	Unigene34748_All//gi|110747150|gb|AB689394.1|//0.00E+00//gibberellic acid receptor [Gossypium hirsutum]	Unigene34748_All//1.00E-161//AT3G63010| GIDIB (GA INSENSITIVE DWARF1B); hydrolase	Unigene34748_All//0.00E+00//TC159088				nr +
Unigene34751_All	1391	2.03	0.80	1.42	16.69	7.43	6.49	6.78	14.33	3.29	-1.34E+00	5.15E-04	Down	-5.20E-01	1.90E-01		-1.17E+00	6.12E-27	Down	-1.36E+00	4.38E-30	Down	1.08E+00	1.41E-20	Up	-1.04E+00	5.92E-10	Down	Unigene34751_All//gi|297835048|ref|XP_002885406.1|//1.00E-130//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331246|gb|EFH61665.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34751_All//2.00E-119//AT1G51170| protein kinase family protein	Unigene34751_All//0.00E+00//gi|48743497|gb|CO074016.1|CO074016				nr +
Unigene34753_All	1660	1.23	1.25	2.60	9.81	3.51	3.92	11.92	33.59	2.47	2.59E-02	9.74E-01		1.08E+00	4.56E-04	Up	-1.48E+00	1.53E-27	Down	-1.32E+00	2.09E-20	Down	1.49E+00	1.59E-92	Up	-2.27E+00	2.78E-60	Down	Unigene34753_All//gi|297835048|ref|XP_002885406.1|//1.00E-135//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331246|gb|EFH61665.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34753_All//6.00E-124//AT3G20830| protein kinase family protein	Unigene34753_All//0.00E+00//TC175904				nr -
Unigene34759_All	942	1.44	2.47	0.28	6.66	10.16	4.70	0.58	0.18	5.08	7.77E-01	6.36E-02		-2.35E+00	7.62E-04	Down	6.09E-01	5.52E-04		-5.04E-01	3.43E-02		-1.72E+00	7.23E-02		3.12E+00	8.45E-21	Up	Unigene34759_All//gi|22408144 9|ref|XP_002306415.1|//6.00E-75//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222855864|gb|EEE93411.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene34759_All//2.00E-66//AT2G43000| anac042 (Arabidopsis NAC domain containing protein 42); transcription factor	Unigene34759_All//0.00E+00//gi|164362553|gb|ES815789.1|ES815789	NAC			nr -
Unigene3476_All	660	6.66	132.66	27.11	13.96	126.31	59.81	14.80	49.77	70.74	4.32E+00	0.00E+00	Up	2.03E+00	2.77E-36	Up	3.18E+00	0.00E+00	Up	2.10E+00	1.20E-91	Up	1.75E+00	1.27E-68	Up	2.26E+00	2.44E-138	Up	Unigene3476_All//gi|15241248|ref|NP_200466.1|//9.00E-20//OXS3 (OXIDATIVE STRESS 3) [Arabidopsis thaliana]	Unigene3476_All//2.00E-19//AT5G66550| OXS3 (OXIDATIVE STRESS 3)	Unigene3476_All//0.00E+00//TC158437			GO:0006950//GO:0010038//GO:0016604	nr -
Unigene34760_All	1097	1.43	2.77	2.23	1.23	1.57	2.51	14.38	14.40	231.33	9.54E-01	8.06E-03		6.42E-01	1.36E-01		3.56E-01	5.38E-01		1.03E+00	6.79E-03		2.60E-03	1.02E+00		4.01E+00	0.00E+00	Up	Unigene34760_All//gi|224094238|ref|XP_002310103.1|//3.00E-76//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222853006|gb|EEE90553.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene34760_All//9.00E-68//AT2G43000| anac042 (Arabidopsis NAC domain containing protein 42); transcription factor	Unigene34760_All//0.00E+00//TC143285	NAC			nr +
Unigene34761_All	1015	9.95	6.09	5.98	13.84	14.49	8.59	0.75	0.37	2.55	-7.08E-01	8.27E-05		-7.34E-01	8.52E-05		6.59E-02	7.37E-01		-6.89E-01	2.27E-06		-1.02E+00	1.69E-01		1.77E+00	2.38E-06	Up	Unigene34761_All//gi|224094238|ref|XP_002310103.1|//1.00E-72//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222853006|gb|EEE90553.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene34761_All//7.00E-62//AT2G43000| anac042 (Arabidopsis NAC domain containing protein 42); transcription factor	Unigene34761_All//0.00E+00//ES836669	NAC			nr +
Unigene34763_All	830	6.05	4.52	5.77	7.08	6.68	9.58	6.21	6.14	14.78	-4.22E-01	1.21E-01		-6.77E-02	8.10E-01		-8.44E-02	7.87E-01		4.35E-01	3.95E-02		-1.66E-02	9.78E-01		1.25E+00	1.45E-16	Up	Unigene34763_All//gi|27261729|gb|AAN86061.1|//1.00E-46//geranylgeranyl diphosphate synthase [Citrus unshiu]	Unigene34763_All//6.00E-42//AT2G34630| geranyl diphosphate synthase, putative / GPPS, putative / dimethylallyltransferase, putative / prenyl transferase, putative	Unigene34763_All//0.00E+00//CO078011		ko00900|Terpenoid backbone biosynthesis		nr +
Unigene34766_All	781	1.54	0.26	0.34	0.06	0.09	0.12	7.80	4.55	13.36	-2.57E+00	5.35E-04	Down	-2.18E+00	3.05E-03		4.67E-01	9.58E-01		8.59E-01	7.94E-01		-7.77E-01	2.71E-04		7.78E-01	5.48E-07		Unigene34766_All//gi|115432146|gb|AB197350.1|//8.00E-67//cold-induced wall associated kinase [Ammopiptanthus mongolicus]	Unigene34766_All//4.00E-61//AT1G16120| WAKL1 (wall associated kinase-like 1); kinase	Unigene34766_All//2.00E-143//DT462732		ko04626|Plant-pathogen interaction		nr +
Unigene34767_All	874	1.68	0.70	2.25	0.17	0.20	0.16	5.51	1.15	9.94	-1.27E+00	2.39E-02		4.28E-01	3.96E-01		2.04E-01	9.50E-01		-1.42E-01	9.43E-01		-2.26E+00	9.92E-15	Down	8.50E-01	8.66E-07		Unigene34767_All//gi|115432146|gb|AB197350.1|//5.00E-93//cold-induced wall associated kinase [Ammopiptanthus mongolicus]	Unigene34767_All//2.00E-79//AT1G16120| WAKL1 (wall associated kinase-like 1); kinase	Unigene34767_All//1.00E-172//DT462732		ko04626|Plant-pathogen interaction		nr -
Unigene34768_All	3028	1.09	0.28	1.53	0.12	0.25	0.15	2.68	2.73	7.43	-1.94E+00	4.11E-07	Down	4.91E-01	9.78E-02		1.12E+00	1.98E-01		3.73E-01	7.32E-01		2.78E-02	9.04E-01		1.47E+00	8.94E-38	Up	Unigene34768_All//gi|68159722|gb|AN86486.1|//1.00E-135//RF01 [Arabidopsis thaliana]	Unigene34768_All//4.00E-129//AT1G16120| WAKL1 (wall associated kinase-like 1); kinase	Unigene34768_All//0.00E+00//DF462732				nr -
Unigene34769_All	2546	2.40	6.47	2.95	4.97	5.78	5.45	8.12	11.97	11.14	1.43E+00	2.60E-21	Up	2.95E-01	2.11E-01		2.17E-01	1.67E-01		1.32E-01	4.74E-01		5.60E-01	1.53E-10		4.56E-01	2.77E-07		Unigene34769_All//gi|18407090|ref|NP_566076.1|//0.00E+00//phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana] >gi|42571253|ref|NP_973700.1| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana] >gi|169304125|gb|AAL31898.1|AF419566_1 At2g46500/F11C10.19 [Arabidopsis thaliana] >gi|4415931|gb|AAD20161.1| expressed protein [Arabidopsis thaliana] >gi|20197828|gb|AAM15268.1| expressed protein [Arabidopsis thaliana] >gi|27363382|gb|AAO11610.1| At2g46500/F11C10.19 [Arabidopsis thaliana]	Unigene34769_All//0.00E+00//AT2G46500| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	Unigene34769_All//0.00E+00//gi|164358378|gb|ES828860.1|ES828860				nr +
Unigene3477_All	1239	2.66	2.74	3.44	20.34	26.29	14.43	3.82	1.86	0.90	4.25E-02	9.11E-01		3.70E-01	2.44E-01		3.70E-01	3.00E-05		-4.95E-01	2.53E-06		-1.04E+00	3.04E-05	Down	-2.09E+00	1.32E-13	Down	Unigene3477_All//gi|115488670|ref|NP_001066822.1|//1.00E-49//Os12g0501400 [Oryza sativa Japonica Group] >gi|77558832|gb|ABA98629.1| universal stress protein family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113649329|dbj|BAF29841.1| Os12g0501400 [Oryza sativa Japonica Group]	Unigene3477_All//2.00E-38//AT1G69080| universal stress protein (USP) family protein	Unigene3477_All//0.00E+00//TC155971			GO:0048764//GO:0050896	nr -
Unigene34775_All	726	2.88	0.42	0.00	3.02	2.94	3.36	3.61	0.86	2.41	-2.78E+00	6.12E-07	Down	-1.15E+01	1.96E-11	Down	-3.79E-02	9.29E-01		1.54E-01	7.19E-01		-2.06E+00	1.66E-07	Down	-5.81E-01	8.46E-02		Unigene34775_All//gi|3913525|sp|O48901.1|DPOD1_SOYBN//1.00E-115//RecName: Full=DNA polymerase delta catalytic subunit >gi|2895198|gb|AAC18443.1| DNA polymerase delta [Glycine max]	Unigene34775_All//4.00E-99//AT5G63960| EMB2780 (EMBRYO DEFECTIVE 2780); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding	Unigene34775_All//2.00E-84//CO083523		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr -
Unigene34776_All	2887	2.43	1.26	1.59	4.71	4.00	3.36	7.21	2.61	3.33	-9.42E-01	2.48E-05		-6.15E-01	7.70E-03		-2.37E-01	1.39E-01		-4.86E-01	1.21E-03		-1.47E+00	3.89E-34	Down	-1.12E+00	2.95E-23	Down	Unigene34776_All//gi|115484523|ref|NP_001067405.1|//0.00E+00//Os11g0186400 [Oryza sativa Japonica Group] >gi|13124219|sp|Q9LRE6.1|DPOD1_ORYSJ RecName: Full=DNA polymerase delta catalytic subunit >gi|91885570|dbj|BAE95573.1| OsPol delta large subunit [Oryza sativa Japonica Group] >gi|62734232|gb|AAX96341.1| dna polymerase delta catalytic subunit (ec 2.7.7.7) [Oryza sativa Japonica Group] >gi|113644627|dbj|BAF27768.1| Os11g0186400 [Oryza sativa Japonica Group]	Unigene34776_All//0.00E+00//AT5G63960| EMB2780 (EMBRYO DEFECTIVE 2780); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding	Unigene34776_All//0.00E+00//gi|48822358|gb|CO123671.1|CO123671		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +
Unigene34777_All	1121	5.37	15.23	7.89	4.67	6.17	6.24	2.64	3.06	1.99	1.50E+00	8.24E-24	Up	5.55E-01	6.07E-03		4.04E-01	7.50E-02		4.21E-01	6.76E-02		2.12E-01	5.31E-01		-4.08E-01	2.03E-01		Unigene34777_All//gi|115455957|ref|NP_001051579.1|//1.00E-115//Os03g0799700 [Oryza sativa Japonica Group] >gi|108711581|gb|ABF99376.1| GTP1/OBG family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550050|dbj|BAF13493.1| Os03g0799700 [Oryza sativa Japonica Group]	Unigene34777_All//1.00E-26//AT5G18570| GTP1/OBG family protein					nr -
Unigene34778_All	1743	6.90	18.40	8.52	5.63	6.54	6.50	5.02	4.20	2.88	1.41E+00	2.79E-40	Up	3.04E-01	5.16E-02		2.16E-01	2.46E-01		2.08E-01	2.79E-01		-2.59E-01	1.67E-01		-8.02E-01	2.56E-06		Unigene34778_All//gi|115455957|ref|NP_001051579.1|//1.00E-108//Os03g0799700 [Oryza sativa Japonica Group] >gi|108711581|gb|ABF99376.1| GTP1/OBG family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550050|dbj|BAF13493.1| Os03g0799700 [Oryza sativa Japonica Group]	Unigene34778_All//2.00E-30//AT5G18570| GTP1/OBG family protein					nr -
Unigene34780_All	1686	2.08	2.04	2.24	0.92	1.70	1.69	2.51	0.97	0.40	-2.49E-02	9.58E-01		1.09E-01	7.36E-01		8.88E-01	1.48E-02		8.82E-01	1.87E-02		-1.38E+00	6.24E-07	Down	-2.64E+00	5.80E-16	Down	Unigene34780_All//gi|90265158|emb|CAH67784.1|//2.00E-63//H0201G08.11 [Oryza sativa (indica cultivar-group)]	Unigene34780_All//9.00E-55//AT2G17975| zinc finger (Ran-binding) family protein	Unigene34780_All//0.00E+00//TC159424				nr +
Unigene34782_All	711	11.11	6.84	6.89	9.60	3.73	1.97	1.13	3.17	7.06	-7.00E-01	6.91E-04		-6.89E-01	1.32E-03		-1.36E+00	2.13E-10	Down	-2.29E+00	2.27E-18	Down	1.49E+00	1.81E-04	Up	2.64E+00	1.63E-18	Up	Unigene34782_All//gi|115468544|ref|NP_001057871.1|//2.00E-14//Os06g0561000 [Oryza sativa Japonica Group] >gi|75112464|sp|Q5Z8T3.1|MI10X_ORYSJ RecName: Full=Probable inositol oxygenase; AltName: Full=Myo-inositol oxygenase; Short=MI oxygenase >gi|113565911|dbj|BAF19785.1| Os06g0561000 [Oryza sativa Japonica Group]	Unigene34782_All//2.00E-14//AT1G14520| MIOX1 (MYO-INISITOL OXYGENASE); inositol oxygenase/ oxidoreductase	Unigene34782_All//3.00E-105//TC136365		ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene34783_All	1380	9.40	8.52	4.51	6.57	2.82	1.96	1.87	4.12	8.98	-1.43E-01	3.97E-01		-1.06E+00	1.96E-10	Down	-1.22E+00	1.56E-11	Down	-1.74E+00	4.11E-17	Down	1.14E+00	5.99E-07	Up	2.26E+00	2.12E-37	Up	Unigene34783_All//gi|192338750|gb|ACF04280.1|//5.00E-76//myo-inositol oxygenase [Eucalyptus grandis]	Unigene34783_All//5.00E-72//AT1G14520| MIOX1 (MYO-INISITOL OXYGENASE); inositol oxygenase/ oxidoreductase	Unigene34783_All//0.00E+00//TC136365		ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene34784_All	1071	58.48	36.19	23.47	28.28	14.98	8.86	4.82	13.35	20.98	-6.92E-01	1.36E-24		-1.32E+00	4.85E-68	Down	-9.16E-01	1.55E-23		-1.68E+00	5.25E-53	Down	1.47E+00	9.96E-24	Up	2.12E+00	4.55E-62	Up	Unigene34784_All//gi|192338750|gb|ACF04280.1|//1.00E-142//myo-inositol oxygenase [Eucalyptus grandis]	Unigene34784_All//2.00E-139//AT1G14520| MIOX1 (MYO-INISITOL OXYGENASE); inositol oxygenase/ oxidoreductase	Unigene34784_All//0.00E+00//TC136365		ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism		nr -

Unigene34787_All	1717	3.14	5.70	4.50	2.23	3.29	1.87	2.12	0.95	1.35	8.60E-01	3.46E-06		5.19E-01	1.81E-02		5.58E-01	2.33E-02		-2.58E-01	4.65E-01		-1.16E+00	7.76E-05	Down	-6.54E-01	1.82E-02		Unigene34787_All//gi|117940084|sp|Q0WVE9.2|PLST1_ARATH//1.00E-150//RecName: Full=Probable plastidic glucose transporter 1 >gi|53828535|gb|AAU94377.1| Atlg05030 [Arabidopsis thaliana] >gi|55733727|gb|AAV59260.1| Atlg05030 [Arabidopsis thaliana]	Unigene34787_All//2.00E-143//AT1G05030| hexose transporter, putative	Unigene34787_All//2.00E-21//FL577065				nr -
Unigene34789_All	808	4.34	7.65	4.22	7.03	7.25	9.84	7.17	17.64	30.27	8.18E-01	6.01E-04		-4.07E-02	9.15E-01		4.38E-02	8.83E-01		4.85E-01	2.00E-02		1.30E+00	9.69E-20	Up	2.08E+00	1.03E-65	Up	Unigene34789_All//gi|18396768|ref|NP_564307.1|//2.00E-92//NSL1 (necrotic spotted lesions 1) [Arabidopsis thaliana] >gi|6560762|gb|AAF16762.1|AC010155 _15 F3M18.18 [Arabidopsis thaliana]	Unigene34789_All//3.00E-93//AT1G28380| NSL1 (necrotic spotted lesions 1)	Unigene34789_All//3.00E-47//DR453833				nr +
Unigene34790_All	1188	2.11	4.61	2.33	2.01	3.13	3.08	5.37	17.20	28.20	1.12E+00	1.73E-05	Up	1.41E-01	7.12E-01		6.37E-01	4.34E-02		6.14E-01	6.18E-02		1.68E+00	1.43E-40	Up	2.39E+00	1.32E-106	Up	Unigene34790_All//gi|18396768|ref|NP_564307.1|//1.00E-118//NSL1 (necrotic spotted lesions 1) [Arabidopsis thaliana] >gi|6560762|gb|AAF16762.1|AC010155 _15 F3M18.18 [Arabidopsis thaliana]	Unigene34790_All//1.00E-112//AT1G28380| NSL1 (necrotic spotted lesions 1)	Unigene34790_All//0.00E+00//DT459750				nr +
Unigene34791_All	1744	0.63	2.12	0.95	1.31	1.92	1.81	3.73	7.05	15.78	1.75E+00	6.09E-07	Up	5.87E-01	2.72E-01		5.44E-01	1.15E-01		4.64E-01	2.14E-01		9.16E-01	4.27E-10		2.08E+00	6.23E-74	Up	Unigene34791_All//gi|18396768|ref|NP_564307.1|//1.00E-142//NSL1 (necrotic spotted lesions 1) [Arabidopsis thaliana] >gi|6560762|gb|AAF16762.1|AC010155 _15 F3M18.18 [Arabidopsis thaliana]	Unigene34791_All//3.00E-132//AT1G28380| NSL1 (necrotic spotted lesions 1)	Unigene34791_All//0.00E+00//DT459750				nr -
Unigene34792_All	2308	0.75	3.32	1.50	1.12	1.84	2.31	3.79	9.40	18.28	2.15E+00	1.47E-17	Up	1.00E+00	3.98E-03		7.10E-01	1.38E-02		1.04E+00	5.61E-05	Up	1.31E+00	5.48E-30	Up	2.27E+00	7.10E-126	Up	Unigene34792_All//gi|92870237|gb|ABE79564.1|//1.00E-175//Membrane attack complex component/perforin/complement C9 [Medicago truncatula]	Unigene34792_All//3.00E-143//AT1G28380| NSL1 (necrotic spotted lesions 1)	Unigene34792_All//0.00E+00//DT459750				nr -
Unigene34793_All	803	3.26	3.91	2.19	4.03	2.36	1.57	2.90	0.78	1.04	2.64E-01	4.67E-01		-5.74E-01	1.61E-01		-7.74E-01	1.79E-02		-1.36E+00	1.04E-04	Down	-1.89E+00	4.26E-06	Down	-1.47E+00	1.01E-04	Down	Unigene34793_All//gi|83853834|gb|ABC47866.1|//3.00E-41//remorin [Glycine max]	Unigene34793_All//3.00E-26//AT1G45207| remorin family protein	Unigene34793_All//0.00E+00//gi|48828998|gb|CO127388.1|CO127388				nr -
Unigene34794_All	2220	6.72	5.89	5.68	11.60	9.09	5.13	4.23	2.11	2.69	-1.90E-01	2.25E-01		-2.41E-01	1.38E-01		-3.52E-01	4.96E-04		-1.18E+00	1.15E-26	Down	-1.00E+00	4.48E-09	Down	-6.51E-01	6.16E-05		Unigene34794_All//gi|83853834|gb|ABC47866.1|//1.00E-148//remorin [Glycine max]	Unigene34794_All//3.00E-118//AT1G45207| remorin family protein	Unigene34794_All//0.00E+00//TC137573				nr +
Unigene34795_All	2305	15.57	68.56	16.96	26.71	29.07	33.23	32.23	54.18	74.77	2.14E+00	0.00E+00	Up	1.23E-01	2.21E-01		1.22E-01	7.60E-02		3.15E-01	4.93E-08		7.49E-01	1.11E-67		1.21E+00	1.46E-211	Up	Unigene34795_All//gi|9294626|dbj|BAB02965.1|//0.00E+00//dem protein [Arabidopsis thaliana]	Unigene34795_All//0.00E+00//AT3G19240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), Vacuolar import and degradation, Vid27-related (InterPro:IPR013863); BEST Arabidopsis thaliana protein match is: dem protein-related / defective embryo and meristems protein-related (TAIR:AT4G33400.1); Has 206 Blast hits to 202 proteins in 88 species: Archae - 0; Bacteria - 0; Metazoa - 11; Fungi - 117; Plants - 38; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink).	Unigene34795_All//0.00E+00//TC134917				nr -
Unigene34796_All	3384	2.16	0.97	2.05	4.28	5.15	4.14	2.46	1.17	3.51	-1.15E+00	2.27E-07	Down	-8.15E-02	7.22E-01		2.65E-01	5.12E-02		-5.02E-02	7.67E-01		-1.07E+00	6.13E-09	Down	5.11E-01	3.45E-04		Unigene34796_All//gi|264664462|sp|C0LGE0.1|Y1765_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g07650; Flags: Precursor >gi|224589982|gb|ACN59225.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene34796_All//0.00E+00//AT1G07650| leucine-rich repeat transmembrane protein kinase, putative	Unigene34796_All//0.00E+00//gi|73862538|gb|DT465277.1|DT465277		ko04626|Plant-pathogen interaction		nr +
Unigene34799_All	359	6.85	3.53	5.04	21.51	21.10	10.69	3.77	1.05	0.67	-9.57E-01	1.83E-02		-4.42E-01	3.09E-01		-2.74E-02	9.07E-01		-1.01E+00	1.11E-06	Down	-1.85E+00	9.22E-04	Down	-2.50E+00	2.46E-05	Down			Unigene34799_All//1.00E-81//gi|73860311|gb|DT463050.1|DT463050				
Unigene3480_All	1578	127.98	73.60	85.44	54.87	48.64	55.12	47.02	23.33	19.52	-7.98E-01	1.85E-99		-5.83E-01	1.54E-55		-1.74E-01	1.38E-03		6.80E-03	9.40E-01		-1.01E+00	6.56E-67	Down	-1.27E+00	7.89E-99	Down	Unigene3480_All//gi|225434133|ref|XP_002277485.1|//1.00E-178//PREDICTED: O-acetylserine(thiol)-lyase [Vitis vinifera]	Unigene3480_All//3.00E-154//AT2G43750| OASB (O-ACETYLSERINE (THIOL) LYASE B); cysteine synthase	Unigene3480_All//0.00E+00//TC156199		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0000097//GO:0006563//GO:0016835//GO:0048037	nr -
Unigene34804_All	2117	3.06	1.36	2.24	6.07	6.73	2.84	1.48	0.79	0.47	-1.17E+00	9.84E-07	Down	-4.53E-01	6.50E-02		1.50E-01	3.92E-01		-1.10E+00	3.48E-12	Down	-9.04E-01	3.97E-03		-1.65E+00	5.47E-07	Down	Unigene34804_All//gi|124359162|gb|ABN05685.1|//8.00E-75//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene34804_All//3.00E-27//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene34804_All//7.00E-155//gi|73860311|gb|DT463050.1|DT463050				nr +
Unigene34805_All	1550	2.67	3.66	4.88	2.31	1.87	1.34	3.46	3.64	1.59	4.57E-01	7.06E-02		8.71E-01	8.01E-05		-3.10E-01	3.70E-01		-7.88E-01	1.47E-02		7.15E-02	7.75E-01		-1.12E+00	1.06E-06	Down	Unigene34805_All//gi|7527730|gb|AAF63179.1|AC010657_15//1.00E-17//T5E21.3 [Arabidopsis thaliana]	Unigene34805_All//5.00E-16//AT1G14530| THB1 (TOM THREE HOMOLOG 1); virion binding	Unigene34805_All//0.00E+00//CO114754				nr -
Unigene34808_All	2732	101.44	106.12	73.93	8.13	11.39	6.83	2.69	2.97	1.20	6.51E-02	4.46E-02		-4.56E-01	6.96E-49		4.87E-01	5.55E-08		-2.52E-01	3.81E-02		1.40E-01	5.16E-01		-1.17E+00	1.93E-09	Down	Unigene34808_All//gi|12030956|gb|AH88068.1|//0.00E+00//photosystem II protein D1 [Phaseolus vulgaris]	Unigene34808_All//0.00E+00//ATCG00020| Encodes chlorophyll binding protein D1, a part of the photosystem II reaction center core	Unigene34808_All//0.00E+00//TC129710		ko00195|Photosynthesis		nr +
Unigene34815_All	1031	4.47	4.47	3.93	4.25	4.48	4.73	3.36	1.54	1.47	2.10E-03	9.94E-01		-1.86E-01	5.61E-01		7.40E-02	8.26E-01		1.54E-01	6.17E-01		-1.13E+00	1.75E-04	Down	-1.20E+00	4.83E-05	Down	Unigene34815_All//gi|15451126|gb|AK96834.1|//1.00E-100//Unknown protein [Arabidopsis thaliana]	Unigene34815_All//1.00E-101//AT1G70480| unknown protein	Unigene34815_All//0.00E+00//gi|109878563|gb|DW507533.1|DW507533				nr -
Unigene34816_All	1921	2.83	1.95	4.13	3.19	3.35	2.84	1.43	0.85	0.66	-5.37E-01	3.65E-02		5.44E-01	1.16E-02		7.17E-02	8.23E-01		-1.65E-01	5.63E-01		-7.54E-01	2.60E-02		-1.11E+00	8.40E-04	Down	Unigene34816_All//gi|15451126|gb|AK96834.1|//5.00E-87//Unknown protein [Arabidopsis thaliana]	Unigene34816_All//2.00E-88//AT1G70480| unknown protein	Unigene34816_All//0.00E+00//gi|109878563|gb|DW507533.1|DW507533				nr -
Unigene34817_All	2481	12.38	19.69	21.76	18.83	23.89	16.15	15.06	19.76	6.57	6.69E-01	3.05E-18		8.14E-01	5.19E-27		3.43E-01	5.77E-08		-2.22E-01	5.02E-03		3.92E-01	6.05E-09		-1.20E+00	6.28E-46	Down	Unigene34817_All//gi|224130824|ref|XP_002328385.1|//0.00E+00//sodium proton exchanger [Populus trichocarpa] >gi|222838100|gb|EEE76465.1| sodium proton exchanger [Populus trichocarpa]	Unigene34817_All//0.00E+00//AT3G05030| NHX2 (SODIUM HYDROGEN EXCHANGER 2); sodium ion transmembrane transporter/ sodium:hydrogen antiporter	Unigene34817_All//0.00E+00//TC154409				nr +
Unigene34818_All	1984	19.09	15.83	14.14	23.15	21.75	25.54	40.75	19.00	20.30	-2.70E-01	2.24E-03		-4.33E-01	1.28E-06		-9.01E-02	3.21E-01		1.42E-01	8.24E-02		-1.10E+00	1.46E-83	Down	-1.01E+00	3.54E-74	Down	Unigene34818_All//gi|15223593|ref|NP_173390.1|//1.00E-148//pfkB-type carbohydrate kinase family protein [Arabidopsis thaliana] >gi|8778428|gb|AAF79436.1|AC025808 _18 F18O14.35 [Arabidopsis thaliana] >gi|9795587|gb|AAF98405.1|AC024609 _6 Unknown protein [Arabidopsis thaliana] >gi|28466957|gb|AAO44087.1| Atlg19600 [Arabidopsis thaliana]	Unigene34818_All//2.00E-149//AT1G19600| pfkB-type carbohydrate kinase family protein	Unigene34818_All//0.00E+00//gi|164247076|gb|EX171906.1|EX171906		ko03050|Proteasome		nr +
Unigene34820_All	2382	22.76	5.40	8.65	31.62	18.59	34.66	77.83	31.23	77.94	-2.07E+00	3.01E-116	Down	-1.40E+00	2.50E-64	Down	-7.66E-01	1.08E-42		1.32E-01	3.12E-02		-1.32E+00	1.73E-253	Down	1.90E-03	9.71E-01		Unigene34820_All//gi|225429228|ref|XP_002263457.1|//0.00E+00//PREDICTED: similar to Heat shock 70 kDa protein, mitochondrial [Vitis vinifera]	Unigene34820_All//0.00E+00//AT5G09590| MTHSC70-2 (MITOCHONDRIAL HSP70 2); ATP binding	Unigene34820_All//0.00E+00//gi|164273409|gb|ES818087.1|ES818087		ko03018|RNA degradation		nr +
Unigene34821_All	1061	6.90	6.83	10.89	11.32	9.54	10.51	11.72	8.43	5.44	-1.57E-02	9.64E-01		6.58E-01	1.41E-04		-2.46E-01	1.55E-01		-1.06E-01	6.15E-01		-4.75E-01	9.05E-04		-1.11E+00	4.60E-14	Down	Unigene34821_All//gi|4586308|dbj|BAA76348.1|//1.00E-101//protoporphyrinogen IX oxidase [Glycine max]	Unigene34821_All//4.00E-95//AT5G14220| HEMG2; electron carrier/ oxidoreductase/ protoporphyrinogen oxidase	Unigene34821_All//0.00E+00//gi|164339659|gb|ES805577.1|ES805577		ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene34823_All	592	10.08	31.75	26.09	8.41	10.59	10.38	1.57	0.92	1.48	1.66E+00	6.25E-30	Up	1.37E+00	2.90E-18	Up	3.31E-01	1.85E-01		3.02E-01	2.46E-01		-7.76E-01	2.35E-01		-8.58E-02	8.95E-01		Unigene34823_All//gi|124365579|gb|ABN08813.1|//2.00E-75//HNH nuclease [Medicago truncatula]	Unigene34823_All//1.00E-74//AT2G23840| HNH endonuclease domain-containing protein	Unigene34823_All//1.00E-128//CO087212				nr -
Unigene34824_All	698	9.00	22.00	16.40	6.07	8.73	8.35	1.09	1.44	2.28	1.29E+00	3.56E-17	Up	8.67E-01	7.24E-07		5.26E-01	2.63E-02		4.60E-01	7.06E-02		3.98E-01	5.45E-01		1.07E+00	1.93E-02		Unigene34824_All//gi|124365579|gb|ABN08813.1|//1.00E-22//HNH nuclease [Medicago truncatula]	Unigene34824_All//1.00E-20//AT2G23840| HNH endonuclease domain-containing protein	Unigene34824_All//0.00E+00//DW496977				nr +
Unigene34826_All	211	0.50	6.72	1.01	1.18	1.31	1.71	0.40	1.58	0.19	3.76E+00	3.98E-06	Up	1.03E+00	5.91E-01		1.45E-01	9.61E-01		5.37E-01	6.94E-01		1.98E+00	1.44E-01		-1.09E+00	6.76E-01								
Unigene34827_All	890	3.12	3.64	4.91	3.08	2.36	2.08	4.18	2.54	1.57	2.26E-01	5.36E-01		6.55E-01	3.07E-02		-3.83E-01	3.22E-01		-5.65E-01	1.48E-01		-7.21E-01	1.10E-02		-1.42E+00	1.10E-06	Down	Unigene34827_All//gi|225468852|ref|XP_002266296.1|//6.00E-06//PREDICTED: hypothetical protein isoform 2 [Vitis vinifera]		Unigene34827_All//3.00E-99//gi|48803105|gb|CO104419.1|CO104419				nr -
Unigene34829_All	1690	9.04	13.16	9.26	17.60	31.05	33.38	43.43	55.92	127.98	5.42E-01	2.96E-06		3.53E-02	8.24E-01		8.19E-01	2.47E-32		9.24E-01	1.67E-38		3.65E-01	1.62E-14		1.56E+00	0.00E+00	Up	Unigene34829_All//gi|18850954|gb|ACD56638.1|//0.00E+00//trehalose synthase-like protein [Gossypioides kirkii]	Unigene34829_All//0.00E+00//AT1G06410| ATTPS7; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase	Unigene34829_All//0.00E+00//gi|164283632|gb|ES821638.1|ES821638		ko00500|Starch and sucrose metabolism		nr -
Unigene34831_All	3557	6.35	2.66	3.70	14.31	11.50	6.97	10.32	3.54	4.46	-1.25E+00	5.22E-24	Down	-7.81E-01	6.95E-11		-3.16E-01	4.30E-06		-1.04E+00	1.33E-42	Down	-1.54E+00	2.79E-64	Down	-1.21E+00	7.09E-46	Down	Unigene34831_All//gi|9280691|gb|AAF86560.1|AC069252_19//0.00E+00//F2E2.13 [Arabidopsis thaliana]	Unigene34831_All//3.00E-175//AT1G22060| LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT1G22900.1); Has 67094 Blast hits to 30189 proteins in 1408 species: Archae - 880; Bacteria - 6261; Metazoa - 35085; Fungi - 5326; Plants - 2622; Viruses - 293; Other Eukaryotes - 16627 (source: NCBI BLink).	Unigene34831_All//0.00E+00//TC174850		ko03440|Homologous recombination//ko03450|Non-homologous end-joining		nr +
Unigene34832_All	1684	46.17	38.27	46.93	24.79	20.39	27.65	30.00	19.31	13.51	-2.71E-01	4.85E-06		2.35E-02	7.36E-01		-2.82E-01	3.01E-04		1.58E-01	6.20E-02		-6.36E-01	4.28E-21		-1.15E+00	4.84E-58	Down	Unigene34832_All//gi|297849846|ref|XP_002892804.1|//1.00E-105//ATWHY1/PTAC1 [Arabidopsis lyrata subsp. lyrata] >gi|297338646|gb|EFH69063.1| ATWHY1/PTAC1 [Arabidopsis lyrata subsp. lyrata]	Unigene34832_All//2.00E-101//AT1G14410| WHY1 (WHIRLY 1); DNA binding / telomeric DNA binding	Unigene34832_All//0.00E+00//TC134876	PBF-2-like			nr +

Unigene34835_All	1345	5.37	14.69	11.72	3.93	4.69	5.14	5.34	11.87	8.59	1.45E+00	4.49E-26	Up	1.13E+00	7.89E-14	Up	2.55E-01	3.21E-01		3.88E-01	9.73E-02		1.15E+00	2.37E-18	Up	6.85E-01	2.68E-06		Unigene34835_All//gi|89540402|gb|AAF82216.1|AC067971_24//1.00E-134//ESTs gb|AI990254, gb|T76141 and gb|AA004864 come from this gene [Arabidopsis thaliana] >gi|27311555|gb|AAO00743.1| expressed protein [Arabidopsis thaliana] >gi|31711836|gb|AAP68274.1| At1g07040 [Arabidopsis thaliana]	Unigene34835_All//6.00E-133//AT1G07040| unknown protein	Unigene34835_All//0.00E+00//TC133005				nr +
Unigene34836_All	3115	5.56	2.51	5.16	8.52	6.43	5.73	3.64	2.08	2.29	-1.15E+00	2.73E-16	Down	-1.07E-01	4.98E-01		-4.06E-01	3.35E-05		-5.74E-01	1.90E-08		-8.07E-01	1.03E-07		-6.68E-01	5.31E-06		Unigene34836_All//gi|238479829|ref|NP_001154629.1|//0.00E+00//alpha-amylase/ catalytic/ cation binding [Arabidopsis thaliana] >gi|283777466|gb|ADB29066.1| branching enzyme 1 [Arabidopsis thaliana]	Unigene34836_All//0.00E+00//AT3G20440| alpha-amylase/ catalytic/ cation binding	Unigene34836_All//0.00E+00//TC146384		ko00500|Starch and sucrose metabolism		nr +
Unigene34838_All	2307	5.22	5.45	6.76	4.84	4.28	3.97	2.69	1.00	1.54	6.24E-02	7.16E-01		3.75E-01	1.21E-02		-1.75E-01	3.59E-01		-2.83E-01	1.20E-01		-1.44E+00	2.01E-10	Down	-8.10E-01	8.31E-05		Unigene34838_All//gi|162462150|ref|NP_001105879.1|//2.00E-92//chloroplast RNA processing1 [Zea mays] >gi|3289002|gb|AAC25599.1| CRP1 [Zea mays]	Unigene34838_All//4.00E-85//AT5G42310| pentatricopeptide (PPR) repeat-containing protein	Unigene34838_All//0.00E+00//TC168283				nr +
Unigene34839_All	2218	2.74	2.97	3.58	5.88	7.50	7.03	6.00	3.00	4.06	1.18E-01	6.10E-01		3.87E-01	7.95E-02		3.50E-01	8.98E-03		2.56E-01	9.11E-02		-1.00E+00	1.59E-12	Down	-5.65E-01	2.42E-05		Unigene34839_All//gi|224146265|ref|XP_002325942.1|//0.00E+00//tubulin folding cofactor [Populus trichocarpa] >gi|222862817|gb|EEF00324.1| tubulin folding cofactor [Populus trichocarpa]	Unigene34839_All//2.00E-176//AT1G71440| PF1 (PF1IFFERLING)	Unigene34839_All//0.00E+00//gi|73860674|gb|DT463413.1|DT463413				nr +
Unigene34484_All	1165	57.67	485.47	230.41	134.86	109.45	89.24	24.61	22.82	11.59	3.07E+00	0.00E+00	Up	2.00E+00	0.00E+00	Up	-3.01E-01	3.10E-16		-5.96E-01	2.80E-50		-1.09E-01	3.08E-01		-1.09E+00	2.15E-30	Down	Unigene34484_All//gi|15228108|ref|NP_178507.1|//5.00E-48//XERICO; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|42570685|ref|NP_973416.1| XERICO; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|11692878|gb|AAG40042.1|AF324691_1 T23O15.13 [Arabidopsis thaliana]	Unigene34484_All//4.00E-35//AT2G04240| XERICO; protein binding / zinc ion binding	Unigene34484_All//0.00E+00//CO120533			GO:0006714//GO:0006970//GO:0009725//GO:0009743//GO:0046914	nr -
Unigene34840_All	620	3.04	5.23	0.34	1.29	1.22	1.60	2.66	6.54	4.05	7.84E-01	2.31E-02		-3.14E+00	1.27E-06	Down	-7.32E-02	9.08E-01		3.18E-01	6.73E-01		1.30E+00	3.60E-06	Up	6.06E-01	8.04E-02		Unigene34840_All//gi|157679144|dbj|BAF80451.1|//2.00E-52//MYB-related transcription factor [Nicotiana tabacum]	Unigene34840_All//7.00E-38//AT5G16600| MYB43 (myb domain protein 43; DNA binding / transcription factor	Unigene34840_All//3.00E-129//gi|73862804|gb|DT465543.1|DT465543	MYB			nr -
Unigene34841_All	1212	11.18	18.60	13.44	4.81	14.97	26.16	4.99	15.93	5.16	7.35E-01	2.85E-10		2.66E-01	7.85E-02		1.64E+00	3.99E-33	Up	2.44E+00	1.23E-88	Up	1.68E+00	2.91E-38	Up	4.89E-02	8.31E-01		Unigene34841_All//gi|157679144|dbj|BAF80451.1|//5.00E-90//MYB-related transcription factor [Nicotiana tabacum]	Unigene34841_All//1.00E-78//AT5G16600| MYB43 (myb domain protein 43; DNA binding / transcription factor	Unigene34841_All//0.00E+00//DW519609	MYB			nr +
Unigene34845_All	1190	16.22	25.42	22.87	17.50	16.64	16.70	15.60	33.40	41.58	6.48E-01	5.46E-11		4.95E-01	3.73E-06		-7.26E-02	6.12E-01		-6.74E-02	6.50E-01		1.10E+00	2.58E-41	Up	1.41E+00	2.27E-77	Up	Unigene34845_All//gi|226531560|ref|NP_001148610.1|//6.00E-55//LOC100282226 [Zea mays] >gi|195620806|gb|ACG32233.1| proline-rich polypeptide 6 isoform 1 [Zea mays]	Unigene34845_All//4.00E-56//AT5G16940| carbon-sulfur lyase	Unigene34845_All//0.00E+00//TC152760				nr +
Unigene34846_All	1823	10.88	34.63	18.52	22.82	22.72	30.47	82.71	78.43	53.87	1.67E+00	2.74E-100	Up	7.68E-01	1.62E-15		-5.90E-03	9.49E-01		4.17E-01	1.04E-09		-7.65E-02	6.68E-02		-6.19E-01	5.28E-60		Unigene34846_All//gi|98960887|gb|AB58927.1|//4.00E-59//At5g24610 [Arabidopsis thaliana]	Unigene34846_All//2.00E-60//AT5G24610| unknown protein	Unigene34846_All//0.00E+00//TC134736				nr -
Unigene34847_All	1875	13.56	40.64	15.79	28.53	38.70	39.38	6.16	10.41	3.91	1.58E+00	5.21E-112	Up	2.20E-01	4.40E-02		4.40E-01	5.40E-15		4.65E-01	2.33E-15		7.58E-01	1.76E-11		-6.55E-01	6.44E-06		Unigene34847_All//gi|111038269|gb|ABR03531.1|//1.00E-164//class II knotted-like homeobox protein [Prunus persica] >gi|215983122|gb|ACJ71731.1| class II knotted-like homeobox transcription factor [Prunus persica]	Unigene34847_All//3.00E-116//AT4G32040| KNAT5 (KNOTTED1-LIKE HOMEOBOX GENE 5); transcription activator/ transcription factor	Unigene34847_All//0.00E+00//TC175385	HB			nr -
Unigene34850_All	1419	2.58	4.11	2.59	4.04	4.37	2.32	3.96	1.77	3.48	6.70E-01	6.44E-03		4.60E-03	9.95E-01		1.14E-01	6.98E-01		-7.97E-01	1.08E-03		-1.17E+00	4.16E-07	Down	-1.87E-01	4.30E-01		Unigene34850_All//gi|224059590|ref|XP_002299922.1|//1.00E-116//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222847180|gb|EEE84727.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene34850_All//3.00E-91//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene34850_All//0.00E+00//TC136749		ko04626|Plant-pathogen interaction		nr -
Unigene34851_All	2258	1.34	1.17	1.04	1.21	1.28	0.62	4.77	2.05	5.82	-2.04E-01	6.01E-01		-3.73E-01	3.41E-01		7.82E-02	8.53E-01		-9.69E-01	1.05E-02		-1.22E+00	9.35E-14	Down	2.86E-01	3.98E-02		Unigene34851_All//gi|224132258|ref|XP_002328224.1|//1.00E-127//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837739|gb|EEE76104.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene34851_All//4.00E-83//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene34851_All//0.00E+00//TC136749		ko04626|Plant-pathogen interaction		nr -
Unigene34852_All	599	34.33	108.36	65.52	43.08	48.58	54.36	33.67	62.10	62.19	1.66E+00	5.18E-102	Up	9.33E-01	9.10E-25		1.73E-01	1.07E-01		3.36E-01	3.26E-04		8.83E-01	3.25E-27		8.85E-01	5.10E-28		Unigene34852_All//gi|59860157|gb|AA309646.1|//5.00E-70//aldehyde dehydrogenase family 7 member A1 [Euphorbia characias]	Unigene34852_All//2.00E-65//AT1G54100| ALDH7B4 (Aldehyde Dehydrogenase 7B4); 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Unigene34852_All//0.00E+00//gi|13354255|gb|BG444603.1|BG444603		ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00350|Tyrosine metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr -
Unigene34853_All	1775	87.55	320.06	136.83	92.86	112.52	132.77	66.81	126.96	90.88	1.87E+00	0.00E+00	Up	6.44E-01	8.07E-80		2.77E-01	2.42E-17		5.16E-01	1.15E-57		9.26E-01	2.70E-174		4.44E-01	2.32E-35		Unigene34853_All//gi|59860157|gb|AA309646.1|//0.00E+00//aldehyde dehydrogenase family 7 member A1 [Euphorbia characias]	Unigene34853_All//0.00E+00//AT1G54100| ALDH7B4 (Aldehyde Dehydrogenase 7B4); 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Unigene34853_All//0.00E+00//TC167315		ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00350|Tyrosine metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr +
Unigene34858_All	1536	8.24	15.97	9.36	4.70	11.01	10.59	8.15	13.96	8.87	9.54E-01	6.89E-17		1.83E-01	2.74E-01		1.23E+00	3.24E-20	Up	1.17E+00	1.23E-16	Up	7.77E-01	4.89E-13		1.23E-01	4.13E-01		Unigene34858_All//gi|15010738|gb|AAK74028.1|//1.00E-86//At2g39570/F12L6.23 [Arabidopsis thaliana] >gi|23308377|gb|AAN18158.1| At2g39570/F12L6.23 [Arabidopsis thaliana]	Unigene34858_All//5.00E-88//AT2G39570| ACT domain-containing protein	Unigene34858_All//0.00E+00//TC135845				nr +
Unigene34859_All	1589	11.23	25.13	14.11	8.34	14.00	14.47	9.31	18.20	7.07	1.16E+00	5.03E-37	Up	3.29E-01	7.09E-03		7.47E-01	6.06E-12		7.95E-01	1.52E-12		9.67E-01	1.05E-24		-3.98E-01	1.73E-03		Unigene34859_All//gi|297823847|ref|XP_002878806.1|//1.00E-149//ACT domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325645|gb|EFH56065.1| ACT domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene34859_All//1.00E-149//AT2G39570| ACT domain-containing protein	Unigene34859_All//0.00E+00//TC135845				nr +
Unigene3486_All	1047	2.45	3.48	2.80	5.99	3.59	3.11	3.96	1.88	1.60	5.09E-01	1.20E-01		1.92E-01	6.26E-01		-7.42E-01	7.07E-04		-9.49E-01	4.29E-05		-1.08E+00	6.74E-05	Down	-1.31E+00	1.31E-06	Down		Unigene3486_All//2.00E-116//TC160879				
Unigene34864_All	1648	19.11	14.88	19.26	21.94	18.95	22.28	14.16	6.54	10.64	-3.61E-01	1.75E-04		1.09E-02	9.36E-01		-2.12E-01	1.79E-02		2.19E-02	8.51E-01		-1.11E+00	3.66E-25	Down	-4.13E-01	2.75E-05		Unigene34864_All//gi|193788742|gb|AGF20470.1|//1.00E-121//At4g12840 [Arabidopsis thaliana]	Unigene34864_All//1.00E-129//AT4G18530| unknown protein	Unigene34864_All//0.00E+00//TC148233				nr -
Unigene34865_All	473	0.66	0.00	1.35	11.90	6.04	3.82	106.37	32.16	106.46	-9.37E+00	3.65E-02		1.03E+00	2.81E-01		-9.78E-01	2.68E-05		-1.64E+00	5.47E-10	Down	-1.73E+00	6.36E-103	Down	1.20E-03	9.85E-01		Unigene34865_All//gi|224057862|ref|XP_002299361.1|//5.00E-45//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene34865_All//1.00E-44//AT5G13320| PBS3 (AVRPPHB SUSCEPTIBLE 3)	Unigene34865_All//5.00E-106//ES825712				nr -
Unigene34867_All	1698	11.37	35.63	21.64	16.75	8.40	8.96	216.48	207.01	143.96	1.65E+00	2.91E-94	Up	9.28E-01	4.70E-23		-9.97E-01	1.97E-25		-9.02E-01	3.86E-19		-6.45E-02	1.10E-02		-5.89E-01	9.36E-133		Unigene34867_All//gi|224057862|ref|XP_002299361.1|//1.00E-178//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene34867_All//4.00E-162//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene34867_All//0.00E+00//TC169017				nr +

Unigene3487_All	1647	85.99	12.74	26.48	39.41	37.93	47.19	13.76	4.11	7.98	-2.76E+00	0.00E+00	Down	-1.70E+00	5.56E-224	Down	-5.53E-02	5.13E-01		2.60E-01	7.26E-06		-1.74E+00	2.09E-47	Down	-7.86E-01	1.94E-14		Unigene3487_All//gi|18394444|ref|NP_564015.1|//3.00E-88//tropomyosin-related [Arabidopsis thaliana] >gi|42571515|ref|NP_973848.1| tropomyosin-related [Arabidopsis thaliana] >gi|51316870|sp|Q8LE98.1|ICR1_ARATH RecName: Full=Interactor of constitutive active ROPs 1 >gi|89000951|gb|ABD59065.1| At1g17140 [Arabidopsis thaliana]	Unigene3487_All//6.00E-74//AT1G78430| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 8 growth stages; BEST Arabidopsis thaliana protein match is: tropomyosin-related (TAIR:AT1G17140.2); Has 36552 Blast hits to 19717 proteins in 1278 species: Archae - 377; Bacteria - 3766; Metazoa - 19812; Fungi - 2701; Plants - 1105; Viruses - 197; Other Eukaryotes - 8594 (source: NCBI BLink).	Unigene3487_All//0.00E+00//TC160514				nr -
Unigene34870_All	3643	0.26	0.71	0.60	0.82	0.76	0.77	1.49	1.42	1.37	1.46E+00	4.25E-04	Up	1.21E+00	8.61E-03		-1.18E-01	7.87E-01		-9.41E-02	8.02E-01		-6.25E-02	8.08E-01		-1.20E-01	6.27E-01		Unigene34870_All//gi|225446426|ref|XP_002276115.1|//0.00E+00//PREDICTED: similar to haloacid dehalogenase-like hydrolase family protein [Vitis vinifera]	Unigene34870_All//0.00E+00//AT5G44240| haloacid dehalogenase-like hydrolase family protein	Unigene34870_All//0.00E+00//TC144036				nr -
Unigene34872_All	2989	3.24	6.59	2.58	11.88	12.11	6.98	6.07	5.38	3.45	1.03E+00	2.20E-15	Up	-3.26E-01	1.03E-01		2.71E-02	8.11E-01		-7.67E-01	3.83E-18		-1.73E-01	1.80E-01		-8.14E-01	2.04E-12		Unigene34872_All//gi|21928151|gb|AAM78103.1|//9.00E-91//AT3g53540/F4P12_240 [Arabidopsis thaliana] >gi|23308447|gb|AAN18193.1| At3g53540/F4P12_240 [Arabidopsis thaliana]	Unigene34872_All//7.00E-131//AT3G53540| unknown protein	Unigene34872_All//0.00E+00//TC160135				nr +
Unigene34873_All	1130	0.00	0.00	0.00	0.00	0.06	0.00	11.86	2.26	4.27	null	null		null	null		5.93E+00	6.09E-01		null	null		-2.39E+00	2.05E-42	Down	-1.48E+00	3.71E-23	Down	Unigene34873_All//gi|159138927|gb|ABW89463.1|//1.00E-175//glutamine synthetase [Gossypium raimondii]	Unigene34873_All//9.00E-169//AT5G37600| ATGSR1; copper ion binding / glutamate-ammonia ligase	Unigene34873_All//0.00E+00//gi|78342884|gb|DT563158.1|DT563158		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene34874_All	1438	28.16	46.37	38.77	231.06	158.22	122.14	153.21	49.99	52.97	7.20E-01	7.65E-28		4.61E-01	1.64E-10		-5.46E-01	1.34E-102		-9.20E-01	1.54E-225		-1.62E+00	0.00E+00	Down	-1.53E+00	0.00E+00	Down	Unigene34874_All//gi|159138921|gb|ABW89460.1|//0.00E+00//glutamine synthetase [Gossypium herbaceum] >gi|159138933|gb|ABW89466.1| glutamine synthetase [Gossypium hirsutum]	Unigene34874_All//0.00E+00//AT5G37600| ATGSR1; copper ion binding / glutamate-ammonia ligase	Unigene34874_All//0.00E+00//TC129771		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene34875_All	788	3.05	6.30	4.19	4.87	8.26	6.36	3.76	3.13	1.87	1.04E+00	1.36E-04	Up	4.56E-01	2.13E-01		7.63E-01	5.31E-04		3.86E-01	1.79E-01		-2.63E-01	4.54E-01		-1.01E+00	1.44E-03		Unigene34875_All//gi|27261731|gb|AAN86062.1|//9.00E-97//sugar transporter [Citrus unshiu]	Unigene34875_All//1.00E-89//AT1G79820| SGB1 (SUPPRESSOR OF G PROTEIN BETA1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene34875_All//0.00E+00//gi|5047194|gb|AI728342.1|AI728342				nr +
Unigene34876_All	455	0.35	0.45	0.47	0.66	2.35	1.29	2.51	0.09	1.05	3.69E-01	8.16E-01		4.40E-01	7.75E-01		1.84E+00	1.02E-02		9.74E-01	3.46E-01		-4.77E+00	5.39E-07	Down	-1.26E+00	2.42E-02		Unigene34876_All//gi|7715596|gb|AAF68114.1|AC010793_9//2.00E-26//F20B17.24 [Arabidopsis thaliana]	Unigene34876_All//1.00E-27//AT1G79820| SGB1 (SUPPRESSOR OF G PROTEIN BETA1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene34876_All//7.00E-65//gi|5047194|gb|AI728342.1|AI728342				nr +
Unigene34877_All	2240	5.47	15.52	9.37	13.34	17.82	16.47	5.53	3.23	3.66	1.51E+00	8.57E-48	Up	7.77E-01	4.40E-10		4.17E-01	9.71E-08		3.04E-01	5.27E-04		-7.77E-01	6.93E-08		-5.94E-01	2.01E-05		Unigene34877_All//gi|30699453|ref|NP_850983.1|//0.00E+00//SGB1 (SUPPRESSOR OF G PROTEIN BETA1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|30699455|ref|NP_178100.3| SGB1 (SUPPRESSOR OF G PROTEIN BETA1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|117940111|sp|Q2V4B9.2|PLST3_ARATH RecName: Full=Probable plastidic glucose transporter 3 >gi|222424748|dbj|BAH20327.1| AT1G79820 [Arabidopsis thaliana]	Unigene34877_All//0.00E+00//AT1G79820| SGB1 (SUPPRESSOR OF G PROTEIN BETA1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene34877_All//0.00E+00//TC168227				nr +
Unigene34879_All	2143	7.37	6.15	8.35	25.01	20.91	16.33	18.70	5.70	11.86	-2.62E-01	7.29E-02		1.79E-01	2.36E-01		-2.59E-01	1.45E-04		-6.15E-01	1.66E-18		-1.72E+00	1.83E-81	Down	-6.57E-01	2.06E-18		Unigene34879_All//gi|125664136|gb|ABN51065.1|//1.00E-109//basic helix-loop-helix protein [Sesamum indicum]	Unigene34879_All//6.00E-72//AT1G10120| DNA binding / transcription factor	Unigene34879_All//0.00E+00//TC171804	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr +
Unigene34883_All	958	10.76	13.75	16.12	6.08	8.23	8.30	18.49	11.82	8.28	3.54E-01	2.50E-02		5.83E-01	7.04E-05		4.36E-01	3.45E-02		4.48E-01	3.34E-02		-6.45E-01	4.01E-08		-1.16E+00	3.55E-21	Down	Unigene34883_All//gi|297823391|ref|XP_002879578.1|//4.00E-70//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297325417|gb|EFH55837.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	Unigene34883_All//4.00E-66//AT2G35820| unknown protein	Unigene34883_All//0.00E+00//TC164733				nr -
Unigene34884_All	3584	0.57	0.68	0.62	2.38	3.83	2.76	4.48	1.61	5.68	2.53E-01	5.56E-01		1.32E-01	7.55E-01		6.90E-01	1.19E-06		2.16E-01	3.02E-01		-1.48E+00	8.06E-27	Down	3.42E-01	1.43E-03		Unigene34884_All//gi|116060285|emb|CAL55621.1|//1.00E-11//Myosin class II heavy chain (ISS) [Ostreococcus tauri]	Unigene34884_All//1.00E-13//AT1G76740| unknown protein	Unigene34884_All//0.00E+00//TC162305		ko03040|Spliceosome		nr -
Unigene34885_All	2381	56.76	95.81	74.94	12.82	15.89	15.16	4.55	4.27	2.21	7.55E-01	9.21E-102		4.01E-01	5.01E-25		3.10E-01	1.79E-04		2.41E-01	8.49E-03		-9.18E-02	6.48E-01		-1.04E+00	2.68E-11	Down	Unigene34885_All//gi|297844608|ref|XP_002890185.1|//0.00E+00//oxidoreductase/ transcriptional repressor [Arabidopsis lyrata subsp. lyrata] >gi|297336027|gb|EFH66444.1| oxidoreductase/ transcriptional repressor [Arabidopsis lyrata subsp. lyrata]	Unigene34885_All//0.00E+00//AT1G16720| HCF173 (high chlorophyll fluorescence phenotype 173); binding / catalytic/ transcription repressor	Unigene34885_All//0.00E+00//TC132945		ko00941|Flavonoid biosynthesis		nr -
Unigene3489_All	1365	11.61	13.59	16.70	11.61	19.60	122.19	14.00	32.36	30.03	2.26E-01	9.51E-02		5.24E-01	9.15E-06		7.56E-01	1.46E-14		3.40E+00	0.00E+00	Up	1.21E+00	2.79E-53	Up	1.10E+00	1.03E-43	Up	Unigene3489_All//gi|15238973|ref|NP_196677.1|//1.00E-83//APT5 (Adenine phosphoribosyltransferase 5); adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|8953378|emb|CAB96651.1| adenine phosphoribosyltransferase-like protein [Arabidopsis thaliana]	Unigene3489_All//5.00E-85//AT5G11160| APT5 (Adenine phosphoribosyltransferase 5); adenine phosphoribosyltransferase	Unigene3489_All//0.00E+00//TC151392		ko00230|Purine metabolism	GO:0015103//GO:0016020//GO:0016763//GO:0043096//GO:0044444	nr -
Unigene34890_All	850	5.48	3.22	2.88	3.34	0.97	3.88	15.92	114.82	13.26	-7.67E-01	5.96E-03		-9.27E-01	1.53E-03		-1.78E+00	1.27E-06	Down	2.16E-01	5.99E-01		2.85E+00	0.00E+00	Up	-2.63E-01	5.67E-02		Unigene34890_All//gi|90856223|gb|ABE01402.1|//1.00E-28//ATP-sulfurylase [Camellia sinensis]	Unigene34890_All//1.00E-26//AT3G22890| APS1 (ATP SULFURYLASE 1); sulfate adenylyltransferase (ATP)	Unigene34890_All//0.00E+00//TC142059		ko00230|Purine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr +
Unigene34891_All	1968	42.78	13.26	14.91	20.83	11.64	52.74	38.84	281.70	44.25	-1.69E+00	1.63E-136	Down	-1.52E+00	1.99E-113	Down	-8.40E-01	2.17E-27		1.34E+00	7.76E-128	Up	2.86E+00	0.00E+00	Up	1.88E-01	1.46E-04		Unigene34891_All//gi|90856223|gb|ABE01402.1|//0.00E+00//ATP-sulfurylase [Camellia sinensis]	Unigene34891_All//0.00E+00//AT3G22890| APS1 (ATP SULFURYLASE 1); sulfate adenylyltransferase (ATP)	Unigene34891_All//0.00E+00//TC147953		ko00230|Purine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr +
Unigene34893_All	1624	2.26	5.77	2.26	11.29	27.48	13.63	30.67	28.08	61.77	1.36E+00	1.43E-11	Up	4.70E-03	9.95E-01		1.28E+00	8.96E-57	Up	2.72E-01	2.44E-02		-1.27E-01	8.53E-02		1.01E+00	5.77E-92	Up	Unigene34893_All//gi|110737096|dbj|BAF00500.1|//1.00E-100//thaumatin-like protein [Arabidopsis thaliana]	Unigene34893_All//4.00E-101//AT4G38660| thaumatin, putative	Unigene34893_All//0.00E+00//TC179458				nr +
Unigene34895_All	1048	8.09	7.06	7.16	2.61	0.89	1.03	2.82	5.98	0.84	-1.96E-01	3.75E-01		-1.75E-01	4.27E-01		-1.56E+00	2.16E-05	Down	-1.34E+00	5.07E-04	Down	1.08E+00	4.81E-07	Up	-1.76E+00	3.55E-07	Down	Unigene34895_All//gi|75154955|sp|Q8LBB7.1|LOG5_ARATH//9.00E-90//RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG5; AltName: Full=Protein LONELY GUY 5 >gi|21592909|gb|AAM64859.1| lysine decarboxylase-like protein [Arabidopsis thaliana] >gi|111074284|gb|ABH04515.1| At4g35190 [Arabidopsis thaliana]	Unigene34895_All//1.00E-81//AT4G35190| unknown protein	Unigene34895_All//0.00E+00//gi|109890771|gb|DW519735.1|DW519735				nr +
Unigene34896_All	855	2.45	2.31	3.11	6.18	2.54	3.12	1.73	1.61	1.30	-8.28E-02	8.46E-01		3.47E-01	3.83E-01		-1.28E+00	1.78E-07	Down	-9.87E-01	1.21E-04		-1.02E-01	8.39E-01		-4.08E-01	3.98E-01			Unigene34896_All//1.00E-04//AT3G20230| 50S ribosomal protein L18 family	Unigene34896_All//2.00E-20//TC156827				
Unigene349_All	3013	1.82	3.82	3.73	5.94	3.74	3.55	9.44	10.51	5.95	1.07E+00	7.57E-10	Up	1.03E+00	8.40E-09	Up	-6.67E-01	2.60E-08		-7.41E-01	6.54E-09		1.55E-01	9.86E-02		-6.67E-01	1.19E-13		Unigene349_All//gi|30689808|ref|NP_850422.1|//2.00E-55//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|20147226|gb|AAM10328.1| At2g44720/F16B22.21 [Arabidopsis thaliana] >gi|23308467|gb|AAN18203.1| At2g44720/F16B22.21 [Arabidopsis thaliana]	Unigene349_All//1.00E-25//AT2G44710| RNA recognition motif (RRM)-containing protein	Unigene349_All//0.00E+00//gi|73848829|gb|DT457849.1|DT457849		ko03040|Spliceosome		nr -
Unigene34900_All	2498	27.00	12.72	23.70	28.22	28.81	13.31	163.15	65.84	42.88	-1.09E+00	5.88E-56	Down	-1.88E-01	6.26E-03		3.00E-02	7.28E-01		-1.08E+00	3.82E-63	Down	-1.31E+00	0.00E+00	Down	-1.93E+00	0.00E+00	Down	Unigene34900_All//gi|224066913|ref|XP_002302276.1|//0.00E+00//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222844002|gb|EEE81549.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene34900_All//0.00E+00//AT1G77990| AST56; sulfate transmembrane transporter	Unigene34900_All//0.00E+00//TC150451				nr +
Unigene34901_All	2365	0.93	1.89	1.91	2.44	3.22	2.71	7.63	7.79	5.46	1.02E+00	4.41E-04	Up	1.04E+00	4.87E-04	Up	3.97E-01	6.36E-02		1.50E-01	6.06E-01		2.99E-02	8.29E-01		-4.84E-01	1.90E-05		Unigene34901_All//gi|226498198|ref|NP_001151569.1|//1.00E-50//ATP binding protein [Zea mays] >gi|195647818|gb|ACG43377.1| ATP binding protein [Zea mays]	Unigene34901_All//6.00E-43//AT4G38470| protein kinase family protein	Unigene34901_All//0.00E+00//TC176884				nr +
Unigene34902_All	1114	2.77	1.05	0.86	18.20	13.57	7.38	7.21	2.40	1.97	-1.41E+00	1.45E-04	Down	-1.69E+00	2.20E-05	Down	-4.24E-01	2.05E-04		-1.30E+00	1.25E-24	Down	-1.59E+00	3.16E-15	Down	-1.87E+00	1.17E-19	Down	Unigene34902_All//gi|145700967|gb|ABR04325.2|//1.00E-107//ROP-like protein [Medicago truncatula]	Unigene34902_All//2.00E-98//AT4G28950| ROP9 (RHO-RELATED PROTEIN FROM PLANTS 9); GTP binding	Unigene34902_All//0.00E+00//TC142677		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene34903_All	905	6.76	3.19	3.00	12.33	11.00	8.38	9.95	2.72	3.74	-1.08E+00	8.95E-06	Down	-1.17E+00	4.23E-06	Down	-1.65E-01	3.95E-01		-5.56E-01	8.66E-04		-1.87E+00	3.70E-21	Down	-1.41E+00	7.07E-15	Down	Unigene34903_All//gi|145700967|gb|ABR04325.2|//1.00E-104//ROP-like protein [Medicago truncatula]	Unigene34903_All//6.00E-89//AT4G28950| ROP9 (RHO-RELATED PROTEIN FROM PLANTS 9); GTP binding	Unigene34903_All//0.00E+00//gi|164259518|gb|ES824870.1|ES824870		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene34905_All	2433	2.09	61.92	2.08	3.60	10.90	12.31	12.03	33.38	316.84	4.89E+00	0.00E+00	Up	-4.70E-03	1.00E+00		1.60E+00	1.38E-46	Up	1.77E+00	1.20E-55	Up	1.47E+00	1.40E-131	Up	4.72E+00	0.00E+00	Up	Unigene34905_All//gi|224126261|ref|XP_002319796.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222858172|gb|EEE95719.1| GRAS family transcription factor [Populus trichocarpa]	Unigene34905_All//9.00E-138//AT1G50600| SCL5; transcription factor	Unigene34905_All//0.00E+00//TC144692	GRAS			nr +

Unigene34911_All	2906	2.50	2.69	1.81	8.79	7.13	6.31	7.06	1.78	3.92	1.02E-01	6.34E-01		-4.64E-01	4.37E-02		-3.02E-01	3.61E-03		-4.79E-01	4.58E-06		-1.98E+00	4.08E-51	Down	-8.48E-01	7.30E-15		Unigene34911_All//gi|30689779|ref|NP_174032.2|//0.00E+00//galactosyltransferase family protein [Arabidopsis thaliana] >gi|221271942|sp|Q8GXG6.2|BGLTH_ARATH RecName: Full=Probable beta-L,3-galactosyltransferase 17	Unigene34911_All//0.00E+00//AT1G27120| galactosyltransferase family protein	Unigene34911_All//0.00E+00//gi|78325610|gb|DT545884.1|DT545884				nr -
Unigene34913_All	2757	7.42	2.83	4.60	21.54	15.68	20.26	22.85	15.37	12.92	-1.39E+00	1.98E-25	Down	-6.91E-01	3.88E-08		-4.58E-01	1.39E-13		-8.79E-02	2.84E-01		-5.72E-01	9.90E-22		-8.23E-01	1.22E-41		Unigene34913_All//gi|30689895|ref|NP_850429.1|//1.00E-138//EMB2766 (EMBRYO DEFECTIVE 2766); structural constituent of nuclear pore [Arabidopsis thaliana]	Unigene34913_All//6.00E-58//AT2G45000| EMB2766 (EMBRYO DEFECTIVE 2766); structural constituent of nuclear pore	Unigene34913_All//0.00E+00//TC173177		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene34914_All	1619	0.55	0.22	0.26	2.25	1.77	1.17	4.18	1.32	1.33	-1.33E+00	7.96E-02		-1.06E+00	1.76E-01		-3.47E-01	3.10E-01		-9.39E-01	3.27E-03		-1.67E+00	7.90E-14	Down	-1.65E+00	3.83E-14	Down	Unigene34914_All//gi|30689895|ref|NP_850429.1|//1.00E-144//EMB2766 (EMBRYO DEFECTIVE 2766); structural constituent of nuclear pore [Arabidopsis thaliana]	Unigene34914_All//2.00E-91//AT2G45000| EMB2766 (EMBRYO DEFECTIVE 2766); structural constituent of nuclear pore	Unigene34914_All//0.00E+00//TC173177		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03018|RNA degradation//ko03020|RNA polymerase		nr -
Unigene34915_All	2752	0.17	0.15	0.02	0.52	0.45	0.51	0.63	0.20	0.35	-2.16E-01	8.17E-01		-3.15E+00	4.00E-02		-2.21E-01	7.05E-01		-4.52E-02	9.45E-01		-1.67E+00	3.96E-04	Down	-8.59E-01	4.40E-02		Unigene34915_All//gi|30689895|ref|NP_850429.1|//1.00E-172//EMB2766 (EMBRYO DEFECTIVE 2766); structural constituent of nuclear pore [Arabidopsis thaliana]	Unigene34915_All//2.00E-92//AT2G45000| EMB2766 (EMBRYO DEFECTIVE 2766); structural constituent of nuclear pore	Unigene34915_All//0.00E+00//TC173177		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene34916_All	2986	0.54	0.80	1.25	10.33	5.93	4.37	53.82	28.76	28.75	5.54E-01	1.84E-01		1.20E+00	3.85E-04	Up	-8.01E-01	4.45E-19		-1.24E+00	1.75E-34	Down	-9.04E-01	1.24E-119		-9.05E-01	4.64E-123		Unigene34916_All//gi|224102205|ref|XP_002312589.1|//0.00E+00//pho1-like protein [Populus trichocarpa] >gi|222852409|gb|EEE89956.1| pho1-like protein [Populus trichocarpa]	Unigene34916_All//0.00E+00//AT3G23430| PHO1 (phosphate 1)	Unigene34916_All//0.00E+00//TC1530076				nr +
Unigene34917_All	2630	5.11	47.59	31.42	10.15	28.90	41.47	27.14	34.33	25.13	3.22E+00	0.00E+00	Up	2.62E+00	4.71E-228	Up	1.51E+00	4.20E-123	Up	2.03E+00	2.39E-242	Up	3.39E-01	3.01E-12		-1.11E-01	5.81E-02		Unigene34917_All//gi|297808737|ref|XP_002872252.1|//0.00E+00//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318089|gb|EFH48511.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34917_All//0.00E+00//AT5G27920| F-box family protein	Unigene34917_All//0.00E+00//TC171795		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene3492_All	1447	1.77	4.27	1.84	2.07	2.67	3.00	15.66	18.72	12.20	1.27E+00	3.25E-07	Up	5.46E-02	8.95E-01		3.68E-01	2.77E-01		5.37E-01	7.34E-02		2.57E-01	7.34E-03		-3.61E-01	3.28E-04		Unigene3492_All//gi|224127272|ref|XP_002320031.1|//1.00E-153//f-box family protein [Populus trichocarpa] >gi|222860804|gb|EEE98346.1| f-box family protein [Populus trichocarpa]	Unigene3492_All//3.00E-107//AT5G43190| F-box family protein (FBX6)	Unigene3492_All//0.00E+00//TC160297				nr +
Unigene34920_All	2689	51.27	190.56	66.85	23.84	29.07	29.83	18.32	17.00	19.33	1.89E+00	0.00E+00	Up	3.83E-01	3.49E-23		2.86E-01	1.68E-07		3.23E-01	9.19E-09		-1.07E-01	1.60E-01		7.79E-02	2.98E-01		Unigene34920_All//gi|53828515|gb|AY94367.1|//1.00E-117//At1g65020 [Arabidopsis thaliana] >gi|55167914|gb|AAV43789.1| At1g65020 [Arabidopsis thaliana]	Unigene34920_All//1.00E-108//AT1G65020| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum, plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: NERD (InterPro:IPR011528); Has 53 Blast hits to 53 proteins in 19 species: Archae - 0; Bacteria - 18; Metazoa - 9; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	Unigene34920_All//0.00E+00//TC148608		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene34921_All	572	18.48	19.13	28.39	54.52	83.92	78.33	110.36	35.51	72.29	5.04E-02	7.80E-01		6.20E-01	1.36E-05		6.22E-01	1.72E-18		5.23E-01	1.08E-11		-1.64E+00	1.43E-119	Down	-6.10E-01	4.57E-25		Unigene34921_All//gi|224066625|ref|XP_002302169.1|//1.00E-102//cellulose synthase [Populus trichocarpa] >gi|222843895|gb|EEE81442.1| cellulose synthase [Populus trichocarpa]	Unigene34921_All//4.00E-95//AT4G39350| CESA2 (CELLULOSE SYNTHASE A2); cellulose synthase/ transferase, transferring glycosyl groups	Unigene34921_All//0.00E+00//TC161742				nr -
Unigene34922_All	395	50.86	50.67	60.13	116.15	168.95	166.48	171.15	51.11	99.55	-5.50E-03	9.86E-01		2.41E-01	4.81E-02		5.41E-01	5.80E-20		5.19E-01	1.09E-16		-1.74E+00	4.04E-140	Down	-7.82E-01	6.13E-41		Unigene34922_All//gi|47078494|gb|AAT09895.1|//4.00E-69//cellulose synthase [Populus tremula x Populus tremuloides]	Unigene34922_All//9.00E-63//AT5G64740| CESA6 (CELLULOSE SYNTHASE 6); cellulose synthase/ transferase, transferring glycosyl groups	Unigene34922_All//0.00E+00//TC146137				nr -
Unigene34923_All	1479	9.55	4.39	6.23	30.28	31.18	22.66	135.33	41.34	60.28	-1.12E+00	5.92E-13	Down	-6.17E-01	6.43E-05		4.21E-02	6.81E-01		-4.18E-01	5.00E-08		-1.71E+00	0.00E+00	Down	-1.17E+00	2.05E-232	Down	Unigene34923_All//gi|224066625|ref|XP_002302169.1|//1.00E-157//cellulose synthase [Populus trichocarpa] >gi|222843895|gb|EEE81442.1| cellulose synthase [Populus trichocarpa]	Unigene34923_All//5.00E-135//AT4G39350| CESA2 (CELLULOSE SYNTHASE A2); cellulose synthase/ transferase, transferring glycosyl groups	Unigene34923_All//0.00E+00//TC170744				nr +
Unigene34924_All	1560	50.21	42.35	53.97	23.57	37.88	49.39	65.70	22.77	48.42	-2.45E-01	3.44E-05		1.04E-01	1.11E-01		6.85E-01	9.20E-27		1.07E+00	1.90E-66	Up	-1.53E+00	1.38E-175	Down	-4.40E-01	1.49E-22		Unigene34924_All//gi|8778991|gb|AAF79906.1|AC022472.15//4.00E-11//Contains similarity to nuclear protein ZAP from Mus musculus gb|AB033168. ESTs gb|AV521697, gb|AV440130 come from this gene [Arabidopsis thaliana]		Unigene34924_All//0.00E+00//TC155603				nr +
Unigene34926_All	1816	13.71	14.23	14.78	15.17	13.20	10.42	8.45	5.22	3.80	5.33E-02	6.49E-01		1.08E-01	4.02E-01		-2.01E-01	5.96E-02		-5.42E-01	6.03E-08		-6.94E-01	5.17E-08		-1.16E+00	2.42E-18	Down	Unigene34926_All//gi|297793045|ref|XP_002864407.1|//0.00E+00//beta-amylase 6 [Arabidopsis lyrata subsp. lyrata] >gi|297310242|gb|EFH40666.1| beta-amylase 6 [Arabidopsis lyrata subsp. lyrata]	Unigene34926_All//0.00E+00//AT5G55700| BAM4 (BETA-AMYLASE 4); beta-amylase/ catalytic/ cation binding	Unigene34926_All//0.00E+00//TC149391		ko00500|Starch and sucrose metabolism		nr +
Unigene34929_All	2174	7.58	28.76	7.62	8.59	4.66	14.79	9.34	24.65	23.97	1.92E+00	1.46E-120	Up	6.90E-03	9.87E-01		-8.84E-01	7.99E-14		7.84E-01	6.59E-17		1.40E+00	9.18E-81	Up	1.36E+00	8.27E-77	Up	Unigene34929_All//gi|30684565|ref|NP_851036.1|//0.00E+00//ZIFL1 (ZINC INDUCED FACILITATOR-like 1); tetracycline:hydrogen antiporter [Arabidopsis thaliana] >gi|14517414|gb|AAK62597.1| AT5g13750/MXE10_2 [Arabidopsis thaliana] >gi|17065582|gb|AAL32945.1| transporter-like protein [Arabidopsis thaliana] >gi|20857393|gb|AAM26717.1| AT5g13750/MXE10_2 [Arabidopsis thaliana]	Unigene34929_All//4.00E-179//AT5G13750| ZIFL1 (ZINC INDUCED FACILITATOR-like 1); tetracycline:hydrogen antiporter	Unigene34929_All//0.00E+00//TC138433				nr +
Unigene3493_All	1311	8.94	2.98	16.25	19.00	15.05	46.95	4.39	58.57	23.34	-1.59E+00	5.99E-18	Down	8.62E-01	4.37E-12		-3.36E-01	1.19E-03		1.31E+00	5.65E-73	Up	3.74E+00	0.00E+00	Up	2.41E+00	2.29E-98	Up	Unigene3493_All//gi|15235124|ref|NP_192787.1|//1.00E-125//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|4115913|gb|AAD03424.1| contains similarity to Iron/Ascorbate family of oxidoreductases (Pfam: PF00671, Score=307.1, E=2.2e-88, N=1) [Arabidopsis thaliana]	Unigene3493_All//1.00E-122//AT4G10090| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene3493_All//0.00E+00//TC131771		ko00941|Flavonoid biosynthesis		nr -
Unigene34930_All	2528	4.74	2.75	2.40	7.00	6.57	4.82	10.40	5.22	4.18	-7.88E-01	1.67E-06		-9.81E-01	1.26E-08		-9.15E-02	5.73E-01		-5.36E-01	2.88E-05		-9.94E-01	1.41E-23		-1.32E+00	1.18E-37	Down	Unigene34930_All//gi|9755453|gb|AAF98214.1|AC007152.10//9.00E-36//Hypothetical protein [Arabidopsis thaliana]	Unigene34930_All//2.00E-33//AT1G67040| unknown protein	Unigene34930_All//0.00E+00//ES817872				nr -
Unigene34933_All	609	5.67	11.90	10.58	12.68	11.93	10.98	6.53	3.98	13.87	1.07E+00	1.58E-06	Up	9.00E-01	2.03E-04		-8.77E-02	7.37E-01		-2.08E-01	3.96E-01		-7.13E-01	8.92E-03		1.09E+00	1.57E-09	Up	Unigene34933_All//gi|224072707|ref|XP_002303842.1|//2.00E-09//predicted protein [Populus trichocarpa] >gi|222841274|gb|EEE78821.1| predicted protein [Populus trichocarpa]	Unigene34933_All//7.00E-06//AT2G32070| CCR4-NOT transcription complex protein, putative	Unigene34933_All//0.00E+00//TC133818		ko03018|RNA degradation		nr -
Unigene34934_All	1414	16.21	35.30	18.04	21.35	24.11	21.88	45.99	42.42	78.10	1.12E+00	1.12E-43	Up	1.55E-01	2.15E-01		1.75E-01	7.13E-02		3.54E-02	7.61E-01		-1.17E-01	6.89E-02		7.64E-01	2.11E-63		Unigene34934_All|75337365|sp|Q9SKZ2.2|CAF1G_ARATH//1.00E-121//RecName: Full=Probable CCR4-associated factor 1 homolog 7	Unigene34934_All//6.00E-123//AT2G32070| CCR4-NOT transcription complex protein, putative	Unigene34934_All//0.00E+00//TC139546		ko03018|RNA degradation		nr +
Unigene34939_All	3684	0.27	0.99	0.61	0.54	0.91	0.56	0.94	1.02	0.96	1.88E+00	1.89E-07	Up	1.17E+00	1.00E-02		7.45E-01	2.55E-02		6.01E-02	9.18E-01		1.18E-01	7.06E-01		3.23E-02	9.35E-01		Unigene34939_All//gi|186517170|ref|NP_195462.3|//0.00E+00//SRFR1 (SUPPRESSOR OF RPS4-RLD 1); protein complex scaffold [Arabidopsis thaliana]	Unigene34939_All//0.00E+00//AT4G37460| SRFR1 (SUPPRESSOR OF RPS4-RLD 1); protein complex scaffold	Unigene34939_All//0.00E+00//TC158463				nr +
Unigene3494_All	1106	81.41	47.33	66.30	49.23	55.73	23.81	14.07	5.97	3.21	-7.83E-01	3.03E-43		-2.96E-01	1.28E-07		1.79E-01	7.52E-03		-1.05E+00	2.93E-46	Down	-1.24E+00	5.58E-20	Down	-2.13E+00	4.37E-44	Down	Unigene3494_All//gi|292653563|gb|AB534298.1|//1.00E-101//aquaporin SIP1;7 [Gossypium hirsutum]	Unigene3494_All//3.00E-44//AT3G04090| SIP1A (SMALL AND BASIC INTRINSIC PROTEIN 1A); water channel	Unigene3494_All//0.00E+00//TC142226			GO:0044464	nr +
Unigene34940_All	1651	7.76	25.47	9.64	15.99	15.02	15.40	8.25	9.06	10.62	1.71E+00	1.88E-69	Up	3.13E-01	3.73E-02		-9.07E-02	4.86E-01		-5.43E-02	6.92E-01		1.36E-01	3.73E-01		3.65E-01	1.69E-03		Unigene34940_All//gi|225441497|ref|XP_002280258.1|//1.00E-147//PREDICTED: SINA2p isoform 2 [Vitis vinifera] >gi|225441499|ref|XP_002280243.1| PREDICTED: SINA2p isoform 1 [Vitis vinifera] >gi|4584257|emb|CAB40578.1| SINA2p [Vitis vinifera]	Unigene34940_All//2.00E-148//AT3G58040| SINA12 (SEVEN IN ABSENTIA OF ARABIDOPSIS 2); protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene34940_All//0.00E+00//DW508584		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene34941_All	1479	10.40	10.11	6.77	17.11	16.58	13.80	14.58	11.02	6.90	-4.14E-02	7.86E-01		-6.20E-01	2.51E-05		-4.56E-02	7.58E-01		-3.10E-01	4.44E-03		-4.04E-01	1.31E-04		-1.08E+00	6.74E-23	Down	Unigene34941_All//gi|16648923|gb|AAL24313.1|//5.00E-09//Unknown protein [Arabidopsis thaliana]		Unigene34941_All//0.00E+00//TC158263				nr -

Unigene34946_All	1530	52.53	25.83	32.23	83.74	79.63	103.93	128.03	68.10	65.15	-1.02E+00	1.68E-60	Down	-7.05E-01	3.66E-31		-7.26E-02	1.58E-01		3.12E-01	1.10E-15		-9.11E-01	1.58E-147		-9.75E-01	9.75E-170		Unigene34946_All//gi|15228692|ref|NP_191771.1|//0.00E+00//tRNA synthetase class II (G, H, P and S) family protein [Arabidopsis thaliana] >gi|30695549|ref|NP_850736.1| tRNA synthetase class II (G, H, P and S) family protein [Arabidopsis thaliana] >gi|6899922|emb|CAB71872.1| multifunctional aminoacyl-tRNA ligase-like protein [Arabidopsis thaliana] >gi|16648885|gb|AAL24294.1| multifunctional aminoacyl-tRNA ligase-like protein [Arabidopsis thaliana] >gi|22136084|gb|AAM91120.1| multifunctional aminoacyl-tRNA ligase-like protein [Arabidopsis thaliana]	Unigene34946_All//0.00E+00//AT3G62120| tRNA synthetase class II (G, H, P and S) family protein	Unigene34946_All//0.00E+00//TC155297		ko00970|Aminoacyl-tRNA biosynthesis		nr +
Unigene34948_All	2948	12.90	5.10	7.59	41.53	30.25	30.46	37.02	17.96	24.65	-1.34E+00	4.76E-44	Down	-7.66E-01	2.56E-17		-4.57E-01	1.94E-27		-4.48E-01	1.48E-23		-1.04E+00	3.31E-103	Down	-5.87E-01	8.23E-40		Unigene34948_All//gi|75337688|sp|Q9SUQ3.1|Y4374_ARATH//0.00E+00//RecName: Full=Probable inactive receptor kinase At4g23740; Flags: Precursor >gi|224589628|gb|ACN59347.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene34948_All//0.00E+00//AT4G23740| leucine-rich repeat transmembrane protein kinase, putative	Unigene34948_All//0.00E+00//gi|78322774|gb|DT543048.1|DT543048		ko04626|Plant-pathogen interaction		nr +
Unigene34949_All	228	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.20	5.77	null	null		null	null		null	null		null	null		1.11E+01	1.02E-03		1.25E+01	1.73E-09	Up	Unigene34949_All//gi|18423233|ref|NP_568750.1|//1.00E-26//ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding [Arabidopsis thaliana] >gi|1169544|sp|P42762.1|ERD1_ARATH RecName: Full=ERD1 protein, chloroplastic; Flags: Precursor >gi|497629|dbj|BAA04506.1| ERD1 protein [Arabidopsis thaliana] >gi|10177198|dbj|BAB10330.1| Erd1 protein precursor [Arabidopsis thaliana]	Unigene34949_All//4.00E-28//AT5G51070| ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding					nr +
Unigene34950_All	3022	0.97	14.72	2.01	1.57	1.69	5.14	2.63	9.34	36.54	3.92E+00	1.76E-183	Up	1.05E+00	3.27E-05	Up	1.07E-01	7.60E-01		1.72E+00	8.33E-28	Up	1.83E+00	1.23E-62	Up	3.80E+00	0.00E+00	Up	Unigene34950_All//gi|18423233|ref|NP_568750.1|//0.00E+00//ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding [Arabidopsis thaliana] >gi|1169544|sp|P42762.1|ERD1_ARATH RecName: Full=ERD1 protein, chloroplastic; Flags: Precursor >gi|497629|dbj|BAA04506.1| ERD1 protein [Arabidopsis thaliana] >gi|10177198|dbj|BAB10330.1| Erd1 protein precursor [Arabidopsis thaliana]	Unigene34950_All//0.00E+00//AT5G51070| ERD1 (EARLY RESPONSIVE TO DEHYDRATION 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding	Unigene34950_All//0.00E+00//TC139533				nr +
Unigene34951_All	932	11.23	9.19	10.34	18.17	15.56	11.05	16.88	11.39	5.26	-2.89E-01	1.17E-01		-1.19E-01	5.75E-01		-2.24E-01	1.12E-01		-7.18E-01	4.61E-08		-5.67E-01	5.74E-06		-1.68E+00	1.51E-32	Down	Unigene34951_All//gi|224094264|ref|XP_002310116.1|//1.00E-99//heavy metal ATPase [Populus trichocarpa] >gi|222853019|gb|EEE90566.1| heavy metal ATPase [Populus trichocarpa]	Unigene34951_All//6.00E-93//AT4G37270| HMA1; ATPase/ cadmium-transporting ATPase/ calcium-transporting ATPase/ copper-exporting ATPase/ zinc transporting ATPase	Unigene34951_All//0.00E+00//TC138364				nr -
Unigene34952_All	2401	11.42	10.72	12.22	18.26	13.70	11.78	14.19	8.27	5.08	-9.10E-02	4.34E-01		9.79E-02	3.94E-01		-4.15E-01	1.59E-08		-6.33E-01	5.16E-16		-7.80E-01	2.26E-20		-1.48E+00	5.60E-58	Down	Unigene34952_All//gi|15235511|ref|NP_195444.1|//0.00E+00//HMA1; ATPase/ cadmium-transporting ATPase/ calcium-transporting ATPase/ copper-exporting ATPase/ zinc transporting ATPase [Arabidopsis thaliana] >gi|126413808|sp|Q9XGH5.2|AHM1_ARATH RecName: Full=Probable cadmium/zinc-transporting ATPase HMA1, chloroplastic; Flags: Precursor >gi|4006855|emb|CAB16773.1| Cu2+-transporting ATPase-like protein [Arabidopsis thaliana] >gi|7270710|emb|CAB80393.1| Cu2+-transporting ATPase-like protein [Arabidopsis thaliana]	Unigene34952_All//0.00E+00//AT4G37270| HMA1; ATPase/ cadmium-transporting ATPase/ calcium-transporting ATPase/ copper-exporting ATPase/ zinc transporting ATPase	Unigene34952_All//0.00E+00//TC138364				nr +
Unigene34954_All	1876	4.13	4.21	10.73	17.68	17.20	9.34	14.76	33.95	10.13	2.97E-02	9.02E-01		1.38E+00	8.62E-24	Up	-4.01E-02	7.55E-01		-9.21E-01	5.38E-23		1.20E+00	9.30E-76	Up	-5.43E-01	1.65E-09		Unigene34954_All//gi|15232096|ref|NP_186784.1|//1.00E-175//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana]	Unigene34954_All//2.00E-170//AT3G01350| proton-dependent oligopeptide transport (POT) family protein	Unigene34954_All//0.00E+00//CO119524				nr -
Unigene34955_All	2398	22.65	54.83	28.58	9.93	12.11	14.75	0.00	0.03	0.00	1.28E+00	2.05E-139	Up	3.36E-01	2.28E-07		2.86E-01	3.54E-03		5.71E-01	7.38E-11		5.13E+00	4.01E-01		null	null		Unigene34955_All//gi|32364696|gb|AAP80385.1|//0.00E+00//ABC transporter [Gossypium hirsutum]	Unigene34955_All//0.00E+00//AT1G17840| WBC11 (WHITE-BROWN COMPLEX HOMOLOG PROTEIN 11); ATPase, coupled to transmembrane movement of substances / fatty acid transporter	Unigene34955_All//0.00E+00//TC152862		ko03010|Spliceosome//ko02010|ABC transporters		nr +
Unigene34956_All	786	5.46	9.86	9.55	6.78	14.81	11.95	12.43	13.77	8.92	8.54E-01	4.96E-05		8.07E-01	2.63E-04		1.13E+00	2.55E-12	Up	8.18E-01	9.46E-06		1.48E-01	3.97E-01		-4.78E-01	2.65E-03		Unigene34956_All//gi|6633847|gb|AAF19706.1|AC008047.13//1.00E-64//P2K11.19 [Arabidopsis thaliana]	Unigene34956_All//2.00E-59//AT1G63430| leucine-rich repeat transmembrane protein kinase, putative	Unigene34956_All//0.00E+00//ES846546		ko04626|Plant-pathogen interaction		nr +
Unigene34957_All	2297	2.94	6.88	3.04	5.05	9.76	7.00	10.40	11.45	7.30	1.23E+00	2.07E-16	Up	4.76E-02	8.43E-01		9.50E-01	7.98E-18		4.70E-01	6.06E-04		1.38E-01	1.99E-01		-5.10E-01	1.58E-07		Unigene34957_All//gi|90399213|emb|CAJ86176.1|//1.00E-179//H0306F12.6 [Oryza sativa (indica cultivar-group)]	Unigene34957_All//9.00E-154//AT1G63430| leucine-rich repeat transmembrane protein kinase, putative	Unigene34957_All//0.00E+00//CO128688				nr -
Unigene3496_All	1583	34.21	8.99	14.97	7.87	3.70	2.60	0.11	0.05	0.05	-1.93E+00	1.90E-105	Down	-1.19E+00	1.94E-50	Down	-1.09E+00	4.13E-13	Down	-1.60E+00	1.08E-20	Down	-1.02E+00	6.14E-01		-1.09E+00	5.52E-01		Unigene3496_All//gi|118572295|sp|Q8LB19.2|EDL16_ARATH//1.00E-160//RecName: Full=Sugar transporter ERD6-like 16 >gi|17381265|gb|AAL36051.1| AT5g18840/F17K4_90 [Arabidopsis thaliana] >gi|233090019|gb|AAN18269.1| At5g18840/F17K4_90 [Arabidopsis thaliana]	Unigene3496_All//8.00E-180//AT2G48020| sugar transporter, putative	Unigene3496_All//0.00E+00//TC145382			GO:0006810//GO:0022857//GO:0031224	nr -
Unigene34962_All	990	0.32	0.05	0.38	1.11	1.39	0.55	1.32	0.21	0.68	-2.63E+00	1.31E-01		2.48E-01	8.23E-01		3.30E-01	6.09E-01		-1.02E+00	1.30E-01		-2.65E+00	3.03E-05	Down	-9.53E-01	5.85E-02		Unigene34962_All//gi|115463371|ref|NP_001055285.1|//1.00E-41//Os05g0354300 [Oryza sativa Japonica Group] >gi|113578836|dbj|BAF17199.1| Os05g0354300 [Oryza sativa Japonica Group]	Unigene34962_All//2.00E-25//AT5G05560| EMB2771 (EMBRYO DEFECTIVE 2771); ubiquitin-protein ligase	Unigene34962_All//0.00E+00//ES845204		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene34965_All	1751	7.59	6.19	6.05	10.13	10.03	8.67	19.92	9.55	8.55	-2.94E-01	6.69E-02		-3.27E-01	4.92E-02		-1.40E-02	9.33E-01		-2.25E-01	1.16E-01		-1.06E+00	1.90E-34	Down	-1.22E+00	3.90E-44	Down	Unigene34965_All//gi|297792369|ref|XP_002864069.1|//1.00E-140//sumo activating enzyme 1b [Arabidopsis lyrata subsp. lyrata] >gi|297309904|gb|EFH40328.1| sumo activating enzyme 1b [Arabidopsis lyrata subsp. lyrata]	Unigene34965_All//1.00E-129//AT5G50580| SAE1B (SUMO-ACTIVATING ENZYME 1B); SUMO activating enzyme	Unigene34965_All//0.00E+00//gi|21101481|gb|BQ413794.1|BQ413794		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene34968_All	1928	19.05	46.65	26.90	96.53	75.26	96.07	34.91	32.06	41.49	1.29E+00	1.96E-97	Up	4.98E-01	3.37E-11		-3.59E-01	1.49E-26		-6.90E-03	9.02E-01		-1.23E-01	4.80E-02		2.49E-01	1.12E-06		Unigene34968_All//gi|240256160|ref|NP_195174.6|//1.00E-173//catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|259016223|sp|Q9M069.2|E137_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 7; AltName: Full=(1->3)-beta-glucan endohydrolase 7; Short=(1->3)-beta-glucanase 7; AltName: Full=Beta-1,3-endoglucanase 7; Short=Beta-1,3-glucanase 7; Flags: Precursor	Unigene34968_All//3.00E-170//AT4G34480| catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene34968_All//0.00E+00//TC132011		ko00500|Starch and sucrose metabolism		nr -
Unigene34969_All	457	9.39	4.21	13.98	9.59	10.40	3.95	0.65	0.91	0.70	-1.16E+00	1.13E-04	Down	5.75E-01	1.84E-02		1.16E-01	7.44E-01		-1.28E+00	1.15E-05	Down	4.98E-01	6.33E-01		1.07E-01	9.45E-01									ESTscan -
Unigene34970_All	1724	15.11	9.61	14.24	8.93	9.39	5.11	2.65	2.25	0.95	-6.53E-01	9.92E-10		-8.60E-02	5.04E-01		7.24E-02	6.79E-01		-8.06E-01	7.07E-09		-2.32E-01	3.96E-01		-1.48E+00	1.61E-08	Down	Unigene34970_All//gi|226497282|ref|NP_001148515.1|//1.00E-33//pro-resilin [Zea mays] >gi|195619956|gb|ACG31808.1| pro-resilin precursor [Zea mays]	Unigene34970_All//1.00E-20//AT3G06130| heavy-metal-associated domain-containing protein	Unigene34970_All//9.00E-49//TC148013				nr +
Unigene34973_All	2416	0.26	0.42	0.68	0.70	0.43	0.56	0.95	0.31	0.63	6.90E-01	3.18E-01		1.39E+00	1.19E-02		-7.13E-01	1.48E-01		-3.22E-01	5.65E-01		-1.60E+00	6.24E-05	Down	-5.93E-01	1.05E-01		Unigene34973_All//gi|115435238|ref|NP_001042377.1|//0.00E+00//Os01g0212100 [Oryza sativa Japonica Group] >gi|113531908|dbj|BAF04291.1| Os01g0212100 [Oryza sativa Japonica Group]	Unigene34973_All//0.00E+00//AT4G18465| RNA helicase, putative	Unigene34973_All//0.00E+00//gi|78347092|gb|DT567366.1|DT567366				nr +
Unigene34975_All	2852	4.16	3.38	4.93	30.76	10.90	4.20	3.16	2.37	2.07	-3.03E-01	7.50E-02		2.43E-01	1.41E-01		-1.50E+00	3.87E-149	Down	-2.87E+00	3.40E-301	Down	-4.12E-01	1.81E-02		-6.11E-01	2.35E-04		Unigene34975_All//gi|115461711|ref|NP_001054455.1|//0.00E+00//Os05g0113300 [Oryza sativa Japonica Group] >gi|113578006|dbj|BAF16369.1| Os05g0113300 [Oryza sativa Japonica Group]	Unigene34975_All//0.00E+00//AT5G41610| ATCHX18; monovalent cation:proton antiporter/ sodium:hydrogen antiporter	Unigene34975_All//0.00E+00//TC156885				nr +

Unigene34979_All	526	12.14	9.06	12.35	9.09	19.77	15.63	15.51	14.30	12.88	-4.22E-01	7.50E-02		2.54E-02	9.31E-01		1.12E+00	5.81E-11	Up	7.81E-01	8.66E-05		-1.17E-01	6.05E-01		-2.69E-01	1.45E-01		Unigene34979_All|gi|297808071|ref|XP_002871919.1|//2.00E-54//phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317756|gb|EFH48178.1|phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34979_All//7.00E-48//AT5G20060| phospholipase/carboxylesterase family protein	Unigene34979_All//0.00E+00//gi|21093960|gb|BQ406285.1|BQ406285		ko00564|Glycerophospholipid metabolism		nr +
Unigene3498_All	2097	17.29	3.79	8.10	2.97	1.20	0.47	0.08	0.04	0.15	-2.19E+00	2.07E-83	Down	-1.09E+00	1.32E-29	Down	-1.31E+00	5.68E-09	Down	-2.65E+00	7.30E-20	Down	-1.01E+00	6.14E-01		9.15E-01	4.53E-01		Unigene3498_All|gi|117940159|sp|P93051.2|ERDL7_ARATH//0.00E+00//RecName: Full=Sugar transporter ERD6-like 7	Unigene3498_All//0.00E+00//AT2G48020| sugar transporter, putative	Unigene3498_All//0.00E+00//TC145382			GO:0006810//GO:0008152//GO:0009536//GO:0016628//GO:0022891//GO:0031224	nr +
Unigene34985_All	1283	31.44	17.77	21.25	83.44	65.09	59.63	42.77	19.45	17.95	-8.23E-01	1.65E-21		-5.65E-01	5.76E-11		-3.58E-01	2.13E-15		-4.85E-01	7.74E-24		-1.14E+00	5.05E-60	Down	-1.25E+00	6.70E-72	Down	Unigene34985_All|gi|297818246|ref|XP_002877006.1|//1.00E-118//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322844|gb|EFH53265.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene34985_All//3.00E-107//AT3G26935| zinc finger (DHHC type) family protein	Unigene34985_All//0.00E+00//gi|164350634|gb|ES819941.1|ES819941				nr +
Unigene34986_All	1873	24.58	29.03	8.27	11.30	10.59	12.01	19.48	33.27	67.98	2.40E-01	9.89E-04		-1.57E+00	3.47E-65	Down	-9.41E-02	5.31E-01		8.73E-02	5.51E-01		7.72E-01	5.85E-36		1.80E+00	9.26E-281	Up	Unigene34986_All|gi|8469220|sp|Q9SQI3.1|FATB_GOSHI//0.00E+00//RecName: Full=Myristoyl-acyl carrier protein thioesterase, chloroplastic; AltName: Full=16:0-acyl-carrier protein thioesterase; Short=16:0-ACP thioesterase; AltName: Full=Acyl-[acyl-carrier-protein] hydrolase; AltName: Full=PATE; Flags: Precursor >gi|6048397|gb|AAF02215.1|AF076535_1 palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]	Unigene34986_All//2.00E-163//AT1G08510| FATB (fatty acyl-ACP thioesterases B); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase	Unigene34986_All//0.00E+00//TC149015		ko00061|Fatty acid biosynthesis		nr +
Unigene34988_All	1503	1.60	0.88	1.03	4.18	3.25	1.05	5.94	2.61	2.60	-8.69E-01	3.39E-02		-6.40E-01	1.37E-01		-3.60E-01	1.34E-01		-1.99E+00	2.80E-14	Down	-1.18E+00	4.63E-11	Down	-1.19E+00	1.47E-11	Down	Unigene34988_All|gi|297844898|ref|XP_002890330.1|//1.00E-127//brl1-ems-suppressor 1 [Arabidopsis lyrata subsp. lyrata] >gi|297336172|gb|EFH66589.1| brl1-ems-suppressor 1 [Arabidopsis lyrata subsp. lyrata]	Unigene34988_All//2.00E-111//AT1G75080| BZR1 (BRASSINAZOLE-RESISTANT 1); DNA binding / transcription regulator/ transcription repressor	Unigene34988_All//0.00E+00//TC147738	BES1			nr +
Unigene3499_All	542	45.66	19.16	20.63	55.97	49.18	45.25	81.75	70.79	61.89	-1.25E+00	3.70E-26	Down	-1.15E+00	6.49E-22	Down	-1.87E-01	6.76E-02		-3.07E-01	1.73E-03		-2.08E-01	4.91E-03		-4.02E-01	8.38E-09		Unigene3499_All|gi|223452474|gb|ACM89564.1|//2.00E-67//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene3499_All//2.00E-52//AT1G53730| SRF6 (STRUBBELIG-RECEPTOR FAMILY 6); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene3499_All//0.00E+00//TC148661		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004871//GO:0006464//GO:0007167//GO:0031224//GO:0043410//GO:0032559//GO:0043231	nr -
Unigene34997_All	2337	68.37	107.21	55.37	55.55	55.86	115.76	12.25	19.37	34.23	6.49E-01	9.32E-86		-3.04E-01	1.25E-13		8.10E-03	8.95E-01		1.06E+00	1.39E-229	Up	6.61E-01	2.84E-20		1.48E+00	1.21E-133	Up	Unigene34997_All|gi|198400319|gb|ACH87168.1|//1.00E-171//senescence-related protein [Camellia sinensis]	Unigene34997_All//5.00E-128//AT2G17840| ERD7 (EARLY-RESPONSIVE TO DEHYDRATION 7)	Unigene34997_All//0.00E+00//TC169390				nr +
Unigene34998_All	2568	2.93	4.87	3.90	3.14	1.45	1.44	5.98	2.83	3.68	7.32E-01	4.89E-06		4.10E-01	3.26E-02		-1.12E+00	5.00E-09	Down	-1.12E+00	3.62E-08	Down	-1.08E+00	5.49E-16	Down	-7.01E-01	2.03E-08		Unigene34998_All|gi|30678282|ref|NP_186759.2|//0.00E+00//HYP1 (HYPOTHETICAL PROTEIN 1) [Arabidopsis thaliana] >gi|27311785|gb|AAO00858.1|Unknown protein [Arabidopsis thaliana] >gi|30725512|gb|AAP37778.1|At3g01100 [Arabidopsis thaliana]	Unigene34998_All//0.00E+00//AT1G69450| LOCATED IN: endomembrane system, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF221 (InterPro:IPR003864); BEST Arabidopsis thaliana protein match is: HYP1 (HYPOTHETICAL PROTEIN 1) (TAIR:AT3G01100.1); Has 911 Blast hits to 825 proteins in 137 species: Archae - 0; Bacteria - 0; Metazoa - 152; Fungi - 442; Plants - 243; Viruses - 0; Other Eukaryotes - 74 (source: NCBI BLink).	Unigene34998_All//0.00E+00//TC160469				nr -
Unigene34999_All	1484	24.40	146.00	86.19	60.66	131.13	109.96	33.82	63.76	108.78	2.58E+00	0.00E+00	Up	1.82E+00	1.72E-223	Up	1.11E+00	8.23E-198	Up	8.58E-01	1.02E-97		9.15E-01	4.18E-72		1.69E+00	0.00E+00	Up			Unigene34999_All//0.00E+00//gi|13247400|gb|BF270356.2|BF270356				
Unigene3500_All	1705	4.88	58.63	9.87	1.08	2.85	7.13	1.64	17.55	10.91	3.59E+00	0.00E+00	Up	1.02E+00	1.49E-12	Up	1.40E+00	2.48E-07	Up	2.72E+00	1.80E-38	Up	3.42E+00	1.18E-135	Up	2.74E+00	3.41E-69	Up	Unigene3500_All|gi|224117120|ref|XP_002317481.1|//0.00E+00//aminotransferase family protein [Populus trichocarpa] >gi|222860546|gb|EEE98093.1|aminotransferase family protein [Populus trichocarpa]	Unigene3500_All//5.00E-175//AT5G53970| aminotransferase, putative	Unigene3500_All//0.00E+00//CO122015		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0016846//GO:0044237//GO:0048037//GO:0070547	nr -
Unigene35000_All	1240	16.08	4.54	2.62	11.93	6.72	6.37	52.75	24.74	22.39	-1.83E+00	1.85E-36	Down	-2.62E+00	8.74E-55	Down	-8.28E-01	6.20E-10		-9.05E-01	2.75E-10		-1.09E+00	6.05E-67	Down	-1.24E+00	9.64E-84	Down	Unigene35000_All|gi|18421009|ref|NP_568484.1|//4.00E-16//meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana] >gi|16604304|gb|AAL24158.1|AT5g26280/T19G15_130 [Arabidopsis thaliana] >gi|27363366|gb|AAO11602.1|At5g26280/T19G15_130 [Arabidopsis thaliana]	Unigene35000_All//3.00E-17//AT5G26280| meprin and TRAF homology domain-containing protein / MATH domain-containing protein					nr -
Unigene35001_All	531	1.48	0.10	0.30	1.03	0.13	1.45	3.11	1.02	0.90	-3.95E+00	8.54E-04	Down	-2.30E+00	1.79E-02		-2.99E+00	9.38E-03		4.87E-01	5.91E-01		-1.60E+00	8.96E-04	Down	-1.79E+00	1.90E-04	Down								
Unigene35002_All	1158	13.83	3.59	2.30	7.66	4.94	4.68	30.60	12.02	13.25	-1.95E+00	5.23E-32	Down	-2.59E+00	1.67E-43	Down	-6.33E-01	4.31E-04		-7.10E-01	1.76E-04		-1.35E+00	9.44E-51	Down	-1.21E+00	3.69E-44	Down	Unigene35002_All|gi|18401489|ref|NP_566576.1|//2.00E-23//meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana]	Unigene35002_All//1.00E-24//AT3G17380| meprin and TRAF homology domain-containing protein / MATH domain-containing protein					nr -
Unigene35007_All	1520	15.35	12.50	9.00	8.98	8.13	6.66	2.98	1.48	2.59	-2.96E-01	1.03E-02		-7.70E-01	5.91E-11		-1.43E-01	4.21E-01		-4.32E-01	4.33E-03		-1.00E+00	8.68E-05	Down	-1.98E-01	4.63E-01		Unigene35007_All|gi|209574320|sp|Q84WN0.2|Y4920_ARATH//1.00E-132//RecName: Full=Uncharacterized protein At4g37920, chloroplastic; Flags: Precursor	Unigene35007_All//2.00E-128//AT4G37920| unknown protein	Unigene35007_All//0.00E+00//CO096944				nr -
Unigene35009_All	2946	3.87	2.79	2.86	9.33	16.08	9.12	4.69	1.11	3.83	-4.75E-01	4.86E-03		-4.39E-01	1.33E-02		7.85E-01	3.50E-27		-3.32E-02	7.94E-01		-2.08E+00	5.96E-37	Down	-2.94E-01	2.88E-02		Unigene35009_All|gi|195614560|gb|ACG29110.1|//1.00E-153//receptor-kinase isolog [Zea mays]	Unigene35009_All//2.00E-118//AT1G10850| ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene35009_All//0.00E+00//TC163488				nr -
Unigene3501_All	744	35.30	70.62	51.03	72.38	97.34	97.49	46.43	43.37	59.17	1.00E+00	3.51E-38	Up	5.32E-01	2.35E-09		4.27E-01	3.08E-14		4.30E-01	3.84E-13		-9.84E-02	3.10E-01		3.50E-01	5.97E-07		Unigene3501_All|gi|224102883|ref|XP_002312841.1|//3.00E-21//ethylene-insensitive 3a [Populus trichocarpa] >gi|222849249|gb|EEE86796.1|ethylene-insensitive 3a [Populus trichocarpa]		Unigene3501_All//0.00E+00//ES801686			GO:0000160//GO:0001071//GO:0003676//GO:0006952//GO:0009725//GO:0009756//GO:0010468//GO:0043231	nr +
Unigene35011_All	1126	36.52	42.52	38.45	34.46	39.36	43.56	80.47	62.51	187.80	2.20E-01	5.37E-03		7.41E-02	4.40E-01		1.92E-01	1.81E-02		3.38E-01	4.69E-06		-3.64E-01	6.01E-14		1.22E+00	2.39E-262	Up	Unigene35011_All|gi|297844672|ref|XP_002890217.1|//1.00E-158//alanine aminotransferase [Arabidopsis lyrata subsp. lyrata] >gi|297336059|gb|EFH66476.1|alanine aminotransferase [Arabidopsis lyrata subsp. lyrata]	Unigene35011_All//2.00E-152//AT1G17290| AlaAT1 (ALANINE AMINOTRANSFERAS); ATP binding / L-alanine:2-oxoglutarate aminotransferase	Unigene35011_All//0.00E+00//TC137511		ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene35013_All	1972	130.17	67.40	95.43	64.39	62.62	115.11	7.42	29.71	5.29	-9.50E-01	2.11E-169		-4.48E-01	9.19E-44		-4.02E-02	5.01E-01		8.38E-01	1.97E-130		2.00E+00	3.57E-146	Up	-4.87E-01	1.26E-04		Unigene35013_All|gi|152214139|ref|NP_177024.1|//0.00E+00//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|5734721|gb|AAD19986.1|AC008075_19 Similar to gb|AF023472 peptide transporter from Hordeum vulgare and is a member of the PF|00854 Peptide transporter family. ESTs gb|T41927 and gb|AA395024 come from this gene [Arabidopsis thaliana] >gi|20147231|gb|AAM10330.1|At1g68570/F24J5_7 [Arabidopsis thaliana] >gi|25090385|gb|AAN72289.1|At1g68570/F24J5_7 [Arabidopsis thaliana] >gi|110742209|dbj|BAE99031.1|peptide transporter like [Arabidopsis thaliana]	Unigene35013_All//0.00E+00//AT1G68570| proton-dependent oligopeptide transport (POT) family protein	Unigene35013_All//0.00E+00//CO091810				nr +
Unigene35014_All	3608	2.44	1.56	1.15	7.81	8.58	5.24	19.98	11.63	11.16	-6.44E-01	9.05E-04		-1.08E+00	1.61E-07	Down	1.35E-01	2.22E-01		-5.75E-01	5.70E-09		-7.81E-01	2.77E-42		-8.40E-01	3.50E-49		Unigene35014_All|gi|22655012|gb|AAM98097.1|//0.00E+00//At1g73080/F3N23_28 [Arabidopsis thaliana]	Unigene35014_All//0.00E+00//AT1G73080| PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase	Unigene35014_All//0.00E+00//DW500111		ko04626|Plant-pathogen interaction		nr +
Unigene35015_All	2846	2.90	2.14	2.23	8.14	10.05	5.97	5.36	0.98	3.89	-4.43E-01	2.93E-02		-3.84E-01	7.67E-02		3.05E-01	1.85E-03		-4.48E-01	5.31E-05		-2.45E+00	1.98E-49	Down	-4.63E-01	1.94E-04		Unigene35015_All|gi|18423656|ref|NP_568811.1|//1.00E-156//ATK3 (ARABIDOPSIS THALIANA KINESIN 3); ATPase/ microtubule binding / microtubule motor [Arabidopsis thaliana] >gi|1170621|sp|P46875.1|ATK3_ARATH RecName: Full=Kinesin-3; AltName: Full=Kinesin-like protein C >gi|1438844|dbj|BAA04674.1| heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana] >gi|27808616|gb|AAO24588.1|At5g54670 [Arabidopsis thaliana] >gi|110736249|dbj|BAF00095.1|heavy chain polypeptide of kinesin like protein [Arabidopsis thaliana]	Unigene35015_All//7.00E-158//AT5G54670| ATK3 (ARABIDOPSIS THALIANA KINESIN 3); ATPase/ microtubule binding / microtubule motor	Unigene35015_All//0.00E+00//TC144793				nr -

Unigene35017_All	1507	8.51	230.28	20.53	10.41	22.60	41.57	31.11	69.47	127.34	4.76E+00	0.00E+00	Up	1.27E+00	4.16E-32	Up	1.12E+00	5.55E-35	Up	2.00E+00	2.75E-136	Up	1.16E+00	3.74E-117	Up	2.03E+00	0.00E+00	Up	Unigene35017_All//gi|297813353|ref|XP_002874660.1|//1.00E-173//UDP-D-glucose/UDP-D-galactose 4-epimerase 5 [Arabidopsis lyrata subsp. lyrata] >gi|297320497|gb|EFH50919.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 5 [Arabidopsis lyrata subsp. lyrata]	Unigene35017_All//2.00E-174//AT4G10960| UGE5 (UDP-D-glucose/UDP-D-galactose 4-epimerase 5); UDP-glucose 4-epimerase/ protein dimerization	Unigene35017_All//0.00E+00//TC132041		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism		nr -
Unigene35018_All	957	26.63	14.72	18.86	16.45	14.14	14.49	8.13	5.76	2.37	-8.55E-01	9.36E-15		-4.97E-01	7.60E-06		-2.18E-01	1.44E-01		-1.83E-01	2.47E-01		-4.96E-01	8.01E-03		-1.78E+00	8.99E-18	Down	Unigene35018_All//gi|1039355|emb|CAA63093.1|//6.00E-76//alcohol dehydrogenase [Solanum tuberosum]	Unigene35018_All//1.00E-34//AT1G32780| alcohol dehydrogenase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr +
Unigene35019_All	1669	14.77	9.47	10.75	7.79	8.98	7.36	8.13	4.11	1.89	-6.40E-01	5.84E-09		-4.58E-01	5.52E-05		2.04E-01	1.97E-01		-8.18E-02	6.71E-01		-9.86E-01	2.09E-12		-2.11E+00	5.45E-38	Down	Unigene35019_All//gi|1039355|emb|CAA63093.1|//1.00E-129//alcohol dehydrogenase [Solanum tuberosum]	Unigene35019_All//1.00E-63//AT1G22440| alcohol dehydrogenase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr +
Unigene3502_All	923	3.12	6.26	5.08	6.80	5.97	5.04	5.08	3.94	2.68	1.01E+00	6.12E-05	Up	7.04E-01	1.54E-02		-1.88E-01	4.85E-01		-4.32E-01	7.41E-02		-3.68E-01	1.55E-01		-9.26E-01	1.34E-04				Unigene3502_All//1.00E-172//gi|21098312|gb|BQ410625.1|BQ410625					
Unigene35022_All	914	9.45	4.49	4.43	8.01	7.20	9.19	14.53	8.69	6.84	-1.07E+00	1.08E-07	Down	-1.09E+00	1.64E-07	Down	-1.55E-01	5.52E-01		1.98E-01	4.05E-01		-7.41E-01	8.36E-08		-1.09E+00	1.48E-14	Down	Unigene35022_All//gi|21554173|gb|AAM63252.1|//1.00E-13//chaperone GrpE-like protein [Arabidopsis thaliana]	Unigene35022_All//2.00E-10//AT5G55200| co-chaperone grpE protein, putative	Unigene35022_All//0.00E+00//TC144100				nr -
Unigene35023_All	993	21.97	12.91	10.51	30.10	20.60	24.47	38.53	19.82	14.64	-7.67E-01	1.03E-10		-1.06E+00	2.95E-17	Down	-5.47E-01	1.28E-09		-2.99E-01	2.58E-03		-9.59E-01	4.97E-32		-1.40E+00	2.15E-59	Down	Unigene35023_All//gi|4455201|emb|CAB36524.1|//2.00E-81//grpE like protein [Arabidopsis thaliana] >gi|7269530|emb|CAB79533.1| grpE like protein [Arabidopsis thaliana]	Unigene35023_All//7.00E-74//AT4G26780| AR192; adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization	Unigene35023_All//0.00E+00//TC170295				nr -
Unigene35025_All	1719	15.71	19.16	15.74	17.91	13.60	41.14	29.98	34.45	13.44	2.87E-01	2.62E-03		2.90E-03	1.00E+00		-3.97E-01	1.02E-05		1.20E+00	1.60E-73	Up	2.01E-01	1.40E-03		-1.16E+00	1.10E-59	Down	Unigene35025_All//gi|297821068|ref|XP_002878417.1|//1.00E-105//arginine/serine-rich splicing factor 31 [Arabidopsis lyrata subsp. lyrata] >gi|297324255|gb|EFH54676.1| arginine/serine-rich splicing factor 31 [Arabidopsis lyrata subsp. lyrata]	Unigene35025_All//3.00E-86//AT3G61860| RSP31; RNA binding / nucleic acid binding / nucleotide binding	Unigene35025_All//0.00E+00//TC156807		ko03040|Spliceosome		nr +
Unigene35026_All	724	3.18	4.90	3.90	4.54	4.28	2.68	2.45	0.81	0.72	6.24E-01	5.75E-02		2.94E-01	4.58E-01		-8.52E-02	8.11E-01		-7.60E-01	2.60E-02		-1.60E+00	5.26E-04	Down	-1.78E+00	1.06E-04	Down	Unigene35026_All//gi|222424331|dbj|BAH20122.1|//8.00E-55//AT3G28760 [Arabidopsis thaliana]	Unigene35026_All//2.00E-42//AT3G28760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: 3-dehydroquinate synthase, prokaryotic-type (InterPro:IPR002812); Has 259 Blast hits to 259 proteins in 76 species: Archae - 86; Bacteria - 48; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 86 (source: NCBI BLink).	Unigene35026_All//0.00E+00//TC150466				nr -
Unigene35027_All	1550	10.46	7.16	10.17	9.64	10.44	7.78	2.46	1.35	1.00	-5.48E-01	7.07E-05		-4.13E-02	7.90E-01		1.15E-01	5.06E-01		-3.10E-01	3.90E-02		-8.65E-01	2.01E-03		-1.29E+00	4.81E-06	Down	Unigene35027_All//gi|222424331|dbj|BAH20122.1|//1.00E-143//AT3G28760 [Arabidopsis thaliana]	Unigene35027_All//7.00E-131//AT3G28760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: 3-dehydroquinate synthase, prokaryotic-type (InterPro:IPR002812); Has 259 Blast hits to 259 proteins in 76 species: Archae - 86; Bacteria - 48; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 86 (source: NCBI BLink).	Unigene35027_All//0.00E+00//TC148571				nr +
Unigene35031_All	2559	15.05	7.58	8.24	22.46	27.75	16.70	21.58	4.95	6.21	-9.89E-01	9.71E-28		-8.69E-01	1.34E-21		3.05E-01	1.14E-07		-4.28E-01	1.56E-10		-2.12E+00	4.05E-149	Down	-1.80E+00	6.15E-123	Down	Unigene35031_All//gi|9758198|dbj|BAB08672.1|//0.00E+00//receptor-like protein kinase [Arabidopsis thaliana] >gi|224589719|gb|ACN59391.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene35031_All//0.00E+00//AT5G51560| leucine-rich repeat transmembrane protein kinase, putative	Unigene35031_All//0.00E+00//TC134344		ko04626|Plant-pathogen interaction		nr -
Unigene35036_All	830	0.76	1.65	1.86	0.78	1.99	1.74	1.53	2.77	4.22	1.12E+00	5.30E-02		1.30E+00	2.33E-02		1.35E+00	9.24E-03		1.16E+00	4.25E-02		8.58E-01	2.27E-02		1.47E+00	1.43E-06	Up	Unigene35036_All//gi|283135892|gb|ADB11337.1|//3.00E-24//theta class glutathione transferase GSTT1 [Populus trichocarpa]	Unigene35036_All//7.00E-21//AT5G41210| ATGSTT1 (GLUTATHIONE S-TRANSFERASE THETA 1); glutathione transferase	Unigene35036_All//2.00E-103//TC147657				nr -
Unigene35037_All	1443	5.73	9.97	5.31	1.55	1.98	3.54	9.08	23.43	21.04	8.00E-01	8.38E-08		-1.09E-01	6.11E-01		3.51E-01	3.94E-01		1.19E+00	9.34E-06	Up	1.37E+00	2.00E-49	Up	1.21E+00	7.75E-38	Up	Unigene35037_All//gi|283135892|gb|ADB11337.1|//3.00E-81//theta class glutathione transferase GSTT1 [Populus trichocarpa]	Unigene35037_All//5.00E-75//AT5G41210| ATGSTT1 (GLUTATHIONE S-TRANSFERASE THETA 1); glutathione transferase	Unigene35037_All//0.00E+00//gi|78344489|gb|DT564763.1|DT564763		ko00480|Glutathione metabolism//ko00350|Tyrosine metabolism		nr +
Unigene35038_All	270	8.33	5.82	8.48	16.79	14.28	12.55	16.60	2.17	5.46	-5.18E-01	2.27E-01		2.54E-02	9.71E-01		-2.33E-01	4.52E-01		-4.20E-01	1.58E-01		-2.94E+00	3.84E-18	Down	-1.60E+00	2.73E-09	Down	Unigene35038_All//gi|15240726|ref|NP_196339.1|//1.00E-32//ATBAG3 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 3); protein binding [Arabidopsis thaliana] >gi|16226483|gb|AAL16179.1|AF42841 1_1 AT5g07220/T28J14_160 [Arabidopsis thaliana]	Unigene35038_All//4.00E-34//AT5G07220| ATBAG3 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 3); protein binding	Unigene35038_All//6.00E-132//gi|109890825|gb|DW519789.1|DW519789				nr +
Unigene35039_All	2059	18.68	8.34	13.73	42.99	38.47	36.67	20.60	5.52	5.69	-1.16E+00	7.23E-36	Down	-4.44E-01	5.44E-07		-1.61E-01	3.16E-03		-2.29E-01	2.42E-05		-1.90E+00	4.80E-99	Down	-1.86E+00	6.42E-99	Down	Unigene35039_All//gi|145359142|ref|NP_200019.2|//1.00E-101//ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1); protein binding [Arabidopsis thaliana]	Unigene35039_All//2.00E-99//AT5G52060| ATBAG1 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 1); protein binding	Unigene35039_All//0.00E+00//TC158133				nr +
Unigene35040_All	942	0.00	1.02	0.00	0.32	0.26	1.68	0.09	0.62	5.37	1.00E+01	1.38E-05	Up	null	null		-3.10E-01	8.20E-01		2.40E+00	8.62E-05	Up	2.79E+00	8.26E-03		5.90E+00	6.12E-33	Up			Unigene35040_All//9.00E-140//TC142619					ESTscan -
Unigene35041_All	3890	0.87	16.50	2.12	11.76	11.31	11.65	4.36	70.42	9.84	4.24E+00	9.17E-280	Up	1.28E+00	4.41E-09	Up	-5.53E-02	5.86E-01		-1.36E-02	9.05E-01		4.01E+00	0.00E+00	Up	1.18E+00	2.79E-45	Up	Unigene35041_All//gi|15225945|ref|NP_182147.1|//2.00E-39//BAG6 (BCL-2-ASSOCIATED ATHANOGENE 6); calmodulin binding / protein binding [Arabidopsis thaliana]	Unigene35041_All//3.00E-31//AT2G46240| BAG6 (BCL-2-ASSOCIATED ATHANOGENE 6); calmodulin binding / protein binding	Unigene35041_All//0.00E+00//TC142619				nr -
Unigene35043_All	1882	15.21	6.70	8.83	14.98	14.45	13.44	11.68	3.75	5.02	-1.18E+00	1.49E-27	Down	-7.85E-01	1.04E-13		-5.16E-02	6.93E-01		-1.57E-01	1.73E-01		-1.64E+00	3.32E-42	Down	-1.22E+00	3.80E-28	Down	Unigene35043_All//gi|22331222|ref|NP_188715.2|//1.00E-134//oxidoreductase family protein [Arabidopsis thaliana]	Unigene35043_All//2.00E-114//AT3G20790| oxidoreductase family protein	Unigene35043_All//0.00E+00//TC142076				nr +
Unigene35046_All	833	1.88	2.55	1.73	4.90	2.69	3.04	5.99	4.67	2.97	4.39E-01	3.33E-01		-1.27E-01	8.07E-01		-8.68E-01	2.06E-03		-6.92E-01	2.14E-02		-3.60E-01	1.50E-01		-1.01E+00	1.76E-05	Down	Unigene35046_All//gi|18407307|ref|NP_564784.1|//9.00E-25//DNA-binding storekeeper protein-related [Arabidopsis thaliana] >gi|4505074|gb|AAD21418.1| Unknown protein [Arabidopsis thaliana] >gi|222424594|dbj|BAH20252.1|AT1G61730 [Arabidopsis thaliana]	Unigene35046_All//4.00E-16//AT1G61730| DNA-binding storekeeper protein-related	Unigene35046_All//1.00E-169//gi|164285997|gb|ES800208.1|ES800208	GeBP			nr +
Unigene35047_All	928	14.10	9.56	5.74	17.12	17.40	16.16	36.13	18.56	26.14	-5.61E-01	3.06E-04		-1.30E+00	2.87E-14	Down	2.34E-02	8.97E-01		-8.38E-02	6.13E-01		-9.61E-01	2.77E-28		-4.67E-01	8.49E-09		Unigene35047_All//gi|18407307|ref|NP_564784.1|//1.00E-25//DNA-binding storekeeper protein-related [Arabidopsis thaliana] >gi|4505074|gb|AAD21418.1| Unknown protein [Arabidopsis thaliana] >gi|222424594|dbj|BAH20252.1|AT1G61730 [Arabidopsis thaliana]	Unigene35047_All//4.00E-16//AT1G61730| DNA-binding storekeeper protein-related	Unigene35047_All//0.00E+00//TC175421	GeBP			nr +
Unigene35048_All	1972	0.58	3.44	1.05	2.15	1.47	1.74	2.21	2.10	1.23	2.56E+00	3.85E-19	Up	8.51E-01	6.95E-02		-5.50E-01	5.50E-02		-3.03E-01	3.56E-01		-7.37E-02	7.93E-01		-8.42E-01	8.07E-04		Unigene35048_All//gi|115477753|ref|NP_001062472.1|//4.00E-92//Os08g0556000 [Oryza sativa Japonica Group] >gi|113624441|dbj|BAF24386.1|Os08g0556000 [Oryza sativa Japonica Group]	Unigene35048_All//1.00E-98//AT3G13060| ECT5; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: YT521-B-like protein (InterPro:IPR007275); BEST Arabidopsis thaliana protein match is: ECT2; protein binding (TAIR:AT5G13460.1); Has 1007 Blast hits to 965 proteins in 147 species: Archae - 0; Bacteria - 8; Metazoa - 528; Fungi - 103; Plants - 235; Viruses - 0; Other Eukaryotes - 133 (source: NCBI BLink).	Unigene35048_All//0.00E+00//C0079741				nr -
Unigene35049_All	2085	23.41	34.61	32.26	17.11	28.29	24.85	3.93	8.38	18.84	5.64E-01	9.20E-20		4.62E-01	1.36E-12		7.26E-01	1.53E-29		5.38E-01	3.94E-14		1.09E+00	2.08E-18	Up	2.26E+00	1.20E-116	Up	Unigene35049_All//gi|9294580|dbj|BAB02861.1|//0.00E+00//receptor-like protein kinase-like protein [Arabidopsis thaliana] >gi|224589583|gb|ACN59225.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene35049_All//0.00E+00//AT3G28450| leucine-rich repeat transmembrane protein kinase, putative	Unigene35049_All//0.00E+00//TC131756				nr +
Unigene3505_All	1089	11.43	35.27	16.48	20.49	23.37	26.00	17.47	32.97	29.23	1.63E+00	6.97E-59	Up	5.27E-01	9.45E-05		1.89E-01	9.98E-02		3.44E-01	6.79E-04		9.16E-01	6.45E-28		7.43E-01	4.83E-18		Unigene3505_All//gi|38603862|gb|AAR24676.1|//2.00E-64//At3g53490 [Arabidopsis thaliana]	Unigene3505_All//5.00E-44//AT3G53490| unknown protein	Unigene3505_All//0.00E+00//TC173584				nr -
Unigene35050_All	1792	52.32	69.13	122.84	64.38	66.74	89.22	43.06	21.46	19.54	4.02E-01	2.54E-18		1.23E+00	2.23E-215	Up	5.19E-02	3.76E-01		4.71E-01	2.48E-33		-1.00E+00	7.22E-69	Down	-1.14E+00	8.68E-87	Down	Unigene35050_All//gi|211906466|gb|ACJ11726.1|//0.00E+00//serine hydroxymethyltransferase [Gossypium hirsutum]	Unigene35050_All//0.00E+00//AT4G13930| SHM4 (serine hydroxymethyltransferase 4); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene35050_All//0.00E+00//TC176819		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr -
Unigene35051_All	1771	4.58	5.98	8.93	4.30	9.96	6.40	1.55	3.02	1.93	3.85E-01	3.09E-02		9.64E-01	6.83E-11		1.21E+00	1.27E-20	Up	5.73E-01	5.72E-04		9.61E-01	3.48E-05		3.18E-01	2.98E-01		Unigene35051_All//gi|289466351|gb|ADC94861.1|//7.00E-93//HSP transcription factor [Vitis pseudoreticulata]	Unigene35051_All//4.00E-67//AT4G11660| AT-HSFB2B; transcription factor/ transcription repressor	Unigene35051_All//0.00E+00//gi|13244151|gb|BE054274.2|BE054274	HSF			nr -

Unigene35052_All	2551	98.14	30.25	116.19	13.57	11.64	5.58	5.95	4.05	2.44	-1.70E+00	0.00E+00	Down	2.44E-01	2.09E-16		-2.22E-01	1.45E-02		-1.28E+00	9.67E-41	Down	-5.56E-01	1.29E-05		-1.29E+00	2.13E-21	Down	Unigene35052_All//gi|297795741|ref|XP_002865755.1|//0.00E+00//ATFR07 FR07 [Arabidopsis lyrata subsp. lyrata] >gi|297311590|gb|EFH42014.1| ATFR07/FR07 [Arabidopsis lyrata subsp. lyrata]	Unigene35052_All//0.00E+00//AT5G49740| ATFR07 (FERRIC REDUCTION OXIDASE 7); ferric-chelate reductase/ oxidoreductase	Unigene35052_All//0.00E+00//TC148634		ko04626|Plant-pathogen interaction		nr -
Unigene35053_All	1845	12.02	33.70	18.21	11.83	14.95	17.45	23.58	71.52	63.22	1.49E+00	1.89E-83	Up	5.99E-01	3.35E-10		3.38E-01	6.14E-04		5.62E-01	1.11E-09		1.60E+00	3.63E-241	Up	1.42E+00	5.71E-183	Up	Unigene35053_All//gi|73919864|sp|Q9FIK7.1|THIC2_ARATH//0.00E+00//RecName: Full=Probable acetyl-CoA acetyltransferase, cytosolic 2; AltName: Full=Cytosolic acetoacetyl-CoA thiolase 2; Short=Thiolase 2 >gi|10177908|dbj|BAB11319.1| acetoacyl-CoA-thiolase [Arabidopsis thaliana] >gi|216180008|gb|AAM67058.1| acetoacyl-CoA-thiolase [Arabidopsis thaliana] >gi|119935899|gb|ABM06028.1| At5g47720 [Arabidopsis thaliana] >gi|222423167|dbj|BAH19561.1| AT5G47720 [Arabidopsis thaliana]	Unigene35053_All//2.00E-170//AT5G47720| acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative	Unigene35053_All//0.00E+00//TC152978		ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00900|Terpenoid backbone biosynthesis//ko00072|Synthesis and degradation of ketone bodies		nr -
Unigene35057_All	467	1.46	1.19	1.71	1.92	3.61	5.42	3.08	2.60	3.07	-2.87E-01	7.10E-01		2.32E-01	7.49E-01		9.12E-01	7.48E-02		1.50E+00	3.08E-04	Up	-2.46E-01	6.37E-01		-3.30E-03	9.90E-01		Unigene35057_All//gi|16416383|dbj|BAB70612.1|//1.00E-17//anthocyanin-related membrane protein 1 [Arabidopsis thaliana]	Unigene35057_All//7.00E-19//AT3G59310| unknown protein	Unigene35057_All//2.00E-102//TC158356				nr -
Unigene35064_All	1431	4.50	2.83	3.27	81.11	30.20	20.70	12.59	7.21	2.34	-6.67E-01	4.04E-03		-4.58E-01	6.33E-02		-1.43E+00	3.14E-183	Down	-1.97E+00	4.67E-253	Down	-8.03E-01	1.06E-11		-2.43E+00	1.52E-59	Down	Unigene35064_All//gi|186511471|ref|NP_001118919.1|//1.00E-22//UNE12 (unfertilized embryo sac 12); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene35064_All//5.00E-24//AT4G02590| UNE12 (unfertilized embryo sac 12); DNA binding / transcription factor	Unigene35064_All//0.00E+00//D9517829	bHLH			nr -
Unigene35065_All	2056	3.66	1.80	3.03	45.16	19.08	11.62	12.40	7.91	3.22	-1.03E+00	2.11E-06	Down	-2.74E-01	2.42E-01		-1.24E+00	2.41E-118	Down	-1.96E+00	6.65E-201	Down	-6.49E-01	1.94E-11		-1.95E+00	1.04E-63	Down	Unigene35065_All//gi|226495509|ref|NP_001152044.1|//3.00E-76//LOC100285681 [Zea mays] >gi|195652123|gb|ACG45529.1| bHLH transcription factor [Zea mays]	Unigene35065_All//1.00E-47//AT4G02590| UNE12 (unfertilized embryo sac 12); DNA binding / transcription factor	Unigene35065_All//0.00E+00//TC133515	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr -
Unigene35066_All	1216	37.13	48.63	50.40	20.77	18.29	18.76	21.45	68.36	17.56	3.89E-01	1.13E-08		4.41E-01	1.27E-10		-1.83E-01	1.10E-01		-1.47E-01	2.32E-01		1.67E+00	6.10E-162	Up	-2.89E-01	2.11E-03		Unigene35066_All//gi|70927822|gb|AZ15733.1|//8.00E-31//DT-related protein [Oryza sativa Japonica Group]	Unigene35066_All//5.00E-27//AT2G41250| haloacid dehalogenase-like hydrolase family protein	Unigene35066_All//0.00E+00//TC167611				nr +
Unigene35067_All	1184	235.89	250.05	301.42	108.59	104.85	95.71	44.21	151.97	43.17	8.41E-02	6.75E-03		3.54E-01	2.73E-39		-5.06E-02	3.62E-01		-1.82E-01	4.98E-05		1.78E+00	0.00E+00	Up	-3.43E-02	6.48E-01		Unigene35067_All//gi|226501694|ref|NP_001147144.1|//1.00E-118//rhythmically expressed protein [Zea mays] >gi|195607682|gb|ACG25671.1| rhythmically expressed protein [Zea mays]	Unigene35067_All//3.00E-103//AT2G41250| haloacid dehalogenase-like hydrolase family protein	Unigene35067_All//0.00E+00//TC167611				nr -
Unigene35073_All	1370	3.86	1.89	3.46	5.05	4.25	4.09	4.47	3.54	4.51	-1.03E+00	9.01E-05	Down	-1.57E-01	6.08E-01		-2.51E-01	3.04E-01		-3.06E-01	2.05E-01		-3.39E-01	1.33E-01		1.04E-02	9.73E-01		Unigene35073_All//gi|15240416|ref|NP_200300.1|//2.00E-93//RNA binding [Arabidopsis thaliana] >gi|75170294|sp|Q9FFU1.1|CAF2M_ARATH RecName: Full=CRS2-associated factor 2, mitochondrial; Flags: Precursor	Unigene35073_All//1.00E-94//AT5G54890| RNA binding	Unigene35073_All//0.00E+00//gi|78336807|gb|DT557081.1|DT557081				nr -
Unigene35076_All	3132	7.72	10.52	8.01	11.32	10.34	10.31	25.16	18.60	57.06	4.46E-01	1.84E-06		5.32E-02	6.66E-01		-1.32E-01	1.86E-01		-1.35E-01	1.91E-01		-4.36E-01	9.45E-17		1.18E+00	4.62E-210	Up	Unigene35076_All//gi|22328857|ref|NP_680734.1|//1.00E-120//ENDO4 (endonuclease 4); T/G mismatch-specific endonuclease/ endonuclease/ nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease [Arabidopsis thaliana]	Unigene35076_All//2.00E-121//AT4G21585| ENDO4 (endonuclease 4); T/G mismatch-specific endonuclease/ endonuclease/ nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease	Unigene35076_All//0.00E+00//TC167912				nr +
Unigene35078_All	890	0.53	2.22	1.91	1.96	1.74	1.73	1.95	1.31	0.90	2.07E+00	7.23E-05	Up	1.86E+00	1.15E-03		-1.70E-01	7.62E-01		-1.83E-01	7.14E-01		-5.67E-01	2.16E-01		-1.12E+00	9.40E-03		Unigene35078_All//gi|224141357|ref|XP_002324039.1|//1.00E-114//f-box family protein [Populus trichocarpa] >gi|222867041|gb|EEF04172.1| f-box family protein [Populus trichocarpa]		Unigene35078_All//2.00E-159//gi|164319321|gb|ES808133.1|ES808133				nr +
Unigene35081_All	2473	22.09	12.76	13.50	27.84	21.67	28.75	57.87	30.30	25.34	-7.91E-01	5.36E-27		-7.10E-01	1.23E-21		-3.62E-01	3.08E-10		4.63E-02	5.76E-01		-9.33E-01	1.68E-112		-1.19E+00	4.93E-172	Down	Unigene35081_All//gi|115475758|ref|NP_001061475.1|//0.00E+00//Os08g0295300 (Oryza sativa Japonica Group) >gi|113623444|dbj|BAF23389.1| Os08g0295300 [Oryza sativa Japonica Group]	Unigene35081_All//0.00E+00//AT5G26830| threonyl-tRNA synthetase / threonine--tRNA ligase (THRRS)	Unigene35081_All//0.00E+00//TC145574		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene35084_All	3238	13.46	16.15	14.90	17.25	16.36	17.34	27.15	29.24	11.01	2.63E-01	3.76E-04		1.47E-01	8.78E-02		-7.64E-02	3.69E-01		7.60E-03	9.45E-01		1.07E-01	3.96E-02		-1.30E+00	1.13E-121	Down	Unigene35084_All//gi|87240964|gb|AB032822.1|//0.00E+00//Protein kinase; U box [Medicago truncatula]	Unigene35084_All//0.00E+00//AT2G45910| protein kinase family protein / U-box domain-containing protein	Unigene35084_All//3.00E-13//gi|164326641|gb|ES827039.1|ES827039		ko04626|Plant-pathogen interaction		nr -
Unigene35085_All	378	3.05	8.85	4.93	3.03	6.92	6.93	8.95	11.06	5.06	1.54E+00	2.01E-05	Up	6.95E-01	1.61E-01		1.19E+00	2.00E-03		1.19E+00	2.63E-03		3.05E-01	2.87E-01		-8.23E-01	4.45E-03				Unigene35085_All//6.00E-108//gi|21091788|gb|BQ404101.1|BQ404101				
Unigene35086_All	1528	13.15	28.39	17.77	23.86	21.88	24.18	24.71	23.63	18.95	1.11E+00	2.26E-37	Up	4.35E-01	5.30E-05		-1.25E-01	2.10E-01		1.89E-02	8.74E-01		-6.43E-02	5.14E-01		-3.83E-01	4.72E-07		Unigene35086_All//gi|15220181|ref|NP_172535.1|//1.00E-103//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|67037423|gb|AAY63560.1| RING domain protein [Arabidopsis thaliana]	Unigene35086_All//4.00E-94//AT1G10650| protein binding / zinc ion binding	Unigene35086_All//0.00E+00//TC163249				nr -
Unigene35090_All	1968	116.29	32.93	49.46	21.72	22.08	10.21	3.12	7.11	1.70	-1.82E+00	0.00E+00	Down	-1.23E+00	6.50E-224	Down	2.40E-02	8.19E-01		-1.09E+00	1.03E-38	Down	1.19E+00	4.72E-17	Up	-8.74E-01	2.75E-05		Unigene35090_All//gi|22329164|ref|NP_195179.2|//2.00E-50//CIB1 (CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75299602|sp|Q8GY61.1|BH063_ARATH RecName: Full=Transcription factor bHLH63; AltName: Full=Transcription factor EN 84; AltName: Full=bHLH transcription factor bHLH063; AltName: Full=Basic helix-loop-helix protein 63; Short=bHLH 63; Short=AtbHLH63 >gi|28950907|gb|AAO63377.1| At4g34530 [Arabidopsis thaliana]	Unigene35090_All//5.00E-51//AT4G34530| CIB1 (CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1); DNA binding / transcription factor	Unigene35090_All//0.00E+00//TC141372	bHLH	ko04712|Circadian rhythm - plant		nr -
Unigene35092_All	1057	2.92	2.92	2.17	4.57	3.55	1.97	8.16	17.20	9.23	1.80E-03	9.97E-01		-4.31E-01	2.51E-01		-3.64E-01	1.95E-01		-1.22E+00	9.02E-06	Down	1.08E+00	1.02E-18	Up	1.78E-01	3.12E-01		Unigene35092_All//gi|1438881|gb|AAC49375.1|//5.00E-57//GmCK2p [Glycine max]	Unigene35092_All//3.00E-50//AT1G71697| ATCK1 (CHOLINE KINASE 1); choline kinase	Unigene35092_All//0.00E+00//C0127907		ko00564|Glycerophospholipid metabolism		nr -
Unigene35095_All	1758	110.27	84.51	129.49	65.82	73.08	55.29	19.70	11.98	8.59	-3.84E-01	5.34E-26		2.32E-01	1.16E-11		1.51E-01	6.32E-04		-2.52E-01	5.86E-08		-7.17E-01	5.27E-18		-1.20E+00	1.33E-42	Down	Unigene35095_All//gi|46093878|gb|AAS79792.1|//0.00E+00//sucrose phosphate phosphatase [Malus x domestica]	Unigene35095_All//0.00E+00//AT2G35840| sucrose-phosphatase 1 (SPP1)	Unigene35095_All//0.00E+00//TC139409				nr -
Unigene35098_All	1913	40.12	37.08	46.79	37.68	37.82	55.53	12.53	9.46	4.27	-1.14E-01	7.80E-02		2.22E-01	1.11E-04		5.30E-03	9.61E-01		5.59E-01	2.32E-30		-4.06E-01	4.53E-05		-1.55E+00	6.68E-44	Down	Unigene35098_All//gi|15231700|ref|NP_190855.1|//1.00E-158//calmodulin-binding family protein [Arabidopsis thaliana] >gi|24111367|gb|AAN46807.1| At3g52870/F8J2_40 [Arabidopsis thaliana]	Unigene35098_All//1.00E-152//AT3G52870| calmodulin-binding family protein	Unigene35098_All//0.00E+00//TC164920				nr -
Unigene3510_All	1255	4.59	4.72	5.39	4.17	8.51	5.90	7.07	1.50	2.92	4.27E-02	8.71E-01		2.33E-01	3.65E-01		1.03E+00	7.27E-10	Up	5.02E-01	2.07E-02		-2.24E+00	3.52E-26	Down	-1.28E+00	1.03E-12	Down	Unigene3510_All//gi|18421959|ref|NP_568578.1|//2.00E-70//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|15724298|gb|AAL06542.1|AF412089_1 AT5g40210/MSN9_110 [Arabidopsis thaliana] >gi|24111287|gb|AAN46767.1| At5g40210/MSN9_110 [Arabidopsis thaliana]	Unigene3510_All//4.00E-64//AT5G40210| nodulin MtN21 family protein	Unigene3510_All//0.00E+00//TC149422				nr -
Unigene35101_All	331	0.32	3.06	0.32	0.75	1.98	2.46	0.00	0.00	0.12	3.28E+00	3.79E-04	Up	2.58E-02	1.00E+00		1.39E+00	1.51E-01		1.71E+00	4.57E-02		null	null		6.91E+00	6.45E-01									ESTscan +
Unigene35102_All	989	0.00	13.06	1.35	1.56	7.73	11.74	1.54	8.66	11.32	1.37E+01	3.77E-74	Up	1.04E+01	2.40E-07	Up	2.31E+00	8.38E-22	Up	2.91E+00	2.00E-39	Up	2.49E+00	1.45E-28	Up	2.88E+00	3.63E-44	Up	Unigene35102_All//gi|144225753|emb|CAM84273.1|//5.00E-97//abscisic insensitive 1B [Populus tremula]	Unigene35102_All//5.00E-93//AT5G57050| ABI2 (ABA INSENSITIVE 2); protein serine/threonine phosphatase	Unigene35102_All//2.00E-73//DW239305				nr -
Unigene35103_All	1956	0.29	9.25	1.17	0.43	4.63	5.61	0.86	3.01	4.58	4.97E+00	6.85E-87	Up	1.99E+00	4.68E-05	Up	3.42E+00	1.86E-38	Up	3.70E+00	2.74E-46	Up	1.80E+00	2.03E-13	Up	2.41E+00	2.87E-29	Up	Unigene35103_All//gi|144225753|emb|CAM84273.1|//1.00E-110//abscisic insensitive 1B [Populus tremula]	Unigene35103_All//2.00E-110//AT5G57050| ABI2 (ABA INSENSITIVE 2); protein serine/threonine phosphatase	Unigene35103_All//1.00E-100//DW239305				nr -
Unigene35104_All	1669	0.47	0.27	0.54	5.37	2.19	3.14	16.74	43.45	26.57	-7.83E-01	3.28E-01		2.06E-01	7.64E-01		-1.30E+00	1.60E-12	Down	-7.75E-01	3.74E-05		1.38E+00	4.03E-106	Up	6.66E-01	1.23E-20		Unigene35104_All//gi|259121415|gb|ACV92027.1|//1.00E-113//WRKY transcription factor 25 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene35104_All//5.00E-78//AT5G28650| WRKY74; calmodulin binding / transcription factor	Unigene35104_All//2.00E-52//TC142040	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene35105_All	1574	0.20	0.42	0.41	2.12	2.34	2.32	5.94	9.90	2.40	1.07E+00	2.37E-01		1.03E+00	2.81E-01		1.43E-01	7.18E-01		1.32E-01	7.01E-01		7.39E-01	5.85E-09		-1.30E+00	9.51E-14	Down	Unigene35105_All//gi|259121415|gb|ACV92027.1|//1.00E-130//WRKY transcription factor 25 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene35105_All//8.00E-77//AT5G28650| WRKY74; calmodulin binding / transcription factor	Unigene35105_All//3.00E-48//gi|109837413|gb|DW235974.1|DW235974	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene35106_All	2560	21.93	10.43	18.51	14.30	15.24	11.56	0.38	0.42	0.22	-1.07E+00	9.84E-46	Down	-2.44E-01	9.86E-04		9.17E-02	3.76E-01		-3.08E-01	4.50E-04		1.60E-01	7.82E-01		-8.02E-01	1.83E-01		Unigene35106_All//gi|225445364|ref|XP_002284885.1|//0.00E+00//PREDICTED: similar to ATFDR4/FDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances [Vitis vinifera]	Unigene35106_All//0.00E+00//AT2G26910| FDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances	Unigene35106_All//0.00E+00//TC142553		ko03040|Spliceosome//ko02010|ABC transporters		nr +

Unigene35107_All	2881	3.54	2.39	3.70	6.41	6.88	9.14	10.29	6.04	4.96	-5.66E-01	1.53E-03		6.19E-02	7.48E-01		1.02E-01	5.15E-01		5.11E-01	7.15E-07		-7.69E-01	1.89E-17		-1.05E+00	7.97E-30	Down	Unigene35107_All//gi|30683900|ref|NP_180412.2|//0.00E+00//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75154217|sp|Q8LT53.1|C3H24_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 24; Short=AtC3H24 >gi|22135822|gb|AAM91097.1|At2g28450/T1B3.3 [Arabidopsis thaliana] >gi|25090447|gb|AAN72304.1|At2g28450/T1B3.3 [Arabidopsis thaliana]	Unigene35107_All//0.00E+00//AT2G28450| zinc finger (CCCH-type) family protein	Unigene35107_All//0.00E+00//gi|78345517|gb|DT565791.1|DT565791	C3H	ko00350|Tyrosine metabolism//ko00450|Selenoamino acid metabolism//ko00340|Histidine metabolism		nr -
Unigene35109_All	2436	10.33	4.20	6.69	12.29	12.07	16.54	14.87	16.87	35.18	-1.30E+00	4.56E-28	Down	-6.27E-01	2.07E-08		-2.58E-02	8.19E-01		4.28E-01	1.52E-07		1.81E-01	2.10E-02		1.24E+00	2.38E-109	Up	Unigene35109_All//gi|15232838|ref|NP_186851.1|//0.00E+00//AK3 (ASPARTATE KINASE 3); aspartate kinase [Arabidopsis thaliana] >gi|75336806|sp|Q9ST02.1|AK3_ARATH RecName: Full=Aspartokinase 3, chloroplastic; AltName: Full=Aspartate kinase 3; Flags: Precursor	Unigene35109_All//0.00E+00//AT3G02020| AK3 (ASPARTATE KINASE 3); aspartate kinase	Unigene35109_All//0.00E+00//ES851112		ko00270|Cysteine and methionine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00300|Lysine biosynthesis		nr -
Unigene3511_All	797	1.58	3.62	4.74	5.06	5.06	2.89	1.49	2.62	1.00	1.20E+00	1.47E-03		1.59E+00	5.33E-06	Up	-2.20E-03	9.86E-01		-8.09E-01	7.11E-03		8.20E-01	4.01E-02		-5.71E-01	2.93E-01						Unigene3511_All//0.00E+00//DW008901				
Unigene35114_All	3099	8.76	3.38	5.79	17.36	13.31	13.52	19.39	46.62	41.03	-1.37E+00	7.07E-33	Down	-5.98E-01	2.47E-08		-3.83E-01	5.47E-09		-3.60E-01	2.34E-07		1.27E+00	1.50E-185	Up	1.08E+00	4.67E-130	Up	Unigene35114_All//gi|15239414|ref|NP_200879.1|//0.00E+00//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|9759335|dbj|BAB09844.1|retroelement pol polyprotein-like [Arabidopsis thaliana]	Unigene35114_All//0.00E+00//AT5G60710| zinc finger (C3HC4-type RING finger) family protein	Unigene35114_All//0.00E+00//TC132821				nr +
Unigene35116_All	331	0.00	0.92	2.25	1.35	1.14	3.96	0.00	0.38	0.48	9.84E+00	4.43E-02		1.11E+01	3.27E-04	Up	-2.43E-01	8.21E-01		1.55E+00	1.29E-02		8.57E+00	2.40E-01		8.91E+00	1.40E-01		Unigene35116_All//gi|297819432|ref|XP_002877599.1|//2.00E-07//ALDH10A9 [Arabidopsis lyrata subsp. lyrata] >gi|297323437|gb|EFH53858.1|ALDH10A9 [Arabidopsis lyrata subsp. lyrata]	Unigene35116_All//1.00E-08//AT3G48170| ALDH10A9; 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Unigene35116_All//7.00E-163//TC172037		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene35117_All	2043	101.52	213.27	184.77	129.64	212.66	272.22	17.57	9.86	8.23	1.07E+00	0.00E+00	Up	8.64E-01	2.04E-206		7.14E-01	1.60E-210		1.07E+00	0.00E+00	Up	-8.33E-01	6.38E-24		-1.09E+00	2.64E-38	Down	Unigene35117_All//gi|134285028|gb|AB069575.1|//0.00E+00//betaine-aldehyde dehydrogenase [Jatropha curcas] >gi|134290688|gb|AB070350.1|betaine-aldehyde dehydrogenase [Jatropha curcas]	Unigene35117_All//0.00E+00//AT1G74920| ALDH10A8; 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Unigene35117_All//0.00E+00//TC134080		ko00260|Glycine, serine and threonine metabolism		nr -
Unigene35118_All	1779	10.29	3.08	3.86	7.56	3.95	6.73	9.01	12.31	2.28	-1.74E+00	1.72E-31	Down	-1.41E+00	1.77E-22	Down	-9.37E-01	4.30E-11		-1.68E-01	3.45E-01		4.51E-01	1.56E-05		-1.98E+00	3.09E-41	Down	Unigene35118_All//gi|297828519|ref|XP_002882142.1|//1.00E-137//endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327981|gb|EFH58401.1|endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35118_All//6.00E-133//AT2G48030|endonuclease/exonuclease/phosphatase family protein	Unigene35118_All//0.00E+00//gi|109872929|gb|DW501904.1|DW501904				nr +
Unigene35119_All	3308	14.73	5.97	6.15	13.61	11.38	10.43	9.45	9.44	11.96	-1.30E+00	6.40E-54	Down	-1.26E+00	1.74E-49	Down	-2.59E-01	6.06E-04		-3.84E-01	5.52E-07		-1.10E-03	1.02E+00		3.40E-01	4.57E-06		Unigene35119_All//gi|15219152|ref|NP_173617.1|//0.00E+00//ATPIPSK1 (PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE 1); 1-phosphatidylinositol-4-phosphate 5-kinase/ actin filament binding / actin monomer binding / phosphatidylinositol phosphate kinase [Arabidopsis thaliana] >gi|75218151|sp|Q56YP2.1|PI5K1_ARATH RecName: Full=Phosphatidylinositol-4-phosphate 5-kinase 1; Short=AtPIP5K1; AltName: Full=1-phosphatidylinositol-4-phosphate kinase 1; AltName: Full=PtdIns(4)P-5-kinase 1; AltName: Full=Diphosphoinositide kinase 1 >gi|62319907|dbj|BAD93975.1|phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]	Unigene35119_All//0.00E+00//AT1G21980| ATPIPSK1 (PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE 1); 1-phosphatidylinositol-4-phosphate 5-kinase/ actin filament binding / actin monomer binding / phosphatidylinositol phosphate kinase	Unigene35119_All//0.00E+00//TC133757		ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene35124_All	2230	12.97	9.61	12.58	10.05	13.54	14.30	8.23	7.52	3.72	-4.33E-01	1.60E-05		-4.41E-02	7.02E-01		4.30E-01	2.69E-06		5.08E-01	4.06E-08		-1.31E-01	3.34E-01		-1.15E+00	1.59E-21	Down	Unigene35124_All//gi|115437340|ref|NP_001043271.1|//0.00E+00//Os01g0541900 [Oryza sativa Japonica Group] >gi|76222723|sp|Q5JJY4.1|P2C04_ORYSJ RecName: Full=Protein kinase and PP2C-like domain-containing protein; Includes: RecName: Full=Probable serine/threonine-protein kinase Os01g0541900; Includes: RecName: Full=Probable protein phosphatase 2C 4; Short=OsPP2C04 >gi|113532802|dbj|BAF05185.1|Os01g0541900 [Oryza sativa Japonica Group]	Unigene35124_All//0.00E+00//AT2G40860| protein kinase family protein / protein phosphatase 2C (PP2C) family protein	Unigene35124_All//0.00E+00//TC168705				nr -
Unigene35127_All	675	6.28	5.25	5.84	6.35	8.16	9.97	70.22	32.20	35.83	-2.57E-01	3.92E-01		-1.05E-01	7.31E-01		3.63E-01	1.72E-01		6.52E-01	3.77E-03		-1.12E+00	4.66E-51	Down	-9.71E-01	1.86E-41		Unigene35127_All//gi|30690360|ref|NP_850886.1|//7.00E-76//catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana] >gi|42573483|ref|NP_974838.1|catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana]	Unigene35127_All//2.00E-76//AT5G26600| catalytic/ pyridoxal phosphate binding	Unigene35127_All//0.00E+00//TC149910				nr +
Unigene35128_All	1938	6.72	8.63	13.85	14.03	17.96	19.34	44.51	29.96	22.30	3.60E-01	9.02E-03		1.04E+00	1.78E-20	Up	3.56E-01	3.16E-05		4.63E-01	4.79E-08		-5.71E-01	2.23E-29		-9.97E-01	5.30E-78		Unigene35128_All//gi|225450446|ref|XP_002279795.1|//0.00E+00//PREDICTED: similar to catalytic/ pyridoxal phosphate binding [Vitis vinifera]	Unigene35128_All//0.00E+00//AT5G26600| catalytic/ pyridoxal phosphate binding	Unigene35128_All//0.00E+00//TC145734		ko00450|Selenoamino acid metabolism//ko00730|Thiamine metabolism		nr -
Unigene35129_All	2622	3.23	4.48	5.75	21.05	40.95	20.34	4.31	3.17	2.01	4.72E-01	4.46E-03		8.30E-01	3.02E-08		9.60E-01	6.13E-86		-4.94E-02	6.13E-01		-4.41E-01	3.69E-03		-1.10E+00	8.55E-13	Down	Unigene35129_All//gi|225432122|ref|XP_002263974.1|//0.00E+00//PREDICTED: similar to boron transporter [Vitis vinifera]	Unigene35129_All//0.00E+00//AT2G47160| BOR1 (REQUIRES HIGH BORON 1); anion exchanger/ boron transporter	Unigene35129_All//0.00E+00//TC164014				nr +
Unigene35131_All	1425	3.27	5.90	5.53	6.78	2.85	6.59	1.72	0.29	3.30	8.53E-01	2.23E-05		7.59E-01	4.12E-04		-1.25E+00	9.99E-13	Down	-4.09E-02	8.58E-01		-2.55E+00	6.67E-09	Down	9.39E-01	1.17E-04		Unigene35131_All//gi|240255859|ref|NP_680693.5|//6.00E-20//ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene35131_All//3.00E-21//AT4G15233| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene35131_All//1.00E-19//gi|78329805|gb|DT550079.1|DT550079				nr -
Unigene35132_All	4619	0.03	0.13	0.00	0.00	0.04	0.09	1.98	6.71	18.43	1.95E+00	6.04E-02		-5.09E+00	2.44E-01		5.48E+00	1.57E-01		6.46E+00	1.36E-02		1.76E+00	2.44E-65	Up	3.22E+00	0.00E+00	Up	Unigene35132_All//gi|75321780|sp|Q59274.1|PDR3_TOBAC//0.00E+00//RecName: Full=Pleiotropic drug resistance protein 3; AltName: Full=NtPDR3 >gi|55056942|emb|CAH39853.1| PDR-like ABC transporter [Nicotiana tabacum]	Unigene35132_All//0.00E+00//AT3G53480| PDR9 (PLEIOTROPIC DRUG RESISTANCE 9); ATPase, coupled to transmembrane movement of substances	Unigene35132_All//9.00E-11//TC177387		ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene35135_All	2028	36.89	30.56	28.23	19.26	24.84	16.44	6.96	2.51	3.52	-2.72E-01	6.89E-06		-3.86E-01	3.62E-10		3.67E-01	1.02E-07		-2.29E-01	9.15E-03		-1.47E+00	1.78E-23	Down	-9.86E-01	2.72E-13		Unigene35135_All//gi|115450825|ref|NP_001049013.1|//1.00E-177//Os03g0157300 [Oryza sativa Japonica Group] >gi|113547484|dbj|BAF10927.1|Os03g0157300 [Oryza sativa Japonica Group]	Unigene35135_All//1.00E-175//AT4G35920| MCA1 (mid1-complementing activity 1)	Unigene35135_All//0.00E+00//TC170673				nr +
Unigene35138_All	1580	24.64	11.16	20.86	7.50	4.62	5.12	1.53	1.11	1.21	-1.14E+00	2.60E-35	Down	-2.40E-01	8.84E-03		-7.00E-01	3.75E-06		-5.52E-01	6.18E-04		-4.57E-01	2.33E-01		-3.34E-01	3.64E-01		Unigene35138_All//gi|17065222|gb|AL32765.1|//1.00E-141//Unknown protein [Arabidopsis thaliana]	Unigene35138_All//4.00E-120//AT1G05140| membrane-associated zinc metalloprotease, putative	Unigene35138_All//0.00E+00//TC162538				nr +
Unigene35140_All	1530	25.37	10.70	15.17	8.73	4.79	3.78	1.52	1.83	0.65	-1.25E+00	2.54E-40	Down	-7.42E-01	9.93E-17		-8.64E-01	1.17E-09		-1.21E+00	1.25E-14	Down	2.68E-01	4.62E-01		-1.22E+00	9.07E-04	Down	Unigene35140_All//gi|17065222|gb|AL32765.1|//1.00E-164//Unknown protein [Arabidopsis thaliana]	Unigene35140_All//5.00E-144//AT1G05140| membrane-associated zinc metalloprotease, putative	Unigene35140_All//0.00E+00//TC162538				nr +
Unigene35142_All	2014	5.51	4.40	3.17	6.16	5.97	8.30	6.00	2.84	3.26	-3.23E-01	6.68E-02		-7.96E-01	7.37E-06		-4.56E-02	8.40E-01		4.30E-01	1.45E-03		-1.08E+00	8.71E-13	Down	-8.79E-01	1.16E-09		Unigene35142_All//gi|225427967|ref|XP_002277572.1|//0.00E+00//PREDICTED: similar to FIO1 (FIONA1) [Vitis vinifera]	Unigene35142_All//3.00E-161//AT2G21070| FIO1 (FIONA1); methyltransferase	Unigene35142_All//0.00E+00//TC149932				nr -
Unigene35143_All	1452	17.12	10.96	8.36	36.33	57.75	86.81	37.36	64.22	63.43	-6.43E-01	4.28E-09		-1.03E+00	1.07E-18	Down	6.69E-01	2.54E-36		1.26E+00	1.49E-140	Up	7.82E-01	1.67E-54		7.64E-01	5.31E-53		Unigene35143_All//gi|297718133|gb|AD893659.2|//1.00E-17//indole-3-acetic acid inducible 26 [Arabidopsis thaliana]	Unigene35143_All//1.00E-13//AT3G16500| PAP1 (PHYTOCHROME-ASSOCIATED PROTEIN 1); transcription factor	Unigene35143_All//0.00E+00//TC132338				nr -
Unigene35144_All	2965	1.16	2.56	1.58	3.46	2.72	3.15	7.70	6.48	5.71	1.14E+00	1.93E-07	Up	4.41E-01	1.38E-01		-3.49E-01	4.89E-02		-1.34E-01	5.31E-01		-2.48E-01	1.99E-02		-4.31E-01	1.50E-05		Unigene35144_All//gi|42573025|ref|NP_974609.1|//1.00E-134//calcineurin-like phosphoesterase family protein [Arabidopsis thaliana] >gi|186513242|ref|NP_001119045.1|calcineurin-like phosphoesterase family protein [Arabidopsis thaliana] >gi|31711726|gb|AAP68219.1|At4g24730 [Arabidopsis thaliana]	Unigene35144_All//2.00E-135//AT4G24730| calcineurin-like phosphoesterase family protein	Unigene35144_All//0.00E+00//TC161823				nr +
Unigene35145_All	3796	1.16	0.92	0.51	4.21	4.98	4.40	5.49	3.68	3.41	-3.30E-01	2.69E-01		-1.20E+00	1.03E-04	Down	2.42E-01	6.76E-02		6.35E-02	6.83E-01		-5.78E-01	6.92E-08		-6.87E-01	9.37E-11		Unigene35145_All//gi|116310281|emb|CAH67300.1|//0.00E+00//OSIGBa0102D10.3 [Oryza sativa (indica cultivar-group)]	Unigene35145_All//5.00E-161//AT1G21730| kinesin-related protein (MKRP1)	Unigene35145_All//2.00E-29//TC134216				nr +

Unigene3515_All	1627	10.00	6.10	7.63	12.83	10.69	11.38	6.44	5.39	3.09	-7.12E-01	2.65E-07		-3.91E-01	7.10E-03		-2.63E-01	2.86E-02		-1.73E-01	2.03E-01		-2.57E-01	1.30E-01		-1.06E+00	2.59E-11	Down	Unigene3515_All//gi|30682162|ref|NP_192993.2|//4.00E-23//F-box family protein [Arabidopsis thaliana] >gi|145333023|ref|NP_001078377.1| F-box family protein [Arabidopsis thaliana] >gi|142989747|sp|Q9SU30.2|FB233_ARATH RecName: Full=F-box protein At4g12560	Unigene3515_All//1.00E-23//AT4G12560| F-box family protein	Unigene3515_All//0.00E+00//gi|164361808|gb|ES819102.1|ES819102				nr -
Unigene35150_All	1220	9.01	13.37	11.04	194.72	288.01	198.57	59.47	24.05	20.34	5.70E-01	3.38E-05		2.94E-01	7.83E-02		5.65E-01	1.73E-112		2.82E-02	5.08E-01		-1.31E+00	2.84E-98	Down	-1.55E+00	1.95E-130	Down	Unigene35150_All//gi|9665091|gb|AAF97282.1|AC010164_4//1.00E-105//Hypothetical protein [Arabidopsis thaliana] >gi|17979549|gb|AAL50109.1| At1g33800/F14M2_23 [Arabidopsis thaliana] >gi|20453345|gb|AAM19911.1| At1g33800/F14M2_23 [Arabidopsis thaliana]	Unigene35150_All//1.00E-99//AT1G33800| unknown protein	Unigene35150_All//0.00E+00//TC136179				nr +
Unigene35151_All	1247	0.84	0.65	0.68	7.75	4.78	5.54	40.04	2.45	3.10	-3.68E-01	5.90E-01		-2.97E-01	6.42E-01		-6.98E-01	4.17E-05		-4.84E-01	8.56E-03		-4.03E+00	2.94E-259	Down	-3.69E+00	5.42E-250	Down	Unigene35151_All//gi|9665091|gb|AAF97282.1|AC010164_4//1.00E-103//Hypothetical protein [Arabidopsis thaliana] >gi|17979549|gb|AAL50109.1| At1g33800/F14M2_23 [Arabidopsis thaliana] >gi|20453345|gb|AAM19911.1| At1g33800/F14M2_23 [Arabidopsis thaliana]	Unigene35151_All//1.00E-99//AT1G33800| unknown protein	Unigene35151_All//2.00E-175//TC136179				nr +
Unigene35156_All	714	0.95	3.55	2.01	2.93	3.23	3.99	3.20	2.81	3.40	1.90E+00	1.79E-05	Up	1.08E+00	6.63E-02		1.41E-01	8.04E-01		4.44E-01	2.67E-01		-1.87E-01	6.29E-01		9.00E-02	8.07E-01		Unigene35156_All//gi|115464863|ref|NP_001056031.1|//2.00E-08//Os05g0513900 [Oryza sativa Japonica Group] >gi|113579582|dbj|BAF17945.1| Os05g0513900 [Oryza sativa Japonica Group]	Unigene35156_All//3.00E-09//AT2G14260| PIP: aminopeptidase	Unigene35156_All//4.00E-157//gi|21093459|gb|BQ405772.1|BQ405772		ko00330|Arginine and proline metabolism		nr +
Unigene35158_All	1972	12.79	12.18	16.66	7.63	8.33	12.25	7.55	2.50	7.94	-7.04E-02	5.90E-01		3.82E-01	8.70E-05		1.27E-01	4.43E-01		6.84E-01	2.90E-10		-1.59E+00	1.02E-27	Down	7.31E-02	6.12E-01		Unigene35158_All//gi|229609829|gb|ACQ83530.1|//1.00E-172//CBL-interacting protein kinase 14 [Vitis vinifera]	Unigene35158_All//2.00E-137//AT5G57630| CIPK21 (CBL-interacting protein kinase 21); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene35158_All//0.00E+00//TC137996		ko04140|Regulation of autophagy		nr -
Unigene35159_All	2031	2.22	3.24	3.22	1.94	1.75	2.18	1.27	0.41	0.71	5.50E-01	1.68E-02		5.42E-01	2.49E-02		-1.50E-01	6.57E-01		1.70E-01	6.37E-01		-1.63E+00	1.43E-05	Down	-8.47E-01	1.24E-02		Unigene35159_All//gi|229609829|gb|ACQ83530.1|//0.00E+00//CBL-interacting protein kinase 14 [Vitis vinifera]	Unigene35159_All//2.00E-152//AT5G57630| CIPK21 (CBL-interacting protein kinase 21); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene35159_All//0.00E+00//gi|164350647|gb|ES831384.1|ES831384		ko04140|Regulation of autophagy		nr +
Unigene3516_All	1484	37.27	215.55	76.07	29.27	41.23	57.98	22.22	56.98	74.55	2.53E+00	0.00E+00	Up	1.03E+00	6.77E-83	Up	4.94E-01	1.18E-15		9.86E-01	3.80E-65		1.36E+00	2.80E-121	Up	1.75E+00	1.88E-233	Up	Unigene3516_All//gi|295913545|gb|ADG58020.1|//3.00E-38//transcription factor [Lycoris longituba]	Unigene3516_All//4.00E-23//AT1G32700| zinc-binding family protein	Unigene3516_All//0.00E+00//TC147946	PLATZ			nr -
Unigene35160_All	1430	71.86	153.89	78.50	62.84	218.94	440.01	15.76	45.51	33.18	1.10E+00	6.97E-184	Up	1.28E-01	1.75E-02		1.80E+00	0.00E+00	Up	2.81E+00	0.00E+00	Up	1.53E+00	1.20E-111	Up	1.07E+00	1.64E-48	Up	Unigene35160_All//gi|223452540|gb|ACM89597.1|//1.00E-154//leucine rich repeat protein [Glycine max]	Unigene35160_All//2.00E-150//AT3G20820| leucine-rich repeat family protein	Unigene35160_All//0.00E+00//TC151330		ko04626|Plant-pathogen interaction		nr -
Unigene35162_All	2524	0.66	1.55	1.50	2.33	2.05	2.31	3.90	3.94	3.77	1.22E+00	1.30E-04	Up	1.18E+00	4.46E-04	Up	-1.87E-01	5.14E-01		-1.28E-02	9.53E-01		1.40E-02	9.67E-01		-4.91E-02	7.80E-01		Unigene35162_All//gi|145338256|ref|NP_187459.2|//7.00E-79//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene35162_All//1.00E-67//AT3G08020| protein binding / zinc ion binding	Unigene35162_All//0.00E+00//gi|78324290|gb|DT544564.1|DT544564				nr +
Unigene35163_All	1834	37.46	26.94	21.51	99.41	100.38	76.68	41.34	12.42	19.33	-4.76E-01	4.42E-14		-8.00E-01	3.62E-33		1.39E-02	8.13E-01		-3.75E-01	3.87E-25		-1.73E+00	6.52E-156	Down	-1.10E+00	3.88E-80	Down	Unigene35163_All//gi|16209720|gb|AAL14415.1|//1.00E-60//At2g35880/F11F19.21 [Arabidopsis thaliana] >gi|20197995|gb|AAD21469.2| expressed protein [Arabidopsis thaliana]	Unigene35163_All//2.00E-45//AT2G35880| FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32330.3); Has 14997 Blast hits to 8919 proteins in 586 species: Archae - 10; Bacteria - 1037; Metazoa - 6567; Fungi - 1700; Plants - 594; Viruses - 59; Other Eukaryotes - 5030 (source: NCBI BLink).	Unigene35163_All//0.00E+00//TC133602				nr +
Unigene35165_All	978	15.19	5.08	8.22	8.46	5.14	2.22	0.52	0.09	1.43	-1.58E+00	1.88E-22	Down	-8.86E-01	5.41E-09		-7.18E-01	1.17E-04		-1.93E+00	5.95E-18	Down	-2.60E+00	2.05E-02		1.46E+00	4.26E-03		Unigene35165_All//gi|42567801|ref|NP_568258.2|//1.00E-98//dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2) [Arabidopsis thaliana] >gi|28194047|gb|AAO33381.1|AF46575 5_1 dihydropyrimidine amidohydrolase [Arabidopsis thaliana] >gi|9759387|dbj|BAB10038.1| dihydropyrimidinase [Arabidopsis thaliana]	Unigene35165_All//2.00E-96//AT5G12200| dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2)	Unigene35165_All//7.00E-36//ES816078		ko00240|Pyrimidine metabolism//ko00410|beta-Alanine metabolism//ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene35166_All	2389	15.81	2.16	6.24	9.49	3.53	2.33	0.09	0.09	0.57	-2.87E+00	1.18E-118	Down	-1.34E+00	2.45E-42	Down	-1.43E+00	6.33E-36	Down	-2.03E+00	1.29E-51	Down	-1.64E-02	1.02E+00		2.68E+00	1.36E-05	Up	Unigene35166_All//gi|42567801|ref|NP_568258.2|//1.00E-163//dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2) [Arabidopsis thaliana] >gi|28194047|gb|AAO33381.1|AF46575 5_1 dihydropyrimidine amidohydrolase [Arabidopsis thaliana] >gi|9759387|dbj|BAB10038.1| dihydropyrimidinase [Arabidopsis thaliana]	Unigene35166_All//2.00E-162//AT5G12200| dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2)	Unigene35166_All//0.00E+00//ES807046		ko00240|Pyrimidine metabolism//ko00410|beta-Alanine metabolism//ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene35167_All	798	4.07	4.00	3.00	30.40	21.88	17.94	25.54	22.00	8.79	-2.32E-02	9.65E-01		-4.37E-01	2.34E-01		-4.75E-01	3.17E-06		-7.61E-01	2.10E-12		-2.15E-01	6.36E-02		-1.54E+00	5.87E-37	Down	Unigene35167_All//gi|290578589|gb|ADB51189.1|//2.00E-16//globulin [Vitis berlandieri x Vitis riparia]	Unigene35167_All//3.00E-11//AT1G07750| cupin family protein	Unigene35167_All//3.00E-145//TC130805				nr +
Unigene35168_All	1987	14.14	12.42	8.25	123.55	89.34	54.19	82.18	69.20	52.31	-1.87E-01	8.43E-02		-7.77E-01	3.02E-13		-4.68E-01	4.66E-57		-1.19E+00	4.49E-254	Down	-2.48E-01	3.16E-12		-6.52E-01	3.80E-71		Unigene35168_All//gi|290578589|gb|ADB51189.1|//3.00E-82//globulin [Vitis berlandieri x Vitis riparia]	Unigene35168_All//1.00E-45//AT1G07750| cupin family protein	Unigene35168_All//0.00E+00//ES822138				nr -
Unigene3517_All	1149	7.97	4.28	2.13	13.14	9.68	6.56	3.94	3.38	2.60	-8.98E-01	3.01E-06		-1.90E+00	2.86E-17	Down	-4.41E-01	1.14E-03		-1.00E+00	2.66E-12	Down	-2.19E-01	4.33E-01		-5.99E-01	1.45E-02		Unigene3517_All//gi|227438217|gb|ACF30598.1|//3.00E-14//disease resistance protein [Brassica rapa subsp. pekinensis]		Unigene3517_All//2.00E-24//TC157110			GO:0005488	nr -
Unigene35170_All	1895	2.10	4.41	4.16	5.20	11.98	7.77	0.00	0.00	0.00	1.07E+00	1.95E-07	Up	9.87E-01	5.61E-06		1.20E+00	3.43E-26	Up	5.78E-01	5.16E-05		null	null		null	null		Unigene35170_All//gi|224140641|ref|XP_002323690.1|//0.00E+00//auxin efflux carrier component, auxin transport protein [Populus trichocarpa] >gi|222868320|gb|EEF05451.1| auxin efflux carrier component, auxin transport protein [Populus trichocarpa]	Unigene35170_All//1.00E-169//AT5G01990| auxin efflux carrier family protein	Unigene35170_All//0.00E+00//gi|48803661|gb|CO104975.1|CO104975				nr +
Unigene35173_All	1670	2.29	5.70	3.86	2.80	1.81	2.62	33.42	85.19	44.51	1.32E+00	2.74E-11	Up	7.54E-01	1.76E-03		-6.28E-01	1.79E-02		-9.61E-02	7.49E-01		1.35E+00	9.01E-202	Up	4.14E-01	7.49E-15		Unigene35173_All//gi|225452181|ref|XP_002265308.1|//0.00E+00//PREDICTED: similar to LHT1 (LYSINE HISTIDINE TRANSPORTER 1); amino acid transmembrane transporter [Vitis vinifera]	Unigene35173_All//4.00E-179//AT5G40780| LHT1; amino acid transmembrane transporter	Unigene35173_All//0.00E+00//TC146709				nr +
Unigene35174_All	2774	9.79	20.90	12.17	16.23	13.69	26.33	21.28	42.22	55.75	1.09E+00	1.46E-48	Up	3.14E-01	1.19E-03		-2.46E-01	1.24E-03		6.98E-01	6.75E-31		9.89E-01	3.05E-101		1.39E+00	6.53E-234	Up	Unigene35174_All//gi|15240634|ref|NP_199832.1|//0.00E+00//QS (QUINOLINATE SYNTHASE); 4 iron, 4 sulfur cluster binding / enzyme activator/ protein homodimerization/ quinolinate synthetase A [Arabidopsis thaliana]	Unigene35174_All//0.00E+00//AT5G50210| QS (QUINOLINATE SYNTHASE); 4 iron, 4 sulfur cluster binding / enzyme activator/ protein homodimerization/ quinolinate synthetase A	Unigene35174_All//0.00E+00//TC176610		ko00760|Nicotinate and nicotinamide metabolism		nr +
Unigene35178_All	3039	27.10	16.19	22.01	24.54	29.19	18.09	5.70	6.44	1.44	-7.43E-01	2.88E-36		-3.00E-01	3.47E-07		2.50E-01	1.13E-06		-4.40E-01	3.74E-14		1.74E-01	1.54E-01		-1.98E+00	1.13E-44	Down	Unigene35178_All//gi|1771162|emb|CAA67430.1|//0.00E+00//SBT2 [Solanum lycopersicum] >gi|3687307|emb|CAA07000.1| subtilisin-like protease [Solanum lycopersicum]	Unigene35178_All//0.00E+00//AT5G51750| ATSBT1.3 (ARABIDOPSIS THALIANA SUBTILASE 1.3); identical protein binding / serine-type endopeptidase	Unigene35178_All//0.00E+00//TC161117				nr +
Unigene35179_All	1009	8.82	15.57	7.92	12.54	12.93	7.34	5.15	4.10	2.49	8.21E-01	8.73E-09		-1.55E-01	4.81E-01		4.47E-02	8.18E-01		-7.73E-01	6.02E-07		-3.30E-01	1.84E-01		-1.05E+00	5.78E-06	Down	Unigene35179_All//gi|242096250|ref|XP_002438615.1|//1.00E-06//hypothetical protein SORBIDRAFT_10g022850 [Sorghum bicolor] >gi|241916838|gb|EER89982.1| hypothetical protein SORBIDRAFT_10g022850 [Sorghum bicolor]		Unigene35179_All//1.00E-58//TC168210				nr +
Unigene35181_All	1939	9.31	4.31	4.15	17.50	18.75	27.41	46.34	21.30	27.00	-1.11E+00	4.68E-16	Down	-1.17E+00	1.38E-16	Down	1.00E-01	3.37E-01		6.48E-01	5.97E-20		-1.12E+00	1.19E-95	Down	-7.79E-01	8.32E-54		Unigene35181_All//gi|133711722|gb|AB036543.1|//0.00E+00//plastid enolase [Helianthus annuus]	Unigene35181_All//0.00E+00//AT1G74030| enolase, putative	Unigene35181_All//0.00E+00//gi|78354821|gb|DT575095.1|DT575095		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation		nr -
Unigene35182_All	919	2.90	5.40	3.42	1.57	1.27	0.44	2.30	3.32	5.16	8.96E-01	9.47E-04		2.36E-01	5.41E-01		-3.03E-01	5.95E-01		-1.83E+00	1.94E-03		5.29E-01	1.04E-01		1.17E+00	2.70E-06	Up	Unigene35182_All//gi|224143627|ref|XP_002325021.1|//1.00E-118//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222866455|gb|EEF03586.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene35182_All//3.00E-102//AT1G35190| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene35182_All//0.00E+00//gi|73860852|gb|DT463591.1|DT463591				nr -
Unigene35183_All	765	0.96	3.31	1.53	0.26	0.81	0.06	1.38	2.62	2.08	1.79E+00	4.01E-05	Up	6.78E-01	3.04E-01		1.64E+00	1.06E-01		-2.14E+00	3.47E-01		9.25E-01	2.36E-02		5.92E-01	1.95E-01					Unigene35183_All//9.00E-155//gi|13351654|gb|BG442002.1|BG442002				

Unigene35185_All	2701	14.51	16.00	13.09	54.41	45.46	52.27	0.81	21.01	2.21	1.41E-01	1.09E-01			-1.48E-01	1.29E-01		-2.59E-01	1.58E-11			-5.78E-02	2.58E-01		4.69E+00	0.00E+00	Up	1.44E+00	2.27E-10	Up	Unigene35185_All//gi|84453182|dbj|BAE71188.1|//1.00E-100//BEL1-like homeodomain transcription factor [Trifolium pratense]	Unigene35185_All//5.00E-66//AT2G35940| BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene35185_All//0.00E+00//TC166443	HB			nr -
Unigene35186_All	2609	1.08	1.65	1.73	6.13	5.17	5.99	0.08	1.15	0.31	6.08E-01	3.80E-02			6.80E-01	2.21E-02		-2.44E-01	8.85E-02			-3.32E-02	8.48E-01		3.83E+00	2.02E-15	Up	1.91E+00	1.08E-02		Unigene35186_All//gi|84453182|dbj|BAE71188.1|//1.00E-139//BEL1-like homeodomain transcription factor [Trifolium pratense]	Unigene35186_All//1.00E-82//AT2G35940| BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene35186_All//0.00E+00//TC166443	HB			nr +
Unigene35187_All	2813	4.89	2.61	1.59	1.91	3.11	3.00	14.43	11.47	14.20	-9.05E-01	4.26E-09			-1.62E+00	1.10E-20	Down	7.01E-01	1.49E-04			6.51E-01	9.29E-04		-3.31E-01	9.73E-06		-2.26E-02	7.94E-01		Unigene35187_All//gi|22345212|gb|ACM89533.1|//0.00E+00//protein kinase [Glycine max]	Unigene35187_All//0.00E+00//AT5G59700| protein kinase, putative	Unigene35187_All//0.00E+00//gi|73865085|gb|DT467824.1|DT467824		ko04626|Plant-pathogen interaction		nr +
Unigene35190_All	983	16.82	15.36	16.25	1.17	2.38	3.03	0.99	2.00	1.54	-1.31E-01	3.91E-01			-4.96E-02	7.49E-01		1.03E+00	1.24E-02			1.38E+00	2.09E-04	Up	1.01E+00	1.45E-02		6.39E-01	1.73E-01		Unigene35190_All//gi|22330270|ref|NP_175981.2|//2.00E-96//ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75161659|sp|Q8VZK9.1|CSLE1_ARATH RecName: Full=Cellulose synthase-like protein E1; Short=AtCslE1	Unigene35190_All//2.00E-88//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene35190_All//0.00E+00//TC178738				nr +
Unigene35191_All	1076	1.17	2.92	1.53	6.53	4.61	3.61	35.05	29.33	254.66	1.32E+00	2.83E-04	Up		3.95E-01	4.55E-01		-5.02E-01	1.79E-02			-8.55E-01	7.99E-05		-2.57E-01	1.18E-03		2.86E+00	0.00E+00	Up	Unigene35191_All//gi|22330270|ref|NP_175981.2|//1.00E-73//ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75161659|sp|Q8VZK9.1|CSLE1_ARATH RecName: Full=Cellulose synthase-like protein E1; Short=AtCslE1	Unigene35191_All//6.00E-75//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene35191_All//0.00E+00//gi|13355118|gb|BG445550.1|BG445550				nr -
Unigene352_All	762	11.12	6.72	2.94	136.30	77.86	54.47	22.03	7.30	4.60	-7.28E-01	2.44E-04			-1.92E+00	3.04E-16	Down	-8.08E-01	1.95E-64			-1.32E+00	2.45E-127	Down	-1.59E+00	3.44E-31	Down	-2.26E+00	5.63E-51	Down	Unigene352_All//gi|170293773|gb|ACB12931.1|//7.00E-94//pectate lyase 1-27 [Populus tremula x Populus tremuloides]	Unigene352_All//2.00E-80//AT1G04680| pectate lyase family protein	Unigene352_All//0.00E+00//TC174630		ko00040|Pentose and glucuronate interconversions		nr +
Unigene35201_All	1754	44.86	44.60	41.53	107.92	76.25	63.32	41.58	29.07	17.92	-8.40E-03	9.14E-01			-1.11E-01	9.74E-02		-5.01E-01	5.45E-50			-7.69E-01	7.92E-95		-5.16E-01	6.10E-21		-1.21E+00	9.97E-91	Down	Unigene35201_All//gi|19568098|gb|AAL89456.1|//0.00E+00//osmotic stress-activated protein kinase [Nicotiana tabacum]	Unigene35201_All//7.00E-161//AT1G60940| SNRK2.10 (SNF1-RELATED PROTEIN KINASE 2.10); kinase	Unigene35201_All//0.00E+00//TC133150				nr -
Unigene35203_All	1852	17.12	127.44	31.23	62.91	55.97	71.65	10.71	127.64	6.71	2.90E+00	0.00E+00	Up		8.67E-01	4.06E-32		-1.69E-01	2.22E-04			1.88E-01	2.07E-05		3.58E+00	0.00E+00	Up	-6.74E-01	5.81E-10		Unigene35203_All//gi|30690149|ref|NP_851079.1|//9.00E-95//NOL1/NOP2/sun family protein [Arabidopsis thaliana] >gi|30690152|ref|NP_197990.2|NOL1/NOP2/sun family protein [Arabidopsis thaliana]	Unigene35203_All//3.00E-96//AT5G26180| NOL1/NOP2/sun family protein	Unigene35203_All//0.00E+00//TC156058				nr -
Unigene35204_All	2623	7.10	2.67	3.53	9.72	7.15	3.77	5.63	0.72	1.59	-1.41E+00	8.72E-24	Down		-1.01E+00	1.31E-13	Down	-4.43E-01	8.56E-06			-1.37E+00	3.48E-33	Down	-2.97E+00	5.49E-59	Down	-1.82E+00	5.16E-34	Down	Unigene35204_All//gi|18406005|ref|NP_565976.1|//0.00E+00//TTL3 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 3); binding / protein binding [Arabidopsis thaliana] >gi|13605845|gb|AAK32908.1|AF367321_1_1 At2g42580/F14N22.15 [Arabidopsis thaliana] >gi|20198077|gb|AAD22995.2| expressed protein [Arabidopsis thaliana] >gi|23506041|gb|AAN28880.1| At2g42580/F14N22.15 [Arabidopsis thaliana]	Unigene35204_All//0.00E+00//AT2G42580| TTL3 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 3); binding / protein binding	Unigene35204_All//0.00E+00//gi|109865572|gb|DW494548.1|DW494548		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene35208_All	2421	5.10	3.43	2.33	6.15	7.67	4.57	10.37	2.69	6.89	-5.71E-01	3.67E-04			-1.13E+00	5.48E-11	Down	3.18E-01	1.24E-02			-4.29E-01	2.89E-03		-1.95E+00	7.52E-61	Down	-5.89E-01	6.12E-10		Unigene35208_All//gi|30684447|ref|NP_193591.2|//0.00E+00//proline-rich family protein [Arabidopsis thaliana] >gi|22135814|gb|AAM91093.1|AT4g18560/F28J12_220 [Arabidopsis thaliana] >gi|28416477|gb|AAO42769.1|At4g18560/F28J12_220 [Arabidopsis thaliana]	Unigene35208_All//4.00E-123//AT4G18570| proline-rich family protein	Unigene35208_All//0.00E+00//TC178387		ko03040|Spliceosome		nr +
Unigene35214_All	1978	6.11	5.76	4.77	12.47	14.54	14.09	27.45	42.51	55.37	-8.42E-02	6.20E-01			-3.59E-01	3.96E-02		2.22E-01	3.15E-02			1.76E-01	1.20E-01		6.31E-01	4.13E-34		1.01E+00	1.05E-100	Up	Unigene35214_All//gi|297823651|ref|XP_002879708.1|//4.00E-59//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297325547|gb|EFH55967.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene35214_All//4.00E-58//AT2G37770| aldo/keto reductase family protein	Unigene35214_All//0.00E+00//TC154247		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene35216_All	3432	1.68	1.33	0.62	3.24	3.76	2.78	7.19	0.61	2.14	-3.36E-01	1.91E-01			-1.43E+00	1.27E-07	Down	2.17E-01	2.07E-01			-2.21E-01	2.42E-01		-3.56E+00	2.28E-116	Down	-1.75E+00	1.52E-53	Down	Unigene35216_All//gi|15228607|ref|NP_187018.1|//0.00E+00//C2 domain-containing protein [Arabidopsis thaliana]	Unigene35216_All//0.00E+00//AT3G03680| C2 domain-containing protein	Unigene35216_All//0.00E+00//gi|78330459|gb|DT550733.1|DT550733				nr -
Unigene35217_All	1579	2.62	0.99	1.69	3.31	4.08	3.06	6.83	1.51	2.17	-1.40E+00	8.73E-06	Down		-6.35E-01	4.40E-02		3.00E-01	2.31E-01			-1.14E-01	6.80E-01		-2.18E+00	1.36E-30	Down	-1.65E+00	4.67E-22	Down	Unigene35217_All//gi|141448032|gb|AB087608.1|//1.00E-151//chloroplast phosphoenolpyruvate/phosphate translocator [Pisum sativum]	Unigene35217_All//7.00E-123//AT5G33320| CUE1 (CAB UNDEREXPRESSED 1); antiporter/ triose-phosphate transmembrane transporter	Unigene35217_All//0.00E+00//gi|78337487|gb|DT557761.1|DT557761				nr +
Unigene35218_All	1704	2.00	0.48	1.47	3.24	2.16	2.25	7.02	1.79	3.34	-2.07E+00	6.67E-08	Down		-4.42E-01	2.23E-01		-5.86E-01	1.52E-02			-5.26E-01	3.95E-02		-1.97E+00	7.03E-30	Down	-1.07E+00	6.30E-13	Down	Unigene35218_All//gi|118196907|gb|ABK78670.1|//1.00E-154//plastid phosphoenolpyruvate/phosphate translocator [Brassica napus] >gi|187940348|gb|ACD39395.1| plastid phosphoenolpyruvate/phosphate translocator [Brassica napus]	Unigene35218_All//1.00E-127//AT5G33320| CUE1 (CAB UNDEREXPRESSED 1); antiporter/ triose-phosphate transmembrane transporter	Unigene35218_All//0.00E+00//gi|78345200|gb|DT565474.1|DT565474				nr +
Unigene35219_All	404	0.26	0.75	0.66	7.15	5.46	3.58	8.06	1.86	9.57	1.54E+00	3.23E-01			1.35E+00	4.09E-01		-3.91E-01	3.13E-01			-9.99E-01	6.40E-03		-2.11E+00	2.09E-09	Down	2.47E-01	3.94E-01		Unigene35219_All//gi|224128073|ref|XP_002320237.1|//5.00E-18//catechol o-methyltransferase related [Populus trichocarpa] >gi|222861010|gb|EEE98552.1| catechol o-methyltransferase related [Populus trichocarpa]	Unigene35219_All//1.00E-09//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene35219_All//0.00E+00//TC145383		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene35220_All	368	0.00	0.00	0.14	0.81	0.28	2.33	11.03	5.34	5.74	null	null			7.18E+00	6.35E-01		-1.53E+00	2.98E-01			1.52E+00	6.17E-02		-1.05E+00	1.24E-04	Down	-9.43E-01	3.37E-04		Unigene35220_All//gi|284437809|gb|ADB85561.1|//9.00E-14//O-methyltransferase-like protein [Prunus mume]	Unigene35220_All//3.00E-08//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene35220_All//7.00E-120//TC139144		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene35221_All	1254	8.93	4.97	8.92	41.95	25.95	54.85	71.04	31.56	50.99	-8.45E-01	8.17E-07			-1.80E-03	9.91E-01		-6.93E-01	4.13E-25			3.87E-01	2.15E-10		-1.17E+00	1.65E-101	Down	-4.78E-01	7.72E-23		Unigene35221_All//gi|224128073|ref|XP_002320237.1|//1.00E-135//catechol o-methyltransferase related [Populus trichocarpa] >gi|222861010|gb|EEE98552.1| catechol o-methyltransferase related [Populus trichocarpa]	Unigene35221_All//9.00E-96//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene35221_All//0.00E+00//TC145383		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene35223_All	1332	195.14	93.62	182.70	223.64	190.04	187.43	200.99	142.14	152.18	-1.06E+00	1.49E-205	Down		-9.51E-02	5.63E-03		-2.35E-01	4.68E-19			-2.55E-01	6.27E-20		-5.00E-01	2.20E-70		-4.01E-01	1.61E-48		Unigene35223_All//gi|468562|emb|CAA83436.1|//1.00E-172//sucrose carrier [Ricinus communis]	Unigene35223_All//1.00E-163//AT1G22710| SUC2 (SUCROSE-PROTON SYMPORTER 2); carbohydrate transmembrane transporter/ sucrose transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter	Unigene35223_All//0.00E+00//TC151803				nr -
Unigene35224_All	958	16.11	7.09	12.95	0.62	0.29	0.09	25.24	17.93	9.19	-1.18E+00	2.86E-15	Down		-3.15E-01	3.96E-02		-1.12E+00	2.26E-01			-2.73E+00	1.74E-02		-4.94E-01	5.72E-07		-1.46E+00	2.27E-40	Down	Unigene35224_All//gi|224089140|ref|XP_002308645.1|//1.00E-81//anion exchanger family protein [Populus trichocarpa] >gi|222854621|gb|EEE92168.1| anion exchanger family protein [Populus trichocarpa]	Unigene35224_All//1.00E-41//AT1G15460| BOR4 (REQUIRES HIGH BORON 4); anion exchanger	Unigene35224_All//1.00E-83//C0127117				nr -
Unigene35225_All	2443	19.23	10.52	21.12	0.61	0.45	0.33	17.29	44.43	12.00	-8.71E-01	2.26E-27			1.35E-01	1.06E-01		-4.39E-01	4.27E-01			-8.78E-01	1.13E-01		1.36E+00	4.26E-156	Up	-5.27E-01	2.67E-13		Unigene35225_All//gi|224058707|ref|XP_002299613.1|//0.00E+00//anion exchanger family protein [Populus trichocarpa] >gi|222846871|gb|EEE84418.1| anion exchanger family protein [Populus trichocarpa]	Unigene35225_All//0.00E+00//AT1G15460| BOR4 (REQUIRES HIGH BORON 4); anion exchanger	Unigene35225_All//2.00E-103//C0127117				nr +
Unigene35227_All	385	8.70	2.11	11.76	10.22	7.96	8.09	4.50	2.39	7.55	-2.05E+00	1.07E-07	Down		4.35E-01	1.48E-01		-3.61E-01	2.62E-01			-3.37E-01	3.16E-01		-9.15E-01	4.03E-02		7.46E-01	1.84E-02		Unigene35227_All//gi|296932945|gb|ADH93593.1|//5.00E-20//SNF5-type chromatin-remodeling complex protein [Glycine max] >gi|297179845|gb|ADI23919.1| SNF5 [Glycine max]	Unigene35227_All//8.00E-21//AT3G17590| BSH (BUSHY GROWTH); chromatin binding / protein binding	Unigene35227_All//6.00E-139//ES794507				nr +
Unigene35229_All	2539	2.84	2.14	1.97	6.42	5.76	4.71	7.14	6.26	15.55	-4.13E-01	6.18E-02			-5.29E-01	2.07E-02		-1.55E-01	3.20E-01			-4.45E-01	1.07E-03		-1.92E-01	1.33E-01		1.12E+00	2.07E-43	Up	Unigene35229_All//gi|140072137|gb|AB084804.1|//1.00E-179//Sugar transporter superfamily [Medicago truncatula]	Unigene35229_All//1.00E-163//AT5G12260| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: glycosyltransferase family protein 2 (TAIR:AT5G60700.1); Has 66 Blast hits to 66 proteins in 22 species: Archae - 0; Bacteria - 6; Metazoa - 0; Fungi - 12; Plants - 29; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink).	Unigene35229_All//0.00E+00//TC174142				nr +
Unigene35231_All	2540	13.97	2.93	6.29	17.14	12.15	23.13	12.18	5.28	8.20	-2.25E+00	1.48E-84	Down		-1.15E+00	2.12E-31	Down	-4.97E-01	1.27E-11			4.33E-01	6.91E-11		-1.21E+00	1.78E-37	Down	-5.71E-01	2.03E-11		Unigene35231_All//gi|297816148|ref|XP_002875957.1|//0.00E+00//EMB1796 [Arabidopsis lyrata subsp. lyrata] >gi|297321795|gb|EFH52216.1| EMB1796 [Arabidopsis lyrata subsp. lyrata]	Unigene35231_All//0.00E+00//AT3G49240| emb1796 (embryo defective 1796); ATP binding	Unigene35231_All//0.00E+00//TC130580				nr +

Unigene35232_All	1424	18.11	21.56	21.84	33.41	22.10	23.69	28.09	28.76	10.66	2.52E-01	1.22E-02		2.70E-01	8.84E-03		-5.96E-01	1.84E-17		-4.96E-01	2.28E-11		3.43E-02	7.13E-01		-1.40E+00	3.52E-62	Down	Unigene35232_All//gi|297816096|ref|XP_002875931.1|//7.00E-45//membrane-associated progesterone binding protein 3 [Arabidopsis lyrata subsp. lyrata] >gi|297321769|gb|EFH52190.1| membrane-associated progesterone binding protein 3 [Arabidopsis lyrata subsp. lyrata]	Unigene35232_All//3.00E-46//AT3G48890| ATMP2; heme binding	Unigene35232_All//0.00E+00//gi|48812173|gb|CO113486.1|CO113486				nr -
Unigene35233_All	3150	3.36	9.06	5.53	8.16	12.62	15.28	6.56	21.64	12.51	1.43E+00	1.38E-36	Up	7.20E-01	1.60E-07		6.29E-01	1.23E-15		9.05E-01	7.21E-32		1.72E+00	1.92E-138	Up	9.30E-01	4.35E-32		Unigene35233_All//gi|34499887|gb|AAQ73529.1|//1.00E-100//early flowering 3 [Mesembryanthemum crystallinum]	Unigene35233_All//4.00E-78//AT2G25930| ELF3 (EARLY FLOWERING 3); protein C-terminus binding / transcription factor	Unigene35233_All//0.00E+00//CO081427		ko04712|Circadian rhythm - plant		nr +
Unigene35236_All	2247	12.08	5.43	7.49	19.22	22.24	18.85	14.83	13.04	15.32	-1.15E+00	3.33E-25	Down	-6.90E-01	1.44E-10		2.10E-01	4.46E-03		-2.78E-02	7.79E-01		-1.85E-01	3.64E-02		4.70E-02	6.28E-01		Unigene35236_All//gi|28416687|gb|AA042874.1|//0.00E+00//At1g70550 [Arabidopsis thaliana]	Unigene35236_All//0.00E+00//AT1G70750| unknown protein	Unigene35236_All//0.00E+00//NP508247				nr -
Unigene35237_All	610	4.29	2.08	1.57	4.33	3.44	1.70	3.33	1.78	0.59	-1.05E+00	7.80E-03		-1.45E+00	6.62E-04	Down	-3.30E-01	4.24E-01		-1.35E+00	6.28E-04	Down	-9.01E-01	2.61E-02		-2.50E+00	1.27E-07	Down	Unigene35237_All//gi|226530818|ref|NP_001148776.1|//1.00E-56//cysteine-type peptidase [Zea mays] >gi|195622072|gb|ACG32866.1| cysteine-type peptidase [Zea mays]	Unigene35237_All//1.00E-54//AT5G04250| OTU-like cysteine protease family protein	Unigene35237_All//0.00E+00//TC174360				nr -
Unigene35238_All	1363	3.49	1.04	2.31	4.20	5.20	3.21	3.66	0.95	1.75	-1.75E+00	9.48E-09	Down	-6.00E-01	3.87E-02		3.08E-01	1.88E-01		-3.87E-01	1.37E-01		-1.95E+00	1.12E-12	Down	-1.06E+00	7.75E-06	Down	Unigene35238_All//gi|226530818|ref|NP_001148776.1|//1.00E-89//cysteine-type peptidase [Zea mays] >gi|195622072|gb|ACG32866.1| cysteine-type peptidase [Zea mays]	Unigene35238_All//7.00E-81//AT5G03330| OTU-like cysteine protease family protein	Unigene35238_All//0.00E+00//TC173767				nr -
Unigene35239_All	1317	1.39	0.96	0.89	10.86	8.63	5.18	3.72	0.95	2.39	-5.32E-01	2.70E-01		-6.45E-01	2.07E-01		-3.31E-01	2.29E-02		-1.07E+00	6.26E-13	Down	-1.97E+00	1.18E-12	Down	-6.40E-01	6.16E-03		Unigene35239_All//gi|226530818|ref|NP_001148776.1|//1.00E-78//cysteine-type peptidase [Zea mays] >gi|195622072|gb|ACG32866.1| cysteine-type peptidase [Zea mays]	Unigene35239_All//1.00E-75//AT5G04250| OTU-like cysteine protease family protein	Unigene35239_All//0.00E+00//AF121190				nr -
Unigene35240_All	898	4.54	1.30	5.51	2.22	0.81	0.40	0.00	0.00	0.09	-1.81E+00	6.13E-08	Down	2.79E-01	3.58E-01		-1.46E+00	8.85E-04	Down	-2.46E+00	3.20E-06	Down	null	null		6.47E+00	4.04E-01		Unigene35240_All//gi|6573167|gb|AAF17576.1|AF202182_1//7.00E-93//2'-hydroxy isoflavone/dihydroflavonol reductase homolog [Glycine max]	Unigene35240_All//1.00E-72//AT2G45400| BEN1; binding / catalytic/ coenzyme binding / oxidoreductase, acting on CH-OH group of donors	Unigene35240_All//0.00E+00//TC138378		ko00941|Flavonoid biosynthesis		nr +
Unigene35241_All	857	2.44	2.66	0.75	8.66	14.43	6.43	0.00	0.00	0.00	1.24E-01	7.62E-01		-1.71E+00	6.07E-04	Down	7.36E-01	1.09E-06		-4.30E-01	4.92E-02		null	null		null	null		Unigene35241_All//gi|6573167|gb|AAF17576.1|AF202182_1//9.00E-83//2'-hydroxy isoflavone/dihydroflavonol reductase homolog [Glycine max]	Unigene35241_All//3.00E-67//AT2G45400| BEN1; binding / catalytic/ coenzyme binding / oxidoreductase, acting on CH-OH group of donors	Unigene35241_All//0.00E+00//TC137347		ko00941|Flavonoid biosynthesis		nr -
Unigene35242_All	1183	9.60	5.31	7.25	13.52	12.72	7.75	1.50	0.39	0.03	-8.54E-01	5.30E-07		-4.05E-01	2.34E-02		-8.76E-02	6.07E-01		-8.03E-01	3.85E-09		-1.95E+00	5.37E-05	Down	-5.48E+00	8.92E-12	Down	Unigene35242_All//gi|124360320|gb|ABN08333.1|//1.00E-113//NAD-dependent epimerase/dehydratase [Medicago truncatula]	Unigene35242_All//4.00E-89//AT2G45400| BEN1; binding / catalytic/ coenzyme binding / oxidoreductase, acting on CH-OH group of donors	Unigene35242_All//0.00E+00//TC1600034		ko00941|Flavonoid biosynthesis		nr +
Unigene35243_All	1608	1.04	8.07	3.78	1.24	1.22	1.32	5.50	6.13	2.28	2.95E+00	6.83E-42	Up	1.86E+00	2.45E-11	Up	-2.17E-02	9.48E-01		9.12E-02	8.58E-01		1.59E-01	3.95E-01		-1.27E+00	1.48E-12	Down	Unigene35243_All//gi|15982862|gb|AAL09778.1|//1.00E-127//AT4g32140/F10N7_50 [Arabidopsis thaliana] >gi|21360499|gb|AAM47365.1| AT4g32140/F10N7_50 [Arabidopsis thaliana]	Unigene35243_All//1.00E-113//AT4G32140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF6, transmembrane (InterPro:IPR000620); BEST Arabidopsis thaliana protein match is: membrane protein (TAIR:AT3G07080.1); Has 1078 Blast hits to 1078 proteins in 273 species: Archae - 20; Bacteria - 294; Metazoa - 244; Fungi - 147; Plants - 41; Viruses - 0; Other Eukaryotes - 332 (source: NCBI BLink).	Unigene35243_All//0.00E+00//TC154349				nr -
Unigene35244_All	1733	0.72	5.38	2.06	0.52	0.91	0.76	2.51	3.71	1.36	2.89E+00	1.27E-29	Up	1.51E+00	2.50E-05	Up	8.21E-01	1.26E-01		5.47E-01	3.98E-01		5.64E-01	6.60E-03		-8.90E-01	4.13E-04		Unigene35244_All//gi|90399340|emb|CAJ86111.1|//1.00E-112//H0811D08.4 [Oryza sativa (indica cultivar-group)]	Unigene35244_All//5.00E-93//AT4G32140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF6, transmembrane (InterPro:IPR000620); BEST Arabidopsis thaliana protein match is: membrane protein (TAIR:AT3G07080.1); Has 1078 Blast hits to 1078 proteins in 273 species: Archae - 20; Bacteria - 294; Metazoa - 244; Fungi - 147; Plants - 41; Viruses - 0; Other Eukaryotes - 332 (source: NCBI BLink).	Unigene35244_All//0.00E+00//TC154349				nr -
Unigene35245_All	785	20.00	11.10	19.13	7.87	12.02	17.95	4.85	9.53	20.25	-8.49E-01	2.76E-09		-6.39E-02	6.88E-01		6.11E-01	5.88E-04		1.19E+00	7.39E-15	Up	9.75E-01	4.43E-07		2.06E+00	1.42E-42	Up	Unigene35245_All//gi|75158446|sp|Q8RUN2.1|LOG1_ARATH//3.00E-97//RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1; AltName: Full=Protein LONELY GUY 1 >gi|20197602|gb|AAM15149.1| expressed protein [Arabidopsis thaliana] >gi|20197733|gb|AAM15229.1| expressed protein [Arabidopsis thaliana]	Unigene35245_All//3.00E-90//AT2G28305| unknown protein	Unigene35245_All//0.00E+00//TC155733				nr -
Unigene35246_All	781	6.97	3.89	3.07	0.96	0.62	0.12	0.65	0.16	2.60	-8.40E-01	1.03E-03		-1.18E+00	1.42E-05	Down	-6.32E-01	4.37E-01		-3.05E+00	3.33E-03		-2.02E+00	5.20E-02		2.00E+00	6.22E-06	Up	Unigene35246_All//gi|75272473|sp|Q8L8B8.1|LOG3_ARATH//2.00E-93//RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG3; AltName: Full=Protein LONELY GUY 3	Unigene35246_All//1.00E-86//AT2G37210| Encodes a protein of unknown function. It has been crystallized and shown to be structurally almost identical to the protein encoded by At5g11950.	Unigene35246_All//0.00E+00//ES812867				nr +
Unigene35247_All	1006	9.62	12.54	12.23	6.49	6.57	11.22	5.09	9.31	21.31	3.82E-01	1.78E-02		3.46E-01	4.48E-02		1.89E-02	9.62E-01		7.91E-01	1.94E-06		8.72E-01	2.58E-07		2.07E+00	2.84E-57	Up	Unigene35247_All//gi|75158446|sp|Q8RUN2.1|LOG1_ARATH//1.00E-100//RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG1; AltName: Full=Protein LONELY GUY 1 >gi|20197602|gb|AAM15149.1| expressed protein [Arabidopsis thaliana] >gi|20197733|gb|AAM15229.1| expressed protein [Arabidopsis thaliana]	Unigene35247_All//4.00E-93//AT2G28305| unknown protein	Unigene35247_All//0.00E+00//TC155733				nr -
Unigene35248_All	2660	1.85	1.47	1.86	6.33	4.73	6.96	9.76	4.79	5.72	-3.34E-01	2.35E-01		1.00E-02	9.95E-01		-4.22E-01	9.31E-04		1.37E-01	3.78E-01		-1.03E+00	1.66E-24	Down	-7.71E-01	6.77E-16		Unigene35248_All//gi|30680505|ref|NP_179480.2|//0.00E+00//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene35248_All//0.00E+00//AT2G18900| transducin family protein / WD-40 repeat family protein	Unigene35248_All//0.00E+00//CO131341				nr -
Unigene35249_All	860	8.33	47.84	9.60	45.53	35.32	35.61	30.28	21.97	43.08	2.52E+00	3.64E-111	Up	2.04E-01	3.83E-01		-3.66E-01	3.32E-06		-3.55E-01	2.09E-05		-4.63E-01	1.02E-06		5.09E-01	4.57E-11		Unigene35249_All//gi|297802270|ref|XP_002869019.1|//5.00E-34//transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297314855|gb|EFH45278.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene35249_All//5.00E-38//AT2G23790| unknown protein	Unigene35249_All//0.00E+00//TC142026				nr -
Unigene35250_All	1925	1.49	14.08	2.16	9.57	4.90	4.25	15.00	10.86	21.17	3.24E+00	4.34E-95	Up	5.29E-01	9.26E-02		-9.66E-01	8.50E-16		-1.17E+00	4.17E-19	Down	-4.67E-01	1.91E-07		4.97E-01	1.25E-11		Unigene35250_All//gi|297802270|ref|XP_002869019.1|//1.00E-36//transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297314855|gb|EFH45278.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene35250_All//3.00E-39//AT2G23790| unknown protein	Unigene35250_All//0.00E+00//TC142026				nr -
Unigene35252_All	2544	8.97	7.99	10.13	10.24	11.75	9.73	5.09	7.66	28.80	-1.67E-01	1.80E-01		1.76E-01	1.45E-01		1.98E-01	5.40E-02		-7.40E-02	5.97E-01		5.90E-01	1.16E-07		2.50E+00	7.15E-245	Up	Unigene35252_All//gi|7076798|emb|CAB75913.1|//0.00E+00//probable serine/threonine-specific protein kinase [Arabidopsis thaliana]	Unigene35252_All//0.00E+00//AT3G55550| lectin protein kinase, putative	Unigene35252_All//0.00E+00//TC144105		ko04626|Plant-pathogen interaction		nr -
Unigene35253_All	2018	0.67	5.72	2.35	2.32	4.81	9.38	76.49	139.35	142.16	3.09E+00	5.31E-39	Up	1.80E+00	1.25E-08	Up	1.05E+00	2.51E-09	Up	2.01E+00	7.14E-42	Up	8.65E-01	8.64E-194		8.94E-01	1.50E-213		Unigene35253_All//gi|116804319|gb|ABK27327.1|//0.00E+00//vacuolar citrate/H+ symporter [Citrus sinensis]	Unigene35253_All//0.00E+00//AT5G47560| TDT (TONOPLAST DICARBOXYLATE TRANSPORTER); malate transmembrane transporter/ sodium:dicarboxylate symporter	Unigene35253_All//0.00E+00//gi|109864658|gb|DW493634.1|DW493634				nr +
Unigene35254_All	2212	18.14	14.04	17.55	46.84	52.66	48.65	25.73	8.54	15.36	-3.70E-01	1.12E-05		-4.79E-02	6.18E-01		1.69E-01	2.37E-04		5.48E-02	3.92E-01		-1.59E+00	1.23E-103	Down	-7.44E-01	8.18E-32		Unigene35254_All//gi|83853834|gb|ABC47866.1|//1.00E-162//remorin [Glycine max]	Unigene35254_All//7.00E-119//AT1G45207| remorin family protein	Unigene35254_All//0.00E+00//TC142648				nr +
Unigene3526_All	1774	5.37	20.45	7.74	8.93	12.73	14.28	14.90	9.28	10.94	1.93E+00	1.75E-70	Up	5.29E-01	7.64E-04		5.12E-01	1.85E-06		6.78E-01	1.41E-10		-6.82E-01	7.67E-13		-4.46E-01	1.27E-06		Unigene3526_All//gi|18414983|ref|NP_567543.1|//1.00E-143//AGD8 (ARF-GAP DOMAIN 8): ARF GTPase activator/ DNA binding / zinc ion binding [Arabidopsis thaliana] >gi|75244593|sp|Q8H100.1|AGD8_ARATH RecName: Full=Probable ADP-ribosylation factor GTPase-activating protein AGD8; Short=ARF GAP AGD8; AltName: Full=Protein ARF-GAP DOMAIN 8; Short=AtAGD8	Unigene3526_All//5.00E-131//AT4G17890| AGD8 (ARF-GAP DOMAIN 8); ARF GTPase activator/ DNA binding / zinc ion binding	Unigene3526_All//0.00E+00//TC171854		ko04144|Endocytosis		nr -

Unigene35260_All	2033	4.04	2.94	5.84	3.72	2.86	3.29	11.65	14.10	313.07	-4.58E-01	2.47E-02		5.32E-01	1.86E-03		-3.80E-01	7.24E-02		-1.80E-01	4.71E-01		2.76E-01	2.74E-03		4.75E+00	0.00E+00	Up	Unigene35260_All//gi|94442475|gb|ABF19025.1|/4.00E-33//At5g40690 [Arabidopsis thaliana]	Unigene35260_All//2.00E-29//AT3G01710| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27350.1); Has 1029 Blast hits to 851 proteins in 111 species: Archae - 0; Bacteria - 24; Metazoa - 456; Fungi - 52; Plants - 192; Viruses - 7; Other Eukaryotes - 298 (source: NCBI BLink).	Unigene35260_All//0.00E+00//gi|109881552|gb|DW510522.1|DW510522				nr +
Unigene35261_All	1081	12.29	17.30	19.06	11.80	9.52	7.60	9.54	4.52	5.71	4.93E-01	1.14E-04		6.33E-01	3.97E-07		-3.09E-01	5.11E-02		-6.34E-01	3.82E-05		-1.08E+00	5.26E-11	Down	-7.40E-01	1.84E-06		Unigene35261_All//gi|297802642|ref|XP_002869205.1|//3.00E-86//carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315041|gb|EFH45464.1| carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35261_All//1.00E-85//AT4G33580| carbonic anhydrase family protein / carbonate dehydratase family protein	Unigene35261_All//0.00E+00//gi|48741776|gb|C0072295.1|C0072295		ko00910|Nitrogen metabolism		nr +
Unigene35262_All	972	2.42	1.36	2.36	2.46	1.38	0.46	0.52	0.60	0.45	-8.38E-01	4.35E-02		-4.02E-02	9.38E-01		-8.32E-01	3.36E-02		-2.40E+00	3.65E-07	Down	2.06E-01	8.00E-01		-2.12E-01	7.92E-01		Unigene35262_All//gi|297802642|ref|XP_002869205.1|//6.00E-47//carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315041|gb|EFH45464.1| carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35262_All//2.00E-46//AT4G33580| carbonic anhydrase family protein / carbonate dehydratase family protein	Unigene35262_All//0.00E+00//TC1134616		ko00910|Nitrogen metabolism		nr -
Unigene35263_All	1294	9.87	11.00	8.89	10.89	6.49	7.15	5.88	2.87	1.63	1.57E-01	3.45E-01		-1.51E-01	3.93E-01		-7.47E-01	5.15E-08		-6.07E-01	3.03E-05		-1.03E+00	7.87E-08	Down	-1.85E+00	2.38E-18	Down	Unigene35263_All//gi|297802642|ref|XP_002869205.1|//1.00E-89//carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315041|gb|EFH45464.1| carbonic anhydrase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35263_All//1.00E-88//AT4G33580| carbonic anhydrase family protein / carbonate dehydratase family protein	Unigene35263_All//0.00E+00//gi|48741776|gb|C0072295.1|C0072295		ko00910|Nitrogen metabolism		nr +
Unigene35266_All	2033	6.54	15.48	8.96	53.88	67.04	59.23	26.39	41.45	32.80	1.24E+00	1.49E-32	Up	4.55E-01	7.35E-04		3.15E-01	3.63E-15		1.36E-01	5.05E-03		6.51E-01	4.65E-36		3.14E-01	2.28E-08		Unigene35266_All//gi|225446337|ref|XP_002272136.1|//6.00E-69//PREDICTED: similar to ring domain containing protein isoform 2 [Vitis vinifera] >gi|225446339|ref|XP_002272107.1| PREDICTED: similar to ring domain containing protein isoform 1 [Vitis vinifera]	Unigene35266_All//8.00E-42//AT4G03510| RMA1; protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene35266_All//0.00E+00//TC162232		ko04146|Peroxisome		nr -
Unigene35267_All	2088	2.98	4.03	1.17	2.86	2.03	5.13	2.65	1.04	0.65	4.34E-01	3.18E-02		-1.35E+00	1.66E-07	Down	-4.97E-01	3.41E-02		8.40E-01	9.80E-07		-1.35E+00	1.29E-08	Down	-2.03E+00	2.81E-15	Down	Unigene35267_All//gi|38194466|gb|AAR13240.1|//0.00E+00//KUP-related potassium transporter [Lotus japonicus]	Unigene35267_All//2.00E-129//AT2G30070| ATKT1 (POTASSIUM TRANSPORTER 1); potassium ion transmembrane transporter	Unigene35267_All//0.00E+00//gi|78327698|gb|DT547972.1|DT547972				nr +
Unigene35268_All	486	9.15	6.46	4.16	10.97	11.69	13.47	2.00	1.55	5.98	-5.02E-01	8.18E-02		-1.14E+00	1.91E-04	Down	9.22E-02	7.85E-01		2.97E-01	2.35E-01		-3.70E-01	5.87E-01		1.58E+00	3.88E-06	Up			Unigene35268_All//1.00E-32//TC140230				
Unigene35271_All	2758	2.30	6.25	2.59	4.12	5.12	8.30	4.49	19.50	10.13	1.44E+00	1.23E-22	Up	1.73E-01	4.84E-01		3.14E-01	3.78E-02		1.01E+00	1.87E-18	Up	2.12E+00	2.18E-144	Up	1.17E+00	3.67E-33	Up	Unigene35271_All//gi|115455533|ref|NP_001051367.1|//1.00E-129//Os03g0764300 [Oryza sativa Japonica Group] >gi|108711235|gb|ABF99030.1| Protein kinase domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|108711236|gb|ABF99031.1| Protein kinase domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549838|dbj|BAF13281.1| Os03g0764300 [Oryza sativa Japonica Group]	Unigene35271_All//1.00E-105//AT5G66850| MAPKKK5; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene35271_All//0.00E+00//gi|78342197|gb|DT562471.1|DT562471		ko04626|Plant-pathogen interaction		nr +
Unigene35272_All	2829	4.18	3.56	1.62	4.31	4.00	3.74	5.72	3.21	3.46	-2.30E-01	1.91E-01		-1.37E+00	5.03E-14	Down	-1.07E-01	5.87E-01		-2.08E-01	2.51E-01		-8.36E-01	2.62E-11		-7.25E-01	2.63E-09		Unigene35272_All//gi|42565615|ref|NP_190175.2|//0.00E+00//RUS1 (ROOT UVB SENSITIVE 1) [Arabidopsis thaliana]	Unigene35272_All//2.00E-175//AT3G45890| RUS1 (ROOT UVB SENSITIVE 1)	Unigene35272_All//0.00E+00//ES807323				nr -
Unigene35275_All	765	14.64	4.70	5.85	25.66	17.74	30.35	58.42	19.50	28.43	-1.64E+00	5.98E-18	Down	-1.32E+00	1.11E-12	Down	-5.33E-01	3.16E-06		2.42E-01	4.24E-02		-1.58E+00	6.43E-81	Down	-1.04E+00	1.13E-43	Down	Unigene35275_All//gi|297848606|ref|XP_002892184.1|//5.00E-15//ATPHB2 [Arabidopsis lyrata subsp. lyrata] >gi|297338026|gb|EFH68443.1| ATPHB2 [Arabidopsis lyrata subsp. lyrata]	Unigene35275_All//3.00E-15//AT2G20530| ATPHB6 (PROHIBITIN 6)	Unigene35275_All//0.00E+00//TC154106				nr -
Unigene35276_All	835	18.42	9.47	10.27	21.48	22.35	28.67	75.45	40.54	32.68	-9.61E-01	4.83E-11		-8.43E-01	1.35E-08		5.76E-02	7.41E-01		4.17E-01	1.45E-04		-8.96E-01	1.11E-46		-1.21E+00	9.84E-78	Down	Unigene35276_All//gi|297848606|ref|XP_002892184.1|//5.00E-22//ATPHB2 [Arabidopsis lyrata subsp. lyrata] >gi|297338026|gb|EFH68443.1| ATPHB2 [Arabidopsis lyrata subsp. lyrata]	Unigene35276_All//3.00E-22//AT1G03860| ATPHB2 (PROHIBITIN 2)	Unigene35276_All//0.00E+00//TC153736				nr -
Unigene35277_All	2857	2.93	6.93	5.16	5.25	7.36	8.54	7.06	5.94	6.07	1.24E+00	9.48E-21	Up	8.17E-01	6.85E-08		4.89E-01	1.31E-05		7.02E-01	8.19E-11		-2.49E-01	2.95E-02		-2.19E-01	5.00E-02		Unigene35277_All//gi|110289573|gb|AAP35009.2|//9.00E-65//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene35277_All//0.00E+00//AT5G47400| unknown protein	Unigene35277_All//0.00E+00//TC173839		ko00600|Sphingolipid metabolism		nr +
Unigene3528_All	226	0.00	0.00	0.00	0.00	0.00	0.00	3.55	0.37	0.53	null	null		null	null		null	null		null	null		-3.26E+00	4.48E-04	Down	-2.75E+00	9.43E-04	Down	Unigene3528_All//gi|115464141|ref|NP_001055670.1|//4.00E-10//Os05g0441400 [Oryza sativa Japonica Group] >gi|113579221|dbj|BAF17584.1| Os05g0441400 [Oryza sativa Japonica Group]	Unigene3528_All//9.00E-09//AT5G04820| OFP13 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 13)	Unigene3528_All//7.00E-54//ES843522			GO:0043231	nr -
Unigene35283_All	1929	3.55	1.76	3.06	5.73	5.48	8.62	11.49	27.21	23.67	-1.01E+00	8.52E-06	Down	-2.14E-01	3.95E-01		-6.50E-02	7.76E-01		5.88E-01	1.02E-05		1.24E+00	4.40E-66	Up	1.04E+00	1.41E-44	Up	Unigene35283_All//gi|14334163|gb|AAK60564.1|AF383149_1/1.00E-147//armadillo repeat-containing protein [Nicotiana tabacum]	Unigene35283_All//1.00E-38//AT1G20780| SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein ligase	Unigene35283_All//0.00E+00//TC163821				nr +
Unigene35285_All	1903	6.46	5.43	7.19	21.75	21.71	19.53	2.60	0.57	0.71	-2.50E-01	1.37E-01		1.55E-01	3.92E-01		-2.60E-03	9.76E-01		-1.55E-01	8.62E-02		-2.19E+00	1.72E-14	Down	-1.87E+00	2.23E-12	Down	Unigene35285_All//gi|224131672|ref|XP_002321149.1|//0.00E+00//glycosyl hydrolase family 9 [Populus trichocarpa] >gi|222861922|gb|EEE99464.1| glycosyl hydrolase family 9 [Populus trichocarpa]	Unigene35285_All//0.00E+00//AT2G32990| AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene35285_All//0.00E+00//TC173807		ko00500|Starch and sucrose metabolism		nr +
Unigene35286_All	1940	10.49	6.16	4.56	22.47	26.52	27.52	20.29	15.84	12.98	-7.67E-01	4.75E-10		-1.20E+00	1.57E-19	Down	2.39E-01	7.78E-04		2.93E-01	3.87E-05		-3.58E-01	2.47E-06		-6.45E-01	1.59E-17		Unigene35286_All//gi|297851732|ref|XP_002893747.1|//0.00E+00//galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339889|gb|EFH70006.1| galactosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35286_All//1.00E-178//AT1G32930| galactosyltransferase family protein	Unigene35286_All//0.00E+00//TC158969				nr -
Unigene35287_All	2479	9.58	20.32	13.10	16.20	19.77	20.86	25.69	61.20	57.42	1.08E+00	1.10E-41	Up	4.52E-01	3.39E-06		2.87E-01	5.92E-05		3.65E-01	3.15E-07		1.25E+00	1.31E-191	Up	1.16E+00	7.69E-163	Up	Unigene35287_All//gi|297810977|ref|XP_002873372.1|//0.00E+00//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319209|gb|EFH49631.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35287_All//0.00E+00//AT5G08560| transducin family protein / WD-40 repeat family protein	Unigene35287_All//0.00E+00//TC156067		ko03040|Spliceosome		nr +
Unigene35289_All	3344	4.99	5.23	2.42	15.13	11.44	15.64	20.46	15.36	12.85	6.68E-02	6.38E-01		-1.04E+00	5.81E-13	Down	-4.04E-01	2.63E-09		4.73E-02	6.40E-01		-4.13E-01	2.31E-13		-6.70E-01	7.54E-32		Unigene35289_All//gi|285309967|emb|CBE71057.1|//0.00E+00//aconitate hydratase 3 [Citrus clementina]	Unigene35289_All//0.00E+00//AT2G05710| aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative	Unigene35289_All//0.00E+00//TC165358		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene35294_All	2102	3.16	2.48	2.10	4.79	3.72	5.74	64.65	31.14	42.23	-3.48E-01	1.35E-01		-5.88E-01	1.38E-02		-3.64E-01	4.11E-02		2.61E-01	1.38E-01		-1.05E+00	1.61E-130	Down	-6.14E-01	1.53E-53		Unigene35294_All//gi|115458664|ref|NP_001052932.1|//0.00E+00//Os04g0449500 [Oryza sativa Japonica Group] >gi|38344840|emb|CAE01571.2| OSJNBa0064H22.21 [Oryza sativa (japonica cultivar-group)] >gi|113564503|dbj|BAF14846.1| Os04g0449500 [Oryza sativa Japonica Group] >gi|116310074|emb|CAH67095.1| H0818E04.12 [Oryza sativa (indica cultivar-group)]	Unigene35294_All//0.00E+00//AT4G37030| unknown protein	Unigene35294_All//0.00E+00//CO128331				nr +
Unigene35296_All	359	4.52	0.56	3.41	9.71	8.63	7.67	3.06	3.61	1.66	-3.00E+00	6.72E-06	Down	-4.05E-01	4.48E-01		-1.70E-01	6.26E-01		-3.40E-01	3.47E-01		2.37E-01	6.52E-01		-8.79E-01	1.15E-01		Unigene35296_All//gi|4097543|gb|AAD09505.1|//3.00E-13//ATFP1 [Arabidopsis thaliana]		Unigene35296_All//1.00E-158//TC151495				nr -
Unigene35297_All	462	6.34	1.65	1.61	16.93	11.85	13.69	3.84	10.31	3.54	-1.95E+00	1.91E-06	Down	-1.97E+00	3.42E-06	Down	-5.14E-01	9.39E-03		-3.07E-01	1.71E-01		1.42E+00	4.53E-08	Up	-1.21E-01	7.73E-01		Unigene35297_All//gi|4097543|gb|AAD09505.1|//1.00E-09//ATFP1 [Arabidopsis thaliana]		Unigene35297_All//0.00E+00//TC151495				nr -
Unigene35298_All	808	26.23	8.40	13.25	115.35	102.58	122.58	70.59	71.02	45.46	-1.64E+00	1.88E-33	Down	-9.85E-01	7.24E-15		-1.69E-01	1.19E-03		8.77E-02	1.41E-01		8.80E-03	9.26E-01		-6.35E-01	2.46E-24		Unigene35298_All//gi|4097543|gb|AAD09505.1|//1.00E-18//ATFP1 [Arabidopsis thaliana]		Unigene35298_All//0.00E+00//TC173796				nr +
Unigene35299_All	2544	3.06	2.13	1.30	6.95	10.57	7.23	7.69	3.66	4.04	-5.24E-01	1.21E-02		-1.24E+00	3.25E-08	Down	6.05E-01	4.77E-10		5.58E-02	7.15E-01		-1.07E+00	5.74E-20	Down	-9.30E-01	1.78E-16		Unigene35299_All//gi|262263163|dbj|BAI48084.1|//2.00E-71//centromere protein C homologue [Nicotiana tabacum]	Unigene35299_All//2.00E-52//AT1G15660| CENP-C (CENTROMERE PROTEIN C)	Unigene35299_All//4.00E-129//gi|164316185|gb|EX168997.1|EX168997				nr -
Unigene353_All	2136	129.14	16.70	20.67	238.25	151.57	86.92	35.09	9.94	13.63	-2.95E+00	0.00E+00	Down	-2.64E+00	0.00E+00	Down	-6.53E-01	1.83E-216		-1.45E+00	0.00E+00	Down	-1.82E+00	8.81E-165	Down	-1.36E+00	1.35E-111	Down	Unigene353_All//gi|170293773|gb|ACB12931.1|//0.00E+00//pectate lyase 1-27 [Populus tremula x Populus tremuloides]	Unigene353_All//3.00E-176//AT1G04680| pectate lyase family protein	Unigene353_All//0.00E+00//TC139359		ko00040|Pentose and glucuronate interconversions		nr -
Unigene3530_All	1029	26.19	9.55	17.70	8.47	5.79	3.91	0.99	1.26	1.66	-1.45E+00	1.42E-35	Down	-5.65E-01	1.49E-07		-5.49E-01	2.83E-03		-1.12E+00	1.08E-08	Down	3.53E-01	5.36E-01		7.56E-01	8.05E-02		Unigene3530_All//gi|15241977|ref|NP_201090.1|//1.00E-116//phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis thaliana]	Unigene3530_All//1.00E-113//AT5G62840| phosphoglycerate/bisphosphoglycerate mutase family protein	Unigene3530_All//0.00E+00//gi|164367091|gb|ES849755.1|ES849755				nr +
Unigene35300_All	4525	1.11	2.32	0.74	2.48	1.72	1.27	3.87	6.01	9.14	1.06E+00	5.30E-09	Up	-5.82E-01	3.86E-02		-5.26E-01	9.18E-04		-9.66E-01	8.28E-09		6.36E-01	9.37E-12		1.24E+00	4.22E-53	Up	Unigene35300_All//gi|15982852|gb|AAL09773.1|//1.00E-166//AT5g66850/MUB21_11 [Arabidopsis thaliana]	Unigene35300_All//1.00E-143//AT5G66850| MAPKKK5; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene35300_All//0.00E+00//TC142966		ko04626|Plant-pathogen interaction		nr -

Unigene35301_All	1233	7.55	3.95	6.35	10.46	6.00	4.40	21.16	18.44	6.17	-9.37E-01	9.43E-07		-2.51E-01	2.39E-01		-8.01E-01	2.81E-08		-1.25E+00	6.06E-15	Down	-1.98E-01	5.05E-02		-1.78E+00	1.18E-57	Down	Unigene35301_All//gi|297794509|ref|XP_002865139.1|//1.00E-29//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310974|gb|EFH41398.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35301_All//4.00E-29//AT5G47140| zinc finger (GATA type) family protein	Unigene35301_All//0.00E+00//TC149889	C2C2-GATA			nr +
Unigene35302_All	2148	4.90	3.92	5.97	5.47	4.65	4.23	8.82	10.18	2.63	-3.22E-01	7.60E-02		2.87E-01	9.33E-02		-2.35E-01	1.78E-01		-3.73E-01	2.70E-02		2.07E-01	6.52E-02		-1.74E+00	5.43E-41	Down	Unigene35302_All//gi|297800334|ref|XP_002868051.1|//1.00E-136//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313887|gb|EFH44310.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35302_All//4.00E-106//AT4G17570| zinc finger (GATA type) family protein	Unigene35302_All//0.00E+00//TC149889	C2C2-GATA			nr +
Unigene35303_All	434	1.45	5.25	2.21	3.90	4.76	2.19	18.31	10.02	8.63	1.86E+00	6.77E-05	Up	6.10E-01	3.86E-01		2.87E-01	5.78E-01		-8.37E-01	1.03E-01		-8.71E-01	2.50E-06		-1.09E+00	4.52E-09	Down	Unigene35303_All//gi|18425204|ref|NP_569051.1|//8.00E-46//ATARLA1D (ADP-ribosylation factor-like A1D); GTP binding [Arabidopsis thaliana] >gi|15450888|gb|AAK96715.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana] >gi|17978675|gb|AAL47331.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana] >gi|21593081|gb|AAM65030.1| ADP-ribosylation factor-like protein [Arabidopsis thaliana]	Unigene35303_All//7.00E-44//AT5G67560| ATARLA1D (ADP-ribosylation factor-like A1D); GTP binding	Unigene35303_All//0.00E+00//TC164715				nr -
Unigene35307_All	2535	9.33	45.87	12.86	15.35	18.75	14.31	14.73	21.47	14.68	2.30E+00	5.97E-281	Up	4.63E-01	1.82E-06		2.89E-01	7.42E-05		-1.01E-01	3.25E-01		5.44E-01	2.70E-17		-4.80E-03	9.73E-01		Unigene35307_All//gi|18650616|gb|AAL75907.1|//1.00E-129//AT4g03420/F9H3_4 [Arabidopsis thaliana] >gi|20452247|gb|AAM19862.1| AT4g03420/F9H3_4 [Arabidopsis thaliana]	Unigene35307_All//4.00E-122//AT4G03420| unknown protein	Unigene35307_All//0.00E+00//TC143805				nr -
Unigene35308_All	1873	18.21	56.00	37.67	1.99	1.89	1.95	12.30	29.86	13.02	1.62E+00	3.53E-159	Up	1.05E+00	1.66E-53	Up	-7.50E-02	8.25E-01		-3.04E-02	9.43E-01		1.28E+00	2.18E-73	Up	8.15E-02	4.78E-01		Unigene35308_All//gi|224123398|ref|XP_002320305.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222871340|gb|EEF08471.1| cytochrome P450 [Populus trichocarpa]	Unigene35308_All//2.00E-139//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene35308_All//2.00E-80//C0076766		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene35309_All	2326	1.03	3.05	1.30	2.66	3.57	3.53	61.26	105.68	57.34	1.56E+00	7.83E-11	Up	3.35E-01	4.02E-01		4.26E-01	3.35E-02		4.12E-01	4.75E-02		7.87E-01	4.66E-144		-9.53E-02	1.73E-02		Unigene35309_All//gi|15221488|ref|NP_177038.1|//0.00E+00//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|12229673|sp|Q9SX33.1|ALA9_ARATH RecName: Full=Putative phospholipid-transporting ATPase 9; Short=AtALA9; AltName: Full=Aminophospholipid flippase 9 >gi|5734708|gb|AAD49973.1|AC008075_6 Similar to gb|AF067820 ATPase II from Homo sapiens and is a member of PF|00122 E1-E2 ATPases family [Arabidopsis thaliana]	Unigene35309_All//0.00E+00//AT1G68710| haloacid dehalogenase-like hydrolase family protein	Unigene35309_All//0.00E+00//C0120262				nr -
Unigene3531_All	1320	1.43	1.88	1.05	4.00	3.00	6.67	4.10	2.37	1.60	3.99E-01	3.40E-01		-4.44E-01	3.90E-01		-4.15E-01	1.10E-01		7.38E-01	1.14E-04		-7.88E-01	5.56E-04		-1.36E+00	8.24E-09	Down	Unigene3531_All//gi|63054325|gb|AAY28930.1|//6.00E-92//sucrose responsive element binding protein [Vitis vinifera]	Unigene3531_All//7.00E-60//AT5G67300| MYBR1 (MYB DOMAIN PROTEIN R1); DNA binding / transcription factor	Unigene3531_All//0.00E+00//gi|78337989|gb|DT558263.1|DT558263	MYB		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene35310_All	1951	18.69	12.02	12.88	20.35	25.68	13.52	12.09	5.59	8.05	-6.36E-01	9.82E-13		-5.37E-01	3.73E-09		3.36E-01	1.43E-06		-5.90E-01	6.42E-13		-1.11E+00	2.17E-25	Down	-5.88E-01	2.35E-09		Unigene35310_All//gi|255557353|ref|XP_002519707.1|//0.00E+00//50 kDa ketoacyl-ACP synthase [Ricinus communis] >gi|294668|gb|AAA33873.1| chloroplast beta-ketoacyl-ACP synthase precursor [Ricinus communis] >gi|148791249|gb|ABR12416.1| plastid 3-keto-acyl-ACP synthase I [Ricinus communis] >gi|223541124|gb|EEF42680.1| 50 kDa ketoacyl-ACP synthase [Ricinus communis]	Unigene35310_All//0.00E+00//AT5G46290| KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); catalytic/ fatty-acid synthase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene35310_All//0.00E+00//TC147442		ko00061|Fatty acid biosynthesis		nr -
Unigene35317_All	2530	11.29	2.76	7.62	3.31	4.34	4.34	1.92	2.91	4.47	-2.03E+00	7.34E-60	Down	-5.68E-01	5.10E-08		3.92E-01	2.10E-02		3.91E-01	2.60E-02		5.97E-01	1.84E-03		1.22E+00	9.06E-15	Up	Unigene35317_All//gi|225455491|ref|XP_002280396.1|//1.00E-170//PREDICTED: similar to ZFWD1 (zinc finger WD40 repeat protein 1); nucleic acid binding / zinc ion binding [Vitis vinifera]	Unigene35317_All//2.00E-161//AT5G51980| WD-40 repeat family protein / zfwd2 protein (ZFWD2), putative	Unigene35317_All//0.00E+00//TC173085	C3H	ko00051|Fructose and mannose metabolism		nr -
Unigene35318_All	2027	26.79	8.77	15.08	27.35	24.96	31.28	30.50	27.77	58.57	-1.61E+00	1.98E-82	Down	-8.29E-01	5.57E-28		-1.32E-01	8.01E-02		1.94E-01	4.11E-03		-1.35E-01	3.65E-02		9.42E-01	8.12E-97		Unigene35318_All//gi|240255737|ref|NP_680572.4|//0.00E+00//catalytic/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75151368|sp|Q8GG60.1|P2C52_ARATH RecName: Full=Probable protein phosphatase 2C 52; Short=AtPP2C52 >gi|28951049|gb|AAO63448.1| At4g03415 [Arabidopsis thaliana]	Unigene35318_All//0.00E+00//AT4G03415| catalytic/ protein serine/threonine phosphatase	Unigene35318_All//0.00E+00//TC142874				nr -
Unigene3532_All	911	17.17	11.90	20.98	29.69	27.40	34.36	22.74	14.50	10.36	-5.29E-01	1.70E-04		2.89E-01	3.35E-02		-1.16E-01	3.35E-01		2.11E-01	3.94E-02		-6.50E-01	1.85E-09		-1.13E+00	9.33E-24	Down	Unigene3532_All//gi|20197762|gb|AAD18102.2|//3.00E-63//expressed protein [Arabidopsis thaliana]	Unigene3532_All//8.00E-48//AT4G30996| unknown protein	Unigene3532_All//0.00E+00//TC146509			GO:0044464	nr -
Unigene35322_All	1949	2.74	5.30	3.36	7.39	8.83	7.76	4.84	2.23	5.56	9.54E-01	1.43E-07		2.96E-01	2.41E-01		2.58E-01	6.14E-02		7.17E-02	6.93E-01		-1.12E+00	1.08E-10	Down	2.01E-01	2.17E-01		Unigene35322_All//gi|224113661|ref|XP_002316535.1|//1.00E-142//arogenate/prephenate dehydratase [Populus trichocarpa] >gi|222859600|gb|EEE97147.1| arogenate/prephenate dehydratase [Populus trichocarpa]	Unigene35322_All//8.00E-122//AT1G11790| ADT1 (arogenate dehydratase 1); arogenate dehydratase/ prephenate dehydratase	Unigene35322_All//0.00E+00//TC141641		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene35323_All	2173	16.57	9.12	10.66	29.07	21.82	29.80	30.22	23.93	14.41	-8.62E-01	8.94E-21		-6.36E-01	5.08E-12		-4.14E-01	5.33E-12		3.61E-02	6.77E-01		-3.37E-01	4.98E-09		-1.07E+00	1.09E-66	Down	Unigene35323_All//gi|60459371|gb|AAX20031.1|//1.00E-172//RING-finger protein [Capsicum annuum]	Unigene35323_All//3.00E-163//AT5G14420| RGLG2 (RING domain Ligase2); ubiquitin-protein ligase	Unigene35323_All//0.00E+00//TC130350				nr -
Unigene35324_All	1286	13.95	15.09	16.48	8.72	17.94	14.68	1.12	0.88	0.65	1.13E-01	4.13E-01		2.40E-01	6.64E-02		1.04E+00	2.89E-21	Up	7.52E-01	1.60E-09		-3.49E-01	5.14E-01		-7.81E-01	1.01E-01		Unigene35324_All//gi|224133454|ref|XP_002328046.1|//1.00E-164//aminotransferase family protein [Populus trichocarpa] >gi|222837455|gb|EEE75834.1| aminotransferase family protein [Populus trichocarpa]	Unigene35324_All//8.00E-129//AT5G53970| aminotransferase, putative	Unigene35324_All//0.00E+00//TC138823		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene35325_All	1416	1.03	2.50	1.24	0.77	1.92	1.37	0.15	0.09	0.03	1.28E+00	1.65E-04	Up	2.62E-01	6.33E-01		1.31E+00	5.38E-04	Up	8.26E-01	8.28E-02		-7.53E-01	6.32E-01		-2.41E+00	1.95E-01		Unigene35325_All//gi|224133454|ref|XP_002328046.1|//1.00E-120//aminotransferase family protein [Populus trichocarpa] >gi|222837455|gb|EEE75834.1| aminotransferase family protein [Populus trichocarpa]	Unigene35325_All//3.00E-96//AT5G53970| aminotransferase, putative	Unigene35325_All//0.00E+00//TC138823		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr +
Unigene35327_All	1400	45.03	33.55	45.57	25.37	24.87	28.55	15.25	10.87	5.66	-4.25E-01	1.09E-10		1.70E-02	8.30E-01		-2.89E-02	8.22E-01		1.70E-01	6.23E-02		-4.89E-01	3.69E-06		-1.43E+00	1.00E-34	Down	Unigene35327_All//gi|222423838|dbj|BAH19884.1|//4.00E-72//AT1G21065 [Arabidopsis thaliana]	Unigene35327_All//2.00E-73//AT1G21065| unknown protein	Unigene35327_All//0.00E+00//TC143570				nr -
Unigene35328_All	1072	14.06	8.27	10.53	22.72	23.19	41.67	60.94	64.21	219.97	-7.65E-01	1.29E-07		-4.17E-01	5.83E-03		2.95E-02	8.19E-01		8.75E-01	5.75E-28		7.56E-02	2.56E-01		1.85E+00	0.00E+00	Up	Unigene35328_All//gi|125950374|gb|ABNS8740.1|//0.00E+00//UGT protein [Gossypium hirsutum]	Unigene35328_All//3.00E-66//AT3G11340| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene35328_All//0.00E+00//TC132027		ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene35329_All	885	8.93	6.81	7.94	10.19	8.09	13.63	4.20	1.04	24.53	-3.90E-01	6.46E-02		-1.69E-01	4.69E-01		-3.32E-01	8.55E-02		4.19E-01	1.08E-02		-2.02E+00	4.52E-10	Down	2.54E+00	1.89E-74	Up	Unigene35329_All//gi|125950374|gb|ABNS8740.1|//1.00E-107//UGT protein [Gossypium hirsutum]	Unigene35329_All//5.00E-36//AT5G59590| UGT76E2 (UDP-GLUCOSYL TRANSFERASE 76E2); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase	Unigene35329_All//0.00E+00//TC134046		ko00908|Zeatin biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene3533_All	1422	2.76	6.52	3.18	2.59	7.41	4.73	1.84	2.94	5.49	1.24E+00	4.35E-10	Up	2.06E-01	5.13E-01		1.52E+00	2.52E-17	Up	8.68E-01	1.05E-04		6.73E-01	1.13E-02		1.57E+00	5.35E-15	Up			Unigene3533_All//3.00E-11//TC176666				
Unigene35331_All	1829	32.38	18.42	23.93	85.03	75.76	80.20	54.44	31.76	25.29	-8.14E-01	1.26E-30		-4.36E-01	4.30E-10		-1.67E-01	1.69E-05		-8.43E-02	6.48E-02		-7.77E-01	1.16E-57		-1.11E+00	1.60E-106	Down	Unigene35331_All//gi|30387529|gb|AAP31930.1|//0.00E+00//At3g09570 [Arabidopsis thaliana]	Unigene35331_All//0.00E+00//AT3G09570| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Transmembrane receptor, eukaryota (InterPro:IPR009637); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G18520.1); Has 385 Blast hits to 385 proteins in 83 species: Archae - 0; Bacteria - 2; Metazoa - 216; Fungi - 12; Plants - 132; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).	Unigene35331_All//0.00E+00//TC144454		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase//ko03022|Basal transcription factors		nr +
Unigene35332_All	1630	15.57	9.42	12.71	33.04	22.56	28.79	8.72	5.69	4.35	-7.25E-01	3.00E-11		-2.93E-01	1.10E-02		-5.50E-01	4.19E-17		-1.99E-01	7.24E-03		-6.15E-01	3.45E-06		-1.00E+00	1.02E-13	Down	Unigene35332_All//gi|297831018|ref|XP_002883391.1|//1.00E-145//cbl-interacting protein kinase 7 [Arabidopsis lyrata subsp. lyrata] >gi|297329231|gb|EFH59650.1| cbl-interacting protein kinase 7 [Arabidopsis lyrata subsp. lyrata]	Unigene35332_All//3.00E-125//AT3G23000| CIPK7 (CBL-INTERACTING PROTEIN KINASE 7); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene35332_All//0.00E+00//C0096043		ko04140|Regulation of autophagy		nr +
Unigene35335_All	295	13.83	6.70	5.96	10.81	6.42	7.35	12.04	7.79	7.70	-1.05E+00	6.07E-04	Down	-1.22E+00	1.61E-04	Down	-7.51E-01	2.28E-02		-5.57E-01	1.20E-01		-6.28E-01	3.22E-02		-6.45E-01	2.17E-02		Unigene35335_All//gi|225468332|ref|XP_002270219.1|//1.00E-41//PREDICTED: similar to oligopeptidase A [Vitis vinifera]	Unigene35335_All//1.00E-34//AT5G65620| peptidase M3 family protein / thimet oligopeptidase family protein	Unigene35335_All//4.00E-130//TC169423				nr +

Unigene35336_All	576	8.72	6.16	8.97	7.61	4.96	6.12	22.83	11.03	6.71	-5.02E-01	6.27E-02		4.03E-02	8.91E-01		-6.17E-01	2.57E-02		-3.15E-01	3.21E-01		-1.05E+00	2.87E-13	Down	-1.77E+00	3.08E-29	Down	Unigene35336_All//gi|225468332|ref|XP_002270219.1|//2.00E-13//PREDICTED: similar to oligopeptidase A [Vitis vinifera]	Unigene35336_All//3.00E-12//AT5G10540| peptidase M3 family protein / thimet oligopeptidase family protein	Unigene35336_All//0.00E+00//TC169423				nr +
Unigene35338_All	1847	97.73	251.26	95.14	175.01	108.77	128.62	448.46	701.11	368.86	1.36E+00	0.00E+00	Up	-3.87E-02	4.00E-01		-6.86E-01	1.98E-150		-4.44E-01	1.66E-60		6.45E-01	0.00E+00		-2.82E-01	1.27E-76		Unigene35338_All//gi|295311645|ref|YP_003387228.1|//0.00E+00//cytochrome c oxidase subunit 1 [Citrullus lanatus] >gi|259156773|gb|ACY96635.1| cytochrome c oxidase subunit 1 [Citrullus lanatus]	Unigene35338_All//0.00E+00//ATMG01360| cytochrome c oxidase subunit 1	Unigene35338_All//0.00E+00//gi|164301352|gb|ES813124.1|ES813124		ko00190|Oxidative phosphorylation		nr -
Unigene35340_All	1841	1.34	0.94	1.30	1.46	1.16	0.71	4.80	18.21	5.19	-5.13E-01	2.12E-01		-3.73E-02	9.43E-01		-3.33E-01	4.13E-01		-1.04E+00	6.71E-03		1.92E+00	1.41E-79	Up	1.14E-01	5.50E-01		Unigene35340_All//gi|223452302|gb|ACM89479.1|//1.00E-180//cysteine-rich protein [Glycine max]	Unigene35340_All//4.00E-168//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene35340_All//0.00E+00//TC164246		ko04626|Plant-pathogen interaction		nr -
Unigene35341_All	1250	92.34	52.49	79.92	96.32	72.31	28.62	0.81	3.21	0.16	-8.15E-01	3.78E-59		-2.08E-01	3.08E-05		-4.14E-01	1.83E-22		-1.75E+00	2.40E-223	Down	1.98E+00	1.47E-10	Up	-2.35E+00	5.84E-04	Down	Unigene35341_All//gi|223452302|gb|ACM89479.1|//1.00E-102//cysteine-rich protein [Glycine max]	Unigene35341_All//1.00E-82//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene35341_All//0.00E+00//TC164246		ko04626|Plant-pathogen interaction		nr +
Unigene35345_All	2665	2.38	1.84	1.60	28.39	27.77	20.56	10.38	1.85	4.81	-3.65E-01	1.29E-01		-5.72E-01	2.01E-02		-3.21E-02	6.84E-01		-4.66E-01	7.08E-16		-2.49E+00	9.72E-91	Down	-1.11E+00	2.67E-30	Down	Unigene35345_All//gi|18423656|ref|NP_568811.1|//0.00E+00//ATK3 (ARABIDOPSIS THALIANA KINESIN 3); ATPase/ microtubule binding / microtubule motor [Arabidopsis thaliana] >gi|1170621|sp|P46875.1|ATK3_ARATH RecName: Full=Kinesin-3; AltName: Full=Kinesin-like protein C >gi|4388841|dbj|BAD40674.1| heavy chain polypeptide of kinesin-like protein [Arabidopsis thaliana] >gi|27808616|gb|AAO24588.1| At5g54670 [Arabidopsis thaliana] >gi|110736249|dbj|BAF00095.1| heavy chain polypeptide of kinesin like protein [Arabidopsis thaliana]	Unigene35345_All//0.00E+00//AT5G54670| ATK3 (ARABIDOPSIS THALIANA KINESIN 3); ATPase/ microtubule binding / microtubule motor	Unigene35345_All//0.00E+00//ES805465				nr -
Unigene35347_All	2108	2.16	1.35	2.96	3.59	4.56	3.58	2.61	2.48	6.86	-6.82E-01	1.57E-02		4.53E-01	7.19E-02		3.44E-01	6.97E-02		-5.60E-03	9.76E-01		-7.32E-02	7.71E-01		1.40E+00	8.98E-23	Up	Unigene35347_All//gi|225440644|ref|XP_002274143.1|//2.00E-41//PREDICTED: similar to proton-dependent oligopeptide transport (POT) family protein [Vitis vinifera]	Unigene35347_All//8.00E-29//AT2G37900| proton-dependent oligopeptide transport (POT) family protein	Unigene35347_All//0.00E+00//DT462556				nr +
Unigene35348_All	2114	0.40	0.53	0.03	0.78	0.86	0.75	0.26	0.42	1.19	4.13E-01	5.26E-01		-3.97E+00	9.08E-04	Down	1.51E-01	8.16E-01		-5.66E-02	9.28E-01		6.75E-01	3.28E-01		2.19E+00	6.69E-08	Up	Unigene35348_All//gi|225440644|ref|XP_002274143.1|//2.00E-38//PREDICTED: similar to proton-dependent oligopeptide transport (POT) family protein [Vitis vinifera]	Unigene35348_All//1.00E-29//AT2G37900| proton-dependent oligopeptide transport (POT) family protein	Unigene35348_All//0.00E+00//DT462556				nr +
Unigene3535_All	3190	0.62	1.13	0.92	1.67	1.38	2.28	3.30	5.35	7.04	8.56E-01	8.54E-03		5.59E-01	1.44E-01		-2.74E-01	3.14E-01		4.48E-01	4.34E-02		6.96E-01	7.66E-09		1.09E+00	4.14E-24	Up	Unigene3535_All//gi|297833718|ref|XP_002884741.1|//0.00E+00//lipin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330581|gb|EFH61000.1| lipin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3535_All//0.00E+00//AT3G09560| lipin family protein	Unigene3535_All//0.00E+00//TC169077			GO:0009267//GO:0016791//GO:0044238	nr -
Unigene35351_All	2396	1.35	3.15	1.60	1.46	2.20	2.19	3.58	3.86	2.99	1.22E+00	3.78E-08	Up	2.41E-01	4.78E-01		5.96E-01	1.98E-02		5.87E-01	2.60E-02		1.06E-01	6.20E-01		-2.59E-01	1.50E-01		Unigene35351_All//gi|225449891|ref|XP_002268085.1|//0.00E+00//PREDICTED: similar to ATMUS81; endonuclease/ nucleic acid binding [Vitis vinifera]	Unigene35351_All//1.00E-111//AT4G30870| MUS81 (MMS AND UV SENSITIVE 81); endonuclease/ nucleic acid binding	Unigene35351_All//0.00E+00//TC172740		ko03440|Homologous recombination		nr -
Unigene35352_All	1058	7.12	27.49	4.03	8.05	9.08	10.71	5.32	4.54	3.09	1.95E+00	2.34E-57	Up	-8.23E-01	1.99E-04		1.74E-01	4.23E-01		4.12E-01	1.60E-02		-2.26E-01	3.72E-01		-7.84E-01	3.07E-04		Unigene35352_All//gi|72255607|gb|AA266925.1|//1.00E-116//117M18_6 [Brassica rapa]	Unigene35352_All//7.00E-113//AT5G10050| short-chain dehydrogenase/reductase (SDR) family protein	Unigene35352_All//0.00E+00//TC154613		ko00564|Glycerophospholipid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis//ko00565|Ether lipid metabolism		nr +
Unigene35353_All	447	0.70	1.70	0.95	3.34	2.39	3.33	3.78	0.75	1.87	1.28E+00	1.28E-01		4.40E-01	6.77E-01		-4.85E-01	3.82E-01		-3.90E-03	9.88E-01		-2.34E+00	8.20E-06	Down	-1.02E+00	1.96E-02		Unigene35353_All//gi|109509142|gb|AB634280.1|//1.00E-59//pectin acetylesterase [Eucalyptus globulus subsp. globulus]	Unigene35353_All//3.00E-57//AT2G46930| pectinacetylesterase, putative	Unigene35353_All//0.00E+00//ES816372				nr -
Unigene35354_All	1570	1.77	0.81	1.56	1.75	2.48	1.41	1.67	0.45	1.24	-1.13E+00	3.16E-03		-1.79E-01	6.35E-01		5.06E-01	1.09E-01		-3.08E-01	4.66E-01		-1.88E+00	9.55E-07	Down	-4.25E-01	2.16E-01		Unigene35354_All//gi|72255607|gb|AA266925.1|//1.00E-113//117M18_6 [Brassica rapa]	Unigene35354_All//2.00E-109//AT5G65205| short-chain dehydrogenase/reductase (SDR) family protein	Unigene35354_All//0.00E+00//TC154613		ko00564|Glycerophospholipid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis//ko00565|Ether lipid metabolism		nr +
Unigene35357_All	3270	11.41	5.83	5.10	25.67	19.26	24.98	44.80	14.51	20.77	-9.69E-01	4.66E-26		-1.16E+00	1.65E-33	Down	-4.14E-01	7.70E-16		-3.90E-02	6.25E-01		-1.63E+00	1.38E-274	Down	-1.11E+00	5.61E-157	Down	Unigene35357_All//gi|238479695|ref|NP_001154598.1|//0.00E+00//binding / protein transporter [Arabidopsis thaliana]	Unigene35357_All//0.00E+00//AT3G08947| binding / protein transporter	Unigene35357_All//0.00E+00//TC178647				nr +
Unigene3536_All	1116	13.27	26.15	37.27	13.70	12.74	50.10	102.25	312.19	465.82	9.79E-01	8.40E-21		1.49E+00	1.13E-54	Up	-1.05E-01	5.65E-01		1.87E+00	1.56E-111	Up	1.61E+00	0.00E+00	Up	2.19E+00	0.00E+00	Up	Unigene3536_All//gi|27803890|gb|AAO22065.1|//1.00E-87//NtPRp27-like protein [Solanum tuberosum]	Unigene3536_All//2.00E-87//AT2G15220| secretory protein, putative	Unigene3536_All//0.00E+00//TC140618			GO:0006950//GO:0044464	nr -
Unigene35360_All	615	0.51	0.66	0.43	3.56	1.96	1.03	1.03	1.56	1.88	3.69E-01	7.24E-01		-2.38E-01	8.50E-01		-8.63E-01	3.65E-02		-1.79E+00	9.25E-05	Down	6.00E-01	3.67E-01		8.65E-01	1.14E-01				Unigene35360_All//3.00E-157//TC145919				
Unigene35362_All	2754	1.77	2.32	2.65	42.78	39.75	39.41	12.02	5.02	4.93	3.92E-01	1.01E-01		5.84E-01	9.56E-03		-1.06E-01	3.27E-02		-1.18E-01	1.90E-02		-1.26E+00	8.98E-43	Down	-1.29E+00	1.88E-45	Down	Unigene35362_All//gi|18378991|ref|NP_563659.1|//0.00E+00//BXL2 (BETA-XYLOSIDASE 2); hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|75250279|sp|Q94KD8.1|BXL2_ARATH RecName: Full=Probable beta-D-xylosidase 2; Short=AtBXL2; Flags: Precursor >gi|14194121|gb|AAK56255.1|AF367266_1 At1g02640/T14P4_11 [Arabidopsis thaliana] >gi|23506063|gb|AAN28891.1| At1g02640/T14P4_11 [Arabidopsis thaliana]	Unigene35362_All//0.00E+00//AT1G02640| BXL2 (BETA-XYLOSIDASE 2); hydrolase, hydrolyzing O-glycosyl compounds	Unigene35362_All//0.00E+00//gi|109865827|gb|DW494803.1|DW494803		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr -
Unigene35367_All	994	12.05	7.65	8.68	12.53	13.61	10.22	9.06	4.25	2.32	-6.57E-01	5.73E-05		-4.74E-01	5.60E-03		1.20E-01	5.31E-01		-2.93E-01	8.19E-02		-1.09E+00	6.33E-10	Down	-1.96E+00	2.78E-23	Down	Unigene35367_All//gi|226528437|ref|NP_001148629.1|//5.00E-47//DCL protein [Zea mays] >gi|195619226|gb|ACG31443.1| DCL protein [Zea mays]	Unigene35367_All//8.00E-60//AT3G46630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: defective chloroplasts and leaves protein-related / DCL protein-related (TAIR:AT1G45220.1); Has 102 Blast hits to 102 proteins in 23 species: Archae - 0; Bacteria - 7; Metazoa - 0; Fungi - 0; Plants - 88; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	Unigene35367_All//0.00E+00//TC136546				nr -
Unigene35368_All	1416	12.38	4.58	10.49	14.63	12.26	6.28	14.21	7.85	11.93	-1.43E+00	6.56E-23	Down	-2.39E-01	1.03E-01		-2.56E-01	3.52E-02		-1.22E+00	9.39E-23	Down	-8.56E-01	2.20E-14		-2.53E-01	2.17E-02		Unigene35368_All//gi|75168878|sp|Q9C518.1|TCP8_ARATH//9.00E-72//RecName: Full=Transcription factor TCP8 >gi|30725660|gb|AAP37852.1| At1g58100 [Arabidopsis thaliana]	Unigene35368_All//2.00E-44//AT1G58100| TCP family transcription factor, putative	Unigene35368_All//0.00E+00//TC153099	TCP			nr +
Unigene35369_All	2454	8.63	2.60	8.25	15.53	13.56	5.59	5.43	2.76	3.99	-1.73E+00	5.33E-36	Down	-6.65E-02	6.16E-01		-1.96E-01	2.53E-02		-1.47E+00	3.25E-55	Down	-9.76E-01	5.22E-12		-4.43E-01	9.65E-04		Unigene35369_All//gi|75168878|sp|Q9C518.1|TCP8_ARATH//5.00E-87//RecName: Full=Transcription factor TCP8 >gi|30725660|gb|AAP37852.1| At1g58100 [Arabidopsis thaliana]	Unigene35369_All//1.00E-54//AT1G58100| TCP family transcription factor, putative	Unigene35369_All//0.00E+00//TC153099	TCP			nr -
Unigene3537_All	219	23.65	72.42	30.39	42.08	47.80	52.38	58.50	179.02	251.77	1.61E+00	1.78E-24	Up	3.62E-01	1.40E-01		1.84E-01	3.63E-01		3.16E-01	7.26E-02		1.61E+00	6.20E-73	Up	2.11E+00	1.10E-149	Up	Unigene3537_All//gi|38016531|gb|AAA80760L1|//1.00E-97//fiber quinone-oxidoreductase [Gossypium barbadense]		Unigene3537_All//1.00E-120//TC175536				nr -
Unigene35370_All	1608	6.57	4.25	3.41	17.78	13.66	8.88	8.60	2.83	2.73	-6.28E-01	3.33E-04		-9.46E-01	2.76E-07		-3.80E-01	5.49E-05		-1.00E+00	7.61E-23	Down	-1.60E+00	5.44E-26	Down	-1.66E+00	3.96E-28	Down	Unigene35370_All//gi|124359459|gb|AB032255.2|//1.00E-130//Esterase/lipase/thioesterase [Medicago truncatula]	Unigene35370_All//2.00E-127//AT3G30380| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: Alpha/beta hydrolase fold-1 (InterPro:IPR000073); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01690.1); Has 3127 Blast hits to 3124 proteins in 513 species: Archae - 3; Bacteria - 775; Metazoa - 627; Fungi - 135; Plants - 158; Viruses - 6; Other Eukaryotes - 1423 (source: NCBI BLink).	Unigene35370_All//8.00E-43//DW498652				nr -
Unigene35371_All	2046	1.28	2.67	2.47	2.97	4.71	4.00	2.91	2.86	4.24	1.06E+00	4.21E-05	Up	9.51E-01	6.42E-04		6.66E-01	1.39E-04		4.28E-01	3.95E-02		-2.69E-02	9.27E-01		5.43E-01	1.41E-03		Unigene35371_All//gi|297823655|ref|XP_002879710.1|//1.00E-168//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325549|gb|EFH55969.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35371_All//4.00E-155//AT2G37840| protein kinase family protein	Unigene35371_All//0.00E+00//ES818583		ko04140|Regulation of autophagy		nr +

Unigene35373_All	2149	41.73	35.44	26.34	51.78	41.97	54.41	44.48	27.25	19.58	-2.36E-01	1.88E-05		-6.64E-01	2.68E-31		-3.03E-01	8.77E-12		7.14E-02	2.07E-01		-7.07E-01	4.21E-47		-1.18E+00	4.75E-114	Down	Unigene35373_All//gi|30698814|ref|NP_177324.2|//1.00E-120//F-actin capping protein beta subunit family protein [Arabidopsis thaliana] >gi|34222650|sp|Q9M9G7.1|CAPZB_ARATH RecName: Full=Probable F-actin-capping protein subunit beta; AltName: Full=CapZ-beta >gi|7239506|gb|AAF43232.1|AC012654_16 Similar to the F-actin capping protein beta subunit from Dictyostelium discoideum gi|115598 [Arabidopsis thaliana] >gi|117958773|gb|ABK59688.1|At1g71790 [Arabidopsis thaliana]	Unigene35373_All//3.00E-116//AT1G71790| F-actin capping protein beta subunit family protein	Unigene35373_All//0.00E+00//gi|78329005|gb|DT549279.1|DT549279				nr -
Unigene35374_All	2556	5.85	14.11	9.04	13.95	11.13	13.82	16.38	16.74	15.96	1.27E+00	1.97E-38	Up	6.27E-01	8.63E-08		-3.27E-01	1.04E-04		-1.42E-02	9.12E-01		3.21E-02	7.19E-01		-3.71E-02	6.61E-01		Unigene35374_All//gi|79362498|ref|NP_175420.3|//0.00E+00//DNA-directed DNA polymerase/ damaged DNA binding [Arabidopsis thaliana] >gi|46394839|gb|AA591582.1| DNA-directed polymerase kappa [Arabidopsis thaliana]	Unigene35374_All//0.00E+00//AT1G49980| DNA-directed DNA polymerase/ damaged DNA binding	Unigene35374_All//0.00E+00//gi|78329408|gb|DT549682.1|DT549682				nr +
Unigene35375_All	1600	165.01	38.22	60.54	357.01	260.01	144.10	77.43	11.65	20.59	-2.11E+00	0.00E+00	Down	-1.45E+00	0.00E+00	Down	-4.57E-01	2.90E-127		-1.31E+00	0.00E+00	Down	-2.73E+00	0.00E+00	Down	-1.91E+00	3.57E-299	Down	Unigene35375_All//gi|157273658|gb|ABV27483.1|//0.00E+00//fasciclin-like arabinogalactan protein 12 [Gossypium hirsutum]	Unigene35375_All//6.00E-133//AT2G45470| FLA8 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 8)	Unigene35375_All//0.00E+00//TC131022		ko04141|Protein processing in endoplasmic reticulum/ko03420|Nucleotide excision repair		nr +
Unigene35376_All	1674	6.84	11.96	5.98	2.47	2.76	7.34	31.67	67.51	77.92	8.05E-01	1.21E-10		-1.95E-01	3.09E-01		1.58E-01	6.15E-01		1.57E+00	1.49E-19	Up	1.09E+00	6.47E-115	Up	1.30E+00	5.39E-178	Up	Unigene35376_All//gi|42567704|ref|NP_196298.2|//7.00E-63//myb family transcription factor [Arabidopsis thaliana]	Unigene35376_All//6.00E-61//AT5G06800| myb family transcription factor	Unigene35376_All//3.00E-11//TC143924	G2-like			nr +
Unigene35379_All	1448	16.69	4.62	3.57	69.66	30.61	22.36	71.71	12.99	11.67	-1.85E+00	5.41E-45	Down	-2.23E+00	6.74E-55	Down	-1.19E+00	2.77E-119	Down	-1.64E+00	2.26E-170	Down	-2.46E+00	0.00E+00	Down	-2.62E+00	0.00E+00	Down	Unigene35379_All//gi|224088196|ref|XP_002308365.1|//0.00E+00//actin 3 [Populus trichocarpa] >gi|224137838|ref|XP_002322664.1| actin 7 [Populus trichocarpa] >gi|222854341|gb|EEE91888.1| actin 3 [Populus trichocarpa] >gi|222867294|gb|EEF04425.1| actin 7 [Populus trichocarpa] >gi|301331528|gb|ADK70741.1| actin [Populus tomentosa] >gi|301331531|gb|ADK70742.1| actin [Populus tomentosa] >gi|301331533|gb|ADK70743.1| actin [Populus tomentosa] >gi|301331536|gb|ADK70744.1| actin [Populus tomentosa] >gi|301331540|gb|ADK70745.1| actin [Populus tomentosa] >gi|301331543|gb|ADK70746.1| actin [Populus tomentosa] >gi|301331546|gb|ADK70747.1| actin [Populus tomentosa] >gi|301331549|gb|ADK70748.1| actin [Populus tomentosa] >gi|301331552|gb|ADK70749.1| actin [Populus tomentosa] >gi|301331555|gb|ADK70750.1| actin [Populus tomentosa] >gi|301331558|gb|ADK70751.1| actin	Unigene35379_All//0.00E+00//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene35379_All//0.00E+00//TC176834		ko04145|Phagosome		nr +
Unigene3538_All	1720	9.34	26.31	13.72	19.20	19.54	18.41	65.26	72.66	158.59	1.49E+00	2.40E-61	Up	5.55E-01	1.67E-06		2.52E-02	8.20E-01		-6.10E-02	6.35E-01		1.55E-01	2.41E-04		1.28E+00	0.00E+00	Up	Unigene3538_All//gi|38016531|gb|AAR07601.1|//2.00E-32//fiber quinone-oxidoreductase [Gossypium barbadense]	Unigene3538_All//2.00E-19//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene3538_All//0.00E+00//gi|78339631|gb|DT559905.1|DT559905			GO:0008152//GO:0009528//GO:0009534//GO:0016655//GO:0046914	nr +
Unigene35380_All	3001	2.13	1.03	0.92	4.76	4.49	2.77	9.62	1.69	3.68	-1.05E+00	1.06E-05	Down	-1.20E+00	1.41E-06	Down	-8.66E-02	6.15E-01		-7.83E-01	6.34E-08		-2.51E+00	6.80E-96	Down	-1.39E+00	1.18E-44	Down	Unigene35380_All//gi|22331291|ref|NP_189009.2|//0.00E+00//KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor [Arabidopsis thaliana] >gi|21703149|gb|AAM74514.1| AT3g23670|MDR19_16 [Arabidopsis thaliana] >gi|23268687|gb|AAN16470.1| phragmoplast-associated kinesin-related protein 1-like protein [Arabidopsis thaliana] >gi|23268689|gb|AAN16471.1| phragmoplast-associated kinesin-related protein 1-like protein [Arabidopsis thaliana]	Unigene35380_All//0.00E+00//AT3G23670| KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor	Unigene35380_All//0.00E+00//ES824306				nr +
Unigene35382_All	1449	3.50	7.45	3.49	6.19	4.14	4.58	21.74	31.87	32.94	1.09E+00	1.39E-09	Up	-4.70E-03	1.00E+00		-5.82E-01	1.22E-03		-4.34E-01	2.61E-02		5.52E-01	3.37E-15		6.00E-01	1.60E-18	Down	Unigene35382_All//gi|224082532|ref|XP_002306731.1|//6.00E-26//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222856180|gb|EEE93727.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene35382_All//1.00E-05//AT1G34190| anac017 (Arabidopsis NAC domain containing protein 17); transcription factor	Unigene35382_All//0.00E+00//TC174628	NAC			nr -
Unigene35388_All	725	10.68	0.56	2.86	2.06	1.28	0.25	3.21	0.69	0.44	-4.26E+00	1.79E-34	Down	-1.90E+00	1.18E-14	Down	-6.85E-01	1.99E-01		-3.05E+00	7.42E-06	Down	-2.21E+00	2.77E-07	Down	-2.87E+00	7.21E-10	Down	Unigene35388_All//gi|18416824|ref|NP_567758.1|//3.00E-59//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|30687361|ref|NP_849451.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75161442|sp|Q8VY93.1|GDL66_ARATH RecName: Full=GDSL esterase/lipase At4g26790; AltName: Full=Extracellular lipase At4g26790; Flags: Precursor	Unigene35388_All//2.00E-60//AT4G26790| GDSL-motif lipase/hydrolase family protein	Unigene35388_All//0.00E+00//gi|109863350|gb|DW492327.1|DW492327				nr +
Unigene35389_All	1896	21.08	0.96	4.83	2.44	1.73	0.98	2.05	1.34	0.67	-4.45E+00	3.98E-182	Down	-2.13E+00	1.59E-85	Down	-5.02E-01	6.77E-02		-1.32E+00	3.11E-06	Down	-6.10E-01	2.83E-02		-1.61E+00	3.31E-08	Down	Unigene35389_All//gi|18416824|ref|NP_567758.1|//1.00E-135//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|30687361|ref|NP_849451.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75161442|sp|Q8VY93.1|GDL66_ARATH RecName: Full=GDSL esterase/lipase At4g26790; AltName: Full=Extracellular lipase At4g26790; Flags: Precursor	Unigene35389_All//2.00E-136//AT4G26790| GDSL-motif lipase/hydrolase family protein	Unigene35389_All//0.00E+00//TC149939				nr -
Unigene35390_All	4255	1.43	0.74	1.21	6.59	5.60	3.59	10.25	5.87	4.88	-9.50E-01	8.83E-05		-2.33E-01	4.01E-01		-2.35E-01	2.14E-02		-8.78E-01	4.84E-18		-8.04E-01	3.23E-27		-1.07E+00	7.34E-45	Down	Unigene35390_All//gi|115448815|ref|NP_001048187.1|//0.00E+00//Os02g0760200 [Oryza sativa Japonica Group] >gi|113537718|dbj|BAF10101.1| Os02g0760200 [Oryza sativa Japonica Group]	Unigene35390_All//0.00E+00//AT5G65440| unknown protein	Unigene35390_All//0.00E+00//gi|78344640|gb|DT564914.1|DT564914				nr +
Unigene35391_All	1568	36.80	26.72	18.10	40.66	77.70	39.86	26.91	13.65	13.26	-4.62E-01	2.31E-11		-1.02E+00	4.30E-42	Down	9.34E-01	3.32E-93		-2.87E-02	7.21E-01		-9.80E-01	1.75E-36		-1.02E+00	3.87E-40	Down	Unigene35391_All//gi|119444239|gb|ABL75361.1|//1.00E-149//xyloglucan endotransglycosylase precursor [Populus tremula x Populus tremuloides]	Unigene35391_All//1.00E-129//AT4G03210| XTH9 (XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 9); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene35391_All//0.00E+00//TC164853				nr -
Unigene35393_All	1710	23.74	7.67	14.01	5.83	5.16	3.09	4.97	5.06	2.42	-1.63E+00	8.20E-63	Down	-7.61E-01	3.18E-18		-1.77E-01	3.91E-01		-9.15E-01	2.88E-07		2.58E-02	9.11E-01		-1.04E+00	5.34E-09	Down	Unigene35393_All//gi|156138809|dbj|BAF75896.1|//1.00E-123//glucosyltransferase [Cyclamen persicum]	Unigene35393_All//2.00E-106//AT4G01070| GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene35393_All//0.00E+00//TC147977		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene35394_All	2129	2.04	1.00	1.60	5.62	4.06	4.18	6.35	2.57	3.33	-1.03E+00	4.67E-04	Down	-3.50E-01	2.65E-01		-4.68E-01	2.48E-03		-4.26E-01	9.43E-03		-1.31E+00	6.06E-19	Down	-9.32E-01	1.03E-11		Unigene35394_All//gi|42566850|ref|NP_193292.3|//0.00E+00//MAA3 (MAGATAMA 3) [Arabidopsis thaliana] >gi|209574484|gb|ACI63222.1| MAA3 [Arabidopsis thaliana]	Unigene35394_All//0.00E+00//AT4G15570| MAA3 (MAGATAMA 3)	Unigene35394_All//0.00E+00//DW231523		ko03040|Spliceosome//ko03030|DNA replication		nr +
Unigene35395_All	2635	2.48	0.83	0.89	5.24	2.46	4.34	6.13	1.43	3.22	-1.59E+00	2.47E-10	Down	-1.48E+00	5.83E-09	Down	-1.09E+00	1.55E-14	Down	-2.72E-01	9.01E-02		-2.10E+00	1.65E-43	Down	-9.29E-01	9.94E-14		Unigene35395_All//gi|297827231|ref|XP_002881498.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327337|gb|EFH57757.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene35395_All//0.00E+00//AT2G37230| pentatricopeptide (PPR) repeat-containing protein	Unigene35395_All//0.00E+00//TC174886				nr +
Unigene35397_All	710	3.17	1.14	2.25	3.09	2.18	2.86	7.32	13.95	16.83	-1.47E+00	9.69E-04	Down	-4.94E-01	2.73E-01		-5.00E-01	2.53E-01		-1.09E-01	8.04E-01		9.30E-01	1.77E-08		1.20E+00	3.25E-15	Up	Unigene35397_All//gi|212717155|gb|ACJ37419.1|//5.00E-27//NBS-LRR disease resistance protein [Glycine max]	Unigene35397_All//1.00E-12//AT3G44670| ATP binding / nucleoside-triphosphatase/ nucleoside binding / protein binding / transmembrane receptor	Unigene35397_All//0.00E+00//TC162835		ko04626|Plant-pathogen interaction		nr -
Unigene354_All	2224	25.13	5.51	6.06	248.76	163.13	69.86	34.01	6.18	11.11	-2.19E+00	3.06E-128	Down	-2.05E+00	3.25E-114	Down	-6.09E-01	9.44E-208		-1.83E+00	0.00E+00	Down	-2.46E+00	3.83E-244	Down	-1.61E+00	1.35E-144	Down	Unigene354_All//gi|170293773|gb|ACB12931.1|//0.00E+00//pectate lyase 1-27 [Populus tremula x Populus tremuloides]	Unigene354_All//0.00E+00//AT1G04680| pectate lyase family protein	Unigene354_All//0.00E+00//TC169849		ko00040|Pentose and glucuronate interconversions		nr +
Unigene3540_All	1147	17.74	73.15	28.60	132.77	141.46	182.66	134.47	106.95	99.54	2.04E+00	4.81E-175	Up	6.89E-01	1.36E-12		9.16E-02	3.02E-02		4.60E-01	8.73E-42		-3.30E-01	2.10E-19		-4.34E-01	1.31E-32		Unigene3540_All//gi|60932254|gb|AAX37335.1|//1.00E-145//UDP-glucuronic acid decarboxylase 2 [Populus tomentosa]	Unigene3540_All//5.00E-144//AT3G62830| AUD1; UDP-glucuronate decarboxylase/ catalytic/ dTDP-glucose 4,6-dehydratase	Unigene3540_All//0.00E+00//TC136608		ko00523|Polyketide sugar unit biosynthesis		nr -
Unigene35401_All	1592	5.36	2.20	2.71	4.38	2.88	4.26	2.76	2.55	1.58	-1.29E+00	6.95E-10	Down	-9.84E-01	2.32E-06		-6.07E-01	3.63E-03		-4.19E-02	8.78E-01		-1.17E-01	6.77E-01		-8.09E-01	1.17E-03		Unigene35401_All//gi|226503603|ref|NP_001148558.1|//1.00E-136//para-hydroxybenzoate--polyprenyltransferase [Zea mays] >gi|195620420|gb|ACG32040.1| para-hydroxybenzoate--polyprenyltransferase [Zea mays]	Unigene35401_All//2.00E-113//AT4G23660| AtPPT1 (Arabidopsis thaliana polyprenyltransferase 1); 4-hydroxybenzoate nonaprenyltransferase	Unigene35401_All//0.00E+00//gi|78352695|gb|DT572969.1|DT572969		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +

Unigene35402_All	985	7.54	94.24	6.87	6.32	21.71	13.53	13.31	10.52	65.36	3.64E+00	0.00E+00	Up	-1.36E-01	5.93E-01		1.78E+00	1.05E-43	Up	1.10E+00	1.91E-12	Up	-3.39E-01	1.74E-02		2.30E+00	1.54E-194	Up	Unigene35402_All//gi|112819971|gb|ABI23959.1|//3.00E-86//WRKY transcription factor 2 [Gossypium hirsutum]	Unigene35402_All//9.00E-35//AT2G25000| WRKY60; transcription factor	Unigene35402_All//0.00E+00//gi|73860760|gb|DT463499.1|DT463499	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene35403_All	1907	7.82	74.56	8.43	7.91	25.05	13.52	6.78	6.73	50.51	3.25E+00	0.00E+00	Up	1.09E-01	5.08E-01		1.66E+00	9.34E-89	Up	7.73E-01	2.29E-13		-1.19E-02	9.69E-01		2.90E+00	0.00E+00	Up	Unigene35403_All//gi|112819971|gb|ABI23959.1|//1.00E-171//WRKY transcription factor 2 [Gossypium hirsutum]	Unigene35403_All//1.00E-63//AT1G80840| WRKY40; transcription factor	Unigene35403_All//0.00E+00//TC130114	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene35407_All	3477	1.87	0.83	0.72	5.09	4.53	3.05	10.34	7.50	7.12	-1.17E+00	9.83E-07	Down	-1.37E+00	5.05E-08	Down	-1.68E-01	2.50E-01		-7.37E-01	9.58E-09		-4.63E-01	6.17E-09		-5.39E-01	6.76E-12		Unigene35407_All//gi|140053517|gb|ABE79572.2|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene35407_All//0.00E+00//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene35407_All//0.00E+00//TC138395				nr +
Unigene35408_All	1485	193.22	116.80	115.86	256.22	272.33	307.26	269.00	176.11	132.80	-7.26E-01	9.07E-120		-7.38E-01	2.14E-119		8.80E-02	3.06E-04		2.62E-01	8.93E-32		-6.11E-01	2.84E-150		-1.02E+00	0.00E+00	Down	Unigene35408_All//gi|211906446|gb|ACJ11716.1|//0.00E+00//adenosine kinase [Gossypium hirsutum]	Unigene35408_All//3.00E-172//AT5G03300| ADK2 (ADENOSINE KINASE 2); adenosine kinase/ copper ion binding / kinase	Unigene35408_All//0.00E+00//TC134512		ko00230|Purine metabolism		nr +
Unigene35411_All	2496	2.62	4.69	3.05	8.24	11.95	15.02	2.81	8.09	4.18	8.40E-01	5.41E-07		2.20E-01	3.64E-01		5.36E-01	5.08E-09		8.66E-01	3.78E-23		1.52E+00	5.83E-35	Up	5.73E-01	1.91E-04		Unigene35411_All//gi|224121242|ref|XP_002318534.1|//0.00E+00//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222859207|gb|EEE96754.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene35411_All//9.00E-112//AT1G27180| disease resistance protein (TIR-NBS-LRR class), putative	Unigene35411_All//0.00E+00//ES803522				nr +
Unigene35412_All	2503	6.94	7.71	8.06	10.13	7.88	5.03	8.13	6.21	2.64	1.52E-01	2.70E-01		2.16E-01	1.13E-01		-3.62E-01	3.71E-04		-1.01E+00	1.58E-20	Down	-3.87E-01	3.94E-04		-1.62E+00	1.08E-39	Down	Unigene35412_All//gi|5454195|gb|AAD43610.1|AC005698.9//6.00E-25//T3P18.9 [Arabidopsis thaliana]	Unigene35412_All//3.00E-26//AT1G62530| unknown protein	Unigene35412_All//0.00E+00//gi|164326255|gb|ES828265.1|ES828265				nr +
Unigene35413_All	1547	14.27	11.96	16.69	10.85	12.29	10.92	12.93	13.83	6.34	-2.56E-01	3.47E-02		2.26E-01	5.34E-02		1.79E-01	2.01E-01		8.90E-03	9.50E-01		9.77E-02	4.38E-01		-1.03E+00	9.62E-20	Down	Unigene35413_All//gi|164604992|dbj|BAF98292.1|//1.00E-120//2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase [Hevea brasiliensis]	Unigene35413_All//6.00E-105//AT2G02500| ISPD; 2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	Unigene35413_All//0.00E+00//TC137211		ko00900|Terpenoid backbone biosynthesis		nr +
Unigene35415_All	682	0.15	1.41	0.16	2.63	2.17	1.06	1.36	0.37	0.93	3.20E+00	6.55E-04	Up	2.61E-02	1.00E+00		-2.76E-01	5.85E-01		-1.31E+00	8.11E-03		-1.89E+00	6.92E-03		-5.45E-01	3.80E-01		Unigene35415_All//gi|20197242|gb|AAC28772.2|//4.00E-26//expressed protein [Arabidopsis thaliana]	Unigene35415_All//5.00E-39//AT5G01620| unknown protein	Unigene35415_All//0.00E+00//CO120227				nr -
Unigene35416_All	1681	2.02	3.26	3.93	8.33	9.57	5.88	3.67	0.17	1.97	6.86E-01	7.12E-03		9.57E-01	6.48E-05		2.00E-01	1.88E-01		-5.01E-01	6.71E-04		-4.40E+00	2.34E-34	Down	-9.01E-01	1.49E-05		Unigene35416_All//gi|20197242|gb|AAC28772.2|//1.00E-100//expressed protein [Arabidopsis thaliana]	Unigene35416_All//1.00E-174//AT5G01620| unknown protein	Unigene35416_All//0.00E+00//CO120228				nr +
Unigene3542_All	990	51.85	23.70	42.28	22.89	18.54	14.92	3.72	2.87	2.66	-1.13E+00	1.66E-45	Down	-2.94E-01	1.29E-04		-3.04E-01	6.29E-03		-6.18E-01	2.94E-08		-3.72E-01	2.20E-01		-4.84E-01	8.22E-02		Unigene3542_All//gi|73761699|gb|AAZ83349.1|//4.00E-51//MAP kinase [Gossypium hirsutum]	Unigene3542_All//1.00E-38//AT3G14720| ATMPK19; MAP kinase	Unigene3542_All//5.00E-163//CO105739			GO:0000166//GO:0004674	nr +
Unigene35420_All	1487	4.01	4.77	4.15	1.91	3.82	1.52	3.24	0.82	1.45	2.50E-01	2.84E-01		5.05E-02	8.43E-01		1.00E+00	2.90E-05	Up	-3.31E-01	4.14E-01		-1.99E+00	1.23E-12	Down	-1.16E+00	1.97E-06	Down	Unigene35420_All//gi|53370641|gb|AU89136.1|//2.00E-11//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene35420_All//9.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene35420_All//0.00E+00//gi|13353059|gb|BG443407.1|BG443407				nr -
Unigene35422_All	1295	6.46	13.89	15.30	57.05	57.09	37.35	23.80	12.23	11.57	1.10E+00	8.76E-16	Up	1.24E+00	4.88E-20	Up	1.10E-03	9.89E-01		-6.11E-01	5.20E-25		-9.60E-01	5.02E-26		-1.04E+00	1.68E-30	Down	Unigene35422_All//gi|15242391|ref|NP_197082.1|//4.00E-71//pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] >gi|9755623|emb|CAC01777.1| proline-rich protein [Arabidopsis thaliana] >gi|27311645|gb|AAO00788.1| proline-rich protein [Arabidopsis thaliana] >gi|53828649|gb|AAL94434.1| At5g15780 [Arabidopsis thaliana]	Unigene35422_All//6.00E-37//AT5G15780| pollen Ole e 1 allergen and extensin family protein	Unigene35422_All//0.00E+00//gi|109865457|gb|DW494433.1|DW494433		ko03040|Spliceosome		nr -
Unigene35423_All	1429	2.78	5.78	6.00	24.30	25.42	14.41	14.41	4.62	4.27	1.05E+00	3.49E-07	Up	1.11E+00	1.23E-07	Up	6.53E-02	5.66E-01		-7.54E-01	3.27E-17		-1.64E+00	1.16E-39	Down	-1.76E+00	6.17E-45	Down	Unigene35423_All//gi|87241486|gb|AB033344.1|//2.00E-78//Pollen Ole e 1 allergen and extensin [Medicago truncatula]	Unigene35423_All//7.00E-37//AT5G15780| pollen Ole e 1 allergen and extensin family protein	Unigene35423_All//0.00E+00//gi|109865457|gb|DW494433.1|DW494433		ko03040|Spliceosome		nr +
Unigene35425_All	1688	31.09	13.39	19.31	53.03	53.37	57.74	38.70	18.22	58.98	-1.22E+00	3.33E-52	Down	-6.87E-01	1.11E-19		9.10E-03	9.03E-01		1.23E-01	2.93E-02		-1.09E+00	2.72E-66	Down	6.08E-01	1.39E-38		Unigene35425_All//gi|224124762|ref|XP_002329942.1|//0.00E+00//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222871964|gb|EEF09095.1| glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene35425_All//0.00E+00//AT5G47780| GAUT4 (Galacturonosyltransferase 4); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups	Unigene35425_All//0.00E+00//TC156150				nr +
Unigene35427_All	1777	12.16	6.30	13.96	9.98	11.24	10.14	2.81	0.92	3.25	-9.48E-01	6.83E-15		2.00E-01	1.01E-01		1.72E-01	2.13E-01		2.31E-02	9.00E-01		-1.61E+00	5.67E-10	Down	2.12E-01	3.64E-01		Unigene35427_All//gi|108735959|gb|ABG00264.1|//4.00E-94//Tic21 [Pisum sativum]	Unigene35427_All//4.00E-88//AT2G15290| TIC21 (TRANSLOCON AT INNER MEMBRANE OF CHLOROPLASTS 21); copper uptake transmembrane transporter/ iron ion transmembrane transporter/ protein homodimerization	Unigene35427_All//0.00E+00//TC135153				nr -
Unigene35428_All	1651	7.00	4.48	3.39	70.12	83.01	86.00	14.88	8.18	8.13	-6.44E-01	1.08E-04		-1.05E+00	3.13E-09	Down	2.44E-01	1.59E-09		2.95E-01	1.05E-12		-8.64E-01	1.27E-17		-8.72E-01	1.96E-18		Unigene35428_All//gi|115452129|ref|NP_001049665.1|//1.00E-134//Os03g0267500 [Oryza sativa Japonica Group] >gi|113548136|dbj|BAF11579.1| Os03g0267500 [Oryza sativa Japonica Group]	Unigene35428_All//1.00E-161//AT5G05840| unknown protein	Unigene35428_All//0.00E+00//TC154972				nr +
Unigene35429_All	1589	27.33	84.06	48.16	35.05	53.92	61.25	64.42	71.39	73.58	1.62E+00	1.19E-202	Up	8.17E-01	2.53E-38		6.21E-01	1.18E-32		8.05E-01	1.74E-52		1.48E-01	9.25E-04		1.92E-01	5.13E-06		Unigene35429_All//gi|297813953|ref|XP_002874860.1|//0.00E+00//two-pore channel 1 [Arabidopsis lyrata subsp. lyrata] >gi|297320697|gb|EFH51119.1| two-pore channel 1 [Arabidopsis lyrata subsp. lyrata]	Unigene35429_All//0.00E+00//AT4G03560| ATTPC1 (TWO-PORE CHANNEL 1); calcium channel/ voltage-gated calcium channel	Unigene35429_All//0.00E+00//TC158793				nr -
Unigene3543_All	1830	4.06	2.13	1.75	6.72	4.44	6.47	9.33	8.13	24.30	-9.29E-01	1.72E-05		-1.22E+00	1.17E-07	Down	-5.98E-01	5.86E-05		-5.64E-02	7.58E-01		-1.99E-01	1.29E-01		1.38E+00	4.34E-67	Up	Unigene3543_All//gi|45387415|gb|AAS60198.1|//0.00E+00//hexokinase 6 [Nicotiana tabacum]	Unigene3543_All//1.00E-157//AT1G50460| HKL1 (HEXOKINASE-LIKE 1); ATP binding / fructokinase/ glucokinase/ hexokinase	Unigene3543_All//0.00E+00//DW234768		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism	GO:0004396//GO:0006007//GO:0006970//GO:0032559//GO:0043231	nr -
Unigene35433_All	1750	3.17	1.65	1.22	4.21	3.25	4.46	6.06	1.91	2.91	-9.41E-01	2.17E-04		-1.38E+00	5.34E-07	Down	-3.76E-01	8.10E-02		8.37E-02	7.21E-01		-1.67E+00	2.92E-21	Down	-1.06E+00	2.37E-11	Down	Unigene35433_All//gi|240254494|ref|NP_179656.4|//0.00E+00//ATP binding / protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Unigene35433_All//0.00E+00//AT2G20635| ATP binding / protein kinase/ protein serine/threonine kinase	Unigene35433_All//0.00E+00//TC149468				nr -
Unigene35436_All	616	1.70	0.99	1.64	2.75	1.45	1.17	2.20	0.48	2.33	-7.83E-01	2.34E-01		-4.85E-02	9.57E-01		-9.20E-01	5.65E-02		-1.23E+00	1.61E-02		-2.21E+00	1.58E-04	Down	8.41E-02	8.72E-01		Unigene35436_All//gi|38344244|emb|CAD41337.2|//1.00E-17//Os991113_30.21 [Oryza sativa (japonica cultivar-group)]	Unigene35436_All//2.00E-10//AT3G09510| nucleic acid binding	Unigene35436_All//0.00E+00//TC156867				nr -
Unigene35437_All	509	11.00	13.24	11.72	16.05	14.82	10.56	4.57	1.72	1.72	2.68E-01	2.61E-01		9.13E-02	7.19E-01		-1.15E-01	6.11E-01		-6.04E-01	2.51E-03		-1.41E+00	2.82E-04	Down	-1.41E+00	1.83E-04	Down			Unigene35437_All//2.00E-158//gi|13350854|gb|BG441202.1|BG441202				ESTscan -
Unigene35438_All	906	4.04	1.57	2.23	6.87	3.88	3.89	2.89	1.38	1.54	-1.37E+00	4.35E-05	Down	-8.56E-01	1.08E-02		-8.26E-01	1.65E-04		-8.22E-01	4.03E-04		-1.06E+00	2.42E-03		-9.11E-01	6.75E-03		Unigene35438_All//gi|297727877|ref|NP_001176302.1|//1.00E-23//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1| Os11g0106066 [Oryza sativa Japonica Group]	Unigene35438_All//1.00E-13//AT3G09510| nucleic acid binding	Unigene35438_All//0.00E+00//TC156867				nr -
Unigene35439_All	956	7.55	4.03	6.85	9.64	7.53	6.09	3.45	1.62	2.00	-9.07E-01	3.52E-05		-1.41E-01	5.86E-01		-3.57E-01	5.87E-02		-6.62E-01	3.60E-04		-1.09E+00	3.88E-04	Down	-7.86E-01	7.32E-03		Unigene35439_All//gi|38344244|emb|CAD41337.2|//8.00E-15//Os991113_30.21 [Oryza sativa (japonica cultivar-group)]	Unigene35439_All//3.00E-12//AT3G09510| nucleic acid binding	Unigene35439_All//0.00E+00//gi|13350854|gb|BG441202.1|BG441202				nr +
Unigene35440_All	1280	5.80	14.09	5.82	9.73	11.49	8.43	11.20	20.47	14.38	1.28E+00	8.30E-20	Up	4.90E-03	1.00E+00		2.40E-01	1.22E-01		-2.06E-01	2.49E-01		8.71E-01	5.73E-19		3.61E-01	1.41E-03		Unigene35440_All//gi|18425169|ref|NP_569047.1|//3.00E-85//SKIP2 (SKP1/ASK1 INTERACTING PROTEIN 2); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75272932|sp|Q9FE83.1|SKIP2_ARATH RecName: Full=F-box protein SKIP2; AltName: Full=SKP1-interacting partner 2 >gi|10716949|gb|AAG21977.1| SKP1 interacting partner 2 [Arabidopsis thaliana] >gi|27311735|gb|AAO00833.1| SKP1 interacting partner 2 (SKIP2) [Arabidopsis thaliana] >gi|31711938|gb|AAP68325.1| At5g67250 [Arabidopsis thaliana]	Unigene35440_All//1.00E-86//AT5G67250| SKIP2 (SKP1/ASK1 INTERACTING PROTEIN 2); ubiquitin-protein ligase	Unigene35440_All//0.00E+00//ES830912		ko04626|Plant-pathogen interaction//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene35441_All	1917	0.93	3.70	2.39	3.07	4.62	2.90	3.93	7.46	6.19	2.00E+00	6.34E-15	Up	1.36E+00	7.97E-06	Up	5.90E-01	1.44E-03		-8.15E-02	7.58E-01		9.26E-01	8.53E-12		6.58E-01	4.56E-06		Unigene35441_All//gi|18425169|ref|NP_569047.1|//0.00E+00//SKIP2 (SKP1/ASK1 INTERACTING PROTEIN 2); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75272932|sp|Q9FE83.1|SKIP2_ARATH RecName: Full=F-box protein SKIP2; AltName: Full=SKP1-interacting partner 2 >gi|10716949|gb|AAG21977.1| SKP1 interacting partner 2 [Arabidopsis thaliana] >gi|27311735|gb|AAO00833.1| SKP1 interacting partner 2 (SKIP2) [Arabidopsis thaliana] >gi|31711938|gb|AAP68325.1| At5g67250 [Arabidopsis thaliana]	Unigene35441_All//0.00E+00//AT5G67250| SKIP2 (SKP1/ASK1 INTERACTING PROTEIN 2); ubiquitin-protein ligase	Unigene35441_All//0.00E+00//gi|78343629|gb|DT563903.1|DT563903		ko04626|Plant-pathogen interaction//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene35442_All	2719	7.20	1.23	1.94	14.09	10.01	5.23	9.36	1.32	4.32	-2.55E+00	3.00E-54	Down	-1.89E+00	4.02E-36	Down	-4.94E-01	3.50E-10		-1.43E+00	4.69E-53	Down	-2.82E+00	3.84E-96	Down	-1.11E+00	3.13E-28	Down	Unigene35442_All//gi|224165009|ref|XP_002313653.1|//0.00E+00//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222850061|gb|EEE87608.1| nucleobase ascorbate transporter [Populus trichocarpa]	Unigene35442_All//0.00E+00//AT2G27810| xanthine/uracil permease family protein	Unigene35442_All//0.00E+00//TC154374				nr -

Unigene35443_All	2265	3.70	5.91	8.30	9.24	11.96	12.42	8.89	6.27	7.92	6.76E-01	1.13E-05		1.17E+00	2.68E-17	Up	3.73E-01	1.55E-04		4.27E-01	1.84E-05		-5.02E-01	4.22E-06		-1.67E-01	1.49E-01		Unigene35443_All//gi|15239582|ref|NP_197384.1|//0.00E+00//SPL7 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 7); DNA binding / transcription factor [Arabidopsis thaliana] >gi|67461538|sp|Q8S9G8.2|SPL7_ARATH RecName: Full=Squamosa promoter-binding-like protein 7 >gi|13605912|gb|AAK32941.1|AF367355.1 AT5g18830/F17K4_80 [Arabidopsis thaliana] >gi|5931635|emb|CAB56574.1| squamosa promoter binding protein-like 7 [Arabidopsis thaliana] >gi|5931637|emb|CAB56575.1| squamosa promoter binding protein-like 7 [Arabidopsis thaliana]	Unigene35443_All//7.00E-168//AT5G18830| SPL7 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 7); DNA binding / transcription factor	Unigene35443_All//1.00E-162//ES799562	SBP			nr -
Unigene35444_All	2567	1.83	4.70	2.92	7.82	14.98	12.67	4.04	4.40	1.58	1.36E+00	1.09E-14	Up	6.73E-01	2.30E-03		9.38E-01	9.33E-30		6.96E-01	5.16E-14		1.24E-01	4.93E-01		-1.35E+00	6.23E-16	Down	Unigene35444_All//gi|115446743|ref|NP_001047151.1|//0.00E+00//Os02g0562300 [Oryza sativa Japonica Group] >gi|113536682|dbj|BAF09065.1| Os02g0562300 [Oryza sativa Japonica Group]	Unigene35444_All//0.00E+00//AT2G18750| calmodulin-binding protein	Unigene35444_All//0.00E+00//TC149311		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene35446_All	2229	2.49	5.48	2.80	5.05	6.49	8.25	12.12	22.86	26.06	1.14E+00	1.73E-11	Up	1.68E-01	5.31E-01		3.61E-01	1.27E-02		7.07E-01	2.06E-08		9.15E-01	3.27E-39		1.10E+00	7.36E-62	Up	Unigene35446_All//gi|15224105|ref|NP_180001.1|//0.00E+00//potassium channel tetramerisation domain-containing protein [Arabidopsis thaliana] >gi|56236038|gb|AAV84475.1| At2g24240 [Arabidopsis thaliana] >gi|56790194|gb|AAK30014.1| At2g24240 [Arabidopsis thaliana]	Unigene35446_All//0.00E+00//AT2G24240| potassium channel tetramerisation domain-containing protein	Unigene35446_All//0.00E+00//TC130098				nr +
Unigene35448_All	1788	9.57	32.90	28.59	10.92	10.32	35.39	2.91	4.02	2.03	1.78E+00	2.87E-102	Up	1.58E+00	4.13E-73	Up	-8.13E-02	5.94E-01		1.70E+00	2.71E-110	Up	4.67E-01	1.77E-02		-5.21E-01	2.19E-02		Unigene35448_All//gi|226494043|ref|NP_001150498.1|//5.00E-65//LOC100284129 [Zea mays] >gi|195639632|gb|ACG39284.1| pathogen-related protein [Zea mays]	Unigene35448_All//4.00E-55//AT1G78780| pathogenesis-related family protein	Unigene35448_All//0.00E+00//TC144906				nr -
Unigene35449_All	1849	18.73	13.24	18.09	17.32	14.47	7.99	6.91	6.71	6.08	-5.01E-01	3.60E-08		-5.07E-02	6.24E-01		-2.60E-01	5.07E-03		-1.12E+00	2.32E-30	Down	-4.07E-02	8.06E-01		-1.85E-01	2.15E-01		Unigene35449_All//gi|15232059|ref|NP_189337.1|//2.00E-70//AT-TCP20; transcription factor [Arabidopsis thaliana] >gi|75273954|sp|Q9LSD5.1|TCP20_ARATH RecName: Full=Transcription factor TCP20	Unigene35449_All//2.00E-61//AT3G27010| AT-TCP20; transcription factor	Unigene35449_All//0.00E+00//gi|78354309|gb|DT574583.1|DT574583	TCP			nr -
Unigene3545_All	1423	1.47	2.96	4.64	3.36	2.54	2.09	3.09	3.00	2.18	1.01E+00	7.90E-04	Up	1.66E+00	1.44E-10	Up	-4.03E-01	1.49E-01		-6.82E-01	1.26E-02		-4.46E-02	8.82E-01		-5.01E-01	4.55E-02		Unigene3545_All//gi|115434224|ref|NP_001041870.1|//3.00E-07//Os01g0120700 [Oryza sativa Japonica Group] >gi|113531401|dbj|BAF03784.1| Os01g0120700 [Oryza sativa Japonica Group]		Unigene3545_All//0.00E+00//TC132238				nr +
Unigene35450_All	1975	44.24	4.28	17.23	166.85	63.20	23.85	26.82	10.05	5.67	-3.37E+00	0.00E+00	Down	-1.36E+00	1.21E-99	Down	-1.40E+00	0.00E+00	Down	-2.81E+00	0.00E+00	Down	-1.42E+00	2.53E-81	Down	-2.24E+00	8.32E-158	Down	Unigene35450_All//gi|22331260|ref|NP_188894.2|//1.00E-54//senescence-associated protein-related [Arabidopsis thaliana]	Unigene35450_All//4.00E-54//AT3G22550| senescence-associated protein-related	Unigene35450_All//0.00E+00//TC147108				nr +
Unigene35452_All	1710	2.14	4.44	1.68	12.03	7.53	11.52	3.66	3.47	2.35	1.05E+00	1.15E-06	Up	-3.49E-01	3.21E-01		-6.76E-01	1.11E-09		-6.32E-02	6.81E-01		-7.63E-02	7.44E-01		-6.37E-01	1.75E-03		Unigene35452_All//gi|224068644|ref|XP_002326164.1|//1.00E-138//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222833357|gb|EEE71834.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene35452_All//1.00E-72//AT4G36920| AP2 (APETALA 2); transcription factor	Unigene35452_All//0.00E+00//CO105897	AP2-EREBP			nr -
Unigene35454_All	2802	3.66	1.48	2.03	8.14	6.38	10.61	9.57	4.39	8.91	-1.30E+00	5.91E-12	Down	-8.48E-01	5.18E-06		-3.52E-01	1.18E-03		3.81E-01	9.06E-05		-1.13E+00	3.04E-29	Down	-1.02E-01	3.39E-01		Unigene35454_All//gi|75318355|sp|Q49289.1|RH29_ARATH//0.00E+00//RecName: Full=Putative DEAD-box ATP-dependent RNA helicase 29 >gi|2829912|gb|AAC00620.1| Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Unigene35454_All//0.00E+00//AT1G77030| ATP binding / ATP-dependent helicase/ RNA binding / helicase/ hydrolase, acting on acid anhydrides, in phosphorus-containing anhydrides / nucleic acid binding	Unigene35454_All//0.00E+00//gi|164360878|gb|ES851392.1|ES851392				nr -
Unigene35455_All	1690	7.65	29.02	19.19	13.12	18.07	13.87	16.94	22.41	12.23	1.92E+00	1.00E-94	Up	1.33E+00	6.22E-36	Up	4.63E-01	3.41E-07		8.05E-02	5.82E-01		4.04E-01	1.82E-07		-4.69E-01	1.04E-07		Unigene35455_All//gi|297853292|ref|XP_002894527.1|//1.00E-139//BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297340369|gb|EFH70786.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene35455_All//1.00E-134//AT1G55760| BTB/POZ domain-containing protein	Unigene35455_All//0.00E+00//TC149255				nr +
Unigene35456_All	2209	62.08	14.68	31.58	203.97	201.98	151.07	8.13	3.35	2.81	-2.08E+00	1.63E-294	Down	-9.75E-01	7.52E-92		-1.41E-02	6.52E-01		-4.33E-01	2.64E-80		-1.28E+00	3.45E-24	Down	-1.53E+00	1.85E-32	Down	Unigene35456_All//gi|225455386|ref|XP_002278061.1|//0.00E+00//PREDICTED: similar to pectin methylesterase 1 [Vitis vinifera]	Unigene35456_All//0.00E+00//AT3G49220| pectinesterase family protein	Unigene35456_All//0.00E+00//TC135285		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene35457_All	447	3.04	0.57	2.50	5.24	2.23	3.33	0.66	0.19	0.36	-2.42E+00	3.35E-04	Down	-2.83E-01	6.05E-01		-1.23E+00	1.83E-03		-6.52E-01	1.27E-01		-1.82E+00	2.11E-01		-8.93E-01	4.71E-01		Unigene35457_All//gi|186911832|gb|ACC95131.1|//2.00E-09//COL3 [Beta vulgaris subsp. vulgaris]	Unigene35457_All//3.00E-08//AT1G28050| zinc finger (B-box type) family protein	Unigene35457_All//0.00E+00//TC136544	C2C2-CO-like			nr +
Unigene35458_All	1844	4.97	2.06	3.73	9.24	5.96	3.65	1.42	1.02	0.82	-1.27E+00	2.39E-10	Down	-4.15E-01	4.07E-02		-6.33E-01	2.78E-07		-1.34E+00	1.08E-21	Down	-4.79E-01	1.83E-01		-7.92E-01	1.79E-02		Unigene35458_All//gi|297851244|ref|XP_002893503.1|//6.00E-50//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339345|gb|EFH69762.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35458_All//8.00E-49//AT2G33500| zinc finger (B-box type) family protein	Unigene35458_All//0.00E+00//gi|78343647|gb|DT563921.1|DT563921	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene35459_All	1621	16.33	8.50	12.38	18.07	15.72	15.52	11.19	8.12	5.36	-9.42E-01	7.14E-18		-3.99E-01	2.74E-04		-2.01E-01	5.01E-02		-2.20E-01	3.70E-02		-4.62E-01	6.48E-05		-1.06E+00	6.55E-19	Down	Unigene35459_All//gi|15225064|ref|NP_181461.1|//6.00E-86//PGP1 (PHOSPHATIDYLGLYCEROLPHOSPHATE SYNTHASE 1); CDP-alcohol phosphatidyltransferase/ CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase [Arabidopsis thaliana] >gi|13365519|dbj|BAB39133.1| phosphatidylglycerolphosphate synthase [Arabidopsis thaliana] >gi|15778125|dbj|BAB68508.1| phophoglycerolphosphate synthase [Arabidopsis thaliana] >gi|89274135|gb|ABD65588.1| At2g39290 [Arabidopsis thaliana]	Unigene35459_All//1.00E-86//AT2G39290| PGP1 (PHOSPHATIDYLGLYCEROLPHOSPHATE SYNTHASE 1); CDP-alcohol phosphatidyltransferase/ CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidyltransferase	Unigene35459_All//0.00E+00//TC153317		ko00564|Glycerophospholipid metabolism		nr +
Unigene35461_All	219	0.72	0.23	0.00	19.11	21.86	10.11	3.67	2.29	39.84	-1.63E+00	4.89E-01		-9.49E+00	2.44E-01		1.94E-01	5.43E-01		-9.19E-01	1.75E-03		-6.80E-01	3.53E-01		3.44E+00	7.77E-41	Up	Unigene35461_All//gi|223452412|gb|ACM89533.1|//1.00E-07//protein kinase [Glycine max]	Unigene35461_All//3.00E-08//AT3G46290| protein kinase, putative	Unigene35461_All//1.00E-70//gi|78326187|gb|DT546461.1|DT546461				nr +
Unigene35462_All	1041	3.12	1.75	2.51	33.78	30.76	25.47	9.50	9.84	35.17	-8.31E-01	1.57E-02		-3.14E-01	4.00E-01		-1.35E-01	1.74E-01		-4.08E-01	3.48E-06		4.97E-02	7.87E-01		1.89E+00	2.03E-86	Up	Unigene35462_All//gi|15227790|ref|NP_179901.1|//3.00E-35//protein kinase family protein [Arabidopsis thaliana] >gi|75317972|sp|Q22187.1|Y2232_ARATH RecName: Full=Probable receptor-like protein kinase At2g23200; Flags: Precursor	Unigene35462_All//1.00E-35//AT2G23200| protein kinase family protein	Unigene35462_All//0.00E+00//gi|78326187|gb|DT546461.1|DT546461				nr +
Unigene35465_All	1957	0.11	0.21	0.00	0.08	0.25	0.18	0.91	0.81	0.33	9.54E-01	4.14E-01		-6.74E+00	1.46E-01		1.69E+00	1.66E-01		1.27E+00	3.82E-01		-1.61E-01	7.21E-01		-1.48E+00	8.13E-04	Down	Unigene35465_All//gi|32250969|gb|AAP74222.1|//1.00E-166//RST1 [Arabidopsis thaliana]	Unigene35465_All//4.00E-163//AT3G27670| RST1 (RESURRECTION1); binding	Unigene35465_All//0.00E+00//gi|78327030|gb|DT547304.1|DT547304				nr -
Unigene35466_All	2812	2.33	1.06	1.17	4.98	4.22	4.21	9.53	6.32	7.59	-1.13E+00	1.79E-06	Down	-9.86E-01	4.54E-05		-2.37E-01	1.34E-01		-2.42E-01	1.34E-01		-5.94E-01	2.42E-10		-3.28E-01	3.56E-04		Unigene35466_All//gi|42566010|ref|NP_191322.3|//0.00E+00//exostosin family protein [Arabidopsis thaliana] >gi|44917463|gb|AAS49056.1| At3g57630 [Arabidopsis thaliana] >gi|46931284|gb|AAT06446.1| At3g57630 [Arabidopsis thaliana]	Unigene35466_All//9.00E-158//AT3G57630| exostosin family protein	Unigene35466_All//9.00E-158//ES793786				nr -
Unigene35467_All	1700	55.89	32.34	36.40	75.13	85.60	79.04	61.56	20.80	34.10	-7.89E-01	2.95E-46		-6.19E-01	2.65E-29		1.88E-01	2.31E-06		7.31E-02	1.56E-01		-1.57E+00	1.25E-185	Down	-8.52E-01	9.11E-73		Unigene35467_All//gi|73761691|gb|AAZ83345.1|//0.00E+00//24-sterol C-methyltransferase [Gossypium hirsutum]	Unigene35467_All//4.00E-170//AT5G13710| SMT1 (STEROL METHYLTRANSFERASE 1); sterol 24-C-methyltransferase	Unigene35467_All//0.00E+00//TC129633		ko00100|Steroid biosynthesis		nr -
Unigene35468_All	1972	3.98	2.29	2.16	6.82	5.76	3.55	5.30	4.34	2.32	-7.99E-01	1.19E-04		-8.82E-01	4.72E-05		-2.43E-01	1.31E-01		-9.42E-01	4.96E-10		-2.86E-01	8.61E-02		-1.19E+00	2.54E-13	Down	Unigene35468_All//gi|224099365|ref|XP_002311456.1|//5.00E-52//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222851276|gb|EEE88823.1| AP2/EBP domain-containing transcription factor [Populus trichocarpa]	Unigene35468_All//8.00E-24//AT1G68550| AP2 domain-containing transcription factor, putative	Unigene35468_All//0.00E+00//TC161866	AP2-EREBP			nr -
Unigene35470_All	903	5.33	3.31	8.37	14.01	9.34	8.40	26.36	23.56	10.46	-6.87E-01	1.20E-02		6.52E-01	3.08E-03		-5.85E-01	6.72E-05		-7.38E-01	1.83E-06		-1.62E-01	1.41E-01		-1.33E+00	7.62E-35	Down	Unigene35470_All//gi|29373077|gb|AAO72533.1|//1.00E-16//pyruvate decarboxylase 1 [Lotus corniculatus]	Unigene35470_All//2.00E-16//AT5G01320| pyruvate decarboxylase, putative	Unigene35470_All//7.00E-156//gi|164277220|gb|ES820805.1|ES820805		ko00010|Glycolysis / Gluconeogenesis//ko00380|Tryptophan metabolism		nr -
Unigene35471_All	848	21.90	15.95	34.35	63.56	50.39	43.57	38.09	39.68	17.81	-4.57E-01	3.59E-04		6.49E-01	3.32E-10		-3.35E-01	4.10E-07		-5.45E-01	4.38E-15		5.88E-02	5.88E-01		-1.10E+00	1.06E-34	Down	Unigene35471_All//gi|224112525|ref|XP_002316220.1|//1.00E-44//high mobility group family [Populus trichocarpa] >gi|222862260|gb|EEF02391.1| high mobility group family [Populus trichocarpa]	Unigene35471_All//2.00E-34//AT3G51880| HMGB1 (HIGH MOBILITY GROUP B 1); DNA binding / chromatin binding / structural constituent of chromatin / transcription factor	Unigene35471_All//0.00E+00//TC147911		ko03410|Base excision repair		nr +
Unigene35472_All	1075	53.88	28.42	52.36	75.25	64.19	38.95	61.24	130.75	77.01	-9.23E-01	6.12E-37		-4.13E-02	6.33E-01		-2.29E-01	2.44E-05		-9.50E-01	2.70E-58		1.09E+00	2.81E-143	Up	3.31E-01	3.99E-11		Unigene35472_All//gi|90093310|gb|ABD85168.1|//5.00E-88//At3g22970 [Arabidopsis thaliana]	Unigene35472_All//4.00E-78//AT3G22970| unknown protein	Unigene35472_All//0.00E+00//gi|78351723|gb|DT571997.1|DT571997				nr +
Unigene35473_All	873	25.11	12.65	20.19	37.72	24.85	14.85	22.76	52.52	29.48	-9.89E-01	3.95E-16		-3.15E-01	1.15E-02		-6.02E-01	1.92E-12		-1.35E+00	1.12E-41	Down	1.21E+00	4.52E-55	Up	3.73E-01	6.93E-05		Unigene35473_All//gi|90093310|gb|ABD85168.1|//9.00E-44//At3g22970 [Arabidopsis thaliana]	Unigene35473_All//4.00E-45//AT3G22970| unknown protein	Unigene35473_All//0.00E+00//TC169775				nr -

Unigene35474_All	1878	2.23	1.97	3.23	2.65	3.58	8.13	2.23	1.76	4.52	-1.78E-01	5.84E-01		5.36E-01	3.36E-02		4.31E-01	5.95E-02		1.62E+00	3.74E-25	Up	-3.42E-01	2.28E-01		1.02E+00	1.05E-08	Up	Unigene35474_All//gi|15235527|ref|NP_194630.1|//0.00E+00//AIM1 (ABNORMAL INFLORESCENCE MERISTEM); enoyl-CoA hydratase [Arabidopsis thaliana] >gi|4337025|gb|AAD18041.1| AIM1 protein [Arabidopsis thaliana] >gi|4972047|emb|CAB43915.1| AIM1 protein [Arabidopsis thaliana] >gi|7269799|emb|CAB79639.1| AIM1 protein [Arabidopsis thaliana] >gi|16648891|gb|AAL24297.1| AIM1 protein [Arabidopsis thaliana]	Unigene35474_All//0.00E+00//AT4G29010| AIM1 (ABNORMAL INFLORESCENCE MERISTEM); enoyl-CoA hydratase	Unigene35474_All//0.00E+00//TC145733		ko00592|alpha-Linolenic acid metabolism		nr -
Unigene35476_All	1654	5.66	7.29	12.27	46.74	48.51	55.70	11.81	4.50	9.61	3.65E-01	2.80E-02		1.12E+00	2.33E-17	Up	5.35E-02	4.69E-01		2.53E-01	1.63E-06		-1.39E+00	9.83E-30	Down	-2.97E-01	7.08E-03		Unigene35476_All//gi|15232503|ref|NP_191008.1|//1.00E-133//aspartyl protease family protein [Arabidopsis thaliana] >gi|7288018|emb|CAB81805.1| nucleoid DNA-binding-like protein [Arabidopsis thaliana] >gi|17979257|gb|AAL49945.1| AT3g54400/T12E18_90 [Arabidopsis thaliana] >gi|21700851|gb|AAM70549.1| AT3g54400/T12E18_90 [Arabidopsis thaliana]	Unigene35476_All//1.00E-116//AT3G54400| aspartyl protease family protein	Unigene35476_All//0.00E+00//TC165698				nr -
Unigene3548_All	2598	7.43	4.23	4.73	9.11	10.15	6.61	12.48	5.81	12.82	-8.12E-01	1.77E-10		-6.50E-01	5.21E-07		1.57E-01	1.80E-01		-4.63E-01	2.23E-05		-1.10E+00	3.69E-34	Down	3.85E-02	6.84E-01		Unigene3548_All//gi|240255941|ref|NP_567501.4|//1.00E-173//binding [Arabidopsis thaliana]	Unigene3548_All//3.00E-162//AT4G16490| binding	Unigene3548_All//0.00E+00//TC168319			GO:0003824	nr +
Unigene35480_All	2519	0.25	9.82	3.07	3.28	8.82	10.85	1.49	0.93	1.82	5.30E+00	1.67E-122	Up	3.62E+00	2.23E-29	Up	1.43E+00	3.72E-33	Up	1.72E+00	6.17E-49	Up	-6.85E-01	1.51E-02		2.84E-01	2.74E-01		Unigene35480_All//gi|15238082|ref|NP_198961.1|//0.00E+00//fringe-related protein [Arabidopsis thaliana] >gi|53828537|gb|AAU94378.1| At5g41460 [Arabidopsis thaliana] >gi|57444904|gb|AAW50706.1| At5g41460 [Arabidopsis thaliana]	Unigene35480_All//4.00E-176//AT5G41460| fringe-related protein	Unigene35480_All//0.00E+00//TC171764				nr +
Unigene35481_All	1969	16.98	18.30	17.17	27.80	35.99	64.66	190.14	178.24	651.52	1.08E-01	2.85E-01		1.63E-02	8.86E-01		3.72E-01	6.65E-11		1.22E+00	4.02E-135	Up	-9.32E-02	9.85E-05		1.78E+00	0.00E+00	Up	Unigene35481_All//gi|4334057|gb|AAK60517.1|AF332974_1/0.00E+00//P450 monooxygenase [Gossypium arboreum]	Unigene35481_All//4.00E-127//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene35481_All//0.00E+00//TC132911		ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene35482_All	422	0.99	1.68	1.01	2.36	1.63	3.21	3.91	8.72	4.06	7.61E-01	3.62E-01		2.54E-02	1.00E+00		-5.33E-01	4.45E-01		4.44E-01	4.72E-01		1.16E+00	7.13E-05	Up	5.51E-02	9.19E-01		Unigene35482_All//gi|18252325|gb|AAL66194.1|AF386512_1/8.00E-41//cytochrome P450 [Pyrus communis]	Unigene35482_All//8.00E-20//AT3G26320| CYP71B36; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene35482_All//3.00E-147//ES819398		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene35483_All	852	2.21	0.59	2.38	6.67	5.01	5.25	4.62	0.34	1.22	-1.89E+00	2.73E-04	Down	1.03E-01	8.17E-01		-4.11E-01	9.88E-02		-3.45E-01	1.96E-01		-3.75E+00	9.43E-20	Down	-1.92E+00	2.23E-10	Down	Unigene35483_All//gi|18252325|gb|AAL66194.1|AF386512_1/4.00E-59//cytochrome P450 [Pyrus communis]	Unigene35483_All//1.00E-33//AT3G48270| CYP71A26; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene35483_All//0.00E+00//TC135966		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene35484_All	1178	2.53	6.37	6.74	4.36	7.42	8.89	46.87	52.44	66.62	1.33E+00	3.65E-09	Up	1.41E+00	4.51E-10	Up	7.70E-01	3.09E-05		1.03E+00	5.21E-09	Up	1.62E-01	1.00E-02		5.07E-01	2.49E-22		Unigene35484_All//gi|18252325|gb|AAL66194.1|AF386512_1/1.00E-107//cytochrome P450 [Pyrus communis]	Unigene35484_All//7.00E-61//AT3G26300| CYP71B34; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene35484_All//0.00E+00//TC143410		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene35486_All	1725	27.24	37.39	52.57	59.81	54.94	45.63	5.49	2.69	2.12	4.57E-01	2.27E-12		9.49E-01	2.98E-58		-1.23E-01	1.91E-02		-3.90E-01	1.38E-15		-1.03E+00	1.66E-09	Down	-1.37E+00	6.01E-15	Down	Unigene35486_All//gi|18411523|ref|NP_567209.1|//1.00E-126//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|73622092|sp|Q9M158.2|Y4105_ARATH RecName: Full=Uncharacterized protein At4g01050 >gi|15982915|gb|AAL09804.1| AT4g01050/F2N1_31 [Arabidopsis thaliana] >gi|16323194|gb|AAL15331.1| AT4g01050/F2N1_31 [Arabidopsis thaliana] >gi|21700911|gb|AAM70579.1| AT4g01050/F2N1_31 [Arabidopsis thaliana]	Unigene35486_All//8.00E-101//AT4G01050| hydroxyproline-rich glycoprotein family protein	Unigene35486_All//0.00E+00//TC135900				nr +
Unigene35487_All	826	10.20	13.56	14.83	30.94	26.72	35.65	50.47	174.06	23.15	4.11E-01	1.69E-02		5.40E-01	1.28E-03		-2.11E-01	5.63E-02		2.05E-01	5.46E-02		1.79E+00	0.00E+00	Up	-1.12E+00	2.75E-46	Down	Unigene35487_All//gi|300509026|gb|ADK24219.1|//4.00E-44//cinnamoyl-CoA reductase [Hibiscus cannabinus]	Unigene35487_All//1.00E-40//AT1G15950| CCR1 (CINNAMOYL COA REDUCTASE 1); cinnamoyl-CoA reductase	Unigene35487_All//0.00E+00//gi|109825294|gb|DW224027.1|DW224027		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene35488_All	913	31.81	40.79	38.44	128.27	127.56	122.33	114.52	422.72	71.69	3.59E-01	4.36E-05		2.73E-01	4.43E-03		-8.10E-03	8.99E-01		-6.84E-02	2.30E-01		1.88E+00	0.00E+00	Up	-6.76E-01	7.14E-49		Unigene35488_All//gi|300509026|gb|ADK24219.1|//1.00E-152//cinnamoyl-CoA reductase [Hibiscus cannabinus]	Unigene35488_All//1.00E-136//AT1G15950| CCR1 (CINNAMOYL COA REDUCTASE 1); cinnamoyl-CoA reductase	Unigene35488_All//0.00E+00//gi|78340777|gb|DT561051.1|DT561051		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene35489_All	1086	0.67	0.79	0.78	2.71	2.16	1.95	9.93	13.01	2.71	2.34E-01	7.28E-01		2.18E-01	7.57E-01		-3.28E-01	3.96E-01		-4.69E-01	2.23E-01		3.90E-01	3.75E-03		-1.87E+00	4.93E-26	Down	Unigene35489_All//gi|300509026|gb|ADK24219.1|//5.00E-80//cinnamoyl-CoA reductase [Hibiscus cannabinus]	Unigene35489_All//2.00E-71//AT1G15950| CCR1 (CINNAMOYL COA REDUCTASE 1); cinnamoyl-CoA reductase	Unigene35489_All//0.00E+00//AI731964		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene35490_All	1540	101.07	33.30	35.41	49.13	49.64	40.62	11.20	11.05	15.00	-1.60E+00	1.97E-233	Down	-1.51E+00	3.95E-208	Down	1.48E-02	8.45E-01		-2.75E-01	2.64E-06		-2.02E-02	8.97E-01		4.22E-01	2.14E-05		Unigene35490_All//gi|15241573|ref|NP_196445.1|//1.00E-155//HEMC (HYDROXYMETHYLBILANE SYNTHASE); hydroxymethylbilane synthase [Arabidopsis thaliana] >gi|2495179|sp|Q43316.1|HEM3_ARATH RecName: Full=Porphobilinogen deaminase, chloroplastic; Short=PBG; AltName: Full=Pre-uroporphyrinogen synthase; AltName: Full=Hydroxymethylbilane synthase; Short=HMBS; Flags: Precursor >gi|16930521|gb|AAL31946.1|AF419614_1 AT5g08280/F8L15_10 [Arabidopsis thaliana] >gi|313150|emb|CAA51941.1| hydroxymethylbilane synthase [Arabidopsis thaliana] >gi|313838|emb|CAA52061.1| hydroxymethylbilane synthase [Arabidopsis thaliana] >gi|10178270|emb|CAC08328.1| hydroxymethylbilane synthase [Arabidopsis thaliana]	Unigene35490_All//7.00E-144//AT5G08280| HEMC (HYDROXYMETHYLBILANE SYNTHASE); hydroxymethylbilane synthase	Unigene35490_All//0.00E+00//TC173026		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene35492_All	580	0.00	0.00	0.00	0.86	0.12	0.62	7.87	1.30	43.96	null	null		null	null		-2.86E+00	1.78E-02		-4.64E-01	6.59E-01		-2.60E+00	2.54E-16	Down	2.48E+00	7.89E-85	Up	Unigene35492_All//gi|47716659|gb|AAT37529.1|//7.00E-60//purple acid phosphatase 1 [Solanum tuberosum]	Unigene35492_All//9.00E-61//AT3G17790| PAP17; acid phosphatase/ phosphatase/ protein serine/threonine phosphatase	Unigene35492_All//0.00E+00//gi|73861800|gb|DT464539.1|DT464539		ko00740|Riboflavin metabolism		nr +
Unigene35493_All	2044	3.43	1.96	2.37	1.32	1.26	3.07	6.21	1.80	39.37	-8.09E-01	2.61E-04		-5.33E-01	2.19E-02		-5.87E-02	8.75E-01		1.22E+00	3.15E-07	Up	-1.79E+00	9.13E-28	Down	2.67E+00	7.80E-289	Up	Unigene35493_All//gi|18401643|ref|NP_566587.1|//1.00E-128//PAP17; acid phosphatase/ phosphatase/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75274605|sp|Q9SCX8.1|PPA17_ARATH RecName: Full=Purple acid phosphatase 17; AltName: Full=Acid phosphatase type 5; AltName: Full=Peroxidase; Flags: Precursor >gi|6624897|emb|CAB63938.1| acid phosphatase type 5 [Arabidopsis thaliana] >gi|9294483|dbj|BAB02702.1| purple acid phosphatase-like protein [Arabidopsis thaliana] >gi|10278031|emb|CAC09923.1| acid phosphatase type 5 [Arabidopsis thaliana] >gi|27808574|gb|AAO24567.1| At3g17790 [Arabidopsis thaliana] >gi|110736187|dbj|BAF00065.1| acid phosphatase type 5 [Arabidopsis thaliana]	Unigene35493_All//2.00E-129//AT3G17790| PAP17; acid phosphatase/ phosphatase/ protein serine/threonine phosphatase	Unigene35493_All//0.00E+00//TC142524		ko00740|Riboflavin metabolism		nr -
Unigene35498_All	2375	4.16	4.54	3.79	26.41	22.62	15.92	20.17	7.37	8.15	1.26E-01	5.16E-01		-1.36E-01	5.20E-01		-2.23E-01	4.17E-04		-7.30E-01	4.88E-29		-1.45E+00	2.16E-76	Down	-1.31E+00	4.32E-67	Down	Unigene35498_All//gi|15217774|ref|NP_174113.1|//0.00E+00//MAP65-8 (MICROTUBULE-ASSOCIATED PROTEIN 65-8) [Arabidopsis thaliana]	Unigene35498_All//0.00E+00//AT1G27920| MAP65-8 (MICROTUBULE-ASSOCIATED PROTEIN 65-8)	Unigene35498_All//0.00E+00//gi|164348532|gb|ES803951.1|ES803951				nr -
Unigene35499_All	622	1.26	0.49	0.17	2.00	2.33	1.96	2.99	0.40	1.22	-1.37E+00	9.59E-02		-2.88E+00	6.35E-03		2.16E-01	7.52E-01		-3.04E-02	9.47E-01		-2.89E+00	8.75E-08	Down	-1.30E+00	2.09E-03		Unigene35499_All//gi|1708025|sp|P52425.1|GPDA_CUPLA//5.00E-62//RecName: Full=Glycerol-3-phosphate dehydrogenase [NAD+] >gi|840731|emb|CAA56125.1| glycerol-3-phosphate dehydrogenase (NAD+) [Cuphea lanceolata]	Unigene35499_All//6.00E-35//AT5G40610| glycerol-3-phosphate dehydrogenase (NAD+) / GPDH	Unigene35499_All//8.00E-121//EX165268		ko00564|Glycerophospholipid metabolism		nr +

Unigene355_All	791	4.89	4.80	4.91	5.79	5.35	5.20	16.78	16.70	7.76	-2.69E-02	9.48E-01		5.80E-03	1.00E+00		-1.14E-01	7.37E-01		-1.57E-01	6.16E-01		-7.50E-03	9.97E-01		-1.11E+00	3.97E-15	Down	Unigene355_All//gi|115463991|ref|NP_001055595.1|//8.00E-17//0s05g0424800 [Oryza sativa Japonica Group] >gi|53980856|gb|AAV24777.1| unknow protein [Oryza sativa Japonica Group] >gi|113579146|dbj|BAF17509.1| Os05g0424800 [Oryza sativa Japonica Group]	Unigene355_All//1.00E-15//AT1G71900| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF803 (InterPro:IPR008521); BEST Arabidopsis thaliana protein match is: permease-related (TAIR:AT1G34470.1); Has 875 Blast hits to 858 proteins in 150 species: Archae - 0; Bacteria - 55; Metazoa - 361; Fungi - 238; Plants - 146; Viruses - 0; Other Eukaryotes - 75 (source: NCBI BLink).	Unigene355_All//0.00E+00//gi|6461906|gb|AW187470.1|AW187470				nr +
Unigene3550_All	362	17.92	22.26	17.06	10.87	13.79	13.60	36.79	93.06	58.55	3.12E-01	1.39E-01		-7.08E-02	7.74E-01		3.43E-01	2.32E-01		3.23E-01	2.79E-01		1.34E+00	1.03E-47	Up	6.70E-01	1.92E-10		Unigene3550_All//gi|42571103|ref|NP_973625.1|//5.00E-21//SLT1 (sodium- and lithium-tolerant 1) [Arabidopsis thaliana]	Unigene3550_All//2.00E-22//AT2G37570| SLT1 (sodium- and lithium-tolerant 1)	Unigene3550_All//0.00E+00//TC147359			GO:0006972	nr +
Unigene35500_All	1887	4.10	1.66	2.57	5.04	3.83	4.07	6.41	1.84	2.60	-1.30E+00	3.37E-09	Down	-6.76E-01	1.86E-03		-3.96E-01	2.98E-02		-3.09E-01	1.18E-01		-1.80E+00	8.19E-27	Down	-1.30E+00	1.61E-17	Down	Unigene35500_All//gi|1708025|sp|P52425.1|GPDA_CUPLA//1.00E-172//RecName: Full=Glycerol-3-phosphate dehydrogenase [NAD+] >gi|840731|emb|CAA56125.1| glycerol-3-phosphate dehydrogenase (NAD+) [Cuphea lanceolata]	Unigene35500_All//2.00E-164//AT5G40610| glycerol-3-phosphate dehydrogenase (NAD+) / GPDH	Unigene35500_All//0.00E+00//EX165268		ko00564|Glycerophospholipid metabolism	nr +
Unigene35501_All	784	0.40	0.13	1.43	1.33	0.53	2.65	10.84	4.85	3.40	-1.63E+00	2.76E-01		1.83E+00	1.24E-02		-1.34E+00	3.95E-02		9.90E-01	2.94E-02		-1.16E+00	2.86E-10	Down	-1.67E+00	8.27E-18	Down	Unigene35501_All//gi|6686400|gb|AAF23834.1|AC007234_6//1.00E-47//F1E22.18 [Arabidopsis thaliana]	Unigene35501_All//2.00E-48//AT1G65840| ATPAO4 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 4); amine oxidase/ polyamine oxidase	Unigene35501_All//2.00E-149//ES833707			nr +
Unigene35502_All	1813	2.22	1.43	0.94	3.57	2.07	8.02	25.42	14.11	12.11	-6.41E-01	3.50E-02		-1.24E+00	1.36E-04	Down	-7.87E-01	2.44E-04		1.17E+00	7.12E-15	Up	-8.49E-01	1.85E-31		-1.07E+00	3.38E-47	Down	Unigene35502_All//gi|15218830|ref|NP_176759.1|//1.00E-158//ATPAO4 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 4); amine oxidase/ polyamine oxidase [Arabidopsis thaliana] >gi|75151901|sp|Q8H191.1|PAO4_ARATH RecName: Full=Probable polyamine oxidase 4; Short=AtPAO4; AltName: Full=Amine oxidase 2	Unigene35502_All//2.00E-159//AT1G65840| ATPAO4 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 4); amine oxidase/ polyamine oxidase	Unigene35502_All//0.00E+00//TC171637			nr +
Unigene35504_All	368	0.00	0.00	0.00	0.00	0.00	0.00	3.22	4.32	0.43	null	null		null	null		null	null		null	null		4.24E-01	4.00E-01		-2.89E+00	2.03E-05	Down	Unigene35504_All//gi|45478053|gb|AA86357.1|//6.00E-30//(-)-germacrene D synthase [Vitis vinifera]	Unigene35504_All//2.00E-20//AT1G70080| terpene synthase/cyclase family protein	Unigene35504_All//8.00E-129//gi|48818489|gb|CO119802.1|CO119802		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis	nr -
Unigene35505_All	1876	2.73	8.64	5.36	13.06	19.44	22.44	0.18	0.16	0.17	1.66E+00	5.15E-26	Up	9.73E-01	2.78E-07		5.73E-01	2.80E-12		7.80E-01	8.36E-22		-2.09E-01	8.50E-01		-8.57E-02	9.47E-01		Unigene35505_All//gi|3970689|emb|CAA77191.1|//1.00E-177//(+)-delta-cadinene synthase [Gossypium arboreum]	Unigene35505_All//2.00E-111//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene35505_All//0.00E+00//TC145985		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis	nr +
Unigene35509_All	1777	5.65	2.14	6.32	4.63	5.33	4.93	1.59	0.54	1.32	-1.40E+00	5.04E-13	Down	1.62E-01	3.88E-01		2.04E-01	3.26E-01		9.22E-02	7.05E-01		-1.56E+00	9.71E-06	Down	-2.69E-01	4.27E-01		Unigene35509_All//gi|297833220|ref|XP_002884492.1|//1.00E-151//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330332|gb|EFH60751.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35509_All//5.00E-152//AT3G05140| KBK2 (Rop Binding protein Kinases 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene35509_All//0.00E+00//AI730476		ko04626|Plant-pathogen interaction	nr -
Unigene35511_All	1077	1.46	1.27	3.26	1.53	1.09	1.89	4.40	3.84	6.99	-1.98E-01	6.85E-01		1.16E+00	8.51E-04	Up	-4.90E-01	3.41E-01		3.06E-01	5.50E-01		-1.95E-01	4.88E-01		6.69E-01	2.85E-04		Unigene35511_All//gi|48958479|gb|AAT47792.1|//2.00E-40//At1g72510 [Arabidopsis thaliana] >gi|51536554|gb|AAU05515.1| At1g72510 [Arabidopsis thaliana]	Unigene35511_All//8.00E-42//AT1G72510| unknown protein	Unigene35511_All//0.00E+00//TC132733			nr +
Unigene35512_All	1832	35.87	82.67	58.86	7.83	6.20	9.29	23.86	16.31	16.90	1.20E+00	9.75E-147	Up	7.15E-01	1.03E-42		-3.36E-01	2.04E-02		2.47E-01	8.60E-02		-5.49E-01	2.68E-14		-4.98E-01	1.70E-12		Unigene35512_All//gi|2160148|gb|AAB60770.1|//2.00E-87//EST gb|H37044 comes from this gene [Arabidopsis thaliana]	Unigene35512_All//8.00E-89//AT1G62250| unknown protein	Unigene35512_All//0.00E+00//TC139372			nr +
Unigene35513_All	1145	4.66	3.76	8.14	3.61	1.56	2.25	5.10	3.36	0.73	-3.09E-01	2.46E-01		8.04E-01	3.96E-05		-1.21E+00	1.78E-05	Down	-6.84E-01	2.20E-02		-6.02E-01	6.03E-03		-2.80E+00	4.02E-23	Down	Unigene35513_All//gi|15238001|ref|NP_199517.1|//3.00E-38//senescence-associated protein-related [Arabidopsis thaliana]	Unigene35513_All//1.00E-32//AT5G47060| senescence-associated protein-related	Unigene35513_All//4.00E-164//gi|48779064|gb|CO088430.1|CO088430			nr -
Unigene35514_All	807	6.22	4.08	13.20	3.58	2.18	3.25	4.30	2.90	1.53	-6.09E-01	2.29E-02		1.08E+00	5.06E-09	Up	-7.18E-01	4.16E-02		-1.41E-01	7.14E-01		-5.67E-01	5.77E-02		-1.49E+00	1.04E-06	Down	Unigene35514_All//gi|15238001|ref|NP_199517.1|//2.00E-38//senescence-associated protein-related [Arabidopsis thaliana]	Unigene35514_All//8.00E-33//AT5G47060| senescence-associated protein-related	Unigene35514_All//0.00E+00//gi|48779064|gb|CO088430.1|CO088430			nr -
Unigene35515_All	1741	211.00	41.21	46.86	306.12	263.30	302.11	89.54	12.80	28.58	-2.36E+00	0.00E+00	Down	-2.17E+00	0.00E+00	Down	-2.17E-01	3.56E-29		-1.90E-02	5.06E-01		-2.81E+00	0.00E+00	Down	-1.65E+00	4.11E-306	Down	Unigene35515_All//gi|115456087|ref|NP_001051644.1|//1.00E-122//Os03g0807700 [Oryza sativa Japonica Group] >gi|108711660|gb|ABF99455.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550115|dbj|BAF13538.1| Os03g0807700 [Oryza sativa Japonica Group]	Unigene35515_All//9.00E-148//AT3G08030| unknown protein	Unigene35515_All//0.00E+00//TC129718			nr -
Unigene35516_All	1341	120.13	91.40	197.83	17.87	49.43	73.79	13.40	1.62	3.45	-3.94E-01	8.10E-23		7.20E-01	7.17E-106		1.47E+00	4.13E-103	Up	2.05E+00	4.27E-222	Up	-3.05E+00	1.62E-73	Down	-1.96E+00	1.59E-45	Down	Unigene35516_All//gi|240248438|gb|ACS45396.1|//1.00E-147//myo-inositol oxygenase [Solanum lycopersicum]	Unigene35516_All//2.00E-142//AT1G14520| MIOX1 (MYO-INISITOL OXYGENASE); inositol oxygenase/ oxidoreductase	Unigene35516_All//0.00E+00//TC132092		ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism	nr -
Unigene35517_All	789	0.80	7.96	1.28	1.45	4.54	9.16	12.27	35.60	38.37	3.32E+00	6.18E-23	Up	6.88E-01	3.42E-01		1.64E+00	7.50E-07	Up	2.66E+00	1.89E-22	Up	1.54E+00	6.63E-49	Up	1.64E+00	2.80E-59	Up	Unigene35517_All//gi|115436224|ref|NP_001042870.1|//2.00E-56//Os01g0314100 [Oryza sativa Japonica Group] >gi|113532401|dbj|BAF04784.1| Os01g0314100 [Oryza sativa Japonica Group]	Unigene35517_All//2.00E-55//AT3G06850| BCE2; acetyltransferase/ alpha-ketoacid dehydrogenase/ dihydrolipoamide branched chain acyltransferase	Unigene35517_All//1.00E-129//TC146612		ko00280|Valine, leucine and isoleucine degradation	nr -
Unigene35518_All	1875	1.76	34.10	6.42	5.53	19.19	29.75	37.86	102.47	156.40	4.28E+00	2.06E-280	Up	1.87E+00	4.27E-22	Up	1.80E+00	2.05E-74	Up	2.43E+00	1.13E-154	Up	1.44E+00	3.53E-299	Up	2.05E+00	0.00E+00	Up	Unigene35518_All//gi|15231314|ref|NP_187341.1|//1.00E-157//BCE2; acetyltransferase/ alpha-ketoacid dehydrogenase/ dihydrolipoamide branched chain acyltransferase [Arabidopsis thaliana] >gi|30680036|ref|NP_850527.1| BCE2; acetyltransferase/ alpha-ketoacid dehydrogenase/ dihydrolipoamide branched chain acyltransferase [Arabidopsis thaliana] >gi|7549628|gb|AAF63813.1| branched chain alpha-keto acid dehydrogenase E2 subunit [Arabidopsis thaliana] >gi|21554337|gb|AAM63444.1| branched chain alpha-keto acid dehydrogenase E2 subunit [Arabidopsis thaliana] >gi|222423008|dbj|BAH19487.1| AT3G06850 [Arabidopsis thaliana] >gi|222424240|dbj|BAH20078.1| AT3G06850 [Arabidopsis thaliana]	Unigene35518_All//5.00E-158//AT3G06850| BCE2; acetyltransferase/ alpha-ketoacid dehydrogenase/ dihydrolipoamide branched chain acyltransferase	Unigene35518_All//0.00E+00//TC145829		ko00280|Valine, leucine and isoleucine degradation	nr +
Unigene35519_All	1580	8.11	1.64	2.36	18.25	10.35	6.72	50.82	62.38	32.43	-2.31E+00	6.81E-32	Down	-1.78E+00	5.56E-22	Down	-8.18E-01	1.54E-18		-1.44E+00	1.27E-40	Down	2.96E-01	1.88E-10		-6.48E-01	4.03E-35		Unigene35519_All//gi|18405635|ref|NP_566831.1|//1.00E-135//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|13937165|gb|AAK50076.1|AF372936_1 AT3g28050/MMG15_6 [Arabidopsis thaliana] >gi|22137010|gb|AAM91350.1| At3g28050/MMG15_6 [Arabidopsis thaliana]	Unigene35519_All//5.00E-121//AT3G28050| nodulin MtN21 family protein	Unigene35519_All//0.00E+00//TC168187			nr -
Unigene3552_All	1256	318.76	512.42	427.40	137.54	172.09	169.36	265.43	264.42	94.74	6.85E-01	3.41E-241		4.23E-01	4.00E-82		3.23E-01	5.74E-25		3.00E-01	2.13E-19		-5.50E-03	8.70E-01		-1.49E+00	0.00E+00	Down	Unigene3552_All//gi|2253415|gb|AAB62937.1|//5.00E-69//stress-induced cysteine proteinase [Lavatera thuringiaca]	Unigene3552_All//3.00E-56//AT4G39090| RD19 (RESPONSIVE TO DEHYDRATION 19); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene3552_All//0.00E+00//TC150900			GO:0004175//GO:0019538	nr +
Unigene35523_All	2107	47.83	23.86	38.26	89.51	58.72	65.85	22.62	77.12	21.82	-1.00E+00	3.09E-73	Down	-3.22E-01	9.43E-10		-6.08E-01	9.53E-71		-4.43E-01	2.62E-35		1.77E+00	0.00E+00	Up	-5.17E-02	5.39E-01		Unigene35523_All//gi|30688168|ref|NP_173714.2|//0.00E+00//LPR1 (Low Phosphate Root1); copper ion binding / oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor [Arabidopsis thaliana]	Unigene35523_All//0.00E+00//AT1G23010| LPR1 (Low Phosphate Root1); copper ion binding / oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor	Unigene35523_All//0.00E+00//TC140940		ko00910|Nitrogen metabolism	nr +
Unigene35524_All	2248	0.28	0.32	0.33	1.15	0.77	0.88	0.32	1.02	0.14	1.76E-01	8.17E-01		2.48E-01	7.45E-01		-5.89E-01	1.26E-01		-3.82E-01	3.76E-01		1.68E+00	3.15E-05	Up	-1.17E+00	1.09E-01		Unigene35524_All//gi|30688168|ref|NP_173714.2|//0.00E+00//LPR1 (Low Phosphate Root1); copper ion binding / oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor [Arabidopsis thaliana]	Unigene35524_All//0.00E+00//AT1G23010| LPR1 (Low Phosphate Root1); copper ion binding / oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor	Unigene35524_All//0.00E+00//TC140940		ko00910|Nitrogen metabolism	nr +
Unigene35525_All	2481	2.45	1.12	1.01	4.76	4.72	3.88	5.74	3.69	2.94	-1.12E+00	5.08E-06	Down	-1.28E+00	7.98E-07	Down	-1.20E-02	9.58E-01		-2.95E-01	9.01E-02		-6.39E-01	1.39E-06		-9.67E-01	5.25E-13		Unigene35525_All//gi|223452412|gb|ACN89533.1|//0.00E+00//protein kinase [Glycine max]	Unigene35525_All//0.00E+00//AT5G59700| protein kinase, putative	Unigene35525_All//0.00E+00//AI731050		ko04626|Plant-pathogen interaction		nr -
Unigene35529_All	1665	20.74	48.57	20.05	62.29	77.08	92.74	84.54	117.96	54.17	1.23E+00	5.37E-81	Up	-4.86E-02	6.41E-01		3.07E-01	1.16E-13		5.74E-01	5.50E-46		4.81E-01	2.65E-48		-6.42E-01	7.19E-60		Unigene35529_All//gi|22327990|ref|NP_200888.2|//1.00E-29//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|28416657|gb|AAO42859.1| At5g60800 [Arabidopsis thaliana]	Unigene35529_All//3.00E-10//AT5G60800| heavy-metal-associated domain-containing protein	Unigene35529_All//0.00E+00//gi|78345451|gb|DT565725.1|DT565725			nr -

Unigene35530_A11	2542	7.08	6.86	8.69	10.03	7.83	8.67	11.23	6.03	4.67	-4.63E-02	7.41E-01		2.96E-01	1.74E-02		-3.58E-01	4.20E-04		-2.11E-01	6.84E-02		-8.96E-01	1.38E-21		-1.27E+00	2.16E-38	Down	Unigene35530_A11//gi|42569818|ref|NP_181616.3|//0.00E+00//DPE2 (DISPROPORTIONATING ENZYME 2); 4-alpha-glucanotransferase/ heteroglycan binding [Arabidopsis thaliana] >gi|34098849|gb|AAQ56807.1| At2g40840 [Arabidopsis thaliana]	Unigene35530_A11//0.00E+00//AT2G40840| DPE2 (DISPROPORTIONATING ENZYME 2); 4-alpha-glucanotransferase/ heteroglycan binding	Unigene35530_A11//0.00E+00//TC151379		ko00500|Starch and sucrose metabolism		nr -
Unigene35538_A11	812	1.48	3.87	4.13	1.47	3.18	3.17	11.25	9.52	7.16	1.38E+00	1.62E-04	Up	1.48E+00	6.16E-05	Up	1.11E+00	4.18E-03		1.11E+00	5.59E-03		-2.40E-01	1.95E-01		-6.51E-01	8.00E-05		Unigene35538_A11//gi|75337365|sp|Q9SKZ2.2|CAF1G_ARATH//3.00E-45//RecName: Full=Probable CCR4-associated factor 1 homolog 7	Unigene35538_A11//5.00E-46//AT2G32070| CCR4-NOT transcription complex protein, putative	Unigene35538_A11//0.00E+00//TC151000		ko03018|RNA degradation		nr -
Unigene3554_A11	627	2.92	2.91	2.04	12.00	9.61	6.70	6.00	1.93	2.99	-5.60E-03	9.86E-01		-5.19E-01	3.11E-01		-3.20E-01	1.45E-01		-8.41E-01	5.41E-05		-1.63E+00	7.80E-08	Down	-1.01E+00	2.63E-04	Down	Unigene3554_A11//gi|13899059|gb|AAK48951.1|AF370524_1//7.00E-35//Unknown protein [Arabidopsis thaliana]	Unigene3554_A11//6.00E-31//AT5G06610| unknown protein	Unigene3554_A11//9.00E-170//gi|78330686|gb|DT550960.1|DT550960				nr +
Unigene35540_A11	416	4.91	5.85	6.02	9.70	6.79	10.64	4.47	3.01	1.34	2.53E-01	5.56E-01		2.95E-01	4.93E-01		-5.15E-01	8.41E-02		1.34E-01	6.97E-01		-5.69E-01	1.93E-01		-1.74E+00	9.21E-05	Down				Unigene35540_A11//6.00E-170//gi|6461821|gb|AW187385.1|AW187385				
Unigene35541_A11	632	5.22	4.65	5.06	10.17	7.14	9.65	4.68	3.11	2.14	-1.66E-01	6.15E-01		-4.50E-02	9.07E-01		-5.11E-01	2.22E-02		-7.58E-02	7.65E-01		-5.91E-01	7.20E-02		-1.13E+00	4.06E-04	Down				Unigene35541_A11//5.00E-82//AW187385				
Unigene35543_A11	2036	1.85	1.52	1.96	3.89	2.25	2.48	3.78	2.07	1.58	-2.85E-01	3.83E-01		8.43E-02	7.89E-01		-7.90E-01	3.41E-05		-6.47E-01	1.42E-03		-8.66E-01	4.17E-06		-1.25E+00	7.51E-11	Down	Unigene35543_A11//gi|297820436|ref|XP_002878101.1|//0.00E+00//CIP111 [Arabidopsis lyrata subsp. lyrata] >gi|297323939|gb|EFH54360.1| CIP111 [Arabidopsis lyrata subsp. lyrata]	Unigene35543_A11//0.00E+00//AT3G56690| CIP111 (CAM INTERACTING PROTEIN 111); ATPase/ calmodulin binding	Unigene35543_A11//0.00E+00//TC173047		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene35544_A11	2448	8.14	10.00	6.96	18.64	14.60	20.77	25.67	40.84	55.85	2.96E-01	8.55E-03		-2.26E-01	9.65E-02		-3.52E-01	1.15E-06		1.56E-01	5.03E-02		6.70E-01	8.19E-45		1.12E+00	3.46E-148	Up	Unigene35544_A11//gi|297805954|ref|XP_002870861.1|//1.00E-152//serine/threonine protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316697|gb|EFH47120.1| serine/threonine protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35544_A11//7.00E-139//AT1G66880| serine/threonine protein kinase family protein	Unigene35544_A11//0.00E+00//TC177699		ko04626|Plant-pathogen interaction		nr -
Unigene35545_A11	1798	14.67	43.26	14.30	14.82	30.74	11.05	19.16	9.04	6.40	1.56E+00	6.62E-112	Up	-3.60E-02	7.69E-01		1.05E+00	1.98E-51	Up	-4.23E-01	3.67E-05		-1.08E+00	3.35E-35	Down	-1.58E+00	2.31E-64	Down	Unigene35545_A11//gi|297800470|ref|XP_002868119.1|//0.00E+00//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313955|gb|EFH44378.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35545_A11//3.00E-153//AT4G16563| aspartyl protease family protein	Unigene35545_A11//2.00E-157//gi|109837727|gb|DW236288.1|DW236288				nr -
Unigene35546_A11	2141	12.98	62.01	10.42	13.54	24.62	29.26	19.69	40.66	36.69	2.26E+00	0.00E+00	Up	-3.16E-01	3.56E-03		8.63E-01	2.05E-35		1.11E+00	1.02E-57	Up	1.05E+00	8.71E-83	Up	8.98E-01	1.59E-59		Unigene35546_A11//gi|224134993|ref|XP_002321956.1|//2.00E-91//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222868952|gb|EEF06083.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene35546_A11//1.00E-72//AT3G49530| anac062 (Arabidopsis NAC domain containing protein 62); transcription factor	Unigene35546_A11//0.00E+00//gi|78344516|gb|DT564790.1|DT564790	NAC			nr +
Unigene35547_A11	2161	1.38	2.67	1.55	1.64	2.60	1.88	0.98	0.66	2.01	9.54E-01	1.34E-04		1.70E-01	6.17E-01		6.66E-01	6.07E-03		2.01E-01	5.75E-01		-5.73E-01	1.53E-01		1.04E+00	5.32E-05	Up	Unigene35547_A11//gi|15237921|ref|NP_197812.1|//0.00E+00//phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana] >gi|10177083|dbj|BAB10389.1| ubiquitin [Arabidopsis thaliana] >gi|110741569|dbj|BAE98733.1| ubiquitin [Arabidopsis thaliana]	Unigene35547_A11//0.00E+00//AT5G24240| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	Unigene35547_A11//0.00E+00//gi|164359311|gb|ES811376.1|ES811376				nr +
Unigene35548_A11	1581	24.32	312.06	151.73	11.56	28.95	45.71	17.44	56.68	76.28	3.68E+00	0.00E+00	Up	2.64E+00	0.00E+00	Up	1.32E+00	5.17E-61	Up	1.98E+00	1.02E-155	Up	1.70E+00	9.16E-179	Up	2.13E+00	0.00E+00	Up	Unigene35548_A11//gi|226506630|ref|NP_001149686.1|//1.00E-69//carbonic anhydrase [Zea mays] >gi|195629458|gb|ACG36370.1| carbonic anhydrase [Zea mays]	Unigene35548_A11//1.00E-66//AT1G58180| carbonic anhydrase family protein / carbonate dehydratase family protein	Unigene35548_A11//0.00E+00//TC164409		ko00910|Nitrogen metabolism		nr +
Unigene35549_A11	2870	4.87	2.33	2.76	8.83	7.15	7.70	13.82	6.28	6.07	-1.06E+00	8.73E-12	Down	-8.16E-01	1.76E-07		-3.05E-01	3.37E-03		-1.99E-01	8.79E-02		-1.14E+00	1.11E-43	Down	-1.19E+00	4.79E-48	Down	Unigene35549_A11//gi|297852630|ref|XP_002894196.1|//0.00E+00//nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297340038|gb|EFH70455.1| nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene35549_A11//0.00E+00//AT1G49540| nucleotide binding	Unigene35549_A11//0.00E+00//TC132963				nr -
Unigene3555_A11	1321	2.14	2.99	2.18	9.77	6.78	4.51	7.36	1.96	4.77	4.84E-01	1.22E-01		2.54E-02	9.65E-01		-5.27E-01	3.06E-04		-1.11E+00	1.63E-12	Down	-1.91E+00	2.06E-23	Down	-6.28E-01	8.16E-05		Unigene3555_A11//gi|13899059|gb|AAK48951.1|AF370524_1//1.00E-135//Unknown protein [Arabidopsis thaliana]	Unigene3555_A11//2.00E-131//AT5G06610| unknown protein	Unigene3555_A11//0.00E+00//gi|78330981|gb|DT551255.1|DT551255			GO:0005488	nr +
Unigene35550_A11	732	4.72	4.91	5.38	1.91	2.82	1.73	1.96	3.71	4.14	5.91E-02	8.60E-01		1.90E-01	5.90E-01		5.67E-01	2.26E-01		-1.41E-01	7.97E-01		9.18E-01	7.17E-03		1.07E+00	6.52E-04	Up	Unigene35550_A11//gi|6682869|dbj|BAA88921.1|//5.00E-41//sigma factor [Nicotiana tabacum]	Unigene35550_A11//1.00E-39//AT1G64860| SIGA (SIGMA FACTOR A); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor	Unigene35550_A11//0.00E+00//TC144283	Sigma70-like			nr +
Unigene35555_A11	981	13.81	47.57	22.20	12.69	13.55	12.80	18.40	112.86	59.45	1.78E+00	2.18E-81	Up	6.85E-01	1.67E-08		9.40E-02	6.08E-01		1.17E-02	9.43E-01		2.62E+00	0.00E+00	Up	1.69E+00	4.70E-118	Up	Unigene35555_A11//gi|206584343|gb|ACI15344.1|//1.00E-80//NAC domain protein NAC3 [Gossypium hirsutum] >gi|206584353|gb|ACI15349.1| NAC domain protein NAC3 [Gossypium hirsutum]	Unigene35555_A11//2.00E-32//AT1G01720| ATAF1; transcription activator/ transcription factor	Unigene35555_A11//0.00E+00//TC156640	NAC			nr +
Unigene35556_A11	1200	4.05	22.76	8.43	2.32	4.51	3.05	8.95	69.10	31.11	2.49E+00	7.15E-73	Up	1.06E+00	2.84E-08	Up	9.55E-01	1.05E-04		3.91E-01	2.59E-01		2.95E+00	0.00E+00	Up	1.80E+00	1.88E-82	Up	Unigene35556_A11//gi|206584343|gb|ACI15344.1|//1.00E-171//NAC domain protein NAC3 [Gossypium hirsutum] >gi|206584353|gb|ACI15349.1| NAC domain protein NAC3 [Gossypium hirsutum]	Unigene35556_A11//1.00E-114//AT1G01720| ATAF1; transcription activator/ transcription factor	Unigene35556_A11//0.00E+00//TC151374	NAC			nr -
Unigene35560_A11	1947	22.90	55.48	33.37	34.72	35.74	24.33	18.65	17.32	23.86	1.28E+00	7.99E-115	Up	5.43E-01	3.81E-16		4.20E-02	6.12E-01		-5.13E-01	7.26E-17		-1.07E-01	2.43E-01		3.55E-01	1.84E-07		Unigene35560_A11//gi|186701214|gb|ACY31241.1|//1.00E-134//aldose 1-epimerase family protein [Arabidopsis halleri]	Unigene35560_A11//8.00E-135//AT4G23730| aldose 1-epimerase family protein	Unigene35560_A11//0.00E+00//gi|78329650|gb|DT549924.1|DT549924				nr +
Unigene35561_A11	1581	10.62	34.81	11.79	15.22	14.75	22.34	26.66	48.67	30.59	1.71E+00	1.52E-90	Up	1.50E-01	3.14E-01		-4.55E-02	7.69E-01		5.54E-01	2.62E-10		8.68E-01	7.26E-54		1.98E-01	3.78E-03		Unigene35561_A11//gi|2168137|emb|CAA66149.1|//3.00E-61//PKF1 [Fagus sylvatica]	Unigene35561_A11//1.00E-53//AT5G58950| protein kinase family protein	Unigene35561_A11//0.00E+00//gi|164337091|gb|ES811640.1|ES811640		ko04626|Plant-pathogen interaction		nr +
Unigene35562_A11	1126	1.53	3.96	1.61	1.42	1.16	1.80	3.75	3.82	1.80	1.37E+00	5.49E-06	Up	6.84E-02	8.91E-01		-2.85E-01	6.01E-01		3.50E-01	4.78E-01		2.60E-02	9.49E-01		-1.06E+00	4.74E-05	Down	Unigene35562_A11//gi|2168137|emb|CAA66149.1|//9.00E-34//PKF1 [Fagus sylvatica]	Unigene35562_A11//7.00E-28//AT5G58950| protein kinase family protein	Unigene35562_A11//0.00E+00//gi|164337091|gb|ES811640.1|ES811640				nr +
Unigene35563_A11	816	11.54	10.49	14.16	43.34	38.15	27.84	49.69	47.69	17.33	-1.37E-01	5.07E-01		2.95E-01	1.05E-01		-1.84E-01	4.72E-02		-6.39E-01	3.03E-13		-5.94E-02	5.34E-01		-1.52E+00	2.56E-71	Down	Unigene35563_A11//gi|31747031|gb|AAP57672.1|//5.00E-06//MutT-like protein [Cucumis sativus]	Unigene35563_A11//4.00E-06//AT2G01670| atnudt17 (Arabidopsis thaliana Nudix hydrolase homolog 17); hydrolase	Unigene35563_A11//0.00E+00//TC142601				nr -
Unigene35564_A11	1392	3.35	3.09	4.97	9.81	7.57	6.29	21.84	16.15	6.12	-1.13E-01	6.86E-01		5.72E-01	1.39E-02		-3.73E-01	1.12E-02		-6.40E-01	1.55E-05		-4.35E-01	5.96E-07		-1.83E+00	5.49E-70	Down	Unigene35564_A11//gi|15223919|ref|NP_172939.1|//1.00E-56//atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase >gi|68565943|sp|Q9LQU5.1|NUD18_ARATH RecName: Full=Nudix hydrolase 18, mitochondrial; Short=AtNUDT18; Flags: Precursor >gi|8778216|gb|AAF79225.1|AC006917_10 F10B6.26 [Arabidopsis thaliana]	Unigene35564_A11//7.00E-55//AT1G14860| atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase	Unigene35564_A11//0.00E+00//TC142601				nr -
Unigene35565_A11	1342	2.18	2.23	2.38	6.64	7.31	4.04	8.98	5.89	2.26	2.90E-02	9.55E-01		1.25E-01	7.21E-01		1.38E-01	5.47E-01		-7.18E-01	1.40E-04		-6.09E-01	2.64E-05		-1.99E+00	1.75E-31	Down	Unigene35565_A11//gi|15223919|ref|NP_172939.1|//6.00E-64//atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase >gi|68565943|sp|Q9LQU5.1|NUD18_ARATH RecName: Full=Nudix hydrolase 18, mitochondrial; Short=AtNUDT18; Flags: Precursor >gi|8778216|gb|AAF79225.1|AC006917_10 F10B6.26 [Arabidopsis thaliana]	Unigene35565_A11//3.00E-65//AT1G14860| atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase	Unigene35565_A11//0.00E+00//TC142601				nr -
Unigene35567_A11	857	32.91	21.70	29.70	38.42	38.29	34.20	77.90	38.87	33.89	-6.01E-01	3.95E-09		-1.48E-01	2.12E-01		-4.80E-03	9.64E-01		-1.68E-01	1.03E-01		-1.00E+00	1.63E-59	Down	-1.20E+00	1.13E-81	Down	Unigene35567_A11//gi|115466690|ref|NP_001056944.1|//1.00E-156//Os06g0173100 [Oryza sativa Japonica Group] >gi|113594984|dbj|BAF18858.1| Os06g0173100 [Oryza sativa Japonica Group]	Unigene35567_A11//6.00E-146//AT3G05530| RPT5A (REGULATORY PARTICLE TRIPLE-A ATPASE 5A); ATPase/ calmodulin binding	Unigene35567_A11//0.00E+00//TC131521		ko03050|Proteasome		nr -
Unigene35571_A11	1865	14.08	20.19	9.28	15.55	15.99	21.26	37.88	61.14	86.68	5.19E-01	2.49E-09		-6.02E-01	3.53E-08		4.07E-02	7.76E-01		4.52E-01	3.90E-08		6.91E-01	1.04E-53		1.19E+00	2.09E-193	Up	Unigene35571_A11//gi|17065506|gb|AAL32907.1|//1.00E-161//Unknown protein [Arabidopsis thaliana] >gi|53829653|gb|AU194136.1| At2g19160 [Arabidopsis thaliana]	Unigene35571_A11//1.00E-160//AT4G30060| unknown protein	Unigene35571_A11//0.00E+00//TC174000				nr -
Unigene35572_A11	2522	4.17	2.59	2.83	5.89	5.86	6.09	12.69	6.21	6.27	-6.86E-01	9.36E-05		-5.60E-01	2.22E-03		-7.00E-03	9.64E-01		4.88E-02	7.70E-01		-1.03E+00	3.28E-30	Down	-1.02E+00	1.77E-30	Down	Unigene35572_A11//gi|297808393|ref|XP_002872080.1|//0.00E+00//CPSF100 [Arabidopsis lyrata subsp. lyrata] >gi|297317917|gb|EFH48339.1| CPSF100 [Arabidopsis lyrata subsp. lyrata]	Unigene35572_A11//0.00E+00//AT5G23880| CPSF100 (CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 100); DNA binding / protein binding	Unigene35572_A11//0.00E+00//TC149988				nr +
Unigene35573_A11	2477	86.54	38.81	47.30	26.87	23.66	12.89	25.19	12.17	11.64	-1.16E+00	1.77E-195	Down	-8.72E-01	7.86E-119		-1.83E-01	3.66E-03		-1.06E+00	1.93E-57	Down	-1.05E+00	5.31E-60	Down	-1.11E+00	8.78E-68	Down	Unigene35573_A11//gi|15220100|ref|NP_178147.1|//0.00E+00//sulfate transmembrane transporter [Arabidopsis thaliana]	Unigene35573_A11//3.00E-173//AT1G80310| sulfate transmembrane transporter	Unigene35573_A11//0.00E+00//TC159472				nr -
Unigene35576_A11	2074	11.20	11.51	9.60	11.89	23.53	21.78	3.63	0.77	1.82	3.89E-02	7.51E-01		-2.22E-01	7.67E-02		9.85E-01	8.65E-41		8.73E-01	3.49E-28		-2.24E+00	2.31E-22	Down	-9.92E-01	1.44E-07		Unigene35576_A11//gi|297799788|ref|XP_002867778.1|//1.00E-168//ubiquitin thiolesterase [Arabidopsis lyrata subsp. lyrata] >gi|297313614|gb|EFH44037.1| ubiquitin thiolesterase [Arabidopsis lyrata subsp. lyrata]	Unigene35576_A11//5.00E-123//AT4G22290| ubiquitin thiolesterase	Unigene35576_A11//0.00E+00//gi|78350110|gb|DT570384.1|DT570384				nr -
Unigene3558_A11	1327	2.92	23.14	6.90	0.71	1.69	2.01	0.67	3.12	12.07	2.99E+00	1.17E-99	Up	1.24E+00	1.38E-09	Up	1.24E+00	3.57E-03		1.49E+00	2.02E-04	Up	2.22E+00	2.00E-12	Up	4.17E+00	1.74E-86	Up	Unigene3558_A11//gi|15220348|ref|NP_172600.1|//1.00E-117//S-locus lectin protein kinase family protein [Arabidopsis thaliana]	Unigene3558_A11//3.00E-114//AT1G11330| S-locus lectin protein kinase family protein	Unigene3558_A11//0.00E+00//C0081719		ko04626|Plant-pathogen interaction		nr -
Unigene35580_A11	2271	12.49	7.54	11.09	24.39	3.94	2.47	10.89	1.79	2.14	-7.28E-01	1.50E-12		-1.71E-01	1.41E-01		-2.63E+00	1.45E-201	Down	-3.31E+00	1.50E-218	Down	-2.61E+00	9.34E-86	Down	-2.35E+00	2.80E-78	Down	Unigene35580_A11//gi|256258969|gb|ACU64894.1|//6.00E-81//UDP-T1 [Oryza officinalis]	Unigene35580_A11//5.00E-29//AT3G16520| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene35580_A11//0.00E+00//gi|78344184|gb|DT564458.1|DT564458		ko00940|Phenylpropanoid biosynthesis		nr +

Unigene35581_All	679	5.93	2.84	5.18	1.83	2.64	0.73	1.25	0.00	0.23	-1.07E+00	5.39E-04	Down	-1.97E-01	5.68E-01		5.24E-01	3.10E-01		-1.33E+00	3.28E-02		-1.03E+01	4.39E-06	Down	-2.41E+00	1.68E-03		Unigene35581_All//gi|18416659|ref|NP_567737.1|//8.00E-17//CIL [Arabidopsis thaliana] >gi|13991648|gb|AAK51446.1|AF339388_1 CIL [Arabidopsis thaliana] >gi|126352272|gb|ABO09881.1| At4g25990 [Arabidopsis thaliana]	Unigene35581_All//1.00E-06//AT5G57180| CIA2 (CHLOROPLAST IMPORT APPARATUS 2); transcription regulator	Unigene35581_All//2.00E-174//TC151139	Orphans			nr +
Unigene35583_All	1757	43.27	30.31	26.43	13.81	12.52	11.39	1.30	0.48	0.66	-5.14E-01	1.04E-17		-7.11E-01	5.55E-30		-1.41E-01	2.62E-01		-2.78E-01	1.42E-02		-1.45E+00	2.26E-04	Down	-9.83E-01	7.13E-03		Unigene35583_All//gi|30696840|ref|NP_568852.2|//2.00E-60//CIA2 (CHLOROPLAST IMPORT APPARATUS 2); transcription regulator [Arabidopsis thaliana] >gi|75180536|sp|Q9LU68.1|CIA2_ARATH RecName: Full=Protein CHLOROPLAST IMPORT APPARATUS 2; Flags: Precursor >gi|13991646|gb|AAK51445.1|AF339387_1 CIA2 [Arabidopsis thaliana] >gi|222423094|dbj|BAH19527.1| AT5G57180 [Arabidopsis thaliana]	Unigene35583_All//2.00E-38//AT5G57180| CIA2 (CHLOROPLAST IMPORT APPARATUS 2); transcription regulator	Unigene35583_All//0.00E+00//TC130980	Orphans			nr -
Unigene35584_All	633	12.81	9.37	6.31	13.22	11.70	13.84	23.31	25.88	23.54	-4.52E-01	2.76E-02		-1.02E+00	1.96E-06	Down	-1.77E-01	4.38E-01		6.62E-02	7.64E-01		1.51E-01	2.81E-01		1.40E-02	9.45E-01		Unigene35584_All//gi|297845138|ref|XP_002890450.1|//9.00E-12//heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297336292|gb|EFH66709.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene35584_All//6.00E-11//AT1G21660| heat shock protein binding	Unigene35584_All//8.00E-158//TC177657				nr +
Unigene35585_All	1039	14.65	7.32	10.20	7.86	8.65	9.00	2.77	1.45	1.65	-1.00E+00	1.11E-11	Down	-5.23E-01	4.27E-04		1.38E-01	5.51E-01		1.95E-01	3.80E-01		-9.34E-01	4.67E-03		-7.47E-01	1.84E-02		Unigene35585_All//gi|18400144|ref|NP_566463.1|//1.00E-70//UKF 4-related [Arabidopsis thaliana] >gi|14423484|gb|AAK62424.1|AF389979_1 Unknown protein [Arabidopsis thaliana]	Unigene35585_All//4.00E-65//AT3G13740| UKF 4-related	Unigene35585_All//0.00E+00//TC147447				nr +
Unigene35586_All	1673	21.77	37.46	59.14	68.13	66.42	82.58	19.76	12.87	12.69	7.83E-01	2.81E-30		1.44E+00	1.68E-123	Up	-3.66E-02	5.62E-01		2.78E-01	4.00E-11		-6.19E-01	1.75E-13		-6.39E-01	1.22E-14		Unigene35586_All//gi|185487419|gb|ACC77744.1|//1.00E-169//homogentisate phytyltransferase [Manihot esculenta]	Unigene35586_All//4.00E-144//AT2G18950| HPT1 (HOMOGENTISATE PHYTYLTRANSFERASE 1); homogentisate phytyltransferase/ prenyltransferase	Unigene35586_All//0.00E+00//TC136806		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene35587_All	1804	2.78	25.84	5.61	9.00	18.17	35.12	6.28	9.34	7.51	3.21E+00	2.86E-162	Up	1.01E+00	9.66E-08	Up	1.01E+00	8.52E-29	Up	1.96E+00	7.03E-135	Up	5.72E-01	2.07E-06		2.58E-01	6.28E-02		Unigene35587_All//gi|297614182|gb|AD148429.1|//1.00E-161//trichome birefringence [Arabidopsis thaliana]	Unigene35587_All//1.00E-162//AT5G06700| unknown protein	Unigene35587_All//1.00E-75//TC173837				nr +
Unigene35588_All	2166	4.13	2.67	2.16	13.32	10.68	6.26	7.30	1.16	2.32	-6.31E-01	1.03E-03		-9.33E-01	3.82E-06		-3.18E-01	8.97E-04		-1.09E+00	2.37E-26	Down	-2.66E+00	3.69E-56	Down	-1.66E+00	5.46E-32	Down	Unigene35588_All//gi|30692580|ref|NP_174446.2|//0.00E+00//ROPGEF14; Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana]	Unigene35588_All//2.00E-178//AT1G31650| ROPGEF14; Rho guanyl-nucleotide exchange factor	Unigene35588_All//0.00E+00//TC142959				nr +
Unigene35589_All	1417	32.79	4.36	12.93	333.41	184.50	61.16	14.32	3.66	3.35	-2.91E+00	5.47E-148	Down	-1.34E+00	4.50E-52	Down	-8.54E-01	0.00E+00		-2.45E+00	0.00E+00	Down	-1.97E+00	4.23E-50	Down	-2.10E+00	4.81E-56	Down	Unigene35589_All//gi|284504570|gb|ADB90475.1|//0.00E+00//pectate lyase [Gossypium herbaceum]	Unigene35589_All//0.00E+00//AT4G24780| pectate lyase family protein	Unigene35589_All//0.00E+00//TC129615		ko00040|Pentose and glucuronate interconversions		nr +
Unigene35590_All	2061	13.02	33.26	11.19	40.87	38.36	43.48	34.36	15.64	23.70	1.35E+00	7.64E-80	Up	-2.19E-01	5.69E-02		-9.14E-02	1.51E-01		8.91E-02	1.59E-01		-1.14E+00	4.13E-77	Down	-5.36E-01	2.31E-22		Unigene35590_All//gi|16226325|gb|AAL16135.1|AF423803_1/0.00E+00//AT3g05910/P2010_3 [Arabidopsis thaliana]	Unigene35590_All//0.00E+00//AT3G05910| pectinacetylesterase, putative	Unigene35590_All//0.00E+00//TC168416				nr +
Unigene35594_All	2314	1.63	5.15	2.46	4.95	4.57	5.13	8.13	5.65	7.20	1.66E+00	2.77E-19	Up	5.97E-01	2.21E-02		-1.16E-01	5.62E-01		5.20E-02	7.89E-01		-5.24E-01	3.67E-06		-1.76E-01	1.40E-01		Unigene35594_All//gi|224132436|ref|XP_002328269.1|//0.00E+00//glycosyltransferase, family GT8 [Populus trichocarpa] >gi|222837784|gb|EEE76149.1| glycosyltransferase, family GT8 [Populus trichocarpa]	Unigene35594_All//0.00E+00//AT4G38270| GAUT3 (Galacturonosyltransferase 3); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups	Unigene35594_All//0.00E+00//DN801682				nr -
Unigene35597_All	1388	15.72	3.54	8.33	51.68	29.90	15.75	9.87	2.86	2.81	-2.15E+00	2.54E-49	Down	-9.17E-01	1.24E-13		-7.90E-01	7.38E-43		-1.71E+00	3.04E-129	Down	-1.79E+00	6.10E-30	Down	-1.81E+00	1.86E-31	Down	Unigene35597_All//gi|195646722|gb|ACG42829.1|//1.00E-64//acetylglucosaminyltransferase [Zea mays]	Unigene35597_All//1.00E-65//AT5G15050| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	Unigene35597_All//0.00E+00//TC170669				nr -
Unigene35598_All	1584	14.43	3.58	8.64	40.19	22.26	12.57	11.58	2.59	2.11	-2.01E+00	2.06E-47	Down	-7.41E-01	4.35E-10		-8.52E-01	2.06E-43		-1.68E+00	3.86E-111	Down	-2.16E+00	3.84E-51	Down	-2.46E+00	1.98E-61	Down	Unigene35598_All//gi|195657301|gb|ACG48118.1|//1.00E-159//acetylglucosaminyltransferase [Zea mays]	Unigene35598_All//4.00E-152//AT5G15050| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	Unigene35598_All//0.00E+00//TC179360				nr +
Unigene3560_All	1728	12.14	9.47	7.61	14.15	13.19	10.51	19.55	13.28	7.82	-3.58E-01	3.08E-03		-6.74E-01	5.37E-08		-1.02E-01	4.45E-01		-4.30E-01	6.53E-05		-5.58E-01	1.48E-11		-1.32E+00	1.89E-48	Down	Unigene3560_All//gi|42567081|ref|NP_194117.3|//1.00E-142//PHD finger protein-related [Arabidopsis thaliana] >gi|42573007|ref|NP_974600.1| PHD finger protein-related [Arabidopsis thaliana] >gi|145333865|ref|NP_001078436.1| PHD finger protein-related [Arabidopsis thaliana]	Unigene3560_All//4.00E-111//AT4G23860| PHD finger protein-related	Unigene3560_All//0.00E+00//DW230951				nr +
Unigene35603_All	1996	5.22	0.89	3.87	2.97	1.38	5.36	7.39	19.14	19.30	-2.55E+00	3.46E-29	Down	-4.31E-01	2.11E-02		-1.11E+00	1.14E-06	Down	8.53E-01	6.96E-07		1.37E+00	4.71E-56	Up	1.38E+00	1.60E-58	Up	Unigene35603_All//gi|221062075|ref|XP_002300742.1|//0.00E+00//cytokinin oxidase [Populus trichocarpa] >gi|222842468|gb|EEE80015.1| cytokinin oxidase [Populus trichocarpa]	Unigene35603_All//0.00E+00//AT1G75450| CKX5 (CYTOKININ OXIDASE 5); cytokinin dehydrogenase	Unigene35603_All//0.00E+00//TC167647		ko00908|Zeatin biosynthesis		nr +
Unigene35604_All	3221	10.25	14.00	10.25	28.66	27.22	22.53	10.47	6.32	4.51	4.50E-01	1.17E-08		0.00E+00	1.00E+00		-7.43E-02	2.35E-01		-3.47E-01	2.31E-11		-7.29E-01	4.66E-18		-1.21E+00	1.93E-42	Down	Unigene35604_All//gi|223452462|gb|ACM89558.1|//0.00E+00//protein kinase family protein [Glycine max]	Unigene35604_All//0.00E+00//AT5G56890| protein kinase family protein	Unigene35604_All//0.00E+00//TC139390		ko04626|Plant-pathogen interaction		nr -
Unigene35605_All	1943	26.17	13.98	26.12	13.69	14.96	14.18	7.22	2.22	2.05	-9.05E-01	1.69E-31		-3.10E-03	9.96E-01		1.28E-01	2.74E-01		5.06E-02	6.72E-01		-1.71E+00	8.96E-29	Down	-1.82E+00	2.34E-32	Down	Unigene35605_All//gi|15231261|ref|NP_187958.1|//0.00E+00//OVA5 (OVULE ABORTION 5); ATP binding / aminoacyl-tRNA ligase/ lysine-tRNA ligase/ nucleic acid binding / nucleotide binding [Arabidopsis thaliana] >gi|9280001|dbj|BAB01756.1| lysyl-tRNA synthetase [Arabidopsis thaliana]	Unigene35605_All//0.00E+00//AT3G13490| OVA5 (OVULE ABORTION 5); ATP binding / aminoacyl-tRNA ligase/ lysine-tRNA ligase/ nucleic acid binding / nucleotide binding	Unigene35605_All//0.00E+00//TC175807		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene35608_All	1230	105.79	40.00	77.02	13.61	14.39	10.02	1.99	1.02	0.36	-1.40E+00	1.97E-160	Down	-4.58E-01	2.33E-23		8.06E-02	6.12E-01		-4.41E-01	9.93E-04		-9.68E-01	7.64E-03		-2.48E+00	5.44E-09	Down	Unigene35608_All//gi|226531508|ref|NP_001149014.1|//2.00E-43//rhodanese-like domain containing protein [Zea mays] >gi|195610936|gb|ACG27298.1| rhodanese-like domain containing protein [Zea mays] >gi|195624004|gb|ACG33832.1| rhodanese-like domain containing protein [Zea mays]	Unigene35608_All//6.00E-33//AT4G27700| rhodanese-like domain-containing protein	Unigene35608_All//0.00E+00//TC131850				nr +
Unigene35609_All	1204	17.47	37.50	22.07	20.77	19.42	25.66	17.98	28.99	18.40	1.10E+00	2.06E-38	Up	3.37E-01	2.28E-03		-9.69E-02	4.58E-01		3.05E-01	1.72E-03		6.89E-01	5.96E-17		3.31E-02	7.78E-01		Unigene35609_All//gi|73761695|gb|AZE82347.1|//1.00E-77//ethylene-responsive element-binding factor [Gossypium hirsutum]	Unigene35609_All//3.00E-44//AT1G50640| ERF3 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 3); DNA binding / protein binding / transcription factor/ transcription repressor	Unigene35609_All//0.00E+00//DW507757	AP2-EREBP			nr +
Unigene3561_All	2459	1.85	0.56	2.69	15.82	9.98	10.30	11.04	14.02	13.82	-1.73E+00	2.53E-08	Down	5.37E-01	2.52E-02		-6.64E-01	2.41E-17		-6.19E-01	9.61E-14		3.45E-01	2.44E-05		3.24E-01	6.05E-05		Unigene3561_All//gi|121308607|dbj|BAF18699.1|//0.00E+00//PERK1-like protein kinase [Nicotiana tabacum]	Unigene3561_All//7.00E-167//AT3G24550| ATPERK1 (PROLINE EXTENSIN-LIKE RECEPTOR KINASE 1); ATP binding / protein kinase	Unigene3561_All//0.00E+00//gi|164318864|gb|ES818355.1|ES818355		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism	GO:0004672//GO:0004871//GO:0006464//GO:0016021//GO:0003259//GO:0043231	nr -
Unigene35613_All	1771	3.69	15.42	5.05	3.94	3.52	4.79	1.89	1.98	1.24	2.06E+00	5.42E-58	Up	4.52E-01	2.61E-02		-1.62E-01	5.40E-01		2.84E-01	1.94E-01		7.19E-02	8.22E-01		-6.08E-01	3.69E-02		Unigene35613_All//gi|124245039|gb|ABM92419.1|//1.00E-176//chloroplast HSP70 [Cucumis sativus]	Unigene35613_All//3.00E-177//AT4G24280| cpHsc70-1 (chloroplast heat shock protein 70-1); ATP binding	Unigene35613_All//0.00E+00//TC174980		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03018|RNA degradation		nr -
Unigene35614_All	2043	9.01	7.32	6.07	12.29	8.09	8.16	11.94	15.06	46.53	-3.01E-01	2.27E-02		-5.70E-01	1.83E-05		-6.03E-01	1.23E-09		-5.91E-01	1.96E-08		3.35E-01	1.27E-04		1.96E+00	4.52E-235	Up	Unigene35614_All//gi|18399065|ref|NP_566384.1|//0.00E+00//xanthine/uracil permease family protein [Arabidopsis thaliana] >gi|75207346|sp|Q9SRK7.1|AZG1_ARATH RecName: Full=Adenine/guanine permease AZG1; AltName: Full=Protein AZAGUANINE RESISTANT 1; Short=AtAzg1; AltName: Full=AzgA-homolog protein >gi|31365735|gb|AAQ65179.1| At3g10960 [Arabidopsis thaliana]	Unigene35614_All//0.00E+00//AT3G10960| xanthine/uracil permease family protein	Unigene35614_All//0.00E+00//TC162601				nr -
Unigene35616_All	1334	48.75	71.29	46.50	20.76	33.27	44.28	5.17	9.05	13.89	5.48E-01	1.40E-24		-6.81E-02	3.88E-01		6.80E-01	5.67E-20		1.09E+00	5.34E-53	Up	8.10E-01	3.29E-08		1.43E+00	7.20E-30	Up	Unigene35616_All//gi|30678254|ref|NP_671784.2|//6.00E-89//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana]	Unigene35616_All//3.00E-90//AT2G06025| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene35616_All//0.00E+00//TC171608				nr +
Unigene35617_All	2425	592.08	218.89	481.07	79.42	79.02	61.25	17.23	8.53	6.42	-1.44E+00	0.00E+00	Down	-3.00E-01	1.09E-114		-7.10E-03	8.82E-01		-3.75E-01	1.55E-26		-1.01E+00	3.44E-38	Down	-1.42E+00	1.14E-66	Down	Unigene35617_All//gi|3738261|dbj|BAA33803.1|//0.00E+00//chloroplast phosphoglycerate kinase [Populus nigra]	Unigene35617_All//0.00E+00//AT1G56190| phosphoglycerate kinase, putative	Unigene35617_All//0.00E+00//TC133469		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene35618_All	2321	4.46	3.14	1.63	10.82	6.91	4.53	10.95	5.76	8.75	-5.06E-01	4.38E-03		-1.45E+00	1.74E-13	Down	-6.46E-01	7.91E-11		-1.25E+00	1.14E-28	Down	-9.26E-01	2.27E-20		-3.23E-01	6.57E-04		Unigene35618_All//gi|15809986|gb|AAL06920.1|//1.00E-176//AT3g19540/T31J18_4 [Arabidopsis thaliana] >gi|22137022|gb|AAM91356.1| At3g19540/T31J18_4 [Arabidopsis thaliana]	Unigene35618_All//1.00E-156//AT3G19540| unknown protein	Unigene35618_All//0.00E+00//TC156418				nr -

Unigene35619_All	1352	76.59	45.69	46.55	26.82	25.65	18.64	10.85	29.28	158.21	-7.45E-01	1.21E-45		-7.18E-01	2.44E-41		-6.46E-02	5.64E-01		-5.25E-01	1.01E-09		1.43E+00	7.52E-62	Up	3.87E+00	0.00E+00	Up	Unigene35619_All//gi|85540956|sp|Q8GXG1.2|ASPG2_ARATH//1.00E-155//RecName: Full=Probable isoaspartyl peptidase/L-asparaginase 2; AltName: Full=L-asparagine amidohydrolase 2; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase 2 subunit alpha; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase 2 subunit beta; Flags: Precursor >gi|9294462|dbj|BAB02681.1| l-asparaginase (l-asparagine amidohydrolase) [Arabidopsis thaliana] >gi|89000945|gb|ABD59062.1| At3g16150 [Arabidopsis thaliana]	Unigene35619_All//3.00E-156//AT3G16150| L-asparaginase, putative / L-asparagine amidohydrolase, putative	Unigene35619_All//0.00E+00//TC130807				nr +
Unigene3562_All	1623	3.35	5.46	3.48	21.15	19.41	17.48	8.49	6.41	4.05	7.05E-01	2.77E-04		5.29E-02	8.43E-01		-1.23E-01	2.33E-01		-2.75E-01	2.87E-03		-4.05E-01	2.90E-03		-1.07E+00	1.05E-14	Down	Unigene3562_All//gi|297811575|ref|XP_002873671.1|//1.00E-136//aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319508|gb|EFH49930.1| aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3562_All//9.00E-130//AT3G01590| aldose 1-epimerase family protein	Unigene3562_All//0.00E+00//TC146651				nr -
Unigene35620_All	1837	17.23	17.65	12.38	108.14	144.53	98.44	6.03	4.32	1.43	3.49E-02	7.38E-01		-4.77E-01	1.27E-06		4.18E-01	2.64E-49		-1.36E-01	1.82E-04		-4.80E-01	1.68E-03		-2.07E+00	1.55E-30	Down	Unigene35620_All//gi|349379|gb|AAA63765.1|//1.00E-106//HAHB-1 [Helianthus annuus]	Unigene35620_All//3.00E-96//AT1G69780| ATHB13; DNA binding / sequence-specific DNA binding / transcription factor	Unigene35620_All//0.00E+00//TC144521	HB			nr +
Unigene35621_All	1264	21.57	18.52	24.06	50.56	32.75	25.73	15.92	9.06	6.65	-2.20E-01	4.37E-02		1.58E-01	1.54E-01		-6.27E-01	1.69E-25		-9.75E-01	3.83E-48		-8.13E-01	3.00E-13		-1.26E+00	3.83E-27	Down	Unigene35621_All//gi|33465891|gb|AAQ19327.1|//2.00E-24//bZIP-like protein [Oryza sativa Japonica Group]	Unigene35621_All//6.00E-12//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene35621_All//0.00E+00//gi|13246195|gb|BE052035.2|BE052035				nr -
Unigene35622_All	1814	2.77	2.40	2.64	8.05	6.45	2.37	2.77	1.08	1.63	-2.05E-01	4.69E-01		-6.77E-02	8.10E-01		-3.18E-01	2.83E-02		-1.77E+00	9.31E-28	Down	-1.36E+00	5.92E-08	Down	-7.71E-01	8.36E-04		Unigene35622_All//gi|9945082|gb|AAG03119.1|AC004133_13//2.00E-43//F5A9.24 [Arabidopsis thaliana]	Unigene35622_All//2.00E-22//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene35622_All//0.00E+00//gi|13246195|gb|BE052035.2|BE052035				nr -
Unigene35624_All	1677	46.02	21.97	40.96	97.25	126.39	50.55	11.37	5.86	5.37	-1.07E+00	3.88E-62	Down	-1.68E-01	9.01E-03		3.78E-01	1.05E-32		-9.44E-01	8.02E-116		-9.57E-01	2.52E-16		-1.08E+00	2.01E-20	Down	Unigene35624_All//gi|297725701|ref|NP_001175214.1|//2.00E-52//Os07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1| Os07g0501200 [Oryza sativa Japonica Group]	Unigene35624_All//3.00E-27//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene35624_All//3.00E-85//TC159820				nr -
Unigene35626_All	1568	7.81	20.26	7.00	12.74	27.50	15.06	14.26	42.04	125.13	1.38E+00	2.69E-38	Up	-1.59E-01	3.93E-01		1.11E+00	1.02E-43	Up	2.42E-01	4.09E-02		1.56E+00	3.03E-116	Up	3.13E+00	0.00E+00	Up	Unigene35626_All//gi|15225326|ref|NP_180221.1|//2.00E-77//AR781 [Arabidopsis thaliana] >gi|2739378|gb|AAC14501.1| AR781, similar to yeast pheromone receptor [Arabidopsis thaliana] >gi|23297321|gb|AAN12941.1| AR781 [Arabidopsis thaliana]	Unigene35626_All//2.00E-44//AT2G26530| AR781	Unigene35626_All//0.00E+00//gi|164277841|gb|ES809478.1|ES809478				nr +
Unigene35627_All	3582	4.10	23.06	10.36	3.48	6.65	6.88	3.71	7.74	9.02	2.49E+00	1.35E-219	Up	1.34E+00	1.81E-41	Up	9.36E-01	1.71E-18		9.86E-01	5.07E-19		1.06E+00	1.62E-27	Up	1.28E+00	6.73E-44	Up	Unigene35627_All//gi|297723367|ref|NP_001174047.1|//1.00E-120//Os04g0564700 [Oryza sativa Japonica Group] >gi|255675694|dbj|BAH92775.1| Os04g0564700 [Oryza sativa Japonica Group]	Unigene35627_All//0.00E+00//AT4G35560| FUNCTIONS IN: molecular_function unknown; LOCATED IN: CUL4 RING ubiquitin ligase complex; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), WD40 repeat (InterPro:IPR001680), WD40/YVTN repeat-like (InterPro:IPR015943), Lethal giant larvae (Lgl) like, C-terminal (InterPro:IPR013905); BEST Arabidopsis thaliana protein match is: transducin family protein / WD-40 repeat family protein (TAIR:AT5G05570.1); Has 562 Blast hits to 546 proteins in 129 species: Archae - 0; Bacteria - 20; Metazoa - 305; Fungi - 89; Plants - 43; Viruses - 0; Other Eukaryotes - 105 (source: NCBI BLink).	Unigene35627_All//0.00E+00//CO112120				nr +
Unigene35628_All	2459	17.79	10.61	8.86	24.61	20.31	24.92	21.70	12.14	13.97	-7.45E-01	1.05E-19		-1.01E+00	4.03E-31	Down	-2.78E-01	1.03E-05		1.81E-02	8.36E-01		-8.38E-01	1.64E-35		-6.36E-01	7.02E-23		Unigene35628_All//gi|18394153|ref|NP_563957.1|//5.00E-77//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|30683962|ref|NP_849663.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	Unigene35628_All//8.00E-60//AT1G14710| hydroxyproline-rich glycoprotein family protein	Unigene35628_All//0.00E+00//gi|78347795|gb|DT568069.1|DT568069		ko03040|Spliceosome		nr +
Unigene35633_All	3145	1.73	1.11	0.63	4.39	3.79	1.85	3.97	3.44	4.08	-6.38E-01	1.24E-02		-1.47E+00	1.85E-07	Down	-2.12E-01	1.92E-01		-1.24E+00	8.42E-16	Down	-2.04E-01	1.95E-01		4.05E-02	7.94E-01		Unigene35633_All//gi|297802800|ref|XP_002869284.1|//1.00E-101//lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315120|gb|EFH45543.1| lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35633_All//5.00E-95//AT4G32300| SD2-5 (S-DOMAIN-2 5); carbohydrate binding / kinase/ protein kinase	Unigene35633_All//0.00E+00//gi|109865008|gb|DW493984.1|DW493984		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism		nr -
Unigene35634_All	2183	43.31	32.80	50.84	8.83	7.67	5.67	1.18	0.98	0.49	-4.01E-01	3.89E-14		2.31E-01	5.11E-06		-2.04E-01	1.25E-01		-6.40E-01	1.57E-07		-2.75E-01	4.72E-01		-1.26E+00	3.03E-04	Down	Unigene35634_All//gi|297801048|ref|XP_002868408.1|//0.00E+00//adenylate kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314244|gb|EFH44667.1| adenylate kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35634_All//0.00E+00//AT5G35170| adenylate kinase family protein	Unigene35634_All//0.00E+00//TC133913		ko00230|Purine metabolism		nr +
Unigene35639_All	1681	209.63	199.69	261.63	22.85	21.78	17.36	12.27	9.90	5.14	-7.00E-02	1.48E-02		3.20E-01	5.15E-40		-6.93E-02	5.31E-01		-3.97E-01	2.18E-06		-3.11E-01	4.79E-03		-1.26E+00	1.18E-27	Down	Unigene35639_All//gi|119368480|ref|YP_913168.1|//1.00E-77//maturase [Gossypium barbadense] >gi|218526556|sp|A0ZZ16.1|MATK_GOSBA RecName: Full=Maturase K; AltName: Full=Intron maturase >gi|119224842|dbj|BAF41228.1| maturase [Gossypium barbadense]	Unigene35639_All//9.00E-46//ATCG00040| Encodes a maturase located in the trnK intron in the chloroplast genome.	Unigene35639_All//0.00E+00//TC163105				nr +
Unigene35644_All	2369	2.92	7.49	5.04	4.39	4.08	5.34	6.26	6.12	7.18	1.36E+00	2.45E-21	Up	7.88E-01	3.61E-06		-1.06E-01	5.97E-01		2.81E-01	9.80E-02		-3.32E-02	8.30E-01		1.97E-01	1.15E-01		Unigene35644_All//gi|42569297|ref|NP_180077.3|//1.00E-163//formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] >gi|160013996|sp|Q9SK28.2|FH18_ARATH RecName: Full=Formin-like protein 18; Short=AtFH18	Unigene35644_All//1.00E-138//AT2G25050| formin homology 2 domain-containing protein / FH2 domain-containing protein	Unigene35644_All//0.00E+00//gi|164318805|gb|ES808112.1|ES808112		ko03040|Spliceosome		nr -
Unigene35645_All	2231	1.43	3.38	2.17	2.95	2.82	2.87	2.12	2.42	3.18	1.24E+00	2.25E-08	Up	6.02E-01	3.54E-02		-6.13E-02	8.08E-01		-3.60E-02	9.04E-01		1.87E-01	4.71E-01		5.83E-01	2.21E-03		Unigene35645_All//gi|240256452|ref|NP_200624.5|//0.00E+00//actin binding [Arabidopsis thaliana]	Unigene35645_All//9.00E-143//AT2G25050| formin homology 2 domain-containing protein / FH2 domain-containing protein	Unigene35645_All//0.00E+00//TC161989		ko03040|Spliceosome		nr -
Unigene35647_All	1035	14.36	9.55	8.80	25.12	14.84	20.86	11.44	4.32	4.20	-5.89E-01	4.73E-05		-7.07E-01	2.57E-06		-7.60E-01	9.01E-15		-2.68E-01	1.40E-02		-1.40E+00	1.47E-18	Down	-1.45E+00	5.44E-20	Down			Unigene35647_All//0.00E+00//gi|164342029|gb|ES793410.1|ES793410				
Unigene35649_All	1492	0.81	0.07	0.18	3.84	5.54	2.78	6.97	1.79	3.71	-3.57E+00	3.63E-05	Down	-2.18E+00	3.05E-03		5.29E-01	6.78E-03		-4.63E-01	6.94E-02		-1.96E+00	7.34E-26	Down	-9.09E-01	7.08E-09		Unigene35649_All//gi|18408804|ref|NP_564900.1|//4.00E-91//remorin family protein [Arabidopsis thaliana] >gi|11072019|gb|AAG28898.1|AC008113_14 F12A21.28 [Arabidopsis thaliana]	Unigene35649_All//8.00E-67//AT1G67590| remorin family protein	Unigene35649_All//0.00E+00//TC159342				nr -
Unigene35650_All	1510	0.62	0.64	1.41	4.02	3.90	3.59	5.54	2.44	3.51	3.18E-02	9.83E-01		1.18E+00	1.19E-02		-4.56E-02	8.59E-01		-1.65E-01	5.65E-01		-1.19E+00	1.80E-10	Down	-6.60E-01	1.39E-04		Unigene35650_All//gi|18408804|ref|NP_564900.1|//6.00E-88//remorin family protein [Arabidopsis thaliana] >gi|11072019|gb|AAG28898.1|AC008113_14 F12A21.28 [Arabidopsis thaliana]	Unigene35650_All//1.00E-78//AT1G67590| remorin family protein	Unigene35650_All//0.00E+00//CO131895				nr -
Unigene35651_All	1783	8.45	8.89	4.33	28.41	28.04	31.84	12.66	9.14	5.21	7.38E-02	6.18E-01		-9.65E-01	2.10E-10		-1.90E-02	8.31E-01		1.64E-01	2.68E-02		-4.70E-01	4.52E-06		-1.28E+00	3.54E-31	Down	Unigene35651_All//gi|8569096|gb|AAF76441.1|AC015445_8//1.00E-132//ESTs gb|AI994059, gb|T43740 come from this gene [Arabidopsis thaliana]	Unigene35651_All//2.00E-104//AT3G19080| unknown protein	Unigene35651_All//0.00E+00//gi|164285039|gb|ES805969.1|ES805969				nr +
Unigene35654_All	2557	6.94	2.54	3.60	12.72	9.60	13.34	27.12	47.57	28.67	-1.45E+00	1.41E-23	Down	-9.45E-01	9.54E-12		-4.06E-01	3.06E-06		6.80E-02	5.68E-01		8.11E-01	2.06E-75		8.02E-02	1.87E-01		Unigene35654_All//gi|224116528|ref|XP_002331919.1|//0.00E+00//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222874591|gb|EEF11722.1| oligopeptide transporter OPT family [Populus trichocarpa]	Unigene35654_All//0.00E+00//AT3G17650| YSL5 (YELLOW STRIPE LIKE 5); oligopeptide transporter	Unigene35654_All//0.00E+00//TC151019				nr +
Unigene35657_All	1782	1.17	0.71	1.17	2.15	1.68	1.82	3.16	1.31	1.39	-7.24E-01	1.03E-01		-1.11E-02	1.00E+00		-3.57E-01	2.78E-01		-2.38E-01	4.97E-01		-1.26E+00	5.63E-08	Down	-1.19E+00	1.46E-07	Down	Unigene35657_All//gi|14335066|gb|AAK59797.1|//1.00E-56//AT5g57120/MCL3_6 [Arabidopsis thaliana] >gi|22135789|gb|AAM91051.1| AT5g57120/MCL3_6 [Arabidopsis thaliana]	Unigene35657_All//5.00E-38//AT5G57120| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: LisH dimerisation motif (InterPro:IPR006594), SRP40, C-terminal (InterPro:IPR007718); Has 90949 Blast hits to 45608 proteins in 1620 species: Archae - 300; Bacteria - 8281; Metazoa - 37603; Fungi - 8095; Plants - 3374; Viruses - 548; Other Eukaryotes - 32748 (source: NCBI BLink).	Unigene35657_All//0.00E+00//ES817791				nr -

Unigene35658_All	975	3.54	5.46	8.57	5.98	4.70	5.19	6.24	11.62	17.20	6.24E-01	1.61E-02		1.28E+00	3.75E-09	Up	-3.48E-01	1.65E-01		-2.04E-01	4.76E-01		8.96E-01	4.77E-09		1.46E+00	4.20E-28	Up	Unigene35658_All//gi|75161682|sp|Q8VZQ0.1|NRX3_ARATH//4.00E-50//RecName: Full=Probable nucleoredoxin 3; Short=AtNrx3	Unigene35658_All//2.00E-51//AT4G31240| INVOLVED IN: cell redox homeostasis; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Thioredoxin fold (InterPro:IPR012335), Thioredoxin-like (InterPro:IPR017936), Thioredoxin-like fold (InterPro:IPR012336), C1-like (InterPro:IPR011424); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G60420.1); Has 1190 Blast hits to 724 proteins in 157 species: Archae - 0; Bacteria - 225; Metazoa - 381; Fungi - 0; Plants - 174; Viruses - 0; Other Eukaryotes - 410 (source: NCBI BLink).	Unigene35658_All//0.00E+00//C0112117				nr +
Unigene35659_All	1552	8.36	14.07	16.92	12.29	13.91	18.25	11.36	27.79	29.37	7.51E-01	2.46E-10		1.02E+00	2.99E-19	Up	1.78E-01	1.65E-01		5.70E-01	8.44E-09		1.29E+00	1.44E-57	Up	1.37E+00	5.23E-68	Up	Unigene35659_All//gi|75161682|sp|Q8VZQ0.1|NRX3_ARATH//1.00E-111//RecName: Full=Probable nucleoredoxin 3; Short=AtNrx3	Unigene35659_All//5.00E-113//AT4G31240| INVOLVED IN: cell redox homeostasis; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Thioredoxin fold (InterPro:IPR012335), Thioredoxin-like (InterPro:IPR017936), Thioredoxin-like fold (InterPro:IPR012336), C1-like (InterPro:IPR011424); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G60420.1); Has 1190 Blast hits to 724 proteins in 157 species: Archae - 0; Bacteria - 225; Metazoa - 381; Fungi - 0; Plants - 174; Viruses - 0; Other Eukaryotes - 410 (source: NCBI BLink).	Unigene35659_All//0.00E+00//TC166494				nr +
Unigene3566_All	1431	4.61	5.95	6.10	3.34	1.47	2.65	1.30	1.05	0.67	3.69E-01	6.92E-02		4.06E-01	5.04E-02		-1.19E+00	4.31E-06	Down	-3.34E-01	2.62E-01		-3.06E-01	5.09E-01		-9.60E-01	1.93E-02		Unigene3566_All//gi|297820152|ref|XP_002877959.1|//0.00E+00//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323797|gb|EFH54218.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3566_All//0.00E+00//AT3G54140| PTR1 (PEPTIDE TRANSPORTER 1); dipeptide transporter/ transporter/ tripeptide transporter	Unigene3566_All//0.00E+00//TC174587			GO:0006857//GO:0008152//GO:0015198//GO:0031224	nr +
Unigene35661_All	1802	22.07	17.38	31.65	1.24	1.93	1.58	0.77	1.81	0.51	-3.45E-01	4.77E-05		5.20E-01	3.21E-13		6.34E-01	5.49E-02		3.44E-01	3.99E-01		1.22E+00	9.63E-05	Up	-6.07E-01	2.13E-01		Unigene35661_All//gi|224127426|ref|XP_002320071.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222860844|gb|EEE98386.1| cytochrome P450 [Populus trichocarpa]	Unigene35661_All//6.00E-173//AT2G45510| CYP704A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene35661_All//0.00E+00//TC178534		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene35664_All	2639	42.84	21.70	24.15	71.07	64.56	88.26	96.14	46.72	57.70	-9.82E-01	3.52E-79		-8.27E-01	1.85E-57		-1.39E-01	9.97E-05		3.13E-01	8.34E-23		-1.04E+00	2.25E-238	Down	-7.37E-01	1.97E-136		Unigene35664_All//gi|87162860|gb|AB028655.1|//1.00E-168//K+ channel tetramerisation [Medicago truncatula]	Unigene35664_All//8.00E-141//AT3G09030| potassium channel tetramerisation domain-containing protein	Unigene35664_All//0.00E+00//TC178347				nr -
Unigene35667_All	559	2.71	2.72	0.38	17.29	25.20	14.38	9.38	8.75	12.97	2.70E-03	9.97E-01		-2.83E+00	5.52E-05	Down	5.43E-01	1.17E-04		-2.66E-01	1.90E-01		-1.01E-01	7.02E-01		4.68E-01	1.34E-02		Unigene35667_All//gi|297811761|ref|XP_002873764.1|//4.00E-08//octicosapeptide/Phox/Bem1p domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319601|gb|EFH50023.1| octicosapeptide/Phox/Bem1p domain-containing protein [Arabidopsis lyrata subsp. lyrata]		Unigene35667_All//0.00E+00//TC147515				nr +
Unigene35670_All	2264	119.32	49.93	35.87	51.51	31.33	23.10	36.21	18.53	33.33	-1.26E+00	1.32E-280	Down	-1.73E+00	0.00E+00	Down	-7.17E-01	9.36E-59		-1.16E+00	1.13E-115	Down	-9.66E-01	1.45E-68		-1.20E-01	2.51E-02		Unigene35670_All//gi|500753|gb|AAA74456.1|//0.00E+00//nitrite reductase [Phaseolus vulgaris]	Unigene35670_All//0.00E+00//AT2G15620| NIR1 (NITRITE REDUCTASE 1); ferredoxin-nitrate reductase/ nitrite reductase (NO-forming)	Unigene35670_All//0.00E+00//TC155184		ko00910|Nitrogen metabolism		nr +
Unigene35671_All	1684	49.00	52.93	89.74	274.36	75.64	71.63	61.54	44.77	81.52	1.11E-01	6.22E-02		8.73E-01	3.05E-84		-1.86E+00	0.00E+00	Down	-1.94E+00	0.00E+00	Down	-4.59E-01	7.64E-24		4.06E-01	9.37E-26		Unigene35671_All//gi|60592456|gb|AA328838.1|//1.00E-136//zinc transporter protein ZIP2 [Fragaria x ananassa]	Unigene35671_All//2.00E-85//AT1G05300| ZIP5; cation transmembrane transporter/ metal ion transmembrane transporter	Unigene35671_All//0.00E+00//TC157926				nr +
Unigene35675_All	1951	2.74	4.91	5.65	2.78	3.85	4.03	2.93	3.15	3.00	8.44E-01	6.54E-06		1.05E+00	7.91E-09	Up	4.67E-01	2.66E-02		5.33E-01	1.03E-02		1.06E-01	6.49E-01		3.70E-02	8.85E-01		Unigene35675_All//gi|297795789|ref|XP_002865779.1|//0.00E+00//nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297311614|gb|EFH42038.1| nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene35675_All//0.00E+00//AT5G50230| nucleotide binding	Unigene35675_All//0.00E+00//TC164507				nr -
Unigene35676_All	1456	3.81	4.77	3.95	8.21	6.60	4.00	2.96	2.15	3.17	3.24E-01	1.59E-01		5.24E-02	8.43E-01		-3.15E-01	5.47E-02		-1.04E+00	1.98E-10	Down	-4.60E-01	8.48E-02		9.98E-02	7.03E-01		Unigene35676_All//gi|90093310|gb|AB085168.1|//4.00E-90//At3g22970 [Arabidopsis thaliana]	Unigene35676_All//6.00E-80//AT2G38820| unknown protein	Unigene35676_All//0.00E+00//TC134568				nr +
Unigene35677_All	1206	2.17	0.67	0.79	19.29	12.05	11.31	7.78	9.74	8.99	-1.69E+00	5.80E-05	Down	-1.45E+00	6.62E-04	Down	-6.79E-01	5.80E-11		-7.70E-01	3.65E-12		3.23E-01	3.41E-02		2.07E-01	2.00E-01		Unigene35677_All//gi|42567992|ref|NP_197554.2|//7.00E-85//ATBRXL4 (BREVIS RADIX-LIKE 4) [Arabidopsis thaliana] >gi|75151601|sp|Q8GZ92.1|BRXL4_ARATH RecName: Full=Protein Brevis radix-like 4; Short=AtBRXL4	Unigene35677_All//4.00E-86//AT5G20540| ATBRXL4 (BREVIS RADIX-LIKE 4)	Unigene35677_All//0.00E+00//gi|78335406|gb|DT555680.1|DT555680				nr -
Unigene35678_All	1948	1.50	0.91	0.71	12.63	8.38	6.00	7.16	4.63	6.71	-7.24E-01	4.64E-02		-1.08E+00	5.08E-03		-5.92E-01	3.59E-09		-1.07E+00	5.26E-22	Down	-6.28E-01	2.66E-06		-9.46E-02	5.47E-01		Unigene35678_All//gi|42567992|ref|NP_197554.2|//1.00E-139//ATBRXL4 (BREVIS RADIX-LIKE 4) [Arabidopsis thaliana] >gi|75151601|sp|Q8GZ92.1|BRXL4_ARATH RecName: Full=Protein Brevis radix-like 4; Short=AtBRXL4	Unigene35678_All//3.00E-130//AT5G20540| ATBRXL4 (BREVIS RADIX-LIKE 4)	Unigene35678_All//0.00E+00//TC161373				nr -
Unigene35680_All	1417	3.10	0.72	2.37	2.85	4.86	5.45	3.40	2.39	1.18	-2.12E+00	2.81E-10	Down	-3.90E-01	2.15E-01		7.71E-01	2.88E-04		9.37E-01	6.40E-06		-5.10E-01	3.96E-02		-1.53E+00	2.70E-09	Down	Unigene35680_All//gi|15234006|ref|NP_193610.1|//1.00E-100//DOT4 (DEFECTIVELY ORGANIZED TRIBUTARIES 4) [Arabidopsis thaliana] >gi|75206861|sp|Q9SN39.1|PP320_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g18750, chloroplastic; Flags: Precursor	Unigene35680_All//4.00E-101//AT4G18750| DOT4 (DEFECTIVELY ORGANIZED TRIBUTARIES 4)	Unigene35680_All//0.00E+00//TC175864				nr +
Unigene35682_All	1200	12.86	12.50	9.98	57.58	44.28	21.60	15.54	6.55	3.52	-4.14E-02	7.85E-01		-3.65E-01	1.52E-02		-3.79E-01	3.60E-11		-1.41E+00	6.87E-94	Down	-1.25E+00	4.43E-24	Down	-2.14E+00	6.05E-53	Down	Unigene35682_All//gi|124359162|gb|ABN05685.1|//6.00E-19//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene35682_All//4.00E-12//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene35682_All//0.00E+00//TC141086				nr -
Unigene35683_All	1131	111.95	128.44	94.21	54.39	43.42	64.77	82.47	176.64	128.57	1.98E-01	3.50E-06		-2.49E-01	1.12E-07		-3.25E-01	1.22E-07		2.52E-01	2.77E-05		1.10E+00	9.04E-205	Up	6.41E-01	2.56E-61		Unigene35683_All//gi|297842942|ref|XP_002889352.1|//3.00E-99//peroxisomal biogenesis factor 11 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335194|gb|EFH65611.1| peroxisomal biogenesis factor 11 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35683_All//1.00E-99//AT1G01820| PEX11C (PEROXIN 11C)	Unigene35683_All//0.00E+00//TC147122				nr +
Unigene35684_All	867	24.98	25.13	14.56	17.64	17.91	16.30	52.03	34.32	24.17	8.40E-03	9.70E-01		-7.79E-01	2.03E-10		2.22E-02	9.04E-01		-1.14E-01	5.09E-01		-6.00E-01	3.70E-17		-1.11E+00	9.65E-49	Down	Unigene35684_All//gi|116317926|emb|CAH65949.1|//2.00E-84//H0716A07.7 [Oryza sativa (indica cultivar-group)]	Unigene35684_All//1.00E-77//AT1G01090| PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-transferring)	Unigene35684_All//0.00E+00//gi|164269301|gb|ES813735.1|ES813735		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)//ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis		nr +
Unigene35686_All	1321	35.13	16.46	21.85	52.91	50.81	31.56	24.20	17.91	17.49	-1.09E+00	3.47E-39	Down	-6.85E-01	2.20E-17		-5.85E-02	4.50E-01		-7.46E-01	1.86E-33		-4.34E-01	3.04E-07		-4.68E-01	1.79E-08		Unigene35686_All//gi|115455173|ref|NP_001051187.1|//6.00E-83//Os03g0735300 [Oryza sativa Japonica Group] >gi|108710938|gb|ABF98733.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549658|dbj|BAF13101.1| Os03g0735300 [Oryza sativa Japonica Group]	Unigene35686_All//1.00E-54//AT3G07030| nucleic acid binding	Unigene35686_All//0.00E+00//gi|78341201|gb|DT561475.1|DT561475		ko03040|Spliceosome		nr +
Unigene35688_All	2067	12.50	4.41	7.45	10.46	7.03	7.58	9.16	1.84	2.14	-1.50E+00	8.23E-36	Down	-7.48E-01	1.66E-11		-5.73E-01	1.09E-07		-4.64E-01	5.48E-05		-2.32E+00	2.34E-57	Down	-2.10E+00	2.16E-52	Down	Unigene35688_All//gi|297799538|ref|XP_002867653.1|//1.00E-149//allinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313489|gb|EFH43912.1| allinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35688_All//2.00E-137//AT4G24670| TAR2 (TRYPTOPHAN AMINOTRANSFERASE RELATED 2); L-tryptophan:2-oxoglutarate aminotransferase/ L-tryptophan:pyruvate aminotransferase/ carbon-sulfur lyase	Unigene35688_All//0.00E+00//gi|164252584|gb|ES826793.1|ES826793				nr +
Unigene3569_All	1767	65.35	32.09	49.42	81.30	53.05	50.07	28.09	14.62	13.48	-1.03E+00	5.97E-87	Down	-4.03E-01	1.53E-16		-6.16E-01	3.26E-55		-6.99E-01	4.63E-61		-9.42E-01	3.71E-40		-1.06E+00	6.23E-50	Down	Unigene3569_All//gi|115476382|ref|NP_001061787.1|//5.00E-59//Os08g0411300 [Oryza sativa Japonica Group] >gi|113623756|dbj|BAF23701.1| Os08g0411300 [Oryza sativa Japonica Group]	Unigene3569_All//3.00E-89//AT4G39840| unknown protein	Unigene3569_All//0.00E+00//TC133472				nr -
Unigene35693_All	1121	9.99	3.84	7.98	4.98	4.30	5.96	1.55	1.49	1.35	-1.38E+00	4.46E-14	Down	-3.24E-01	7.94E-02		-2.11E-01	4.49E-01		2.61E-01	3.11E-01		-5.22E-02	9.23E-01		-1.95E-01	6.45E-01		Unigene35693_All//gi|145339954|ref|NP_567251.2|//8.00E-96//binding / catalytic/ oxidoreductase [Arabidopsis thaliana]	Unigene35693_All//1.00E-88//AT4G03140| binding / catalytic/ oxidoreductase	Unigene35693_All//0.00E+00//gi|164271695|gb|ES796829.1|ES796829		ko00906|Carotenoid biosynthesis		nr +
Unigene35694_All	593	6.53	3.33	1.44	7.56	9.00	7.77	4.42	7.40	6.05	-9.70E-01	1.93E-03		-2.18E+00	5.41E-09	Down	2.52E-01	3.89E-01		3.92E-02	9.19E-01		7.43E-01	3.88E-03		4.52E-01	1.14E-01				Unigene35694_All//5.00E-162//gi|108890086|gb|DW519054.1|DW519054				

Unigene35696_All	1639	1.98	1.95	2.31	3.89	4.73	4.99	4.41	2.09	1.82	-2.32E-02	9.65E-01		2.21E-01	5.26E-01		2.81E-01	2.15E-01		3.58E-01	9.29E-02		-1.08E+00	5.97E-08	Down	-1.27E+00	1.71E-10	Down	Unigene35696_All//gi|18397649|ref|NP_565365.1|//1.00E-130//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|42570775|ref|NP_973461.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|20197262|gb|AAM15000.1| Expressed protein [Arabidopsis thaliana]	Unigene35696_All//7.00E-123//AT2G14835| zinc finger (C3HC4-type RING finger) family protein	Unigene35696_All//0.00E+00//gi|48801467|gb|CO102781.1|CO102781				nr +
Unigene35697_All	1934	3.87	4.24	4.85	5.69	4.18	5.53	5.92	6.89	2.86	1.34E-01	5.58E-01		3.25E-01	1.11E-01		-4.44E-01	6.67E-03		-4.06E-02	8.45E-01		2.19E-01	1.42E-01		-1.05E+00	4.85E-12	Down	Unigene35697_All|gi|297829288|ref|XP_002882526.1|//0.00E+00//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328366|gb|EFH58785.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35697_All//0.00E+00//AT3G07400| lipase class 3 family protein	Unigene35697_All//0.00E+00//TC153620				nr +
Unigene35698_All	1202	17.59	87.77	19.67	39.91	55.61	48.28	137.15	196.22	154.75	2.32E+00	8.58E-258	Up	1.62E-01	2.13E-01		4.79E-01	4.19E-16		2.75E-01	5.51E-05		5.17E-01	6.62E-66		1.74E-01	1.21E-07		Unigene35698_All|gi|297804388|ref|XP_002870078.1|//3.00E-95//zinc-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315914|gb|EFH46337.1| zinc-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35698_All//8.00E-89//AT4G17900| zinc-binding family protein	Unigene35698_All//0.00E+00//TC153837	PLATZ			nr +
Unigene35699_All	1768	2.60	2.24	1.17	2.79	4.27	2.55	3.78	1.11	1.53	-2.20E-01	4.53E-01		-1.15E+00	1.22E-04	Down	6.13E-01	2.64E-03		-1.27E-01	6.92E-01		-1.77E+00	9.25E-15	Down	-1.30E+00	4.64E-10	Down	Unigene35699_All|gi|224071513|ref|XP_002303496.1|//0.00E+00//f-box family protein [Populus trichocarpa] >gi|222840928|gb|EEE78475.1| f-box family protein [Populus trichocarpa]	Unigene35699_All//1.00E-143//AT5G07670| F-box family protein	Unigene35699_All//0.00E+00//gi|48878780|gb|CO129802.1|CO129802		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene3570_All	1815	3.14	2.51	5.25	14.82	20.28	24.36	16.19	4.63	10.07	-3.23E-01	2.16E-01		7.41E-01	1.22E-04		4.53E-01	3.01E-08		7.17E-01	7.92E-20		-1.81E+00	2.45E-64	Down	-6.84E-01	1.08E-14		Unigene3570_All|gi|22326581|ref|NP_195946.2|//0.00E+00//LAC11 (laccase 11); laccase [Arabidopsis thaliana] >gi|75331174|sp|Q8VZA1.1|LAC11_ARATH RecName: Full=Laccase-11; AltName: Full=Benzenediol:oxygen oxidoreductase 11; AltName: Full=Urishiol oxidase 11; AltName: Full=Diphenol oxidase 11; Flags: Precursor >gi|17473695|gb|AAL38304.1| laccase (diphenol oxidase)-like protein [Arabidopsis thaliana] >gi|20148527|gb|AAM10154.1| laccase (diphenol oxidase)-like protein [Arabidopsis thaliana]	Unigene3570_All//0.00E+00//AT5G03260| LAC11 (laccase 11); laccase	Unigene3570_All//8.00E-77//TC158657		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0031410//GO:0046914	nr -
Unigene35703_All	1983	5.17	9.81	6.12	10.53	9.60	14.67	22.52	37.92	54.42	9.24E-01	6.73E-13		2.44E-01	1.75E-01		-1.32E-01	3.32E-01		4.79E-01	9.26E-07		7.52E-01	2.62E-41		1.27E+00	5.66E-143	Up	Unigene35703_All|gi|79516777|ref|NP_197441.3|//1.00E-08//SMG7 [Arabidopsis thaliana] >gi|159461469|gb|ABW96769.1| SMG7-like protein [Arabidopsis thaliana]	Unigene35703_All//4.00E-35//AT5G19400| SMG7	Unigene35703_All//0.00E+00//gi|18099393|gb|BM358647.1|BM358647				nr -
Unigene35704_All	1868	1.09	2.39	0.97	2.45	3.59	3.70	4.96	6.51	9.47	1.13E+00	1.20E-04	Up	-1.73E-01	7.00E-01		5.51E-01	1.27E-02		5.92E-01	7.81E-03		3.94E-01	7.29E-03		9.34E-01	5.51E-15		Unigene35704_All|gi|18146966|dbj|BAB82502.1|//4.00E-61//cig3 [Nicotiana tabacum]	Unigene35704_All//4.00E-35//AT5G19400| SMG7	Unigene35704_All//0.00E+00//gi|109884972|gb|DW513942.1|DW513942				nr +
Unigene35705_All	1578	3.78	7.29	13.16	12.50	10.63	40.70	4.58	3.50	8.61	9.47E-01	2.98E-08		1.80E+00	6.08E-36	Up	-2.34E-01	6.61E-02		1.70E+00	1.43E-112	Up	-3.90E-01	5.03E-02		9.10E-01	2.95E-11		Unigene35705_All|gi|297847058|ref|XP_002891410.1|//0.00E+00//glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] >gi|297337252|gb|EFH67669.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	Unigene35705_All//0.00E+00//AT1G48100| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene35705_All//0.00E+00//gi|109850584|gb|DW479563.1|DW479563		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene35708_All	804	61.30	32.58	59.67	13.88	8.65	6.24	3.10	1.25	0.79	-9.12E-01	6.27E-31		-3.88E-02	6.59E-01		-6.82E-01	1.37E-05		-1.15E+00	1.63E-11	Down	-1.31E+00	3.60E-04	Down	-1.97E+00	4.57E-07	Down	Unigene35708_All|gi|18420570|ref|NP_568077.1|//2.00E-82//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana]	Unigene35708_All//4.00E-83//AT4G39970| haloacid dehalogenase-like hydrolase family protein	Unigene35708_All//0.00E+00//gi|109876681|gb|DW505655.1|DW505655		ko00740|Riboflavin metabolism		nr +
Unigene35709_All	319	9.18	3.81	6.84	0.78	0.76	0.71	1.06	0.26	0.25	-1.27E+00	7.30E-04	Down	-4.24E-01	2.77E-01		-4.73E-02	9.51E-01		-1.41E-01	9.29E-01		-2.02E+00	1.36E-01		-2.09E+00	1.07E-01		Unigene35709_All|gi|22022552|gb|AAM83233.1|//2.00E-15//AT4g39970/T5J17_140 [Arabidopsis thaliana] >gi|23505871|gb|AAN28795.1| At4g39970/T5J17_140 [Arabidopsis thaliana]	Unigene35709_All//8.00E-17//AT4G39970| haloacid dehalogenase-like hydrolase family protein	Unigene35709_All//3.00E-97//DR455956				nr +
Unigene3571_All	1107	14.70	53.28	6.83	42.07	31.54	36.23	86.16	98.54	137.08	1.86E+00	1.47E-108	Up	-1.11E+00	8.01E-14	Down	-4.16E-01	4.64E-09		-2.16E-01	6.71E-03		1.94E-01	1.45E-05		6.70E-01	4.00E-69		Unigene3571_All|gi|297821154|ref|XP_002878460.1|//5.00E-34//ATBZIP53 [Arabidopsis lyrata subsp. lyrata] >gi|297324298|gb|EFH54719.1| ATBZIP53 [Arabidopsis lyrata subsp. lyrata]	Unigene3571_All//2.00E-34//AT3G62420| ATBZIP53 (BASIC REGION/LEUCINE ZIPPER MOTIF 53); DNA binding / protein heterodimerization/ sequence-specific DNA binding / transcription factor	Unigene3571_All//0.00E+00//gi|109852686|gb|DW481665.1|DW481665	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0003677//GO:0006351//GO:0046983	nr -
Unigene35710_All	1324	53.39	25.72	46.33	8.50	8.30	6.00	1.09	1.99	1.11	-1.05E+00	7.71E-56	Down	-2.05E-01	2.01E-03		-3.54E-02	8.52E-01		-5.02E-01	2.71E-03		8.73E-01	1.20E-02		3.62E-02	9.60E-01		Unigene35710_All|gi|18420570|ref|NP_568077.1|//1.00E-121//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana]	Unigene35710_All//3.00E-120//AT4G39970| haloacid dehalogenase-like hydrolase family protein	Unigene35710_All//0.00E+00//gi|109876681|gb|DW505655.1|DW505655		ko00740|Riboflavin metabolism		nr +
Unigene35717_All	1062	38.28	35.35	27.43	61.87	54.18	61.79	44.23	28.14	21.34	-1.15E-01	2.18E-01		-4.81E-01	2.06E-08		-1.91E-01	2.42E-03		-1.80E-03	9.78E-01		-6.53E-01	1.48E-20		-1.05E+00	9.74E-47	Down	Unigene35717_All|gi|169589|gb|AAA33847.1|//7.00E-94//spliceosomal protein [Solanum tuberosum]	Unigene35717_All//6.00E-74//AT2G30260| U2B'' (U2 small nuclear ribonucleoprotein B); RNA binding / nucleic acid binding / nucleotide binding	Unigene35717_All//0.00E+00//TC153472		ko03040|Spliceosome		nr -
Unigene35719_All	1539	6.05	3.03	4.74	41.88	32.11	18.96	6.57	1.58	2.07	-9.98E-01	2.06E-07		-3.52E-01	8.24E-02		-3.84E-01	1.11E-10		-1.14E+00	6.13E-63	Down	-2.06E+00	8.56E-27	Down	-1.66E+00	6.51E-21	Down	Unigene35719_All|gi|15240633|ref|NP_196850.1|//5.00E-68//IQD11 (IQ-domain 11); calmodulin binding [Arabidopsis thaliana]	Unigene35719_All//2.00E-64//AT5G13460| IQD11 (IQ-domain 11); calmodulin binding	Unigene35719_All//0.00E+00//TC148875				nr +
Unigene3572_All	1685	59.25	37.38	55.84	35.80	26.65	29.19	9.41	5.43	3.90	-6.65E-01	4.03E-36		-8.54E-02	1.57E-01		-4.26E-01	4.27E-12		-2.95E-01	8.32E-06		-7.93E-01	3.47E-10		-1.27E+00	7.55E-22	Down	Unigene3572_All|gi|18404699|ref|NP_565885.1|//1.00E-108//CXIP2 (CAX-INTERACTING PROTEIN 2); electron carrier/ protein disulfide oxidoreductase [Arabidopsis thaliana] >gi|119570634|sp|Q8GTF6.2|GRS16_ARATH RecName: Full=Monothiol glutaredoxin-S16, chloroplastic; Short=AtGrxS16; AltName: Full=CAXIP1-like protein; Flags: Precursor >gi|3335374|gb|AAC27175.1| expressed protein [Arabidopsis thaliana] >gi|27752307|gb|AA019648.1| CAXIP1-like protein [Arabidopsis thaliana]	Unigene3572_All//1.00E-102//AT2G38270| CXIP2 (CAX-INTERACTING PROTEIN 2); electron carrier/ protein disulfide oxidoreductase	Unigene3572_All//0.00E+00//TC143466			GO:0015036//GO:0019725//GO:0043231	nr +
Unigene35720_All	475	0.88	0.85	3.03	17.62	11.82	6.66	0.89	0.18	0.08	-4.62E-02	9.80E-01		1.78E+00	4.43E-03		-5.76E-01	2.13E-03		-1.40E+00	1.03E-11	Down	-2.34E+00	5.46E-02		-3.41E+00	1.24E-02		Unigene35720_All|gi|15237584|ref|NP_196016.1|//2.00E-15//IQD12 (IQ-domain 12); calmodulin binding [Arabidopsis thaliana]	Unigene35720_All//1.00E-06//AT5G13460| IQD11 (IQ-domain 11); calmodulin binding	Unigene35720_All//0.00E+00//DN779899				nr +
Unigene35721_All	1686	0.43	0.12	0.63	4.64	3.51	1.42	1.18	0.40	0.28	-1.85E+00	4.08E-02		5.40E-01	4.18E-01		-4.01E-01	5.03E-02		-1.71E+00	1.93E-14	Down	-1.57E+00	2.71E-04	Down	-2.06E+00	4.43E-06	Down	Unigene35721_All|gi|15240633|ref|NP_196850.1|//7.00E-58//IQD11 (IQ-domain 11); calmodulin binding [Arabidopsis thaliana]	Unigene35721_All//8.00E-56//AT5G13460| IQD11 (IQ-domain 11); calmodulin binding	Unigene35721_All//0.00E+00//TC148875				nr -
Unigene35722_All	997	18.26	17.64	18.59	29.53	25.63	29.08	17.51	9.43	5.91	-5.04E-02	7.24E-01		2.54E-02	8.66E-01		-2.04E-01	4.48E-02		-2.20E-02	8.64E-01		-8.93E-01	1.86E-13		-1.57E+00	1.36E-32	Down			Unigene35722_All//0.00E+00//TC156046				
Unigene35727_All	1478	40.00	23.31	25.80	29.93	43.03	62.95	11.24	9.95	8.38	-7.79E-01	2.05E-28		-6.33E-01	3.55E-19		5.24E-01	5.19E-18		1.07E+00	9.06E-81	Up	-1.76E-01	1.96E-01		-4.23E-01	3.59E-04		Unigene35727_All|gi|68131790|gb|AN88179.1|//0.00E+00//fiber expressed protein [Gossypium hirsutum]	Unigene35727_All//7.00E-66//AT1G61260| unknown protein	Unigene35727_All//0.00E+00//TC129650				nr +
Unigene35728_All	2532	6.05	2.94	2.63	14.15	7.33	11.72	8.48	23.11	5.22	-1.04E+00	1.82E-12	Down	-1.20E+00	7.27E-15	Down	-9.48E-01	2.08E-29		-2.72E-01	2.60E-03		1.45E+00	1.99E-92	Up	-7.00E-01	2.21E-11		Unigene35728_All|gi|1217967|emb|CAA65291.1|//0.00E+00//high affinity sulphate transporter [Hordeum vulgare subsp. vulgare] >gi|28300414|gb|AM034714.1| high-affinity sulfate transporter HvST1 [Hordeum vulgare subsp. vulgare]	Unigene35728_All//0.00E+00//AT1G22150| SULTR1;3; sulfate transmembrane transporter	Unigene35728_All//0.00E+00//ES813014				nr -
Unigene35729_All	1767	6.04	6.19	4.04	17.62	12.14	9.94	21.01	6.65	7.67	3.62E-02	8.46E-01		-5.81E-01	1.34E-03		-5.37E-01	1.10E-09		-8.26E-01	4.83E-18		-1.66E+00	4.20E-72	Down	-1.45E+00	2.70E-61	Down	Unigene35729_All|gi|195622042|gb|ACG32851.1|//1.00E-113//IQD1 [Zea mays]	Unigene35729_All//7.00E-90//AT5G03040| IQD2 (IQ-domain 2); calmodulin binding	Unigene35729_All//0.00E+00//TC177173				nr +
Unigene3573_All	1219	37.94	45.18	26.25	42.09	61.64	54.28	40.86	17.66	61.83	2.52E-01	4.65E-04		-5.31E-01	3.17E-11		5.50E-01	3.75E-23		3.67E-01	3.89E-09		-1.21E+00	3.61E-60	Down	5.98E-01	1.39E-28		Unigene3573_All|gi|7670832|gb|AAF66242.1|AF243180_1|//3.00E-63//dicyanin [Solanum lycopersicum]	Unigene3573_All//3.00E-28//AT1G45063| copper ion binding / electron carrier	Unigene3573_All//0.00E+00//TC167872				nr -
Unigene35731_All	2149	2.19	6.44	2.13	3.15	3.61	4.12	6.12	11.42	3.97	1.55E+00	2.44E-20	Up	-4.02E-02	8.98E-01		1.94E-01	4.23E-01		3.86E-01	5.46E-02		9.00E-01	8.69E-19		-6.25E-01	3.68E-06		Unigene35731_All|gi|9651530|gb|AAF91178.1|AF203700_1|//0.00E+00//ClpB [Phaseolus lunatus]	Unigene35731_All//0.00E+00//AT2G25140| CLPB4 (CASEIN LYTIC PROTEINASE B4); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding	Unigene35731_All//0.00E+00//ES812266				nr +
Unigene35733_All	496	4.54	3.78	7.84	9.94	8.68	13.84	11.00	6.15	4.50	-2.63E-01	5.55E-01		7.89E-01	1.47E-02		-1.96E-01	5.32E-01		4.77E-01	3.70E-02		-8.38E-01	2.33E-04		-1.29E+00	2.91E-08	Down	Unigene35733_All|gi|297806991|ref|XP_002871379.1|//7.00E-46//mthsc70-2 [Arabidopsis lyrata subsp. lyrata] >gi|297317216|gb|EFH47638.1| mthsc70-2 [Arabidopsis lyrata subsp. lyrata]	Unigene35733_All//2.00E-41//AT5G09590| MTHSC70-2 (MITOCHONDRIAL HSP70 2); ATP binding	Unigene35733_All//0.00E+00//BE055811		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03018|RNA degradation		nr -
Unigene35736_All	1232	6.50	11.27	19.19	4.45	3.19	10.45	4.43	2.82	2.04	7.94E-01	1.76E-07		1.56E+00	1.71E-33	Up	-4.81E-01	5.28E-02		1.23E+00	2.35E-14	Up	-6.53E-01	4.06E-03		-1.12E+00	8.69E-07	Down	Unigene35736_All|gi|130369073|emb|CAJ90831.1|//3.00E-88//MYBPA1 protein [Vitis vinifera]	Unigene35736_All//1.00E-52//AT3G13540| ATMYB5 (MYB DOMAIN PROTEIN 5); DNA binding / transcription factor	Unigene35736_All//0.00E+00//gi|78348401|gb|DT568675.1|DT568675	MYB			nr +
Unigene35737_All	699	4.94	2.83	4.34	5.27	3.79	3.42	5.63	4.84	2.05	-8.05E-01	1.50E-02		-1.86E-01	6.29E-01		-4.75E-01	1.36E-01		-6.23E-01	5.33E-02		-2.16E-01	4.84E-01		-1.46E+00	2.86E-07	Down	Unigene35737_All|gi|87241300|gb|AB033158.1|//1.00E-41//Syntaxin, N-terminal [Medicago truncatula]	Unigene35737_All//3.00E-20//AT5G46860| VAM3; SNAP receptor	Unigene35737_All//0.00E+00//gi|11204305|gb|BF273235.1|BF273235		ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport		nr -
Unigene35739_All	836	0.50	1.09	1.59	0.83	0.78	1.13	1.92	0.80	0.19	1.12E+00	1.30E-01		1.67E+00	9.89E-03		-9.21E-02	8.95E-01		4.44E-01	5.74E-01		-1.26E+00	7.60E-03		-3.33E+00	5.33E-08	Down	Unigene35739_All|gi|87241300|gb|AB033158.1|//8.00E-39//Syntaxin, N-terminal [Medicago truncatula]	Unigene35739_All//1.00E-18//AT5G46860| VAM3; SNAP receptor	Unigene35739_All//0.00E+00//gi|11204305|gb|BF273235.1|BF273235		ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport		nr +
Unigene35740_All	1001	23.94	13.26	20.37	22.34	19.09	13.13	5.24	4.93	1.79	-8.52E-01	7.66E-14		-2.33E-01	5.68E-02		-2.27E-01	5.56E-02		-7.67E-01	1.22E-11		-8.82E-02	7.27E-01		-1.55E+00	3.17E-10	Down	Unigene35740_All|gi|87241300|gb|AB033158.1|//1.00E-97//Syntaxin, N-terminal [Medicago truncatula]	Unigene35740_All//6.00E-58//AT5G46860| VAM3; SNAP receptor	Unigene35740_All//0.00E+00//gi|78343517|gb|DT563791.1|DT563791		ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport		nr -

Unigene35741_All	2935	9.34	7.91	7.67	11.71	14.58	9.76	15.53	5.88	11.20	-2.41E-01	2.48E-02			-2.84E-01	1.03E-02		3.17E-01	3.68E-05		-2.64E-01	4.50E-03		-1.40E+00	6.06E-69	Down	-4.72E-01	7.62E-12		Unigene35741_All//gi|115474123|ref|NP_001060660.1|//1.00E-131//0s07g0682100 [Oryza sativa Japonica Group] >gi|122166929|sp|Q0D3J9.1|C3H53_ORYSJ RecName: Full=Zinc finger CCCH domain-containing protein 53; Short=OsC3H53 >gi|113612196|dbj|BAF22574.1|0s07g0682100 [Oryza sativa Japonica Group]	Unigene35741_All//3.00E-74//AT5G12440| nucleic acid binding / nucleotide binding / zinc ion binding	Unigene35741_All//0.00E+00//TC150820	C3H			nr +
Unigene35742_All	2990	1.12	0.83	0.66	2.02	1.54	1.03	2.19	0.99	0.87	-4.32E-01	2.14E-01			-7.65E-01	3.06E-02		-3.85E-01	1.12E-01		-9.73E-01	4.24E-05		-1.14E+00	6.22E-08	Down	-1.34E+00	2.75E-10	Down	Unigene35742_All//gi|115474123|ref|NP_001060660.1|//1.00E-138//0s07g0682100 [Oryza sativa Japonica Group] >gi|122166929|sp|Q0D3J9.1|C3H53_ORYSJ RecName: Full=Zinc finger CCCH domain-containing protein 53; Short=OsC3H53 >gi|113612196|dbj|BAF22574.1|0s07g0682100 [Oryza sativa Japonica Group]	Unigene35742_All//2.00E-77//AT5G12440| nucleic acid binding / nucleotide binding / zinc ion binding	Unigene35742_All//0.00E+00//TC150820	C3H			nr -
Unigene35743_All	1994	3.44	2.59	3.18	4.20	4.96	3.17	1.06	0.27	0.58	-4.07E-01	7.43E-02			-1.13E-01	6.31E-01		2.40E-01	2.28E-01		-4.05E-01	4.83E-02		-1.96E+00	7.64E-06	Down	-8.72E-01	2.17E-02		Unigene35743_All//gi|205688046|sp|Q10M00.2|C3H22_ORYSJ//4.00E-91//RecName: Full=Zinc finger CCCH domain-containing protein 22; Short=OsC3H22 >gi|108707943|gb|ABF95738.1| Zinc finger C-x8-C-x5-C-x3-H type family protein, expressed [Oryza sativa (Japonica cultivar-group)]	Unigene35743_All//2.00E-63//AT3G51950| zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein	Unigene35743_All//0.00E+00//TC150820	C3H			nr -
Unigene35744_All	1235	4.02	6.61	3.10	6.57	7.28	4.10	3.29	1.79	1.16	7.15E-01	4.32E-04			-3.75E-01	2.01E-01		1.47E-01	5.40E-01		-6.83E-01	6.20E-04		-8.74E-01	1.20E-03		-1.50E+00	8.70E-08	Down	Unigene35744_All//gi|115441063|ref|NP_001041811.1|//5.00E-25//0s01g0850000 [Oryza sativa Japonica Group] >gi|113534342|dbj|BAF06725.1|0s01g0850000 [Oryza sativa Japonica Group]	Unigene35744_All//4.00E-14//AT2G39870| unknown protein	Unigene35744_All//0.00E+00//gi|78331841|gb|DT552115.1|DT552115				nr -
Unigene35745_All	2292	214.37	118.16	203.52	52.05	67.28	38.09	4.19	2.61	1.23	-8.59E-01	1.28E-273			-7.50E-02	2.27E-03		3.70E-01	5.60E-23		-4.51E-01	3.01E-23		-6.83E-01	3.38E-05		-1.76E+00	1.67E-21	Down	Unigene35745_All//gi|16648734|gb|AL235559.1|//3.00E-68//AT4g23890/T32A16_60 [Arabidopsis thaliana]	Unigene35745_All//2.00E-75//AT4G23890| unknown protein	Unigene35745_All//0.00E+00//TC174358				nr -
Unigene35746_All	1827	11.03	18.78	14.57	27.13	34.17	61.26	14.81	6.02	20.76	7.68E-01	2.25E-16			4.03E-01	2.28E-04		3.33E-01	6.09E-08		1.18E+00	2.43E-112	Up	-1.30E+00	7.45E-37	Down	4.87E-01	1.60E-10		Unigene35746_All//gi|15233136|ref|NP_191055.1|//2.00E-92//PLA IIIA (PATATIN-LIKE PROTEIN 6) [Arabidopsis thaliana]	Unigene35746_All//6.00E-84//AT3G54950| PLA IIIA (PATATIN-LIKE PROTEIN 6)	Unigene35746_All//0.00E+00//TC156530				nr +
Unigene35749_All	1465	8.57	18.57	10.87	51.48	47.06	43.16	50.91	84.33	49.14	1.12E+00	6.84E-24	Up		3.43E-01	2.13E-02		-1.30E-01	3.88E-02		-2.54E-01	1.59E-05		7.28E-01	1.00E-63		-5.11E-02	4.20E-01		Unigene35749_All//gi|37051125|dbj|BAC81659.1|//2.00E-71//DNA binding with one finger 2 protein [Pisum sativum]	Unigene35749_All//5.00E-37//AT2G28510| Dof-type zinc finger domain-containing protein	Unigene35749_All//0.00E+00//TC148861	C2C2-Dof			nr +
Unigene3575_All	1217	38.35	11.78	10.90	45.68	41.11	37.04	75.84	32.18	34.08	-1.70E+00	9.67E-77	Down		-1.82E+00	4.93E-81	Down	-1.52E-01	3.79E-02		-3.03E-01	1.18E-05		-1.24E+00	1.07E-114	Down	-1.15E+00	9.52E-106	Down	Unigene3575_All//gi|4557063|gb|AAD25202.1|//1.00E-43//expressed protein [Arabidopsis thaliana]		Unigene3575_All//0.00E+00//TC145931			GO:0009526//GO:0031410	nr -
Unigene35751_All	1008	0.10	0.00	0.00	0.40	0.44	0.72	0.42	0.46	4.35	-6.70E+00	3.71E-01			-6.70E+00	3.93E-01		1.68E-01	9.04E-01		8.59E-01	3.42E-01		1.21E-01	9.07E-01		3.37E+00	1.76E-20	Up	Unigene35751_All//gi|297833532|ref|XP_002884648.1|//4.00E-29//asparaginyl-tRNA synthetase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297330488|gb|EFH60907.1|asparaginyl-tRNA synthetase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene35751_All//6.00E-28//AT3G07420| NS2; asparagine-tRNA ligase			ko00970|Aminoacyl-tRNA biosynthesis		nr +
Unigene35755_All	2357	2.02	9.37	1.40	3.04	1.99	3.10	10.28	21.24	39.26	2.21E+00	2.14E-51	Up		-5.28E-01	7.03E-02		-6.15E-01	2.66E-03		2.85E-02	9.28E-01		1.05E+00	5.04E-48	Up	1.93E+00	1.79E-224	Up	Unigene35755_All//gi|30686949|ref|NP_194292.2|//6.00E-76//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|28951011|gb|AAO63429.1|At4g25620 [Arabidopsis thaliana]	Unigene35755_All//9.00E-54//AT4G25620| hydroxyproline-rich glycoprotein family protein	Unigene35755_All//0.00E+00//gi|164360149|gb|ES844957.1|ES844957				nr +
Unigene35756_All	1046	11.00	11.00	7.74	4.86	8.16	3.58	1.21	4.52	2.21	-1.10E-03	9.94E-01			-5.08E-01	3.61E-03		7.49E-01	6.35E-05		-4.39E-01	1.13E-01		1.90E+00	1.22E-11	Up	8.65E-01	1.71E-02		Unigene35756_All//gi|224125294|ref|XP_002319550.1|//1.00E-104//amidase family protein [Populus trichocarpa] >gi|222857926|gb|EEE95473.1|amidase family protein [Populus trichocarpa]	Unigene35756_All//7.00E-56//AT3G17970| atToc64-III (Arabidopsis thaliana translocon at the outer membrane of chloroplasts 64-III); binding / carbon-nitrogen ligase, with glutamine as amido-N-donor	Unigene35756_All//0.00E+00//TC132026			ko00970|Aminoacyl-tRNA biosynthesis	nr -
Unigene35757_All	1494	5.50	4.92	4.95	2.53	5.42	2.72	0.79	2.21	1.28	-1.61E-01	4.61E-01			-1.50E-01	5.17E-01		1.10E+00	2.40E-08	Up	1.03E-01	7.56E-01		1.48E+00	3.99E-06	Up	6.92E-01	8.87E-02		Unigene35757_All//gi|115456912|ref|NP_001052056.1|//1.00E-127//0s04g0118100 [Oryza sativa Japonica Group] >gi|32451277|emb|CAE01284.1|OSJNBa0020P07.1 [Oryza sativa (Japonica cultivar-group)] >gi|113563627|dbj|BAF13970.1|0s04g0118100 [Oryza sativa Japonica Group]	Unigene35757_All//9.00E-101//AT1G08980| AMI1 (AMIDASE 1); amidase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds / indoleacetamide hydrolase	Unigene35757_All//0.00E+00//TC132026			ko00970|Aminoacyl-tRNA biosynthesis	nr +
Unigene3576_All	1337	5.40	2.35	3.27	7.38	7.16	6.01	11.16	13.38	7.45	-1.20E+00	1.06E-07	Down		-7.26E-01	1.33E-03		-4.31E-02	8.26E-01		-2.95E-01	1.32E-01		2.61E-01	3.25E-02		-5.84E-01	3.52E-06		Unigene3576_All//gi|151347473|gb|AB501349.1|//1.00E-142//hypersensitive-induced response protein [Carica papaya]	Unigene3576_All//3.00E-134//AT5G62740| band 7 family protein	Unigene3576_All//0.00E+00//TC178247				nr +
Unigene35761_All	1712	2.54	1.21	0.75	4.39	3.72	2.82	6.72	2.08	1.79	-1.06E+00	3.11E-04	Down		-1.76E+00	9.88E-08	Down	-2.40E-01	3.05E-01		-6.38E-01	2.28E-03		-1.69E+00	1.64E-23	Down	-1.91E+00	2.08E-28	Down	Unigene35761_All//gi|79485764|ref|NP_194202.3|//0.00E+00//ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene35761_All//0.00E+00//AT4G24710| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene35761_All//0.00E+00//gi|78340732|gb|DT561006.1|DT561006		ko04144|Endocytosis		nr +
Unigene35765_All	786	5.59	2.32	2.91	10.20	6.62	4.42	1.94	2.82	1.01	-1.27E+00	2.21E-05	Down		-9.41E-01	1.90E-03		-6.25E-01	1.07E-03		-1.21E+00	5.21E-09	Down	5.41E-01	1.69E-01		-9.34E-01	4.27E-02		Unigene35765_All//gi|124359339|gb|AB028498.2|//9.00E-08//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]		Unigene35765_All//5.00E-175//TC174171				nr +
Unigene35766_All	1275	7.18	3.14	4.55	8.01	6.18	2.73	2.45	3.47	1.78	-1.19E+00	1.78E-09	Down		-6.58E-01	8.63E-04		-3.73E-01	3.40E-02		-1.55E+00	2.21E-16	Down	5.02E-01	5.43E-02		-4.62E-01	1.33E-01		Unigene35766_All//gi|124359162|gb|AB002685.1|//7.00E-20//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene35766_All//9.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene35766_All//7.00E-132//gi|72273229|gb|DT049049.1|DT049049				nr -
Unigene35768_All	2294	4.22	5.17	3.27	14.38	14.28	15.65	13.75	20.08	29.21	2.93E-01	8.63E-02			-3.66E-01	6.38E-02		-1.01E-02	9.37E-01		1.23E-01	2.34E-01		5.46E-01	6.91E-15		1.09E+00	1.81E-69	Up	Unigene35768_All//gi|297803380|ref|XP_002869674.1|//1.00E-177//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315510|gb|EFH45933.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35768_All//8.00E-149//AT4G25390| protein kinase family protein	Unigene35768_All//0.00E+00//ES798836		ko04626|Plant-pathogen interaction		nr -
Unigene3577_All	232	5.86	3.93	13.77	14.39	16.77	10.51	8.20	4.86	6.18	-5.77E-01	3.19E-01			1.23E+00	8.83E-04	Up	2.21E-01	5.58E-01		-4.53E-01	2.05E-01		-7.54E-01	7.44E-02		-4.08E-01	3.33E-01								ESTscan +
Unigene35773_All	1573	42.21	27.09	29.86	72.20	58.73	56.88	42.95	22.90	17.42	-6.40E-01	9.60E-23			-4.99E-01	3.22E-14		-2.98E-01	1.26E-11		-3.44E-01	1.20E-13		-9.07E-01	4.81E-51		-1.30E+00	1.08E-93	Down	Unigene35773_All//gi|297812135|ref|XP_002873951.1|//8.00E-93//elongation factor 1B alpha-subunit 2 [Arabidopsis lyrata subsp. lyrata] >gi|297319788|gb|EFH50210.1|elongation factor 1B alpha-subunit 2 [Arabidopsis lyrata subsp. lyrata]	Unigene35773_All//3.00E-69//AT5G19510| elongation factor 1B alpha-subunit 2 (eEF1Balpha2)	Unigene35773_All//0.00E+00//TC144712				nr -
Unigene35774_All	918	0.80	2.26	1.33	1.19	2.48	2.36	2.03	5.37	4.47	1.50E+00	1.41E-03			7.42E-01	2.46E-01		1.05E+00	1.23E-02		9.84E-01	2.63E-02		1.41E+00	3.44E-08	Up	1.14E+00	2.06E-05	Up	Unigene35774_All//gi|79313157|ref|NP_001030658.1|//2.00E-68//DNA binding [Arabidopsis thaliana]	Unigene35774_All//9.00E-10//AT3G07565| DNA binding	Unigene35774_All//0.00E+00//gi|21095288|gb|BQ407601.1|BQ407601				nr +
Unigene35775_All	1382	10.45	17.16	8.94	17.19	16.40	26.01	7.13	19.87	21.42	7.16E-01	2.58E-10			-2.25E-01	1.69E-01		-6.86E-02	6.07E-01		5.97E-01	6.41E-12		1.48E+00	3.00E-45	Up	1.59E+00	4.07E-55	Up	Unigene35775_All//gi|15229471|ref|NP_187413.1|//2.00E-98//DNA binding [Arabidopsis thaliana]	Unigene35775_All//7.00E-100//AT3G07565| DNA binding	Unigene35775_All//0.00E+00//gi|78340590|gb|DT560864.1|DT560864				nr -
Unigene35778_All	788	0.66	0.71	1.01	0.51	0.61	1.03	1.29	6.79	0.56	9.11E-02	9.32E-01			6.10E-01	4.41E-01		2.75E-01	8.20E-01		1.03E+00	2.17E-01		2.40E+00	2.49E-17	Up	-1.21E+00	4.17E-02		Unigene35778_All//gi|79565313|ref|NP_180417.2|//9.00E-58//LBD11 (LOB DOMAIN-CONTAINING PROTEIN 11) [Arabidopsis thaliana]	Unigene35778_All//1.00E-48//AT1G07900| LBD1 (LOB DOMAIN-CONTAINING PROTEIN 1)	Unigene35778_All//0.00E+00//gi|109885381|gb|DW514351.1|DW514351		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene3578_All	1052	5.22	5.92	9.06	8.48	8.35	7.30	9.61	7.39	2.88	1.82E-01	4.75E-01			7.95E-01	3.85E-05		-2.21E-02	9.20E-01		-2.16E-01	3.25E-01		-3.78E-01	2.10E-02		-1.74E+00	3.47E-22	Down							
Unigene35780_All	984	5.00	16.63	5.90	2.68	1.26	4.59	0.52	3.44	1.98	1.73E+00	7.32E-28	Up		2.39E-01	3.98E-01		-1.09E+00	2.85E-03		7.75E-01	6.32E-03		2.74E+00	6.79E-13	Up	1.94E+00	1.51E-05	Up	Unigene35780_All//gi|297843580|ref|XP_002889671.1|//3.00E-61//LOB domain protein 1 [Arabidopsis lyrata subsp. lyrata] >gi|297335513|gb|EFH65930.1| LOB domain protein 1 [Arabidopsis lyrata subsp. lyrata]	Unigene35780_All//2.00E-46//AT2G28500| LBD11 (LOB DOMAIN-CONTAINING PROTEIN 11)	Unigene35780_All//5.00E-89//TC133806		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene35781_All	1439	4.54	9.19	9.92	12.57	12.13	9.86	3.06	2.64	3.79	1.02E+00	2.04E-10	Up		1.13E+00	1.43E-12	Up	-5.07E-02	7.78E-01		-3.51E-01	7.48E-03		-2.09E-01	4.67E-01		3.12E-01	1.79E-01		Unigene35781_All//gi|18406854|ref|NP_566051.1|//1.00E-156//calcineurin B subunit-related [Arabidopsis thaliana]	Unigene35781_All//4.00E-149//AT2G45670| calcineurin B subunit-related	Unigene35781_All//0.00E+00//gi|78349263|gb|DT569537.1|DT569537		ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr -
Unigene35784_All	919	12.92	30.82	16.98	10.35	14.76	11.65	19.09	18.28	13.70	1.25E+00	9.50E-30	Up		3.94E-01	8.06E-03		5.12E-01	4.06E-04		1.70E-01	4.03E-01		-6.25E-02	6.48E-01		-4.79E-01	3.10E-05		Unigene35784_All//gi|115444495|ref|NP_001046627.1|//4.00E-39//0s02g0170200 [Oryza sativa Japonica Group] >gi|113535558|dbj|BAF07941.1|0s02g0170200 [Oryza sativa Japonica Group]	Unigene35784_All//2.00E-26//AT1G79200| unknown protein	Unigene35784_All//0.00E+00//TC151045		ko03040|Spliceosome		nr +
Unigene35785_All	2428	4.81	0.88	0.15	8.15	5.25	2.98	10.43	1.96	3.20	-2.45E+00	3.25E-31	Down		-4.97E+00	1.82E-54	Down	-6.34E-01	2.18E-08		-1.45E+00	2.67E-28	Down	-2.41E+00	3.60E-80	Down	-1.70E+00	7.40E-53	Down	Unigene35785_All//gi|50540766|gb|AAT17922.1|//5.00E-78//expressed protein [Oryza sativa Japonica Group]	Unigene35785_All//7.00E-75//AT1G75150| unknown protein	Unigene35785_All//0.00E+00//ES810364				nr +
Unigene35786_All	1246	38.72	65.43	24.87	77.20	75.59	81.12	55.48	68.87	116.35	7.57E-01	5.87E-37			-6.38E-01	5.42E-16		-3.05E-02	6.54E-01		7.15E-02	2.43E-01		3.12E-01	4.28E-10		1.07E+00	3.14E-145	Up	Unigene35786_All//gi|259121417|gb|ACV92028.1|//1.00E-109//WRKY transcription factor 26 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene35786_All//9.00E-61//AT2G23320| WRKY15; calmodulin binding / transcription factor	Unigene35786_All//0.00E+00//gi|164270590|gb|ES852046.1|ES852046	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene35787_All	2201	38.96	114.00	71.49	39.38	78.71	97.32	74.07	89.93	104.91	1.55E+00	0.00E+00	Up		8.76E-01	3.74E-88		9.99E-01	4.39E-148		1.31E+00	3.44E-253	Up	2.80E-01	3.06E-18		5.02E-01	9.06E-63		Unigene35787_All//gi|256387096|gb|ACU80550.1|//0.00E+00//Dof1 protein [Jatropha curcas]	Unigene35787_All//1.00E-113//AT3G47500| CDF3 (CYCLING DOF FACTOR 3); DNA binding / protein binding / transcription factor	Unigene35787_All//0.00E+00//gi|78334440|gb|DT554714.1|DT554714	C2C2-Dof			nr -
Unigene35789_All	720	23.40	12.95	9.39	44.07	39.98	36.07	29.42	11.96	7.19	-8.54E-01	5.38E-10			-1.32E+00	1.23E-18	Down	-1.41E-01	1.82E-01		-2.89E-01	2.62E-03		-1.30E+00	5.42E-29	Down	-2.03E+00	4.00E-56	Down	Unigene35789_All//gi|42362268|gb|AAS13367.1|//5.00E-41//cyclin-dependent kinases regulatory subunit [Glycine max]	Unigene35789_All//2.00E-38//AT2G27960| CKS1 (CYCLIN-DEPENDENT KINASE-SUBUNIT 1); cyclin-dependent protein kinase/ protein binding	Unigene35789_All//0.00E+00//gi|21101265|gb|BQ413578.1|BQ413578				nr -

Unigene35790_All	1824	156.42	142.42	139.02	200.60	188.77	151.09	19.42	20.44	7.93	-1.35E-01	7.78E-06		-1.70E-01	3.01E-08		-8.76E-02	6.84E-04		-4.09E-01	1.03E-58		7.35E-02	4.40E-01		-1.29E+00	4.96E-49	Down	Unigene35790_All//gi|45752764|gb|AS76280.1|/1.00E-75//At5g41850 [Arabidopsis thaliana]	Unigene35790_All//3.00E-70//AT5G41850| unknown protein	Unigene35790_All//0.00E+00//TC154860				nr +
Unigene35793_All	1455	7.30	3.69	2.78	14.35	13.11	10.46	7.44	3.04	3.56	-9.84E-01	3.72E-08		-1.39E+00	5.67E-13	Down	-1.30E-01	3.46E-01		-4.56E-01	1.06E-04		-1.29E+00	4.96E-15	Down	-1.06E+00	1.16E-11	Down	Unigene35793_All//gi|133907524|gb|AB042262.1|//1.00E-114//AT-hook DNA-binding protein [Gossypium hirsutum]	Unigene35793_All//6.00E-66//AT2G45850| DNA-binding family protein	Unigene35793_All//0.00E+00//gi|78324325|gb|DT544599.1|DT544599				nr -
Unigene35797_All	772	17.01	28.55	21.73	33.10	36.84	37.15	21.41	45.15	42.11	7.47E-01	2.47E-10		3.53E-01	1.40E-02		1.55E-01	1.65E-01		1.66E-01	1.38E-01		1.08E+00	3.65E-35	Up	9.76E-01	9.46E-29		Unigene35797_All//gi|22652534|gb|AN03743.1|/6.00E-61//ankyrin-kinase protein [Arabidopsis thaliana]	Unigene35797_All//3.00E-62//AT2G31800| ankyrin protein kinase, putative	Unigene35797_All//0.00E+00//CO069626				nr +
Unigene35798_All	669	2.42	1.36	2.55	3.65	2.52	4.93	0.76	2.44	1.91	-8.31E-01	1.08E-01		7.12E-02	8.90E-01		-5.33E-01	1.88E-01		4.34E-01	2.30E-01		1.68E+00	6.05E-04	Up	1.33E+00	1.23E-02				Unigene35798_All//3.00E-148//DW498461				
Unigene35799_All	1628	5.37	3.95	4.15	3.49	4.72	3.80	11.89	8.29	4.58	-4.41E-01	2.49E-02		-3.70E-01	7.94E-02		4.35E-01	3.83E-02		1.24E-01	6.60E-01		-5.20E-01	3.03E-06		-1.38E+00	6.39E-30	Down	Unigene35799_All//gi|15238260|ref|NP_201288.1|//1.00E-100//programmed cell death 2 C-terminal domain-containing protein [Arabidopsis thaliana] >gi|15724302|gb|AAL06544.1|AF41209 1_1 AT5g64830/MXK3_5 [Arabidopsis thaliana] >gi|109946415|gb|ABG48386.1| At5g64830 [Arabidopsis thaliana]	Unigene35799_All//1.00E-95//AT5G64830| programmed cell death 2 C-terminal domain-containing protein	Unigene35799_All//0.00E+00//TC131415				nr -
Unigene35802_All	1171	6.39	16.70	4.59	9.57	10.88	10.53	7.55	4.25	7.01	1.39E+00	4.09E-24	Up	-4.76E-01	3.46E-02		1.85E-01	3.09E-01		1.38E-01	4.69E-01		-8.29E-01	1.87E-06		-1.07E-01	6.00E-01				Unigene35802_All//2.00E-144//gi|109862414|gb|DW491391.1|DW491391				
Unigene35803_All	1383	39.69	34.29	45.01	92.35	92.70	93.00	42.92	28.65	20.65	-2.11E-01	4.01E-03		1.82E-01	1.19E-02		5.40E-03	9.38E-01		1.01E-02	8.72E-01		-5.83E-01	3.12E-21		-1.06E+00	3.36E-59	Down	Unigene35803_All//gi|18406048|ref|NP_566842.1|//1.00E-160//pectinesterase family protein [Arabidopsis thaliana] >gi|75311628|sp|Q9LVQ0.1|PME31_ARATH RecName: Full=Pectinesterase 31; Short=PE 31; AltName: Full=Pectin methylesterase 31; Short=AtPME31 >gi|9294028|dbj|BAB01985.1| pectin methylesterase-like protein [Arabidopsis thaliana]	Unigene35803_All//2.00E-156//AT3G29090| pectinesterase family protein	Unigene35803_All//0.00E+00//TC1139273		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene35805_All	792	13.21	7.10	5.24	23.27	16.17	25.32	68.12	23.01	24.95	-8.96E-01	5.31E-07		-1.33E+00	5.16E-12	Down	-5.25E-01	9.67E-06		1.22E-01	4.09E-01		-1.57E+00	4.74E-96	Down	-1.45E+00	3.33E-88	Down	Unigene35805_All//gi|461736|sp|Q05046.1|CH62_CUCMA//1.00E-116//RecName: Full=Chaperonin CPN60-2, mitochondrial; AltName: Full=HSP60-2; Flags: Precursor >gi|478786|pir||S29316 chaperonin 60 - cucurbit >gi|12546|emb|CAA50218.1| chaperonin 60 [Cucurbita cv. Kurokawa Amakuri]	Unigene35805_All//3.00E-105//AT3G23990| HSP60 (HEAT SHOCK PROTEIN 60); ATP binding	Unigene35805_All//0.00E+00//TC1130859		ko03018|RNA degradation		nr -
Unigene35806_All	847	12.66	5.08	3.46	20.00	13.58	19.25	56.36	19.39	21.02	-1.32E+00	1.19E-12	Down	-1.87E+00	9.81E-20	Down	-5.58E-01	6.87E-06		-5.49E-02	7.24E-01		-1.54E+00	5.90E-83	Down	-1.42E+00	5.19E-76	Down	Unigene35806_All//gi|461736|sp|Q05046.1|CH62_CUCMA//1.00E-139//RecName: Full=Chaperonin CPN60-2, mitochondrial; AltName: Full=HSP60-2; Flags: Precursor >gi|478786|pir||S29316 chaperonin 60 - cucurbit >gi|12546|emb|CAA50218.1| chaperonin 60 [Cucurbita cv. Kurokawa Amakuri]	Unigene35806_All//5.00E-137//AT3G23990| HSP60 (HEAT SHOCK PROTEIN 60); ATP binding	Unigene35806_All//0.00E+00//TC140996		ko03018|RNA degradation		nr -
Unigene35811_All	1556	20.48	12.90	12.15	9.86	7.68	2.70	38.29	30.51	20.05	-6.67E-01	3.87E-12		-7.53E-01	3.36E-14		-3.61E-01	8.84E-03		-1.87E+00	1.76E-31	Down	-3.27E-01	6.98E-08		-9.33E-01	1.25E-48		Unigene35811_All//gi|223452335|gb|ACM89495.1|//1.00E-156//protein kinase family protein [Glycine max]	Unigene35811_All//2.00E-133//AT2G18890| protein kinase family protein	Unigene35811_All//0.00E+00//gi|78325111|gb|DT545385.1|DT545385		ko04626|Plant-pathogen interaction		nr +
Unigene35812_All	1695	5.40	5.47	4.52	15.78	19.32	17.80	12.95	2.07	4.72	1.82E-02	9.46E-01		-2.56E-01	2.33E-01		2.92E-01	1.30E-03		1.74E-01	1.10E-01		-2.64E+00	2.79E-77	Down	-1.45E+00	1.39E-36	Down	Unigene35812_All//gi|18417196|ref|NP_567809.1|//3.00E-88//reticulon family protein [Arabidopsis thaliana] >gi|229891746|sp|Q8LDG3.2|RTNLR_ARATH RecName: Full=Reticulon-like protein B18; Short=ArRTNLB18	Unigene35812_All//3.00E-82//AT4G28430| reticulon family protein	Unigene35812_All//0.00E+00//gi|84175285|gb|DR463933.1|DR463933				nr +
Unigene35815_All	527	39.91	18.84	36.58	130.82	139.31	83.56	73.89	46.55	43.09	-1.08E+00	7.22E-18	Down	-1.26E-01	3.82E-01		9.07E-02	1.93E-01		-6.47E-01	8.02E-26		-6.67E-01	8.23E-18		-7.78E-01	8.95E-24		Unigene35815_All//gi|115454699|ref|NP_001050950.1|//2.00E-32//Os03g0690000 [Oryza sativa Japonica Group] >gi|75120259|sp|Q6AVK1.1|U727_ORYSJ RecName: Full=UPF0727 protein >gi|224493392|sp|A2XKU9.1|U727_ORYSI RecName: Full=UPF0727 protein >gi|50838962|gb|AAT81723.1| striated muscle activator-like protein [Oryza sativa Japonica Group] >gi|108710488|gb|ABF98283.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549421|dbj|BAF12864.1| Os03g0690000 [Oryza sativa Japonica Group]	Unigene35815_All//2.00E-33//AT4G33640| unknown protein	Unigene35815_All//0.00E+00//TC164879				nr +
Unigene35816_All	529	7.02	4.41	8.25	32.39	19.59	12.21	23.10	11.54	12.88	-6.73E-01	3.46E-02		2.33E-01	4.59E-01		-7.25E-01	3.59E-09		-1.41E+00	1.76E-23	Down	-1.00E+00	1.55E-11	Down	-8.43E-01	3.87E-09		Unigene35816_All//gi|75155025|sp|Q8LBN7.1|U727_ARATH//2.00E-20//RecName: Full=UPF0727 protein At4g33640 >gi|98961013|gb|ABF58990.1| At4g33640 [Arabidopsis thaliana]	Unigene35816_All//1.00E-21//AT4G33640| unknown protein	Unigene35816_All//0.00E+00//TC164879				nr -
Unigene35817_All	581	11.26	25.38	11.18	15.35	16.95	14.07	10.33	7.27	6.38	1.17E+00	2.46E-14	Up	-9.60E-03	9.93E-01		1.43E-01	5.26E-01		-1.25E-01	6.07E-01		-5.08E-01	1.95E-02		-6.96E-01	8.40E-04				Unigene35817_All//0.00E+00//TC169622				
Unigene35819_All	751	1.67	2.90	0.64	6.96	4.81	6.37	9.96	13.86	4.67	7.95E-01	6.74E-02		-1.39E+00	3.39E-02		-5.33E-01	3.49E-02		-1.28E-01	6.78E-01		4.76E-01	2.69E-03		-1.09E+00	1.10E-08	Down	Unigene35819_All//gi|20330766|gb|AAM19129.1|AC103891_9//3.00E-54//Putative RING zinc finger protein [Oryza sativa Japonica Group]	Unigene35819_All//5.00E-47//AT3G27710| zinc finger protein-related	Unigene35819_All//0.00E+00//ES813491				nr +
Unigene35820_All	2022	1.86	0.80	1.11	5.10	5.42	3.77	6.82	7.28	5.87	-1.22E+00	1.75E-04	Down	-7.52E-01	2.30E-02		8.67E-02	6.87E-01		-4.34E-01	1.54E-02		9.41E-02	5.61E-01		-2.15E-01	1.22E-01		Unigene35820_All//gi|297802536|ref|XP_002869152.1|//0.00E+00//IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297314988|gb|EFH45411.1| IBR domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene35820_All//0.00E+00//AT2G16090| zinc finger protein-related	Unigene35820_All//0.00E+00//ES812022				nr -
Unigene35822_All	1487	5.88	3.99	5.48	10.72	12.78	15.06	14.39	12.73	6.75	-5.60E-01	4.09E-03		-1.01E-01	6.27E-01		2.54E-01	5.09E-02		4.91E-01	1.38E-05		-1.76E-01	1.32E-01		-1.09E+00	4.23E-23	Down	Unigene35822_All//gi|152926164|gb|ABS32235.1|//3.00E-92//protein kinase [Carica papaya]	Unigene35822_All//2.00E-89//AT5G14720| protein kinase family protein	Unigene35822_All//0.00E+00//TC178781				nr +
Unigene35824_All	1119	7.06	8.24	9.33	11.31	9.39	9.61	11.00	5.98	5.02	2.23E-01	2.71E-01		4.02E-01	3.22E-02		-2.69E-01	1.00E-01		-2.35E-01	1.78E-01		-8.80E-01	1.68E-09		-1.13E+00	2.03E-14	Down	Unigene35824_All//gi|20197972|gb|AAD25844.2|//1.00E-60//expressed protein [Arabidopsis thaliana] >gi|20198213|gb|AAM15465.1| expressed protein [Arabidopsis thaliana] >gi|107738176|gb|ABF83655.1| At2g04340 [Arabidopsis thaliana]	Unigene35824_All//6.00E-62//AT2G04340| unknown protein	Unigene35824_All//0.00E+00//TC167177				nr -
Unigene35825_All	1340	1.56	1.63	2.66	2.68	1.82	1.25	1.55	0.78	1.16	5.81E-02	9.01E-01		7.70E-01	2.39E-02		-5.53E-01	8.17E-02		-1.10E+00	6.58E-04	Down	-9.88E-01	1.38E-02		-4.15E-01	2.97E-01		Unigene35825_All//gi|20197972|gb|AAD25844.2|//1.00E-60//expressed protein [Arabidopsis thaliana] >gi|20198213|gb|AAM15465.1| expressed protein [Arabidopsis thaliana] >gi|107738176|gb|ABF83655.1| At2g04340 [Arabidopsis thaliana]	Unigene35825_All//7.00E-62//AT2G04340| unknown protein	Unigene35825_All//0.00E+00//TC167177				nr +
Unigene35828_All	1441	8.86	2.71	3.66	6.53	2.96	3.45	7.10	2.93	8.21	-1.71E+00	1.32E-21	Down	-1.28E+00	1.29E-13	Down	-1.14E+00	8.86E-11	Down	-9.22E-01	5.46E-07		-1.28E+00	4.56E-14	Down	2.10E-01	1.73E-01		Unigene35828_All//gi|28416689|gb|AAO42875.1|//1.00E-165//At3g50340 [Arabidopsis thaliana]	Unigene35828_All//4.00E-142//AT3G50340| unknown protein	Unigene35828_All//0.00E+00//CO094210				nr -
Unigene35830_All	1704	1.66	6.60	2.03	1.96	1.70	1.64	1.94	1.84	3.93	1.99E+00	3.13E-23	Up	2.93E-01	4.01E-01		-2.07E-01	5.88E-01		-2.53E-01	4.99E-01		-7.32E-02	8.25E-01		1.02E+00	4.57E-07	Up	Unigene35830_All//gi|297726473|ref|NP_001175600.1|//7.00E-23//Os08g0422350 [Oryza sativa Japonica Group] >gi|255678483|dbj|BAH94328.1| Os08g0422350 [Oryza sativa Japonica Group]	Unigene35830_All//8.00E-42//AT5G57830| unknown protein	Unigene35830_All//0.00E+00//gi|78332506|gb|DT552780.1|DT552780				nr -
Unigene35838_All	1575	2.39	2.09	0.85	3.32	3.17	2.78	1.37	2.23	1.77	-1.94E-01	5.69E-01		-1.50E+00	1.54E-05	Down	-6.70E-02	8.14E-01		-2.56E-01	3.94E-01		7.03E-01	1.67E-02		3.71E-01	2.73E-01		Unigene35838_All//gi|224126071|ref|XP_002329654.1|//1.00E-143//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222870535|gb|EEF07666.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene35838_All//9.00E-118//AT5G57390| AIL5 (AINTEGUMENTA-LIKE 5); DNA binding / transcription factor	Unigene35838_All//0.00E+00//gi|78346784|gb|DT567058.1|DT567058	AP2-EREBP			nr +
Unigene3584_All	3615	0.41	0.14	0.44	19.31	8.19	5.75	12.89	5.91	2.71	-1.53E+00	7.80E-03		1.25E-01	8.05E-01		-1.24E+00	3.28E-88	Down	-1.75E+00	2.94E-129	Down	-1.13E+00	3.04E-50	Down	-2.25E+00	2.22E-139	Down	Unigene3584_All//gi|15230845|ref|NP_189177.1|//0.00E+00//AFH1 (FORMIN HOMOLOGY 1); actin binding / actin filament binding / protein binding [Arabidopsis thaliana] >gi|75274615|sp|Q9SE97.1|FH1_ARATH RecName: Full=Formin-like protein 1; Short=AtFH1; Short=AtFORMIN-8; Flags: Precursor >gi|6503010|gb|AAF14548.1| formin-like protein AHF1 [Arabidopsis thaliana] >gi|9279730|dbj|BAB01320.1| formin-like protein [Arabidopsis thaliana]	Unigene3584_All//0.00E+00//AT3G25500| AFH1 (FORMIN HOMOLOGY 1); actin binding / actin filament binding / protein binding	Unigene3584_All//0.00E+00//gi|78326284|gb|DT546558.1|DT546558		ko03040|Spliceosome//ko03018|RNA degradation	GO:0003779//GO:0007010//GO:0016020	nr -
Unigene35840_All	1166	111.24	22.29	25.44	160.59	145.69	75.53	65.38	7.85	9.26	-2.32E+00	0.00E+00	Down	-2.13E+00	8.49E-278	Down	-1.41E-01	7.66E-05		-1.09E+00	4.13E-168	Down	-3.06E+00	0.00E+00	Down	-2.82E+00	1.47E-295	Down	Unigene35840_All//gi|119444239|gb|ABL75361.1|//1.00E-149//xyloglucan endotransglycosylase precursor [Populus tremula x Populus tremuloides]	Unigene35840_All//4.00E-127//AT4G03210| XTH9 (XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 9); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene35840_All//0.00E+00//TC141157				nr -

Unigene35841_All	2060	9.37	11.61	7.63	49.31	39.58	24.62	30.93	19.76	11.04	3.09E-01	6.60E-03		-2.98E-01	2.72E-02		-3.17E-01	1.08E-11		-1.00E+00	8.88E-80	Down	-6.46E-01	3.86E-27		-1.49E+00	5.44E-108	Down	Unigene35841_All//gi|115455589|ref|NP_001051395.1|//1.00E-176//Os03g0769400 [Oryza sativa Japonica Group] >gi|40539077|gb|AAR57334.1| expressed protein [Oryza sativa Japonica Group] >gi|50872443|gb|AAT85043.1| expressed protein [Oryza sativa Japonica Group] >gi|113549866|dbj|BAF13309.1| Os03g0769400 [Oryza sativa Japonica Group]	Unigene35841_All//0.00E+00//AT3G50780| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: PRL1-interacting factor-related (TAIR:AT1G63850.1); Has 173 Blast hits to 173 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 0; Plants - 164; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene35841_All//0.00E+00//TC169139				nr -
Unigene35845_All	1667	11.96	19.82	4.60	10.40	14.27	13.76	16.66	23.67	18.21	7.29E-01	1.71E-14		-1.38E+00	1.67E-23	Down	4.57E-01	1.30E-05		4.04E-01	3.33E-04		5.06E-01	2.54E-11		1.28E-01	1.77E-01		Unigene35845_All//gi|158516796|gb|ABW70161.1|//1.00E-156//SINA3 [Medicago truncatula]	Unigene35845_All//2.00E-135//AT3G61790| seven in absentia (SINA) family protein	Unigene35845_All//0.00E+00//TC158917		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene35846_All	1268	19.10	65.97	17.89	48.60	56.41	41.64	28.74	32.40	102.39	1.79E+00	6.31E-146	Up	-9.48E-02	4.70E-01		2.15E-01	2.91E-04		-2.23E-01	8.98E-04		1.73E-01	2.88E-02		1.83E+00	7.81E-293	Up	Unigene35846_All//gi|87241270|gb|AB033128.1|//3.00E-92//Zinc finger, RING-type; Thioredoxin-related [Medicago truncatula]	Unigene35846_All//4.00E-77//AT2G39720| RHC2A; protein binding / zinc ion binding	Unigene35846_All//0.00E+00//TC132229				nr -
Unigene35847_All	1034	3.90	8.97	5.82	7.23	10.29	7.95	4.21	5.17	5.01	1.20E+00	1.21E-09	Up	5.79E-01	2.21E-02		5.10E-01	2.38E-03		1.38E-01	5.83E-01		2.97E-01	2.35E-01		2.50E-01	3.12E-01		Unigene35847_All//gi|8778872|gb|AAF79871.1|AC000348_24//2.00E-50//T7N9.26 [Arabidopsis thaliana]	Unigene35847_All//3.00E-43//AT1G27200| unknown protein	Unigene35847_All//0.00E+00//TC154178				nr +
Unigene35848_All	2288	2.72	10.50	2.09	7.16	8.80	5.25	5.03	3.80	4.72	1.95E+00	1.98E-47	Up	-3.78E-01	1.38E-01		2.98E-01	1.46E-02		-4.48E-01	9.36E-04		-4.04E-01	7.55E-03		-9.11E-02	6.10E-01		Unigene35848_All//gi|8778872|gb|AAF79871.1|AC000348_24//0.00E+00//T7N9.26 [Arabidopsis thaliana]	Unigene35848_All//6.00E-176//AT1G27200| unknown protein	Unigene35848_All//0.00E+00//TC154178				nr -
Unigene35850_All	2654	2.50	3.61	1.91	0.79	1.30	1.45	5.26	9.34	39.46	5.27E-01	4.53E-03		-3.93E-01	1.09E-01		7.19E-01	2.86E-02		8.76E-01	5.05E-03		8.29E-01	1.31E-16		2.91E+00	0.00E+00	Up	Unigene35850_All//gi|225434959|ref|XP_002281079.1|//3.00E-63//PREDICTED: similar to GTP1/OBG family member [Vitis vinifera]	Unigene35850_All//1.00E-40//AT5G02390| unknown protein	Unigene35850_All//2.00E-07//DT051216				nr +
Unigene35851_All	1370	4.16	5.03	5.44	4.25	3.97	7.65	0.52	2.59	2.06	2.73E-01	2.42E-01		3.87E-01	9.10E-02		-9.92E-02	7.43E-01		8.46E-01	1.12E-06		2.31E+00	3.09E-11	Up	1.98E+00	7.83E-08	Up	Unigene35851_All//gi|224513796|gb|ACN65116.1|//3.00E-86//2-alkenal reductase [Artemisia annua]	Unigene35851_All//1.00E-82//AT3G03080| NADP-dependent oxidoreductase, putative	Unigene35851_All//0.00E+00//gi|48740861|gb|CO071380.1|CO071380				nr -
Unigene35852_All	1686	2.58	3.46	2.56	9.19	6.17	9.05	9.35	17.70	53.38	4.24E-01	9.00E-02		-9.80E-03	9.98E-01		-5.75E-01	1.06E-05		-2.13E-02	9.14E-01		9.20E-01	1.65E-23		2.51E+00	2.03E-302	Up	Unigene35852_All//gi|21555734|gb|AM63923.1|//3.00E-68//carnitine racemase like protein [Arabidopsis thaliana]	Unigene35852_All//1.00E-60//AT4G14430| IBR10 (INDOLE-3-BUTYRIC ACID RESPONSE 10); catalytic/ dodecenoyl-CoA delta-isomerase	Unigene35852_All//0.00E+00//gi|109872877|gb|DW501852.1|DW501852		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism		nr +
Unigene35853_All	3142	1.22	0.81	0.97	6.48	6.37	5.66	9.34	2.09	4.12	-5.92E-01	5.91E-02		-3.32E-01	3.38E-01		-2.62E-02	8.55E-01		-1.95E-01	1.45E-01		-2.16E+00	3.03E-81	Down	-1.18E+00	1.97E-35	Down	Unigene35853_All//gi|18414189|ref|NP_567426.1|//0.00E+00//phragmoplast-associated kinesin-related protein 2 (PAKRP2) [Arabidopsis thaliana] >gi|16973451|gb|AAL32293.1|AF320248_1 phragmoplast-associated kinesin-related protein 2 [Arabidopsis thaliana] >gi|16973453|gb|AAL32294.1|AF320249_1 phragmoplast-associated kinesin-related protein 2 [Arabidopsis thaliana]	Unigene35853_All//0.00E+00//AT4G14330| phragmoplast-associated kinesin-related protein 2 (PAKRP2)	Unigene35853_All//0.00E+00//TC173797				nr -
Unigene35858_All	2082	2.41	2.04	2.58	4.67	5.46	2.08	2.11	2.31	1.55	-2.39E-01	3.83E-01		9.86E-02	7.17E-01		2.26E-01	2.23E-01		-1.16E+00	3.16E-10	Down	1.28E-01	6.24E-01		-4.46E-01	7.73E-02		Unigene35858_All//gi|297795889|ref|XP_002865829.1|//0.00E+00//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311664|gb|EFH42088.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35858_All//5.00E-173//AT5G50900| armadillo/beta-catenin repeat family protein	Unigene35858_All//0.00E+00//TC138361				nr +
Unigene35861_All	1686	22.19	25.91	37.24	41.28	43.46	49.24	26.91	17.28	7.47	2.24E-01	7.08E-03		7.47E-01	4.58E-27		7.45E-02	3.15E-01		2.54E-01	5.42E-06		-6.39E-01	3.41E-19		-1.85E+00	3.02E-105	Down	Unigene35861_All//gi|59275987|dbj|BAD89561.1|//1.00E-175//NGMTP1 [Nicotiana glauca]	Unigene35861_All//7.00E-71//AT2G46800| ZAT (ZINC TRANSPORTER OF ARABIDOPSIS THALIANA); inorganic anion transmembrane transporter/ metal ion transmembrane transporter/ zinc ion transmembrane transporter	Unigene35861_All//0.00E+00//TC152457				nr -
Unigene35863_All	2012	7.78	3.37	3.86	3.39	4.60	2.94	0.00	0.00	0.04	-1.20E+00	7.51E-16	Down	-1.01E+00	1.49E-11	Down	4.41E-01	1.80E-02		-2.06E-01	4.22E-01		null	null		5.31E+00	4.04E-01		Unigene35863_All//gi|22475197|gb|AAM97322.1|//0.00E+00//homeodomain protein GhHOX2 [Gossypium hirsutum]	Unigene35863_All//0.00E+00//AT5G46880| HB-7 (HOMEOBOX-7); DNA binding / transcription factor	Unigene35863_All//0.00E+00//TC129563	HB			nr +
Unigene35864_All	2113	24.07	24.17	26.84	26.52	31.78	31.31	23.07	14.95	10.78	6.20E-03	9.62E-01		1.57E-01	4.35E-02		2.61E-01	1.45E-05		2.40E-01	1.83E-04		-6.26E-01	7.93E-20		-1.10E+00	6.57E-52	Down	Unigene35864_All//gi|15222037|ref|NP_177629.1|//0.00E+00//ADP-glucose pyrophosphorylase family protein [Arabidopsis thaliana] >gi|30699054|ref|NP_849886.1| ADP-glucose pyrophosphorylase family protein [Arabidopsis thaliana] >gi|13937224|gb|AAK50104.1|AF372967_1 At1g74910/F9E10_24 [Arabidopsis thaliana] >gi|21700877|gb|AAM70562.1| At1g74910/F9E10_24 [Arabidopsis thaliana]	Unigene35864_All//0.00E+00//AT1G74910| ADP-glucose pyrophosphorylase family protein	Unigene35864_All//0.00E+00//TC135096		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene35868_All	644	1.79	2.20	0.91	2.78	2.03	0.84	1.90	2.14	1.11	3.02E-01	6.11E-01		-9.75E-01	1.46E-01		-4.55E-01	3.59E-01		-1.73E+00	7.60E-04	Down	1.70E-01	7.38E-01		-7.74E-01	1.40E-01		Unigene35868_All//gi|79325247|ref|NP_001031709.1|//9.00E-09//ABC1 family protein [Arabidopsis thaliana]	Unigene35868_All//5.00E-10//AT4G24810| ABC1 family protein	Unigene35868_All//3.00E-102//TC167740				nr +
Unigene3587_All	1139	6.20	36.70	11.03	10.45	3.93	6.46	52.97	13.47	33.30	2.57E+00	3.48E-115	Up	8.31E-01	5.25E-07		-1.41E+00	9.61E-19	Down	-6.94E-01	1.44E-05		-1.98E+00	2.94E-148	Down	-6.70E-01	3.71E-28		Unigene3587_All//gi|225440392|ref|XP_002267559.1|//1.00E-132//PREDICTED: ripening-related protein-like [Vitis vinifera]	Unigene3587_All//1.00E-118//AT5G02230| haloacid dehalogenase-like hydrolase family protein	Unigene3587_All//0.00E+00//TC137468			GO:0003824	nr -
Unigene35871_All	2008	42.76	86.70	56.64	35.15	42.50	38.69	60.26	76.22	119.60	1.02E+00	5.31E-129	Up	4.06E-01	1.62E-16		2.74E-01	1.58E-07		1.38E-01	2.89E-02		3.39E-01	3.63E-20		9.89E-01	1.51E-211		Unigene35871_All//gi|9294678|dbj|BAB03027.1|//0.00E+00//glutamine-fructose-6-phosphate transaminase 2 [Arabidopsis thaliana]	Unigene35871_All//0.00E+00//AT3G24090| glutamine-fructose-6-phosphate transaminase (isomerizing)/ sugar binding / transaminase/	Unigene35871_All//0.00E+00//TC163238		ko00520|Amino sugar and nucleotide sugar metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene35873_All	1013	15.96	57.42	16.40	15.79	24.20	27.73	34.48	35.44	34.21	1.85E+00	3.06E-106	Up	3.93E-02	7.97E-01		6.17E-01	1.65E-09		8.13E-01	8.96E-16		3.99E-02	6.81E-01		-1.09E-02	9.26E-01		Unigene35873_All//gi|30695448|ref|NP_564623.2|//7.00E-51//sodium/calcium exchanger family protein / calcium-binding EF hand family protein [Arabidopsis thaliana]	Unigene35873_All//4.00E-52//AT1G53210| sodium/calcium exchanger family protein / calcium-binding EF hand family protein	Unigene35873_All//0.00E+00//TC175884				nr +
Unigene35875_All	1861	13.21	8.60	6.32	15.61	14.32	15.05	11.02	13.07	24.30	-6.19E-01	1.83E-08		-1.06E+00	2.34E-19	Down	-1.24E-01	2.86E-01		-5.26E-02	6.85E-01		2.46E-01	1.64E-02		1.14E+00	6.69E-51	Up	Unigene35875_All//gi|15231865|ref|NP_190939.1|//1.00E-176//AGD6; ARF GTPase activator/ DNA binding / zinc ion binding [Arabidopsis thaliana] >gi|79314905|ref|NP_001030854.1| AGD6; ARF GTPase activator/ DNA binding / zinc ion binding [Arabidopsis thaliana] >gi|75264634|sp|Q9M354.1|AGD6_ARATH RecName: Full=Probable ADP-ribosylation factor GTPase-activating protein AGD6; Short=ARF GAP AGD6; AltName: Full=Protein ARF-GAP DOMAIN 6; Short=AtAGD6; AltName: Full=Protein ZIGA2 >gi|134031918|gb|ABO45696.1| At3g53710 [Arabidopsis thaliana]	Unigene35875_All//1.00E-157//AT3G53710| AGD6; ARF GTPase activator/ DNA binding / zinc ion binding	Unigene35875_All//0.00E+00//TC169135		ko04144|Endocytosis		nr +
Unigene35877_All	1358	1.16	2.31	1.65	1.72	1.72	0.86	3.14	2.40	1.23	1.00E+00	4.71E-03		5.11E-01	2.54E-01		2.00E-04	9.89E-01		-9.96E-01	1.69E-02		-3.90E-01	1.53E-01		-1.35E+00	4.32E-07	Down	Unigene35877_All//gi|297846208|ref|XP_002890985.1|//1.00E-117//zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336827|gb|EFH67244.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35877_All//8.00E-104//AT1G32360| zinc finger (CCCH-type) family protein	Unigene35877_All//0.00E+00//gi|78328644|gb|DT548918.1|DT548918	C3H	ko04146|Peroxisome		nr -
Unigene35878_All	1632	8.82	3.42	3.43	15.20	11.08	12.34	12.33	3.61	4.52	-1.37E+00	1.10E-17	Down	-1.36E+00	7.51E-17	Down	-4.57E-01	5.96E-06		-3.01E-01	6.60E-03		-1.77E+00	3.79E-43	Down	-1.45E+00	1.88E-33	Down	Unigene35878_All//gi|224067864|ref|XP_002302571.1|//1.00E-158//tetrahydrofolate dehydrogenase/cyclohydrolase [Populus trichocarpa] >gi|222844297|gb|EEE81844.1| tetrahydrofolate dehydrogenase/cyclohydrolase [Populus trichocarpa]	Unigene35878_All//2.00E-147//AT4G00620| tetrahydrofolate dehydrogenase/cyclohydrolase, putative	Unigene35878_All//0.00E+00//TC141022				nr -
Unigene35879_All	2262	8.30	7.91	7.91	10.72	14.98	17.47	18.82	54.56	69.52	-7.06E-02	6.22E-01		-7.01E-02	6.19E-01		4.82E-01	1.67E-08		7.04E-01	3.07E-17		1.54E+00	2.36E-212	Up	1.88E+00	0.00E+00	Up	Unigene35879_All//gi|115434156|ref|NP_001041836.1|//1.00E-126//Os01g0115600 [Oryza sativa Japonica Group] >gi|113531367|dbj|BAF03750.1| Os01g0115600 [Oryza sativa Japonica Group]	Unigene35879_All//2.00E-100//AT1G66910| protein kinase, putative	Unigene35879_All//0.00E+00//TC142439		ko04626|Plant-pathogen interaction		nr +
Unigene3588_All	748	2.24	4.20	5.48	5.53	3.45	3.38	2.03	1.51	1.70	9.08E-01	1.01E-02		1.29E+00	6.28E-05	Up	-6.79E-01	1.69E-02		-7.09E-01	1.73E-02		-4.32E-01	4.02E-01		-2.56E-01	6.16E-01		Unigene3588_All//gi|297836072|ref|XP_002885918.1|//4.00E-31//CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331758|gb|EFH62177.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene3588_All//2.00E-27//AT2G14520| CBS domain-containing protein	Unigene3588_All//2.00E-94//CO099327			GO:0016020//GO:0031410	nr +
Unigene35881_All	1083	1.06	1.31	0.59	0.37	2.96	1.54	5.27	4.28	3.90	3.02E-01	6.11E-01		-8.49E-01	2.06E-01		3.01E+00	3.56E-12	Up	2.07E+00	2.60E-04	Up	-2.99E-01	2.11E-01		-4.35E-01	4.53E-02		Unigene35881_All//gi|166811|gb|AAA18854.1|//2.00E-17//protein kinase [Arabidopsis thaliana]	Unigene35881_All//1.00E-18//AT4G13020| MHK; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene35881_All//2.00E-144//gi|164341878|gb|ES851807.1|ES851807				nr -

Unigene35882_All	2848	0.53	0.04	0.26	5.12	3.42	3.01	3.90	5.31	6.14	-3.90E+00	9.44E-07	Down	-1.03E+00	7.23E-02		-5.83E-01	1.59E-05		-7.66E-01	8.28E-08		4.44E-01	5.39E-04		6.53E-01	1.99E-08		Unigene35882_All//gi|75219581|sp|Q49318.1|Y2317_ARATH//0.00E+00//Rec Name: Full=Probable leucine-rich repeat receptor-like protein kinase At2g33170; Flags: Precursor >gi|224589939|gb|ACN59303.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene35882_All//0.00E+00//AT2G33170| leucine-rich repeat transmembrane protein kinase, putative	Unigene35882_All//0.00E+00//TC163302				nr +
Unigene35884_All	881	8.73	18.86	7.80	15.72	17.75	17.17	9.07	14.94	10.85	1.11E+00	8.33E-15	Up	-1.63E-01	4.96E-01		1.75E-01	2.77E-01		1.28E-01	4.66E-01		7.20E-01	2.13E-07		2.59E-01	1.27E-01		Unigene35884_All//gi|224061867|ref|XP_002300638.1|//2.00E-62//bromodomain protein [Populus trichocarpa] >gi|222842364|gb|EEE79911.1| bromodomain protein [Populus trichocarpa]	Unigene35884_All//3.00E-33//AT1G20670| DNA-binding bromodomain-containing protein	Unigene35884_All//0.00E+00//gi|78338479|gb|DT558753.1|DT558753				nr +
Unigene35885_All	613	2.90	4.79	2.78	8.94	18.99	9.87	2.35	3.75	5.26	7.24E-01	4.68E-02		-6.21E-02	9.06E-01		1.09E+00	1.18E-11	Up	1.43E-01	6.39E-01		6.77E-01	7.39E-02		1.17E+00	1.45E-04	Up	Unigene35885_All//gi|224061867|ref|XP_002300638.1|//4.00E-08//bromodomain protein [Populus trichocarpa] >gi|222842364|gb|EEE79911.1| bromodomain protein [Populus trichocarpa]		Unigene35885_All//0.00E+00//TC148509				nr +
Unigene35890_All	1720	18.40	9.49	11.80	6.95	5.23	5.15	2.02	0.85	0.35	-9.56E-01	9.70E-22		-6.42E-01	8.22E-11		-4.12E-01	8.89E-03		-4.34E-01	8.14E-03		-1.24E+00	4.10E-05	Down	-2.54E+00	1.14E-12	Down	Unigene35890_All//gi|297805172|ref|XP_002870470.1|//1.00E-179//HCF109 [Arabidopsis lyrata subsp. lyrata] >gi|297316306|gb|EFH46729.1| HCF109 [Arabidopsis lyrata subsp. lyrata]	Unigene35890_All//2.00E-171//AT5G36170| HCF109 (HIGH CHLOROPHYLL FLUORESCENT 109); translation release factor/ translation release factor, codon specific	Unigene35890_All//0.00E+00//gi|164258347|gb|ES803265.1|ES803265				nr -
Unigene35891_All	1361	1.46	6.29	4.26	2.53	4.02	3.58	2.61	5.77	4.92	2.11E+00	4.07E-19	Up	1.55E+00	1.58E-08	Up	6.72E-01	6.44E-03		5.05E-01	7.17E-02		1.15E+00	2.27E-09	Up	9.14E-01	4.94E-06		Unigene35891_All//gi|42573011|ref|NP_974602.1|//9.00E-66//pleckstrin homology (PH) domain-containing protein-related [Arabidopsis thaliana] >gi|145333884|ref|NP_001078437.1| pleckstrin homology (PH) domain-containing protein-related [Arabidopsis thaliana]	Unigene35891_All//1.00E-65//AT4G23895| pleckstrin homology (PH) domain-containing protein-related	Unigene35891_All//0.00E+00//gi|48778350|gb|CO087716.1|CO087716				nr +
Unigene35893_All	2867	13.40	6.80	5.83	23.77	22.99	24.48	25.16	8.62	10.84	-9.77E-01	3.77E-27		-1.20E+00	3.11E-36	Down	-4.81E-02	5.52E-01		4.25E-02	6.29E-01		-1.55E+00	7.81E-126	Down	-1.21E+00	8.39E-90	Down	Unigene35893_All//gi|18147592|dbj|BAB83088.1|//0.00E+00//cycloartenol 1 synthase [Betula platyphylla]	Unigene35893_All//0.00E+00//AT2G07050| CAS1 (cycloartenol synthase 1); cycloartenol synthase	Unigene35893_All//0.00E+00//TC134460		ko00100|Steroid biosynthesis		nr +
Unigene35894_All	1603	17.01	1.20	7.18	7.30	3.65	5.97	9.18	1.20	1.44	-3.82E+00	1.74E-111	Down	-1.24E+00	2.19E-27	Down	-1.00E+00	8.79E-11		-2.90E-01	9.92E-02		-2.94E+00	4.18E-58	Down	-2.67E+00	2.60E-54	Down	Unigene35894_All//gi|225440514|ref|XP_002274763.1|//0.00E+00//PREDICTED: similar to glyoxal oxidase [Vitis vinifera]	Unigene35894_All//0.00E+00//AT3G53950| glyoxal oxidase-related	Unigene35894_All//0.00E+00//ES832440				nr -
Unigene35895_All	1836	72.87	37.86	55.60	124.83	151.75	141.96	15.43	3.00	4.04	-9.44E-01	9.12E-88		-3.90E-01	5.45E-18		2.82E-01	8.17E-25		1.86E-01	9.19E-10		-2.36E+00	2.09E-87	Down	-1.93E+00	4.07E-70	Down	Unigene35895_All//gi|157273654|gb|ABV27481.1|//0.00E+00//fasciclin-like arabinogalactan protein 10 [Gossypium hirsutum]	Unigene35895_All//6.00E-123//AT5G55730| FLA1 (FASCICLIN-LIKE ARAB INOGALACTAN 1)	Unigene35895_All//0.00E+00//TC131841				nr -
Unigene35897_All	875	0.48	0.00	0.00	0.34	0.75	0.46	1.55	3.34	4.19	-8.90E+00	1.05E-02		-8.90E+00	1.56E-02		1.13E+00	2.38E-01		4.43E-01	7.01E-01		1.11E+00	7.66E-04	Up	1.44E+00	1.17E-06	Up	Unigene35897_All//gi|29029006|gb|AA064882.1|//4.00E-11//At5g13560 [Arabidopsis thaliana]	Unigene35897_All//3.00E-09//AT2G37370| unknown protein					nr +
Unigene35898_All	2228	0.23	0.23	0.17	0.89	1.21	1.30	1.39	4.01	7.62	-4.62E-02	9.76E-01		-4.89E-01	6.32E-01		4.31E-01	3.04E-01		5.37E-01	1.64E-01		1.54E+00	4.44E-16	Up	2.46E+00	3.96E-56	Up	Unigene35898_All//gi|29029006|gb|AA064882.1|//1.00E-123//At5g13560 [Arabidopsis thaliana]	Unigene35898_All//1.00E-127//AT2G37370| unknown protein					nr -
Unigene35902_All	1356	1.62	1.46	2.32	1.76	1.85	1.30	7.83	1.63	1.26	-1.53E-01	7.13E-01		5.16E-01	1.62E-01		7.22E-02	8.76E-01		-4.41E-01	3.15E-01		-2.26E+00	1.65E-31	Down	-2.63E+00	9.52E-39	Down	Unigene35902_All//gi|225457654|ref|XP_002275693.1|//1.00E-137//PREDICTED: similar to cinnamoyl-CoA reductase family [Vitis vinifera]	Unigene35902_All//3.00E-109//AT2G33590| cinnamoyl-CoA reductase family	Unigene35902_All//0.00E+00//gi|78346547|gb|DT566821.1|DT566821		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene35904_All	1663	23.03	10.85	15.85	32.29	38.99	27.38	12.20	2.14	7.09	-1.09E+00	4.38E-32	Down	-5.39E-01	1.21E-09		2.72E-01	8.61E-06		-2.38E-01	9.63E-04		-2.51E+00	1.35E-67	Down	-7.83E-01	5.81E-13		Unigene35904_All//gi|30725596|gb|AP37820.1|//1.00E-126//At1g29790 [Arabidopsis thaliana]	Unigene35904_All//2.00E-105//AT1G29790| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: Golgi apparatus, plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: methyltransferase (TAIR:AT5G40830.2); Has 127 Blast hits to 127 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 127; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene35904_All//0.00E+00//TC156429				nr -
Unigene35906_All	470	0.11	0.00	3.97	0.32	0.15	3.84	0.09	0.09	0.00	-6.80E+00	6.11E-01		5.15E+00	4.94E-09	Up	-1.12E+00	5.83E-01		3.60E+00	1.06E-07	Up	-1.77E-02	1.00E+00		-6.49E+00	6.12E-01					Unigene35906_All//2.00E-90//EV484228					
Unigene35907_All	1121	2.66	1.49	5.04	3.11	1.84	2.05	2.41	15.96	1.85	-8.35E-01	2.08E-02		9.20E-01	4.32E-04		-7.55E-01	1.57E-02		-5.98E-01	7.36E-02		2.72E+00	5.14E-65	Up	-3.85E-01	2.56E-01		Unigene35907_All//gi|53370641|gb|AAU89136.1|//2.00E-20//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene35907_All//1.00E-12//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene35907_All//3.00E-140//gi|78335762|gb|DT556036.1|DT556036				nr +
Unigene35909_All	3131	0.74	0.91	1.50	2.13	1.30	1.86	5.21	4.87	5.61	3.02E-01	4.24E-01		1.03E+00	4.58E-04	Up	-7.16E-01	7.09E-04		-1.96E-01	4.56E-01		-9.73E-02	5.19E-01		1.06E-01	4.21E-01		Unigene35909_All//gi|145334203|ref|NP_001078482.1|//0.00E+00//DNA-directed DNA polymerase family protein [Arabidopsis thaliana] >gi|62241195|dbj|BAD93700.1| helicase and polymerase containing protein TEBICHI [Arabidopsis thaliana]	Unigene35909_All//0.00E+00//AT4G32700| DNA-directed DNA polymerase family protein	Unigene35909_All//0.00E+00//CO085611				nr +
Unigene3591_All	1239	3.50	9.28	9.24	3.14	4.64	2.70	0.65	0.44	0.77	1.41E+00	9.06E-15	Up	1.40E+00	4.49E-14	Up	5.66E-01	2.00E-02		-2.17E-01	5.42E-01		-5.64E-01	4.30E-01		2.51E-01	6.76E-01		Unigene3591_All//gi|53370641|gb|AAU89136.1|//6.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene3591_All//1.00E-07//AT3G09510| nucleic acid binding	Unigene3591_All//0.00E+00//TC156036				nr -
Unigene35912_All	1658	30.07	26.31	35.94	43.38	32.05	16.51	7.85	6.58	5.45	-1.93E-01	1.35E-02		2.57E-01	3.17E-04		-4.37E-01	5.18E-15		-1.39E+00	1.26E-95	Down	-2.56E-01	8.41E-02		-5.26E-01	1.02E-04		Unigene35912_All//gi|37202104|gb|AAQ89667.1|//3.00E-86//At5g25170 [Arabidopsis thaliana]	Unigene35912_All//1.00E-82//AT5G25170| unknown protein	Unigene35912_All//0.00E+00//TC168555				nr +
Unigene35915_All	2257	12.03	9.16	11.09	7.02	6.65	5.72	46.01	11.70	21.36	-3.93E-01	1.59E-04		-1.18E-01	3.47E-01		-7.74E-02	6.39E-01		-2.94E-01	4.29E-02		-1.97E+00	1.15E-254	Down	-1.11E+00	3.30E-111	Down	Unigene35915_All//gi|18075958|emb|CAD12836.1|//0.00E+00//diphosphonucleotide phosphatase 1 [Lupinus luteus]	Unigene35915_All//0.00E+00//AT1G13750| calcineurin-like phosphoesterase family protein	Unigene35915_All//0.00E+00//gi|78352840|gb|DT573114.1|DT573114				nr -
Unigene35916_All	2974	15.34	12.08	16.38	5.76	6.07	4.59	3.34	1.57	1.30	-3.45E-01	1.14E-05		9.48E-02	2.96E-01		7.45E-02	6.38E-01		-3.29E-01	1.59E-02		-1.09E+00	9.29E-11	Down	-1.36E+00	1.61E-15	Down	Unigene35916_All//gi|15221411|ref|NP_177623.1|//0.00E+00//PTAC2 (PLASTID TRANSCRIPTIONALLY ACTIVE2) [Arabidopsis thaliana] >gi|75194055|sp|Q9S7Q2.1|PP124_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g74850, chloroplastic; AltName: Full=Protein PLASTID TRANSCRIPTIONALLY ACTIVE 2; Flags: Precursor >gi|8882738|gb|AAD55291.1|AC008263_22 Contains 3 PF|01535 DUF17 domains [Arabidopsis thaliana]	Unigene35916_All//0.00E+00//AT1G74850| PTAC2 (PLASTID TRANSCRIPTIONALLY ACTIVE2)	Unigene35916_All//0.00E+00//TC175626				nr +
Unigene35917_All	1134	2.72	7.06	1.64	4.39	7.99	4.18	2.16	6.16	5.45	1.37E+00	3.44E-10	Up	-7.28E-01	4.95E-02		8.62E-01	1.94E-06		-7.10E-02	8.08E-01		1.51E+00	2.00E-12	Up	1.33E+00	1.41E-09	Up	Unigene35917_All//gi|15982759|gb|AAL09720.1|//2.00E-33//At1g80000/F19K16_3 [Arabidopsis thaliana] >gi|28416531|gb|AAO42796.1| At1g80000/F19K16_3 [Arabidopsis thaliana] >gi|222423722|dbj|BAH19827.1| AT1G80000 [Arabidopsis thaliana]	Unigene35917_All//1.00E-31//AT1G80000| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: CASC3/Barentsz eIF4AIII binding (InterPro:IPR018545); BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT1G15280.2); Has 2243 Blast hits to 1704 proteins in 212 species: Archae - 16; Bacteria - 151; Metazoa - 691; Fungi - 281; Plants - 163; Viruses - 64; Other Eukaryotes - 877 (source: NCBI BLink).	Unigene35917_All//0.00E+00//gi|84164963|gb|DR453611.1|DR453611				nr -
Unigene35919_All	2114	7.05	8.29	5.89	13.48	10.59	8.95	12.68	4.88	9.74	2.34E-01	9.41E-02		-2.59E-01	1.03E-01		-3.48E-01	2.57E-04		-5.91E-01	1.83E-09		-1.38E+00	8.06E-40	Down	-3.80E-01	3.23E-05		Unigene35919_All//gi|34365761|gb|AAQ65192.1|//1.00E-154//At3g08670 [Arabidopsis thaliana]	Unigene35919_All//4.00E-100//AT3G08670| unknown protein	Unigene35919_All//0.00E+00//TC136119		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene3592_All	1288	1.38	14.60	8.56	9.09	16.50	20.83	4.53	3.44	1.76	3.40E+00	4.00E-69	Up	2.63E+00	9.34E-31	Up	8.60E-01	2.14E-14		1.20E+00	4.81E-28	Up	-3.97E-01	7.88E-02		-1.36E+00	1.83E-09	Down	Unigene3592_All//gi|115548293|dbj|BAF34362.1|//1.00E-153//beta-fructofuranosidase [Citrus sinensis]	Unigene3592_All//2.00E-133//AT1G12240| ATBETAFRUCT4; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene3592_All//0.00E+00//TC157380		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr +
Unigene35920_All	1341	28.40	36.24	22.36	21.06	20.70	13.54	0.44	5.89	0.24	3.51E-01	3.72E-06		-3.45E-01	1.24E-04		-2.52E-02	8.31E-01		-6.38E-01	1.13E-10		3.74E+00	6.47E-39	Up	-8.93E-01	2.71E-01		Unigene35920_All//gi|297813755|ref|XP_002874761.1|//1.00E-110//CYP706A4 [Arabidopsis lyrata subsp. lyrata] >gi|297320598|gb|EFH51020.1| CYP706A4 [Arabidopsis lyrata subsp. lyrata]	Unigene35920_All//3.00E-111//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene35920_All//0.00E+00//TC179067		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene35923_All	1127	70.33	43.12	66.24	44.60	73.12	67.08	2.48	7.19	7.25	-7.06E-01	5.40E-32		-8.64E-02	2.17E-01		7.13E-01	6.14E-40		5.89E-01	7.99E-24		1.54E+00	1.06E-14	Up	1.55E+00	2.65E-15	Up	Unigene35923_All//gi|107738372|gb|ABF83685.1|//3.00E-16//At2g42760 [Arabidopsis thaliana]	Unigene35923_All//1.00E-15//AT2G42760| unknown protein	Unigene35923_All//0.00E+00//TC135559				nr -
Unigene35927_All	1319	42.64	150.93	63.95	21.45	30.36	39.58	11.99	23.99	37.72	1.82E+00	0.00E+00	Up	5.85E-01	1.23E-23		5.01E-01	1.19E-10		8.84E-01	3.65E-33		1.00E+00	1.75E-28	Up	1.65E+00	1.16E-97	Up	Unigene35927_All//gi|116268423|gb|ABJ96380.1|//4.00E-87//expressed protein [Prunus persica]	Unigene35927_All//7.00E-83//AT5G10490| MSL2 (MscS-LIKE 2); ion channel	Unigene35927_All//0.00E+00//TC148551				nr +
Unigene35928_All	1203	29.01	69.12	40.72	39.71	49.78	49.52	73.91	140.92	79.78	1.25E+00	6.63E-86	Up	4.89E-01	2.63E-10		3.26E-01	2.30E-07		3.18E-01	1.63E-06		9.31E-01	2.12E-132		1.10E-01	2.56E-02		Unigene35928_All//gi|115475029|ref|NP_001061111.1|//1.00E-32//Os08g0175200 [Oryza sativa Japonica Group] >gi|113623080|dbj|BAF23025.1| Os08g0175200 [Oryza sativa Japonica Group]	Unigene35928_All//6.00E-11//AT1G34220| unknown protein	Unigene35928_All//0.00E+00//TC166059				nr +
Unigene35932_All	2803	3.68	3.04	2.24	3.32	9.20	22.30	13.85	34.65	52.97	-2.76E-01	1.35E-01		-7.14E-01	1.10E-04		1.47E+00	3.25E-40	Up	2.75E+00	5.58E-199	Up	1.32E+00	8.46E-134	Up	1.94E+00	0.00E+00	Up	Unigene35932_All//gi|289721345|gb|ADD17684.1|//0.00E+00//beta-glucosidase [Vitis vinifera]	Unigene35932_All//0.00E+00//AT1G26560| BGLU40 (BETA GLUCOSIDASE 40); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene35932_All//0.00E+00//TC140980		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr +

Unigene35933_All	1335	37.74	27.37	22.66	16.46	14.99	13.87	9.37	4.60	3.94	-4.64E-01	4.23E-10		-7.36E-01	2.89E-21		-1.35E-01	3.08E-01		-2.47E-01	4.43E-02		-1.03E+00	3.03E-12	Down	-1.25E+00	4.88E-17	Down	Unigene35933_All//gi|83265567|gb|ABB97536.1|//7.00E-84//microtubule-associated protein [Nicotiana benthamiana]	Unigene35933_All//7.00E-65//AT5G08120| MBP2C (MICROTUBULE BINDING PROTEIN 2C); protein binding	Unigene35933_All//0.00E+00//DR463926				nr +
Unigene35934_All	1798	7.54	4.96	2.58	7.59	9.35	16.08	6.09	6.65	9.86	-6.04E-01	7.37E-05		-1.55E+00	4.20E-19	Down	3.00E-01	2.79E-02		1.08E+00	8.54E-26	Up	1.26E-01	4.60E-01		6.95E-01	2.08E-09		Unigene35934_All//gi|11131528|sp|Q9SEA0.1|CCS_CITSI//0.00E+00//RecName: Full=Capsanthin/capsorubin synthase, chromoplast; Flags: Precursor >gi|6580973|gb|AAF18389.1|AF169241_1 capsanthin/capsorubin synthase [Citrus sinensis] >gi|237664127|gb|ACE09634.1| lycopene beta-cyclase [Citrus sinensis]	Unigene35934_All//3.00E-158//AT3G10230| LYC (LYCOPENE CYCLASE); lycopene beta cyclase	Unigene35934_All//0.00E+00//TC170373		ko00906|Carotenoid biosynthesis		nr +
Unigene35935_All	1678	2.65	3.90	3.78	3.41	4.68	3.61	1.54	0.90	0.45	5.56E-01	1.60E-02		5.11E-01	3.87E-02		4.55E-01	2.70E-02		7.92E-02	7.67E-01		-7.77E-01	2.70E-02		-1.77E+00	2.04E-06	Down	Unigene35935_All//gi|297810979|ref|XP_002873373.1|//1.00E-119//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319210|gb|EFH49632.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35935_All//4.00E-116//AT5G08580| calcium-binding EF hand family protein	Unigene35935_All//0.00E+00//gi|11203916|gb|BF272846.1|BF272846				nr -
Unigene35936_All	3116	1.86	1.85	1.28	4.88	7.61	5.94	8.01	10.77	17.66	-7.80E-03	9.88E-01		-5.40E-01	3.74E-02		6.43E-01	6.91E-10		2.85E-01	3.27E-02		4.28E-01	2.20E-07		1.14E+00	9.12E-62	Up	Unigene35936_All//gi|15234429|ref|NP_190870.1|//0.00E+00//8120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding [Arabidopsis thaliana] >gi|3402758|emb|CAA20204.1| serine/threonine kinase-like protein [Arabidopsis thaliana] >gi|7269936|emb|CAB81246.1| serine/threonine kinase-like protein [Arabidopsis thaliana] >gi|157086543|gb|ABV21215.1| At4g21390 [Arabidopsis thaliana]	Unigene35936_All//0.00E+00//AT4G21390| 8120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding	Unigene35936_All//4.00E-126//CK640429		ko04626|Plant-pathogen interaction		nr +
Unigene35940_All	983	10.75	23.09	12.73	19.21	13.84	9.37	33.08	39.84	39.84	1.10E+00	1.06E-19	Up	2.44E-01	1.66E-01		-4.73E-01	5.94E-05		-1.04E+00	4.51E-16	Down	2.68E-01	5.18E-04		2.68E-01	3.68E-04					Unigene35940_All//0.00E+00//TC174789				
Unigene35942_All	617	1.27	2.14	1.21	7.35	5.41	2.93	3.70	1.22	3.49	7.47E-01	2.05E-01		-7.41E-02	9.35E-01		-4.41E-01	1.19E-01		-1.33E+00	3.85E-06	Down	-1.60E+00	6.24E-05	Down	-8.58E-02	8.15E-01					Unigene35942_All//0.00E+00//BF275533				
Unigene35943_All	2307	11.07	7.29	6.00	25.41	21.81	15.86	28.17	7.86	18.93	-6.02E-01	2.27E-08		-8.83E-01	6.57E-15		-2.21E-01	8.23E-04		-6.81E-01	4.53E-24		-1.84E+00	3.42E-145	Down	-5.74E-01	3.61E-23		Unigene35943_All//gi|15221404|ref|NP_177008.1|//0.00E+00//protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] >gi|79320902|ref|NP_001031252.1| protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] >gi|75191032|sp|Q9M9C6.1|P2C15_ARATH RecName: Full=Probable protein phosphatase 2C 15; Short=AtPP2C15	Unigene35943_All//0.00E+00//AT1G68410| protein phosphatase 2C-related / PP2C-related	Unigene35943_All//0.00E+00//TC174191				nr -
Unigene35945_All	1868	13.36	4.04	5.13	13.79	13.01	10.76	61.90	44.88	17.47	-1.73E+00	4.37E-42	Down	-1.38E+00	2.24E-29	Down	-8.32E-02	5.44E-01		-3.58E-01	7.43E-04		-4.64E-01	4.96E-27		-1.83E+00	1.92E-262	Down	Unigene35945_All//gi|15231700|ref|NP_190855.1|//1.00E-158//calmodulin-binding family protein [Arabidopsis thaliana] >gi|24111367|gb|AAN46807.1| At3g52870/F8J2_40 [Arabidopsis thaliana]	Unigene35945_All//2.00E-153//AT3G52870| calmodulin-binding family protein	Unigene35945_All//0.00E+00//TC173024				nr -
Unigene35948_All	1611	3.83	1.64	1.82	5.16	4.89	5.13	5.09	2.46	2.18	-1.23E+00	6.41E-07	Down	-1.08E+00	1.89E-05	Down	-7.72E-02	7.69E-01		-9.40E-03	9.59E-01		-1.05E+00	1.51E-08	Down	-1.23E+00	3.81E-11	Down	Unigene35948_All//gi|115447851|ref|NP_001047705.1|//6.00E-77//Os02g0672400 [Oryza sativa Japonica Group] >gi|113537236|dbj|BAF09619.1| Os02g0672400 [Oryza sativa Japonica Group]	Unigene35948_All//5.00E-83//AT1G09290| unknown protein	Unigene35948_All//0.00E+00//TC172196				nr +
Unigene35949_All	533	1.77	0.76	1.00	29.53	24.68	26.35	6.35	1.96	2.02	-1.22E+00	9.43E-02		-8.23E-01	2.71E-01		-2.59E-01	7.15E-02		-1.64E-01	3.11E-01		-1.69E+00	1.88E-07	Down	-1.65E+00	1.70E-07	Down	Unigene35949_All//gi|297833894|ref|XP_002884829.1|//1.00E-35//steroid hormone receptor/ transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297330669|gb|EFH61088.1| steroid hormone receptor/ transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene35949_All//7.00E-43//AT2G40320| unknown protein	Unigene35949_All//2.00E-145//gi|54117475|gb|CO492984.1|CO492984				nr +
Unigene3595_All	877	15.51	5.20	9.53	20.51	12.02	23.53	50.14	20.59	17.17	-1.58E+00	1.56E-20	Down	-7.02E-01	8.51E-06		-7.71E-01	1.26E-10		1.99E-01	1.34E-01		-1.28E+00	2.60E-58	Down	-1.55E+00	3.05E-79	Down	Unigene3595_All//gi|282848242|gb|AD02902.1|//3.00E-31//mitochondrial import inner membrane translocase subunit Tim8/small zinc finger-like protein [Jatropha curcas]	Unigene3595_All//9.00E-28//AT5G50810| TIM8; P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene3595_All//0.00E+00//gi|164360319|gb|EX167967.1|EX167967		GO:0005758//GO:0006612//GO:0008320//GO:0019866//GO:0043169		nr +
Unigene35950_All	1338	1.33	0.91	1.39	33.21	33.87	21.74	11.47	3.31	2.83	-5.49E-01	2.61E-01		6.72E-02	8.92E-01		2.84E-02	8.12E-01		-6.11E-01	2.71E-15		-1.79E+00	1.32E-33	Down	-2.02E+00	1.42E-40	Down	Unigene35950_All//gi|297833894|ref|XP_002884829.1|//1.00E-155//steroid hormone receptor/ transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297330669|gb|EFH61088.1| steroid hormone receptor/ transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene35950_All//0.00E+00//AT2G40320| unknown protein	Unigene35950_All//0.00E+00//TC171671				nr +
Unigene35951_All	691	5.45	8.29	5.32	9.52	9.77	13.01	8.20	16.09	19.03	6.04E-01	1.51E-02		-3.60E-02	9.25E-01		3.76E-02	8.94E-01		4.51E-01	2.09E-02		9.73E-01	4.34E-10		1.21E+00	6.14E-17	Up	Unigene35951_All//gi|58743302|gb|AAW81729.1|//4.00E-46//At1g62305 [Arabidopsis thaliana] >gi|61656151|gb|AAX49378.1| At1g62305 [Arabidopsis thaliana]	Unigene35951_All//5.00E-48//AT1G11940| unknown protein	Unigene35951_All//0.00E+00//TC151479				nr -
Unigene35952_All	1705	3.65	5.56	4.37	8.71	7.80	11.42	5.28	8.19	16.03	6.06E-01	1.17E-03		2.60E-01	2.70E-01		-1.59E-01	3.23E-01		3.91E-01	1.68E-03		6.32E-01	2.30E-06		1.60E+00	1.31E-51	Up	Unigene35952_All//gi|58743302|gb|AAW81729.1|//1.00E-121//At1g62305 [Arabidopsis thaliana] >gi|61656151|gb|AAX49378.1| At1g62305 [Arabidopsis thaliana]	Unigene35952_All//5.00E-119//AT1G11940| unknown protein	Unigene35952_All//0.00E+00//TC151479				nr -
Unigene35953_All	1740	0.18	0.70	0.49	0.69	0.95	0.83	0.75	1.15	2.18	1.95E+00	4.09E-03		1.44E+00	8.22E-02		4.67E-01	4.04E-01		2.74E-01	6.49E-01		6.14E-01	1.38E-01		1.53E+00	2.02E-07	Up	Unigene35953_All//gi|58743302|gb|AAW81729.1|//1.00E-126//At1g62305 [Arabidopsis thaliana] >gi|61656151|gb|AAX49378.1| At1g62305 [Arabidopsis thaliana]	Unigene35953_All//6.00E-124//AT1G11940| unknown protein	Unigene35953_All//0.00E+00//TC151479				nr +
Unigene35958_All	1958	22.98	12.09	8.21	46.28	60.46	38.66	84.47	12.94	45.54	-9.27E-01	4.37E-29		-1.48E+00	1.23E-58	Down	3.86E-01	4.13E-19		-2.60E-01	1.01E-06		-2.71E+00	0.00E+00	Down	-8.92E-01	1.38E-123		Unigene35958_All//gi|224058355|ref|XP_002299486.1|//0.00E+00//high mobility group family [Populus trichocarpa] >gi|222846744|gb|EEE84291.1| high mobility group family [Populus trichocarpa]	Unigene35958_All//4.00E-77//AT4G23800| high mobility group (HMG1/2) family protein	Unigene35958_All//0.00E+00//TC163360		ko03410|Base excision repair		nr +
Unigene35959_All	1092	28.94	105.70	92.85	20.16	49.73	65.80	29.27	123.47	156.55	1.87E+00	1.02E-213	Up	1.68E+00	1.66E-158	Up	1.30E+00	1.34E-70	Up	1.71E+00	2.79E-126	Up	2.08E+00	0.00E+00	Up	2.42E+00	0.00E+00	Up	Unigene35959_All//gi|89258512|gb|ABD65465.1|//1.00E-117//protein phosphatase 2C [Gossypium hirsutum]	Unigene35959_All//9.00E-84//AT3G11410| PP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA); protein binding / protein serine/threonine phosphatase	Unigene35959_All//0.00E+00//gi|78345378|gb|DT565652.1|DT565652				nr +
Unigene3596_All	749	2.17	3.25	3.06	5.65	2.99	2.53	2.54	2.06	0.85	5.85E-01	1.51E-01		4.98E-01	2.62E-01		-9.20E-01	8.33E-04		-1.16E+00	8.36E-05	Down	-2.99E-01	5.16E-01		-1.58E+00	2.42E-04	Down	Unigene3596_All//gi|124359162|gb|AB005885.1|//9.00E-17//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene3596_All//9.00E-06//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene3596_All//2.00E-10//TC135700				nr -
Unigene35960_All	1581	17.44	15.86	19.10	6.02	4.40	3.63	1.34	1.69	0.45	-1.37E-01	2.33E-01		1.31E-01	2.46E-01		-4.52E-01	1.13E-02		-7.30E-01	5.87E-05		3.40E-01	3.69E-01		-1.56E+00	1.14E-04	Down	Unigene35960_All//gi|48310194|gb|AAT41772.1|//4.00E-65//At2g46100 [Arabidopsis thaliana] >gi|50198900|gb|AAT70469.1| At2g46100 [Arabidopsis thaliana]	Unigene35960_All//5.00E-66//AT2G46100| unknown protein	Unigene35960_All//0.00E+00//TC169896				nr -
Unigene35961_All	1785	5.77	7.10	6.59	8.07	7.81	7.51	15.28	16.11	34.79	2.98E-01	7.02E-02		1.91E-01	3.11E-01		-4.58E-02	8.19E-01		-1.02E-01	5.85E-01		7.65E-02	4.95E-01		1.19E+00	4.07E-74	Up	Unigene35961_All//gi|21693562|gb|AAM75346.1|AF520810_1//1.00E-110//DNA-binding protein phosphatase 2C [Nicotiana tabacum]	Unigene35961_All//1.00E-87//AT2G25620| protein phosphatase 2C, putative / PP2C, putative	Unigene35961_All//0.00E+00//TC175287	DBP			nr +
Unigene35962_All	3315	0.35	0.31	0.34	5.76	4.57	5.72	10.45	2.77	7.40	-1.84E-01	7.48E-01		-4.17E-02	9.65E-01		-3.33E-01	6.44E-03		-8.30E-03	9.47E-01		-1.91E+00	8.87E-82	Down	-4.97E-01	4.81E-10		Unigene35962_All//gi|87240323|gb|ABD32181.1|//0.00E+00//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene35962_All//5.00E-95//AT2G27230| LHW (LONESOME HIGHWAY); protein homodimerization/ transcription activator/ transcription factor	Unigene35962_All//0.00E+00//CO081500	bHLH			nr -
Unigene35964_All	525	4.29	3.67	6.59	8.63	8.66	4.99	8.70	4.86	4.25	-2.25E-01	5.92E-01		6.22E-01	7.52E-02		3.90E-03	9.98E-01		-7.91E-01	4.78E-03		-8.41E-01	8.46E-04		-1.03E+00	3.21E-05	Down	Unigene35964_All//gi|297796721|ref|XP_002866245.1|//5.00E-47//transport protein particle component Bet3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312080|gb|EFH62504.1| transport protein particle component Bet3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene35964_All//7.00E-48//AT5G58030| transport protein particle (TRAPP) component Bet3 family protein	Unigene35964_All//0.00E+00//gi|164274896|gb|ES813841.1|ES813841				nr +
Unigene35965_All	492	6.38	2.68	6.60	13.36	10.29	9.36	6.02	2.89	1.05	-1.25E+00	5.13E-04	Down	4.92E-02	8.95E-01		-3.77E-01	1.02E-01		-5.13E-01	2.62E-02		-1.06E+00	1.20E-03		-2.51E+00	7.90E-11	Down	Unigene35965_All//gi|195624916|gb|ACG34288.1|//3.00E-31//transport protein particle subunit trs31 [Zea mays]	Unigene35965_All//1.00E-31//AT5G58030| transport protein particle (TRAPP) component Bet3 family protein	Unigene35965_All//4.00E-128//DR462029				nr -
Unigene35967_All	1664	4.91	1.61	3.42	32.21	22.58	28.99	6.00	5.40	3.30	-1.60E+00	6.59E-13	Down	-5.19E-01	1.47E-02		-5.13E-01	5.07E-15		-1.52E-01	4.98E-02		-1.51E-01	4.12E-01		-8.60E-01	7.35E-08		Unigene35967_All//gi|79549667|ref|NP_178303.2|//1.00E-135//nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana]	Unigene35967_All//3.00E-115//AT1G68130| AtIDD14 (Arabidopsis thaliana Indeterminate(ID)-Domain 14); nucleic acid binding / transcription factor/ zinc ion binding	Unigene35967_All//0.00E+00//TC158298	C2H2			nr +
Unigene35971_All	1849	6.90	17.21	6.77	15.22	15.35	12.41	18.59	23.96	28.10	1.32E+00	5.99E-36	Up	-2.88E-02	8.76E-01		1.17E-02	9.38E-01		-2.95E-01	4.17E-03		3.66E-01	2.68E-07		5.96E-01	7.15E-20		Unigene35971_All//gi|115488588|ref|NP_001066781.1|//7.00E-96//Os12g0485400 [Oryza sativa Japonica Group] >gi|122248588|sp|Q2QQS5.1|CCT14_ORYSJ RecName: Full=Cyclin-T1-4; Short=CycT1:4 >gi|113649288|dbj|BAF29800.1| Os12g0485400 [Oryza sativa Japonica Group]	Unigene35971_All//3.00E-91//AT5G45190| cyclin family protein	Unigene35971_All//0.00E+00//TC156485				nr +
Unigene35974_All	1425	46.78	163.46	46.45	54.01	58.36	118.50	77.44	101.04	140.06	1.81E+00	0.00E+00	Up	-1.01E-02	9.03E-01		1.12E-01	6.91E-02		1.13E+00	5.76E-160	Up	3.84E-01	8.71E-24		8.55E-01	5.55E-138		Unigene35974_All//gi|79592093|ref|NP_850045.2|//1.00E-111//TET8 (TETRASPANIN8) [Arabidopsis thaliana]	Unigene35974_All//2.00E-86//AT2G23810| TET8 (TETRASPANIN8)	Unigene35974_All//0.00E+00//TC161574				nr +

Unigene35979_All	2167	38.70	46.13	43.20	29.49	30.99	33.10	13.19	8.22	6.29	2.53E-01	1.00E-06		1.59E-01	6.22E-03		7.13E-02	3.57E-01		1.66E-01	9.63E-03		-6.83E-01	7.76E-14		-1.07E+00	1.46E-29	Down	Unigene35979_All//gi|224126051|ref|XP_002329649.1|//0.00E+00//4-Coumarate:CoA ligase [Populus trichocarpa] >gi|222870530|gb|EEF07661.1| 4-Coumarate:CoA ligase [Populus trichocarpa]	Unigene35979_All//0.00E+00//AT3G21240| 4CL2 (4-COUMARATE:COA LIGASE 2); 4-coumarate-CoA ligase	Unigene35979_All//0.00E+00//TC159384		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene3598_All	887	37.81	35.19	38.18	57.90	62.19	98.17	53.82	188.25	209.57	-1.04E-01	3.32E-01		1.41E-02	9.04E-01		1.03E-01	2.04E-01		7.62E-01	9.64E-43		1.81E+00	0.00E+00	Up	1.96E+00	0.00E+00	Up	Unigene3598_All//gi|192910680|gb|ACF06448.1|//7.00E-71//annexin [Elaeis guineensis]	Unigene3598_All//1.00E-52//AT1G68090| ANN5; calcium ion binding / calcium-dependent phospholipid binding	Unigene3598_All//0.00E+00//TC131838			GO:0005543//GO:0046872	nr +
Unigene35981_All	823	5.98	3.94	2.20	3.09	3.89	4.72	11.51	15.03	7.55	-6.01E-01	2.63E-02		-1.44E+00	1.18E-06	Down	3.34E-01	3.84E-01		6.12E-01	5.24E-02		3.86E-01	8.04E-03		-6.08E-01	1.68E-04		Unigene35981_All//gi|115474471|ref|NP_001060832.1|//2.00E-20//Os08g0112600 [Oryza sativa Japonica Group] >gi|113622801|dbj|BAF22746.1|Os08g0112600 [Oryza sativa Japonica Group]	Unigene35981_All//4.00E-29//AT1G33810| unknown protein	Unigene35981_All//0.00E+00//gi|109874691|gb|DW503665.1|DW503665				nr +
Unigene35984_All	2408	32.44	11.80	22.47	31.55	15.52	17.74	1.09	1.30	0.43	-1.46E+00	2.78E-102	Down	-5.30E-01	1.95E-18		-1.02E+00	1.53E-70	Down	-8.30E-01	1.17E-43		2.58E-01	4.49E-01		-1.34E+00	1.25E-04	Down	Unigene35984_All//gi|37548634|gb|AAN12272.1|//0.00E+00//subtilisin-like protease C1 [Glycine max] >gi|405566678|gb|AAO02075.4| subtilisin-like protease C1 [Glycine max]	Unigene35984_All//5.00E-173//AT5G59100| subtilase family protein	Unigene35984_All//0.00E+00//TC175719				nr +
Unigene35986_All	282	1.30	0.18	0.94	4.42	2.44	0.00	1.80	1.19	0.42	-2.85E+00	7.80E-02		-4.60E-01	6.97E-01		-8.55E-01	1.47E-01		-1.21E+01	8.64E-08	Down	-6.02E-01	5.31E-01		-2.09E+00	3.64E-02		Unigene35986_All//gi|15809976|gb|AAL06915.1|//2.00E-39//AT5g67280/K3G17_4 [Arabidopsis thaliana]	Unigene35986_All//1.00E-40//AT5G67280| RLK (Receptor-like kinase); ATP binding / kinase/ protein serine/threonine kinase	Unigene35986_All//2.00E-57//gi|48803775|gb|CO105089.1|CO105089		ko04626|Plant-pathogen interaction		nr +
Unigene35987_All	2496	4.13	1.46	2.22	16.62	8.88	5.56	9.05	4.54	2.25	-1.50E+00	1.18E-14	Down	-8.96E-01	1.46E-06		-9.04E-01	2.21E-31		-1.58E+00	1.01E-66	Down	-9.95E-01	2.08E-20		-2.01E+00	8.22E-59	Down	Unigene35987_All//gi|115477948|ref|NP_001062569.1|//1.00E-170//Os09g0110100 [Oryza sativa Japonica Group] >gi|113630802|dbj|BAF24483.1|Os09g0110100 [Oryza sativa Japonica Group]	Unigene35987_All//1.00E-138//AT4G34220| leucine-rich repeat transmembrane protein kinase, putative	Unigene35987_All//0.00E+00//TC168186				nr +
Unigene35988_All	428	0.61	0.95	2.12	5.00	3.22	3.90	19.66	9.18	2.89	6.32E-01	6.01E-01		1.79E+00	3.07E-02		-6.37E-01	1.39E-01		-3.58E-01	4.59E-01		-1.10E+00	2.14E-09	Down	-2.77E+00	1.34E-32	Down			Unigene35988_All//8.00E-154//gi|164243175|gb|ES837893.1|ES837893		ko00270|Cysteine and methionine metabolism//ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism//ko00410|beta-Alanine metabolism		kegg -
Unigene35989_All	1362	6.65	5.39	7.35	68.06	63.71	51.80	123.55	51.49	29.63	-3.01E-01	1.30E-01		1.45E-01	4.82E-01		-9.53E-02	1.06E-01		-3.94E-01	2.54E-14		-1.26E+00	1.82E-215	Down	-2.06E+00	0.00E+00	Down	Unigene35989_All//gi|18150158|dbj|BAB83649.1|//1.00E-148//spermine synthase [Arabidopsis thaliana] >gi|18150160|dbj|BAB83650.1| spermine synthase [Arabidopsis thaliana] >gi|18150162|dbj|BAB83651.1| spermine synthase [Arabidopsis thaliana] >gi|18150164|dbj|BAB83652.1| spermine synthase [Arabidopsis thaliana] >gi|18150166|dbj|BAB83653.1| spermine synthase [Arabidopsis thaliana]	Unigene35989_All//3.00E-147//AT5G19530| ACL5 (ACAULIS 5); spermine synthase/ thermospermine synthase	Unigene35989_All//0.00E+00//TC158504		ko00270|Cysteine and methionine metabolism//ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism//ko00410|beta-Alanine metabolism		nr -
Unigene35991_All	1081	16.60	5.11	7.64	52.99	39.53	42.28	10.33	9.74	4.31	-1.70E+00	7.64E-30	Down	-1.12E+00	1.68E-15	Down	-4.23E-01	2.33E-11		-3.26E-01	1.44E-06		-8.37E-02	6.22E-01		-1.26E+00	1.88E-15	Down	Unigene35991_All//gi|67003902|gb|AAV60842.1|//1.00E-141//plastidic hexokinase [Solanum lycopersicum]	Unigene35991_All//1.00E-120//AT1G47840| HXK3 (HEXOKINASE 3); ATP binding / fructokinase/ glucokinase/ hexokinase	Unigene35991_All//0.00E+00//gi|109859262|gb|DW488241.1|DW488241		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism		nr -
Unigene35992_All	1787	4.92	1.30	3.40	18.51	12.60	11.02	4.00	2.55	1.29	-1.92E+00	1.62E-17	Down	-5.34E-01	8.60E-03		-5.55E-01	7.75E-11		-7.48E-01	3.12E-16		-6.49E-01	8.47E-04		-1.63E+00	1.34E-14	Down	Unigene35992_All//gi|67003902|gb|AAV60842.1|//0.00E+00//plastidic hexokinase [Solanum lycopersicum]	Unigene35992_All//2.00E-169//AT1G47840| HXK3 (HEXOKINASE 3); ATP binding / fructokinase/ glucokinase/ hexokinase	Unigene35992_All//0.00E+00//TC136024		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism		nr +
Unigene35993_All	1011	25.10	40.70	32.13	46.91	39.51	25.60	22.62	22.03	8.55	6.97E-01	1.39E-16		3.56E-01	2.90E-04		-2.48E-01	7.76E-04		-8.74E-01	6.58E-30		-3.81E-02	7.57E-01		-1.40E+00	3.69E-36	Down	Unigene35993_All//gi|124359162|gb|ABN05685.1|//6.00E-11//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene35993_All//2.00E-12//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene35993_All//0.00E+00//TC152025				nr +
Unigene35994_All	1288	24.13	36.86	34.77	23.09	24.78	27.98	37.16	27.71	17.32	0.57E-01	3.15E-15		5.27E-01	9.32E-11		1.02E-01	3.71E-01		2.77E-01	2.03E-03		-4.23E-01	5.45E-10		-1.10E+00	2.78E-51	Down	Unigene35994_All//gi|4103987|gb|AAD01907.1|//1.00E-141//5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum] >gi|6002383|emb|CAB56756.1| 5,10-methylenetetrahydrofolate dehydrogenase: 5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]	Unigene35994_All//2.00E-139//AT3G12290| tetrahydrofolate dehydrogenase/cyclohydrolase, putative	Unigene35994_All//0.00E+00//TC130126				nr -
Unigene35995_All	1023	2.51	2.08	1.20	4.82	4.68	1.81	2.60	2.00	0.90	-2.69E-01	5.10E-01		-1.07E+00	1.07E-02		-4.31E-02	8.79E-01		-1.41E+00	3.22E-07	Down	-3.79E-01	3.02E-01		-1.54E+00	1.42E-05	Down	Unigene35995_All//gi|166203240|gb|ABY84660.1|//3.00E-62//transcription factor [Glycine max]	Unigene35995_All//2.00E-40//AT2G30590| WRKY21; calmodulin binding / transcription factor	Unigene35995_All//0.00E+00//ES833557	WRKY			nr -
Unigene35996_All	1516	3.14	1.47	1.65	5.45	6.84	3.52	3.10	2.76	1.29	-1.09E+00	9.70E-05	Down	-9.28E-01	1.32E-03		3.26E-01	7.39E-02		-6.34E-01	1.36E-03		-1.67E-01	5.66E-01		-1.27E+00	4.77E-07	Down	Unigene35996_All//gi|166203240|gb|ABY84660.1|//1.00E-116//transcription factor [Glycine max]	Unigene35996_All//4.00E-86//AT2G30590| WRKY21; calmodulin binding / transcription factor	Unigene35996_All//0.00E+00//ES833557	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene35998_All	2603	0.46	0.43	0.86	1.84	2.35	2.08	2.44	1.08	2.40	-1.11E-01	8.45E-01		8.94E-01	4.60E-02		3.58E-01	1.55E-01		1.81E-01	5.54E-01		-1.18E+00	4.69E-08	Down	-2.00E-02	9.47E-01		Unigene35998_All//gi|186501175|ref|NP_179383.2|//0.00E+00//binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor [Arabidopsis thaliana]	Unigene35998_All//0.00E+00//AT2G17930| binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor	Unigene35998_All//0.00E+00//CO110904				nr +
Unigene35999_All	1803	14.02	8.94	9.07	40.53	37.01	29.31	28.87	26.40	14.41	-6.49E-01	2.27E-09		-6.28E-01	1.80E-08		-1.31E-01	4.02E-02		-4.68E-01	1.85E-15		-1.29E-01	7.44E-02		-1.00E+00	6.88E-48	Down	Unigene35999_All//gi|297797389|ref|XP_002866579.1|//0.00E+00//UVB-resistance 8 [Arabidopsis lyrata subsp. lyrata] >gi|297312414|gb|EFH42838.1| UVB-resistance 8 [Arabidopsis lyrata subsp. lyrata]	Unigene35999_All//0.00E+00//AT5G63860| UVR8 (UVB-RESISTANCE 8); chromatin binding / guanyl-nucleotide exchange factor	Unigene35999_All//0.00E+00//TC138082		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene36_All	1079	18.23	57.38	23.20	67.22	72.03	52.57	52.51	43.62	32.49	1.65E+00	5.50E-97	Up	3.47E-01	2.34E-03		9.97E-02	1.30E-01		-3.55E-01	2.02E-09		-2.68E-01	2.08E-05		-6.93E-01	4.78E-28		Unigene36_All//gi|24461849|gb|AAN62336.1|AF506028_3/1.00E-145//CTV_2 [Citrus trifoliata]	Unigene36_All//7.00E-121//AT1G80490| TPR1 (TOPLESS-RELATED 1)	Unigene36_All//0.00E+00//TC157431		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene3600_All	3307	0.52	0.77	1.22	12.98	16.39	13.14	13.44	10.01	8.04	5.53E-01	1.67E-01		1.23E+00	1.45E-04	Up	3.36E-01	4.46E-07		1.69E-02	8.78E-01		-4.25E-01	2.14E-09		-7.42E-01	6.30E-25		Unigene3600_All//gi|297832162|ref|XP_002883963.1|//0.00E+00//RNA-dependent RNA polymerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329803|gb|EFH60222.1| RNA-dependent RNA polymerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3600_All//0.00E+00//AT2G19930| RNA-dependent RNA polymerase family protein	Unigene3600_All//0.00E+00//CA992900				nr -
Unigene36000_All	474	0.11	0.32	0.45	1.16	1.67	3.81	14.72	35.89	18.99	1.54E+00	5.31E-01		2.03E+00	3.61E-01		5.32E-01	5.40E-01		1.72E+00	9.05E-04	Up	1.29E+00	4.72E-23	Up	3.68E-01	3.02E-02		Unigene36000_All//gi|217073560|gb|ACJ85140.1|//1.00E-05//unknown [Medicago truncatula]		Unigene36000_All//4.00E-97//TC161964				nr +
Unigene36001_All	1178	5.95	4.30	3.98	43.72	43.96	77.67	61.81	156.93	120.53	-4.69E-01	3.59E-02		-5.81E-01	1.20E-02		7.90E-03	9.46E-01		8.29E-01	7.44E-52		1.34E+00	2.56E-260	Up	9.64E-01	3.81E-120		Unigene36001_All//gi|18400020|ref|NP_565539.1|//7.00E-88//NIC1 (NICOTINAMIDASE 1); catalytic/ nicotinamidase [Arabidopsis thaliana] >gi|20197887|gb|AAM15300.1| expressed protein [Arabidopsis thaliana]	Unigene36001_All//1.00E-85//AT2G22570| NIC1 (NICOTINAMIDASE 1); catalytic/ nicotinamidase	Unigene36001_All//0.00E+00//TC161964				nr -
Unigene36002_All	716	5.77	2.62	3.12	3.41	5.00	3.91	5.55	4.85	15.52	-1.14E+00	1.87E-04	Down	-8.86E-01	4.65E-03		5.53E-01	9.27E-02		1.98E-01	6.36E-01		-1.96E-01	5.35E-01		1.48E+00	2.60E-19	Up	Unigene36002_All//gi|6730631|gb|AAF27052.1|AC008262_1/1.00E-90//F4N2.2 [Arabidopsis thaliana]	Unigene36002_All//1.00E-88//AT1G69040| ACR4 (ACT REPEAT 4); amino acid binding	Unigene36002_All//2.00E-90//gi|109870195|gb|DW499171.1|DW499171				nr -
Unigene36004_All	2182	1.29	0.74	0.88	34.66	23.36	24.82	48.46	11.07	12.23	-8.01E-01	3.15E-02		-5.60E-01	1.52E-01		-5.69E-01	2.34E-25		-4.82E-01	7.90E-17		-2.13E+00	4.31E-286	Down	-1.99E+00	5.26E-269	Down	Unigene36004_All//gi|18379219|ref|NP_563698.1|//1.00E-96//acid phosphatase class B family protein [Arabidopsis thaliana] >gi|13926198|gb|AAK49578.1|AF370572_1 Similar to acid phosphatase [Arabidopsis thaliana] >gi|16226693|gb|AAL16234.1|AF428465_1 At1g04040/F21M11_2 [Arabidopsis thaliana] >gi|4204285|gb|AAD10666.1| Similar to acid phosphatase [Arabidopsis thaliana]	Unigene36004_All//6.00E-88//AT1G04040| acid phosphatase class B family protein	Unigene36004_All//0.00E+00//TC158235		ko03010|Ribosome		nr +
Unigene36005_All	738	1.99	1.37	0.72	1.08	0.84	3.43	1.83	1.36	2.81	-5.32E-01	3.39E-01		-1.46E+00	1.49E-02		-3.63E-01	6.23E-01		1.67E+00	7.87E-05	Up	-4.32E-01	4.16E-01		6.15E-01	1.13E-01		Unigene36005_All//gi|225461042|ref|XP_002278794.1|//1.00E-24//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene36005_All//1.00E-08//AT4G21780| unknown protein	Unigene36005_All//0.00E+00//TC167301				nr +
Unigene36007_All	465	3.26	2.51	2.86	4.71	3.55	0.78	1.45	0.99	1.88	-3.81E-01	4.78E-01		-1.89E-01	7.21E-01		-4.07E-01	3.61E-01		-2.60E+00	3.56E-07	Down	-5.57E-01	4.89E-01		3.74E-01	5.86E-01				Unigene36007_All//2.00E-136//gi|109887240|gb|DW516209.1|DW516209				
Unigene36009_All	1609	3.45	5.26	2.09	14.15	15.00	8.62	5.57	1.43	4.90	6.10E-01	2.16E-03		-7.25E-01	5.92E-03		8.46E-02	5.66E-01		-7.15E-01	1.50E-10		-1.96E+00	1.90E-22	Down	-1.84E-01	3.17E-01		Unigene36009_All//gi|30682967|ref|NP_193208.2|//5.00E-21//PPD2; dioxygenase/ metal ion binding [Arabidopsis thaliana] >gi|75151364|sp|Q8GY55.1|TIF4B_ARATH RecName: Full=Protein TIFY 4B; AltName: Full=Protein PEAPOD 2	Unigene36009_All//9.00E-22//AT4G14720| PPD2; dioxygenase/ metal ion binding	Unigene36009_All//0.00E+00//TC149149	Tify	ko04626|Plant-pathogen interaction		nr +
Unigene3601_All	1134	7.52	5.05	4.65	30.53	25.78	23.90	15.62	8.44	5.27	-5.75E-01	3.67E-03		-6.94E-01	7.34E-04		-2.44E-01	6.30E-03		-3.54E-01	7.75E-05		-8.88E-01	1.58E-13		-1.57E+00	4.27E-33	Down	Unigene3601_All//gi|297820146|ref|XP_002877956.1|//3.00E-57//reticulon family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323794|gb|EFH54215.1| reticulon family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3601_All//2.00E-48//AT3G54120| reticulon family protein (RTNLB12)	Unigene3601_All//0.00E+00//TC134472			GO:0043231	nr -

Unigene36010_All	256	0.00	0.79	0.00	1.17	1.08	0.00	0.99	1.63	5.29	9.63E+00	1.36E-01		null	null		-1.18E-01	9.00E-01		-1.02E+01	3.99E-02		7.20E-01	5.07E-01		2.42E+00	4.42E-05	Up	Unigene36010_All//gi|255584507|ref|XP_002532982.1|//9.00E-20//DNA binding protein, putative [Ricinus communis] >gi|223527246|gb|EEF29406.1| DNA binding protein, putative [Ricinus communis]	Unigene36010_All//2.00E-05//AT1G30320| remorin family protein	Unigene36010_All//2.00E-119//TC148890				nr +
Unigene36011_All	2369	1.21	1.37	0.36	2.80	3.07	4.58	9.24	13.53	40.36	1.72E-01	6.05E-01		-1.76E+00	2.58E-05	Down	1.33E-01	6.15E-01		7.10E-01	2.85E-05		5.50E-01	1.00E-10		2.13E+00	2.31E-262	Up	Unigene36011_All//gi|297845966|ref|XP_002890864.1|//1.00E-134//remorin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336706|gb|EFH67123.1| remorin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36011_All//2.00E-102//AT1G30320| remorin family protein	Unigene36011_All//0.00E+00//gi|78343600|gb|DT563874.1|DT563874				nr +
Unigene36013_All	2198	7.69	3.14	4.07	14.35	9.90	14.94	11.66	5.23	6.51	-1.29E+00	5.18E-19	Down	-9.18E-01	1.02E-10		-5.35E-01	9.91E-10		5.83E-02	6.13E-01		-1.16E+00	3.30E-29	Down	-8.41E-01	4.11E-18		Unigene36013_All//gi|30725462|gb|AF37753.1|//0.00E+00//At4g28200 [Arabidopsis thaliana]	Unigene36013_All//0.00E+00//AT4G28200| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: RNA processing; LOCATED IN: intracellular; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: RNA-processing protein, HAT helix (InterPro:IPR003107), U3 small nucleolar RNA-associated protein 6 (InterPro:IPR013949); Has 352 Blast hits to 342 proteins in 144 species: Archae - 0; Bacteria - 0; Metazoa - 111; Fungi - 130; Plants - 24; Viruses - 0; Other Eukaryotes - 87 (source: NCBI BLink).	Unigene36013_All//0.00E+00//gi|164251052|gb|ES793689.1|ES793689				nr +
Unigene36015_All	993	34.35	57.15	56.04	45.30	52.16	48.48	52.54	64.27	18.17	7.34E-01	1.21E-24		7.06E-01	7.67E-22		2.03E-01	5.20E-03		9.80E-02	2.84E-01		2.91E-01	7.29E-07		-1.53E+00	1.33E-92	Down	Unigene36015_All//gi|167961875|dbj|BAG09382.1|//1.00E-130//peroxisomal glycolate oxidase [Glycine max]	Unigene36015_All//6.00E-123//AT3G14420| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene36015_All//0.00E+00//TC134274		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene36016_All	2216	63.09	27.96	30.49	21.83	18.51	12.53	1.97	0.00	0.23	-1.17E+00	1.33E-130	Down	-1.05E+00	1.52E-105	Down	-2.38E-01	1.15E-03		-8.00E-01	2.63E-26		-1.09E+01	8.04E-31	Down	-3.07E+00	4.47E-19	Down	Unigene36016_All//gi|30696940|ref|NP_200588.2|//0.00E+00//CER3 (ECERIFERUM 3); binding / catalytic/ iron ion binding / oxidoreductase [Arabidopsis thaliana] >gi|75151993|sp|Q8HIZ0.1|WAX2_ARATH RecName: Full=Protein WAX2; AltName: Full=Protein YORE-YORE; AltName: Full=Protein FACELESS POLLEN 1 >gi|22900949|gb|AAN06975.1| cuticle protein [Arabidopsis thaliana] >gi|37051339|dbj|BAC81644.1| YORE-YORE protein [Arabidopsis thaliana] >gi|40714041|dbj|BAD06945.1| faceless pollen-1 [Arabidopsis thaliana]	Unigene36016_All//6.00E+00//AT5G57800| CER3 (ECERIFERUM 3); binding / catalytic/ iron ion binding / oxidoreductase	Unigene36016_All//0.00E+00//TC142175		ko00100|Steroid biosynthesis		nr +
Unigene36020_All	605	5.71	5.19	3.70	9.06	6.72	12.24	11.74	10.50	3.16	-1.37E-01	6.78E-01		-6.27E-01	7.35E-02		-4.31E-01	8.68E-02		4.35E-01	4.83E-02		-1.61E-01	4.76E-01		-1.89E+00	1.05E-17	Down	Unigene36020_All//gi|38566540|gb|AR24160.1|//7.00E-24//At5g11630 [Arabidopsis thaliana] >gi|40823768|gb|AA892303.1| At5g11630 [Arabidopsis thaliana]	Unigene36020_All//8.00E-20//AT5G11630| unknown protein	Unigene36020_All//1.00E-147//gi|109879006|gb|DW507976.1|DW507976				nr -
Unigene36022_All	634	1.07	1.04	1.68	5.34	4.24	1.14	6.14	1.52	2.51	-4.62E-02	9.69E-01		6.47E-01	3.62E-01		-3.35E-01	3.39E-01		-2.23E+00	4.16E-09	Down	-2.02E+00	1.70E-10	Down	-1.29E+00	3.97E-06	Down	Unigene36022_All//gi|38566540|gb|AR24160.1|//8.00E-16//At5g11630 [Arabidopsis thaliana] >gi|40823768|gb|AA892303.1| At5g11630 [Arabidopsis thaliana]	Unigene36022_All//6.00E-13//AT5G11630| unknown protein	Unigene36022_All//5.00E-51//gi|109879006|gb|DW507976.1|DW507976				nr +
Unigene36027_All	2194	1.43	1.78	1.84	2.70	3.86	2.90	2.29	2.38	7.17	3.14E-01	3.37E-01		3.67E-01	2.58E-01		5.15E-01	7.62E-03		1.03E-01	6.86E-01		5.44E-02	8.36E-01		1.65E+00	3.22E-31	Up	Unigene36027_All//gi|212717149|gb|ACJ37416.1|//1.00E-123//stress-induced receptor-like kinase [Glycine max]	Unigene36027_All//5.00E-81//AT4G18250| receptor serine/threonine kinase, putative	Unigene36027_All//0.00E+00//ES806075		ko04626|Plant-pathogen interaction		nr -
Unigene36034_All	1584	13.15	10.27	9.65	18.96	17.83	12.89	10.46	10.32	3.65	-3.57E-01	3.39E-03		-4.46E-01	3.54E-04		-8.92E-02	4.51E-01		-5.57E-01	5.09E-09		-2.03E-02	8.99E-01		-1.52E+00	1.08E-29	Down	Unigene36034_All//gi|226510081|ref|NP_001152651.1|//2.00E-60//calmodulin [Zea mays] >gi|195658577|gb|ACG48756.1| calmodulin [Zea mays]	Unigene36034_All//1.00E-55//AT3G03000| calmodulin, putative	Unigene36034_All//2.00E-102//DW243162		ko04626|Plant-pathogen interaction		nr -
Unigene36035_All	1084	22.35	10.98	12.97	35.57	33.70	48.04	48.52	26.26	20.76	-1.02E+00	9.12E-19	Down	-7.85E-01	1.03E-11		-7.77E-02	4.61E-01		4.34E-01	9.24E-10		-8.86E-01	2.20E-38		-1.22E+00	1.59E-66	Down	Unigene36035_All//gi|49617539|gb|AT67464.1|//1.00E-135//succinyl-CoA ligase alpha 2 subunit [Solanum lycopersicum]	Unigene36035_All//6.00E-111//AT5G23250| succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative	Unigene36035_All//0.00E+00//gi|78334242|gb|DT554516.1|DT554516		ko00020|Citrate cycle (TCA cycle)//ko00640|Propanoate metabolism		nr -
Unigene36036_All	1184	22.14	46.05	23.03	28.19	45.02	28.88	56.89	97.39	210.53	1.06E+00	3.10E-43	Up	5.67E-02	6.25E-01		6.76E-01	1.28E-23		3.47E-02	7.55E-01		7.76E-01	2.28E-66		1.89E+00	0.00E+00	Up	Unigene36036_All//gi|18395724|ref|NP_564236.1|//1.00E-79//myb family transcription factor [Arabidopsis thaliana] >gi|13926312|gb|AAK49622.1|AF37290 6_1 At1g25550/F2J7_21 [Arabidopsis thaliana] >gi|27363342|gb|AAO11590.1| At1g25550/F2J7_21 [Arabidopsis thaliana]	Unigene36036_All//6.00E-81//AT1G25550| myb family transcription factor	Unigene36036_All//0.00E+00//TC153086	G2-like			nr -
Unigene3604_All	505	1.04	3.41	2.11	3.35	2.86	6.71	8.62	5.13	2.60	1.72E+00	1.41E-03		1.03E+00	1.43E-01		-2.28E-01	6.59E-01		1.00E+00	3.00E-03		-7.49E-01	3.75E-03		-1.73E+00	5.83E-10	Down							
Unigene36040_All	2016	1.06	2.99	1.95	8.85	9.62	8.60	12.18	34.97	52.09	1.49E+00	8.91E-09	Up	8.77E-01	6.35E-03		1.21E-01	4.24E-01		-4.03E-02	7.90E-01		1.52E+00	6.55E-120	Up	2.10E+00	6.90E-283	Up	Unigene36040_All//gi|297793071|ref|XP_002864420.1|//1.00E-139//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310255|gb|EFH40679.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36040_All//1.00E-120//AT5G55970| zinc finger (C3HC4-type RING finger) family protein	Unigene36040_All//0.00E+00//TC173249				nr +
Unigene36042_All	332	2.21	5.19	3.53	6.60	7.26	8.57	6.24	2.39	1.92	1.23E+00	1.58E-02		6.78E-01	3.04E-01		1.37E-01	8.05E-01		3.76E-01	3.60E-01		-1.38E+00	8.02E-04	Down	-1.70E+00	4.43E-05	Down	Unigene36042_All//gi|205830837|sp|Q8L7E5.2|WIT1_ARATH//3.00E-19//RecName: Full=WPP domain-interacting tail-anchored protein 1	Unigene36042_All//1.00E-20//AT5G11390| unknown protein					nr +
Unigene36043_All	2501	4.06	3.36	4.66	7.83	7.92	6.48	9.59	6.35	4.30	-2.71E-01	1.47E-01		2.00E-01	2.86E-01		1.63E-02	9.23E-01		-2.72E-01	3.61E-02		-5.94E-01	2.40E-09		-1.16E+00	3.39E-28	Down	Unigene36043_All//gi|205830837|sp|Q8L7E5.2|WIT1_ARATH//1.00E-150//RecName: Full=WPP domain-interacting tail-anchored protein 1	Unigene36043_All//1.00E-131//AT5G11390| unknown protein					nr +
Unigene36044_All	1555	89.64	36.72	41.02	77.11	58.37	36.97	22.30	6.13	5.30	-1.29E+00	1.46E-150	Down	-1.13E+00	2.63E-118	Down	-4.02E-01	3.41E-21		-1.06E+00	2.68E-103	Down	-1.86E+00	4.93E-79	Down	-2.07E+00	1.13E-93	Down	Unigene36044_All//gi|15451206|gb|AB96874.1|//5.00E-93//Unknown protein [Arabidopsis thaliana] >gi|23197698|gb|AAN15376.1| Unknown protein [Arabidopsis thaliana]	Unigene36044_All//2.00E-84//AT3G18050| unknown protein	Unigene36044_All//0.00E+00//TC132773				nr -
Unigene36045_All	700	4.78	5.14	10.04	13.45	12.40	14.52	6.89	9.02	11.67	1.04E-01	7.47E-01		1.07E+00	4.54E-06	Up	-1.18E-01	5.92E-01		1.10E-01	6.37E-01		3.89E-01	7.31E-02		7.61E-01	1.76E-05		Unigene36045_All//gi|3256068|emb|CAA74397.1|//3.00E-63//Heat Shock Factor 3 [Arabidopsis thaliana]	Unigene36045_All//3.00E-49//AT3G02990| ATHSFA1E; DNA binding / transcription factor	Unigene36045_All//1.00E-178//TC141036	HSF			nr -
Unigene36047_All	638	2.38	1.11	2.34	5.15	5.34	8.00	3.51	3.08	8.74	-1.10E+00	4.35E-02		-2.52E-02	9.84E-01		5.23E-02	9.00E-01		6.34E-01	1.73E-02		-1.90E-01	6.25E-01		1.32E+00	1.39E-08	Up	Unigene36047_All//gi|15228440|ref|NP_186949.1|//1.00E-27//ATHSFA1E; DNA binding / transcription factor [Arabidopsis thaliana] >gi|21431799|sp|Q9SCW5.2|HFA1E_ARATH RecName: Full=Heat stress transcription factor A-1e; Short=AtHsfA1e; AltName: Full=Heat shock factor protein 2; Short=HSF 2; AltName: Full=Heat shock transcription factor 2; Short=HSTF 2; AltName: Full=AtHsf-06 >gi|11074198|gb|AB8040472.1| At3g02990 [Arabidopsis thaliana]	Unigene36047_All//2.00E-27//AT3G02990| ATHSFA1E; DNA binding / transcription factor	Unigene36047_All//0.00E+00//EX165337	HSF			nr -
Unigene36048_All	394	3.98	2.57	7.03	5.31	2.01	4.13	4.94	3.18	4.65	-6.31E-01	2.31E-01		8.19E-01	3.85E-02		-1.40E+00	9.86E-04	Down	-3.64E-01	4.57E-01		-6.33E-01	1.35E-01		-8.58E-02	8.34E-01		Unigene36048_All//gi|5734618|dbj|BAA88349.1|//5.00E-27//formiminotransferase-cyclodeaminase-like [Oryza sativa Japonica Group] >gi|55296213|dbj|BAD67931.1| formiminotransferase-cyclodeaminase-like [Oryza sativa Japonica Group]	Unigene36048_All//4.00E-27//AT2G20830| folic acid binding / transferase	Unigene36048_All//1.00E-121//TC148750				nr -
Unigene36050_All	1642	13.64	12.53	9.47	92.26	87.98	93.13	38.24	15.27	12.37	-1.22E-01	3.56E-01		-5.26E-01	1.03E-05		-6.85E-02	1.46E-01		1.36E-02	7.93E-01		-1.32E+00	6.17E-87	Down	-1.63E+00	1.48E-121	Down	Unigene36050_All//gi|60932273|gb|AAX37336.1|//0.00E+00//UDP-glucuronic acid decarboxylase 3 [Populus tomentosa]	Unigene36050_All//4.00E-176//AT3G46440| UXS5; UDP-glucuronate decarboxylase/ catalytic	Unigene36050_All//0.00E+00//TC163374		ko00523|Polyketide sugar unit biosynthesis		nr +
Unigene36053_All	1569	2.17	0.97	2.51	2.79	1.76	1.93	2.78	2.16	2.13	-1.16E+00	6.70E-04	Down	2.13E-01	5.32E-01		-6.70E-01	1.45E-02		-5.35E-01	7.05E-02		-3.63E-01	1.83E-01		-3.80E-01	1.40E-01		Unigene36053_All//gi|297611935|ref|NP_001068018.2|//1.00E-144//Os11g0533100 [Oryza sativa Japonica Group] >gi|255680143|dbj|BAF28381.2| Os11g0533100 [Oryza sativa Japonica Group]	Unigene36053_All//4.00E-174//AT3G02060| DEAD/DEAH box helicase, putative	Unigene36053_All//0.00E+00//gi|48746422|gb|CO076941.1|CO076941		ko03440|Homologous recombination		nr +
Unigene36054_All	1887	38.43	38.96	62.03	37.57	37.81	21.76	70.15	48.22	30.21	1.98E-02	7.78E-01		6.91E-01	1.12E-43		9.40E-03	9.08E-01		-7.88E-01	2.64E-37		-5.41E-01	1.52E-40		-1.22E+00	2.89E-164	Down	Unigene36054_All//gi|224137688|ref|XP_002327188.1|//1.00E-169//cytochrome P450 [Populus trichocarpa] >gi|222835503|gb|EEE73938.1| cytochrome P450 [Populus trichocarpa]	Unigene36054_All//5.00E-138//AT5G10600| CYP81K2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene36054_All//0.00E+00//TC134865		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene36055_All	1711	13.82	11.19	10.77	4.98	6.44	11.01	7.91	7.57	8.45	-3.04E-01	7.79E-03		-3.60E-01	2.21E-03		3.71E-01	3.02E-02		1.14E+00	1.55E-18	Up	-6.24E-02	6.99E-01		9.61E-02	5.31E-01		Unigene36055_All//gi|62869545|gb|AAY17949.1|//1.00E-158//ring zinc finger protein [Artemisia desertorum]	Unigene36055_All//4.00E-152//AT2G28840| ankyrin repeat family protein	Unigene36055_All//0.00E+00//TC155644				nr +

Unigene36057_All	1883	5.17	2.56	5.60	5.58	4.55	2.81	8.35	1.11	3.17	-1.02E+00	6.63E-08	Down	1.16E-01	5.86E-01		-2.94E-01	1.03E-01		-9.92E-01	1.22E-08		-2.91E+00	1.49E-61	Down	-1.40E+00	6.10E-25	Down	Unigene36057_All//gi|229597364|gb|ACQ82802.1|//0.00E+00//vacuolar invertase [Gossypium hirsutum]	Unigene36057_All//0.00E+00//AT1G12240| ATBETAFRUCT4| beta-fructofuranosidase| hydrolase, hydrolyzing O-glycosyl compounds	Unigene36057_All//0.00E+00//TC162693		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene36058_All	1702	4.67	21.91	3.19	4.65	10.86	10.19	1.94	3.07	6.18	2.23E+00	4.08E-87	Up	-5.50E-01	1.07E-02		1.22E+00	5.58E-22	Up	1.13E+00	8.67E-17	Up	6.64E-01	4.40E-03		1.67E+00	1.22E-21	Up	Unigene36058_All//gi|29028306|gb|AA062313.1|//0.00E+00//UDP-glucose dehydrogenase [Colocasia esculenta]	Unigene36058_All//0.00E+00//AT5G15490| UDP-glucose 6-dehydrogenase, putative	Unigene36058_All//0.00E+00//gi|78341431|gb|DT561705.1|DT561705		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene36059_All	1523	24.39	34.63	27.13	16.58	24.13	21.74	12.21	26.21	21.14	5.06E-01	3.48E-12		1.54E-01	1.01E-01		5.41E-01	3.49E-11		3.90E-01	1.95E-05		1.10E+00	1.19E-41	Up	7.91E-01	3.02E-20		Unigene36059_All//gi|224105109|ref|XP_002313690.1|//5.00E-42//f-box family protein [Populus trichocarpa] >gi|222850098|gb|EEE87645.1| f-box family protein [Populus trichocarpa]	Unigene36059_All//3.00E-34//AT2G17030| F-box family protein	Unigene36059_All//0.00E+00//TC164036				nr +
Unigene36062_All	1735	3.59	2.28	4.02	2.18	1.96	1.25	0.00	0.02	0.64	-6.56E-01	5.51E-03		1.64E-01	5.15E-01		-1.51E-01	6.61E-01		-8.04E-01	1.00E-02		4.59E+00	6.34E-01		9.33E+00	4.36E-08	Up	Unigene36062_All//gi|224589671|gb|ACN59367.1|//1.00E-151//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene36062_All//2.00E-134//AT5G14210| leucine-rich repeat transmembrane protein kinase, putative	Unigene36062_All//2.00E-154//gi|48740426|gb|CO070945.1|CO070945		ko04626|Plant-pathogen interaction		nr +
Unigene36063_All	1709	1.04	2.88	2.09	5.54	6.97	5.44	5.57	3.89	3.05	1.47E+00	3.88E-07	Up	1.00E+00	3.35E-03		3.32E-01	4.54E-02		-2.48E-02	9.24E-01		-5.18E-01	1.84E-03		-8.66E-01	1.29E-07		Unigene36063_All//gi|15242078|ref|NP_197587.1|//1.00E-171//glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Unigene36063_All//3.00E-173//AT5G20870| glycosyl hydrolase family 17 protein	Unigene36063_All//0.00E+00//gi|78329547|gb|DT549821.1|DT549821		ko00500|Starch and sucrose metabolism		nr +
Unigene36065_All	2584	6.18	0.65	0.37	13.36	4.14	3.81	10.01	1.89	1.88	-3.25E+00	5.12E-57	Down	-4.06E+00	1.01E-65	Down	-1.69E+00	3.12E-70	Down	-1.81E+00	2.84E-67	Down	-2.40E+00	1.23E-81	Down	-2.41E+00	1.45E-84	Down	Unigene36065_All//gi|18378991|ref|NP_563659.1|//0.00E+00//BXL2 (BETA-XYLOSIDASE 2); hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|75250279|sp|Q94KD8.1|BXL2_ARATH RecName: Full=Probable beta-D-xylosidase 2; Short=AtBXL2; Flags: Precursor >gi|14194121|gb|AAK56255.1|AF367266.1 At1g02640/T14P4_11 [Arabidopsis thaliana] >gi|23506063|gb|AAN28891.1| At1g02640/T14P4_11 [Arabidopsis thaliana]	Unigene36065_All//0.00E+00//AT1G02640| BXL2 (BETA-XYLOSIDASE 2); hydrolase, hydrolyzing O-glycosyl compounds	Unigene36065_All//0.00E+00//TC177844		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr -
Unigene36066_All	1404	19.86	40.38	16.65	44.53	58.96	42.75	45.68	49.06	82.26	1.02E+00	1.04E-42	Up	-2.55E-01	2.16E-02		4.05E-01	1.01E-14		-5.88E-02	4.80E-01		1.03E-01	1.04E-01		8.49E-01	3.57E-79		Unigene36066_All//gi|16974548|gb|AAL31190.1|//3.00E-26//AT4g32020/F10N7_170 [Arabidopsis thaliana] >gi|21928043|gb|AAM78050.1| AT4g32020/F10N7_170 [Arabidopsis thaliana]	Unigene36066_All//4.00E-11//AT4G32020| unknown protein	Unigene36066_All//0.00E+00//gi|78337925|gb|DT558199.1|DT558199				nr -
Unigene36067_All	1578	37.43	72.25	61.42	52.72	73.67	76.22	1.63	4.40	1.92	9.49E-01	3.55E-75		7.14E-01	2.02E-38		4.83E-01	3.47E-28		5.32E-01	2.36E-31		1.43E+00	1.93E-11	Up	2.31E-01	4.92E-01		Unigene36067_All//gi|115476924|ref|NP_001062058.1|//6.00E-80//Os08g0480200 [Oryza sativa Japonica Group] >gi|113624027|dbj|BAF23972.1| Os08g0480200 [Oryza sativa Japonica Group]	Unigene36067_All//7.00E-69//AT2G36690| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene36067_All//0.00E+00//gi|78344048|gb|DT564322.1|DT564322		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr -
Unigene36069_All	297	0.18	2.39	0.00	0.00	0.23	0.61	4.70	9.43	19.99	3.76E+00	2.36E-03		-7.46E+00	6.23E-01		7.86E+00	6.09E-01		9.25E+00	1.94E-01		1.01E+00	2.85E-03		2.09E+00	1.19E-16	Up			Unigene36069_All//6.00E-58//DW232275					
Unigene3607_All	1023	18.05	59.68	27.74	33.50	93.65	112.44	6.90	13.56	33.45	1.73E+00	1.82E-101	Up	6.20E-01	3.14E-09		1.48E+00	2.76E-151	Up	1.75E+00	8.93E-209	Up	9.75E-01	1.96E-12		2.28E+00	1.16E-102	Up	Unigene3607_All//gi|224082518|ref|XP_002335471.1|//4.00E-10//predicted protein [Populus trichocarpa] >gi|224096243|ref|XP_002310589.1| predicted protein [Populus trichocarpa] >gi|222834230|gb|EEE72707.1| predicted protein [Populus trichocarpa] >gi|222853492|gb|EEE91039.1| predicted protein [Populus trichocarpa]		Unigene3607_All//0.00E+00//TC165474				nr +
Unigene36070_All	1039	3.42	19.56	5.84	21.67	53.16	37.82	81.02	181.83	296.59	2.51E+00	5.67E-55	Up	7.71E-01	2.03E-03		1.29E+00	3.74E-71	Up	8.03E-01	2.08E-21		1.17E+00	5.12E-213	Up	1.87E+00	0.00E+00	Up	Unigene36070_All//gi|226500126|ref|NP_001149571.1|//2.00E-49//lactoylglutathione lyase [Zea mays] >gi|195628124|gb|ACG35892.1| lactoylglutathione lyase [Zea mays]	Unigene36070_All//8.00E-44//AT1G80160| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene36070_All//0.00E+00//TC171335				nr -
Unigene36074_All	1621	3.87	2.53	2.83	5.41	4.95	4.57	3.52	1.32	1.87	-6.13E-01	9.13E-03		-4.55E-01	6.91E-02		-1.28E-01	5.82E-01		-2.43E-01	2.61E-01		-1.42E+00	1.65E-09	Down	-9.15E-01	2.58E-05		Unigene36074_All//gi|115443823|ref|NP_001045691.1|//1.00E-125//Os02g0117900 [Oryza sativa Japonica Group] >gi|41052840|dbj|BAD07731.1| leaf senescence related protein-like [Oryza sativa Japonica Group] >gi|41053244|dbj|BAD07612.1| leaf senescence related protein-like [Oryza sativa Japonica Group] >gi|113535222|dbj|BAF07605.1| Os02g0117900 [Oryza sativa Japonica Group]	Unigene36074_All//3.00E-157//AT5G64470| unknown protein					nr +
Unigene36075_All	1215	3.79	8.63	4.69	20.50	32.68	25.35	29.82	35.67	33.54	1.19E+00	1.29E-10	Up	3.07E-01	2.54E-01		6.73E-01	1.48E-17		3.06E-01	1.65E-03		2.58E-01	4.19E-04		1.70E-01	2.69E-02		Unigene36075_All//gi|15529234|gb|AAK97711.1|//8.00E-26//AT3g15630/MSJ11_3 [Arabidopsis thaliana] >gi|16974391|gb|AAL31121.1| AT3g15630/MSJ11_3 [Arabidopsis thaliana]	Unigene36075_All//4.00E-27//AT3G15630| unknown protein	Unigene36075_All//0.00E+00//TC143329				nr -
Unigene36079_All	1805	18.00	18.89	22.21	15.23	13.62	10.23	1.36	1.62	0.60	6.97E-02	5.20E-01		3.03E-01	5.81E-04		-1.61E-01	1.52E-01		-5.74E-01	9.84E-09		2.55E-01	4.78E-01		-1.19E+00	8.55E-04	Down	Unigene36079_All//gi|42570805|ref|NP_973476.1|//1.00E-116//tetracycline transporter [Arabidopsis thaliana]	Unigene36079_All//6.00E-110//AT2G16990| tetracycline transporter	Unigene36079_All//0.00E+00//TC151593				nr +
Unigene36081_All	3477	1.75	1.78	1.06	6.00	7.42	5.10	8.41	1.39	2.88	2.65E-02	9.30E-01		-7.24E-01	3.81E-03		3.05E-01	3.42E-03		-2.34E-01	6.84E-02		-2.59E+00	1.19E-100	Down	-1.55E+00	3.70E-53	Down	Unigene36081_All//gi|42569244|ref|NP_178846.2|//0.00E+00//kinesin motor protein-related [Arabidopsis thaliana]	Unigene36081_All//0.00E+00//AT2G22610| kinesin motor protein-related	Unigene36081_All//0.00E+00//TC144773				nr +
Unigene36082_All	1420	1.58	16.13	4.76	3.37	11.88	23.54	7.95	27.11	23.54	3.35E+00	6.09E-83	Up	1.59E+00	3.35E-10	Up	1.82E+00	1.54E-35	Up	2.81E+00	7.33E-109	Up	1.77E+00	1.54E-81	Up	1.57E+00	6.04E-61	Up	Unigene36082_All//gi|297822091|ref|XP_002878928.1|//2.00E-64//ATHSFA2 [Arabidopsis lyrata subsp. lyrata] >gi|297324767|gb|EFH55187.1| ATHSFA2 [Arabidopsis lyrata subsp. lyrata]	Unigene36082_All//2.00E-65//AT2G26150| ATHSFA2; DNA binding / transcription factor	Unigene36082_All//0.00E+00//TC158707	HSF			nr -
Unigene36083_All	3277	1.17	1.36	1.66	8.01	13.48	7.15	4.04	8.14	3.34	2.23E-01	4.57E-01		5.08E-01	5.96E-02		7.51E-01	1.57E-23		-1.64E-01	1.70E-01		1.01E+00	1.60E-24	Up	-2.73E-01	5.02E-02		Unigene36083_All//gi|14010521|gb|AAK52034.1|AF363826_1//6.00E-84//Pto-like kinase SG5-3e [Phaseolus vulgaris]	Unigene36083_All//1.00E-75//AT5G59700| protein kinase, putative					nr -
Unigene36084_All	662	56.51	24.19	35.31	16.40	5.67	15.21	6.83	38.95	2.89	-1.22E+00	7.85E-38	Down	-6.78E-01	6.79E-14		-1.53E+00	2.29E-19	Down	-1.09E-01	6.29E-01		2.51E+00	2.39E-85	Up	-1.24E+00	1.18E-06	Down	Unigene36084_All//gi|60280217|gb|AAX16493.1|//3.00E-56//UDP-glucose:flavonoid 7-O-glucosyltransferase [Malus x domestica]	Unigene36084_All//3.00E-43//AT4G14090| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene36084_All//0.00E+00//gi|78323735|gb|DT544009.1|DT544009		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr -
Unigene36085_All	655	13.18	12.15	7.72	8.97	4.78	6.14	1.48	43.26	0.55	-1.18E-01	6.05E-01		-7.71E-01	1.62E-04		-9.08E-01	6.28E-05		-5.48E-01	2.55E-02		4.87E+00	2.54E-165	Up	-1.44E+00	2.09E-02		Unigene36085_All//gi|14192682|gb|AAK54465.1|//5.00E-60//cold-induced glucosyl transferase [Solanum sogarandinum]	Unigene36085_All//2.00E-48//AT4G15550| IAGLU (INDOLE-3-ACETATE BETA-D-GLUCOSYLTRANSFERASE); UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene36085_All//0.00E+00//TC139712		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr +
Unigene36086_All	1516	29.68	15.98	15.03	10.25	6.29	11.05	7.78	72.70	4.39	-8.94E-01	2.24E-27		-9.81E-01	9.85E-31		-7.04E-01	5.62E-08		1.09E-01	5.12E-01		3.22E+00	0.00E+00	Up	-8.26E-01	1.38E-08		Unigene36086_All//gi|209954707|dbj|BAG80544.1|//1.00E-167//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene36086_All//2.00E-123//AT1G05560| UGT75B1 (UDP-GLUCOSYLTRANSFERASE 75B1); UDP-glucose:4-aminobenzoate acylglucosyltransferase/ UDP-glucosyltransferase/ UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring glycosyl groups	Unigene36086_All//0.00E+00//TC168115		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr -
Unigene36087_All	1751	4.51	1.82	3.07	9.50	7.95	17.95	47.79	207.86	1290.47	-1.31E+00	1.99E-09	Down	-5.55E-01	1.03E-02		-2.58E-01	6.30E-02		9.18E-01	1.81E-21		2.12E+00	0.00E+00	Up	4.76E+00	0.00E+00	Up	Unigene36087_All//gi|79527284|ref|NP_568556.3|//0.00E+00//hydrolase [Arabidopsis thaliana]	Unigene36087_All//0.00E+00//AT5G38200| hydrolase					nr +
Unigene36089_All	1545	5.45	9.35	4.96	2.03	3.97	4.30	7.25	6.47	8.59	7.78E-01	1.69E-07		-1.36E-01	5.63E-01		9.66E-01	2.38E-05		1.08E+00	2.25E-06	Up	-1.66E-01	3.46E-01		2.44E-01	8.40E-02		Unigene36089_All//gi|297844838|ref|XP_002890300.1|//7.00E-91//AGL102 [Arabidopsis lyrata subsp. lyrata] >gi|297336142|gb|EFH66559.1| AGL102 [Arabidopsis lyrata subsp. lyrata]	Unigene36089_All//4.00E-90//AT1G18750| AGL65 (AGAMOUS-LIKE 65); DNA binding / transcription factor	Unigene36089_All//0.00E+00//TC175079	MADS			nr -
Unigene36094_All	1396	51.20	101.96	109.55	27.05	33.50	31.71	17.17	15.00	7.45	9.94E-01	3.51E-101		1.10E+00	1.60E-124	Up	3.09E-01	2.38E-05		2.29E-01	4.97E-03		-1.95E-01	6.82E-02		-1.21E+00	4.65E-30	Down	Unigene36094_All//gi|15222771|ref|NP_175972.1|//1.00E-137//BTB/POZ domain-containing protein [Arabidopsis thaliana] >gi|63147370|gb|AAY34158.1| At1g55760 [Arabidopsis thaliana]	Unigene36094_All//1.00E-138//AT1G55760| BTB/POZ domain-containing protein	Unigene36094_All//0.00E+00//TC172543				nr +
Unigene36095_All	1698	20.43	25.72	28.69	6.48	5.92	4.60	1.87	1.23	5.47	3.32E-01	3.77E-05		4.90E-01	2.77E-10		-1.31E-01	5.32E-01		-4.95E-01	3.58E-03		-6.02E-01	5.52E-02		1.55E+00	2.78E-17	Up	Unigene36095_All//gi|62752942|gb|AAX98670.1|//2.00E-51//HDZip I protein [Glycine max]	Unigene36095_All//4.00E-30//AT3G01470| ATHB-1 (ARABIDOPSIS THALIANA HOMEOBOX 1); DNA binding / protein homodimerization/ sequence-specific DNA binding / transcription activator/ transcription factor	Unigene36095_All//0.00E+00//TC146073	HB			nr +
Unigene36097_All	1787	4.16	3.69	3.22	7.02	7.26	5.74	8.75	6.76	4.06	-1.74E-01	4.47E-01		-3.70E-01	1.10E-01		4.85E-02	8.31E-01		-2.92E-01	8.19E-02		-3.73E-01	3.36E-03		-1.11E+00	1.46E-17	Down	Unigene36097_All//gi|18412056|ref|NP_565185.1|//1.00E-113//POLD3; DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|4836868|gb|AAD30571.1|AC007260_2 Hypothetical protein [Arabidopsis thaliana]	Unigene36097_All//3.00E-86//AT1G78650| POLD3; DNA-directed DNA polymerase	Unigene36097_All//0.00E+00//gi|13354689|gb|BG445037.1|BG445037		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +

Unigene361_All	3326	3.71	1.48	2.88	21.48	20.17	13.06	10.88	8.78	5.63	-1.33E+00	1.19E-14	Down	-3.65E-01	3.33E-02		-9.07E-02	1.97E-01		-7.17E-01	5.44E-32		-3.09E-01	1.14E-04		-9.51E-01	8.29E-31		Unigene361_All//gi|225030806|gb|ACN79516.1|//0.00E+00//auxin response factor 3b [Lotus japonicus]	Unigene361_All//5.00E-162//AT2G33860| ETT (ETTIN); DNA binding / transcription factor	Unigene361_All//0.00E+00//gi|78352599|gb|DT572873.1|DT572873	ARF			nr -
Unigene3610_All	1905	1.10	2.05	1.51	4.00	7.45	9.25	1.15	2.19	1.97	8.99E-01	3.90E-03		4.58E-01	2.44E-01		8.96E-01	2.01E-10		1.21E+00	6.99E-19	Up	9.27E-01	5.00E-04		7.68E-01	5.04E-03		Unigene3610_All//gi|224121242|ref|XP_002318534.1|//1.00E-180//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222859207|gb|EEE96754.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene3610_All//1.00E-154//AT1G27170| ATP binding / protein binding / transmembrane receptor	Unigene3610_All//0.00E+00//TC147843		ko04626|Plant-pathogen interaction		nr +
Unigene36100_All	1165	5.84	3.22	4.02	16.51	12.53	7.52	9.65	3.77	3.35	-8.59E-01	1.42E-04		-5.38E-01	2.31E-02		-3.97E-01	8.05E-04		-1.13E+00	6.89E-19	Down	-1.36E+00	8.01E-17	Down	-1.53E+00	1.54E-20	Down	Unigene36100_All//gi|224096832|ref|XP_002310753.1|//1.00E-117//f-box family protein [Populus trichocarpa] >gi|222853656|gb|EEE91203.1| f-box family protein [Populus trichocarpa]	Unigene36100_All//9.00E-29//AT5G60850| OBP4; DNA binding / transcription factor	Unigene36100_All//0.00E+00//ES829611	C2C2-Dof			nr +
Unigene36101_All	1709	2.97	2.02	1.68	2.30	2.10	1.24	24.76	6.75	6.22	-5.59E-01	3.64E-02		-8.20E-01	3.14E-03		-1.36E-01	6.98E-01		-8.91E-01	3.45E-03		-1.88E+00	3.55E-97	Down	-1.99E+00	1.63E-108	Down	Unigene36101_All//gi|209954729|dbj|BAG80555.1|//1.00E-169//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene36101_All//4.00E-126//AT2G36780| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene36101_All//0.00E+00//TC144945		ko00908|Zeatin biosynthesis		nr -
Unigene36102_All	2216	26.04	4.25	18.43	3.93	3.37	3.00	1.45	0.34	0.76	-2.61E+00	1.12E-163	Down	-4.99E-01	2.06E-12		-2.22E-01	3.04E-01		-3.93E-01	5.01E-02		-2.09E+00	3.37E-09	Down	-9.41E-01	1.69E-03		Unigene36102_All//gi|225434642|ref|XP_002279786.1|//1.00E-180//PREDICTED: similar to binding [Vitis vinifera]	Unigene36102_All//1.00E-128//AT2G29670| binding	Unigene36102_All//0.00E+00//TC174325				nr -
Unigene36103_All	3105	37.61	8.00	27.99	0.93	1.22	0.47	0.25	0.19	0.05	-2.23E+00	1.47E-274	Down	-4.26E-01	1.72E-18		3.91E-01	2.44E-01		-9.99E-01	6.40E-03		-3.79E-01	6.35E-01		-2.26E+00	4.68E-03		Unigene36103_All//gi|225459996|ref|XP_002270813.1|//0.00E+00//PREDICTED: sucrose-phosphate synthase 1 [Vitis vinifera] >gi|58825798|gb|AAW82754.1| sucrose-phosphate synthase 1 [Vitis vinifera]	Unigene36103_All//0.00E+00//AT4G10120| ATSPS4F; sucrose-phosphate synthase/ transferase, transferring glycosyl groups	Unigene36103_All//1.00E-06//TC137668		ko00500|Starch and sucrose metabolism		nr +
Unigene36104_All	2095	13.49	4.79	7.22	0.19	0.41	0.37	0.04	0.00	0.00	-1.49E+00	9.70E-39	Down	-9.02E-01	5.30E-17		1.11E+00	1.63E-01		9.46E-01	2.73E-01		-5.34E+00	4.03E-01		-5.34E+00	3.58E-01		Unigene36104_All//gi|225459996|ref|XP_002270813.1|//0.00E+00//PREDICTED: sucrose-phosphate synthase 1 [Vitis vinifera] >gi|58825798|gb|AAW82754.1| sucrose-phosphate synthase 1 [Vitis vinifera]	Unigene36104_All//0.00E+00//AT4G10120| ATSPS4F; sucrose-phosphate synthase/ transferase, transferring glycosyl groups			ko00500|Starch and sucrose metabolism		nr +
Unigene36106_All	843	16.20	12.62	15.10	33.68	20.47	31.07	54.07	45.51	26.98	-3.60E-01	1.98E-02		-1.02E-01	5.85E-01		-7.19E-01	1.22E-14		-1.16E-01	3.40E-01		-2.48E-01	5.02E-04		-1.00E+00	4.82E-42	Down	Unigene36106_All//gi|18650620|gb|AAL75909.1|//7.00E-56//AT3g50440/T20E23_40 [Arabidopsis thaliana] >gi|22635406|gb|AAM88295.1| At3g50440/T20E23_40 [Arabidopsis thaliana]	Unigene36106_All//4.00E-57//AT3G50440| MES10 (METHYL ESTERASE 10); hydrolase/ hydrolase, acting on ester bonds / methyl jasmonate esterase	Unigene36106_All//0.00E+00//TC147531		ko00901|Indole alkaloid biosynthesis		nr -
Unigene36110_All	1067	1.32	2.85	0.50	4.11	4.39	1.69	3.01	2.59	1.98	1.11E+00	2.37E-03		-1.41E+00	2.12E-02		9.53E-02	8.07E-01		-1.28E+00	1.15E-05	Down	-2.20E-01	5.33E-01		-6.06E-01	4.21E-02		Unigene36110_All//gi|75272473|sp|Q8L8B8.1|LOG3_ARATH//2.00E-63//RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG3; AltName: Full=Protein LONELY GUY 3	Unigene36110_All//3.00E-64//AT2G37210| Encodes a protein of unknown function. It has been crystallized and shown to be structurally almost identical to the protein encoded by At5g11950.	Unigene36110_All//0.00E+00//TC157691				nr +
Unigene36113_All	1329	39.60	16.47	36.50	28.19	31.53	32.22	10.34	4.18	7.43	-1.27E+00	9.11E-56	Down	-1.18E-01	1.59E-01		1.62E-01	6.24E-02		1.93E-01	2.42E-02		-1.31E+00	3.07E-19	Down	-4.76E-01	2.96E-04		Unigene36113_All//gi|297851624|ref|XP_002890693.1|//1.00E-98//AT-IE [Arabidopsis lyrata subsp. lyrata] >gi|297339535|gb|EFH69952.1| AT-IE [Arabidopsis lyrata subsp. lyrata]	Unigene36113_All//1.00E-98//AT1G31860| AT-IE; phosphoribosyl-AMP cyclohydrolase/ phosphoribosyl-ATP diphosphatase	Unigene36113_All//0.00E+00//TC146771		ko00340|Histidine metabolism		nr +
Unigene36114_All	1779	2.24	1.74	2.07	5.74	7.07	4.34	3.90	1.34	1.84	-3.64E-01	2.44E-01		-1.14E-01	7.21E-01		3.00E-01	6.78E-02		-4.03E-01	2.67E-02		-1.54E+00	9.74E-13	Down	-1.09E+00	5.02E-08	Down	Unigene36114_All//gi|283488499|gb|ADB22471.1|//0.00E+00//UDP-D-glucuronic acid 4-epimerase [Gossypium hirsutum]	Unigene36114_All//0.00E+00//AT4G00110| GAE3 (UDP-D-GLUCURONATE 4-EPIMERASE 3); UDP-glucuronate 4-epimerase/ catalytic	Unigene36114_All//0.00E+00//TC137614		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene36117_All	1753	34.14	4.57	6.17	19.86	15.09	7.83	11.58	4.89	6.95	-2.90E+00	4.92E-190	Down	-2.47E+00	1.27E-153	Down	-3.97E-01	2.17E-06		-1.34E+00	6.36E-44	Down	-1.24E+00	4.68E-26	Down	-7.35E-01	1.04E-11		Unigene36117_All//gi|3540181|gb|AAC34331.1|//1.00E-129//Unknown protein [Arabidopsis thaliana] >gi|40823449|gb|AAR92283.1| At1g10020 [Arabidopsis thaliana] >gi|46518421|gb|AAS99692.1| At1g10020 [Arabidopsis thaliana]	Unigene36117_All//6.00E-158//AT4G29310| unknown protein	Unigene36117_All//0.00E+00//TC144255				nr +
Unigene3612_All	974	54.31	31.73	33.24	64.24	51.19	52.40	60.08	31.28	27.98	-7.75E-01	2.72E-25		-7.08E-01	7.13E-21		-3.27E-01	7.46E-08		-2.94E-01	5.67E-06		-9.42E-01	4.02E-47		-1.10E+00	1.27E-62	Down	Unigene3612_All//gi|224081865|ref|XP_002306507.1|//1.00E-103//porin/voltage-dependent anion-selective channel protein [Populus trichocarpa] >gi|222855956|gb|EEE93503.1| porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	Unigene3612_All//2.00E-95//AT5G67500| VDAC2 (VOLTAGE DEPENDENT ANION CHANNEL 2); voltage-gated anion channel	Unigene3612_All//0.00E+00//TC155915			GO:0005244//GO:0006811//GO:0009526//GO:0030312//GO:0031966//GO:0051707	nr -
Unigene36120_All	1569	188.07	662.93	357.61	135.38	175.14	244.73	64.03	124.75	51.92	1.82E+00	0.00E+00	Up	9.27E-01	0.00E+00		3.72E-01	5.69E-41		8.54E-01	1.01E-227		9.62E-01	2.07E-161		-3.02E-01	2.12E-11		Unigene36120_All//gi|87240834|gb|AB032692.1|//1.00E-100//2OG-Fe(II) oxygenase [Medicago truncatula]	Unigene36120_All//3.00E-90//AT1G03400| 2-oxoglutarate-dependent dioxygenase, putative	Unigene36120_All//0.00E+00//TC164157		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene36121_All	845	66.69	73.10	73.04	37.67	54.12	68.68	19.01	37.44	39.04	1.32E-01	6.68E-02		1.31E-01	8.29E-02		5.23E-01	5.13E-13		8.67E-01	1.29E-35		9.78E-01	1.94E-27		1.04E+00	3.43E-32	Up	Unigene36121_All//gi|224993380|gb|ACN76469.1|//9.00E-27//CBL-interacting protein kinase 12 [Populus euphratica]	Unigene36121_All//8.00E-26//AT1G01140| CIPK9 (CBL-INTERACTING PROTEIN KINASE 9); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene36121_All//0.00E+00//gi|164348830|gb|EX165283.1|EX165283				nr +
Unigene36122_All	1052	18.85	36.22	27.13	22.82	25.70	36.79	67.36	86.89	154.20	9.42E-01	2.59E-25		5.25E-01	4.53E-07		1.71E-01	1.32E-01		6.89E-01	2.75E-16		3.67E-01	2.95E-14		1.19E+00	3.06E-194	Up	Unigene36122_All//gi|297812691|ref|XP_002874229.1|//2.00E-63//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320066|gb|EFH50488.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36122_All//2.00E-37//AT5G24870| zinc finger (C3HC4-type RING finger) family protein	Unigene36122_All//0.00E+00//TC152905				nr -
Unigene36126_All	422	0.99	1.68	0.38	4.60	4.65	0.96	3.11	0.40	1.23	7.61E-01	3.62E-01		-1.39E+00	2.80E-01		1.48E-02	9.89E-01		-2.26E+00	1.51E-05	Down	-2.97E+00	8.34E-06	Down	-1.34E+00	9.65E-03		Unigene36126_All//gi|18421483|ref|NP_568529.1|//1.00E-11//iqd33 (IQ-domain 33); calmodulin binding [Arabidopsis thaliana]	Unigene36126_All//6.00E-13//AT5G35670| iqd33 (IQ-domain 33); calmodulin binding	Unigene36126_All//2.00E-105//C0105172				nr +
Unigene36127_All	1600	11.09	4.47	8.52	42.37	31.19	12.05	17.49	2.22	6.75	-1.31E+00	2.54E-20	Down	-3.80E-01	6.10E-03		-4.42E-01	1.74E-14		-1.81E+00	3.48E-132	Down	-2.98E+00	1.30E-111	Down	-1.37E+00	1.11E-42	Down	Unigene36127_All//gi|18421483|ref|NP_568529.1|//9.00E-79//iqd33 (IQ-domain 33); calmodulin binding [Arabidopsis thaliana]	Unigene36127_All//4.00E-80//AT5G35670| iqd33 (IQ-domain 33); calmodulin binding	Unigene36127_All//0.00E+00//TC144139				nr +
Unigene3613_All	990	43.92	4.40	12.80	22.89	25.57	16.42	11.10	12.71	4.02	-3.32E+00	1.77E-157	Down	-1.78E+00	2.13E-73	Down	1.59E-01	1.83E-01		-4.79E-01	1.82E-05		1.95E-01	2.20E-01		-1.46E+00	6.04E-19	Down	Unigene3613_All//gi|15235150|ref|NP_193705.1|//5.00E-48//RING; protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene3613_All//6.00E-44//AT4G19700| RING; protein binding / zinc ion binding	Unigene3613_All//6.00E-175//gi|11206137|gb|BF275067.1|BF275067			GO:0005488//GO:0009725	nr -
Unigene36133_All	1398	4.57	3.73	3.62	21.06	14.95	16.38	4.96	5.11	1.80	-2.91E-01	2.36E-01		-3.36E-01	1.86E-01		-4.94E-01	5.79E-08		-3.63E-01	2.16E-04		4.37E-02	8.48E-01		-1.47E+00	2.73E-12	Down	Unigene36133_All//gi|37202104|gb|AAQ89667.1|//3.00E-87//At5g25170 [Arabidopsis thaliana]	Unigene36133_All//2.00E-87//AT5G25170| unknown protein	Unigene36133_All//0.00E+00//TC152541				nr +
Unigene36134_All	1290	52.24	110.06	65.72	63.18	65.21	73.35	10.68	17.37	7.44	1.08E+00	9.93E-115	Up	3.31E-01	9.70E-09		4.58E-02	5.50E-01		2.15E-01	4.37E-05		7.01E-01	1.72E-11		-5.22E-01	7.05E-05		Unigene36134_All//gi|15238156|ref|NP_199575.1|//2.00E-58//NF-YB2 (NUCLEAR FACTOR Y, SUBUNIT B2); transcription factor [Arabidopsis thaliana] >gi|75262442|sp|Q9FGJ3.1|NFYB2_ARATH RecName: Full=Nuclear transcription factor Y subunit B-2; Short=AtNF-YB-2; AltName: Full=Transcriptional activator HAP3B >gi|14326580|gb|AAK60334.1|AF385744_1 AT5g47640/MNJ7_23 [Arabidopsis thaliana] >gi|18700234|gb|AAL77727.1| AT5g47640/MNJ7_23 [Arabidopsis thaliana]	Unigene36134_All//6.00E-55//AT5G47640| NF-YB2 (NUCLEAR FACTOR Y, SUBUNIT B2); transcription factor	Unigene36134_All//0.00E+00//TC168815	CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication		nr +
Unigene36137_All	1109	93.37	143.14	126.95	19.49	36.89	41.54	9.95	18.50	18.11	6.17E-01	7.17E-50		4.43E-01	8.05E-24		9.20E-01	1.22E-30		1.09E+00	2.39E-41	Up	8.95E-01	1.03E-15		8.64E-01	6.46E-15		Unigene36137_All//gi|19310484|gb|AAL84976.1|//9.00E-98//AT3g29240/MXO21_9 [Arabidopsis thaliana] >gi|22634969|gb|AAM98077.1| AT3g29240/MXO21_9 [Arabidopsis thaliana] >gi|28416521|gb|AAO42791.1| AT3g29240/MXO21_9 [Arabidopsis thaliana]	Unigene36137_All//8.00E-95//AT3G29240| unknown protein	Unigene36137_All//0.00E+00//TC130195				nr +
Unigene36139_All	2055	8.40	3.48	4.07	17.11	11.75	14.94	14.28	4.23	6.38	-1.27E+00	6.18E-19	Down	-1.05E+00	1.97E-13	Down	-5.43E-01	4.49E-11		-1.96E-01	4.12E-02		-1.76E+00	9.55E-62	Down	-1.16E+00	1.30E-34	Down	Unigene36139_All//gi|46095227|gb|AAS80150.1|//0.00E+00//ACT11D09.4 [Cucumis melo]	Unigene36139_All//8.00E-173//AT1G10270| GRP23 (GLUTAMINE-RICH PROTEIN23); binding	Unigene36139_All//0.00E+00//TC175732				nr +
Unigene3614_All	1041	34.33	31.69	27.78	43.98	45.05	51.11	60.03	27.26	39.11	-1.16E-01	2.46E-01		-3.06E-01	1.17E-03		3.49E-02	7.50E-01		2.17E-01	3.26E-03		-1.14E+00	2.13E-68	Down	-6.18E-01	2.24E-25		Unigene3614_All//gi|30682715|ref|NP_180103.2|//8.00E-72//carbohydrate binding [Arabidopsis thaliana]	Unigene3614_All//8.00E-63//AT2G25310| carbohydrate binding	Unigene3614_All//0.00E+00//TC148946			GO:0005488//GO:0008238//GO:0031410//GO:0043231	nr -
Unigene36140_All	2216	1.18	0.48	0.50	1.80	1.04	1.14	2.63	0.43	0.86	-1.30E+00	1.23E-03		-1.23E+00	3.28E-03		-7.89E-01	6.01E-03		-6.56E-01	3.23E-02		-2.60E+00	1.14E-20	Down	-1.61E+00	6.91E-12	Down	Unigene36140_All//gi|46095227|gb|AAS80150.1|//0.00E+00//ACT11D09.4 [Cucumis melo]	Unigene36140_All//0.00E+00//AT1G10270| GRP23 (GLUTAMINE-RICH PROTEIN23); binding	Unigene36140_All//0.00E+00//TC175732				nr +
Unigene36141_All	1303	8.83	5.29	5.48	7.03	7.27	5.27	2.82	0.96	0.18	-7.40E-01	9.97E-06		-6.90E-01	6.88E-05		4.71E-02	8.27E-01		-4.17E-01	3.10E-02		-1.55E+00	3.48E-07	Down	-3.94E+00	6.32E-20	Down	Unigene36141_All//gi|115457076|ref|NP_001052138.1|//5.00E-63//Os04g0166600 [Oryza sativa Japonica Group] >gi|113563709|dbj|BAF14052.1| Os04g0166600 [Oryza sativa Japonica Group]	Unigene36141_All//4.00E-47//AT1G19330| unknown protein	Unigene36141_All//0.00E+00//gi|78331127|gb|DT551401.1|DT551401				nr +
Unigene36142_All	1231	3.66	5.56	5.49	4.98	4.64	4.70	6.70	6.01	3.33	6.04E-01	7.16E-03		5.88E-01	1.27E-02		-1.00E-01	7.32E-01		-8.39E-02	7.49E-01		-1.56E-01	4.46E-01		-1.01E+00	2.18E-08	Down	Unigene36142_All//gi|22326767|ref|NP_196828.2|//6.00E-88//transcription regulator [Arabidopsis thaliana]	Unigene36142_All//3.00E-89//AT5G13240| transcription regulator	Unigene36142_All//0.00E+00//TC155292				nr +
Unigene36143_All	1587	4.85	2.91	5.07	118.68	107.82	93.43	19.85	10.96	8.71	-7.38E-01	4.28E-04		6.41E-02	7.74E-01		-1.39E-01	9.57E-05		-3.45E-01	2.38E-22		-8.57E-01	4.26E-22		-1.19E+00	2.31E-38	Down	Unigene36143_All//gi|297817972|ref|XP_002876869.1|//1.00E-154//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322707|gb|EFH53128.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36143_All//3.00E-155//AT2G03200| aspartyl protease family protein	Unigene36143_All//0.00E+00//TC138272				nr +
Unigene36144_All	1329	9.05	6.06	7.97	19.98	18.37	23.55	22.08	10.63	12.83	-5.79E-01	3.74E-04		-1.84E-01	3.30E-01		-1.21E-01	3.17E-01		2.37E-01	1.76E-02		-1.05E+00	8.01E-29	Down	-7.83E-01	2.48E-18		Unigene36144_All//gi|8778482|gb|AAF79490.1|AC022492_34//4.00E-12//F1L3.4 [Arabidopsis thaliana]	Unigene36144_All//6.00E-08//AT5G42905| nucleic acid binding / ribonuclease H	Unigene36144_All//0.00E+00//ES799295				nr -

Unigene36146_All	430	31.03	11.55	37.65	18.54	13.53	8.93	24.09	10.59	4.82	-1.43E+00	1.81E-17	Down	2.79E-01	6.34E-02		-4.54E-01	2.24E-02		-1.05E+00	2.42E-07	Down	-1.19E+00	9.59E-13	Down	-2.32E+00	8.13E-33	Down	Unigene36146_All//gi|15237158|ref|NP_200058.1|//4.00E-50//MATE efflux protein-related [Arabidopsis thaliana]	Unigene36146_All//3.00E-51//AT5G52450| MATE efflux protein-related	Unigene36146_All//3.00E-144//TC160792				nr -
Unigene36147_All	1855	37.88	14.67	42.17	22.85	12.92	13.59	29.45	17.33	7.50	-1.37E+00	1.09E-83	Down	1.55E-01	1.63E-02		-8.23E-01	2.59E-27		-7.50E-01	9.76E-21		-7.65E-01	3.61E-31		-1.97E+00	3.65E-138	Down	Unigene36147_All//gi|15237158|ref|NP_200058.1|//1.00E-175//MATE efflux protein-related [Arabidopsis thaliana]	Unigene36147_All//8.00E-177//AT5G52450| MATE efflux protein-related	Unigene36147_All//0.00E+00//TC158342				nr -
Unigene36148_All	848	7.77	5.02	3.70	11.75	9.99	6.60	9.02	3.55	2.49	-6.31E-01	5.76E-03		-1.07E+00	1.01E-05	Down	-2.34E-01	2.29E-01		-8.31E-01	2.82E-06		-1.35E+00	1.45E-11	Down	-1.86E+00	1.50E-18	Down	Unigene36148_All//gi|3702368|emb|CAA05054.1|//8.00E-60//alpha subunit of F-actin capping protein [Arabidopsis thaliana]	Unigene36148_All//2.00E-60//AT3G05520| F-actin capping protein alpha subunit family protein	Unigene36148_All//0.00E+00//TC142456				nr +
Unigene36149_All	1585	5.97	3.16	3.33	12.13	7.95	7.58	3.12	0.87	1.73	-9.17E-01	1.23E-06		-8.45E-01	1.38E-05		-6.09E-01	1.20E-07		-6.79E-01	2.86E-08		-1.84E+00	9.45E-12	Down	-8.48E-01	2.93E-04		Unigene36149_All//gi|297829078|ref|XP_002882421.1|//1.00E-123//alpha subunit of F-actin capping protein [Arabidopsis lyrata subsp. lyrata] >gi|297328261|gb|EFH58680.1| alpha subunit of F-actin capping protein [Arabidopsis lyrata subsp. lyrata]	Unigene36149_All//2.00E-122//AT3G05520| F-actin capping protein alpha subunit family protein	Unigene36149_All//0.00E+00//TC129838				nr +
Unigene36150_All	1987	1.82	0.33	0.78	1.91	1.06	1.09	2.11	3.49	3.49	-2.45E+00	4.20E-10	Down	-1.23E+00	3.96E-04	Down	-8.50E-01	3.99E-03		-8.04E-01	1.00E-02		7.29E-01	2.34E-04		7.28E-01	1.70E-04		Unigene36150_All//gi|224020979|ref|YP_002608212.1|//8.00E-88//apocytochrome b [Carica papaya] >gi|170522391|gb|ACB20501.1| apocytochrome b [Carica papaya]	Unigene36150_All//1.00E-56//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.	Unigene36150_All//0.00E+00//TC168148		ko00190|Oxidative phosphorylation		nr +
Unigene36152_All	1164	69.22	63.69	75.85	18.49	25.00	14.55	4.90	1.97	3.56	-1.20E-01	5.45E-02		1.32E-01	3.17E-02		4.35E-01	3.26E-06		-3.46E-01	3.50E-03		-1.31E+00	1.64E-08	Down	-4.62E-01	3.27E-02		Unigene36152_All//gi|15218435|ref|NP_177984.1|//2.00E-86//emb1473 (embryo defective 1473); structural constituent of ribosome [Arabidopsis thaliana] >gi|75314103|sp|Q9SY19.1|RK13_ARATH RecName: Full=50S ribosomal protein L13, chloroplastic; AltName: Full=CL13; AltName: Full=Protein EMBRYO DEFECTIVE 1473; Flags: Precursor >gi|4836870|gb|AAD30573.1|AC007260_4 50S Ribosomal protein L13 [Arabidopsis thaliana] >gi|7572808|emb|CAA60775.1| ribosomal protein L13 [Arabidopsis thaliana]	Unigene36152_All//9.00E-83//AT1G78630| emb1472 (embryo defective 1473); structural constituent of ribosome	Unigene36152_All//0.00E+00//TC161587		ko03010|Ribosome		nr -
Unigene36154_All	1078	1.02	1.93	1.38	4.07	6.17	7.21	1.26	0.27	0.07	9.19E-01	4.07E-02		4.41E-01	4.26E-01		6.00E-01	6.51E-03		8.25E-01	6.07E-05		-2.21E+00	1.58E-04	Down	-4.09E+00	7.07E-08	Down	Unigene36154_All//gi|18414255|ref|NP_568121.1|//1.00E-93//RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding [Arabidopsis thaliana] >gi|2723477|dbj|BAA24074.1| GTP-binding protein [Arabidopsis thaliana] >gi|7378638|emb|CAB83314.1| AtRab GTP-binding protein [Arabidopsis thaliana]	Unigene36154_All//2.00E-86//AT5G03530| RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding	Unigene36154_All//0.00E+00//TC161007				nr -
Unigene36155_All	756	8.44	4.22	5.85	3.89	4.01	2.63	5.98	3.10	2.16	-1.00E+00	2.38E-05		-5.30E-01	3.06E-02		4.41E-02	9.25E-01		-5.65E-01	1.34E-01		-9.51E-01	1.89E-04		-1.47E+00	2.40E-08	Down	Unigene36155_All//gi|18414255|ref|NP_568121.1|//2.00E-87//RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding [Arabidopsis thaliana] >gi|2723477|dbj|BAA24074.1| GTP-binding protein [Arabidopsis thaliana] >gi|7378638|emb|CAB83314.1| AtRab GTP-binding protein [Arabidopsis thaliana]	Unigene36155_All//9.00E-89//AT5G03530| RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding	Unigene36155_All//0.00E+00//TC157371				nr +
Unigene36156_All	1630	42.66	27.17	40.18	7.30	7.67	4.85	18.26	18.54	7.72	-6.51E-01	1.69E-24		-8.63E-02	2.43E-01		7.03E-02	7.44E-01		-5.91E-01	2.29E-04		2.18E-02	8.41E-01		-1.24E+00	7.55E-39	Down	Unigene36156_All//gi|18411840|ref|NP_565170.1|//1.00E-117//methyltransferase-related [Arabidopsis thaliana] >gi|75329938|sp|Q8LBV4.1|Y1814_ARATH RecName: Full=Uncharacterized methyltransferase At1g78140, chloroplastic; Flags: Precursor	Unigene36156_All//2.00E-117//AT1G78140| methyltransferase-related	Unigene36156_All//0.00E+00//C00791660		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00100|Steroid biosynthesis		nr +
Unigene36158_All	1247	17.12	4.88	6.45	10.19	8.20	4.93	6.98	5.06	7.06	-1.81E+00	1.33E-38	Down	-1.41E+00	5.84E-26	Down	-3.13E-01	4.80E-02		-1.05E+00	3.14E-11	Down	-4.65E-01	8.22E-03		1.56E-02	9.57E-01		Unigene36158_All//gi|119935833|gb|ABM06007.1|//2.00E-78//At5g17640 [Arabidopsis thaliana]	Unigene36158_All//1.00E-79//AT5G17640| unknown protein	Unigene36158_All//0.00E+00//gi|78332493|gb|DT552767.1|DT552767				nr -
Unigene36159_All	1959	14.80	3.44	4.35	6.87	5.59	3.02	6.26	6.06	3.50	-2.10E+00	1.36E-63	Down	-1.77E+00	1.41E-48	Down	-2.97E-01	5.47E-02		-1.18E+00	2.58E-14	Down	-4.68E-02	7.83E-01		-8.40E-01	4.13E-09		Unigene36159_All//gi|119935833|gb|ABM06007.1|//0.00E+00//At5g17640 [Arabidopsis thaliana]	Unigene36159_All//2.00E-179//AT5G17640| unknown protein	Unigene36159_All//0.00E+00//TC155368				nr +
Unigene3616_All	1468	11.80	11.91	8.49	16.83	18.91	20.21	11.15	8.43	5.51	1.35E-02	9.44E-01		-4.75E-01	6.04E-04		1.68E-01	1.35E-01		2.64E-01	9.31E-03		-4.03E-01	1.08E-03		-1.02E+00	5.16E-16	Down	Unigene3616_All//gi|32339703|gb|AAQ14331.1|AF283506.1|9.00E-72//MYC1 [Catharanthus roseus]	Unigene3616_All//7.00E-64//AT1G59640| ZCW32; DNA binding / transcription factor	Unigene3616_All//0.00E+00//TC151506	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0010468//GO:0043231	nr +
Unigene36160_All	987	35.46	34.45	39.98	43.51	41.24	50.38	44.64	29.01	22.28	-4.20E-02	6.80E-01		1.73E-01	6.81E-02		-7.72E-02	4.38E-01		2.12E-01	5.95E-03		-6.22E-01	8.16E-18		-1.00E+00	1.17E-40	Down	Unigene36160_All//gi|226505058|ref|NP_001146955.1|//2.00E-62//LOC100280564 [Zea mays] >gi|195665816|gb|ACG24738.1| trafficking protein particle complex protein 2 [Zea mays] >gi|195648512|gb|ACG43724.1| trafficking protein particle complex protein 2 [Zea mays]	Unigene36160_All//1.00E-67//AT1G08500| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: transport, ER to Golgi vesicle-mediated transport; LOCATED IN: intracellular; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Sedlin (InterPro:IPR006722), Longin-like (InterPro:IPR011012); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G20930.1); Has 437 Blast hits to 435 proteins in 138 species: Archae - 0; Bacteria - 0; Metazoa - 248; Fungi - 75; Plants - 53; Viruses - 0; Other Eukaryotes - 61 (source: NCBI BLink).	Unigene36160_All//0.00E+00//TC139456				nr +
Unigene36161_All	1775	15.65	3.05	16.53	26.16	22.47	19.24	19.27	7.44	8.91	-2.36E+00	4.00E-70	Down	7.87E-02	5.15E-01		-2.19E-01	3.93E-03		-4.43E-01	3.65E-09		-1.37E+00	2.19E-50	Down	-1.11E+00	1.59E-37	Down	Unigene36161_All//gi|8655992|gb|AAF78265.1|AC020576_9//0.00E+00//Contains similarity to aminoacylase from Sus scrofa domestica gi|S27010 and contains a peptidase M20 PF|01546 domain. ESTs gb|H76043, gb|AA394953, gb|AI995115, gb|AA651481 come from this gene [Arabidopsis thaliana] >gi|109946615|gb|ABG48486.1| At1g48820 [Arabidopsis thaliana]	Unigene36161_All//0.00E+00//AT1G44820| aminoacylase, putative / N-acyl-L-amino-acid amidohydrolase, putative	Unigene36161_All//0.00E+00//TC131818		ko00330|Arginine and proline metabolism		nr -
Unigene36162_All	1438	4.11	6.69	4.63	3.98	6.20	4.59	3.00	5.75	8.92	7.03E-01	1.44E-04		1.71E-01	5.09E-01		6.39E-01	5.00E-04		2.03E-01	4.49E-01		9.40E-01	2.45E-07		1.57E+00	4.68E-24	Up	Unigene36162_All//gi|197312901|gb|ACH63231.1|//6.00E-71//translation initiation factor [Rheum australe]	Unigene36162_All//3.00E-50//AT2G04520| eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative	Unigene36162_All//0.00E+00//TC165563				nr +
Unigene36164_All	1661	27.12	6.68	6.80	148.93	106.00	75.89	110.60	18.82	26.89	-2.02E+00	1.64E-93	Down	-2.00E+00	7.31E-89	Down	-4.91E-01	9.09E-63		-9.73E-01	1.60E-184		-2.55E+00	0.00E+00	Down	-2.04E+00	0.00E+00	Down	Unigene36164_All//gi|219810208|gb|ACL36352.1|//0.00E+00//fasciclin-like arabinogalactan protein [Gossypium hirsutum]	Unigene36164_All//6.00E-115//AT4G12730| FLA2 (FASCICLIN-LIKE ARABINOGALACTAN 2)	Unigene36164_All//0.00E+00//TC132215				nr +
Unigene36165_All	404	4.40	2.88	3.56	6.66	6.39	7.60	8.27	4.14	3.45	-6.10E-01	2.16E-01		-3.07E-01	5.62E-01		-5.87E-02	8.75E-01		1.91E-01	6.29E-01		-9.99E-01	1.01E-03		-1.26E+00	3.09E-05	Down			Unigene36165_All//4.00E-174//BF269144				
Unigene36166_All	1050	2.94	3.33	0.76	7.54	5.87	8.00	7.21	2.95	3.98	1.80E-01	5.92E-01		-1.95E+00	2.13E-06	Down	-3.62E-01	8.10E-02		8.49E-02	7.07E-01		-1.29E+00	8.89E-11	Down	-8.55E-01	3.95E-06				Unigene36166_All//0.00E+00//TC138241				
Unigene36167_All	1305	2.93	4.23	2.12	2.71	2.27	2.18	9.53	20.91	11.42	5.32E-01	3.68E-02		-4.64E-01	1.62E-01		-2.56E-01	4.76E-01		-3.14E-01	3.95E-01		1.13E+00	4.21E-30	Up	2.61E-01	4.54E-02		Unigene36167_All//gi|30695682|ref|NP_191845.2|//1.00E-142//esterase/lipase/thioesterase family protein [Arabidopsis thaliana]	Unigene36167_All//4.00E-143//AT3G62860| esterase/lipase/thioesterase family protein	Unigene36167_All//0.00E+00//TC135657		ko00561|Glycerolipid metabolism		nr +
Unigene36168_All	1568	19.69	10.24	11.34	68.78	34.33	25.15	53.39	7.92	14.30	-9.43E-01	9.82E-21		-7.96E-01	4.46E-15		-1.00E+00	1.07E-96	Down	-1.45E+00	2.90E-152	Down	-2.75E+00	0.00E+00	Down	-1.90E+00	7.69E-201	Down	Unigene36168_All//gi|79507883|ref|NP_196320.2|//1.00E-172//aspartic-type endopeptidase [Arabidopsis thaliana]	Unigene36168_All//4.00E-162//AT5G07030| aspartic-type endopeptidase	Unigene36168_All//0.00E+00//TC172009				nr +
Unigene36171_All	1398	30.31	12.00	28.42	49.14	41.50	47.88	14.64	12.35	13.25	-1.34E+00	5.59E-49	Down	-9.33E-02	3.50E-01		-2.44E-01	4.06E-05		-3.75E-02	6.45E-01		-2.46E-01	3.10E-02		-1.44E-01	2.20E-01		Unigene36171_All//gi|32815933|gb|AAP88351.1|//3.00E-48//At5g41960 [Arabidopsis thaliana]	Unigene36171_All//9.00E-47//AT5G41960| unknown protein	Unigene36171_All//0.00E+00//TC148701				nr +
Unigene36172_All	642	2.69	1.10	1.33	4.35	3.97	3.10	4.02	0.85	0.37	-1.28E+00	1.19E-02		-1.02E+00	5.26E-02		-1.31E-01	7.69E-01		-4.89E-01	2.17E-01		-2.25E+00	3.87E-08	Down	-3.43E+00	9.72E-13	Down	Unigene36172_All//gi|71480741|gb|AAB85402.2|//4.00E-56//beta-1,3-glucanase [Camellia sinensis]	Unigene36172_All//2.00E-44//AT1G66250| glycosyl hydrolase family 17 protein	Unigene36172_All//2.00E-100//TC132814		ko00500|Starch and sucrose metabolism		nr -
Unigene36173_All	1730	4.17	2.75	2.77	10.91	10.05	5.27	9.02	0.99	2.49	-6.00E-01	5.72E-03		-5.91E-01	9.17E-03		-1.19E-01	4.27E-01		-1.05E+00	2.02E-16	Down	-3.19E+00	1.04E-66	Down	-1.86E+00	5.71E-37	Down	Unigene36173_All//gi|71480741|gb|AAB85402.2|//0.00E+00//beta-1,3-glucanase [Camellia sinensis]	Unigene36173_All//0.00E+00//AT1G66250| glycosyl hydrolase family 17 protein	Unigene36173_All//0.00E+00//gi|164366783|gb|ES791181.1|ES791181		ko00500|Starch and sucrose metabolism		nr +
Unigene36174_All	1619	1.33	1.28	1.38	19.20	14.78	8.40	7.89	4.47	3.27	-4.62E-02	9.25E-01		6.01E-02	8.94E-01		-3.77E-01	2.69E-05		-1.19E+00	1.01E-32	Down	-8.20E-01	8.01E-09		-1.27E+00	9.72E-18	Down	Unigene36174_All//gi|297790413|ref|XP_002863099.1|//3.00E-33//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297795351|ref|XP_002865560.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308918|gb|EFH39338.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311395|gb|EFH41819.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36174_All//1.00E-30//AT5G42200| zinc finger (C3HC4-type RING finger) family protein	Unigene36174_All//0.00E+00//DW227527				nr +
Unigene36177_All	240	3.27	1.06	0.67	3.11	2.30	3.76	10.57	3.48	3.49	-1.63E+00	5.37E-02		-2.30E+00	1.79E-02		-4.40E-01	5.85E-01		2.74E-01	7.10E-01		-1.60E+00	2.15E-05	Down	-1.60E+00	1.31E-05	Down			Unigene36177_All//6.00E-110//TC148370				
Unigene36181_All	1353	9.82	3.82	6.49	2.36	3.31	1.50	3.31	1.36	2.50	-1.36E+00	2.71E-16	Down	-5.97E-01	1.88E-04		4.90E-01	9.12E-02		-6.50E-01	6.53E-02		-1.29E+00	1.16E-06	Down	-4.04E-01	1.07E-01		Unigene36181_All//gi|295881692|gb|ADG36590.1|//2.00E-87//ALCATRAZ/SPATULA-like protein [Prunus persica]	Unigene36181_All//2.00E-45//AT4G36930| SPT (SPATULA); DNA binding / transcription factor	Unigene36181_All//0.00E+00//TC173293	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr -

Unigene36182_All	1613	22.38	17.53	18.78	39.53	30.78	22.32	5.58	3.03	1.38	-3.53E-01	7.90E-05		-2.53E-01	7.98E-03		-3.61E-01	1.75E-09		-8.25E-01	2.50E-36		-8.81E-01	3.46E-07		-2.01E+00	4.75E-24	Down	Unigene36182_All//gi|18404466|ref|NP_565865.1|//3.00E-39//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565090|sp|Q80927.2|ATL2J_ARATH RecName: Full=RING-H2 finger protein ATL2J >gi|20197250|gb|AAC23649.2| Expressed protein [Arabidopsis thaliana] >gi|89111920|gb|ABD60732.1| At2g37580 [Arabidopsis thaliana]	Unigene36182_All//3.00E-30//AT2G37580| zinc finger (C3HC4-type RING finger) family protein	Unigene36182_All//0.00E+00//ES831775				nr -
Unigene36184_All	566	11.46	3.13	4.61	5.02	3.77	3.11	2.39	1.40	0.84	-1.87E+00	9.84E-13	Down	-1.31E+00	1.54E-07	Down	-4.11E-01	2.88E-01		-6.89E-01	6.76E-02		-7.69E-01	1.39E-01		-1.50E+00	3.72E-03		Unigene36184_All//gi|154813794|gb|ABS86962.1|//5.00E-12//omega-3 fatty acid desaturase [Descurainia sophia]	Unigene36184_All//3.00E-13//AT2G29980| FAD3 (FATTY ACID DESATURASE 3); omega-3 fatty acid desaturase	Unigene36184_All//1.00E-168//DT455847		ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene36185_All	1313	173.18	74.87	126.70	40.25	53.19	51.35	23.25	9.26	11.95	-1.21E+00	1.47E-222	Down	-4.51E-01	2.66E-39		4.02E-01	2.55E-12		3.51E-01	1.25E-08		-1.33E+00	7.76E-43	Down	-9.60E-01	1.60E-26		Unigene36185_All//gi|110725975|gb|ABG88131.1|//1.00E-153//chloroplast omega-3 fatty acid desaturase [Olea europaea]	Unigene36185_All//3.00E-133//AT3G11170| FAD7 (FATTY ACID DESATURASE 7); omega-3 fatty acid desaturase	Unigene36185_All//0.00E+00//TC146456		ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene36188_All	1960	0.56	0.80	1.49	1.65	1.53	2.14	1.57	2.26	3.01	5.16E-01	3.38E-01		1.41E+00	3.58E-04	Up	-1.12E-01	7.90E-01		3.75E-01	2.38E-01		5.22E-01	4.47E-02		9.34E-01	1.39E-05		Unigene36188_All//gi|225426280|ref|XP_002265207.1|//0.00E+00//PREDICTED: similar to 3-oxoacyl-[acyl-carrier-protein] synthase [Vitis vinifera]	Unigene36188_All//1.00E-174//AT5G46290| KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); catalytic/ fatty-acid synthase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene36188_All//0.00E+00//ES838267		ko00061|Fatty acid biosynthesis		nr -
Unigene36190_All	1081	226.13	216.41	273.24	130.69	134.56	135.03	74.20	68.90	33.28	-6.34E-02	7.88E-02		2.73E-01	3.36E-20		4.21E-02	4.37E-01		4.72E-02	3.89E-01		-1.07E-01	6.24E-02		-1.16E+00	2.51E-92	Down	Unigene36190_All//gi|164604996|dbj|BAF98294.1|//4.00E-90//2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [Hevea brasiliensis]	Unigene36190_All//8.00E-85//AT1G63970| ISPF; 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	Unigene36190_All//0.00E+00//gi|109889458|gb|DW518426.1|DW518426		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene36191_All	1527	0.82	2.22	2.02	2.35	2.12	2.90	2.24	2.68	2.11	1.43E+00	4.89E-05	Up	1.30E+00	6.31E-04	Up	-1.48E-01	6.82E-01		3.03E-01	3.45E-01		2.58E-01	3.92E-01		-8.59E-02	7.74E-01		Unigene36191_All//gi|15230381|ref|NP_188575.1|//1.00E-127//pseudouridine synthase family protein [Arabidopsis thaliana] >gi|75274073|sp|Q9LT72.1|PUS4_ARATH RecName: Full=RNA pseudourine synthase 4, mitochondrial; AltName: Full=RNA-uridine isomerase 4; AltName: Full=RNA pseudouridylate synthase 4; Flags: Precursor >gi|134031916|gb|AB045695.1| At3g19440 [Arabidopsis thaliana]	Unigene36191_All//6.00E-128//AT3G19440| pseudouridine synthase family protein	Unigene36191_All//0.00E+00//TC138007		ko00240|Pyrimidine metabolism		nr +
Unigene36192_All	1079	69.92	60.34	64.95	15.42	13.60	10.09	1.61	2.48	3.91	-2.13E-01	5.02E-04		-1.07E-01	1.28E-01		-1.82E-01	2.26E-01		-6.12E-01	3.74E-06		6.26E-01	7.24E-02		1.28E+00	1.70E-06	Up	Unigene36192_All//gi|8569098|gb|AAF76413.1|AC015445	10//3.00E-41//ESTs gb|F20048, gb|F20049 come from this gene [Arabidopsis thaliana]	Unigene36192_All//1.00E-33//AT1G50020| unknown protein	Unigene36192_All//0.00E+00//TC149297				nr +
Unigene36193_All	1232	16.61	34.47	27.84	17.06	13.16	10.23	12.59	8.04	7.31	1.05E+00	1.13E-33	Up	7.45E-01	5.42E-15		-3.74E-01	9.47E-04		-7.38E-01	2.59E-10		-6.48E-01	2.96E-07		-7.85E-01	3.64E-10		Unigene36193_All//gi|91694293|gb|AB541798.1|//1.00E-158//gamma-tocopherol methyltransferase [Gossypium hirsutum]	Unigene36193_All//9.00E-128//AT1G64970| G-TMT (GAMMA-TOCOPHEROL METHYLTRANSFERASE); tocopherol O-methyltransferase	Unigene36193_All//0.00E+00//gi|78323889|gb|DT544163.1|DT544163		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00100|Steroid biosynthesis		nr -
Unigene36195_All	1806	2.64	1.91	1.98	3.72	2.57	1.50	16.60	7.73	9.26	-4.67E-01	9.45E-02		-4.16E-01	1.56E-01		-5.33E-01	1.37E-02		-1.31E+00	1.21E-08	Down	-1.10E+00	1.41E-31	Down	-8.41E-01	4.83E-21		Unigene36195_All//gi|231903|sp|P29463.1|TPT_SOLTU//1.00E-149//RecName: Full=Triose phosphate/phosphate translocator, chloroplastic; Short=cTPT; AltName: Full=E29; Flags: Precursor >gi|21587|emb|CAA47430.1| triose phosphate translocator [Solanum tuberosum]	Unigene36195_All//5.00E-128//AT5G46110| APE2 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT 2); antiporter/ triose-phosphate transmembrane transporter	Unigene36195_All//0.00E+00//TC168729				nr -
Unigene36196_All	2496	5.76	3.86	3.05	9.60	13.82	11.24	19.21	2.24	8.17	-5.80E-01	8.30E-05		-9.18E-01	3.17E-09		5.26E-01	4.80E-10		2.27E-01	3.50E-02		-3.10E+00	1.60E-198	Down	-1.23E+00	2.22E-61	Down	Unigene36196_All//gi|9989057|gb|AAG10820.1|AC011808.8//7.00E-23//Hypothetical protein [Arabidopsis thaliana] >gi|38603812|gb|AAR24651.1| At1g16630 [Arabidopsis thaliana] >gi|110738771|dbj|BAF01309.1| Hypothetical protei [Arabidopsis thaliana]	Unigene36196_All//4.00E-11//AT1G16630| unknown protein	Unigene36196_All//0.00E+00//gi|164313113|gb|ES828100.1|ES828100				nr -
Unigene36197_All	2192	4.80	1.57	1.72	13.66	9.96	4.57	31.21	7.30	19.47	-1.61E+00	1.66E-16	Down	-1.48E+00	5.67E-14	Down	-4.56E-01	4.86E-07		-1.58E+00	4.13E-48	Down	-2.10E+00	2.09E-181	Down	-6.81E-01	9.91E-33		Unigene36197_All//gi|15219996|ref|NP_173716.1|//0.00E+00//armadillo/beta-catenin repeat family protein / U-box domain-containing protein [Arabidopsis thaliana] >gi|172045744|sp|Q8GUG9.2|PUB11_ARATH RecName: Full=U-box domain-containing protein 11; AltName: Full=Plant U-box protein 11	Unigene36197_All//0.00E+00//AT1G23030| armadillo/beta-catenin repeat family protein / U-box domain-containing protein	Unigene36197_All//0.00E+00//TC179229		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene36199_All	831	6.36	49.15	10.06	1.74	8.20	7.12	10.53	14.69	16.35	2.95E+00	9.36E-131	Up	6.62E-01	1.43E-03		2.24E+00	8.73E-19	Up	2.03E+00	1.47E-13	Up	4.80E-01	9.09E-04		6.34E-01	1.90E-06		Unigene36199_All//gi|31747031|gb|AAP57672.1|//2.00E-06//MutT-like protein [Cucumis sativus]	Unigene36199_All//5.00E-06//AT1G73540| atmudt21 (Arabidopsis thaliana Nudix hydrolase homolog 21); hydrolase	Unigene36199_All//0.00E+00//gi|48745654|gb|C0076173.1|C0076173				nr +
Unigene36200_All	1284	16.30	87.37	20.24	10.82	22.18	15.90	10.44	12.21	20.04	2.42E+00	1.01E-288	Up	3.12E-01	5.63E-03		1.04E+00	6.56E-26	Up	5.55E-01	2.95E-06		2.26E-01	9.39E-02		9.41E-01	1.13E-21		Unigene36200_All//gi|15221055|ref|NP_173266.1|//4.00E-54//atmudt4 (Arabidopsis thaliana Nudix hydrolase homolog 4); hydrolase >gi|68565940|sp|Q9LE73.1|NUDT4_ARATH RecName: Full=Nudix hydrolase 4; Short=ATNUDT4; AltName: Full=ADP-ribose pyrophosphatase; AltName: Full=NADH pyrophosphatase >gi|6714298|gb|AAF25994.1|AC013354_13 F15H18.18 [Arabidopsis thaliana] >gi|8671772|gb|AAF78378.1|AC069551_11 T10022.27 [Arabidopsis thaliana] >gi|27765008|gb|AAO23625.1| At1g18300 [Arabidopsis thaliana]	Unigene36200_All//2.00E-55//AT1G18300| atmudt4 (Arabidopsis thaliana Nudix hydrolase homolog 4); hydrolase	Unigene36200_All//0.00E+00//TC165592				nr -
Unigene36201_All	801	21.95	13.09	17.15	55.66	44.37	58.36	33.57	20.09	12.14	-7.45E-01	2.13E-08		-3.56E-01	1.11E-02		-3.27E-01	9.46E-06		6.83E-02	4.80E-01		-7.41E-01	6.04E-15		-1.47E+00	3.00E-45	Down			Unigene36201_All//0.00E+00//TC178122				
Unigene36206_All	625	5.53	11.43	2.98	1.99	2.87	3.76	7.17	1.07	2.10	1.05E+00	2.82E-06	Up	-8.90E-01	1.06E-02		5.24E-01	3.10E-01		9.15E-01	2.99E-02		-2.74E+00	5.94E-17	Down	-1.77E+00	1.54E-10	Down	Unigene36206_All//gi|225454428|ref|XP_002276498.1|//3.00E-48//PREDICTED: similar to Os11g0118600 [Vitis vinifera]	Unigene36206_All//3.00E-19//AT3G08600| unknown protein					nr -
Unigene36207_All	1595	2.00	1.24	1.57	3.22	4.27	1.59	3.53	1.91	2.55	-6.92E-01	4.56E-02		-3.51E-01	3.60E-01		4.10E-01	7.28E-02		-1.02E+00	9.42E-05	Down	-8.82E-01	8.40E-05		-4.69E-01	3.16E-02		Unigene36207_All//gi|145358849|ref|NP_199258.3|//1.00E-117//methyltransferase [Arabidopsis thaliana]	Unigene36207_All//4.00E-119//AT5G44450| methyltransferase	Unigene36207_All//0.00E+00//TC155452				nr -
Unigene36208_All	1098	47.84	63.54	51.60	46.64	49.77	44.38	3.50	21.28	7.73	4.10E-01	5.19E-11		1.09E-01	1.80E-01		9.38E-02	2.63E-01		-7.15E-02	4.40E-01		2.60E+00	1.46E-80	Up	1.14E+00	2.87E-10	Up	Unigene36208_All//gi|4966370|gb|AA034701.1|AC006341_29//7.00E-21//>F3009.30 [Arabidopsis thaliana] >gi|22655156|gb|AAM98168.1| expressed protein [Arabidopsis thaliana] >gi|30023742|gb|AAP13404.1| At1g16500 [Arabidopsis thaliana]	Unigene36208_All//4.00E-19//AT1G16500| unknown protein	Unigene36208_All//0.00E+00//gi|109886967|gb|DW515936.1|DW515936				nr +
Unigene36209_All	1544	8.54	8.20	8.79	6.19	8.54	9.62	27.41	12.80	19.22	-5.78E-02	7.25E-01		4.25E-02	8.03E-01		4.64E-01	1.83E-03		6.36E-01	7.41E-06		-1.10E+00	5.67E-44	Down	-5.12E-01	1.05E-12		Unigene36209_All//gi|145328256|ref|NP_001077874.1|//1.00E-176//UPS2 (UREIDE PERMEASE 2) [Arabidopsis thaliana] >gi|145359873|ref|NP_178451.2| UPS2 (UREIDE PERMEASE 2) [Arabidopsis thaliana] >gi|68566151|sp|Q97Q89.2|UPS2_ARATH RecName: Full=Ureide permease 2; Short=AtUPS2	Unigene36209_All//3.00E-165//AT2G03530| UPS2 (UREIDE PERMEASE 2)	Unigene36209_All//0.00E+00//CO112131				nr +
Unigene3621_All	2174	9.48	5.76	1.91	15.79	15.95	12.71	13.81	3.13	4.69	-7.20E-01	3.45E-09		-2.31E+00	4.79E-49	Down	1.48E-02	9.03E-01		-3.12E-01	5.92E-04		-2.14E+00	4.45E-82	Down	-1.56E+00	5.91E-55	Down	Unigene3621_All//gi|29029014|gb|AA064886.1|//0.00E+00//At4g13370 [Arabidopsis thaliana]	Unigene3621_All//0.00E+00//AT4G13370| unknown protein	Unigene3621_All//0.00E+00//TC175872				nr -
Unigene36210_All	1641	2.39	1.57	0.75	3.31	2.41	3.08	4.41	1.91	1.68	-6.03E-01	5.05E-02		-1.68E+00	1.27E-06	Down	-4.55E-01	7.10E-02		-1.02E-01	7.15E-01		-1.21E+00	2.29E-09	Down	-1.40E+00	6.36E-12	Down	Unigene36210_All//gi|255642813|gb|ACU21593.1|//1.00E-117//expressed protein 1 [Triticum aestivum]	Unigene36210_All//7.00E-137//AT3G07210| unknown protein	Unigene36210_All//0.00E+00//gi|13354230|gb|BG444578.1|BG444578				nr +
Unigene36213_All	935	2.41	1.19	0.74	5.01	6.30	2.46	2.22	1.61	0.94	-1.01E+00	1.81E-02		-1.70E+00	3.72E-04	Down	3.31E-01	2.06E-01		-1.02E+00	2.04E-04	Down	-4.62E-01	2.65E-01		-1.24E+00	1.64E-03		Unigene36213_All//gi|124359162|gb|ABN05685.1|//4.00E-38//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene36213_All//2.00E-21//ATMG00310| hypothetical protein	Unigene36213_All//7.00E-116//ES821533				nr -
Unigene36214_All	1609	1.59	3.40	2.55	3.56	3.15	3.51	4.52	3.97	4.11	1.09E+00	2.70E-05	Up	6.77E-01	3.11E-02		-1.79E-01	5.42E-01		-2.11E-02	9.53E-01		-1.86E-01	3.95E-01		-1.37E-01	5.27E-01		Unigene36214_All//gi|21553404|gb|AAM62497.1|//1.00E-142//26S proteasome regulatory particle chain RPT6-like protein [Arabidopsis thaliana]	Unigene36214_All//3.00E-140//AT4G27680| NSP1 protein, putative / intramitochondrial sorting protein, putative	Unigene36214_All//0.00E+00//gi|78343380|gb|DT563654.1|DT563654		ko00230|Purine metabolism		nr +
Unigene36215_All	967	5.46	3.98	5.01	8.35	8.19	8.27	14.73	10.16	4.57	-4.57E-01	8.15E-02		-1.25E-01	6.45E-01		-2.70E-02	9.06E-01		-1.37E-02	9.43E-01		-5.37E-01	4.82E-05		-1.69E+00	1.06E-29	Down	Unigene36215_All//gi|15231714|ref|NP_191519.1|//2.00E-33//NRPBB; DNA-directed RNA polymerase [Arabidopsis thaliana]	Unigene36215_All//8.00E-35//AT3G59600| NRPBB; DNA-directed RNA polymerase	Unigene36215_All//0.00E+00//gi|21089459|gb|BQ401772.1|BQ401772		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene36216_All	875	51.12	48.30	32.13	80.73	57.69	68.49	67.60	41.51	22.86	-8.21E-02	3.65E-01		-6.70E-01	3.76E-16		-4.85E-01	9.05E-18		-2.37E-01	1.18E-04		-7.04E-01	3.32E-29		-1.56E+00	3.50E-108	Down	Unigene36216_All//gi|15231714|ref|NP_191519.1|//2.00E-61//NRPBB; DNA-directed RNA polymerase [Arabidopsis thaliana]	Unigene36216_All//8.00E-63//AT3G59600| NRPBB; DNA-directed RNA polymerase	Unigene36216_All//0.00E+00//TC143820		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene36217_All	1826	3.84	4.66	3.67	1.91	3.79	4.85	38.14	3.52	8.44	2.80E-01	1.79E-01		-6.34E-02	7.89E-01		9.89E-01	3.44E-06		1.34E+00	2.08E-11	Up	-3.44E+00	0.00E+00	Down	-2.18E+00	1.76E-199	Down	Unigene36217_All//gi|297841569|ref|XP_002888666.1|//1.00E-155//exostosin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334507|gb|EFH64925.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36217_All//3.00E-151//AT1G68470| exostosin family protein	Unigene36217_All//0.00E+00//gi|48828183|gb|CO126573.1|CO126573				nr +
Unigene36220_All	1423	15.22	9.72	13.43	9.59	10.79	18.47	3.77	8.58	5.15	-6.47E-01	4.19E-08		-1.80E-01	1.76E-01		1.70E-01	3.00E-01		9.45E-01	6.28E-19		1.18E+00	7.78E-15	Up	4.49E-01	1.71E-02		Unigene36220_All//gi|164562231|gb|ABY61030.1|//2.00E-68//zinc finger-homeodomain protein 1 [Cucumis sativus]	Unigene36220_All//5.00E-42//AT5G39760| AtHB23 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 23); DNA binding / transcription factor	Unigene36220_All//0.00E+00//TC166659	zf-HD			nr +

Unigene36221_All	2823	1.67	1.04	1.43	2.52	1.22	1.68	8.07	7.54	4.52	-6.80E-01	1.39E-02		-2.19E-01	4.73E-01		-1.05E+00	2.72E-07	Down	-5.87E-01	6.89E-03		-9.92E-02	4.10E-01		-8.38E-01	4.10E-16		Unigene36221_All//gi|255588681|ref|XP_002534684.1|//9.00E-48//conserved hypothetical protein [Ricinus communis] >gi|223524768|gb|EEF27698.1| conserved hypothetical protein [Ricinus communis]		Unigene36221_All//0.00E+00//TC151270				nr +
Unigene36224_All	621	1.01	1.71	0.69	7.70	3.83	3.93	2.59	4.04	0.90	7.61E-01	2.48E-01		-5.60E-01	5.53E-01		-1.01E+00	8.21E-05	Down	-9.72E-01	3.50E-04		6.42E-01	7.50E-02		-1.53E+00	1.16E-03		Unigene36224_All//gi|222423859|dbj|BAH19894.1|//7.00E-29//AT5G14420 [Arabidopsis thaliana]	Unigene36224_All//9.00E-28//AT5G14420| RGLG2 (RING domain Ligase2); ubiquitin-protein ligase	Unigene36224_All//0.00E+00//gi|109875162|gb|DW504136.1|DW504136			GO:0006725//GO:0016020//GO:0042445	nr +
Unigene36225_All	1678	2.71	5.95	1.24	26.63	13.28	12.89	4.38	6.55	3.73	1.13E+00	1.85E-09	Up	-1.13E+00	1.65E-04	Down	-1.00E+00	2.90E-40	Down	-1.05E+00	5.85E-38	Down	5.79E-01	1.48E-04		-2.34E-01	2.43E-01		Unigene36225_All//gi|222423859|dbj|BAH19894.1|//1.00E-147//AT5G14420 [Arabidopsis thaliana]	Unigene36225_All//6.00E-151//AT5G14420| RGLG2 (RING domain Ligase2); ubiquitin-protein ligase	Unigene36225_All//0.00E+00//TC172813				nr +
Unigene36226_All	1341	34.22	33.06	34.03	11.14	18.41	16.00	2.08	13.18	4.13	-4.96E-02	6.15E-01		-7.90E-03	9.49E-01		7.24E-01	1.55E-12		5.22E-01	6.34E-06		2.66E+00	1.07E-62	Up	9.89E-01	9.82E-06		Unigene36226_All//gi|30696431|ref|NP_176255.2|//1.00E-147//ECHID (ENOYL-COA HYDRATASE/ISOMERASE D); catalytic/ naphthoate synthase [Arabidopsis thaliana] >gi|192571726|gb|ACF04808.1| At1g60550 [Arabidopsis thaliana]	Unigene36226_All//5.00E-142//AT1G60550| ECHID (ENOYL-COA HYDRATASE/ISOMERASE D); catalytic/ naphthoate synthase	Unigene36226_All//0.00E+00//ES822697		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene36228_All	785	1.00	0.90	0.95	0.76	1.18	0.86	1.29	0.91	3.40	-1.46E-01	8.37E-01		-7.42E-02	9.35E-01		6.37E-01	4.18E-01		1.81E-01	8.43E-01		-5.14E-01	4.07E-01		1.40E+00	6.86E-05	Up	Unigene36228_All//gi|224146489|ref|XP_002326924.1|//3.00E-72//global transcription factor group [Populus trichocarpa] >gi|222862899|gb|EEF00406.1| global transcription factor group [Populus trichocarpa]	Unigene36228_All//1.00E-71//AT1G06230| GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding	Unigene36228_All//1.00E-95//TC141211			GO:0008415//GO:0009292//GO:0009987//GO:0043231//GO:0048513	nr -
Unigene3623_All	2027	0.54	0.28	1.34	1.89	2.65	1.80	3.71	1.32	2.36	-9.79E-01	1.34E-01		1.31E+00	1.43E-03		4.86E-01	6.04E-02		-6.83E-02	8.47E-01		-1.49E+00	3.71E-13	Down	-6.55E-01	3.64E-04		Unigene3623_All//gi|224072881|ref|XP_002303925.1|//0.00E+00//RNA polymerase IV subunit [Populus trichocarpa] >gi|222841357|gb|EEE78904.1| RNA polymerase IV subunit [Populus trichocarpa]	Unigene3623_All//0.00E+00//AT2G40030| NRPD1B; DNA binding / DNA-directed RNA polymerase			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003676//GO:0006305//GO:0016246//GO:0034062//GO:0044451//GO:0055029	nr -
Unigene36231_All	3554	0.24	0.67	0.45	1.12	1.31	1.33	1.23	1.03	1.61	1.51E+00	5.37E-04	Up	9.33E-01	8.84E-02		2.22E-01	5.01E-01		2.51E-01	4.23E-01		-2.44E-01	4.08E-01		3.98E-01	6.92E-02		Unigene36231_All//gi|15221424|ref|NP_172113.1|//1.00E-123//GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding [Arabidopsis thaliana] >gi|30679613|ref|NP_849601.1| GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding [Arabidopsis thaliana] >gi|8841128|gb|AAF80229.1|AC025290_9 Contains similarity to a Ring3 protein from Homo sapiens gi|133157 and contains a bromodomain PF|00439. EST gb|F14211 comes from this gene [Arabidopsis thaliana]	Unigene36231_All//2.00E-97//AT1G06230| GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding	Unigene36231_All//0.00E+00//TC141211			GO:0005515	nr -
Unigene36236_All	933	17.05	14.88	27.57	35.19	44.59	33.21	37.93	29.83	14.77	-1.96E-01	1.94E-01		6.93E-01	3.95E-10		3.42E-01	1.02E-05		-8.35E-02	4.84E-01		-3.46E-01	1.73E-05		-1.36E+00	6.61E-53	Down	Unigene36236_All//gi|62752942|gb|AY98670.1|//6.00E-62//HDZip I protein [Glycine max]	Unigene36236_All//4.00E-28//AT3G01470| ATHB-1 (ARABIDOPSIS THALIANA HOMEOBOX 1); DNA binding / protein homodimerization/ sequence-specific DNA binding / transcription activator/ transcription factor	Unigene36236_All//0.00E+00//gi|109879064|gb|DW508034.1|DW508034	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene36237_All	1654	35.21	17.55	21.38	32.53	30.98	18.81	17.97	11.09	11.66	-1.00E+00	1.19E-42	Down	-7.20E-01	1.45E-23		-7.03E-02	4.24E-01		-7.90E-01	1.48E-28		-6.96E-01	8.12E-15		-6.24E-01	9.27E-13		Unigene36237_All//gi|18416788|ref|NP_567751.1|//1.00E-164//sucrase-related [Arabidopsis thaliana] >gi|21536780|gb|AAM61112.1| sucrase-like protein [Arabidopsis thaliana]	Unigene36237_All//5.00E-137//AT4G26620| sucrase-related	Unigene36237_All//0.00E+00//gi|48749721|gb|CO080240.1|CO080240				nr -
Unigene36238_All	2158	3.01	3.12	1.48	4.73	4.55	3.96	4.90	5.95	7.16	5.48E-02	8.15E-01		-1.02E+00	2.70E-05	Down	-5.73E-02	8.16E-01		-2.59E-01	1.88E-01		2.80E-01	5.76E-02		5.48E-01	9.19E-06		Unigene36238_All//gi|42415865|gb|AS15800.1|//1.00E-127//heat shock factor protein hsf8-related [Glycine max]	Unigene36238_All//1.00E-71//AT1G32330| ATHSFA1D; DNA binding / transcription factor	Unigene36238_All//0.00E+00//ES807393	HSF		GO:0031410	nr -
Unigene3624_All	701	43.14	14.46	15.42	59.76	52.56	76.15	61.70	31.00	26.99	-1.58E+00	8.07E-45	Down	-1.48E+00	1.60E-39	Down	-1.85E-01	2.68E-02		3.50E-01	6.49E-07		-9.93E-01	3.30E-38		-1.19E+00	1.18E-52	Down	Unigene3624_All//gi|192910854|gb|AC06535.1|//3.00E-63//60S ribosomal protein L27 [Elaeis guineensis]	Unigene3624_All//7.00E-64//AT4G15000| 60S ribosomal protein L27 (RPL27C)	Unigene3624_All//0.00E+00//gi|164320824|gb|ES826486.1|ES826486		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +
Unigene36242_All	1859	10.30	15.45	23.60	49.60	33.16	18.22	9.39	2.74	7.54	5.85E-01	7.08E-09		1.20E+00	2.98E-41	Up	-5.81E-01	5.35E-32		-1.44E+00	2.74E-129	Down	-1.78E+00	1.19E-37	Down	-3.16E-01	6.90E-03		Unigene36242_All//gi|21593371|gb|AM65320.1|//1.00E-114//mutT domain protein-like [Arabidopsis thaliana]	Unigene36242_All//2.00E-116//AT5G47240| atnudt8 (Arabidopsis thaliana Nudix hydrolase homolog 8); hydrolase	Unigene36242_All//0.00E+00//TC162318				nr -
Unigene36243_All	1548	0.78	0.82	0.38	2.51	2.76	2.19	2.32	1.00	3.19	7.40E-02	9.06E-01		-1.04E+00	1.14E-01		1.36E-01	7.05E-01		-1.98E-01	5.90E-01		-1.22E+00	4.10E-05	Down	4.59E-01	5.26E-02		Unigene36243_All//gi|297797804|ref|XP_002866786.1|//1.00E-169//guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312622|gb|EFH43045.1| guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36243_All//6.00E-159//AT4G38200| guanine nucleotide exchange family protein	Unigene36243_All//6.00E-31//BE053450		ko04626|Plant-pathogen interaction	GO:0005083//GO:0032011//GO:0044464	nr +
Unigene36244_All	1714	0.61	1.39	0.99	2.41	2.79	3.69	1.06	0.88	2.88	1.19E+00	4.89E-03		7.04E-01	1.81E-01		2.11E-01	5.21E-01		6.13E-01	8.95E-03		-2.73E-01	5.70E-01		1.44E+00	1.02E-08	Up	Unigene36244_All//gi|297797804|ref|XP_002866786.1|//1.00E-130//guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312622|gb|EFH43045.1| guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36244_All//2.00E-113//AT4G35380| guanine nucleotide exchange family protein	Unigene36244_All//3.00E-24//BE053450		ko04626|Plant-pathogen interaction		nr -
Unigene36246_All	1669	1.63	3.37	3.89	37.85	39.02	33.93	21.05	20.76	6.95	1.05E+00	4.15E-05	Up	1.26E+00	4.22E-07	Up	4.39E-02	6.06E-01		-1.57E-01	2.42E-02		-2.01E-02	8.42E-01		-1.60E+00	1.08E-66	Down	Unigene36246_All//gi|17978991|gb|AL47456.1|//5.00E-22//AT3g51720/T18N14_100 [Arabidopsis thaliana] >gi|21360437|gb|AAM47334.1| AT3g51720/T18N14_100 [Arabidopsis thaliana]	Unigene36246_All//9.00E-52//AT2G40480| unknown protein	Unigene36246_All//0.00E+00//TC137471				nr +
Unigene36248_All	2557	7.69	5.21	5.54	33.14	32.05	24.67	14.93	5.31	8.46	-5.62E-01	5.77E-06		-4.74E-01	2.33E-04		-4.81E-02	5.18E-01		-4.26E-01	4.64E-15		-1.49E+00	1.76E-63	Down	-8.20E-01	1.97E-25		Unigene36248_All//gi|297853576|ref|XP_002894669.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340511|gb|EFH70928.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36248_All//0.00E+00//AT1G56720| protein kinase family protein	Unigene36248_All//0.00E+00//TC158763		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0032559//GO:0043231	nr +
Unigene36250_All	1674	9.88	7.93	6.04	2.32	1.87	2.46	24.20	21.17	6.47	-3.17E-01	2.38E-02		-7.09E-01	5.54E-07		-3.10E-01	3.41E-01		8.10E-02	8.06E-01		-1.93E-01	1.41E-02		-1.90E+00	1.08E-97	Down	Unigene36250_All//gi|121309739|dbj|BAF44192.1|//1.00E-137//SNF1-related kinase [Solanum lycopersicum]	Unigene36250_All//9.00E-117//AT4G33950| OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase	Unigene36250_All//0.00E+00//TC159504				nr +
Unigene36251_All	2092	9.50	6.93	5.50	74.32	61.27	28.73	15.32	5.75	4.78	-4.56E-01	2.16E-04		-7.90E-01	8.04E-10		-2.79E-01	6.43E-14		-1.37E+00	4.00E-201	Down	-1.41E+00	2.50E-49	Down	-1.68E+00	2.56E-65	Down	Unigene36251_All//gi|82469976|gb|AB877236.1|//1.00E-172//patellin 1 [Cucurbita pepo]	Unigene36251_All//5.00E-132//AT1G72160| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene36251_All//0.00E+00//TC133727				nr +
Unigene36252_All	599	2.45	9.98	1.42	6.57	5.63	10.10	18.35	27.14	44.16	2.03E+00	6.00E-13	Up	-7.82E-01	1.75E-01		-2.22E-01	5.30E-01		6.21E-01	9.86E-03		5.65E-01	4.29E-06		1.27E+00	2.08E-35	Up	Unigene36252_All//gi|255574893|ref|XP_002528353.1|//2.00E-10//conserved hypothetical protein [Ricinus communis] >gi|223532221|gb|EEF34025.1| conserved hypothetical protein [Ricinus communis]		Unigene36252_All//2.00E-140//gi|189098396|gb|FG551548.1|FG551548				nr -
Unigene36253_All	1017	1.59	0.70	0.73	2.30	3.05	7.02	12.64	18.41	32.16	-1.19E+00	2.32E-02		-1.12E+00	4.20E-02		4.05E-01	2.94E-01		1.61E+00	5.96E-12	Up	5.43E-01	1.78E-06		1.35E+00	7.71E-48	Up	Unigene36253_All//gi|255574893|ref|XP_002528353.1|//2.00E-22//conserved hypothetical protein [Ricinus communis] >gi|223532221|gb|EEF34025.1| conserved hypothetical protein [Ricinus communis]	Unigene36253_All//9.00E-06//AT4G21865| unknown protein	Unigene36253_All//0.00E+00//gi|189098396|gb|FG551548.1|FG551548				nr -
Unigene36254_All	825	1.65	5.96	3.03	9.72	8.06	19.38	28.29	34.35	74.03	1.85E+00	1.23E-09	Up	8.80E-01	3.64E-02		-2.71E-01	2.13E-01		9.95E-01	9.96E-13		2.80E-01	2.52E-03		1.39E+00	1.26E-92	Up	Unigene36254_All//gi|117168113|gb|ABK32139.1|//2.00E-08//At4g21865 [Arabidopsis thaliana]	Unigene36254_All//2.00E-08//AT4G21865| unknown protein	Unigene36254_All//0.00E+00//gi|189098396|gb|FG551548.1|FG551548				nr -
Unigene36255_All	3355	2.29	0.47	0.46	5.84	4.29	1.84	6.05	1.76	1.38	-2.29E+00	3.28E-19	Down	-2.32E+00	1.36E-18	Down	-4.44E-01	1.30E-04		-1.66E+00	4.87E-34	Down	-1.78E+00	6.57E-44	Down	-2.13E+00	2.72E-57	Down	Unigene36255_All//gi|145339083|ref|NP_189852.2|//0.00E+00//nucleotide binding [Arabidopsis thaliana]	Unigene36255_All//0.00E+00//AT3G42660| nucleotide binding	Unigene36255_All//0.00E+00//gi|164291549|gb|ES833440.1|ES833440			GO:0031410	nr -
Unigene36256_All	948	4.30	15.82	13.20	0.53	0.22	0.62	0.36	0.97	0.76	1.88E+00	1.85E-28	Up	1.62E+00	7.60E-19	Up	-1.27E+00	2.22E-01		2.37E-01	7.98E-01		1.44E+00	3.26E-02		1.08E+00	1.41E-01		Unigene36256_All//gi|300608164|emb|CAZ86692.1|//1.00E-111//epoxide hydrolase 1 [Prunus persica]	Unigene36256_All//1.00E-96//AT2G26740| ATSEH (Arabidopsis thaliana soluble epoxide hydrolase); epoxide hydrolase	Unigene36256_All//0.00E+00//TC134055			GO:0006950//GO:0009725//GO:0016803	nr +
Unigene36257_All	1273	6.58	13.14	8.12	7.79	7.71	26.40	16.27	38.45	22.19	9.98E-01	1.28E-12		3.03E-01	1.19E-01		-1.45E-02	9.52E-01		1.76E+00	7.16E-62	Up	1.24E+00	2.48E-61	Up	4.47E-01	5.00E-07		Unigene36257_All//gi|300608164|emb|CAZ86692.1|//1.00E-127//epoxide hydrolase 1 [Prunus persica]	Unigene36257_All//2.00E-107//AT2G26740| ATSEH (Arabidopsis thaliana soluble epoxide hydrolase); epoxide hydrolase	Unigene36257_All//0.00E+00//TC130791				nr +
Unigene36258_All	415	0.00	0.00	0.13	0.00	0.17	0.00	3.36	2.01	0.48	null	null		7.00E+00	6.35E-01		7.38E+00	6.09E-01		null	null		-7.39E-01	1.46E-01		-2.81E+00	4.25E-06	Down			Unigene36258_All//6.00E-102//gi|48822483|gb|CO123796.1|CO123796				
Unigene36260_All	1572	7.36	21.63	9.11	13.82	15.86	14.02	19.04	24.54	17.11	1.56E+00	4.70E-49	Up	3.09E-01	5.26E-02		1.99E-01	8.45E-02		2.11E-02	8.97E-01		3.66E-01	1.86E-06		-1.55E-01	9.58E-02		Unigene36260_All//gi|297828674|ref|XP_002882219.1|//1.00E-72//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328059|gb|EFH58478.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36260_All//5.00E-63//AT3G02290| zinc finger (C3HC4-type RING finger) family protein	Unigene36260_All//0.00E+00//TC162472			GO:0009743//GO:0046914	nr +
Unigene36262_All	1577	0.86	3.95	0.81	3.60	12.95	12.11	3.32	4.27	6.47	2.20E+00	8.26E-15	Up	-9.01E-02	8.77E-01		1.85E+00	7.67E-44	Up	1.75E+00	4.68E-35	Up	3.60E-01	8.69E-02		9.60E-01	2.13E-09		Unigene36262_All//gi|281185543|gb|ADA54554.1|//3.00E-65//CONSTANS-like protein [Medicago truncatula] >gi|281185545|gb|ADA54555.1| CONSTANS-like protein [Medicago truncatula]	Unigene36262_All//9.00E-55//AT2G33500| zinc finger (B-box type) family protein	Unigene36262_All//2.00E-15//gi|48799412|gb|CO100726.1|CO100726	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene36268_All	2048	10.50	6.38	9.23	27.39	22.48	12.33	0.35	0.20	0.12	-7.18E-01	1.65E-09		-1.86E-01	1.60E-01		-2.85E-01	1.40E-05		-1.15E+00	1.92E-55	Down	-7.82E-01	3.10E-01		-1.59E+00	3.62E-02		Unigene36268_All//gi|226377504|gb|ACO52508.1|//1.00E-160//transcription factor APETALA2 [Vitis vinifera]	Unigene36268_All//8.00E-87//AT4G36920| AP2 (APETALA 2); transcription factor	Unigene36268_All//0.00E+00//TC150865	AP2-EREBP			nr -
Unigene36269_All	1599	75.59	115.92	110.03	17.01	51.77	37.06	7.43	10.87	17.74	6.17E-01	3.53E-58		5.42E-01	1.55E-42		1.61E+00	1.24E-146	Up	1.12E+00	1.48E-55	Up	5.49E-01	3.45E-06		1.26E+00	2.18E-37	Up	Unigene36269_All//gi|89000907|gb|AB059043.1|//4.00E-88//At2g39650 [Arabidopsis thaliana]	Unigene36269_All//3.00E-86//AT2G39650| unknown protein	Unigene36269_All//0.00E+00//TC152915			GO:0043231	nr -

Unigene36270_All	1727	3.51	2.85	4.72	4.04	3.31	3.48	1.54	0.48	0.76	-3.04E-01	2.24E-01		4.25E-01	4.89E-02		-2.87E-01	2.23E-01		-2.15E-01	3.89E-01		-1.67E+00	6.26E-06	Down	-1.02E+00	2.37E-03		Unigene36270_All//gi|60652317|gb|AX332231.1|//1.00E-135//plastid alpha-amylase [Malus x domestica]	Unigene36270_All//2.00E-134//AT1G69830| AMY3 (ALPHA-AMYLASE-LIKE 3); alpha-amylase	Unigene36270_All//0.00E+00//TC164469		ko00500|Starch and sucrose metabolism	GO:0016160//GO:0044238//GO:0046872	nr +
Unigene36274_All	1023	12.17	7.97	10.98	22.69	14.61	21.37	7.73	5.11	2.84	-6.10E-01	1.32E-04		-1.48E-01	4.09E-01		-6.35E-01	8.92E-10		-8.67E-02	5.44E-01		-5.98E-01	1.15E-03		-1.44E+00	1.38E-13	Down			Unigene36274_All//2.00E-128//gi|164246323|gb|ES836761.1|ES836761				
Unigene36275_All	1261	6.14	16.35	8.36	18.80	17.50	18.23	20.59	25.59	15.01	1.41E+00	4.13E-26	Up	4.45E-01	1.59E-02		-1.03E-01	4.44E-01		-4.47E-02	7.34E-01		3.14E-01	2.37E-04		-4.56E-01	9.17E-07		Unigene36275_All//gi|211906448|gb|ACJ11717.1|//1.00E-138//alpha-soluble NSF attachment protein [Gossypium hirsutum]	Unigene36275_All//2.00E-110//AT2G56190| ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN 2); binding / soluble NSF attachment protein	Unigene36275_All//0.00E+00//CO099805				nr -
Unigene36276_All	1592	8.41	9.77	8.03	14.86	19.25	14.64	11.66	5.30	28.10	2.16E-01	1.50E-01		-6.77E-02	6.96E-01		3.73E-01	4.80E-05		-2.20E-02	8.84E-01		-1.14E+00	8.17E-21	Down	1.27E+00	1.88E-59	Up	Unigene36276_All//gi|18395601|ref|NP_565304.1|//1.00E-158//ACR5; amino acid binding [Arabidopsis thaliana] >gi|79316674|ref|NP_001030965.1|ACR5; amino acid binding [Arabidopsis thaliana] >gi|222424419|dbj|BAH20165.1|AT2G03730 [Arabidopsis thaliana]	Unigene36276_All//2.00E-159//AT2G03730| ACR5; amino acid binding	Unigene36276_All//0.00E+00//TC165770			GO:0031406	nr +
Unigene36277_All	2067	2.58	2.94	4.12	3.95	4.63	3.78	3.19	1.31	8.50	1.88E-01	4.62E-01		6.75E-01	1.02E-03		2.29E-01	2.70E-01		-6.43E-02	7.78E-01		-1.28E+00	2.24E-09	Down	1.41E+00	5.42E-28	Up	Unigene36277_All//gi|42572033|ref|NP_974107.1|//0.00E+00//ACR4 (ACT REPEAT 4); amino acid binding [Arabidopsis thaliana]	Unigene36277_All//0.00E+00//AT1G69040| ACR4 (ACT REPEAT 4); amino acid binding	Unigene36277_All//0.00E+00//TC165770			GO:0003006//GO:0004672//GO:0006520//GO:0008356//GO:0009725//GO:0010102//GO:0016020//GO:0016023//GO:0031406	nr -
Unigene36279_All	1051	4.38	8.68	5.88	3.65	3.31	3.82	18.91	25.89	92.15	9.86E-01	4.07E-07		4.24E-01	9.39E-02		-1.41E-01	6.88E-01		6.75E-02	8.51E-01		4.53E-01	9.75E-07		2.29E+00	1.21E-290	Up	Unigene36279_All//gi|18416366|ref|NP_568237.1|//2.00E-22//protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] >gi|75301248|sp|Q8LAY8.1|P2C69_ARATH RecName: Full=Probable protein phosphatase 2C 69; Short=AtPP2C69 >gi|21593115|gb|AAM65064.1|protein phosphatase 2C-like protein [Arabidopsis thaliana]	Unigene36279_All//1.00E-23//AT5G10740| protein phosphatase 2C-related / PP2C-related	Unigene36279_All//2.00E-45//TC160328			GO:0004721//GO:0006464//GO:0043169//GO:0043234	nr -
Unigene3628_All	1006	0.31	1.51	1.01	15.10	14.38	13.60	56.28	10.47	21.35	2.28E+00	2.68E-04	Up	1.69E+00	2.74E-02		-7.11E-02	6.87E-01		-1.51E-01	3.79E-01		-2.43E+00	6.21E-180	Down	-1.40E+00	9.82E-88	Down	Unigene3628_All//gi|15238989|ref|NP_199660.1|//3.00E-21//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|106879149|gb|ABF82604.1|At5g48490 [Arabidopsis thaliana]	Unigene3628_All//4.00E-19//AT5G48490| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene3628_All//0.00E+00//TC163377			GO:0006810	nr -
Unigene36280_All	1102	33.66	67.96	61.13	25.04	24.87	29.84	17.84	19.42	30.15	1.01E+00	2.73E-55	Up	8.61E-01	7.13E-37		-9.80E-03	9.47E-01		2.53E-01	8.57E-03		1.22E-01	3.26E-01		7.57E-01	2.09E-19		Unigene36280_All//gi|30689144|ref|NP_194903.2|//6.00E-97//WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75303285|sp|Q8RXV3.1|P2C59_ARATH RecName: Full=Probable protein phosphatase 2C 59; Short=AtPP2C59; AltName: Full=Protein phosphatase 2C WIN2; Short=PP2C WIN2; AltName: Full=HopW1-1-interacting protein 2	Unigene36280_All//3.00E-98//AT4G31750| WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase	Unigene36280_All//0.00E+00//TC150612			GO:0004721//GO:0006464//GO:0006952//GO:0016020//GO:0031410//GO:0043169//GO:0043231//GO:0043234	nr -
Unigene36281_All	1221	12.04	34.32	15.44	14.97	20.56	27.96	81.72	137.64	84.87	1.51E+00	8.38E-58	Up	3.59E-01	7.47E-03		4.58E-01	6.67E-06		9.01E-01	1.39E-22		7.52E-01	2.23E-91		5.45E-02	3.04E-01		Unigene36281_All//gi|152287497|ref|NP_191142.1|//1.00E-120//EPC1 (ECTOPICALLY PARTING CELLS); UDP-glucosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene36281_All//2.00E-121//AT3G55830| EPC1 (ECTOPICALLY PARTING CELLS); UDP-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene36281_All//0.00E+00//TC134016			GO:0016757//GO:0043231//GO:0044444	nr +
Unigene36282_All	983	11.39	26.55	15.49	47.33	47.75	52.33	43.53	78.53	96.25	1.22E+00	2.32E-26	Up	4.44E-01	2.98E-03		1.26E-02	9.04E-01		1.45E-01	7.29E-02		8.51E-01	2.72E-52		1.14E+00	3.49E-106	Up	Unigene36282_All//gi|259490269|ref|NP_001159012.1|//6.00E-50//remorin [Zea mays] >gi|195628632|gb|ACG36146.1|remorin [Zea mays]	Unigene36282_All//8.00E-36//AT5G23750| remorin family protein	Unigene36282_All//2.00E-171//gi|21093198|gb|BQ405511.1|BQ405511			GO:0007154//GO:0016020//GO:0043168	nr +
Unigene36286_All	1046	13.01	6.54	11.86	17.67	21.17	16.97	3.88	8.99	9.98	-9.92E-01	2.37E-10		-1.33E-01	4.44E-01		2.61E-01	2.69E-02		-5.83E-02	6.94E-01		1.21E+00	5.10E-12	Up	1.36E+00	4.11E-16	Up	Unigene36286_All//gi|9758979|dbj|BAB09489.1|//6.00E-21//disease resistance protein-like [Arabidopsis thaliana]	Unigene36286_All//2.00E-18//AT5G45060| disease resistance protein (TIR-NBS-LRR class), putative	Unigene36286_All//2.00E-42//ES795903				nr +
Unigene36287_All	1503	9.85	39.17	25.40	4.01	6.97	10.67	30.10	80.14	177.67	1.99E+00	7.06E-119	Up	1.37E+00	3.84E-44	Up	7.96E-01	1.68E-06		1.41E+00	9.76E-22	Up	1.41E+00	4.00E-183	Up	2.56E+00	0.00E+00	Up	Unigene36287_All//gi|13937213|gb|AK50099.1|AF372961_1//1.00E-116//AT3g51000/F24M12_40 [Arabidopsis thaliana] >gi|6562252|emb|CAB62622.1|epoxide hydrolase-like protein [Arabidopsis thaliana] >gi|18491129|gb|AL69533.1|AT3g51000/F24M12_40 [Arabidopsis thaliana]	Unigene36287_All//2.00E-117//AT3G51000| epoxide hydrolase, putative	Unigene36287_All//0.00E+00//gi|13349623|gb|BG439973.1|BG439973				nr +
Unigene36289_All	1957	7.27	7.53	4.08	13.21	11.88	11.35	29.19	20.89	12.91	5.11E-02	7.42E-01		-8.33E-01	7.40E-08		-1.54E-01	1.92E-01		-2.19E-01	5.41E-02		-4.83E-01	9.24E-15		-1.18E+00	7.41E-68	Down	Unigene36289_All//gi|297817406|ref|XP_002876586.1|//0.00E+00//guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322424|gb|EFH52845.1|guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36289_All//0.00E+00//AT3G60860| guanine nucleotide exchange family protein	Unigene36289_All//0.00E+00//TC134586		ko04626|Plant-pathogen interaction	GO:0005083//GO:0009553//GO:0032011//GO:0043231//GO:0044444	nr -
Unigene3629_All	267	0.00	2.85	1.20	2.05	0.90	1.69	0.00	0.00	0.00	1.15E+01	1.77E-04	Up	1.02E+01	4.52E-02		-1.18E+00	2.25E-01		-2.79E-01	7.57E-01		null	null		null	null				Unigene3629_All//6.00E-61//TC178594				
Unigene36290_All	2029	2.53	2.42	0.79	4.93	5.04	3.63	7.11	1.69	3.61	-6.11E-02	8.19E-01		-1.68E+00	1.77E-08	Down	3.06E-02	8.94E-01		-4.44E-01	1.47E-02		-2.07E+00	3.13E-38	Down	-9.76E-01	2.42E-13		Unigene36290_All//gi|224079069|ref|XP_002305737.1|//0.00E+00//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222848701|gb|EEE86248.1|nucleobase ascorbate transporter [Populus trichocarpa]	Unigene36290_All//0.00E+00//AT2G34190| xanthine/uracil permease family protein	Unigene36290_All//0.00E+00//TC129603			GO:0005215//GO:0006810//GO:0044464	nr +
Unigene36291_All	1611	51.51	29.57	42.57	40.14	31.74	32.80	17.48	8.85	8.23	-8.01E-01	1.68E-41		-2.75E-01	3.13E-06		-3.39E-01	1.39E-08		-2.91E-01	4.71E-06		-9.82E-01	9.88E-25		-1.09E+00	7.17E-30	Down	Unigene36291_All//gi|18402572|ref|NP_566659.1|//1.00E-158//TGD2 (TRIGALACTOSYLDIACYLGLYCEROL2); lipid transporter/ phospholipid binding [Arabidopsis thaliana] >gi|75274119|sp|Q9LTR2.1|TGD2_ARATH RecName: Full=Protein TRIGALACTOSYLDIACYLGLYCEROL 2, chloroplastic; AltName: Full=ABC transporter I family member 15; Short=ABC transporter ABCI.15; Short=AtABCI15; Flags: Precursor >gi|15081676|gb|AAK82493.1|AT3g20320/MQC12_7 [Arabidopsis thaliana] >gi|20334840|gb|AAM16176.1|AT3g20320/MQC12_7 [Arabidopsis thaliana]	Unigene36291_All//4.00E-146//AT3G20320| TGD2 (TRIGALACTOSYLDIACYLGLYCEROL2); lipid transporter/ phospholipid binding	Unigene36291_All//0.00E+00//TC154112				nr -
Unigene36293_All	921	87.54	88.03	126.39	24.56	27.74	17.56	25.80	11.25	13.71	7.90E-03	9.20E-01		5.30E-01	3.21E-27		1.76E-01	1.32E-01		-4.84E-01	1.52E-05		-1.20E+00	1.27E-28	Down	-9.12E-01	3.30E-19		Unigene36293_All//gi|134142800|gb|AB061734.1|//1.00E-158//mitochondrial glycine decarboxylase complex P-protein [Populus tremuloides]	Unigene36293_All//3.00E-144//AT4G33010| AtGLDP1 (Arabidopsis thaliana glycine decarboxylase P-protein 1); catalytic/ glycine dehydrogenase (decarboxylating)/ pyridoxal phosphate binding	Unigene36293_All//0.00E+00//TC137790		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene36294_All	1028	261.25	177.64	331.52	38.52	41.37	32.38	6.00	2.64	2.75	-5.57E-01	4.61E-70		3.44E-01	1.36E-35		1.03E-01	2.87E-01		-2.51E-01	3.49E-03		-1.18E+00	6.62E-08	Down	-1.13E+00	1.27E-07	Down	Unigene36294_All//gi|134142800|gb|AB061734.1|//0.00E+00//mitochondrial glycine decarboxylase complex P-protein [Populus tremuloides]	Unigene36294_All//8.00E-164//AT4G33010| AtGLDP1 (Arabidopsis thaliana glycine decarboxylase P-protein 1); catalytic/ glycine dehydrogenase (decarboxylating)/ pyridoxal phosphate binding	Unigene36294_All//0.00E+00//TC137790		ko00260|Glycine, serine and threonine metabolism	GO:0006546//GO:0016642//GO:0048037	nr +
Unigene36295_All	756	2.08	6.64	2.11	3.36	5.83	2.15	31.32	42.35	18.81	1.68E+00	1.19E-08	Up	2.54E-02	9.81E-01		7.95E-01	4.39E-03		-6.44E-01	1.13E-01		4.35E-01	2.80E-07		-7.35E-01	1.65E-13				Unigene36295_All//4.00E-154//TC166566				
Unigene36296_All	1019	4.52	11.83	8.62	9.14	6.39	3.90	38.34	38.68	18.81	1.39E+00	3.39E-15	Up	9.32E-01	4.72E-06		-5.17E-01	3.63E-03		-1.23E+00	1.16E-10	Down	1.27E-02	9.03E-01		-1.03E+00	1.24E-37	Down			Unigene36296_All//0.00E+00//TC130741				
Unigene36297_All	1455	0.83	0.52	0.15	12.33	4.95	31.57	53.29	21.23	62.13	-6.63E-01	2.79E-01		-2.50E+00	1.15E-03		-1.32E+00	3.13E-25	Down	1.36E+00	7.42E-58	Up	-1.33E+00	1.09E-107	Down	2.21E-01	4.22E-06		Unigene36297_All//gi|27464177|gb|AA015998.1|AF516879_1//1.00E-129//expansin [Glycine max]	Unigene36297_All//3.00E-117//AT1G20190| ATEXPA11 (ARABIDOPSIS THALIANA EXPANSIN 11)	Unigene36297_All//0.00E+00//TC143599				nr +
Unigene36298_All	2124	1.06	4.75	0.93	4.13	2.33	2.30	3.94	6.91	3.45	2.16E+00	3.86E-23	Up	-1.91E-01	6.53E-01		-8.22E-01	4.77E-06		-8.46E-01	9.30E-06		8.09E-01	8.61E-10		-1.92E-01	3.15E-01		Unigene36298_All//gi|22328569|ref|NP_192893.2|//1.00E-176//bromo-adjacent homology (BAH) domain-containing protein [Arabidopsis thaliana]	Unigene36298_All//2.00E-148//AT4G11560| bromo-adjacent homology (BAH) domain-containing protein	Unigene36298_All//0.00E+00//TC176296		ko00270|Cysteine and methionine metabolism	GO:0006350	nr +
Unigene363_All	2318	14.36	16.85	13.81	18.91	39.43	47.72	69.04	44.18	52.14	2.31E-01	8.59E-03		-5.63E-02	6.20E-01		1.06E+00	5.68E-86	Up	1.34E+00	1.85E-135	Up	-6.44E-01	1.58E-66		-4.05E-01	7.70E-30		Unigene363_All//gi|157812633|gb|AB980356.1|//0.00E+00//phosphoenolpyruvate carboxylase [Gossypium hirsutum]	Unigene363_All//0.00E+00//AT3G14940| ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase	Unigene363_All//0.00E+00//TC131208		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene36300_All	2103	3.04	1.78	2.00	9.55	10.09	6.61	1.59	2.60	3.60	-7.68E-01	9.93E-04		-6.02E-01	1.38E-02		7.95E-02	5.94E-01		-5.29E-01	9.27E-06		7.13E-01	1.67E-03		1.18E+00	1.03E-09	Up	Unigene36300_All//gi|37983539|gb|AR006289.1|//0.00E+00//5-phosphoribosyl-1-pyrophosphate amidotransferase [Nicotiana tabacum]	Unigene36300_All//0.00E+00//AT4G34740| ATASE2 (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 2); amidophosphoribosyltransferase	Unigene36300_All//0.00E+00//gi|78322975|gb|DT543249.1|DT543249		ko00230|Purine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0006144//GO:0006163//GO:0009064//GO:0009887//GO:0016763//GO:0030312//GO:0043169//GO:0044435//GO:0051536	nr -
Unigene36301_All	1547	0.61	1.70	0.10	135.89	103.11	96.69	58.16	96.32	24.00	1.48E+00	2.96E-04	Up	-2.56E+00	4.40E-03		-3.98E-01	2.48E-36		-4.91E-01	2.19E-47		7.28E-01	1.28E-76		-1.28E+00	7.32E-121	Down	Unigene36301_All//gi|167858185|gb|ACA04033.1|//1.00E-164//galactinol synthase 4 [Populus trichocarpa x Populus deltoides]	Unigene36301_All//2.00E-157//AT2G47180| AtGolS1 (Arabidopsis thaliana galactinol synthase 1); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene36301_All//0.00E+00//TC134217				nr -
Unigene36303_All	2711	1.60	1.53	0.86	7.96	7.34	5.00	5.85	2.85	4.01	-6.38E-02	8.28E-01		-8.90E-01	3.45E-03		-1.16E-01	4.07E-01		-6.71E-01	5.02E-09		-1.04E+00	1.63E-15	Down	-5.44E-01	7.73E-06		Unigene36303_All//gi|289540923|gb|ADD09595.1|//1.00E-154//bZIP transcription factor [Trifolium repens]	Unigene36303_All//7.00E-124//AT4G39790| unknown protein	Unigene36303_All//0.00E+00//TC140351				nr -
Unigene36307_All	2639	2.50	1.67	1.15	4.79	6.41	3.87	5.26	0.62	0.97	-5.81E-01	1.12E-02		-1.12E+00	4.24E-06	Down	4.18E-01	1.22E-03		-3.10E-01	6.18E-02		-3.09E+00	1.28E-57	Down	-2.44E+00	2.33E-46	Down	Unigene36307_All//gi|205933555|gb|AC105081.1|//1.00E-166//receptor-like protein kinase HGK1 [Glycine max] >gi|206584431|gb|AC115357.1|RHG1 [Glycine max] >gi|226693207|dbj|BAH56603.1|receptor-like kinase [Glycine max]	Unigene36307_All//0.00E+00//AT3G51740| IMK2 (INFLORESCENCE MERISTEM RECEPTOR-LIKE KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene36307_All//0.00E+00//D8463276			GO:0006464//GO:0016301//GO:0031224//GO:0032559	nr -

Unigene36308_All	1294	10.63	61.40	26.79	39.77	103.31	52.74	22.81	12.79	23.71	2.53E+00	4.00E-215	Up	1.33E+00	1.25E-38	Up	1.38E+00	3.18E-189	Up	4.07E-01	2.75E-11		-8.34E-01	7.43E-20		5.58E-02	6.08E-01		Unigene36308_All//gi|297728309|ref|NP_001176518.1|//7.00E-44//Os11g0437600 [Oryza sativa Japonica Group] >gi|108864340|gb|ABA93251.2| uncharacterized plant-specific domain TIG801615 family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255680055|dbj|BAH95246.1| Os11g0437600 [Oryza sativa Japonica Group]	Unigene36308_All//2.00E-79//AT3G07350| unknown protein	Unigene36308_All//0.00E+00//TC160316				nr +
Unigene36309_All	1728	15.05	6.45	10.51	23.75	21.32	17.77	31.61	6.92	7.22	-1.22E+00	1.96E-26	Down	-5.18E-01	2.37E-06		-1.56E-01	7.63E-02		-4.19E-01	2.02E-07		-2.19E+00	1.73E-153	Down	-2.13E+00	1.31E-152	Down	Unigene36309_All//gi|141448072|gb|AB087612.1|//1.00E-155//chloroplast pentose phosphate transporter [Glycine max]	Unigene36309_All//5.00E-143//AT5G17630| glucose-6-phosphate/phosphate translocator, putative	Unigene36309_All//0.00E+00//gi|164329470|gb|ES805520.1|ES805520			GO:0006996//GO:0009555//GO:0015119//GO:0015291//GO:0016020//GO:0043231//GO:0051707	nr +
Unigene36312_All	3002	3.10	2.38	2.87	16.48	16.44	6.23	3.01	0.70	0.54	-3.82E-01	4.56E-02		-1.11E-01	6.34E-01		-3.50E-03	9.64E-01		-1.40E+00	1.47E-66	Down	-2.11E+00	7.27E-25	Down	-2.47E+00	6.83E-31	Down	Unigene36312_All//gi|32526673|dbj|BAC79196.1|//1.00E-162//bzip-like transcription factor-like protein [Oryza sativa Japonica Group] >gi|52076085|dbj|BAD46598.1| bzip-like transcription factor-like [Oryza sativa Japonica Group]	Unigene36312_All//6.00E-54//AT2G27090| unknown protein	Unigene36312_All//0.00E+00//TC166931				nr -
Unigene36313_All	2523	0.95	0.76	0.32	2.51	1.92	1.02	0.32	0.00	0.03	-3.22E-01	4.35E-01		-1.59E+00	4.53E-04	Down	-3.82E-01	1.05E-01		-1.30E+00	4.81E-08	Down	-8.31E+00	8.58E-06	Down	-3.33E+00	2.47E-04	Down	Unigene36313_All//gi|32526673|dbj|BAC79196.1|//1.00E-166//bzip-like transcription factor-like protein [Oryza sativa Japonica Group] >gi|52076085|dbj|BAD46598.1| bzip-like transcription factor-like [Oryza sativa Japonica Group]	Unigene36313_All//2.00E-62//AT2G27090| unknown protein	Unigene36313_All//0.00E+00//TC130437				nr +
Unigene36316_All	1536	0.58	0.96	1.07	0.13	0.22	0.26	3.63	1.36	1.53	7.24E-01	1.89E-01		8.92E-01	9.63E-02		7.90E-01	5.96E-01		1.03E+00	4.28E-01		-1.42E+00	2.80E-09	Down	-1.25E+00	4.70E-08	Down	Unigene36316_All//gi|124558720|gb|ABN13969.1|//1.00E-23//1-deoxy-D-xylulose 5-phosphate reductoisomerase [Gossypium barbadense]	Unigene36316_All//0.00E+00//AT5G62790| DXR (1-DEOXY-D-XYLULOSE 5-PHOSPHATE REDUCTOISOMERASE); 1-deoxy-D-xylulose-5-phosphate reductoisomerase	Unigene36316_All//0.00E+00//gi|21092733|gb|BQ405046.1|BQ405046		ko00900|Terpenoid backbone biosynthesis	GO:0006721//GO:0016616//GO:0043169	nr +
Unigene36318_All	972	17.01	42.12	25.42	34.64	29.65	50.65	38.89	59.30	48.61	1.31E+00	1.47E-45	Up	5.80E-01	2.76E-07		-2.25E-01	1.49E-02		5.48E-01	7.24E-14		6.09E-01	3.39E-22		3.22E-01	1.87E-06		Unigene36318_All//gi|289540943|gb|ADD09614.1|//2.00E-58//zinc ion binding protein [Trifolium repens]	Unigene36318_All//5.00E-34//AT4G39140| protein binding / zinc ion binding	Unigene36318_All//0.00E+00//TC135145			GO:0016020//GO:0046872	nr -
Unigene36319_All	1695	4.88	3.86	2.17	8.20	10.63	8.55	9.20	1.58	4.00	-3.39E-01	1.03E-01		-1.17E+00	5.68E-08	Down	3.74E-01	3.06E-03		6.09E-02	7.22E-01		-2.54E+00	8.10E-53	Down	-1.20E+00	7.65E-20	Down	Unigene36319_All//gi|857397|dbj|BAA09466.1|//0.00E+00//mitotic cyclin a2-type [Glycine max]	Unigene36319_All//1.00E-156//AT1G44110| CYCA1;1 (Cyclin A1;1); cyclin-dependent protein kinase regulator	Unigene36319_All//0.00E+00//EX172322			GO:0009987//GO:0043231	nr +
Unigene36320_All	1497	31.35	20.21	18.50	48.95	42.26	60.73	44.43	21.67	22.99	-6.34E-01	4.82E-16		-7.61E-01	5.37E-21		-2.12E-01	2.65E-04		3.11E-01	3.31E-09		-1.04E+00	1.70E-62	Down	-9.50E-01	8.37E-56		Unigene36320_All//gi|6685535|sp|P56820.1|EIF3D_ARATH//0.00E+00//RecName: Full=Eukaryotic translation initiation factor 3 subunit D; Short=eIF3d; AltName: Full=eIF-3-zeta; AltName: Full=p66 >gi|5262788|emb|CAB45893.1| translation initiation factor eIF3-like protein [Arabidopsis thaliana] >gi|7268895|emb|CAB79098.1| translation initiation factor eIF3-like protein [Arabidopsis thaliana] >gi|208879518|gb|ACI31304.1| At4g20980 [Arabidopsis thaliana] >gi|222423664|dbj|BAH19799.1| AT4G20980 [Arabidopsis thaliana]	Unigene36320_All//0.00E+00//AT4G20980| eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative	Unigene36320_All//0.00E+00//ES816965			GO:0006412//GO:0008135//GO:0009536	nr -
Unigene36328_All	935	4.48	3.09	3.76	7.62	8.03	4.35	5.83	3.84	2.05	-5.35E-01	7.31E-02		-2.52E-01	4.28E-01		7.57E-02	8.02E-01		-8.09E-01	1.64E-04		-6.02E-01	8.26E-03		-1.51E+00	2.84E-10	Down	Unigene36328_All//gi|186506028|ref|NP_565857.2|//3.00E-62//DNA binding / sequence-specific DNA binding [Arabidopsis thaliana]	Unigene36328_All//1.00E-63//AT2G37020| DNA binding / sequence-specific DNA binding	Unigene36328_All//0.00E+00//gi|73865494|gb|DT468232.1|DT468232			GO:0003677	nr -
Unigene36329_All	1111	13.89	4.29	6.09	16.59	14.10	14.19	8.45	6.43	4.05	-1.70E+00	1.11E-25	Down	-1.19E+00	1.03E-14	Down	-2.34E-01	7.79E-02		-2.26E-01	1.05E-01		-3.93E-01	2.12E-02		-1.06E+00	3.50E-10	Down	Unigene36329_All//gi|186506028|ref|NP_565857.2|//1.00E-103//DNA binding / sequence-specific DNA binding [Arabidopsis thaliana]	Unigene36329_All//3.00E-104//AT2G37020| DNA binding / sequence-specific DNA binding	Unigene36329_All//0.00E+00//TC140961			GO:0003677	nr -
Unigene3633_All	1360	37.09	21.24	24.59	57.87	59.48	46.29	39.02	20.65	13.18	-8.04E-01	1.08E-25		-5.93E-01	1.05E-14		3.95E-02	6.04E-01		-3.22E-01	1.36E-08		-9.18E-01	4.78E-41		-1.57E+00	3.17E-97	Down	Unigene3633_All//gi|15229382|ref|NP_191857.1|//2.00E-54//CYCP1;1 (cyclin p1;1); cyclin-dependent protein kinase [Arabidopsis thaliana] >gi|147637975|sp|Q8LB60.2|CCU1_ARATH RecName: Full=Cyclin-U3-1; Short=CycU3:1; AltName: Full=Cyclin-P1.1; Short=CycP1:1	Unigene3633_All//4.00E-49//AT3G63120| CYCP1;1 (cyclin p1;1); cyclin-dependent protein kinase	Unigene3633_All//0.00E+00//TC155994			GO:0016772	nr +
Unigene36330_All	1182	3.23	265.61	13.92	5.82	47.22	54.30	12.38	65.31	134.31	6.36E+00	0.00E+00	Up	2.11E+00	3.95E-35	Up	3.02E+00	1.10E-212	Up	3.22E+00	6.42E-240	Up	2.40E+00	2.45E-241	Up	3.44E+00	0.00E+00	Up	Unigene36330_All//gi|439489|dbj|BAA05077.1|//1.00E-42//zinc-finger DNA binding protein [Petunia x hybrida]	Unigene36330_All//9.00E-30//AT3G49930| zinc finger (C2H2 type) family protein	Unigene36330_All//0.00E+00//gi|109860299|gb|DW489278.1|DW489278	C2H2			nr -
Unigene36331_All	1503	7.62	53.37	3.86	5.34	12.62	10.01	17.38	52.20	287.27	2.81E+00	1.29E-243	Up	-9.81E-01	2.78E-08		1.24E+00	4.40E-23	Up	9.07E-01	2.23E-10		1.59E+00	1.01E-141	Up	4.05E+00	0.00E+00	Up	Unigene36331_All//gi|13539578|emb|CAC35703.1|//3.00E-99//photoperiod responsive protein [Solanum tuberosum subsp. andigena]	Unigene36331_All//4.00E-73//AT3G18710| PUB29 (PLANT U-BOX 29); ubiquitin-protein ligase	Unigene36331_All//0.00E+00//TC131077			GO:0009743//GO:0019787//GO:0032446	nr -
Unigene36333_All	1240	50.72	270.14	37.06	70.02	98.39	105.81	61.75	94.58	181.17	2.41E+00	0.00E+00	Up	-4.53E-01	2.22E-11		4.91E-01	1.89E-30		5.96E-01	9.17E-42		6.15E-01	3.89E-45		1.55E+00	0.00E+00	Up	Unigene36333_All//gi|63054325|gb|AY28930.1|//8.00E-95//sucrose responsive element binding protein [Vitis vinifera]	Unigene36333_All//4.00E-57//AT2G23290| AtMYB70 (myb domain protein 70); DNA binding / transcription factor	Unigene36333_All//0.00E+00//TC130139	MYB		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene36334_All	713	61.79	68.22	46.30	73.99	70.37	30.66	14.94	9.91	8.88	1.43E-01	7.99E-02		-4.16E-01	4.21E-07		-7.24E-02	4.18E-01		-1.27E+00	6.19E-61	Down	-5.93E-01	1.34E-04		-7.50E-01	8.90E-07		Unigene36334_All//gi|297725595|ref|NP_001175161.1|//2.00E-10//Os07g0417700 [Oryza sativa Japonica Group] >gi|255677700|dbj|BAH93889.1| Os07g0417700 [Oryza sativa Japonica Group]	Unigene36334_All//3.00E-06//AT3G25270| nucleic acid binding	Unigene36334_All//2.00E-07//DW501117				nr +
Unigene36335_All	2839	2.71	1.46	0.90	5.67	6.14	4.14	14.52	8.29	7.66	-8.88E-01	2.63E-05		-1.59E+00	1.71E-11	Down	1.15E-01	4.80E-01		-4.54E-01	8.89E-04		-8.09E-01	4.98E-26		-9.22E-01	2.84E-33		Unigene36335_All//gi|15228982|ref|NP_191223.1|//0.00E+00//exocyst complex subunit Sec15-like family protein [Arabidopsis thaliana] >gi|24418676|sp|Q9LXX6.1|EXOC6_ARATH RecName: Full=Probable exocyst complex component 6; AltName: Full=Exocyst complex component Sec15	Unigene36335_All//0.00E+00//AT3G56640| exocyst complex subunit Sec15-like family protein	Unigene36335_All//0.00E+00//TC147206			GO:0043234//GO:0048278	nr +
Unigene36337_All	1996	1.52	0.33	0.56	3.64	2.69	2.06	3.94	2.01	3.99	-2.20E+00	1.18E-07	Down	-1.44E+00	2.24E-04	Down	-4.37E-01	3.93E-02		-8.23E-01	1.04E-04		-9.71E-01	2.32E-07		1.89E-02	9.46E-01		Unigene36337_All//gi|209529755|gb|ACI49772.1|//1.00E-170//At5g01100 [Arabidopsis thaliana]	Unigene36337_All//0.00E+00//AT2G37980| unknown protein	Unigene36337_All//0.00E+00//TC177247			GO:0009536	nr -
Unigene36339_All	1568	4.97	13.48	8.76	6.99	9.00	11.03	4.53	6.10	5.13	1.44E+00	1.94E-27	Up	8.18E-01	2.12E-07		3.66E-01	1.30E-02		6.58E-01	4.30E-07		4.30E-01	1.03E-02		1.80E-01	3.56E-01		Unigene36339_All//gi|87162555|gb|AB028350.1|//1.00E-156//Protein phosphatase 2C-like [Medicago truncatula]	Unigene36339_All//5.00E-154//AT3G05640| protein phosphatase 2C, putative / PP2C, putative	Unigene36339_All//0.00E+00//TC168339				nr +
Unigene3634_All	1601	0.23	1.61	1.10	2.86	3.29	7.84	46.69	43.15	188.19	2.82E+00	1.97E-08	Up	2.26E+00	1.32E-04	Up	2.01E-01	5.20E-01		1.45E+00	6.91E-18	Up	-1.14E-01	5.47E-02		2.01E+00	0.00E+00	Up	Unigene3634_All//gi|26224736|gb|AAN76362.1|//3.00E-81//serpin-like protein [Citrus x paradisi]	Unigene3634_All//7.00E-69//AT1G47710| serpin, putative / serine protease inhibitor, putative	Unigene3634_All//0.00E+00//TC166774			GO:0004866//GO:0005576	nr +
Unigene36341_All	1500	14.16	11.79	13.17	20.26	24.91	22.31	14.74	9.06	6.85	-2.65E-01	3.17E-02		-1.05E-01	4.51E-01		2.98E-01	3.63E-04		1.39E-01	1.93E-01		-7.03E-01	2.01E-11		-1.11E+00	2.58E-24	Down	Unigene36341_All//gi|52627091|gb|AAL84672.1|//1.00E-143//At5g42470 [Arabidopsis thaliana] >gi|55167890|gb|AAV43777.1| At5g42470 [Arabidopsis thaliana]	Unigene36341_All//3.00E-144//AT5G42470| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Brain and reproductive organ-expressed (InterPro:IPR010358); Has 125 Blast hits to 120 proteins in 32 species: Archae - 0; Bacteria - 0; Metazoa - 108; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink).	Unigene36341_All//0.00E+00//TC139869				nr -
Unigene36343_All	2132	0.47	0.45	0.47	1.26	0.95	0.81	2.10	2.10	4.82	-4.62E-02	9.58E-01		2.55E-02	9.90E-01		-4.05E-01	3.13E-01		-6.48E-01	9.71E-02		-3.10E-03	1.02E+00		1.20E+00	3.71E-13	Up	Unigene36343_All//gi|297814269|ref|XP_002875018.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320855|gb|EFH51277.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36343_All//0.00E+00//AT4G00710| BSK3 (BR-SIGNALING KINASE 3); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase	Unigene36343_All//0.00E+00//TC139845			GO:0004672//GO:0004871//GO:0006464//GO:0016020//GO:0032559//GO:0043401	nr +
Unigene36344_All	1024	119.36	24.59	44.98	94.23	61.91	70.66	28.74	3.71	4.94	-2.28E+00	1.51E-294	Down	-1.41E+00	1.04E-146	Down	-6.06E-01	4.32E-36		-4.15E-01	2.39E-16		-2.95E+00	2.83E-116	Down	-2.54E+00	5.27E-102	Down	Unigene36344_All//gi|13605511|gb|AK32749.1|AF361581_1//3.00E-31//AT4g35320/F23E12_120 [Arabidopsis thaliana] >gi|16323284|gb|AAL15397.1| AT4g35320/F23E12_120 [Arabidopsis thaliana]	Unigene36344_All//4.00E-27//AT4G35320| unknown protein	Unigene36344_All//0.00E+00//gi|48742930|gb|CO073449.1|CO073449				nr -
Unigene36345_All	1352	5.65	2.02	3.27	13.56	8.66	6.55	8.41	2.13	1.27	-1.48E+00	7.00E-11	Down	-7.89E-01	3.20E-04		-6.47E-01	4.47E-08		-1.05E+00	5.48E-16	Down	-1.98E+00	1.37E-28	Down	-2.73E+00	3.52E-43	Down	Unigene36345_All//gi|30678332|ref|NP_186790.2|//8.00E-59//RNase H domain-containing protein [Arabidopsis thaliana] >gi|145331720|ref|NP_001078087.1| RNase H domain-containing protein [Arabidopsis thaliana]	Unigene36345_All//4.00E-68//AT3G01410| RNase H domain-containing protein	Unigene36345_All//0.00E+00//gi|73849080|gb|DT458100.1|DT458100			GO:0004518	nr +
Unigene36347_All	644	1.06	3.30	4.55	2.78	3.74	2.88	0.98	1.95	3.09	1.65E+00	4.95E-04	Up	2.11E+00	1.07E-06	Up	4.27E-01	3.27E-01		4.62E-02	9.42E-01		9.83E-01	7.13E-02		1.65E+00	1.08E-04	Up	Unigene36347_All//gi|146233385|gb|ABQ14360.1|//4.00E-30//abscisic acid ABA receptor [Populus trichocarpa]	Unigene36347_All//3.00E-29//AT1G52920| GPCR (G PROTEIN COUPLED RECEPTOR); abscisic acid binding / catalytic	Unigene36347_All//7.00E-146//TC143065			GO:0004871//GO:0005488//GO:0043231//GO:0044425	nr +
Unigene36349_All	1285	4.03	5.48	2.90	3.37	3.03	4.67	2.80	5.53	5.74	4.43E-01	4.69E-02		-4.75E-01	8.85E-02		-1.55E-01	6.16E-01		4.71E-01	5.82E-02		9.83E-01	7.58E-07		1.04E+00	7.39E-08	Up	Unigene36349_All//gi|146233385|gb|ABQ14360.1|//1.00E-137//abscisic acid ABA receptor [Populus trichocarpa]	Unigene36349_All//3.00E-128//AT1G52920| GPCR (G PROTEIN COUPLED RECEPTOR); abscisic acid binding / catalytic	Unigene36349_All//0.00E+00//EX169975				nr +
Unigene36350_All	1214	80.25	66.61	75.71	37.42	34.21	39.73	30.40	21.90	13.98	-2.69E-01	2.88E-07		-8.40E-02	1.72E-01		-1.30E-01	1.33E-01		8.64E-02	3.58E-01		-4.74E-01	1.60E-09		-1.12E+00	6.91E-41	Down	Unigene36350_All//gi|48310049|gb|AAT41743.1|//2.00E-46//At3g09860 [Arabidopsis thaliana] >gi|52218784|gb|AAU29462.1| At3g09860 [Arabidopsis thaliana]	Unigene36350_All//9.00E-48//AT3G09860| unknown protein	Unigene36350_All//0.00E+00//TC156810				nr +

Unigene36351_All	1353	4.33	2.36	1.89	2.32	1.63	1.10	2.69	1.64	2.21	-8.76E-01	3.63E-04		-1.20E+00	4.86E-06	Down	-5.10E-01	1.45E-01		-1.07E+00	2.12E-03		-7.15E-01	1.28E-02		-2.83E-01	3.42E-01		Unigene36351_All//gi|297841587|ref|XP_002886675.1|//1.00E-134//transcription factor perianthia [Arabidopsis lyrata subsp. lyrata] >gi|297334516|gb|EFH64934.1| transcription factor perianthia [Arabidopsis lyrata subsp. lyrata]	Unigene36351_All//2.00E-100//AT1G68640| PAN (PERIANTHIA); DNA binding / transcription factor	Unigene36351_All//0.00E+00//gi|164364091|gb|ES839197.1|ES839197	bZIP			nr -
Unigene36352_All	837	2.94	1.70	3.37	3.99	3.99	3.18	7.22	3.25	2.43	-7.94E-01	4.88E-02		1.99E-01	6.19E-01		1.20E-03	9.92E-01		-3.25E-01	3.93E-01		-1.15E+00	1.76E-07	Down	-1.57E+00	6.44E-12	Down	Unigene36352_All//gi|5714658|gb|AAD48018.1|//3.00E-98//Rab GTP-binding protein Rab11a [Gossypium hirsutum]	Unigene36352_All//5.00E-91//AT5G47520| AtRABA5a (Arabidopsis Rab GTPase homolog A5a); GTP binding	Unigene36352_All//0.00E+00//TC154653			GO:0003824//GO:0006810//GO:0016020//GO:0032561//GO:0035556	nr +
Unigene36353_All	1624	2.29	1.03	2.10	4.23	3.44	3.78	3.18	2.34	0.81	-1.15E+00	3.89E-04	Down	-1.24E-01	7.05E-01		-3.01E-01	1.97E-01		-1.63E-01	5.41E-01		-4.40E-01	6.84E-02		-1.97E+00	9.04E-14	Down	Unigene36353_All//gi|5714658|gb|AAD48018.1|//3.00E-97//Rab GTP-binding protein Rab11a [Gossypium hirsutum]	Unigene36353_All//1.00E-90//AT5G47520| AtRABA5a (Arabidopsis Rab GTPase homolog A5a); GTP binding	Unigene36353_All//0.00E+00//TC176096			GO:0003824//GO:0006810//GO:0016020//GO:0032561//GO:0035556	nr -
Unigene36354_All	1699	39.23	34.00	47.45	7.62	8.09	5.82	3.33	1.92	1.55	-2.07E-01	1.65E-03		2.74E-01	4.62E-06		8.52E-02	6.41E-01		-3.89E-01	1.39E-02		-7.97E-01	3.38E-04		-1.11E+00	6.56E-07	Down	Unigene36354_All//gi|18394414|ref|NP_564010.1|//1.00E-102//uridylyltransferase-related [Arabidopsis thaliana] >gi|9802776|gb|AAF99845.1|AC051629_12 Unknown protein [Arabidopsis thaliana] >gi|14423502|gb|AAK62433.1|AF386988_1 Unknown protein [Arabidopsis thaliana] >gi|30023784|gb|AAP13425.1|At1g16880 [Arabidopsis thaliana]	Unigene36354_All//1.00E-103//AT1G16880| uridylyltransferase-related	Unigene36354_All//0.00E+00//TC164352			GO:0009532//GO:0009534//GO:0031406	nr -
Unigene36356_All	1578	11.27	7.22	12.35	2.08	4.58	5.64	14.20	17.38	18.86	-6.42E-01	1.02E-06		1.32E-01	3.80E-01		1.14E+00	6.21E-08	Up	1.44E+00	1.31E-12	Up	2.91E-01	1.98E-03		4.09E-01	2.21E-06		Unigene36356_All//gi|209954705|dbj|BAG80543.1|//1.00E-142//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene36356_All//4.00E-140//AT1G65680| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene36356_All//8.00E-09//TC141753		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00908|Zeatin biosynthesis//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr +
Unigene36364_All	291	1.62	1.22	1.10	1.54	1.89	4.04	19.03	10.20	2.60	-4.09E-01	6.69E-01		-5.60E-01	6.28E-01		2.97E-01	8.18E-01		1.39E+00	3.52E-02		-9.00E-01	7.03E-05		-2.87E+00	1.55E-22	Down	Unigene36364_All//gi|192910686|gb|ACF06451.1|//9.00E-39//QM-like protein [Elaeis guineensis]	Unigene36364_All//1.00E-38//AT1G14320| SMC52 (SUPPRESSOR OF ACAULIS 52); structural constituent of ribosome	Unigene36364_All//5.00E-105//TC130761		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene36366_All	574	114.49	66.38	81.45	124.54	114.88	142.89	109.31	59.42	54.55	-7.86E-01	5.30E-32		-4.91E-01	1.13E-13		-1.16E-01	7.96E-02		1.98E-01	6.01E-04		-8.80E-01	4.39E-45		-1.00E+00	1.51E-57	Down	Unigene36366_All//gi|11036950|gb|AAG27431.1|//3.00E-74//QM-like protein [Elaeis guineensis]	Unigene36366_All//3.00E-71//AT1G66580| 60S ribosomal protein L10 (RPL10C)	Unigene36366_All//0.00E+00//TC133379		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene36367_All	409	133.30	89.69	91.79	122.65	144.81	164.75	240.04	104.23	110.17	-5.72E-01	1.60E-15		-5.38E-01	2.04E-13		2.40E-01	2.47E-04		4.26E-01	4.68E-12		-1.20E+00	7.97E-117	Down	-1.12E+00	1.05E-107	Down	Unigene36367_All//gi|192910686|gb|ACF06451.1|//8.00E-72//QM-like protein [Elaeis guineensis]	Unigene36367_All//1.00E-69//AT1G14320| SMC52 (SUPPRESSOR OF ACAULIS 52); structural constituent of ribosome	Unigene36367_All//0.00E+00//gi|11205319|gb|BF274249.1|BF274249		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene36370_All	781	0.27	2.34	0.82	1.79	4.72	5.61	6.23	13.70	7.09	3.12E+00	1.05E-06	Up	1.61E+00	1.11E-01		1.40E+00	1.07E-05	Up	1.65E+00	7.97E-08	Up	1.14E+00	2.41E-12	Up	1.88E-01	4.36E-01		Unigene36370_All//gi|145327751|ref|NP_001077851.1|//4.00E-22//lactoylglutathione lyase family protein / glyoxalase I family protein [Arabidopsis thaliana]	Unigene36370_All//2.00E-23//AT1G80160| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene36370_All//1.00E-101//C0120887			GO:0003824//GO:0044238//GO:0044464	nr -
Unigene36371_All	1019	13.50	47.04	11.71	25.96	72.01	86.60	190.86	310.82	185.43	1.80E+00	1.20E-84	Up	-2.06E-01	2.34E-01		1.47E+00	1.28E-114	Up	1.74E+00	4.28E-159	Up	7.04E-01	8.92E-153		-4.16E-02	2.72E-01		Unigene36371_All//gi|5902371|gb|AAD55473.1|AC009322_13//8.00E-76//Hypothetical protein [Arabidopsis thaliana]	Unigene36371_All//1.00E-74//AT1G80160| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene36371_All//0.00E+00//TC134971			GO:0003824//GO:0044238//GO:0044464	nr +
Unigene36372_All	1323	31.52	31.21	38.92	12.99	13.01	10.58	3.29	2.69	1.60	-1.40E-02	8.89E-01		3.04E-01	6.94E-05		2.70E-03	9.90E-01		-2.96E-01	3.28E-02		-2.94E-01	2.97E-01		-1.04E+00	4.31E-05	Down	Unigene36372_All//gi|77744917|gb|ABB02412.1|//3.00E-71//chloroplast lipocalin [Glycine max]	Unigene36372_All//6.00E-62//AT3G47860| apolipoprotein D-related	Unigene36372_All//0.00E+00//TC141615			GO:0043231	nr +
Unigene36373_All	1162	113.06	52.11	85.10	34.94	31.00	27.13	8.19	7.63	3.74	-1.12E+00	1.67E-113	Down	-4.10E-01	2.57E-19		-1.73E-01	4.54E-02		-3.65E-01	7.54E-06		-1.03E-01	6.30E-01		-1.13E+00	2.35E-11	Down	Unigene36373_All//gi|38679313|gb|AAR26478.1|//1.00E-124//harpin binding protein 1 [Gossypium hirsutum]	Unigene36373_All//9.00E-82//AT3G23400| plastid-lipid associated protein PAP / fibrillin family protein	Unigene36373_All//0.00E+00//TC143802			GO:0009534//GO:0009570//GO:0016020//GO:0044436//GO:0051234	nr -
Unigene36374_All	1916	29.33	11.95	19.34	42.14	34.60	48.77	44.88	20.90	21.48	-1.29E+00	1.31E-61	Down	-6.00E-01	1.12E-16		-2.85E-01	8.95E-08		2.11E-01	7.52E-05		-1.10E+00	3.74E-89	Down	-1.06E+00	2.01E-86	Down	Unigene36374_All//gi|4194878|sp|Q9SA34.1|IMDH2_ARATH//0.00E+00//Rec Name: Full=Probable inosine-5'-monophosphate dehydrogenase; Short=IMP dehydrogenase; Short=IMPDH; Short=IMPD >gi|4966356|gb|AAD34687.1|AC006341_15 Strong similarity to gb|L34684 inosine monophosphate dehydrogenase (IMPDH) from Arabidopsis thaliana and is a member of the PF|00478 IMP dehydrogenase family	Unigene36374_All//0.00E+00//AT1G16350| inosine-5'-monophosphate dehydrogenase, putative	Unigene36374_All//0.00E+00//TC139067		ko00230|Purine metabolism	GO:0009168//GO:0016616//GO:0043169	nr -
Unigene36376_All	1842	2.67	4.15	2.75	2.89	3.10	5.47	16.25	4.79	4.22	6.38E-01	2.45E-03		4.06E-02	8.91E-01		1.01E-01	7.59E-01		9.18E-01	2.72E-07		-1.76E+00	2.21E-63	Down	-1.95E+00	1.26E-74	Down	Unigene36376_All//gi|260401276|gb|ACX37118.1|//0.00E+00//MATE transporter [Medicago truncatula]	Unigene36376_All//0.00E+00//AT3G59030| TT12 (TRANSPARENT TESTA 12); antiporter/ solute:hydrogen antiporter/ transmembrane transporter/ transporter	Unigene36376_All//0.00E+00//gi|78343049|gb|DT563323.1|DT563323			GO:0000325//GO:0003006//GO:0009813//GO:0015298//GO:0015893	nr +
Unigene36377_All	545	0.67	0.37	0.20	1.92	3.03	1.49	1.32	4.14	1.46	-8.54E-01	4.89E-01		-1.78E+00	2.34E-01		6.60E-01	2.18E-01		-3.64E-01	6.33E-01		1.65E+00	4.73E-05	Up	1.49E-01	8.23E-01		Unigene36377_All//gi|224129686|ref|XP_002320646.1|//5.00E-41//glutaredoxin [Populus trichocarpa] >gi|222861419|gb|EEE98961.1| glutaredoxin [Populus trichocarpa]	Unigene36377_All//1.00E-38//AT2G30540| glutaredoxin family protein	Unigene36377_All//2.00E-127//TC158121			GO:0015036//GO:0019725//GO:0044464	nr -
Unigene36378_All	778	8.20	6.32	15.74	38.80	42.71	22.52	0.98	2.63	1.08	-3.77E-01	1.16E-01		9.40E-01	2.88E-08		1.39E-01	1.82E-01		-7.85E-01	4.28E-16		1.43E+00	6.34E-04	Up	1.37E-01	8.36E-01		Unigene36378_All//gi|224129686|ref|XP_002320646.1|//2.00E-41//glutaredoxin [Populus trichocarpa] >gi|222861419|gb|EEE98961.1| glutaredoxin [Populus trichocarpa]	Unigene36378_All//8.00E-40//AT2G30540| glutaredoxin family protein	Unigene36378_All//0.00E+00//TC158121			GO:0015036//GO:0019725//GO:0044464	nr +
Unigene36380_All	1714	16.67	12.15	10.66	26.88	20.65	23.53	22.45	11.61	7.81	-4.56E-01	6.31E-06		-6.45E-01	6.54E-10		-3.80E-01	1.10E-07		-1.92E-01	1.86E-02		-9.52E-01	8.34E-32		-1.52E+00	5.86E-68	Down	Unigene36380_All//gi|15219673|ref|NP_171915.1|//1.00E-147//tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	Unigene36380_All//1.00E-147//AT1G04190| tetratricopeptide repeat (TPR)-containing protein	Unigene36380_All//0.00E+00//TC163166				nr +
Unigene36381_All	883	5.10	1.84	3.50	10.44	8.46	8.95	4.02	2.89	2.08	-1.47E+00	1.12E-06	Down	-5.43E-01	7.16E-02		-3.03E-01	1.19E-01		-2.22E-01	3.04E-01		-4.78E-01	1.10E-01		-9.55E-01	7.66E-04		Unigene36381_All//gi|15216226|dbj|BAB63262.1|//5.00E-40//CIG2 [Nicotiana tabacum]	Unigene36381_All//1.00E-27//AT2G05830| eukaryotic translation initiation factor 2B family protein / eIF-2B family protein	Unigene36381_All//1.00E-92//BQ403684			GO:0006412//GO:0016861//GO:0032561//GO:0033353//GO:0043231//GO:0043234	nr +
Unigene36383_All	1110	13.39	7.76	6.86	29.75	27.27	26.28	29.41	12.69	7.64	-7.87E-01	7.48E-08		-9.65E-01	2.89E-10		-1.26E-01	2.33E-01		-1.79E-01	7.71E-02		-1.21E+00	8.17E-40	Down	-1.94E+00	3.65E-81	Down	Unigene36383_All//gi|193290377|gb|ABV65001.1|//1.00E-125//14-3-3b protein [Gossypium hirsutum]	Unigene36383_All//5.00E-113//AT1G35160| GF14 PHI (GF14 PROTEIN PHI CHAIN); protein binding / protein phosphorylated amino acid binding	Unigene36383_All//0.00E+00//TC144149				nr +
Unigene36385_All	1974	5.73	4.95	3.80	15.07	17.76	14.39	13.34	4.79	3.23	-2.09E-01	2.46E-01		-5.90E-01	7.62E-04		2.37E-01	8.42E-03		-6.61E-02	6.22E-01		-1.48E+00	1.52E-43	Down	-2.05E+00	2.98E-70	Down	Unigene36385_All//gi|15237291|ref|NP_200098.1|//0.00E+00//ABC transporter family protein [Arabidopsis thaliana] >gi|75334041|sp|Q9FLX5.1|ABBG_ARATH RecName: Full=ABC transporter G family member 8; Short=ABC transporter ABCG.8; Short=AtABCG8; AltName: Full=Probable white-brown complex homolog protein 8; Short=AtWBC8 >gi|10177100|dbj|BAB10434.1| ABC transporter-like protein [Arabidopsis thaliana]	Unigene36385_All//0.00E+00//AT5G52860| ABC transporter family protein	Unigene36385_All//0.00E+00//TC130896		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015405//GO:0044464	nr -
Unigene36386_All	2993	0.66	11.34	1.99	1.33	3.97	10.53	3.66	13.38	45.84	4.09E+00	1.82E-144	Up	1.58E+00	4.79E-09	Up	1.58E+00	1.31E-20	Up	2.98E+00	2.08E-109	Up	1.87E+00	1.95E-91	Up	3.65E+00	0.00E+00	Up	Unigene36386_All//gi|297726959|ref|NP_001175843.1|//0.00E+00//Os09g0423000 [Oryza sativa Japonica Group] >gi|255678905|dbj|BAAH94571.1| Os09g0423000 [Oryza sativa Japonica Group]	Unigene36386_All//0.00E+00//AT2G24130| leucine-rich repeat transmembrane protein kinase, putative	Unigene36386_All//5.00E-141//DN800051		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016301//GO:0044464	nr -
Unigene3639_All	1938	2.00	1.78	0.74	5.01	5.86	5.06	6.20	0.99	2.34	-1.68E-01	5.95E-01		-1.43E+00	2.49E-05	Down	2.26E-01	2.23E-01		1.28E-02	9.46E-01		-2.64E+00	1.47E-42	Down	-1.40E+00	2.24E-19	Down	Unigene3639_All//gi|102139848|gb|ABF70006.1|//1.00E-94//transport protein-related [Musa acuminata]	Unigene3639_All//1.00E-98//AT1G49870| LOCATED IN: chloroplast; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; BEST Arabidopsis thaliana protein match is: MBD10; DNA binding / methyl-CpG binding (TAIR:AT1G15340.1); Has 5602 Blast hits to 4205 proteins in 368 species: Archae - 30; Bacteria - 406; Metazoa - 2889; Fungi - 302; Plants - 153; Viruses - 8; Other Eukaryotes - 1814 (source: NCBI BLink)。				GO:0043231	nr +
Unigene36391_All	1918	2.56	3.65	5.69	1.04	1.85	1.98	0.00	0.00	0.00	5.08E-01	2.28E-02		1.15E+00	4.37E-10	Up	8.32E-01	9.15E-03		9.29E-01	3.13E-03		null	null		null	null		Unigene36391_All//gi|6671365|gb|AAF23176.1|AF216497_1//0.00E+00//P-glycoprotein [Gossypium hirsutum]	Unigene36391_All//0.00E+00//AT4G25960| PGP2 (P-GLYCOPROTEIN 2); ATPase, coupled to transmembrane movement of substances	Unigene36391_All//0.00E+00//TC141861		ko02010|ABC transporters	GO:0006810//GO:0031224//GO:0032559//GO:0042626//GO:0043231	nr -
Unigene36392_All	1868	5.99	2.50	3.62	12.27	10.21	13.03	11.59	5.15	5.01	-1.26E+00	2.04E-12	Down	-7.27E-01	3.64E-05		-2.64E-01	1.98E-02		8.72E-02	5.30E-01		-1.17E+00	2.75E-25	Down	-1.21E+00	2.24E-27	Down	Unigene36392_All//gi|60498651|dbj|BAD90709.1|//2.00E-45//plastid DNA-binding protein [Prunus x yedoensis]	Unigene36392_All//1.00E-34//AT3G52170| DNA binding	Unigene36392_All//0.00E+00//gi|48778779|gb|CO088145.1|CO088145				nr +
Unigene36393_All	1883	0.89	0.22	1.39	2.72	1.57	3.38	0.58	0.33	0.61	-2.05E+00	3.19E-04	Down	6.40E-01	1.21E-01		-7.93E-01	1.28E-03		3.12E-01	2.23E-01		-8.10E-01	1.69E-01		7.18E-02	9.11E-01		Unigene36393_All//gi|60498651|dbj|BAD90709.1|//1.00E-49//plastid DNA-binding protein [Prunus x yedoensis]	Unigene36393_All//3.00E-39//AT3G52170| DNA binding	Unigene36393_All//0.00E+00//TC167598				nr -
Unigene36394_All	1422	15.01	2.67	3.56	13.80	15.55	9.12	4.25	7.11	3.75	-2.49E+00	1.41E-57	Down	-2.08E+00	1.78E-44	Down	1.72E-01	1.80E-01		-5.99E-01	7.07E-07		7.42E-01	3.81E-06		-1.80E-01	4.32E-01		Unigene36394_All//gi|6942322|gb|AAF32409.1|AF230276_1//1.00E-123//alpha-expansin 3 [Triphysaria versicolor]	Unigene36394_All//4.00E-113//AT2G03090| ATEXPA15 (ARABIDOPSIS THALIANA EXPANSIN A15)	Unigene36394_All//0.00E+00//TC133082				nr -
Unigene36395_All	1053	15.11	46.48	7.99	35.43	60.99	29.25	84.48	83.59	225.11	1.62E+00	1.17E-74	Up	-9.19E-01	3.84E-10		7.84E-01	1.27E-36		-2.77E-01	1.62E-03		-1.53E-02	8.08E-01		1.41E+00	0.00E+00	Up	Unigene36395_All//gi|171452362|dbj|BAG15872.1|//1.00E-133//transcription factor [Bruguiera gymnorhiza]	Unigene36395_All//3.00E-120//AT2G40140| CZF1; transcription factor	Unigene36395_All//0.00E+00//TC144396	C3H			nr -

Unigene36396_All	1955	12.26	7.70	13.76	13.02	9.78	6.01	9.47	3.40	3.85	-6.71E-01	2.03E-09		1.66E-01	1.58E-01		-4.14E-01	3.60E-05		-1.12E+00	3.25E-24	Down	-1.48E+00	8.20E-31	Down	-1.30E+00	3.22E-26	Down	Unigene36396_All//gi|224125528|ref|XP_002329827.1|//6.00E-82//f-box family protein [Populus trichocarpa] >gi|222870889|gb|EEF08020.1| f-box family protein [Populus trichocarpa]	Unigene36396_All//3.00E-37//AT1G28310| Dof-type zinc finger domain-containing protein	Unigene36396_All//0.00E+00//TC175368	C2C2-Dof		GO:0005488	nr +
Unigene36397_All	1429	3.37	14.29	7.38	1.88	5.06	5.15	2.51	3.42	2.98	2.08E+00	4.08E-44	Up	1.13E+00	1.60E-09	Up	1.43E+00	5.08E-11	Up	1.45E+00	1.07E-10	Up	4.44E-01	7.49E-02		2.46E-01	3.69E-01		Unigene36397_All//gi|289707891|gb|ADD16956.1|//4.00E-68//C4C4-type RING finger protein [Vitis pseudoreticulata]	Unigene36397_All//6.00E-38//AT3G48070| protein binding / zinc ion binding	Unigene36397_All//0.00E+00//TC172366		ko03018|RNA degradation		nr +
Unigene36399_All	1673	15.70	11.75	13.30	7.47	7.76	6.13	4.32	2.35	1.74	-4.18E-01	7.98E-05		-2.39E-01	3.89E-02		5.42E-02	8.10E-01		-2.86E-01	9.03E-02		-8.80E-01	6.41E-06		-1.31E+00	5.92E-11	Down	Unigene36399_All//gi|225452797|ref|XP_002278099.1|//0.00E+00//PREDICTED: similar to DEG8/DEG8 (DEGP PROTEASE 8); peptidase/ serine-type peptidase/ trypsin [Vitis vinifera]	Unigene36399_All//6.00E-178//AT5G39830| DEG8; peptidase/ serine-type peptidase	Unigene36399_All//1.00E-29//gi|78331816|gb|DT552090.1|DT552090			GO:0004175//GO:0005488//GO:0009534//GO:0009765//GO:0016628//GO:0019538//GO:0044436	nr +
Unigene3640_All	1463	46.38	40.24	43.68	31.43	56.73	44.36	3.99	10.51	13.37	-2.05E-01	1.64E-03		-8.67E-02	2.46E-01		8.52E-01	1.82E-54		4.97E-01	2.85E-15		1.40E+00	1.11E-23	Up	1.75E+00	6.93E-42	Up	Unigene3640_All//gi|78711803|gb|ABB49053.1|//1.00E-129//carotenoid beta-ring hydroxylase [Citrus sinensis]	Unigene3640_All//9.00E-109//AT5G52570| BETA-OHASE 2 (BETA-CAROTENE HYDROXYLASE 2); carotene beta-ring hydroxylase	Unigene3640_All//0.00E+00//TC165712		ko00906|Carotenoid biosynthesis		nr -
Unigene36400_All	1472	33.23	22.20	14.69	51.17	38.72	37.71	39.78	28.11	9.39	-5.82E-01	1.92E-14		-1.18E+00	9.47E-45	Down	-4.02E-01	1.61E-13		-4.40E-01	2.66E-14		-5.01E-01	4.09E-16		-2.08E+00	8.64E-159	Down	Unigene36400_All//gi|37625023|gb|AAQ96335.1|//0.00E+00//ribosomal protein L3A [Nicotiana tabacum]	Unigene36400_All//0.00E+00//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene36400_All//0.00E+00//TC130945		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene36402_All	2305	36.20	21.39	33.71	15.93	16.82	10.27	3.85	4.32	1.92	-7.59E-01	4.09E-38		-1.03E-01	1.18E-01		7.88E-02	4.57E-01		-6.34E-01	1.55E-13		1.64E-01	3.86E-01		-1.01E+00	5.95E-09	Down	Unigene36402_All//gi|297792999|ref|XP_002864384.1|//0.00E+00//trigger factor type chaperone family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310219|gb|EFH40643.1| trigger factor type chaperone family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36402_All//0.00E+00//AT5G55220| trigger factor type chaperone family protein	Unigene36402_All//0.00E+00//TC171971			GO:0006810//GO:0009526//GO:0009532//GO:0044267	nr -
Unigene36404_All	1813	6.32	7.85	7.43	2.80	2.77	10.31	1.45	9.71	3.05	3.13E-01	4.04E-02		2.34E-01	1.68E-01		-1.53E-02	9.48E-01		1.88E+00	8.68E-38	Up	2.75E+00	1.63E-64	Up	1.08E+00	1.78E-06	Up	Unigene36404_All//gi|87162753|gb|ABD28548.1|//8.00E-93//Protein kinase; Type I EGF [Medicago truncatula]	Unigene36404_All//4.00E-78//AT1G21230| WAK5 (WALL ASSOCIATED KINASE 5); kinase/ protein serine/threonine kinase	Unigene36404_All//2.00E-16//DR456209		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr -
Unigene36406_All	1914	6.70	5.32	4.95	13.01	9.48	9.11	14.67	6.73	8.35	-3.32E-01	3.97E-02		-4.36E-01	8.48E-03		-4.57E-01	5.58E-06		-5.15E-01	1.15E-06		-1.12E+00	1.43E-30	Down	-8.13E-01	1.05E-18		Unigene36406_All//gi|15232462|ref|NP_188748.1|//1.00E-167//PUR7 (PURIN 7); phosphoribosylaminoimidazolesuccinocarboxamide synthase [Arabidopsis thaliana] >gi|79313319|ref|NP_001030739.1| PUR7 (PURIN 7); phosphoribosylaminoimidazolesuccinocarboxamide synthase [Arabidopsis thaliana] >gi|26454658|sp|P38025.2|PUR7_ARATH RecName: Full=Phosphoribosylaminoimidazole-succinocarboxamide synthase, chloroplastic; AltName: Full=SAICAR synthetase; Flags: Precursor >gi|11994271|dbj|BAB01454.1| 5'-phosphoribosyl-4-(N-succinocarboxamide)-5- aminoimidazole synthetase [Arabidopsis thaliana]	Unigene36406_All//7.00E-160//AT3G21110| PUR7 (PURIN 7); phosphoribosylaminoimidazolesuccinocarboxamide synthase	Unigene36406_All//0.00E+00//TC170596		ko00230|Purine metabolism		nr -
Unigene36407_All	1275	5.91	2.27	4.76	3.59	3.27	4.00	3.48	1.48	1.03	-1.38E+00	9.04E-10	Down	-3.12E-01	1.79E-01		-1.37E-01	6.61E-01		1.55E-01	6.41E-01		-1.24E+00	2.76E-06	Down	-1.76E+00	2.40E-10	Down	Unigene36407_All//gi|297809443|ref|XP_002872605.1|//1.00E-141//signal-responsive protein [Arabidopsis lyrata subsp. lyrata] >gi|297318442|gb|EFH48864.1| signal-responsive protein [Arabidopsis lyrata subsp. lyrata]	Unigene36407_All//2.00E-125//AT4G11640| ATSR (ARABIDOPSIS THALIANA SERINE RACEMASE); serine racemase	Unigene36407_All//0.00E+00//TC155709		ko00260|Glycine, serine and threonine metabolism//ko00290|Valine, leucine and isoleucine biosynthesis	GO:0008152	nr -
Unigene36409_All	1652	330.08	146.06	274.73	74.33	76.54	59.11	2.66	4.23	2.56	-1.18E+00	0.00E+00	Down	-2.65E-01	9.70E-35		4.23E-02	4.72E-01		-3.31E-01	1.13E-13		6.67E-01	7.27E-04		-5.83E-02	8.28E-01		Unigene36409_All//gi|15241221|ref|NP_197494.1|//2.00E-72//plastid-lipid associated protein PAP-related / fibrillin-related [Arabidopsis thaliana] >gi|75163992|sp|Q941D3.1|PAP8_ARATH RecName: Full=Probable plastid-lipid-associated protein 8, chloroplastic; AltName: Full=Fibrillin-8; Flags: Precursor >gi|15529232|gb|AAK97710.1| AT5g19940/F28I16_90 [Arabidopsis thaliana] >gi|16974385|gb|AAL31118.1| AT5g19940/F28I16_90 [Arabidopsis thaliana]	Unigene36409_All//4.00E-70//AT5G19940| plastid-lipid associated protein PAP-related / fibrillin-related	Unigene36409_All//0.00E+00//gi|48782332|gb|CO089890.1|CO089890			GO:0009526	nr -
Unigene3641_All	503	4.99	9.57	4.45	4.36	5.68	6.64	4.20	10.22	9.43	9.39E-01	6.86E-04		-1.67E-01	6.79E-01		3.83E-01	3.37E-01		6.09E-01	7.90E-02		1.28E+00	1.74E-07	Up	1.17E+00	2.70E-06	Up	Unigene3641_All//gi|90654203|gb|ABD95976.1|//1.00E-19//serine/threonine kinase [Nicotiana tabacum]	Unigene3641_All//1.00E-15//AT5G02290| NAK; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene3641_All//4.00E-128//CO087684			GO:0004672//GO:0006464//GO:0006952//GO:0032559//GO:0043231	nr +
Unigene36410_All	1297	4.48	3.05	2.09	4.72	3.80	4.88	5.87	4.38	3.81	-5.55E-01	2.45E-02		-1.10E+00	2.60E-05	Down	-3.15E-01	2.06E-01		4.54E-02	8.78E-01		-4.21E-01	2.82E-02		-6.24E-01	6.29E-04		Unigene36410_All//gi|114050605|gb|ABI49152.1|//2.00E-79//At2g43110 [Arabidopsis thaliana]	Unigene36410_All//4.00E-68//AT2G43110| unknown protein	Unigene36410_All//0.00E+00//gi|11206844|gb|BF275774.1|BF275774			GO:0043231	nr +
Unigene36411_All	531	7.69	16.03	5.52	13.79	14.01	7.82	3.66	3.31	1.65	1.06E+00	1.93E-07	Up	-4.79E-01	1.40E-01		2.25E-02	9.45E-01		-8.18E-01	1.10E-04		-1.48E-01	7.33E-01		-1.15E+00	4.53E-03		Unigene36411_All//gi|297727877|ref|NP_001176302.1|//1.00E-122//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1| Os11g0106066 [Oryza sativa Japonica Group]		Unigene36411_All//5.00E-23//TC135955				nr +
Unigene36413_All	569	3.31	8.91	3.65	6.57	8.05	5.64	2.38	1.69	1.33	1.43E+00	4.43E-07	Up	1.41E-01	7.48E-01		2.94E-01	3.42E-01		-2.21E-01	5.46E-01		-4.93E-01	3.67E-01		-8.38E-01	8.98E-02			Unigene36413_All//4.00E-11//TC176628				
Unigene36414_All	1019	0.92	1.79	1.05	0.78	1.42	0.31	0.87	0.66	0.08	9.54E-01	4.89E-02		1.77E-01	7.73E-01		8.60E-01	1.31E-01		-1.33E+00	1.06E-01		-4.09E-01	5.62E-01		-3.48E+00	7.33E-05	Down	Unigene36414_All//gi|297727877|ref|NP_001176302.1|//3.00E-10//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1| Os11g0106066 [Oryza sativa Japonica Group]	Unigene36414_All//1.00E-05//AT3G25270| nucleic acid binding	Unigene36414_All//9.00E-23//TC135955				nr +
Unigene36415_All	1966	1.81	1.91	1.76	29.34	12.91	7.44	3.70	1.04	1.28	7.57E-02	8.13E-01		-3.97E-02	9.17E-01		-1.18E+00	4.65E-68	Down	-1.98E+00	1.22E-126	Down	-1.83E+00	9.55E-17	Down	-1.53E+00	1.09E-13	Down	Unigene36415_All//gi|297832296|ref|XP_002884030.1|//1.00E-108//tetracycline transporter [Arabidopsis lyrata subsp. lyrata] >gi|297329870|gb|EFH60289.1| tetracycline transporter [Arabidopsis lyrata subsp. lyrata]	Unigene36415_All//9.00E-102//AT2G16990| tetracycline transporter	Unigene36415_All//0.00E+00//TC179285			GO:0006810	nr -
Unigene36416_All	365	70.81	148.40	70.47	86.12	92.17	96.88	33.82	58.40	47.37	1.07E+00	1.14E-43	Up	-7.10E-03	9.76E-01		9.80E-02	3.82E-01		1.70E-01	8.37E-02		7.88E-01	2.87E-13		4.86E-01	2.89E-05		Unigene36416_All//gi|222423852|dbj|BAH19891.1|//4.00E-24//AT5G64170 [Arabidopsis thaliana]	Unigene36416_All//2.00E-25//AT5G64170| dentin sialophosphoprotein-related	Unigene36416_All//0.00E+00//TC171248				nr +
Unigene36417_All	776	1.42	6.20	3.43	1.16	1.95	2.15	11.71	11.26	8.06	2.13E+00	3.41E-11	Up	1.28E+00	2.02E-03		7.57E-01	1.71E-01		8.98E-01	8.51E-02		-5.75E-02	7.68E-01		-5.39E-01	1.09E-03		Unigene36417_All//gi|222423852|dbj|BAH19891.1|//3.00E-22//AT5G64170 [Arabidopsis thaliana]	Unigene36417_All//2.00E-23//AT5G64170| dentin sialophosphoprotein-related	Unigene36417_All//1.00E-178//TC173578				nr +
Unigene36418_All	1555	10.90	31.67	7.16	13.97	18.54	17.02	37.36	49.75	95.33	1.54E+00	1.21E-69	Up	-6.07E-01	1.30E-05		4.08E-01	1.55E-05		2.85E-01	8.05E-03		4.13E-01	5.47E-15		1.35E+00	6.13E-215	Up	Unigene36418_All//gi|15229865|ref|NP_187788.1|//1.00E-141//SYP121 (SYNTAXIN OF PLANTS 121); SNAP receptor/ protein anchor [Arabidopsis thaliana] >gi|28380149|sp|Q9ZS24.1|SY121_ARATH RecName: Full=Syntaxin-121; Short=AtSYP121; AltName: Full=Syntaxin-related protein At-Syr1 >gi|4206789|gb|AAD11809.1| syntaxin-related protein At-SYR1 [Arabidopsis thaliana]	Unigene36418_All//2.00E-120//AT3G11820| SYP121 (SYNTAXIN OF PLANTS 121); SNAP receptor/ protein anchor	Unigene36418_All//0.00E+00//TC153586		ko04130|SNARE interactions in vesicular transport		nr -
Unigene3642_All	1859	5.49	7.17	7.45	4.29	6.19	6.95	2.73	6.74	5.81	3.85E-01	1.35E-02		4.40E-01	5.27E-03		5.29E-01	9.07E-04		6.97E-01	5.75E-06		1.31E+00	1.38E-17	Up	1.09E+00	5.70E-12	Up	Unigene3642_All//gi|223452416|gb|ACN89535.1|//1.00E-159//protein kinase [Glycine max]	Unigene3642_All//2.00E-144//AT2G28930| APK1B; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene3642_All//0.00E+00//CO087683		ko04626|Plant-pathogen interaction		nr +
Unigene36421_All	1034	0.81	1.32	0.98	1.64	0.83	1.31	4.38	2.30	1.81	7.09E-01	2.15E-01		2.73E-01	6.75E-01		-9.76E-01	4.19E-02		-3.22E-01	5.65E-01		-9.25E-01	2.74E-04		-1.27E+00	7.05E-07	Down			Unigene36421_All//1.00E-126//gi|13245419|gb|BE053968.2|BE053968				
Unigene36425_All	1318	22.27	39.98	6.71	13.15	13.40	7.13	11.16	1.62	5.71	8.44E-01	5.68E-29		-1.73E+00	7.77E-48	Down	2.72E-02	8.70E-01		-8.84E-01	1.63E-11		-2.79E+00	4.59E-55	Down	-9.67E-01	2.14E-13		Unigene36425_All//gi|224149524|ref|XP_002336822.1|//1.00E-42//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|148372095|gb|ABQ62979.1| TINY-like protein [Populus trichocarpa] >gi|222836958|gb|EEE75351.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene36425_All//1.00E-27//AT5G25810| tny (TINY); DNA binding / transcription factor	Unigene36425_All//0.00E+00//TC137037	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0016049//GO:0043231	nr +
Unigene36427_All	3106	31.79	41.39	36.04	10.79	13.69	10.25	1.63	5.73	6.44	3.81E-01	3.11E-17		1.81E-01	4.41E-04		3.43E-01	7.07E-06		-7.44E-02	5.25E-01		1.81E+00	2.52E-39	Up	1.98E+00	1.35E-50	Up	Unigene36427_All//gi|240254220|ref|NP_174979.5|//0.00E+00//PMI1 (PLASTID MOVEMENT IMPAIRED1) [Arabidopsis thaliana]	Unigene36427_All//0.00E+00//AT1G42550| PMI1 (PLASTID MOVEMENT IMPAIRED1)	Unigene36427_All//0.00E+00//gi|78341465|gb|DT561739.1|DT561739			GO:0007010//GO:0009658//GO:0016020	nr -
Unigene36430_All	1561	9.15	4.03	5.19	13.59	10.28	10.82	21.26	6.35	9.60	-1.18E+00	3.45E-14	Down	-8.19E-01	1.11E-07		-4.03E-01	3.02E-04		-3.29E-01	6.07E-03		-1.74E+00	3.62E-69	Down	-1.15E+00	2.97E-38	Down	Unigene36430_All//gi|18419731|ref|NP_567990.1|//1.00E-152//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75248494|sp|Q8VY85.1|PP351_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g35850, mitochondrial; Flags: Precursor	Unigene36430_All//6.00E-153//AT4G35850| pentatricopeptide (PPR) repeat-containing protein	Unigene36430_All//0.00E+00//TC170658				nr +
Unigene36436_All	1243	1.60	2.65	2.74	4.61	5.76	6.36	3.13	2.66	6.41	7.28E-01	3.32E-02		7.78E-01	2.60E-02		3.22E-01	1.63E-01		4.64E-01	2.72E-02		-2.36E-01	4.34E-01		1.03E+00	2.10E-08	Up	Unigene36436_All//gi|3193327|gb|AAC19309.1|//7.00E-72//F6N15.10 gene product [Arabidopsis thaliana]	Unigene36436_All//4.00E-107//AT4G00058| unknown protein					nr -
Unigene36437_All	882	18.98	32.17	22.94	23.72	24.05	23.15	26.75	23.55	13.32	7.61E-01	1.77E-13		2.73E-01	3.92E-02		1.99E-02	9.00E-01		-3.55E-02	8.01E-01		-1.84E-01	9.14E-02		-1.01E+00	2.70E-22	Down	Unigene36437_All//gi|24899755|gb|AAN65092.1|//1.00E-41//Unknown protein [Arabidopsis thaliana]	Unigene36437_All//4.00E-32//AT5G16660| unknown protein	Unigene36437_All//0.00E+00//gi|109890040|gb|DW519008.1|DW519008			GO:0009526//GO:0009534	nr -

Unigene36438_All	1707	5.67	8.43	10.92	11.32	12.39	9.60	0.89	0.20	1.33	5.72E-01	1.05E-04		9.45E-01	2.43E-12		1.30E-01	3.52E-01		-2.38E-01	7.48E-02		-2.19E+00	5.96E-05	Down	5.77E-01	1.17E-01		Unigene36438_All//gi|18407336|ref|NP_564285.1|//1.00E-178//GPT2; antiporter/ glucose-6-phosphate transmembrane transporter [Arabidopsis thaliana]	Unigene36438_All//8.00E-159//AT1G61800| GPT2; antiporter/ glucose-6-phosphate transmembrane transporter	Unigene36438_All//0.00E+00//TC139269			GO:0031224//GO:0051234	nr -
Unigene36441_All	2131	6.11	16.03	7.47	6.05	11.04	10.38	12.64	69.53	31.91	1.39E+00	9.02E-42	Up	2.89E-01	5.54E-02		8.66E-01	4.38E-16		7.78E-01	1.08E-11		2.46E+00	0.00E+00	Up	1.34E+00	2.57E-97	Up	Unigene36441_All//gi|15234357|ref|NP_192096.1|//0.00E+00//tolB protein-related [Arabidopsis thaliana]	Unigene36441_All//0.00E+00//AT4G01870| tolB protein-related	Unigene36441_All//0.00E+00//TC165577				nr +
Unigene36443_All	2832	9.99	14.13	9.42	15.27	17.89	32.12	18.32	38.25	63.71	5.00E-01	2.93E-09		-8.54E-02	4.83E-01		2.28E-01	1.59E-03		1.07E+00	5.21E-79	Up	1.06E+00	2.16E-105	Up	1.80E+00	0.00E+00	Up	Unigene36443_All//gi|240256144|ref|NP_567926.4|//2.00E-44//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene36443_All//2.00E-38//AT4G33565| protein binding / zinc ion binding	Unigene36443_All//0.00E+00//TC137075			GO:0046872	nr +
Unigene36444_All	1892	4.04	10.20	4.70	8.16	5.08	8.98	17.59	26.91	14.47	1.34E+00	1.38E-22	Up	2.19E-01	3.17E-01		-6.85E-01	1.44E-07		1.37E-01	3.87E-01		6.14E-01	5.70E-20		-2.82E-01	5.99E-04		Unigene36444_All//gi|297848856|ref|XP_002892309.1|//0.00E+00//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338151|gb|EFH68568.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36444_All//0.00E+00//AT1G05840| aspartyl protease family protein	Unigene36444_All//7.00E-99//gi|21097053|gb|BQ409366.1|BQ409366			GO:0004175//GO:0019538//GO:0031224	nr +
Unigene36445_All	1752	1.46	1.13	0.79	2.39	1.85	1.80	4.49	1.60	2.11	-3.76E-01	3.63E-01		-8.89E-01	3.21E-02		-3.70E-01	2.25E-01		-4.04E-01	1.99E-01		-1.49E+00	1.12E-13	Down	-1.09E+00	5.52E-09	Down	Unigene36445_All//gi|15230837|ref|NP_189170.1|//1.00E-129//CAF1 family ribonuclease [Arabidopsis thaliana] >gi|75162449|sp|Q8WWC3.1|PARNL_ARATH RecName: Full=Poly(A)-specific ribonuclease PARN-like; AltName: Full=Polyadenylate-specific ribonuclease-like protein >gi|17065176|gb|AAL32742.1| Unknown protein [Arabidopsis thaliana] >gi|30725444|gb|AAP37744.1| At3g25430 [Arabidopsis thaliana]	Unigene36445_All//2.00E-130//AT3G25430| CAF1 family ribonuclease	Unigene36445_All//0.00E+00//DV849475		ko03018|RNA degradation	GO:0043231	nr -
Unigene36446_All	1676	4.59	3.54	2.29	6.54	5.38	3.50	3.13	2.34	3.99	-3.76E-01	7.88E-02		-1.00E+00	5.49E-06	Down	-2.81E-01	1.13E-01		-9.00E-01	9.83E-08		-4.16E-01	8.26E-02		3.52E-01	8.16E-02		Unigene36446_All//gi|224074167|ref|XP_002304283.1|//1.00E-122//formyltetrahydrofolate deformylase [Populus trichocarpa] >gi|222841715|gb|EEE79262.1| formyltetrahydrofolate deformylase [Populus trichocarpa]	Unigene36446_All//5.00E-107//AT5G47435| formyltetrahydrofolate deformylase, putative	Unigene36446_All//0.00E+00//gi|164309517|gb|ES804544.1|ES804544		ko00630|Glyoxylate and dicarboxylate metabolism//ko00670|One carbon pool by folate	GO:0009058//GO:0016741//GO:0043231	nr -
Unigene36448_All	644	10.56	82.22	15.21	10.60	42.51	44.32	36.90	75.93	160.47	2.96E+00	4.69E-170	Up	5.27E-01	5.82E-03		2.00E+00	2.07E-65	Up	2.06E+00	5.68E-65	Up	1.04E+00	1.78E-46	Up	2.12E+00	1.36E-282	Up	Unigene36448_All//gi|9972376|gb|AAG10626.1|AC022521_4//4.00E-59//Unknown protein [Arabidopsis thaliana]	Unigene36448_All//3.00E-56//AT4G02075| PIT1 (pitchoun 1); protein binding / zinc ion binding	Unigene36448_All//0.00E+00//TC153109		ko04141|Protein processing in endoplasmic reticulum	GO:0016020//GO:0043231//GO:0046914	nr -
Unigene36449_All	572	1.56	16.57	5.77	4.35	17.64	8.61	4.80	6.58	25.56	3.41E+00	3.70E-35	Up	1.89E+00	1.38E-06	Up	2.02E+00	2.12E-24	Up	9.83E-01	2.68E-04		4.53E-01	1.21E-01		2.41E+00	2.20E-47	Up	Unigene36449_All//gi|9972376|gb|AAG10626.1|AC022521_4//1.00E-40//Unknown protein [Arabidopsis thaliana]	Unigene36449_All//2.00E-40//AT4G02075| PIT1 (pitchoun 1); protein binding / zinc ion binding	Unigene36449_All//0.00E+00//DR453590		ko04141|Protein processing in endoplasmic reticulum	GO:0016020//GO:0043231//GO:0046914	nr +
Unigene3645_All	456	0.69	3.33	1.05	1.31	1.89	3.07	2.97	3.39	3.32	2.28E+00	2.68E-04	Up	6.10E-01	5.87E-01		5.26E-01	5.45E-01		1.23E+00	3.60E-02		1.93E-01	6.95E-01		1.62E-01	7.30E-01		Unigene3645_All//gi|79313155|ref|NP_001030657.1|//7.00E-24//DNA binding [Arabidopsis thaliana]	Unigene3645_All//5.00E-25//AT3G07565| DNA binding	Unigene3645_All//6.00E-161//ES828260				nr -
Unigene36458_All	1323	53.23	88.24	77.72	134.61	99.45	151.40	109.87	267.20	61.19	7.29E-01	2.46E-49		5.46E-01	1.98E-25		-4.37E-01	1.54E-36		1.70E-01	1.51E-06		1.28E+00	0.00E+00	Up	-8.45E-01	3.32E-99		Unigene36458_All//gi|297840523|ref|XP_002888143.1|//1.00E-173//DC1 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333984|gb|EFH64402.1| DC1 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene36458_All//3.00E-168//AT1G60420| DC1 domain-containing protein	Unigene36458_All//0.00E+00//TC132472				nr +
Unigene36459_All	1751	2.45	1.24	0.46	3.07	3.62	4.98	8.04	3.49	2.68	-9.78E-01	9.23E-04		-2.43E+00	3.75E-11	Down	2.36E-01	3.74E-01		6.96E-01	3.00E-04		-1.21E+00	1.72E-17	Down	-1.58E+00	7.82E-27	Down	Unigene36459_All//gi|224057862|ref|XP_002299361.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene36459_All//0.00E+00//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene36459_All//0.00E+00//ES830314			GO:0009725//GO:0016881//GO:0043231//GO:0048878	nr +
Unigene3646_All	1162	3.56	8.02	4.31	2.49	3.76	4.86	5.49	6.26	7.03	1.17E+00	2.35E-09	Up	2.76E-01	3.61E-01		5.98E-01	3.75E-02		9.66E-01	1.03E-04		1.88E-01	4.03E-01		3.55E-01	4.85E-02		Unigene3646_All//gi|15229471|ref|NP_187413.1|//8.00E-53//DNA binding [Arabidopsis thaliana]	Unigene3646_All//5.00E-54//AT3G07565| DNA binding	Unigene3646_All//0.00E+00//TC168389				nr -
Unigene36460_All	439	4.05	5.77	4.61	3.63	7.06	8.13	8.28	15.90	15.34	5.10E-01	2.09E-01		1.86E-01	6.80E-01		9.59E-01	5.51E-03		1.16E+00	4.12E-04	Up	9.41E-01	2.55E-06		8.89E-01	7.99E-06		Unigene36460_All//gi|3850585|gb|AAC72125.1|//1.00E-32//ESTs gb|H36966, gb|R65511, gb|T42324 and gb|T20569 come from this gene [Arabidopsis thaliana]	Unigene36460_All//1.00E-23//AT1G03290| unknown protein	Unigene36460_All//2.00E-167//TC155392				nr +
Unigene36462_All	1858	3.89	2.75	3.15	12.71	11.58	12.54	23.23	8.95	13.42	-4.97E-01	2.32E-02		-3.02E-01	2.10E-01		-1.34E-01	3.05E-01		-1.89E-02	9.06E-01		-1.38E+00	1.36E-63	Down	-7.92E-01	5.05E-27		Unigene36462_All//gi|116309921|emb|CAH66954.1|//5.00E-10//OSIGBa0147H17.2 [Oryza sativa (indica cultivar-group)]	Unigene36462_All//6.00E-81//AT5G03670| unknown protein	Unigene36462_All//0.00E+00//ES848746				nr -
Unigene36463_All	1254	67.09	44.12	48.37	86.44	68.87	73.51	50.20	34.86	20.87	-6.05E-01	6.18E-26		-4.72E-01	3.66E-16		-3.28E-01	3.04E-13		-2.34E-01	1.34E-06		-5.26E-01	8.62E-19		-1.27E+00	1.03E-83	Down	Unigene36463_All//gi|75164899|sp|Q94A20.1|BI1L_ARATH//1.00E-105//RecName: Full=BI1-like protein >gi|15215827|gb|AAK91458.1| AT4g15470/d13775w [Arabidopsis thaliana] >gi|20453267|gb|AAM19872.1| AT4g15470/d13775w [Arabidopsis thaliana]	Unigene36463_All//6.00E-84//AT4G15470| EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0005 (InterPro:IPR006214); BEST Arabidopsis thaliana protein match is: glutamate binding (TAIR:AT1G03070.1); Has 4000 Blast hits to 3999 proteins in 955 species: Archae - 0; Bacteria - 1775; Metazoa - 750; Fungi - 92; Plants - 143; Viruses - 77; Other Eukaryotes - 1163 (source: NCBI BLink).	Unigene36463_All//0.00E+00//TC137896			GO:0031224	nr +
Unigene36464_All	2316	0.45	0.59	0.14	2.65	2.47	2.42	5.59	1.28	3.96	3.87E-01	5.01E-01		-1.71E+00	2.35E-02		-1.00E-01	7.32E-01		-1.30E-01	6.37E-01		-2.12E+00	1.86E-35	Down	-4.98E-01	2.50E-04		Unigene36464_All//gi|18411254|ref|NP_567155.1|//0.00E+00//XSP1 (xylem serine peptidase 1); identical protein binding / serine-type endopeptidase [Arabidopsis thaliana] >gi|71153422|sp|Q9LLL8.1|XSP1_ARATH RecName: Full=Xylem serine proteinase 1; Short=AtXSP1; AltName: Full=Cucumisin-like protein; Flags: Precursor >gi|6708179|gb|AAF25830.1|AF190794_1 subtilisin-type serine endopeptidase XSP1 [Arabidopsis thaliana]	Unigene36464_All//0.00E+00//AT4G00230| XSP1 (xylem serine peptidase 1); identical protein binding / serine-type endopeptidase	Unigene36464_All//3.00E-117//gi|78327452|gb|DT547726.1|DT547726			GO:0004175//GO:0005515//GO:0005618//GO:0016628//GO:0019538//GO:0044092	nr +
Unigene36467_All	1172	70.53	32.77	45.66	9.22	10.78	7.09	2.78	2.46	1.19	-1.11E+00	1.81E-70	Down	-6.27E-01	3.49E-26		2.25E-01	1.92E-01		-3.79E-01	3.22E-02		-1.75E-01	6.34E-01		-1.22E+00	6.24E-05	Down	Unigene36467_All//gi|116311029|emb|CAH67960.1|//1.00E-58//OSIGBa0142D02-OSIGBa0101B20.3 [Oryza sativa (indica cultivar-group)]	Unigene36467_All//2.00E-64//AT2G35410| 33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative	Unigene36467_All//0.00E+00//TC151430			GO:0003676//GO:0009532//GO:0032991	nr -
Unigene36468_All	1935	2.30	1.39	2.50	33.49	11.96	10.81	64.22	47.11	9.33	-7.28E-01	1.10E-02		1.24E-01	6.63E-01		-1.49E+00	5.32E-109	Down	-1.63E+00	7.41E-109	Down	-4.47E-01	3.98E-27		-2.78E+00	0.00E+00	Down	Unigene36468_All//gi|6091551|gb|AAF01764.2|AF184277_1//4.00E-43//homeodomain-leucine zipper protein 56 [Glycine max]	Unigene36468_All//8.00E-17//AT3G22430| ATHB6; DNA binding / protein binding / sequence-specific DNA binding / transcription activator/ transcription factor	Unigene36468_All//0.00E+00//gi|164265057|gb|ES800393.1|ES800393	HB		GO:0003677//GO:0006350//GO:0009738//GO:0010468//GO:0010556	nr +
Unigene36469_All	286	24.88	14.70	24.76	29.44	19.51	27.63	17.30	11.69	5.99	-7.59E-01	5.37E-04		-6.80E-03	1.00E+00		-5.94E-01	1.45E-03		-9.11E-02	6.73E-01		-5.65E-01	1.97E-02		-1.53E+00	1.52E-09	Down	Unigene36469_All//255585857|ref|XP_002533603.1|//5.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223526504|gb|EEF28772.1| conserved hypothetical protein [Ricinus communis]	Unigene36469_All//1.00E-06//AT2G27775| unknown protein	Unigene36469_All//2.00E-141//gi|11203779|gb|BF272709.1|BF272709				nr -
Unigene36471_All	385	4.35	3.29	3.32	5.56	1.07	2.58	1.54	2.39	0.21	-4.02E-01	4.19E-01		-3.90E-01	4.60E-01		-2.37E+00	3.13E-07	Down	-1.11E+00	1.19E-02		6.35E-01	3.48E-01		-2.89E+00	4.53E-03		Unigene36471_All//gi|20197455|gb|AAM15080.1|//2.00E-13//Expressed protein [Arabidopsis thaliana] >gi|116325954|gb|ABJ98578.1| At2g27775 [Arabidopsis thaliana]	Unigene36471_All//2.00E-11//AT2G27775| unknown protein	Unigene36471_All//0.00E+00//DW513185				nr -
Unigene36472_All	619	3.47	2.29	1.55	3.06	2.61	2.41	10.31	5.54	3.02	-5.97E-01	1.74E-01		-1.16E+00	1.29E-02		-2.26E-01	6.37E-01		-3.45E-01	4.99E-01		-8.98E-01	1.78E-05		-1.77E+00	1.16E-14	Down	Unigene36472_All//gi|20197455|gb|AAM15080.1|//2.00E-14//Expressed protein [Arabidopsis thaliana] >gi|116325954|gb|ABJ98578.1| At2g27775 [Arabidopsis thaliana]	Unigene36472_All//3.00E-12//AT2G27775| unknown protein	Unigene36472_All//0.00E+00//gi|13248493|gb|BF270780.2|BF270780				nr +
Unigene36473_All	1911	1.01	2.36	1.78	3.91	4.09	4.49	7.32	2.97	3.79	1.22E+00	3.36E-05	Up	8.16E-01	1.97E-02		6.50E-02	8.22E-01		2.00E-01	3.93E-01		-1.30E+00	1.89E-19	Down	-9.49E-01	2.01E-12		Unigene36473_All//gi|28530394|emb|CAA63954.1|//0.00E+00//phosphoinositide-specific phospholipase C [Solanum tuberosum]	Unigene36473_All//3.00E-179//AT3G08510| ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C	Unigene36473_All//0.00E+00//TC146670		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0004629	nr -
Unigene36475_All	1333	25.87	10.68	18.98	18.09	14.83	13.76	8.63	3.42	7.32	-1.28E+00	3.24E-37	Down	-4.47E-01	2.03E-06		-2.87E-01	8.17E-03		-3.95E-01	3.01E-04		-1.34E+00	8.76E-17	Down	-2.37E-01	1.22E-01		Unigene36475_All//gi|259563723|gb|ACW83060.1|//1.00E-149//glycosyltransferase family GT8 protein [Populus deltoides]	Unigene36475_All//8.00E-133//AT3G50760| GATL2 (Galacturonosyltransferase-like 2); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene36475_All//0.00E+00//DW241745		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene36476_All	866	85.37	70.50	87.19	109.87	113.68	109.36	28.66	23.50	13.75	-2.76E-01	5.65E-06		3.05E-02	6.67E-01		4.93E-02	4.54E-01		-6.70E-03	9.36E-01		-2.86E-01	4.14E-03		-1.06E+00	2.04E-25	Down			Unigene36476_All//0.00E+00//TC176505				
Unigene36478_All	2001	8.26	6.81	6.15	10.56	12.17	8.96	15.49	7.44	5.69	-2.79E-01	4.86E-02		-4.27E-01	2.84E-03		2.05E-01	7.83E-02		-2.38E-01	6.25E-02		-1.06E+00	1.40E-30	Down	-1.44E+00	9.47E-51	Down	Unigene36478_All//gi|56121882|gb|AAT42222.1|//2.00E-27//At5g40700 [Arabidopsis thaliana] >gi|63003888|gb|AAY25473.1| At5g40700 [Arabidopsis thaliana]	Unigene36478_All//6.00E-63//AT3G01710| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27350.1); Has 1029 Blast hits to 851 proteins in 111 species: Archae - 0; Bacteria - 24; Metazoa - 456; Fungi - 52; Plants - 192; Viruses - 7; Other Eukaryotes - 298 (source: NCBI BLink).	Unigene36478_All//0.00E+00//TC163015				nr -

Unigene36479_All	1251	10.25	7.78	7.96	16.53	18.55	7.40	16.39	5.88	6.62	-3.98E-01	1.24E-02		-3.64E-01	2.99E-02		1.67E-01	1.82E-01		-1.16E+00	5.75E-21	Down	-1.48E+00	4.70E-34	Down	-1.31E+00	3.11E-29	Down	Unigene36479_All//gi|8778446|gb|AAF79454.1|AC025808.36//7.00E-94//F18014.5 [Arabidopsis thaliana]	Unigene36479_All//3.00E-95//AT1G19330| unknown protein	Unigene36479_All//0.00E+00//TC141920				nr -
Unigene36483_All	1827	10.51	4.55	3.61	4.39	4.03	5.76	3.98	1.81	2.53	-1.21E+00	2.20E-19	Down	-1.54E+00	1.19E-26	Down	-1.22E-01	6.15E-01		3.92E-01	2.96E-02		-1.14E+00	1.13E-08	Down	-6.54E-01	4.76E-04		Unigene36483_All//gi|30680811|ref|NP_849992.1|//3.00E-98//tRNA/rRNA methyltransferase (SpoU) family protein [Arabidopsis thaliana] >gi|17065308|gb|AAL32808.1| Unknown protein [Arabidopsis thaliana]	Unigene36483_All//2.00E-126//AT2G19870| tRNA/rRNA methyltransferase (SpoU) family protein	Unigene36483_All//0.00E+00//DT046836			GO:0003676//GO:0008168//GO:0009536//GO:0016467	nr +
Unigene36486_All	1286	177.96	75.26	124.84	45.51	44.21	34.42	2.60	2.34	1.46	-1.24E+00	2.57E-233	Down	-5.11E-01	1.05E-49		-4.20E-02	6.18E-01		-4.03E-01	1.19E-09		-1.51E-01	6.34E-01		-8.35E-01	4.19E-03		Unigene36486_All//gi|115452417|ref|NP_001049809.1|//2.00E-33//Os03g0293100 [Oryza sativa Japonica Group] >gi|113548280|dbj|BAF11723.1| Os03g0293100 [Oryza sativa Japonica Group]	Unigene36486_All//3.00E-31//AT3G56010| unknown protein	Unigene36486_All//0.00E+00//TC152772			GO:0009534	nr -
Unigene36487_All	1392	3.23	1.57	2.41	5.65	6.95	5.35	4.40	3.54	2.43	-1.05E+00	2.90E-04	Down	-4.24E-01	1.62E-01		2.98E-01	1.24E-01		-7.89E-02	7.33E-01		-3.14E-01	1.64E-01		-8.56E-01	3.85E-05		Unigene36487_All//gi|37202038|gb|AAQ89634.1|//1.00E-146//At1g14020 [Arabidopsis thaliana] >gi|110739513|dbj|BAF01665.1| growth regulator like protein [Arabidopsis thaliana] >gi|110739824|dbj|BAF01818.1| growth regulator like protein [Arabidopsis thaliana]	Unigene36487_All//4.00E-135//AT1G14020| unknown protein	Unigene36487_All//0.00E+00//gi|48879429|gb|CO130451.1|CO130451				nr -
Unigene36489_All	1687	12.47	7.00	9.82	4.22	3.72	3.86	1.48	0.30	1.30	-8.33E-01	8.14E-12		-3.45E-01	6.39E-03		-1.85E-01	4.53E-01		-1.31E-01	6.35E-01		-2.31E+00	3.74E-08	Down	-1.87E-01	6.10E-01		Unigene36489_All//gi|15234586|ref|NP_193908.1|//0.00E+00//pseudouridine synthase family protein [Arabidopsis thaliana] >gi|75212600|sp|Q9SVS0.1|PUS6_ARATH RecName: Full=RNA pseudouridine synthase 6, chloroplastic; AltName: Full=RNA-uridine isomerase 6; AltName: Full=RNA pseudouridylate synthase 6; Flags: Precursor	Unigene36489_All//0.00E+00//AT4G21770| pseudouridine synthase family protein	Unigene36489_All//0.00E+00//CO112458			GO:0003676//GO:0009451//GO:0009536//GO:0016866	nr -
Unigene3649_All	1823	8.93	5.86	9.06	8.44	7.90	9.44	23.49	8.51	10.07	-6.06E-01	1.08E-05		2.07E-02	9.00E-01		-9.68E-02	5.79E-01		1.61E-01	3.06E-01		-1.47E+00	2.32E-69	Down	-1.22E+00	3.89E-54	Down	Unigene3649_All//gi|15231911|ref|NP_187456.1|//0.00E+00//SCPL27 (serine carboxypeptidase-like 27); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75337170|sp|Q8SF85.1|SCP27_ARATH RecName: Full=Serine carboxypeptidase-like 27; Flags: Precursor >gi|50253506|gb|AAT71955.1| At3g07990 [Arabidopsis thaliana] >gi|53850527|gb|AAU95440.1| At3g07990 [Arabidopsis thaliana]	Unigene3649_All//0.00E+00//AT3G07990| SCPL27 (serine carboxypeptidase-like 27); serine-type carboxypeptidase	Unigene3649_All//0.00E+00//TC137039		ko00460|Cyanoamino acid metabolism		nr +
Unigene36490_All	1700	6.49	3.25	7.30	48.29	36.38	32.86	8.68	2.66	3.16	-9.99E-01	1.20E-08		1.69E-01	3.71E-01		-4.09E-01	4.11E-15		-5.55E-01	1.95E-23		-1.71E+00	2.68E-30	Down	-1.46E+00	6.24E-25	Down	Unigene36490_All//gi|225467303|ref|XP_002262661.1|//1.00E-172//PREDICTED: similar to auxin-responsive protein-related, partial [Vitis vinifera]	Unigene36490_All//2.00E-172//AT2G04850| auxin-responsive protein-related	Unigene36490_All//0.00E+00//TC142039			GO:0016491	nr -
Unigene36491_All	1126	40.94	50.58	43.37	33.49	31.81	41.31	60.79	139.05	73.03	3.05E-01	1.28E-05		8.32E-02	3.75E-01		-7.45E-02	4.98E-01		3.03E-01	7.83E-05		1.19E+00	2.84E-183	Up	2.65E-01	1.47E-07		Unigene36491_All//gi|224589537|gb|ACN59302.1|//1.00E-125//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene36491_All//1.00E-126//AT2G31880| leucine-rich repeat transmembrane protein kinase, putative	Unigene36491_All//0.00E+00//TC149364		ko04626|Plant-pathogen interaction	GO:0004672//GO:0031410	nr +
Unigene36492_All	2007	28.60	4.92	7.93	45.77	33.37	42.62	75.54	21.78	34.88	-2.54E+00	1.98E-157	Down	-1.85E+00	3.39E-102	Down	-4.56E-01	1.45E-20		-1.03E-01	8.86E-02		-1.79E+00	0.00E+00	Down	-1.12E+00	6.77E-164	Down	Unigene36492_All//gi|25090254|sp|Q9ZT91.1|EFTM_ARATH//0.00E+00//RecName: Full=Elongation factor Tu, mitochondrial; Flags: Precursor >gi|3924612|gb|AAC79113.1| mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi|4263511|gb|AAD15337.1| mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi|7269778|emb|CAB77778.1| mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi|22531166|gb|AAM97087.1| mitochondrial elongation factor Tu [Arabidopsis thaliana] >gi|31576381|gb|AAP19517.1| At4g02930 [Arabidopsis thaliana] >gi|110742332|dbj|BAE99090.1| mitochondrial elongation factor Tu [Arabidopsis thaliana]	Unigene36492_All//0.00E+00//AT4G02930| elongation factor Tu, putative / EF-Tu, putative	Unigene36492_All//0.00E+00//TC134098		ko04626|Plant-pathogen interaction	GO:0006412//GO:0008135//GO:0010038//GO:0016772//GO:0017111//GO:0030312//GO:0032559//GO:0032561//GO:0043231//GO:0046914	nr -
Unigene36496_All	867	2.41	5.61	3.69	11.66	16.88	9.90	2.88	4.44	3.72	1.22E+00	1.58E-05	Up	6.10E-01	9.40E-02		5.33E-01	1.12E-04		-2.37E-01	2.30E-01		6.24E-01	2.55E-02		3.71E-01	2.31E-01		Unigene36496_All//gi|124359162|gb|ABN05685.1|//4.00E-19//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene36496_All//3.00E-05//AT3G09510| nucleic acid binding	Unigene36496_All//0.00E+00//TC175511			GO:0005488	nr -
Unigene36498_All	970	7.17	7.89	6.53	5.29	5.47	4.42	1.87	0.56	1.52	1.37E-01	5.64E-01		-1.35E-01	6.12E-01		4.76E-02	8.78E-01		-2.58E-01	3.95E-01		-1.74E+00	1.71E-04	Down	-3.03E-01	4.88E-01		Unigene36498_All//gi|297819370|ref|XP_002877568.1|//2.00E-53//esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323406|gb|EFH53827.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36498_All//2.00E-54//AT3G47590| esterase/lipase/thioesterase family protein	Unigene36498_All//0.00E+00//TC170286				nr +
Unigene36499_All	1583	62.90	37.45	75.18	148.06	107.61	125.25	137.39	239.92	38.86	-7.48E-01	3.43E-44		2.57E-01	1.07E-07		-4.60E-01	6.57E-53		-2.41E-01	2.60E-14		8.04E-01	7.01E-231		-1.82E+00	0.00E+00	Down	Unigene36499_All//gi|148887523|gb|ABR15365.1|//0.00E+00//calreticulin [Triticum aestivum]	Unigene36499_All//1.00E-144//AT1G08450| CRT3 (CALRETICULIN 3); calcium ion binding / unfolded protein binding	Unigene36499_All//0.00E+00//TC135138		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	GO:0005515//GO:0031410//GO:0043231//GO:0044267//GO:0046872	nr +
Unigene36500_All	1843	32.14	26.28	24.50	49.11	46.69	65.97	95.02	52.27	45.44	-2.90E-01	2.31E-05		-3.91E-01	2.24E-08		-7.29E-02	2.56E-01		4.26E-01	2.86E-21		-8.62E-01	2.45E-120		-1.06E+00	1.83E-175	Down	Unigene36500_All//gi|226506470|ref|NP_001151538.1|//0.00E+00//eukaryotic peptide chain release factor subunit 1-1 [Zea mays] >gi|195647508|gb|ACG43222.1| eukaryotic peptide chain release factor subunit 1-1 [Zea mays]	Unigene36500_All//0.00E+00//AT3G26618| ERF1-3 (eukaryotic release factor 1-3); translation release factor	Unigene36500_All//0.00E+00//TC174543			GO:0003747//GO:0006412//GO:0044424	nr +
Unigene36503_All	1449	26.86	17.27	12.61	49.16	64.71	137.83	79.66	213.71	602.72	-6.37E-01	1.46E-13		-1.09E+00	1.21E-31	Down	3.97E-01	5.39E-16		1.49E+00	1.49E-287	Up	1.42E+00	0.00E+00	Up	2.92E+00	0.00E+00	Up	Unigene36503_All//gi|33469564|gb|AAQ19807.1|//0.00E+00//polygalacturonase-inhibiting protein [Gossypium barbadense] >gi|33469566|gb|AAQ19808.1| polygalacturonase-inhibiting protein [Gossypium barbadense]	Unigene36503_All//8.00E-123//AT5G06860| PGIP1 (POLYGALACTURONASE INHIBITING PROTEIN 1); protein binding	Unigene36503_All//0.00E+00//TC129661		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene36508_All	2174	1.28	0.07	0.17	2.98	2.90	1.12	3.33	1.06	1.25	-4.19E+00	1.74E-12	Down	-2.89E+00	7.82E-09	Down	-3.94E-02	8.78E-01		-1.41E+00	3.06E-09	Down	-1.65E+00	1.43E-14	Down	-1.42E+00	3.55E-12	Down	Unigene36508_All//gi|32483159|emb|CAE02147.1|//5.00E-27//OSJNBa0081G05.2 [Oryza sativa (japonica cultivar-group)] >gi|116309213|emb|CAH66305.1| OSIGBa0135K14.2 [Oryza sativa (indica cultivar-group)] >gi|116309230|emb|CAH66320.1| OSIGBa0150M16.3 [Oryza sativa (indica cultivar-group)]	Unigene36508_All//4.00E-09//AT1G40390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Endonuclease/exonuclease/phosphatase (InterPro:IPR005135), RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43760.1); Has 480 Blast hits to 479 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 480; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene36508_All//5.00E-20//ES803923			GO:0005488	nr -
Unigene36509_All	1258	9.90	19.58	17.14	12.04	21.68	31.09	33.68	52.19	62.29	9.84E-01	8.28E-18		7.92E-01	1.12E-10		8.49E-01	5.63E-18		1.37E+00	5.41E-50	Up	6.32E-01	7.13E-27		8.87E-01	3.48E-58		Unigene36509_All//gi|183979104|emb|CAP08301.1|//1.00E-104//DNA-binding protein [Vitis thunbergii]	Unigene36509_All//4.00E-58//AT1G13960| WRKY4; DNA binding / transcription factor	Unigene36509_All//0.00E+00//TC132314	WRKY	ko04626|Plant-pathogen interaction	GO:0006350	nr -
Unigene36511_All	877	2.98	1.16	3.40	2.50	1.85	2.94	5.21	2.43	4.18	-1.37E+00	7.23E-04	Down	1.89E-01	6.29E-01		-4.38E-01	3.14E-01		2.32E-01	6.29E-01		-1.10E+00	1.82E-05	Down	-3.17E-01	2.13E-01		Unigene36511_All//gi|240254165|ref|NP_173884.5|//8.00E-51//UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Arabidopsis thaliana]	Unigene36511_All//4.00E-52//AT1G25054| UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	Unigene36511_All//0.00E+00//TC160354			GO:0001071//GO:0008654//GO:0010468//GO:0016811//GO:0043231	nr +
Unigene36512_All	1430	1.32	0.50	0.78	1.74	1.11	1.17	3.43	1.29	1.95	-1.41E+00	4.09E-03		-7.52E-01	1.34E-01		-6.53E-01	9.36E-02		-5.76E-01	1.65E-01		-1.42E+00	3.12E-08	Down	-8.15E-01	5.20E-04		Unigene36512_All//gi|240254165|ref|NP_173884.5|//1.00E-100//UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [Arabidopsis thaliana]	Unigene36512_All//3.00E-102//AT1G25054| UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase	Unigene36512_All//0.00E+00//TC160354			GO:0001071//GO:0008654//GO:0010468//GO:0016811	nr -
Unigene36514_All	1395	12.08	11.95	9.08	18.03	19.87	10.30	7.55	5.15	2.80	-1.52E-02	9.33E-01		-4.11E-01	3.80E-03		1.40E-01	2.28E-01		-8.09E-01	3.35E-14		-5.50E-01	4.37E-04		-1.43E+00	1.35E-17	Down	Unigene36514_All//gi|115457076|ref|NP_001052138.1|//8.00E-67//Os04g0166600 [Oryza sativa Japonica Group] >gi|113563709|dbj|BAF14052.1| Os04g0166600 [Oryza sativa Japonica Group]	Unigene36514_All//1.00E-46//AT1G19330| unknown protein	Unigene36514_All//0.00E+00//TC142033				nr -
Unigene36516_All	1325	1.26	1.26	1.33	3.05	1.98	2.97	4.91	2.43	2.41	-1.80E-03	9.94E-01		6.98E-02	8.91E-01		-6.25E-01	3.16E-02		-3.83E-02	9.22E-01		-1.02E+00	1.16E-06	Down	-1.03E+00	4.80E-07	Down	Unigene36516_All//gi|18417838|ref|NP_567879.1|//1.00E-142//UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter-related [Arabidopsis thaliana]	Unigene36516_All//3.00E-116//AT4G31600| UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter-related	Unigene36516_All//0.00E+00//gi|48815451|gb|CO116764.1|CO116764				nr +
Unigene36519_All	583	0.45	0.09	0.00	2.73	1.83	0.62	1.38	0.65	0.96	-2.37E+00	2.14E-01		-8.81E+00	8.56E-02		-5.79E-01	2.71E-01		-2.14E+00	2.07E-04	Down	-1.09E+00	1.29E-01		-5.26E-01	4.35E-01		Unigene36519_All//gi|21553556|gb|AM62649.1|//6.00E-69//protein kinase-like protein [Arabidopsis thaliana]	Unigene36519_All//4.00E-70//AT5G39010| protein kinase-related	Unigene36519_All//7.00E-124//DW519595		ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0016020//GO:0032559//GO:0043401	nr -
Unigene3652_All	534	12.64	5.69	9.57	13.81	7.61	15.98	8.23	4.15	4.18	-1.15E+00	7.84E-07	Down	-4.01E-01	9.74E-02		-8.60E-01	1.53E-05		2.11E-01	3.55E-01		-9.89E-01	1.38E-04		-9.79E-01	1.05E-04				Unigene3652_All//9.00E-148//gi|109844102|gb|DW242660.1|DW242660				

Unigene36520_All	2284	1.28	0.95	0.28	14.83	8.67	5.64	5.04	2.89	1.48	-4.27E-01	2.46E-01			-2.20E+00	5.40E-07	Down	-7.75E-01	9.17E-20		-1.40E+00	2.40E-45	Down	-8.00E-01	1.00E-07		-1.76E+00	1.27E-25	Down	Unigene36520_All//gi|15232406|ref|NP_190971.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana] >gi|7630023|emb|CAB88365.1|protein kinase-like protein [Arabidopsis thaliana] >gi|15450846|gb|AAK96694.1|protein kinase-like protein [Arabidopsis thaliana] >gi|25083647|gb|AAV72100.1|protein kinase-like protein [Arabidopsis thaliana]	Unigene36520_All//0.00E+00//AT3G54030| protein kinase family protein	Unigene36520_All//0.00E+00//DW519595		ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene36521_All	1286	11.55	18.87	11.10	13.44	15.74	25.46	18.77	55.97	86.71	7.08E-01	2.34E-10			-5.83E-02	7.21E-01		2.28E-01	7.44E-02		9.22E-01	1.72E-22		1.58E+00	7.48E-129	Up	2.21E+00	0.00E+00	Up	Unigene36521_All//gi|6679689|dbj|BAD99112.1|//2.00E-63//dynein light chain [Vicia faba]	Unigene36521_All//1.00E-32//AT5G20110| dynein light chain, pstative	Unigene36521_All//0.00E+00//gi|78331352|gb|DT551626.1|DT551626			GO:0003774//GO:0005488//GO:0009987//GO:0015630	nr -
Unigene36524_All	1423	13.20	13.03	16.39	3.26	4.65	7.17	4.28	3.73	8.85	-1.84E-02	9.06E-01			3.12E-01	9.24E-03		5.13E-01	2.26E-02		1.14E+00	3.07E-10	Up	-1.98E-01	4.02E-01		1.05E+00	5.03E-13	Up	Unigene36524_All//gi|260513718|gb|ACX42571.1|//2.00E-83//CONSTANS-like zinc finger protein [Glycine max]	Unigene36524_All//2.00E-80//AT2G47890| zinc finger (B-box type) family protein	Unigene36524_All//0.00E+00//TC144622	C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0010468	nr -
Unigene36527_All	1910	20.33	11.27	14.66	54.27	42.98	50.29	64.37	38.60	30.81	-8.50E-01	7.24E-22			-4.71E-01	8.69E-08		-3.37E-01	2.60E-13		-1.10E-01	4.69E-02		-7.38E-01	6.14E-65		-1.06E+00	3.48E-123	Down	Unigene36527_All//gi|74273625|gb|AB001880.1|//0.00E+00//sterol delta-7 reductase DWF5 [Gossypium hirsutum]	Unigene36527_All//0.00E+00//AT1G50430| DWF5 (DWARF 5); sterol delta7 reductase	Unigene36527_All//0.00E+00//TC157178		ko00100|Steroid biosynthesis	GO:0016129//GO:0016628//GO:0031227	nr -
Unigene36528_All	2199	4.64	3.23	2.42	10.24	7.99	7.99	3.38	2.19	1.65	-5.24E-01	3.41E-03			-9.38E-01	5.78E-07		-3.59E-01	1.03E-03		-3.58E-01	1.82E-03		-6.31E-01	9.13E-04		-1.04E+00	5.33E-08	Down	Unigene36528_All//gi|115480133|ref|NP_001063660.1|//2.00E-14//Os09g0514500 [Oryza sativa Japonica Group] >gi|317114477|dbj|BAC77633.1|aleurone layer morphogenesis protein [Oryza sativa Japonica Group] >gi|113631893|dbj|BAF25574.1|Os09g0514500 [Oryza sativa Japonica Group]	Unigene36528_All//3.00E-42//AT1G05950| unknown protein	Unigene36528_All//0.00E+00//TC130527				nr -
Unigene36529_All	1572	19.24	3.26	12.60	22.82	14.63	13.93	1.29	0.58	1.12	-2.56E+00	4.40E-84	Down		-6.10E-01	1.58E-09		-6.41E-01	4.63E-15		-7.11E-01	4.06E-16		-1.14E+00	5.27E-03		-2.11E-01	6.05E-01		Unigene36529_All//gi|79484897|ref|NP_567694.2|//1.00E-155//YSL1 (YELLOW STRIPE LIKE 1); oligopeptide transporter [Arabidopsis thaliana] >gi|160359043|sp|Q6R3L0.2|YSL1_ARATH RecName: Full=Metal-nicotianamine transporter YSL1; AltName: Full=Protein YELLOW STRIPE LIKE 1; Short=AtYSL1	Unigene36529_All//2.00E-147//AT4G24120| YSL1 (YELLOW STRIPE LIKE 1); oligopeptide transporter					nr +
Unigene3653_All	589	1.60	1.81	1.72	2.54	1.29	2.15	3.30	0.57	2.10	1.76E-01	7.74E-01			1.03E-01	8.77E-01		-9.80E-01	5.91E-02		-2.41E-01	6.82E-01		-2.54E+00	3.67E-07	Down	-6.55E-01	1.01E-01				Unigene3653_All//0.00E+00//BG446032					
Unigene36531_All	1050	0.80	2.99	1.83	1.57	0.98	2.97	1.09	7.24	5.96	1.91E+00	1.19E-06	Up		1.20E+00	1.64E-02		-6.70E-01	1.82E-01		9.23E-01	9.20E-03		2.74E+00	3.89E-28	Up	2.45E+00	4.09E-21	Up	Unigene36531_All//gi|4337001|gb|AAD18030.1|//7.00E-36//Tsi1-interacting protein TSIP1 [Nicotiana tabacum]	Unigene36531_All//2.00E-35//AT2G24860| chaperone protein dnaJ-related	Unigene36531_All//4.00E-167//TC159135			GO:0005515//GO:0043231//GO:0044267	nr -
Unigene36532_All	1079	18.23	30.34	18.46	14.82	16.88	27.46	13.44	54.46	73.22	7.35E-01	1.49E-14			1.77E-02	9.09E-01		1.88E-01	1.86E-01		8.90E-01	2.92E-19		2.02E+00	3.47E-148	Up	2.45E+00	3.49E-257	Up	Unigene36532_All//gi|4337001|gb|AAD18030.1|//7.00E-89//Tsi1-interacting protein TSIP1 [Nicotiana tabacum]	Unigene36532_All//3.00E-43//AT2G24860| chaperone protein dnaJ-related	Unigene36532_All//0.00E+00//TC159135			GO:0005515//GO:0043231//GO:0044267	nr -
Unigene36533_All	1549	12.90	8.73	8.04	15.08	16.12	13.09	8.38	3.43	4.40	-5.63E-01	4.57E-06			-6.82E-01	8.50E-08		9.57E-02	4.78E-01		-2.04E-01	9.49E-02		-1.29E+00	6.77E-18	Down	-9.30E-01	3.08E-11		Unigene36533_All//gi|22331752|ref|NP_190825.2|//1.00E-114//ATP binding [Arabidopsis thaliana] >gi|18377853|gb|AAL67113.1|AT3g52570/F2206_50 [Arabidopsis thaliana] >gi|20453341|gb|AAM19909.1|AT3g52570/F2206_50 [Arabidopsis thaliana]	Unigene36533_All//3.00E-113//AT3G52570| ATP binding	Unigene36533_All//0.00E+00//TC150527				nr +
Unigene36534_All	2507	10.94	4.87	8.22	14.58	12.95	13.10	5.57	0.95	2.43	-1.17E+00	6.49E-26	Down		-4.12E-01	1.25E-04		-1.71E-01	6.44E-02		-1.55E-01	1.14E-01		-2.55E+00	1.97E-47	Down	-1.19E+00	1.23E-17	Down	Unigene36534_All//gi|15220455|ref|NP_176918.1|//0.00E+00//leucine-rich repeat family protein [Arabidopsis thaliana] >gi|3176660|gb|AAC18784.1| Similar to ERECTA receptor protein kinase gb|U47029 from A. thaliana [Arabidopsis thaliana] >gi|224589465|gb|ACN59266.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene36534_All//0.00E+00//AT1G67510| leucine-rich repeat family protein	Unigene36534_All//0.00E+00//TC155305			GO:0004672//GO:0006464//GO:0007167//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene36535_All	1082	14.07	9.46	8.86	23.16	24.25	23.12	18.95	8.42	8.36	-5.73E-01	5.94E-05			-6.68E-01	6.48E-06		6.66E-02	6.06E-01		-2.10E-03	9.84E-01		-1.17E+00	5.72E-24	Down	-1.18E+00	4.67E-25	Down	Unigene36535_All//gi|48310199|gb|AAT41773.1|//4.00E-58//At5g24600 [Arabidopsis thaliana] >gi|50198891|gb|AAT70465.1|At5g24600 [Arabidopsis thaliana]	Unigene36535_All//4.00E-55//AT3G18215| unknown protein	Unigene36535_All//0.00E+00//gi|109856813|gb|DW485792.1|DW485792			GO:0016020	nr +
Unigene36536_All	2409	70.17	163.07	72.79	22.44	22.96	29.30	0.05	0.10	0.00	1.22E+00	0.00E+00	Up		5.28E-02	2.55E-01		3.31E-02	7.42E-01		3.85E-01	1.43E-10		9.82E-01	5.17E-01		-5.72E+00	2.00E-01		Unigene36536_All//gi|22331230|ref|NP_188746.2|//0.00E+00//ABC transporter family protein [Arabidopsis thaliana] >gi|109896158|sp|Q8RWI9.2|AB15G_ARATH RecName: Full=ABC transporter G family member 15; Short=ABC transporter ABCG.15; Short=AtABCG15; AltName: Full=White-brown complex homolog protein 15; Short=AtWBC15; AltName: Full=White-brown complex homolog protein 22; Short=AtWBC22	Unigene36536_All//0.00E+00//AT3G21090| ABC transporter family protein	Unigene36536_All//0.00E+00//TC140077		ko03040|Spliceosome//ko02010|ABC transporters	GO:0006633//GO:0006970//GO:0009725//GO:0015405//GO:0015604//GO:0017111//GO:0032559//GO:0044464	nr -
Unigene36537_All	2135	4.19	1.95	4.12	11.74	11.40	8.04	6.04	3.23	2.15	-1.11E+00	2.60E-08	Down		-2.62E-02	9.11E-01		-4.15E-02	7.85E-01		-5.46E-01	2.21E-07		-9.03E-01	2.48E-10		-1.49E+00	1.07E-22	Down	Unigene36537_All//gi|30725324|gb|AF37684.1|//3.00E-52//At3g01680 [Arabidopsis thaliana]	Unigene36537_All//1.00E-53//AT3G01680| unknown protein	Unigene36537_All//0.00E+00//TC145686				nr +
Unigene36540_All	1189	5.19	2.22	3.85	64.14	37.82	14.17	14.72	2.78	1.54	-1.23E+00	6.41E-07	Down		-4.31E-01	8.87E-02		-7.62E-01	8.25E-43		-2.18E+00	1.26E-189	Down	-2.41E+00	1.64E-55	Down	-3.26E+00	8.20E-79	Down	Unigene36540_All//gi|18201934|gb|AK92458.3|AF398149_1/6.00E-41//kinesin-like protein heavy chain [Arabidopsis thaliana]	Unigene36540_All//2.00E-38//AT3G44730| kinesin motor protein-related	Unigene36540_All//0.00E+00//TC135621			GO:0000166//GO:0003774	nr +
Unigene36541_All	605	5.45	6.95	12.23	4.61	6.32	9.63	8.81	12.99	8.49	3.52E-01	2.48E-01			1.17E+00	3.34E-07	Up	4.54E-01	1.63E-01		1.06E+00	1.54E-05	Up	5.61E-01	2.44E-03		-5.19E-02	8.33E-01		Unigene36541_All//gi|110738363|dbj|BAF01108.1|//5.00E-59//protein kinase [Arabidopsis thaliana]	Unigene36541_All//3.00E-60//AT4G32660| AME3; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene36541_All//0.00E+00//CO126408			GO:0004672//GO:0006464//GO:0032559//GO:0043231	nr +
Unigene36543_All	1198	45.64	248.86	173.13	56.09	83.93	38.08	11.79	3.11	11.61	2.45E+00	0.00E+00	Up		1.92E+00	0.00E+00	Up	5.81E-01	4.90E-34		-5.59E-01	1.64E-19		-1.92E+00	4.74E-34	Down	-2.24E-02	8.92E-01		Unigene36543_All//gi|87241486|gb|AB033344.1|//2.00E-72//Pollen Ole e 1 allergen and extensin [Medicago truncatula]	Unigene36543_All//5.00E-38//AT5G15780| pollen Ole e 1 allergen and extensin family protein	Unigene36543_All//0.00E+00//gi|78324253|gb|DT544527.1|DT544527		ko03040|Spliceosome		nr +
Unigene36545_All	2988	0.11	0.20	1.02	0.30	0.39	0.50	0.78	0.52	0.77	9.53E-01	3.14E-01			3.27E+00	8.11E-11	Up	3.85E-01	5.89E-01		7.33E-01	1.98E-01		-5.88E-01	1.23E-01		-9.10E-03	9.73E-01		Unigene36545_All//gi|224062137|ref|XP_002360773.1|//1.00E-172//jumonji domain protein [Populus trichocarpa] >gi|222842499|gb|EEE80046.1|jumonji domain protein [Populus trichocarpa]	Unigene36545_All//4.00E-165//AT1G08620| transcription factor	Unigene36545_All//0.00E+00//TC166128				nr -
Unigene36546_All	1753	4.98	3.73	2.13	9.86	11.59	6.72	15.73	5.15	10.23	-4.19E-01	3.45E-02			-1.23E+00	5.18E-09	Down	2.33E-01	6.67E-02		-5.52E-01	2.08E-05		-1.61E+00	1.83E-51	Down	-6.21E-01	8.67E-12		Unigene36546_All//gi|15231175|ref|NP_190797.1|//1.00E-104//IQ03 (IQ-domain 3); calmodulin binding [Arabidopsis thaliana]	Unigene36546_All//1.00E-74//AT3G52290| IQD3 (IQ-domain 3); calmodulin binding	Unigene36546_All//0.00E+00//gi|164334055|gb|ES816874.1|ES816874			GO:0016020	nr -
Unigene36547_All	2002	8.96	6.38	8.88	16.92	16.96	17.33	25.13	12.80	11.14	-4.91E-01	1.67E-04			-1.30E-02	9.47E-01		3.40E-03	9.78E-01		3.42E-02	7.57E-01		-9.74E-01	6.35E-43		-1.17E+00	1.49E-59	Down	Unigene36547_All//gi|79473201|ref|NP_193072.2|//1.00E-163//catalytic [Arabidopsis thaliana]	Unigene36547_All//6.00E-164//AT4G13360| catalytic	Unigene36547_All//0.00E+00//TC147804		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism		nr +
Unigene3655_All	1344	3.66	27.45	2.50	15.97	64.46	46.47	9.15	13.25	13.25	2.91E+00	2.28E-116	Up		-5.52E-01	5.26E-02		2.01E+00	2.20E-208	Up	1.54E+00	7.06E-95	Up	5.33E-01	4.98E-06		5.33E-01	3.13E-06		Unigene3655_All//gi|18396229|ref|NP_566175.1|//5.00E-86//LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41) [Arabidopsis thaliana] >gi|27805498|sp|Q9M886.1|LBD41_ARATH RecName: Full=LOB domain-containing protein 41; AltName: Full=ASYMMETRIC LEAVES 2-like protein 38; Short=AS2-like protein 38 >gi|17227172|gb|AAL38040.1|AF447895_1 LOB DOMAIN 41 [Arabidopsis thaliana] >gi|19699326|gb|AAL91273.1|AT3g02550/F16B3_18 [Arabidopsis thaliana] >gi|21689615|gb|AAM67429.1|AT3g02550/F16B3_18 [Arabidopsis thaliana] >gi|219807152|dbj|BAH10582.1|ASYMMETRIC LEAVES2-like 38 protein [Arabidopsis thaliana]	Unigene3655_All//3.00E-80//AT3G02550| LBD41 (LOB DOMAIN-CONTAINING PROTEIN 41)	Unigene3655_All//0.00E+00//TC161269		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene36550_All	970	36.35	57.04	32.99	67.02	80.27	71.28	32.17	101.26	35.24	6.50E-01	1.50E-19			-1.40E-01	1.77E-01		2.60E-01	2.46E-06		8.90E-02	2.33E-01		1.65E+00	2.36E-188	Up	1.32E-01	1.35E-01		Unigene36550_All//gi|18396059|ref|NP_564263.1|//6.00E-54//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|9295734|gb|AAF87040.1|AC006535_18 T24P13.19 [Arabidopsis thaliana] >gi|13605625|gb|AAK32806.1|AF361638_1 At1g26800/T24P13_21 [Arabidopsis thaliana] >gi|15450675|gb|AAO96609.1|At1g26800/T24P13_21 [Arabidopsis thaliana] >gi|15777873|gb|AAL05897.1|At1g26800/T24P13_21 [Arabidopsis thaliana]	Unigene36550_All//6.00E-54//AT1G26800| zinc finger (C3HC4-type RING finger) family protein	Unigene36550_All//0.00E+00//gi|109876500|gb|DW505474.1|DW505474			GO:0016914	nr +

Unigene36554_All	1088	3.08	4.19	2.69	2.29	1.42	2.03	1.55	0.96	0.26	4.46E-01	1.21E-01		-1.93E-01	6.19E-01		-6.85E-01	7.79E-02		-1.71E-01	6.71E-01		-6.95E-01	1.29E-01		-2.60E+00	9.91E-07	Down	Unigene36554_All//gi|20197943|gb|AAM15322.1|//4.00E-78//Expressed protein [Arabidopsis thaliana]	Unigene36554_All//1.00E-57//AT2G36885| unknown protein				GO:0009536	nr +
Unigene36555_All	404	6.48	45.90	11.47	12.95	14.58	7.15	3.98	129.84	0.99	2.83E+00	4.86E-57	Up	8.25E-01	4.76E-03		1.71E-01	5.54E-01		-8.56E-01	8.80E-04		5.03E+00	0.00E+00	Up	-2.01E+00	5.95E-05	Down	Unigene36555_All//gi|159138935|gb|ABW89467.1|//2.00E-32//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene36555_All//6.00E-28//AT2G29500| 17.6 kDa class I small heat shock protein (HSP17.6B-CI)	Unigene36555_All//0.00E+00//gi|21101419|gb|BQ413732.1|BQ413732			GO:0044424//GO:0050896	nr -
Unigene36556_All	1136	119.84	359.99	160.22	95.02	98.79	82.10	9.12	134.66	6.10	1.59E+00	0.00E+00	Up	4.19E-01	1.21E-27		5.61E-02	3.42E-01		-2.11E-01	1.60E-05		3.88E+00	0.00E+00	Up	-5.80E-01	1.62E-04		Unigene36556_All//gi|159138935|gb|ABW89467.1|//2.00E-81//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene36556_All//2.00E-55//AT2G29500| 17.6 kDa class I small heat shock protein (HSP17.6B-CI)	Unigene36556_All//0.00E+00//TC150366			GO:0044424//GO:0050896	nr -
Unigene36558_All	1264	88.75	47.66	53.12	49.46	36.61	23.12	3.51	1.19	1.36	-8.97E-01	1.30E-67		-7.40E-01	3.62E-47		-4.34E-01	6.15E-13		-1.10E+00	3.96E-57	Down	-1.56E+00	1.42E-08	Down	-1.37E+00	1.69E-07	Down	Unigene36558_All//gi|300793596|tpg|DAA33864.1|//1.00E-121//TPA: TPA_inf: aquaporin PIP2;4 [Gossypium hirsutum]	Unigene36558_All//2.00E-125//AT4G35100| PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel	Unigene36558_All//0.00E+00//TC141725				nr +
Unigene36559_All	1878	8.86	1.08	2.78	51.11	40.25	9.79	11.26	1.11	2.29	-3.04E+00	1.25E-55	Down	-1.67E+00	5.01E-26	Down	-3.45E-01	6.44E-13		-2.38E+00	8.20E-267	Down	-3.34E+00	3.49E-94	Down	-2.30E+00	2.78E-65	Down	Unigene36559_All//gi|42563104|ref|NP_177183.2|//1.00E-126//nodulin MtN21 family protein [Arabidopsis thaliana]	Unigene36559_All//2.00E-115//AT1G70260| nodulin MtN21 family protein	Unigene36559_All//0.00E+00//TC139500				nr -
Unigene3656_All	1373	2.67	39.49	6.71	2.32	3.49	8.98	2.22	12.57	13.46	3.89E+00	5.76E-222	Up	1.33E+00	1.18E-10	Up	5.86E-01	3.10E-02		1.95E+00	2.54E-26	Up	2.50E+00	3.84E-57	Up	2.60E+00	4.36E-65	Up	Unigene3656_All//gi|224146569|ref|XP_002336318.1|//1.00E-139//amino acid permease [Populus trichocarpa] >gi|222834652|gb|EEE73115.1| amino acid permease [Populus trichocarpa]	Unigene3656_All//2.00E-113//AT5G23810| AAP7; amino acid transmembrane transporter	Unigene3656_All//0.00E+00//TC163111				nr -
Unigene36561_All	1866	4.96	223.97	15.47	14.95	52.56	48.91	29.89	44.77	61.53	5.50E+00	0.00E+00	Up	1.64E+00	9.89E-44	Up	1.81E+00	1.10E-205	Up	1.71E+00	7.65E-161	Up	5.83E-01	1.61E-29		1.04E+00	1.44E-110	Up	Unigene36561_All//gi|124057819|gb|ABD72603.1|//0.00E+00//raffinose synthase [Cucumis sativus]	Unigene36561_All//0.00E+00//AT5G40390| SIP1 (seed imbibition 1-like); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene36561_All//0.00E+00//TC162566		ko00052|Galactose metabolism	GO:0004672//GO:0005985//GO:0006464//GO:0006950//GO:0008378//GO:0009312//GO:0009536//GO:0019406//GO:0023060//GO:0032559	nr -
Unigene36562_All	1106	22.99	18.33	18.78	40.81	37.89	35.16	62.04	44.59	26.62	-3.27E-01	2.73E-03		-2.92E-01	1.12E-02		-1.07E-01	2.33E-01		-2.15E-01	8.13E-03		-4.77E-01	3.60E-17		-1.22E+00	3.96E-86	Down	Unigene36562_All//gi|75338884|sp|Q9ZR40.1|U2A2B_NICPL//1.00E-128//RecName: Full=Splicing factor U2af large subunit B; AltName: Full=U2 small nuclear ribonucleoprotein auxiliary factor large subunit B; Short=U2 snRNP auxiliary factor large subunit B; AltName: Full=U2 auxiliary factor 65 kDa subunit B; AltName: Full=NpU2AF65b >gi|3850821|emb|CAA77135.1| U2 snRNP auxiliary factor, large subunit [Nicotiana plumbaginifolia]	Unigene36562_All//3.00E-120//AT1G60900| U2 snRNP auxiliary factor large subunit, putative	Unigene36562_All//0.00E+00//ES803534		ko03040|Spliceosome		nr +
Unigene36563_All	1957	9.46	40.08	15.40	42.59	37.34	25.59	31.46	17.28	17.65	2.08E+00	1.14E-167	Up	7.02E-01	5.15E-12		-1.90E-01	5.35E-04		-7.35E-01	8.52E-39		-8.64E-01	5.41E-43		-8.34E-01	1.27E-41		Unigene36563_All//gi|268374460|gb|AC204445.1|//7.00E-79//bHLH1 transcription factor [Hevea brasiliensis]	Unigene36563_All//6.00E-31//AT1G29950| transcription factor/ transcription regulator	Unigene36563_All//0.00E+00//TC171247	bHLH		GO:0010468//GO:0043231	nr -
Unigene36565_All	1706	1.44	1.93	1.28	2.60	2.40	1.93	1.04	1.67	2.50	4.22E-01	2.28E-01		-1.72E-01	6.75E-01		-1.14E-01	7.43E-01		-4.27E-01	1.56E-01		6.79E-01	4.18E-02		1.26E+00	2.09E-06	Up	Unigene36565_All//gi|224105735|ref|XP_002313916.1|//1.00E-113//single myb histone [Populus trichocarpa] >gi|222850324|gb|EEE87871.1| single myb histone [Populus trichocarpa]	Unigene36565_All//1.00E-81//AT1G49950| DNA-binding protein, putative	Unigene36565_All//0.00E+00//gi|78323800|gb|DT544074.1|DT544074	MYB-related		GO:0009987//GO:0043229	nr +
Unigene36566_All	1806	0.35	1.82	1.95	2.62	2.17	1.70	2.79	0.79	2.82	2.39E+00	6.05E-09	Up	2.49E+00	1.60E-09	Up	-2.70E-01	3.67E-01		-6.24E-01	2.42E-02		-1.82E+00	8.72E-12	Down	1.94E-02	9.60E-01		Unigene36566_All//gi|224118358|ref|XP_002317799.1|//0.00E+00//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222858472|gb|EEE96019.1| olippopeptide transporter OPT family [Populus trichocarpa]	Unigene36566_All//0.00E+00//AT4G27730| OPT6 (OLIGOPEPTIDE TRANSPORTER 1); oligopeptide transporter	Unigene36566_All//0.00E+00//TC152622			GO:0015197//GO:0015833//GO:0016020	nr -
Unigene36567_All	1219	58.20	73.20	100.03	14.87	27.03	61.58	41.34	55.03	128.41	3.31E-01	1.47E-09		7.81E-01	2.56E-56		8.62E-01	3.26E-22		2.05E+00	7.14E-169	Up	4.13E-01	4.54E-13		1.64E+00	9.10E-301	Up	Unigene36567_All//gi|18700129|gb|AAL77676.1|//1.00E-129//At2g36630/T1011.26 [Arabidopsis thaliana] >gi|22137236|gb|AAM91463.1| At2g36630/T1011.26 [Arabidopsis thaliana]	Unigene36567_All//2.00E-103//AT2G36630| unknown protein	Unigene36567_All//0.00E+00//TC130953			GO:0044464	nr +
Unigene36576_All	1107	23.25	6.00	4.86	26.59	18.57	28.40	43.39	15.10	17.85	-1.96E+00	2.10E-51	Down	-2.26E+00	1.69E-59	Down	-5.18E-01	1.23E-08		9.45E-02	4.22E-01		-1.52E+00	3.69E-82	Down	-1.28E+00	2.96E-65	Down	Unigene36576_All//gi|192910792|gb|ACF06504.1|//7.00E-63//60S ribosomal protein L28 [Elaeis guineensis]	Unigene36576_All//2.00E-60//AT4G29410| 60S ribosomal protein L28 (RPL28C)	Unigene36576_All//0.00E+00//TC143895		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0030312	nr -
Unigene36579_All	2309	0.88	1.95	0.67	9.02	10.72	10.58	4.01	3.57	5.06	1.14E+00	8.89E-05	Up	-4.02E-01	3.83E-01		2.50E-01	2.39E-02		2.31E-01	4.80E-02		-1.69E-01	3.89E-01		3.34E-01	2.32E-02		Unigene36579_All//gi|224145173|ref|XP_002325552.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222862427|gb|EEE99933.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene36579_All//0.00E+00//AT1G71960| ABC transporter family protein	Unigene36579_All//0.00E+00//TC140272		ko03040|Spliceosome//ko02010|ABC transporters	GO:0017111//GO:0032559//GO:0044464	nr +
Unigene3658_All	3349	0.75	0.70	0.37	0.71	0.90	0.20	10.68	2.00	4.29	-1.08E-01	7.80E-01		-1.04E+00	1.40E-02		3.42E-01	3.89E-01		-1.82E+00	3.18E-05	Down	-2.42E+00	1.76E-113	Down	-1.31E+00	9.21E-51	Down	Unigene3658_All//gi|224056903|ref|XP_002299081.1|//0.00E+00//tir-nbs resistance protein [Populus trichocarpa] >gi|222846339|gb|EEE83886.1| tir-nbs resistance protein [Populus trichocarpa]	Unigene3658_All//0.00E+00//AT5G56220| nucleoside-triphosphatase/ nucleotide binding	Unigene3658_All//0.00E+00//TC174775				nr +
Unigene36581_All	1249	68.91	31.52	66.04	96.04	50.73	76.55	0.00	0.44	0.80	-1.13E+00	9.76E-76	Down	-6.14E-02	3.83E-01		-9.21E-01	3.78E-93		-3.27E-01	3.99E-13		8.76E+00	5.36E-04	Up	9.64E+00	3.00E-07	Up	Unigene36581_All//gi|18252325|gb|AAL66194.1|AF386512_1/1.00E-111//cytochrome P450 [Pyrus communis]	Unigene36581_All//2.00E-67//AT5G07990| TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	Unigene36581_All//0.00E+00//TC134811		ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0016491//GO:0046914	nr -
Unigene36582_All	1134	10.57	6.84	7.04	21.13	22.05	20.51	119.76	137.03	58.99	-6.28E-01	1.18E-04		-5.85E-01	5.65E-04		6.13E-02	6.52E-01		-4.29E-02	7.44E-01		1.94E-01	1.26E-07		-1.02E+00	2.01E-127	Down	Unigene36582_All//gi|5882745|gb|AAD55298.1|AC008263_29/1.00E-139//P25A4.24 [Arabidopsis thaliana]	Unigene36582_All//2.00E-135//AT1G74790| catalytic	Unigene36582_All//0.00E+00//TC152042				nr +
Unigene36583_All	1486	2.71	1.98	0.75	3.79	3.59	3.31	2.05	2.70	4.18	-4.55E-01	1.36E-01		-1.85E+00	1.20E-07	Down	-7.67E-02	8.16E-01		-1.93E-01	4.97E-01		3.98E-01	1.58E-01		1.03E+00	1.06E-06	Up	Unigene36583_All//gi|238479361|ref|NP_001154534.1|//1.00E-120//binding [Arabidopsis thaliana] >gi|240254532|ref|NP_180101.4| binding [Arabidopsis thaliana]	Unigene36583_All//5.00E-122//AT2G25290| binding	Unigene36583_All//0.00E+00//CO079568				nr -
Unigene36587_All	1655	1.49	0.43	0.39	4.48	7.07	4.28	3.40	1.26	2.05	-1.79E+00	4.83E-05	Down	-1.94E+00	3.26E-05	Down	6.58E-01	2.49E-05		-6.60E-02	7.85E-01		-1.43E+00	1.92E-09	Down	-7.32E-01	7.28E-04		Unigene36587_All//gi|223452402|gb|ACM89528.1|//1.00E-155//serine/threonine-specific protein kinase-like protein [Glycine max]	Unigene36587_All//3.00E-150//AT3G58690| protein kinase family protein	Unigene36587_All//0.00E+00//CO081668		ko04626|Plant-pathogen interaction		nr +
Unigene36588_All	1710	0.55	0.65	0.06	2.83	3.60	2.40	1.48	0.42	0.75	2.43E-01	6.82E-01		-3.14E+00	1.33E-03		3.51E-01	1.61E-01		-2.34E-01	4.57E-01		-1.84E+00	2.33E-06	Down	-9.93E-01	3.92E-03		Unigene36588_All//gi|297817182|ref|XP_002876474.1|//1.00E-167//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322312|gb|EFH52733.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36588_All//2.00E-158//AT3G58690| protein kinase family protein	Unigene36588_All//0.00E+00//gi|78349978|gb|DT570252.1|DT570252		ko04626|Plant-pathogen interaction		nr +
Unigene36589_All	2685	1.31	0.66	1.45	14.99	8.95	6.06	7.67	1.88	20.00	-9.83E-01	3.00E-03		1.49E-01	6.37E-01		-7.44E-01	7.91E-22		-1.31E+00	1.07E-48	Down	-2.03E+00	1.03E-52	Down	1.38E+00	4.04E-81	Up	Unigene36589_All//gi|155242172|gb|ABT18098.1|//0.00E+00//FERONIA receptor-like kinase [Cardamine flexuosa]	Unigene36589_All//6.00E-175//AT5G39000| protein kinase family protein	Unigene36589_All//0.00E+00//ES806067		ko04626|Plant-pathogen interaction	GO:0006468//GO:0007275//GO:0009856//GO:0016020//GO:0016301//GO:0044426	nr -
Unigene3659_All	914	5.95	15.08	10.08	9.70	10.66	10.03	17.95	27.21	24.06	1.34E+00	2.15E-16	Up	7.60E-01	1.12E-04		1.36E-01	5.60E-01		4.82E-02	8.33E-01		6.00E-01	8.02E-10		4.23E-01	3.37E-05		Unigene3659_All//gi|224146489|ref|XP_002326024.1|//5.00E-32//global transcription factor group [Populus trichocarpa] >gi|222862899|gb|EEF00406.1| global transcription factor group [Populus trichocarpa]	Unigene3659_All//2.00E-12//AT1G06230| GTE4 (GLOBAL TRANSCRIPTION FACTOR GROUP E 4); DNA binding	Unigene3659_All//0.00E+00//TC164546				nr -
Unigene36591_All	1174	4.81	16.57	9.57	31.95	28.01	37.70	3.13	3.38	4.38	1.78E+00	2.75E-34	Up	9.92E-01	2.77E-08		-1.90E-01	3.32E-02		2.39E-01	3.25E-03		1.10E-01	7.19E-01		4.83E-01	3.64E-02		Unigene36591_All//gi|224134959|ref|XP_002327532.1|//7.00E-62//f-box family protein [Populus trichocarpa] >gi|222836086|gb|EEE74507.1| f-box family protein [Populus trichocarpa]	Unigene36591_All//1.00E-30//AT3G21270| ADOF2; DNA binding / transcription factor	Unigene36591_All//0.00E+00//TC178035	C2C2-Dof		GO:0005488//GO:0009743//GO:0010468//GO:0050794	nr +
Unigene36593_All	2260	4.35	0.92	1.04	2.31	2.32	1.52	31.04	5.33	15.37	-2.24E+00	9.01E-24	Down	-2.07E+00	1.27E-20	Down	1.00E-03	9.95E-01		-6.08E-01	2.00E-02		-2.54E+00	2.59E-235	Down	-1.01E+00	2.21E-65	Down	Unigene36593_All//gi|62318763|dbj|BAB93796.1|//3.00E-71//glutamic acid-rich protein [Arabidopsis thaliana]	Unigene36593_All//8.00E-88//AT3G05130| unknown protein	Unigene36593_All//0.00E+00//TC138257				nr -
Unigene36595_All	2072	14.14	6.09	20.84	2.64	1.73	0.94	1.10	0.52	0.35	-1.22E+00	1.88E-29	Down	5.60E-01	1.63E-11		-6.14E-01	1.10E-02		-1.50E+00	1.33E-08	Down	-1.07E+00	4.85E-03		-1.67E+00	2.12E-05	Down	Unigene36595_All//gi|13560977|gb|AK30294.1|AF353207_1/0.00E+00//beta-amylase [Castanea crenata]	Unigene36595_All//0.00E+00//AT2G32290| BAM6 (BETA-AMYLASE 6); beta-amylase/ catalytic/ cation binding	Unigene36595_All//2.00E-84//TC170168		ko00500|Starch and sucrose metabolism	GO:0005976//GO:0009536//GO:0016160//GO:0043167	nr -
Unigene36596_All	1358	14.45	10.67	6.55	22.82	20.72	21.48	34.84	24.90	23.26	-4.37E-01	4.43E-04		-1.14E+00	2.19E-17	Down	-1.39E-01	1.94E-01		-8.68E-02	4.77E-01		-4.85E-01	1.87E-12		-5.83E-01	1.42E-17		Unigene36596_All//gi|15242483|ref|NP_190387.1|//1.00E-105//AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding [Arabidopsis thaliana] >gi|75171186|sp|Q9FK68.1|RA1C_ARATH RecName: Full=Ras-related protein RABA1c >gi|9758678|dbj|BAB09217.1| Rab-type small GTP-binding protein-like [Arabidopsis thaliana]	Unigene36596_All//2.00E-106//AT5G45750| AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding	Unigene36596_All//0.00E+00//TC133948				nr -
Unigene36597_All	1214	9.70	5.26	6.32	15.76	15.29	11.87	5.43	2.27	1.94	-8.83E-01	1.32E-07		-6.19E-01	3.05E-04		-4.35E-02	8.04E-01		-4.09E-01	1.04E-03		-1.26E+00	3.78E-09	Down	-1.49E+00	5.55E-12	Down	Unigene36597_All//gi|259121425|gb|ACV92032.1|//6.00E-70//WRKY transcription factor 30 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene36597_All//2.00E-47//AT4G30935| WRKY32; transcription factor	Unigene36597_All//0.00E+00//gi|78351230|gb|DT571504.1|DT571504	WRKY	ko04626|Plant-pathogen interaction	GO:0005488//GO:0009987//GO:0010467	nr -
Unigene36598_All	1854	16.06	3.83	7.78	5.59	6.15	3.31	0.00	0.00	0.00	-2.07E+00	6.77E-64	Down	-1.04E+00	1.12E-22	Down	1.38E-01	5.07E-01		-7.54E-01	1.31E-05		null	null		null	null		Unigene36598_All//gi|224074945|ref|XP_002304502.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222841934|gb|EEE79481.1| cytochrome P450 [Populus trichocarpa]	Unigene36598_All//0.00E+00//AT2G45970| CYP86A8; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene36598_All//0.00E+00//DN804257		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0016712//GO:0016713//GO:0032787	nr +
Unigene36599_All	1439	16.62	69.97	8.77	18.24	21.56	12.24	8.05	42.58	114.50	2.07E+00	5.45E-214	Up	-9.22E-01	5.22E-15		2.41E-01	1.27E-02		-5.76E-01	2.07E-08		2.40E+00	5.97E-192	Up	3.83E+00	0.00E+00	Up	Unigene36599_All//gi|32815937|gb|AAP88353.1|//3.00E-52//At1g21010 [Arabidopsis thaliana]	Unigene36599_All//7.00E-47//AT1G21010| unknown protein	Unigene36599_All//0.00E+00//TC169383			GO:0031981	nr +

Unigene366_All	2682	0.94	0.93	0.54	10.68	11.13	5.78	6.10	1.85	3.02	-1.66E-02	9.84E-01		-8.05E-01	5.48E-02		5.98E-02	6.19E-01		-8.87E-01	9.82E-19		-1.72E+00	9.17E-34	Down	-1.02E+00	5.16E-16	Down	Unigene366_All//gi|79316590|ref|NP_001030957.1|//1.00E-160//MYB88 (myb domain protein 88); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene366_All//1.00E-152//AT2G02820| MYB88 (myb domain protein 88); DNA binding / transcription factor	Unigene366_All//0.00E+00//ES830223	MYB			nr -
Unigene3660_All	2284	2.15	1.69	0.89	2.84	3.56	3.24	4.94	5.75	5.98	-3.53E-01	2.10E-01		-1.28E+00	1.10E-05	Down	3.28E-01	1.23E-01		1.94E-01	4.39E-01		2.17E-01	1.48E-01		2.76E-01	4.39E-02		Unigene3660_All//gi|186510672|ref|NP_190039.2|//0.00E+00//HIRA (Arabidopsis homolog of histone chaperone HIRA); nucleotide binding / protein binding [Arabidopsis thaliana]	Unigene3660_All//0.00E+00//AT3G44530| HIRA (Arabidopsis homolog of histone chaperone HIRA); nucleotide binding / protein binding	Unigene3660_All//0.00E+00//gi|164327433|gb|ES806626.1|ES806626				nr -
Unigene36600_All	1295	1.54	1.10	1.48	3.73	1.99	3.66	3.07	1.10	1.88	-4.87E-01	2.93E-01		-5.26E-02	9.19E-01		-9.04E-01	3.82E-04		-2.71E-02	9.42E-01		-1.48E+00	2.95E-07	Down	-7.10E-01	7.04E-03		Unigene36600_All//gi|297814019|ref|XP_002874893.1|//1.00E-110//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297320730|gb|EFH51152.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene36600_All//2.00E-110//AT4G02820| pentatricopeptide (PPR) repeat-containing protein	Unigene36600_All//0.00E+00//gi|78340407|gb|DT560681.1|DT560681			GO:0043231	nr +
Unigene36603_All	415	35.30	88.27	44.65	30.85	58.08	57.68	11.10	16.32	13.06	1.32E+00	1.66E-41	Up	3.39E-01	1.29E-02		9.13E-01	5.98E-18		9.03E-01	4.79E-16		5.55E-01	5.93E-03		2.34E-01	3.37E-01		Unigene36603_All//gi|225446337|ref|XP_002272136.1|//3.00E-27//PREDICTED: similar to ring domain containing protein isoform 2 [Vitis vinifera] >gi|225446339|ref|XP_002272107.1| PREDICTED: similar to ring domain containing protein isoform 1 [Vitis vinifera]	Unigene36603_All//8.00E-26//AT4G27470| zinc finger (C3HC4-type RING finger) family protein	Unigene36603_All//0.00E+00//gi|109849809|gb|DW478788.1|DW478788		ko04146|Peroxisome	GO:0006511//GO:0006950//GO:0009725//GO:0019787//GO:0031090//GO:0032446//GO:0043231//GO:0044425//GO:0046914	nr +
Unigene36604_All	1022	101.47	233.76	94.41	89.93	163.25	154.67	20.19	26.83	17.74	1.20E+00	5.14E-231	Up	-1.04E-01	7.29E-02		8.60E-01	3.32E-111		7.82E-01	7.42E-81		4.10E-01	8.89E-06		-1.87E-01	9.69E-02		Unigene36604_All//gi|225446337|ref|XP_002272136.1|//2.00E-65//PREDICTED: similar to ring domain containing protein isoform 2 [Vitis vinifera] >gi|225446339|ref|XP_002272107.1| PREDICTED: similar to ring domain containing protein isoform 1 [Vitis vinifera]	Unigene36604_All//3.00E-32//AT4G03510| RMA1; protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene36604_All//0.00E+00//TC138619		ko04146|Peroxisome	GO:0006511//GO:0006950//GO:0009725//GO:0019787//GO:0031090//GO:0032446//GO:0046914	nr +
Unigene36605_All	1390	3.20	1.39	3.64	4.44	4.38	2.79	1.58	1.59	2.98	-1.21E+00	4.26E-05	Down	1.86E-01	5.34E-01		-1.93E-02	9.48E-01		-6.69E-01	4.35E-03		1.09E-02	1.02E+00		9.14E-01	4.58E-04		Unigene36605_All//gi|297851072|ref|XP_002893417.1|//1.00E-130//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297339259|gb|EFH69676.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene36605_All//3.00E-126//AT1G26090| unknown protein	Unigene36605_All//0.00E+00//gi|109858164|gb|DW487143.1|DW487143			GO:0043231	nr +
Unigene36607_All	1339	4.61	33.87	26.88	13.39	6.61	34.84	12.22	5.71	11.16	2.88E+00	1.86E-141	Up	2.54E+00	4.32E-96	Up	-1.02E+00	8.87E-17	Down	1.38E+00	3.08E-60	Up	-1.10E+00	1.80E-17	Down	-1.31E-01	3.37E-01		Unigene36607_All//gi|115465829|ref|NP_001056514.1|//2.00E-59//Os05g0595300 [Oryza sativa Japonica Group] >gi|113580065|dbj|BAF18428.1| Os05g0595300 [Oryza sativa Japonica Group]	Unigene36607_All//1.00E-58//AT5G53420| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: CCT domain (InterPro:IPR001022); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27900.2); Has 863 Blast hits to 863 proteins in 62 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 840; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).	Unigene36607_All//0.00E+00//TC132939	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr -
Unigene36608_All	1610	1.01	1.64	2.75	1.98	1.39	2.30	3.36	4.62	2.72	7.00E-01	7.23E-02		1.45E+00	4.27E-06	Up	-5.10E-01	1.40E-01		2.16E-01	5.65E-01		4.59E-01	1.75E-02		-3.04E-01	1.91E-01		Unigene36608_All//gi|124359343|gb|ABD28505.2|//2.00E-44//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene36608_All//9.00E-13//AT5G42905| nucleic acid binding / ribonuclease H	Unigene36608_All//2.00E-09//FL576736				nr -
Unigene36610_All	2491	0.25	0.33	0.30	4.70	3.07	2.50	11.73	5.67	3.65	3.69E-01	6.22E-01		2.48E-01	7.45E-01		-6.15E-01	5.92E-05		-9.09E-01	2.41E-08		-1.05E+00	1.97E-28	Down	-1.69E+00	7.11E-60	Down	Unigene36610_All//gi|15217599|ref|NP_177332.1|//0.00E+00//MATE efflux family protein [Arabidopsis thaliana] >gi|7239514|gb|AAF43240.1|AC012654_24 Contains similarity to the ZF14 mRNA from Arabidopsis thaliana gb|AB028198; It is a member of the uncharacterized membrane protein family PF|01554 >gi|29468190|gb|AAO65439.1| NIC2 [Arabidopsis thaliana]	Unigene36610_All//0.00E+00//AT1G71870| MATE efflux family protein				GO:0015291//GO:0015893//GO:0044464	nr -
Unigene36611_All	1274	3.66	4.61	1.76	4.81	4.38	9.78	8.70	14.37	21.95	3.36E-01	1.87E-01		-1.06E+00	3.32E-04	Down	-1.35E-01	6.07E-01		1.02E+00	1.63E-10	Up	7.25E-01	4.55E-10		1.34E+00	1.64E-10	Up	Unigene36611_All//gi|21700765|gb|AC38144.1|//1.00E-128//phosphoglycerate mutase-like protein [Glycine max]	Unigene36611_All//3.00E-117//AT1G58280| LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61460.6); Has 337 Blast hits to 337 proteins in 68 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 175; Plants - 69; Viruses - 0; Other Eukaryotes - 89 (source: NCBI BLink).	Unigene36611_All//0.00E+00//TC137260				nr +
Unigene36614_All	1865	3.45	6.49	2.57	1.74	1.42	1.28	5.55	9.97	15.02	9.12E-01	3.65E-08		-4.25E-01	8.52E-02		-2.88E-01	4.38E-01		-4.36E-01	2.34E-01		8.44E-01	4.74E-13		1.43E+00	4.18E-45	Up	Unigene36614_All//gi|226497956|ref|NP_001147720.1|//1.00E-137//serine/threonine-protein kinase Cx32 [Zea mays] >gi|195613312|gb|ACG28486.1| serine/threonine-protein kinase Cx32 [Zea mays]	Unigene36614_All//6.00E-119//AT2G17220| protein kinase, putative	Unigene36614_All//0.00E+00//gi|73864313|gb|DT467052.1|DT467052				nr -
Unigene36615_All	1322	0.83	1.42	2.13	3.73	3.54	2.05	2.24	2.66	2.41	7.71E-01	1.06E-01		1.36E+00	7.25E-04	Up	-7.46E-02	8.29E-01		-8.64E-01	1.18E-03		2.46E-01	4.43E-01		1.07E-01	7.39E-01		Unigene36615_All//gi|124360549|gb|ABD33126.2|//2.00E-56//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene36615_All//1.00E-10//AT4G20520| RNA binding / RNA-directed DNA polymerase	Unigene36615_All//1.00E-25//C0109005				nr -
Unigene36617_All	1012	4.50	1.40	5.16	3.54	6.09	3.88	1.59	0.83	0.79	-1.68E+00	5.27E-08	Down	1.97E-01	5.01E-01		7.81E-01	5.91E-04		1.32E-01	6.89E-01		-9.43E-01	4.30E-02		-1.01E+00	2.40E-02		Unigene36617_All//gi|22711564|gb|AAM01179.2|AC113336_31//9.00E-06//Putative retroelement [Oryza sativa Japonica Group]		Unigene36617_All//4.00E-93//DW498715				nr -
Unigene3662_All	1466	5.57	2.38	2.03	12.67	11.72	8.47	6.49	6.10	6.77	-1.22E+00	7.77E-09	Down	-1.45E+00	9.75E-11	Down	-1.13E-01	4.57E-01		-5.81E-01	3.02E-06		-8.89E-02	6.32E-01		6.04E-02	7.35E-01		Unigene3662_All//gi|224128494|ref|XP_002320346.1|//1.00E-118//f-box family protein [Populus trichocarpa] >gi|222861119|gb|EEE98861.1| f-box family protein [Populus trichocarpa]	Unigene3662_All//2.00E-112//AT4G02440| EID1 (EMPFINDLICHER IM DUNKELROTEN LICHT 1); ubiquitin-protein ligase	Unigene3662_All//0.00E+00//TC142664				nr -
Unigene36625_All	1443	19.54	8.25	11.18	5.94	5.51	3.29	8.41	12.05	12.53	-1.24E+00	2.14E-29	Down	-8.06E-01	4.06E-14		-1.07E-01	6.30E-01		-8.53E-01	1.02E-05		5.19E-01	1.16E-05		5.76E-01	4.09E-07		Unigene36625_All//gi|124359159|gb|ABD28369.2|//1.00E-130//Zinc finger, CCCH-type; Sugar transporter superfamily [Medicago truncatula]	Unigene36625_All//2.00E-87//AT3G02830| ZFN1 (ZINC FINGER PROTEIN 1); DNA binding / nuclease/ nucleic acid binding	Unigene36625_All//0.00E+00//DW517457	C3H	ko04141|Protein processing in endoplasmic reticulum	GO:0005488	nr +
Unigene36626_All	1073	25.75	69.79	37.67	55.80	98.27	42.13	5.60	1.21	3.38	1.44E+00	1.27E-95	Up	5.49E-01	1.80E-10		8.16E-01	2.40E-64		-4.05E-01	5.96E-10		-2.21E+00	1.11E-17	Down	-7.28E-01	4.91E-04		Unigene36626_All//gi|3608141|gb|AAC36174.1|//1.00E-25//expressed protein [Arabidopsis thaliana] >gi|107738167|gb|ABF83654.1| At2g35470 [Arabidopsis thaliana]	Unigene36626_All//1.00E-10//AT2G35470| unknown protein	Unigene36626_All//0.00E+00//TC151987				nr +
Unigene36627_All	749	6.85	10.69	2.63	9.18	9.10	13.45	13.32	16.24	17.92	6.43E-01	1.73E-03		-1.38E+00	1.63E-06	Down	-1.18E-02	9.55E-01		5.51E-01	2.04E-03		2.86E-01	5.99E-02		4.28E-01	1.39E-03		Unigene36627_All//gi|115443601|ref|NP_001045580.1|//4.00E-22//Os02g0100200 [Oryza sativa Japonica Group] >gi|113535111|dbj|BAF07494.1| Os02g0100200 [Oryza sativa Japonica Group]	Unigene36627_All//2.00E-30//AT5G04670| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: nucleic acid binding (TAIR:AT4G32620.2); Has 197 Blast hits to 193 proteins in 56 species: Archae - 0; Bacteria - 2; Metazoa - 139; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 13 (source: NCBI BLink).	Unigene36627_All//0.00E+00//gi|109873477|gb|DW502452.1|DW502452				nr -
Unigene36629_All	2022	0.96	1.03	0.61	3.20	2.74	1.36	2.36	2.91	3.57	1.02E-01	8.15E-01		-6.61E-01	1.77E-01		-2.24E-01	3.84E-01		-1.23E+00	1.21E-07	Down	3.03E-01	1.95E-01		5.94E-01	1.65E-03		Unigene36629_All//gi|115459306|ref|NP_001053253.1|//1.00E-172//Os04g0505400 [Oryza sativa Japonica Group] >gi|32490023|emb|CAE05562.1| OSJNBb0116K07.15 [Oryza sativa (japonica cultivar-group)] >gi|113561824|dbj|BAF15167.1| Os04g0505400 [Oryza sativa Japonica Group] >gi|116310257|emb|CAH67264.1| OSIGBa0145C12.1 [Oryza sativa (indica cultivar-group)]	Unigene36629_All//0.00E+00//AT3G50120| unknown protein	Unigene36629_All//0.00E+00//gi|50506087|gb|AT731835.1|AT731835			GO:0044464	nr -
Unigene3663_All	745	7.37	15.98	4.72	20.59	56.48	69.72	38.53	149.74	187.00	1.12E+00	6.86E-11	Up	-6.45E-01	1.52E-02		1.46E+00	1.23E-64	Up	1.76E+00	2.60E-95	Up	1.96E+00	7.92E-270	Up	2.28E+00	0.00E+00	Up	Unigene3663_All//gi|19911187|dbj|BAB86920.1|//2.00E-60//glucosyltransferase-2 [Vigna angularis]	Unigene3663_All//4.00E-37//AT3G11340| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene3663_All//0.00E+00//TC149055		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene36633_All	1411	7.90	20.76	33.40	195.13	193.21	385.92	1.17	0.53	0.31	1.39E+00	4.67E-36	Up	2.08E+00	1.97E-98	Up	-1.42E-02	7.49E-01		9.84E-01	0.00E+00		-1.13E+00	1.43E-02		-1.91E+00	8.63E-05	Down	Unigene36633_All//gi|116871384|gb|ABK30788.1|//1.00E-133//xyloglucan endotransglycosylase 1 [Litchi chinensis]	Unigene36633_All//1.00E-116//AT3G44990| XTH8 (XYLOGLUCAN ENDO-TRANSGLYCOSYLASE-RELATED 8); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene36633_All//0.00E+00//TC131681				nr -

Unigene36635_All	1753	0.72	0.61	1.94	5.83	4.22	2.63	3.86	1.81	1.20	-2.39E-01	6.68E-01		1.44E+00	7.73E-05	Up	-4.64E-01	6.46E-03		-1.15E+00	1.66E-10	Down	-1.09E+00	1.25E-07	Down	-1.68E+00	1.88E-14	Down	Unigene36635_All//gi|301073323|gb|ADK56449.1|//1.00E-36//acyl-CoA-binding protein [Vitis vinifera]	Unigene36635_All//4.00E-29//AT4G24230| ACBP3 (ACYL-COA-BINDING DOMAIN 3); acyl-CoA binding	Unigene36635_All//0.00E+00//TC154976			GO:0005504//GO:0010038//GO:0044421	nr -
Unigene36636_All	1174	5.75	3.24	5.08	16.29	11.85	7.16	2.56	1.78	2.65	-8.29E-01	2.52E-04		-1.79E-01	4.82E-01		-4.59E-01	8.83E-05		-1.19E+00	3.49E-20	Down	-5.23E-01	1.12E-01		4.99E-02	8.90E-01		Unigene36636_All//gi|77999238|gb|ABB16966.1|//9.00E-53//adenylate kinase family-like protein [Solanum tuberosum]	Unigene36636_All//7.00E-52//AT3G01820| adenylate kinase family protein	Unigene36636_All//0.00E+00//gi|78341915|gb|DT562189.1|DT562189		ko00230|Purine metabolism	GO:0019205//GO:0032559//GO:0034641	nr -
Unigene36637_All	1082	159.96	35.40	85.93	47.60	41.56	49.42	9.65	14.18	27.14	-2.18E+00	0.00E+00	Down	-8.97E-01	1.14E-100		-1.96E-01	7.26E-03		5.40E-02	5.70E-01		5.55E-01	1.23E-05		1.49E+00	5.48E-50	Up	Unigene36637_All//gi|259479222|dbj|BAI40146.1|//5.00E-69//glutathione S-transferase 1 [Diospyros kaki]	Unigene36637_All//1.00E-66//AT1G39700| ATGSTU16 (GLUTATHIONE S-TRANSFERASE TAU 16); glutathione transferase	Unigene36637_All//0.00E+00//TC173243		ko00480|Glutathione metabolism	GO:0009404//GO:0009536//GO:0016829	nr -
Unigene3664_All	976	70.49	72.11	62.80	66.20	63.26	71.31	157.34	79.52	47.72	3.27E-02	6.42E-01		-1.67E-01	1.54E-02		-6.55E-02	4.16E-01		1.07E-01	1.34E-01		-9.84E-01	8.31E-132		-1.72E+00	0.00E+00	Down	Unigene3664_All//gi|225432398|ref|XP_002277251.1|//6.00E-44//PREDICTED: similar to plastid acyl carrier protein [Vitis vinifera]	Unigene3664_All//1.00E-25//AT1G54580| ACP2 (ACYL CARRIER PROTEIN 2); acyl carrier	Unigene3664_All//0.00E+00//gi|109890183|gb|DW519147.1|DW519147		ko00190|Oxidative phosphorylation		nr -
Unigene36641_All	1691	5.32	2.58	5.98	5.57	6.54	5.61	6.58	3.53	4.92	-1.05E+00	1.07E-07	Down	1.69E-01	3.94E-01		2.32E-01	2.19E-01		1.06E-02	9.55E-01		-8.96E-01	6.56E-09		-4.17E-01	4.98E-03		Unigene36641_All//gi|124359876|gb|ABN06170.1|//1.00E-177//Regulator of chromosome condensation/beta-lactamase-inhibitor protein II [Medicago truncatula]	Unigene36641_All//2.00E-148//AT5G60870| regulator of chromosome condensation (RCC1) family protein	Unigene36641_All//0.00E+00//gi|11206801|gb|BF275731.1|BF275731		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene36642_All	1384	15.46	18.01	8.93	19.36	18.79	25.68	31.22	67.22	87.82	2.20E-01	5.45E-02		-7.93E-01	1.38E-10		-4.38E-02	7.63E-01		4.07E-01	3.35E-06		1.11E+00	9.35E-97	Up	1.49E+00	1.37E-204	Up	Unigene36642_All//gi|89000969|gb|ABD59074.1|//1.00E-124//At4g25030 [Arabidopsis thaliana] >gi|222424032|dbj|BAH19977.1| AT4G25030 [Arabidopsis thaliana]	Unigene36642_All//3.00E-106//AT4G25030| unknown protein	Unigene36642_All//0.00E+00//TC149117				nr -
Unigene36646_All	849	10.78	7.76	9.35	25.35	23.16	17.08	5.38	4.53	2.25	-4.75E-01	1.30E-02		-2.07E-01	3.45E-01		-1.30E-01	3.33E-01		-5.70E-01	6.70E-07		-2.48E-01	3.81E-01		-1.26E+00	8.28E-07	Down	Unigene36646_All//gi|124359981|gb|ABN07997.1|//2.00E-08//contains similarity to reverse transcriptase, related [Medicago truncatula]	Unigene36646_All//8.00E-09//AT3G09510| nucleic acid binding	Unigene36646_All//0.00E+00//TC168330				nr +
Unigene36647_All	1492	2.67	3.43	3.00	19.87	24.12	14.35	6.80	33.87	6.01	3.64E-01	1.84E-01		1.70E-01	6.10E-01		2.80E-01	1.18E-03		-4.69E-01	1.07E-06		2.32E+00	1.49E-151	Up	-1.79E-01	2.99E-01		Unigene36647_All//gi|6651292|gb|AAF22256.1|//1.00E-93//myb-related transcription factor [Pimpinella brachycarpa]	Unigene36647_All//1.00E-80//AT4G22680| MYB85 (myb domain protein 85); DNA binding / transcription activator/ transcription factor	Unigene36647_All//0.00E+00//gi|78326281|gb|DT546555.1|DT546555	MYB		GO:0001071//GO:0006351//GO:0010468//GO:0030528//GO:0043231	nr +
Unigene36648_All	1276	173.57	204.46	279.06	87.88	111.89	98.79	30.35	18.51	10.46	2.36E-01	2.58E-14		6.85E-01	2.95E-130		3.49E-01	4.53E-19		1.69E-01	2.36E-04		-7.14E-01	6.98E-20		-1.54E+00	2.64E-69	Down	Unigene36648_All//gi|18397039|ref|NP_566241.1|//1.00E-119//DRT102 (DNA-DAMAGE-REPAIR/TOLERATION 2) [Arabidopsis thaliana] >gi|148872800|sp|Q05212.2|DR102_ARATH RecName: Full=DNA-damage-repair/toleration protein DRT102 >gi|15529165|gb|AA97677.1| AT3g04880/T9J14_17 [Arabidopsis thaliana] >gi|23505883|gb|AAN28801.1| At3g04880/T9J14_17 [Arabidopsis thaliana]	Unigene36648_All//6.00E-121//AT3G04880| DRT102 (DNA-DAMAGE-REPAIR/TOLERATION 2)	Unigene36648_All//0.00E+00//TC134463				nr +
Unigene3665_All	958	15.57	79.44	34.18	21.16	28.07	41.01	9.18	28.05	23.62	2.35E+00	3.25E-189	Up	1.14E+00	1.82E-28	Up	4.08E-01	3.42E-05		9.55E-01	1.79E-28		1.61E+00	3.86E-50	Up	1.36E+00	5.91E-34	Up	Unigene3665_All//gi|15241727|ref|NP_201026.1|//2.00E-58//embryo-specific protein-related [Arabidopsis thaliana] >gi|38603856|gb|AAR24673.1| At5g62200 [Arabidopsis thaliana]	Unigene3665_All//2.00E-49//AT5G62200| embryo-specific protein-related	Unigene3665_All//0.00E+00//gi|13355056|gb|BG445488.1|BG445488				nr +
Unigene36650_All	1187	1.28	1.45	2.06	1.68	2.20	2.17	1.64	1.30	3.62	1.83E-01	6.99E-01		6.91E-01	1.04E-01		3.93E-01	3.51E-01		3.70E-01	3.88E-01		-3.31E-01	4.51E-01		1.15E+00	1.16E-05	Up	Unigene36650_All//gi|224131110|ref|XP_002321003.1|//1.00E-102//Mg2+ and Zn2+/H+ antiporter, atmhx1-like protein [Populus trichocarpa] >gi|222861776|gb|EEE99318.1| Mg2+ and Zn2+/H+ antiporter, atmhx1-like protein [Populus trichocarpa]	Unigene36650_All//3.00E-95//AT2G47600| ATMHX (ARABIDOPSIS THALIANA MAGNESIUM/PROTON EXCHANGER); calcium:sodium antiporter/ cation:cation antiporter				GO:0000041//GO:0015298//GO:0031090//GO:0031224//GO:0070838	nr +
Unigene36652_All	1539	5.07	0.59	1.76	10.45	8.28	8.42	6.18	1.22	3.05	-3.10E+00	8.13E-27	Down	-1.52E+00	5.79E-11	Down	-3.37E-01	1.27E-02		-3.12E-01	2.91E-02		-2.34E+00	1.75E-29	Down	-1.02E+00	1.09E-09	Down	Unigene36652_All//gi|227463008|gb|ACP39956.1|//1.00E-177//pentatricopeptide repeat protein [Gossypium hirsutum] >gi|227463010|gb|ACP39957.1| pentatricopeptide repeat protein [Gossypium hirsutum]	Unigene36652_All//3.00E-138//AT1G61870| PPR336 (pentatricopeptide repeat 336)	Unigene36652_All//0.00E+00//gi|164274066|gb|ES806810.1|ES806810		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0043231	nr -
Unigene36660_All	1249	12.78	10.99	19.91	14.52	15.05	14.57	10.16	4.08	4.15	-2.17E-01	1.41E-01		6.40E-01	1.31E-08		5.23E-02	7.70E-01		5.40E-03	9.69E-01		-1.31E+00	5.29E-18	Down	-1.29E+00	4.16E-18	Down	Unigene36660_All//gi|297827029|ref|XP_002881397.1|//1.00E-127//At2g35450 [Arabidopsis lyrata subsp. lyrata] >gi|297327236|gb|EFH57656.1| At2g35450 [Arabidopsis lyrata subsp. lyrata]	Unigene36660_All//1.00E-127//AT2G35450| catalytic/ hydrolase	Unigene36660_All//0.00E+00//TC137966				nr +
Unigene36661_All	1342	1.01	0.08	0.56	0.63	0.31	0.57	1.23	0.93	0.42	-3.75E+00	5.95E-06	Down	-8.68E-01	1.47E-01		-1.04E+00	1.62E-01		-1.41E-01	8.54E-01		-3.95E-01	4.03E-01		-1.56E+00	7.74E-04	Down	Unigene36661_All//gi|297827029|ref|XP_002881397.1|//1.00E-127//At2g35450 [Arabidopsis lyrata subsp. lyrata] >gi|297327236|gb|EFH57656.1| At2g35450 [Arabidopsis lyrata subsp. lyrata]	Unigene36661_All//1.00E-127//AT2G35450| catalytic/ hydrolase	Unigene36661_All//0.00E+00//TC144898				nr +
Unigene36662_All	2090	3.55	1.75	3.57	2.57	3.02	2.23	3.36	1.52	1.56	-1.03E+00	2.54E-06	Down	4.90E-03	1.00E+00		2.28E-01	3.93E-01		-2.10E-01	4.69E-01		-1.14E+00	1.90E-08	Down	-1.10E+00	2.66E-08	Down	Unigene36662_All//gi|224140669|ref|XP_002323703.1|//1.00E-178//tetratricopeptide repeat-containing protein [Populus trichocarpa] >gi|222868333|gb|EEF05464.1| tetratricopeptide repeat-containing protein [Populus trichocarpa]	Unigene36662_All//6.00E-168//AT1G33400| tetratricopeptide repeat (TPR)-containing protein	Unigene36662_All//0.00E+00//TC147231				nr -
Unigene36668_All	1969	18.76	14.31	18.28	25.68	22.44	25.16	47.97	18.85	24.16	-3.91E-01	8.74E-06		-3.72E-02	7.17E-01		-1.95E-01	8.36E-03		-2.93E-02	7.46E-01		-1.35E+00	5.12E-134	Down	-9.90E-01	2.37E-84		Unigene36668_All//gi|30694211|ref|NP_567017.2|//0.00E+00//HEXO1 (BETA-HEXOSAMINIDASE 1); beta-N-acetylhexosaminidase/ hexosaminidase/ hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|157154097|emb|CAM35467.1| beta-N-acetylhexosaminidase [Arabidopsis thaliana]	Unigene36668_All//0.00E+00//AT3G55260| HEXO1 (BETA-HEXOSAMINIDASE 1); beta-N-acetylhexosaminidase/ hexosaminidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene36668_All//0.00E+00//TC152920		ko00520|Amino sugar and nucleotide sugar metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series//ko00603|Glycosphingolipid biosynthesis - globo series	GO:0005618//GO:0015929//GO:0043167//GO:0043231//GO:0044238	nr +
Unigene36669_All	1657	24.19	7.46	18.45	2.80	2.95	0.87	0.51	0.30	0.36	-1.70E+00	1.13E-65	Down	-3.91E-01	6.81E-06		7.79E-02	8.41E-01		-1.68E+00	1.33E-08	Down	-7.54E-01	2.78E-01		-5.01E-01	4.47E-01		Unigene36669_All//gi|224085968|ref|XP_002307758.1|//1.00E-134//high mobility group family [Populus trichocarpa] >gi|222857207|gb|EEE94754.1| high mobility group family [Populus trichocarpa]	Unigene36669_All//5.00E-100//AT1G76110| high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein	Unigene36669_All//0.00E+00//DR460911			GO:0010468	nr +
Unigene3667_All	262	1.20	1.74	1.22	1.71	1.31	1.72	4.20	1.28	0.61	5.39E-01	6.02E-01		2.54E-02	1.00E+00		-3.81E-01	7.22E-01		1.06E-02	1.00E+00		-1.72E+00	5.68E-03		-2.79E+00	6.37E-05	Down	Unigene3667_All//gi|115469344|ref|NP_001058271.1|//2.00E-18//Os06g0660700 [Oryza sativa Japonica Group] >gi|113596311|dbj|BAF20185.1| Os06g0660700 [Oryza sativa Japonica Group]	Unigene3667_All//1.00E-18//AT5G05080| UBC22 (ubiquitin-conjugating enzyme 22); ubiquitin-protein ligase	Unigene3667_All//2.00E-119//gi|78347460|gb|DT567734.1|DT567734		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene36670_All	1133	6.14	3.94	5.12	8.05	6.20	8.89	10.86	6.27	4.43	-6.42E-01	3.79E-03		-2.62E-01	2.89E-01		-3.76E-01	4.55E-02		1.44E-01	5.00E-01		-7.92E-01	4.44E-08		-1.29E+00	1.29E-17	Down	Unigene36670_All//gi|115478765|ref|NP_001062976.1|//2.00E-88//Os09g0359900 [Oryza sativa Japonica Group] >gi|113631209|dbj|BAF24890.1| Os09g0359900 [Oryza sativa Japonica Group]	Unigene36670_All//2.00E-99//AT4G14000| unknown protein	Unigene36670_All//0.00E+00//TC134502			GO:0043231	nr +
Unigene36672_All	2620	9.96	11.35	9.06	10.36	13.96	9.29	24.51	59.09	15.62	1.88E-01	7.44E-02		-1.37E-01	2.66E-01		4.30E-01	1.66E-07		-1.57E-01	1.82E-01		1.27E+00	1.39E-199	Up	-6.51E-01	1.89E-28		Unigene36672_All//gi|213268485|gb|ACJ45013.1|//0.00E+00//NPR1-1 protein [Glycine max]	Unigene36672_All//3.00E-175//AT5G45110| NPR3 (NPR1-LIKE PROTEIN 3); protein binding	Unigene36672_All//0.00E+00//TC168742			GO:0005488	nr +
Unigene36675_All	958	2.13	4.18	7.11	3.33	5.79	3.68	1.68	1.79	1.41	9.72E-01	1.59E-03		1.74E+00	1.29E-11	Up	7.98E-01	9.87E-04		1.44E-01	6.75E-01		9.30E-02	8.42E-01		-2.46E-01	6.20E-01					Unigene36675_All//0.00E+00//CO123647				
Unigene36676_All	593	4.94	2.39	6.65	5.38	5.28	4.49	8.27	3.74	3.63	-1.05E+00	4.51E-03		4.28E-01	1.96E-01		-2.49E-02	9.50E-01		-2.59E-01	5.00E-01		-1.15E+00	3.65E-06	Down	-1.19E+00	1.01E-06	Down	Unigene36676_All//gi|42572893|ref|NP_974543.1|//4.00E-14//WRNEXO (WERNER SYNDROME-LIKE EXONUCLEASE); 3'-5' exonuclease/ nucleic acid binding / protein binding [Arabidopsis thaliana] >gi|75327902|sp|Q84LH3.1|WEX_ARATH RecName: Full=Werner Syndrome-like exonuclease >gi|28195109|gb|AAO33765.1| Werner Syndrome-like exonuclease [Arabidopsis thaliana] >gi|38603882|gb|AAR24686.1| At4g13870 [Arabidopsis thaliana]	Unigene36676_All//2.00E-15//AT4G13870| WRNEXO (WERNER SYNDROME-LIKE EXONUCLEASE); 3'-5' exonuclease/ nucleic acid binding / protein binding	Unigene36676_All//3.00E-77//ES808983			GO:0004527//GO:0005488//GO:0034641//GO:0044464	nr +
Unigene36679_All	1810	7.31	5.68	4.68	9.83	9.36	11.23	12.43	5.82	6.34	-3.64E-01	2.06E-02		-6.45E-01	5.64E-05		-6.99E-02	6.59E-01		1.93E-01	1.54E-01		-1.09E+00	1.26E-23	Down	-9.71E-01	3.69E-20		Unigene36679_All//gi|3377805|gb|AAC28178.1|//1.00E-155//T2H3.12 [Arabidopsis thaliana]	Unigene36679_All//5.00E-140//AT4G02220| zinc finger (MYND type) family protein / programmed cell death 2 C-terminal domain-containing protein	Unigene36679_All//0.00E+00//EV487666			GO:0046872	nr +
Unigene3668_All	434	0.12	0.23	0.00	1.15	0.71	0.42	1.75	0.00	0.64	9.53E-01	7.26E-01		-6.91E+00	6.23E-01		-6.85E-01	5.15E-01		-1.46E+00	1.93E-01		-1.08E+01	1.68E-05	Down	-1.45E+00	4.46E-02					Unigene3668_All//2.00E-58//TC149777				
Unigene36681_All	1367	4.02	66.50	25.36	6.38	8.21	9.02	28.45	43.72	31.33	4.05E+00	0.00E+00	Up	2.66E+00	3.17E-97	Up	3.65E-01	3.16E-02		5.00E-01	1.72E-03		6.20E-01	1.04E-23		1.39E-01	6.89E-02		Unigene36681_All//gi|224096656|ref|XP_002310688.1|//3.00E-97//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222853591|gb|EEE91138.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene36681_All//3.00E-77//AT1G66010| NAC1; transcription factor	Unigene36681_All//0.00E+00//CO109521	NAC		GO:0001071//GO:0003006//GO:0009755//GO:0048528	nr +
Unigene36683_All	1743	12.79	2.06	9.75	16.80	12.39	10.42	7.20	4.70	5.12	-2.63E+00	5.88E-64	Down	-3.92E-01	1.20E-03		-4.40E-01	1.66E-06		-6.90E-01	1.30E-12		-6.16E-01	1.37E-05		-4.93E-01	3.61E-04		Unigene36683_All//gi|110739125|dbj|BAF01479.1|//0.00E+00//protein kinase like protein [Arabidopsis thaliana]	Unigene36683_All//1.00E-169//AT3G44610| protein kinase family protein	Unigene36683_All//0.00E+00//TC136504			GO:0004672//GO:0006464//GO:0009536//GO:0032559	nr -
Unigene36684_All	367	2.28	3.87	7.25	2.44	3.10	1.23	1.61	0.57	1.30	7.61E-01	1.74E-01		1.67E+00	1.07E-04	Up	3.42E-01	6.20E-01		-9.89E-01	1.96E-01		-1.50E+00	9.13E-02		-3.08E-01	6.78E-01		Unigene36684_All//gi|115461366|ref|NP_001054283.1|//3.00E-10//Os04g0679900 [Oryza sativa Japonica Group] >gi|32487399|emb|CAE05733.1| OSJNBb0017101.13 [Oryza sativa (japonica cultivar-group)] >gi|113568854|dbj|BAF16197.1| Os04g0679900 [Oryza sativa Japonica Group]	Unigene36684_All//8.00E-10//AT2G20740| unknown protein				GO:0044464	nr +

Unigene36685_All	595	5.63	6.81	10.83	5.11	3.59	4.17	4.48	1.55	2.01	2.76E-01	3.83E-01		9.44E-01	1.01E-04		-5.09E-01	1.55E-01		-2.91E-01	4.68E-01		-1.53E+00	2.46E-05	Down	-1.16E+00	6.53E-04	Down	Unigene36685_All//gi|115461366|ref|NP_001054283.1|//7.00E-10//Os04g0679900 [Oryza sativa Japonica Group] >gi|32487399|emb|CAE05733.1|OSJNB0017101.13 [Oryza sativa (japonica cultivar-group)] >gi|113565854|dbj|BAF16197.1|Os04g0679900 [Oryza sativa Japonica Group]	Unigene36685_All//3.00E-08//AT2G20230| LOCATED IN: plasma membrane, vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 16 growth stages; CONTAINS InterPro DOMAIN/s: Tetraspanin (InterPro:IPR018499); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G28770.1); Has 91 Blast hits to 91 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 90; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).			ko03420|Nucleotide excision repair//ko03022|Basal transcription factors		nr +
Unigene36686_All	1294	12.37	638.85	161.23	63.83	131.25	335.41	17.58	102.33	28.08	5.69E+00	0.00E+00	Up	3.70E+00	0.00E+00	Up	1.04E+00	5.82E-155	Up	2.39E+00	0.00E+00	Up	2.54E+00	0.00E+00	Up	6.76E-01	1.72E-17		Unigene36686_All//gi|15238868|ref|NP_200198.1|//1.00E-55//plastocyanin-like domain-containing protein [Arabidopsis thaliana] >gi|109946411|gb|ABG48384.1|At5g53870 [Arabidopsis thaliana]	Unigene36686_All//5.00E-39//AT5G53870| plastocyanin-like domain-containing protein	Unigene36686_All//0.00E+00//TC145004				nr -
Unigene36687_All	689	2.73	15.59	5.56	5.93	6.10	5.83	47.19	28.45	38.86	2.51E+00	2.70E-29	Up	1.03E+00	1.80E-03		4.05E-02	9.13E-01		-2.32E-02	9.46E-01		-7.30E-01	1.81E-17		-2.80E-01	7.56E-04		Unigene36687_All//gi|108862168|gb|ABG21877.1|//5.00E-38//EF hand family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene36687_All//2.00E-31//AT3G10300| calcium-binding EF hand family protein	Unigene36687_All//0.00E+00//gi|48816271|gb|CO117584.1|CO117584		ko04626|Plant-pathogen interaction	GO:0016872	nr -
Unigene36688_All	1074	13.93	32.60	12.44	27.27	19.69	29.39	104.60	77.36	101.15	1.23E+00	2.19E-35	Up	-1.63E-01	3.34E-01		-4.70E-01	2.77E-07		1.08E-01	3.52E-01		-4.35E-01	1.88E-23		-4.83E-02	3.50E-01		Unigene36688_All//gi|225441918|ref|XP_002284505.1|//1.00E-117//PREDICTED: similar to calcium-binding EF hand family protein [Vitis vinifera]	Unigene36688_All//5.00E-87//AT5G04170| calcium-binding EF hand family protein	Unigene36688_All//0.00E+00//TC162214		ko04626|Plant-pathogen interaction	GO:0046872	nr +
Unigene36690_All	1956	18.08	39.35	26.79	16.50	9.86	13.81	11.82	16.13	6.88	1.12E+00	6.86E-67	Up	5.67E-01	3.80E-14		-7.43E-01	1.46E-17		-2.57E-01	7.77E-03		4.48E-01	1.53E-07		-7.80E-01	1.48E-14		Unigene36690_All//gi|183229552|gb|ACO60274.1|//0.00E+00//aluminum-activated citrate transporter [Glycine max]	Unigene36690_All//4.00E-166//AT1G51340| MATE efflux family protein	Unigene36690_All//0.00E+00//TC176101			GO:0015291//GO:0015893//GO:0044464	nr +
Unigene36694_All	2111	3.02	0.79	2.19	2.52	2.87	2.67	3.87	2.75	3.36	-1.93E+00	4.61E-13	Down	-4.62E-01	6.15E-02		1.85E-01	5.25E-01		8.29E-02	7.64E-01		-4.90E-01	7.07E-03		-2.03E-01	2.93E-01		Unigene36694_All//gi|29028890|gb|AA064824.1|//1.00E-107//At1g20410 [Arabidopsis thaliana]	Unigene36694_All//8.00E-111//AT1G20410| unknown protein	Unigene36694_All//0.00E+00//gi|78348405|gb|DT568679.1|DT568679			GO:0003676//GO:0009451//GO:0016866//GO:0043231	nr -
Unigene36696_All	1740	1.02	1.46	1.07	5.04	1.80	2.34	6.56	9.49	4.67	5.10E-01	2.09E-01		6.71E-02	8.92E-01		-1.48E+00	5.40E-15	Down	-1.11E+00	1.20E-08	Down	5.32E-01	1.24E-05		-4.90E-01	7.67E-04					Unigene36696_All//0.00E+00//DW488774				
Unigene36698_All	1855	14.47	1.80	2.61	23.60	15.83	5.36	11.69	3.51	5.76	-3.00E+00	1.71E-88	Down	-2.47E+00	5.51E-69	Down	-5.76E-01	3.62E-15		-2.14E+00	1.69E-106	Down	-1.73E+00	4.36E-45	Down	-1.02E+00	3.97E-21	Down	Unigene36698_All//gi|297833520|ref|XP_002884642.1|//0.00E+00//glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] >gi|297330482|gb|EFH60901.1|glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	Unigene36698_All//0.00E+00//AT3G07320| glycosyl hydrolase family 17 protein	Unigene36698_All//0.00E+00//TC159161		ko00500|Starch and sucrose metabolism	GO:0005618//GO:0016798//GO:0043167//GO:0044238	nr -
Unigene36699_All	814	57.40	186.37	69.47	69.27	73.95	111.91	32.93	26.70	38.91	1.70E+00	4.42E-246	Up	2.75E-01	1.65E-04		9.42E-02	2.28E-01		6.92E-01	6.97E-38		-3.03E-01	1.45E-03		2.41E-01	4.87E-03		Unigene36699_All//gi|3860249|gb|AAC73017.1|//1.00E-35//expressed protein [Arabidopsis thaliana]	Unigene36699_All//6.00E-35//AT2G27830| FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT4G22760.1); Has 68 Blast hits to 68 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene36699_All//0.00E+00//gi|73859999|gb|DT462738.1|DT462738				nr +
Unigene3670_All	2219	5.59	18.31	4.46	6.58	9.16	9.08	19.30	25.11	77.16	1.71E+00	4.85E-67	Up	-3.24E-01	6.07E-02		4.77E-01	3.15E-05		4.65E-01	1.12E-04		3.79E-01	1.58E-09		2.00E+00	0.00E+00	Up	Unigene3670_All//gi|18397204|ref|NP_564333.1|//0.00E+00//CAD1 (constitutively activated cell death 1) [Arabidopsis thaliana] >gi|186506018|gb|AAL75908.1|At1g29690/F15D2_24 [Arabidopsis thaliana] >gi|133778820|gb|AB038750.1|At1g29690 [Arabidopsis thaliana]	Unigene3670_All//0.00E+00//AT1G29690| CAD1 (constitutively activated cell death 1)	Unigene3670_All//0.00E+00//TC169996				nr +
Unigene36700_All	984	9.41	4.27	5.20	224.21	106.84	68.53	62.05	14.99	11.90	-1.14E+00	6.07E-09	Down	-8.57E-01	1.36E-05		-1.07E+00	4.04E-220	Down	-1.71E+00	0.00E+00	Down	-2.05E+00	2.47E-157	Down	-2.38E+00	1.25E-195	Down	Unigene36700_All//gi|297797417|ref|XP_002866593.1|//4.00E-50//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312428|gb|EFH42852.1|protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36700_All//2.00E-42//AT5G64080| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene36700_All//0.00E+00//TC140992			GO:0005488//GO:0006810//GO:0031225	nr -
Unigene36701_All	2118	6.20	1.67	2.74	13.69	9.32	9.81	10.94	3.97	5.62	-1.89E+00	2.33E-25	Down	-1.18E+00	2.06E-12	Down	-5.55E-01	1.40E-09		-4.81E-01	7.86E-07		-1.46E+00	8.57E-38	Down	-9.60E-01	2.35E-20		Unigene36701_All//gi|15231273|ref|NP_187965.1|//0.00E+00//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|42572413|ref|NP_974302.1|glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|42572415|ref|NP_974303.1|glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|38257734|sp|Q94CD8.1|E134_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 4; AltName: Full=(1->3)-beta-glucan endohydrolase 4; Short=(1->3)-beta-glucanase 4; AltName: Full=Beta-1,3-endoglucanase 4; Short=Beta-1,3-glucanase 4; Flags: Precursor >gi|222423996|dbj|BAH19959.1|AT3G13560 [Arabidopsis thaliana]	Unigene36701_All//8.00E-172//AT3G13560| glycosyl hydrolase family 17 protein	Unigene36701_All//0.00E+00//gi|109881296|gb|DW510266.1|DW510266		ko00500|Starch and sucrose metabolism	GO:0016798//GO:0031225//GO:0043167//GO:0044238	nr -
Unigene36702_All	2268	20.05	8.51	5.00	33.14	39.08	30.77	41.74	12.00	15.88	-1.24E+00	1.67E-46	Down	-2.00E+00	4.52E-90	Down	2.38E-01	4.28E-06		-1.07E-01	1.14E-01		-1.80E+00	1.26E-204	Down	-1.39E+00	1.73E-145	Down	Unigene36702_All//gi|2190419|emb|CAA73973.1|//0.00E+00//dem [Solanum lycopersicum]	Unigene36702_All//0.00E+00//AT4G33400| dem protein-related / defective embryo and meristems protein-related	Unigene36702_All//0.00E+00//TC137627			GO:0016020//GO:0043231//GO:0044444	nr -
Unigene36703_All	2417	0.74	0.34	0.13	0.62	0.83	0.62	2.71	0.47	1.01	-1.13E+00	2.21E-02		-2.48E+00	4.58E-05	Down	4.18E-01	4.06E-01		-4.00E-03	9.88E-01		-2.54E+00	1.63E-22	Down	-1.43E+00	2.78E-11	Down	Unigene36703_All//gi|2190419|emb|CAA73973.1|//0.00E+00//dem [Solanum lycopersicum]	Unigene36703_All//0.00E+00//AT4G33400| dem protein-related / defective embryo and meristems protein-related	Unigene36703_All//0.00E+00//TC137627			GO:0016020//GO:0043231//GO:0044444	nr +
Unigene36709_All	1208	4.85	4.91	5.42	23.09	19.98	13.42	6.23	3.46	1.68	1.68E-02	9.68E-01		1.61E-01	5.42E-01		-2.09E-01	4.65E-02		-7.83E-01	7.34E-15		-8.49E-01	8.23E-06		-1.89E+00	1.17E-18	Down	Unigene36709_All//gi|30687337|ref|NP_173561.2|//3.00E-38//emb2170 (embryo defective 2170) [Arabidopsis thaliana] >gi|62867637|gb|AAY17422.1|At1g21390 [Arabidopsis thaliana] >gi|89111926|gb|ABD60735.1|At1g21390 [Arabidopsis thaliana]	Unigene36709_All//1.00E-22//AT1G76880| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: emb2170 (embryo defective 2170) (TAIR:AT1G21390.1); Has 33 Blast hits to 33 proteins in 14 species: Archae - 0; Bacteria - 4; Metazoa - 2; Fungi - 7; Plants - 14; Viruses - 2; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene36709_All//0.00E+00//TC147328				nr -
Unigene3671_All	552	45.69	30.38	35.21	58.30	47.29	56.86	47.64	47.17	18.62	-5.89E-01	5.58E-08		-3.76E-01	8.97E-04		-3.02E-01	8.21E-04		-3.59E-02	7.52E-01		-1.43E-02	9.14E-01		-1.36E+00	2.50E-39	Down	Unigene3671_All//gi|18400721|ref|NP_565585.1|//1.00E-30//SDF2 (STROMAL CELL-DERIVED FACTOR 2-LIKE PROTEIN PRECURSOR) [Arabidopsis thaliana] >gi|24212393|sp|Q93ZE8.1|SDF2_ARATH RecName: Full=Stromal cell-derived factor 2-like protein; Short=SDF2-like protein; Flags: Precursor >gi|16209645|gb|AAL14383.1|At2g25110/F13D4.70 [Arabidopsis thaliana] >gi|23505803|gb|AAN28761.1|At2g25110/F13D4.70 [Arabidopsis thaliana]	Unigene3671_All//1.00E-23//AT2G25110| SDF2 (STROMAL CELL-DERIVED FACTOR 2-LIKE PROTEIN PRECURSOR)	Unigene3671_All//8.00E-170//gi|78325866|gb|DT546140.1|DT546140				nr -
Unigene36711_All	3214	0.50	1.36	0.60	1.35	0.78	1.91	1.59	8.52	8.08	1.43E+00	3.46E-06	Up	2.41E-01	6.24E-01		-7.86E-01	3.99E-03		5.03E-01	3.88E-02		2.42E+00	9.01E-87	Up	2.34E+00	7.44E-81	Up	Unigene36711_All//gi|240254179|ref|NP_174268.7|//0.00E+00//RKF1 (RECEPTOR-LIKE KINASE IN FLOWERS 1); ATP binding / kinase/ protein serine/threonine kinase/ receptor signaling protein serine/threonine kinase [Arabidopsis thaliana] >gi|75334468|sp|Q9FXF2.1|RKF1_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase RFK1; AltName: Full=Receptor-like kinase in flowers 1; Flags: Precursor >gi|9972369|gb|AAG10619.1|AC008030_19 Receptor-like serine/threonine kinase (RFK1) [Arabidopsis thaliana]	Unigene36711_All//0.00E+00//AT1G29750| RKF1 (RECEPTOR-LIKE KINASE IN FLOWERS 1); ATP binding / kinase/ protein serine/threonine kinase/ receptor signaling protein serine/threonine kinase	Unigene36711_All//0.00E+00//TC163829		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674//GO:0008152	nr +
Unigene36712_All	1376	4.18	2.58	3.41	3.19	3.00	3.48	9.28	6.65	4.02	-6.98E-01	4.66E-03		-2.97E-01	2.74E-01		-8.52E-02	8.19E-01		1.27E-01	7.00E-01		-4.80E-01	6.50E-04		-1.21E+00	1.98E-16	Down	Unigene36712_All//gi|224109720|ref|XP_002315289.1|//1.00E-11//global transcription factor group [Populus trichocarpa] >gi|222864329|gb|EEF01460.1|global transcription factor group [Populus trichocarpa]	Unigene36712_All//3.00E-26//AT3G27420| unknown protein	Unigene36712_All//0.00E+00//TC165478				nr -
Unigene36713_All	1453	8.21	1.81	7.99	6.86	8.89	6.75	2.42	1.78	2.50	-2.18E+00	1.09E-27	Down	-3.93E-02	8.31E-01		3.74E-01	1.58E-02		-2.37E-02	9.26E-01		-4.38E-01	1.48E-01		4.70E-02	8.87E-01		Unigene36713_All//gi|149789412|gb|ABR29877.1|//0.00E+00//phosphoenol pyruvate carboxylase [Ricinus communis]	Unigene36713_All//5.00E-160//AT1G68750| ATPPC4; phosphoenolpyruvate carboxylase	Unigene36713_All//0.00E+00//gi|78336761|gb|DT557035.1|DT557035		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0004611//GO:0009060//GO:0071704	nr +

Unigene36715_All	1208	30.79	16.02	29.93	11.88	8.95	10.99	3.01	1.45	0.89	-9.43E-01	7.86E-25		-4.10E-02	6.90E-01		-4.08E-01	3.80E-03		-1.12E-01	5.40E-01		-1.05E+00	2.96E-04	Down	-1.76E+00	1.23E-08	Down	Unigene36715_All|gi|121308621|dbj|BAF43703.1|//1.00E-128//Chlorophyllase 1 [Glycine max]	Unigene36715_All//1.00E-107//AT5G43860| ATCLH2; chlorophyllase	Unigene36715_All//0.00E+00//TC178520		ko00860|Porphyrin and chlorophyll metabolism	GO:0004091//GO:0031410//GO:0043231	nr -
Unigene36716_All	935	89.76	88.60	103.60	81.41	74.25	78.35	56.07	25.79	19.64	-1.87E-02	7.77E-01		2.07E-01	1.79E-04		-1.33E-01	3.20E-02		-5.53E-02	4.75E-01		-1.12E+00	4.90E-56	Down	-1.51E+00	1.99E-91	Down	Unigene36716_All|gi|194466266|gb|ACF74362.1|//8.00E-73//perchloric acid soluble translation inhibitor protein [Arachis hypogaea]	Unigene36716_All//2.00E-65//AT3G20390| endoribonuclease L-PSP family protein	Unigene36716_All//0.00E+00//TC159873			GO:0009536//GO:0010038	nr +
Unigene36718_All	964	41.19	39.58	34.97	36.95	42.15	36.26	57.94	31.30	22.23	-5.77E-02	5.74E-01		-2.37E-01	9.17E-03		1.90E-01	2.65E-02		-2.70E-02	8.03E-01		-8.88E-01	6.94E-41		-1.38E+00	5.37E-85	Down	Unigene36718_All|gi|226505142|ref|NP_001149258.1|//3.00E-48//ribosomal protein S12 (homolog) [Zea mays] >gi|195625842|gb|ACG34751.1| 40S ribosomal protein S12 [Zea mays]	Unigene36718_All//4.00E-49//AT2G32060| 40S ribosomal protein S12 (RPS12C)	Unigene36718_All//0.00E+00//TC163989		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279//GO:0043231	nr +
Unigene36719_All	1548	1.52	1.90	0.89	2.51	2.80	2.39	16.50	5.37	15.65	3.20E-01	3.81E-01		-7.66E-01	8.04E-02		1.59E-01	6.29E-01		-6.92E-02	8.42E-01		-1.62E+00	4.54E-48	Down	-7.63E-02	4.97E-01		Unigene36719_All|gi|224113331|ref|XP_002316459.1|//1.00E-124//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222865499|gb|EEF02630.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene36719_All//1.00E-75//AT3G54320| WRI1 (WRINKLED 1); DNA binding / transcription factor	Unigene36719_All//0.00E+00//TC150196	AP2-EREBP		GO:0003676//GO:0006096//GO:0006350//GO:0006611//GO:0010468//GO:0034285//GO:0043231	nr -
Unigene3672_All	1471	7.04	14.60	6.84	16.19	30.17	31.26	41.88	65.63	86.58	1.05E+00	2.25E-17	Up	-4.17E-02	8.31E-01		8.99E-01	6.08E-32		9.49E-01	6.31E-33		6.48E-01	7.03E-41		1.05E+00	9.84E-124	Up	Unigene3672_All|gi|28558782|gb|AAO45753.1|//1.00E-102//RING/C3HC4/PHD zinc finger-like protein [Cucumis melo]	Unigene3672_All//4.00E-70//AT3G05200| ATL6; protein binding / zinc ion binding	Unigene3672_All//0.00E+00//TC144485				nr +
Unigene36720_All	2076	1.36	4.08	1.13	3.22	5.16	5.07	3.50	5.03	3.91	1.58E+00	4.90E-13	Up	-2.70E-01	5.06E-01		6.82E-01	3.28E-05		6.57E-01	1.44E-04		5.23E-01	8.98E-04		1.60E-01	4.12E-01		Unigene36720_All|gi|115472801|ref|NP_001059999.1|//2.00E-56//Os07g0563800 [Oryza sativa Japonica Group] >gi|50510178|dbj|BAD31272.1| ARF GAP-like zinc finger-containing protein-like [Oryza sativa Japonica Group] >gi|113611535|dbj|BAF21913.1|Os07g0563800 [Oryza sativa Japonica Group] >gi|219969152|gb|ACJ54910.1| GAP-like zinc-finger containing protein [Oryza sativa Japonica Group]	Unigene36720_All//7.00E-49//AT5G54310| AGD5 (ARF-GAP domain 5); ARF GTPase activator/ DNA binding / zinc ion binding	Unigene36720_All//8.00E-25//EX169189		ko04144|Endocytosis	GO:0003006//GO:0005083//GO:0032850//GO:0044431//GO:0046914	nr +
Unigene36721_All	933	9.20	19.17	12.44	13.45	15.58	15.49	28.87	34.00	22.50	1.06E+00	9.45E-15	Up	4.36E-01	1.29E-02		2.11E-01	1.88E-01		2.03E-01	2.22E-01		2.36E-01	7.50E-03		-3.59E-01	8.37E-05		Unigene36721_All|gi|297853274|ref|XP_002894518.1|//1.00E-88//WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340360|gb|EFH70777.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36721_All//6.00E-83//AT1G55680| WD-40 repeat family protein	Unigene36721_All//0.00E+00//TC137174		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis//ko03018|RNA degradation//ko03420|Nucleotide excision repair//ko03022|Basal transcription factors	GO:0019897//GO:0031461	nr +
Unigene36724_All	1212	0.82	0.38	0.48	1.32	0.94	0.60	0.52	1.59	1.22	-1.12E+00	1.09E-01		-7.63E-01	2.94E-01		-4.88E-01	3.53E-01		-1.14E+00	3.09E-02		1.60E+00	2.94E-04	Up	1.22E+00	1.17E-02		Unigene36724_All|gi|18390437|ref|NP_563717.1|//6.00E-44//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|15450836|gb|AAK96689.1| Unknown protein [Arabidopsis thaliana] >gi|30725482|gb|AAP37763.1|At1g04790 [Arabidopsis thaliana]	Unigene36724_All//5.00E-35//AT1G04790| zinc finger (C3HC4-type RING finger) family protein	Unigene36724_All//2.00E-157//DR457287			GO:0005488	nr +
Unigene36725_All	1139	5.60	3.38	10.80	0.44	2.09	1.98	0.07	0.00	0.00	-7.29E-01	1.75E-03		9.46E-01	2.20E-08		2.25E+00	8.41E-07	Up	2.18E+00	5.88E-06	Up	-6.21E+00	4.03E-01		-6.21E+00	3.58E-01		Unigene36725_All|gi|14334057|gb|AK60517.1|AF332974_1/1.00E-107//P450 monooxygenase [Gossypium arboreum]	Unigene36725_All//6.00E-43//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene36725_All//0.00E+00//DR456127		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0046872	nr -
Unigene36726_All	1643	2.83	2.22	5.06	0.00	0.82	0.58	0.00	0.00	0.00	-3.52E-01	2.22E-01		8.35E-01	6.47E-05		9.67E+00	2.67E-08	Up	9.17E+00	1.13E-05	Up	null	null		null	null		Unigene36726_All|gi|14334057|gb|AK60517.1|AF332974_1/1.00E-146//P450 monooxygenase [Gossypium arboreum]	Unigene36726_All//4.00E-100//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene36726_All//0.00E+00//DR456127		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene36727_All	996	0.32	0.10	0.00	0.35	1.07	0.73	1.83	0.46	10.28	-1.63E+00	2.76E-01		-8.30E+00	4.90E-02		1.61E+00	2.12E-02		1.05E+00	2.35E-01		-1.98E+00	3.39E-05	Down	2.49E+00	1.06E-34	Up	Unigene36727_All|gi|14334057|gb|AK60517.1|AF332974_1/3.00E-68//P450 monooxygenase [Gossypium arboreum]	Unigene36727_All//2.00E-44//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene36727_All//0.00E+00//ES819299		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506	nr -
Unigene36728_All	1735	2.80	2.45	3.96	0.40	1.43	1.12	0.00	0.00	0.00	-1.93E-01	5.07E-01		4.98E-01	3.49E-02		1.83E+00	1.45E-05	Up	1.48E+00	2.31E-03		null	null		null	null		Unigene36728_All|gi|14334057|gb|AK60517.1|AF332974_1/0.00E+00//P450 monooxygenase [Gossypium arboreum]	Unigene36728_All//4.00E-108//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene36728_All//0.00E+00//DR456127		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0016491	nr -
Unigene36729_All	1325	18.60	40.11	25.88	12.59	12.58	16.16	24.12	23.94	28.26	1.11E+00	1.47E-45	Up	4.77E-01	4.14E-07		-1.80E-03	9.87E-01		3.59E-01	2.46E-03		-1.09E-02	9.34E-01		2.29E-01	3.46E-03		Unigene36729_All|gi|30698229|ref|NP_201446.2|//9.00E-63//phosphatidic acid phosphatase-related / PAP2-related [Arabidopsis thaliana] >gi|34146858|gb|AAQ62437.1|At5g66450 [Arabidopsis thaliana]	Unigene36729_All//3.00E-60//AT5G66450| phosphatidic acid phosphatase-related / PAP2-related	Unigene36729_All//0.00E+00//TC151098		ko00510|N-Glycan biosynthesis	GO:0043231	nr +
Unigene36730_All	340	0.00	3.28	1.25	3.52	2.03	1.59	0.25	0.98	0.94	1.17E+01	2.00E-06	Up	1.03E+01	1.38E-02		-7.96E-01	1.87E-01		-1.14E+00	7.15E-02		1.98E+00	1.44E-01		1.91E+00	1.54E-01		Unigene36730_All|gi|290490572|dbj|BAI79273.1|//1.00E-31//LysM type receptor kinase [Lotus japonicus]	Unigene36730_All//5.00E-22//AT3G21630| CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase	Unigene36730_All//9.00E-150//gi|78336809|gb|DT557083.1|DT557083		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0043170//GO:0044237//GO:0044238	nr -
Unigene36732_All	1596	4.69	2.57	2.34	9.11	4.96	2.72	4.79	1.18	0.80	-8.66E-01	5.27E-05		-1.01E+00	7.46E-06	Down	-8.77E-01	9.82E-11		-1.75E+00	3.12E-27	Down	-2.02E+00	4.87E-20	Down	-2.59E+00	1.27E-27	Down	Unigene36732_All|gi|79346260|ref|NP_173302.2|//1.00E-141//IBS1 (IMPAIRED IN BABA-INDUCED STERILITY 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene36732_All//2.00E-141//AT1G18670| IBS1 (IMPAIRED IN BABA-INDUCED STERILITY 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene36732_All//0.00E+00//DW517146			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene36734_All	1853	1.07	4.07	1.87	4.73	5.26	6.56	3.65	6.61	8.26	1.92E+00	3.87E-15	Up	8.00E-01	2.11E-02		1.53E-01	4.93E-01		4.71E-01	3.62E-03		8.56E-01	4.59E-09		1.18E+00	1.14E-18	Up	Unigene36734_All|gi|297822773|ref|XP_002879269.1|//1.00E-135//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325108|gb|EFH55528.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36734_All//3.00E-112//AT2G30580| DRIP2 (DREB2A-INTERACTING PROTEIN 2); protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene36734_All//0.00E+00//CO093180				nr -
Unigene36735_All	1108	45.14	105.18	45.75	63.80	86.03	115.44	64.87	57.49	81.04	1.22E+00	2.34E-115	Up	1.93E-02	8.27E-01		4.31E-01	6.47E-19		8.56E-01	2.82E-76		-1.74E-01	2.24E-03		3.21E-01	2.12E-11		Unigene36735_All|gi|30695448|ref|NP_564623.2|//1.00E-131//sodium/calcium exchanger family protein / calcium-binding EF hand family protein [Arabidopsis thaliana]	Unigene36735_All//2.00E-132//AT1G53210| sodium/calcium exchanger family protein / calcium-binding EF hand family protein	Unigene36735_All//0.00E+00//TC149923				nr +
Unigene36739_All	945	7.81	6.49	4.90	25.88	14.50	8.08	4.34	3.32	1.94	-2.67E-01	2.33E-01		-6.71E-01	2.66E-03		-8.36E-01	2.38E-16		-1.68E+00	4.50E-43	Down	-3.88E-01	1.66E-01		-1.16E+00	1.36E-05	Down							
Unigene3674_All	1344	4.87	5.50	5.27	30.84	21.34	22.48	59.14	29.33	21.55	1.78E-01	4.37E-01		1.15E-01	6.20E-01		-5.31E-01	1.82E-12		-4.56E-01	1.17E-08		-1.01E+00	9.43E-72	Down	-1.46E+00	1.39E-130	Down	Unigene3674_All|gi|224103505|ref|XP_002313083.1|//1.00E-149//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222849491|gb|EEE57035.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene3674_All//1.00E-125//AT3G19000| oxidoreductase, 20G-Fe(II) oxygenase family protein	Unigene3674_All//0.00E+00//TC143847		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr -
Unigene36741_All	951	14.69	14.71	14.67	18.12	13.69	32.15	9.34	6.37	3.02	1.60E-03	9.92E-01		-1.90E-03	9.90E-01		-4.05E-01	1.33E-03		8.27E-01	1.31E-17		-5.51E-01	1.40E-03		-1.63E+00	5.91E-18	Down		Unigene36741_All//0.00E+00//gi|72268947|gb|DT046941.1|DT046941					
Unigene36742_All	1072	1.90	2.08	1.49	94.42	54.22	72.25	54.82	22.54	20.29	1.28E-01	7.57E-01		-3.53E-01	4.55E-01		-8.00E-01	8.50E-62		-3.86E-01	5.10E-15		-1.28E+00	1.55E-77	Down	-1.43E+00	1.60E-94	Down	Unigene36742_All|gi|214011869|gb|ACJ61689.1|//7.00E-82//WOX4 [Solanum lycopersicum] >gi|214011873|gb|ACJ61691.1| WOX4 [Solanum lycopersicum]	Unigene36742_All//5.00E-62//AT1G46480| WOX4 (WUSCHEL RELATED HOMEOBOX 4); transcription factor	Unigene36742_All//0.00E+00//gi|109839409|gb|DW237970.1|DW237970	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene36743_All	1680	3.33	4.22	2.12	5.07	4.98	3.79	10.92	6.64	4.65	3.42E-01	1.33E-01		-6.50E-01	1.35E-02		-2.57E-02	9.09E-01		-4.20E-01	3.80E-02		-7.18E-01	6.14E-10		-1.23E+00	4.97E-24	Down	Unigene36743_All|gi|297796559|ref|XP_002866164.1|//1.00E-122//histone acetyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311999|gb|EFH42423.1| histone acetyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36743_All//1.00E-114//AT5G56740| HAG2 (HISTONE ACETYLTRANSFERASE OF THE GNAT FAMILY 2); H4 histone acetyltransferase/ histone acetyltransferase	Unigene36743_All//0.00E+00//TC138851			GO:0006325//GO:0008080	nr +
Unigene36744_All	657	0.32	8.33	0.89	0.83	2.41	4.19	0.77	3.37	3.76	4.71E+00	1.09E-25	Up	1.49E+00	1.53E-01		1.53E+00	4.53E-03		2.33E+00	1.10E-07	Up	2.13E+00	1.18E-06	Up	2.28E+00	3.80E-08	Up		Unigene36744_All//9.00E-161//TC175684					
Unigene36745_All	1108	3.64	35.03	6.34	5.44	19.39	42.35	9.54	25.76	37.65	3.27E+00	2.91E-137	Up	8.03E-01	4.71E-04		1.83E+00	1.02E-45	Up	2.96E+00	1.51E-161	Up	1.43E+00	6.79E-45	Up	1.98E+00	8.54E-105	Up	Unigene36745_All|gi|16648748|gb|AAL25566.1|//1.00E-35//AT5g02020/T7H20_70 [Arabidopsis thaliana] >gi|20334906|gb|AAM16209.1|AT5g02020/T7H20_70 [Arabidopsis thaliana]	Unigene36745_All//6.00E-32//AT5G02020| unknown protein	Unigene36745_All//0.00E+00//TC175684				nr -
Unigene36746_All	1394	43.65	21.77	49.96	47.53	42.61	26.57	7.95	1.80	1.11	-1.00E+00	1.72E-44	Down	1.95E-01	3.67E-03		-1.58E-01	1.56E-02		-8.39E-01	7.83E-39		-2.14E+00	8.53E-31	Down	-2.83E+00	9.58E-44	Down	Unigene36746_All|gi|297832042|ref|XP_002883903.1|//2.00E-42//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329743|gb|EFH60162.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36746_All//3.00E-40//AT2G15580| zinc finger (C3HC4-type RING finger) family protein	Unigene36746_All//0.00E+00//TC148680			GO:0043231//GO:0046914	nr -
Unigene36747_All	1246	11.93	9.31	11.15	16.19	14.92	12.00	10.52	4.06	3.17	-3.57E-01	1.54E-02		-9.64E-02	5.90E-01		-1.18E-01	4.18E-01		-4.33E-01	3.24E-04		-1.37E+00	8.11E-20	Down	-1.73E+00	2.20E-28	Down	Unigene36747_All|gi|22328740|ref|NP_193438.2|//1.00E-140//UGLYAH (UREIDOGLYCINE AMINOHYDROLASE); transcription factor [Arabidopsis thaliana] >gi|296248910|gb|ADH04164.1| ureidoglycine aminohydrolase [Arabidopsis thaliana]	Unigene36747_All//2.00E-130//AT4G17050| UGLYAH (UREIDOGLYCINE AMINOHYDROLASE); transcription factor	Unigene36747_All//0.00E+00//TC154142				nr -

Unigene36748_All	1131	3.56	3.00	9.98	4.58	4.35	4.31	16.93	2.11	2.25	-2.47E-01	4.30E-01			1.49E+00	3.72E-15	Up	-7.32E-02	8.27E-01		-8.69E-02	7.58E-01		-3.01E+00	2.69E-77	Down	-2.91E+00	3.54E-77	Down	Unigene36748_All//gi|115465627|ref|NP_001056413.1|//2.00E-64//0s05g0578500 [Oryza sativa Japonica Group] >gi|113579964|dbj|BAF18327.1| Os05g0578500 [Oryza sativa Japonica Group]	Unigene36748_All//3.00E-59//AT5G14700| cinnamoyl-CoA reductase-related	Unigene36748_All//0.00E+00//TC148083		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis	GO:0008152//GO:0016491	nr +
Unigene36749_All	1051	28.87	30.90	32.22	29.95	33.81	42.28	49.00	35.19	22.21	9.80E-02	3.75E-01			1.58E-01	1.34E-01		1.75E-01	6.55E-02		4.97E-01	1.19E-10		-4.77E-01	3.88E-13		-1.14E+00	2.45E-58	Down	Unigene36749_All//gi|297609769|ref|NP_001063604.2|//1.00E-105//0s09g0505700 [Oryza sativa Japonica Group] >gi|60390595|sp|Q9SE42.1|RPE1_ORYSJ RecName: Full=Ribulose-phosphate 3-epimerase, cytoplasmic isoform; AltName: Full=Ribulose-5-phosphate-epimerase; AltName: Full=Cyt-RPEase; AltName: Full=RPEcyt; AltName: Full=Pentose-5-phosphate 3-epimerase; Short=PPE >gi|28373310|pdb|1H1Y|A Chain A, The Structure Of The Cytosolic D-Ribulose-5-Phosphate 3- Epimerase From Rice Complexed With Sulfate >gi|28373311|pdb|1H1Y|B Chain B, The Structure Of The Cytosolic D-Ribulose-5-Phosphate 3- Epimerase From Rice Complexed With Sulfate >gi|28373312|pdb|1H1Z|A Chain A, The Structure Of The Cytosolic D-Ribulose-5-Phosphate 3- Epimerase From Rice Complexed With Sulfate And Zinc >gi|28373313|pdb|1H1Z|B Chain B, The Structure Of The Cytosolic D-Ribulose-5-Phosphate 3- Epimerase From Rice Complexed With Sulfate And Zinc	Unigene36749_All//6.00E-106//AT1G63290| ribulose-phosphate 3-epimerase, cytosolic, putative / pentose-5-phosphate 3-epimerase, putative	Unigene36749_All//0.00E+00//TC161164		ko00710|Carbon fixation in photosynthetic organisms//ko00040|Pentose and glucuronate interconversions//ko00030|Pentose phosphate pathway	GO:0016857//GO:0044238	nr -
Unigene3675_All	971	1.24	1.41	1.86	2.21	1.88	2.42	3.00	1.98	1.35	1.85E-01	7.28E-01			5.89E-01	2.42E-01		-2.31E-01	6.06E-01		1.33E-01	7.61E-01		-6.02E-01	6.89E-02		-1.15E+00	3.57E-04	Down			Unigene3675_All//1.00E-49//DR455784				
Unigene36750_All	1467	1.46	0.62	0.40	2.82	1.81	1.32	2.85	1.20	4.78	-1.23E+00	5.86E-03			-1.87E+00	1.90E-04	Down	-6.41E-01	2.48E-02		-1.09E+00	2.46E-04	Down	-1.25E+00	4.57E-06	Down	7.44E-01	1.11E-04		Unigene36750_All//gi|219291116|gb|ACL13991.1|//5.00E-72//At2g33360 [Arabidopsis thaliana]	Unigene36750_All//2.00E-65//AT2G33360| unknown protein	Unigene36750_All//5.00E-56//gi|78348807|gb|DT569081.1|DT569081			GO:0043231	nr +
Unigene36751_All	1099	15.90	11.30	9.35	27.92	20.93	26.47	23.89	12.06	10.66	-4.93E-01	1.93E-04			-7.66E-01	2.65E-08		-4.16E-01	3.64E-06		-7.73E-02	5.29E-01		-9.87E-01	2.79E-23		-1.16E+00	3.83E-31	Down	Unigene36751_All//gi|115448445|ref|NP_001048002.1|//8.00E-56//Os02g0728700 [Oryza sativa Japonica Group] >gi|113537533|dbj|BAF09916.1| Os02g0728700 [Oryza sativa Japonica Group]	Unigene36751_All//3.00E-55//AT5G38720| unknown protein	Unigene36751_All//0.00E+00//TC145611				nr -
Unigene36752_All	1846	3.03	1.10	0.61	2.40	1.64	1.10	21.23	5.75	8.37	-1.47E+00	4.58E-08	Down	-2.32E+00	1.02E-13	Down	-5.49E-01	4.82E-02		-1.13E+00	8.39E-05	Down	-1.88E+00	1.26E-90	Down	-1.34E+00	2.46E-57	Down	Unigene36752_All//gi|116248667|gb|ABJ90468.1|//0.00E+00//beta-ketoacyl-ACP synthase I [Jatropha curcas]	Unigene36752_All//0.00E+00//AT5G46290| KAS I (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE I); catalytic/ fatty-acid synthase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene36752_All//0.00E+00//TC163346		ko00061|Fatty acid biosynthesis	GO:0004312//GO:0006631//GO:0043231	nr +
Unigene36754_All	1629	18.05	13.41	20.76	11.25	10.19	7.68	3.30	2.23	1.22	-4.29E-01	1.59E-05			2.02E-01	4.71E-02		-1.43E-01	3.22E-01		-5.51E-01	1.13E-05		-5.62E-01	1.47E-02		-1.43E+00	2.14E-09	Down	Unigene36754_All//gi|158427472|gb|ABK38331.1|//1.00E-149//chloroplast fructose-1,6-bisphosphatase II [Fragaria x ananassa] >gi|190151803|gb|ACE63522.1| chloroplast fructose-1,6-bisphosphatase [Fragaria x ananassa]	Unigene36754_All//5.00E-128//AT5G64380| fructose-1,6-bisphosphatase family protein	Unigene36754_All//0.00E+00//TC171484		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway	GO:0008152//GO:0016787	nr -
Unigene36755_All	888	16.03	6.68	6.54	26.48	19.43	22.89	49.52	47.59	31.45	-1.26E+00	1.46E-15	Down	-1.29E+00	2.00E-15	Down	-4.47E-01	1.80E-05		-2.10E-01	8.23E-02		-5.74E-02	5.35E-01		-6.55E-01	5.38E-20		Unigene36755_All//gi|115481716|ref|NP_001064451.1|//9.00E-68//Os10g0369000 [Oryza sativa Japonica Group] >gi|20043025|gb|AAM08833.1|AC113335_13 Putative glutamyl-tRNA synthetase [Oryza sativa Japonica Group] >gi|31431616|gb|AAP53367.1| glutamyl-tRNA synthetase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639060|dbj|BAF26365.1| Os10g0369000 [Oryza sativa Japonica Group]	Unigene36755_All//4.00E-67//AT5G26710| glutamate-tRNA ligase, putative / glutamyl-tRNA synthetase, putatuve / GluRS, putative	Unigene36755_All//0.00E+00//DT463544		ko00970|Aminoacyl-tRNA biosynthesis//ko00860|Porphyrin and chlorophyll metabolism	GO:0004812//GO:0006418//GO:0032559//GO:0043231	nr -
Unigene36757_All	2690	6.87	4.41	4.81	2.02	2.25	1.90	0.22	0.00	0.06	-6.39E-01	6.64E-07			-5.13E-01	1.15E-04		1.59E-01	5.87E-01		-8.94E-02	7.48E-01		-7.78E+00	2.39E-04	Down	-1.89E+00	3.22E-02		Unigene36757_All//gi|32364696|gb|AAP80385.1|//0.00E+00//ABC transporter [Gossypium hirsutum]	Unigene36757_All//0.00E+00//AT1G17840| WBC11 (WHITE-BROWN COMPLEX HOMOLOG PROTEIN 11); ATPase, coupled to transmembrane movement of substances / fatty acid transporter	Unigene36757_All//0.00E+00//TC131069		ko03040|Spliceosome//ko02010|ABC transporters	GO:0005319//GO:0009986//GO:0015604//GO:0015909//GO:0016020//GO:0017111//GO:0032559	nr +
Unigene36758_All	1446	3.26	3.82	3.98	3.07	3.38	5.03	8.71	8.70	4.19	2.30E-01	3.78E-01			2.88E-01	2.90E-01		1.41E-01	6.57E-01		7.14E-01	8.51E-04		-2.20E-03	1.02E+00		-1.06E+00	2.64E-13	Down	Unigene36758_All//gi|21593200|gb|AM65149.1|//1.00E-103//similar to eyes absent protein [Arabidopsis thaliana]	Unigene36758_All//9.00E-104//AT2G35320| ATEYA (Arabidopsis thaliana EYES ABSENT homolog); protein tyrosine phosphatase, metal-dependent	Unigene36758_All//0.00E+00//TC178484				nr -
Unigene3676_All	1297	29.04	15.51	15.89	42.52	39.98	38.13	31.46	19.98	13.61	-9.05E-01	1.56E-23			-8.70E-01	3.36E-21		-8.86E-02	2.93E-01		-1.57E-01	3.88E-02		-6.55E-01	4.45E-18		-1.21E+00	8.62E-51	Down	Unigene3676_All//gi|18397064|ref|NP_565353.1|//5.00E-68//adenylate cyclase [Arabidopsis thaliana] >gi|4557062|gb|AAD22501.1| expressed protein [Arabidopsis thaliana] >gi|15010776|gb|AAK74047.1| At2g11890/F23M2.5 [Arabidopsis thaliana] >gi|15810059|gb|AAL06955.1| At2g11890/F23M2.5 [Arabidopsis thaliana]	Unigene3676_All//4.00E-59//AT2G11890| adenylate cyclase	Unigene3676_All//0.00E+00//TC150619				nr -
Unigene36760_All	213	0.74	2.62	0.75	0.00	0.49	0.21	1.39	8.83	7.11	1.83E+00	9.02E-02			2.54E-02	1.00E+00		8.92E+00	4.56E-01		7.73E+00	6.96E-01		2.67E+00	2.89E-07	Up	2.35E+00	1.89E-05	Up	Unigene36760_All//gi|3914368|sp|Q39639.1|PLSB_CUCSA//6.00E-11//RecName: Full=Glycerol-3-phosphate acyltransferase, chloroplastic; Short=GPAT; Flags: Precursor >gi|167519|gb|AAA33122.1| glycerol-3-phosphate acyltransferase precursor [Cucumis sativus] >gi|444331|prf||1906380A glycerol phosphate acyltransferase	Unigene36760_All//1.00E-11//AT1G32200| ATS1; glycerol-3-phosphate O-acyltransferase	Unigene36760_All//7.00E-51//TC169142		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0003006//GO:0004497//GO:0006633//GO:0006950//GO:0006996//GO:0008374//GO:0009532//GO:0009725//GO:0016705//GO:0031224//GO:0046471//GO:0046872	nr +
Unigene36761_All	930	49.96	54.10	46.15	15.85	23.14	18.99	25.23	127.50	53.72	1.15E-01	1.63E-01			-1.14E-01	2.13E-01		5.46E-01	7.30E-07		2.60E-01	6.29E-02		2.34E+00	0.00E+00	Up	1.09E+00	3.00E-52	Up	Unigene36761_All//gi|179743220|dbj|BAB78529.1|//1.00E-84//glycerol-3-phosphate acyltransferase [Citrus unshiu]	Unigene36761_All//1.00E-82//AT1G32200| ATS1; glycerol-3-phosphate O-acyltransferase	Unigene36761_All//0.00E+00//TC134915		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0003006//GO:0004497//GO:0006633//GO:0006950//GO:0006996//GO:0008374//GO:0009532//GO:0009725//GO:0016705//GO:0031224//GO:0046471//GO:0046872	nr +
Unigene36763_All	1008	0.10	4.93	0.32	1.63	2.15	3.32	2.10	6.26	8.46	5.57E+00	2.99E-25	Up	1.61E+00	3.05E-01		4.00E-01	4.05E-01		1.02E+00	2.61E-03		1.58E+00	5.13E-12	Up	2.01E+00	1.70E-22	Up	Unigene36763_All//gi|240254348|ref|NP_177256.4|//2.00E-36//heat shock protein binding [Arabidopsis thaliana]	Unigene36763_All//1.00E-37//AT1G71000| heat shock protein binding	Unigene36763_All//0.00E+00//TC157334			GO:0005515	nr +
Unigene36765_All	1601	4.02	3.77	3.29	6.85	7.87	5.22	6.36	0.89	1.02	-9.40E-02	6.91E-01			-2.88E-01	2.56E-01		2.02E-01	2.58E-01		-3.91E-01	2.51E-02		-2.84E+00	4.09E-39	Down	-2.64E+00	2.17E-37	Down	Unigene36765_All//gi|31711872|gb|AP68292.1|//1.00E-159//At5g11730 [Arabidopsis thaliana]	Unigene36765_All//8.00E-161//AT5G11730| unknown protein	Unigene36765_All//3.00E-64//gi|109887238|gb|DW516207.1|DW516207				nr +
Unigene36766_All	1813	11.77	8.58	9.46	7.45	18.27	13.18	10.80	10.49	8.42	-4.57E-01	1.18E-04			-3.16E-01	1.25E-02		1.30E+00	9.52E-43	Up	8.24E-01	8.59E-14		-4.18E-02	7.52E-01		-3.60E-01	9.74E-04		Unigene36766_All//gi|224112417|ref|XP_002316182.1|//1.00E-122//amino acid transporter [Populus trichocarpa] >gi|222865222|gb|EEF02353.1| amino acid transporter [Populus trichocarpa]	Unigene36766_All//2.00E-114//AT3G56200| amino acid transporter family protein	Unigene36766_All//0.00E+00//TC174411			GO:0015837//GO:0016020//GO:0022804	nr -
Unigene36768_All	1366	4.90	3.78	3.82	7.84	9.30	6.55	5.35	2.91	2.48	-3.74E-01	1.09E-01			-3.60E-01	1.42E-01		2.47E-01	1.46E-01		-2.60E-01	1.70E-01		-8.81E-01	5.39E-06		-1.11E+00	1.05E-08	Down	Unigene36768_All//gi|22331064|ref|NP_566459.2|//6.00E-66//FUS9 (FUSCA 9); protein binding / ubiquitin-protein ligase [Arabidopsis thaliana] >gi|55976602|sp|Q9LJD7.1|COP10_ARATH RecName: Full=Constitutive photomorphogenesis protein 10 >gi|20065779|gb|AAK57749.1| ubiquitin-conjugating enzyme COP10 [Arabidopsis thaliana] >gi|110728728|dbj|BAF01288.1| ubiquitin-conjugating enzyme COP10 [Arabidopsis thaliana]	Unigene36768_All//7.00E-64//AT3G13550| FUS9 (FUSCA 9); protein binding / ubiquitin-protein ligase	Unigene36768_All//0.00E+00//TC132380		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0006464//GO:0009640//GO:0019787//GO:0031410//GO:0043231//GO:0060255	nr +
Unigene36770_All	1312	6.10	3.48	6.05	7.59	5.41	3.34	2.90	0.54	0.64	-8.12E-01	7.91E-05			-1.28E-02	9.76E-01		-4.90E-01	4.36E-03		-1.19E+00	9.12E-11	Down	-2.42E+00	1.08E-12	Down	-2.19E+00	1.03E-11	Down	Unigene36770_All//gi|56550681|gb|AAY97794.1|//3.00E-31//At5g67350 [Arabidopsis thaliana] >gi|59958292|gb|AAX12856.1| At5g67350 [Arabidopsis thaliana]	Unigene36770_All//1.00E-20//AT5G67350| unknown protein	Unigene36770_All//0.00E+00//gi|48740567|gb|CO071086.1|CO071086				nr +
Unigene36775_All	2388	47.61	14.85	21.92	17.75	14.23	11.76	14.00	5.06	6.62	-1.68E+00	8.90E-183	Down	-1.12E+00	2.22E-95	Down	-3.19E-01	2.91E-05		-5.94E-01	6.73E-14		-1.47E+00	1.62E-54	Down	-1.08E+00	4.98E-35	Down	Unigene36775_All//gi|2499535|sp|Q41364.1|SOT1_SPIOL//0.00E+00//RecName: Full=2-oxoglutarate/malate translocator, chloroplastic; Flags: Precursor >gi|595681|gb|AAA68148.1| 2-oxoglutarate/malate translocator [Spinacia oleracea]	Unigene36775_All//2.00E-160//AT5G12860| DiT1 (dicarboxylate transporter 1); oxoglutarate:malate antiporter	Unigene36775_All//0.00E+00//TC147942			GO:0009528//GO:0015740//GO:0030001//GO:0031224//GO:0051707	nr -
Unigene36776_All	1905	0.00	0.00	0.00	0.00	0.14	0.00	22.04	3.80	17.11	null	null		null	null		7.18E+00	7.01E-02		null	null		-2.54E+00	1.06E-140	Down	-3.66E-01	3.49E-07		Unigene36776_All//gi|15223699|ref|NP_173419.1|//0.00E+00//glyoxal oxidase-related [Arabidopsis thaliana] >gi|16604507|gb|AAL24259.1| At1g19900/F6F9_4 [Arabidopsis thaliana]	Unigene36776_All//0.00E+00//AT1G75620| glyoxal oxidase-related	Unigene36776_All//0.00E+00//TC171989			GO:0008152//GO:0016899	nr +

Unigene36777_All	1855	0.00	0.00	0.00	0.00	0.04	0.00	27.15	5.36	15.42	null	null		null	null		5.21E+00	6.09E-01		null	null		-2.34E+00	2.54E-153	Down	-8.16E-01	5.29E-33		Unigene36777_All//gi|15223699|ref|NP_173419.1|//0.00E+00//glyoxal oxidase-related [Arabidopsis thaliana] >gi|16604507|gb|AAL24259.1|At1g19900/F6F9_4 [Arabidopsis thaliana]	Unigene36777_All//0.00E+00//AT1G19900| glyoxal oxidase-related	Unigene36777_All//0.00E+00//TC171989			GO:0008152//GO:0016899	nr +
Unigene36778_All	2511	2.27	1.25	1.85	13.47	19.58	24.30	19.45	9.27	5.49	-8.60E-01	5.63E-04		-3.00E-01	2.70E-01		5.40E-01	8.97E-15		8.51E-01	2.56E-36		-1.07E+00	1.81E-48	Down	-1.82E+00	3.55E-111	Down	Unigene36778_All//gi|15235527|ref|NP_194630.1|//0.00E+00//AIM1 (ABNORMAL INFLORESCENCE MERISTEM); enoyl-CoA hydratase [Arabidopsis thaliana] >gi|4337025|gb|AAD18041.1| AIM1 protein [Arabidopsis thaliana] >gi|4972047|emb|CAB43915.1| AIM1 protein [Arabidopsis thaliana] >gi|7269799|emb|CAB79659.1| AIM1 protein [Arabidopsis thaliana] >gi|16648891|gb|AAL24297.1| AIM1 protein [Arabidopsis thaliana]	Unigene36778_All//0.00E+00//AT4G29010| AIM1 (ABNORMAL INFLORESCENCE MERISTEM); enoyl-CoA hydratase	Unigene36778_All//0.00E+00//TC130995		ko00592|alpha-Linolenic acid metabolism	GO:0009062//GO:0009536//GO:0009791//GO:0016836//GO:0016856//GO:0030212//GO:0042579//GO:0048037	nr +
Unigene36779_All	1625	4.25	2.49	3.15	4.75	5.57	2.64	2.37	1.67	0.34	-7.69E-01	5.66E-04		-4.34E-01	6.77E-02		2.30E-01	2.85E-01		-8.48E-01	3.59E-05		-5.02E-01	7.68E-02		-2.79E+00	2.08E-15	Down	Unigene36779_All//gi|219879368|gb|ACL51016.1|//1.00E-52//squamosa promoter-binding protein [Citrus trifoliata]	Unigene36779_All//2.00E-41//AT5G50570| squamosa promoter-binding protein, putative	Unigene36779_All//0.00E+00//C0113054	SBP		GO:0010468	nr +
Unigene3678_All	1351	3.83	7.65	7.65	10.10	17.89	25.11	8.20	13.49	14.89	9.97E-01	4.36E-08		9.96E-01	1.01E-07		8.25E-01	3.11E-15		1.31E+00	8.99E-41	Up	7.18E-01	7.02E-10		8.61E-01	7.17E-15		Unigene3678_All//gi|297793185|ref|XP_002864477.1|//1.00E-152//ndr family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310312|gb|EFH40736.1| ndr family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3678_All//2.00E-152//AT5G56750| Ndr family protein	Unigene3678_All//0.00E+00//TC142892				nr -
Unigene36780_All	1916	1.91	1.30	1.92	4.39	3.61	3.58	4.21	1.51	3.81	-5.61E-01	8.05E-02		4.70E-03	9.95E-01		-2.83E-01	1.73E-01		-2.94E-01	1.72E-01		-1.49E+00	5.71E-14	Down	-1.48E-01	4.60E-01		Unigene36780_All//gi|44681380|gb|AS47630.1|//0.00E+00//At1g64650 [Arabidopsis thaliana] >gi|45773902|gb|AS76755.1| At1g64650 [Arabidopsis thaliana]	Unigene36780_All//0.00E+00//AT1G64650| LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27720.1); Has 565 Blast hits to 562 proteins in 197 species: Archae - 7; Bacteria - 312; Metazoa - 76; Fungi - 39; Plants - 85; Viruses - 0; Other Eukaryotes - 46 (source: NCBI BLink).	Unigene36780_All//1.00E-82//TC153367			GO:0031410	nr +
Unigene36782_All	1537	97.29	35.57	52.04	40.74	37.17	37.64	9.79	6.44	4.95	-1.45E+00	5.98E-194	Down	-9.03E-01	4.99E-88		-1.32E-01	5.84E-02		-1.14E-01	1.29E-01		-6.04E-01	2.50E-06		-9.84E-01	4.50E-14		Unigene36782_All//gi|297811925|ref|XP_002873846.1|//1.00E-95//EMB1241 [Arabidopsis lyrata subsp. lyrata] >gi|297319683|gb|EFH50105.1| EMB1241 [Arabidopsis lyrata subsp. lyrata]	Unigene36782_All//2.00E-87//AT5G17710| EMB1241 (embryo defective 1241); adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization	Unigene36782_All//0.00E+00//TC156716			GO:0003006//GO:0005515//GO:0005739//GO:0009532//GO:0009987//GO:0016914	nr -
Unigene36786_All	1394	0.26	0.80	0.42	0.32	0.52	1.17	0.61	0.96	0.60	1.61E+00	1.95E-02		6.78E-01	4.83E-01		6.90E-01	4.47E-01		1.86E+00	9.27E-04	Up	6.61E-01	2.14E-01		-1.53E-02	9.71E-01		Unigene36786_All//gi|222423371|dbj|BAH19658.1|//6.00E-95//AT3G59090 [Arabidopsis thaliana]	Unigene36786_All//2.00E-78//AT3G59090| EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: TOM1 (TOBAMOVIRUS MULTIPLICATION 1); protein binding (TAIR:AT4G21790.1); Has 115 Blast hits to 115 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 108; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene36786_All//0.00E+00//TC158661			GO:0044464	nr +
Unigene36789_All	1362	5.07	2.90	2.66	4.86	4.20	2.22	5.37	1.23	2.43	-8.05E-01	3.11E-04		-9.32E-01	6.67E-05		-2.13E-01	4.04E-01		-1.13E+00	6.94E-07	Down	-2.13E+00	2.03E-20	Down	-1.15E+00	4.28E-09	Down	Unigene36789_All//gi|226713356|sp|B1B5D4.1|NXJA2_WHEAT//3.00E-18//RecName: Full=Ninja-family protein 2; AltName: Full=ABI five-binding protein B1; Short=ABI5-binding protein B1; Short=TaAFP-B1 >gi|169788695|dbj|BAG12828.1| ABI5 binding protein B1 [Triticum aestivum]	Unigene36789_All//4.00E-19//AT3G29575| AFP3 (ABI FIVE BINDING PROTEIN 3)	Unigene36789_All//0.00E+00//TC174437			GO:0005488	nr -
Unigene36790_All	2154	397.12	64.97	344.52	72.96	50.53	17.03	1.00	0.17	1.48	-2.61E+00	0.00E+00	Down	-2.05E-01	2.30E-33		-5.30E-01	5.37E-46		-2.10E+00	0.00E+00	Down	-2.52E+00	8.42E-08	Down	5.64E-01	6.21E-02		Unigene36790_All//gi|83628262|gb|AB326011.1|//0.00E+00//carotenoid cleavage dioxygenase 4a [Citrus clementina]	Unigene36790_All//0.00E+00//AT4G19170| NCED4 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 4)	Unigene36790_All//0.00E+00//TC166104		ko00906|Carotenoid biosynthesis	GO:0005488//GO:0009570//GO:0016701	nr +
Unigene36791_All	1050	37.92	55.45	63.34	34.96	26.83	13.89	11.60	11.78	9.18	5.48E-01	2.42E-15		7.40E-01	3.35E-28		-3.82E-01	2.73E-06		-1.33E+00	1.05E-45	Down	2.29E-02	9.03E-01		-3.37E-01	1.85E-02		Unigene36791_All//gi|23306390|gb|AAN17422.1|//4.00E-16//Unknown protein [Arabidopsis thaliana] >gi|24899779|gb|AAN65104.1| Unknown protein [Arabidopsis thaliana]	Unigene36791_All//1.00E-20//AT3G21710| unknown protein	Unigene36791_All//0.00E+00//CD485555				nr -
Unigene36797_All	1799	6.81	2.14	2.66	17.28	11.98	9.39	11.45	2.90	8.39	-1.67E+00	4.59E-20	Down	-1.35E+00	2.92E-14	Down	-5.28E-01	2.18E-09		-8.80E-01	5.04E-20		-1.98E+00	3.92E-51	Down	-4.48E-01	2.16E-05		Unigene36797_All//gi|90655934|gb|AB096566.1|//0.00E+00//Rhg4-like receptor kinase II [Glycine max]	Unigene36797_All//2.00E-136//AT1G66150| TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase	Unigene36797_All//0.00E+00//TC149123			GO:0004672//GO:0006464//GO:0031224//GO:0032559	nr -
Unigene36802_All	1245	10.13	4.68	9.50	9.36	7.74	7.51	2.00	2.92	1.38	-1.11E+00	1.69E-11	Down	-9.31E-02	6.42E-01		-2.74E-01	1.09E-01		-3.18E-01	6.74E-02		5.44E-01	6.24E-02		-5.42E-01	1.18E-01				Unigene36802_All//0.00E+00//AW186863				
Unigene36805_All	687	11.42	13.79	17.75	17.69	20.00	10.98	9.79	5.84	4.58	2.72E-01	1.65E-01		6.36E-01	1.49E-04		1.77E-01	3.12E-01		-6.88E-01	1.32E-05		-7.45E-01	2.22E-04		-1.09E+00	6.69E-08	Down	Unigene36805_All//gi|297810667|ref|XP_002873217.1|//3.00E-55//signal recognition particle binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297319054|gb|EFH49476.1| signal recognition particle binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene36805_All//4.00E-49//AT5G05670| signal recognition particle binding	Unigene36805_All//0.00E+00//gi|11207904|gb|BF276834.1|BF276834		ko03060|Protein export	GO:0000166//GO:0004871//GO:0016020//GO:0043231	nr -
Unigene36807_All	1553	5.42	1.08	5.59	0.64	0.84	1.43	17.86	14.05	1.85	-2.33E+00	2.04E-21	Down	4.32E-02	8.40E-01		3.93E-01	5.44E-01		1.15E+00	8.64E-03		-3.46E-01	1.76E-04		-3.27E+00	3.66E-125	Down	Unigene36807_All//gi|224055717|ref|XP_002298618.1|//1.00E-130//f-box family protein [Populus trichocarpa] >gi|222845876|gb|EEE83423.1| f-box family protein [Populus trichocarpa]	Unigene36807_All//3.00E-104//AT3G27150| kelch repeat-containing F-box family protein	Unigene36807_All//0.00E+00//gi|84167964|gb|DR456612.1|DR456612				nr +
Unigene36809_All	1466	3.78	8.36	8.17	1.12	1.15	0.77	0.00	0.00	0.00	1.14E+00	1.27E-11	Up	1.11E+00	1.89E-10	Up	3.77E-02	9.55E-01		-5.42E-01	3.16E-01		null	null		null	null				Unigene36809_All//1.00E-96//DW501876				
Unigene36810_All	863	20.98	36.87	43.50	4.79	8.42	5.50	0.00	0.00	0.00	8.14E-01	9.23E-17		1.05E+00	7.41E-29	Up	8.13E-01	7.85E-05		1.98E-01	5.44E-01		null	null		null	null		Unigene36810_All//gi|222423500|dbj|BAH19720.1|//1.00E-25//AT1G10657 [Arabidopsis thaliana]	Unigene36810_All//5.00E-27//AT1G10657| unknown protein	Unigene36810_All//0.00E+00//DW501876			GO:0044464	nr -
Unigene36811_All	1450	10.93	5.70	3.82	13.33	7.34	8.04	8.95	5.13	6.81	-9.41E-01	5.39E-11		-1.52E+00	1.27E-21	Down	-8.61E-01	1.10E-13		-7.30E-01	2.33E-09		-8.03E-01	1.16E-08		-3.94E-01	3.96E-03		Unigene36811_All//gi|297817082|ref|XP_002876424.1|//1.00E-116//guanylate kinase-encoding gene 1 [Arabidopsis lyrata subsp. lyrata] >gi|297322262|gb|EFH52683.1| guanylate kinase-encoding gene 1 [Arabidopsis lyrata subsp. lyrata]	Unigene36811_All//2.00E-114//AT3G57550| AGK2 (GUANYLATE KINASE); guanylate kinase	Unigene36811_All//0.00E+00//TC157361		ko00230|Purine metabolism		nr -
Unigene36814_All	806	14.35	26.40	19.29	16.87	18.46	26.56	32.42	21.88	13.20	8.80E-01	5.43E-13		4.27E-01	3.91E-03		1.30E-01	4.53E-01		6.55E-01	1.53E-08		-5.67E-01	2.28E-09		-1.30E+00	1.49E-36	Down	Unigene36814_All//gi|115488000|ref|NP_001066487.1|//2.00E-39//Os12g0244200 [Oryza sativa Japonica Group] >gi|77554416|gb|ABA97212.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113648994|dbj|BAF29506.1| Os12g0244200 [Oryza sativa Japonica Group]	Unigene36814_All//2.00E-41//AT3G01740| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Ribosomal protein L37, mitochondrial (InterPro:IPR013370); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G14290.1); Has 117 Blast hits to 117 proteins in 58 species: Archae - 0; Bacteria - 0; Metazoa - 56; Fungi - 22; Plants - 27; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink).	Unigene36814_All//0.00E+00//TC149884			GO:0043231	nr +
Unigene36815_All	1049	18.55	61.01	35.64	17.52	15.10	13.82	36.07	78.85	59.44	1.72E+00	1.19E-105	Up	9.42E-01	5.42E-24		-2.15E-01	1.12E-01		-3.42E-01	8.53E-03		1.13E+00	8.02E-89	Up	7.20E-01	9.35E-33		Unigene36815_All//gi|225430575|ref|XP_002263122.1|//2.00E-29//PREDICTED: similar to GDU1 [Vitis vinifera]	Unigene36815_All//8.00E-26//AT5G57685| AtGDC3 (Arabidopsis thaliana GLUTAMINE DUMPER 3)	Unigene36815_All//5.00E-83//gi|109886475|gb|DW515445.1|DW515445				nr -
Unigene36816_All	1737	4.70	18.26	6.10	6.88	9.26	9.33	12.15	10.11	19.33	1.96E+00	6.64E-63	Up	3.77E-01	4.46E-02		4.28E-01	1.29E-03		4.40E-01	1.35E-03		-2.65E-01	1.64E-02		6.71E-01	4.88E-16		Unigene36816_All//gi|115434566|ref|NP_001042041.1|//1.00E-139//Os01g0151600 [Oryza sativa Japonica Group] >gi|113531572|dbj|BAF03955.1| Os01g0151600 [Oryza sativa Japonica Group]	Unigene36816_All//1.00E-160//AT5G59960| unknown protein	Unigene36816_All//0.00E+00//TC148558				nr -
Unigene36817_All	1259	15.54	9.02	13.66	22.51	21.58	22.60	20.85	11.29	9.62	-7.86E-01	4.55E-10		-1.86E-01	1.87E-01		-6.11E-02	6.18E-01		5.50E-03	9.59E-01		-8.86E-01	1.45E-19		-1.12E+00	3.73E-29	Down	Unigene36817_All//gi|18401429|ref|NP_565650.1|//1.00E-153//NLP1 (NITRILASE-LIKE PROTEIN 1); N-carbamoylputrescine amidase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds [Arabidopsis thaliana] >gi|222424030|dbj|BAH19976.1| AT2G27450 [Arabidopsis thaliana]	Unigene36817_All//4.00E-154//AT2G27450| NLP1 (NITRILASE-LIKE PROTEIN 1); N-carbamoylputrescine amidase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds	Unigene36817_All//0.00E+00//TC133539		ko00240|Pyrimidine metabolism//ko00460|Cyanoamino acid metabolism//ko00410|beta-Alanine metabolism//ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene36818_All	1767	3.29	4.90	1.87	10.88	12.84	11.14	14.24	5.04	7.30	5.77E-01	3.30E-03		-8.15E-01	1.49E-03		2.39E-01	4.21E-02		3.43E-02	8.21E-01		-1.50E+00	2.08E-42	Down	-9.63E-01	3.95E-22		Unigene36818_All//gi|18403316|ref|NP_565767.1|//1.00E-137//spindle checkpoint protein-related [Arabidopsis thaliana] >gi|20196848|gb|AAB50673.2| expressed protein [Arabidopsis thaliana]	Unigene36818_All//1.00E-138//AT2G33560| spindle checkpoint protein-related	Unigene36818_All//0.00E+00//TC155175				nr -

Unigene36819_All	1298	1.61	2.77	2.87	12.86	9.68	8.87	4.40	13.81	2.33	7.82E-01	1.60E-02		8.33E-01	1.21E-02		-4.09E-01	1.47E-03		-5.35E-01	5.43E-05		1.65E+00	7.03E-35	Up	-9.15E-01	2.58E-05		Unigene36819_All//gi|219560134|gb|ACL27273.1|//6.00E-82//homeodomain leucine-zipper 1 [Capsicum annuum]	Unigene36819_All//7.00E-75//AT4G37790| HAT22; transcription factor	Unigene36819_All//0.00E+00//BG447194	HB		GO:0001071//GO:0003677//GO:0006351//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene36820_All	1383	23.53	38.10	25.37	11.92	12.65	31.28	79.36	117.35	150.51	6.95E-01	6.36E-21		1.09E-01	3.13E-01		8.53E-02	6.09E-01		1.39E+00	1.19E-56	Up	5.64E-01	2.40E-53		9.23E-01	9.81E-164		Unigene36820_All//gi|223452536|gb|ACM89595.1|//4.00E-90//leucine-rich repeat family protein [Glycine max]	Unigene36820_All//7.00E-70//AT3G43740| leucine-rich repeat family protein	Unigene36820_All//0.00E+00//TC139997		ko04626|Plant-pathogen interaction	GO:0004871//GO:0005488//GO:0016772//GO:0023060//GO:0031410	nr -
Unigene36822_All	3213	1.66	1.17	1.01	0.76	0.98	1.34	9.09	6.80	25.79	-5.09E-01	4.97E-02		-7.16E-01	7.83E-03		3.60E-01	3.43E-01		8.14E-01	5.38E-03		-4.19E-01	2.64E-06		1.50E+00	2.42E-141	Up	Unigene36822_All//gi|224134585|ref|XP_002321859.1|//0.00E+00//cationic amino acid transporter [Populus trichocarpa] >gi|222868855|gb|EEF05986.1| cationic amino acid transporter [Populus trichocarpa]	Unigene36822_All//0.00E+00//AT4G21120| AAT1 (AMINO ACID TRANSPORTER 1); L-glutamate transmembrane transporter/ L-lysine transmembrane transporter/ arginine transmembrane transporter/ cationic amino acid transmembrane transporter	Unigene36822_All//0.00E+00//TC152173			GO:0015172//GO:0015174//GO:0015809//GO:0015813//GO:0031224	nr -
Unigene36823_All	2454	0.64	0.78	0.65	0.65	1.00	1.14	4.05	7.89	18.73	2.95E-01	5.42E-01		2.55E-02	9.81E-01		6.17E-01	1.39E-01		8.13E-01	3.23E-02		9.62E-01	1.16E-16		2.21E+00	9.72E-133	Up	Unigene36823_All//gi|115467228|ref|NP_001057213.1|//0.00E+00//Os06g0229200 [Oryza sativa Japonica Group] >gi|113595253|dbj|BAF19127.1| Os06g0229200 [Oryza sativa Japonica Group]	Unigene36823_All//0.00E+00//AT1G26810| GALT1 (GALACTOSYLTRANSFERASE1); UDP-galactose:N-glycan beta-1,3-galactosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene36823_All//0.00E+00//TC159159			GO:0016020//GO:0031410//GO:0033692//GO:0035250//GO:0043231	nr -
Unigene36824_All	2173	38.24	31.57	43.67	16.94	21.68	15.21	0.91	2.15	2.51	-2.76E-01	1.28E-06		1.92E-01	6.55E-04		3.56E-01	7.34E-07		-1.55E-01	1.13E-01		1.24E+00	1.50E-06	Up	1.46E+00	1.11E-09	Up	Unigene36824_All//gi|297807403|ref|XP_002871585.1|//1.00E-170//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317422|gb|EFH47844.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene36824_All//3.00E-163//AT5G13770| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene36825_All	3752	1.58	1.31	0.68	10.71	7.65	8.94	14.54	25.62	19.09	-2.67E-01	3.03E-01		-1.21E+00	3.52E-06	Down	-4.87E-01	2.12E-10		-2.61E-01	2.07E-03		8.18E-01	1.22E-60		3.93E-01	3.86E-13		Unigene36825_All//gi|224128722|ref|XP_002328950.1|//0.00E+00//glycosyltransferase, CAZy family GT2 [Populus trichocarpa] >gi|222839184|gb|EEE77535.1| glycosyltransferase, CAZy family GT2 [Populus trichocarpa]	Unigene36825_All//0.00E+00//AT5G16910| CSLD2 (CELLULOSE-SYNTHASE LIKE D2); cellulose synthase/ transferase, transferring glycosyl groups	Unigene36825_All//0.00E+00//TC148605		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0006950//GO:0009250//GO:0016759//GO:0031228//GO:0042546//GO:0045229//GO:0048588	nr +
Unigene36826_All	1239	17.40	16.03	25.06	13.27	9.45	8.97	8.77	7.62	3.09	-1.18E-01	3.70E-01		5.26E-01	1.20E-07		-4.90E-01	1.21E-04		-5.65E-01	2.28E-05		-2.02E-01	2.36E-01		-1.51E+00	1.66E-19	Down	Unigene36826_All//gi|6664314|gb|AAF22896.1|AC006922.13//2.00E-62//T27G7.21 [Arabidopsis thaliana]	Unigene36826_All//7.00E-66//AT1G08530| unknown protein	Unigene36826_All//0.00E+00//TC136801			GO:0009536//GO:0031410	nr +
Unigene3683_All	1668	6.96	15.58	8.27	8.72	10.22	10.18	4.56	3.78	5.95	1.16E+00	2.37E-24	Up	2.48E-01	1.37E-01		2.29E-01	1.07E-01		2.23E-01	1.31E-01		-2.70E-01	1.83E-01		3.82E-01	1.68E-02		Unigene3683_All//gi|82570159|gb|AB883643.1|//3.00E-26//PIF-like orf1 [Daucus carota]	Unigene3683_All//6.00E-08//AT5G05800| unknown protein	Unigene3683_All//6.00E-161//ES792505				nr -
Unigene36830_All	1061	7.40	17.62	8.03	13.66	20.12	11.54	3.67	2.80	6.68	1.25E+00	7.51E-20	Up	1.19E-01	6.21E-01		5.59E-01	4.39E-07		-2.44E-01	1.26E-01		-3.90E-01	1.77E-01		8.66E-01	7.23E-06		Unigene36830_All//gi|15229025|ref|NP_190419.1|//3.00E-88//sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	Unigene36830_All//1.00E-44//AT5G23680| sterile alpha motif (SAM) domain-containing protein	Unigene36830_All//0.00E+00//TC166356				nr +
Unigene36835_All	1561	1.07	2.79	1.30	2.46	3.35	2.17	4.14	3.86	3.19	1.38E+00	6.24E-06	Up	2.73E-01	5.85E-01		4.49E-01	9.17E-02		-1.79E-01	6.38E-01		-1.04E-01	6.47E-01		-3.77E-01	6.46E-02		Unigene36835_All//gi|22327003|ref|NP_197704.2|//3.00E-59//peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana]	Unigene36835_All//5.00E-54//AT5G22130| peptidoglycan-binding LysM domain-containing protein	Unigene36835_All//0.00E+00//TC172065				nr -
Unigene3684_All	1544	9.86	8.57	6.66	14.00	12.24	10.15	2.88	2.08	1.37	-2.03E-01	1.87E-01		-5.67E-01	1.29E-04		-1.94E-01	1.21E-01		-4.64E-01	5.48E-05		-4.64E-01	7.68E-02		-1.07E+00	2.32E-05	Down	Unigene3684_All//gi|16323145|gb|AAL15307.1|//1.00E-82//AT5g11000/T30N20_270 [Arabidopsis thaliana] >gi|21436003|gb|AAM51579.1| AT5g11000/T30N20_270 [Arabidopsis thaliana]	Unigene3684_All//5.00E-73//AT5G11000| unknown protein	Unigene3684_All//0.00E+00//TC155412				nr -
Unigene36840_All	1338	5.79	4.20	5.49	3.98	4.66	5.23	4.04	3.22	1.73	-4.61E-01	2.84E-02		-7.55E-02	7.37E-01		2.26E-01	4.05E-01		3.93E-01	8.94E-02		-3.30E-01	1.72E-01		-1.23E+00	1.15E-07	Down	Unigene36840_All//gi|297818456|ref|XP_002877111.1|//1.00E-121//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297322949|gb|EFH53370.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene36840_All//5.00E-113//AT3G28480| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene36840_All//0.00E+00//gi|11199564|gb|BF268569.1|BF268569		ko00330|Arginine and proline metabolism		nr -
Unigene36842_All	625	79.53	38.51	53.93	86.48	79.83	86.06	120.75	46.95	58.32	-1.05E+00	5.14E-39	Down	-5.60E-01	3.63E-13		-1.15E-01	1.47E-01		-6.90E-03	9.53E-01		-1.36E+00	4.42E-109	Down	-1.05E+00	2.11E-74	Down	Unigene36842_All//gi|76161008|gb|ABA04967.1|//3.00E-62//glycoprotein-like protein [Solanum tuberosum]	Unigene36842_All//2.00E-61//AT4G27090| 60S ribosomal protein L14 (RPL14B)	Unigene36842_All//0.00E+00//gi|164262081|gb|ES798721.1|ES798721		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0031981	nr -
Unigene36844_All	743	84.85	32.73	12.33	55.04	49.68	25.10	42.05	9.90	9.81	-1.37E+00	1.31E-75	Down	-2.78E+00	5.07E-185	Down	-1.48E-01	9.69E-02		-1.13E+00	1.69E-39	Down	-2.09E+00	9.96E-83	Down	-2.10E+00	6.04E-86	Down	Unigene36844_All//gi|224123270|ref|XP_002319037.1|//4.00E-55//histone 2 [Populus trichocarpa] >gi|222857413|gb|EEE94960.1| histone 2 [Populus trichocarpa]	Unigene36844_All//1.00E-39//AT1G08880| H2AXA; DNA binding	Unigene36844_All//0.00E+00//gi|109828713|gb|DW227332.1|DW227332			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr -
Unigene36845_All	1804	40.08	19.49	43.77	2.82	3.74	2.35	0.23	0.09	0.77	-1.04E+00	6.65E-56	Down	1.27E-01	5.32E-02		4.10E-01	7.51E-02		-2.59E-01	3.95E-01		-1.34E+00	2.24E-01		1.72E+00	1.09E-03		Unigene36845_All//gi|297842251|ref|XP_002888907.1|//5.00E-60//J-domain protein required for chloroplast accumulation response 1 [Arabidopsis lyrata subsp. lyrata] >gi|297334848|gb|EFH65266.1| J-domain protein required for chloroplast accumulation response 1 [Arabidopsis lyrata subsp. lyrata]	Unigene36845_All//1.00E-47//AT1G75100| JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULATION RESPONSE 1); heat shock protein binding	Unigene36845_All//0.00E+00//TC135807			GO:0005515	nr -
Unigene36847_All	832	13.46	105.97	24.70	24.49	79.71	28.93	24.54	53.95	82.89	2.98E+00	1.55E-284	Up	8.76E-01	5.29E-12		1.70E+00	1.55E-127	Up	2.41E-01	3.96E-02		1.14E+00	4.14E-49	Up	1.76E+00	7.31E-147	Up	Unigene36847_All//gi|115445141|ref|NP_001046350.1|//9.00E-11//Os02g0227100 [Oryza sativa Japonica Group] >gi|113535881|dbj|BAF08264.1| Os02g0227100 [Oryza sativa Japonica Group]	Unigene36847_All//7.00E-11//AT5G36550| OXS3 (OXIDATIVE STRESS 3)	Unigene36847_All//0.00E+00//DW519596				nr +
Unigene36848_All	1449	3.14	0.87	0.85	5.19	3.42	3.12	3.71	1.44	1.90	-1.85E+00	5.40E-09	Down	-1.89E+00	8.05E-09	Down	-6.01E-01	2.57E-03		-7.36E-01	4.07E-04		-1.36E+00	1.78E-08	Down	-9.66E-01	1.89E-05		Unigene36848_All//gi|297805680|ref|XP_002870724.1|//1.00E-142//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316560|gb|EFH46983.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36848_All//9.00E-125//AT5G40140| armadillo/beta-catenin repeat family protein / U-box domain-containing protein	Unigene36848_All//0.00E+00//DW236769			GO:0019787//GO:0032446	nr -
Unigene36854_All	1001	43.85	36.14	35.27	189.70	168.22	160.58	140.15	75.45	57.59	-2.79E-01	5.85E-04		-3.14E-01	1.71E-04		-1.73E-01	4.42E-07		-2.41E-01	1.24E-11		-8.93E-01	1.74E-102		-1.28E+00	1.92E-189	Down	Unigene36854_All//gi|285028876|gb|ADC34699.1|//6.00E-50//elicitor responsive gene 3 [Triticum aestivum]	Unigene36854_All//1.00E-43//AT1G63220| C2 domain-containing protein	Unigene36854_All//0.00E+00//TC170038		ko04626|Plant-pathogen interaction		nr -
Unigene36855_All	815	6.03	2.86	10.58	18.46	11.11	16.18	9.55	6.72	4.64	-1.08E+00	9.20E-05	Down	8.11E-01	7.35E-05		-7.32E-01	3.04E-08		-1.90E-01	2.39E-01		-5.07E-01	6.65E-03		-1.04E+00	2.39E-08	Down	Unigene36855_All//gi|15224165|ref|NP_179430.1|//8.00E-97//TTN5 (TITAN 5); GTP binding / GTPase [Arabidopsis thaliana] >gi|11131460|sp|Q92PX1.1|ARF5_ARATH RecName: Full=Probable ADP-ribosylation factor At2g18390 >gi|20514265|gb|AAM22961.1|AF486852_1 ARL2 G-protein [Arabidopsis thaliana]	Unigene36855_All//3.00E-89//AT2G18390| TTN5 (TITAN 5); GTP binding / GTPase	Unigene36855_All//0.00E+00//TC156929			GO:0003006//GO:0007010//GO:0007349//GO:0009606//GO:0017111//GO:0032561//GO:0035556//GO:0043623//GO:0044464//GO:0060089	nr -
Unigene36858_All	962	46.61	50.51	17.71	102.68	54.77	36.67	57.14	8.43	8.28	1.16E-01	1.68E-01		-1.40E+00	2.62E-53	Down	-9.07E-01	9.40E-75		-1.49E+00	2.12E-144	Down	-2.76E+00	3.94E-202	Down	-2.79E+00	1.59E-210	Down	Unigene36858_All//gi|15223416|ref|NP_171656.1|//2.00E-64//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|79316252|ref|NP_001030928.1| heavy-metal-associated domain-containing protein [Arabidopsis thaliana]	Unigene36858_All//3.00E-26//AT1G01490| heavy-metal-associated domain-containing protein	Unigene36858_All//4.00E-133//DW497785		ko03040|Spliceosome	GO:0006812//GO:0043169	nr -
Unigene36859_All	861	41.93	75.56	38.04	75.16	81.59	163.08	252.16	366.02	535.76	8.50E-01	5.45E-36		-1.41E-01	1.68E-01		1.19E-01	7.84E-02		1.12E+00	4.61E-130	Up	5.38E-01	2.78E-94		1.09E+00	0.00E+00	Up	Unigene36859_All//gi|47824991|gb|AAT38764.1|//2.00E-58//Putative ATPase protein, identical [Solanum demissum]	Unigene36859_All//7.00E-46//AT3G28540| AAA-type ATPase family protein	Unigene36859_All//0.00E+00//TC153266			GO:0009725//GO:0017111//GO:0032559//GO:0043231	nr +
Unigene3686_All	1577	3.28	1.06	0.81	3.29	3.30	4.10	8.45	4.13	3.51	-1.63E+00	1.17E-08	Down	-2.02E+00	8.87E-11	Down	5.30E-03	9.92E-01		3.18E-01	2.08E-01		-1.03E+00	4.68E-13	Down	-1.27E+00	2.11E-18	Down	Unigene3686_All//gi|6730701|gb|AAF27096.1|AC011809_5//1.00E-120//Unknown protein [Arabidopsis thaliana]	Unigene3686_All//1.00E-121//AT1G18850| unknown protein	Unigene3686_All//0.00E+00//gi|13351090|gb|BG441438.1|BG441438				nr -
Unigene36861_All	1143	6.68	1.68	5.08	19.13	15.88	15.69	3.18	1.68	1.71	-1.99E+00	4.65E-16	Down	-3.96E-01	8.04E-02		-2.69E-01	2.06E-02		-2.87E-01	1.72E-02		-9.19E-01	1.41E-03		-8.97E-01	1.29E-03		Unigene36861_All//gi|157932074|gb|ABW05088.1|//1.00E-67//ovate-like protein [Nicotiana tabacum]	Unigene36861_All//1.00E-30//AT2G18500| OFP7 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 7)	Unigene36861_All//0.00E+00//gi|78351423|gb|DT571697.1|DT571697				nr -
Unigene36864_All	1528	1.64	1.59	2.54	4.04	2.95	2.54	5.15	2.16	2.58	-4.63E-02	9.17E-01		6.30E-01	5.20E-02		-4.54E-01	5.12E-02		-6.69E-01	4.35E-03		-1.25E+00	1.10E-10	Down	-9.96E-01	6.53E-08		Unigene36864_All//gi|46931324|gb|AAT06466.1|//1.00E-132//At1g09800 [Arabidopsis thaliana]	Unigene36864_All//5.00E-131//AT1G09800| tRNA pseudouridine synthase family protein	Unigene36864_All//0.00E+00//TC150721			GO:0006399//GO:0009451//GO:0016853	nr +
Unigene36868_All	1584	7.47	6.01	8.14	30.79	17.44	10.26	8.43	3.03	2.44	-3.12E-01	6.72E-02		1.24E-01	4.99E-01		-8.20E-01	3.21E-31		-1.58E+00	1.40E-78	Down	-1.47E+00	2.27E-22	Down	-1.79E+00	3.23E-30	Down	Unigene36868_All//gi|195646710|gb|ACG42823.1|//1.00E-119//membrane protein [Zea mays]	Unigene36868_All//5.00E-86//AT2G46890| oxidoreductase, acting on the CH-CH group of donors	Unigene36868_All//0.00E+00//TC134133			GO:0016491//GO:0031224//GO:0031410//GO:0044238	nr +
Unigene36869_All	1393	6.42	18.55	4.89	7.90	14.81	12.68	28.74	59.65	42.53	1.53E+00	1.49E-36	Up	-3.93E-01	5.63E-02		9.06E-01	3.21E-15		6.82E-01	1.22E-07		1.05E+00	6.86E-80	Up	5.65E-01	1.41E-20		Unigene36869_All//gi|224106071|ref|XP_002314033.1|//1.00E-24//predicted protein [Populus trichocarpa] >gi|222850441|gb|EEE87988.1| predicted protein [Populus trichocarpa]	Unigene36869_All//3.00E-20//AT3G52105| unknown protein	Unigene36869_All//0.00E+00//DR452304			GO:0031410	nr +
Unigene3687_All	319	155.81	268.91	360.06	156.94	152.31	301.70	151.63	112.68	87.92	7.87E-01	1.59E-41		1.21E+00	3.67E-109	Up	-4.31E-02	6.43E-01		9.43E-01	1.19E-67		-4.28E-01	2.70E-10		-7.86E-01	7.90E-30		Unigene3687_All//gi|21616051|emb|CAC86003.1|//1.00E-27//aspartic proteinase [Theobroma cacao]	Unigene3687_All//4.00E-15//AT1G62290| aspartyl protease family protein	Unigene3687_All//3.00E-165//TC173224				nr +
Unigene36870_All	398	1.97	1.15	0.00	0.63	0.87	0.91	2.76	0.63	0.10	-7.83E-01	3.28E-01		-1.09E+01	2.22E-04	Down	4.67E-01	7.79E-01		5.37E-01	6.94E-01		-2.13E+00	1.11E-03		-4.79E+00	4.55E-07	Down			Unigene36870_All//2.00E-141//gi|13352878|gb|BG443226.1|BG443226				
Unigene36872_All	1718	3.56	8.49	2.76	9.42	9.40	12.15	13.34	15.25	24.93	1.25E+00	1.12E-15	Up	-3.69E-01	1.49E-01		-3.50E-03	9.77E-01		3.66E-01	2.33E-03		1.94E-01	5.64E-02		9.02E-01	4.28E-33		Unigene36872_All//gi|4874305|gb|AAD31367.1|//2.00E-81//expressed protein [Arabidopsis thaliana]	Unigene36872_All//1.00E-14//AT2G25670| unknown protein	Unigene36872_All//0.00E+00//gi|78354136|gb|DT574410.1|DT574410			GO:0046914	nr +

Unigene36873_All	1401	4.59	14.03	8.25	8.11	10.37	19.76	22.30	23.66	26.64	1.61E+00	4.35E-30	Up	8.44E-01	1.18E-06		3.56E-01	1.43E-02		1.29E+00	2.67E-32	Up	8.51E-02	3.97E-01		2.57E-01	9.45E-04		Unigene36873_All//gi|89540152|gb|AAF82225.1|AC069143.1//1.00E-99//Contains similarity to a HSPC326 mRNA from Homo sapiens gb|AF161444. EST gb|AI997162 comes from this gene [Arabidopsis thaliana]	Unigene36873_All//1.00E-97//AT1G19140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ubiquinone biosynthetic process; LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: COQ9 (InterPro:IPR013718), Ubiquinone biosynthesis protein COQ9 (InterPro:IPR012762); Has 598 Blast hits to 598 proteins in 175 species: Archae - 0; Bacteria - 149; Metazoa - 114; Fungi - 60; Plants - 22; Viruses - 0; Other Eukaryotes - 253 (source: NCBI BLink).	Unigene36873_All//0.00E+00//TC132136			GO:0006743//GO:0043231	nr +
Unigene36874_All	1373	15.43	31.63	16.25	13.90	15.52	15.23	13.86	18.51	10.91	1.04E+00	1.84E-33	Up	7.44E-02	6.12E-01		1.60E-01	2.30E-01		1.32E-01	3.59E-01		4.18E-01	1.44E-05		-3.45E-01	1.88E-03		Unigene36874_All//gi|297833526|ref|XP_002884645.1|//1.00E-106//carboxyl terminus of hsc70-interacting protein [Arabidopsis lyrata subsp. lyrata] >gi|297330485|gb|EFH60904.1|carboxyl terminus of hsc70-interacting protein [Arabidopsis lyrata subsp. lyrata]	Unigene36874_All//3.00E-107//AT3G07370| CHIP (CARBOXYL TERMINUS OF HSC70-INTERACTING PROTEIN); ubiquitin-protein ligase	Unigene36874_All//0.00E+00//TC163135		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0019787//GO:0032446//GO:0043234	nr +
Unigene36875_All	2204	9.16	5.54	6.09	13.54	14.14	12.73	13.27	6.13	7.66	-7.26E-01	3.90E-09		-5.90E-01	3.02E-06		6.27E-02	6.17E-01		-8.94E-02	4.70E-01		-1.12E+00	1.99E-31	Down	-7.93E-01	1.21E-18		Unigene36875_All//gi|20138107|sp|Q9ESQ1.1|FUT1_PEA//0.00E+00//RecName: Full=Galactoside 2-alpha-L-fucosyltransferase; AltName: Full=Xyloglucan alpha-(1,2)-fucosyltransferase; AltName: Full=PsFT1 >gi|7453579|gb|AAF62896.1|AF223643_1 xyloglucan fucosyltransferase [Pisum sativum]	Unigene36875_All//7.00E-170//AT2G03210| FUT2 (FUCOSYLTRANSFERASE 2); fucosyltransferase/ transferase, transferring glycosyl groups	Unigene36875_All//0.00E+00//TC138301			GO:0005794//GO:0016020//GO:0031127//GO:0070882	nr -
Unigene36876_All	1023	138.60	94.90	164.59	115.89	115.73	99.33	44.26	32.85	20.99	-5.47E-01	3.86E-36		2.48E-01	6.44E-10		-2.10E-03	9.68E-01		-2.22E-01	1.46E-06		-4.30E-01	9.06E-10		-1.08E+00	7.78E-47	Down	Unigene36876_All//gi|18399355|ref|NP_566400.1|//2.00E-40//MD-2-related lipid recognition domain-containing protein / ML domain-containing protein [Arabidopsis thaliana]	Unigene36876_All//3.00E-39//AT3G11780| MD-2-related lipid recognition domain-containing protein / ML domain-containing protein	Unigene36876_All//0.00E+00//TC174117			GO:0030312//GO:0031224//GO:0031410//GO:0043231	nr -
Unigene36878_All	1624	11.28	6.30	6.92	17.48	15.46	8.82	8.80	1.11	2.75	-8.39E-01	1.64E-10		-7.05E-01	1.36E-07		-1.78E-01	9.82E-02		-9.88E-01	3.72E-22		-2.99E+00	1.61E-57	Down	-1.68E+00	1.42E-29	Down	Unigene36878_All//gi|13605601|gb|AAK32794.1|AF361626_1//4.00E-56//At1g54460/F20021_28 [Arabidopsis thaliana] >gi|15777865|gb|AAL05893.1|At1g54460/F20021_28 [Arabidopsis thaliana]	Unigene36878_All//2.00E-48//AT1G54460| FUCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: WDL1 (TAIR:AT3G04630.3); Has 393 Blast hits to 375 proteins in 76 species: Archae - 0; Bacteria - 3; Metazoa - 143; Fungi - 38; Plants - 160; Viruses - 0; Other Eukaryotes - 49 (source: NCBI BLink).	Unigene36878_All//0.00E+00//TC178499				nr +
Unigene36882_All	1229	9.79	3.67	2.34	4.66	3.14	1.95	3.58	1.56	2.66	-1.42E+00	1.14E-15	Down	-2.07E+00	4.65E-25	Down	-5.71E-01	1.59E-02		-1.26E+00	4.85E-07	Down	-1.19E+00	6.37E-06	Down	-4.29E-01	9.12E-02		Unigene36882_All//gi|15223699|ref|NP_173419.1|//1.00E-121//glyoxal oxidase-related [Arabidopsis thaliana] >gi|16604507|gb|AAL24259.1|At1g19900/F6F9_4 [Arabidopsis thaliana]	Unigene36882_All//8.00E-123//AT1G19900| glyoxal oxidase-related	Unigene36882_All//0.00E+00//TC146860				nr +
Unigene36884_All	1465	1.75	0.93	0.58	11.73	9.52	10.39	28.17	7.50	9.25	-9.06E-01	2.18E-02		-1.59E+00	2.80E-04	Down	-3.01E-01	2.26E-02		-1.75E-01	2.46E-01		-1.91E+00	5.08E-97	Down	-1.61E+00	1.03E-78	Down	Unigene36884_All//gi|297829390|ref|XP_002882577.1|//1.00E-115//alphavirus core protein family [Arabidopsis lyrata subsp. lyrata] >gi|297328417|gb|EFH58836.1|alphavirus core protein family [Arabidopsis lyrata subsp. lyrata]	Unigene36884_All//4.00E-88//AT3G08640| alphavirus core protein family	Unigene36884_All//0.00E+00//TC147777		ko04146|Peroxisome	GO:0043231	nr -
Unigene36887_All	1475	10.54	8.83	8.05	15.67	13.89	15.25	25.77	11.76	8.99	-2.55E-01	8.41E-02		-3.88E-01	9.26E-03		-1.74E-01	1.57E-01		-3.94E-02	7.69E-01		-1.13E+00	1.64E-41	Down	-1.52E+00	7.49E-67	Down	Unigene36887_All//gi|48958523|gb|AAT47814.1|//1.00E-124//At5g63220 [Arabidopsis thaliana]	Unigene36887_All//2.00E-125//AT5G63220| unknown protein	Unigene36887_All//0.00E+00//TC151494				nr +
Unigene3689_All	1786	6.44	7.09	8.94	16.40	23.45	30.12	5.14	16.10	3.99	1.38E-01	4.23E-01		4.73E-01	1.10E-03		5.16E-01	1.14E-11		8.77E-01	1.04E-33		1.65E+00	2.52E-55	Up	-3.64E-01	3.00E-02		Unigene3689_All//gi|297851126|ref|XP_002890444.1|//1.00E-143//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339286|gb|EFH69703.1|transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3689_All//3.00E-138//AT1G24530| transducin family protein / WD-40 repeat family protein	Unigene3689_All//0.00E+00//TC133910		ko03040|Spliceosome		nr -
Unigene36890_All	1583	35.93	13.44	21.13	53.68	47.03	39.49	47.38	27.35	27.68	-1.42E+00	1.40E-71	Down	-7.66E-01	1.32E-25		-1.91E-01	4.17E-04		-4.43E-01	3.06E-16		-7.93E-01	4.13E-45		-7.75E-01	1.11E-44		Unigene36890_All//gi|224107417|ref|XP_002314474.1|//0.00E+00//dehydroquinate dehydratase/ shikimate dehydrogenase [Populus trichocarpa] >gi|222863514|gb|EEF00645.1|dehydroquinate dehydratase/ shikimate dehydrogenase [Populus trichocarpa]	Unigene36890_All//0.00E+00//AT3G06350| MEE32 (MATERNAL EFFECT EMBRYO ARREST 32); 3-dehydroquinate dehydratase/ NADP or NADPH binding / binding / catalytic/ shikimate 5-dehydrogenase	Unigene36890_All//0.00E+00//TC133124		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0000166//GO:0003006//GO:0008652//GO:0009532//GO:0016616//GO:0016836	nr -
Unigene36891_All	2385	3.14	139.30	11.39	10.21	7.19	9.20	6.28	100.38	7.12	5.47E+00	0.00E+00	Up	1.86E+00	4.99E-49	Up	-5.06E-01	5.75E-07		-1.50E-01	2.30E-01		4.00E+00	0.00E+00	Up	1.81E-01	1.53E-01		Unigene36891_All//gi|186898205|gb|ACC93947.1|//0.00E+00//heat-shock protein 70 [Hevea brasiliensis]	Unigene36891_All//0.00E+00//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene36891_All//0.00E+00//TC166610		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr -
Unigene36892_All	1441	7.23	3.34	4.03	10.13	8.51	11.16	19.60	10.06	9.12	-1.11E+00	1.27E-09	Down	-8.43E-01	4.84E-06		-2.52E-01	9.62E-02		1.40E-01	3.94E-01		-9.62E-01	5.79E-24		-1.10E+00	1.02E-30	Down	Unigene36892_All//gi|13936812|gb|AAK49947.1|AF335551_1//1.00E-176//TGF-beta receptor-interacting protein 1 [Phaseolus vulgaris]	Unigene36892_All//2.00E-157//AT2G46280| TRIP-1 (TGF-BETA RECEPTOR INTERACTING PROTEIN 1); nucleotide binding / protein binding	Unigene36892_All//0.00E+00//gi|164342800|gb|ES848566.1|ES848566				nr +
Unigene36896_All	1625	1.09	1.96	1.84	32.89	26.87	22.54	7.44	2.16	2.99	8.44E-01	1.54E-02		7.45E-01	4.88E-02		-2.92E-01	1.45E-05		-5.45E-01	5.55E-15		-1.78E+00	1.81E-26	Down	-1.31E+00	9.39E-18	Down	Unigene36896_All//gi|224133394|ref|XP_002328031.1|//1.00E-136//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222837440|gb|EEE75819.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene36896_All//3.00E-107//AT4G28500| ANAC073 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 73); transcription activator/ transcription factor	Unigene36896_All//8.00E-43//TC162791	NAC			nr +
Unigene36897_All	907	3.29	3.74	5.75	6.87	22.63	35.25	2.66	1.66	3.95	1.87E-01	6.18E-01		8.07E-01	3.06E-03		1.72E+00	4.63E-40	Up	2.36E+00	7.78E-86	Up	-6.80E-01	6.49E-02		5.73E-01	4.19E-02		Unigene36897_All//gi|157679144|dbj|BAF80451.1|//6.00E-62//MYB-related transcription factor [Nicotiana tabacum]	Unigene36897_All//2.00E-50//AT1G66230| MYB20 (myb domain protein 20); DNA binding / transcription factor	Unigene36897_All//4.00E-83//DW519609	MYB		GO:0006350//GO:0009725//GO:0043231	nr +
Unigene36898_All	4963	0.04	0.00	0.06	0.43	0.85	0.57	7.63	3.13	7.05	-5.40E+00	1.22E-01		6.10E-01	6.24E-01		9.72E-01	6.93E-04		4.10E-01	3.09E-01		-1.28E+00	2.18E-50	Down	-1.15E-01	1.73E-01		Unigene36898_All//gi|4235644|gb|AAD13304.1|//0.00E+00//polyprotein [Solanum lycopersicum]	Unigene36898_All//2.00E-20//ATMG00860| hypothetical protein	Unigene36898_All//4.00E-87//DT047810			GO:0003676//GO:0003824//GO:0006259//GO:0043229	nr -
Unigene36899_All	3141	0.03	0.00	0.03	0.25	0.26	0.35	3.41	1.33	2.69	-5.06E+00	3.71E-01		2.58E-02	1.00E+00		5.25E-02	9.65E-01		4.44E-01	5.39E-01		-1.36E+00	5.25E-16	Down	-3.41E-01	2.68E-02		Unigene36899_All//gi|4235644|gb|AAD13304.1|//0.00E+00//polyprotein [Solanum lycopersicum]	Unigene36899_All//6.00E-12//ATMG00860| hypothetical protein	Unigene36899_All//1.00E-52//ES791882			GO:0003676//GO:0004175//GO:0006260//GO:0006325//GO:0019538//GO:0034061//GO:0043231//GO:0044427//GO:0046914	nr -
Unigene36900_All	1101	27.89	64.11	69.26	53.52	61.05	61.86	12.25	47.60	83.62	1.20E+00	2.41E-68	Up	1.31E+00	1.71E-82	Up	1.90E-01	2.51E-03		2.09E-01	1.10E-03		1.96E+00	4.72E-127	Up	2.77E+00	0.00E+00	Up	Unigene36900_All//gi|224100869|ref|XP_002312046.1|//8.00E-48//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222851866|gb|EEE89413.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene36900_All//3.00E-37//AT4G36920| AP2 (APETALA 2); transcription factor	Unigene36900_All//0.00E+00//gi|11203047|gb|BF272052.1|BF272052	AP2-EREBP		GO:0006350//GO:0010073//GO:0050793//GO:0050794	nr -
Unigene36902_All	717	16.56	11.17	8.76	26.96	69.30	55.05	40.57	55.61	37.34	-5.69E-01	5.20E-04		-9.19E-01	9.67E-08		1.36E+00	3.73E-69	Up	1.03E+00	2.30E-32	Up	4.55E-01	1.51E-09		-1.20E-01	2.20E-01		Unigene36902_All//gi|110737096|dbj|BAF00500.1|//1.00E-41//thaumatin-like protein [Arabidopsis thaliana]	Unigene36902_All//5.00E-43//AT4G38660| thaumatin, putative	Unigene36902_All//0.00E+00//gi|48798343|gb|CO099657.1|CO099657			GO:0009607//GO:0031224	nr +
Unigene36906_All	1188	1.37	1.92	1.97	1.55	2.35	1.25	4.66	3.80	1.84	4.91E-01	2.47E-01		5.31E-01	2.35E-01		5.98E-01	1.18E-01		-3.07E-01	5.67E-01		-2.95E-01	2.27E-01		-1.34E+00	8.17E-09	Down	Unigene36906_All//gi|297800018|ref|XP_002867893.1|//6.00E-63//EMB1895 [Arabidopsis lyrata subsp. lyrata] >gi|297313729|gb|EFH44152.1|EMB1895 [Arabidopsis lyrata subsp. lyrata]	Unigene36906_All//3.00E-55//AT4G20060| EMB1895 (EMBRYO DEFECTIVE 1895); binding	Unigene36906_All//0.00E+00//TC161925				nr +
Unigene36907_All	822	31.00	83.77	47.48	31.27	42.94	42.42	44.80	106.57	95.86	1.43E+00	1.45E-87	Up	6.15E-01	2.73E-12		4.58E-01	4.43E-08		4.40E-01	6.42E-07		1.25E+00	1.42E-110	Up	1.10E+00	8.53E-83	Up	Unigene36907_All//gi|297830310|ref|XP_002883037.1|//9.00E-56//ubiquitin-conjugating enzyme 31 [Arabidopsis lyrata subsp. lyrata] >gi|297328877|gb|EFH59296.1|ubiquitin-conjugating enzyme 31 [Arabidopsis lyrata subsp. lyrata]	Unigene36907_All//6.00E-47//AT3G17000| UBC32 (ubiquitin-conjugating enzyme 32); ubiquitin-protein ligase	Unigene36907_All//0.00E+00//TC138220		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0019787//GO:0019941	nr -
Unigene36909_All	1724	3.76	2.29	1.39	10.66	11.09	9.12	16.51	6.57	7.88	-7.15E-01	1.95E-03		-1.44E+00	1.56E-08	Down	5.62E-02	7.46E-01		-2.26E-01	1.05E-01		-1.33E+00	4.81E-40	Down	-1.07E+00	2.44E-29	Down	Unigene36909_All//gi|297810135|ref|XP_002872951.1|//0.00E+00//At4g00460 [Arabidopsis lyrata subsp. lyrata] >gi|297318788|gb|EFH49210.1|At4g00460 [Arabidopsis lyrata subsp. lyrata]	Unigene36909_All//7.00E-171//AT4G00460| Rho guanyl-nucleotide exchange factor	Unigene36909_All//0.00E+00//TC141986			GO:0005088	nr +
Unigene36910_All	966	52.43	22.71	34.12	43.94	42.53	22.16	7.09	3.59	2.56	-1.21E+00	7.51E-50	Down	-6.20E-01	6.28E-16		-4.70E-02	6.42E-01		-9.87E-01	8.02E-33		-9.82E-01	1.28E-06		-1.47E+00	3.26E-12	Down	Unigene36910_All//gi|283135880|gb|ADB11331.1|//3.00E-92//phi class glutathione transferase GSTF2 [Populus trichocarpa]	Unigene36910_All//2.00E-49//AT2G47730| AT6STF8 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE PHI 8); glutathione binding / glutathione transferase	Unigene36910_All//0.00E+00//TC135048		ko00480|Glutathione metabolism	GO:0016765	nr -
Unigene36911_All	1659	3.50	1.99	2.44	7.24	6.66	4.71	6.50	2.24	3.19	-8.18E-01	8.94E-04		-5.21E-01	4.43E-02		-1.19E-01	5.61E-01		-6.20E-01	1.01E-04		-1.54E+00	2.88E-19	Down	-1.02E+00	5.46E-11	Down	Unigene36911_All//gi|9295718|gb|AAF87024.1|AC006535_2//1.00E-102//T24P13.3 [Arabidopsis thaliana]	Unigene36911_All//1.00E-102//AT1G69430| unknown protein	Unigene36911_All//0.00E+00//CO132878			GO:0031410	nr +
Unigene36913_All	1257	10.74	8.47	10.93	10.26	7.20	9.05	24.96	50.27	22.44	-3.43E-01	2.78E-02		2.54E-02	8.87E-01		-5.11E-01	4.90E-04		-1.81E-01	3.16E-01		1.01E+00	5.64E-57	Up	-1.54E-01	8.95E-02		Unigene36913_All//gi|28558782|gb|AAO43753.1|//1.00E-111//RING/C3HC4/PHD zinc finger-like protein [Cucumis melo]	Unigene36913_All//1.00E-72//AT3G05200| ATL6; protein binding / zinc ion binding	Unigene36913_All//0.00E+00//TC155930			GO:0005488//GO:0009743//GO:0016020//GO:0019787//GO:0032446	nr -

Unigene36914_All	744	39.59	56.87	32.42	105.19	92.66	77.64	86.27	117.52	192.82	5.22E-01	1.75E-10		-2.88E-01	6.45E-03		-1.83E-01	1.39E-03		-4.38E-01	1.07E-14		4.46E-01	2.93E-19		1.16E+00	4.55E-164	Up	Unigene36914_All||gi|226533162|ref|NP_001148880.1||1.00E-68||glycogen synthase kinase-3 MsK-3 [Zea mays] >gi|195622888|gb|ACG33274.1|glycogen synthase kinase-3 MsK-3 [Zea mays]	Unigene36914_All||1.00E-67||AT5G26751| ATSK11; protein kinase/ protein serine/threonine kinase	Unigene36914_All||0.00E+00||gi|73861208|gb|DT463947.1|DT463947			GO:0004672||GO:0006464||GO:0032559	nr +
Unigene36919_All	2688	0.47	0.74	0.73	22.41	19.78	15.89	3.27	0.93	1.72	6.54E-01	1.54E-01		6.50E-01	1.79E-01		-1.80E-01	7.57E-03		-4.95E-01	3.35E-14		-1.81E+00	7.78E-20	Down	-9.28E-01	7.03E-08		Unigene36919_All||gi|15218202|ref|NP_177929.1||0.00E+00||glycosyl hydrolase family 3 protein [Arabidopsis thaliana] >gi|259585708|sp|Q9SGZ5.2|BXL7_ARATH RecName: Full=Probable beta-D-xylosidase 7; Short=AtBXL7; Flags: Precursor >gi|18086336|gb|AAL57631.1|At1g78060/F28K19_32 [Arabidopsis thaliana]	Unigene36919_All||0.00E+00||AT1G78060| glycosyl hydrolase family 3 protein	Unigene36919_All||0.00E+00||TC175456		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0005576||GO:0005618||GO:0009536||GO:0015926||GO:0031410||GO:0044238	nr +
Unigene36920_All	939	12.98	20.72	27.79	43.40	35.39	34.00	31.56	43.84	24.23	6.75E-01	7.69E-08		1.10E+00	1.27E-21	Up	-2.94E-01	1.86E-04		-3.52E-01	1.59E-05		4.74E-01	1.54E-10		-3.82E-01	1.03E-05		Unigene36920_All||gi|115460364|ref|NP_001053782.1||2.00E-16||Os04g0603400 [Oryza sativa Japonica Group] >gi|38344154|emb|CAE01828.2|OSJNBa0041A02.21 [Oryza sativa (japonica cultivar-group)] >gi|113565353|dbj|BAF15696.1|Os04g0603400 [Oryza sativa Japonica Group] >gi|116309664|emb|CAH66713.1|OSIGBa0118P15.3 [Oryza sativa (indica cultivar-group)]	Unigene36920_All||9.00E-10||AT5G43150| unknown protein	Unigene36920_All||0.00E+00||TC160728			GO:0043231	nr +
Unigene36921_All	642	6.03	15.78	16.17	34.53	28.75	23.99	20.02	11.65	10.55	1.39E+00	7.11E-13	Up	1.42E+00	3.79E-13	Up	-2.64E-01	2.23E-02		-5.25E-01	3.25E-06		-7.81E-01	3.23E-08		-9.24E-01	4.95E-11		Unigene36921_All||gi|284520976|gb|ADB92063.1||9.00E-06||universal stress protein [Jatropha curcas]		Unigene36921_All||7.00E-106||ES793035				nr +
Unigene36922_All	1340	3.90	2.34	2.82	99.26	66.71	81.26	29.91	11.54	13.47	-7.36E-01	4.76E-03		-4.69E-01	9.13E-02		-5.73E-01	6.47E-45		-2.89E-01	1.50E-11		-1.37E+00	5.50E-59	Down	-1.15E+00	3.17E-46	Down	Unigene36922_All||gi|27765046|gb|AAO23644.1||1.00E-129||At5g67210 [Arabidopsis thaliana]	Unigene36922_All||1.00E-119||AT5G67210| unknown protein	Unigene36922_All||0.00E+00||TC155913				nr +
Unigene36924_All	1234	4.28	4.35	5.91	18.45	12.75	30.45	16.27	6.84	6.75	2.35E-02	9.48E-01		4.65E-01	4.24E-02		-5.33E-01	3.95E-07		7.23E-01	3.55E-17		-1.25E+00	5.48E-26	Down	-1.27E+00	1.95E-27	Down	Unigene36924_All||gi|61651585|dbj|BAD91162.1||1.00E-161||gibberellin 3-beta hydroxylase [Prunus subhirtella]	Unigene36924_All||1.00E-122||AT1G15550| GA3OX1 (GIBBERELLIN 3-OXIDASE 1); gibberellin 3-beta-dioxygenase/ transcription factor binding	Unigene36924_All||0.00E+00||gi|164260197|gb|ES799727.1|ES799727		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr -
Unigene36926_All	1310	2.00	2.40	0.93	4.56	3.65	1.76	0.16	0.06	0.06	2.64E-01	4.67E-01		-1.10E+00	8.04E-03		-3.21E-01	2.04E-01		-1.38E+00	2.68E-08	Down	-1.34E+00	4.30E-01		-1.41E+00	3.80E-01		Unigene36926_All||gi|15228789|ref|NP_191158.1||1.00E-115||ESK1 (ESKIMO 1) [Arabidopsis thaliana]	Unigene36926_All||1.00E-112||AT3G55990| ESK1 (ESKIMO 1)	Unigene36926_All||8.00E-101||EE592863				nr +
Unigene3693_All	1172	17.32	57.85	18.40	18.49	24.42	22.58	13.31	13.91	15.64	1.74E+00	6.11E-114	Up	8.73E-02	5.42E-01		4.01E-01	2.41E-05		2.89E-01	7.25E-03		6.32E-02	6.58E-01		2.32E-01	4.80E-02		Unigene3693_All||gi|297808001|ref|XP_002871884.1||8.00E-76||zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317721|gb|EFH48143.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3693_All||5.00E-51||AT5G19430| zinc finger (C3HC4-type RING finger) family protein	Unigene3693_All||0.00E+00||gi|78337376|gb|DT557650.1|DT557650				nr +
Unigene36930_All	2028	1.52	6.25	6.93	3.56	5.25	10.60	0.88	1.07	23.44	2.04E+00	8.39E-27	Up	2.19E+00	1.65E-31	Up	5.59E-01	7.85E-04		1.57E+00	6.17E-34	Up	2.92E-01	4.93E-01		4.74E+00	1.83E-277	Up	Unigene36930_All||gi|164653234|gb|ABY65110.1||0.00E+00||beta-ocimene synthase [Phaseolus lunatus]	Unigene36930_All||1.00E-120||AT4G16740| ATTPS03; (E)-beta-ocimene synthase/ myrcene synthase	Unigene36930_All||0.00E+00||gi|164346763|gb|ES823798.1|ES823798		ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0016829	nr +
Unigene36931_All	1138	6.90	45.73	27.47	19.65	47.48	109.50	19.25	32.14	75.65	2.73E+00	1.84E-153	Up	1.99E+00	7.36E-62	Up	1.27E+00	8.74E-68	Up	2.48E+00	0.00E+00	Up	7.40E-01	5.82E-20		1.97E+00	8.93E-215	Up	Unigene36931_All||gi|115460364|ref|NP_001053782.1||8.00E-122||Os04g0603400 [Oryza sativa Japonica Group] >gi|38344154|emb|CAE01828.2|OSJNBa0041A02.21 [Oryza sativa (japonica cultivar-group)] >gi|113565353|dbj|BAF15696.1|Os04g0603400 [Oryza sativa Japonica Group] >gi|116309664|emb|CAH66713.1|OSIGBa0118P15.3 [Oryza sativa (indica cultivar-group)]	Unigene36931_All||5.00E-08||AT5G43150| unknown protein	Unigene36931_All||0.00E+00||TC136991			GO:0043231	nr +
Unigene36932_All	1577	5.71	16.29	2.90	11.59	9.02	12.09	12.01	14.84	24.58	1.51E+00	9.17E-36	Up	-9.75E-01	1.38E-06		-3.62E-01	3.39E-03		6.01E-02	6.78E-01		3.05E-01	2.94E-03		1.03E+00	2.11E-37	Up	Unigene36932_All||gi|222422812|dbj|BAH19394.1||1.00E-61||AT4G37180 [Arabidopsis thaliana]	Unigene36932_All||3.00E-59||AT4G37180| myb family transcription factor	Unigene36932_All||0.00E+00||TC163909	G2-like			nr +
Unigene36934_All	1043	7.17	2.09	2.81	10.13	9.41	13.16	22.94	13.38	21.01	-1.78E+00	1.16E-13	Down	-1.35E+00	5.90E-09	Down	-1.06E-01	5.95E-01		3.79E-01	1.39E-02		-7.78E-01	1.71E-14		-1.27E-01	2.41E-01		Unigene36934_All||gi|75099990|sp|Q80920.1|PYL4_ARATH||4.00E-58||RecName: Full=Abscisic acid receptor PYL4; AltName: Full=PYR1-like protein 4; AltName: Full=ABA1-binding protein 2; AltName: Full=Regulatory components of ABA receptor 10 >gi|3395441|gb|AAC28773.1|expressed protein [Arabidopsis thaliana] >gi|14517502|gb|AAK62641.1|At2g38310/T19C21.20 [Arabidopsis thaliana] >gi|15809748|gb|AAL06802.1|At2g38310/T19C21.20 [Arabidopsis thaliana]	Unigene36934_All||2.00E-59||AT2G38310| unknown protein	Unigene36934_All||2.00E-42||gi|109881683|gb|DW510653.1|DW510653			GO:0004871||GO:0005488||GO:0009755	nr -
Unigene36935_All	677	0.93	1.95	1.34	7.06	16.53	25.42	6.31	6.36	7.94	1.07E+00	7.10E-02		5.28E-01	4.79E-01		1.23E+00	1.72E-13	Up	1.85E+00	5.18E-34	Up	1.17E-02	1.00E+00		3.33E-01	1.51E-01		Unigene36935_All||gi|115445155|ref|NP_001046357.1||2.00E-32||Os02g0228900 [Oryza sativa Japonica Group] >gi|75258740|sp|Q6H543.1|IAA7_ORYSJ RecName: Full=Auxin-responsive protein IAA7; AltName: Full=Indoleacetic acid-induced protein 7 >gi|113535888|dbj|BAF08271.1|Os02g0228900 [Oryza sativa Japonica Group]	Unigene36935_All||4.00E-30||AT1G51950| IAA18 (INDOLE-3-ACETIC ACID INDUCIBLE 18); transcription factor	Unigene36935_All||0.00E+00||TC169001			GO:0005515||GO:0006412||GO:0009755||GO:0010468||GO:0043231	nr -
Unigene36936_All	1881	0.19	2.07	0.91	8.00	12.81	27.66	6.45	5.93	10.63	3.41E+00	9.04E-15	Up	2.22E+00	2.12E-04	Up	6.80E-01	5.02E-11		1.79E+00	8.47E-98	Up	-1.21E-01	4.83E-01		7.21E-01	3.95E-11		Unigene36936_All||gi|25296228|pir||T52144||7.00E-46||auxin-induced protein IAA18 [imported] - Arabidopsis thaliana (fragment) >gi|2618725|gb|AAB84355.1| IAA18 [Arabidopsis thaliana]	Unigene36936_All||1.00E-45||AT1G51950| IAA18 (INDOLE-3-ACETIC ACID INDUCIBLE 18); transcription factor	Unigene36936_All||0.00E+00||TC169001			GO:0001071||GO:0003676||GO:0005515||GO:0006351||GO:0006412||GO:0006801||GO:0009970||GO:0009718||GO:0009725||GO:0010182||GO:0010468||GO:0016021||GO:0016791||GO:0019637||GO:0043231	nr -
Unigene36938_All	925	83.54	36.04	67.93	30.27	35.14	26.07	6.81	7.00	4.87	-1.21E+00	2.66E-76	Down	-2.99E-01	1.01E-06		2.16E-01	2.48E-02		-2.15E-01	4.69E-02		4.03E-02	8.68E-01		-4.85E-01	1.74E-02		Unigene36938_All||emb|CAL91513.1||4.00E-37||SHW1 protein [Arabidopsis thaliana]	Unigene36938_All||9.00E-18||AT1G69935| SHW1 (SHORT HYPOCOTYL IN WHITE LIGHT1)	Unigene36938_All||0.00E+00||TC161119			GO:0009536||GO:0009640	nr +
Unigene36939_All	1099	8.14	3.27	7.66	44.33	26.98	20.10	33.55	21.68	27.11	-1.31E+00	1.17E-10	Down	-8.87E-02	6.72E-01		-7.17E-01	1.10E-24		-1.14E+00	1.56E-47	Down	-6.30E-01	2.23E-15		-3.07E-01	7.13E-05		Unigene36939_All||gi|66271061|gb|AY432808.1||2.00E-19||Pbl7 [Gossypium hirsutum]		Unigene36939_All||0.00E+00||TC172678				nr +
Unigene36941_All	1273	9.45	7.68	7.40	42.73	30.32	34.09	121.39	111.07	34.55	-2.99E-01	7.69E-02		-3.53E-01	4.43E-02		-4.95E-01	2.61E-14		-3.26E-01	2.86E-06		-1.28E-01	7.72E-04		-1.81E+00	0.00E+00	Down	Unigene36941_All||gi|211906506|gb|ACJ11746.1||0.00E+00||luminal binding protein [Gossypium hirsutum]	Unigene36941_All||0.00E+00||AT5G28540| BIP1; ATP binding	Unigene36941_All||0.00E+00||gi|78352643|gb|DT572917.1|DT572917		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0008152||GO:0016628||GO:0032559||GO:0044432||GO:0050896	nr +
Unigene36944_All	1811	5.72	9.04	7.94	7.01	8.58	15.51	16.86	11.54	6.51	6.60E-01	1.68E-06		4.73E-01	2.13E-03		2.90E-01	4.38E-02		1.15E+00	2.12E-27	Up	-5.47E-01	3.60E-10		-1.37E+00	2.31E-46	Down	Unigene36944_All||0.00E+00||AT1G50420| SCL3; transcription factor	Unigene36944_All||0.00E+00||CO073496	GRAS			GO:0001071||GO:0003676||GO:0006351||GO:0009725||GO:0010468||GO:0043231	nr +
Unigene36947_All	1609	0.52	1.76	1.99	1.67	1.69	2.30	0.95	1.22	1.71	1.76E+00	1.53E-05	Up	1.93E+00	1.48E-06	Up	1.62E-02	9.78E-01		4.61E-01	1.72E-01		3.68E-01	4.00E-01		8.53E-01	9.34E-03		Unigene36947_All||gi|15228881|ref|NP_188308.1||1.00E-168||glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	Unigene36947_All||7.00E-157||AT3G16850| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene36947_All||0.00E+00||DW501410		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553||GO:0044238||GO:0045229	nr -
Unigene36948_All	1672	5.35	14.09	6.50	5.75	9.25	10.83	3.59	5.87	68.29	1.40E+00	3.13E-29	Up	2.80E-01	1.39E-01		6.85E-01	2.40E-07		9.14E-01	1.62E-12		7.10E-01	1.32E-05		4.25E+00	0.00E+00	Up	Unigene36948_All||gi|297796137|ref|XP_002865953.1||1.00E-141||hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311788|gb|EFH42212.1|hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36948_All||6.00E-142||AT5G53050| hydrolase, alpha/beta fold family protein	Unigene36948_All||0.00E+00||CO097335				nr -
Unigene3695_All	2014	8.81	25.26	13.48	8.43	9.68	8.41	40.56	25.67	68.16	1.52E+00	1.18E-70	Up	6.15E-01	9.72E-09		1.98E-01	1.43E-01		-4.30E-03	9.73E-01		-6.60E-01	7.94E-36		7.49E-01	5.73E-76		Unigene3695_All||gi|15223556|ref|NP_173376.1||0.00E+00||KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups [Arabidopsis thaliana] >gi|75311386|sp|Q9LN49.1|KCS4_ARATH RecName: Full=3-ketoacyl-CoA synthase 4; Short=KCS-4; AltName: Full=Very long-chain fatty acid condensing enzyme 4; Short=VLCFA condensing enzyme 4 >gi|8778420|gb|AAF79428.1|AC025808_10 F18O14.21 [Arabidopsis thaliana] >gi|190610070|gb|ACE79746.1|At1g19440 [Arabidopsis thaliana]	Unigene3695_All||0.00E+00||AT1G19440| KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene3695_All||0.00E+00||TC177704		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr +
Unigene36951_All	1815	3.57	4.13	2.14	26.38	23.18	12.42	3.89	0.62	0.81	2.09E-01	3.74E-01		-7.39E-01	2.14E-03		-1.86E-01	1.57E-02		-1.09E+00	3.41E-43	Down	-2.65E+00	2.53E-25	Down	-2.26E+00	6.47E-22	Down	Unigene36951_All||gi|15232389|ref|NP_188722.1||1.00E-156||ATNEK5 (NIMA-RELATED KINASE5); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene36951_All||2.00E-150||AT3G20860| ATNEK5 (NIMA-RELATED KINASE5); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene36951_All||0.00E+00||ES818513				nr +

Unigene36952_All	735	22.57	18.20	16.81	23.18	18.74	16.90	20.19	16.04	9.00	-3.10E-01	2.64E-02			-4.25E-01	2.91E-03		-3.07E-01	2.06E-02			-4.56E-01	5.65E-04		-3.32E-01	1.22E-02		-1.17E+00	5.03E-18	Down	Unigene36952_All//gi|18420256|ref|NP_568396.1|//7.00E-64//RBX1 (RING-BOX 1); protein binding [Arabidopsis thaliana] >gi|37537976|sp|Q940X7.1|RBX1A_ARATH RecName: Full=RING-box protein 1a; AltName: Full=RBX1a-At; AltName: Full=At-Rbx1;1; AltName: Full=RBX1-2; AltName: Full=Protein RING of cullins 1 >gi|16180265|gb|AAL13435.1| ring box-1-like protein [Arabidopsis thaliana] >gi|18252991|gb|AAL62422.1| ring-box protein - like [Arabidopsis thaliana] >gi|21389679|gb|AAM48038.1| ring-box protein-like [Arabidopsis thaliana] >gi|21592528|gb|AAM64477.1| ring-box protein-like [Arabidopsis thaliana]	Unigene36952_All//2.00E-58//AT5G20570| RBX1 (RING-BOX 1); protein binding	Unigene36952_All//0.00E+00//TC153564		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair	GO:0031461//GO:0032446//GO:0046914	nr -
Unigene36955_All	2111	1.12	1.42	1.26	2.03	1.21	1.67	2.56	1.52	1.21	3.45E-01	3.69E-01		1.78E-01	6.46E-01		-7.50E-01	6.54E-03			-2.82E-01	3.98E-01		-7.50E-01	1.01E-03		-1.09E+00	1.86E-06	Down	Unigene36955_All//gi|124359510|gb|ABD28627.2|//5.00E-39//RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H [Medicago truncatula]	Unigene36955_All//3.00E-08//AT4G20520| RNA binding / RNA-directed DNA polymerase	Unigene36955_All//0.00E+00//ES815015			GO:0005488	nr +
Unigene36956_All	1711	10.27	3.44	5.82	14.73	11.79	13.51	13.59	4.64	6.05	-1.58E+00	2.06E-26	Down	-8.20E-01	2.64E-09		-3.21E-01	1.97E-03		-1.24E-01	3.36E-01		-1.55E+00	3.20E-41	Down	-1.17E+00	9.16E-28	Down	Unigene36956_All//gi|95147286|gb|AB557278.1|//0.00E+00//At3g28700 [Arabidopsis thaliana]	Unigene36956_All//0.00E+00//AT3G28700| unknown protein	Unigene36956_All//0.00E+00//TC136959			GO:0043231//GO:0046914	nr -
Unigene36959_All	951	2.37	4.96	2.07	5.60	3.98	5.32	4.62	2.15	2.97	1.07E+00	1.61E-04	Up	-1.91E-01	6.53E-01		-4.93E-01	5.03E-02		-7.55E-02	7.94E-01		-1.10E+00	2.58E-05	Down	-6.37E-01	1.04E-02		Unigene36959_All//gi|297796531|ref|XP_002866150.1|//1.00E-115//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311985|gb|EFH42409.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene36959_All//3.00E-107//AT5G56450| mitochondrial substrate carrier family protein	Unigene36959_All//0.00E+00//TC174757			GO:0006810//GO:0019866//GO:0031224	nr +
Unigene3696_All	1713	3.51	0.89	1.09	6.11	4.74	5.27	7.95	2.37	4.77	-1.98E+00	9.05E-13	Down	-1.69E+00	6.60E-10	Down	-3.64E-01	3.64E-02		-2.12E-01	2.89E-01		-1.75E+00	6.95E-29	Down	-7.37E-01	3.48E-08		Unigene3696_All//gi|297799892|ref|XP_002867830.1|//1.00E-162//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297313666|gb|EFH44089.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene3696_All//3.00E-159//AT4G21705| pentatricopeptide (PPR) repeat-containing protein	Unigene3696_All//0.00E+00//TC179354				nr -
Unigene36960_All	1721	2.25	1.12	0.84	2.29	1.50	1.08	7.22	3.79	2.22	-1.01E+00	1.30E-03		-1.43E+00	2.49E-05	Down	-6.08E-01	4.04E-02		-1.09E+00	3.80E-04	Down	-9.31E-01	1.81E-10		-1.70E+00	2.76E-26	Down	Unigene36960_All//gi|224100569|ref|XP_002311927.1|//0.00E+00//aminophospholipid ATPase [Populus trichocarpa] >gi|222851747|gb|EEE89294.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene36960_All//0.00E+00//AT5G04930| ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	Unigene36960_All//0.00E+00//TC150628			GO:0005548//GO:0006869//GO:0009206//GO:0031224//GO:0032559//GO:0042625//GO:0046872	nr -
Unigene36963_All	2161	0.44	0.59	0.22	11.20	11.27	49.20	368.67	288.43	312.46	4.28E-01	4.74E-01		-9.74E-01	2.00E-01		8.10E-03	9.55E-01		2.13E+00	6.70E-252	Up	-3.54E-01	3.86E-110		-2.39E-01	7.19E-54		Unigene36963_All//gi|20269071|emb|CAD29733.1|//0.00E+00//pectin methylesterase [Sesbania rostrata]	Unigene36963_All//2.00E-177//AT1G11580| PMEPCRA (METHYLESTERASE PCR A); enzyme inhibitor/ pectinesterase	Unigene36963_All//0.00E+00//C0132597		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0030234//GO:0030312//GO:0071555	nr +
Unigene36966_All	1580	3.84	14.34	6.30	25.95	33.48	25.87	17.10	29.10	38.68	1.90E+00	2.53E-43	Up	7.14E-01	1.46E-04		3.68E-01	4.41E-08		-4.40E-03	9.59E-01		7.67E-01	1.93E-26		1.18E+00	5.39E-72	Up	Unigene36966_All//gi|115440519|ref|NP_001044539.1|//2.00E-36//Os01g0801200 [Oryza sativa Japonica Group] >gi|113534070|dbj|BAF06453.1| Os01g0801200 [Oryza sativa Japonica Group]	Unigene36966_All//5.00E-48//AT5G03990| unknown protein	Unigene36966_All//0.00E+00//TC146349				nr +
Unigene36967_All	1202	1.48	7.42	2.39	1.91	1.86	1.24	2.25	1.91	2.09	2.33E+00	2.24E-22	Up	6.93E-01	7.43E-02		-3.39E-02	9.37E-01		-6.21E-01	1.51E-01		-2.35E-01	5.40E-01		-1.09E-01	7.44E-01		Unigene36967_All//gi|115486503|ref|NP_001068395.1|//3.00E-59//Os11g0657200 [Oryza sativa Japonica Group] >gi|113645617|dbj|BAF28758.1| Os11g0657200 [Oryza sativa Japonica Group]	Unigene36967_All//4.00E-60//AT4G02485| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene36967_All//0.00E+00//EE592940				nr -
Unigene3697_All	2110	1.93	0.77	0.73	10.88	7.43	5.80	7.09	2.63	2.70	-1.33E+00	2.20E-05	Down	-1.40E+00	1.92E-05	Down	-5.52E-01	1.27E-07		-9.08E-01	9.98E-16		-1.43E+00	7.59E-24	Down	-1.39E+00	1.04E-23	Down	Unigene3697_All//gi|115455585|ref|NP_001051393.1|//1.00E-150//Os03g0769000 [Oryza sativa Japonica Group] >gi|113549864|dbj|BAF13307.1| Os03g0769000 [Oryza sativa Japonica Group]	Unigene3697_All//1.00E-168//AT5G66600| unknown protein	Unigene3697_All//0.00E+00//TC166544				nr -
Unigene36974_All	658	5.41	0.15	2.35	0.38	0.10	0.41	0.06	0.00	0.24	-5.13E+00	8.73E-18	Down	-1.20E+00	5.45E-04	Down	-1.85E+00	2.75E-01		1.22E-01	9.44E-01		-6.01E+00	6.57E-01		1.91E+00	3.77E-01		Unigene36974_All//gi|115489504|ref|NP_001067239.1|//2.00E-19//Os12g0608900 [Oryza sativa Japonica Group] >gi|77556479|gb|ABA99275.1| Protein kinase domain containing protein [Oryza sativa (Japonica cultivar-group)] >gi|113649746|dbj|BAF30258.1| Os12g0608900 [Oryza sativa Japonica Group]		Unigene36974_All//1.00E-168//gi|109856731|gb|DW485710.1|DW485710	ko04626|Plant-pathogen interaction//ko03040|Spliceosome	GO:0000166//GO:0003676//GO:0004674//GO:0031410//GO:0044238//GO:0044260	nr +
Unigene36975_All	1769	3.22	1.60	2.08	4.62	1.07	1.10	4.57	14.01	13.15	-1.01E+00	6.41E-05	Down	-6.34E-01	1.46E-02		-2.11E+00	8.82E-23	Down	-2.07E+00	2.03E-19	Down	1.62E+00	1.48E-46	Up	1.53E+00	3.78E-41	Up	Unigene36975_All//gi|115489498|ref|NP_001067236.1|//1.00E-109//Os12g0608500 [Oryza sativa Japonica Group] >gi|77556475|gb|ABA99271.1| Protein kinase domain containing protein, expressed [Oryza sativa (Japonica cultivar-group)] >gi|113649743|dbj|BAF30255.1| Os12g0608500 [Oryza sativa Japonica Group]	Unigene36975_All//4.00E-96//AT5G10530| lectin protein kinase, putative	Unigene36975_All//3.00E-175//gi|109856731|gb|DW485710.1|DW485710	ko04626|Plant-pathogen interaction		nr -
Unigene36976_All	577	73.54	59.45	80.66	40.92	54.85	46.49	42.79	21.37	21.68	-3.07E-01	1.89E-04		1.33E-01	1.38E-01		4.23E-01	2.21E-06		1.84E-01	1.10E-01		-1.00E+00	1.76E-22	Down	-9.81E-01	2.11E-22		Unigene36976_All//gi|295687231|gb|ADG27841.1|//3.00E-61//triosephosphate isomerase [Gossypium hirsutum]	Unigene36976_All//1.00E-48//AT2G21170| TIM (TRIOSEPHOSPHATE ISOMERASE); catalytic/ triose-phosphate isomerase	Unigene36976_All//4.00E-141//gi|11209248|gb|BF278178.1|BF278178		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00562|Inositol phosphate metabolism//ko00051|Fructose and mannose metabolism	GO:0000003//GO:0005488//GO:0005576//GO:0006071//GO:0006641//GO:0009526//GO:0009532//GO:0009657//GO:0015977//GO:0016861//GO:0019682//GO:0048364	nr -
Unigene36977_All	1768	2.49	3.04	1.20	3.69	3.00	4.16	6.39	6.24	7.08	2.89E-01	2.85E-01		-1.04E+00	6.04E-04	Down	-2.99E-01	2.18E-01		1.74E-01	4.88E-01		-3.29E-02	8.55E-01		1.48E-01	3.49E-01		Unigene36977_All//gi|18424537|ref|NP_568948.1|//2.00E-59//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75170898|sp|Q9FIT7.1|PP442_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g61990, mitochondrial; Flags: Precursor	Unigene36977_All//1.00E-60//AT5G61990| pentatricopeptide (PPR) repeat-containing protein	Unigene36977_All//0.00E+00//gi|164352088|gb|ES839079.1|ES839079				nr +
Unigene36978_All	1242	4.17	1.88	4.03	6.42	2.83	1.42	1.84	1.75	1.06	-1.15E+00	1.92E-05	Down	-4.94E-02	8.63E-01		-1.18E+00	1.01E-09	Down	-2.18E+00	3.66E-20	Down	-7.11E-02	8.62E-01		-7.96E-01	2.81E-02		Unigene36978_All//gi|38603962|gb|AAR24726.1|//1.00E-47//At5g03110 [Arabidopsis thaliana] >gi|46681450|gb|AAS42665.1| At5g03110 [Arabidopsis thaliana]	Unigene36978_All//5.00E-31//AT5G03110| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; BEST Arabidopsis thaliana protein match is: protamine P1 family protein (TAIR:AT2G37100.1); Has 43 Blast hits to 42 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene36978_All//0.00E+00//gi|78332358|gb|DT552632.1|DT552632			GO:0016020	nr -
Unigene3698_All	1540	12.60	30.34	25.69	12.78	17.64	18.15	27.78	41.36	35.16	1.27E+00	2.05E-49	Up	1.03E+00	3.11E-29	Up	4.66E-01	1.57E-06		5.07E-01	3.67E-07		5.74E-01	4.34E-22		3.40E-01	6.23E-08		Unigene3698_All//gi|18418356|ref|NP_567950.1|//0.00E+00//MCCB (3-METHYLCROTONYL-COA CARBOXYLASE); biotin carboxylase/ methylcrotonoyl-CoA carboxylase [Arabidopsis thaliana] >gi|20455074|sp|Q8LG08.1|MCCB_ARATH RecName: Full=Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial; Short=MCCase subunit beta; AltName: Full=3-methylcrotonyl-CoA:carbon dioxide ligase subunit beta; AltName: Full=3-methylcrotonyl-CoA carboxylase 2; Flags: Precursor >gi|7021222|gb|AAF35258.1|AF059510_1 3-methylcrotonyl-CoA carboxylase non-biotinylated subunit [Arabidopsis thaliana] >gi|7021224|gb|AAF35259.1|AF059511_1 3-methylcrotonyl-CoA carboxylase nonbiotinylated subunit [Arabidopsis thaliana] >gi|23198352|gb|AAN15703.1| Unknown protein [Arabidopsis thaliana]	Unigene3698_All//0.00E+00//AT4G3430 30| MCCB (3-METHYLCROTONYL-COA CARBOXYLASE); biotin carboxylase/ methylcrotonoyl-CoA carboxylase	Unigene3698_All//0.00E+00//TC133117		ko00280|Valine, leucine and isoleucine degradation		nr -
Unigene36983_All	402	0.39	1.64	0.40	2.85	2.14	1.69	5.89	1.98	6.64	2.07E+00	3.93E-02		2.53E-02	1.00E+00		-4.12E-01	5.39E-01		-7.58E-01	2.45E-01		-1.58E+00	5.47E-05	Down	1.73E-01	6.31E-01				Unigene36983_All//1.00E-72//TC133115				

Unigene36988_All	1612	4.97	25.46	12.92	15.61	10.72	7.26	7.32	4.95	20.19	2.36E+00	1.43E-102	Up	1.38E+00	1.30E-24	Up	-5.41E-01	4.92E-08		-1.10E+00	1.51E-23	Down	-5.63E-01	1.23E-04		1.46E+00	7.40E-54	Up	Unigene36988_All//gi|297728309|ref|NP_001176518.1|//1.00E-35//Os11g0437600 [Oryza sativa Japonica Group] >gi|108864340|gb|ABA93251.2| uncharacterized plant-specific domain TIG801615 family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|255680055|dbj|BAH95246.1| Os11g0437600 [Oryza sativa Japonica Group]	Unigene36988_All//9.00E-67//AT3G07350| unknown protein	Unigene36988_All//0.00E+00//gi|78339782|gb|DT560056.1|DT560056				nr -
Unigene36989_All	1560	35.28	47.97	24.68	38.93	47.08	47.77	16.13	45.87	28.40	4.43E-01	1.75E-13		-5.16E-01	1.42E-12		2.75E-01	1.37E-06		2.95E-01	5.20E-07		1.51E+00	3.88E-120	Up	8.16E-01	5.26E-29		Unigene36989_All//gi|15240535|ref|NP_199781.1|//4.00E-92//DNA-binding protein-related [Arabidopsis thaliana] >gi|119657378|tpd|FAA00288.1| TPA: AT-hook motif nuclear localized protein 17 [Arabidopsis thaliana]	Unigene36989_All//7.00E-67//AT5G49700| DNA-binding protein-related	Unigene36989_All//0.00E+00//TC172408				nr -
Unigene36990_All	1419	5.35	12.32	8.48	9.69	14.00	11.24	25.80	241.38	164.38	1.20E+00	1.52E-17	Up	6.66E-01	8.06E-05		5.31E-01	4.18E-06		2.14E-01	1.67E-01		3.23E+00	0.00E+00	Up	2.67E+00	0.00E+00	Up	Unigene36990_All//gi|30698042|ref|NP_201258.2|//3.00E-74//XND1; transcription factor [Arabidopsis thaliana] >gi|107738104|gb|ABF83636.1| At5g64530 [Arabidopsis thaliana]	Unigene36990_All//4.00E-64//AT5G64530| XND1; transcription factor	Unigene36990_All//0.00E+00//EX164587	NAC		GO:0001071//GO:0003676//GO:0010087//GO:0010468//GO:0012501//GO:0048513	nr +
Unigene36994_All	316	18.71	10.74	12.81	32.95	40.65	27.87	30.64	12.43	11.47	-8.00E-01	1.03E-03		-5.47E-01	3.29E-02		3.03E-01	6.00E-02		-2.41E-01	2.19E-01		-1.30E+00	1.01E-13	Down	-1.42E+00	4.99E-16	Down	Unigene36994_All//gi|124484373|dbj|BAF46297.1|//1.00E-19//caffeoyl-CoA O-methyltransferase [Ipomoea nil]	Unigene36994_All//6.00E-21//AT4G26220| caffeoyl-CoA 3-O-methyltransferase, putative			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0005488//GO:0008171//GO:0044237//GO:0044238//GO:0044444	nr +
Unigene36995_All	1083	8.84	7.16	7.13	20.15	16.63	17.60	25.73	12.81	8.20	-3.05E-01	1.15E-01		-3.10E-01	1.28E-01		-2.77E-01	1.70E-02		-1.95E-01	1.31E-01		-1.01E+00	2.03E-25	Down	-1.65E+00	2.07E-55	Down	Unigene36995_All//gi|30580368|sp|Q9C5D7.1|CAMT3_ARATH//9.00E-92//RecName: Full=Probable caffeoyl-CoA O-methyltransferase At4g26220; AltName: Full=Trans-caffeoyl-CoA 3-O-methyltransferase; Short=CCoAOMT; Short=CCoAMT	Unigene36995_All//5.00E-93//AT4G26220| caffeoyl-CoA 3-O-methyltransferase, putative	Unigene36995_All//2.00E-159//ES791145		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003676//GO:0006259//GO:0008171//GO:0044444	nr -
Unigene36997_All	892	104.93	78.05	35.82	74.50	81.92	44.05	82.81	133.96	126.13	-4.27E-01	1.24E-15		-1.55E+00	9.21E-130	Down	1.37E-01	3.11E-02		-7.58E-01	9.14E-33		6.94E-01	9.61E-57		6.07E-01	2.26E-43		Unigene36997_All//gi|110749713|gb|AB698382.1|//4.00E-41//lateral organ boundaries domain protein [Saragana korshinskii]	Unigene36997_All//8.00E-31//AT5G67420| LBD37 (LOB DOMAIN-CONTAINING PROTEIN 37)	Unigene36997_All//0.00E+00//gi|164301225|gb|ES790765.1|ES790765				nr +
Unigene36998_All	732	15.01	23.47	12.95	69.28	45.16	60.16	66.14	42.20	213.83	6.45E-01	1.53E-06		-2.13E-01	2.68E-01		-6.17E-01	8.92E-20		-2.04E-01	7.65E-03		-6.48E-01	6.22E-21		1.69E+00	0.00E+00	Up	Unigene36998_All//gi|18409649|ref|NP_564995.1|//6.00E-64//caleosin-related family protein [Arabidopsis thaliana] >gi|15810177|gb|AL06990.1| At1g70670/F5A18_15 [Arabidopsis thaliana] >gi|23505789|gb|AAN28754.1| At1g70670/F5A18_15 [Arabidopsis thaliana]	Unigene36998_All//3.00E-65//AT1G70670| caleosin-related family protein	Unigene36998_All//0.00E+00//TC149929			GO:0043231	nr -
Unigene36999_All	1253	5.60	2.87	4.84	11.37	5.96	3.57	3.58	2.27	1.08	-9.63E-01	1.70E-05		-2.08E-01	3.85E-01		-9.31E-01	1.35E-11		-1.67E+00	4.05E-25	Down	-6.57E-01	9.93E-03		-1.73E+00	3.25E-10	Down								
Unigene3700_All	1255	11.84	4.64	8.44	5.08	4.14	2.59	1.65	0.63	0.92	-1.35E+00	6.77E-18	Down	-4.88E-01	1.22E-03		-2.94E-01	2.31E-01		-9.72E-01	2.41E-05		-1.38E+00	8.02E-04	Down	-8.43E-01	2.82E-02		Unigene3700_All//gi|14517466|gb|AAK62623.1|//4.00E-68//AT3g52150/F4F15_260 [Arabidopsis thaliana] >gi|23507783|gb|AAN38695.1| At3g52150/F4F15_260 [Arabidopsis thaliana]	Unigene3700_All//1.00E-67//AT3G52155| LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078); Has 1050 Blast hits to 1050 proteins in 239 species: Archae - 0; Bacteria - 476; Metazoa - 0; Fungi - 0; Plants - 22; Viruses - 0; Other Eukaryotes - 552 (source: NCBI BLink).	Unigene3700_All//0.00E+00//TC139330				nr +
Unigene37000_All	1194	1.97	5.60	2.68	3.55	5.65	10.40	19.83	22.23	36.97	1.51E+00	8.70E-10	Up	4.40E-01	2.33E-01		6.73E-01	1.91E-03		1.55E+00	1.95E-19	Up	1.65E-01	1.12E-01		8.99E-01	7.23E-34		Unigene37000_All//gi|217793794|gb|ACK56111.1|//3.00E-58//ELF4-like protein [Gossypium arboreum]	Unigene37000_All//2.00E-44//AT1G17455| ELF4-L4 (ELF4-Like 4)	Unigene37000_All//0.00E+00//TC167828				nr +
Unigene37001_All	576	1.64	7.39	2.68	4.58	2.87	5.18	1.03	0.94	10.65	2.18E+00	3.21E-10	Up	7.14E-01	2.04E-01		-6.76E-01	7.16E-02		1.75E-01	6.75E-01		-1.24E-01	8.84E-01		3.37E+00	2.03E-28	Up			Unigene37001_All//0.00E+00//DR238152				
Unigene37002_All	1034	2.48	4.95	2.94	3.47	2.03	5.24	0.86	0.81	11.37	9.97E-01	2.01E-04		2.44E-01	5.33E-01		-7.72E-01	1.18E-02		5.96E-01	2.12E-02		-8.71E-02	9.03E-01		3.73E+00	1.63E-58	Up			Unigene37002_All//0.00E+00//TC137008				
Unigene37003_All	1663	1.04	1.58	1.09	2.04	2.32	4.92	7.88	15.10	16.67	6.10E-01	1.21E-01		6.85E-02	8.91E-01		1.87E-01	6.11E-01		1.27E+00	9.26E-10	Up	9.39E-01	1.46E-20		1.08E+00	5.25E-29	Up	Unigene37003_All//gi|79470337|ref|NP_192950.2|//1.00E-132//aminomethyltransferase [Arabidopsis thaliana] >gi|30725630|gb|AAP37837.1| At4g12130 [Arabidopsis thaliana]	Unigene37003_All//6.00E-132//AT4G12130| aminomethyltransferase	Unigene37003_All//0.00E+00//gi|78343223|gb|DT563497.1|DT563497			GO:0016741	nr -
Unigene37007_All	577	4.62	3.60	2.31	3.02	3.76	7.98	5.72	1.52	2.97	-3.61E-01	3.75E-01		-1.00E+00	1.38E-02		3.15E-01	5.34E-01		1.40E+00	1.35E-06	Up	-1.91E+00	1.93E-08	Down	-9.45E-01	1.39E-03		Unigene37007_All//gi|15232342|ref|NP_191609.1|//1.00E-68//CER7 (ECERIFERUM 7); 3'-5'-exoribonuclease/ RNA binding [Arabidopsis thaliana] >gi|42572741|ref|NP_974466.1| CER7 (ECERIFERUM 7); 3'-5'-exoribonuclease/ RNA binding [Arabidopsis thaliana] >gi|7287998|emb|CAB81836.1| nucleolar autoantigen-like protein [Arabidopsis thaliana] >gi|113196170|gb|ABI31441.1| CER7 [Arabidopsis thaliana]	Unigene37007_All//8.00E-70//AT3G60500| CER7 (ECERIFERUM 7); 3'-5'-exoribonuclease/ RNA binding	Unigene37007_All//0.00E+00//gi|48805596|gb|C0106910.1|C0106910		ko03018|RNA degradation	GO:0003676//GO:0006633//GO:0008408//GO:0010467//GO:0043231	nr -
Unigene37008_All	1189	2.82	1.41	2.46	5.36	3.68	3.57	5.26	2.78	2.35	-1.00E+00	3.26E-03		-1.93E-01	6.19E-01		-5.44E-01	1.46E-02		-5.87E-01	1.15E-02		-9.22E-01	1.35E-05		-1.17E+00	4.13E-08	Down	Unigene37008_All//gi|15232342|ref|NP_191609.1|//1.00E-125//CER7 (ECERIFERUM 7); 3'-5'-exoribonuclease/ RNA binding [Arabidopsis thaliana] >gi|42572741|ref|NP_974466.1| CER7 (ECERIFERUM 7); 3'-5'-exoribonuclease/ RNA binding [Arabidopsis thaliana] >gi|7287998|emb|CAB81836.1| nucleolar autoantigen-like protein [Arabidopsis thaliana] >gi|113196170|gb|ABI31441.1| CER7 [Arabidopsis thaliana]	Unigene37008_All//2.00E-126//AT3G60500| CER7 (ECERIFERUM 7); 3'-5'-exoribonuclease/ RNA binding	Unigene37008_All//0.00E+00//gi|48805596|gb|C0106910.1|C0106910		ko03018|RNA degradation	GO:0003676//GO:0008408//GO:0010467	nr +
Unigene37009_All	1026	182.56	133.64	244.76	95.99	85.35	168.86	246.18	46.32	34.17	-4.50E-01	1.56E-33		4.23E-01	1.29E-38		-1.70E-01	7.91E-04		8.15E-01	5.50E-95		-2.41E+00	0.00E+00	Down	-2.85E+00	0.00E+00	Down	Unigene37009_All//gi|283135858|gb|ADB11320.1|//8.00E-90//tau class glutathione transferase GSTU22 [Populus trichocarpa]	Unigene37009_All//7.00E-72//AT1G10370| ER099 (EARLY-RESPONSIVE TO DEHYDRATION 9); glutathione transferase	Unigene37009_All//0.00E+00//gi|164245003|gb|ES809073.1|ES809073		ko00480|Glutathione metabolism	GO:0009404//GO:0009536//GO:0016740//GO:0016846	nr +
Unigene37010_All	1961	11.37	7.42	11.70	16.16	21.02	7.83	0.47	0.45	0.20	-6.16E-01	1.09E-07		4.22E-02	7.46E-01		3.80E-01	8.78E-07		-1.04E+00	5.35E-27	Down	-8.36E-02	9.05E-01		-1.22E+00	5.14E-02		Unigene37010_All//gi|115436258|ref|NP_001042887.1|//1.00E-39//Os01g0319200 [Oryza sativa Japonica Group] >gi|113532418|dbj|BAF04801.1| Os01g0319200 [Oryza sativa Japonica Group]	Unigene37010_All//2.00E-21//AT5G11290| unknown protein	Unigene37010_All//3.00E-144//gi|109878713|gb|DW507683.1|DW507683				nr +
Unigene37012_All	819	6.58	5.63	3.58	5.53	8.83	21.29	131.38	168.82	739.33	-2.25E-01	3.95E-01		-8.80E-01	1.05E-03		6.74E-01	1.18E-03		1.94E+00	7.69E-37	Up	3.62E-01	1.48E-20		2.49E+00	0.00E+00	Up	Unigene37012_All//gi|224137294|ref|XP_002327090.1|//4.00E-65//cytochrome P450 [Populus trichocarpa] >gi|222835405|gb|EEE73840.1| cytochrome P450 [Populus trichocarpa]	Unigene37012_All//4.00E-40//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene37012_All//0.00E+00//TC141300		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0016491//GO:0046872	nr +
Unigene37014_All	795	11.52	4.72	3.82	10.90	8.88	13.35	14.68	8.83	9.42	-1.29E+00	1.42E-10	Down	-1.59E+00	1.29E-13	Down	-2.96E-01	1.46E-01		2.92E-01	1.20E-01		-7.33E-01	7.77E-07		-6.40E-01	9.14E-06		Unigene37014_All//gi|115452257|ref|NP_001049729.1|//1.00E-40//Os03g0278800 [Oryza sativa Japonica Group] >gi|113548200|dbj|BAF11643.1| Os03g0278800 [Oryza sativa Japonica Group]	Unigene37014_All//3.00E-39//AT2G37510| RNA-binding protein, putative	Unigene37014_All//0.00E+00//gi|73850592|gb|DT459612.1|DT459612		ko03010|Ribosome//ko03040|Spliceosome	GO:0003676//GO:0043231	nr -
Unigene37015_All	1333	3.57	1.41	2.40	2.54	2.79	2.37	3.90	1.98	2.21	-1.34E+00	3.17E-06	Down	-5.76E-01	4.71E-02		1.35E-01	7.38E-01		-9.96E-02	7.81E-01		-9.82E-01	3.19E-05		-8.19E-01	3.13E-04		Unigene37015_All//gi|18414678|ref|NP_567502.1|//4.00E-92//YbaK/prolyl-tRNA synthetase-related [Arabidopsis thaliana] >gi|15451034|gb|AAK96788.1| Unknown protein [Arabidopsis thaliana]	Unigene37015_All//6.00E-91//AT4G16510| YbaK/prolyl-tRNA synthetase-related	Unigene37015_All//0.00E+00//gi|78353356|gb|DT573630.1|DT573630				nr +
Unigene37016_All	1234	2.63	0.29	1.21	4.04	2.37	3.48	2.64	2.10	2.36	-3.19E+00	8.17E-12	Down	-1.12E+00	2.13E-03		-7.67E-01	2.26E-03		-2.15E-01	4.76E-01		-3.29E-01	3.20E-01		-1.63E-01	6.10E-01		Unigene37016_All//gi|297830972|ref|XP_002883368.1|//8.00E-77//structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata] >gi|297329208|gb|EFH59627.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	Unigene37016_All//2.00E-72//AT3G22450| structural constituent of ribosome	Unigene37016_All//0.00E+00//gi|48741322|gb|C0071841.1|C0071841		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene37017_All	1392	45.33	21.33	32.29	80.88	70.85	80.95	61.75	18.23	17.54	-1.09E+00	1.64E-52	Down	-4.90E-01	4.42E-13		-1.91E-01	3.15E-05		1.30E-03	9.81E-01		-1.76E+00	2.17E-180	Down	-1.82E+00	9.06E-194	Down	Unigene37017_All//gi|16649113|gb|AAL24408.1|//0.00E+00//phosphoglucomutase [Arabidopsis thaliana] >gi|20148521|gb|AAM10151.1| phosphoglucomutase [Arabidopsis thaliana]	Unigene37017_All//0.00E+00//AT1G23190| phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative	Unigene37017_All//0.00E+00//TC139043		ko00500|Starch and sucrose metabolism//ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway	GO:0009536//GO:0010038//GO:0016020//GO:0016868//GO:0019318//GO:0046872	nr +
Unigene37018_All	657	39.58	21.83	38.58	52.77	47.75	47.84	35.65	25.06	17.22	-8.59E-01	3.82E-15		-3.69E-02	7.64E-01		-1.44E-01	1.48E-01		-1.41E-01	1.71E-01		-5.08E-01	4.17E-07		-1.05E+00	1.04E-23	Down	Unigene37018_All//gi|297808071|ref|XP_002871919.1|//2.00E-54//phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317756|gb|EFH48178.1| phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37018_All//2.00E-48//AT5G20060| phospholipase/carboxylesterase family protein	Unigene37018_All//0.00E+00//gi|48749030|gb|C0079549.1|C0079549		ko00564|Glycerophospholipid metabolism	GO:0016788	nr -
Unigene3702_All	2344	1.85	0.56	0.43	2.06	2.23	1.10	23.02	19.01	40.65	-1.72E+00	6.76E-08	Down	-2.10E+00	1.42E-09	Down	1.15E-01	7.29E-01		-9.08E-01	7.56E-04		-2.76E-01	1.87E-05		8.21E-01	6.49E-62		Unigene3702_All//gi|38112427|gb|AAR11299.1|//0.00E+00//lectin-like receptor kinase 7;2 [Medicago truncatula]	Unigene3702_All//2.00E-163//AT5G59260| lectin protein kinase, putative	Unigene3702_All//7.00E-10//EX170099		ko04626|Plant-pathogen interaction		nr -

Unigene37022_All	1024	1.43	0.69	3.85	2.53	2.19	2.21	1.11	1.67	0.54	-1.05E+00	5.84E-02		1.43E+00	2.02E-05	Up	-2.11E-01	6.04E-01		-1.98E-01	6.45E-01		5.86E-01	2.03E-01		-1.03E+00	5.95E-02		Unigene37022_All//gi|297832112|ref|XP_002883938.1|//5.00E-74//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329778|gb|EFH60197.1|leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37022_All//2.00E-65//AT2G20210| leucine-rich repeat family protein	Unigene37022_All//0.00E+00//ES841393				nr -
Unigene37024_All	1176	23.80	17.79	28.66	14.61	14.08	10.45	27.58	13.01	8.84	-4.20E-01	4.06E-05		2.68E-01	6.53E-03		-5.32E-02	7.69E-01		-4.84E-01	2.17E-04		-1.08E+00	3.42E-33	Down	-1.64E+00	6.63E-64	Down	Unigene37024_All//gi|8403820|ref|NP_566732.1|//1.00E-89//dienelactone hydrolase family protein [Arabidopsis thaliana] >gi|17381244|gb|AAL36041.1|AT3g23600/MDB19_9 [Arabidopsis thaliana] >gi|20453365|gb|AAM19921.1|AT3g23600/MDB19_9 [Arabidopsis thaliana] >gi|21536848|gb|AAM61180.1|contains similarity to endo-1,3-1,4-beta-D-glucanase [Arabidopsis thaliana]	Unigene37024_All//4.00E-82//AT3G23600| dienelactone hydrolase family protein	Unigene37024_All//0.00E+00//TC152808			GO:0004091//GO:0005576//GO:0006970//GO:0016020//GO:0043231	nr +
Unigene37028_All	1057	8.86	4.51	6.45	11.31	5.64	6.32	17.92	10.24	39.88	-9.76E-01	3.36E-07		-4.58E-01	2.06E-02		-1.00E+00	4.31E-11	Down	-8.39E-01	1.67E-07		-8.07E-01	2.29E-12		1.15E+00	2.29E-48	Up	Unigene37028_All//gi|2003388|gb|AG43551.1|AF211533_1//3.00E-44//Avr9/CF-9 rapidly elicited protein 146 [Nicotiana tabacum]	Unigene37028_All//1.00E-40//AT1G52140| unknown protein	Unigene37028_All//0.00E+00//TC137792				nr -
Unigene3703_All	1701	13.29	5.03	6.17	6.35	4.37	3.29	2.01	1.08	1.36	-1.40E+00	2.59E-28	Down	-1.11E+00	5.11E-19	Down	-5.39E-01	8.67E-04		-9.49E-01	2.81E-08		-8.97E-01	2.61E-03		-5.68E-01	4.88E-02		Unigene3703_All//gi|83281193|dbj|BAD15110.2|//0.00E+00//similar to CDK5 regulatory subunit-associated protein [Nicotiana tabacum]	Unigene3703_All//0.00E+00//AT4G36390| radical SAM domain-containing protein / TRAM domain-containing protein	Unigene3703_All//0.00E+00//TC171391				nr -
Unigene37032_All	1253	9.31	7.56	3.57	9.66	9.67	5.84	6.85	3.50	5.34	-3.00E-01	7.95E-02		-1.38E+00	4.61E-14	Down	2.00E-03	9.97E-01		-7.26E-01	4.56E-06		-9.68E-01	6.35E-08		-3.59E-01	3.93E-02		Unigene37032_All//gi|15226727|ref|NP_181594.1|//5.00E-85//bZIP transcription factor family protein [Arabidopsis thaliana]	Unigene37032_All//4.00E-78//AT2G40620| bZIP transcription factor family protein	Unigene37032_All//0.00E+00//TC131009	bZIP		GO:0005488	nr +
Unigene37033_All	1478	0.81	36.55	0.43	2.86	6.17	6.23	2.66	4.41	78.14	5.49E+00	6.74E-272	Up	-9.13E-01	1.57E-01		1.11E+00	1.67E-09	Up	1.12E+00	4.40E-09	Up	7.30E-01	3.77E-04		4.88E+00	0.00E+00	Up	Unigene37033_All//gi|195549553|gb|ACG50004.1|//1.00E-145//salt responsive protein 2 [Solanum lycopersicum]	Unigene37033_All//8.00E-144//AT5G12010| unknown protein	Unigene37033_All//0.00E+00//TC150879				nr +
Unigene37034_All	1114	8.13	151.60	44.55	6.62	12.67	29.80	0.84	8.48	6.83	4.22E+00	0.00E+00	Up	2.46E+00	4.30E-127	Up	9.37E-01	3.88E-11		2.17E+00	1.84E-80	Up	3.34E+00	2.71E-42	Up	3.03E+00	7.92E-32	Up	Unigene37034_All//gi|226500952|ref|NP_001150046.1|//1.00E-127//LOC100283673 [Zea mays] >gi|195636298|gb|ACG37617.1| MAPK activating protein [Zea mays]	Unigene37034_All//5.00E-124//AT4G21570| unknown protein	Unigene37034_All//2.00E-163//TC138019				nr +
Unigene37035_All	2072	8.89	6.68	5.47	14.02	12.35	16.28	21.45	9.38	13.44	-4.13E-01	1.40E-03		-6.99E-01	1.53E-07		-1.83E-01	8.29E-02		2.16E-01	2.58E-02		-1.19E+00	1.41E-52	Down	-6.74E-01	3.23E-21		Unigene37035_All//gi|225468815|ref|XP_002263544.1|//0.00E+00//PREDICTED: similar to EMB2762 (EMBRYO DEFECTIVE 2762) [Vitis vinifera]	Unigene37035_All//8.00E-178//AT2G17250| EMB2762 (EMBRYO DEFECTIVE 2762)	Unigene37035_All//0.00E+00//gi|13356550|gb|BG446898.1|BG446898				nr +
Unigene37039_All	1240	2.41	4.21	2.28	2.57	3.25	3.06	2.93	15.24	4.40	8.07E-01	2.11E-03		-7.96E-02	8.31E-01		3.38E-01	3.15E-01		2.51E-01	4.77E-01		2.38E+00	7.66E-59	Up	5.86E-01	8.00E-03		Unigene37039_All//gi|186510070|ref|NP_188099.2|//1.00E-110//MSL5 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 5) [Arabidopsis thaliana]	Unigene37039_All//1.00E-102//AT3G14810| MSL5 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 5)	Unigene37039_All//0.00E+00//gi|164278004|gb|ES825436.1|ES825436			GO:0006810//GO:0044464	nr -
Unigene3704_All	1577	1.06	1.06	2.03	20.44	13.82	6.19	1.29	3.42	2.63	-1.90E-03	9.94E-01		9.32E-01	1.04E-02		-5.64E-01	6.79E-11		-1.72E+00	1.00E-58	Down	1.41E+00	6.59E-09	Up	1.03E+00	9.34E-05	Up	Unigene3704_All//gi|224072174|ref|XP_002303637.1|//0.00E+00//proline transporter [Populus trichocarpa] >gi|222841069|gb|EEE78616.1|proline transporter [Populus trichocarpa]	Unigene3704_All//0.00E+00//AT5G41800| amino acid transporter family protein	Unigene3704_All//0.00E+00//TC142250				nr +
Unigene37041_All	485	19.85	15.67	13.07	30.50	83.71	67.70	43.94	60.41	32.04	-3.41E-01	7.27E-02		-6.03E-01	1.68E-03		1.46E+00	2.03E-62	Up	1.15E+00	3.65E-32	Up	4.59E-01	2.40E-07		-4.56E-01	1.05E-05		Unigene37041_All//gi|5051760|emb|CAB45053.1|//2.00E-57//thaumatin-like protein [Arabidopsis thaliana] >gi|7269268|emb|CAB79328.1|thaumatin-like protein [Arabidopsis thaliana]	Unigene37041_All//1.00E-58//AT4G24180| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to other organism; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Thaumatin, pathogenesis-related (InterPro:IPR001938); BEST Arabidopsis thaliana protein match is: thaumatin, putative (TAIR:AT4G38660.2); Has 1060 Blast hits to 1045 proteins in 143 species: Archae - 0; Bacteria - 22; Metazoa - 46; Fungi - 45; Plants - 935; Viruses - 3; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene37041_All//0.00E+00//TC140552			GO:0009607//GO:0031224	nr +
Unigene37042_All	684	34.57	18.30	23.82	78.58	191.66	167.12	39.19	54.87	39.49	-9.18E-01	2.08E-15		-5.37E-01	3.42E-06		1.29E+00	2.82E-167	Up	1.09E+00	1.49E-101	Up	4.86E-01	4.45E-10		1.10E-02	9.39E-01		Unigene37042_All//gi|110737096|dbj|BAF00500.1|//2.00E-57//thaumatin-like protein [Arabidopsis thaliana]	Unigene37042_All//3.00E-63//AT4G36000| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to other organism; LOCATED IN: cellular_component unknown; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Thaumatin, pathogenesis-related (InterPro:IPR001938); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24180.1); Has 1043 Blast hits to 945 proteins in 126 species: Archae - 0; Bacteria - 6; Metazoa - 42; Fungi - 41; Plants - 948; Viruses - 2; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene37042_All//0.00E+00//TC140552			GO:0031224	nr +
Unigene37043_All	1091	4.60	2.28	2.78	5.34	4.89	4.68	11.01	5.17	5.40	-1.02E+00	1.74E-04	Down	-7.27E-01	9.17E-03		-1.27E-01	6.42E-01		-1.92E-01	4.98E-01		-1.09E+00	6.68E-13	Down	-1.03E+00	3.68E-12	Down	Unigene37043_All//gi|227204413|dbj|BAH57058.1|//1.00E-29//AT5G12320 [Arabidopsis thaliana]	Unigene37043_All//2.00E-25//AT5G12320| ankyrin repeat family protein	Unigene37043_All//0.00E+00//TC177989			GO:0006519	nr -
Unigene37048_All	1027	3.11	2.12	3.21	14.50	20.82	17.06	5.39	3.26	1.67	-5.51E-01	1.16E-01		4.88E-02	8.95E-01		5.22E-01	2.44E-06		2.35E-01	1.02E-01		-7.28E-01	1.21E-03		-1.69E+00	4.12E-12	Down	Unigene37048_All//gi|225580063|gb|ACN94269.1|//7.00E-88//R283 Myb4b C2 repressor motif protein [Vitis vinifera]	Unigene37048_All//7.00E-72//AT4G38620| MYB4; DNA binding / transcription factor	Unigene37048_All//0.00E+00//TC165806	MYB		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene37049_All	1949	4.19	4.91	4.48	293.42	233.08	255.80	23.30	16.36	11.12	2.31E-01	2.39E-01		9.76E-02	6.41E-01		-3.32E-01	5.38E-70		-1.98E-01	1.97E-23		-5.10E-01	4.53E-13		-1.07E+00	2.56E-46	Down	Unigene37049_All//gi|224112579|ref|XP_002316233.1|//0.00E+00//laccase 3 [Populus trichocarpa] >gi|222865273|gb|EEF02404.1|laccase 3 [Populus trichocarpa]	Unigene37049_All//0.00E+00//AT5G01190| LAC10 (laccase 10); laccase	Unigene37049_All//0.00E+00//TC143117		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0016682//GO:0031410//GO:0046914	nr +
Unigene3705_All	1681	17.80	37.74	27.88	7.73	12.13	8.92	1.16	2.54	1.04	1.08E+00	2.67E-52	Up	6.47E-01	6.24E-16		6.49E-01	1.07E-08		2.06E-01	2.03E-01		1.13E+00	2.33E-05	Up	-1.50E-01	7.10E-01		Unigene3705_All//gi|124301082|gb|ABN04793.1|//1.00E-104//At4g24750 [Arabidopsis thaliana]	Unigene3705_All//1.00E-97//AT4G24750| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763); BEST Arabidopsis thaliana protein match is: rhodanese-like domain-containing protein (TAIR:AT3G08920.1); Has 222 Blast hits to 222 proteins in 59 species: Archae - 8; Bacteria - 82; Metazoa - 0; Fungi - 0; Plants - 88; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink).	Unigene3705_All//0.00E+00//TC145301		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene37050_All	494	2.33	1.13	3.02	4.24	4.04	2.01	16.86	9.05	8.31	-1.05E+00	1.01E-01		3.73E-01	5.11E-01		-6.70E-02	8.77E-01		-1.07E+00	1.61E-02		-8.97E-01	6.81E-07		-1.02E+00	1.20E-08	Down	Unigene37050_All//gi|223452460|gb|ACM89557.1|//5.00E-22//receptor-like protein kinase [Glycine max]	Unigene37050_All//7.00E-20//AT1G07650| leucine-rich repeat transmembrane protein kinase, putative	Unigene37050_All//0.00E+00//TC167179		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152	nr -
Unigene37051_All	690	3.56	0.29	4.01	11.91	9.48	6.09	19.30	2.24	1.15	-3.60E+00	5.09E-10	Down	1.71E-01	6.52E-01		-3.29E-01	1.09E-01		-9.69E-01	1.17E-06		-3.11E+00	1.15E-55	Down	-4.06E+00	3.65E-72	Down	Unigene37051_All//gi|223452460|gb|ACM89557.1|//2.00E-21//receptor-like protein kinase [Glycine max]	Unigene37051_All//6.00E-20//AT1G29720| protein kinase family protein	Unigene37051_All//0.00E+00//TC161349		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674//GO:0008152//GO:0016491	nr +
Unigene37052_All	901	21.43	7.14	7.03	42.18	32.10	44.81	24.78	8.58	10.48	-1.59E+00	4.70E-29	Down	-1.61E+00	1.76E-28	Down	-3.94E-01	7.76E-07		8.72E-02	3.94E-01		-1.53E+00	7.44E-39	Down	-1.24E+00	2.34E-29	Down	Unigene37052_All//gi|225470846|ref|XP_002266597.1|//6.00E-88//PREDICTED: similar to nascent polypeptide associated complex alpha [Vitis vinifera]	Unigene37052_All//2.00E-58//AT3G12390| nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative	Unigene37052_All//0.00E+00//TC132501			GO:0005840//GO:0006810//GO:0006970	nr +
Unigene37056_All	1493	2.38	0.98	0.89	2.84	2.03	2.60	3.31	1.88	1.92	-1.28E+00	1.51E-04	Down	-1.42E+00	6.59E-05	Down	-4.83E-01	9.80E-02		-1.25E-01	6.88E-01		-8.21E-01	6.41E-04		-7.86E-01	7.47E-04		Unigene37056_All//gi|297794983|ref|XP_002865376.1|//1.00E-98//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297311211|gb|EFH41635.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene37056_All//1.00E-129//AT5G44230| pentatricopeptide (PPR) repeat-containing protein	Unigene37056_All//0.00E+00//gi|109850936|gb|DW479915.1|DW479915				nr -
Unigene37057_All	215	0.00	4.71	0.00	2.78	0.32	2.10	0.00	0.19	8.71	1.22E+01	7.26E-06	Up	null	null		-3.12E+00	4.87E-03		-4.04E-01	6.73E-01		7.60E+00	6.34E-01		1.31E+01	1.95E-13	Up							
Unigene37058_All	2101	0.97	8.10	0.05	1.26	0.87	2.86	11.03	4.30	60.81	3.06E+00	8.49E-57	Up	-4.26E+00	6.89E-09	Down	-5.33E-01	1.64E-01		1.19E+00	1.19E-06	Up	-1.36E+00	6.75E-34	Down	2.46E+00	0.00E+00	Up	Unigene37058_All//gi|224126717|ref|XP_002319909.1|//1.00E-130//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372108|gb|ABQ62985.1| RAP2-like protein [Populus trichocarpa] >gi|222858285|gb|EEE95832.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene37058_All//7.00E-43//AT2G20880| AP2 domain-containing transcription factor, putative	Unigene37058_All//0.00E+00//C0106720	AP2-EREBP		GO:0006350//GO:0043231	nr +
Unigene37059_All	952	10.06	6.76	5.20	13.45	13.02	13.28	9.90	7.90	32.35	-5.73E-01	1.97E-03		-9.51E-01	1.03E-06		-4.64E-02	8.31E-01		-1.77E-02	9.37E-01		-3.26E-01	6.07E-02		1.71E+00	1.61E-63	Up	Unigene37059_All//gi|22531416|emb|CAD30274.1|//1.00E-117//IAA16 protein [Gossypium hirsutum]	Unigene37059_All//9.00E-50//AT3G04730| IAA16; transcription factor	Unigene37059_All//0.00E+00//TC130814			GO:0009725//GO:0009987//GO:0010467	nr +
Unigene3706_All	886	0.30	0.00	0.00	2.19	7.93	2.34	6.92	2.03	9.22	-8.21E+00	6.70E-02		-8.21E+00	8.56E-02		1.85E+00	2.61E-15	Up	9.68E-02	8.48E-01		-1.77E+00	1.19E-13	Down	4.14E-01	2.01E-02		Unigene3706_All//gi|283132373|dbj|BAI63592.1|//4.00E-45//BTB/POZ domain-containing protein [Lotus japonicus]	Unigene3706_All//4.00E-43//AT3G48360| BT2 (BTB AND TAZ DOMAIN PROTEIN 2); protein binding / transcription factor/ transcription regulator	Unigene3706_All//0.00E+00//EX168343		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene37060_All	609	21.13	10.07	9.01	7.69	8.54	7.42	9.03	3.09	2.88	-1.07E+00	4.92E-11	Down	-1.23E+00	5.28E-13	Down	1.51E-01	6.13E-01		-5.21E-02	8.74E-01		-1.55E+00	2.61E-10	Down	-1.65E+00	1.30E-11	Down	Unigene37060_All//gi|109946601|gb|AB618479.1|//5.00E-97//At5g18460 [Arabidopsis thaliana]	Unigene37060_All//3.00E-98//AT5G18460| unknown protein	Unigene37060_All//0.00E+00//gi|78324750|gb|DT545024.1|DT545024			GO:0031410	nr -

Unigene37061_All	1847	10.31	5.08	7.44	5.96	4.53	3.77	4.81	2.26	3.41	-1.02E+00	7.11E-15	Down	-4.71E-01	3.27E-04		-3.96E-01	1.75E-02		-6.63E-01	7.47E-05		-1.09E+00	1.03E-09	Down	-4.96E-01	3.08E-03		Unigene37061_All//gi|109946601|gb|ABG48479.1|//1.00E-175//At5g18460 [Arabidopsis thaliana]	Unigene37061_All//6.00E-175//AT5G18460| unknown protein	Unigene37061_All//0.00E+00//gi|78354832|gb|DT575106.1|DT575106				nr +
Unigene37063_All	394	5.05	7.20	3.38	3.41	6.12	8.02	6.65	10.93	6.57	5.13E-01	1.73E-01		-5.79E-01	2.40E-01		8.42E-01	3.92E-02		1.23E+00	5.18E-04	Up	7.16E-01	6.03E-03		-1.76E-02	9.73E-01		Unigene37063_All//gi|227202702|dbj|BAH56824.1|//1.00E-21//AT3G12350 [Arabidopsis thaliana]	Unigene37063_All//7.00E-13//AT3G12350| F-box family protein	Unigene37063_All//2.00E-111//gi|78339182|gb|DT559456.1|DT559456			GO:0005488	nr +
Unigene37064_All	1843	4.23	12.59	6.10	4.22	4.45	5.07	5.37	10.57	9.23	1.57E+00	3.03E-34	Up	5.27E-01	2.79E-03		7.68E-02	7.82E-01		2.67E-01	1.96E-01		9.77E-01	3.42E-17		7.82E-01	6.41E-11		Unigene37064_All//gi|157951155|dbj|BAB03143.1|//1.00E-109//ankyrin-like protein [Arabidopsis thaliana]	Unigene37064_All//4.00E-101//AT3G12350| F-box family protein	Unigene37064_All//0.00E+00//gi|78339182|gb|DT559456.1|DT559456				nr +
Unigene37065_All	983	100.06	141.70	136.46	33.75	40.99	29.82	4.99	4.21	2.07	5.02E-01	1.81E-30		4.48E-01	4.17E-23		2.80E-01	5.06E-04		-1.79E-01	7.65E-02		-2.45E-01	3.67E-01		-1.27E+00	2.26E-07	Down	Unigene37065_All//gi|225380890|gb|ACN38686.1|//3.00E-99//dehydroascorbate reductase [Malus x domestica]	Unigene37065_All//4.00E-99//AT5G16710| DHAR3 (dehydroascorbate reductase 1); glutathione dehydrogenase (ascorbate)	Unigene37065_All//0.00E+00//gi|109878389|gb|DW507360.1|DW507360		ko00480|Glutathione metabolism//ko00350|Tyrosine metabolism	GO:0005488//GO:0006464//GO:0009526//GO:0009532//GO:0015038	nr +
Unigene37067_All	344	14.75	104.28	24.15	35.48	32.03	40.04	258.60	323.43	413.67	2.82E+00	9.92E-110	Up	7.11E-01	6.44E-04		-1.47E-01	4.30E-01		1.75E-01	3.21E-01		3.23E-01	1.20E-13		6.78E-01	3.17E-66				Unigene37067_All//4.00E-146//TC139498				
Unigene37069_All	1239	35.39	51.45	43.45	28.22	41.27	46.48	18.09	6.04	13.38	5.40E-01	2.73E-16		2.96E-01	7.44E-05		5.48E-01	9.06E-16		7.20E-01	8.14E-26		-1.58E+00	5.94E-41	Down	-4.35E-01	1.53E-05		Unigene37069_All//gi|5042435|gb|AAD38274.1|AC006193_30//1.00E-123//Unknown protein [Arabidopsis thaliana] >gi|34146814|gb|AAQ62415.1|At1g61980 [Arabidopsis thaliana]	Unigene37069_All//5.00E-124//AT1G61980| unknown protein	Unigene37069_All//0.00E+00//TC136280				nr +
Unigene3707_All	1321	0.00	0.00	0.00	1.92	3.73	1.13	4.42	0.70	7.45	null	null		null	null		9.55E-01	2.42E-04		-7.70E-01	5.39E-02		-2.67E+00	3.25E-21	Down	7.54E-01	2.44E-06		Unigene3707_All//gi|15242656|ref|NP_201121.1|//1.00E-103//BT1 (BTB AND TAZ DOMAIN PROTEIN 1); protein binding / transcription regulator [Arabidopsis thaliana] >gi|36955895|gb|AAQ87004.1| BTB and TAZ domain protein 1 [Arabidopsis thaliana] >gi|38603810|gb|AAR24650.1|At5g63160 [Arabidopsis thaliana]	Unigene3707_All//6.00E-98//AT5G63160| BT1 (BTB AND TAZ DOMAIN PROTEIN 1); protein binding / transcription regulator	Unigene3707_All//0.00E+00//TC177284		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene37070_All	2310	3.62	5.62	1.34	9.75	5.47	13.41	9.94	11.94	10.28	6.32E-01	5.33E-05		-1.44E+00	7.57E-11	Down	-8.33E-01	5.14E-15		4.61E-01	1.03E-06		2.65E-01	5.13E-03		4.85E-02	6.68E-01		Unigene37070_All//gi|145335038|ref|NP_171852.2|//9.00E-99//NAF1 (NUCLEAR ASSEMBLY FACTOR 1) [Arabidopsis thaliana] >gi|9280664|gb|AAF86533.1|AC002560_26 F21B7.15 [Arabidopsis thaliana]	Unigene37070_All//1.00E-67//AT1G03530| NAF1 (NUCLEAR ASSEMBLY FACTOR 1)	Unigene37070_All//0.00E+00//TC161068		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene37071_All	342	5.20	3.70	1.87	4.81	1.41	4.49	9.89	7.82	1.63	-4.90E-01	3.25E-01		-1.48E+00	5.78E-03		-1.77E+00	4.68E-04	Down	-9.83E-02	8.59E-01		-3.39E-01	2.92E-01		-2.60E+00	1.04E-12	Down	Unigene37071_All//gi|115475557|ref|NP_001061375.1|//4.00E-13//Os08g0250700 [Oryza sativa Japonica Group] >gi|113623344|dbj|BAF23289.1|Os08g0250700 [Oryza sativa Japonica Group]	Unigene37071_All//8.00E-11//AT3G25580| thioredoxin-related	Unigene37071_All//6.00E-157//TC136784			GO:0019725	nr +
Unigene37079_All	1440	30.05	26.46	19.12	54.90	46.99	40.55	71.32	43.62	32.40	-1.83E-01	3.10E-02		-6.52E-01	5.98E-15		-2.24E-01	4.81E-05		-4.37E-01	8.91E-15		-7.09E-01	8.72E-51		-1.14E+00	5.02E-115	Down	Unigene37079_All//gi|15450794|gb|AAO96668.1|//1.00E-110//transmembrane protein FT27/PFT27-like [Arabidopsis thaliana] >gi|21537321|gb|AAM61662.1| transmembrane protein FT27/PFT27-like [Arabidopsis thaliana] >gi|32362303|gb|AAF80179.1|At5g36290 [Arabidopsis thaliana]	Unigene37079_All//1.00E-93//AT5G36290| unknown protein	Unigene37079_All//0.00E+00//TC174949			GO:0031410	nr +
Unigene3708_All	1574	6.22	33.70	11.71	22.66	33.49	40.77	26.19	53.00	41.26	2.44E+00	7.85E-138	Up	9.13E-01	1.48E-11		5.64E-01	4.64E-17		8.48E-01	6.75E-38		1.02E+00	9.00E-76	Up	6.56E-01	5.19E-29		Unigene3708_All//gi|15240744|ref|NP_196342.1|//1.00E-127//ATRBL3 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 3) [Arabidopsis thaliana] >gi|7546703|emb|CAB87281.1| membrane protein [Arabidopsis thaliana] >gi|16648762|gb|AAL25572.1|AT5g07250/T28J14_190 [Arabidopsis thaliana] >gi|20466143|gb|AAM19993.1|AT5g07250/T28J14_190 [Arabidopsis thaliana]	Unigene3708_All//6.00E-79//AT5G07250| ATRBL3 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 3)	Unigene3708_All//0.00E+00//TC143724				nr +
Unigene37080_All	1832	5.83	12.34	6.25	10.20	13.51	12.13	11.56	9.72	9.31	1.08E+00	4.75E-19	Up	1.01E-01	6.25E-01		4.06E-01	8.33E-05		2.50E-01	4.02E-02		-2.51E-01	2.39E-02		-3.13E-01	2.88E-03		Unigene37080_All//gi|18394964|ref|NP_564136.1|//1.00E-160//transcription factor [Arabidopsis thaliana] >gi|8920640|gb|AAF81382.1|AC036104_11 Contains weak similarity to DNA-binding protein (GT-1a) from Nicotiana tabacum gb|M93436 [Arabidopsis thaliana]	Unigene37080_All//8.00E-123//AT1G21200| transcription factor	Unigene37080_All//0.00E+00//gi|109875045|gb|DW504019.1|DW504019			GO:0003676	nr -
Unigene37081_All	2145	32.05	9.38	19.59	41.52	37.95	32.13	11.04	5.77	4.53	-1.77E+00	2.36E-119	Down	-7.11E-01	4.09E-27		-1.30E-01	2.14E-02		-3.70E-01	2.55E-12		-9.37E-01	2.19E-19		-1.28E+00	9.86E-33	Down	Unigene37081_All//gi|297814043|ref|XP_002874905.1|//1.00E-176//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320742|gb|EFH51164.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37081_All//2.00E-169//AT4G02630| protein kinase family protein	Unigene37081_All//0.00E+00//gi|164263254|gb|ES807940.1|ES807940		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004713//GO:0004871//GO:0006464//GO:0032559	nr +
Unigene37083_All	1171	2.64	32.32	3.77	2.89	14.09	23.64	13.90	30.73	202.46	3.62E+00	2.58E-146	Up	5.18E-01	8.81E-02		2.28E+00	2.51E-46	Up	3.03E+00	1.32E-97	Up	1.14E+00	5.58E-40	Up	3.86E+00	0.00E+00	Up	Unigene37083_All//gi|259121375|gb|ACV92007.1|//1.00E-101//WRKY transcription factor 5 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene37083_All//2.00E-70//AT1G80840| WRKY40; transcription factor	Unigene37083_All//0.00E+00//TC148447	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0010467	nr -
Unigene37086_All	1910	3.42	5.01	2.62	9.88	7.28	4.00	10.58	12.28	7.28	5.50E-01	3.05E-03		-3.86E-01	1.21E-01		-4.41E-01	2.01E-04		-1.31E+00	4.44E-23	Down	2.14E-01	4.46E-02		-5.40E-01	4.17E-07		Unigene37086_All//gi|115483498|ref|NP_001065419.1|//0.00E+00//Os10g0565300 [Oryza sativa Japonica Group] >gi|113639951|dbj|BAF27256.1|Os10g0565300 [Oryza sativa Japonica Group]	Unigene37086_All//0.00E+00//AT4G17140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pleckstrin homology (InterPro:IPR001849); BEST Arabidopsis thaliana protein match is: phosphoinositide binding (TAIR:AT1G48090.2); Has 1924 Blast hits to 1182 proteins in 161 species: Archae - 0; Bacteria - 16; Metazoa - 911; Fungi - 304; Plants - 271; Viruses - 0; Other Eukaryotes - 422 (source: NCBI BLink).	Unigene37086_All//0.00E+00//TC148809			GO:0033036//GO:0043231	nr +
Unigene37087_All	1031	2.44	0.88	1.24	230.18	238.07	201.90	10.99	6.57	3.94	-1.46E+00	4.79E-04	Down	-9.75E-01	2.06E-02		4.87E-02	1.99E-01		-1.89E-01	2.74E-09		-7.43E-01	8.42E-07		-1.48E+00	8.63E-20	Down	Unigene37087_All//gi|150416577|gb|ABR68796.1|//1.00E-125//arabinogalactan protein 4 [Gossypium hirsutum]	Unigene37087_All//3.00E-56//AT5G60490| FLA12	Unigene37087_All//0.00E+00//TC150633			GO:0016020	nr +
Unigene37088_All	961	45.08	28.16	38.46	20.89	22.50	20.68	9.11	4.48	9.99	-6.79E-01	1.04E-16		-2.29E-01	8.13E-03		1.07E-01	4.49E-01		-1.47E-02	9.34E-01		-1.02E+00	9.05E-09	Down	1.34E-01	4.69E-01		Unigene37088_All//gi|115454377|ref|NP_001050789.1|//2.00E-31//Os03g0651000 [Oryza sativa Japonica Group] >gi|62733418|gb|AAX95535.1| Putative Glutamyl-tRNA(Gln) amidotransferase, C subunit [Oryza sativa Japonica Group] >gi|108710125|gb|ABF97920.1| glutamyl-tRNA amidotransferase, C subunit family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549260|dbj|BAF12703.1|Os03g0651000 [Oryza sativa Japonica Group]	Unigene37088_All//2.00E-30//AT4G32915| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: regulation of translational fidelity; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Glu-tRNAGln amidotransferase, C subunit (InterPro:IPR003837); Has 1227 Blast hits to 1227 proteins in 425 species: Archae - 17; Bacteria - 884; Metazoa - 0; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 309 (source: NCBI BLink).	Unigene37088_All//0.00E+00//gi|109874664|gb|DW503638.1|DW503638		ko00970|Aminoacyl-tRNA biosynthesis	GO:0003824//GO:0006448//GO:0009536	nr -
Unigene37089_All	2226	14.22	5.62	8.78	9.60	6.95	8.38	7.65	6.74	4.87	-1.34E+00	8.25E-37	Down	-6.96E-01	2.28E-12		-4.67E-01	2.09E-05		-1.96E-01	1.34E-01		-1.83E-01	1.65E-01		-6.53E-01	2.89E-08		Unigene37089_All//gi|88909724|sp|Q8GK20.2|YS390_ARATH//0.00E-00//Rec Name: Full=Uncharacterized protein At5g03900; Flags: Precursor	Unigene37089_All//2.00E-174//AT5G03900| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: FeS cluster biogenesis (InterPro:IPR000361); Has 98 Blast hits to 98 proteins in 40 species: Archae - 0; Bacteria - 53; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink).	Unigene37089_All//0.00E+00//DR458079			GO:0009526	nr -
Unigene3709_All	1674	12.44	5.90	8.81	13.69	11.85	11.09	14.75	13.43	14.85	-1.08E+00	1.61E-17	Down	-4.98E-01	6.40E-05		-2.08E-01	8.00E-02		-3.04E-01	8.73E-03		-1.35E-01	2.30E-01		9.80E-03	9.52E-01		Unigene3709_All//gi|113367246|gb|AB134680.1|//1.00E-105//bZIP transcription factor bZIP121 [Glycine max]	Unigene3709_All//6.00E-88//AT2G16770| DNA binding / transcription factor	Unigene3709_All//0.00E+00//TC179395	bZIP			nr -
Unigene37090_All	1334	5.10	3.57	4.87	8.22	5.78	3.39	3.99	2.01	1.08	-5.14E-01	2.29E-02		-6.62E-02	7.82E-01		-5.07E-01	1.71E-03		-1.28E+00	3.32E-13	Down	-9.94E-01	2.01E-05		-1.89E+00	1.74E-13	Down	Unigene37090_All//gi|124360746|gb|ABN08723.1|//8.00E-11//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene37090_All//4.00E-10//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene37090_All//6.00E-179//TC136056				nr -
Unigene37091_All	283	4.81	0.72	1.13	5.28	4.87	3.51	3.29	2.66	1.97	-2.75E+00	1.08E-04	Down	-2.09E+00	1.95E-03		-1.18E-01	8.23E-01		-5.89E-01	3.04E-01		-3.06E-01	6.21E-01		-7.38E-01	2.33E-01				Unigene37091_All//9.00E-159//TC137666				ESTscan +
Unigene37094_All	1385	34.07	82.97	36.41	5.07	5.69	11.84	1.98	1.42	1.06	1.28E+00	3.85E-123	Up	9.56E-02	2.79E-01		1.67E-01	5.06E-01		1.22E+00	6.26E-18	Up	-4.85E-01	1.64E-01		-8.99E-01	5.97E-03		Unigene37094_All//gi|144925078|gb|ABP03876.1|//1.00E-120//Hly-III related proteins [Medicago truncatula]	Unigene37094_All//1.00E-71//AT5G20270| HHP1 (HEPTAHELICAL TRANSMEMBRANE PROTEIN1); receptor	Unigene37094_All//0.00E+00//TC151992			GO:0004871//GO:0006970//GO:0009719//GO:0031224//GO:0034285	nr +
Unigene37095_All	1172	12.59	8.82	6.68	32.01	29.00	18.50	10.61	1.43	4.15	-5.13E-01	4.13E-04		-9.15E-01	2.19E-09		-1.42E-01	1.35E-01		-7.91E-01	3.96E-20		-2.89E+00	1.77E-48	Down	-1.35E+00	4.86E-19	Down	Unigene37095_All//gi|297794689|ref|XP_002865229.1|//2.00E-57//NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311064|gb|EFH41488.1| NLI interacting factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37095_All//9.00E-55//AT5G45700| NLI interacting factor (NIF) family protein	Unigene37095_All//0.00E+00//TC174926			GO:0016791	nr -

Unigene37096_All	1164	5.35	1.65	1.46	14.51	10.41	4.89	12.06	8.04	10.30	-1.69E+00	9.09E-11	Down	-1.87E+00	1.18E-11	Down	-4.78E-01	1.40E-04		-1.57E+00	4.00E-27	Down	-5.84E-01	1.15E-05		-2.27E-01	9.85E-02		Unigene37096_All//gi|15229606|ref|NP_190544.1|//1.00E-111//AtRLP44 (Receptor Like Protein 44); protein binding [Arabidopsis thaliana] >gi|30102624|gb|AAP21230.1|At3g49750 [Arabidopsis thaliana]	Unigene37096_All//2.00E-91//AT3G49750| AtRLP44 (Receptor Like Protein 44); protein binding	Unigene37096_All//0.00E+00//DN779584		ko04626|Plant-pathogen interaction	GO:0043231	nr +
Unigene37098_All	1500	4.33	7.30	5.18	5.61	5.33	6.80	16.52	6.13	7.73	7.54E-01	1.26E-05		2.61E-01	2.54E-01		-7.56E-02	7.70E-01		2.78E-01	1.51E-01		-1.43E+00	5.25E-39	Down	-1.10E+00	9.05E-27	Down	Unigene37098_All//gi|226509304|ref|NP_001149563.1|//1.00E-135//LOC100283189 [Zea mays] >gi|195628028|gb|ACG35814.1| NADP-dependent oxidoreductase P1 [Zea mays]	Unigene37098_All//4.00E-132//AT1G65560| allyl alcohol dehydrogenase, putative	Unigene37098_All//0.00E+00//ES825728				nr -
Unigene37099_All	1325	9.24	22.49	20.17	43.91	59.38	138.39	20.20	81.70	62.06	1.28E+00	2.27E-32	Up	1.13E+00	4.68E-23	Up	4.36E-01	5.86E-16		1.66E+00	0.00E+00	Up	2.02E+00	4.22E-272	Up	1.62E+00	3.89E-156	Up	Unigene37099_All//gi|297796583|ref|XP_002866176.1|//7.00E-45//AT5g56980/MEM17_10 [Arabidopsis lyrata subsp. lyrata] >gi|297312011|gb|EFH42435.1|AT5g56980/MEM17_10 [Arabidopsis lyrata subsp. lyrata]	Unigene37099_All//5.00E-36//AT5G56980| unknown protein	Unigene37099_All//0.00E+00//TC136700				nr -
Unigene3710_All	624	1.68	1.62	0.68	8.14	4.41	3.47	1.56	0.40	0.38	-4.62E-02	9.57E-01		-1.30E+00	7.46E-02		-8.83E-01	3.49E-04		-1.23E+00	4.12E-06	Down	-1.96E+00	4.44E-03		-2.02E+00	2.47E-03		Unigene3710_All//gi|17064874|gb|AAL32591.1|//3.00E-16//Unknown protein [Arabidopsis thaliana] >gi|27311933|gb|AAO00932.1|Unknown protein [Arabidopsis thaliana]	Unigene3710_All//2.00E-17//AT4G14200| unknown protein	Unigene3710_All//0.00E+00//gi|164350639|gb|ES819946.1|ES819946				nr +
Unigene37100_All	1308	2.36	1.24	1.67	4.15	3.53	1.97	7.43	3.00	2.53	-9.29E-01	8.94E-03		-5.00E-01	1.85E-01		-2.35E-01	4.07E-01		-1.08E+00	2.21E-05	Down	-1.31E+00	7.10E-14	Down	-1.56E+00	2.29E-18	Down	Unigene37100_All//gi|240256302|ref|NP_197227.4|//6.00E-94//catalytic/ transferase [Arabidopsis thaliana]	Unigene37100_All//3.00E-82//AT5G17250| catalytic/ transferase	Unigene37100_All//0.00E+00//TC161744			GO:0043231	nr +
Unigene37108_All	1274	4.64	4.18	3.72	4.73	4.05	5.39	8.06	5.84	3.10	-1.52E-01	5.74E-01		-3.19E-01	2.39E-01		-2.23E-01	4.06E-01		1.88E-01	4.82E-01		-4.66E-01	3.55E-03		-1.38E+00	2.43E-16	Down	Unigene37108_All//gi|30102890|gb|AAP21363.1|//4.00E-24//At4g38290 [Arabidopsis thaliana]	Unigene37108_All//2.00E-25//AT4G38280| unknown protein	Unigene37108_All//0.00E+00//TC164146				nr +
Unigene3711_All	1659	0.98	2.44	1.38	3.48	4.19	3.43	1.15	0.88	1.18	1.32E+00	2.84E-05	Up	4.97E-01	2.62E-01		2.68E-01	2.77E-01		-2.21E-02	9.48E-01		-3.79E-01	4.07E-01		3.71E-02	9.50E-01		Unigene3711_All//gi|17064874|gb|AAL32591.1|//2.00E-16//Unknown protein [Arabidopsis thaliana] >gi|27311933|gb|AAO00932.1|Unknown protein [Arabidopsis thaliana]	Unigene3711_All//1.00E-17//AT4G14200| unknown protein	Unigene3711_All//0.00E+00//gi|164350639|gb|ES819946.1|ES819946				nr +
Unigene37111_All	809	8.02	5.45	8.62	7.14	6.73	5.42	5.12	1.76	1.87	-5.58E-01	1.59E-02		1.05E-01	6.58E-01		-8.69E-02	7.86E-01		-4.00E-01	1.23E-01		-1.54E+00	6.15E-08	Down	-1.45E+00	1.35E-07	Down	Unigene37111_All//gi|2494127|gb|AAB80636.1|//1.00E-98//Contains similarity to Mycobacterium LIPB gene (gb|Q104041) [Arabidopsis thaliana]	Unigene37111_All//2.00E-89//AT1G04640| LIP2 (LIPOYLTRANSFERASE 2); lipoyltransferase	Unigene37111_All//0.00E+00//ES847401		ko00785|Lipoic acid metabolism	GO:0008415//GO:0009105//GO:0018065//GO:0043231	nr +
Unigene37117_All	1152	45.46	8.44	12.80	60.93	52.76	75.27	95.42	27.90	45.16	-2.43E+00	1.74E-136	Down	-1.83E+00	9.07E-92	Down	-2.08E-01	5.20E-04		3.05E-01	1.64E-08		-1.77E+00	4.79E-233	Down	-1.08E+00	6.36E-113	Down	Unigene37117_All//gi|17367847|sp|Q9XF97.1|RL4_PRUAR//1.00E-161//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32206.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene37117_All//6.00E-152//AT3G09630| 60S ribosomal protein L4/L1 (RPLA4)	Unigene37117_All//0.00E+00//TC133143		ko03010|Ribosome		nr -
Unigene37120_All	272	0.58	5.40	1.57	2.56	1.14	3.65	13.83	11.83	21.38	3.23E+00	1.15E-05	Up	1.44E+00	2.53E-01		-1.17E+00	1.61E-01		5.11E-01	4.92E-01		-2.26E-01	4.71E-01		6.28E-01	3.18E-03		Unigene37120_All//gi|297829824|ref|XP_002882794.1|//2.00E-24//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328634|gb|EFH59053.1|oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene37120_All//9.00E-26//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene37120_All//2.00E-128//TC134433		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0008152//GO:0016701//GO:0016706	nr -
Unigene37121_All	1590	0.46	3.54	1.31	1.22	0.89	1.59	12.29	8.91	16.79	2.94E+00	2.15E-18	Up	1.50E+00	2.09E-03		-4.61E-01	3.22E-01		3.81E-01	3.95E-01		-4.63E-01	3.03E-05		4.50E-01	9.08E-07		Unigene37121_All//gi|297829824|ref|XP_002882794.1|//1.00E-110//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328634|gb|EFH59053.1|oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene37121_All//3.00E-111//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene37121_All//0.00E+00//TC134433		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0016491	nr -
Unigene37122_All	801	25.67	23.15	11.97	28.36	21.02	26.84	42.44	31.36	33.37	-1.49E-01	2.63E-01		-1.10E+00	3.36E-17	Down	-4.32E-01	5.05E-05		-7.95E-02	5.96E-01		-4.37E-01	1.02E-07		-3.47E-01	1.65E-05		Unigene37122_All//gi|18398673|ref|NP_566360.1|//8.00E-73//ankyrin repeat family protein [Arabidopsis thaliana] >gi|89001029|gb|ABD59104.1|At3g09890 [Arabidopsis thaliana]	Unigene37122_All//1.00E-66//AT3G09890| ankyrin repeat family protein	Unigene37122_All//0.00E+00//gi|78322849|gb|DT543123.1|DT543123				nr +
Unigene37123_All	865	33.51	24.72	28.50	58.28	64.09	54.51	38.57	22.66	16.03	-4.39E-01	1.19E-05		-2.34E-01	3.27E-02		1.37E-01	7.02E-02		-9.65E-02	2.77E-01		-7.67E-01	1.95E-19		-1.27E+00	8.45E-45	Down	Unigene37123_All//gi|15229863|ref|NP_187151.1|//5.00E-77//transport protein particle (TRAPP) component Bet3 family protein [Arabidopsis thaliana]	Unigene37123_All//2.00E-78//AT3G05000| transport protein particle (TRAPP) component Bet3 family protein	Unigene37123_All//0.00E+00//TC134834			GO:0003006//GO:0005506//GO:0006164//GO:0009975	nr -
Unigene37124_All	1032	177.39	99.08	167.80	42.86	71.07	40.48	0.00	0.57	0.23	-8.40E-01	1.81E-98		-8.02E-02	6.29E-02		7.30E-01	5.45E-37		-8.25E-02	3.98E-01		9.15E+00	2.81E-04	Up	7.86E+00	4.39E-02		Unigene37124_All//gi|42565672|ref|NP_566886.2|//2.00E-97//PTAC16 (PLASTID TRANSCRIPTIONALLY ACTIVE 16); binding / catalytic [Arabidopsis thaliana]	Unigene37124_All//6.00E-84//AT3G46780| PTAC16 (PLASTID TRANSCRIPTIONALLY ACTIVE 16); binding / catalytic	Unigene37124_All//0.00E+00//TC133990			GO:0000229//GO:0009526//GO:0009534	nr +
Unigene37125_All	1116	73.93	128.31	98.29	51.06	141.17	116.59	23.19	39.96	57.76	7.95E-01	4.66E-70		4.11E-01	2.59E-16		1.47E+00	6.17E-245	Up	1.19E+00	2.18E-133	Up	7.85E-01	1.04E-26		1.32E+00	3.07E-90	Up	Unigene37125_All//gi|89258512|gb|AB065465.1|//1.00E-126//protein phosphatase 2C [Gossypium hirsutum]	Unigene37125_All//1.00E-84//AT3G11410| PP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA); protein binding / protein serine/threonine phosphatase	Unigene37125_All//0.00E+00//TC173820			GO:0004721//GO:0005488//GO:0006950//GO:0009738//GO:0010118	nr -
Unigene37130_All	1569	0.20	0.68	1.09	147.79	86.80	82.01	295.10	229.81	237.53	1.76E+00	1.43E-02		2.44E+00	7.80E-05	Up	-7.68E-01	1.42E-131		-8.50E-01	1.05E-137		-3.61E-01	1.34E-66		-3.13E-01	1.52E-52		Unigene37130_All//gi|18394832|ref|NP_564107.1|//1.00E-155//AT5B75.2; identical protein binding / serine-type endopeptidase [Arabidopsis thaliana] >gi|8778982|gb|AAF79897.1|AC022472_6 Contains similarity to p69c gene from Lycopersicon esculentum gb|Y17277 and is a member of subtilase family PF|00082. ESTs gb|T22485, gb|R65370, gb|AA651071 come from this gene [Arabidopsis thaliana]	Unigene37130_All//3.00E-152//AT1G20160| AT5B75.2; identical protein binding / serine-type endopeptidase	Unigene37130_All//0.00E+00//gi|109847156|gb|DW476136.1|DW476136		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene37133_All	988	35.27	30.51	14.34	71.14	43.18	57.05	46.35	32.19	19.96	-2.09E-01	2.75E-02		-1.30E+00	3.24E-37	Down	-7.20E-01	8.82E-36		-3.19E-01	1.34E-07		-5.26E-01	7.08E-14		-1.22E+00	2.35E-57	Down	Unigene37133_All//gi|15218053|ref|NP_172962.1|//3.00E-40//RHA2A; protein binding / ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana] >gi|50401214|sp|Q9ZT50.1|RHA2A_ARATH RecName: Full=E3 ubiquitin-protein ligase RHA2A; AltName: Full=RING-H2 zinc finger protein RHA2a >gi|5103808|gb|AAD39638.1|AC007591_3 Identical to gb|AF078822 RING-H2 finger RHA2a protein from Arabidopsis thaliana. ESTs gb|N37587, gb|T04684, gb|AA394318, gb|Z35014 and gb|AA713343 come from this gene >gi|3796569|gb|AAC68671.1| RING-H2 finger protein RHA2a [Arabidopsis thaliana] >gi|19715570|gb|AAL91611.1|At1g15100/F9L1_3 [Arabidopsis thaliana] >gi|20334914|gb|AAM16213.1|At1g15100/F9L1_3 [Arabidopsis thaliana] >gi|66865898|gb|AAY57583.1| RING finger family protein [Arabidopsis thaliana]	Unigene37133_All//3.00E-41//AT1G15100| RHA2A; protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene37133_All//0.00E+00//gi|109874925|gb|DW503899.1|DW503899			GO:0006970//GO:0009738//GO:0019787//GO:0032446//GO:0046914//GO:0080134	nr -
Unigene37136_All	962	1.41	13.38	1.83	3.06	1.58	0.70	4.35	1.87	5.01	3.24E+00	1.89E-45	Up	3.69E-01	4.72E-01		-9.56E-01	5.29E-03		-2.12E+00	1.62E-07	Down	-1.22E+00	7.61E-06	Down	2.04E-01	4.30E-01		Unigene37136_All//gi|221329408|gb|ACM18110.1|//2.00E-32//growth-regulating factor 10 [Oryza sativa Indica Group]	Unigene37136_All//3.00E-29//AT3G13960| AtGRF5 (GROWTH-REGULATING FACTOR 5); transcription activator	Unigene37136_All//1.00E-154//DR461662	GRF			nr +
Unigene3714_All	1409	5.61	4.78	5.37	11.17	9.53	7.18	14.40	10.56	6.28	-2.29E-01	3.02E-01		-6.32E-02	7.74E-01		-2.29E-01	1.19E-01		-6.38E-01	2.99E-06		-4.48E-01	3.86E-05		-1.20E+00	2.31E-25	Down	Unigene3714_All//gi|21741227|emb|CAD40938.1|//4.00E-87//OSJNBO048E02.14 [Oryza sativa (japonica cultivar-group)] >gi|116309718|emb|CAH66763.1|OSIGBa0115M15.1 [Oryza sativa (indica cultivar-group)]		Unigene3714_All//0.00E+00//TC148557				nr +
Unigene37142_All	472	2.66	1.83	0.23	3.59	2.48	2.58	2.78	3.36	2.36	-5.44E-01	3.75E-01		-3.56E+00	4.96E-05	Down	-5.33E-01	3.00E-01		-4.74E-01	3.86E-01		2.77E-01	6.01E-01		-2.33E-01	6.34E-01		Unigene37142_All//gi|10241605|emb|CAC09581.1|//2.00E-14//protein kinase [Fagus sylvatica]		Unigene37142_All//0.00E+00//TC164044			GO:0004672//GO:0006464	nr -
Unigene37145_All	1732	1.66	1.90	2.03	22.55	24.77	19.32	18.19	8.83	8.03	1.95E-01	6.05E-01		2.88E-01	4.05E-01		1.36E-01	1.28E-01		-2.23E-01	1.14E-02		-1.04E+00	2.67E-30	Down	-1.18E+00	6.03E-38	Down	Unigene37145_All//gi|85001715|gb|AB068411.1|//0.00E+00//cytochrome P450 monooxygenase CYP701A16 [Glycine max]	Unigene37145_All//0.00E+00//AT5G25900| GA3 (GA REQUIRING 3); ent-kaurene oxidase/ oxygen binding	Unigene37145_All//0.00E+00//TC151422		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00904|Diterpenoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0009527//GO:0009685//GO:0010476//GO:0016491//GO:0033231	nr -
Unigene37146_All	1845	0.09	0.08	0.29	1.70	1.44	0.76	1.35	0.84	0.43	-4.65E-02	9.89E-01		1.76E+00	1.29E-01		-2.43E-01	5.41E-01		-1.16E+00	9.08E-04	Down	-6.90E-01	5.52E-02		-1.65E+00	1.01E-05	Down	Unigene37146_All//gi|85001715|gb|AB068411.1|//0.00E+00//cytochrome P450 monooxygenase CYP701A16 [Glycine max]	Unigene37146_All//0.00E+00//AT5G25900| GA3 (GA REQUIRING 3); ent-kaurene oxidase/ oxygen binding	Unigene37146_All//0.00E+00//TC137207		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0009527//GO:0009685//GO:0010476//GO:0016491//GO:0033231	nr -

Unigene37147_All	1348	2.83	1.35	1.46	3.07	1.79	1.27	2.35	2.05	2.81	-1.07E+00	7.77E-04	Down	-9.55E-01	3.69E-03		-7.78E-01	5.58E-03		-1.27E+00	2.52E-05	Down	-2.01E-01	5.76E-01		2.55E-01	3.81E-01		Unigene37147_All//gi|61611694|gb|AAX47176.1|//2.00E-79//expressed protein [Pisum sativum]	Unigene37147_All//1.00E-52//AT2G25920| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: 3'-5' exonuclease domain-containing protein / K homology domain-containing protein / KH domain-containing protein (TAIR:AT2G25910.2); Has 84 Blast hits to 79 proteins in 34 species: Archae - 0; Bacteria - 23; Metazoa - 11; Fungi - 12; Plants - 23; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink).	Unigene37147_All//0.00E+00//CO117654				nr +
Unigene37148_All	965	51.56	93.83	65.17	39.54	59.02	47.92	77.77	126.69	263.43	8.64E-01	3.34E-51		3.38E-01	6.74E-07		5.78E-01	3.26E-19		2.77E-01	3.51E-04		7.04E-01	1.72E-59		1.76E+00	0.00E+00	Up	Unigene37148_All//gi|94442475|gb|ABF19025.1|//2.00E-43//At5g40690 [Arabidopsis thaliana]	Unigene37148_All//6.00E-40//AT5G40690| INVOLVED IN: biological_process unknown; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: EF-HAND 1 (InterPro:IPR018247); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41730.1); Has 208 Blast hits to 177 proteins in 46 species: Archae - 0; Bacteria - 4; Metazoa - 51; Fungi - 25; Plants - 42; Viruses - 6; Other Eukaryotes - 80 (source: NCBI BLink).	Unigene37148_All//0.00E+00//DW504564				nr -
Unigene37149_All	1489	1.93	1.05	0.46	4.05	2.68	1.64	3.58	0.76	0.78	-8.73E-01	1.79E-02		-2.06E+00	2.21E-06	Down	-5.94E-01	9.38E-03		-1.31E+00	9.19E-08	Down	-2.24E+00	5.42E-16	Down	-2.21E+00	2.98E-16	Down	Unigene37149_All//gi|30696854|ref|NP_176536.2|//1.00E-93//DNA-binding family protein [Arabidopsis thaliana] >gi|119657354|tpd|FAA00276.1| TPA: AT-hook motif nuclear localized protein 5 [Arabidopsis thaliana]	Unigene37149_All//4.00E-85//AT1G63470| DNA-binding family protein	Unigene37149_All//0.00E+00//ES797488				nr +
Unigene37150_All	1032	4.36	6.38	4.70	8.21	6.07	5.03	17.62	15.11	8.34	5.50E-01	1.68E-02		1.07E-01	7.08E-01		-4.34E-01	2.43E-02		-7.05E-01	2.87E-04		-2.22E-01	7.37E-02		-1.08E+00	2.05E-19	Down			Unigene37150_All//0.00E+00//TC166503				
Unigene37151_All	1563	10.18	2.24	3.48	5.20	5.79	2.75	0.62	0.53	0.56	-2.19E+00	7.36E-37	Down	-1.55E+00	2.29E-22	Down	1.58E-01	4.96E-01		-9.20E-01	4.20E-06		-2.18E-01	7.24E-01		-1.50E-01	7.92E-01		Unigene37151_All//gi|157101244|dbj|BAF79953.1|//2.00E-79//receptor-like kinase [Marchantia polymorpha]	Unigene37151_All//2.00E-73//AT3G26700| protein kinase family protein	Unigene37151_All//0.00E+00//TC174921				nr -
Unigene37152_All	469	0.78	3.67	1.14	2.76	18.80	17.91	4.51	30.39	32.36	2.23E+00	1.09E-04	Up	5.40E-01	6.10E-01		2.77E+00	1.13E-30	Up	2.70E+00	1.84E-26	Up	2.75E+00	1.68E-52	Up	2.84E+00	6.76E-59	Up	Unigene37152_All//gi|242199346|gb|ACS87994.1|//6.00E-25//UDP-glucosyltransferase family 1 protein [Citrus sinensis]	Unigene37152_All//4.00E-10//AT1G22280| AtUGT85A3 (UDP-glucosyl transferase 85A3); glucuronosyltransferase/ transcription factor/ transferase, transferring glycosyl groups	Unigene37152_All//0.00E+00//TC160427		ko00460|Cyanoamino acid metabolism	GO:0016757	nr -
Unigene37153_All	1081	1.69	7.27	2.02	9.17	29.88	35.76	22.80	82.86	127.96	2.10E+00	1.58E-17	Up	2.54E-01	5.98E-01		1.70E+00	3.67E-62	Up	1.96E+00	2.34E-82	Up	1.86E+00	1.78E-202	Up	2.49E+00	0.00E+00	Up	Unigene37153_All//gi|242199346|gb|ACS87994.1|//3.00E-92//UDP-glucosyltransferase family 1 protein [Citrus sinensis]	Unigene37153_All//3.00E-49//AT1G22370| AtUGT85A5 (UDP-glucosyl transferase 85A5); glucuronosyltransferase/ transferase, transferring glycosyl groups	Unigene37153_All//0.00E+00//TC149055		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis	GO:0016757	nr -
Unigene37154_All	1627	0.80	0.97	1.93	1.50	1.21	0.61	3.38	4.91	2.18	2.64E-01	6.09E-01		1.26E+00	7.51E-04	Up	-3.14E-01	4.67E-01		-1.30E+00	1.60E-03		5.38E-01	3.35E-03		-6.33E-01	3.89E-03		Unigene37154_All//gi|75170629|sp|Q9FHK4.1|Y5519_ARATH//8.00E-22//RecName: Full=Uncharacterized protein At5g05190 >gi|30725434|gb|AAP37739.1| At5g05190 [Arabidopsis thaliana]	Unigene37154_All//5.00E-21//AT5G05190| unknown protein	Unigene37154_All//9.00E-89//gi|73864793|gb|DT467532.1|DT467532			GO:0005488	nr +
Unigene37156_All	1111	9.14	3.97	7.14	5.43	6.76	4.11	2.74	0.90	1.54	-1.20E+00	1.53E-10	Down	-3.55E-01	6.53E-02		3.17E-01	1.60E-01		-4.02E-01	1.11E-01		-1.60E+00	2.55E-06	Down	-8.30E-01	6.98E-03		Unigene37156_All//gi|87116616|gb|ABD19672.1|//5.00E-69//At3g15110 [Arabidopsis thaliana]	Unigene37156_All//1.00E-50//AT3G15110| unknown protein	Unigene37156_All//0.00E+00//TC179140			GO:0009534	nr +
Unigene37157_All	762	20.60	28.19	17.68	55.83	61.50	43.86	15.98	51.28	20.60	4.53E-01	1.30E-04		-2.20E-01	1.57E-01		1.40E-01	9.45E-02		-3.48E-01	1.23E-05		1.68E+00	3.98E-77	Up	3.66E-01	3.02E-03		Unigene37157_All//gi|256857790|gb|ACV31209.1|//8.00E-09//auxin/indole-3-acetic acid 3 [Solanum tuberosum]	Unigene37157_All//7.00E-09//AT3G04730| IAA16; transcription factor	Unigene37157_All//0.00E+00//gi|161240965|gb|ES830021.1|ES830021				nr +
Unigene37158_All	2226	2.04	1.25	0.65	1.54	2.27	1.56	2.98	3.27	4.46	-7.08E-01	1.22E-02		-1.66E+00	1.75E-07	Down	5.59E-01	3.43E-02		1.69E-02	9.59E-01		1.32E-01	5.74E-01		5.80E-01	2.42E-04		Unigene37158_All//gi|223635613|sp|B3H672.1|PF317_ARATH//6.00E-58//RecName: Full=Pentatricopeptide repeat-containing protein At4g17616	Unigene37158_All//2.00E-50//AT4G17616| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT1G03100.1); Has 497 Blast hits to 452 proteins in 24 species: Archae - 0; Bacteria - 2; Metazoa - 6; Fungi - 0; Plants - 485; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).					nr -
Unigene3716_All	1347	2.56	0.90	2.65	6.14	3.30	2.38	5.65	3.35	1.45	-1.51E+00	1.85E-05	Down	4.71E-02	8.94E-01		-8.97E-01	1.46E-06		-1.37E+00	3.90E-11	Down	-7.54E-01	6.14E-05		-1.96E+00	8.29E-20	Down	Unigene3716_All//gi|15219436|ref|NP_175096.1|//1.00E-138//ATPUP11; purine transmembrane transporter [Arabidopsis thaliana] >gi|75176558|sp|Q9LPF6.1|PUP11_ARATH RecName: Full=Probable purine permease 11; Short=AtPUP11 >gi|8653985|gb|AF78258.1|AC020576_2 Contains similarity to purine permease from Arabidopsis thaliana gb|AF078531. EST gb|AI997301 comes from this gene >gi|17065412|gb|AAL32860.1| Unknown protein [Arabidopsis thaliana] >gi|28058999|gb|AAO29976.1| Unknown protein [Arabidopsis thaliana]	Unigene3716_All//3.00E-115//AT1G44750| ATPUP11; purine transmembrane transporter	Unigene3716_All//0.00E+00//TC154562				nr +
Unigene37161_All	972	11.25	12.20	12.82	16.55	14.91	7.20	6.48	6.24	1.80	1.17E-01	5.29E-01		1.88E-01	3.04E-01		-1.50E-01	3.36E-01		-1.20E+00	2.30E-17	Down	-5.59E-02	8.11E-01		-1.85E+00	2.73E-15	Down	Unigene37161_All//gi|18418598|ref|NP_567979.1|//2.00E-83//cyclase family protein [Arabidopsis thaliana] >gi|13937204|gb|AAK50095.1|AF372956_1 AT4g35220/F23E12_220 [Arabidopsis thaliana] >gi|18491127|gb|AAL69532.1| AT4g35220/F23E12_220 [Arabidopsis thaliana]	Unigene37161_All//9.00E-85//AT4G35220| cyclase family protein	Unigene37161_All//0.00E+00//TC158981			GO:0006970//GO:0030312//GO:0031410	nr +
Unigene37162_All	1197	0.96	0.08	1.82	1.96	0.98	0.60	1.84	1.82	0.13	-3.51E+00	6.57E-05	Down	9.24E-01	4.33E-02		-1.00E+00	1.10E-02		-1.70E+00	1.02E-04	Down	-1.66E-02	1.00E+00		-3.79E+00	8.31E-12	Down	Unigene37162_All//gi|297802428|ref|XP_002869098.1|//1.00E-51//cyclase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314934|gb|EFH45357.1| cyclase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37162_All//5.00E-53//AT4G35220| cyclase family protein	Unigene37162_All//0.00E+00//TC158981			GO:0006970//GO:0030312	nr -
Unigene37163_All	1087	0.58	7.37	2.25	1.37	0.98	2.33	3.70	6.04	6.19	3.67E+00	1.24E-31	Up	1.96E+00	2.81E-05	Up	-4.85E-01	3.82E-01		7.59E-01	6.18E-02		7.08E-01	5.31E-04		7.45E-01	1.54E-04		Unigene37163_All//gi|188509937|gb|ACD56623.1|//1.00E-116//ERD2-like protein [Gossypium raimondii]	Unigene37163_All//1.00E-64//AT1G29330| ERD2 (ENDOPLASMIC RETICULUM RETENTION DEFECTIVE 2); KDEL sequence binding / receptor	Unigene37163_All//0.00E+00//TC178135			GO:0004871//GO:0005048//GO:0006810//GO:0031090//GO:0031224//GO:0031410//GO:0035437//GO:0043231	nr +
Unigene37164_All	1082	52.37	17.94	20.03	90.24	87.27	56.10	29.97	21.98	38.18	-1.55E+00	5.04E-81	Down	-1.39E+00	1.34E-66	Down	-4.83E-02	4.66E-01		-6.86E-01	2.96E-40		-4.47E-01	1.04E-07		3.49E-01	1.46E-06		Unigene37164_All//gi|15235668|ref|NP_193070.1|//1.00E-154//leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] >gi|75337952|sp|Q9T0K5.1|LRX3_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 3; Short=LRR/EXTENSIN3; Short=AtLRX3; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|4584539|emb|CAB40769.1| extensin-like protein [Arabidopsis thaliana] >gi|7268037|emb|CAB78376.1| extensin-like protein [Arabidopsis thaliana]	Unigene37164_All//5.00E-46//AT4G13340| leucine-rich repeat family protein / extensin family protein	Unigene37164_All//6.00E-89//DW487868		ko03040|Spliceosome	GO:0000902//GO:0030154//GO:0044464	nr +
Unigene37166_All	1448	2.24	1.96	1.80	3.61	3.33	2.12	3.39	1.36	3.00	-1.93E-01	6.11E-01		-3.14E-01	4.00E-01		-1.18E-01	6.99E-01		-7.68E-01	2.87E-03		-1.32E+00	1.74E-07	Down	-1.76E-01	5.01E-01		Unigene37166_All//gi|297598416|ref|XP_001045553.2|//1.00E-100//Os01g0974300 [Oryza sativa Japonica Group] >gi|255674124|dbj|BAF07467.2| Os01g0974300 [Oryza sativa Japonica Group]	Unigene37166_All//2.00E-167//AT3G12590| unknown protein	Unigene37166_All//2.00E-154//TC130770				nr +
Unigene37168_All	916	3.03	2.71	2.67	0.71	1.20	0.74	1.89	0.73	0.26	-1.60E-01	6.64E-01		-1.79E-01	6.35E-01		7.67E-01	2.69E-01		6.50E-02	9.49E-01		-1.37E+00	2.67E-03		-2.86E+00	1.61E-07	Down	Unigene37168_All//gi|297804228|ref|XP_002869998.1|//4.00E-46//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297315834|gb|EFH46257.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene37168_All//6.00E-45//AT4G19160| unknown protein	Unigene37168_All//0.00E+00//TC176726				nr -
Unigene3717_All	1443	1.67	44.24	16.02	2.07	3.68	9.77	9.23	24.27	92.85	4.73E+00	4.43E-298	Up	3.26E+00	5.72E-80	Up	8.27E-01	8.85E-04		2.24E+00	1.20E-35	Up	1.40E+00	9.85E-53	Up	3.33E+00	0.00E+00	Up	Unigene3717_All//gi|124359676|gb|ABD32341.2|//1.00E-116//N-6 Adenine-specific DNA methylase; Homeodomain-related [Medicago truncatula]	Unigene3717_All//1.00E-97//AT4G21440| ATMYB102 (ARABIDOPSIS MYB-LIKE 102); DNA binding / transcription factor	Unigene3717_All//5.00E-121//gi|73860948|gb|DT463687.1|DT463687	MYB			nr -

Unigene37171_All	1416	2.40	0.79	0.68	4.22	3.16	5.07	5.52	4.96	8.02	-1.61E+00	7.48E-06	Down	-1.83E+00	1.84E-06	Down	-4.17E-01	8.35E-02		2.65E-01	2.78E-01		-1.56E-01	4.66E-01		5.38E-01	2.42E-04		Unigene37171_All//gi|15233139|ref|NP_191712.1|//1.00E-155//PANB2; 3-methyl-2-oxobutanoate hydroxymethyltransferase [Arabidopsis thaliana] >gi|42572757|ref|NP_974474.1| PANB2; 3-methyl-2-oxobutanoate hydroxymethyltransferase [Arabidopsis thaliana] >gi|6850844|emb|CAB71083.1| 3-methyl-2-oxobutanoate hydroxy-methyl-transferase-like protein [Arabidopsis thaliana] >gi|21593121|gb|AAM65076.1| 3-methyl-2-oxobutanoate hydroxy-methyl-transferase-like protein [Arabidopsis thaliana] >gi|94442441|gb|ABF19008.1| At3g61530 [Arabidopsis thaliana]	Unigene37171_All//4.00E-155//AT3G61530| PANB2: 3-methyl-2-oxobutanoate hydroxymethyltransferase	Unigene37171_All//0.00E+00//gi|164349564|gb|EX170709.1|EX170709		ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene37172_All	933	7.07	113.61	11.02	26.70	25.28	24.11	4.80	11.78	8.80	4.01E+00	0.00E+00	Up	6.41E-01	5.24E-04		-7.85E-02	5.62E-01		-1.47E-01	2.36E-01		1.29E+00	2.53E-15	Up	8.73E-01	1.00E-06		Unigene37172_All//gi|159138941|gb|ABW89470.1|//7.00E-84//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene37172_All//5.00E-58//AT2G29500| 17.6 kDa class I small heat shock protein (HSP17.6B-CI)	Unigene37172_All//0.00E+00//gi|310725555|gb|CA992834.1|CA992834			GO:0044424//GO:0050896	nr +
Unigene37173_All	920	0.63	0.33	0.00	0.70	0.30	0.49	4.04	9.59	1.30	-9.21E-01	3.43E-01		-9.29E+00	2.60E-03		-1.23E+00	1.60E-01		-5.20E-01	5.88E-01		1.25E+00	9.01E-12	Up	-1.64E+00	4.54E-08	Down	Unigene37173_All//gi|296149181|gb|ADG96405.1|//5.00E-89//S-locus receptor kinase [Olea europaea]	Unigene37173_All//3.00E-92//AT4G27300| S-locus protein kinase, putative	Unigene37173_All//2.00E-45//gi|164366409|gb|ES802621.1|ES802621		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene37174_All	3158	0.17	0.29	0.35	0.46	0.50	0.94	5.36	11.92	33.34	8.02E-01	2.71E-01		1.10E+00	1.10E-01		1.33E-01	8.25E-01		1.05E+00	4.14E-03		1.15E+00	2.14E-42	Up	2.64E+00	0.00E+00	Up	Unigene37174_All//gi|240256087|ref|NP_194459.4|//0.00E+00//ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene37174_All//0.00E+00//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene37174_All//2.00E-54//TC154318		ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488	nr +
Unigene37178_All	1414	18.61	8.10	20.67	0.74	0.58	0.45	1.02	0.15	0.39	-1.20E+00	5.04E-26	Down	1.52E-01	1.86E-01		-3.40E-01	5.96E-01		-7.26E-01	3.02E-01		-2.78E+00	5.95E-06	Down	-1.37E+00	5.50E-03		Unigene37178_All//gi|254946546|gb|ACT91266.1|//2.00E-41//DWARF27 [Oryza sativa Japonica Group]	Unigene37178_All//2.00E-32//AT1G03055| unknown protein					nr +
Unigene37181_All	1351	3.02	1.91	2.44	15.41	15.32	6.59	4.76	1.45	2.27	-6.59E-01	2.83E-02		-3.06E-01	3.63E-01		-8.80E-03	9.61E-01		-1.23E+00	4.63E-23	Down	-1.71E+00	1.22E-13	Down	-1.07E+00	2.56E-07	Down	Unigene37181_All//gi|224082031|ref|XP_002306554.1|//1.00E-154//F-box family protein [Populus trichocarpa] >gi|222856003|gb|EEE93550.1| f-box family protein [Populus trichocarpa]	Unigene37181_All//2.00E-132//AT5G49980| AFB5 (Auxin F-Box protein 5); ubiquitin-protein ligase	Unigene37181_All//0.00E+00//TC168480		ko04626|Plant-pathogen interaction		nr +
Unigene37182_All	618	83.65	72.07	71.17	100.43	111.55	77.76	91.54	71.01	42.61	-2.15E-01	4.42E-03		-2.33E-01	2.86E-03		1.52E-01	1.91E-02		-3.69E-01	9.48E-09		-3.66E-01	4.17E-09		-1.10E+00	1.27E-60	Down	Unigene37182_All//gi|20269051|emb|CAC84706.1|//8.00E-81//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene37182_All//2.00E-43//AT5G65670| IAA9 (INDOLE-3-ACETIC ACID INDUCIBLE 9); transcription factor	Unigene37182_All//0.00E+00//TC131927			GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr +
Unigene37183_All	1028	187.19	9.27	54.86	32.56	26.70	24.38	5.14	7.28	6.32	-4.34E+00	0.00E+00	Down	-1.77E+00	0.00E+00	Down	-2.87E-01	1.25E-03		-4.17E-01	3.74E-06		5.01E-01	8.78E-03		2.97E-01	1.57E-01		Unigene37183_All//gi|15228108|ref|NP_178507.1|//2.00E-35//XERICO; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|42570685|ref|NP_973416.1| XERICO; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|11692878|gb|AAG40042.1|AF32469 1_1 T23015.13 [Arabidopsis thaliana]	Unigene37183_All//2.00E-31//AT2G04240| XERICO; protein binding / zinc ion binding	Unigene37183_All//0.00E+00//TC146102			GO:0006714//GO:0006970//GO:0009725//GO:0009743//GO:0046914	nr -
Unigene37184_All	2272	2.49	1.09	1.05	2.43	1.70	1.87	6.66	1.58	2.40	-1.19E+00	4.18E-06	Down	-1.24E+00	3.99E-06	Down	-5.20E-01	3.36E-02		-3.81E-01	1.53E-01		-2.07E+00	3.89E-40	Down	-1.47E+00	6.04E-26	Down	Unigene37184_All//gi|40241245|emb|CAF02297.1|//1.00E-125//cysteine-rich polycomb-like protein [Lotus japonicus] >gi|40241253|emb|CAF02298.1| cysteine-rich polycomb-like protein [Lotus japonicus]	Unigene37184_All//2.00E-60//AT4G14770| TCX2 (TESMIN/TSO1-LIKE CXC 2); transcription factor	Unigene37184_All//0.00E+00//TC179260	CPP			nr -
Unigene37185_All	1610	19.04	15.30	14.62	18.13	19.36	23.40	16.68	22.79	98.80	-3.16E-01	1.31E-03		-3.82E-01	1.64E-04		9.44E-02	4.23E-01		3.68E-01	1.61E-05		4.51E-01	1.02E-08		2.57E+00	0.00E+00	Up	Unigene37185_All//gi|63029722|gb|AY27752.1|//1.00E-171//12-oxophytodienoate reductase [Hevea brasiliensis]	Unigene37185_All//1.00E-162//AT2G06050| OPR3 (OPDA-REDUCTASE 3); 12-oxophytodienoate reductase	Unigene37185_All//0.00E+00//TC179247		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene37186_All	1141	3.58	9.37	2.61	5.81	6.79	8.83	13.75	11.94	8.87	1.39E+00	1.47E-13	Up	-4.53E-01	1.56E-01		2.26E-01	3.30E-01		6.04E-01	6.76E-04		-2.03E-01	1.38E-01		-6.32E-01	2.63E-07		Unigene37186_All//gi|225432153|ref|XP_002265997.1|//4.00E-90//PREDICTED: similar to catalytic [Vitis vinifera]	Unigene37186_All//8.00E-80//AT3G17365| catalytic/ methyltransferase	Unigene37186_All//0.00E+00//CO077692			GO:0016741	nr -
Unigene37188_All	1400	4.04	6.26	4.98	3.45	3.47	1.61	4.50	4.00	1.99	6.34E-01	1.16E-03		3.04E-01	2.15E-01		7.00E-03	9.88E-01		-1.10E+00	5.39E-05	Down	-1.70E-01	4.81E-01		-1.18E+00	2.96E-08	Down	Unigene37188_All//gi|297845164|ref|XP_002890463.1|//1.00E-159//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336305|gb|EFH66722.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37188_All//3.00E-158//AT1G21760| FBP7 (F-BOX PROTEIN 7)	Unigene37188_All//0.00E+00//TC139049				nr -
Unigene3719_All	2022	9.91	8.60	8.95	8.72	8.48	6.92	1.21	0.60	0.39	-2.05E-01	1.18E-01		-1.46E-01	3.07E-01		-4.03E-02	8.26E-01		-3.33E-01	1.29E-02		-1.02E+00	5.18E-03		-1.62E+00	1.55E-05	Down	Unigene3719_All//gi|9778416|ref|NP_178316.1|//1.00E-134//AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding >gi|41059987|emb|CAF18564.1| ID1-like zinc finger protein 2 [Arabidopsis thaliana]	Unigene3719_All//3.00E-117//AT2G02070| AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding	Unigene3719_All//0.00E+00//ES809194	C2H2			nr -
Unigene37193_All	1304	3.41	2.25	3.88	14.36	8.13	7.48	6.68	2.63	2.72	-5.98E-01	3.72E-02		1.86E-01	5.34E-01		-8.21E-01	2.98E-12		-9.41E-01	1.05E-13		-1.35E+00	4.86E-13	Down	-1.30E+00	9.02E-13	Down	Unigene37193_All//gi|30694417|ref|NP_199211.2|//5.00E-85//PDLP1 (PLASMODESMATA-LOCATED PROTEIN 1) [Arabidopsis thaliana] >gi|158563851|sp|Q8GXV7.2|CRR56_ARATH RecName: Full=Cysteine-rich repeat secretory protein 56; Flags: Precursor	Unigene37193_All//1.00E-76//AT5G43980| PDLP1 (PLASMODESMATA-LOCATED PROTEIN 1)				GO:0005911//GO:0010496	nr +
Unigene37194_All	1260	38.29	10.42	10.86	125.05	99.86	105.95	122.28	15.13	34.65	-1.88E+00	8.69E-91	Down	-1.82E+00	7.05E-84	Down	-3.25E-01	1.07E-18		-2.39E-01	1.17E-09		-3.02E+00	0.00E+00	Down	-1.82E+00	0.00E+00	Down	Unigene37194_All//gi|157273638|gb|ABV27473.1|//1.00E-146//fasciclin-like arabinogalactan protein 2 [Gossypium hirsutum]	Unigene37194_All//8.00E-58//AT2G04780| FLA7 (FASCICLIN-LIKE ARABINOOGALACTAN 7)	Unigene37194_All//0.00E+00//TC130600			GO:0031225	nr +
Unigene37195_All	562	5.49	1.80	6.92	2.57	1.53	1.37	2.03	0.89	2.06	-1.61E+00	2.25E-05	Down	3.33E-01	3.30E-01		-7.47E-01	1.63E-01		-9.12E-01	1.06E-01		-1.19E+00	4.02E-02		1.72E-02	9.72E-01		Unigene37195_All//gi|225464144|ref|XP_002266805.1|//2.00E-36//PREDICTED: similar to bile acid:sodium symporter [Vitis vinifera]	Unigene37195_All//1.00E-24//AT3G56160| bile acid:sodium symporter	Unigene37195_All//1.00E-51//TC145525			GO:0005343//GO:0030001//GO:0044464	nr -
Unigene37196_All	1555	12.28	5.96	10.99	2.27	3.17	1.71	5.08	2.93	2.28	-1.04E+00	2.32E-15	Down	-1.60E-01	2.68E-01		4.77E-01	8.21E-02		-4.09E-01	2.37E-01		-7.95E-01	1.63E-05		-1.16E+00	6.65E-10	Down	Unigene37196_All//gi|225464144|ref|XP_002266805.1|//1.00E-142//PREDICTED: similar to bile acid:sodium symporter [Vitis vinifera]	Unigene37196_All//6.00E-116//AT3G56160| bile acid:sodium symporter	Unigene37196_All//0.00E+00//TC145525			GO:0005343//GO:0030001//GO:0044464	nr +
Unigene37197_All	1358	3.66	0.97	2.98	4.33	3.70	2.86	12.11	8.06	8.13	-1.92E+00	3.23E-10	Down	-2.97E-01	3.21E-01		-2.26E-01	4.07E-01		-5.98E-01	1.41E-02		-5.87E-01	1.52E-06		-5.76E-01	1.41E-06		Unigene37197_All//gi|115456445|ref|NP_001051823.1|//2.00E-20//Os03g0836200 [Oryza sativa Japonica Group] >gi|108711961|gb|ABF99756.1| RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|108711962|gb|ABF99757.1| RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|108711963|gb|ABF99758.1| RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|108711964|gb|ABF99759.1| RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550294|dbj|BAF13737.1| Os03g0836200 [Oryza sativa Japonica Group]		Unigene37197_All//0.00E+00//TC154397			GO:0003677//GO:0009791//GO:0044424//GO:0048527//GO:0048608	nr +
Unigene37199_All	1231	36.51	67.46	32.83	13.88	13.73	64.13	101.46	446.85	212.69	8.86E-01	4.84E-49		-1.53E-01	8.50E-02		-1.52E-02	9.28E-01		2.21E+00	3.65E-195	Up	2.14E+00	0.00E+00	Up	1.07E+00	1.68E-261	Up	Unigene37199_All//gi|124359974|gb|ABN07990.1|//4.00E-98//SAM (and some other nucleotide) binding motif [Medicago truncatula]	Unigene37199_All//2.00E-90//AT2G41380| embryo-abundant protein-related	Unigene37199_All//0.00E+00//gi|13247650|gb|BF271517.2|BF271517			GO:0010038//GO:0016741//GO:0043231	nr +
Unigene372_All	444	0.94	0.00	0.00	4.49	0.78	2.85	8.00	6.87	2.06	-9.88E+00	1.05E-02		-9.88E+00	1.56E-02		-2.53E+00	2.94E-07	Down	-6.56E-01	1.63E-01		-2.19E-01	5.06E-01		-1.95E+00	1.24E-09	Down	Unigene372_All//gi|297853362|ref|XP_002894562.1|//3.00E-33//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340404|gb|EFH70821.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene372_All//1.00E-32//AT1G56130| leucine-rich repeat family protein / protein kinase family protein	Unigene372_All//7.00E-68//CO076745				nr -
Unigene37200_All	1478	10.05	26.77	20.46	21.20	22.46	27.35	15.91	24.01	17.66	1.41E+00	1.74E-49	Up	1.03E+00	2.11E-22	Up	8.33E-02	4.73E-01		3.67E-01	7.31E-06		5.94E-01	1.99E-13		1.51E-01	1.36E-01		Unigene37200_All//gi|297828824|ref|XP_002882294.1|//1.00E-129//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328134|gb|EFH58553.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37200_All//7.00E-117//AT3G03440| armadillo/beta-catenin repeat family protein	Unigene37200_All//0.00E+00//gi|164298641|gb|ES809340.1|ES809340				nr -
Unigene37201_All	780	1.07	2.08	4.30	2.17	1.94	3.59	4.44	11.68	13.23	9.54E-01	6.65E-02		2.00E+00	3.78E-07	Up	-1.61E-01	7.82E-01		7.25E-01	5.78E-02		1.39E+00	2.77E-14	Up	1.57E+00	1.58E-19	Up			Unigene37201_All//0.00E+00//TC178512				
Unigene37203_All	1453	5.65	30.34	13.41	17.76	21.16	17.06	2.30	1.70	1.97	2.42E+00	8.81E-114	Up	1.25E+00	8.12E-20	Up	2.53E-01	8.77E-03		-5.76E-02	6.73E-01		-4.38E-01	1.61E-01		-2.20E-01	4.88E-01		Unigene37203_All//gi|15241097|ref|NP_200406.1|//1.00E-163//transporter-related [Arabidopsis thaliana] >gi|91807050|gb|ABE66252.1| transporter-like [Arabidopsis thaliana]	Unigene37203_All//4.00E-155//AT5G55950| transporter-related					nr +
Unigene37204_All	960	16.68	10.35	17.75	111.82	125.15	124.29	30.61	17.76	13.11	-6.89E-01	7.76E-07		8.99E-02	5.89E-01		1.63E-01	3.48E-04		1.53E-01	1.51E-03		-7.85E-01	6.84E-18		-1.22E+00	1.75E-37	Down	Unigene37204_All//gi|6694693|gb|AAF25357.1|AF210061_1//1.00E-75//dirigent protein [Forsythia x intermedia]	Unigene37204_All//4.00E-49//AT4G23690| disease resistance-responsive family protein / dirigent family protein	Unigene37204_All//0.00E+00//TC168181				nr -
Unigene37209_All	910	3.85	11.92	5.21	4.60	5.22	4.76	2.60	3.26	2.71	1.63E+00	3.56E-17	Up	4.35E-01	1.40E-01		1.84E-01	5.76E-01		5.13E-02	8.89E-01		3.26E-01	3.59E-01		6.10E-02	8.78E-01		Unigene37209_All//gi|300175972|emb|CBK22189.2|//6.00E-06//unnamed protein product [Blastocystis hominis]		Unigene37209_All//8.00E-54//gi|73860658|gb|DT463397.1|DT463397				nr -

Unigene3721_All	2225	4.89	7.22	3.97	6.96	6.31	6.76	11.99	25.38	12.39	5.62E-01	5.16E-05		-3.00E-01	1.12E-01		-1.41E-01	3.91E-01		-4.28E-02	7.92E-01		1.08E+00	6.33E-57	Up	4.73E-02	6.50E-01		Unigene3721_All//gi|31711872|gb|AAP68292.1|//1.00E-166//At5g11730 [Arabidopsis thaliana]	Unigene3721_All//6.00E-168//AT5G11730| unknown protein	Unigene3721_All//0.00E+00//gi|109887239|gb|DW516208.1|DW516208			nr +
Unigene37213_All	704	1.71	4.82	3.03	2.05	1.66	1.41	1.98	1.66	2.26	1.50E+00	2.62E-05	Up	8.24E-01	7.51E-02		-3.03E-01	5.95E-01		-5.40E-01	3.59E-01		-2.54E-01	6.33E-01		1.92E-01	6.75E-01				Unigene37213_All//5.00E-116//BF274633				
Unigene37215_All	788	44.15	35.88	52.98	71.24	55.89	52.38	62.51	46.20	26.49	-2.99E-01	1.15E-03		2.63E-01	2.58E-03		-3.50E-01	5.49E-08		-4.44E-01	5.85E-11		-4.36E-01	8.42E-11		-1.24E+00	1.81E-63	Down	Unigene37215_All//gi|115481880|ref|NP_001064533.1|//2.00E-41//Os10g0397200 [Oryza sativa Japonica Group] >gi|19881736|gb|AAM01137.1|AC10888 4_19 Putative Transcription initiation factor IIE, beta subunit [Oryza sativa Japonica Group] >gi|113639142|dbj|BAF26447.1|Os10g0397200 [Oryza sativa Japonica Group]	Unigene37215_All//3.00E-34//AT4G20330| transcription initiation factor-related	Unigene37215_All//0.00E+00//TC137928		ko03022|Basal transcription factors	GO:0005667//GO:0006352//GO:0008135//GO:0030528	nr +
Unigene37217_All	791	53.58	41.06	25.58	66.00	47.15	63.66	53.56	30.38	22.46	-3.84E-01	2.53E-06		-1.07E+00	3.81E-33	Down	-4.85E-01	2.79E-13		-5.20E-02	5.98E-01		-8.18E-01	3.19E-27		-1.25E+00	9.56E-56	Down	Unigene37217_All//gi|115454741|ref|NP_001050971.1|//6.00E-19//Os03g0694700 [Oryza sativa Japonica Group] >gi|108710535|gb|ABF98330.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549442|dbj|BAF12885.1|Os03g0694700 [Oryza sativa Japonica Group]	Unigene37217_All//2.00E-27//AT3G26360| unknown protein	Unigene37217_All//0.00E+00//TC161268			GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr -
Unigene37219_All	1689	5.36	5.64	5.33	13.18	17.35	17.70	7.11	1.36	5.68	7.37E-02	7.08E-01		-8.30E-03	9.92E-01		3.96E-01	2.39E-05		4.25E-01	1.04E-05		-2.39E+00	6.71E-38	Down	-3.23E-01	2.58E-02		Unigene37219_All//gi|30692765|ref|NP_174563.2|//1.00E-152//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|75154301|sp|Q8L868.1|E1311_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 11; AltName: Full=(1->3)-beta-glucan endohydrolase 11; Short=(1->3)-beta-glucanase 11; AltName: Full=Beta-1,3-endoglucanase 11; Short=Beta-1,3-glucanase 11; Flags: Precursor	Unigene37219_All//2.00E-146//AT1G32860| glycosyl hydrolase family 17 protein	Unigene37219_All//0.00E+00//gi|78346333|gb|DT566607.1|DT566607		ko00500|Starch and sucrose metabolism		nr +
Unigene37220_All	1286	2.24	1.73	3.31	14.06	9.10	4.67	2.99	2.37	3.44	-3.68E-01	3.37E-01		5.66E-01	6.75E-02		-6.27E-01	1.42E-07		-1.59E+00	1.47E-29	Down	-3.35E-01	2.58E-01		2.01E-01	4.66E-01		Unigene37220_All//gi|297832316|ref|XP_002884040.1|//6.00E-94//peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329880|gb|EFH60299.1|peptidoglycan-binding LysM domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene37220_All//3.00E-84//AT2G17120| LYM2 (LYSM DOMAIN GPI-ANCHORED PROTEIN 2 PRECURSOR)	Unigene37220_All//0.00E+00//TC130643		ko04626|Plant-pathogen interaction	GO:0031225	nr +
Unigene37221_All	1297	2.18	1.25	0.78	2.92	2.68	1.92	3.42	1.71	3.35	-8.01E-01	3.15E-02		-1.48E+00	2.89E-04	Down	-1.22E-01	7.45E-01		-6.08E-01	5.61E-02		-1.00E+00	1.04E-04	Down	-3.19E-02	9.21E-01		Unigene37221_All//gi|115447467|ref|NP_001047513.1|//7.00E-95//Os02g0634600 [Oryza sativa Japonica Group] >gi|113537044|dbj|BAF09427.1|Os02g0634600 [Oryza sativa Japonica Group]	Unigene37221_All//2.00E-97//AT5G23200| unknown protein	Unigene37221_All//4.00E-41//TC136279				nr -
Unigene37223_All	1233	11.16	18.29	35.89	204.43	170.00	128.09	20.40	20.10	11.60	7.13E-01	8.84E-10		1.69E+00	1.67E-69	Up	-2.66E-01	1.86E-20		-6.74E-01	3.32E-100		-2.15E-02	8.59E-01		-8.15E-01	6.68E-17		Unigene37223_All//gi|205326623|gb|ACI03401.1|//1.00E-139//peroxidase 1 [Litchi chinensis]	Unigene37223_All//1.00E-97//AT5G05340| peroxidase, putative	Unigene37223_All//0.00E+00//TC169676		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene37225_All	1091	4.51	3.02	3.27	19.59	11.49	45.49	15.46	22.26	15.63	-5.79E-01	3.30E-02		-4.63E-01	1.09E-01		-7.70E-01	1.69E-12		1.22E+00	8.77E-53	Up	5.26E-01	9.74E-08		1.54E-02	9.29E-01		Unigene37225_All//gi|5902391|gb|AAD55493.1|AC008148_3//1.00E-42//Unknown protein [Arabidopsis thaliana] >gi|17622444|gb|AAG40399.1|AF325047_1 At1g70780 [Arabidopsis thaliana] >gi|15146214|gb|AAK83590.1|At1g70780/F5A18_4 [Arabidopsis thaliana] >gi|23506215|gb|AAN31119.1|At1g70780/F5A18_4 [Arabidopsis thaliana]	Unigene37225_All//5.00E-44//AT1G70780| unknown protein	Unigene37225_All//0.00E+00//TC145629				nr -
Unigene37226_All	1114	6.72	5.96	5.21	11.45	10.20	9.16	10.29	9.98	4.72	-1.73E-01	4.48E-01		-3.66E-01	1.12E-01		-1.66E-01	3.47E-01		-3.21E-01	4.97E-02		-4.35E-02	8.03E-01		-1.12E+00	2.36E-13	Down	Unigene37226_All//gi|225459685|ref|XP_002285888.1|//1.00E-109//PREDICTED: similar to BTB/POZ domain-containing protein [Vitis vinifera]	Unigene37226_All//9.00E-86//AT4G08455| BTB/POZ domain-containing protein	Unigene37226_All//0.00E+00//TC137021				nr +
Unigene37227_All	1012	1.03	2.85	1.00	3.15	3.03	4.02	3.97	2.81	1.50	1.46E+00	1.63E-04	Up	-4.85E-02	9.57E-01		-5.69E-02	8.72E-01		3.50E-01	2.91E-01		-4.99E-01	7.18E-02		-1.41E+00	4.31E-07	Down	Unigene37227_All//gi|40241237|emb|CAF02296.1|//1.00E-87//Rho GDP dissociation inhibitor 2 [Medicago truncatula] >gi|87241144|gb|ABD33002.1| RHO protein GDP dissociation inhibitor [Medicago truncatula]	Unigene37227_All//4.00E-84//AT3G07880| Rho GDP-dissociation inhibitor family protein	Unigene37227_All//0.00E+00//TC167182				nr +
Unigene37229_All	1179	24.45	57.93	30.08	31.52	24.86	27.62	64.73	95.33	54.06	1.24E+00	5.70E-70	Up	2.99E-01	1.59E-03		-3.43E-01	2.76E-05		-1.91E-01	4.08E-02		5.58E-01	1.60E-36		-2.60E-01	6.97E-07		Unigene37229_All//gi|7433647|pir||S72532//5.00E-22//acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor - cucurbit >gi|1694621|dbj|BAA11117.1| 3-ketoacyl-CoA thiolase [Cucurbita cv. Kurokawa Amakuri]	Unigene37229_All//2.00E-21//AT2G33150| PKT3 (PEROXISOMAL 3-KETOACYL-COA THIOLASE 3); acetyl-CoA C-acyltransferase	Unigene37229_All//0.00E+00//gi|48808048|gb|CO109362.1|CO109362		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene3723_All	1842	0.26	0.17	0.06	1.11	1.44	1.99	2.48	0.59	1.56	-6.31E-01	5.54E-01		-2.14E+00	1.03E-01		3.77E-01	3.77E-01		8.41E-01	8.96E-03		-2.07E+00	1.36E-12	Down	-6.71E-01	5.82E-03		Unigene3723_All//gi|9280323|dbj|BAB01702.1|//7.00E-71//kinesin (centromeric protein)-like protein [Arabidopsis thaliana]	Unigene3723_All//7.00E-53//AT3G17360| POK1 (PHRAGMOPLASTORIENTING KINESIN 1); ATP binding / microtubule motor					nr +
Unigene37230_All	1209	4.41	4.11	3.04	10.55	9.91	8.37	9.44	4.32	5.63	-1.04E-01	6.90E-01		-5.39E-01	4.79E-02		-8.97E-02	6.20E-01		-3.34E-01	4.03E-02		-1.13E+00	5.83E-13	Down	-7.45E-01	4.06E-07		Unigene37230_All//gi|12718822|dbj|BAB32405.1|//0.00E+00//NQK1 MAPKK [Nicotiana tabacum]	Unigene37230_All//4.00E-159//AT5G56580| MKK6 (MAP KINASE KINASE 6); MAP kinase kinase/kinase	Unigene37230_All//0.00E+00//TC178168		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene37231_All	1542	0.41	0.89	0.14	4.98	2.75	2.34	3.07	2.74	3.93	1.12E+00	5.30E-02		-1.56E+00	1.29E-01		-8.57E-01	1.02E-05		-1.09E+00	2.04E-07	Down	-1.66E-01	5.68E-01		3.55E-01	9.91E-02		Unigene37231_All//gi|42564100|ref|NP_187868.2|//1.00E-157//protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|79313205|ref|NP_001030682.1|protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|75273276|sp|Q9LHJ9.1|P2C38_ARATH RecName: Full=Probable protein phosphatase 2C 38; Short=AtPP2C38 >gi|9294356|dbj|BAB02253.1|protein phosphatase 2C [Arabidopsis thaliana] >gi|28466963|gb|AAO44090.1|At3g12620 [Arabidopsis thaliana] >gi|222424096|dbj|BAH20008.1|AT3G12620 [Arabidopsis thaliana] >gi|222424228|dbj|BAH20072.1|AT3G12620 [Arabidopsis thaliana]	Unigene37231_All//5.00E-159//AT3G12620| protein phosphatase 2C family protein / PP2C family protein	Unigene37231_All//0.00E+00//TC177582				nr +
Unigene37233_All	1117	22.53	24.00	15.68	24.08	18.84	24.06	32.17	16.54	15.59	9.10E-02	4.43E-01		-5.23E-01	2.95E-06		-3.55E-01	3.14E-04		-1.50E-03	9.87E-01		-9.60E-01	3.40E-30		-1.05E+00	1.14E-35	Down	Unigene37233_All//gi|297797487|ref|XP_002866628.1|//1.00E-111//ribosomal protein L15 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312463|gb|EFH42887.1|ribosomal protein L15 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37233_All//2.00E-88//AT5G44670| ribosomal protein L15 family protein	Unigene37233_All//0.00E+00//TC158768		ko03010|Ribosome		nr +
Unigene37234_All	1513	6.74	3.55	4.79	29.83	15.82	12.03	5.42	4.31	2.95	-9.26E-01	3.44E-07		-4.95E-01	8.30E-03		-9.15E-01	7.95E-35		-1.31E+00	1.07E-54	Down	-3.31E-01	7.86E-02		-8.78E-01	7.86E-07		Unigene37234_All//gi|15231396|ref|NP_187368.1|//1.00E-52//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|56381891|gb|AAV85664.1|At3g07120 [Arabidopsis thaliana] >gi|88531344|gb|AAW78594.1|At3g07120 [Arabidopsis thaliana]	Unigene37234_All//2.00E-40//AT3G07120| zinc finger (C3HC4-type RING finger) family protein	Unigene37234_All//0.00E+00//gi|48800165|gb|CO101479.1|CO101479				nr -
Unigene37235_All	1543	1.02	2.66	3.31	3.71	6.58	6.26	6.19	7.34	7.31	1.39E+00	1.14E-05	Up	1.70E+00	1.27E-08	Up	8.26E-01	1.07E-06		7.55E-01	3.15E-05		2.45E-01	1.32E-01		2.39E-01	1.24E-01		Unigene37235_All//gi|87244449|gb|AB034616.1|//1.00E-104//green ripe-like 1 [Solanum lycopersicum]	Unigene37235_All//2.00E-79//AT2G26070| RTE1 (REVERSION-TO-ETHYLENE SENSITIVITY1)	Unigene37235_All//0.00E+00//TC171411				nr +
Unigene37236_All	1496	5.67	3.22	2.85	21.04	26.63	24.54	1.70	1.68	10.97	-8.16E-01	4.21E-05		-9.93E-01	2.06E-06		3.40E-01	1.90E-05		2.22E-01	1.56E-02		-1.66E-02	9.98E-01		2.69E+00	4.28E-60	Up	Unigene37236_All//gi|259563723|gb|ACW83060.1|//1.00E-170//glycosyltransferase family GT8 protein [Populus deltoides]	Unigene37236_All//4.00E-154//AT1G19300| PARVUS (PARVUS); polygalacturonate 4-alpha-galacturonosyltransferase/transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene37236_All//0.00E+00//TC131412				nr +
Unigene37240_All	1149	23.18	64.34	24.19	28.57	29.49	49.61	40.48	59.91	51.66	1.47E+00	9.32E-98	Up	6.18E-02	6.18E-01		4.57E-02	7.12E-01		7.96E-01	2.46E-30		5.66E-01	3.31E-23		3.52E-01	3.76E-09		Unigene37240_All//gi|10241603|emb|CAC09580.1|//1.00E-109//protein kinase (PK) [Fagus sylvatica]	Unigene37240_All//2.00E-88//AT5G58950| protein kinase family protein	Unigene37240_All//0.00E+00//TC134376		ko04626|Plant-pathogen interaction		nr +
Unigene37241_All	732	6.29	14.12	7.20	23.48	21.87	27.58	15.36	34.26	34.51	1.17E+00	3.36E-10	Up	1.95E-01	5.03E-01		-1.02E-01	5.44E-01		2.32E-01	7.60E-02		1.16E+00	1.42E-28	Up	1.17E+00	7.34E-30	Up	Unigene37241_All//gi|7769863|gb|AAF69541.1|AC008007_16//2.00E-45//F12M16.29 [Arabidopsis thaliana]	Unigene37241_All//8.00E-47//AT1G53400| unknown protein	Unigene37241_All//0.00E+00//gi|164272515|gb|ES804437.1|ES804437				nr -
Unigene37242_All	1039	1.06	3.22	0.67	4.22	4.81	5.43	6.80	8.97	6.25	1.61E+00	1.03E-05	Up	-6.66E-01	3.35E-01		1.88E-01	5.49E-01		3.65E-01	1.74E-01		4.01E-01	1.93E-02		-1.21E-01	5.96E-01		Unigene37242_All//gi|7769863|gb|AAF69541.1|AC008007_16//6.00E-42//F12M16.29 [Arabidopsis thaliana]	Unigene37242_All//5.00E-43//AT1G53400| unknown protein	Unigene37242_All//0.00E+00//gi|164272515|gb|ES804437.1|ES804437				nr +
Unigene37244_All	1576	3.85	17.84	10.98	9.29	18.68	25.10	10.54	8.12	15.02	2.21E+00	3.37E-65	Up	1.51E+00	1.67E-23	Up	1.01E+00	1.21E-25	Up	1.43E+00	3.46E-54	Up	-3.78E-01	2.11E-03		5.10E-01	1.97E-07		Unigene37244_All//gi|15238395|ref|NP_201331.1|//1.00E-154//GCL1 (GCR2-LIKE 1); catalytic [Arabidopsis thaliana] >gi|10178190|dbj|BAB11664.1| G protein-coupled receptor-like protein [Arabidopsis thaliana] >gi|16604356|gb|AAL24184.1|AT5g65280/MQN23_23 [Arabidopsis thaliana]	Unigene37244_All//1.00E-153//AT5G65280| GCL1 (GCR2-LIKE 1); catalytic	Unigene37244_All//0.00E+00//TC141111				nr -

Unigene37245_All	1658	0.63	0.06	0.64	2.16	1.70	2.89	10.28	15.65	65.74	-3.37E+00	2.13E-04	Down	2.54E-02	9.89E-01		-3.45E-01	3.18E-01		4.17E-01	1.51E-01		6.07E-01	2.06E-10		2.68E+00	0.00E+00	Up	Unigene37245_All//gi|240256087|ref|NP_194459.4|//1.00E-149//ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene37245_All//7.00E-150//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene37245_All//3.00E-27//TC154318		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism		nr -
Unigene37246_All	1077	9.33	5.08	5.74	15.68	17.04	17.24	34.19	32.44	73.94	-8.76E-01	1.54E-06		-7.02E-01	1.79E-04		1.20E-01	4.41E-01		1.37E-01	3.80E-01		-7.58E-02	4.26E-01		1.11E+00	1.57E-85	Up	Unigene37246_All//gi|18379261|ref|NP_565267.1|//1.00E-132//epsin N-terminal homology (ENTH) domain-containing protein [Arabidopsis thaliana] >gi|46395897|sp|Q8LBH2.2|CAP8_ARATH RecName: Full=Putative clathrin assembly protein At2g01600 >gi|15983438|gb|AAL11587.1|AF424593_1 At2g01600/F219.22 [Arabidopsis thaliana] >gi|20197399|gb|AAM15059.1| expressed protein [Arabidopsis thaliana]	Unigene37246_All//8.00E-127//AT2G01600| epsin N-terminal homology (ENTH) domain-containing protein	Unigene37246_All//0.00E+00//TC177163				nr -
Unigene37247_All	1612	4.87	2.83	2.87	9.67	8.10	7.09	4.25	7.55	11.20	-7.83E-01	1.62E-04		-7.61E-01	4.22E-04		-2.57E-01	7.63E-02		-4.48E-01	1.30E-03		8.28E-01	1.47E-08		1.40E+00	2.90E-28	Up	Unigene37247_All//gi|6692100|gb|AAF24565.1|AC007764_7//1.00E-21//P22C12.16 [Arabidopsis thaliana] >gi|9896119|gb|ABF59043.1| At1g61080 [Arabidopsis thaliana]	Unigene37247_All//4.00E-34//AT5G52870| unknown protein	Unigene37247_All//0.00E+00//gi|78337063|gb|DT557337.1|DT557337				nr -
Unigene37248_All	629	8.65	7.25	4.06	24.95	28.08	31.38	17.07	20.13	28.56	-2.55E-01	3.55E-01		-1.09E+00	5.56E-05	Down	1.71E-01	2.50E-01		3.31E-01	8.55E-03		2.38E-01	1.19E-01		7.43E-01	1.41E-10					Unigene37248_All//0.00E+00//gi|109871912|gb|DW500888.1|DW500888				
Unigene37249_All	606	9.76	5.27	3.08	4.69	4.72	9.02	7.54	6.28	4.67	-8.89E-01	2.81E-04		-1.67E+00	1.49E-09	Down	9.50E-03	9.90E-01		9.45E-01	1.93E-04		-2.64E-01	3.47E-01		-6.91E-01	4.48E-03					Unigene37249_All//7.00E-152//TC162815				
Unigene37254_All	2007	0.10	0.30	0.11	2.53	2.85	2.07	5.90	1.48	3.61	1.54E+00	1.22E-01		2.47E-02	1.00E+00		1.70E-01	5.66E-01		-2.90E-01	3.23E-01		-2.00E+00	4.77E-30	Down	-7.07E-01	8.60E-07		Unigene37254_All//gi|13877693|gb|AAK43924.1|AF370605_1//0.00E+00//axi 1 protein-like protein [Arabidopsis thaliana] >gi|3128192|gb|AAC16096.1| similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana]	Unigene37254_All//0.00E+00//AT2G44500| unknown protein	Unigene37254_All//0.00E+00//TC143215				nr +
Unigene37259_All	1639	0.19	6.46	1.88	1.55	3.76	5.73	2.99	1.48	5.40	5.08E+00	1.81E-51	Up	3.30E+00	4.54E-11	Up	1.28E+00	4.28E-08	Up	1.89E+00	2.67E-19	Up	-1.02E+00	3.24E-05	Down	8.51E-01	6.52E-07		Unigene37259_All//gi|18395813|ref|NP_566139.1|//0.00E+00//5'-AMP-activated protein kinase beta-1 subunit-related [Arabidopsis thaliana]	Unigene37259_All//0.00E+00//AT3G01510| 5'-AMP-activated protein kinase beta-1 subunit-related	Unigene37259_All//0.00E+00//TC140851				nr -
Unigene37261_All	1490	3.72	30.84	27.16	16.55	17.59	279.22	1.65	28.16	13.26	3.05E+00	3.96E-152	Up	2.87E+00	3.74E-123	Up	8.78E-02	5.20E-01		4.08E+00	0.00E+00	Up	4.10E+00	1.55E-219	Up	3.01E+00	5.39E-81	Up	Unigene37261_All//gi|31074969|gb|AF421361.1|//6.00E-58//erg-1 [Solanum tuberosum]	Unigene37261_All//4.00E-49//AT5G64260| EXL2 (EXORDIUM LIKE 2)	Unigene37261_All//0.00E+00//TC148678				nr -
Unigene37262_All	1340	7.46	22.05	23.72	23.79	17.73	19.18	2.68	3.06	2.62	1.56E+00	5.23E-43	Up	1.67E+00	2.27E-49	Up	-4.24E-01	1.33E-06		-3.11E-01	1.05E-03		1.89E-01	5.42E-01		-3.58E-02	9.20E-01		Unigene37262_All//gi|90093310|gb|ABD85168.1|//2.00E-69//At3g22970 [Arabidopsis thaliana]	Unigene37262_All//9.00E-54//AT3G22970| unknown protein	Unigene37262_All//0.00E+00//gi|78328683|gb|DT548957.1|DT548957				nr +
Unigene37264_All	1075	17.18	18.05	24.82	0.65	1.60	1.01	3.97	1.01	1.45	7.14E-02	6.11E-01		5.31E-01	9.21E-07		1.30E+00	9.73E-03		6.36E-01	3.73E-01		-1.97E+00	3.68E-11	Down	-1.46E+00	7.58E-08	Down	Unigene37264_All//gi|190684635|gb|ACE82565.1|//1.00E-141//epoxide hydrolase [Nicotiana benthamiana]	Unigene37264_All//5.00E-124//AT3G05600| epoxide hydrolase, putative	Unigene37264_All//0.00E+00//gi|164260751|gb|ES846465.1|ES846465				nr +
Unigene37267_All	895	3.10	3.00	2.56	17.03	12.39	14.38	160.95	850.53	169.99	-4.63E-02	9.11E-01		-2.76E-01	4.99E-01		-4.59E-01	6.09E-04		-2.44E-01	1.15E-01		2.40E+00	0.00E+00	Up	7.89E-02	4.62E-02		Unigene37267_All//gi|283136100|gb|ADB11369.1|//3.00E-83//tau class glutathione transferase GSTU43 [Populus trichocarpa]	Unigene37267_All//5.00E-52//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	Unigene37267_All//0.00E+00//TC158719		ko00480|Glutathione metabolism		nr -
Unigene37270_All	707	16.72	9.82	8.81	20.64	15.00	21.34	26.91	12.71	10.14	-7.68E-01	3.38E-06		-9.24E-01	8.72E-08		-4.61E-01	8.04E-04		4.75E-02	7.81E-01		-1.08E+00	9.26E-20	Down	-1.41E+00	2.37E-30	Down	Unigene37270_All//gi|62751093|dbj|BAD95794.1|//2.00E-57//similar to 60S ribosomal protein L35 [Solanum lycopersicum]	Unigene37270_All//4.00E-56//AT5G02610| 60S ribosomal protein L35 (RPL35D)	Unigene37270_All//0.00E+00//TC143219		ko03010|Ribosome		nr -
Unigene37271_All	1308	20.80	9.80	6.51	64.74	52.39	36.57	17.23	3.96	5.79	-1.09E+00	5.49E-23	Down	-1.68E+00	2.32E-42	Down	-3.05E-01	3.30E-09		-8.24E-01	5.21E-48		-2.12E+00	4.33E-61	Down	-1.57E+00	4.22E-42	Down	Unigene37271_All//gi|224132502|ref|XP_002328301.1|//4.00E-68//GATA zinc finger protein regulating nitrogen assimilation [Populus trichocarpa] >gi|222837816|gb|EEE76181.1| GATA zinc finger protein regulating nitrogen assimilation [Populus trichocarpa]	Unigene37271_All//2.00E-33//AT1G08000| zinc finger (GATA type) family protein	Unigene37271_All//0.00E+00//TC151531	C2C2-GATA			nr -
Unigene37273_All	2485	40.26	19.29	40.29	16.48	18.55	12.85	0.34	0.37	1.72	-1.06E+00	1.11E-79	Down	1.00E-03	1.00E+00		1.71E-01	3.42E-02		-3.59E-01	9.91E-06		1.21E-01	8.54E-01		2.33E+00	7.73E-14	Up	Unigene37273_All//gi|15222513|ref|NP_174474.1|//0.00E+00//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75169173|sp|Q9C672.1|PPR68_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g31920	Unigene37273_All//0.00E+00//AT1G31920| pentatricopeptide (PPR) repeat-containing protein	Unigene37273_All//0.00E+00//TC137267				nr -
Unigene37276_All	633	3.14	5.04	3.45	4.80	4.95	6.21	3.21	1.65	0.88	6.83E-01	4.93E-02		1.35E-01	7.52E-01		4.44E-02	9.23E-01		3.71E-01	2.69E-01		-9.58E-01	1.83E-02		-1.86E+00	1.51E-05	Down	Unigene37276_All//gi|115461370|ref|NP_001054285.1|//2.00E-44//Os04g0680300 [Oryza sativa Japonica Group] >gi|32487404|emb|CAE05738.1| OSJNB00017101.18 [Oryza sativa (japonica cultivar-group)] >gi|113565856|dbj|BAF16199.1| Os04g0680300 [Oryza sativa Japonica Group]	Unigene37276_All//4.00E-37//AT4G21720| unknown protein	Unigene37276_All//0.00E+00//DW508164				nr -
Unigene37277_All	683	4.90	0.67	0.86	5.11	3.28	6.35	3.22	11.87	2.10	-2.88E+00	4.63E-11	Down	-2.52E+00	3.61E-09	Down	-6.40E-01	4.33E-02		3.14E-01	3.33E-01		1.88E+00	2.88E-19	Up	-6.16E-01	9.86E-02		Unigene37277_All//gi|15233747|ref|NP_194153.1|//2.00E-42//VEP1 (VEIN PATTERNING 1); binding / catalytic [Arabidopsis thaliana] >gi|21592923|gb|AAM64873.1| induced upon wounding stress [Arabidopsis thaliana] >gi|30725632|gb|AAP37838.1| At4g24220 [Arabidopsis thaliana] >gi|156187111|gb|ABU55811.1| progesterone 5-beta-reductase [Arabidopsis thaliana]	Unigene37277_All//3.00E-32//AT4G24220| VEP1 (VEIN PATTERNING 1); binding / catalytic	Unigene37277_All//0.00E+00//CO092012				nr -
Unigene37278_All	649	11.69	10.38	11.24	33.85	24.78	49.83	62.61	479.33	71.39	-1.71E-01	4.50E-01		-5.65E-02	8.06E-01		-4.50E-01	3.25E-05		5.58E-01	1.31E-09		2.94E+00	0.00E+00	Up	1.89E-01	7.17E-03		Unigene37278_All//gi|15233747|ref|NP_194153.1|//2.00E-62//VEP1 (VEIN PATTERNING 1); binding / catalytic [Arabidopsis thaliana] >gi|21592923|gb|AAM64873.1| induced upon wounding stress [Arabidopsis thaliana] >gi|30725632|gb|AAP37838.1| At4g24220 [Arabidopsis thaliana] >gi|156187111|gb|ABU55811.1| progesterone 5-beta-reductase [Arabidopsis thaliana]	Unigene37278_All//6.00E-46//AT4G24220| VEP1 (VEIN PATTERNING 1); binding / catalytic	Unigene37278_All//0.00E+00//gi|21094916|gb|BQ407229.1|BQ407229				nr -
Unigene37280_All	1243	73.49	43.21	55.69	52.30	44.27	39.35	40.04	14.69	10.16	-7.66E-01	2.62E-42		-4.00E-01	4.67E-13		-2.41E-01	8.93E-05		-4.10E-01	5.52E-11		-1.45E+00	7.20E-79	Down	-1.98E+00	2.74E-126	Down	Unigene37280_All//gi|297842881|ref|XP_002889322.1|//6.00E-93//oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335163|gb|EFH65581.1| oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37280_All//5.00E-93//AT1G79870| oxidoreductase family protein	Unigene37280_All//0.00E+00//TC138029		ko00620|Pyruvate metabolism//ko00260|Glycine, serine and threonine metabolism//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene37281_All	1329	1.69	4.00	9.54	15.74	9.56	7.75	75.68	30.32	52.82	1.24E+00	3.91E-06	Up	2.49E+00	3.03E-33	Up	-7.19E-01	6.26E-11		-1.02E+00	2.05E-17	Down	-1.32E+00	3.37E-138	Down	-5.19E-01	1.24E-29		Unigene37281_All//gi|13162619|gb|AAO09635.1|//1.00E-130//zinc transporter [Medicago truncatula] >gi|87241265|gb|ABD33123.1| Zinc/iron permease [Medicago truncatula]	Unigene37281_All//6.00E-100//AT5G59520| ZIP2; copper ion transmembrane transporter/ transferase, transferring glycosyl groups / zinc ion transmembrane transporter	Unigene37281_All//0.00E+00//TC170301				nr +
Unigene37282_All	699	27.69	25.81	22.24	22.52	21.23	25.59	37.02	18.18	15.39	-1.02E-01	4.72E-01		-3.16E-01	1.81E-02		-8.49E-02	6.03E-01		1.84E-01	2.15E-01		-1.03E+00	1.98E-24	Down	-1.27E+00	6.21E-35	Down	Unigene37282_All//gi|299855523|gb|ADJ57303.1|//2.00E-59//defender against cell death 1 [Gossypium hirsutum]	Unigene37282_All//2.00E-50//AT1G32210| ATDAD1 (DEFENDER AGAINST APOPTOTIC DEATH 1)	Unigene37282_All//0.00E+00//TC152387		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis		nr +
Unigene37283_All	1684	13.73	5.02	3.89	18.81	19.65	19.93	28.20	14.87	14.62	-1.45E+00	1.71E-30	Down	-1.82E+00	1.90E-40	Down	6.28E-02	5.97E-01		8.29E-02	4.83E-01		-9.23E-01	3.49E-37		-9.48E-01	6.55E-40		Unigene37283_All//gi|297844274|ref|XP_002890018.1|//2.00E-82//nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335860|gb|EFH66277.1| nuclear transport factor 2 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37283_All//4.00E-69//AT2G03640| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene37283_All//0.00E+00//gi|48815056|gb|CO116369.1|CO116369		ko03040|Spliceosome		nr -
Unigene37284_All	1277	6.51	40.47	4.80	20.44	61.75	53.05	40.66	69.62	155.27	2.64E+00	1.11E-146	Up	-4.42E-01	3.79E-02		1.60E+00	2.41E-138	Up	1.38E+00	5.67E-87	Up	7.76E-01	2.33E-51		1.93E+00	0.00E+00	Up	Unigene37284_All//gi|171452000|dbj|BAG15844.1|//2.00E-74//zinc-finger protein [Bruguiera gymnorhiza]	Unigene37284_All//7.00E-46//AT1G27730| STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding	Unigene37284_All//0.00E+00//TC137100	C2H2			nr +
Unigene37285_All	752	11.34	6.00	5.66	29.54	21.61	22.22	62.52	31.62	46.83	-9.19E-01	4.38E-06		-1.00E+00	1.57E-06	Down	-4.51E-01	2.77E-05		-4.11E-01	3.20E-04		-9.83E-01	8.17E-41		-4.17E-01	6.91E-10		Unigene37285_All//gi|224120498|ref|XP_002331062.1|//1.00E-81//vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa] >gi|222872992|gb|EEF10123.1| vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa]	Unigene37285_All//6.00E-80//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene37285_All//0.00E+00//TC151755		ko00190|Oxidative phosphorylation		nr -
Unigene37286_All	971	1.19	2.77	1.43	11.34	9.50	6.33	43.28	185.13	61.17	1.22E+00	1.97E-03		2.66E-01	6.23E-01		-2.55E-01	1.58E-01		-8.42E-01	5.32E-07		2.10E+00	0.00E+00	Up	4.99E-01	1.18E-16		Unigene37286_All//gi|15451136|gb|AAK96839.1|//4.00E-90//periaxin-like protein [Arabidopsis thaliana]	Unigene37286_All//5.00E-07//AT5G09530| hydroxyproline-rich glycoprotein family protein	Unigene37286_All//0.00E+00//TC152654		ko03040|Spliceosome		nr +

Unigene37287_All	2478	0.91	3.48	1.42	0.36	0.39	0.95	5.65	13.24	20.51	1.94E+00	2.60E-17	Up	6.44E-01	6.16E-02		1.05E-01	9.03E-01		1.39E+00	1.21E-03		1.23E+00	8.25E-41	Up	1.86E+00	2.03E-117	Up	Unigene37287_All//gi|92870237|gb|ABE79564.1|//0.00E+00//Membrane attack complex component/perforin/complement C9 [Medicago truncatula]	Unigene37287_All//0.00E+00//AT4G24290| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: NSL1 (necrotic spotted lesions 1) (TAIR:AT1G28380.1); Has 124 Blast hits to 124 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 41; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene37287_All//0.00E+00//TC161677				nr -
Unigene37288_All	1266	2.48	2.76	3.49	6.30	4.92	3.14	9.69	7.30	15.80	1.55E-01	6.30E-01		4.94E-01	1.06E-01		-3.55E-01	8.51E-02		-1.00E+00	7.86E-07	Down	-4.09E-01	4.98E-03		7.06E-01	9.24E-11		Unigene37288_All//gi|297603462|ref|NP_001051070.2|//6.00E-82//Os04g0647300 [Oryza sativa Japonica Group] >gi|255678832|dbj|BAF15984.2|Os04g0647300 [Oryza sativa Japonica Group]	Unigene37288_All//6.00E-66//AT5G10790| UBP22 (UBIQUITIN-SPECIFIC PROTEASE 22); ubiquitin thiolesterase/ ubiquitin-specific protease/ zinc ion binding	Unigene37288_All//0.00E+00//TC170115			nr -
Unigene37293_All	1471	7.01	11.71	10.72	9.11	16.81	20.63	21.64	31.34	32.45	7.41E-01	3.78E-08		6.13E-01	2.37E-05		8.84E-01	1.88E-17		1.18E+00	5.77E-31	Up	5.34E-01	2.45E-14		5.84E-01	1.01E-17		Unigene37293_All//gi|224066231|ref|XP_002302037.1|//1.00E-139//ABC transporter family protein [Populus trichocarpa] >gi|222843763|gb|EEE81310.1| ABC transporter family protein [Populus trichocarpa]	Unigene37293_All//1.00E-123//AT1G03905| ABC transporter family protein	Unigene37293_All//0.00E+00//TC168749	ko03018|RNA degradation		nr -
Unigene37296_All	2492	6.32	5.77	2.31	9.87	9.00	9.12	12.89	8.18	11.72	-1.30E-01	3.91E-01		-1.45E+00	3.47E-20	Down	-1.35E-01	2.87E-01		-1.15E-01	3.93E-01		-6.56E-01	1.91E-14		-1.38E-01	1.26E-01		Unigene37296_All//gi|222424052|dbj|BAH19987.1|//0.00E+00//AT1G73930| unknown protein	Unigene37296_All//0.00E+00//AT1G73930| unknown protein	Unigene37296_All//0.00E+00//TC159499			nr +
Unigene37298_All	1388	1.70	1.24	0.92	3.52	2.75	2.21	6.76	10.54	16.27	-4.51E-01	2.83E-01		-8.82E-01	4.40E-02		-3.53E-01	2.11E-01		-6.69E-01	1.34E-02		6.40E-01	9.28E-07		1.27E+00	2.29E-30	Up	Unigene37298_All//gi|224093334|ref|XP_002309886.1|//1.00E-124//photoperiod-response-like protein [Populus trichocarpa] >gi|224093344|ref|XP_002309891.1| photoperiod-response-like protein [Populus trichocarpa] >gi|222852789|gb|EEE90336.1| photoperiod-response-like protein [Populus trichocarpa] >gi|222852794|gb|EEE90341.1| photoperiod-response-like protein [Populus trichocarpa]	Unigene37298_All//3.00E-105//AT5G61660| U-box domain-containing protein	Unigene37298_All//0.00E+00//gi|164364903|gb|ES810624.1|ES810624	ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene37299_All	514	0.61	0.00	0.41	2.04	4.29	3.43	3.29	4.96	9.84	-9.25E+00	3.65E-02		-5.59E-01	6.63E-01		1.08E+00	1.21E-02		7.52E-01	1.39E-01		5.92E-01	9.90E-02		1.58E+00	4.57E-10	Up	Unigene37299_All//gi|4249381|gb|AAD14478.1|//5.00E-08//Strong similarity to gb|AF039376 Evelknievel retrotransposon polyprotein from Arabidopsis arenosa [Arabidopsis thaliana]		Unigene37299_All//0.00E+00//TC168633			nr +
Unigene373_All	3440	0.68	0.71	1.01	16.44	4.41	6.76	26.14	24.02	9.16	4.69E-02	9.20E-01		5.56E-01	1.13E-01		-1.90E+00	1.35E-135	Down	-1.28E+00	4.11E-66	Down	-1.22E-01	2.00E-02		-1.51E+00	3.30E-156	Down	Unigene373_All//gi|297653362|ref|XP_002894562.1|//0.00E+00//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340404|gb|EFH70821.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene373_All//0.00E+00//AT1G56145| leucine-rich repeat family protein / protein kinase family protein	Unigene373_All//0.00E+00//TC133493	ko04626|Plant-pathogen interaction		nr -
Unigene3730_All	817	3.33	5.46	2.87	13.60	11.38	30.02	18.06	22.30	118.20	7.13E-01	1.30E-02		-2.16E-01	6.19E-01		-2.57E-01	1.53E-01		1.14E+00	6.64E-24	Up	3.05E-01	1.03E-02		2.71E+00	0.00E+00	Up	Unigene3730_All//gi|300507127|gb|ADK23939.1|//8.00E-90//3FAD [Gossypium hirsutum]	Unigene3730_All//2.00E-80//AT5G05580| FAD8 (FATTY ACID DESATURASE 8); omega-3 fatty acid desaturase	Unigene3730_All//0.00E+00//TC168802	ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene37300_All	1482	1.73	1.50	1.37	2.49	7.13	4.39	1.08	3.86	11.34	-2.02E-01	6.10E-01		-3.41E-01	4.07E-01		1.52E+00	1.86E-17	Up	8.19E-01	3.33E-04		1.83E+00	2.30E-13	Up	3.39E+00	4.79E-77	Up	Unigene37300_All//gi|90265044|emb|CAH67640.1|//7.00E-17//H0102C09.1 [Oryza sativa (indica cultivar-group)]	Unigene37300_All//2.00E-06//AT5G48050| unknown protein	Unigene37300_All//0.00E+00//gi|78352252|gb|DT572526.1|DT572526			nr +
Unigene37304_All	977	36.36	26.03	20.00	57.00	49.10	59.63	57.56	24.64	24.14	-4.82E-01	7.67E-08		-8.62E-01	1.01E-19		-2.15E-01	1.62E-03		6.50E-02	4.58E-01		-1.22E+00	5.02E-69	Down	-1.25E+00	1.04E-73	Down	Unigene37304_All//gi|15230011|ref|NP_187210.1|//2.00E-90//RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome [Arabidopsis thaliana] >gi|21431838|sp|P42791.2|RL182_ARATH RecName: Full=60S ribosomal protein L18-2 >gi|14335090|gb|AAK59824.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] >gi|16974509|gb|AAL31164.1| AT3g05590/F18C1_14 [Arabidopsis thaliana]	Unigene37304_All//1.00E-91//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome	Unigene37304_All//0.00E+00//TC150222	ko03010|Ribosome		nr -
Unigene37308_All	833	29.02	16.61	12.91	39.95	27.86	33.40	54.31	22.98	25.20	-8.05E-01	9.64E-13		-1.17E+00	4.61E-22	Down	-5.20E-01	9.66E-10		-2.58E-01	6.41E-03		-1.24E+00	7.00E-57	Down	-1.11E+00	5.73E-49	Down	Unigene37308_All//gi|209967445|gb|ACJ02351.1|//1.00E-59//60S ribosomal protein L31 [Vernicia fordii]	Unigene37308_All//3.00E-43//AT5G36710| 60S ribosomal protein L31 (RPL31C)	Unigene37308_All//0.00E+00//gi|84174904|gb|DR463552.1|DR463552		ko03010|Ribosome		nr +
Unigene3731_All	1062	0.94	1.29	0.60	3.89	3.89	10.29	7.05	6.34	55.22	4.61E-01	4.11E-01		-6.38E-01	3.90E-01		-8.00E-04	9.87E-01		1.40E+00	7.59E-15	Up	-1.53E-01	4.89E-01		2.97E+00	4.67E-236	Up	Unigene3731_All//gi|300507127|gb|ADK23939.1|//1.00E-107//3FAD [Gossypium hirsutum]	Unigene3731_All//8.00E-95//AT5G05580| FAD8 (FATTY ACID DESATURASE 8); omega-3 fatty acid desaturase	Unigene3731_All//0.00E+00//TC168802	ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene37310_All	1176	4.40	25.89	3.12	5.17	7.50	7.18	8.16	13.11	7.55	2.56E+00	1.09E-83	Up	-4.95E-01	7.63E-02		5.37E-01	4.20E-03		4.75E-01	1.83E-02		6.84E-01	7.28E-08		-1.12E-01	5.58E-01		Unigene37310_All//gi|259121427|gb|ACV92033.1|//2.00E-70//WRKY transcription factor 31 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene37310_All//1.00E-37//AT5G49520| WRKY48; transcription factor	Unigene37310_All//0.00E+00//gi|73860919|gb|DT463658.1|DT463658	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene37311_All	1672	6.60	5.55	5.10	10.40	9.04	5.81	12.49	5.60	7.84	-2.52E-01	1.62E-01		-3.74E-01	4.13E-02		-2.02E-01	1.56E-01		-8.40E-01	1.21E-10		-1.16E+00	5.41E-24	Down	-6.72E-01	2.10E-10		Unigene37311_All//gi|224132502|ref|XP_002328301.1|//2.00E-57//GATA zinc finger protein regulating nitrogen assimilation [Populus trichocarpa] >gi|222837816|gb|EEE76181.1| GATA zinc finger protein regulating nitrogen assimilation [Populus trichocarpa]	Unigene37311_All//2.00E-32//AT1G08010| zinc finger (GATA type) family protein	Unigene37311_All//0.00E+00//gi|78323642|gb|DT543916.1|DT543916	C2C2-GATA		nr -
Unigene37312_All	1285	14.94	7.14	12.31	23.76	21.65	24.04	21.02	9.17	10.39	-1.07E+00	5.44E-16	Down	-2.80E-01	4.02E-02		-1.34E-01	2.22E-01		1.67E-02	9.03E-01		-1.20E+00	1.97E-32	Down	-1.02E+00	6.86E-26	Down	Unigene37312_All//gi|15241434|ref|NP_196957.1|//1.00E-159//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|108385403|gb|ABF85783.1| At5g14530 [Arabidopsis thaliana]	Unigene37312_All//1.00E-160//AT5G14530| transducin family protein / WD-40 repeat family protein	Unigene37312_All//0.00E+00//TC154347			nr +
Unigene37314_All	1358	5.70	3.92	6.98	12.77	18.74	16.66	18.87	10.68	5.34	-5.42E-01	9.69E-03		2.92E-01	1.50E-01		5.54E-01	3.19E-08		3.84E-01	7.56E-04		-8.21E-01	6.77E-17		-1.82E+00	1.50E-58	Down	Unigene37314_All//gi|158563847|sp|Q8LER2.2|ADEL6_ARATH//0.00E+00//RecName: Full=Alcohol dehydrogenase-like 6 >gi|19310538|gb|AAL85002.1| AT5g24760/T4C12_30 [Arabidopsis thaliana] >gi|20334800|gb|AAM16261.1| AT5g24760/T4C12_30 [Arabidopsis thaliana]	Unigene37314_All//0.00E+00//AT5G24760| alcohol dehydrogenase, putative	Unigene37314_All//0.00E+00//TC146613	ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr +
Unigene37315_All	1687	49.65	13.70	47.76	14.00	14.94	13.31	0.00	0.77	0.19	-1.86E+00	5.22E-155	Down	-5.62E-02	4.08E-01		9.43E-02	4.85E-01		-7.30E-02	6.31E-01		9.59E+00	3.67E-09	Up	7.56E+00	1.34E-02		Unigene37315_All//gi|187711143|gb|ACD14144.1|//0.00E+00//limonoid UDP-glucosyltransferase [Citrus x paradisi]	Unigene37315_All//3.00E-158//AT4G15480| UGT84A1; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene37315_All//0.00E+00//gi|78338844|gb|DT559118.1|DT559118		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr -
Unigene37316_All	1756	5.24	2.83	2.58	10.52	11.81	6.64	11.34	3.31	4.06	-8.91E-01	3.27E-06		-1.02E+00	3.05E-07	Down	1.66E-01	2.22E-01		-6.66E-01	9.98E-08		-1.78E+00	7.03E-43	Down	-1.48E+00	3.41E-34	Down	Unigene37316_All//gi|44917443|gb|AAS49046.1|//2.00E-64//At2g30820 [Arabidopsis thaliana] >gi|52412271|gb|AAU45205.1| At2g30820 [Arabidopsis thaliana]	Unigene37316_All//4.00E-85//AT1G06660| unknown protein	Unigene37316_All//0.00E+00//D8462440			nr +
Unigene37317_All	1794	0.82	1.10	0.00	1.67	1.86	1.59	1.48	0.54	0.98	4.32E-01	3.69E-01		-9.67E+00	5.25E-08	Down	1.60E-01	6.91E-01		-7.10E-02	8.58E-01		-1.47E+00	4.62E-05	Down	-6.04E-01	6.93E-02		Unigene37317_All//gi|44917443|gb|AAS49046.1|//3.00E-68//At2g30820 [Arabidopsis thaliana] >gi|52412271|gb|AAU45205.1| At2g30820 [Arabidopsis thaliana]	Unigene37317_All//2.00E-87//AT1G06660| unknown protein	Unigene37317_All//0.00E+00//gi|78347756|gb|DT568030.1|DT568030			nr -
Unigene37320_All	1214	70.34	143.66	115.45	71.89	132.07	79.76	34.55	40.18	26.68	1.03E+00	2.12E-131	Up	7.15E-01	1.89E-55		8.77E-01	1.73E-110		1.50E-01	5.98E-03		2.18E-01	1.74E-03		-3.73E-01	2.04E-07		Unigene37320_All//gi|255542772|ref|XP_002512449.1|//5.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223548410|gb|EEF49901.1| conserved hypothetical protein [Ricinus communis]		Unigene37320_All//0.00E+00//gi|78333488|gb|DT553762.1|DT553762			nr +
Unigene37325_All	1662	2.99	4.27	3.72	1.71	2.94	4.67	5.19	6.71	12.44	5.13E-01	2.02E-02		3.14E-01	2.34E-01		7.84E-01	2.76E-03		1.45E+00	2.98E-11	Up	3.72E-01	1.65E-02		1.26E+00	1.10E-27	Up	Unigene37325_All//gi|224104985|ref|XP_002313644.1|//0.00E+00//proline transporter [Populus trichocarpa] >gi|222850052|gb|EEE87599.1| proline transporter [Populus trichocarpa]	Unigene37325_All//3.00E-156//AT1G08230| amino acid transporter family protein	Unigene37325_All//0.00E+00//TC163288			nr -

Unigene37326_All	1407	233.38	99.83	172.20	21.49	20.17	17.43	0.33	1.81	0.82	-1.23E+00	0.00E+00	Down	-4.39E-01	9.21E-54		-9.17E-02	4.41E-01		-3.02E-01	2.12E-03		2.45E+00	7.84E-09	Up	1.31E+00	1.95E-02		Unigene37326_All//gi|18399397|ref|NP_565476.1|//1.00E-114//GPRI1 (GBF'S PRO-RICH REGION-INTERACTING FACTOR 1); transcription factor/ transcription regulator [Arabidopsis thaliana] >gi|13311003|gb|AAK16743.1| golden2-like transcription factor [Arabidopsis thaliana] >gi|13432088|gb|AAK20120.1| golden2-like protein 1 [Arabidopsis thaliana] >gi|15451040|gb|AAK96791.1| Unknown protein [Arabidopsis thaliana] >gi|17221599|dbj|BAB78466.1| GPRI1 [Arabidopsis thaliana] >gi|20198041|gb|AAD21709.2| expressed protein [Arabidopsis thaliana] >gi|20198084|gb|AAM15392.1| expressed protein [Arabidopsis thaliana]	Unigene37326_All//2.00E-100//AT2G20570| GPRI1 (GBF'S PRO-RICH REGION-INTERACTING FACTOR 1); transcription factor/ transcription regulator	Unigene37326_All//0.00E+00//gi|48776760|gb|CO086126.1|CO086126	G2-like	ko03040|Spliceosome		nr +
Unigene37329_All	794	4.28	3.77	5.10	39.15	38.08	37.14	6.60	2.90	4.16	-1.86E-01	6.17E-01		2.51E-01	4.39E-01		-4.00E-02	7.70E-01		-7.59E-02	5.36E-01		-1.19E+00	7.07E-07	Down	-6.65E-01	3.11E-03		Unigene37329_All//gi|116310885|emb|CAH67825.1|//4.00E-08//B0616E02-H0507E05.1 [Oryza sativa (indica cultivar-group)]	Unigene37329_All//4.00E-24//AT1G63310| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: oxidoreductase, acting on NADH or NADPH (TAIR:AT1G75260.1); Has 35 Blast hits to 35 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene37329_All//0.00E+00//TC152026				nr +
Unigene37330_All	1020	39.34	80.03	75.07	25.00	27.04	27.28	2.65	2.50	4.22	1.02E+00	2.95E-61	Up	9.32E-01	7.87E-48		1.13E-01	3.52E-01		1.25E-01	3.07E-01		-8.59E-02	8.11E-01		6.69E-01	8.12E-03		Unigene37330_All//gi|254692064|emb|CBA10126.1|//2.00E-83//PME inhibitor [Nicotiana benthamiana]	Unigene37330_All//8.00E-34//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene37330_All//0.00E+00//gi|164319252|gb|ES794654.1|ES794654		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene37331_All	1627	7.56	4.95	2.85	4.78	4.44	3.08	0.18	0.23	0.12	-6.10E-01	1.48E-04		-1.41E+00	3.56E-15	Down	-1.04E-01	6.68E-01		-6.32E-01	2.07E-03		3.46E-01	7.38E-01		-5.72E-01	6.28E-01		Unigene37331_All//gi|40850578|gb|AB986009.1|//0.00E+00//crinkly4-like protein [Musa acuminata]	Unigene37331_All//0.00E+00//AT3G59420| ACR4 (ARABIDOPSIS CRINKLY4); kinase/ transmembrane receptor protein kinase	Unigene37331_All//0.00E+00//TC149774		ko04626|Plant-pathogen interaction		nr -
Unigene37334_All	1069	0.29	0.00	0.00	3.26	2.06	0.25	2.61	2.27	1.27	-8.20E+00	3.65E-02		-8.20E+00	4.90E-02		-6.62E-01	3.64E-02		-3.69E+00	2.33E-15	Down	-2.03E-01	6.08E-01		-1.04E+00	1.44E-03		Unigene37334_All//gi|28950973|gb|AC063410.1|//1.00E-118//At1g23340 [Arabidopsis thaliana]	Unigene37334_All//2.00E-102//AT1G70550| unknown protein	Unigene37334_All//1.00E-86//gi|78329842|gb|DT550116.1|DT550116				nr +
Unigene37335_All	1837	0.40	0.28	0.20	8.19	5.45	2.58	1.91	2.41	1.84	-5.32E-01	5.13E-01		-9.75E-01	2.64E-01		-5.86E-01	9.91E-06		-1.67E+00	2.35E-26	Down	3.36E-01	2.22E-01		-5.14E-02	8.72E-01		Unigene37335_All//gi|28950973|gb|AC063410.1|//0.00E+00//At1g23340 [Arabidopsis thaliana]	Unigene37335_All//4.00E-173//AT1G70550| unknown protein	Unigene37335_All//7.00E-176//gi|78329842|gb|DT550116.1|DT550116				nr +
Unigene37337_All	1333	30.54	6.65	6.35	17.23	14.65	8.10	0.10	0.03	0.06	-2.20E+00	4.02E-94	Down	-2.27E+00	2.75E-94	Down	-2.34E-01	4.29E-02		-1.09E+00	4.57E-21	Down	-1.60E+00	5.34E-01		-6.71E-01	7.19E-01		Unigene37337_All//gi|9294638|dbj|BAB02977.1|//1.00E-67//glycolate oxidase [Arabidopsis thaliana]	Unigene37337_All//6.00E-69//AT3G14130| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene37337_All//0.00E+00//gi|73850349|gb|DT459369.1|DT459369		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene37339_All	1308	2.20	0.66	1.30	3.62	1.42	3.38	4.62	1.60	1.31	-1.74E+00	1.44E-05	Down	-7.56E-01	5.03E-02		-1.35E+00	2.99E-07	Down	-9.65E-02	7.46E-01		-1.53E+00	4.03E-11	Down	-1.82E+00	1.94E-14	Down	Unigene37339_All//gi|231610|sp|P29790.1|ATPG_TOBAC//1.00E-136//RecName: Full=ATP synthase gamma chain, chloroplastic; AltName: Full=F-ATPase gamma subunit; Flags: Precursor >gi|19785|emb|CAA45152.1| ATP synthase (gamma subunit) [Nicotiana tabacum]	Unigene37339_All//3.00E-128//AT1G15700| ATPC2; enzyme regulator	Unigene37339_All//0.00E+00//TC171680		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr +
Unigene37340_All	953	16.31	114.31	58.50	74.12	322.85	340.31	27.37	41.80	58.48	2.81E+00	0.00E+00	Up	1.84E+00	3.99E-99	Up	2.12E+00	0.00E+00	Up	2.20E+00	0.00E+00	Up	6.11E-01	1.11E-15		1.10E+00	1.28E-58	Up	Unigene37340_All//gi|18412668|ref|NP_565230.1|//2.00E-43//binding [Arabidopsis thaliana] >gi|5902369|gb|AAD55471.1|AC009322_11 Unknown protein [Arabidopsis thaliana]	Unigene37340_All//9.00E-29//AT5G20190| binding	Unigene37340_All//0.00E+00//TC165464				nr -
Unigene37341_All	706	20.45	18.16	15.99	30.98	29.51	39.60	59.77	27.41	32.90	-1.72E-01	2.86E-01		-3.55E-01	2.38E-02		-7.00E-02	6.15E-01		3.54E-01	4.85E-04		-1.12E+00	1.56E-45	Down	-8.61E-01	2.05E-30		Unigene37341_All//gi|116292768|gb|ABJ97690.1|//5.00E-89//EBP1 [Solanum tuberosum]	Unigene37341_All//1.00E-78//AT3G51800| ATG2; aminopeptidase/ metalloexopeptidase	Unigene37341_All//0.00E+00//gi|13355664|gb|BG446012.1|BG446012				nr +
Unigene37345_All	3339	1.28	0.52	1.12	5.83	6.46	3.63	0.63	0.70	0.68	-1.32E+00	1.55E-05	Down	-2.03E-01	5.35E-01		1.46E-01	2.85E-01		-6.86E-01	1.59E-08		1.47E-01	7.14E-01		1.03E-01	7.85E-01		Unigene37345_All//gi|15242342|ref|NP_197062.1|//1.00E-105//LNG1 (LONGIFOLIA1) [Arabidopsis thaliana]	Unigene37345_All//4.00E-79//AT1G74160| unknown protein	Unigene37345_All//0.00E+00//TC165117				nr -
Unigene37348_All	1119	11.32	8.33	10.28	55.60	31.70	15.01	26.30	6.13	3.92	-4.42E-01	5.58E-03		-1.39E-01	4.41E-01		-8.11E-01	6.03E-39		-1.89E+00	2.84E-128	Down	-2.10E+00	1.09E-78	Down	-2.75E+00	2.70E-111	Down	Unigene37348_All//gi|27808522|gb|AC024541.1|//3.00E-36//At4g33985 [Arabidopsis thaliana]	Unigene37348_All//2.00E-31//AT4G33985| unknown protein	Unigene37348_All//0.00E+00//TC141664		ko03040|Spliceosome		nr +
Unigene37349_All	963	7.61	5.68	6.97	13.14	11.66	12.57	24.76	11.81	8.60	-4.21E-01	5.46E-02		-1.27E-01	6.28E-01		-1.73E-01	3.25E-01		-6.40E-02	7.22E-01		-1.07E+00	4.47E-24	Down	-1.52E+00	1.62E-42	Down			Unigene37349_All//5.00E-163//TC165524				
Unigene37350_All	1114	2.77	1.82	2.63	12.25	10.05	10.05	15.03	13.92	6.69	-6.07E-01	8.64E-02		-7.59E-02	8.35E-01		-2.86E-01	6.29E-02		-2.85E-01	7.44E-02		-1.11E-01	4.38E-01		-1.17E+00	2.79E-20	Down			Unigene37350_All//0.00E+00//TC175638				
Unigene37352_All	1127	3.11	3.64	1.28	5.26	5.53	4.09	4.35	4.56	5.02	2.28E-01	4.72E-01		-1.29E+00	2.79E-04	Down	7.23E-02	8.25E-01		-3.64E-01	1.58E-01		6.79E-02	7.94E-01		2.06E-01	3.84E-01		Unigene37352_All//gi|255580791|ref|XP_002531216.1|//6.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223529176|gb|EEF31152.1| conserved hypothetical protein [Ricinus communis]		Unigene37352_All//4.00E-167//DW227095				nr +
Unigene37353_All	1846	3.12	2.91	2.80	26.26	20.91	7.36	21.03	22.89	23.39	-9.97E-02	6.91E-01		-1.56E-01	5.93E-01		-3.28E-01	3.05E-06		-1.83E+00	4.73E-96	Down	1.23E-01	1.36E-01		1.54E-01	4.00E-02		Unigene37353_All//gi|224080717|ref|XP_002306215.1|//1.00E-168//lysine/histidine transporter [Populus trichocarpa] >gi|222849179|gb|EEE86726.1| lysine/histidine transporter [Populus trichocarpa]	Unigene37353_All//1.00E-122//AT4G35180| LHT7 (Lys/His transporter 7); amino acid transmembrane transporter	Unigene37353_All//0.00E+00//TC164480				nr +
Unigene37354_All	1107	1.13	2.29	3.22	2.52	2.64	2.33	6.15	3.66	4.17	1.01E+00	1.17E-02		1.51E+00	2.50E-05	Up	6.94E-02	8.73E-01		-1.16E-01	7.65E-01		-7.48E-01	1.88E-04		-5.59E-01	4.03E-03		Unigene37354_All//gi|148270944|gb|AB053642.1|//2.00E-49//60S ribosomal protein L32A [Cucumis melo]	Unigene37354_All//9.00E-47//AT4G18100| 60S ribosomal protein L32 (RPL32A)	Unigene37354_All//1.00E-170//TC144900		ko03010|Ribosome		nr -
Unigene37355_All	1461	8.34	5.79	5.54	13.71	10.11	4.51	4.28	1.69	0.65	-5.27E-01	1.14E-03		-5.91E-01	4.33E-04		-4.39E-01	1.27E-04		-1.60E+00	4.64E-33	Down	-1.34E+00	1.44E-09	Down	-2.71E+00	6.69E-24	Down	Unigene37355_All//gi|297725701|ref|NP_001175214.1|//2.00E-19//Os07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1| Os07g0501200 [Oryza sativa Japonica Group]	Unigene37355_All//2.00E-13//AT3G25270| nucleic acid binding	Unigene37355_All//2.00E-175//DW229962				nr -
Unigene37357_All	1060	3.75	8.13	5.12	6.39	6.40	6.22	10.85	11.59	8.98	1.12E+00	4.36E-08	Up	4.50E-01	9.79E-02		1.90E-03	9.99E-01		-3.91E-02	8.90E-01		9.56E-02	6.02E-01		-2.72E-01	7.07E-02		Unigene37357_All//gi|21592748|gb|AAM64697.1|//5.00E-37//PRT1 [Arabidopsis thaliana]	Unigene37357_All//1.00E-37//AT3G24800| PRT1 (PROTEOLYSIS 1); ubiquitin-protein ligase	Unigene37357_All//0.00E+00//TC177531				nr +
Unigene37359_All	1803	39.84	194.19	69.29	62.44	94.96	97.69	50.70	124.58	92.65	2.29E+00	0.00E+00	Up	7.98E-01	7.68E-60		6.05E-01	5.41E-62		6.46E-01	1.70E-64		1.30E+00	3.31E-299	Up	8.70E-01	5.11E-119		Unigene37359_All//gi|110736458|dbj|BAF00197.1|//8.00E-10//enoyl-CoA hydratase like protein [Arabidopsis thaliana]	Unigene37359_All//4.00E-11//AT4G16210| ECHIA (ENOYL-COA HYDRATASE/ISOMERASE A); catalytic	Unigene37359_All//0.00E+00//gi|164299579|gb|ES813070.1|ES813070		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism		nr -
Unigene3736_All	2261	1.57	0.92	0.73	6.46	5.60	3.86	6.43	3.16	2.27	-7.76E-01	1.71E-02		-1.11E+00	1.34E-03		-2.04E-01	1.97E-01		-7.44E-01	1.91E-07		-1.03E+00	4.57E-14	Down	-1.50E+00	1.11E-25	Down	Unigene3736_All//gi|122172235|sp|Q0GZS3.1|USP_CUCME//0.00E+00//RecName: Full=UDP-sugar pyrophosphorylase; AltName: Full=UDP-galactose/glucose pyrophosphorylase; Short=UG6Pase >gi|88954061|gb|ABD59006.1| UDP-galactose/glucose pyrophosphorylase [Cucumis melo]	Unigene3736_All//0.00E+00//AT5G52560| ATUSP (ARABIDOPSIS THALIANA UDP-SUGAR PYROPHOSPHORYLASE); UTP-monosaccharide-1-phosphate uridylyltransferase/ UTP:arabinose-1-phosphate uridylyltransferase/ UTP:galactose-1-phosphate uridylyltransferase/ UTP:glucose-1-phosphate uridylyltransferase/ UTP:xy	Unigene3736_All//0.00E+00//TC179044		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene37360_All	657	1.19	11.41	2.59	0.23	1.00	1.17	0.77	1.02	0.49	3.26E+00	8.73E-27	Up	1.12E+00	3.58E-02		2.13E+00	3.78E-02		2.36E+00	1.34E-02		3.99E-01	6.48E-01		-6.71E-01	4.48E-01		Unigene37360_All//gi|114329246|gb|ABI64152.1|//1.00E-67//hydroxymethylbutenyl diphosphate reductase [Camptotheca acuminata]	Unigene37360_All//2.00E-64//AT4G34350| HDR (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE REDUCTASE); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase/ 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Unigene37360_All//0.00E+00//TC138347		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene37362_All	1379	5.27	4.41	2.43	8.81	10.79	10.58	16.71	2.12	4.54	-2.58E-01	2.56E-01		-1.12E+00	1.24E-06	Down	2.92E-01	4.85E-02		2.63E-01	9.33E-02		-2.98E+00	5.77E-92	Down	-1.88E+00	4.23E-55	Down	Unigene37362_All//gi|115646844|gb|ABJ17137.1|//4.00E-90//At4g02800 [Arabidopsis thaliana]	Unigene37362_All//2.00E-91//AT4G02800| unknown protein	Unigene37362_All//0.00E+00//TC177282				nr +
Unigene37365_All	1046	10.00	5.09	8.91	7.67	7.60	2.20	2.22	1.80	1.52	-9.76E-01	5.93E-08		-1.67E-01	3.91E-01		-1.18E-02	9.52E-01		-1.80E+00	7.03E-16	Down	-3.06E-01	4.43E-01		-5.45E-01	1.33E-01		Unigene37365_All//gi|297842595|ref|XP_002889179.1|//5.00E-69//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335020|gb|EFH65435.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37365_All//3.00E-69//AT1G78210| hydrolase, alpha/beta fold family protein	Unigene37365_All//0.00E+00//TC147452				nr -
Unigene37366_All	871	4.63	9.31	5.69	5.49	4.86	3.32	7.14	7.44	8.32	1.01E+00	1.25E-06	Up	2.98E-01	3.18E-01		-1.75E-01	5.77E-01		-7.26E-01	7.68E-03		5.98E-02	7.96E-01		2.22E-01	2.76E-01		Unigene37366_All//gi|22535608|dbj|BAC10782.1|//6.00E-10//HGWP repeat containing protein-like [Oryza sativa Japonica Group]		Unigene37366_All//4.00E-114//BP276244				nr -
Unigene37367_All	344	0.00	0.00	0.00	1.88	1.30	0.92	3.56	3.65	0.81	null	null		null	null		-5.33E-01	5.38E-01		-1.03E+00	2.68E-01		3.23E-02	9.83E-01		-2.14E+00	3.24E-04	Down	Unigene37367_All//gi|14326489|gb|AA660290.1|AF385697_1//1.00E-20//AT5g10580/F12B17_70 [Arabidopsis thaliana] >gi|18700208|gb|AAL77714.1| AT5g10580/F12B17_70 [Arabidopsis thaliana]	Unigene37367_All//4.00E-22//AT5G10580| unknown protein	Unigene37367_All//4.00E-78//TC133038				nr +

Unigene37368_All	1250	2.80	0.57	0.43	364.52	144.46	129.06	419.69	313.40	67.25	-2.31E+00	3.50E-09	Down	-2.72E+00	2.23E-10	Down	-1.34E+00	0.00E+00	Down	-1.50E+00	0.00E+00	Down	-4.21E-01	2.20E-100		-2.64E+00	0.00E+00	Down	Unigene37368_All//gi|14326489|gb|AAK60290.1|AF385697_1/2.00E-82//AT5g10580/F12B17_70 [Arabidopsis thaliana] >gi|18700208|gb|AAL77714.1|AT5g10580/F12B17_70 [Arabidopsis thaliana]	Unigene37368_All//2.00E-92//AT4G31330| unknown protein	Unigene37368_All//0.00E+00//TC133038				nr +
Unigene37369_All	1912	0.11	0.00	0.06	8.88	2.23	2.91	6.30	2.89	4.73	-6.77E+00	1.22E-01		-9.75E-01	6.21E-01		-1.99E+00	1.22E-43	Down	-1.61E+00	2.30E-28	Down	-1.13E+00	1.27E-13	Down	-4.14E-01	3.59E-03		Unigene37369_All//gi|227121314|gb|ACP19347.1|//0.00E+00//phosphate transporter [Glycine max]	Unigene37369_All//2.00E-163//AT1G76430| phosphate transporter family protein				nr +
Unigene37370_All	983	2.93	75.67	3.95	3.09	9.28	13.28	3.57	7.74	12.69	4.69E+00	0.00E+00	Up	4.34E-01	1.91E-01		1.59E+00	4.80E-16	Up	2.10E+00	1.28E-30	Up	1.12E+00	9.30E-09	Up	1.83E+00	9.47E-29	Up	Unigene37370_All//gi|19911579|dbj|BAB86893.1|//5.00E-76//syringolide-induced protein 1-3-1B [Glycine max]	Unigene37370_All//4.00E-71//AT5G04760| myb family transcription factor	Unigene37370_All//0.00E+00//TC143121	MYB	ko04712|Circadian rhythm - plant		nr +
Unigene37371_All	2208	1.61	0.96	1.54	5.71	6.13	3.74	2.89	0.47	2.42	-7.41E-01	2.28E-02		-6.20E-02	8.57E-01		1.03E-01	5.84E-01		-6.09E-01	8.64E-05		-2.61E+00	1.21E-22	Down	-2.58E-01	2.30E-01		Unigene37371_All//gi|9280691|gb|AAF86560.1|AC069252_19/1.00E-166//F2E2.13 [Arabidopsis thaliana]	Unigene37371_All//1.00E-149//AT1G22060| LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT1G22000.1); Has 67094 Blast hits to 30189 proteins in 1408 species: Archae - 880; Bacteria - 6261; Metazoa - 35085; Fungi - 5326; Plants - 2622; Viruses - 293; Other Eukaryotes - 16627 (source: NCBI BLink).	Unigene37371_All//0.00E+00//gi|109857375|gb|DW486354.1|DW486354				nr -
Unigene37372_All	1124	27.51	25.02	27.38	32.35	29.56	32.06	33.03	22.91	15.60	-1.37E-01	2.03E-01		-6.70E-03	9.74E-01		-1.30E-01	1.87E-01		-1.29E-02	9.22E-01		-5.28E-01	1.72E-11		-1.08E+00	6.60E-39	Down	Unigene37372_All//gi|115482774|ref|NP_001061980.1|//1.00E-47//Os10g0500500 [Oryza sativa Japonica Group] >gi|31432894|gb|AAP54470.1| ribosomal protein S18 containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639589|dbj|BAF26894.1|Os10g0500500 [Oryza sativa Japonica Group]	Unigene37372_All//7.00E-44//AT1G07210| 30S ribosomal protein S18 family	Unigene37372_All//0.00E+00//ES845491		ko03010|Ribosome		nr +
Unigene37373_All	1953	12.94	24.49	16.17	3.09	4.43	6.36	4.29	8.32	5.65	9.21E-01	2.11E-30		3.21E-01	1.39E-03		5.20E-01	6.28E-03		1.04E+00	9.03E-11	Up	9.58E-01	4.93E-14		3.99E-01	7.93E-03		Unigene37373_All//gi|159895659|gb|ABX10440.1|//0.00E+00//3-ketoacyl-CoA synthase 10 [Gossypium hirsutum]	Unigene37373_All//0.00E+00//AT1G01120| KCS1 (3-KETOACYL-COA SYNTHASE 1); acyltransferase/ fatty acid elongase	Unigene37373_All//0.00E+00//TC135385		ko00061|Fatty acid biosynthesis		nr +
Unigene37375_All	1177	16.49	14.03	19.18	1.35	1.96	1.84	1.65	0.39	0.20	-2.33E-01	7.70E-02		2.18E-01	8.59E-02		5.34E-01	2.24E-01		4.44E-01	3.51E-01		-2.08E+00	8.32E-06	Down	-3.02E+00	8.70E-09	Down	Unigene37375_All//gi|186478451|ref|NP_172824.3|//1.00E-118//phospholipase C/ phosphoric diester hydrolase [Arabidopsis thaliana] >gi|8920573|gb|AAF81295.1|AC027656_12 Contains similarity to MAP3K-like protein kinase from Arabidopsis thaliana gb|Z99707	Unigene37375_All//2.00E-119//AT1G13080| phospholipase C/ phosphoric diester hydrolase	Unigene37375_All//0.00E+00//ES806491				nr -
Unigene37378_All	1381	1.97	16.25	13.30	16.63	33.41	41.83	0.00	0.06	0.00	3.04E+00	2.37E-74	Up	2.76E+00	1.12E-53	Up	1.01E+00	5.30E-40	Up	1.33E+00	1.49E-70	Up	5.92E+00	4.01E-01		null	null		Unigene37378_All//gi|256773105|dbj|BAI22477.1|//1.00E-172//delta 1-pyrroline-5-carboxylate synthase [Vigna unguiculata]	Unigene37378_All//2.00E-156//AT2G39800| P5CS1 (DELTA1-PYRROLINE-5-CARBOXYLATE SYNTHASE 1); delta1-pyrroline-5-carboxylate synthetase	Unigene37378_All//2.00E-104//CO105373		ko00330|Arginine and proline metabolism		nr +
Unigene37379_All	1398	1.95	1.41	0.88	6.59	10.20	11.92	38.29	43.92	84.01	-4.61E-01	2.34E-01		-1.15E+00	4.47E-03		6.29E-01	6.11E-06		8.55E-01	2.11E-10		1.98E-01	1.31E-03		1.13E+00	1.49E-129	Up	Unigene37379_All//gi|259496080|gb|ACW82829.1|//1.00E-111//F-box/kelch protein [Vitis vinifera]	Unigene37379_All//1.00E-57//AT1G23390| kelch repeat-containing F-box family protein	Unigene37379_All//0.00E+00//DW242305				nr +
Unigene3738_All	1447	2.57	1.33	1.21	7.64	9.95	8.02	1.37	1.85	3.19	-9.48E-01	3.03E-03		-1.08E+00	1.32E-03		3.80E-01	8.53E-03		6.98E-02	7.13E-01		4.29E-01	2.37E-01		1.22E+00	1.55E-06	Up	Unigene3738_All//gi|42569342|ref|NP_180199.3|//1.00E-104//chalcone isomerase [Arabidopsis thaliana]	Unigene3738_All//7.00E-106//AT2G26310| chalcone isomerase	Unigene3738_All//0.00E+00//TC147397				nr +
Unigene37382_All	1959	8.41	1.06	0.87	11.34	6.05	2.33	13.04	9.75	4.68	-2.99E+00	3.22E-54	Down	-3.27E+00	6.51E-57	Down	-9.07E-01	4.36E-17		-2.28E+00	8.62E-59	Down	-4.19E-01	1.26E-05		-1.48E+00	1.76E-43	Down	Unigene37382_All//gi|3540181|gb|AAC34331.1|//0.00E+00//Unknown protein [Arabidopsis thaliana] >gi|40823449|gb|AAR92283.1|At1g10020 [Arabidopsis thaliana] >gi|46518421|gb|AAS99692.1|At1g10020 [Arabidopsis thaliana]	Unigene37382_All//3.00E-172//AT1G10020| unknown protein	Unigene37382_All//0.00E+00//TC132274				nr -
Unigene37384_All	1140	4.54	2.44	3.64	10.01	4.38	4.99	3.41	2.68	3.77	-8.94E-01	6.97E-04		-3.19E-01	2.64E-01		-1.19E+00	6.98E-14	Down	-1.00E+00	1.74E-09	Down	-3.50E-01	2.37E-01		1.46E-01	6.01E-01		Unigene37384_All//gi|297834288|ref|XP_002885026.1|//3.00E-65//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297330866|gb|EFH61285.1|protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene37384_All//2.00E-59//AT3G36690| zinc finger (C3HC4-type RING finger) family protein	Unigene37384_All//0.00E+00//TC149295				nr +
Unigene37387_All	358	5.55	3.96	9.82	17.25	11.54	13.12	9.92	3.50	12.35	-4.87E-01	2.93E-01		8.22E-01	1.66E-02		-5.80E-01	1.01E-02		-3.95E-01	1.13E-01		-1.50E+00	1.14E-06	Down	3.16E-01	2.27E-01				Unigene37387_All//3.00E-177//TC138602				ESTscan +
Unigene37389_All	2404	0.98	3.37	0.78	4.85	8.71	4.23	15.23	22.50	26.45	1.78E+00	1.09E-14	Up	-3.37E-01	4.37E-01		8.45E-01	8.67E-14		-1.98E-01	2.97E-01		5.63E-01	3.00E-18		7.96E-01	1.53E-39		Unigene37389_All//gi|297810217|ref|XP_002872992.1|//0.00E+00//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318829|gb|EFH49251.1|armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37389_All//0.00E+00//AT5G01830| armadillo/beta-catenin repeat family protein / U-box domain-containing protein	Unigene37389_All//0.00E+00//TC151624		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene3739_All	546	92.09	213.35	127.08	247.98	285.83	371.56	43.36	126.08	236.62	1.21E+00	4.22E-114	Up	4.65E-01	4.37E-13		2.05E-01	6.79E-08		5.83E-01	5.30E-62		1.54E+00	3.59E-119	Up	2.45E+00	0.00E+00	Up	Unigene3739_All//gi|116265932|gb|ABJ91214.1|//9.00E-67//CBL-interacting protein kinase 7 [Populus trichocarpa] >gi|116265934|gb|ABJ91215.1| CBL-interacting protein kinase 8 [Populus trichocarpa]	Unigene3739_All//9.00E-65//AT4G30960| SIP3 (SOS3-INTERACTING PROTEIN 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene3739_All//0.00E+00//gi|78328065|gb|DT548339.1|DT548339		ko04140|Regulation of autophagy		nr -
Unigene37395_All	1706	8.13	6.33	5.96	15.62	13.14	13.16	11.13	5.56	4.95	-3.61E-01	1.83E-02		-4.47E-01	4.60E-03		-2.50E-01	1.69E-02		-2.48E-01	2.32E-02		-1.00E+00	1.93E-17	Down	-1.17E+00	6.98E-23	Down	Unigene37395_All//gi|145359470|ref|NP_200812.2|//1.00E-162//NRPC1; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding / zinc ion binding [Arabidopsis thaliana]	Unigene37395_All//2.00E-151//AT5G60040| NRPC1; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding / zinc ion binding	Unigene37395_All//0.00E+00//gi|48807648|gb|CO108962.1|CO108962		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene37396_All	2524	8.52	0.70	0.30	22.08	12.80	5.26	8.51	0.83	0.74	-3.60E+00	7.89E-84	Down	-4.85E+00	3.20E-99	Down	-7.87E-01	3.40E-33		-2.07E+00	8.26E-130	Down	-3.36E+00	2.83E-96	Down	-3.52E+00	1.42E-103	Down	Unigene37396_All//gi|224067164|ref|XP_002302387.1|//0.00E+00//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222844113|gb|EEE81660.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene37396_All//3.00E-105//AT4G37750| ANT (AINTEGUMENTA); DNA binding / transcription factor	Unigene37396_All//0.00E+00//TC165949	AP2-EREBP			nr -
Unigene37397_All	1017	4.89	11.51	6.02	7.69	5.52	5.06	8.73	8.79	3.49	1.24E+00	1.85E-12	Up	3.01E-01	2.44E-01		-4.79E-01	1.67E-02		-6.03E-01	3.27E-03		1.06E-02	9.90E-01		-1.32E+00	2.10E-13	Down		Unigene37397_All//4.00E-05//AT5G27320| GIDIC (GA INSENSITIVE DWARFIC); hydrolase	Unigene37397_All//3.00E-32//ES845548				nr +
Unigene374_All	2654	5.13	12.85	3.21	14.13	11.78	15.15	25.01	73.48	50.44	1.33E+00	7.72E-39	Up	-6.75E-01	1.86E-05		-2.63E-01	1.78E-03		9.98E-02	3.26E-01		1.55E+00	0.00E+00	Up	1.01E+00	8.50E-123	Up	Unigene374_All//gi|6056376|gb|AAF02840.1|AC009894_11//0.00E+00//Similar to serine/threonine kinases [Arabidopsis thaliana]	Unigene374_All//0.00E+00//AT1G56130| leucine-rich repeat family protein / protein kinase family protein	Unigene374_All//0.00E+00//TC173885		ko04626|Plant-pathogen interaction		nr +
Unigene37400_All	1033	196.42	65.78	76.55	61.73	71.04	30.60	4.54	3.80	1.08	-1.58E+00	1.07E-297	Down	-1.36E+00	6.64E-231	Down	2.03E-01	5.84E-04		-1.01E+00	4.33E-51	Down	-2.57E-01	3.55E-01		-2.07E+00	2.17E-13	Down	Unigene37400_All//gi|48310189|gb|AAT41771.1|//9.00E-84//At5g42680 [Arabidopsis thaliana] >gi|52218794|gb|AAU29467.1|At5g42680 [Arabidopsis thaliana]	Unigene37400_All//4.00E-85//AT5G42680| unknown protein	Unigene37400_All//0.00E+00//TC135217				nr +
Unigene37401_All	1533	3.11	3.67	4.48	6.17	4.76	5.07	5.32	6.87	2.62	2.40E-01	3.62E-01		5.29E-01	2.45E-02		-3.75E-01	4.16E-02		-2.85E-01	1.56E-01		3.68E-01	2.19E-02		-1.02E+00	1.78E-08	Down	Unigene37401_All//gi|75127116|sp|Q6NPF8.1|U497B_ARATH/8.00E-69//RecName: Full=UPF0497 membrane protein At2g37200 >gi|38454082|gb|AAR20735.1|At2g37200 [Arabidopsis thaliana] >gi|38604002|gb|AAR24744.1|At2g37200 [Arabidopsis thaliana]	Unigene37401_All//4.00E-70//AT2G37200| integral membrane protein, putative	Unigene37401_All//0.00E+00//gi|109862498|gb|DW491475.1|DW491475				nr +
Unigene37402_All	829	124.46	46.21	91.98	161.64	173.80	86.84	4.85	7.41	2.55	-1.43E+00	6.28E-131	Down	-4.36E-01	4.24E-17		1.05E-01	1.79E-02		-8.96E-01	2.73E-87		6.13E-01	3.91E-03		-9.28E-01	4.48E-04		Unigene37402_All//gi|115440593|ref|NP_001044576.1|//1.00E-12//Os01g0808900 [Oryza sativa Japonica Group] >gi|113534107|dbj|BAF06490.1|Os01g0808900 [Oryza sativa Japonica Group]	Unigene37402_All//7.00E-08//AT2G41180| sigA-binding protein-related	Unigene37402_All//0.00E+00//TC152095				nr -
Unigene37403_All	1484	6.28	8.40	7.71	21.18	19.05	24.38	15.44	7.13	3.54	4.21E-01	9.22E-03		2.98E-01	1.03E-01		-1.53E-01	1.44E-01		2.03E-01	3.10E-02		-1.12E+00	8.71E-25	Down	-2.12E+00	3.68E-64	Down	Unigene37403_All//gi|4581119|gb|AAD24609.1|//1.00E-115//expressed protein [Arabidopsis thaliana]	Unigene37403_All//1.00E-102//AT2G16760| FUNCTIONS IN: molecular_function unknown; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Six-bladed beta-propeller, TolB-like (InterPro:IPR011042); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G47370.1); Has 78 Blast hits to 78 proteins in 24 species: Archae - 0; Bacteria - 32; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene37403_All//0.00E+00//TC146160				nr -
Unigene37408_All	830	106.72	69.47	68.20	119.61	100.61	129.67	142.73	76.14	39.45	-6.19E-01	1.95E-28		-6.46E-01	1.71E-29		-2.50E-01	1.86E-07		1.16E-01	2.96E-02		-9.07E-01	7.88E-89		-1.86E+00	7.29E-275	Down	Unigene37408_All//gi|225440831|ref|XP_002282071.1|//4.00E-68//PREDICTED: similar to ubiquitin fusion protein [Vitis vinifera] >gi|71040673|gb|AAZ20285.1|ubiquitin fusion protein [Arachis hypogaea] >gi|192910738|gb|ACF06477.1|ubiquitin fusion protein [Elaeis guineensis] >gi|284433784|gb|ADB85098.1|ubiquitin C variant [Jatropha curcas]	Unigene37408_All//7.00E-69//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene37408_All//0.00E+00//gi|109875869|gb|DW504843.1|DW504843		ko03010|Ribosome		nr -

Unigene3741_All	1679	6.89	5.01	7.36	11.24	11.61	13.13	20.07	11.38	8.97	-4.59E-01	6.15E-03		9.55E-02	6.34E-01		4.59E-02	8.04E-01		2.23E-01	7.37E-02		-8.19E-01	7.14E-22		-1.16E+00	1.40E-39	Down	Unigene3741_All//gi|224099887|ref|XP_002311660.1|//0.00E+00//magnesium transporter [Populus trichocarpa] >gi|222851480|gb|EEE89027.1|magnesium transporter [Populus trichocarpa]	Unigene3741_All//9.00E-137//AT5G61560| magnesium transporter CorA-like family protein (MRS2-2)	Unigene3741_All//0.00E+00//TC134628				nr -
Unigene37411_All	1889	2.16	6.49	6.79	5.33	5.51	5.48	1.01	0.13	0.53	1.59E+00	1.21E-18	Up	1.65E+00	6.40E-20	Up	4.75E-02	8.26E-01		3.96E-02	8.61E-01		-2.92E+00	4.98E-08	Down	-9.34E-01	2.11E-02		Unigene37411_All|gi|42562033|ref|NP_172772.2|//0.00E+00//glycosyl hydrolase family 5 protein / cellulase family protein [Arabidopsis thaliana] >gi|51536480|gb|AAU05478.1|At1g13130 [Arabidopsis thaliana]	Unigene37411_All//0.00E+00//AT1G13130| glycosyl hydrolase family 5 protein / cellulase family protein	Unigene37411_All//2.00E-74//TC141992				nr +
Unigene37413_All	986	35.71	80.22	39.21	15.46	30.70	41.77	15.18	21.15	20.32	1.17E+00	3.18E-73	Up	1.35E-01	1.71E-01		9.90E-01	1.31E-25		1.43E+00	2.03E-56	Up	4.79E-01	7.84E-06		4.21E-01	8.70E-05		Unigene37413_All|gi|222424195|dbj|BAH20056.1|//3.00E-69//AT2G25670 [Arabidopsis thaliana]	Unigene37413_All//1.00E-19//AT2G25670| unknown protein	Unigene37413_All//0.00E+00//TC160108				nr +
Unigene37415_All	2305	0.32	1.34	0.51	7.02	6.05	3.37	9.54	12.17	8.85	2.08E+00	3.16E-07	Up	6.77E-01	3.04E-01		-2.15E-01	1.44E-01		-1.06E+00	2.21E-14	Down	3.51E-01	1.29E-04		-1.08E-01	3.62E-01		Unigene37415_All|gi|297828041|ref|XP_002881903.1|//1.00E-155//3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327742|gb|EFH58162.1| 3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37415_All//2.00E-142//AT2G43420| 3-beta hydroxysteroid dehydrogenase/isomerase family protein	Unigene37415_All//0.00E+00//gi|78345401|gb|DT565675.1|DT565675		ko00100|Steroid biosynthesis		nr +
Unigene37416_All	2524	0.06	0.14	0.08	0.77	0.65	0.48	1.66	0.76	0.68	1.18E+00	3.72E-01		4.40E-01	7.75E-01		-2.33E-01	6.16E-01		-6.72E-01	1.58E-01		-1.12E+00	3.18E-05	Down	-1.29E+00	1.54E-06	Down	Unigene37416_All|gi|297828041|ref|XP_002881903.1|//1.00E-156//3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327742|gb|EFH58162.1| 3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37416_All//2.00E-148//AT2G43420| 3-beta hydroxysteroid dehydrogenase/isomerase family protein	Unigene37416_All//0.00E+00//gi|78345401|gb|DT565675.1|DT565675		ko00940|Phenylpropanoid biosynthesis//ko00100|Steroid biosynthesis		nr -
Unigene37418_All	838	11.49	61.49	30.82	14.03	35.30	30.18	52.17	51.77	74.59	2.42E+00	1.08E-132	Up	1.42E+00	6.78E-32	Up	1.33E+00	8.12E-40	Up	1.11E+00	2.17E-23	Up	-1.11E-02	9.14E-01		5.16E-01	1.70E-18		Unigene37418_All|gi|225445069|ref|XP_002280317.1|//6.00E-06//PREDICTED: similar to protein kinase family protein / WD-40 repeat family protein [Vitis vinifera]	Unigene37418_All//0.00E+00//gi|164242737|gb|ES799593.1|ES799593		ko04140|Regulation of autophagy		nr -
Unigene37420_All	1091	17.07	6.27	5.71	14.06	9.00	10.47	3.91	2.83	1.72	-1.45E+00	1.44E-24	Down	-1.58E+00	7.83E-27	Down	-6.45E-01	8.18E-07		-4.25E-01	2.66E-03		-4.65E-01	8.26E-02		-1.19E+00	5.69E-06	Down	Unigene37420_All|gi|1053065|gb|AAA80679.1|//4.00E-93//small GTP-binding protein [Solanum lycopersicum]	Unigene37420_All//2.00E-84//AT3G11730| ATFP8; GTP binding / GTP-dependent protein binding / myosin XI tail binding	Unigene37420_All//0.00E+00//TC163854				nr +
Unigene37421_All	1400	3.14	3.08	1.14	3.42	3.52	2.97	3.81	2.87	4.30	-2.92E-02	9.35E-01		-1.46E+00	4.02E-06	Down	4.22E-02	9.02E-01		-2.03E-01	5.20E-01		-4.09E-01	8.60E-02		1.75E-01	4.52E-01		Unigene37421_All|gi|115453133|ref|NP_001050167.1|//2.00E-78//0s03g0363700 [Oryza sativa Japonica Group] >gi|113548638|dbj|BAF12081.1|Os03g0363700 [Oryza sativa Japonica Group]	Unigene37421_All//9.00E-73//AT5G18950| pentatricopeptide (PPR) repeat-containing protein	Unigene37421_All//5.00E-16//gi|164321176|gb|ES791758.1|ES791758				nr -
Unigene37425_All	924	31.20	10.91	23.63	54.13	38.27	53.18	19.81	19.22	15.65	-1.52E+00	2.33E-40	Down	-4.01E-01	1.24E-04		-5.00E-01	1.95E-13		-2.55E-02	7.83E-01		-4.35E-02	7.50E-01		-3.40E-01	2.71E-03		Unigene37425_All|gi|18406916|ref|NP_564765.1|//1.00E-41//MEE9 (maternal effect embryo arrest 9) [Arabidopsis thaliana]	Unigene37425_All//1.00E-26//AT1G60870| MEE9 (maternal effect embryo arrest 9)	Unigene37425_All//0.00E+00//TC155398				nr -
Unigene37426_All	1344	14.56	15.80	20.72	24.31	21.93	23.15	20.95	20.87	10.14	1.18E-01	3.78E-01		5.09E-01	1.43E-06		-1.49E-01	1.48E-01		-7.06E-02	5.61E-01		-5.80E-03	9.90E-01		-1.05E+00	3.26E-28	Down	Unigene37426_All|gi|115447029|ref|NP_001047294.1|//2.00E-94//0s02g0592500 [Oryza sativa Japonica Group] >gi|113536825|dbj|BAF09208.1|Os02g0592500 [Oryza sativa Japonica Group]	Unigene37426_All//1.00E-67//AT5G27830| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Folate receptor, conserved region (InterPro:IPR018143); Has 46 Blast hits to 46 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 16; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryotes - 16 (source: NCBI BLink).	Unigene37426_All//0.00E+00//TC142234				nr +
Unigene37429_All	1124	23.13	59.37	18.76	46.67	47.95	61.24	54.96	77.16	131.46	1.36E+00	2.50E-78	Up	-3.02E-01	7.49E-03		3.90E-02	6.80E-01		3.92E-01	1.22E-10		4.90E-01	1.65E-22		1.26E+00	6.61E-192	Up	Unigene37429_All|gi|15450826|gb|AAK96684.1|//1.00E-66//Unknown protein [Arabidopsis thaliana] >gi|881967223|gb|ARD43004.1|At5g42570 [Arabidopsis thaliana]	Unigene37429_All//6.00E-55//AT1G11905| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular protein transport; LOCATED IN: endomembrane system, integral to membrane, endoplasmic reticulum; CONTAINS InterPro DOMAIN/s: B-cell receptor-associated 31-like (InterPro:IPR008417); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G42570.1); Has 65 Blast hits to 65 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 65; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene37429_All//0.00E+00//TC161022				nr -
Unigene3743_All	1529	1.47	0.36	1.22	4.27	2.61	5.49	4.15	1.61	1.25	-2.01E+00	2.56E-05	Down	-2.72E-01	5.60E-01		-7.08E-01	9.63E-04		3.64E-01	8.11E-02		-1.36E+00	6.97E-10	Down	-1.73E+00	3.86E-14	Down	Unigene3743_All|gi|22328346|ref|NP_567268.2|//1.00E-125//Met-10+ like family protein / kelch repeat-containing protein [Arabidopsis thaliana] >gi|75162488|sp|Q8W4K1.1|TYW23_ARATH RecName: Full=tRNA wybutosine-synthesizing protein 2/3/4; Includes: RecName: Full=tRNA wybutosine-synthesizing protein 3 homolog; Includes: RecName: Full=tRNA wybutosine synthesizing protein 2 homolog >gi|17064868|gb|AAL32588.1|Unknown protein [Arabidopsis thaliana] >gi|30725408|gb|AAP37726.1|At4g04670 [Arabidopsis thaliana]	Unigene3743_All//3.00E-126//AT4G04670| Met-10+ like family protein / kelch repeat-containing protein	Unigene3743_All//0.00E+00//TC172281				nr -
Unigene37433_All	1575	2.13	22.78	14.20	0.95	1.97	2.09	0.40	0.77	3.59	3.42E+00	2.97E-132	Up	2.74E+00	6.71E-65	Up	1.05E+00	2.34E-03		1.14E+00	9.17E-04	Up	9.34E-01	9.20E-02		3.16E+00	9.39E-25	Up	Unigene37433_All|gi|15235354|ref|NP_195164.1|//1.00E-138//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|29028888|gb|AAO64823.1|At4g34380 [Arabidopsis thaliana]	Unigene37433_All//6.00E-138//AT4G34380| transducin family protein / WD-40 repeat family protein	Unigene37433_All//1.00E-38//gi|78327177|gb|DT547451.1|DT547451		ko03040|Spliceosome		nr -
Unigene37434_All	901	8.77	5.46	3.72	15.09	15.63	17.19	51.81	68.84	103.64	-6.85E-01	8.99E-04		-1.24E+00	2.82E-08	Down	5.05E-02	8.18E-01		1.88E-01	2.39E-01		4.10E-01	5.04E-12		1.00E+00	2.51E-84	Up	Unigene37434_All|gi|5899651|gb|AAX11684.1|//1.00E-69//perakine reductase [Rauvolfia serpentina]	Unigene37434_All//2.00E-53//AT1G60730| aldo/keto reductase family protein	Unigene37434_All//0.00E+00//ES820673				nr -
Unigene37435_All	554	5.86	2.56	4.42	14.03	10.01	11.17	6.94	4.30	4.75	-1.19E+00	6.96E-04	Down	-4.05E-01	2.71E-01		-4.87E-01	1.49E-02		-3.29E-01	1.37E-01		-6.92E-01	1.28E-02		-5.49E-01	4.15E-02		Unigene37435_All|gi|55956974|emb|CAI11451.1|//5.00E-18//alpha-1,6-xylosyltransferase [Gossypium raimondii]	Unigene37435_All//1.00E-17//AT4G02500| XT2 (UDP-XYLOSYLTRANSFERASE 2); UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups / xyloglucan 6-xylosyltransferase	Unigene37435_All//0.00E+00//TC174476				nr -
Unigene37436_All	555	3.21	3.93	2.30	5.30	5.65	3.50	8.53	5.72	2.73	2.93E-01	5.14E-01		-4.77E-01	3.67E-01		9.25E-02	8.22E-01		-5.98E-01	1.10E-01		-5.76E-01	2.03E-02		-1.65E+00	4.28E-10	Down	Unigene37436_All|gi|55956974|emb|CAI11451.1|//6.00E-18//alpha-1,6-xylosyltransferase [Gossypium raimondii]	Unigene37436_All//2.00E-17//AT4G02500| XT2 (UDP-XYLOSYLTRANSFERASE 2); UDP-xylosyltransferase/ transferase/ transferase, transferring glycosyl groups / xyloglucan 6-xylosyltransferase	Unigene37436_All//1.00E-159//gi|109868773|gb|DW497749.1|DW497749				nr +
Unigene37438_All	1346	17.41	19.95	18.08	15.99	19.24	16.17	24.22	15.37	7.19	1.96E-01	7.80E-02		5.41E-02	6.66E-01		2.67E-01	1.20E-02		1.66E-02	9.26E-01		-6.56E-01	1.19E-14		-1.75E+00	2.17E-70	Down	Unigene37438_All|gi|150036255|gb|ABR67418.1|//1.00E-127//mitochondrial FAD carrier [Cucumis melo]	Unigene37438_All//3.00E-109//AT3G05290| PNC1 (PEROXISOMAL ADENINE NUCLEOTIDE CARRIER 1); ADP transmembrane transporter/ ATP transmembrane transporter/ binding	Unigene37438_All//0.00E+00//TC141852		ko04146|Peroxisome		nr -
Unigene37439_All	1442	1.63	1.69	0.48	11.12	11.25	8.99	6.83	9.83	4.92	4.68E-02	9.20E-01		-1.77E+00	1.68E-04	Down	1.60E-02	9.37E-01		-3.07E-01	3.23E-02		5.24E-01	7.65E-05		-4.74E-01	2.74E-03		Unigene37439_All|gi|297720585|ref|NP_001172654.1|//3.00E-26//0s01g0850200 [Oryza sativa Japonica Group] >gi|20166570|dbj|BAB89518.1| zinc finger protein-like [Oryza sativa Japonica Group] >gi|20805170|dbj|BAB92839.1| zinc finger protein-like [Oryza sativa Japonica Group] >gi|255673877|dbj|BAH91384.1|Os01g0850200 [Oryza sativa Japonica Group]	Unigene37439_All//4.00E-25//AT5G05830| zinc finger (C3HC4-type RING finger) family protein	Unigene37439_All//4.00E-35//DW511249				nr +
Unigene37441_All	947	5.36	44.30	11.86	53.29	65.31	39.25	35.63	18.10	4.63	3.05E+00	9.56E-139	Up	1.15E+00	2.60E-10	Up	2.94E-01	2.54E-06		-4.41E-01	8.13E-10		-9.77E-01	3.12E-29		-2.94E+00	3.59E-137	Down	Unigene37441_All|gi|18424977|ref|NP_569016.1|//6.00E-44//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|75180337|sp|Q9LSK9.1|Y5566_ARATH RecName: Full=Uncharacterized protein At5g65660 >gi|30102568|gb|AAP21202.1|At5g65660 [Arabidopsis thaliana]	Unigene37441_All//6.00E-38//AT5G65660| hydroxyproline-rich glycoprotein family protein	Unigene37441_All//0.00E+00//gi|109872253|gb|DW501228.1|DW501228				nr +

Unigene37442_All	778	1.95	5.54	2.33	4.03	2.43	1.34	4.08	5.21	4.97	1.51E+00	1.44E-06	Up	2.55E-01	6.40E-01		-7.29E-01	2.95E-02		-1.60E+00	1.20E-05	Down	3.54E-01	2.18E-01		2.85E-01	3.23E-01		Unigene37442_All//gi|242068605|ref|XP_002449579.1|//5.00E-07//hypothetical protein SORBIDRAFT_05g019550 [Sorghum bicolor]>gi|241935422|gb|EES08567.1|hypothetical protein SORBIDRAFT_05g019550 [Sorghum bicolor]						nr +
Unigene37443_All	1332	2.16	1.83	1.76	4.94	5.45	4.24	7.84	6.09	3.44	-2.43E-01	5.32E-01		-2.97E-01	4.49E-01		1.44E-01	5.88E-01		-2.20E-01	3.94E-01		-3.65E-01	2.36E-02		-1.19E+00	2.54E-13	Down	Unigene37443_All//gi|15241163|ref|NP_197474.1|//1.00E-168//pectinesterase family protein [Arabidopsis thaliana]>gi|75304460|sp|Q8VY23.1|PME53_ARATH RecName: Full=Probable pectinesterase 53; Short=PE 53; AltName: Full=Pectin methylesterase 53; Short=AtPME53; Flags: Precursor	Unigene37443_All//2.00E-155//AT5G19730| pectinesterase family protein	Unigene37443_All//0.00E+00//TC178716		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene37444_All	852	1.17	3.57	2.69	41.75	26.15	25.39	5.86	8.49	5.56	1.61E+00	2.70E-05	Up	1.20E+00	7.42E-03		-6.75E-01	2.43E-16		-7.17E-01	3.26E-16		5.35E-01	5.92E-03		-7.36E-02	7.65E-01		Unigene37444_All//gi|297794215|ref|XP_002861992.1|//6.00E-26//expressed protein [Arabidopsis lyrata subsp. lyrata]>gi|297310827|gb|EFH41251.1|expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene37444_All//0.00E+00//TC161282				nr +
Unigene37445_All	1170	1.97	1.52	2.37	1.96	2.18	0.19	9.21	3.82	5.18	-3.76E-01	3.75E-01		2.66E-01	5.14E-01		1.53E-01	7.64E-01		-3.34E+00	1.90E-09	Down	-1.27E+00	1.19E-14	Down	-8.32E-01	5.18E-08		Unigene37445_All//gi|79607902|ref|NP_974371.2|//9.00E-67//nodulin MtN21 family protein [Arabidopsis thaliana]	Unigene37445_All//4.00E-63//AT5G40240| nodulin MtN21 family protein	Unigene37445_All//4.00E-170//DW500109				nr -
Unigene37447_All	1150	39.45	31.33	41.03	48.86	40.84	47.13	64.19	31.44	24.01	-3.33E-01	2.53E-05		5.67E-02	5.60E-01		-2.59E-01	9.47E-05		-5.21E-02	5.74E-01		-1.03E+00	1.27E-68	Down	-1.42E+00	1.14E-116	Down	Unigene37447_All//gi|98961025|gb|AB588996.1|//1.00E-25//At5g62575 [Arabidopsis thaliana]	Unigene37447_All//6.00E-27//AT5G62575| unknown protein	Unigene37447_All//0.00E+00//gi|164271828|gb|ES809369.1|ES809369				nr +
Unigene37448_All	978	12.36	18.75	17.48	24.35	33.24	24.94	13.96	28.72	34.50	6.02E-01	3.14E-06		5.00E-01	3.26E-04		4.49E-01	2.98E-07		3.45E-02	7.92E-01		1.04E+00	5.37E-27	Up	1.31E+00	5.33E-47	Up	Unigene37448_All//gi|18422223|ref|NP_568606.1|//2.00E-74//abscisic acid-responsive HVA22 family protein [Arabidopsis thaliana]>gi|57012602|sp|Q8LE10.2|HA221_ARATH RecName: Full=HVA22-like protein i; Short=AtHVA22i >gi|94142437|gb|ABF19006.1|At5g42560 [Arabidopsis thaliana]	Unigene37448_All//1.00E-75//AT5G42560| abscisic acid-responsive HVA22 family protein	Unigene37448_All//0.00E+00//TC138663				nr +
Unigene3745_All	1261	0.75	1.29	1.82	1.62	1.31	1.33	1.94	0.80	1.96	7.84E-01	1.31E-01		1.28E+00	4.54E-03		-3.05E-01	5.37E-01		-2.90E-01	5.68E-01		-1.29E+00	5.10E-04	Down	1.04E-02	9.74E-01		Unigene3745_All//gi|87241031|gb|AB032889.1|//1.00E-90//AAA ATPase; 26S proteasome subunit P45 [Medicago truncatula]>gi|124360940|gb|ABN08912.1| AAA ATPase; 26S proteasome subunit P45 [Medicago truncatula]	Unigene3745_All//7.00E-76//AT4G29040| RPT2a (regulatory particle AAA-ATPase 2a); ATPase	Unigene3745_All//0.00E+00//TC137127		ko03050|Proteasome		nr -
Unigene37450_All	859	13.16	16.34	12.65	14.73	15.79	20.50	29.04	16.40	12.38	3.13E-01	4.29E-02		-5.71E-02	7.59E-01		1.01E-01	5.90E-01		4.77E-01	2.37E-04		-8.25E-01	1.37E-16		-1.23E+00	3.16E-32	Down	Unigene37450_All//gi|115488570|ref|NP_001066772.1|//5.00E-33//Os12g0481200 [Oryza sativa Japonica Group]>gi|108862675|gb|ABA98488.2|expressed protein [Oryza sativa (japonica cultivar-group)]>gi|113649279|dbj|BAF29791.1|Os12g0481200 [Oryza sativa Japonica Group]	Unigene37450_All//3.00E-31//AT1G21930| unknown protein	Unigene37450_All//0.00E+00//gi|109881995|gb|DW510965.1|DW510965				nr +
Unigene37454_All	535	6.06	5.78	1.49	6.42	6.18	4.47	7.90	14.22	5.21	-6.97E-02	8.39E-01		-2.02E+00	5.55E-07	Down	-5.62E-02	8.69E-01		-5.22E-01	1.30E-01		8.47E-01	7.60E-06		-6.00E-01	1.83E-02		Unigene37454_All//gi|15241598|ref|NP_196452.1|//2.00E-50//GRAM domain-containing protein / ABA-responsive protein-related [Arabidopsis thaliana]>gi|75172412|sp|Q9FTA0.1|GEML4_ARATH RecName: Full=GEM-like protein 4	Unigene37454_All//1.00E-51//AT5G08350| GRAM domain-containing protein / ABA-responsive protein-related	Unigene37454_All//0.00E+00//TC140324				nr +
Unigene37455_All	575	5.46	10.31	7.13	17.33	22.22	17.20	11.25	13.74	2.91	9.17E-01	1.87E-04		3.85E-01	2.32E-01		3.59E-01	2.22E-02		-1.05E-02	9.50E-01		2.88E-01	1.41E-01		-1.95E+00	7.90E-17	Down	Unigene37455_All//gi|15241598|ref|NP_196452.1|//3.00E-37//GRAM domain-containing protein / ABA-responsive protein-related [Arabidopsis thaliana]>gi|75172412|sp|Q9FTA0.1|GEML4_ARATH RecName: Full=GEM-like protein 4	Unigene37455_All//2.00E-38//AT5G08350| GRAM domain-containing protein / ABA-responsive protein-related	Unigene37455_All//0.00E+00//TC144471				nr +
Unigene37459_All	1722	16.26	1.27	2.81	35.49	14.82	5.69	13.58	1.33	4.58	-3.68E+00	4.21E-111	Down	-2.53E+00	5.72E-74	Down	-1.26E+00	1.28E-79	Down	-2.64E+00	2.33E-191	Down	-3.35E+00	2.47E-104	Down	-1.57E+00	2.14E-43	Down	Unigene37459_All//gi|36957267|gb|AAQ87025.1|//0.00E+00//pectate lyase-like protein [Brassica napus]	Unigene37459_All//5.00E-165//AT5G04310| pectate lyase family protein	Unigene37459_All//0.00E+00//gi|78347710|gb|DT567984.1|DT567984		ko00040|Pentose and glucuronate interconversions		nr -
Unigene37463_All	1971	9.05	6.22	5.27	14.58	12.74	11.09	12.59	6.43	6.08	-5.41E-01	3.49E-05		-7.81E-01	9.96E-09		-1.95E-01	6.16E-02		-3.95E-01	6.29E-05		-9.71E-01	1.76E-21		-1.05E+00	4.71E-25	Down	Unigene37463_All//gi|297798186|ref|XP_002866977.1|//1.00E-156//hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]>gi|297312813|gb|EFH43236.1|hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37463_All//2.00E-104//AT4G37130| hydroxyproline-rich glycoprotein family protein	Unigene37463_All//0.00E+00//TC140495		ko03022|Basal transcription factors		nr +
Unigene37464_All	1028	180.02	52.74	230.56	61.20	59.12	23.68	2.26	0.08	0.47	-1.77E+00	0.00E+00	Down	3.57E-01	1.00E-26		-4.99E-02	5.55E-01		-1.37E+00	1.75E-81	Down	-4.80E+00	7.37E-14	Down	-2.28E+00	7.89E-08	Down	Unigene37464_All//gi|224080780|ref|XP_002306227.1|//7.00E-76//cytochrome P450 [Populus trichocarpa]>gi|222849191|gb|EEE86738.1|cytochrome P450 [Populus trichocarpa]	Unigene37464_All//1.00E-75//AT1G12740| CYP97A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene37464_All//0.00E+00//TC165458		ko00905|Brassinosteroid biosynthesis		nr +
Unigene37466_All	1493	2.35	2.07	2.53	4.74	4.64	7.47	12.74	6.16	5.60	-1.82E-01	6.20E-01		1.09E-01	7.36E-01		-3.14E-02	8.99E-01		6.57E-01	8.31E-05		-1.05E+00	8.02E-19	Down	-1.19E+00	1.93E-23	Down	Unigene37466_All//gi|42568687|ref|NP_200941.2|//1.00E-138//rRNA processing protein-related [Arabidopsis thaliana]	Unigene37466_All//2.00E-113//AT5G61530| rRNA processing protein-related	Unigene37466_All//0.00E+00//TC172130		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene37467_All	674	0.00	0.15	1.42	27.12	23.96	13.40	96.67	68.65	21.87	7.23E+00	3.86E-01		1.05E+01	2.46E-05	Up	-1.79E-01	2.06E-01		-1.02E+00	3.71E-15	Down	-4.94E-01	2.15E-17		-2.14E+00	2.65E-183	Down	Unigene37467_All//gi|153805698|gb|ABS52574.1|//4.00E-93//nodulin family protein [Gossypium hirsutum]	Unigene37467_All//1.00E-73//AT1G21890| nodulin MtN21 family protein	Unigene37467_All//0.00E+00//gi|48828609|gb|CO126999.1|CO126999				nr -
Unigene37468_All	1530	1.57	0.50	0.80	2.02	1.98	1.98	6.02	3.61	2.06	-1.66E+00	1.53E-04	Down	-9.75E-01	2.41E-02		-2.74E-02	9.44E-01		-2.95E-02	9.49E-01		-7.40E-01	1.18E-05		-1.55E+00	2.33E-17	Down	Unigene37468_All//gi|77416925|gb|AB481858.1|//1.00E-132//brittle 1 protein-like [Solanum tuberosum]	Unigene37468_All//2.00E-107//AT4G32400| SIS1 (SODIUM HYPERSENSITIVE 1); binding / nucleotide transmembrane transporter/ transporter	Unigene37468_All//6.00E-99//TC158634				nr -
Unigene3747_All	1222	3.08	3.32	5.10	7.87	7.04	3.95	2.70	1.09	1.01	1.06E-01	7.25E-01		7.26E-01	3.16E-03		-1.59E-01	4.50E-01		-9.92E-01	5.81E-08		-1.30E+00	3.38E-05	Down	-1.42E+00	5.00E-06	Down	Unigene3747_All//gi|297725701|ref|NP_001175214.1|//4.00E-34//Os07g0501200 [Oryza sativa Japonica Group]>gi|255677791|dbj|BAH93942.1|Os07g0501200 [Oryza sativa Japonica Group]	Unigene3747_All//2.00E-11//ATMG00310| hypothetical protein	Unigene3747_All//0.00E+00//TC148050				nr +
Unigene37471_All	1139	5.70	18.28	9.77	8.00	7.74	12.21	13.33	15.49	15.53	1.68E+00	7.95E-34	Up	7.79E-01	1.07E-05		-4.84E-02	8.26E-01		6.10E-01	3.48E-05		2.17E-01	8.69E-02		2.21E-01	6.68E-02		Unigene37471_All//gi|15235657|ref|NP_195483.1|//3.00E-95//HHP4 (heptahelical protein 4); receptor [Arabidopsis thaliana]	Unigene37471_All//2.00E-96//AT4G37680| HHP4 (heptahelical protein 4); receptor	Unigene37471_All//0.00E+00//TC149722				nr +
Unigene37472_All	1763	3.09	5.98	4.83	9.04	8.11	7.15	12.33	6.90	25.87	9.54E-01	1.05E-07		6.47E-01	1.65E-03		-1.58E-01	3.13E-01		-3.39E-01	1.69E-02		-8.37E-01	6.35E-15		1.07E+00	2.30E-46	Up	Unigene37472_All//gi|222423371|dbj|BAH19658.1|//1.00E-98//AT3G59090 [Arabidopsis thaliana]	Unigene37472_All//6.00E-70//AT3G50090| EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: TOM1 (TOBAMOVIRUS MULTIPLICATION 1); protein binding (TAIR:AT4G21790.1); Has 115 Blast hits to 115 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 108; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene37472_All//0.00E+00//TC163449				nr +
Unigene37474_All	935	2.85	4.82	4.67	2.98	2.06	2.03	6.15	3.67	2.00	7.57E-01	7.84E-03		7.11E-01	1.89E-02		-5.33E-01	1.56E-01		-5.57E-01	1.51E-01		-7.47E-01	7.00E-04		-1.62E+00	8.10E-12	Down							
Unigene37475_All	1813	1.13	1.17	0.85	2.89	2.24	1.59	7.09	0.99	1.49	6.06E-02	8.97E-01		-4.02E-01	3.83E-01		-3.64E-01	1.71E-01		-8.56E-01	8.80E-04		-2.84E+00	4.17E-49	Down	-2.25E+00	6.02E-39	Down	Unigene37475_All//gi|15231911|ref|NP_187456.1|//0.00E+00//SCPL27 (serine carboxypeptidase-like 27); serine-type carboxypeptidase [Arabidopsis thaliana]>gi|75337170|sp|Q9SFB5.1|SCP27_ARATH RecName: Full=Serine carboxypeptidase-like 27; Flags: Precursor >gi|50233506|gb|AAT71955.1|At3g07990 [Arabidopsis thaliana]>gi|53850527|gb|AAU95440.1|At3g07990 [Arabidopsis thaliana]	Unigene37475_All//0.00E+00//AT3G07990| SCPL27 (serine carboxypeptidase-like 27); serine-type carboxypeptidase	Unigene37475_All//0.00E+00//gi|78336900|gb|DT557174.1|DT557174		ko00460|Cyanoamino acid metabolism		nr +
Unigene37476_All	1150	0.82	0.26	0.56	1.39	0.48	0.55	6.95	2.04	1.84	-1.63E+00	3.13E-02		-5.59E-01	4.39E-01		-1.53E+00	2.44E-03		-1.33E+00	1.23E-02		-1.77E+00	1.39E-17	Down	-1.92E+00	3.53E-20	Down	Unigene37476_All//gi|56121894|gb|AAV74228.1|//3.00E-79//At3g60670 [Arabidopsis thaliana]>gi|57222190|gb|AAK39002.1|At3g60670 [Arabidopsis thaliana]	Unigene37476_All//9.00E-76//AT3G60670| zinc-binding protein, putative	Unigene37476_All//0.00E+00//gi|109874438|gb|DW503412.1|DW503412	PLATZ			nr +
Unigene37478_All	846	1.36	0.00	0.00	0.47	1.51	1.01	1.00	0.54	0.89	-1.04E+01	9.91E-07	Down	-1.04E+01	2.60E-06	Down	1.68E+00	7.61E-03		1.11E+00	1.67E-01		-8.79E-01	2.07E-01		-1.60E-01	7.94E-01		Unigene37478_All//gi|56121894|gb|AAV74228.1|//2.00E-71//At3g60670 [Arabidopsis thaliana]>gi|57222190|gb|AAK39002.1|At3g60670 [Arabidopsis thaliana]	Unigene37478_All//2.00E-67//AT3G60670| zinc-binding protein, putative	Unigene37478_All//0.00E+00//gi|109882058|gb|DW511028.1|DW511028	PLATZ			nr +
Unigene37480_All	1449	1.77	0.91	0.85	24.72	8.75	7.73	3.01	1.76	1.18	-9.61E-01	1.52E-02		-1.07E+00	1.07E-02		-1.50E+00	4.20E-61	Down	-1.68E+00	1.03E-62	Down	-7.72E-01	2.81E-03		-1.35E+00	3.57E-07	Down	Unigene37480_All//gi|124359713|gb|ABD32380.2|//8.00E-65//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene37480_All//2.00E-58//AT1G22490| basic helix-loop-helix (bHLH) family protein	Unigene37480_All//1.00E-65//TC157801	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene37481_All	1535	7.06	7.59	7.32	8.66	5.11	9.33	13.99	10.48	6.96	1.06E-01	5.84E-01		5.30E-02	7.76E-01		-7.61E-01	7.97E-08		1.06E-01	5.66E-01		-4.17E-01	8.01E-05		-1.01E+00	1.79E-20	Down	Unigene37481_All//gi|30699851|ref|NP_177364.2|//1.00E-132//oxidoreductase family protein [Arabidopsis thaliana]	Unigene37481_All//2.00E-133//AT1G72190| oxidoreductase family protein	Unigene37481_All//0.00E+00//TC142942		ko00260|Glycine, serine and threonine metabolism//ko00630|Glyoxylate and dicarboxylate metabolism		nr +

Unigene37482_All	971	32.71	33.50	18.21	30.47	38.44	36.33	21.12	3.23	6.24	3.46E-02	7.39E-01		-8.45E-01	4.03E-17		3.35E-01	4.98E-05		2.54E-01	5.89E-03		-2.71E+00	3.19E-74	Down	-1.76E+00	7.04E-45	Down	Unigene37482_All//gi|115393868|gb|ABI96983.1|//2.00E-91//phytocyanin-like arabinogalactan-protein [Gossypium hirsutum] >gi|115393870|gb|ABI96984.1| phytocyanin-like arabinogalactan-protein [Gossypium hirsutum]	Unigene37482_All//2.00E-47//AT2G25060| plastocyanin-like domain-containing protein	Unigene37482_All//0.00E+00//TC156874				nr -
Unigene37484_All	2100	0.02	0.56	0.86	1.92	2.39	3.18	3.83	6.75	18.17	4.48E+00	1.19E-05	Up	5.11E+00	9.43E-09	Up	3.17E-01	2.79E-01		7.28E-01	1.20E-03		8.19E-01	1.17E-09		2.25E+00	1.19E-112	Up	Unigene37484_All//gi|30693481|ref|NP_851107.1|//1.00E-146//structural constituent of ribosome [Arabidopsis thaliana]	Unigene37484_All//8.00E-122//AT5G39785| structural constituent of ribosome					nr -
Unigene37485_All	1110	85.13	43.27	72.01	50.58	43.09	30.43	18.17	13.22	8.08	-9.76E-01	1.15E-65		-2.42E-01	1.26E-05		-2.31E-01	5.92E-04		-7.33E-01	3.36E-26		-4.59E-01	2.58E-05		-1.17E+00	2.68E-24	Down	Unigene37485_All//gi|225454700|ref|XP_002270495.1|//8.00E-40//PREDICTED: similar to 0s03g0854000 [Vitis vinifera]	Unigene37485_All//9.00E-49//AT5G46720| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Butirosin biosynthesis, BtrG-like (InterPro:IPR013024), AIG2-like (InterPro:IPR009298); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G02910.1); Has 249 Blast hits to 249 proteins in 85 species: Archae - 5; Bacteria - 65; Metazoa - 121; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink).	Unigene37485_All//0.00E+00//gi|109870602|gb|DW499578.1|DW499578				nr +
Unigene37486_All	1286	1.30	1.93	0.66	2.63	3.35	3.16	1.32	1.85	3.00	5.68E-01	1.59E-01		-9.75E-01	6.91E-02		3.46E-01	2.79E-01		2.63E-01	4.46E-01		4.94E-01	1.95E-01		1.19E+00	1.88E-05	Up	Unigene37486_All//gi|157169067|gb|ABV25893.1|//0.00E+00//starch synthase isoform I [Manihot esculenta]	Unigene37486_All//0.00E+00//AT5G24300| SS1I (SUPPRESSOR OF SALICYLIC ACID INSENSITIVITY 1); starch synthase/ transferase, transferring glycosyl groups	Unigene37486_All//0.00E+00//CO112593		ko00500|Starch and sucrose metabolism		nr -
Unigene37488_All	1324	3.48	1.99	1.45	3.50	2.86	2.80	2.91	2.08	1.20	-8.05E-01	4.12E-03		-1.26E+00	2.85E-05	Down	-2.91E-01	3.23E-01		-3.23E-01	2.93E-01		-4.80E-01	9.15E-02		-1.27E+00	5.67E-06	Down	Unigene37488_All//gi|56744240|gb|AW28560.1|//1.00E-106//At3g03210 [Arabidopsis thaliana]	Unigene37488_All//2.00E-98//AT3G03210| unknown protein	Unigene37488_All//3.00E-48//gi|72281352|gb|DT052931.1|DT052931				nr +
Unigene37493_All	1951	44.92	21.01	37.58	7.10	7.71	4.31	0.04	0.17	0.12	-1.10E+00	1.29E-73	Down	-2.57E-01	7.45E-06		1.20E-01	5.03E-01		-7.21E-01	9.16E-07		1.98E+00	1.44E-01		1.50E+00	3.39E-01		Unigene37493_All//gi|13605708|gb|AAX32847.1|AF361838.1|//0.00E+00//AT5g59750/mth12_150 [Arabidopsis thaliana] >gi|9758840|dbj|BAB09512.1| GTP cyclohydrolase II; 3,4-dihydroxy-2-butanone-4-phoshate synthase [Arabidopsis thaliana] >gi|15215752|gb|AAK91421.1| AT5g59750/mth12_150 [Arabidopsis thaliana] >gi|27363454|gb|AAO11646.1| At5g59750/mth12_150 [Arabidopsis thaliana]	Unigene37493_All//0.00E+00//AT5G59750| riboflavin biosynthesis protein, putative	Unigene37493_All//0.00E+00//TC132513		ko00740|Riboflavin metabolism		nr -
Unigene37494_All	596	13.34	1.70	5.99	24.41	14.39	27.43	83.78	41.23	41.44	-2.97E+00	2.73E-26	Down	-1.16E+00	1.44E-07	Down	-7.63E-01	1.53E-08		1.69E-01	2.90E-01		-1.02E+00	3.76E-46	Down	-1.02E+00	6.19E-47	Down	Unigene37494_All//gi|8778823|gb|AAF79822.1|AC026875.2||3.00E-53//T6D22.2 [Arabidopsis thaliana]	Unigene37494_All//7.00E-42//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene37494_All//0.00E+00//gi|21103043|gb|BQ415356.1|BQ415356				nr +
Unigene37495_All	1725	0.79	1.59	3.03	0.84	1.36	1.62	15.22	4.26	20.42	1.01E+00	8.65E-03		1.94E+00	2.26E-10	Up	6.97E-01	9.87E-02		9.55E-01	1.15E-02		-1.84E+00	7.86E-59	Down	4.24E-01	8.19E-08		Unigene37495_All//gi|74273312|gb|AB401324.1|//1.00E-178//epoxide hydrolase [Gossypium hirsutum]	Unigene37495_All//5.00E-50//AT4G02340| epoxide hydrolase, putative	Unigene37495_All//0.00E+00//TC131648				nr +
Unigene37496_All	1261	5.93	14.10	6.67	62.85	70.54	41.01	28.70	20.75	12.29	1.25E+00	7.56E-19	Up	1.69E-01	4.46E-01		1.66E-01	2.14E-03		-6.16E-01	3.53E-27		-4.68E-01	3.57E-09		-1.22E+00	5.28E-46	Down	Unigene37496_All//gi|40233087|gb|AA88341.1|//1.00E-101//homeodomain protein HB2 [Populus tomentosa]	Unigene37496_All//9.00E-88//AT4G35550| WOX13 (WUSCHEL-RELATED HOMEOBOX 13); DNA binding / transcription factor	Unigene37496_All//78.00E+00//TC148918	HB			nr -
Unigene37499_All	1812	0.64	2.40	1.20	2.78	5.49	5.71	6.60	6.14	4.18	1.92E+00	5.20E-09	Up	9.24E-01	4.33E-02		9.84E-01	1.29E-08		1.04E+00	5.02E-09	Up	-1.06E-01	5.52E-01		-6.61E-01	3.52E-06		Unigene37499_All//gi|30686502|ref|NP_850841.1|//1.00E-142//AAA-type ATPase family protein [Arabidopsis thaliana] >gi|9759053|dbj|BAB09575.1| AAA-type ATPase-like protein [Arabidopsis thaliana]	Unigene37499_All//7.00E-122//AT5G17760| AAA-type ATPase family protein	Unigene37499_All//9.00E-12//gi|78344432|gb|DT564706.1|DT564706				nr -
Unigene3750_All	1552	2.36	1.60	1.06	22.47	13.51	8.61	9.81	4.07	1.77	-5.61E-01	8.05E-02		-1.15E+00	7.41E-04	Down	-7.34E-01	1.62E-18		-1.38E+00	5.09E-46	Down	-1.27E+00	2.29E-20	Down	-2.47E+00	1.99E-51	Down	Unigene3750_All//gi|224114479|ref|XP_002332364.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222874681|gb|EEF11812.1| GRAS family transcription factor [Populus trichocarpa]	Unigene3750_All//3.00E-146//AT4G37650| SHR (SHORT ROOT); protein binding / sequence-specific DNA binding / transcription factor	Unigene3750_All//1.00E-109//gi|164285084|gb|ES814639.1|ES814639	GRAS			nr -
Unigene37500_All	449	2.10	1.81	2.13	7.66	4.68	3.52	1.32	0.74	0.44	-2.16E-01	7.32E-01		2.54E-02	9.91E-01		-7.11E-01	2.49E-02		-1.12E+00	7.35E-04	Down	-8.24E-01	3.48E-01		-1.57E+00	6.49E-02		Unigene37500_All//gi|124359162|gb|ABN05685.1|//1.00E-17//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene37500_All//1.00E-08//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene37500_All//2.00E-37//BE052035				nr -
Unigene37501_All	611	4.62	2.40	6.62	19.65	13.92	7.91	4.15	1.44	0.26	-9.43E-01	1.17E-02		5.18E-01	1.06E-01		-4.97E-01	1.18E-03		-1.31E+00	5.53E-15	Down	-1.53E+00	4.18E-05	Down	-3.99E+00	4.83E-14	Down			Unigene37501_All//1.00E-36//BF275236				
Unigene37502_All	893	1.23	0.23	1.07	5.69	2.70	1.52	1.28	0.19	0.18	-2.44E+00	1.50E-03		-1.97E-01	7.50E-01		-1.08E+00	1.43E-05	Down	-1.91E+00	4.70E-11	Down	-2.77E+00	7.62E-05	Down	-2.84E+00	3.60E-05	Down			Unigene37502_All//3.00E-38//BF275236				
Unigene3751_All	1963	5.41	9.94	7.81	21.04	16.84	31.73	2.00	4.75	12.60	8.77E-01	6.56E-12		5.30E-01	3.29E-04		-3.21E-01	3.35E-05		5.93E-01	6.02E-20		1.25E+00	2.14E-12	Up	2.65E+00	9.21E-89	Up	Unigene3751_All//gi|15237647|ref|NP_196039.1|//4.00E-30//PKS4 (phytochrome kinase substrate 4) [Arabidopsis thaliana] >gi|75173226|sp|Q9FYE2.1|PKS4_ARATH RecName: Full=Protein PHYTOCHROME KINASE SUBSTRATE 4 >gi|9955574|emb|CAC05501.1| phytochrome kinase substrate 1-like protein [Arabidopsis thaliana] >gi|51315394|gb|AAT99802.1| At5g04190 [Arabidopsis thaliana] >gi|66543333|gb|AAX22264.1| At5g04190 [Arabidopsis thaliana]	Unigene3751_All//4.00E-21//AT5G04190| PKS4 (phytochrome kinase substrate 4)	Unigene3751_All//0.00E+00//CO102833				nr +
Unigene37510_All	918	164.77	145.61	177.21	55.67	60.84	55.30	18.65	10.38	9.03	-1.78E-01	2.21E-05		1.05E-01	1.81E-02		1.28E-01	9.30E-02		-9.80E-03	9.33E-01		-8.46E-01	4.04E-12		-1.05E+00	1.67E-17	Down	Unigene37510_All//gi|225447290|ref|XP_002279657.1|//1.00E-100//PREDICTED: similar to EMB2394 (EMBRYO DEFECTIVE 2394); structural constituent of ribosome [Vitis vinifera]	Unigene37510_All//6.00E-90//AT1G05190| emb2394 (embryo defective 2394); structural constituent of ribosome	Unigene37510_All//0.00E+00//gi|164271977|gb|ES823648.1|ES823648		ko03010|Ribosome		nr +
Unigene37511_All	481	3.15	14.01	12.29	4.25	6.37	9.39	1.05	1.48	1.41	2.15E+00	1.42E-15	Up	1.96E+00	7.74E-12	Up	5.86E-01	1.05E-01		1.14E+00	6.37E-05	Up	4.86E-01	5.42E-01		4.17E-01	6.01E-01				Unigene37511_All//1.00E-112//ES837011				ESTscan +
Unigene37512_All	897	2.80	3.67	7.12	1.67	2.76	2.22	0.38	0.37	0.84	3.91E-01	2.63E-01		1.35E+00	1.01E-07	Up	7.30E-01	7.12E-02		4.11E-01	4.09E-01		-1.65E-02	1.02E+00		1.16E+00	1.06E-01		Unigene37512_All//gi|224068372|ref|XP_002302728.1|//6.00E-13//predicted protein [Populus trichocarpa] >gi|222844454|gb|EEE82001.1| predicted protein [Populus trichocarpa]		Unigene37512_All//3.00E-112//ES837011				nr -
Unigene37514_All	1722	27.59	17.15	22.79	17.39	18.36	14.63	11.76	2.99	3.86	-6.86E-01	1.54E-18		-2.76E-01	6.34E-04		7.85E-02	5.27E-01		-2.49E-01	1.44E-02		-1.98E+00	2.77E-50	Down	-1.61E+00	5.02E-39	Down	Unigene37514_All//gi|38604456|gb|AAR24912.1|//1.00E-164//fructokinase 3 [Solanum lycopersicum]	Unigene37514_All//5.00E-133//AT1G66330| pfkB-type carbohydrate kinase family protein	Unigene37514_All//0.00E+00//TC168961		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene37517_All	2055	0.56	0.74	1.92	6.40	4.16	2.04	7.00	1.22	0.87	4.01E-01	4.53E-01		1.78E+00	3.73E-07	Up	-6.23E-01	1.33E-05		-1.65E+00	9.81E-23	Down	-2.52E+00	3.51E-48	Down	-3.00E+00	5.31E-60	Down	Unigene37517_All//gi|15237312|ref|NP_197731.1|//0.00E+00//disease resistance family protein / LRR family protein [Arabidopsis thaliana] >gi|9759078|dbj|BAB09556.1| disease resistance protein-like [Arabidopsis thaliana]	Unigene37517_All//0.00E+00//AT5G23400| disease resistance family protein / LRR family protein	Unigene37517_All//0.00E+00//TC178363		ko04626|Plant-pathogen interaction		nr -
Unigene3752_All	2075	1.08	2.47	1.64	12.12	5.83	5.55	12.18	19.14	8.93	1.19E+00	1.42E-05	Up	5.99E-01	8.79E-02		-1.06E+00	7.69E-25	Down	-1.13E+00	2.61E-24	Down	6.51E-01	1.98E-17		-4.49E-01	1.93E-06		Unigene3752_All//gi|15238363|ref|NP_201321.1|//2.00E-37//VQ motif-containing protein [Arabidopsis thaliana] >gi|49917435|gb|AAS49042.1| At5g65170 [Arabidopsis thaliana] >gi|46931270|gb|AAT06439.1| At5g65170 [Arabidopsis thaliana]	Unigene3752_All//7.00E-20//AT5G65170| VQ motif-containing protein	Unigene3752_All//0.00E+00//gi|109826075|gb|DW224796.1|DW224796				nr -
Unigene37522_All	1386	8.57	5.89	5.96	6.11	7.21	5.18	8.36	5.04	3.48	-5.42E-01	9.59E-04		-5.25E-01	2.16E-03		2.38E-01	2.30E-01		-2.38E-01	2.87E-01		-7.31E-01	9.15E-07		-1.27E+00	4.21E-16	Down	Unigene37522_All//gi|11181932|emb|CAC16135.1|//1.00E-119//endonuclease III homologue [Arabidopsis thaliana]	Unigene37522_All//3.00E-111//AT2G31450| endonuclease-related	Unigene37522_All//0.00E+00//CO093647		ko03410|Base excision repair		nr -
Unigene37526_All	789	2.45	43.28	5.94	1.01	1.66	1.89	10.50	60.12	57.21	4.14E+00	1.65E-146	Up	1.28E+00	1.97E-05	Up	7.15E-01	2.46E-01		9.03E-01	1.09E-01		2.52E+00	5.58E-157	Up	2.45E+00	3.63E-147	Up	Unigene37526_All//gi|18417474|ref|NP_567835.1|//1.00E-77//CFIM-25 [Arabidopsis thaliana] >gi|150816674|gb|AAR82492.1| AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|20147173|gb|AAM10303.1| AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|21554114|gb|AAM63194.1| mRNA cleavage factor subunit-like protein [Arabidopsis thaliana]	Unigene37526_All//5.00E-63//AT4G29820| CFIM-25	Unigene37526_All//0.00E+00//TC161737				nr +
Unigene37527_All	815	42.11	34.75	34.17	63.14	46.22	57.80	48.92	30.41	20.09	-2.77E-01	2.96E-03		-3.02E-01	1.77E-03		-4.50E-01	1.91E-11		-1.28E-01	1.24E-01		-6.86E-01	4.05E-19		-1.28E+00	1.74E-54	Down	Unigene37527_All//gi|297808085|ref|XP_002871926.1|//6.00E-25//ribosomal protein L36 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317763|gb|EFH48185.1| ribosomal protein L36 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37527_All//4.00E-26//AT5G20180| ribosomal protein L36 family protein	Unigene37527_All//0.00E+00//gi|13247626|gb|BF271402.2|BF271402		ko03010|Ribosome		nr -

Unigene3753_All	1067	3.48	2.80	1.85	7.84	7.00	5.16	5.59	2.74	2.46	-3.13E-01	3.52E-01		-9.15E-01	6.10E-03		-1.63E-01	4.81E-01		-6.03E-01	2.21E-03		-1.03E+00	2.95E-06	Down	-1.18E+00	6.58E-08	Down	Unigene3753_All//gi|18391394|ref|NP_563908.1|//1.00E-109//ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / binding / microtubule motor [Arabidopsis thaliana] >gi|75173334|sp|Q9FZ06.1|ARK3_ARATH RecName: Full=Armadillo repeat-containing kinesin-like protein 3; AltName: Full=Phosphatidic acid kinase >gi|9954168|gb|AAG08965.1|AF159052_1 kinesin-like protein [Arabidopsis thaliana] >gi|162958327|dbj|BAF95587.1| armadillo repeat kinesin3 [Arabidopsis thaliana]	Unigene3753_All//1.00E-103//AT1G12430| ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / binding / microtubule motor	Unigene3753_All//0.00E+00//gi|164269381|gb|ES830435.1|ES830435				nr -
Unigene37531_All	1788	2.93	6.83	3.04	3.04	4.03	3.23	2.39	3.79	2.03	1.22E+00	9.12E-13	Up	5.40E-02	8.43E-01		4.07E-01	6.61E-02		9.04E-02	7.43E-01		6.65E-01	9.24E-04		-2.36E-01	3.86E-01		Unigene37531_All//gi|47497362|dbj|BAD19401.1|//2.00E-42//DNAJ heat shock N-terminal domain-containing protein-like [Oryza sativa Japonica Group]	Unigene37531_All//4.00E-32//AT5G16650| DNAJ heat shock N-terminal domain-containing protein	Unigene37531_All//0.00E+00//gi|48790620|gb|CO091934.1|CO091934				nr -
Unigene37532_All	1726	3.36	1.32	3.46	19.77	9.54	5.18	11.81	9.44	6.62	-1.35E+00	1.89E-07	Down	3.83E-02	8.88E-01		-1.05E+00	2.83E-33	Down	-1.93E+00	1.14E-72	Down	-3.22E-01	3.57E-03		-8.34E-01	2.18E-14		Unigene37532_All//gi|18700103|gb|AAL77663.1|//1.00E-158//AT5g10770/T30N20_40 [Arabidopsis thaliana] >gi|24111269|gb|AAN46758.1| At5g10770/T30N20_40 [Arabidopsis thaliana]	Unigene37532_All//3.00E-140//AT5G10770| chloroplast nucleoid DNA-binding protein, putative	Unigene37532_All//0.00E+00//TC137010				nr +
Unigene37533_All	1882	5.95	2.77	2.09	9.79	8.69	9.41	11.86	8.28	4.91	-1.10E+00	3.98E-10	Down	-1.51E+00	2.81E-15	Down	-1.72E-01	2.26E-01		-5.81E-02	6.96E-01		-5.18E-01	5.09E-07		-1.27E+00	1.80E-30	Down	Unigene37533_All//gi|297816078|ref|XP_002875922.1|//0.00E+00//glutamate-1-semialdehyde 2,1-aminomutase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297321760|gb|EFH52181.1| glutamate-1-semialdehyde 2,1-aminomutase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene37533_All//0.00E+00//AT3G48730| GSA2 (glutamate-1-semialdehyde 2,1-aminomutase 2); catalytic/ glutamate-1-semialdehyde 2,1-aminomutase/ pyridoxal phosphate binding / transaminase	Unigene37533_All//0.00E+00//TC153660		ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene37535_All	781	2.81	9.47	10.36	20.47	15.04	30.13	16.94	19.91	26.73	1.75E+00	3.80E-13	Up	1.88E+00	3.64E-15	Up	-4.46E-01	6.48E-04		5.57E-01	3.67E-07		2.33E-01	8.49E-02		6.58E-01	5.47E-10		Unigene37535_All//gi|186501250|ref|NP_849973.3|//8.00E-62//metal ion binding [Arabidopsis thaliana]	Unigene37535_All//4.00E-63//AT2G18196| metal ion binding	Unigene37535_All//4.00E-21//DN800214				nr -
Unigene37536_All	1444	1.09	1.61	0.48	4.38	2.07	1.19	4.57	3.10	3.56	5.70E-01	1.75E-01		-1.18E+00	3.61E-02		-1.08E+00	8.06E-07	Down	-1.88E+00	2.12E-13	Down	-5.61E-01	6.15E-03		-3.60E-01	7.62E-02		Unigene37536_All//gi|28850915|gb|AA063381.1|//9.00E-42//At3g46110 [Arabidopsis thaliana]	Unigene37536_All//6.00E-53//AT5G39790| unknown protein	Unigene37536_All//0.00E+00//TC144912				nr -
Unigene37537_All	992	1.27	0.51	1.40	3.31	1.39	2.28	2.22	2.32	2.37	-1.31E+00	3.41E-02		1.41E-01	7.97E-01		-1.26E+00	9.96E-05	Down	-5.42E-01	1.25E-01		6.43E-02	8.78E-01		9.64E-02	7.94E-01		Unigene37537_All//gi|225464836|ref|XP_002272323.1|//1.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene37539_All	1299	5.36	3.63	2.62	3.22	1.86	2.02	1.50	0.84	0.74	-5.62E-01	1.14E-02		-1.03E+00	1.09E-05	Down	-7.96E-01	4.30E-03		-6.76E-01	2.28E-02		-8.40E-01	4.31E-02		-1.02E+00	1.07E-02		Unigene37539_All//gi|115448127|ref|NP_001047843.1|//1.00E-28//Os02g0701300 [Oryza sativa Japonica Group] >gi|51039837|tpg|DAA05208.1| TPA_exp: growth-regulating factor 4 [Oryza sativa (japonica cultivar-group)] >gi|113537374|dbj|BAF09757.1| Os02g0701300 [Oryza sativa Japonica Group]	Unigene37539_All//8.00E-28//AT5G53660| AtGRF7 (GROWTH-REGULATING FACTOR 7); transcription activator	Unigene37539_All//0.00E+00//TC143364	GRF			nr +
Unigene37540_All	991	31.04	6.19	5.32	30.16	21.09	13.03	17.54	0.59	1.33	-2.33E+00	2.12E-76	Down	-2.54E+00	8.07E-82	Down	-5.16E-01	1.07E-08		-1.21E+00	3.43E-32	Down	-4.89E+00	3.27E-102	Down	-3.72E+00	6.06E-88	Down	Unigene37540_All//gi|105829831|gb|ABF74705.1|//7.00E-43//At4g28310 [Arabidopsis thaliana]	Unigene37540_All//2.00E-25//AT4G28310| unknown protein	Unigene37540_All//0.00E+00//ES792341				nr +
Unigene37541_All	1204	3.13	0.88	0.31	2.11	1.06	0.98	8.95	6.14	2.32	-1.82E+00	1.82E-07	Down	-3.34E+00	1.80E-13	Down	-9.96E-01	7.86E-03		-1.11E+00	5.08E-03		-5.43E-01	4.35E-04		-1.95E+00	1.70E-27	Down	Unigene37541_All//gi|50253584|gb|AAT71994.1|//3.00E-68//At3g25640 [Arabidopsis thaliana]	Unigene37541_All//5.00E-62//AT5G23100| unknown protein	Unigene37541_All//0.00E+00//TC152250				nr +
Unigene37545_All	545	2.50	7.16	6.16	11.06	10.17	12.43	2.33	2.38	2.56	1.52E+00	4.21E-06	Up	1.30E+00	3.27E-04	Up	-1.21E-01	6.58E-01		1.69E-01	5.29E-01		3.07E-02	9.85E-01		1.37E-01	7.79E-01		Unigene37545_All//gi|121281798|gb|ABM53472.1|//3.00E-58//eIF5A [Rosa chinensis]	Unigene37545_All//6.00E-53//AT1G69410| ELF5A-3 (EUKARYOTIC ELONGATION FACTOR 5A-3); translation initiation factor	Unigene37545_All//9.00E-142//DR454324				nr -
Unigene37546_All	308	3.06	10.69	6.92	9.70	10.06	17.01	0.82	2.85	1.29	1.81E+00	1.69E-06	Up	1.18E+00	1.19E-02		5.23E-02	9.05E-01		8.10E-01	1.79E-03		1.79E+00	1.27E-02		6.51E-01	5.44E-01		Unigene37546_All//gi|121281798|gb|ABM53472.1|//3.00E-25//eIF5A [Rosa chinensis]	Unigene37546_All//2.00E-21//AT1G69410| ELF5A-3 (EUKARYOTIC ELONGATION FACTOR 5A-3); translation initiation factor	Unigene37546_All//5.00E-105//DW517809				nr -
Unigene37547_All	462	0.11	5.37	1.73	3.45	3.95	4.40	0.37	0.45	0.43	5.57E+00	9.50E-13	Up	3.93E+00	1.25E-03		1.95E-01	7.43E-01		3.51E-01	4.78E-01		3.05E-01	8.36E-01		2.36E-01	8.83E-01					Unigene37547_All//5.00E-112//DW239987				
Unigene37548_All	767	2.39	10.37	6.11	7.86	11.58	11.31	0.33	0.93	0.73	2.12E+00	6.20E-18	Up	1.36E+00	6.80E-06	Up	5.60E-01	2.58E-03		5.25E-01	7.47E-03		1.49E+00	6.15E-02		1.14E+00	1.91E-01		Unigene37548_All//gi|124226|sp|P24922.1|IF5A2_NICPL//5.00E-58//RecName: Full=Eukaryotic translation initiation factor 5A-2; Short=eIF-5A-2; AltName: Full=eIF-4D >gi|19702|emb|CAA45104.1| eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]	Unigene37548_All//4.00E-52//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor	Unigene37548_All//4.00E-154//TC153096				nr -
Unigene37549_All	1998	5.79	8.83	4.80	12.62	12.81	14.90	6.71	15.12	16.01	6.09E-01	3.94E-06		-2.71E-01	1.39E-01		2.16E-02	8.77E-01		2.40E-01	1.99E-02		1.17E+00	5.19E-35	Up	1.26E+00	4.91E-42	Up	Unigene37549_All//gi|15239081|ref|NP_196715.1|//0.00E+00//FAD-binding domain-containing protein [Arabidopsis thaliana]	Unigene37549_All//0.00E+00//AT5G11540| FAD-binding domain-containing protein	Unigene37549_All//0.00E+00//DR459048		ko00053|Ascorbate and aldarate metabolism		nr +
Unigene37550_All	952	5.88	2.61	5.15	10.41	9.84	10.96	2.44	4.57	2.34	-1.17E+00	5.82E-06	Down	-1.93E-01	4.95E-01		-8.18E-02	7.17E-01		7.37E-02	7.13E-01		9.02E-01	5.20E-04		-5.99E-02	8.81E-01		Unigene37550_All//gi|4204289|gb|AAD10670.1|//1.00E-21//Unknown protein [Arabidopsis thaliana]	Unigene37550_All//4.00E-21//AT5G44060| unknown protein	Unigene37550_All//0.00E+00//TC174538				nr -
Unigene37551_All	2020	14.45	8.95	8.25	17.24	15.60	17.28	19.59	16.93	9.57	-6.91E-01	7.70E-12		-8.09E-01	1.09E-14		-1.44E-01	1.47E-01		3.80E-03	9.69E-01		-2.11E-01	7.31E-03		-1.03E+00	1.65E-38	Down	Unigene37551_All//gi|3121130|sp|O22212.1|PRP4_ARATH RecName: Full=U4/U6 small nuclear ribonucleoprotein PRP4-like protein; AltName: Full=Protein EMBRYO DEFECTIVE 2776 >gi|58652074|gb|AAW80862.1| At2g41500 [Arabidopsis thaliana]	Unigene37551_All//1.00E-179//AT2G41500| EMB2776; nucleotide binding	Unigene37551_All//0.00E+00//TC147974		ko03040|Spliceosome		nr +
Unigene37552_All	1494	1.05	0.37	0.36	56.92	11.89	39.54	7.41	3.22	2.29	-1.49E+00	6.73E-03		-1.56E+00	7.38E-03		-2.26E+00	2.81E-257	Down	-5.26E-01	5.31E-22		-1.20E+00	6.64E-14	Down	-1.69E+00	2.24E-23	Down	Unigene37552_All//gi|257831443|gb|ACV71022.1|//7.00E-24//UPA23 [Capsicum annuum]	Unigene37552_All//5.00E-22//AT3G44940| unknown protein	Unigene37552_All//0.00E+00//TC171932		ko03040|Spliceosome		nr -
Unigene37553_All	1117	12.83	10.98	10.34	38.13	34.25	32.67	10.64	24.85	7.38	-2.25E-01	1.49E-01		-3.11E-01	5.07E-02		-1.55E-01	7.20E-02		-2.23E-01	7.65E-03		1.22E+00	2.06E-34	Up	-5.27E-01	2.17E-04		Unigene37553_All//gi|166203244|gb|ABB18662.1|//5.00E-55//transcription factor [Glycine max]	Unigene37553_All//3.00E-40//AT3G56400| WRKY70; transcription factor/ transcription repressor	Unigene37553_All//0.00E+00//CO089978	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene37556_All	990	6.61	7.78	8.39	11.87	11.93	10.13	14.31	10.30	5.43	2.36E-01	2.94E-01		3.45E-01	1.13E-01		6.80E-03	9.75E-01		-2.30E-01	2.11E-01		-4.74E-01	3.62E-04		-1.40E+00	1.44E-22	Down	Unigene37556_All//gi|18398701|ref|NP_565433.1|//2.00E-98//anaphase-promoting complex, subunit 10 family / APC10 family [Arabidopsis thaliana] >gi|34395513|sp|Q9ZFW2.2|APC10_ARATH RecName: Full=Anaphase-promoting complex subunit 10; Short=APC10; AltName: Full=Cyclosome subunit 10 >gi|20197809|gb|AAD15507.2| expressed protein [Arabidopsis thaliana] >gi|90567996|gb|ABD94068.1| At2g18290 [Arabidopsis thaliana]	Unigene37556_All//2.00E-91//AT2G18290| anaphase-promoting complex, subunit 10 family / APC10 family	Unigene37556_All//0.00E+00//TC141358		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene37557_All	468	6.04	3.36	5.46	4.04	2.87	2.03	4.61	2.68	1.02	-8.47E-01	2.31E-02		-1.45E-01	7.02E-01		-4.95E-01	3.07E-01		-9.97E-01	3.60E-02		-7.82E-01	4.54E-02		-2.17E+00	6.08E-07	Down	Unigene37557_All//gi|225427310|ref|XP_002282053.1|//1.00E-22//PREDICTED: similar to pentatricopeptide repeat-containing protein At1g32415 [Vitis vinifera]	Unigene37557_All//2.00E-10//AT1G32410| vacuolar protein sorting 55 family protein / VPS55 family protein	Unigene37557_All//3.00E-144//TC150052				nr +
Unigene37558_All	725	44.31	37.53	58.39	28.45	33.68	29.47	10.61	6.98	5.22	-2.40E-01	1.44E-02		3.98E-01	2.25E-06		2.44E-01	3.02E-02		5.08E-02	7.16E-01		-6.06E-01	1.18E-03		-1.02E+00	4.38E-08	Down	Unigene37558_All//gi|225427310|ref|XP_002282053.1|//6.00E-58//PREDICTED: similar to pentatricopeptide repeat-containing protein At1g32415 [Vitis vinifera]	Unigene37558_All//8.00E-44//AT1G32410| vacuolar protein sorting 55 family protein / VPS55 family protein	Unigene37558_All//0.00E+00//TC150052				nr +
Unigene3756_All	1052	13.78	29.48	17.06	25.76	27.50	27.00	17.68	25.31	20.22	1.10E+00	1.98E-26	Up	3.08E-01	2.77E-02		9.41E-02	4.48E-01		6.81E-02	6.21E-01		5.17E-01	3.46E-08		1.94E-01	7.88E-02		Unigene3756_All//gi|192913012|gb|ACF06614.1|//2.00E-52//holocarboxylase synthetase [Elaeis guineensis]	Unigene3756_All//1.00E-36//AT4G09830| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP009193 (InterPro:IPR016549); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64780.1); Has 56 Blast hits to 56 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene3756_All//0.00E+00//TC148730				nr -
Unigene3563_All	1189	2.07	2.43	6.94	9.09	13.53	20.97	3.59	2.64	2.71	2.32E-01	5.54E-01		1.75E+00	5.08E-14	Up	5.73E-01	1.06E-05		1.21E+00	2.09E-26	Up	-4.46E-01	9.75E-02		-4.04E-01	1.18E-01		Unigene3563_All//gi|13446373|gb|AAK20904.1|//9.00E-19//plastid-targeted protein 3 [Craterostigma plantagineum]	Unigene3563_All//2.00E-05//AT2G14095| unknown protein	Unigene3563_All//1.00E-16//CO097117				nr +
Unigene37564_All	593	46.06	235.92	56.75	71.99	106.67	154.68	206.84	522.06	702.05	2.36E+00	0.00E+00	Up	3.01E-01	2.01E-03		5.67E-01	1.27E-20		1.10E+00	2.37E-83	Up	1.34E+00	0.00E+00	Up	1.76E+00	0.00E+00	Up	Unigene37564_All//gi|1332579|emb|CAA66667.1|//1.00E-105//polyubiquitin [Pinus sylvestris]	Unigene37564_All//7.00E-106//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene37564_All//0.00E+00//TC145816				nr -
Unigene37565_All	1142	23.32	6.34	14.18	21.29	18.21	7.04	2.30	0.62	1.60	-1.88E+00	2.22E-50	Down	-7.18E-01	4.52E-11		-2.25E-01	4.53E-02		-1.60E+00	8.28E-40	Down	-1.88E+00	9.55E-07	Down	-5.16E-01	1.27E-01		Unigene37565_All//gi|227206194|dbj|BAH57152.1|//6.00E-31//AT3G15095 [Arabidopsis thaliana]	Unigene37565_All//3.00E-25//AT3G15095| unknown protein	Unigene37565_All//0.00E+00//gi|78350800|gb|DT571074.1|DT571074				nr -
Unigene37570_All	877	1.01	0.64	1.09	2.10	2.04	2.42	0.63	2.43	1.27	-6.74E-01	3.69E-01		1.08E-01	8.75E-01		-4.16E-02	9.26E-01		2.04E-01	6.86E-01		1.96E+00	7.46E-06	Up	1.02E+00	6.87E-02					Unigene37570_All//0.00E+00//BQ413308				

Unigene37571_All	303	3.80	2.01	0.18	4.44	2.39	7.90	0.84	3.59	2.10	-9.21E-01	1.43E-01			-4.43E+00	2.72E-05	Down	-8.95E-01	1.07E-01		8.32E-01	4.64E-02		2.10E+00	1.40E-03		1.33E+00	1.00E-01		Unigene37571_All//gi|4433048|dbj|BAA21017.1|/1.00E-23//DNA-binding protein [Daucus carota]	Unigene37571_All//6.00E-11//AT2G22430| ATHB6; DNA binding / protein binding / sequence-specific DNA binding / transcription activator/ transcription factor	Unigene37571_All//8.00E-147//TC158717	HB			nr +
Unigene37572_All	959	19.80	7.03	10.66	20.99	12.93	25.95	3.84	6.58	2.87	-1.49E+00	2.72E-26	Down	-8.94E-01	1.83E-11		-6.99E-01	4.91E-10		3.06E-01	5.63E-03		7.79E-01	1.99E-04		-4.20E-01	1.36E-01		Unigene37572_All//gi|49659431|dbj|BAD27254.1|//9.00E-51//SlHDL1 [Silene latifolia]	Unigene37572_All//2.00E-36//AT2G22430| ATHB6; DNA binding / protein binding / sequence-specific DNA binding / transcription activator/ transcription factor	Unigene37572_All//0.00E+00//gi|82755451|gb|DV849013.1|DV849013	HB			nr +
Unigene37575_All	1339	13.79	11.69	10.50	5.65	8.92	5.26	2.78	1.34	1.19	-2.38E-01	7.77E-02		-3.94E-01	3.52E-03		6.58E-01	1.95E-05		-1.04E-01	6.85E-01		-1.05E+00	2.48E-04	Down	-1.22E+00	1.63E-05	Down	Unigene37575_All//gi|115477278|ref|NP_001062235.1|/1.00E-108//Os08g0515800 [Oryza sativa Japonica Group] >gi|113624204|dbj|BAF24149.1|Os08g0515800 [Oryza sativa Japonica Group]	Unigene37575_All//2.00E-97//AT4G38160| pde191 (pigment defective 191)	Unigene37575_All//0.00E+00//TC157279				nr -
Unigene37577_All	1768	1.63	0.89	1.45	10.76	8.18	4.01	4.21	0.61	0.45	-8.74E-01	1.79E-02		-1.71E-01	6.46E-01		-3.96E-01	9.07E-04		-1.42E+00	1.81E-26	Down	-2.78E+00	4.83E-28	Down	-3.22E+00	1.39E-33	Down	Unigene37577_All//gi|297824789|ref|XP_002880277.1|//0.00E+00//At2g47010/F14M4.16 [Arabidopsis lyrata subsp. lyrata] >gi|297326116|gb|EFH56536.1|At2g47010/F14M4.16 [Arabidopsis lyrata subsp. lyrata]	Unigene37577_All//0.00E+00//AT2G47010| unknown protein	Unigene37577_All//0.00E+00//TC165022				nr +
Unigene37579_All	2115	1.93	0.26	0.45	7.80	6.82	2.97	3.10	0.95	1.96	-2.87E+00	2.50E-13	Down	-2.09E+00	5.64E-09	Down	-1.93E-01	1.94E-01		-1.39E+00	2.88E-22	Down	-1.71E+00	7.20E-14	Down	-6.62E-01	8.56E-04		Unigene37579_All//gi|224082398|ref|XP_002306678.1|//0.00E+00//auxin efflux carrier component [Populus trichocarpa] >gi|222856127|gb|EEE93674.1| auxin efflux carrier component [Populus trichocarpa]	Unigene37579_All//0.00E+00//AT1G77110| PIN6 (PIN-FORMED 6); auxin:hydrogen symporter/ transporter	Unigene37579_All//0.00E+00//gi|78344013|gb|DT564287.1|DT564287				nr +
Unigene3758_All	2118	21.54	1.72	1.51	16.89	8.88	7.74	40.36	5.74	18.94	-3.64E+00	2.38E-179	Down	-3.84E+00	2.67E-180	Down	-9.28E-01	2.64E-28		-1.13E+00	2.97E-34	Down	-2.81E+00	0.00E+00	Down	-1.09E+00	1.24E-89	Down	Unigene3758_All//gi|15234688|ref|NP_193932.1|//0.00E+00//sks4 (SKU5 Similar 4); copper ion binding / oxidoreductase [Arabidopsis thaliana] >gi|2961346|emb|CAA18104.1|pectinesterase like protein [Arabidopsis thaliana] >gi|7269046|emb|CAB79156.1|pectinesterase like protein [Arabidopsis thaliana] >gi|196989977|gb|AAL91224.1|pectinesterase-like protein [Arabidopsis thaliana] >gi|317119964|gb|ADP88338.1|At4g22010 [Arabidopsis thaliana]	Unigene3758_All//0.00E+00//AT4G22010| sks4 (SKU5 Similar 4); copper ion binding / oxidoreductase	Unigene3758_All//0.00E+00//TC132575		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene37580_All	1727	6.97	3.96	1.97	12.00	11.09	5.94	5.07	0.82	2.56	-8.15E-01	7.11E-07		-1.82E+00	2.92E-21	Down	-1.14E-01	4.24E-01		-1.02E+00	4.72E-17	Down	-2.62E+00	6.12E-31	Down	-9.85E-01	1.44E-08		Unigene37580_All//gi|2443885|gb|AAB71478.1|//8.00E-22//Unknown protein [Arabidopsis thaliana] >gi|30017227|gb|AAP12847.1|At1g61170 [Arabidopsis thaliana]	Unigene37580_All//1.00E-09//AT1G61170| unknown protein	Unigene37580_All//0.00E+00//ES801341				nr -
Unigene37584_All	548	2.39	2.77	2.72	8.91	5.53	4.62	5.63	2.29	2.91	2.17E-01	6.71E-01		1.89E-01	7.21E-01		-6.88E-01	7.27E-03		-9.49E-01	4.05E-04		-1.30E+00	6.66E-05	Down	-9.54E-01	1.90E-03		Unigene37584_All//gi|75183398|sp|Q9MZV6.1|Y3972_ARATH//7.00E-45//RecName: Full=Uncharacterized protein At3g49720 >gi|222424727|dbj|BAH20317.1|AT3G49720 [Arabidopsis thaliana]	Unigene37584_All//6.00E-35//AT3G49720| unknown protein	Unigene37584_All//0.00E+00//gi|13248315|gb|BF275246.2|BF275246				nr -
Unigene37585_All	811	3.81	1.50	1.25	5.41	4.29	3.45	3.08	1.03	1.33	-1.34E+00	2.54E-04	Down	-1.61E+00	4.40E-05	Down	-3.34E-01	2.74E-01		-6.47E-01	2.53E-02		-1.58E+00	3.22E-05	Down	-1.21E+00	6.07E-04	Down	Unigene37585_All//gi|115434486|ref|NP_001042001.1|//1.00E-74//Os01g0144000 [Oryza sativa Japonica Group] >gi|113531532|dbj|BAF03915.1|Os01g0144000 [Oryza sativa Japonica Group]	Unigene37585_All//3.00E-74//AT3G49720| unknown protein	Unigene37585_All//0.00E+00//TC170926				nr +
Unigene37586_All	940	1.17	2.91	2.38	3.34	2.38	4.04	2.38	0.89	0.68	1.32E+00	8.34E-04	Up	1.03E+00	2.31E-02		-4.88E-01	1.65E-01		2.74E-01	4.44E-01		-1.42E+00	3.28E-04	Down	-1.81E+00	7.47E-06	Down	Unigene37586_All//gi|75183398|sp|Q9MZV6.1|Y3972_ARATH//2.00E-94//RecName: Full=Uncharacterized protein At3g49720 >gi|222424727|dbj|BAH20317.1|AT3G49720 [Arabidopsis thaliana]	Unigene37586_All//4.00E-85//AT3G49720| unknown protein	Unigene37586_All//0.00E+00//TC170926				nr -
Unigene37587_All	1572	0.93	1.48	0.75	3.80	2.54	2.36	4.06	22.44	4.76	6.70E-01	1.11E-01		-3.23E-01	5.91E-01		-5.82E-01	1.15E-02		-6.91E-01	3.84E-03		2.47E+00	3.94E-114	Up	2.30E-01	2.47E-01		Unigene37587_All//gi|1685005|gb|AAB36653.1|//1.00E-143//immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]	Unigene37587_All//4.00E-126//AT2G15490| UGT73B4 (UDP-GLYCOSYLTRANSFERASE 73B4); UDP-glucosyltransferase/ UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene37587_All//0.00E+00//TC143715		ko00908|Zeatin biosynthesis		nr -
Unigene37589_All	776	1.75	0.52	6.04	3.08	1.46	3.03	4.09	1.29	4.57	-1.75E+00	4.61E-03		1.78E+00	1.92E-08	Up	-1.07E+00	5.67E-03		-2.59E-02	9.56E-01		-1.66E+00	7.42E-07	Down	1.61E-01	6.01E-01		Unigene37589_All//gi|86559335|gb|AB004075.1|//2.00E-62//YSL transporter 3 [Noccaea caerulescens]	Unigene37589_All//2.00E-61//AT5G53550| YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	Unigene37589_All//2.00E-57//CK640489				nr +
Unigene37590_All	1263	0.41	0.84	4.22	0.83	0.79	1.00	4.02	1.22	3.38	1.02E+00	1.27E-01		3.35E+00	4.80E-19	Up	-6.70E-02	9.06E-01		2.74E-01	6.79E-01		-1.71E+00	5.80E-11	Down	-2.51E-01	3.13E-01		Unigene37590_All//gi|86559335|gb|AB004075.1|//1.00E-120//YSL transporter 3 [Noccaea caerulescens]	Unigene37590_All//3.00E-118//AT5G53550| YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	Unigene37590_All//3.00E-57//CK640489				nr +
Unigene37591_All	1164	4.00	2.44	1.69	5.73	5.41	4.31	3.60	3.59	5.54	-7.15E-01	1.04E-02		-1.24E+00	3.41E-05	Down	-8.31E-02	7.77E-01		-4.13E-01	7.80E-02		-2.10E-03	1.01E+00		6.25E-01	1.87E-03		Unigene37591_All//gi|3785977|gb|AAC67324.1|//1.00E-151//similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana] >gi|20260420|gb|AAM13108.1|similar to axi 1 protein [Arabidopsis thaliana] >gi|22136280|gb|AAM91218.1|similar to axi 1 protein [Arabidopsis thaliana] >gi|110742513|dbj|BAE99174.1|similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana]	Unigene37591_All//3.00E-134//AT2G01480| unknown protein	Unigene37591_All//0.00E+00//CO085849				nr +
Unigene37592_All	805	43.61	56.96	26.53	70.98	60.79	77.48	81.78	62.25	34.30	3.85E-01	8.39E-07		-7.17E-01	2.31E-14		-2.24E-01	8.32E-04		1.26E-01	8.53E-02		-3.94E-01	7.68E-12		-1.25E+00	3.74E-86	Down	Unigene37592_All//gi|240254411|ref|NP_178110.6|//3.00E-55//ATP binding [Arabidopsis thaliana]	Unigene37592_All//9.00E-55//AT1G79920| ATP binding	Unigene37592_All//0.00E+00//TC138215		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene37593_All	1156	3.67	3.16	3.55	19.78	24.07	27.35	7.68	2.10	1.55	-2.16E-01	4.86E-01		-4.77E-02	8.83E-01		2.83E-01	4.93E-03		4.68E-01	5.25E-07		-1.87E+00	6.21E-21	Down	-2.31E+00	4.81E-28	Down	Unigene37593_All//gi|115440079|ref|NP_001044319.1|//2.00E-27//Os01g0760900 [Oryza sativa Japonica Group] >gi|75106329|sp|Q6JMF2.1|ABIL5_ORYSJ RecName: Full=Probable protein ABIL5; AltName: Full=Abl interactor-like protein 5 >gi|113533850|dbj|BAF06233.1|Os01g0760900 [Oryza sativa Japonica Group]	Unigene37593_All//3.00E-16//AT2G46225| ABIL1 (Abi-1-like 1)	Unigene37593_All//0.00E+00//gi|164314621|gb|ES814765.1|ES814765				nr +
Unigene37594_All	889	129.89	105.39	107.82	190.40	179.73	203.57	141.25	80.63	55.57	-3.02E-01	2.46E-10		-2.69E-01	4.57E-08		-8.32E-02	4.60E-02		9.64E-02	1.73E-02		-8.09E-01	1.27E-77		-1.35E+00	1.17E-182	Down	Unigene37594_All//gi|168480809|gb|ACA24498.1|//2.00E-93//pseudouridine synthase and archaeosine transglycosylase-like protein [Cucumis sativus]	Unigene37594_All//4.00E-88//AT1G09150| pseudouridine synthase and archaeosine transglycosylase (PUA) domain-containing protein	Unigene37594_All//0.00E+00//TC139448				nr +
Unigene37595_All	689	9.42	8.16	6.57	14.60	11.45	5.18	1.10	0.36	0.06	-2.06E-01	3.90E-01		-5.19E-01	3.29E-02		-3.52E-01	4.95E-02		-1.50E+00	2.69E-15	Down	-1.60E+00	3.70E-02		-4.26E+00	8.65E-05	Down	Unigene37595_All//gi|296088269|emb|CBI35777.3|//1.00E-13//unnamed protein product [Vitis vinifera]	Unigene37595_All//9.00E-05//AT3G23930| unknown protein	Unigene37595_All//0.00E+00//gi|109829096|gb|DW227690.1|DW227690				nr -
Unigene37596_All	771	66.23	44.82	47.79	79.53	65.74	25.66	1.65	0.92	0.31	-5.63E-01	3.11E-14		-4.71E-01	5.16E-10		-2.75E-01	1.11E-05		-1.63E+00	4.89E-103	Down	-8.36E-01	1.23E-01		-2.41E+00	7.19E-05	Down	Unigene37596_All//gi|225433334|ref|XP_002282600.1|//2.00E-36//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene37596_All//9.00E-17//AT4G13540| unknown protein	Unigene37596_All//7.00E-128//gi|73858750|gb|DT461489.1|DT461489				nr +
Unigene37598_All	1278	1.92	3.33	1.79	4.05	2.51	2.72	2.65	0.95	2.87	7.91E-01	7.28E-03		-1.03E-01	8.01E-01		-6.94E-01	4.95E-03		-5.75E-01	2.93E-02		-1.48E+00	2.84E-06	Down	1.16E-01	6.92E-01		Unigene37598_All//gi|297596373|ref|NP_001042181.2|//1.00E-07//Os01g0228800 [Oryza sativa Japonica Group] >gi|255673022|dbj|BAF04395.2|Os01g0228800 [Oryza sativa Japonica Group]	Unigene37598_All//8.00E-10//AT3G24630| unknown protein					nr +
Unigene37599_All	1291	1.54	1.22	1.07	5.21	5.01	4.30	7.07	2.04	3.52	-3.40E-01	4.60E-01		-5.22E-01	2.81E-01		-5.49E-02	8.27E-01		-2.76E-01	2.70E-01		-1.79E+00	2.50E-20	Down	-1.01E+00	3.27E-09	Down	Unigene37599_All//gi|72004127|gb|AAZ66047.1|//1.00E-151//fused [Arabidopsis thaliana]	Unigene37599_All//6.00E-153//AT1G50240| FU (FUSED); protein serine/threonine kinase					nr -
Unigene376_All	2391	83.07	50.56	38.02	37.98	31.40	36.08	25.80	24.47	16.53	-7.16E-01	4.14E-81		-1.13E+00	1.59E-168	Down	-2.75E-01	3.92E-08		-7.41E-02	2.54E-01		-7.62E-02	2.86E-01		-6.42E-01	8.82E-27		Unigene376_All//gi|124245039|gb|ABW92419.1|//0.00E+00//chloroplast HSP70 [Cucumis sativus]	Unigene376_All//0.00E+00//AT4G24280| cpHsc70-1 (chloroplast heat shock protein 70-1); ATP binding	Unigene376_All//0.00E+00//TC148473		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03018|RNA degradation		nr +
Unigene3760_All	1452	0.32	2.90	0.81	6.90	19.19	22.49	1.92	1.01	0.77	3.16E+00	7.50E-15	Up	1.31E+00	5.10E-02		1.48E+00	1.01E-43	Up	1.71E+00	1.64E-57	Up	-9.32E-01	5.56E-03		-1.32E+00	8.46E-05	Down	Unigene3760_All//gi|18420811|ref|NP_568449.1|//1.00E-110//copper-binding family protein [Arabidopsis thaliana]	Unigene3760_All//6.00E-64//AT5G24580| copper-binding family protein	Unigene3760_All//0.00E+00//TC146549				nr +
Unigene37601_All	496	14.24	25.95	7.09	8.64	9.79	11.20	7.93	11.63	6.43	8.66E-01	5.75E-08		-1.01E+00	1.39E-05	Down	1.81E-01	5.79E-01		3.75E-01	1.64E-01		5.53E-01	1.26E-02		-3.03E-01	2.80E-01					Unigene37601_All//5.00E-66//gi|78328091|gb|DT548365.1|DT548365				
Unigene37602_All	1451	0.79	0.35	0.11	2.13	1.50	1.21	2.24	2.22	1.92	-1.18E+00	6.62E-02		-2.85E+00	6.02E-04	Down	-5.10E-01	1.50E-01		-8.10E-01	2.18E-02		-1.66E-02	9.92E-01		-2.23E-01	4.86E-01		Unigene37602_All//gi|79313347|ref|NP_001030753.1|//1.00E-66//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	Unigene37602_All//1.00E-06//AT3G23900| RNA recognition motif (RRM)-containing protein	Unigene37602_All//1.00E-102//gi|164318910|gb|ES828737.1|ES828737		ko03040|Spliceosome		nr +
Unigene37603_All	1219	0.82	2.16	6.60	4.45	2.43	88.33	8.25	65.80	79.32	1.41E+00	5.42E-04	Up	3.02E+00	6.00E-26	Up	-8.75E-01	2.31E-04		4.31E+00	0.00E+00	Up	2.99E+00	0.00E+00	Up	3.26E+00	0.00E+00	Up	Unigene37603_All//gi|115435944|ref|NP_001042730.1|//1.00E-08//Os01g0276600 [Oryza sativa Japonica Group] >gi|6539567|dbj|BAA88184.1| zinc finger protein -like [Oryza sativa Japonica Group] >gi|113532261|dbj|BAF04644.1|Os01g0276600 [Oryza sativa Japonica Group]	Unigene37603_All//5.00E-07//AT3G19950| zinc finger (C3HC4-type RING finger) family protein	Unigene37603_All//3.00E-26//gi|48802343|gb|CO103657.1|CO103657				nr +
Unigene37607_All	1475	3.37	0.45	0.94	4.76	2.57	1.19	15.02	1.70	4.86	-2.92E+00	2.42E-16	Down	-1.84E+00	2.92E-09	Down	-8.91E-01	1.31E-05		-2.00E+00	5.57E-16	Down	-3.14E+00	2.79E-93	Down	-1.63E+00	2.03E-43	Down	Unigene37607_All//gi|23345025|gb|AAN17504.1|//1.00E-178//microsomal omega-3 fatty acid desaturase [Betula pendula]	Unigene37607_All//1.00E-164//AT2G29980| FAD3 (FATTY ACID DESATURASE 3); omega-3 fatty acid desaturase	Unigene37607_All//0.00E+00//TC142859		ko01040|Biosynthesis of unsaturated fatty acids		nr +

Unigene37608_All	1047	91.20	215.07	86.05	179.42	144.12	144.59	125.35	243.35	116.62	1.24E+00	2.04E-227	Up	-8.38E-02	1.80E-01		-3.16E-01	3.81E-21		-3.11E-01	1.89E-18		9.57E-01	4.67E-208		-1.04E-01	1.23E-02		Unigene37608_All//gi|290795719|gb|AD064698.1|//3.00E-48//glycine and proline rich protein 3 [Glycine max]		Unigene37608_All//0.00E+00//TC138149		ko03040|Spliceosome		nr -
Unigene37609_All	709	78.96	46.17	49.72	126.40	123.95	154.15	355.24	173.61	159.64	-7.74E-01	1.14E-26		-6.67E-01	6.39E-20		-2.82E-02	7.03E-01		2.86E-01	1.92E-09		-1.03E+00	1.35E-233	Down	-1.15E+00	3.15E-287	Down	Unigene37609_All//gi|33415263|gb|AAQ18140.1|/1.00E-94//enolase [Gossypium barbadense]	Unigene37609_All//3.00E-86//AT2G36530| LOS2; copper ion binding / phosphopyruvate hydratase	Unigene37609_All//0.00E+00//TC155632		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation		nr -
Unigene3761_All	1138	19.59	85.62	21.57	37.60	58.25	40.96	40.20	49.58	113.07	2.13E+00	4.80E-214	Up	1.39E-01	2.74E-01		6.32E-01	4.75E-26		1.23E-01	1.64E-01		3.03E-01	1.38E-06		1.49E+00	1.52E-216	Up	Unigene3761_All//gi|295913545|gb|ADG38020.1|/7.00E-40//transcription factor [Lycoris longituba]	Unigene3761_All//5.00E-27//AT1G32700| zinc-binding family protein	Unigene3761_All//0.00E+00//TC168963	PLATZ			nr -
Unigene37613_All	439	16.33	10.50	11.52	12.60	15.69	17.18	7.22	5.81	2.90	-6.37E-01	3.52E-03		-5.03E-01	2.86E-02		3.17E-01	1.81E-01		4.48E-01	3.96E-02		-3.15E-01	3.57E-01		-1.31E+00	2.70E-05	Down			Unigene37613_All//1.00E-137//TC155325				
Unigene37614_All	1090	10.42	8.41	6.25	7.95	8.21	9.12	6.48	2.65	3.33	-3.08E-01	7.75E-02		-7.36E-01	2.53E-05		4.67E-02	8.35E-01		1.97E-01	3.49E-01		-1.29E+00	4.07E-10	Down	-9.62E-01	7.63E-07		Unigene37614_All//gi|18396223|ref|NP_565333.1|//2.00E-83//ORG4 (OBP3-RESPONSIVE GENE 4) [Arabidopsis thaliana]	Unigene37614_All//8.00E-85//AT2G06010| ORG4 (OBP3-RESPONSIVE GENE 4)	Unigene37614_All//0.00E+00//TC155325				nr -
Unigene37619_All	1232	0.89	2.59	0.73	1.82	1.17	2.27	3.74	4.68	12.42	1.54E+00	3.26E-05	Up	-2.79E-01	6.54E-01		-6.32E-01	1.31E-01		3.21E-01	4.46E-01		3.24E-01	1.65E-01		1.73E+00	1.42E-32	Up	Unigene37619_All//gi|219842168|dbj|BAH10641.1|/1.00E-168//2-methyl-6-phytylbenzoquinone methyltranferase [Hevea brasiliensis]	Unigene37619_All//1.00E-141//AT3G63410| APG1 (ALBINO OR PALE GREEN MUTANT 1); 2-methyl-6-phytyl-1,4-benzoquinone methyltransferase/ S-adenosylmethionine-dependent methyltransferase/ methyltransferase	Unigene37619_All//0.00E+00//gi|78343905|gb|DT564179.1|DT564179		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene37621_All	1058	12.51	12.12	6.85	20.53	21.12	15.32	8.03	4.23	3.95	-4.63E-02	7.76E-01		-8.70E-01	7.26E-08		4.12E-02	8.08E-01		-4.22E-01	2.60E-04		-9.26E-01	2.35E-07		-1.02E+00	8.03E-09	Down	Unigene37621_All//gi|297808049|ref|XP_002871908.1|//5.00E-92//aminoacyl-tRNA hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297317745|gb|EFH48167.1| aminoacyl-tRNA hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene37621_All//2.00E-88//AT5G19830| aminoacyl-tRNA hydrolase	Unigene37621_All//0.00E+00//TC132632				nr -
Unigene37622_All	1024	22.79	37.75	32.19	42.61	50.61	40.84	27.62	126.49	9.92	7.28E-01	8.25E-17		4.98E-01	2.22E-07		2.48E-01	4.32E-04		-6.13E-02	5.59E-01		2.20E+00	0.00E+00	Up	-1.48E+00	5.36E-48	Down	Unigene37622_All//gi|82697965|gb|AB889017.1|/3.00E-81/CXE carboxylesterase [Actinidia deliciosa]	Unigene37622_All//9.00E-62//AT1G49650| cell death associated protein-related	Unigene37622_All//0.00E+00//gi|21094940|gb|BQ407253.1|BQ407253				nr -
Unigene37623_All	661	11.71	9.28	6.28	15.52	17.71	11.48	8.89	2.47	3.56	-3.37E-01	1.21E-01		-8.99E-01	3.92E-05		1.90E-01	3.05E-01		-4.36E-01	1.53E-02		-1.85E+00	6.88E-14	Down	-1.32E+00	3.79E-09	Down	Unigene37623_All//gi|225470696|ref|XP_002263439.1|/8.00E-51//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297741055|emb|CBI31786.3| unnamed protein product [Vitis vinifera]	Unigene37623_All//7.00E-36//AT5G52220| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Chromosome transmission fidelity protein 8 (InterPro:IPR018607); Has 85 Blast hits to 85 proteins in 45 species: Archae - 0; Bacteria - 0; Metazoa - 54; Fungi - 13; Plants - 11; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	Unigene37623_All//0.00E+00//DW517445				nr +
Unigene37624_All	1011	7.61	7.27	17.01	32.72	31.98	56.73	2.13	3.72	2.80	-6.60E-02	7.60E-01		1.16E+00	9.32E-16	Up	-3.27E-02	8.09E-01		7.94E-01	2.08E-30		8.03E-01	4.38E-03		3.92E-01	2.43E-01		Unigene37624_All//gi|297823945|ref|XP_002879855.1|/2.00E-37//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325694|gb|EFH56114.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37624_All//3.00E-27//AT3G25710| BHLH32 (BASIC HELIX-LOOP-HELIX 32); DNA binding / transcription factor	Unigene37624_All//0.00E+00//TC144211	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr -
Unigene37625_All	1348	5.12	2.82	2.01	7.69	7.00	7.87	5.49	5.95	3.01	-8.62E-01	1.19E-04		-1.35E+00	2.92E-08	Down	-1.35E-01	5.30E-01		3.47E-02	8.78E-01		1.17E-01	6.10E-01		-8.65E-01	4.16E-06		Unigene37625_All//gi|30685461|ref|NP_180843.2|//1.00E-45//proline-rich family protein [Arabidopsis thaliana]	Unigene37625_All//4.00E-37//AT2G32840| proline-rich family protein	Unigene37625_All//0.00E+00//gi|78322939|gb|DT543213.1|DT543213				nr +
Unigene37626_All	1197	1.18	4.78	4.09	1.12	1.84	2.19	0.00	0.00	0.03	2.02E+00	2.35E-12	Up	1.79E+00	7.38E-09	Up	7.13E-01	1.04E-01		9.62E-01	1.46E-02		null	null		5.06E+00	6.45E-01		Unigene37626_All//gi|6671365|gb|AAF23176.1|AF216497_1//0.00E+00//P-glycoprotein [Gossypium hirsutum]	Unigene37626_All//1.00E-175//AT4G25960| PGP2 (P-GLYCOPROTEIN 2: ATPase, coupled to transmembrane movement of substances	Unigene37626_All//0.00E+00//TC141861		ko02010|ABC transporters		nr -
Unigene37627_All	511	4.51	2.88	4.79	1.66	1.95	6.28	5.13	10.80	7.72	-6.48E-01	1.23E-01		8.95E-02	8.26E-01		2.38E-01	7.85E-01		1.92E+00	4.32E-07	Up	1.07E+00	3.22E-06	Up	5.89E-01	2.69E-02		Unigene37627_All//gi|297794281|ref|XP_002865025.1|//1.00E-26//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310860|gb|EFH41284.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37627_All//8.00E-28//AT5G67140| F-box family protein					nr -
Unigene37628_All	945	8.53	9.49	11.78	4.80	7.36	7.74	14.63	32.38	24.41	1.55E-01	4.60E-01		4.66E-01	9.03E-03		6.18E-01	3.91E-03		6.91E-01	1.21E-03		1.15E+00	3.57E-34	Up	7.39E-01	3.31E-13		Unigene37628_All//gi|15240225|ref|NP_201515.1|//1.00E-86//F-box family protein [Arabidopsis thaliana] >gi|75262475|sp|Q9FH99.1|FB302_ARATH RecName: Full=F-box protein At5g67140	Unigene37628_All//2.00E-88//AT5G67140| F-box family protein			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene37630_All	1085	52.71	15.13	27.48	167.49	95.66	40.96	51.09	17.03	21.77	-1.80E+00	1.66E-101	Down	-9.39E-01	3.17E-36		-8.08E-01	9.87E-113		-2.03E+00	0.00E+00	Down	-1.59E+00	1.98E-100	Down	-1.23E+00	1.38E-70	Down	Unigene37630_All//gi|124359162|gb|ABN05685.1|//1.00E-15//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene37630_All//3.00E-08//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene37630_All//0.00E+00//gi|11202012|gb|BF271017.1|BF271017				nr +
Unigene37631_All	1213	4.23	1.50	3.95	4.85	4.71	2.94	1.43	0.38	1.58	-1.49E+00	1.27E-07	Down	-9.75E-02	7.24E-01		-4.03E-02	8.77E-01		-7.20E-01	2.79E-03		-1.91E+00	8.45E-05	Down	1.42E-01	7.34E-01		Unigene37631_All//gi|15219271|ref|NP_175737.1|//6.00E-97//TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 1); binding [Arabidopsis thaliana] >gi|75336154|sp|Q9MAH1.1|TTL1_ARATH RecName: Full=TPR repeat-containing thioredoxin TTL1; AltName: Full=Tetratricopeptide repeat thioredoxin-like 1 >gi|7769858|gb|AAF69536.1|AC008007_11 F12M16.20 [Arabidopsis thaliana] >gi|30102668|gb|AAP21252.1| At1g53300 [Arabidopsis thaliana]	Unigene37631_All//2.00E-77//AT1G53300| TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 1); binding	Unigene37631_All//0.00E+00//gi|78345626|gb|DT565900.1|DT565900				nr +
Unigene37634_All	595	8.44	1.79	2.60	6.53	4.86	13.13	11.87	4.99	5.83	-2.24E+00	1.94E-12	Down	-1.70E+00	1.93E-08	Down	-4.26E-01	1.72E-01		1.01E+00	1.16E-06	Up	-1.25E+00	1.17E-09	Down	-1.03E+00	1.60E-07	Down	Unigene37634_All//gi|20197493|gb|AB03357.2|//4.00E-23//expressed protein [Arabidopsis thaliana] >gi|88010967|gb|ABD38880.1| At2g15000 [Arabidopsis thaliana]	Unigene37634_All//5.00E-14//AT2G15000| unknown protein	Unigene37634_All//0.00E+00//TC163397				nr -
Unigene37635_All	734	4.06	1.66	1.60	2.99	1.78	5.29	9.10	3.87	3.75	-1.29E+00	5.17E-04	Down	-1.35E+00	5.59E-04	Down	-7.44E-01	7.45E-02		8.25E-01	7.81E-03		-1.23E+00	5.35E-09	Down	-1.28E+00	7.86E-10	Down	Unigene37635_All//gi|20197493|gb|AB03357.2|//2.00E-24//expressed protein [Arabidopsis thaliana] >gi|88010967|gb|ABD38880.1| At2g15000 [Arabidopsis thaliana]	Unigene37635_All//2.00E-15//AT2G15000| unknown protein	Unigene37635_All//0.00E+00//TC163397				nr -
Unigene37636_All	1745	1.29	0.23	0.70	10.28	5.68	5.23	3.08	2.56	1.14	-2.47E+00	1.32E-06	Down	-8.77E-01	4.95E-02		-8.55E-01	1.43E-12		-9.75E-01	6.51E-14		-2.64E-01	2.95E-01		-1.43E+00	2.14E-09	Down	Unigene37636_All//gi|115456723|ref|NP_001051962.1|//2.00E-81//Os03g0858600 [Oryza sativa Japonica Group] >gi|108712208|gb|ABG00003.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550433|dbj|BAF13876.1| Os03g0858600 [Oryza sativa Japonica Group]	Unigene37636_All//8.00E-117//AT5G51670| unknown protein	Unigene37636_All//0.00E+00//TC178814				nr -
Unigene37639_All	1201	50.58	37.97	43.81	72.05	70.88	91.83	64.42	32.78	29.06	-4.14E-01	7.12E-10		-2.07E-01	4.04E-03		-2.36E-02	7.72E-01		3.50E-01	1.28E-13		-9.75E-01	1.08E-65		-1.15E+00	4.17E-88	Down	Unigene37639_All//gi|297820218|ref|XP_002877992.1|/1.00E-126//alpha subunit of tryptophan synthase [Arabidopsis lyrata subsp. lyrata] >gi|297323830|gb|EFH54251.1| alpha subunit of tryptophan synthase [Arabidopsis lyrata subsp. lyrata]	Unigene37639_All//3.00E-126//AT3G54640| TSA1 (TRYPTOPHAN SYNTHASE ALPHA CHAIN); tryptophan synthase	Unigene37639_All//0.00E+00//TC134669		ko00260|Glycine, serine and threonine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr +
Unigene3764_All	1773	4.57	5.00	3.39	11.15	4.60	26.16	0.00	0.07	0.13	1.29E-01	5.57E-01		-4.31E-01	4.63E-02		-1.28E+00	1.78E-26	Down	1.23E+00	3.02E-50	Up	6.14E+00	2.40E-01		7.07E+00	4.39E-02		Unigene3764_All//gi|224137498|ref|XP_002327141.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222835456|gb|EEE73891.1| cytochrome P450 [Populus trichocarpa]	Unigene3764_All//0.00E+00//AT3G19270| CYP707A4; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	Unigene3764_All//2.00E-145//gi|3325852|gb|AI054738.1|AI054738		ko00906|Carotenoid biosynthesis		nr -
Unigene37640_All	1336	15.23	12.25	7.57	26.66	20.03	18.12	43.58	68.83	49.56	-3.15E-01	1.14E-02		-1.01E+00	7.77E-15	Down	-4.13E-01	5.64E-07		-5.57E-01	1.43E-10		6.59E-01	3.90E-40		1.86E-01	1.30E-03		Unigene37640_All//gi|14596045|gb|AK68750.1|//1.00E-105//Unknown protein [Arabidopsis thaliana]	Unigene37640_All//1.00E-106//AT1G14740| unknown protein	Unigene37640_All//0.00E+00//TC141799				nr -
Unigene37642_All	1264	8.24	8.42	7.08	16.39	19.26	14.97	14.55	6.02	6.21	3.14E-02	8.73E-01		-2.19E-01	2.69E-01		2.33E-01	4.06E-02		-1.31E-01	3.66E-01		-1.27E+00	1.51E-24	Down	-1.23E+00	5.79E-24	Down	Unigene37642_All//gi|184152895|ref|NP_567582.1|//5.00E-37//EMB3006 (embryo defective 3006) [Arabidopsis thaliana] >gi|28372912|gb|AAO39938.1| At4g19350 [Arabidopsis thaliana]	Unigene37642_All//2.00E-38//AT4G19350| EMB3006 (embryo defective 3006)	Unigene37642_All//0.00E+00//TC137466				nr +
Unigene37643_All	839	84.56	31.89	43.41	51.77	47.82	12.54	3.83	0.85	3.18	-1.41E+00	4.35E-88	Down	-9.62E-01	1.26E-46		-1.15E-01	2.08E-01		-2.05E+00	1.14E-99	Down	-2.18E+00	1.29E-09	Down	-2.68E-01	4.00E-01		Unigene37643_All//gi|256002927|gb|ACU32707.1|//2.00E-61//bHLH transcription factor PTF1 [Glycine max]	Unigene37643_All//2.00E-43//AT3G57800| basic helix-loop-helix (bHLH) family protein	Unigene37643_All//0.00E+00//gi|21092290|gb|BQ404603.1|BQ404603	bHLH	ko04712|Circadian rhythm - plant		nr -
Unigene37644_All	934	19.27	10.36	17.50	7.15	4.28	5.46	2.54	0.40	0.73	-8.95E-01	1.90E-11		-1.39E-01	3.73E-01		-7.41E-01	4.51E-04		-3.87E-01	1.03E-01		-2.65E+00	5.79E-09	Down	-1.81E+00	4.17E-06	Down	Unigene37644_All//gi|62086401|dbj|BAD91803.1|//2.00E-66//cyclo-DOPA 5-O-glucosyltransferase [Mirabilis jalapa]	Unigene37644_All//1.00E-46//AT5G12890| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene37644_All//0.00E+00//TC136287		ko00908|Zeatin biosynthesis		nr +
Unigene37645_All	622	1.51	2.04	1.88	1.60	4.32	1.82	1.02	3.02	1.92	4.28E-01	4.74E-01		3.15E-01	6.23E-01		1.43E+00	2.06E-04	Up	1.81E-01	7.84E-01		1.57E+00	4.37E-04	Up	9.14E-01	8.92E-02		Unigene37645_All//gi|115445113|ref|NP_001046336.1|//1.00E-16//Os02g0224800 [Oryza sativa Japonica Group] >gi|113535867|dbj|BAF08250.1| Os02g0224800 [Oryza sativa Japonica Group]	Unigene37645_All//1.00E-08//AT5G56750| Ndr family protein	Unigene37645_All//5.00E-20//TC174584				nr +
Unigene37648_All	1694	30.21	7.15	12.04	13.88	13.21	12.45	1.47	0.22	0.45	-2.08E+00	4.30E-110	Down	-1.33E+00	2.69E-56	Down	-7.10E-02	6.16E-01		-1.57E-01	2.24E-01		-2.73E+00	1.13E-09	Down	-1.72E+00	4.94E-06	Down	Unigene37648_All//gi|289186762|gb|ACH56523.2|//0.00E+00//flavonoid 3-glucosyltransferase [Gossypium hirsutum]	Unigene37648_All//9.00E-102//AT5G17050| UGT78D2 (UDP-GLUCOSYL TRANSFERASE 78D2); UDP-glycosyltransferase/ anthocyanidin 3-O-glucosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene37648_All//0.00E+00//TC166134		ko00944|Flavone and flavonol biosynthesis//ko00942|Anthocyanin biosynthesis		nr -

Unigene37650_All	1689	9.70	5.46	4.13	4.63	12.54	5.03	2.43	0.37	1.53	-8.29E-01	2.70E-09		-1.23E+00	2.16E-16	Down	1.44E+00	5.27E-32	Up	1.19E-01	6.44E-01		-2.71E+00	2.30E-15	Down	-6.63E-01	1.03E-02		Unigene37650_All//gi|15239346|ref|NP_201434.1|//1.00E-147//leucine-rich repeat family protein [Arabidopsis thaliana]	Unigene37650_All//6.00E-147//AT5G66330| leucine-rich repeat family protein	Unigene37650_All//0.00E+00//gi|78351499|gb|DT571773.1|DT571773		ko04626|Plant-pathogen interaction		nr -
Unigene37651_All	1248	14.38	7.71	9.94	13.85	11.98	10.82	8.30	3.75	4.02	-8.99E-01	1.74E-11		-5.33E-01	8.16E-05		-2.10E-01	1.39E-01		-3.56E-01	8.04E-03		-1.15E+00	4.01E-12	Down	-1.05E+00	6.55E-11	Down	Unigene37651_All//gi|115467706|ref|NP_001057452.1|//3.00E-37//0s06g0300700 [Oryza sativa Japonica Group] >gi|113595492|dbj|BAF19366.1|0s06g0300700 [Oryza sativa Japonica Group]	Unigene37651_All//1.00E-39//AT5G17070| unknown protein	Unigene37651_All//0.00E+00//TC142264				nr +
Unigene37655_All	1024	1.07	0.79	1.61	1.22	1.41	1.63	4.75	3.63	2.18	-4.39E-01	4.95E-01		5.87E-01	2.72E-01		2.16E-01	7.52E-01		4.24E-01	4.48E-01		-3.86E-01	1.29E-01		-1.12E+00	3.54E-06	Down	Unigene37655_All//gi|225454595|ref|XP_002267912.1|//6.00E-29//PREDICTED: similar to protein kinase family protein [Vitis vinifera]	Unigene37655_All//8.00E-10//AT5G35980| protein kinase family protein	Unigene37655_All//0.00E+00//DW503257				nr -
Unigene37663_All	770	53.07	79.56	74.07	21.09	30.05	51.15	6.75	24.05	32.44	5.84E-01	5.79E-18		4.81E-01	1.54E-11		5.11E-01	1.40E-06		1.28E+00	2.41E-45	Up	1.83E+00	1.68E-41	Up	2.26E+00	1.32E-74	Up	Unigene37663_All//gi|284433802|gb|ADB85107.1|//2.00E-42//translation initiation factor-like protein [Jatropha curcas]	Unigene37663_All//6.00E-38//AT5G54940| eukaryotic translation initiation factor SUI1, putative	Unigene37663_All//0.00E+00//TC149484				nr -
Unigene37665_All	2266	2.68	1.68	1.79	5.30	5.65	4.07	1.96	0.42	1.13	-6.75E-01	4.79E-03		-5.85E-01	2.02E-02		9.36E-02	6.18E-01		-3.82E-01	2.14E-02		-2.21E+00	3.17E-13	Down	-8.00E-01	1.25E-03		Unigene37665_All//gi|17064962|gb|AAL32635.1|//0.00E+00//Unknown protein [Arabidopsis thaliana]	Unigene37665_All//0.00E+00//AT5G13760| unknown protein	Unigene37665_All//0.00E+00//TC152070				nr -
Unigene37666_All	875	8.79	3.42	2.92	11.10	7.75	8.21	10.24	7.31	4.74	-1.36E+00	9.32E-10	Down	-1.59E+00	1.71E-11	Down	-5.18E-01	2.82E-03		-4.36E-01	1.89E-02		-4.87E-01	4.72E-03		-1.11E+00	1.70E-10	Down	Unigene37666_All//gi|297829774|ref|XP_002882769.1|//8.00E-45//cornichon family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328609|gb|EFH59028.1|cornichon family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37666_All//1.00E-39//AT3G12180| cornichon family protein	Unigene37666_All//0.00E+00//gi|109891311|gb|DW520274.1|DW520274				nr -
Unigene37667_All	311	17.50	13.03	8.39	8.81	9.30	8.42	16.45	14.65	9.10	-4.25E-01	1.02E-01		-1.06E+00	8.56E-05	Down	7.83E-02	8.53E-01		-6.48E-02	8.82E-01		-1.67E-01	5.44E-01		-8.55E-01	1.99E-04		Unigene37667_All//gi|108936784|emb|CAJ34818.1|//1.00E-21//methionine sulfoxide reductase [Plantago major]	Unigene37667_All//6.00E-22//AT4G21860| MSRB2 (methionine sulfoxide reductase B 2); peptide-methionine-(S)-S-oxide reductase	Unigene37667_All//8.00E-147//TC153811				nr -
Unigene3767_All	1068	28.81	18.69	17.10	60.68	48.24	18.56	7.72	2.43	2.76	-6.24E-01	1.61E-10		-7.52E-01	1.06E-13		-3.31E-01	2.82E-08		-1.71E+00	3.02E-116	Down	-1.67E+00	9.79E-17	Down	-1.48E+00	1.08E-14	Down	Unigene3767_All//gi|31506015|gb|AAP48989.1|//1.00E-53//expansin [Sambucus nigra]	Unigene3767_All//3.00E-53//AT2G39700| ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	Unigene3767_All//0.00E+00//ES823571				nr -
Unigene37670_All	627	4.76	12.93	5.18	18.27	24.71	11.02	14.84	20.00	10.42	1.44E+00	5.00E-11	Up	1.23E-01	7.22E-01		4.36E-01	1.32E-03		-7.30E-01	8.09E-06		4.31E-01	2.63E-03		-5.10E-01	1.80E-03		Unigene37670_All//gi|297613682|gb|AD148274.1|//1.00E-16//uridine cytidine kinase [Carica papaya]	Unigene37670_All//2.00E-16//AT1G55810| uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative	Unigene37670_All//0.00E+00//TC173927		ko00240|Pyrimidine metabolism		nr +
Unigene37671_All	1396	9.52	10.96	4.62	12.45	12.70	13.04	6.75	9.91	8.36	2.03E-01	1.86E-01		-1.04E+00	1.87E-10	Down	2.87E-02	8.60E-01		6.61E-02	6.91E-01		5.53E-01	3.81E-05		3.08E-01	3.76E-02		Unigene37671_All//gi|30680596|ref|NP_849613.1|//2.00E-99//armadillo/beta-catenin repeat family protein [Arabidopsis thaliana]	Unigene37671_All//1.00E-100//AT1G08315| armadillo/beta-catenin repeat family protein	Unigene37671_All//0.00E+00//TC166531				nr +
Unigene37673_All	923	7.37	10.38	4.79	2.91	2.35	1.86	49.75	176.74	119.77	4.94E-01	8.03E-03		-6.22E-01	8.04E-03		-3.10E-01	4.54E-01		-6.48E-01	9.71E-02		1.83E+00	0.00E+00	Up	1.27E+00	2.00E-145	Up	Unigene37673_All//gi|18414384|ref|NP_567458.1|//2.00E-11//VQ motif-containing protein [Arabidopsis thaliana]		Unigene37673_All//2.00E-54//gi|73863925|gb|DT466664.1|DT466664				nr +
Unigene37674_All	1292	6.28	5.57	5.81	2.74	2.75	1.43	0.39	1.04	1.36	-1.73E-01	4.26E-01		-1.11E-01	6.05E-01		4.10E-03	1.00E+00		-9.34E-01	4.03E-03		1.40E+00	9.01E-03		1.79E+00	1.28E-04	Up	Unigene37674_All//gi|16604537|gb|AAL24274.1|//1.00E-148//At2g46910/F14M4.26 [Arabidopsis thaliana]	Unigene37674_All//1.00E-136//AT2G46915| unknown protein	Unigene37674_All//0.00E+00//DR452510				nr +
Unigene37678_All	845	38.58	28.54	18.40	72.92	64.63	74.40	80.96	38.19	50.87	-4.35E-01	3.78E-06		-1.07E+00	1.16E-25	Down	-1.74E-01	9.13E-03		2.89E-02	7.20E-01		-1.08E+00	3.76E-69	Down	-6.70E-01	7.54E-32		Unigene37678_All//gi|68149762|gb|AY97868.1|//4.00E-45//cytoplasmic ribosomal protein S13 [Solanum lycopersicum]	Unigene37678_All//9.00E-46//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene37678_All//0.00E+00//gi|13352180|gb|BG442528.1|BG442528		ko03010|Ribosome		nr -
Unigene3768_All	805	11.31	19.95	12.04	38.55	45.86	27.88	8.19	41.12	34.54	8.19E-01	6.06E-09		9.02E-02	6.50E-01		2.50E-01	3.78E-03		-4.67E-01	6.24E-07		2.33E+00	4.71E-100	Up	2.08E+00	1.73E-74	Up	Unigene3768_All//gi|297824199|ref|XP_002879982.1|//1.00E-36//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325821|gb|EFH56241.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3768_All//2.00E-25//AT2G42360| zinc finger (C3HC4-type RING finger) family protein	Unigene3768_All//4.00E-09//TC159723		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene37681_All	627	2.17	8.89	5.44	20.10	36.69	33.85	19.29	13.33	17.66	2.03E+00	3.71E-12	Up	1.33E+00	2.34E-04	Up	8.68E-01	8.58E-16		7.52E-01	1.25E-10		-5.33E-01	2.35E-04		-1.27E-01	4.28E-01		Unigene37681_All//gi|18394637|ref|NP_564059.1|//3.00E-34//PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding [Arabidopsis thaliana] >gi|9795591|gb|AAF98409.1|ACO26238_1 Hypothetical protein [Arabidopsis thaliana] >gi|30017221|gb|AAP12844.1|At1g18650 [Arabidopsis thaliana]	Unigene37681_All//1.00E-35//AT1G18650| PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding	Unigene37681_All//0.00E+00//gi|13356848|gb|BG447196.1|BG447196				nr -
Unigene37682_All	611	12.67	6.14	4.62	84.14	59.06	34.22	20.14	2.39	3.00	-1.05E+00	9.77E-07	Down	-1.46E+00	2.98E-10	Down	-5.11E-01	2.57E-14		-1.30E+00	2.43E-61	Down	-3.07E+00	6.38E-51	Down	-2.75E+00	6.07E-47	Down	Unigene37682_All//gi|15233171|ref|NP_191723.1|//9.00E-18//AGP20 [Arabidopsis thaliana] >gi|75153616|sp|Q9SZT3.1|AGP20_ARATH RecName: Full=Arabinogalactan peptide 20; Short=AG-peptide 20; Flags: Precursor >gi|98960995|gb|ABF58981.1|At3g61640 [Arabidopsis thaliana]	Unigene37682_All//1.00E-12//AT3G61640| AGP20	Unigene37682_All//0.00E+00//gi|164271060|gb|ES809343.1|ES809343				nr +
Unigene37684_All	598	6.91	3.98	14.60	8.66	4.95	7.85	3.32	3.56	4.80	-7.95E-01	7.73E-03		1.08E+00	1.81E-07	Up	-8.07E-01	9.78E-04		-1.41E-01	6.36E-01		1.01E-01	8.07E-01		5.30E-01	1.01E-01		Unigene37684_All//gi|2425107|gb|AAB70837.1|//1.00E-21//glutathione reductase (NADPH) [Vitis vinifera]	Unigene37684_All//1.00E-21//AT3G54660| GR (GLUTATHIONE REDUCTASE); ATP binding / glutathione-disulfide reductase	Unigene37684_All//0.00E+00//TC144522		ko00480|Glutathione metabolism		nr -
Unigene37685_All	1160	27.47	17.82	23.87	34.05	27.01	28.46	31.53	10.20	15.49	-6.24E-01	7.12E-11		-2.03E-01	5.39E-02		-3.34E-01	2.38E-05		-2.59E-01	2.49E-03		-1.63E+00	3.98E-69	Down	-1.03E+00	3.67E-35	Down	Unigene37685_All//gi|18423981|ref|NP_568858.1|//1.00E-106//GS1; catalytic/ hydrolase [Arabidopsis thaliana] >gi|21536767|gb|AAM61099.1| GS1-like protein [Arabidopsis thaliana]	Unigene37685_All//2.00E-101//AT5G37440| GS1; catalytic/ hydrolase	Unigene37685_All//0.00E+00//TC132752		ko00740|Riboflavin metabolism		nr +
Unigene37687_All	942	10.05	10.06	8.42	16.92	14.44	8.01	4.85	2.93	1.61	8.00E-04	9.97E-01		-2.55E-01	2.23E-01		-2.29E-01	1.16E-01		-1.08E+00	1.36E-14	Down	-7.27E-01	3.82E-03		-1.59E+00	2.32E-09	Down	Unigene37687_All//gi|124359306|gb|ABN05799.1|//1.00E-102//EXS, C-terminal [Medicago truncatula]	Unigene37687_All//3.00E-102//AT5G35730| EXS family protein / ERD1/XPR1/SYG1 family protein	Unigene37687_All//0.00E+00//ES820385				nr +
Unigene3769_All	1216	1.68	2.13	0.92	8.36	6.34	3.86	3.93	2.61	2.03	3.41E-01	3.83E-01		-8.68E-01	6.77E-02		-3.98E-01	2.26E-02		-1.11E+00	5.58E-10	Down	-5.89E-01	1.69E-02		-9.52E-01	7.58E-05		Unigene3769_All//gi|15238143|ref|NP_199572.1|//2.00E-35//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68566286|sp|Q8VGJ6.1|ATL5M_ARATH RecName: Full=RING-H2 finger protein ATL5M; Flags: Precursor >gi|98960905|gb|ABF58936.1|At5g47610 [Arabidopsis thaliana]	Unigene3769_All//9.00E-37//AT5G47610| zinc finger (C3HC4-type RING finger) family protein	Unigene3769_All//0.00E+00//CA994184				nr -
Unigene37690_All	779	6.99	221.80	5.40	9.40	22.81	14.67	11.78	15.72	23.32	4.99E+00	0.00E+00	Up	-3.71E-01	1.78E-01		1.28E+00	1.31E-22	Up	6.42E-01	9.80E-05		4.17E-01	4.19E-03		9.86E-01	1.01E-16		Unigene37690_All//gi|54261723|gb|AAV31165.1|//1.00E-27//At3g03280 [Arabidopsis thaliana] >gi|57222180|gb|AAN38997.1|At3g03280 [Arabidopsis thaliana]	Unigene37690_All//3.00E-29//AT5G17350| unknown protein	Unigene37690_All//0.00E+00//gi|109825303|gb|DW224036.1|DW224036				nr +
Unigene37691_All	1409	0.45	1.58	0.87	4.99	4.20	9.14	54.67	63.90	48.63	1.83E+00	1.03E-04	Up	9.64E-01	1.38E-01		-2.46E-01	3.11E-01		8.74E-01	1.82E-08		2.25E-01	4.85E-06		-1.69E-01	1.55E-03		Unigene37691_All//gi|22328578|ref|NP_192945.2|//1.00E-105//DNA-binding family protein [Arabidopsis thaliana] >gi|17979485|gb|AAL50079.1|AT4g12080/F16J13_150 [Arabidopsis thaliana] >gi|23506149|gb|AAN31086.1|At4g12080/F16J13_150 [Arabidopsis thaliana] >gi|118420990|dbj|BAF37220.1| AT-hook motif nuclear localized protein 1 [Arabidopsis thaliana]	Unigene37691_All//7.00E-60//AT4G12080| DNA-binding family protein	Unigene37691_All//0.00E+00//TC147841				nr -
Unigene37692_All	394	0.40	2.70	0.54	1.90	1.22	1.03	5.26	4.77	4.95	2.76E+00	8.45E-04	Up	4.40E-01	7.75E-01		-6.32E-01	4.37E-01		-8.78E-01	3.08E-01		-1.40E-01	7.33E-01		-8.58E-02	8.26E-01		Unigene37692_All//gi|115452485|ref|NP_001049843.1|//2.00E-20//Os03g0298400 [Oryza sativa Japonica Group] >gi|17297987|dbj|BAB78491.1| 26S proteasome regulatory particle triple-A ATPase subunit2b [Oryza sativa Japonica Group] >gi|113548314|dbj|BAF11757.1|Os03g0298400 [Oryza sativa Japonica Group]	Unigene37692_All//4.00E-21//AT4G29040| RPT2a (regulatory particle AAA-ATPase 2a); ATPase	Unigene37692_All//5.00E-155//ES841963		ko03050|Proteasome		nr -
Unigene37694_All	223	4.69	0.23	1.91	12.06	11.89	5.06	2.09	0.00	0.36	-4.37E+00	3.91E-05	Down	-1.30E+00	7.46E-02		-2.08E-02	9.61E-01		-1.25E+00	1.20E-03		-1.10E+01	1.71E-03		-2.55E+00	2.35E-02		Unigene37694_All//gi|255558366|ref|XP_002520210.1|//1.00E-09//aldo-keto reductase, putative [Ricinus communis] >gi|223540702|gb|EEF42265.1| aldo-keto reductase, putative [Ricinus communis]		Unigene37694_All//4.00E-117//gi|78332585|gb|DT552859.1|DT552859				nr +
Unigene37695_All	1147	4.15	2.87	1.72	10.38	10.57	4.84	2.91	0.33	1.01	-5.32E-01	5.51E-02		-1.27E+00	1.77E-05	Down	2.59E-02	9.02E-01		-1.10E+00	2.27E-11	Down	-3.15E+00	1.34E-14	Down	-1.53E+00	9.89E-07	Down	Unigene37695_All//gi|40781598|gb|AAB38808.1|//1.00E-129//reductase 2 [Hydrangea macrophylla] >gi|40781601|gb|AAB89810.1|reductase 2 [Hydrangea macrophylla]	Unigene37695_All//3.00E-117//AT1G59950| aldo/keto reductase, putative	Unigene37695_All//0.00E+00//gi|78336494|gb|DT556768.1|DT556768		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr -
Unigene37696_All	1587	1.71	0.83	1.38	4.71	4.04	2.39	6.85	3.53	1.83	-1.05E+00	6.56E-03		-3.18E-01	4.28E-01		-2.22E-01	3.37E-01		-9.78E-01	3.34E-06		-9.56E-01	1.22E-09		-1.90E+00	8.43E-27	Down	Unigene37696_All//gi|108711353|gb|ABF99148.1|//3.00E-61//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene37696_All//8.00E-65//AT1G06780| GAUT6 (Galacturonosyltransferase 6); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups				nr +
Unigene37697_All	678	12.66	7.32	6.83	14.69	15.03	13.19	21.26	9.37	13.34	-7.89E-01	6.51E-05		-8.89E-01	1.60E-05		3.29E-02	8.82E-01		-1.56E-01	4.72E-01		-1.18E+00	2.32E-17	Down	-6.73E-01	1.79E-07		Unigene37697_All//gi|195604664|gb|ACG24162.1|//1.00E-56//small nuclear ribonucleoprotein Sm D1 [Zea mays]	Unigene37697_All//8.00E-46//AT4G02840| small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative	Unigene37697_All//0.00E+00//gi|109858464|gb|DW487443.1|DW487443		ko03040|Spliceosome		nr +

Unigene3770_All	1851	9.13	16.21	13.03	12.59	3.74	5.03	22.00	23.12	14.64	8.28E-01	2.71E-16		5.13E-01	7.18E-06		-1.75E+00	4.57E-50	Down	-1.33E+00	5.39E-29	Down	7.20E-02	4.11E-01		-5.88E-01	1.76E-15		Unigene3770_All//gi|197209780|dbj|BAG88829.1|//1.00E-141//cytochrome P450 8BD6 [Glycyrrhiza uralensis]	Unigene3770_All//1.00E-130//AT2G32440| KAO2 (ENT-KAURENOIC ACID HYDROXYLASE 2); ent-kaurenoate oxidase/ oxygen binding	Unigene3770_All//0.00E+00//CO099590		ko00904|Diterpenoid biosynthesis		nr -
Unigene37700_All	948	15.95	16.20	14.21	16.66	17.33	16.34	9.46	7.94	4.08	2.20E-02	8.98E-01		-1.67E-01	3.17E-01		5.68E-02	7.70E-01		-2.77E-02	8.79E-01		-2.53E-01	1.73E-01		-1.21E+00	6.42E-12	Down			Unigene37700_All//3.00E-81//gi|78344134|gb|DT564108.1|DT564108				
Unigene37704_All	1246	7.43	1.55	1.67	16.51	6.02	37.95	74.48	41.43	102.57	-2.27E+00	1.09E-22	Down	-2.16E+00	1.84E-20	Down	-1.45E+00	1.22E-33	Down	1.20E+00	2.46E-49	Up	-8.46E-01	3.74E-62		4.62E-01	2.89E-30		Unigene37704_All//gi|31074969|gb|AAP42136.1|//1.00E-108//erg-1 [Solanum tuberosum]	Unigene37704_All//8.00E-108//AT5G64260| EXL2 (EXORDIUM LIKE 2)	Unigene37704_All//0.00E+00//TC176216				nr +
Unigene37705_All	1189	34.72	30.00	35.96	18.35	12.97	8.36	2.35	2.46	0.77	-2.11E-01	1.42E-02		5.08E-02	6.35E-01		-5.00E-01	3.58E-06		-1.13E+00	2.20E-21	Down	6.83E-02	8.49E-01		-1.61E+00	4.09E-06	Down	Unigene37705_All//gi|297604810|ref|NP_001056147.2|//9.00E-43//Os05g0534100 [Oryza sativa Japonica Group] >gi|255676521|dbj|BAF18061.2|Os05g0534100 [Oryza sativa Japonica Group]	Unigene37705_All//1.00E-88//AT3G61770| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Acid phosphatase/vanadium-dependent haloperoxidase related (InterPro:IPR003823); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67600.1); Has 613 Blast hits to 613 proteins in 199 species: Archae - 0; Bacteria - 356; Metazoa - 0; Fungi - 0; Plants - 104; Viruses - 0; Other Eukaryotes - 153 (source: NCBI BLink).	Unigene37705_All//0.00E+00//TC161516				nr -
Unigene37706_All	1277	9.30	16.70	4.50	3.55	4.10	2.23	0.03	0.03	0.00	8.45E-01	3.35E-12		-1.05E+00	1.95E-09	Down	2.08E-01	5.06E-01		-6.72E-01	1.74E-02		-1.75E-02	1.00E+00		-5.05E+00	6.12E-01		Unigene37706_All//gi|50512303|gb|AAT77550.1|//3.00E-68//90C3 [Solanum pimpinellifolium]	Unigene37706_All//4.00E-45//AT2G25440| AtRLP20 (Receptor Like Protein 20); kinase/ protein binding					nr -
Unigene37709_All	1425	2.28	2.03	1.38	4.44	2.59	2.79	2.70	5.37	14.65	-1.68E-01	6.14E-01		-7.19E-01	4.60E-02		-7.80E-01	3.37E-04		-6.71E-01	3.73E-03		9.91E-01	2.15E-07		2.44E+00	3.00E-68	Up	Unigene37709_All//gi|15218427|ref|NP_177375.1|//5.00E-65//ATL3; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|68565343|sp|Q9XF63.1|ATL1P_ARATH RecName: Full=RING-H2 finger protein ATL1P; AltName: Full=RING-H2 finger protein ATL3 >gi|4928397|gb|AAD33581.1|AF132013_1 RING-H2 zinc finger protein ATL3 [Arabidopsis thaliana] >gi|12323672|gb|AAG51805.1|AC06775_4_21 RING-H2 zinc finger protein ATL3; 90350-91324 [Arabidopsis thaliana] >gi|12325277|gb|AAG52584.1|AC016529_15 RING-H2 zinc finger protein (ATL3); 86824-85850 [Arabidopsis thaliana] >gi|33589686|gb|AAQ22609.1|At1g72310 [Arabidopsis thaliana] >gi|110743698|dbj|BAE99686.1|RING-H2 zinc finger protein [Arabidopsis thaliana]	Unigene37709_All//6.00E-41//AT1G72310| ATL3; protein binding / zinc ion binding	Unigene37709_All//0.00E+00//TC179554				nr -
Unigene3771_All	828	16.30	61.93	52.03	13.30	28.40	43.15	2.09	3.18	2.79	1.93E+00	4.28E-99	Up	1.67E+00	4.82E-67	Up	1.10E+00	1.82E-23	Up	1.70E+00	1.62E-62	Up	6.03E-01	8.66E-02		4.15E-01	2.68E-01		Unigene3771_All//gi|297790891|ref|XP_002863330.1|//2.00E-36//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309165|gb|EFH39589.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3771_All//5.00E-37//AT5G47610| zinc finger (C3HC4-type RING finger) family protein	Unigene3771_All//0.00E+00//gi|31406632|gb|CD485667.1|CD485667		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene37712_All	794	5.27	13.78	8.85	10.85	12.36	10.64	20.23	23.79	19.17	1.39E+00	7.97E-14	Up	7.48E-01	1.12E-03		1.88E-01	3.74E-01		-2.91E-02	9.11E-01		2.34E-01	5.16E-02		-7.82E-02	6.01E-01		Unigene37712_All//gi|15236597|ref|NP_193499.1|//2.00E-28//CKB2; protein kinase CK2 regulator [Arabidopsis thaliana] >gi|729882|sp|P40229.1|CSK2C_ARATH RecName: Full=Casein kinase II subunit beta'; Short=CK II beta' >gi|467975|gb|AAA53234.1| casein kinase II beta subunit CKB2 [Arabidopsis thaliana] >gi|2245122|emb|CAB10544.1| casein kinase II beta chain CKB2 [Arabidopsis thaliana] >gi|7268516|emb|CAB78767.1| casein kinase II beta chain CKB2 [Arabidopsis thaliana] >gi|21554030|gb|AAM63111.1| casein kinase II beta chain CKB2 [Arabidopsis thaliana] >gi|28950839|gb|AAO63343.1|At4g17640 [Arabidopsis thaliana]	Unigene37712_All//1.00E-29//AT4G17640| CKB2; protein kinase CK2 regulator	Unigene37712_All//0.00E+00//gi|48821078|gb|CO122391.1|CO122391		ko04712|Circadian rhythm - plant		nr -
Unigene37717_All	982	5.97	4.49	4.34	15.02	13.11	8.19	17.61	10.30	7.18	-4.11E-01	9.96E-02		-4.60E-01	7.85E-02		-1.95E-01	2.21E-01		-8.75E-01	9.89E-10		-7.74E-01	1.28E-10		-1.29E+00	2.01E-24	Down	Unigene37717_All//gi|76262500|gb|AB441400.1|//2.00E-20//pherophorin-C2 protein precursor [Chlamydomonas reinhardtii]		Unigene37717_All//0.00E+00//gi|164310093|gb|ES846177.1|ES846177		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene37718_All	414	1.52	8.57	5.40	3.13	1.66	4.25	1.02	0.81	0.29	2.50E+00	4.89E-10	Up	1.83E+00	1.63E-04	Up	-9.11E-01	1.09E-01		4.44E-01	4.05E-01		-3.39E-01	7.30E-01		-1.82E+00	9.22E-02		Unigene37718_All//gi|255560113|ref|XP_002521074.1|//4.00E-35//hypothetical protein RCOM_1719350 [Ricinus communis] >gi|223539643|gb|EEF41225.1| hypothetical protein RCOM_1719350 [Ricinus communis]	Unigene37718_All//1.00E-20//AT3G07150| unknown protein	Unigene37718_All//0.00E+00//gi|109888716|gb|DW517685.1|DW517685				nr -
Unigene37719_All	952	2.25	2.93	5.03	3.24	2.86	2.09	1.38	0.97	0.71	3.78E-01	3.35E-01		1.16E+00	7.10E-05	Up	-1.83E-01	6.20E-01		-6.36E-01	7.59E-02		-5.11E-01	3.55E-01		-9.53E-01	5.85E-02		Unigene37719_All//gi|255560113|ref|XP_002521074.1|//3.00E-47//hypothetical protein RCOM_1719350 [Ricinus communis] >gi|223539643|gb|EEF41225.1| hypothetical protein RCOM_1719350 [Ricinus communis]	Unigene37719_All//1.00E-29//AT3G07150| unknown protein	Unigene37719_All//2.00E-168//gi|109888716|gb|DW517685.1|DW517685				nr +
Unigene3772_All	1068	4.07	7.31	4.59	4.76	2.97	4.14	3.44	4.70	6.90	8.46E-01	5.45E-05		1.74E-01	5.79E-01		-6.82E-01	6.45E-03		-1.99E-01	5.11E-01		4.47E-01	6.79E-02		1.00E+00	1.72E-07	Up	Unigene3772_All//gi|15233768|ref|NP_192657.1|//9.00E-36//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75311758|sp|Q9M0R0.1|BH081_ARATH RecName: Full=Transcription factor bHLH81; AltName: Full=Transcription factor EN 72; AltName: Full=bHLH transcription factor bHLH081; AltName: Full=Basic helix-loop-helix protein 81; Short=bHLH 81; Short=AtbHLH81 >gi|34146832|gb|AAQ62424.1|At4g09180 [Arabidopsis thaliana]	Unigene3772_All//9.00E-28//AT4G09180| basic helix-loop-helix (bHLH) family protein	Unigene3772_All//0.00E+00//gi|48790427|gb|CO091741.1|CO091741	bHLH			nr -
Unigene37720_All	798	45.50	8.64	33.70	24.47	17.95	8.55	0.74	0.26	0.55	-2.40E+00	2.40E-93	Down	-4.33E-01	2.19E-06		-4.47E-01	1.17E-04		-1.52E+00	8.27E-30	Down	-1.50E+00	9.13E-02		-4.34E-01	6.08E-01		Unigene37720_All//gi|239056176|emb|CAQ58610.1|//7.00E-26//Unknown gene [Vitis vinifera]	Unigene37720_All//2.00E-10//AT5G01015| unknown protein	Unigene37720_All//0.00E+00//ES845321				nr -
Unigene37723_All	682	3.68	10.70	4.61	15.56	28.78	64.57	24.74	188.69	54.68	1.54E+00	6.40E-11	Up	3.23E-01	3.93E-01		8.87E-01	4.97E-14		2.05E+00	2.23E-99	Up	2.93E+00	0.00E+00	Up	1.14E+00	2.47E-42	Up	Unigene37723_All//gi|224116328|ref|XP_002331955.1|//9.00E-42//glutaredoxin C9 [Populus trichocarpa] >gi|222874732|gb|EEF11863.1| glutaredoxin C9 [Populus trichocarpa]	Unigene37723_All//7.00E-34//AT1G28480| GRX480; electron carrier/ protein disulfide oxidoreductase	Unigene37723_All//0.00E+00//gi|109835188|gb|DW233752.1|DW233752				nr +
Unigene37724_All	811	9.29	7.68	7.75	21.07	19.79	19.99	17.78	7.52	6.53	-2.74E-01	2.19E-01		-2.62E-01	2.63E-01		-9.06E-02	5.87E-01		-7.56E-02	6.45E-01		-1.24E+00	1.16E-18	Down	-1.44E+00	4.32E-24	Down	Unigene37724_All//gi|9797761|gb|AAF98579.1|AC013427_22//4.00E-33//Contains similarity to PIR7A protein from Oryza sativa gb|Z34271 and contains an alpha/beta hydrolase fold PF|00561 [Arabidopsis thaliana]	Unigene37724_All//8.00E-22//AT1G26355| SPIL1 (SPIRAL1-LIKE1)	Unigene37724_All//0.00E+00//TC144788				nr +
Unigene37725_All	1461	1.36	0.73	0.22	3.07	3.11	2.50	1.45	0.69	1.04	-9.02E-01	4.85E-02		-2.64E+00	6.10E-06	Down	1.99E-02	9.58E-01		-2.93E-01	3.57E-01		-1.08E+00	6.86E-03		-4.82E-01	2.12E-01		Unigene37725_All//gi|297851726|ref|XP_002893744.1|//1.00E-142//glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] >gi|297339586|gb|EFH70003.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	Unigene37725_All//3.00E-137//AT1G32860| glycosyl hydrolase family 17 protein	Unigene37725_All//0.00E+00//ES831927		ko00500|Starch and sucrose metabolism		nr -
Unigene37728_All	1023	221.30	87.97	124.72	1714.33	902.69	880.27	146.10	49.76	28.00	-1.33E+00	3.69E-257	Down	-8.27E-01	7.83E-115		-9.25E-01	0.00E+00		-9.62E-01	0.00E+00		-1.55E+00	4.48E-262	Down	-2.38E+00	0.00E+00	Down	Unigene37728_All//gi|66271031|gb|AY43793.1|//1.00E-145//E6-4 [Gossypium hirsutum]	Unigene37728_All//1.00E-22//AT2G33850| unknown protein	Unigene37728_All//0.00E+00//TC129868				nr -
Unigene37729_All	743	9.65	158.96	4.52	14.41	10.52	32.64	21.34	41.51	44.77	4.04E+00	0.00E+00	Up	-1.10E+00	2.26E-06	Down	-4.54E-01	6.18E-03		1.18E+00	7.75E-25	Up	9.60E-01	5.32E-26		1.07E+00	5.08E-34	Up	Unigene37729_All//gi|6899646|gb|AAF31023.1|AC012189_5//6.00E-26//EST gb|AB015130 comes from this gene [Arabidopsis thaliana]	Unigene37729_All//1.00E-28//AT2G01300| unknown protein	Unigene37729_All//0.00E+00//gi|109854773|gb|DW483752.1|DW483752				nr -
Unigene37731_All	676	5.80	1.95	3.86	12.53	17.42	15.03	15.07	1.98	4.36	-1.57E+00	1.89E-06	Down	-5.89E-01	7.02E-02		4.76E-01	2.75E-03		2.63E-01	1.83E-01		-2.93E+00	2.43E-40	Down	-1.79E+00	3.06E-23	Down	Unigene37731_All//gi|4056461|gb|AAC98034.1|//5.00E-70//F5G8.34 [Arabidopsis thaliana] >gi|66792642|gb|AAY56423.1|At1g23790 [Arabidopsis thaliana]	Unigene37731_All//6.00E-70//AT1G23790| unknown protein	Unigene37731_All//0.00E+00//gi|109850564|gb|DW479543.1|DW479543				nr +
Unigene37732_All	991	32.31	14.16	18.38	13.62	11.61	7.25	3.07	2.45	2.69	-1.19E+00	4.45E-31	Down	-8.14E-01	3.16E-16		-2.31E-01	1.56E-01		-9.11E-01	1.52E-09		-3.29E-01	3.44E-01		-1.90E-01	5.86E-01		Unigene37732_All//gi|87241277|gb|ABD33135.1|//1.00E-27//80C09_19, related [Medicago truncatula]	Unigene37732_All//2.00E-18//AT2G29180| unknown protein	Unigene37732_All//0.00E+00//gi|84157631|gb|DN826678.1|DN826678				nr -

Unigene37734_All	1083	0.14	0.51	0.30	0.14	0.00	0.08	7.69	17.60	10.23	1.83E+00	9.02E-02		1.03E+00	4.71E-01		-7.11E+00	1.65E-01		-7.27E-01	7.15E-01		1.19E+00	5.31E-23	Up	4.11E-01	6.00E-03		Unigene37734_All//gi|124361158|gb|ABN09130.1|//9.00E-34//DC1; C1-like [Medicago truncatula]	Unigene37734_All//2.00E-36//AT2G16050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: DC1 (InterPro:IPR004146); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G20990.1); Has 719 Blast hits to 448 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 717; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene37734_All//0.00E+00//DV849172				nr -
Unigene37736_All	767	15.21	16.12	10.76	22.15	18.95	15.19	19.51	10.84	8.10	8.36E-02	6.19E-01		-4.99E-01	3.97E-03		-2.25E-01	1.09E-01		-5.44E-01	3.37E-05		-8.48E-01	9.73E-11		-1.27E+00	1.28E-20	Down	Unigene37736_All//gi|29839555|sp|Q8LSQ8.1|Y5486_ARATH//3.00E-63//RecName: Full=Uncharacterized protein At5g64816; Flags: Precursor >gi|98961067|gb|ABF59017.1| At5g64816 [Arabidopsis thaliana] >gi|222424148|dbj|BAH20033.1| AT5G64816 [Arabidopsis thaliana]	Unigene37736_All//gi|AT5G64816| unknown protein	Unigene37736_All//0.00E+00//TC157958				nr -
Unigene37737_All	955	6.46	5.15	4.41	15.44	12.91	12.20	2.21	0.70	1.17	-3.29E-01	1.83E-01		-5.54E-01	2.65E-02		-2.58E-01	8.45E-02		-3.40E-01	2.25E-02		-1.66E+00	7.98E-05	Down	-9.22E-01	1.54E-02			Unigene37737_All//5.00E-06//AT1G73430| sec34-like family protein	Unigene37737_All//6.00E-33//CO496941				
Unigene37739_All	681	65.54	83.78	92.19	86.75	84.50	86.35	79.72	88.69	37.15	3.54E-01	3.49E-07		4.92E-01	3.66E-13		-3.81E-02	6.63E-01		-6.80E-03	9.52E-01		1.54E-01	1.64E-02		-1.10E+00	4.39E-58	Down	Unigene37739_All//gi|225443562|ref|XP_002277951.1|//8.00E-43//PREDICTED: similar to Os07g0631100 [Vitis vinifera]	Unigene37739_All//8.00E-00//AT5G46030| unknown protein	Unigene37739_All//0.00E+00//gi|164349253|gb|ES812725.1|ES812725				nr -
Unigene37742_All	1376	1.83	1.47	1.12	12.53	8.81	6.17	1.08	4.40	0.67	-3.09E-01	4.43E-01		-7.02E-01	9.42E-02		-5.08E-01	3.97E-05		-1.02E+00	2.03E-14	Down	2.03E+00	4.53E-16	Up	-6.92E-01	1.40E-01		Unigene37742_All//gi|115473283|ref|NP_001060240.1|//1.00E-30//Os07g0608200 [Oryza sativa Japonica Group] >gi|113611776|dbj|BAF22154.1| Os07g0608200 [Oryza sativa Japonica Group] >gi|148921404|dbj|BAF64441.1| HAP2 subunit of HAP complex [Oryza sativa Japonica Group]	Unigene37742_All//2.00E-23//AT1G17590| NF-YA8 (NUCLEAR FACTOR Y, SUBUNIT A8); transcription factor	Unigene37742_All//0.00E+00//TC170304	CCAAT			nr +
Unigene37744_All	1291	1.09	2.47	0.99	2.97	5.39	4.20	7.11	1.97	1.42	1.18E+00	9.53E-04	Up	-1.45E-01	7.90E-01		8.59E-01	4.88E-05		4.99E-01	5.80E-02		-1.85E+00	3.20E-21	Down	-2.32E+00	3.49E-29	Down	Unigene37744_All//gi|15239503|ref|NP_197955.1|//4.00E-84//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|71660770|sp|P69781.1|GAT12_ARATH RecName: Full=GATA transcription factor 12	Unigene37744_All//2.00E-66//AT5G25830| zinc finger (GATA type) family protein	Unigene37744_All//0.00E+00//DN781360	C2C2-GATA			nr +
Unigene37745_All	767	43.32	29.07	30.96	51.44	45.75	50.76	59.70	43.87	27.37	-5.76E-01	6.99E-10		-4.84E-01	4.39E-07		-1.69E-01	5.61E-02		-1.92E-02	8.62E-01		-4.45E-01	1.97E-10		-1.13E+00	8.52E-51	Down	Unigene37745_All//gi|28932772|gb|AA060427.1|//2.00E-64//FPh1 [Gossypium hirsutum]	Unigene37745_All//9.00E-57//AT5G20060| phospholipase/carboxylesterase family protein	Unigene37745_All//0.00E+00//TC135864		ko00564|Glycerophospholipid metabolism		nr -
Unigene37747_All	829	1.45	2.69	3.92	21.27	21.81	18.20	4.18	3.23	2.02	8.90E-01	3.87E-02		1.43E+00	1.29E-04	Up	3.59E-02	8.25E-01		-2.25E-01	1.16E-01		-3.74E-01	2.35E-01		-1.05E+00	2.88E-04	Down	Unigene37747_All//gi|28372878|gb|AA039921.1|//1.00E-19//At4g37445 [Arabidopsis thaliana]	Unigene37747_All//1.00E-33//AT4G37445| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: calcium-binding EF hand family protein (TAIR:AT1G648S0.1); Has 34 Blast hits to 34 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 34; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).				nr +
Unigene37749_All	784	11.68	10.66	10.66	13.66	13.18	9.74	4.42	2.13	2.74	-1.31E-01	5.36E-01		-1.31E-01	5.57E-01		-5.20E-02	8.23E-01		-4.89E-01	4.71E-03		-1.05E+00	4.21E-04	Down	-6.89E-01	1.56E-02		Unigene37749_All//gi|121631|sp|P27484.1|GRP2_NICSY//2.00E-55//RecName: Full=Glycine-rich protein 2 >gi|19743|emb|CAA42622.1| nsGRP-2 [Nicotiana sylvestris]	Unigene37749_All//9.00E-29//AT2G21060| ATGRP2B (GLYCINE-RICH PROTEIN 2B); DNA binding / nucleic acid binding / zinc ion binding	Unigene37749_All//0.00E+00//TC172375	CSD			nr +
Unigene37751_All	976	4.56	3.22	3.49	1.07	1.87	3.56	0.52	2.78	2.94	-5.01E-01	8.18E-02		-3.84E-01	2.20E-01		8.03E-01	1.01E-01		1.73E+00	9.85E-07	Up	2.42E+00	3.13E-09	Up	2.50E+00	2.77E-10	Up	Unigene37751_All//gi|32815941|gb|AAP88355.1|//6.00E-42//At5g67620 [Arabidopsis thaliana]	Unigene37751_All//1.00E-32//AT5G67620| unknown protein	Unigene37751_All//0.00E+00//DW507104				nr +
Unigene37754_All	757	35.46	141.97	41.29	26.59	49.04	60.02	52.95	139.41	37.94	2.00E+00	4.69E-218	Up	2.20E-01	3.71E-02		8.83E-01	5.19E-26		1.17E+00	7.84E-46	Up	1.40E+00	9.43E-158	Up	-4.81E-01	7.27E-11		Unigene37754_All//gi|166203244|gb|ABY84662.1|//2.00E-16//transcription factor [Glycine max]	Unigene37754_All//1.00E-10//AT3G56400| WRKY70; transcription factor/ transcription repressor	Unigene37754_All//0.00E+00//gi|164330647|gb|ES839518.1|ES839518	WRKY			nr +
Unigene37757_All	852	0.12	0.06	0.38	0.41	0.16	0.05	1.49	0.49	0.33	-1.05E+00	6.84E-01		1.61E+00	3.05E-01		-1.34E+00	3.08E-01		-2.95E+00	8.30E-02		-1.60E+00	4.42E-03		-2.19E+00	1.97E-04	Down	Unigene37757_All//gi|42567385|ref|NP_195162.2|//4.00E-87//protease-related [Arabidopsis thaliana] >gi|83310184|gb|AAT41770.1| At4g34360 [Arabidopsis thaliana] >gi|50198934|gb|AAT70470.1| At4g34360 [Arabidopsis thaliana]	Unigene37757_All//1.00E-103//AT4G34360| protease-related	Unigene37757_All//0.00E+00//TC144232				nr -
Unigene37762_All	750	28.60	169.98	54.67	51.94	52.85	81.96	57.73	102.76	73.78	2.57E+00	0.00E+00	Up	9.35E-01	5.96E-26		2.50E-02	8.20E-01		6.58E-01	1.34E-23		8.32E-01	3.14E-50		3.54E-01	1.13E-08		Unigene37762_All//gi|290886187|gb|ADD69807.1|//6.00E-35//copper transport protein ATOX1 [Hevea brasiliensis]	Unigene37762_All//4.00E-30//AT1G66240| ATX1 (ARABIDOPSIS HOMOLOG OF ANTI-OXIDANT 1); metal ion binding	Unigene37762_All//0.00E+00//gi|13248756|gb|BF278325.2|BF278325				nr +
Unigene37763_All	666	5.42	12.63	6.88	3.14	1.86	2.71	26.22	14.12	4.61	1.22E+00	5.25E-09	Up	3.43E-01	2.58E-01		-7.55E-01	7.83E-02		-2.12E-01	6.63E-01		-8.93E-01	1.86E-13		-2.51E+00	5.64E-60	Down	Unigene37763_All//gi|8920587|gb|AAF81309.1|AC061957_5//6.00E-38//Contains a weak similarity to a farnesylated protein GMFP5 mRNA from Glycine max gb|U64916. ESTs gb|AI993148, gb|T44360 come from this gene [Arabidopsis thaliana]	Unigene37763_All//2.00E-20//AT1G01490| heavy-metal-associated domain-containing protein	Unigene37763_All//3.00E-111//EX165152				nr +
Unigene37764_All	1230	5.44	2.14	2.81	3.08	3.70	3.56	5.02	4.28	5.47	-1.35E+00	1.92E-08	Down	-9.52E-01	6.31E-05		2.64E-01	4.14E-01		2.11E-01	5.32E-01		-2.29E-01	3.35E-01		1.25E-01	5.93E-01		Unigene37764_All//gi|297843300|ref|XP_002889531.1|//1.00E-76//tyrosine specific protein phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335373|gb|EFH65790.1| tyrosine specific protein phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37764_All//7.00E-77//AT1G05000| tyrosine specific protein phosphatase family protein	Unigene37764_All//0.00E+00//gi|109867527|gb|DW496503.1|DW496503				nr +
Unigene37766_All	995	44.01	2.75	18.62	2.25	1.94	1.54	4.67	2.02	0.96	-4.00E+00	2.92E-185	Down	-1.24E+00	1.74E-43	Down	-2.17E-01	6.15E-01		-5.46E-01	2.22E-01		-1.21E+00	2.33E-06	Down	-2.28E+00	7.16E-15	Down	Unigene37766_All//gi|34015078|gb|AAQ56281.1|//9.00E-39//ethylene receptor [Litchi chinensis]	Unigene37766_All//1.00E-08//AT4G14860| atofp11 (Arabidopsis thaliana ovate family protein 11)	Unigene37766_All//1.00E-37//ES794718				nr -
Unigene37768_All	856	5.32	55.40	13.81	14.08	8.17	14.25	37.49	98.43	154.98	3.38E+00	6.03E-173	Up	1.38E+00	3.47E-14	Up	-7.86E-01	1.54E-07		1.66E-02	9.46E-01		1.39E+00	1.58E-125	Up	2.05E+00	0.00E+00	Up	Unigene37768_All//gi|297825155|ref|XP_002880460.1|//6.00E-44//homeobox-leucine zipper protein 9 [Arabidopsis lyrata subsp. lyrata] >gi|297326299|gb|EFH56719.1| homeobox-leucine zipper protein 9 [Arabidopsis lyrata subsp. lyrata]	Unigene37768_All//3.00E-42//AT4G37790| HAT22; transcription factor	Unigene37768_All//0.00E+00//gi|41578550|gb|CK640555.1|CK640555	HB			nr -
Unigene37775_All	660	13.48	10.82	16.86	46.49	31.46	34.90	19.09	14.50	6.64	-3.16E-01	1.16E-01		3.23E-01	7.86E-02		-5.63E-01	2.27E-10		-4.14E-01	1.27E-05		-3.97E-01	5.74E-03		-1.52E+00	7.57E-23	Down	Unigene37775_All//gi|225451780|ref|XP_002277757.1|//6.00E-09//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene37775_All//3.00E-05//AT3G29780| RALFL27 (ralf-like 27); signal transducer	Unigene37775_All//0.00E+00//gi|164245376|gb|ES851900.1|ES851900				nr +
Unigene37777_All	661	23.59	20.39	18.05	51.47	59.39	53.23	99.91	37.75	58.70	-2.10E-01	1.62E-01		-3.86E-01	9.45E-03		2.06E-01	1.66E-02		4.83E-02	6.83E-01		-1.40E+00	6.10E-100	Down	-7.67E-01	9.41E-39		Unigene37777_All//gi|47078494|gb|AAT09895.1|//2.00E-17//cellulose synthase [Populus tremula x Populus tremuloides]	Unigene37777_All//2.00E-17//AT4G39350| CESA2 (CELLULOSE SYNTHASE A2); cellulose synthase/ transferase, transferring glycosyl groups	Unigene37777_All//0.00E+00//gi|109886538|gb|DW515508.1|DW515508				nr -
Unigene37778_All	1276	6.11	16.88	7.39	18.23	15.25	13.52	16.80	17.85	22.67	1.47E+00	9.86E-29	Up	2.74E-01	1.84E-01		-2.58E-01	2.22E-02		-4.31E-01	9.93E-05		8.76E-02	4.83E-01		4.32E-01	8.61E-07		Unigene37778_All//gi|225465921|ref|XP_002270142.1|//6.00E-40//PREDICTED: similar to glutaredoxin family protein [Vitis vinifera]	Unigene37778_All//2.00E-39//AT5G13810| glutaredoxin family protein	Unigene37778_All//0.00E+00//TC130717				nr +
Unigene37780_All	2736	16.45	74.69	37.54	25.54	35.88	36.83	41.37	44.61	33.68	2.18E+00	0.00E+00	Up	1.19E+00	2.06E-95	Up	4.90E-01	1.59E-24		5.28E-01	5.28E-26		1.09E-01	1.48E-02		-2.97E-01	2.56E-12				Unigene37780_All//0.00E+00//gi|21100583|gb|BQ412896.1|BQ412896				
Unigene37781_All	1225	34.94	12.37	39.69	13.46	16.98	6.56	0.07	0.00	0.07	-1.50E+00	1.32E-58	Down	1.84E-01	2.70E-02		3.35E-01	4.32E-03		-1.04E+00	3.86E-14	Down	-6.11E+00	4.03E-01		-8.62E-02	9.72E-01		Unigene37781_All//gi|15240938|ref|NP_188667.1|//2.00E-24//rhomboid family protein [Arabidopsis thaliana] >gi|145334671|ref|NP_001078681.1| rhomboid family protein [Arabidopsis thaliana] >gi|46518449|gb|AAS99706.1| At5g38510 [Arabidopsis thaliana]	Unigene37781_All//1.00E-25//AT5G38510| rhomboid family protein	Unigene37781_All//0.00E+00//CO080584				nr +
Unigene37782_All	1154	9.61	2.72	9.55	2.59	3.58	1.33	0.00	0.00	0.00	-1.82E+00	1.66E-20	Down	-9.00E-03	9.85E-01		4.67E-01	1.30E-01		-9.61E-01	7.48E-03		null	null		null	null		Unigene37782_All//gi|115445857|ref|NP_001046708.1|//7.00E-13//Os02g0326700 [Oryza sativa Japonica Group] >gi|46390267|dbj|BAD15696.1| rhomboid family protein-like [Oryza sativa Japonica Group] >gi|46390870|dbj|BAD16387.1| rhomboid family protein-like [Oryza sativa Japonica Group] >gi|113536239|dbj|BAF08622.1| Os02g0326700 [Oryza sativa Japonica Group]	Unigene37782_All//3.00E-14//AT5G38510| rhomboid family protein	Unigene37782_All//0.00E+00//CO080584				nr +
Unigene37784_All	729	25.98	21.27	12.42	55.96	52.81	65.92	63.57	28.49	32.63	-2.89E-01	2.67E-02		-1.07E+00	4.36E-15	Down	-8.37E-02	4.10E-01		2.36E-01	2.27E-03		-1.16E+00	2.97E-52	Down	-9.62E-01	5.71E-40		Unigene37784_All//gi|51067769|gb|AAD39835.1|AF057024_1//2.00E-10//Ran-binding protein siRanBP [Arabidopsis thaliana]		Unigene37784_All//0.00E+00//gi|78343436|gb|DT563710.1|DT563710				nr -
Unigene37785_All	1388	2.34	0.99	4.03	0.83	0.72	1.95	2.56	4.22	4.08	-1.25E+00	4.28E-04	Down	7.86E-01	2.70E-03		-1.98E-01	7.77E-01		1.24E+00	1.44E-03		7.20E-01	9.64E-04		6.72E-01	1.92E-03		Unigene37785_All//gi|122214588|sp|Q2EA54.1|U5970_ARATH//1.00E-29//RecName: Full=UPF0497 membrane protein At4g11655	Unigene37785_All//4.00E-24//AT4G11655| transmembrane protein, putative	Unigene37785_All//8.00E-24//TC166625				nr +

Unigene37786_All	815	11.94	3.48	6.86	28.97	14.07	26.10	11.10	8.62	5.23	-1.78E+00	1.57E-17	Down	-8.00E-01	2.87E-05		-1.04E+00	8.71E-23	Down	-1.51E-01	2.39E-01		-3.66E-01	3.73E-02		-1.09E+00	3.33E-10	Down			Unigene37786_All//9.00E-35//gi|78343885|gb|DT564159.1|DT564159				
Unigene37787_All	1052	11.09	8.53	6.33	31.87	25.86	28.29	13.38	7.07	5.76	-3.80E-01	2.45E-02		-8.10E-01	2.76E-06		-3.01E-01	6.23E-04		-1.72E-01	8.98E-02		-9.20E-01	1.52E-11		-1.22E+00	2.71E-18	Down			Unigene37787_All//2.00E-156//gi|13352215|gb|BG442563.1|BG442563				
Unigene37788_All	1271	1.73	1.59	0.75	4.43	4.71	2.27	2.10	1.58	0.85	-1.17E-01	7.78E-01		-1.20E+00	9.38E-03		9.01E-02	7.83E-01		-9.62E-01	9.93E-05		-4.09E-01	2.56E-01		-1.31E+00	1.48E-04	Down	Unigene37788_All//gi|15240531|ref|NP_200365.1|//1.00E-165//TRN1 (TORNADO 1) [Arabidopsis thaliana]	Unigene37788_All//1.00E-161//AT5G55540| TRN1 (TORNADO 1)				nr +
Unigene3779_All	2132	2.41	2.42	1.20	8.15	5.90	6.93	10.07	12.80	20.37	1.14E-02	9.87E-01		-1.00E+00	3.06E-04	Down	-4.68E-01	1.55E-04		-2.35E-01	1.00E-01		3.46E-01	2.09E-04		1.02E+00	1.17E-10	Up	Unigene3779_All//gi|115477887|ref|NP_001062539.1|//1.00E-171//Os08g0566000 [Oryza sativa Japonica Group] >gi|113624508|dbj|BAF24453.1|Os08g0566000 [Oryza sativa Japonica Group]	Unigene3779_All//0.00E+00//AT5G32470| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Haem oxygenase-like, multi-helical (InterPro:IPR016084), TENA/THI-4 protein/Coenzyme PQQ biosynthesis protein C (InterPro:IPR004305); Has 1039 Blast hits to 1039 proteins in 384 species: Archae - 43; Bacteria - 698; Metazoa - 2; Fungi - 110; Plants - 26; Viruses - 0; Other Eukaryotes - 160 (source: NCBI BLink).	Unigene3779_All//0.00E+00//ES830699		ko00730|Thiamine metabolism		nr +
Unigene37792_All	637	4.93	1.99	3.43	5.94	6.87	7.87	6.90	6.30	6.38	-1.31E+00	3.06E-04	Down	-5.24E-01	1.56E-01		2.08E-01	5.58E-01		4.05E-01	1.53E-01		-1.32E-01	6.32E-01		-1.14E-01	6.67E-01		Unigene37792_All//gi|18415262|ref|NP_567580.1|//2.00E-43//integral membrane family protein [Arabidopsis thaliana] >gi|16974593|gb|AAL31201.1|AT4g19180/T18B16_150 [Arabidopsis thaliana] >gi|23506177|gb|AAN31100.1|At4g19180/T18B16_150 [Arabidopsis thaliana]	Unigene37792_All//6.00E-29//AT4G19185| integral membrane family protein	Unigene37792_All//0.00E+00//TC163046			nr -
Unigene37793_All	596	1.76	1.36	2.23	4.93	4.16	3.03	4.68	2.81	1.07	-3.68E-01	5.90E-01		3.47E-01	5.78E-01		-2.45E-01	5.56E-01		-7.02E-01	5.60E-02		-7.39E-01	2.78E-02		-2.13E+00	1.49E-08	Down	Unigene37793_All//gi|18415262|ref|NP_567580.1|//1.00E-55//integral membrane family protein [Arabidopsis thaliana] >gi|16974593|gb|AAL31201.1|AT4g19180/T18B16_150 [Arabidopsis thaliana] >gi|23506177|gb|AAN31100.1|At4g19180/T18B16_150 [Arabidopsis thaliana]	Unigene37793_All//4.00E-41//AT4G19185| integral membrane family protein	Unigene37793_All//0.00E+00//gi|78344306|gb|DT564580.1|DT564580			nr +
Unigene37795_All	1452	2.74	1.26	0.55	3.43	4.32	3.58	2.27	0.75	0.69	-1.12E+00	3.10E-04	Down	-2.32E+00	7.42E-10	Down	3.31E-01	1.85E-01		6.02E-02	8.48E-01		-1.60E+00	8.77E-07	Down	-1.73E+00	9.62E-08	Down	Unigene37795_All//gi|297601699|ref|NP_001051288.2|//7.00E-29//Os03g0750900 (Oryza sativa Japonica Group) >gi|255674903|dbj|BAF13202.2|Os03g0750900 (Oryza sativa Japonica Group)	Unigene37795_All//6.00E-61//AT4G17240| unknown protein	Unigene37795_All//0.00E+00//gi|78331126|gb|DT551400.1|DT551400			nr +
Unigene37797_All	843	7.39	54.40	18.95	101.64	93.26	120.11	7.12	7.24	5.62	2.88E+00	3.09E-143	Up	1.36E+00	1.31E-18	Up	-1.24E-01	3.35E-02		2.41E-01	1.61E-06		2.34E-02	9.42E-01		-3.41E-01	1.13E-01		Unigene37797_All//gi|15223925|ref|NP_177261.1|//7.00E-53//heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related [Arabidopsis thaliana] >gi|28372824|gb|AAO39894.1|Att gi710550 [Arabidopsis thaliana]	Unigene37797_All//3.00E-54//AT1G71050| heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	Unigene37797_All//0.00E+00//TC172464			nr -
Unigene37800_All	710	9.51	7.64	10.13	18.17	17.75	16.48	37.81	22.31	16.89	-3.16E-01	1.79E-01		9.10E-02	7.02E-01		-3.38E-02	8.50E-01		-1.41E-01	4.54E-01		-7.61E-01	1.33E-15		-1.16E+00	9.47E-32	Down	Unigene37800_All//gi|282848240|gb|ADB02901.1|//1.00E-31//protein transport protein SEC61 subunit gamma [Jatropha curcas]	Unigene37800_All//5.00E-22//AT5G50160| protein transport protein SEC61 gamma subunit, putative	Unigene37800_All//0.00E+00//TC170473		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export	nr -
Unigene37806_All	1622	11.13	23.96	14.02	1.84	1.76	1.31	0.08	0.15	0.22	1.11E+00	2.26E-33	Up	3.33E-01	5.98E-03		-6.45E-02	8.59E-01		-4.94E-01	1.95E-01		9.83E-01	5.17E-01		1.50E+00	2.03E-01		Unigene37806_All//gi|10178872|emb|CAC08442.1|//1.00E-148//(1-4)-beta-mannan endohydrolase [Coffea arabica]	Unigene37806_All//1.00E-134//AT5G66460| (1-4)-beta-mannan endohydrolase, putative	Unigene37806_All//0.00E+00//TC164936			nr -
Unigene37807_All	1428	1.47	0.35	0.86	5.02	2.41	1.01	7.25	1.76	1.59	-2.05E+00	4.33E-05	Down	-7.73E-01	9.77E-02		-1.06E+00	1.90E-07	Down	-2.31E+00	1.52E-19	Down	-2.05E+00	3.15E-27	Down	-2.19E+00	1.41E-30	Down	Unigene37807_All//gi|38345392|emb|CAD41244.2|//6.00E-79//OSJNBa0067K08.21 [Oryza sativa (japonica cultivar-group)]	Unigene37807_All//6.00E-89//AT5G57770| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Pleckstrin-like, plant (InterPro:IPR013666), Protein of unknown function DUF828, plant (InterPro:IPR008546); Has 104 Blast hits to 104 proteins in 9 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 102; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene37807_All//6.00E-34//CA993859			nr -
Unigene37808_All	376	2.23	0.54	0.57	0.93	0.92	2.88	4.39	0.89	3.18	-2.05E+00	1.68E-02		-1.97E+00	2.71E-02		-1.82E-02	9.58E-01		1.64E+00	2.06E-02		-2.30E+00	1.36E-05	Down	-4.64E-01	3.05E-01		Unigene37808_All//gi|15224950|ref|NP_182002.1|//2.00E-46//CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase [Arabidopsis thaliana] >gi|75278850|sp|Q80513.1|CCU41_ARATH RecName: Full=Cyclin-U4-1; Short=CycU4;1; AltName: Full=Cyclin-P4.1; Short=CycP4;1 >gi|62867623|gb|AAY17415.1|At2g44740 [Arabidopsis thaliana] >gi|66841350|gb|AAY57312.1|At2g44740 [Arabidopsis thaliana]	Unigene37808_All//1.00E-47//AT2G44740| CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	Unigene37808_All//1.00E-87//gi|13349771|gb|BG440121.1|BG440121			nr +
Unigene37809_All	878	9.48	1.50	3.09	6.07	4.12	3.60	8.14	1.43	5.85	-2.66E+00	1.70E-24	Down	-1.62E+00	1.16E-12	Down	-5.60E-01	2.39E-02		-7.54E-01	3.11E-03		-2.51E+00	3.40E-24	Down	-4.76E-01	1.24E-02		Unigene37809_All//gi|15224950|ref|NP_182002.1|//4.00E-78//CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase [Arabidopsis thaliana] >gi|75278850|sp|Q80513.1|CCU41_ARATH RecName: Full=Cyclin-U4-1; Short=CycU4;1; AltName: Full=Cyclin-P4.1; Short=CycP4;1 >gi|62867623|gb|AAY17415.1|At2g44740 [Arabidopsis thaliana] >gi|66841350|gb|AAY57312.1|At2g44740 [Arabidopsis thaliana]	Unigene37809_All//2.00E-79//AT2G44740| CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	Unigene37809_All//1.00E-144//gi|13349771|gb|BG440121.1|BG440121			nr +
Unigene3781_All	1155	17.12	18.69	26.14	8.67	9.63	13.26	10.62	3.08	4.04	1.26E-01	3.49E-01		6.10E-01	1.58E-09		1.52E-01	4.48E-01		6.13E-01	1.12E-05		-1.79E+00	6.89E-27	Down	-1.40E+00	1.28E-19	Down	Unigene3781_All//gi|285309967|emb|CBE71057.1|//1.00E-52//aconitate hydratase 3 [Citrus clementina]	Unigene3781_All//2.00E-51//AT2G05710| aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative	Unigene3781_All//0.00E+00//gi|13246348|gb|BE054514.2|BE054514		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene37810_All	884	6.39	4.70	5.90	10.26	10.67	8.23	5.64	8.04	11.72	-4.44E-01	7.89E-02		-1.15E-01	6.63E-01		5.76E-02	8.29E-01		-3.18E-01	1.18E-01		5.10E-01	9.63E-03		1.05E+00	5.79E-11	Up	Unigene37810_All//gi|18401970|ref|NP_566616.1|//7.00E-34//MKS1 (MAP kinase substrate 1); protein binding [Arabidopsis thaliana] >gi|110279050|sp|Q8LGD5.2|MKS1_ARATH RecName: Full=Protein MKS1; AltName: Full=Protein MAP kinase 4 substrate 1 >gi|88196717|gb|ABD43001.1|At3g18690 [Arabidopsis thaliana]	Unigene37810_All//8.00E-34//AT3G18690| MKS1 (MAP kinase substrate 1); protein binding	Unigene37810_All//1.00E-21//TC144019			nr +
Unigene37812_All	746	10.03	9.31	4.07	8.41	8.26	8.72	1.76	2.13	1.71	-1.08E-01	6.17E-01		-1.30E+00	1.77E-08	Down	-2.61E-02	9.20E-01		5.12E-02	8.58E-01		2.77E-01	6.01E-01		-4.00E-02	9.54E-01		Unigene37812_All//gi|240255425|ref|NP_189188.4|//5.00E-61//calcium ion binding [Arabidopsis thaliana] >gi|48310609|gb|AAT41852.1|At3g25600 [Arabidopsis thaliana]	Unigene37812_All//9.00E-52//AT3G25600| calcium ion binding	Unigene37812_All//0.00E+00//gi|109871424|gb|DW500400.1|DW500400		ko04626|Plant-pathogen interaction		nr -
Unigene37813_All	619	6.59	4.42	3.10	8.93	7.73	7.88	36.00	24.31	20.47	-5.77E-01	5.63E-02		-1.09E+00	6.24E-04	Down	-2.08E-01	4.60E-01		-1.81E-01	5.43E-01		-5.66E-01	4.26E-08		-8.15E-01	4.54E-15		Unigene37813_All//gi|154269260|gb|ABS72190.1|//2.00E-20//chaperonin [Corchorus olitorius]	Unigene37813_All//4.00E-15//AT5G20890| chaperonin, putative	Unigene37813_All//0.00E+00//gi|164261262|gb|ES811004.1|ES811004			nr +
Unigene37815_All	1260	3.78	1.69	4.06	6.76	5.79	5.84	2.35	1.43	1.99	-1.16E+00	3.97E-05	Down	1.03E-01	7.13E-01		-2.23E-01	3.11E-01		-2.11E-01	3.54E-01		-7.20E-01	2.65E-02		-2.38E-01	4.78E-01		Unigene37815_All//gi|30682540|ref|NP_680156.2|//3.00E-62//regulator of chromosome condensation (RCC1) family protein / LVB-resistance protein-related [Arabidopsis thaliana]	Unigene37815_All//2.00E-63//AT5G08710| regulator of chromosome condensation (RCC1) family protein / LVB-resistance protein-related	Unigene37815_All//3.00E-143//EV498777		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene37817_All	1009	13.33	0.05	0.00	2.47	1.30	0.72	91.73	26.10	73.68	-8.05E+00	3.36E-76	Down	-1.37E+01	4.16E-75	Down	-9.29E-01	1.44E-02		-1.79E+00	2.71E-05	Down	-1.81E+00	2.50E-202	Down	-3.16E-01	1.96E-11		Unigene37817_All//gi|15221483|ref|NP_176439.1|//3.00E-64//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|5454192|gb|AAD43607.1|AC005698_6 T3P18_6 [Arabidopsis thaliana]	Unigene37817_All//2.00E-33//AT1G62500| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene37817_All//0.00E+00//TC171610		ko03018|RNA degradation		nr +
Unigene37819_All	1272	3.25	1.99	3.22	1.10	1.76	1.74	4.09	1.18	0.72	-7.06E-01	1.80E-02		-1.16E-02	9.94E-01		6.82E-01	1.16E-01		6.66E-01	1.34E-01		-1.79E+00	7.36E-12	Down	-2.50E+00	2.28E-18	Down			Unigene37819_All//1.00E-07//CO112306				
Unigene3782_All	1240	36.96	19.70	27.66	22.82	26.35	23.49	39.11	22.08	6.10	-9.08E-01	1.27E-28		-4.19E-01	1.98E-07		2.08E-01	3.10E-02		4.20E-02	7.26E-01		-8.25E-01	1.71E-31		-2.68E+00	4.41E-178	Down	Unigene3782_All//gi|77548630|gb|AB491427.1|//2.00E-63//Sulfotransferase domain containing protein [Oryza sativa (japonica cultivar-group)]	Unigene3782_All//3.00E-64//AT2G14920| STA4 (SULFOTRANSFERASE 4A); brassinosteroid sulfotransferase/sulfotransferase	Unigene3782_All//2.00E-107//TC153081		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism		nr -

Unigene37821_All	1573	41.71	406.58	81.31	59.98	98.38	156.56	148.32	349.80	224.85	3.29E+00	0.00E+00	Up	9.63E-01	4.22E-84		7.14E-01	5.77E-75		1.38E+00	0.00E+00	Up	1.24E+00	0.00E+00	Up	6.00E-01	8.29E-132		Unigene37821_All//gi|225426282|ref|XP_002266388.1|//5.00E-70//PREDICTED: similar to B2 protein [Vitis vinifera]	Unigene37821_All//5.00E-47//AT3G27090| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G42050.1); Has 642 Blast hits to 564 proteins in 35 species: Archae - 0; Bacteria - 2; Metazoa - 12; Fungi - 0; Plants - 155; Viruses - 0; Other Eukaryotes - 473 (source: NCBI BLink).	Unigene37821_All//0.00E+00//TC137691				nr +
Unigene37823_All	2435	12.83	12.09	11.66	23.51	17.90	19.07	21.27	11.35	10.39	-8.55E-02	4.34E-01		-1.38E-01	2.20E-01		-3.93E-01	5.86E-10		-3.02E-01	8.90E-06		-9.07E-01	2.74E-39		-1.03E+00	4.48E-50	Down	Unigene37823_All//gi|44917431|gb|AAS49040.1|//0.00E+00//At1g31780 [Arabidopsis thaliana]	Unigene37823_All//0.00E+00//AT1G31780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Conserved oligomeric complex COG6 (InterPro:IPR010490); Has 281 Blast hits to 279 proteins in 131 species: Archae - 0; Bacteria - 2; Metazoa - 132; Fungi - 106; Plants - 21; Viruses - 0; Other Eukaryotes - 20 (source: NCBI BLink).	Unigene37823_All//0.00E+00//TC130948				nr +
Unigene37826_All	1003	1.77	4.34	5.63	11.27	14.45	13.01	13.19	3.75	7.15	1.29E+00	1.90E-05	Up	1.67E+00	3.50E-09	Up	3.59E-01	1.35E-02		2.07E-01	2.34E-01		-1.81E+00	1.45E-29	Down	-8.84E-01	1.42E-10		Unigene37826_All//gi|1526417|dbj|BAA08475.1|//5.00E-99//ribonuclease [Pyrus pyrifolia]	Unigene37826_All//8.00E-89//AT1G26820| RNS3 (RIBONUCLEASE 3); RNA binding / endoribonuclease/ ribonuclease T2	Unigene37826_All//0.00E+00//TC132559				nr -
Unigene37828_All	1106	17.65	15.39	16.90	18.69	20.14	18.99	30.74	13.76	13.90	-1.97E-01	1.37E-01		-6.23E-02	6.57E-01		1.08E-01	4.46E-01		2.27E-02	8.90E-01		-1.16E+00	1.15E-38	Down	-1.14E+00	5.62E-39	Down	Unigene37828_All//gi|297804254|ref|XP_002870011.1|//1.00E-68//cyclic phosphodiesterase [Arabidopsis lyrata subsp. lyrata] >gi|297315847|gb|EFH16270.1| cyclic phosphodiesterase [Arabidopsis lyrata subsp. lyrata]	Unigene37828_All//3.00E-59//AT4G18930| cyclic phosphodiesterase	Unigene37828_All//0.00E+00//gi|78324086|gb|DT544360.1|DT544360				nr +
Unigene37829_All	1585	5.15	11.51	7.66	6.38	8.97	10.86	8.00	14.45	9.45	1.16E+00	2.86E-17	Up	5.73E-01	6.58E-04		4.92E-01	4.94E-04		7.67E-01	5.18E-09		8.53E-01	3.96E-16		2.40E-01	6.77E-02		Unigene37829_All//gi|110931850|gb|ABH02924.1|//1.00E-37//MYB transcription factor MYB131 [Glycine max]	Unigene37829_All//4.00E-11//AT1G18330| EPR1 (EARLY-PHYTOCHROME-RESPONSIVE1); DNA binding / transcription factor	Unigene37829_All//0.00E+00//TC140800	MYB-related	ko04712|Circadian rhythm - plant		nr -
Unigene3783_All	1447	4.30	9.59	6.81	9.33	16.42	12.55	3.33	3.87	1.24	1.16E+00	2.87E-13	Up	6.62E-01	4.65E-04		8.16E-01	1.03E-14		4.28E-01	8.86E-04		2.17E-01	3.99E-01		-1.43E+00	1.72E-08	Down	Unigene3783_All//gi|15241087|ref|NP_196808.1|//5.00E-41//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565316|sp|Q9LZV8.1|ATL5A_ARATH RecName: Full=RING-H2 finger protein ATL5A >gi|38454090|gb|AAR20739.1| At5g01880 [Arabidopsis thaliana] >gi|386040016|gb|AAR24751.1| At5g01880 [Arabidopsis thaliana]	Unigene3783_All//5.00E-34//AT5G01880| zinc finger (C3HC4-type RING finger) family protein	Unigene3783_All//0.00E+00//TC164977				nr +
Unigene37830_All	1380	1.29	5.54	1.70	2.56	2.82	2.78	2.36	4.57	47.29	2.10E+00	3.92E-17	Up	3.97E-01	3.82E-01		1.38E-01	7.20E-01		1.18E-01	7.26E-01		9.55E-01	6.45E-06		4.33E+00	0.00E+00	Up	Unigene37830_All//gi|90399172|emb|CAH68354.1|//6.00E-20//H00723C07.4 [Oryza sativa (indica cultivar-group)]		Unigene37830_All//0.00E+00//gi|78332051|gb|DT552325.1|DT552325				nr +
Unigene37831_All	1091	1.77	1.76	1.76	5.34	5.02	12.71	9.07	11.61	86.10	-7.80E-03	9.81E-01		-1.41E-02	9.99E-01		-9.02E-02	7.72E-01		1.25E+00	9.10E-16	Up	3.56E-01	1.37E-02		3.25E+00	0.00E+00	Up	Unigene37831_All//gi|300507127|gb|ADK23939.1|//1.00E-150//3FAD [Gossypium hirsutum]	Unigene37831_All//6.00E-87//AT3G11170| FAD7 (FATTY ACID DESATURASE 7); omega-3 fatty acid desaturase	Unigene37831_All//0.00E+00//TC168802		ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene37832_All	1785	0.64	0.94	0.36	1.98	1.76	4.10	17.27	21.10	90.50	5.39E-01	2.94E-01		-8.49E-01	2.06E-01		-1.75E-01	6.16E-01		1.05E+00	1.17E-06	Up	2.89E-01	2.39E-04		2.39E+00	0.00E+00	Up	Unigene37832_All//gi|30683515|ref|NP_180312.2|//1.00E-134//binding [Arabidopsis thaliana]	Unigene37832_All//9.00E-114//AT2G27430| binding	Unigene37832_All//0.00E+00//ES810069				nr -
Unigene37833_All	1336	6.62	2.20	1.75	9.47	8.87	12.47	21.61	4.57	10.20	-1.59E+00	9.48E-14	Down	-1.92E+00	7.44E-17	Down	-9.51E-02	6.01E-01		3.97E-01	3.53E-03		-2.24E+00	9.72E-84	Down	-1.08E+00	1.62E-30	Down			Unigene37833_All//0.00E+00//gi|48805741|gb|CO107055.1|CO107055				
Unigene37834_All	1062	188.49	77.82	111.26	270.27	250.64	312.78	224.38	98.66	85.57	-1.28E+00	3.85E-213	Down	-7.61E-01	6.96E-88		-1.09E-01	1.54E-04		2.11E-01	1.57E-15		-1.19E+00	5.05E-276	Down	-1.39E+00	0.00E+00	Down	Unigene37834_All//gi|17367847|sp|Q9XF97.1|RL4_PRUAR//1.00E-158//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32206.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene37834_All//3.00E-145//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)	Unigene37834_All//0.00E+00//TC135151		ko03010|Ribosome		nr +
Unigene37836_All	845	1.55	1.14	0.69	5.60	2.08	1.98	4.35	3.22	0.71	-4.42E-01	4.41E-01		-1.16E+00	6.45E-02		-1.43E+00	6.80E-08	Down	-1.50E+00	1.50E-07	Down	-4.37E-01	1.39E-01		-2.62E+00	7.14E-14	Down	Unigene37836_All//gi|2688828|gb|AAB88878.1|//4.00E-50//ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]	Unigene37836_All//2.00E-46//AT5G20400| oxidoreductase, 2OG-Fe(II) oxygenase family protein			ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr +
Unigene37839_All	1697	0.86	1.22	2.42	11.68	12.74	10.17	3.46	2.59	1.74	5.04E-01	2.63E-01		1.48E+00	6.60E-06	Up	1.25E-01	3.68E-01		-2.01E-01	1.38E-01		-4.21E-01	5.95E-02		-9.95E-01	3.91E-06		Unigene37839_All//gi|31711834|gb|AAP68273.1|//1.00E-80//At3g54290 [Arabidopsis thaliana]	Unigene37839_All//5.00E-82//AT3G54290| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Hasemerythrin/HHE cation-binding motif (InterPro:IPR012312); Has 35 Blast hits to 35 proteins in 7 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene37839_All//1.00E-66//DN801525				nr -
Unigene37840_All	1807	1.30	0.56	0.09	1.90	1.77	1.37	7.16	2.91	2.43	-1.22E+00	4.07E-03		-3.88E+00	1.31E-09	Down	-1.02E-01	8.10E-01		-4.69E-01	1.81E-01		-1.30E+00	5.61E-18	Down	-1.56E+00	2.84E-24	Down	Unigene37840_All//gi|33412004|emb|CAE22479.1|//1.00E-129//3g18730 [Arabidopsis thaliana]	Unigene37840_All//1.00E-109//AT3G18730| TSK (TONSOKU); protein binding	Unigene37840_All//4.00E-122//BM358708				nr -
Unigene37841_All	647	16.98	176.13	16.54	31.41	40.45	52.42	19.60	81.20	34.48	3.37E+00	0.00E+00	Up	-3.78E-02	8.44E-01		3.65E-01	3.04E-04		7.39E-01	3.88E-16		2.05E+00	3.02E-135	Up	8.15E-01	5.31E-15				Unigene37841_All//7.00E-146//TC152879				
Unigene37842_All	475	31.72	545.20	27.91	57.57	69.74	111.62	74.59	283.86	162.21	4.10E+00	0.00E+00	Up	-1.85E-01	2.55E-01		2.77E-01	2.34E-03		9.55E-01	2.78E-38		1.93E+00	0.00E+00	Up	1.12E+00	9.91E-84	Up	Unigene37842_All//gi|4263700|gb|AAD15386.1|//1.00E-17//expressed protein [Arabidopsis thaliana]	Unigene37842_All//1.00E-05//AT3G22240| unknown protein	Unigene37842_All//0.00E+00//gi|109825209|gb|DW223943.1|DW223943				nr +
Unigene37843_All	1323	0.16	2.41	1.21	4.10	5.23	5.63	5.21	6.38	7.05	3.93E+00	1.50E-13	Up	2.93E+00	2.09E-05	Up	3.50E-01	1.33E-01		4.57E-01	3.67E-02		2.93E-01	1.22E-01		4.36E-01	8.05E-03		Unigene37843_All//gi|224087429|ref|XP_002308163.1|//1.00E-129//GRAS family transcription factor [Populus trichocarpa] >gi|222854139|gb|EEE91686.1| GRAS family transcription factor [Populus trichocarpa]	Unigene37843_All//8.00E-93//AT2G37650| scarecrow-like transcription factor 9 (SCL9)	Unigene37843_All//4.00E-13//TC175537	GRAS			nr +
Unigene37844_All	671	3.90	3.70	6.19	5.05	5.80	6.53	3.91	2.68	1.37	-7.54E-02	8.43E-01		6.67E-01	3.27E-02		2.00E-01	5.86E-01		3.71E-01	2.31E-01		-5.45E-01	1.27E-01		-1.52E+00	2.13E-05	Down			Unigene37844_All//8.00E-07//TC156792				
Unigene37849_All	1067	13.44	6.98	6.84	23.67	19.94	23.24	10.34	72.78	61.61	-9.45E-01	4.40E-10		-9.75E-01	4.34E-10		-2.47E-01	2.22E-02		-2.66E-02	8.47E-01		2.82E+00	1.70E-290	Up	2.57E+00	4.52E-227	Up	Unigene37849_All//gi|4510354|gb|AAD21443.1|//8.00E-52//expressed protein [Arabidopsis thaliana] >gi|15450733|gb|AAK96638.1| At2g36220/F2H17.17 [Arabidopsis thaliana] >gi|18491123|gb|AAL69530.1| At2g36220/F2H17.17 [Arabidopsis thaliana]	Unigene37849_All//2.00E-46//AT2G36220| unknown protein	Unigene37849_All//0.00E+00//TC139542				nr -
Unigene3785_All	1469	2.71	1.72	2.50	3.66	6.05	3.66	1.47	3.61	0.54	-6.50E-01	3.35E-02		-1.14E-01	7.21E-01		7.24E-01	7.72E-05		-1.50E-03	9.92E-01		1.30E+00	7.51E-08	Up	-1.44E+00	2.65E-04	Down	Unigene3785_All//gi|292653525|gb|ADE34280.1|//4.00E-94//aquaporin PIP1;11 [Gossypium hirsutum]	Unigene3785_All//5.00E-83//AT1G01620| PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1C); water channel	Unigene3785_All//2.00E-33//EX166998				nr +
Unigene37852_All	1090	2.35	3.21	1.03	2.65	2.24	2.69	5.78	12.12	9.87	4.48E-01	1.84E-01		-1.20E+00	4.45E-03		-2.41E-01	5.44E-01		2.29E-02	9.48E-01		1.07E+00	1.16E-13	Up	7.72E-01	4.31E-07		Unigene37852_All//gi|18396691|ref|NP_566214.1|//4.00E-73//ATAPRL5 (APR-like 5) [Arabidopsis thaliana]	Unigene37852_All//1.00E-70//AT3G03860| ATAPRL5 (APR-like 5)	Unigene37852_All//3.00E-155//AW187478				nr -
Unigene37853_All	1366	2.45	5.71	3.00	2.48	4.21	3.64	10.55	26.83	12.92	1.22E+00	2.05E-08	Up	2.92E-01	3.86E-01		7.64E-01	1.29E-03		5.53E-01	4.36E-02		1.35E+00	2.81E-52	Up	2.92E-01	1.30E-02		Unigene37853_All//gi|18396691|ref|NP_566214.1|//6.00E-83//ATAPRL5 (APR-like 5) [Arabidopsis thaliana]	Unigene37853_All//2.00E-80//AT3G03860| ATAPRL5 (APR-like 5)	Unigene37853_All//4.00E-158//AW187478				nr +
Unigene37854_All	1311	1.80	3.40	1.18	6.42	7.12	6.03	39.02	364.56	67.40	9.21E-01	1.41E-03		-6.09E-01	1.61E-01		1.49E-01	5.21E-01		-9.11E-02	6.73E-01		3.22E+00	0.00E+00	Up	7.88E-01	1.06E-53		Unigene37854_All//gi|283136110|gb|ADB11374.1|//2.00E-69//tau class glutathione transferase GSTU50 [Populus trichocarpa]	Unigene37854_All//2.00E-42//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	Unigene37854_All//0.00E+00//TC171132		ko00480|Glutathione metabolism		nr +
Unigene37855_All	1756	9.83	14.80	14.46	1.08	1.55	0.57	4.82	3.05	0.95	5.90E-01	3.22E-08		5.57E-01	5.32E-07		5.23E-01	1.87E-01		-9.30E-01	5.00E-02		-6.61E-01	1.88E-04		-2.34E+00	3.82E-27	Down	Unigene37855_All//gi|226506030|ref|NP_001147552.1|//1.00E-107//transposon protein Mutator sub-class [Zea mays] >gi|195612146|gb|ACG27903.1| transposon protein Mutator sub-class [Zea mays]	Unigene37855_All//1.00E-83//AT5G10250| DOT3 (DEFECTIVELY ORGANIZED TRIBUTARIES 3); protein binding / signal transducer	Unigene37855_All//0.00E+00//DW505831				nr +
Unigene37856_All	1128	8.12	4.49	2.83	3.27	1.86	1.76	7.80	1.56	7.77	-8.54E-01	8.25E-06		-1.52E+00	9.57E-13	Down	-8.11E-01	6.96E-03		-8.91E-01	4.89E-03		-2.32E+00	4.04E-27	Down	-4.90E-03	9.73E-01		Unigene37856_All//gi|15224950|ref|NP_182002.1|//1.00E-65//CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase [Arabidopsis thaliana] >gi|75278850|sp|Q80513.1|CCU41_ARATH RecName: Full=Cyclin-U4-1; Short=CycU4;1; AltName: Full=Cyclin-P4.1; Short=CycP4;1 >gi|62867623|gb|AAY17415.1| At2g44740 [Arabidopsis thaliana] >gi|66841350|gb|AAY57312.1| At2g44740 [Arabidopsis thaliana]	Unigene37856_All//5.00E-66//AT2G44740| CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	Unigene37856_All//0.00E+00//gi|109870185|gb|DW499161.1|DW499161				nr -
Unigene37858_All	1155	1.54	1.18	0.78	7.03	0.54	3.87	10.32	4.45	10.24	-3.79E-01	4.35E-01		-9.75E-01	5.87E-02		-3.71E+00	9.06E-42	Down	-8.61E-01	1.59E-05		-1.21E+00	4.50E-15	Down	-1.11E-02	9.65E-01		Unigene37858_All//gi|289466357|gb|ADC93864.1|//1.00E-110//NAC transcription factor [Vitis pseudoreticulata]	Unigene37858_All//1.00E-88//AT2G17040| anac036 (Arabidopsis NAC domain containing protein 36); transcription factor	Unigene37858_All//0.00E+00//gi|73861829|gb|DT464568.1|DT464568	NAC			nr +

Unigene37861_All	1278	7.37	17.56	5.75	6.12	5.85	4.88	5.16	12.10	18.05	1.25E+00	1.06E-23	Up	-3.58E-01	7.65E-02		-6.57E-02	8.14E-01		-3.28E-01	1.36E-01		1.23E+00	1.16E-19	Up	1.81E+00	1.34E-51	Up	Unigene37861_All//gi|115476412|ref|NP_001061802.1|//1.00E-177//Os08g0414300 [Oryza sativa Japonica Group] >gi|113623771|dbj|BAF23716.1|Os08g0414300 [Oryza sativa Japonica Group]	Unigene37861_All//2.00E-16//AT4G38060| unknown protein	Unigene37861_All//0.00E+00//TC179570				nr -
Unigene37862_All	1207	20.59	67.34	36.57	7.55	16.35	17.51	5.22	10.84	20.43	1.71E+00	3.53E-133	Up	8.29E-01	7.36E-23		1.11E+00	2.84E-20	Up	1.21E+00	1.10E-22	Up	1.05E+00	2.82E-13	Up	1.97E+00	8.64E-62	Up	Unigene37862_All//gi|79510333|ref|NP_568230.2|//1.00E-121//MSL2 (MscS-LIKE 2); ion channel [Arabidopsis thaliana]	Unigene37862_All//2.00E-110//AT5G10490| MSL2 (MscS-LIKE 2); ion channel	Unigene37862_All//0.00E+00//TC148551				nr +
Unigene37863_All	1714	1.31	40.71	0.75	4.48	27.52	10.38	3.28	10.27	17.43	4.95E+00	0.00E+00	Up	-8.16E-01	6.86E-02		2.62E+00	3.46E-155	Up	1.21E+00	3.38E-19	Up	1.65E+00	4.42E-34	Up	2.41E+00	5.56E-96	Up	Unigene37863_All//gi|87241270|gb|AB033128.1|//1.00E-70//Zinc finger, RING-type; Thioredoxin-related [Medicago truncatula]	Unigene37863_All//4.00E-53//AT3G46620| zinc finger (C3HC4-type RING finger) family protein	Unigene37863_All//0.00E+00//TC142363				nr -
Unigene37866_All	883	4.38	7.00	7.12	11.00	8.93	9.82	10.77	8.19	4.42	6.75E-01	4.47E-03		6.99E-01	4.29E-03		-3.01E-01	1.10E-01		-1.64E-01	4.53E-01		-3.96E-01	1.94E-02		-1.28E+00	1.10E-13	Down	Unigene37866_All//gi|7259352|dbj|BAA92781.1|//1.00E-79//nonclathrin coat protein zeta1-COP [Solanum lycopersicum]	Unigene37866_All//2.00E-61//AT1G60970| clathrin adaptor complex small chain family protein	Unigene37866_All//0.00E+00//TC176067				nr +
Unigene37868_All	490	14.95	3.00	4.46	8.95	7.87	12.44	12.34	7.93	10.41	-2.32E+00	1.44E-18	Down	-1.75E+00	1.87E-12	Down	-1.85E-01	5.74E-01		4.76E-01	5.25E-02		-6.37E-01	2.93E-03		-2.46E-01	2.70E-01					Unigene37868_All//8.00E-31//DW235752				
Unigene37869_All	642	32.84	19.65	15.43	23.98	23.55	30.46	16.00	12.70	13.78	-7.41E-01	8.07E-10		-1.09E+00	2.39E-17	Down	-2.61E-02	8.77E-01		3.45E-01	6.02E-03		-3.34E-01	4.21E-02		-2.16E-01	1.95E-01					Unigene37869_All//7.00E-38//DW235752				
Unigene37870_All	947	33.48	32.21	34.92	10.73	11.53	10.59	4.29	2.16	1.18	-5.58E-02	6.09E-01		6.07E-02	6.14E-01		1.03E-01	6.12E-01		-1.94E-02	9.39E-01		-9.87E-01	2.78E-04		-1.86E+00	2.86E-10	Down	Unigene37870_All//gi|28372880|gb|AA039922.1|//3.00E-43//At5g52960 [Arabidopsis thaliana]	Unigene37870_All//1.00E-44//AT5G52960| unknown protein	Unigene37870_All//0.00E+00//TC134554				nr +
Unigene37871_All	1162	2.16	5.58	2.34	1.93	1.48	1.90	3.09	5.50	15.19	1.37E+00	2.37E-08	Up	1.13E-01	7.71E-01		-3.81E-01	3.95E-01		-1.85E-02	9.56E-01		8.31E-01	6.54E-05		2.30E+00	7.81E-54	Up									
Unigene37873_All	1364	2.84	21.69	2.50	8.03	16.46	6.79	16.06	7.11	22.87	2.93E+00	2.51E-94	Up	-1.84E-01	6.09E-01		1.03E+00	1.73E-20	Up	-2.43E-01	1.98E-01		-1.18E+00	1.02E-25	Down	5.10E-01	1.63E-09		Unigene37873_All//gi|110931710|gb|ABH02854.1|//2.00E-72//MYB transcription factor MYB124 [Glycine max]	Unigene37873_All//4.00E-46//AT4G37260| MYB73 (MYB DOMAIN PROTEIN 73); DNA binding / transcription factor	Unigene37873_All//0.00E+00//TC155579	MYB			nr +
Unigene37874_All	728	23.43	73.01	27.80	11.43	16.89	17.74	79.86	90.65	57.30	1.64E+00	2.57E-82	Up	2.47E-01	6.54E-02		5.63E-01	2.21E-04		6.35E-01	3.58E-05		1.83E-01	2.13E-03		-4.79E-01	2.98E-15		Unigene37874_All//gi|167178664|gb|ABZ10963.1|//4.00E-24//class 1 knox protein [Kalanchoe x houghtonii]	Unigene37874_All//7.00E-24//AT5G25220| KNAT3 (KNOTTED1-LIKE HOMEOBOX GENE 3); transcription activator/ transcription factor	Unigene37874_All//0.00E+00//TC135932	HB			nr -
Unigene37876_All	1029	2.03	3.10	2.02	7.02	3.45	6.54	2.26	1.91	1.24	6.09E-01	7.98E-02		-1.12E-02	1.00E+00		-1.03E+00	3.84E-07	Down	-1.02E-01	6.97E-01		-2.43E-01	5.62E-01		-8.67E-01	1.58E-02		Unigene37876_All//gi|256674141|gb|ACV04900.1|//1.00E-138//callose synthase 5 [Arabidopsis thaliana]	Unigene37876_All//3.00E-114//AT2G13680| CALS5 (CALLOSE SYNTHASE 5); 1,3-beta-glucan synthase	Unigene37876_All//0.00E+00//gi|21101006|gb|BQ413319.1|BQ413319				nr -
Unigene37877_All	748	4.34	10.57	6.26	5.79	8.56	7.55	3.17	3.13	5.75	1.28E+00	3.70E-09	Up	5.31E-01	7.12E-02		5.64E-01	1.31E-02		3.81E-01	1.51E-01		-1.66E-02	1.00E+00		8.62E-01	7.08E-04		Unigene37877_All//gi|15238001|ref|NP_199517.1|//1.00E-37//senescence-associated protein-related [Arabidopsis thaliana]	Unigene37877_All//2.00E-31//AT4G17670| senescence-associated protein-related	Unigene37877_All//0.00E+00//TC156771				nr +
Unigene37879_All	982	0.05	2.68	1.19	0.86	0.70	1.84	0.73	2.64	1.91	5.65E+00	1.38E-13	Up	4.48E+00	1.90E-05	Up	-2.98E-01	6.93E-01		1.09E+00	2.78E-02		1.85E+00	1.60E-06	Up	1.38E+00	1.22E-03		Unigene37879_All//gi|255577958|ref|XP_002529851.1|//3.00E-07//ribophorin II, putative [Ricinus communis] >gi|223530679|gb|EEF32552.1|ribophorin II, putative [Ricinus communis]						nr -
Unigene37880_All	993	16.28	22.09	18.50	27.39	29.89	34.98	60.89	50.97	29.29	4.41E-01	1.68E-04		1.84E-01	2.12E-01		1.26E-01	2.75E-01		3.53E-01	8.25E-05		-2.56E-01	2.47E-05		-1.06E+00	2.49E-60	Down	Unigene37880_All//gi|18390562|ref|NP_563747.1|//1.00E-64//selenoprotein family protein [Arabidopsis thaliana]	Unigene37880_All//7.00E-66//AT1G05720| selenoprotein family protein	Unigene37880_All//0.00E+00//TC171307				nr -
Unigene37883_All	1656	8.91	2.69	2.41	8.93	10.58	7.15	9.78	2.62	4.35	-1.73E+00	3.50E-25	Down	-1.89E+00	3.24E-27	Down	2.45E-01	7.66E-02		-3.22E-01	3.14E-02		-1.90E+00	3.25E-38	Down	-1.17E+00	1.29E-19	Down	Unigene37883_All//gi|15225258|ref|NP_180187.1|//1.00E-143//IQ06 (IQ-domain 6); calmodulin binding [Arabidopsis thaliana] >gi|119935823|gb|ABM06004.1|At2g26180 [Arabidopsis thaliana]	Unigene37883_All//2.00E-106//AT2G26180| IQ06 (IQ-domain 6); calmodulin binding	Unigene37883_All//0.00E+00//gi|164363156|gb|ES839170.1|ES839170				nr -
Unigene37885_All	1651	7.95	20.65	7.68	10.38	9.64	12.58	11.63	20.18	19.30	1.38E+00	4.24E-41	Up	-5.13E-02	7.68E-01		-1.07E-01	5.20E-01		2.78E-01	2.64E-02		7.95E-01	1.39E-20		7.32E-01	1.26E-17		Unigene37885_All//gi|30698743|ref|NP_177231.2|//1.00E-152//protein kinase family protein [Arabidopsis thaliana] >gi|193870477|gb|ACF22895.1|At1g70740 [Arabidopsis thaliana]	Unigene37885_All//2.00E-143//AT1G70740| protein kinase family protein	Unigene37885_All//0.00E+00//TC151005		ko04626|Plant-pathogen interaction		nr -
Unigene37886_All	1119	1.36	4.44	3.05	3.92	4.00	3.96	4.61	4.07	1.78	1.71E+00	8.53E-09	Up	1.17E+00	1.01E-03		3.02E-02	9.43E-01		1.39E-02	9.62E-01		-1.79E-01	5.09E-01		-1.37E+00	1.46E-08	Down	Unigene37886_All//gi|22329715|ref|NP_173580.2|//4.00E-21//wound-responsive family protein [Arabidopsis thaliana] >gi|196991100|gb|AAL90916.1|At1g21610/F24J8_11 [Arabidopsis thaliana] >gi|21928029|gb|AAM78043.1|At1g21610/F24J8_11 [Arabidopsis thaliana]	Unigene37886_All//2.00E-22//AT1G21610| wound-responsive family protein	Unigene37886_All//0.00E+00//TC158852				nr -
Unigene37888_All	1121	10.03	3.75	2.33	9.02	7.43	4.92	9.24	3.99	3.77	-1.42E+00	9.51E-15	Down	-2.11E+00	4.58E-24	Down	-2.79E-01	1.36E-01		-8.76E-01	6.82E-07		-1.21E+00	3.58E-13	Down	-1.29E+00	5.47E-15	Down	Unigene37888_All//gi|79399060|ref|NP_187859.2|//2.00E-87//PSF2 [Arabidopsis thaliana] >gi|37999772|sp|Q9C7A8.2|PSF2_ARATH RecName: Full=DNA replication complex GINS protein PSF2 >gi|38603928|gb|AAR24709.1|At3g12530 [Arabidopsis thaliana] >gi|58652096|gb|AAW80873.1|At3g12530 [Arabidopsis thaliana]	Unigene37888_All//1.00E-88//AT3G12530| PSF2	Unigene37888_All//0.00E+00//TC163405				nr -
Unigene37891_All	1575	2.03	2.77	2.06	9.68	6.78	6.85	12.13	11.15	25.65	4.49E-01	1.28E-01		2.54E-02	9.60E-01		-5.14E-01	1.07E-04		-4.98E-01	3.84E-04		-1.23E-01	3.63E-01		1.08E+00	8.76E-42	Up	Unigene37891_All//gi|259121393|gb|ACV92016.1|//1.00E-97//WRKY transcription factor 14 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene37891_All//1.00E-73//AT4G24240| WRKY7; calmodulin binding / transcription factor	Unigene37891_All//0.00E+00//TC157676	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene37892_All	486	19.92	38.89	66.62	27.16	37.69	52.32	27.58	24.08	26.48	9.65E-01	1.92E-13		1.74E+00	2.34E-53	Up	4.73E-01	1.05E-04		9.46E-01	2.44E-18		-1.96E-01	1.98E-01		-5.88E-02	6.95E-01					Unigene37892_All//0.00E+00//TC164116				
Unigene37893_All	1628	12.86	11.80	11.15	14.01	14.85	10.57	13.79	8.93	3.92	-1.24E-01	3.70E-01		-2.05E-01	1.30E-01		8.34E-02	5.44E-01		-4.07E-01	2.99E-04		-6.26E-01	1.35E-09		-1.82E+00	3.15E-51	Down	Unigene37893_All//gi|50725037|dbj|BAD32839.1|//8.00E-35//agenet domain-containing protein-like [Oryza sativa Japonica Group] >gi|51090873|dbj|BAD35446.1|agenet domain-containing protein-like [Oryza sativa Japonica Group]	Unigene37893_All//1.00E-35//AT4G32440| agenet domain-containing protein	Unigene37893_All//0.00E+00//TC178830				nr -
Unigene37894_All	1216	2.54	2.63	3.94	0.16	0.91	0.15	16.59	3.92	24.28	4.83E-02	8.99E-01		6.35E-01	2.72E-02		2.47E+00	1.07E-03		-1.41E-01	9.35E-01		-2.08E+00	1.76E-53	Down	5.50E-01	3.14E-10		Unigene37894_All//gi|297853362|ref|XP_002894562.1|//1.00E-104//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340404|gb|EFH70821.1|leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37894_All//4.00E-102//AT1G56145| leucine-rich repeat family protein / protein kinase family protein	Unigene37894_All//0.00E+00//TC161714		ko04626|Plant-pathogen interaction		nr -
Unigene37895_All	699	27.25	39.87	49.29	62.57	67.54	39.74	11.61	5.26	5.13	5.49E-01	8.62E-08		8.55E-01	6.39E-19		1.10E-01	2.12E-01		-6.55E-01	5.91E-17		-1.14E+00	1.26E-09	Down	-1.18E+00	2.00E-10	Down	Unigene37895_All//gi|297795511|ref|XP_002865640.1|//1.00E-19//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314475|gb|EFH41899.1|protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37895_All//5.00E-21//AT5G48490| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene37895_All//0.00E+00//TC161621				nr +
Unigene37896_All	1693	0.00	0.00	0.06	1.41	0.73	2.53	19.15	4.79	3.32	null	null		5.98E+00	3.98E-01		-9.48E-01	1.49E-02		8.44E-01	3.88E-03		-2.00E+00	2.99E-81	Down	-2.53E+00	8.58E-112	Down	Unigene37896_All//gi|30684813|ref|NP_188445.2|//1.00E-127//transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|27808590|gb|AAO24575.1|At3g18170 [Arabidopsis thaliana]	Unigene37896_All//2.00E-120//AT3G18170| transferase, transferring glycosyl groups	Unigene37896_All//3.00E-76//DN802248				nr -
Unigene37898_All	1138	5.88	2.36	3.04	13.96	11.98	9.21	12.15	5.25	5.88	-1.32E+00	3.32E-08	Down	-9.52E-01	6.31E-05		-2.21E-01	1.36E-01		-6.01E-01	9.80E-06		-1.21E+00	2.85E-17	Down	-1.05E+00	2.71E-14	Down	Unigene37898_All//gi|17227092|gb|AAL38006.1|AF443117_1/3.00E-88//LIM domain protein [Gossypium hirsutum]	Unigene37898_All//2.00E-76//AT3G35770| LIM domain-containing protein	Unigene37898_All//0.00E+00//TC142024	LIM			nr +
Unigene37899_All	1000	11.51	5.57	7.46	4.53	5.34	4.52	8.41	2.84	2.31	-1.05E+00	1.27E-09	Down	-6.27E-01	3.02E-04		2.36E-01	4.23E-01		-5.40E-03	9.81E-01		-1.57E+00	1.26E-15	Down	-1.86E+00	2.07E-20	Down	Unigene37899_All//gi|93115321|gb|ABE98329.1|//1.00E-62//SRC2-like protein [Nicotiana benthamiana]	Unigene37899_All//4.00E-31//AT1G09070| SRC2 (SOYBEAN GENE REGULATED BY COLD-2); protein binding	Unigene37899_All//0.00E+00//TC138421		ko03040|Spliceosome		nr -
Unigene379_All	1799	2.47	2.34	2.16	1.91	3.94	2.74	3.76	1.79	3.06	-8.06E-02	7.79E-01		-1.94E-01	5.49E-01		1.05E+00	7.11E-07	Up	5.18E-01	6.24E-02		-1.07E+00	1.94E-07	Down	-2.99E-01	1.41E-01		Unigene379_All//0.00E+00//gi|79586698|ref|NP_680116.2|//0.00E+00//REF6 (RELATIVE OF EARLY FLOWERING 6); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|50513173|gb|AAT77779.1|relative of early flowering 6 [Arabidopsis thaliana]	Unigene379_All//0.00E+00//AT3G48430| REF6 (RELATIVE OF EARLY FLOWERING 6); nucleic acid binding / transcription factor/ zinc ion binding	Unigene379_All//1.00E-143//ES814405	Jumonji			nr -
Unigene37900_All	963	6.52	4.68	1.82	12.98	12.55	11.12	20.46	2.34	6.08	-4.77E-01	4.37E-02		-1.84E+00	1.72E-11	Down	-4.89E-02	8.20E-01		-2.24E-01	2.06E-01		-3.13E+00	1.42E-82	Down	-1.75E+00	7.73E-43	Down	Unigene37900_All//gi|149944345|gb|ABR46215.1|//3.00E-86//At3g12870 [Arabidopsis thaliana]	Unigene37900_All//1.00E-66//AT3G12870| unknown protein	Unigene37900_All//0.00E+00//ES825631				nr -
Unigene37901_All	1108	6.04	16.33	5.82	12.95	13.49	14.39	15.61	24.90	29.74	1.43E+00	1.78E-23	Up	-5.57E-02	8.20E-01		5.90E-02	7.70E-01		1.52E-01	3.58E-01		6.74E-01	4.43E-13		9.30E-01	5.80E-27		Unigene37901_All//gi|297832820|ref|XP_002884292.1|//7.00E-69//structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata] >gi|297330132|gb|EFH60551.1|structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	Unigene37901_All//2.00E-63//AT3G01170| structural constituent of ribosome	Unigene37901_All//0.00E+00//TC143269				nr +
Unigene37902_All	1635	9.82	4.46	4.62	11.52	7.39	10.88	14.27	4.29	6.97	-1.14E+00	6.27E-15	Down	-1.09E+00	2.66E-13	Down	-6.40E-01	3.99E-08		-8.16E-02	6.31E-01		-1.73E+00	2.07E-48	Down	-1.03E+00	4.38E-23	Down	Unigene37902_All//gi|30693135|ref|NP_190477.2|//2.00E-97//ribosomal protein S9 family protein [Arabidopsis thaliana] >gi|30387523|gb|AAP31927.1|At3g49080 [Arabidopsis thaliana]	Unigene37902_All//2.00E-94//AT3G49080| ribosomal protein S9 family protein	Unigene37902_All//0.00E+00//BG440435		ko03010|Ribosome		nr +

Unigene37904_All	782	50.78	12.31	5.04	38.73	23.69	10.97	82.18	9.14	12.38	-2.04E+00	1.00E-83	Down	-3.33E+00	2.65E-139	Down	-7.09E-01	3.16E-15		-1.82E+00	1.70E-59	Down	-3.17E+00	6.79E-272	Down	-2.73E+00	8.95E-241	Down	Unigene37904_All//gi|15241016|ref|NP_198119.1|//2.00E-59//HTA7 (HISTONE H2A 7); DNA binding [Arabidopsis thaliana] >gi|75306451|sp|Q94F49.1|H2A5_ARATH RecName: Full=Probable histone H2A.5; AltName: Full=HTA7 >gi|14326516|gb|AAK60303.1|AF385711_1 AT5g27670/F15A18_130 [Arabidopsis thaliana] >gi|18700220|gb|AAL77720.1|AT5g27670/F15A18_130 [Arabidopsis thaliana]	Unigene37904_All//6.00E-33//AT5G27670| HTA7 (HISTONE H2A 7); DNA binding	Unigene37904_All//0.00E+00//gi|164247090|gb|ES806627.1|ES806627				nr -
Unigene37905_All	712	0.29	7.12	0.07	3.22	2.18	2.66	2.73	2.11	2.18	4.60E+00	1.70E-23	Up	-1.97E+00	3.81E-01		-5.64E-01	1.75E-01		-2.73E-01	5.68E-01		-3.70E-01	3.99E-01		-3.24E-01	4.35E-01		Unigene37905_All//gi|68989120|dbj|BAE06227.1|//1.00E-100//heat shock protein [Solanum lycopersicum]	Unigene37905_All//0.00E+00//gi|109879807|gb|DW508777.1|DW508777	Unigene37905_All//0.00E+00//gi|109879807|gb|DW508777.1|DW508777				nr +
Unigene37908_All	1137	25.95	18.63	24.17	39.30	30.35	40.08	23.06	14.70	11.07	-4.79E-01	1.40E-06		-1.03E-01	4.01E-01		-3.73E-01	3.23E-07		2.83E-02	7.68E-01		-6.49E-01	9.80E-12		-1.06E+00	9.26E-27	Down	Unigene37908_All//gi|107738334|gb|ABF83678.1|//4.00E-43//At3g07640 [Arabidopsis thaliana]	Unigene37908_All//2.00E-44//AT3G07640| unknown protein	Unigene37908_All//0.00E+00//TC166378				nr +
Unigene37909_All	966	1.90	1.05	1.93	23.72	18.14	9.26	5.16	1.90	1.57	-8.54E-01	7.59E-02		2.53E-02	9.77E-01		-3.87E-01	3.06E-04		-1.36E+00	1.45E-29	Down	-1.44E+00	1.47E-08	Down	-1.72E+00	3.16E-11	Down	Unigene37909_All//gi|18394953|ref|NP_564135.1|//2.00E-56//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|111074298|gb|AB104522.1|At1g21090 [Arabidopsis thaliana]	Unigene37909_All//4.00E-45//AT1G21090| hydroxyproline-rich glycoprotein family protein	Unigene37909_All//0.00E+00//TC146827				nr +
Unigene37910_All	1041	4.72	1.70	2.81	7.80	9.43	9.72	13.08	6.99	5.93	-1.47E+00	3.22E-07	Down	-7.48E-01	8.11E-03		2.73E-01	1.61E-01		3.17E-01	9.62E-02		-9.05E-01	6.81E-11		-1.14E+00	4.60E-16	Down	Unigene37910_All//gi|146286094|sp|Q0WW26.2|COPG_ARATH//1.00E-134//RecName: Full=Coatomer subunit gamma; AltName: Full=Gamma-coat protein; Short=Gamma-COP >gi|222424705|dbj|BAH20306.1|AT4G34450 [Arabidopsis thaliana]	Unigene37910_All//4.00E-129//AT4G34450| coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	Unigene37910_All//0.00E+00//gi|78337737|gb|DT558011.1|DT558011				nr +
Unigene37913_All	1138	33.42	72.49	37.67	53.89	49.66	59.73	31.77	26.15	22.09	1.12E+00	3.88E-71	Up	1.72E-01	5.59E-02		-1.18E-01	1.04E-01		1.49E-01	2.83E-02		-2.81E-01	4.98E-04		-5.24E-01	2.00E-11		Unigene37913_All//gi|44681340|gb|AAS47610.1|//2.00E-57//At1g32260 [Arabidopsis thaliana] >gi|45733860|gb|AAS76734.1|At1g32260 [Arabidopsis thaliana]	Unigene37913_All//3.00E-49//AT1G32260| unknown protein	Unigene37913_All//0.00E+00//TC161639				nr -
Unigene37914_All	1395	12.45	4.14	3.28	21.57	13.70	22.86	24.85	9.83	10.34	-1.59E+00	2.74E-26	Down	-1.92E+00	8.10E-33	Down	-6.55E-01	3.44E-13		8.37E-02	4.76E-01		-1.34E+00	3.75E-49	Down	-1.27E+00	1.89E-46	Down	Unigene37914_All//gi|15231102|ref|NP_191425.1|//1.00E-100//60S ribosomal protein-related [Arabidopsis thaliana]	Unigene37914_All//3.00E-93//AT3G58860| 60S ribosomal protein-related	Unigene37914_All//0.00E+00//gi|164297800|gb|ES813015.1|ES813015		ko03010|Ribosome		nr -
Unigene37916_All	1495	0.63	1.66	1.78	8.86	5.67	3.81	5.77	2.21	1.76	1.40E+00	8.73E-04	Up	1.50E+00	3.87E-04	Up	-6.45E-01	5.65E-06		-1.22E+00	9.61E-15	Down	-1.39E+00	1.81E-13	Down	-1.71E+00	1.08E-18	Down	Unigene37916_All//gi|297803650|ref|XP_002869209.1|//1.00E-129//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297315545|gb|EFH45968.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene37916_All//6.00E-116//AT4G24630| receptor/ zinc ion binding	Unigene37916_All//0.00E+00//gi|84165724|gb|DR454372.1|DR454372				nr +
Unigene37917_All	773	16.18	19.14	17.02	27.45	24.90	31.84	13.13	11.41	5.57	2.43E-01	1.15E-01		7.29E-02	6.71E-01		-1.41E-01	3.06E-01		2.14E-01	7.04E-02		-2.02E-01	2.53E-01		-1.24E+00	9.11E-14	Down			Unigene37917_All//7.00E-97//BF268507				
Unigene37923_All	1784	20.56	9.26	15.01	2.82	4.00	4.46	0.50	0.73	0.49	-1.15E+00	1.08E-33	Down	-4.54E-01	6.03E-07		5.03E-01	1.98E-02		6.60E-01	1.19E-03		5.45E-01	3.22E-01		-1.87E-02	9.66E-01		Unigene37923_All//gi|15241092|ref|NP_195812.1|//0.00E+00//STN8; kinase/ protein kinase [Arabidopsis thaliana]	Unigene37923_All//4.00E-178//AT5G01920| STN8; kinase/ protein kinase	Unigene37923_All//0.00E+00//TC135611		ko04626|Plant-pathogen interaction		nr -
Unigene37924_All	1134	4.61	2.99	1.31	10.32	10.69	5.85	4.06	1.47	2.53	-6.24E-01	1.68E-02		-1.81E+00	1.70E-09	Down	5.02E-02	8.31E-01		-8.18E-01	4.41E-07		-1.46E+00	3.89E-08	Down	-6.84E-01	4.67E-03		Unigene37924_All//gi|15235179|ref|NP_192801.1|//1.00E-95//glutaredoxin family protein [Arabidopsis thaliana] >gi|4115916|gb|AAD03427.1| F3H7.9 gene product [Arabidopsis thaliana]	Unigene37924_All//7.00E-84//AT4G10630| glutaredoxin family protein	Unigene37924_All//0.00E+00//TC175802				nr +
Unigene37925_All	2027	46.95	12.62	21.44	23.72	15.95	18.34	0.77	0.37	1.08	-1.90E+00	8.08E-181	Down	-1.13E+00	2.81E-81	Down	-5.72E-01	2.07E-16		-3.71E-01	5.49E-07		-1.06E+00	2.63E-02		4.86E-01	2.01E-01		Unigene37925_All//gi|297836364|ref|XP_002886064.1|//0.00E+00//nodulin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331904|gb|EFH62323.1| nodulin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37925_All//0.00E+00//AT2G16660| nodulin family protein	Unigene37925_All//0.00E+00//TC166778				nr -
Unigene37926_All	2055	3.11	1.90	1.30	8.05	11.50	8.02	22.22	22.29	15.57	-7.10E-01	2.28E-03		-1.26E+00	5.13E-07	Down	5.14E-01	8.79E-07		-4.70E-03	9.71E-01		4.60E-03	9.91E-01		-5.13E-01	1.07E-13		Unigene37926_All//gi|224137338|ref|XP_002327101.1|//0.00E+00//lysine/histidine transporter [Populus trichocarpa] >gi|222835416|gb|EEE73851.1|lysine/histidine transporter [Populus trichocarpa]	Unigene37926_All//0.00E+00//AT1G47670| amino acid transporter family protein	Unigene37926_All//0.00E+00//TC142375				nr +
Unigene37927_All	1172	13.44	8.30	9.50	19.42	15.63	16.65	29.33	17.80	12.27	-6.95E-01	7.90E-07		-5.01E-01	5.95E-04		-3.13E-01	4.59E-03		-2.23E-01	6.97E-02		-7.21E-01	4.90E-18		-1.26E+00	1.36E-45	Down	Unigene37927_All//gi|284449853|emb|CBJ19441.1|//2.00E-96//nucleotide-sensitive chloride conductance regulator [Citrus clementina]	Unigene37927_All//2.00E-72//AT5G62290| nucleotide-sensitive chloride conductance regulator (ICln) family protein	Unigene37927_All//0.00E+00//TC132370				nr -
Unigene37929_All	1709	0.92	0.89	0.84	5.31	4.41	12.79	6.93	5.80	8.37	-4.61E-02	9.40E-01		-1.27E-01	8.07E-01		-2.66E-01	1.87E-01		1.27E+00	3.93E-25	Up	-2.57E-01	1.00E-01		2.73E-01	4.06E-02		Unigene37929_All//gi|110289449|gb|AAP54700.2|//9.00E-10//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene37929_All//1.00E-49//AT5G03670| unknown protein	Unigene37929_All//5.00E-38//BF269706				nr -
Unigene3793_All	1045	4.36	1.26	4.33	5.01	2.11	1.34	2.75	2.68	2.33	-1.79E+00	1.18E-08	Down	-8.20E-03	1.00E+00		-1.25E+00	4.19E-07	Down	-1.90E+00	2.55E-11	Down	-3.80E-02	9.30E-01		-2.43E-01	4.76E-01		Unigene3793_All//gi|186521214|ref|NP_001119190.1|//1.00E-40//BIM1; DNA binding / protein binding / transcription factor [Arabidopsis thaliana] >gi|209572593|sp|Q9LEZ3.2|BIM1_ARATH RecName: Full=Transcription factor BIM1; AltName: Full=BES1-interacting Myc-like protein 1; AltName: Full=Transcription factor EN 126; AltName: Full=bHLH transcription factor bHLH046; AltName: Full=Basic helix-loop-helix protein 46; Short=bHLH 46; Short=AtbHLH46	Unigene3793_All//2.00E-22//AT5G08130| BIM1; DNA binding / protein binding / transcription factor	Unigene3793_All//0.00E+00//gi|78348103|gb|DT568377.1|DT568377	bHLH			nr +
Unigene37930_All	1544	0.95	0.92	1.41	0.77	1.45	1.49	1.37	24.74	0.52	-4.62E-02	9.43E-01		5.76E-01	2.13E-01		9.05E-01	3.36E-02		9.46E-01	2.66E-02		4.18E+00	1.42E-202	Up	-1.41E+00	3.88E-04	Down	Unigene37930_All//gi|297817324|ref|XP_002876545.1|//1.00E-113//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297322383|gb|EFH52804.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene37930_All//1.00E-113//AT2G44800| oxidoreductase, 2OG-Fe(II) oxygenase family protein			ko00941|Flavonoid biosynthesis		nr -
Unigene37932_All	731	3.08	0.83	2.33	4.23	2.83	3.34	2.72	1.72	1.69	-1.89E+00	5.88E-05	Down	-4.01E-01	3.92E-01		-5.80E-01	9.32E-02		-3.41E-01	3.89E-01		-6.64E-01	1.09E-01		-6.86E-01	8.11E-02		Unigene37932_All//gi|297791163|ref|XP_002863466.1|//4.00E-32//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297309301|gb|EFH39725.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene37932_All//6.00E-33//AT5G45610| unknown protein	Unigene37932_All//0.00E+00//gi|73851683|gb|DT460703.1|DT460703				nr +
Unigene37933_All	2544	0.00	0.30	0.27	0.63	1.22	1.40	2.63	4.70	10.91	8.22E+00	1.77E-04	Up	8.09E+00	6.16E-04	Up	9.59E-01	5.51E-03		1.16E+00	4.12E-04	Up	8.39E-01	1.33E-08		2.06E+00	1.89E-73	Up	Unigene37933_All//gi|15239586|ref|NP_197387.1|//0.00E+00//inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis thaliana] >gi|19310427|gb|AAL84950.1|AT5g18860/F17K4_110 [Arabidopsis thaliana] >gi|22137232|gb|AAM91461.1|AT5g18860/F17K4_110 [Arabidopsis thaliana]	Unigene37933_All//0.00E+00//AT5G18860| inosine-uridine preferring nucleoside hydrolase family protein					nr -
Unigene37935_All	819	51.23	63.29	48.37	66.24	69.00	75.44	114.92	73.69	56.47	3.05E-01	3.48E-05		-8.29E-02	3.85E-01		5.89E-02	5.22E-01		1.88E-01	6.41E-03		-6.41E-01	3.95E-39		-1.02E+00	5.14E-89	Down	Unigene37935_All//gi|115473055|ref|NP_001060126.1|//3.00E-59//Os07g0585800 [Oryza sativa Japonica Group] >gi|50509945|dbj|BAD30267.1| NADH-ubiquinone oxidoreductase-related-like protein [Oryza sativa Japonica Group] >gi|113611662|dbj|BAF22040.1|Os07g0585800 [Oryza sativa Japonica Group]	Unigene37935_All//2.00E-58//AT5G67590| FR01 (FROSTBITE1); NADH dehydrogenase (ubiquinone)	Unigene37935_All//0.00E+00//gi|11199540|gb|BF268545.1|BF268545		ko00190|Oxidative phosphorylation		nr -
Unigene37938_All	824	5.02	3.69	4.20	5.08	5.68	6.14	16.52	9.28	8.17	-4.43E-01	1.42E-01		-2.56E-01	4.23E-01		1.63E-01	6.07E-01		2.74E-01	3.68E-01		-8.32E-01	1.48E-09		-1.02E+00	1.86E-13	Down	Unigene37938_All//gi|195657267|gb|ACG48101.1|//5.00E-28//cytochrome c oxidase subunit [Zea mays]	Unigene37938_All//4.00E-29//AT5G57815| cytochrome c oxidase subunit 6b, putative	Unigene37938_All//0.00E+00//gi|109880793|gb|DW509763.1|DW509763		ko00190|Oxidative phosphorylation		nr -
Unigene37939_All	1208	1.65	0.25	0.44	2.64	1.60	1.65	2.80	1.31	1.62	-2.71E+00	1.84E-06	Down	-1.90E+00	3.07E-04	Down	-7.25E-01	2.86E-02		-6.82E-01	5.11E-02		-1.09E+00	3.25E-04	Down	-7.93E-01	6.10E-03		Unigene37939_All//gi|22328607|ref|NP_193141.2|//1.00E-153//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|223635650|sp|Q23266.3|PP308_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g14050, mitochondrial; Flags: Precursor	Unigene37939_All//1.00E-154//AT4G14050| pentatricopeptide (PPR) repeat-containing protein	Unigene37939_All//0.00E+00//TC131968				nr -
Unigene37941_All	1046	4.80	1.40	1.27	12.10	5.73	2.94	7.64	11.15	3.16	-1.77E+00	2.29E-09	Down	-1.92E+00	8.24E-10	Down	-1.08E+00	4.16E-13	Down	-2.04E+00	2.90E-29	Down	5.45E-01	2.26E-04		-1.27E+00	1.75E-11	Down	Unigene37941_All//gi|15235150|ref|NP_193705.1|//4.00E-70//RING; protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene37941_All//1.00E-63//AT4G19700| RING; protein binding / zinc ion binding	Unigene37941_All//0.00E+00//TC146703				nr +
Unigene37945_All	859	5.12	5.60	5.27	298.07	303.46	246.01	22.59	10.36	9.37	1.31E-01	6.31E-01		4.25E-02	8.93E-01		2.59E-02	5.51E-01		-2.77E-01	4.39E-20		-1.12E+00	2.30E-21	Down	-1.27E+00	1.56E-26	Down	Unigene37945_All//gi|157273646|gb|ABV27477.1|//1.00E-125//fasciclin-like arabinogalactan protein 6 [Gossypium hirsutum]	Unigene37945_All//3.00E-48//AT5G03170| FLA11	Unigene37945_All//0.00E+00//DW478779				nr +
Unigene37946_All	1364	11.74	14.86	8.16	7.27	7.22	5.30	12.46	2.73	2.98	3.40E-01	6.10E-03		-5.25E-01	2.76E-04		-9.40E-03	9.58E-01		-4.56E-01	1.24E-02		-2.19E+00	3.35E-48	Down	-2.06E+00	4.04E-46	Down	Unigene37946_All//gi|76559872|tpe|CAI56323.1|//0.00E+00//TPA: leucoanthocyanidin reductase 2 [Gossypium arboreum]	Unigene37946_All//3.00E-63//AT1G75290| oxidoreductase, acting on NADH or NADPH	Unigene37946_All//0.00E+00//gi|78333570|gb|DT553844.1|DT553844		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism		nr -

Unigene37949_All	1015	12.63	6.14	9.92	7.56	7.57	3.74	2.83	0.95	1.33	-1.04E+00	1.54E-10	Down	-3.49E-01	3.87E-02		1.40E-03	9.98E-01		-1.02E+00	1.02E-06	Down	-1.58E+00	6.51E-06	Down	-1.09E+00	7.71E-04	Down	Unigene37949_All//gi|297728381|ref|NP_001176554.1//1.00E-36//Os11g0497350 [Oryza sativa Japonica Group] >gi|77550981|gb|ABA93778.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255680113|dbj|BAH95282.1| Os11g0497350 [Oryza sativa Japonica Group]	Unigene37949_All//5.00E-59//AT4G22190| unknown protein	Unigene37949_All//0.00E+00//gi|78345519|gb|DT565793.1|DT565793				nr -
Unigene37950_All	907	25.50	54.69	41.27	22.74	15.38	15.49	41.77	24.24	17.35	1.10E+00	4.43E-42	Up	6.95E-01	1.68E-14		-5.64E-01	3.58E-07		-5.54E-01	2.39E-06		-7.85E-01	8.00E-23		-1.27E+00	8.48E-51	Down	Unigene37950_All//gi|117650695|gb|ABK54297.1|//1.00E-68//glycine-rich protein [Gossypium hirsutum]		Unigene37950_All//0.00E+00//TC161487		ko03040|Spliceosome		nr -
Unigene37951_All	1669	2.07	0.61	1.60	5.04	3.49	2.76	8.16	7.86	2.39	-1.77E+00	1.18E-06	Down	-3.75E-01	2.97E-01		-5.33E-01	4.71E-03		-8.70E-01	8.58E-06		-5.29E-02	7.36E-01		-1.77E+00	2.19E-30	Down	Unigene37951_All//gi|259121409|gb|ACV92024.1|//6.00E-90//WRKY transcription factor 22 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene37951_All//1.00E-38//AT2G30590| WRKY21; calmodulin binding / transcription factor	Unigene37951_All//1.00E-07//DV437954	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene37953_All	1798	0.09	1.86	0.06	26.82	11.53	6.15	0.47	1.16	8.44	4.41E+00	2.87E-15	Up	-5.60E-01	7.75E-01		-1.22E+00	1.60E-59	Down	-2.12E+00	4.03E-116	Down	1.31E+00	1.39E-03		4.17E+00	6.73E-82	Up	Unigene37953_All//gi|84406257|ref|NP_564731.1|//0.00E+00//ZF14; antiporter/ drug transporter/ transporter [Arabidopsis thaliana] >gi|8979940|gb|AAF82254.1|AC008051_5 [identical to gene ZF14 from Arabidopsis thaliana gb|AB028198 and is a member of an uncharacterized integral membrane protein UPF PF|01554 family >gi|6520161|dbj|BAA87939.1| ZF14 [Arabidopsis thaliana]	Unigene37953_All//2.00E-180//AT1G58340| ZF14; antiporter/ drug transporter/ transporter	Unigene37953_All//2.00E-12//TC161363				nr +
Unigene37954_All	1268	2.81	9.23	12.05	52.56	38.97	23.83	0.00	0.00	0.13	1.72E+00	7.22E-20	Up	2.10E+00	1.41E-32	Up	-4.32E-01	1.22E-13		-1.14E+00	7.29E-65	Down	null	null		6.97E+00	1.40E-01		Unigene37954_All//gi|124365521|gb|ABN09755.1|//1.00E-111//Proteinase inhibitor I4, serpin [Medicago truncatula]	Unigene37954_All//2.00E-98//AT1G55230| unknown protein	Unigene37954_All//0.00E+00//gi|109873693|gb|DW502668.1|DW502668				nr -
Unigene37955_All	1411	10.86	6.54	4.91	18.43	15.23	12.45	12.82	7.17	8.53	-7.33E-01	3.02E-07		-1.15E+00	8.18E-14	Down	-2.75E-01	8.27E-03		-5.66E-01	4.26E-08		-8.39E-01	1.31E-12		-5.89E-01	2.09E-07		Unigene37955_All//gi|182623790|gb|ACB88833.1|//1.00E-167//At1g63160 [Arabidopsis thaliana]	Unigene37955_All//1.00E-165//AT1G63160| replication factor C 40 kDa, putative	Unigene37955_All//0.00E+00//gi|78352231|gb|DT572505.1|DT572505		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03430|Mismatch repair		nr -
Unigene37958_All	1464	0.00	0.00	0.00	2.76	1.06	0.52	87.07	20.36	19.43	null	null		null	null		-1.38E+00	1.76E-06	Down	-2.39E+00	1.15E-11	Down	-2.10E+00	0.00E+00	Down	-2.16E+00	0.00E+00	Down	Unigene37958_All//gi|30315245|gb|AF308841.1|//1.00E-139//nectarin 5 [Nicotiana langsdorffii x Nicotiana sanderae]	Unigene37958_All//1.00E-108//AT5G44360| FAD-binding domain-containing protein	Unigene37958_All//0.00E+00//TC143305		ko00620|Pyruvate metabolism		nr -
Unigene37959_All	1352	29.64	28.00	29.46	19.09	18.95	15.40	12.01	8.47	5.01	-8.25E-02	3.81E-01		-8.90E-03	9.45E-01		-1.03E-02	9.46E-01		-3.10E-01	4.05E-03		-5.04E-01	4.17E-05		-1.26E+00	4.06E-22	Down	Unigene37959_All//gi|297799952|ref|XP_002867860.1|//1.00E-103//EMB1417 [Arabidopsis lyrata subsp. lyrata] >gi|297313696|gb|EFH44119.1| EMB1417 [Arabidopsis lyrata subsp. lyrata]	Unigene37959_All//4.00E-95//AT4G21190| emb1417 (embryo defective 1417)	Unigene37959_All//0.00E+00//TC137381				nr -
Unigene37961_All	1714	1.31	1.45	2.61	0.90	1.23	2.06	8.09	16.80	7.67	1.42E-01	7.20E-01		9.92E-01	9.49E-04		4.44E-01	3.52E-01		1.19E+00	3.42E-04	Up	1.05E+00	3.02E-28	Up	-7.71E-02	6.13E-01		Unigene37961_All//gi|223452548|gb|ACM89601.1|//9.00E-96//disease resistance protein [Glycine max]	Unigene37961_All//6.00E-78//AT2G33060| AtRLP27 (Receptor Like Protein 27); kinase/ protein binding	Unigene37961_All//0.00E+00//ES836854				nr +
Unigene37964_All	677	22.18	6.81	6.84	25.31	17.65	13.41	1.37	1.17	1.18	-1.70E+00	3.77E-25	Down	-1.70E+00	5.35E-24	Down	-5.20E-01	2.66E-05		-9.17E-01	4.52E-12		-2.28E-01	7.18E-01		-2.23E-01	7.07E-01		Unigene37964_All//gi|16604505|gb|AAL24258.1|//1.00E-58//At1g47530/F16N3_20 [Arabidopsis thaliana] >gi|27764936|gb|AAO23589.1| At1g47530/F16N3_20 [Arabidopsis thaliana]	Unigene37964_All//1.00E-57//AT1G47530| ripening-responsive protein, putative	Unigene37964_All//0.00E+00//DW227626				nr -
Unigene37965_All	1653	12.03	3.92	3.99	11.87	10.48	8.31	1.02	0.40	0.27	-1.62E+00	9.87E-31	Down	-1.59E+00	7.07E-29	Down	-1.80E-01	1.80E-01		-5.16E-01	2.04E-05		-1.34E+00	3.79E-03		-1.95E+00	5.40E-05	Down	Unigene37965_All//gi|5668808|gb|AAD46034.1|AC007519_19//1.00E-172//F16N3_20 [Arabidopsis thaliana]	Unigene37965_All//1.00E-156//AT1G47530| ripening-responsive protein, putative	Unigene37965_All//4.00E-162//DW227626				nr +
Unigene37966_All	1434	7.77	6.61	7.32	15.63	14.02	11.87	13.77	4.90	5.28	-2.34E-01	1.98E-01		-8.73E-02	6.36E-01		-1.57E-01	2.23E-01		-3.97E-01	4.96E-04		-1.49E+00	3.18E-33	Down	-1.38E+00	1.17E-30	Down	Unigene37966_All//gi|297813551|ref|XP_002874659.1|//1.00E-129//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320196|gb|EFH50918.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37966_All//1.00E-127//AT4G10955| lipase class 3 family protein	Unigene37966_All//0.00E+00//TC150142				nr -
Unigene37967_All	1201	10.37	1.90	2.66	9.66	7.05	4.78	2.68	1.84	1.92	-2.45E+00	3.45E-33	Down	-1.96E+00	2.83E-24	Down	-4.54E-01	4.05E-03		-1.02E+00	7.68E-10	Down	-5.37E-01	8.77E-02		-4.76E-01	1.15E-01		Unigene37967_All//gi|158302693|dbj|BAF85832.1|//1.00E-55//alpha-1,2-fucosidase [Lilium longiflorum]	Unigene37967_All//4.00E-53//AT4G34260| FUC95A; 1,2-alpha-L-fucosidase	Unigene37967_All//1.00E-164//gi|164256585|gb|ES817939.1|ES817939				nr +
Unigene37968_All	943	2.72	0.48	0.56	1.16	0.62	1.34	7.98	2.30	2.45	-2.49E+00	1.74E-07	Down	-2.27E+00	2.07E-06	Down	-9.05E-01	1.55E-01		2.07E-01	7.34E-01		-1.79E+00	7.42E-17	Down	-1.70E+00	2.74E-16	Down	Unigene37968_All//gi|20197493|gb|AAD03357.2|//3.00E-20//expressed protein [Arabidopsis thaliana] >gi|88010967|gb|ABD38880.1| At2g15000 [Arabidopsis thaliana]	Unigene37968_All//3.00E-22//AT2G15000| unknown protein	Unigene37968_All//0.00E+00//TC146711				nr -
Unigene3797_All	614	9.80	24.67	27.84	11.03	15.76	21.48	33.88	55.34	75.14	1.33E+00	8.81E-18	Up	1.51E+00	4.22E-23	Up	5.14E-01	3.82E-03		9.61E-01	4.87E-10		7.08E-01	2.71E-17		1.15E+00	1.66E-52	Up	Unigene3797_All//gi|297819888|ref|XP_002877827.1|//8.00E-54//acyl-CoA oxidase 4 [Arabidopsis lyrata subsp. lyrata] >gi|297323665|gb|EFH54086.1| acyl-CoA oxidase 4 [Arabidopsis lyrata subsp. lyrata]	Unigene3797_All//1.00E-54//AT3G51840| ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase	Unigene3797_All//0.00E+00//TC144658		ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation		nr -
Unigene37970_All	963	9.67	28.73	11.89	3.93	3.54	3.42	2.68	0.43	2.36	1.57E+00	1.39E-40	Up	2.98E-01	1.03E-01		-1.51E-01	6.61E-01		-2.00E-01	5.93E-01		-2.63E+00	1.34E-09	Down	-1.84E-01	6.10E-01		Unigene37970_All//gi|38566650|gb|AB24215.1|//1.00E-64//At1g35180 [Arabidopsis thaliana] >gi|51536528|gb|AAU05502.1| At3g16870 [Arabidopsis thaliana]	Unigene37970_All//5.00E-66//AT1G35180| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; CONTAINS InterPro DOMAIN/s: TRAM, LAG1 and CLN8 homology (InterPro:IPR006634); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G35170.1); Has 128 Blast hits to 128 proteins in 42 species: Archae - 0; Bacteria - 0; Metazoa - 49; Fungi - 4; Plants - 41; Viruses - 3; Other Eukaryotes - 31 (source: NCBI BLink).	Unigene37970_All//0.00E+00//TC177135				nr -
Unigene37972_All	797	11.69	26.57	15.30	8.31	8.17	5.27	15.70	15.99	19.64	1.19E+00	1.36E-20	Up	3.89E-01	2.36E-02		-2.57E-02	9.19E-01		-6.58E-01	3.50E-03		2.66E-02	8.81E-01		3.23E-01	9.52E-03		Unigene37972_All//gi|297821186|ref|XP_002878476.1|//2.00E-08//AT3g62770/F26K9_200 [Arabidopsis lyrata subsp. lyrata] >gi|297324314|gb|EFH54735.1| AT3g62770/F26K9_200 [Arabidopsis lyrata subsp. lyrata]	Unigene37972_All//6.00E-09//AT3G62770| AtATG18a	Unigene37972_All//0.00E+00//ES793101				nr +
Unigene37973_All	1180	12.46	6.23	10.29	15.20	13.48	14.58	33.97	12.01	16.04	-1.00E+00	2.80E-11	Down	-2.76E-01	8.30E-02		-1.73E-01	2.29E-01		-5.96E-02	6.91E-01		-1.50E+00	3.22E-67	Down	-1.08E+00	5.95E-42	Down	Unigene37973_All//gi|21554213|gb|AAM63292.1|//2.00E-83//C-8,7 sterol isomerase [Arabidopsis thaliana]	Unigene37973_All//1.00E-67//AT1G20050| HYD1 (HYDRA1); C-8 sterol isomerase	Unigene37973_All//0.00E+00//TC158940		ko00100|Steroid biosynthesis		nr -
Unigene37974_All	914	94.97	73.01	160.51	172.01	182.73	103.57	19.29	16.28	3.44	-3.79E-01	7.83E-12		7.57E-01	4.25E-64		8.72E-02	3.78E-02		-7.32E-01	2.73E-72		-2.45E-01	4.86E-02		-2.49E+00	6.54E-60	Down	Unigene37974_All//gi|18411783|ref|NP_565167.1|//2.00E-23//senescence-associated protein-related [Arabidopsis thaliana] >gi|65737767|gb|AAF17687.1|AC009243_14 F28K19.24 [Arabidopsis thaliana]	Unigene37974_All//9.00E-25//AT1G78020| senescence-associated protein-related	Unigene37974_All//0.00E+00//gi|48742277|gb|CO072796.1|CO072796				nr -
Unigene37975_All	1294	1.82	4.89	3.62	2.23	1.49	0.94	1.73	1.10	0.06	1.43E+00	1.17E-08	Up	9.93E-01	6.71E-04		-5.83E-01	1.05E-01		-1.24E+00	7.77E-04	Down	-6.57E-01	8.80E-02		-4.81E+00	6.33E-14	Down	Unigene37975_All//gi|13383303|dbj|BAB39482.1|//0.00E+00//endo-1,4-beta glucanase [Populus alba]	Unigene37975_All//6.00E-125//AT1G02800| AtCEL2; cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene37975_All//0.00E+00//gi|78354042|gb|DT574316.1|DT574316		ko00500|Starch and sucrose metabolism		nr -
Unigene37976_All	1426	2.16	1.42	2.24	7.20	9.76	7.38	30.36	6.62	13.58	-6.07E-01	8.64E-02		4.97E-02	8.95E-01		4.39E-01	2.43E-03		3.63E-02	8.71E-01		-2.20E+00	4.63E-122	Down	-1.16E+00	1.57E-50	Down	Unigene37976_All//gi|8409089|ref|NP_564938.1|//3.00E-87//myb family transcription factor [Arabidopsis thaliana]	Unigene37976_All//1.00E-67//AT1G68670| myb family transcription factor	Unigene37976_All//0.00E+00//TC156523	G2-like			nr +
Unigene37978_All	1474	20.23	9.32	10.91	13.28	15.14	13.36	14.28	8.90	8.03	-1.12E+00	2.41E-26	Down	-8.91E-01	1.44E-17		1.89E-01	1.32E-01		8.40E-03	9.49E-01		-6.82E-01	2.16E-10		-8.32E-01	9.06E-15		Unigene37978_All//gi|18395021|ref|NP_564148.1|//1.00E-159//emb1968 (embryo defective 1968); ATP binding / ATPase/ DNA binding / DNA clamp loader/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana] >gi|17065122|gb|AAL32715.1| Similar replication factor C, 37-kDa subunit [Arabidopsis thaliana] >gi|34098857|gb|AAQ56811.1| At1g21690 [Arabidopsis thaliana]	Unigene37978_All//9.00E-149//AT1G21690| emb1968 (embryo defective 1968); ATP binding / ATPase/ DNA binding / DNA clamp loader/ nucleoside-triphosphatase/ nucleotide binding	Unigene37978_All//0.00E+00//gi|78338873|gb|DT559147.1|DT559147		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03430|Mismatch repair		nr +
Unigene37979_All	1076	1.60	1.70	1.39	2.73	3.65	2.98	3.46	3.03	7.00	7.93E-02	8.69E-01		-2.12E-01	6.65E-01		4.18E-01	1.98E-01		1.26E-01	7.35E-01		-1.91E-01	5.61E-01		1.02E+00	8.55E-08	Up	Unigene37979_All//gi|42573473|ref|NP_974833.1|//5.00E-18//transcription elongation factor-related [Arabidopsis thaliana]	Unigene37979_All//7.00E-17//AT5G25520| transcription elongation factor-related	Unigene37979_All//0.00E+00//gi|78326354|gb|DT546628.1|DT546628				nr -
Unigene3798_All	594	20.96	42.05	23.49	30.19	36.23	42.12	67.48	80.50	58.08	1.00E+00	1.18E-18	Up	1.64E-01	3.53E-01		2.63E-01	2.79E-02		4.81E-01	6.01E-06		2.55E-01	2.44E-04		-2.16E-01	4.13E-03		Unigene3798_All//gi|25992529|gb|AAN77145.1|//2.00E-37//fiber protein Fb2 [Gossypium barbadense]	Unigene3798_All//2.00E-22//AT3G05700| INVOLVED IN: response to water deprivation; CONTAINS InterPro DOMAIN/s: Drought induced 19 (InterPro:IPR008598); BEST Arabidopsis thaliana protein match is: drought-responsive family protein (TAIR:AT5G26990.1); Has 167 Blast hits to 167 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 38; Fungi - 0; Plants - 128; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene3798_All//0.00E+00//gi|109835544|gb|DW234107.1|DW234107				nr -
Unigene37981_All	1410	4.94	4.35	3.36	11.34	12.09	9.19	5.49	1.63	2.32	-1.83E-01	4.38E-01		-5.54E-01	1.72E-02		9.22E-02	5.87E-01		-3.03E-01	3.58E-02		-1.75E+00	8.70E-17	Down	-1.24E+00	8.77E-11	Down	Unigene37981_All//gi|2739044|gb|AAB94598.1|//1.00E-151//polyphosphoinositide binding protein SshIp [Glycine max]	Unigene37981_All//2.00E-127//AT5G47730| SEC14 cytosolic factor, putative / polyphosphoinositide-binding protein, putative	Unigene37981_All//0.00E+00//TC174252				nr -
Unigene37984_All	1296	15.06	14.97	8.01	38.48	42.41	41.89	36.41	6.16	7.81	-8.10E-03	9.74E-01		-9.10E-01	4.05E-12		1.40E-01	6.34E-02		1.23E-01	1.31E-01		-2.56E+00	6.85E-160	Down	-2.22E+00	5.72E-139	Down	Unigene37984_All//gi|59125543|emb|CAB56195.1|//1.00E-129//Knolle [Capsicum annuum]	Unigene37984_All//4.00E-119//AT1G08360| SYP111 (SYNTAXIN OF PLANTS 111); SNAP receptor	Unigene37984_All//0.00E+00//TC136111		ko04130|SNARE interactions in vesicular transport		nr +

Unigene37986_All	2240	0.21	1.65	0.48	1.29	1.45	1.61	5.30	5.24	13.66	2.97E+00	2.01E-12	Up	1.18E+00	9.59E-02		1.64E-01	6.89E-01		3.23E-01	3.78E-01		-1.66E-02	9.42E-01		1.36E+00	1.14E-45	Up	Unigene37986_All//gi|145326682|ref|NP_001077788.1|//1.00E-131//protein kinase family protein [Arabidopsis thaliana]	Unigene37986_All//2.00E-111//AT1G67890| protein kinase family protein	Unigene37986_All//0.00E+00//TC157905				nr -
Unigene37987_All	1481	2.33	6.19	2.27	2.19	2.72	3.20	10.31	13.55	19.85	1.41E+00	5.66E-12	Up	-4.17E-02	9.13E-01		3.15E-01	3.41E-01		5.51E-01	5.08E-02		3.94E-01	3.40E-04		9.46E-01	7.99E-25		Unigene37987_All//gi|297817142|ref|XP_002876454.1|//1.00E-159//seven in absentia family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322292|gb|EFH52713.1| seven in absentia family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37987_All//6.00E-156//AT3G58040| SINAT2 (SEVEN IN ABSENTIA OF ARABIDOPSIS 2); protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene37987_All//0.00E+00//gi|78343779|gb|DT564053.1|DT564053		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene37989_All	988	39.29	31.44	18.32	71.54	45.38	57.37	283.85	197.60	99.07	-3.22E-01	1.87E-04		-1.10E+00	5.75E-32	Down	-6.57E-01	1.34E-30		-3.19E-01	1.22E-07		-5.23E-01	7.25E-80		-1.52E+00	0.00E+00	Down	Unigene37989_All//gi|288563554|gb|ADC53692.1|//1.00E-111//heat shock protein 90-1 [Cryptocoryne ciliata]	Unigene37989_All//1.00E-73//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Unigene37989_All//0.00E+00//gi|78351369|gb|DT571643.1|DT571643		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene37990_All	656	1.99	10.66	4.71	3.34	9.24	5.23	2.77	3.95	4.01	2.42E+00	1.73E-18	Up	1.24E+00	1.05E-03		1.47E+00	1.13E-09	Up	6.47E-01	5.68E-02		5.11E-01	1.53E-01		5.32E-01	1.16E-01					Unigene37990_All//2.00E-07//gi|13246027|gb|BE052628.2|BE052628				
Unigene37992_All	1391	15.80	9.73	8.61	28.76	34.26	26.27	40.64	5.26	11.77	-7.00E-01	2.63E-09		-8.75E-01	9.84E-13		2.53E-01	6.29E-04		-1.31E-01	1.75E-01		-2.95E+00	7.50E-223	Down	-1.79E+00	5.62E-125	Down	Unigene37992_All//gi|210148100|gb|ACJ09092.1|//1.00E-161//cyclin-dependent kinase B [Populus tomentosa]	Unigene37992_All//2.00E-154//AT1G20930| CDKB2;2 (CYCLIN-DEPENDENT KINASE B2;2); cyclin-dependent protein kinase/ kinase	Unigene37992_All//0.00E+00//TC144597				nr +
Unigene37993_All	1418	1.37	11.04	3.72	9.03	4.35	6.31	9.57	18.60	9.36	3.02E+00	1.62E-51	Up	1.45E+00	3.91E-07	Up	-1.05E+00	8.63E-13	Down	-5.18E-01	8.27E-04		9.58E-01	2.75E-22		-3.29E-02	8.30E-01		Unigene37993_All//gi|7670832|gb|AAF66242.1|AF243180_1//3.00E-88//dicyanin [Solanum lycopersicum]	Unigene37993_All//8.00E-22//AT5G26330| plastocyanin-like domain-containing protein / mavicyanin, putative	Unigene37993_All//0.00E+00//gi|78324765|gb|DT545039.1|DT545039		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene37994_All	1394	177.87	67.35	160.78	26.77	28.14	24.30	0.06	0.06	0.00	-1.40E+00	1.36E-304	Down	-1.46E-01	1.44E-05		7.21E-02	5.15E-01		-1.40E-01	1.58E-01		-1.67E-02	1.01E+00		-5.92E+00	3.58E-01		Unigene37994_All//gi|15222966|ref|NP_172837.1|//1.00E-131//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|46518397|gb|AAS99680.1|At1g13820 [Arabidopsis thaliana] >gi|83104156|gb|AAT41824.1|At1g13820 [Arabidopsis thaliana]	Unigene37994_All//4.00E-132//AT1G13820| hydrolase, alpha/beta fold family protein	Unigene37994_All//0.00E+00//TC145607				nr +
Unigene37995_All	958	12.12	4.44	4.50	35.31	23.11	35.36	18.62	12.35	9.65	-1.45E+00	1.20E-15	Down	-1.43E+00	1.11E-14	Down	-6.11E-01	4.12E-13		2.10E-03	9.84E-01		-5.93E-01	3.80E-07		-9.49E-01	1.34E-15		Unigene37995_All//gi|499068|emb|CAA54506.1|//1.00E-93//GTPase [Glycine max]	Unigene37995_All//9.00E-90//AT1G05810| RABA5E (RAB GTPASE HOMOLOG A5E); GTP binding	Unigene37995_All//0.00E+00//TC135499				nr -
Unigene37996_All	1741	0.75	2.12	1.50	17.05	13.45	21.04	33.37	30.44	33.87	1.50E+00	9.99E-06	Up	9.96E-01	1.53E-02		-3.43E-01	2.38E-04		3.03E-01	5.83E-04		-1.33E-01	4.80E-02		2.14E-02	7.64E-01		Unigene37996_All//gi|224115584|ref|XP_002317072.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222860137|gb|EEE97684.1|cytochrome P450 [Populus trichocarpa]	Unigene37996_All//3.00E-109//AT5G36110| CYP716A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene37996_All//0.00E+00//TC154874		ko00906|Carotenoid biosynthesis		nr +
Unigene37998_All	932	32.50	20.22	40.74	76.38	92.55	91.97	6.90	1.52	8.85	-6.85E-01	4.44E-12		3.26E-01	3.20E-04		2.77E-01	8.91E-08		2.68E-01	9.74E-07		-2.18E+00	1.62E-18	Down	3.60E-01	4.40E-02		Unigene37998_All//gi|297793807|ref|XP_002864788.1|//9.00E-50//invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310623|gb|EFH41047.1|invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene37998_All//7.00E-50//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene37998_All//0.00E+00//gi|164367945|gb|ES804915.1|ES804915		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene37999_All	1266	0.87	2.24	2.23	2.12	1.63	1.50	18.03	16.67	10.26	1.37E+00	4.19E-04	Up	1.36E+00	7.25E-04	Up	-3.81E-01	3.34E-01		-5.04E-01	2.11E-01		-1.13E-01	3.55E-01		-8.14E-01	2.13E-15		Unigene37999_All//gi|224072174|ref|XP_002330637.1|//1.00E-171//proline transporter [Populus trichocarpa] >gi|222841069|gb|EEE78616.1|proline transporter [Populus trichocarpa]	Unigene37999_All//7.00E-146//AT5G41800| amino acid transporter family protein	Unigene37999_All//4.00E-75//TC142250				nr -
Unigene38_All	2619	4.10	8.84	6.95	14.51	18.18	16.71	17.00	13.96	15.24	1.11E+00	2.71E-20	Up	7.64E-01	1.34E-08		3.25E-01	6.00E-06		2.03E-01	1.51E-02		-2.84E-01	7.48E-05		-1.57E-01	3.19E-02		Unigene38_All//gi|24461849|gb|AAN62336.1|AF506028_3//0.00E+00//CTV.2 [Citrus trifoliata]	Unigene38_All//0.00E+00//AT1G15750| TPL (TOPLESS); protein binding / protein homodimerization/ transcription repressor	Unigene38_All//0.00E+00//TC177482				nr -
Unigene380_All	4343	3.78	3.82	4.61	8.22	6.10	4.88	8.26	7.33	3.94	1.23E-02	9.54E-01		2.85E-01	3.12E-02		-4.32E-01	1.48E-07		-7.54E-01	1.06E-17		-1.71E-01	4.63E-02		-1.07E+00	1.13E-36	Down	Unigene380_All//gi|79586698|ref|NP_680116.2|//0.00E+00//REF6 (RELATIVE OF EARLY FLOWERING 6); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|50513173|gb|AAT77779.1|relative of early flowering 6 [Arabidopsis thaliana]	Unigene380_All//2.00E-172//AT3G48430| REF6 (RELATIVE OF EARLY FLOWERING 6); nucleic acid binding / transcription factor/ zinc ion binding	Unigene380_All//0.00E+00//TC151749	Jumonji			nr +
Unigene3800_All	2056	0.71	2.49	0.96	1.82	1.49	1.60	1.89	1.32	1.49	1.80E+00	1.12E-09	Up	4.28E-01	3.96E-01		-2.86E-01	4.05E-01		-1.80E-01	6.39E-01		-5.18E-01	6.56E-02		-3.43E-01	2.18E-01		Unigene3800_All//gi|297851436|ref|XP_002893599.1|//1.00E-106//kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339441|gb|EFH69858.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3800_All//3.00E-107//AT1G30090| kelch repeat-containing F-box family protein	Unigene3800_All//7.00E-167//gi|21096754|gb|BQ409067.1|BQ409067				nr -
Unigene38000_All	1299	3.58	1.48	2.01	7.86	8.62	8.03	7.23	1.32	3.62	-1.27E+00	1.10E-05	Down	-8.36E-01	4.15E-03		1.32E-01	5.32E-01		3.09E-02	8.98E-01		-2.45E+00	9.28E-31	Down	-9.98E-01	2.67E-09		Unigene38000_All//gi|15240974|ref|NP_195762.1|//9.00E-68//glutaredoxin family protein [Arabidopsis thaliana]	Unigene38000_All//2.00E-53//AT5G01420| glutaredoxin family protein	Unigene38000_All//0.00E+00//ES800675				nr -
Unigene38001_All	1030	11.28	7.97	6.05	19.78	14.34	10.00	14.86	6.09	10.64	-5.01E-01	2.64E-03		-8.99E-01	2.44E-07		-4.64E-01	3.97E-05		-9.85E-01	5.70E-16		-1.29E+00	6.69E-21	Down	-4.82E-01	9.91E-05		Unigene38001_All//gi|38016521|gb|AAR07596.1|//1.00E-62//fiber protein Fb34 [Gossypium barbadense]	Unigene38001_All//6.00E-44//AT1G61065| unknown protein	Unigene38001_All//0.00E+00//TC149802				nr +
Unigene38002_All	1281	9.88	9.22	3.99	23.14	28.01	21.37	21.55	4.11	6.10	-1.01E-01	5.85E-01		-1.31E+00	5.06E-14	Down	2.76E-01	1.45E-03		-1.15E-01	3.33E-01		-2.39E+00	1.71E-86	Down	-1.82E+00	4.59E-63	Down	Unigene38002_All//gi|3176683|gb|AAC18806.1|//3.00E-69//F1707.12 [Arabidopsis thaliana] >gi|50897240|gb|AAT85759.1|At1g70340 [Arabidopsis thaliana]	Unigene38002_All//3.00E-76//AT1G23790| unknown protein	Unigene38002_All//0.00E+00//ES842448				nr +
Unigene38003_All	1222	7.24	5.68	1.66	10.07	11.67	10.13	17.61	3.11	10.20	-3.49E-01	7.82E-02		-2.13E+00	3.12E-19	Down	2.13E-01	1.90E-01		8.30E-03	9.60E-01		-2.50E+00	3.44E-71	Down	-7.87E-01	8.33E-14		Unigene38003_All//gi|115454921|ref|NP_001051061.1|//4.00E-75//Os03g0712100 [Oryza sativa Japonica Group] >gi|108710726|gb|ABF98521.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549532|dbj|BAF12975.1|Os03g0712100 [Oryza sativa Japonica Group]	Unigene38003_All//6.00E-20//AT4G37110| protein binding / zinc ion binding	Unigene38003_All//0.00E+00//TC130470				nr -
Unigene38004_All	1130	1.44	3.68	2.12	2.91	3.02	2.76	3.14	3.81	3.31	1.36E+00	1.42E-05	Up	5.63E-01	1.96E-01		5.23E-02	9.00E-01		-7.73E-02	8.37E-01		2.78E-01	3.34E-01		7.64E-02	7.93E-01		Unigene38004_All//gi|28466915|gb|AA044066.1|//3.00E-75//At5g20120 [Arabidopsis thaliana]	Unigene38004_All//6.00E-69//AT5G20120| unknown protein	Unigene38004_All//0.00E+00//gi|109847246|gb|DW476226.1|DW476226				nr -
Unigene38005_All	1108	7.65	5.99	5.24	17.53	10.97	12.43	10.04	4.19	3.92	-3.53E-01	8.26E-02		-5.46E-01	8.50E-03		-6.77E-01	3.46E-09		-4.96E-01	4.72E-05		-1.26E+00	6.16E-15	Down	-1.36E+00	3.70E-17	Down	Unigene38005_All//gi|15809944|gb|AAL06899.1|//1.00E-104//AT5g21070/T10F18_100 [Arabidopsis thaliana] >gi|18958048|gb|AAL79597.1|AT5g21070/T10F18_100 [Arabidopsis thaliana]	Unigene38005_All//8.00E-106//AT5G21070| unknown protein	Unigene38005_All//0.00E+00//TC155043				nr -
Unigene38006_All	1479	4.88	4.69	2.52	21.42	13.64	7.30	19.10	20.74	9.29	-5.68E-02	8.01E-01		-9.54E-01	2.89E-05		-6.51E-01	1.01E-13		-1.55E+00	9.90E-50	Down	1.19E-01	2.37E-01		-1.04E+00	6.09E-28	Down	Unigene38006_All//gi|224093334|ref|XP_002309886.1|//1.00E-124//photoperiod-response-like protein [Populus trichocarpa] >gi|224093344|ref|XP_002309891.1|photoperiod-response-like protein [Populus trichocarpa] >gi|222852789|gb|EEE90336.1|photoperiod-response-like protein [Populus trichocarpa] >gi|222852794|gb|EEE90341.1|photoperiod-response-like protein [Populus trichocarpa]	Unigene38006_All//1.00E-111//AT5G64660| U-box domain-containing protein	Unigene38006_All//0.00E+00//gi|78328468|gb|DT548742.1|DT548742		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene38012_All	1685	4.81	10.40	10.14	10.64	9.32	12.54	14.05	13.67	11.23	1.11E+00	1.37E-15	Up	1.08E+00	6.41E-14	Up	-1.92E-01	1.71E-01		2.37E-01	6.25E-02		-4.00E-02	7.36E-01		-3.23E-01	1.04E-03		Unigene38012_All//gi|15235456|ref|NP_193007.1|//1.00E-131//armadillo/beta-catenin repeat family protein [Arabidopsis thaliana] >gi|11074334|gb|AH004540.1|At4g12710 [Arabidopsis thaliana]	Unigene38012_All//9.00E-124//AT4G12710| armadillo/beta-catenin repeat family protein	Unigene38012_All//0.00E+00//TC170257				nr +
Unigene38014_All	1564	15.66	11.53	13.55	3.85	5.77	7.39	0.46	0.05	0.00	-4.41E-01	6.08E-05		-2.08E-01	8.74E-02		5.82E-01	1.50E-03		9.40E-01	1.40E-08		-3.11E+00	1.40E-03		-8.84E+00	1.78E-05	Down	Unigene38014_All//gi|224106263|ref|XP_002314106.1|//0.00E+00//ammonium transporter [Populus trichocarpa] >gi|222850514|gb|EEE88061.1|ammonium transporter [Populus trichocarpa]	Unigene38014_All//6.00E-158//AT1G64780| ATAMT1;2 (AMMONIUM TRANSPORTER 1;2); ammonium transmembrane transporter	Unigene38014_All//0.00E+00//gi|78323589|gb|DT543863.1|DT543863				nr +
Unigene38016_All	1584	1.65	0.22	1.48	2.17	1.35	1.54	0.96	0.84	1.41	-2.88E+00	8.50E-09	Down	-1.59E-01	6.90E-01		-6.87E-01	3.06E-02		-4.95E-01	1.51E-01		-1.87E-01	7.07E-01		5.52E-01	1.40E-01		Unigene38016_All//gi|224118674|ref|XP_002317879.1|//2.00E-49//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222858552|gb|EEE96099.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene38016_All//2.00E-17//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene38016_All//0.00E+00//TC176102				nr +
Unigene38017_All	1406	1.45	0.97	1.06	5.88	3.43	4.21	2.98	1.22	1.76	-5.77E-01	2.05E-01		-4.53E-01	3.56E-01		-7.78E-01	2.85E-05		-4.83E-01	1.69E-02		-1.29E+00	2.70E-06	Down	-7.61E-01	2.94E-03		Unigene38017_All//gi|18410430|ref|NP_567034.1|//1.00E-133//Met-10+ like family protein [Arabidopsis thaliana]	Unigene38017_All//7.00E-135//AT3G56120| Met-10+ like family protein	Unigene38017_All//0.00E+00//TC177142				nr +
Unigene38018_All	1260	0.83	3.58	2.62	4.19	3.61	5.99	5.13	8.53	6.54	2.11E+00	2.15E-10	Up	1.66E+00	1.30E-05	Up	-2.16E-01	4.50E-01		5.14E-01	1.61E-02		7.32E-01	2.47E-06		3.50E-01	5.08E-02		Unigene38018_All//gi|224106505|ref|XP_002314189.1|//7.00E-91//f-box family protein [Populus trichocarpa] >gi|222850597|gb|EEE88144.1| f-box family protein [Populus trichocarpa]	Unigene38018_All//1.00E-38//AT3G55370| OBP3 (OBF-BINDING PROTEIN 3); DNA binding / transcription factor	Unigene38018_All//0.00E+00//gi|164258357|gb|ES804340.1|ES804340	C2C2-Dof			nr -
Unigene38019_All	1161	7.03	1.53	4.91	6.44	8.93	3.97	18.68	16.56	17.64	-2.20E+00	2.09E-19	Down	-5.19E-01	1.47E-02		4.72E-01	6.04E-03		-6.98E-01	8.52E-04		-1.74E-01	1.35E-01		-8.30E-02	4.96E-01		Unigene38019_All//gi|3759184|dbj|BAA33810.1|//1.00E-134//phi-1 [Nicotiana tabacum]	Unigene38019_All//8.00E-120//AT4G08950| EXO (EXORDIUM)	Unigene38019_All//0.00E+00//TC134763				nr -

Unigene38020_All	326	7.38	7.15	9.47	12.84	26.41	26.60	2.85	2.82	2.44	-4.63E-02	9.19E-01		3.60E-01	3.57E-01		1.04E+00	3.48E-08	Up	1.05E+00	8.49E-08	Up	-1.66E-02	1.02E+00		-2.23E-01	7.07E-01		Unigene38020_All//gi|30725336|gb|AP37690.1|//7.00E-19//At5g41560 [Arabidopsis thaliana]	Unigene38020_All//2.00E-19//AT5G41560| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin ligase, Det1/DDB1-complexing (InterPro:IPR018276); Has 59 Blast hits to 59 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 46; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene38020_All//7.00E-129//CO496712				nr -
Unigene38021_All	620	0.68	3.19	0.52	6.51	10.00	6.56	2.93	2.16	2.25	2.24E+00	2.78E-05	Up	-3.90E-01	7.17E-01		6.19E-01	7.05E-03		1.06E-02	9.73E-01		-4.43E-01	3.31E-01		-3.83E-01	3.72E-01		Unigene38021_All//gi|30725336|gb|AP37690.1|//3.00E-32//At5g41560 [Arabidopsis thaliana]	Unigene38021_All//2.00E-33//AT5G41560| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin ligase, Det1/DDB1-complexing (InterPro:IPR018276); Has 59 Blast hits to 59 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 46; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene38021_All//0.00E+00//gi|54121203|gb|CO496712.1|CO496712				nr -
Unigene38022_All	685	68.59	8.21	8.78	184.13	74.45	59.34	60.49	9.21	12.16	-3.06E+00	1.37E-157	Down	-2.97E+00	2.98E-147	Down	-1.31E+00	7.12E-174	Down	-1.63E+00	6.26E-212	Down	-2.71E+00	9.93E-150	Down	-2.32E+00	1.73E-128	Down	Unigene38022_All//gi|15236175|ref|NP_194362.1|//5.00E-13//AGP13 (arabinogalactan protein 13) [Arabidopsis thaliana] >gi|752077711|sp|Q96SQ3.1|AGP13_ARATH RecName: Full=Arabinogalactan peptide 13; Short=AG-peptide 13; Flags: Precursor >gi|10880503|gb|AAG24281.1|AF195894_1 arabinogalactan protein [Arabidopsis thaliana] >gi|89111816|gb|ABD60680.1| At4g26320 [Arabidopsis thaliana]	Unigene38022_All//0.00E+00//CD486585				nr +
Unigene38024_All	1702	0.40	0.86	1.44	9.78	8.98	8.23	4.17	2.38	1.83	1.11E+00	4.53E-02		1.85E+00	6.30E-05	Up	-1.22E-01	4.54E-01		-2.49E-01	8.63E-02		-8.09E-01	3.66E-05		-1.19E+00	2.17E-09	Down	Unigene38024_All//gi|42568160|ref|NP_198534.2|//1.00E-172//SUS5; UDP-glycosyltransferase/ sucrose synthase [Arabidopsis thaliana]	Unigene38024_All//2.00E-173//AT5G37180| SUS5; UDP-glycosyltransferase/ sucrose synthase	Unigene38024_All//0.00E+00//TC143548		ko00500|Starch and sucrose metabolism		nr -
Unigene38028_All	1151	0.68	1.28	2.22	2.73	1.83	2.67	1.95	1.20	1.49	9.05E-01	1.00E-01		1.70E+00	1.20E-04	Up	-5.79E-01	9.02E-02		-3.12E-02	9.44E-01		-7.00E-01	6.86E-02		-3.88E-01	3.12E-01		Unigene38028_All//gi|7444442|pir||T02887//2.00E-49//gag/pol polyprotein - maize retrotransposon Hopscotch >gi|531389|gb|AAA57005.1| copia-like retrotransposon Hopscotch polyprotein [Zea mays]	Unigene38028_All//2.00E-37//AT4G23160| protein kinase family protein	Unigene38028_All//0.00E+00//BG446103				nr +
Unigene38029_All	816	15.58	14.72	12.73	18.92	16.63	15.72	19.95	32.17	100.48	-8.23E-02	6.18E-01		-2.92E-01	8.96E-02		-1.87E-01	2.29E-01		-2.68E-01	7.40E-02		6.89E-01	5.78E-13		2.33E+00	2.48E-252	Up	Unigene38029_All//gi|224071573|ref|XP_002303522.1|//7.00E-42//SAUR family protein [Populus trichocarpa] >gi|222840954|gb|EEE78501.1| SAUR family protein [Populus trichocarpa]	Unigene38029_All//3.00E-40//AT4G22620| auxin-responsive family protein	Unigene38029_All//0.00E+00//gi|164280182|gb|ES820156.1|ES820156				nr -
Unigene3803_All	2859	0.07	1.47	0.00	2.82	2.08	5.06	1.80	6.43	15.27	4.33E+00	7.05E-19	Up	-6.19E+00	1.46E-01		-4.38E-01	2.74E-02		8.41E-01	7.20E-09		1.83E+00	2.77E-41	Up	3.08E+00	2.04E-182	Up	Unigene3803_All//gi|109676362|gb|AB637663.1|//0.00E+00//CCHC-type integrase [Populus trichocarpa]	Unigene3803_All//5.00E-141//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene3803_All//0.00E+00//TC169127		ko04626|Plant-pathogen interaction		nr +
Unigene38032_All	1267	0.04	0.08	0.00	24.61	21.61	19.39	6.47	2.74	2.17	9.54E-01	7.26E-01		-5.37E+00	6.23E-01		-1.88E-01	6.06E-02		-3.44E-01	3.04E-04		-1.24E+00	5.62E-11	Down	-1.58E+00	6.45E-16	Down	Unigene38032_All//gi|224130664|ref|XP_002320897.1|//1.00E-154//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222861670|gb|EEE99212.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene38032_All//6.00E-106//AT2G46770| EMB2301 (EMBRYO DEFECTIVE 2301); transcription activator/ transcription factor	Unigene38032_All//0.00E+00//TC164045	NAC			nr -
Unigene38034_All	1162	0.18	2.09	0.92	3.09	5.04	22.43	14.45	20.14	90.44	3.54E+00	1.12E-09	Up	2.35E+00	3.61E-03		7.07E-01	2.71E-03		2.86E+00	1.10E-86	Up	4.80E-01	1.82E-06		2.65E+00	0.00E+00	Up	Unigene38034_All//gi|224061332|ref|XP_002300430.1|//1.00E-140//gibberellin 2-oxidase [Populus trichocarpa] >gi|222847688|gb|EEE85235.1| gibberellin 2-oxidase [Populus trichocarpa]	Unigene38034_All//1.00E-106//AT1G78440| ATGA2OX1 (gibberellin 2-oxidase 1); gibberellin 2-beta-dioxygenase	Unigene38034_All//0.00E+00//TC143881		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene38035_All	2365	0.60	1.65	1.28	1.92	2.23	3.44	5.35	4.81	7.21	1.47E+00	7.94E-06	Up	1.10E+00	3.53E-03		2.17E-01	4.72E-01		8.43E-01	2.67E-05		-1.53E-01	3.56E-01		4.32E-01	2.31E-04					Unigene38035_All//0.00E+00//CO087208				
Unigene38037_All	1542	9.87	11.17	15.47	7.33	7.39	6.85	3.13	2.36	0.57	1.78E-01	2.19E-01		6.48E-01	1.87E-08		1.15E-02	9.58E-01		-9.76E-02	6.22E-01		-4.07E-01	1.09E-01		-2.46E+00	9.70E-17	Down	Unigene38037_All//gi|224068707|ref|XP_002302805.1|//2.00E-97//outward rectifying potassium channel [Populus trichocarpa] >gi|222844531|gb|EEE82078.1| outward rectifying potassium channel [Populus trichocarpa]	Unigene38037_All//5.00E-72//AT4G01840| KCO5 (CA2+ ACTIVATED OUTWARD RECTIFYING K+ CHANNEL 5); outward rectifier potassium channel	Unigene38037_All//0.00E+00//TC159727				nr -
Unigene38040_All	705	12.02	25.95	24.70	17.74	22.76	24.86	41.56	51.58	33.06	1.11E+00	3.55E-16	Up	1.04E+00	2.03E-13	Up	3.60E-01	8.24E-03		4.87E-01	1.82E-04		3.12E-01	9.50E-05		-3.30E-01	1.60E-04		Unigene38040_All//gi|18404804|ref|NP_566789.1|//2.00E-31//regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana]	Unigene38040_All//1.00E-32//AT3G26100| regulator of chromosome condensation (RCC1) family protein	Unigene38040_All//0.00E+00//gi|73852453|gb|DT461473.1|DT461473				nr -
Unigene38041_All	1696	1.05	0.00	0.06	3.58	1.22	1.68	46.92	123.00	45.17	-1.00E+01	2.68E-10	Down	-4.06E+00	1.42E-07	Down	-1.56E+00	2.83E-11	Down	-1.09E+00	4.38E-06	Down	1.39E+00	0.00E+00	Up	-5.47E-02	3.70E-01		Unigene38041_All//gi|224101641|ref|XP_002314260.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222870199|gb|EEF07330.1| cytochrome P450 [Populus trichocarpa]	Unigene38041_All//1.00E-159//AT1G61950| CYP89A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene38041_All//4.00E-66//TC153079		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene38042_All	1275	4.14	1.71	2.80	5.08	5.35	4.96	8.22	6.26	28.62	-1.28E+00	2.25E-06	Down	-5.67E-01	3.83E-02		7.43E-02	8.17E-01		-3.45E-02	9.07E-01		-3.93E-01	1.38E-02		1.80E+00	9.91E-81	Up	Unigene38042_All//gi|225453303|ref|XP_002268524.1|//1.00E-152//PREDICTED: similar to LOL3 (LSD ONE LIKE 3); caspase/ cysteine-type endopeptidase [Vitis vinifera]	Unigene38042_All//1.00E-123//AT1G02170| AMC1 (METACASPASE 1); cysteine-type endopeptidase	Unigene38042_All//0.00E+00//TC141447				nr +
Unigene38043_All	1380	9.71	8.22	12.93	8.27	7.39	5.99	5.76	1.79	2.31	-2.39E-01	1.38E-01		4.13E-01	2.55E-03		-1.62E-01	3.98E-01		-4.65E-01	5.47E-03		-1.69E+00	2.08E-16	Down	-1.32E+00	5.12E-12	Down	Unigene38043_All//gi|18397077|ref|NP_564328.1|//9.00E-51//COR414-TM1 [Arabidopsis thaliana]	Unigene38043_All//1.00E-49//AT1G29395| COR414-TM1	Unigene38043_All//0.00E+00//TC129953				nr -
Unigene38044_All	890	2.18	3.99	2.15	38.51	41.25	33.04	5.42	3.38	2.33	8.74E-01	7.74E-03		-1.41E-02	9.99E-01		9.91E-02	3.42E-01		-2.21E-01	2.06E-02		-6.80E-01	5.34E-03		-1.22E+00	7.55E-07	Down	Unigene38044_All//gi|10798750|dbj|BAB16427.1|//7.00E-55//NtE1G-E80 [Nicotiana tabacum]	Unigene38044_All//8.00E-48//AT3G54040| photoassimilate-responsive protein-related	Unigene38044_All//0.00E+00//TC158097				nr +
Unigene38045_All	1125	27.53	20.81	28.31	89.71	88.92	73.43	31.16	11.55	12.61	-4.04E-01	2.98E-05		3.99E-02	7.18E-01		-1.28E-02	8.41E-01		-2.89E-01	6.10E-09		-1.43E+00	6.40E-55	Down	-1.31E+00	3.12E-49	Down	Unigene38045_All//gi|34395875|sp|Q84MC0.1|GP14_ARATH//2.00E-65//RecName: Full=Uncharacterized GPI-anchored protein At3g06035; Flags: Precursor >gi|30102608|gb|AAP21222.1| At3g06035 [Arabidopsis thaliana]	Unigene38045_All//6.00E-64//AT3G06035| unknown protein	Unigene38045_All//0.00E+00//gi|109870746|gb|DW499722.1|DW499722				nr +
Unigene38046_All	1171	6.39	4.41	3.64	16.51	14.17	12.80	8.59	1.64	1.87	-5.34E-01	1.24E-02		-8.13E-01	2.53E-04		-2.20E-01	9.20E-02		-3.66E-01	3.47E-03		-2.39E+00	6.46E-32	Down	-2.20E+00	6.88E-30	Down	Unigene38046_All//gi|5912543|emb|CAB56195.1|//1.00E-121//Knolle [Capsicum annuum]	Unigene38046_All//2.00E-110//AT1G68560| SYP111 (SYNTAXIN OF PLANTS 111); SNAP receptor	Unigene38046_All//0.00E+00//TC153710		ko04130|SNARE interactions in vesicular transport		nr -
Unigene38048_All	2215	0.19	0.78	0.31	6.52	7.77	8.07	8.27	2.62	4.08	2.04E+00	2.81E-04	Up	7.26E-01	3.96E-01		2.53E-01	6.84E-02		3.08E-01	2.24E-02		-1.66E+00	8.28E-36	Down	-1.02E+00	7.83E-18	Down	Unigene38048_All//gi|297800138|ref|XP_002867953.1|//0.00E+00//early-responsive to dehydration 3 [Arabidopsis lyrata subsp. lyrata] >gi|297313789|gb|EFH44212.1| early-responsive to dehydration 3 [Arabidopsis lyrata subsp. lyrata]	Unigene38048_All//0.00E+00//AT4G19120| EDS3 (early-responsive to dehydration 3)	Unigene38048_All//0.00E+00//TC140614				nr -
Unigene38049_All	990	0.48	0.31	0.22	5.08	5.60	4.52	39.38	99.55	48.65	-6.31E-01	5.54E-01		-1.14E+00	3.32E-01		1.40E-01	6.28E-01		-1.70E-01	6.00E-01		1.34E+00	4.59E-138	Up	3.05E-01	5.11E-06		Unigene38049_All//gi|152221222|ref|NP_172287.1|//4.00E-94//ACA7 (ALPHA CARBONIC ANHYDRASE 7); carbonate dehydratase/ zinc ion binding [Arabidopsis thaliana]	Unigene38049_All//2.00E-95//AT1G08080| ACA7 (ALPHA CARBONIC ANHYDRASE 7); carbonate dehydratase/ zinc ion binding	Unigene38049_All//0.00E+00//TC179117		ko00910|Nitrogen metabolism		nr +
Unigene38050_All	1602	0.95	0.25	0.93	19.71	16.40	12.97	4.94	1.90	2.29	-1.90E+00	1.25E-03		-2.52E-02	9.84E-01		-2.66E-01	4.37E-03		-6.04E-01	7.84E-11		-1.37E+00	2.88E-12	Down	-1.11E+00	2.59E-09	Down	Unigene38050_All//gi|20197242|gb|AC28772.2|//1.00E-140//expressed protein [Arabidopsis thaliana]	Unigene38050_All//7.00E-142//AT2G38320| unknown protein					nr +
Unigene38053_All	1062	3.65	2.43	4.16	5.82	5.06	3.57	6.81	0.31	2.06	-5.83E-01	6.13E-02		1.91E-01	5.57E-01		-2.01E-01	4.56E-01		-7.03E-01	2.67E-03		-4.43E+00	2.28E-40	Down	-1.72E+00	6.53E-16	Down	Unigene38053_All//gi|3695061|gb|AAC62625.1|//1.00E-102//rac GTPase activating protein 2 [Lotus japonicus]	Unigene38053_All//1.00E-82//AT2G46710| rac GTPase activating protein, putative	Unigene38053_All//0.00E+00//TC160147				nr -
Unigene38054_All	1603	20.69	7.21	9.10	14.76	10.01	7.55	47.87	11.99	12.85	-1.52E+00	1.30E-46	Down	-1.18E+00	9.08E-31	Down	-5.60E-01	4.78E-08		-9.67E-01	6.24E-18		-2.00E+00	4.35E-191	Down	-1.90E+00	7.96E-184	Down	Unigene38054_All//gi|115466160|ref|NP_001056679.1|//1.00E-119//Os06g0129200 [Oryza sativa Japonica Group] >gi|113594719|dbj|BAF18593.1| Os06g0129200 [Oryza sativa Japonica Group]	Unigene38054_All//7.00E-94//AT3G05675| protein binding	Unigene38054_All//0.00E+00//TC150434				nr +
Unigene38055_All	1037	12.21	18.76	24.49	7.35	4.52	4.53	0.49	0.93	0.54	6.20E-01	7.24E-07		1.00E+00	2.75E-18	Up	-7.03E-01	3.29E-04		-6.98E-01	7.35E-04		9.22E-01	1.49E-01		1.36E-01	8.76E-01		Unigene38055_All//gi|18420047|ref|NP_568381.1|//1.00E-115//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]	Unigene38055_All//2.00E-116//AT5G19850| hydrolase, alpha/beta fold family protein					nr +
Unigene38057_All	1552	1.96	1.21	2.33	3.63	4.22	4.04	2.62	1.00	0.56	-6.95E-01	5.15E-02		2.55E-01	4.64E-01		2.17E-01	4.15E-01		1.57E-01	5.86E-01		-1.39E+00	8.53E-07	Down	-2.21E+00	1.30E-12	Down	Unigene38057_All//gi|15221480|ref|NP_172132.1|//2.00E-78//ubiquitin thiolesterase [Arabidopsis thaliana] >gi|6692684|gb|AAF24818.1|AC007592_11 F12K11.21 [Arabidopsis thaliana] >gi|52627099|gb|AAU84676.1| At1g06440 [Arabidopsis thaliana] >gi|60543349|gb|AAX22272.1| At1g06440 [Arabidopsis thaliana]	Unigene38057_All//1.00E-73//AT1G06440| ubiquitin thiolesterase					nr +

Unigene38058_All	1726	4.61	3.46	2.84	12.38	11.71	14.50	4.83	9.69	3.53	-4.12E-01	4.85E-02		-6.99E-01	1.09E-03		-8.03E-02	5.88E-01		2.28E-01	4.83E-02		1.01E+00	1.53E-15	Up	-4.51E-01	9.82E-03		Unigene38058_All//gi|115439195|ref|NP_001043877.1|//1.00E-76//Os01g0681000 [Oryza sativa Japonica Group] >gi|113533408|dbj|BAF05791.1|Os01g0681000 [Oryza sativa Japonica Group]	Unigene38058_All//1.00E-72//AT5G53390| unknown protein	Unigene38058_All//0.00E+00//gi|78324726|gb|DT545000.1|DT545000				nr +
Unigene38059_All	690	0.30	3.97	1.08	3.18	7.04	12.76	4.72	11.63	9.24	3.71E+00	3.29E-11	Up	1.83E+00	5.05E-02		1.15E+00	1.48E-05	Up	2.01E+00	1.29E-19	Up	1.30E+00	1.70E-11	Up	9.69E-01	2.74E-06		Unigene38059_All//gi|224054404|ref|XP_002298243.1|//1.00E-64//histidine phosphotransfer protein [Populus trichocarpa] >gi|222845501|gb|EEE83048.1|histidine phosphotransfer protein [Populus trichocarpa]	Unigene38059_All//6.00E-49//AT3G16360| AHP4 (HPT PHOSPHOTRANSMITTER 4); histidine phosphotransfer kinase/ transferase, transferring phosphorus-containing groups					nr +
Unigene38060_All	819	28.24	5.69	11.38	41.24	22.41	7.39	21.53	13.93	10.31	-2.31E+00	4.45E-57	Down	-1.31E+00	3.17E-25	Down	-8.80E-01	1.81E-24		-2.48E+00	1.73E-98	Down	-6.28E-01	9.67E-08		-1.06E+00	2.18E-18	Down	Unigene38060_All//gi|124360549|gb|ABD33126.2|//7.00E-29//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene38060_All//3.00E-18//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene38060_All//0.00E+00//TC171513				nr +
Unigene38061_All	738	25.31	247.99	13.64	11.07	29.16	25.21	31.62	150.93	114.44	3.29E+00	0.00E+00	Up	-8.92E-01	2.93E-11		1.40E+00	3.29E-31	Up	1.19E+00	2.17E-19	Up	2.25E+00	0.00E+00	Up	1.86E+00	7.10E-194	Up	Unigene38061_All//gi|255572081|ref|XP_002526981.1|//3.00E-06//ctp synthase, putative [Ricinus communis] >gi|223533672|gb|EEF35408.1| ctp synthase, putative [Ricinus communis]		Unigene38061_All//0.00E+00//gi|73861862|gb|DT464601.1|DT464601				nr -
Unigene38062_All	1099	9.52	22.78	20.50	21.35	36.82	40.44	5.31	6.92	9.50	1.26E+00	1.64E-26	Up	1.11E+00	5.83E-19	Up	7.86E-01	2.56E-23		9.22E-01	2.49E-30		3.83E-01	4.83E-02		8.39E-01	7.82E-08		Unigene38062_All//gi|117958758|gb|ABK59684.1|//4.00E-13//At4g32030 [Arabidopsis thaliana]	Unigene38062_All//5.00E-07//AT4G32030| unknown protein	Unigene38062_All//0.00E+00//gi|109828702|gb|DW227321.1|DW227321				nr -
Unigene38063_All	1239	8.87	38.48	15.73	1.21	1.70	8.24	0.07	0.03	1.03	2.12E+00	2.64E-104	Up	8.27E-01	2.12E-10		4.91E-01	3.07E-01		2.77E+00	5.13E-33	Up	-1.02E+00	7.24E-01		3.92E+00	4.24E-07	Up	Unigene38063_All//gi|15226724|ref|NP_179223.1|//1.00E-164//KCS9 (3-KETOACYL-COA SYNTHASE 9); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups [Arabidopsis thaliana] >gi|752061887|sp|Q9SX11.1|KCS9_ARATH RecName: Full=3-ketoacyl-CoA synthase 9; Short=KCS-9; AltName: Full=Very long-chain fatty acid condensing enzyme 9; Short=VLCFA condensing enzyme 9	Unigene38063_All//3.00E-161//AT2G16280| KCS9 (3-KETOACYL-COA SYNTHASE 9); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene38063_All//0.00E+00//TC157876				nr +
Unigene38065_All	1246	4.33	11.87	7.86	1.00	0.80	0.76	3.73	4.80	1.82	1.46E+00	8.58E-20	Up	8.63E-01	6.16E-06		-3.19E-01	6.08E-01		-3.93E-01	5.49E-01		3.62E-01	1.09E-01		-1.03E+00	2.62E-05	Down	Unigene38065_All//gi|3550661|emb|CAA04670.1|//1.00E-113//39 kDa EF-Hand containing protein [Solanum tuberosum]	Unigene38065_All//8.00E-101//AT4G38810| calcium-binding EF hand family protein	Unigene38065_All//0.00E+00//gi|84151237|gb|DN800592.1|DN800592				nr +
Unigene38066_All	567	101.69	50.04	24.42	63.52	80.90	43.81	65.92	29.85	26.56	-1.02E+00	1.58E-43	Down	-2.06E+00	2.82E-118	Down	3.49E-01	1.79E-06		-5.36E-01	5.32E-10		-1.14E+00	1.87E-41	Down	-1.31E+00	8.09E-53	Down	Unigene38066_All//gi|15232146|ref|NP_189372.1|//7.00E-70//histone H3 [Arabidopsis thaliana] >gi|15238433|ref|NP_201339.1|histone H3 [Arabidopsis thaliana] >gi|18390992|ref|NP_563838.1|histone H3 [Arabidopsis thaliana] >gi|18416261|ref|NP_568227.1|histone H3 [Arabidopsis thaliana] >gi|18416264|ref|NP_568228.1|histone H3 [Arabidopsis thaliana] >gi|115441249|ref|NP_001044904.1|Os01g0866200 [Oryza sativa Japonica Group] >gi|115458352|ref|NP_001052776.1|Os04g0419600 [Oryza sativa Japonica Group] >gi|115464121|ref|NP_001055660.1|Os05g0438700 [Oryza sativa Japonica Group] >gi|115466556|ref|NP_001056877.1|Os06g0160100 [Oryza sativa Japonica Group] >gi|115484259|ref|NP_001065791.1|Os11g0155900 [Oryza sativa Japonica Group] >gi|212721652|ref|NP_001131276.1|histone H3.2 [Zea mays] >gi|297724495|ref|NP_001174611.1|Os06g0159501 [Oryza sativa	Unigene38066_All//2.00E-55//AT5G65360| histone H3	Unigene38066_All//0.00E+00//gi|73846661|gb|DT455681.1|DT455681				nr +
Unigene38067_All	795	8.49	5.99	1.81	4.51	5.33	2.84	22.44	3.42	3.91	-5.03E-01	2.66E-02		-2.23E+00	1.14E-15	Down	2.40E-01	4.83E-01		-6.68E-01	4.07E-02		-2.72E+00	8.26E-65	Down	-2.52E+00	1.30E-61	Down	Unigene38067_All//gi|15232146|ref|NP_189372.1|//1.00E-69//histone H3 [Arabidopsis thaliana] >gi|15238433|ref|NP_201339.1|histone H3 [Arabidopsis thaliana] >gi|18390992|ref|NP_563838.1|histone H3 [Arabidopsis thaliana] >gi|18416261|ref|NP_568227.1|histone H3 [Arabidopsis thaliana] >gi|18416264|ref|NP_568228.1|histone H3 [Arabidopsis thaliana] >gi|115441249|ref|NP_001044904.1|Os01g0866200 [Oryza sativa Japonica Group] >gi|115458352|ref|NP_001052776.1|Os04g0419600 [Oryza sativa Japonica Group] >gi|115464121|ref|NP_001055660.1|Os05g0438700 [Oryza sativa Japonica Group] >gi|115466556|ref|NP_001056877.1|Os06g0160100 [Oryza sativa Japonica Group] >gi|115484259|ref|NP_001065791.1|Os11g0155900 [Oryza sativa Japonica Group] >gi|212721652|ref|NP_001131276.1|histone H3.2 [Zea mays] >gi|297724495|ref|NP_001174611.1|Os06g0159501 [Oryza sativa	Unigene38067_All//3.00E-60//AT5G65360| histone H3	Unigene38067_All//0.00E+00//TC152201				nr +
Unigene38069_All	909	0.00	0.00	0.00	0.00	0.00	0.00	3.12	5.98	0.96	null	null		null	null		null	null		null	null		9.40E-01	4.33E-05		-1.69E+00	1.33E-06	Down	Unigene38069_All//gi|115465379|ref|NP_001056289.1|//6.00E-67//Os05g0557500 [Oryza sativa Japonica Group] >gi|113578640|dbj|BAF18203.1|Os05g0557500 [Oryza sativa Japonica Group]	Unigene38069_All//8.00E-67//AT4G21700| unknown protein	Unigene38069_All//0.00E+00//CO096440				nr -
Unigene38070_All	3015	0.00	0.00	0.00	0.00	0.00	0.00	3.14	6.10	1.29	null	null		null	null		null	null		null	null		9.57E-01	9.26E-16		-1.28E+00	1.57E-13	Down	Unigene38070_All//gi|115439151|ref|NP_001043855.1|//6.00E-73//Os01g0678000 [Oryza sativa Japonica Group] >gi|113533386|dbj|BAF05769.1|Os01g0678000 [Oryza sativa Japonica Group]	Unigene38070_All//6.00E-114//AT4G21700| unknown protein	Unigene38070_All//0.00E+00//CO096440				nr +
Unigene38071_All	693	28.54	8.26	13.37	32.63	15.11	10.88	28.25	1.27	1.84	-1.79E+00	3.48E-35	Down	-1.09E+00	2.13E-16	Down	-1.11E+00	3.05E-24	Down	-1.58E+00	1.16E-36	Down	-4.48E+00	2.51E-109	Down	-3.94E+00	1.81E-103	Down	Unigene38071_All//gi|194708826|gb|ACF88497.1|//2.00E-37//At5g41050 [Arabidopsis thaliana]	Unigene38071_All//4.00E-49//AT5G13140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pollen Ole e 1 allergen and extensin (InterPro:IPR006041); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G26960.1); Has 90 Blast hits to 85 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 5; Fungi - 0; Plants - 83; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene38071_All//0.00E+00//TC148425				nr -
Unigene38072_All	1039	5.24	6.24	4.25	13.23	15.08	11.04	9.24	2.05	3.64	2.53E-01	3.06E-01		-3.00E-01	2.85E-01		1.89E-01	2.27E-01		-2.61E-01	1.08E-01		-2.17E+00	3.35E-27	Down	-1.34E+00	1.05E-14	Down	Unigene38072_All//gi|30678573|ref|NP_171846.2|//2.00E-48//kinase interacting family protein [Arabidopsis thaliana] >gi|79316376|ref|NP_001030943.1|kinase interacting family protein [Arabidopsis thaliana] >gi|51536438|gb|AAU05457.1|At1g03470 [Arabidopsis thaliana] >gi|52421277|gb|AAU45208.1|At1g03470 [Arabidopsis thaliana]	Unigene38072_All//1.00E-44//AT1G03470| kinase interacting family protein	Unigene38072_All//0.00E+00//TC130616				nr +
Unigene38073_All	715	37.25	22.75	18.77	53.79	55.87	63.54	146.65	70.03	75.44	-7.11E-01	2.08E-11		-9.89E-01	1.24E-18		5.48E-02	5.96E-01		2.41E-01	2.57E-03		-1.07E+00	8.38E-103	Down	-9.59E-01	8.33E-89		Unigene38073_All//gi|140072168|gb|ABO84810.1|//6.00E-63//Cytochrome c, monohaem [Medicago truncatula]	Unigene38073_All//6.00E-53//AT5G40810| cytochrome c1, putative	Unigene38073_All//0.00E+00//TC144037		ko00190|Oxidative phosphorylation		nr +

Unigene38074_All	1148	13.44	8.12	10.30	17.44	15.96	24.12	33.59	21.08	13.26	-7.27E-01	3.38E-07		-3.85E-01	1.03E-02		-1.28E-01	3.68E-01		4.67E-01	3.22E-06		-6.72E-01	6.76E-18		-1.34E+00	2.35E-56	Down	Unigene38074_All//gi|38454156|gb|AAR20772.1|//3.00E-65//At5g14440 [Arabidopsis thaliana] >gi|38604030|gb|AAR24758.1| At5g14440 [Arabidopsis thaliana]	Unigene38074_All//4.00E-42//AT5G14440| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Surfeit locus 2 (InterPro:IPR008833); BEST Arabidopsis thaliana protein match is: surfeit locus protein 2 family protein / SURF2 family protein (TAIR:AT5G40570.1); Has 6533 Blast hits to 4299 proteins in 259 species: Archae - 4; Bacteria - 127; Metazoa - 2727; Fungi - 698; Plants - 260; Viruses - 77; Other Eukaryotes - 2640 (source: NCBI BLink).	Unigene38074_All//0.00E+00//TC170790				nr -
Unigene38075_All	1139	17.87	47.11	39.93	8.66	10.25	13.96	0.15	0.07	0.80	1.40E+00	7.58E-66	Up	1.16E+00	1.03E-40	Up	2.43E-01	1.71E-01		6.89E-01	4.66E-07		-1.02E+00	6.14E-01		2.44E+00	1.06E-03		Unigene38075_All//gi|115455069|ref|NP_001051135.1|//9.00E-10//Os03g0726400 [Oryza sativa Japonica Group] >gi|41469273|gb|AAS07155.1| expressed protein [Oryza sativa Japonica Group] >gi|50428733|gb|AAT77084.1| expressed protein [Oryza sativa Japonica Group] >gi|108710851|gb|ABF98646.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549606|dbj|BAF13049.1| Os03g0726400 [Oryza sativa Japonica Group]	Unigene38075_All//1.00E-08//AT2G22795| unknown protein				nr +
Unigene38076_All	1420	1.73	4.82	7.65	0.95	0.75	1.40	0.06	0.00	0.11	1.48E+00	1.02E-09	Up	2.14E+00	7.76E-24	Up	-3.33E-01	5.81E-01		5.63E-01	2.43E-01		-5.89E+00	4.03E-01		9.15E-01	6.24E-01		Unigene38076_All//gi|115455069|ref|NP_001051135.1|//1.00E-09//Os03g0726400 [Oryza sativa Japonica Group] >gi|41469273|gb|AAS07155.1| expressed protein [Oryza sativa Japonica Group] >gi|50428733|gb|AAT77084.1| expressed protein [Oryza sativa Japonica Group] >gi|108710851|gb|ABF98646.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549606|dbj|BAF13049.1| Os03g0726400 [Oryza sativa Japonica Group]	Unigene38076_All//1.00E-08//AT2G22795| unknown protein				nr -
Unigene38079_All	1306	8.69	12.88	6.93	2.14	4.90	4.53	0.10	0.13	1.83	5.67E-01	2.74E-05		-3.27E-01	7.34E-02		1.20E+00	1.19E-07	Up	1.08E+00	8.82E-06	Up	3.99E-01	8.14E-01		4.24E+00	1.75E-13	Up	Unigene38079_All//gi|15228830|ref|NP_191828.1|//2.00E-44//ATL5 (ATL5); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|68565315|sp|Q9LZJ6.1|ATL3L_ARATH RecName: Full=RING-H2 finger protein ATL3L; AltName: Full=RING-H2 finger protein ATL5 >gi|7362749|emb|CAB83119.1| RING-H2 zinc finger protein ATL5 [Arabidopsis thaliana] >gi|32189289|gb|AAP75799.1| At3g62690 [Arabidopsis thaliana] >gi|110736661|dbj|BAF90294.1| RING-H2 zinc finger protein ATL5 [Arabidopsis thaliana]	Unigene38079_All//2.00E-24//AT3G62690| ATL5 (ATL5); protein binding / zinc ion binding	Unigene38079_All//0.00E+00//gi|78325156|gb|DT545430.1|DT545430			nr -
Unigene3808_All	1236	348.00	338.00	448.06	60.70	62.91	38.95	22.13	12.48	10.28	-4.21E-02	1.27E-01		3.65E-01	2.88E-64		5.17E-02	5.05E-01		-6.40E-01	1.57E-27		-8.27E-01	3.43E-18		-1.11E+00	6.72E-30	Down	Unigene3808_All//gi|134142800|gb|ABO61734.1|//1.00E-164//mitochondrial glycine decarboxylase complex P-protein [Populus tremuloides]	Unigene3808_All//9.00E-144//AT4G33010| AtGLDP1 (Arabidopsis thaliana glycine decarboxylase P-protein 1); catalytic/ glycine dehydrogenase (decarboxylating)/ pyridoxal phosphate binding	Unigene3808_All//0.00E+00//TC136190		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene38080_All	1172	3.21	7.95	3.95	4.55	4.14	5.13	16.56	12.98	10.37	1.31E+00	6.23E-11	Up	2.99E-01	3.38E-01		-1.35E-01	6.35E-01		1.72E-01	5.50E-01		-3.51E-01	1.88E-03		-6.76E-01	8.30E-10		Unigene38080_All//gi|297798522|ref|XP_002867145.1|//1.00E-116//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297312981|gb|EFH43404.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene38080_All//3.00E-116//AT4G33910| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene38080_All//0.00E+00//TC171841		ko00330|Arginine and proline metabolism		nr -
Unigene38081_All	1031	2.59	21.23	4.65	5.85	6.91	8.50	4.39	13.99	11.13	3.04E+00	2.54E-72	Up	8.45E-01	3.20E-03		2.42E-01	3.13E-01		5.40E-01	5.54E-03		1.67E+00	1.08E-28	Up	1.34E+00	2.98E-17	Up	Unigene38081_All//gi|297843106|ref|XP_002889434.1|//1.00E-111//glutamate binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297335276|gb|EFH65693.1| glutamate binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene38081_All//1.00E-95//AT1G03070| glutamate binding	Unigene38081_All//0.00E+00//gi|5048552|gb|AT729700.1|AT729700				nr -
Unigene38082_All	1060	0.39	2.34	0.90	0.80	0.84	1.15	0.88	1.97	1.09	2.57E+00	1.98E-07	Up	1.20E+00	1.15E-01		8.03E-02	9.41E-01		5.26E-01	4.24E-01		1.17E+00	3.80E-03		3.13E-01	5.99E-01		Unigene38082_All//gi|297843106|ref|XP_002889434.1|//1.00E-107//glutamate binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297335276|gb|EFH65693.1| glutamate binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene38082_All//1.00E-91//AT1G03070| glutamate binding	Unigene38082_All//0.00E+00//gi|5048552|gb|AT729700.1|AT729700				nr -
Unigene38084_All	805	2.21	5.22	6.68	4.33	5.48	6.73	1.68	1.40	3.51	1.24E+00	5.11E-05	Up	1.60E+00	2.68E-08	Up	3.38E-01	2.85E-01		6.36E-01	1.32E-02		-2.62E-01	6.63E-01		1.06E+00	1.15E-03				Unigene38084_All//0.00E+00//gi|73863784|gb|DT466523.1|DT466523				
Unigene38086_All	1060	1.18	4.45	2.21	5.78	4.61	4.90	1.56	3.00	6.31	1.91E+00	1.31E-09	Up	9.00E-01	3.97E-02		-3.25E-01	1.88E-01		-2.38E-01	3.86E-01		9.46E-01	2.44E-03		2.02E+00	6.23E-18	Up	Unigene38086_All//gi|2346972|dbj|BAA21920.1|//6.00E-50//ZPT2-11 [Petunia x hybrida]	Unigene38086_All//1.00E-35//AT2G28200| nucleic acid binding / transcription factor/ zinc ion binding	Unigene38086_All//0.00E+00//gi|109872792|gb|DW501767.1|DW501767	C2H2			nr +
Unigene38088_All	845	2.48	2.40	0.76	2.30	2.85	3.05	1.55	1.14	56.34	-4.62E-02	9.26E-01		-1.71E+00	6.07E-04	Down	3.11E-01	5.14E-01		4.06E-01	3.46E-01		-4.47E-01	4.05E-01		5.18E+00	2.65E-291	Up	Unigene38088_All//gi|224137172|ref|XP_002327054.1|//7.00E-51//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222835369|gb|EEE73804.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene38088_All//1.00E-44//AT2G44840| ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	Unigene38088_All//1.00E-114//ES851528	AP2-EREBP			nr +
Unigene38092_All	828	5.18	3.12	6.17	3.91	1.87	2.78	0.71	0.35	1.25	-7.31E-01	1.24E-02		2.53E-01	3.85E-01		-1.06E+00	9.98E-04	Down	-4.91E-01	1.72E-01		-1.02E+00	2.40E-01		8.07E-01	1.68E-01		Unigene38092_All//gi|297821086|ref|XP_002878426.1|//5.00E-64//O-methyltransferase family 3 protein [Arabidopsis lyrata subsp. lyrata] >gi|297324264|gb|EFH54685.1| O-methyltransferase family 3 protein [Arabidopsis lyrata subsp. lyrata]	Unigene38092_All//1.00E-64//AT3G62000| O-methyltransferase family 3 protein	Unigene38092_All//0.00E+00//TC139901		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene38097_All	1301	19.22	16.12	6.63	23.20	19.32	8.40	13.00	16.19	9.65	-2.54E-01	2.44E-02		-1.54E+00	2.00E-34	Down	-2.64E-01	5.80E-03		-1.47E+00	1.61E-43	Down	3.17E-01	3.56E-03		-4.31E-01	2.48E-04		Unigene38097_All//gi|82734195|emb|CAJ44131.1|//4.00E-19//fimbriata protein [Misopates orontium]	Unigene38097_All//1.00E-17//AT1G30950| UFO (UNUSUAL FLORAL ORGANS); transcription factor binding / ubiquitin-protein ligase	Unigene38097_All//0.00E+00//gi|78326249|gb|DT546523.1|DT546523				nr -
Unigene38098_All	799	5.83	5.01	8.20	10.16	8.53	5.37	10.95	5.86	3.64	-2.18E-01	4.55E-01		4.92E-01	4.31E-02		-2.52E-01	2.48E-01		-9.20E-01	4.20E-06		-9.03E-01	2.87E-07		-1.59E+00	4.15E-17	Down			Unigene38098_All//0.00E+00//gi|21101628|gb|BQ413953.1|BQ413953				
Unigene38099_All	1826	1.63	1.17	0.58	12.41	10.28	5.42	7.62	2.33	10.73	-4.87E-01	1.84E-01		-1.49E+00	1.77E-04	Down	-2.72E-01	1.65E-02		-1.20E+00	4.24E-24	Down	-1.71E+00	1.52E-28	Down	4.95E-01	5.11E-06		Unigene38099_All//gi|19911587|dbj|BAB86897.1|//0.00E+00//syringolide-induced protein B13-1-1 [Glycine max]	Unigene38099_All//0.00E+00//AT4G39830| L-ascorbate oxidase, putative	Unigene38099_All//0.00E+00//TC140875		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene38100_All	1642	0.83	2.01	0.13	1.94	1.09	30.17	36.74	9.93	24.19	1.28E+00	3.03E-04	Up	-2.68E+00	2.60E-04	Down	-8.32E-01	1.12E-02		3.96E+00	4.29E-220	Up	-1.89E+00	1.53E-139	Down	-6.03E-01	1.61E-23		Unigene38100_All//gi|190896584|gb|ACE96805.1|//1.00E-151//aspartyl protease [Populus tremula] >gi|190896586|gb|ACE96806.1| aspartyl protease [Populus tremula] >gi|190896588|gb|ACE96807.1| aspartyl protease [Populus tremula] >gi|190896590|gb|ACE96808.1| aspartyl protease [Populus tremula] >gi|190896592|gb|ACE96809.1| aspartyl protease [Populus tremula] >gi|190896594|gb|ACE96810.1| aspartyl protease [Populus tremula] >gi|190896596|gb|ACE96811.1| aspartyl protease [Populus tremula] >gi|190896598|gb|ACE96812.1| aspartyl protease [Populus tremula] >gi|190896600|gb|ACE96813.1| aspartyl protease [Populus tremula] >gi|190896602|gb|ACE96814.1| aspartyl protease [Populus tremula]	Unigene38100_All//5.00E-143//AT1G09750| chloroplast nucleoid DNA-binding protein-related	Unigene38100_All//0.00E+00//gi|78351811|gb|DT572085.1|DT572085				nr -
Unigene38101_All	1345	9.30	6.52	6.30	10.78	11.27	8.83	20.24	6.81	8.74	-5.13E-01	1.32E-03		-5.63E-01	6.82E-04		6.38E-02	7.43E-01		-2.87E-01	6.30E-02		-1.57E+00	3.75E-49	Down	-1.21E+00	2.50E-34	Down	Unigene38101_All//gi|225440994|ref|XP_002283576.1|//0.00E+00//PREDICTED: similar to FK (FACKEL); deltai4-sterol reductase [Vitis vinifera]	Unigene38101_All//3.00E-158//AT3G52940| FK (FACKEL); deltai4-sterol reductase	Unigene38101_All//0.00E+00//DR452531		ko00100|Steroid biosynthesis		nr +

Unigene38102_All	1359	7.51	7.12	5.02	12.83	12.39	9.90	13.53	4.58	5.22	-7.62E-02	6.83E-01		-5.82E-01	1.76E-03		-5.02E-02	7.82E-01		-3.73E-01	4.98E-03		-1.56E+00	3.91E-33	Down	-1.38E+00	2.30E-28	Down	Unigene38102_All//gi|115482338|ref|NP_001064762.1|//3.00E-35//Os10g0457400 (Oryza sativa Japonica Group)>gi|110289183|gb|AAF54098.2| expressed protein (Oryza sativa (japonica cultivar-group))>gi|113639371|dbj|BAF26676.1|Os10g0457400 (Oryza sativa Japonica Group)	Unigene38102_All//6.00E-21//AT5G04320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: meiotic chromosome segregation; LOCATED IN: chromosome, centromeric region, nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Shugoshin, C-terminal (InterPro:IPR011515); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G10440.1); Has 951 Blast hits to 743 proteins in 147 species: Archae - 0; Bacteria - 61; Metazoa - 474; Fungi - 60; Plants - 48; Viruses - 0; Other Eukaryotes - 308 (source: NCBI BLink).	Unigene38102_All//0.00E+00//ES801417				nr +
Unigene38103_All	462	2.60	5.15	3.92	5.39	10.88	6.75	1.83	1.45	2.16	9.85E-01	1.78E-02		5.89E-01	2.42E-01		1.01E+00	8.29E-05	Up	3.23E-01	4.06E-01		-3.39E-01	6.62E-01		2.36E-01	6.82E-01		Unigene38103_All//gi|18396813|ref|NP_564310.1|//1.00E-06//SYP61 (SYNTAXIN OF PLANTS 61); SNAP receptor [Arabidopsis thaliana]>gi|28380156|sp|Q94617.1|SYP61_ARATH RecName: Full=Syntaxin-61; Short=AtSYP61; AltName: Full=Osmotic stress-sensitive mutant 1>gi|16041650|gb|AAK40222.2|AF355754_1 syntaxin of plants 61 [Arabidopsis thaliana]	Unigene38103_All//9.00E-08//AT1G28490| SYP61 (SYNTAXIN OF PLANTS 61); SNAP receptor	Unigene38103_All//6.00E-130//ES836063		ko04130|SNARE interactions in vesicular transport		nr -
Unigene38106_All	1266	25.04	12.81	19.43	35.49	27.31	26.83	11.19	8.95	5.16	-9.68E-01	3.42E-22		-3.66E-01	2.35E-04		-3.78E-01	1.98E-07		-4.04E-01	1.39E-07		-3.23E-01	1.83E-02		-1.12E+00	3.88E-16	Down	Unigene38106_All//gi|297838943|ref|XP_002887353.1|//1.00E-104//6-phosphogluconate dehydrogenase NAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]>gi|297333194|gb|EFH63612.1| 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene38106_All//9.00E-104//AT1G71180| 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein	Unigene38106_All//0.00E+00//TC160374		ko00903|Limonene and pinene degradation//ko00280|Valine, leucine and isoleucine degradation		nr -
Unigene38107_All	699	47.16	67.05	94.77	51.31	60.30	44.45	47.18	45.26	27.41	5.08E-01	5.44E-11		1.01E+00	4.63E-47	Up	2.33E-01	3.90E-03		-2.07E-01	2.75E-02		-5.98E-02	5.84E-01		-7.83E-01	1.69E-20					Unigene38107_All//5.00E-147//TC164314				
Unigene38108_All	1483	5.64	10.08	8.47	10.45	10.45	7.83	2.68	3.72	6.26	8.36E-01	1.18E-08		5.86E-01	3.78E-04		3.00E-04	9.98E-01		-4.17E-01	3.12E-03		4.73E-01	3.98E-02		1.22E+00	2.37E-12	Up	Unigene38108_All//gi|18412918|ref|NP_565249.1|//1.00E-130//phospholipid/glycerol acyltransferase family protein [Arabidopsis thaliana]	Unigene38108_All//4.00E-114//AT1G68950| phospholipid/glycerol acyltransferase family protein	Unigene38108_All//0.00E+00//gi|78323659|gb|DT543933.1|DT543933		ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr -
Unigene38109_All	1059	76.18	45.21	72.86	40.92	42.40	34.25	20.36	6.55	5.15	-7.53E-01	2.52E-36		-6.43E-02	3.76E-01		5.12E-02	6.00E-01		-2.57E-01	1.53E-03		-1.64E+00	2.48E-41	Down	-1.98E+00	2.66E-55	Down	Unigene38109_All//gi|38603876|gb|AAR24683.1|//7.00E-70//At2g31670 [Arabidopsis thaliana]>gi|38638692|gb|AAR25640.1|At2g31670 [Arabidopsis thaliana]	Unigene38109_All//3.00E-56//AT2G31670| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: peroxisome, chloroplast stroma, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 16 growth stages; CONTAINS InterPro DOMAIN/s: Stress responsive alpha-beta barrel (InterPro:IPR013097), Dimeric alpha-beta barrel (InterPro:IPR011008); BEST Arabidopsis thaliana protein match is: DABB1 (DIMERIC A/B BARREL DOMAINS-PROTEIN 1) (TAIR:AT1G51360.1); Has 138 Blast hits to 135 proteins in 38 species: Archae - 0; Bacteria - 51; Metazoa - 0; Fungi - 4; Plants - 74; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene38109_All//0.00E+00//TC166230				nr +
Unigene38110_All	925	4.92	2.47	1.73	4.25	3.05	2.39	1.69	0.27	0.34	-9.97E-01	4.82E-04		-1.51E+00	1.33E-06	Down	-4.79E-01	1.16E-01		-8.31E-01	6.42E-03		-2.64E+00	4.08E-06	Down	-2.30E+00	1.48E-05	Down	Unigene38110_All//gi|238481201|ref|NP_001154694.1|//2.00E-70//nucleobase:cation symporter [Arabidopsis thaliana]	Unigene38110_All//1.00E-71//AT5G03560| nucleobase:cation symporter					nr +
Unigene38111_All	691	72.08	64.09	70.82	57.38	38.22	27.71	168.94	117.28	86.48	-1.70E-01	3.21E-02		-2.55E-02	7.75E-01		-5.86E-01	3.26E-14		-1.05E+00	6.23E-34	Down	-5.27E-01	3.55E-34		-9.66E-01	5.43E-100		Unigene38111_All//gi|182702251|sp|A0ZZ93.1|YCF1_GOSBA//4.00E-67//RecName: Full=Putative membrane protein ycf1>gi|119224919|dbj|BAF41305.1|Hypothetical protein [Gossypium barbadense]	Unigene38111_All//1.00E-33//ATCG01130| hypothetical protein	Unigene38111_All//0.00E+00//TC130435				nr +
Unigene38112_All	1551	19.33	34.76	13.32	27.33	21.76	24.61	139.49	501.12	288.71	8.47E-01	9.20E-30		-5.37E-01	1.18E-07		-3.29E-01	1.50E-05		-1.52E-01	9.12E-02		1.85E+00	0.00E+00	Up	1.05E+00	0.00E+00	Up	Unigene38112_All//gi|15229901|ref|NP_190005.1|//1.00E-136//pyridine nucleotide-disulphide oxidoreductase family protein [Arabidopsis thaliana]>gi|30725576|gb|AAP37810.1|At3g44190 [Arabidopsis thaliana]	Unigene38112_All//3.00E-132//AT3G44190| pyridine nucleotide-disulphide oxidoreductase family protein	Unigene38112_All//0.00E+00//TC162424		ko00190|Oxidative phosphorylation		nr +
Unigene38113_All	698	3.00	3.85	3.74	2.07	2.12	1.94	1.70	5.33	2.00	3.60E-01	3.75E-01		3.18E-01	4.37E-01		3.57E-02	9.64E-01		-9.25E-02	8.76E-01		1.65E+00	7.69E-08	Up	2.36E-01	6.46E-01		Unigene38113_All//gi|297835372|ref|XP_002885568.1|//2.00E-87//mate efflux family protein [Arabidopsis lyrata subsp. lyrata]>gi|297331408|gb|EFH61827.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38113_All//1.00E-78//AT3G23550| MATE efflux family protein	Unigene38113_All//0.00E+00//TC173391				nr -
Unigene38115_All	830	123.24	84.06	85.91	188.87	164.38	230.99	185.83	96.18	84.67	-5.52E-01	9.77E-27		-5.21E-01	3.20E-23		-2.00E-01	1.08E-07		2.90E-01	1.68E-16		-9.50E-01	7.81E-125		-1.13E+00	2.61E-171	Down	Unigene38115_All//gi|46397044|sp|Q9M5L0.1|RL35_EUPES//1.00E-57//RecName: Full=60S ribosomal protein L35>gi|6984224|gb|AAF34800.1|AF227980_1 60S ribosomal protein L35 [Euphorbia esula]	Unigene38115_All//9.00E-56//AT5G02610| 60S ribosomal protein L35 (RPL35D)	Unigene38115_All//0.00E+00//TC155272		ko03010|Ribosome		nr -
Unigene38117_All	1322	0.32	0.42	0.56	55.84	33.47	22.34	5.21	1.74	3.95	4.13E-01	6.37E-01		8.33E-01	3.39E-01		-7.38E-01	3.03E-39		-1.32E+00	2.02E-90	Down	-1.58E+00	3.80E-13	Down	-4.01E-01	4.05E-02		Unigene38117_All//gi|1167486|emb|CAA64615.1|//3.00E-94//transcription factor [Solanum lycopersicum]	Unigene38117_All//5.00E-83//AT1G63910| AtMYB103 (myb domain protein 103); DNA binding / transcription activator/ transcription factor	Unigene38117_All//5.00E-164//gi|54115907|gb|CO491416.1|CO491416	MYB			nr -
Unigene38118_All	817	7.62	7.57	7.23	27.93	18.17	12.22	4.66	2.40	2.39	-1.04E-02	9.85E-01		-7.50E-02	7.68E-01		-6.20E-01	3.09E-09		-1.19E+00	3.86E-24	Down	-9.54E-01	6.88E-04		-9.63E-01	4.22E-04		Unigene38118_All//gi|76262500|gb|AB441400.1|//4.00E-19//pherophorin-C2 protein precursor [Chlamydomonas reinhardtii]		Unigene38118_All//0.00E+00//TC160030		ko03040|Spliceosome		nr -
Unigene3812_All	1235	71.81	49.60	83.69	13.59	12.55	7.79	2.70	1.46	0.74	-5.34E-01	5.82E-22		2.21E-01	2.99E-05		-1.16E-01	4.77E-01		-8.03E-01	1.40E-09		-8.94E-01	3.09E-03		-1.87E+00	1.30E-08	Down	Unigene3812_All//gi|18398129|ref|NP_566327.1|//1.00E-121//ATAB2; RNA binding [Arabidopsis thaliana]	Unigene3812_All//3.00E-112//AT3G08010| ATAB2; RNA binding	Unigene3812_All//0.00E+00//TC131257				nr +
Unigene38120_All	809	1.68	3.95	1.45	1.97	2.43	1.95	4.81	2.69	2.56	1.23E+00	5.85E-04	Up	-2.16E-01	7.04E-01		3.00E-01	5.69E-01		-1.21E-02	9.73E-01		-8.40E-01	2.37E-03		-9.09E-01	7.17E-04					Unigene38120_All//0.00E+00//AW186870				
Unigene38122_All	976	10.72	4.78	6.93	16.23	12.91	17.82	42.54	16.06	21.10	-1.17E+00	2.31E-10	Down	-6.30E-01	5.82E-04		-3.30E-01	1.60E-02		1.34E-01	3.93E-01		-1.41E+00	3.47E-63	Down	-1.01E+00	6.36E-39	Down	Unigene38122_All//gi|195658145|gb|ACG48540.1|//1.00E-16//60S ribosomal protein L23 [Zea mays]	Unigene38122_All//5.00E-18//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene38122_All//0.00E+00//TC174626		ko03010|Ribosome		nr -
Unigene38123_All	691	4.77	2.35	5.16	7.71	8.37	4.84	7.53	4.11	2.48	-1.02E+00	2.92E-03		1.14E-01	7.31E-01		1.18E-01	6.97E-01		-6.73E-01	8.58E-03		-8.72E-01	1.99E-04		-1.60E+00	1.27E-10	Down	Unigene38123_All//gi|16197625|gb|AL13436.1|//2.00E-48//anaphase promoting complex subunit 11 [Arabidopsis thaliana]	Unigene38123_All//5.00E-32//AT3G05870| APC11; protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene38123_All//1.00E-42//TC173511		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene38124_All	1136	2.35	1.38	1.41	3.07	3.21	3.18	2.46	0.74	2.77	-7.65E-01	4.65E-02		-7.40E-01	6.77E-02		6.60E-02	8.60E-01		5.12E-02	9.04E-01		-1.74E+00	1.76E-06	Down	1.74E-01	5.94E-01		Unigene38124_All//gi|222422925|dbj|BAH19449.1|//1.00E-126//AT2G27900 [Arabidopsis thaliana]	Unigene38124_All//3.00E-103//AT2G27900| unknown protein	Unigene38124_All//0.00E+00//ES852368				nr +
Unigene38125_All	1513	1.24	0.50	2.15	20.38	7.62	20.75	5.98	12.13	12.82	-1.31E+00	7.13E-03		7.86E-01	2.86E-02		-1.42E+00	2.13E-48	Down	2.57E-02	8.33E-01		1.02E+00	2.25E-17	Up	1.10E+00	3.86E-21	Up	Unigene38125_All//gi|30962522|dbj|BAC76729.1|//0.00E+00//alpha-amylase [Vigna angularis]	Unigene38125_All//5.00E-173//AT4G25000| AMY1 (ALPHA-AMYLASE-LIKE); alpha-amylase	Unigene38125_All//0.00E+00//TC134812		ko00500|Starch and sucrose metabolism		nr +
Unigene38126_All	612	1.11	1.57	2.26	12.29	10.18	7.90	4.15	2.53	0.98	5.01E-01	4.72E-01		1.03E+00	8.63E-02		-2.71E-01	2.27E-01		-6.38E-01	2.28E-03		-7.14E-01	4.46E-02		-2.09E+00	1.16E-07	Down	Unigene38126_All//gi|115479095|ref|NP_001063141.1|//2.00E-18//Os09g0408500 (Oryza sativa Japonica Group)>gi|113631374|dbj|BAF25055.1|Os09g0408500 (Oryza sativa Japonica Group)	Unigene38126_All//2.00E-16//AT3G25855| unknown protein	Unigene38126_All//0.00E+00//gi|109889408|gb|DW518376.1|DW518376				nr +
Unigene38127_All	1082	7.40	3.23	6.15	36.09	21.99	6.34	0.31	0.15	1.25	-1.20E+00	2.12E-08	Down	-2.66E-01	2.41E-01		-7.15E-01	8.74E-20		-2.51E+00	2.45E-115	Down	-1.02E+00	3.99E-01		2.00E+00	3.24E-04	Up	Unigene38127_All//gi|224118954|ref|XP_002317948.1|//4.00E-82//f-box family protein [Populus trichocarpa]>gi|222858621|gb|EEE96168.1| f-box family protein [Populus trichocarpa]	Unigene38127_All//5.00E-42//AT5G60850| OBP4; DNA binding / transcription factor	Unigene38127_All//0.00E+00//gi|78338373|gb|DT558647.1|DT558647	C2C2-Dof			nr +
Unigene38131_All	1008	130.39	91.74	80.09	4.40	4.03	1.43	0.17	0.00	0.08	-5.07E-01	2.17E-29		-7.03E-01	1.79E-50		-1.26E-01	7.05E-01		-1.62E+00	7.49E-08	Down	-7.39E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene38131_All//gi|4754913|gb|AAD29049.1|AF132854|//8.00E-31//carbonic anhydrase isoform 1 [Gossypium hirsutum]	Unigene38131_All//1.00E-21//AT5G14740| CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding	Unigene38131_All//6.00E-101//gi|84148283|gb|DN779583.1|DN779583		ko00910|Nitrogen metabolism		nr -
Unigene38142_All	978	2.84	1.97	2.99	5.91	5.88	3.19	3.16	4.15	1.43	-5.26E-01	1.64E-01		7.88E-02	8.31E-01		-6.90E-03	9.69E-01		-8.91E-01	2.43E-04		3.94E-01	1.62E-01		-1.15E+00	2.40E-04	Down	Unigene38142_All//gi|267881836|gb|ACN32513.1|//1.00E-103//mitogen-activated protein kinase [Malus x domestica]	Unigene38142_All//7.00E-98//AT2G43790| ATMPK6 (ARABIDOPSIS THALIANA MAP KINASE 6); MAP kinase/ kinase	Unigene38142_All//1.00E-148//ES804798		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene38143_All	783	19.65	18.70	16.80	27.36	22.25	34.55	29.97	16.49	10.02	-7.10E-02	6.38E-01		-2.26E-01	1.51E-01		-2.98E-01	1.00E-02		3.37E-01	1.21E-03		-8.62E-01	8.36E-17		-1.58E+00	4.76E-44	Down	Unigene38143_All//gi|30725284|gb|AAP37664.1|//8.00E-40//At2g43810 [Arabidopsis thaliana]>gi|222423635|dbj|BAH19786.1|AT2G43810 [Arabidopsis thaliana]	Unigene38143_All//4.00E-41//AT2G43810| small nuclear ribonucleoprotein F, putative / U6 snRNA-associated Sm-like protein, putative / Sm protein F, putative	Unigene38143_All//0.00E+00//gi|109873263|gb|DW502238.1|DW502238		ko03040|Spliceosome//ko03018|RNA degradation		nr +
Unigene38145_All	1438	16.88	9.87	11.96	9.08	8.53	8.32	14.26	7.79	4.96	-7.75E-01	5.02E-12		-4.97E-01	1.32E-05		-9.04E-02	6.17E-01		-1.25E-01	5.00E-01		-8.72E-01	4.35E-15		-1.52E+00	1.20E-36	Down	Unigene38145_All//gi|54035683|sp|Q81221.1|ACT_GOSHI//0.00E+00//RecName: Full=Actin>gi|3420239|gb|AAC31886.1| actin [Gossypium hirsutum]	Unigene38145_All//0.00E+00//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene38145_All//0.00E+00//TC135077		ko04145|Phagosome		nr -
Unigene38146_All	993	1.42	1.84	1.72	2.26	4.23	2.23	3.19	6.57	3.45	3.69E-01	4.44E-01		2.71E-01	6.27E-01		9.06E-01	1.55E-03		-1.85E-02	9.56E-01		1.04E+00	6.99E-07	Up	1.12E-01	7.16E-01									
Unigene38147_All	1320	3.92	1.77	6.45	18.08	8.74	4.62	9.16	11.59	1.06	-1.15E+00	1.92E-05	Down	7.18E-01	4.75E-04		-1.05E+00	2.94E-23	Down	-1.97E+00	3.27E-52	Down	3.39E-01	9.10E-03		-3.12E+00	1.91E-52	Down	Unigene38147_All//gi|87240777|gb|AB032635.1|//1.00E-119//Leucine-rich repeat, plant specific [Medicago truncatula]	Unigene38147_All//6.00E-111//AT4G06744| leucine-rich repeat family protein / extensin family protein			ko04626|Plant-pathogen interaction		nr +

Unigene38149_All	743	95.49	55.99	60.92	142.67	101.03	58.29	13.49	16.03	8.79	-7.70E-01	2.65E-33		-6.48E-01	7.03E-24		-4.98E-01	8.59E-28		-1.29E+00	4.09E-125	Down	2.49E-01	1.12E-01		-6.17E-01	8.17E-05		Unigene38149_All//gi|62526422|gb|AA84649.1|//1.00E-16//methionine rich arabinogalactan [Solanum lycopersicum]	Unigene38149_All//0.00E+00//gi|21091810|gb|BQ404123.1|BQ404123		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene38150_All	691	26.58	12.32	21.27	67.48	76.64	70.46	103.28	30.67	37.01	-1.11E+00	2.69E-16	Down	-3.21E-01	1.97E-02		1.84E-01	1.20E-02		6.24E-02	5.19E-01		-1.75E+00	7.44E-149	Down	-1.48E+00	3.28E-120	Down	Unigene38150_All//gi|162955859|gb|ABY25305.1|//3.00E-65//pyrophosphate-dependent phosphofructokinase alpha subunit [[Citrus sinensis x Poncirus trifoliata]	Unigene38150_All//3.00E-51//AT1G76550| pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative	Unigene38150_All//0.00E+00//gi|164243941|gb|ES808365.1|ES808365		ko00051|Fructose and mannose metabolism		nr +
Unigene38152_All	902	8.35	3.93	7.26	1.49	1.64	2.25	2.02	0.74	0.80	-1.09E+00	6.02E-07	Down	-2.02E-01	3.98E-01		1.39E-01	8.24E-01		5.96E-01	2.13E-01		-1.44E+00	1.28E-03		-1.34E+00	1.76E-03		Unigene38152_All//gi|15237618|ref|NP_201220.1|//4.00E-69//methylase family protein [Arabidopsis thaliana] >gi|15451004|gb|AAK96773.1|Unknown protein [Arabidopsis thaliana] >gi|30725624|gb|AAP37834.1|At5g64156 [Arabidopsis thaliana]	Unigene38152_All//8.00E-62//AT5G64150| methylase family protein	Unigene38152_All//0.00E+00//gi|48790481|gb|CO091795.1|CO091795				nr +
Unigene38153_All	594	20.08	71.65	24.20	10.82	12.06	29.65	36.87	87.18	34.61	1.84E+00	3.35E-77	Up	2.69E-01	9.51E-02		1.57E-01	5.44E-01		1.45E+00	6.61E-25	Up	1.24E+00	5.95E-65	Up	-9.14E-02	4.42E-01		Unigene38153_All//gi|18397866|ref|NP_565376.1|//2.00E-14//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|66865916|gb|AAY57592.1| RING finger family protein [Arabidopsis thaliana] >gi|49944335|gb|ABR46210.1|At2g15580 [Arabidopsis thaliana] >gi|222423846|dbj|BAH19888.1|AT2G15580 [Arabidopsis thaliana]	Unigene38153_All//1.00E-15//AT2G15580| zinc finger (C3HC4-type RING finger) family protein	Unigene38153_All//0.00E+00//TC139538				nr -
Unigene38154_All	1249	23.67	33.51	48.56	10.37	14.14	6.18	0.24	1.07	0.64	5.02E-01	1.06E-09		1.04E+00	3.14E-45	Up	4.48E-01	3.43E-04		-7.46E-01	1.03E-06		2.18E+00	2.12E-04	Up	1.43E+00	4.39E-02		Unigene38154_All//gi|146552062|gb|ABQ42205.1|//2.00E-53//dehydration-responsive element binding protein 6 [Glycine max]	Unigene38154_All//9.00E-45//AT2G35700| EKF38 (ERF FAMILY PROTEIN 38); DNA binding / transcription factor	Unigene38154_All//0.00E+00//TC177300	AP2-EREBP			nr -
Unigene38156_All	1391	0.98	3.75	0.96	2.15	2.85	4.81	35.65	69.41	67.76	1.94E+00	8.77E-11	Up	-3.13E-02	9.77E-01		4.06E-01	2.13E-01		1.16E+00	4.14E-07	Up	9.61E-01	8.34E-80		9.26E-01	5.31E-75					Unigene38156_All//0.00E+00//TC165125				
Unigene38158_All	461	6.13	11.98	13.86	4.11	5.38	4.31	0.00	0.00	0.00	9.67E-01	1.63E-04		1.18E+00	2.17E-06	Up	3.89E-01	3.80E-01		7.01E-02	9.04E-01		null	null		null	null		Unigene38158_All//gi|17226662|gb|AAL37896.1|AF443118_1//4.00E-45//polyphosphoinositide binding protein [Gossypium hirsutum]	Unigene38158_All//1.00E-25//AT1G01630| SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative	Unigene38158_All//8.00E-148//ES839043				nr -
Unigene38159_All	830	4.60	8.42	14.05	2.82	3.32	2.18	0.00	0.10	0.00	8.72E-01	9.31E-05		1.61E+00	1.66E-17	Up	2.35E-01	5.86E-01		-3.74E-01	4.05E-01		6.65E+00	4.01E-01		null	null		Unigene38159_All//gi|17226662|gb|AAL37896.1|AF443118_1//1.00E-133//polyphosphoinositide binding protein [Gossypium hirsutum]	Unigene38159_All//6.00E-87//AT1G01630| SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative	Unigene38159_All//0.00E+00//TC145391				nr +
Unigene3816_All	889	73.68	60.53	85.83	67.97	75.53	98.25	102.73	40.81	37.06	-2.84E-01	1.23E-05		2.20E-01	4.59E-04		1.52E-01	2.01E-02		5.32E-01	6.62E-23		-1.33E+00	2.75E-127	Down	-1.47E+00	3.94E-152	Down	Unigene3816_All//gi|239056192|emb|CAQ58629.1|//1.00E-133//pyruvate kinase [Vitis vinifera]	Unigene3816_All//1.00E-132//AT5G08570| pyruvate kinase, putative	Unigene3816_All//0.00E+00//gi|78339794|gb|DT560068.1|DT560068		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene38160_All	1085	480.00	698.44	1077.22	272.30	256.38	329.67	62.15	40.14	26.00	5.41E-01	1.65E-186		1.17E+00	0.00E+00	Up	-8.69E-02	3.11E-03		2.76E-01	1.59E-27		-6.31E-01	1.68E-27		-1.26E+00	1.15E-88	Down	Unigene38160_All//gi|116265932|gb|ABJ91214.1|//1.00E-125//CBL-interacting protein kinase 7 [Populus trichocarpa] >gi|116265934|gb|ABJ91215.1| CBL-interacting protein kinase 8 [Populus trichocarpa]	Unigene38160_All//8.00E-122//AT4G30960| SIP3 (SOS3-INTERACTING PROTEIN 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene38160_All//0.00E+00//TC142051		ko04140|Regulation of autophagy		nr -
Unigene38161_All	1461	1.72	1.70	1.49	6.79	4.55	2.41	4.63	0.83	2.21	-1.65E-02	9.84E-01		-2.02E-01	6.09E-01		-5.77E-01	6.67E-04		-1.49E+00	4.96E-15	Down	-2.48E+00	1.23E-22	Down	-1.07E+00	1.15E-07	Down	Unigene38161_All//gi|212717159|gb|ACJ37421.1|//1.00E-157//NBS-LRR disease resistance protein [Glycine max]	Unigene38161_All//8.00E-139//AT5G23400| disease resistance family protein / LRR family protein	Unigene38161_All//0.00E+00//TC178363		ko04626|Plant-pathogen interaction		nr -
Unigene38162_All	1663	0.44	1.04	0.45	2.13	0.95	1.22	4.14	4.73	4.46	1.23E+00	1.58E-02		2.53E-02	9.95E-01		-1.16E+00	1.64E-04	Down	-7.99E-01	1.40E-02		1.89E-01	3.74E-01		1.05E-01	6.23E-01		Unigene38162_All//gi|8778278|gb|AAF79287.1|AC068602_10//1.00E-103//T14D16.17 [Arabidopsis thaliana]	Unigene38162_All//7.00E-105//AT1G19025| DNA cross-link repair protein-related	Unigene38162_All//1.00E-60//DR458386				nr -
Unigene38163_All	1227	8.83	10.24	10.03	9.46	8.50	8.58	7.10	4.05	3.54	2.15E-01	2.14E-01		1.84E-01	3.22E-01		-1.54E-01	4.23E-01		-1.41E-01	4.67E-01		-8.08E-01	3.88E-06		-1.00E+00	8.86E-09	Down	Unigene38163_All//gi|297609887|ref|NP_001063818.2|//6.00E-76//0s09g0542000 [Oryza sativa Japonica Group] >gi|255679102|dbj|BAF25732.2|Os09g0542000 [Oryza sativa Japonica Group]	Unigene38163_All//1.00E-44//AT1G76010| nucleic acid binding	Unigene38163_All//0.00E+00//TC155707				nr -
Unigene38166_All	802	5.02	1.90	2.59	10.43	25.93	8.50	2.21	1.56	1.14	-1.41E+00	1.03E-05	Down	-9.56E-01	2.70E-03		1.31E+00	1.70E-27	Up	-2.95E-01	1.72E-01		-5.02E-01	2.66E-01		-9.55E-01	2.36E-02		Unigene38166_All//gi|255585816|ref|XP_002533586.1|//2.00E-20//conserved hypothetical protein [Ricinus communis] >gi|223526530|gb|EEF28791.1|conserved hypothetical protein [Ricinus communis]		Unigene38166_All//0.00E+00//TC166172				nr +
Unigene38167_All	660	48.99	210.43	42.52	56.61	117.97	75.89	40.55	59.08	43.64	2.10E+00	2.67E-300	Up	-2.04E-01	4.90E-02		1.06E+00	3.57E-73	Up	4.23E-01	5.10E-09		5.43E-01	1.32E-12		1.06E-01	2.93E-01		Unigene38167_All//gi|300079018|gb|ADJ67440.1|//2.00E-43//ethylene response factor 11 [Actinidia deliciosa]	Unigene38167_All//2.00E-37//AT5G51190| AP2 domain-containing transcription factor, putative	Unigene38167_All//0.00E+00//DW509271	AP2-EREBP			nr +
Unigene3817_All	1864	16.42	3.02	4.11	8.31	6.37	3.20	12.41	30.70	21.35	-2.44E+00	1.43E-80	Down	-2.00E+00	1.80E-60	Down	-3.83E-01	4.76E-03		-1.38E+00	1.30E-20	Down	1.31E+00	1.37E-77	Up	7.83E-01	2.07E-24		Unigene3817_All//gi|292677823|dbj|BAI99253.1|//1.00E-158//trehalose 6-phosphate phosphatase [Nicotiana tabacum]	Unigene3817_All//7.00E-145//AT5G51460| ATTPPA; trehalose-phosphatase	Unigene3817_All//0.00E+00//TC159648		ko00500|Starch and sucrose metabolism		nr -
Unigene38171_All	1398	1.24	0.94	0.50	3.46	2.56	1.65	6.02	2.09	3.45	-3.90E-01	4.27E-01		-1.32E+00	1.40E-02		-4.32E-01	1.13E-01		-1.07E+00	8.15E-05	Down	-1.52E+00	4.75E-15	Down	-8.04E-01	3.99E-06		Unigene38171_All//gi|297810641|ref|XP_002888202.1|//2.00E-99//ZCF125 [Arabidopsis lyrata subsp. lyrata] >gi|297340043|gb|EFH64461.1|ZCF125 [Arabidopsis lyrata subsp. lyrata]	Unigene38171_All//5.00E-86//AT1G59540| ZCF125; ATP binding / microtubule motor					nr -
Unigene38173_All	1466	1.18	2.45	0.94	0.95	1.29	2.46	1.67	1.68	13.89	1.06E+00	1.29E-03		-3.19E-01	5.53E-01		4.41E-01	3.93E-01		1.37E+00	3.59E-05	Up	8.10E-03	1.02E+00		3.05E+00	1.35E-84	Up	Unigene38173_All//gi|28416689|gb|AA042875.1|//1.00E-40//At3g50340 [Arabidopsis thaliana]	Unigene38173_All//2.00E-51//AT2G22790| unknown protein	Unigene38173_All//0.00E+00//CO091549				nr +
Unigene38174_All	1498	1.64	0.07	0.32	4.16	2.67	1.93	2.99	1.40	1.04	-4.60E+00	9.56E-12	Down	-2.36E+00	1.94E-06	Down	-6.40E-01	3.97E-03		-1.11E+00	2.56E-06	Down	-1.10E+00	2.17E-05	Down	-1.53E+00	1.02E-08	Down	Unigene38174_All//gi|297597115|ref|NP_001043456.2|//1.00E-107//0s01g0592900 [Oryza sativa Japonica Group] >gi|53791584|dbj|BAD52706.1| DEAH helicase isoform 5-like [Oryza sativa Japonica Group] >gi|255673416|dbj|BAF05370.2|Os01g0592900 [Oryza sativa Japonica Group]	Unigene38174_All//2.00E-105//AT1G79950| helicase-related	Unigene38174_All//0.00E+00//CO106654				nr -
Unigene38175_All	1606	1.50	0.69	0.33	8.78	3.88	3.23	2.79	0.78	0.84	-1.11E+00	7.36E-03		-2.18E+00	8.53E-06	Down	-1.18E+00	1.00E-16	Down	-1.44E+00	4.43E-20	Down	-1.84E+00	1.12E-10	Down	-1.73E+00	3.25E-10	Down	Unigene38175_All//gi|18402763|ref|NP_564553.1|//1.00E-153//phospholipase C/ phosphoric diester hydrolase [Arabidopsis thaliana] >gi|10120435|gb|AAG13060.1|AC011807_19 Unknown protein [Arabidopsis thaliana]	Unigene38175_All//3.00E-154//AT1G49740| phospholipase C/ phosphoric diester hydrolase	Unigene38175_All//0.00E+00//TC144796				nr -
Unigene38177_All	1037	0.56	3.52	0.92	2.59	9.60	3.75	3.02	4.35	16.17	2.66E+00	5.14E-11	Up	7.36E-01	3.23E-01		1.89E+00	4.32E-22	Up	5.30E-01	9.91E-02		5.29E-01	3.97E-02		2.42E+00	1.58E-54	Up	Unigene38177_All//gi|15238685|ref|NP_200137.1|//1.00E-10//AGP22 (ARABINOGALACTAN PROTEIN 22) [Arabidopsis thaliana] >gi|75171157|sp|Q9FK16.1|AGP22_ARATH RecName: Full=Arabinogalactan peptide 22; Short=AG-peptide 22; Flags: Precursor >gi|38566508|gb|AAR24144.1|At5g53250 [Arabidopsis thaliana] >gi|40823626|gb|AAR92294.1|At5g53250 [Arabidopsis thaliana]		Unigene38177_All//0.00E+00//gi|164370393|gb|ES849855.1|ES849855				nr -
Unigene38178_All	1712	1.96	9.41	4.11	7.45	9.92	12.29	8.15	30.05	8.52	2.27E+00	9.94E-39	Up	1.07E+00	4.54E-06	Up	4.13E-01	1.39E-03		7.23E-01	7.02E-10		1.88E+00	2.42E-118	Up	6.36E-02	6.61E-01		Unigene38178_All//gi|297798136|ref|XP_002866952.1|//1.00E-166//CYP81D8 [Arabidopsis lyrata subsp. lyrata] >gi|297312788|gb|EFH43211.1|CYP81D8 [Arabidopsis lyrata subsp. lyrata]	Unigene38178_All//5.00E-154//AT4G37370| CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene3818_All	2084	2.01	1.12	0.84	1.60	1.02	0.48	3.08	6.62	3.98	-8.45E-01	4.45E-03		-1.25E+00	8.50E-05	Down	-6.45E-01	4.74E-02		-1.75E+00	1.07E-06	Down	1.10E+00	6.30E-15	Up	3.67E-01	3.94E-02		Unigene3818_All//gi|292677823|dbj|BAI99253.1|//1.00E-163//trehalose 6-phosphate phosphatase [Nicotiana tabacum]	Unigene3818_All//2.00E-149//AT5G51460| ATTPPA; trehalose-phosphatase	Unigene3818_All//0.00E+00//TC159648		ko00500|Starch and sucrose metabolism		nr +
Unigene38181_All	899	73.85	208.60	45.55	40.39	50.98	36.57	17.50	50.95	12.32	1.50E+00	1.94E-253	Up	-6.97E-01	2.29E-25		3.36E-01	4.59E-06		-1.43E-01	1.50E-01		1.54E+00	1.01E-79	Up	-5.06E-01	3.39E-05		Unigene38181_All//gi|87241016|gb|ABD32874.1|//1.00E-28//VQ [Medicago truncatula]	Unigene38181_All//2.00E-16//AT3G56880| VQ motif-containing protein	Unigene38181_All//0.00E+00//TC156967				nr -
Unigene38182_All	1221	12.13	6.06	12.39	23.66	24.93	25.08	12.29	7.46	3.75	-1.00E+00	2.33E-11	Down	3.05E-02	8.52E-01		7.53E-02	5.64E-01		8.38E-02	4.87E-01		-7.20E-01	2.51E-08		-1.71E+00	7.44E-32	Down	Unigene38182_All//gi|16323109|gb|AAL15289.1|//2.00E-45//AT3g12650/T2E22_103 [Arabidopsis thaliana] >gi|21360415|gb|AAM47323.1|AT3g12650/T2E22_103 [Arabidopsis thaliana]	Unigene38182_All//1.00E-30//AT3G12650| unknown protein	Unigene38182_All//0.00E+00//TC159390				nr -
Unigene38185_All	913	2.46	0.83	1.46	2.84	2.41	0.64	4.49	4.12	1.88	-1.57E+00	5.19E-04	Down	-7.57E-01	9.05E-02		-2.33E-01	5.89E-01		-2.14E+00	8.77E-07	Down	-1.25E-01	6.68E-01		-1.26E+00	3.15E-06	Down							
Unigene38186_All	1791	8.12	1.36	5.68	0.06	0.04	0.00	20.16	4.20	0.93	-2.58E+00	5.04E-41	Down	-5.16E-01	7.04E-04		-5.30E-01	8.16E-01		-5.80E+00	3.99E-01		-2.26E+00	1.03E-105	Down	-4.43E+00	8.04E-207	Down	Unigene38186_All//gi|224139828|ref|XP_002323296.1|//1.00E-154//cytochrome P450 [Populus trichocarpa] >gi|222867926|gb|EEF05057.1|cytochrome P450 [Populus trichocarpa]	Unigene38186_All//3.00E-138//AT5G06905| CYP712A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene38189_All	953	9.77	22.28	22.63	43.33	69.05	81.94	1.60	0.75	0.42	1.19E+00	9.83E-21	Up	1.21E+00	6.19E-21	Up	6.72E-01	7.74E-29		9.19E-01	1.09E-52		-1.10E+00	2.32E-02		-1.93E+00	1.54E-04	Down	Unigene38189_All//gi|226506334|ref|NP_001152619.1|//7.00E-45//lactoylglutathione lyase [Zea mays] |gi|195658267|gb|ACG48601.1|lactoylglutathione lyase [Zea mays]	Unigene38189_All//2.00E-40//AT1G80160| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene38189_All//0.00E+00//gi|48752168|gb|CO082687.1|CO082687				nr -

Unigene3819_All	509	5.14	7.76	5.13	4.50	3.72	4.17	18.03	13.30	3.91	5.95E-01	5.35E-02		-3.80E-03	9.92E-01		-2.75E-01	5.66E-01		-1.10E-01	7.96E-01		-4.38E-01	1.06E-02		-2.20E+00	2.18E-27	Down	Unigene3819_All|gi|38257656|sp|Q8LEK2.1|FA18_ARATH//1.00E-05//RecName: Full=Uncharacterized FAM18-like protein At1g09330 >gi|28466859|gb|AAO44038.1|At1g09330 [Arabidopsis thaliana]	Unigene3819_All//6.00E-07//AT1G09330| unknown protein	Unigene3819_All//2.00E-161//TC150971				nr +
Unigene38190_All	738	8.15	43.74	6.42	11.00	17.68	11.69	40.05	63.77	63.21	2.42E+00	2.02E-83	Up	-3.44E-01	1.90E-01		6.85E-01	2.86E-06		8.73E-02	6.91E-01		6.71E-01	1.37E-21		6.59E-01	2.92E-21		Unigene38190_All//gi|171452362|dbj|BAG15872.1|//4.00E-44//transcription factor [Bruguiera gymnorhiza]	Unigene38190_All//1.00E-19//AT2G40140| CZF1; transcription factor	Unigene38190_All//0.00E+00//TC142808	C3H			nr +
Unigene38193_All	1053	26.83	29.45	17.75	38.70	31.30	47.18	42.44	28.98	19.48	1.34E-01	2.13E-01		-5.96E-01	1.32E-08		-3.06E-01	9.32E-05		2.86E-01	1.17E-04		-5.51E-01	1.11E-14		-1.12E+00	1.80E-49	Down	Unigene38193_All//gi|15081799|gb|AAK82554.1|//2.00E-70//At1g05070/T7A14_6 [Arabidopsis thaliana] >gi|22655016|gb|AAM88099.1|At1g05070/T7A14_6 [Arabidopsis thaliana]	Unigene38193_All//4.00E-56//AT1G05070| unknown protein	Unigene38193_All//0.00E+00//gi|164343010|gb|ES803009.1|ES803009				nr +
Unigene38194_All	1264	51.12	21.41	43.06	6.11	11.33	7.22	0.57	0.43	0.85	-1.26E+00	1.76E-67	Down	-2.48E-01	2.93E-04		8.92E-01	1.98E-10		2.41E-01	2.58E-01		-4.03E-01	6.23E-01		5.82E-01	3.17E-01		Unigene38194_All//gi|8778672|gb|AAF79680.1|AC022314_21/1.00E-72//F9C16.20 [Arabidopsis thaliana]	Unigene38194_All//9.00E-75//AT1G44000| unknown protein	Unigene38194_All//0.00E+00//TC143935				nr +
Unigene38196_All	1914	0.77	0.71	0.42	1.15	1.60	1.18	1.55	6.05	8.16	-9.87E-02	8.47E-01		-8.75E-01	1.34E-01		4.84E-01	1.93E-01		4.29E-02	9.43E-01		1.97E+00	8.54E-29	Up	2.40E+00	2.84E-50	Up	Unigene38196_All//gi|259121421|gb|ACV92030.1|//1.00E-173//WRKY transcription factor 28 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene38196_All//3.00E-104//AT1G62300| WRKY6; transcription factor	Unigene38196_All//0.00E+00//TC165797	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene3820_All	1030	55.88	61.25	42.03	87.83	76.39	64.94	63.63	42.04	30.63	1.32E-01	6.33E-02		-4.11E-01	7.32E-09		-2.01E-01	1.01E-04		-4.36E-01	1.00E-16		-5.98E-01	2.23E-24		-1.05E+00	3.49E-65	Down	Unigene3820_All//gi|38257656|sp|Q8LEK2.1|FA18_ARATH//6.00E-90//RecName: Full=Uncharacterized FAM18-like protein At1g09330 >gi|28466859|gb|AAO44038.1|At1g09330 [Arabidopsis thaliana]	Unigene3820_All//3.00E-91//AT1G09330| unknown protein	Unigene3820_All//0.00E+00//TC145553				nr -
Unigene38200_All	616	21.06	50.26	37.26	24.91	37.17	40.32	79.28	124.57	82.78	1.25E+00	1.77E-32	Up	8.23E-01	4.94E-12		5.78E-01	5.35E-08		6.95E-01	7.90E-11		6.52E-01	5.47E-33		6.24E-02	4.15E-01					Unigene38200_All//0.00E+00//gi|164300100|gb|ES834790.1|ES834790				
Unigene38201_All	1156	25.16	11.31	29.39	3.23	2.44	1.88	0.80	0.72	0.62	-1.15E+00	5.53E-27	Down	2.24E-01	2.50E-02		-4.04E-01	2.15E-01		-7.85E-01	1.27E-02		-1.54E-01	8.08E-01		-3.75E-01	5.57E-01		Unigene38201_All//gi|15081662|gb|AAK82486.1|//1.00E-103//AT4g28740/F16A16_150 [Arabidopsis thaliana] >gi|20147175|gb|AAM10304.1|AT4g28740/F16A16_150 [Arabidopsis thaliana]	Unigene38201_All//2.00E-101//AT4G28740| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: LPA1 (LOW PSII ACCUMULATION1); binding (TAIR:AT1G02910.1); Has 65 Blast hits to 65 proteins in 19 species: Archae - 0; Bacteria - 17; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene38201_All//0.00E+00//TC175082				nr -
Unigene38202_All	674	8.31	19.70	4.11	19.59	19.57	10.39	8.34	4.59	5.26	1.25E+00	3.37E-14	Up	-1.02E+00	1.24E-04	Down	-1.30E-03	9.87E-01		-9.15E-01	2.03E-09		-8.63E-01	1.19E-04		-6.65E-01	2.09E-03		Unigene38202_All//gi|32815867|gb|AF98333.1|//1.00E-46//At3g08850 [Arabidopsis thaliana]	Unigene38202_All//7.00E-21//AT3G08890| unknown protein	Unigene38202_All//0.00E+00//TC161474				nr -
Unigene38203_All	538	6.61	3.30	9.80	8.43	7.49	13.01	7.86	6.76	3.92	-1.00E+00	2.25E-03		5.67E-01	3.81E-02		-1.70E-01	5.93E-01		6.27E-01	4.40E-03		-2.18E-01	4.56E-01		-1.00E+00	1.07E-04	Down				Unigene38203_All//3.00E-64//DW234639				
Unigene38205_All	1328	6.97	1.56	2.61	2.21	2.41	1.67	2.01	0.35	0.60	-2.16E+00	2.25E-21	Down	-1.42E+00	1.03E-11	Down	1.24E-01	7.87E-01		-4.09E-01	2.98E-01		-2.53E+00	1.53E-09	Down	-1.74E+00	1.78E-06	Down	Unigene38205_All//gi|15223380|ref|NP_174012.1|//1.00E-110//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75216976|sp|Q9ZVG8.1|PPR60_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g26900, mitochondrial; Flags: Precursor >gi|4262179|gb|AAD14496.1|Hypothetical protein [Arabidopsis thaliana]	Unigene38205_All//7.00E-107//AT1G26900| pentatricopeptide (PPR) repeat-containing protein	Unigene38205_All//0.00E+00//ES835639				nr -
Unigene38206_All	546	72.44	193.40	109.13	113.50	102.49	123.17	231.84	535.38	305.72	1.42E+00	1.65E-131	Up	5.91E-01	3.39E-17		-1.47E-01	3.24E-02		1.18E-01	9.82E-02		1.21E+00	0.00E+00	Up	3.99E-01	3.37E-30		Unigene38206_All//gi|223452524|gb|ACM89589.1|//5.00E-51//leucine-rich repeat protein [Glycine max]	Unigene38206_All//5.00E-47//AT5G21090| leucine-rich repeat protein, putative	Unigene38206_All//0.00E+00//TC154032				nr -
Unigene38207_All	1107	5.06	15.70	8.71	7.47	7.65	7.79	23.18	47.46	32.03	1.63E+00	3.24E-27	Up	7.84E-01	4.40E-05		3.48E-02	8.89E-01		6.10E-02	7.91E-01		1.03E+00	2.78E-49	Up	4.66E-01	3.31E-09		Unigene38207_All//gi|223452524|gb|ACM89589.1|//1.00E-38//leucine-rich repeat protein [Glycine max]	Unigene38207_All//7.00E-35//AT3G43740| leucine-rich repeat family protein	Unigene38207_All//2.00E-165//DT051320		ko04626|Plant-pathogen interaction		nr -
Unigene38208_All	1135	1.71	4.02	2.58	7.59	9.59	6.57	2.31	0.37	1.16	1.24E+00	2.44E-05	Up	5.97E-01	1.23E-01		3.37E-01	5.54E-02		-2.10E-01	3.53E-01		-2.65E+00	7.81E-10	Down	-9.96E-01	3.20E-03		Unigene38208_All//gi|257831433|gb|ACV71017.1|//4.00E-41//UPA17 [Capsicum annuum]	Unigene38208_All//5.00E-22//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene38208_All//0.00E+00//ES830922	GRF			nr -
Unigene3821_All	1063	14.52	9.25	14.78	37.86	43.60	34.03	1.87	0.67	0.11	-6.51E-01	4.52E-06		2.54E-02	8.78E-01		2.04E-01	9.00E-03		-1.54E-01	9.59E-02		-1.48E+00	5.15E-04	Down	-4.06E+00	3.04E-11	Down	Unigene3821_All//gi|171190270|gb|AC842441.1|//1.00E-134//aquaporin PIP2;4 [Gossypium hirsutum]	Unigene3821_All//2.00E-126//AT2G16850| PIP2;8 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;8); water channel	Unigene3821_All//0.00E+00//TC130059				nr +
Unigene38210_All	1317	1.11	1.89	1.29	1.51	1.18	0.93	10.50	4.09	5.72	7.61E-01	5.91E-02		2.18E-01	6.56E-01		-3.63E-01	4.54E-01		-7.09E-01	1.31E-01		-1.36E+00	1.61E-20	Down	-8.77E-01	7.22E-11		Unigene38210_All//gi|29294217|dbj|BAB02119.1|//1.00E-90//ubiquinol-cytochrome c1 reductase cytochrome c1 precursor-like protein [Arabidopsis thaliana] >gi|15451172|gb|AAK96857.1|endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana] >gi|20148415|gb|AAM10098.1|endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]	Unigene38210_All//7.00E-36//AT1G10950| endomembrane protein 70, putative	Unigene38210_All//0.00E+00//gi|84165643|gb|DR454291.1|DR454291				nr +
Unigene38214_All	975	7.67	2.81	7.05	4.45	3.04	5.37	0.87	0.51	0.41	-1.45E+00	2.24E-10	Down	-1.23E-01	6.35E-01		-5.49E-01	5.14E-02		2.74E-01	3.54E-01		-7.54E-01	2.78E-01		-1.09E+00	9.98E-02		Unigene38214_All//gi|15235537|ref|NP_195454.1|//1.00E-80//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75213666|sp|Q9SZT8.1|PP354_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g37380, chloroplastic; Flags: Precursor	Unigene38214_All//2.00E-69//AT4G37380| pentatricopeptide (PPR) repeat-containing protein	Unigene38214_All//0.00E+00//CO120970				nr +
Unigene38215_All	1742	0.30	6.28	5.78	0.49	0.42	0.44	0.39	0.58	2.13	4.39E+00	5.64E-49	Up	4.27E+00	3.34E-43	Up	-2.28E-01	7.78E-01		-1.42E-01	8.54E-01		5.68E-01	3.79E-01		2.45E+00	8.27E-13	Up	Unigene38215_All//gi|294861500|gb|ADF45512.1|//1.00E-90//type 2 ribosome-inactivating protein precursor [Camellia sinensis]		Unigene38215_All//7.00E-179//gi|78338048|gb|DT558322.1|DT558322				nr -
Unigene38216_All	1889	0.00	0.00	0.06	5.51	4.32	4.81	14.50	5.20	14.02	null	null		5.82E+00	3.98E-01		-3.51E-01	4.51E-02		-1.98E-01	3.30E-01		-1.48E+00	2.79E-45	Down	-4.85E-02	6.40E-01		Unigene38216_All//gi|297810079|ref|XP_002874923.1|//0.00E+00//pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320760|gb|EFH51182.1|pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38216_All//0.00E+00//AT1G02810| pectinesterase family protein	Unigene38216_All//0.00E+00//TC138774		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene38217_All	856	3.30	2.37	2.86	5.47	3.14	2.27	0.99	0.29	0.84	-4.79E-01	2.07E-01		-2.06E-01	6.31E-01		-8.02E-01	2.05E-03		-1.27E+00	6.02E-06	Down	-1.75E+00	1.64E-02		-2.38E-01	7.02E-01		Unigene38217_All//gi|297803668|ref|XP_002869718.1|//1.00E-105//ATGWD2/GWD3 [Arabidopsis lyrata subsp. lyrata] >gi|297315554|gb|EFH45977.1|ATGWD2/GWD3 [Arabidopsis lyrata subsp. lyrata]	Unigene38217_All//2.00E-105//AT4G24450| PWD (PHOSPHOGLUCAN, WATER DIKINASE); ATP binding / kinase	Unigene38217_All//1.00E-12//DW506388				nr -
Unigene38218_All	1666	2.95	5.47	8.02	2.54	5.66	3.31	0.18	0.30	0.24	8.91E-01	3.85E-06		1.44E+00	4.43E-17	Up	1.16E+00	1.84E-10	Up	3.80E-01	1.60E-01		7.61E-01	4.22E-01		4.29E-01	6.61E-01		Unigene38218_All//gi|170676246|gb|ACB30062.1|//1.00E-110//transcription factor [Capsicum annuum]	Unigene38218_All//8.00E-98//AT4G27240| zinc finger (C2H2 type) family protein	Unigene38218_All//2.00E-18//TC138486	C2H2			nr +
Unigene38224_All	1042	2.76	1.56	0.72	1.63	1.88	2.08	4.26	1.32	1.72	-8.28E-01	2.44E-02		-1.95E+00	5.30E-06	Down	2.13E-01	6.94E-01		3.56E-01	4.64E-01		-1.69E+00	1.74E-09	Down	-1.31E+00	5.07E-07	Down	Unigene38224_All//gi|30681147|ref|NP_172416.2|//1.00E-104//haspin-related [Arabidopsis thaliana] >gi|3482920|gb|AAC33205.1|Hypothetical protein [Arabidopsis thaliana]	Unigene38224_All//4.00E-102//AT1G09450| haspin-related	Unigene38224_All//0.00E+00//gi|78332499|gb|DT552773.1|DT552773				nr +
Unigene38229_All	961	1.58	4.53	0.78	24.67	18.99	39.29	5.06	13.27	15.21	1.52E+00	9.90E-07	Up	-1.03E+00	7.23E-02		-3.78E-01	3.33E-04		6.71E-01	3.23E-15		1.39E+00	1.33E-19	Up	1.59E+00	1.11E-27	Up	Unigene38229_All//gi|15238851|ref|NP_200194.1|//2.00E-20//VQ motif-containing protein [Arabidopsis thaliana] >gi|13926342|gb|AAK49634.1|AF372918_1 AT5g53830/MGN6_22 [Arabidopsis thaliana] >gi|22135787|gb|AAM91050.1|AT5g53830/MGN6_22 [Arabidopsis thaliana]	Unigene38229_All//3.00E-15//AT5G53830| VQ motif-containing protein	Unigene38229_All//0.00E+00//TC134606				nr -
Unigene3823_All	1295	19.64	55.91	61.93	57.66	129.26	126.88	1.18	0.23	1.51	1.51E+00	2.66E-99	Up	1.66E+00	8.75E-123	Up	1.16E+00	5.04E-183	Up	1.14E+00	1.51E-156	Up	-2.38E+00	2.15E-05	Down	3.59E-01	3.89E-01		Unigene3823_All//gi|224056449|ref|XP_002298862.1|//4.00E-66//outward rectifying potassium channel [Populus trichocarpa] >gi|222846120|gb|EEE83667.1|outward rectifying potassium channel [Populus trichocarpa]	Unigene3823_All//3.00E-52//AT5G55630| ATKCO1; calcium-activated potassium channel/ ion channel/ outward rectifier potassium channel	Unigene3823_All//0.00E+00//TC131293				nr -
Unigene38230_All	882	1.13	2.93	2.60	2.15	2.15	2.51	4.51	4.74	6.91	1.38E+00	7.70E-04	Up	1.20E+00	7.42E-03		7.00E-04	9.89E-01		2.25E-01	6.34E-01		7.26E-02	8.04E-01		6.17E-01	2.93E-03					Unigene38230_All//2.00E-147//gi|164344999|gb|ES843254.1|ES843254				
Unigene38231_All	707	31.97	19.35	20.64	54.61	57.18	65.67	103.10	50.49	68.52	-7.24E-01	4.29E-10		-6.32E-01	1.04E-07		6.65E-02	5.50E-01		2.66E-01	6.22E-04		-1.03E+00	8.72E-68	Down	-5.89E-01	4.03E-27		Unigene38231_All//gi|9294217|dbj|BAB02119.1|//1.00E-90//ubiquinol-cytochrome c1 reductase cytochrome c1 precursor-like protein [Arabidopsis thaliana]	Unigene38231_All//4.00E-85//AT5G40810| cytochrome c1, putative	Unigene38231_All//0.00E+00//gi|78336970|gb|DT557244.1|DT557244		ko00190|Oxidative phosphorylation		nr -
Unigene38232_All	1650	3.96	1.57	1.36	3.59	3.76	2.79	0.10	0.00	0.00	-1.34E+00	3.27E-08	Down	-1.55E+00	1.61E-09	Down	6.44E-02	8.22E-01		-3.64E-01	1.58E-01		-6.68E+00	1.34E-01		-6.68E+00	1.08E-01		Unigene38232_All//gi|297612088|ref|NP_001068172.2|//2.00E-43//Os11g0587300 [Oryza sativa Japonica Group] >gi|255680218|dbj|BAF28535.2|Os11g0587300 [Oryza sativa Japonica Group]	Unigene38232_All//1.00E-26//AT3G63430| unknown protein	Unigene38232_All//3.00E-101//gi|211100072|gb|BQ412385.1|BQ412385				nr +

Unigene38234_All	1034	1.52	0.54	0.72	3.85	2.40	2.14	4.42	0.85	1.31	-1.49E+00	6.73E-03			-1.07E+00	5.45E-02			-6.85E-01	1.84E-02			-8.49E-01	5.02E-03			-2.38E+00	8.42E-15	Down	-1.75E+00	1.34E-10	Down	Unigene38234_All//gi|115483442|ref|NP_001065391.1|//2.00E-06//Os10g0562000 [Oryza sativa Japonica Group] >gi|31433517|gb|AAP55022.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113639923|dbj|BAF27228.1| Os10g0562000 [Oryza sativa Japonica Group]	Unigene38234_All//8.00E-07//AT3G60380| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT4G16790.1); Has 5716 Blast hits to 3635 proteins in 329 species: Archae - 2; Bacteria - 249; Metazoa - 2628; Fungi - 569; Plants - 209; Viruses - 24; Other Eukaryotes - 2035 (source: NCBI BLink).	Unigene38234_All//0.00E+00//TC169685				nr +
Unigene38235_All	1091	4.94	2.65	3.81	4.16	4.26	3.15	1.86	0.88	0.40	-9.00E-01	4.88E-04			-3.76E-01	1.75E-01			3.63E-02	9.20E-01			-4.01E-01	1.83E-01			-1.08E+00	8.18E-03		-2.21E+00	1.05E-06	Down	Unigene38235_All//gi|75296458|sp|Q7XSK0.2|BGL18_ORYSJ//2.00E-93//RecName: Full=Beta-glucosidase 18; Short=Os4bglu18; Flags: Precursor >gi|38345329|emb|CAE54546.1| OSJNBa0004N05.26 [Oryza sativa (japonica cultivar-group)] >gi|38345687|emb|CAE01910.2| OSJNBb0070J16.3 [Oryza sativa (japonica cultivar-group)] >gi|116310833|emb|CAH67620.1| OSIGBa0140J09.1 [Oryza sativa (indica cultivar-group)]	Unigene38235_All//3.00E-82//AT1G61810| BGLU45 (BETA-GLUCOSIDASE 45); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene38235_All//0.00E+00//TC137692		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr +
Unigene38236_All	1049	2.59	0.48	1.88	1.42	2.46	0.65	0.93	0.16	0.80	-2.42E+00	1.10E-07	Down	-4.66E-01	2.47E-01			7.89E-01	4.33E-02			-1.14E+00	3.85E-02			-2.54E+00	6.41E-04	Down	-2.17E-01	7.07E-01		Unigene38236_All//gi|75296458|sp|Q7XSK0.2|BGL18_ORYSJ//1.00E-101//RecName: Full=Beta-glucosidase 18; Short=Os4bglu18; Flags: Precursor >gi|38345329|emb|CAE54546.1| OSJNBa0004N05.26 [Oryza sativa (japonica cultivar-group)] >gi|38345687|emb|CAE01910.2| OSJNBb0070J16.3 [Oryza sativa (japonica cultivar-group)] >gi|116310833|emb|CAH67620.1| OSIGBa0140J09.1 [Oryza sativa (indica cultivar-group)]	Unigene38236_All//2.00E-90//AT1G61810| BGLU45 (BETA-GLUCOSIDASE 45); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene38236_All//0.00E+00//TC137692		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr +
Unigene38238_All	3826	0.08	0.13	0.00	0.82	0.30	0.15	5.98	5.11	2.53	6.89E-01	4.99E-01		-6.36E+00	4.90E-02			-1.47E+00	1.32E-05	Down	-2.42E+00	2.73E-09	Down	-2.26E-01	3.60E-02		-1.24E+00	5.06E-30	Down					Unigene38238_All//2.00E-20//TC166641				
Unigene3824_All	507	13.00	10.79	5.88	11.89	10.26	13.09	5.84	6.76	3.38	-2.69E-01	2.64E-01		-1.14E+00	2.70E-06	Down	-2.13E-01	4.25E-01		1.39E-01	6.35E-01		2.12E-01	5.31E-01		-7.89E-01	1.15E-02		Unigene3824_All//9.00E-42//AT1G73090| unknown protein	Unigene3824_All//5.00E-66//gi|78328542|gb|DT548816.1|DT548816				nr -
Unigene38240_All	2097	4.14	73.50	10.87	1.78	1.28	1.44	0.10	0.20	0.08	4.15E+00	0.00E+00	Up	1.39E+00	2.84E-27	Up	-4.76E-01	1.33E-01		-3.04E-01	3.96E-01		9.83E-01	3.73E-01		-4.07E-01	7.55E-01		Unigene38240_All//gi|54400096|emb|CAH64542.1|//0.00E-00//alpha-dioxygenase 2 [Solanum lycopersicum] >gi|266631441|emb|CAZ68079.1| alpha-dioxygenase 2 enzyme [Solanum lycopersicum]	Unigene38240_All//0.00E+00//AT1G73680| pathogen-responsive alpha-dioxygenase, putative	Unigene38240_All//0.00E+00//TC167331		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene38241_All	1255	0.67	0.32	1.02	0.64	0.96	0.36	2.06	3.53	23.01	-1.05E+00	1.74E-01		6.10E-01	3.33E-01		5.97E-01	3.69E-01		-8.19E-01	3.19E-01		7.81E-01	2.32E-03		3.49E+00	2.66E-135	Up					Unigene38241_All//0.00E+00//gi|21103569|gb|BQ415882.1|BQ415882				
Unigene38242_All	1030	10.31	116.05	13.70	7.45	12.80	18.99	44.00	145.51	117.70	3.49E+00	0.00E+00	Up	4.10E-01	8.98E-03		7.82E-01	7.99E-08		1.35E+00	1.02E-24	Up	1.73E+00	5.87E-305	Up	1.42E+00	1.99E-189	Up	Unigene38242_All//gi|167427545|gb|ABZ80409.1|//9.00E-78//hairpin-inducing protein [Casuarina glauca]	Unigene38242_All//2.00E-52//AT2G35980| YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	Unigene38242_All//0.00E+00//TC133073		ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport		nr +
Unigene38244_All	958	5.63	1.27	1.50	4.78	2.84	4.57	18.93	6.81	8.11	-2.15E+00	1.16E-12	Down	-1.91E+00	2.03E-10	Down	-7.52E-01	4.43E-03		-6.50E-02	8.38E-01		-1.48E+00	4.02E-30	Down	-1.22E+00	1.72E-23	Down	Unigene38244_All//gi|266944|sp|P29766.1|RL8_SOLLC//1.00E-143//RecName: Full=60S ribosomal protein L8; AltName: Full=L2; AltName: Full=Ribosomal protein TL2 >gi|19343|emb|CAA45863.1| ribosomal protein L2 [Solanum lycopersicum]	Unigene38244_All//4.00E-122//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene38244_All//0.00E+00//TC162347		ko03010|Ribosome		nr -
Unigene38246_All	595	5.28	8.26	2.24	2.18	4.57	2.66	5.97	8.08	5.36	6.47E-01	1.70E-02		-1.24E+00	9.77E-04	Down	1.07E+00	4.33E-03		2.87E-01	6.43E-01		4.37E-01	8.27E-02		-1.56E-01	6.09E-01		Unigene38246_All//gi|15224422|ref|NP_181336.1|//9.00E-48//chaperone protein dnaJ-related [Arabidopsis thaliana]	Unigene38246_All//5.00E-49//AT2G38000| chaperone protein dnaJ-related	Unigene38246_All//0.00E+00//gi|11209683|gb|BF278613.1|BF278613				nr +
Unigene38252_All	614	4.94	8.67	7.72	3.16	6.90	3.02	18.66	21.03	26.93	8.10E-01	1.81E-03		6.43E-01	2.60E-02		1.12E+00	8.80E-05	Up	-6.93E-02	8.97E-01		1.73E-01	2.74E-01		5.29E-01	8.94E-06		Unigene38252_All//gi|4928460|gb|AAD33596.1|AF133127_1//2.00E-08//thioredoxin h [Hevea brasiliensis]	Unigene38252_All//3.00E-05//AT1G11530| ATCCXS1 (C-terminal cysteine residue is changed to a serine 1); protein disulfide isomerase	Unigene38252_All//5.00E-82//gi|84152257|gb|DN801612.1|DN801612				nr +
Unigene38253_All	603	4.95	4.79	4.68	10.74	7.14	9.29	44.94	14.97	12.35	-4.63E-02	9.06E-01		-7.96E-02	8.31E-01		-5.89E-01	7.08E-03		-2.10E-01	4.28E-01		-1.59E+00	1.63E-49	Down	-1.86E+00	8.10E-64	Down					Unigene38253_All//2.00E-180//gi|164240889|gb|ES822580.1|ES822580				
Unigene38255_All	1017	3.04	1.49	1.26	2.35	1.79	0.98	2.62	2.88	2.86	-1.02E+00	4.17E-03		-1.27E+00	8.14E-04	Down	-3.90E-01	3.59E-01		-1.27E+00	2.28E-03		1.35E-01	7.03E-01		1.27E-01	7.03E-01		Unigene38255_All//gi|145338580|ref|NP_188247.2|//4.00E-94//TRZ4 (TRNASE Z 4); 3'-tRNA processing endoribonuclease/ catalytic [Arabidopsis thaliana]	Unigene38255_All//1.00E-95//AT3G16260| TRZ4 (TRNASE Z 4); 3'-tRNA processing endoribonuclease/ catalytic	Unigene38255_All//0.00E+00//TC179296				nr -
Unigene38256_All	861	4.80	11.42	4.89	11.40	10.88	11.91	45.82	87.67	80.46	1.25E+00	9.17E-11	Up	2.54E-02	9.51E-01		-6.73E-02	7.83E-01		6.31E-02	7.57E-01		9.36E-01	6.41E-60		8.13E-01	1.71E-44		Unigene38256_All//gi|15227057|ref|NP_178390.1|//5.00E-33//kelch repeat-containing F-box family protein [Arabidopsis thaliana] >gi|79316620|ref|NP_001030959.1| kelch repeat-containing F-box family protein [Arabidopsis thaliana] >gi|79316634|ref|NP_001030960.1| kelch repeat-containing F-box family protein [Arabidopsis thaliana] >gi|142994697|sp|Q8L736.2|SK111_ARATH RecName: Full=F-box/kelch-repeat protein SKIP11; AltName: Full=SKP1-interacting partner 11 >gi|16974560|gb|AAL31196.1| At2g02870/T17M13.4 [Arabidopsis thaliana] >gi|25090100|gb|AAN72228.1| At2g02870/T17M13.4 [Arabidopsis thaliana] >gi|222423827|dbj|BAH19879.1| AT2G02870 [Arabidopsis thaliana]	Unigene38256_All//2.00E-32//AT2G02870| kelch repeat-containing F-box family protein	Unigene38256_All//0.00E+00//TC166035				nr -
Unigene38257_All	738	66.57	37.90	51.23	73.98	55.62	74.23	39.64	29.34	17.27	-8.13E-01	1.76E-25		-3.78E-01	1.15E-06		-4.12E-01	2.42E-10		4.90E-03	9.49E-01		-4.34E-01	1.05E-06		-1.20E+00	3.51E-36	Down	Unigene38257_All//gi|18397961|ref|NP_566309.1|//5.00E-60//electron carrier/ iron-sulfur cluster binding [Arabidopsis thaliana] >gi|297829298|ref|XP_002882531.1| electron carrier/ iron ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|14423424|gb|AAK62394.1|AF386949_1 [unknown protein [Arabidopsis thaliana] >gi|297328371|gb|EFH58790.1| electron carrier/ iron ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene38257_All//3.00E-61//AT3G07480| electron carrier/ iron-sulfur cluster binding	Unigene38257_All//0.00E+00//TC151389		ko04626|Plant-pathogen interaction		nr +
Unigene38258_All	982	21.53	475.06	58.13	42.21	125.50	135.03	56.75	73.42	181.79	4.46E+00	0.00E+00	Up	1.43E+00	1.00E-70	Up	1.57E+00	7.57E-212	Up	1.68E+00	2.25E-227	Up	3.72E-01	1.17E-11		1.68E+00	0.00E+00	Up	Unigene38258_All//gi|15724294|gb|AAL06540.1|AF412087_1//2.00E-29//AT3g45210/T14D3_150 [Arabidopsis thaliana] >gi|20334744|gb|AAM16233.1| AT3g45210/T14D3_150 [Arabidopsis thaliana]	Unigene38258_All//5.00E-33//AT5G60680| unknown protein	Unigene38258_All//0.00E+00//gi|109868877|gb|DW497853.1|DW497853				nr -
Unigene3826_All	1157	25.37	160.59	15.74	74.57	63.33	30.84	51.38	15.71	37.98	2.66E+00	0.00E+00	Up	-6.89E-01	2.55E-11		-2.36E-01	6.34E-06		-1.27E+00	9.28E-100	Down	-1.71E+00	7.23E-120	Down	-4.36E-01	3.05E-13		Unigene3826_All//gi|28301674|emb|CAB63264.3|//1.00E-70//calcium-binding protein [Lotus japonicus]	Unigene3826_All//3.00E-55//AT3G07490| AGD11 (ARF-GAP domain 11); calcium ion binding	Unigene3826_All//0.00E+00//TC139630		ko04626|Plant-pathogen interaction		nr -
Unigene38261_All	871	6.31	7.91	6.42	12.24	13.48	8.92	2.48	5.52	4.53	3.27E-01	1.56E-01		2.54E-02	9.39E-01		1.40E-01	4.87E-01		-4.57E-01	8.90E-03		1.16E+00	4.07E-06	Up	8.71E-01	1.12E-03						Unigene38261_All//1.00E-18//ES820359				
Unigene38264_All	944	2.55	2.47	0.79	8.81	5.58	5.69	2.19	2.83	2.95	-4.62E-02	9.19E-01		-1.69E+00	2.30E-04	Down	-6.59E-01	4.07E-04		-6.30E-01	1.40E-03		3.69E-01	3.16E-01		4.29E-01	2.01E-01		Unigene38264_All//gi|297845902|ref|XP_002890832.1|//1.00E-111//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297336674|gb|EFH67091.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene38264_All//3.00E-100//AT1G29800| phosphoinositide binding / zinc ion binding	Unigene38264_All//5.00E-95//ES797221		ko04145|Phagosome//ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene38265_All	345	77.65	38.33	33.80	97.32	95.02	131.96	253.80	137.26	108.43	-1.02E+00	1.80E-20	Down	-1.20E+00	1.98E-25	Down	-3.45E-02	7.99E-01		4.39E-01	8.25E-09		-8.87E-01	1.80E-63		-1.23E+00	1.53E-110	Down	Unigene38265_All//gi|297812919|ref|XP_002874343.1|//3.00E-49//60S ribosomal protein L18 [Arabidopsis lyrata subsp. lyrata] >gi|297320180|gb|EFH50602.1| 60S ribosomal protein L18 [Arabidopsis lyrata subsp. lyrata]	Unigene38265_All//2.00E-50//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome	Unigene38265_All//2.00E-169//ES837275		ko03010|Ribosome		nr -
Unigene38266_All	697	18.99	9.16	6.72	20.23	17.34	28.32	59.93	22.91	21.72	-1.05E+00	4.86E-11	Down	-1.50E+00	8.18E-18	Down	-2.22E-01	1.62E-01		4.85E-01	6.43E-05		-1.39E+00	2.33E-62	Down	-1.46E+00	1.48E-69	Down	Unigene38266_All//gi|115452937|ref|NP_001050069.1|//3.00E-49//Os03g0341100 [Oryza sativa Japonica Group] >gi|113548540|dbj|BAF11983.1| Os03g0341100 [Oryza sativa Japonica Group]	Unigene38266_All//6.00E-42//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome	Unigene38266_All//0.00E+00//TC153002		ko03010|Ribosome		nr +
Unigene38268_All	929	6.59	9.76	8.77	4.29	18.13	13.52	4.46	11.38	8.02	5.67E-01	3.04E-03		4.12E-01	5.63E-02		2.08E+00	3.61E-42	Up	1.66E+00	1.71E-21	Up	1.35E+00	9.84E-16	Up	8.46E-01	6.44E-06		Unigene38268_All//gi|50404477|gb|AAT76903.1|//5.00E-47//IAA type protein [Elaeis guineensis]	Unigene38268_All//4.00E-38//AT3G04730| IAA16; transcription factor	Unigene38268_All//0.00E+00//gi|18099172|gb|BM358426.1|BM358426				nr -

Unigene38269_All	900	6.34	13.06	8.58	14.83	15.53	18.22	11.27	12.35	7.35	1.04E+00	9.85E-10	Up	4.37E-01	4.90E-02		6.66E-02	7.42E-01		2.96E-01	3.87E-02		1.32E-01	4.58E-01		-6.18E-01	7.16E-05		Unigene38269_All//gi|192913012|gb|ACF06614.1|//5.00E-47//holocarboxylase synthetase [Elaeis guineensis]	Unigene38269_All//7.00E-33//AT4G09830| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP009193 (InterPro:IPR016549); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64780.1); Has 56 Blast hits to 56 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene38269_All//0.00E+00//TC149362				nr -
Unigene38270_All	1226	181.42	138.20	223.08	42.18	37.33	33.56	5.55	1.81	1.36	-3.93E-01	6.02E-31		2.98E-01	4.62E-22		-1.76E-01	1.77E-02		-3.30E-01	4.07E-06		-1.62E+00	2.16E-13	Down	-2.02E+00	1.66E-18	Down	Unigene38270_All//gi|75162595|sp|Q8K593.1|LGLC_ARATH//1.00E-140//RecName: Full=Probable lactoylglutathione lyase, chloroplast; AltName: Full=Glyoxalase I; Flags: Precursor >gi|16930396|gb|AAL31884.1|AF419651_1 At1g67280/F1N21_10 [Arabidopsis thaliana] >gi|19310505|gb|AAL84986.1| At1g67280/F1N21_10 [Arabidopsis thaliana]	Unigene38270_All//6.00E-142//AT1G67280| lactoylglutathione lyase, putative / glyoxalase I, putative	Unigene38270_All//0.00E+00//TC139355		ko00620|Pyruvate metabolism		nr -
Unigene38271_All	701	12.54	33.25	24.38	26.22	23.82	17.85	43.61	48.95	22.96	1.41E+00	3.15E-29	Up	9.60E-01	1.22E-11		-1.38E-01	3.47E-01		-5.55E-01	9.43E-06		1.67E-01	5.92E-02		-9.26E-01	4.79E-25		Unigene38271_All//gi|297840125|ref|XP_002887944.1|//2.00E-84//protease-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333785|gb|EFH64203.1| protease-associated domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene38271_All//2.00E-85//AT1G63690| protease-associated (PA) domain-containing protein	Unigene38271_All//0.00E+00//TC148186				nr +
Unigene38272_All	1393	1.80	0.07	1.15	2.11	1.24	0.58	4.01	1.77	1.60	-4.63E+00	4.98E-12	Down	-6.53E-01	1.23E-01		-7.72E-01	2.61E-02		-1.85E+00	2.03E-06	Down	-1.18E+00	3.57E-07	Down	-1.32E+00	9.76E-09	Down	Unigene38272_All//gi|240254392|ref|NP_177883.5|//7.00E-27//binding [Arabidopsis thaliana]	Unigene38272_All//2.00E-38//AT1G77600| binding	Unigene38272_All//0.00E+00//ES804045				nr -
Unigene38273_All	830	19.73	8.00	11.55	3.30	3.03	2.23	34.18	9.32	9.17	-1.30E+00	1.25E-18	Down	-7.73E-01	6.17E-08		-1.24E-01	7.84E-01		-5.65E-01	1.48E-01		-1.88E+00	2.26E-65	Down	-1.90E+00	1.76E-68	Down	Unigene38273_All//gi|89274227|gb|AB065631.1|//6.00E-76//Streptomyces cyclase/dehydrase family protein [Brassica oleracea]	Unigene38273_All//5.00E-75//AT4G17870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Streptomyces cyclase/dehydrase (InterPro:IPR005031); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G46290.1); Has 177 Blast hits to 177 proteins in 18 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 177; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene38273_All//0.00E+00//gi|109872783|gb|DW501758.1|DW501758				nr -
Unigene38274_All	1415	1.85	2.18	0.23	2.85	4.14	3.73	6.10	0.86	2.25	2.41E-01	5.19E-01		-3.03E+00	9.96E-09	Down	5.37E-01	2.65E-02		3.89E-01	1.59E-01		-2.83E+00	4.49E-33	Down	-1.44E+00	1.20E-14	Down	Unigene38274_All//gi|38345316|emb|CAE03386.2|//2.00E-37//OSJNBa0004N05.10 [Oryza sativa (japonica cultivar-group)]	Unigene38274_All//1.00E-23//AT5G44040| unknown protein	Unigene38274_All//0.00E+00//DW518146				nr -
Unigene38275_All	1173	9.32	20.69	12.98	5.82	10.39	5.47	0.18	0.32	1.09	1.15E+00	1.98E-22	Up	4.78E-01	1.31E-03		8.37E-01	4.27E-08		-8.97E-02	7.15E-01		8.32E-01	4.67E-01		2.59E+00	3.78E-05	Up	Unigene38275_All//gi|164562217|gb|ABV61023.1|//2.00E-85//zinc finger homeodomain protein 1 [Saruma henryi]	Unigene38275_All//1.00E-61//AT4G24660| ATHB22 (HOMEOBOX PROTEIN 22); DNA binding / transcription factor	Unigene38275_All//0.00E+00//TC149750	zf-HD			nr -
Unigene38276_All	576	92.56	41.52	82.74	81.21	76.46	89.54	20.63	22.71	16.53	-1.16E+00	4.79E-49	Down	-1.62E-01	4.43E-02		-8.68E-02	3.41E-01		1.41E-01	8.12E-02		1.39E-01	4.02E-01		-3.19E-01	2.85E-02		Unigene38276_All//gi|3293261|gb|AAC25687.1|//1.00E-25//cystathionine gamma-synthase precursor [Arabidopsis thaliana]	Unigene38276_All//1.00E-16//AT3G01120| MTO1 (METHIONINE OVERACCUMULATION 1); cystathionine gamma-synthase	Unigene38276_All//0.00E+00//gi|78329977|gb|DT550251.1|DT550251		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr -
Unigene38277_All	1021	3.54	8.19	1.56	43.81	62.63	110.23	49.90	168.33	191.51	1.21E+00	7.24E-09	Up	-1.18E+00	6.34E-04	Down	5.16E-01	1.34E-17		1.33E+00	3.48E-137	Up	1.75E+00	0.00E+00	Up	1.94E+00	0.00E+00	Up	Unigene38277_All//gi|89258498|gb|AB065462.1|//2.00E-87//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene38277_All//6.00E-58//AT2G47140| short-chain dehydrogenase/reductase (SDR) family protein	Unigene38277_All//4.00E-142//gi|3325781|gb|AI054667.1|AI054667		ko00906|Carotenoid biosynthesis		nr -
Unigene3828_All	1225	45.87	44.34	49.90	134.80	135.94	126.09	185.83	105.77	63.58	-4.90E-02	5.68E-01		1.22E-01	1.15E-01		1.21E-02	8.19E-01		-9.64E-02	2.40E-02		-8.13E-01	2.30E-141		-1.55E+00	0.00E+00	Down	Unigene3828_All//gi|2963361|emb|CAA50575.1|//1.00E-62//cytochrome b5 [Nicotiana tabacum]	Unigene3828_All//4.00E-59//AT2G32720| CB5-B (CYTOCHROME B5 ISOFORM B); heme binding	Unigene3828_All//0.00E+00//TC138135		ko00910|Nitrogen metabolism		nr +
Unigene38280_All	1027	31.08	28.37	28.67	40.65	36.31	35.22	23.92	11.44	7.76	-1.32E-01	2.16E-01		-1.16E-01	3.04E-01		-1.63E-01	5.87E-02		-2.07E-01	1.59E-02		-1.06E+00	1.26E-24	Down	-1.62E+00	6.41E-48	Down	Unigene38280_All//gi|15226156|ref|NP_180930.1|//3.00E-59//CUTA; copper ion binding [Arabidopsis thaliana] >gi|73620711|sp|P93009.1|CUTA_ARATH RecName: Full=Protein CutA, chloroplastic; AltName: Full=Copper-binding protein CutA; Short=AtCUTA; Flags: Precursor >gi|12963361|gb|AAK11228.1|AF327524_1 copper-binding protein CUTA [Arabidopsis thaliana]	Unigene38280_All//2.00E-60//AT2G33740| CUTA; copper ion binding	Unigene38280_All//0.00E+00//TC142265				nr -
Unigene38281_All	931	6.41	8.65	19.28	22.90	31.25	59.04	11.90	2.51	2.91	4.34E-01	3.67E-02		1.59E+00	3.65E-26	Up	4.49E-01	1.55E-06		1.37E+00	6.90E-70	Up	-2.24E+00	1.49E-32	Down	-2.03E+00	9.77E-30	Down	Unigene38281_All//gi|34146816|gb|AAQ62416.1|//3.00E-61//At5g65340 [Arabidopsis thaliana]	Unigene38281_All//2.00E-63//AT2G22460| unknown protein	Unigene38281_All//0.00E+00//TC162764				nr +
Unigene38284_All	1047	34.93	40.31	27.97	31.35	22.99	35.54	36.59	46.35	17.43	2.07E-01	1.52E-02		-3.21E-01	5.39E-04		-4.48E-01	1.94E-07		1.81E-01	5.49E-02		3.41E-01	4.91E-07		-1.07E+00	2.22E-39	Down	Unigene38284_All//gi|29826242|gb|AA091861.1|//9.00E-49//TGB12K interacting protein 2 [Nicotiana tabacum]	Unigene38284_All//1.00E-45//AT4G35450| AKR2 (ANKYRIN REPEAT-CONTAINING PROTEIN 2); protein binding	Unigene38284_All//0.00E+00//TC175653				nr -
Unigene38285_All	1261	168.04	56.09	104.60	25.99	26.00	14.04	0.23	0.13	0.06	-1.58E+00	0.00E+00	Down	-6.84E-01	2.63E-77		2.00E-04	9.98E-01		-8.89E-01	1.97E-21		-8.24E-01	5.40E-01		-1.89E+00	1.68E-01		Unigene38285_All//gi|164459312|gb|ABY57763.1|//1.00E-150//extracellular Ca2+ sensing receptor [Glycine max]	Unigene38285_All//2.00E-123//AT5G23060| CaS (Calcium sensing receptor)	Unigene38285_All//0.00E+00//TC139902				nr +
Unigene38288_All	955	1.53	2.49	3.85	3.08	2.20	2.65	4.74	3.28	8.22	7.01E-01	8.95E-02		1.33E+00	1.20E-04	Up	-4.85E-01	1.84E-01		-2.17E-01	6.19E-01		-5.29E-01	3.90E-02		7.95E-01	1.20E-05		Unigene38288_All//gi|115439343|ref|NP_001043951.1|//6.00E-09//Os01g0694200 [Oryza sativa Japonica Group] >gi|113533482|dbj|BAF05865.1|Os01g0694200 [Oryza sativa Japonica Group]		Unigene38288_All//3.00E-146//AW187267				nr +
Unigene38289_All	681	17.06	46.28	14.47	16.60	13.91	15.05	26.82	60.94	44.11	1.44E+00	1.15E-40	Up	-2.38E-01	2.03E-01		-2.56E-01	1.50E-01		-1.41E-01	4.76E-01		1.18E+00	1.65E-48	Up	7.18E-01	3.76E-16		Unigene38289_All//gi|183979104|emb|CAP08301.1|//1.00E-32//DNA-binding protein [Vitis thunbergii]	Unigene38289_All//3.00E-23//AT2G03340| WRKY3; transcription factor	Unigene38289_All//0.00E+00//gi|210999924|gb|BQ412237.1|BQ412237	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene3829_All	1287	93.10	126.38	128.10	63.83	94.42	94.85	24.70	18.77	11.17	4.41E-01	4.12E-28		4.61E-01	8.98E-30		5.65E-01	4.89E-39		5.72E-01	3.60E-36		-3.96E-01	3.25E-06		-1.14E+00	1.61E-36	Down	Unigene3829_All//gi|238836224|gb|AC861392.1|//1.00E-174//phytoene synthase protein [Fragaria x ananassa]	Unigene3829_All//1.00E-147//AT5G17230| phytoene synthase (PSY) / geranylgeranyl-diphosphate geranylgeranyl transferase	Unigene3829_All//0.00E+00//TC134139		ko00906|Carotenoid biosynthesis		nr -
Unigene38295_All	759	24.61	24.77	21.26	30.26	25.00	34.04	2.17	1.10	0.47	9.20E-03	9.69E-01		-2.11E-01	1.39E-01		-2.75E-01	1.43E-02		1.70E-01	1.55E-01		-9.80E-01	3.31E-02		-2.20E+00	1.44E-05	Down	Unigene38295_All//gi|116309502|emb|CAH66569.1|//6.00E-22//OSIGBa0148P16.3 [Oryza sativa (indica cultivar-group)]	Unigene38295_All//5.00E-17//AT3G48550| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: nucleic acid binding / transcription factor/ zinc ion binding (TAIR:AT2G01940.3); Has 40 Blast hits to 40 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene38295_All//0.00E+00//DW505845				nr -
Unigene38299_All	1173	6.96	21.94	21.06	13.50	16.38	10.20	1.30	0.46	0.58	1.66E+00	8.91E-41	Up	1.60E+00	3.91E-36	Up	2.79E-01	2.84E-02		-4.04E-01	3.74E-03		-1.49E+00	2.91E-03		-1.17E+00	1.25E-02		Unigene38299_All//gi|300267101|gb|EF151286.1|//1.00E-06//hypothetical protein VOLCADRAFT_87950 [Volvox carteri f. nagariensis]		Unigene38299_All//4.00E-53//DW232722				nr -
Unigene3830_All	1557	150.81	40.71	86.77	43.58	33.86	17.78	0.16	0.16	0.26	-1.89E+00	0.00E+00	Down	-7.98E-01	7.66E-112		-3.64E-01	3.25E-10		-1.29E+00	2.21E-80	Down	-1.60E-02	1.02E+00		6.52E-01	5.44E-01		Unigene3830_All//gi|115463661|ref|NP_001055430.1|//1.00E-129//Os05g0388600 [Oryza sativa Japonica Group] >gi|113578981|dbj|BAF17344.1|Os05g0388600 [Oryza sativa Japonica Group]	Unigene3830_All//7.00E-109//AT5G12470| unknown protein	Unigene3830_All//0.00E+00//TC156037				nr +

Unigene38302_All	1793	0.12	0.90	0.18	1.11	0.33	1.41	4.83	19.28	154.64	2.95E+00	9.24E-06	Up	6.11E-01	6.24E-01		-1.77E+00	8.96E-05	Down	3.44E-01	4.37E-01		2.00E+00	4.12E-86	Up	5.00E+00	0.00E+00	Up	Unigene38302_All//gi|8778214|gb|AAF79223.1|AC006917,8//1.00E-165//P10B6.18 [Arabidopsis thaliana]	Unigene38302_All//2.00E-171//AT1G14780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24290.2); Has 119 Blast hits to 118 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 14; Fungi - 0; Plants - 105; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene38302_All//0.00E+00//gi|109864394|gb|DW493370.1|DW493370				nr +
Unigene38304_All	1547	0.27	0.62	0.07	3.90	2.32	2.89	11.07	4.97	5.15	1.20E+00	9.57E-02		-1.98E+00	1.51E-01		-7.51E-01	8.10E-04		-4.31E-01	8.30E-02		-1.15E+00	9.56E-20	Down	-1.10E+00	5.46E-19	Down	Unigene38304_All//gi|71041104|gb|AAZ20440.1|/1.00E-83//MYB24 [Malus x domestica]	Unigene38304_All//3.00E-61//AT5G65790| MYB68 (MYB DOMAIN PROTEIN 68); DNA binding / transcription factor	Unigene38304_All//1.00E-44//gi|109890159|gb|DW519123.1|DW519123	MYB			nr +
Unigene38305_All	1153	0.27	23.34	0.00	3.41	12.90	5.76	0.99	2.57	61.40	6.42E+00	2.12E-143	Up	-8.09E+00	4.90E-02		1.92E+00	1.24E-33	Up	7.55E-01	8.22E-04		1.38E+00	4.21E-05	Up	5.95E+00	0.00E+00	Up	Unigene38305_All//gi|224123482|ref|XP_002330325.1|/2.00E-57//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222871360|gb|EEF08491.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene38305_All//1.00E-32//AT4G34410| RRTF1 ((REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor	Unigene38305_All//0.00E+00//gi|78324872|gb|DT545146.1|DT545146	AP2-EREBP			nr -
Unigene38307_All	717	0.95	0.92	2.08	22.65	13.74	9.32	6.49	3.61	5.50	-4.62E-02	9.69E-01		1.13E+00	4.89E-02		-7.22E-01	1.20E-08		-1.28E+00	2.47E-19	Down	-8.44E-01	7.12E-04		-2.38E-01	3.58E-01		Unigene38307_All//gi|15529149|gb|AA897669.1|/2.00E-62//AT3g21550/MIL23_11 [Arabidopsis thaliana] >gi|16974353|gb|AAL31102.1| AT3g21550/MIL23_11 [Arabidopsis thaliana]	Unigene38307_All//6.00E-60//AT3G21550| unknown protein	Unigene38307_All//0.00E+00//TC133915				nr -
Unigene38309_All	943	1.28	0.16	0.34	0.85	0.58	0.67	1.30	1.15	0.42	-2.98E+00	1.58E-04	Down	-1.91E+00	7.10E-03		-5.33E-01	5.10E-01		-3.34E-01	6.86E-01		-1.74E-01	7.49E-01		-1.62E+00	3.49E-03		Unigene38309_All//gi|18405960|ref|NP_565971.1|//3.00E-58//protein kinase C substrate, heavy chain-related [Arabidopsis thaliana] >gi|20197489|gb|AAD23722.2| expressed protein [Arabidopsis thaliana]	Unigene38309_All//2.00E-54//AT2G42390| protein kinase C substrate, heavy chain-related	Unigene38309_All//0.00E+00//gi|109877603|gb|DW506576.1|DW506576		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene3831_All	1389	1.92	5.18	0.88	1.97	3.79	2.73	0.61	0.78	105.75	1.43E+00	9.22E-10	Up	-1.12E+00	6.04E-03		9.43E-01	1.59E-04		4.70E-01	1.55E-01		3.62E-01	5.69E-01		7.44E+00	0.00E+00	Up	Unigene3831_All//gi|297836190|ref|XP_002885977.1|//3.00E-23//calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297331817|gb|EFH62236.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene3831_All//3.00E-20//AT2G15760| calmodulin-binding protein	Unigene3831_All//0.00E+00//gi|164268395|gb|ES831124.1|ES831124				nr +
Unigene38310_All	779	17.80	14.05	15.38	30.57	22.68	23.36	21.33	10.52	7.26	-3.41E-01	2.64E-02		-2.11E-01	2.19E-01		-4.31E-01	3.28E-05		-3.88E-01	4.35E-04		-1.02E+00	7.71E-16	Down	-1.55E+00	1.02E-30	Down	Unigene38310_All//gi|88010951|gb|AB358877.1|/6.00E-40//At1g05205 [Arabidopsis thaliana]	Unigene38310_All//3.00E-41//AT1G05205| unknown protein	Unigene38310_All//0.00E+00//TC166657				nr +
Unigene38312_All	845	49.60	21.71	25.08	35.55	26.45	29.24	26.42	13.11	9.81	-1.19E+00	1.41E-40	Down	-9.84E-01	9.05E-29		-4.27E-01	2.57E-06		-2.82E-01	4.62E-03		-1.01E+00	1.05E-20	Down	-1.43E+00	2.78E-36	Down	Unigene38312_All//gi|225463238|ref|XP_002273609.1|/5.00E-44//PREDICTED: similar to structural constituent of ribosome [Vitis vinifera]	Unigene38312_All//5.00E-20//AT5G45590| unknown protein	Unigene38312_All//0.00E+00//TC172023				nr +
Unigene38313_All	887	2.48	65.86	0.72	5.50	15.92	5.14	1.19	14.80	66.83	4.73E+00	7.10E-273	Up	-1.78E+00	2.71E-04	Down	1.53E+00	1.74E-23	Up	-9.79E-02	7.39E-01		3.63E+00	7.17E-63	Up	5.81E+00	0.00E+00	Up	Unigene38313_All//gi|224069196|ref|XP_002326298.1|//6.00E-66//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|148372128|gb|ABQ62995.1| RAP2-like protein [Populus trichocarpa] >gi|222833491|gb|EEE71968.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene38313_All//5.00E-44//AT1G19210| AP2 domain-containing transcription factor, putative	Unigene38313_All//0.00E+00//TC149990	AP2-EREBP			nr +
Unigene38317_All	607	10.08	5.51	5.35	11.90	6.98	5.21	7.04	4.61	3.68	-8.72E-01	2.76E-04		-9.14E-01	2.56E-04		-7.70E-01	1.30E-04		-1.19E+00	4.81E-08	Down	-6.09E-01	2.06E-02		-9.37E-01	2.48E-04		Unigene38317_All//gi|115469788|ref|NP_001058493.1|//3.00E-44//Os06g0702700 [Oryza sativa Japonica Group] >gi|113596533|dbj|BAF20407.1| Os06g0702700 [Oryza sativa Japonica Group]	Unigene38317_All//3.00E-39//AT2G24390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Butirosin biosynthesis, BtrG-like (InterPro:IPR013024), AIG2-like (InterPro:IPR009288); BEST Arabidopsis thaliana protein match is: avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related (TAIR:AT4G31310.1); Has 204 Blast hits to 204 proteins in 63 species: Archae - 15; Bacteria - 49; Metazoa - 0; Fungi - 38; Plants - 61; Viruses - 0; Other Eukaryotes - 41 (source: NCBI BLink).	Unigene38317_All//2.00E-177//TC152591				nr +
Unigene38319_All	811	0.52	6.50	1.90	3.01	2.63	4.29	15.95	32.62	25.84	3.65E+00	6.74E-21	Up	1.88E+00	1.93E-03		-1.93E-01	6.50E-01		5.11E-01	1.38E-01		1.03E+00	3.71E-25	Up	6.96E-01	5.65E-11		Unigene38319_All//gi|224075517|ref|XP_002304662.1|//3.00E-09//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842094|gb|EEE79641.1| NAC domain protein, IPR003441 [Populus trichocarpa]		Unigene38319_All//0.00E+00//gi|109868552|gb|DW497528.1|DW497528				nr +
Unigene3832_All	1195	2.19	3.73	2.90	2.58	2.07	0.91	1.06	1.36	1.30	7.69E-01	7.36E-03		4.04E-01	2.51E-01		-3.17E-01	4.02E-01		-1.51E+00	3.39E-05	Down	3.62E-01	4.56E-01		2.93E-01	5.53E-01		Unigene3832_All//gi|75213194|sp|Q9SX85.1|SEC3A_ARATH//1.00E-158//RecName: Full=Exocyst complex component SEC3A >gi|5668806|gb|AAD46032.1|AC007519_17 Strong similarity to F16N3.17 from Arabidopsis thalian BAC gb|AC007519 [Arabidopsis thaliana]	Unigene3832_All//2.00E-159//AT1G47550| unknown protein	Unigene3832_All//4.00E-115//TC169454				nr +
Unigene38320_All	710	10.39	126.89	88.20	17.05	180.91	369.70	13.04	166.36	16.44	3.61E+00	0.00E+00	Up	3.09E+00	2.37E-205	Up	3.41E+00	0.00E+00	Up	4.44E+00	0.00E+00	Up	3.67E+00	0.00E+00	Up	3.34E-01	2.32E-02		Unigene38320_All//gi|297823659|ref|XP_002879712.1|//7.00E-40//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325551|gb|EFH55971.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38320_All//3.00E-34//AT2G37870| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene38320_All//9.00E-158//gi|164243185|gb|ES842373.1|ES842373				nr -
Unigene38322_All	982	54.56	22.39	32.92	16.59	14.83	13.15	8.91	5.28	4.02	-1.28E+00	4.59E-58	Down	-7.29E-01	3.34E-22		-1.61E-01	3.04E-01		-3.35E-01	1.72E-02		-7.56E-01	1.40E-05		-1.15E+00	9.01E-11	Down	Unigene38322_All//gi|297833622|ref|XP_002884693.1|//1.00E-88//elongation factor P (EF-P) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330533|gb|EFH60952.1| elongation factor P (EF-P) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38322_All//9.00E-87//AT3G08740| elongation factor P (EF-P) family protein	Unigene38322_All//0.00E+00//gi|109857909|gb|DW486888.1|DW486888				nr +
Unigene38323_All	787	6.38	50.09	17.73	12.91	9.54	9.07	3.76	2.97	4.30	2.97E+00	3.46E-127	Up	1.47E+00	2.29E-18	Up	-4.37E-01	1.12E-02		-5.10E-01	4.11E-03		-3.39E-01	3.34E-01		1.94E-01	5.51E-01		Unigene38323_All//gi|219842174|dbj|BAH10644.1|//1.00E-97//tocopherol cyclase [Hevea brasiliensis]	Unigene38323_All//6.00E-89//AT4G32770| VTE1 (VITAMIN E DEFICIENT 1); tocopherol cyclase	Unigene38323_All//0.00E+00//gi|164343584|gb|ES830984.1|ES830984		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene38324_All	1212	5.74	4.56	2.11	9.82	14.35	10.10	17.30	2.31	3.81	-3.33E-01	1.44E-01		-1.44E+00	3.55E-09	Down	5.47E-01	1.15E-05		3.99E-02	8.42E-01		-2.90E+00	1.15E-81	Down	-2.18E+00	8.07E-61	Down	Unigene38324_All//gi|255545204|ref|XP_002513663.1|//3.00E-42//conserved hypothetical protein [Ricinus communis] >gi|223547571|gb|EEF49066.1| conserved hypothetical protein [Ricinus communis]		Unigene38324_All//0.00E+00//TC145524				nr +
Unigene3833_All	998	9.91	10.66	4.54	33.04	17.08	17.92	33.00	38.19	38.36	1.06E-01	6.08E-01		-1.13E+00	6.62E-09	Down	-9.52E-01	2.81E-27		-8.83E-01	2.53E-21		2.11E-01	8.81E-03		2.17E-01	5.07E-03		Unigene3833_All//gi|15724294|gb|AAL06540.1|AF412087_1//8.00E-26//AT3g45210/T14D3_150 [Arabidopsis thaliana] >gi|20334744|gb|AAM16233.1| AT3g45210/T14D3_150 [Arabidopsis thaliana]	Unigene3833_All//1.00E-31//AT5G60680| unknown protein	Unigene3833_All//0.00E+00//gi|164246228|gb|ES827823.1|ES827823				nr +
Unigene38330_All	962	3.10	2.05	1.16	50.07	38.19	22.86	6.99	3.35	2.40	-5.94E-01	1.01E-01		-1.42E+00	3.22E-04	Down	-3.91E-01	2.17E-08		-1.13E+00	2.53E-46	Down	-1.06E+00	2.64E-07	Down	-1.54E+00	8.73E-13	Down	Unigene38330_All//gi|15222421|ref|NP_177128.1|//5.00E-68//ATHVA22C [Arabidopsis thaliana] >gi|57012624|sp|Q9SZ84.1|HA22C_ARATH RecName: Full=HVA22-like protein c; Short=AtHVA22c >gi|4884946|gb|AAD31886.1|AF141978_1 AtHVA22c [Arabidopsis thaliana] >gi|12325187|gb|AAG52538.1|AC013289_5 AtHVA22c; 50565-49239 [Arabidopsis thaliana] >gi|4884936|gb|AAD31881.1| AtHVA22c [Arabidopsis thaliana] >gi|21536712|gb|AAM61044.1| AtHVA22c [Arabidopsis thaliana]	Unigene38330_All//2.00E-69//AT1G69700| ATHVA22C	Unigene38330_All//0.00E+00//DW507846				nr -
Unigene38331_All	1079	9.41	3.48	4.98	27.61	23.36	18.46	36.28	11.08	12.07	-1.44E+00	1.30E-13	Down	-9.16E-01	1.08E-06		-2.41E-01	1.40E-02		-5.81E-01	1.36E-09		-1.71E+00	2.45E-79	Down	-1.59E+00	2.05E-73	Down	Unigene38331_All//gi|15237758|ref|NP_201274.1|//2.00E-06//neurofilament triplet H protein-related [Arabidopsis thaliana] >gi|29029084|gb|AAO64921.1| At5g64690 [Arabidopsis thaliana]		Unigene38331_All//0.00E+00//TC142362				nr +

Unigene38332_All	1042	7.28	4.86	7.26	7.22	7.53	9.41	10.31	8.30	4.47	-5.82E-01	5.85E-03		-4.80E-03	1.00E+00		6.18E-02	8.36E-01		3.82E-01	4.30E-02		-3.12E-01	5.35E-02		-1.20E+00	6.15E-14	Down	Unigene38332_All//gi|42573748|ref|NP_974970.1|//3.00E-93//yrdC protein-related [Arabidopsis thaliana]	Unigene38332_All//1.00E-94//AT5G60590| yrdC protein-related	Unigene38332_All//0.00E+00//TC168135				nr -
Unigene38333_All	1088	1.30	6.24	3.33	7.88	4.08	4.94	24.21	31.00	15.20	2.26E+00	1.13E-16	Up	1.36E+00	9.94E-05	Up	-9.48E-01	2.14E-07		-6.73E-01	5.01E-04		3.57E-01	1.61E-05		-6.72E-01	7.11E-13		Unigene38333_All//gi|15294284|gb|AAB95319.1|AF410333_1//1.00E-101//AT3g62730/F26B9_160 [Arabidopsis thaliana] >gi|20147275|gb|AAM10351.1|AT3g62730/F26B9_160 [Arabidopsis thaliana]	Unigene38333_All//2.00E-102//AT3G62730| unknown protein	Unigene38333_All//0.00E+00//TC134498				nr +
Unigene38338_All	1973	1.30	1.08	1.43	3.31	3.77	2.86	1.99	0.68	1.03	-2.69E-01	5.10E-01		1.39E-01	7.15E-01		1.89E-01	4.54E-01		-2.09E-01	4.27E-01		-1.56E+00	1.20E-07	Down	-9.53E-01	3.78E-04		Unigene38338_All//gi|30681096|ref|NP_179660.2|//9.00E-93//glycosyl hydrolase family 5 protein / cellulase family protein [Arabidopsis thaliana] >gi|75233455|sp|Q7Y223.1|MAN2_ARATH RecName: Full=Mannan endo-1,4-beta-mannosidase 2; AltName: Full=Beta-mannanase 2; AltName: Full=Endo-beta-1,4-mannanase 2; Short=AtMAN2; Flags: Precursor >gi|109134159|gb|ABG25077.1|At2g20680 [Arabidopsis thaliana]	Unigene38338_All//1.00E-88//AT2G20680| glycosyl hydrolase family 5 protein / cellulase family protein	Unigene38338_All//0.00E+00//EE592873				nr -
Unigene38339_All	802	0.72	2.27	1.39	2.24	1.89	2.59	2.21	2.14	6.26	1.66E+00	1.30E-03		9.58E-01	1.54E-01		-2.43E-01	6.16E-01		2.12E-01	6.74E-01		-5.14E-02	9.23E-01		1.50E+00	2.58E-09	Up	Unigene38339_All//gi|75181359|sp|Q9LZX1.1|Y5175_ARATH//5.00E-21//RecName: Full=UPF0706 protein At5g01750 >gi|13926237|gb|AAK49593.1|AF372877_1 AT5g01750/T20L15_20 [Arabidopsis thaliana] >gi|22655412|gb|AAM88298.1|At5g01750/T20L15_20 [Arabidopsis thaliana]	Unigene38339_All//6.00E-36//AT2G30270| unknown protein	Unigene38339_All//0.00E+00//TC177311				nr -
Unigene38340_All	934	20.05	22.62	19.84	37.28	29.86	28.24	6.61	6.18	13.61	1.74E-01	1.80E-01		-1.55E-02	9.28E-01		-3.20E-01	1.81E-04		-4.01E-01	5.87E-06		-9.79E-02	6.78E-01		1.04E+00	5.08E-13	Up	Unigene38340_All//gi|88900406|gb|ABD57515.1|//3.00E-15//At4g02040 [Arabidopsis thaliana]	Unigene38340_All//5.00E-11//AT4G02040| unknown protein	Unigene38340_All//0.00E+00//TC165274				nr +
Unigene38341_All	2372	0.44	0.30	0.56	1.91	1.02	0.61	4.90	10.80	5.78	-5.61E-01	3.82E-01		3.47E-01	5.78E-01		-9.11E-01	5.64E-04		-1.65E+00	3.18E-08	Down	1.14E+00	1.65E-28	Up	2.37E-01	8.80E-02		Unigene38341_All//gi|224066759|ref|XP_002302201.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222843927|gb|EEE81474.1| GRAS family transcription factor [Populus trichocarpa]	Unigene38341_All//5.00E-172//AT1G21450| SCL1 (SCARECROW-LIKE 1); transcription factor	Unigene38341_All//2.00E-167//gi|78339787|gb|DT560061.1|DT560061	GRAS			nr +
Unigene38344_All	593	92.38	49.05	51.99	16.46	46.86	162.76	53.19	69.99	269.80	-9.13E-01	2.13E-34		-8.29E-01	3.25E-28		1.51E+00	4.96E-45	Up	3.31E+00	0.00E+00	Up	3.96E-01	7.60E-08		2.34E+00	0.00E+00	Up	Unigene38344_All//gi|74273617|gb|AB01476.1|//3.00E-65//ACC oxidase AC04 [Gossypium hirsutum]	Unigene38344_All//1.00E-46//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene38344_All//0.00E+00//TC129657		ko00270|Cysteine and methionine metabolism		nr -
Unigene38345_All	683	18.54	8.31	15.44	29.39	17.95	17.85	2.29	4.10	3.73	-1.16E+00	3.10E-12	Down	-2.64E-01	1.34E-01		-7.12E-01	2.58E-10		-7.19E-01	1.84E-09		8.40E-01	1.22E-02		7.05E-01	3.93E-02					Unigene38345_All//1.00E-24//gi|164325842|gb|ES828255.1|ES828255				
Unigene38349_All	1217	0.64	0.17	0.18	2.78	0.82	1.22	8.48	25.14	10.84	-1.95E+00	2.62E-02		-1.88E+00	4.13E-02		-1.76E+00	1.07E-07	Down	-1.18E+00	4.22E-04	Down	1.57E+00	8.41E-55	Up	3.54E-01	9.50E-03		Unigene38349_All//gi|94136581|gb|ACF33513.1|//1.00E-136//salicylic acid methyl transferase-like protein [Glycine max]	Unigene38349_All//4.00E-129//AT4G36470| S-adenosyl-L-methionine:carboxyl methyltransferase family protein	Unigene38349_All//0.00E+00//ES829240		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene38350_All	784	0.53	2.33	1.02	2.29	2.50	1.44	4.26	6.40	5.74	2.12E+00	1.13E-04	Up	9.32E-01	2.56E-01		1.30E-01	8.35E-01		-6.67E-01	1.86E-01		5.87E-01	1.44E-02		4.31E-01	8.67E-02					Unigene38350_All//0.00E+00//TC172109				
Unigene38354_All	1543	0.34	0.26	0.38	4.07	2.28	1.52	6.66	1.63	1.06	-3.68E-01	6.83E-01		1.63E-01	8.50E-01		-8.38E-01	1.24E-04		-1.42E+00	4.64E-09	Down	-2.03E+00	8.17E-27	Down	-2.65E+00	7.03E-38	Down	Unigene38354_All//gi|294769202|gb|ADF36482.1|//0.00E+00//high-affinity potassium transporter protein 2 [Gossypium hirsutum]	Unigene38354_All//0.00E+00//AT5G14880| potassium transporter, putative	Unigene38354_All//0.00E+00//ES808336				nr +
Unigene38355_All	577	13.33	14.40	5.91	12.95	11.46	16.12	8.94	8.69	11.74	1.12E-01	6.04E-01		-1.17E+00	1.66E-07	Down	-1.77E-01	4.68E-01		3.16E-01	1.17E-01		-4.05E-02	8.85E-01		3.93E-01	4.85E-02					Unigene38355_All//1.00E-08//DW517301				
Unigene38356_All	759	6.69	28.71	7.16	8.40	9.21	20.77	42.50	79.46	45.66	2.10E+00	1.60E-47	Up	9.79E-02	7.17E-01		1.33E-01	6.03E-01		1.31E+00	4.75E-19	Up	9.03E-01	3.14E-45		1.04E-01	2.51E-01		Unigene38356_All//gi|70609694|gb|AAD50072.1|//4.00E-41//hypoxia-responsive family protein [Citrus sinensis]	Unigene38356_All//7.00E-28//AT3G05550| hypoxia-responsive family protein	Unigene38356_All//0.00E+00//TC158407				nr +
Unigene38358_All	922	0.11	0.22	0.75	3.13	18.45	15.14	9.54	34.18	72.68	9.54E-01	6.21E-01		2.73E+00	1.40E-02		2.56E+00	2.09E-54	Up	2.27E+00	5.62E-36	Up	1.84E+00	1.34E-70	Up	2.93E+00	6.01E-266	Up	Unigene38358_All//gi|115450803|ref|NP_001049002.1|//2.00E-73//Os03g0154100 [Oryza sativa Japonica Group] >gi|108706247|gb|ABF94042.1| FAD binding domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547473|dbj|BAF10916.1|Os03g0154100 [Oryza sativa Japonica Group]	Unigene38358_All//6.00E-69//AT4G38540| monooxygenase, putative (MO2)	Unigene38358_All//2.00E-128//gi|48750026|gb|CO080545.1|CO080545				nr +
Unigene38359_All	1219	2.45	2.04	5.37	1.14	1.92	0.82	0.10	0.00	0.00	-2.64E-01	4.79E-01		1.14E+00	3.35E-06	Up	7.47E-01	7.48E-02		-4.89E-01	4.09E-01		-6.70E+00	2.35E-01		-6.70E+00	2.00E-01		Unigene38359_All//gi|38344225|emb|CAE03693.2|//3.00E-06//OSJNBb0026E15.13 [Oryza sativa (japonica cultivar-group)]						nr -
Unigene38360_All	625	10.13	22.46	18.40	15.62	18.51	14.24	14.68	14.58	7.46	1.15E+00	2.92E-13	Up	8.61E-01	7.86E-07		2.45E-01	1.70E-01		-1.34E-01	5.48E-01		-1.00E-02	9.92E-01		-9.77E-01	7.85E-09		Unigene38360_All//gi|109134221|gb|ABG25108.1|//9.00E-27//At5g63905 [Arabidopsis thaliana]		Unigene38360_All//0.00E+00//gi|21091535|gb|BQ403848.1|BQ403848				nr -
Unigene38362_All	611	6.94	7.38	7.15	10.27	7.27	7.61	45.26	29.96	21.91	8.96E-02	7.55E-01		4.31E-02	8.93E-01		-4.99E-01	2.84E-02		-4.32E-01	7.41E-02		-5.95E-01	1.10E-10		-1.05E+00	1.08E-27	Down	Unigene38362_All//gi|5230728|gb|AAD40979.1|AF089851_1//2.00E-39//peroxisomal copper-containing amine oxidase [Glycine max]	Unigene38362_All//5.00E-36//AT2G42490| copper amine oxidase, putative	Unigene38362_All//0.00E+00//TC141748		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene38364_All	921	2.67	5.61	4.16	3.84	3.66	1.81	1.33	2.54	1.30	1.07E+00	6.58E-05	Up	6.41E-01	4.98E-02		-6.77E-02	8.36E-01		-1.08E+00	8.97E-04	Down	9.33E-01	1.24E-02		-3.69E-02	9.60E-01		Unigene38364_All//gi|115456649|ref|NP_001051925.1|//5.00E-48//Os03g0852600 [Oryza sativa Japonica Group] >gi|113550396|dbj|BAF13839.1|Os03g0852600 [Oryza sativa Japonica Group]	Unigene38364_All//4.00E-46//AT3G56830| unknown protein	Unigene38364_All//0.00E+00//TC144111				nr +
Unigene38365_All	757	6.15	3.41	3.02	18.03	5.55	3.46	90.87	47.21	26.00	-8.50E-01	2.38E-03		-1.02E+00	5.01E-04	Down	-1.70E+00	3.48E-28	Down	-2.38E+00	3.89E-38	Down	-9.45E-01	1.40E-55		-1.81E+00	5.02E-154	Down	Unigene38365_All//gi|197725474|gb|ACH72969.1|//2.00E-22//major latex-like protein [Panax ginseng]	Unigene38365_All//1.00E-22//AT1G70830| MLP28 (MLP-LIKE PROTEIN 28)	Unigene38365_All//0.00E+00//DW505476				nr -
Unigene38367_All	617	94.72	98.22	59.72	135.80	70.27	100.57	40.09	225.44	62.31	5.23E-02	5.18E-01		-6.65E-01	1.15E-20		-9.51E-01	1.07E-68		-4.33E-01	2.19E-15		2.49E+00	0.00E+00	Up	6.36E-01	1.10E-16		Unigene38367_All//gi|47779324|gb|AAT38561.1|//3.00E-38//mitochondrial serine acetyltransferase [Thlaspi goesingense]	Unigene38367_All//5.00E-30//AT3G13110| ATSERAT2;2 (SERINE ACETYLTRANSFERASE 2;2); serine O-acetyltransferase	Unigene38367_All//0.00E+00//TC165999		ko00270|Cysteine and methionine metabolism|ko00920|Sulfur metabolism		nr +
Unigene38369_All	668	21.54	29.43	23.20	67.04	55.93	40.50	8.48	4.19	4.53	4.50E-01	2.94E-04		1.07E-01	5.25E-01		-2.61E-01	5.47E-04		-7.27E-01	9.69E-21		-1.02E+00	6.69E-06	Down	-9.04E-01	3.40E-05		Unigene38369_All//gi|115479781|ref|NP_001063484.1|//1.00E-08//Os09g0480100 [Oryza sativa Japonica Group] >gi|113631717|dbj|BAF25398.1|Os09g0480100 [Oryza sativa Japonica Group]	Unigene38369_All//1.00E-18//AT3G13275| unknown protein	Unigene38369_All//0.00E+00//DW496699				nr +
Unigene38371_All	825	13.83	12.28	8.84	10.08	8.18	11.22	27.11	12.51	10.53	-1.71E-01	3.66E-01		-6.45E-01	2.15E-04		-3.02E-01	1.48E-01		1.54E-01	4.89E-01		-1.12E+00	3.38E-24	Down	-1.36E+00	6.29E-34	Down	Unigene38371_All//gi|192910790|gb|ACF06503.1|//1.00E-57//structural constituent of ribosome [Elaeis guineensis]	Unigene38371_All//1.00E-45//AT1G07830| ribosomal protein L29 family protein	Unigene38371_All//0.00E+00//TC149175				nr +
Unigene38372_All	626	6.69	31.32	7.06	8.12	25.14	12.84	29.45	85.39	48.49	2.23E+00	4.91E-46	Up	7.85E-02	7.94E-01		1.63E+00	1.46E-28	Up	6.62E-01	1.06E-03		1.54E+00	2.28E-92	Up	7.20E-01	2.19E-16		Unigene38372_All//gi|224127502|ref|XP_002320090.1|//3.00E-59//f-box family protein [Populus trichocarpa] >gi|222860863|gb|EEE98405.1| f-box family protein [Populus trichocarpa]	Unigene38372_All//4.00E-54//AT3G61060| AtFP2-A13 (Arabidopsis thaliana phloem protein 2-A13); carbohydrate binding	Unigene38372_All//0.00E+00//CO105320				nr +
Unigene38373_All	721	12.63	8.08	24.15	7.60	11.99	3.70	0.23	0.29	0.22	-6.44E-01	7.17E-04		9.36E-01	2.19E-11		6.58E-01	4.28E-04		-1.04E+00	3.64E-05	Down	3.05E-01	8.36E-01		-8.62E-02	9.65E-01		Unigene38373_All//gi|30685117|ref|NP_188519.2|//8.00E-26//binding / catalytic/ coenzyme binding [Arabidopsis thaliana] >gi|25083201|gb|AAN72050.1| Unknown protein [Arabidopsis thaliana] >gi|30725480|gb|AAP37762.1|At3g18890 [Arabidopsis thaliana]	Unigene38373_All//4.00E-27//AT3G18890| binding / catalytic/ coenzyme binding					nr -
Unigene38374_All	1683	1.31	136.74	19.84	1.84	19.38	42.18	0.00	0.15	0.95	6.71E+00	0.00E+00	Up	3.93E+00	4.72E-135	Up	3.40E+00	2.40E-138	Up	4.52E+00	0.00E+00	Up	7.22E+00	4.31E-02		9.89E+00	1.85E-11	Up	Unigene38374_All//gi|75102139|sp|Q39846.1|SBP65_SOYBN//4.00E-59//RecName: Full=Seed biotin-containing protein SBP65; AltName: Full=Seed biotinylated protein of 65 kDa; AltName: Full=BP75 >gi|1389897|gb|AAC61783.1| LEA protein [Glycine max]	Unigene38374_All//7.00E-25//AT2G42560| late embryogenesis abundant domain-containing protein / LEA domain-containing protein					nr -
Unigene38375_All	451	60.91	71.90	40.26	80.41	72.15	72.50	130.97	69.51	52.03	2.40E-01	1.40E-02		-5.97E-01	2.07E-08		-1.56E-01	9.96E-02		-1.49E-01	1.34E-01		-9.14E-01	2.74E-45		-1.33E+00	6.04E-85	Down	Unigene38375_All//gi|40850676|gb|AAR23816.2|//4.00E-32//betaine-aldehyde dehydrogenase [Gossypium hirsutum]	Unigene38375_All//4.00E-31//AT3G48170| ALDH10A9; 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Unigene38375_All//0.00E+00//gi|21100390|gb|BQ412703.1|BQ412703		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene38376_All	500	11.20	13.17	7.46	38.16	54.75	51.22	4.57	4.18	1.59	2.35E-01	3.46E-01		-5.87E-01	2.59E-02		5.21E-01	6.04E-08		4.25E-01	5.59E-05		-1.28E-01	7.45E-01		-1.52E+00	8.08E-05	Down	Unigene38376_All//gi|255710053|gb|ACL30848.1|//7.00E-32//cold-regulated LTCOR12 [Jatropha curcas]	Unigene38376_All//4.00E-28//AT2G18420| Encodes a Gibberellin-regulated GASA/GAST/Snakin family protein	Unigene38376_All//0.00E+00//gi|109869894|gb|DW498870.1|DW498870				nr -
Unigene38377_All	1021	17.53	14.04	13.72	8.44	7.69	7.08	11.55	8.80	4.21	-3.20E-01	1.68E-02		-3.54E-01	1.07E-02		-1.34E-01	5.60E-01		-2.54E-01	2.38E-01		-3.93E-01	8.53E-03		-1.46E+00	4.40E-20	Down	Unigene38377_All//gi|15238662|ref|NP_197286.1|//7.00E-06//chaperone protein dnaJ-related [Arabidopsis thaliana]	Unigene38377_All//1.00E-45//AT5G17840| chaperone protein dnaJ-related	Unigene38377_All//0.00E+00//TC160244				nr +

Unigene38378_All	795	72.26	264.18	74.22	51.07	151.43	55.05	75.63	401.03	125.53	1.87E+00	0.00E+00	Up	3.85E-02	6.25E-01		1.57E+00	3.58E-206	Up	1.08E-01	2.50E-01		2.41E+00	0.00E+00	Up	7.31E-01	3.26E-53		Unigene38378_All//gi|15218686|ref|NP_174170.1|//4.00E-31//GRX480; electron carrier/ protein disulfide oxidoreductase [Arabidopsis thaliana] >gi|75204928|sp|Q95GP6.1|GRXC9_ARATH RecName: Full=Glutaredoxin-C9; Short=AtGrxC9 >gi|6560751|gb|AAF16751.1|AC010155_4 F3M18.8 [Arabidopsis thaliana] >gi|17622208|gb|AAL40382.1|AF325030_1 At1g28480 [Arabidopsis thaliana] >gi|117168135|gb|ABK32150.1|At1g28480 [Arabidopsis thaliana] >gi|226348214|gb|ACO50423.1|glutaredoxin [Arabidopsis thaliana]	Unigene38378_All//2.00E-23//AT1G28480| GRX480; electron carrier/ protein disulfide oxidoreductase	Unigene38378_All//0.00E+00//TC151442				nr +
Unigene3838_All	320	11.94	12.98	10.98	14.48	16.68	35.57	91.03	102.79	214.13	1.22E-01	6.82E-01		-1.20E-01	7.12E-01		2.04E-01	5.09E-01		1.30E+00	9.16E-14	Up	1.75E-01	5.17E-02		1.23E+00	9.59E-87	Up	Unigene3838_All//gi|15242536|ref|NP_198817.1|//8.00E-27//AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene3838_All//3.00E-28//AT5G40010| AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene3838_All//5.00E-102//TC133425				nr +
Unigene38380_All	1104	31.99	68.11	41.38	58.34	82.00	63.57	70.51	91.24	70.37	1.09E+00	1.87E-62	Up	3.72E-01	4.39E-06		4.91E-01	1.03E-22		1.24E-01	7.18E-02		3.72E-01	5.65E-16		-2.80E-03	9.72E-01		Unigene38380_All//gi|224131746|ref|XP_002328098.1|//9.00E-37//ethylene-insensitive 3b [Populus trichocarpa] >gi|222837613|gb|EEE75978.1|ethylene-insensitive 3b [Populus trichocarpa]	Unigene38380_All//2.00E-10//AT3G20770| EIN3 (ETHYLENE-INSENSITIVE3); transcription factor	Unigene38380_All//0.00E+00//TC171233	EIL			nr -
Unigene38381_All	634	36.72	43.80	49.39	36.46	35.52	30.49	47.08	42.06	20.36	2.54E-01	1.66E-02		4.27E-01	1.70E-05		-3.75E-02	8.20E-01		-2.58E-01	2.91E-02		-1.63E-01	9.13E-02		-1.21E+00	2.02E-37	Down	Unigene38381_All//gi|20334820|gb|AAU61166.1|//2.00E-55//At1g12050/F12F1_8 [Arabidopsis thaliana]	Unigene38381_All//1.00E-56//AT1G12050| fumarylacetoacetase, putative	Unigene38381_All//0.00E+00//gi|164346807|gb|ES832055.1|ES832055		ko00350|Tyrosine metabolism		nr -
Unigene38385_All	753	0.42	1.88	0.78	1.98	3.29	1.62	2.81	2.72	1.75	2.18E+00	6.84E-04	Up	9.00E-01	3.77E-01		7.30E-01	7.12E-02		-2.93E-01	6.38E-01		-4.57E-02	9.27E-01		-6.85E-01	7.07E-02					Unigene38385_All//3.00E-53//gi|73943537|gb|DT526845.1|DT526845				
Unigene38387_All	479	8.96	16.61	14.01	14.98	10.42	14.61	58.17	36.82	22.29	8.91E-01	1.85E-05		6.45E-01	6.29E-03		-5.23E-01	1.21E-02		-3.52E-02	9.01E-01		-6.60E-01	9.20E-13		-1.38E+00	6.21E-43	Down	Unigene38387_All//gi|17978970|gb|AL47446.1|//7.00E-16//At2g36580/F10I1.21 [Arabidopsis thaliana]	Unigene38387_All//4.00E-17//AT2G36580| pyruvate kinase, putative	Unigene38387_All//0.00E+00//TC167448		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene38388_All	1512	1.76	0.94	1.16	2.83	2.07	1.61	5.70	3.21	1.90	-9.11E-01	1.83E-02		-6.03E-01	1.38E-01		-4.51E-01	1.23E-01		-8.13E-01	5.05E-03		-8.31E-01	2.42E-06		-1.59E+00	7.43E-17	Down	Unigene38388_All//gi|240256029|ref|NP_193884.6|//1.00E-155//nucleotide binding [Arabidopsis thaliana]	Unigene38388_All//2.00E-139//AT4G21530| nucleotide binding	Unigene38388_All//0.00E+00//DN759649				nr +
Unigene38389_All	1092	2.83	3.71	3.36	3.01	3.28	1.32	1.05	0.23	0.04	3.93E-01	2.10E-01		2.51E-01	4.68E-01		1.23E-01	7.73E-01		-1.19E+00	5.26E-04	Down	-2.19E+00	6.83E-04	Down	-4.84E+00	2.34E-07	Down	Unigene38389_All//gi|242085310|ref|XP_002443080.1|//1.00E-07//hypothetical protein SORBIDRAFT_08g007680 [Sorghum bicolor] >gi|241943773|gb|EES16918.1|hypothetical protein SORBIDRAFT_08g007680 [Sorghum bicolor]		Unigene38389_All//8.00E-36//DR461178				nr +
Unigene3839_All	592	8.93	19.17	12.23	19.52	33.33	52.64	60.14	91.15	275.30	1.10E+00	3.11E-10	Up	4.55E-01	4.78E-02		7.72E-01	3.21E-11		1.43E+00	1.17E-42	Up	6.00E-01	2.51E-20		2.19E+00	0.00E+00	Up	Unigene3839_All//gi|15242536|ref|NP_198817.1|//6.00E-60//AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene3839_All//3.00E-61//AT5G40010| AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene3839_All//0.00E+00//TC133425				nr +
Unigene38391_All	761	3.44	2.46	3.29	4.06	4.16	1.72	3.39	1.70	1.26	-4.81E-01	2.23E-01		-6.38E-02	8.77E-01		3.67E-02	9.44E-01		-1.24E+00	5.07E-04	Down	-9.93E-01	4.86E-03		-1.43E+00	5.84E-05	Down	Unigene38391_All//gi|125579912|gb|EAZ21058.1|//4.00E-06//hypothetical protein OsJ_36702 [Oryza sativa Japonica Group]						nr +
Unigene38392_All	1210	0.82	0.42	0.09	1.07	0.77	1.12	2.62	0.59	3.89	-9.72E-01	1.58E-01		-3.22E+00	7.83E-04	Down	-4.78E-01	4.24E-01		6.51E-02	9.33E-01		-2.16E+00	2.10E-09	Down	5.68E-01	1.84E-02		Unigene38392_All//gi|15226012|ref|NP_179089.1|//6.00E-81//NPY2 (NAKED PINS IN YUC MUTANTS 2); protein binding / signal transducer [Arabidopsis thaliana]	Unigene38392_All//8.00E-68//AT2G14820| NPY2 (NAKED PINS IN YUC MUTANTS 2); protein binding / signal transducer	Unigene38392_All//7.00E-129//gi|164259394|gb|ES812161.1|ES812161				nr +
Unigene38393_All	748	33.71	95.45	41.36	26.97	52.76	45.77	35.89	53.87	70.62	1.50E+00	4.06E-97	Up	2.95E-01	3.98E-03		9.68E-01	3.99E-32		7.63E-01	3.54E-17		5.86E-01	9.02E-15		9.76E-01	3.15E-46		Unigene38393_All//gi|14423428|gb|AK62396.1|AF386951_1//2.00E-38//Unknown protein [Arabidopsis thaliana]	Unigene38393_All//1.00E-39//AT1G27290| unknown protein	Unigene38393_All//0.00E+00//ES809813				nr -
Unigene38397_All	627	35.30	76.37	47.05	40.52	40.37	56.90	44.57	50.39	42.51	1.11E+00	2.26E-41	Up	4.15E-01	5.57E-05		-5.40E-03	9.65E-01		4.90E-01	1.83E-08		1.77E-01	5.42E-02		-6.85E-02	5.32E-01		Unigene38397_All//gi|297821252|ref|XP_002878509.1|//3.00E-62//glutamate binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324347|gb|EFH54768.1|glutamate binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene38397_All//3.00E-57//AT3G63310| glutamate binding	Unigene38397_All//0.00E+00//TC132000				nr +
Unigene38398_All	421	72.33	42.73	53.50	126.13	124.65	105.45	136.48	43.19	72.30	-7.60E-01	2.12E-14		-4.35E-01	1.63E-05		-1.70E-02	8.48E-01		-2.58E-01	3.32E-04		-1.66E+00	3.31E-111	Down	-9.17E-01	1.46E-45		Unigene38398_All//gi|6831665|sp|O65731.1|RS5_CICAR//2.00E-39//RecName: Full=40S ribosomal protein S5 >gi|3043428|emb|CAA06491.1| 40S ribosomal protein S5 [Cicer arietinum]	Unigene38398_All//3.00E-40//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	Unigene38398_All//0.00E+00//gi|11210690|gb|BF279620.1|BF279620		ko03010|Ribosome		nr +
Unigene3840_All	1941	0.00	5.19	0.05	2.77	2.40	2.33	7.34	5.51	10.04	1.23E+01	8.99E-58	Up	5.78E+00	3.98E-01		-2.11E-01	4.62E-01		-2.52E-01	3.93E-01		-4.13E-01	1.94E-03		4.51E-01	3.40E-05		Unigene3840_All//gi|224482639|gb|ACN50176.1|//0.00E+00//pectinesterase [Annona cherimola]	Unigene3840_All//0.00E+00//AT1G76160| sks5 (SKU5 Similar 5); copper ion binding / oxidoreductase	Unigene3840_All//0.00E+00//TC134529		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene38400_All	1044	7.67	4.17	5.66	13.74	10.65	15.70	39.45	19.82	18.81	-8.77E-01	2.17E-05		-4.38E-01	4.52E-02		-3.67E-01	1.02E-02		1.93E-01	2.16E-01		-9.93E-01	1.97E-36		-1.07E+00	3.75E-42	Down	Unigene38400_All//gi|115488728|ref|NP_001066851.1|//1.00E-26//Os12g0508300 [Oryza sativa Japonica Group] >gi|297722587|ref|NP_001173657.1|Os03g0773150 [Oryza sativa Japonica Group] >gi|113649358|dbj|BAF29870.1|Os12g0508300 [Oryza sativa Japonica Group] >gi|149391293|gb|ABR25664.1| 40S ribosomal protein S29 [Oryza sativa Indica Group] >gi|255674934|dbj|BAH92385.1|Os03g0773150 [Oryza sativa Japonica Group]	Unigene38400_All//2.00E-26//AT4G33865| 40S ribosomal protein S29 (RPS29C)	Unigene38400_All//0.00E+00//gi|78349367|gb|DT569641.1|DT569641		ko03010|Ribosome		nr +
Unigene38402_All	908	14.52	34.10	8.03	17.34	70.31	46.36	17.60	22.74	63.75	1.23E+00	1.45E-31	Up	-8.54E-01	1.30E-07		2.02E+00	3.23E-154	Up	1.42E+00	9.57E-57	Up	3.70E-01	6.75E-04		1.86E+00	3.29E-133	Up	Unigene38402_All//gi|171452000|dbj|BAG15864.1|//4.00E-60//zinc-finger protein [Bruguiera gymnorhiza]	Unigene38402_All//1.00E-45//AT1G27730| STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding	Unigene38402_All//0.00E+00//TC143706	C2H2			nr +
Unigene38403_All	1330	1.34	0.80	0.76	1.84	2.43	1.32	2.80	0.82	1.14	-7.42E-01	1.29E-01		-8.14E-01	1.15E-01		4.07E-01	2.75E-01		-4.71E-01	2.74E-01		-1.78E+00	1.29E-08	Down	-1.30E+00	5.86E-06	Down	Unigene38403_All//gi|76880192|dbj|BAE45867.1|//1.00E-98//UDP-N-acetylmuramoylalanine-D-glutamate ligase [Physcomitrella patens]		Unigene38403_All//0.00E+00//CO113811				nr -
Unigene38404_All	791	108.28	23.12	45.31	0.82	0.61	0.69	2.35	3.38	2.27	-2.23E+00	9.66E-201	Down	-1.26E+00	1.89E-86	Down	-4.26E-01	6.08E-01		-2.57E-01	7.57E-01		5.24E-01	1.37E-01		-5.34E-02	9.11E-01		Unigene38404_All//gi|193806744|sp|Q6LFK5.2|CML44_ARATH//1.00E-27//RecName: Full=Probable calcium-binding protein CML44; AltName: Full=Calmodulin-like protein 44	Unigene38404_All//9.00E-26//AT1G21550| calcium-binding protein, putative	Unigene38404_All//0.00E+00//DW499365		ko04626|Plant-pathogen interaction		nr -
Unigene38405_All	471	2.00	7.42	3.05	11.11	25.08	35.96	30.61	42.15	24.02	1.89E+00	3.02E-07	Up	6.10E-01	2.96E-01		1.18E+00	2.53E-13	Up	1.70E+00	8.73E-30	Up	4.62E-01	2.77E-05		-3.50E-01	7.00E-03									
Unigene38406_All	1402	14.26	2.71	3.72	22.60	15.06	11.21	12.55	3.70	2.24	-2.39E+00	1.49E-51	Down	-1.94E+00	4.64E-38	Down	-5.86E-01	1.96E-11		-1.01E+00	1.29E-25	Down	-1.76E+00	1.53E-37	Down	-2.48E+00	1.13E-59	Down	Unigene38406_All//gi|124360117|gb|ABN08133.1|//1.00E-113//Heat shock protein DnaJ [Medicago truncatula]	Unigene38406_All//3.00E-107//AT3G12170| DNAJ heat shock N-terminal domain-containing protein	Unigene38406_All//0.00E+00//TC135023				nr -
Unigene38407_All	1008	3.84	1.31	1.11	7.26	4.54	6.27	2.27	0.29	1.26	-1.56E+00	2.82E-06	Down	-1.79E+00	4.30E-07	Down	-6.77E-01	7.46E-04		-2.12E-01	4.03E-01		-2.96E+00	1.24E-09	Down	-8.41E-01	2.05E-02	Down	Unigene38407_All//gi|18394294|ref|NP_563984.1|//4.00E-68//mitochondrial glycoprotein family protein / MAM33 family protein [Arabidopsis thaliana] >gi|8927665|gb|AAF82156.1|AC034256_20 Contains weak similarity to saAprg41 from Emericella nidulans gb|Y17330. EST gb|AI997956 comes from this gene [Arabidopsis thaliana] >gi|15215660|gb|AAK91375.1|At1g15870/F7H2_19 [Arabidopsis thaliana] >gi|20334884|gb|AAM16198.1|At1g15870/F7H2_19 [Arabidopsis thaliana]	Unigene38407_All//2.00E-69//AT1G15870| mitochondrial glycoprotein family protein / MAM33 family protein					nr +
Unigene38408_All	911	44.57	36.88	26.60	13.89	17.16	7.54	1.35	0.92	0.31	-2.73E-01	1.28E-03		-7.45E-01	1.37E-17		3.05E-01	3.19E-02		-8.82E-01	1.50E-08		-5.53E-01	3.30E-01		-2.14E+00	3.24E-04	Down	Unigene38408_All//gi|115451263|ref|NP_001049232.1|//2.00E-29//Os03g0191200 [Oryza sativa Japonica Group] >gi|108706605|gb|ABF94400.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547703|dbj|BAF11146.1|Os03g0191200 [Oryza sativa Japonica Group]	Unigene38408_All//1.00E-34//AT1G78170| unknown protein	Unigene38408_All//0.00E+00//TC136794				nr -
Unigene38409_All	448	23.24	17.53	13.19	45.59	33.97	46.47	84.37	36.20	40.37	-4.07E-01	2.32E-02		-8.17E-01	9.14E-06		-4.24E-01	1.87E-04		2.77E-02	8.61E-01		-1.22E+00	1.79E-46	Down	-1.06E+00	1.73E-38	Down				Unigene38409_All//0.00E+00//gi|21095885|gb|BQ408198.1|BQ408198				
Unigene38412_All	746	2.60	10.94	4.78	24.71	24.97	21.92	7.31	0.90	3.68	2.08E+00	6.55E-18	Up	8.82E-01	9.57E-03		1.54E-02	9.33E-01		-1.73E-01	2.32E-01		-3.03E+00	1.35E-22	Down	-9.89E-01	1.06E-05		Unigene38412_All//gi|225451585|ref|XP_002275581.1|//6.00E-11//PREDICTED: similar to Tetratricopeptide-like helical [Vitis vinifera]	Unigene38412_All//2.00E-08//AT1G12845| unknown protein	Unigene38412_All//0.00E+00//TC164908				nr +
Unigene38415_All	1107	11.72	5.58	5.00	9.36	9.43	5.06	4.66	0.79	0.29	-1.07E+00	4.09E-11	Down	-1.23E+00	4.55E-13	Down	1.01E-02	9.68E-01		-8.88E-01	3.44E-07		-2.56E+00	5.34E-18	Down	-4.02E+00	4.53E-28	Down	Unigene38415_All//gi|89111299|dbj|BAE80324.1|//1.00E-105//cyclin D3-1 [Camellia sinensis]	Unigene38415_All//2.00E-70//AT5G67260| CYCD3;2 (CYCLIN D3;2); cyclin-dependent protein kinase	Unigene38415_All//0.00E+00//gi|73847055|gb|DT456075.1|DT456075				nr +

Unigene38416_All	713	15.48	13.00	13.37	18.30	11.11	14.32	22.42	19.29	11.12	-2.52E-01	1.62E-01		-2.12E-01	2.70E-01		-7.21E-01	4.81E-07		-3.55E-01	2.60E-02		-2.17E-01	1.06E-01		-1.01E+00	1.55E-15	Down	Unigene38416_All//gi|16648677|gb|AAL25531.1|//2.00E-19//At1g22140/F2E2_13 [Arabidopsis thaliana] >gi|20334900|gb|AAM16206.1| At1g22140/F2E2_13 [Arabidopsis thaliana]	Unigene38416_All//5.00E-09//AT1G22140| unknown protein	Unigene38416_All//0.00E+00//TC161705				nr -
Unigene38417_All	572	50.58	21.35	25.69	99.11	72.78	121.83	163.95	66.71	53.63	-1.24E+00	3.65E-30	Down	-9.77E-01	8.15E-20		-4.45E-01	2.43E-12		2.98E-01	1.07E-06		-1.30E+00	1.74E-125	Down	-1.61E+00	1.04E-178	Down	Unigene38417_All//gi|225431804|ref|XP_002272727.1|//4.00E-39//PREDICTED: similar to 60S ribosomal protein L19 (Vitis vinifera)	Unigene38417_All//5.00E-30//AT4G02230| 60S ribosomal protein L19 (RPL19C)	Unigene38417_All//0.00E+00//gi|78343954|gb|DT564228.1|DT564228		ko03010|Ribosome		nr +
Unigene38419_All	662	2.45	6.28	5.31	40.86	32.20	42.09	119.50	154.75	120.84	1.36E+00	1.42E-05	Up	1.12E+00	1.32E-03		-3.44E-01	4.81E-04		4.29E-02	7.26E-01		3.73E-01	2.60E-16		1.61E-02	7.94E-01		Unigene38419_All//gi|15235514|ref|NP_195447.1|//4.00E-36//MEE59 (maternal effect embryo arrest 59) [Arabidopsis thaliana] >gi|14517512|gb|AAK62646.1| AT4g37300/CTA10_60 [Arabidopsis thaliana] >gi|15809770|gb|AAL06813.1| AT4g37300/CTA10_60 [Arabidopsis thaliana]	Unigene38419_All//2.00E-37//AT4G37300| MEE59 (maternal effect embryo arrest 59)	Unigene38419_All//0.00E+00//gi|109856637|gb|DW485616.1|DW485616				nr -
Unigene38420_All	911	6.32	1.89	2.40	11.32	14.17	4.96	8.08	1.79	1.27	-1.74E+00	2.27E-10	Down	-1.40E+00	2.30E-07	Down	3.25E-01	4.09E-02		-1.19E+00	3.34E-11	Down	-2.17E+00	4.65E-21	Down	-2.67E+00	1.56E-27	Down	Unigene38420_All//gi|15235984|ref|NP_195680.1|//6.00E-59//heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related [Arabidopsis thaliana]	Unigene38420_All//3.00E-60//AT4G39700| heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	Unigene38420_All//0.00E+00//TC139884				nr -
Unigene38421_All	506	0.21	1.10	0.53	1.28	0.75	1.79	2.92	0.99	0.16	2.41E+00	3.93E-02		1.35E+00	4.09E-01		-7.74E-01	3.81E-01		4.80E-01	5.50E-01		-1.56E+00	2.28E-03		-4.21E+00	1.00E-08	Down	Unigene38421_All//gi|110739416|dbj|BAF01618.1|//9.00E-59//beta-galactosidase like protein [Arabidopsis thaliana]	Unigene38421_All//1.00E-59//AT5G63800| MUM2 (MUCILAGE-MODIFIED 2); beta-galactosidase			ko00052|Galactose metabolism/ko00600|Sphingolipid metabolism/ko00511|Other glycan degradation		nr -
Unigene38422_All	1473	0.64	0.14	0.90	1.86	1.66	1.99	2.93	1.93	1.22	-2.22E+00	6.65E-03		4.99E-01	3.93E-01		-1.64E-01	6.94E-01		9.96E-02	7.98E-01		-6.02E-01	2.15E-02		-1.27E+00	1.49E-06	Down	Unigene38422_All//gi|297793965|ref|XP_002864867.1|//1.00E-172//beta-galactosidase 6 [Arabidopsis lyrata subsp. lyrata] >gi|297310702|gb|EFH41126.1| beta-galactosidase 6 [Arabidopsis lyrata subsp. lyrata]	Unigene38422_All//2.00E-173//AT5G63800| MUM2 (MUCILAGE-MODIFIED 2); beta-galactosidase	Unigene38422_All//1.00E-13//C0074493		ko00052|Galactose metabolism/ko00600|Sphingolipid metabolism/ko00511|Other glycan degradation		nr +
Unigene38423_All	595	70.35	31.08	42.60	69.91	69.33	87.37	70.70	37.79	41.78	-1.18E+00	8.38E-40	Down	-7.24E-01	2.95E-17		-1.19E-02	9.10E-01		3.22E-01	7.16E-06		-9.04E-01	6.84E-32		-7.59E-01	1.43E-24		Unigene38423_All//gi|223469963|gb|ACM00324.1|//2.00E-88//GDP-D-mannose-3',5'-epimerase [Ribes nigrum]	Unigene38423_All//7.00E-87//AT5G28840| GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-mannose 3,5-epimerase/ NAD or NADH binding / catalytic	Unigene38423_All//0.00E+00//TC1317759		ko00520|Amino sugar and nucleotide sugar metabolism/ko00053|Ascorbate and aldarate metabolism/ko00051|Fructose and mannose metabolism		nr +
Unigene38424_All	849	0.00	0.06	0.25	2.11	2.68	35.06	13.30	26.73	86.53	5.90E+00	6.16E-01		7.97E+00	1.41E-01		3.42E-01	4.72E-01		4.05E+00	1.78E-134	Up	1.01E+00	6.91E-21	Up	2.70E+00	1.11E-267	Up	Unigene38424_All//gi|8778991|gb|AAF79906.1|AC022472_15//5.00E-10//Contains similarity to nuclear protein ZAP from Mus musculus gb|AB033168. ESTs gb|AV521697, gb|AV440130 come from this gene [Arabidopsis thaliana]		Unigene38424_All//5.00E-24//TC145758				nr +
Unigene38425_All	1417	2.07	1.00	0.75	3.23	1.92	1.91	5.58	1.30	1.24	-1.05E+00	4.51E-03		-1.46E+00	2.55E-04	Down	-7.53E-01	4.43E-03		-7.58E-01	6.56E-03		-2.10E+00	1.08E-21	Down	-2.17E+00	2.55E-23	Down	Unigene38425_All//gi|42569202|ref|NP_179694.2|//1.00E-117//MCM10 [Arabidopsis thaliana]	Unigene38425_All//1.00E-108//AT2G20980| MCM10	Unigene38425_All//0.00E+00//gi|164317468|gb|ES845203.1|ES845203				nr -
Unigene38426_All	1289	0.61	1.85	0.99	0.97	1.42	1.93	1.38	6.16	2.84	1.60E+00	2.78E-04	Up	7.03E-01	2.54E-01		5.52E-01	2.87E-01		9.96E-01	1.44E-02		2.16E+00	1.91E-22	Up	1.05E+00	2.16E-04	Up	Unigene38426_All//gi|297842639|ref|XP_002889201.1|//1.00E-159//mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335042|gb|EFH65460.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene38426_All//4.00E-143//AT1G78610| MSL6 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 6)	Unigene38426_All//0.00E+00//TC178511				nr +
Unigene38427_All	848	8.08	18.40	16.33	7.70	8.37	9.32	18.15	21.39	17.24	1.19E+00	2.08E-15	Up	1.01E+00	2.07E-10	Up	1.20E-01	6.39E-01		2.76E-01	2.25E-01		2.37E-01	5.32E-02		-7.40E-02	6.09E-01		Unigene38427_All//gi|11072018|gb|AAC28897.1|AC008113_13//6.00E-52//F12A21.27 [Arabidopsis thaliana] >gi|89274151|gb|ABD65596.1| At1g67600 [Arabidopsis thaliana]	Unigene38427_All//6.00E-55//AT3G21610| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Acid phosphatase/vanadium-dependent haloperoxidase related (InterPro:IPR003832); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67600.1); Has 626 Blast hits to 626 proteins in 204 species: Archae - 0; Bacteria - 365; Metazoa - 0; Fungi - 0; Plants - 103; Viruses - 0; Other Eukaryotes - 158 (source: NCBI BLink).	Unigene38427_All//0.00E+00//TC138757				nr +
Unigene38429_All	1782	0.38	0.88	0.78	8.08	6.71	4.94	1.68	0.61	0.78	1.21E+00	2.47E-02		1.03E+00	8.63E-02		-2.69E-01	7.49E-02		-7.09E-01	8.08E-07		-1.47E+00	1.39E-05	Down	-1.11E+00	4.59E-04	Down	Unigene38429_All//gi|15983811|gb|AAL10502.1|//1.00E-155//AT5g60720/mup24_130 [Arabidopsis thaliana] >gi|27363288|gb|AAO11563.1| At5g60720/mup24_130 [Arabidopsis thaliana]	Unigene38429_All//5.00E-144//AT5G60720| unknown protein	Unigene38429_All//0.00E+00//DN804358				nr +
Unigene3843_All	2657	3.11	1.11	0.44	5.83	5.57	4.28	9.50	1.24	3.13	-1.49E+00	7.88E-12	Down	-2.82E+00	8.75E-25	Down	-6.52E-02	7.18E-01		-4.45E-01	1.49E-03		-2.93E+00	3.25E-99	Down	-1.60E+00	3.59E-48	Down	Unigene3843_All//gi|150036248|gb|AB867411.1|//0.00E+00//kinesin [Cucumis melo]	Unigene3843_All//0.00E+00//AT5G27550| ATP binding / microtubule motor	Unigene3843_All//0.00E+00//gi|78354836|gb|DT575110.1|DT575110				nr -
Unigene38430_All	1352	7.08	17.80	3.58	2.25	1.38	7.05	20.55	46.12	42.52	1.33E+00	9.77E-28	Up	-9.83E-01	4.76E-07		-7.09E-01	3.86E-02		1.65E+00	2.43E-16	Up	1.17E+00	8.24E-71	Up	1.05E+00	1.98E-56	Up	Unigene38430_All//gi|224075453|ref|XP_002304640.1|//4.00E-62//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222842072|gb|EEE79619.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene38430_All//9.00E-38//AT5G13330| Rap2.6L (related to AP2 6L); DNA binding / transcription factor	Unigene38430_All//0.00E+00//gi|109849878|gb|DW478857.1|DW478857	AP2-EREBP			nr +
Unigene38433_All	1277	10.78	0.87	4.63	2.11	1.00	1.95	1.09	0.29	0.41	-3.63E+00	4.21E-54	Down	-1.22E+00	1.15E-13	Down	-1.08E+00	2.86E-03		-1.15E-01	7.73E-01		-1.89E+00	5.91E-04	Down	-1.43E+00	4.53E-03		Unigene38433_All//gi|42568685|ref|NP_200935.2|//3.00E-54//PIF7 (PHYTOCHROME-INTERACTING FACTOR7); DNA binding / double-stranded DNA binding / transcription factor [Arabidopsis thaliana] >gi|182676517|sp|Q570R7.2|PIF7_ARATH RecName: Full=Transcription factor PIF7; AltName: Full=Phytochrome-interacting factor 7; AltName: Full=Transcription factor EN 109; AltName: Full=bHLH transcription factor bHLH072; AltName: Full=Basic helix-loop-helix protein 72; Short=bHLH 72; Short=AtbHLH72	Unigene38433_All//2.00E-36//AT5G61270| PIF7 (PHYTOCHROME-INTERACTING FACTOR7); DNA binding / double-stranded DNA binding / transcription factor	Unigene38433_All//0.00E+00//TC148000	bHLH		ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	nr -
Unigene38434_All	843	4.28	6.97	1.58	4.37	9.76	5.09	6.32	6.69	2.22	7.03E-01	4.01E-03		-1.44E+00	4.63E-05	Down	1.16E+00	3.24E-09	Up	2.19E-01	5.14E-01		8.29E-02	7.36E-01		-1.51E+00	5.06E-10	Down	Unigene38434_All//gi|255538714|ref|XP_002510422.1|//2.00E-23//conserved hypothetical protein [Ricinus communis] >gi|223551123|gb|EEF52609.1| conserved hypothetical protein [Ricinus communis]	Unigene38434_All//1.00E-10//AT5G66410| unknown protein	Unigene38434_All//0.00E+00//TC161475				nr +
Unigene38435_All	781	2.34	5.32	4.57	8.55	6.92	6.42	16.73	17.82	11.94	1.18E+00	1.16E-04	Up	9.62E-01	4.80E-03		-3.04E-01	2.01E-01		-4.13E-01	7.80E-02		9.13E-02	5.92E-01		-4.87E-01	3.16E-04		Unigene38435_All//gi|115454287|ref|NP_001050744.1|//9.00E-37//Os03g0640400 [Oryza sativa Japonica Group] >gi|108710031|gb|ABF97826.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549215|dbj|BAF12658.1| Os03g0640400 [Oryza sativa Japonica Group]	Unigene38435_All//4.00E-45//AT3G29130| unknown protein	Unigene38435_All//0.00E+00//gi|109876074|gb|DW505048.1|DW505048				nr +
Unigene38439_All	691	7.12	3.96	7.32	3.03	4.88	2.88	0.12	0.79	1.56	-8.46E-01	1.81E-03		4.07E-02	8.91E-01		6.90E-01	3.91E-02		-7.43E-02	8.82E-01		2.68E+00	1.38E-02		3.67E+00	7.75E-06	Up	Unigene38439_All//gi|228481103|gb|ACQ42250.1|//1.00E-109//blue light photoreceptor [Fragaria x ananassa]	Unigene38439_All//9.00E-100//AT3G45780| PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase	Unigene38439_All//0.00E+00//TC158920				nr +
Unigene3844_All	1117	1.78	1.91	1.86	9.32	6.50	3.19	3.22	2.21	1.75	9.81E-02	8.17E-01		6.29E-02	8.93E-01		-5.19E-01	1.80E-03		-1.55E+00	1.49E-16	Down	-5.43E-01	6.42E-02		-8.81E-01	1.69E-03				Unigene3844_All//2.00E-42//FL577416				
Unigene38440_All	1407	12.79	6.19	13.97	4.60	4.63	3.85	13.31	7.93	5.63	-1.05E+00	1.31E-14	Down	1.27E-01	4.01E-01		7.20E-03	9.85E-01		-2.57E-01	3.21E-01		-7.47E-01	8.29E-11		-1.24E+00	9.63E-25	Down	Unigene38440_All//gi|2346972|dbj|BAA21920.1|//1.00E-60//ZPT2-11 [Petunia x hybrida]	Unigene38440_All//1.00E-42//AT5G03510| zinc finger (C2H2 type) family protein	Unigene38440_All//0.00E+00//ES828084	C2H2			nr +
Unigene38441_All	807	13.03	67.81	31.34	5.62	13.91	36.49	4.45	14.71	23.84	2.38E+00	4.33E-138	Up	1.27E+00	3.50E-26	Up	1.31E+00	6.77E-15	Up	2.70E+00	4.40E-92	Up	1.72E+00	9.30E-25	Up	2.42E+00	2.14E-62	Up	Unigene38441_All//gi|239056193|emb|CAQ88630.1|//9.00E-59//Unknown gene [Vitis vinifera]	Unigene38441_All//5.00E-43//AT2G38640| unknown protein	Unigene38441_All//0.00E+00//gi|109853695|gb|DW482674.1|DW482674				nr -
Unigene38442_All	467	5.94	2.39	2.85	4.59	5.68	8.12	3.08	5.19	6.57	-1.31E+00	7.32E-04	Down	-1.06E+00	7.86E-03		3.08E-01	4.86E-01		8.25E-01	8.82E-03		7.54E-01	3.93E-02		1.09E+00	4.88E-04	Up			Unigene38442_All//1.00E-44//DW238033				
Unigene38447_All	1026	1.22	0.15	0.42	2.77	3.32	3.43	2.14	2.40	2.80	-3.05E+00	9.00E-05	Down	-1.56E+00	1.90E-02		2.64E-01	4.98E-01		3.11E-01	3.90E-01		1.66E-01	6.60E-01		3.84E-01	2.47E-01		Unigene38447_All//gi|124359162|gb|ABN05685.1|//4.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]						nr +
Unigene3845_All	1113	2.16	2.09	2.49	3.00	2.48	1.91	3.23	5.75	1.50	-4.62E-02	9.19E-01		2.02E-01	6.43E-01		-2.77E-01	4.55E-01		-6.53E-01	5.61E-02		8.31E-01	6.54E-05		-1.10E+00	1.13E-04	Down			Unigene3845_All//4.00E-167//gi|13352367|gb|BG442715.1|BG442715				
Unigene38450_All	448	61.78	84.15	66.56	37.14	59.42	47.99	28.50	11.66	62.51	4.46E-01	2.90E-07		1.08E-01	3.70E-01		6.78E-01	4.61E-12		3.70E-01	1.73E-03		-1.29E+00	1.33E-17	Down	1.13E+00	1.58E-31	Up	Unigene38450_All//gi|30685380|ref|NP_850825.1|//3.00E-01//ankyrin repeat family protein [Arabidopsis thaliana]		Unigene38450_All//0.00E+00//TC175160				nr -
Unigene38452_All	1517	1.52	10.19	2.35	2.36	2.68	15.57	10.48	32.90	78.84	2.75E+00	3.19E-46	Up	6.32E-01	6.46E-02		1.80E-01	5.94E-01		2.72E+00	1.73E-74	Up	1.65E+00	1.13E-95	Up	2.91E+00	0.00E+00	Up	Unigene38452_All//gi|158564572|gb|AB674474.1|//1.00E-161//mitochondrial phosphate transporter [Paeonia suffruticosa]	Unigene38452_All//4.00E-138//AT5G14040| mitochondrial phosphate transporter	Unigene38452_All//0.00E+00//DT464191				nr +

Unigene38453_All	777	39.73	14.67	32.21	15.96	25.13	10.40	7.73	10.60	8.51	-1.44E+00	6.29E-40	Down	-3.03E-01	3.15E-03		6.55E-01	1.80E-08		-6.18E-01	7.87E-05		4.56E-01	1.23E-02		1.40E-01	5.46E-01		Unigene38453_All//gi|297790316|ref|XP_002863057.1|//2.00E-43//glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297824891|ref|XP_002880328.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308863|gb|EFH39316.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326167|gb|EFH56587.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38453_All//8.00E-45//AT3G62950| glutaredoxin family protein	Unigene38453_All//0.00E+00//DW513727				nr -
Unigene38457_All	542	54.35	24.68	65.73	37.87	52.42	28.33	1.09	0.39	0.66	-1.14E+00	9.30E-27	Down	2.74E-01	3.98E-03		4.69E-01	6.86E-07		-4.19E-01	4.56E-04		-1.50E+00	9.13E-02		-7.23E-01	3.71E-01		Unigene38457_All//gi|152312245|ref|NP_190164.1|//5.00E-52//PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase [Arabidopsis thaliana] >gi|79314333|ref|NP_001030814.1| PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase [Arabidopsis thaliana] >gi|25090817|sp|O48963.1|PHOT1_ARATH RecName: Full=Phototropin-1; AltName: Full=Non-phototropic hypocotyl protein 1; AltName: Full=Root phototropism protein 1 >gi|2832241|gb|AAC01753.1| nonphototropic hypocotyl 1 [Arabidopsis thaliana] >gi|7019644|emb|CAB75791.1| nonphototropic hypocotyl 1 [Arabidopsis thaliana]	Unigene38457_All//1.00E-44//AT3G45780| PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase	Unigene38457_All//4.00E-144//TC158920				nr +
Unigene3846_All	1105	0.43	1.38	1.30	0.36	0.22	0.61	29.35	12.90	103.33	1.69E+00	3.43E-03		1.61E+00	8.67E-03		-7.25E-01	5.46E-01		7.66E-01	4.10E-01		-1.19E+00	3.12E-38	Down	1.82E+00	2.60E-254	Up	Unigene3846_All//gi|75297894|sp|Q84MB3.1|ACH1_ARATH//7.00E-79//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene3846_All//4.00E-80//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene3846_All//0.00E+00//TC146757		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene38460_All	1283	23.77	32.50	59.27	42.32	12.70	39.46	5.11	17.43	7.42	4.51E-01	4.18E-08		1.32E+00	7.92E-83	Up	-1.74E+00	4.84E-115	Down	-1.01E-01	2.30E-01		1.77E+00	1.05E-47	Up	5.39E-01	8.50E-04		Unigene38460_All//gi|144905104|dbj|BAF56427.1|//7.00E-108//cysteine proteinase [Lotus japonicus]	Unigene38460_All//1.00E-96//AT2G27420| cysteine proteinase, putative	Unigene38460_All//0.00E+00//TC130544				nr +
Unigene38461_All	422	17.85	24.13	19.31	17.71	25.13	36.82	19.94	24.17	15.48	4.35E-01	1.62E-02		1.13E-01	6.28E-01		5.05E-01	2.68E-03		1.06E+00	1.39E-13	Up	2.78E-01	1.01E-01		-3.65E-01	3.81E-02		Unigene38461_All//gi|87162555|gb|ABQ28350.1|//1.00E-45//Protein phosphatase 2C-like [Medicago truncatula]	Unigene38461_All//3.00E-45//AT5G27930| protein phosphatase 2C, putative / PP2C, putative	Unigene38461_All//0.00E+00//TC146797				nr -
Unigene38462_All	745	9.34	6.73	6.65	59.04	45.30	20.67	6.30	1.07	1.66	-4.72E-01	3.52E-02		-4.91E-01	3.66E-02		-3.82E-01	1.99E-07		-1.51E+00	2.49E-66	Down	-2.56E+00	1.72E-16	Down	-1.93E+00	3.07E-12	Down	Unigene38462_All//gi|18407486|ref|NP_566114.1|//1.00E-17//AGP26 (ARABINOGALACTAN PROTEIN 26) [Arabidopsis thaliana] >gi|119361080|sp|Q94F57.2|AGP26_ARATH RecName: Full=Classical arabinogalactan protein 26; Flags: Precursor >gi|3738305|gb|AAC63647.1| expressed protein [Arabidopsis thaliana] >gi|20197561|gb|AAM15130.1| expressed protein [Arabidopsis thaliana]		Unigene38462_All//0.00E+00//gi|109868431|gb|DW497407.1|DW497407				nr +
Unigene38463_All	726	11.82	19.26	13.50	6.59	11.43	11.88	5.36	11.97	17.40	7.05E-01	2.85E-06		1.91E-01	3.67E-01		7.95E-01	2.97E-05		8.51E-01	1.15E-05		1.16E+00	1.78E-10	Up	1.70E+00	2.33E-26	Up	Unigene38463_All//gi|255555915|ref|XP_002518993.1|//1.00E-43//plastidal glycerol-phosphate acyltransferase [Ricinus communis] >gi|223541980|gb|EEF43526.1| plastidal glycerol-phosphate acyltransferase [Ricinus communis]	Unigene38463_All//6.00E-40//AT1G32200| ATS1; glycerol-3-phosphate O-acyltransferase	Unigene38463_All//0.00E+00//DN817406		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr +
Unigene38468_All	728	12.86	41.06	25.16	131.93	128.75	105.53	28.17	30.77	45.20	1.67E+00	5.91E-48	Up	9.68E-01	1.33E-12		-3.51E-02	6.16E-01		-3.22E-01	2.42E-10		1.28E-01	2.86E-01		6.82E-01	3.44E-16		Unigene38468_All//gi|87162905|gb|ABQ28700.1|//1.00E-31//ATP binding , related [Medicago truncatula] >gi|124360477|gb|ABN08487.1| ATP binding , related [Medicago truncatula]	Unigene38468_All//4.00E-17//AT5G24010| protein kinase family protein	Unigene38468_All//0.00E+00//TC146738				nr +
Unigene3847_All	1313	14.27	4.05	6.85	3.11	2.15	3.23	8.57	5.79	35.95	-1.82E+00	4.71E-34	Down	-1.06E+00	9.18E-15	Down	-5.33E-01	7.03E-02		5.56E-02	8.78E-01		-5.64E-01	1.82E-04		2.07E+00	1.83E-125	Up	Unigene3847_All//gi|75297894|sp|Q84MB3.1|ACH1_ARATH//1.00E-100//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene3847_All//1.00E-100//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene3847_All//0.00E+00//TC158223		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene38470_All	635	7.83	4.79	3.35	9.18	7.65	9.25	3.00	2.44	2.95	-7.09E-01	8.24E-03		-1.22E+00	2.20E-05	Down	-2.64E-01	3.16E-01		1.06E-02	9.66E-01		-2.99E-01	5.16E-01		-2.31E-02	9.67E-01		Unigene38470_All//gi|297597655|ref|NP_001044334.2|//1.00E-23//Os01g0763300 [Oryza sativa Japonica Group] >gi|255673707|dbj|BAF06248.2| Os01g0763300 [Oryza sativa Japonica Group]	Unigene38470_All//2.00E-35//AT5G08060| unknown protein	Unigene38470_All//4.00E-104//ES824591				nr -
Unigene38471_All	583	4.22	1.13	1.28	7.60	3.48	2.71	26.40	24.37	44.76	-1.90E+00	2.20E-05	Down	-1.72E+00	1.55E-04	Down	-1.13E+00	2.85E-05	Down	-1.49E+00	5.02E-07	Down	-1.15E-01	4.41E-01		7.62E-01	1.36E-15		Unigene38471_All//gi|14625425|dbj|BAB61919.1|//8.00E-74//calmodulin NtCaM13 [Nicotiana tabacum]	Unigene38471_All//1.00E-70//AT4G14640| CAM8 (CALMODULIN 8); calcium ion binding	Unigene38471_All//0.00E+00//TC144739		ko04626|Plant-pathogen interaction		nr +
Unigene38472_All	1389	1.92	0.44	0.15	3.34	2.73	2.31	3.29	0.30	1.26	-2.13E+00	1.40E-06	Down	-3.65E+00	2.31E-10	Down	-2.90E-01	3.23E-01		-5.31E-01	6.29E-02		-3.45E+00	2.25E-21	Down	-1.38E+00	9.60E-08	Down	Unigene38472_All//gi|42362341|gb|AAS13373.1|//1.00E-152//weel [Glycine max]	Unigene38472_All//3.00E-134//AT1G02970| WEE1 (ARABIDOPSIS WEE1 KINASE HOMOLOG); kinase/ protein kinase	Unigene38472_All//0.00E+00//gi|54119256|gb|CO494765.1|CO494765				nr +
Unigene38473_All	1183	1.15	1.93	2.34	0.59	1.31	1.18	632.95	81.19	14.92	7.45E-01	7.75E-02		1.03E+00	9.83E-03		1.15E+00	3.22E-02		1.01E+00	8.41E-02		-2.96E+00	0.00E+00	Down	-5.41E+00	0.00E+00	Down	Unigene38473_All//gi|46577788|gb|AT01414.1|//1.00E-135//iron regulated transporter [Cucumis sativus]	Unigene38473_All//2.00E-102//AT1G31260| ZIP10 (ZINC TRANSPORTER 10 PRECURSOR); cation transmembrane transporter/ metal ion transmembrane transporter	Unigene38473_All//0.00E+00//TC148511				nr -
Unigene38474_All	914	7.50	13.08	14.45	43.27	25.73	20.85	5.74	2.24	1.74	8.03E-01	1.15E-06		9.46E-01	6.00E-09		-7.50E-01	9.21E-22		-1.05E+00	5.17E-34	Down	-1.36E+00	3.00E-08	Down	-1.72E+00	9.85E-12	Down	Unigene38474_All//gi|18411783|ref|NP_565167.1|//2.00E-32//senescence-associated protein-related [Arabidopsis thaliana] >gi|6573767|gb|AAF17687.1|AC009243_14 F28K19.24 [Arabidopsis thaliana]	Unigene38474_All//3.00E-31//AT1G78020| senescence-associated protein-related	Unigene38474_All//0.00E+00//gi|109874332|gb|DW503306.1|DW503306				nr +
Unigene38475_All	955	225.17	60.06	65.91	1190.43	812.64	989.29	171.64	61.36	73.46	-1.91E+00	0.00E+00	Down	-1.77E+00	0.00E+00	Down	-5.51E-01	0.00E+00		-2.67E-01	1.76E-81		-1.48E+00	1.47E-268	Down	-1.22E+00	1.34E-205	Down	Unigene38475_All//gi|7387766|sp|Q39967.3|ALL5_HEVBR//3.00E-20//RecName: Full=Major latex allergen Hev b 5; AltName: Allergen=Hev b 5 >gi|1480457|gb|AAC49447.1| latex allergen Hev b 5 [Hevea brasiliensis] >gi|1493836|gb|AAC49448.1| latex pI 3.5 protein Hev b 5 [Hevea brasiliensis]		Unigene38475_All//0.00E+00//TC131661		ko00190|Oxidative phosphorylation		nr -
Unigene38476_All	1075	3.11	3.21	2.08	6.30	4.36	2.39	2.56	0.47	0.30	4.12E-02	9.14E-01		-5.82E-01	1.03E-01		-5.33E-01	1.33E-02		-1.40E+00	1.63E-09	Down	-2.45E+00	1.70E-09	Down	-3.11E+00	1.99E-12	Down	Unigene38476_All//gi|6730717|gb|AAF27112.1|AC011809_21//1.00E-116//Putative protein kinase [Arabidopsis thaliana]	Unigene38476_All//7.00E-104//AT1G18670| IBS1 (IMPAIRED IN BABA-INDUCED STERILITY 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene38476_All//4.00E-22//gi|78332918|gb|DT553192.1|DT553192				nr +
Unigene38478_All	1273	3.45	10.31	8.20	0.39	0.68	0.43	0.00	0.00	0.00	1.58E+00	9.60E-20	Up	1.25E+00	6.56E-11	Up	7.89E-01	3.21E-01		1.22E-01	9.21E-01		null	null		null	null		Unigene38478_All//gi|115439873|ref|NP_001044216.1|//3.00E-88//Os01g0743200 [Oryza sativa Japonica Group] >gi|20521423|dbj|BAB91933.1| pectin methyl esterase-like [Oryza sativa Japonica Group] >gi|113533747|dbj|BAF06130.1| Os01g0743200 [Oryza sativa Japonica Group]	Unigene38478_All//3.00E-86//AT5G19730| pectinesterase family protein	Unigene38478_All//0.00E+00//gi|78350296|gb|DT570570.1|DT570570		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene3848_All	1216	20.48	13.67	23.30	23.84	31.52	34.24	16.45	9.59	4.75	-5.84E-01	8.72E-08		1.86E-01	1.03E-01		4.03E-01	5.15E-07		5.22E-01	6.73E-11		-7.78E-01	2.89E-12		-1.79E+00	7.07E-45	Down	Unigene3848_All//gi|15224802|ref|NP_179548.1|//1.00E-122//TET2 (TETRASPANIN2) [Arabidopsis thaliana] >gi|40822966|gb|AAR92249.1| At2g19580 [Arabidopsis thaliana] >gi|46518389|gb|AAS99676.1| At2g19580 [Arabidopsis thaliana]	Unigene3848_All//1.00E-94//AT2G19580| TET2 (TETRASPANIN2)	Unigene3848_All//0.00E+00//TC129684				nr -
Unigene38480_All	1969	0.03	0.10	0.00	22.74	21.72	14.43	3.31	2.91	0.40	1.95E+00	3.75E-01		-4.73E+00	6.23E-01		-6.64E-02	5.16E-01		-6.57E-01	2.01E-17		-1.85E-01	4.22E-01		-3.03E+00	8.24E-28	Down	Unigene38480_All//gi|224087431|ref|XP_002308164.1|//0.00E+00//laccase 110b [Populus trichocarpa] >gi|222854140|gb|EEE91687.1| laccase 110b [Populus trichocarpa]	Unigene38480_All//0.00E+00//AT5G60020| LAC17 (laccase 17); laccase	Unigene38480_All//0.00E+00//TC136693		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene38481_All	813	0.64	1.87	0.39	4.90	3.30	2.78	36.40	151.09	5.83	1.54E+00	6.71E-03		-7.12E-01	4.97E-01		-5.69E-01	5.46E-02		-8.20E-01	6.76E-03		2.05E+00	0.00E+00	Up	-2.64E+00	3.04E-107	Down	Unigene38481_All//gi|297791393|ref|XP_002863581.1|//3.00E-48//FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297309416|gb|EFH39840.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene38481_All//2.00E-49//AT1G30760| FAD-binding domain-containing protein	Unigene38481_All//0.00E+00//TC153328				nr +

Unigene38482_All	885	3.61	2.92	2.83	2.76	2.06	0.97	1.67	1.94	0.72	-3.05E-01	3.81E-01			-3.51E-01	3.60E-01		-4.20E-01	3.11E-01			-1.51E+00	3.09E-04	Down	2.12E-01	6.38E-01		-1.22E+00	1.09E-02		Unigene38482_All//gi|77553129|gb|AB595925.1|//2.9E-86//Amidase family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene38482_All//6.00E-48//AT5G44440| AtFAAH (Arabidopsis thaliana fatty acid amide hydrolase); N-(long-chain-acyl)ethanolamine deacylase/ amidase	Unigene38482_All//0.00E+00//TC156538		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene38484_All	910	1.84	1.17	1.40	1.64	1.97	2.23	1.95	0.96	0.53	-6.54E-01	1.99E-01			-3.90E-01	4.60E-01		2.61E-01	6.21E-01			4.44E-01	3.75E-01		-1.02E+00	2.09E-02		-1.89E+00	4.84E-05	Down	Unigene38484_All//gi|158828301|gb|ABW81176.1|//7.00E-12//non-LTR reverse transcriptase [Arabidopsis cebennensis]						nr -
Unigene38486_All	1447	25.24	6.02	17.74	9.40	5.35	3.15	0.18	0.00	0.06	-2.07E+00	3.79E-78	Down	-5.09E-01	2.23E-08		-8.12E-01	7.03E-09			-1.58E+00	4.44E-22	Down	-7.45E+00	4.04E-02		-1.67E+00	2.56E-01		Unigene38486_All//gi|21536954|gb|AM61295.1|//1.00E-122//GDSL-motif lipase/hydrolase-like protein [Arabidopsis thaliana]	Unigene38486_All//1.00E-122//AT5G45960| GDSL-motif lipase/hydrolase family protein	Unigene38486_All//0.00E+00//gi|164252502|gb|ES821222.1|ES821222				nr +
Unigene38487_All	2634	0.38	0.50	0.24	1.19	0.82	1.32	7.45	1.86	5.99	4.06E-01	4.87E-01		-6.38E-01	3.90E-01		-5.33E-01	1.24E-01			1.48E-01	6.77E-01		-2.00E+00	1.42E-49	Down	-3.14E-01	4.15E-03		Unigene38487_All//gi|2098713|gb|AAB57671.1|//0.00E+00//pectinesterase [Citrus sinensis]	Unigene38487_All//0.00E+00//AT2G45220| pectinesterase family protein	Unigene38487_All//2.00E-07//TC151968		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene38489_All	856	106.72	46.88	94.68	24.73	24.18	20.26	0.74	0.05	0.09	-1.19E+00	4.73E-87	Down	-1.73E-01	3.00E-03		-3.28E-02	8.22E-01			-2.88E-01	1.88E-02		-3.92E+00	9.80E-04	Down	-2.99E+00	2.58E-03		Unigene38489_All//gi|297823651|ref|XP_002879708.1|//1.00E-99//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297325547|gb|EFH55967.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene38489_All//5.00E-92//AT2G37770| aldo/keto reductase family protein	Unigene38489_All//0.00E+00//TC144579		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene3849_All	1475	15.18	8.38	14.48	21.65	16.95	14.51	59.48	28.90	37.33	-8.57E-01	4.15E-13		-6.86E-02	6.21E-01		-3.53E-01	7.30E-05			-5.77E-01	4.05E-10		-1.04E+00	7.37E-83	Down	-6.72E-01	8.88E-41		Unigene3849_All//gi|18417667|ref|NP_567854.1|//1.00E-141//scpl29 (serine carboxypeptidase-like 29); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75332010|sp|Q94YQ7.1|SCP29_ARATH RecName: Full=Serine carboxypeptidase-like 29; Flags: Precursor	Unigene3849_All//2.00E-142//AT4G30810| scpl29 (serine carboxypeptidase-like 29); serine-type carboxypeptidase	Unigene3849_All//0.00E+00//TC132509		ko00460|Cyanoamino acid metabolism		nr +
Unigene38492_All	572	1.56	3.10	1.58	1.74	4.70	4.11	4.80	3.80	3.90	9.96E-01	4.45E-02		2.54E-02	9.92E-01		1.43E+00	2.06E-04	Up	1.24E+00	3.56E-03		-3.39E-01	3.60E-01		-3.01E-01	3.80E-01					Unigene38492_All//8.00E-170//ES845513					
Unigene38493_All	1339	0.16	0.53	0.16	1.79	0.82	6.21	9.76	19.07	75.33	1.76E+00	5.60E-02		2.56E-02	1.00E+00		-1.12E+00	4.01E-03		1.80E+00	4.51E-16	Up	9.67E-01	6.48E-22		2.95E+00	0.00E+00	Up	Unigene38493_All//gi|259121391|gb|ACV92015.1|//5.00E-91//WRKY transcription factor 13 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene38493_All//5.00E-47//AT2G47260| WRKY23; transcription factor	Unigene38493_All//0.00E+00//gi|78339426|gb|DT559700.1|DT559700	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene38495_All	707	3.18	50.38	3.84	3.73	7.55	8.94	2.69	18.39	5.86	3.98E+00	1.25E-148	Up	2.72E-01	5.09E-01		1.02E+00	4.39E-05	Up	1.26E+00	1.36E-07	Up	2.77E+00	2.72E-48	Up	1.12E+00	2.44E-05	Up	Unigene38495_All//gi|12003400|gb|AAG43557.1|AF211539.1|/9.00E-08//Avr9/Cf-9 rapidly elicited protein 65 [Nicotiana tabacum]		Unigene38495_All//0.00E+00//TC169089				nr +
Unigene38496_All	924	3.74	3.24	5.47	9.43	5.66	8.02	4.44	1.72	1.16	-2.08E-01	5.59E-01		5.51E-01	4.93E-02		-7.36E-01	4.59E-05		-2.35E-01	2.85E-01		-1.37E+00	1.05E-06	Down	-1.93E+00	7.83E-11	Down				Unigene38496_All//0.00E+00//TC137373				
Unigene38498_All	798	18.82	45.02	25.36	27.72	27.27	25.86	28.82	30.64	14.98	1.26E+00	9.25E-38	Up	4.30E-01	7.12E-04		-2.33E-02	8.67E-01		-9.98E-02	4.79E-01		8.82E-02	4.57E-01		-9.45E-01	1.07E-19		Unigene38498_All//gi|32709122|gb|AAP86780.1|//7.00E-58//Mal d 1-associated protein [Malus x domestica]	Unigene38498_All//9.00E-45//AT2G35900| unknown protein	Unigene38498_All//0.00E+00//gi|109877672|gb|DW506645.1|DW506645				nr -
Unigene3850_All	1715	2.04	2.33	3.23	8.19	5.70	3.24	1.95	1.22	0.79	1.91E-01	5.65E-01		6.60E-01	1.25E-02		-5.23E-01	1.71E-04		-1.34E+00	5.99E-18	Down	-6.77E-01	2.53E-02		-1.30E+00	1.83E-05	Down	Unigene3850_All//gi|224131930|ref|XP_002321213.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222861986|gb|EEE99528.1| cytochrome P450 [Populus trichocarpa]	Unigene3850_All//1.00E-111//AT3G50660| DWF4 (DWARF 4); steroid 22-alpha hydroxylase			ko00905|Brassinosteroid biosynthesis		nr -
Unigene38500_All	720	4.65	3.03	2.37	0.42	2.25	2.01	2.17	1.10	1.83	-6.20E-01	6.63E-02		-9.75E-01	6.09E-03		2.44E+00	3.72E-05	Up	2.27E+00	3.41E-04	Up	-9.78E-01	3.94E-02		-2.51E-01	6.18E-01		Unigene38500_All//gi|297839353|ref|XP_002887558.1|//2.00E-82//nodulin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333399|gb|EFH63817.1| nodulin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38500_All//3.00E-82//AT1G74780| nodulin family protein	Unigene38500_All//5.00E-73//TC154702				nr +
Unigene38502_All	487	17.94	44.01	21.21	40.30	40.94	42.75	87.86	110.80	29.04	1.29E+00	8.36E-24	Up	2.42E-01	2.28E-01		2.27E-02	8.86E-01		8.52E-02	5.85E-01		3.35E-01	1.74E-07		-1.60E+00	7.43E-81	Down	Unigene38502_All//gi|222423327|dbj|BAH19733.1|//1.00E-51//AT4G12400| stress-inducible protein, putative	Unigene38502_All//6.00E-53//AT4G12400| stress-inducible protein, putative	Unigene38502_All//0.00E+00//gi|21103741|gb|BQ416054.1|BQ416054				nr +
Unigene38503_All	702	16.62	7.15	7.81	28.95	18.30	20.14	66.13	44.83	41.60	-1.22E+00	3.23E-12	Down	-1.09E+00	7.32E-10	Down	-6.62E-01	3.02E-09		-5.24E-01	9.99E-06		-5.61E-01	1.07E-15		-6.69E-01	7.97E-22		Unigene38503_All//gi|107953708|gb|ABF85694.1|//2.00E-71//inorganic pyrophosphatase [Nicotiana rustica]	Unigene38503_All//3.00E-70//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene38503_All//0.00E+00//TC142855		ko00190|Oxidative phosphorylation		nr -
Unigene38505_All	660	10.70	107.10	17.67	19.02	32.82	18.75	6.21	7.35	6.16	3.32E+00	1.33E-253	Up	7.23E-01	2.58E-05		7.87E-01	1.12E-12		-2.07E-02	9.29E-01		2.41E-01	3.78E-01		-1.33E-02	9.67E-01		Unigene38505_All//gi|15233117|ref|NP_191705.1|//2.00E-64//BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|297820998|ref|XP_002878382.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata] >gi|4689366|gb|AAD27870.1|AF134155_1 BRH1 RING finger protein [Arabidopsis thaliana] >gi|6850837|emb|CAB71076.1| RING finger protein [Arabidopsis thaliana] >gi|21554590|gb|AAM63625.1| RING finger protein [Arabidopsis thaliana] >gi|297324220|gb|EFH54641.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata]	Unigene38505_All//1.00E-65//AT3G61460| BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding	Unigene38505_All//0.00E+00//gi|109874868|gb|DW503842.1|DW503842				nr -
Unigene38506_All	929	0.90	5.29	2.46	6.27	2.04	1.99	50.70	117.15	50.86	2.55E+00	5.48E-14	Up	1.45E+00	1.55E-03		-1.62E+00	1.78E-11	Down	-1.65E+00	1.91E-10	Down	1.21E+00	4.46E-130	Up	4.50E-03	9.71E-01		Unigene38506_All//gi|300836821|gb|ADK38538.1|//1.00E-76//methylketone synthase Ib [Solanum lycopersicum]	Unigene38506_All//4.00E-52//AT2G23610| MES3 (METHYL ESTERASE 3); hydrolase, acting on ester bonds / methyl indole-3-acetate esterase/ methyl jasmonate esterase	Unigene38506_All//0.00E+00//gi|109878098|gb|DW507071.1|DW507071		ko00901|Indole alkaloid biosynthesis		nr -
Unigene38508_All	1512	0.42	0.10	0.63	11.73	7.93	5.62	14.74	15.73	12.65	-2.05E+00	4.46E-02		6.10E-01	3.86E-01		-5.66E-01	2.87E-06		-1.06E+00	9.00E-16	Down	9.40E-02	4.31E-01		-2.21E-01	3.62E-02		Unigene38508_All//gi|53828519|gb|AY94369.1|//2.00E-73//At1g78110 [Arabidopsis thaliana] >gi|55167926|gb|AAV43795.1| At1g78110 [Arabidopsis thaliana]	Unigene38508_All//7.00E-70//AT1G78110| unknown protein	Unigene38508_All//3.00E-144//gi|109847232|gb|DW476212.1|DW476212				nr -
Unigene38512_All	504	12.15	19.81	9.83	21.74	17.42	15.68	56.12	44.45	28.06	7.05E-01	1.00E-04		-3.06E-01	2.43E-01		-3.20E-01	6.47E-02		-4.72E-01	5.84E-03		-3.36E-01	2.36E-04		-1.00E+00	2.52E-26	Down	Unigene38512_All//gi|222424564|dbj|BAH20237.1|//7.00E-44//AT2G01970 [Arabidopsis thaliana]	Unigene38512_All//1.00E-36//AT2G01970| endomembrane protein 70, putative	Unigene38512_All//0.00E+00//TC139516				nr -
Unigene38514_All	761	10.86	29.36	15.32	17.48	23.76	28.84	38.89	56.24	58.79	1.43E+00	7.27E-29	Up	4.96E-01	4.11E-03		4.43E-01	3.35E-04		7.23E-01	2.82E-10		5.32E-01	2.73E-13		5.96E-01	2.96E-17					Unigene38514_All//0.00E+00//TC153755					
Unigene38515_All	809	18.56	10.46	10.93	32.33	27.75	12.00	3.19	0.52	0.89	-8.28E-01	1.42E-08		-7.65E-01	3.27E-07		-2.20E-01	4.14E-02		-1.43E+00	2.18E-36	Down	-2.63E+00	1.34E-09	Down	-1.85E+00	9.39E-07	Down	Unigene38515_All//gi|30691739|ref|NP_198216.2|//2.00E-38//AN3 (ANGUSTIFOLIA 3); protein binding / transcription coactivator [Arabidopsis thaliana] >gi|21539890|gb|AAM52881.1| GRF1-interacting factor 1 [Arabidopsis thaliana]	Unigene38515_All//2.00E-32//AT5G28640| AN3 (ANGUSTIFOLIA 3); protein binding / transcription coactivator	Unigene38515_All//0.00E+00//gi|164293571|gb|ES818224.1|ES818224				nr -
Unigene38516_All	724	4.48	2.45	4.56	4.82	6.23	8.23	16.70	9.41	5.45	-8.71E-01	1.14E-02		2.54E-02	9.60E-01		3.72E-01	2.23E-01		7.74E-01	1.28E-03		-8.28E-01	1.63E-08		-1.62E+00	7.33E-24	Down	Unigene38516_All//gi|145359623|ref|NP_201203.2|//1.00E-42//SAL1; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase [Arabidopsis thaliana]	Unigene38516_All//2.00E-35//AT5G63980| SAL1; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase	Unigene38516_All//0.00E+00//gi|48752561|gb|CO083080.1|CO083080		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism		nr -
Unigene38517_All	884	15.57	18.17	22.53	10.14	23.88	7.00	4.16	5.34	44.98	2.23E-01	1.31E-01		5.33E-01	2.79E-05		1.24E+00	2.01E-25	Up	-5.35E-01	5.02E-03		3.61E-01	1.65E-01		3.43E+00	1.07E-183	Up	Unigene38517_All//gi|149944287|gb|ABR46186.1|//1.00E-36//At4g21445 [Arabidopsis thaliana]	Unigene38517_All//7.00E-38//AT4G21445| unknown protein					nr -
Unigene38518_All	525	33.19	12.84	13.29	44.88	38.04	69.16	20.94	13.85	15.33	-1.37E+00	2.63E-21	Down	-1.32E+00	2.45E-19	Down	-2.39E-01	3.60E-02		6.24E-01	5.90E-13		-5.96E-01	9.36E-05		-4.50E-01	2.55E-03										
Unigene38519_All	487	14.29	14.98	17.06	15.85	13.79	19.94	12.50	0.86	3.11	6.84E-02	7.60E-01		2.56E-01	2.46E-01		-2.02E-01	3.90E-01		3.31E-01	8.84E-02		-3.86E+00	5.27E-31	Down	-2.01E+00	1.80E-16	Down	Unigene38519_All//gi|15233171|ref|NP_191723.1|//4.00E-21//AGP20 [Arabidopsis thaliana] >gi|75183616|sp|Q9M373.1|AGP20_ARATH RecName: Full=Arabinogalactan peptide 20; Short=AG-peptide 20; Flags: Precursor >gi|98960995|gb|ABF58981.1| At3g61640 [Arabidopsis thaliana]	Unigene38519_All//2.00E-16//AT3G61640| AGP20	Unigene38519_All//4.00E-171//TC177810				nr +
Unigene38520_All	1117	1.17	0.45	0.38	46.25	29.69	24.83	15.18	7.56	4.35	-1.37E+00	2.40E-02		-1.62E+00	1.33E-02		-6.40E-01	1.99E-21		-8.98E-01	5.11E-34		-1.01E+00	8.64E-16	Down	-1.80E+00	1.72E-38	Down	Unigene38520_All//gi|15237490|ref|NP_199482.1|//1.00E-119//TRN2 (TORNADO 2) [Arabidopsis thaliana] >gi|9758506|dbj|BAB08914.1| senescence-associated protein 5-like protein [Arabidopsis thaliana] >gi|56381915|gb|AAV85676.1| At5g46700 [Arabidopsis thaliana] >gi|110740669|dbj|BAE98437.1| senescence-associated protein 5-like protein [Arabidopsis thaliana]	Unigene38520_All//1.00E-102//AT5G46700| TRN2 (TORNADO 2)	Unigene38520_All//0.00E+00//DW235272				nr -
Unigene38523_All	830	8.83	4.33	6.16	12.96	6.72	9.69	14.26	7.50	8.02	-1.03E+00	3.06E-06	Down	-5.19E-01	2.23E-02		-9.48E-01	3.83E-09		-4.21E-01	1.63E-02		-9.27E-01	6.11E-10		-8.31E-01	1.07E-08		Unigene38523_All//gi|28416791|gb|AAO42926.1|//1.00E-24//At4g39300 [Arabidopsis thaliana]	Unigene38523_All//6.00E-26//AT4G39300| unknown protein	Unigene38523_All//0.00E+00//gi|109876900|gb|DW505874.1|DW505874				nr +
Unigene38524_All	988	18.27	8.15	5.66	17.34	28.82	51.84	1.07	2.24	7.46	-1.16E+00	2.95E-17	Down	-1.69E+00	1.27E-28	Down	7.33E-01	1.12E-14		1.58E+00	1.02E-80	Up	1.07E+00	5.89E-03		2.80E+00	1.60E-28	Up	Unigene38524_All//gi|225433371|ref|XP_002282929.1|//6.00E-71//PREDICTED: similar to glutathione S-transferase [Vitis vinifera]	Unigene38524_All//6.00E-38//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	Unigene38524_All//0.00E+00//TC155908		ko00480|Glutathione metabolism		nr -
Unigene38525_All	879	12.74	6.00	9.87	5.27	6.58	4.26	8.71	7.66	10.06	-1.09E+00	6.16E-10	Down	-3.67E-01	4.38E-02		3.21E-01	2.25E-01		-3.06E-01	3.23E-01		-1.86E-01	3.93E-01		2.09E-01	2.52E-01		Unigene38525_All//gi|297800462|ref|XP_002868115.1|//4.00E-51//histidine triad family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313951|gb|EFH44374.1| histidine triad family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38525_All//7.00E-52//AT4G16566| histidine triad family protein / HIT family protein	Unigene38525_All//0.00E+00//TC141346				nr +

Unigene38527_All	1035	12.54	6.51	16.62	1.20	2.20	3.80	0.00	0.00	0.00	-9.45E-01	3.28E-09		4.07E-01	3.73E-03		8.68E-01	4.03E-02		1.66E+00	4.08E-07	Up	null	null		null	null		Unigene38527_All//gi|18407481|ref|NP_566113.1|//3.00E-90//CRR6 (chlororespiratory reduction 6) [Arabidopsis thaliana] >gi|11692910|gb|AAG40058.1|AF324707_1 At2g47910 [Arabidopsis thaliana] >gi|3738303|gb|AAC03645.1| expressed protein [Arabidopsis thaliana] >gi|15010782|gb|AAK74050.1| T9J23.7/T9J23.7 [Arabidopsis thaliana] >gi|15899758|gb|AAL06807.1| At2g47910/T9J23.7 [Arabidopsis thaliana] >gi|20197562|gb|AAM15131.1| expressed protein [Arabidopsis thaliana]	Unigene38527_All//1.00E-91//AT2G47910| CRR6 (chlororespiratory reduction 6)	Unigene38527_All//0.00E+00//TC141347				nr +
Unigene38529_All	1087	16.32	12.96	8.13	16.82	13.97	13.25	7.90	6.88	7.73	-3.33E-01	1.31E-02		-1.00E+00	6.19E-13	Down	-2.68E-01	3.99E-02		-3.44E-01	8.50E-03		-1.98E-01	3.19E-01		-3.00E-02	8.85E-01		Unigene38529_All//gi|224094957|ref|XP_002310304.1|//2.00E-96//methionine sulfoxide reductase type [Populus trichocarpa] >gi|222853207|gb|EEE90754.1| methionine sulfoxide reductase type [Populus trichocarpa]	Unigene38529_All//2.00E-94//AT2G18030| peptide methionine sulfoxide reductase family protein	Unigene38529_All//0.00E+00//TC132896				nr -
Unigene38530_All	581	18.28	54.94	14.94	29.15	22.64	34.13	67.68	123.23	99.01	1.59E+00	1.91E-47	Up	-2.91E-01	1.32E-01		-3.65E-01	4.85E-03		2.27E-01	8.77E-02		8.65E-01	7.92E-50		5.49E-01	4.96E-19		Unigene38530_All//gi|159895671|gb|ABX10446.1|//2.00E-47//ethanolamine-phosphate cytidylyltransferase 2 [Gossypium hirsutum]	Unigene38530_All//3.00E-21//AT2G38670| PECT1 (PHOSPHORYLETHANOLAMINE CYTIDYLYLTRANSFERASE 1); ethanolamine-phosphate cytidylyltransferase	Unigene38530_All//0.00E+00//DR044156		ko00564|Glycerophospholipid metabolism		nr +
Unigene38531_All	856	7.46	3.79	4.91	8.55	9.74	7.39	2.86	0.98	1.77	-9.77E-01	3.49E-05		-6.02E-01	1.38E-02		1.87E-01	4.23E-01		-2.12E-01	4.03E-01		-1.55E+00	4.79E-05	Down	-6.96E-01	4.53E-02		Unigene38531_All//gi|242073486|ref|XP_002446679.1|//5.00E-06//hypothetical protein SORBIDRAFT_06g020406 [Sorghum bicolor] >gi|241937862|gb|EES11007.1| hypothetical protein SORBIDRAFT_06g020406 [Sorghum bicolor]		Unigene38531_All//1.00E-09//ES852136				nr +
Unigene38532_All	843	0.12	81.38	3.85	0.77	0.82	4.34	12.19	28.26	49.05	9.36E+00	0.00E+00	Up	4.96E+00	2.63E-15	Up	8.89E-02	9.49E-01		2.50E+00	7.74E-11	Up	1.21E+00	2.93E-29	Up	2.01E+00	7.45E-106	Up	Unigene38532_All//gi|15236529|ref|NP_192597.1|//2.00E-54//heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related [Arabidopsis thaliana] >gi|3377812|gb|AAC28185.1| contains similarity to heavy-metal-associated domain containing proteins (Pfam: HMA,hm, score: 12.02) [Arabidopsis thaliana]	Unigene38532_All//6.00E-56//AT4G08570| heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	Unigene38532_All//0.00E+00//TC178741				nr -
Unigene38535_All	899	8.61	6.31	10.07	7.37	9.19	5.27	3.53	2.37	1.33	-4.48E-01	3.39E-02		2.25E-01	2.96E-01		3.19E-01	1.32E-01		-4.82E-01	3.75E-02		-5.73E-01	6.95E-02		-1.41E+00	8.85E-06	Down					Unigene38535_All//8.00E-131//TC166523				
Unigene38537_All	978	802.63	736.00	1090.48	131.31	162.88	109.12	4.11	7.48	13.08	-1.25E-01	1.23E-12		4.42E-01	1.03E-176		3.11E-01	3.31E-17		-2.67E-01	1.00E-09		8.65E-01	8.03E-06		1.67E+00	4.45E-26	Up	Unigene38537_All//gi|297852864|ref|XP_002894313.1|//7.00E-24//photosystem II 5 kD protein [Arabidopsis lyrata subsp. lyrata] >gi|297340155|gb|EFH70572.1| photosystem II 5 kD protein [Arabidopsis lyrata subsp. lyrata]	Unigene38537_All//2.00E-16//AT1G81400| photosystem II 5 kD protein	Unigene38537_All//0.00E+00//gi|164247129|gb|ES810191.1|ES810191				nr -
Unigene38538_All	786	3.59	7.99	6.71	9.44	10.25	5.98	3.77	1.33	2.64	1.15E+00	2.09E-06	Up	9.00E-01	9.25E-04		1.19E-01	6.14E-01		-6.60E-01	1.71E-03		-1.50E+00	1.09E-05	Down	-5.15E-01	1.04E-01			Unigene38538_All//4.00E-05//AT2G33240| XID; motor/ protein binding	Unigene38538_All//6.00E-14//DT463172				
Unigene38540_All	513	14.28	13.24	7.06	11.65	13.69	13.56	7.75	7.01	6.99	-1.10E-01	6.17E-01		-1.02E+00	7.73E-06	Down	2.33E-01	3.45E-01		2.19E-01	4.06E-01		-1.45E-01	6.36E-01		-1.49E-01	6.05E-01		Unigene38540_All//gi|224072218|ref|XP_002303658.1|//6.00E-53//f-box family protein [Populus trichocarpa] >gi|222841090|gb|EEE78637.1| f-box family protein [Populus trichocarpa]	Unigene38540_All//3.00E-47//AT4G10925| F-box family protein	Unigene38540_All//8.00E-105//gi|72273813|gb|DT049343.1|DT049343				nr -
Unigene38542_All	1257	4.99	3.39	2.12	17.91	11.81	12.07	25.80	6.32	4.03	-5.61E-01	1.73E-02		-1.24E+00	9.93E-07	Down	-6.01E-01	1.17E-08		-5.69E-01	3.56E-07		-2.03E+00	7.66E-83	Down	-2.68E+00	2.58E-119	Down	Unigene38542_All//gi|18405770|ref|NP_565953.1|//1.00E-62//MIZ1 (mizu-kussei 1) [Arabidopsis thaliana] >gi|2818701|gb|AAB84348.1| expressed protein [Arabidopsis thaliana] >gi|109946471|gb|ABG48414.1| At2g41660 [Arabidopsis thaliana]	Unigene38542_All//9.00E-64//AT2G41660| MIZ1 (mizu-kussei 1)	Unigene38542_All//0.00E+00//TC148386				nr +
Unigene38543_All	958	0.05	8.57	2.17	3.90	3.81	7.45	1.06	0.79	0.08	7.29E+00	4.58E-45	Up	5.31E+00	3.65E-10	Up	-3.36E-02	9.18E-01		9.34E-01	1.70E-05		-4.32E-01	5.03E-01		-3.67E+00	1.15E-05	Down	Unigene38543_All//gi|32364488|gb|AA061677.1|//3.00E-42//AKIN beta2 [Medicago truncatula]	Unigene38543_All//3.00E-33//AT4G16360| AMP-activated protein kinase	Unigene38543_All//0.00E+00//TC165533				nr +
Unigene38545_All	1153	0.23	0.00	0.00	57.59	23.21	18.96	9.24	7.47	2.73	-7.83E+00	6.70E-02		-7.83E+00	8.56E-02		-1.31E+00	4.29E-92	Down	-1.60E+00	1.12E-108	Down	-3.07E-01	5.86E-02		-1.76E+00	1.02E-23	Down	Unigene38545_All//gi|224085656|ref|XP_002307652.1|//1.00E-109//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222857101|gb|EEE94648.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene38545_All//7.00E-74//AT4G28530| anac074 (Arabidopsis NAC domain containing protein 74); transcription factor	Unigene38545_All//0.00E+00//TC143526	NAC			nr -
Unigene38546_All	906	2.14	1.73	0.76	13.14	9.50	4.44	4.95	0.92	2.37	-3.02E-01	5.29E-01		-1.48E+00	3.61E-03		-4.68E-01	2.56E-03		-1.57E+00	3.14E-19	Down	-2.42E+00	7.76E-15	Down	-1.06E+00	2.59E-05	Down	Unigene38546_All//gi|105830048|gb|AB874712.1|//1.00E-89//At1g80690 [Arabidopsis thaliana]	Unigene38546_All//4.00E-81//AT1G80690| unknown protein	Unigene38546_All//0.00E+00//gi|48778070|gb|C0087436.1|C0087436				nr +
Unigene38547_All	547	6.03	12.23	7.59	21.86	17.69	23.78	8.89	4.36	3.64	1.02E+00	1.05E-05	Up	3.34E-01	3.05E-01		-3.05E-01	6.50E-02		1.22E-01	5.22E-01		-1.03E+00	2.88E-05	Down	-1.29E+00	1.92E-07	Down	Unigene38547_All//gi|14190467|gb|AAX55714.1|AF380633_1/5.00E-16//At3g13171 [Arabidopsis thaliana] >gi|15809712|gb|AAL06784.1| At3g13171 [Arabidopsis thaliana]	Unigene38547_All//5.00E-13//AT3G13175| unknown protein	Unigene38547_All//0.00E+00//TC165964				nr -
Unigene38548_All	991	1.90	16.82	3.65	19.91	22.83	23.20	32.68	32.48	27.38	3.15E+00	4.14E-57	Up	9.43E-01	5.28E-03		1.98E-01	1.06E-01		2.21E-01	7.11E-02		-9.10E-03	9.52E-01		-2.56E-01	2.32E-03		Unigene38548_All//gi|164564739|dbj|BAF98220.1|//3.00E-18//CM0216.380.nc [Lotus japonicus]	Unigene38548_All//5.00E-28//AT4G34560| unknown protein					nr +
Unigene38549_All	984	64.28	33.73	54.06	12.45	13.79	6.06	0.39	0.34	0.40	-9.31E-01	7.64E-41		-2.50E-01	3.05E-04		1.47E-01	4.17E-01		-1.04E+00	1.03E-10	Down	-1.87E-01	8.57E-01		6.64E-02	9.66E-01		Unigene38549_All//gi|297804700|ref|XP_002870234.1|//4.00E-89//photosystem II reaction center PsbP family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316070|gb|EFH46493.1| photosystem II reaction center PsbP family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38549_All//5.00E-85//AT4G15510| photosystem II reaction center PsbP family protein	Unigene38549_All//0.00E+00//TC131192		ko00195|Photosynthesis		nr -
Unigene38550_All	972	2.69	0.42	0.22	4.77	4.78	2.83	2.31	0.22	0.70	-2.69E+00	3.11E-08	Down	-3.62E+00	4.17E-10	Down	5.00E-03	9.95E-01		-7.50E-01	6.84E-03		-3.42E+00	1.03E-10	Down	-1.73E+00	1.59E-05	Down	Unigene38550_All//gi|145340316|ref|NP_193430.3|//2.00E-08//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|110738029|dbj|BAF00949.1| kinase like protein [Arabidopsis thaliana]	Unigene38550_All//9.00E-10//AT4G16970| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase					nr +
Unigene38551_All	978	3.80	3.83	2.34	6.62	9.58	4.34	1.64	0.17	0.29	1.35E-02	9.86E-01		-6.98E-01	3.66E-02		5.32E-01	3.21E-03		-6.09E-01	7.93E-03		-3.26E+00	1.49E-07	Down	-2.53E+00	2.96E-06	Down	Unigene38551_All//gi|15236232|ref|NP_192210.1|//1.00E-122//leucine-rich repeat family protein [Arabidopsis thaliana] >gi|91806626|gb|ABE66040.1| leucine-rich repeat family protein [Arabidopsis thaliana]	Unigene38551_All//8.00E-118//AT1G03440| leucine-rich repeat family protein	Unigene38551_All//7.00E-107//TC173657		ko04626|Plant-pathogen interaction		nr +
Unigene38553_All	1482	8.26	7.42	10.20	3.16	1.00	0.91	0.57	3.98	0.27	-1.55E-01	3.80E-01		3.05E-01	4.92E-02		-1.66E+00	1.24E-09	Down	-1.79E+00	1.99E-09	Down	2.80E+00	1.77E-22	Up	-1.09E+00	9.98E-02		Unigene38553_All//gi|87162753|gb|AB028548.1|//8.00E-79//Protein kinase; Type I EGF [Medicago truncatula]	Unigene38553_All//2.00E-51//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase	Unigene38553_All//8.00E-15//DT467466				nr +
Unigene38554_All	1187	1.72	5.42	3.01	4.78	5.74	4.41	0.32	0.42	0.13	1.66E+00	1.00E-10	Up	8.06E-01	1.78E-02		2.64E-01	2.95E-01		-1.16E-01	6.95E-01		3.98E-01	6.52E-01		-1.26E+00	2.48E-01		Unigene38554_All//gi|108706753|gb|ABF94548.1|//8.00E-58//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene38554_All//1.00E-72//AT1G49890| unknown protein	Unigene38554_All//0.00E+00//gi|13353152|gb|BG443500.1|BG443500				nr -
Unigene38555_All	1162	13.82	6.32	5.09	12.65	10.34	2.37	2.04	0.36	0.45	-1.13E+00	9.91E-15	Down	-1.44E+00	2.38E-20	Down	-2.90E-01	4.75E-02		-2.42E+00	1.02E-41	Down	-2.50E+00	1.92E-08	Down	-2.19E+00	1.28E-07	Down	Unigene38555_All//gi|38564296|gb|AAR23727.1|//3.00E-35//At5g19260 [Arabidopsis thaliana] >gi|44022143|gb|AAS46641.1| At5g19260 [Arabidopsis thaliana]	Unigene38555_All//1.00E-28//AT5G19260| unknown protein	Unigene38555_All//0.00E+00//DW489206				nr +
Unigene38556_All	1133	10.58	10.33	3.85	42.21	42.88	42.57	0.34	0.04	0.00	-3.37E-02	8.48E-01		-1.46E+00	1.55E-15	Down	2.29E-02	8.16E-01		1.24E-02	9.12E-01		-3.19E+00	3.12E-02		-8.39E+00	4.19E-03		Unigene38556_All//gi|121490210|emb|CAK55186.1|//1.00E-117//pinene synthase [Quercus ilex]	Unigene38556_All//4.00E-101//AT3G25830| ATTPS-CIN (terpene synthase-like sequence-1,8-cineole); (E)-beta-ocimene synthase/ myrcene synthase	Unigene38556_All//0.00E+00//TC149686		ko00902|Monoterpenoid biosynthesis		nr +
Unigene38559_All	2106	1.37	0.22	0.43	8.52	5.98	4.37	11.02	5.89	8.29	-2.66E+00	6.94E-09	Down	-1.67E+00	5.32E-05	Down	-5.09E-01	2.52E-05		-9.61E-01	1.37E-13		-9.03E-01	6.09E-18		-4.12E-01	3.08E-05		Unigene38559_All//gi|223452498|gb|ACM89576.1|//0.00E+00//protein kinase [Glycine max]	Unigene38559_All//2.00E-133//AT5G15080| protein kinase, putative	Unigene38559_All//0.00E+00//TC174260				nr +
Unigene38562_All	773	4.67	9.05	11.16	36.28	30.25	43.88	16.90	26.33	19.22	9.54E-01	2.17E-05		1.26E+00	3.19E-09	Up	-2.62E-01	8.92E-03		2.74E-01	3.27E-03		6.40E-01	4.48E-09		1.86E-01	1.74E-01		Unigene38562_All//gi|261532843|gb|ACX85428.1|//1.00E-74//calmodulin isoform 1 [Solanum tuberosum]	Unigene38562_All//2.00E-74//AT3G43810| CAM7 (CALMODULIN 7); calcium ion binding	Unigene38562_All//0.00E+00//gi|164255386|gb|ES798602.1|ES798602		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr +
Unigene38564_All	1252	1.92	2.79	1.36	3.94	3.55	3.32	3.04	1.00	0.92	5.39E-01	1.06E-01		-4.98E-01	2.46E-01		-1.51E-01	6.08E-01		-2.47E-01	4.13E-01		-1.60E+00	1.04E-07	Down	-1.72E+00	9.32E-09	Down	Unigene38564_All//gi|224078478|ref|XP_002305547.1|//1.00E-107//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222848511|gb|EEE86058.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene38564_All//3.00E-84//AT2G17040| anac036 (Arabidopsis NAC domain containing protein 36); transcription factor	Unigene38564_All//0.00E+00//TC170871	NAC			nr +
Unigene38565_All	1109	1.42	1.74	1.10	15.50	7.17	3.18	34.85	15.38	2.51	2.95E-01	5.42E-01		-3.58E-01	5.20E-01		-1.11E+00	1.62E-18	Down	-2.29E+00	1.27E-45	Down	-1.18E+00	4.64E-45	Down	-3.79E+00	7.98E-198	Down	Unigene38565_All//gi|297796145|ref|XP_002865957.1|//6.00E-83//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311792|gb|EFH42216.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38565_All//5.00E-80//AT5G53190| nodulin MtN3 family protein					nr +

Unigene38568_All	866	7.19	3.28	2.77	115.73	163.43	70.98	13.28	4.97	3.13	-1.13E+00	3.09E-06	Down	-1.38E+00	9.42E-08	Down	4.98E-01	3.34E-36		-7.05E-01	2.18E-43		-1.42E+00	2.70E-18	Down	-2.09E+00	7.01E-32	Down	Unigene38568_All//gi|226497984|ref|NP_001150100.1|//2.00E-18//LOC100283729 [Zea mays] >gi|195605708|gb|ACG24684.1| NAP16kDa protein [Zea mays] >gi|195617226|gb|ACG30443.1| NAP16kDa protein [Zea mays] >gi|195628432|gb|ACG36046.1| NAP16kDa protein [Zea mays] >gi|195636726|gb|ACG37831.1| NAP16kDa protein [Zea mays] >gi|195646128|gb|ACG42532.1| NAP16kDa protein [Zea mays] >gi|195648182|gb|ACG43559.1| NAP16kDa protein [Zea mays]	Unigene38568_All//2.00E-14//AT4G23496| SP1L5 (SPIRAL1-LIKE5)	Unigene38568_All//0.00E+00//TC164502				nr +
Unigene38569_All	687	15.69	17.63	12.25	15.59	13.63	12.75	17.66	13.08	7.19	1.68E-01	3.56E-01		-3.57E-01	5.46E-02		-1.93E-01	3.13E-01		-2.90E-01	1.20E-01		-4.33E-01	2.96E-03		-1.30E+00	1.90E-17	Down	Unigene38569_All//gi|17065494|gb|AAL32901.1|//3.00E-28//Unknown protein [Arabidopsis thaliana] >gi|30102802|gb|AAP21319.1| At5g22280 [Arabidopsis thaliana]	Unigene38569_All//3.00E-24//AT3G44280| unknown protein	Unigene38569_All//0.00E+00//DW511530				nr -
Unigene38570_All	665	1.49	0.00	1.68	2.25	2.64	3.87	2.86	1.51	1.38	-1.05E+01	7.45E-06	Down	1.70E-01	7.78E-01		2.33E-01	6.80E-01		7.85E-01	4.98E-02		-9.24E-01	2.84E-02		-1.05E+00	9.64E-03		Unigene38570_All//gi|20385491|gb|AAM21312.1|AF371327_1//2.00E-47//EMB514 [Arabidopsis thaliana]	Unigene38570_All//6.00E-46//AT5G62410| Encodes a protein DOMINO1 that belongs to a plant-specific gene family sharing a common motif present in the tomato DEFECTIVE CHLOROPLASTS AND LEAVES (LeDCL) protein. DOMINO1 is located in the nucleus. Arabidopsis embryos carrying the domino1 mutation grow slowly in comparison with wild type embryos and reach only the globular stage at desiccation. The primary defect of the mutation at the cellular level is the large size of the nucleolus that can be observed soon after fertilization in the nuclei of both the embryo and the endosperm. DOMINO1 might have a role in ribosome biogenesis and in determining the rate of cell division.	Unigene38570_All//0.00E+00//gi|13350670|gb|BG441018.1|BG441018				nr -
Unigene38571_All	1112	6.30	3.69	5.51	19.40	20.90	16.04	8.86	1.92	2.26	-7.73E-01	4.75E-04		-1.95E-01	4.20E-01		1.08E-01	4.30E-01		-2.74E-01	2.47E-02		-2.21E+00	1.72E-28	Down	-1.97E+00	1.47E-25	Down	Unigene38571_All//gi|297849186|ref|XP_002892474.1|//4.00E-49//VAMP/synaptobrevin-associated protein 27-2 [Arabidopsis lyrata subsp. lyrata] >gi|297338316|gb|EFH68733.1| VAMP/synaptobrevin-associated protein 27-2 [Arabidopsis lyrata subsp. lyrata]	Unigene38571_All//3.00E-48//AT1G08820| VAP27-2 (VAMP/SYNAPTOBREVIN-ASSOCIATED PROTEIN 27-2); structural molecule	Unigene38571_All//0.00E+00//TC148377				nr +
Unigene38573_All	838	3.43	8.47	2.41	4.76	1.27	2.91	2.02	3.44	3.61	1.30E+00	1.89E-08	Up	-5.08E-01	1.97E-01		-1.90E+00	6.72E-10	Down	-7.08E-01	2.01E-02		7.70E-01	1.95E-02		8.40E-01	6.81E-03		Unigene38573_All//gi|15241290|ref|NP_197519.1|//5.00E-59//binding [Arabidopsis thaliana]	Unigene38573_All//3.00E-42//AT5G20190| binding	Unigene38573_All//0.00E+00//TC175355				nr +
Unigene38576_All	994	5.26	5.66	5.04	4.96	6.03	10.63	17.31	28.13	41.88	1.04E-01	6.81E-01		-6.39E-02	8.17E-01		2.81E-01	2.97E-01		1.10E+00	5.03E-10	Up	7.00E-01	4.03E-14		1.27E+00	9.71E-56	Up	Unigene38576_All//gi|5002232|gb|AAD37373.1|AF145234_1//9.00E-80//NADPH:quinone oxidoreductase [Arabidopsis thaliana]	Unigene38576_All//1.00E-80//AT3G27890| NQR (NADPH:QUINONE OXIDOREDUCTASE); FMN reductase	Unigene38576_All//0.00E+00//TC153034				nr +
Unigene38577_All	1947	0.81	2.29	1.42	13.10	14.61	11.32	5.15	2.43	6.32	1.51E+00	8.87E-07	Up	8.19E-01	3.85E-02		1.57E-01	1.60E-01		-2.11E-01	6.84E-02		-1.09E+00	7.80E-11	Down	2.97E-01	3.93E-02		Unigene38577_All//gi|115451143|ref|NP_001049172.1|//2.00E-99//Os03g0181800 [Oryza sativa Japonica Group] >gi|24960751|gb|AAN65445.1| Hypothetical protein [Oryza sativa Japonica Group] >gi|108706524|gb|ABF94319.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547643|dbj|BAF11086.1| Os03g0181800 [Oryza sativa Japonica Group]	Unigene38577_All//1.00E-126//AT3G14170| unknown protein	Unigene38577_All//0.00E+00//TC177212				nr +
Unigene38580_All	2690	0.21	0.23	0.06	0.43	0.56	0.55	23.12	23.17	7.92	7.87E-02	9.41E-01		-1.85E+00	9.61E-02		4.03E-01	5.14E-01		3.79E-01	5.26E-01		2.90E-03	1.01E+00		-1.55E+00	1.19E-111	Down	Unigene38580_All//gi|18147596|dbj|BAB83088.1|//0.00E+00//beta-amyrin synthase [Betula platyphylla]	Unigene38580_All//0.00E+00//AT1G78955| CAS1 (Cameliol C synthase 1); beta-amyrin synthase	Unigene38580_All//0.00E+00//CO128033		ko00100|Steroid biosynthesis		nr -
Unigene38581_All	1809	0.23	0.00	0.35	8.70	3.24	3.40	9.16	6.24	1.04	-7.85E+00	1.05E-02		6.10E-01	5.09E-01		-1.43E+00	4.39E-25	Down	-1.36E+00	1.76E-20	Down	-5.55E-01	4.97E-06		-3.15E+00	2.80E-72	Down	Unigene38581_All//gi|42475462|dbj|BAD10885.1|//7.00E-98//zinc finger protein [Malus x domestica]	Unigene38581_All//6.00E-77//AT3G50700| AtIDD2 (Arabidopsis thaliana Indeterminate(ID)-Domain 2); nucleic acid binding / transcription factor/ zinc ion binding	Unigene38581_All//0.00E+00//ES815778	C2H2			nr +
Unigene38582_All	773	38.65	64.43	45.05	52.97	45.62	28.34	6.73	8.92	3.35	7.37E-01	7.00E-22		2.21E-01	2.49E-02		-2.16E-01	8.88E-03		-9.03E-01	2.50E-27		4.07E-01	4.60E-02		-1.01E+00	1.30E-05	Down		Unigene38582_All//6.00E-06//AT1G10000| nucleic acid binding / ribonuclease H	Unigene38582_All//3.00E-93//TC148688				
Unigene38586_All	823	8.65	5.05	5.24	13.74	17.66	16.63	30.77	5.74	11.57	-7.76E-01	4.01E-04		-7.22E-01	1.54E-03		3.62E-01	1.24E-02		2.75E-01	8.90E-02		-2.42E+00	1.15E-80	Down	-1.41E+00	2.89E-40	Down	Unigene38586_All//gi|34395875|sp|Q8HCO.1|GP14_ARATH//3.00E-63//RecName: Full=Uncharacterized GPI-anchored protein At3g06035; Flags: Precursor >gi|30102608|gb|AAP21222.1| At3g06035 [Arabidopsis thaliana]	Unigene38586_All//4.00E-55//AT3G06035| unknown protein	Unigene38586_All//0.00E+00//gi|109882320|gb|DW511290.1|DW511290				nr +
Unigene38587_All	1035	25.17	13.85	18.06	28.59	16.37	30.55	99.18	30.37	44.03	-8.62E-01	2.95E-15		-4.79E-01	1.27E-05		-8.05E-01	1.82E-18		9.55E-02	4.13E-01		-1.71E+00	2.59E-206	Down	-1.17E+00	2.41E-120	Down	Unigene38587_All//gi|30680258|ref|NP_566306.3|//2.00E-45//AIR12; extracellular matrix structural constituent [Arabidopsis thaliana]	Unigene38587_All//2.00E-45//AT3G07390| AIR12; extracellular matrix structural constituent	Unigene38587_All//0.00E+00//TC150436				nr +
Unigene38589_All	543	27.17	23.24	35.11	62.11	59.23	190.97	115.55	99.52	96.11	-2.26E-01	1.41E-01		3.70E-01	5.42E-03		-6.84E-02	5.53E-01		1.62E+00	2.89E-169	Up	-2.15E-01	3.56E-04		-2.66E-01	4.86E-06		Unigene38589_All//gi|283136142|gb|ADB11390.1|//7.00E-42//tau class glutathione transferase GSTU24 [Populus trichocarpa]	Unigene38589_All//4.00E-37//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	Unigene38589_All//0.00E+00//gi|164294039|gb|ES807289.1|ES807289		ko00480|Glutathione metabolism		nr -
Unigene3859_All	1033	40.67	25.21	39.69	600.18	677.61	567.27	43.18	23.10	19.24	-6.90E-01	1.15E-16		-3.51E-02	7.15E-01		1.75E-01	4.90E-25		-8.14E-02	5.25E-05		-9.02E-01	1.11E-33		-1.17E+00	2.21E-52	Down	Unigene3859_All//gi|451544|gb|AAA79364.1|//1.00E-125//proline-rich cell wall protein [Gossypium barbadense]		Unigene3859_All//0.00E+00//TC132208		ko03040|Spliceosome		nr +
Unigene38590_All	1157	4.43	3.59	2.21	6.72	7.89	3.28	4.35	1.34	1.10	-3.03E-01	2.71E-01		-1.00E+00	3.06E-04	Down	2.32E-01	2.77E-01		-1.03E+00	5.57E-07	Down	-1.70E+00	8.88E-11	Down	-1.98E+00	1.60E-13	Down	Unigene38590_All//gi|30686452|ref|NP_181098.2|//7.00E-58//BPC7 (BASIC PENTACYSTEINE 7); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene38590_All//3.00E-58//AT2G35550| BPC7 (BASIC PENTACYSTEINE 7); DNA binding / transcription factor	Unigene38590_All//0.00E+00//TC167366	BBR/BPC			nr -
Unigene38591_All	1068	5.09	3.08	3.99	1.96	3.00	1.65	0.87	0.94	4.40	-7.24E-01	4.47E-03		-3.53E-01	2.06E-01		6.14E-01	7.91E-02		-2.48E-01	6.39E-01		1.09E-01	8.63E-01		2.34E+00	3.28E-15	Up	Unigene38591_All//gi|38175497|dbj|BAD01195.1|//1.00E-62//F-box protein family-like protein [Oryza sativa Japonica Group] >gi|38175774|dbj|BAD01468.1| F-box protein family-like protein [Oryza sativa Japonica Group]	Unigene38591_All//1.00E-60//AT2G01620| MEE11 (maternal effect embryo arrest 11)					nr +
Unigene38597_All	2561	0.00	0.00	0.00	0.04	0.00	0.00	11.62	15.31	28.28	null	null		null	null		-5.28E+00	3.13E-01		-5.28E+00	3.99E-01		3.97E-01	1.68E-07		1.28E+00	2.54E-97	Up	Unigene38597_All//gi|168034532|ref|XP_001769766.1|//0.00E+00//potassium transporter [Physcomitrella patens subsp. patens] >gi|162678875|gb|EDQ65328.1| potassium transporter [Physcomitrella patens subsp. patens]	Unigene38597_All//7.00E-143//AT1G31120| KUP10; potassium ion transmembrane transporter	Unigene38597_All//0.00E+00//TC145012				nr +
Unigene38598_All	551	1.61	1.38	0.39	7.87	5.69	2.79	2.46	0.30	0.58	-2.27E-01	7.27E-01		-2.06E+00	1.78E-02		-4.68E-01	1.05E-01		-1.50E+00	6.13E-07	Down	-3.02E+00	4.74E-06	Down	-2.09E+00	1.85E-04	Down	Unigene38598_All//gi|124359162|gb|ABN05685.1|//2.00E-10//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene38598_All//1.00E-35//gi|78336635|gb|DT556909.1|DT556909				nr -
Unigene38599_All	827	4.68	3.61	3.22	19.64	12.62	9.07	1.94	0.76	0.53	-3.73E-01	2.37E-01		-5.40E-01	1.00E-01		-6.38E-01	4.62E-07		-1.12E+00	1.25E-15	Down	-1.36E+00	4.47E-03		-1.87E+00	1.38E-04	Down	Unigene38599_All//gi|124359162|gb|ABN05685.1|//3.00E-11//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene38599_All//5.00E-05//AT3G09510| nucleic acid binding	Unigene38599_All//0.00E+00//gi|109852641|gb|DW481620.1|DW481620				nr -
Unigene38601_All	735	0.85	6.34	1.67	0.61	2.62	5.04	0.98	1.76	1.79	2.89E+00	4.24E-15	Up	9.64E-01	1.38E-01		2.10E+00	3.43E-05	Up	3.05E+00	2.19E-13	Up	8.50E-01	1.12E-01		8.71E-01	8.59E-02		Unigene38601_All//gi|222631198|gb|EEE63330.1|//9.00E-06//hypothetical protein Os_I_18141 [Oryza sativa Japonica Group]		Unigene38601_All//4.00E-12//TC179044				nr -
Unigene38602_All	475	19.28	61.02	86.55	16.15	5.94	22.72	6.94	3.96	2.01	1.66E+00	4.84E-46	Up	2.17E+00	1.86E-90	Up	-1.44E+00	1.26E-12	Down	4.93E-01	4.39E-03		-8.10E-01	7.67E-03		-1.79E+00	4.52E-08	Down	Unigene38602_All//gi|19962|emb|CAA41437.1|//1.00E-60//pathogenesis-related protein 4A [Nicotiana tabacum]	Unigene38602_All//3.00E-38//AT3G04720| PR4 (PATHOGENESIS-RELATED 4); chitin binding	Unigene38602_All//0.00E+00//gi|31073097|gb|CA993376.1|CA993376				nr +
Unigene38603_All	1362	0.54	1.97	1.06	1.61	1.09	1.26	2.58	1.60	1.14	1.87E+00	1.12E-05	Up	9.73E-01	9.57E-02		-5.66E-01	1.87E-01		-3.53E-01	4.57E-01		-6.91E-01	1.87E-02		-1.18E+00	5.54E-05	Down	Unigene38603_All//gi|224131902|ref|XP_002328136.1|//1.00E-135//mitochondrial phosphate carrier protein [Populus trichocarpa] >gi|222837651|gb|EEE76016.1| mitochondrial phosphate carrier protein [Populus trichocarpa]	Unigene38603_All//2.00E-124//AT2G17270| mitochondrial substrate carrier family protein	Unigene38603_All//0.00E+00//DW518289				nr -
Unigene38604_All	1127	0.46	0.09	0.95	7.03	4.46	7.05	3.15	2.15	1.41	-2.37E+00	4.75E-02		1.03E+00	1.43E-01		-6.56E-01	6.36E-04		5.10E-03	9.82E-01		-5.51E-01	6.20E-02		-1.16E+00	6.35E-05	Down	Unigene38604_All//gi|46931334|gb|AAO66471.1|//1.00E-77//At1g77855 [Arabidopsis thaliana]	Unigene38604_All//3.00E-79//AT1G77855| unknown protein	Unigene38604_All//2.00E-15//TC175176				nr -
Unigene38606_All	881	8.20	60.85	55.73	8.54	1.17	2.51	1.82	0.95	0.18	2.89E+00	4.21E-168	Up	2.77E+00	9.17E-144	Up	-2.86E+00	3.46E-30	Down	-1.77E+00	1.54E-14	Down	-9.43E-01	4.30E-02		-3.33E+00	5.33E-08	Down	Unigene38606_All//gi|88193285|gb|AAV34889.2|//1.00E-89//osmotin-like [Theobroma cacao]	Unigene38606_All//1.00E-77//AT4G11650| AT0SM34 (osmotin 34)	Unigene38606_All//0.00E+00//TC136094				nr +
Unigene38608_All	1814	0.55	0.36	1.00	7.52	4.48	2.32	98.78	8.71	4.48	-5.94E-01	3.82E-01		8.65E-01	8.81E-02		-7.48E-01	8.37E-08		-1.70E+00	1.17E-24	Down	-3.50E+00	0.00E+00	Down	-4.46E+00	0.00E+00	Down	Unigene38608_All//gi|224120220|ref|XP_002330994.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222872924|gb|EEF10055.1| cytochrome P450 [Populus trichocarpa]	Unigene38608_All//0.00E+00//AT2G42250| CYP71A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene38608_All//0.00E+00//TC137811		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00380|Tryptophan metabolism//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene38609_All	715	8.78	4.32	9.76	18.18	16.66	19.01	0.71	8.65	0.89	-1.02E+00	1.92E-05	Down	1.52E-01	5.53E-01		-1.26E-01	5.06E-01		6.43E-02	7.14E-01		3.61E+00	9.84E-30	Up	3.29E-01	6.60E-01				Unigene38609_All//7.00E-140//gi|109833632|gb|DW232197.1|DW232197				

Unigene38610_All	707	47.95	13.04	30.88	52.91	53.33	72.82	2.93	25.72	6.59	-1.88E+00	5.40E-64	Down	-6.35E-01	2.50E-11		1.14E-02	9.25E-01		4.61E-01	1.00E-10		3.13E+00	3.73E-76	Up	1.17E+00	3.08E-06	Up	Unigene38610_All//gi|18398482|ref|NP_564405.1|//4.00E-65//LOL1 (LSD ONE LIKE 1); DNA binding [Arabidopsis thaliana] >gi|186479127|ref|NP_001117399.1| LOL1 (LSD ONE LIKE 1); DNA binding [Arabidopsis thaliana] >gi|16323143|gb|AAL15306.1| At1g32540/T9G5_1 [Arabidopsis thaliana] >gi|21436015|gb|AAM51585.1| At1g32540/T9G5_1 [Arabidopsis thaliana] >gi|33867796|gb|AAQ55219.1| LSD1-like [Arabidopsis thaliana]	Unigene38610_All//1.00E-54//AT1G32540| LOL1 (LSD ONE LIKE 1); DNA binding	Unigene38610_All//0.00E+00//gi|48790746|gb|C0092060.1|C0092060				nr +
Unigene38611_All	880	9.99	6.79	9.02	21.06	13.97	21.76	20.80	11.49	6.16	-5.56E-01	4.22E-03		-1.48E-01	5.12E-01		-5.92E-01	4.85E-07		4.74E-02	7.51E-01		-8.56E-01	3.71E-13		-1.76E+00	4.65E-10	Down	Unigene38611_All//gi|98960945|gb|AB558956.1|//1.00E-38//At5g27990 [Arabidopsis thaliana]	Unigene38611_All//2.00E-28//AT5G27990| unknown protein	Unigene38611_All//0.00E+00//TC146866				nr +
Unigene38612_All	478	5.91	60.53	14.71	158.51	72.98	83.05	28.92	22.38	31.00	3.36E+00	6.47E-105	Up	1.31E+00	3.82E-08	Up	-1.12E+00	1.74E-81	Down	-9.33E-01	6.20E-53		-3.70E-01	6.86E-03		1.00E-01	5.00E-01		Unigene38612_All//gi|18407840|ref|NP_566871.1|//6.00E-11//PSK1; growth factor [Arabidopsis thaliana] >gi|29428768|sp|Q8LA14.2|PSK6_ARATH RecName: Full=Putative phytosulfokines 6; Short=AtPSK6; Short=AtPSK3_2; Contains: RecName: Full=Phytosulfokine-alpha-like; Short=PSK-alpha-like; Short=Phytosulfokine-a-like; Contains: RecName: Full=Phytosulfokine-beta; Short=PSK-beta; Short=Phytosulfokine-b; Flags: Precursor >gi|27808144|dbj|BAB72177.2| phytosulfokine precursor 3_2 [Arabidopsis thaliana] >gi|88010851|gb|ABD38863.1| At3g44735 [Arabidopsis thaliana]	Unigene38612_All//4.00E-11//AT3G44735| PSK1; growth factor	Unigene38612_All//0.00E+00//DW505488				nr +
Unigene38613_All	1454	0.22	0.45	0.40	13.40	8.81	9.16	2.09	0.55	0.85	1.07E+00	2.37E-01		9.00E-01	3.77E-01		-6.05E-01	1.24E-07		-5.48E-01	6.31E-06		-1.94E+00	5.46E-08	Down	-1.30E+00	4.73E-05	Down	Unigene38613_All//gi|115452395|ref|NP_001049798.1|//1.00E-119//Os03g0291200 [Oryza sativa Japonica Group] >gi|108707605|gb|ABF95400.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548269|dbj|BAF11712.1| Os03g0291200 [Oryza sativa Japonica Group]	Unigene38613_All//2.00E-166//AT5G01360| EXPRESSED IN: 13 plant structures: EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF231, plant (InterPro:IPR004253); BEST Arabidopsis thaliana protein match is: ESK1 (ESKIMO 1) (TAIR:AT3G55990.1); Has 710 Blast hits to 702 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 2; Plants - 705; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene38613_All//0.00E+00//TC133183				nr -
Unigene38614_All	401	0.26	0.00	0.53	1.86	0.77	2.48	16.34	46.80	65.07	-8.03E+00	3.71E-01		1.03E+00	5.91E-01		-1.27E+00	1.12E-01		4.11E-01	6.02E-01		1.52E+00	2.34E-32	Up	1.99E+00	2.12E-66	Up	Unigene38614_All//gi|224111880|ref|XP_002316010.1|//6.00E-33//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene38614_All//7.00E-17//AT2G46960| CYP709B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene38614_All//0.00E+00//gi|164268290|gb|ES813717.1|ES813717	ko00908|Zeatin biosynthesis//ko00591|Linoleic acid metabolism		nr -
Unigene38615_All	225	0.00	0.00	0.24	1.55	0.31	1.41	26.50	63.90	118.63	null	null		7.89E+00	6.35E-01		-2.34E+00	1.01E-01		-1.41E-01	9.12E-01		1.27E+00	2.99E-19	Up	2.16E+00	2.60E-75	Up	Unigene38615_All//gi|224111880|ref|XP_002316010.1|//3.00E-22//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene38615_All//2.00E-09//AT2G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene38615_All//2.00E-112//gi|73860637|gb|DT463376.1|DT463376		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	nr +
Unigene38616_All	705	0.30	0.58	0.45	0.99	0.98	0.77	12.83	23.89	69.22	9.54E-01	4.14E-01		6.10E-01	6.24E-01		-1.81E-02	9.61E-01		-3.64E-01	6.81E-01		8.97E-01	4.43E-13		2.43E+00	5.38E-158	Up	Unigene38616_All//gi|224111880|ref|XP_002316010.1|//2.00E-42//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene38616_All//6.00E-28//AT2G46960| CYP709B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene38616_All//0.00E+00//gi|73860637|gb|DT463376.1|DT463376		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	nr -
Unigene38617_All	1214	3.23	2.30	1.27	3.49	5.79	5.88	4.70	57.22	4.36	-4.94E-01	1.14E-01		-1.35E+00	5.47E-05	Down	7.30E-01	5.22E-04		7.53E-01	4.96E-04		3.61E+00	0.00E+00	Up	-1.07E-01	6.39E-01		Unigene38617_All//gi|115469074|ref|NP_001058136.1|//5.00E-97//Os06g0634300 [Oryza sativa Japonica Group] >gi|51535772|dbj|BAD37816.1| MutT domain protein-like [Oryza sativa Japonica Group] >gi|51535894|dbj|BAD37977.1| MutT domain protein-like [Oryza sativa Japonica Group] >gi|113596176|dbj|BAF20050.1| Os06g0634300 [Oryza sativa Japonica Group]	Unigene38617_All//3.00E-89//AT4G25434| ATNUDT10 (Arabidopsis thaliana Nudix hydrolase homolog 10); ADP-ribose diphosphatase/ NAD or NADH binding / catalytic	Unigene38617_All//0.00E+00//TC165900				nr +
Unigene38619_All	788	2.32	1.22	2.09	3.22	3.89	2.12	3.27	1.27	1.31	-9.28E-01	5.39E-02		-1.50E-01	7.51E-01		2.71E-01	5.19E-01		-6.04E-01	1.37E-01		-1.36E+00	1.76E-04	Down	-1.32E+00	1.79E-04	Down	Unigene38619_All//gi|59709749|gb|AAP72282.2|//7.00E-54//calcium-dependent calmodulin-independent protein kinase isoform 2 [Cicer arietinum]	Unigene38619_All//6.00E-52//AT5G12480| CPK7 (calmodulin-domain protein kinase 7); ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene38619_All//2.00E-97//TC133932	ko04626|Plant-pathogen interaction		nr +
Unigene3862_All	1209	731.50	360.60	584.69	83.97	108.95	121.56	35.04	63.37	79.55	-1.02E+00	0.00E+00	Down	-3.23E-01	1.19E-81		3.76E-01	3.24E-20		5.34E-01	1.96E-38		8.55E-01	3.03E-52		1.18E+00	1.32E-113	Up	Unigene3862_All//gi|18404224|ref|NP_564616.1|//1.00E-102//peroxisomal membrane protein-related [Arabidopsis thaliana]	Unigene3862_All//2.00E-98//AT1G52870| peroxisomal membrane protein-related	Unigene3862_All//0.00E+00//TC165523	ko04146|Peroxisome		nr -
Unigene38622_All	4593	0.09	0.12	0.26	0.02	0.02	0.00	18.85	3.25	1.36	4.14E-01	6.37E-01		1.49E+00	3.04E-02		-5.33E-01	8.16E-01		-4.44E+00	3.99E-01		-2.54E+00	1.26E-289	Down	-3.79E+00	0.00E+00	Down	Unigene38622_All//gi|75321780|sp|Q5W274.1|PDR3_TOBAC//0.00E+00//RecName: Full=Pleiotropic drug resistance protein 3; AltName: Full=NtPDR3 >gi|50056942|emb|CAH39853.1| PDR-like ABC transporter [Nicotiana tabacum]	Unigene38622_All//0.00E+00//AT4G15215| PDR13; ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene38622_All//8.00E-33//TC147767	ko03040|Spliceosome//ko02010|ABC transporters		nr +
Unigene38624_All	1030	0.61	0.30	0.83	1.79	1.04	0.75	4.06	2.60	1.90	-1.05E+00	2.50E-01		4.40E-01	5.83E-01		-7.88E-01	8.70E-02		-1.26E+00	9.32E-03		-6.46E-01	1.49E-02		-1.10E+00	2.75E-05	Down	Unigene38624_All//gi|6692688|gb|AAF24822.1|AC007592_15//1.00E-133//F12K11.17 [Arabidopsis thaliana]	Unigene38624_All//3.00E-126//AT1G06490| ATGSL07 (glucan synthase-like 7); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups	Unigene38624_All//3.00E-140//C0074626				nr +
Unigene38627_All	350	20.63	2.03	10.04	24.20	13.58	32.26	27.78	12.66	11.38	-3.35E+00	1.01E-26	Down	-1.04E+00	6.06E-06	Down	-8.34E-01	5.49E-06		4.15E-01	1.55E-02		-1.13E+00	2.95E-11	Down	-1.29E+00	5.19E-14	Down	Unigene38627_All//gi|196166898|gb|ACG70968.1|//2.00E-46//cyclophilin [Ziziphus jujuba]	Unigene38627_All//1.00E-36//AT3G56070| ROC2 (ROTAMASE CYCLOPHILIN 2); cyclosporin A binding / peptidyl-prolyl cis-trans isomerase	Unigene38627_All//0.00E+00//gi|13243838|gb|BE053498.2|BE053498				nr -
Unigene38628_All	1127	7.43	1.66	3.17	8.44	6.51	11.06	21.35	5.82	8.41	-2.16E+00	2.07E-19	Down	-1.23E+00	1.12E-08	Down	-3.75E-01	4.10E-02		3.90E-01	1.66E-02		-1.87E+00	1.68E-55	Down	-1.34E+00	1.43E-35	Down	Unigene38628_All//gi|196166898|gb|ACG70968.1|//5.00E-90//cyclophilin [Ziziphus jujuba]	Unigene38628_All//1.00E-73//AT3G56070| ROC2 (ROTAMASE CYCLOPHILIN 2); cyclosporin A binding / peptidyl-prolyl cis-trans isomerase	Unigene38628_All//0.00E+00//gi|31073951|gb|CA994230.1|CA994230				nr -
Unigene38629_All	946	25.66	31.76	29.16	71.88	59.73	96.58	96.94	58.36	47.46	3.08E-01	2.08E-03		1.84E-01	1.12E-01		-2.67E-01	6.19E-06		4.26E-01	3.69E-16		-7.32E-01	5.43E-48		-1.03E+00	1.64E-87	Down	Unigene38629_All//gi|297527459|ref|XP_002881612.1|//5.00E-93//AMMECR1 family [Arabidopsis lyrata subsp. lyrata] >gi|297327451|gb|EFH57871.1| AMMECR1 family [Arabidopsis lyrata subsp. lyrata]	Unigene38629_All//2.00E-93//AT2G38710| AMMECR1 family	Unigene38629_All//0.00E+00//gi|78326138|gb|DT546412.1|DT546412				nr +
Unigene38630_All	661	0.40	2.30	0.89	14.09	9.43	5.19	17.97	25.10	23.51	2.54E+00	9.21E-05	Up	1.16E+00	2.47E-01		-5.80E-01	9.78E-04		-1.44E+00	1.87E-13	Down	4.82E-01	7.36E-05		3.87E-01	1.78E-03		Unigene38630_All//gi|115456727|ref|NP_001051964.1|//1.00E-42//Os03g0858800 [Oryza sativa Japonica Group] >gi|108712210|gb|ABG00005.1| MATE efflux family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550435|dbj|BAF13878.1| Os03g0858800 [Oryza sativa Japonica Group]	Unigene38630_All//4.00E-33//AT4G22790| MATE efflux family protein	Unigene38630_All//0.00E+00//gi|48803654|gb|C0104968.1|C0104968				nr +
Unigene38631_All	777	226.45	102.38	182.57	20.90	24.64	51.44	2.18	4.73	0.56	-1.15E+00	6.23E-158	Down	-3.11E-01	1.61E-15		2.38E-01	7.05E-02		1.30E+00	3.40E-47	Up	1.12E+00	1.14E-04	Up	-1.95E+00	5.40E-05	Down	Unigene38631_All//gi|224137836|ref|XP_002326452.1|//5.00E-26//predicted protein [Populus trichocarpa] >gi|222833774|gb|EEE72251.1| predicted protein [Populus trichocarpa]		Unigene38631_All//0.00E+00//TC144648				nr +
Unigene38632_All	968	44.59	37.95	18.92	42.51	11.70	22.63	0.17	0.09	0.08	-2.33E-01	5.10E-03		-1.24E+00	1.21E-42	Down	-1.86E+00	4.30E-96	Down	-9.10E-01	8.18E-28		-1.02E+00	6.14E-01		-1.09E+00	5.52E-01		Unigene38632_All//gi|21322711|emb|CAD22154.1|//1.00E-63//pherophorin-drl protein [Volvox carteri f. nagariensis]		Unigene38632_All//9.00E-63//gi|164259792|gb|ES846441.1|ES846441	ko03040|Spliceosome		nr +

Unigene38633_All	1353	11.25	7.45	4.01	13.66	10.05	18.43	16.66	7.07	9.28	-5.95E-01	3.11E-05		-1.49E+00	3.42E-20	Down	-4.42E-01	2.28E-04		4.32E-01	5.35E-05		-1.24E+00	1.53E-28	Down	-8.45E-01	3.80E-16		Unigene38633_All//gi|15240059|ref|NP_199210.1|//1.00E-26//TOM22-V (TRANSLOCASE OF OUTER MEMBRANE 22-V); P-P-bond-hydrolysis-driven protein transmembrane transporter [Arabidopsis thaliana] >gi|24212685|sp|Q9FKN9.3|TO222_ARATH RecName: Full=Mitochondrial import receptor subunit TOM22 homolog 2; AltName: Full=Translocase of outer membrane 22 kDa subunit homolog 2; AltName: Full=Mitochondrial import receptor subunit TOM9-2; AltName: Full=Translocase of outer membrane 9 kDa subunit TOM9-2 >gi|15529292|gb|AAK97740.1|AT5g43970/MRH10_8 [Arabidopsis thaliana] >gi|16974415|gb|AAL31133.1|AT5g43970/MRH10_8 [Arabidopsis thaliana]	Unigene38633_All//5.00E-21//AT1G04070| TOM22-1 (TRANSLOCASE OF OUTER MEMBRANE 22-I); P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene38633_All//0.00E+00//gi|109874781|gb|DW503755.1|DW503755				nr -
Unigene38635_All	767	9.96	9.58	4.17	5.00	2.78	3.77	2.09	1.58	1.35	-5.62E-02	7.96E-01		-1.26E+00	3.15E-08	Down	-8.45E-01	3.91E-03		-4.08E-01	2.21E-01		-4.07E-01	3.95E-01		-6.33E-01	1.58E-01		Unigene38635_All//gi|90399315|emb|CAJ86209.1|//6.00E-43//H0101F08.8 [Oryza sativa (indica cultivar-group)]	Unigene38635_All//0.00E+00//gi|109883125|gb|DW512095.1|DW512095	MYB			nr +
Unigene38638_All	589	5.42	11.61	3.07	2.71	4.97	6.44	39.27	102.61	46.53	1.10E+00	1.85E-06	Up	-8.18E-01	2.49E-02		8.77E-01	1.47E-02		1.25E+00	9.04E-05	Up	1.39E+00	1.47E-89	Up	2.45E-01	8.18E-03		Unigene38638_All//gi|192910812|gb|ACF06514.1|//3.00E-16//synaptobrevin 1 [Elaeis guineensis]	Unigene38638_All//9.00E-69//AT2G33120| SAR1 (SYNAPTOBREVIN-RELATED PROTEIN 1)	Unigene38638_All//2.00E-32//CO084949		ko04130|SNARE interactions in vesicular transport		nr -
Unigene38640_All	1673	1.53	0.55	0.70	0.45	0.68	0.70	2.78	8.44	7.60	-1.49E+00	3.29E-04	Down	-1.13E+00	7.05E-03		6.05E-01	3.84E-01		6.52E-01	3.31E-01		1.60E+00	1.62E-26	Up	1.45E+00	2.94E-21	Up	Unigene38640_All//gi|18398327|ref|NP_566341.1|//1.00E-144//protein kinase family protein [Arabidopsis thaliana]	Unigene38640_All//7.00E-133//AT3G09010| protein kinase family protein	Unigene38640_All//7.00E-176//ES810755		ko04626|Plant-pathogen interaction		nr +
Unigene38642_All	750	72.83	46.01	37.20	132.11	110.38	113.03	206.33	67.71	38.78	-6.63E-01	5.18E-20		-9.69E-01	1.93E-36		-2.59E-01	5.82E-08		-2.25E-01	1.04E-05		-1.61E+00	4.49E-285	Down	-2.41E+00	0.00E+00	Down	Unigene38642_All//gi|261280336|gb|ACM67305.2|//3.00E-72//triosphosphate isomerase-like protein type I [Dimocarpus longan]	Unigene38642_All//4.00E-69//AT3G55440| TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase	Unigene38642_All//0.00E+00//TC156712		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00562|Inositol phosphate metabolism//ko00051|Fructose and mannose metabolism		nr +
Unigene38643_All	1126	0.98	1.35	1.14	2.17	3.21	2.41	3.23	1.26	2.76	4.68E-01	3.85E-01		2.18E-01	7.02E-01		5.67E-01	8.28E-02		1.51E-01	7.12E-01		-1.36E+00	5.89E-06	Down	-2.27E-01	4.51E-01		Unigene38643_All//gi|8843863|dbj|BAA97389.1|//3.00E-26//acid phosphatase [Arabidopsis thaliana] >gi|62326502|dbj|BAD95053.1| acid phosphatase [Arabidopsis thaliana] >gi|87116594|gb|ABD19661.1|At5g51260 [Arabidopsis thaliana]	Unigene38643_All//8.00E-28//AT5G51260| acid phosphatase, putative	Unigene38643_All//4.00E-10//TC148205		ko03010|Ribosome		nr +
Unigene38644_All	2394	0.33	0.59	0.33	1.44	0.88	0.58	1.40	3.89	1.91	8.54E-01	1.28E-01		2.53E-02	9.94E-01		-7.10E-01	2.49E-02		-1.30E+00	1.14E-04	Down	1.48E+00	6.78E-16	Up	4.56E-01	6.50E-02		Unigene38644_All//gi|24960749|gb|AAN65443.1|//1.00E-122//Putative transposase [Oryza sativa Japonica Group]	Unigene38644_All//2.00E-98//AT4G38180| FRS5 (FAR1-related sequence 5); zinc ion binding	Unigene38644_All//0.00E+00//ES804190				nr +
Unigene38645_All	1269	0.45	3.87	1.01	1.69	1.49	1.82	13.76	10.28	56.13	3.09E+00	6.09E-17	Up	1.15E+00	6.95E-02		-1.78E-01	7.12E-01		1.05E-01	8.18E-01		-4.21E-01	3.84E-04		2.03E+00	3.97E-184	Up	Unigene38645_All//gi|18416997|ref|NP_568287.1|//1.00E-39//JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10) [Arabidopsis thaliana] >gi|75163798|sp|Q93ZM9.1|TIF9_ARATH RecName: Full=Protein TIFY 9; AltName: Full=Protein JASMONATE-ASSOCIATED 1; AltName: Full=Jasmonate ZIM domain-containing protein 10 >gi|159123333|gb|AAL08300.1|AT5g13220/T31B5_40 [Arabidopsis thaliana] >gi|19548009|gb|AAL87368.1|AT5g13220/T31B5_40 [Arabidopsis thaliana]	Unigene38645_All//8.00E-39//AT5G13220| JAZ10 (JASMONATE-ZIM-DOMAIN PROTEIN 10)	Unigene38645_All//0.00E+00//gi|164292615|gb|ES841761.1|ES841761	Tify			nr -
Unigene38646_All	956	21.18	23.90	22.95	640.65	579.06	550.46	44.98	26.14	12.25	1.75E-01	1.56E-01		1.16E-01	3.82E-01		-1.46E-01	1.27E-15		-2.19E-01	2.61E-30		-7.83E-01	1.15E-25		-1.88E+00	9.29E-102	Down	Unigene38646_All//gi|297838641|ref|XP_002887202.1|//2.00E-71//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297333043|gb|EFH63461.1|expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene38646_All//0.00E+00//DW500418		ko03040|Spliceosome		nr -
Unigene38651_All	792	1.32	7.10	4.44	8.93	20.57	20.47	19.22	21.80	64.89	2.43E+00	4.75E-15	Up	1.75E+00	2.51E-06	Up	1.20E+00	6.51E-19	Up	1.20E+00	3.66E-17	Up	1.82E-01	1.67E-01		1.76E+00	1.30E-109	Up	Unigene38651_All//gi|224087806|ref|XP_002308234.1|//1.00E-27//predicted protein [Populus trichocarpa] >gi|222854210|gb|EEE91757.1|predicted protein [Populus trichocarpa]		Unigene38651_All//0.00E+00//TC160023				nr +
Unigene38652_All	480	206.01	39.27	50.25	189.92	172.10	223.75	97.07	29.87	42.91	-2.39E+00	1.13E-252	Down	-2.04E+00	6.53E-200	Down	-1.42E-01	9.35E-03		2.37E-01	1.18E-06		-1.70E+00	2.01E-93	Down	-1.18E+00	1.52E-55	Down	Unigene38652_All//gi|146454512|gb|ABQ41922.1|//9.00E-55//60S ribosomal protein large subunit 9 [Sonneratia ovata] >gi|156633792|gb|ABU90895.1|ribosomal protein L9 [Sonneratia alba] >gi|156633794|gb|ABU90896.1|ribosomal protein L9 [Sonneratia alba] >gi|156633796|gb|ABU90897.1|ribosomal protein L9 [Sonneratia alba] >gi|156633798|gb|ABU90898.1|ribosomal protein L9 [Sonneratia alba] >gi|156633800|gb|ABU90899.1|ribosomal protein L9 [Sonneratia alba] >gi|156633802|gb|ABU90900.1|ribosomal protein L9 [Sonneratia alba] >gi|156633804|gb|ABU90901.1|ribosomal protein L9 [Sonneratia alba] >gi|156633806|gb|ABU90902.1|ribosomal protein L9 [Sonneratia alba] >gi|156633808|gb|ABU90903.1|ribosomal protein L9 [Sonneratia alba] >gi|156633810|gb|ABU90904.1|ribosomal protein L9 [Sonneratia alba] >gi|156633812|gb|ABU90905.1|ribosomal protein L9 [Sonneratia alba] >gi|156633814|gb|ABU90906.1|ribosomal protein L9 [Sonneratia alba] >gi|156633816|gb|ABU90907.1|ribosomal protein L9 [Sonneratia	Unigene38652_All//6.00E-53//AT1G33140| PGY2 (PIGGYBACK2); structural constituent of ribosome	Unigene38652_All//0.00E+00//TC137377		ko03010|Ribosome		nr -
Unigene38653_All	660	16.49	17.58	6.45	24.83	19.51	18.75	14.35	7.03	4.59	9.25E-02	6.12E-01		-1.35E+00	9.59E-13	Down	-3.48E-01	8.97E-03		-4.05E-01	3.02E-03		-1.03E+00	1.66E-09	Down	-1.65E+00	2.45E-19	Down			Unigene38653_All//0.00E+00//TC167015				
Unigene38659_All	522	2.00	0.19	0.92	0.57	0.86	0.69	1.94	0.48	2.14	-3.37E+00	2.13E-04	Down	-1.13E+00	1.17E-01		5.83E-01	6.26E-01		2.74E-01	8.33E-01		-2.02E+00	2.83E-03		1.37E-01	8.65E-01								
Unigene3866_All	1453	0.58	1.88	1.10	1.54	2.25	2.46	1.75	3.77	4.22	1.71E+00	3.49E-05	Up	9.32E-01	8.84E-02		5.45E-01	1.19E-01		6.71E-01	4.22E-02		1.11E+00	1.79E-06	Up	1.27E+00	6.01E-09	Up	Unigene3866_All//gi|10177316|dbj|BAB10642.1|//2.00E-34//kinesin-like protein [Arabidopsis thaliana]	Unigene3866_All//1.00E-35//AT5G60930| chromosome-associated kinesin, putative	Unigene3866_All//7.00E-12//TC129989				nr -
Unigene38661_All	805	4.55	7.43	5.29	4.95	9.41	18.63	7.51	15.89	9.80	7.07E-01	3.53E-03		2.18E-01	5.04E-01		9.27E-01	4.24E-06		1.91E+00	4.52E-31	Up	1.08E+00	1.68E-13	Up	3.84E-01	3.56E-02		Unigene38661_All//gi|297725791|ref|NP_001175259.1|//2.00E-37//Os07g0564400 [Oryza sativa Japonica Group] >gi|255677889|dbj|BAH93987.1|Os07g0564400 [Oryza sativa Japonica Group]	Unigene38661_All//3.00E-47//AT5G63690| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Nucleic acid-binding, OB-fold-like (InterPro:IPR016027), Nucleic acid-binding, OB-fold (InterPro:IPR012340); Has 165 Blast hits to 164 proteins in 56 species: Archae - 3; Bacteria - 0; Metazoa - 135; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink).					nr +
Unigene38663_All	1014	1.24	0.50	0.95	6.14	6.49	2.49	2.08	1.73	3.14	-1.31E+00	3.41E-02		-3.90E-01	5.38E-01		7.90E-02	8.02E-01		-1.30E+00	5.96E-08	Down	-2.68E-01	5.40E-01		5.92E-01	4.97E-02		Unigene38663_All//gi|32483159|emb|CAE02147.1|//6.00E-22//OSJNBa0081G05.2 [Oryza sativa (japonica cultivar-group)] >gi|116309213|emb|CAH66305.1|OS1GBa0135K14.2 [Oryza sativa (indica cultivar-group)] >gi|116309230|emb|CAH66320.1|OS1GBa0150M16.3 [Oryza sativa (indica cultivar-group)]		Unigene38663_All//1.00E-37//TC137548				nr -
Unigene38664_All	1220	1.59	1.91	1.48	2.61	2.17	1.11	5.65	6.68	1.60	2.68E-01	5.39E-01		-9.66E-02	8.35E-01		-2.66E-01	4.86E-01		-1.23E+00	4.09E-04	Down	2.42E-01	2.24E-01		-1.82E+00	2.39E-16	Down	Unigene38664_All//gi|297607562|ref|NP_001060171.2|//4.00E-50//Os07g0596300 [Oryza sativa Japonica Group] >gi|255677941|dbj|BAF22085.2|Os07g0596300 [Oryza sativa Japonica Group]	Unigene38664_All//6.00E-41//AT5G07650| formin homology 2 domain-containing protein / FH2 domain-containing protein	Unigene38664_All//3.00E-112//TC146284				nr -
Unigene38666_All	1080	1.55	0.38	0.00	1.52	1.05	1.97	2.78	0.85	1.29	-2.05E+00	3.19E-04	Down	-1.06E+01	3.83E-09	Down	-5.33E-01	3.08E-01		3.69E-01	4.54E-01		-1.71E+00	9.31E-07	Down	-1.11E+00	4.59E-04	Down	Unigene38666_All//gi|145338580|ref|NP_188247.2|//1.00E-105//TRZ4 (TRNASE Z 4); 3''-tRNA processing endoribonuclease/ catalytic [Arabidopsis thaliana]	Unigene38666_All//8.00E-87//AT3G16260| TRZ4 (TRNASE Z 4); 3''-tRNA processing endoribonuclease/ catalytic					nr -
Unigene38668_All	730	1.08	3.12	3.65	4.64	3.25	4.83	5.73	6.93	6.33	1.54E+00	6.01E-04	Up	1.76E+00	5.21E-05	Up	-5.12E-01	1.24E-01		5.66E-02	8.91E-01		2.73E-01	2.94E-01		1.43E-01	5.92E-01		Unigene38668_All//gi|115445545|ref|NP_001046552.1|//3.00E-16//Os02g0279800 [Oryza sativa Japonica Group] >gi|113536083|dbj|BAF08466.1|Os02g0279800 [Oryza sativa Japonica Group]	Unigene38668_All//3.00E-19//AT4G25225| unknown protein	Unigene38668_All//2.00E-41//TC159332				nr +
Unigene38669_All	842	11.93	824.49	225.77	44.90	83.68	230.05	29.07	77.49	65.91	6.11E+00	0.00E+00	Up	4.24E+00	0.00E+00	Up	8.98E-01	1.61E-50		2.36E+00	0.00E+00	Up	1.41E+00	1.28E-99	Up	1.18E+00	9.88E-66	Up	Unigene38669_All//gi|15227642|ref|NP_178443.1|//6.00E-29//nodulin-related [Arabidopsis thaliana]	Unigene38669_All//3.00E-20//AT2G03440| nodulin-related	Unigene38669_All//0.00E+00//TC156909				nr +

Unigene3867_All	1003	19.30	48.35	22.67	32.63	50.16	54.84	37.52	69.26	81.58	1.32E+00	6.99E-55	Up	2.32E-01	6.52E-02		6.20E-01	2.99E-19		7.49E-01	1.94E-26		8.84E-01	3.12E-50		1.12E+00	7.12E-89	Up	Unigene3867_All//gi|260223734|emb|CAZ15514.1|//8.00E-39//basic-leucine zipper [Humulus lupulus]	Unigene3867_All//7.00E-16//AT2G41070| EEL (ENHANCED EM LEVEL); DNA binding / transcription factor	Unigene3867_All//0.00E+00//TC169033	bZIP			nr +
Unigene38671_All	772	3.46	12.80	3.93	9.49	33.36	19.83	9.91	18.08	162.24	1.89E+00	4.00E-19	Up	1.86E-01	6.32E-01		1.81E+00	5.13E-54	Up	1.06E+00	1.49E-13	Up	8.67E-01	2.00E-10		4.03E+00	0.00E+00	Up	Unigene38671_All//gi|224110988|ref|XP_002315707.1|//4.00E-74//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222864747|gb|EEF01878.1| AP2/EBP domain-containing transcription factor [Populus trichocarpa]	Unigene38671_All//7.00E-50//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene38671_All//4.00E-52//TC178583	AP2-EREBP			nr -
Unigene38672_All	980	2.67	1.24	1.25	2.69	3.34	3.46	3.24	1.54	1.75	-1.11E+00	5.16E-03		-1.09E+00	8.04E-03		3.09E-01	4.20E-01		3.60E-01	3.32E-01		-1.08E+00	6.26E-04	Down	-8.88E-01	3.18E-03		Unigene38672_All//gi|297596230|ref|NP_001042218.2|//2.00E-08//Os01g0182400 [Oryza sativa Japonica Group] >gi|552962270|dbj|BAD68050.1| myb/SANT domain protein -like [Oryza sativa Japonica Group] >gi|255672943|dbj|BAF04132.2| Os01g0182400 [Oryza sativa Japonica Group]	Unigene38672_All//6.00E-22//AT4G39080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thaliana protein match is: TKI1 (TSL-kinase interacting protein 1); DNA binding / transcription factor (TAIR:AT2G36960.2); Has 39 Blast hits to 35 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).				nr -
Unigene38673_All	1028	13.59	8.18	8.91	25.44	23.68	22.89	63.01	27.36	26.47	-7.32E-01	1.17E-06		-6.09E-01	8.88E-05		-1.03E-01	4.17E-01		-1.52E-01	2.08E-01		-1.20E+00	2.56E-77	Down	-1.25E+00	1.56E-84	Down	Unigene38673_All//gi|6716760|gb|AAF26735.1|//2.00E-96//methionine synthase [Coffea arabica]	Unigene38673_All//2.00E-95//AT5G17920| ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase	Unigene38673_All//0.00E+00//gi|109827829|gb|DW226491.1|DW226491		ko00270|Cysteine and methionine metabolism		nr +
Unigene38674_All	1139	0.51	1.16	0.00	3.76	6.41	14.63	28.55	27.85	65.83	1.19E+00	4.50E-02		-8.98E+00	2.60E-03		7.69E-01	1.82E-04		1.96E+00	1.25E-35	Up	-3.55E-02	7.31E-01		1.21E+00	1.97E-91	Up	Unigene38674_All//gi|18558997|gb|AAL73112.1|//0.00E+00//bacterial-induced peroxidase [Gossypium hirsutum]	Unigene38674_All//4.00E-117//AT5G39580| peroxidase, putative	Unigene38674_All//0.00E+00//TC143237		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene38675_All	1158	2.17	1.36	1.15	10.20	8.92	6.01	9.02	3.83	4.47	-6.77E-01	8.94E-02		-9.16E-01	2.91E-02		-1.93E-01	2.98E-01		-7.63E-01	2.08E-06		-1.24E+00	1.11E-13	Down	-1.01E+00	1.81E-10	Down	Unigene38675_All//gi|5051760|emb|CAB45053.1|//7.00E-96//thaumatin-like protein [Arabidopsis thaliana] >gi|7269268|emb|CAB79328.1| thaumatin-like protein [Arabidopsis thaliana]	Unigene38675_All//7.00E-87//AT4G24180| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to other organism; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Thaumatin, pathogenesis-related (InterPro:IPR001938); BEST Arabidopsis thaliana protein match is: thaumatin, putative (TAIR:AT4G38660.2); Has 1060 Blast hits to 1045 proteins in 143 species: Archae - 0; Bacteria - 22; Metazoa - 46; Fungi - 45; Plants - 935; Viruses - 3; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene38675_All//7.00E-67//gi|78346648|gb|DT566922.1|DT566922				nr -
Unigene38677_All	635	32.38	34.15	30.27	50.36	44.09	49.36	33.29	30.80	16.00	7.68E-02	5.86E-01		-9.71E-02	5.03E-01		-1.92E-01	5.02E-02		-2.90E-02	7.98E-01		-1.12E-01	3.82E-01		-1.06E+00	1.00E-21	Down	Unigene38677_All//gi|15224916|ref|NP_181989.1|//1.00E-37//RAB6A; GTP binding / protein binding [Arabidopsis thaliana] >gi|75318653|sp|Q8GS01.1|RBH1B_ARATH RecName: Full=Ras-related protein RABH1B >gi|107738267|gb|ABF83670.1| At2g44610 [Arabidopsis thaliana] >gi|741994|prf||2008312A GTP-binding protein	Unigene38677_All//2.00E-30//AT2G44610| RAB6A; GTP binding / protein binding	Unigene38677_All//0.00E+00//TC139606				nr +
Unigene38678_All	1427	2.68	1.14	1.31	10.61	9.34	4.62	3.14	0.88	1.28	-1.24E+00	1.25E-04	Down	-1.04E+00	1.71E-03		-1.84E-01	2.42E-01		-1.20E+00	2.37E-16	Down	-1.84E+00	1.11E-10	Down	-1.29E+00	5.99E-07	Down	Unigene38678_All//gi|238478319|ref|NP_001154301.1|//1.00E-125//armadillo/beta-catenin repeat family protein / kinesin motor family protein [Arabidopsis thaliana]	Unigene38678_All//3.00E-126//AT1G01950| armadillo/beta-catenin repeat family protein / kinesin motor family protein	Unigene38678_All//0.00E+00//TC144386				nr +
Unigene3868_All	1388	3.17	1.64	0.38	10.12	6.97	3.25	8.07	0.09	3.90	-9.47E-01	1.12E-03		-3.05E+00	2.07E-14	Down	-5.38E-01	1.06E-04		-1.64E+00	4.72E-24	Down	-6.48E+00	4.89E-74	Down	-1.05E+00	8.84E-12	Down	Unigene3868_All//gi|30689007|ref|NP_850369.1|//4.00E-78//bZIP transcription factor family protein [Arabidopsis thaliana]	Unigene3868_All//6.00E-72//AT2G42380| bZIP transcription factor family protein	Unigene3868_All//0.00E+00//ES802062	bZIP			nr -
Unigene38681_All	1116	13.27	16.57	13.46	16.65	17.19	22.06	18.34	16.29	7.35	3.21E-01	1.44E-02		2.03E-02	9.09E-01		4.58E-02	8.07E-01		4.06E-01	1.76E-04		-1.71E-01	1.53E-01		-1.32E+00	1.52E-29	Down	Unigene38681_All//gi|16604420|gb|AAL24216.1|//3.00E-87//AT3g25550/WWL2_17 [Arabidopsis thaliana] >gi|19699216|gb|AAL90974.1| AT3g25550/WWL2_17 [Arabidopsis thaliana]	Unigene38681_All//2.00E-88//AT3G25545| unknown protein	Unigene38681_All//0.00E+00//TC134178				nr +
Unigene38683_All	520	9.56	19.49	4.20	11.02	9.01	13.72	21.38	45.41	26.43	1.03E+00	2.60E-08	Up	-1.19E+00	3.56E-05	Down	-2.91E-01	2.75E-01		3.17E-01	1.84E-01		1.09E+00	1.92E-24	Up	3.06E-01	2.35E-02				Unigene38683_All//3.00E-138//gi|164248214|gb|ES814237.1|ES814237				
Unigene38686_All	645	58.24	138.58	69.76	88.66	73.09	80.94	94.46	110.42	87.71	1.25E+00	4.59E-92	Up	2.60E-01	1.86E-03		-2.79E-01	1.81E-05		-1.31E-01	8.71E-02		2.25E-01	5.76E-05		-1.07E-01	9.78E-02		Unigene38686_All//gi|195623032|gb|ACG33346.1|//2.00E-17//endothelial differentiation-related factor 1 [Zea mays]	Unigene38686_All//5.00E-12//AT3G42680| MBF1A (MULTIPROTEIN BRIDGING FACTOR 1A); DNA binding / transcription coactivator	Unigene38686_All//0.00E+00//TC135836				nr +
Unigene38687_All	1175	1.29	0.60	1.59	5.64	4.43	5.50	4.50	1.96	2.17	-1.10E+00	4.35E-02		2.97E-01	5.65E-01		-3.50E-01	1.35E-01		-3.68E-02	9.00E-01		-1.20E+00	5.09E-07	Down	-1.05E+00	4.73E-06	Down	Unigene38687_All//gi|14091849|gb|AAS3852.1|AC016781_6//6.00E-14//Putative retroelement [Oryza sativa Japonica Group]		Unigene38687_All//0.00E+00//gi|78331989|gb|DT552263.1|DT552263				nr +
Unigene38688_All	1419	0.00	0.04	0.08	2.95	1.65	1.75	569.90	126.80	90.32	5.16E+00	6.16E-01		6.23E+00	3.98E-01		-8.38E-01	2.58E-03		-7.52E-01	1.07E-02		-2.17E+00	0.00E+00	Down	-2.66E+00	0.00E+00	Down	Unigene38688_All//gi|15236282|ref|NP_195242.1|//1.00E-104//O-methyltransferase family 2 protein [Arabidopsis thaliana] >gi|4455342|emb|CAB36723.1| O-methyltransferase-like protein [Arabidopsis thaliana] >gi|7270467|emb|CAB80233.1| O-methyltransferase-like protein [Arabidopsis thaliana] >gi|20466674|gb|AAM20654.1| O-methyltransferase-like protein [Arabidopsis thaliana] >gi|23198188|gb|AAN15621.1| O-methyltransferase-like protein [Arabidopsis thaliana]	Unigene38688_All//2.00E-102//AT4G35160| O-methyltransferase family 2 protein	Unigene38688_All//0.00E+00//TC177360		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene3869_All	829	8.77	5.68	4.82	8.05	7.68	8.34	11.32	5.34	8.65	-6.26E-01	3.81E-03		-8.65E-01	1.31E-04		-6.74E-02	8.16E-01		4.99E-02	8.57E-01		-1.08E+00	3.60E-10	Down	-3.88E-01	1.81E-02		Unigene3869_All//gi|20197762|gb|AAD18102.2|//1.00E-40//expressed protein [Arabidopsis thaliana]	Unigene3869_All//5.00E-44//AT4G30996| unknown protein	Unigene3869_All//0.00E+00//gi|21103833|gb|BQ416146.1|BQ416146				nr +
Unigene38691_All	922	2.50	0.66	0.46	4.65	2.73	2.25	2.52	2.54	1.21	-1.92E+00	3.76E-05	Down	-2.43E+00	2.90E-06	Down	-7.69E-01	5.18E-03		-1.04E+00	3.27E-04	Down	9.40E-03	1.02E+00		-1.06E+00	3.54E-03		Unigene38691_All//gi|15228825|ref|NP_188906.1|//2.00E-64//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75274241|sp|Q9LJJ4.1|PP248_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g22670, mitochondrial; Flags: Precursor	Unigene38691_All//1.00E-59//AT3G22670| pentatricopeptide (PPR) repeat-containing protein	Unigene38691_All//0.00E+00//TC174147				nr +
Unigene38693_All	935	1.34	0.87	0.74	4.21	4.49	4.35	3.35	1.56	1.53	-6.31E-01	2.93E-01		-8.59E-01	1.74E-01		9.43E-02	8.20E-01		4.67E-02	9.04E-01		-1.10E+00	5.48E-04	Down	-1.13E+00	2.73E-04	Down	Unigene38693_All//gi|297823237|ref|XP_002879501.1|//3.00E-30//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297325340|gb|EFH55760.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene38693_All//1.00E-29//AT2G34540| unknown protein	Unigene38693_All//1.00E-132//gi|109885532|gb|DW514502.1|DW514502				nr -
Unigene38695_All	1171	0.36	0.00	0.32	1.87	1.24	2.16	3.90	1.07	1.84	-8.48E+00	1.05E-02		-1.67E-01	8.79E-01		-6.00E-01	1.60E-01		2.07E-01	6.41E-01		-1.86E+00	4.55E-11	Down	-1.09E+00	1.38E-05	Down	Unigene38695_All//gi|163889364|gb|ABY48134.1|//2.00E-89//bHLH transcription factor [Medicago truncatula]	Unigene38695_All//1.00E-60//AT5G65640| bHLH093 (beta HLH protein 93); DNA binding / transcription factor	Unigene38695_All//0.00E+00//TC161640	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene38696_All	669	15.80	8.10	7.08	24.05	26.25	12.69	1.45	2.06	1.25	-9.63E-01	7.24E-08		-1.16E+00	7.59E-10	Down	1.26E-01	4.24E-01		-9.22E-01	1.75E-11		5.04E-01	3.48E-01		-2.17E-01	7.07E-01		Unigene38696_All//gi|224146315|ref|XP_002325961.1|//1.00E-07//predicted protein [Populus trichocarpa] >gi|222862836|gb|EEF00343.1| predicted protein [Populus trichocarpa]		Unigene38696_All//0.00E+00//gi|21093207|gb|BQ405520.1|BQ405520				nr -
Unigene38698_All	563	1.02	0.00	2.36	31.94	20.12	14.52	43.56	36.75	14.93	-1.00E+01	1.52E-03		1.21E+00	5.06E-02		-6.67E-01	2.44E-08		-1.14E+00	8.73E-18	Down	-2.45E-01	1.64E-02		-1.54E+00	1.62E-44	Down	Unigene38698_All//gi|115459422|ref|NP_001053311.1|//1.00E-47//Os04g0515400 [Oryza sativa Japonica Group] >gi|32482945|emb|CAE02349.1| OSJNBa0072M01.10 [Oryza sativa (japonica cultivar-group)] >gi|38345698|emb|CAE01918.2| OSJNBa0070J16.14 [Oryza sativa (japonica cultivar-group)] >gi|113568882|dbj|BAF15225.1| Os04g0515400 [Oryza sativa Japonica Group] >gi|116310843|emb|CAH67630.1| OSIGba0140J09.11 [Oryza sativa (indica cultivar-group)]	Unigene38698_All//1.00E-35//AT3G25400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: NTP Pyrophosphohydrolase MazG-related, RS21-C6 (InterPro:IPR011394), EAR (InterPro:IPR009039), NTP pyrophosphohydrolase MazG, putative catalytic core (InterPro:IPR004518); Has 572 Blast hits to 572 proteins in 181 species: Archae - 11; Bacteria - 286; Metazoa - 71; Fungi - 1; Plants - 31; Viruses - 0; Other Eukaryotes - 172 (source: NCBI BLink).	Unigene38698_All//0.00E+00//ES828589				nr +

Unigene3870_All	937	3.46	1.30	2.33	4.20	3.60	4.05	4.92	2.27	3.87	-1.42E+00	8.53E-05	Down	-5.71E-01	1.18E-01		-2.22E-01	5.30E-01		-5.29E-02	8.85E-01		-1.11E+00	1.33E-05	Down	-3.46E-01	1.69E-01		Unigene3870_All//gi|115459264|ref|NP_001053232.1|//9.00E-54//Os04g0501800 [Oryza sativa Japonica Group] >gi|21740509|emb|CAD41488.1|OSJNBa0029802.27 [Oryza sativa (japonica cultivar-group)] >gi|113564803|dbj|BAF15146.1|Os04g0501800 [Oryza sativa Japonica Group]	Unigene3870_All//4.00E-58//AT4G30996| unknown protein	Unigene3870_All//0.00E+00//TC144207				nr -
Unigene38700_All	1300	0.89	0.55	0.45	59.66	28.24	10.87	2.83	0.45	0.40	-6.98E-01	2.66E-01		-9.75E-01	1.46E-01		-1.08E+00	1.36E-78	Down	-2.46E+00	2.57E-223	Down	-2.65E+00	1.51E-13	Down	-2.83E+00	5.50E-15	Down	Unigene38700_All//gi|15217873|ref|NP_174144.1|//1.00E-112//PUP1 (PURINE PERMEASE 1); purine nucleoside transmembrane transporter/ purine transmembrane transporter [Arabidopsis thaliana] >gi|75173386|sp|Q9FZ96.1|PUP1_ARATH RecName: Full=Purine permease 1; Short=AtPUP1 >gi|9795614|gb|AAF98432.1|AC021044_11 purine permease [Arabidopsis thaliana]	Unigene38700_All//5.00E-114//AT1G28230| PUP1 (PURINE PERMEASE 1); purine nucleoside transmembrane transporter/ purine transmembrane transporter	Unigene38700_All//0.00E+00//TC168675				nr +
Unigene38701_All	899	2.33	0.23	2.49	3.93	2.26	1.66	1.60	1.67	1.02	-3.37E+00	3.53E-08	Down	9.58E-02	8.22E-01		-8.00E-01	9.48E-03		-1.25E+00	1.51E-04	Down	6.59E-02	9.05E-01		-6.50E-01	1.74E-01		Unigene38701_All//gi|218199235|gb|EEC81662.1|//8.00E-06//hypothetical protein Osl_25211 [Oryza sativa Indica Group]		Unigene38701_All//2.00E-11//TC133829				nr -
Unigene38702_All	890	1.35	1.02	1.44	1.29	1.63	1.22	1.90	2.40	0.40	-4.00E-01	5.15E-01		8.69E-02	8.84E-01		3.36E-01	5.83E-01		-8.00E-02	9.09E-01		3.34E-01	4.23E-01		-2.24E+00	8.65E-06	Down	Unigene38702_All//gi|47824985|gb|AAT38758.1|//3.00E-07//Putative gag-pol polyprotein, identical [Solanum demissum]		Unigene38702_All//2.00E-08//BF269227				nr +
Unigene38705_All	340	37.86	22.95	20.20	41.46	35.04	38.26	148.23	56.92	47.57	-7.22E-01	4.49E-06		-9.06E-01	3.70E-08		-2.43E-01	1.19E-01		-1.16E-01	5.21E-01		-1.38E+00	1.55E-74	Down	-1.64E+00	9.42E-99	Down	Unigene38705_All//gi|82623403|gb|AB88716.1|//5.00E-10//40S ribosomal protein S19-like [Solanum tuberosum]	Unigene38705_All//2.00E-10//AT5G61170| 40S ribosomal protein S19 (RPS19C)	Unigene38705_All//3.00E-171//gi|21103743|gb|BQ416056.1|BQ416056	ko03010|Ribosome			nr +
Unigene38709_All	711	3.61	39.62	176.60	0.28	0.00	0.38	1.61	0.41	16.64	3.46E+00	6.62E-105	Up	5.61E+00	0.00E+00	Up	-8.13E+00	8.42E-02		4.44E-01	7.63E-01		-1.96E+00	1.69E-03		3.37E+00	3.25E-54	Up	Unigene38709_All//gi|416662|sp|P32765.1|ASP_THECC//1.00E-69//RecName: Full=21 kDa seed protein; Flags: Precursor >gi|99954|pir||S16252 trypsin inhibitor homolog - soybean >gi|21909|emb|CAA39860.1| 21 kDa seed protein [Theobroma cacao]	Unigene38709_All//4.00E-24//AT1G17860| trypsin and protease inhibitor family protein / Kunitz family protein	Unigene38709_All//0.00E+00//TC133081				nr +
Unigene38710_All	712	0.29	5.76	19.45	0.35	0.34	30.95	3.21	0.18	10.07	4.29E+00	2.44E-18	Up	6.05E+00	6.67E-71	Up	-4.74E-02	9.51E-01		6.47E+00	1.37E-125	Up	-4.19E+00	1.33E-12	Down	1.65E+00	9.38E-15	Up	Unigene38710_All//gi|416662|sp|P32765.1|ASP_THECC//3.00E-72//RecName: Full=21 kDa seed protein; Flags: Precursor >gi|99954|pir||S16252 trypsin inhibitor homolog - soybean >gi|21909|emb|CAA39860.1| 21 kDa seed protein [Theobroma cacao]	Unigene38710_All//2.00E-24//AT1G17860| trypsin and protease inhibitor family protein / Kunitz family protein	Unigene38710_All//0.00E+00//TC161422				nr +
Unigene38712_All	561	1.59	2.17	0.76	0.98	1.41	1.29	3.54	0.97	1.49	4.51E-01	4.56E-01		-1.06E+00	1.76E-01		5.32E-01	5.40E-01		3.99E-01	6.51E-01		-1.87E+00	2.98E-05	Down	-1.25E+00	2.01E-03									
Unigene38715_All	1103	1.09	1.10	2.03	3.48	1.53	3.40	3.41	3.26	11.96	1.51E-02	9.86E-01		8.94E-01	4.60E-02		-1.18E+00	5.44E-05	Down	-3.32E-02	9.33E-01		-6.61E-02	8.31E-01		1.81E+00	6.48E-30	Up								
Unigene38716_All	678	9.26	18.68	15.00	25.72	22.30	18.92	26.07	36.49	22.92	1.01E+00	5.79E-10	Up	6.96E-01	1.78E-04		-2.06E-01	1.47E-01		-4.43E-01	7.07E-04		4.86E-01	6.39E-07		-1.86E-01	1.31E-01		Unigene38716_All//gi|15220062|ref|NP_173172.1|//1.00E-21//UBC34 (ubiquitin-conjugating enzyme 34); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|145323930|ref|NP_001077554.1|UBC34 (ubiquitin-conjugating enzyme 34); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75313457|sp|Q9SH17.1|UBC34_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 34; AltName: Full=Ubiquitin carrier protein 34 >gi|5734741|gb|AAD50006.1|AC007651_1 Similar to Ubiquitin Conjugating Enzyme [Arabidopsis thaliana] >gi|27765034|gb|AAO23638.1|At1g17280 [Arabidopsis thaliana]	Unigene38716_All//7.00E-23//AT1G17280| UBC34 (ubiquitin-conjugating enzyme 34); ubiquitin-protein ligase	Unigene38716_All//0.00E+00//TC151834	ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis			nr -
Unigene38717_All	588	5.25	1.90	2.72	5.34	1.29	4.15	19.41	20.47	15.99	-1.47E+00	8.07E-05	Down	-9.50E-01	1.07E-02		-2.05E+00	1.07E-08	Down	-3.64E-01	3.43E-01		7.65E-02	6.44E-01		-2.80E-01	6.38E-02		Unigene38717_All//gi|15221451|ref|NP_172122.1|//6.00E-35//copper-binding family protein [Arabidopsis thaliana]	Unigene38717_All//4.00E-32//AT1G06330| copper-binding family protein	Unigene38717_All//0.00E+00//DT464862				nr +
Unigene38718_All	1985	0.92	0.00	0.43	2.61	4.37	4.51	0.96	0.46	0.04	-9.85E+00	1.34E-10	Down	-1.10E+00	3.06E-02		7.44E-01	6.06E-05		7.88E-01	3.29E-05		-1.05E+00	1.31E-02		-4.58E+00	1.36E-11	Down	Unigene38718_All//gi|15218867|ref|NP_176767.1|//0.00E+00//regulator of chromosome condensation (RCC1) family protein / zinc finger protein-related [Arabidopsis thaliana] >gi|6227017|gb|AAF06053.1|AC009513_9 Contains PF|00169 Pleckstrin homology domain, 6 PF|00415 Regulator of chromosome condensation (RCC1) domains and a PF|01363 FYVE Zinc finger domain [Arabidopsis thaliana]	Unigene38718_All//3.00E-170//AT1G65920| regulator of chromosome condensation (RCC1) family protein / zinc finger protein-related	Unigene38718_All//0.00E+00//TC167924	ko04120|Ubiquitin mediated proteolysis			nr -
Unigene38719_All	653	82.13	58.27	53.41	107.18	119.81	106.23	188.87	69.45	79.37	-4.95E-01	5.95E-12		-6.21E-01	7.07E-17		1.61E-01	6.44E-03		-1.28E-02	8.83E-01		-1.44E+00	5.74E-194	Down	-1.25E+00	4.03E-160	Down	Unigene38719_All//gi|242205330|gb|ACS88359.1|//1.00E-111//cellulose synthase catalytic subunit [Gossypium hirsutum]	Unigene38719_All//2.00E-96//AT5G05170| CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene38719_All//0.00E+00//TC138090				nr -
Unigene38720_All	770	2.31	0.99	4.50	19.41	17.22	20.47	8.18	4.40	3.05	-1.23E+00	1.38E-02		9.60E-01	5.72E-03		-1.73E-01	2.91E-01		7.69E-02	6.59E-01		-8.96E-01	2.12E-05		-1.42E+00	8.72E-11	Down	Unigene38720_All//gi|11238318|gb|AB117896.1|//2.00E-51//invertase inhibitor [Coffea canephora]	Unigene38720_All//1.00E-22//AT5G46940| invertase/pectin methylesterase inhibitor family protein					nr -
Unigene38721_All	1144	0.82	0.49	0.98	3.35	1.99	3.47	4.25	3.73	1.46	-7.57E-01	2.86E-01		2.48E-01	6.90E-01		-7.55E-01	1.04E-02		5.12E-02	8.96E-01		-1.90E-01	4.95E-01		-1.54E+00	1.80E-09	Down	Unigene38721_All//gi|224038406|gb|ACN38307.1|//1.00E-83//eukaryotic translation initiation factor 4e [Carica papaya]	Unigene38721_All//4.00E-75//AT4G18040| EIF4E (EUKARYOTIC TRANSLATION INITIATION FACTOR 4E); RNA binding / RNA cap binding / protein binding / translation initiation factor	Unigene38721_All//0.00E+00//TC178249				nr -
Unigene38723_All	307	3.07	13.20	1.73	39.59	64.83	77.82	44.76	189.92	109.39	2.11E+00	2.11E-09	Up	-8.23E-01	2.71E-01		7.12E-01	6.74E-10		9.75E-01	3.94E-18		2.09E+00	2.53E-153	Up	1.29E+00	6.27E-46	Up	Unigene38723_All//gi|227053553|gb|ACP18875.1|//1.00E-37//beta-galactosidase pBG(a) [Carica papaya]	Unigene38723_All//7.00E-39//AT3G13750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene38723_All//2.00E-166//EV486173		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation	GO:0005618//GO:0006950//GO:0015925//GO:0030246//GO:0043167//GO:0044238	nr +
Unigene38726_All	631	2.49	0.16	0.34	2.45	3.06	1.65	4.42	1.85	2.65	-3.95E+00	5.06E-07	Down	-2.88E+00	3.27E-05	Down	3.21E-01	5.66E-01		-5.72E-01	3.09E-01		-1.25E+00	2.62E-04	Down	-7.38E-01	2.22E-02		Unigene38726_All//gi|42563365|ref|NP_178113.3|//5.00E-13//helicase-related [Arabidopsis thaliana]	Unigene38726_All//2.00E-14//AT1G79950| helicase-related	Unigene38726_All//0.00E+00//gi|48805339|gb|CO106653.1|CO106653			GO:0003676//GO:0003678//GO:0032559//GO:0034641//GO:0042623//GO:0043231	nr -
Unigene38729_All	910	17.48	1.73	3.69	111.18	89.12	156.33	59.70	51.72	81.82	-3.34E+00	3.43E-58	Down	-2.25E+00	1.31E-36	Down	-3.19E-01	8.44E-12		4.92E-01	3.77E-32		-2.07E-01	1.62E-03		4.55E-01	1.52E-17		Unigene38729_All//gi|22947852|gb|AAN07898.1|//5.00E-64//xyloglucan endotransglycosylase [Malus x domestica] >gi|187372984|gb|ACD03226.1|xyloglucan endotransglucosylase/hydrolase 2 [Malus x domestica]	Unigene38729_All//2.00E-63//AT4G30270| MERI5B (meristem-5); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene38729_All//0.00E+00//gi|84169281|gb|DR457929.1|DR457929			GO:0005576//GO:0016758//GO:0016798//GO:0030312//GO:0044042	nr +
Unigene38730_All	636	40.97	21.91	43.20	40.49	47.16	49.92	7.11	11.96	28.88	-9.03E-01	1.88E-16		7.66E-02	5.46E-01		2.20E-01	2.90E-02		3.02E-01	1.63E-03		7.50E-01	6.80E-05		2.02E+00	8.09E-48	Up	Unigene38730_All//gi|63029722|gb|AAY27752.1|//2.00E-07//12-oxophytodienoate reductase [Hevea brasiliensis]	Unigene38730_All//7.00E-06//AT2G06050| OPR3 (OPDA-REDUCTASE 3); 12-oxophytodienoate reductase	Unigene38730_All//0.00E+00//TC143666	ko00592|alpha-Linolenic acid metabolism		GO:0000166//GO:0006633//GO:0016628//GO:0042579	nr +
Unigene38731_All	901	0.99	0.34	0.53	3.54	2.48	0.80	3.38	2.18	1.11	-1.55E+00	4.56E-02		-8.92E-01	2.46E-01		-5.10E-01	1.40E-01		-2.14E+00	3.25E-08	Down	-6.32E-01	4.88E-02		-1.61E+00	1.28E-06	Down	Unigene38731_All//gi|8778648|gb|AAF79656.1|AC025416.30//1.00E-56//FS011.10 [Arabidopsis thaliana]	Unigene38731_All//1.00E-53//AT1G62870| unknown protein				GO:0005488	nr -
Unigene38732_All	870	5.71	1.28	11.20	3.44	7.68	7.58	10.74	0.58	0.87	-2.16E+00	8.65E-12	Down	9.71E-01	4.70E-07		1.16E+00	1.38E-07	Up	1.14E+00	7.48E-07	Up	-4.22E+00	2.16E-50	Down	-3.63E+00	1.52E-46	Down	Unigene38732_All//gi|3341443|emb|CAA11075.1|//6.00E-88//acid phosphatase [Glycine max]	Unigene38732_All//3.00E-62//AT4G25150| acid phosphatase, putative	Unigene38732_All//0.00E+00//gi|109827326|gb|DW226018.1|DW226018	ko03010|Ribosome		GO:0016791//GO:0031410	nr +
Unigene38733_All	521	69.79	13.32	17.78	72.09	38.67	96.22	124.49	127.23	129.61	-2.39E+00	4.35E-93	Down	-1.97E+00	1.21E-70	Down	-8.99E-01	3.65E-28		4.17E-01	8.53E-09		3.15E-02	6.54E-01		5.82E-02	3.80E-01		Unigene38733_All//gi|211906496|gb|ACJ11741.1|//6.00E-94//heat shock protein 70 [Gossypium hirsutum]	Unigene38733_All//3.00E-94//AT5G02500| HSC70-1 (HEAT SHOCK COGNATE PROTEIN 70-1); ATP binding	Unigene38733_All//0.00E+00//gi|78324073|gb|DT544347.1|DT544347	ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		GO:0005576//GO:0005840//GO:0006950//GO:0009536//GO:0010038//GO:0016020//GO:0016628//GO:0019899//GO:0030312//GO:0031981//GO:0032559//GO:0044267//GO:0051707	nr -
Unigene38736_All	753	2.50	2.22	3.18	13.36	22.32	13.26	1.57	0.06	0.79	-1.72E-01	7.01E-01		3.47E-01	4.14E-01		7.40E-01	5.47E-09		-1.17E-02	9.46E-01		-4.82E+00	2.83E-07	Down	-9.86E-01	6.53E-02		Unigene38736_All//gi|162146|gb|AAB17194.1|//1.00E-104//laccase [Liriodendron tulipifera]	Unigene38736_All//5.00E-101//AT2G29130| LAC2 (laccase 2); laccase	Unigene38736_All//0.00E+00//TC150942	ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism			nr +
Unigene3874_All	904	2.32	2.86	2.24	2.59	4.69	3.75	4.82	4.07	1.54	3.04E-01	4.46E-01		-4.86E-02	9.25E-01		8.55E-01	2.72E-03		5.33E-01	1.29E-01		-2.44E-01	4.08E-01		-1.64E+00	2.46E-09	Down	Unigene3874_All//gi|238480867|ref|NP_001154257.1|//1.00E-31//zinc finger protein (LSD1) [Arabidopsis thaliana]	Unigene3874_All//5.00E-33//AT4G20380| zinc finger protein (LSD1)	Unigene3874_All//4.00E-148//ES829625				nr -
Unigene38740_All	321	7.66	4.58	2.32	6.67	5.69	5.49	10.80	23.18	26.44	-7.43E-01	6.62E-02		-1.72E+00	1.55E-04	Down	-2.31E-01	6.06E-01		-2.82E-01	5.68E-01		1.10E+00	2.03E-08	Up	1.29E+00	2.79E-12	Up	Unigene38740_All//gi|61651608|dbj|BAD91177.1|//1.00E-52//plastidic phosphate translocator-like protein2 [Mesembryanthemum crystallinum]	Unigene38740_All//9.00E-52//AT3G11320| organic anion transmembrane transporter	Unigene38740_All//2.00E-119//TC155027			GO:0031224	nr -
Unigene38742_All	654	2.72	1.47	2.93	3.88	3.26	4.70	2.26	0.32	0.73	-8.86E-01	6.99E-02		1.08E-01	8.14E-01		-2.51E-01	5.58E-01		2.74E-01	4.92E-01		-2.82E+00	3.44E-06	Down	-1.63E+00	1.09E-03				Unigene38742_All//8.00E-07//TC137737				
Unigene38743_All	336	18.53	7.24	13.47	41.22	39.05	23.12	35.61	20.15	17.31	-1.36E+00	5.47E-08	Down	-4.60E-01	6.73E-02		-7.80E-02	6.67E-01		-8.34E-01	1.65E-08		-8.21E-01	2.47E-08		-1.04E+00	2.21E-12	Down		Unigene38743_All//2.00E-05//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene38743_All//5.00E-71//gi|48744656|gb|CO075175.1|CO075175				
Unigene38744_All	750	11.65	23.58	11.50	18.80	18.87	27.40	28.41	31.43	33.15	1.02E+00	1.07E-13	Up	-1.85E-02	9.48E-01		5.70E-03	9.78E-01		5.44E-01	4.28E-06		1.46E-01	2.01E-01		2.22E-01	2.46E-02		Unigene38744_All//gi|222424195|dbj|BAH20056.1|//3.00E-60//AT2G25670| [Arabidopsis thaliana]	Unigene38744_All//1.00E-27//AT2G25670| unknown protein	Unigene38744_All//0.00E+00//TC153788			GO:0046914	nr -
Unigene38746_All	249	14.50	9.16	6.20	9.20	12.72	5.99	70.64	22.66	22.88	-6.63E-01	4.02E-02		-1.23E+00	3.96E-04	Down	4.67E-01	2.02E-01		-6.21E-01	1.51E-01		-1.64E+00	5.59E-34	Down	-1.63E+00	1.29E-34	Down			Unigene38746_All//2.00E-125//TC148307				
Unigene38747_All	1119	1.22	2.81	4.71	0.98	1.66	0.85	0.00	0.11	0.04	1.21E+00	8.00E-04	Up	1.95E+00	1.43E-10	Up	7.63E-01	1.16E-01		-2.09E-01	7.42E-01		6.81E+00	2.40E-01		5.15E+00	6.45E-01		Unigene38747_All//gi|297842986|ref|XP_002889374.1|//1.00E-132//tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335216|gb|EFH65633.1|tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene38747_All//2.00E-104//AT1G01320| tetratricopeptide repeat (TPR)-containing protein	Unigene38747_All//0.00E+00//CA994256				nr +

Unigene38748_All	1005	64.92	5.24	27.66	6.39	3.02	1.26	0.55	0.37	0.08	-3.63E+00	1.61E-255	Down	-1.23E+00	8.27E-64	Down	-1.08E+00	5.61E-07	Down	-2.35E+00	7.32E-18	Down	-5.47E-01	5.52E-01		-2.79E+00	7.96E-03		Unigene38748_All//gi|115468494|ref|NP_001057846.1|//1.00E-39//Os06g0554200 [Oryza sativa Japonica Group] >gi|113595886|dbj|BAF19760.1| Os06g0554200 [Oryza sativa Japonica Group]	Unigene38748_All//3.00E-39//AT5G25810| unknown protein	Unigene38748_All//0.00E+00//CO098132				nr -
Unigene38749_All	2134	0.27	1.40	0.17	1.59	1.08	1.42	1.51	1.29	2.37	2.38E+00	3.97E-08	Up	-6.27E-01	5.27E-01		-5.54E-01	9.11E-02		-1.63E-01	6.70E-01		-2.20E-01	5.33E-01		6.55E-01	4.47E-03		Unigene38749_All//gi|18415314|ref|NP_567587.1|//6.00E-45//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene38749_All//3.00E-64//AT1G13630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT3G22470.1); Has 23967 Blast hits to 5877 proteins in 185 species: Archae - 3; Bacteria - 26; Metazoa - 708; Fungi - 595; Plants - 21695; Viruses - 0; Other Eukaryotes - 940 (source: NCBI BLink).	Unigene38749_All//0.00E+00//DR463554				nr -
Unigene38750_All	723	3.55	0.98	0.96	2.69	2.33	1.81	1.29	1.27	1.98	-1.85E+00	2.00E-05	Down	-1.89E+00	3.13E-05	Down	-2.03E-01	6.79E-01		-5.69E-01	2.36E-01		-1.66E-02	1.02E+00		6.25E-01	1.99E-01		Unigene38750_All//gi|87241294|gb|AB033152.1|//1.00E-105//Helicase, C-terminal; Haem peroxidase, plant/fungal/bacterial [Medicago truncatula]	Unigene38750_All//2.00E-118//AT3G02060| DEAD/DEAH box helicase, putative	Unigene38750_All//0.00E+00//TC140721		ko03440|Homologous recombination	GO:0001071//GO:0003677//GO:0006259//GO:0006351//GO:0032559//GO:0042623//GO:0043231	nr +
Unigene38751_All	577	34.09	36.53	31.19	49.47	37.42	61.91	94.45	43.39	41.63	9.96E-02	4.60E-01		-1.28E-01	3.92E-01		-4.03E-01	1.78E-05		3.24E-01	2.66E-04		-1.12E+00	2.23E-58	Down	-1.18E+00	3.54E-65	Down	Unigene38751_All//gi|99083509|gb|AB966654.1|//3.00E-99//EBP1 [Ammopiptanthus mongolicus] >gi|146336945|gb|ABQ23586.1| EBP1 [Ammopiptanthus mongolicus]	Unigene38751_All//5.00E-78//AT3G51800| ATG2; aminopeptidase/ metalloexopeptidase	Unigene38751_All//0.00E+00//gi|164358000|gb|ES812859.1|ES812859			GO:0008237//GO:0008238//GO:0019538	nr -
Unigene38753_All	239	23.21	20.56	11.36	40.64	28.82	34.01	52.19	49.67	31.84	-1.74E-01	5.26E-01		-1.03E+00	1.10E-04	Down	-4.96E-01	4.39E-03		-2.57E-01	2.03E-01		-7.14E-02	6.63E-01		-7.13E-01	3.40E-07		Unigene38753_All//gi|297843258|ref|XP_002889510.1|//2.00E-30//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335352|gb|EFH65769.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38753_All//3.00E-25//AT1G04510| transducin family protein / WD-40 repeat family protein	Unigene38753_All//3.00E-130//ES827487		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0019787//GO:0032446//GO:0043234	nr +
Unigene38757_All	532	1.87	7.24	3.00	2.72	3.17	3.31	2.78	3.30	5.62	1.95E+00	3.26E-08	Up	6.84E-01	2.15E-01		2.24E-01	7.06E-01		2.86E-01	6.26E-01		2.46E-01	6.30E-01		1.01E+00	1.34E-03		Unigene38757_All//gi|238417984|ref|NP_001154633.1|//7.00E-13//RNA polymerase transcriptional regulation mediator-related [Arabidopsis thaliana]	Unigene38757_All//3.00E-05//AT3G21350| RNA polymerase transcriptional regulation mediator-related	Unigene38757_All//2.00E-87//TC174279			GO:0005488//GO:0006355//GO:0016251//GO:0043231//GO:0043234	nr -
Unigene38758_All	555	305.63	229.34	340.51	2445.74	2170.97	1388.18	13.86	29.82	15.58	-4.14E-01	3.22E-26		1.56E-01	6.05E-05		-1.72E-01	5.70E-47		-8.17E-01	0.00E+00		1.10E+00	7.85E-18	Up	1.68E-01	3.78E-01		Unigene38758_All//gi|115468306|ref|NP_001057752.1|//4.00E-23//Os06g0523300 [Oryza sativa Japonica Group] >gi|113595792|dbj|BAF19666.1| Os06g0523300 [Oryza sativa Japonica Group]	Unigene38758_All//2.00E-18//AT5G41761| unknown protein	Unigene38758_All//0.00E+00//gi|109875336|gb|DW504310.1|DW504310				nr -
Unigene3876_All	931	6.80	10.99	10.18	6.37	8.25	7.28	4.77	10.64	3.34	6.93E-01	1.05E-04		5.82E-01	2.66E-03		3.73E-01	8.29E-02		1.93E-01	4.69E-01		1.16E+00	8.63E-12	Up	-5.15E-01	3.88E-02		Unigene3876_All//gi|15225894|ref|NP_180326.1|//1.00E-44//zinc finger (AN1-like) family protein [Arabidopsis thaliana] >gi|75219978|sp|Q9ZN19.1|SAP3_ARATH RecName: Full=Zinc finger A20 and AN1 domain-containing stress-associated protein 3; Short=AtSAP3	Unigene3876_All//4.00E-41//AT2G27580| zinc finger (AN1-like) family protein	Unigene3876_All//0.00E+00//gi|109891511|gb|DW520474.1|DW520474				nr +
Unigene38760_All	362	15.18	14.14	14.42	10.60	8.09	9.61	21.14	16.40	8.14	-1.02E-01	6.90E-01		-7.41E-02	7.81E-01		-3.90E-01	2.26E-01		-1.41E-01	6.96E-01		-3.67E-01	5.85E-02		-1.38E+00	2.49E-12	Down	Unigene38760_All//gi|195605878|gb|ACG24769.1|//5.00E-15//small nuclear ribonucleoprotein F [Zea mays]	Unigene38760_All//2.00E-14//AT3G59810| small nuclear ribonucleoprotein F, putative / U6 snRNA-associated Sm-like protein, putative / Sm protein F, putative	Unigene38760_All//0.00E+00//gi|164278814|gb|ES833351.1|ES833351		ko03040|Spliceosome//ko03018|RNA degradation	GO:0005488//GO:0030529//GO:0043231	nr -
Unigene38762_All	688	17.34	4.86	8.51	59.95	42.94	22.58	14.50	2.98	4.52	-1.83E+00	3.08E-22	Down	-1.03E+00	3.36E-09	Down	-4.81E-01	1.92E-10		-1.41E+00	7.17E-56	Down	-2.28E+00	4.76E-30	Down	-1.68E+00	5.68E-21	Down	Unigene38762_All//gi|224112122|ref|XP_002316090.1|//3.00E-09//predicted protein [Populus trichocarpa] >gi|222865130|gb|EEF02261.1| predicted protein [Populus trichocarpa]		Unigene38762_All//0.00E+00//TC140304				nr +
Unigene38765_All	677	0.23	0.00	0.00	1.18	1.78	0.67	10.99	5.12	6.83	-7.86E+00	2.15E-01		-7.86E+00	2.44E-01		5.97E-01	3.69E-01		-8.20E-01	3.19E-01		-1.10E+00	1.99E-08	Down	-6.87E-01	2.04E-04		Unigene38765_All//gi|6630448|gb|AAF19536.1|AC007190_4//7.00E-08//F23N19.5 [Arabidopsis thaliana]						nr -
Unigene38768_All	808	12.69	17.94	20.50	397.65	405.21	133.59	8.32	3.41	3.55	4.99E-01	6.98E-04		6.92E-01	9.68E-07		2.72E-02	4.58E-01		-1.57E+00	0.00E+00	Down	-1.29E+00	1.34E-09	Down	-1.23E+00	2.55E-09	Down	Unigene38768_All//gi|4432836|gb|AAD20685.1|//6.00E-17//expressed protein [Arabidopsis thaliana] >gi|26450173|dbj|BAC42205.1| GPI-anchored protein [Arabidopsis thaliana]	Unigene38768_All//3.00E-18//AT2G28410| unknown protein	Unigene38768_All//0.00E+00//DW505784			GO:0031224	nr -
Unigene38769_All	447	51.62	61.10	39.67	44.13	47.69	56.88	78.60	88.73	33.78	2.43E-01	2.39E-02		-3.80E-01	1.40E-03		1.12E-01	4.37E-01		3.66E-01	6.22E-04		1.75E-01	3.00E-02		-1.22E+00	2.15E-44	Down	Unigene38769_All//gi|115461008|ref|NP_001054104.1|//1.00E-19//Os04g0653100 [Oryza sativa Japonica Group] >gi|32488879|emb|CAE03551.1| OSJNBa0060006.17 [Oryza sativa (japonica cultivar-group)] >gi|113565675|dbj|BAF16018.1| Os04g0653100 [Oryza sativa Japonica Group]	Unigene38769_All//7.00E-15//AT3G43520| unknown protein	Unigene38769_All//0.00E+00//TC143299			GO:0009526//GO:0031224	nr +
Unigene38771_All	429	29.03	22.80	29.05	45.63	48.48	48.74	64.65	33.51	24.52	-3.49E-01	3.30E-02		9.00E-04	9.95E-01		8.73E-02	5.63E-01		9.51E-02	5.24E-01		-9.48E-01	5.17E-23		-1.40E+00	1.93E-43	Down	Unigene38771_All//gi|2499489|sp|Q41141.1|PFPB_RICCO//8.00E-77//RecName: Full=Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta; Short=PFP; AltName: Full=6-phosphofructokinase, pyrophosphate dependent; AltName: Full=Pyrophosphate-dependent 6-phosphofructose-1-kinase; AltName: Full=PP1-PFK >gi|483536|emb|CAA83683.1| pyrophosphate-dependent phosphofructokinase beta subunit [Ricinus communis]	Unigene38771_All//7.00E-68//AT1G12000| pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative	Unigene38771_All//0.00E+00//gi|164287598|gb|ES800503.1|ES800503		ko00051|Fructose and mannose metabolism	GO:0006007//GO:0008443//GO:0010038//GO:0010316//GO:0030312//GO:0032559//GO:0043231	nr -
Unigene38772_All	463	177.30	167.44	134.79	245.31	213.53	259.67	221.99	111.76	84.84	-8.26E-02	2.08E-01		-3.96E-01	1.48E-11		-2.00E-01	1.03E-05		8.21E-02	1.29E-01		-9.90E-01	2.65E-89		-1.39E+00	8.96E-157	Down	Unigene38772_All//gi|115476070|ref|NP_001061631.1|//4.00E-50//Os08g0359500 [Oryza sativa Japonica Group] >gi|75132349|sp|Q6YYB0.1|Y8359_ORYSJ RecName: Full=Uncharacterized protein Os08g0359500 >gi|113623600|dbj|BAF23545.1| Os08g0359500 [Oryza sativa Japonica Group]	Unigene38772_All//4.00E-35//AT4G02450| glycine-rich protein	Unigene38772_All//0.00E+00//gi|109836530|gb|DW235091.1|DW235091			GO:0016020	nr +
Unigene38773_All	507	18.47	39.98	26.47	27.02	26.08	45.25	72.30	82.27	57.60	1.11E+00	6.07E-18	Up	5.19E-01	1.14E-03		-5.10E-02	8.06E-01		7.44E-01	3.09E-11		1.86E-01	1.63E-02		-3.28E-01	2.23E-05		Unigene38773_All//gi|149727917|gb|ABR28337.1|//8.00E-10//MYB transcription factor MYB49 [Medicago truncatula]		Unigene38773_All//0.00E+00//TC131424			GO:0015031//GO:0044464	nr -
Unigene38776_All	429	2.56	8.27	2.73	2.79	3.69	6.53	12.81	29.33	41.14	1.69E+00	2.08E-06	Up	9.25E-02	8.81E-01		4.06E-01	4.93E-01		1.23E+00	1.29E-03		1.19E+00	1.83E-15	Up	1.68E+00	4.96E-36	Up	Unigene38776_All//gi|257219566|gb|ACV50436.1|//7.00E-15//Avr9/Cf-9 rapidly elicited protein [Jatropha curcas]	Unigene38776_All//9.00E-07//AT1G32928| unknown protein	Unigene38776_All//0.00E+00//TC150328			GO:0006950	nr +
Unigene38779_All	419	47.58	38.21	41.94	81.08	85.88	67.48	55.90	36.91	25.20	-3.16E-01	1.19E-02		-1.82E-01	1.95E-01		8.30E-02	4.59E-01		-2.65E-01	4.51E-03		-5.99E-01	2.81E-09		-1.15E+00	2.48E-27	Down	Unigene38779_All//gi|166343835|gb|ABV88660.1|//3.00E-77//beta-tubulin 14 [Gossypium hirsutum]	Unigene38779_All//2.00E-77//AT2G29550| TUB7; structural constituent of cytoskeleton	Unigene38779_All//0.00E+00//TC155176		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene3878_All	1617	2.46	0.72	1.58	1.91	2.15	1.26	3.90	1.81	2.12	-1.77E+00	1.48E-07	Down	-6.38E-01	4.70E-02		1.71E-01	6.51E-01		-6.04E-01	9.44E-02		-1.11E+00	2.63E-07	Down	-8.79E-01	1.87E-05		Unigene3878_All//gi|183963417|ref|NP_564283.1|//1.00E-133//NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding [Arabidopsis thaliana] >gi|9802536|gb|AAF99738.1|AC004557_17 F17L21.25 [Arabidopsis thaliana] >gi|16226498|gb|AAL16183.1|AF424115_1 Atlg27460/F17L21_26 [Arabidopsis thaliana] >gi|33589668|gb|AAQ22600.1| Atlg27460/F17L21_26 [Arabidopsis thaliana]	Unigene3878_All//3.00E-128//AT1G27460| NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding	Unigene3878_All//0.00E+00//TC142974				nr -
Unigene38780_All	511	11.98	4.16	6.46	5.07	12.26	12.20	1.24	0.82	1.56	-1.52E+00	3.20E-09	Down	-8.91E-01	3.59E-04		1.27E+00	3.48E-08	Up	1.27E+00	1.50E-07	Up	-6.02E-01	4.67E-01		3.29E-01	6.33E-01		Unigene38780_All//gi|224137836|ref|XP_002326452.1|//3.00E-24//predicted protein [Populus trichocarpa] >gi|222833774|gb|EEE72251.1| predicted protein [Populus trichocarpa]		Unigene38780_All//0.00E+00//TC149959				nr +
Unigene38781_All	635	6.51	5.27	1.17	17.73	16.70	18.85	23.10	37.25	44.86	-3.06E-01	3.32E-01		-2.47E+00	5.50E-11	Down	-8.61E-02	6.69E-01		8.83E-02	6.59E-01		6.89E-01	9.12E-12		9.57E-01	1.52E-24					Unigene38781_All//0.00E+00//TC152976				
Unigene38783_All	720	6.54	3.31	13.24	4.98	4.54	3.64	1.59	1.39	1.00	-9.84E-01	4.43E-04		1.02E+00	2.07E-07	Up	-1.33E-01	7.26E-01		-4.53E-01	1.86E-01		-1.87E-01	7.39E-01		-6.71E-01	2.20E-01					Unigene38783_All//9.00E-07//TC179092				
Unigene38784_All	579	19.25	54.87	39.45	13.59	37.17	29.48	2.19	6.57	7.09	1.51E+00	5.46E-44	Up	1.04E+00	2.51E-17	Up	1.45E+00	5.44E-33	Up	1.12E+00	3.15E-16	Up	1.58E+00	1.39E-07	Up	1.69E+00	4.34E-09	Up				Unigene38784_All//2.00E-127//TC147144				
Unigene38786_All	752	60.11	182.40	82.78	211.05	399.94	362.09	163.55	375.22	213.76	1.60E+00	1.73E-204	Up	4.62E-01	1.14E-11		9.22E-01	2.79E-225		7.79E-01	6.31E-138		1.20E+00	0.00E+00	Up	3.86E-01	1.89E-27		Unigene38786_All//gi|148645874|gb|ABR01222.1|//1.00E-107//MYB10 [Gossypium hirsutum]	Unigene38786_All//2.00E-19//AT1G22640| MYB3 (MYB DOMAIN PROTEIN 3); DNA binding / transcription factor	Unigene38786_All//0.00E+00//TC155209	MYB		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene38788_All	398	4.86	6.37	3.75	10.76	8.91	9.65	39.62	23.21	13.51	3.88E-01	3.49E-01		-3.77E-01	4.36E-01		-2.72E-01	3.92E-01		-1.58E-01	6.28E-01		-7.72E-01	1.02E-09		-1.55E+00	3.89E-29	Down			Unigene38788_All//0.00E+00//gi|109867421|gb|DW496397.1|DW496397				

Unigene3879_All	1526	43.41	43.93	55.48	6.30	5.66	3.20	1.66	1.29	0.47	1.73E-02	8.17E-01		3.54E-01	8.19E-10		-1.54E-01	4.75E-01		-9.79E-01	8.46E-08		-3.69E-01	3.32E-01		-1.82E+00	1.48E-06	Down	Unigene3879_All//gi|149390435|ref|YP_001294263.1|//2.00E-09//cytochrome b6/f complex subunit VIII [Illicium oligandrum] >gi|215275450|sp|A6MWT7.1|PETN_ILLOL RecName: Full=Cytochrome b6-f complex subunit 8; AltName: Full=Cytochrome b6-f complex subunit VIII; AltName: Full=Cytochrome b6-f complex subunit petN >gi|50250320|emb|CAF28586.1| petN [Nymphaea alba] >gi|147917388|gb|ABQ52512.1| cytochrome b6/f complex subunit VIII [Illicium oligandrum]		Unigene3879_All//0.00E+00//TC167416		ko00195|Photosynthesis		nr +
Unigene38792_All	425	92.82	56.39	76.05	227.39	199.00	173.21	82.37	81.33	37.96	-7.19E-01	8.10E-17		-2.88E-01	1.30E-03		-1.92E-01	1.22E-04		-3.93E-01	8.41E-15		-1.84E-02	8.57E-01		-1.12E+00	1.22E-38	Down	Unigene38792_All//gi|223452472|gb|ACM89563.1|//2.00E-55//receptor-like protein kinase [Glycine max]	Unigene38792_All//7.00E-44//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene38792_All//0.00E+00//TC159380		ko04626|Plant-pathogen interaction	GO:0003006//GO:0004702//GO:0005982//GO:0006464//GO:0006950//GO:0007167//GO:0009933//GO:0010073//GO:0016160//GO:0016628//GO:0031224//GO:0031410//GO:0032559//GO:0043231	nr -
Unigene38793_All	575	9.10	5.64	3.52	8.14	11.56	7.15	40.07	10.39	11.78	-6.90E-01	8.10E-03		-1.37E+00	1.42E-06	Down	5.05E-01	2.47E-02		-1.88E-01	5.67E-01		-1.95E+00	6.13E-56	Down	-1.77E+00	1.36E-50	Down	Unigene38793_All|gi|1173043|sp|P46291.1|RL38_SOLLC//1.00E-29//RecName: Full=60S ribosomal protein L38 >gi|313027|emb|CAA49599.1| ribosomal protein L38 [Solanum lycopersicum] >gi|77745467|gb|ABB02632.1| ribosomal protein L38-like [Solanum tuberosum]	Unigene38793_All//1.00E-30//AT3G59540| 60S ribosomal protein L38 (RPL38B)	Unigene38793_All//0.00E+00//TC162410		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr -
Unigene38796_All	330	36.15	13.20	27.27	31.10	26.92	27.92	52.27	24.70	16.54	-1.45E+00	4.01E-16	Down	-4.07E-01	1.91E-02		-2.08E-01	2.96E-01		-1.56E-01	4.64E-01		-1.08E+00	5.60E-18	Down	-1.66E+00	5.82E-35	Down	Unigene38796_All|gi|211906476|gb|ACJ11731.1|//2.00E-11//ascorbate peroxidase [Gossypium hirsutum] >gi|254036190|gb|ACT56517.1| cytosolic ascorbate peroxidase [Gossypium hirsutum]	Unigene38796_All//3.00E-09//AT1G07890| APX1 (ascorbate peroxidase 1); L-ascorbate peroxidase	Unigene38796_All//0.00E+00//gi|11205034|gb|BF273964.1|BF273964		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0004601//GO:0005506//GO:0006950//GO:0008152	nr +
Unigene38798_All	508	6.28	4.89	3.67	8.83	11.79	9.51	12.90	6.01	6.27	-3.62E-01	3.16E-01		-7.76E-01	3.32E-02		4.18E-01	8.96E-02		1.08E-01	7.18E-01		-1.10E+00	1.55E-07	Down	-1.04E+00	3.54E-07	Down	Unigene38798_All//gi|297802420|ref|XP_002869094.1|//7.00E-84//At4g35335 [Arabidopsis lyrata subsp. lyrata] >gi|297314930|gb|EFH45353.1| At4g35335 [Arabidopsis lyrata subsp. lyrata]	Unigene38798_All//1.00E-84//AT4G35335| nucleotide-sugar transmembrane transporter/ sugar:hydrogen symporter	Unigene38798_All//0.00E+00//TC148595			GO:0001071//GO:0003677//GO:0005402//GO:0006351//GO:0008643//GO:0012505//GO:0015144//GO:0031224//GO:0043231	nr -
Unigene38799_All	586	10.45	31.30	6.18	11.90	20.63	24.51	42.79	78.24	72.88	1.58E+00	1.96E-27	Up	-7.58E-01	2.31E-03		7.93E-01	2.20E-07		1.04E+00	2.40E-12	Up	8.71E-01	1.37E-32		7.68E-01	2.59E-25		Unigene38799_All//gi|927025|gb|AAC37515.1|//3.00E-36//SPF1-like DNA-binding protein [Cucumis sativus]	Unigene38799_All//2.00E-25//AT3G01080| WRKY58; transcription factor	Unigene38799_All//0.00E+00//TC145302	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0010468//GO:0043231	nr -
Unigene388_All	2481	19.95	8.58	9.74	16.16	13.49	20.59	7.65	4.51	3.03	-1.22E+00	2.05E-49	Down	-1.03E+00	9.82E-37	Down	-2.61E-01	1.25E-03		3.49E-01	1.25E-06		-7.61E-01	2.82E-11		-1.33E+00	5.71E-28	Down	Unigene388_All|gi|115439151|ref|NP_001043855.1|//3.00E-26//Os01g0678000 [Oryza sativa Japonica Group] >gi|113533386|dbj|BAF05769.1| Os01g0678000 [Oryza sativa Japonica Group]	Unigene388_All//9.00E-60//AT4G21700| unknown protein	Unigene388_All//0.00E+00//TC160808				nr -
Unigene38800_All	482	10.20	23.34	28.17	6.82	17.86	17.99	9.47	10.58	14.13	1.19E+00	2.08E-11	Up	1.47E+00	9.76E-18	Up	1.39E+00	1.49E-12	Up	1.40E+00	7.47E-12	Up	1.59E-01	5.70E-01		5.77E-01	3.06E-03					Unigene38800_All//6.00E-07//TC139364				
Unigene38801_All	432	36.33	33.31	33.28	71.38	78.68	71.20	43.06	20.90	23.42	-1.25E-01	4.15E-01		-1.27E-01	4.30E-01		1.40E-01	1.67E-01		-3.70E-03	9.70E-01		-1.04E+00	2.93E-18	Down	-8.79E-01	2.34E-14		Unigene38801_All|gi|192910838|gb|ACF06527.1|//3.00E-33//secretory carrier membrane protein [Elaeis guineensis]	Unigene38801_All//4.00E-14//AT2G20840| secretory carrier membrane protein (SCAMP) family protein	Unigene38801_All//0.00E+00//gi|11206398|gb|BF275328.1|BF275328			GO:0005768//GO:0006897//GO:0031224	nr +
Unigene38802_All	611	4.62	9.29	5.93	12.31	14.09	25.06	10.59	13.00	4.50	1.01E+00	7.15E-05	Up	3.58E-01	3.07E-01		1.95E-01	3.92E-01		1.03E+00	8.54E-13	Up	2.96E-01	1.32E-01		-1.23E+00	4.61E-09	Down	Unigene38802_All//gi|108710350|gb|ABF98145.1|//6.00E-13//expressed protein [Oryza sativa (japonica cultivar-group)]		Unigene38802_All//2.00E-130//TC171399			GO:0008152//GO:0008483	nr -
Unigene38805_All	664	1.42	0.00	0.08	4.28	2.23	0.95	0.45	0.44	0.96	-1.05E+01	1.46E-05	Down	-4.14E+00	2.90E-04	Down	-9.39E-01	7.35E-03		-2.17E+00	1.76E-07	Down	-1.66E-02	1.02E+00		1.11E+00	1.64E-01		Unigene38805_All|gi|24461866|gb|AAN62353.1|AF506028_20//7.00E-26//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene38805_All//8.00E-14//AT1G12280| disease resistance protein (CC-NBS-LRR class), putative	Unigene38805_All//4.00E-55//ES816451		ko04626|Plant-pathogen interaction	GO:0005488	nr -
Unigene38810_All	972	1.40	1.15	0.66	1.79	2.16	1.35	3.35	2.49	1.23	-2.87E-01	6.02E-01		-1.09E+00	7.48E-02		2.69E-01	5.94E-01		-4.13E-01	4.39E-01		-4.25E-01	1.83E-01		-1.45E+00	4.08E-06	Down				Unigene38810_All//6.00E-175//DR461469				
Unigene38811_All	531	4.83	15.27	14.64	1.78	0.52	2.55	3.98	67.85	83.73	1.66E+00	2.30E-13	Up	1.60E+00	9.20E-12	Up	-1.78E+00	1.22E-02		5.18E-01	4.01E-01		4.09E+00	2.52E-188	Up	4.39E+00	7.89E-248	Up								ESTscan -
Unigene38815_All	649	9.92	2.65	5.09	19.57	22.07	36.05	0.00	0.64	0.12	-1.90E+00	6.77E-13	Down	-9.63E-01	7.77E-05		1.73E-01	3.11E-01		8.81E-01	4.37E-15		9.33E+00	3.65E-03		6.94E+00	4.04E-01		Unigene38815_All|gi|225456461|ref|XP_002284464.1|//5.00E-39//PREDICTED: similar to bHLH transcription factor Upa20 [Vitis vinifera]	Unigene38815_All//6.00E-13//AT5G50915| basic helix-loop-helix (bHLH) family protein	Unigene38815_All//0.00E+00//gi|109886105|gb|DW515075.1|DW515075	bHLH			nr -
Unigene38816_All	532	2.07	2.19	1.80	4.40	3.24	4.92	5.96	1.34	2.25	8.50E-02	8.94E-01		-1.97E-01	7.50E-01		-4.43E-01	3.04E-01		1.62E-01	6.91E-01		-2.16E+00	2.10E-09	Down	-1.41E+00	8.85E-06	Down	Unigene38816_All|gi|298201211|gb|AD160301.1|//6.00E-35//ER luminal protein receptor 2b [Nicotiana benthamiana]	Unigene38816_All//3.00E-35//AT3G25040| ER lumen protein retaining receptor, putative / HDEL receptor, putative	Unigene38816_All//0.00E+00//TC172848			GO:0004871//GO:0005048//GO:0006810//GO:0031090//GO:0031224//GO:0043410//GO:0035437//GO:0043231	nr +
Unigene38818_All	494	78.80	29.75	14.12	67.16	65.87	45.80	147.64	33.00	68.55	-1.41E+00	1.53E-48	Down	-2.48E+00	1.77E-100	Down	-2.79E-02	8.42E-01		-5.52E-01	9.70E-10		-2.16E+00	3.47E-201	Down	-1.11E+00	2.52E-78	Down	Unigene38818_All|gi|297808385|ref|XP_002872076.1|//1.00E-91//tubulin beta-8 [Arabidopsis lyrata subsp. lyrata] >gi|297317913|gb|EFH48335.1| tubulin beta-8 [Arabidopsis lyrata subsp. lyrata]	Unigene38818_All//1.00E-83//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene38818_All//0.00E+00//ES813385		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043231//GO:0043623	nr -
Unigene38819_All	950	0.22	1.01	0.00	1.15	1.01	2.85	2.31	35.06	37.66	2.20E+00	6.58E-03		-7.78E+00	1.46E-01		-1.85E-01	8.01E-01		1.31E+00	8.44E-04	Up	3.92E+00	8.66E-169	Up	4.02E+00	8.70E-188	Up	Unigene38819_All|gi|30060337|gb|AAP13348.1|//9.00E-58//transcription factor GT-3b [Arabidopsis thaliana]	Unigene38819_All//3.00E-25//AT2G38250| DNA-binding protein-related	Unigene38819_All//1.00E-169//TC166469	Trihelix		GO:0003676//GO:0010468//GO:0031981	nr +
Unigene38821_All	508	7.00	8.78	6.71	5.59	4.95	4.71	8.91	3.87	3.14	3.26E-01	2.74E-01		-6.21E-02	8.57E-01		-1.76E-01	6.59E-01		-2.46E-01	5.62E-01		-1.20E+00	3.85E-06	Down	-1.51E+00	1.29E-08	Down	Unigene38821_All|gi|4432834|gb|AAD20683.1|//5.00E-20//expressed protein [Arabidopsis thaliana] >gi|16648716|gb|AAL25550.1| At2g28430/T1B3.5 [Arabidopsis thaliana] >gi|20334920|gb|AAM16216.1| At2g28430/T1B3.5 [Arabidopsis thaliana]	Unigene38821_All//6.00E-17//AT2G28430| unknown protein	Unigene38821_All//0.00E+00//BF275582				nr +
Unigene38822_All	539	1.84	1.69	1.88	0.83	1.47	0.59	2.20	2.56	0.52	-1.24E-01	8.42E-01		2.54E-02	9.90E-01		8.21E-01	3.28E-01		-5.04E-01	6.49E-01		2.20E-01	6.68E-01		-2.09E+00	5.32E-04	Down	Unigene38822_All|gi|4432834|gb|AAD20683.1|//3.00E-22//expressed protein [Arabidopsis thaliana] >gi|16648716|gb|AAL25550.1| At2g28430/T1B3.5 [Arabidopsis thaliana] >gi|20334920|gb|AAM16216.1| At2g28430/T1B3.5 [Arabidopsis thaliana]	Unigene38822_All//3.00E-17//AT2G28430| unknown protein	Unigene38822_All//0.00E+00//BF275582				nr -
Unigene38823_All	522	4.51	6.99	10.71	9.16	13.13	15.40	2.27	3.76	2.44	6.32E-01	4.97E-02		1.25E+00	3.73E-06	Up	5.19E-01	1.84E-02		7.49E-01	2.02E-04		7.31E-01	7.85E-02		1.07E-01	8.40E-01		Unigene38823_All|gi|297809153|ref|XP_002872460.1|//4.00E-28//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318297|gb|EFH48719.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38823_All//5.00E-29//AT4G09750| short-chain dehydrogenase/reductase (SDR) family protein	Unigene38823_All//0.00E+00//ES852245			GO:0008152//GO:0016628	nr -
Unigene38831_All	481	15.77	32.87	14.72	37.08	25.20	25.16	52.21	57.87	40.58	1.06E+00	4.07E-13	Up	-9.92E-02	6.63E-01		-5.57E-01	3.80E-06		-5.59E-01	1.15E-05		1.48E-01	1.45E-01		-3.64E-01	1.28E-04					Unigene38831_All//0.00E+00//TC177303				
Unigene38833_All	561	73.58	173.87	77.64	58.16	52.11	103.37	31.05	86.80	134.29	1.24E+00	3.70E-99	Up	7.75E-02	4.12E-01		-1.58E-01	1.16E-01		8.30E-01	4.31E-33		1.48E+00	5.68E-80	Up	2.11E+00	3.72E-205	Up	Unigene38833_All|gi|75127082|sp|Q6NM02.1|Y4445_ARATH//7.00E-19//RecName: Full=Uncharacterized protein At4g14450, chloroplastic; Flags: Precursor >gi|38603896|gb|AAR24693.1| At4g14450 [Arabidopsis thaliana] >gi|41349908|gb|AAS00339.1| At4g14450 [Arabidopsis thaliana]	Unigene38833_All//2.00E-10//AT4G14450| unknown protein	Unigene38833_All//0.00E+00//gi|84171422|gb|DR460070.1|DR460070				nr +
Unigene38834_All	459	8.32	27.82	18.45	10.74	11.78	11.81	40.81	49.08	20.31	1.74E+00	5.27E-22	Up	1.15E+00	5.94E-08	Up	1.33E-01	6.61E-01		1.36E-01	6.48E-01		2.66E-01	1.23E-02		-1.01E+00	6.42E-18	Down	Unigene38834_All|gi|297850392|ref|XP_002893077.1|//2.00E-08//protein IQ-DOMAIN 32 [Arabidopsis lyrata subsp. lyrata] >gi|297338919|gb|EFH69336.1| protein IQ-DOMAIN 32 [Arabidopsis lyrata subsp. lyrata]	Unigene38834_All//1.00E-09//AT1G18870| iqd32 (IQ-domain 32); calmodulin binding	Unigene38834_All//3.00E-138//gi|164277515|gb|ES852171.1|ES852171			GO:0009526//GO:0016020	nr -
Unigene38835_All	1124	0.74	0.18	1.33	4.92	3.89	2.13	1.88	0.33	1.28	-2.05E+00	1.68E-02		8.33E-01	1.43E-01		-3.38E-01	1.96E-01		-1.21E+00	1.97E-06	Down	-2.49E+00	1.42E-07	Down	-5.60E-01	1.43E-01		Unigene38835_All|gi|42561693|ref|NP_171946.2|//1.00E-72//PDLP2 (PLASMODESMATA-LOCATED PROTEIN 2) [Arabidopsis thaliana] >gi|75127023|sp|Q6NM73.1|CRR3_ARATH RecName: Full=Cysteine-rich repeat secretory protein 3; Flags: Precursor >gi|38566686|gb|AAR24233.1| At1g04520 [Arabidopsis thaliana] >gi|45992918|gb|AAS68113.1| At1g04520 [Arabidopsis thaliana]	Unigene38835_All//7.00E-71//AT1G04520| PDLP2 (PLASMODESMATA-LOCATED PROTEIN 2)	Unigene38835_All//2.00E-39//TC139402			GO:0005911//GO:0010496	nr -
Unigene38836_All	1143	2.24	2.93	3.03	2.88	3.49	3.00	2.92	1.39	3.35	3.83E-01	2.70E-01		4.33E-01	2.28E-01		2.81E-01	4.14E-01		6.21E-02	8.78E-01		-1.07E+00	4.42E-04	Down	1.95E-01	5.18E-01		Unigene38836_All|gi|30679594|ref|NP_195851.2|//1.00E-47//PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene38836_All//1.00E-41//AT5G02310| PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase				GO:0003824	nr +
Unigene38839_All	476	4.18	3.30	5.48	5.97	8.39	2.37	3.02	3.25	0.42	-3.40E-01	4.60E-01		3.92E-01	3.60E-01		4.92E-01	1.14E-01		-1.33E+00	4.10E-04	Down	1.05E-01	8.30E-01		-2.85E+00	2.40E-06	Down				Unigene38839_All//6.00E-07//CO099437				
Unigene38841_All	1400	0.22	0.47	0.61	1.71	0.79	1.29	2.30	1.46	11.47	1.07E+00	2.37E-01		1.44E+00	8.22E-02		-1.12E+00	4.01E-03		-4.04E-01	3.67E-01		-6.50E-01	3.63E-02		2.32E+00	1.12E-49	Up	Unigene38841_All|gi|145334247|ref|NP_001078504.1|//4.00E-99//MAPKKK21; ATP binding / protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Unigene38841_All//4.00E-98//AT5G67080| MAPKKK19; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene38841_All//0.00E+00//gi|78333718|gb|DT553992.1|DT553992		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr -
Unigene38842_All	360	11.92	25.76	28.40	29.61	11.96	25.34	25.96	54.10	23.02	1.11E+00	1.31E-08	Up	1.25E+00	9.16E-11	Up	-1.31E+00	5.25E-15	Down	-2.25E-01	2.46E-01		1.06E+00	1.58E-19	Up	-1.73E-01	3.42E-01					Unigene38842_All//2.00E-58//DW508219				
Unigene38844_All	500	4.92	4.66	3.20	5.48	6.75	5.69	4.14	2.51	1.67	-7.73E-02	8.44E-01		-6.22E-01	1.44E-01		3.01E-01	4.24E-01		5.45E-02	9.09E-01		-7.25E-01	7.22E-02		-1.31E+00	9.85E-04	Down				Unigene38844_All//0.00E+00//BF270665				
Unigene38845_All	873	1.62	1.04	1.71	5.99	2.33	2.53	2.71	0.91	1.73	-6.31E-01	2.56E-01		7.78E-02	8.88E-01		-1.36E+00	4.26E-08	Down	-1.24E+00	2.34E-06	Down	-1.58E+00	5.47E-05	Down	-6.45E-01	6.93E-02		Unigene38845_All|gi|297610205|ref|NP_001064277.2|//4.00E-07//Os10g0191000 [Oryza sativa Japonica Group] >gi|255679263|dbj|BAF26191.2| Os10g0191000 [Oryza sativa Japonica Group]	Unigene38845_All//6.00E-05//AT2G13980| nucleic acid binding	Unigene38845_All//0.00E+00//TC146858				nr -

Unigene38846_All	497	8.74	7.75	6.96	15.64	13.03	9.36	3.49	2.35	0.96	-1.73E-01	5.89E-01		-3.27E-01	3.03E-01		-2.64E-01	2.33E-01		-7.40E-01	2.90E-04		-5.67E-01	2.16E-01		-1.86E+00	7.67E-05	Down	Unigene38846_All//gi|126363763|dbj|BAF47748.1|//2.00E-26//ADP-glucose pyrophosphorylase beta subunit IbAGPb2 [Ipomoea batatas]	Unigene38846_All//3.00E-19//AT4G39210| APL3; glucose-1-phosphate adenylyltransferase	Unigene38846_All//0.00E+00//DR459606		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0009536//GO:0070566	nr +
Unigene38847_All	371	1.97	1.23	2.44	0.94	1.30	1.22	2.51	2.25	0.43	-6.84E-01	3.86E-01		3.06E-01	6.57E-01		4.67E-01	7.04E-01		3.73E-01	7.32E-01		-1.54E-01	8.08E-01		-2.55E+00	5.79E-04	Down	Unigene38847_All//gi|255568577|ref|XP_002525262.1|//6.00E-19//conserved hypothetical protein [Ricinus communis] >gi|223535420|gb|EEF37090.1| conserved hypothetical protein [Ricinus communis]	Unigene38847_All//5.00E-07//AT4G37608| unknown protein	Unigene38847_All//0.00E+00//gi|109873432|gb|DR502407.1|DR502407			GO:0043231	nr +
Unigene38849_All	1269	18.14	4.47	2.81	5.26	5.10	1.00	0.00	0.00	0.00	-2.02E+00	4.88E-48	Down	-2.69E+00	3.63E-65	Down	-4.42E-02	8.58E-01		-2.40E+00	4.83E-19	Down	null	null		null	null		Unigene38849_All//gi|73761705|gb|AZ83352.1|//1.00E-164//myb transcription factor MYB30 [Gossypium hirsutum]	Unigene38849_All//1.00E-87//AT3G28910| MYB30 (MYB DOMAIN PROTEIN 30); DNA binding / transcription factor	Unigene38849_All//0.00E+00//TC168071	MYB		GO:0000038//GO:0009725//GO:0033554//GO:0051707	nr +
Unigene38850_All	576	11.17	4.84	8.69	5.71	6.22	4.23	2.42	1.52	2.97	-1.21E+00	5.23E-07	Down	-3.63E-01	1.45E-01		1.23E-01	7.73E-01		-4.31E-01	2.29E-01		-6.69E-01	1.94E-01		2.96E-01	5.24E-01		Unigene38850_All//gi|75099212|sp|Q64818.1|Y2309_ARATH//1.00E-34//RecName: Full=Uncharacterized protein At2g23090 >gi|3169182|gb|AAC17825.1| Expressed protein [Arabidopsis thaliana] >gi|15450484|gb|AAK96535.1| At2g23090/F21P24.15 [Arabidopsis thaliana] >gi|15912199|gb|AAL08233.1| At2g23090/F21P24.15 [Arabidopsis thaliana] >gi|23565759|gb|AAN28739.1| At2g23090/F21P24.15 [Arabidopsis thaliana]	Unigene38850_All//9.00E-29//AT2G23090| unknown protein	Unigene38850_All//0.00E+00//gi|21092747|gb|BQ405060.1|BQ405060				nr -
Unigene38851_All	478	9.41	20.25	13.37	22.93	19.31	26.27	31.22	29.03	21.00	1.10E+00	7.24E-09	Up	5.06E-01	3.98E-02		-2.48E-01	1.69E-01		1.96E-01	2.82E-01		-1.05E-01	5.02E-01		-5.72E-01	5.40E-06		Unigene38851_All//gi|224105299|ref|XP_002313759.1|//1.00E-76//global transcription factor group [Populus trichocarpa] >gi|222850167|gb|EEE87714.1| global transcription factor group [Populus trichocarpa]	Unigene38851_All//5.00E-49//AT4G08350| GTA2 (GLOBAL TRANSCRIPTION FACTOR GROUP A2); structural constituent of ribosome / transcription elongation regulator/ transcription factor	Unigene38851_All//0.00E+00//gi|78347179|gb|DT567453.1|DT567453			GO:0005198//GO:0006355//GO:0006368//GO:0030528//GO:0030529	nr -
Unigene38852_All	532	52.22	42.76	53.45	44.66	40.65	44.65	20.98	11.00	10.18	-2.88E-01	5.96E-03		3.35E-02	7.73E-01		-1.36E-01	2.93E-01		-3.00E-04	9.97E-01		-9.32E-01	1.69E-09		-1.04E+00	1.20E-11	Down			Unigene38852_All//1.00E-106//gi|78352004|gb|DT572278.1|DT572278				
Unigene38853_All	629	10.81	0.64	2.88	24.39	25.95	8.19	3.76	1.66	2.72	-4.07E+00	2.08E-29	Down	-1.91E+00	4.93E-13	Down	8.93E-02	6.04E-01		-1.58E+00	7.93E-25	Down	-1.18E+00	1.66E-03		-4.67E-01	2.00E-01		Unigene38853_All//gi|15232059|ref|NP_189337.1|//6.00E-28//AT-TCP20; transcription factor [Arabidopsis thaliana] >gi|75273954|sp|Q9LSD5.1|TCP20_ARATH RecName: Full=Transcription factor TCP20	Unigene38853_All//5.00E-22//AT3G27010| AT-TCP20; transcription factor	Unigene38853_All//3.00E-154//TC177765	TCP			nr -
Unigene38855_All	758	0.83	1.67	1.26	5.98	5.86	3.10	5.86	2.21	1.79	1.01E+00	9.38E-02		6.10E-01	3.86E-01		-2.92E-02	9.24E-01		-9.49E-01	7.10E-04		-1.41E+00	1.77E-07	Down	-1.71E+00	5.05E-10	Down	Unigene38855_All//gi|15237147|ref|NP_197678.1|//6.00E-48//harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana]	Unigene38855_All//9.00E-49//AT5G22870| harpin-induced protein-related / HIN1-related / harpin-responsive protein-related					nr -
Unigene38857_All	498	24.27	12.31	10.48	19.21	15.00	24.76	43.21	20.73	9.52	-9.79E-01	4.16E-09		-1.21E+00	5.75E-12	Down	-3.56E-01	5.37E-02		3.66E-01	2.65E-02		-1.06E+00	1.59E-21	Down	-2.18E+00	2.07E-62	Down	Unigene38857_All//gi|115441727|ref|NP_001045143.1|//3.00E-19//Os01g0908400 [Oryza sativa Japonica Group] >gi|20804891|dbj|BAB92572.1| P0497H05.16 [Oryza sativa Japonica Group] >gi|113534674|dbj|BAF07057.1| Os01g0908400 [Oryza sativa Japonica Group]	Unigene38857_All//3.00E-20//AT1G67785| unknown protein	Unigene38857_All//0.00E+00//gi|13246666|gb|BE052360.2|BE052360			GO:0030961//GO:0031410//GO:0043231	nr -
Unigene38858_All	765	0.96	1.46	0.70	26.89	14.85	8.86	9.51	1.31	3.18	6.06E-01	3.59E-01		-4.60E-01	6.02E-01		-8.56E-01	2.10E-14		-1.60E+00	5.98E-34	Down	-2.86E+00	2.96E-28	Down	-1.58E+00	2.93E-14	Down	Unigene38858_All//gi|115441397|ref|NP_001044978.1|//1.00E-29//Os01g0878000 [Oryza sativa Japonica Group] >gi|113534509|dbj|BAF06892.1| Os01g0878000 [Oryza sativa Japonica Group]	Unigene38858_All//7.00E-31//AT1G09812| unknown protein	Unigene38858_All//2.00E-69//TC149235			GO:0043231	nr -
Unigene38859_All	672	2.18	3.47	5.31	5.41	4.82	7.26	6.92	10.88	8.48	6.70E-01	1.11E-01		1.28E+00	2.38E-04	Up	-1.68E-01	6.22E-01		4.24E-01	1.38E-01		6.53E-01	6.73E-04		2.93E-01	1.99E-01				Unigene38859_All//4.00E-169//TC164546				
Unigene38862_All	738	0.85	47.65	31.03	6.41	22.30	46.39	0.00	0.23	0.16	5.81E+00	3.80E-181	Up	5.19E+00	3.56E-110	Up	1.80E+00	3.78E-34	Up	2.85E+00	1.43E-113	Up	7.82E+00	1.39E-01		7.34E+00	2.43E-01								
Unigene38869_All	469	4.91	8.64	7.27	11.79	10.57	10.01	37.95	26.02	18.94	8.16E-01	7.17E-03		5.66E-01	1.09E-01		-1.57E-01	5.85E-01		-2.35E-01	4.08E-01		-5.45E-01	3.12E-06		-1.00E+00	5.74E-17	Down	Unigene38869_All//gi|195658123|gb|ACG48529.1|//9.00E-20//small nuclear ribonucleoprotein Sm D3 [Zea mays]	Unigene38869_All//3.00E-13//AT1G20580| small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative	Unigene38869_All//0.00E+00//gi|164310861|gb|ES835540.1|ES835540		ko03040|Spliceosome	GO:0005488//GO:0030529//GO:0031981	nr +
Unigene38872_All	466	11.23	17.07	13.60	36.35	36.95	38.38	63.96	57.31	31.89	6.05E-01	3.35E-03		2.76E-01	2.84E-01		2.37E-02	8.91E-01		7.86E-02	6.19E-01		-1.58E-01	1.02E-01		-1.00E+00	7.00E-28	Down	Unigene38872_All//gi|211906444|gb|ACJ11715.1|//1.00E-55//fructokinase [Gossypium hirsutum]	Unigene38872_All//2.00E-48//AT3G59480| pfkB-type carbohydrate kinase family protein	Unigene38872_All//0.00E+00//gi|84163845|gb|DR452493.1|DR452493		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism	GO:0004396//GO:0019321//GO:0032559	nr -
Unigene38875_All	2737	0.50	2.28	0.70	1.20	2.10	1.22	0.42	0.82	6.45	2.20E+00	8.26E-15	Up	4.95E-01	3.22E-01		8.07E-01	6.63E-04		2.37E-02	9.43E-01		9.83E-01	1.01E-02		3.95E+00	1.31E-91	Up	Unigene38875_All//gi|224139488|ref|XP_002323136.1|//1.00E-95//autoinhibited calcium ATPase [Populus trichocarpa] >gi|222867766|gb|EEF04897.1| autoinhibited calcium ATPase [Populus trichocarpa]	Unigene38875_All//4.00E-33//AT3G63380| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12)	Unigene38875_All//0.00E+00//gi|73862493|gb|DT465232.1|DT465232			GO:0005488//GO:0016787//GO:0022857	nr -
Unigene38876_All	1134	0.55	1.25	1.55	2.33	1.40	0.60	2.76	2.25	1.16	1.18E+00	3.93E-02		1.48E+00	5.78E-03		-7.37E-01	4.69E-02		-1.96E+00	3.07E-06	Down	-2.95E-01	3.96E-01		-1.25E+00	6.54E-05	Down	Unigene38876_All//gi|79533267|ref|NP_199834.2|//1.00E-100//nucleotide binding [Arabidopsis thaliana] >gi|40823395|gb|AAR92280.1| At5g50230 [Arabidopsis thaliana] >gi|56381931|gb|AAV85684.1| At5g50230 [Arabidopsis thaliana]	Unigene38876_All//2.00E-86//AT5G50230| nucleotide binding	Unigene38876_All//4.00E-136//gi|164535617|gb|ES848658.1|ES848658		ko03040|Spliceosome	GO:0004683	nr -
Unigene38878_All	526	13.03	18.88	14.88	17.14	29.59	14.85	33.60	72.31	69.07	5.35E-01	3.29E-03		1.92E-01	3.98E-01		7.88E-01	2.99E-09		-2.07E-01	3.47E-01		1.11E+00	5.64E-40	Up	1.04E+00	1.81E-35	Up	Unigene38878_All//gi|29028824|gb|AA064791.1|//5.00E-07//At1g68490 [Arabidopsis thaliana]	Unigene38878_All//3.00E-08//AT1G68490| unknown protein	Unigene38878_All//2.00E-90//ES810021				nr +
Unigene38879_All	700	69.14	39.74	34.00	70.31	61.29	113.23	146.53	59.83	45.99	-7.99E-01	2.09E-24		-1.02E+00	2.28E-35	Down	-1.98E-01	8.13E-03		6.88E-01	1.16E-32		-1.29E+00	2.10E-136	Down	-1.67E+00	6.82E-206	Down	Unigene38879_All//gi|39477719|emb|CAA10101.1|//7.00E-27//ribosomal protein S28 [Prunus persica] >gi|39477721|emb|CAA10102.1| ribosomal protein S28 [Prunus persica] >gi|3947723|emb|CAA10103.1| ribosomal protein S28 [Prunus persica]	Unigene38879_All//1.00E-18//AT5G64140| RPS28 (RIBOSOMAL PROTEIN S28); structural constituent of ribosome	Unigene38879_All//0.00E+00//TC161809		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene3888_All	614	26.59	15.18	13.10	100.36	79.36	50.68	114.51	123.89	71.63	-8.08E-01	6.47E-09		-1.02E+00	2.86E-12	Down	-3.39E-01	3.25E-08		-9.86E-01	2.75E-47		1.14E-01	5.28E-02		-6.77E-01	2.93E-33		Unigene3888_All//gi|193290377|gb|AB165001.1|//3.00E-13//14-3-3b protein [Gossypium hirsutum]	Unigene3888_All//4.00E-05//AT4G09000| 14-3-3-like protein GF14 chi / general regulatory factor 1 (GRF1)	Unigene3888_All//2.00E-152//BF271729				nr +
Unigene38880_All	670	10.78	13.46	6.60	10.93	10.84	6.81	37.80	16.16	17.60	3.21E-01	1.07E-01		-7.08E-01	1.74E-03		-1.13E-02	9.56E-01		-6.83E-01	1.27E-03		-1.23E+00	1.30E-31	Down	-1.10E+00	1.28E-27	Down	Unigene38880_All//gi|257219558|gb|ACV50432.1|//7.00E-21//mitochondrial ATP synthase 6kDa subunit [Jatropha curcas]	Unigene38880_All//3.00E-19//AT5G59613| unknown protein	Unigene38880_All//0.00E+00//TC164429			GO:0003824//GO:0005746	nr +
Unigene38881_All	539	0.19	9.21	3.16	4.07	7.73	9.89	2.51	23.34	11.16	5.57E+00	2.99E-25	Up	4.03E+00	2.79E-07	Up	9.27E-01	1.28E-03		1.28E+00	1.17E-06	Up	3.22E+00	3.41E-54	Up	2.15E+00	1.75E-17	Up	Unigene38881_All//gi|255555005|ref|XP_002518540.1|//8.00E-18//conserved hypothetical protein [Ricinus communis] >gi|223542385|gb|EEF43927.1| conserved hypothetical protein [Ricinus communis]		Unigene38881_All//1.00E-171//TC178164				nr +
Unigene38882_All	506	7.13	12.52	9.68	24.12	32.87	50.07	7.35	11.65	7.64	8.11E-01	5.63E-04		4.40E-01	1.32E-01		4.47E-01	5.75E-04		1.05E+00	9.87E-22	Up	6.64E-01	2.28E-03		5.47E-02	8.56E-01		Unigene38882_All//gi|186503441|ref|NP_001118397.1|//7.00E-09//CPu0BF6 (Conserved peptide upstream open reading frame 6) [Arabidopsis thaliana]	Unigene38882_All//4.00E-10//AT2G27228| CPu0BF6 (Conserved peptide upstream open reading frame 6)					nr -
Unigene38884_All	587	14.89	25.38	18.78	20.20	18.83	20.39	15.85	58.31	15.81	7.70E-01	1.38E-07		3.35E-01	6.97E-02		-1.01E-01	6.11E-01		1.36E-02	9.50E-01		1.88E+00	8.63E-79	Up	-3.00E-03	9.83E-01		Unigene38884_All//gi|297807251|ref|XP_002871509.1|//2.00E-44//carbon-nitrogen hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317346|gb|EFH47768.1| carbon-nitrogen hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38884_All//2.00E-34//AT5G12040| carbon-nitrogen hydrolase family protein	Unigene38884_All//0.00E+00//TC143798			GO:0008152//GO:0009536//GO:0016815//GO:0046914	nr +
Unigene38885_All	444	8.84	5.02	2.76	40.84	23.97	75.17	2.86	8.38	2.33	-8.16E-01	8.07E-03		-1.68E+00	1.27E-06	Down	-7.69E-01	1.16E-10		8.80E-01	2.98E-21		1.55E+00	3.08E-07	Up	-2.92E-01	5.99E-01		Unigene38885_All//gi|11596186|gb|AAG38521.1|AF283536_1|//7.00E-29//cystatin-like protein [Citrus x paradisi]	Unigene38885_All//2.00E-24//AT5G47550| cysteine protease inhibitor, putative / cystatin, putative	Unigene38885_All//0.00E+00//gi|109880555|gb|DW509525.1|DW509525			GO:0004866//GO:0030312	nr +
Unigene38886_All	607	34.48	35.89	56.67	41.44	56.33	59.45	34.62	20.45	16.47	5.81E-02	6.49E-01		7.17E-01	4.28E-14		4.43E-01	2.01E-07		5.21E-01	1.80E-09		-7.59E-01	2.39E-12		-1.07E+00	4.70E-22	Down	Unigene38886_All//gi|15239755|ref|NP_200292.1|//1.00E-33//TSB1 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT 1); tryptophan synthase [Arabidopsis thaliana] >gi|136251|sp|P14671.1|TRPB1_ARATH RecName: Full=Tryptophan synthase beta chain 1, chloroplastic; Flags: Precursor >gi|14194117|gb|AAK56253.1|AF367264_1 AT5g54810/MBG8_7 [Arabidopsis thaliana] >gi|166892|gb|AAA32878.1| tryptophan synthase beta subunit [Arabidopsis thaliana] >gi|9758261|dbj|BAB08760.1| tryptophan synthase beta chain 1 precursor [Arabidopsis thaliana] >gi|21592983|gb|AAM64932.1| tryptophan synthase beta chain 1 precursor [Arabidopsis thaliana] >gi|22137210|gb|AAN91450.1| AT5g54810/MBG8_7 [Arabidopsis thaliana] >gi|110742593|dbj|BAE99210.1| tryptophan synthase beta chain 1 precursor [Arabidopsis thaliana]	Unigene38886_All//2.00E-31//AT5G54810| TSB1 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT 1); tryptophan synthase	Unigene38886_All//0.00E+00//TC133825		ko00260|Glycine, serine and threonine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0006568//GO:0006970//GO:0008652//GO:0009532//GO:0009683//GO:0016836//GO:0048037	nr -

Unigene38887_All	416	52.57	22.66	14.72	82.03	57.94	95.32	40.35	15.27	18.77	-1.21E+00	3.84E-22	Down	-1.84E+00	9.63E-39	Down	-5.01E-01	2.25E-09		2.17E-01	1.36E-02		-1.40E+00	6.60E-26	Down	-1.10E+00	1.22E-18	Down	Unigene38887_All//gi|297820930|ref|XP_002878348.1|//1.00E-24//40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata] >gi|297324186|gb|EFH54607.1| 40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata]	Unigene38887_All//6.00E-26//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene38887_All//1.00E-164//TC158660		ko03010|Ribosome	GO:0000904//GO:0005198//GO:0009536//GO:0009887//GO:0010467//GO:0015935//GO:0003012//GO:0031410//GO:0031981//GO:0033205	nr -
Unigene38891_All	868	2.23	3.15	0.74	4.88	3.77	2.24	5.36	3.32	4.82	4.99E-01	1.97E-01		-1.60E+00	1.93E-03		-3.72E-01	2.23E-01		-1.12E+00	1.30E-04	Down	-6.90E-01	5.64E-03		-1.53E-01	5.84E-01					Unigene38891_All//6.00E-110//TC140597					
Unigene38892_All	346	36.59	42.76	42.48	68.67	66.58	75.97	43.14	21.38	42.26	2.25E-01	1.44E-01		2.15E-01	1.89E-01		-4.47E-02	7.74E-01		1.46E-01	2.28E-01		-1.01E+00	3.84E-14	Down	-2.97E-02	8.41E-01		Unigene38892_All//gi|255554567|ref|XP_002518322.1|//8.00E-06//bromodomain-containing protein, putative [Ricinus communis] >gi|223542542|gb|EEF44082.1| bromodomain-containing protein, putative [Ricinus communis]		Unigene38892_All//8.00E-138//TC144797			GO:0016740	nr +
Unigene38894_All	534	103.66	73.44	116.57	48.41	36.89	52.52	55.82	22.62	28.80	-4.97E-01	2.10E-12		1.69E-01	2.01E-02		-3.92E-01	8.22E-05		1.18E-01	3.40E-01		-1.30E+00	1.10E-40	Down	-9.55E-01	1.04E-25		Unigene38894_All//gi|117650693|gb|ABK54296.1|//2.00E-11//glycine-rich protein [Gossypium hirsutum]		Unigene38894_All//0.00E+00//TC169335				nr -
Unigene38895_All	862	25.25	4.53	8.09	1.27	1.36	0.73	0.00	0.00	0.00	-2.48E+00	2.01E-58	Down	-1.64E+00	5.09E-33	Down	9.53E-02	9.01E-01		-7.94E-01	2.34E-01		null	null		null	null		Unigene38895_All//gi|41745624|gb|AAS10177.1|//1.00E-80//YABBY-like transcription factor GRAMINIFOLIA [Antirrhinum majus]	Unigene38895_All//1.00E-64//AT2G45190| AFO (ABNORMAL FLORAL ORGANS); protein binding / transcription factor/ transcription regulator	Unigene38895_All//0.00E+00//gi|164358442|gb|ES837796.1|ES837796	C2C2-YABBY		GO:0001708//GO:0003676//GO:0009908//GO:0009943//GO:0010468//GO:0043231//GO:0048507	nr -
Unigene38896_All	921	0.40	0.28	0.75	2.06	2.13	1.67	2.39	0.77	2.94	-5.32E-01	6.27E-01		9.18E-01	3.11E-01		5.23E-02	9.35E-01		-3.02E-01	5.68E-01		-1.63E+00	7.07E-05	Down	3.01E-01	3.89E-01		Unigene38896_All//gi|108864075|gb|ABA91813.2|//5.00E-79//Armadillo/beta-catenin-like repeat family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene38896_All//7.00E-62//AT1G77460| binding				GO:0003824//GO:0043231	nr +
Unigene38898_All	729	15.57	8.90	11.54	17.49	17.38	26.95	68.15	39.04	32.30	-8.08E-01	1.91E-06		-4.32E-01	1.48E-02		-9.10E-03	9.55E-01		6.24E-01	2.71E-07		-8.04E-01	7.43E-31		-1.08E+00	2.33E-51	Down	Unigene38898_All//gi|223469631|gb|ACM90156.1|//1.00E-33//40S ribosomal protein S15-like protein [Jatropha curcas]	Unigene38898_All//2.00E-34//AT1G04270| RPS15 (CYTOSOLIC RIBOSOMAL PROTEIN S15); structural constituent of ribosome	Unigene38898_All//0.00E+00//TC144411		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009532//GO:0010467//GO:0015935//GO:0016020	nr +
Unigene38899_All	855	4.10	14.64	10.28	6.87	6.32	7.03	17.75	19.26	13.47	1.84E+00	3.65E-23	Up	1.33E+00	3.91E-10	Up	-1.21E-01	6.63E-01		3.12E-02	9.29E-01		1.18E-01	4.08E-01		-3.99E-01	1.43E-03					Unigene38899_All//0.00E+00//gi|13244951|gb|BE051998.2|BE051998				
Unigene38901_All	590	1.51	1.03	2.08	4.90	3.91	2.68	4.16	1.42	1.82	-5.49E-01	4.42E-01		4.62E-01	4.60E-01		-3.25E-01	4.09E-01		-8.70E-01	1.78E-02		-1.55E+00	4.79E-05	Down	-1.19E+00	8.55E-04	Down									
Unigene38902_All	757	0.28	0.07	0.63	0.66	0.59	0.78	1.95	0.50	0.89	-2.05E+00	3.34E-01		1.20E+00	3.02E-01		-1.54E-01	8.50E-01		2.37E-01	7.98E-01		-1.98E+00	2.39E-04	Down	-1.13E+00	1.72E-02									
Unigene38903_All	561	1.68	2.98	4.46	4.88	0.74	3.14	56.75	63.92	17.82	8.28E-01	1.04E-01		1.41E+00	1.15E-03		-2.73E+00	1.24E-10	Down	-6.37E-01	9.98E-02		1.72E-01	4.51E-02		-1.67E+00	2.26E-64	Down	Unigene38903_All//gi|124359513|gb|ABN05946.1|//3.00E-22//TIR [Medicago truncatula]	Unigene38903_All//4.00E-14//AT1G72860| disease resistance protein (TIR-NBS-LRR class), putative	Unigene38903_All//2.00E-81//TC140957			GO:0005488//GO:0009987	nr -
Unigene38904_All	812	1.42	0.62	0.92	5.71	3.60	2.34	2.81	2.52	3.29	-1.18E+00	6.62E-02		-6.27E-01	3.56E-01		-6.62E-01	1.25E-02		-1.29E+00	5.21E-06	Down	-1.57E-01	6.95E-01		2.25E-01	5.43E-01		Unigene38904_All//gi|297833452|ref|XP_002884608.1|//2.00E-75//glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] >gi|297330448|gb|EFH60867.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	Unigene38904_All//3.00E-64//AT3G16850| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene38904_All//0.00E+00//DW501411			GO:0004553//GO:0005618//GO:0031410//GO:0043231//GO:0044238//GO:0045229	nr +
Unigene38905_All	566	2.03	2.95	4.70	3.08	4.20	2.39	5.53	2.22	4.65	5.39E-01	2.94E-01		1.21E+00	3.27E-03		4.47E-01	3.09E-01		-3.64E-01	4.94E-01		-1.32E+00	4.68E-05	Down	-2.51E-01	4.37E-01					Unigene38905_All//6.00E-109//gi|48811204|gb|CO112517.1|CO112517				
Unigene38906_All	581	7.20	18.92	2.66	11.92	10.73	4.66	3.86	2.66	4.73	1.39E+00	5.57E-14	Up	-1.44E+00	9.41E-06	Down	-1.52E-01	5.54E-01		-1.35E+00	2.72E-09	Down	-5.35E-01	1.71E-01		2.95E-01	3.97E-01		Unigene38906_All//gi|119720804|gb|ABL97972.1|//1.00E-13//serine-rich protein [Brassica rapa]	Unigene38906_All//2.00E-13//AT5G11090| serine-rich protein-related	Unigene38906_All//6.00E-177//DW234094				nr +
Unigene3891_All	1014	14.03	20.54	10.14	112.60	120.93	92.95	31.40	11.75	9.19	5.49E-01	4.93E-06		-4.70E-01	2.43E-03		1.03E-01	3.56E-02		-2.77E-01	2.81E-09		-1.42E+00	2.70E-49	Down	-1.77E+00	7.11E-70	Down	Unigene3891_All//gi|195623654|gb|ACG33657.1|//4.00E-07//serine/arginine repetitive matrix protein 1 [Zea mays]	Unigene3891_All//2.00E-28//AT3G42725| unknown protein	Unigene3891_All//0.00E+00//TC136350		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene38915_All	2195	7.63	3.92	6.67	1.18	1.36	0.33	0.00	0.00	0.40	-9.59E-01	6.48E-12		-1.93E-01	2.13E-01		2.10E-01	5.98E-01		-1.84E+00	1.09E-05	Down	null	null		8.64E+00	2.05E-06	Up	Unigene38915_All//gi|15239979|ref|NP_201453.1|//0.00E+00//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75171133|sp|Q9FJY7.1|PP449_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g66520 >gi|10177533|dbj|BAB10928.1| selenium-binding protein-like [Arabidopsis thaliana]	Unigene38915_All//0.00E+00//AT5G66520| pentatricopeptide (PPR) repeat-containing protein	Unigene38915_All//0.00E+00//TC146587				nr +
Unigene38916_All	696	6.39	46.23	17.90	26.41	40.52	33.29	36.51	41.74	14.83	2.85E+00	1.11E-99	Up	1.49E+00	1.15E-16	Up	6.18E-01	6.82E-11		3.34E-01	3.44E-03		1.93E-01	4.32E-02		-1.30E+00	1.01E-35	Down				Unigene38916_All//0.00E+00//TC146208					
Unigene38917_All	774	3.52	10.61	5.44	9.46	21.89	10.91	0.93	0.92	1.54	1.59E+00	8.78E-13	Up	6.29E-01	4.35E-02		1.21E+00	7.82E-20	Up	2.06E-01	3.78E-01		-1.66E-02	1.02E+00		7.34E-01	1.73E-01		Unigene38917_All//gi|297801758|ref|XP_002868763.1|//4.00E-26//invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314599|gb|EFH45022.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene38917_All//5.00E-25//AT5G38610| invertase/pectin methylesterase inhibitor family protein					nr +
Unigene38918_All	670	2.50	13.39	4.77	0.89	2.11	1.48	5.93	11.42	14.09	2.42E+00	1.44E-23	Up	9.32E-01	1.04E-02		1.24E+00	3.03E-02		7.33E-01	3.21E-01		9.45E-01	6.89E-07		1.25E+00	6.45E-13	Up	Unigene38918_All//gi|12003402|gb|AAG43558.1|AF211540_1|//2.00E-16//Avr9/Cf-9 rapidly elicited protein 75 [Nicotiana tabacum]		Unigene38918_All//0.00E+00//DW499650				nr -
Unigene3892_All	1515	0.28	1.54	1.12	2.47	1.18	1.79	3.94	3.70	1.84	2.48E+00	9.11E-07	Up	2.03E+00	5.19E-04	Up	-1.06E+00	3.47E-04	Down	-4.63E-01	1.62E-01		-9.01E-02	7.16E-01		-1.10E+00	4.06E-07	Down	Unigene3892_All//gi|297819496|ref|XP_002877631.1|//1.00E-112//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297323469|gb|EFH53890.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene3892_All//6.00E-107//AT3G48770| ATP binding / DNA binding	Unigene3892_All//0.00E+00//TC163335				nr +
Unigene38921_All	384	36.65	10.42	9.57	45.92	28.97	51.75	116.49	31.35	43.05	-1.81E+00	1.03E-25	Down	-1.94E+00	6.24E-27	Down	-6.65E-01	3.74E-08		1.72E-01	2.22E-01		-1.89E+00	4.88E-104	Down	-1.44E+00	2.72E-72	Down	Unigene38921_All//gi|15229845|ref|NP_187143.1|//5.00E-51//40S ribosomal protein S24 (RPS24A) [Arabidopsis thaliana] >gi|11134742|sp|Q08S17.1|RS241_ARATH RecName: Full=40S ribosomal protein S24-1 >gi|15215672|gb|AAK91381.1| AT3g04920/T9J14_13 [Arabidopsis thaliana] >gi|20334888|gb|AAM16200.1| AT3g04920/T9J14_13 [Arabidopsis thaliana]	Unigene38921_All//8.00E-48//AT3G04920| 40S ribosomal protein S24 (RPS24A)	Unigene38921_All//0.00E+00//TC173416		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0031981	nr +
Unigene38924_All	1075	0.63	1.65	1.44	0.97	1.86	2.86	2.36	1.17	3.08	1.38E+00	6.71E-03		1.18E+00	3.71E-02		9.33E-01	4.16E-02		1.55E+00	2.97E-05	Up	-1.02E+00	4.34E-03		3.82E-01	2.09E-01										ESTscan -
Unigene38925_All	344	40.91	28.43	40.25	51.99	33.13	63.68	37.36	22.60	17.37	-5.25E-01	4.30E-04		-2.37E-02	8.95E-01		-6.50E-01	5.92E-08		2.93E-01	1.49E-02		-7.25E-01	2.50E-07		-1.10E+00	1.69E-14	Down	Unigene38925_All//gi|164449274|gb|ABV56102.1|//7.00E-23//eukaryotic initiation factor iso4E [Cucumis sativus]	Unigene38925_All//5.00E-18//AT5G35620| LSP1 (LOSS OF SUSCEPTIBILITY TO POTYVIRUS 1); RNA 7-methylguanosine cap binding / RNA binding / translation initiation factor	Unigene38925_All//2.00E-123//TC150977			GO:0006412//GO:0008135//GO:0044424	nr +
Unigene38929_All	315	21.92	9.01	22.15	37.00	41.32	39.43	45.90	25.34	21.63	-1.28E+00	3.99E-08	Down	1.44E-02	9.72E-01		1.59E-01	3.86E-01		9.15E-02	6.36E-01		-8.57E-01	1.39E-10		-1.09E+00	8.95E-16	Down	Unigene38929_All//gi|30246971|sp|O04450.1|TCPE_ARATH//1.00E-34//RecName: Full=T-complex protein 1 subunit epsilon; Short=TCP-1-epsilon; AltName: Full=CCT-epsilon >gi|9743353|gb|AAF97977.1|AC000103_27 F21J9.17 [Arabidopsis thaliana] >gi|19715605|gb|AAL91625.1| At1g24510/F21J9_150 [Arabidopsis thaliana] >gi|23463047|gb|AAN33193.1| At1g24510/F21J9_150 [Arabidopsis thaliana]	Unigene38929_All//4.00E-36//AT1G24510| T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative	Unigene38929_All//4.00E-167//gi|164342238|gb|ES830933.1|ES830933			GO:0005515//GO:0016020//GO:0032559//GO:0044267//GO:0044424	nr -
Unigene38930_All	811	3.87	1.75	2.56	3.26	1.53	5.23	1.04	4.79	3.98	-1.15E+00	1.33E-03		-5.96E-01	1.08E-01		-1.09E+00	2.85E-03		6.85E-01	2.10E-02		2.20E+00	1.35E-11	Up	1.93E+00	1.37E-08	Up	Unigene38930_All//gi|18390725|ref|NP_563780.1|//6.00E-60//LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6) [Arabidopsis thaliana] >gi|56236136|gb|AAV84524.1| At1g07090 [Arabidopsis thaliana] >gi|88193786|gb|ABD42982.1| At1g07090 [Arabidopsis thaliana]	Unigene38930_All//3.00E-58//AT1G07090| LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6)	Unigene38930_All//0.00E+00//gi|78353662|gb|DT573936.1|DT573936				nr +
Unigene38931_All	950	5.34	2.29	1.63	2.73	1.88	3.23	0.31	1.85	1.72	-1.22E+00	8.87E-06	Down	-1.72E+00	1.28E-08	Down	-5.33E-01	1.69E-01		2.46E-01	5.50E-01		2.57E+00	1.41E-06	Up	2.46E+00	4.32E-06	Up	Unigene38931_All//gi|18390725|ref|NP_563780.1|//3.00E-60//LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6) [Arabidopsis thaliana] >gi|56236136|gb|AAV84524.1| At1g07090 [Arabidopsis thaliana] >gi|88193786|gb|ABD42982.1| At1g07090 [Arabidopsis thaliana]	Unigene38931_All//4.00E-58//AT1G07090| LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6)	Unigene38931_All//0.00E+00//gi|78353662|gb|DT573936.1|DT573936			GO:0043231	nr -
Unigene38932_All	634	0.00	4.08	2.02	13.36	10.59	11.90	8.54	3.16	3.27	1.20E+01	1.06E-14	Up	1.10E+01	4.68E-07	Up	-3.35E-01	9.62E-02		-1.67E-01	4.82E-01		-1.43E+00	3.78E-09	Down	-1.39E+00	4.68E-09	Down	Unigene38932_All//gi|225436069|ref|XP_002272311.1|//1.00E-14//PREDICTED: similar to Hsp20/alpha crystallin family protein [Vitis vinifera]	Unigene38932_All//3.00E-17//AT1G54400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to heat; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: HSP20-like chaperone (InterPro:IPR008978); BEST Arabidopsis thaliana protein match is: heat shock family protein (TAIR:AT2G27140.1); Has 35 Blast hits to 35 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene38935_All	665	4.72	1.60	1.44	3.60	2.07	1.77	3.75	14.83	1.92	-1.56E+00	2.90E-05	Down	-1.71E+00	1.46E-05	Down	-7.96E-01	4.23E-02		-1.03E+00	1.26E-02		1.98E+00	6.86E-25	Up	-9.69E-01	5.22E-03					Unigene38935_All//8.00E-07//ES806034					
Unigene38936_All	472	2.88	4.19	2.03	11.71	11.89	8.13	6.27	2.75	3.80	5.39E-01	2.41E-01		-5.05E-01	3.82E-01		2.16E-02	9.59E-01		-5.26E-01	3.95E-02		-1.19E+00	3.08E-04	Down	-7.23E-01	2.04E-02		Unigene38936_All//gi|115463805|ref|NP_001055502.1|//3.00E-19//Os05g0404300 [Oryza sativa Japonica Group] >gi|113579053|dbj|BAF17416.1| Os05g0404300 [Oryza sativa Japonica Group]	Unigene38936_All//7.00E-20//AT5G18920| unknown protein					nr +

Unigene38938_All	440	0.83	3.57	1.45	2.94	2.35	1.95	9.03	4.84	54.96	2.10E+00	4.40E-04	Up	8.03E-01	3.88E-01		-3.26E-01	5.86E-01		-5.94E-01	3.41E-01		-8.99E-01	1.01E-03		2.61E+00	4.90E-85	Up	Unigene38938_All//gi|15919089|emb|CAC86996.1|//1.00E-13//ATP citrate lyase b-subunit [Lupinus albus]	Unigene38938_All//3.00E-14//AT1G10670| ACLA-1; ATP citrate synthase	Unigene38938_All//0.00E+00//TC179563		ko00020|Citrate cycle (TCA cycle)	GO:0004774//GO:0005982//GO:0006084//GO:0006633//GO:0006779//GO:0008361//GO:0009908//GO:0016109//GO:0032559//GO:0043234//GO:0043479//GO:0044444//GO:0048827//GO:2000026	nr +
Unigene3894_All	850	31.58	15.92	14.35	31.41	37.31	37.57	60.83	21.19	31.07	-9.88E-01	1.47E-19		-1.14E+00	1.81E-23	Down	2.48E-01	8.99E-03		2.58E-01	8.13E-03		-1.52E+00	2.70E-88	Down	-9.69E-01	5.10E-45		Unigene3894_All//gi|54039313|sp|P62302.1|RS13_SOYBN/3.00E-80//RecName: Full=40S ribosomal protein S13 >gi|44662862|gb|AAS47510.1| ribosomal protein S13 [Glycine max] >gi|161367348|gb|ABX71080.1| ribosomal protein S13 [Glycine max]	Unigene3894_All//9.00E-78//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene3894_All//0.00E+00//TC176312		ko03010|Ribosome		nr +
Unigene38940_All	648	3.55	5.94	3.37	4.92	5.74	4.88	5.02	10.06	8.55	7.42E-01	1.73E-02		-7.65E-02	8.59E-01		2.22E-01	5.42E-01		-1.21E-02	9.66E-01		1.00E+00	1.60E-06	Up	7.66E-01	4.88E-04		Unigene38940_All//gi|21261784|emb|CAD32500.1|//3.00E-16//protein kinase Ck2 regulatory subunit 2 [Nicotiana tabacum]	Unigene38940_All//0.00E+00//gi|13353740|gb|BG444088.1|BG444088	Unigene38940_All//0.00E+00//TC176312		ko04712|Circadian rhythm - plant	GO:0005488//GO:0006464//GO:0019207//GO:0043234	nr +
Unigene38941_All	686	74.97	217.01	140.42	45.53	139.50	166.43	47.21	82.80	43.61	1.53E+00	2.57E-208	Up	9.05E-01	3.29E-57		1.62E+00	5.98E-171	Up	1.87E+00	1.69E-227	Up	8.11E-01	1.23E-35		-1.14E-01	2.16E-01		Unigene38941_All//gi|15225213|ref|NP_180161.1|//3.00E-51//ATCTH; transcription factor [Arabidopsis thaliana] >gi|75220235|sp|082307.1|C3H23_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 23; Short=AtC3H23; AltName: Full=Protein ATCTH >gi|14030625|gb|AAK52987.1|AF375403_1 At2g25900/F17H15.7 [Arabidopsis thaliana] >gi|22136536|gb|AAM91054.1| At2g25900/F17H15.7 [Arabidopsis thaliana]	Unigene38941_All//3.00E-49//AT2G25900| ATCTH; transcription factor	Unigene38941_All//0.00E+00//gi|78353461|gb|DT573735.1|DT573735	C3H		GO:0001071//GO:0003676//GO:0010468//GO:0044424//GO:0046914	nr -
Unigene38942_All	562	12.66	5.14	7.11	14.45	11.09	13.50	32.65	16.36	12.90	-1.30E+00	1.65E-08	Down	-8.33E-01	2.68E-04		-3.82E-01	5.87E-02		-9.78E-02	6.95E-01		-9.97E-01	8.78E-17		-1.34E+00	3.14E-27	Down	Unigene38942_All//gi|195616008|gb|ACG29834.1|//5.00E-49//eukaryotic translation initiation factor 3 subunit 6-interacting protein [Zea mays]	Unigene38942_All//9.00E-60//AT5G25757| unknown protein	Unigene38942_All//0.00E+00//TC152320			GO:0008135//GO:0016020	nr +
Unigene38944_All	953	222.57	197.52	206.63	17.77	62.29	57.25	2.48	3.46	2.13	-1.72E-01	8.74E-07		-1.07E-01	4.75E-03		1.81E+00	4.63E-124	Up	1.69E+00	1.82E-94	Up	4.80E-01	1.27E-01		-2.21E-01	5.75E-01		Unigene38944_All//gi|15236529|ref|NP_192597.1|//7.00E-59//heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related [Arabidopsis thaliana] >gi|3377812|gb|AAC28185.1| contains similarity to heavy-metal-associated domain containing proteins (Pfam: HMA.hm, score: 12.02) [Arabidopsis thaliana]	Unigene38944_All//5.00E-56//AT4G08570| heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related	Unigene38944_All//0.00E+00//TC150940			GO:0006812//GO:0043169	nr +
Unigene38946_All	959	0.44	3.17	2.22	3.74	3.41	3.86	3.44	5.97	4.74	2.86E+00	5.99E-10	Up	2.35E+00	1.17E-05	Up	-1.33E-01	7.26E-01		4.62E-02	9.12E-01		7.96E-01	3.22E-04		4.62E-01	6.30E-02		Unigene38946_All//gi|9802525|gb|AAF99727.1|AC004557_6//2.00E-22//F17L21.7 [Arabidopsis thaliana]		Unigene38946_All//8.00E-85//BE054355			GO:0005488	nr -
Unigene38948_All	448	9.93	27.82	5.35	12.23	17.29	23.89	32.09	64.19	56.47	1.49E+00	2.78E-17	Up	-8.92E-01	2.96E-03		5.00E-01	1.46E-02		9.66E-01	2.47E-08		1.00E+00	6.06E-26	Up	8.15E-01	6.46E-17		Unigene38948_All//gi|226529461|ref|NP_001149830.1|//5.00E-36//LOC100283457 [Zea mays] >gi|195634915|gb|ACG36926.1| thioredoxin [Zea mays]	Unigene38948_All//1.00E-40//AT3G07090| unknown protein	Unigene38948_All//0.00E+00//gi|78323966|gb|DT544240.1|DT544240			GO:0043231	nr +
Unigene38949_All	550	69.35	47.26	60.51	148.45	108.82	146.17	42.66	21.66	13.18	-5.53E-01	1.65E-10		-1.97E-01	3.89E-02		-4.48E-01	9.15E-18		-2.23E-02	7.55E-01		-9.78E-01	1.32E-20		-1.69E+00	1.29E-48	Down	Unigene38949_All//gi|283101068|gb|ADB08692.1|//3.00E-26//nucleolar RNA-binding Nop10p-like protein [Wolffia arrhiza]	Unigene38949_All//2.00E-26//AT2G20490| NOP10; RNA binding	Unigene38949_All//0.00E+00//TC172929			GO:0000741//GO:0005488//GO:0016604//GO:0032991	nr +
Unigene3895_All	1032	26.82	13.99	11.09	259.11	300.24	99.65	0.49	0.85	0.19	-9.39E-01	1.51E-18		-1.27E+00	8.68E-29	Down	2.13E-01	2.99E-16		-1.38E+00	0.00E+00	Down	7.91E-01	2.41E-01		-1.35E+00	1.40E-01		Unigene3895_All//gi|4249385|gb|AAD14482.1|AAD14482//1.00E-58//T2K10.11 [Arabidopsis thaliana]	Unigene3895_All//9.00E-59//AT1G60060| unknown protein	Unigene3895_All//0.00E+00//gi|109833094|gb|DW231659.1|DW231659				nr -
Unigene38950_All	575	1.55	1.32	2.59	1.91	1.68	2.83	3.24	1.02	0.69	-2.27E-01	7.27E-01		7.45E-01	1.91E-01		-1.85E-01	8.01E-01		5.69E-01	3.06E-01		-1.67E+00	2.33E-04	Down	-2.22E+00	3.02E-06	Down	Unigene38950_All//gi|297832646|ref|XP_002884205.1|//2.00E-09//EDA27/NOP10 [Arabidopsis lyrata subsp. lyrata] >gi|297330045|gb|EFH60464.1| EDA27/NOP10 [Arabidopsis lyrata subsp. lyrata]	Unigene38950_All//2.00E-10//AT2G20490| NOP10; RNA binding	Unigene38950_All//0.00E+00//CO098555				nr -
Unigene38951_All	438	26.76	21.86	16.78	41.97	39.31	42.59	35.81	17.18	26.29	-2.91E-01	8.99E-02		-6.73E-01	8.68E-05		-9.44E-02	5.43E-01		2.11E-02	9.06E-01		-1.06E+00	6.49E-16	Down	-4.46E-01	2.67E-04		Unigene38951_All//gi|226443504|gb|ACO57639.1|//7.00E-31//protein phosphatase 2A catalytic subunit [Castanea mollissima]	Unigene38951_All//2.00E-29//AT2G42500| PP2A-4; hydrolase/protein serine/threonine phosphatase	Unigene38951_All//0.00E+00//TC136244			GO:0006464//GO:0008287//GO:0016020//GO:0016791//GO:0031981//GO:0043169	nr -
Unigene38952_All	1157	1.31	0.39	1.47	4.05	3.04	1.25	3.87	0.98	1.72	-1.73E+00	2.69E-03		1.68E-01	7.31E-01		-4.15E-01	1.40E-01		-1.70E+00	8.54E-09	Down	-1.99E+00	8.67E-12	Down	-1.17E+00	4.38E-06	Down	Unigene38952_All//gi|297822877|ref|XP_002876321.1|//8.00E-60//EMB1381 [Arabidopsis lyrata subsp. lyrata] >gi|297325160|gb|EFH55580.1| EMB1381 [Arabidopsis lyrata subsp. lyrata]	Unigene38952_All//1.00E-58//AT2G31340| emb1381 (embryo defective 1381)				GO:0005488	nr -
Unigene38957_All	749	1.26	1.96	2.28	3.52	4.00	2.65	3.27	1.06	3.99	6.42E-01	2.37E-01		8.55E-01	1.04E-01		1.82E-01	6.59E-01		-4.10E-01	3.27E-01		-1.63E+00	2.44E-05	Down	2.85E-01	3.90E-01		Unigene38957_All//gi|297825637|ref|XP_002880701.1|//7.00E-75//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297326540|gb|EFH56960.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene38957_All//3.00E-70//AT2G25730| unknown protein					nr -
Unigene3896_All	1489	5.66	3.74	2.68	49.81	57.40	17.93	0.20	0.22	0.05	-5.96E-01	2.76E-03		-1.08E+00	3.48E-07	Down	2.05E-01	1.43E-04		-1.47E+00	2.68E-107	Down	1.76E-01	8.80E-01		-1.89E+00	1.68E-01		Unigene3896_All//gi|4249385|gb|AAD14482.1|AAD14482//1.00E-135//T2K10.11 [Arabidopsis thaliana]	Unigene3896_All//1.00E-135//AT1G60060| unknown protein	Unigene3896_All//0.00E+00//TC138265				nr +
Unigene38960_All	409	8.19	2.73	2.34	4.14	3.87	8.83	32.25	13.59	7.01	-1.59E+00	1.13E-05	Down	-1.80E+00	2.83E-06	Down	-9.66E-02	8.34E-01		1.09E+00	7.77E-04	Up	-1.25E+00	2.83E-17	Down	-2.20E+00	5.62E-39	Down			Unigene38960_All//0.00E+00//TC163053				
Unigene38962_All	824	1.27	3.32	2.07	3.20	3.09	2.74	1.90	0.71	0.87	1.39E+00	4.77E-04	Up	7.04E-01	1.81E-01		-5.11E-02	8.94E-01		-2.26E-01	6.28E-01		-1.42E+00	3.64E-03		-1.13E+00	1.41E-02		Unigene38962_All//gi|22655129|gb|AAM98155.1|//6.00E-47//expressed protein [Arabidopsis thaliana] >gi|32189307|gb|AAP75808.1| At3g03320 [Arabidopsis thaliana]	Unigene38962_All//3.00E-48//AT3G03320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: ProFAR isomerase-like (InterPro:IPR010539), ASCH domain (InterPro:IPR007374); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G43465.1); Has 65 Blast hits to 65 proteins in 18 species: Archae - 31; Bacteria - 2; Metazoa - 1; Fungi - 0; Plants - 13; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink).	Unigene38962_All//0.00E+00//TC176482				nr +
Unigene38963_All	1189	0.75	1.19	1.03	1.30	1.04	1.33	2.35	2.71	0.77	6.74E-01	2.31E-01		4.62E-01	4.60E-01		-3.17E-01	5.71E-01		3.37E-02	9.46E-01		2.06E-01	5.61E-01		-1.61E+00	4.09E-06	Down	Unigene38963_All//gi|24461866|gb|AAN62353.1|AF506028_20//8.00E-62//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene38963_All//2.00E-35//AT1G12290| disease resistance protein (CC-NBS-LRR class), putative	Unigene38963_All//1.00E-90//ES832022		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016787	nr -
Unigene38964_All	732	158.25	154.71	188.19	32.32	39.85	29.12	7.51	3.03	2.61	-3.27E-02	5.90E-01		2.50E-01	2.31E-08		3.02E-01	1.86E-03		-1.51E-01	2.38E-01		-1.31E+00	3.23E-08	Down	-1.52E+00	1.90E-10	Down	Unigene38964_All//gi|15224451|ref|NP_181349.1|//9.00E-41//PSRP4 (PLASTID-SPECIFIC RIBOSOMAL PROTEIN 4); structural constituent of ribosome [Arabidopsis thaliana] >gi|75275034|sp|080439.1|RR31_ARATH RecName: Full=30S ribosomal protein S31, chloroplastic; AltName: Full=Plastid-specific 30S ribosomal protein 4; Short=PSRP-4; Flags: Precursor >gi|7578852|gb|AAF64153.1|AF236826_1 plastid-specific ribosomal protein 4 precursor [Arabidopsis thaliana] >gi|3333362|gb|AAC27163.1| 30S ribosomal protein S31 [Arabidopsis thaliana] >gi|15529182|gb|AAK97685.1| At2g38140/F16M14.7 [Arabidopsis thaliana] >gi|16974357|gb|AAL31104.1| At2g38140/F16M14.7 [Arabidopsis thaliana] >gi|21618289|gb|AAM67339.1| 30S ribosomal protein S31 [Arabidopsis thaliana]	Unigene38964_All//3.00E-13//AT2G38140| PSRP4 (PLASTID-SPECIFIC RIBOSOMAL PROTEIN 4); structural constituent of ribosome	Unigene38964_All//0.00E+00//gi|164281424|gb|ES792195.1|ES792195			GO:0009536//GO:0010467//GO:0030529	nr +
Unigene38965_All	447	66.13	45.46	31.45	87.37	75.73	98.61	147.93	75.27	67.11	-5.41E-01	4.97E-08		-1.07E+00	1.78E-23	Down	-2.06E-01	1.58E-02		1.75E-01	4.09E-02		-9.75E-01	2.86E-56		-1.14E+00	1.49E-74	Down	Unigene38965_All//gi|6094040|sp|O65743.1|RL24_CICAR//6.00E-21//RecName: Full=60S ribosomal protein L24 >gi|2961300|emb|CAA12358.1| ribosomal protein L24 [Cicer arietinum]		Unigene38965_All//3.00E-175//gi|164267349|gb|ES823566.1|ES823566		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr +
Unigene38966_All	701	3.28	3.54	1.67	16.06	4.18	17.78	11.04	2.38	3.47	1.09E-01	7.77E-01		-9.75E-01	2.78E-02		-1.94E+00	4.59E-28	Down	1.47E-01	4.44E-01		-2.21E+00	1.48E-22	Down	-1.67E+00	2.73E-16	Down	Unigene38966_All//gi|18405136|ref|NP_565910.1|//1.00E-19//RTFL8 (ROTUNDIFOLIA LIKE 8) [Arabidopsis thaliana] >gi|20197045|gb|AAM14893.1| Expressed protein [Arabidopsis thaliana] >gi|42822055|tpg|DAA02282.1| TPA_exp: DVL11 [Arabidopsis thaliana]	Unigene38966_All//7.00E-17//AT2G39705| RTFL8 (ROTUNDIFOLIA LIKE 8)	Unigene38966_All//1.00E-64//ES815245			GO:0048513	nr +
Unigene38967_All	655	178.37	137.47	116.34	174.01	169.92	69.23	3.29	0.57	0.24	-3.76E-01	2.14E-15		-6.17E-01	1.10E-35		-3.43E-02	5.85E-01		-1.33E+00	9.71E-141	Down	-2.52E+00	8.42E-08	Down	-3.76E+00	1.57E-11	Down	Unigene38967_All//gi|114050611|gb|ABI49455.1|//1.00E-08//At3g06070 [Arabidopsis thaliana]	Unigene38967_All//7.00E-10//AT3G06070| unknown protein	Unigene38967_All//0.00E+00//TC138537				nr -

Unigene38968_All	397	35.32	16.08	23.20	27.73	34.61	32.19	31.95	21.16	32.71	-1.14E+00	4.52E-13	Down	-6.06E-01	9.23E-05		3.20E-01	3.69E-02		2.15E-01	2.23E-01		-5.94E-01	2.45E-05		3.41E-02	8.29E-01		Unigene38968_All//gi|15242792|ref|NP_201156.1|//5.00E-39//GAMMA CAL1 (GAMMA CARBONIC ANHYDRASE LIKE 1); carbonate dehydratase [Arabidopsis thaliana] >gi|25091501|sp|Q9FMV1.1|UMP7_ARATH RecName: Full=Uncharacterized protein At5g63510, mitochondrial	Unigene38968_All//2.00E-38//AT5G63510| GAMMA CAL1 (GAMMA CARBONIC ANHYDRASE LIKE 1); carbonate dehydratase	Unigene38968_All//0.00E+00//TC156976			GO:0003824//GO:0043231	nr +
Unigene38969_All	396	34.88	31.09	25.01	37.11	20.70	29.08	27.01	55.41	59.66	-1.66E-01	3.24E-01		-4.80E-01	2.30E-03		-8.42E-01	3.78E-10		-3.52E-01	1.79E-02		1.04E+00	3.78E-21	Up	1.14E+00	4.25E-27	Up	Unigene38969_All//gi|6692098|gb|AAF24563.1|AC007764.5//8.00E-72//F22C12.10 [Arabidopsis thaliana]	Unigene38969_All//4.00E-73//AT1G64140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: loricrin-related (TAIR:AT5G64550.1); Has 2298 Blast hits to 1429 proteins in 121 species: Archae - 0; Bacteria - 42; Metazoa - 1626; Fungi - 29; Plants - 243; Viruses - 9; Other Eukaryotes - 349 (source: NCBI BLink).	Unigene38969_All//0.00E+00//gi|48751679|gb|CO082198.1|CO082198				nr +
Unigene38970_All	385	41.18	21.32	15.49	51.37	43.83	59.94	100.70	51.57	38.60	-9.50E-01	3.71E-11		-1.41E+00	1.90E-19	Down	-2.29E-01	7.31E-02		2.23E-01	6.81E-02		-9.66E-01	8.07E-33		-1.38E+00	2.23E-59	Down	Unigene38970_All//gi|15229631|ref|NP_190560.1|//4.00E-30//60S ribosomal protein L26 (RPL26A) [Arabidopsis thaliana] >gi|297816242|ref|XP_002876004.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|27735242|sp|P51414.2|RL261_ARATH RecName: Full=60S ribosomal protein L26-1 >gi|6723436|emb|CAB66929.1| 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana] >gi|297321842|gb|EFH52263.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene38970_All//1.00E-13//AT3G49910| 60S ribosomal protein L26 (RPL26A)	Unigene38970_All//0.00E+00//gi|164335974|gb|ES799061.1|ES799061		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0006950//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene38971_All	279	0.75	1.09	0.76	0.54	1.85	0.65	1.97	1.20	9.57	5.39E-01	6.71E-01		2.54E-02	1.00E+00		1.79E+00	1.26E-01		2.74E-01	9.05E-01		-7.17E-01	4.22E-01		2.28E+00	9.98E-09	Up			Unigene38971_All//1.00E-25//TC167145					
Unigene38977_All	899	1.75	0.23	2.55	3.66	2.11	2.26	3.20	2.74	0.66	-2.95E+00	1.18E-05	Down	5.45E-01	2.27E-01		-7.96E-01	1.36E-02		-6.94E-01	4.28E-02		-2.22E-01	5.52E-01		-2.27E+00	2.01E-09	Down			Unigene38977_All//1.00E-49//BF277609					
Unigene3898_All	791	114.63	130.61	181.09	37.72	75.71	35.40	0.86	2.85	1.71	1.88E-01	2.75E-04		6.60E-01	3.06E-49		1.01E+00	1.04E-51	Up	-9.17E-02	4.58E-01		1.74E+00	2.28E-05	Up	1.00E+00	4.48E-02		Unigene3898_All//gi|4755200|gb|AAD29067.1|//3.00E-36//expressed protein [Arabidopsis thaliana]	Unigene3898_All//7.00E-28//AT4G13500| unknown protein	Unigene3898_All//0.00E+00//TC153232				nr +
Unigene38982_All	641	2.86	4.66	3.07	4.35	2.15	1.41	3.36	4.56	3.98	7.07E-01	5.01E-02		1.06E-01	8.15E-01		-1.02E+00	3.99E-03		-1.63E+00	3.22E-05	Down	4.40E-01	1.96E-01		2.42E-01	5.18E-01									
Unigene38983_All	556	12.05	14.03	9.86	14.42	11.40	14.30	74.60	70.81	36.54	2.21E-01	3.31E-01		-2.88E-01	2.43E-01		-3.40E-01	1.01E-01		-1.29E-02	9.47E-01		-7.52E-02	4.03E-01		-1.03E+00	5.12E-40	Down	Unigene38983_All//gi|1808656|emb|CAA71762.1|//1.00E-46//Ubiquitin activating enzyme E1 [Nicotiana tabacum]	Unigene38983_All//4.00E-33//AT2G30110| ATUBA1; ubiquitin activating enzyme/ ubiquitin-protein ligase	Unigene38983_All//0.00E+00//gi|82756396|gb|DV849958.1|DV849958		ko04120|Ubiquitin mediated proteolysis	GO:0008641//GO:0009607//GO:0010038//GO:0016020//GO:0019787//GO:0019941//GO:0032446//GO:0032559	nr +
Unigene38985_All	534	21.07	12.81	13.96	32.00	38.88	27.32	40.22	18.47	24.02	-7.18E-01	2.29E-05		-5.94E-01	7.32E-04		2.81E-01	2.00E-02		-2.28E-01	1.18E-01		-1.12E+00	1.66E-23	Down	-7.44E-01	1.45E-12		Unigene38985_All//gi|1170898|sp|P46487.1|MDMM_EUCGU//1.00E-62//RecName: Full=Malate dehydrogenase, mitochondrial; Flags: Precursor >gi|473206|emb|CAA55383.1| mitochondrial malate dehydrogenase [Eucalyptus gunnii]	Unigene38985_All//1.00E-59//AT3G15020| malate dehydrogenase (NAD), mitochondrial, putative	Unigene38985_All//0.00E+00//gi|78348220|gb|DT568494.1|DT568494		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005576//GO:0006007//GO:0006952//GO:0009060//GO:0016615//GO:0031980//GO:0043648//GO:0046914	nr -
Unigene38987_All	519	19.15	25.87	19.19	34.75	30.39	28.28	71.77	35.92	30.63	4.34E-01	5.00E-03		2.40E-03	9.97E-01		-1.93E-01	1.65E-01		-2.97E-01	2.72E-02		-9.99E-01	2.48E-33		-1.23E+00	1.29E-47	Down	Unigene38982_All//gi|12229923|sp|Q9M4T8.1|PSA5_SOYBN//4.00E-24//RecName: Full=Proteasome subunit alpha type-5; AltName: Full=20S proteasome alpha subunit E; AltName: Full=20S proteasome subunit alpha-5 >gi|7839483|gb|AAF70292.1|AF255338_1 20S proteasome subunit [Glycine max]	Unigene38987_All//9.00E-24//AT3G14290| PAE2; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene38987_All//0.00E+00//gi|18098842|gb|BM358108.1|BM358108		ko03050|Proteasome	GO:0004175//GO:0005839//GO:0005840//GO:0010038//GO:0016020//GO:0019941//GO:0043231	nr -
Unigene38988_All	713	3.16	14.64	4.48	6.71	5.60	3.04	47.08	157.33	51.18	2.21E+00	1.34E-24	Up	5.06E-01	1.67E-01		-2.60E-01	3.86E-01		-1.14E+00	3.15E-05	Down	1.74E+00	4.68E-231	Up	1.20E-01	1.60E-01		Unigene38988_All//gi|34365641|gb|AAQ65132.1|//2.00E-16//At3g48180 [Arabidopsis thaliana]	Unigene38988_All//1.00E-14//AT1G19020| unknown protein	Unigene38988_All//0.00E+00//DW480218			GO:0006950	nr +
Unigene3899_All	1425	66.35	49.78	63.49	52.26	54.59	53.66	150.04	23.11	34.97	-4.14E-01	5.67E-15		-6.35E-02	3.35E-01		6.29E-02	3.90E-01		3.80E-02	6.14E-01		-2.70E+00	0.00E+00	Down	-2.10E+00	0.00E+00	Down	Unigene3899_All//gi|295687229|gb|ADG27840.1|//1.00E-114//chalcone isomerase [Gossypium hirsutum]	Unigene3899_All//2.00E-69//AT5G05270| chalcone-flavanone isomerase family protein	Unigene3899_All//0.00E+00//TC151931		ko00941|Flavonoid biosynthesis		nr +
Unigene38993_All	641	445.01	286.31	358.30	175.79	192.59	174.45	207.77	132.17	96.09	-6.36E-01	2.07E-94		-3.13E-01	4.50E-25		1.32E-01	4.48E-03		-1.10E-02	8.68E-01		-6.53E-01	8.67E-57		-1.11E+00	1.50E-143	Down	Unigene38993_All//gi|3219766|sp|P93584.1|ACT9_SOLTU//1.00E-117//RecName: Full=Actin-82 >gi|1498370|gb|AAB40096.1| actin [Solanum tuberosum]	Unigene38993_All//2.00E-117//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene38993_All//0.00E+00//gi|13353633|gb|BG443981.1|BG443981		ko04145|Phagosome		nr -
Unigene38994_All	584	12.18	33.84	9.85	14.59	13.27	17.25	18.53	11.09	13.23	1.47E+00	1.27E-26	Up	-3.07E-01	2.04E-01		-1.37E-01	5.54E-01		2.42E-01	2.29E-01		-7.41E-01	1.68E-06		-4.86E-01	1.20E-03		Unigene38994_All//gi|115466524|ref|NP_001066861.1|//2.00E-15//Os06g0157800 (Oryza sativa Japonica Group) >gi|113594901|dbj|BAF18775.1| Os06g0157800 [Oryza sativa Japonica Group]	Unigene38994_All//2.00E-15//AT5G67490| unknown protein	Unigene38994_All//0.00E+00//gi|109885336|gb|DW514306.1|DW514306				nr -
Unigene38997_All	521	1.41	5.25	3.27	2.87	1.59	5.89	64.76	305.57	153.93	1.90E+00	7.24E-06	Up	1.22E+00	2.32E-02		-8.55E-01	1.02E-01		1.04E+00	3.68E-03		2.24E+00	0.00E+00	Up	1.25E+00	2.56E-103	Up	Unigene38997_All//gi|297816226|ref|XP_002875996.1|//9.00E-15//ATPSK4 [Arabidopsis lyrata subsp. lyrata] >gi|297321834|gb|EFH52255.1| ATPSK4 [Arabidopsis lyrata subsp. lyrata]	Unigene38997_All//2.00E-09//AT3G49780| ATPSK4 (PHYTOSULFOKINE 4 PRECURSOR); growth factor	Unigene38997_All//2.00E-25//TC156906			GO:0032502//GO:0044421	nr -
Unigene38998_All	461	11.46	6.48	4.85	16.10	14.19	16.85	12.56	6.53	8.12	-8.22E-01	1.57E-03		-1.24E+00	8.55E-06	Down	-1.82E-01	4.49E-01		6.57E-02	7.84E-01		-9.45E-01	2.02E-05		-6.29E-01	3.07E-03				Unigene38998_All//1.00E-174//gi|11203927|gb|BF272857.1|BF272857					
Unigene390_All	553	1.14	1.01	1.73	3.24	1.37	2.45	4.51	3.70	1.44	-1.72E-01	8.29E-01		6.10E-01	3.86E-01		-1.24E+00	7.41E-03		-4.04E-01	4.43E-01		-2.85E-01	4.62E-01		-1.65E+00	1.01E-05	Down	Unigene390_All//gi|186494184|ref|NP_177125.3|//9.00E-86//CUL3B (CULLIN 3B); protein binding / ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene390_All//5.00E-87//AT1G69670| CUL3B (CULLIN 3B); protein binding / ubiquitin-protein ligase	Unigene390_All//0.00E+00//TC155743		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene39002_All	329	4.13	3.08	0.65	2.73	2.72	3.02	5.01	9.78	2.18	-4.25E-01	4.51E-01		-2.68E+00	2.60E-04	Down	-2.20E-03	9.78E-01		1.48E-01	8.42E-01		9.65E-01	1.86E-03		-1.20E+00	7.29E-03									
Unigene39003_All	752	3.48	0.67	0.50	0.99	1.97	1.86	1.97	9.00	1.59	-2.37E+00	3.10E-07	Down	-2.81E+00	3.91E-08	Down	9.87E-01	7.54E-02		9.06E-01	1.23E-01		2.19E+00	1.34E-19	Up	-3.08E-01	5.38E-01									
Unigene39006_All	733	10.21	27.37	15.69	30.58	30.82	34.38	7.44	6.16	8.42	1.42E+00	1.09E-25	Up	6.20E-01	3.40E-04		1.11E-02	9.53E-01		1.69E-01	1.65E-01		-2.73E-01	2.68E-01		1.79E-01	4.30E-01				Unigene39006_All//9.00E-124//TC171691					
Unigene39007_All	514	7.23	18.53	13.05	22.39	19.09	23.55	26.73	27.24	21.55	1.36E+00	8.81E-12	Up	8.53E-01	3.07E-04		-2.30E-01	1.99E-01		7.29E-02	6.94E-01		2.71E-02	8.70E-01		-3.11E-01	2.06E-02		Unigene39007_All//gi|23237802|dbj|BAC16370.1|//4.00E-36//aspartic proteinase 4 [Glycine max]	Unigene39007_All//3.00E-36//AT1G62290| aspartyl protease family protein	Unigene39007_All//0.00E+00//TC162258			GO:0004175//GO:0019538//GO:0043231	nr -
Unigene3901_All	906	20.33	125.16	23.39	27.99	79.44	77.57	52.31	167.04	323.72	2.62E+00	0.00E+00	Up	2.03E-01	1.32E-01		1.51E+00	4.07E-116	Up	1.47E+00	1.15E-99	Up	1.68E+00	3.88E-295	Up	2.63E+00	0.00E+00	Up	Unigene3901_All//gi|225434421|ref|XP_002272040.1|//2.00E-78//PREDICTED: similar to DNA-binding protein [Vitis vinifera]	Unigene3901_All//2.00E-17//AT5G07100| WRKY26; transcription factor	Unigene3901_All//0.00E+00//gi|78326789|gb|DT547063.1|DT547063	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene39010_All	497	4.63	4.08	5.57	4.01	4.71	4.36	6.13	4.29	2.32	-1.84E-01	6.47E-01		2.66E-01	5.14E-01		2.33E-01	6.13E-01		1.22E-01	7.88E-01		-5.14E-01	1.16E-01		-1.40E+00	1.56E-05	Down			Unigene39010_All//8.00E-108//TC130611					
Unigene39011_All	395	21.06	40.28	31.01	44.52	30.77	35.10	40.67	24.55	15.03	9.36E-01	6.75E-11		5.58E-01	8.64E-04		-5.33E-01	1.22E-05		-3.43E-01	1.03E-02		-7.29E-01	5.08E-09		-1.44E+00	1.54E-26	Down	Unigene39011_All//gi|7862066|gb|AAF70460.1|AF240445_1//8.00E-08//polyubiquitin [Populus tremula x Populus tremuloides]	Unigene39011_All//3.00E-07//AT1G31340| RUB1 (RELATED TO UBIQUITIN 1); protein binding	Unigene39011_All//5.00E-164//TC166692				nr +
Unigene39012_All	1083	0.58	0.47	0.20	4.00	2.86	3.09	9.49	23.77	66.80	-3.09E-01	7.01E-01		-1.56E+00	1.29E-01		-4.84E-01	9.17E-02		-3.75E-01	2.30E-01		1.33E+00	4.27E-36	Up	2.82E+00	1.56E-275	Up	Unigene39012_All//gi|224139824|ref|XP_002323294.1|//1.00E-143//cytochrome P450 [Populus trichocarpa] >gi|222867924|gb|EEF05055.1| cytochrome P450 [Populus trichocarpa]	Unigene39012_All//3.00E-96//AT5G06900| CYP93D1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00380|Tryptophan metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0016491	nr -
Unigene39013_All	653	5.45	20.17	5.63	15.79	27.11	12.17	25.19	23.94	40.75	1.89E+00	2.87E-25	Up	4.65E-02	8.94E-01		7.80E-01	2.81E-10		-3.76E-01	4.01E-02		-7.34E-02	6.54E-01		6.94E-01	1.20E-13		Unigene39013_All//gi|224136918|ref|XP_002322448.1|//2.00E-14//f-box family protein [Populus trichocarpa] >gi|222869444|gb|EEF06575.1| f-box family protein [Populus trichocarpa]	Unigene39013_All//4.00E-14//AT1G63090| AtPP2-A11 (Phloem protein 2-A11); carbohydrate binding	Unigene39013_All//7.00E-177//gi|78353864|gb|DT574138.1|DT574138			GO:0005488	nr +
Unigene39014_All	1094	0.00	0.74	0.19	3.14	2.46	3.10	8.70	2.94	3.39	9.53E+00	9.38E-05	Up	7.61E+00	1.41E-01		-3.56E-01	3.14E-01		-2.11E-02	9.58E-01		-1.56E+00	1.56E-17	Down	-1.36E+00	7.25E-15	Down	Unigene39014_All//gi|110931832|gb|ABH02915.1|//2.00E-56//MYB transcription factor MYB94 [Glycine max]	Unigene39014_All//1.00E-41//AT5G22260| AtMYB19 (myb domain protein 19); DNA binding / transcription factor	Unigene39014_All//0.00E+00//TC175799	MYB		GO:0001071//GO:0003676//GO:0006351//GO:0010033//GO:0010468//GO:0043231	nr +
Unigene39017_All	1113	35.30	19.85	16.65	1.97	3.74	2.64	1.18	0.79	0.36	-8.31E-01	2.71E-21		-1.08E+00	1.35E-31	Down	9.27E-01	1.28E-03		4.22E-01	2.88E-01		-5.79E-01	2.83E-01		-1.72E+00	1.48E-03		Unigene39017_All//gi|5103824|gb|AAD39654.1|AC007591_19//3.00E-18//EST gb|N65467 comes from this gene [Arabidopsis thaliana]	Unigene39017_All//2.00E-19//AT1G15260| unknown protein	Unigene39017_All//0.00E+00//ES804729				nr -
Unigene39018_All	1603	16.29	7.40	15.48	0.65	0.95	0.11	0.08	0.00	0.10	-1.14E+00	8.43E-24	Down	-7.33E-02	5.83E-01		5.34E-01	3.52E-01		-2.53E+00	1.22E-03		-6.31E+00	2.35E-01		3.30E-01	8.51E-01		Unigene39018_All//gi|227053577|gb|ACF18876.1|//0.00E+00//subtilisin-like serine protease [Carica papaya]	Unigene39018_All//0.00E+00//AT2G04160| AIR3; serine-type endopeptidase	Unigene39018_All//1.00E-155//TC174671			GO:0004175//GO:0005515//GO:0009725//GO:0010101//GO:0016628//GO:0019538//GO:0044092	nr +
Unigene39019_All	866	1.51	5.15	5.35	38.94	25.37	48.29	21.68	34.41	13.29	1.77E+00	2.55E-08	Up	1.82E+00	1.37E-08	Up	-6.18E-01	2.46E-13		3.11E-01	1.35E-04		6.67E-01	8.06E-14		-7.05E-01	3.38E-10		Unigene39019_All//gi|8096279|dbj|BAA95794.1|//4.00E-41//DC1.2 homologue [Nicotiana tabacum]	Unigene39019_All//7.00E-38//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene39019_All//0.00E+00//DW502487		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene39022_All	490	9.08	5.58	5.43	7.62	4.99	8.94	3.19	1.45	1.06	-7.01E-01	1.42E-02		-7.40E-01	1.37E-02		-6.12E-01	4.49E-02		2.30E-01	4.84E-01		-1.14E+00	1.72E-02		-1.59E+00	9.20E-04	Down			Unigene39022_All//0.00E+00//TC167942					
Unigene39025_All	1072	83.51	64.52	69.24	22.72	31.70	17.99	0.08	0.70	0.00	-3.72E-01	8.77E-12		-2.70E-01	1.78E-06		4.81E-01	1.75E-08		-3.37E-01	2.25E-03		3.15E+00	9.54E-04	Up	-6.30E+00	3.58E-01		Unigene39025_All//gi|70779014|gb|AAZ08051.1|//5.00E-91//wax synthase [Petunia x hybrida]	Unigene39025_All//7.00E-72//AT5G53390| unknown protein	Unigene39025_All//1.00E-49//TC154959				nr -
Unigene39026_All	388	3.37	3.26	1.10	1.67	0.80	1.51	6.65	2.15	2.36	-4.63E-02	9.48E-01		-1.62E+00	1.33E-02		-1.06E+00	2.26E-01		-1.41E-01	8.73E-01		-1.63E+00	1.43E-05	Down	-1.49E+00	3.19E-05	Down								
Unigene39027_All	534	1.37	1.90	1.10	2.33	1.55	1.44	4.12	0.78	0.37	4.68E-01	4.89E-01		-3.23E-01	6.81E-01		-5.92E-01	3.18E-01		-6.98E-01	2.66E-01		-2.40E+00	1.55E-07	Down	-3.46E+00	4.87E-11	Down								
Unigene39028_All	1077	18.80	3.43	4.15	27.61	13.08	4.86	9.58	0.89	2.92	-2.45E+00	1.07E-53	Down	-2.18E+00	8.16E-45	Down	-1.08E+00	3.01E-30	Down	-2.51E+00	9.46E-88	Down	-3.42E+00	2.79E-47	Down	-1.71E+00	3.55E-22	Down	Unigene39028_All//gi|87240479|gb|ABD32337.1|//3.00E-94//Major sperm protein [Medicago truncatula]	Unigene39028_All//1.00E-78//AT4G21450| vesicle-associated membrane family protein / VAMP family protein	Unigene39028_All//0.00E+00//gi|164342132|gb|ES807825.1|ES807825			GO:0016020	nr -
Unigene39029_All	1223	0.00	0.17	0.17	3.46	4.39	2.40	9.99	2.36	7.52	7.37E+00	1.36E-01		7.44E+00	1.41E-01		3.43E-01	2.13E-01		-5.28E-01	7.89E-02		-2.08E+00	1.03E-32	Down	-4.09E-01	3.76E-03		Unigene39029_All//gi|195613296|gb|ACG28478.1|//3.00E-28//serine/threonine kinase-like protein [Zea mays]	Unigene39029_All//1.00E-25//AT5G48540| 33 kDa secretory protein-related					nr +
Unigene39030_All	1873	0.06	0.65	1.17	0.05	0.74	3.33	36.59	18.90	735.07	3.54E+00	4.02E-05	Up	4.38E+00	1.03E-09	Up	3.79E+00	2.00E-06	Up	5.97E+00	1.80E-34	Up	-9.53E-01	3.58E-56		4.33E+00	0.00E+00	Up	Unigene39030_All//gi|3970689|emb|CAA77191.1|//0.00E+00//(+)-delta-cadinene synthase [Gossypium arboreum]	Unigene39030_All//7.00E-116//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene39030_All//0.00E+00//TC129577		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0010334//GO:0046872	nr -

Unigene39031_All	896	1.52	1.53	1.19	5.45	1.23	1.81	30.53	46.65	312.40	8.20E-03	9.87E-01		-3.53E-01	5.65E-01		-2.15E+00	4.45E-14	Down	-1.59E+00	2.30E-08	Down	6.12E-01	1.86E-16		3.36E+00	0.00E+00	Up	Unigene39031_All//gi|94442475|gb|AB196025.1|//1.00E-45//At5g40690 [Arabidopsis thaliana]	Unigene39031_All//7.00E-44//AT5G40690| INVOLVED IN: biological_process unknown; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: EF-HAND 1 (InterPro:IPR018247); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41720.1); Has 208 Blast hits to 177 proteins in 46 species: Archae - 0; Bacteria - 4; Metazoa - 51; Fungi - 25; Plants - 42; Viruses - 6; Other Eukaryotes - 80 (source: NCBI BLink).	Unigene39031_All//0.00E+00//gi|73865044|gb|DT467783.1|DT467783				nr +
Unigene39032_All	1728	0.27	0.23	0.12	0.46	0.76	1.02	4.62	7.52	25.41	-2.16E-01	8.17E-01		-1.14E+00	3.32E-01		7.16E-01	2.46E-01		1.14E+00	2.35E-02		7.02E-01	5.01E-07		2.46E+00	5.28E-144	Up	Unigene39032_All//gi|15237625|ref|NP_188949.1|//1.00E-140//potassium channel tetramerisation domain-containing protein [Arabidopsis thaliana] >gi|54606858|gb|AAV34777.1|At5g41330 [Arabidopsis thaliana]	Unigene39032_All//4.00E-134//AT5G41330| potassium channel tetramerisation domain-containing protein	Unigene39032_All//0.00E+00//gi|78333134|gb|DT553408.1|DT553408				nr -
Unigene39034_All	1998	4.19	0.66	0.67	0.55	0.38	2.12	1.93	16.92	18.86	-2.67E+00	9.78E-25	Down	-2.65E+00	1.55E-23	Down	-5.33E-01	4.20E-01		1.95E+00	2.12E-09	Up	3.14E+00	2.68E-141	Up	3.29E+00	1.13E-167	Up	Unigene39034_All//gi|295393250|gb|ADG03462.1|//0.00E+00//9-cis-epoxycarotenoid dioxygenase [Gossypium hirsutum]	Unigene39034_All//0.00E+00//AT3G14440| NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	Unigene39034_All//0.00E+00//TC169835		ko00906|Carotenoid biosynthesis	GO:0016701	nr -
Unigene39035_All	957	38.38	15.99	18.03	24.36	24.47	17.89	4.20	1.05	0.83	-1.26E+00	5.43E-39	Down	-1.09E+00	8.11E-30	Down	6.40E-03	9.69E-01		-4.46E-01	5.45E-05		-2.00E+00	1.02E-10	Down	-2.33E+00	2.78E-13	Down	Unigene39035_All//gi|98286617|gb|AAG00240.1|AC002130_5//1.00E-106//F1N21.15 [Arabidopsis thaliana] >gi|40823166|gb|AAB92263.1|At1g67330 [Arabidopsis thaliana] >gi|45752704|gb|AAS76250.1|At1g67330 [Arabidopsis thaliana]	Unigene39035_All//1.00E-107//AT1G67330| unknown protein	Unigene39035_All//5.00E-83//TC134341			GO:0031410	nr -
Unigene39036_All	1736	20.61	64.77	43.19	12.91	15.06	35.56	11.25	34.57	57.35	1.65E+00	2.56E-175	Up	1.07E+00	1.77E-58	Up	2.22E-01	4.26E-02		1.46E+00	8.50E-87	Up	1.62E+00	7.27E-112	Up	2.35E+00	0.00E+00	Up	Unigene39036_All//gi|240256381|ref|NP_568561.4|//1.00E-112//transferase/ transferase, transferring acyl groups other than amino-acyl groups [Arabidopsis thaliana] >gi|15450469|gb|AAK96528.1|At5g39050/MXF12_60 [Arabidopsis thaliana] >gi|25090341|gb|AAN72280.1|At5g39050/MXF12_60 [Arabidopsis thaliana]	Unigene39036_All//3.00E-112//AT5G39050| transferase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene39036_All//0.00E+00//TC139201				nr +
Unigene39037_All	1303	5.14	0.86	2.57	10.67	5.76	11.47	9.41	2.47	3.67	-2.59E+00	2.89E-19	Down	-9.97E-01	2.95E-05		-8.89E-01	1.68E-10		1.05E-01	5.64E-01		-1.93E+00	9.18E-30	Down	-1.36E+00	7.10E-19	Down	Unigene39037_All//gi|31711824|gb|AAP68268.1|//1.00E-118//At5g47680 [Arabidopsis thaliana]	Unigene39037_All//2.00E-87//AT5G47680| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: tRNA (guanine-N1-)-methyltransferase (InterPro:IPR016009), tRNA (guanine-N(1)-)-methyltransferase, metazoa (InterPro:IPR016653), tRNA (guanine-N1-)-methyltransferase, eukaryotic (InterPro:IPR007356); Has 9601 Blast hits to 4663 proteins in 357 species: Archae - 22; Bacteria - 498; Metazoa - 3588; Fungi - 1024; Plants - 270; Viruses - 29; Other Eukaryotes - 4170 (source: NCBI BLink).	Unigene39037_All//0.00E+00//TC137974				nr +
Unigene39038_All	995	21.30	19.81	19.11	42.35	33.54	35.54	15.21	8.78	6.45	-1.04E-01	4.32E-01		-1.57E-01	2.48E-01		-3.37E-01	9.61E-06		-2.53E-01	2.19E-03		-7.93E-01	9.04E-10		-1.24E+00	4.01E-20	Down			Unigene39038_All//1.00E-142//gi|164327530|gb|ES838540.1|ES838540				
Unigene39039_All	620	9.03	6.13	6.70	16.79	16.83	10.93	4.84	3.57	2.31	-5.59E-01	2.62E-02		-4.31E-01	1.10E-01		3.10E-03	9.92E-01		-6.20E-01	3.42E-04		-4.38E-01	1.90E-01		-1.07E+00	7.05E-04	Down	Unigene39039_All//gi|3695061|gb|AAC62625.1|//2.00E-20//rac GTPase activating protein 2 [Lotus japonicus]	Unigene39039_All//8.00E-18//AT2G46710| rac GTPase activating protein, putative	Unigene39039_All//0.00E+00//gi|109825543|gb|DW224269.1|DW224269			GO:0023060//GO:0044464	nr +
Unigene3904_All	1343	2.88	4.41	2.50	3.52	4.38	2.66	7.46	3.21	3.38	6.15E-01	1.17E-02		-2.07E-01	5.52E-01		3.15E-01	2.29E-01		-4.08E-01	1.62E-01		-1.22E+00	7.04E-13	Down	-1.14E+00	4.49E-12	Down			Unigene3904_All//0.00E+00//TC156639				
Unigene39040_All	1777	0.00	2.77	0.42	0.45	0.68	1.17	3.24	15.52	6.84	1.14E+01	5.13E-28	Up	8.71E+00	3.27E-04	Up	5.97E-01	3.69E-01		1.38E+00	2.77E-03		2.26E+00	1.16E-80	Up	1.08E+00	3.55E-13	Up	Unigene39040_All//gi|113205290|gb|AB134329.1|//2.00E-43//Integrase core domain containing protein [Solanum demissum]	Unigene39040_All//4.00E-26//AT4G23160| protein kinase family protein	Unigene39040_All//0.00E+00//DR463391			GO:0003676//GO:0006259//GO:0046914	nr -
Unigene39042_All	1058	10.93	3.98	9.56	3.96	4.72	1.28	0.00	0.00	0.11	-1.46E+00	9.53E-16	Down	-1.93E-01	3.13E-01		2.55E-01	4.03E-01		-1.63E+00	1.67E-07	Down	null	null		6.82E+00	2.43E-01		Unigene39042_All//gi|72384490|gb|AA267606.1|//1.00E-106//80A08_21 [Brassica rapa subsp. pekinensis]	Unigene39042_All//2.00E-93//AT5G10250| DOT3 (DEFECTIVELY ORGANIZED TRIBUTARIES 3); protein binding / signal transducer				GO:0005488//GO:0009314//GO:0009606//GO:0009888//GO:0010051//GO:0030522//GO:0048364//GO:0060089	nr +
Unigene39043_All	653	104.00	79.53	139.44	88.87	129.88	137.22	580.92	295.58	152.34	-3.87E-01	9.22E-10		4.23E-01	2.22E-14		5.47E-01	7.68E-26		6.27E-01	2.28E-31		-9.75E-01	0.00E+00		-1.93E+00	0.00E+00	Down	Unigene39043_All//gi|146432257|gb|AB241112.1|//1.00E-89//GDP-mannose-3',5'-epimerase [Vitis vinifera]	Unigene39043_All//1.00E-87//AT5G28840| GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-mannose 3,5-epimerase/ NAD or NADH binding / catalytic	Unigene39043_All//0.00E+00//gi|109847467|gb|DW476447.1|DW476447		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00051|Fructose and mannose metabolism	GO:0008152//GO:0016857//GO:0048037	nr +
Unigene39044_All	335	1.72	5.60	2.07	2.53	2.57	1.75	10.73	1.87	7.14	1.70E+00	8.73E-04	Up	2.66E-01	7.36E-01		2.37E-02	9.92E-01		-5.28E-01	5.03E-01		-2.52E+00	1.48E-12	Down	-5.88E-01	3.55E-02				Unigene39044_All//6.00E-46//DW229665				
Unigene39045_All	1517	0.00	0.00	0.00	0.59	0.64	2.68	15.08	42.62	74.58	null	null		null	null		1.05E-01	9.03E-01		2.18E+00	2.74E-10	Up	1.50E+00	1.12E-107	Up	2.31E+00	0.00E+00	Up	Unigene39045_All//gi|15217667|ref|NP_174087.1|//1.00E-29//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|218563530|sp|Q9SFZ3.2|BHLH10_ARATH RecName: Full=Transcription factor bHLH110; AltName: Full=Transcription factor EN 59; AltName: Full=bHLH transcription factor bHLH110; AltName: Full=Basic helix-loop-helix protein 110; Short=bHLH 110; Short=AtbHLH110	Unigene39045_All//5.00E-29//AT1G27660| ethylene-responsive protein -related		bHLH			nr +
Unigene39048_All	1175	0.09	0.00	0.00	0.51	0.18	1.15	8.67	8.32	29.67	-6.48E+00	3.71E-01		-6.48E+00	3.93E-01		-1.53E+00	1.01E-01		1.18E+00	4.74E-02		-5.91E-02	7.47E-01		1.77E+00	1.05E-75	Up	Unigene39048_All//gi|224092694|ref|XP_002309700.1|//1.00E-180//histidine kinase cytokinin receptor [Populus trichocarpa] >gi|222855676|gb|EEE93223.1|histidine kinase cytokinin receptor [Populus trichocarpa]	Unigene39048_All//4.00E-142//GI10720| AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase		Orphans	ko04712|Circadian rhythm - plant	GO:0004673//GO:0004871//GO:0016310//GO:0023060//GO:0044238//GO:0044260	nr -
Unigene3905_All	1816	1.15	1.37	1.08	8.45	4.55	2.51	4.75	0.92	0.79	2.47E-01	5.64E-01		-8.71E-02	8.46E-01		-8.93E-01	1.27E-11		-1.75E+00	8.81E-29	Down	-2.37E+00	3.53E-27	Down	-2.59E+00	4.53E-31	Down	Unigene3905_All//gi|115441817|ref|NP_001045188.1|//3.00E-82//Os01g0915600 [Oryza sativa Japonica Group] >gi|113534719|dbj|BAF07102.1|Os01g0915600 [Oryza sativa Japonica Group]	Unigene3905_All//2.00E-65//AT5G48560| basic helix-loop-helix (bHLH) family protein	Unigene3905_All//0.00E+00//TC144761	bHLH	ko04712|Circadian rhythm - plant		nr -
Unigene39051_All	783	8.82	10.87	4.01	78.76	106.91	44.30	9.29	2.46	1.27	3.02E-01	1.42E-01		-1.14E+00	1.70E-06	Down	4.41E-01	2.49E-17		-8.30E-01	1.54E-35		-1.92E+00	7.82E-18	Down	-2.87E+00	2.50E-29	Down	Unigene39051_All//gi|119331580|gb|ABL63116.1|//1.00E-74//DNA-binding protein [Catharanthus roseus]	Unigene39051_All//6.00E-57//AT1G69780| AHBH13; DNA binding / sequence-specific DNA binding / transcription factor	Unigene39051_All//0.00E+00//TC141945	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene39053_All	1268	613.70	794.61	1526.11	126.81	162.92	180.76	9.20	16.55	20.17	3.73E-01	6.13E-125		1.31E+00	0.00E+00	Up	3.61E-01	2.42E-29		5.11E-01	2.99E-55		8.46E-01	1.14E-14		1.13E+00	7.91E-29	Up	Unigene39053_All//gi|18394095|ref|NP_563944.1|//5.00E-84//SBH2 (SPHINGOID BASE HYDROXYLASE 2); catalytic/ sphingosine hydroxylase [Arabidopsis thaliana] >gi|13666750|gb|AAK32868.1|AF36185_6_1 At1g14290/F14L17_4 [Arabidopsis thaliana] >gi|24797014|gb|AAN64519.1|At1g14290/F14L17_4 [Arabidopsis thaliana]	Unigene39053_All//4.00E-70//AT1G69640| SBH1 (SPHINGOID BASE HYDROXYLASE 1); catalytic/ sphingosine hydroxylase	Unigene39053_All//0.00E+00//TC136408		ko00100|Steroid biosynthesis	GO:0009639//GO:0016491//GO:0030148//GO:0031410//GO:0043231	nr -
Unigene39054_All	807	8.04	5.27	6.53	6.67	4.01	1.96	2.41	0.57	0.99	-6.08E-01	8.41E-03		-3.00E-01	2.37E-01		-7.33E-01	2.30E-03		-1.77E+00	1.42E-10	Down	-2.08E+00	8.32E-06	Down	-1.29E+00	1.71E-03		Unigene39054_All//gi|301015573|gb|ADK47527.1|//6.00E-73//NOA1/RIF1 protein [Medicago truncatula]	Unigene39054_All//1.00E-66//AT3G47450| NOA1 (NO ASSOCIATED 1); GTPase/ nitric-oxide synthase	Unigene39054_All//0.00E+00//TC155401		ko04626|Plant-pathogen interaction//ko00330|Arginine and proline metabolism	GO:0006950//GO:0009536//GO:0009668//GO:0010565//GO:0016709//GO:0017111//GO:0042221//GO:0048827//GO:0060255	nr +
Unigene39055_All	947	9.83	4.44	7.53	1.05	1.27	1.38	1.21	1.19	0.97	-1.15E+00	4.42E-09	Down	-3.84E-01	5.62E-02		2.75E-01	7.00E-01		3.95E-01	5.45E-01		-1.67E-02	1.01E+00		-3.17E-01	5.87E-01		Unigene39055_All//gi|224054805|ref|XP_002298367.1|//8.00E-44//predicted protein [Populus trichocarpa] >gi|222845625|gb|EEE83172.1|predicted protein [Populus trichocarpa]	Unigene39055_All//2.00E-30//AT2G28780| unknown protein	Unigene39055_All//2.00E-08//TC153125				nr -
Unigene39056_All	617	3.65	0.08	0.00	4.60	1.84	5.12	74.76	76.21	21.05	-5.47E+00	1.15E-11	Down	-1.18E+01	2.68E-12	Down	-1.32E+00	1.81E-04	Down	1.55E-01	6.78E-01		2.76E-02	7.44E-01		-1.83E+00	2.39E-105	Down	Unigene39056_All//gi|57233444|gb|AAW48295.1|//1.00E-30//pore-forming toxin-like protein HFr-2 [Triticum aestivum]		Unigene39056_All//2.00E-174//TC159407				nr -
Unigene39058_All	1264	0.25	1.24	0.51	0.51	0.49	1.43	6.69	8.80	149.30	2.32E+00	1.67E-04	Up	1.03E+00	2.81E-01		-6.30E-02	9.25E-01		1.48E+00	3.49E-03		3.95E-01	1.07E-02		4.48E+00	0.00E+00	Up	Unigene39058_All//gi|259121375|gb|ACV92007.1|//8.00E-98//WRKY transcription factor 5 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene39058_All//6.00E-61//AT1G80840| WRKY40; transcription factor	Unigene39058_All//0.00E+00//gi|84149715|gb|DN781015.1|DN781015	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0010467	nr +
Unigene39059_All	1059	1.33	1.10	1.06	4.19	6.37	3.54	0.36	1.07	1.69	-2.78E-01	6.08E-01		-3.37E-01	5.79E-01		6.06E-01	5.48E-03		-2.42E-01	4.58E-01		1.57E+00	9.26E-03		2.24E+00	5.44E-06	Up	Unigene39059_All//gi|115479373|ref|NP_001063280.1|//1.00E-107//Os09g0440200 [Oryza sativa Japonica Group] >gi|113631513|dbj|BAF25194.1|Os09g0440200 [Oryza sativa Japonica Group]	Unigene39059_All//6.00E-111//AT2G26270| unknown protein	Unigene39059_All//2.00E-119//gi|164342689|gb|ES830952.1|ES830952				nr +
Unigene3906_All	1060	4.49	3.20	3.32	4.98	5.65	5.62	33.86	16.09	20.03	-4.88E-01	7.83E-02		-4.38E-01	1.37E-01		1.82E-01	5.35E-01		1.75E-01	5.46E-01		-1.07E+00	4.14E-36	Down	-7.57E-01	4.99E-21		Unigene3906_All//gi|283135892|gb|AB113537.1|//2.00E-98//theta class glutathione transferase GSTT1 [Populus trichocarpa]	Unigene3906_All//5.00E-87//AT5G41210| ATGSTT1 (GLUTATHIONE S-TRANSFERASE THETA 1); glutathione transferase	Unigene3906_All//0.00E+00//TC138117		ko00480|Glutathione metabolism//ko00350|Tyrosine metabolism		nr +

Unigene39060_All	657	3.58	2.16	1.13	5.16	3.09	2.13	8.17	4.20	11.10	-7.31E-01	7.80E-02		-1.66E+00	3.38E-04	Down	-7.38E-01	2.06E-02		-1.27E+00	1.63E-04	Down	-9.61E-01	3.30E-05		4.41E-01	1.97E-02		Unigene39060_All//gi|224094296|ref|XP_002310129.1|//3.00E-69//SET domain protein [Populus trichocarpa] >gi|222853032|gb|EEE90579.1| SET domain protein [Populus trichocarpa]	Unigene39060_All//2.00E-64//AT2G23380| CLF (CURLY LEAF); transcription factor	Unigene39060_All//0.00E+00//CO116292			GO:0001071//GO:0003006//GO:0003676//GO:0006479//GO:0009292//GO:0009887//GO:0016279//GO:0040029	nr -
Unigene39062_All	955	59.61	276.75	119.38	3.13	7.86	21.42	0.49	1.44	0.50	2.22E+00	0.00E+00	Up	1.00E+00	4.43E-80	Up	1.33E+00	2.57E-10	Up	2.78E+00	5.80E-66	Up	1.57E+00	3.34E-03		3.97E-02	9.76E-01		Unigene39062_All//gi|193806744|sp|Q9LPK5.2|CML44_ARATH//4.00E-31//RecName: Full=Probable calcium-binding protein CML44; AltName: Full=Calmodulin-like protein 44	Unigene39062_All//2.00E-29//AT1G21550| calcium-binding protein, putative	Unigene39062_All//9.00E-137//TC162383		ko04626|Plant-pathogen interaction	GO:0046872	nr +
Unigene39064_All	1281	5.19	1.98	3.08	1.09	1.48	1.06	8.19	9.98	3.39	-1.39E+00	8.92E-09	Down	-7.54E-01	1.48E-03		4.41E-01	3.93E-01		-4.18E-02	9.52E-01		2.87E-01	5.18E-02		-1.27E+00	8.99E-15	Down	Unigene39064_All//gi|224123754|ref|XP_002319156.1|//3.00E-79//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222857532|gb|EEE95079.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene39064_All//4.00E-29//AT5G19790| RAP2.11 (related to AP2 11); DNA binding / transcription factor		AP2-EREBP		GO:0006350//GO:0010468//GO:0043231	nr +
Unigene39066_All	1244	13.46	4.81	6.51	5.17	5.70	5.23	0.61	0.24	0.22	-1.49E+00	4.66E-23	Down	-1.05E+00	4.33E-13	Down	1.43E-01	5.83E-01		1.73E-02	9.56E-01		-1.38E+00	6.73E-02		-1.45E+00	4.46E-02		Unigene39066_All//gi|124360986|gb|ABN08958.1|//5.00E-84//Leucine-rich repeat; Leucine-rich repeat, cysteine-containing type [Medicago truncatula]	Unigene39066_All//2.00E-77//AT3G05660| ArRLP33 (Receptor Like Protein 33); kinase/ protein binding				GO:0003824	nr +
Unigene39068_All	1147	0.91	2.34	1.07	6.60	5.55	9.37	12.53	18.47	55.68	1.36E+00	6.75E-04	Up	2.27E-01	7.03E-01		-2.49E-01	2.79E-01		5.06E-01	3.47E-03		5.60E-01	1.37E-07		2.15E+00	4.74E-178	Up	Unigene39068_All//gi|15217736|ref|NP_176653.1|//1.00E-09//CP5 [Arabidopsis thaliana] >gi|5042409|gb|AAD32248.1|AC006193_4 Putative membrane related protein [Arabidopsis thaliana]	Unigene39068_All//5.00E-11//AT1G64720| CP5	Unigene39068_All//1.00E-124//CO111343			GO:0043231	nr +
Unigene39069_All	586	6.70	1.82	7.27	25.84	13.81	7.17	7.72	0.71	0.27	-1.88E+00	4.74E-08	Down	1.19E-01	7.03E-01		-9.04E-01	1.01E-11		-1.85E+00	1.17E-30	Down	-3.44E+00	4.10E-21	Down	-4.83E+00	1.15E-27	Down	Unigene39069_All//gi|117168149|gb|ABK32157.1|//3.00E-40//At1g61667 [Arabidopsis thaliana]	Unigene39069_All//3.00E-40//AT5G54530| unknown protein	Unigene39069_All//0.00E+00//gi|109888708|gb|DW517677.1|DW517677				nr +
Unigene39070_All	755	14.21	6.64	20.17	22.17	25.04	20.58	1.46	1.49	0.63	-1.10E+00	1.13E-09	Down	5.06E-01	6.52E-04		1.76E-01	2.16E-01		-1.08E-01	5.15E-01		3.78E-02	9.76E-01		-1.20E+00	3.41E-02		Unigene39070_All//gi|18415864|ref|NP_567651.1|//2.00E-39//AKT2/3 (ARABIDOPSIS POTASSIUM TRANSPORT 2/3); cyclic nucleotide binding / inward rectifier potassium channel/ protein binding [Arabidopsis thaliana] >gi|14887668|sp|Q38898.1|AKT2_ARATH RecName: Full=Potassium channel AKT2/3 >gi|1100898|gb|AAA97865.1| potassium channel [Arabidopsis thaliana] >gi|110739319|dbj|BAF01572.1| potassium channel [Arabidopsis thaliana]	Unigene39070_All//1.00E-31//AT4G22200| AKT2/3 (ARABIDOPSIS POTASSIUM TRANSPORT 2/3); cyclic nucleotide binding / inward rectifier potassium channel/ protein binding				GO:0005249//GO:0005515//GO:0006811//GO:0006873//GO:0009725//GO:0016020//GO:0043231	nr +
Unigene39074_All	1134	1.06	3.93	1.41	0.66	0.18	0.20	4.14	2.80	1.62	1.89E+00	5.06E-09	Up	4.09E-01	4.46E-01		-1.85E+00	2.53E-02		-1.73E+00	5.00E-02		-5.63E-01	2.39E-02		-1.36E+00	9.58E-08	Down	Unigene39074_All//gi|30687337|ref|NP_173561.2|//1.00E-13//emb2170 (embryo defective 2170) [Arabidopsis thaliana] >gi|62867637|gb|AAV17422.1| At1g21390 [Arabidopsis thaliana] >gi|89111926|gb|ABD60735.1| At1g21390 [Arabidopsis thaliana]	Unigene39074_All//9.00E-12//AT1G21390| emb2170 (embryo defective 2170)	Unigene39074_All//0.00E+00//TC147495				nr +
Unigene39076_All	1079	8.10	7.56	2.67	2.95	4.79	1.59	2.94	7.55	14.33	-9.90E-02	6.21E-01		-1.60E+00	3.87E-13	Down	6.96E-01	6.32E-03		-8.93E-01	9.76E-03		1.36E+00	1.92E-12	Up	2.29E+00	5.52E-47	Up	Unigene39076_All//gi|62566193|gb|AAX85983.1|//8.00E-98//NAC6 protein [Glycine max] >gi|66394520|gb|AAY46126.1| NAC domain protein NAC6 [Glycine max]	Unigene39076_All//4.00E-73//AT2G17040| anac036 (Arabidopsis NAC domain containing protein 36); transcription factor	Unigene39076_All//0.00E+00//CO085881	NAC		GO:0003676//GO:0010468	nr +
Unigene39077_All	1040	8.25	347.72	98.92	3.02	8.44	23.32	0.81	1.61	7.01	5.40E+00	0.00E+00	Up	3.58E+00	0.00E+00	Up	1.48E+00	4.46E-14	Up	2.95E+00	3.01E-83	Up	9.83E-01	3.14E-02		3.11E+00	3.03E-31	Up	Unigene39077_All//gi|18407444|ref|NP_566110.1|//3.00E-47//benzodiazepine receptor-related [Arabidopsis thaliana] >gi|16226870|gb|AAL16286.1|AF428356_1 At2g47770/F17A22.16 [Arabidopsis thaliana] >gi|3738290|gb|AAC03632.1| expressed protein [Arabidopsis thaliana]	Unigene39077_All//8.00E-39//AT2G47770| benzodiazepine receptor-related	Unigene39077_All//0.00E+00//TC146799			GO:0016020	nr -
Unigene39078_All	1023	0.20	0.10	1.41	5.16	0.88	3.31	6.45	4.00	19.71	-1.05E+00	5.64E-01		2.78E+00	1.05E-04	Up	-2.56E+00	8.77E-19	Down	-6.41E-01	1.32E-02		-6.87E-01	7.35E-04		1.61E+00	1.24E-38	Up	Unigene39078_All//gi|292668977|gb|ADE41143.1|//1.00E-72//AP2 domain class transcription factor [Malus x domestica]	Unigene39078_All//2.00E-22//AT3G16770| ATEBP (ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN); DNA binding / protein binding / transcription activator/ transcription factor	Unigene39078_All//0.00E+00//TC133532	AP2-EREBP		GO:0006350//GO:0050789	nr +
Unigene39079_All	913	5.27	11.27	4.96	23.35	18.10	15.63	45.57	44.41	75.23	1.10E+00	2.96E-09	Up	-8.88E-02	7.57E-01		-3.67E-01	1.10E-03		-5.79E-01	5.06E-07		-3.73E-02	6.78E-01		7.23E-01	3.12E-36		Unigene39079_All//gi|187942405|gb|ACD40011.1|//9.00E-66//pollen-specific C2 domain containing protein [Nicotiana sp. variant "Rastroensis"]	Unigene39079_All//1.00E-64//AT5G37740| C2 domain-containing protein	Unigene39079_All//0.00E+00//TC150953				nr +
Unigene3908_All	1031	7.82	3.44	4.49	4.25	4.44	3.72	2.05	1.70	3.28	-1.18E+00	2.47E-08	Down	-7.98E-01	1.74E-04		6.32E-02	8.47E-01		-1.91E-01	5.73E-01		-2.68E-01	5.40E-01		6.80E-01	1.92E-02		Unigene3908_All//gi|297799026|ref|XP_002867397.1|//2.00E-60//thioredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313233|gb|EFH43656.1| thioredoxin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3908_All//2.00E-57//AT4G29670| thioredoxin family protein	Unigene3908_All//0.00E+00//TC153511				nr -
Unigene39080_All	2136	17.46	12.98	16.70	0.09	0.35	0.15	10.99	12.64	4.74	-4.29E-01	9.20E-07		-6.44E-02	5.55E-01		1.93E+00	3.36E-02		6.66E-01	6.47E-01		2.02E-01	4.07E-02		-1.21E+00	9.34E-30	Down	Unigene39080_All//gi|15226866|ref|NP_178316.1|//1.00E-134//At1DD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding >gi|41059987|emb|CAF18564.1| ID1-like zinc finger protein 2 [Arabidopsis thaliana]	Unigene39080_All//1.00E-110//AT2G02070| AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding	Unigene39080_All//0.00E+00//TC175377	C2H2		GO:0005488	nr +
Unigene39082_All	941	1.00	0.22	0.34	3.02	2.45	1.06	3.73	4.00	2.71	-2.22E+00	6.65E-03		-1.56E+00	4.90E-02		-3.00E-01	4.59E-01		-1.51E+00	7.59E-05	Down	1.00E-01	7.41E-01		-4.61E-01	1.08E-01		Unigene39082_All//gi|16040952|dbj|BAB69683.1|//1.00E-117//receptor kinase 5 [Brassica rapa]	Unigene39082_All//4.00E-117//AT4G21380| ARK3 (A. THALIANA RECEPTOR KINASE 3); kinase/ transmembrane receptor protein serine/threonine kinase					nr -
Unigene39083_All	1816	0.00	0.06	0.12	1.23	0.70	0.85	7.64	3.91	3.03	5.80E+00	3.86E-01		6.87E+00	1.41E-01		-8.15E-01	4.54E-02		-5.46E-01	2.22E-01		-9.65E-01	3.00E-12		-1.33E+00	1.10E-20	Down	Unigene39083_All//gi|224103771|ref|XP_002313187.1|//0.00E+00//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222849595|gb|EEE87142.1| nucleobase ascorbate transporter [Populus trichocarpa]	Unigene39083_All//0.00E+00//AT1G49960| xanthine/uracil permease family protein	Unigene39083_All//0.00E+00//TC172512			GO:0005215//GO:0006810//GO:0044464	nr -
Unigene39086_All	1181	2.04	3.78	4.96	2.19	3.50	1.68	0.25	0.14	0.24	8.90E-01	2.03E-03		1.28E+00	1.15E-06	Up	6.74E-01	2.18E-02		-3.82E-01	3.76E-01		-8.24E-01	5.40E-01		-8.60E-02	9.52E-01		Unigene39086_All//gi|30694417|ref|NP_199211.2|//8.00E-89//PDLP1 (PLASMODESMATA-LOCATED PROTEIN 1) [Arabidopsis thaliana] >gi|158563851|sp|Q8GXV7.2|CRR56_ARATH RecName: Full=Cysteine-rich repeat secretory protein 56; Flags: Precursor	Unigene39086_All//4.00E-69//AT5G43980| PDLP1 (PLASMODESMATA-LOCATED PROTEIN 1)				GO:0005911//GO:0010196	nr +
Unigene39089_All	766	17.90	15.48	13.49	25.95	17.53	30.84	45.04	35.74	19.19	-2.09E-01	2.00E-01		-4.08E-01	1.07E-02		-5.66E-01	5.86E-07		2.49E-01	3.45E-02		-3.34E-01	4.57E-05		-1.23E+00	2.73E-44	Down	Unigene39089_All//gi|30983940|gb|AAP40645.1|//2.00E-76//clathrin coat assembly protein [Gossypium barbadense]	Unigene39089_All//6.00E-74//AT1G47830| clathrin coat assembly protein, putative	Unigene39089_All//0.00E+00//TC147916		ko04144|Endocytosis	GO:0005488//GO:0015031//GO:0022892//GO:0030118//GO:0043231	nr +
Unigene3909_All	987	2.86	2.46	3.94	116.44	75.15	47.73	18.93	24.10	3.87	-2.16E-01	5.90E-01		4.60E-01	1.60E-01		-6.32E-01	3.13E-46		-1.29E+00	7.61E-135	Down	3.48E-01	5.53E-04		-2.29E+00	1.47E-57	Down	Unigene3909_All//gi|224085656|ref|XP_002307652.1|//3.00E-93//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222857101|gb|EEE94648.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene3909_All//5.00E-75//AT4G28530| anac074 (Arabidopsis NAC domain containing protein 74); transcription factor	Unigene3909_All//0.00E+00//TC146830	NAC			nr -
Unigene39090_All	1276	0.00	3.49	28.67	1.02	0.78	224.44	48.87	47.69	554.59	1.18E+01	2.11E-25	Up	1.48E+01	1.15E-207	Up	-3.75E-01	5.57E-01		7.79E+00	0.00E+00	Up	-3.53E-02	6.19E-01		3.50E+00	0.00E+00	Up	Unigene39090_All//gi|268638403|gb|ACZ17543.1|//1.00E-137//oxidoreductase [Capsicum annuum]	Unigene39090_All//2.00E-132//AT3G11180| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene39090_All//0.00E+00//TC151847		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr +
Unigene39091_All	1441	0.07	0.00	0.52	2.04	0.79	0.06	14.49	5.86	4.09	-6.18E+00	3.71E-01		2.83E+00	8.52E-03		-1.37E+00	7.79E-05	Down	-5.02E+00	8.53E-16	Down	-1.31E+00	7.30E-29	Down	-1.82E+00	5.20E-48	Down	Unigene39091_All//gi|211906542|gb|ACJ11761.1|//1.00E-146//class III peroxidase [Gossypium hirsutum]	Unigene39091_All//8.00E-113//AT4G30170| peroxidase, putative	Unigene39091_All//0.00E+00//DR462751		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene39094_All	688	23.65	56.71	38.00	20.92	32.98	55.86	49.53	123.69	204.46	1.26E+00	4.13E-41	Up	6.84E-01	4.60E-10		6.57E-01	8.22E-10		1.42E+00	1.00E-51	Up	1.32E+00	7.32E-117	Up	2.05E+00	0.00E+00	Up	Unigene39094_All//gi|297843432|ref|XP_002889597.1|//6.00E-62//acyl-CoA oxidase ACX3 [Arabidopsis lyrata subsp. lyrata] >gi|297335439|gb|EFH65856.1| acyl-CoA oxidase ACX3 [Arabidopsis lyrata subsp. lyrata]	Unigene39094_All//1.00E-62//AT1G06290| ACX3 (ACYL-COA OXIDASE 3); acyl-CoA oxidase	Unigene39094_All//0.00E+00//gi|73864632|gb|DT467371.1|DT467371		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids	GO:0009062//GO:0015002//GO:0016634//GO:0030554//GO:0042579	nr -
Unigene39095_All	1187	0.18	2.22	2.33	0.80	1.28	2.78	7.73	29.40	12.49	3.65E+00	1.07E-10	Up	3.73E+00	5.55E-11	Up	6.79E-01	2.26E-01		1.80E+00	1.00E-06	Up	1.93E+00	4.79E-83	Up	6.92E-01	5.95E-08		Unigene39095_All//gi|124365521|gb|ABN09755.1|//1.00E-108//Proteinase inhibitor I4, serpin [Medicago truncatula]	Unigene39095_All//3.00E-109//AT1G55230| unknown protein	Unigene39095_All//0.00E+00//CO129484			GO:0044464	nr -
Unigene39096_All	1225	0.26	0.04	0.96	1.50	3.26	3.83	4.83	4.78	3.61	-2.63E+00	1.31E-01		1.90E+00	8.12E-03		1.12E+00	1.70E-04	Up	1.35E+00	2.24E-06	Up	-1.66E-02	9.73E-01		-4.21E-01	4.87E-02		Unigene39096_All//gi|73761689|gb|AA283344.1|//1.00E-157//ACC oxidase 3 [Gossypium hirsutum]	Unigene39096_All//7.00E-117//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene39096_All//0.00E+00//TC141644		ko00270|Cysteine and methionine metabolism		nr -
Unigene39097_All	669	71.01	30.14	14.65	35.37	31.86	26.46	67.37	12.00	15.30	-1.24E+00	1.39E-48	Down	-2.28E+00	9.62E-111	Down	-1.51E-01	2.26E-01		-4.19E-01	1.41E-04		-2.49E+00	9.97E-148	Down	-2.14E+00	1.46E-126	Down	Unigene39097_All//gi|195617694|gb|ACG30677.1|//2.00E-52//histone H4 [Zea mays]	Unigene39097_All//1.00E-37//AT5G59970| histone H4	Unigene39097_All//0.00E+00//TC164717			GO:0000785//GO:0003676//GO:0006950//GO:0009536//GO:0016020//GO:0031981//GO:0034728	nr +
Unigene39099_All	1799	7703.87	2325.53	4940.50	669.82	766.99	529.33	5.52	5.81	3.39	-1.73E+00	0.00E+00	Down	-6.41E-01	0.00E+00		1.95E-01	1.18E-60		-3.40E-01	5.10E-136		7.26E-02	6.91E-01		-7.05E-01	8.14E-06		Unigene39099_All//gi|12620883|gb|AA561121.1|AF329933_1//0.00E+00//ribulose-1,5-bisphosphate carboxylase/oxygenase activase 2 [Gossypium hirsutum]	Unigene39099_All//0.00E+00//AT2G39730| RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	Unigene39099_All//0.00E+00//TC176440		ko03050|Proteasome	GO:0005576//GO:0006952//GO:0008047//GO:0009314//GO:0009526//GO:0009534//GO:0009570//GO:0030312//GO:0032559	nr -
Unigene3910_All	421	1.74	0.96	0.63	3.31	2.29	3.43	34.85	30.68	10.03	-8.54E-01	3.05E-01		-1.46E+00	1.12E-01		-5.33E-01	3.45E-01		5.12E-02	9.45E-01		-1.84E-01	2.07E-01		-1.80E+00	2.83E-33	Down	Unigene3910_All//gi|211906506|gb|ACJ11746.1|//4.00E-25//luminal binding protein [Gossypium hirsutum]	Unigene3910_All//5.00E-25//AT5G42020| BIP2; ATP binding	Unigene3910_All//0.00E+00//TC179555		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr -

Unigene39101_All	928	8.34	2.13	3.44	4.40	2.60	8.37	2.05	1.17	1.29	-1.97E+00	4.37E-16	Down	-1.28E+00	1.62E-08	Down	-7.61E-01	7.29E-03		9.27E-01	7.29E-06		-8.08E-01	5.51E-02		-6.71E-01	9.77E-02		Unigene39101_All//gi|15226346|ref|NP_178286.1|//1.00E-109//VIT1 (vacuolar iron transporter 1); iron ion transmembrane transporter [Arabidopsis thaliana] >gi|36962697|gb|AAQ57602.1| vacuolar iron transporter [Arabidopsis thaliana] >gi|115311431|gb|AB193896.1| At2g01770 [Arabidopsis thaliana]	Unigene39101_All//7.00E-81//AT2G01770| VIT1 (vacuolar iron transporter 1); iron ion transmembrane transporter	Unigene39101_All//0.00E+00//DN781133			GO:0044464	nr -
Unigene39103_All	1069	8.61	86.74	4.03	0.37	0.26	1.82	0.08	6.84	3.88	3.33E+00	0.00E+00	Up	-1.09E+00	5.59E-08	Down	-5.33E-01	6.16E-01		2.28E+00	1.81E-05	Up	6.43E+00	4.84E-48	Up	5.61E+00	1.51E-26	Up	Unigene39103_All//gi|297827171|ref|XP_002881468.1|//2.00E-73//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327307|gb|EFH57727.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39103_All//2.00E-65//AT2G36780| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene39103_All//0.00E+00//TC132849		ko00908|Zeatin biosynthesis	GO:0009411//GO:0016128//GO:0035251//GO:0051553	nr -
Unigene39104_All	397	0.00	0.13	0.00	4.52	1.30	1.48	1.28	0.21	0.40	7.00E+00	6.16E-01		null	null		-1.80E+00	1.91E-04	Down	-1.61E+00	1.49E-03		-2.60E+00	2.05E-02		-1.67E+00	7.78E-02				Unigene39104_All//3.00E-88//gi|109888314|gb|DW517283.1|DW517283				
Unigene39105_All	739	1.13	0.96	2.74	37.14	20.46	13.69	7.44	4.86	4.15	-2.39E-01	7.25E-01		1.27E+00	8.67E-03		-8.61E-01	3.17E-19		-1.44E+00	1.38E-38	Down	-6.13E-01	6.85E-03		-8.41E-01	1.38E-04		Unigene39105_All//gi|297727037|ref|NP_001175882.1|//2.00E-20//Os09g0472700 [Oryza sativa Japonica Group] >gi|255678972|dbj|BAH94610.1| Os09g0472700 [Oryza sativa Japonica Group]	Unigene39105_All//7.00E-20//AT2G18660| EXLB3 (EXPANSIN-LIKE B3 PRECURSOR)	Unigene39105_All//0.00E+00//gi|109888314|gb|DW517283.1|DW517283				nr +
Unigene39106_All	1237	37.64	17.70	25.83	5.92	8.38	2.48	0.21	0.07	0.06	-1.09E+00	5.09E-39	Down	-5.43E-01	9.65E-12		5.01E-01	3.34E-03		-1.25E+00	9.09E-09	Down	-1.60E+00	3.10E-01		-1.67E+00	2.56E-01		Unigene39106_All//gi|297835184|ref|XP_002885474.1|//7.00E-67//CYCP2_1 [Arabidopsis lyrata subsp. lyrata] >gi|297331314|gb|EFH61733.1| CYCP2_1 [Arabidopsis lyrata subsp. lyrata]	Unigene39106_All//4.00E-60//AT3G21870| CYCP2;1 (cyclin p2;1); cyclin-dependent protein kinase	Unigene39106_All//0.00E+00//CO081350			GO:0005488//GO:0007049//GO:0016772	nr +
Unigene39107_All	461	3.63	5.28	8.20	5.19	6.27	8.92	3.94	6.89	6.91	5.39E-01	1.92E-01		1.18E+00	4.46E-04	Up	2.75E-01	5.26E-01		7.81E-01	9.29E-03		8.05E-01	9.68E-03		8.10E-01	7.14E-03		Unigene39107_All//gi|15230209|ref|NP_188511.1|//6.00E-06//protein kinase family protein [Arabidopsis thaliana]		Unigene39107_All//3.00E-150//gi|78333180|gb|DT553454.1|DT553454				nr -
Unigene39108_All	1280	1.19	0.87	0.33	6.07	2.99	1.48	4.89	1.44	1.49	-4.45E-01	3.94E-01		-1.83E+00	2.74E-03		-1.02E+00	1.29E-07	Down	-2.03E+00	4.57E-18	Down	-1.77E+00	6.99E-14	Down	-1.71E+00	9.32E-14	Down	Unigene39108_All//gi|13937145|gb|AK50066.1|AF372926.1|//1.00E-169//AT5g20410/F5O24_300 [Arabidopsis thaliana] >gi|18700258|gb|AL177739.1| AT5g20410/F5O24_300 [Arabidopsis thaliana]	Unigene39108_All//3.00E-163//AT5G20410| MGD2; 1,2-diacylglycerol 3-beta-galactosyltransferase/ UDP-galactosyltransferase/ transferase, transferring glycosyl groups	Unigene39108_All//0.00E+00//TC143721		ko00561|Glycerolipid metabolism		nr -
Unigene39109_All	1064	7.97	20.43	17.22	42.28	98.55	123.77	0.04	0.00	0.00	1.36E+00	6.17E-26	Up	1.11E+00	1.17E-15	Up	1.22E+00	1.94E-123	Up	1.55E+00	1.70E-201	Up	-5.31E+00	6.57E-01		-5.31E+00	6.12E-01		Unigene39109_All//gi|156739648|gb|ABU93483.1|//1.00E-146//xyloglucan endotraglucosylase/hydrolase [Vigna angularis]	Unigene39109_All//8.00E-138//AT2G36870| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene39109_All//0.00E+00//gi|48780358|gb|CO089724.1|CO089724				nr -
Unigene3911_All	928	34.56	42.10	16.87	139.30	91.51	110.91	287.90	252.62	64.69	2.85E-01	1.02E-03		-1.03E+00	5.16E-24	Down	-6.06E-01	2.75E-48		-3.29E-01	3.25E-14		-1.89E-01	7.58E-12		-2.15E+00	0.00E+00	Down	Unigene3911_All//gi|211906506|gb|AC111746.1|//1.00E-106//luminal binding protein [Gossypium hirsutum]	Unigene3911_All//4.00E-89//AT5G28540| BIP1; ATP binding	Unigene3911_All//0.00E+00//TC130608		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr -
Unigene39110_All	1309	28.18	15.79	19.77	20.93	19.94	9.52	0.00	0.00	0.06	-8.35E-01	3.23E-20		-5.11E-01	1.60E-08		-6.99E-02	5.82E-01		-1.14E+00	9.24E-27	Down	null	null		5.93E+00	4.04E-01		Unigene39110_All//gi|224074945|ref|XP_002304502.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222841934|gb|EEE79481.1| cytochrome P450 [Populus trichocarpa]	Unigene39110_All//4.00E-174//AT2G45970| CYP86A8; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene39110_All//0.00E+00//gi|48795256|gb|CO096570.1|CO096570		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016712	nr +
Unigene39111_All	793	16.96	14.25	22.36	23.43	21.63	50.12	20.53	24.30	35.07	-2.51E-01	1.22E-01		3.99E-01	3.81E-03		-1.16E-01	4.51E-01		1.10E+00	4.95E-36	Up	2.43E-01	3.93E-02		7.73E-01	6.05E-17		Unigene39111_All//gi|297829900|ref|XP_002882832.1|//3.00E-46//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328672|gb|EFH59091.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene39111_All//7.00E-47//AT3G13610| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene39111_All//0.00E+00//gi|13350383|gb|BG440731.1|BG440731		ko00941|Flavonoid biosynthesis	GO:0009699//GO:0012501//GO:0016705	nr +
Unigene39112_All	1033	1.87	0.10	1.24	1.93	3.00	0.96	3.36	0.89	1.70	-4.26E+00	6.09E-09	Down	-5.99E-01	2.29E-01		6.37E-01	7.31E-02		-1.00E+00	2.91E-02		-1.91E+00	7.29E-09	Down	-9.84E-01	6.39E-04		Unigene39112_All//gi|9755453|gb|AAF98214.1|AC007152_10//8.00E-57//Hypothetical protein [Arabidopsis thaliana]	Unigene39112_All//1.00E-58//AT1G67040| unknown protein					nr +
Unigene39113_All	547	4.78	3.43	1.95	5.10	6.67	2.15	3.48	4.74	10.49	-4.81E-01	2.23E-01		-1.30E+00	2.00E-03		3.88E-01	2.63E-01		-1.25E+00	9.65E-04	Down	4.46E-01	2.25E-01		1.59E+00	2.07E-11	Up	Unigene39113_All//gi|113911568|gb|AB148270.1|//2.00E-22//histidine kinase 2 [Lotus japonicus]	Unigene39113_All//1.00E-13//AT2G01830| WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase	Unigene39113_All//2.00E-25//TC152619	Orphans		GO:0006468//GO:0006952//GO:0009267//GO:0009744//GO:0009755//GO:0009784//GO:0009845//GO:0010015//GO:0010260//GO:0015698//GO:0016791//GO:0019901//GO:0023060//GO:2000026	nr -
Unigene39114_All	759	0.21	0.73	0.14	2.56	1.32	0.71	3.73	3.80	6.67	1.83E+00	9.02E-02		-5.60E-01	7.75E-01		-9.60E-01	3.00E-02		-1.84E+00	1.99E-04	Down	2.58E-02	9.68E-01		8.37E-01	3.11E-04		Unigene39114_All//gi|113911568|gb|AB148270.1|//2.00E-42//histidine kinase 2 [Lotus japonicus]	Unigene39114_All//6.00E-31//AT2G01830| WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase	Unigene39114_All//4.00E-52//TC152619	Orphans		GO:0006351//GO:0006468//GO:0006952//GO:0009267//GO:0009744//GO:0009755//GO:0009784//GO:0009845//GO:0010015//GO:0010260//GO:0015698//GO:0016791//GO:0019901//GO:0023060//GO:0032559//GO:0044464//GO:2000026	nr -
Unigene39115_All	1211	11.02	5.06	6.64	26.82	25.79	12.83	0.42	0.14	0.26	-1.12E+00	2.96E-12	Down	-7.31E-01	4.75E-06		-5.64E-02	6.17E-01		-1.06E+00	1.77E-28	Down	-1.60E+00	1.07E-01		-6.71E-01	4.48E-01		Unigene39115_All//gi|45752754|gb|AS76275.1|//2.00E-37//At4g21500 [Arabidopsis thaliana]	Unigene39115_All//4.00E-16//AT4G21500| unknown protein					nr -
Unigene39116_All	1126	4.55	14.44	13.71	24.29	40.64	37.90	0.60	0.67	0.07	1.67E+00	3.43E-26	Up	1.59E+00	1.30E-22	Up	7.43E-01	6.50E-24		6.42E-01	6.98E-16		1.53E-01	8.31E-01		-3.09E+00	1.45E-03		Unigene39116_All//gi|15229310|ref|NP_187101.1|//2.00E-75//LSH2 (LIGHT SENSITIVE HYPOCOTYLS 2) [Arabidopsis thaliana]	Unigene39116_All//6.00E-53//AT5G28490| LSH1 (LIGHT-DEPENDENT SHORT HYPOCOTYLS 1)	Unigene39116_All//1.00E-22//ES798424			GO:0000902//GO:0009536//GO:0009639	nr +
Unigene39117_All	965	1.08	4.31	3.53	2.94	2.46	4.73	0.92	2.51	2.44	1.99E+00	5.37E-09	Up	1.70E+00	5.79E-06	Up	-2.57E-01	5.38E-01		6.84E-01	1.60E-02		1.45E+00	1.39E-04	Up	1.40E+00	1.92E-04	Up	Unigene39117_All//gi|14030731|gb|AK53040.1|AF375456_1//1.00E-96//AT5g65380/MXA5_11 [Arabidopsis thaliana] >gi|23506079|gb|AAN28899.1| At5g65380/MXA5_11 [Arabidopsis thaliana]	Unigene39117_All//5.00E-98//AT5G65380| ripening-responsive protein, putative	Unigene39117_All//0.00E+00//TC164998			GO:0003006//GO:0015291//GO:0015893//GO:0044464	nr +
Unigene39118_All	1964	2.80	1.44	2.09	4.41	3.49	5.89	8.40	3.83	4.67	-9.53E-01	1.98E-04		-4.22E-01	1.23E-01		-3.39E-01	8.55E-02		4.16E-01	1.38E-02		-1.13E+00	1.80E-18	Down	-8.48E-01	3.98E-12		Unigene39118_All//gi|297597139|ref|NP_001043490.2|//4.00E-24//Os01g0600300 [Oryza sativa Japonica Group] >gi|255673428|dbj|BAF05404.2| Os01g0600300 [Oryza sativa Japonica Group]	Unigene39118_All//2.00E-33//AT5G11780| unknown protein	Unigene39118_All//0.00E+00//CO498236				nr -
Unigene39119_All	802	6.33	2.08	2.99	24.72	12.71	11.43	1.21	1.93	4.52	-1.60E+00	2.69E-08	Down	-1.08E+00	1.19E-04	Down	-9.60E-01	8.80E-17		-1.11E+00	6.88E-19	Down	6.69E-01	1.65E-01		1.90E+00	2.37E-09	Up	Unigene39119_All//gi|60617257|gb|AX31277.1|//2.00E-80//MLO1 [Capsicum annuum]	Unigene39119_All//6.00E-64//AT1G61560| MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding	Unigene39119_All//0.00E+00//gi|3325743|gb|AI054629.1|AI054629			GO:0009987//GO:0010260//GO:0031224//GO:0050832	nr +
Unigene3912_All	505	3.94	2.61	5.59	5.62	6.34	7.24	6.45	5.13	3.00	-5.94E-01	1.98E-01		5.05E-01	2.05E-01		1.74E-01	6.65E-01		3.66E-01	3.02E-01		-3.29E-01	3.20E-01		-1.10E+00	2.52E-04	Down	Unigene3912_All//gi|18410289|ref|NP_565057.1|//7.00E-07//BNS (BONSAI) [Arabidopsis thaliana] >gi|90862932|gb|ABE02390.1| At1g73177 [Arabidopsis thaliana]	Unigene3912_All//4.00E-08//AT1G73177| BNS (BONSAI)	Unigene3912_All//3.00E-52//TC161720				nr -
Unigene39120_All	1489	0.46	0.00	0.07	6.76	3.40	1.58	4.57	1.77	0.86	-8.84E+00	4.10E-04	Down	-2.68E+00	1.69E-02		-9.91E-01	3.24E-09		-2.10E+00	3.41E-24	Down	-1.37E+00	1.24E-10	Down	-2.42E+00	7.24E-23	Down	Unigene39120_All//gi|9989054|gb|AAG10817.1|AC011808_5//7.00E-78//Putative retroelement polyprotein [Arabidopsis thaliana]	Unigene39120_All//2.00E-68//AT4G23160| protein kinase family protein	Unigene39120_All//0.00E+00//AI725813			GO:0005488	nr -
Unigene39123_All	738	7.09	10.02	9.60	13.50	8.73	11.02	12.95	3.45	5.56	5.00E-01	2.07E-02		4.37E-01	6.12E-02		-6.30E-01	1.78E-04		-2.93E-01	1.32E-01		-1.91E+00	5.47E-23	Down	-1.22E+00	9.83E-13	Down	Unigene39123_All//gi|3759177|dbj|BAA33806.1|//4.00E-57//3-phosphoserine phosphatase [Arabidopsis thaliana] >gi|3759179|dbj|BAA33807.1| 3-phosphoserin phosphatase [Arabidopsis thaliana]	Unigene39123_All//2.00E-58//AT1G18640| PSP (3-PHOSPHOSERINE PHOSPHATASE); phosphoserine phosphatase	Unigene39123_All//0.00E+00//gi|11207133|gb|BF276063.1|BF276063		ko00260|Glycine, serine and threonine metabolism	GO:0006563//GO:0009536//GO:0016791	nr +
Unigene39124_All	1080	0.87	0.84	0.00	10.56	4.43	4.01	3.01	3.87	1.29	-4.62E-02	9.60E-01		-9.77E+00	3.34E-05	Down	-1.25E+00	5.36E-15	Down	-1.40E+00	1.29E-15	Down	3.61E-01	2.00E-01		-1.22E+00	6.24E-05	Down	Unigene39124_All//gi|15220238|ref|NP_174819.1|//5.00E-19//VQ motif-containing protein [Arabidopsis thaliana]	Unigene39124_All//1.00E-18//AT1G35830| VQ motif-containing protein	Unigene39124_All//1.00E-65//gi|48777327|gb|CO086693.1|CO086693				nr +
Unigene39125_All	896	4.03	11.14	5.88	4.95	14.91	3.58	0.57	0.51	1.25	1.47E+00	9.99E-14	Up	5.46E-01	4.56E-02		1.59E+00	1.81E-23	Up	-4.67E-01	1.18E-01		-1.42E-01	8.76E-01		1.14E+00	4.43E-02									
Unigene39126_All	530	1.18	3.73	4.42	3.48	5.33	14.74	2.87	2.92	9.25	1.65E+00	8.01E-04	Up	1.90E+00	6.83E-05	Up	6.15E-01	1.04E-01		2.08E+00	2.67E-18	Up	2.29E-02	9.96E-01		1.69E+00	1.23E-10	Up			Unigene39126_All//2.00E-71//TC148214				
Unigene39127_All	791	5.16	5.51	4.38	40.49	30.87	25.07	12.88	4.44	5.14	9.46E-02	7.44E-01		-2.38E-01	4.70E-01		-3.92E-01	8.54E-06		-6.92E-01	8.44E-14		-1.54E+00	2.77E-18	Down	-1.33E+00	2.75E-15	Down	Unigene39127_All//gi|44681464|gb|AS47672.1|//3.00E-36//At3g06145 [Arabidopsis thaliana]	Unigene39127_All//2.00E-37//AT3G06145| unknown protein	Unigene39127_All//0.00E+00//TC168638				nr +
Unigene39129_All	891	17.09	14.73	7.53	20.07	20.75	22.35	18.17	16.65	16.45	-2.14E-01	1.58E-01		-1.18E+00	2.26E-14	Down	4.83E-02	7.97E-01		1.55E-01	2.78E-01		-1.26E-01	3.93E-01		-1.44E-01	2.87E-01		Unigene39129_All//gi|20198239|gb|AD26906.2|//5.00E-52//expressed protein [Arabidopsis thaliana]	Unigene39129_All//8.00E-21//AT2G18270| unknown protein	Unigene39129_All//0.00E+00//TC151947		ko03040|Spliceosome		nr -
Unigene39130_All	810	5.04	2.75	1.91	5.60	5.82	10.98	97.30	31.94	53.12	-8.72E-01	3.89E-03		-1.40E+00	1.92E-05	Down	5.76E-02	8.60E-01		9.73E-01	4.13E-07		-1.61E+00	2.23E-145	Down	-8.73E-01	2.59E-57		Unigene39130_All//gi|38184116|gb|AAD03487.1|//9.00E-56//proline-rich cell wall protein [Medicago sativa]	Unigene39130_All//1.00E-27//AT3G22142| structural constituent of cell wall	Unigene39130_All//2.00E-51//gi|109838930|gb|DW237491.1|DW237491			GO:0006810	nr +
Unigene39132_All	909	0.81	0.11	0.82	17.32	8.45	10.48	5.77	5.61	10.47	-2.85E+00	6.26E-03		2.54E-02	9.95E-01		-1.04E+00	3.58E-15	Down	-7.24E-01	1.21E-07		-4.01E-02	8.85E-01		8.61E-01	1.66E-07		Unigene39132_All//gi|15235604|ref|NP_195470.1|//3.00E-51//LBD39 (LOB DOMAIN-CONTAINING PROTEIN 39) [Arabidopsis thaliana] >gi|29428053|sp|Q8GZE8.1|LBD39_ARATH RecName: Full=LOB domain-containing protein 39; AltName: Full=ASYMMETRIC LEAVES 2-like protein 41; Short=AS2-like protein 41 >gi|219807158|dbj|BAH10585.1| ASYMMETRIC LEAVES2-like 41 protein [Arabidopsis thaliana]	Unigene39132_All//2.00E-50//AT4G37540| LBD39 (LOB DOMAIN-CONTAINING PROTEIN 39)	Unigene39132_All//0.00E+00//TC170004		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene39133_All	1367	1.00	0.96	1.21	5.58	3.98	4.10	3.77	1.41	2.21	-4.63E-02	9.46E-01		2.79E-01	6.20E-01		-4.86E-01	1.64E-02		-4.45E-01	3.86E-02		-1.42E+00	1.09E-08	Down	-7.69E-01	7.33E-04		Unigene39133_All//gi|148611499|gb|ABQ95989.1|//1.00E-126//phospholipase A1 [Capsicum annuum]	Unigene39133_All//3.00E-121//AT2G31100| triacylglycerol lipase					nr +
Unigene39134_All	1082	0.10	1.36	0.49	4.01	5.51	5.01	2.81	10.16	4.60	3.81E+00	2.22E-06	Up	2.35E+00	5.87E-02		4.59E-01	6.03E-02		3.23E-01	2.47E-01		1.85E+00	2.64E-25	Up	7.10E-01	2.27E-03		Unigene39134_All//gi|163889364|gb|ABY48134.1|//1.00E-71//bHLH transcription factor [Medicago truncatula]	Unigene39134_All//1.00E-52//AT5G65640| bHLH093 (beta HLH protein 93); DNA binding / transcription factor	Unigene39134_All//0.00E+00//TC179415	bHLH	ko04626|Plant-pathogen interaction		nr -

Unigene39136_All	805	25.41	11.90	20.24	37.99	34.48	25.13	56.88	20.98	22.76	-1.10E+00	1.04E-17	Down	-3.28E-01	1.10E-02		-1.40E-01	1.95E-01		-5.96E-01	2.83E-10		-1.44E+00	4.05E-72	Down	-1.32E+00	3.08E-65	Down	Unigene39136_All//gi|115447137|ref|NP_001047348.1|//2.00E-56//0s02g0601300 [Oryza sativa Japonica Group] >gi|113536879|dbj|BAF09262.1| Os02g0601300 [Oryza sativa Japonica Group] >gi|119434402|gb|ABL75274.1| glyceralde-3-phosphate dehydrogenase [Oryza sativa]	Unigene39136_All//3.00E-55//AT3G04120| GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)// glyceraldehyde-3-phosphate dehydrogenase	Unigene39136_All//0.00E+00//gi|73850518|gb|DT459538.1|DT459538		ko00010|Glycolysis / Gluconeogenesis	GO:0000166//GO:0006007//GO:0008943//GO:0044424	nr +
Unigene39137_All	810	38.56	19.08	31.23	35.24	33.37	19.68	42.65	22.65	12.69	-1.02E+00	1.26E-23	Down	-3.04E-01	2.77E-03		-7.85E-02	5.47E-01		-8.40E-01	4.40E-17		-9.13E-01	9.20E-27		-1.75E+00	2.24E-74	Down	Unigene39137_All//gi|297819918|ref|XP_002877842.1|//1.00E-54//ATRPB13.6 [Arabidopsis lyrata subsp. lyrata] >gi|297323680|gb|EFH54101.1| ATRPB13.6 [Arabidopsis lyrata subsp. lyrata]	Unigene39137_All//3.00E-55//AT3G52090| NRP811; DNA binding / DNA-directed RNA polymerase	Unigene39137_All//0.00E+00//TC163646		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003676//GO:0005515//GO:0010467//GO:0016591//GO:0034062//GO:0005029	nr +
Unigene39138_All	820	1.91	0.12	0.26	2.79	5.84	2.20	4.59	7.08	6.95	-3.95E+00	5.06E-07	Down	-2.88E+00	3.27E-05	Down	1.06E+00	6.34E-05	Up	-3.43E-01	4.58E-01		6.27E-01	4.30E-03		5.98E-01	5.51E-03		Unigene39138_All//gi|302142043|emb|CBI19246.3|//7.00E-06//unnamed protein product [Vitis vinifera]		Unigene39138_All//0.00E+00//TC143597				nr -
Unigene39139_All	590	7.09	43.63	13.27	32.67	27.72	34.45	14.48	17.00	13.03	2.62E+00	7.99E-73	Up	9.03E-01	3.14E-05		-2.37E-01	6.61E-02		7.62E-02	6.42E-01		2.32E-01	1.87E-01		-1.52E-01	4.28E-01		Unigene39139_All//gi|255555923|ref|XP_002518997.1|//3.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223541984|gb|EEF43530.1| conserved hypothetel protein [Ricinus communis]		Unigene39139_All//0.00E+00//TC175110				nr +
Unigene3914_All	747	17.02	13.84	15.83	14.94	11.29	13.97	15.40	9.46	7.57	-2.99E-01	6.77E-02		-1.05E-01	5.87E-01		-4.03E-01	1.42E-02		-9.70E-02	6.29E-01		-7.03E-01	2.46E-06		-1.02E+00	1.22E-11	Down	Unigene3914_All//gi|18410289|ref|NP_565057.1|//3.00E-22//BNS (BONSAI) [Arabidopsis thaliana] >gi|90962932|gb|ABE02390.1| At1g73177 [Arabidopsis thaliana]	Unigene3914_All//1.00E-15//AT1G73177| BNS (BONSAI)	Unigene3914_All//0.00E+00//TC161720		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene39141_All	1553	0.07	0.20	0.00	1.06	2.68	2.79	16.33	7.51	13.98	1.54E+00	3.23E-01		-6.07E+00	3.93E-01		1.34E+00	5.18E-06	Up	1.40E+00	3.14E-06	Up	-1.12E+00	1.45E-27	Down	-2.25E-01	2.14E-02		Unigene39141_All//gi|15218391|ref|NP_177366.1|//4.00E-82//basic helix-loop-helix (bHLH) family protein (bHLH096) [Arabidopsis thaliana] >gi|75308860|sp|Q9C774.1|BH096_ARATH RecName: Full=Transcription factor bHLH96; AltName: Full=Transcription factor EN 15; AltName: Full=bHLH transcription factor bHLH096; AltName: Full=Basic helix-loop-helix protein 96; Short=bHLH 96; Short=AtbHLH96 >gi|20520637|emb|CAD30833.1| basic-helix-loop-helix transcription factor [Arabidopsis thaliana]	Unigene39141_All//5.00E-72//AT1G72210| basic helix-loop-helix (bHLH) family protein (bHLH096)	Unigene39141_All//0.00E+00//gi|78337922|gb|DT558196.1|DT558196	bHLH	ko04626|Plant-pathogen interaction	GO:0010468//GO:0043231	nr -
Unigene39142_All	1578	1.29	2.25	0.57	12.88	13.16	8.47	4.21	1.54	1.31	7.98E-01	1.48E-02		-1.17E+00	1.47E-02		3.09E-02	8.30E-01		-6.04E-01	3.29E-07		-1.45E+00	2.82E-11	Down	-1.68E+00	3.36E-14	Down	Unigene39142_All//gi|30102530|gb|AAP21183.1|//3.00E-83//At1g72880 [Arabidopsis thaliana]	Unigene39142_All//2.00E-75//AT1G72880| acid phosphatase survival protein SurE, putative	Unigene39142_All//0.00E+00//TC161887		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00760|Nicotinate and nicotinamide metabolism	GO:0008252//GO:0043231	nr -
Unigene39144_All	856	2.02	2.31	0.68	5.59	5.91	4.48	7.51	1.61	2.09	1.95E-01	6.59E-01		-1.56E+00	4.51E-03		8.20E-02	8.21E-01		-3.17E-01	2.94E-01		-2.22E+00	5.89E-19	Down	-1.84E+00	1.53E-15	Down	Unigene39144_All//gi|3551257|dbj|BAA32827.1|//7.00E-11//98b [Daucus carota]	Unigene39144_All//1.00E-09//AT5G01910| unknown protein	Unigene39144_All//0.00E+00//gi|164252443|gb|ES810271.1|ES810271				nr +
Unigene39146_All	604	3.90	3.19	0.62	3.79	3.31	2.47	12.74	3.74	2.90	-2.90E-01	4.94E-01		-2.66E+00	5.47E-07	Down	-1.98E-01	6.53E-01		-6.21E-01	1.51E-01		-1.77E+00	6.20E-17	Down	-2.13E+00	3.19E-22	Down	Unigene39146_All//gi|297850248|ref|XP_002893005.1|//2.00E-15//3-phosphoserine phosphatase [Arabidopsis lyrata subsp. lyrata] >gi|297338847|gb|EFH69264.1| 3-phosphoserine phosphatase [Arabidopsis lyrata subsp. lyrata]	Unigene39146_All//2.00E-16//AT1G18640| PSP (3-PHOSPHOSERINE PHOSPHATASE); phosphoserine phosphatase	Unigene39146_All//0.00E+00//TC170559		ko00260|Glycine, serine and threonine metabolism	GO:0006563//GO:0009536//GO:0016791	nr -
Unigene39147_All	762	5.56	4.26	3.35	5.69	4.16	4.68	5.72	3.73	2.82	-3.86E-01	2.05E-01		-7.30E-01	1.80E-02		-4.52E-01	1.19E-01		-2.81E-01	3.98E-01		-6.16E-01	1.78E-02		-1.02E+00	6.49E-05	Down	Unigene39147_All//gi|91107221|gb|ABE11612.1|//4.00E-42//SWIb domain-containing protein [Solanum chacoense]	Unigene39147_All//2.00E-40//AT4G26810| SWIB complex BAF60b domain-containing protein	Unigene39147_All//0.00E+00//gi|109878079|gb|DW507052.1|DW507052				nr +
Unigene39148_All	764	6.64	3.12	7.46	2.93	4.55	3.55	1.00	0.27	0.99	-1.09E+00	5.58E-05	Down	1.67E-01	5.58E-01		6.34E-01	5.49E-02		2.74E-01	5.28E-01		-1.86E+00	1.82E-02		-7.70E-03	9.84E-01		Unigene39148_All//gi|15231226|ref|NP_190160.1|//7.00E-75//hydrolase family protein / HAD-superfamily protein [Arabidopsis thaliana]	Unigene39148_All//9.00E-76//AT3G45740| hydrolase family protein / HAD-superfamily protein	Unigene39148_All//5.00E-98//TC134345			GO:0003824//GO:0043231//GO:0046914	nr +
Unigene39149_All	822	7.07	13.44	13.99	13.45	36.19	31.15	21.09	14.03	15.85	9.28E-01	1.04E-07		9.86E-01	2.17E-08		1.43E+00	1.87E-44	Up	1.21E+00	2.60E-27	Up	-5.88E-01	7.24E-07		-4.12E-01	3.80E-04		Unigene39149_All//gi|95103172|gb|ABF51526.1|//8.00E-71//MADS box transcription factor [Populus tomentosa]	Unigene39149_All//1.00E-45//AT4G11880| AGL14 (agamous-like 14); DNA binding / transcription factor	Unigene39149_All//0.00E+00//CO074529	MADS		GO:0001071//GO:0003677//GO:0006351//GO:0009409//GO:0010468//GO:0043231//GO:0048506	nr +
Unigene3915_All	1012	10.86	11.92	5.52	20.97	15.52	15.40	25.23	11.19	12.95	1.34E-01	4.53E-01		-9.75E-01	6.85E-08		-4.35E-01	8.81E-05		-4.46E-01	1.32E-04		-1.17E+00	9.36E-30	Down	-9.62E-01	1.96E-22		Unigene3915_All//gi|195625786|gb|CG34723.1|//1.00E-112//seven transmembrane domain protein [Zea mays]	Unigene3915_All//5.00E-113//AT1G47640| unknown protein	Unigene3915_All//0.00E+00//TC139119				nr -
Unigene39150_All	1534	0.00	0.63	0.35	3.90	4.09	4.36	9.10	4.85	10.80	9.29E+00	1.38E-05	Up	8.44E+00	4.04E-03		6.82E-02	8.42E-01		1.61E-01	5.57E-01		-9.07E-01	3.41E-11		2.48E-01	4.43E-02		Unigene39150_All//gi|53857147|gb|AAP03880.2|//1.00E-149//Avr9/Cf-9 induced kinase 1 [Nicotiana tabacum]	Unigene39150_All//3.00E-133//AT2G05940| protein kinase, putative	Unigene39150_All//0.00E+00//TC154062				nr +
Unigene39152_All	1452	16.47	5.03	6.23	11.25	9.96	9.64	10.66	5.73	8.92	-1.71E+00	6.08E-40	Down	-1.40E+00	8.48E-29	Down	-1.76E-01	2.47E-01		-2.23E-01	1.36E-01		-8.96E-01	4.42E-12		-2.57E-01	4.39E-02		Unigene39152_All//gi|297847266|ref|XP_002891514.1|//4.00E-71//EMB1273 [Arabidopsis lyrata subsp. lyrata] >gi|297337356|gb|EFH67773.1| EMB1273 [Arabidopsis lyrata subsp. lyrata]	Unigene39152_All//6.00E-64//AT1G49510| emb1273 (embryo defective 1273)	Unigene39152_All//0.00E+00//TC133159			GO:0003006	nr +
Unigene39154_All	808	1.23	3.76	0.92	1.42	0.94	0.89	2.04	4.24	5.52	1.61E+00	2.70E-05	Up	-4.15E-01	5.72E-01		-5.97E-01	3.41E-01		-6.65E-01	3.16E-01		1.06E+00	4.48E-04	Up	1.44E+00	6.56E-08	Up	Unigene39154_All//gi|238478527|ref|NP_001154349.1|//4.00E-22//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|259016409|sp|P0CSE2.2|Y1839_ARATH RecName: Full=Probable serine/threonine-protein kinase At1g18390; Flags: Precursor	Unigene39154_All//1.00E-19//AT1G18390| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase				GO:0016301	nr -
Unigene39155_All	1014	1.96	0.75	0.63	2.90	4.25	2.67	4.63	1.36	2.55	-1.39E+00	3.51E-03		-1.64E+00	1.31E-03		5.51E-01	6.02E-02		-1.17E-01	7.57E-01		-1.77E+00	1.33E-10	Down	-8.58E-01	3.74E-04		Unigene39155_All//gi|116047949|gb|ABJ53200.1|//1.00E-109//myosin VIII-1 [Nicotiana benthamiana]	Unigene39155_All//4.00E-99//AT3G19960| ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor	Unigene39155_All//0.00E+00//TC157476			GO:0015405//GO:0015629//GO:0016020//GO:0017111//GO:0030029//GO:0003259//GO:0044444	nr -
Unigene39158_All	833	4.21	7.60	1.92	11.72	7.19	7.86	4.06	2.26	1.00	8.53E-01	2.93E-04		-1.13E+00	1.16E-03		-7.04E-01	3.16E-05		-5.76E-01	1.40E-03		-8.47E-01	4.71E-03		-2.02E+00	1.48E-09	Down			Unigene39158_All//0.00E+00//DR461340				
Unigene39159_All	1674	0.09	3.42	0.06	0.12	1.05	1.24	5.91	4.42	16.99	5.19E+00	3.23E-28	Up	-5.61E-01	7.75E-01		3.14E+00	4.78E-07	Up	3.38E+00	2.14E-08	Up	-4.19E-01	1.08E-02		1.52E+00	5.58E-50	Up	Unigene39159_All//gi|224127045|ref|XP_002329370.1|//1.00E-126//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222870420|gb|EEF07551.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene39159_All//8.00E-58//AT2G20880| AP2 domain-containing transcription factor, putative	Unigene39159_All//1.00E-44//CO106720	AP2-EREBP		GO:0006350//GO:0010468//GO:0043231	nr +
Unigene3916_All	1476	5.53	1.03	1.05	7.76	5.18	6.61	3.67	1.08	2.40	-2.42E+00	1.02E-21	Down	-2.40E+00	1.50E-20	Down	-5.84E-01	1.73E-04		-2.32E-01	2.13E-01		-1.77E+00	3.96E-12	Down	-6.10E-01	5.76E-03		Unigene3916_All//gi|15223910|ref|NP_172934.1|//1.00E-165//semialdehyde dehydrogenase family protein [Arabidopsis thaliana] >gi|17979524|gb|AAL50097.1| At1g14810/F1O86_6 [Arabidopsis thaliana] >gi|20856224|gb|AAM26654.1| At1g14810/F1O86_6 [Arabidopsis thaliana]	Unigene3916_All//3.00E-161//AT1G14810| semialdehyde dehydrogenase family protein	Unigene3916_All//0.00E+00//gi|78334145|gb|DT554419.1|DT554419		ko00270|Cysteine and methionine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00300|Lysine biosynthesis		nr +
Unigene39160_All	1760	0.56	0.75	0.61	2.07	1.64	2.16	11.41	25.34	21.68	4.06E-01	4.87E-01		9.94E-02	8.79E-01		-3.30E-01	3.22E-01		6.10E-02	8.72E-01		1.15E+00	8.66E-50	Up	9.26E-01	6.85E-31		Unigene39160_All//gi|297827551|ref|XP_002881658.1|//1.00E-38//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327497|gb|EFH57917.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39160_All//8.00E-35//AT2G39490| F-box family protein	Unigene39160_All//0.00E+00//ES810677				nr +
Unigene39163_All	1693	1.92	1.17	1.82	16.80	7.85	5.12	14.51	12.52	12.02	-7.15E-01	3.73E-02		-7.08E-02	8.43E-01		-1.10E+00	8.62E-30	Down	-1.71E+00	1.93E-51	Down	-2.13E-01	4.06E-02		-2.71E-01	5.50E-03		Unigene39163_All//gi|30692538|gb|AAP33475.1|//0.00E+00//polygalacturonase-like protein [Fragaria x ananassa]	Unigene39163_All//0.00E+00//AT3G61490| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene39163_All//0.00E+00//CO132686		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004553//GO:0030312//GO:0044238//GO:0045229	nr -
Unigene39164_All	1115	1.50	0.23	0.67	2.99	3.49	2.92	3.68	0.45	2.50	-2.72E+00	1.40E-05	Down	-1.17E+00	3.09E-02		2.21E-01	5.58E-01		-3.75E-02	9.33E-01		-3.03E+00	3.64E-17	Down	-5.56E-01	3.20E-02		Unigene39164_All//gi|18087521|gb|AAL58895.1|AF462799_1/3.00E-28//AT3g17120/K14A17_24 [Arabidopsis thaliana]	Unigene39164_All//2.00E-11//AT3G17120| unknown protein	Unigene39164_All//0.00E+00//ES817020				nr +
Unigene39165_All	1432	0.95	1.27	0.45	3.17	3.46	3.88	15.94	11.53	40.87	4.23E-01	3.85E-01		-1.09E+00	7.48E-02		1.30E-01	6.93E-01		2.93E-01	2.99E-01		-4.68E-01	4.39E-06		1.36E+00	6.27E-86	Up	Unigene39165_All//gi|115472321|ref|NP_001059759.1|//3.00E-95//Os07g0511000 [Oryza sativa Japonica Group] >gi|113611295|dbj|BAF21673.1| Os07g0511000 [Oryza sativa Japonica Group]	Unigene39165_All//1.00E-114//AT5G55060| unknown protein	Unigene39165_All//3.00E-76//gi|78346556|gb|DT566830.1|DT566830			GO:0043231	nr -
Unigene39166_All	1251	6.82	4.05	2.30	10.19	6.06	10.72	13.32	6.21	9.62	-7.51E-01	1.48E-04		-1.57E+00	1.88E-12	Down	-7.51E-01	2.22E-07		7.29E-02	6.72E-01		-1.10E+00	7.82E-18	Down	-4.70E-01	7.23E-05		Unigene39166_All//gi|18398935|ref|NP_565446.1|//1.00E-113//metaxin-related [Arabidopsis thaliana] >gi|3176710|gb|AAD12026.1| expressed protein [Arabidopsis thaliana] >gi|17979483|gb|AAL50078.1| At2g19080/T20K24.9 [Arabidopsis thaliana] >gi|22655436|gb|AAM98310.1| At2g19080/T20K24.9 [Arabidopsis thaliana]	Unigene39166_All//1.00E-88//AT2G19080| metaxin-related	Unigene39166_All//0.00E+00//TC153976				nr +

Unigene39167_All	1333	0.00	0.00	0.40	0.82	0.39	14.03	36.00	16.77	180.30	null	null		8.64E+00	4.04E-03		-1.09E+00	8.45E-02		4.09E+00	4.56E-85	Up	-1.10E+00	5.23E-50	Down	2.32E+00	0.00E+00	Up	Unigene39167_All//gi|15219988|ref|NP_173145.1|//5.00E-91//SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors [Arabidopsis thaliana] >gi|75220747|sp|Q8W224.1|SRG1_ARATH RecName: Full=Protein SRG1; Short=AtSRG1; AltName: Full=Protein SENESCENCE-RELATED GENE 1 >gi|5734767|gb|AAD50032.1|AC007651_27 SRG1 Protein [Arabidopsis thaliana] >gi|479047|emb|CAA55654.1| SRG1 [Arabidopsis thaliana] >gi|15081819|gb|AAK82564.1|F6I1.30/F6I1.30 [Arabidopsis thaliana] >gi|22655018|gb|AAM98100.1|At1g17020/F6I1.30 [Arabidopsis thaliana]	Unigene39167_All//6.00E-88//AT1G17020| SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc	Unigene39167_All//0.00E+00//DW513674		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr +
Unigene39170_All	710	3.32	7.14	6.68	3.44	6.64	13.55	2.86	1.82	5.84	1.11E+00	4.94E-05	Up	1.01E+00	5.13E-04	Up	9.51E-01	3.68E-04		1.98E+00	5.24E-21	Up	-6.47E-01	1.15E-01		1.03E+00	9.34E-05	Up			Unigene39170_All//0.00E+00//TC178064				
Unigene39172_All	905	30.81	44.62	77.32	89.34	101.25	176.76	243.26	418.47	249.46	5.34E-01	2.00E-10		1.33E+00	4.48E-77	Up	1.81E-01	5.84E-04		9.85E-01	1.65E-120		7.83E-01	1.23E-219		3.63E-02	3.12E-01		Unigene39172_All//gi|224126143|ref|XP_002319765.1|//1.00E-102//hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase-like protein [Populus trichocarpa] >gi|222858141|gb|EEE95688.1|hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase-like protein [Populus trichocarpa]	Unigene39172_All//1.00E-78//AT5G17540| transferase family protein	Unigene39172_All//0.00E+00//gi|109848982|gb|DW477961.1|DW477961		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016413	nr +
Unigene39173_All	868	32.25	66.26	25.21	10.96	10.79	20.08	4.82	20.95	22.21	1.04E+00	2.40E-44	Up	-3.55E-01	9.08E-04		-2.26E-02	9.14E-01		8.74E-01	3.06E-11		2.12E+00	2.99E-49	Up	2.20E+00	6.74E-56	Up	Unigene39173_All//gi|35187445|gb|AQ84314.1|//1.00E-41//fiber protein Fb25 [Gossypium barbadense]	Unigene39173_All//2.00E-22//AT5G43260| chaperone protein dnaJ-related	Unigene39173_All//0.00E+00//TC157618			GO:0005515//GO:0044267	nr +
Unigene39174_All	535	54.57	93.29	66.59	71.97	94.29	150.09	34.22	25.55	41.10	7.74E-01	9.34E-24		2.87E-01	2.44E-03		3.90E-01	1.46E-08		1.06E+00	1.76E-68	Up	-4.22E-01	2.61E-04		2.65E-01	1.13E-02		Unigene39174_All//gi|297847712|ref|XP_002891737.1|//2.00E-34//sodium/calcium exchanger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337579|gb|EFH67996.1|sodium/calcium exchanger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39174_All//3.00E-33//AT1G53210| sodium/calcium exchanger family protein / calcium-binding EF hand family protein	Unigene39174_All//0.00E+00//TC171858			GO:0005773//GO:0000810//GO:0031090//GO:0031224//GO:0046872	nr +
Unigene39175_All	1032	4.97	2.01	2.99	7.00	5.64	4.38	3.32	1.09	2.43	-1.30E+00	2.26E-06	Down	-7.31E-01	7.99E-03		-3.12E-01	1.63E-01		-6.78E-01	1.52E-03		-1.60E+00	5.16E-07	Down	-4.48E-01	1.25E-01		Unigene39175_All//gi|15238599|ref|NP_200813.1|//1.00E-97//PRL1-interacting factor-related [Arabidopsis thaliana]	Unigene39175_All//3.00E-99//AT5G60050| PRL1-interacting factor-related	Unigene39175_All//0.00E+00//TC178923			GO:0043231	nr -
Unigene39177_All	580	4.96	2.27	1.56	5.15	4.45	2.73	5.32	2.09	1.92	-1.13E+00	2.63E-03		-1.67E+00	5.32E-05	Down	-2.11E-01	5.91E-01		-9.19E-01	1.05E-02		-1.35E+00	3.86E-05	Down	-1.47E+00	5.86E-06	Down	Unigene39177_All//gi|15224916|ref|NP_181989.1|//4.00E-20//RAB6A; GTP binding / protein binding [Arabidopsis thaliana] >gi|75318653|sp|Q8H501.1|RBH1B_ARATH RecName: Full=Ras-related protein RABH1B >gi|107738267|gb|ABF83670.1|At2g44610 [Arabidopsis thaliana] >gi|741994|prf||2008312A GTP-binding protein	Unigene39177_All//7.00E-13//AT2G44610| RAB6A; GTP binding / protein binding	Unigene39177_All//0.00E+00//gi|164280176|gb|ES820150.1|ES820150			GO:0003824//GO:0005626//GO:0016020//GO:0032561//GO:0035556//GO:0046903	nr -
Unigene39179_All	1471	0.50	0.17	0.00	1.05	1.59	0.71	4.43	1.34	1.08	-1.53E+00	7.78E-02		-8.96E+00	4.13E-04	Down	6.01E-01	1.62E-01		-5.72E-01	3.09E-01		-1.73E+00	5.21E-14	Down	-2.03E+00	8.35E-18	Down	Unigene39179_All//gi|15219161|ref|NP_177996.1|//1.00E-37//F-box family protein [Arabidopsis thaliana] >gi|75288062|sp|Q9ZV93.1|FDL10_ARATH RecName: Full=F-box/FBD/LRR-repeat protein At1g78750 >gi|3834319|gb|AAC83035.1| Similar to gi|2244754 heat shock transcription factor HSF30 homolog from Arabidopsis thaliana chromosome 4 contig gb|Z97335	Unigene39179_All//4.00E-39//AT1G78750| F-box family protein	Unigene39179_All//2.00E-123//TC147261				nr -
Unigene39180_All	537	65.47	64.26	47.10	209.37	220.46	186.20	33.62	9.96	7.20	-2.71E-02	7.88E-01		-4.75E-01	3.18E-07		7.45E-02	1.65E-01		-1.69E-01	5.55E-04		-1.75E+00	2.85E-38	Down	-2.22E+00	1.02E-53	Down	Unigene39180_All//gi|94807644|gb|AB747119.1|//6.00E-20//At1g31335 [Arabidopsis thaliana]	Unigene39180_All//2.00E-10//AT1G31335| unknown protein	Unigene39180_All//0.00E+00//gi|132483951|gb|BF275633.2|BF275633			GO:0016020	nr +
Unigene39182_All	756	5.12	9.72	5.63	68.33	54.66	43.97	0.06	1.88	0.37	9.24E-01	2.24E-05		1.38E-01	6.49E-01		-3.22E-01	2.15E-06		-6.36E-01	6.19E-19		5.07E+00	8.39E-09	Up	2.72E+00	9.93E-02		Unigene39182_All//gi|30680258|ref|NP_566306.3|//3.00E-41//AIR12; extracellular matrix structural constituent [Arabidopsis thaliana]	Unigene39182_All//9.00E-40//AT3G07390| AIR12; extracellular matrix structural constituent	Unigene39182_All//0.00E+00//TC136702			GO:0016020//GO:0031410	nr -
Unigene39184_All	341	55.85	19.91	12.49	62.23	68.06	44.63	126.96	29.05	62.62	-1.49E+00	3.45E-26	Down	-2.16E+00	9.83E-42	Down	1.29E-01	3.21E-01		-4.80E-01	3.61E-05		-2.13E+00	2.79E-117	Down	-1.02E+00	4.33E-41	Down	Unigene39184_All//gi|166343845|gb|AB598665.1|//9.00E-63//beta-tubulin 19 [Gossypium hirsutum]	Unigene39184_All//5.00E-41//AT5G62700| TUB3; GTP binding / GTPase/ structural molecule	Unigene39184_All//0.00E+00//ES831934		ko04145|Phagosome	GO:0006970//GO:0007017//GO:0010038//GO:0015630//GO:0016020//GO:0017111//GO:0030312//GO:0031981//GO:0032561//GO:0043234//GO:0043623	nr -
Unigene39186_All	1918	23.05	9.19	13.91	17.19	13.27	19.12	14.99	14.10	15.70	-1.33E+00	2.05E-50	Down	-7.29E-01	2.08E-18		-3.74E-01	1.68E-05		1.53E-01	1.20E-01		-8.84E-02	4.08E-01		6.70E-02	5.24E-01		Unigene39186_All//gi|113205448|gb|ABI34400.1|//4.00E-86//Putative mandelonitrile lyase, related [Solanum demissum]	Unigene39186_All//8.00E-71//AT1G14180| protein binding / zinc ion binding	Unigene39186_All//0.00E+00//gi|109847591|gb|DW476571.1|DW476571			GO:0005488//GO:0044464	nr +
Unigene39188_All	765	6.84	2.78	1.25	1.95	2.52	0.94	3.54	0.82	3.33	-1.30E+00	1.91E-06	Down	-2.45E+00	1.23E-13	Down	3.68E-01	4.84E-01		-1.05E+00	5.67E-02		-2.11E+00	6.37E-08	Down	-8.58E-02	8.00E-01				Unigene39188_All//0.00E+00//gi|109876141|gb|DW505115.1|DW505115				
Unigene39189_All	2559	0.16	0.04	0.35	0.91	0.55	0.30	6.06	3.66	3.22	-2.05E+00	1.20E-01		1.11E+00	1.49E-01		-7.30E-01	6.94E-02		-1.61E+00	2.00E-04	Down	-7.29E-01	9.52E-09		-9.12E-01	7.40E-13		Unigene39189_All//gi|224112451|ref|XP_002332774.1|//2.00E-33//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834669|gb|EEE73132.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene39189_All//4.00E-07//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene39189_All//2.00E-10//ES850138		ko04626|Plant-pathogen interaction		nr +
Unigene39191_All	608	6.11	5.33	7.09	8.44	7.99	3.71	3.89	0.34	1.18	-1.96E-01	5.67E-01		2.16E-01	5.06E-01		-7.96E-02	8.17E-01		-1.18E+00	7.48E-06	Down	-3.50E+00	1.70E-11	Down	-1.72E+00	8.87E-06	Down	Unigene39191_All//gi|297826979|ref|XP_002881372.1|//6.00E-37//AICARFT/IMPCHase bienzyme family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327211|gb|EFH57631.1|AICARFT/IMPCHase bienzyme family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39191_All//1.00E-38//AT2G35040| AICARFT/IMPCHase bienzyme family protein	Unigene39191_All//3.00E-123//gi|78351170|gb|DT571444.1|DT571444		ko00230|Purine metabolism//ko00670|One carbon pool by folate	GO:0003676//GO:0006950//GO:0009168//GO:0009526//GO:0009532//GO:0010467//GO:0016742//GO:0019238//GO:0034062	nr -
Unigene39192_All	492	46.58	69.00	33.55	61.76	47.38	47.46	50.01	35.25	106.16	5.67E-01	8.20E-10		-4.73E-01	6.13E-05		-3.82E-01	2.62E-05		-3.80E-01	7.37E-05		-5.05E-01	2.47E-07		1.09E+00	3.13E-54	Up			Unigene39192_All//0.00E+00//TC168554				
Unigene3920_All	923	28.97	17.07	13.67	29.58	21.68	37.29	96.65	30.43	34.27	-7.63E-01	7.95E-13		-1.08E+00	1.27E-21	Down	-4.48E-01	2.69E-06		3.34E-01	2.20E-04		-1.67E+00	2.08E-173	Down	-1.50E+00	2.17E-152	Down	Unigene3920_All//gi|12580855|emb|CAC27136.1|//4.00E-97//40S ribosomal protein S2 [Picea abies]	Unigene3920_All//3.00E-96//AT1G58684| 40S ribosomal protein S2, putative	Unigene3920_All//0.00E+00//TC143126		ko03010|Ribosome		nr +
Unigene39200_All	577	2.81	3.07	3.51	2.07	3.28	3.29	3.00	2.83	13.67	1.29E-01	7.79E-01		3.19E-01	5.10E-01		6.64E-01	1.70E-01		6.66E-01	1.78E-01		-8.88E-02	8.49E-01		2.19E+00	4.16E-23	Up			Unigene39200_All//9.00E-102//ES791926				
Unigene39201_All	530	1.58	2.96	1.91	99.35	71.01	63.48	60.87	36.35	25.11	9.08E-01	8.56E-02		2.73E-01	6.75E-01		-4.84E-01	2.40E-13		-6.46E-01	8.10E-20		-7.44E-01	7.08E-18		-1.28E+00	6.33E-44	Down							
Unigene39202_All	794	367.70	182.13	306.69	64.43	92.85	54.38	0.27	0.74	0.30	-1.01E+00	1.45E-214	Down	-2.62E-01	1.86E-18		5.27E-01	4.69E-21		-2.45E-01	9.43E-04		1.47E+00	1.02E-01		1.77E-01	9.08E-01		Unigene39202_All//gi|115489236|ref|NP_001067105.1|//3.00E-48//Os12g0575000 [Oryza sativa Japonica Group] >gi|77556201|gb|ABA98997.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649612|dbj|BAF30124.1|Os12g0575000 [Oryza sativa Japonica Group]	Unigene39202_All//5.00E-16//AT5G08050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: thylakoid, chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1118 (InterPro:IPR009500), Uncharacterised conserved protein UCP022207 (InterPro:IPR016801); Has 41 Blast hits to 41 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene39202_All//0.00E+00//TC161812			GO:0009534	nr -
Unigene39203_All	585	1.61	0.87	1.46	1.28	7.77	8.80	4.55	8.00	8.10	-8.94E-01	2.14E-01		-1.45E-01	8.31E-01		2.60E+00	6.51E-15	Up	2.78E+00	6.57E-17	Up	8.13E-01	1.05E-03		8.32E-01	5.47E-04		Unigene39203_All//gi|77551963|gb|ABA94760.1|//8.00E-08//Protein kinase domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene39203_All//9.00E-08//AT2G34320| nucleic acid binding					nr +
Unigene39204_All	617	35.28	21.84	20.28	81.06	61.73	78.10	81.07	50.33	37.84	-6.91E-01	4.75E-09		-7.99E-01	6.92E-11		-3.93E-01	8.79E-09		-5.36E-02	5.93E-01		-6.88E-01	7.09E-24		-1.10E+00	2.10E-53	Down	Unigene39204_All//gi|6730705|gb|AAF27100.1|AC011809_9//9.00E-30//Putative phospatase 2A inhibitor [Arabidopsis thaliana]	Unigene39204_All//3.00E-19//AT1G74560| NRP1 (NAP1-RELATED PROTEIN 1); DNA binding / chromatin binding / histone binding	Unigene39204_All//0.00E+00//TC130464			GO:0003676//GO:0005515//GO:0006950//GO:0009755//GO:0010038//GO:0010102//GO:0034728//GO:0043231//GO:0048869//GO:0051707	nr +
Unigene39205_All	529	2.77	2.78	3.93	4.52	3.97	0.60	1.60	0.16	1.13	4.40E-03	9.94E-01		5.04E-01	2.86E-01		-1.87E-01	6.70E-01		-2.92E+00	1.02E-08	Down	-3.34E+00	2.51E-04	Down	-5.01E-01	4.47E-01		Unigene39205_All//gi|212292507|gb|ACJ24185.1|//8.00E-08//CAPRICE [Gossypium hirsutum] >gi|212292511|gb|ACJ24187.1|CAPRICE [Gossypium hirsutum] >gi|212292515|gb|ACJ24189.1|CAPRICE [Gossypium hirsutum] >gi|212292519|gb|ACJ24191.1|CAPRICE [Gossypium hirsutum]		Unigene39205_All//2.00E-121//TC159137			GO:0003676//GO:0010468//GO:0043231	nr -
Unigene39206_All	331	3.48	9.34	12.55	9.48	4.99	2.18	6.51	1.14	3.37	1.43E+00	1.28E-04	Up	1.85E+00	6.53E-08	Up	-9.25E-01	5.02E-03		-2.12E+00	5.38E-08	Down	-2.52E+00	8.42E-08	Down	-9.51E-01	1.16E-02		Unigene39206_All//gi|212292507|gb|ACJ24185.1|//1.00E-21//CAPRICE [Gossypium hirsutum] >gi|212292511|gb|ACJ24187.1|CAPRICE [Gossypium hirsutum] >gi|212292515|gb|ACJ24189.1|CAPRICE [Gossypium hirsutum] >gi|212292519|gb|ACJ24191.1|CAPRICE [Gossypium hirsutum]	Unigene39206_All//2.00E-09//AT1G01380| ETC1 (ENHANCER OF TRY AND CPC 1); DNA binding / transcription factor	Unigene39206_All//8.00E-144//TC166877	MYB-related		GO:0003676//GO:0010468//GO:0043231	nr +

Unigene39208_All	679	124.68	137.90	135.99	30.15	39.00	26.21	5.98	2.77	1.06	1.46E-01	9.55E-03		1.25E-01	3.79E-02		3.71E-01	2.09E-04		-2.02E-01	1.30E-01		-1.11E+00	5.17E-05	Down	-2.50E+00	1.76E-14	Down	Unigene39208_All//gi|297815948|ref|XP_002875857.1|/2.00E-32//bundle-sheath defective protein 2 family [Arabidopsis lyrata subsp. lyrata] >gi|297321695|gb|EFH52116.1| bundle-sheath defective protein 2 family [Arabidopsis lyrata subsp. lyrata]	Unigene39208_All//4.00E-33//AT3G47650| bundle-sheath defective protein 2 family / bsd2 family	Unigene39208_All//0.00E+00//TC163788			GO:0005515//GO:0009536//GO:0044267	nr -
Unigene39209_All	731	2.08	2.63	3.13	2.45	4.33	4.39	2.60	3.14	0.76	3.44E-01	4.67E-01		5.94E-01	1.81E-01		8.21E-01	1.67E-02		8.38E-01	1.62E-02		2.73E-01	5.12E-01		-1.77E+00	5.92E-05	Down	Unigene39209_All//gi|124359162|gb|ABN05685.1|/1.00E-08//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene39209_All//2.00E-164//ES801598				nr +
Unigene3921_All	918	25.42	23.73	31.61	11.72	10.77	10.18	1.20	1.09	3.43	-9.90E-02	4.35E-01		3.15E-01	2.94E-03		-1.23E-01	5.48E-01		-2.03E-01	3.09E-01		-1.32E-01	8.19E-01		1.52E+00	3.01E-06	Up	Unigene3921_All//gi|75151174|sp|Q8GXB1.1|U548_ARATH//3.00E-84//RecName: Full=UPF0548 protein At2g17695	Unigene3921_All//2.00E-85//AT2G17695| unknown protein	Unigene3921_All//0.00E+00//TC137550				nr -
Unigene39210_All	937	1.17	5.19	8.18	14.89	10.40	7.81	1.44	0.00	0.34	2.15E+00	2.13E-11	Up	2.80E+00	5.32E-23	Up	-5.17E-01	2.12E-04		-9.31E-01	3.48E-10		-1.05E+01	1.30E-09	Down	-2.09E+00	1.85E-04	Down	Unigene39210_All//gi|290579513|gb|ADD51352.1|//7.00E-93//TT2 like MYB transcriptoin factor [Theobroma cacao]	Unigene39210_All//2.00E-56//AT3G13540| ATMYB5 (MYB DOMAIN PROTEIN 5); DNA binding / transcription factor	Unigene39210_All//0.00E+00//gi|78328361|gb|DT548635.1|DT548635	MYB		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene39211_All	988	0.58	2.31	0.81	4.39	5.09	3.98	2.27	1.95	0.65	1.99E+00	2.91E-05	Up	4.73E-01	5.65E-01		2.14E-01	4.98E-01		-1.41E-01	6.76E-01		-2.21E-01	6.18E-01		-1.81E+00	7.47E-06	Down	Unigene39211_All//gi|79557632|ref|NP_179585.3|//4.00E-50//GC1 (Golgin Candidate 1) [Arabidopsis thaliana] >gi|85681038|sp|Q8SSN9.2|GOGC1_ARATH RecName: Full=Golgin candidate 1; Short=AtGC1; AltName: Full=Golgin-84 >gi|44917433|gb|AAS49041.1| At2g19950 [Arabidopsis thaliana]	Unigene39211_All//2.00E-51//AT2G19950| GC1 (Golgin Candidate 1)	Unigene39211_All//6.00E-141//AI728600			GO:0043231	nr -
Unigene39213_All	975	0.75	1.14	0.44	1.02	3.57	1.39	1.65	4.50	16.67	6.06E-01	3.59E-01		-7.82E-01	3.80E-01		1.80E+00	1.68E-07	Up	4.44E-01	4.72E-01		1.45E+00	1.13E-07	Up	3.34E+00	1.47E-73	Up	Unigene39213_All//gi|224085109|ref|XP_002335302.1|/1.00E-12//predicted protein [Populus trichocarpa] >gi|222833249|gb|EEE71726.1| predicted protein [Populus trichocarpa]						nr -
Unigene39216_All	450	12.21	8.56	5.68	8.52	3.44	3.81	3.76	3.16	0.62	-5.13E-01	4.43E-02		-1.10E+00	4.16E-05	Down	-1.31E+00	9.85E-06	Down	-1.16E+00	1.99E-04	Down	-2.51E-01	6.29E-01		-2.60E+00	9.91E-07	Down	Unigene39216_All//gi|12039277|gb|AG46067.1|AC079830.7//1.00E-06//expressed protein {Oryza sativa Japonica Group} >gi|108710365|gb|ABF98160.1| expressed protein {Oryza sativa (japonica cultivar-group)}	Unigene39216_All//7.00E-08//AT4G10810| unknown protein	Unigene39216_All//4.00E-91//AW187354				nr +
Unigene39218_All	448	6.31	4.86	5.94	11.23	8.69	8.37	5.95	4.76	2.67	-3.75E-01	3.34E-01		-8.56E-02	8.22E-01		-3.71E-01	1.72E-01		-4.25E-01	1.29E-01		-3.22E-01	3.97E-01		-1.16E+00	6.53E-04	Down			Unigene39218_All//5.00E-07//ES838442				
Unigene39219_All	1692	0.49	0.18	0.13	0.88	0.57	0.59	2.50	3.09	1.13	-1.46E+00	6.69E-02		-1.97E+00	2.71E-02		-6.32E-01	2.38E-01		-5.89E-01	3.04E-01		3.05E-01	2.26E-01		-1.14E+00	1.27E-05	Down	Unigene39219_All//gi|223452286|gb|ACM89471.1|//7.00E-48//FERONIA receptor-like kinase [Glycine max]	Unigene39219_All//3.00E-49//AT3G04690| protein kinase family protein	Unigene39219_All//0.00E+00//gi|21101440|gb|BQ413753.1|BQ413753			GO:0004672//GO:0043231//GO:0044444	nr -
Unigene3922_All	884	22.43	2.81	2.65	289.87	186.67	92.22	7.32	2.36	1.80	-3.00E+00	2.40E-65	Down	-3.08E+00	1.26E-64	Down	-6.35E-01	8.03E-104		-1.65E+00	0.00E+00	Down	-1.63E+00	7.07E-13	Down	-2.02E+00	1.36E-17	Down	Unigene3922_All//gi|17154773|gb|AAL35979.1|AF104392.1//7.00E-57//extensin-like protein [Cucumis sativus]	Unigene3922_All//4.00E-33//AT2G10940| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene3922_All//0.00E+00//TC137856				nr -
Unigene39220_All	501	0.31	1.92	1.49	0.70	1.99	2.79	0.59	2.25	3.66	2.62E+00	2.34E-03		2.25E+00	2.35E-02		1.52E+00	3.74E-02		2.01E+00	1.35E-03		1.93E+00	2.12E-03		2.63E+00	3.47E-07	Up	Unigene39220_All//gi|297841723|ref|XP_002888743.1|//2.00E-65//ATNRT1:2 [Arabidopsis lyrata subsp. lyrata] >gi|297334584|gb|EFH65002.1| ATNRT1:2 [Arabidopsis lyrata subsp. lyrata]	Unigene39220_All//5.00E-58//AT1G69850| ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter				GO:0015833//GO:0016020//GO:0046872//GO:0051707	nr +
Unigene39221_All	365	9.75	3.47	8.32	8.19	8.21	8.54	14.83	10.19	7.09	-1.49E+00	1.58E-05	Down	-2.29E-01	5.25E-01		3.40E-03	9.97E-01		6.02E-02	8.91E-01		-5.41E-01	1.88E-02		-1.06E+00	2.84E-06	Down	Unigene39221_All//gi|261351264|gb|ACX71299.1|//3.00E-30//RNA-binding protein RZ-1 [Capsicum annuum]	Unigene39221_All//6.00E-28//AT3G26420| ATRZ-1A; RNA binding / nucleotide binding	Unigene39221_All//1.00E-136//gi|109867013|gb|DW495989.1|DW495989		ko03010|Ribosome//ko03040|Spliceosome	GO:0009409//GO:0046914	nr +
Unigene39222_All	466	7.52	3.48	1.71	5.67	5.91	8.53	35.48	14.98	12.31	-1.11E+00	8.77E-04	Down	-2.13E+00	5.56E-08	Down	6.13E-02	8.94E-01		5.90E-01	5.95E-02		-1.24E+00	2.26E-21	Down	-1.53E+00	8.50E-30	Down	Unigene39222_All//sp|049169|EF1A_MANES//7.00E-06//Elongation factor 1-alpha OS=Manihot esculenta GN=EF1 PE=3 SV=1		Unigene39222_All//0.00E+00//TC159452				swissprot +
Unigene39223_All	541	70.70	65.19	105.22	17.13	36.66	34.98	2.11	0.85	3.98	-1.17E-01	2.25E-01		5.74E-01	1.26E-15		1.10E+00	6.38E-20	Up	1.03E+00	8.50E-16	Up	-1.31E+00	2.45E-02		9.14E-01	1.58E-02		Unigene39223_All//gi|17865457|sp|O82150.2|FTSH_TOBAC//6.00E-18//RecName: Full=Cell division protease ftsH homolog, chloroplastic; AltName: Full=DS9; Flags: Precursor >gi|5804782|dbj|BAA33755.2| chloroplast FtsH protease [Nicotiana tabacum]	Unigene39223_All//2.00E-12//AT5G42270| VAR1 (VARIEGATED 1); ATP-dependent peptidase/ ATPase/ metallopeptidase	Unigene39223_All//1.00E-159//gi|21091020|gb|BQ403333.1|BQ403333				nr +
Unigene39224_All	922	1.25	1.87	0.58	2.54	2.69	2.84	2.57	0.27	0.60	5.82E-01	2.41E-01		-1.11E+00	9.93E-02		8.27E-02	8.57E-01		1.62E-01	6.91E-01		-3.24E+00	8.82E-11	Down	-2.09E+00	3.31E-07	Down	Unigene39224_All//gi|297740866|emb|CBI31048.3|//7.00E-10//unnamed protein product [Vitis vinifera]						nr -
Unigene39225_All	1412	0.93	0.25	0.38	2.33	2.27	1.12	6.83	1.12	2.06	-1.88E+00	3.39E-03		-1.30E+00	4.12E-02		-3.79E-02	9.11E-01		-1.06E+00	1.88E-03		-2.60E+00	1.03E-33	Down	-1.73E+00	4.84E-21	Down	Unigene39225_All//gi|309791663|ref|NP_568885.2|//0.00E+00//SQD2 (sulfoquinovosyldiacylglycerol 2); UDP-glycosyltransferase/ UDP-sulfoquinovose:DAG sulfoquinovosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|203002857|gb|AAM18913.1|AF454354_1 sulfolipid synthase [Arabidopsis thaliana]	Unigene39225_All//0.00E-00//AT5G01220| SQD2 (sulfoquinovosyldiacylglycerol 2); UDP-glycosyltransferase/ UDP-sulfoquinovose:DAG sulfoquinovosyltransferase/ transferase, transferring glycosyl groups	Unigene39225_All//0.00E+00//gi|109842782|gb|DW241340.1|DW241340		ko00561|Glycerolipid metabolism		nr -
Unigene39228_All	827	17.27	0.92	6.50	4.22	3.41	2.29	6.24	8.04	3.90	-4.23E+00	4.51E-63	Down	-1.41E+00	1.49E-17	Down	-3.04E-01	3.89E-01		-8.78E-01	7.31E-03		3.66E-01	8.37E-02		-6.77E-01	2.87E-03		Unigene39228_All//gi|44889030|sp|P54152.2|MSRA_PRAAN//5.00E-88//RecName: Full=Peptide methionine sulfoxide reductase; AltName: Full=Protein-methionine-S-oxide reductase; AltName: Full=Peptide-methionine (S)-S-oxide reductase; Short=Peptide Met(O) reductase; AltName: Full=Fruit-ripening protein E4 >gi|31455408|emb|CAA93442.2| methionine sulfoxide reductase [Fragaria x ananassa]	Unigene39228_All//5.00E-72//AT5G61640| PMSR1 (PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 1); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor / peptide-methionine-(S)-S-oxide reductase	Unigene39228_All//0.00E+00//gi|109883584|gb|DW512554.1|DW512554				nr +
Unigene39229_All	612	7.52	1.66	2.52	8.22	5.74	5.17	6.63	1.43	1.56	-2.18E+00	3.92E-11	Down	-1.58E+00	4.69E-07	Down	-5.19E-01	4.53E-02		-6.70E-01	1.15E-02		-2.21E+00	3.63E-12	Down	-2.09E+00	8.87E-12	Down	Unigene39229_All//gi|117168079|gb|ABK32122.1|//1.00E-06//At5g54970 [Arabidopsis thaliana]	Unigene39229_All//1.00E-06//AT5G54970| unknown protein	Unigene39229_All//3.00E-92//ES793053				nr +
Unigene3923_All	934	3.53	20.02	8.61	10.88	19.61	14.46	19.87	36.16	33.27	2.50E+00	2.11E-50	Up	1.29E+00	6.16E-09	Up	8.50E-01	3.07E-12		4.10E-01	7.75E-03		8.64E-01	6.95E-24		7.43E-01	1.13E-17		Unigene3923_All//gi|224127502|ref|XP_002320090.1|//1.00E-59//f-box family protein [Populus trichocarpa] >gi|222860863|gb|EEE98405.1| f-box family protein [Populus trichocarpa]	Unigene3923_All//2.00E-50//AT3G61060| AtPP2-A13 (Arabidopsis thaliana phloem protein 2-A13); carbohydrate binding	Unigene3923_All//0.00E+00//gi|48804003|gb|CO105317.1|CO105317				nr -
Unigene39230_All	1009	2.23	1.46	1.16	17.92	16.69	7.21	7.63	1.70	1.07	-6.15E-01	1.47E-01		-9.41E-01	3.61E-02		-1.03E-01	5.26E-01		-1.31E+00	2.51E-22	Down	-2.17E+00	6.64E-22	Down	-2.84E+00	1.15E-30	Down	Unigene39230_All//gi|3927834|gb|AAC79591.1|//6.00E-07//expressed protein [Arabidopsis thaliana] >gi|98961099|gb|ABF59033.1| At2g28870 [Arabidopsis thaliana]	Unigene39230_All//4.00E-13//AT5G02420| unknown protein	Unigene39230_All//0.00E+00//DW504073				nr -
Unigene39235_All	719	5.02	11.70	8.96	0.97	0.48	1.38	10.41	25.34	32.86	1.22E+00	5.25E-09	Up	8.36E-01	5.43E-04		-1.02E+00	2.25E-01		5.11E-01	4.92E-01		1.28E+00	1.40E-24	Up	1.66E+00	5.60E-47	Up	Unigene39235_All//gi|297834874|ref|XP_002885319.1|//2.00E-15//beta-1,4-xylosidase [Arabidopsis lyrata subsp. lyrata] >gi|297331159|gb|EFH61578.1| beta-1,4-xylosidase [Arabidopsis lyrata subsp. lyrata]	Unigene39235_All//6.00E-15//AT3G19615| unknown protein	Unigene39235_All//0.00E+00//ES809679				nr +
Unigene39241_All	1077	4.18	22.63	14.29	1.06	1.09	0.25	0.67	0.19	1.26	2.44E+00	1.54E-63	Up	1.77E+00	3.13E-26	Up	3.13E-02	9.74E-01		-2.08E+00	2.95E-03		-1.78E+00	2.79E-02		9.14E-01	6.62E-02		Unigene39241_All//gi|170676246|gb|ACB30362.1|//5.00E-29//transcription factor [Capsicum annuum]	Unigene39241_All//3.00E-27//AT4G27240| zinc finger (C2H2 type) family protein	Unigene39241_All//0.00E+00//TC152989	C2H2			nr -
Unigene39242_All	770	0.88	0.79	1.52	2.91	1.07	0.82	1.54	0.87	1.29	-1.62E-01	8.32E-01		7.84E-01	2.38E-01		-1.44E+00	4.34E-04	Down	-1.83E+00	5.88E-05	Down	-8.24E-01	1.42E-01		-2.49E-01	6.27E-01		Unigene39242_All//gi|42573559|ref|NP_974876.1|//3.00E-06//ATARP9 (ACTIN-RELATED PROTEIN 9); DNA binding / protein binding [Arabidopsis thaliana]	Unigene39242_All//2.00E-07//AT5G43500| ATARP9 (ACTIN-RELATED PROTEIN 9); DNA binding / protein binding	Unigene39242_All//7.00E-26//TC170678				nr +
Unigene39243_All	573	0.37	0.53	0.74	16.87	14.96	12.93	7.82	1.75	2.22	5.39E-01	6.71E-01		1.03E+00	3.96E-01		-1.73E-01	4.16E-01		-3.84E-01	4.22E-02		-2.16E+00	5.24E-13	Down	-1.81E+00	7.07E-11	Down	Unigene39243_All//gi|297828261|ref|XP_002882013.1|//2.00E-12//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297327852|gb|EFH58272.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	Unigene39243_All//3.00E-12//AT2G45450| ZPR1 (LITTLE ZIPPER 1); protein binding	Unigene39243_All//0.00E+00//gi|109882988|gb|DW511958.1|DW511958				nr -
Unigene39244_All	1000	10.31	14.74	26.20	10.31	16.70	16.85	0.00	0.00	0.00	5.17E-01	3.90E-04		1.35E+00	9.70E-30	Up	6.96E-01	4.39E-08		7.08E-01	8.87E-08		null	null		null	null		Unigene39244_All//gi|3193285|gb|AAC19269.1|//1.00E-40//T14P8.18 [Arabidopsis thaliana] >gi|7268997|emb|CAB80730.1| AT4g02370 [Arabidopsis thaliana]	Unigene39244_All//7.00E-42//AT4G02370| unknown protein	Unigene39244_All//0.00E+00//gi|109884559|gb|DW513529.1|DW513529				nr +
Unigene39245_All	855	3.18	7.29	3.36	1.17	1.77	0.53	6.82	14.52	7.92	1.20E+00	1.09E-06	Up	7.99E-02	8.31E-01		6.05E-01	2.97E-01		-1.14E+00	1.09E-01		1.09E+00	2.78E-13	Up	2.15E-01	3.15E-01		Unigene39245_All//gi|12003392|gb|AAG43553.1|AF211535.1//2.00E-36//Avr9/Cf-9 rapidly elicited protein 194 [Nicotiana tabacum]	Unigene39245_All//4.00E-27//AT5G41810| unknown protein	Unigene39245_All//0.00E+00//TC149693				nr -
Unigene39246_All	769	2.04	207.03	9.76	6.74	22.48	18.56	41.57	79.30	57.97	6.66E+00	0.00E+00	Up	2.26E+00	1.06E-17	Up	1.74E+00	3.01E-34	Up	1.46E+00	2.01E-20	Up	9.32E-01	3.42E-48		4.80E-01	6.58E-12		Unigene39246_All//gi|124057819|gb|ABD72603.1|//8.00E-83//raffinose synthase [Cucumis sativus]	Unigene39246_All//7.00E-81//AT5G40390| SIP1 (seed imbibition 1-like); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene39246_All//0.00E+00//TC151873		ko00052|Galactose metabolism		nr +
Unigene39248_All	497	10.42	7.85	6.43	14.63	10.74	10.00	40.92	12.36	13.87	-4.09E-01	1.27E-01		-6.97E-01	1.11E-02		-4.46E-01	3.44E-02		-5.50E-01	1.08E-02		-1.73E+00	4.43E-42	Down	-1.56E+00	1.24E-37	Down	Unigene39248_All//gi|192910756|gb|ACF06486.1|//2.00E-39//60S ribosomal protein L11 [Elaeis guineensis] >gi|192910758|gb|ACF06487.1| 60S ribosomal protein L11 [Elaeis guineensis]	Unigene39248_All//2.00E-29//AT5G45775| 60S ribosomal protein L11 (RPL11D)	Unigene39248_All//3.00E-123//gi|13350567|gb|BG440915.1|BG440915		ko03010|Ribosome		nr +
Unigene39249_All	790	5.17	2.12	5.93	23.77	17.70	11.43	89.70	74.23	102.32	-1.29E+00	3.74E-05	Down	1.99E-01	5.20E-01		-4.26E-01	3.57E-04		-1.06E+00	1.67E-16	Down	-2.73E-01	8.80E-07		1.90E-01	2.30E-04				Unigene39249_All//0.00E+00//TC135598				

Unigene39252_All	563	11.52	7.74	5.30	6.72	12.42	7.54	3.68	3.86	5.66	-5.74E-01	1.31E-02		-1.12E+00	4.95E-06	Down	8.85E-01	2.75E-05		1.65E-01	6.18E-01		6.91E-02	8.71E-01		6.21E-01	3.92E-02		Unigene39252_All//gi|89540 61|gb|AAF82234.1|AC069143.10//1.00E-18//T12988.11 [Arabidopsis thaliana]	Unigene39252_All//1.00E-18//AT1G19240| unknown protein	Unigene39252_All//0.00E+00//TC169698				nr -
Unigene39255_All	575	2.18	8.55	6.39	11.87	14.91	12.96	34.04	31.40	33.33	1.97E+00	2.21E-10	Up	1.55E+00	1.17E-05	Up	3.29E-01	1.08E-01		1.27E-01	6.44E-01		-1.17E-01	3.82E-01		-3.08E-02	8.07E-01		Unigene39255_All//gi|211906524|gb|ACJ11755.1|//6.00E-62//UDP-D-xylose 4-epimerase [Gossypium hirsutum]	Unigene39255_All//1.00E-57//AT1G30620| MUR4 (MURUS 4); UDP-arabinose 4-epimerase/ catalytic	Unigene39255_All//0.00E+00//TC170055		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene39256_All	779	5.78	2.08	0.89	1.92	0.53	0.99	6.68	1.61	2.30	-1.47E+00	1.12E-06	Down	-2.70E+00	4.27E-13	Down	-1.85E+00	5.94E-04	Down	-9.61E-01	8.02E-02		-2.05E+00	4.40E-14	Down	-1.54E+00	4.77E-10	Down	Unigene39256_All//gi|37202082|gb|AAQ89656.1|//4.00E-32//At5g38700 [Arabidopsis thaliana]	Unigene39256_All//4.00E-29//AT5G38700| unknown protein	Unigene39256_All//0.00E+00//TC144849				nr -
Unigene39257_All	492	19.35	55.20	17.43	18.43	23.31	31.94	16.93	17.75	16.11	1.51E+00	1.00E-37	Up	-1.52E-01	4.74E-01		3.39E-01	4.55E-02		7.94E-01	9.38E-09		6.87E-02	7.32E-01		-7.12E-02	7.11E-01		Unigene39257_All//gi|3860249|gb|AAC73017.1|//2.00E-13//expressed protein [Arabidopsis thaliana]	Unigene39257_All//1.00E-14//AT2G27830| FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT4G22760.1); Has 68 Blast hits to 68 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene39257_All//0.00E+00//gi|73859999|gb|DT462738.1|DT462738				nr +
Unigene39259_All	840	5.85	7.36	3.93	5.52	8.57	9.30	4.68	2.79	1.47	3.30E-01	1.82E-01		-5.75E-01	4.41E-02		6.36E-01	2.37E-03		7.54E-01	2.35E-04		-7.48E-01	6.34E-03		-1.67E+00	1.07E-08	Down	Unigene39259_All//gi|224068426|ref|XP_002302742.1|//4.00E-47//histone H1 [Populus trichocarpa] >gi|222844468|gb|EEE82015.1| histone H1 [Populus trichocarpa]	Unigene39259_All//4.00E-12//AT2G18050| HIS1-3 (HISTONE H1-3); DNA binding / nucleosomal DNA binding	Unigene39259_All//0.00E+00//gi|164342607|gb|ES815083.1|ES815083				nr +
Unigene3926_All	1225	1.45	1.32	3.69	1.95	2.78	3.28	2.28	2.22	2.11	-1.34E-01	7.71E-01		1.35E+00	1.14E-05	Up	5.12E-01	1.38E-01		7.49E-01	1.40E-02		-3.87E-02	9.30E-01		-1.08E-01	7.50E-01		Unigene3926_All//gi|79510333|ref|NP_568230.2|//6.00E-63//MSL2 (MscS-LIKE 2); ion channel [Arabidopsis thaliana]	Unigene3926_All//4.00E-62//AT5G10490| MSL2 (MscS-LIKE 2); ion channel	Unigene3926_All//0.00E+00//TC161993				nr -
Unigene39260_All	1399	11.67	8.15	13.93	0.21	1.01	0.13	0.57	0.15	0.20	-5.18E-01	1.63E-04		2.56E-01	6.01E-02		2.24E+00	3.44E-04	Up	-7.26E-01	6.39E-01		-1.94E+00	1.17E-02		-1.53E+00	3.04E-02		Unigene39260_All//gi|15222937|ref|NP_172827.1|//1.00E-156//CYP78A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|8920576|gb|AAF81298.1|AC027656_15 Strong similarity to cytochrome P-450 from Phalaenopsis sp. SM9108 gb|U34744. It contains a cytochrome P450 domain PF|00067. EST gb|T45256 comes from this gene [Arabidopsis thaliana] >gi|63003816|gb|AAY25437.1| At1g13710 [Arabidopsis thaliana] >gi|115646887|gb|ABJ17153.1| At1g13710 [Arabidopsis thaliana]	Unigene39260_All//1.00E-143//AT1G13710| CYP78A5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene39260_All//5.00E-19//BQ406852		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene39262_All	494	4.34	9.74	2.48	11.50	10.46	7.50	8.13	6.94	4.11	1.17E+00	3.56E-05	Up	-8.09E-01	7.86E-02		-1.37E-01	6.19E-01		-6.17E-01	1.29E-02		-2.29E-01	4.44E-01		-9.83E-01	2.13E-04				Unigene39262_All//0.00E+00//TC151653				
Unigene39263_All	1069	4.26	2.32	2.34	9.74	9.37	9.38	4.86	1.13	1.12	-8.75E-01	2.06E-03		-8.63E-01	3.55E-03		-5.52E-02	8.11E-01		-5.44E-02	7.92E-01		-2.10E+00	1.72E-14	Down	-2.12E+00	3.60E-15	Down	Unigene39263_All//gi|18410877|ref|NP_567060.1|//6.00E-33//PDCB5 (PLASMODESMATA CALLOSE-BINDING PROTEIN 5); callose binding / polysaccharide binding [Arabidopsis thaliana] >gi|116247775|sp|Q9MZK6.2|E13L1_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase-like protein 1; Flags: Precursor >gi|107738196|gb|ABF83659.1| At3g58100 [Arabidopsis thaliana]	Unigene39263_All//3.00E-34//AT3G58100| PDCB5 (PLASMODESMATA CALLOSE-BINDING PROTEIN 5); callose binding / polysaccharide binding	Unigene39263_All//0.00E+00//TC133248				nr +
Unigene39265_All	778	36.52	48.78	34.50	36.75	37.58	63.04	217.00	315.89	497.37	4.18E-01	1.42E-06		-8.21E-02	5.05E-01		3.20E-02	8.30E-01		7.79E-01	3.21E-25		5.42E-01	1.03E-74		1.20E+00	0.00E+00	Up	Unigene39265_All//gi|195610442|gb|ACG27051.1|//2.00E-92//cytidine/deoxycytidylate deaminase family protein [Zea mays]	Unigene39265_All//1.00E-77//AT5G28050| cytidine/deoxycytidylate deaminase family protein	Unigene39265_All//0.00E+00//gi|73860937|gb|DT463676.1|DT463676				nr +
Unigene39266_All	831	0.19	0.24	0.51	1.32	1.86	2.23	4.07	8.80	3.88	3.69E-01	8.16E-01		1.44E+00	2.53E-01		5.00E-01	3.86E-01		7.57E-01	1.27E-01		1.11E+00	2.06E-08	Up	-6.79E-02	8.24E-01		Unigene39266_All//gi|183979104|emb|CAP08301.1|//4.00E-90//DNA-binding protein [Vitis thunbergii]	Unigene39266_All//5.00E-68//AT1G13960| WRKY4; DNA binding / transcription factor	Unigene39266_All//6.00E-79//ES838637	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene39268_All	888	0.00	0.00	0.00	6.62	1.86	1.32	29.52	52.15	20.01	null	null		null	null		-1.83E+00	1.11E-13	Down	-2.32E+00	3.35E-16	Down	8.21E-01	7.76E-30		-5.61E-01	1.55E-09		Unigene39268_All//gi|14326489|gb|AK60290.1|AF385697_1//2.00E-88//AT5g10580/F12B17_70 [Arabidopsis thaliana] >gi|18700208|gb|AAL77714.1| AT5g10580/F12B17_70 [Arabidopsis thaliana]	Unigene39268_All//4.00E-73//AT4G31330| unknown protein	Unigene39268_All//5.00E-61//TC133038				nr -
Unigene39269_All	293	28.75	23.00	19.81	28.90	39.61	38.84	130.16	101.28	36.85	-3.22E-01	1.21E-01		-5.37E-01	9.95E-03		4.55E-01	4.80E-03		4.27E-01	1.21E-02		-3.62E-01	2.78E-06		-1.82E+00	1.02E-86	Down	Unigene39269_All//gi|297814115|ref|XP_002874941.1|//1.00E-48//Os01g0254000 [Arabidopsis lyrata subsp. lyrata] >gi|297320778|gb|EFH51200.1| Os01g0254000 [Arabidopsis lyrata subsp. lyrata]	Unigene39269_All//9.00E-37//AT4G02080| ATSAR2 (ARABIDOPSIS THALIANA SECRETION-ASSOCIATED RAS SUPER FAMILY 2); GTP binding	Unigene39269_All//4.00E-161//DT467916		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene39270_All	536	19.03	11.72	13.71	13.75	15.61	11.46	9.47	2.42	9.74	-6.99E-01	9.16E-05		-4.73E-01	1.18E-02		1.83E-01	4.33E-01		-2.63E-01	2.68E-01		-1.97E+00	4.44E-13	Down	4.07E-02	8.82E-01		Unigene39270_All//gi|226499248|ref|NP_001150489.1|//2.00E-13//AGP16 [Zea mays] >gi|195639584|gb|ACG39260.1| AGP16 [Zea mays]	Unigene39270_All//1.00E-05//AT3G61640| AGP20	Unigene39270_All//1.00E-100//DW506393				nr +
Unigene39271_All	756	4.78	4.83	5.71	4.55	6.88	5.74	2.74	1.22	0.69	1.51E-02	9.84E-01		2.57E-01	4.08E-01		5.97E-01	2.02E-02		3.35E-01	2.99E-01		-1.17E+00	3.81E-03		-2.00E+00	4.09E-06	Down	Unigene39271_All//gi|224082500|ref|XP_002306718.1|//9.00E-17//predicted protein [Populus trichocarpa] >gi|222856167|gb|EEE93714.1| predicted protein [Populus trichocarpa]						nr -
Unigene39272_All	945	6.92	3.75	2.76	5.75	6.92	12.66	0.22	0.44	0.17	-8.83E-01	1.34E-04		-1.33E+00	1.09E-07	Down	2.69E-01	2.96E-01		1.14E+00	6.49E-12	Up	9.84E-01	3.73E-01		-4.08E-01	7.55E-01		Unigene39272_All//gi|107738065|gb|ABF83626.1|//2.00E-11//At4g33800 [Arabidopsis thaliana]						nr +
Unigene39273_All	985	2.82	0.10	0.97	3.03	2.62	1.97	4.98	0.72	2.06	-4.77E+00	1.87E-13	Down	-1.53E+00	2.23E-04	Down	-2.11E-01	5.91E-01		-6.22E-01	9.03E-02		-2.79E+00	8.74E-19	Down	-1.27E+00	2.26E-07	Down	Unigene39273_All//gi|115436170|ref|NP_001042843.1|//1.00E-08//Os01g0306100 [Oryza sativa Japonica Group] >gi|113532374|dbj|BAF04757.1| Os01g0306100 [Oryza sativa Japonica Group]		Unigene39273_All//0.00E+00//TC1131870				nr -
Unigene39274_All	528	0.50	1.63	4.84	2.74	1.70	0.86	2.56	3.01	15.62	1.72E+00	3.49E-02		3.29E+00	3.27E-09	Up	-6.90E-01	2.06E-01		-1.68E+00	3.92E-03		2.31E-01	6.19E-01		2.61E+00	1.64E-29	Up			Unigene39274_All//0.00E+00//DW506312				
Unigene39277_All	869	3.31	1.81	1.96	5.73	6.02	2.34	0.29	0.38	0.23	-8.73E-01	1.79E-02		-7.56E-01	5.03E-02		7.14E-02	8.20E-01		-1.29E+00	1.90E-06	Down	3.99E-01	7.24E-01		-3.49E-01	7.66E-01		Unigene39277_All//gi|15242330|ref|NP_199329.1|//1.00E-72//root hair defective 3 GTP-binding (RHD3) family protein [Arabidopsis thaliana] >gi|9759601|dbj|BAB11389.1| GTP-binding protein-like; root hair defective 3 protein-like [Arabidopsis thaliana]	Unigene39277_All//5.00E-74//AT5G45160| root hair defective 3 GTP-binding (RHD3) family protein	Unigene39277_All//1.00E-114//gi|78334181|gb|DT554455.1|DT554455				nr +
Unigene39278_All	609	4.73	0.92	3.41	1.88	0.96	0.52	3.54	1.44	0.46	-2.37E+00	6.91E-08	Down	-4.71E-01	2.40E-01		-9.69E-01	1.14E-01		-1.86E+00	6.47E-03		-1.30E+00	1.18E-03		-2.95E+00	1.88E-09	Down							
Unigene39279_All	650	0.80	6.86	2.21	6.59	3.76	5.00	106.22	191.81	92.00	3.09E+00	2.09E-15	Up	1.46E+00	1.58E-02		-8.09E-01	3.19E-03		-3.98E-01	2.01E-01		8.53E-01	3.53E-84		-2.07E-01	2.05E-04		Unigene39279_All//gi|297790792|ref|XP_002863281.1|//7.00E-55//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297309115|gb|EFH39540.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene39279_All//1.00E-55//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene39279_All//0.00E+00//TC147786				nr +
Unigene3928_All	1405	0.22	0.83	0.45	1.99	1.54	0.77	3.13	4.05	2.24	1.89E+00	6.32E-03		1.03E+00	2.81E-01		-3.63E-01	3.52E-01		-1.36E+00	3.51E-04	Down	3.70E-01	1.11E-01		-4.83E-01	5.51E-02		Unigene3928_All//gi|28558781|gb|AAO45752.1|//1.00E-143//pol protein [Cucumis melo]		Unigene3928_All//0.00E+00//NP822053				nr +
Unigene39282_All	938	4.91	2.43	0.57	3.61	3.89	1.44	3.56	0.45	1.66	-1.01E+00	3.60E-04	Down	-3.11E+00	2.19E-15	Down	1.08E-01	8.02E-01		-1.32E+00	9.81E-05	Down	-3.00E+00	5.98E-14	Down	-1.10E+00	2.05E-04	Down	Unigene39282_All//gi|297834520|ref|XP_002885142.1|//5.00E-40//IQ-domain 26 [Arabidopsis lyrata subsp. lyrata] >gi|297330982|gb|EFH61401.1| IQ-domain 26 [Arabidopsis lyrata subsp. lyrata]	Unigene39282_All//2.00E-40//AT3G16490| IQD26 (IQ-domain 26); calmodulin binding	Unigene39282_All//0.00E+00//gi|109854601|gb|DW483580.1|DW483580				nr -
Unigene39283_All	714	2.56	2.27	0.97	2.37	2.94	1.90	9.77	8.02	3.40	-1.76E-01	6.99E-01		-1.40E+00	7.28E-03		3.11E-01	5.56E-01		-3.22E-01	5.65E-01		-2.85E-01	1.79E-01		-1.52E+00	5.23E-13	Down	Unigene39283_All//gi|88900376|gb|ABD57500.1|//2.00E-27//At5g40460 [Arabidopsis thaliana]	Unigene39283_All//2.00E-23//AT5G40460| unknown protein					nr -
Unigene39284_All	747	1.75	2.03	0.07	3.27	2.40	3.81	1.81	1.45	1.01	2.17E-01	6.71E-01		-4.62E+00	4.46E-06	Down	-4.47E-01	2.87E-01		2.21E-01	6.27E-01		-3.16E-01	5.76E-01		-8.38E-01	8.98E-02								ESTscan -
Unigene39286_All	559	20.78	9.52	11.62	59.88	70.84	34.18	0.00	0.00	0.00	-1.13E+00	7.74E-11	Down	-8.38E-01	1.34E-06		2.42E-01	3.58E-03		-8.09E-01	1.01E-18		null	null		null	null		Unigene39286_All//gi|21314547|gb|AAM46999.1|AF512541_1//2.00E-30//alpha-expansin precursor [Gossypium hirsutum]	Unigene39286_All//3.00E-24//AT3G29030| EXPA5 (EXPANSIN A5)	Unigene39286_All//0.00E+00//TC138762				nr -
Unigene39287_All	511	30.72	25.19	65.55	4.78	6.27	4.15	1.49	1.06	1.33	-2.86E-01	4.85E-02		1.09E+00	1.96E-27	Up	3.92E-01	3.02E-01		-2.02E-01	6.49E-01		-4.86E-01	5.25E-01		-1.68E-01	7.94E-01		Unigene39287_All//gi|224088838|ref|XP_002308562.1|//6.00E-37//precursor of carboxylase p-protein 1, glycine decarboxylase complex [Populus trichocarpa] >gi|222854538|gb|EEE92085.1| precursor of carboxylase p-protein 1, glycine decarboxylase complex [Populus trichocarpa]	Unigene39287_All//5.00E-27//AT4G33010| AtGLDP1 (Arabidopsis thaliana glycine decarboxylase P-protein 1); catalytic/ glycine dehydrogenase (decarboxylating)/ pyridoxal phosphate binding	Unigene39287_All//0.00E+00//gi|84157296|gb|DN826343.1|DN826343		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene39288_All	570	3.30	2.84	1.49	2.53	2.84	1.98	12.76	6.09	4.89	-2.16E-01	6.26E-01		-1.14E+00	2.33E-02		1.64E-01	8.10E-01		-3.56E-01	5.58E-01		-1.07E+00	6.80E-08	Down	-1.38E+00	7.71E-12	Down	Unigene39288_All//gi|21617942|gb|AAM66992.1|//2.00E-30//mitochondrial import inner membrane translocase subunit Tim9 [Arabidopsis thaliana]	Unigene39288_All//1.00E-31//AT3G46560| TIM9; P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene39288_All//0.00E+00//TC167781				nr +

Unigene39289_All	629	19.55	11.92	9.40	19.48	12.15	18.09	13.11	9.50	8.87	-7.13E-01	9.79E-06		-1.06E+00	6.78E-10	Down	-6.81E-01	4.56E-06		-1.07E-01	6.07E-01		-4.64E-01	1.06E-02		-5.64E-01	1.22E-03		Unigene39289_All//gi|15231455|ref|NP_190240.1|//4.00E-39//TIM9; P-P-bond-hydrolysis-driven protein transmembrane transporter [Arabidopsis thaliana] >gi|12643936|sp|Q9XGX9.2|TIM9_ARATH RecName: Full=Mitochondrial import inner membrane translocase subunit Tim9; AltName: Full=Protein EMBRYO DEFECTIVE 2474 >gi|6523059|emb|CAB62326.1| small zinc finger-like protein TIM9 [Arabidopsis thaliana]	Unigene39289_All//2.00E-40//AT3G46560| TIM9; P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene39289_All//0.00E+00//TC167781				nr +
Unigene3929_All	943	9.15	26.11	8.24	32.06	39.40	20.21	46.90	87.18	52.13	1.51E+00	2.83E-34	Up	-1.51E-01	5.05E-01		2.97E-01	3.99E-04		-6.66E-01	3.05E-12		8.95E-01	1.95E-60		1.53E-01	2.86E-02		Unigene3929_All//gi|226491243|ref|NP_001146854.1|//4.00E-53//RING zinc finger protein-like [Zea mays] >gi|195604260|gb|ACG23960.1|RING zinc finger protein-like [Zea mays]	Unigene3929_All//4.00E-43//AT5G20885| zinc finger (C3HC4-type RING finger) family protein	Unigene3929_All//0.00E+00//TC147634				nr -
Unigene39290_All	1025	16.49	1.58	0.52	19.54	29.93	23.00	0.00	0.00	0.00	-3.38E+00	1.71E-62	Down	-4.99E+00	4.02E-79	Down	6.16E-01	9.65E-12		2.36E-01	4.76E-02		null	null		null	null		Unigene39290_All//gi|88697586|gb|AB048785.1|//1.00E-155//alpha-expansin 1 [Gossypium hirsutum] >gi|187936328|gb|ACD37707.1| alpha expansin [Gossypium hirsutum]	Unigene39290_All//4.00E-97//AT2G40610| ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	Unigene39290_All//0.00E+00//gi|78343769|gb|DT564043.1|DT564043				nr -
Unigene39292_All	891	9.87	6.31	5.86	1.06	3.63	2.89	4.46	0.38	0.18	-6.44E-01	9.04E-04		-7.52E-01	1.99E-04		1.77E+00	7.29E-07	Up	1.44E+00	4.05E-04	Up	-3.57E+00	3.23E-19	Down	-4.64E+00	7.64E-24	Down	Unigene39292_All//gi|38564292|gb|AK23725.1|//4.00E-39//At5g62280 [Arabidopsis thaliana] >gi|45592914|gb|AAS68111.1|At5g62280 [Arabidopsis thaliana]	Unigene39292_All//2.00E-36//AT5G62280| unknown protein					nr -
Unigene39293_All	812	7.09	2.75	5.25	3.37	3.60	3.17	1.04	1.13	0.83	-1.37E+00	1.55E-07	Down	-4.34E-01	1.00E-01		9.54E-02	8.24E-01		-8.99E-02	8.24E-01		1.21E-01	8.54E-01		-3.20E-01	6.25E-01				Unigene39293_All//1.00E-09//TC150482				
Unigene39294_All	413	9.63	12.51	4.13	15.56	15.68	13.23	34.50	20.85	24.40	3.78E-01	1.61E-01		-1.22E+00	1.86E-04	Down	1.07E-02	9.71E-01		-2.34E-01	3.82E-01		-7.27E-01	4.63E-08		-4.99E-01	1.06E-04		Unigene39294_All//gi|115482422|ref|NP_001061804.1|//1.00E-50//Os10g0466300 [Oryza sativa Japonica Group] >gi|113639413|dbj|BAF26718.1|Os10g0466300 [Oryza sativa Japonica Group]	Unigene39294_All//4.00E-36//AT1G04510| transducin family protein / WD-40 repeat family protein	Unigene39294_All//4.00E-177//ESS00384		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene39295_All	833	0.38	2.43	0.26	3.47	3.22	3.04	7.87	8.48	20.80	2.69E+00	1.81E-06	Up	-5.60E-01	6.63E-01		-1.05E-01	8.17E-01		-1.92E-01	6.34E-01		1.08E-01	6.36E-01		1.40E+00	2.51E-27	Up	Unigene39295_All//gi|225446048|ref|XP_002268885.1|//2.00E-39//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene39295_All//8.00E-30//AT4G30230| unknown protein	Unigene39295_All//0.00E+00//DW514259				nr +
Unigene39296_All	1575	0.00	0.19	0.24	0.00	0.17	0.06	48.62	35.03	19.48	7.59E+00	4.43E-02		7.89E+00	2.50E-02		7.45E+00	7.01E-02		5.84E+00	4.76E-01		-4.73E-01	8.27E-19		-1.32E+00	2.39E-108	Down	Unigene39296_All//gi|300498294|gb|ADK23849.1|//1.00E-91//WRKY72 [Solanum lycopersicum]	Unigene39296_All//2.00E-60//AT5G15130| WRKY72; transcription factor	Unigene39296_All//6.00E-19//TC164018	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene39297_All	743	6.55	13.43	4.23	3.49	2.04	2.13	3.47	1.46	3.65	1.04E+00	2.65E-08	Up	-6.31E-01	2.70E-02		-7.74E-01	3.93E-02		-7.13E-01	7.29E-02		-1.25E+00	5.15E-04	Down	7.09E-02	8.44E-01				Unigene39297_All//0.00E+00//TC172435				
Unigene39299_All	536	10.84	23.73	17.39	20.72	17.60	16.68	50.72	83.83	44.82	1.13E+00	8.26E-12	Up	6.82E-01	4.74E-04		-2.36E-01	1.95E-01		-3.13E-01	8.02E-02		7.25E-01	1.64E-23		-1.79E-01	6.33E-02		Unigene39299_All//gi|24461867|gb|AN62354.1|AF506028_23//5.00E-17//CTV.22 [Citrus trifoliata]	Unigene39299_All//5.00E-12//AT1G15780| unknown protein	Unigene39299_All//0.00E+00//TC153162				nr +
Unigene39300_All	529	4.45	1.34	2.92	20.34	12.17	8.79	12.47	19.44	8.36	-1.73E+00	1.14E-04	Down	-6.09E-01	1.61E-01		-7.41E-01	3.57E-06		-1.21E+00	6.11E-12	Down	6.41E-01	5.34E-05		-5.77E-01	3.54E-03				Unigene39300_All//0.00E+00//gi|18099162|gb|BM358416.1|BM358416				
Unigene39301_All	937	0.78	0.22	1.36	4.84	3.75	2.07	0.72	1.83	3.15	-1.85E+00	4.08E-02		8.03E-01	2.01E-01		-3.68E-01	2.09E-01		-1.22E+00	1.73E-05	Down	1.34E+00	3.54E-03		2.12E+00	7.86E-09	Up	Unigene39301_All//gi|225431419|ref|XP_002279961.1|//2.00E-55//PREDICTED: similar to HB2 homeodomain protein isoform 2 [Vitis vinifera]	Unigene39301_All//6.00E-49//AT4G35550| WOX13 (WUSCHEL-RELATED HOMEOBOX 13); DNA binding / transcription factor	Unigene39301_All//0.00E+00//DW496927	HB			nr +
Unigene39303_All	383	67.62	141.03	103.86	85.71	77.68	116.98	87.87	115.89	74.89	1.06E+00	4.28E-43	Up	6.19E-01	1.21E-12		-1.42E-01	1.65E-01		4.49E-01	5.34E-09		3.99E-01	1.88E-08		-2.31E-01	5.34E-03		Unigene39303_All//gi|9802746|gb|AAF99815.1|AC034257_7//4.00E-24//Similar to developmental protein [Arabidopsis thaliana]	Unigene39303_All//7.00E-15//AT1G17730| VPS46.1 (VACUOLAR PROTEIN SORTING 46.1)	Unigene39303_All//2.00E-179//TC140484		ko04144|Endocytosis		nr +
Unigene39305_All	502	0.21	2.62	0.42	0.60	0.14	0.00	1.18	1.58	1.27	3.65E+00	1.28E-05	Up	1.03E+00	5.91E-01		-2.12E+00	1.65E-01		-9.22E+00	3.99E-02		4.24E-01	5.77E-01		1.07E-01	9.01E-01									
Unigene39307_All	448	30.72	14.14	29.00	46.70	44.27	51.72	18.31	11.76	9.43	-1.12E+00	1.42E-12	Down	-8.28E-02	6.16E-01		-7.70E-02	6.04E-01		1.47E-01	2.63E-01		-6.39E-01	3.81E-04		-9.58E-01	9.28E-08		Unigene39307_All//gi|639834|emb|CAA58823.1|//6.00E-23//NADH dehydrogenase [Solanum tuberosum]	Unigene39307_All//8.00E-11//AT5G08530| CI51 (51 kDa subunit of complex I); 4 iron, 4 sulfur cluster binding / FMN binding / NAD or NADH binding / NADH dehydrogenase (ubiquinone)/ oxidoreductase, acting on NADH or NADPH	Unigene39307_All//1.00E-177//TC157832		ko00190|Oxidative phosphorylation		nr -
Unigene39308_All	3281	1.00	0.43	0.65	0.18	0.20	0.44	11.39	21.77	30.89	-1.22E+00	5.01E-04	Down	-6.30E-01	7.86E-02		1.30E-01	9.05E-01		1.27E+00	2.66E-02		9.34E-01	1.46E-56		1.44E+00	8.55E-162	Up	Unigene39308_All//gi|297597467|ref|NP_001044016.2|//1.00E-106//Os01g0706400 [Oryza sativa Japonica Group] >gi|56784921|dbj|BAD82253.1| MAPK activating protein-like [Oryza sativa Japonica Group] >gi|255673607|dbj|BAF05930.2|Os01g0706400 [Oryza sativa Japonica Group]	Unigene39308_All//5.00E-76//AT2G19710| unknown protein	Unigene39308_All//0.00E+00//gi|3325916|gb|AI054802.1|AI054802				nr -
Unigene39312_All	418	24.16	21.09	21.53	22.40	19.77	18.26	54.42	37.20	19.54	-1.96E-01	3.21E-01		-1.66E-01	4.06E-01		-1.80E-01	3.96E-01		-2.95E-01	1.41E-01		-5.49E-01	7.72E-08		-1.48E+00	8.67E-39	Down	Unigene39312_All//gi|17380185|sp|O82531.1|PSB1_PETHY//7.00E-20//RecName: Full=Proteasome subunit beta type-1; AltName: Full=20S proteasome alpha subunit F; AltName: Full=20S proteasome subunit beta-6 >gi|3608485|gb|AAC35983.1|proteasome beta subunit [Petunia x hybrida]	Unigene39312_All//2.00E-17//AT3G60820| PBB1; peptidase/ threonine-type endopeptidase	Unigene39312_All//0.00E+00//gi|84168775|gb|DR457423.1|DR457423		ko03050|Proteasome		nr +
Unigene39313_All	1607	0.00	0.00	0.00	0.00	0.04	0.14	6.63	5.96	26.06	null	null		null	null		5.42E+00	6.09E-01		7.13E+00	1.19E-01		-1.55E-01	4.01E-01		1.97E+00	8.92E-105	Up	Unigene39313_All//gi|13161397|dbj|BAB33033.1|//1.00E-165//CPRD2 [Vigna unguiculata]	Unigene39313_All//1.00E-134//AT1G30700| FAD-binding domain-containing protein	Unigene39313_All//0.00E+00//TC170571		ko00620|Pyruvate metabolism//ko00908|Zeatin biosynthesis		nr +
Unigene39314_All	482	62.74	136.03	80.98	67.07	80.94	68.12	5.79	0.61	3.14	1.12E+00	1.19E-56	Up	3.68E-01	3.11E-05		2.71E-01	1.02E-03		2.23E-02	8.59E-01		-3.25E+00	1.19E-12	Down	-8.82E-01	6.45E-03		Unigene39314_All//gi|10798750|dbj|BAB16427.1|//6.00E-47//NtEIG-E80 [Nicotiana tabacum]	Unigene39314_All//2.00E-38//AT3G54040| photoassimilate-responsive protein-related	Unigene39314_All//0.00E+00//gi|109834928|gb|DW233493.1|DW233493				nr +
Unigene39315_All	1027	2.14	0.59	0.62	11.01	9.25	11.17	9.59	11.48	5.55	-1.85E+00	9.28E-05	Down	-1.78E+00	2.71E-04	Down	-2.51E-01	1.59E-01		2.07E-02	9.34E-01		2.59E-01	9.88E-02		-7.90E-01	7.62E-07		Unigene39315_All//gi|297842663|ref|XP_002889213.1|//3.00E-68//At1g78815 [Arabidopsis lyrata subsp. lyrata] >gi|297335054|gb|EFH65472.1|At1g78815 [Arabidopsis lyrata subsp. lyrata]	Unigene39315_All//3.00E-66//AT1G78815| LSH7 (LIGHT SENSITIVE HYPOCOTYLS 7)	Unigene39315_All//0.00E+00//TC138660				nr -
Unigene39317_All	353	133.10	46.22	172.12	63.50	19.02	7.29	25.03	7.22	1.81	-1.53E+00	5.03E-66	Down	3.71E-01	7.83E-08		-1.74E+00	1.21E-47	Down	-3.12E+00	8.36E-84	Down	-1.79E+00	1.11E-19	Down	-3.79E+00	1.14E-45	Down	Unigene39317_All//gi|255631336|gb|ACU16035.1|//8.00E-06//unknown [Glycine max]		Unigene39317_All//6.00E-145//FL576427				nr +
Unigene39318_All	495	34.77	32.14	38.83	7.35	4.80	2.74	3.93	2.79	2.49	-1.14E-01	4.43E-01		1.59E-01	2.68E-01		-6.14E-01	4.76E-02		-1.42E+00	1.49E-05	Down	-4.96E-01	2.44E-01		-6.55E-01	1.01E-01									
Unigene39319_All	970	1.08	0.10	0.05	2.82	1.85	1.49	0.78	5.13	0.33	-3.37E+00	2.13E-04	Down	-4.30E+00	9.00E-05	Down	-6.14E-01	9.73E-02		-9.23E-01	1.48E-02		2.71E+00	1.99E-18	Up	-1.26E+00	7.70E-02				Unigene39319_All//1.00E-117//C0083955				
Unigene3932_All	1442	12.88	11.88	13.59	20.45	23.14	16.69	20.08	22.49	46.69	-1.17E-01	4.05E-01		7.73E-02	6.22E-01		1.78E-01	6.97E-02		-2.93E-01	3.46E-03		1.63E-01	7.51E-02		1.22E+00	1.99E-83	Up	Unigene3932_All//gi|297847710|ref|XP_002891736.1|//1.00E-61//F12M16.10 [Arabidopsis lyrata subsp. lyrata] >gi|297337578|gb|EFH67995.1|F12M16.10 [Arabidopsis lyrata subsp. lyrata]	Unigene3932_All//2.00E-57//AT1G53190| zinc finger (C3HC4-type RING finger) family protein	Unigene3932_All//0.00E+00//TC173683				nr -
Unigene39320_All	712	2.43	8.97	2.24	19.10	11.46	9.26	7.84	20.25	8.50	1.89E+00	1.38E-12	Up	-1.12E-01	8.19E-01		-7.37E-01	1.38E-07		-1.04E+00	6.58E-12	Down	1.37E+00	1.41E-21	Up	1.18E-01	6.16E-01		Unigene39320_All//gi|30682547|ref|NP_849375.1|//6.00E-10//four F5 protein-related / 4F5 protein-related [Arabidopsis thaliana] >gi|28416731|gb|AAO42896.1|At4g13612 [Arabidopsis thaliana]		Unigene39320_All//0.00E+00//TC169707				nr +
Unigene39321_All	553	16.46	18.60	21.67	17.21	19.18	20.17	61.55	26.76	16.93	1.76E-01	3.78E-01		3.96E-01	2.23E-02		1.57E-01	4.54E-01		2.30E-01	2.28E-01		-1.20E+00	6.39E-41	Down	-1.86E+00	6.94E-80	Down	Unigene39321_All//gi|192910686|gb|ACF06451.1|//2.00E-18//QM-like protein [Elaeis guineensis]	Unigene39321_All//1.00E-15//AT1G26910| 60S ribosomal protein L10 (RPL10B)	Unigene39321_All//0.00E+00//TC161859		ko03010|Ribosome		nr -
Unigene39322_All	538	2.04	2.45	1.88	3.33	3.90	3.19	2.99	0.93	0.89	2.62E-01	6.27E-01		-1.19E-01	8.50E-01		2.28E-01	6.44E-01		-6.34E-02	9.11E-01		-1.68E+00	6.74E-04	Down	-1.75E+00	2.96E-04	Down	Unigene39322_All//gi|42567218|ref|NP_194584.3|//4.00E-61//RabGAP/TBC domain-containing protein [Arabidopsis thaliana] >gi|119935837|gb|ABM06008.1|At4g28550 [Arabidopsis thaliana]	Unigene39322_All//2.00E-62//AT4G28550| RabGAP/TBC domain-containing protein	Unigene39322_All//3.00E-120//DR463251				nr -
Unigene39324_All	576	0.64	2.38	0.09	1.04	3.41	2.12	2.64	2.68	3.67	1.90E+00	2.58E-03		-2.78E+00	1.03E-01		1.72E+00	3.49E-04	Up	1.03E+00	1.07E-01		2.29E-02	9.96E-01		4.72E-01	2.28E-01		Unigene39324_All//gi|86279638|gb|ABC94473.1| type 2 diacylglycerol acyltransferase [Vernicia fordii] >gi|86279638|gb|ABC94474.1| type 2 diacylglycerol acyltransferase [Vernicia fordii]	Unigene39324_All//1.00E-56//AT3G51520| diacylglycerol acyltransferase family	Unigene39324_All//0.00E+00//CO498385				nr -
Unigene39325_All	443	15.94	4.46	4.93	30.25	27.05	37.42	111.38	68.40	58.36	-1.84E+00	1.75E-13	Down	-1.69E+00	1.49E-11	Down	-1.61E-01	3.52E-01		3.07E-01	3.00E-02		-7.03E-01	1.74E-24		-9.32E-01	2.34E-40		Unigene39325_All//gi|7340791|emb|CAA63107.1|//2.00E-38//ribosomal protein L23 [Spinacia oleracea]	Unigene39325_All//2.00E-27//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene39325_All//0.00E+00//TC155794		ko03010|Ribosome		nr +
Unigene39331_All	666	1.18	0.15	1.20	0.45	1.60	2.17	2.35	2.45	3.23	-2.95E+00	3.66E-03		2.54E-02	9.94E-01		1.84E+00	1.02E-02		2.27E+00	3.41E-04	Up	5.93E-02	9.13E-01		4.60E-01	2.37E-01		Unigene39331_All//gi|38346143|emb|CAD40681.2|//3.00E-20//OSJNB0118P14.3 [Oryza sativa (japonica cultivar-group)]						nr +
Unigene39332_All	720	0.36	0.99	3.18	2.01	11.72	8.84	3.29	14.40	24.07	1.44E+00	1.06E-01		3.13E+00	5.83E-08	Up	2.55E+00	7.17E-27	Up	2.14E+00	1.70E-15	Up	2.13E+00	1.43E-28	Up	2.87E+00	8.09E-68	Up	Unigene39332_All//gi|2808682|emb|CAA05267.1|//6.00E-23//Hcr9-4C [Solanum habrochaites]	Unigene39332_All//8.00E-23//AT1G45616| AtRLP6 (Receptor Like Protein 6); protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene39333_All	969	4.27	8.00	2.53	6.32	15.49	28.29	10.60	11.00	15.01	9.07E-01	1.75E-05		-7.55E-01	1.57E-02		1.29E+00	1.82E-19	Up	2.16E+00	3.74E-66	Up	5.29E-02	7.69E-01		5.01E-01	8.78E-05		Unigene39333_All//gi|224060467|ref|XP_002300214.1|//5.00E-41//SAUR family protein [Populus trichocarpa] >gi|222847472|gb|EEE85019.1| SAUR family protein [Populus trichocarpa]	Unigene39333_All//5.00E-11//AT5G53590| auxin-responsive family protein					nr +
Unigene39334_All	329	28.15	22.33	42.41	39.37	50.66	73.03	25.19	58.56	64.30	-3.34E-01	8.54E-02		5.91E-01	1.42E-04		3.64E-01	6.17E-03		8.92E-01	8.86E-16		1.22E+00	6.21E-24	Up	1.35E+00	2.11E-31	Up		Unigene39334_All//6.00E-06//AT5G18650| zinc finger (C3HC4-type RING finger) family protein	Unigene39334_All//9.00E-76//TC135860		ko04120|Ubiquitin mediated proteolysis		kegg +
Unigene39335_All	722	125.08	538.21	112.92	83.14	137.55	212.81	71.27	182.12	457.92	2.11E+00	0.00E+00	Up	-1.48E-01	1.37E-02		7.26E-01	1.24E-49		1.36E+00	1.41E-192	Up	1.35E+00	2.91E-187	Up	2.68E+00	0.00E+00	Up	Unigene39335_All//gi|206584339|gb|ACI15342.1|//2.00E-29//NAC domain protein NAC2 [Gossypium hirsutum] >gi|206584351|gb|ACI15348.1| NAC domain protein NAC2 [Gossypium hirsutum]	Unigene39335_All//7.00E-14//AT1G01720| ATAF1; transcription activator/ transcription factor	Unigene39335_All//0.00E+00//TC131344	NAC			nr -
Unigene39337_All	364	24.29	40.65	37.89	33.67	37.37	64.02	48.44	173.96	54.07	7.43E-01	3.87E-07		6.41E-01	4.08E-05		1.51E-01	4.03E-01		9.27E-01	2.51E-16		1.84E+00	1.54E-141	Up	1.59E-01	1.82E-01		Unigene39337_All//gi|86371808|gb|ABB89042.1|//3.00E-57//glutathione reductase [Vigna unguiculata]	Unigene39337_All//2.00E-54//AT3G24170| ATGR1 (glutathione-disulfide reductase); FAD binding / NADP or NADPH binding / glutathione-disulfide reductase/ oxidoreductase	Unigene39337_All//2.00E-135//TC132998		ko00480|Glutathione metabolism		nr -

Unigene39338_All	964	0.16	3.00	0.11	1.09	0.79	1.17	1.89	3.25	3.10	4.20E+00	7.47E-13	Up	-5.59E-01	7.75E-01		-4.66E-01	5.02E-01		1.10E-01	8.80E-01		7.86E-01	1.22E-02		7.17E-01	2.16E-02				Unigene39338_All//0.00E+00//ES805958				
Unigene3934_All	1191	75.16	54.46	92.95	9.87	10.61	9.67	5.33	1.23	2.64	-4.65E-01	2.12E-17		3.06E-01	9.02E-10		1.04E-01	5.91E-01		-2.97E-02	8.90E-01		-2.12E+00	1.15E-17	Down	-1.01E+00	1.07E-06	Down	Unigene3934_All//gi|6587814|gb|AAF18505.1|AC010924.18//1.00E-132//ESTs gb|A1992412, gb|A1994629 come from this gene [Arabidopsis thaliana]	Unigene3934_All//2.00E-120//AT1G16080| unknown protein	Unigene3934_All//0.00E+00//TC134922				nr +
Unigene39340_All	682	1.76	3.57	1.41	0.51	0.86	1.32	2.29	0.74	0.76	1.02E+00	1.34E-02		-3.28E-01	6.27E-01		7.48E-01	4.81E-01		1.37E+00	7.76E-02		-1.64E+00	1.02E-03		-1.59E+00	9.20E-04	Down	Unigene39340_All//gi|18399682|ref|NP_566428.1|//1.00E-56//atnudt16 (Arabidopsis thaliana Nudix hydrolase homolog 16); hydrolase >gi|68565942|sp|Q9LJR1.1|NUD16_ARATH RecName: Full=Nudix hydrolase 16, mitochondrial; Short=AtNUDT16; Flags: Precursor >gi|11762150|gb|AAG40353.1|AF32500 1_1 AT3g12600 [Arabidopsis thaliana] >gi|13926332|gb|AAK49630.1|AF37291 4_1 AT3g12600/T2E22_108 [Arabidopsis thaliana] >gi|27363312|gb|AAO11575.1| At3g12600/T2E22_108 [Arabidopsis thaliana]	Unigene39340_All//5.00E-48//AT3G12600| atnudt16 (Arabidopsis thaliana Nudix hydrolase homolog 16); hydrolase	Unigene39340_All//0.00E+00//TC178880				nr +
Unigene39341_All	738	3.76	21.76	18.76	3.24	5.93	7.34	10.89	7.65	8.21	2.53E+00	5.74E-44	Up	2.32E+00	2.44E-33	Up	8.71E-01	1.84E-03		1.18E+00	5.01E-06	Up	-5.10E-01	5.43E-03		-4.08E-01	2.29E-02		Unigene39341_All//gi|4432836|gb|AAD20685.1|//4.00E-19//expressed protein [Arabidopsis thaliana] >gi|26450173|dbj|BAC42205.1| GPI-anchored protein [Arabidopsis thaliana]	Unigene39341_All//2.00E-15//AT2G28410| unknown protein	Unigene39341_All//0.00E+00//gi|109873513|gb|DW502488.1|DW502488				nr -
Unigene39342_All	501	22.56	25.79	16.16	26.05	27.49	32.72	72.91	30.12	31.09	1.93E-01	2.52E-01		-4.82E-01	6.48E-03		7.78E-02	6.83E-01		3.29E-01	1.96E-02		-1.28E+00	4.34E-48	Down	-1.23E+00	8.84E-47	Down	Unigene39342_All//gi|42565437|gb|AAS20989.1|//4.00E-27//60S ribosomal protein L13 [Hyacinthus orientalis]	Unigene39342_All//6.00E-20//AT3G49010| ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1): structural constituent of ribosome	Unigene39342_All//0.00E+00//gi|109840107|gb|DW238668.1|DW238668		ko03010|Ribosome		nr -
Unigene39345_All	224	0.47	5.43	0.48	2.22	0.31	2.22	0.76	4.48	0.18	3.54E+00	4.02E-05	Up	2.51E-02	1.00E+00		-2.85E+00	1.78E-02		-3.90E-03	9.87E-01		2.57E+00	4.79E-04	Up	-2.09E+00	3.13E-01									
Unigene39346_All	412	1.65	0.86	0.52	2.18	1.67	2.63	1.44	4.36	3.48	-9.39E-01	2.77E-01		-1.68E+00	8.70E-02		-3.81E-01	6.05E-01		2.74E-01	6.70E-01		1.60E+00	4.89E-04	Up	1.28E+00	9.57E-03									
Unigene39349_All	1748	1.65	0.61	0.43	0.91	0.28	0.83	9.34	3.92	3.44	-1.44E+00	2.02E-04	Down	-1.95E+00	5.30E-06	Down	-1.73E+00	7.76E-04	Down	-1.41E-01	7.89E-01		-1.25E+00	2.65E-21	Down	-1.44E+00	4.89E-27	Down	Unigene39349_All//gi|115459964|ref|NP_001053582.1|//4.00E-39//Os04g0566600 [Oryza sativa Japonica Group] >gi|21741799|emb|CAD41286.1| OSJNBa0005N02.4 [Oryza sativa (japonica cultivar-group)] >gi|113565153|dbj|BAF15496.1| Os04g0566600 [Oryza sativa Japonica Group]	Unigene39349_All//2.00E-25//AT1G14600| DNA binding / transcription factor	Unigene39349_All//0.00E+00//TC177190	G2-like			nr -
Unigene3935_All	1359	37.58	21.14	42.40	25.73	25.26	23.40	6.28	2.40	4.13	-8.30E-01	2.18E-27		1.74E-01	2.19E-02		-2.65E-02	8.13E-01		-1.37E-01	1.86E-01		-1.39E+00	2.11E-13	Down	-6.05E-01	4.08E-04		Unigene3935_All//gi|228480464|gb|ACQ41893.1|//1.00E-152//cinnamoyl-CoA reductase [Camellia oleifera]	Unigene3935_All//1.00E-146//AT5G58890| cinnamoyl-CoA reductase family	Unigene3935_All//0.00E+00//TC147252		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene39350_All	289	4.89	6.66	3.69	11.89	5.84	5.16	24.29	11.57	4.41	4.47E-01	3.56E-01		-4.08E-01	4.86E-01		-1.03E+00	9.87E-04	Down	-1.21E+00	3.02E-04	Down	-1.07E+00	1.15E-07	Down	-2.46E+00	4.85E-24	Down			Unigene39350_All//8.00E-73//TC173981				
Unigene39351_All	461	12.37	82.54	32.80	11.13	15.39	16.65	26.23	43.16	62.74	2.74E+00	1.02E-112	Up	1.41E+00	1.46E-18	Up	4.67E-01	3.23E-02		5.82E-01	5.49E-03		7.18E-01	1.02E-10		1.26E+00	3.14E-38	Up	Unigene39351_All//gi|18407840|ref|NP_566871.1|//5.00E-12//PSK1; growth factor [Arabidopsis thaliana] >gi|29428768|sp|Q8LA14.2|PSK6_ARATH RecName: Full=Putative phytosulfokines 6; Short=AtPSK6; Short=AtPSK3_2; Contains: RecName: Full=Phytosulfokine-alpha-like; Short=PSK-alpha-like; Short=Phytosulfokine-a-like; Contains: RecName: Full=Phytosulfokine-beta; Short=PSK-beta; Short=Phytosulfokine-b; Flags: Precursor >gi|27808144|dbj|BAB72177.2| phytosulfokine precursor 3_2 [Arabidopsis thaliana] >gi|88010851|gb|ABD38863.1| At3g44735 [Arabidopsis thaliana]	Unigene39351_All//3.00E-13//AT3G44735| PSK1; growth factor	Unigene39351_All//0.00E+00//TC164757				nr -
Unigene39352_All	513	9.28	29.93	11.73	14.76	14.57	29.84	37.99	332.57	91.40	1.69E+00	3.01E-25	Up	3.38E-01	2.00E-01		-1.90E-02	9.42E-01		1.02E+00	1.31E-12	Up	3.13E+00	0.00E+00	Up	1.27E+00	4.66E-62	Up			Unigene39352_All//3.00E-157//gi|109884468|gb|DW513438.1|DW513438				
Unigene39353_All	289	50.69	839.46	117.74	98.59	289.66	359.90	32.19	160.24	59.00	4.05E+00	0.00E+00	Up	1.22E+00	6.45E-33	Up	1.55E+00	1.35E-141	Up	1.87E+00	5.73E-207	Up	2.32E+00	6.47E-139	Up	8.74E-01	4.71E-13		Unigene39353_All//gi|1107526|emb|CAA61158.1|//3.00E-22//SIEP1L protein [Beta vulgaris subsp. vulgaris]	Unigene39353_All//8.00E-16//AT1G78830| curculin-like (mannose-binding) lectin family protein	Unigene39353_All//2.00E-162//gi|109865314|gb|DW494290.1|DW494290				nr +
Unigene39354_All	311	17.83	28.35	24.66	28.67	39.31	50.97	32.22	73.92	58.67	6.69E-01	5.77E-04		4.67E-01	3.53E-02		4.55E-01	3.54E-03		8.30E-01	1.79E-09		1.20E+00	1.04E-27	Up	8.65E-01	1.16E-13		Unigene39354_All//gi|190148357|gb|ACE63261.1|//1.00E-36//histidine kinase 3 [Betula pendula]	Unigene39354_All//1.00E-26//AT1G27320| AHK3 (ARABIDOPSIS HISTIDINE KINASE 3); cytokinin receptor/ osmosensor/ protein histidine kinase	Unigene39354_All//3.00E-168//C0110785	Orphans			nr +
Unigene39355_All	489	54.67	33.88	25.48	61.33	50.42	60.40	64.41	59.49	42.45	-6.90E-01	6.64E-11		-1.10E+00	3.34E-22	Down	-2.83E-01	2.99E-03		-2.19E-02	8.63E-01		-1.15E-01	2.43E-01		-6.02E-01	1.15E-12		Unigene39355_All//gi|297849408|ref|XP_002892585.1|//2.00E-20//ADP-ribosylation factor [Arabidopsis lyrata subsp. lyrata] >gi|297338427|gb|EFH68844.1| ADP-ribosylation factor [Arabidopsis lyrata subsp. lyrata]	Unigene39355_All//1.00E-21//AT3G62290| ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding	Unigene39355_All//0.00E+00//gi|21099841|gb|BQ412154.1|BQ412154				nr -
Unigene39356_All	2662	0.00	0.00	0.00	5.76	0.71	0.36	9.18	26.86	7.95	null	null		null	null		-3.02E+00	6.33E-65	Down	-4.02E+00	2.77E-71	Down	1.55E+00	7.07E-125	Up	-2.08E-01	3.82E-02		Unigene39356_All//gi|297727859|ref|NP_001176293.1|//3.00E-84//Os11g0100300 [Oryza sativa Japonica Group] >gi|77548278|gb|ABA91075.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255679678|dbj|BAH95021.1| Os11g0100300 [Oryza sativa Japonica Group]	Unigene39356_All//3.00E-176//AT2G28780| unknown protein					nr +
Unigene39359_All	608	23.66	52.17	18.92	36.13	28.09	34.39	49.86	71.97	47.44	1.14E+00	1.06E-28	Up	-3.23E-01	4.25E-02		-3.63E-01	1.03E-03		-7.12E-02	6.13E-01		5.30E-01	1.86E-13		-7.18E-02	4.81E-01		Unigene39359_All//gi|15225415|ref|NP_182039.1|//3.00E-18//PVA12 (PLANT VAP HOMOLOG 12); structural molecule [Arabidopsis thaliana] >gi|30023716|gb|AAP13391.1| At2g45140 [Arabidopsis thaliana]		Unigene39359_All//0.00E+00//TC160547				nr -
Unigene39360_All	951	0.11	1.07	0.28	1.89	1.38	0.66	3.65	2.59	2.89	3.28E+00	3.79E-04	Up	1.35E+00	4.09E-01		-4.55E-01	3.59E-01		-1.50E+00	2.75E-03		-4.92E-01	1.05E-01		-3.35E-01	2.60E-01		Unigene39360_All//gi|124360728|gb|ABN08705.1|//2.00E-60//DOT; Homeodomain-related [Medicago truncatula]	Unigene39360_All//3.00E-32//AT5G44180| homeobox transcription factor, putative	Unigene39360_All//5.00E-15//gi|73865338|gb|DT468076.1|DT468076	HB			nr -
Unigene39362_All	558	0.38	0.91	0.57	41.60	18.76	11.25	25.08	3.52	3.57	1.28E+00	2.31E-01		6.10E-01	6.24E-01		-1.15E+00	3.08E-26	Down	-1.89E+00	5.27E-48	Down	-2.83E+00	2.65E-53	Down	-2.81E+00	1.22E-54	Down	Unigene39362_All//gi|255547379|ref|XP_002514747.1|//7.00E-14//conserved hypothetical protein [Ricinus communis] >gi|223546351|gb|EEF47853.1| conserved hypothetical protein [Ricinus communis]	Unigene39362_All//5.00E-05//AT3G47510| unknown protein					nr -
Unigene39367_All	249	7.56	8.14	10.27	11.40	14.52	10.70	16.47	37.77	40.00	1.06E-01	8.10E-01		4.40E-01	2.98E-01		3.49E-01	3.20E-01		-9.17E-02	8.15E-01		1.20E+00	8.41E-12	Up	1.28E+00	4.41E-14	Up	Unigene39367_All//gi|224130568|ref|XP_002320873.1|//6.00E-06//predicted protein [Populus trichocarpa] >gi|222861646|gb|EEE99188.1| predicted protein [Populus trichocarpa]	Unigene39367_All//7.00E-07//AT2G46550| unknown protein	Unigene39367_All//2.00E-48//gi|78348265|gb|DT568539.1|DT568539				nr -
Unigene39368_All	863	32.98	147.84	81.14	123.06	290.92	219.69	109.69	245.74	198.73	2.16E+00	3.42E-286	Up	1.30E+00	1.32E-74	Up	1.24E+00	2.43E-303	Up	8.36E-01	1.43E-108		1.16E+00	3.12E-238	Up	8.57E-01	3.07E-119		Unigene39368_All//gi|29164798|gb|AAO65149.1|//1.00E-41//auxin repressed protein [Gossypium barbadense]	Unigene39368_All//3.00E-17//AT2G33830| dormancy/auxin associated family protein	Unigene39368_All//0.00E+00//gi|78337282|gb|DT557556.1|DT557556				nr -
Unigene39369_All	341	3.22	3.12	2.65	4.82	6.06	5.03	21.57	9.68	6.54	-4.63E-02	9.55E-01		-2.80E-01	6.54E-01		3.30E-01	5.26E-01		6.21E-02	9.25E-01		-1.16E+00	5.94E-09	Down	-1.72E+00	3.65E-16	Down			Unigene39369_All//2.00E-135//gi|109887154|gb|DW516123.1|DW516123				
Unigene3937_All	225	0.00	1.80	0.47	0.22	0.61	0.40	0.38	2.23	7.79	1.08E+01	1.36E-02		8.89E+00	3.98E-01		1.47E+00	6.19E-01		8.59E-01	7.94E-01		2.57E+00	2.28E-02		4.37E+00	3.23E-10	Up			Unigene3937_All//6.00E-79//C0102970				
Unigene39373_All	530	0.79	4.49	0.60	2.63	2.47	1.79	2.63	2.52	2.63	2.51E+00	5.46E-07	Up	-3.90E-01	7.17E-01		-9.21E-02	8.58E-01		-5.56E-01	3.52E-01		-6.10E-02	9.18E-01		-9.00E-04	9.95E-01		Unigene39373_All//gi|98961075|gb|AB59021.1|//2.00E-10//At3g15760 [Arabidopsis thaliana]	Unigene39373_All//6.00E-08//AT1G52565| unknown protein	Unigene39373_All//4.00E-14//TC171639				nr +
Unigene39374_All	221	23.20	12.84	16.87	26.37	24.00	24.73	37.50	10.97	16.04	-8.54E-01	1.26E-03		-4.60E-01	1.02E-01		-1.36E-01	6.14E-01		-9.29E-02	7.29E-01		-1.77E+00	3.12E-18	Down	-1.22E+00	3.13E-11	Down	Unigene39374_All//gi|62751093|dbj|BAB95794.1|//2.00E-15//similar to to 60S ribosomal protein L35 [Solanum lycopersicum]	Unigene39374_All//3.00E-14//AT3G09500| 60S ribosomal protein L35 (RPL35A)	Unigene39374_All//3.00E-99//gi|164296145|gb|ES840914.1|ES840914		ko03010|Ribosome		nr +
Unigene39376_All	527	1.89	0.00	4.34	4.92	6.47	1.97	4.09	2.62	5.44	-1.09E+01	7.45E-06	Down	1.20E+00	7.42E-03		3.96E-01	2.74E-01		-1.32E+00	9.02E-04	Down	-6.45E-01	1.03E-01		4.12E-01	2.11E-01								
Unigene39378_All	224	51.15	32.35	23.30	45.59	65.64	70.37	78.90	113.07	113.65	-6.61E-01	7.80E-05		-1.13E+00	2.58E-10	Down	5.26E-01	1.34E-04		6.26E-01	4.99E-06		5.19E-01	7.05E-08		5.27E-01	2.42E-08		Unigene39378_All//gi|195607028|gb|ACG25344.1|//2.00E-36//protein kinase G11A [Zea mays]	Unigene39378_All//5.00E-37//AT5G55910| D6PK (D6 PROTEIN KINASE); kinase/ protein kinase	Unigene39378_All//2.00E-116//TC137884				nr -
Unigene3938_All	1473	6.61	27.18	10.99	8.45	5.35	21.22	7.64	19.49	17.55	2.04E+00	1.38E-83	Up	7.34E-01	2.95E-07		-6.59E-01	7.59E-06		1.33E+00	3.17E-38	Up	1.35E+00	2.11E-41	Up	1.20E+00	6.46E-32	Up	Unigene3938_All//gi|206572099|gb|ACI13682.1|//1.00E-116//NAC domain protein [Malus x domestica]	Unigene3938_All//1.00E-83//AT5G61430| NAC100 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 100); transcription factor	Unigene3938_All//0.00E+00//TC144148	NAC			nr +
Unigene39381_All	375	0.70	2.16	0.00	0.66	0.83	2.41	1.47	0.00	0.11	1.63E+00	5.05E-02		-9.45E+00	8.56E-02		3.15E-01	8.38E-01		1.86E+00	2.18E-02		-1.05E+01	4.61E-04	Down	-3.79E+00	2.03E-03				Unigene39381_All//5.00E-16//ES803332				
Unigene39382_All	624	2.68	4.06	7.68	3.51	6.24	5.21	2.57	1.54	1.34	5.98E-01	1.35E-01		1.52E+00	5.54E-07	Up	8.28E-01	5.94E-03		5.69E-01	1.11E-01		-7.41E-01	1.15E-01		-9.42E-01	3.51E-02				Unigene39382_All//4.00E-36//ES803332				
Unigene39384_All	318	16.95	46.53	20.09	14.26	24.26	48.15	18.22	77.81	21.55	1.46E+00	8.58E-20	Up	2.46E-01	3.53E-01		7.67E-01	1.15E-04		1.76E+00	2.62E-28	Up	2.09E+00	8.17E-66	Up	2.42E-01	2.44E-01				Unigene39384_All//7.00E-101//TC136687				
Unigene39385_All	980	0.43	0.93	2.17	1.52	2.92	2.03	1.81	0.94	2.85	1.12E+00	1.30E-01		2.35E+00	1.17E-05	Up	9.36E-01	1.01E-02		4.11E-01	4.09E-01		-9.50E-01	3.09E-02		6.51E-01	4.50E-02		Unigene39385_All//gi|225432116|ref|XP_002274451.1|//1.00E-133//PREDICTED: similar to vacuolar protein sorting 13C protein-like [Vitis vinifera]	Unigene39385_All//1.00E-117//AT1G48090| phosphoinositide binding					nr +
Unigene39386_All	578	6.16	2.37	6.36	3.88	5.78	6.56	1.98	0.65	1.17	-1.38E+00	5.13E-05	Down	4.64E-02	8.94E-01		5.75E-01	9.27E-02		7.59E-01	1.62E-02		-1.60E+00	7.50E-03		-7.53E-01	1.68E-01		Unigene39386_All//gi|15239573|ref|NP_200229.1|//1.00E-10//PTAC15 (PLASTID TRANSCRIPTIONALLY ACTIVE15) [Arabidopsis thaliana]	Unigene39386_All//6.00E-12//AT5G54180| PTAC15 (PLASTID TRANSCRIPTIONALLY ACTIVE15)					nr -
Unigene39387_All	330	69.60	118.69	73.26	53.14	53.11	61.18	88.53	65.86	41.89	7.70E-01	1.15E-18		7.39E-02	5.95E-01		-6.00E-04	9.92E-01		2.03E-01	1.33E-01		-4.27E-01	1.65E-06		-1.08E+00	1.12E-30	Down			Unigene39387_All//2.00E-175//gi|109826916|gb|DW225625.1|DW225625				
Unigene39389_All	1339	0.70	0.00	1.99	1.38	0.41	0.64	9.28	6.84	4.91	-9.46E+00	1.46E-05	Down	1.50E+00	3.87E-04	Up	-1.74E+00	2.18E-04	Down	-1.10E+00	2.24E-02		-4.42E-01	2.11E-03		-9.19E-01	1.32E-10		Unigene39389_All//gi|240254350|ref|NP_177276.4|//2.00E-27//DNA binding / transcription factor [Arabidopsis thaliana]	Unigene39389_All//4.00E-22//AT1G71200| DNA binding / transcription factor		b6LLH			nr +
Unigene39394_All	584	8.87	161.81	10.76	35.57	144.52	79.35	19.76	41.44	107.24	4.19E+00	0.00E+00	Up	2.79E-01	2.82E-01		2.02E+00	2.81E-204	Up	1.16E+00	1.18E-45	Up	1.07E+00	2.31E-24	Up	2.44E+00	2.02E-203	Up			Unigene39394_All//4.00E-138//gi|109876927|gb|DW505901.1|DW505901				
Unigene39395_All	959	1.64	1.53	1.06	2.96	4.02	2.03	0.49	0.57	2.53	-9.52E-02	8.47E-01		-6.34E-01	2.47E-01		4.42E-01	1.71E-01		-5.48E-01	1.53E-01		2.24E-01	7.92E-01		2.39E+00	2.07E-08	Up	Unigene39395_All//gi|18420914|ref|NP_568469.1|//8.00E-99//phosphate translocator-related [Arabidopsis thaliana]	Unigene39395_All//4.00E-100//AT5G25400| phosphate translocator-related	Unigene39395_All//0.00E+00//TC141120				nr +

Unigene39396_All	438	2.51	2.20	1.70	7.62	4.56	2.78	4.63	3.05	1.91	-1.91E-01	7.45E-01		-5.60E-01	3.93E-01		-7.41E-01	2.10E-02		-1.45E+00	2.75E-05	Down	-6.02E-01	1.43E-01		-1.28E+00	1.41E-03									
Unigene39397_All	478	77.17	177.98	103.60	76.91	162.67	171.02	17.07	33.93	75.18	1.21E+00	8.47E-83	Up	4.25E-01	3.43E-08		1.08E+00	1.83E-75	Up	1.15E+00	1.03E-79	Up	9.91E-01	9.12E-15		2.14E+00	9.67E-100	Up			Unigene39397_All//2.00E-108//DW508052					
Unigene394_All	585	4.29	3.46	2.64	8.34	7.06	6.79	9.18	3.72	3.54	-3.09E-01	4.43E-01		-7.02E-01	9.42E-02		-2.41E-01	4.22E-01		-2.97E-01	3.23E-01		-1.30E+00	5.42E-08	Down	-1.37E+00	6.84E-09	Down	Unigene394_All//gi|108707957|gb|AB F95752.1|/6.00E-09//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene394_All//8.00E-06//AT1G72410| COP1-interacting protein-related	Unigene394_All//0.00E+00//gi|164336129|gb|ES847547.1|ES847547				nr +
Unigene3940_All	899	137.99	66.62	76.35	203.36	198.72	276.36	196.45	113.81	151.87	-1.05E+00	5.20E-97	Down	-8.54E-01	1.56E-66		-3.33E-02	5.06E-01		4.43E-01	4.95E-46		-7.88E-01	5.53E-104		-3.71E-01	4.47E-28		Unigene3940_All//gi|39725278|emb|CAC85228.1|/2.00E-99//salt tolerance protein 2 [Beta vulgaris]	Unigene3940_All//1.00E-44//AT4G17520| nuclear RNA-binding protein, putative	Unigene3940_All//0.00E+00//TC135072				nr +
Unigene39403_All	378	4.43	8.18	7.61	9.75	7.20	4.66	6.71	3.43	5.27	8.85E-01	1.29E-02		7.80E-01	4.42E-02		-4.38E-01	1.71E-01		-1.07E+00	7.95E-04	Down	-9.69E-01	6.42E-03		-3.49E-01	3.34E-01		Unigene39403_All//gi|255082856|ref|XP_002504414.1|//7.00E-10//glycogen synthase kinase 3 [Micromonas sp. RCC299] >gi|226519682|gb|ACO65672.1| glycogen synthase kinase 3 [Micromonas sp. RCC299]	Unigene39403_All//5.00E-11//AT1G57870| ATSK42 (ARABIDOPSIS SHAGGY-LIKE KINASE 42); ATP binding / protein kinase/ protein serine/threonine kinase	Unigene39403_All//2.00E-34//TC178887				nr +
Unigene39404_All	1820	0.00	0.11	0.06	0.33	1.21	13.13	3.39	10.56	36.42	6.80E+00	1.36E-01		5.87E+00	3.98E-01		1.88E+00	3.62E-05	Up	5.32E+00	1.23E-126	Up	1.64E+00	5.91E-37	Up	3.42E+00	2.05E-305	Up	Unigene39404_All//gi|193734712|gb|ACF19982.1|/1.00E-146//MYC2 [Hevea brasiliensis]	Unigene39404_All//4.00E-57//AT4G00870| basic helix-loop-helix (bHLH) family protein	Unigene39404_All//0.00E+00//CO102490	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene39405_All	989	30.21	29.82	28.91	21.46	17.06	16.03	15.65	8.49	6.61	-1.87E-02	8.71E-01		-6.32E-02	6.21E-01		-3.31E-01	3.88E-03		-4.21E-01	3.25E-04		-8.81E-01	8.90E-12		-1.24E+00	1.10E-20	Down	Unigene39405_All//gi|297821635|ref|XP_002876700.1|/1.00E-89//metal-dependent phosphohydrolase HD domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297324539|gb|EFH54959.1| metal-dependent phosphohydrolase HD domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene39405_All//2.00E-84//AT2G23820| metal-dependent phosphohydrolase HD domain-containing protein	Unigene39405_All//0.00E+00//TC140489				nr -
Unigene39406_All	1098	0.38	0.78	1.12	1.09	2.04	2.30	0.85	1.48	2.54	1.04E+00	1.72E-01		1.55E+00	2.13E-02		9.05E-01	3.36E-02		1.08E+00	7.33E-03		8.09E-01	8.07E-02		1.58E+00	6.18E-06	Up	Unigene39406_All//gi|162463339|ref|NP_001105293.1|/1.00E-140//target of rapamycin [Zea mays] >gi|58429948|gb|AAW78347.1| target of rapamycin [Zea mays]	Unigene39406_All//1.00E-95//AT1G50030| TOR (TARGET OF RAPAMYCIN); 1-phosphatidylinositol-3-kinase/ protein binding					nr -
Unigene3941_All	1459	2.51	8.86	3.03	6.49	8.33	10.59	16.05	20.77	22.12	1.82E+00	1.35E-23	Up	2.71E-01	3.89E-01		3.61E-01	2.57E-02		7.07E-01	3.66E-07		3.72E-01	2.24E-05		4.62E-01	2.44E-08		Unigene3941_All//gi|150036255|gb|ABR67418.1|/1.00E-137//mitochondrial FAD carrier [Cucumis melo]	Unigene3941_All//3.00E-115//AT3G05290| PNC1 (PEROXISOMAL ADENINE NUCLEOTIDE CARRIER 1); ADP transmembrane transporter/ ATP transmembrane transporter/ binding	Unigene3941_All//0.00E+00//TC145835		ko04146|Peroxisome		nr -
Unigene39410_All	579	1.08	50.84	0.00	1.38	5.17	2.57	3.65	12.13	42.52	5.55E+00	6.77E-149	Up	-1.01E+01	1.41E-03		1.91E+00	5.44E-07	Up	9.03E-01	1.09E-01		1.73E+00	4.76E-15	Up	3.54E+00	5.30E-117	Up	Unigene39410_All//gi|75127082|sp|Q6NM02.1||4445_ARATH//1.00E-13//RecName: Full=Uncharacterized protein At4g14450, chloroplastic; Flags: Precursor >gi|38603896|gb|AAR24693.1| At4g14450 [Arabidopsis thaliana] >gi|41349908|gb|AAS00339.1| At4g14450 [Arabidopsis thaliana]	Unigene39410_All//1.00E-05//AT4G14450| unknown protein	Unigene39410_All//0.00E+00//gi|109875320|gb|DW504294.1|DW504294				nr +
Unigene39411_All	1145	0.82	0.27	1.53	1.87	1.65	0.28	1.00	0.99	2.51	-1.63E+00	3.13E-02		9.00E-01	8.21E-02		-1.78E-01	7.12E-01		-2.76E+00	1.89E-07	Down	-1.66E-02	1.01E+00		1.33E+00	6.91E-05	Up	Unigene39411_All//gi|2865427|gb|AAC02666.1|/6.00E-12//polyprotein [Arabidopsis thaliana]		Unigene39411_All//7.00E-58//gi|78350168|gb|DT570442.1|DT570442				nr -
Unigene39415_All	414	23.13	23.13	26.11	3.97	10.81	18.87	10.42	11.11	8.28	3.00E-04	9.99E-01		1.75E-01	3.90E-01		1.45E+00	4.10E-07	Up	2.25E+00	4.50E-20	Up	9.23E-02	7.35E-01		-3.32E-01	2.05E-01				Unigene39415_All//1.00E-78//TC168145					
Unigene39417_All	777	77.44	59.60	133.71	11.60	21.49	67.95	897.68	393.37	433.71	-3.78E-01	2.16E-08		7.88E-01	9.69E-49		8.89E-01	4.87E-12		2.55E+00	7.26E-155	Up	-1.19E+00	0.00E+00	Down	-1.05E+00	0.00E+00	Down	Unigene39417_All//gi|300793598|tpg|DAA33865.1|/1.00E-81//TPA: TPA_inf: aquaporin PIP2;10 [Gossypium hirsutum]	Unigene39417_All//2.00E-58//AT2G37170| PIP2B (PLASMA MEMBRANE INTRINSIC PROTEIN 2); water channel	Unigene39417_All//0.00E+00//TC165706				nr -
Unigene39421_All	536	4.00	9.55	13.01	1.86	1.61	1.10	0.16	3.35	2.90	1.25E+00	5.19E-06	Up	1.70E+00	1.59E-11	Up	-2.11E-01	7.79E-01		-7.63E-01	2.89E-01		4.41E+00	2.75E-10	Up	4.20E+00	6.62E-09	Up			Unigene39421_All//5.00E-26//CD486453					
Unigene39427_All	473	0.33	2.36	0.00	1.58	0.58	1.05	1.70	0.44	0.25	2.83E+00	5.03E-04	Up	-8.37E+00	2.44E-01		-1.44E+00	7.43E-02		-5.89E-01	4.87E-01		-1.94E+00	1.17E-02		-2.75E+00	9.43E-04	Down								
Unigene39429_All	545	1.92	0.19	0.49	1.74	2.34	1.82	3.26	2.15	1.39	-3.37E+00	2.13E-04	Down	-1.97E+00	1.13E-02		4.29E-01	5.32E-01		7.01E-02	9.38E-01		-6.02E-01	1.78E-01		-1.23E+00	4.20E-03		Unigene39429_All//gi|9294626|dbj|BAB02965.1|/3.00E-88//dem protein [Arabidopsis thaliana]	Unigene39429_All//1.00E-80//AT3G19240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), Vacuolar import and degradation, Vid27-related (InterPro:IPR013863); BEST Arabidopsis thaliana protein match is: dem protein-related / defective embryo and meristems protein-related (TAIR:AT4G33400.1); Has 206 Blast hits to 202 proteins in 88 species: Archae - 0; Bacteria - 0; Metazoa - 11; Fungi - 117; Plants - 38; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink).	Unigene39429_All//0.00E+00//DT462703				nr -
Unigene3943_All	1393	2.67	11.79	6.65	7.62	22.35	20.81	4.80	3.81	7.84	2.14E+00	7.51E-37	Up	1.32E+00	1.43E-10	Up	1.55E+00	1.48E-52	Up	1.45E+00	1.62E-40	Up	-3.32E-01	1.21E-01		7.08E-01	2.59E-06		Unigene3943_All//gi|55375996|gb|AAV50009.1|/1.00E-120//anthranilate N-hydroxycinnamoyl/benzoyltransferase [Malus x domestica]	Unigene3943_All//2.00E-92//AT5G67150| transferase family protein	Unigene3943_All//0.00E+00//DW232948		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene39431_All	427	62.37	44.50	62.10	65.33	111.53	64.94	74.26	84.77	162.15	-4.87E-01	3.44E-06		-6.10E-03	9.82E-01		7.72E-01	1.57E-26		-8.60E-03	9.50E-01		1.91E-01	2.30E-02		1.13E+00	5.85E-76	Up	Unigene39431_All//gi|183041149|dbj|BAG24402.1|/3.00E-17//bZIP protein [Glycine max]	Unigene39431_All//2.00E-08//AT5G28770| BZOZH3; DNA binding / protein heterodimerization/ transcription factor	Unigene39431_All//0.00E+00//TC138505	bZIP			nr +
Unigene39433_All	368	26.30	16.94	10.56	38.99	39.96	40.62	21.83	14.20	12.67	-6.35E-01	5.52E-04		-1.32E+00	5.92E-11	Down	3.55E-02	8.38E-01		5.94E-02	7.23E-01		-6.21E-01	6.51E-04		-7.85E-01	1.08E-05				Unigene39433_All//8.00E-135//TC160693					
Unigene39434_All	439	33.61	57.13	39.42	62.18	56.40	73.66	166.14	151.57	78.95	7.66E-01	4.08E-12		2.30E-01	1.21E-01		-1.41E-01	2.26E-01		2.44E-01	1.22E-02		-1.32E-01	2.37E-02		-1.07E+00	1.52E-74	Down	Unigene39434_All//gi|17977975|emb|CAC80989.1|/1.00E-24//translation initiation factor (eIF-1A) [Beta vulgaris]	Unigene39434_All//8.00E-17//AT2G04520| eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative	Unigene39434_All//0.00E+00//gi|21099905|gb|BQ412218.1|BQ412218				nr -
Unigene39435_All	828	4.30	1.53	1.93	9.63	5.03	5.24	3.98	1.41	1.20	-1.49E+00	1.58E-05	Down	-1.16E+00	8.62E-04	Down	-9.36E-01	8.77E-07		-8.78E-01	1.33E-05		-1.49E+00	3.28E-06	Down	-1.73E+00	9.62E-08	Down			Unigene39435_All//5.00E-92//DW502145					
Unigene39436_All	815	1.22	1.62	1.83	2.08	1.44	2.44	3.99	2.31	0.78	4.06E-01	4.87E-01		5.85E-01	3.07E-01		-5.33E-01	3.00E-01		2.31E-01	6.48E-01		-7.92E-01	9.78E-03		-2.35E+00	5.17E-11	Down	Unigene39436_All//gi|297744587|emb|CBI37849.3|/2.00E-06//unnamed protein product [Vitis vinifera]		Unigene39436_All//8.00E-140//gi|78351821|gb|DT572095.1|DT572095				nr +
Unigene3944_All	1401	4.71	2.75	4.52	37.37	24.70	16.09	6.58	2.21	2.02	-7.76E-01	7.02E-04		-5.71E-02	8.16E-01		-5.97E-01	3.02E-19		-1.22E+00	1.95E-56	Down	-1.58E+00	3.44E-17	Down	-1.70E+00	9.07E-20	Down	Unigene3944_All//gi|300793633|tpg|DAA33875.1|/1.00E-147//TPA: TPA_inf: aquaporin NIP6;1 [Gossypium hirsutum]	Unigene3944_All//4.00E-93//AT1G80760| NIP6;1 (NOD26-LIKE INTRINSIC PROTEIN 6;1); boron transporter/ glycerol transmembrane transporter/ urea transmembrane transporter/ water channel/ water transporter	Unigene3944_All//0.00E+00//TC158461				nr +
Unigene39441_All	329	31.17	26.64	19.58	44.51	30.04	39.26	5.65	2.92	1.82	-2.26E-01	2.36E-01		-6.71E-01	2.93E-04		-5.67E-01	2.62E-05		-1.81E-01	2.79E-01		-9.53E-01	2.57E-02		-1.64E+00	1.88E-04	Down		Unigene39441_All//2.00E-06//AT4G09190| RNase H domain-containing protein	Unigene39441_All//1.00E-118//ES818849			ESTscan -
Unigene39442_All	517	1.72	4.12	5.87	2.99	5.00	4.02	2.94	8.08	3.54	1.26E+00	5.48E-03		1.77E+00	1.21E-05	Up	7.42E-01	5.92E-02		4.28E-01	3.90E-01		1.46E+00	2.14E-07	Up	2.68E-01	5.53E-01		Unigene39442_All//gi|119888002|gb|ABM05953.1|/3.00E-07//proline-rich protein [Gossypium hirsutum]	Unigene39442_All//1.00E-05//AT4G16380| metal ion binding	Unigene39442_All//4.00E-125//DN803752				nr +
Unigene39446_All	1180	1.42	1.20	0.27	1.86	1.81	1.53	1.40	1.03	4.02	-2.39E-01	6.10E-01		-2.39E+00	1.21E-04	Down	-3.79E-02	9.29E-01		-2.79E-01	5.68E-01		-4.44E-01	3.64E-01		1.52E+00	4.91E-09	Up	Unigene39446_All//gi|15234617|ref|NP_194739.1|/2.00E-40//tRNA-splicing endonuclease positive effector-related [Arabidopsis thaliana]	Unigene39446_All//7.00E-34//AT4G30100| tRNA-splicing endonuclease positive effector-related	Unigene39446_All//2.00E-42//TC147059				nr +
Unigene39447_All	1051	0.10	1.11	0.41	0.47	0.56	1.72	6.64	32.93	17.47	3.48E+00	7.08E-05	Up	2.02E+00	1.39E-01		2.33E-01	8.26E-01		1.86E+00	4.17E-04	Up	2.31E+00	1.15E-103	Up	1.40E+00	1.03E-28	Up	Unigene39447_All//gi|41619312|gb|AAS10073.1|/3.00E-65//MYB transcription factor [Arabidopsis thaliana]	Unigene39447_All//7.00E-56//AT4G05100| AtMYB74 (myb domain protein 74); DNA binding / transcription factor	Unigene39447_All//0.00E+00//TC141121	MYB			nr +
Unigene39448_All	988	4.08	4.10	3.02	6.81	5.61	5.39	6.98	4.53	3.10	8.90E-03	9.83E-01		-4.34E-01	1.81E-01		-2.79E-01	2.46E-01		-3.36E-01	1.65E-01		-6.24E-01	1.70E-03		-1.17E+00	7.31E-09	Down	Unigene39448_All//gi|297599681|ref|NP_001047583.2|/2.00E-92//Os02g0649400 [Oryza sativa Japonica Group] >gi|255671132|dbj|BAF09497.2| Os02g0649400 [Oryza sativa Japonica Group]	Unigene39448_All//3.00E-92//AT3G50790| late embryogenesis abundant protein, putative / LEA protein, putative	Unigene39448_All//0.00E+00//TC177788				nr -
Unigene39449_All	1814	2.51	0.56	1.91	28.18	17.98	4.68	0.40	3.55	0.20	-2.17E+00	6.43E-11	Down	-3.95E-01	1.97E-01		-6.48E-01	1.01E-21		-2.59E+00	1.60E-156	Down	3.16E+00	1.42E-27	Up	-1.00E+00	1.66E-01		Unigene39449_All//gi|119507461|dbj|BAF42038.1|/1.00E-119//pectin methylesterase 1 [Pyrus communis]	Unigene39449_All//1.00E-115//AT3G49220| pectinesterase family protein	Unigene39449_All//0.00E+00//TC137161		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene3945_All	1833	6.42	18.85	6.30	4.38	6.48	6.87	0.00	0.00	0.00	1.55E+00	9.75E-50	Up	-2.68E-02	8.91E-01		5.67E-01	2.69E-04		6.52E-01	2.84E-05		null	null		null	null		Unigene3945_All//gi|57233444|gb|AAW48295.1|/3.00E-85//pore-forming toxin-like protein HFr-2 [Triticum aestivum]		Unigene3945_All//0.00E+00//TC148656				nr +
Unigene39450_All	469	8.48	3.67	9.42	6.80	6.53	4.72	2.25	1.16	0.59	-1.21E+00	1.22E-04	Down	1.53E-01	6.34E-01		-5.69E-02	8.72E-01		-5.27E-01	1.42E-01		-9.60E-01	1.12E-01		-1.92E+00	2.21E-03				Unigene39450_All//2.00E-31//TC160101		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		kegg -
Unigene39451_All	477	0.99	10.84	1.67	1.46	5.34	10.60	1.24	2.28	0.75	3.46E+00	1.33E-19	Up	7.62E-01	3.62E-01		1.87E+00	7.42E-06	Up	2.86E+00	4.60E-17	Up	8.77E-01	1.39E-01		-7.23E-01	3.71E-01									
Unigene39452_All	760	1.17	2.40	1.05	1.51	1.63	0.89	4.45	0.33	2.67	1.04E+00	3.37E-02		-1.55E-01	8.24E-01		1.14E-01	8.71E-01		-7.58E-01	2.45E-01		-3.75E+00	4.42E-17	Down	-7.35E-01	1.09E-02		Unigene39452_All//gi|145351606|ref|NP_567903.3|//5.00E-75//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene39452_All//2.00E-76//AT4G32710| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene39452_All//9.00E-07//TC178099		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism		nr +
Unigene39454_All	880	18.37	56.25	36.13	13.81	18.70	25.87	9.71	16.48	12.90	1.61E+00	5.06E-75	Up	9.76E-01	1.06E-21		4.38E-01	8.25E-04		9.05E-01	2.38E-15		7.64E-01	7.53E-09		4.11E-01	5.34E-03				Unigene39454_All//2.00E-110//DN803832					
Unigene39457_All	733	0.50	5.32	3.05	1.22	4.13	5.36	2.31	2.11	3.26	3.41E+00	9.04E-15	Up	2.61E+00	1.40E-06	Up	1.76E+00	2.24E-06	Up	2.13E+00	1.06E-09	Up	-1.29E-01	7.82E-01		4.99E-01	1.68E-01									
Unigene39459_All	903	17.44	2.41	5.31	1.82	2.40	2.75	0.47	0.56	0.88	-2.85E+00	1.87E-49	Down	-1.72E+00	1.49E-25	Down	4.00E-01	4.05E-01		5.96E-01	1.55E-01		2.46E-01	7.84E-01		9.14E-01	1.85E-01		Unigene39459_All//gi|18422702|ref|NP_568866.1|/9.00E-50//bHLH071 (beta HLH protein 71); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75283539|sp|Q6X0X0.1|BH071_ARATH RecName: Full=Transcription factor bHLH71; AltName: Full=Transcription factor EN 17; AltName: Full=bHLH transcription factor bHLH071; AltName: Full=Basic helix-loop-helix protein 71; Short=bHLH 71; Short=AtbHLH71 >gi|105830423|gb|ABF74724.1| At5g46690 [Arabidopsis thaliana]	Unigene39459_All//3.00E-40//AT5G46690| bHLH071 (beta HLH protein 71); DNA binding / transcription factor	Unigene39459_All//4.00E-83//gi|78335657|gb|DT555931.1|DT555931	bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene3946_All	1449	6.43	10.14	16.54	30.77	34.17	52.64	10.88	15.26	8.96	6.58E-01	6.75E-06		1.36E+00	8.82E-28	Up	1.51E-01	5.65E-02		7.75E-01	1.29E-38		4.88E-01	2.59E-06		-2.80E-01	2.53E-02		Unigene3946_All//gi|4585877|gb|AAD25550.1|AC005850_7//1.00E-108//Hypothetical protein [Arabidopsis thaliana]	Unigene3946_All//7.00E-105//AT1G61600| unknown protein	Unigene3946_All//0.00E+00//TC169377				nr +
Unigene39460_All	466	6.85	3.59	5.37	5.34	4.43	4.17	2.54	6.37	2.48	-9.33E-01	7.39E-03		-3.51E-01	3.60E-01		-2.70E-01	5.50E-01		-3.59E-01	4.07E-01		1.33E+00	7.41E-05	Up	-3.52E-02	9.63E-01									

Unigene39462_All	648	4.76	9.93	5.42	4.30	6.06	3.35	0.46	1.03	1.23	1.06E+00	8.08E-06	Up	1.87E-01	6.21E-01		4.93E-01	1.18E-01		-3.64E-01	3.82E-01		1.18E+00	1.44E-01		1.43E+00	4.39E-02		Unigene39462_All//gi|14423428|gb|AK622396.1|AF386951_1//3.00E-30//Unknown protein [Arabidopsis thaliana]	Unigene39462_All//1.00E-31//AT1G27290| unknown protein	Unigene39462_All//8.00E-47//TC141561				nr +
Unigene39463_All	535	0.88	0.38	0.60	1.68	1.54	0.93	2.13	1.80	0.45	-1.22E+00	2.72E-01		-5.60E-01	6.28E-01		-1.18E-01	8.51E-01		-8.52E-01	2.63E-01		-2.48E-01	6.60E-01		-2.26E+00	3.40E-04	Down	Unigene39463_All//gi|124359163|gb|ABN05686.1|//8.00E-12//Zinc finger, CCHC-type [Medicago truncatula]		Unigene39463_All//6.00E-07//ES792704				nr -
Unigene39464_All	510	3.59	6.86	3.55	4.40	1.89	5.49	8.87	5.74	3.44	9.33E-01	4.93E-03		-1.64E-02	9.96E-01		-1.22E+00	2.63E-03		3.21E-01	4.46E-01		-6.29E-01	1.31E-02		-1.37E+00	1.40E-07	Down	Unigene39464_All//gi|28416737|gb|AA042899.1|//1.00E-13//At3g18510 [Arabidopsis thaliana]		Unigene39464_All//4.00E-11//DR459031				nr -
Unigene39465_All	824	0.00	0.12	0.13	0.73	0.92	3.12	12.21	43.88	82.72	6.94E+00	3.86E-01		7.01E+00	3.98E-01		3.42E-01	7.20E-01		2.11E+00	1.86E-06	Up	1.85E+00	4.08E-81	Up	2.76E+00	3.72E-254	Up	Unigene39465_All//gi|225441993|ref|XP_002271332.1|//9.00E-43//PREDICTED: similar to GTP binding / translation initiation factor [Vitis vinifera]	Unigene39465_All//8.00E-44//AT3G14260| unknown protein					nr -
Unigene39468_All	1047	0.40	5.13	1.73	2.71	2.57	21.91	0.16	1.16	1.33	3.68E+00	2.05E-21	Up	2.11E+00	2.08E-04	Up	-8.01E-02	8.22E-01		3.01E+00	1.78E-80	Up	2.84E+00	3.39E-05	Up	3.04E+00	2.08E-06	Up	Unigene39468_All//gi|257831443|gb|ACY71022.1|//1.00E-47//TPA23 [Capsicum annuum]	Unigene39468_All//2.00E-33//AT2G28690| unknown protein	Unigene39468_All//5.00E-12//DR452606				nr -
Unigene39469_All	510	1.64	5.07	2.19	2.44	2.63	5.93	0.91	1.56	0.55	1.63E+00	1.16E-04	Up	4.18E-01	5.32E-01		1.09E-01	8.71E-01		1.28E+00	4.62E-04	Up	7.72E-01	2.88E-01		-7.38E-01	4.26E-01		Unigene39469_All//gi|9795613|gb|AAF98431.1|AC021044_10//8.00E-37//Unknown protein [Arabidopsis thaliana]	Unigene39469_All//3.00E-32//AT1G28240| unknown protein	Unigene39469_All//4.00E-45//CO073778				nr +
Unigene3947_All	1603	0.26	1.39	1.73	2.05	2.62	3.35	0.76	1.20	0.65	2.41E+00	2.46E-06	Up	2.73E+00	2.27E-08	Up	3.54E-01	2.74E-01		7.09E-01	5.71E-03		6.49E-01	1.28E-01		-2.43E-01	6.29E-01		Unigene3947_All//gi|4585877|gb|AAD25550.1|AC005850_7//1.00E-105//Hypothetical protein [Arabidopsis thaliana]	Unigene3947_All//3.00E-101//AT1G61600| unknown protein	Unigene3947_All//0.00E+00//TC169377				nr +
Unigene39470_All	850	4.49	1.19	1.32	1.93	4.17	4.30	1.64	0.39	0.80	-1.91E+00	5.16E-08	Down	-1.77E+00	6.54E-07	Down	1.11E+00	5.01E-04	Up	1.15E+00	3.70E-04	Up	-2.06E+00	2.51E-04	Down	-1.04E+00	3.24E-02		Unigene39470_All//gi|15236687|ref|NP_194942.1|//5.00E-66//ATVAMP711 (ARABIDOPSIS THALIANA VESICLE-ASSOCIATED MEMBRANE PROTEIN 711) [Arabidopsis thaliana] >gi|27805754|sp|O49377.2|VA711_ARATH RecName: Full=Vesicle-associated membrane protein 711; Short=AtVAMP711; AltName: Full=v-SNARE synaptobrevin 7C; Short=AtVAMP7C >gi|16612292|gb|AAL27509.1|AF439840_1 AT4g32150/F10N7_40 [Arabidopsis thaliana] >gi|3858935|emb|CAA16574.1| synaptobrevin-like protein [Arabidopsis thaliana] >gi|4103357|gb|AAD01748.1| vesicle-associated membrane protein 7C [Arabidopsis thaliana] >gi|7270119|emb|CAB79933.1| synaptobrevin-like protein [Arabidopsis thaliana] >gi|21593706|gb|AAM65673.1| synaptobrevin-like protein [Arabidopsis thaliana] >gi|21928069|gb|AAM78063.1| AT4g32150/F10N7_40 [Arabidopsis thaliana] >gi|110740910|dbj|BAE98551.1|	Unigene39470_All//2.00E-67//AT4G32150| ATVAMP711 (ARABIDOPSIS THALIANA VESICLE-ASSOCIATED MEMBRANE PROTEIN 711)	Unigene39470_All//0.00E+00//DW504159		ko04130|SNARE interactions in vesicular transport		nr +
Unigene39474_All	798	0.33	0.13	0.13	2.06	1.29	1.92	2.33	0.42	1.70	-1.37E+00	3.83E-01		-1.30E+00	4.36E-01		-6.70E-01	1.82E-01		-9.83E-02	8.59E-01		-2.48E+00	1.05E-06	Down	-4.58E-01	2.74E-01		Unigene39474_All//gi|240255326|ref|NP_187803.4|//2.00E-40//RNA binding [Arabidopsis thaliana]	Unigene39474_All//1.00E-41//AT3G11964| RNA binding					nr +
Unigene39476_All	236	25.27	13.96	18.28	39.47	37.06	40.00	87.43	50.12	43.55	-8.57E-01	4.24E-04		-4.68E-01	6.95E-02		-9.09E-02	6.87E-01		1.91E-02	9.45E-01		-8.03E-01	2.82E-13		-1.01E+00	1.31E-19	Down	Unigene39476_All//gi|21362874|sp|Q9ATF5.1|RL18A_CASSA//2.00E-18//RecName: Full=60S ribosomal protein L18a >gi|13430184|gb|AAK25759.1|AF334839_1 ribosomal protein L18a [Castanea sativa]	Unigene39476_All//3.00E-17//AT2G34480| 60S ribosomal protein L18A (RPL18aB)	Unigene39476_All//4.00E-114//gi|109890319|gb|DW519283.1|DW519283		ko03010|Ribosome		nr +
Unigene39478_All	388	7.69	8.23	14.82	12.07	12.78	4.66	4.14	2.69	1.64	9.81E-02	7.77E-01		9.47E-01	2.57E-04		8.27E-02	8.22E-01		-1.37E+00	1.26E-06	Down	-6.21E-01	1.91E-01		-1.33E+00	3.75E-03				Unigene39478_All//9.00E-98//CO099437				
Unigene39479_All	356	12.79	10.39	5.68	21.83	18.86	25.25	26.25	33.58	19.58	-2.99E-01	3.16E-01		-1.17E+00	1.04E-04	Down	-2.11E-01	3.60E-01		2.10E-01	3.45E-01		3.55E-01	1.76E-02		-4.23E-01	9.97E-03		Unigene39479_All//gi|162459484|ref|NP_001105726.1|//2.00E-17//eukaryotic translation initiation factor 3 subunit A [Zea mays] >gi|6685541|sp|Q9QHR2.1|EIF3A_MAIZE RecName: Full=Eukaryotic translation initiation factor 3 subunit A; Short=eIF3a; AltName: Full=eIF-3-theta; AltName: Full=Eukaryotic translation initiation factor 3 large subunit >gi|5106764|gb|AAD39834.1|AF073329_1 eukaryotic translation initiation factor 3 large subunit [Zea mays]		Unigene39479_All//1.00E-155//gi|109831035|gb|DW229594.1|DW229594				nr -
Unigene39481_All	1023	2.51	1.54	1.46	4.77	4.68	4.64	7.81	2.37	5.34	-7.07E-01	7.30E-02		-7.82E-01	5.87E-02		-2.84E-02	9.23E-01		-4.19E-02	9.04E-01		-1.72E+00	6.45E-17	Down	-5.50E-01	1.96E-03		Unigene39481_All//gi|63087714|emb|CAI93172.1|//1.00E-89//beta-1,3-glucuronosyltransferase [Gossypium raimondii]	Unigene39481_All//8.00E-81//AT1G27600| glycosyl transferase family 43 protein	Unigene39481_All//0.00E+00//ES851983				nr +
Unigene39482_All	1625	2.22	6.83	0.72	0.67	2.08	4.25	0.91	0.69	8.78	1.62E+00	2.01E-17	Up	-1.62E+00	6.79E-06	Down	1.62E+00	2.26E-06	Up	2.66E+00	1.76E-21	Up	-3.91E-01	4.42E-01		3.27E+00	2.14E-63	Up	Unigene39482_All//gi|15224120|ref|NP_179409.1|//0.00E+00//ATMPK7 (ARABIDOPSIS THALIANA MAP KINASE 7); MAP kinase/ kinase [Arabidopsis thaliana] >gi|21431797|sp|Q39027.2|MPK7_ARATH RecName: Full=Mitogen-activated protein kinase 7; Short=MAP kinase 7; Short=AtMPK7 >gi|4874286|gb|AAD31349.1| MAP kinase (ATMPK7) [Arabidopsis thaliana] >gi|110739420|dbj|BAF01620.1| MAP kinase [Arabidopsis thaliana]	Unigene39482_All//0.00E+00//AT2G18170| ATMPK7 (ARABIDOPSIS THALIANA MAP KINASE 7); MAP kinase/ kinase	Unigene39482_All//0.00E+00//TC146174		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene39483_All	693	23.63	23.03	36.73	486.57	311.16	181.31	0.12	0.24	0.00	-3.71E-02	8.03E-01		6.36E-01	1.03E-08		-6.45E-01	1.57E-140		-1.42E+00	0.00E+00	Down	9.83E-01	6.33E-01		-6.93E+00	3.58E-01		Unigene39483_All//gi|21322711|emb|CAD22154.1|//1.00E-43//pherophorin-dz1 protein [Volvox carteri f. nagariensis]		Unigene39483_All//1.00E-39//AI731546				nr +
Unigene39484_All	1114	0.19	0.00	0.29	0.36	1.98	1.74	2.62	7.05	22.60	-7.55E+00	1.22E-01		6.10E-01	6.24E-01		2.47E+00	5.62E-07	Up	2.29E+00	1.81E-05	Up	1.43E+00	7.09E-13	Up	3.11E+00	2.40E-106	Up	Unigene39484_All//gi|118500901|gb|ABK97619.1|//1.00E-159//1-aminocyclopropane-1-carboxylic acid oxidase [Durio zibethinus]	Unigene39484_All//3.00E-127//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene39484_All//0.00E+00//TC137620		ko00270|Cysteine and methionine metabolism		nr +
Unigene39486_All	399	36.32	23.37	19.49	64.92	54.54	60.22	84.45	30.06	34.25	-6.36E-01	1.46E-05		-8.99E-01	5.54E-09		-2.51E-01	1.80E-02		-1.09E-01	3.96E-01		-1.49E+00	4.48E-56	Down	-1.30E+00	3.41E-47	Down			Unigene39486_All//2.00E-163//gi|164302713|gb|ES837133.1|ES837133				
Unigene39488_All	1454	3.74	7.88	2.38	4.86	7.06	4.94	1.74	0.83	1.01	1.07E+00	6.54E-10	Up	-6.53E-01	1.44E-02		5.37E-01	1.66E-03		2.18E-02	9.46E-01		-1.07E+00	2.88E-03		-7.83E-01	2.17E-02		Unigene39488_All//gi|15225258|ref|NP_180187.1|//1.00E-130//IQ06 (IQ-domain 6); calmodulin binding [Arabidopsis thaliana] >gi|119935823|gb|ABM06004.1|At2g26180 [Arabidopsis thaliana]	Unigene39488_All//3.00E-109//AT2G26180| IQ06 (IQ-domain 6); calmodulin binding	Unigene39488_All//0.00E+00//TC133521				nr +
Unigene39489_All	497	2.63	6.02	4.29	7.82	39.42	6.09	7.49	4.54	1.28	1.19E+00	1.27E-03		7.04E-01	1.31E-01		2.33E+00	1.78E-56	Up	-3.61E-01	2.83E-01		-7.21E-01	1.10E-02		-2.55E+00	1.37E-13	Down	Unigene39489_All//gi|225447659|ref|XP_002275321.1|//2.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene39489_All//8.00E-06//AT4G10270| wound-responsive family protein	Unigene39489_All//0.00E+00//TC145255				nr -
Unigene3949_All	2049	0.69	0.99	1.38	1.14	2.08	2.05	3.24	4.39	7.14	5.21E-01	2.52E-01		9.99E-01	1.10E-02		8.67E-01	2.25E-03		8.43E-01	4.38E-03		4.37E-01	1.18E-02		1.14E+00	5.11E-17	Up	Unigene3949_All//gi|18412037|ref|NP_565183.1|//3.00E-84//LZF1 (LIGHT-REGULATED ZINC FINGER PROTEIN 1); transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|52788299|sp|Q9SYM2.2|STHY_ARATH RecName: Full=Probable salt tolerance-like protein At1g78600 >gi|20260418|gb|AAM13107.1| highly similar to rice zinc finger protein [Arabidopsis thaliana] >gi|30023798|gb|AAP13432.1| At1g78600 [Arabidopsis thaliana]	Unigene3949_All//4.00E-52//AT1G78600| LZF1 (LIGHT-REGULATED ZINC FINGER PROTEIN 1); transcription factor/ zinc ion binding	Unigene3949_All//0.00E+00//TC154927	DEB	ko04712|Circadian rhythm - plant		nr -
Unigene39494_All	427	22.67	31.68	8.85	47.48	33.71	35.22	53.17	54.52	53.37	4.83E-01	1.61E-03		-1.36E+00	1.93E-11	Down	-4.94E-01	1.16E-05		-4.31E-01	3.29E-04		3.61E-02	7.65E-01		5.30E-03	9.74E-01				Unigene39494_All//3.00E-122//TC160083				
Unigene39497_All	424	98.22	111.26	103.11	91.52	76.67	99.06	100.32	83.39	48.48	1.80E-01	2.66E-02		7.00E-02	4.71E-01		-2.56E-01	2.00E-03		1.14E-01	2.30E-01		-2.67E-01	3.06E-04		-1.05E+00	2.89E-42	Down	Unigene39497_All//gi|225453502|ref|XP_002277890.1|//4.00E-32//PREDICTED: similar to sec61beta family protein [Vitis vinifera]	Unigene39497_All//6.00E-18//AT3G60540| sec61beta family protein	Unigene39497_All//0.00E+00//TC170032		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export		nr -
Unigene39498_All	718	1.02	2.96	2.30	1.67	0.19	3.77	43.69	254.73	177.22	1.54E+00	9.72E-04	Up	1.17E+00	3.12E-02		-3.12E+00	1.54E-05	Down	1.18E+00	2.36E-03		2.54E+00	0.00E+00	Up	2.02E+00	0.00E+00	Up	Unigene39498_All//gi|290578583|gb|ADD51186.1|//4.00E-77//tumor-related protein [Vitis berlandieri x Vitis riparia]	Unigene39498_All//2.00E-55//AT1G17860| trypsin and protease inhibitor family protein / Kunitz family protein	Unigene39498_All//0.00E+00//TC160466				nr -
Unigene395_All	3789	4.46	4.28	4.65	9.85	9.51	6.34	6.80	2.38	3.55	-5.97E-02	6.84E-01		6.07E-02	6.84E-01		-5.08E-02	6.35E-01		-6.35E-01	8.43E-14		-1.51E+00	5.93E-44	Down	-9.35E-01	1.33E-21		Unigene395_All//gi|115452817|ref|NP_001050009.1|//2.00E-94//Os03g0330300 [Oryza sativa Japonica Group] >gi|108707956|gb|ABF95751.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548480|dbj|BAF11923.1| Os03g0330300 [Oryza sativa Japonica Group]	Unigene395_All//5.00E-17//AT3G14172| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: COP1-interacting protein-related (TAIR:AT1G72410.1); Has 2665 Blast hits to 1956 proteins in 215 species: Archae - 2; Bacteria - 189; Metazoa - 878; Fungi - 141; Plants - 132; Viruses - 5; Other Eukaryotes - 1318 (source: NCBI BLink).	Unigene395_All//0.00E+00//TC137311				nr -

Unigene3950_All	1458	45.47	4.10	7.27	13.26	7.91	8.21	12.09	6.48	5.52	-3.47E+00	8.16E-250	Down	-2.65E+00	4.76E-184	Down	-7.45E-01	9.81E-11		-6.92E-01	1.44E-08		-9.00E-01	9.25E-14		-1.13E+00	2.74E-20	Down	Unigene3950_All//gi|12230623|sp|Q9ZUA4.1|ROC1_ARATH//3.00E-90//RecName: Full=Ribonucleoprotein At2g37220, chloroplastic; Flags: Precursor >gi|15081717|gb|AAK82513.1| At2g37220/F365.1 [Arabidopsis thaliana]	Unigene3950_All//2.00E-78//AT2G37220| 29 kDa ribonucleoprotein, chlorcplast, putative / RNA-binding protein cp29, putative	Unigene3950_All//0.00E+00//gi|164260228|gb|ES800915.1|ES800915		ko03040|Spliceosome		nr -
Unigene39500_All	403	2.34	6.29	2.91	4.82	5.81	2.69	3.88	2.18	3.56	1.43E+00	6.15E-04	Up	3.15E-01	6.23E-01		2.69E-01	5.74E-01		-8.42E-01	7.33E-02		-8.34E-01	7.87E-02		-1.25E-01	7.79E-01		Unigene39500_All//gi|224121846|ref|XP_002318887.1|//2.00E-21//cytochrome P450 [Populus trichocarpa] >gi|222859360|gb|EEE96907.1| cytochrome P450 [Populus trichocarpa]	Unigene39500_All//6.00E-14//AT1G13080| CYP71B2 (CYTOCHROME P450 71B2); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene39503_All	926	6.55	4.05	1.50	23.94	21.20	16.05	1.83	1.31	0.34	-6.95E-01	3.75E-03		-2.13E+00	2.13E-13	Down	-1.76E-01	1.63E-01		-5.77E-01	3.11E-07		-4.81E-01	3.10E-01		-2.41E+00	3.07E-06	Down	Unigene39503_All|gi|15226800|ref|NP_181012.1|//1.00E-105//PID (PINOID); kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|7208442|gb|AAF40202.1| protein kinase PINOID [Arabidopsis thaliana]	Unigene39503_All//5.00E-103//AT2G34650| PID (PINOID); kinase/ protein kinase/ protein serine/threonine kinase	Unigene39503_All//0.00E+00//TC155583				nr +
Unigene39504_All	590	10.38	46.98	17.78	76.41	70.91	85.20	122.33	86.57	75.42	2.18E+00	4.51E-63	Up	7.77E-01	2.14E-05		-1.08E-01	2.31E-01		1.57E-01	5.08E-02		-4.99E-01	1.61E-19		-6.98E-01	6.20E-36		Unigene39504_All|gi|15229334|ref|NP_191842.1|//7.00E-15//AUD1; UDP-glucuronate decarboxylase/ catalytic/ dTDP-glucose 4,6-dehydratase [Arabidopsis thaliana] >gi|186511349|ref|NP_001118893.1| AUD1; UDP-glucuronate decarboxylase/ catalytic/ dTDP-glucose 4,6-dehydratase [Arabidopsis thaliana] >gi|7362763|emb|CAB83133.1| dTDP-glucose 4-6-dehydratase homolog D18 [Arabidopsis thaliana] >gi|25605953|gb|AAN28836.1| At3g62830/F26K9_260 [Arabidopsis thaliana]	Unigene39504_All//3.00E-14//AT3G62830| AUD1; UDP-glucuronate decarboxylase/ catalytic/ dTDP-glucose 4,6-dehydratase	Unigene39504_All//2.00E-164//gi|11209530|gb|BF278460.1|BF278460		ko00523|Polyketide sugar unit biosynthesis		nr +
Unigene39506_All	1075	0.19	4.20	3.37	1.25	7.24	8.82	0.43	1.28	2.74	4.43E+00	1.69E-20	Up	4.11E+00	2.72E-15	Up	2.53E+00	1.17E-24	Up	2.82E+00	3.14E-31	Up	1.57E+00	3.34E-03		2.66E+00	2.91E-11	Up	Unigene39506_All|gi|18409228|ref|NP_564956.1|//1.00E-55//AFP1 (ABI FIVE BINDING PROTEIN) [Arabidopsis thaliana] >gi|75180099|sp|Q9LQ98.1|AFP1_ARATH RecName: Full=Ninja-family protein AFP1; AltName: Full=ABI five-binding protein 1; Short=ABI5-binding protein 1 >gi|6730641|gb|AAF27062.1|AC008262_11 F4N2.22 [Arabidopsis thaliana] >gi|22531038|gb|AAM97023.1| expressed protein [Arabidopsis thaliana] >gi|23197982|gb|AAN15518.1| expressed protein [Arabidopsis thaliana]	Unigene39506_All//2.00E-39//AT3G29575| AFP3 (ABI FIVE BINDING PROTEIN 3)	Unigene39506_All//2.00E-45//gi|48747452|gb|C0077971.1|C0077971				nr +
Unigene39508_All	735	7.69	3.24	5.14	5.56	7.64	6.57	0.86	1.14	1.30	-1.25E+00	1.57E-06	Down	-5.80E-01	2.71E-02		4.59E-01	7.11E-02		2.43E-01	4.39E-01		3.98E-01	5.94E-01		5.92E-01	3.46E-01		Unigene39508_All|gi|42562487|ref|NP_174606.2|//3.00E-58//tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	Unigene39508_All//2.00E-50//AT1G31400| tetratricopeptide repeat (TPR)-containing protein	Unigene39508_All//0.00E+00//TC162423				nr -
Unigene39509_All	648	44.09	54.19	47.09	30.13	32.73	29.90	57.09	33.99	27.85	2.98E-01	1.17E-03		9.50E-02	4.00E-01		1.19E-01	4.04E-01		-1.13E-02	9.44E-01		-7.48E-01	1.38E-20		-1.04E+00	3.98E-36	Down	Unigene39509_All|gi|18087587|gb|AALS8924.1|AF462838_1//5.00E-56//AT5g47570/MNJ7_16 [Arabidopsis thaliana] >gi|20453263|gb|AAM19870.1| AT5g47570/MNJ7_16 [Arabidopsis thaliana]	Unigene39509_All//2.00E-57//AT5G47570| unknown protein	Unigene39509_All//0.00E+00//TC156233				nr -
Unigene3951_All	943	3.99	5.96	4.52	2.06	3.80	2.63	3.14	1.77	1.35	5.78E-01	2.15E-02		1.77E-01	6.01E-01		8.82E-01	5.28E-03		3.55E-01	4.23E-01		-8.24E-01	1.10E-02		-1.22E+00	1.59E-04	Down	Unigene3951_All|gi|98961083|gb|ABF59025.1|//1.00E-47//At3g27340 [Arabidopsis thaliana]	Unigene3951_All//1.00E-45//AT3G27340| unknown protein	Unigene3951_All//0.00E+00//DV850162				nr +
Unigene39512_All	594	52.32	15.78	24.20	9.73	12.93	9.81	7.19	5.98	2.55	-1.73E+00	1.97E-52	Down	-1.11E+00	4.02E-26	Down	4.10E-01	5.24E-02		1.18E-02	9.62E-01		-2.65E-01	3.66E-01		-1.50E+00	4.10E-08	Down	Unigene39512_All|gi|225452851|ref|XP_002283710.1|//7.00E-12//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296082934|emb|CBI22235.3| unnamed protein product [Vitis vinifera]		Unigene39512_All//0.00E+00//gi|13246505|gb|BE053609.2|BE053609				nr +
Unigene39513_All	247	30.71	19.08	19.62	37.51	34.85	36.94	96.03	32.32	20.65	-6.87E-01	1.14E-03		-6.47E-01	3.30E-03		-1.06E-01	6.16E-01		-2.24E-02	9.35E-01		-1.57E+00	7.53E-43	Down	-2.22E+00	4.42E-70	Down	Unigene39513_All|gi|192912996|gb|ACF06606.1|//3.00E-30//60S ribosomal protein L13E [Elaeis guineensis]	Unigene39513_All//2.00E-28//AT3G49010| ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome	Unigene39513_All//2.00E-137//gi|21100733|gb|BQ413046.1|BQ413046		ko03010|Ribosome		nr +
Unigene39514_All	720	0.00	0.00	0.00	8.37	2.34	3.58	7.34	3.42	2.71	null	null		null	null		-1.84E+00	4.37E-14	Down	-1.23E+00	4.11E-07	Down	-1.10E+00	3.31E-06	Down	-1.44E+00	2.57E-09	Down	Unigene39514_All|gi|30686409|ref|NP_564087.2|//5.00E-26//ATRL5 (ARABIDOPSIS RAD-LIKE 5); DNA binding / transcription factor [Arabidopsis thaliana] >gi|41618974|gb|AAS09994.1| MYB transcription factor [Arabidopsis thaliana] >gi|87133605|gb|ABD24443.1| RAD-like protein 5 [Arabidopsis thaliana]	Unigene39514_All//2.00E-27//AT1G19510| ATRL5 (ARABIDOPSIS RAD-LIKE 5); DNA binding / transcription factor	Unigene39514_All//0.00E+00//TC155450	MYB-related			nr +
Unigene39515_All	624	19.96	12.10	14.59	146.57	79.30	42.41	3.79	0.80	0.77	-7.22E-01	6.68E-06		-4.52E-01	7.18E-03		-8.86E-01	1.47E-66		-1.79E+00	7.10E-175	Down	-2.24E+00	1.69E-07	Down	-2.31E+00	4.68E-08	Down	Unigene39515_All|gi|464981|sp|P35135.1|UBC4_SOLLC//3.00E-74//RecName: Full=Ubiquitin-conjugating enzyme E2-17 kDa; AltName: Full=Ubiquitin-protein ligase; AltName: Full=Ubiquitin carrier protein >gi|388207|gb|AAA34125.1| ubiquitin carrier protein [Solanum lycopersicum] >gi|83283973|gb|ABC01894.1| ubiquitin-conjugating enzyme E2-like protein [Solanum tuberosum] >gi|213494485|gb|ACJ48964.1| ubiquitin conjugating enzyme [Solanum lycopersicum]	Unigene39515_All//5.00E-75//AT1G64230| ubiquitin-conjugating enzyme, putative	Unigene39515_All//0.00E+00//TC153585		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene39517_All	706	11.86	3.16	2.04	12.28	12.73	5.89	0.12	0.18	0.00	-1.91E+00	1.20E-16	Down	-2.54E+00	1.85E-22	Down	5.23E-02	8.25E-01		-1.06E+00	5.26E-08	Down	5.68E-01	7.82E-01		-6.90E+00	3.58E-01		Unigene39517_All|gi|224103097|ref|XP_002312924.1|//2.00E-42//SAUR family protein [Populus trichocarpa] >gi|222849332|gb|EEE86879.1| SAUR family protein [Populus trichocarpa]	Unigene39517_All//2.00E-31//AT1G29510| SAUR68 (SMALL AUXIN UPREGULATED 68)	Unigene39517_All//0.00E+00//BG444136				nr +
Unigene39519_All	834	4.08	39.43	9.83	1.08	2.39	2.11	0.20	0.00	0.10	3.27E+00	1.63E-116	Up	1.27E+00	6.23E-09	Up	1.16E+00	1.14E-02		9.74E-01	5.32E-02		-7.66E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene39519_All|gi|115464331|ref|NP_001055765.1|//1.00E-26//Os05g0462000 [Oryza sativa Japonica Group] >gi|113579316|dbj|BAF17679.1| Os05g0462000 [Oryza sativa Japonica Group]	Unigene39519_All//2.00E-26//AT5G02580| unknown protein	Unigene39519_All//2.00E-63//TC157651				nr -
Unigene39521_All	724	2.67	1.82	0.37	7.84	5.76	6.43	5.90	2.42	1.98	-5.55E-01	2.36E-01		-2.86E+00	2.95E-06	Down	-4.47E-01	7.01E-02		-2.88E-01	2.98E-01		-1.28E+00	2.29E-06	Down	-1.57E+00	1.13E-08	Down	Unigene39521_All|gi|297845392|ref|XP_002890577.1|//8.00E-52//dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336419|gb|EFH66836.1| dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39521_All//1.00E-45//AT1G23220| dynein light chain type 1 family protein	Unigene39521_All//0.00E+00//TC161501				nr -
Unigene39525_All	795	0.53	2.61	1.21	7.64	8.75	6.48	2.66	1.26	0.50	2.31E+00	1.07E-05	Up	1.20E+00	1.15E-01		1.95E-01	4.57E-01		-2.39E-01	3.86E-01		-1.08E+00	6.86E-03		-2.41E+00	1.32E-07	Down	Unigene39525_All|gi|15239833|ref|NP_196760.1|//3.00E-19//proline-rich family protein [Arabidopsis thaliana]		Unigene39525_All//6.00E-11//gi|109869227|gb|DW498203.1|DW498203		ko03040|Spliceosome		nr -
Unigene39526_All	242	79.56	70.14	69.31	34.38	37.99	47.96	65.87	38.86	29.47	-1.82E-01	1.81E-01		-1.99E-01	1.55E-01		1.44E-01	5.42E-01		4.81E-01	3.78E-03		-7.61E-01	1.33E-09		-1.16E+00	3.76E-19	Down	Unigene39526_All|gi|15224809|ref|NP_181933.1|//3.00E-33//COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase [Arabidopsis thaliana] >gi|20139375|sp|Q80575.1|RISB_ARATH RecName: Full=6,7-dimethyl-8-ribityllumazine synthase, chloroplastic; Short=DMRL synthase; Short=Lumazine synthase; Flags: Precursor >gi|5532610|gb|AAD44810.1|AF148649_1 6,7-dimethyl-8-ribityllumazine synthase precursor [Arabidopsis thaliana] >gi|3212862|gb|AAC23413.1| 6,7-dimethyl-8-ribityllumazine synthase precursor [Arabidopsis thaliana]	Unigene39526_All//1.00E-34//AT2G44050| COS1 (COI1 SUPPRESSOR1); 6,7-dimethyl-8-ribityllumazine synthase	Unigene39526_All//1.00E-129//TC170411		ko00740|Riboflavin metabolism		nr +
Unigene39528_All	655	0.64	1.47	0.73	5.78	2.73	2.55	10.33	5.55	2.07	1.20E+00	9.57E-02		1.95E-01	8.39E-01		-1.08E+00	2.44E-04	Down	-1.18E+00	1.78E-04	Down	-8.96E-01	9.79E-06		-2.32E+00	1.09E-21	Down								
Unigene39529_All	554	4.16	4.21	4.42	1.35	0.06	1.96	1.14	1.96	1.08	1.79E-02	9.86E-01		8.95E-02	8.26E-01		-4.44E+00	1.31E-04	Down	5.37E-01	4.55E-01		7.77E-01	1.94E-01		-8.58E-02	9.19E-01		Unigene39529_All|gi|116056034|emb|CAL58587.1|//3.00E-08//Nucleolar GTPase/ATPase p130 (1SS) [Ostreococcus tauri]		Unigene39529_All//0.00E+00//ES791473				nr +

Unigene3953_All	1421	5.63	4.60	3.86	11.39	6.59	11.89	16.22	7.97	7.32	-2.92E-01	1.72E-01		-5.46E-01	1.11E-02		-7.90E-01	5.32E-10		6.12E-02	6.96E-01		-1.02E+00	8.54E-22	Down	-1.15E+00	7.70E-27	Down	Unigene3953_All//gi|30697571|ref|NP_851242.1|//1.00E-143//PPAN (PETER PAN-LIKE PROTEIN) [Arabidopsis thaliana] >gi|24212091|sp|Q9ASU7.1|PPAN_ARATH RecName: Full=Peter Pan-like protein >gi|13605686|gb|AAK32836.1|AF36182 4_1 AT5g61770/mac9_70 [Arabidopsis thaliana] >gi|15810077|gb|AAL06964.1| At1g06730/F4H5_22 [Arabidopsis thaliana] >gi|17979000|gb|AAL47460.1| AT5g61770/mac9_70 [Arabidopsis thaliana]	Unigene3953_All//4.00E-129//AT5G61770| PPAN (PETER PAN-LIKE PROTEIN)	Unigene3953_All//0.00E+00//TC141298				nr +
Unigene39530_All	365	6.45	3.75	4.67	16.38	7.26	10.39	1.85	1.37	1.53	-7.83E-01	5.88E-02		-4.67E-01	2.92E-01		-1.17E+00	2.42E-07	Down	-6.56E-01	6.14E-03		-4.32E-01	6.12E-01		-2.78E-01	6.89E-01		Unigene39530_All//gi|297805570|ref|XP_002870669.1|//2.00E-21//ATUK/UPRT1 [Arabidopsis lyrata subsp. lyrata] >gi|297316505|gb|EFH46928.1| ATUK/UPRT1 [Arabidopsis lyrata subsp. lyrata]	Unigene39530_All//7.00E-22//AT5G40870| AtUK/UPRT1 (Uridine kinase/Uracil phosphoribosyltransferase 1); ATP binding / kinase/ uracil phosphoribosyltransferase/ uridine kinase	Unigene39530_All//0.00E+00//TC166310		ko00240|Pyrimidine metabolism		nr -
Unigene39531_All	322	9.91	11.64	14.06	12.07	7.27	13.89	24.16	18.17	11.01	2.32E-01	4.87E-01		5.04E-01	9.27E-02		-7.31E-01	1.26E-02		2.03E-01	5.49E-01		-4.11E-01	3.06E-02		-1.13E+00	1.79E-09	Down	Unigene39531_All//gi|24899705|gb|AN65067.1|//2.00E-21//Similar to CGI-126 protein [Arabidopsis thaliana]	Unigene39531_All//7.00E-23//AT1G27530| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin-conjugating enzyme/RWD-like (InterPro:IPR016135), Ubiquitin-fold modifier-conjugating enzyme 1 (InterPro:IPR014806); Has 183 Blast hits to 183 proteins in 80 species: Archae - 0; Bacteria - 0; Metazoa - 126; Fungi - 0; Plants - 21; Viruses - 0; Other Eukaryotes - 36 (source: NCBI BLink).	Unigene39531_All//5.00E-136//TC152577				nr -
Unigene39532_All	676	41.49	10.42	14.49	91.89	55.88	78.03	101.82	67.58	58.52	-1.99E+00	2.20E-57	Down	-1.52E+00	7.07E-38	Down	-7.18E-01	1.86E-31		-2.36E-01	3.82E-04		-5.91E-01	4.35E-25		-7.99E-01	3.16E-43		Unigene39532_All//gi|211906474|gb|ACJ11730.1|//7.00E-47//glycine-rich RNA-binding protein [Gossypium hirsutum]	Unigene39532_All//9.00E-08//AT2G21660| CCR2 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	Unigene39532_All//2.00E-127//gi|13349511|gb|BG439854.1|BG439854		ko03040|Spliceosome		nr +
Unigene39533_All	639	0.16	1.03	0.92	1.09	2.48	0.92	0.60	0.20	4.55	2.65E+00	1.49E-02		2.48E+00	3.75E-02		1.18E+00	2.57E-02		-2.48E-01	7.56E-01		-1.60E+00	1.81E-01		2.93E+00	3.29E-12	Up	Unigene39533_All//gi|283362118|dbj|BAI65912.1|//2.00E-28//UDP-sugar:glycosyltransferase [Forsythia x intermedia]	Unigene39533_All//9.00E-20//AT3G21750| UGT71B1 (UDP-GLUCOSYL TRANSFERASE 71B1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene39533_All//0.00E+00//gi|78339233|gb|DT559507.1|DT559507				nr +
Unigene39534_All	690	5.23	1.47	1.70	10.32	7.09	3.86	0.00	0.00	0.12	-1.83E+00	3.14E-07	Down	-1.62E+00	6.79E-06	Down	-5.43E-01	9.18E-03		-1.42E+00	3.33E-10	Down	null	null		6.85E+00	4.04E-01		Unigene39534_All//gi|283362118|dbj|BAI65912.1|//1.00E-36//UDP-sugar:glycosyltransferase [Forsythia x intermedia]	Unigene39534_All//5.00E-29//AT3G21780| UGT71B6 (UDP-glucosyl transferase 71B6); UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring glycosyl groups	Unigene39534_All//1.00E-101//gi|78339233|gb|DT559507.1|DT559507				nr +
Unigene39535_All	729	0.00	0.00	0.29	9.91	3.97	4.34	10.85	4.30	2.68	null	null		8.19E+00	1.41E-01		-1.32E+00	1.85E-10	Down	-1.19E+00	4.81E-08	Down	-1.33E+00	8.96E-12	Down	-2.02E+00	2.80E-21	Down	Unigene39535_All//gi|9294048|dbj|BAB02005.1|//3.00E-14//protein kinase-like protein [Arabidopsis thaliana]	Unigene39535_All//2.00E-14//AT3G24535| unknown protein					nr -
Unigene39536_All	730	4.73	8.26	8.68	3.21	7.55	5.44	0.17	0.11	0.44	8.04E-01	8.75E-04		8.76E-01	3.35E-04		1.23E+00	6.25E-07	Up	7.64E-01	1.28E-02		-6.02E-01	7.66E-01		1.33E+00	2.93E-01		Unigene39536_All//gi|75334522|sp|Q9FVX2.1|CML25_ARATH//2.00E-43//RecName: Full=Probable calcium-binding protein CML25; AltName: Full=Calmodulin-like protein 25 >gi|9743349|gb|AAF97973.1|AC000103_23 F21J9.28 [Arabidopsis thaliana] >gi|91805849|gb|ABE65653.1| polcalcin [Arabidopsis thaliana]	Unigene39536_All//1.00E-40//AT1G24620| polcalcin, putative / calcium-binding pollen allergen, putative	Unigene39536_All//5.00E-33//TC156088		ko04626|Plant-pathogen interaction		nr +
Unigene39537_All	668	6.58	4.70	2.15	6.64	5.77	4.53	3.61	2.69	2.56	-4.84E-01	9.63E-02		-1.61E+00	5.78E-07	Down	-2.01E-01	5.49E-01		-5.51E-01	5.91E-02		-4.23E-01	2.68E-01		-4.92E-01	1.68E-01		Unigene39537_All//gi|124301042|gb|ABN04773.1|//1.00E-72//At5g57230 [Arabidopsis thaliana]	Unigene39537_All//7.00E-74//AT5G57230| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Thioredoxin-like fold (InterPro:IPR012336); Has 18 Blast hits to 18 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene39537_All//1.00E-51//ES802430				nr -
Unigene39539_All	664	0.71	3.13	0.88	1.95	1.14	1.84	5.60	8.81	4.38	2.14E+00	2.88E-05	Up	3.15E-01	7.19E-01		-7.74E-01	1.77E-01		-8.70E-02	8.93E-01		6.53E-01	2.78E-03		-3.55E-01	2.11E-01		Unigene39539_All//gi|15228749|ref|NP_191142.1|//2.00E-08//EPC1 (ECTOPICALLY PARTING CELLS); UDP-glucosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene39539_All//1.00E-09//AT3G55830| EPC1 (ECTOPICALLY PARTING CELLS); UDP-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene39539_All//0.00E+00//EX164438				nr -
Unigene39540_All	957	1.26	0.32	0.22	2.19	1.76	1.75	4.46	1.88	2.75	-1.98E+00	3.72E-03		-2.50E+00	1.15E-03		-3.10E-01	5.23E-01		-3.24E-01	4.99E-01		-1.25E+00	3.87E-06	Down	-7.00E-01	5.63E-03		Unigene39540_All//gi|115463371|ref|NP_001055285.1|//6.00E-32//Os05g0354300 [Oryza sativa Japonica Group] >gi|113578836|dbj|BAF17199.1| Os05g0354300 [Oryza sativa Japonica Group]	Unigene39540_All//5.00E-18//AT5G05560| EMB2771 (EMBRYO DEFECTIVE 2771); ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis		nr +
Unigene39541_All	1117	1.45	8.39	3.10	2.50	3.24	4.89	4.35	4.08	3.00	2.53E+00	7.39E-26	Up	1.09E+00	1.78E-03		3.74E-01	2.90E-01		9.70E-01	1.31E-04		-9.39E-02	7.27E-01		-5.39E-01	2.22E-02		Unigene39541_All//gi|7572929|emb|CAB87430.1|//6.00E-07//alpha-galactosidase-like protein [Arabidopsis thaliana]	Unigene39541_All//3.00E-08//AT3G56310| alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative	Unigene39541_All//0.00E+00//TC139892		ko00561|Glycerolipid metabolism//ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00603|Glycosphingolipid biosynthesis - globo series		nr +
Unigene39543_All	951	0.94	0.53	0.34	7.07	4.45	3.28	5.91	4.22	2.93	-8.12E-01	2.68E-01		-1.48E+00	6.99E-02		-6.67E-01	1.61E-03		-1.11E+00	8.61E-07	Down	-4.87E-01	3.18E-02		-1.01E+00	4.79E-06	Down	Unigene39543_All//gi|15778154|dbj|BAB88527.1|//2.00E-16//14-3-3 protein [Nicotiana tabacum]	Unigene39543_All//1.00E-12//AT2G42590| GRF9 (GENERAL REGULATORY FACTOR 9); calcium ion binding / protein binding / protein phosphorylated amino acid binding	Unigene39543_All//1.00E-64//gi|21093489|gb|BQ405802.1|BQ405802				nr +
Unigene39545_All	636	107.77	82.46	97.12	98.92	75.10	52.69	155.83	333.38	180.09	-3.86E-01	8.20E-10		-1.50E-01	3.20E-02		-3.98E-01	3.93E-11		-9.09E-01	3.46E-42		1.10E+00	9.60E-217	Up	2.09E-01	8.58E-07		Unigene39545_All//gi|15242741|ref|NP_195958.1|//2.00E-18//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|7378619|emb|CAB83295.1| farnesylated protein-like [Arabidopsis thaliana] >gi|16604513|gb|AAL24262.1| At5g03380/C160EPL23M [Arabidopsis thaliana] >gi|21591780|gb|AAM64219.1| cadmium induced protein CdI19 [Arabidopsis thaliana] >gi|21655291|gb|AAM65357.1| At5g03380/C160EPL23M [Arabidopsis thaliana]	Unigene39545_All//1.00E-19//AT5G03380| heavy-metal-associated domain-containing protein	Unigene39545_All//0.00E+00//TC169585				nr -
Unigene39548_All	634	4.21	2.00	4.20	9.74	7.50	3.49	0.67	0.92	0.25	-1.07E+00	5.82E-03		-3.20E-03	9.93E-01		-3.78E-01	1.14E-01		-1.48E+00	1.76E-09	Down	4.69E-01	6.13E-01		-1.41E+00	1.73E-01		Unigene39548_All//gi|297794349|ref|XP_002865059.1|//2.00E-74//maf family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310894|gb|EFH41318.1| maf family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39548_All//1.00E-73//AT5G66550| Maf family protein	Unigene39548_All//0.00E+00//CO081163				nr -
Unigene39549_All	251	20.85	7.47	11.46	30.36	23.19	32.21	135.26	64.11	55.87	-1.48E+00	1.09E-07	Down	-8.64E-01	1.55E-03		-3.89E-01	6.31E-02		8.50E-02	7.14E-01		-1.08E+00	2.29E-34	Down	-1.28E+00	4.54E-46	Down	Unigene39549_All//gi|115464537|ref|NP_001055868.1|//2.00E-36//Os05g0482700 [Oryza sativa Japonica Group] >gi|113579419|dbj|BAF17782.1| Os05g0482700 [Oryza sativa Japonica Group]	Unigene39549_All//5.00E-37//AT1G09780| 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative	Unigene39549_All//9.00E-140//TC138989		ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene3955_All	1133	3.46	6.04	1.50	2.51	2.40	2.59	11.68	31.76	32.70	8.02E-01	3.66E-04		-1.20E+00	2.56E-04	Down	-6.18E-02	8.68E-01		4.81E-02	9.22E-01		1.44E+00	5.72E-57	Up	1.49E+00	1.77E-62	Up	Unigene3955_All//gi|292668893|gb|ADE41101.1|//4.00E-70//AP2 domain class transcription factor [Malus x domestica]	Unigene3955_All//6.00E-56//AT5G47230| ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5); DNA binding / transcription activator/ transcription factor	Unigene3955_All//0.00E+00//gi|78343252|gb|DT563526.1|DT563526	AP2-EREBP			nr +
Unigene39551_All	330	2.54	7.22	2.10	3.47	0.94	2.87	2.18	1.39	1.69	1.51E+00	5.37E-04	Up	-2.74E-01	7.05E-01		-1.89E+00	3.06E-03		-2.73E-01	6.89E-01		-6.45E-01	4.01E-01		-3.66E-01	6.05E-01		Unigene39551_All//gi|15237292|ref|NP_200099.1|//9.00E-12//unknown protein [Arabidopsis thaliana] >gi|10177101|dbj|BAB10435.1| unnamed protein product [Arabidopsis thaliana] >gi|15028097|gb|AAK76579.1| unknown protein [Arabidopsis thaliana] >gi|20258915|gb|AAM14151.1| unknown protein [Arabidopsis thaliana]		Unigene39551_All//2.00E-45//TC148061				nr +

Unigene39552_All	879	8.39	3.34	7.39	2.15	1.65	1.03	0.53	0.10	0.00	-1.33E+00	4.75E-09	Down	-1.83E-01	4.40E-01		-3.88E-01	4.26E-01		-1.07E+00	2.45E-02		-2.48E+00	3.38E-02		-9.05E+00	1.09E-03		Unigene39552_All//gi|225460761|ref|XP_002276224.1|//1.00E-147//PREDICTED: similar to mitochondrial transcription termination factor family protein / mTERF family protein [Vitis vinifera]	Unigene39552_All//1.00E-132//AT5G55580| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene39552_All//0.00E+00//TC173851				nr -
Unigene39554_All	510	1.74	5.17	5.74	5.57	4.79	1.86	3.48	2.87	3.98	1.57E+00	1.55E-04	Up	1.72E+00	2.78E-05	Up	-2.16E-01	5.92E-01		-1.58E+00	4.06E-05	Down	-2.80E-01	5.63E-01		1.94E-01	6.43E-01											
Unigene39555_All	611	3.51	4.23	4.44	6.11	4.79	2.96	5.88	1.50	2.02	2.69E-01	5.11E-01		3.40E-01	3.89E-01		-3.52E-01	2.95E-01		-1.05E+00	8.72E-04	Down	-1.97E+00	1.83E-09	Down	-1.54E+00	3.10E-07	Down	Unigene39555_All//gi|6685428|sp|Q9ZTN2.1|ERD2_PETHY//3.00E-66//RecName: Full=ER lumen protein retaining receptor; AltName: Full=HDEL receptor; AltName: Full=PGP169-12 >gi|4105782|gb|AAD02548.1| PGPS/D6 [Petunia x hybrida]	Unigene39555_All//6.00E-57//AT3G25040| ER lumen protein retaining receptor, putative / HDEL receptor, putative	Unigene39555_All//1.00E-125//TC131790				nr +
Unigene39557_All	568	24.13	16.50	14.25	40.08	38.32	32.68	35.06	13.69	15.01	-5.48E-01	2.92E-04		-7.60E-01	1.38E-06		-6.49E-02	6.36E-01		-2.95E-01	1.17E-02		-1.36E+00	3.71E-29	Down	-1.22E+00	1.01E-25	Down	Unigene39557_All//gi|75294330|sp|Q6ZL94.1|SUCA_ORYSJ//5.00E-71//RecName: Full=Probable succinyl-CoA ligase (GDP-forming) subunit alpha, mitochondrial; AltName: Full=Succinyl-CoA synthetase subunit alpha; Short=SCS-alpha; Flags: Precursor	Unigene39557_All//6.00E-62//AT5G23250| succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative	Unigene39557_All//0.00E+00//TC131503		ko00020|Citrate cycle (TCA cycle)//ko00640|Propanoate metabolism		nr +
Unigene39559_All	1091	4.75	6.55	6.54	2.69	1.61	2.73	2.36	0.42	0.77	4.64E-01	3.63E-02		4.62E-01	4.57E-02		-7.43E-01	3.25E-02		2.04E-02	9.53E-01		-2.49E+00	4.40E-09	Down	-1.62E+00	8.62E-06	Down	Unigene39559_All//gi|22854880|gb|AN09798.1|//1.00E-104//benzoyl coenzyme A: benzyl alcohol benzoyl transferase [Nicotiana tabacum]	Unigene39559_All//1.00E-70//AT5G17540| transferase family protein			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene3956_All	1556	5.65	1.95	3.49	12.52	8.43	15.01	27.15	11.58	24.76	-1.53E+00	5.37E-13	Down	-6.95E-01	5.91E-04		-5.70E-01	6.41E-07		2.62E-01	2.61E-02		-1.23E+00	2.10E-52	Down	-1.33E-01	8.66E-02		Unigene3956_All//gi|15223941|ref|NP_177867.1|//1.00E-133//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]	Unigene3956_All//2.00E-134//AT1G77420| hydrolase, alpha/beta fold family protein	Unigene3956_All//0.00E+00//TC142525		ko00561|Glycerolipid metabolism		nr +
Unigene39560_All	1445	0.91	1.72	1.07	0.52	0.52	1.53	1.87	1.85	3.86	9.25E-01	2.23E-02		2.40E-01	6.41E-01		1.99E-02	1.00E+00		1.57E+00	5.28E-04	Up	-1.66E-02	9.97E-01		1.04E+00	3.21E-06	Up	Unigene39560_All//gi|301318140|gb|ADK66985.1|//1.00E-160//chloride channel ClC7 [Vitis vinifera]	Unigene39560_All//3.00E-131//AT4G35440| CLC-E (CHLORIDE CHANNEL E); ion channel/ voltage-gated chloride channel					nr -
Unigene39561_All	544	2.69	7.27	2.35	6.68	4.43	6.39	15.39	12.83	10.98	1.43E+00	1.02E-05	Up	-1.97E-01	7.14E-01		-5.93E-01	5.71E-02		-6.44E-02	8.63E-01		-2.62E-01	1.72E-01		-4.86E-01	5.04E-03		Unigene39561_All//gi|1449179|dbj|BAA13101.1|//1.00E-53//N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]	Unigene39561_All//8.00E-32//AT4G04910| NSF (N-ethylmaleimide sensitive factor); ATP binding / binding / nucleoside-triphosphatase/ nucleotide binding	Unigene39561_All//0.00E+00//gi|18101361|gb|BM360615.1|BM360615				nr +
Unigene39564_All	611	117.32	83.34	173.43	38.40	55.18	39.62	0.00	1.03	0.65	-4.93E-01	1.30E-15		5.64E-01	9.74E-28		5.23E-01	1.01E-09		4.51E-02	7.33E-01		1.00E+01	1.47E-04	Up	9.35E+00	3.96E-03		Unigene39564_All//gi|11387206|sp|Q9THX6.1|APX4_SOLLC//2.00E-29//RecName: Full=Putative L-ascorbate peroxidase, chloroplastic; AltName: Full=Thylakoid lumenal 29 kDa protein; Short=TL29; AltName: Full=P29; AltName: Full=LeAPx09; Flags: Precursor	Unigene39564_All//1.00E-21//AT4G09010| APX4 (ASCORBATE PEROXIDASE 4); heme binding / peroxidase	Unigene39564_All//0.00E+00//gi|11205206|gb|BF274136.1|BF274136		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene39565_All	342	17.59	35.26	26.00	35.98	40.38	33.41	42.77	48.40	40.77	1.00E+00	2.18E-09	Up	5.64E-01	5.09E-03		1.66E-01	3.32E-01		-1.07E-01	6.05E-01		1.78E-01	1.90E-01		-6.92E-02	6.47E-01		Unigene39565_All//gi|17933310|gb|AAL48237.1|AF446365_1//9.00E-10//At1g10950/T19D16_13 [Arabidopsis thaliana] >gi|15451172|gb|AAK96857.1| endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana] >gi|20148415|gb|AAM10098.1| endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]	Unigene39565_All//8.00E-08//AT1G10950| endomembrane protein 70, putative	Unigene39565_All//2.00E-21//TC170451				nr +
Unigene39566_All	732	9.94	16.47	21.68	11.30	6.96	6.91	19.64	1.66	0.49	7.30E-01	8.10E-06		1.13E+00	6.62E-14	Up	-6.98E-01	1.81E-04		-7.09E-01	3.22E-04		-3.57E+00	4.91E-68	Down	-5.33E+00	2.28E-91	Down	Unigene39566_All//gi|224104361|ref|XP_002313411.1|//6.00E-47//copper transporter [Populus trichocarpa] >gi|222849819|gb|EEE87366.1| copper transporter [Populus trichocarpa]	Unigene39566_All//6.00E-34//AT5G59030| COPT1 (copper transporter 1); copper ion transmembrane transporter	Unigene39566_All//0.00E+00//gi|164241069|gb|EV486201.1|EV486201				nr -
Unigene39569_All	969	6.32	1.93	2.80	6.43	8.35	5.87	1.40	0.60	0.49	-1.71E+00	1.03E-10	Down	-1.17E+00	4.23E-06	Down	3.78E-01	6.93E-02		-1.30E-01	6.32E-01		-1.21E+00	2.08E-02		-1.50E+00	3.72E-03		Unigene39569_All//gi|30023726|gb|AAP13396.1|//6.00E-38//At1g68330 [Arabidopsis thaliana]	Unigene39569_All//1.00E-34//AT1G68330| unknown protein					nr +
Unigene3957_All	1132	155.76	166.69	173.02	177.52	135.64	70.14	4.89	5.91	2.11	9.78E-02	1.31E-02		1.52E-01	7.29E-05		-3.88E-01	3.97E-33		-1.34E+00	7.52E-251	Down	2.72E-01	2.18E-01		-1.21E+00	1.10E-07	Down	Unigene3957_All//gi|224131668|ref|XP_002321148.1|//1.00E-103//nitrate transporter, H+/oligopeptide symporter POT family [Populus trichocarpa] >gi|222861921|gb|EEE99463.1| nitrate transporter, H+/oligopeptide symporter POT family [Populus trichocarpa]	Unigene3957_All//4.00E-84//AT3G21670| nitrate transporter (NTP3)	Unigene3957_All//0.00E+00//TC139318				nr -
Unigene39572_All	732	2.86	0.69	1.67	1.02	1.27	0.99	0.23	0.17	0.05	-2.05E+00	4.33E-05	Down	-7.73E-01	9.77E-02		3.15E-01	7.04E-01		-4.83E-02	9.50E-01		-4.31E-01	7.93E-01		-2.09E+00	3.13E-01											
Unigene39573_All	1350	8.99	4.54	4.89	1.03	1.12	0.87	0.00	0.06	0.56	-9.85E-01	3.12E-09		-8.78E-01	2.25E-07		1.19E-01	8.39E-01		-2.48E-01	6.85E-01		5.95E+00	4.01E-01		9.13E+00	1.39E-05	Up	Unigene39573_All//gi|115455333|ref|NP_001051267.1|//3.00E-86//Os03g0748300 [Oryza sativa Japonica Group] >gi|108711077|gb|ABF98872.1| Aldose 1-epimerase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549738|dbj|BAF13181.1| Os03g0748300 [Oryza sativa Japonica Group]	Unigene39573_All//4.00E-85//AT1G55370| carbohydrate binding / catalytic	Unigene39573_All//0.00E+00//TC133623				nr +
Unigene39574_All	511	123.07	116.81	291.57	155.58	57.68	35.35	4.96	15.46	4.99	-7.54E-02	3.32E-01		1.24E+00	3.25E-148	Up	-1.43E+00	2.41E-126	Down	-2.14E+00	5.85E-193	Down	1.64E+00	1.25E-15	Up	7.30E-03	9.82E-01			Unigene39574_All//8.00E-136//TC168086						
Unigene39577_All	819	192.80	132.64	215.99	250.65	153.38	179.33	187.55	104.62	76.08	-5.40E-01	2.90E-39		1.64E-01	4.52E-05		-7.09E-01	3.89E-101		-4.83E-01	6.01E-45		-8.42E-01	1.64E-101		-1.30E+00	4.53E-212	Down	Unigene39577_All//gi|224065681|ref|XP_002301918.1|//7.00E-26//high mobility group family [Populus trichocarpa] >gi|222843644|gb|EEE81191.1| high mobility group family [Populus trichocarpa]	Unigene39577_All//3.00E-23//AT1G20696| HMGB3 (HIGH MOBILITY GROUP B 3); DNA binding / chromatin binding / structural constituent of chromatin / transcription factor	Unigene39577_All//0.00E+00//TC168621		ko03410|Base excision repair		nr -
Unigene39578_All	836	1.31	0.18	0.25	10.96	10.13	9.40	3.24	2.75	8.72	-2.85E+00	4.77E-04	Down	-2.37E+00	2.97E-03		-1.14E-01	5.94E-01		-2.22E-01	3.05E-01		-2.35E-01	5.40E-01		1.43E+00	2.59E-12	Up	Unigene39578_All//gi|18409123|ref|NP_564943.1|//1.00E-11//CLE12 (CLAVATA3/ESR-RELATED 12); protein binding / receptor binding [Arabidopsis thaliana] >gi|89111846|gb|ABD60695.1| Atlg68795 [Arabidopsis thaliana]	Unigene39578_All//6.00E-09//AT1G68795| CLE12 (CLAVATA3/ESR-RELATED 12); protein binding / receptor binding	Unigene39578_All//0.00E+00//TC150443				nr +
Unigene39579_All	621	13.48	5.14	13.89	48.29	88.56	65.09	2.38	11.17	5.45	-1.39E+00	7.44E-11	Down	4.33E-02	8.41E-01		8.75E-01	8.45E-38		4.31E-01	1.22E-07		2.23E+00	1.89E-20	Up	1.19E+00	6.82E-05	Up	Unigene39579_All//gi|299810231|gb|ADJ53039.1|//1.00E-14//embryo-abundant protein [Pinus pinaster]	Unigene39579_All//7.00E-08//AT5G48540| 33 kDa secretory protein-related					nr +
Unigene3958_All	1289	1.58	1.38	2.48	4.14	3.07	2.56	5.67	5.38	2.47	-2.02E-01	6.34E-01		6.47E-01	7.69E-02		-4.29E-01	9.56E-02		-6.93E-01	6.73E-03		-7.62E-02	7.28E-01		-1.20E+00	1.04E-09	Down		Unigene3958_All//0.00E+00//TC130553						
Unigene39581_All	525	7.67	9.07	9.64	12.43	16.46	13.76	33.26	28.66	15.33	2.42E-01	3.94E-01		3.29E-01	2.53E-01		4.06E-01	3.97E-02		1.47E-01	5.82E-01		-2.15E-01	9.12E-02		-1.12E+00	1.01E-19	Down	Unigene39581_All//gi|226500554|ref|NP_001150505.1|//1.00E-08//peptidyl-prolyl cis-trans isomerase 1 [Zea mays] >gi|195639680|gb|ACG39308.1| peptidyl-prolyl cis-trans isomerase 1 [Zea mays]	Unigene39581_All//5.00E-09//AT2G18040| PIN1AT (PEPTIDYLPROLYL CIS/TRANS ISOMERASE, NIMA-INTERACTING 1); peptidyl-prolyl cis-trans isomerase	Unigene39581_All//2.00E-164//ES816050				nr +
Unigene39582_All	283	2.40	2.15	1.32	5.28	3.41	4.95	26.15	10.19	6.76	-1.62E-01	8.32E-01		-8.68E-01	3.51E-01		-6.32E-01	2.38E-01		-9.41E-02	8.70E-01		-1.36E+00	2.33E-11	Down	-1.95E+00	3.82E-19	Down			Unigene39582_All//1.00E-52//gi|21096162|gb|BQ408475.1|BQ408475				
Unigene39583_All	228	0.46	2.67	5.37	2.62	4.68	4.16	15.58	21.08	10.66	2.54E+00	2.46E-02		3.55E+00	6.10E-05	Up	8.37E-01	2.29E-01		6.66E-01	3.93E-01		4.37E-01	8.27E-02		-5.47E-01	5.29E-02			Unigene39583_All//6.00E-79//TC144505					
Unigene39587_All	588	4.54	3.88	2.90	1.61	3.22	1.15	2.37	0.43	0.95	-2.27E-01	5.81E-01		-6.47E-01	1.12E-01		1.00E+00	3.42E-02		-4.82E-01	5.18E-01		-2.48E+00	3.36E-05	Down	-1.32E+00	7.95E-03		Unigene39587_All//gi|227202676|dbj|BAH56811.1|//3.00E-39//AT2G31810 [Arabidopsis thaliana]	Unigene39587_All//2.00E-38//AT2G31810| acetolactate synthase small subunit, putative	Unigene39587_All//1.00E-70//CO082881		ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis//ko00660|C5-Branched dibasic acid metabolism		nr +
Unigene39588_All	500	14.44	35.16	15.44	1.99	4.68	3.34	0.00	0.00	0.00	1.28E+00	2.02E-19	Up	9.68E-02	6.66E-01		1.23E+00	2.92E-03		7.46E-01	1.57E-01		null	null		null	null		Unigene39588_All//gi|47174868|gb|AAT12424.1|//7.00E-38//male-specific transcription factor MMS87.2 [Marchantia polymorpha]	Unigene39588_All//8.00E-30//AT3G21175| ZML1 (ZIM-LIKE 1); sequence-specific DNA binding / transcription factor/ zinc ion binding	Unigene39588_All//0.00E+00//TC137044	C2C2-GATA	ko04712|Circadian rhythm - plant		nr -
Unigene3959_All	774	6.08	5.63	4.06	9.33	8.28	8.40	9.83	19.22	27.85	-1.12E-01	6.86E-01		-5.84E-01	4.51E-02		-1.73E-01	4.92E-01		-1.51E-01	5.64E-01		9.67E-01	4.07E-13		1.50E+00	2.69E-37	Up	Unigene3959_All//gi|61651608|dbj|BAD91177.1|//3.00E-71//plastidic phosphate translocator-like protein2 [Mesembryanthemum crystallinum]	Unigene3959_All//6.00E-72//AT5G05820| phosphate translocator-related	Unigene3959_All//0.00E+00//DR458342				nr +
Unigene39592_All	968	14.59	5.97	13.70	1.03	1.25	0.56	0.26	0.09	0.08	-1.29E+00	6.09E-16	Down	-9.14E-02	6.22E-01		2.75E-01	7.00E-01		-8.78E-01	2.20E-01		-1.60E+00	3.10E-01		-1.67E+00	2.56E-01		Unigene39592_All//gi|15230137|ref|NP_189105.1|//1.00E-80//ROPGEF8; Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana]	Unigene39592_All//1.00E-80//AT3G24620| ROPGEF8; Rho guanyl-nucleotide exchange factor	Unigene39592_All//1.00E-12//TC136788				nr +
Unigene39593_All	504	4.46	0.60	1.06	24.12	20.02	26.88	66.94	83.43	57.94	-2.89E+00	1.15E-07	Down	-2.08E+00	3.39E-05	Down	-2.69E-01	1.08E-01		1.57E-01	3.95E-01		3.18E-01	1.58E-05		-2.08E-01	1.26E-02		Unigene39593_All//gi|149392729|gb|ABR26167.1|//2.00E-29//cytosol aminopeptidase [Oryza sativa Indica Group]	Unigene39593_All//2.00E-27//AT2G24200| cytosol aminopeptidase	Unigene39593_All//0.00E+00//gi|18100416|gb|BM359670.1|BM359670		ko00480|Glutathione metabolism		nr +
Unigene39594_All	366	16.30	47.76	21.82	33.62	44.31	62.07	52.91	72.06	42.56	1.55E+00	1.95E-25	Up	4.21E-01	5.33E-02		3.99E-01	2.82E-03		8.85E-01	9.18E-15		4.46E-01	2.23E-06		-3.14E-01	4.46E-03		Unigene39594_All//gi|45476565|gb|AAS65948.1|//6.00E-17//At5g11600 [Arabidopsis thaliana] >gi|46359849|gb|AAS88788.1| At5g11600 [Arabidopsis thaliana]	Unigene39594_All//2.00E-09//AT5G11600| unknown protein	Unigene39594_All//3.00E-165//DR453809				nr -
Unigene39595_All	684	26.39	19.93	11.68	30.01	29.75	25.75	38.45	26.76	24.64	-4.05E-01	1.97E-03		-1.18E+00	8.48E-17	Down	-1.22E-02	9.41E-01		-2.21E-01	9.10E-02		-5.23E-01	3.04E-08		-6.42E-01	6.25E-12		Unigene39595_All//gi|124360846|gb|ABN08818.1|//2.00E-89//Mov34-1 [Medicago truncatula]	Unigene39595_All//6.00E-76//AT1G10860| TIF3H1; translation initiation factor	Unigene39595_All//0.00E+00//TC152925				nr -
Unigene39597_All	594	16.65	18.43	12.55	15.01	18.09	18.25	47.19	32.44	16.90	1.46E-01	4.34E-01		-4.08E-01	3.53E-02		2.69E-01	1.47E-01		2.82E-01	1.32E-01		-5.41E-01	3.05E-09		-1.48E+00	9.09E-48	Down	Unigene39597_All//gi|2511598|emb|CAA74030.1|//1.00E-42//multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana]	Unigene39597_All//6.00E-44//AT1G56450| PBG1; peptidase/ threonine-type endopeptidase	Unigene39597_All//0.00E+00//gi|21099596|gb|BQ411909.1|BQ411909		ko03050|Proteasome		nr -

Unigene39598_All	641	55.83	25.69	25.17	232.05	172.66	147.12	135.88	100.41	57.24	-1.12E+00	1.66E-31	Down	-1.15E+00	1.33E-31	Down	-4.27E-01	2.81E-29		-6.58E-01	1.03E-56		-4.36E-01	1.82E-18		-1.25E+00	8.24E-113	Down	Unigene39598_All//gi|223635320|sp|A4PU48.1|METK_MEDTR//5.00E-71//RecName: Full=S-adenosylmethionine synthase; Short=AdoMet synthase; AltName: Full=Methionine adenosyltransferase; Short=MAT >gi|140055593|gb|ABO80948.1| S-adenosylmethionine synthetase [Medicago truncatula]	Unigene39598_All//2.00E-59//AT4G01850| SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase	Unigene39598_All//0.00E+00//gi|21100606|gb|BQ412919.1|BQ412919		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -
Unigene39599_All	826	0.70	0.98	0.64	2.11	2.04	1.04	2.87	6.88	3.33	4.94E-01	5.26E-01		-1.12E-01	9.07E-01		-4.72E-02	9.17E-01		-1.02E+00	4.05E-02		1.26E+00	4.97E-08	Up	2.15E-01	5.55E-01		Unigene39599_All//gi|224069342|ref|XP_002302960.1|//9.00E-46//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222844686|gb|EEE82233.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene39599_All//3.00E-17|AT3G25510| disease resistance protein (TIR-NBS-LRR class), putative	Unigene39599_All//3.00E-179//TC174987		ko04626|Plant-pathogen interaction		nr +
Unigene396_All	3720	3.85	2.02	2.75	11.21	11.19	6.05	6.06	1.71	2.39	-9.35E-01	6.38E-10		-4.88E-01	1.54E-03		-2.20E-03	9.80E-01		-8.91E-01	3.35E-27		-1.83E+00	2.90E-50	Down	-1.34E+00	2.31E-33	Down	Unigene396_All//gi|115452817|ref|NP_001050009.1|//1.00E-153//Os03g0330300 [Oryza sativa Japonica Group] >gi|108707956|gb|ABF95751.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548180|dbj|BAF11923.1| Os03g0330300 [Oryza sativa Japonica Group]	Unigene396_All//5.00E-21//AT3G14172| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: COP1-interacting protein-related (TAIR:AT1G72410.1); Has 2665 Blast hits to 1956 proteins in 215 species: Archae - 2; Bacteria - 189; Metazoa - 878; Fungi - 141; Plants - 132; Viruses - 5; Other Eukaryotes - 1318 (source: NCBI BLink).	Unigene396_All//0.00E+00//gi|164336129|gb|ES847547.1|ES847547				nr -
Unigene3960_All	1640	14.55	13.84	16.75	21.26	15.39	8.48	2.53	0.38	0.39	-7.18E-02	5.95E-01		2.04E-01	7.63E-02		-4.66E-01	1.95E-08		-1.33E+00	3.79E-43	Down	-2.72E+00	1.33E-15	Down	-2.70E+00	5.11E-16	Down	Unigene3960_All//gi|56744299|gb|AAW28578.1|//0.00E+00//Putative gag-pol polyprotein, identical [Solanum demissum]		Unigene3960_All//7.00E-108//NP822049				nr -
Unigene39601_All	2057	0.10	0.57	0.31	0.39	0.50	0.92	16.98	45.53	68.41	2.48E+00	9.79E-04	Up	1.61E+00	1.11E-01		3.74E-01	6.04E-01		1.25E+00	9.82E-03		1.42E+00	4.08E-144	Up	2.01E+00	0.00E+00	Up	Unigene39601_All//gi|56109840|emb|CAI30145.1|//1.00E-171//glycosyltransferase [Medicago truncatula]	Unigene39601_All//5.00E-158//AT2G41640| transferase, transferring glycosyl groups	Unigene39601_All//0.00E+00//TC169024				nr +
Unigene39604_All	521	5.12	4.47	8.18	13.10	10.64	5.46	6.90	4.49	2.22	-1.95E-01	6.15E-01		6.75E-01	2.78E-02		-3.00E-01	2.03E-01		-1.26E+00	2.71E-08	Down	-6.19E-01	3.36E-02		-1.64E+00	8.14E-08	Down			Unigene39604_All//6.00E-07//gi|78333209|gb|DT553483.1|DT553483				
Unigene39606_All	551	1.42	4.23	2.90	3.89	5.00	5.66	2.15	1.67	3.54	1.57E+00	4.09E-04	Up	1.03E+00	6.23E-02		3.63E-01	3.83E-01		5.41E-01	1.40E-01		-3.65E-01	5.42E-01		7.22E-01	7.13E-02				Unigene39606_All//5.00E-128//DW482075				
Unigene39607_All	1740	1.08	0.12	0.64	2.12	0.95	0.88	3.26	0.94	0.87	-3.22E+00	3.75E-07	Down	-7.52E-01	1.34E-01		-1.16E+00	1.15E-04	Down	-1.26E+00	8.55E-05	Down	-1.80E+00	6.29E-13	Down	-1.90E+00	2.15E-14	Down	Unigene39607_All//gi|297606861|ref|NP_001059107.2|//6.00E-58//Os07g0193600 [Oryza sativa Japonica Group] >gi|255677581|dbj|BAF21021.2| Os07g0193600 [Oryza sativa Japonica Group]	Unigene39607_All//1.00E-49//AT5G25580| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 8 growth stages; BEST Arabidopsis thaliana protein match is: aminoacyl-tRNA synthetase family (TAIR:AT1G18950.1); Has 138 Blast hits to 138 proteins in 63 species: Archae - 0; Bacteria - 4; Metazoa - 48; Fungi - 29; Plants - 30; Viruses - 1; Other Eukaryotes - 26 (source: NCBI BLink).	Unigene39607_All//0.00E+00//ES799938				nr +
Unigene39609_All	306	10.94	7.95	23.14	20.02	16.99	17.86	1.38	1.37	0.91	-4.61E-01	1.78E-01		1.08E+00	3.38E-06	Up	-2.37E-01	3.64E-01		-1.65E-01	5.63E-01		-1.66E-02	1.02E+00		-6.00E-01	5.53E-01		Unigene39609_All//gi|255575295|ref|XP_002528851.1|//9.00E-07//F-box/leucine rich repeat protein, putative [Ricinus communis] >gi|223532053|gb|EEF33863.1| F-box/leucine rich repeat protein, putative [Ricinus communis]						nr -
Unigene3961_All	1465	33.64	10.76	14.94	110.17	94.07	52.59	46.84	81.85	51.83	-1.65E+00	3.61E-77	Down	-1.17E+00	1.15E-44	Down	-2.28E-01	5.65E-10		-1.07E+00	2.76E-140	Down	8.05E-01	1.63E-73		1.46E-01	7.49E-03		Unigene3961_All//gi|224131644|ref|XP_002328073.1|//0.00E+00//arogenate/prephenate dehydratase [Populus trichocarpa] >gi|222837588|gb|EEE75953.1| arogenate/prephenate dehydratase [Populus trichocarpa]	Unigene3961_All//8.00E-166//AT2G27820| PDT (PREPHENATE DEHYDRATASE 1); arogenate dehydratase/ prephenate dehydratase	Unigene3961_All//0.00E+00//TC135675		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr +
Unigene39610_All	665	1.42	3.73	2.88	2.85	2.07	2.99	0.57	1.76	3.71	1.40E+00	8.73E-04	Up	1.03E+00	3.81E-02		-4.59E-01	3.35E-01		7.01E-02	9.04E-01		1.62E+00	6.24E-03		2.70E+00	1.13E-09	Up			Unigene39610_All//2.00E-161//TC140143				
Unigene39611_All	401	17.74	19.08	10.76	20.99	23.27	28.04	73.28	48.57	20.66	1.05E-01	6.27E-01		-7.22E-01	1.54E-03		1.49E-01	5.21E-01		4.18E-01	1.49E-02		-5.93E-01	3.00E-11		-1.83E+00	2.79E-67	Down	Unigene39611_All//gi|222424799|dbj|BAH20352.1|//7.00E-26//AT1G54270 [Arabidopsis thaliana]	Unigene39611_All//4.00E-27//AT1G54270| EIF4A-2; ATP-dependent helicase/ translation initiation factor	Unigene39611_All//1.00E-136//BQ409833				nr -
Unigene39612_All	370	1.41	10.41	5.90	3.90	4.56	5.25	8.57	22.37	21.86	2.88E+00	1.60E-12	Up	2.06E+00	4.88E-05	Up	2.24E-01	7.06E-01		4.27E-01	3.94E-01		1.38E+00	6.50E-13	Up	1.35E+00	1.61E-12	Up	Unigene39612_All//gi|297819888|ref|XP_002877827.1|//2.00E-07//acyl-CoA oxidase 4 [Arabidopsis lyrata subsp. lyrata] >gi|297323665|gb|EFH54086.1| acyl-CoA oxidase 4 [Arabidopsis lyrata subsp. lyrata]	Unigene39612_All//8.00E-09//AT3G51840| ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase	Unigene39612_All//1.00E-164//CO121054		ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation		nr +
Unigene39613_All	763	2.19	1.00	0.91	27.42	9.48	1.78	1.27	0.22	1.51	-1.14E+00	2.63E-02		-1.27E+00	1.95E-02		-1.53E+00	5.36E-37	Down	-3.95E+00	5.94E-96	Down	-2.54E+00	6.41E-04	Down	2.49E-01	6.41E-01		Unigene39613_All//gi|79565313|ref|NP_180417.2|//8.00E-43//LBD11 (LOB DOMAIN-CONTAINING PROTEIN 11) [Arabidopsis thaliana]	Unigene39613_All//5.00E-34//AT1G07900| LBD1 (LOB DOMAIN-CONTAINING PROTEIN 1)	Unigene39613_All//0.00E+00//gi|73862495|gb|DT465234.1|DT465234		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene39615_All	525	5.68	1.83	4.87	8.07	6.03	5.68	2.01	0.64	0.91	-1.63E+00	2.60E-05	Down	-2.23E-01	5.86E-01		-4.19E-01	1.61E-01		-5.06E-01	9.46E-02		-1.66E+00	8.55E-03		-1.14E+00	4.77E-02		Unigene39615_All//gi|30697827|ref|NP_177089.2|//2.00E-27//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|193806277|sp|P0CCT4.1|PP110_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g69290	Unigene39615_All//7.00E-21//AT1G69290| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene39616_All	552	2.18	24.42	9.65	2.53	5.12	7.20	3.14	4.32	6.13	3.49E+00	9.83E-51	Up	2.15E+00	5.84E-12	Up	1.02E+00	5.45E-03		1.51E+00	2.25E-06	Up	4.59E-01	2.36E-01		9.66E-01	9.93E-04				Unigene39616_All//7.00E-07//TC175622				
Unigene39617_All	923	50.68	19.98	43.21	54.29	39.06	36.06	3.80	1.95	1.73	-1.34E+00	2.58E-54	Down	-2.30E-01	5.53E-03		-4.75E-01	2.70E-12		-5.90E-01	3.68E-16		-9.65E-01	1.05E-03		-1.14E+00	8.79E-05	Down	Unigene39617_All//gi|297810639|ref|XP_002873203.1|//8.00E-46//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319040|gb|EFH49462.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39617_All//1.00E-37//AT3G10910| zinc finger (C3HC4-type RING finger) family protein	Unigene39617_All//0.00E+00//TC173081				nr +
Unigene39619_All	483	4.22	11.64	5.29	4.54	5.56	4.11	1.75	2.16	0.17	1.46E+00	4.97E-08	Up	3.25E-01	4.32E-01		2.93E-01	5.14E-01		-1.41E-01	7.49E-01		3.05E-01	6.58E-01		-3.41E+00	1.35E-04	Down			Unigene39619_All//6.00E-07//TC149029				
Unigene39620_All	365	10.32	17.91	17.51	3.68	5.28	5.44	16.91	12.60	8.19	7.95E-01	5.73E-04		7.62E-01	1.65E-03		5.20E-01	3.03E-01		5.63E-01	2.43E-01		-4.25E-01	5.02E-02		-1.05E+00	7.09E-07	Down	Unigene39620_All//gi|145910320|gb|ABP98813.1|//2.00E-06//chloroplast biotin carboxylase [Gossypium hirsutum]		Unigene39620_All//0.00E+00//gi|109869532|gb|DW498508.1|DW498508				nr +
Unigene39621_All	295	8.34	2.40	1.08	12.50	7.24	12.71	39.70	10.63	14.04	-1.79E+00	4.83E-05	Down	-2.94E+00	5.16E-08	Down	-7.88E-01	8.91E-03		2.42E-02	9.53E-01		-1.90E+00	6.38E-28	Down	-1.50E+00	8.18E-21	Down			Unigene39621_All//3.00E-152//TC173896				
Unigene39622_All	306	67.37	95.54	52.03	150.42	98.69	147.00	179.48	287.11	84.10	5.04E-01	4.43E-07		-3.73E-01	3.38E-03		-6.08E-01	1.63E-17		-3.32E-02	7.26E-01		6.78E-01	2.96E-40		-1.09E+00	4.54E-58	Down	Unigene39622_All//gi|288310312|gb|ADC45395.1|//9.00E-52//HSP90-1 [Glycine max]	Unigene39622_All//4.00E-31//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Unigene39622_All//2.00E-123//gi|78331215|gb|DT551489.1|DT551489		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene39627_All	900	0.23	0.00	0.00	36.42	25.71	17.41	0.09	0.65	0.00	-7.86E+00	1.22E-01		-7.86E+00	1.46E-01		-5.02E-01	4.71E-09		-1.06E+00	9.20E-29	Down	2.79E+00	8.26E-03		-6.55E+00	3.58E-01		Unigene39627_All//gi|54042995|gb|AAV28488.1|//1.00E-113//homeodomain protein ARBORKNOX1 [Populus tremula x Populus alba]	Unigene39627_All//2.00E-107//AT1G62360| STM (SHOOT MERISTEMLESS); transcription factor	Unigene39627_All//0.00E+00//TC172748	HB			nr -
Unigene39628_All	911	1.78	0.39	1.11	5.96	8.58	6.59	26.69	16.33	7.08	-2.19E+00	2.05E-04	Down	-6.81E-01	2.14E-01		5.26E-01	9.37E-03		1.46E-01	6.38E-01		-7.08E-01	1.24E-12		-1.91E+00	2.06E-59	Down	Unigene39628_All//gi|4249380|gb|AAD14477.1|//2.00E-44//ESTs gb|237637, gb|AA042498 and gb|AA042269 come from this gene [Arabidopsis thaliana]	Unigene39628_All//2.00E-42//AT1G60010| unknown protein	Unigene39628_All//0.00E+00//TC164121				nr -
Unigene3963_All	1258	7.24	17.40	7.28	11.25	8.60	11.92	10.42	8.74	5.67	1.27E+00	1.75E-23	Up	8.70E-03	9.89E-01		-3.88E-01	6.74E-03		8.39E-02	6.31E-01		-2.54E-01	8.54E-02		-8.78E-01	2.25E-10		Unigene3963_All//gi|297811177|ref|XP_002873472.1|//1.00E-130//catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297319309|gb|EFH49731.1| catalytic/ coenzyme binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene3963_All//1.00E-120//AT5G10730| binding / catalytic/ coenzyme binding	Unigene3963_All//0.00E+00//TC149371				nr +
Unigene39630_All	305	19.56	16.95	11.17	10.62	10.39	6.22	49.63	21.10	11.63	-2.07E-01	4.14E-01		-8.08E-01	1.39E-03		-3.15E-02	9.30E-01		-7.72E-01	2.49E-02		-1.23E+00	2.15E-19	Down	-2.09E+00	6.59E-42	Down	Unigene39630_All//gi|300269009|gb|EFJ53189.1|//4.00E-08//histone H2B [Volvox carteri f. nagariensis]	Unigene39630_All//2.00E-09//AT5G59910| HTB4; DNA binding	Unigene39630_All//2.00E-162//gi|164273387|gb|ES815950.1|ES815950				nr -
Unigene39631_All	938	4.63	2.75	4.09	4.30	3.23	3.66	3.88	2.67	1.27	-7.49E-01	9.91E-03		-1.80E-01	5.91E-01		-4.13E-01	1.78E-01		-2.33E-01	4.94E-01		-5.36E-01	6.64E-02		-1.61E+00	1.06E-07	Down			Unigene39631_All//0.00E+00//TC179175				
Unigene39633_All	326	1.12	0.62	0.00	5.50	4.33	2.08	12.45	5.26	6.23	-8.54E-01	4.89E-01		-1.01E+01	2.78E-02		-3.45E-01	5.12E-01		-1.40E+00	4.83E-03		-1.24E+00	7.61E-06	Down	-9.98E-01	1.59E-04				Unigene39633_All//3.00E-165//gi|13245259|gb|BE052155.2|BE052155				
Unigene39634_All	560	4.20	9.50	8.27	3.20	1.91	2.90	3.40	0.60	0.64	1.18E+00	1.06E-05	Up	9.77E-01	8.84E-04		-7.48E-01	1.12E-01		-1.41E-01	7.72E-01		-2.51E+00	6.21E-07	Down	-2.41E+00	6.35E-07	Down	Unigene39634_All//gi|224059066|ref|XP_002299700.1|//2.00E-20//predicted protein [Populus trichocarpa] >gi|222846958|gb|EEE84505.1| predicted protein [Populus trichocarpa]		Unigene39634_All//3.00E-169//DT459198				nr +
Unigene39635_All	1114	3.76	0.55	0.72	3.49	2.60	1.14	1.44	0.71	0.82	-2.78E+00	3.08E-13	Down	-2.39E+00	1.02E-10	Down	-4.26E-01	1.72E-01		-1.62E+00	5.69E-07	Down	-1.02E+00	2.97E-02		-8.10E-01	6.84E-02		Unigene39635_All//gi|297812115|ref|XP_002873941.1|//1.00E-157//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319778|gb|EFH50200.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39635_All//8.00E-152//AT5G19330| armadillo/beta-catenin repeat family protein / BTB/POZ domain-containing protein	Unigene39635_All//5.00E-34//TC160738				nr -
Unigene39636_All	808	1.23	0.25	1.25	6.54	1.92	3.80	1.62	0.41	0.05	-2.29E+00	4.05E-03		2.55E-02	9.90E-01		-1.77E+00	9.02E-12	Down	-7.82E-01	2.26E-03		-1.97E+00	6.34E-04	Down	-5.04E+00	1.60E-08	Down	Unigene39636_All//gi|297843300|ref|XP_002888531.1|//4.00E-77//tyrosine specific protein phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335373|gb|EFH65790.1| tyrosine specific protein phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39636_All//5.00E-78//AT1G05000| tyrosine specific protein phosphatase family protein	Unigene39636_All//0.00E+00//TC137937				nr +

Unigene39637_All	1373	0.00	0.30	0.19	1.74	0.70	1.64	3.76	7.43	0.90	8.21E+00	1.36E-02		7.60E+00	8.01E-02		-1.31E+00	7.97E-04	Down	-8.25E-02	8.57E-01		9.83E-01	1.77E-09		-2.06E+00	1.51E-14	Down	Unigene39637_All//gi|15235633|ref|NP_195474.1|//1.00E-150//HLS1 (HOOKLESS 1); N-acetyltransferase [Arabidopsis thaliana] >gi|4468983|emb|CAB38297.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|7270740|emb|CAB80423.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|51969462|dbj|BAD43423.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|51970376|dbj|BAD43880.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|11074338|gb|AB804542.1| At4g37580 [Arabidopsis thaliana]	Unigene39637_All//1.00E-151//AT4G37580| HLS1 (HOOKLESS 1); N-acetyltransferase					nr -
Unigene39640_All	1151	0.09	0.26	0.14	0.00	0.06	0.24	4.89	10.57	89.78	1.54E+00	3.23E-01		6.11E-01	7.48E-01		5.90E+00	6.09E-01		7.88E+00	7.02E-02		1.11E+00	1.83E-13	Up	4.20E+00	0.00E+00	Up	Unigene39640_All//gi|15220787|ref|NP_173769.1|//1.00E-36//SR02 (SIMILAR TO RCD ONE 2); NAD+ ADP-ribosyltransferase [Arabidopsis thaliana] >gi|4056438|gb|AAC98011.1| F508.11 [Arabidopsis thaliana] >gi|63003772|gb|AAY25415.1| At1g23550 [Arabidopsis thaliana]	Unigene39640_All//5.00E-38//AT1G23550| SR02 (SIMILAR TO RCD ONE 2); NAD+ ADP-ribosyltransferase					nr +
Unigene39641_All	1471	0.21	0.21	0.00	0.20	0.00	0.09	0.89	3.75	25.97	-4.60E-02	9.84E-01		-7.74E+00	4.90E-02		-7.67E+00	2.01E-02		-1.14E+00	4.57E-01		2.07E+00	4.80E-15	Up	4.87E+00	2.71E-226	Up	Unigene39641_All//gi|15220787|ref|NP_173769.1|//3.00E-63//SR02 (SIMILAR TO RCD ONE 2); NAD+ ADP-ribosyltransferase [Arabidopsis thaliana] >gi|4056438|gb|AAC98011.1| F508.11 [Arabidopsis thaliana] >gi|63003772|gb|AAY25415.1| At1g23550 [Arabidopsis thaliana]	Unigene39641_All//2.00E-44//AT1G23550| SR02 (SIMILAR TO RCD ONE 2); NAD+ ADP-ribosyltransferase					nr +
Unigene39642_All	291	47.29	19.85	19.40	72.24	65.32	89.71	87.32	46.68	45.04	-1.25E+00	7.07E-15	Down	-1.29E+00	8.56E-15	Down	-1.45E-01	2.90E-01		3.12E-01	3.55E-03		-9.04E-01	1.39E-19		-9.55E-01	4.62E-22		Unigene39642_All//gi|116292768|gb|ABJ97699.1|//7.00E-44//EBP1 [Solanum tuberosum]	Unigene39642_All//1.00E-34//AT3G51800| ATG2; aminopeptidase/ metalloexopeptidase	Unigene39642_All//1.00E-163//TC131957				nr +
Unigene39643_All	598	5.77	2.03	8.73	3.33	3.63	1.66	1.13	1.05	2.60	-1.51E+00	1.85E-05	Down	5.96E-01	2.96E-02		1.23E-01	8.36E-01		-1.00E+00	2.91E-02		-1.10E-01	8.90E-01		1.20E+00	1.02E-02		Unigene39643_All//gi|297798030|ref|XP_002866899.1|//4.00E-30//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312735|gb|EFH43158.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39643_All//1.00E-30//AT4G39955| hydrolase, alpha/beta fold family protein	Unigene39643_All//0.00E+00//TC147452				nr +
Unigene39644_All	677	0.46	0.52	0.16	2.43	3.46	1.13	6.25	5.37	34.48	1.76E-01	8.83E-01		-1.56E+00	3.30E-01		5.10E-01	2.45E-01		-1.10E+00	3.43E-02		-2.18E-01	4.56E-01		2.47E+00	3.78E-77	Up	Unigene39644_All//gi|225456016|ref|XP_002277098.1|//7.00E-15//PREDICTED: hypothetical protein [Vitis vinifera]						nr +
Unigene39645_All	662	4.74	0.77	1.05	2.03	1.30	1.36	2.30	1.01	0.72	-2.63E+00	1.55E-09	Down	-2.18E+00	2.17E-07	Down	-6.44E-01	2.63E-01		-5.74E-01	3.45E-01		-1.19E+00	1.47E-02		-1.67E+00	7.06E-04	Down	Unigene39645_All//gi|15228894|ref|NP_191192.1|//3.00E-30//N2,N2-dimethylguanosine tRNA methyltransferase family protein [Arabidopsis thaliana] >gi|7572931|emb|CAB87432.1| N2,N2-dimethylguanosine tRNA methyltransferases-like protein [Arabidopsis thaliana]	Unigene39645_All//1.00E-31//AT3G56330| N2,N2-dimethylguanosine tRNA methyltransferase family protein	Unigene39645_All//0.00E+00//ES800657				nr -
Unigene39646_All	1396	1.12	0.29	1.83	0.79	0.12	0.49	2.30	5.63	6.08	-1.95E+00	7.99E-04	Down	7.03E-01	8.93E-02		-2.67E+00	1.89E-04	Down	-6.94E-01	3.11E-01		1.29E+00	3.96E-11	Up	1.40E+00	8.64E-14	Up	Unigene39646_All//gi|15223284|ref|NP_171611.1|//2.00E-53//NGA3 (NGATHA3); transcription factor [Arabidopsis thaliana] >gi|75192354|sp|Q9MAV1.1|NGA3_ARATH RecName: Full=B3 domain-containing transcription factor NGA3; AltName: Full=Protein NGATHA3 >gi|6715649|gb|AAF26476.1|AC007323_17 T25K16.3 [Arabidopsis thaliana] >gi|227060706|gb|ACP18973.1| NGATHA3 [Arabidopsis thaliana]	Unigene39646_All//2.00E-53//AT2G46870| NGA1 (NGATHA1); transcription factor	Unigene39646_All//0.00E+00//gi|164354332|gb|ES805253.1|ES805253	ABI3VP1			nr +
Unigene39647_All	931	0.84	1.63	0.06	1.50	1.59	1.84	4.54	4.85	2.01	9.54E-01	7.82E-02		-3.88E+00	1.60E-03		8.63E-02	8.96E-01		2.99E-01	6.11E-01		9.44E-02	7.30E-01		-1.18E+00	7.98E-06	Down	Unigene39647_All//gi|297829424|ref|XP_002882594.1|//9.00E-50//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328434|gb|EFH58853.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene39647_All//2.00E-50//AT3G08970| ATERDJ3A; oxidoreductase	Unigene39647_All//3.00E-87//TC178503				nr +
Unigene39648_All	448	0.47	1.24	0.59	4.45	8.76	3.53	2.08	12.97	4.71	1.41E+00	1.69E-01		3.47E-01	7.97E-01		9.78E-01	1.05E-03		-3.34E-01	5.02E-01		2.64E+00	7.21E-21	Up	1.18E+00	2.47E-03					Unigene39648_All//5.00E-07//TC159158				
Unigene3965_All	1641	12.40	6.36	8.47	7.26	5.31	10.82	22.26	6.55	19.64	-9.63E-01	2.00E-14		-5.50E-01	1.22E-05		-4.51E-01	3.84E-03		5.76E-01	7.17E-06		-1.77E+00	2.35E-77	Down	-1.81E-01	2.55E-02		Unigene3965_All//gi|42761392|dbj|BAD11660.1|//1.00E-143//uridylyl transferase-like [Oryza sativa Japonica Group]	Unigene3965_All//1.00E-144//AT1G69040| ACR4 (ACT REPEAT 4); amino acid binding	Unigene3965_All//0.00E+00//TC141518				nr -
Unigene39650_All	816	1.73	1.24	0.26	2.44	3.38	1.83	5.65	0.77	2.29	-4.79E-01	3.91E-01		-2.73E+00	1.56E-04	Down	4.67E-01	2.43E-01		-4.19E-01	3.88E-01		-2.88E+00	2.87E-18	Down	-1.30E+00	3.44E-07	Down	Unigene39650_All//gi|297839631|ref|XP_002887697.1|//5.00E-81//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333538|gb|EFH63956.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39650_All//1.00E-72//AT1G77720| protein kinase family protein	Unigene39650_All//0.00E+00//gi|78322945|gb|DT543219.1|DT543219				nr -
Unigene39653_All	1443	0.22	1.23	0.89	2.83	2.39	7.42	0.38	0.70	0.44	2.50E+00	2.34E-05	Up	2.03E+00	3.44E-03		-2.46E-01	4.51E-01		1.39E+00	2.32E-14	Up	8.68E-01	1.64E-01		2.14E-01	7.73E-01		Unigene39653_All//gi|145359157|ref|NP_200047.3|//0.00E+00//ATEX070A2 (exocyst subunit EX070 family protein A2); protein binding [Arabidopsis thaliana]	Unigene39653_All//0.00E+00//AT5G52340| ATEX070A2 (exocyst subunit EX070 family protein A2); protein binding	Unigene39653_All//6.00E-62//DT049948				nr -
Unigene39655_All	1052	0.10	0.34	0.30	0.85	0.85	1.16	10.21	26.02	20.15	1.76E+00	2.18E-01		1.61E+00	3.05E-01		-2.00E-03	9.78E-01		4.44E-01	5.00E-01		1.35E+00	2.07E-39	Up	9.81E-01	3.26E-19		Unigene39655_All//gi|222423216|dbj|BAH19585.1|//3.00E-83//AT2G20900 [Arabidopsis thaliana] >gi|222424359|dbj|BAH20135.1| AT2G20900 [Arabidopsis thaliana]	Unigene39655_All//3.00E-75//AT2G20900| diacylglycerol kinase, putative	Unigene39655_All//9.00E-91//TC146210		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	nr +
Unigene39656_All	624	5.45	0.73	0.94	1.76	0.39	1.52	17.96	9.91	14.62	-2.90E+00	2.62E-11	Down	-2.54E+00	2.17E-09	Down	-2.18E+00	1.20E-03		-2.09E-01	7.42E-01		-8.57E-01	2.20E-08		-2.97E-01	5.11E-02		Unigene39656_All//gi|116310418|emb|CAH67426.1|//5.00E-22//OSIGBa0150F01.6 [Oryza sativa (indica cultivar-group)]	Unigene39656_All//2.00E-15//AT3G20180| metal ion binding	Unigene39656_All//8.00E-13//FL577622				nr +
Unigene39658_All	359	3.64	29.50	18.99	7.63	17.27	28.43	68.90	230.28	69.69	3.02E+00	5.08E-35	Up	2.38E+00	3.77E-17	Up	1.18E+00	3.15E-07	Up	1.90E+00	4.35E-21	Up	1.74E+00	1.84E-170	Up	1.65E-02	8.97E-01					Unigene39658_All//4.00E-07//DT048855				
Unigene39659_All	742	0.00	2.32	0.00	1.07	0.88	2.31	31.28	216.70	311.25	1.12E+01	7.99E-10	Up	null	null		-2.85E-01	7.21E-01		1.11E+00	3.09E-02		2.79E+00	0.00E+00	Up	3.31E+00	0.00E+00	Up	Unigene39659_All//gi|224969393|gb|ACN71235.1|//8.00E-18//bZIP transcription factor [Tamarix hispida]	Unigene39659_All//1.00E-16//AT5G49450| AtbZIP1 (Arabidopsis thaliana basic leucine-zipper 1); DNA binding / protein heterodimerization/ transcription factor		bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene3966_All	2292	1.32	0.51	0.35	4.69	2.88	1.83	6.83	1.19	2.89	-1.38E+00	2.10E-04	Down	-1.93E+00	3.31E-06	Down	-7.03E-01	1.12E-05		-1.36E+00	3.63E-14	Down	-2.53E+00	1.59E-52	Down	-1.24E+00	7.41E-21	Down	Unigene3966_All//gi|212717139|gb|AGJ37411.1|//0.00E+00//receptor-like protein kinase [Glycine max]	Unigene3966_All//0.00E+00//AT4G36180| leucine-rich repeat family protein	Unigene3966_All//0.00E+00//gi|78345818|gb|DT566092.1|DT566092		ko04626|Plant-pathogen interaction		nr +
Unigene39660_All	671	1.72	1.21	3.25	6.76	3.70	4.04	5.36	1.37	1.42	-5.06E-01	4.09E-01		9.24E-01	4.33E-02		-8.71E-01	9.94E-04		-7.42E-01	8.27E-03		-1.97E+00	1.83E-09	Down	-1.91E+00	1.80E-09	Down				Unigene39660_All//9.00E-87//DT500553				
Unigene39661_All	2228	0.02	0.16	0.02	0.29	0.49	1.52	74.37	13.39	43.90	2.76E+00	9.59E-02		2.43E-02	9.95E-01		7.67E-01	2.69E-01		2.39E+00	1.38E-09	Up	-2.47E+00	0.00E+00	Down	-7.61E-01	1.89E-94		Unigene39661_All//gi|30725324|gb|AK257684.1|//1.00E-115//At3g01680 [Arabidopsis thaliana]	Unigene39661_All//4.00E-117//AT3G01680| unknown protein	Unigene39661_All//0.00E+00//ES831165				nr +
Unigene39664_All	847	0.49	0.00	0.50	26.99	7.44	8.26	24.86	18.31	17.12	-8.95E+00	1.05E-02		2.55E-02	1.00E+00		-1.86E+00	2.14E-53	Down	-1.71E+00	3.14E-41	Down	-4.41E-01	3.48E-05		-5.38E-01	2.48E-07		Unigene39664_All//gi|113367166|gb|ABI34640.1|//5.00E-63//bZIP transcription factor bZIP35 [Glycine max]	Unigene39664_All//2.00E-38//AT1G13600| AtbZIP58 (Arabidopsis thaliana basic leucine-zipper 58); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor		bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene39665_All	1045	1.45	0.63	0.66	4.48	7.61	9.38	0.45	2.24	0.11	-1.20E+00	2.75E-02		-1.13E+00	4.79E-02		7.65E-01	9.06E-05		1.07E+00	6.55E-09	Up	2.33E+00	9.94E-08	Up	-1.96E+00	5.82E-02		Unigene39665_All//gi|297795599|ref|XP_002865684.1|//1.00E-114//male sterility MS5 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311519|gb|EFH41943.1| male sterility MS5 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39665_All//2.00E-112//AT5G48850| ATSDI1 (SULPHUR DEFICIENCY-INDUCED 1); binding	Unigene39665_All//1.00E-133//gi|164317959|gb|EV485945.1|EV485945				nr +
Unigene39667_All	700	0.75	2.53	1.37	2.06	16.38	26.58	1.15	1.97	4.33	1.76E+00	9.42E-04	Up	8.74E-01	2.38E-01		2.99E+00	4.28E-43	Up	3.69E+00	3.08E-78	Up	7.80E-01	1.32E-01		1.91E+00	5.09E-08	Up	Unigene39667_All//gi|224131232|ref|XP_002321033.1|//8.00E-38//glutaredoxin [Populus trichocarpa] >gi|222861806|gb|EEE99348.1| glutaredoxin [Populus trichocarpa]	Unigene39667_All//4.00E-38//AT3G62930| glutaredoxin family protein	Unigene39667_All//1.00E-76//TC155902				nr +
Unigene39670_All	517	12.14	31.75	13.18	34.21	34.97	35.73	38.85	66.70	80.60	1.39E+00	2.29E-20	Up	1.19E-01	6.15E-01		3.18E-02	8.39E-01		6.29E-02	7.05E-01		7.80E-01	1.34E-20		1.05E+00	2.19E-41	Up	Unigene39670_All//gi|259121417|gb|ACV92028.1|//2.00E-24//WRKY transcription factor 26 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene39670_All//2.00E-20//AT2G23320| WRKY15; calmodulin binding / transcription factor	Unigene39670_All//3.00E-138//DW514531	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene39671_All	1350	0.00	0.00	0.00	9.30	1.63	1.24	0.06	0.00	0.00	null	null		null	null		-2.51E+00	2.78E-43	Down	-2.91E+00	7.90E-44	Down	-5.97E+00	4.03E-01		-5.97E+00	3.58E-01		Unigene39671_All//gi|262316884|emb|CAZ64538.1|//1.00E-174//inward rectifying shaker-like K+ channel [Vitis vinifera]	Unigene39671_All//1.00E-155//AT2G26650| AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel	Unigene39671_All//0.00E+00//gi|78341379|gb|DT561653.1|DT561653				nr +
Unigene39673_All	439	5.72	10.50	7.76	5.11	4.39	1.85	1.35	2.29	1.63	8.77E-01	1.92E-03		4.40E-01	2.23E-01		-2.17E-01	6.15E-01		-1.46E+00	8.28E-04	Down	7.61E-01	2.28E-01		2.77E-01	6.90E-01					Unigene39673_All//5.00E-07//BG441208				
Unigene39674_All	538	3.79	1.88	0.79	3.15	2.37	1.85	5.11	4.89	5.11	-1.01E+00	2.58E-02		-2.26E+00	3.27E-05	Down	-4.11E-01	4.28E-01		-7.70E-01	1.33E-01		-6.17E-02	8.69E-01		3.00E-04	9.99E-01		Unigene39674_All//gi|115460452|ref|NP_001053826.1|//1.00E-11//Os04g0610000 [Oryza sativa Japonica Group] >gi|113565397|dbj|BAF15740.1| Os04g0610000 [Oryza sativa Japonica Group]		Unigene39674_All//0.00E+00//gi|78329536|gb|DT549810.1|DT549810				nr +
Unigene39675_All	444	4.01	2.17	5.52	10.21	3.96	3.97	2.76	3.29	0.09	-8.86E-01	6.99E-02		4.62E-01	2.84E-01		-1.37E+00	4.05E-07	Down	-1.36E+00	2.26E-06	Down	2.55E-01	6.58E-01		-4.94E+00	6.14E-08	Down				Unigene39675_All//5.00E-07//ES798070				

Unigene39676_All	982	2.24	1.39	0.65	5.94	5.72	4.37	0.90	0.38	0.77	-6.84E-01	1.15E-01		-1.78E+00	2.71E-04	Down	-5.43E-02	8.32E-01		-4.42E-01	8.03E-02		-1.24E+00	6.79E-02		-2.30E-01	7.05E-01		Unigene39676_All//gi|79501722|ref|NP_195675.2|//4.00E-84//GGT2 (GAMMA-GLUTAMYL TRANSPEPTIDASE 2); gamma-glutamyltransferase/ glutathione gamma-glutamylcysteinyltransferase [Arabidopsis thaliana]	Unigene39676_All//3.00E-85//AT4G39650| GGT2 (GAMMA-GLUTAMYL TRANSPEPTIDASE 2); gamma-glutamyltransferase/ glutathione gamma-glutamylcysteinyltransferase	Unigene39676_All//1.00E-71//TC130431		ko00480|Glutathione metabolism//ko00460|Cyanoamino acid metabolism//ko00450|Selenoamino acid metabolism//ko00590|Arachidonic acid metabolism//ko00430|Taurine and hypotaurine metabolism		nr +
Unigene39678_All	2163	0.00	0.80	0.12	0.05	0.06	0.15	5.20	19.30	40.85	9.64E+00	7.99E-10	Up	6.94E+00	8.01E-02		4.67E-01	8.76E-01		1.67E+00	3.09E-01		1.89E+00	7.86E-97	Up	2.97E+00	0.00E+00	Up	Unigene39678_All//gi|91806405|gb|ABE65930.1|//0.00E+00//exocyst subunit EXO70 family protein [Arabidopsis thaliana]	Unigene39678_All//5.00E-178//AT3G09520| ATEXO70H4 (exocyst subunit EXO70 family protein H4); protein binding	Unigene39678_All//3.00E-117//gi|78340229|gb|DT560503.1|DT560503				nr +
Unigene39679_All	893	0.47	1.93	1.85	5.91	5.28	3.19	9.56	4.21	2.81	2.04E+00	2.81E-04	Up	1.98E+00	8.05E-04	Up	-1.63E-01	5.88E-01		-8.92E-01	4.90E-04		-1.18E+00	1.28E-10	Down	-1.77E+00	2.75E-19	Down	Unigene39679_All//gi|15237147|ref|NP_197678.1|//8.00E-83//harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana]	Unigene39679_All//4.00E-38//AT5G22870| harpin-induced protein-related / HIN1-related / harpin-responsive protein-related					nr -
Unigene3968_All	1625	4.86	4.46	4.75	28.14	17.80	22.93	13.43	5.25	8.85	-1.25E-01	6.00E-01		-3.31E-02	8.90E-01		-6.61E-01	3.86E-20		-2.96E-01	1.35E-04		-1.36E+00	8.24E-32	Down	-6.01E-01	4.87E-09		Unigene3968_All//gi|30680274|ref|NP_849972.1|//1.00E-151//AAA-type ATPase family protein [Arabidopsis thaliana] >gi|51968516|dbj|BAD42950.1| AAA-type ATPase like protein [Arabidopsis thaliana] >gi|51968792|dbj|BAD43088.1| AAA-type ATPase like protein [Arabidopsis thaliana] >gi|51971357|dbj|BAD44343.1| AAA-type ATPase like protein [Arabidopsis thaliana] >gi|111074238|gb|AB804492.1|At2g18193 [Arabidopsis thaliana]	Unigene3968_All//1.00E-145//AT2G18193| AAA-type ATPase family protein	Unigene3968_All//0.00E+00//TC134787				nr -
Unigene39680_All	836	14.52	5.39	10.19	11.68	4.12	1.40	0.00	0.00	0.19	-1.43E+00	5.32E-16	Down	-5.11E-01	2.53E-03		-1.50E+00	5.73E-17	Down	-3.06E+00	6.78E-36	Down	null	null		7.57E+00	1.40E-01		Unigene39680_All//gi|297822233|ref|XP_002878999.1|//5.00E-59//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324838|gb|EFH55258.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene39680_All//1.00E-59//AT2G26695| binding / zinc ion binding					nr +
Unigene39681_All	272	3.85	3.73	2.74	2.93	3.54	3.99	19.74	17.82	6.74	-4.63E-02	9.57E-01		-4.89E-01	4.78E-01		2.75E-01	7.47E-01		4.44E-01	5.39E-01		-1.47E-01	5.97E-01		-1.55E+00	1.77E-10	Down			Unigene39681_All//1.00E-111//gi|73860739|gb|DT463478.1|DT463478				
Unigene39682_All	379	2.76	4.95	3.79	8.02	7.00	6.67	13.61	8.49	3.15	8.41E-01	7.75E-02		4.58E-01	4.15E-01		-1.97E-01	5.97E-01		-2.65E-01	5.02E-01		-6.81E-01	3.69E-03		-2.11E+00	5.95E-15	Down			Unigene39682_All//2.00E-132//gi|164307920|gb|ES807655.1|ES807655				
Unigene39684_All	687	3.88	7.82	3.64	7.03	14.74	8.61	1.17	0.85	1.22	1.01E+00	1.13E-04	Up	-9.25E-02	8.12E-01		1.07E+00	6.50E-10	Up	2.92E-01	2.81E-01		-4.57E-01	5.36E-01		5.86E-02	9.50E-01								
Unigene39688_All	404	0.52	3.51	1.58	2.59	2.64	1.57	3.14	2.48	3.65	2.76E+00	7.72E-05	Up	1.61E+00	1.11E-01		2.92E-02	9.80E-01		-7.26E-01	3.02E-01		-3.39E-01	5.58E-01		2.17E-01	6.44E-01								
Unigene39691_All	465	2.48	1.09	1.03	1.29	2.22	2.33	8.27	4.22	2.40	-1.18E+00	6.62E-02		-1.26E+00	6.41E-02		7.89E-01	2.74E-01		8.59E-01	2.17E-01		-9.70E-01	5.22E-04		-1.79E+00	2.81E-09	Down	Unigene39691_All//gi|37202072|gb|AAQ89651.1|//1.00E-31//At5g51960 [Arabidopsis thaliana]	Unigene39691_All//9.00E-33//AT5G51960| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: ATP synthase assembly factor FMC1, mitochondrial (InterPro:IPR018471); Has 18 Blast hits to 18 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 18; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene39691_All//0.00E+00//gi|109881700|gb|DW510670.1|DW510670				nr +
Unigene39693_All	828	2.97	7.71	2.57	0.36	0.67	0.22	15.78	27.81	59.52	1.38E+00	2.70E-08	Up	-2.07E-01	6.35E-01		8.82E-01	4.21E-01		-7.26E-01	6.39E-01		8.18E-01	3.73E-15		1.92E+00	2.44E-118	Up	Unigene39693_All//gi|106879177|gb|ABF82618.1|//2.00E-13//At5g38300 [Arabidopsis thaliana]	Unigene39693_All//4.00E-11//AT5G38300| unknown protein	Unigene39693_All//2.00E-14//BM359153				nr +
Unigene39694_All	528	51.92	15.35	43.16	4.15	4.24	0.68	0.48	0.71	1.21	-1.76E+00	2.17E-47	Down	-2.67E-01	1.64E-02		3.03E-02	9.58E-01		-2.60E+00	3.56E-07	Down	5.68E-01	6.37E-01		1.33E+00	1.00E-01		Unigene39694_All//gi|240255271|ref|NP_186985.5|//4.00E-12//binding / catalytic/ oxidoreductase [Arabidopsis thaliana]	Unigene39694_All//9.00E-06//AT3G03350| binding / catalytic/ oxidoreductase	Unigene39694_All//0.00E+00//gi|109884197|gb|DW513167.1|DW513167				nr +
Unigene39695_All	624	2.85	2.92	5.80	3.83	3.31	3.26	0.47	1.27	2.49	3.62E-02	9.58E-01		1.03E+00	2.52E-03		-2.11E-01	6.15E-01		-2.35E-01	6.33E-01		1.42E+00	5.34E-02		2.39E+00	1.16E-05	Up	Unigene39695_All//gi|57955929|gb|AB006388.1|//4.00E-70//CBL1 [Gossypium hirsutum]	Unigene39695_All//2.00E-64//AT4G17615| CBL1 (CALCINEURIN B-LIKE PROTEIN 1); calcium ion binding	Unigene39695_All//0.00E+00//gi|48812035|gb|CO113348.1|CO113348		ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene39696_All	347	21.11	10.51	17.80	45.94	46.84	37.61	14.26	8.43	7.81	-1.01E+00	4.55E-06	Down	-2.46E-01	3.09E-01		2.80E-02	8.72E-01		-2.88E-01	4.72E-02		-7.58E-01	1.61E-03		-8.69E-01	2.10E-04		Unigene39696_All//gi|30841446|gb|AAP34361.1|//6.00E-43//fiber protein Fb14 [Gossypium barbadense] >gi|66271051|gb|AAY43803.1| Fb14 [Gossypium hirsutum]	Unigene39696_All//4.00E-37//AT2G47690| NADH-ubiquinone oxidoreductase-related	Unigene39696_All//3.00E-159//BE053626		ko00190|Oxidative phosphorylation		nr -
Unigene39697_All	693	1.43	0.66	0.69	2.95	3.98	1.56	6.10	3.26	2.41	-1.12E+00	1.09E-01		-1.05E+00	1.48E-01		4.32E-01	2.95E-01		-9.14E-01	4.37E-02		-9.06E-01	6.01E-04		-1.34E+00	6.25E-07	Down	Unigene39697_All//gi|30841446|gb|AAP34361.1|//2.00E-42//fiber protein Fb14 [Gossypium barbadense] >gi|66271051|gb|AAY43803.1| Fb14 [Gossypium hirsutum]	Unigene39697_All//2.00E-36//AT2G47690| NADH-ubiquinone oxidoreductase-related	Unigene39697_All//0.00E+00//TC160689		ko00190|Oxidative phosphorylation		nr +
Unigene39698_All	403	8.57	39.48	14.67	33.99	26.32	34.07	45.53	113.36	49.33	2.20E+00	5.71E-37	Up	7.75E-01	2.21E-03		-3.69E-01	1.21E-02		3.20E-03	9.85E-01		1.32E+00	9.35E-63	Up	1.16E-01	3.56E-01				Unigene39698_All//6.00E-133//DW238310				
Unigene397_All	3596	5.60	3.09	5.02	7.36	7.08	6.08	4.68	1.95	2.84	-8.60E-01	6.11E-12		-1.58E-01	2.58E-01		-5.58E-02	6.72E-01		-2.75E-01	1.07E-02		-1.26E+00	3.45E-22	Down	-7.22E-01	1.36E-09		Unigene397_All//gi|115452817|ref|NP_001050009.1|//1.00E-160//0s03g0330300 [Oryza sativa Japonica Group] >gi|108707956|gb|ABF95751.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548480|dbj|BAF11923.1| Os03g0330300 [Oryza sativa Japonica Group]	Unigene397_All//4.00E-21//AT1G72410| COP1-interacting protein-related	Unigene397_All//0.00E+00//TC137311				nr +
Unigene3970_All	1142	22.50	31.81	33.25	27.57	24.48	19.06	17.99	14.46	8.93	5.00E-01	1.76E-08		5.64E-01	2.53E-10		-1.71E-01	9.14E-02		-5.32E-01	1.00E-08		-3.16E-01	4.19E-03		-1.01E+00	1.08E-19	Down	Unigene3970_All//gi|15223970|ref|NP_177275.1|//1.00E-127//SAG18 (SENESCENCE ASSOCIATED GENE 18) [Arabidopsis thaliana] >gi|208876514|gb|ACI31302.1| At1g71190 [Arabidopsis thaliana]	Unigene3970_All//2.00E-119//AT1G71190| SAG18 (SENESCENCE ASSOCIATED GENE 18)	Unigene3970_All//0.00E+00//TC147458				nr +
Unigene39700_All	403	10.65	5.53	9.51	10.63	7.95	5.16	0.52	0.10	0.30	-9.44E-01	1.33E-03		-1.62E-01	6.41E-01		-4.20E-01	1.56E-01		-1.04E+00	3.27E-04	Down	-2.34E+00	2.37E-01		-8.23E-01	5.99E-01		Unigene39700_All//gi|208436371|gb|ACI28534.1|//2.00E-22//shikimate O-hydroxycinnamoyl transferase [Trifolium pratense]	Unigene39700_All//6.00E-18//AT5G48930| HCT (HYDROXYCINNAMOYL-COA SHIKIMATE/QUINATE HYDROXYCINNAMOYL TRANSFERASE); quinate O-hydroxycinnamoyltransferase/ shikimate O-hydroxycinnamoyltransferase/ transferase	Unigene39700_All//1.00E-72//TC147324		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene39701_All	364	4.60	7.93	10.09	5.34	9.37	6.33	26.72	33.30	6.90	7.87E-01	3.32E-02		1.13E+00	8.24E-04	Up	8.11E-01	1.32E-02		2.46E-01	6.31E-01		3.18E-01	3.43E-02		-1.95E+00	6.18E-25	Down			Unigene39701_All//2.00E-160//TC178375				
Unigene39702_All	858	60.31	32.24	51.76	16.84	39.61	11.90	2.02	0.05	2.79	-9.03E-01	6.11E-32		-2.21E-01	4.96E-03		1.23E+00	9.60E-41	Up	-5.01E-01	5.30E-04		-5.37E+00	5.76E-11	Down	4.64E-01	2.00E-01		Unigene39702_All//gi|70609692|gb|AAZ05071.1|//1.00E-104//cytochrome P450 [Citrus sinensis]	Unigene39702_All//7.00E-54//AT4G36380| ROT3 (ROTUNDIFOLIA 3); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding / steroid hydroxylase	Unigene39702_All//0.00E+00//TC163156		ko00905|Brassinosteroid biosynthesis		nr +
Unigene39703_All	463	11.07	20.14	12.65	2.69	1.64	1.56	3.84	2.08	0.52	8.63E-01	5.74E-06		1.92E-01	4.81E-01		-7.17E-01	2.26E-01		-7.85E-01	2.08E-01		-8.85E-01	4.34E-02		-2.89E+00	9.05E-08	Down							
Unigene39704_All	330	9.35	165.52	12.91	53.89	219.86	80.75	31.13	57.12	162.61	4.15E+00	2.14E-234	Up	4.65E-01	1.37E-01		2.03E+00	3.01E-176	Up	5.83E-01	1.19E-08		8.76E-01	5.33E-14		2.38E+00	8.75E-170	Up	Unigene39704_All//gi|15241248|ref|NP_200466.1|//9.00E-12//OXS3 (OXIDATIVE STRESS 3) [Arabidopsis thaliana]	Unigene39704_All//4.00E-13//AT5G56550| OXS3 (OXIDATIVE STRESS 3)	Unigene39704_All//2.00E-113//gi|109876927|gb|DW505901.1|DW505901				nr +
Unigene39705_All	781	1.27	64.42	2.66	3.64	9.26	14.05	7.04	16.75	14.84	5.66E+00	1.29E-256	Up	1.06E+00	2.44E-02		1.35E+00	3.60E-10	Up	1.95E+00	1.83E-23	Up	1.25E+00	3.39E-17	Up	1.08E+00	1.45E-12	Up	Unigene39705_All//gi|297798220|ref|XP_002866994.1|//1.00E-60//homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata] >gi|297312830|gb|EFH43253.1| homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata]	Unigene39705_All//3.00E-42//AT4G36740| ATHB40 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 40); DNA binding / transcription factor	Unigene39705_All//0.00E+00//gi|164353340|gb|ES793985.1|ES793985	HB			nr -
Unigene39706_All	331	2.05	4.44	4.02	7.83	4.37	4.78	21.84	14.02	10.35	1.11E+00	4.53E-02		9.69E-01	1.15E-01		-8.41E-01	2.39E-02		-7.13E-01	7.29E-02		-6.40E-01	9.28E-04		-1.08E+00	3.08E-08	Down			Unigene39706_All//9.00E-153//gi|109873378|gb|DW502353.1|DW502353				
Unigene39707_All	669	1.09	346.20	20.93	0.15	5.10	33.75	0.25	0.56	2.80	8.30E+00	0.00E+00	Up	4.26E+00	5.09E-60	Up	5.10E+00	1.05E-18	Up	7.82E+00	3.17E-134	Up	1.15E+00	3.27E-01		3.47E+00	2.57E-09	Up	Unigene39707_All//gi|6630452|gb|AAF19540.1|AC007190_8//1.00E-09//F23N19.19 [Arabidopsis thaliana] >gi|38603860|gb|AAR24675.1| At1g62840 [Arabidopsis thaliana]	Unigene39707_All//6.00E-11//AT1G62840| unknown protein					nr +

Unigene39709_All	1473	0.00	0.07	0.07	1.08	1.01	5.12	13.66	11.26	13.93	6.10E+00	3.86E-01		6.18E+00	3.98E-01		-1.07E-01	8.20E-01		2.24E+00	2.52E-19	Up	-2.78E-01	1.37E-02		2.78E-02	8.23E-01		Unigene39709_All//gi|22330390|ref|NP_683462.1|//3.00E-24//basic helix-loop-helix (bHLH) family protein (bHLH125) [Arabidopsis thaliana] >gi|75311449|sp|Q9LQ08.1|BH125_ARATH RecName: Full=Transcription factor bHLH125; AltName: Full=Transcription factor EN 2; AltName: Full=bHLH transcription factor bHLH125; AltName: Full=Basic helix-loop-helix protein 125; Short=bHLH 125; Short=AtbHLH125 >gi|8493586|gb|AAF75809.1|AC011000_12 Contains similarity to Mitf from Mesocricetus auratus gb|AF029900, and contains a Helix-loop-helix DNA-binding PF|00010 domain [Arabidopsis thaliana] >gi|20805890|gb|AAM28882.1|AF506369_1 basic helix-loop-helix transcription factor bHLH125 [Arabidopsis thaliana] >gi|30102596|gb|AAP21216.1|At1g62975 [Arabidopsis thaliana]	Unigene39709_All//6.00E-19//AT5G51780| basix helix-loop-helix (bHLH) family protein		bHLH			nr -
Unigene39710_All	744	1.69	0.89	2.58	1.00	0.19	0.24	157.30	137.97	72.61	-9.31E-01	1.21E-01		6.10E-01	2.20E-01		-2.44E+00	5.60E-03		-2.05E+00	2.45E-02		-1.89E-01	1.10E-05		-1.12E+00	1.00E-126	Down	Unigene39710_All//gi|215271818|emb|CAN87006.1|//3.00E-88//hexose transporter 1 [Hevea brasiliensis]	Unigene39710_All//2.00E-71//AT1G11260| STP1 (SUGAR TRANSPORTER 1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene39710_All//0.00E+00//gi|84158532|gb|DN827579.1|DN827579				nr +
Unigene39711_All	1069	1.17	1.04	0.70	4.01	4.12	5.49	8.46	1.60	1.79	-1.72E-01	7.55E-01		-7.52E-01	2.32E-01		4.11E-02	9.11E-01		4.55E-01	7.28E-02		-2.40E+00	6.08E-29	Down	-2.24E+00	1.35E-27	Down	Unigene39711_All//gi|297795355|ref|XP_002865562.1|//1.00E-117//peroxidase 64 [Arabidopsis lyrata subsp. lyrata] >gi|297311397|gb|EFH41821.1|peroxidase 64 [Arabidopsis lyrata subsp. lyrata]	Unigene39711_All//5.00E-118//AT5G42180| peroxidase 64 (PER64) (P64) (PRXR4)	Unigene39711_All//0.00E+00//TC145326		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene39712_All	1106	1.32	0.82	0.82	3.42	3.71	3.39	6.04	1.47	0.94	-6.84E-01	2.15E-01		-6.95E-01	2.36E-01		1.14E-01	7.75E-01		-1.43E-02	9.57E-01		-2.04E+00	1.07E-17	Down	-2.69E+00	2.96E-25	Down	Unigene39712_All//gi|225626267|gb|ACN97183.1|//1.00E-143//peroxidase [Populus trichocarpa]	Unigene39712_All//7.00E-132//AT5G42180| peroxidase 64 (PER64) (P64) (PRXR4)	Unigene39712_All//0.00E+00//TC145326		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene39713_All	490	105.82	92.45	61.73	109.79	110.12	97.33	104.84	51.01	55.61	-1.95E-01	1.04E-02		-7.78E-01	5.48E-24		4.30E-03	9.66E-01		-1.74E-01	2.15E-02		-1.04E+00	1.04E-48	Down	-9.15E-01	1.11E-40		Unigene39713_All//gi|226509527|ref|NP_001150550.1|//3.00E-29//LOC100284182 [Zea mays] >gi|226958587|ref|NP_001152931.1|40S ribosomal protein S30 [Zea mays] >gi|195611292|gb|ACG27476.1|40S ribosomal protein S30 [Zea mays] >gi|195618628|gb|ACG31144.1|40S ribosomal protein S30 [Zea mays] >gi|195618890|gb|ACG31275.1|40S ribosomal protein S30 [Zea mays] >gi|195640126|gb|ACG39531.1|40S ribosomal protein S30 [Zea mays] >gi|195651375|gb|ACG45155.1|40S ribosomal protein S30 [Zea mays] >gi|195656311|gb|ACG47623.1|40S ribosomal protein S30 [Zea mays]	Unigene39713_All//4.00E-22//AT5G56670| 40S ribosomal protein S30 (RPS30C)	Unigene39713_All//0.00E+00//TC170648		ko03010|Ribosome		nr -
Unigene39714_All	738	7.94	1.99	3.90	1.76	3.64	1.77	0.00	0.11	0.16	-2.00E+00	1.54E-12	Down	-1.03E+00	6.90E-05	Down	1.05E+00	5.37E-03		1.61E-02	9.80E-01		6.82E+00	4.01E-01		7.34E+00	2.43E-01		Unigene39714_All//gi|18398482|ref|NP_564405.1|//2.00E-70//LOL1 (LSD ONE LIKE 1); DNA binding [Arabidopsis thaliana] >gi|186479127|ref|NP_001117399.1|LOL1 (LSD ONE LIKE 1); DNA binding [Arabidopsis thaliana] >gi|163323143|gb|AAL15306.1|At1g32540/T9G5_1 [Arabidopsis thaliana] >gi|21436015|gb|AAM51585.1|At1g32540/T9G5_1 [Arabidopsis thaliana] >gi|33867796|gb|AAQ55219.1| LSD1-like [Arabidopsis thaliana]	Unigene39714_All//7.00E-64//AT1G32540| LOL1 (LSD ONE LIKE 1); DNA binding	Unigene39714_All//0.00E+00//TC145771				nr +
Unigene39719_All	366	23.73	26.72	25.46	29.81	30.48	65.52	54.18	47.51	40.38	1.71E-01	3.77E-01		1.02E-01	6.12E-01		3.24E-02	8.76E-01		1.14E+00	3.42E-23	Up	-1.90E-01	1.16E-01		-4.24E-01	8.19E-05		Unigene39719_All//gi|300608164|emb|CAZ86692.1|//4.00E-33//epoxide hydrolase 1 [Prunus persica]	Unigene39719_All//1.00E-32//AT2G26740| ATSEH (Arabidopsis thaliana soluble epoxide hydrolase); epoxide hydrolase	Unigene39719_All//0.00E+00//CO082151				nr -
Unigene39720_All	572	1.65	0.80	1.02	0.26	0.72	0.87	4.58	7.82	15.46	-1.05E+00	1.43E-01		-6.85E-01	3.69E-01		1.47E+00	2.79E-01		1.73E+00	1.45E-01		7.71E-01	2.49E-03		1.75E+00	1.58E-19	Up	Unigene39720_All//gi|145335397|ref|NP_172597.2|//6.00E-34//ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene39720_All//4.00E-35//AT1G11300| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene39720_All//9.00E-173//TC149497				nr +
Unigene39722_All	1618	0.97	0.25	0.00	0.99	0.81	0.34	11.45	4.03	8.74	-1.95E+00	7.99E-04	Down	-9.92E+00	1.42E-08	Down	-2.85E-01	6.01E-01		-1.56E+00	4.07E-03		-1.51E+00	1.21E-31	Down	-3.89E-01	5.19E-04		Unigene39722_All//gi|240256153|ref|NP_567936.5|//0.00E+00//CER4 (ECERIFERUM 4); fatty acyl-CoA reductase (alcohol-forming)/ oxidoreductase, acting on the CH-CH group of donors [Arabidopsis thaliana] >gi|75163749|sp|Q93ZB9.1|FACR3_ARATH RecName: Full=Fatty acyl-CoA reductase 3; AltName: Full=Protein ECERIFERUM 4 >gi|16323107|gb|AAL15288.1|AT4g33790/T16L1_280 [Arabidopsis thaliana]	Unigene39722_All//3.00E-173//AT4G33790| CER4 (ECERIFERUM 4); fatty acyl-CoA reductase (alcohol-forming)/ oxidoreductase, acting on the CH-CH group of donors	Unigene39722_All//0.00E+00//TC149409		ko04146|Peroxisome	GO:0006633//GO:0016620//GO:0043231	nr -
Unigene39723_All	268	1.95	14.18	4.57	6.69	22.74	14.66	1.26	2.65	3.72	2.86E+00	2.76E-12	Up	1.23E+00	6.00E-02		1.77E+00	1.70E-12	Up	1.13E+00	2.65E-04	Up	1.07E+00	1.67E-01		1.56E+00	1.33E-02					Unigene39723_All//3.00E-07//TC165464					
Unigene39724_All	1885	0.53	0.62	0.11	1.19	0.38	0.55	156.29	23.35	47.30	2.29E-01	6.94E-01		-2.22E+00	7.49E-03		-1.63E+00	8.57E-05	Down	-1.11E+00	9.63E-03		-2.74E+00	0.00E+00	Down	-1.72E+00	0.00E+00	Down	Unigene39724_All//gi|73647513|gb|AAZ79355.1|//0.00E+00//aldehyde dehydrogenase [Vitis pseudoreticulata]	Unigene39724_All//0.00E+00//AT3G48000| ALDH2B4 (ALDEHYDE DEHYDROGENASE 2B4); 3-chloroallyl aldehyde dehydrogenase/ ATP binding / aldehyde dehydrogenase (NAD)	Unigene39724_All//1.00E-146//EG702325		ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0004030//GO:0008152//GO:0009536//GO:0010038//GO:0032559	nr +
Unigene39725_All	509	0.31	0.20	0.21	4.80	3.65	5.32	43.36	155.19	63.71	-6.31E-01	7.27E-01		-5.60E-01	7.75E-01		-3.93E-01	3.47E-01		1.51E-01	7.12E-01		1.84E+00	8.52E-176	Up	5.55E-01	2.47E-11		Unigene39725_All//gi|15221214|ref|NP_172677.1|//2.00E-40//flavin-containing monooxygenase family protein / FMO family protein [Arabidopsis thaliana] >gi|10086520|gb|AAG12580.1|AC022522_13 Hypothetical protein [Arabidopsis thaliana] >gi|67633370|gb|AAT78610.1|flavin-containing monooxygenase family protein [Arabidopsis thaliana] >gi|111074200|gb|ABH04473.1|At1g12130 [Arabidopsis thaliana]	Unigene39725_All//1.00E-37//AT1G12130| flavin-containing monooxygenase family protein / FMO family protein	Unigene39725_All//1.00E-57//TC129641		ko00380|Tryptophan metabolism//ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0005789//GO:0008152//GO:0016709//GO:0030554	nr +
Unigene39726_All	765	4.58	8.41	6.26	1.11	1.04	1.00	2.82	1.20	0.89	8.76E-01	1.78E-04		4.51E-01	1.26E-01		-9.66E-02	8.77E-01		-1.42E-01	8.53E-01		-1.23E+00	1.98E-03		-1.67E+00	3.80E-05	Down				Unigene39726_All//2.00E-29//ES809754					
Unigene39727_All	512	3.17	0.99	4.16	4.09	0.74	1.85	1.98	4.24	1.79	-1.68E+00	2.38E-03		3.93E-01	4.00E-01		-2.47E+00	2.22E-07	Down	-1.14E+00	1.08E-02		1.10E+00	5.13E-03		-1.47E-01	7.92E-01					Unigene39727_All//0.00E+00//BG443327					
Unigene39729_All	412	1.02	1.97	0.13	1.69	2.42	2.08	1.64	3.25	4.74	9.54E-01	2.28E-01		-2.98E+00	6.45E-02		5.18E-01	5.07E-01		2.99E-01	6.86E-01		9.83E-01	5.99E-02		1.53E+00	3.17E-04	Up				Unigene39729_All//0.00E+00//EV482806					
Unigene3973_All	1355	1.97	4.79	3.81	2.57	2.03	2.97	48.21	75.08	30.43	1.28E+00	1.27E-07	Up	9.53E-01	5.47E-04		-3.40E-01	3.18E-01		2.05E-01	5.66E-01		6.39E-01	5.65E-42		-6.64E-01	6.04E-30		Unigene3973_All//gi|30690409|ref|NP_850456.1|//4.00E-52//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene3973_All//8.00E-49//AT2G46495| zinc finger (C3HC4-type RING finger) family protein	Unigene3973_All//7.00E-09//TC154738				nr +
Unigene39730_All	654	2.88	0.00	1.14	3.88	2.53	2.35	2.65	1.15	0.73	-1.15E+01	6.73E-11	Down	-1.34E+00	8.77E-03		-6.20E-01	1.09E-01		-7.26E-01	7.01E-02		-1.20E+00	7.57E-03		-1.86E+00	7.67E-05	Down	Unigene39730_All//gi|226493492|ref|NP_001148424.1|//6.00E-37//glucan endo-1,3-beta-glucosidase 4 [Zea mays] >gi|195619194|gb|ACG31427.1|glucan endo-1,3-beta-glucosidase 4 precursor [Zea mays] >gi|195619278|gb|ACG31469.1|glucan endo-1,3-beta-glucosidase 4 precursor [Zea mays]	Unigene39730_All//6.00E-37//glucan endo-1,3-beta-glucosidase 4 (Zea mays) (InterPro:IPR012946); BEST Arabidopsis thaliana protein match is: E13L3 (GLUCAN ENDO-1,3-BETA-GLUCOSIDASE-LIKE PROTEIN 3); callose binding / polysaccharide binding (TAIR:AT5G08000.1); Has 804 Blast hits to 768 proteins in 66 species: Archae - 0; Bacteria - 9; Metazoa - 8; Fungi - 36; Plants - 728; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).	Unigene39730_All//0.00E+00//gi|21095175|gb|BQ407488.1|BQ407488			GO:0003824	nr +

Unigene39731_All	1028	0.66	0.25	0.00	1.02	1.27	1.36	2.39	0.81	0.08	-1.43E+00	1.16E-01		-9.37E+00	7.64E-04	Down	3.23E-01	6.11E-01		4.21E-01	4.92E-01		-1.55E+00	4.79E-05	Down	-4.94E+00	2.14E-15	Down	Unigene39731_All//gi|226493492|ref|NP_001148424.1|//1.00E-40//glucan endo-1,3-beta-glucosidase 4 [Zea mays] >gi|195619194|gb|ACG31427.1| glucan endo-1,3-beta-glucosidase 4 precursor [Zea mays] >gi|195619278|gb|ACG31469.1| glucan endo-1,3-beta-glucosidase 4 precursor [Zea mays]	Unigene39731_All//2.00E-38//AT4G13600| EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 12 growth stages; CONTAINS InterPro DOMAIN/s: X8 (InterPro:IPR012946); BEST Arabidopsis thaliana protein match is: E13L3 (GLUCAN ENDO-1,3-BETA-GLUCOSIDASE-LIKE PROTEIN 3); callose binding / polysaccharide binding (TAIR:AT5G08000.1); Has 804 Blast hits to 768 proteins in 66 species: Archae - 0; Bacteria - 9; Metazoa - 8; Fungi - 36; Plants - 728; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).	Unigene39731_All//0.00E+00//gi|21103815|gb|BQ416128.1|BQ416128			GO:0003824	nr -
Unigene39734_All	408	0.38	0.75	0.13	2.81	3.21	2.99	0.62	3.79	0.68	9.54E-01	5.03E-01		-1.56E+00	5.33E-01		1.92E-01	8.06E-01		8.99E-02	9.06E-01		2.61E+00	5.83E-06	Up	1.37E-01	9.29E-01								
Unigene39735_All	1504	0.07	3.77	0.21	1.13	0.27	1.47	16.50	19.65	16.08	5.76E+00	3.32E-29	Up	1.61E+00	3.05E-01		-2.04E+00	6.77E-05	Down	3.86E-01	4.10E-01		2.52E-01	5.91E-03		-3.75E-02	7.38E-01		Unigene39735_All//gi|46518427|gb|AS99695.1|//1.00E-141//At5g47530 [Arabidopsis thaliana]	Unigene39735_All//2.00E-137//AT5G47530| auxin-responsive protein, putative	Unigene39735_All//8.00E-12//TC175130				nr -
Unigene39738_All	649	0.48	1.87	0.98	1.54	2.44	1.25	1.95	0.26	0.74	1.95E+00	4.09E-03		1.03E+00	2.81E-01		6.69E-01	2.24E-01		-2.93E-01	6.89E-01		-2.92E+00	1.46E-05	Down	-1.41E+00	8.06E-03		Unigene39738_All//gi|79478570|ref|NP_193732.2|//7.00E-38//FRS1 (FAR1-related sequence 1); zinc ion binding [Arabidopsis thaliana] >gi|75109056|sp|Q8LBY2.1|FRS1_ARATH RecName: Full=Protein FAR1-RELATED SEQUENCE 1 >gi|54306432|gb|AAV33403.1| FAR1-related 1 protein [Arabidopsis thaliana]	Unigene39738_All//2.00E-32//AT4G19990| FRS1 (FAR1-related sequence 1); zinc ion binding	Unigene39738_All//3.00E-12//ES794029	FAR1		GO:0001071//GO:0006631//GO:0006970//GO:0009536//GO:0010017//GO:0016620//GO:0030528//GO:0046914	nr +
Unigene39739_All	810	1.61	0.56	0.79	0.37	1.06	1.73	0.89	0.41	0.93	-1.52E+00	1.35E-02		-1.03E+00	9.64E-02		1.53E+00	5.80E-02		2.23E+00	5.33E-04	Up	-1.10E+00	1.49E-01		7.46E-02	9.33E-01		Unigene39739_All//gi|79478570|ref|NP_193732.2|//2.00E-85//FRS1 (FAR1-related sequence 1); zinc ion binding [Arabidopsis thaliana] >gi|75109056|sp|Q8LBY2.1|FRS1_ARATH RecName: Full=Protein FAR1-RELATED SEQUENCE 1 >gi|54306432|gb|AAV33403.1| FAR1-related 1 protein [Arabidopsis thaliana]	Unigene39739_All//5.00E-40//AT4G19990| FRS1 (FAR1-related sequence 1); zinc ion binding	Unigene39739_All//4.00E-12//ES794029	FAR1		GO:0001071//GO:0005488//GO:0006631//GO:0006970//GO:0007602//GO:0009536//GO:0010017//GO:0016620//GO:0030528//GO:0048511	nr +
Unigene39741_All	746	3.51	7.27	6.78	6.14	4.20	2.66	9.80	7.73	6.36	1.05E+00	5.58E-05	Up	9.51E-01	6.42E-04		-5.48E-01	4.40E-02		-1.21E+00	1.96E-05	Down	-3.43E-01	8.81E-02		-6.26E-01	7.94E-04		Unigene39741_All//gi|217075412|gb|ACJ86066.1|//1.00E-06//unknown [Medicago truncatula]	Unigene39741_All//7.00E-07//AT5G06240| emb2735 (embryo defective 2735)	Unigene39741_All//0.00E+00//TC138144				nr +
Unigene39742_All	617	2.88	4.93	5.96	5.97	13.39	14.05	0.00	0.00	0.00	7.73E-01	3.08E-02		1.05E+00	1.91E-03		1.16E+00	2.53E-09	Up	1.23E+00	6.98E-10	Up	null	null		null	null		Unigene39742_All//gi|83853809|gb|ABC47842.1|//5.00E-47//membrane protein-like protein [Glycine max]	Unigene39742_All//5.00E-30//AT2G25737| unknown protein	Unigene39742_All//7.00E-109//TC171545			GO:0031224	nr -
Unigene39744_All	620	1.10	0.33	0.26	2.25	2.11	2.62	1.23	1.82	3.66	-1.75E+00	6.23E-02		-2.09E+00	4.38E-02		-9.21E-02	8.58E-01		2.21E-01	6.77E-01		5.68E-01	3.44E-01		1.58E+00	5.86E-05	Up	Unigene39744_All//gi|42565171|ref|NP_189132.2|//2.00E-29//DNA binding [Arabidopsis thaliana]	Unigene39744_All//7.00E-17//AT3G24880| DNA binding				GO:0003676//GO:0010468//GO:0043231	nr -
Unigene39746_All	539	0.00	0.00	0.00	3.70	1.21	1.34	2.90	2.09	3.18	null	null		null	null		-1.61E+00	3.01E-04	Down	-1.46E+00	1.84E-03		-4.71E-01	3.45E-01		1.31E-01	7.63E-01		Unigene39746_All//gi|224141469|ref|XP_002324094.1|//8.00E-99//glycosyltransferase [Populus trichocarpa] >gi|222867096|gb|EEF04227.1| glycosyltransferase [Populus trichocarpa]	Unigene39746_All//1.00E-86//AT3G01040| GAUT13 (Galacturonosyltransferase 13); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene39746_All//2.00E-71//TC172780			GO:0005975//GO:0008194	nr +
Unigene39747_All	514	0.00	0.10	0.10	2.13	2.95	4.66	2.39	1.63	0.39	6.62E+00	6.16E-01		6.69E+00	6.35E-01		4.67E-01	4.26E-01		1.13E+00	6.94E-03		-5.53E-01	3.30E-01		-2.62E+00	4.02E-05	Down	Unigene39747_All//gi|18401821|ref|NP_566604.1|//2.00E-35//reticulon family protein (RTNLB9) [Arabidopsis thaliana] >gi|75273624|sp|Q9M_Q65.1|RTNL1_ARATH RecName: Full=Reticulon-like protein B9; Short=AtRTNLB9 >gi|9279659|dbj|BAB01175.1| seed maturation protein-like [Arabidopsis thaliana] >gi|89111912|gb|ABD60728.1| At3g18260 [Arabidopsis thaliana]	Unigene39747_All//9.00E-37//AT3G18260| reticulon family protein (RTNLB9)				GO:0043231	nr -
Unigene39748_All	2385	0.04	0.00	0.00	0.04	0.12	0.00	13.97	1.45	12.61	-5.46E+00	3.71E-01		-5.46E+00	3.93E-01		1.47E+00	4.20E-01		-5.39E+00	3.99E-01		-3.26E+00	4.07E-145	Down	-1.48E-01	9.27E-02		Unigene39748_All//gi|115607575|gb|AB116556.1|//0.00E+00//Fe(III)-chelate reductase [Citrus junos]	Unigene39748_All//0.00E+00//AT5G23980| FRO4 (FERRIC REDUCTION OXIDASE 4); ferric-chelate reductase	Unigene39748_All//0.00E+00//CO092661		ko04626|Plant-pathogen interaction	GO:0008152//GO:0016723//GO:0030554//GO:0031224//GO:0046914//GO:0050664	nr +
Unigene3975_All	707	2.89	21.86	21.54	20.01	40.04	53.92	0.12	0.06	0.00	2.92E+00	2.93E-49	Up	2.90E+00	5.42E-47	Up	1.00E+00	2.13E-24	Up	1.43E+00	5.09E-52	Up	-1.02E+00	7.24E-01		-6.90E+00	3.58E-01		Unigene3975_All//gi|225449372|ref|XP_002282355.1|//1.00E-109//PREDICTED: pyrroline-5-carboxylate synthetase [Vitis vinifera]	Unigene3975_All//5.00E-93//AT3G55610| P5CS2 (DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHASE 2); catalytic/ glutamate 5-kinase/ glutamate-5-semialdehyde dehydrogenase/ oxidoreductase	Unigene3975_All//0.00E+00//DR458250		ko00330|Arginine and proline metabolism		nr -
Unigene39750_All	695	1.43	0.36	0.08	0.79	1.59	0.97	2.07	1.20	1.20	-1.97E+00	9.93E-03		-4.22E+00	1.62E-04	Down	1.01E+00	1.37E-01		3.06E-01	7.22E-01		-7.82E-01	1.20E-01		-7.81E-01	1.01E-01		Unigene39750_All//gi|240256029|ref|NP_193884.6|//6.00E-84//nucleotide binding [Arabidopsis thaliana]	Unigene39750_All//1.00E-85//AT4G21530| nucleotide binding	Unigene39750_All//1.00E-27//TC169539				nr +
Unigene39751_All	1074	0.54	3.35	1.34	4.08	3.01	2.02	7.79	7.82	3.89	2.64E+00	8.66E-11	Up	1.32E+00	2.70E-02		-4.38E-01	1.32E-01		-1.02E+00	3.89E-04	Down	5.10E-03	1.02E+00		-1.00E+00	1.97E-08	Down			Unigene39751_All//3.00E-29//ES805854				
Unigene39752_All	475	3.86	4.59	4.48	12.69	13.85	19.68	7.92	6.86	3.27	2.51E-01	5.89E-01		2.18E-01	6.12E-01		1.26E-01	6.37E-01		6.33E-01	6.34E-04		-2.07E-01	5.20E-01		-1.28E+00	6.91E-06	Down			Unigene39752_All//6.00E-07//EX165938				
Unigene39757_All	349	12.44	2.03	6.41	8.71	5.53	5.82	9.09	7.07	5.37	-2.61E+00	7.44E-13	Down	-9.57E-01	1.70E-03		-6.56E-01	5.68E-02		-5.80E-01	1.15E-01		-3.63E-01	2.71E-01		-7.60E-01	1.12E-02		Unigene39757_All//gi|3122703|sp|O02644.1|RL23A_FRIAG//2.00E-33//RecName: Full=60S ribosomal protein L23A >gi|2641201|gb|AAB68652.1| ribosomal protein L23a [Fritillaria agrestis]	Unigene39757_All//4.00E-21//AT2G39460| RPL23AA (RIBOSOMAL PROTEIN L23AA); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene39757_All//0.00E+00//TC142945		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene39758_All	756	1.38	1.21	0.56	6.46	2.23	1.43	0.50	1.00	0.79	-1.98E-01	7.41E-01		-1.30E+00	7.46E-02		-1.53E+00	5.83E-09	Down	-2.17E+00	1.71E-12	Down	9.83E-01	1.89E-01		6.51E-01	4.23E-01		Unigene39758_All//gi|164564743|dbj|BAF98224.1|//3.00E-35//CM02216.420.nc [Lotus japonicus]	Unigene39758_All//8.00E-34//AT4G34580| COW1 (CAN OF WORMS1); phosphatidylinositol transporter/ transporter	Unigene39758_All//1.00E-70//CO126010				nr -
Unigene39759_All	330	29.97	20.42	16.46	51.78	44.77	53.79	127.74	59.27	42.37	-5.53E-01	2.36E-03		-8.64E-01	5.41E-06		-2.10E-01	1.42E-01		5.49E-02	7.22E-01		-1.11E+00	2.08E-44	Down	-1.59E+00	2.69E-79	Down	Unigene39759_All//gi|297833934|ref|XP_002884849.1|//2.00E-20//40S ribosomal protein S14 [Arabidopsis lyrata subsp. lyrata] >gi|297330689|gb|EFH61108.1| 40S ribosomal protein S14 [Arabidopsis lyrata subsp. lyrata]	Unigene39759_All//4.00E-15//AT3G52580| 40S ribosomal protein S14 (RPS14C)	Unigene39759_All//0.00E+00//gi|13245584|gb|BE053629.2|BE053629		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0031981	nr +
Unigene3976_All	1613	6.97	20.64	1.95	8.89	9.29	2.63	13.92	6.43	6.62	1.57E+00	1.85E-48	Up	-1.84E+00	3.37E-20	Down	6.23E-02	7.52E-01		-1.76E+00	4.35E-27	Down	-1.12E+00	2.84E-24	Down	-1.07E+00	1.56E-23	Down	Unigene3976_All//gi|18409445|ref|NP_564983.1|//1.00E-162//LGT8 (GLUCOSYL TRANSFERASE FAMILY 8); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|186494322|ref|NP_001117576.1| LGT8 (GLUCOSYL TRANSFERASE FAMILY 8); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|75097066|sp|Q04536.1|GATL9_ARATH RecName: Full=Probable galacturonosyltransferase-like 9; AltName: Full=Like glycosyl transferase 8 >gi|2194142|gb|AAB61117.1| ESTs gb|N38288,gb|T43486,gb|AA395242 come from this gene [Arabidopsis thaliana]	Unigene3976_All//1.00E-160//AT1G70090| LGT8 (GLUCOSYL TRANSFERASE FAMILY 8); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene3976_All//0.00E+00//TC140522				nr +
Unigene39760_All	1169	0.00	1.73	1.46	4.43	7.07	12.63	0.58	0.75	1.40	1.08E+01	1.54E-11	Up	1.05E+01	2.20E-09	Up	6.74E-01	4.36E-04		1.51E+00	3.76E-22	Up	3.76E-01	6.11E-01		1.27E+00	5.37E-03		Unigene39760_All//gi|38112198|gb|AAR11193.1|//1.00E-135//9-cis-epoxycarotenoid dioxygenase 1 [Vitis vinifera]	Unigene39760_All//1.00E-128//AT3G14440| NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	Unigene39760_All//2.00E-95//gi|78348871|gb|DT569145.1|DT569145		ko00906|Carotenoid biosynthesis		nr +
Unigene39761_All	793	1.45	0.51	0.00	3.52	3.04	1.59	5.01	0.74	0.95	-1.51E+00	2.31E-02		-1.05E+01	2.60E-06	Down	-2.11E-01	6.08E-01		-1.14E+00	2.41E-03		-2.76E+00	3.25E-15	Down	-2.39E+00	1.60E-13	Down	Unigene39761_All//gi|22331750|ref|NP_680125.1|//7.00E-26//OFP6 (OVATE FAMILY PROTEIN 6) [Arabidopsis thaliana]	Unigene39761_All//7.00E-29//AT2G36026| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF623, plant (InterPro:IPR006458); BEST Arabidopsis thaliana protein match is: OFP6 (OVATE FAMILY PROTEIN 6) (TAIR:AT3G52525.1); Has 230 Blast hits to 230 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 228; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene39761_All//0.00E+00//gi|18098798|gb|BM358064.1|BM358064				nr +
Unigene39764_All	1067	0.00	0.00	0.10	47.34	20.78	23.07	18.82	28.36	11.84	null	null		6.64E+00	3.98E-01		-1.19E+00	7.12E-60	Down	-1.04E+00	3.21E-42	Down	5.91E-01	1.72E-11		-6.69E-01	5.74E-10		Unigene39764_All//gi|82569705|gb|AB883474.1|//1.00E-109//beta-expansin precursor [Solanum lycopersicum]	Unigene39764_All//2.00E-87//AT1G65680| ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2)	Unigene39764_All//0.00E+00//TC140534			GO:0000003//GO:0031410	nr -
Unigene39765_All	880	1.13	3.57	2.12	0.68	0.27	0.98	3.56	1.80	0.86	1.66E+00	1.23E-05	Up	9.07E-01	7.01E-02		-1.31E+00	1.56E-01		5.22E-01	5.23E-01		-9.78E-01	1.90E-03		-2.05E+00	4.58E-09	Down	Unigene39765_All//gi|56681317|gb|AW21275.1|//1.00E-120//glutamine synthetase [Saccharum officinarum]	Unigene39765_All//4.00E-81//AT5G37600| ATGSR1; copper ion binding / glutamate-ammonia ligase	Unigene39765_All//0.00E+00//TC177144		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006541//GO:0016211//GO:0032559	nr +
Unigene39766_All	650	4.91	1.95	4.34	2.30	1.59	0.97	2.21	1.29	0.74	-1.33E+00	2.14E-04	Down	-1.77E-01	6.11E-01		-5.33E-01	3.21E-01		-1.24E+00	2.45E-02		-7.82E-01	1.20E-01		-1.59E+00	1.64E-03				Unigene39766_All//4.00E-172//ES826291				ESTscan +

Unigene39767_All	2108	0.00	0.00	0.13	0.80	0.08	0.17	7.56	3.31	2.31	null	null		6.98E+00	8.01E-02		-3.30E+00	4.59E-08	Down	-2.23E+00	7.57E-05	Down	-1.19E+00	2.48E-19	Down	-1.71E+00	8.11E-34	Down	Unigene39767_All//gi|15219567|ref|NP_171880.1|//1.00E-125//MGP (Magpie); nucleic acid binding / protein binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|75339114|sp|Q9ZW46.1|MGP_ARATH RecName: Full=Zinc finger protein MAGPIE >gi|30017249|gb|AAP12858.1|At1g03840 [Arabidopsis thaliana]	Unigene39767_All//2.00E-127//AT1G03840| MGP (Magpie); nucleic acid binding / protein binding / transcription factor/ zinc ion binding	Unigene39767_All//1.00E-171//TC134372	C2H2		GO:0043231//GO:0046914	nr -
Unigene39768_All	867	0.60	0.23	0.68	3.91	1.27	2.50	3.76	2.07	7.67	-1.37E+00	1.97E-01		1.63E-01	8.50E-01		-1.62E+00	7.02E-07	Down	-6.44E-01	5.76E-02		-8.57E-01	5.16E-03		1.03E+00	3.97E-07	Up	Unigene39768_All//gi|38564296|gb|AAR23727.1|//1.00E-31//At5g19260 [Arabidopsis thaliana] >gi|44022143|gb|AAS46641.1|At5g19260 [Arabidopsis thaliana]	Unigene39768_All//2.00E-22//AT5G19260| unknown protein					nr +
Unigene39769_All	612	0.94	1.49	3.92	5.13	6.36	9.22	4.35	1.43	1.69	6.64E-01	3.75E-01		2.06E+00	1.87E-05	Up	3.10E-01	3.65E-01		8.47E-01	6.39E-04		-1.60E+00	1.26E-05	Down	-1.36E+00	8.58E-05	Down	Unigene39769_All//gi|20197119|gb|AAD11992.2|//1.00E-29//expressed protein [Arabidopsis thaliana]	Unigene39769_All//8.00E-31//AT2G41200| unknown protein					nr +
Unigene39770_All	445	2.00	1.37	2.15	1.90	1.24	0.41	1.43	0.19	0.09	-5.49E-01	4.42E-01		1.08E-01	8.75E-01		-6.20E-01	4.13E-01		-2.23E+00	9.52E-03		-2.92E+00	4.19E-03		-3.99E+00	5.82E-04	Down	Unigene39770_All//gi|8886947|gb|AAF80633.1|AC069251_26//1.00E-10//F2D10.24 [Arabidopsis thaliana]	Unigene39770_All//1.00E-11//AT1G20750| helicase-related	Unigene39770_All//3.00E-113//ES833956			GO:0005488//GO:0016818	nr +
Unigene39773_All	637	2.22	0.72	0.92	3.68	2.27	3.33	15.13	38.58	4.44	-1.63E+00	6.15E-03		-1.27E+00	3.55E-02		-6.95E-01	8.45E-02		-1.41E-01	7.41E-01		1.35E+00	1.83E-35	Up	-1.77E+00	1.06E-21	Down	Unigene39773_All//gi|255571322|ref|XP_002526610.1|//9.00E-06//mgatp-energized glutathione s-conjugate pump, putative [Ricinus communis] >gi|223534050|gb|EEF35769.1|mgatp-energized glutathione s-conjugate pump, putative [Ricinus communis]		Unigene39773_All//7.00E-69//TC155326			GO:0003824	nr +
Unigene39779_All	822	12.86	34.09	22.16	4.24	3.02	2.03	0.10	0.00	0.44	1.41E+00	5.38E-35	Up	7.85E-01	5.50E-09		-4.92E-01	1.35E-01		-1.06E+00	1.22E-03		-6.69E+00	4.03E-01		2.08E+00	1.01E-01		Unigene39779_All//gi|8778243|gb|AAF79252.1|AC023279_1//3.00E-34//F12K21.2 [Arabidopsis thaliana] >gi|98961039|gb|ABF59003.1|At1g34640 [Arabidopsis thaliana]	Unigene39779_All//7.00E-26//AT1G34640| unknown protein	Unigene39779_All//0.00E+00//TC161883			GO:0005789//GO:0016787//GO:0031224//GO:0051605	nr -
Unigene3978_All	1629	13.81	8.12	12.68	19.69	19.45	17.22	19.52	6.59	7.70	-7.67E-01	5.22E-11		-1.23E-01	3.77E-01		-1.81E-02	8.73E-01		-1.94E-01	5.66E-02		-1.57E+00	6.85E-57	Down	-1.34E+00	1.28E-46	Down	Unigene3978_All//gi|238481582|ref|NP_001154784.1|//1.00E-143//BNR/Asp-box repeat family protein [Arabidopsis thaliana]	Unigene3978_All//3.00E-144//AT5G57700| BNR/Asp-box repeat family protein	Unigene3978_All//0.00E+00//TC161338				nr +
Unigene39780_All	1257	0.12	0.56	0.47	1.23	0.99	1.15	1.82	0.53	4.12	2.18E+00	2.50E-02		1.90E+00	8.48E-02		-3.17E-01	5.71E-01		-9.56E-02	8.64E-01		-1.77E+00	1.47E-05	Down	1.18E+00	6.23E-07	Up	Unigene39780_All//gi|10129653|emb|CAC08248.1|//1.00E-104//VPS13-like protein [Arabidopsis thaliana]	Unigene39780_All//5.00E-100//AT5G24740| INVOLVED IN: protein localization; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Vacuolar protein sorting-associated protein (InterPro:IPR009543); BEST Arabidopsis thaliana protein match is: phosphoinositide binding (TAIR:AT1G48090.2); Has 1782 Blast hits to 981 proteins in 148 species: Archae - 0; Bacteria - 0; Metazoa - 1018; Fungi - 290; Plants - 104; Viruses - 0; Other Eukaryotes - 370 (source: NCBI BLink).					nr +
Unigene39781_All	1197	1.14	0.08	1.25	0.37	0.20	1.21	0.21	0.94	1.83	-3.75E+00	5.95E-06	Down	1.32E-01	8.01E-01		-8.95E-01	4.13E-01		1.69E+00	4.38E-03		2.15E+00	8.74E-04	Up	3.11E+00	7.22E-10	Up	Unigene39781_All//gi|226290819|gb|ACO40485.1|//1.00E-111//terpene synthase [Actinidia deliciosa]	Unigene39781_All//1.00E-79//AT1G61120| TPS04 (TERPENE SYNTHASE 04); (E,E)-geranyllinalool synthase	Unigene39781_All//4.00E-07//CO114033		ko00904|Diterpenoid biosynthesis	GO:0006950//GO:0009719//GO:0016101//GO:0016838//GO:0043231	nr +
Unigene39785_All	1252	0.00	0.00	0.00	0.16	0.28	0.04	5.84	1.40	12.73	null	null		null	null		7.89E-01	5.96E-01		-2.14E+00	3.47E-01		-2.06E+00	1.36E-19	Down	1.12E+00	4.44E-18	Up	Unigene39785_All//gi|226507536|ref|NP_001148133.1|//1.00E-14//WAK53a - OsWAK receptor-like protein kinase [Zea mays] >gi|195616018|gb|ACG29839.1|WAK53a - OsWAK receptor-like protein kinase [Zea mays]	Unigene39785_All//1.00E-09//AT1G79670| RF01 (RESISTANCE TO FUSARIUM OXYSPORUM 1); kinase	Unigene39785_All//0.00E+00//TC169886			GO:0016740	nr +
Unigene39786_All	338	48.45	19.04	27.89	72.51	77.02	94.87	111.95	52.92	65.77	-1.35E+00	1.39E-19	Down	-7.97E-01	2.48E-08		8.71E-02	5.24E-01		3.88E-01	3.14E-05		-1.08E+00	2.01E-38	Down	-7.67E-01	1.32E-22		Unigene39786_All//gi|15220431|ref|NP_176910.1|//3.00E-37//60S ribosomal protein L17 (RPL17B) [Arabidopsis thaliana] >gi|297838479|ref|XP_002887121.1|60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata] >gi|27735241|sp|P51413.2|RL172_ARATH RecName: Full=60S ribosomal protein L17-2 >gi|3176668|gb|AAC18792.1| Similar to ribosomal protein L17 gb|X62724 from Hordeum vulgare. ESTs gb|Z34728, gb|F19974, gb|T75677 and gb|Z33937 come from this gene [Arabidopsis thaliana] >gi|14596149|gb|AAK68802.1|ribosomal protein L17-like protein [Arabidopsis thaliana] >gi|110736681|dbj|BAF00304.1|ribosomal protein L17-like protein [Arabidopsis thaliana] >gi|297332962|gb|EFH63380.1| 60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata]	Unigene39786_All//1.00E-38//AT1G67430| 60S ribosomal protein L17 (RPL17B)	Unigene39786_All//3.00E-177//gi|13243645|gb|BE055023.2|BE055023		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0016787//GO:0019538//GO:0033279	nr +
Unigene39788_All	662	0.63	0.92	3.14	1.05	1.72	1.16	3.64	7.32	2.47	5.39E-01	5.63E-01		2.31E+00	1.92E-05	Up	7.04E-01	3.06E-01		1.39E-01	8.78E-01		1.01E+00	4.21E-05	Up	-5.61E-01	1.12E-01									
Unigene39789_All	1440	0.00	0.00	0.00	0.00	0.05	0.00	143.08	30.94	12.95	null	null		null	null		5.58E+00	6.09E-01		null	null		-2.21E+00	0.00E+00	Down	-3.47E+00	0.00E+00	Down	Unigene39789_All//gi|48675345|dbj|BAD22820.1|//0.00E+00//nitrate transporter [Prunus persica]	Unigene39789_All//2.00E-168//AT1G12110| NRT1.1; nitrate transmembrane transporter/ transporter	Unigene39789_All//0.00E+00//TC165574			GO:0015833//GO:0031224	nr -
Unigene3979_All	2491	1.43	1.69	0.77	4.72	4.48	6.18	10.40	5.02	5.45	2.41E-01	4.32E-01		-8.92E-01	9.02E-03		-7.55E-02	7.15E-01		3.90E-01	6.47E-03		-1.05E+00	1.81E-25	Down	-9.32E-01	1.29E-21		Unigene3979_All//gi|150036250|gb|AB867413.1|//0.00E+00//NPK1-like kinase [Cucumis melo]	Unigene3979_All//1.00E-173//AT1G54960| ANP2; MAP kinase kinase kinase/ kinase	Unigene3979_All//0.00E+00//TC149417		ko04626|Plant-pathogen interaction		nr +
Unigene39791_All	403	6.75	8.17	7.27	3.46	6.92	5.38	4.93	11.20	4.05	2.76E-01	4.30E-01		1.06E-01	7.77E-01		1.00E+00	6.76E-03		6.36E-01	1.61E-01		1.18E+00	5.57E-06	Up	-2.83E-01	4.99E-01		Unigene39791_All//gi|11539465\8|gb|AB197245.1|//8.00E-22//PHD6 [Glycine max]	Unigene39791_All//2.00E-21//AT5G26210| AL4 (ALFIN-LIKE 4); DNA binding / methylated histone residue binding	Unigene39791_All//1.00E-106//DW488532	Alfin-like		GO:0046914	nr -
Unigene39792_All	562	3.17	2.25	1.90	1.68	2.21	1.13	1.43	0.00	0.07	-4.90E-01	3.25E-01		-7.40E-01	1.46E-01		3.89E-01	5.68E-01		-5.82E-01	4.37E-01		-1.05E+01	8.58E-06	Down	-4.33E+00	4.54E-05	Down	Unigene39792_All//gi|297802294|ref|XP_002869031.1|//2.00E-25//At4g36570 [Arabidopsis lyrata subsp. lyrata] >gi|38566494|gb|AAR24137.1|At4g36570 [Arabidopsis thaliana] >gi|40823588|gb|AAR92291.1|At4g36570 [Arabidopsis thaliana] >gi|297314867|gb|EFH45290.1|At4g36570 [Arabidopsis lyrata subsp. lyrata]	Unigene39792_All//4.00E-18//AT1G19510| ATRL5 (ARABIDOPSIS RAD-LIKE 5); DNA binding / transcription factor	Unigene39792_All//0.00E+00//TC137422	MYB-related		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene39795_All	592	0.97	4.28	0.72	1.26	2.56	1.45	3.14	5.08	5.18	2.14E+00	3.00E-06	Up	-4.34E-01	6.23E-01		1.02E+00	6.18E-02		2.00E-01	7.89E-01		6.94E-01	3.13E-02		7.22E-01	1.88E-02		Unigene39795_All//gi|15228792|ref|NP_188895.1|//2.00E-42//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|11994288|dbj|BAB01471.1|alanine acetyl transferase-like protein [Arabidopsis thaliana] >gi|124301058|gb|ABN04781.1|At3g22560 [Arabidopsis thaliana]	Unigene39795_All//3.00E-43//AT3G22560| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene39795_All//0.00E+00//TC144981			GO:0016407//GO:0044464	nr -
Unigene39796_All	909	0.52	0.50	0.70	4.77	4.66	4.52	3.02	1.70	1.36	-4.61E-02	9.78E-01		4.41E-01	6.23E-01		-3.31E-02	9.12E-01		-7.66E-02	8.06E-01		-8.30E-01	1.42E-02		-1.15E+00	5.37E-04	Down	Unigene39796_All//gi|13877549|gb|AAK43852.1|AF370475_1//1.00E-31//Unknown protein [Arabidopsis thaliana]	Unigene39796_All//4.00E-29//AT3G07510| unknown protein	Unigene39796_All//0.00E+00//TC140630			GO:0044464	nr -
Unigene39800_All	1570	0.33	0.42	0.07	0.41	0.44	0.66	1.13	1.76	2.77	3.32E-01	6.80E-01		-2.30E+00	6.76E-02		8.88E-02	9.49E-01		6.82E-01	3.45E-01		6.35E-01	6.23E-02		1.29E+00	1.08E-06	Up	Unigene39800_All//gi|297846702|ref|XP_002891232.1|//2.00E-16//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337074|gb|EFH67491.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39800_All//2.00E-15//AT1G60360| zinc finger (C3HC4-type RING finger) family protein	Unigene39800_All//0.00E+00//DT465859			GO:0005488//GO:0043231	nr -
Unigene39804_All	404	4.14	1.63	4.22	3.33	6.99	2.24	4.81	1.66	1.58	-1.35E+00	1.01E-02		2.54E-02	9.79E-01		1.07E+00	3.51E-03		-5.74E-01	3.45E-01		-1.54E+00	4.03E-04	Down	-1.61E+00	1.60E-04	Down	Unigene39804_All//gi|6587849|gb|AAF18538.1|AC006551_24//5.00E-27//Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	Unigene39804_All//1.00E-12//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene39804_All//6.00E-25//TC131141			GO:0003676//GO:0006260//GO:0034061//GO:0043231	nr -
Unigene39805_All	1098	1.57	5.77	0.82	2.31	1.57	2.71	8.63	21.51	102.54	1.88E+00	2.14E-12	Up	-9.32E-01	7.71E-02		-5.61E-01	1.55E-01		2.31E-01	5.91E-01		1.32E+00	6.68E-33	Up	3.57E+00	0.00E+00	Up	Unigene39805_All//gi|228480908|gb|ACQ42220.1|//2.00E-99//RZ83 transcription factor WYR108-like protein 1 [Vitis vinifera]	Unigene39805_All//1.00E-70//AT3G06490| MYB108 (myb domain protein 108); DNA binding / transcription factor	Unigene39805_All//1.00E-105//gi|78345617|gb|DT565891.1|DT565891	MYB		GO:0001071//GO:0006351//GO:0006970//GO:0009725//GO:0051707	nr +
Unigene39806_All	1606	0.13	0.06	0.03	0.99	0.73	0.82	7.06	9.37	2.70	-1.05E+00	5.64E-01		-1.97E+00	3.81E-01		-4.45E-01	4.08E-01		-2.84E-01	6.38E-01		4.09E-01	1.57E-03		-1.38E+00	5.63E-18	Down	Unigene39806_All//gi|147805709|emb|CAN65018.1|//9.00E-10//hypothetical protein [Vitis vinifera]					GO:0005488	nr +
Unigene39807_All	717	2.41	1.13	0.37	5.97	2.26	2.52	4.72	6.82	2.89	-1.09E+00	2.99E-02		-2.70E+00	2.40E-05	Down	-1.40E+00	5.16E-07	Down	-1.25E+00	2.33E-05	Down	5.32E-01	2.99E-02		-7.07E-01	1.43E-02				Unigene39807_All//2.00E-07//TC159490				
Unigene39808_All	480	19.84	3.48	5.66	16.50	26.40	18.54	23.69	53.38	52.79	-2.51E+00	3.12E-26	Down	-1.81E+00	8.27E-17	Down	6.78E-01	5.22E-06		1.68E-01	4.67E-01		1.17E+00	9.36E-30	Up	1.16E+00	1.72E-29	Up							
Unigene39809_All	341	0.15	1.04	0.00	0.73	2.32	1.85	0.62	2.08	3.74	2.76E+00	9.59E-02		-7.26E+00	6.23E-01		1.67E+00	5.20E-02		1.34E+00	1.74E-01		1.75E+00	3.21E-02		2.59E+00	3.78E-05	Up	Unigene39809_All//gi|239056192|emb|CAQ58629.1|//1.00E-20//pyruvate kinase [Vitis vinifera]	Unigene39809_All//2.00E-20//AT5G08570| pyruvate kinase, putative	Unigene39809_All//2.00E-52//BQ401381		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0006007//GO:0010038//GO:0016020//GO:0016301//GO:0031420//GO:0032559//GO:0044424	nr -
Unigene3981_All	1525	3.16	4.45	2.55	2.65	2.89	2.10	6.27	9.62	14.11	4.96E-01	2.86E-02		-3.08E-01	3.07E-01		1.28E-01	7.25E-01		-3.32E-01	3.18E-01		6.19E-01	2.01E-06		1.17E+00	1.10E-25	Up	Unigene3981_All//gi|75312309|sp|Q9M9K3.1|PP19_ARATH//1.00E-159//RecName: Full=Serine/threonine-protein phosphatase PP1 isozyme 9 >gi|34365687|gb|AAQ65155.1|At3g05580 [Arabidopsis thaliana]	Unigene3981_All//6.00E-158//AT3G05580| serine/threonine protein phosphatase, putative	Unigene3981_All//0.00E+00//gi|164246072|gb|ES811835.1|ES811835				nr -

Unigene39810_All	469	2.45	2.16	1.14	0.74	2.06	2.70	0.27	4.63	1.95	-1.84E-01	7.48E-01		-1.11E+00	9.93E-02		1.47E+00	4.80E-02		1.86E+00	4.55E-03		4.10E+00	8.27E-12	Up	2.85E+00	3.18E-04	Up	Unigene39810_All//gi|9759351|dbj|BAB10006.1|//7.00E-19//pyruvate kinase [Arabidopsis thaliana] >gi|110739085|dbj|BAF01459.1| pyruvate kinase [Arabidopsis thaliana]	Unigene39810_All//3.00E-19//AT5G08570| pyruvate kinase, putative	Unigene39810_All//2.00E-56//BQ401381		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0006007//GO:0016301//GO:0031420	nr -
Unigene39811_All	380	14.18	54.54	65.86	197.42	175.80	84.27	16.69	17.60	18.24	1.94E+00	6.89E-41	Up	2.22E+00	1.01E-56	Up	-1.67E-01	5.03E-03		-1.23E+00	5.76E-82	Down	7.65E-02	7.34E-01		1.28E-01	5.71E-01					Unigene39811_All//2.00E-95//TC140326				
Unigene39813_All	538	0.10	1.22	0.89	2.50	1.66	0.92	3.14	1.86	7.41	3.65E+00	4.10E-03		3.19E+00	3.48E-02		-5.87E-01	3.15E-01		-1.44E+00	1.59E-02		-7.54E-01	9.64E-02		1.24E+00	7.19E-06	Up	Unigene39813_All//gi|224067186|ref|XP_002302398.1|//5.00E-06//predicted protein [Populus trichocarpa] >gi|222844124|gb|EEE81671.1| predicted protein [Populus trichocarpa]						nr -
Unigene39814_All	511	5.73	5.26	1.88	13.06	9.23	8.31	5.13	3.84	2.81	-1.26E-01	7.21E-01		-1.61E+00	7.17E-05	Down	-5.01E-01	2.20E-02		-6.53E-01	3.60E-03		-4.16E-01	2.51E-01		-8.70E-01	9.44E-03					Unigene39814_All//0.00E+00//gi|21103863|gb|BQ416176.1|BQ416176				
Unigene39817_All	458	11.77	11.28	4.42	11.31	10.53	7.59	57.42	31.76	27.23	-6.03E-02	8.17E-01		-1.41E+00	4.87E-07	Down	-1.04E-01	7.48E-01		-5.75E-01	2.93E-02		-8.55E-01	1.74E-18		-1.08E+00	1.39E-27	Down				Unigene39817_All//7.00E-142//gi|31022764|gb|CA993043.1|CA993043				
Unigene39818_All	472	0.33	23.40	2.37	1.16	5.91	16.46	4.03	20.54	16.88	6.14E+00	5.07E-58	Up	2.83E+00	7.34E-04	Up	2.35E+00	2.77E-08	Up	3.83E+00	1.05E-33	Up	2.35E+00	4.07E-30	Up	2.07E+00	8.71E-22	Up				Unigene39818_All//6.00E-07//gi|164242995|gb|ES821903.1|ES821903				
Unigene39819_All	536	9.27	1.89	2.19	10.13	4.43	6.49	20.43	8.50	6.47	-2.29E+00	1.15E-12	Down	-2.09E+00	8.89E-11	Down	-1.19E+00	6.95E-07	Down	-6.43E-01	1.14E-02		-1.27E+00	8.58E-15	Down	-1.66E+00	1.69E-22	Down	Unigene39819_All//gi|45773776|gb|AAS76692.1|//3.00E-39//At4g18590 [Arabidopsis thaliana] >gi|46339785|gb|AAS88756.1| At4g18590 [Arabidopsis thaliana]	Unigene39819_All//4.00E-38//AT4G18590| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Replication factor A protein 3 (InterPro:IPR013970), Nucleic acid-binding, OB-fold-like (InterPro:IPR016027); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G52630.2); Has 58 Blast hits to 58 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 26; Fungi - 2; Plants - 26; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene39819_All//0.00E+00//gi|21089690|gb|BQ402015.1|BQ402015			GO:0031410	nr +
Unigene39820_All	664	3.70	1.68	1.28	7.73	4.87	3.40	4.78	2.27	0.90	-1.14E+00	5.46E-03		-1.53E+00	5.92E-04	Down	-6.65E-01	7.70E-03		-1.18E+00	7.48E-06	Down	-1.08E+00	6.26E-04	Down	-2.41E+00	5.06E-11	Down	Unigene39820_All//gi|88900376|gb|AB057500.1|//8.00E-29//At5g40460 [Arabidopsis thaliana]	Unigene39820_All//2.00E-15//AT5G40460| unknown protein	Unigene39820_All//4.00E-169//DW511790				nr +
Unigene39822_All	1915	0.05	0.11	0.00	0.05	0.11	0.00	17.64	2.55	5.16	9.54E-01	6.21E-01		-5.77E+00	3.93E-01		1.05E+00	6.12E-01		-5.70E+00	3.99E-01		-2.79E+00	1.00E-125	Down	-1.77E+00	3.42E-74	Down	Unigene39822_All//gi|224087611|ref|XP_002308196.1|//0.00E+00//laccase 110a [Populus trichocarpa] >gi|222854172|gb|EEE91719.1| laccase 110a [Populus trichocarpa]	Unigene39822_All//0.00E+00//AT3G09220| LACT (laccase 7); laccase	Unigene39822_All//5.00E-66//gi|78331794|gb|DT552068.1|DT552068		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0003006//GO:0005576//GO:0009808//GO:0010038//GO:0016682//GO:0046914	nr +
Unigene39825_All	389	4.98	10.94	9.99	17.29	12.13	10.10	33.69	40.72	49.26	1.14E+00	1.62E-04	Up	1.01E+00	2.01E-03		-5.12E-01	1.87E-02		-7.75E-01	4.82E-04		2.73E-01	3.63E-02		5.48E-01	6.36E-07		Unigene39825_All//gi|224136690|ref|XP_002326921.1|//2.00E-07//predicted protein [Populus trichocarpa] >gi|222835236|gb|EEE73671.1| predicted protein [Populus trichocarpa]		Unigene39825_All//4.00E-134//TC156896				nr +
Unigene39826_All	949	0.22	0.80	0.73	8.24	5.70	4.24	3.07	8.72	3.78	1.86E+00	3.73E-02		1.73E+00	7.67E-02		-5.33E-01	6.90E-03		-9.60E-01	2.75E-06		1.50E+00	1.61E-14	Up	2.98E-01	3.21E-01		Unigene39826_All//gi|6899646|gb|AAF31023.1|AC012189_5//6.00E-20//EST gb|AB015130 comes from this gene [Arabidopsis thaliana]	Unigene39826_All//3.00E-20//AT2G01300| unknown protein	Unigene39826_All//0.00E+00//TC147505			GO:0006952	nr -
Unigene39828_All	473	22.34	8.89	22.18	47.81	31.30	69.61	28.34	64.15	14.07	-1.33E+00	1.18E-12	Down	-1.08E-02	9.77E-01		-6.11E-01	6.24E-09		5.42E-01	2.64E-09		1.18E+00	1.97E-35	Up	-1.01E+00	3.74E-13	Down	Unigene39828_All//gi|255550081|ref|XP_002516091.1|//2.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223544577|gb|EEF46093.1| conserved hypothetical protein [Ricinus communis]		Unigene39828_All//6.00E-13//DW516108				nr +
Unigene39829_All	1180	0.98	0.17	0.32	1.18	0.93	1.00	3.30	1.06	1.35	-2.51E+00	8.99E-04	Down	-1.63E+00	2.13E-02		-3.40E-01	5.62E-01		-2.48E-01	6.85E-01		-1.63E+00	4.57E-08	Down	-1.29E+00	3.97E-06	Down				Unigene39829_All//4.00E-19//gi|84171934|gb|DR460582.1|DR460582				
Unigene39830_All	897	21.23	16.38	19.47	14.77	14.51	16.31	11.27	7.55	5.02	-3.74E-01	3.36E-03		-1.25E-01	4.00E-01		-2.57E-02	8.86E-01		1.43E-01	4.08E-01		-5.78E-01	3.06E-04		-1.17E+00	1.46E-12	Down	Unigene39830_All//gi|90823167|gb|AB201085.1|//8.00E-60//BTF3 [Nicotiana benthamiana]	Unigene39830_All//8.00E-52//AT1G73230| nascent polypeptide-associated complex (NAC) domain-containing protein	Unigene39830_All//0.00E+00//gi|11209703|gb|BP278633.1|BP278633				nr +
Unigene39832_All	1450	0.36	0.31	0.48	4.67	3.63	1.87	1.11	0.49	0.36	-1.98E-01	8.20E-01		4.04E-01	6.09E-01		-3.63E-01	1.11E-01		-1.32E+00	8.34E-09	Down	-1.18E+00	1.24E-02		-1.63E+00	6.02E-04	Down	Unigene39832_All//gi|224120270|ref|XP_002318288.1|//1.00E-119//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222858961|gb|EEE96508.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene39832_All//9.00E-86//AT1G12260| ANAC007 (ARABIDOPSIS NAC 007); transcription factor	Unigene39832_All//6.00E-108//TC173274	NAC		GO:0001071//GO:0010468	nr +
Unigene39833_All	600	1.57	4.73	3.11	15.53	18.71	11.89	0.28	0.07	0.07	1.59E+00	6.48E-05	Up	9.85E-01	4.87E-02		2.69E-01	1.35E-01		-3.85E-01	4.67E-02		-2.02E+00	3.67E-01		-2.09E+00	3.13E-01					Unigene39833_All//0.00E+00//DW501803				
Unigene39834_All	1329	0.63	0.53	0.48	1.46	1.79	0.51	2.42	1.98	0.96	-2.39E-01	7.25E-01		-3.90E-01	6.41E-01		2.90E-01	5.55E-01		-1.52E+00	1.52E-03		-2.87E-01	4.05E-01		-1.33E+00	1.87E-05	Down	Unigene39834_All//gi|9759309|dbj|BAB09815.1|//4.00E-26//non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	Unigene39834_All//6.00E-14//AT5G42905| nucleic acid binding / ribonuclease H	Unigene39834_All//1.00E-13//DT468956				nr +
Unigene39835_All	1495	2.80	0.58	0.14	0.43	0.48	0.60	5.23	3.35	6.80	-2.28E+00	1.06E-10	Down	-4.30E+00	5.02E-18	Down	1.59E-01	8.68E-01		4.80E-01	5.50E-01		-6.41E-01	5.22E-04		3.77E-01	1.69E-02		Unigene39835_All//gi|224097692|ref|XP_002311043.1|//0.00E+00//proline transporter [Populus trichocarpa] >gi|222850863|gb|EEE88410.1| proline transporter [Populus trichocarpa]	Unigene39835_All//6.00E-125//AT1G08230| amino acid transporter family protein	Unigene39835_All//2.00E-12//CO092095			GO:0031224	nr +
Unigene39838_All	849	0.37	1.07	1.19	2.76	3.73	1.49	0.70	2.12	0.89	1.54E+00	4.51E-02		1.69E+00	2.74E-02		4.36E-01	2.37E-01		-8.89E-01	3.33E-02		1.60E+00	4.89E-04	Up	3.55E-01	6.16E-01		Unigene39838_All//gi|15224955|ref|NP_181414.1|//2.00E-32//calmodulin-binding protein-related [Arabidopsis thaliana]	Unigene39838_All//1.00E-33//AT2G38800| calmodulin-binding protein-related	Unigene39838_All//0.00E+00//ES805909			GO:0005515	nr -
Unigene39839_All	1027	2.75	0.44	0.47	5.09	3.99	6.11	2.96	1.59	0.43	-2.63E+00	1.19E-08	Down	-2.56E+00	5.78E-08	Down	-3.52E-01	1.90E-01		2.63E-01	3.21E-01		-9.01E-01	4.73E-03		-2.80E+00	2.18E-12	Down	Unigene39839_All//gi|297820370|ref|XP_002878068.1|//5.00E-65//prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323906|gb|EFH54327.1| prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39839_All//2.00E-39//AT3G56110| PRA1.B1 (PRENYLATED RAB ACCEPTOR 1.B1)	Unigene39839_All//3.00E-146//gi|78354437|gb|DT574711.1|DT574711			GO:0006810//GO:0043231	nr +
Unigene39841_All	651	0.08	0.16	0.25	1.45	1.48	0.69	3.77	3.53	1.35	9.54E-01	7.26E-01		1.61E+00	5.11E-01		2.67E-02	9.87E-01		-1.07E+00	1.45E-01		-9.33E-02	8.08E-01		-1.48E+00	5.68E-05	Down	Unigene39841_All//gi|15225471|ref|NP_182065.1|//1.00E-53//LBD19 (LOB DOMAIN-CONTAINING PROTEIN 19) [Arabidopsis thaliana] >gi|29427560|sp|Q22132.1|LBD19_ARATH RecName: Full=LOB domain-containing protein 19; AltName: Full=ASYMMETRIC LEAVES 2-like protein 23; Short=AS2-like protein 23 >gi|219807122|dbj|BAH10567.1| ASYMMETRIC LEAVES2-like 23 protein [Arabidopsis thaliana]	Unigene39841_All//4.00E-54//AT2G45410| LBD19 (LOB DOMAIN-CONTAINING PROTEIN 19)		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene39842_All	1454	462.32	413.89	580.44	185.69	304.40	262.66	5.29	15.92	12.38	-1.60E-01	3.94E-17		3.28E-01	2.65E-80		7.13E-01	5.82E-214		5.00E-01	3.41E-88		1.59E+00	1.86E-42	Up	1.23E+00	3.17E-23	Up	Unigene39842_All//gi|224071632|ref|XP_002303546.1|//1.00E-147//cytochrome P450 [Populus trichocarpa] >gi|222840978|gb|EEE78525.1| cytochrome P450 [Populus trichocarpa]	Unigene39842_All//9.00E-110//AT2G45550| CYP76C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene39842_All//0.00E+00//TC134567		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene39843_All	796	6.90	3.69	2.21	4.07	5.97	5.56	0.80	0.00	2.10	-9.03E-01	4.08E-04		-1.64E+00	8.99E-09	Down	5.54E-01	4.37E-02		4.51E-01	1.34E-01		-9.64E+00	1.23E-04	Down	1.40E+00	2.16E-03		Unigene39843_All//gi|125950374|gb|ABN58740.1|//1.00E-109//UGT protein [Gossypium hirsutum]	Unigene39843_All//2.00E-50//AT3G11340| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene39843_All//0.00E+00//TC166770		ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis	GO:0035251	nr -
Unigene39844_All	1047	0.40	0.92	0.61	2.09	2.47	4.57	0.85	0.52	1.79	1.20E+00	9.57E-02		6.10E-01	5.09E-01		2.37E-01	6.00E-01		1.13E+00	4.57E-05	Up	-7.08E-01	2.97E-01		1.08E+00	9.46E-03		Unigene39844_All//gi|145327195|ref|NP_001077799.1|//3.00E-06//CLE45 (CLAVATA3/ESR-RELATED 45) [Arabidopsis thaliana]	Unigene39844_All//2.00E-07//AT1G69588| CLE45 (CLAVATA3/ESR-RELATED 45)	Unigene39844_All//1.00E-09//DW500136				nr -
Unigene39846_All	1127	0.46	1.75	1.23	1.99	2.26	1.36	2.29	1.37	4.31	1.92E+00	1.74E-04	Up	1.40E+00	2.28E-02		1.85E-01	6.93E-01		-5.46E-01	2.22E-01		-7.38E-01	3.61E-02		9.14E-01	1.29E-04		Unigene39846_All//gi|297746481|emb|CBI16537.3|//1.00E-133//unnamed protein product [Vitis vinifera]	Unigene39846_All//3.00E-47//AT1G55325| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: TRAP240 (InterPro:IPR009401); Has 190 Blast hits to 182 proteins in 65 species: Archae - 0; Bacteria - 45; Metazoa - 113; Fungi - 3; Plants - 23; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink).	Unigene39846_All//5.00E-34//DW488490				nr -
Unigene39848_All	516	112.35	50.77	52.94	130.81	110.91	166.74	252.45	138.59	127.16	-1.15E+00	1.67E-52	Down	-1.09E+00	1.76E-46	Down	-2.38E-01	7.50E-05		3.50E-01	9.21E-11		-8.65E-01	3.19E-90		-9.89E-01	5.74E-116		Unigene39848_All//gi|192912994|gb|ACF06605.1|//1.00E-41//60S ribosomal protein L13E [Elaeis guineensis]	Unigene39848_All//3.00E-33//AT3G49010| ATRBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome	Unigene39848_All//0.00E+00//gi|21099308|gb|BQ411621.1|BQ411621		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene3985_All	2429	1.77	0.88	1.51	6.60	5.60	1.60	0.96	0.77	0.80	-1.01E+00	6.24E-04	Down	-2.24E-01	4.89E-01		-2.38E-01	9.97E-02		-2.05E+00	4.63E-37	Down	-3.06E-01	4.43E-01		-2.53E-01	5.16E-01		Unigene3985_All//gi|297795135|ref|XP_002865452.1|//1.00E-176//tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297311287|gb|EFH41711.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene3985_All//2.00E-169//AT5G43120| tetratricopeptide repeat (TPR)-containing protein	Unigene3985_All//0.00E+00//TC142146				nr +

Unigene39850_All	282	36.55	19.76	19.64	68.36	55.44	65.98	105.85	35.13	46.48	-8.87E-01	8.29E-07		-8.96E-01	1.46E-06		-3.02E-01	1.41E-02		-5.11E-02	7.27E-01		-1.59E+00	9.94E-55	Down	-1.19E+00	2.30E-36	Down	Unigene39850_All//gi|225453305|ref|XP_002268650.1|/9.00E-22//PREDICTED: similar to protein synthesis initiation factor-like [Vitis vinifera]	Unigene39850_All//2.00E-22//AT3G10950| 60S ribosomal protein L37a (RPL37aB)	Unigene39850_All//5.00E-120//TC164665		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043169	nr -
Unigene39854_All	263	45.95	80.53	31.38	67.43	63.24	67.32	224.74	382.68	80.13	8.09E-01	2.56E-11		-5.50E-01	1.14E-03		-9.25E-02	5.65E-01		-2.40E-03	9.84E-01		7.68E-01	5.12E-57		-1.49E+00	1.98E-100	Down	Unigene39854_All//gi|25992539|gb|AAN77149.1|/4.00E-41//fiber protein Fb9 [Gossypium barbadense]	Unigene39854_All//2.00E-24//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Unigene39854_All//3.00E-146//gi|13353427|gb|BG443775.1|BG443775		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr +
Unigene39857_All	701	8.73	15.40	4.10	4.90	6.04	7.22	0.66	1.01	0.28	8.18E-01	2.89E-06		-1.09E+00	1.64E-05	Down	3.01E-01	3.53E-01		5.57E-01	3.95E-02		6.11E-01	4.27E-01		-1.22E+00	2.00E-01		Unigene39857_All//gi|107738282|gb|ABF83672.1|/1.00E-64//At1g51100 [Arabidopsis thaliana]	Unigene39857_All//1.00E-51//AT1G51100| unknown protein	Unigene39857_All//0.00E+00//AT729421			GO:0009532	nr +
Unigene3986_All	1072	22.11	22.36	33.58	41.08	36.88	26.96	35.22	17.35	11.93	1.61E-02	9.09E-01		6.03E-01	5.30E-11		-1.56E-01	6.43E-02		-6.07E-01	5.43E-15		-1.02E+00	5.05E-35	Down	-1.56E+00	3.50E-69	Down	Unigene3986_All//gi|297797884|ref|XP_002866826.1|/4.00E-58//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312662|gb|EFH43085.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3986_All//4.00E-59//AT4G38960| zinc finger (B-box type) family protein	Unigene3986_All//0.00E+00//gi|161434428|gb|ES825724.1|ES825724	DBB	ko04712|Circadian rhythm - plant		nr -
Unigene39860_All	612	6.50	3.15	4.70	4.80	3.04	4.28	4.28	3.89	1.30	-1.05E+00	7.25E-04	Down	-4.68E-01	1.48E-01		-6.60E-01	6.01E-02		-1.66E-01	6.90E-01		-1.38E-01	7.14E-01		-1.72E+00	2.76E-06	Down	Unigene39860_All//gi|13605738|gb|AK32862.1|AF361850_1/1.00E-32//AT5g49540/K6M13_9 [Arabidopsis thaliana] >gi|22136552|gb|AAM91062.1|AT5g49540/K6M13_9 [Arabidopsis thaliana]	Unigene39860_All//3.00E-27//AT5G49540| unknown protein	Unigene39860_All//4.00E-67//gi|84152950|gb|DN802305.1|DN802305				nr -
Unigene39863_All	675	7.52	7.21	15.23	7.08	5.00	3.55	1.44	0.50	0.47	-6.12E-02	8.20E-01		1.02E+00	6.08E-08	Up	-5.03E-01	6.13E-02		-9.98E-01	2.41E-04		-1.54E+00	1.90E-02		-1.61E+00	1.12E-02		Unigene39863_All//gi|115465643|ref|NP_001056421.1|/4.00E-13//Os05g0579600 [Oryza sativa Japonica Group] >gi|113579972|dbj|BAF18335.1|Os05g0579600 [Oryza sativa Japonica Group]	Unigene39863_All//4.00E-12//AT1G75250| ATRL6 (ARABIDOPSIS RAD-LIKE 6); transcription factor	Unigene39863_All//3.00E-43//DT455683	MYB-related		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene39864_All	557	9.68	15.10	13.48	22.09	14.16	17.51	32.26	227.96	15.02	6.42E-01	1.27E-03		4.79E-01	3.30E-02		-6.42E-01	1.54E-05		-3.35E-01	4.40E-02		2.82E+00	0.00E+00	Up	-1.10E+00	7.35E-20	Down	Unigene39864_All//gi|124488472|gb|ABN12320.1|/2.00E-24//benzoquinone reductase [Gossypium hirsutum]	Unigene39864_All//2.00E-19//AT4G27270| quinone reductase family protein	Unigene39864_All//0.00E+00//TC171939			GO:0000166//GO:0006350//GO:0016655	nr +
Unigene39865_All	437	25.26	8.12	12.55	42.29	38.77	61.49	119.78	40.17	35.74	-1.64E+00	1.04E-17	Down	-1.01E+00	2.36E-08	Down	-1.25E-01	4.07E-01		5.40E-01	1.13E-07		-1.58E+00	4.20E-94	Down	-1.74E+00	5.94E-112	Down	Unigene39865_All//gi|209967445|gb|ACJ02351.1|/3.00E-42//60S ribosomal protein L31 [Vernicia fordii]	Unigene39865_All//4.00E-40//AT5G56710| 60S ribosomal protein L31 (RPL31C)	Unigene39865_All//0.00E+00//gi|13245046|gb|BE054305.2|BE054305		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene39866_All	524	10.88	21.18	22.87	13.21	13.67	17.58	37.68	67.80	25.93	9.60E-01	3.74E-08		1.07E+00	7.01E-10	Up	4.88E-02	8.51E-01		4.12E-01	3.39E-02		8.47E-01	2.56E-24		-5.40E-01	5.82E-07					Unigene39866_All//0.00E+00//TC155526				
Unigene39867_All	848	8.88	8.13	10.11	36.24	30.54	24.98	4.19	1.28	1.97	-1.29E-01	5.96E-01		1.86E-01	3.86E-01		-2.47E-01	9.84E-03		-5.37E-01	1.16E-08		-1.71E+00	7.24E-08	Down	-1.09E+00	1.54E-04	Down	Unigene39867_All//gi|297815530|ref|XP_002875648.1|/3.00E-70//harpin-induced family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321486|gb|EFH51907.1| harpin-induced family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39867_All//4.00E-65//AT3G44220| harpin-induced family protein / HIN1 family protein / harpin-responsive family protein	Unigene39867_All//0.00E+00//TC147372			GO:0002252//GO:0005618	nr -
Unigene39868_All	428	0.61	3.55	1.87	0.93	4.02	3.48	0.89	2.34	1.68	2.54E+00	9.21E-05	Up	1.61E+00	6.67E-02		2.11E+00	1.06E-04	Up	1.90E+00	1.38E-03		1.40E+00	2.82E-02		9.14E-01	2.12E-01					Unigene39868_All//5.00E-07//TC161780				
Unigene3987_All	1361	17.41	54.62	38.77	16.95	21.00	19.91	6.46	8.29	6.44	1.65E+00	8.32E-116	Up	1.15E+00	7.56E-47	Up	3.09E-01	1.55E-03		2.33E-01	3.38E-02		3.60E-01	2.00E-02		-4.90E-03	9.73E-01		Unigene3987_All//gi|148595730|emb|CAM12544.1|/2.00E-64//YA6 [Antirrhinum majus]	Unigene3987_All//2.00E-40//AT1G30500| NF-YA7 (NUCLEAR FACTOR Y, SUBUNIT A7); specific transcriptional repressor/ transcription factor	Unigene3987_All//0.00E+00//TC157983	CCAAT			nr +
Unigene39870_All	1940	2.83	0.99	1.13	0.92	0.60	1.77	2.03	4.61	4.29	-1.51E+00	2.87E-08	Down	-1.33E+00	1.33E-06	Down	-6.15E-01	2.02E-01		9.37E-01	5.05E-03		1.19E+00	4.19E-11	Up	1.08E+00	2.42E-09	Up	Unigene39870_All//gi|226495381|ref|NP_001149327.1|/9.00E-47//zinc finger, C3HC4 type family protein [Zea mays] >gi|195626422|gb|ACG35041.1| zinc finger, C3HC4 type family protein [Zea mays]	Unigene39870_All//4.00E-43//AT5G05830| zinc finger (C3HC4-type RING finger) family protein	Unigene39870_All//6.00E-87//TC163633				nr -
Unigene39871_All	605	2.59	2.51	0.62	2.55	2.56	3.51	0.98	1.17	3.36	-4.63E-02	9.40E-01		-2.07E+00	7.92E-04	Down	5.00E-03	9.92E-01		4.59E-01	3.39E-01		2.63E-01	7.21E-01		1.78E+00	3.39E-05	Up	Unigene39871_All//gi|297800428|ref|XP_002868098.1|/1.00E-12//hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313934|gb|EFH43357.1| hydroxyproline-rich glycoprotein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39871_All//2.00E-08//AT3G60380| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT4G16790.1); Has 5716 Blast hits to 3635 proteins in 329 species: Archae - 2; Bacteria - 249; Metazoa - 2628; Fungi - 569; Plants - 209; Viruses - 24; Other Eukaryotes - 2035 (source: NCBI BLink).					nr -
Unigene39872_All	843	7.57	11.60	8.97	13.71	14.46	31.77	421.85	464.66	870.83	6.16E-01	7.79E-04		2.44E-01	3.04E-01		7.70E-02	7.13E-01		1.21E+00	1.39E-28	Up	1.40E-01	8.19E-10		1.05E+00	0.00E+00	Up	Unigene39872_All//gi|40218371|gb|AB83118.1|/6.00E-81//secretory laccase [Gossypium arboreum]	Unigene39872_All//2.00E-49//AT5G09360| LAC14 (laccase 14); laccase	Unigene39872_All//0.00E+00//TC143100		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0016491	nr +
Unigene39873_All	273	2.11	4.83	3.12	1.82	2.27	3.31	4.65	1.68	0.73	1.19E+00	4.50E-02		5.66E-01	4.61E-01		3.15E-01	7.84E-01		8.59E-01	2.70E-01		-1.46E+00	8.32E-03		-2.67E+00	2.31E-05	Down			Unigene39873_All//2.00E-20//gi|54115229|gb|CO490738.1|CO490738				
Unigene39874_All	410	0.64	1.73	0.13	0.36	1.43	0.88	3.40	1.63	0.29	1.44E+00	1.06E-01		-2.30E+00	2.43E-01		1.97E+00	7.03E-02		1.27E+00	3.82E-01		-1.06E+00	3.74E-02		-3.55E+00	2.28E-07	Down			Unigene39874_All//5.00E-13//gi|54115229|gb|CO490738.1|CO490738				
Unigene39875_All	1064	1.23	0.86	1.15	4.87	4.34	2.38	0.12	0.20	0.11	-5.20E-01	3.69E-01		-9.48E-02	8.72E-01		-1.67E-01	5.81E-01		-1.03E+00	6.97E-05	Down	7.20E-01	6.32E-01		-8.60E-02	9.69E-01		Unigene39875_All//gi|242056489|ref|XP_002457390.1|/7.00E-07//hypothetical protein SORBIDRAFT_03g006560 [Sorghum bicolor] >gi|241929365|gb|EES02510.1| hypothetical protein SORBIDRAFT_03g006560 [Sorghum bicolor]	Unigene39875_All//7.00E-06//AT3G25270| nucleic acid binding					nr +
Unigene39877_All	576	0.36	2.82	1.85	3.89	3.29	2.35	0.95	0.22	1.52	2.95E+00	9.24E-06	Up	2.35E+00	3.61E-03		-2.43E-01	5.93E-01		-7.26E-01	9.38E-02		-2.13E+00	3.31E-02		6.73E-01	3.05E-01					Unigene39877_All//5.00E-23//gi|54115824|gb|CO491333.1|CO491333				
Unigene39879_All	1037	0.45	0.78	2.52	2.02	1.46	1.96	0.45	0.00	0.27	7.84E-01	3.23E-01		2.47E+00	3.62E-07	Up	-4.66E-01	3.11E-01		-4.19E-02	9.39E-01		-8.81E+00	1.71E-03		-7.38E-01	4.26E-01		Unigene39879_All//gi|257831433|gb|ACV71017.1|/3.00E-34//TPA17 [Capsicum annuum]	Unigene39879_All//4.00E-35//AT4G37740| AtGRF2 (GROWTHREGULATING FACTOR 2); transcription activator	Unigene39879_All//0.00E+00//gi|78348751|gb|DT569025.1|DT569025	GRF		GO:0010468//GO:0016817//GO:0030528//GO:0032559//GO:0043231//GO:0048827	nr +
Unigene39881_All	437	4.91	5.57	8.29	17.67	10.87	10.75	13.45	7.65	6.02	1.81E-01	6.45E-01		7.55E-01	2.50E-02		-7.00E-01	3.10E-04		-7.17E-01	4.72E-04		-8.14E-01	1.90E-04		-1.16E+00	1.28E-07	Down			Unigene39881_All//0.00E+00//TC178397				
Unigene39882_All	518	0.00	0.98	2.16	1.44	2.19	1.92	0.00	0.00	1.15	9.93E+00	4.04E-03		1.11E+01	3.43E-06	Up	6.05E-01	3.84E-01		4.11E-01	6.02E-01		null	null		1.02E+01	1.75E-04	Up	Unigene39882_All//gi|115469242|ref|NP_001058220.1|/4.00E-24//Os06g0649900 [Oryza sativa Japonica Group] >gi|113596260|dbj|BAF20134.1|Os06g0649900 [Oryza sativa Japonica Group]		Unigene39882_All//2.00E-90//ES830600				nr -
Unigene39883_All	1200	0.09	0.59	0.36	0.25	1.26	1.58	0.00	0.24	1.39	2.76E+00	9.14E-03		2.03E+00	1.39E-01		2.34E+00	1.15E-04	Up	2.67E+00	3.00E-06	Up	7.93E+00	2.35E-02		1.04E+01	5.04E-12	Up	Unigene39883_All//gi|115469242|ref|NP_001058220.1|/4.00E-25//Os06g0649900 [Oryza sativa Japonica Group] >gi|113596260|dbj|BAF20134.1|Os06g0649900 [Oryza sativa Japonica Group]		Unigene39883_All//2.00E-49//ES830600				nr -
Unigene39884_All	908	3.46	2.57	4.16	2.25	0.46	3.38	1.77	0.64	0.44	-4.30E-01	2.30E-01		2.68E-01	4.22E-01		-2.31E+00	1.08E-06	Down	5.89E-01	1.10E-01		-1.46E+00	2.51E-03		-2.01E+00	5.95E-05	Down	Unigene39884_All//gi|224125984|ref|XP_002319727.1|/3.00E-91//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222858103|gb|EEE95650.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene39884_All//4.00E-57//AT5G17850| cation exchanger, putative (CAX8)	Unigene39884_All//0.00E+00//TC178088			GO:0006810//GO:0031224	nr +
Unigene39885_All	361	2.46	4.21	10.03	2.76	6.68	9.13	0.70	1.04	2.54	7.73E-01	1.48E-01		2.03E+00	9.01E-08	Up	1.27E+00	1.76E-03		1.73E+00	2.20E-06	Up	5.68E-01	6.37E-01		1.85E+00	6.88E-03								
Unigene39887_All	1272	0.49	0.88	0.42	19.86	15.81	12.71	3.06	3.06	1.32	8.28E-01	2.04E-01		-2.38E-01	7.75E-01		-3.29E-01	1.43E-03		-6.43E-01	9.31E-10		-1.00E-03	9.96E-01		-1.22E+00	1.09E-05	Down	Unigene39887_All//gi|4836889|gb|AAD30592.1|AC007369_2//2.00E-81//Hypothetical protein [Arabidopsis thaliana]	Unigene39887_All//1.00E-73//AT1G20990| DC1 domain-containing protein	Unigene39887_All//0.00E+00//ES821810			GO:0046872	nr +
Unigene39888_All	634	1.57	6.23	1.51	1.65	3.64	1.85	2.07	0.26	1.26	1.99E+00	1.32E-08	Up	-5.27E-02	9.54E-01		1.14E+00	6.16E-03		1.67E-01	7.91E-01		-2.97E+00	8.34E-06	Down	-7.18E-01	1.54E-01								
Unigene39890_All	498	9.04	6.21	2.46	20.61	13.62	18.59	31.75	23.84	11.04	-5.42E-01	5.86E-02		-1.88E+00	1.24E-08	Down	-5.97E-01	3.12E-04		-1.48E-01	4.76E-01		-4.14E-01	9.87E-04		-1.52E+00	1.82E-28	Down	Unigene39890_All//gi|255957394|emb|CBA13551.1|/3.00E-28//cytosolic chaperonin, delta subunit [Glycine max]	Unigene39890_All//4.00E-29//AT3G18190| chaperonin, putative	Unigene39890_All//0.00E+00//gi|109873742|gb|DW502717.1|DW502717			GO:0005515//GO:0010038//GO:0032559//GO:0044267//GO:0044424	nr +
Unigene39891_All	602	3.82	1.52	3.27	3.23	3.43	3.23	0.42	3.33	0.79	-1.34E+00	2.11E-03		-2.25E-01	6.42E-01		8.88E-02	8.63E-01		-5.00E-04	9.95E-01		2.98E+00	1.47E-08	Up	9.14E-01	3.38E-01								
Unigene39892_All	427	8.09	3.32	4.36	17.50	10.81	6.88	4.16	1.08	4.76	-1.28E+00	1.80E-04	Down	-8.90E-01	1.06E-02		-6.95E-01	4.47E-04		-1.35E+00	6.42E-10	Down	-1.95E+00	5.37E-05	Down	1.94E-01	6.43E-01		Unigene39892_All//gi|30684882|ref|NP_850163.1|/3.00E-12//tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	Unigene39892_All//9.00E-09//AT2G31240| tetratricopeptide repeat (TPR)-containing protein	Unigene39892_All//0.00E+00//gi|13248429|gb|BF275924.2|BF275924				nr +
Unigene39893_All	731	0.93	3.54	1.38	4.09	4.80	5.93	1.74	2.52	1.36	1.93E+00	1.16E-05	Up	5.73E-01	4.04E-01		2.33E-01	5.61E-01		5.37E-01	7.34E-02		5.36E-01	2.29E-01		-3.49E-01	5.15E-01		Unigene39893_All//gi|224086542|ref|XP_002307906.1|/1.00E-24//histone acetyltransferase complex component [Populus trichocarpa] >gi|222853882|gb|EEE91429.1| histone acetyltransferase complex component [Populus trichocarpa]	Unigene39893_All//5.00E-18//AT4G16420| ADA2B (HOMOLOG OF YEAST ADA2 2B); DNA binding / transcription coactivator/ transcription factor	Unigene39893_All//0.00E+00//gi|78333894|gb|DT554168.1|DT554168			GO:0001071//GO:0003676//GO:0003712//GO:0003824//GO:0008283//GO:0009409//GO:0009725//GO:0010468//GO:0043231//GO:0046914	nr +

Unigene39898_All	1072	0.68	0.19	0.40	1.12	1.38	1.05	12.03	5.81	7.66	-1.85E+00	4.08E-02		-7.82E-01	3.80E-01		3.09E-01	5.98E-01		-8.24E-02	9.06E-01		-1.05E+00	4.85E-13	Down	-6.52E-01	1.85E-06		Unigene39898_All//gi|18405401|ref|NP_565933.1|//2.00E-68//LBD15 (LOB DOMAIN-CONTAINING PROTEIN 15) [Arabidopsis thaliana] >gi|29427824|sp|Q8L5T5.2|LBD15_ARATH RecName: Full=LOB domain-containing protein 15; AltName: Full=ASYMMETRIC LEAVES 2-like protein 11; Short=AS2-like protein 11 >gi|17227160|gb|AAL38034.1|AF447889_1 LOB DOMAIN 15 [Arabidopsis thaliana] >gi|2651309|gb|AAB87589.1| expressed protein [Arabidopsis thaliana] >gi|91806339|gb|ABE65897.1| LOB domain protein 15/lateral organ boundaries domain protein 15 [Arabidopsis thaliana] >gi|94442507|gb|ABF19041.1| At2g40470 [Arabidopsis thaliana] >gi|219807098|dbj|BAH10555.1| ASYMMETRIC LEAVES2-like 11 protein [Arabidopsis thaliana]	Unigene39898_All//2.00E-66//AT2G40470| LBD15 (LOB DOMAIN-CONTAINING PROTEIN 15)	Unigene39898_All//5.00E-40//DW519375		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0005488//GO:0043231	nr +
Unigene39899_All	544	15.20	33.07	23.00	7.05	7.53	9.55	6.22	5.92	6.22	1.12E+00	3.50E-16	Up	5.98E-01	2.96E-04		9.54E-02	8.19E-01		4.37E-01	1.13E-01		-7.18E-02	8.26E-01		1.60E-03	9.97E-01				Unigene39899_All//0.00E+00//TC164399				
Unigene3990_All	1663	20.89	23.67	31.67	7.22	14.06	7.06	0.92	2.21	1.72	1.81E-01	4.44E-02		6.00E-01	1.13E-15		9.62E-01	5.86E-19		-3.19E-02	8.78E-01		1.27E+00	1.59E-05	Up	9.14E-01	4.40E-03		Unigene3990_All//gi|297839731|ref|XP_002887747.1|//7.00E-79//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333588|gb|EFH64006.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene3990_All//8.00E-74//AT1G78600| LZF1 (LIGHT-REGULATED ZINC FINGER PROTEIN 1); transcription factor/ zinc ion binding	Unigene3990_All//0.00E+00//ES818371	DEB	ko04712|Circadian rhythm - plant		nr -
Unigene39901_All	739	0.14	1.37	0.29	0.67	1.68	2.26	1.43	1.58	2.37	3.28E+00	3.79E-04	Up	1.03E+00	5.91E-01		1.32E+00	3.54E-02		1.75E+00	1.36E-03		1.47E-01	7.92E-01		7.30E-01	8.78E-02		Unigene39901_All//gi|115455521|ref|NP_001051361.1|//2.00E-10//Os03g0762500 [Oryza sativa Japonica Group] >gi|113549832|dbj|BAF13275.1| Os03g0762500 [Oryza sativa Japonica Group]	Unigene39901_All//2.00E-08//AT5G43150| unknown protein				GO:0043231	nr -
Unigene39902_All	404	0.78	2.01	1.19	2.34	1.79	2.79	2.72	1.76	0.39	1.37E+00	9.21E-02		6.11E-01	5.86E-01		-3.88E-01	5.85E-01		2.55E-01	6.91E-01		-6.30E-01	2.93E-01		-2.79E+00	6.37E-05	Down			Unigene39902_All//5.00E-07//DW227861				
Unigene39903_All	381	7.55	26.60	13.84	5.62	4.70	2.25	0.55	0.77	1.15	1.82E+00	1.27E-18	Up	8.73E-01	1.28E-03		-2.59E-01	5.87E-01		-1.32E+00	3.01E-03		4.69E-01	7.06E-01		1.05E+00	2.98E-01		Unigene39903_All//gi|115472965|ref|NP_001060081.1|//2.00E-13//Os07g0575800 [Oryza sativa Japonica Group] >gi|113611617|dbj|BAF21995.1| Os07g0575800 [Oryza sativa Japonica Group]	Unigene39903_All//9.00E-12//AT5G19850| hydrolase, alpha/beta fold family protein	Unigene39903_All//1.00E-16//gi|164314228|gb|ES837291.1|ES837291			GO:0003824//GO:0043231	nr +
Unigene39904_All	513	0.31	0.59	1.25	2.14	2.28	2.11	6.59	3.75	1.63	9.54E-01	5.03E-01		2.03E+00	5.58E-02		9.54E-02	9.01E-01		-1.59E-02	9.71E-01		-8.15E-01	6.49E-03		-2.02E+00	1.48E-09	Down			Unigene39904_All//6.00E-07//gi|11208223|gb|BF277153.1|BF277153				
Unigene39905_All	633	53.56	107.82	80.51	70.28	64.95	74.56	44.75	57.31	42.42	1.01E+00	4.10E-50	Up	5.88E-01	1.16E-14		-1.14E-01	2.06E-01		8.54E-02	3.75E-01		3.57E-01	7.02E-06		-7.72E-02	4.65E-01		Unigene39905_All//gi|209484089|gb|ACI47519.1|//1.00E-11//iron-sulfer cluster scaffold protein ISU1 [Eucalyptus grandis]	Unigene39905_All//4.00E-11//AT4G22220| ISU1; structural molecule	Unigene39905_All//0.00E+00//gi|78333703|gb|DT553977.1|DT553977			GO:0031163//GO:0043231//GO:0046914//GO:0051540	nr +
Unigene39907_All	462	12.80	8.77	15.56	8.52	16.10	23.46	0.55	1.54	1.55	-5.45E-01	2.56E-02		2.82E-01	2.40E-01		9.18E-01	6.46E-06		1.46E+00	1.24E-15	Up	1.49E+00	6.15E-02		1.50E+00	4.94E-02		Unigene39907_All//gi|30679852|ref|NP_849962.1|//1.00E-27//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75244359|sp|Q8GWA9.1|PP157_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g17033	Unigene39907_All//9.00E-29//AT2G17033| pentatricopeptide (PPR) repeat-containing protein	Unigene39907_All//2.00E-123//BM359181				nr +
Unigene39909_All	718	3.79	7.83	8.08	4.02	3.02	2.14	1.00	0.52	0.33	1.05E+00	4.15E-05	Up	1.09E+00	2.68E-05	Up	-4.13E-01	2.79E-01		-9.12E-01	1.29E-02		-9.34E-01	2.26E-01		-1.59E+00	3.62E-02		Unigene39909_All//gi|297727877|ref|NP_001176302.1|//2.00E-11//Os11g0106066 [Oryza sativa Japonica Group] >gi|255679693|dbj|BAH95030.1| Os11g0106066 [Oryza sativa Japonica Group]	Unigene39909_All//2.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene39909_All//0.00E+00//BF273775				nr -
Unigene3991_All	675	0.62	0.60	0.32	0.15	0.26	0.67	3.07	0.37	1.06	-4.63E-02	9.80E-01		-9.74E-01	4.11E-01		7.89E-01	7.71E-01		2.18E+00	1.03E-01		-3.05E+00	5.12E-09	Down	-1.53E+00	1.72E-04	Down	Unigene3991_All//gi|124360281|gb|ABN08294.1|//7.00E-81//Cyclin-like F-box [Medicago truncatula]	Unigene3991_All//1.00E-75//AT1G10780| F-box family protein	Unigene3991_All//0.00E+00//DW496622				nr -
Unigene39910_All	575	2.37	0.53	0.93	3.12	0.96	4.40	4.93	4.22	3.88	-2.16E+00	9.05E-04	Down	-1.35E+00	2.93E-02		-1.70E+00	3.60E-04	Down	4.96E-01	2.37E-01		-2.25E-01	5.48E-01		-3.45E-01	3.08E-01				Unigene39910_All//0.00E+00//gi|72279662|gb|DT052145.1|DT052145				ESTscan -
Unigene39911_All	411	4.07	3.82	1.94	2.18	2.93	2.31	3.19	3.25	0.39	-9.21E-02	8.47E-01		-1.07E+00	4.69E-02		4.27E-01	5.52E-01		8.10E-02	9.31E-01		2.92E-02	9.87E-01		-3.04E+00	3.54E-06	Down	Unigene39911_All//gi|241899123|gb|ACS71641.1|//8.00E-08//ACC oxidase [Boea hygrometrica]	Unigene39911_All//2.00E-06//AT1G12010| 1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative	Unigene39911_All//7.00E-40//ES831910		ko00270|Cysteine and methionine metabolism	GO:0003824//GO:0008152	nr -
Unigene39912_All	926	0.00	0.00	0.00	0.75	1.56	0.88	80.68	6.14	18.93	null	null		null	null		1.05E+00	6.14E-02		2.21E-01	7.78E-01		-3.72E+00	0.00E+00	Down	-2.09E+00	1.60E-203	Down	Unigene39912_All//gi|109900626|gb|ABG47806.1|//5.00E-46//pectin methlyesterase inhibitor protein 1 [Capsicum annuum] >gi|110631514|gb|ABG81102.1| pectin methlyesterase inhibitor protein 1 [Capsicum annuum]	Unigene39912_All//1.00E-36//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene39912_All//7.00E-11//DW502487		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene39913_All	875	4.84	45.40	13.51	21.18	69.30	85.84	13.67	31.91	31.01	3.23E+00	6.73E-139	Up	1.48E+00	9.60E-16	Up	1.71E+00	2.55E-117	Up	2.02E+00	1.01E-165	Up	1.22E+00	1.51E-34	Up	1.18E+00	1.35E-32	Up	Unigene39913_All//gi|255572539|ref|XP_002527204.1|//4.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223533469|gb|EEF35217.1| conserved hypothetical protein [Ricinus communis]	Unigene39913_All//2.00E-06//AT4G32340| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: binding (TAIR:AT1G80130.1); Has 2680 Blast hits to 1282 proteins in 184 species: Archae - 2; Bacteria - 433; Metazoa - 1247; Fungi - 71; Plants - 657; Viruses - 13; Other Eukaryotes - 257 (source: NCBI BLink).	Unigene39913_All//0.00E+00//TC165464				nr -
Unigene39914_All	467	3.25	48.82	13.57	5.01	6.93	11.61	0.18	1.16	3.33	3.91E+00	7.05E-94	Up	2.06E+00	1.83E-13	Up	4.67E-01	1.95E-01		1.21E+00	3.03E-06	Up	2.68E+00	1.38E-02		4.20E+00	6.61E-09	Up	Unigene39914_All//gi|297720569|ref|NP_001172646.1|//6.00E-16//Os01g0843700 [Oryza sativa Japonica Group] >gi|255673865|dbj|BAH91376.1| Os01g0843700 [Oryza sativa Japonica Group]					GO:0031410	nr -
Unigene39915_All	620	4.56	1.72	4.29	3.78	3.50	1.68	0.48	0.61	0.45	-1.41E+00	2.94E-04	Down	-8.56E-02	8.22E-01		-1.10E-01	8.22E-01		-1.17E+00	5.07E-03		3.46E-01	7.38E-01		-8.59E-02	9.52E-01		Unigene39915_All//gi|75265624|sp|Q9SCP4.1|PP279_ARATH//3.00E-37//RecName: Full=Pentatricopeptide repeat-containing protein At3g53170 >gi|6630737|emb|CAB64220.1| nodulin / glutamate-ammonia ligase-like protein [Arabidopsis thaliana]	Unigene39915_All//7.00E-35//AT3G53170| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: glutamine biosynthetic process; LOCATED IN: nucleolus; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT5G48730.1); Has 17188 Blast hits to 5538 proteins in 167 species: Archae - 1; Bacteria - 16; Metazoa - 307; Fungi - 211; Plants - 16025; Viruses - 0; Other Eukaryotes - 628 (source: NCBI BLink).				GO:0043231	nr +
Unigene39916_All	530	1.68	2.49	5.93	3.76	2.34	2.39	1.44	0.47	1.43	5.67E-01	3.41E-01		1.82E+00	5.14E-06	Up	-6.85E-01	1.25E-01		-6.56E-01	1.63E-01		-1.60E+00	3.70E-02		-7.80E-03	9.84E-01		Unigene39916_All//gi|297831228|ref|XP_002883496.1|//2.00E-39//glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata] >gi|297329336|gb|EFH59755.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata]	Unigene39916_All//5.00E-39//AT3G24040| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	Unigene39916_All//3.00E-144//gi|21096815|gb|BQ409128.1|BQ409128			GO:0008194//GO:0043231	nr +
Unigene39917_All	1046	0.40	0.92	0.87	1.48	1.88	0.43	2.55	5.99	5.98	1.20E+00	9.57E-02		1.11E+00	1.49E-01		3.46E-01	5.18E-01		-1.77E+00	1.65E-03		1.23E+00	1.70E-08	Up	1.23E+00	1.11E-08	Up			Unigene39917_All//5.00E-83//TC139249				
Unigene3992_All	1378	1.63	0.96	0.43	1.81	1.37	1.08	3.99	1.00	2.46	-7.72E-01	6.92E-02		-1.94E+00	8.10E-05	Down	-3.95E-01	3.36E-01		-7.41E-01	6.85E-02		-1.99E+00	2.49E-14	Down	-6.99E-01	1.43E-03		Unigene3992_All//gi|124360281|gb|ABN08294.1|//1.00E-105//Cyclin-like F-box [Medicago truncatula]	Unigene3992_All//2.00E-98//AT1G10780| F-box family protein	Unigene3992_All//0.00E+00//DW496622				nr +
Unigene39920_All	507	25.59	5.60	19.85	2.75	4.08	2.14	0.08	0.00	5.58	-2.19E+00	2.64E-30	Down	-3.67E-01	2.77E-02		5.67E-01	2.26E-01		-3.64E-01	5.56E-01		-6.38E+00	6.57E-01		6.06E+00	1.04E-18	Up	Unigene39920_All//gi|15217873|ref|NP_174144.1|//6.00E-27//PUP1 (PURINE PERMEASE 1); purine nucleoside transmembrane transporter/ purine transmembrane transporter [Arabidopsis thaliana] >gi|75173386|sp|Q9FZ96.1|PUP1_ARATH RecName: Full=Purine permease 1; Short=AtPUP1 >gi|9795614|gb|AAF98432.1|AC021044_11 purine permease [Arabidopsis thaliana]	Unigene39920_All//3.00E-28//AT1G28230| PUP1 (PURINE PERMEASE 1); purine nucleoside transmembrane transporter/ purine transmembrane transporter				GO:0005337//GO:0006863//GO:0009267//GO:0015205//GO:0016021	nr +
Unigene39921_All	556	0.94	0.91	0.86	4.84	4.46	2.27	4.71	1.73	3.58	-4.63E-02	9.76E-01		-1.27E-01	8.98E-01		-1.18E-01	8.04E-01		-1.09E+00	4.53E-03		-1.45E+00	6.76E-05	Down	-3.96E-01	2.51E-01		Unigene39921_All//gi|297599775|ref|NP_001047802.2|//4.00E-40//Os02g0693500 [Oryza sativa Japonica Group] >gi|255671179|dbj|BAF09716.2| Os02g0693500 [Oryza sativa Japonica Group]	Unigene39921_All//3.00E-43//AT4G17790| INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (InterPro:IPR015414); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G71940.1); Has 2258 Blast hits to 2258 proteins in 517 species: Archae - 4; Bacteria - 1129; Metazoa - 188; Fungi - 22; Plants - 104; Viruses - 0; Other Eukaryotes - 811 (source: NCBI BLink).	Unigene39921_All//0.00E+00//gi|164353648|gb|ES849349.1|ES849349			GO:0031410	nr +

Unigene39923_All	1251	0.25	0.16	1.70	10.43	6.19	3.39	0.95	0.53	0.13	-6.31E-01	6.22E-01			2.76E+00	1.21E-06	Up	-7.52E-01	1.48E-07			-1.62E+00	4.64E-22	Down	-8.24E-01	1.42E-01		-2.89E+00	2.03E-05	Down	Unigene39923_All//gi|115473321|ref|XP_001060259.1|//6.00E-18//0s07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene39923_All//2.00E-17//AT3G09510| nucleic acid binding	Unigene39923_All//2.00E-67//gi|78335693|gb|DT553967.1|DT555967				nr +
Unigene39925_All	710	2.58	0.14	0.53	55.08	40.98	25.06	6.85	0.71	1.29	-4.18E+00	2.18E-08	Down	-2.30E+00	8.05E-05	Down	-4.26E-01	4.80E-08		-1.14E+00	5.83E-38	Down	-3.28E+00	9.74E-22	Down	-2.41E+00	1.73E-16	Down	Unigene39925_All//gi|124502497|gb|ABN13629.1|//3.00E-49//blue copper-like protein [Gossypium hirsutum]	Unigene39925_All//1.00E-25//AT1G72230| plastocyanin-like domain-containing protein	Unigene39925_All//0.00E+00//TC177324			GO:0006091//GO:0031410//GO:0046914	nr -
Unigene39927_All	736	2.13	1.38	0.80	1.62	2.62	0.25	1.44	0.51	0.65	-6.31E-01	2.31E-01		-1.42E+00	1.34E-02		6.90E-01	1.53E-01		-2.73E+00	2.36E-04	Down	-1.49E+00	1.64E-02		-1.14E+00	4.77E-02		Unigene39927_All//gi|224125028|ref|XP_002329873.1|//2.00E-98//GRAS family transcription factor [Populus trichocarpa] >gi|222871110|gb|EEF08241.1| GRAS family transcription factor [Populus trichocarpa]	Unigene39927_All//8.00E-47//AT3G60630| scarecrow transcription factor family protein	Unigene39927_All//3.00E-173//gi|48793763|gb|CO095077.1|CO095077	GRAS		GO:0010468	nr +
Unigene39928_All	290	5.95	1.40	2.20	7.90	8.67	6.07	5.98	1.87	8.93	-2.09E+00	1.98E-04	Down	-1.43E+00	8.21E-03		1.34E-01	8.06E-01		-3.80E-01	4.02E-01		-1.67E+00	3.96E-04	Down	5.79E-01	9.03E-02				Unigene39928_All//3.00E-134//gi|78326105|gb|DT546379.1|DT546379				
Unigene3993_All	1195	45.67	21.33	29.45	2.63	2.82	2.42	5.02	7.34	4.87	-1.10E+00	3.10E-46	Down	-6.33E-01	9.90E-18		1.05E-01	8.12E-01		-1.19E-01	7.47E-01		5.48E-01	1.62E-03		-4.57E-02	8.46E-01		Unigene3993_All//gi|15231396|ref|NP_187368.1|//9.00E-48//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|56381891|gb|AAV85664.1| At3g07120 [Arabidopsis thaliana] >gi|58531344|gb|AAW78594.1| At3g07120 [Arabidopsis thaliana]	Unigene3993_All//1.00E-22//AT3G25030| zinc finger (C3HC4-type RING finger) family protein	Unigene3993_All//0.00E+00//TC155211				nr -
Unigene39930_All	1605	3.46	0.06	0.50	2.86	3.71	5.63	0.00	0.00	0.00	-5.78E+00	5.93E-29	Down	-2.80E+00	1.28E-16	Down	3.78E-01	1.35E-01		9.79E-01	2.82E-07		null	null		null	null		Unigene39930_All//gi|152411147|ref|NP_197465.1|//0.00E+00//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana]	Unigene39930_All//0.00E+00//AT5G19640| proton-dependent oligopeptide transport (POT) family protein	Unigene39930_All//1.00E-53//TC168493			GO:0015833//GO:0044464	nr +
Unigene39931_All	1558	0.20	0.00	0.07	10.20	6.45	4.73	0.33	0.30	0.15	-7.65E+00	3.65E-02		-1.56E+00	3.30E-01		-6.60E-01	2.54E-07		-1.11E+00	3.39E-15	Down	-1.42E-01	8.76E-01		-1.09E+00	2.28E-01		Unigene39931_All//gi|224115540|ref|XP_002317059.1|//1.00E-142//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222860124|gb|EEE97671.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene39931_All//7.00E-83//AT2G46770| EMB2301 (EMBRYO DEFECTIVE 2301); transcription activator/ transcription factor	Unigene39931_All//4.00E-97//TC156365	NAC		GO:0009699//GO:0009832//GO:0009900//GO:0016564//GO:0032502//GO:0043231	nr +
Unigene39932_All	821	10.01	15.43	22.96	22.75	19.04	18.10	7.52	7.59	6.70	6.25E-01	8.03E-05		1.20E+00	4.58E-18	Up	-2.57E-01	4.65E-02		-3.30E-01	1.08E-02		1.27E-02	9.90E-01		-1.67E-01	4.68E-01		Unigene39932_All//gi|225464958|ref|XP_002276137.1|//4.00E-08//PREDICTED: hypothetical protein [Vitis vinifera] >gi|147841156|emb|CAN66263.1| hypothetical protein [Vitis vinifera] >gi|296084917|emb|CBI28326.3| unnamed protein product [Vitis vinifera]	Unigene39932_All//4.00E-06//AT1G67190| F-box family protein	Unigene39932_All//0.00E+00//ES796183				nr +
Unigene39934_All	663	2.84	0.92	0.96	5.41	1.97	1.36	9.12	0.88	0.12	-1.63E+00	1.19E-03		-1.56E+00	2.80E-03		-1.45E+00	2.92E-06	Down	-1.99E+00	2.14E-08	Down	-3.37E+00	1.49E-27	Down	-6.25E+00	4.78E-41	Down	Unigene39934_All//gi|224080516|ref|XP_002306147.1|//3.00E-43//SAUR family protein [Populus trichocarpa] >gi|222849111|gb|EEE86658.1| SAUR family protein [Populus trichocarpa]	Unigene39934_All//2.00E-41//AT1G75580| auxin-responsive protein, putative	Unigene39934_All//1.00E-64//TC157705			GO:0009725	nr -
Unigene39935_All	2051	0.05	0.05	0.10	0.00	0.00	0.35	12.41	7.07	135.48	-4.60E-02	9.88E-01		1.03E+00	5.91E-01		null	null		8.46E+00	2.31E-04	Up	-8.12E-01	1.80E-16		3.45E+00	0.00E+00	Up	Unigene39935_All//gi|18404979|ref|NP_565902.1|//0.00E+00//MLO12 (MILDEW RESISTANCE LOCUS O 12); calmodulin binding [Arabidopsis thaliana] >gi|21903435|sp|O80961.2|MLO12_ARATH RecName: Full=MLO-like protein 12; Short=AtMlo12; Short=AtMlo18 >gi|14091594|gb|AAK53805.1|AF36957 3_1 membrane protein Mlo12 [Arabidopsis thaliana] >gi|20197259|gb|AAC28997.2| similar to Mlo proteins from H. vulgare [Arabidopsis thaliana]	Unigene39935_All//0.00E+00//AT2G39200| MLO12 (MILDEW RESISTANCE LOCUS O 12); calmodulin binding	Unigene39935_All//0.00E+00//DN799901			GO:0009987//GO:0010260//GO:0031224//GO:0050832	nr +
Unigene39936_All	437	1.08	1.16	2.68	3.99	3.78	1.03	4.35	2.39	1.55	1.06E-01	9.23E-01		1.32E+00	5.10E-02		-7.70E-02	8.69E-01		-1.95E+00	2.67E-04	Down	-8.65E-01	4.03E-02		-1.49E+00	4.57E-04	Down	Unigene39936_All//gi|15241106|ref|NP_198149.1|//4.00E-39//binding [Arabidopsis thaliana]	Unigene39936_All//3.00E-40//AT5G27970| binding					nr +
Unigene39937_All	795	7.37	6.50	7.37	9.65	7.58	8.64	5.90	3.94	1.75	-1.81E-01	4.90E-01		-6.00E-04	9.98E-01		-3.48E-01	1.01E-01		-1.60E-01	5.14E-01		-5.82E-01	1.96E-02		-1.75E+00	7.49E-11	Down	Unigene39937_All//gi|116793503|gb|ABK26771.1|//8.00E-06//unknown [Picea sitchensis]		Unigene39937_All//0.00E+00//DW499134				nr +
Unigene39939_All	569	0.55	1.78	0.66	3.76	2.18	0.87	1.78	1.47	1.26	1.69E+00	2.14E-02		2.48E-01	8.23E-01		-7.89E-01	6.06E-02		-2.11E+00	1.29E-05	Down	-2.80E-01	6.37E-01		-5.01E-01	3.99E-01				Unigene39939_All//1.00E-171//ES847724				
Unigene39941_All	843	0.99	0.66	0.63	4.31	4.74	1.61	3.31	0.30	1.47	-5.87E-01	4.26E-01		-6.53E-01	3.96E-01		1.36E-01	7.21E-01		-1.42E+00	1.49E-05	Down	-3.48E+00	2.29E-13	Down	-1.18E+00	3.83E-04	Down	Unigene39941_All//gi|297834848|ref|XP_002885306.1|//1.00E-65//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331146|gb|EFH61565.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39941_All//1.00E-58//AT3G19090| protein kinase family protein	Unigene39941_All//3.00E-65//ES800996		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism	GO:0004175//GO:0004672//GO:0006464//GO:0016020//GO:0031410//GO:0032559	nr +
Unigene39942_All	738	10.21	2.61	7.14	5.87	5.37	8.26	0.69	1.30	0.22	-1.97E+00	1.19E-15	Down	-5.15E-01	2.10E-02		-1.30E-01	6.96E-01		4.93E-01	4.39E-02		9.22E-01	1.49E-01		-1.67E+00	7.78E-02		Unigene39942_All//gi|15221439|ref|NP_177024.1|//3.00E-14//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|5734721|gb|AAD49986.1|AC008075_19 Similar to gb|AF023472 peptide transporter from Hordeum vulgare and is a member of the PF|00854 Peptide transporter family. ESTs gb|T41927 and gb|AA395024 come from this gene [Arabidopsis thaliana] >gi|20147231|gb|AAM10330.1| At1g68570/F24J5_7 [Arabidopsis thaliana] >gi|25090385|gb|AAN72289.1| At1g68570/F24J5_7 [Arabidopsis thaliana] >gi|110742209|dbj|BAE99031.1| peptide transporter like [Arabidopsis thaliana]	Unigene39942_All//-1.67E+00| 7.78E-02 proton-dependent oligopeptide transport (POT) family protein	Unigene39942_All//3.00E-114//C0094698			GO:0015833//GO:0031224	nr +
Unigene39944_All	430	0.00	1.30	0.50	7.53	4.08	3.15	1.47	1.46	0.37	1.03E+01	2.18E-03		8.95E+00	1.41E-01		-8.83E-01	6.45E-03		-1.26E+00	2.89E-04	Down	-1.66E-02	1.02E+00		-1.99E+00	2.04E-02									
Unigene39945_All	745	2.18	2.11	0.50	2.54	2.82	1.39	2.84	4.99	7.91	-4.63E-02	9.39E-01		-2.12E+00	5.11E-04	Down	1.50E-01	8.01E-01		-8.66E-01	7.02E-02		8.15E-01	4.04E-03		1.48E+00	1.32E-10	Up	Unigene39945_All//gi|24461866|gb|AA62353.1|AF506028_20//5.00E-61//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene39945_All//2.00E-51//AT1G12280| disease resistance protein (CC-NBS-LRR class), putative	Unigene39945_All//4.00E-166//ES852122		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016787	nr +
Unigene39948_All	747	0.77	2.37	0.43	1.67	6.45	5.99	1.64	1.57	0.59	1.62E+00	1.94E-03		-8.49E-01	3.97E-01		1.95E+00	2.55E-11	Up	1.84E+00	3.47E-09	Up	-6.73E-02	9.14E-01		-1.48E+00	6.62E-03				Unigene39948_All//0.00E+00//gi|21102990|gb|BQ415303.1|BQ415303				
Unigene39949_All	705	2.82	1.80	0.76	4.38	3.32	2.75	1.20	0.95	2.03	-6.50E-01	1.53E-01		-1.90E+00	3.07E-04	Down	-3.99E-01	2.78E-01		-6.69E-01	6.16E-02		-3.38E-01	6.62E-01		7.62E-01	1.12E-01		Unigene39949_All//gi|225424454|ref|XP_002281633.1|//1.00E-70//PREDICTED: similar to anthranilate synthase beta subunit [Vitis vinifera]	Unigene39949_All//4.00E-71//AT1G25220| ASB1 (ANTHRANILATE SYNTHASE BETA SUBUNIT 1); anthranilate synthase	Unigene39949_All//1.00E-132//TC155581		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0006568//GO:0006970//GO:0009064//GO:0009536//GO:0009725//GO:0009850//GO:0016833//GO:0048527//GO:0051707	nr -
Unigene3995_All	1366	1.26	0.48	0.19	5.94	2.34	2.31	6.07	2.78	2.27	-1.39E+00	7.05E-03		-2.70E+00	2.40E-05	Down	-1.34E+00	5.46E-12	Down	-1.36E+00	7.06E-11	Down	-1.12E+00	1.41E-09	Down	-1.42E+00	8.17E-14	Down	Unigene3995_All//gi|225030804|gb|ACN79515.1|//2.00E-37//auxin response factor 3a [Lotus japonicus]		Unigene3995_All//3.00E-48//TC132130				nr -
Unigene39950_All	742	1.27	0.34	0.79	28.20	11.14	8.95	3.65	7.27	1.18	-1.89E+00	1.53E-02		-6.85E-01	3.69E-01		-1.34E+00	3.57E-30	Down	-1.66E+00	3.61E-36	Down	9.95E-01	1.78E-05		-1.63E+00	4.80E-06	Down	Unigene39950_All//gi|113367188|gb|ABI34651.1|//8.00E-53//bZIP transcription factor bZIP73A [Glycine max]	Unigene39950_All//6.00E-39//AT3G30530| ATBZIP42 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 42); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene39950_All//0.00E+00//TC160692	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0043231	nr +
Unigene39951_All	807	0.13	0.57	0.33	1.05	2.13	0.90	4.72	1.24	32.93	2.12E+00	9.59E-02		1.35E+00	4.09E-01		1.02E+00	4.17E-02		-2.29E-01	7.51E-01		-1.92E+00	1.04E-09	Down	2.80E+00	4.23E-101	Up	Unigene39951_All//gi|15225361|ref|NP_182011.1|//8.00E-39//ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor [Arabidopsis thaliana] >gi|57012834|sp|Q8LSK1.2|ERF99_ARATH RecName: Full=Ethylene-responsive transcription factor 13; Short=AtERF13; AltName: Full=Ethylene-responsive element-binding factor 13; Short=EREBP-13	Unigene39951_All//1.00E-29//AT2G44840| ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	Unigene39951_All//4.00E-40//DT467806	AP2-EREBP		GO:0000160//GO:0001071//GO:0003676//GO:0006351//GO:0009743//GO:0010468//GO:0043231	nr +
Unigene39952_All	348	4.81	12.09	11.17	4.58	8.61	8.83	1.82	1.80	1.49	1.33E+00	1.77E-05	Up	1.22E+00	2.37E-04	Up	9.10E-01	1.00E-02		9.46E-01	8.12E-03		-1.66E-02	1.02E+00		-2.92E-01	6.84E-01		Unigene39952_All//gi|7768153|emb|CAB90634.1|//4.00E-10//protein phosphatase 2C (PP2C) [Fagus sylvatica]	Unigene39952_All//3.00E-09//AT4G38520| protein phosphatase 2C family protein / PP2C family protein	Unigene39952_All//2.00E-40//TC174839			GO:0004721	nr +
Unigene39953_All	1255	16.68	14.62	30.04	1.03	0.58	0.58	0.81	0.10	0.41	-1.90E-01	1.36E-01		8.49E-01	2.08E-20		-8.41E-01	1.44E-01		-8.42E-01	1.64E-01		-3.02E+00	1.08E-04	Down	-9.70E-01	9.93E-02		Unigene39953_All//gi|158934007|emb|CAJ40777.1|//1.00E-114//alpha galactosidase precursor [Coffea arabica]	Unigene39953_All//1.00E-114//AT1G29050| unknown protein	Unigene39953_All//0.00E+00//TC159045				nr -
Unigene39956_All	515	5.89	3.15	3.31	168.30	161.88	84.63	16.09	4.71	3.95	-9.04E-01	1.16E-02		-8.33E-01	2.63E-02		-5.62E-02	4.20E-01		-9.92E-01	5.08E-67		-1.77E+00	3.12E-18	Down	-2.03E+00	2.10E-22	Down	Unigene39956_All//gi|255558960|ref|XP_002520503.1|//2.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223540345|gb|EEF41916.1| conserved hypothetical protein [Ricinus communis]		Unigene39956_All//0.00E+00//gi|109886155|gb|DW515125.1|DW515125				nr +
Unigene39958_All	632	81.88	89.95	44.49	46.50	80.64	149.71	96.00	72.02	69.21	1.36E-01	7.17E-02		-8.80E-01	1.82E-29		7.94E-01	8.62E-30		1.69E+00	1.59E-163	Up	-4.15E-01	5.17E-12		-4.72E-01	1.77E-15		Unigene39958_All//gi|29839387|sp|Q9948F6.1|FR13_SOYBN//3.00E-40//RecName: Full=Ferritin-3, chloroplastic; AltName: Full=SFerH-3; Flags: Precursor >gi|15487307|dbj|BAB94536.1| ferritin [Glycine max]	Unigene39958_All//5.00E-28//AT5G01600| ATFER1; ferric iron binding / iron ion binding	Unigene39958_All//0.00E+00//gi|109881079|gb|DW510049.1|DW510049		ko00860|Porphyrin and chlorophyll metabolism	GO:0000041//GO:0005506//GO:0008152//GO:0009536//GO:0016724//GO:0030005	nr -
Unigene3996_All	1508	3.61	1.58	1.13	4.56	4.70	4.88	5.24	4.46	3.49	-1.19E+00	6.03E-06	Down	-1.68E+00	6.60E-09	Down	4.53E-02	8.64E-01		9.88E-02	6.73E-01		-2.33E-01	2.47E-01		-5.88E-01	9.85E-04		Unigene3996_All//gi|262070706|gb|ACY08824.1|//2.00E-10//low molecular weight glutenin subunit D3-6 [Aegilops tauschii]		Unigene3996_All//0.00E+00//TC161581				nr +

Unigene39960_All	2082	0.00	0.00	0.00	0.00	0.00	0.00	84.19	11.08	12.57	null	null		null	null		null	null		null	null		-2.93E+00	0.00E+00	Down	-2.74E+00	0.00E+00	Down	Unigene39960_All//gi|224084952|ref|XP_002307454.1|//0.00E+00//nramp transporter [Populus trichocarpa] >gi|222856903|gb|EEE94450.1| nramp transporter [Populus trichocarpa]	Unigene39960_All//8.00E-159//AT1G80830| NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter	Unigene39960_All//3.00E-12//DN804497			GO:0044464//GO:0051234	nr +
Unigene39962_All	510	3.39	0.60	1.57	3.22	4.05	3.90	0.83	0.82	0.55	-2.51E+00	2.66E-05	Down	-1.11E+00	3.59E-02		3.30E-01	5.26E-01		2.74E-01	6.17E-01		-1.66E-02	1.02E+00		-6.00E-01	5.53E-01		Unigene39962_All//gi|15233788|ref|NP_194163.1|//9.00E-49//ubiquitin thiolesterase [Arabidopsis thaliana]	Unigene39962_All//2.00E-31//AT4G24320| ubiquitin thiolesterase				GO:0019941//GO:0043231	nr +
Unigene39964_All	584	6.90	83.64	21.97	4.86	2.24	4.64	12.02	21.04	13.17	3.60E+00	4.82E-188	Up	1.67E+00	3.12E-20	Up	-1.12E+00	1.40E-03		-6.74E-02	8.73E-01		8.08E-01	2.59E-08		1.32E-01	5.37E-01		Unigene39964_All//gi|297848320|ref|XP_002892041.1|//3.00E-40//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337883|gb|EFH68300.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39964_All//8.00E-41//AT3G61220| short-chain dehydrogenase/reductase (SDR) family protein	Unigene39964_All//0.00E+00//TC154214			GO:0005618//GO:0016616	nr +
Unigene39965_All	1229	0.47	0.04	0.43	25.58	10.23	1.47	2.10	1.84	0.23	-3.51E+00	9.02E-03		-1.12E-01	9.07E-01		-1.32E+00	2.91E-44	Down	-4.12E+00	9.22E-149	Down	-1.93E-01	6.47E-01		-3.21E+00	4.85E-12	Down	Unigene39965_All//gi|225455352|ref|XP_002277097.1|//1.00E-110//PREDICTED: similar to ABIL3 (ABL INTERACTOR-LIKE PROTEIN 3) [Vitis vinifera]	Unigene39965_All//3.00E-80//AT5G24310| ABIL3 (ABL INTERACTOR-LIKE PROTEIN 3)	Unigene39965_All//0.00E+00//ES823487			GO:0000904//GO:0005856//GO:0048513	nr +
Unigene39968_All	651	0.16	0.00	0.33	11.25	5.71	3.19	2.60	3.08	0.37	-7.33E+00	3.71E-01		1.03E+00	5.91E-01		-9.77E-01	1.03E-06		-1.82E+00	9.85E-15	Down	2.46E-01	5.97E-01		-2.82E+00	2.86E-07	Down								
Unigene3997_All	1965	1.44	4.38	5.07	3.95	9.76	8.32	0.95	0.30	0.32	1.61E+00	1.50E-13	Up	1.82E+00	1.04E-17	Up	1.30E+00	4.31E-25	Up	1.07E+00	1.27E-14	Up	-1.67E+00	2.33E-04	Down	-1.55E+00	3.64E-04	Down	Unigene3997_All//gi|82623417|gb|AB887123.1|//1.00E-166//aspartic protease precursor-like [Solanum tuberosum]	Unigene3997_All//3.00E-144//AT1G11910| aspartyl protease family protein	Unigene3997_All//0.00E+00//DW237417				nr -
Unigene39971_All	324	5.17	3.91	0.99	1.23	1.81	0.84	0.91	0.26	0.61	-4.02E-01	4.19E-01		-2.39E+00	1.21E-04	Down	5.55E-01	5.99E-01		-5.56E-01	6.38E-01		-1.82E+00	2.11E-01		-5.71E-01	6.28E-01		Unigene39971_All//gi|297809703|ref|XP_002872735.1|//4.00E-35//inositol monophosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318572|gb|EFH48994.1| inositol monophosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39971_All//3.00E-36//AT4G05090| inositol monophosphatase family protein	Unigene39971_All//7.00E-61//TC160047		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism	GO:0008252//GO:0009536//GO:0016312//GO:0044237	nr -
Unigene39973_All	448	0.00	0.45	0.00	7.01	3.23	14.32	43.41	29.29	25.88	8.82E+00	1.36E-01		null	null		-1.12E+00	6.95E-04	Down	1.03E+00	8.94E-06	Up	-5.68E-01	3.42E-07		-7.46E-01	1.55E-11		Unigene39973_All//gi|224134741|ref|XP_002321895.1|//3.00E-06//predicted protein [Populus trichocarpa] >gi|222868891|gb|EEF06022.1| predicted protein [Populus trichocarpa]		Unigene39973_All//8.00E-09//DW008516				nr -
Unigene39974_All	475	2.31	6.19	2.02	15.31	9.71	15.97	148.74	373.17	250.94	1.42E+00	2.07E-04	Up	-1.97E-01	7.50E-01		-6.56E-01	1.16E-03		6.11E-02	7.98E-01		1.33E+00	9.99E-245	Up	7.55E-01	6.40E-67		Unigene39974_All//gi|224120498|ref|XP_002331062.1|//5.00E-08//vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa] >gi|222872992|gb|EEF10123.1| vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa]	Unigene39974_All//2.00E-08//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene39974_All//5.00E-174//gi|72275545|gb|DT050186.1|DT050186		ko00190|Oxidative phosphorylation		nr +
Unigene39975_All	575	84.44	120.20	140.49	11.09	23.36	14.22	0.15	0.00	0.00	5.09E-01	6.50E-16		7.34E-01	1.12E-33		1.07E+00	3.72E-13	Up	3.58E-01	9.29E-02		-7.20E+00	4.03E-01		-7.20E+00	3.58E-01		Unigene39975_All//gi|6587827|gb|AAF18516.1|AC006551_2//5.00E-33//Unknown protein [Arabidopsis thaliana] >gi|150106608|gb|AAK73963.1| At1g22630/F12K8_2 [Arabidopsis thaliana] >gi|19699248|gb|AAL90990.1| At1g22630/F12K8_2 [Arabidopsis thaliana]	Unigene39975_All//7.00E-24//AT1G22630| unknown protein	Unigene39975_All//1.00E-140//gi|84151437|gb|DN800792.1|DN800792			GO:0005515//GO:0043231//GO:0044267	nr +
Unigene39978_All	796	116.60	62.57	108.31	23.09	20.68	11.52	1.59	0.37	0.40	-8.98E-01	3.48E-56		-1.07E-01	8.33E-02		-1.59E-01	2.75E-01		-1.00E+00	6.49E-15	Down	-2.12E+00	4.16E-04	Down	-1.99E+00	4.87E-04	Down	Unigene39978_All//gi|297804780|ref|XP_002870274.1|//2.00E-46//Terredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316110|gb|EFH46533.1| ferredoxin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene39978_All//3.00E-47//AT4G14890| ferredoxin family protein	Unigene39978_All//0.00E+00//gi|161424278|gb|ES808346.1|ES808346		ko00195|Photosynthesis	GO:0006091//GO:0009536//GO:0043169//GO:0051536	nr -
Unigene39979_All	585	13.68	25.55	20.30	4.60	4.53	12.43	2.46	4.00	2.18	9.01E-01	1.05E-09		5.69E-01	8.41E-04		-2.08E-02	9.61E-01		1.43E+00	2.17E-10	Up	7.03E-01	6.01E-02		-1.73E-01	7.13E-01		Unigene39979_All//gi|114329246|gb|AB164152.1|//1.00E-94//hydroxymethylbutenyl diphosphate reductase [Camptotheca acuminata]	Unigene39979_All//4.00E-84//AT4G34350| HDR (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE REDUCTASE); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase/ 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Unigene39979_All//0.00E+00//CO072954		ko00900|Terpenoid backbone biosynthesis	GO:0006090//GO:0006721//GO:0009532//GO:0016726//GO:0042221//GO:0052592	nr -
Unigene3998_All	1006	5.25	1.81	2.49	17.28	12.01	10.60	39.04	26.17	19.13	-1.53E+00	3.90E-08	Down	-1.08E+00	8.74E-05	Down	-5.24E-01	1.93E-05		-7.06E-01	4.90E-08		-5.77E-01	4.52E-14		-1.03E+00	6.13E-38	Down	Unigene3998_All//gi|117950163|gb|AB658465.1|//4.00E-83//LIM domain protein GLIMlb [Populus tremula x Populus alba]	Unigene3998_All//1.00E-78//AT1G10200| WLIM1; transcription factor/ zinc ion binding	Unigene3998_All//0.00E+00//TC148238	LIM			nr -
Unigene39981_All	239	20.36	41.77	48.13	12.30	17.43	19.46	0.53	1.40	0.50	1.04E+00	2.65E-08	Up	1.24E+00	7.30E-12	Up	5.04E-01	9.63E-02		6.63E-01	1.84E-02		1.40E+00	2.76E-01		-8.57E-02	9.69E-01					Unigene39981_All//3.00E-75//TC149489				
Unigene39984_All	463	2.03	2.41	1.73	8.50	9.00	3.80	0.27	0.54	0.34	2.43E-01	6.82E-01		-2.38E-01	7.23E-01		8.24E-02	8.14E-01		-1.16E+00	1.61E-04	Down	9.83E-01	5.17E-01		3.29E-01	8.51E-01					Unigene39984_All//5.00E-07//TC130237				
Unigene39986_All	435	1.20	0.93	1.47	1.60	3.25	2.28	1.07	3.94	2.47	-3.68E-01	6.83E-01		2.88E-01	7.25E-01		1.02E+00	7.53E-02		5.11E-01	4.92E-01		1.88E+00	1.20E-04	Up	1.21E+00	3.74E-02					Unigene39986_All//5.00E-07//TC163973				
Unigene39988_All	517	186.92	80.46	73.13	346.29	271.35	273.43	330.06	127.65	114.58	-1.22E+00	1.19E-95	Down	-1.35E+00	2.36E-109	Down	-3.52E-01	1.26E-24		-3.41E-01	8.70E-21		-1.37E+00	5.70E-248	Down	-1.53E+00	1.02E-299	Down	Unigene39988_All//gi|211906518|gb|ACJ11752.1|//1.00E-15//glyceraldehyde-3-phosphate dehydrogenase C subunit [Gossypium hirsutum]	Unigene39988_All//4.00E-14//AT3G04120| GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene39988_All//2.00E-179//ES818844		ko00010|Glycolysis / Gluconeogenesis	GO:0000166//GO:0006007//GO:0008943//GO:0044424	nr -
Unigene39989_All	289	1.81	2.63	2.21	8.79	5.36	2.19	0.88	0.00	1.38	5.39E-01	5.02E-01		2.89E-01	7.25E-01		-7.13E-01	6.16E-02		-2.01E+00	3.48E-06	Down	-9.78E+00	4.04E-02		6.51E-01	5.44E-01									
Unigene3999_All	1519	6.13	1.40	3.89	4.79	6.91	3.84	3.06	4.15	6.48	-2.13E+00	3.63E-21	Down	-6.56E-01	7.91E-04		5.30E-01	1.65E-03		-3.20E-01	1.68E-01		4.40E-01	3.94E-02		1.08E+00	7.28E-11	Up	Unigene3999_All//gi|79549667|ref|NP_178303.2|//1.00E-124//nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana]	Unigene3999_All//8.00E-102//AT1G68130| AtIDD14 (Arabidopsis thaliana Indeterminate(ID)-Domain 14); nucleic acid binding / transcription factor/ zinc ion binding	Unigene3999_All//0.00E+00//TC162445	C2H2			nr -
Unigene39990_All	514	0.61	0.30	0.21	10.37	8.51	5.10	8.55	3.74	2.79	-1.05E+00	4.43E-01		-1.56E+00	3.30E-01		-2.86E-01	3.08E-01		-1.02E+00	6.13E-05	Down	-1.19E+00	6.37E-06	Down	-1.62E+00	3.21E-09	Down				Unigene39990_All//4.00E-20//FL577046				
Unigene39991_All	510	7.08	2.38	3.13	8.69	4.39	5.84	2.16	3.03	2.58	-1.57E+00	5.65E-06	Down	-1.18E+00	6.34E-04	Down	-9.86E-01	2.31E-04		-5.73E-01	4.83E-02		4.92E-01	3.23E-01		2.58E-01	6.23E-01		Unigene39991_All//gi|297606541|ref|NP_001058631.2|//1.00E-44//Os06g0726600 [Oryza sativa Japonica Group] >gi|54291134|dbj|BAD61807.1| MAP kinase activating protein-like [Oryza sativa Japonica Group] >gi|255677415|dbj|BAF20545.2| Os06g0726600 [Oryza sativa Japonica Group]	Unigene39991_All//4.00E-61//AT4G38360| unknown protein	Unigene39991_All//1.00E-85//TC174598			GO:0031410//GO:0043231	nr +
Unigene39993_All	761	5.16	7.06	11.90	2.23	1.72	2.14	0.00	0.00	0.00	4.53E-01	8.22E-02		1.21E+00	4.39E-09	Up	-3.72E-01	4.82E-01		-5.89E-02	9.21E-01		null	null		null	null		Unigene39993_All//gi|115476344|ref|NP_001061768.1|//2.00E-30//Os08g0405700 [Oryza sativa Japonica Group] >gi|113623737|dbj|BAF23682.1| Os08g0405700 [Oryza sativa Japonica Group]	Unigene39993_All//3.00E-22//AT2G28660| copper-binding family protein				GO:0000041//GO:0009536//GO:0043169	nr -
Unigene39997_All	536	5.08	1.32	1.39	11.90	8.54	7.92	2.84	0.78	2.01	-1.94E+00	5.15E-06	Down	-1.87E+00	1.94E-05	Down	-4.77E-01	3.53E-02		-5.87E-01	1.15E-02		-1.86E+00	3.50E-04	Down	-5.01E-01	2.87E-01		Unigene39997_All//gi|297844940|ref|XP_002890351.1|//2.00E-27//glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata] >gi|297336193|gb|EFH66610.1| glycosyl transferase family 1 protein [Arabidopsis lyrata subsp. lyrata]		Unigene39997_All//0.00E+00//gi|164336394|gb|ES799882.1|ES799882			GO:0016740//GO:0043231	nr -
Unigene40000_All	434	13.50	4.90	3.93	12.51	7.38	11.86	44.52	20.22	10.46	-1.46E+00	2.26E-08	Down	-1.78E+00	2.38E-10	Down	-7.62E-01	1.40E-03		-7.67E-02	7.86E-01		-1.14E+00	1.09E-21	Down	-2.09E+00	4.13E-53	Down	Unigene40000_All//gi|225433375|ref|XP_002285608.1|//7.00E-20//PREDICTED: similar to GroEL-like chaperone, ATPase [Vitis vinifera]	Unigene40000_All//3.00E-12//AT3G23990| HSP60 (HEAT SHOCK PROTEIN 60); ATP binding	Unigene40000_All//0.00E+00//gi|11202099|gb|BF271104.1|BF271104		ko03018|RNA degradation	GO:0005515//GO:0006457//GO:0032559//GO:0043231//GO:0050896	nr +
Unigene40001_All	584	14.33	22.21	19.97	15.87	12.09	17.63	4.63	2.36	2.05	6.32E-01	5.33E-05		4.78E-01	5.85E-03		-3.92E-01	3.42E-02		1.52E-01	4.81E-01		-9.72E-01	4.54E-03		-1.18E+00	4.69E-04	Down				Unigene40001_All//1.00E-107//TC152831				
Unigene40003_All	538	4.08	2.35	4.85	4.26	3.90	1.60	0.63	1.94	2.07	-7.95E-01	6.58E-02		2.48E-01	5.65E-01		-1.26E-01	8.08E-01		-1.42E+00	9.93E-04	Down	1.63E+00	1.04E-02		1.72E+00	4.13E-03		Unigene40003_All//gi|228480908|gb|ACQ42220.1|//5.00E-70//R283 transcription factor MYB108-like protein 1 [Vitis vinifera]	Unigene40003_All//9.00E-54//AT5G49620| AtMYB78 (myb domain protein 78); DNA binding / transcription factor	Unigene40003_All//4.00E-82//gi|78345617|gb|DT565891.1|DT565891	MYB		GO:0001071//GO:0003676//GO:0006351//GO:0006970//GO:0009725//GO:0010468//GO:0043231//GO:0051707	nr +
Unigene40004_All	1088	0.00	0.00	0.00	0.00	0.00	2.45	3.07	6.88	31.45	null	null		null	null		null	null		1.13E+01	5.75E-16	Up	1.16E+00	3.66E-09	Up	3.36E+00	5.18E-155	Up	Unigene40004_All//gi|117957301|gb|ABK59085.1|//1.00E-109//peroxidase 1 [Sesbania rostrata]	Unigene40004_All//2.00E-85//AT5G38400| peroxidase, putative	Unigene40004_All//4.00E-142//DN817134		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0046872	nr +
Unigene40006_All	523	2.30	2.71	0.20	1.24	0.13	1.21	5.58	11.67	1.60	2.38E-01	6.50E-01		-3.50E+00	8.78E-05	Down	-3.23E+00	2.48E-03		-3.44E-02	9.53E-01		1.06E+00	1.03E-06	Up	-1.80E+00	2.59E-07	Down	Unigene40006_All//gi|4530126|gb|AAD21872.1|//2.00E-23//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene40006_All//2.00E-09//AT4G23150| protein kinase family protein	Unigene40006_All//3.00E-58//TC172433			GO:0000166//GO:0004672	nr -
Unigene40008_All	304	10.15	8.00	5.43	10.32	7.36	11.44	50.90	24.20	9.04	-3.44E-01	3.56E-01		-9.03E-01	1.51E-02		-4.88E-01	1.65E-01		1.48E-01	6.77E-01		-1.07E+00	5.26E-16	Down	-2.49E+00	7.52E-53	Down	Unigene40008_All//gi|300257527|gb|EFJ41774.1|//2.00E-09//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]		Unigene40008_All//1.00E-161//gi|164281481|gb|ES795614.1|ES795614		ko03010|Ribosome		nr +
Unigene40011_All	470	1.34	1.40	1.25	43.45	38.61	18.16	9.72	4.18	4.41	6.92E-02	9.50E-01		-1.00E-01	9.15E-01		-1.71E-01	2.01E-01		-1.26E+00	1.53E-23	Down	-1.22E+00	2.76E-06	Down	-1.14E+00	5.69E-06	Down				Unigene40011_All//5.00E-177//gi|164265263|gb|ES812241.1|ES812241				
Unigene40012_All	270	95.53	48.23	71.79	21.40	45.66	204.07	43.38	68.42	223.83	-9.86E-01	9.31E-19		-4.12E-01	2.07E-04		1.09E+00	1.96E-12	Up	3.25E+00	8.38E-208	Up	6.58E-01	1.10E-08		2.37E+00	1.78E-189	Up	Unigene40012_All//gi|74273617|gb|AB081476.1|//2.00E-31//ACC oxidase ACO4 [Gossypium hirsutum]	Unigene40012_All//7.00E-25//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene40012_All//6.00E-129//gi|21093896|gb|BQ406209.1|BQ406209		ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016641	nr +
Unigene40015_All	358	83.74	47.98	55.63	94.76	72.91	115.56	304.35	190.07	88.13	-8.04E-01	1.46E-15		-5.90E-01	6.12E-09		-3.78E-01	9.49E-06		2.86E-01	5.23E-04		-6.79E-01	5.87E-50		-1.79E+00	2.55E-240	Down	Unigene40015_All//gi|225431910|ref|XP_002276776.1|//4.00E-17//PREDICTED: similar to 60S ribosomal protein L29 [Vitis vinifera]	Unigene40015_All//4.00E-15//AT3G06680| 60S ribosomal protein L29 (RPL29B)	Unigene40015_All//0.00E+00//TC170288		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613//GO:0031981	nr +

Unigene40016_All	1095	0.33	1.06	1.65	0.09	0.72	0.12	5.10	4.81	6.88	1.67E+00	1.33E-02		2.31E+00	8.14E-05	Up	2.99E+00	2.96E-03		4.43E-01	8.61E-01		-8.37E-02	7.34E-01		4.32E-01	2.02E-02		Unigene40016_All//gi|164521127|gb|ABY60423.1|//3.00E-54//dormancy associated MADS-box 2 [Euphorbia esula]	Unigene40016_All//3.00E-38//AT2G22540| SVP (SHORT VEGETATIVE PHASE); transcription factor/ translation repressor, nucleic acid binding	Unigene40016_All//2.00E-45//gi|84151065|gb|DS800420.1|DS800420	MADS		GO:0001071//GO:0003677//GO:0006350//GO:0009628//GO:0009908//GO:0010074//GO:0010468//GO:0030371//GO:0043231	nr +
Unigene40019_All	1057	2.48	6.04	1.31	0.71	0.81	1.20	8.24	10.00	49.26	1.29E+00	1.45E-07	Up	-9.18E-01	2.49E-02		2.04E-01	8.40E-01		7.59E-01	2.30E-01		2.80E-01	9.05E-02		2.58E+00	2.18E-180	Up	Unigene40019_All//gi|30017255|gb|AAP12861.1|//3.00E-67//At2g40095 [Arabidopsis thaliana]	Unigene40019_All//5.00E-63//AT2G40095| unknown protein	Unigene40019_All//0.00E+00//gi|84152465|gb|DN801820.1|DN801820			GO:0003824//GO:0009267	nr +
Unigene40002_All	1372	13.08	9.64	11.29	16.88	10.49	11.03	19.48	12.89	7.55	-4.40E-01	7.61E-04		-2.12E-01	1.44E-01		-6.86E-01	4.01E-11		-6.15E-01	2.40E-08		-5.96E-01	2.23E-10		-1.37E+00	1.80E-40	Down	Unigene4002_All//gi|21592979|gb|AAM64928.1|//1.00E-144//galactose-1-phosphate uridyl transferase-like protein [Arabidopsis thaliana]	Unigene4002_All//8.00E-117//AT5G18200| UTP:galactose-1-phosphate uridylyltransferase/ ribose-5-phosphate adenylyltransferase	Unigene4002_All//0.00E+00//TC162313		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism		nr -
Unigene40020_All	359	1.17	1.98	7.27	0.97	0.96	1.51	3.30	2.44	2.22	7.61E-01	3.62E-01		2.64E+00	1.14E-07	Up	-1.81E-02	9.58E-01		6.36E-01	5.61E-01		-4.32E-01	4.54E-01		-5.71E-01	2.93E-01				Unigene40020_All//0.00E+00//BF277006					
Unigene40024_All	1402	0.00	0.00	0.00	0.00	0.00	0.00	4.31	6.44	0.00	null	null		null	null		null	null		null	null		5.78E-01	7.02E-04		-1.21E+01	1.79E-44	Down	Unigene40024_All//gi|242070913|ref|XP_002450733.1|//4.00E-13//hypothetical protein SORBIDRAFT_05g016477 [Sorghum bicolor]>gi|241936576|gb|EES09721.1|hypothetical protein SORBIDRAFT_05g016477 [Sorghum bicolor]		Unigene40024_All//1.00E-53//gi|78348172|gb|DT568446.1|DT568446				nr +
Unigene40027_All	263	35.61	13.10	19.23	60.80	51.98	54.78	60.93	40.68	40.75	-1.44E+00	1.09E-12	Down	-8.89E-01	5.95E-06		-2.26E-01	1.22E-01		-1.50E-01	3.62E-01		-5.83E-01	2.52E-06		-5.80E-01	1.64E-06		Unigene40027_All//gi|56784185|dbj|BAD81570.1|//7.00E-42//clathrin-associated protein unc-101-like [Oryza sativa Japonica Group]>gi|56785137|dbj|BAD81792.1|clathrin-associated protein unc-101-like [Oryza sativa Japonica Group]	Unigene40027_All//8.00E-43//AT1G60780| HAP13 (HAPLESS 13); protein binding	Unigene40027_All//4.00E-142//TC139619			GO:0005488//GO:0015031//GO:0030118//GO:0030119	nr -
Unigene40028_All	597	0.00	17.74	0.00	1.92	1.90	5.98	0.42	7.07	10.54	1.41E+01	1.07E-60	Up	null	null		-1.18E-02	9.64E-01		1.64E+00	2.01E-06	Up	4.06E+00	2.54E-22	Up	4.63E+00	1.32E-36	Up	Unigene40028_All//gi|297834362|ref|XP_002885063.1|//5.00E-13//zinc finger family protein [Arabidopsis lyrata subsp. lyrata]>gi|297330903|gb|EFH61322.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40028_All//1.00E-11//AT1G60360| zinc finger (C3HC4-type RING finger) family protein	Unigene40028_All//0.00E+00//TC175063			GO:0005488	nr +
Unigene4003_All	1611	6.37	17.52	7.80	4.64	8.36	12.45	6.80	14.14	20.65	1.46E+00	3.01E-37	Up	2.93E-01	9.00E-02		8.50E-01	4.18E-09		1.42E+00	2.02E-27	Up	1.06E+00	1.35E-22	Up	1.60E+00	1.03E-62	Up	Unigene4003_All//gi|88196763|gb|ABD43024.1|//1.00E-33//At4g01960 [Arabidopsis thaliana]	Unigene4003_All//3.00E-16//AT4G01960| unknown protein	Unigene4003_All//0.00E+00//TC133809				nr -
Unigene40034_All	315	0.50	4.66	3.21	4.90	3.72	4.44	0.94	1.99	0.63	3.23E+00	1.15E-05	Up	2.69E+00	2.09E-03		-3.99E-01	4.68E-01		-1.41E-01	7.94E-01		1.08E+00	1.99E-01		-5.71E-01	6.28E-01									ESTscan +
Unigene40036_All	321	14.67	14.84	24.72	8.22	14.16	20.82	28.58	20.05	45.92	1.65E-02	9.75E-01		7.53E-01	4.37E-04		7.84E-01	4.25E-03		1.34E+00	1.01E-08	Up	-5.11E-01	2.59E-03		6.84E-01	8.91E-08		Unigene40036_All//gi|222424262|dbj|BAH20088.1|//5.00E-18//AT3G58610 [Arabidopsis thaliana]	Unigene40036_All//1.00E-16//AT3G58610| ketol-acid reductoisomerase	Unigene40036_All//6.00E-160//TC148331		ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis	GO:0003824//GO:0005576//GO:0008652//GO:0009526//GO:0009532//GO:0010038//GO:0030312//GO:0042802//GO:0046914//GO:0050661	nr -
Unigene40040_All	1032	0.51	0.00	0.41	0.97	0.80	1.40	4.55	0.85	2.05	-8.99E+00	2.92E-03		-2.97E-01	7.50E-01		-2.70E-01	7.00E-01		5.37E-01	3.76E-01		-2.42E+00	1.78E-15	Down	-1.15E+00	3.35E-06	Down	Unigene40040_All//gi|42571241|ref|NP_973694.1|//1.00E-143//DTA2 (DOWNSTREAM TARGET OF AGL15 2) [Arabidopsis thaliana]>gi|49117445|gb|AAS49047.1|At2g45830 [Arabidopsis thaliana]>gi|46931276|gb|AAT06442.1|At2g45830 [Arabidopsis thaliana]	Unigene40040_All//2.00E-144//AT2G45830| DTA2 (DOWNSTREAM TARGET OF AGL15 2)					nr +
Unigene40043_All	302	1.56	1.85	3.00	3.30	1.25	2.24	4.62	3.18	1.32	2.43E-01	7.77E-01		9.43E-01	2.26E-01		-1.40E+00	3.79E-02		-5.57E-01	4.47E-01		-5.38E-01	3.07E-01		-1.81E+00	6.10E-04	Down	Unigene40043_All//gi|115455355|ref|NP_001051278.1|//6.00E-49//Os03g0749800 [Oryza sativa Japonica Group]>gi|113549749|dbj|BAF13192.1|Os03g0749800 [Oryza sativa Japonica Group]	Unigene40043_All//6.00E-45//AT5G20930| TSL (TOUSLED); kinase/ protein serine/threonine kinase	Unigene40043_All//1.00E-117//gi|21096091|gb|BQ408404.1|BQ408404			GO:0004672//GO:0006464//GO:0032559//GO:0043231	nr +
Unigene40045_All	352	18.73	19.86	18.00	77.98	55.27	57.61	89.24	65.42	41.54	8.50E-02	7.13E-01		-5.71E-02	8.16E-01		-4.97E-01	1.60E-07		-4.37E-01	1.45E-05		-4.48E-01	1.66E-07		-1.10E+00	4.48E-34	Down	Unigene40045_All//gi|211906438|gb|ACJ11712.1|//4.00E-07//UDP-D-glucose dehydrogenase [Gossypium hirsutum]	Unigene40045_All//1.00E-07//AT5G39320| UDP-glucose 6-dehydrogenase, putative	Unigene40045_All//0.00E+00//gi|11204424|gb|BF273354.1|BF273354		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene40046_All	712	0.73	2.92	1.72	1.47	1.50	0.70	7.07	3.17	2.57	1.99E+00	7.20E-05	Up	1.23E+00	6.00E-02		2.93E-02	9.80E-01		-1.07E+00	1.19E-01		-1.16E+00	2.23E-06	Down	-1.46E+00	4.43E-09	Down			Unigene40046_All//0.00E+00//TC177610					
Unigene40047_All	455	63.70	13.25	4.92	49.05	47.60	26.70	0.74	0.28	7.79	-2.27E+00	1.07E-69	Down	-3.70E+00	3.72E-111	Down	-4.31E-02	7.91E-01		-8.77E-01	1.81E-14		-1.43E+00	2.58E-01		3.39E+00	9.25E-17	Up			Unigene40047_All//4.00E-131//DT459120					
Unigene40048_All	3399	0.05	0.00	0.00	0.03	0.02	0.08	13.15	3.65	15.66	-5.53E+00	2.15E-01		-5.53E+00	2.44E-01		-5.29E-01	8.16E-01		1.44E+00	4.09E-01		-1.85E+00	1.47E-100	Down	2.52E-01	7.83E-05		Unigene40048_All//gi|225442485|ref|XP_002278313.1|//0.00E+00//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene40048_All//0.00E+00//AT1G59870| PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	Unigene40048_All//0.00E+00//TC136716		ko03040|Spliceosome//ko02010|ABC transporters	GO:0000041//GO:0000166//GO:0009526//GO:0009941//GO:0015082//GO:0016020//GO:0016887//GO:0019762//GO:0050832//GO:0052482//GO:0071365	nr +
Unigene40049_All	653	5.29	1.94	3.34	0.99	1.05	1.24	0.00	0.00	0.12	-1.45E+00	3.41E-05	Down	-6.62E-01	5.75E-02		8.89E-02	9.49E-01		3.28E-01	7.01E-01		null	null		6.93E+00	4.04E-01		Unigene40049_All//gi|13899099|gb|AAK48971.1|AF370544_1/3.00E-35//cyclin delta-3 [Arabidopsis thaliana]>gi|20148339|gb|AAM10060.1| cyclin delta-3 [Arabidopsis thaliana]>gi|110738184|dbj|BAF01023.1|cyclin delta-3 [Arabidopsis thaliana]	Unigene40049_All//2.00E-36//AT4G34090| unknown protein	Unigene40049_All//7.00E-177//gi|48739377|gb|CO069896.1|CO069896			GO:0009532	nr -
Unigene4005_All	1412	19.08	14.53	19.01	15.45	13.34	8.86	47.37	20.90	26.55	-3.93E-01	1.74E-04		-5.70E-03	9.85E-01		-2.12E-01	8.25E-02		-8.02E-01	3.05E-12		-1.18E+00	1.86E-77	Down	-8.35E-01	2.73E-45		Unigene4005_All//gi|115444011|ref|NP_001045785.1|//7.00E-67//Os02g0130600 [Oryza sativa Japonica Group]>gi|113535316|dbj|BAF07699.1|Os02g0130600 [Oryza sativa Japonica Group]	Unigene4005_All//6.00E-102//AT2G47115| unknown protein	Unigene4005_All//0.00E+00//TC141159				nr +
Unigene40051_All	547	1750.02	521.98	1195.64	235.96	336.29	167.86	2.47	1.30	1.75	-1.75E+00	0.00E+00	Down	-5.50E-01	8.22E-236		5.11E-01	2.76E-49		-4.91E-01	2.45E-29		-9.29E-01	7.36E-02		-5.01E-01	3.22E-01		Unigene40051_All//gi|297840471|ref|XP_002888117.1|//1.00E-39//fed A [Arabidopsis lyrata subsp. lyrata]>gi|297333958|gb|EFH64376.1| fed A [Arabidopsis lyrata subsp. lyrata]	Unigene40051_All//8.00E-38//AT1G60950| FED A; 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding	Unigene40051_All//0.00E+00//TC152952		ko00195|Photosynthesis	GO:0006091//GO:0009532//GO:0043169//GO:0051536	nr -
Unigene40052_All	501	1.46	1.21	0.00	11.34	1.65	3.52	15.19	2.84	2.54	-2.69E-01	7.19E-01		-1.05E+01	4.13E-04	Down	-2.78E+00	3.92E-22	Down	-1.69E+00	1.76E-10	Down	-2.42E+00	1.08E-24	Down	-2.58E+00	2.21E-27	Down	Unigene40052_All//gi|224117684|ref|XP_002317642.1|//1.00E-89//aquaporin, MIP family, NIP subfamily [Populus trichocarpa]>gi|222860707|gb|EEE98254.1|aquaporin, MIP family, NIP subfamily [Populus trichocarpa]	Unigene40052_All//2.00E-18//AT4G10380| NIP5;1; arsenite transmembrane transporter/ boron transporter/ water channel	Unigene40052_All//2.00E-90//TC138001			GO:0005372//GO:0010036//GO:0015103//GO:0015166//GO:0015563//GO:0015698//GO:0031224//GO:0042887//GO:0043231//GO:0044459	nr -
Unigene40053_All	811	1.42	1.37	1.12	3.69	0.76	1.45	5.63	2.73	10.27	-4.63E-02	9.53E-01		-3.47E-01	6.16E-01		-2.27E+00	2.15E-09	Down	-1.35E+00	2.30E-04	Down	-1.04E+00	4.31E-05	Down	8.67E-01	9.70E-07		Unigene40053_All//gi|224091959|ref|XP_002309417.1|//8.00E-71//NAC domain protein, IPR003441 [Populus trichocarpa]>gi|222855393|gb|EEE92940.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene40053_All//8.00E-55//AT5G22380| anac090 (Arabidopsis NAC domain containing protein 90); transcription factor	Unigene40053_All//0.00E+00//gi|48777712|gb|CO087078.1|CO087078	NAC		GO:0003676//GO:0010468	nr +
Unigene40055_All	449	508.76	313.83	387.34	57.47	66.42	76.45	27.40	60.97	41.97	-6.97E-01	7.06E-89		-3.93E-01	8.91E-31		2.09E-01	4.08E-02		4.12E-01	4.07E-06		1.15E+00	5.41E-31	Up	6.15E-01	3.49E-08				Unigene40055_All//2.00E-170//CO079993					
Unigene40057_All	477	0.77	0.64	0.22	3.55	2.45	0.66	4.43	13.93	4.18	-2.69E-01	8.01E-01		-1.78E+00	2.34E-01		-5.33E-01	3.00E-01		-2.42E+00	2.78E-05	Down	1.65E+00	2.02E-13	Up	-8.58E-02	8.24E-01				Unigene40057_All//4.00E-14//EV488869					
Unigene40059_All	1289	0.41	0.55	0.54	12.91	8.84	6.48	3.02	0.49	1.42	4.39E-01	6.16E-01		4.04E-01	6.09E-01		-5.46E-01	1.40E-05		-9.94E-01	2.40E-13		-2.63E+00	3.51E-14	Down	-1.09E+00	6.94E-05	Down	Unigene40059_All//gi|87240518|gb|AB032376.1|//1.00E-125//Lipolytic enzyme, G-D-S-L [Medicago truncatula]>gi|124361052|gb|ABN09024.1|Lipolytic enzyme, G-D-S-L [Medicago truncatula]	Unigene40059_All//5.00E-123//AT1G54790| GDSL-motif lipase/hydrolase family protein	Unigene40059_All//0.00E+00//TC159845				nr +
Unigene4006_All	1626	0.26	9.69	3.34	1.69	2.41	16.08	92.73	179.75	139.75	5.23E+00	1.17E-77	Up	3.70E+00	4.29E-21	Up	5.19E-01	9.78E-02		3.25E+00	1.11E-98	Up	9.55E-01	1.01E-237		5.92E-01	7.05E-83		Unigene4006_All//gi|288310302|gb|ADC45390.1|//1.00E-152//branched chain amino acid transaminase [Cucumis melo]	Unigene4006_All//6.00E-146//AT1G10070| ATBCAT-2 (ARABIDOPSIS THALIANA BRANCHED-CHAIN AMINO ACID TRANSAMINASE 2); branched-chain-amino-acid transaminase/ catalytic	Unigene4006_All//0.00E+00//TC137798		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene40062_All	879	0.00	0.00	0.00	0.00	0.00	0.00	3.51	10.70	18.81	null	null		null	null		null	null		null	null		1.61E+00	5.60E-18	Up	2.42E+00	9.82E-54	Up	Unigene40062_All//gi|158828300|gb|ABW81175.1|//5.00E-09//non-LTR retrotransposon transposase [Arabidopsis cebennensis]	Unigene40062_All//5.00E-06//AT5G42905| nucleic acid binding / ribonuclease H					nr -
Unigene40063_All	833	0.69	0.61	0.64	1.91	1.94	1.30	0.25	0.70	3.06	-1.84E-01	8.25E-01		-1.12E-01	9.07E-01		2.19E-02	9.79E-01		-5.56E-01	3.10E-01		1.47E+00	1.02E-01		3.59E+00	8.40E-13	Up	Unigene40063_All//gi|297846200|ref|XP_002890981.1|//5.00E-86//ATMKK10 [Arabidopsis lyrata subsp. lyrata]>gi|297336823|gb|EFH67240.1|ATMKK10 [Arabidopsis lyrata subsp. lyrata]	Unigene40063_All//9.00E-83//AT1G32320| ATMKK10; MAP kinase kinase/ kinase	Unigene40063_All//9.00E-106//TC178080		ko04626|Plant-pathogen interaction	GO:0000160//GO:0000166//GO:0004712//GO:0006468//GO:0006555//GO:0006970//GO:0009700//GO:0010557//GO:0019887	nr -
Unigene40064_All	705	4.60	3.16	4.99	3.96	2.74	3.40	2.58	1.48	0.45	-5.41E-01	1.20E-01		1.16E-01	7.30E-01		-5.33E-01	1.56E-01		-2.21E-01	6.23E-01		-7.99E-01	6.56E-02		-2.51E+00	6.12E-07	Down	Unigene40064_All//gi|115480663|ref|NP_001063925.1|//7.00E-38//Os09g0560300 [Oryza sativa Japonica Group]>gi|113632158|dbj|BAF25839.1|Os09g0560300 [Oryza sativa Japonica Group]	Unigene40064_All//4.00E-33//AT4G00585| unknown protein	Unigene40064_All//0.00E+00//TC163534			GO:0005746//GO:0030964//GO:0043094	nr -
Unigene40065_All	596	2.63	0.68	2.32	3.59	4.56	2.12	2.27	1.47	3.61	-1.95E+00	7.99E-04	Down	-1.81E-01	7.22E-01		3.45E-01	4.17E-01		-7.60E-01	8.66E-02		-6.24E-01	2.33E-01		6.69E-01	7.75E-02		Unigene40065_All//gi|30684602|ref|NP_850606.1|//1.00E-11//ATRBL14 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 14); zinc ion binding [Arabidopsis thaliana]>gi|75247670|sp|Q8RXW0.1|Y3761_ARATH RecName: Full=Uncharacterized protein At3g17611	Unigene40065_All//5.00E-05//AT3G17611| ATRBL14 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 14); zinc ion binding	Unigene40065_All//8.00E-87//gi|78346546|gb|DT566820.1|DT566820			GO:0031224//GO:0046914	nr -
Unigene40066_All	348	0.60	5.53	4.59	1.43	9.99	5.06	0.24	2.40	2.18	3.20E+00	3.42E-07	Up	2.93E+00	2.09E-05	Up	2.80E+00	2.37E-12	Up	1.82E+00	6.24E-04	Up	3.31E+00	3.10E-04	Up	3.16E+00	6.82E-04	Up			Unigene40066_All//2.00E-117//EV488733					
Unigene40067_All	442	4.14	8.83	7.95	14.31	15.43	20.74	0.38	0.66	0.81	1.09E+00	5.36E-04	Up	9.41E-01	6.30E-03		1.08E-01	6.99E-01		5.35E-01	4.71E-03		7.91E-01	5.63E-01		1.08E+00	3.50E-01				Unigene40067_All//3.00E-119//EX167392					
Unigene40068_All	456	1.72	1.67	0.00	2.95	1.21	2.28	1.30	0.73	1.57	-4.62E-02	9.66E-01		-1.07E+01	2.21E-04	Down	-1.29E+00	2.02E-02		-3.73E-01	5.53E-01		-8.24E-01	3.48E-01		2.77E-01	6.90E-01		Unigene40068_All//gi|115453829|ref|NP_001050515.1|//3.00E-24//Os03g0569800 [Oryza sativa Japonica Group]>gi|113548986|dbj|BAF12429.1|Os03g0569800 [Oryza sativa Japonica Group]	Unigene40068_All//6.00E-56//AT1G30290| unknown protein	Unigene40068_All//1.00E-121//ES824293			GO:0043231	nr +

Unigene4007_All	1296	35.85	18.26	27.61	31.25	34.36	36.56	3.26	4.06	9.44	-9.73E-01	1.72E-32		-3.77E-01	2.60E-06		1.37E-01	1.15E-01		2.26E-01	3.94E-03		3.17E-01	2.03E-01		1.53E+00	3.72E-22	Up	Unigene4007_All//gi|224055285|ref|XP_002298461.1|//1.00E-120//f-box family protein [Populus trichocarpa] >gi|222845719|gb|EEE83266.1| f-box family protein [Populus trichocarpa]	Unigene4007_All//9.00E-107//AT2G32560| F-box family protein	Unigene4007_All//0.00E+00//gi|78348152|gb|DT568426.1|DT568426				nr -
Unigene40070_All	364	66.69	27.70	43.01	127.27	130.84	169.73	178.06	93.47	74.86	-1.27E+00	3.79E-26	Down	-6.33E-01	2.92E-08		3.98E-02	6.98E-01		4.15E-01	1.23E-10		-9.30E-01	4.74E-51		-1.25E+00	1.82E-84	Down	Unigene40070_All|gi|225431804|ref|XP_002272727.1|//1.00E-42//PREDICTED: similar to 60S ribosomal protein L19 [Vitis vinifera]	Unigene40070_All//7.00E-40//AT3G16780| 60S ribosomal protein L19 (RPL19B)	Unigene40070_All//1.00E-173//gi|78343954|gb|DT564228.1|DT564228		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene40071_All	710	0.66	0.14	0.23	3.37	0.87	1.27	1.19	0.59	1.40	-2.22E+00	7.76E-02		-1.56E+00	2.04E-01		-1.95E+00	2.46E-06	Down	-1.40E+00	8.07E-04	Down	-1.02E+00	1.41E-01		2.36E-01	6.82E-01		Unigene40071_All|gi|22327586|ref|NP_680395.1|//9.00E-37//mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana]	Unigene40071_All//7.00E-67//AT4G19650| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Mitochodrial transcription termination factor-related (InterPro:IPR003690); BEST Arabidopsis thaliana protein match is: mitochondrial transcription termination factor-related / mTERF-related (TAIR:AT5G45113.1); Has 110 Blast hits to 107 proteins in 9 species: Archae - 0; Bacteria - 2; Metazoa - 3; Fungi - 0; Plants - 105; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene40075_All	384	41.42	29.82	41.46	53.97	56.85	68.69	145.23	89.90	67.85	-4.74E-01	6.86E-04		1.50E-03	9.91E-01		7.52E-02	6.16E-01		3.48E-01	9.45E-04		-6.92E-01	8.39E-27		-1.10E+00	2.55E-59	Down	Unigene40075_All|gi|82623413|gb|AB887121.1|//1.00E-26//ribosomal protein S27-like protein-like [Solanum tuberosum]	Unigene40075_All//3.00E-27//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome	Unigene40075_All//0.00E+00//TC159451		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0022613//GO:0030312//GO:0043169	nr -
Unigene40076_All	470	42.52	20.48	20.96	4.35	7.03	3.08	0.27	0.00	0.25	-1.05E+00	2.56E-16	Down	-1.02E+00	7.34E-15	Down	6.95E-01	4.01E-02		-4.99E-01	2.99E-01		-8.08E+00	2.35E-01		-8.59E-02	9.69E-01		Unigene40076_All|gi|21592651|gb|AM64600.1|//8.00E-30//rhodanese-like family protein [Arabidopsis thaliana]	Unigene40076_All//1.00E-27//AT3G08920| rhodanese-like domain-containing protein	Unigene40076_All//0.00E+00//CA993825			GO:0009536	nr +
Unigene40077_All	481	62.55	23.81	25.46	33.76	29.71	43.85	24.26	183.87	50.44	-1.39E+00	3.44E-37	Down	-1.30E+00	4.13E-32	Down	-1.84E-01	2.25E-01		3.77E-01	1.54E-03		2.92E+00	0.00E+00	Up	1.06E+00	1.42E-24	Up	Unigene40077_All|gi|34099827|gb|AAQ57202.1|//3.00E-36//adenosine 5' phosphosulfate reductase [Populus tremula x Populus alba]	Unigene40077_All//3.00E-27//AT4G04610| APR1 (APS REDUCTASE 1); adenylyl-sulfate reductase	Unigene40077_All//0.00E+00//TC149017			GO:0000097//GO:0000103//GO:0009532//GO:0016671//GO:0019725//GO:0031976	nr +
Unigene40078_All	825	0.76	0.25	1.10	13.95	7.47	4.87	2.46	1.72	2.03	-1.63E+00	9.23E-02		5.28E-01	4.79E-01		-9.01E-01	5.59E-09		-1.52E+00	8.90E-18	Down	-5.14E-01	2.21E-01		-2.79E-01	5.01E-01					Unigene40078_All//2.00E-174//C0120076				
Unigene4008_All	1322	4.35	11.04	5.52	7.20	6.56	5.53	7.29	7.49	5.48	1.34E+00	2.41E-17	Up	3.42E-01	1.44E-01		-1.33E-01	5.67E-01		-3.79E-01	4.74E-02		3.92E-02	8.36E-01		-4.11E-01	1.09E-02		Unigene4008_All|gi|115447531|ref|NP_001047545.1|//1.00E-63//Os02g0640200 [Oryza sativa Japonica Group] >gi|113537076|dbj|BAF09459.1|Os02g0640200 [Oryza sativa Japonica Group]		Unigene4008_All//0.00E+00//TC153539				nr -
Unigene40082_All	649	0.00	1.02	0.16	24.41	15.02	16.49	13.81	23.06	27.38	9.99E+00	6.25E-04	Up	7.36E+00	3.98E-01		-7.01E-01	4.72E-08		-5.66E-01	3.33E-05		7.39E-01	1.20E-08		9.87E-01	2.03E-16		Unigene40082_All|gi|297848908|ref|XP_002892335.1|//4.00E-37//agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297338177|gb|EFH68594.1|agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene40082_All//9.00E-34//AT1G06340| agenet domain-containing protein	Unigene40082_All//0.00E+00//TC164739				nr +
Unigene40083_All	783	0.00	0.00	0.00	1.53	0.09	8.13	0.32	0.96	1.63	null	null		null	null		-4.12E+00	7.48E-07	Down	2.41E+00	7.72E-18	Up	1.57E+00	4.21E-02		2.33E+00	1.17E-04	Up	Unigene40083_All|gi|162461600|ref|NP_001105417.1|//2.00E-14//extensin precursor [Zea mays] >gi|119712|sp|P14918.1|EXTN_MAIZE RecName: Full=Extensin; AltName: Full=Proline-rich glycoprotein; Flags: Precursor >gi|226756|prf||1604465A cell wall protein	Unigene40083_All//2.00E-11//AT5G14920| gibberellin-regulated family protein	Unigene40083_All//3.00E-19//gi|109886045|gb|DW515015.1|DW515015		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0044464	nr -
Unigene40084_All	1416	0.00	0.00	0.00	1.23	0.00	2.11	0.60	0.83	2.87	null	null		null	null		-1.03E+01	5.67E-13	Down	7.74E-01	3.47E-02		4.69E-01	4.16E-01		2.26E+00	8.67E-13	Up	Unigene40084_All|gi|115434038|ref|NP_001041777.1|//2.00E-09//Os01g0106600 [Oryza sativa Japonica Group] >gi|113531308|dbj|BAF03691.1|Os01g0106600 [Oryza sativa Japonica Group]	Unigene40084_All//3.00E-25//AT2G44630| unknown protein	Unigene40084_All//8.00E-52//gi|109874804|gb|DW503778.1|DW503778				nr +
Unigene40085_All	442	2.84	4.93	2.77	3.94	0.55	0.92	2.87	4.92	3.61	7.95E-01	6.74E-02		-3.60E-02	9.71E-01		-2.85E+00	3.02E-07	Down	-2.10E+00	1.14E-04	Down	7.77E-01	4.63E-02		3.29E-01	4.87E-01		Unigene40085_All|gi|145335397|ref|NP_172597.2|//4.00E-30//ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene40085_All//8.00E-27//AT1G11300| ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene40085_All//2.00E-129//C0081719		ko04626|Plant-pathogen interaction		nr +
Unigene40086_All	615	13.95	27.93	17.14	20.82	18.81	29.67	41.11	106.77	48.39	1.00E+00	5.26E-13	Up	2.97E-01	1.23E-01		-1.46E-01	4.23E-01		5.11E-01	5.53E-05		1.38E+00	2.73E-96	Up	2.35E-01	8.06E-03		Unigene40086_All|gi|224137404|ref|XP_002322549.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222867179|gb|EEF04310.1|predicted protein [Populus trichocarpa]	Unigene40086_All//8.00E-05//AT3G22200| POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase/ 4-aminobutyrate:pyruvate transaminase	Unigene40086_All//4.00E-135//gi|164291588|gb|EV486291.1|EV486291				nr -
Unigene40087_All	446	23.11	11.02	25.19	12.62	8.57	8.81	1.04	0.56	0.98	-1.07E+00	5.65E-09	Down	1.24E-01	5.32E-01		-5.58E-01	1.99E-02		-5.19E-01	4.07E-02		-8.91E-01	3.83E-01		-8.58E-02	9.34E-01		Unigene40087_All|gi|240256063|ref|NP_194259.4|//3.00E-15//DNA photolyase [Arabidopsis thaliana]	Unigene40087_All//9.00E-16//AT4G25290| DNA photolyase	Unigene40087_All//3.00E-110//gi|109850492|gb|DW479471.1|DW479471			GO:0006259//GO:0016829//GO:0043231	nr +
Unigene40088_All	671	5.77	1.81	6.03	0.74	3.23	2.09	0.13	0.50	0.00	-1.67E+00	7.24E-07	Down	6.39E-02	8.40E-01		2.12E+00	7.65E-06	Up	1.49E+00	1.20E-02		1.98E+00	1.44E-01		-6.98E+00	3.58E-01		Unigene40088_All|gi|115489594|ref|NP_001067284.1|//7.00E-07//Os12g0616800 [Oryza sativa Japonica Group] >gi|77557066|gb|ABA99862.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|77557067|gb|ABA99863.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649791|dbj|BAF30303.1|Os12g0616800 [Oryza sativa Japonica Group]	Unigene40088_All//5.00E-08//AT2G34610| unknown protein	Unigene40088_All//0.00E+00//TC145035				nr -
Unigene40089_All	393	97.19	212.48	162.46	55.64	50.82	35.40	196.34	283.64	99.04	1.13E+00	3.29E-73	Up	7.41E-01	3.69E-27		-1.31E-01	3.23E-01		-6.53E-01	9.67E-09		5.31E-01	4.13E-33		-9.87E-01	8.52E-69					Unigene40089_All//0.00E+00//gi|82756240|gb|DV849802.1|DV849802				
Unigene4009_All	1363	68.71	27.84	51.96	39.62	36.76	23.49	0.12	0.12	0.06	-1.30E+00	2.82E-103	Down	-4.03E-01	1.52E-13		-1.08E-01	1.77E-01		-7.54E-01	1.78E-26		-1.64E-02	1.02E+00		-1.09E+00	5.52E-01		Unigene4009_All|gi|166865122|gb|AB201816.1|//0.00E+00//cinnamyl alcohol dehydrogenase [Gossypium hirsutum] >gi|211906488|gb|ACJ11737.1|mannitol dehydrogenase [Gossypium hirsutum]	Unigene4009_All//2.00E-148//AT4G39330| CAD9 (CINNAMYL ALCOHOL DEHYDROGENASE 9); binding / catalytic/ oxidoreductase/ zinc ion binding	Unigene4009_All//0.00E+00//TC145297		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene40091_All	915	9.61	35.44	15.77	88.79	96.00	98.67	427.75	61.57	199.80	1.88E+00	4.71E-61	Up	7.15E-01	2.77E-06		1.13E-01	5.68E-02		1.52E-01	7.36E-03		-2.80E+00	0.00E+00	Down	-1.10E+00	0.00E+00	Down	Unigene40091_All|gi|110816009|gb|AB691752.1|//7.00E-50//HyPRP2 [Gossypium hirsutum]	Unigene40091_All//3.00E-35//AT1G62510| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene40091_All//0.00E+00//gi|109827204|gb|DW225901.1|DW225901			GO:0005488//GO:0006810//GO:0016020//GO:0031410	nr -
Unigene40092_All	1626	1.74	0.25	0.20	1.10	0.19	0.00	8.68	10.87	4.02	-2.80E+00	3.39E-09	Down	-3.14E+00	1.08E-09	Down	-2.53E+00	1.40E-06	Down	-1.01E+01	3.23E-11	Down	3.24E-01	6.91E-03		-1.11E+00	5.36E-16	Down	Unigene40092_All|gi|35187439|gb|AAQ84311.1|//7.00E-41//fiber protein Fb17 [Gossypium barbadense]	Unigene40092_All//2.00E-05//AT2G20950| EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Phospholipase-like, arabidopsis (InterPro:IPR007942); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G38550.1); Has 618 Blast hits to 562 proteins in 105 species: Archae - 7; Bacteria - 22; Metazoa - 391; Fungi - 75; Plants - 96; Viruses - 2; Other Eukaryotes - 25 (source: NCBI BLink).	Unigene40092_All//1.00E-26//TC149710				nr +
Unigene40095_All	622	535.15	1084.75	1101.30	47.17	61.78	63.61	1.70	1.08	0.32	1.02E+00	0.00E+00	Up	1.04E+00	0.00E+00	Up	3.89E-01	1.23E-06		4.31E-01	1.66E-07		-6.61E-01	2.78E-01		-2.41E+00	3.46E-04	Down	Unigene40095_All|gi|98961027|gb|AB758997.1|//2.00E-17//At5g55620 [Arabidopsis thaliana]	Unigene40095_All//3.00E-18//AT5G55620| unknown protein	Unigene40095_All//0.00E+00//gi|84165095|gb|DR453743.1|DR453743				nr +
Unigene40105_All	487	2.04	6.87	3.06	1.53	2.05	2.04	2.60	1.20	2.86	1.75E+00	2.41E-06	Up	5.85E-01	3.07E-01		4.19E-01	5.85E-01		4.11E-01	6.02E-01		-1.12E+00	3.93E-02		1.37E-01	7.79E-01					Unigene40105_All//0.00E+00//gi|109875159|gb|DW504133.1|DW504133				
Unigene40106_All	671	13.10	4.83	11.11	6.38	4.72	2.42	0.19	0.19	0.12	-1.44E+00	6.57E-12	Down	-2.38E-01	2.73E-01		-4.35E-01	1.40E-01		-1.40E+00	2.90E-06	Down	-1.61E-02	1.02E+00		-6.71E-01	7.19E-01		Unigene40106_All|gi|37921345|gb|AP55675.1|//9.00E-10//geranylgeranyl reductase [Prunus persica]	Unigene40106_All//8.00E-09//AT1G74470| geranylgeranyl reductase	Unigene40106_All//2.00E-38//TC148880		ko00900|Terpenoid backbone biosynthesis//ko00860|Porphyrin and chlorophyll metabolism	GO:0006399//GO:0006779//GO:0016491//GO:0030554	nr -
Unigene40108_All	394	12.22	2.57	4.73	3.92	6.38	3.67	0.32	0.00	0.00	-2.25E+00	5.30E-12	Down	-1.37E+00	4.29E-06	Down	7.03E-01	8.12E-02		-9.56E-02	8.64E-01		-8.33E+00	2.35E-01		-8.33E+00	2.00E-01		Unigene40108_All|gi|108862372|gb|AB496334.2|//1.00E-27//WW domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene40108_All//3.00E-07//AT4G08910| unknown protein	Unigene40108_All//4.00E-146//gi|11208468|gb|BF277398.1|BF277398				nr -
Unigene40111_All	1005	1.98	4.49	3.02	1.73	2.09	0.90	3.58	5.07	3.41	1.18E+00	5.48E-05	Up	6.10E-01	1.05E-01		2.69E-01	5.94E-01		-9.49E-01	5.80E-02		5.05E-01	3.53E-02		-6.89E-02	8.13E-01		Unigene40111_All|gi|224107357|ref|XP_002333530.1|//2.00E-23//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837125|gb|EEE75504.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene40111_All//5.00E-06//AT1G69545| leucine-rich repeat family protein	Unigene40111_All//5.00E-160//TC138390				nr -
Unigene40114_All	439	364.70	151.55	289.30	274.03	238.38	163.78	481.55	314.56	181.59	-1.27E+00	1.27E-168	Down	-3.34E-01	3.62E-16		-2.01E-01	4.53E-06		-7.43E-01	7.82E-57		-6.14E-01	1.34E-80		-1.41E+00	0.00E+00	Down	Unigene40114_All|gi|254047060|gb|ACT63839.1|//1.00E-72//cydophilin [Gossypium hirsutum]	Unigene40114_All//6.00E-59//AT2G21130| peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase	Unigene40114_All//0.00E+00//gi|13243554|gb|BE053625.2|BE053625			GO:0005488//GO:0016859//GO:0044267//GO:0044424	nr +
Unigene40115_All	347	10.71	49.65	7.52	8.76	15.48	12.76	33.02	48.90	25.03	2.21E+00	3.43E-40	Up	-5.10E-01	1.35E-01		8.22E-01	8.71E-04		5.43E-01	6.67E-02		5.67E-01	2.33E-06		-4.00E-01	6.37E-03					Unigene40115_All//6.00E-151//gi|72860034|gb|DT462773.1|DT462773				

Unigene40118_All	659	109.80	73.97	108.36	23.36	41.91	21.25	0.00	1.33	1.51	-5.70E-01	3.05E-20		-1.91E-02	7.95E-01		8.43E-01	5.25E-18		-1.37E-01	4.16E-01		1.04E+01	2.86E-06	Up	1.06E+01	3.00E-07	Up	Unigene40118_All//gi|2493694|sp|Q41387.1|PSBW_SPIOL//2.00E-34//RecName: Full=Photosystem II reaction center W protein, chloroplastic; AltName: Full=PSII 6.1 kDa protein; Flags: Precursor >gi|728716|emb|CAA59409.1| protein of photosystem II [Spinacia oleracea]	Unigene40118_All//4.00E-22//AT2G30570| PSBW (PHOTOSYSTEM II REACTION CENTER W)	Unigene40118_All//0.00E+00//C0097901		ko00195|Photosynthesis	GO:0009521//GO:0009534	nr -
Unigene40119_All	283	5.55	2.69	0.56	4.93	4.75	5.43	57.97	15.21	13.51	-1.05E+00	4.79E-02		-3.30E+00	8.04E-06	Down	-5.46E-02	9.11E-01		1.39E-01	8.01E-01		-1.93E+00	1.39E-39	Down	-2.10E+00	1.54E-45	Down							Unigene40119_All//4.00E-93//TC133357				
Unigene40123_All	1337	0.31	0.57	0.40	0.89	2.32	2.67	10.40	24.32	6.38	8.61E-01	2.93E-01		3.47E-01	7.06E-01		1.37E+00	9.45E-05	Up	1.58E+00	4.05E-06	Up	1.23E+00	3.06E-40	Up	-7.06E-01	8.33E-08		Unigene40123_All//gi|6715637|gb|AAF26464.1|AC007323_5//1.00E-111//T25K16.17 [Arabidopsis thaliana]	Unigene40123_All//7.00E-108//AT1G01180| unknown protein					nr -
Unigene40124_All	318	3.13	3.51	6.70	11.91	6.93	10.23	2.79	0.39	0.38	1.65E-01	7.79E-01		1.10E+00	1.82E-02		-7.81E-01	8.47E-03		-2.19E-01	5.45E-01		-2.82E+00	5.65E-04	Down	-2.89E+00	3.04E-04	Down								
Unigene40125_All	511	7.78	2.97	1.46	1.36	1.01	1.24	3.64	2.54	0.86	-1.39E+00	1.49E-05	Down	-2.42E+00	2.50E-10	Down	-4.33E-01	6.06E-01		-1.41E-01	8.66E-01		-5.22E-01	2.33E-01		-2.09E+00	7.81E-06	Down	Unigene40125_All//gi|115455233|ref|NP_001051217.1|//3.00E-115//Os03g0740200 [Oryza sativa Japonica Group] >gi|113549688|dbj|BAF13131.1| Os03g0740200 [Oryza sativa Japonica Group]	Unigene40125_All//7.00E-36//AT2G23690| unknown protein	Unigene40125_All//1.00E-48//DN758474			GO:0005488	nr +
Unigene40126_All	340	0.62	8.20	1.41	0.73	2.84	4.78	3.61	5.41	14.30	3.74E+00	1.82E-11	Up	1.20E+00	3.02E-01		1.95E+00	1.16E-02		2.71E+00	1.65E-05	Up	5.85E-01	1.83E-01		1.99E+00	5.71E-13	Up								
Unigene40127_All	300	4.01	3.38	1.60	1.33	1.15	2.26	0.56	3.76	1.33	-2.48E-01	6.62E-01		-1.33E+00	4.65E-02		-2.11E-01	8.25E-01		7.66E-01	4.10E-01		2.74E+00	9.94E-05	Up	1.24E+00	2.51E-01				Unigene40127_All//3.00E-07//ES812645				
Unigene40128_All	333	2.67	7.46	6.72	14.51	8.89	2.85	23.11	25.98	14.00	1.48E+00	4.79E-04	Up	1.33E+00	3.85E-03		-7.06E-01	6.02E-03		-2.35E+00	1.42E-13	Down	1.69E-01	3.98E-01		-7.23E-01	7.06E-05				Unigene40128_All//6.00E-40//TC172720				
Unigene40129_All	332	5.04	9.62	14.11	5.10	4.67	3.67	131.04	123.88	49.08	9.31E-01	7.72E-03		1.48E+00	1.20E-06	Up	-1.28E-01	8.22E-01		-4.74E-01	3.86E-01		-8.11E-02	3.59E-01		-1.42E+00	6.06E-69	Down	Unigene40129_All//gi|393707|emb|CAA47926.1|//3.00E-16//3-ketoacyl-CoA thiolase; acetyl-CoA acyltransferase [Cucumis sativus]	Unigene40129_All//4.00E-15//AT2G33150| PKT3 (PEROXISOMAL 3-KETOACYL-COA THIOLASE 3); acetyl-CoA C-acyltransferase	Unigene40129_All//0.00E+00//gi|21099905|gb|BQ411218.1|BQ411218		ko04146|Peroxisome//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids	GO:0016408	nr -
Unigene40131_All	552	0.28	0.28	0.19	0.36	0.62	0.82	2.76	4.39	8.52	-4.64E-02	9.89E-01		-5.60E-01	7.75E-01		7.89E-01	5.96E-01		1.18E+00	3.38E-01		6.71E-01	6.79E-02		1.63E+00	9.04E-10	Up			Unigene40131_All//4.00E-79//gi|164365079|gb|ES840312.1|ES840312				
Unigene40132_All	355	45.39	94.77	72.45	34.24	32.88	38.93	87.18	106.55	43.43	1.06E+00	3.61E-27	Up	6.75E-01	1.11E-09		-5.83E-02	7.91E-01		1.85E-01	2.88E-01		2.89E-01	2.25E-04		-1.01E+00	5.79E-29	Down	Unigene40132_All//gi|21593125|gb|AAM65074.1|//1.00E-28//Bax inhibitor-1 like [Arabidopsis thaliana]	Unigene40132_All//5.00E-30//AT5G47120| ATBI1 (BAX INHIBITOR 1)	Unigene40132_All//1.00E-167//TC166118			GO:0005488//GO:0006631//GO:0006950//GO:0006984//GO:0012505//GO:0031224//GO:0043066//GO:0043231	nr -
Unigene40134_All	443	51.38	42.55	41.35	59.48	37.00	65.35	36.36	20.85	11.06	-2.72E-01	2.12E-02		-3.13E-01	1.02E-02		-6.85E-01	1.52E-12		1.36E-01	2.41E-01		-8.02E-01	1.54E-10		-1.72E+00	2.91E-34	Down			Unigene40134_All//2.00E-49//TC165688				
Unigene40135_All	598	1.31	4.75	1.51	1.08	1.61	0.91	1.13	1.19	2.40	1.85E+00	7.02E-06	Up	2.06E-01	7.64E-01		5.74E-01	4.52E-01		-2.57E-01	7.57E-01		7.09E-02	9.42E-01		1.08E+00	2.54E-02				Unigene40135_All//1.00E-91//TC156537				
Unigene40137_All	291	2.70	8.36	2.74	6.16	10.30	11.48	1.74	1.87	1.64	1.63E+00	1.87E-04	Up	2.54E-02	9.94E-01		7.40E-01	3.89E-02		8.98E-01	8.17E-03		9.89E-02	9.21E-01		-8.58E-02	9.30E-01				Unigene40137_All//2.00E-116//gi|78348864|gb|DT569138.1|DT569138				
Unigene40139_All	608	0.17	0.00	0.00	12.29	5.49	1.04	25.59	16.15	9.57	-7.43E+00	3.71E-01		-7.43E+00	3.93E-01		-1.16E+00	6.59E-09	Down	-3.56E+00	1.12E-31	Down	-6.64E-01	1.47E-07		-1.42E+00	2.74E-25	Down	Unigene40139_All//gi|4587555|gb|AAD25786.1|AC006577_22//5.00E-17//F1511.22 [Arabidopsis thaliana]	Unigene40139_All//5.00E-15//AT1G54120| unknown protein	Unigene40139_All//0.00E+00//TC161490			GO:0030312//GO:0044424	nr -
Unigene4014_All	863	1.64	1.41	1.23	1.85	1.32	2.20	6.17	3.73	2.86	-2.16E-01	6.80E-01		-4.08E-01	4.86E-01		-4.88E-01	3.53E-01		2.51E-01	6.21E-01		-7.27E-01	1.58E-03		-1.11E+00	1.47E-06	Down	Unigene4014_All//gi|224130070|ref|XP_002320745.1|//1.00E-40//glycosyltransferase [Populus trichocarpa] >gi|222861518|gb|EEE90960.1| glycosyltransferase [Populus trichocarpa]	Unigene4014_All//5.00E-34//AT3G61130| GAUT1 (GALACTURONOSYLTRANSFERASE 1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups	Unigene4014_All//2.00E-91//TC155011				nr -
Unigene40140_All	457	1.37	6.99	6.87	2.94	3.84	4.74	0.65	1.28	2.62	2.35E+00	1.63E-08	Up	2.32E+00	5.71E-08	Up	3.85E-01	4.89E-01		6.89E-01	1.28E-01		9.83E-01	2.59E-01		2.01E+00	7.79E-04	Up			Unigene40140_All//6.00E-124//DT527382				
Unigene40142_All	614	1.96	0.00	0.35	0.24	0.17	0.00	2.62	3.27	2.73	-1.09E+01	5.01E-07	Down	-2.50E+00	1.15E-03		-5.32E-01	7.85E-01		-7.93E+00	2.33E-01		3.20E-01	4.62E-01		5.86E-02	9.12E-01				Unigene40142_All//3.00E-09//TC161633				
Unigene40143_All	470	17.25	14.77	12.12	9.01	11.06	13.16	14.57	10.94	5.59	-2.24E-01	3.07E-01		-5.09E-01	1.71E-02		2.96E-01	3.10E-01		5.47E-01	2.25E-02		-4.14E-01	4.28E-02		-1.38E+00	3.49E-11	Down	Unigene40143_All//gi|167599639|gb|ABZ88805.1|//1.00E-31//ATP synthase subunit H protein [Hevea brasiliensis]	Unigene40143_All//3.00E-31//AT5G55290| ATP synthase subunit H family protein	Unigene40143_All//2.00E-105//TC157948		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0003824//GO:0015077//GO:0015988//GO:0031410//GO:0033176//GO:0043231	nr +
Unigene40144_All	1067	0.78	0.14	0.60	2.43	0.52	1.65	57.73	47.01	14.86	-2.46E+00	6.70E-03		-3.90E-01	6.41E-01		-2.23E+00	4.73E-08	Down	-5.56E-01	1.72E-01		-2.97E-01	6.99E-07		-1.96E+00	4.96E-154	Down	Unigene40144_All//gi|57233444|gb|AA48295.1|//2.00E-32//pore-forming toxin-like protein Hfr-2 [Triticum aestivum]		Unigene40144_All//3.00E-97//TC159407				nr +
Unigene40146_All	361	0.14	0.00	0.59	3.45	0.76	1.38	2.11	2.43	0.99	-7.18E+00	6.11E-01		2.03E+00	3.61E-01		-2.18E+00	4.83E-04	Down	-1.33E+00	3.28E-02		2.06E-01	7.54E-01		-1.09E+00	1.21E-01				Unigene40146_All//4.00E-07//gi|13355982|gb|BG446270.1|BG446270				
Unigene40147_All	651	3.86	19.38	3.11	21.50	90.72	25.53	22.08	27.74	11.26	2.33E+00	1.91E-31	Up	-3.12E-01	4.62E-01		2.08E+00	8.46E-148	Up	2.48E-01	9.04E-02		3.29E-01	5.50E-03		-9.72E-01	3.23E-13		Unigene40147_All//gi|15234987|ref|NP_192765.1|//6.00E-24//wound-responsive family protein [Arabidopsis thaliana] >gi|3695408|gb|AAC62808.1| contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi|4538956|emb|CAB39780.1| probable wound-induced protein [Arabidopsis thaliana] >gi|7267724|emb|CAB78150.1| probable wound-induced protein [Arabidopsis thaliana] >gi|21553934|gb|AAM63015.1| probable wound-induced protein [Arabidopsis thaliana] >gi|90962948|gb|ABE02398.1| At4g10270 [Arabidopsis thaliana]	Unigene40147_All//3.00E-25//AT4G10270| wound-responsive family protein	Unigene40147_All//0.00E+00//TC159545				nr +
Unigene40148_All	410	76.82	56.23	31.56	63.54	86.76	35.03	50.84	89.20	107.95	-4.50E-01	2.57E-06		-1.28E+00	4.46E-33	Down	4.49E-01	6.81E-08		-8.59E-01	3.15E-16		8.11E-01	2.91E-23		1.09E+00	3.89E-46	Up	Unigene40148_All//gi|297816246|ref|XP_002876006.1|//1.00E-36//LOB domain protein 38 [Arabidopsis lyrata subsp. lyrata] >gi|297321844|gb|EFH52265.1| LOB domain protein 38 [Arabidopsis lyrata subsp. lyrata]	Unigene40148_All//7.00E-38//AT3G49940| LBD38 (LOB DOMAIN-CONTAINING PROTEIN 38)	Unigene40148_All//0.00E+00//gi|78327889|gb|DT548163.1|DT548163				nr +
Unigene40149_All	1591	0.46	0.00	0.20	1.22	1.21	0.57	25.41	10.01	8.14	-8.85E+00	2.11E-04	Down	-1.20E+00	1.80E-01		-1.07E-02	9.65E-01		-1.11E+00	1.82E-02		-1.34E+00	1.62E-57	Down	-1.64E+00	1.52E-79	Down	Unigene40149_All//gi|48431269|gb|AAT44124.1|//4.00E-92//F3H-like protein [Saussurea medusa]	Unigene40149_All//6.00E-63//AT5G24530| DMR6 (DOWNY MILDEW RESISTANT 6); oxidoreductase/ oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene40149_All//0.00E+00//DW479710		ko00941|Flavonoid biosynthesis	GO:0016491	nr -
Unigene40150_All	216	22.53	82.34	81.11	43.13	58.51	193.62	38.56	32.89	40.02	1.87E+00	1.92E-33	Up	1.85E+00	1.69E-31	Up	4.40E-01	4.16E-03		2.17E+00	4.63E-101	Up	-2.29E-01	2.39E-01		5.37E-02	7.76E-01		Unigene40150_All//gi|256032164|gb|AAD55762.2|//3.00E-32//chloroplast 1-hydroxy-2-methyl-butenyl 4-diphosphate reductase [Nicotiana tabacum]	Unigene40150_All//6.00E-32//AT4G34350| HDR (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE REDUCTASE); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase/ 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Unigene40150_All//6.00E-119//gi|13349931|gb|BG440280.1|BG440280		ko00900|Terpenoid backbone biosynthesis	GO:0006090//GO:0006721//GO:0009532//GO:0016726//GO:0042221//GO:0052592	nr -
Unigene40152_All	948	1.66	0.37	0.51	1.89	1.71	0.95	2.05	0.26	1.05	-2.15E+00	3.32E-04	Down	-1.71E+00	3.82E-03		-1.48E-01	7.95E-01		-9.89E-01	4.36E-02		-2.96E+00	2.83E-08	Down	-9.66E-01	1.58E-02		Unigene40152_All//gi|297802010|ref|XP_002868889.1|//8.00E-53//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297314725|gb|EFH45148.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene40152_All//2.00E-25//AT2G21500| protein binding / zinc ion binding	Unigene40152_All//0.00E+00//gi|109878353|gb|DW507324.1|DW507324			GO:0005488//GO:0016020	nr +
Unigene40153_All	651	0.72	3.66	2.04	6.66	9.31	6.04	21.04	12.58	12.85	2.34E+00	1.67E-06	Up	1.50E+00	1.84E-02		4.84E-01	4.33E-02		-1.41E-01	6.76E-01		-7.42E-01	4.93E-08		-7.11E-01	8.69E-08		Unigene40153_All//gi|297738666|emb|CBI27911.3|//3.00E-26//unnamed protein product [Vitis vinifera]	Unigene40153_All//8.00E-13//AT3G60310| unknown protein	Unigene40153_All//0.00E+00//TC174026				nr +
Unigene40155_All	249	3.36	0.61	0.21	7.20	7.33	3.81	2.21	0.00	2.08	-2.46E+00	6.70E-03		-3.97E+00	9.08E-04	Down	2.53E-02	9.69E-01		-9.19E-01	6.19E-02		-1.11E+01	4.61E-04	Down	-8.58E-02	9.27E-01		Unigene40155_All//gi|224057579|ref|XP_002299277.1|//3.00E-10//predicted protein [Populus trichocarpa] >gi|222846535|gb|EEE84082.1| predicted protein [Populus trichocarpa]						nr -
Unigene40158_All	559	3.00	1.63	9.24	1.51	1.97	1.86	0.23	0.00	0.14	-8.76E-01	8.26E-02		1.63E+00	3.44E-08	Up	3.80E-01	6.01E-01		2.95E-01	6.93E-01		-7.83E+00	2.35E-01		-6.71E-01	7.19E-01		Unigene40158_All//gi|224142619|ref|XP_002324652.1|//2.00E-22//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222866086|gb|EEF03217.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene40158_All//1.00E-14//AT1G15360| SHN1 (SHINE 1); DNA binding / sequence-specific DNA binding / transcription factor	Unigene40158_All//0.00E+00//ES805836	AP2-EREBP		GO:0000160//GO:0001071//GO:0003677//GO:0006351//GO:0006633//GO:0006950//GO:0010468//GO:0043231	nr +
Unigene4016_All	1497	26.91	8.87	14.41	45.06	38.90	45.50	47.25	17.67	16.26	-1.60E+00	8.13E-61	Down	-9.02E-01	5.43E-24		-2.12E-01	5.19E-04		1.40E-02	8.72E-01		-1.42E+00	1.14E-108	Down	-1.54E+00	3.68E-126	Down	Unigene4016_All//gi|51701647|sp|P83291.2|NCB5R_ARATH//1.00E-150//RecName: Full=NADH-cytochrome b5 reductase-like protein; Short=B5R >gi|21592883|gb|AAM64833.1| cytochrome-b5 reductase-like protein [Arabidopsis thaliana] >gi|89000937|gb|ABD59058.1| At5g20080 [Arabidopsis thaliana] >gi|110742032|dbj|BAE98853.1| cytochrome-b5 reductase - like protein [Arabidopsis thaliana]	Unigene4016_All//2.00E-142//AT5G20080| NADH-cytochrome b5 reductase, putative	Unigene4016_All//0.00E+00//TC134035		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene40160_All	287	2.92	46.79	6.12	1.91	1.32	0.31	0.15	3.20	2.50	4.00E+00	2.12E-56	Up	1.07E+00	4.06E-02		-5.33E-01	5.85E-01		-2.60E+00	2.93E-02		4.44E+00	1.66E-05	Up	4.08E+00	2.41E-04	Up			Unigene40160_All//4.00E-90//gi|48816051|gb|CO117364.1|CO117364				
Unigene40161_All	312	11.07	146.32	23.55	7.98	3.20	10.28	3.12	8.71	3.58	3.72E+00	9.16E-181	Up	1.09E+00	1.76E-06	Up	-1.32E+00	5.45E-04	Down	3.65E-01	3.42E-01		1.48E+00	3.46E-05	Up	1.98E-01	7.17E-01				Unigene40161_All//2.00E-135//gi|48816051|gb|CO117364.1|CO117364				
Unigene40166_All	714	1.91	1.42	0.90	0.56	1.54	1.71	4.44	1.23	2.06	-4.25E-01	4.51E-01		-1.09E+00	7.48E-02		1.47E+00	3.09E-02		1.61E+00	1.36E-02		-1.85E+00	7.50E-08	Down	-1.11E+00	3.07E-04	Down	Unigene40166_All//gi|30698782|ref|NP_177277.2|//1.00E-45//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75151609|sp|Q8GZA6.1|PP113_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g71210 >gi|29029058|gb|AAO64908.1| At1g71210 [Arabidopsis thaliana]	Unigene40166_All//3.00E-43//AT1G71210| pentatricopeptide (PPR) repeat-containing protein	Unigene40166_All//0.00E+00//DR462038				nr +
Unigene40167_All	395	1.99	0.00	0.81	6.05	2.09	2.74	24.83	20.00	27.53	-1.10E+01	1.09E-04	Down	-1.30E+00	1.38E-01		-1.53E+00	1.11E-04	Down	-1.14E+00	5.69E-03		-3.12E-01	6.73E-02		1.49E-01	3.76E-01		Unigene40167_All//gi|186516279|ref|NP_001119115.1|//3.00E-06//CPu08F2 (Conserved peptide upstream open reading frame 2) [Arabidopsis thaliana]	Unigene40167_All//1.00E-07//AT4G34588| CPu08F2 (Conserved peptide upstream open reading frame 2)	Unigene40167_All//2.00E-74//TC146684				nr +

Unigene40168_All	491	4.05	2.79	2.60	3.15	2.10	0.64	1.98	0.68	0.81	-5.39E-01	2.35E-01		-6.38E-01	1.87E-01		-5.80E-01	2.80E-01		-2.29E+00	1.35E-04	Down	-1.54E+00	1.90E-02		-1.29E+00	3.62E-02		Unigene40168_All//gi|51536472|gb|AU05474.1|//2.00E-50//At1g78010 [Arabidopsis thaliana] >gi|52421301|gb|AAU45220.1| At1g78010 [Arabidopsis thaliana]	Unigene40168_All//1.00E-51//AT1G78010| tRNA modification GTPase, putative				GO:0008033//GO:0017111//GO:0032561//GO:0035556//GO:0043231	nr +
Unigene4017_All	881	29.99	45.78	52.28	31.27	52.85	52.60	12.33	16.56	24.69	6.10E-01	5.15E-13		8.02E-01	1.54E-22		7.57E-01	4.02E-25		7.50E-01	2.05E-22		4.25E-01	1.22E-03		1.00E+00	2.37E-20	Up	Unigene4017_All//gi|297804846|ref|XP_002870307.1|//2.00E-17//CCAAT-box binding transcription factor subunit B (NF-YB) family [Arabidopsis lyrata subsp. lyrata] >gi|297316143|gb|EFH46566.1| CCAAT-box binding transcription factor subunit B (NF-YB) family [Arabidopsis lyrata subsp. lyrata]	Unigene4017_All//6.00E-13//AT4G14540| NF-YB3 (NUCLEAR FACTOR Y, SUBUNIT B3); transcription factor	Unigene4017_All//3.00E-81//TC158088	CCAAT			nr -
Unigene40171_All	318	100.03	47.32	51.24	119.84	118.79	169.01	175.64	74.00	82.56	-1.08E+00	1.60E-26	Down	-9.65E-01	2.69E-21		-1.26E-02	9.08E-01		4.96E-01	1.07E-12		-1.25E+00	1.37E-70	Down	-1.09E+00	1.20E-58	Down	Unigene40171_All//gi|87240356|gb|AB032214.1|//1.00E-52//Ribosomal protein L34e [Medicago truncatula] >gi|124360947|gb|ABN08915.1| Ribosomal protein L34e [Medicago truncatula]	Unigene40171_All//4.00E-53//AT1G26880| 60S ribosomal protein L34 (RPL34A)	Unigene40171_All//1.00E-179//gi|11207162|gb|BF276092.1|BF276092		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0031981	nr -
Unigene40173_All	982	0.21	0.31	0.27	1.78	1.68	1.01	0.47	0.98	1.66	5.39E-01	6.71E-01		3.47E-01	7.97E-01		-7.70E-02	8.69E-01		-8.11E-01	1.08E-01		1.05E+00	1.03E-01		1.81E+00	2.01E-04	Up						
Unigene40174_All	925	0.79	0.33	0.12	6.14	4.58	3.52	3.34	0.63	0.95	-1.27E+00	1.36E-01		-2.78E+00	1.04E-02		-4.23E-01	8.70E-02		-8.04E-01	1.03E-03		-2.40E+00	2.53E-10	Down	-1.82E+00	9.22E-08	Down	Unigene40174_All//gi|87241323|gb|AB033181.1|//1.00E-110//Pectinacetylesterase [Medicago truncatula]	Unigene40174_All//2.00E-109//AT3G05910| pectinacetylesterase, putative	Unigene40174_All//0.00E+00//TC168416				nr -
Unigene40175_All	1025	0.36	0.74	0.10	7.53	3.46	1.94	6.60	0.16	1.24	1.05E+00	2.05E-01		-1.78E+00	2.34E-01		-1.12E+00	1.02E-08	Down	-1.96E+00	4.28E-17	Down	-5.34E+00	9.97E-42	Down	-2.41E+00	1.24E-22	Down	Unigene40175_All//gi|15239503|ref|NP_197955.1|//6.00E-63//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|71660770|sp|P69781.1|GAT12_ARATH RecName: Full=GATA transcription factor 12	Unigene40175_All//1.00E-58//AT5G25830| zinc finger (GATA type) family protein	Unigene40175_All//0.00E+00//DW503936	C2C2-GATA		GO:0046872	nr -
Unigene40177_All	704	0.45	1.80	0.91	0.00	2.10	1.67	1.02	0.95	1.64	2.01E+00	2.67E-03		1.03E+00	2.81E-01		1.10E+01	3.59E-09	Up	1.07E+01	5.32E-07	Up	-1.04E-01	8.93E-01		6.85E-01	2.12E-01		Unigene40177_All//gi|14488090|gb|AAK63865.1|AF389293_1|2.00E-14//AT5g26741 [Arabidopsis thaliana] >gi|22655444|gb|AAM98314.1| At5g26741/At5g26741 [Arabidopsis thaliana]	Unigene40177_All//8.00E-07//AT5G26731| unknown protein					nr +
Unigene40178_All	740	1.27	0.00	0.14	5.25	4.75	1.83	9.20	4.69	4.90	-1.03E+01	1.46E-05	Down	-3.14E+00	1.33E-03		-1.46E-01	6.72E-01		-1.52E+00	2.04E-06	Down	-9.73E-01	1.70E-06		-9.09E-01	4.11E-06		Unigene40178_All//gi|224122896|ref|XP_002318943.1|//2.00E-49//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222857319|gb|EEE94866.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene40178_All//1.00E-30//AT1G12290| disease resistance protein (CC-NBS-LRR class), putative	Unigene40178_All//0.00E+00//gi|109877710|gb|DW506683.1|DW506683		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016787	nr -
Unigene4018_All	1169	133.47	89.77	93.79	54.33	61.57	77.65	19.24	10.19	8.08	-5.72E-01	4.48E-43		-5.09E-01	9.77E-34		1.80E-01	3.03E-03		5.15E-01	1.66E-22		-9.17E-01	7.52E-18		-1.25E+00	5.71E-30	Down	Unigene4018_All//gi|224057792|ref|XP_002299326.1|//1.00E-104//isomerase peptidyl-prolyl cis-trans isomerase [Populus trichocarpa] >gi|222846584|gb|EEE84131.1| isomerase peptidyl-prolyl cis-trans isomerase [Populus trichocarpa]	Unigene4018_All//4.00E-84//AT5G13120| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	Unigene4018_All//0.00E+00//TC149721				nr +
Unigene40180_All	475	36.90	20.27	20.40	41.84	45.45	67.03	116.34	78.05	55.86	-8.64E-01	1.42E-10		-8.55E-01	6.53E-10		1.19E-01	3.97E-01		6.80E-01	3.29E-13		-5.76E-01	2.13E-19		-1.06E+00	1.94E-55	Down	Unigene40180_All//gi|192910768|gb|ACF06492.1|//5.00E-27//ribosomal L9-like protein [Elaeis guineensis]	Unigene40180_All//3.00E-27//AT1G33140| PG72 (P16GYBACK2); structural constituent of ribosome	Unigene40180_All//0.00E+00//TC133131		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr -
Unigene40181_All	1423	0.00	0.28	0.00	0.28	0.05	0.73	2.14	4.49	38.72	8.15E+00	1.36E-02		null	null		-2.53E+00	5.79E-02		1.38E+00	5.20E-02		1.07E+00	4.70E-07	Up	4.18E+00	7.51E-297	Up	Unigene40181_All//gi|30697417|ref|NP_200878.2|//1.00E-175//glycosyltransferase family protein 2 [Arabidopsis thaliana]	Unigene40181_All//3.00E-169//AT5G60700| glycosyltransferase family protein 2	Unigene40181_All//0.00E+00//DN800298			GO:0003824	nr +
Unigene40183_All	233	6.74	3.48	5.71	9.83	4.73	9.89	9.62	3.23	1.54	-9.53E-01	7.08E-02		-2.38E-01	6.42E-01		-1.06E+00	8.04E-03		7.40E-03	9.88E-01		-1.57E+00	9.33E-05	Down	-2.64E+00	8.10E-09	Down	Unigene40183_All//gi|226499354|ref|NP_001147027.1|//4.00E-11//polyubiquitin containing 7 ubiquitin monomers [Zea mays] >gi|195606596|gb|ACG25128.1| polyubiquitin containing 7 ubiquitin monomers [Zea mays]	Unigene40183_All//6.00E-12//AT5G02240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene40183_All//7.00E-91//DR452779		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene40184_All	436	4.80	1.63	5.37	7.65	6.71	6.84	0.68	0.38	0.37	-1.56E+00	8.94E-04	Down	1.63E-01	7.00E-01		-1.89E-01	6.18E-01		-1.63E-01	6.72E-01		-8.24E-01	5.40E-01		-8.93E-01	4.71E-01					Unigene40184_All//6.00E-16//gi|13353379|gb|BG443727.1|BG443727				
Unigene40185_All	324	3.39	5.79	2.30	5.23	3.61	3.62	17.49	4.39	4.43	7.71E-01	1.06E-01		-5.60E-01	3.93E-01		-5.33E-01	3.00E-01		-5.28E-01	3.21E-01		-2.00E+00	9.35E-15	Down	-1.98E+00	3.88E-15	Down				Unigene40185_All//3.00E-165//TC147407		ko03010|Ribosome		kegg +
Unigene40187_All	1519	0.59	0.57	0.25	0.13	0.29	0.65	2.23	7.51	3.04	-4.63E-02	9.62E-01		-1.25E+00	1.17E-01		1.17E+00	3.47E-01		2.32E+00	3.98E-03		1.75E+00	2.12E-24	Up	4.50E-01	6.74E-02		Unigene40187_All//gi|104294986|gb|ABF72002.1|//4.00E-82//U-box domain-containing protein [Musa acuminata]	Unigene40187_All//1.00E-15//AT1G76390| armadillo/beta-catenin repeat family protein / U-box domain-containing protein	Unigene40187_All//0.00E+00//DT462984				nr -
Unigene40189_All	550	0.29	0.00	0.00	3.26	0.75	0.66	7.53	5.55	12.97	-8.16E+00	2.15E-01		-8.16E+00	2.44E-01		-2.12E+00	2.16E-05	Down	-2.31E+00	2.69E-05	Down	-4.42E-01	1.08E-01		7.83E-01	4.19E-05		Unigene40189_All//gi|224145597|ref|XP_002325700.1|//7.00E-09//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222862575|gb|EEF00082.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]		Unigene40189_All//3.00E-86//CO080430			GO:0005488	nr +
Unigene4019_All	1809	2.95	0.53	1.00	18.75	12.01	4.32	10.21	7.32	5.26	-2.47E+00	9.96E-15	Down	-1.56E+00	5.80E-08	Down	-6.43E-01	2.41E-14		-2.12E+00	1.64E-81	Down	-4.80E-01	2.77E-05		-9.56E-01	2.54E-16		Unigene4019_All//gi|16648748|gb|AAL25566.1|//5.00E-10//AT5g02020/T7H20_70 [Arabidopsis thaliana] >gi|20334906|gb|AAM16209.1| AT5g02020/T7H20_70 [Arabidopsis thaliana]	Unigene4019_All//2.00E-16//AT5G59080| unknown protein	Unigene4019_All//0.00E+00//TC176841				nr +
Unigene40190_All	284	7.37	7.32	5.06	1.23	5.34	3.02	0.89	0.88	0.42	-1.06E-02	9.84E-01		-5.42E-01	2.44E-01		2.12E+00	3.26E-04	Up	1.30E+00	1.07E-01		-1.66E-02	1.02E+00		-1.09E+00	4.28E-01					Unigene40190_All//3.00E-07//ES794141				
Unigene40191_All	470	5.68	2.48	3.63	3.71	2.78	3.27	2.97	0.44	1.02	-1.20E+00	2.39E-03		-6.47E-01	1.12E-01		-4.14E-01	4.20E-01		-1.83E-01	7.14E-01		-2.74E+00	1.03E-05	Down	-1.55E+00	2.47E-03		Unigene40191_All//gi|115456383|ref|NP_001051792.1|//3.00E-22//Os03g0831200 [Oryza sativa Japonica Group] >gi|108711910|gb|ABF99705.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550263|dbj|BAF13706.1| Os03g0831200 [Oryza sativa Japonica Group]	Unigene40191_All//1.00E-17//AT4G16141| sequence-specific DNA binding / transcription factor/ zinc ion binding	Unigene40191_All//4.00E-11//ES804921	C2C2-GATA		GO:0005488	nr +
Unigene40193_All	666	0.00	0.30	1.60	1.27	1.03	0.47	5.97	2.32	4.01	8.25E+00	1.36E-01		1.06E+01	6.62E-06	Up	-2.98E-01	6.93E-01		-1.42E+00	7.33E-02		-1.36E+00	1.78E-06	Down	-5.74E-01	2.98E-02		Unigene40193_All//gi|30984566|gb|AAP42746.1|//3.00E-17//At4g33890 [Arabidopsis thaliana]	Unigene40193_All//2.00E-18//AT4G33890| unknown protein					nr -
Unigene40197_All	1123	0.37	0.14	0.19	7.19	5.64	1.57	1.96	0.37	0.28	-1.46E+00	2.34E-01		-9.74E-01	4.11E-01		-3.49E-01	8.93E-02		-2.20E+00	1.29E-20	Down	-2.40E+00	1.55E-07	Down	-2.79E+00	4.04E-09	Down	Unigene40197_All//gi|190898408|gb|ACE97717.1|//7.00E-63//expressed protein [Populus tremula] >gi|190898410|gb|ACE97718.1| expressed protein [Populus tremula] >gi|190898412|gb|ACE97719.1| expressed protein [Populus tremula] >gi|190898414|gb|ACE97720.1| expressed protein [Populus tremula] >gi|190898416|gb|ACE97721.1| expressed protein [Populus tremula] >gi|190898418|gb|ACE97722.1| expressed protein [Populus tremula] >gi|190898420|gb|ACE97723.1| expressed protein [Populus tremula] >gi|190898422|gb|ACE97724.1| expressed protein [Populus tremula] >gi|190898424|gb|ACE97725.1| expressed protein [Populus tremula] >gi|190898426|gb|ACE97726.1| expressed protein [Populus tremula]	Unigene40197_All//3.00E-88//AT3G17350| unknown protein	Unigene40197_All//0.00E+00//TC146997			GO:0044464	nr +
Unigene40199_All	569	1.38	1.87	1.97	2.45	3.03	3.02	1.63	0.88	0.28	4.39E-01	5.07E-01		5.11E-01	4.34E-01		3.04E-01	5.86E-01		2.99E-01	6.11E-01		-8.91E-01	1.72E-01		-2.55E+00	5.79E-04	Down							
Unigene40200_All	443	4.72	8.69	5.65	1.80	1.87	6.52	0.10	0.19	0.27	8.80E-01	4.96E-03		2.58E-01	5.55E-01		5.23E-02	9.65E-01		1.86E+00	3.34E-06	Up	9.84E-01	7.31E-01		1.50E+00	5.58E-01					Unigene40200_All//5.00E-07//CO132526				
Unigene40201_All	1191	0.97	1.91	0.54	0.67	1.27	0.76	15.73	24.11	75.13	9.86E-01	2.07E-02		-8.49E-01	2.06E-01		9.27E-01	9.02E-02		1.81E-01	8.07E-01		6.16E-01	1.01E-11		2.26E+00	1.98E-264	Up	Unigene40201_All//gi|15235621|ref|NP_193054.1|//7.00E-96//short-chain dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] >gi|17933307|gb|AAL48236.1|AF446363_1 AT4g13180/F17N18_70 [Arabidopsis thaliana] >gi|4753652|emb|CAB41928.1| short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana] >gi|7268020|emb|CAB78360.1| short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana] >gi|20453399|gb|AAM19938.1| AT4g13180/F17N18_70 [Arabidopsis thaliana] >gi|21594913|gb|AAM66055.1| short-chain alcohol dehydrogenase like protein [Arabidopsis thaliana]	Unigene40201_All//3.00E-97//AT4G13180| short-chain dehydrogenase/reductase (SDR) family protein	Unigene40201_All//0.00E+00//TC156780		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0004312//GO:0008152//GO:0010035	nr -
Unigene40202_All	710	21.37	8.85	12.98	3.30	6.60	2.42	0.00	0.00	0.00	-1.27E+00	1.03E-16	Down	-7.20E-01	1.26E-06		1.00E+00	1.94E-04	Up	-4.48E-01	3.12E-01		null	null		null	null		Unigene40202_All//gi|171919810|gb|ACB59077.1|//6.00E-13//Myb-like transcription factor EOBII [Petunia x hybrida]	Unigene40202_All//5.00E-14//AT3G27810| ATMYB21 (ARABIDOPSIS THALIANA MYB DOMAIN PROTEIN 21); DNA binding / transcription factor	Unigene40202_All//1.00E-48//TC138320	MYB		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene40203_All	500	20.82	9.42	14.70	11.06	8.06	9.76	53.36	25.08	20.96	-1.14E+00	5.11E-10	Down	-5.03E-01	6.61E-03		-4.57E-01	6.72E-02		-1.81E-01	5.43E-01		-1.09E+00	1.16E-27	Down	-1.35E+00	1.41E-39	Down	Unigene40203_All//gi|164605523|dbj|BAF98589.1|//1.00E-08//CM02216.550.nc [Lotus japonicus]		Unigene40203_All//2.00E-105//gi|164298195|gb|ES809321.1|ES809321			GO:0006970	nr +

Unigene40204_All	811	0.90	0.00	0.07	6.08	2.21	2.73	2.09	0.62	0.88	-9.82E+00	2.11E-04	Down	-3.78E+00	2.79E-03		-1.46E+00	1.85E-08	Down	-1.16E+00	1.82E-05	Down	-1.75E+00	2.90E-04	Down	-1.24E+00	5.14E-03		Unigene40204_All//gi|224096304|ref|XP_002310601.1|//1.00E-119//cytochrome P450 [Populus trichocarpa] >gi|222853504|gb|EEE91051.1|cytochrome P450 [Populus trichocarpa]	Unigene40204_All//3.00E-112//AT5G09970| CYP78A7; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0009791//GO:0016491//GO:0048522//GO:0048827	nr +
Unigene40205_All	669	1.72	0.83	1.51	2.23	2.16	1.01	2.09	1.31	0.36	-1.05E+00	1.01E-01		-1.86E-01	7.59E-01		-4.72E-02	9.23E-01		-1.14E+00	3.85E-02		-6.69E-01	1.94E-01		-2.55E+00	1.43E-05	Down			Unigene40205_All//1.00E-132//TC170123				
Unigene40206_All	2986	0.12	0.03	0.20	0.48	0.20	0.44	16.16	6.70	6.86	-1.86E+00	1.87E-01		6.77E-01	4.82E-01		-1.30E+00	1.41E-02		-1.42E-01	7.93E-01		-1.27E+00	9.84E-63	Down	-1.24E+00	5.26E-62	Down	Unigene40206_All//gi|28300299|gb|AA037645.1|//0.00E+00//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene40206_All//5.00E-93//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene40206_All//2.00E-177//TC143926		ko04626|Plant-pathogen interaction	GO:0005488	nr -
Unigene40207_All	610	2.40	0.42	1.40	2.20	3.10	2.67	3.74	0.69	1.04	-2.53E+00	1.19E-04	Down	-7.82E-01	1.75E-01		4.94E-01	3.21E-01		2.74E-01	6.20E-01		-2.45E+00	5.49E-08	Down	-1.84E+00	4.73E-06	Down	Unigene40207_All//gi|227202782|dbj|BAH56884.1|//1.00E-15//AT2G18670 [Arabidopsis thaliana]	Unigene40207_All//2.00E-16//AT2G18670| zinc finger (C3HC4-type RING finger) family protein	Unigene40207_All//2.00E-121//DR460582				nr -
Unigene40208_All	374	11.89	7.86	10.54	7.86	11.14	17.63	3.96	2.57	1.92	-5.98E-01	3.72E-02		-1.75E-01	6.00E-01		5.04E-01	9.63E-02		1.17E+00	4.62E-07	Up	-6.22E-01	2.14E-01		-1.05E+00	2.65E-02		Unigene40208_All//gi|4544453|gb|AAD22361.1|//3.00E-12//expressed protein [Arabidopsis thaliana] >gi|117168219|gb|ABX32192.1|At2g22370 [Arabidopsis thaliana]	Unigene40208_All//1.00E-05//AT2G22370| unknown protein	Unigene40208_All//0.00E+00//gi|21094782|gb|BQ407095.1|BQ407095			GO:0006355//GO:0016251//GO:0043234	nr +
Unigene40209_All	636	0.16	0.72	0.33	69.55	36.71	25.85	0.86	1.31	0.31	2.12E+00	9.59E-02		1.03E+00	5.91E-01		-9.22E-01	1.44E-34		-1.43E+00	3.89E-61	Down	6.05E-01	4.04E-01		-1.46E+00	9.76E-02		Unigene40209_All//gi|186510343|ref|NP_001078202.2|//2.00E-72//LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4) [Arabidopsis thaliana]	Unigene40209_All//6.00E-58//AT3G23290| LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4)	Unigene40209_All//0.00E+00//TC146825				nr +
Unigene40210_All	668	0.47	0.76	0.16	3.58	3.35	3.92	2.53	1.75	0.89	6.91E-01	4.99E-01		-1.56E+00	3.30E-01		-9.53E-02	8.21E-01		1.32E-01	7.51E-01		-5.31E-01	2.50E-01		-1.50E+00	9.77E-04	Down	Unigene40210_All//gi|79379437|ref|NP_177526.2|//4.00E-34//structural constituent of ribosome [Arabidopsis thaliana] >gi|40823465|gb|AAR92284.1|At1g73850 [Arabidopsis thaliana] >gi|46518405|gb|AAS99684.1|At1g73850 [Arabidopsis thaliana]	Unigene40210_All//9.00E-26//AT1G73850| structural constituent of ribosome				GO:0005198//GO:0010467//GO:0030529	nr +
Unigene40211_All	699	2.77	0.43	0.15	2.64	2.41	1.81	1.88	0.12	0.74	-2.67E+00	3.17E-06	Down	-4.18E+00	2.32E-08	Down	-1.27E-01	8.13E-01		-5.44E-01	2.82E-01		-3.97E+00	3.35E-07	Down	-1.34E+00	9.65E-03		Unigene40211_All//gi|18056482|emb|CAC83650.1|//8.00E-84//CDC6b protein [Arabidopsis thaliana]	Unigene40211_All//4.00E-85//AT1G07270| cell division control protein CDC6b, putative (CDC6b)				GO:0000166//GO:0007049//GO:0009536	nr -
Unigene40212_All	1274	1.07	0.76	1.42	1.25	1.73	1.49	1.56	0.59	2.10	-4.99E-01	3.80E-01		4.12E-01	4.05E-01		4.67E-01	3.07E-01		2.51E-01	6.21E-01		-1.40E+00	9.38E-04	Down	4.26E-01	2.13E-01		Unigene40212_All//gi|297836048|ref|XP_002885906.1|//7.00E-44//ALDH6B2 [Arabidopsis lyrata subsp. lyrata] >gi|297317746|gb|EFH62165.1|ALDH6B2 [Arabidopsis lyrata subsp. lyrata]	Unigene40212_All//3.00E-44//AT2G14170| ALDH6B2; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase	Unigene40212_All//0.00E+00//gi|78332266|gb|DT552540.1|DT552540		ko00562|Inositol phosphate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism	GO:0006950//GO:0009081//GO:0016620//GO:0043231//GO:0046914	nr +
Unigene40214_All	934	2.02	0.92	1.94	4.32	3.94	2.08	1.67	0.45	0.73	-1.13E+00	1.84E-02		-5.71E-02	9.13E-01		-1.31E-01	7.08E-01		-1.06E+00	4.58E-04	Down	-1.90E+00	2.25E-04	Down	-1.21E+00	8.84E-03		Unigene40214_All//gi|224125028|ref|XP_002329873.1|//2.00E-52//GRAS family transcription factor [Populus trichocarpa] >gi|222871110|gb|EEF08241.1| GRAS family transcription factor [Populus trichocarpa]	Unigene40214_All//3.00E-16//AT3G60630| scarecrow transcription factor family protein	Unigene40214_All//0.00E+00//gi|78349823|gb|DT570097.1|DT570097	GRAS			nr +
Unigene40216_All	644	3.98	1.26	0.74	1.16	1.28	1.47	4.66	6.49	4.08	-1.66E+00	8.88E-05	Down	-2.42E+00	7.24E-07	Down	1.45E-01	8.70E-01		3.44E-01	6.49E-01		4.78E-01	7.83E-02		-1.91E-01	5.85E-01		Unigene40216_All//gi|115484967|ref|NP_001067627.1|//2.00E-06//Os11g0251400 [Oryza sativa Japonica Group] >gi|62733062|gb|AAY95179.1|expressed protein [Oryza sativa Japonica Group] >gi|77549628|gb|ABA92425.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108864196|gb|ABG22429.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108864197|gb|ABG22430.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113644849|dbj|BAF27990.1|Os11g0251400 [Oryza sativa Japonica Group]		Unigene40216_All//7.00E-106//gi|109890353|gb|DW519317.1|DW519317				nr -
Unigene40218_All	648	2.10	3.60	5.09	2.61	3.40	6.76	1.96	3.35	2.40	7.77E-01	6.36E-02		1.28E+00	4.59E-04	Up	3.80E-01	4.24E-01		1.37E+00	4.04E-06	Up	7.77E-01	4.63E-02		2.93E-01	5.53E-01				Unigene40218_All//8.00E-07//ES849681				
Unigene40219_All	1494	0.98	2.41	1.71	0.33	0.18	0.06	24.96	15.50	21.97	1.30E+00	1.18E-04	Up	8.03E-01	5.20E-02		-8.54E-01	4.07E-01		-2.46E+00	4.83E-02		-6.88E-01	5.22E-18		-1.84E-01	2.13E-02		Unigene40219_All//gi|30687527|ref|NP_194455.2|//1.00E-112//dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family [Arabidopsis thaliana]	Unigene40219_All//1.00E-108//AT4G27250| dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family	Unigene40219_All//0.00E+00//gi|78333082|gb|DT553356.1|DT553356		ko00941|Flavonoid biosynthesis	GO:0008152	nr -
Unigene40220_All	447	1.29	3.17	0.95	0.56	1.16	0.61	3.41	7.48	6.15	1.30E+00	2.42E-02		-4.34E-01	6.23E-01		1.05E+00	3.49E-01		1.22E-01	9.44E-01		1.14E+00	2.17E-04	Up	8.53E-01	9.34E-03				Unigene40220_All//5.00E-118//TC153285				
Unigene40221_All	1478	1.31	1.23	1.19	5.93	9.20	3.09	1.97	0.76	2.13	-8.58E-02	8.47E-01		-1.40E-01	7.63E-01		6.34E-01	9.42E-06		-9.43E-01	8.97E-07		-1.37E+00	5.29E-05	Down	1.10E-01	7.33E-01		Unigene40221_All//gi|15227816|ref|NP_179917.1|//2.00E-93//transport protein-related [Arabidopsis thaliana] >gi|75206690|sp|Q9SLN1.1|FPP7_ARATH RecName: Full=Filament-like plant protein 7; Short=AtFPP7	Unigene40221_All//2.00E-77//AT2G23360| transport protein-related	Unigene40221_All//0.00E+00//DT462205				nr -
Unigene40224_All	293	1.07	1.56	1.45	3.74	0.12	1.08	3.46	3.99	2.58	5.39E-01	6.02E-01		4.40E-01	6.77E-01		-4.99E+00	5.16E-07	Down	-1.79E+00	1.01E-02		2.06E-01	7.23E-01		-4.23E-01	4.77E-01				Unigene40224_All//9.00E-48//TC135755				
Unigene40228_All	613	0.51	0.00	1.39	9.26	3.48	3.39	11.17	11.59	15.53	-9.00E+00	3.65E-02		1.44E+00	8.22E-02		-1.41E+00	3.48E-09	Down	-1.45E+00	1.61E-08	Down	5.29E-02	8.15E-01		4.75E-01	3.35E-03		Unigene40228_All//gi|18409123|ref|NP_564943.1|//3.00E-11//CLE12 (CLAVATA3/ESR-RELATED 12); protein binding / receptor binding [Arabidopsis thaliana] >gi|89111846|gb|ABD60695.1|At1g68795 [Arabidopsis thaliana]	Unigene40228_All//9.00E-11//AT1G73965| CLE13 (CLAVATA3/ESR-RELATED 13); protein binding / receptor binding	Unigene40228_All//3.00E-09//DR454415				nr +
Unigene40229_All	254	24.31	49.07	27.88	33.93	26.84	33.96	190.76	175.90	125.16	1.01E+00	7.88E-10	Up	1.98E-01	4.08E-01		-3.38E-01	8.82E-02		1.40E-03	9.97E-01		-1.17E-01	1.27E-01		-6.08E-01	2.50E-19		Unigene40229_All//gi|209865725|gb|ACC66148.3|//3.00E-23//cell division cycle protein [Dimocarpus longan] >gi|221327637|gb|ACM17483.1| cell division cycle protein [Dimocarpus longan]	Unigene40229_All//3.00E-20//AT3G53230| cell division cycle protein 48, putative / CDC48, putative	Unigene40229_All//2.00E-128//EX172244		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene40231_All	719	0.15	6.62	0.44	0.07	0.10	3.58	2.41	5.81	2.16	5.51E+00	3.99E-24	Up	1.61E+00	3.05E-01		4.67E-01	9.58E-01		5.69E+00	5.37E-14	Up	1.27E+00	3.75E-06	Up	-1.58E-01	7.12E-01		Unigene40231_All//gi|193806744|sp|Q9LPK5.2|CML44_ARATH//9.00E-32//RecName: Full=Probable calcium-binding protein CML44; AltName: Full=Calmodulin-like protein 44	Unigene40231_All//6.00E-32//AT1G21550| calcium-binding protein, putative	Unigene40231_All//0.00E+00//DN827375		ko04626|Plant-pathogen interaction		nr +
Unigene40236_All	1169	0.27	1.04	0.09	1.92	1.65	3.79	0.07	0.86	0.61	1.95E+00	4.09E-03		-1.56E+00	3.30E-01		-2.17E-01	6.15E-01		9.81E-01	6.32E-04		3.57E+00	3.07E-05	Up	3.08E+00	1.17E-03		Unigene40236_All//gi|82697961|gb|AB889015.1|//1.00E-109//CXE carboxylesterase [Actinidia deliciosa]	Unigene40236_All//2.00E-92//AT5G16080| AtCXE17 (Arabidopsis thaliana carboxyesterase 17); hydrolase					nr +
Unigene40239_All	484	5.73	9.11	14.96	17.81	25.61	19.69	1.40	0.35	0.99	6.69E-01	2.05E-02		1.38E+00	5.27E-09	Up	5.25E-01	5.84E-04		1.45E-01	5.12E-01		-2.02E+00	1.98E-02		-5.01E-01	5.07E-01				Unigene40239_All//8.00E-108//gi|78323809|gb|DT544083.1|DT544083				
Unigene4024_All	643	60.13	136.88	91.84	16.81	26.94	21.70	19.33	44.59	32.59	1.19E+00	1.58E-83	Up	6.11E-01	4.76E-18		6.80E-01	4.60E-08		3.69E-01	1.60E-02		1.21E+00	1.03E-34	Up	7.53E-01	1.78E-12		Unigene4024_All//gi|8778440|gb|AAF79448.1|AC025808.30//1.00E-23//F18014.16 [Arabidopsis thaliana]	Unigene4024_All//5.00E-25//AT1G19400| unknown protein	Unigene4024_All//0.00E+00//EY198110				nr +
Unigene40241_All	490	1.39	1.96	1.63	1.12	2.25	2.03	2.93	0.68	1.54	5.01E-01	4.72E-01		2.32E-01	7.49E-01		1.01E+00	1.37E-01		8.59E-01	2.35E-01		-2.10E+00	1.56E-04	Down	-9.25E-01	5.24E-02		Unigene40241_All//gi|30697827|ref|NP_177089.2|//1.00E-51//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|193806277|sp|P0C7R4.1|PP110_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g69290	Unigene40241_All//3.00E-45//AT1G69290| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene40244_All	699	0.75	3.33	2.44	2.49	4.09	2.65	1.81	2.87	5.98	2.16E+00	7.36E-06	Up	1.70E+00	2.37E-03		7.13E-01	5.38E-02		8.69E-02	8.76E-01		6.61E-01	1.09E-01		1.72E+00	1.92E-09	Up	Unigene40244_All//gi|156972244|gb|ABU98950.1|//2.00E-16//acyl-CoA oxidase [Glycine max]	Unigene40244_All//1.00E-17//AT3G51840| ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase	Unigene40244_All//2.00E-87//CO121053		ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation		nr +
Unigene40245_All	1126	0.19	0.18	0.09	17.56	11.77	12.19	4.02	1.26	0.57	-4.65E-02	9.88E-01		-9.75E-01	6.20E-01		-5.77E-01	3.69E-07		-5.27E-01	1.23E-05		-1.67E+00	1.55E-09	Down	-2.83E+00	2.96E-18	Down	Unigene40245_All//gi|115438913|ref|NP_001043736.1|//1.00E-113//Os01g0652100 [Oryza sativa Japonica Group] >gi|19571145|dbj|BAB86568.1|lustrin A-like [Oryza sativa Japonica Group] >gi|113533267|dbj|BAF05650.1|Os01g0652100 [Oryza sativa Japonica Group]	Unigene40245_All//2.00E-107//AT3G14850| unknown protein	Unigene40245_All//0.00E+00//TC171343				nr +
Unigene40246_All	1753	0.18	0.20	0.12	0.23	0.22	0.41	12.78	6.41	3.36	1.76E-01	8.83E-01		-5.60E-01	6.63E-01		-7.29E-02	9.25E-01		8.59E-01	3.42E-01		-9.95E-01	2.95E-20		-1.93E+00	2.57E-55	Down	Unigene40246_All//gi|297845276|ref|XP_002890519.1|//0.00E+00//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336361|gb|EFH66778.1|proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40246_All//2.00E-165//AT1G22540| proton-dependent oligopeptide transport (POT) family protein	Unigene40246_All//0.00E+00//TC176037				nr -
Unigene40247_All	1449	1.23	0.73	0.99	2.58	6.42	2.56	0.29	0.43	0.27	-7.42E-01	1.29E-01		-3.07E-01	5.62E-01		1.32E+00	1.69E-12	Up	-1.27E-02	9.62E-01		5.68E-01	5.04E-01		-8.61E-02	9.39E-01		Unigene40247_All//gi|168805188|gb|ACA28679.1|//1.00E-153//male sterility-related protein [Linum usitatissimum] >gi|168805190|gb|ACA28680.1| male sterility-related protein [Linum usitatissimum]	Unigene40247_All//7.00E-138//AT3G11980| MS2 (MALE STERILITY 2); fatty acyl-CoA reductase (alcohol-forming)/ oxidoreductase, acting on the CH-CH group of donors, NAD or NADP as acceptor	Unigene40247_All//2.00E-108//gi|195983100|gb|FL576733.1|FL576733		ko04146|Peroxisome		nr +
Unigene4025_All	958	2.57	5.50	3.39	1.72	2.80	1.56	2.43	3.75	3.16	1.10E+00	3.66E-05	Up	4.02E-01	2.75E-01		7.08E-01	6.64E-02		-1.41E-01	7.85E-01		6.28E-01	3.10E-02		3.81E-01	2.37E-01		Unigene4025_All//gi|8778440|gb|AAF79448.1|AC025808.30//2.00E-23//F18014.16 [Arabidopsis thaliana]	Unigene4025_All//1.00E-24//AT1G19400| unknown protein	Unigene4025_All//0.00E+00//ES804320				nr +
Unigene40250_All	213	22.35	7.61	24.75	17.31	13.58	11.66	27.19	17.07	25.25	-1.55E+00	1.57E-07	Down	1.47E-01	6.36E-01		-3.50E-01	3.03E-01		-5.70E-01	7.96E-02		-6.72E-01	2.20E-03		-1.07E-01	6.37E-01				Unigene40250_All//8.00E-100//gi|13349889|gb|BG440238.1|BG440238				
Unigene40251_All	464	77.80	80.59	92.38	60.01	72.80	72.03	571.42	317.16	110.16	5.08E-02	6.15E-01		2.48E-01	4.11E-03		2.79E-01	1.89E-03		2.63E-01	5.40E-03		-8.49E-01	2.78E-177		-2.38E+00	0.00E+00	Down	Unigene40251_All//gi|89973462|gb|AB853472.1|//1.00E-23//GDP-D-mannose-3',5'-epimerase [Malpighia glabra]	Unigene40251_All//6.00E-23//AT5G28840| GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-mannose 3,5-epimerase/ NAD or NADH binding / catalytic	Unigene40251_All//0.00E+00//TC143049		ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene40253_All	425	1.11	1.79	4.89	2.81	1.05	2.55	0.80	2.56	1.12	6.91E-01	3.76E-01		2.14E+00	5.02E-05	Up	-1.42E+00	1.82E-02		-1.41E-01	8.16E-01		1.68E+00	6.96E-03		4.99E-01	6.12E-01				Unigene40253_All//1.00E-07//ES838061				

Unigene40255_All	726	2.38	1.26	0.44	2.26	2.28	1.68	22.83	7.77	6.97	-9.21E-01	6.50E-02		-2.43E+00	7.48E-05	Down	7.90E-03	9.98E-01		-4.31E-01	4.32E-01		-1.55E+00	1.01E-29	Down	-1.71E+00	4.40E-35	Down	Unigene40255_All//gi|3540195|gb|AAC34345.1|/6.00E-77//Unknown protein [Arabidopsis thaliana]	Unigene40255_All//2.00E-71//AT1G77130| PGSIP2 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 2); transferase, transferring glycosyl groups	Unigene40255_All//0.00E+00//CO123151				nr +
Unigene40257_All	965	1.36	2.15	3.75	1.70	2.50	1.50	0.00	0.00	6.67E-01	1.37E-01		1.47E+00	3.17E-05	Up	5.52E-01	1.95E-01		-1.86E-01	7.15E-01		null	null		null	null		Unigene40257_All//gi|183211896|gb|ACC59198.1|/1.00E-101//1-acyl-sn-glycerol-3-phosphate acyltransferase [Ricinus communis]	Unigene40257_All//4.00E-89//AT3G57650| LPAT2; 1-acylglycerol-3-phosphate O-acyltransferase	Unigene40257_All//0.00E+00//ES819567		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr -
Unigene40258_All	212	15.55	13.86	16.33	39.95	33.14	41.75	149.38	79.65	72.16	-1.66E-01	6.15E-01		7.05E-02	8.36E-01		-2.70E-01	1.99E-01		6.39E-02	7.73E-01		-9.07E-01	2.31E-24		-1.05E+00	9.92E-32	Down	Unigene40258_All//gi|162458637|ref|NP_001105506.1|/2.00E-31//pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays] >gi|3851001|gb|AAC72193.1| pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]	Unigene40258_All//5.00E-32//AT5G50850| MAB1 (MACC1-BOU); catalytic/ pyruvate dehydrogenase (acetyl-transferring)	Unigene40258_All//1.00E-116//ES812420		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)//ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis		nr -
Unigene40260_All	581	0.36	3.31	0.37	1.80	0.53	1.55	5.53	2.66	4.05	3.20E+00	3.42E-07	Up	2.54E-02	1.00E+00		-1.76E+00	8.43E-03		-2.12E-01	7.44E-01		-1.06E+00	7.09E-04	Down	-4.51E-01	1.38E-01									
Unigene40261_All	672	1.48	0.15	0.48	0.52	0.05	0.60	2.83	2.74	2.96	-3.29E+00	3.81E-04	Down	-1.64E+00	3.43E-02		-3.34E+00	4.06E-02		2.21E-01	8.63E-01		-4.91E-02	9.25E-01		6.62E-02	8.84E-01				Unigene40261_All//5.00E-08//TC130103				
Unigene40262_All	432	13.56	3.52	1.97	39.21	22.64	10.87	2.15	0.48	0.00	-1.95E+00	3.69E-12	Down	-2.78E+00	1.91E-17	Down	-7.92E-01	1.69E-10		-1.85E+00	3.08E-34	Down	-2.15E+00	2.94E-03		-1.11E+01	5.47E-07	Down	Unigene40262_All//gi|1524019|ref|NP_201508.1|/5.00E-32//RALFL34 (ralf-like 34); signal transducer [Arabidopsis thaliana]	Unigene40262_All//2.00E-28//AT5G67070| RALFL34 (ralf-like 34); signal transducer	Unigene40262_All//0.00E+00//gi|109888798|gb|DW517767.1|DW517767				nr +
Unigene40266_All	850	0.25	0.12	0.38	3.52	2.23	0.69	3.23	2.36	0.70	-1.05E+00	5.64E-01		6.11E-01	6.24E-01		-6.58E-01	5.84E-02		-2.35E+00	1.37E-08	Down	-4.54E-01	1.98E-01		-2.20E+00	9.40E-09	Down	Unigene40266_All//gi|7340688|emb|CAB82987.1|/1.00E-119//thaumatin-like protein [Arabidopsis thaliana]	Unigene40266_All//2.00E-118//AT5G02140| thaumatin-like protein, putative					nr +
Unigene40267_All	423	1.48	0.84	0.50	2.94	2.77	1.28	4.00	1.19	1.88	-8.24E-01	3.75E-01		-1.56E+00	1.29E-01		-8.91E-02	8.70E-01		-1.20E+00	5.16E-02		-1.75E+00	2.90E-04	Down	-1.09E+00	1.30E-02		Unigene40267_All//gi|297845438|ref|XP_002890600.1|/1.00E-23//GAMMA-ADAPTIN 1 [Arabidopsis lyrata subsp. lyrata] >gi|297336442|gb|EFH66859.1| GAMMA-ADAPTIN 1 [Arabidopsis lyrata subsp. lyrata]	Unigene40267_All//3.00E-22//AT1G23900| GAMMA-ADAPTIN 1 (GAMMA-ADAPTIN 1); binding / clathrin binding / protein binding / protein transporter	Unigene40267_All//2.00E-176//DW499752				nr -
Unigene40269_All	984	7.71	1.75	0.32	16.15	17.22	14.50	0.64	0.17	0.00	-2.14E+00	1.85E-17	Down	-4.57E+00	8.41E-34	Down	9.24E-02	5.87E-01		-1.55E-01	3.46E-01		-1.92E+00	3.09E-02		-9.33E+00	7.11E-05	Down	Unigene40269_All//gi|57222140|gb|AAW38972.1|/1.00E-81//At5g49800 [Arabidopsis thaliana]	Unigene40269_All//3.00E-83//AT5G49800| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, C globular stage, petal differentiation and expansion stage, D bilateral stage; CONTAINS InterPro DOMAIN/s: Lipid-binding START (InterPro:IPR002291); Has 156 Blast hits to 155 proteins in 50 species: Archae - 0; Bacteria - 14; Metazoa - 91; Fungi - 2; Plants - 15; Viruses - 0; Other Eukaryotes - 34 (source: NCBI BLink).	Unigene40269_All//0.00E+00//gi|164334819|gb|ES806200.1|ES806200				nr +
Unigene40271_All	481	14.03	1.47	8.52	8.39	3.29	1.41	2.37	0.43	1.08	-3.25E+00	2.29E-24	Down	-7.19E-01	2.22E-03		-1.35E+00	2.84E-06	Down	-2.57E+00	1.22E-12	Down	-2.45E+00	2.46E-04	Down	-1.14E+00	3.90E-02				Unigene40271_All//9.00E-09//DR463838				
Unigene40273_All	634	859.08	762.60	905.84	30.72	29.82	18.88	94.76	101.65	34.75	-1.72E-01	4.52E-16		7.65E-02	6.45E-04		-4.30E-02	8.05E-01		-7.03E-01	7.42E-09		1.01E-01	1.27E-01		-1.45E+00	5.71E-98	Down	Unigene40273_All//gi|231688|sp|P30567.1|CAT2_GOSHI//3.00E-65//RecName: Full=Catalase isozyme 2 >gi|184488|emb|CAA39998.1| subunit 2 of cotton catalase [Gossypium hirsutum]	Unigene40273_All//4.00E-58//AT4G35090| CAT2 (CATALASE 2); catalase	Unigene40273_All//0.00E+00//gi|109836944|gb|DW235505.1|DW235505		ko04146|Peroxisome//ko00380|Tryptophan metabolism		nr +
Unigene40274_All	346	12.40	3.81	11.23	9.07	13.04	11.10	1.71	1.09	1.84	-1.70E+00	1.04E-07	Down	-1.42E-01	6.36E-01		5.24E-01	6.81E-02		2.91E-01	4.04E-01		-6.54E-01	4.45E-01		1.07E-01	9.01E-01		Unigene40274_All//gi|225429222|ref|XP_002263300.1|/1.00E-28//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene40274_All//2.00E-21//AT5G09580| unknown protein	Unigene40274_All//1.00E-158//ES835743				nr -
Unigene40276_All	740	0.14	0.75	0.79	0.67	2.65	1.65	1.89	1.02	2.75	2.41E+00	3.93E-02		2.49E+00	3.75E-02		1.98E+00	6.34E-05	Up	1.29E+00	4.33E-02		-8.91E-01	7.94E-02		5.42E-01	1.71E-01		Unigene40276_All//gi|42569320|ref|NP_180137.2|/3.00E-87//emb2410 (embryo defective 2410) [Arabidopsis thaliana]	Unigene40276_All//7.00E-83//AT2G25660| emb2410 (embryo defective 2410)	Unigene40276_All//0.00E+00//TC133449				nr +
Unigene40277_All	584	0.81	0.09	1.09	11.52	1.95	1.24	19.11	25.26	2.87	-3.22E+00	2.73E-02		4.41E-01	6.23E-01		-2.57E+00	6.77E-24	Down	-3.22E+00	4.38E-26	Down	4.03E-01	2.12E-03		-2.74E+00	1.67E-42	Down	Unigene40277_All//gi|208427035|gb|ACI26699.1|/6.00E-22//lipid transfer protein [Gossypium hirsutum]	Unigene40277_All//4.00E-13//AT3G18280| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene40277_All//0.00E+00//gi|109884862|gb|DW513832.1|DW513832				nr -
Unigene40279_All	1251	0.38	0.24	0.17	0.72	0.41	0.97	0.61	5.71	4.59	-6.31E-01	5.54E-01		-1.14E+00	3.32E-01		-7.96E-01	2.75E-01		4.43E-01	5.00E-01		3.23E+00	3.65E-31	Up	2.91E+00	2.95E-23	Up	Unigene40279_All//gi|15228637|ref|NP_187030.1|/1.00E-107//SYP131 (SYNTAXIN OF PLANTS 131); SNAP receptor [Arabidopsis thaliana] >gi|28380139|sp|Q9SRV7.1|SY131_ARATH RecName: Full=Putative syntaxin-131; Short=AtSYP131 >gi|6006872|gb|AAF00648.1|AC009540_25 s-syntaxin-like protein [Arabidopsis thaliana]	Unigene40279_All//1.00E-102//AT3G03800| SYP131 (SYNTAXIN OF PLANTS 131); SNAP receptor	Unigene40279_All//0.00E+00//TC176100		ko04130|SNARE interactions in vesicular transport		nr +
Unigene40280_All	1541	0.00	0.00	0.00	0.10	0.04	0.00	105.88	43.45	19.49	null	null		null	null		-1.12E+00	5.83E-01		-6.60E+00	2.33E-01		-1.29E+00	1.04E-214	Down	-2.44E+00	0.00E+00	Down	Unigene40280_All//gi|46577788|gb|AT01414.1|/1.00E-142//iron regulated transporter [Cucumis sativus]	Unigene40280_All//2.00E-121//AT4G19690| IRT1 (iron-regulated transporter 1); cadmium ion transmembrane transporter/ copper uptake transmembrane transporter/ iron ion transmembrane transporter/ manganese ion transmembrane transporter/ zinc ion transmembrane transporter	Unigene40280_All//0.00E+00//TC148511				nr -
Unigene40282_All	451	0.35	1.69	3.54	2.87	2.60	3.50	1.13	1.02	1.33	2.28E+00	1.60E-02		3.35E+00	5.08E-06	Up	-1.46E-01	8.22E-01		2.87E-01	6.43E-01		-1.42E-01	8.76E-01		2.36E-01	7.56E-01									
Unigene40284_All	472	39.13	25.76	21.32	196.41	221.64	208.98	156.49	71.11	132.51	-6.03E-01	2.66E-06		-8.76E-01	8.04E-11		1.74E-01	3.51E-04		8.95E-02	1.32E-01		-1.14E+00	1.27E-80	Down	-2.40E-01	7.09E-06		Unigene40284_All//gi|211906444|gb|ACJ11715.1|/1.00E-56//fructokinase [Gossypium hirsutum]	Unigene40284_All//3.00E-48//AT3G59480| pfkB-type carbohydrate kinase family protein	Unigene40284_All//0.00E+00//gi|11202337|gb|BF271342.1|BF271342		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene40286_All	311	5.22	11.89	9.76	13.45	6.20	4.94	60.50	32.52	36.25	1.19E+00	2.85E-04	Up	9.04E-01	1.57E-02		-1.12E+00	5.85E-05	Down	-1.45E+00	2.03E-06	Down	-8.95E-01	1.68E-14		-7.39E-01	5.26E-11				Unigene40286_All//6.00E-163//TC177009				
Unigene40288_All	606	0.69	1.17	0.35	10.60	6.02	5.66	9.07	0.76	1.84	7.61E-01	3.62E-01		-9.75E-01	4.11E-01		-8.16E-01	1.51E-04		-9.05E-01	7.46E-05		-3.58E+00	2.06E-26	Down	-2.30E+00	1.35E-17	Down	Unigene40288_All//gi|18407840|ref|NP_566871.1|/4.00E-10//PSK1; growth factor [Arabidopsis thaliana] >gi|29428768|sp|Q8LA14.2|PSK6_ARATH RecName: Full=Putative phytosulfokines 6; Short=AtPSK6; Short=AtPSK3_2; Contains: RecName: Full=Phytosulfokine-alpha-like; Short=PSK-alpha-like; Short=Phytosulfokine-a-like; Contains: RecName: Full=Phytosulfokine-beta; Short=PSK-beta; Short=Phytosulfokine-b; Flags: Precursor >gi|27808144|dbj|BAB72177.2| phytosulfokine precursor 3_2 [Arabidopsis thaliana] >gi|88010851|gb|ABD38863.1| At3g44735 [Arabidopsis thaliana]	Unigene40288_All//1.00E-04//AT3G44735| PSK1; growth factor	Unigene40288_All//2.00E-155//DW507648				nr +
Unigene40290_All	443	2.95	7.21	6.49	11.58	10.03	8.67	0.86	0.47	2.25	1.29E+00	3.45E-04	Up	1.14E+00	3.68E-03		-2.08E-01	4.87E-01		-4.19E-01	1.31E-01		-8.65E-01	4.41E-01		1.39E+00	2.47E-02		Unigene40290_All//gi|297806821|ref|XP_002871294.1|/2.00E-18//mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317131|gb|EFH47553.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40290_All//2.00E-19//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein					nr +
Unigene40293_All	580	1.71	2.53	6.43	4.47	6.17	3.89	1.31	1.15	0.96	5.64E-01	3.11E-01		1.91E+00	2.00E-07	Up	4.67E-01	1.64E-01		-1.98E-01	6.43E-01		-1.87E-01	7.91E-01		-4.48E-01	5.31E-01		Unigene40293_All//gi|28804252|dbj|BAC58020.1|/3.00E-07//angustifolia [Ipomoea nil] >gi|28804254|dbj|BAC58021.1| angustifolia [Ipomoea nil]	Unigene40293_All//1.00E-07//AT1G01510| AN (ANGUSTIFOLIA); protein binding	Unigene40293_All//2.00E-10//TC145181				nr +
Unigene40295_All	445	1.41	0.11	0.36	1.01	1.24	1.62	2.28	1.69	6.18	-3.63E+00	5.07E-03		-1.97E+00	6.50E-02		2.97E-01	8.18E-01		6.89E-01	4.48E-01		-4.32E-01	5.03E-01		1.44E+00	3.35E-05	Up			Unigene40295_All//1.00E-161//DW483049				
Unigene40296_All	555	181.57	570.05	385.89	99.45	162.68	90.65	0.15	1.66	0.00	1.65E+00	0.00E+00	Up	1.09E+00	8.04E-172	Up	7.10E-01	2.13E-43		-1.34E-01	8.76E-02		3.44E+00	9.84E-05	Up	-7.25E+00	3.58E-01		Unigene40296_All//gi|45476543|gb|AAS65937.1|/1.00E-27//At2g27385 [Arabidopsis thaliana] >gi|46359825|gb|AAS88776.1| At2g27385 [Arabidopsis thaliana]	Unigene40296_All//3.00E-18//AT2G27385| unknown protein	Unigene40296_All//0.00E+00//DW515441				nr -
Unigene40297_All	1230	0.00	0.08	0.35	0.00	0.00	0.00	5.60	6.42	13.34	6.36E+00	3.86E-01		8.44E+00	1.38E-02		null	null		null	null		1.97E-01	3.51E-01		1.25E+00	6.54E-22	Up	Unigene40297_All//gi|297829824|ref|XP_002882794.1|/1.00E-134//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328634|gb|EFH59053.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene40297_All//1.00E-131//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene40297_All//8.00E-27//TC134433		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene40299_All	688	0.00	0.00	0.00	3.11	2.10	6.56	8.05	21.75	10.25	null	null		null	null		-5.67E-01	1.93E-01		1.08E+00	1.59E-04	Up	1.43E+00	6.53E-24	Up	3.48E-01	7.64E-02		Unigene40299_All//gi|20197330|gb|AAM15027.1|AC005311_15//6.00E-06//CLE7 [Arabidopsis thaliana]	Unigene40299_All//3.00E-06//AT2G31083| CLE5 (CLAVATA3/ESR-RELATED 5); protein binding / receptor binding					nr -
Unigene4030_All	1132	6.15	2.33	2.31	5.41	5.38	5.90	5.86	4.84	3.17	-1.40E+00	3.02E-09	Down	-1.42E+00	6.47E-09	Down	-7.60E-03	9.67E-01		1.26E-01	6.37E-01		-2.78E-01	2.08E-01		-8.89E-01	8.60E-06		Unigene4030_All//gi|75162595|sp|Q8W593.1|LGLC_ARATH//1.00E-130//RecName: Full=Probable lactoylglutathione lyase, chloroplast; AltName: Full=Glyoxalase I; Flags: Precursor >gi|16930396|gb|AAL31884.1|AF419550_1_1 At1g67280/F1N21_10 [Arabidopsis thaliana] >gi|19310505|gb|AAL84986.1| At1g67280/F1N21_10 [Arabidopsis thaliana]	Unigene4030_All//4.00E-126//AT1G67280| lactoylglutathione lyase, putative / glyoxalase I, putative	Unigene4030_All//0.00E+00//CO091764		ko00620|Pyruvate metabolism		nr +

Unigene40300_All	1003	1.30	0.81	1.49	7.20	15.76	12.97	0.30	0.58	0.12	-6.90E-01	2.32E-01		1.89E-01	7.21E-01		1.13E+00	1.15E-16	Up	8.49E-01	3.64E-08		9.83E-01	2.59E-01		-1.31E+00	3.13E-01		Unigene40300_All//gi|18406012|ref|NP_565978.1|//3.00E-77//LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|30689086|ref|NP_850374.1| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|6691165|gb|AAF24517.1|AF218765 _1 177 protein [Arabidopsis thaliana] >gi|4559231|gb|AAD22993.1| expressed protein [Arabidopsis thaliana] >gi|28372972|gb|AAO39968.1| At2g42610 [Arabidopsis thaliana]	Unigene40300_All//2.00E-74//AT2G42610| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10)	Unigene40300_All//0.00E+00//TC135451				nr +
Unigene40301_All	984	0.32	0.62	1.30	3.44	10.71	6.43	0.09	0.09	0.08	9.54E-01	3.14E-01		2.03E+00	3.44E-03		1.64E+00	2.62E-19	Up	9.00E-01	1.07E-04		-1.52E-02	1.01E+00		-8.47E-02	9.72E-01		Unigene40301_All//gi|297836566|ref|XP_002886165.1|//2.00E-59//ATHB24 [Arabidopsis lyrata subsp. lyrata] >gi|297332005|gb|EFH62424.1| ATHB24 [Arabidopsis lyrata subsp. lyrata]	Unigene40301_All//7.00E-55//AT1G75240| AtHB33 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 33); DNA binding / transcription factor	Unigene40301_All//0.00E+00//gi|78331690|gb|DT551964.1|DT551964	zf-HD			nr -
Unigene40303_All	752	2.09	1.82	0.42	0.86	1.14	0.42	1.35	0.50	0.85	-1.98E-01	6.85E-01		-2.30E+00	3.17E-04	Down	4.11E-01	6.11E-01		-1.03E+00	2.68E-01		-1.43E+00	2.36E-02		-6.71E-01	2.53E-01		Unigene40303_All//gi|40538933|gb|AA887190.1|//7.00E-23//expressed protein [Oryza sativa Japonica Group]	Unigene40303_All//1.00E-19//AT4G14240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF21 (InterPro:IPR002550), Cystathionine beta-synthase, core (InterPro:IPR000644); BEST Arabidopsis thaliana protein match is: CBS domain-containing protein-related (TAIR:AT4G14230.1); Has 6770 Blast hits to 6657 proteins in 1347 species: Archae - 62; Bacteria - 4461; Metazoa - 254; Fungi - 179; Plants - 121; Viruses - 0; Other Eukaryotes - 1693 (source: NCBI BLink).	Unigene40303_All//0.00E+00//TC172662				nr -
Unigene40305_All	502	1.25	0.61	0.85	1.19	0.14	0.00	4.55	3.41	3.73	-1.05E+00	2.50E-01		-5.60E-01	5.53E-01		-3.12E+00	4.87E-03		-1.02E+01	7.70E-04	Down	-4.14E-01	2.99E-01		-2.86E-01	4.57E-01		Unigene40305_All//gi|224122896|ref|XP_002318943.1|//6.00E-31//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222857319|gb|EEE94866.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene40305_All//6.00E-19//AT5G05400| disease resistance protein (CC-NBS-LRR class), putative	Unigene40305_All//3.00E-58//TC162123		ko04626|Plant-pathogen interaction		nr +
Unigene40306_All	880	0.48	6.91	3.27	6.79	6.30	4.93	4.37	0.66	0.27	3.86E+00	4.52E-25	Up	2.78E+00	7.69E-09	Up	-1.09E-01	7.04E-01		-4.63E-01	6.17E-02		-2.72E+00	1.70E-14	Down	-4.01E+00	4.66E-21	Down	Unigene40306_All//gi|115449115|ref|NP_001048337.1|//3.00E-56//Os02g0786900 [Oryza sativa Japonica Group] >gi|113537868|dbj|BAF10251.1| Os02g0786900 [Oryza sativa Japonica Group]	Unigene40306_All//6.00E-63//AT4G25780| pathogenesis-related protein, putative	Unigene40306_All//0.00E+00//gi|109874957|gb|DW503931.1|DW503931		ko04626|Plant-pathogen interaction		nr +
Unigene40307_All	655	80.28	46.41	34.15	213.86	245.41	197.00	0.13	0.00	0.00	-7.90E-01	5.56E-26		-1.23E+00	1.19E-51	Down	1.99E-01	1.15E-07		-1.19E-01	9.13E-03		-7.01E+00	4.03E-01		-7.01E+00	3.58E-01		Unigene40307_All//gi|8745402|gb|AAF78903.1|AF248055_1//3.00E-26//proline-rich protein [Glycine max]	Unigene40307_All//2.00E-12//AT2G45180| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene40307_All//0.00E+00//TC140330				nr +
Unigene40308_All	699	0.15	0.43	0.00	5.42	5.32	2.71	63.87	41.74	7.01	1.54E+00	3.23E-01		-7.23E+00	3.93E-01		-2.57E-02	9.42E-01		-9.97E-01	1.40E-03		-6.14E-01	1.18E-17		-3.19E+00	3.56E-196	Down	Unigene40308_All//gi|9294177|dbj|BAB02079.1|//3.00E-30//nodulin-like protein [Arabidopsis thaliana]	Unigene40308_All//4.00E-31//AT3G25190| nodulin, putative	Unigene40308_All//2.00E-137//gi|109868194|gb|DW497167.1|DW497167				nr -
Unigene40311_All	609	0.17	0.50	2.45	0.82	1.24	1.93	1.18	1.17	1.83	1.54E+00	3.23E-01		3.83E+00	3.20E-06	Up	6.05E-01	5.14E-01		1.24E+00	5.89E-02		-1.66E-02	1.02E+00		6.34E-01	2.59E-01		Unigene40311_All//gi|225459056|ref|XP_002285638.1|//7.00E-58//PREDICTED: similar to SAB [Vitis vinifera]	Unigene40311_All//3.00E-36//AT1G68250| SAB (SABRE)					nr +
Unigene40312_All	822	1.08	0.55	0.32	1.94	1.26	1.37	1.70	0.81	0.34	-9.64E-01	1.95E-01		-1.74E+00	3.79E-02		-6.26E-01	2.24E-01		-4.98E-01	3.77E-01		-1.06E+00	3.74E-02		-2.32E+00	4.25E-05	Down	Unigene40312_All//gi|18412056|ref|NP_565185.1|//7.00E-29//POLD3; DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|4836868|gb|AAD30571.1|AC007260 _2 Hypothetical protein [Arabidopsis thaliana]	Unigene40312_All//6.00E-09//AT1G78650| POLD3; DNA-directed DNA polymerase	Unigene40312_All//0.00E+00//ES850046		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +
Unigene40313_All	658	1.99	0.62	1.29	1.36	1.15	2.13	0.58	1.33	2.66	-1.69E+00	7.07E-03		-6.19E-01	3.20E-01		-2.43E-01	7.52E-01		6.43E-01	2.85E-01		1.21E+00	7.78E-02		2.20E+00	8.71E-06	Up									
Unigene40314_All	502	222.42	222.06	162.08	106.28	143.30	156.45	49.78	164.27	136.82	-2.30E-03	9.86E-01		-4.57E-01	5.17E-20		4.31E-01	2.27E-14		5.58E-01	1.74E-22		1.72E+00	1.59E-167	Up	1.46E+00	4.15E-112	Up	Unigene40314_All//gi|31747031|gb|AAP57672.1|//1.00E-06//MutT-like protein [Cucumis sativus]	Unigene40314_All//6.00E-06//AT1G14860| atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase	Unigene40314_All//0.00E+00//TC154246				nr +
Unigene40315_All	383	0.00	2.12	2.64	1.17	1.62	0.35	1.44	8.95	0.52	1.10E+01	9.38E-05	Up	1.14E+01	1.27E-05	Up	4.67E-01	6.35E-01		-1.73E+00	1.61E-01		2.64E+00	1.43E-12	Up	-1.46E+00	9.76E-02		Unigene40315_All//gi|124360058|gb|ABN08074.1|//2.00E-39//Gibberellin regulated protein [Medicago truncatula]	Unigene40315_All//1.00E-22//AT3G02885| GASA5 (GAST1 PROTEIN HOMOLOG 5)	Unigene40315_All//3.00E-23//TC159691				nr -
Unigene40317_All	813	0.26	6.79	0.98	5.33	4.32	3.83	1.40	2.21	0.74	4.72E+00	5.80E-26	Up	1.93E+00	3.42E-02		-3.03E-01	3.19E-01		-4.76E-01	1.16E-01		6.55E-01	1.38E-01		-9.34E-01	8.80E-02		Unigene40317_All//gi|27311725|gb|AA000828.1|//4.00E-26//Unknown protein [Arabidopsis thaliana] >gi|30725702|gb|AAP33873.1| At3g25590 [Arabidopsis thaliana]	Unigene40317_All//1.00E-25//AT3G25590| unknown protein	Unigene40317_All//0.00E+00//gi|78351933|gb|DT572207.1|DT572207				nr +
Unigene40318_All	968	49.35	21.30	41.70	7.10	9.85	5.46	0.17	0.00	0.08	-1.21E+00	2.33E-47	Down	-2.43E-01	2.83E-03		4.73E-01	9.09E-03		-3.80E-01	1.05E-01		-7.45E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene40318_All//gi|115484755|ref|NP_001067521.1|//2.00E-46//Os11g0220300 [Oryza sativa Japonica Group] >gi|108864149|gb|ABA92096.2| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113644743|dbj|BAF27884.1| Os11g0220300 [Oryza sativa Japonica Group]	Unigene40318_All//2.00E-98//AT1G32520| unknown protein	Unigene40318_All//0.00E+00//TC150396				nr -
Unigene40319_All	668	2.82	8.04	6.94	4.77	5.72	3.45	1.27	1.56	1.25	1.51E+00	4.78E-08	Up	1.30E+00	1.65E-05	Up	2.62E-01	4.61E-01		-4.69E-01	1.99E-01		3.05E-01	6.58E-01		-1.55E-02	9.71E-01		Unigene40319_All//gi|227206372|dbj|BAH57241.1|//1.00E-06//AT4G08580 [Arabidopsis thaliana]		Unigene40319_All//1.00E-82//ES837011				nr +
Unigene4032_All	587	0.36	1.55	0.00	1.70	3.46	2.15	19.30	10.97	3.87	2.12E+00	1.04E-02		-8.48E+00	1.45E-01		1.03E+00	2.26E-02		3.44E-01	6.24E-01		-8.16E-01	7.47E-08		-2.32E+00	9.07E-36	Down	Unigene4032_All//gi|224085996|ref|XP_002307770.1|//8.00E-75//acyl:coa ligase [Populus trichocarpa] >gi|222857219|gb|EEE94766.1| acyl:coa ligase [Populus trichocarpa]	Unigene4032_All//7.00E-64//AT1G20510| OPCL1 (OPC-8:0 COA LIGASE1); 4-coumarate-CoA ligase	Unigene4032_All//3.00E-132//ES793429		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene40320_All	486	459.26	77.26	288.82	164.41	236.09	128.43	0.00	0.00	0.08	-2.57E+00	0.00E+00	Down	-6.69E-01	2.42E-78		5.22E-01	5.09E-32		-3.56E-01	2.11E-10		null	null		6.36E+00	6.45E-01		Unigene40320_All//gi|6782440|gb|AAF28387.1|AF151216_1//1.00E-31//proline-rich protein [Nicotiana glauca]	Unigene40320_All//2.00E-15//AT4G38770| PRP4 (PROLINE-RICH PROTEIN 4)	Unigene40320_All//0.00E+00//TC162759				nr -
Unigene40321_All	454	33.08	45.09	38.00	139.79	106.19	146.33	44.70	27.34	20.18	4.47E-01	2.37E-04		2.00E-01	1.82E-01		-3.97E-01	3.55E-11		6.60E-02	4.09E-01		-7.09E-01	1.06E-10		-1.15E+00	1.01E-23	Down	Unigene40321_All//gi|284520976|gb|ADB93063.1|//5.00E-55//universal stress protein [Jatropha curcas]	Unigene40321_All//3.00E-47//AT3G17020| universal stress protein (USP) family protein	Unigene40321_All//0.00E+00//gi|54123123|gb|CO498632.1|CO498632				nr +
Unigene40322_All	518	2.63	1.17	1.44	2.89	1.79	1.83	3.75	1.05	1.38	-1.16E+00	4.51E-02		-8.68E-01	1.47E-01		-6.85E-01	1.99E-01		-6.56E-01	2.40E-01		-1.84E+00	4.63E-05	Down	-1.44E+00	5.63E-04	Down			Unigene40322_All//0.00E+00//gi|73848720|gb|DT457740.1|DT457740				
Unigene40324_All	590	92.32	4.21	35.29	6.08	1.98	1.07	1.22	1.42	0.74	-4.46E+00	3.69E-248	Down	-1.39E+00	4.35E-64	Down	-1.62E+00	3.18E-07	Down	-2.50E+00	5.88E-11	Down	2.18E-01	7.44E-01		-7.14E-01	3.27E-01		Unigene40324_All//gi|41618986|gb|AAS09997.1|//1.00E-28//MYB transcription factor [Arabidopsis thaliana] >gi|88900326|gb|ABD57475.1| At4g39250 [Arabidopsis thaliana]	Unigene40324_All//7.00E-24//AT4G39250| ATRL1 (ARABIDOPSIS RAD-LIKE 1); DNA binding / transcription factor	Unigene40324_All//0.00E+00//TC147941	MYB-related			nr +
Unigene40327_All	484	4.76	7.22	1.65	1.54	1.28	1.96	0.61	0.09	0.33	6.03E-01	6.84E-02		-1.53E+00	9.55E-04	Down	-2.70E-01	7.48E-01		3.44E-01	6.49E-01		-2.82E+00	8.84E-02		-8.93E-01	4.71E-01		Unigene40327_All//gi|18405624|ref|NP_566830.1|//1.00E-30//UVH3 (ULTRAVIOLET HYPERSENSITIVE 3); DNA binding / catalytic/ endonuclease/ nuclease/ single-stranded DNA binding [Arabidopsis thaliana] >gi|56749787|sp|Q9ATY5.1|UVH3_ARATH RecName: Full=DNA repair protein UVH3; AltName: Full=UV hypersensitive protein 3; AltName: Full=XPG homolog; AltName: Full=ERCC5 homolog; AltName: Full=RAD2 homolog; Short=AtUVH3; Short=AtXPG; Short=AtRAD2 >gi|13649704|gb|AAK37472.1| UV hypersensitive protein [Arabidopsis thaliana]	Unigene40327_All//2.00E-20//AT3G28030| UVH3 (ULTRAVIOLET HYPERSENSITIVE 3); DNA binding / catalytic/ endonuclease/ nuclease/ single-stranded DNA binding	Unigene40327_All//3.00E-30//gi|164251595|gb|ES831959.1|ES831959		ko03420|Nucleotide excision repair		nr +
Unigene40329_All	912	2.47	0.28	1.34	0.87	1.59	1.88	1.16	0.46	0.22	-3.15E+00	2.80E-08	Down	-8.77E-01	4.95E-02		8.60E-01	1.31E-01		1.11E+00	3.09E-02		-1.34E+00	2.90E-02		-2.41E+00	3.46E-04	Down	Unigene40329_All//gi|226491754|ref|NP_001148336.1|//2.00E-80//phytosulfokine receptor [Zea mays] >gi|195618028|gb|ACG30844.1| phytosulfokine receptor precursor [Zea mays]	Unigene40329_All//1.00E-81//AT2G25220| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene40329_All//6.00E-64//TC158373		ko04626|Plant-pathogen interaction		nr +
Unigene4033_All	1572	2.13	2.68	1.76	7.83	12.51	10.63	28.00	12.66	3.62	3.29E-01	2.86E-01		-2.74E-01	4.47E-01		6.76E-01	5.34E-09		4.42E-01	1.04E-03		-1.15E+00	7.30E-49	Down	-2.95E+00	4.40E-179	Down	Unigene4033_All//gi|224121930|ref|XP_002318708.1|//3.00E-95//acyl:coa ligase [Populus trichocarpa] >gi|222859381|gb|EEE96928.1| acyl:coa ligase [Populus trichocarpa]	Unigene4033_All//1.00E-74//AT5G63380| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene4033_All//0.00E+00//ES793429		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene40330_All	624	1.68	0.00	0.68	0.80	0.99	0.36	1.76	2.41	0.83	-1.07E+01	3.80E-06	Down	-1.30E+00	7.46E-02		3.15E-01	7.84E-01		-1.14E+00	3.07E-01		4.53E-01	3.78E-01		-1.09E+00	5.40E-02										
Unigene40332_All	547	2.87	0.09	0.19	3.82	5.92	2.89	6.34	0.99	1.09	-4.95E+00	6.38E-08	Down	-3.88E+00	1.55E-06	Down	6.30E-01	6.96E-02		-4.05E-01	3.93E-01		-2.67E+00	6.46E-13	Down	-2.54E+00	1.14E-12	Down	Unigene40332_All//gi|115433974|ref|NP_001041745.1|//2.00E-21//Os01g0101800 [Oryza sativa Japonica Group] >gi|113531276|dbj|BAF03659.1| Os01g0101800 [Oryza sativa Japonica Group]	Unigene40332_All//3.00E-28//AT3G23740| unknown protein	Unigene40332_All//0.00E+00//TC130687				nr +

Unigene40333_All	352	1.64	5.61	2.87	3.96	2.84	3.72	1.80	0.83	1.36	1.78E+00	3.85E-04	Up	8.14E-01	2.51E-01		-4.82E-01	4.04E-01		-9.08E-02	8.82E-01		-1.12E+00	1.80E-01		-4.08E-01	6.19E-01		Unigene40333_All//gi|297810925|ref|XP_002873346.1|//3.00E-13//ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319183|gb|EFH49605.1| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40333_All//3.00E-69//AT5G08180| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	Unigene40333_All//4.00E-32//gi|48799299|gb|CO100613.1|CO100613				nr -
Unigene40334_All	502	0.83	1.11	1.27	2.18	2.40	2.25	4.80	2.08	1.19	4.13E-01	6.37E-01		6.10E-01	5.09E-01		1.37E-01	8.38E-01		4.30E-02	9.42E-01		-1.21E+00	1.19E-03		-2.01E+00	5.00E-07	Down			Unigene40334_All//6.00E-10//gi|3325955|gb|AI054841.1|AI054841				
Unigene40337_All	255	21.95	28.41	19.21	24.42	18.10	22.14	97.66	47.53	25.93	3.72E-01	9.48E-02		-1.93E-01	4.95E-01		-4.32E-01	6.41E-02		-1.41E-01	6.38E-01		-1.04E+00	5.23E-24	Down	-1.91E+00	8.09E-61	Down			Unigene40337_All//8.00E-128//gi|11202934|gb|BF271939.1|BF271939				
Unigene40338_All	621	38.59	15.09	15.95	47.97	34.32	46.18	98.65	31.90	23.80	-1.35E+00	1.62E-28	Down	-1.27E+00	5.09E-25	Down	-4.83E-01	9.65E-08		-5.48E-02	6.63E-01		-1.63E+00	2.39E-115	Down	-2.05E+00	7.17E-163	Down	Unigene40338_All//gi|282848250|gb|ADB02906.1|//4.00E-56//60S ribosomal protein L30 [Jatropha curcas]	Unigene40338_All//7.00E-54//AT1G36240| 60S ribosomal protein L30 (RPL30A)	Unigene40338_All//0.00E+00//TC150586		ko03010|Ribosome		nr +
Unigene40339_All	657	0.80	4.70	2.76	3.34	2.99	4.12	0.84	1.15	0.61	2.56E+00	4.58E-09	Up	1.79E+00	1.06E-03		-1.59E-01	7.48E-01		3.06E-01	4.66E-01		4.53E-01	5.59E-01		-4.64E-01	5.97E-01		Unigene40339_All//gi|4508075|gb|AAD21419.1|//1.00E-54//Unknown protein [Arabidopsis thaliana] >gi|11074464|gb|AB804605.1| At1g61740 [Arabidopsis thaliana]	Unigene40339_All//3.00E-48//AT4G21250| unknown protein					nr -
Unigene4034_All	1458	8.68	2.57	2.67	14.62	11.08	22.43	16.99	6.05	6.61	-1.76E+00	3.27E-22	Down	-1.70E+00	1.98E-20	Down	-4.01E-01	3.20E-04		6.17E-01	1.66E-11		-1.49E+00	1.93E-41	Down	-1.36E+00	2.30E-37	Down	Unigene4034_All//gi|297798228|ref|XP_002866998.1|//1.00E-158//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297312834|gb|EFH43257.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene4034_All//4.00E-143//AT4G36680| pentatricopeptide (PPR) repeat-containing protein	Unigene4034_All//0.00E+00//TC133964				nr -
Unigene40340_All	356	26.45	8.26	23.04	6.44	5.42	2.66	3.33	2.58	2.24	-1.68E+00	9.52E-16	Down	-2.00E-01	3.58E-01		-2.49E-01	5.87E-01		-1.27E+00	2.82E-03		-3.65E-01	5.42E-01		-5.71E-01	2.93E-01				Unigene40340_All//0.00E+00//gi|109862279|gb|DW491256.1|DW491256				
Unigene40342_All	680	0.62	0.45	0.00	4.98	2.13	1.66	7.65	4.55	3.63	-4.61E-01	6.50E-01		-9.27E+00	1.56E-02		-1.23E+00	1.04E-04	Down	-1.59E+00	5.41E-06	Down	-7.50E-01	1.31E-03		-1.07E+00	3.80E-06	Down								
Unigene40343_All	697	0.98	0.15	0.46	2.07	2.08	0.97	1.88	5.16	0.57	-2.73E+00	1.06E-02		-1.09E+00	2.39E-01		1.70E-03	9.89E-01		-1.09E+00	5.14E-02		1.46E+00	1.83E-06	Up	-1.72E+00	1.48E-03				Unigene40343_All//8.00E-07//DW519604				
Unigene40344_All	519	14.62	7.03	10.57	2.69	3.12	3.22	0.00	0.48	0.38	-1.06E+00	1.05E-06	Down	-4.68E-01	3.66E-02		2.15E-01	7.32E-01		2.61E-01	6.36E-01		8.92E+00	4.31E-02		8.58E+00	7.89E-02		Unigene40344_All//gi|18397002|ref|NP_566237.1|//9.00E-47//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75207286|sp|Q9SR00.1|PP213_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g04760, chloroplastic; Flags: Precursor	Unigene40344_All//5.00E-48//AT3G04760| pentatricopeptide (PPR) repeat-containing protein	Unigene40344_All//0.00E+00//gi|164239924|gb|ES832847.1|ES832847				nr +
Unigene40346_All	564	0.28	2.43	1.42	1.41	2.81	1.68	0.30	0.37	1.34	3.12E+00	3.45E-05	Up	2.35E+00	1.46E-02		9.91E-01	6.19E-02		2.51E-01	7.24E-01		3.05E-01	8.36E-01		2.16E+00	6.98E-03		Unigene40346_All//gi|6692110|gb|AAF24575.1|AC007764_17//7.00E-20//F22C12.17 [Arabidopsis thaliana]	Unigene40346_All//2.00E-27//AT1G64065| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G44000.1); Has 69 Blast hits to 69 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene40346_All//5.00E-171//TC156511				nr +
Unigene40351_All	881	0.53	1.09	1.51	22.62	8.29	6.72	7.20	0.57	0.27	1.03E+00	1.45E-01		1.50E+00	1.84E-02		-1.45E+00	2.17E-32	Down	-1.75E+00	2.70E-37	Down	-3.66E+00	6.01E-31	Down	-4.73E+00	3.65E-38	Down	Unigene40351_All//gi|225459623|ref|XP_002284558.1|//4.00E-39//PREDICTED: similar to Os03g0839800 [Vitis vinifera]	Unigene40351_All//3.00E-16//AT1G77400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT1G21695.1); Has 289 Blast hits to 275 proteins in 50 species: Archae - 0; Bacteria - 12; Metazoa - 127; Fungi - 25; Plants - 67; Viruses - 10; Other Eukaryotes - 48 (source: NCBI BLink).	Unigene40351_All//0.00E+00//gi|78342157|gb|DT562431.1|DT562431				nr +
Unigene40352_All	306	2.05	8.78	4.35	6.02	2.25	4.28	0.00	0.00	0.00	2.10E+00	1.94E-06	Up	1.08E+00	7.97E-02		-1.42E+00	2.01E-03		-4.93E-01	3.34E-01		null	null		null	null				Unigene40352_All//4.00E-19//DW508527				
Unigene40353_All	401	21.92	16.43	16.20	14.78	14.34	19.60	43.86	22.51	17.39	-4.16E-01	3.50E-02		-4.36E-01	3.46E-02		-4.38E-02	8.68E-01		4.07E-01	5.82E-02		-9.62E-01	3.01E-15		-1.34E+00	5.25E-26	Down	Unigene40353_All//gi|211906476|gb|ACJ11731.1|//2.00E-17//ascorbate peroxidase [Gossypium hirsutum] >gi|254036190|gb|ACT56517.1| cytosolic ascorbate peroxidase [Gossypium hirsutum]	Unigene40353_All//2.00E-16//AT3G09640| APX2 (ASCORBATE PEROXIDASE 2); L-ascorbate peroxidase	Unigene40353_All//9.00E-98//CO131759		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene40357_All	631	0.00	2.09	0.76	1.97	3.60	3.36	0.00	0.00	0.00	1.10E+01	1.50E-07	Up	9.57E+00	7.48E-03		8.68E-01	4.03E-02		7.69E-01	8.92E-02		null	null		null	null		Unigene40357_All//gi|190358875|sp|P81370.2|TLP_ACTDE//6.00E-70//RecName: Full=Thaumatin-like protein; AltName: Allergen=Act d 2; Flags: Precursor >gi|71057064|emb|CAI38795.2| thaumatin-like protein [Actinidia deliciosa]	Unigene40357_All//2.00E-51//AT4G11650| ATOSM34 (osmotin 34)	Unigene40357_All//4.00E-24//gi|109865793|gb|DW494769.1|DW494769				nr +
Unigene40358_All	453	32.92	33.00	22.22	69.61	162.67	53.04	1.59	2.58	3.52	3.50E-03	9.80E-01		-5.67E-01	1.55E-04		1.22E+00	3.81E-87	Up	-3.92E-01	2.81E-05		7.03E-01	2.23E-01		1.15E+00	1.23E-02				Unigene40358_All//5.00E-69//gi|109851292|gb|DW480271.1|DW480271				
Unigene40359_All	879	0.60	3.17	1.21	0.79	2.04	2.77	1.01	3.90	1.41	2.41E+00	9.55E-08	Up	1.03E+00	1.43E-01		1.36E+00	5.82E-03		1.81E+00	3.76E-05	Up	1.95E+00	6.18E-09	Up	4.76E-01	3.76E-01				Unigene40359_All//9.00E-143//TC133295				
Unigene4036_All	1359	7.39	89.45	9.44	6.96	11.86	8.54	26.10	30.94	19.88	3.60E+00	0.00E+00	Up	3.53E-01	3.57E-02		7.68E-01	3.56E-09		2.94E-01	9.69E-02		2.45E-01	1.05E-03		-3.93E-01	5.50E-07		Unigene4036_All//gi|184013171|ref|NP_565634.1|//7.00E-82//harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana] >gi|42570933|ref|NP_973540.1| harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana] >gi|13877665|gb|AAK43910.1|AF37059 1_1 Unknown protein [Arabidopsis thaliana] >gi|3883338|gb|AAC77866.1| expressed protein [Arabidopsis thaliana] >gi|15450381|gb|AAK96484.1| At2g27080/T20P8.13 [Arabidopsis thaliana] >gi|16974489|gb|AAL31248.1| At2g27080/T20P8.13 [Arabidopsis thaliana]	Unigene4036_All//1.00E-74//AT2G27080| harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	Unigene4036_All//0.00E+00//gi|78341698|gb|DT561972.1|DT561972				nr -
Unigene40360_All	647	1.46	4.70	1.23	2.54	1.60	1.40	1.05	0.39	0.68	1.69E+00	1.34E-05	Up	-2.38E-01	7.23E-01		-6.70E-01	1.82E-01		-8.64E-01	9.70E-02		-1.43E+00	7.83E-02		-6.27E-01	4.03E-01		Unigene40360_All//gi|3176669|gb|AAC18793.1|//7.00E-72//End is cut off [Arabidopsis thaliana]	Unigene40360_All//6.00E-73//AT1G67410| exostosin family protein	Unigene40360_All//0.00E+00//TC137959				nr +
Unigene40361_All	735	87.27	36.74	62.02	10.98	11.10	11.98	0.86	0.57	0.33	-1.25E+00	2.41E-66	Down	-4.93E-01	1.91E-13		1.62E-02	9.48E-01		1.26E-01	6.13E-01		-6.02E-01	4.67E-01		-1.41E+00	7.94E-02		Unigene40361_All//gi|219842168|dbj|BAH10641.1|//1.00E-80//2-methyl-6-phytylbenzoquinone methyltranferase [Hevea brasiliensis]	Unigene40361_All//4.00E-79//AT3G63410| APG1 (ALBINO OR PALE GREEN MUTANT 1); 2-methyl-6-phytyl-1,4-benzoquinone methyltransferase/ S-adenosylmethionine-dependent methyltransferase/ methyltransferase	Unigene40361_All//0.00E+00//TC152960		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene40362_All	1125	0.00	0.09	0.09	0.09	0.18	0.00	29.09	27.90	58.32	6.49E+00	3.86E-01		6.57E+00	3.98E-01		1.05E+00	6.12E-01		-6.47E+00	3.99E-01		-6.01E-02	5.83E-01		1.00E+00	8.10E-60	Up	Unigene40362_All//gi|297814167|ref|XP_002874967.1|//1.00E-118//ATEXPA17 [Arabidopsis lyrata subsp. lyrata] >gi|297320804|gb|EFH51226.1| ATEXPA17 [Arabidopsis lyrata subsp. lyrata]	Unigene40362_All//2.00E-119//AT4G01630| ATEXPA17 (ARABIDOPSIS THALIANA EXPANSIN A17)	Unigene40362_All//4.00E-16//TC143501				nr +
Unigene40363_All	542	0.97	1.03	0.59	1.10	2.29	1.42	6.94	1.93	4.63	9.12E-02	9.32E-01		-7.12E-01	4.97E-01		1.05E+00	9.06E-02		3.61E-01	6.80E-01		-1.85E+00	3.75E-09	Down	-5.84E-01	3.19E-02		Unigene40363_All//gi|15221439|ref|NP_177024.1|//3.00E-32//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|5734721|gb|AAD49986.1|AC008075_19 Similar to gb|AF023472 peptide transporter from Hordeum vulgare and is a member of the PF|00854 Peptide transporter family. ESTs gb|T41927 and gb|AA395024 come from this gene [Arabidopsis thaliana] >gi|20147231|gb|AAM10330.1| At1g68570/F24J5_7 [Arabidopsis thaliana] >gi|25090385|gb|AAN72289.1| At1g68570/F24J5_7 [Arabidopsis thaliana] >gi|110742209|dbj|BAE99031.1| peptide transporter like [Arabidopsis thaliana]	Unigene40363_All//2.00E-33//AT1G68570| proton-dependent oligopeptide transport (POT) family protein					nr -

Unigene40365_All	503	43.06	84.52	67.01	37.34	51.55	63.39	80.27	156.05	175.91	9.73E-01	1.19E-29		6.38E-01	2.26E-11		4.65E-01	2.96E-06		7.64E-01	4.55E-16		9.59E-01	8.52E-65		1.13E+00	1.49E-97	Up	Unigene40365_All//gi|15231059|ref|NP_190752.1|//4.00E-79//ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase [Arabidopsis thaliana] >gi|62286630|sp|Q96329.1|ACOX4_ARATH RecName: Full=Acyl-coenzyme A oxidase 4, peroxisomal; Short=AOX 4; AltName: Full=Short-chain acyl-CoA oxidase; Short=SAOX; Short=AtCX4; Short=At5G6; AltName: Full=G6p >gi|114794822|pdb|2IX5|A Chain A, Short Chain Specific Acyl-Coa Oxidase From Arabidopsis Thaliana, Acx4 In Complex With Acetoacetyl-Coa >gi|114794823|pdb|2IX5|B Chain B, Short Chain Specific Acyl-Coa Oxidase From Arabidopsis Thaliana, Acx4 In Complex With Acetoacetyl-Coa >gi|114794824|pdb|2IX5|C Chain C, Short Chain Specific Acyl-Coa Oxidase From Arabidopsis Thaliana, Acx4 In Complex With Acetoacetyl-Coa >gi|114794825|pdb|2IX5|D Chain D, Short Chain Specific Acyl-Coa Oxidase From Arabidopsis Thaliana, Acx4 In Complex With Acetoacetyl-Coa >gi|165762|gb|AAB18129.1| G6p [Arabidopsis thaliana]	Unigene40365_All//2.00E-80//AT3G51840| ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase	Unigene40365_All//0.00E+00//TC144658		ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation		nr +
Unigene40366_All	576	2.63	0.62	1.20	3.20	1.85	3.06	2.35	0.58	0.90	-2.10E+00	5.39E-04	Down	-1.13E+00	4.79E-02		-7.88E-01	8.70E-02		-6.55E-02	9.04E-01		-2.02E+00	4.01E-04	Down	-1.39E+00	6.70E-03					Unigene40366_All//2.00E-130//ES794606				
Unigene40367_All	1204	3.13	2.86	1.24	2.77	2.49	2.78	3.20	3.19	4.70	-1.29E-01	6.83E-01		-1.34E+00	8.89E-05	Down	-1.56E-01	6.77E-01		1.90E-03	9.99E-01		-9.00E-04	9.97E-01		5.56E-01	1.03E-02		Unigene40367_All//gi|297828049|ref|XP_002881907.1|//6.00E-68//Rab6AP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327746|gb|EFH58166.1| Rab6AP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene40367_All//2.00E-63//AT2G43490| RAB GTPase activator	Unigene40367_All//2.00E-120//DT468421				nr +
Unigene40368_All	581	1.08	0.00	1.47	1.89	3.14	1.79	3.13	10.07	14.81	-1.01E+01	7.91E-04	Down	4.40E-01	5.83E-01		7.36E-01	1.37E-01		-7.73E-02	9.16E-01		1.69E+00	3.11E-12	Up	2.24E+00	6.40E-26	Up	Unigene40368_All//gi|259121401|gb|ACV92020.1|//3.00E-51//WRKY transcription factor 18 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene40368_All//1.00E-41//AT5G13080| WRKY75; transcription factor	Unigene40368_All//0.00E+00//gi|73865567|gb|DT468305.1|DT468305	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene40375_All	1573	0.07	0.00	0.00	1.20	0.90	1.49	2.90	0.82	0.89	-6.06E+00	3.71E-01		-6.06E+00	3.93E-01		-4.23E-01	3.84E-01		3.11E-01	5.02E-01		-1.82E+00	1.03E-10	Down	-1.71E+00	2.82E-10	Down	Unigene40375_All//gi|75100109|sp|O81211.1|RBOHE_ARATH//1.00E-119//RecName: Full=Respiratory burst oxidase homolog protein E; AltName: Full=NADPH oxidase RBOHE; Short=AtRBOHE >gi|3242787|gb|AAC39478.1| respiratory burst oxidase protein E [Arabidopsis thaliana]	Unigene40375_All//1.00E-105//AT1G19230| respiratory burst oxidase protein E (RbohE) / NADPH oxidase			ko04626|Plant-pathogen interaction		nr -
Unigene40376_All	432	7.15	10.09	8.63	6.80	7.57	5.85	9.89	21.96	13.83	4.97E-01	9.00E-02		2.72E-01	4.18E-01		1.55E-01	7.12E-01		-2.17E-01	6.19E-01		1.15E+00	3.09E-11	Up	4.85E-01	2.17E-02		Unigene40376_All//gi|18416834|ref|NP_568264.1|//2.00E-10//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|14586361|emb|CAC42892.1| RING finger-like protein [Arabidopsis thaliana] >gi|21436021|gb|AAM51588.1| AT5g19430/F7K24_180 [Arabidopsis thaliana]	Unigene40376_All//1.00E-11//AT5G12310| zinc finger (C3HC4-type RING finger) family protein	Unigene40376_All//7.00E-111//TC133680				nr +
Unigene40377_All	584	0.00	11.89	0.18	0.34	0.41	0.46	0.14	0.29	11.73	1.35E+01	1.15E-39	Up	7.51E+00	3.98E-01		2.75E-01	8.95E-01		4.44E-01	7.63E-01		9.84E-01	6.33E-01		6.34E+00	1.51E-45	Up	Unigene40377_All//gi|78216290|gb|AB836646.1|//1.00E-34//dehydration-responsive element binding protein 3 [Glycine max]	Unigene40377_All//1.00E-13//AT1G74930| ORA47; DNA binding / transcription factor	Unigene40377_All//0.00E+00//DT049908	AP2-EREBP			nr +
Unigene40378_All	661	0.63	32.20	0.97	0.75	2.97	3.01	0.70	0.51	21.09	5.67E+00	1.48E-108	Up	6.10E-01	5.09E-01		1.98E+00	6.34E-05	Up	2.00E+00	7.99E-05	Up	-4.76E-01	6.59E-01		4.91E+00	3.78E-83	Up	Unigene40378_All//gi|78216290|gb|AB836646.1|//1.00E-57//dehydration-responsive element binding protein 3 [Glycine max]	Unigene40378_All//5.00E-40//AT1G74930| ORA47; DNA binding / transcription factor	Unigene40378_All//1.00E-153//TC157484	AP2-EREBP			nr -
Unigene40380_All	534	2.35	6.26	3.09	2.52	3.03	4.48	1.35	2.27	0.90	1.41E+00	6.99E-05	Up	3.95E-01	4.55E-01		2.67E-01	6.37E-01		8.32E-01	4.64E-02		7.54E-01	1.77E-01		-5.88E-01	4.09E-01									
Unigene40381_All	725	0.43	0.14	2.35	1.99	0.57	1.37	5.89	5.59	1.92	-1.63E+00	2.76E-01		2.44E+00	7.80E-05	Up	-1.81E+00	9.96E-04	Down	-5.40E-01	3.59E-01		-7.49E-02	7.92E-01		-1.61E+00	5.75E-09	Down	Unigene40381_All//gi|13449335|ref|NP_085517.1|//2.00E-37//orfX [Arabidopsis thaliana] >gi|6851021|emb|CAA69741.3| orfX [Arabidopsis thaliana]	Unigene40381_All//8.00E-39//ATMG00570| encodes a protein of unknown function. The transcript has extensive RNA editing at the 3' end. Protein has orthologous in other plants and sequence is similar to E. coli ORFs orf154 and orf131, both of unknown function. So far, similar proteins are found only in plants and prokaryotes.	Unigene40381_All//0.00E+00//gi|164304455|gb|ES850576.1|ES850576				nr +
Unigene40383_All	200	0.00	4.05	0.00	0.25	1.03	0.23	0.85	2.30	2.79	1.20E+01	9.38E-05	Up	null	null		2.05E+00	3.95E-01		-1.42E-01	9.52E-01		1.44E+00	1.67E-01		1.72E+00	5.91E-02									
Unigene40384_All	445	7.17	9.34	3.95	0.67	0.62	0.71	0.19	0.94	2.42	3.81E-01	2.14E-01		-8.61E-01	1.81E-02		-1.18E-01	9.00E-01		8.08E-02	9.50E-01		2.31E+00	5.99E-02		3.67E+00	7.75E-06	Up			Unigene40384_All//3.00E-27//TC175742				
Unigene40391_All	797	2614.79	1572.34	3377.06	293.26	418.41	275.06	1.33	4.93	5.95	-7.34E-01	0.00E+00		3.69E-01	0.00E+00		5.13E-01	1.05E-89		-9.24E-02	8.17E-03		1.89E+00	8.65E-10	Up	2.17E+00	4.87E-14	Up	Unigene40391_All//gi|1181599|dbj|BAA11677.1|//1.00E-101//subunit of photosystem I [Cucumis sativus]	Unigene40391_All//1.00E-80//AT4G12800| PSAL (photosystem I subunit L)	Unigene40391_All//0.00E+00//TC143960		ko00195|Photosynthesis		nr -
Unigene40392_All	801	0.39	0.63	0.33	2.49	1.76	1.47	1.95	0.37	1.59	6.91E-01	4.99E-01		-2.38E-01	8.50E-01		-4.97E-01	2.89E-01		-7.63E-01	1.01E-01		-2.42E+00	1.29E-05	Down	-2.95E-01	5.44E-01		Unigene40392_All//gi|4406824|gb|AAD20132.1|//8.00E-27//expressed protein [Arabidopsis thaliana]	Unigene40392_All//7.00E-21//AT2G17940| unknown protein	Unigene40392_All//3.00E-13//DN817915				nr -
Unigene40393_All	765	1.50	1.92	2.37	6.84	7.20	4.49	1.05	0.00	0.31	3.52E-01	5.29E-01		6.53E-01	2.02E-01		7.50E-02	8.34E-01		-6.08E-01	2.00E-02		-1.00E+01	8.58E-06	Down	-1.75E+00	1.55E-02		Unigene40393_All//gi|192913018|gb|ACF06617.1|//1.00E-103//40S ribosomal protein S8 [Elaeis guineensis]	Unigene40393_All//2.00E-84//AT5G59240| 40S ribosomal protein S8 (RPS8B)	Unigene40393_All//0.00E+00//DR460335		ko03010|Ribosome		nr +
Unigene40394_All	1749	0.12	0.58	0.12	2.02	1.28	0.90	3.41	1.55	2.12	2.28E+00	4.09E-03		2.51E-02	1.00E+00		-6.60E-01	3.53E-02		-1.16E+00	3.83E-04	Down	-1.13E+00	3.33E-07	Down	-6.86E-01	1.05E-03		Unigene40394_All//gi|75299757|sp|Q8HIH9.1|AMO_ARATH//0.00E+00//RecName: Full=Primary amine oxidase; AltName: Full=Amine oxidase [copper-containing]; Flags: Precursor >gi|23297202|gb|AAN12916.1| At1g62810/F23N19_18 [Arabidopsis thaliana]	Unigene40394_All//0.00E+00//AT1G62810| copper amine oxidase, putative	Unigene40394_All//2.00E-25//ES822112		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene40397_All	826	1.39	20.06	7.41	2.11	6.71	5.41	0.00	0.00	0.00	3.85E+00	1.75E-67	Up	2.41E+00	1.12E-15	Up	1.67E+00	1.39E-10	Up	1.36E+00	3.71E-06	Up	null	null		null	null		Unigene40397_All//gi|224124558|ref|XP_002330053.1|//7.00E-19//predicted protein [Populus trichocarpa] >gi|222871478|gb|EEF08609.1| predicted protein [Populus trichocarpa]		Unigene40397_All//0.00E+00//gi|109873755|gb|DW502730.1|DW502730				nr +
Unigene40398_All	1063	0.89	0.10	0.50	0.47	0.91	0.55	1.59	2.08	0.94	-3.22E+00	6.76E-04	Down	-8.23E-01	2.71E-01		9.53E-01	1.98E-01		2.37E-01	7.98E-01		3.89E-01	3.46E-01		-7.64E-01	7.73E-02		Unigene40398_All//gi|124359343|gb|AB028505.2|//5.00E-21//RNA-directed DNA polymerase (Reverse transcriptase); Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene40398_All//4.00E-14//AT5G42905| nucleic acid binding / ribonuclease H					nr -
Unigene40399_All	1448	0.22	0.14	0.81	0.76	0.48	0.31	2.42	3.15	1.10	-6.31E-01	6.22E-01		1.90E+00	8.12E-03		-6.70E-01	3.06E-01		-1.28E+00	5.68E-02		3.77E-01	1.53E-01		-1.14E+00	8.79E-05	Down			Unigene40399_All//0.00E+00//TC136631				
Unigene40401_All	706	263.90	231.46	280.43	54.68	101.06	84.57	1.26	4.74	2.99	-1.89E-01	4.15E-07		8.76E-02	3.12E-02		8.86E-01	4.88E-50		6.29E-01	3.18E-21		1.91E+00	1.52E-08	Up	1.25E+00	1.48E-03		Unigene40401_All//gi|115441459|ref|NP_001045009.1|//2.00E-76//Os01g0882500 [Oryza sativa Japonica Group] >gi|113534540|dbj|BAF06923.1| Os01g0882500 [Oryza sativa Japonica Group]	Unigene40401_All//7.00E-77//AT5G58260| Encodes subunit NDH-N of NAD(P)H:plastoquinone dehydrogenase complex (Ndh complex) present in the thylakoid membrane of chloroplasts. This subunit is thought to be required for Ndh complex assembly.	Unigene40401_All//0.00E+00//gi|109891196|gb|DW520159.1|DW520159				nr -
Unigene40405_All	630	1.99	0.08	0.51	2.45	1.31	1.72	0.00	0.00	0.00	-4.63E+00	3.10E-06	Down	-1.97E+00	4.62E-03		-9.02E-01	7.78E-02		-5.11E-01	3.72E-01		null	null		null	null		Unigene40405_All//gi|14916566|sp|Q9ZWQ9.1|FLS_CITUN//3.00E-80//RecName: Full=Flavonol synthase/flavanone 3-hydroxylase; AltName: Full=CitFLS; Short=FLS >gi|4126403|dbj|BAA36554.1| flavonol synthase [Citrus unshiu]	Unigene40405_All//1.00E-74//AT5G08640| FLS (FLAVONOL SYNTHASE); flavonol synthase	Unigene40405_All//0.00E+00//gi|48755378|gb|CO084097.1|CO084097		ko00941|Flavonoid biosynthesis		nr -
Unigene40407_All	439	0.95	1.39	2.55	3.29	1.57	0.62	2.02	1.24	0.82	5.39E-01	5.63E-01		1.42E+00	4.39E-02		-1.07E+00	4.31E-02		-2.41E+00	1.41E-04	Down	-7.09E-01	2.97E-01		-1.31E+00	4.40E-02		Unigene40407_All//gi|296080895|emb|CBI18827.3|//1.00E-13//unnamed protein product [Vitis vinifera]						nr -
Unigene40409_All	318	1.15	4.14	2.01	3.29	0.87	0.28	1.20	1.31	0.38	1.85E+00	3.97E-03		8.03E-01	3.88E-01		-1.93E+00	4.39E-03		-3.53E+00	9.34E-05	Down	1.35E-01	8.99E-01		-1.67E+00	1.40E-01				Unigene40409_All//4.00E-07//TC159248				
Unigene40410_All	945	0.44	3.27	0.85	0.42	1.06	1.15	0.85	3.18	6.75	2.88E+00	3.48E-10	Up	9.32E-01	2.56E-01		1.33E+00	6.66E-02		1.44E+00	3.84E-02		1.91E+00	1.01E-07	Up	2.99E+00	2.12E-26	Up	Unigene40410_All//gi|12322008|gb|AAG51046.1|AC069473_8//5.00E-39//gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] >gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]						nr +
Unigene40411_All	654	5.12	16.66	17.59	20.87	17.74	11.95	0.65	0.45	0.49	1.70E+00	2.62E-18	Up	1.78E+00	8.06E-20	Up	-2.34E-01	1.46E-01		-8.05E-01	6.17E-08		-5.31E-01	6.34E-01		-4.08E-01	6.54E-01		Unigene40411_All//gi|124359162|gb|AB065683.1|//6.00E-08//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene40411_All//2.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene40411_All//1.00E-08//ES816850				nr -
Unigene40412_All	1509	0.00	0.00	0.00	0.00	0.00	0.00	1.91	6.87	3.14	null	null		null	null		null	null		null	null		1.85E+00	7.26E-24	Up	7.22E-01	2.57E-03		Unigene40412_All//gi|227438287|gb|ACP30633.1|//3.00E-13//disease resistance protein [Brassica rapa subsp. pekinensis]	Unigene40412_All//5.00E-16//AT4G19510| disease resistance protein (TIR-NBS-LRR class), putative	Unigene40412_All//1.00E-19//ES795903				nr +
Unigene40414_All	627	1.50	1.78	0.51	2.22	1.26	0.43	2.16	3.07	4.45	2.43E-01	6.82E-01		-1.56E+00	4.90E-02		-8.17E-01	1.37E-01		-2.36E+00	2.38E-04	Down	5.07E-01	2.40E-01		1.04E+00	1.54E-03		Unigene40414_All//gi|87241270|gb|AB033128.1|//1.00E-15//Zinc finger, RING-type; Thioredoxin-related [Medicago truncatula]	Unigene40414_All//7.00E-14//AT2G39720| RING2A; protein binding / zinc ion binding	Unigene40414_All//5.00E-08//TC159328				nr +
Unigene40415_All	912	0.29	0.06	0.12	0.71	0.19	0.59	3.43	1.60	1.88	-2.37E+00	2.14E-01		-1.30E+00	4.36E-01		-1.91E+00	3.63E-02		-2.57E-01	7.57E-01		-1.10E+00	5.48E-04	Down	-8.69E-01	4.15E-03		Unigene40415_All//gi|38344186|emb|CAE03517.2|//7.00E-63//OSJNBa0053K19.25 [Oryza sativa (japonica cultivar-group)]	Unigene40415_All//4.00E-70//AT4G27010| unknown protein	Unigene40415_All//4.00E-74//DR453399				nr +
Unigene40416_All	325	3.38	12.00	4.42	3.37	7.73	7.23	1.56	9.26	0.74	1.83E+00	1.13E-07	Up	3.88E-01	5.06E-01		1.20E+00	2.46E-03		1.10E+00	9.18E-03		2.57E+00	8.34E-11	Up	-1.09E+00	2.28E-01				Unigene40416_All//4.00E-87//TC155516				

Unigene40417_All	552	218.10	302.09	273.68	44.85	61.14	32.15	37.45	46.11	12.63	4.70E-01	2.67E-32		3.28E-01	9.31E-15		4.47E-01	1.91E-07		-4.80E-01	6.36E-06		3.00E-01	2.20E-03		-1.57E+00	1.69E-38	Down	Unigene40417_All//gi|91208884|ref|YP_538917.1|//1.00E-35//ribosomal protein S16 [Gossypium hirsutum] >gi|122245017|sp|Q2L8Y7.1|RR16_GOSHI RecName: Full=30S ribosomal protein S16, chloroplastic >gi|85667398|gb|ABC73610.1|ribosomal protein S16 [Gossypium hirsutum]	Unigene40417_All//6.00E-24//ATCG00050| Homologous to the bacterial ribosomal protein S16	Unigene40417_All//3.00E-154//TC175183		ko03010|Ribosome		nr -
Unigene40418_All	594	4.58	14.67	9.14	2.77	2.15	7.68	36.87	79.09	95.51	1.68E+00	1.57E-14	Up	9.97E-01	2.03E-04		-3.68E-01	5.00E-01		1.47E+00	5.55E-07	Up	1.10E+00	7.48E-49	Up	1.37E+00	1.00E-84	Up	Unigene40418_All//gi|44917493|gb|AAS49071.1|//3.00E-11//At2g44010 [Arabidopsis thaliana]	Unigene40418_All//2.00E-12//AT2G44010| unknown protein	Unigene40418_All//0.00E+00//gi|164334384|gb|ES800999.1|ES800999				nr +
Unigene40419_All	593	1.59	1.11	1.08	2.77	0.52	4.65	10.77	13.60	9.00	-5.16E-01	4.57E-01		-5.60E-01	4.39E-01		-2.41E+00	9.47E-06	Down	7.45E-01	5.29E-02		3.37E-01	7.58E-02		-2.58E-01	2.30E-01		Unigene40419_All//gi|115435458|ref|NP_001042487.1|//2.00E-19//Os01g0229500 [Oryza sativa Japonica Group] >gi|113532018|dbj|BAF04401.1|Os01g0229500 [Oryza sativa Japonica Group]	Unigene40419_All//8.00E-17//AT3G16175| thioesterase family protein	Unigene40419_All//2.00E-07//ES824893				nr +
Unigene40421_All	618	0.25	1.64	1.55	0.64	1.28	1.32	1.37	1.56	4.38	2.69E+00	1.41E-03		2.61E+00	3.45E-03		9.91E-01	2.40E-01		1.03E+00	2.17E-01		1.85E-01	7.65E-01		1.68E+00	3.24E-06	Up			Unigene40421_All//8.00E-50//TC179124				
Unigene40423_All	516	51.10	11.29	4.33	0.00	0.73	0.35	35.40	1.22	1.16	-2.18E+00	1.85E-60	Down	-3.56E+00	5.16E-98	Down	9.52E+00	1.96E-02		8.45E+00	1.94E-01		-4.86E+00	4.31E-107	Down	-4.93E+00	1.20E-111	Down	Unigene40423_All//gi|117575127|emb|CAL68581.1|//1.00E-25//gamma-thionin [Phaseolus vulgaris]	Unigene40423_All//5.00E-09//AT5G63660| PDF2.5	Unigene40423_All//0.00E+00//gi|164248264|gb|ES821172.1|ES821172				nr -
Unigene40424_All	462	0.57	0.00	0.00	1.94	1.64	2.35	1.74	0.54	0.17	-9.15E+00	6.70E-02		-9.15E+00	8.56E-02		-2.43E-01	7.52E-01		2.74E-01	6.70E-01		-1.68E+00	2.46E-02		-3.33E+00	2.47E-04	Down								
Unigene40425_All	761	1.24	1.46	0.70	5.69	8.73	13.65	0.50	1.59	1.15	2.43E-01	6.82E-01		-8.23E-01	2.71E-01		6.17E-01	5.07E-03		1.26E+00	4.18E-12	Up	1.67E+00	4.19E-03		1.20E+00	6.68E-02		Unigene40425_All//gi|14030679|gb|AAK53014.1|AF375430_1//4.00E-28//AT5g45310/K9E15_9 [Arabidopsis thaliana] >gi|16974513|gb|AAL31166.1|AT5g45310/K9E15_9 [Arabidopsis thaliana]	Unigene40425_All//2.00E-29//AT5G45310| unknown protein	Unigene40425_All//0.00E+00//TC178829				nr +
Unigene40427_All	363	1.59	2.23	0.73	5.35	2.94	1.37	2.91	0.81	1.43	4.94E-01	5.26E-01		-1.11E+00	2.78E-01		-8.64E-01	5.15E-02		-1.97E+00	9.06E-05	Down	-1.85E+00	4.09E-03		-1.03E+00	7.30E-02		Unigene40427_All//gi|115479877|ref|NP_001063532.1|//3.00E-09//Os09g0488800 [Oryza sativa Japonica Group] >gi|113631765|dbj|BAF25446.1|Os09g0488800 [Oryza sativa Japonica Group]	Unigene40427_All//3.00E-07//AT5G12900| unknown protein	Unigene40427_All//4.00E-32//TC149269				nr +
Unigene40429_All	854	0.55	0.36	0.12	2.16	1.13	2.17	2.57	1.03	1.31	-6.31E-01	5.54E-01		-2.14E+00	1.03E-01		-9.35E-01	4.10E-02		6.70E-03	9.92E-01		-1.32E+00	8.35E-04	Down	-9.79E-01	8.63E-03		Unigene40429_All//gi|115435514|ref|NP_001042515.1|//2.00E-44//Os01g0234100 [Oryza sativa Japonica Group] >gi|122235052|sp|Q0JP99.1|Y1341_ORYSJ RecName: Full=B3 domain-containing protein Os01g0234100 >gi|113532046|dbj|BAF04429.1|Os01g0234100 [Oryza sativa Japonica Group]	Unigene40429_All//3.00E-12//AT3G19184| DNA binding	Unigene40429_All//1.00E-49//TC171850	ABI3VP1			nr -
Unigene40432_All	531	10.15	34.26	34.60	1.50	2.92	0.94	0.00	0.00	0.15	1.76E+00	2.15E-31	Up	1.77E+00	4.10E-31	Up	9.59E-01	7.53E-02		-6.82E-01	4.05E-01		null	null		7.23E+00	4.04E-01		Unigene40432_All//gi|115458314|ref|NP_001052757.1|//2.00E-14//Os04g0415000 [Oryza sativa Japonica Group] >gi|32479729|emb|CAE01516.1|OJ991214_12.5 [Oryza sativa (japonica cultivar-group)] >gi|113564328|dbj|BAF14671.1|Os04g0415000 [Oryza sativa Japonica Group] >gi|116309338|emb|CAH66422.1|B0622F05.5 [Oryza sativa (indica cultivar-group)]	Unigene40432_All//2.00E-16//AT5G06270| unknown protein	Unigene40432_All//0.00E+00//TC169010				nr +
Unigene40433_All	399	0.00	0.00	0.00	1.25	1.21	7.02	10.28	4.71	25.76	null	null		null	null		-4.72E-02	9.49E-01		2.49E+00	2.21E-08	Up	-1.12E+00	3.78E-05	Down	1.33E+00	2.93E-15	Up	Unigene40433_All//gi|28466815|gb|AAO40016.1|//6.00E-16//At1g11655 [Arabidopsis thaliana]	Unigene40433_All//3.00E-17//AT1G11655| unknown protein	Unigene40433_All//0.00E+00//gi|21098544|gb|BQ410857.1|BQ410857				nr -
Unigene40437_All	573	112.86	29.89	37.64	320.36	184.86	284.22	475.41	768.15	395.95	-1.92E+00	6.51E-125	Down	-1.58E+00	1.45E-92	Down	-7.93E-01	2.87E-110		-1.73E-01	2.89E-06		6.92E-01	4.17E-206		-2.64E-01	7.25E-23		Unigene40437_All//gi|211906474|gb|ACJ11730.1|//6.00E-75//glycine-rich RNA-binding protein [Gossypium hirsutum]	Unigene40437_All//3.00E-19//AT2G21660| CCR2 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	Unigene40437_All//0.00E+00//gi|13350601|gb|BG440949.1|BG440949		ko03040|Spliceosome		nr +
Unigene40439_All	319	1.31	5.40	3.67	0.47	1.30	2.12	0.53	1.83	0.62	2.04E+00	2.81E-04	Up	1.48E+00	3.04E-02		1.47E+00	2.79E-01		2.18E+00	3.14E-02		1.79E+00	5.30E-02		2.36E-01	8.83E-01									
Unigene40441_All	501	2.09	1.21	2.13	1.39	0.62	0.99	0.34	0.58	2.78	-7.83E-01	2.34E-01		2.53E-02	9.89E-01		-1.17E+00	1.61E-01		-4.89E-01	5.98E-01		7.91E-01	5.63E-01		3.04E+00	2.08E-06	Up	Unigene40441_All//gi|263546703|sp|COLGE4.1|Y1124_ARATH//6.00E-08//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g12460; Flags: Precursor >gi|224580390|gb|ACN59229.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene40441_All//3.00E-09//AT1G12460| leucine-rich repeat transmembrane protein kinase, putative					nr +
Unigene40442_All	272	18.66	9.13	17.23	4.21	6.58	3.32	0.00	0.00	0.00	-1.03E+00	1.29E-04	Down	-1.15E-01	6.83E-01		6.44E-01	2.06E-01		-3.43E-01	6.37E-01		null	null		null	null				Unigene40442_All//9.00E-131//TC170394				ESTscan +
Unigene40444_All	1363	0.00	0.00	0.00	0.00	0.00	0.00	14.67	1.56	0.76	null	null		null	null		null	null		null	null		-3.23E+00	1.89E-86	Down	-4.27E+00	5.85E-112	Down	Unigene40444_All//sp|P0C6B8|SVEP1_RAT//1.00E-08//Sushi, von Willebrand factor type A, EGF and pentraxin domain-containing protein 1 OS=Rattus norvegicus GN=Svep1 PE=1 SV=1						swissprot -
Unigene4045_All	1443	1.56	0.84	1.14	1.07	1.74	1.06	1.05	0.26	0.39	-8.88E-01	3.72E-02		-4.47E-01	3.31E-01		7.03E-01	8.12E-02		-8.20E-03	9.81E-01		-2.02E+00	1.51E-04	Down	-1.45E+00	2.57E-03		Unigene4045_All//gi|226506384|ref|NP_001148210.1|//7.00E-89//SWIB/MDM2 domain containing protein [Zea mays] >gi|195616714|gb|ACG30187.1|SWIB/MDM2 domain containing protein [Zea mays]	Unigene4045_All//5.00E-39//AT3G19080| SWIB complex BAF60b domain-containing protein	Unigene4045_All//0.00E+00//DN779821				nr +
Unigene40450_All	447	0.23	2.27	2.26	0.67	0.15	0.00	2.36	2.99	4.10	3.28E+00	3.79E-04	Up	3.27E+00	5.93E-04	Up	-2.12E+00	1.65E-01		-9.39E+00	3.99E-02		3.40E-01	5.46E-01		7.94E-01	5.64E-02		Unigene40450_All//gi|297849514|ref|XP_002892638.1|//2.00E-35//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338480|gb|EFH68897.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40450_All//6.00E-36//AT1G11350| SD1-13 (S-DOMAIN-1 13); kinase/ protein kinase/ protein serine/threonine kinase	Unigene40450_All//4.00E-60//CO081718		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism		nr -
Unigene40453_All	592	23.95	14.55	18.53	16.07	18.32	7.17	0.14	0.14	0.27	-7.19E-01	1.45E-06		-3.70E-01	1.92E-02		1.89E-01	3.30E-01		-1.16E+00	4.92E-10	Down	-1.63E-02	1.01E+00		9.15E-01	6.24E-01		Unigene40453_All//gi|297736998|emb|CBI26199.3|//7.00E-10//unnamed protein product [Vitis vinifera]	Unigene40453_All//3.00E-05//AT5G19190| unknown protein	Unigene40453_All//7.00E-84//BF276883				nr -
Unigene40455_All	1728	0.00	0.06	0.00	0.00	0.00	0.00	68.14	12.14	15.42	5.87E+00	3.86E-01		null	null		null	null		null	null		-2.49E+00	0.00E+00	Down	-2.14E+00	0.00E+00	Down	Unigene40455_All//gi|38636547|dbj|BAD02939.1|//0.00E+00//high-affinity nitrate transporter [Prunus persica] >gi|48675347|dbj|BAD22821.1|nitrate transporter [Prunus persica]	Unigene40455_All//0.00E+00//AT1G08090| AINRT2;1 (NITRATE TRANSPORTER 2;1); nitrate transmembrane transporter	Unigene40455_All//9.00E-120//CB074791				nr +
Unigene40456_All	584	11.38	3.56	3.10	1.11	0.83	0.77	0.00	0.00	0.00	-1.68E+00	2.67E-11	Down	-1.88E+00	1.86E-12	Down	-4.26E-01	6.08E-01		-5.20E-01	5.88E-01		null	null		null	null			Unigene40456_All//5.00E-05//AT3G14395| unknown protein	Unigene40456_All//0.00E+00//DW512309				
Unigene40458_All	1125	0.19	0.00	0.05	2.17	0.89	0.44	9.25	17.42	4.99	-7.54E+00	1.22E-01		-1.98E+00	3.81E-01		-1.29E+00	8.24E-04	Down	-2.30E+00	6.01E-07	Down	9.14E-01	1.45E-15		-8.89E-01	1.42E-08		Unigene40458_All//gi|297842193|ref|XP_002888978.1|//1.00E-157//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334819|gb|EFH65237.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40458_All//2.00E-158//AT1G74460| GDSL-motif lipase/hydrolase family protein	Unigene40458_All//6.00E-157//TC162868				nr -
Unigene40459_All	454	1.73	2.12	1.52	8.12	11.45	12.53	29.52	17.86	11.14	2.95E-01	6.48E-01		-1.81E-01	8.07E-01		4.96E-01	5.95E-02		6.26E-01	1.20E-02		-7.25E-01	1.33E-07		-1.41E+00	1.37E-21	Down			Unigene40459_All//9.00E-157//gi|13245917|gb|BE055210.2|BE055210				
Unigene40460_All	394	7.57	8.23	6.62	5.06	4.02	4.59	36.49	21.11	18.20	1.21E-01	7.27E-01		-1.93E-01	6.22E-01		-3.31E-01	5.03E-01		-1.41E-01	7.58E-01		-7.89E-01	2.97E-09		-1.00E+00	6.84E-14	Down			Unigene40460_All//2.00E-86//gi|164288852|gb|ES844148.1|ES844148				
Unigene40465_All	428	0.00	1.89	0.62	1.16	1.37	0.53	2.27	2.54	2.89	1.09E+01	9.38E-05	Up	9.28E+00	8.01E-02		2.33E-01	8.26E-01		-1.14E+00	3.07E-01		1.60E-01	7.82E-01		3.45E-01	5.38E-01									
Unigene40467_All	545	0.00	0.37	0.39	5.30	2.09	1.82	3.18	2.38	3.51	8.54E+00	1.36E-01		8.61E+00	1.41E-01		-1.35E+00	1.19E-04	Down	-1.54E+00	5.05E-05	Down	-4.20E-01	3.77E-01		1.42E-01	7.34E-01		Unigene40467_All//gi|146432261|gb|ABQ41114.1|//2.00E-56//monodehydroascorbate reductase [Vitis vinifera]	Unigene40467_All//4.00E-53//AT5G03630| ATMDAR2; monodehydroascorbate reductase (NADH)	Unigene40467_All//2.00E-16//gi|73943604|gb|DT526912.1|DT526912		ko00053|Ascorbate and aldarate metabolism		nr -
Unigene40469_All	357	2.20	6.25	3.13	3.63	3.09	6.07	5.80	6.09	4.58	1.51E+00	8.69E-04	Up	5.11E-01	4.34E-01		-2.33E-01	7.05E-01		7.43E-01	9.72E-02		6.91E-02	8.71E-01		-3.43E-01	3.92E-01		Unigene40469_All//gi|227204473|dbj|BAH57088.1|//3.00E-23//AT2G25280 [Arabidopsis thaliana]	Unigene40469_All//3.00E-24//AT2G25280| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Mediator of ErbB2-driven cell motility (Memo), related (InterPro:IPR002237); Has 742 Blast hits to 742 proteins in 323 species: Archae - 138; Bacteria - 240; Metazoa - 132; Fungi - 82; Plants - 26; Viruses - 0; Other Eukaryotes - 124 (source: NCBI BLink).	Unigene40469_All//8.00E-95//DW499259				nr -
Unigene40471_All	838	1.81	0.54	0.00	5.65	7.07	2.80	1.72	0.45	0.48	-1.73E+00	2.69E-03		-1.08E+01	2.73E-08	Down	3.24E-01	2.17E-01		-1.01E+00	2.22E-04	Down	-1.93E+00	3.78E-04	Down	-1.85E+00	3.87E-04	Down	Unigene40471_All//gi|164605533|dbj|BAF98599.1|//3.00E-40//CM0545.320.nc [Lotus japonicus]	Unigene40471_All//4.00E-16//AT5G02440| unknown protein	Unigene40471_All//0.00E+00//gi|21097636|gb|BQ409949.1|BQ409949				nr +
Unigene40473_All	759	1.65	1.60	1.82	5.05	2.86	0.83	1.17	0.11	0.63	-4.63E-02	9.50E-01		1.41E-01	7.97E-01		-8.22E-01	5.05E-03		-2.60E+00	3.58E-12	Down	-3.41E+00	1.40E-04	Down	-8.93E-01	1.60E-01		Unigene40473_All//gi|159025703|emb|CAN88852.1|//2.00E-75//D1-type cyclin (Populus trichocarpa)	Unigene40473_All//2.00E-31//AT1G70210| CYCD1;1 (CYCLIN D1;1); cyclin-dependent protein kinase regulator	Unigene40473_All//4.00E-166//gi|78324373|gb|DT544647.1|DT544647				nr -
Unigene40474_All	445	5.17	1.14	8.26	5.82	2.01	9.84	0.00	0.00	0.00	-2.18E+00	6.34E-06	Down	6.75E-01	4.51E-02		-1.53E+00	5.11E-05	Down	7.58E-01	8.79E-03		null	null		null	null				Unigene40474_All//2.00E-09//CO105291				
Unigene40475_All	710	1.03	3.78	1.20	0.98	1.41	2.10	3.45	5.30	4.55	1.87E+00	1.12E-05	Up	2.18E-01	7.57E-01		5.18E-01	5.07E-01		1.10E+00	5.01E-02		6.17E-01	2.95E-02		3.96E-01	2.01E-01				Unigene40475_All//4.00E-86//ES844012				

Unigene40476_All	817	0.26	1.61	0.00	0.85	0.46	0.17	3.31	4.09	2.83	2.65E+00	2.16E-04	Up	-8.00E+00	1.45E-01		-8.81E-01	2.99E-01		-2.36E+00	1.69E-02		3.05E-01	3.60E-01		-2.28E-01	5.29E-01		Unigene40476_All//gi|224136103|ref|XP_002327381.1|//6.00E-63//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372101|gb|ABQ62982.1| TINY-like protein [Populus trichocarpa] >gi|222835751|gb|EEE74186.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene40476_All//3.00E-37//AT1G33760| AP2 domain-containing transcription factor, putative	Unigene40476_All//0.00E+00//gi|109827586|gb|DW226261.1|DW226261	AP2-EREBP			nr -
Unigene40477_All	726	0.50	3.21	1.83	2.61	4.79	3.98	0.17	0.17	0.77	2.67E+00	2.76E-07	Up	1.86E+00	4.86E-03		8.78E-01	6.46E-03		6.11E-01	1.09E-01		-1.66E-02	1.02E+00		2.14E+00	2.64E-02		Unigene40477_All//gi|77552183|gb|AB494980.1|//3.00E-22//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene40477_All//2.00E-10//AT5G45530| unknown protein				nr -
Unigene40478_All	387	4.87	1.31	3.44	10.81	12.55	16.81	1.09	1.08	1.34	-1.89E+00	2.73E-04	Down	-5.01E-01	3.23E-01		2.15E-01	5.10E-01		6.36E-01	5.68E-03		-1.66E-02	1.02E+00		2.93E-01	7.27E-01		Unigene40478_All//gi|225461114|ref|XP_002279701.1|//4.00E-07//PREDICTED: similar to putative pentatricopeptide (PPR) repeat-containing protein [Vitis vinifera]					nr +
Unigene40479_All	502	0.00	7.87	0.11	1.89	6.38	5.04	0.00	0.33	0.48	1.29E+01	1.66E-22	Up	6.73E+00	6.35E-01		1.76E+00	1.01E-06	Up	1.42E+00	5.71E-04	Up	8.38E+00	1.39E-01		8.90E+00	4.39E-02				Unigene40479_All//8.00E-102//TC175167				
Unigene40480_All	420	0.50	3.14	3.30	1.66	2.38	1.08	1.81	0.70	1.52	2.65E+00	2.16E-04	Up	2.73E+00	1.78E-04	Up	5.18E-01	5.07E-01		-6.27E-01	4.76E-01		-1.38E+00	6.73E-02		-2.56E-01	6.97E-01		Unigene40480_All//gi|224080099|ref|XP_002306017.1|//4.00E-25//SET domain-containing protein [Populus trichocarpa] >gi|222848981|gb|EEE86528.1| SET domain-containing protein [Populus trichocarpa]	Unigene40480_All//3.00E-16//AT3G56570| SET domain-containing protein				nr +
Unigene40481_All	632	0.00	0.56	0.00	1.66	0.71	0.71	0.87	1.32	3.09	9.13E+00	2.46E-02		null	null		-1.22E+00	5.85E-02		-1.21E+00	7.81E-02		6.05E-01	4.04E-01		1.83E+00	3.51E-05	Up							
Unigene40483_All	862	0.24	0.53	0.25	0.06	0.24	0.31	159.90	30.55	64.43	1.12E+00	3.28E-01		2.53E-02	1.00E+00		2.05E+00	3.94E-01		2.44E+00	2.22E-01		-2.39E+00	0.00E+00	Down	-1.31E+00	1.44E-192	Down	Unigene40483_All//gi|7105717|gb|AAB84202.2|//1.00E-154//plasma membrane proton ATPase [Kosteletzkya virginica]	Unigene40483_All//1.00E-133//AT5G57350| AHA3; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	Unigene40483_All//0.00E+00//CO113495	ko00190|Oxidative phosphorylation		nr +
Unigene40486_All	523	3.10	0.10	2.95	0.48	0.66	1.38	0.00	0.00	0.30	-5.00E+00	3.32E-08	Down	-7.08E-02	8.95E-01		4.67E-01	7.79E-01		1.54E+00	9.17E-02		null	null		8.25E+00	1.40E-01								
Unigene4049_All	1399	44.80	39.48	23.90	71.82	41.52	30.44	9.49	14.34	13.93	-1.83E-01	7.93E-03		-9.06E-01	2.23E-37		-7.90E-01	4.83E-60		-1.24E+00	4.53E-111	Down	5.96E-01	5.53E-08		5.53E-01	3.96E-07		Unigene4049_All//gi|15226223|ref|NP_178238.1|//1.00E-104//ribose-5-phosphate isomerase [Arabidopsis thaliana] >gi|6226027|sp|Q9ZU38.1|RPIA_ARATH RecName: Full=Probable ribose-5-phosphate isomerase; AltName: Full=Phosphoriboisomerase >gi|15809810|gb|AAL06833.1| At2g01290/F10A8.17 [Arabidopsis thaliana] >gi|17978867|gb|AAL47405.1| At2g01290/F10A8.17 [Arabidopsis thaliana]	Unigene4049_All//1.00E-103//AT2G01290| ribose-5-phosphate isomerase	Unigene4049_All//0.00E+00//TC144478	ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway		nr +
Unigene40490_All	877	0.24	0.06	0.00	0.91	0.47	1.24	3.91	27.59	2.50	-2.05E+00	3.34E-01		-7.90E+00	1.45E-01		-9.48E-01	2.21E-01		4.44E-01	5.39E-01		2.82E+00	4.88E-91	Up	-6.44E-01	2.47E-02		Unigene40490_All//gi|3426064|emb|CAA07575.1|//4.00E-65//monooxygenase [Arabidopsis thaliana] >gi|4467141|emb|CAB37510.1| monooxygenase 2 (MO2) [Arabidopsis thaliana] >gi|7270837|emb|CAB80518.1| monooxygenase 2 (MO2) [Arabidopsis thaliana]	Unigene40490_All//4.00E-67//AT4G38540| monooxygenase, putative (MO2)	Unigene40490_All//1.00E-169//TC146874			nr -
Unigene40491_All	445	298.41	217.59	219.22	126.38	142.62	103.52	173.02	107.26	80.84	-4.56E-01	1.59E-24		-4.45E-01	1.29E-22		1.74E-01	8.34E-03		-2.88E-01	2.94E-05		-6.90E-01	1.67E-36		-1.10E+00	1.51E-81	Down	Unigene40491_All//gi|231496|sp|P30167.1|ACT3_SOLTU//8.00E-60//RecName: Full=Actin-58 >gi|21536|emb|CAA29278.1| actin [Solanum tuberosum]	Unigene40491_All//1.00E-60//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene40491_All//0.00E+00//gi|13244825|gb|BE052786.2|BE052786			nr +
Unigene40494_All	673	0.93	0.75	0.55	1.11	2.51	3.15	1.44	0.12	2.90	-3.09E-01	7.01E-01		-7.52E-01	4.11E-01		1.18E+00	2.09E-02		1.51E+00	1.07E-03		-3.54E+00	4.32E-05	Down	1.01E+00	1.27E-02		Unigene40494_All//gi|115471637|ref|NP_001059417.1|//4.00E-16//Os07g0298100 [Oryza sativa Japonica Group] >gi|113610953|dbj|BAF21331.1| Os07g0298100 [Oryza sativa Japonica Group]	Unigene40494_All//1.00E-11//AT3G02125| unknown protein	Unigene40494_All//0.00E+00//gi|73849718|gb|DT458738.1|DT458738			nr -
Unigene40495_All	1025	0.00	0.00	0.00	0.00	0.00	0.00	5.61	1.26	29.81	null	null		null	null		null	null		null	null		-2.15E+00	2.15E-16	Down	2.41E+00	3.78E-98	Up	Unigene40495_All//gi|39636757|gb|AAR29072.1|//9.00E-06//blight resistance protein RGA4 [Solanum bulbocastanum]		Unigene40495_All//2.00E-26//gi|109876995|gb|DW505969.1|DW505969				nr -
Unigene40501_All	682	1.07	0.00	2.26	3.51	1.36	0.66	0.00	0.00	0.00	-1.01E+01	2.11E-04	Down	1.08E+00	5.58E-02		-1.36E+00	5.05E-04	Down	-2.40E+00	3.65E-07	Down	null	null		null	null				Unigene40501_All//1.00E-172//DW243171				ESTscan +
Unigene40502_All	549	13.53	36.46	34.05	4.90	3.39	2.30	6.85	1.14	1.31	1.43E+00	8.50E-26	Up	1.33E+00	5.24E-21	Up	-5.33E-01	1.63E-01		-1.09E+00	4.53E-03		-2.59E+00	1.76E-13	Down	-2.39E+00	7.71E-13	Down	Unigene40502_All//gi|56562175|emb|CAH60890.1|//2.00E-23//carbonic anhydrase [Solanum lycopersicum]	Unigene40502_All//5.00E-23//AT3G01500| CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	Unigene40502_All//3.00E-86//ES838914	ko00910|Nitrogen metabolism		nr -
Unigene40506_All	438	0.00	2.43	0.00	3.98	3.30	4.02	3.09	2.19	0.36	1.12E+01	3.81E-06	Up	null	null		-2.70E-01	6.05E-01		1.47E-02	9.77E-01		-4.93E-01	3.67E-01		-3.09E+00	1.97E-06	Down	Unigene40506_All//gi|116056034|emb|CAL58567.1|//4.00E-19//Nucleolar GTPase/ATPase p130 (ISS) [Ostreococcus tauri]			ko04120|Ubiquitin mediated proteolysis		nr +
Unigene4051_All	765	2.26	2.91	2.65	31.32	23.45	20.43	21.83	9.56	8.12	3.69E-01	3.83E-01		2.29E-01	6.34E-01		-4.17E-01	5.58E-05		-6.17E-01	1.16E-08		-1.19E+00	3.29E-20	Down	-1.43E+00	2.90E-27	Down	Unigene4051_All//gi|30685734|ref|NP_189069.2|//2.00E-22//protein binding [Arabidopsis thaliana] >gi|57222128|gb|AAW38971.1| At2g33510 [Arabidopsis thaliana]	Unigene4051_All//3.00E-12//AT2G33510| protein binding	Unigene4051_All//0.00E+00//DW497103			nr +
Unigene40510_All	351	10.43	8.52	6.83	18.88	13.15	6.82	63.96	42.51	23.61	-2.93E-01	3.76E-01		-6.12E-01	7.02E-02		-5.22E-01	1.72E-02		-1.47E+00	5.22E-10	Down	-5.89E-01	1.07E-08		-1.44E+00	8.61E-37	Down			Unigene40510_All//3.00E-97//BQ413755				
Unigene40512_All	458	5.25	0.89	2.79	4.13	3.76	5.13	0.37	0.55	0.00	-2.57E+00	2.71E-07	Down	-9.13E-01	3.42E-02		-1.37E-01	8.10E-01		3.11E-01	5.02E-01		5.68E-01	6.74E-01		-8.53E+00	1.08E-01		Unigene40512_All//gi|297830924|ref|XP_002883344.1|//1.00E-34//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329184|gb|EFH59603.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene40512_All//3.00E-31//AT3G22150| pentatricopeptide (PPR) repeat-containing protein				nr +
Unigene40513_All	455	1.03	0.45	0.00	6.46	4.31	2.58	3.35	1.47	0.53	-1.22E+00	2.72E-01		-1.00E+01	8.64E-03		-5.82E-01	1.02E-01		-1.32E+00	3.33E-04	Down	-1.19E+00	1.47E-02		-2.67E+00	2.74E-06	Down			Unigene40513_All//9.00E-83//CO109857				
Unigene40514_All	476	3.85	0.00	2.68	1.15	2.53	0.57	2.22	0.70	2.18	-1.19E+01	1.34E-10	Down	-5.19E-01	3.11E-01		1.14E+00	7.32E-02		-1.02E+00	3.29E-01		-1.66E+00	8.55E-03		-2.92E-02	9.70E-01		Unigene40514_All//gi|118572293|sp|Q9LTP6.2|ERL13_ARATH//1.00E-11//RecName: Full=Putative sugar transporter ERD6-like 13	Unigene40514_All//2.00E-12//AT3G20160| sugar transporter, putative	Unigene40514_All//2.00E-49//TC135009			nr +
Unigene40516_All	368	4.27	2.89	1.74	3.52	2.90	0.25	0.46	0.80	0.00	-5.61E-01	2.88E-01		-1.30E+00	2.26E-02		-2.79E-01	6.29E-01		-3.84E+00	4.02E-06	Down	7.91E-01	5.63E-01		-8.84E+00	1.08E-01				Unigene40516_All//3.00E-11//ES847437				
Unigene40517_All	1135	1.38	0.58	0.61	0.92	0.12	0.48	4.66	3.94	1.72	-1.25E+00	1.98E-02		-1.18E+00	3.61E-02		-2.92E+00	1.21E-04	Down	-9.49E-01	1.69E-01		-2.41E-01	3.55E-01		-1.44E+00	2.57E-09	Down	Unigene40517_All//gi|158828302|gb|ABW81177.1|//3.00E-18//gag non-LTR retrotransposase [Arabidopsis cebennensis]	Unigene40517_All//6.00E-06//AT3G01050| nucleic acid binding / zinc ion binding	Unigene40517_All//2.00E-88//BF277456			nr -
Unigene40521_All	899	1.63	4.45	1.78	8.26	9.65	9.14	0.47	0.42	0.09	1.45E+00	7.12E-06	Up	1.25E-01	8.05E-01		2.25E-01	3.11E-01		1.47E-01	5.50E-01		-1.69E-01	8.65E-01		-2.41E+00	3.94E-02		Unigene40521_All//gi|297723217|ref|NP_001173972.1|//2.00E-78//Os04g0465432 [Oryza sativa Japonica Group] >gi|21741223|emb|CAD40934.1| OSJNB00048E02.10 [Oryza sativa (japonica cultivar-group)] >gi|255675536|dbj|BAH92700.1| Os04g0465432 [Oryza sativa Japonica Group]	Unigene40521_All//3.00E-104//AT3G28150| unknown protein	Unigene40521_All//0.00E+00//TC173964			nr +
Unigene40522_All	314	21.99	15.01	21.88	40.61	38.27	34.52	90.75	18.77	29.18	-5.52E-01	1.36E-02		-7.80E-03	9.98E-01		-8.56E-02	6.43E-01		-2.35E-01	1.78E-01		-2.27E+00	4.75E-84	Down	-1.64E+00	4.61E-56	Down			Unigene40522_All//5.00E-71//TC176422				
Unigene40523_All	600	2794.80	1427.11	3154.44	3219.82	2446.80	3685.63	590.65	336.11	196.67	-9.70E-01	0.00E+00		1.75E-01	7.08E-54		-3.96E-01	0.00E+00		1.95E-01	2.37E-86		-8.13E-01	6.64E-220		-1.59E+00	0.00E+00	Down	Unigene40523_All//gi|167367|gb|AAA99868.1|//8.00E-54//peroxidase [Gossypium hirsutum]	Unigene40523_All//2.00E-33//AT4G21960| PRXR1; electron carrier/ heme binding / peroxidase	Unigene40523_All//0.00E+00//gi|31406843|gb|CD485878.1|CD485878		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene40524_All	653	3.12	1.71	0.00	4.27	3.96	1.24	0.06	0.00	0.00	-8.72E-01	5.29E-02		-1.16E+01	3.79E-11	Down	-1.11E-01	8.07E-01		-1.78E+00	7.97E-06	Down	-6.02E+00	6.57E-01		-6.02E+00	6.12E-01		Unigene40524_All//gi|119640513|gb|ABL85473.1|//2.00E-75//glycosyltransferase UGT71A13 [Maclura pomifera]	Unigene40524_All//1.00E-66//AT3G21800| UGT71B8 (UDP-GLUCOSYL TRANSFERASE 71B8); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene40524_All//2.00E-69//gi|109871489|gb|DW500465.1|DW500465		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene4053_All	430	2.68	9.90	5.45	2.90	5.45	3.78	6.69	6.90	8.62	1.89E+00	1.25E-08	Up	1.03E+00	1.94E-02		9.11E-01	2.77E-02		3.85E-01	4.95E-01		4.57E-02	9.07E-01		3.66E-01	1.99E-01				Unigene4053_All//4.00E-60//DW518130				
Unigene40532_All	485	69.26	41.16	25.91	66.66	71.85	49.73	53.61	19.22	29.00	-7.51E-01	1.68E-15		-1.42E+00	5.27E-41	Down	1.08E-01	3.18E-01		-4.23E-01	4.29E-06		-1.48E+00	5.06E-43	Down	-8.87E-01	5.21E-20		Unigene40532_All//gi|225435032|ref|XP_002284277.1|//4.00E-29//PREDICTED: similar to Histone H2B isoform 1 [Vitis vinifera]		Unigene40532_All//3.00E-113//TC148617				nr +
Unigene40533_All	455	3.22	0.67	2.22	1.64	2.27	1.89	0.65	0.55	0.96	-2.27E+00	3.39E-04	Down	-5.34E-01	3.66E-01		4.67E-01	5.51E-01		2.00E-01	7.88E-01		-2.39E-01	8.39E-01		5.66E-01	5.78E-01								ESTscan +
Unigene40534_All	869	6.38	2.22	4.04	1.20	0.63	0.52	0.78	0.38	3.76	-1.53E+00	1.94E-08	Down	-6.58E-01	1.28E-02		-9.25E-01	1.55E-01		-1.21E+00	7.81E-02		-1.02E+00	2.04E-01		2.27E+00	1.81E-10	Up	Unigene40534_All//gi|297825707|ref|XP_002880736.1|//1.00E-73//bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326575|gb|EFH56995.1| bet v I allergen family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40534_All//2.00E-72//AT2G26040| Bet v I allergen family protein	Unigene40534_All//0.00E+00//DW231297			nr -
Unigene40535_All	1561	0.07	0.00	0.00	0.00	0.00	0.00	164.41	4.39	2.86	-6.07E+00	3.71E-01		-6.07E+00	3.93E-01		null	null		null	null		-5.23E+00	0.00E+00	Down	-5.85E+00	0.00E+00	Down	Unigene40535_All//gi|51318208|gb|AAU00158.1|//0.00E+00//root-specific metal transporter [Malus baccata]	Unigene40535_All//1.00E-121//AT1G80830| NRAMP1 (NATURAL RESISTANCE-ASSOCIATED MACROPHAGE PROTEIN 1); inorganic anion transmembrane transporter/ manganese ion transmembrane transporter/ metal ion transmembrane transporter	Unigene40535_All//7.00E-34//DN804497			nr +
Unigene40540_All	1263	0.00	0.00	0.00	0.00	0.00	0.00	26.38	17.61	4.16	null	null		null	null		null	null		null	null		-5.83E-01	2.73E-12		-2.66E+00	1.02E-121	Down	Unigene40540_All//gi|77378044|gb|AAZ79470.2|//3.00E-67//SUPERMAN-like zinc finger protein [Gossypium hirsutum]	Unigene40540_All//6.00E-29//AT2G37740| ZFP10 (ZINC-FINGER PROTEIN 10); nucleic acid binding / transcription factor/ zinc ion binding	Unigene40540_All//1.00E-34//TC130397	C2H2		nr -
Unigene40541_All	797	1.71	1.65	1.27	1.06	2.38	0.74	0.16	0.00	2.35	-4.62E-02	9.46E-01		-4.27E-01	4.72E-01		1.16E+00	1.39E-02		-5.28E-01	5.02E-01		-7.31E+00	2.35E-01		3.88E+00	4.18E-10	Up	Unigene40541_All//gi|224145016|ref|XP_002325496.1|//3.00E-57//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222862371|gb|EEE99877.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene40541_All//4.00E-43//AT4G12010| disease resistance protein (TIR-NBS-LRR class), putative	Unigene40541_All//4.00E-40//gi|164283229|gb|ES851593.1|ES851593				nr +
Unigene40542_All	692	2.12	0.66	1.92	0.22	0.70	0.98	0.00	0.00	1.84	-1.68E+00	4.05E-03		-1.38E-01	7.97E-01		1.69E+00	1.66E-01		2.18E+00	3.14E-02		null	null		1.08E+01	3.29E-09	Up							

Unigene40543_All	1167	0.94	1.13	1.10	1.58	2.83	1.12	2.39	5.55	14.37	2.62E-01	6.27E-01		2.18E-01	7.02E-01		8.43E-01	1.14E-02		-4.93E-01	3.34E-01		1.22E+00	1.48E-08	Up	2.59E+00	9.43E-59	Up	Unigene40543_All//gi|297802268|ref|XP_002869018.1|//1.00E-108//GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314854|gb|EFH45277.1|GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40543_All//1.00E-105//AT4G36830| GNS1/SUR4 membrane family protein	Unigene40543_All//2.00E-14//TC171527				nr -
Unigene40545_All	594	1.59	5.20	2.78	2.43	2.55	1.60	2.06	2.39	13.28	1.71E+00	8.87E-06	Up	8.10E-01	1.35E-01		6.88E-02	9.20E-01		-6.07E-01	2.97E-01		2.13E-01	6.74E-01		2.69E+00	3.66E-29	Up			Unigene40545_All//1.00E-11//TC179099				
Unigene40546_All	346	0.15	0.00	0.15	1.73	1.79	1.57	1.59	1.33	0.00	-7.24E+00	6.11E-01		2.55E-02	9.95E-01		5.22E-02	9.71E-01		-1.41E-01	8.79E-01		-2.58E-01	7.60E-01		-1.06E+01	2.80E-04	Down	Unigene40546_All//gi|297811577|ref|XP_002873672.1|//3.00E-19//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319509|gb|EFH49931.1|armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40546_All//6.00E-20//AT5G14510| armadillo/beta-catenin repeat family protein	Unigene40546_All//5.00E-167//TC171460				nr -
Unigene40548_All	1091	0.00	0.00	0.00	0.00	0.00	0.04	3.10	8.81	23.15	null	null		null	null		null	null		5.37E+00	6.95E-01		1.51E+00	8.77E-17	Up	2.90E+00	1.45E-99	Up	Unigene40548_All//gi|149728036|gb|ABR28343.1|//4.00E-89//MYB transcription factor MYB64 [Medicago truncatula]	Unigene40548_All//6.00E-79//AT5G57620| MYB36 (myb domain protein 36); DNA binding / transcription factor	Unigene40548_All//5.00E-117//TC144511	MYB			nr +
Unigene40549_All	549	0.00	0.18	0.00	2.18	1.32	2.30	2.00	0.38	0.65	7.53E+00	3.86E-01		null	null		-7.25E-01	2.33E-01		8.10E-02	9.13E-01		-2.39E+00	4.11E-04	Down	-1.62E+00	6.27E-03		Unigene40549_All//gi|255537956|ref|XP_002510043.1|//6.00E-06//Squalene monooxygenase, putative [Ricinus communis] >gi|223550744|gb|EEF52230.1|Squalene monooxygenase, putative [Ricinus communis]		Unigene40549_All//0.00E+00//CO130208		ko00100|Steroid biosynthesis		nr -
Unigene40551_All	319	3.12	3.18	8.51	2.19	2.05	2.55	0.80	0.66	0.75	2.77E-02	9.86E-01		1.45E+00	4.85E-04	Up	-9.21E-02	8.95E-01		2.21E-01	7.78E-01		-2.80E-01	8.28E-01		-8.58E-02	9.56E-01									
Unigene40552_All	832	0.50	0.00	0.00	23.41	13.82	10.86	0.10	0.00	0.10	-8.97E+00	1.05E-02		-8.97E+00	1.56E-02		-7.60E-01	3.43E-11		-1.11E+00	1.85E-18	Down	-6.67E+00	4.03E-01		-8.48E-02	9.72E-01		Unigene40552_All//gi|297845654|ref|XP_002890708.1|//8.00E-87//F21J9.14 [Arabidopsis lyrata subsp. lyrata] >gi|297336550|gb|EFH66967.1|F21J9.14 [Arabidopsis lyrata subsp. lyrata]	Unigene40552_All//9.00E-85//AT1G24480| methyltransferase	Unigene40552_All//4.00E-34//gi|78342286|gb|DT562560.1|DT562560				nr +
Unigene40554_All	566	2.03	0.18	0.19	1.32	1.95	0.80	2.24	0.74	1.69	-3.51E+00	6.57E-05	Down	-3.43E+00	1.54E-04	Down	5.60E-01	4.27E-01		-7.27E-01	3.90E-01		-1.60E+00	4.42E-03		-4.08E-01	4.35E-01		Unigene40554_All//gi|42564100|ref|NP_187868.2|//2.00E-79//protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|79313205|ref|NP_001030682.1|protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|75273276|sp|Q9LHJ9.1|P2C38_ARATH RecName: Full=Probable protein phosphatase 2C 38; Short=AtPP2C38 >gi|9294356|dbj|BAB02253.1|protein phosphatase 2C [Arabidopsis thaliana] >gi|28466963|gb|AAO44090.1|At3g12620 [Arabidopsis thaliana] >gi|222424096|dbj|BAH20008.1|AT3G12620 [Arabidopsis thaliana] >gi|222424228|dbj|BAH20072.1|AT3G12620 [Arabidopsis thaliana]	Unigene40554_All//1.00E-80//AT3G12620| protein phosphatase 2C family protein / PP2C family protein	Unigene40554_All//2.00E-139//CO127481				nr +
Unigene40558_All	220	3.57	201.07	33.89	16.30	20.50	50.30	64.19	199.29	134.55	5.82E+00	5.08E-228	Up	3.25E+00	7.91E-26	Up	3.31E-01	2.92E-01		1.63E+00	1.61E-18	Up	1.63E+00	5.53E-83	Up	1.07E+00	2.62E-30	Up			Unigene40558_All//4.00E-114//TC162170				
Unigene4056_All	946	4.26	3.21	3.15	0.37	1.89	3.06	1.97	2.70	1.94	-4.06E-01	1.92E-01		-4.34E-01	1.81E-01		2.36E+00	1.76E-05	Up	3.05E+00	1.51E-10	Up	4.55E-01	2.20E-01		-2.17E-02	9.71E-01		Unigene4056_All//gi|42567949|ref|NP_197404.2|//2.00E-19//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	Unigene4056_All//1.00E-19//AT5G19030| RNA recognition motif (RRM)-containing protein					nr -
Unigene40561_All	574	4.83	1.77	4.55	1.48	1.32	1.02	0.81	0.44	0.90	-1.45E+00	2.37E-04	Down	-8.78E-02	8.19E-01		-1.61E-01	8.14E-01		-5.28E-01	5.02E-01		-8.91E-01	3.83E-01		1.55E-01	8.60E-01		Unigene40561_All//gi|109946589|gb|ABG48473.1|//3.00E-11//At3g19810 [Arabidopsis thaliana]		Unigene40561_All//0.00E+00//TC140026				nr +
Unigene40562_All	285	0.00	0.00	0.00	3.67	3.62	3.80	45.69	2.79	10.62	null	null		null	null		-1.81E-02	9.61E-01		5.12E-02	9.47E-01		-4.04E+00	6.64E-68	Down	-2.10E+00	2.11E-36	Down	Unigene40562_All//gi|297791389|ref|XP_002863579.1|//1.00E-14//FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297309414|gb|EFH39838.1| FAD-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene40562_All//2.00E-13//AT5G44440| FAD-binding domain-containing protein	Unigene40562_All//1.00E-74//TC143305				nr +
Unigene40564_All	993	0.16	0.36	1.34	1.76	3.88	2.09	0.98	0.63	0.96	1.18E+00	3.72E-01		3.08E+00	8.57E-05	Up	1.15E+00	1.61E-04	Up	2.53E-01	6.37E-01		-6.33E-01	3.28E-01		-2.44E-02	9.71E-01		Unigene40564_All//gi|15230158|ref|NP_188497.1|//3.00E-75//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene40564_All//1.00E-68//AT3G18670| ankyrin repeat family protein					nr +
Unigene40568_All	469	0.00	0.00	0.00	1.49	0.44	2.31	72.84	34.04	28.88	null	null		null	null		-1.76E+00	4.11E-02		6.36E-01	3.73E-01		-1.10E+00	1.31E-35	Down	-1.33E+00	1.18E-49	Down	Unigene40568_All//gi|15485716|emb|CAC67491.1|//1.00E-45//selenium binding protein [Lotus japonicus] >gi|15485718|emb|CAC67492.1|selenium binding protein [Lotus japonicus]	Unigene40568_All//1.00E-46//AT3G23800| SBP3 (selenium-binding protein 3); selenium binding	Unigene40568_All//0.00E+00//gi|109839155|gb|DW237716.1|DW237716				nr +
Unigene40569_All	1033	0.20	0.98	0.15	3.38	3.43	5.12	2.29	0.73	0.54	2.28E+00	4.09E-03		-3.90E-01	8.07E-01		2.45E-02	9.53E-01		6.00E-01	2.20E-02		-1.65E+00	2.75E-05	Down	-2.09E+00	3.31E-07	Down	Unigene40569_All//gi|15219457|ref|NP_177480.1|//1.00E-108//SUS6 (SUCROSE SYNTHASE 6); UDP-glycosyltransferase/ sucrose synthase [Arabidopsis thaliana]	Unigene40569_All//1.00E-109//AT1G73370| SUS6 (SUCROSE SYNTHASE 6); UDP-glycosyltransferase/ sucrose synthase	Unigene40569_All//0.00E+00//TC152711		ko00500|Starch and sucrose metabolism		nr -
Unigene40570_All	531	6.60	2.58	2.81	5.35	5.64	9.02	0.96	0.47	0.90	-1.36E+00	7.41E-05	Down	-1.23E+00	4.58E-04	Down	7.74E-02	8.52E-01		7.54E-01	5.96E-03		-1.02E+00	2.88E-01		-8.59E-02	9.30E-01		Unigene40570_All//gi|195627412|gb|ACG35536.1|//1.00E-33//retrotransposon protein [Zea mays]	Unigene40570_All//9.00E-33//AT3G18380| sequence-specific DNA binding / transcription factor	Unigene40570_All//0.00E+00//DW501211				nr -
Unigene40571_All	515	0.41	0.20	0.00	5.51	1.07	1.49	0.57	1.87	1.78	-1.05E+00	5.64E-01		-8.67E+00	1.45E-01		-2.37E+00	2.17E-09	Down	-1.89E+00	2.34E-06	Down	1.70E+00	1.17E-02		1.63E+00	1.45E-02		Unigene40571_All//gi|292630778|sp|Q9FFN2.2|GLYT3_ARATH//3.00E-49//RecName: Full=Probable glycosyltransferase At5g03795	Unigene40571_All//2.00E-50//AT5G03795| LOCATED IN: membrane; EXPRESSED IN: embryo, sepal, flower; EXPRESSED DURING: C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Exostosin-like (InterPro:IPR004263); BEST Arabidopsis thaliana protein match is: exostosin family protein (TAIR:AT3G07620.1); Has 866 Blast hits to 860 proteins in 87 species: Archae - 0; Bacteria - 9; Metazoa - 265; Fungi - 4; Plants - 504; Viruses - 0; Other Eukaryotes - 84 (source: NCBI BLink).	Unigene40571_All//6.00E-38//TC143482				nr +
Unigene40572_All	894	0.70	0.68	1.01	0.95	2.77	1.47	3.88	0.75	2.14	-4.63E-02	9.72E-01		5.28E-01	4.79E-01		1.55E+00	1.52E-04	Up	6.29E-01	3.15E-01		-2.37E+00	2.21E-11	Down	-8.58E-01	2.67E-03		Unigene40572_All//gi|30684540|ref|NP_193617.2|//6.00E-40//ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene40572_All//1.00E-31//AT4G18820| ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding	Unigene40572_All//4.00E-28//TC171199				nr -
Unigene40575_All	410	4.08	2.60	5.71	3.28	3.70	0.66	0.93	0.92	0.29	-6.54E-01	1.99E-01		4.85E-01	2.69E-01		1.72E-01	8.06E-01		-2.31E+00	4.01E-04	Down	-1.66E-02	1.02E+00		-1.67E+00	1.40E-01				Unigene40575_All//5.00E-07//EY484953				
Unigene40576_All	400	0.26	1.77	0.53	10.46	7.92	12.31	2.43	1.67	0.00	2.76E+00	9.14E-03		1.03E+00	5.91E-01		-4.01E-01	1.83E-01		2.35E-01	4.55E-01		-5.40E-01	4.02E-01		-1.12E+01	2.72E-07	Down			Unigene40576_All//0.00E+00//DR458243				
Unigene40578_All	348	20.15	10.48	13.62	17.03	11.97	15.70	73.99	40.35	35.83	-9.42E-01	2.48E-05		-5.65E-01	1.46E-02		-5.09E-01	3.05E-02		-1.17E-01	6.86E-01		-8.75E-01	8.15E-19		-1.05E+00	7.90E-26	Down	Unigene40578_All//gi|223469631|gb|ACM90156.1|//6.00E-24//40S ribosomal protein S15-like protein [Jatropha curcas]	Unigene40578_All//3.00E-25//AT5G09510| 40S ribosomal protein S15 (RPS15D)	Unigene40578_All//0.00E+00//TC154752		ko03010|Ribosome		nr -
Unigene40583_All	1566	0.00	0.00	0.00	0.00	0.00	0.00	17.23	6.75	4.71	null	null		null	null		null	null		null	null		-1.35E+00	5.88E-39	Down	-1.87E+00	6.33E-64	Down	Unigene40583_All//gi|15217667|ref|NP_174087.1|//2.00E-31//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|218563530|sp|Q9SF23.2|BH110_ARATH RecName: Full=Transcription factor bHLH110; AltName: Full=Transcription factor EN 59; AltName: Full=bHLH transcription factor bHLH110; AltName: Full=Basic helix-loop-helix protein 110; Short=bHLH 110; Short=AtbHLH110	Unigene40583_All//4.00E-31//AT1G27660| ethylene-responsive protein -related		bHLH			nr +
Unigene40589_All	340	8.31	5.96	5.17	12.01	6.89	11.03	43.40	21.27	22.73	-4.79E-01	2.07E-01		-6.85E-01	8.02E-02		-8.03E-01	4.48E-03		-1.24E-01	6.98E-01		-1.03E+00	2.40E-14	Down	-9.33E-01	1.03E-12				Unigene40589_All//2.00E-144//TC176674				
Unigene40591_All	455	3.33	3.12	8.19	8.10	9.76	7.84	0.37	1.10	0.09	-9.69E-02	8.47E-01		1.30E+00	1.44E-04	Up	2.69E-01	4.08E-01		-4.71E-02	9.03E-01		1.57E+00	1.18E-01		-2.09E+00	3.13E-01		Unigene40591_All//gi|10737098|dbj|BAF00501.1|//7.00E-11//zinc finger like protein [Arabidopsis thaliana]		Unigene40591_All//3.00E-116//BE053154				nr -
Unigene40592_All	1348	0.08	0.00	0.00	1.00	0.77	0.23	6.59	1.71	12.65	-6.28E+00	3.71E-01		-6.28E+00	3.93E-01		-3.81E-01	5.36E-01		-2.09E+00	1.00E-03		-1.95E+00	4.79E-22	Down	9.41E-01	1.16E-14		Unigene40592_All//gi|3399777|gb|AAC32828.1|//1.00E-63//symbiotic ammonium transporter [Glycine max]	Unigene40592_All//4.00E-59//AT4G37850| basic helix-loop-helix (bHLH) family protein		bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene40595_All	263	3.78	3.08	1.21	5.49	3.67	4.46	39.07	9.22	8.33	-2.94E-01	6.37E-01		-1.64E+00	3.43E-02		-5.83E-01	2.98E-01		-2.99E-01	6.38E-01		-2.08E+00	1.26E-27	Down	-2.23E+00	5.26E-31	Down			Unigene40595_All//7.00E-147//gi|164301351|gb|ES813123.1|ES813123				
Unigene40598_All	241	21.71	62.86	49.71	26.04	53.30	50.60	39.47	95.56	71.74	1.53E+00	8.63E-22	Up	1.20E+00	1.17E-11	Up	1.03E+00	7.57E-12	Up	9.58E-01	2.75E-09		1.28E+00	1.50E-30	Up	8.62E-01	6.25E-13		Unigene40598_All//gi|66710734|emb|CAI98820.1|//5.00E-27//SNF1-related protein kinase regulatory beta subunit 1 [Pisum sativum]	Unigene40598_All//2.00E-26//AT5G21170| 5'-AMP-activated protein kinase beta-2 subunit, putative	Unigene40598_All//8.00E-134//TC146790				nr -
Unigene406_All	857	1.10	0.89	1.18	3.78	3.17	3.16	1.13	1.51	2.93	-3.09E-01	6.29E-01		1.04E-01	8.77E-01		-2.51E-01	5.18E-01		-2.57E-01	5.00E-01		4.14E-01	4.51E-01		1.37E+00	1.54E-04	Up	Unigene406_All//gi|240254592|ref|NP_181219.4|//1.00E-111//binding [Arabidopsis thaliana]	Unigene406_All//1.00E-104//AT2G36810| binding	Unigene406_All//0.00E+00//ES802001				nr +
Unigene4060_All	822	5.98	1.79	1.55	5.21	6.41	7.42	3.34	3.25	3.78	-1.74E+00	5.49E-09	Down	-1.94E+00	8.52E-10	Down	2.99E-01	3.03E-01		5.09E-01	3.71E-02		-3.90E-02	9.29E-01		1.77E-01	6.18E-01		Unigene4060_All//gi|15220076|ref|NP_178136.1|//1.00E-78//PSF1 (PARTNER OF SLD FIVE 1) [Arabidopsis thaliana] >gi|5902373|gb|AAD55475.1|AC009322_15 unknown protein [Arabidopsis thaliana] >gi|34365591|gb|AAQ65107.1|At1g80190 [Arabidopsis thaliana] >gi|51969246|dbj|BAD43315.1|At1g80190 [Arabidopsis thaliana]	Unigene4060_All//5.00E-80//AT1G80190| PSF1 (PARTNER OF SLD FIVE 1)	Unigene4060_All//0.00E+00//ES850894				nr -
Unigene40600_All	374	1.26	0.95	2.85	1.47	0.74	2.05	0.34	1.12	2.45	-4.09E-01	6.69E-01		1.18E+00	9.59E-02		-9.92E-01	3.13E-01		4.87E-01	5.91E-01		1.72E+00	1.35E-01		2.85E+00	3.18E-04	Up	Unigene40600_All//gi|14954332|gb|ABP04242.1|//2.00E-29//calmodulin binding protein-like [Elaeis guineensis]	Unigene40600_All//3.00E-17//AT1G76650| calcium-binding EF hand family protein			ko04626|Plant-pathogen interaction		nr +
Unigene40601_All	301	5.39	1.68	3.18	4.30	4.00	3.60	0.56	3.33	0.53	-1.68E+00	2.36E-03		-7.59E-01	1.59E-01		-1.04E-01	8.43E-01		-2.57E-01	6.87E-01		2.57E+00	4.79E-04	Up	-8.60E-02	9.65E-01				Unigene40601_All//6.00E-52//gi|109872115|gb|DW501091.1|DW501091				

Unigene40603_All	961	1.74	0.47	0.33	2.95	3.15	2.11	3.08	1.61	2.94	-1.88E+00	7.32E-04	Down	-2.39E+00	1.21E-04	Down	9.39E-02	8.23E-01		-4.82E-01	2.20E-01		-9.36E-01	3.91E-03		-6.54E-02	8.46E-01		Unigene40603_All//gi|65736533|dbj|BAD98515.1//1.00E-136//TONSOKU protein [Nicotiana tabacum]	Unigene40603_All//2.00E-80//AT3G18730| TSK (TONSOKU); protein binding					nr +
Unigene40604_All	387	1.49	0.13	0.00	2.45	3.83	2.33	3.28	1.51	0.62	-3.51E+00	9.02E-03		-1.05E+01	2.60E-03		6.46E-01	2.65E-01		-6.74E-02	9.34E-01		-1.12E+00	3.93E-02		-2.41E+00	7.19E-05	Down	Unigene40604_All//gi|79379437|ref|NP_177526.2|//7.00E-31//structural constituent of ribosome [Arabidopsis thaliana] >gi|40823465|gb|AAR92284.1| At1g73850 [Arabidopsis thaliana] >gi|46518405|gb|AAS99684.1| At1g73850 [Arabidopsis thaliana]	Unigene40604_All//4.00E-32//AT1G73850| structural constituent of ribosome	Unigene40604_All//5.00E-155//DR460862				nr +
Unigene40606_All	523	54.72	110.06	75.85	12.38	13.76	15.37	15.12	17.90	11.35	1.01E+00	2.79E-42	Up	4.71E-01	5.92E-08		1.52E-01	5.59E-01		3.12E-01	1.57E-01		2.44E-01	1.80E-01		-4.14E-01	2.22E-02		Unigene40606_All//gi|224065699|ref|XP_002301927.1|//2.00E-43//precursor of protein cell division protease ftsh-like protein [Populus trichocarpa] >gi|222843653|gb|EEE81200.1| precursor of protein cell division protease ftsh-like protein [Populus trichocarpa]	Unigene40606_All//3.00E-42//AT1G50250| FTSH1 (FtsH protease 1); ATP-dependent peptidase/ ATPase/ metallopeptidase	Unigene40606_All//0.00E+00//TC161660				nr +
Unigene40607_All	402	0.13	2.90	0.66	0.37	1.80	0.90	2.94	4.16	8.23	4.48E+00	1.19E-05	Up	2.35E+00	2.39E-01		2.27E+00	1.95E-02		1.27E+00	3.82E-01		4.98E-01	2.92E-01		1.48E+00	2.50E-06	Up	Unigene40607_All//gi|15235668|ref|NP_193070.1|//1.00E-18//leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] >gi|75337952|sp|Q9T085.1|LRX3_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 3; Short=LRR/EXTENSIN3; Short=AtLRX3; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|4584539|emb|CAB40769.1| extensin-like protein [Arabidopsis thaliana] >gi|7268037|emb|CAB78376.1| extensin-like protein [Arabidopsis thaliana]						nr -
Unigene40608_All	572	3.66	4.52	4.10	0.96	4.15	1.03	0.37	0.44	0.21	3.04E-01	4.46E-01		1.63E-01	7.00E-01		2.12E+00	2.44E-06	Up	9.95E-02	9.36E-01		2.46E-01	8.53E-01		-8.23E-01	5.99E-01					Unigene40608_All//7.00E-07//ES794141				
Unigene40609_All	293	2.68	1.73	6.91	3.23	4.82	2.47	2.45	0.57	0.27	-6.31E-01	4.08E-01		1.37E+00	5.21E-03		5.77E-01	3.29E-01		-3.89E-01	6.28E-01		-2.10E+00	1.25E-02		-3.17E+00	8.09E-04	Down				Unigene40609_All//2.00E-17//FL576934				
Unigene40610_All	331	15.02	11.63	8.37	16.40	14.56	16.51	41.64	23.74	12.16	-3.68E-01	1.84E-01		-8.44E-01	2.66E-03		-1.72E-01	5.54E-01		9.30E-03	9.72E-01		-8.11E-01	2.76E-09		-1.78E+00	7.83E-31	Down				Unigene40610_All//5.00E-176//ES827233				
Unigene40611_All	627	1.25	0.48	0.76	0.95	1.54	1.44	2.09	1.00	0.51	-1.37E+00	9.59E-02		-7.12E-01	3.88E-01		6.90E-01	3.61E-01		5.96E-01	4.55E-01		-1.06E+00	4.42E-02		-2.04E+00	3.01E-04	Down	Unigene40611_All//gi|42566730|ref|NP_193010.2|//2.00E-63//adenine-DNA glycosylase-related / MYH-related [Arabidopsis thaliana]	Unigene40611_All//1.00E-57//AT4G12740| adenine-DNA glycosylase-related / MYH-related			ko03410|Base excision repair		nr +
Unigene40612_All	680	0.62	0.45	0.55	0.51	0.30	0.80	5.10	2.34	6.68	-4.61E-01	6.50E-01		-1.67E-01	8.79E-01		-7.55E-01	5.67E-01		6.36E-01	5.61E-01		-1.13E+00	1.75E-04	Down	3.90E-01	1.21E-01					Unigene40612_All//3.00E-71//TC164316				
Unigene40613_All	272	10.77	11.36	8.61	37.54	15.70	22.91	144.25	154.12	34.13	7.71E-02	8.27E-01		-3.23E-01	3.97E-01		-1.26E+00	1.48E-13	Down	-7.12E-01	4.46E-05		9.55E-02	2.67E-01		-2.08E+00	1.99E-106	Down				Unigene40613_All//7.00E-107//TC157469				
Unigene40614_All	438	15.41	41.65	15.68	46.97	80.74	83.32	136.88	225.01	535.09	1.43E+00	1.09E-23	Up	2.54E-02	9.29E-01		7.82E-01	3.20E-20		8.27E-01	6.67E-21		7.17E-01	1.15E-49		1.97E+00	0.00E+00	Up	Unigene40614_All//gi|151934217|gb|ABS18446.1|//1.00E-46//WRKY50 [Glycine max]	Unigene40614_All//3.00E-36//AT2G24570| WRKY17; calmodulin binding / transcription factor	Unigene40614_All//0.00E+00//gi|48750020|gb|CO080539.1|CO080539	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene40615_All	696	0.60	154.99	32.06	1.29	5.44	27.12	0.12	0.12	0.74	8.01E+00	0.00E+00	Up	5.74E+00	3.19E-112	Up	2.08E+00	1.13E-09	Up	4.40E+00	4.10E-90	Up	-1.67E-02	1.01E+00		2.61E+00	1.55E-02		Unigene40615_All//gi|15240040|ref|NP_196821.1|//3.00E-75//SAG29 (SENESCENCE-ASSOCIATED PROTEIN 29) [Arabidopsis thaliana] >gi|9955561|emb|CAC05445.1| senescence-associated protein (SAG29) [Arabidopsis thaliana]	Unigene40615_All//2.00E-76//AT5G13170| SAG29 (SENESCENCE-ASSOCIATED PROTEIN 29)	Unigene40615_All//4.00E-86//gi|54118506|gb|CO494015.1|CO494015				nr +
Unigene40616_All	956	0.00	0.32	0.22	0.10	0.07	0.09	25.92	128.88	47.71	8.31E+00	4.43E-02		7.80E+00	1.41E-01		-5.33E-01	8.16E-01		-1.41E-01	9.50E-01		2.31E+00	0.00E+00	Up	8.81E-01	8.08E-34									
Unigene40618_All	515	0.00	1.48	0.62	0.19	1.81	0.96	1.81	2.03	1.93	1.05E+01	1.76E-04	Up	9.28E+00	4.52E-02		3.22E+00	5.79E-04	Up	2.32E+00	6.88E-02		1.68E-01	7.81E-01		9.86E-02	8.78E-01					Unigene40618_All//6.00E-07//ES835903				
Unigene40622_All	1661	149.97	18.64	88.39	0.18	0.17	0.05	0.00	0.05	0.00	-3.01E+00	0.00E+00	Down	-7.63E-01	7.60E-110		-1.17E-01	9.00E-01		-1.73E+00	2.89E-01		5.65E+00	4.01E-01		null	null		Unigene40622_All//gi|171906258|gb|ACB56926.1|//1.00E-147//glycosyltransferase UGT90A7 [Hieracium pilosella]	Unigene40622_All//1.00E-143//AT2G16890| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene40622_All//0.00E+00//gi|78341183|gb|DT561457.1|DT561457		ko00908|Zeatin biosynthesis		nr +
Unigene40624_All	317	28.55	51.47	27.55	23.26	19.66	28.35	50.55	104.42	90.99	8.50E-01	1.31E-09		-5.17E-02	8.06E-01		-2.42E-01	3.05E-01		2.86E-01	1.72E-01		1.05E+00	5.52E-32	Up	8.48E-01	2.00E-20					Unigene40624_All//2.00E-160//TC174060				
Unigene40625_All	700	0.00	1.30	0.15	0.14	0.44	0.90	595.91	380.64	637.99	1.03E+01	2.62E-05	Up	7.25E+00	3.98E-01		1.64E+00	3.21E-01		2.67E+00	1.83E-02		-6.47E-01	1.93E-173		9.84E-02	3.27E-06		Unigene40625_All//gi|83728526|gb|ABC41951.1|//1.00E-49//FAD-linked oxidoreductase 2 [Glycine max]	Unigene40625_All//3.00E-46//AT5G44400| FAD-binding domain-containing protein	Unigene40625_All//0.00E+00//CO078412				nr +
Unigene40627_All	588	15.66	4.74	3.62	19.40	16.92	22.20	87.94	32.48	26.97	-1.72E+00	5.83E-16	Down	-2.11E+00	7.88E-20	Down	-1.97E-01	2.96E-01		1.94E-01	2.75E-01		-1.44E+00	3.85E-81	Down	-1.71E+00	4.11E-107	Down	Unigene40627_All//gi|115449557|ref|NP_001048495.1|//7.00E-73//Os02g0814700 [Oryza sativa Japonica Group] >gi|115450623|ref|NP_001048912.1| Os03g0129100 [Oryza sativa Japonica Group] >gi|115482426|ref|NP_001064806.1| Os10g0466700 [Oryza sativa Japonica Group] >gi|226494003|ref|NP_001148342.1| 60S ribosomal protein L23 [Zea mays] >gi|226532932|ref|NP_001149366.1| 60S ribosomal protein L23 [Zea mays] >gi|259490208|ref|NP_001159003.1| 60S ribosomal protein L23 [Zea mays] >gi|225433247|ref|XP_002285443.1| PREDICTED: similar to ribosomal protein L17 [Vitis vinifera] >gi|225438001|ref|XP_002273253.1| PREDICTED: similar to ribosomal protein L17 [Vitis vinifera] >gi|134889168|gb|AAK23802.1|AC022457_5 60S ribosomal protein L17 [Oryza sativa Japonica Group] >gi|47847875|dbj|BAD21668.1| 60S ribosomal protein L17 [Oryza	Unigene40627_All//4.00E-73//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene40627_All//0.00E+00//gi|78334876|gb|DT555150.1|DT555150		ko03010|Ribosome		nr -
Unigene40628_All	444	6.13	1.26	3.00	1.57	0.93	1.73	2.38	0.38	0.00	-2.29E+00	3.18E-07	Down	-1.03E+00	1.04E-02		-7.55E-01	3.69E-01		1.39E-01	8.77E-01		-2.66E+00	2.25E-04	Down	-1.12E+01	6.72E-08	Down	Unigene40628_All//gi|225439143|ref|XP_002271738.1|//6.00E-56//PREDICTED: R2R3 MYB60 transcription factor [Vitis vinifera] >gi|193795735|gb|ACF21938.1| R2R3 MYB60 transcription factor [Vitis vinifera]	Unigene40628_All//1.00E-56//AT1G08810| MYB60 (myb domain protein 60); DNA binding / transcription factor	Unigene40628_All//0.00E+00//TC145072	MYB			nr +
Unigene4063_All	1949	3.03	1.51	1.04	5.42	2.92	2.97	4.30	2.32	2.02	-1.01E+00	4.46E-05	Down	-1.55E+00	1.18E-08	Down	-8.94E-01	3.42E-08		-8.69E-01	4.39E-07		-8.91E-01	7.45E-07		-1.09E+00	1.66E-09	Down	Unigene4063_All//gi|56381987|gb|AAV85712.1|//1.00E-156//At2g18850 [Arabidopsis thaliana]	Unigene4063_All//6.00E-149//AT2G18850| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: SET (InterPro:IPR001214); BEST Arabidopsis thaliana protein match is: SET domain-containing protein (TAIR:AT3G07670.1); Has 597 Blast hits to 594 proteins in 119 species: Archae - 0; Bacteria - 0; Metazoa - 207; Fungi - 132; Plants - 162; Viruses - 0; Other Eukaryotes - 96 (source: NCBI BLink).	Unigene4063_All//0.00E+00//TC177481				nr +
Unigene40630_All	242	26.81	10.68	14.52	22.64	22.48	22.40	54.16	12.44	18.11	-1.33E+00	4.68E-08	Down	-8.84E-01	2.51E-04		-1.02E-02	9.65E-01		-1.59E-02	9.45E-01		-2.12E+00	7.02E-36	Down	-1.58E+00	5.37E-25	Down	Unigene40630_All//gi|5725356|emb|CAA10382.2|//4.00E-32//alpha-D-xylosidase [Tropaeolum majus]	Unigene40630_All//4.00E-27//AT1G68560| XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Unigene40630_All//1.00E-129//TC138131		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr +
Unigene40631_All	757	4.84	5.02	1.97	4.67	4.37	4.00	1.17	0.50	0.21	5.33E-02	8.72E-01		-1.30E+00	1.73E-04	Down	-9.74E-02	8.12E-01		-2.25E-01	5.49E-01		-1.24E+00	6.79E-02		-2.48E+00	9.93E-04	Down	Unigene40631_All//gi|297816538|ref|XP_002876152.1|//9.00E-26//ATOFP6/OFP6 [Arabidopsis lyrata subsp. lyrata] >gi|297321990|gb|EFH52411.1| ATOFP6/OFP6 [Arabidopsis lyrata subsp. lyrata]	Unigene40631_All//8.00E-32//AT2G36026| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF623, plant (InterPro:IPR006458); BEST Arabidopsis thaliana protein match is: OFP6 (OVATE FAMILY PROTEIN 6) (TAIR:AT3G52525.1); Has 230 Blast hits to 230 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 228; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene40631_All//2.00E-50//TC160220		ko04144|Endocytosis		nr -
Unigene40632_All	354	11.38	8.44	24.22	12.95	11.38	14.54	1.31	1.42	1.35	-4.30E-01	1.62E-01		1.09E+00	1.90E-07	Up	-1.86E-01	5.57E-01		1.68E-01	6.08E-01		1.09E-01	9.14E-01		3.97E-02	9.76E-01		Unigene40632_All//gi|122242678|sp|Q0WVV0.1|PPR31_ARATH//6.00E-11//RecName: Full=Pentatricopeptide repeat-containing protein At1g10910, chloroplastic; Flags: Precursor >gi|110741600|dbj|BAE98748.1| membrane-associated salt-inducible protein isolog [Arabidopsis thaliana]		Unigene40632_All//1.00E-139//CO074411				nr +
Unigene40634_All	332	5.99	1.68	10.10	0.00	1.04	3.40	0.00	0.00	0.00	-1.83E+00	2.47E-04	Down	7.55E-01	3.26E-02		1.00E+01	3.01E-02		1.17E+01	9.83E-07	Up	null	null		null	null		Unigene40634_All//gi|161089458|gb|ABX37719.1|//2.00E-32//acyltransferase [Vanda hybrid cultivar]	Unigene40634_All//1.00E-28//AT5G17540| transferase family protein	Unigene40634_All//8.00E-101//gi|48817391|gb|CO118704.1|CO118704		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -

Unigene40642_All	439	153.98	85.87	89.52	262.12	154.53	130.96	88.89	45.79	120.06	-8.43E-01	5.92E-37		-7.83E-01	1.89E-31		-7.62E-01	1.57E-64		-1.00E+00	3.35E-90	Down	-9.57E-01	1.51E-32		4.34E-01	1.07E-11		Unigene40642_All//gi|224110514|ref|XP_002315543.1|//4.00E-10//predicted protein [Populus trichocarpa] >gi|222864583|gb|EEF01714.1|predicted protein [Populus trichocarpa]		Unigene40642_All//8.00E-120//gi|78324642|gb|DT544916.1|DT544916				nr -
Unigene40643_All	429	46.83	15.71	26.07	77.10	61.49	92.33	243.63	115.74	80.61	-1.58E+00	5.83E-30	Down	-8.45E-01	4.58E-11		-3.27E-01	2.04E-04		2.60E-01	2.40E-03		-1.07E+00	1.24E-103	Down	-1.60E+00	3.65E-196	Down	Unigene40643_All//gi|215433932|gb|ACJ66780.1|//5.00E-16//omega-3 desaturase [Portulaca oleracea]	Unigene40643_All//1.00E-16//AT3G12915| GTP binding / GTPase	Unigene40643_All//0.00E+00//TC134103				nr +
Unigene40646_All	2324	0.00	0.00	0.00	0.00	0.03	0.00	9.59	3.11	6.74	null	null		null	null		4.89E+00	6.09E-01		null	null		-1.62E+00	3.12E-42	Down	-5.09E-01	4.69E-07		Unigene40646_All//gi|30725324|gb|AAP37684.1|//1.00E-139//At3g01680 [Arabidopsis thaliana]	Unigene40646_All//9.00E-141//AT3G01680| unknown protein	Unigene40646_All//6.00E-72//TC134810				nr -
Unigene40647_All	843	12.91	3.19	6.32	0.77	0.25	0.11	1.76	1.19	0.95	-2.02E+00	5.00E-23	Down	-1.03E+00	1.63E-08	Down	-1.65E+00	6.52E-02		-2.84E+00	1.02E-02		-5.61E-01	2.61E-01		-8.93E-01	5.68E-02		Unigene40647_All//gi|48675345|dbj|BAD22820.1|//1.00E-112//nitrate transporter [Prunus persica]	Unigene40647_All//1.00E-73//AT1G12110| NRT1.1; nitrate transmembrane transporter/ transporter	Unigene40647_All//0.00E+00//gi|78330549|gb|DT550823.1|DT550823				nr -
Unigene40648_All	460	0.68	1.43	1.39	0.54	0.00	1.37	2.48	0.36	1.39	1.07E+00	2.36E-01		1.03E+00	2.81E-01		-9.08E+00	4.18E-02		1.34E+00	1.74E-01		-2.77E+00	7.62E-05	Down	-8.41E-01	1.23E-01		Unigene40648_All//gi|224102345|ref|XP_002312645.1|//2.00E-54//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222852465|gb|EEE90012.1|multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene40648_All//6.00E-31//AT3G13090| ATMRP8; ATPase, coupled to transmembrane movement of substances	Unigene40648_All//5.00E-41//A1055682		ko02010|ABC transporters		nr -
Unigene4065_All	1759	17.13	15.18	18.13	0.54	0.51	1.44	8.48	7.29	8.72	-1.75E-01	9.70E-02		8.19E-02	4.71E-01		-8.02E-02	8.94E-01		1.42E+00	5.71E-04	Up	-2.18E-01	1.20E-01		3.94E-02	7.81E-01		Unigene4065_All//gi|3258575|gb|AAC24385.1|//0.00E+00//Hypothetical protein [Arabidopsis thaliana] >gi|66792704|gb|AAY56454.1|At1g02260 [Arabidopsis thaliana]	Unigene4065_All//0.00E+00//AT1G02260| transmembrane protein, putative	Unigene4065_All//0.00E+00//ES806769				nr -
Unigene40653_All	545	1.06	0.28	1.76	2.47	1.20	3.07	2.87	0.77	1.39	-1.92E+00	7.00E-02		7.36E-01	3.23E-01		-1.04E+00	6.04E-02		3.13E-01	5.94E-01		-1.90E+00	2.25E-04	Down	-1.05E+00	2.17E-02		Unigene40653_All//gi|297818694|ref|XP_002892228.1|//6.00E-57//EMB2748 [Arabidopsis lyrata subsp. lyrata] >gi|297338070|gb|EFH68487.1|EMB2748 [Arabidopsis lyrata subsp. lyrata]	Unigene40653_All//1.00E-58//AT1G04590| FUNCTIONS IN: molecular_function unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: emb1417 (embryo defective 1417) (TAIR:AT4G21190.1); Has 54 Blast hits to 54 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 52; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene40653_All//4.00E-116//DR459069				nr +
Unigene40659_All	357	0.00	0.57	0.00	2.93	0.10	2.78	1.30	1.87	1.23	9.15E+00	1.36E-01		null	null		-4.92E+00	1.16E-06	Down	-7.43E-02	9.22E-01		5.24E-01	5.26E-01		-8.59E-02	9.34E-01		Unigene40659_All//gi|109676372|gb|AB637668.1|//1.00E-42//gag protein [Populus trichocarpa]						nr +
Unigene40662_All	485	1.19	9.82	7.25	1.64	1.63	3.91	0.52	0.26	0.16	3.05E+00	3.29E-16	Up	2.61E+00	4.97E-10	Up	-9.20E-03	9.67E-01		1.25E+00	9.82E-03		-1.02E+00	4.95E-01		-1.67E+00	2.56E-01		Unigene40662_All//gi|224142968|ref|XP_002324799.1|//1.00E-30//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372075|gb|ABQ62969.1| TINY-like protein [Populus trichocarpa] >gi|222866233|gb|EEF03364.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene40662_All//2.00E-25//AT5G11590| TINY2 (TINY2); DNA binding / transcription factor	Unigene40662_All//0.00E+00//TC178420	AP2-EREBP			nr -
Unigene40663_All	666	3.14	0.76	1.44	2.47	3.10	2.64	0.13	0.19	0.12	-2.05E+00	4.33E-05	Down	-1.13E+00	1.70E-02		3.30E-01	5.26E-01		9.96E-02	8.61E-01		5.68E-01	7.82E-01		-8.66E-02	9.72E-01		Unigene40663_All//gi|163889378|gb|ABY48148.1|//1.00E-28//lectin [Medicago truncatula]	Unigene40663_All//2.00E-21//AT5G10530| lectin protein kinase, putative	Unigene40663_All//0.00E+00//TC144439				nr -
Unigene40665_All	723	0.43	0.00	0.00	2.41	0.71	0.25	19.06	3.64	1.87	-8.76E+00	3.65E-02		-8.76E+00	4.90E-02		-1.76E+00	3.19E-04	Down	-3.27E+00	3.65E-07	Down	-2.39E+00	1.82E-43	Down	-3.35E+00	8.64E-64	Down	Unigene40665_All//gi|28950747|gb|AAO63297.1|//3.00E-74//At2g45360 [Arabidopsis thaliana]	Unigene40665_All//2.00E-75//AT2G45360| unknown protein					nr -
Unigene40666_All	841	0.00	8.31	0.25	0.00	0.20	0.16	3.37	11.78	119.18	1.30E+01	5.86E-40	Up	7.98E+00	1.41E-01		7.68E+00	2.27E-01		7.33E+00	3.11E-01		1.81E+00	3.99E-22	Up	5.15E+00	0.00E+00	Up			Unigene40666_All//0.00E+00//gi|73865539|gb|DT468277.1|DT468277				
Unigene40667_All	447	1.99	0.23	1.07	3.34	2.08	3.64	1.51	1.87	4.19	-3.13E+00	1.19E-03		-8.92E-01	2.46E-01		-6.85E-01	1.99E-01		1.22E-01	8.26E-01		3.05E-01	6.47E-01		1.47E+00	6.64E-04	Up	Unigene40667_All//gi|124359633|gb|ABD32307.2|//2.00E-09//Nuclear factor related to kappa-B-binding protein , related [Medicago truncatula]		Unigene40667_All//0.00E+00//gi|73861543|gb|DT464282.1|DT464282				nr -
Unigene40669_All	794	0.13	0.00	0.54	1.51	0.95	0.80	7.14	1.37	5.82	-7.04E+00	3.71E-01		2.03E+00	1.39E-01		-6.58E-01	2.90E-01		-9.19E-01	1.46E-01		-2.38E+00	3.16E-18	Down	-2.94E-01	1.96E-01		Unigene40669_All//gi|28300299|gb|AAO37645.1|//3.00E-46//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene40669_All//1.00E-24//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene40669_All//7.00E-94//TC177573		ko04626|Plant-pathogen interaction		nr -
Unigene4067_All	1278	1.76	2.26	4.04	3.16	2.45	2.16	9.89	18.18	4.71	3.60E-01	3.51E-01		1.20E+00	1.94E-05	Up	-3.65E-01	2.46E-01		-5.51E-01	7.41E-02		8.78E-01	3.71E-17		-1.07E+00	1.27E-13	Down			Unigene4067_All//0.00E+00//gi|164242171|gb|EV488636.1|EV488636				
Unigene40672_All	674	13.66	5.86	4.27	1.55	1.28	1.07	0.00	0.00	0.00	-1.22E+00	7.83E-10	Down	-1.68E+00	1.03E-14	Down	-2.81E-01	6.74E-01		-5.34E-01	4.55E-01		null	null		null	null		Unigene40672_All//gi|15240191|ref|NP_201508.1|//2.00E-34//RALFL34 (ralf-like 34); signal transducer [Arabidopsis thaliana]	Unigene40672_All//6.00E-31//AT5G67070| RALFL34 (ralf-like 34); signal transducer	Unigene40672_All//0.00E+00//gi|13351056|gb|BG441404.1|BG441404				nr +
Unigene40677_All	1219	0.00	0.00	0.00	0.57	0.23	0.00	37.91	15.50	8.95	null	null		null	null		-1.34E+00	1.09E-01		-9.16E+00	1.96E-04	Down	-1.29E+00	1.03E-61	Down	-2.08E+00	2.15E-125	Down	Unigene40677_All//gi|32351452|gb|AAP76387.1|//1.00E-153//class III peroxidase [Gossypium hirsutum]	Unigene40677_All//2.00E-124//AT5G05340| peroxidase, putative	Unigene40677_All//0.00E+00//ES840062		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene40681_All	432	25.07	16.89	28.84	13.26	12.75	9.51	71.94	20.32	25.08	-5.70E-01	9.69E-04		2.02E-01	2.59E-01		-5.62E-02	8.26E-01		-4.79E-01	5.87E-02		-1.82E+00	6.71E-69	Down	-1.52E+00	6.98E-55	Down	Unigene40681_All//gi|35187458|gb|AAQ84320.1|//4.00E-08//acyl-CoA-binding protein [Gossypium barbadense]	Unigene40681_All//1.00E-65//AT1G31812| ACBP6 (acyl-CoA-binding protein 6); acyl-CoA binding / phosphatidylcholine binding	Unigene40681_All//0.00E+00//TC153632				nr -
Unigene40686_All	610	0.26	0.91	1.92	1.80	0.79	0.52	1.18	1.23	1.50	1.83E+00	9.02E-02		2.90E+00	4.34E-04	Up	-1.18E+00	5.94E-02		-1.79E+00	1.01E-02		6.58E-02	9.46E-01		3.50E-01	6.04E-01										
Unigene40689_All	1530	0.00	0.00	0.00	0.36	0.07	0.18	4.06	0.44	1.80	null	null		null	null		-2.41E+00	2.44E-02		-1.02E+00	3.29E-01		-3.22E+00	3.70E-27	Down	-1.18E+00	3.61E-08	Down	Unigene40689_All//gi|9454546|gb|AAF87869.1|AC012561_2//1.00E-121//Unknown protein [Arabidopsis thaliana]	Unigene40689_All//5.00E-116//AT1G50660| unknown protein	Unigene40689_All//1.00E-173//TC168523				nr -
Unigene4069_All	1737	6.87	3.15	3.53	10.61	6.03	5.20	19.67	11.21	13.00	-1.12E+00	4.47E-11	Down	-9.62E-01	2.43E-08		-8.16E-01	5.89E-12		-1.03E+00	1.47E-15	Down	-8.11E-01	8.63E-22		-5.97E-01	1.79E-13		Unigene4069_All//gi|92870993|gb|ABE80154.1|//1.00E-180//Protein kinase [Medicago truncatula]	Unigene4069_All//1.00E-145//AT1G73660| protein kinase family protein	Unigene4069_All//0.00E+00//DW506957				nr +
Unigene40690_All	630	0.00	0.00	0.00	1.34	0.71	0.07	2.35	0.20	1.71	null	null		null	null		-9.20E-01	2.17E-01		-4.23E+00	2.18E-04	Down	-3.56E+00	1.75E-07	Down	-4.60E-01	3.42E-01		Unigene40690_All//gi|15221679|ref|NP_174417.1|//1.00E-39//LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4) [Arabidopsis thaliana] >gi|29428037|sp|Q9SHE9.1|LBD4_ARATH RecName: Full=LOB domain-containing protein 4; AltName: Full=ASYMMETRIC LEAVES 2-like protein 6; Short=AS2-like protein 6 >gi|6692123|gb|AAF24588.1|AC007654_4 T19E23.11 [Arabidopsis thaliana] >gi|50253474|gb|AAT71939.1|At1g31320 [Arabidopsis thaliana] >gi|51972120|gb|AAU15164.1|At1g31320 [Arabidopsis thaliana] >gi|219807088|dbj|BAH10530.1|ASYMMETRIC LEAVES2-like 6 protein [Arabidopsis thaliana]	Unigene40690_All//3.00E-40//AT1G31320| LBD4 (LOB DOMAIN-CONTAINING PROTEIN 4)	Unigene40690_All//4.00E-21//TC178840		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene40692_All	562	2.89	0.09	1.61	2.66	1.90	1.45	0.53	0.37	0.28	-5.00E+00	3.32E-08	Down	-8.41E-01	1.24E-01		-4.85E-01	3.82E-01		-8.78E-01	1.13E-01		-5.02E-01	6.78E-01		-8.93E-01	4.71E-01		Unigene40692_All//gi|224101827|ref|XP_002312436.1|//3.00E-59//auxin efflux carrier component [Populus trichocarpa] >gi|222852256|gb|EEE89803.1| auxin efflux carrier component [Populus trichocarpa]	Unigene40692_All//2.00E-39//AT1G70940| PIN3 (PIN-FORMED 3); auxin:hydrogen symporter/ transporter	Unigene40692_All//2.00E-38//gi|109868413|gb|DW497389.1|DW497389				nr +
Unigene40693_All	635	0.25	0.80	0.50	1.41	0.98	3.77	1.80	1.18	2.07	1.69E+00	1.34E-01		1.03E+00	4.71E-01		-5.33E-01	4.70E-01		1.42E+00	8.62E-04	Up	-6.02E-01	3.08E-01		2.04E-01	6.82E-01		Unigene40693_All//gi|42569036|ref|NP_179058.3|//2.00E-40//CBS domain-containing protein [Arabidopsis thaliana]	Unigene40693_All//7.00E-38//AT2G14520| CBS domain-containing protein					nr -
Unigene40694_All	720	0.00	0.00	0.00	0.35	0.00	0.25	2.53	6.44	2.71	null	null		null	null		-8.43E+00	4.18E-02		-4.63E-01	7.44E-01		1.35E+00	2.44E-07	Up	1.03E-01	8.03E-01										
Unigene40696_All	1057	13.46	2.92	7.86	0.05	0.33	0.09	0.00	0.00	0.00	-2.20E+00	2.30E-33	Down	-7.77E-01	4.82E-07		2.79E+00	1.14E-01		8.60E-01	7.94E-01		null	null		null	null		Unigene40696_All//gi|225446160|ref|XP_002271382.1|//2.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene40696_All//2.00E-17//FL576919				nr +
Unigene40697_All	385	6.39	0.00	1.80	11.90	16.99	4.22	0.55	0.00	0.21	-1.26E+01	3.32E-14	Down	-1.83E+00	7.31E-05	Down	5.14E-01	2.34E-02		-1.50E+00	2.74E-07	Down	-9.10E+00	7.44E-02		-1.41E+00	3.80E-01				Unigene40697_All//3.00E-57//DW507252				
Unigene40700_All	654	0.24	0.31	0.00	0.61	1.47	1.59	3.81	1.47	53.79	3.69E-01	8.16E-01		-7.91E+00	2.44E-01		1.27E+00	8.43E-02		1.38E+00	5.20E-02		-1.38E+00	2.07E-04	Down	3.82E+00	1.76E-177	Up	Unigene40700_All//gi|115472809|ref|NP_001060003.1|//2.00E-61//Os07g0564500 [Oryza sativa Japonica Group] >gi|113611539|dbj|BAF21917.1|Os07g0564500 [Oryza sativa Japonica Group]	Unigene40700_All//7.00E-65//AT1G07180| NDA1 (ALTERNATIVE NAD(P)H DEHYDROGENASE 1); NADH dehydrogenase	Unigene40700_All//0.00E+00//TC173686		ko00190|Oxidative phosphorylation		nr +
Unigene40701_All	573	0.00	1.33	0.93	0.78	1.44	3.63	1.03	1.90	0.76	1.04E+01	1.76E-04	Up	9.86E+00	4.04E-03		8.82E-01	2.92E-01		2.21E+00	1.30E-05	Up	8.77E-01	1.39E-01		-4.34E-01	6.08E-01				Unigene40701_All//2.00E-16//TC134923				
Unigene40702_All	415	14.62	14.77	24.89	4.68	10.21	4.24	0.20	0.20	0.00	1.46E-02	9.74E-01		7.67E-01	3.15E-05		1.12E+00	8.80E-05	Up	-1.41E-01	7.62E-01		-1.71E-02	1.01E+00		-7.67E+00	3.58E-01				Unigene40702_All//3.00E-48//TC141776				
Unigene40704_All	423	8.53	4.31	3.52	11.07	7.49	5.77	35.48	28.36	18.55	-9.85E-01	2.50E-03		-1.28E+00	2.41E-04	Down	-5.64E-01	3.58E-02		-9.41E-01	6.18E-04		-3.23E-01	1.43E-02		-9.35E-01	5.69E-13				Unigene40704_All//0.00E+00//TC129595				
Unigene40706_All	1672	0.00	0.00	0.00	0.00	0.08	0.00	26.22	5.67	1.93	null	null		null	null		6.36E+00	3.18E-01		null	null		-2.21E+00	1.96E-124	Down	-3.76E+00	4.70E-223	Down	Unigene40706_All//gi|297814832|ref|XP_002875299.1|//2.00E-74//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321137|gb|EFH61558.1|transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40706_All//4.00E-64//AT3G26040| transferase family protein	Unigene40706_All//0.00E+00//TC135446		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene40707_All	286	67.87	18.25	41.89	49.81	32.15	18.32	0.00	0.00	0.00	-1.90E+00	2.43E-37	Down	-6.96E-01	7.50E-08		-6.32E-01	3.65E-06		-1.44E+00	2.41E-20	Down	null	null		null	null		Unigene40707_All//gi|115482178|ref|NP_001064682.1|//7.00E-20//Os10g0438600 [Oryza sativa Japonica Group] >gi|31432302|gb|AAP53952.1| GDSL-like Lipase/Acylhydrolase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639291|dbj|BAF26596.1|Os10g0438600 [Oryza sativa Japonica Group]	Unigene40707_All//3.00E-17//AT1G20120| family II extracellular lipase, putative	Unigene40707_All//1.00E-160//TC150885				nr +
Unigene40708_All	1862	0.14	0.05	0.03	0.05	0.06	0.02	1.00	4.85	2.65	-1.37E+00	3.83E-01		-2.30E+00	2.43E-01		5.29E-02	9.66E-01		-1.14E+00	6.76E-01		2.28E+00	4.26E-27	Up	1.41E+00	1.90E-08	Up	Unigene40708_All//gi|133711804|gb|ABO36622.1|//6.00E-75//copia LTR rider [Solanum lycopersicum] >gi|133711819|gb|ABO36636.1| copia LTR rider [Solanum lycopersicum]		Unigene40708_All//8.00E-68//gi|78334423|gb|DT554697.1|DT554697				nr +

Unigene40709_All	393	1.86	1.29	2.03	2.92	4.99	8.50	17.54	13.19	13.99	-5.32E-01	5.13E-01			1.25E-01	8.66E-01		7.77E-01	9.71E-02		1.54E+00	1.28E-05	Up	-4.11E-01	4.35E-02		-3.26E-01	1.03E-01		Unigene40709_All//gi|192913000|gb|ACF06608.1|//5.00E-49//ribosomal protein [Elaeis guineensis]	Unigene40709_All//2.00E-48//AT5G39850| 40S ribosomal protein S9 (RPS9C)	Unigene40709_All//2.00E-101//TC133364		ko03010|Ribosome		nr -
Unigene40713_All	763	0.00	0.27	0.70	2.22	1.08	1.30	90.38	240.70	157.16	8.05E+00	1.36E-01			9.45E+00	4.04E-03		-1.04E+00	3.10E-02		-7.70E-01	1.33E-01		1.41E+00	5.05E-279	Up	7.98E-01	4.32E-74		Unigene40713_All//gi|18652398|gb|AL77102.1|AF472608_1//2.00E-72//carbohydrate oxidase [Lactuca sativa]	Unigene40713_All//3.00E-57//AT1G30710| FAD-binding domain-containing protein	Unigene40713_All//2.00E-20//TC130360				nr -
Unigene40714_All	403	2.86	5.66	8.19	2.23	3.93	3.14	18.05	15.97	6.62	9.86E-01	2.07E-02			1.52E+00	4.86E-05	Up	8.21E-01	1.26E-01		4.96E-01	4.48E-01		-1.76E-01	4.18E-01		-1.45E+00	1.33E-12	Down			Unigene40714_All//3.00E-113//gi|48790084|gb|C0091398.1|C0091398				
Unigene40718_All	277	37.02	22.32	18.65	59.89	44.01	48.42	96.62	30.03	41.42	-7.30E-01	4.29E-05			-9.89E-01	1.40E-07		-4.44E-01	5.07E-04		-3.07E-01	2.93E-02		-1.69E+00	2.48E-53	Down	-1.22E+00	3.53E-34	Down			Unigene40718_All//4.00E-130//gi|09836311|gb|DW234872.1|DW234872				
Unigene40719_All	506	1.14	0.20	1.26	0.39	0.68	0.00	4.01	3.63	1.34	-2.51E+00	2.94E-02			1.51E-01	8.55E-01		7.89E-01	5.96E-01		-8.62E+00	1.33E-01		-1.42E-01	7.30E-01		-1.58E+00	1.35E-04	Down			Unigene40719_All//2.00E-37//gi|09831956|gb|DW230515.1|DW230515				
Unigene4072_All	1209	0.74	1.17	0.44	0.58	0.54	0.86	2.06	0.28	2.41	6.74E-01	2.31E-01			-7.40E-01	3.47E-01		-9.19E-02	8.94E-01		5.75E-01	4.27E-01		-2.90E+00	2.98E-10	Down	2.21E-01	5.29E-01		Unigene4072_All//gi|53828553|gb|AAU94386.1|//6.00E-90//At1g73320 [Arabidopsis thaliana] >gi|57222202|gb|AAW39008.1|At1g73320 [Arabidopsis thaliana]	Unigene4072_All//8.00E-92//AT1G73320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: Expressed protein (TAIR:AT1G08125.1); Has 1043 Blast hits to 1041 proteins in 162 species: Archae - 0; Bacteria - 35; Metazoa - 424; Fungi - 344; Plants - 150; Viruses - 0; Other Eukaryotes - 90 (source: NCBI BLink).	Unigene4072_All//0.00E+00//TC160199				nr +
Unigene40723_All	347	8.44	17.23	15.50	5.02	7.24	7.29	54.59	34.21	16.19	1.03E+00	3.00E-05	Up	8.76E-01	1.10E-03		5.28E-01	2.07E-01		5.37E-01	2.02E-01		-6.74E-01	2.92E-09		-1.75E+00	2.54E-41	Down		Unigene40723_All//6.00E-06//AT5G64400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: CHCH (InterPro:IPR010625); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G09570.1); Has 218 Blast hits to 216 proteins in 80 species: Archae - 0; Bacteria - 10; Metazoa - 66; Fungi - 60; Plants - 47; Viruses - 0; Other Eukaryotes - 35 (source: NCBI BLink).	Unigene40723_All//2.00E-160//TC143297				
Unigene40726_All	370	71.13	98.60	95.56	39.18	41.14	28.44	24.68	80.20	11.20	4.71E-01	1.01E-07			4.26E-01	4.47E-06		7.04E-02	7.04E-01		-4.62E-01	1.46E-03		1.70E+00	1.28E-59	Up	-1.14E+00	4.61E-11	Down			Unigene40726_All//1.00E-158//gi|164341147|gb|ES840186.1|ES840186				
Unigene40727_All	752	0.21	0.40	0.71	3.44	2.15	3.06	0.34	1.83	1.11	9.54E-01	5.03E-01			1.76E+00	1.29E-01		-6.79E-01	7.37E-02		-1.69E-01	7.05E-01		2.44E+00	4.59E-05	Up	1.72E+00	1.56E-02									
Unigene40728_All	371	272.46	298.42	366.87	194.29	302.96	257.35	64.05	133.27	176.54	1.31E-01	1.09E-02			4.29E-01	9.74E-22		6.41E-01	3.83E-45		4.06E-01	1.99E-15		1.06E+00	3.80E-48	Up	1.46E+00	2.21E-107	Up	Unigene40728_All//gi|119640|sp|P10967.1|ACCH3_SOLLC//6.00E-24//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog; AltName: Full=Protein E8 >gi|19199|emb|CAA31789.1| E8 protein [Solanum lycopersicum]	Unigene40728_All//8.00E-18//AT1G06645| oxidoreductase			ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene40729_All	350	3.14	2.03	9.28	37.86	87.86	272.40	0.72	0.24	0.46	-6.31E-01	3.35E-01			1.56E+00	3.80E-05	Up	1.21E+00	5.60E-36	Up	2.85E+00	0.00E+00	Up	-1.60E+00	3.10E-01		-6.71E-01	6.05E-01		Unigene40729_All//gi|3282505|gb|AAC28935.1|//3.00E-14//polyphenol oxidase precursor [Prunus armeniaca]		Unigene40729_All//2.00E-138//TC137424		ko00350|Tyrosine metabolism//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene40732_All	716	0.95	0.64	0.15	8.35	10.63	9.52	2.36	0.23	1.11	-5.77E-01	4.94E-01			-2.68E+00	1.69E-02		3.48E-01	1.11E-01		1.90E-01	4.76E-01		-3.34E+00	4.60E-08	Down	-1.09E+00	1.30E-02		Unigene40732_All//gi|2921334|gb|AAC04717.1|//1.00E-54//MYB-like DNA-binding domain protein [Gossypium hirsutum]	Unigene40732_All//4.00E-43//AT5G14750| ATMYB66 (MYB DOMAIN PROTEIN 66); DNA binding / protein binding / transcription factor/ transcription regulator	Unigene40732_All//4.00E-169//BF276143	MYB			nr -
Unigene40733_All	380	6.88	3.73	6.87	2.36	1.36	0.24	0.22	0.33	0.52	-8.83E-01	2.38E-02			-3.80E-03	9.92E-01		-7.96E-01	2.75E-01		-3.31E+00	5.80E-04	Down	5.69E-01	7.82E-01		1.24E+00	4.68E-01									
Unigene40735_All	2434	0.00	0.02	0.04	1.60	0.24	0.22	16.19	1.43	5.65	4.38E+00	6.16E-01			5.45E+00	3.98E-01		-2.73E+00	6.11E-15	Down	-2.84E+00	1.64E-13	Down	-3.51E+00	5.84E-183	Down	-1.52E+00	2.46E-69	Down	Unigene40735_All//gi|7269720|emb|CAB81453.1|//0.00E+00//receptor protein kinase-like protein [Arabidopsis thaliana] >gi|224589634|gb|ACN59350.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene40735_All//0.00E+00//AT4G28650| leucine-rich repeat transmembrane protein kinase, putative	Unigene40735_All//0.00E+00//TC147887				nr -
Unigene40736_All	611	6.08	7.05	2.88	8.23	3.38	3.33	9.00	10.53	4.63	2.13E-01	4.90E-01			-1.08E+00	1.32E-03		-1.28E+00	3.74E-07	Down	-1.31E+00	1.32E-06	Down	2.28E-01	3.27E-01		-9.58E-01	1.70E-05		Unigene40736_All//gi|186507803|ref|NP_973681.2|//5.00E-06//IQ014; calmodulin binding [Arabidopsis thaliana] >gi|238479554|ref|NP_001154574.1|IQ014; calmodulin binding [Arabidopsis thaliana] >gi|75271938|sp|Q8LFG9.1|IQ014_ARATH RecName: Full=Protein IQ-DOMAIN 14 >gi|30725490|gb|AAP37767.1|At2g43680 [Arabidopsis thaliana] >gi|110741128|dbj|BAE98657.1| SF16 protein [Helianthus annuus] like protein [Arabidopsis thaliana]	Unigene40736_All//1.00E-05//AT1G62970| DNAJ heat shock N-terminal domain-containing protein	Unigene40736_All//1.00E-156//gi|109882248|gb|DW511218.1|DW511218				nr -
Unigene40737_All	703	0.30	0.50	1.14	2.13	1.08	0.39	3.01	0.65	0.23	7.61E-01	5.57E-01			1.93E+00	3.42E-02		-9.80E-01	5.91E-02		-2.46E+00	8.25E-05	Down	-2.20E+00	1.20E-06	Down	-3.73E+00	2.97E-11	Down	Unigene40737_All//gi|297610455|ref|NP_001064559.2|//5.00E-17//Os10g0405500 [Oryza sativa Japonica Group] >gi|255679389|dbj|BAF26473.2|Os10g0405500 [Oryza sativa Japonica Group]	Unigene40737_All//1.00E-17//AT2G46980| unknown protein	Unigene40737_All//0.00E+00//gi|21102851|gb|BQ415164.1|BQ415164				nr -
Unigene40738_All	481	1.85	1.58	4.54	2.90	4.30	0.56	0.70	0.43	0.66	-2.27E-01	7.27E-01			1.30E+00	5.33E-03		5.67E-01	2.26E-01		-2.36E+00	2.38E-04	Down	-6.95E-01	5.77E-01		-8.58E-02	9.47E-01		Unigene40738_All//gi|158828241|gb|ABW81118.1|//8.00E-06//putative tropinone reductase [Boechera divaricarpa]		Unigene40738_All//5.00E-149//C0119586				nr +
Unigene4074_All	1646	29.02	27.24	22.81	33.80	29.33	31.17	43.82	26.56	19.68	-9.12E-02	3.00E-01			-3.48E-01	1.14E-05		-2.05E-01	2.99E-03		-1.17E-01	1.43E-01		-7.22E-01	4.53E-37		-1.16E+00	6.31E-83	Down	Unigene4074_All//gi|18418688|ref|NP_567984.1|//0.00E+00//pantothenate kinase family protein [Arabidopsis thaliana] >gi|23506025|gb|AAN28872.1|At4g35360/F23E12_80 [Arabidopsis thaliana]	Unigene4074_All//2.00E-177//AT4G35360| pantothenate kinase family protein	Unigene4074_All//0.00E+00//TC154723		ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene40740_All	761	6.53	2.40	6.23	1.83	1.00	0.83	0.11	0.05	0.00	-1.45E+00	4.04E-07	Down	-6.87E-02	8.08E-01		-8.81E-01	1.06E-01		-1.14E+00	4.68E-02		-1.02E+00	7.24E-01		-6.80E+00	3.58E-01		Unigene40740_All//gi|403023|emb|CAA52979.1|//3.00E-25//phosphate translocator [Nicotiana tabacum]	Unigene40740_All//1.00E-18//AT5G46110| APE2 (ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT 2); antiporter/ triose-phosphate transmembrane transporter	Unigene40740_All//2.00E-54//ES846633				nr -
Unigene40743_All	341	225.85	151.12	134.45	349.28	270.94	298.53	284.80	143.28	105.73	-5.80E-01	3.87E-22			-7.48E-01	3.94E-33		-3.66E-01	8.47E-18		-2.27E-01	8.43E-07		-9.91E-01	1.50E-84		-1.43E+00	5.56E-155	Down	Unigene40743_All//gi|123192431|gb|ABM73376.1|//2.00E-65//Ran1 [Pisum sativum]	Unigene40743_All//8.00E-67//AT5G20010| RAN-1; GTP binding / GTPase/ protein binding	Unigene40743_All//0.00E+00//gi|21093512|gb|BQ405825.1|BQ405825				nr -
Unigene40745_All	566	13.87	14.41	9.69	16.19	12.65	14.36	45.57	36.70	22.03	5.58E-02	7.92E-01			-5.17E-01	1.76E-02		-3.56E-01	6.04E-02		-1.73E-01	4.36E-01		-3.12E-01	1.27E-03		-1.05E+00	5.81E-26	Down	Unigene40745_All//gi|98961007|gb|ABF58987.1|//4.00E-45//At1g03330 [Arabidopsis thaliana]	Unigene40745_All//2.00E-46//AT1G03330| small nuclear ribonucleoprotein D, putative / snRNP core SM-like protein, putative / U6 snRNA-associated Sm-like protein, putative	Unigene40745_All//0.00E+00//gi|109875097|gb|DW504071.1|DW504071		ko03040|Spliceosome//ko03018|RNA degradation		nr -
Unigene40746_All	587	19.34	14.07	14.42	41.24	35.55	45.16	44.73	28.77	19.14	-4.59E-01	6.71E-03			-4.23E-01	1.73E-02		-2.14E-01	6.02E-02		1.31E-01	2.93E-01		-6.37E-01	2.14E-11		-1.22E+00	1.16E-33	Down	Unigene40746_All//gi|6730705|gb|AAF22100.1|AC011809_9//2.00E-10//Putative phospatase 2A inhibitor [Arabidopsis thaliana]		Unigene40746_All//8.00E-90//TC170685				nr +
Unigene40747_All	2153	0.00	0.00	0.15	0.05	0.00	0.08	10.35	26.09	51.37	null	null			7.21E+00	4.52E-02		-5.53E+00	3.13E-01		8.58E-01	6.95E-01		1.33E+00	1.28E-78	Up	2.31E+00	0.00E+00	Up	Unigene40747_All//gi|223452302|gb|ACN89479.1|//1.00E-156//cysteine-rich protein [Glycine max]	Unigene40747_All//5.00E-148//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene40747_All//7.00E-10//DT468110		ko04626|Plant-pathogen interaction		nr -
Unigene40749_All	543	1.35	4.20	3.92	2.29	2.09	0.58	1.17	0.38	1.10	1.64E+00	3.06E-04	Up	1.54E+00	1.42E-03		-1.32E-01	8.17E-01		-1.98E+00	2.61E-03		-1.60E+00	6.27E-02		-8.59E-02	9.19E-01		Unigene40749_All//gi|224059480|ref|XP_002299867.1|//2.00E-47//GRAS family transcription factor [Populus trichocarpa] >gi|222847125|gb|EEE84672.1| GRAS family transcription factor [Populus trichocarpa]	Unigene40749_All//5.00E-33//AT1G07530| SCL14 (SCARECROW-LIKE 14); transcription factor	Unigene40749_All//3.00E-67//gi|78330552|gb|DT550826.1|DT550826	GRAS			nr -
Unigene4075_All	1306	14.66	21.84	11.82	21.86	20.30	23.48	22.60	20.90	10.80	5.75E-01	1.43E-08			-3.10E-01	2.15E-02		-1.06E-01	3.75E-01		1.04E-01	3.93E-01		-1.13E-01	2.75E-01		-1.07E+00	2.47E-30	Down	Unigene4075_All//gi|225455106|ref|XP_002265766.1|//1.00E-104//PREDICTED: similar to salt tolerance protein S-like protein [Vitis vinifera]	Unigene4075_All//7.00E-78//AT5G53400| nuclear movement family protein	Unigene4075_All//0.00E+00//TC139611		ko03040|Spliceosome		nr -
Unigene40750_All	713	0.29	0.21	0.22	0.00	0.53	0.00	14.23	46.13	28.44	-4.61E-01	7.58E-01			-3.89E-01	8.07E-01		9.05E+00	1.96E-02		null	null		1.70E+00	8.14E-66	Up	9.99E-01	5.87E-19		Unigene40750_All//gi|297796797|ref|XP_002866283.1|//2.00E-67//ATPLC1 [Arabidopsis lyrata subsp. lyrata] >gi|297312118|gb|EFH42542.1|ATPLC1 [Arabidopsis lyrata subsp. lyrata]	Unigene40750_All//2.00E-68//AT5G08510| ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C	Unigene40750_All//5.00E-08//TC164966		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene40754_All	447	1.87	1.81	2.86	1.45	3.85	2.12	112.56	277.52	138.77	-4.63E-02	9.64E-01			6.10E-01	3.33E-01		1.41E+00	5.42E-03		5.51E-01	4.82E-01		1.30E+00	1.90E-166	Up	3.02E-01	2.32E-07		Unigene40754_All//gi|6478218|gb|AAF13743.1|AF109921_1//3.00E-39//caleosin [Sesamum indicum]	Unigene40754_All//2.00E-40//AT2G33380| RD20 (RESPONSIVE TO DESSICATION 20); calcium ion binding	Unigene40754_All//0.00E+00//EX165406				nr +
Unigene40755_All	623	3.70	2.03	1.54	2.32	0.61	0.80	0.34	0.67	0.32	-8.62E-01	4.02E-02			-1.26E+00	5.02E-03		-1.93E+00	5.06E-04	Down	-1.54E+00	7.34E-03		9.84E-01	3.73E-01		-8.58E-02	9.61E-01									

Unigene40764_All	861	0.00	6.94	0.25	0.00	2.40	0.84	0.44	2.62	0.79	1.28E+01	3.95E-34	Up	7.95E+00	1.41E-01		1.12E+01	6.58E-13	Up	9.71E+00	2.31E-04	Up	2.57E+00	2.86E-08	Up	8.32E-01	2.74E-01		Unigene40764_All//gi|15234987|ref|NP_192765.1|//2.00E-23//wound-responsive family protein [Arabidopsis thaliana] >gi|3695408|gb|AAC62808.1| contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi|4538956|emb|CAB39780.1| probable wound-induced protein [Arabidopsis thaliana] >gi|7267724|emb|CAB78150.1| probable wound-induced protein [Arabidopsis thaliana] >gi|21553934|gb|AAM63015.1| probable wound-induced protein [Arabidopsis thaliana] >gi|90962948|gb|ABE02398.1| At4g10270 [Arabidopsis thaliana]	Unigene40764_All//1.00E-24//AT4G10270| wound-responsive family protein	Unigene40764_All//0.00E+00//TC159887				nr +
Unigene40765_All	330	8.24	4.45	6.45	11.62	18.16	8.49	29.47	8.61	31.39	-8.89E-01	1.97E-02		-3.53E-01	3.87E-01		6.44E-01	5.92E-03		-4.54E-01	1.65E-01		-1.77E+00	2.78E-21	Down	9.11E-02	6.08E-01				Unigene40765_All//3.00E-94//gi|78348255|gb|DT568529.1|DT568529				
Unigene40766_All	370	16.26	15.75	10.94	19.79	14.33	24.90	13.60	30.84	35.64	-4.63E-02	8.54E-01		-5.72E-01	2.39E-02		-4.66E-01	2.58E-02		3.31E-01	9.88E-02		1.18E+00	7.26E-14	Up	1.39E+00	1.02E-20	Up	Unigene40766_All//gi|73761699|gb|AA283349.1|//6.00E-12//MAP kinase [Gossypium hirsutum]		Unigene40766_All//9.00E-175//TC154267				nr -
Unigene40768_All	875	0.36	15.75	3.10	0.28	0.47	1.34	0.00	0.00	0.09	5.46E+00	3.19E-69	Up	3.11E+00	2.63E-09	Up	7.30E-01	5.86E-01		2.24E+00	1.82E-03		null	null		6.51E+00	4.04E-01		Unigene40768_All//gi|56709428|emb|CAF32327.1|//3.00E-29//late embryogenesis abundant protein [Pisum sativum]	Unigene40768_All//1.00E-28//AT5G44310| late embryogenesis abundant domain-containing protein / LEA domain-containing protein	Unigene40768_All//0.00E+00//DR458228		ko03040|Spliceosome		nr -
Unigene40771_All	300	22.85	30.91	10.83	25.90	17.33	15.66	6.34	1.81	1.73	4.36E-01	2.25E-02		-1.08E+00	5.56E-06	Down	-5.80E-01	3.13E-03		-7.26E-01	3.78E-04		-1.81E+00	7.18E-05	Down	-1.88E+00	2.70E-05	Down	Unigene40771_All//gi|297843532|ref|XP_002889647.1|//4.00E-19//sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297335489|gb|EFH65906.1| sterol 4-alpha-methyl-oxidase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene40771_All//1.00E-20//AT1G07420| SMO2-1 (STEROL 4-ALPHA-METHYL-OXIDASE 2-1): 4-alpha-methyl-delta7-sterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase	Unigene40771_All//2.00E-92//TC148053		ko00100|Steroid biosynthesis		nr +
Unigene40774_All	293	3.39	2.08	0.55	4.42	1.65	0.92	1.73	0.86	0.14	-7.09E-01	3.05E-01		-2.64E+00	2.71E-03		-1.43E+00	1.25E-02		-2.26E+00	6.70E-04	Down	-1.02E+00	2.88E-01		-3.67E+00	3.75E-03									
Unigene40777_All	459	3.08	2.43	1.97	0.76	1.73	3.54	2.49	5.74	2.60	-3.42E-01	5.48E-01		-6.42E-01	2.75E-01		1.18E+00	1.61E-01		2.22E+00	1.55E-04	Up	1.21E+00	6.58E-04	Up	6.62E-02	9.19E-01				Unigene40777_All//1.00E-180//CA994255				
Unigene40778_All	1049	0.00	0.19	0.96	0.10	0.13	2.02	5.04	2.67	1.71	7.59E+00	1.36E-01		9.91E+00	1.27E-05	Up	4.67E-01	8.76E-01		4.41E+00	2.73E-10	Up	-9.16E-01	8.25E-05		-1.56E+00	2.10E-10	Down			Unigene40778_All//0.00E+00//DR510605				ESTscan +
Unigene4078_All	1255	1.08	14.21	2.25	1.71	1.04	4.39	20.25	71.77	56.38	3.71E+00	1.29E-70	Up	1.05E+00	7.50E-03		-7.11E-01	9.35E-02		1.36E+00	1.80E-07	Up	1.83E+00	2.78E-198	Up	1.48E+00	1.17E-117	Up	Unigene4078_All//gi|18408342|ref|NP_564862.1|//8.00E-79//harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana]	Unigene4078_All//2.00E-50//AT1G65690| harpin-induced protein-related / HIN1-related / harpin-responsive protein-related	Unigene4078_All//0.00E+00//gi|84158832|gb|DN827896.1|DN827896	ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport			nr +
Unigene40780_All	1476	0.28	0.27	0.14	11.71	2.85	0.92	5.30	0.74	1.00	-4.65E-02	9.80E-01		-9.75E-01	4.11E-01		-2.04E+00	7.29E-46	Down	-3.67E+00	7.10E-75	Down	-2.85E+00	3.13E-30	Down	-2.41E+00	4.77E-26	Down	Unigene40780_All//gi|297846520|ref|XP_002891141.1|//1.00E-142//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336983|gb|EFH67400.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40780_All//3.00E-141//AT1G31490| transferase family protein	Unigene40780_All//0.00E+00//gi|84146358|gb|DN760600.1|DN760600	ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis			nr -
Unigene40782_All	286	7.32	1.06	7.82	16.90	15.65	7.90	2.66	1.75	0.70	-2.78E+00	6.12E-07	Down	9.58E-02	8.22E-01		-1.10E-01	7.39E-01		-1.10E+00	5.39E-05	Down	-6.02E-01	4.12E-01		-1.93E+00	1.14E-02				Unigene40782_All//1.00E-145//BQ406357				
Unigene40785_All	285	4.77	3.20	1.12	5.77	2.05	1.90	8.16	2.20	6.15	-5.77E-01	3.19E-01		-2.09E+00	1.95E-03		-1.49E+00	2.61E-03		-1.60E+00	2.71E-03		-1.89E+00	4.26E-06	Down	-4.08E-01	2.71E-01				Unigene40785_All//3.00E-69//TC172413				
Unigene40787_All	1006	0.10	0.15	0.26	0.15	0.00	0.00	2.31	5.36	2.83	5.39E-01	7.79E-01		1.35E+00	4.09E-01		-7.22E+00	1.65E-01		-7.22E+00	2.33E-01		1.21E+00	3.10E-07	Up	3.03E-01	3.71E-01									
Unigene40789_All	973	19.95	9.63	24.90	0.87	1.42	0.42	0.00	0.00	0.25	-1.05E+00	8.73E-16	Down	3.20E-01	6.37E-03		7.02E-01	2.39E-01		-1.06E+00	1.81E-01		null	null		7.94E+00	4.39E-02		Unigene40789_All//gi|54645911|gb|AAV36561.1|//1.00E-64//RDZ2-like protein [Vitis vinifera]	Unigene40789_All//2.00E-48//AT5G25610| RDZ2; nutrient reservoir				nr -
Unigene4079_All	1134	6.18	2.59	4.65	12.21	10.84	10.67	48.10	31.51	22.27	-1.25E+00	5.60E-08	Down	-4.11E-01	8.17E-02		-1.72E-01	3.16E-01		-1.94E-01	2.52E-01		-6.10E-01	3.79E-21		-1.11E+00	4.10E-59	Down	Unigene4079_All//gi|10177953|dbj|BAB11312.1|//3.00E-97//aluminum-induced protein-like [Arabidopsis thaliana] >gi|21537246|gb|AAM61587.1| aluminum-induced protein-like [Arabidopsis thaliana]	Unigene4079_All//2.00E-98//AT5G43830| unknown protein	Unigene4079_All//0.00E+00//TC165134	ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism			nr +
Unigene40791_All	432	7.15	13.02	0.37	11.19	14.83	4.81	3.03	18.77	3.23	8.66E-01	6.00E-04		-4.27E+00	2.57E-13	Down	4.07E-01	8.64E-02		-1.22E+00	9.02E-06	Down	2.63E+00	1.06E-28	Up	8.93E-02	8.64E-01				Unigene40791_All//0.00E+00//EX167366				
Unigene40792_All	1763	0.00	0.00	0.00	0.06	0.12	0.00	9.74	1.35	3.39	null	null		null	null		1.05E+00	6.12E-01		-5.82E+00	3.99E-01		-2.85E+00	1.24E-65	Down	-1.52E+00	8.96E-31	Down	Unigene40792_All//gi|224136035|ref|XP_002322223.1|//1.00E-178//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222869219|gb|EEF06350.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene40792_All//1.00E-144//AT3G10960| xanthine/uracil permease family protein				nr -
Unigene40793_All	352	61.98	262.56	145.23	96.09	89.41	175.26	103.54	187.25	81.49	2.08E+00	1.59E-197	Up	1.23E+00	4.92E-50	Up	-1.04E-01	3.30E-01		8.67E-01	7.14E-38		8.55E-01	4.52E-45		-3.46E-01	8.27E-06				Unigene40793_All//6.00E-74//TC145559				
Unigene40796_All	1215	0.43	142.83	88.62	0.12	0.23	0.26	0.52	0.07	0.79	8.37E+00	0.00E+00	Up	7.69E+00	0.00E+00	Up	8.82E-01	5.95E-01		1.08E+00	4.76E-01		-2.92E+00	4.19E-03		5.92E-01	3.46E-01									
Unigene40798_All	923	0.62	0.16	0.12	0.54	0.22	0.10	5.59	8.15	59.78	-1.92E+00	7.00E-02		-2.43E+00	4.40E-02		-1.27E+00	2.22E-01		-2.46E+00	4.83E-02		5.45E-01	4.14E-03		3.42E+00	8.54E-254	Up	Unigene40798_All//gi|18406390|ref|NP_564747.1|//5.00E-26//ZCF37 [Arabidopsis thaliana] >gi|8778744|gb|AAF79752.1|AC009317_11 T30E16.15 [Arabidopsis thaliana] >gi|6520221|dbj|BAA87954.1| ZCF37 [Arabidopsis thaliana] >gi|89111900|gb|ABD60722.1| At1g59590 [Arabidopsis thaliana]	Unigene40798_All//8.00E-21//AT1G59590| ZCF37	Unigene40798_All//5.00E-15//gi|73861431|gb|DT464170.1|DT464170				nr +
Unigene40799_All	670	0.08	4.39	0.48	1.71	2.47	2.70	12.94	12.35	11.83	5.81E+00	2.84E-15	Up	2.61E+00	1.46E-01		5.29E-01	3.27E-01		6.57E-01	1.96E-01		-6.67E-02	7.35E-01		-1.29E-01	5.11E-01									
Unigene408_All	759	3.10	1.07	1.89	5.64	7.12	4.52	4.96	3.14	4.30	-1.54E+00	4.45E-04	Down	-7.12E-01	1.03E-01		3.36E-01	2.24E-01		-3.20E-01	3.21E-01		-6.60E-01	1.96E-02		-2.04E-01	4.94E-01		Unigene408_All//gi|79512687|ref|NP_196834.3|//3.00E-69//SFC (SCARFACE); ARF GTPase activator/ phosphoinositide binding [Arabidopsis thaliana] >gi|75321812|sp|Q9WTF2.1|AGD3_ARATH RecName: Full=ADP-ribosylation factor GTPase-activating protein AGD3; Short=ARF GAP AGD3; AltName: Full=Protein ARF-GAP DOMAIN 3; Short=AtAGD3; AltName: Full=Protein VASCULAR NETWORK 3; AltName: Full=Protein SCARFACE >gi|55583334|dbj|BAD69588.1| ARF-GAP [Arabidopsis thaliana]	Unigene408_All//9.00E-63//AT5G13300| SFC (SCARFACE); ARF GTPase activator/ phosphoinositide binding	Unigene408_All//0.00E+00//TC158233		ko04144|Endocytosis		nr +
Unigene4080_All	1519	22.66	9.34	13.50	376.64	418.87	320.16	544.27	316.76	227.73	-1.28E+00	2.72E-37	Down	-7.48E-01	4.13E-15		1.53E-01	1.04E-17		-2.34E-01	2.93E-32		-7.81E-01	0.00E+00		-1.26E+00	0.00E+00	Down	Unigene4080_All//gi|258489633|gb|ACV72640.1|//0.00E+00//sucrose synthase 1 [Gossypium hirsutum]	Unigene4080_All//3.00E-90| SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups	Unigene4080_All//0.00E+00//TC169801		ko00500|Starch and sucrose metabolism		nr -
Unigene40803_All	344	1.06	5.01	1.55	2.75	1.60	2.23	0.00	0.24	0.00	2.23E+00	1.09E-04	Up	5.40E-01	6.10E-01		-7.81E-01	2.68E-01		-3.02E-01	6.89E-01		7.92E+00	4.01E-01		null	null		Unigene40803_All//gi|159895661|gb|ABX10441.1|//4.00E-61//3-ketoacyl-CoA synthase 6 [Gossypium hirsutum]	Unigene40803_All//1.00E-37//AT2G28630| KCS12 (3-KETOACYL-COA SYNTHASE 12); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene40803_All//0.00E+00//TC146425				nr -
Unigene40805_All	764	0.00	0.00	0.00	0.13	0.00	0.95	6.25	8.70	12.51	null	null		null	null		-7.03E+00	3.13E-01		2.86E+00	7.12E-03		4.76E-01	2.08E-02		1.00E+00	1.96E-09	Up			Unigene40805_All//2.00E-07//EX169558				
Unigene40808_All	1330	0.08	0.00	0.08	27.83	5.64	35.32	278.35	325.50	737.85	-6.30E+00	3.71E-01		2.54E-02	1.00E+00		-2.30E+00	1.17E-114	Down	3.44E-01	5.39E-06		2.26E-01	4.62E-26		1.41E+00	0.00E+00	Up	Unigene40808_All//gi|19698452|gb|AAL93154.1|AF485268_1/1.00E-162//bacterial-induced class III peroxidase [Gossypium hirsutum]	Unigene40808_All//4.00E-115//AT2G41480| electron carrier/ heme binding / peroxidase	Unigene40808_All//0.00E+00//TC147787		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene40811_All	815	1.67	0.87	0.46	5.99	5.96	0.67	0.31	0.10	0.00	-9.39E-01	1.02E-01		-1.87E+00	4.39E-03		-7.80E-03	9.68E-01		-3.17E+00	8.98E-19	Down	-1.60E+00	3.10E-01		-8.28E+00	3.04E-02		Unigene40811_All//gi|224101833|ref|XP_002334238.1|//3.00E-71//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|148372081|gb|ABQ62972.1| TINY-like protein [Populus trichocarpa] >gi|222870106|gb|EEF07237.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene40811_All//7.00E-39//AT3G60490| AP2 domain-containing transcription factor TINY, putative	Unigene40811_All//0.00E+00//TC151951	AP2-EREBP			nr +
Unigene40812_All	1201	0.00	0.08	0.00	0.00	0.06	0.00	63.30	22.97	3.42	6.40E+00	3.86E-01		null	null		5.84E+00	6.09E-01		null	null		-1.46E+00	3.71E-122	Down	-4.21E+00	0.00E+00	Down	Unigene40812_All//gi|197090689|gb|ACH41745.1|//2.00E-90//ST5a [Brassica rapa subsp. rapa] >gi|197090691|gb|ACH41746.1| ST5a [Brassica rapa subsp. pekinensis] >gi|197090697|gb|ACH41749.1| ST5a [Brassica rapa subsp. pekinensis] >gi|197090723|gb|ACH41762.1| ST5a [Brassica rapa subsp. rapa] >gi|197090725|gb|ACH41763.1| ST5a [Brassica rapa subsp. pekinensis]	Unigene40812_All//6.00E-91//AT1G74100| SOT16 (SULFOTRANSFERASE 16): desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene40812_All//2.00E-160//gi|48780170|gb|CO089536.1|CO089536	ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism			nr -
Unigene40813_All	846	0.12	5.33	1.51	0.12	1.91	3.04	0.30	0.64	2.31	5.43E+00	1.01E-22	Up	3.61E+00	3.41E-05	Up	4.02E+00	8.12E-08	Up	4.69E+00	7.32E-13	Up	1.10E+00	2.36E-01		2.94E+00	1.90E-08	Up								
Unigene40816_All	1327	0.00	0.00	0.00	0.00	0.00	0.00	1.37	1.42	3.30	null	null		null	null		null	null		null	null		4.90E-02	9.27E-01		1.27E+00	1.33E-06	Up	Unigene40816_All//gi|15233666|ref|NP_191136.1|//1.00E-127//short-chain dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] >gi|16612264|gb|AAL27501.1|AF439829_1 AT4g24050/T19F6_40 [Arabidopsis thaliana] >gi|2262111|gb|AAB63619.1| ribitol dehydrogenase isolog [Arabidopsis thaliana] >gi|21928085|gb|AAM78071.1| AT4g24050/T19F6_40 [Arabidopsis thaliana]	Unigene40816_All//4.00E-115//AT4G24050| short-chain dehydrogenase/reductase (SDR) family protein	Unigene40816_All//5.00E-176//gi|78342862|gb|DT563136.1|DT563136		ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism//ko00061|Fatty acid biosynthesis//ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene40817_All	389	1.08	0.26	1.37	6.66	5.93	5.22	2.17	0.21	2.05	-2.05E+00	1.20E-01		3.47E-01	7.06E-01		-1.67E-01	6.99E-01		-3.50E-01	4.08E-01		-3.34E+00	2.51E-04	Down	-8.58E-02	9.02E-01		Unigene40817_All//gi|6664321|gb|AAF22903.1|AC006932_20/3.00E-08//T27G7.8 [Arabidopsis thaliana]	Unigene40817_All//5.00E-05//AT1G08400| chromosome structural maintenance protein-related					nr +

Unigene40818_All	621	4.21	1.31	0.51	5.45	3.27	3.42	0.27	0.00	0.00	-1.69E+00	5.80E-05	Down	-3.03E+00	9.96E-09	Down	-7.38E-01	2.06E-02		-6.74E-01	4.56E-02		-8.09E+00	1.34E-01		-8.09E+00	1.08E-01		Unigene40818_All//gi|115486587|ref|NP_001068437.1|//1.00E-20//Os11g0672900 [Oryza sativa Japonica Group] >gi|77552473|gb|ABA95270.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113645659|dbj|BAF28800.1| Os11g0672900 [Oryza sativa Japonica Group]	Unigene40818_All//3.00E-23//AT3G62630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1645 (InterPro:IPR012442); BEST Arabidopsis thaliana protein match is: calmodulin-binding protein (TAIR:AT2G15760.1); Has 207 Blast hits to 197 proteins in 50 species: Archae - 3; Bacteria - 4; Metazoa - 52; Fungi - 9; Plants - 91; Viruses - 0; Other Eukaryotes - 48 (source: NCBI BLink).	Unigene40818_All//0.00E+00//ES803059				nr +
Unigene40819_All	542	2.99	1.22	2.75	6.80	3.49	3.58	5.23	1.23	1.25	-1.30E+00	1.41E-02		-1.21E-01	8.10E-01		-9.61E-01	1.30E-03		-9.25E-01	3.49E-03		-2.08E+00	3.87E-08	Down	-2.06E+00	2.30E-08	Down			Unigene40819_All//2.00E-62//TC175416				
Unigene40821_All	445	1.06	3.42	2.27	2.69	1.55	0.20	1.33	2.25	1.07	1.69E+00	3.43E-03		1.10E+00	1.33E-01		-7.96E-01	1.87E-01		-3.73E+00	1.43E-05	Down	7.61E-01	2.28E-01		-3.08E-01	6.78E-01									
Unigene40822_All	817	0.13	0.37	2.87	0.73	3.08	7.08	8.49	14.17	16.92	1.54E+00	3.23E-01		4.48E+00	1.53E-10	Up	2.07E+00	1.59E-06	Up	3.27E+00	4.06E-22	Up	7.40E-01	7.08E-07		9.95E-01	3.89E-13		Unigene40822_All//gi|224060299|ref|XP_002300130.1|//1.00E-56//glutaredoxin [Populus trichocarpa] >gi|222847388|gb|EEE84935.1| glutaredoxin [Populus trichocarpa]	Unigene40822_All//3.00E-39//AT3G02000| ROXY1; disulfide oxidoreductase	Unigene40822_All//7.00E-17//DW503331				nr -
Unigene40823_All	1581	0.07	0.00	0.00	0.19	0.20	0.23	31.93	2.96	1.36	-6.05E+00	3.71E-01		-6.05E+00	3.93E-01		5.25E-02	9.98E-01		2.74E-01	8.33E-01		-3.43E+00	6.48E-230	Down	-4.55E+00	4.96E-294	Down	Unigene40823_All//gi|15229594|ref|NP_188446.1|//1.00E-120//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene40823_All//4.00E-122//AT3G18180| transferase, transferring glycosyl groups					
Unigene40825_All	751	0.35	0.27	0.57	1.46	1.51	1.74	4.90	1.45	2.71	-3.68E-01	7.78E-01		7.04E-01	5.54E-01		5.22E-02	9.48E-01		2.57E-01	6.93E-01		-1.76E+00	1.99E-08	Down	-8.56E-01	1.95E-03				Unigene40825_All//4.00E-09//TC175998				
Unigene40827_All	792	2.71	0.77	0.81	7.86	7.83	3.31	1.76	0.69	0.91	-1.82E+00	1.43E-04	Down	-1.75E+00	4.05E-04	Down	-6.60E-03	9.70E-01		-1.25E+00	1.64E-07	Down	-1.36E+00	8.81E-03		-9.60E-01	4.80E-02		Unigene40827_All//gi|30689400|ref|NP_851068.1|//3.00E-60//WD-40 repeat family protein [Arabidopsis thaliana]	Unigene40827_All//1.00E-57//AT5G24320| WD-40 repeat family protein	Unigene40827_All//5.00E-138//C0120903				nr +
Unigene40828_All	694	1.36	1.39	2.15	5.53	2.18	6.96	0.00	1.14	0.17	3.18E-02	9.83E-01		6.63E-01	2.44E-01		-1.34E+00	6.20E-06	Down	3.33E-01	2.66E-01		1.02E+01	1.07E-05	Up	7.43E+00	2.43E-01				Unigene40828_All//7.00E-103//TC177871				
Unigene40829_All	640	0.16	0.87	0.00	0.47	0.48	1.06	2.05	4.77	4.48	2.41E+00	3.93E-02		-7.35E+00	3.93E-01		5.22E-02	9.98E-01		1.18E+00	2.08E-01		1.22E+00	1.83E-04	Up	1.13E+00	5.45E-04	Up			Unigene40829_All//5.00E-11//TC153203				
Unigene40830_All	532	1.38	0.19	1.20	8.24	3.37	3.14	1.99	1.10	2.02	-2.85E+00	6.26E-03		-1.97E-01	7.99E-01		-1.29E+00	2.33E-06	Down	-1.39E+00	2.36E-06	Down	-8.53E-01	1.55E-01		2.52E-02	9.76E-01		Unigene40830_All//gi|118489803|gb|ABK96701.1|//3.00E-09//unknown [Populus trichocarpa x Populus deltoides]							nr +
Unigene40833_All	776	1.28	1.04	1.24	32.93	7.50	3.14	0.33	0.65	0.31	-2.94E-01	6.37E-01		-5.26E-02	9.54E-01		-2.13E+00	7.19E-72	Down	-3.39E+00	3.47E-103	Down	9.83E-01	3.11E-01		-8.59E-02	9.56E-01		Unigene40833_All//gi|115471671|ref|NP_001059434.1|//3.00E-43//Os07g0407900 [Oryza sativa Japonica Group] >gi|113610970|dbj|BAF21348.1| Os07g0407900 [Oryza sativa Japonica Group]	Unigene40833_All//1.00E-30//AT5G27370| unknown protein	Unigene40833_All//0.00E+00//TC148045				nr -
Unigene40834_All	493	22.18	5.65	3.89	1.41	1.54	0.92	1.37	0.00	0.65	-1.97E+00	1.86E-22	Down	-2.51E+00	7.66E-29	Down	1.19E-01	9.05E-01		-6.27E-01	4.76E-01		-1.04E+01	6.34E-05	Down	-1.09E+00	1.50E-01									
Unigene40836_All	409	11.90	6.32	1.56	5.36	7.83	6.74	1.86	0.20	0.97	-9.13E-01	8.46E-04		-2.93E+00	2.52E-15	Down	5.47E-01	1.23E-01		3.30E-01	4.34E-01		-3.19E+00	7.92E-04	Down	-9.34E-01	1.82E-01		Unigene40836_All//gi|94807648|gb|ABF47121.1|//3.00E-10//At5g02220 [Arabidopsis thaliana]	Unigene40836_All//2.00E-11//AT5G02220| unknown protein	Unigene40836_All//2.00E-09//DW504069				nr +
Unigene40837_All	431	1.82	0.00	0.00	1.62	1.68	2.20	3.34	1.26	1.57	-1.08E+01	1.09E-04	Down	-1.08E+01	2.21E-04	Down	5.23E-02	9.65E-01		4.44E-01	5.74E-01		-1.40E+00	6.15E-03		-1.09E+00	2.39E-02		Unigene40837_All//gi|75206292|sp|Q9SJK7.1|TCP11_ARATH//2.00E-13//RecName: Full=Transcription factor TCP11 >gi|38454126|gb|AAR20757.1| At2g37000 [Arabidopsis thaliana] >gi|41349918|gb|AAS00344.1| At2g37000 [Arabidopsis thaliana]	Unigene40837_All//9.00E-10//AT2G37000| TCP family transcription factor, putative	Unigene40837_All//4.00E-20//TC147567	TCP			nr +
Unigene40839_All	321	6.19	3.79	13.77	0.62	2.15	2.25	0.00	0.00	0.00	-7.09E-01	1.20E-01		1.15E+00	1.62E-04	Up	1.79E+00	6.10E-02		1.86E+00	4.71E-02		null	null		null	null										
Unigene40843_All	1394	0.00	0.11	0.00	0.21	0.20	0.45	3.73	24.08	42.21	6.77E+00	2.35E-01		null	null		-1.18E-01	9.00E-01		1.08E+00	2.69E-01		2.69E+00	8.58E-120	Up	3.50E+00	3.27E-276	Up	Unigene40843_All//gi|224064641|ref|XP_002301530.1|//1.00E-118//gibberellin 2-oxidase [Populus trichocarpa] >gi|222843256|gb|EEE80803.1| gibberellin 2-oxidase [Populus trichocarpa]	Unigene40843_All//2.00E-92//AT1G02400| GA2OX6 (GIBBERELLIN 2-OXIDASE 6); gibberellin 2-beta-dioxygenase	Unigene40843_All//0.00E+00//gi|109850348|gb|DW479327.1|DW479327		ko00904|Diterpenoid biosynthesis		nr -
Unigene40844_All	1693	0.00	0.00	0.00	0.03	0.06	0.03	0.67	1.73	7.65	null	null		null	null		1.05E+00	8.08E-01		-1.39E-01	9.52E-01		1.36E+00	6.02E-05	Up	3.50E+00	3.10E-61	Up	Unigene40844_All//gi|223452335|gb|ACM89495.1|//4.00E-63//protein kinase family protein [Glycine max]	Unigene40844_All//3.00E-63//AT2G18890| protein kinase family protein	Unigene40844_All//1.00E-20//DT463342		ko04626|Plant-pathogen interaction		nr -
Unigene40847_All	1315	0.00	0.00	0.00	0.00	0.00	0.00	5.24	2.00	2.85	null	null		null	null		null	null		null	null		-1.39E+00	5.95E-11	Down	-8.80E-01	6.77E-06		Unigene40847_All//gi|223452393|gb|ACM89524.1|//1.00E-107//FERONIA receptor-like kinase [Glycine max]	Unigene40847_All//3.00E-102//AT3G51550| FER (FERONIA); kinase/ protein kinase					nr +
Unigene40848_All	620	1.86	2.45	5.15	2.09	4.89	3.79	0.00	0.00	0.00	4.01E-01	4.53E-01		1.47E+00	1.04E-04	Up	1.23E+00	5.11E-04	Up	8.59E-01	4.18E-02		null	null		null	null		Unigene40848_All//gi|9502375|gb|AAF88082.1|AC025417.10//1.00E-08//T12C24.19 [Arabidopsis thaliana]	Unigene40848_All//7.00E-09//AT1G12660| Predicted to encode a PR (pathogenesis-related) protein. Belongs to the plant thionin (PR-13) family with the following members: At1g66100, At5g36910, At1g72260, At2g15010, At1g12663, At1g12660.					nr +
Unigene4085_All	1628	2.86	2.02	1.80	7.56	6.58	4.19	2.99	1.49	2.69	-5.00E-01	7.65E-02		-6.69E-01	2.23E-02		-2.00E-01	2.58E-01		-8.51E-01	6.98E-08		-1.00E+00	4.32E-05	Down	-1.50E-01	5.82E-01		Unigene4085_All//gi|4914316|gb|AAD32864.1|AC005489_2//7.00E-15//F14N23.2 [Arabidopsis thaliana] >gi|107738163|gb|ABF83653.1| At1g10140 [Arabidopsis thaliana]	Unigene4085_All//3.00E-16//AT1G10140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031279 (InterPro:IPR016972); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G58420.1); Has 38 Blast hits to 38 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene4085_All//0.00E+00//gi|78334630|gb|DT554904.1|DT554904		ko03040|Spliceosome		nr +
Unigene40852_All	1146	1.55	0.13	0.14	2.17	1.47	0.91	3.84	0.73	1.11	-3.55E+00	2.53E-07	Down	-3.48E+00	8.41E-07	Down	-5.62E-01	1.58E-01		-1.26E+00	1.84E-03		-2.40E+00	2.19E-14	Down	-1.79E+00	1.75E-10	Down	Unigene40852_All//gi|49659270|emb|CAE01428.1|//1.00E-91//origin recognition complex 4 subunit [Arabidopsis thaliana]	Unigene40852_All//6.00E-91//AT2G01120| ORC4 (ORIGIN RECOGNITION COMPLEX SUBUNIT 4); protein binding	Unigene40852_All//3.00E-152//EST91241				nr +
Unigene40855_All	1050	0.00	0.43	0.10	0.47	0.26	0.52	11.48	23.45	62.45	8.76E+00	7.43E-03		6.66E+00	3.98E-01		-8.54E-01	4.07E-01		1.22E-01	9.21E-01		1.03E+00	2.05E-23	Up	2.44E+00	2.07E-213	Up	Unigene40855_All//gi|224075293|ref|XP_002304588.1|//2.00E-84//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842020|gb|EEE79567.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene40855_All//8.00E-66//AT3G12910| transcription factor	Unigene40855_All//8.00E-42//CO124002				nr +
Unigene40857_All	814	0.13	0.25	0.13	9.91	7.23	1.39	6.13	0.31	1.52	9.53E-01	6.21E-01		2.45E-02	1.00E+00		-4.55E-01	2.11E-02		-2.84E+00	1.40E-27	Down	-4.31E+00	1.64E-27	Down	-2.01E+00	1.07E-13	Down	Unigene40857_All//gi|118485322|gb|ABK94520.1|//6.00E-13//unknown [Populus trichocarpa]	Unigene40857_All//3.00E-05//AT5G39005| unknown protein	Unigene40857_All//9.00E-146//DW515284				nr +
Unigene40858_All	676	2.01	0.37	1.65	1.69	0.76	1.00	2.63	0.87	2.18	-2.42E+00	3.35E-04	Down	-2.83E-01	6.05E-01		-1.15E+00	6.01E-02		-7.58E-01	2.45E-01		-1.60E+00	5.26E-04	Down	-2.69E-01	5.54E-01		Unigene40858_All//gi|297833250|ref|XP_002884507.1|//2.00E-40//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297330347|gb|EFH60766.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene40858_All//2.00E-28//AT3G05340| pentatricopeptide (PPR) repeat-containing protein	Unigene40858_All//0.00E+00//gi|18099471|gb|BM358725.1|BM358725				nr +
Unigene4086_All	777	4.44	11.54	7.95	8.85	11.83	15.40	15.67	14.85	15.69	1.38E+00	2.38E-11	Up	8.39E-01	6.98E-04		4.20E-01	2.60E-02		8.00E-01	6.64E-07		-7.80E-02	6.32E-01		1.60E-03	9.91E-01		Unigene4086_All//gi|156620978|gb|ABU88852.1|//1.00E-32//lammer-type protein kinase [Sorghum bicolor]	Unigene4086_All//2.00E-25//AT4G32660| AME3; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene4086_All//0.00E+00//gi|164269213|gb|ES808487.1|ES808487				nr -
Unigene40862_All	1788	0.00	0.00	0.00	0.00	0.00	0.00	24.21	1.43	5.79	null	null		null	null		null	null		null	null		-4.09E+00	5.65E-227	Down	-2.06E+00	3.48E-116	Down									
Unigene40863_All	490	0.64	0.00	0.00	2.13	1.48	1.11	8.46	7.93	2.93	-9.32E+00	3.65E-02		-9.32E+00	4.90E-02		-5.33E-01	4.27E-01		-9.49E-01	1.69E-01		-9.22E-02	7.51E-01		-1.53E+00	3.88E-08	Down	Unigene40863_All//gi|254803073|gb|ACT82815.1|//3.00E-17//At1g29270 [Arabidopsis thaliana]	Unigene40863_All//2.00E-18//AT1G29270| unknown protein	Unigene40863_All//0.00E+00//TC167005				nr -
Unigene40864_All	509	7.71	1.10	1.15	15.37	8.12	4.70	0.00	0.00	0.00	-2.82E+00	1.36E-12	Down	-2.74E+00	1.15E-11	Down	-9.20E-01	1.69E-06		-1.71E+00	1.93E-14	Down	null	null		null	null		Unigene40864_All//gi|222139394|gb|ACM45716.1|//1.00E-77//class IV chitinase [Pyrus pyrifolia]	Unigene40864_All//8.00E-78//AT3G54420| ATEP3; chitinase	Unigene40864_All//0.00E+00//gi|109840927|gb|DW239487.1|DW239487		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene40870_All	657	10.91	4.63	11.59	0.99	1.47	1.37	0.13	0.00	4.43	-1.24E+00	5.51E-08	Down	8.72E-02	6.99E-01		5.74E-01	4.52E-01		4.80E-01	5.50E-01		-7.01E+00	4.03E-01		5.10E+00	5.16E-18	Up	Unigene40870_All//gi|297851262|ref|XP_002893512.1|//3.00E-37//ATPUP3 [Arabidopsis lyrata subsp. lyrata] >gi|297339354|gb|EFH69771.1| ATPUP3 [Arabidopsis lyrata subsp. lyrata]	Unigene40870_All//2.00E-36//AT2G33750| ATPUP2; purine transmembrane transporter	Unigene40870_All//0.00E+00//TC177508				nr +
Unigene40871_All	210	35.13	45.36	44.12	46.97	50.18	78.50	10.87	32.04	10.05	3.69E-01	5.24E-02		3.29E-01	1.09E-01		9.54E-02	6.53E-01		7.41E-01	3.38E-08		1.56E+00	1.48E-12	Up	-1.13E-01	7.57E-01		Unigene40871_All//gi|13605704|gb|AAK32845.1|AF361833_1//1.00E-07//At1g26110/F28B23_21 [Arabidopsis thaliana] >gi|18700276|gb|AAL77748.1| At1g26110/F28B23_21 [Arabidopsis thaliana]	Unigene40871_All//7.00E-91//gi|78340889|gb|DT561163.1|DT561163				nr +
Unigene40874_All	452	14.24	1.23	2.12	21.16	8.30	7.09	1.68	5.64	1.32	-3.53E+00	5.61E-25	Down	-2.75E+00	7.19E-19	Down	-1.35E+00	3.70E-14	Down	-1.58E+00	1.07E-15	Down	1.74E+00	5.42E-06	Up	-3.49E-01	6.12E-01		Unigene40874_All//gi|224080516|ref|XP_002306147.1|//6.00E-42//SAUR family protein [Populus trichocarpa] >gi|222849111|gb|EEE86658.1| SAUR family protein [Populus trichocarpa]	Unigene40874_All//3.00E-40//AT4G34760| auxin-responsive family protein	Unigene40874_All//0.00E+00//DW514024				nr +
Unigene40876_All	612	0.34	0.91	1.13	16.52	14.01	5.83	0.41	0.14	0.00	1.41E+00	1.69E-01		1.73E+00	7.67E-02		-2.38E-01	2.19E-01		-1.50E+00	1.78E-15	Down	-1.60E+00	3.10E-01		-8.70E+00	3.04E-02		Unigene40876_All//gi|297845886|ref|XP_002890824.1|//1.00E-37//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336666|gb|EFH67083.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40876_All//4.00E-38//AT1G29660| GDSL-motif lipase/hydrolase family protein	Unigene40876_All//0.00E+00//TC142158				nr +

Unigene40879_All	454	25.93	19.42	16.54	22.71	16.54	20.00	79.44	38.02	21.24	-4.17E-01	1.24E-02		-6.49E-01	1.50E-04		-4.58E-01	6.95E-03		-1.84E-01	3.79E-01		-1.06E+00	1.07E-35	Down	-1.90E+00	3.92E-87	Down	Unigene40879_All//gi|209967447|gb|ACJ02352.1|//4.00E-24//60S ribosomal protein L39 [Vernicia fordii] >gi|257219568|gb|ACV50437.1| 60S ribosomal protein L39 [Jatropha curcas]	Unigene40879_All//5.00E-24//AT4G31985| 60S ribosomal protein L39 (RPL39C)	Unigene40879_All//1.00E-124//gi|73852428|gb|DT461448.1|DT461448		ko03010|Ribosome		nr +
Unigene40880_All	548	21.20	17.66	11.95	27.36	30.35	32.06	111.10	44.08	34.31	-2.63E-01	1.32E-01		-8.27E-01	1.84E-06		1.50E-01	3.39E-01		2.29E-01	1.12E-01		-1.33E+00	3.00E-85	Down	-1.70E+00	6.68E-125	Down	Unigene40880_All//gi|115470525|ref|NP_001058861.1|//1.00E-06//Os07g0139600 [Oryza sativa Japonica Group] >gi|113610397|dbj|BAF20775.1|Os07g0139600 [Oryza sativa Japonica Group]		Unigene40880_All//0.00E+00//TC171246		ko03010|Ribosome		nr -
Unigene40884_All	1280	0.00	0.00	0.00	0.31	0.59	0.07	116.40	4.11	20.51	null	null		null	null		9.27E-01	2.97E-01		-2.14E+00	1.26E-01		-4.82E+00	0.00E+00	Down	-2.50E+00	0.00E+00	Down	Unigene40884_All//gi|297828624|ref|XP_002882194.1|//1.00E-110//peroxidase 27 [Arabidopsis lyrata subsp. lyrata] >gi|297328034|gb|EFH58453.1| peroxidase 27 [Arabidopsis lyrata subsp. lyrata]	Unigene40884_All//3.00E-111//AT3G01190| peroxidase 27 (PER27) (P27) (PRXR7)	Unigene40884_All//1.00E-07//gi|84169298|gb|DR457946.1|DR457946		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene40885_All	686	7.09	1.63	1.55	3.56	5.47	1.98	0.25	0.00	0.12	-2.13E+00	2.31E-11	Down	-2.19E+00	3.31E-11	Down	6.21E-01	4.85E-02		-8.49E-01	3.75E-02		-7.95E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene40885_All//gi|242390093|dbj|BAH80549.1|//2.00E-79//transcription factor GRAS family protein [Eucalyptus grandis]	Unigene40885_All//2.00E-65//AT4G37650| SHR (SHORT ROOT); protein binding / sequence-specific DNA binding / transcription factor	Unigene40885_All//0.00E+00//ES836399	GRAS			nr +
Unigene40886_All	271	0.19	1.50	4.72	6.07	1.40	2.00	0.62	0.62	0.74	2.95E+00	5.91E-02		4.61E+00	5.51E-06	Up	-2.12E+00	5.46E-05	Down	-1.60E+00	2.71E-03		-1.67E-02	1.02E+00		2.36E-01	8.83E-01		Unigene40886_All//gi|115448127|ref|NP_001047843.1|//8.00E-14//Os02g0701300 [Oryza sativa Japonica Group] >gi|51039837|tpg|DAA05208.1| TPA_exp: growth-regulating factor 4 [Oryza sativa (japonica cultivar-group)] >gi|113537374|dbj|BAF09757.1|Os02g0701300 [Oryza sativa Japonica Group]	Unigene40886_All//5.00E-11//AT3G13960| AtGRF5 (GROWTH-REGULATING FACTOR 5); transcription activator	Unigene40886_All//4.00E-105//ES838256	GRF			nr +
Unigene40887_All	636	1.73	0.56	0.42	0.00	0.60	0.00	22.34	1.51	4.13	-1.63E+00	1.82E-02		-2.05E+00	7.42E-03		9.22E+00	1.96E-02		null	null		-3.89E+00	5.54E-72	Down	-2.43E+00	2.96E-47	Down	Unigene40887_All//gi|297793017|ref|XP_002864393.1|//3.00E-13//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310228|gb|EFH40652.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40887_All//7.00E-13//AT5G55460| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene40887_All//6.00E-174//gi|109833658|gb|DW232223.1|DW232223				nr -
Unigene40888_All	1270	0.00	0.00	0.00	0.47	0.08	0.00	26.50	10.43	11.32	null	null		null	null		-2.53E+00	1.36E-02		-8.88E+00	7.70E-04	Down	-1.34E+00	4.43E-48	Down	-1.23E+00	5.31E-43	Down	Unigene40888_All//gi|206812328|gb|AC122425.1|//1.00E-150//pericarp peroxidase 3 [Litchi chinensis]	Unigene40888_All//6.00E-148//AT5G66390| peroxidase 72 (PER72) (P72) (PRXR8)	Unigene40888_All//0.00E+00//BF271891		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene40889_All	282	5.94	6.47	1.89	2.30	3.79	5.77	0.30	0.59	3.11	1.24E-01	7.86E-01		-1.65E+00	3.47E-03		7.21E-01	3.14E-01		1.33E+00	1.30E-02		9.83E-01	6.33E-01		3.37E+00	1.32E-04	Up			Unigene40889_All//2.00E-58//BM360771				
Unigene4089_All	1867	25.53	12.62	18.14	25.24	22.21	14.20	13.41	4.05	3.41	-1.02E+00	9.68E-36	Down	-4.93E-01	3.64E-10		-1.85E-01	1.78E-02		-8.30E-01	2.92E-27		-1.73E+00	1.37E-51	Down	-1.97E+00	1.09E-63	Down	Unigene4089_All//gi|145335950|ref|NP_173489.2|//1.00E-158//ATP binding / protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|87785941|gb|AAF79602.1|AC027665_3 F5M15.3 [Arabidopsis thaliana] >gi|8886951|gb|AAF80637.1|AC069251_30 F2D10.13 [Arabidopsis thaliana]	Unigene4089_All//2.00E-158//AT1G20650| ATP binding / protein kinase/ protein serine/threonine kinase	Unigene4089_All//0.00E+00//TC141940		ko04626|Plant-pathogen interaction		nr -
Unigene40891_All	1424	584.68	539.96	803.57	12.63	14.44	7.20	0.06	0.09	0.56	-1.15E-01	2.03E-11		4.59E-01	6.18E-203		1.93E-01	1.42E-01		-8.11E-01	2.27E-10		5.69E-01	7.82E-01		3.24E+00	3.96E-04	Up	Unigene40891_All//gi|126571484|gb|AB021382.1|//0.00E+00//plastid fructose 1,6 bisphosphate aldolase class 1 [Gossypium arboreum]	Unigene40891_All//0.00E+00//AT4G38970| fructose-bisphosphate aldolase, putative	Unigene40891_All//0.00E+00//TC152482		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene40892_All	447	2.81	1.81	0.24	7.47	4.24	4.24	4.73	3.09	1.69	-6.31E-01	2.93E-01		-3.56E+00	4.96E-05	Down	-8.17E-01	1.04E-02		-8.15E-01	1.56E-02		-6.16E-01	1.26E-01		-1.48E+00	2.15E-04	Down	Unigene40892_All//gi|297822505|ref|XP_002879135.1|//2.00E-09//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324974|gb|EFH55394.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene40892_All//8.00E-10//AT2G27790| nucleic acid binding / nucleotide binding	Unigene40892_All//9.00E-86//TC140645				nr +
Unigene40893_All	465	4.28	0.44	5.04	14.57	12.07	12.43	2.00	3.78	3.00	-3.29E+00	1.16E-07	Down	2.37E-01	6.13E-01		-2.71E-01	2.61E-01		-2.29E-01	3.79E-01		9.16E-01	3.87E-02		5.84E-01	2.39E-01		Unigene40893_All//gi|15232012|ref|NP_187519.1|//1.00E-33//glycine-rich protein [Arabidopsis thaliana] >gi|75207465|sp|Q9SS80.1|U503A_ARATH RecName: Full=UPF0503 protein At3g09070, chloroplastic; Flags: Precursor	Unigene40893_All//2.00E-20//AT3G09070| glycine-rich protein	Unigene40893_All//2.00E-40//ES798205				nr -
Unigene40895_All	1041	3.42	0.29	1.64	2.63	1.32	0.87	0.32	0.00	0.46	-3.55E+00	4.23E-14	Down	-1.06E+00	2.06E-03		-9.92E-01	5.50E-03		-1.60E+00	4.92E-05	Down	-8.34E+00	1.17E-02		4.99E-01	6.12E-01		Unigene40895_All//gi|28558780|gb|AA045751.1|//4.00E-12//gag-protease polyprotein [Cucumis melo]		Unigene40895_All//0.00E+00//TC151060				nr +
Unigene40897_All	558	0.66	0.18	0.29	0.45	0.43	1.46	2.42	4.04	5.64	-1.85E+00	1.87E-01		-1.20E+00	3.96E-01		-4.73E-02	9.51E-01		1.71E+00	4.57E-02		7.38E-01	5.31E-02		1.22E+00	1.00E-04	Up			Unigene40897_All//7.00E-07//ES814995				
Unigene40898_All	489	4.17	4.66	9.15	4.18	2.32	1.75	264.66	347.78	233.41	1.60E-01	6.94E-01		1.13E+00	1.85E-04	Up	-8.46E-01	4.95E-02		-1.25E+00	6.06E-03		3.94E-01	2.64E-29		-1.81E-01	5.59E-06		Unigene40898_All//gi|224137306|ref|XP_002327093.1|//3.00E-26//cytochrome P450 [Populus trichocarpa] >gi|222835408|gb|EEE73843.1| cytochrome P450 [Populus trichocarpa]	Unigene40898_All//4.00E-21//AT4G31950| CYP82C3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene40898_All//0.00E+00//TC156034		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene4090_All	1761	11.65	3.97	12.13	12.76	13.14	9.54	16.16	9.85	10.02	-1.55E+00	6.37E-30	Down	5.81E-02	6.64E-01		4.27E-02	8.00E-01		-4.19E-01	2.15E-04		-7.14E-01	7.69E-15		-6.89E-01	2.01E-14		Unigene4090_All//gi|18650600|gb|AAL75900.1|//1.00E-170//AT4g38220/F20D10_340 [Arabidopsis thaliana]	Unigene4090_All//2.00E-165//AT4G38220| aminoacylase, putative / N-acyl-L-amino-acid amidohydrolase, putative	Unigene4090_All//0.00E+00//TC153973		ko00330|Arginine and proline metabolism		nr +
Unigene40900_All	1563	0.00	0.00	0.00	0.00	0.09	0.00	35.90	8.34	36.14	null	null		null	null		6.46E+00	3.18E-01		null	null		-2.11E+00	9.21E-150	Down	9.90E-03	9.10E-01		Unigene40900_All//gi|38194913|gb|AAR13301.1|//6.00E-86//anthocyanin acyltransferase [Phaseolus vulgaris]	Unigene40900_All//4.00E-64//AT1G03940| transferase family protein	Unigene40900_All//5.00E-07//TC174995		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene40902_All	1186	0.97	0.09	0.00	1.51	2.99	2.93	1.75	0.28	0.87	-3.51E+00	6.57E-05	Down	-9.92E+00	2.60E-06	Down	9.84E-01	1.97E-03		9.55E-01	3.95E-03		-2.63E+00	7.41E-08	Down	-1.00E+00	9.64E-03		Unigene40902_All//gi|15231088|ref|NP_190761.1|//1.00E-116//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|30725344|gb|AAP37694.1| At3g51930 [Arabidopsis thaliana]	Unigene40902_All//9.00E-116//AT3G51930| transducin family protein / WD-40 repeat family protein	Unigene40902_All//9.00E-08//CO125636				nr +
Unigene40903_All	348	0.30	5.82	0.00	0.00	1.98	1.82	2.67	0.72	2.06	4.28E+00	3.01E-09	Up	-8.23E+00	3.93E-01		1.10E+01	3.05E-04	Up	1.08E+01	7.60E-04	Up	-1.89E+00	6.92E-03		-3.75E-01	5.57E-01				Unigene40903_All//3.00E-85//DW495489				
Unigene40907_All	511	9.32	8.53	9.80	17.06	18.40	17.85	30.70	20.78	13.88	-1.28E-01	6.42E-01		7.22E-02	7.97E-01		1.09E-01	6.16E-01		6.56E-02	7.62E-01		-5.63E-01	6.86E-06		-1.15E+00	1.73E-18	Down	Unigene40907_All//gi|224111376|ref|XP_002315832.1|//1.00E-06//predicted protein [Populus trichocarpa] >gi|222864872|gb|EEF02003.1| predicted protein [Populus trichocarpa]	Unigene40907_All//7.00E-05//AT2G02050| NADH-ubiquinone oxidoreductase B18 subunit, putative	Unigene40907_All//0.00E+00//gi|21096915|gb|BQ409228.1|BQ409228		ko00190|Oxidative phosphorylation		nr -
Unigene40909_All	463	805.49	395.51	730.89	95.54	118.92	73.65	0.46	1.44	0.69	-1.03E+00	1.35E-279	Down	-1.40E-01	1.78E-07		3.16E-01	1.87E-06		-3.76E-01	1.29E-06		1.66E+00	4.76E-02		5.92E-01	6.13E-01		Unigene40909_All//gi|21311559|gb|AAM46780.1|AF467803_1//6.00E-56//latex plastidic aldolase-like protein [Hevea brasiliensis]	Unigene40909_All//2.00E-56//AT4G38970| fructose-bisphosphate aldolase, putative	Unigene40909_All//0.00E+00//CD486271		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene40910_All	901	1.10	3.43	0.71	1.00	1.22	1.20	0.38	2.78	0.62	1.64E+00	1.83E-05	Up	-6.38E-01	3.90E-01		2.97E-01	6.88E-01		2.74E-01	6.70E-01		2.89E+00	3.09E-10	Up	7.22E-01	3.99E-01		Unigene40910_All//gi|15238818|ref|NP_196592.1|//1.00E-122//PFK2 (PHOSPHOFRUCTOKINASE 2); 6-phosphofructokinase [Arabidopsis thaliana] >gi|75170846|sp|Q9FIK0.1|K6PF2_ARATH RecName: Full=6-phosphofructokinase 2; AltName: Full=Phosphofructokinase 2; AltName: Full=Phosphohexokinase 2 >gi|10177917|dbj|BAB11328.1| pyrophosphate-fructose-6-phosphate 1-phosphotransferase-like protein [Arabidopsis thaliana] >gi|15982711|gb|AAL09725.1| AT5g47810/MCA23_13 [Arabidopsis thaliana] >gi|19699343|gb|AAL91281.1| AT5g47810/MCA23_13 [Arabidopsis thaliana]	Unigene40910_All//3.00E-105//AT5G47810| PFK2 (PHOSPHOFRUCTOKINASE 2); 6-phosphofructokinase	Unigene40910_All//7.00E-82//DN780534		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene40911_All	974	1.40	1.04	1.37	7.16	8.98	6.35	2.95	1.20	0.98	-4.25E-01	4.51E-01		-3.12E-02	9.77E-01		3.27E-01	1.06E-01		-1.73E-01	4.99E-01		-1.30E+00	1.31E-04	Down	-1.59E+00	3.47E-06	Down			Unigene40911_All//2.00E-57//FL577567				
Unigene40912_All	513	26.93	15.01	16.50	14.27	11.88	8.54	0.49	26.64	0.70	-8.43E-01	3.54E-08		-7.06E-01	6.40E-06		-2.65E-01	2.51E-01		-7.41E-01	4.56E-04		5.75E+00	2.61E-86	Up	4.99E-01	6.27E-01		Unigene40912_All//gi|60280217|gb|AA16493.1|//7.00E-31//UDP-glucose:flavonoid 7-O-glucosyltransferase [Malus x domestica]	Unigene40912_All//2.00E-24//AT1G05530| UGT75B2 (UDP-GLUCOSYL TRANSFERASE 75B2); UDP-glucosyltransferase/ UDP-glycosyltransferase/ abscisic acid glucosyltransferase/ transferase, transferring glycosyl groups	Unigene40912_All//1.00E-156//TC139712		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis		nr +
Unigene40913_All	614	0.00	2.15	1.13	0.49	0.73	1.18	1.38	1.16	0.45	1.11E+01	1.50E-07	Up	1.01E+01	6.16E-04	Up	5.83E-01	6.26E-01		1.27E+00	1.56E-01		-2.51E-01	7.13E-01		-1.60E+00	2.02E-02				Unigene40913_All//3.00E-40//TC135819				
Unigene40914_All	517	21.86	23.23	9.58	16.28	9.32	9.26	14.23	9.05	5.24	8.76E-02	6.06E-01		-1.19E+00	6.16E-11	Down	-8.04E-01	1.24E-05		-8.14E-01	2.99E-05		-6.52E-01	6.52E-04		-1.44E+00	1.11E-12	Down			Unigene40914_All//8.00E-62//DW519039				
Unigene40916_All	887	0.53	0.51	0.84	1.12	1.09	1.12	1.10	0.66	2.87	-4.64E-02	9.78E-01		6.63E-01	4.19E-01		-4.73E-02	9.36E-01		-3.90E-03	9.88E-01		-7.33E-01	2.48E-01		1.39E+00	1.09E-04	Up	Unigene40916_All//gi|240254367|ref|NP_177558.4|//1.00E-38//AtRLP14 (Receptor Like Protein 14); protein binding [Arabidopsis thaliana]	Unigene40916_All//8.00E-29//AT1G74190| AtRLP15 (Receptor Like Protein 15); protein binding			ko04626|Plant-pathogen interaction		nr -
Unigene40918_All	514	0.92	1.08	0.21	4.94	3.95	4.31	4.20	0.24	1.55	2.43E-01	7.77E-01		-2.14E+00	1.03E-01		-3.23E-01	4.48E-01		-1.99E-01	6.47E-01		-4.10E+00	8.83E-12	Down	-1.44E+00	2.65E-04	Down	Unigene40918_All//gi|297831136|ref|XP_002883450.1|//2.00E-78//PAKRP1L [Arabidopsis lyrata subsp. lyrata] >gi|297329290|gb|EFH59709.1| PAKRP1L [Arabidopsis lyrata subsp. lyrata]	Unigene40918_All//7.00E-79//AT3G23670| KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor	Unigene40918_All//2.00E-31//ES836817				nr +

Unigene40919_All	1216	0.13	0.08	0.44	0.04	0.51	0.00	88.00	23.58	23.65	-6.32E-01	7.27E-01		1.76E+00	1.29E-01		3.64E+00	5.37E-03		-5.36E+00	6.35E-01		-1.90E+00	3.21E-249	Down	-1.90E+00	1.01E-255	Down	Unigene40919_All//gi|119888002|gb|ABM05953.1|//5.00E-26//proline-rich protein [Gossypium hirsutum]	Unigene40919_All//5.00E-16//AT4G16380| metal ion binding	Unigene40919_All//7.00E-18//ES846429				nr -
Unigene40920_All	1221	0.04	0.00	0.00	0.04	0.00	0.04	7.13	1.20	2.09	-5.42E+00	6.11E-01		-5.42E+00	6.23E-01		-5.35E+00	5.55E-01		-1.41E-01	9.52E-01		-2.57E+00	3.63E-30	Down	-1.77E+00	9.79E-20	Down	Unigene40920_All//gi|224097756|ref|XP_002334586.1|//1.00E-136//cytochrome P450 [Populus trichocarpa] >gi|22287336|gb|EEF10492.1| cytochrome P450 [Populus trichocarpa]	Unigene40920_All//2.00E-90//AT4G31500| CYP83B1 (CYTOCHROME P450 MONOOXYGENASE 83B1); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding	Unigene40920_All//0.00E+00//TC151895		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr -
Unigene40923_All	475	2.42	1.28	0.45	1.89	1.96	0.95	3.29	0.26	0.59	-9.21E-01	1.43E-01		-2.43E+00	1.85E-03		5.23E-02	9.59E-01		-9.89E-01	1.96E-01		-3.64E+00	5.20E-08	Down	-2.49E+00	5.08E-06	Down	Unigene40923_All//gi|38454112|gb|AAR20750.1|//4.00E-17//At3g28420 [Arabidopsis thaliana]	Unigene40923_All//1.00E-06//AT3G28420| unknown protein					nr +
Unigene40924_All	327	440.49	176.96	253.39	287.76	256.11	368.77	82.75	38.98	38.25	-1.32E+00	6.56E-161	Down	-7.98E-01	9.33E-69		-1.68E-01	1.21E-03		3.58E-01	1.98E-15		-1.09E+00	6.63E-28	Down	-1.11E+00	6.96E-30	Down	Unigene40924_All//gi|2506277|sp|P08927.2|RUBB_PEA//1.00E-51//RecName: Full=RuBisCO large subunit-binding protein subunit beta, chloroplastic; AltName: Full=60 kDa chaperonin subunit beta; AltName: Full=CPN-60 beta; Flags: Precursor >gi|806808|gb|AAA66365.1| chaperonin precursor [Pisum sativum]	Unigene40924_All//2.00E-52//AT5G56500| ATP binding / protein binding	Unigene40924_All//0.00E+00//gi|13349887|gb|BG440236.1|BG440236		ko03018|RNA degradation		nr +
Unigene40926_All	759	0.41	0.40	0.98	1.44	0.95	0.89	1.39	3.47	2.94	-4.64E-02	9.84E-01		1.25E+00	1.54E-01		-6.00E-01	3.53E-01		-6.94E-01	3.11E-01		1.32E+00	2.33E-04	Up	1.08E+00	4.08E-03		Unigene40926_All//gi|52082696|gb|AU25941.1|//5.00E-89//cytochrome b [Vitis vinifera]	Unigene40926_All//5.00E-81//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.			ko00190|Oxidative phosphorylation		nr -
Unigene40927_All	622	0.00	1.63	0.00	1.04	15.89	2.18	0.00	0.00	0.06	1.07E+01	7.26E-06	Up	null	null		3.93E+00	7.54E-47	Up	1.07E+00	7.27E-02		null	null		6.00E+00	6.45E-01		Unigene40927_All//gi|224140209|ref|XP_002323477.1|//2.00E-24//SAUR family protein [Populus trichocarpa] >gi|222868107|gb|EEF05238.1| SAUR family protein [Populus trichocarpa]	Unigene40927_All//2.00E-20//AT3G09870| auxin-responsive family protein	Unigene40927_All//2.00E-81//TC138921				nr +
Unigene40928_All	293	4.11	2.42	5.09	2.04	1.18	0.00	0.29	0.43	0.00	-7.63E-01	2.13E-01		3.09E-01	6.01E-01		-7.96E-01	3.88E-01		-1.10E+01	7.70E-04	Down	5.68E-01	7.82E-01		-8.17E+00	3.58E-01		Unigene40928_All//gi|115486964|ref|NP_001065969.1|//5.00E-16//Os12g0111600 [Oryza sativa Japonica Group] >gi|77553422|gb|ABA96218.1| Hypoxia induced protein conserved region containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113648476|dbj|BAF28988.1| Os12g0111600 [Oryza sativa Japonica Group]	Unigene40928_All//1.00E-10//AT5G27760| hypoxia-responsive family protein	Unigene40928_All//8.00E-42//DW508525				nr -
Unigene40932_All	335	65.13	52.48	72.48	152.27	135.79	304.82	177.20	480.21	144.49	-3.11E-01	9.20E-03		1.54E-01	2.31E-01		-1.65E-01	2.94E-02		1.00E+00	3.12E-79	Up	1.44E+00	4.64E-251	Up	-2.94E-01	8.29E-07		Unigene40932_All//gi|146432261|gb|ABQ41114.1|//2.00E-54//monodehydroascorbate reductase [Vitis vinifera]	Unigene40932_All//8.00E-51//AT5G03630| ATMDAR2; monodehydroascorbate reductase (NADH)	Unigene40932_All//0.00E+00//gi|164250218|gb|ES803630.1|ES803630		ko00053|Ascorbate and aldarate metabolism		nr -
Unigene40935_All	655	0.48	0.77	0.24	6.01	4.47	1.52	0.45	0.00	0.06	6.91E-01	4.99E-01		-9.75E-01	5.06E-01		-4.27E-01	1.66E-01		-1.99E+00	3.90E-09	Down	-8.82E+00	2.17E-02		-2.89E+00	6.76E-02					Unigene40935_All//2.00E-10//DR455591				
Unigene40937_All	347	17.49	8.03	14.89	11.20	13.20	7.42	0.00	0.00	0.11	-1.12E+00	5.08E-06	Down	-2.33E-01	4.01E-01		2.37E-01	4.62E-01		-5.94E-01	5.87E-02		null	null		6.84E+00	6.45E-01					Unigene40937_All//5.00E-22//TC135055				
Unigene40939_All	422	0.00	0.48	0.00	0.00	0.08	0.00	32.96	4.16	30.40	8.91E+00	1.36E-01		null	null		6.35E+00	8.29E-01		null	null		-2.99E+00	6.55E-56	Down	-1.17E-01	4.33E-01		Unigene40939_All//gi|73624747|gb|AAZ79231.1|//1.00E-54//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene40939_All//1.00E-51//AT4G23990| ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups					nr -
Unigene4094_All	1970	2.02	5.22	2.73	1.80	1.43	1.19	11.37	35.60	20.40	1.37E+00	7.90E-13	Up	4.36E-01	1.13E-01		-3.25E-01	3.43E-01		-5.91E-01	7.51E-02		1.65E+00	1.07E-133	Up	8.43E-01	7.66E-28		Unigene4094_All//gi|297814159|ref|XP_002874963.1|//1.00E-91//WRKY DNA-binding protein 47 [Arabidopsis lyrata subsp. lyrata] >gi|297320800|gb|EFH51222.1| WRKY DNA-binding protein 47 [Arabidopsis lyrata subsp. lyrata]	Unigene4094_All//6.00E-66//AT4G01720| WRKY47; transcription factor	Unigene4094_All//3.00E-24//AI730840	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene40940_All	406	0.00	0.00	0.00	0.00	0.00	0.00	3.23	0.21	2.94	null	null		null	null		null	null		null	null		-3.97E+00	3.34E-07	Down	-1.33E-01	7.86E-01		Unigene40940_All//gi|73624747|gb|AAZ79231.1|//3.00E-48//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene40940_All//8.00E-44//AT4G23990| ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups					nr -
Unigene40942_All	1314	0.40	0.54	0.16	7.96	9.43	11.10	2.38	0.38	1.24	4.39E-01	6.16E-01		-1.30E+00	2.42E-01		2.45E-01	1.57E-01		4.80E-01	9.31E-04		-2.64E+00	1.42E-11	Down	-9.38E-01	2.06E-03		Unigene40942_All//gi|297720249|ref|NP_001172486.1|//9.00E-97//Os01g0652800 [Oryza sativa Japonica Group] >gi|195711153|dbj|BAB86576.1| leaf senescence protein-like [Oryza sativa Japonica Group] >gi|20161502|dbj|BAB90425.1| leaf senescence protein-like [Oryza sativa Japonica Group] >gi|255673513|dbj|BAH91216.1| Os01g0652800 [Oryza sativa Japonica Group]	Unigene40942_All//5.00E-113//AT5G15900| unknown protein	Unigene40942_All//0.00E+00//CO106230				nr +
Unigene40943_All	680	0.31	0.00	0.55	15.16	9.12	21.05	524.09	23.30	134.51	-8.27E+00	1.22E-01		8.33E-01	5.16E-01		-7.34E-01	7.36E-06		4.74E-01	1.25E-03		-4.49E+00	0.00E+00	Down	-1.96E+00	0.00E+00	Down	Unigene40943_All//gi|110816009|gb|ABG91752.1|//1.00E-50//RgPRP2 [Gossypium hirsutum]	Unigene40943_All//2.00E-33//AT1G62510| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene40943_All//0.00E+00//TC162945				nr -
Unigene40944_All	365	0.14	0.00	0.29	1.91	1.13	0.00	1.85	2.18	1.20	-7.16E+00	6.11E-01		1.03E+00	7.03E-01		-7.55E-01	3.69E-01		-1.09E+01	1.96E-04	Down	2.31E-01	7.34E-01		-6.26E-01	4.03E-01					Unigene40944_All//4.00E-07//DN760089				
Unigene40949_All	643	1.38	0.47	0.17	4.34	3.80	3.65	4.47	2.02	2.73	-1.55E+00	4.56E-02		-3.06E+00	2.25E-03		-1.90E-01	6.26E-01		-2.48E-01	5.63E-01		-1.15E+00	5.87E-04	Down	-7.14E-01	2.44E-02		Unigene40949_All//gi|297806821|ref|XP_002871294.1|//2.00E-23//mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317131|gb|EFH47553.1| mitochondrial transcription termination factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene40949_All//1.00E-24//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene40949_All//0.00E+00//gi|21102257|gb|BQ414570.1|BQ414570				nr +
Unigene40951_All	374	1.82	1.35	0.00	1.60	1.38	2.05	3.28	7.04	5.01	-4.25E-01	5.97E-01		-1.08E+01	7.64E-04	Down	-2.11E-01	8.23E-01		3.61E-01	6.80E-01		1.10E+00	1.70E-03		6.11E-01	1.40E-01		Unigene40951_All//gi|51536572|gb|AAU05524.1|//8.00E-14//At3g26990 [Arabidopsis thaliana]	Unigene40951_All//4.00E-15//AT3G26990| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF618 (InterPro:IPR006903), Regulation of nuclear pre-mRNA protein (InterPro:IPR006569), ENTH/VHS (InterPro:IPR008942); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G10060.1); Has 815 Blast hits to 806 proteins in 138 species: Archae - 0; Bacteria - 10; Metazoa - 490; Fungi - 159; Plants - 81; Viruses - 1; Other Eukaryotes - 74 (source: NCBI BLink).	Unigene40951_All//0.00E+00//TC138729				nr -
Unigene40952_All	660	0.00	0.00	0.00	0.00	0.00	0.00	52.98	75.36	26.02	null	null		null	null		null	null		null	null		5.08E-01	3.75E-14		-1.03E+00	1.09E-33	Down	Unigene40952_All//gi|297836874|ref|XP_002886319.1|//3.00E-08//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332159|gb|EFH62578.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene40952_All//2.00E-16//DW506003				nr +
Unigene40957_All	644	0.16	7.63	0.00	0.15	1.66	0.14	0.72	0.91	39.84	5.55E+00	5.72E-25	Up	-7.34E+00	3.93E-01		3.42E+00	1.07E-04	Up	-1.41E-01	9.50E-01		3.31E-01	6.88E-01		5.79E+00	9.49E-165	Up	Unigene40957_All//gi|2921338|gb|AAC04719.1|//2.00E-78//MYB-like DNA-binding domain protein [Gossypium hirsutum]	Unigene40957_All//2.00E-45//AT3G06490| MYB108 (myb domain protein 108); DNA binding / transcription factor	Unigene40957_All//0.00E+00//TC146739	MYB			nr +
Unigene40958_All	794	55.29	24.95	53.05	37.20	42.37	37.43	90.95	16.69	23.78	-1.15E+00	5.09E-40	Down	-5.96E-02	5.54E-01		1.88E-01	5.19E-02		8.70E-03	9.50E-01		-2.45E+00	1.23E-231	Down	-1.94E+00	1.17E-177	Down	Unigene40958_All//gi|147776618|emb|CAN63020.1|//8.00E-06//hypothetical protein [Vitis vinifera]		Unigene40958_All//0.00E+00//gi|13356810|gb|BG447158.1|BG447158				nr +
Unigene4096_All	1735	3.41	8.82	11.63	9.30	22.63	24.36	0.15	0.00	0.00	1.37E+00	9.67E-19	Up	1.77E+00	3.51E-34	Up	1.28E+00	7.13E-50	Up	1.39E+00	3.35E-55	Up	-7.19E+00	4.04E-02		-7.19E+00	3.04E-02		Unigene4096_All//gi|224054546|ref|XP_002298314.1|//0.00E+00//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222845572|gb|EEE83119.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene4096_All//3.00E-136//AT3G51860| CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	Unigene4096_All//0.00E+00//ES814991				nr +
Unigene40960_All	419	64.56	553.86	141.32	112.71	617.53	391.92	1087.78	1907.44	2072.46	3.10E+00	0.00E+00	Up	1.13E+00	9.29E-51	Up	2.45E+00	0.00E+00	Up	1.80E+00	0.00E+00	Up	8.10E-01	0.00E+00		9.30E-01	0.00E+00		Unigene40960_All//gi|222423474|dbj|BAH19707.1|//4.00E-12//AT3G15150 [Arabidopsis thaliana]	Unigene40960_All//3.00E-13//AT3G15450| unknown protein	Unigene40960_All//6.00E-167//gi|54115393|gb|CO490902.1|CO490902				nr -
Unigene40966_All	878	0.00	0.40	0.00	0.28	0.51	0.36	1.78	13.52	16.43	8.66E+00	2.46E-02		null	null		8.46E-01	5.14E-01		3.44E-01	7.96E-01		2.92E+00	1.22E-46	Up	3.20E+00	6.12E-63	Up				Unigene40966_All//3.00E-121//DW497762				
Unigene4097_All	2177	7.69	5.98	8.17	8.54	5.13	5.64	11.48	2.30	7.98	-3.63E-01	8.35E-03		8.72E-02	5.90E-01		-7.36E-01	3.87E-10		-5.97E-01	1.61E-06		-2.32E+00	1.78E-75	Down	-5.25E-01	3.43E-08		Unigene4097_All//gi|27597231|dbj|BAC55156.1|//0.00E+00//purple acid phosphatase [Nicotiana tabacum]	Unigene4097_All//0.00E+00//AT2G27190| PAP12 (PURPLE ACID PHOSPHATASE 12); acid phosphatase/ protein serine/threonine phosphatase	Unigene4097_All//0.00E+00//TC157039				nr -
Unigene40978_All	292	24.55	97.69	42.13	17.74	16.39	28.15	19.84	38.50	11.46	1.99E+00	6.21E-58	Up	7.79E-01	3.19E-06		-1.14E-01	7.12E-01		6.66E-01	8.42E-04		9.57E-01	6.08E-10		-7.92E-01	2.12E-04		Unigene40978_All//gi|224111870|ref|XP_002316008.1|//1.00E-10//cytochrome P450 [Populus trichocarpa] >gi|222865048|gb|EEF02179.1| cytochrome P450 [Populus trichocarpa]	Unigene40978_All//4.00E-10//AT3G14620| CYP72A8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene40978_All//7.00E-135//gi|73860942|gb|DT463681.1|DT463681		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +

Unigene40983_All	464	2.03	0.44	0.11	1.18	1.19	0.78	2.10	2.07	0.09	-2.22E+00	6.64E-03		-4.14E+00	2.90E-04	Down	7.90E-03	9.83E-01		-6.01E-01	5.66E-01		-1.66E-02	1.02E+00		-4.61E+00	3.32E-06	Down	Unigene40983_All//gi|297793693|ref|XP_002864731.1|//4.00E-28//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297310566|gb|EFH40990.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene40983_All//6.00E-29//AT5G61400| pentatricopeptide (PPR) repeat-containing protein	Unigene40983_All//4.00E-57//TC178255				nr +
Unigene40985_All	282	1.11	1.62	4.72	117.65	100.25	51.09	1.05	0.74	0.14	5.39E-01	6.02E-01		2.08E+00	2.18E-03		-2.31E-01	1.26E-02		-1.20E+00	2.34E-35	Down	-5.02E-01	6.78E-01		-2.89E+00	6.76E-02			Unigene40985_All//1.00E-55//TC148937				
Unigene40986_All	295	33.52	16.32	22.20	77.17	112.76	52.05	0.00	0.00	0.00	-1.04E+00	2.73E-08	Down	-5.94E-01	1.69E-03		5.47E-01	2.24E-10		-5.68E-01	3.19E-07		null	null		null	null		Unigene40986_All//gi|150022176|gb|ABR57416.1|//4.00E-55//alpha-expansin 3 [Gossypium arboreum] >gi|150022184|gb|ABR57420.1| alpha-expansin 3 [Gossypium hirsutum] >gi|150022186|gb|ABR57421.1| alpha-expansin 3 [Gossypium hirsutum] >gi|150022188|gb|ABR57422.1| alpha-expansin 3 [Gossypium mustelinum] >gi|150022190|gb|ABR57423.1| alpha-expansin 3 [Gossypium raimondii]	Unigene40986_All//4.00E-49//AT3G29030| EXPA5 (EXPANSIN A5)	Unigene40986_All//6.00E-166//ES819675				nr +
Unigene40987_All	1024	0.36	1.04	0.05	0.15	1.21	0.40	1.32	0.82	4.55	1.54E+00	2.81E-02		-2.78E+00	1.03E-01		3.05E+00	6.03E-05	Up	1.44E+00	2.82E-01		-6.95E-01	1.84E-01		1.78E+00	6.49E-11	Up		Unigene40987_All//0.00E+00//ES843568				
Unigene4099_All	933	78.23	34.32	53.02	48.91	55.18	18.83	2.72	1.16	2.01	-1.19E+00	7.54E-70	Down	-5.61E-01	4.39E-19		1.74E-01	2.06E-02		-1.38E+00	1.13E-59	Down	-1.22E+00	7.21E-04	Down	-4.38E-01	2.09E-01		Unigene4099_All//gi|256002927|gb|ACU52707.1|//3.00E-43//bHLH transcription factor PTF1 [Glycine max]	Unigene4099_All//3.00E-37//AT3G57800| basic helix-loop-helix (bHLH) family protein	Unigene4099_All//0.00E+00//TC142667	bHLH			nr -
Unigene40991_All	414	1.14	5.75	4.50	3.25	4.74	2.18	0.92	0.61	1.83	2.34E+00	1.67E-06	Up	1.98E+00	3.17E-04	Up	5.45E-01	2.68E-01		-5.74E-01	3.45E-01		-6.02E-01	6.12E-01		9.92E-01	1.63E-01			Unigene40991_All//3.00E-05//AT1G78630| emb1473 (embryo defective 1473); structural constituent of ribosome	Unigene40991_All//2.00E-37//ES843027		ko03010|Ribosome		kegg -
Unigene40993_All	488	0.21	1.45	0.11	7.96	17.57	4.16	0.95	0.69	0.49	2.76E+00	9.14E-03		-9.75E-01	7.20E-01		1.14E+00	2.25E-09	Up	-9.35E-01	2.32E-03		-4.76E-01	6.59E-01		-9.60E-01	3.13E-01		Unigene40993_All//gi|171452356|dbj|BAG15869.1|//8.00E-28//ankyrin repeat protein [Bruguiera gymnorhiza]	Unigene40993_All//5.00E-28//AT4G10720| ankyrin repeat family protein	Unigene40993_All//2.00E-173//DW477863				nr -
Unigene40995_All	424	7.28	2.75	5.15	7.17	5.36	11.93	8.38	9.76	4.79	-1.41E+00	1.45E-04	Down	-5.00E-01	1.85E-01		-4.19E-01	2.54E-01		7.35E-01	5.64E-03		2.20E-01	4.56E-01		-8.06E-01	4.19E-03		Unigene40995_All//gi|255555073|ref|XP_002518574.1|//1.00E-15//transcription regulator, putative [Ricinus communis] >gi|223542419|gb|EEF43961.1| transcription regulator, putative [Ricinus communis]		Unigene40995_All//2.00E-83//BF271897				nr +
Unigene40997_All	357	0.29	0.28	1.04	0.28	1.16	0.76	2.72	1.99	7.59	-4.60E-02	9.88E-01		1.83E+00	2.13E-01		2.05E+00	1.47E-01		1.44E+00	4.09E-01		-4.53E-01	4.90E-01		1.48E+00	2.56E-05	Up							
Unigene40999_All	426	1.72	1.55	0.50	1.52	2.83	1.91	27.59	6.57	4.49	-1.53E-01	8.35E-01		-1.78E+00	6.00E-02		8.96E-01	1.61E-01		3.28E-01	7.01E-01		-2.07E+00	3.08E-31	Down	-2.62E+00	1.24E-42	Down		Unigene40999_All//6.00E-133//gi|13246586|gb|BE055000.2|BE055000		ko03010|Ribosome		kegg -
Unigene410_All	3357	9.83	5.30	4.46	22.47	21.54	15.26	13.63	7.73	7.58	-8.92E-01	3.00E-20		-1.14E+00	6.83E-29	Down	-6.06E-02	4.15E-01		-5.58E-01	8.67E-22		-8.18E-01	2.56E-29		-8.46E-01	6.58E-32		Unigene410_All//gi|79512687|ref|NP_196834.3|//0.00E+00//SFC (SCARFACE): ARF GTPase activator/ phosphoinositide binding [Arabidopsis thaliana] >gi|75321812|sp|Q5W7F2.1|AGD3_ARATH RecName: Full=ARF-ribosylation factor GTPase-activating protein AGD3; Short=ARF GAP AGD3; AltName: Full=Protein ARF-GAP DOMAIN 3; Short=AtAGD3; AltName: Full=Protein VASCULAR NETWORK 3; AltName: Full=Protein SCARFACE >gi|55583334|dbj|BAD69588.1| ARF-GAP [Arabidopsis thaliana]	Unigene410_All//0.00E+00//AT5G13300| SFC (SCARFACE): ARF GTPase activator/ phosphoinositide binding	Unigene410_All//0.00E+00//TC142516		ko04144|Endocytosis		nr +
Unigene4100_All	1120	0.61	12.12	0.33	12.32	13.84	18.35	55.95	117.48	376.51	4.32E+00	4.26E-60	Up	-8.68E-01	3.51E-01		1.67E-01	3.08E-01		5.75E-01	1.17E-06		1.07E+00	2.06E-129	Up	2.75E+00	0.00E+00	Up	Unigene4100_All//gi|224129252|ref|XP_002328928.1|//4.00E-62//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222839358|gb|EEE77695.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene4100_All//3.00E-38//AT5G13180| ANAC083 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 83); transcription factor	Unigene4100_All//0.00E+00//CO103825	NAC			nr +
Unigene41001_All	1053	0.94	0.58	0.30	0.57	0.92	1.20	4.46	6.19	14.38	-7.09E-01	3.05E-01		-1.64E+00	3.43E-02		6.90E-01	3.61E-01		1.08E+00	8.18E-02		4.74E-01	2.26E-02		1.69E+00	3.41E-31	Up	Unigene41001_All//gi|42572257|ref|NP_974224.1|//1.00E-09//zinc finger (DHHC type) family protein [Arabidopsis thaliana]	Unigene41001_All//7.00E-11//AT3G04970| zinc finger (DHHC type) family protein	Unigene41001_All//0.00E+00//CK640438				nr +
Unigene41003_All	293	8.39	13.32	9.63	6.29	6.11	13.72	9.09	10.41	8.02	6.66E-01	3.16E-02		1.99E-01	6.19E-01		-4.17E-02	9.26E-01		1.12E+00	2.37E-04	Up	1.96E-01	6.02E-01		-1.81E-01	6.11E-01			Unigene41003_All//3.00E-78//CO093602				
Unigene41004_All	896	0.00	3.22	0.00	0.22	0.00	1.01	3.07	8.07	7.03	1.17E+01	1.97E-16	Up	null	null		-7.80E+00	8.42E-02		2.18E+00	9.48E-03		1.40E+00	1.61E-11	Up	1.20E+00	2.24E-08	Up	Unigene41004_All//gi|288310302|gb|ADC45390.1|//1.00E-109//branched chain amino acid transaminase [Cucumis melo]	Unigene41004_All//2.00E-104//AT4G10070| ATBCAT-2 (ARABIDOPSIS THALIANA BRANCHED-CHAIN AMINO ACID TRANSAMINASE 2); branched-chain-amino-acid transaminase/ catalytic	Unigene41004_All//2.00E-165//TC159597		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene41005_All	1522	0.00	0.30	0.11	0.00	0.05	0.24	0.56	2.75	2.30	8.23E+00	7.43E-03		6.71E+00	2.39E-01		5.50E+00	6.09E-01		7.89E+00	2.37E-02		2.31E+00	4.28E-13	Up	2.05E+00	6.02E-10	Up	Unigene41005_All//gi|288310302|gb|ADC45390.1|//1.00E-113//branched chain amino acid transaminase [Cucumis melo]	Unigene41005_All//2.00E-111//AT1G10070| ATBCAT-2 (ARABIDOPSIS THALIANA BRANCHED-CHAIN AMINO ACID TRANSAMINASE 2); branched-chain-amino-acid transaminase/ catalytic	Unigene41005_All//0.00E+00//TC159597		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene41006_All	2163	1.50	0.47	0.94	0.71	0.99	0.84	8.44	26.30	17.42	-1.68E+00	6.53E-06	Down	-6.81E-01	5.92E-02		4.67E-01	3.20E-01		2.26E-01	6.78E-01		1.64E+00	6.92E-108	Up	1.05E+00	4.66E-37	Up	Unigene41006_All//gi|297814159|ref|XP_002874963.1|//1.00E-105//WRKY DNA-binding protein 47 [Arabidopsis lyrata subsp. lyrata] >gi|297320800|gb|EFH51222.1| WRKY DNA-binding protein 47 [Arabidopsis lyrata subsp. lyrata]	Unigene41006_All//4.00E-72//AT4G01720| WRKY47; transcription factor	Unigene41006_All//0.00E+00//TC149870	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene41008_All	526	0.00	0.39	0.61	0.00	0.07	1.80	5.55	5.09	65.21	8.59E+00	1.36E-01		9.25E+00	4.52E-02		6.03E+00	8.29E-01		1.08E+01	1.13E-05	Up	-1.25E-01	7.19E-01		3.56E+00	2.37E-163	Up	Unigene41008_All//gi|224127866|ref|XP_002320183.1|//1.00E-78//GH3 family protein [Populus trichocarpa] >gi|222860956|gb|EEE98498.1| GH3 family protein [Populus trichocarpa]	Unigene41008_All//1.00E-62//AT2G46370| JAR1 (JASMONATE RESISTANT 1); ATP binding / adenylyltransferase/ catalytic/ jasmonate-amino synthetase	Unigene41008_All//4.00E-150//DW520054				nr +
Unigene41009_All	816	0.26	0.50	0.07	0.37	1.27	11.79	1.09	4.87	7.27	9.54E-01	4.14E-01		-1.97E+00	3.81E-01		1.79E+00	1.39E-02		5.01E+00	1.86E-49	Up	2.16E+00	1.39E-11	Up	2.74E+00	1.33E-22	Up	Unigene41009_All//gi|18417145|ref|NP_567799.1|//1.00E-104//ULT1 (ULTRAPETALA1); DNA binding [Arabidopsis thaliana] >gi|6121737|sp|Q86Z38.1|ULT1_ARATH RecName: Full=Protein ULTRAPETALA 1 >gi|110074294|gb|ABH04520.1| At4g28190 [Arabidopsis thaliana]	Unigene41009_All//3.00E-105//AT4G28190| ULT1 (ULTRAPETALA1); DNA binding	Unigene41009_All//0.00E+00//gi|164260455|gb|ES822862.1|ES822862	ULT			nr +
Unigene4101_All	1039	89.94	66.52	65.50	14.72	24.66	19.52	6.31	3.94	2.88	-4.35E-01	3.91E-16		-4.57E-01	6.54E-17		7.44E-01	1.34E-13		4.07E-01	7.70E-04		-6.78E-01	9.06E-04		-1.13E+00	4.10E-08	Down	Unigene4101_All//gi|75275079|sp|P82277.1|RRP2_SPIOL//5.00E-79//RecName: Full=30S ribosomal protein 2, chloroplastic; AltName: Full=Plastid-specific 30S ribosomal protein 2; Short=PSRP-2; Flags: Precursor >gi|7578881|gb|AAF64167.1|AF240462_1 plastid-specific ribosomal protein 2 precursor [Spinacia oleracea]	Unigene4101_All//3.00E-69//AT3G52150| RNA recognition motif (RRM)-containing protein	Unigene4101_All//0.00E+00//TC132038		ko03040|Spliceosome		nr +
Unigene41010_All	642	0.24	1.26	1.24	0.78	1.77	1.06	1.84	0.39	2.36	2.37E+00	1.01E-02		2.35E+00	1.46E-02		1.19E+00	7.15E-02		4.44E-01	6.22E-01		-2.24E+00	4.21E-04	Down	3.55E-01	4.67E-01		Unigene41010_All//gi|297837659|ref|XP_002886711.1|//4.00E-44//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297332552|gb|EFH62970.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene41010_All//2.00E-37//AT1G58227| binding					nr +
Unigene41011_All	543	1.16	0.75	0.00	1.56	2.66	1.91	2.18	0.46	1.76	-6.31E-01	4.75E-01		-1.02E+01	1.41E-03		7.72E-01	1.76E-01		2.95E-01	6.93E-01		-2.24E+00	4.21E-04	Down	-3.08E-01	5.92E-01		Unigene41011_All//gi|5420278|emb|CAB46643.1|//3.00E-31//cyclin A3 [Solanum lycopersicum]	Unigene41011_All//1.00E-22//AT1G47230| cyclin, putative	Unigene41011_All//7.00E-53//gi|78347966|gb|DT568240.1|DT568240				nr -
Unigene41015_All	756	0.21	0.00	0.63	1.71	4.28	1.61	1.34	0.88	2.69	-7.70E+00	2.15E-01		1.61E+00	1.82E-01		1.32E+00	1.09E-04	Up	-8.69E-02	8.93E-01		-6.02E-01	3.45E-01		1.00E+00	1.10E-02		Unigene41015_All//gi|297607353|ref|NP_001059835.2|//4.00E-13//Os07g0527800 [Oryza sativa Japonica Group] >gi|255677834|dbj|BAF21749.2| Os07g0527800 [Oryza sativa Japonica Group]	Unigene41015_All//5.00E-10//AT4G03480| protein binding	Unigene41015_All//1.00E-144//TC170049				nr -
Unigene41017_All	387	0.00	1.96	0.00	4.76	1.42	1.05	4.81	2.38	1.44	1.09E+01	1.76E-04	Up	null	null		-1.74E+00	2.18E-04	Down	-2.18E+00	4.21E-05	Down	-1.02E+00	1.76E-02		-1.74E+00	9.21E-05	Down		Unigene41017_All//4.00E-07//BF268565				
Unigene4102_All	865	5.50	148.44	5.17	18.31	16.32	21.88	10.07	36.14	14.60	4.75E+00	0.00E+00	Up	-9.01E-02	7.55E-01		-1.66E-01	2.97E-01		2.57E-01	5.60E-02		1.84E+00	3.61E-70	Up	5.36E-01	1.04E-04		Unigene4102_All//gi|15225894|ref|NP_180326.1|//9.00E-44//zinc finger (AN1-like) family protein [Arabidopsis thaliana] >gi|75215978|sp|Q9ZNU9.1|SAP3_ARATH RecName: Full=Zinc finger A20 and AN1 domain-containing stress-associated protein 3; Short=AtSAP3	Unigene4102_All//9.00E-41//AT2G27580| zinc finger (AN1-like) family protein	Unigene4102_All//0.00E+00//gi|109827606|gb|DW226281.1|DW226281				nr -
Unigene41020_All	337	4.19	2.86	0.32	5.62	3.68	3.08	21.33	34.11	35.46	-5.53E-01	3.30E-01		-3.73E+00	8.89E-06	Down	-6.11E-01	1.90E-01		-8.66E-01	7.02E-02		6.77E-01	5.64E-06		7.34E-01	3.35E-07			Unigene41020_All//2.00E-92//gi|54118719|gb|CO494228.1|CO494228				
Unigene41022_All	392	0.00	0.26	0.27	1.27	1.67	0.92	1.73	0.00	0.91	8.01E+00	3.86E-01		8.09E+00	3.98E-01		3.93E-01	6.98E-01		-4.63E-01	6.59E-01		-1.08E+01	6.34E-05	Down	-9.16E-01	2.21E-01			Unigene41022_All//2.00E-102//TC179580				
Unigene41024_All	281	3.54	0.00	1.14	2.84	1.72	1.61	1.81	0.89	1.13	-1.18E+01	7.45E-06	Down	-1.64E+00	3.43E-02		-7.25E-01	3.47E-01		-8.20E-01	3.19E-01		-1.02E+00	2.88E-01		-6.71E-01	4.48E-01		Unigene41024_All//gi|297725039|ref|NP_001174883.1|//9.00E-23//Os06g0597400 [Oryza sativa Japonica Group] >gi|255677195|dbj|BAH93611.1| Os06g0597400 [Oryza sativa Japonica Group]	Unigene41024_All//4.00E-23//AT5G43810| ZLL (ZWILLE); translation initiation factor	Unigene41024_All//8.00E-82//TC134250				nr -
Unigene41025_All	779	0.00	0.00	0.00	8.76	3.49	3.54	0.71	0.43	0.82	null	null		null	null		-1.33E+00	5.52E-10	Down	-1.31E+00	9.73E-09	Down	-7.17E-01	4.22E-01		2.14E-01	7.73E-01		Unigene41025_All//gi|224137956|ref|XP_002326482.1|//1.00E-37//cationic amino acid transporter [Populus trichocarpa] >gi|222833804|gb|EEF72281.1| cationic amino acid transporter [Populus trichocarpa]	Unigene41025_All//2.00E-18//AT3G10600| CAT7 (CATIONIC AMINO ACID TRANSPORTER 7); cationic amino acid transmembrane transporter	Unigene41025_All//0.00E+00//TC146944				nr +

Unigene41027_All	633	0.33	0.32	0.50	1.65	0.33	0.78	4.07	4.29	1.38	-4.61E-02	9.88E-01		6.10E-01	6.24E-01		-2.34E+00	9.24E-04	Down	-1.07E+00	1.19E-01		7.50E-02	8.39E-01		-1.56E+00	1.68E-05	Down			Unigene41027_All//2.00E-84//gi|109844272|gb|DW242830.1|DW242830				
Unigene41029_All	356	0.88	0.00	0.00	0.00	0.97	2.92	0.36	1.53	0.22	-9.78E+00	3.65E-02		-9.78E+00	4.90E-02		9.92E+00	3.01E-02		1.15E+01	3.33E-06	Up	2.10E+00	3.71E-02		-6.71E-01	7.19E-01				Unigene41029_All//3.00E-45//DW497935				ESTscan -
Unigene41031_All	690	0.15	3.30	1.39	0.14	0.60	1.18	0.12	0.42	0.69	4.45E+00	1.39E-10	Up	3.19E+00	1.02E-03		2.05E+00	1.47E-01		3.03E+00	2.68E-03		1.79E+00	2.24E-01		2.50E+00	2.51E-02		Unigene41031_All//gi|46931316|gb|AT06462.1|//5.00E-30//At3g27250 [Arabidopsis thaliana]	Unigene41031_All//3.00E-26//AT3G27250| unknown protein					nr +
Unigene41032_All	662	1.90	0.92	0.97	3.99	1.35	1.09	0.96	0.19	0.66	-1.05E+00	8.27E-02		-9.75E-01	1.29E-01		-1.56E+00	3.20E-05	Down	-1.87E+00	6.88E-06	Down	-2.34E+00	1.27E-02		-5.33E-01	4.94E-01		Unigene41032_All//gi|255564697|ref|XP_002523343.1|//2.00E-22//conserved hypothetical protein [Ricinus communis] >gi|223537431|gb|EEF39059.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene41036_All	362	2.17	7.42	2.50	1.10	0.57	1.75	1.05	0.46	0.66	1.77E+00	2.49E-05	Up	2.06E-01	7.64E-01		-9.48E-01	4.21E-01		6.66E-01	4.92E-01		-1.19E+00	3.09E-01		-6.71E-01	5.31E-01				Unigene41036_All//6.00E-37//FL577604				
Unigene41040_All	344	3.50	0.44	1.70	4.49	1.40	3.28	2.83	1.82	1.74	-2.98E+00	1.58E-04	Down	-1.04E+00	1.14E-01		-1.68E+00	1.27E-03		-4.52E-01	4.24E-01		-6.33E-01	3.28E-01		-7.03E-01	2.43E-01		Unigene41040_All//gi|297795789|ref|XP_002865779.1|//7.00E-12//nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297311614|gb|EFH42038.1| nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene41040_All//2.00E-08//AT5G50230| nucleotide binding	Unigene41040_All//1.00E-22//TC164507				nr -
Unigene41044_All	562	5.03	10.82	6.92	5.67	9.93	9.88	0.90	0.67	0.00	1.11E+00	7.11E-06	Up	4.60E-01	1.60E-01		8.07E-01	8.26E-04		8.01E-01	1.38E-03		-4.32E-01	6.18E-01		-9.82E+00	5.54E-04	Down	Unigene41044_All//gi|115435222|ref|NP_001042369.1|//1.00E-35//Os01g0210600 [Oryza sativa Japonica Group] >gi|113531900|dbj|BAF04283.1| Os01g0210600 [Oryza sativa Japonica Group]	Unigene41044_All//5.00E-32//AT5G46230| unknown protein	Unigene41044_All//0.00E+00//gi|164282736|gb|ES848165.1|ES848165				nr +
Unigene41045_All	675	5.19	1.88	3.55	6.49	3.83	6.96	1.38	0.87	0.35	-1.47E+00	2.33E-05	Down	-5.49E-01	1.16E-01		-7.63E-01	4.93E-03		9.96E-02	7.44E-01		-6.69E-01	3.12E-01		-1.96E+00	3.98E-03				Unigene41045_All//5.00E-153//BF273068				
Unigene41046_All	360	1.02	0.28	0.00	1.52	0.86	1.25	14.68	18.46	35.63	-1.85E+00	1.87E-01		-9.99E+00	2.78E-02		-8.22E-01	3.96E-01		-2.79E-01	7.57E-01		3.31E-01	1.24E-01		1.28E+00	7.11E-18	Up			Unigene41046_All//3.00E-174//DT468581				
Unigene41047_All	482	0.22	0.00	0.22	2.79	0.71	1.50	1.05	1.04	1.98	-7.76E+00	3.71E-01		2.57E-02	1.00E+00		-1.97E+00	7.30E-04	Down	-8.96E-01	1.30E-01		-1.65E-02	1.02E+00		9.14E-01	1.38E-01								
Unigene41048_All	398	8.94	6.11	11.64	9.14	11.68	8.28	40.26	31.08	16.62	-5.49E-01	9.40E-02		3.81E-01	2.12E-01		3.54E-01	2.35E-01		-1.41E-01	6.78E-01		-3.73E-01	2.95E-03		-1.28E+00	3.04E-22	Down			Unigene41048_All//2.00E-141//gi|11202080|gb|BF271085.1|BF271085				
Unigene41049_All	1162	0.81	2.01	1.37	0.34	0.09	0.54	3.02	5.11	1.41	1.31E+00	2.46E-03		7.62E-01	1.60E-01		-1.95E+00	1.19E-01		6.66E-01	4.92E-01		7.58E-01	4.64E-04		-1.10E+00	1.38E-04	Down	Unigene41049_All//gi|4530126|gb|AA021872.1|//2.00E-80//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene41049_All//5.00E-46//AT3G22060| receptor protein kinase-related	Unigene41049_All//4.00E-59//TC172433		ko04626|Plant-pathogen interaction		nr -
Unigene4105_All	3082	0.03	0.10	0.00	0.03	0.04	0.03	4.79	1.36	8.73	1.54E+00	3.23E-01		-5.09E+00	3.93E-01		4.69E-01	8.76E-01		-1.41E-01	9.50E-01		-1.82E+00	5.29E-33	Down	8.66E-01	9.27E-20		Unigene4105_All//gi|199601718|dbj|BAG70977.1|//0.00E+00//glycosyl transferase family 2 protein [Musa balbisiana]	Unigene4105_All//0.00E+00//AT5G60700| glycosyltransferase family protein 2	Unigene4105_All//2.00E-162//DT462702				nr +
Unigene41050_All	1447	0.00	0.00	0.00	0.00	0.00	0.00	1.87	3.09	20.98	null	null		null	null		null	null		null	null		7.25E-01	4.44E-03		3.49E+00	2.86E-142	Up	Unigene41050_All//gi|15241569|ref|NP_199290.1|//2.00E-46//DC1 domain-containing protein [Arabidopsis thaliana] >gi|9758381|dbj|BAB08830.1| CHP-rich zinc finger protein-like [Arabidopsis thaliana] >gi|67633858|gb|AAY78853.1| DC1 domain-containing protein [Arabidopsis thaliana]	Unigene41050_All//5.00E-44//AT5G44770| DC1 domain-containing protein	Unigene41050_All//6.00E-139//TC162929				nr +
Unigene41051_All	548	4.58	3.24	2.23	1.73	0.31	0.16	0.00	0.00	0.00	-5.02E-01	2.17E-01		-1.04E+00	1.40E-02		-2.46E+00	1.25E-03		-3.39E+00	3.17E-04	Down	null	null		null	null				Unigene41051_All//7.00E-81//TC170637				
Unigene41052_All	511	1.33	5.75	6.15	5.56	3.77	3.80	0.50	0.65	0.39	2.11E+00	4.94E-07	Up	2.21E+00	1.56E-07	Up	-5.58E-01	1.28E-01		-5.48E-01	1.53E-01		3.98E-01	7.24E-01		-3.49E-01	7.66E-01				Unigene41052_All//1.00E-91//TC163553				
Unigene41053_All	1214	0.26	0.25	0.18	5.05	2.52	1.41	21.73	4.20	3.15	-4.65E-02	9.84E-01		-5.59E-01	6.63E-01		-1.00E+00	6.60E-06		-1.84E+00	1.39E-12	Down	-2.37E+00	6.68E-82	Down	-2.79E+00	2.27E-101	Down	Unigene41053_All//gi|42568214|ref|NP_198840.2|//9.00E-92//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|10177511|dbj|BAB10905.1| nodulin-like protein [Arabidopsis thaliana] >gi|30725298|gb|AAP37671.1| At5g40240 [Arabidopsis thaliana]	Unigene41053_All//8.00E-86//AT5G40240| nodulin MtN21 family protein	Unigene41053_All//3.00E-17//TC169820				nr -
Unigene41054_All	804	5.47	1.58	0.00	0.99	0.17	0.45	32.13	60.72	47.07	-1.79E+00	2.05E-08	Down	-1.24E+01	3.37E-24	Down	-2.53E+00	3.08E-03		-1.14E+00	1.63E-01		9.18E-01	8.29E-38		5.51E-01	6.56E-13		Unigene41054_All//gi|75099990|sp|Q80920.1|PYL4_ARATH//4.00E-64//RecName: Full=Abscisic acid receptor PYL4; AltName: Full=PYR1-like protein 4; AltName: Full=ABI1-binding protein 2; AltName: Full=Regulatory components of ABA receptor 10 >gi|3395441|gb|AAC28773.1| expressed protein [Arabidopsis thaliana] >gi|14517502|gb|AAK62641.1| At2g38310/T19C21.20 [Arabidopsis thaliana] >gi|15809748|gb|AAL06802.1| At2g38310/T19C21.20 [Arabidopsis thaliana]	Unigene41054_All//2.00E-65//AT2G38310| unknown protein	Unigene41054_All//0.00E+00//TC142937				nr +
Unigene41055_All	491	0.64	0.21	1.95	1.22	2.81	4.05	1.21	1.36	0.24	-1.63E+00	2.76E-01		1.61E+00	4.07E-02		1.20E+00	3.86E-02		1.73E+00	4.10E-04	Up	1.76E-01	8.15E-01		-2.31E+00	1.36E-02		Unigene41055_All//gi|258489633|gb|ACV72640.1|//1.00E-77//sucrose synthase 1 [Gossypium hirsutum]	Unigene41055_All//4.00E-74//AT3G43190| SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups	Unigene41055_All//0.00E+00//TC160855		ko00500|Starch and sucrose metabolism		nr -
Unigene41057_All	364	5.61	20.32	7.61	16.97	10.97	7.44	90.14	112.53	66.65	1.86E+00	3.40E-14	Up	4.40E-01	2.72E-01		-6.29E-01	4.94E-03		-1.19E+00	6.02E-07	Down	3.20E-01	1.78E-05		-4.35E-01	1.06E-07				Unigene41057_All//1.00E-90//TC154214				
Unigene41058_All	394	2.39	0.00	0.00	2.53	3.06	3.55	0.86	0.21	0.10	-1.12E+01	1.46E-05	Down	-1.12E+01	3.34E-05	Down	2.75E-01	7.00E-01		4.91E-01	4.19E-01		-2.02E+00	1.36E-01		-3.09E+00	3.92E-02		Unigene41058_All//gi|297806919|ref|XP_002871343.1|//4.00E-16//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317180|gb|EFH47602.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene41058_All//6.00E-12//AT5G08510| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene4106_All	1145	0.00	0.04	0.00	0.22	0.24	0.16	1.85	2.26	28.60	5.47E+00	6.16E-01		null	null		1.46E-01	9.61E-01		-4.63E-01	7.44E-01		2.94E-01	4.34E-01		3.95E+00	1.09E-169	Up	Unigene4106_All//gi|30697417|ref|NP_200878.2|//1.00E-157//glycosyltransferase family protein 2 [Arabidopsis thaliana]	Unigene4106_All//3.00E-153//AT5G60700| glycosyltransferase family protein 2					nr -
Unigene41060_All	266	0.39	3.62	0.00	2.06	0.65	0.85	0.64	1.26	1.95	3.20E+00	6.55E-04	Up	-8.62E+00	3.93E-01		-1.67E+00	9.26E-02		-1.28E+00	2.24E-01		9.83E-01	4.24E-01		1.61E+00	8.80E-02				Unigene41060_All//1.00E-132//TC148376				
Unigene41061_All	346	31.91	45.84	29.55	30.67	22.89	25.45	71.97	77.55	35.12	5.23E-01	1.84E-04		-1.11E-01	5.93E-01		-4.22E-01	1.23E-02		-2.69E-01	1.55E-01		1.08E-01	3.34E-01		-1.04E+00	1.33E-24	Down			Unigene41061_All//4.00E-146//gi|164335267|gb|ES816919.1|ES816919		ko03010|Ribosome		kegg -
Unigene41067_All	353	1.19	0.00	0.00	0.71	0.39	1.02	2.40	1.66	0.34	-1.02E+01	1.05E-02		-1.02E+01	1.56E-02		-8.55E-01	5.73E-01		5.37E-01	6.94E-01		-5.31E-01	4.45E-01		-2.82E+00	5.38E-04	Down			Unigene41067_All//7.00E-55//C0097097				
Unigene4107_All	2050	2.91	4.72	2.78	6.39	5.24	8.42	6.37	12.97	5.93	6.98E-01	1.53E-04		-6.60E-02	7.98E-01		-2.86E-01	7.01E-02		3.97E-01	2.94E-03		1.02E+00	5.44E-25	Up	-1.05E-01	5.10E-01		Unigene4107_All//gi|115434234|ref|NP_001041875.1|//1.00E-127//Os01g0121300 [Oryza sativa Japonica Group] >gi|113531406|dbj|BAF03789.1| Os01g0121300 [Oryza sativa Japonica Group]	Unigene4107_All//0.00E+00//AT1G71110| unknown protein	Unigene4107_All//0.00E+00//TC161833				nr -
Unigene41074_All	982	0.00	0.00	0.00	0.10	0.14	0.00	1.85	3.96	46.45	null	null		null	null		4.67E-01	8.76E-01		-6.67E+00	3.99E-01		1.10E+00	9.51E-05	Up	4.65E+00	2.94E-263	Up	Unigene41074_All//gi|62766606|gb|AY39411.1|//1.00E-112//patatin-like protein [Gossypium hirsutum]	Unigene41074_All//3.00E-92//AT2G26560| PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	Unigene41074_All//5.00E-92//gi|3326630|gb|AI055516.1|AI055516				nr +
Unigene41075_All	530	3.36	0.76	1.81	2.35	1.49	0.68	0.00	0.00	0.00	-2.13E+00	1.23E-04	Down	-8.92E-01	8.34E-02		-6.53E-01	2.80E-01		-1.79E+00	5.55E-03		null	null		null	null				Unigene41075_All//2.00E-07//TC129913				
Unigene41076_All	471	2.33	0.11	0.23	3.07	7.75	3.93	0.00	0.00	0.00	-4.44E+00	2.09E-05	Down	-3.37E+00	2.67E-04	Down	1.34E+00	2.65E-05	Up	3.58E-01	4.95E-01		null	null		null	null		Unigene41076_All//gi|224072455|ref|XP_002303740.1|//3.00E-39//GH3 family protein [Populus trichocarpa] >gi|222841172|gb|EEE78719.1| GH3 family protein [Populus trichocarpa]	Unigene41076_All//8.00E-37//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene41076_All//4.00E-88//TC147747				nr +
Unigene41077_All	351	68.57	34.36	47.64	81.32	100.85	122.37	221.28	103.83	106.24	-9.97E-01	7.32E-18		-5.26E-01	4.54E-06		3.11E-01	3.02E-04		5.90E-01	8.34E-14		-1.09E+00	2.85E-79	Down	-1.06E+00	1.42E-77	Down	Unigene41077_All//gi|57471698|gb|AW50980.1|//2.00E-24//ribosomal protein L36 [Triticum aestivum]	Unigene41077_All//2.00E-23//AT5G02450| 60S ribosomal protein L36 (RPL36C)	Unigene41077_All//1.00E-167//TC164702		ko03010|Ribosome		nr -
Unigene41078_All	723	4.85	6.17	12.74	1.58	1.29	0.25	0.00	0.75	0.22	3.47E-01	2.37E-01		1.39E+00	2.18E-11	Up	-3.01E-01	6.23E-01		-2.66E+00	4.12E-04	Down	9.55E+00	5.36E-04	Up	7.78E+00	1.40E-01		Unigene41078_All//gi|87162753|gb|AB028548.1|//9.00E-67//Protein kinase; Type I EGF [Medicago truncatula]	Unigene41078_All//7.00E-43//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase	Unigene41078_All//9.00E-07//TC166725				nr -
Unigene41079_All	874	1.14	1.16	0.61	11.00	9.26	3.15	1.40	0.77	1.09	2.78E-02	9.86E-01		-9.01E-01	2.22E-01		-2.49E-01	2.08E-01		-1.80E+00	5.61E-19	Down	-8.75E-01	1.13E-01		-3.59E-01	5.10E-01		Unigene41079_All//gi|224589461|gb|ACN59264.1|//1.00E-63//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene41079_All//2.00E-52//AT1G66150| TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase	Unigene41079_All//7.00E-17//TC165297				nr +
Unigene41080_All	1321	0.00	0.00	0.00	0.00	0.00	0.00	10.95	14.21	5.25	null	null		null	null		null	null		null	null		3.76E-01	1.03E-03		-1.06E+00	3.22E-15	Down			Unigene41080_All//9.00E-36//CF932145				
Unigene41081_All	344	1.67	3.24	2.79	3.77	3.20	3.28	10.45	6.56	5.21	9.54E-01	1.40E-01		7.36E-01	3.23E-01		-2.33E-01	7.05E-01		-1.98E-01	7.33E-01		-6.71E-01	2.06E-02		-1.00E+00	3.90E-04	Down			Unigene41081_All//2.00E-89//TC163820				
Unigene41082_All	1874	0.06	0.00	0.00	0.32	0.04	0.00	12.52	7.16	8.31	-5.80E+00	3.71E-01		-5.80E+00	3.92E-01		-3.12E+00	4.87E-03		-8.32E+00	7.70E-04	Down	-8.07E-01	4.23E-15		-5.91E-01	2.15E-09		Unigene41082_All//gi|15227721|ref|NP_180580.1|//0.00E+00//LAC3 (laccase 3); laccase [Arabidopsis thaliana] >gi|143344116|sp|Q56YT0.2|LAC3_ARATH RecName: Full=Laccase-3; AltName: Full=Benzenediol:oxygen oxidoreductase 3; AltName: Full=Urishiol oxidase 3; AltName: Full=Diphenol oxidase 3; Flags: Precursor	Unigene41082_All//0.00E+00//AT2G30210| LAC3 (laccase 3); laccase	Unigene41082_All//2.00E-12//TC165735		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene41083_All	341	427.77	165.08	87.29	280.92	294.16	208.86	247.98	57.97	60.87	-1.37E+00	4.40E-174	Down	-2.29E+00	0.00E+00	Down	6.65E-02	2.87E-01		-4.28E-01	4.24E-17		-2.10E+00	2.67E-224	Down	-2.03E+00	5.15E-221	Down	Unigene41083_All//gi|298712420|emb|CBJ33198.1|//7.00E-45//histone H4 [Ectocarpus siliculosus]	Unigene41083_All//6.00E-33//AT5G59970| histone H4	Unigene41083_All//8.00E-175//TC169994				nr +
Unigene41084_All	433	1.09	0.59	1.72	1.61	1.11	1.67	0.29	0.39	1.93	-8.94E-01	3.89E-01		6.63E-01	4.19E-01		-5.33E-01	5.45E-01		5.13E-02	9.48E-01		3.99E-01	8.14E-01		2.72E+00	8.98E-04	Up	Unigene41084_All//gi|117606933|gb|ABK32021.1|//6.00E-06//vegetative cell wall protein [Chlamydomonas incerta]						nr +
Unigene41085_All	1404	0.00	0.04	0.00	0.14	0.00	0.00	10.24	15.54	5.05	5.17E+00	6.16E-01		null	null		-7.15E+00	8.42E-02		-7.15E+00	1.33E-01		6.02E-01	9.28E-09		-1.02E+00	3.08E-14	Down	Unigene41085_All//gi|301016726|dbj|BAJ11784.1|//2.00E-30//dehydration responsive protein [Corchorus olitorius]		Unigene41085_All//0.00E+00//gi|109849827|gb|DW478806.1|DW478806				nr +
Unigene41087_All	521	1.81	0.58	0.51	3.92	3.04	0.95	0.16	0.32	0.00	-1.63E+00	3.13E-02		-1.82E+00	2.53E-02		-3.67E-01	4.38E-01		-2.04E+00	3.45E-05	Down	9.84E-01	6.33E-01		-7.34E+00	3.58E-01		Unigene41087_All//gi|115489730|ref|NP_001067352.1|//7.00E-58//Os12g0633600 [Oryza sativa Japonica Group] >gi|113649859|dbj|BAF30371.1| Os12g0633600 [Oryza sativa Japonica Group]	Unigene41087_All//4.00E-43//AT1G58520| hydrolase, acting on ester bonds / lipase	Unigene41087_All//9.00E-77//TC172450				nr -
Unigene41089_All	691	0.08	0.37	1.85	1.15	2.04	1.05	4.96	3.15	1.96	2.28E+00	2.34E-01		4.61E+00	5.51E-06	Up	8.25E-01	1.57E-01		-1.41E-01	8.60E-01		-6.56E-01	2.80E-02		-1.34E+00	8.81E-06	Down			Unigene41089_All//3.00E-28//DR455549				
Unigene41090_All	701	0.37	0.43	0.76	0.50	0.15	1.16	4.64	18.60	17.90	2.17E-01	8.65E-01		1.03E+00	3.42E-01		-1.75E+00	1.90E-01		1.22E+00	1.40E-01		2.00E+00	4.57E-33	Up	1.95E+00	2.23E-31	Up			Unigene41090_All//3.00E-65//gi|3326430|gb|AI055316.1|AI055316				

Unigene41093_All	299	6.82	1.36	1.96	13.99	2.99	1.06	0.85	0.28	0.40	-2.33E+00	1.04E-05	Down	-1.80E+00	4.36E-04	Down	-2.22E+00	1.15E-12	Down	-3.73E+00	1.59E-18	Down	-1.60E+00	3.10E-01		-1.09E+00	4.28E-01		Unigene41093_All|gi|11994125|dbj|BAB01127.1||9.00E-15||nodulin MtN21-like protein [Arabidopsis thaliana]	Unigene41093_All||3.00E-13||AT3G28050| nodulin MtN21 family protein	Unigene41093_All||3.00E-106||TC148144				nr -
Unigene41097_All	588	0.00	0.00	0.00	0.00	0.00	0.00	19.63	20.83	1.96	null	null		null	null		null	null		null	null		8.54E-02	6.54E-01		-3.32E+00	3.80E-53	Down	Unigene41097_All|gi|145408590|ref|XP_001152214.1||4.00E-10||ORF124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1|ORF124 [Pinus koraiensis]		Unigene41097_All||3.00E-21||TC134836				nr +
Unigene411_All	1046	3.85	1.70	2.85	3.86	3.13	4.23	5.01	2.96	2.55	-1.18E+00	1.41E-04	Down	-4.34E-01	1.81E-01		-3.03E-01	3.45E-01		1.34E-01	6.97E-01		-7.61E-01	1.04E-03		-9.74E-01	2.11E-05		Unigene411_All|gi|42569749|ref|NP_181418.2||1.00E-141||guanylate-binding family protein [Arabidopsis thaliana]	Unigene411_All||1.00E-134||AT2G38840| guanylate-binding family protein	Unigene411_All||0.00E+00||DR456758				nr -
Unigene4110_All	1296	3.11	4.85	2.55	11.07	8.05	6.17	50.27	41.51	22.72	6.41E-01	6.51E-03		-2.87E-01	3.85E-01		-4.59E-01	9.40E-04		-8.44E-01	5.94E-09		-2.77E-01	1.98E-06		-1.15E+00	4.69E-74	Down	Unigene4110_All|gi|113367238|gb|AB134676.1||3.00E-45||bZIP transcription factor bZIP16 [Glycine max]	Unigene4110_All||8.00E-31||AT5G24800| BZIP9 (BASIC LEUCINE ZIPPER 9); DNA binding / protein heterodimerization/ transcription factor	Unigene4110_All||0.00E+00||TC165148	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene41100_All	298	5.79	1.36	9.29	8.36	8.90	10.15	1.28	0.42	0.94	-2.09E+00	1.98E-04	Down	6.81E-01	8.53E-02		9.03E-02	8.34E-01		2.81E-01	4.81E-01		-1.60E+00	1.81E-01		-4.48E-01	6.41E-01		Unigene41100_All|gi|255542890|ref|XP_002512508.1||5.00E-13||pentatricopeptide repeat-containing protein, putative [Ricinus communis] >gi|223548469|gb|EEF49960.1|pentatricopeptide repeat-containing protein, putative [Ricinus communis]	Unigene41100_All||1.00E-05||AT1G09820| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene41102_All	437	0.00	2.20	2.56	3.76	4.41	9.20	0.97	0.48	0.55	1.11E+01	1.38E-05	Up	1.13E+01	3.43E-06	Up	2.30E-01	6.62E-01		1.29E+00	3.16E-05	Up	-1.02E+00	3.50E-01		-8.23E-01	3.99E-01		Unigene41102_All|gi|18146714|dbj|BAB82419.1||4.00E-14||acid invertase [Citrus unshiu]	Unigene41102_All||3.00E-11||AT1G12240| ATBETAFRUCT4; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene41102_All||0.00E+00||TC146217		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene41103_All	381	2.20	0.13	2.24	0.52	0.54	0.47	1.55	1.65	0.00	-4.05E+00	4.65E-04	Down	2.54E-02	9.93E-01		5.23E-02	9.88E-01		-1.41E-01	9.34E-01		8.29E-02	9.32E-01		-1.06E+01	1.41E-04	Down								
Unigene41106_All	690	0.00	0.00	0.00	0.00	0.00	0.07	79.60	7.75	46.54	null	null		null	null		null	null		6.03E+00	6.95E-01		-3.36E+00	1.85E-245	Down	-7.74E-01	6.84E-33		Unigene41106_All|gi|86156028|gb|ABC86745.1||3.00E-38||pollen-specific protein [Vitis pseudoreticulata]	Unigene41106_All||1.00E-29||AT5G10130| pollen Ole e 1 allergen and extensin family protein	Unigene41106_All||2.00E-84||gi|31073609|gb|CA993888.1|CA993888				nr -
Unigene41107_All	577	0.00	0.35	0.37	1.21	0.24	0.00	4.40	4.85	0.97	8.46E+00	1.36E-01		8.53E+00	1.41E-01		-2.34E+00	1.01E-02		-1.02E+01	1.96E-04	Down	1.43E-01	6.91E-01		-2.19E+00	4.48E-08	Down			Unigene41107_All||7.00E-10||TC169323				
Unigene41108_All	418	0.00	1.70	0.00	0.95	0.66	1.73	6.27	7.60	33.36	1.07E+01	3.33E-04	Up	null	null		-5.33E-01	6.16E-01		8.59E-01	3.42E-01		2.77E-01	4.06E-01		2.41E+00	3.22E-45	Up	Unigene41108_All|gi|224053945|ref|XP_002298051.1||2.00E-10||predicted protein [Populus trichocarpa] >gi|222845309|gb|EEE82856.1|predicted protein [Populus trichocarpa]		Unigene41108_All||5.00E-10||ES790396				nr -
Unigene41109_All	475	46.59	24.75	23.21	70.58	61.69	90.04	114.47	43.91	50.24	-9.13E-01	2.45E-14		-1.01E+00	5.20E-16	Down	-1.94E-01	4.14E-02		3.51E-01	1.01E-05		-1.38E+00	1.74E-80	Down	-1.19E+00	1.44E-65	Down			Unigene41109_All||1.00E-174||gi|164314090|gb|ES814752.1|ES814752				
Unigene41112_All	262	3.20	2.90	2.44	19.39	17.35	22.06	15.17	13.88	59.45	-1.39E-01	8.39E-01		-3.90E-01	6.41E-01		-1.61E-01	5.92E-01		1.86E-01	5.18E-01		-1.28E-01	6.63E-01		1.97E+00	2.24E-39	Up	Unigene41112_All|gi|223452391|gb|ACM89523.1||1.00E-10||protein kinase family protein [Glycine max]	Unigene41112_All||4.00E-08||AT5G24010| protein kinase family protein					nr -
Unigene41113_All	1838	0.00	0.00	0.00	0.22	0.26	0.74	0.48	45.57	1.97	null	null		null	null		2.75E-01	8.20E-01		1.77E+00	4.50E-03		6.56E+00	0.00E+00	Up	2.03E+00	3.95E-10	Up	Unigene41113_All|gi|115440781|ref|NP_001044670.1||1.00E-127||Os01g0825500 [Oryza sativa Japonica Group] >gi|14587357|dbj|BAB61258.1|nodulin-like protein [Oryza sativa Japonica Group] >gi|21104610|dbj|BAB93203.1|nodulin-like protein [Oryza sativa Japonica Group] >gi|113534201|dbj|BAF06584.1|Os01g0825500 [Oryza sativa Japonica Group]	Unigene41113_All||2.00E-45||AT2G30300| nodulin-related					nr +
Unigene41117_All	1653	0.00	0.00	0.00	0.24	0.44	0.33	10.79	1.11	1.16	null	null		null	null		8.60E-01	3.36E-01		4.44E-01	6.78E-01		-3.28E+00	2.95E-78	Down	-3.22E+00	1.52E-79	Down	Unigene41117_All|gi|186499036|ref|NP_001118256.1||1.00E-108||transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene41117_All||2.00E-106||AT2G03360| transferase, transferring glycosyl groups					nr -
Unigene41120_All	632	0.33	1.28	0.42	0.55	1.91	1.36	3.88	5.49	14.06	1.95E+00	2.43E-02		3.48E-01	7.97E-01		1.79E+00	6.51E-03		1.30E+00	1.07E-01		5.00E-01	9.75E-02		1.86E+00	3.91E-21	Up	Unigene41120_All|gi|115338597|gb|AB194388.1||3.00E-16||isopentyl diphosphate isomerase [Gossypium barbadense]	Unigene41120_All||2.00E-15||AT5G16440| IPP1 (ISOPENTENYL DIPHOSPHATE ISOMERASE 1); isopentenyl-diphosphate delta-isomerase	Unigene41120_All||2.00E-96||TC132436		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene41122_All	1993	0.29	0.36	0.21	0.82	0.69	0.93	1.19	0.84	3.40	3.01E-01	6.93E-01		-4.35E-01	6.23E-01		-2.55E-01	6.15E-01		1.72E-01	7.30E-01		-5.02E-01	1.88E-01		1.52E+00	1.83E-12	Up	Unigene41122_All|gi|224075299|ref|XP_002304589.1||4.00E-31||nbs-lrr resistance protein [Populus trichocarpa] >gi|222842021|gb|EEE79568.1|nbs-lrr resistance protein [Populus trichocarpa]	Unigene41122_All||2.00E-20||AT3G46730| disease resistance protein (CC-NBS class), putative			ko04626|Plant-pathogen interaction		nr +
Unigene41123_All	267	0.20	6.26	2.19	2.05	2.84	1.01	0.95	0.16	2.09	5.00E+00	2.47E-08	Up	3.48E+00	1.21E-02		4.67E-01	6.07E-01		-1.02E+00	3.29E-01		-2.60E+00	1.44E-01		1.14E+00	1.91E-01				Unigene41123_All||3.00E-07||TC146732				
Unigene41126_All	1839	0.00	0.00	0.00	0.00	0.00	0.00	7.43	0.34	3.51	null	null		null	null		null	null		null	null		-4.45E+00	5.27E-76	Down	-1.08E+00	7.47E-15	Down	Unigene41126_All|gi|117940159|sp|P93051.2|ERD6_ARATH||1.00E-149||RecName: Full=Sugar transporter ERD6-like 7	Unigene41126_All||7.00E-141||AT2G48020| sugar transporter, putative	Unigene41126_All||0.00E+00||TC145382				nr -
Unigene41128_All	395	1.06	2.31	2.70	1.89	1.39	1.60	0.32	0.74	2.52	1.12E+00	1.30E-01		1.35E+00	6.01E-02		-4.40E-01	5.85E-01		-2.41E-01	7.56E-01		1.21E+00	3.92E-01		2.97E+00	1.11E-04	Up	Unigene41128_All|gi|145358042|ref|NP_197006.2||7.00E-18||SNL2 (SIN3-LIKE 2) [Arabidopsis thaliana] >gi|296439819|sp|Q9LFQ3.2|SNL2_ARATH RecName: Full=Paired amphipathic helix protein Sin3-like 2	Unigene41128_All||2.00E-14||AT5G15020| SNL2 (SIN3-LIKE 2)	Unigene41128_All||6.00E-65||ES814309				nr -
Unigene41129_All	308	301.69	280.49	305.32	1095.59	1359.63	556.77	200.42	39.35	64.03	-1.05E-01	7.31E-02		1.72E-02	7.87E-01		3.12E-01	7.36E-45		-9.77E-01	2.89E-253		-2.35E+00	1.11E-188	Down	-1.65E+00	1.76E-121	Down	Unigene41129_All|gi|73761701|gb|AA283350.1||1.00E-40||aquaporin [Gossypium hirsutum]	Unigene41129_All||6.00E-35||AT2G16850| PIP2;8 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;8); water channel	Unigene41129_All||6.00E-166||gi|13349680|gb|BG440030.1|BG440030				nr +
Unigene4113_All	1367	37.55	26.47	17.41	202.68	101.32	50.19	161.54	16.17	11.19	-5.05E-01	7.46E-12		-1.11E+00	1.31E-42	Down	-1.00E+00	2.16E-247	Down	-2.01E+00	0.00E+00	Down	-3.32E+00	0.00E+00	Down	-3.85E+00	0.00E+00	Down	Unigene4113_All|gi|124109191|gb|ABM91071.1||1.00E-140||xyloglucan endotransglycosylase/hydrolase precursor XTH-14 [Populus tremula x Populus tremuloides]	Unigene4113_All||1.00E-122||AT3G23730| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene4113_All||0.00E+00||TC144610				nr -
Unigene41132_All	1241	0.21	2.45	1.20	2.37	3.44	2.33	1.36	0.17	0.55	3.54E+00	5.79E-12	Up	2.51E+00	1.98E-04	Up	5.39E-01	6.87E-02		-2.41E-02	9.54E-01		-3.02E+00	2.08E-07	Down	-1.32E+00	3.08E-03		Unigene41132_All|gi|15218566|ref|NP_174686.1||2.00E-85||phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] >gi|5091620|gb|AAD29608.1|AC007454_7 Contains similarity to gi|836774 FAB1 protein from Saccharomyces cerevisiae genome gb|BS06617 [Arabidopsis thaliana]	Unigene41132_All||9.00E-83||AT1G34260| phosphatidylinositol-4-phosphate 5-kinase family protein			ko04145|Phagosome//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene41136_All	449	1.63	3.39	4.98	1.89	2.99	2.82	1.22	2.42	2.48	1.05E+00	5.24E-02		1.61E+00	6.62E-04	Up	6.65E-01	2.81E-01		5.78E-01	3.77E-01		9.83E-01	9.75E-02		1.02E+00	6.87E-02		Unigene41136_All|gi|238478362|ref|NP_001154308.1||2.00E-30||binding [Arabidopsis thaliana]	Unigene41136_All||1.00E-31||AT1G05960| binding	Unigene41136_All||1.00E-54||TC147064				nr -
Unigene41139_All	1161	0.00	16.76	5.92	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	6.28E-112	Up	1.25E+01	2.29E-38	Up	null	null		null	null		null	null		null	null		Unigene41139_All|gi|159476624|ref|XP_001696361.1||3.00E-52||vacuolar H(+)-ATPase V0 sector, c/c' subunits [Chlamydomonas reinhardtii] >gi|158282586|gb|EDP08338.1|vacuolar H(+)-ATPase V0 sector, c/c' subunits [Chlamydomonas reinhardtii]	Unigene41139_All||8.00E-51||AT4G34720| AVA-P1; ATPase/ proton-transporting ATPase, rotational mechanism			ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene4114_All	1259	7.56	10.18	6.30	4.87	8.01	4.84	7.29	4.05	2.91	4.29E-01	6.93E-03		-2.63E-01	2.04E-01		7.20E-01	2.28E-05		-7.10E-03	9.72E-01		-8.47E-01	6.80E-07		-1.32E+00	8.16E-14	Down	Unigene4114_All||2.00E-48||AT1G65420| unknown protein		Unigene4114_All||0.00E+00||gi|5048283|gb|AI729431.1|AI729431				nr +
Unigene41141_All	432	1.70	0.23	0.49	2.42	0.72	0.73	1.37	0.00	1.01	-2.85E+00	6.26E-03		-1.78E+00	6.00E-02		-1.76E+00	8.43E-03		-1.73E+00	1.55E-02		-1.04E+01	2.39E-04	Down	-4.34E-01	6.08E-01		Unigene41141_All|gi|255543389|ref|XP_002512757.1||2.00E-06||Tubby protein, putative [Ricinus communis] >gi|223547768|gb|EEF49260.1| Tubby protein, putative [Ricinus communis]		Unigene41141_All||0.00E+00||gi|78352241|gb|DT572515.1|DT572515				nr +
Unigene41142_All	856	0.92	0.00	0.75	1.63	2.78	2.32	1.73	0.54	1.21	-9.84E+00	1.09E-04	Down	-2.97E-01	6.97E-01		7.69E-01	6.35E-02		5.11E-01	3.03E-01		-1.69E+00	1.15E-03		-5.15E-01	2.80E-01		Unigene41142_All|gi|18400752|ref|NP_566511.1||5.00E-96||choline transporter-related [Arabidopsis thaliana]	Unigene41142_All||4.00E-97||AT3G15380| choline transporter-related	Unigene41142_All||0.00E+00||AW187145				nr -
Unigene41143_All	407	3.09	0.50	1.31	2.69	2.88	1.44	0.93	0.21	0.10	-2.63E+00	3.16E-04	Down	-1.24E+00	5.53E-02		9.54E-02	9.01E-01		-9.00E-01	1.81E-01		-2.19E+00	8.75E-02		-3.26E+00	2.22E-02		Unigene41143_All|gi|297822415|ref|XP_002879090.1||1.00E-47||sec23/sec24 transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324929|gb|EFH55349.1|sec23/sec24 transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene41143_All||1.00E-48||AT3G27460| sec23/sec24 transport family protein	Unigene41143_All||7.00E-117||DR457441				nr -
Unigene41144_All	1094	0.00	0.00	0.00	0.00	0.00	0.45	7.61	2.90	23.74	null	null		null	null		null	null		8.83E+00	4.38E-03		-1.39E+00	4.16E-13	Down	1.64E+00	8.39E-51	Up	Unigene41144_All|gi|297850166|ref|XP_002892964.1||3.00E-96||phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297338806|gb|EFH69223.1|phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene41144_All||5.00E-95||AT1G17710| phosphatase	Unigene41144_All||0.00E+00||TC172862				nr -
Unigene41145_All	416	0.00	0.37	0.00	0.00	0.08	0.00	3.56	4.82	9.77	8.51E+00	2.35E-01		null	null		6.37E+00	8.29E-01		null	null		4.39E-01	3.08E-01		1.46E+00	2.02E-07	Up			Unigene41145_All||5.00E-112||DN800146				

Unigene41147_All	404	1.17	0.25	1.45	5.43	2.47	1.12	3.77	0.00	0.99	-2.22E+00	7.76E-02		3.15E-01	7.19E-01		-1.13E+00	5.60E-03		-2.28E+00	3.02E-06	Down	-1.19E+01	8.51E-11	Down	-1.93E+00	1.54E-04	Down	Unigene41147_All//gi|15234961|ref|NP_195625.1|//1.00E-16//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|30692196|ref|NP_849522.1| protein binding / zinc ion binding [Arabidopsis thaliana] >gi|42573229|ref|NP_974711.1| protein binding / zinc ion binding [Arabidopsis thaliana] >gi|42573231|ref|NP_974712.1| protein binding / zinc ion binding [Arabidopsis thaliana] >gi|145334267|ref|NP_001078514.1| protein binding / zinc ion binding [Arabidopsis thaliana] >gi|66865958|gb|AAY57613.1| RING finger family protein [Arabidopsis thaliana]	Unigene41147_All//7.00E-18//AT4G39140| protein binding / zinc ion binding	Unigene41147_All//1.00E-155//C0089808					nr -
Unigene4115_All	1963	1.79	4.34	2.20	6.60	5.44	5.80	4.67	6.39	5.60	1.28E+00	9.49E-10	Up	2.99E-01	3.61E-01		-2.79E-01	8.16E-02		-1.87E-01	3.01E-01		4.51E-01	1.61E-03		2.61E-01	9.51E-02		Unigene4115_All//gi|226496665|ref|NP_001147987.1|//2.00E-92//ribosomal protein L11 methyltransferase containing protein [Zea mays] >gi|195614998|gb|ACG29329.1| ribosomal protein L11 methyltransferase containing protein [Zea mays]	Unigene4115_All//3.00E-85//AT5G44280| RING1A (RING 1A); protein binding / zinc ion binding					nr -
Unigene41151_All	707	0.22	0.07	0.00	6.62	3.75	3.19	3.23	0.41	0.11	-1.63E+00	4.89E-01		-7.79E+00	2.44E-01		-8.21E-01	1.59E-03		-1.05E+00	1.38E-04	Down	-2.96E+00	1.24E-09	Down	-4.84E+00	3.22E-14	Down	Unigene41151_All//gi|224053447|ref|XP_002297821.1|//4.00E-19//predicted protein [Populus trichocarpa] >gi|222845079|gb|EEE82626.1| predicted protein [Populus trichocarpa]	Unigene41151_All//2.00E-06//AT1G55475| unknown protein					nr -
Unigene41152_All	886	0.47	0.23	0.24	0.22	0.08	0.00	9.69	2.64	3.96	-1.05E+00	3.66E-01		-9.75E-01	4.11E-01		-1.53E+00	4.15E-01		-7.81E+00	1.33E-01		-1.87E+00	2.77E-20	Down	-1.29E+00	1.57E-12	Down	Unigene41152_All//gi|157955935|gb|ABW06391.1|//1.00E-106//CBL8 [Gossypium hirsutum]	Unigene41152_All//1.00E-71//AT5G24270| SOS3 (SALT OVERLY SENSITIVE 3); calcium ion binding / calcium-dependent protein serine/threonine phosphatase	Unigene41152_All//0.00E+00//TC156917		ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene41154_All	534	0.00	103.05	34.50	0.00	0.64	1.61	0.00	1.41	4.77	1.67E+01	0.00E+00	Up	1.51E+01	4.68E-104	Up	9.33E+00	3.01E-02		1.07E+01	3.79E-05	Up	1.05E+01	2.07E-05	Up	1.22E+01	2.96E-18	Up	Unigene41154_All//gi|28416855|gb|AA042958.1|//1.00E-11//At5g15190 [Arabidopsis thaliana]		Unigene41154_All//0.00E+00//CA993777				nr +
Unigene41157_All	910	0.92	0.67	0.53	1.20	1.67	1.39	1.72	0.32	0.74	-4.61E-01	5.43E-01		-8.05E-01	3.22E-01		4.67E-01	4.26E-01		2.07E-01	7.34E-01		-2.42E+00	1.29E-05	Down	-1.21E+00	8.84E-03		Unigene41157_All//gi|297831754|ref|XP_002883759.1|//1.00E-71//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297326599|gb|EFH60018.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene41157_All//4.00E-71//AT2G07170| binding					nr -
Unigene41158_All	1879	0.36	0.00	0.00	0.21	0.37	0.36	1.87	1.96	5.15	-8.50E+00	4.10E-04	Down	-8.50E+00	7.64E-04	Down	7.89E-01	4.04E-01		7.65E-01	4.10E-01		6.78E-02	8.29E-01		1.46E+00	1.29E-16	Up	Unigene41158_All//gi|224138866|ref|XP_002322921.1|//1.00E-90//aldose reductase with ABC domain [Populus trichocarpa] >gi|222867551|gb|EEF04682.1| aldose reductase with ABC domain [Populus trichocarpa]	Unigene41158_All//3.00E-63//AT2G37790| aldo/keto reductase family protein	Unigene41158_All//2.00E-133//DR460967		ko00010|Glycolysis / Gluconeogenesis//ko00480|Glutathione metabolism//ko00561|Glycerolipid metabolism		nr -
Unigene41159_All	726	0.00	0.00	0.00	0.00	0.00	0.00	26.73	3.86	9.99	null	null		null	null		null	null		null	null		-2.79E+00	1.38E-72	Down	-1.42E+00	2.38E-31	Down	Unigene41159_All//gi|297848906|ref|XP_002892334.1|//3.00E-58//copper-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338176|gb|EFH68593.1| copper-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene41159_All//9.00E-59//AT1G06330| copper-binding family protein					nr -
Unigene4116_All	1382	3.41	1.21	2.54	5.70	6.08	5.13	7.59	4.81	3.78	-1.49E+00	4.42E-07	Down	-4.22E-01	1.52E-01		9.43E-02	7.11E-01		-1.51E-01	5.44E-01		-6.58E-01	2.71E-05		-1.01E+00	2.00E-10	Down	Unigene4116_All//gi|56744240|gb|AAW28560.1|//1.00E-138//At3g03210 [Arabidopsis thaliana]	Unigene4116_All//2.00E-128//AT3G03210| unknown protein	Unigene4116_All//0.00E+00//gi|164278489|gb|ES796128.1|ES796128				nr +
Unigene41162_All	501	1.15	1.21	0.64	1.89	1.86	0.99	1.52	0.17	0.40	7.92E-02	9.41E-01		-8.49E-01	3.97E-01		-2.57E-02	9.50E-01		-9.30E-01	2.06E-01		-3.19E+00	7.92E-04	Down	-1.93E+00	1.14E-02		Unigene41162_All//gi|224134769|ref|XP_002321901.1|//1.00E-27//predicted protein [Populus trichocarpa] >gi|222868897|gb|EEF06028.1| predicted protein [Populus trichocarpa]	Unigene41162_All//2.00E-15//AT5G52180| unknown protein	Unigene41162_All//0.00E+00//AW186707				nr -
Unigene41163_All	372	2.25	6.67	7.16	7.90	4.35	3.28	1.14	1.91	1.18	1.57E+00	2.51E-04	Up	1.67E+00	1.07E-04	Up	-8.61E-01	1.24E-02		-1.27E+00	5.51E-04	Down	7.49E-01	3.41E-01		5.16E-02	9.74E-01										
Unigene41164_All	342	2.75	1.48	3.74	2.18	2.22	0.00	0.25	0.00	0.00	-8.94E-01	2.14E-01		4.40E-01	4.71E-01		1.99E-02	1.00E+00		-1.11E+01	9.80E-05	Down	-7.95E+00	4.03E-01		-7.95E+00	3.58E-01				Unigene41164_All//4.00E-07//TC165317					ESTscan -
Unigene41165_All	592	0.00	0.00	0.00	2.86	0.87	0.69	1.57	1.34	4.24	null	null		null	null		-1.71E+00	5.29E-04	Down	-2.06E+00	1.87E-04	Down	-2.28E-01	7.18E-01		1.43E+00	8.46E-05	Up	Unigene41165_All//gi|99907093|gb|ABF68753.1|//1.00E-60//MADS box transcription factor [Populus tomentosa]	Unigene41165_All//5.00E-58//AT1G71692| AGL12 (AGAMOUS-LIKE 12); transcription factor		MADS			nr -
Unigene41171_All	362	63.31	32.47	20.15	48.58	36.72	81.72	91.22	27.83	30.81	-9.63E-01	3.89E-16		-1.65E+00	4.91E-35	Down	-4.04E-01	1.22E-03		7.50E-01	1.61E-14		-1.71E+00	4.27E-67	Down	-1.57E+00	7.97E-61	Down	Unigene41171_All//gi|225426162|ref|XP_002278759.1|//2.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene41171_All//2.00E-101//TC137821		ko03010|Ribosome		nr -
Unigene41172_All	553	6.62	1.92	10.11	5.04	3.55	0.74	0.00	0.00	0.22	-1.78E+00	4.41E-07	Down	6.10E-01	2.04E-02		-5.07E-01	1.74E-01		-2.78E+00	1.30E-09	Down	null	null		7.76E+00	2.43E-01		Unigene41172_All//gi|224125294|ref|XP_002319650.1|//4.00E-63//amidase family protein [Populus trichocarpa] >gi|222857926|gb|EEE95473.1| amidase family protein [Populus trichocarpa]	Unigene41172_All//2.00E-38//AT1G08980| AMI1 (AMIDASE 1); amidase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds / indoleacetamide hydrolase	Unigene41172_All//0.00E+00//TC144696				nr +
Unigene41173_All	508	0.62	0.60	0.42	0.69	1.29	1.07	0.67	2.30	2.74	-4.63E-02	9.84E-01		-5.60E-01	6.63E-01		9.08E-01	3.42E-01		6.36E-01	5.61E-01		1.79E+00	3.05E-03		2.04E+00	2.08E-04	Up			Unigene41173_All//2.00E-53//C0131101					
Unigene41176_All	986	4.72	6.01	3.89	7.78	6.18	5.73	53.09	23.19	25.17	3.48E-01	1.65E-01		-2.80E-01	3.73E-01		-3.32E-01	1.21E-01		-4.42E-01	3.90E-02		-1.20E+00	6.00E-62	Down	-1.08E+00	5.26E-54	Down			Unigene41176_All//2.00E-128//gi|21102925|gb|BQ415238.1|BQ415238					ESTscan -
Unigene41178_All	341	10.43	2.67	5.93	8.18	8.28	21.32	0.74	0.61	3.39	-1.96E+00	9.52E-08	Down	-8.14E-01	1.70E-02		1.75E-02	9.73E-01		1.38E+00	7.38E-10	Up	-2.80E-01	8.28E-01		2.19E+00	4.81E-04	Up	Unigene41178_All//gi|147858488|emb|CAN83505.1|//3.00E-12//hypothetical protein [Vitis vinifera]						nr +
Unigene41179_All	370	0.00	0.00	1.44	7.54	7.26	1.59	0.23	1.02	0.22	null	null		1.05E+01	4.04E-03		-5.46E-02	8.83E-01		-2.25E+00	1.13E-07	Down	2.15E+00	9.45E-02		-8.58E-02	9.71E-01				Unigene41179_All//2.00E-104//gi|109826190|gb|DW224911.1|DW224911					
Unigene4118_All	1558	457.52	149.08	337.58	78.01	120.66	66.38	0.92	1.02	0.66	-1.62E+00	0.00E+00	Down	-4.39E-01	2.58E-116		6.29E-01	5.99E-73		-2.33E-01	2.87E-07		1.44E-01	7.67E-01		-4.73E-01	3.37E-01		Unigene4118_All//gi|297847910|ref|XP_002891836.1|//1.00E-115//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297337678|gb|EFH68095.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene4118_All//3.00E-105//AT1G55480| binding / protein binding	Unigene4118_All//0.00E+00//TC129800				nr +
Unigene41183_All	1364	0.00	0.00	0.23	0.00	0.00	0.07	3.44	8.95	2.45	null	null		7.87E+00	4.51E-02		null	null		6.05E+00	4.76E-01		1.38E+00	1.44E-18	Up	-4.88E-01	4.35E-02		Unigene41183_All//gi|145839451|gb|ABP96804.1|//1.00E-117//receptor-like protein kinase [Capsicum annuum]	Unigene41183_All//1.00E-91//AT5G38280| PESK; kinase/ transmembrane receptor protein serine/threonine kinase	Unigene41183_All//0.00E+00//DW511405				nr -
Unigene41185_All	1528	0.00	11.31	3.24	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	2.52E-99	Up	1.17E+01	1.53E-27	Up	null	null		null	null		null	null		null	null		Unigene41185_All//gi|149063401|gb|EDM13724.1|//1.00E-151//rCG21519, isoform CRA_a [Rattus norvegicus] >gi|149063402|gb|EDM13725.1| rCG21519, isoform CRA_a [Rattus norvegicus] >gi|149063403|gb|EDM13726.1| rCG21519, isoform CRA_a [Rattus norvegicus]	Unigene41185_All//1.00E-127//AT3G48000| ALDH2B4 (ALDEHYDE DEHYDROGENASE 2B4); 3-chloroallyl aldehyde dehydrogenase/ ATP binding / aldehyde dehydrogenase (NAD)			ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr +
Unigene41186_All	555	0.09	0.00	0.00	2.69	2.54	2.28	3.66	0.45	0.43	-6.56E+00	6.11E-01		-6.56E+00	6.23E-01		-8.20E-02	8.70E-01		-2.41E-01	6.82E-01		-3.02E+00	9.07E-09	Down	-3.09E+00	2.66E-09	Down	Unigene41186_All//gi|18414767|ref|NP_568147.1|//1.00E-61//clathrin adaptor complexes medium subunit-related [Arabidopsis thaliana] >gi|79327017|ref|NP_001031836.1| clathrin adaptor complexes medium subunit-related [Arabidopsis thaliana] >gi|146286092|sp|Q93Y22.2|COPD_ARATH RecName: Full=Coatomer subunit delta; AltName: Full=Delta-coat protein; Short=Delta-COP >gi|15450769|gb|AAK96656.1| coatomer delta subunit (delta-coat protein) (delta-COP) [Arabidopsis thaliana] >gi|21387083|gb|AAM47945.1| coatomer delta subunit (delta-coat protein) (delta-COP) [Arabidopsis thaliana] >gi|222423821|dbj|BAH19876.1| AT5G05010 [Arabidopsis thaliana]	Unigene41186_All//2.00E-57//AT5G05010| clathrin adaptor complexes medium subunit-related	Unigene41186_All//3.00E-160//ES851549				nr -
Unigene41189_All	393	1.86	0.77	2.30	1.14	2.54	2.87	6.13	0.85	1.62	-1.27E+00	1.36E-01		3.06E-01	6.57E-01		1.16E+00	1.07E-01		1.33E+00	4.76E-02		-2.85E+00	9.15E-10	Down	-1.92E+00	1.18E-06	Down	Unigene41189_All//gi|225410868|ref|XP_002276568.1|//2.00E-22//PREDICTED: similar to glutaredoxin family protein [Vitis vinifera]	Unigene41189_All//2.00E-17//AT5G03870| glutaredoxin family protein					nr +
Unigene4119_All	1541	0.00	0.72	0.21	23.24	33.79	19.55	9.00	12.69	9.64	9.50E+00	2.00E-06	Up	7.70E+00	4.51E-02		5.40E-01	1.30E-15		-2.50E-01	6.13E-03		4.96E-01	7.70E-06		9.97E-02	5.02E-01		Unigene4119_All//gi|77176889|gb|ABA64550.1|//2.00E-34//expansin-like protein precursor [Solanum lycopersicum]	Unigene4119_All//4.00E-29//AT4G38400| ATEXLA2 (ARABIDOPSIS THALIANA EXPANSIN-LIKE A2)	Unigene4119_All//0.00E+00//gi|54122423|gb|CO497932.1|CO497932				nr -
Unigene41190_All	512	11.85	4.45	15.91	1.46	2.49	0.97	0.00	0.00	0.00	-1.41E+00	2.98E-08	Down	4.25E-01	4.89E-02		7.70E-01	2.20E-01		-5.89E-01	4.87E-01		null	null		null	null				Unigene41190_All//6.00E-07//CO100228					
Unigene41194_All	397	1.19	0.64	1.61	0.00	0.00	0.00	0.85	6.74	1.91	-8.94E-01	3.89E-01		4.41E-01	6.23E-01		null	null		null	null		2.98E+00	3.32E-11	Up	1.16E+00	1.06E-01										ESTscan +

Unigene41197_All	518	2.22	8.02	4.01	0.29	0.40	0.44	0.33	0.24	0.31	1.85E+00	2.98E-08	Up	8.51E-01	6.95E-02		4.68E-01	8.25E-01		5.95E-01	7.21E-01		-4.32E-01	7.93E-01		-8.60E-02	9.65E-01		Unigene41197_All//gi|18416824|ref|NP_567758.1|//4.00E-46//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|30687361|ref|NP_849451.1|GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75161442|sp|Q8VY93.1|GDL66_ARATH RecName: Full=GDSL esterase/lipase At4g26790; AltName: Full=Extracellular lipase At4g26790; Flags: Precursor	Unigene41197_All//3.00E-47//AT4G26790| GDSL-motif lipase/hydrolase family protein	Unigene41197_All//2.00E-124//C0090421				nr +
Unigene41198_All	380	1.10	5.20	2.24	0.13	0.54	0.95	0.67	1.54	2.20	2.24E+00	2.78E-05	Up	1.03E+00	2.04E-01		2.05E+00	3.94E-01		2.86E+00	9.45E-02		1.21E+00	1.71E-01		1.72E+00	1.56E-02									
Unigene412_All	881	3.21	2.53	3.51	3.45	5.43	6.20	11.13	3.32	7.14	-3.42E-01	3.67E-01		1.29E-01	7.17E-01		6.56E-01	1.47E-02		8.47E-01	8.10E-04		-1.75E+00	5.47E-21	Down	-6.40E-01	5.45E-05		Unigene412_All//gi|42569749|ref|NP_181418.2|//4.00E-74//guanylate-binding family protein [Arabidopsis thaliana]	Unigene412_All//5.00E-71//AT2G38840| guanylate-binding family protein	Unigene412_All//0.00E+00//TC155950				nr -
Unigene41201_All	377	3.19	5.11	3.39	4.62	8.68	6.59	5.61	7.32	11.73	6.78E-01	1.45E-01		8.68E-02	8.84E-01		9.08E-01	6.65E-03		5.11E-01	2.34E-01		3.84E-01	2.83E-01		1.06E+00	2.99E-05	Up			Unigene41201_All//3.00E-88//gi|164353780|gb|ES790590.1|ES790590				
Unigene41202_All	360	2.33	0.99	1.18	2.21	0.48	4.01	4.35	3.60	1.11	-1.24E+00	1.15E-01		-9.75E-01	2.37E-01		-2.21E+00	7.35E-03		8.59E-01	1.33E-01		-2.72E-01	6.13E-01		-1.97E+00	9.58E-05	Down	Unigene41202_All//gi|255633434|gb|ACU17075.1|//3.00E-06//unknown [Glycine max]		Unigene41202_All//1.00E-81//gi|109872689|gb|DW501664.1|DW501664				nr -
Unigene41203_All	808	0.13	0.44	0.26	0.00	0.00	0.28	1.94	2.33	4.54	1.76E+00	2.18E-01		1.03E+00	5.91E-01		null	null		8.13E+00	1.19E-01		2.66E-01	5.75E-01		1.23E+00	2.01E-05	Up								
Unigene41204_All	476	0.00	0.00	0.11	12.87	4.05	15.28	0.89	0.09	0.84	null	null		6.81E+00	6.35E-01		-1.67E+00	1.57E-12	Down	2.47E-01	3.11E-01		-3.34E+00	1.80E-02		-8.58E-02	9.39E-01		Unigene41204_All//gi|224084318|ref|XP_002307257.1|//6.00E-09//predicted protein [Populus trichocarpa] >gi|222856706|gb|EEE94253.1|predicted protein [Populus trichocarpa]	Unigene41204_All//2.00E-05//AT5G66815| unknown protein	Unigene41204_All//9.00E-12//DR460393				nr +
Unigene4121_All	299	1.05	0.00	1.07	1.67	2.53	0.30	4.81	0.84	2.13	-1.00E+01	3.65E-02		2.55E-02	1.00E+00		6.05E-01	5.14E-01		-2.46E+00	4.83E-02		-2.52E+00	2.00E-05	Down	-1.17E+00	1.53E-02		Unigene4121_All//gi|115489066|ref|NP_001067020.1|//2.00E-43//Os12g0560700 [Oryza sativa Japonica Group] >gi|113649527|dbj|BAF30039.1|Os12g0560700 [Oryza sativa Japonica Group]	Unigene4121_All//8.00E-35//AT4G02060| PRL (PROLIFERA); ATP binding / DNA binding / DNA-dependent ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene4121_All//2.00E-150//gi|164314083|gb|ES814745.1|ES814745		ko03030|DNA replication		nr -
Unigene41211_All	638	0.00	0.00	0.08	1.09	1.51	0.35	1.59	3.41	0.31	null	null		6.38E+00	6.35E-01		4.67E-01	5.47E-01		-1.63E+00	7.45E-02		1.10E+00	5.13E-03		-2.35E+00	5.84E-04	Down	Unigene41211_All//gi|15229901|ref|NP_190005.1|//2.00E-67//pyridine nucleotide-disulphide oxidoreductase family protein [Arabidopsis thaliana] >gi|30725576|gb|AAP37810.1|At3g44190 [Arabidopsis thaliana]	Unigene41211_All//2.00E-68//AT3G44190| pyridine nucleotide-disulphide oxidoreductase family protein	Unigene41211_All//2.00E-22//gi|109875096|gb|DW504070.1|DW504070				nr -
Unigene41213_All	1430	0.00	1.06	0.37	0.14	1.18	2.21	0.33	3.42	4.85	1.01E+01	1.10E-08	Up	8.54E+00	4.04E-03		3.08E+00	1.13E-06	Up	3.99E+00	2.88E-14	Up	3.39E+00	1.87E-22	Up	3.90E+00	5.88E-36	Up								
Unigene41214_All	1106	0.28	1.42	0.19	0.09	0.19	0.29	2.14	9.52	5.98	2.32E+00	1.67E-04	Up	-5.59E-01	6.63E-01		1.05E+00	6.12E-01		1.67E+00	3.09E-01		2.15E+00	2.08E-29	Up	1.48E+00	8.16E-12	Up								
Unigene4122_All	2610	8.42	1.86	2.12	12.73	12.90	9.38	21.67	6.37	9.95	-2.18E+00	2.11E-50	Down	-1.99E+00	2.91E-43	Down	1.95E-02	8.70E-01		-4.41E-01	1.09E-06		-1.77E+00	2.01E-119	Down	-1.12E+00	2.30E-62	Down	Unigene4122_All//gi|34452231|gb|AAQ72567.1|//0.00E+00//mini-chromosome maintenance 7 [Pisum sativum]	Unigene4122_All//0.00E+00//AT4G02060| PRL (PROLIFERA); ATP binding / DNA binding / DNA-dependent ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene4122_All//0.00E+00//TC145352		ko03030|DNA replication		nr -
Unigene41223_All	371	3.67	0.27	1.15	7.52	10.21	7.06	0.00	0.00	0.21	-3.75E+00	5.95E-06	Down	-1.68E+00	8.96E-03		4.41E-01	1.78E-01		-9.08E-02	8.19E-01		null	null		7.75E+00	4.04E-01		Unigene41223_All//gi|4049351|emb|CAA22576.1|//8.00E-35//nodulin-like protein [Arabidopsis thaliana] >gi|7270153|emb|CAB79966.1|nodulin-like protein [Arabidopsis thaliana]	Unigene41223_All//4.00E-32//AT5G53870| plastocyanin-like domain-containing protein	Unigene41223_All//0.00E+00//gi|13351117|gb|BG441465.1|BG441465			GO:0046914	nr +
Unigene41224_All	510	0.21	0.10	0.00	1.66	2.70	0.44	9.29	7.29	3.12	-1.05E+00	6.84E-01		-7.68E+00	3.92E-01		7.02E-01	2.39E-01		-1.91E+00	2.14E-02		-3.48E-01	1.82E-01		-1.57E+00	1.67E-09	Down	Unigene41224_All//gi|115470543|ref|NP_001058870.1|//8.00E-19//Os07g0142300 [Oryza sativa Japonica Group] >gi|34393335|dbj|BAC83283.1| early nodulin 75 precursor-like protein [Oryza sativa Japonica Group] >gi|113610406|dbj|BAF20784.1|Os07g0142300 [Oryza sativa Japonica Group]		Unigene41224_All//0.00E+00//TC166639		ko03040|Spliceosome		nr -
Unigene41227_All	1421	0.00	0.14	0.00	0.00	0.00	0.03	1.64	1.94	5.05	7.16E+00	1.36E-01		null	null		null	null		4.99E+00	6.95E-01		2.46E-01	5.15E-01		1.62E+00	1.94E-14	Up	Unigene41227_All//gi|1346705|sp|P48979.1|PGLR_PRUPE//1.00E-141//RecName: Full=Polygalacturonase; Short=PG; AltName: Full=Pectinase; Flags: Precursor >gi|436420|emb|CAA54150.1|endopolygalacturonase [Prunus persica]	Unigene41227_All//6.00E-128//AT3G59850| polygalacturonase, putative / pectinase, putative			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene41228_All	603	21.00	10.92	9.89	18.34	18.39	24.27	43.89	11.09	13.08	-9.43E-01	5.69E-09		-1.09E+00	1.32E-10	Down	3.80E-03	9.88E-01		4.04E-01	5.96E-03		-1.98E+00	8.64E-66	Down	-1.75E+00	4.43E-57	Down	Unigene41228_All//gi|5725356|emb|CAA10382.2|//2.00E-36//alpha-D-xylosidase [Tropaeolum majus]	Unigene41228_All//2.00E-32//AT1G68560| XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Unigene41228_All//0.00E+00//gi|48749764|gb|CO080283.1|CO080283		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism	GO:0000272//GO:0005488//GO:0005576//GO:0005618//GO:0009536//GO:0010038//GO:0015926	nr +
Unigene4123_All	1040	34.66	30.60	40.04	64.23	55.43	54.11	21.59	15.31	9.00	-1.80E-01	5.73E-02		2.08E-01	2.04E-02		-2.13E-01	5.34E-04		-2.47E-01	9.34E-05		-4.96E-01	1.43E-06		-1.26E+00	2.92E-30	Down			Unigene4123_All//0.00E+00//gi|164267185|gb|ES806452.1|ES806452				ESTscan +
Unigene41233_All	366	2.14	2.22	1.16	5.58	5.55	1.60	0.58	0.23	0.33	4.69E-02	9.69E-01		-8.82E-01	2.95E-01		-7.60E-03	9.72E-01		-1.80E+00	1.71E-04	Down	-1.34E+00	4.29E-01		-8.23E-01	5.99E-01		Unigene41233_All//gi|224101241|ref|XP_002312197.1|//9.00E-29//dicer-like protein [Populus trichocarpa] >gi|222852017|gb|EEE89564.1|dicer-like protein [Populus trichocarpa]	Unigene41233_All//3.00E-25//AT3G03300| DCL2 (DICER-LIKE 2); ATP binding / ATP-dependent helicase/ RNA binding / double-stranded RNA binding / helicase/ nucleic acid binding / ribonuclease III	Unigene41233_All//0.00E+00//TC138289			GO:0003723//GO:0010467//GO:0016891//GO:0032559//GO:0042623//GO:0044464	nr -
Unigene41235_All	511	1.43	3.47	1.15	1.46	6.54	3.01	0.17	0.00	0.00	1.28E+00	1.15E-02		-3.23E-01	6.81E-01		2.16E+00	5.70E-09	Up	1.04E+00	5.90E-02		-7.37E+00	4.03E-01		-7.37E+00	3.58E-01		Unigene41235_All//gi|161610920|gb|ABX75139.1|//7.00E-54//lipase [Gossypium hirsutum]	Unigene41235_All//1.00E-45//AT4G28780| GDSL-motif lipase/hydrolase family protein	Unigene41235_All//6.00E-84//TC137605			GO:0016787//GO:0031410//GO:0044238	nr -
Unigene41236_All	559	0.56	0.82	1.91	1.07	1.11	1.13	0.98	0.90	3.06	5.39E-01	6.02E-01		1.76E+00	1.85E-02		5.22E-02	9.71E-01		8.09E-02	9.45E-01		-1.32E-01	8.80E-01		1.64E+00	4.04E-04	Up	Unigene41236_All//gi|75336836|sp|Q9SZ76.1|RPK2_ARATH//9.00E-36//RecName: Full=LRR receptor-like serine/threonine-protein kinase RPK2; AltName: Full=Receptor-like protein kinase 2; AltName: Full=Protein TOADSTOOL 2; Flags: Precursor	Unigene41236_All//4.00E-37//AT3G02130| RPK2 (RECEPTOR-LIKE PROTEIN KINASE 2); ATP binding / kinase/ protein serine/threonine kinase	Unigene41236_All//4.00E-42//gi|13356651|gb|BG447011.1|BG447011		ko04626|Plant-pathogen interaction	GO:0000166//GO:0000578//GO:0003006//GO:0006950//GO:0009555//GO:0009698//GO:0009856//GO:0016020//GO:0016301//GO:0043231//GO:0044444	nr +
Unigene41241_All	686	3.28	19.28	4.58	1.45	0.30	1.12	1.23	0.24	0.23	2.56E+00	1.23E-36	Up	4.82E-01	1.98E-01		-2.27E+00	1.67E-03		-3.76E-01	6.32E-01		-2.34E+00	2.95E-03		-2.41E+00	1.68E-03		Unigene41241_All//gi|221329408|gb|ACM18110.1|//2.00E-11//growth-regulating factor 10 [Oryza sativa Indica Group]	Unigene41241_All//1.00E-06//AT2G45480| AtGRF9 (GROWTH-REGULATING FACTOR 9); transcription activator	Unigene41241_All//0.00E+00//TC163434	GRF			nr -
Unigene41245_All	507	1.03	1.60	6.30	5.01	4.14	8.82	0.00	0.00	0.00	6.32E-01	4.02E-01		2.61E+00	3.64E-09	Up	-2.74E-01	5.33E-01		8.16E-01	4.24E-03		null	null		null	null				Unigene41245_All//2.00E-07//ES822396				
Unigene41246_All	752	1.25	1.08	0.64	0.73	1.24	0.48	1.24	3.00	7.73	-2.16E-01	7.32E-01		-9.75E-01	2.00E-01		7.63E-01	3.20E-01		-6.01E-01	5.66E-01		1.28E+00	1.02E-03		2.64E+00	2.39E-21	Up			Unigene41246_All//9.00E-121//C0076300				
Unigene41249_All	737	0.99	0.07	0.51	4.19	1.21	0.98	0.98	0.45	0.27	-3.85E+00	1.56E-03		-9.75E-01	2.64E-01		-1.79E+00	3.44E-07	Down	-2.10E+00	8.90E-08	Down	-1.10E+00	1.49E-01		-1.85E+00	1.78E-02		Unigene41249_All//gi|30023726|gb|AAP13396.1|//3.00E-18//At1g68330 [Arabidopsis thaliana]	Unigene41249_All//2.00E-10//AT1G67050| unknown protein	Unigene41249_All//7.00E-131//TC177837				nr -
Unigene41250_All	333	6.91	2.89	5.76	15.26	15.82	9.63	8.13	3.39	8.97	-1.26E+00	3.53E-03		-2.64E-01	5.69E-01		5.23E-02	8.67E-01		-6.64E-01	1.18E-02		-1.26E+00	3.10E-04	Down	1.43E-01	6.61E-01		Unigene41250_All//gi|224092704|ref|XP_002309705.1|//6.00E-24//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222855681|gb|EEE93228.1| cc-nbs-lrr resistance protein [Populus trichocarpa]		Unigene41250_All//9.00E-79//TC165835			GO:0000166	nr +
Unigene41252_All	235	67.68	8.19	33.08	12.51	9.09	4.80	26.63	8.54	3.39	-3.05E+00	2.36E-53	Down	-1.03E+00	3.57E-12	Down	-4.61E-01	2.13E-01		-1.38E+00	1.96E-04	Down	-1.64E+00	1.36E-12	Down	-2.97E+00	2.91E-26	Down			Unigene41252_All//7.00E-116//gi|21090429|gb|BQ402742.1|BQ402742				
Unigene41253_All	492	2.23	0.21	0.00	5.77	4.76	4.13	2.32	0.93	0.65	-3.44E+00	1.19E-04	Down	-1.11E+01	4.93E-06	Down	-2.78E-01	4.97E-01		-4.83E-01	2.20E-01		-1.31E+00	2.45E-02		-1.84E+00	1.97E-03									
Unigene41256_All	647	0.73	0.70	0.91	0.31	1.76	1.54	2.74	1.55	1.42	-4.63E-02	9.78E-01		3.15E-01	7.19E-01		2.51E+00	7.35E-04	Up	2.32E+00	3.97E-03		-8.24E-01	6.07E-02		-9.55E-01	2.36E-02		Unigene41256_All//gi|297817502|ref|XP_002876634.1|//3.00E-08//nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297322472|gb|EFH52893.1|nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene41256_All//4.00E-14//AT3G61690| unknown protein					nr -
Unigene41257_All	564	0.65	0.00	0.00	1.41	0.67	0.00	3.37	1.04	2.33	-9.34E+00	1.96E-02		-9.34E+00	2.78E-02		-1.07E+00	1.62E-01		-1.05E+01	4.90E-05	Down	-1.70E+00	1.53E-04	Down	-5.33E-01	1.95E-01		Unigene41257_All//gi|115440157|ref|NP_001044358.1|//4.00E-67//Os01g0766900 [Oryza sativa Japonica Group] >gi|113533889|dbj|BAF06272.1|Os01g0766900 [Oryza sativa Japonica Group]	Unigene41257_All//3.00E-55//AT4G07960| ATCSLC12 (CELLULOSE-SYNTHASE LIKE C12); cellulose synthase/ transferase, transferring glycosyl groups	Unigene41257_All//1.00E-91//TC166442			GO:0016759//GO:0044464	nr +
Unigene41261_All	240	0.87	3.17	5.55	2.08	3.44	3.76	1.59	2.79	1.83	1.86E+00	3.73E-02		2.67E+00	3.01E-04	Up	7.30E-01	3.87E-01		8.59E-01	2.70E-01		8.14E-01	3.15E-01		2.04E-01	8.26E-01									
Unigene41264_All	223	3.28	5.45	2.39	1.79	0.31	2.03	0.76	4.31	1.07	7.31E-01	2.35E-01		-4.60E-01	6.02E-01		-2.53E+00	5.79E-02		1.81E-01	8.83E-01		2.51E+00	8.00E-04	Up	4.99E-01	7.07E-01				Unigene41264_All//1.00E-06//gi|109884721|gb|DW513691.1|DW513691				
Unigene41266_All	456	0.69	5.22	0.82	0.11	0.45	1.68	0.74	4.40	3.49	2.92E+00	4.35E-08	Up	2.48E-01	8.23E-01		2.05E+00	3.94E-01		3.95E+00	1.02E-03		2.57E+00	2.01E-07	Up	2.24E+00	2.08E-05	Up			Unigene41266_All//4.00E-66//gi|164257249|gb|ES793904.1|ES793904				
Unigene41267_All	1876	0.00	0.00	0.00	0.00	0.00	0.00	0.90	2.25	3.50	null	null		null	null		null	null		null	null		1.32E+00	1.55E-06	Up	1.96E+00	5.95E-17	Up	Unigene41267_All//gi|224128410|ref|XP_002329155.1|//4.00E-35//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222869824|gb|EEF06955.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene41267_All//2.00E-06//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene41267_All//1.00E-91//ES818502		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene41268_All	1692	0.22	0.15	0.25	4.74	3.64	0.88	0.77	0.10	1.60	-5.32E-01	6.27E-01		2.18E-01	8.31E-01		-3.80E-01	6.22E-02		-2.43E+00	4.28E-23	Down	-2.97E+00	8.34E-06	Down	1.05E+00	1.77E-03		Unigene41268_All//gi|223452398|gb|ACM89526.1|//1.00E-164//protein kinase [Glycine max]	Unigene41268_All//2.00E-144//AT3G46290| protein kinase, putative	Unigene41268_All//5.00E-10//TC159391		ko04626|Plant-pathogen interaction		nr -
Unigene41269_All	705	0.59	0.58	0.60	4.24	4.40	4.10	1.14	0.12	2.09	-4.62E-02	9.80E-01		2.55E-02	1.00E+00		5.23E-02	9.05E-01		-4.83E-02	9.13E-01		-3.26E+00	4.48E-04	Down	8.76E-01	6.42E-02		Unigene41269_All//gi|225445342|ref|XP_002281542.1|//1.00E-44//PREDICTED: similar to GRV2 (KATAMARI2); binding / heat shock protein binding [Vitis vinifera]	Unigene41269_All//2.00E-37//AT3G26890| GRV2 (GRAVITROPISM DEFECTIVE 2); binding / heat shock protein binding				GO:0005515//GO:0043231//GO:0050896	nr +
Unigene41271_All	794	0.40	1.15	0.00	0.63	0.95	1.93	3.83	9.21	21.42	1.54E+00	4.51E-02		-8.63E+00	4.90E-02		6.05E-01	5.14E-01		1.62E+00	4.20E-03		1.26E+00	4.03E-10	Up	2.48E+00	7.22E-57	Up			Unigene41271_All//2.00E-08//BG444302				
Unigene41274_All	290	1.08	50.32	34.15	0.86	17.93	13.70	0.00	0.00	0.00	5.54E+00	9.32E-74	Up	4.98E+00	1.33E-46	Up	4.38E+00	2.04E-26	Up	4.00E+00	6.68E-18	Up	null	null		null	null									
Unigene41278_All	239	19.26	11.66	22.50	13.96	15.56	17.39	38.74	16.96	12.67	-7.24E-01	9.88E-03		2.24E-01	4.19E-01		1.56E-01	6.78E-01		3.16E-01	3.44E-01		-1.19E+00	1.43E-11	Down	-1.61E+00	2.06E-18	Down	Unigene41278_All//gi|52851178|emb|CAH58637.1|//7.00E-10//vacuolar H+-ATPase C subunit [Plantago major] >gi|106879597|emb|CAJ38382.1|vacuolar H+-ATPase, subunit C 2 [Plantago major]	Unigene41278_All//1.00E-104//gi|109834765|gb|DW233330.1|DW233330		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0006754//GO:0006818//GO:0015077//GO:0031224//GO:0033176	nr +
Unigene41279_All	730	0.29	0.35	0.44	0.20	1.98	0.68	1.16	3.84	1.64	2.76E-01	8.43E-01		6.10E-01	6.24E-01		3.27E+00	4.70E-06	Up	1.73E+00	1.45E-01		1.73E+00	1.97E-06	Up	4.99E-01	3.58E-01				Unigene41279_All//9.00E-07//EX172314				
Unigene41280_All	274	0.00	0.92	3.11	1.82	1.38	0.82	0.77	1.37	0.44	9.85E+00	7.86E-02		1.16E+01	9.02E-05	Up	-3.95E-01	6.89E-01		-1.14E+00	3.07E-01		8.32E-01	4.67E-01		-8.23E-01	5.99E-01									
Unigene41282_All	378	0.28	4.56	0.85	0.92	1.91	0.60	3.91	1.99	2.53	4.04E+00	1.14E-07	Up	1.61E+00	3.05E-01		1.05E+00	2.40E-01		-6.27E-01	6.21E-01		-9.76E-01	4.66E-02		-6.30E-01	1.82E-01		Unigene41282_All//gi|296084963|emb|CBI28378.3|//3.00E-06//unnamed protein product [Vitis vinifera]	Unigene41282_All//5.00E-06//AT4G10270| wound-responsive family protein	Unigene41282_All//0.00E+00//gi|164279533|gb|ES832304.1|ES832304				nr -

Unigene41283_All	1189	0.18	0.00	0.00	0.21	0.49	0.30	6.54	0.18	1.21	-7.46E+00	1.22E-01			-7.46E+00	1.45E-01		1.23E+00	2.33E-01		5.37E-01	6.94E-01		-5.22E+00	1.91E-47	Down	-2.44E+00	2.66E-26	Down	Unigene41283_All//gi|15229999|ref|NP_188451.1|//9.00E-17//octicosapeptide/Phox/Bemlp (PB1) domain-containing protein [Arabidopsis thaliana] >gi|209529793|gb|ACI49791.1|At3g18230 [Arabidopsis thaliana]	Unigene41283_All//2.00E-06//AT3G18230| octicosapeptide/Phox/Bemlp (PB1) domain-containing protein					nr +
Unigene41291_All	424	0.25	1.67	0.63	2.58	1.14	0.00	1.79	1.18	0.85	2.76E+00	9.14E-03			1.35E+00	4.09E-01		-1.18E+00	5.94E-02		-1.13E+01	7.26E-07	Down	-6.02E-01	4.12E-01		-1.09E+00	1.21E-01							
Unigene41294_All	2248	0.05	0.00	0.00	0.00	0.03	0.04	13.35	24.41	42.94	-5.54E+00	3.71E-01			-5.54E+00	3.92E-01		4.94E+00	6.09E-01		5.33E+00	4.76E-01		8.70E-01	8.26E-39		1.69E+00	7.61E-194	Up	Unigene41294_All//gi|115440305|ref|NP_001044432.1|//1.00E-139//0s01g0779300 [Oryza sativa Japonica Group] >gi|113533963|dbj|BAF06346.1|Os01g0779300 [Oryza sativa Japonica Group]	Unigene41294_All//4.00E-130//AT5G10530| lectin protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene4130_All	1166	23.96	7.95	9.36	29.14	21.88	31.45	26.14	6.27	10.08	-1.59E+00	5.54E-42	Down	-1.36E+00	6.00E-32	Down	-4.13E-01	1.10E-06		1.10E-01	2.97E-01		-2.06E+00	2.24E-79	Down	-1.38E+00	1.91E-46	Down	Unigene4130_All//gi|15450930|gb|AAK96736.1|//6.00E-82//Unknown protein [Arabidopsis thaliana]	Unigene4130_All//3.00E-83//AT5G66860| INVOLVED IN: translation; LOCATED IN: mitochondrion; CONTAINS InterPro DOMAIN/s: Ribosomal protein L25/Gln-tRNA synthetase, anti-codon-binding (InterPro:IPR011035); BEST Arabidopsis thaliana protein match is: 50S ribosomal protein-related (TAIR:AT4G23620.1); Has 2346 Blast hits to 2345 proteins in 433 species: Archae - 0; Bacteria - 930; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 1375 (source: NCBI BLink).	Unigene4130_All//0.00E+00//TC129985		ko03010|Ribosome		nr +
Unigene41300_All	394	0.27	1.54	0.68	1.14	1.84	0.80	2.68	0.42	1.82	2.54E+00	2.46E-02			1.35E+00	4.09E-01		6.90E-01	4.47E-01		-5.04E-01	6.49E-01		-2.66E+00	2.25E-04	Down	-5.60E-01	3.39E-01							
Unigene41301_All	412	2.79	0.00	0.78	2.66	5.35	1.32	0.62	0.51	0.29	-1.14E+01	9.91E-07	Down	-1.85E+00	1.07E-02		1.01E+00	1.88E-02		-1.02E+00	1.30E-01		-2.80E-01	8.28E-01		-1.09E+00	4.28E-01				Unigene41301_All//1.00E-10//gi|109853794|gb|DW482773.1|DW482773				
Unigene41304_All	996	1432.52	641.81	933.85	134.59	159.07	101.80	2.76	1.18	0.96	-1.16E+00	0.00E+00	Down	-6.17E-01	0.00E+00		2.41E-01	9.69E-11		-4.03E-01	2.84E-21		-1.23E+00	3.68E-04	Down	-1.52E+00	1.19E-05	Down	Unigene41304_All//gi|77540210|gb|AB86963.1|//1.00E-136//glyceraldehyde-3-phosphate dehydrogenase A subunit [Glycine max]	Unigene41304_All//0.00E+00//AT1G12900| GAPA-2 (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT 2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene41304_All//0.00E+00//TC132443		ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene41305_All	459	1.14	0.11	1.16	5.64	1.73	0.98	1.84	3.19	2.08	-3.37E+00	1.58E-02		2.53E-02	9.99E-01		-1.71E+00	8.83E-06	Down	-2.52E+00	4.13E-08	Down	7.91E-01	1.12E-01		1.77E-01	7.64E-01				Unigene41305_All//2.00E-46//ES840947				
Unigene41306_All	757	0.00	0.00	0.00	1.71	1.59	1.31	15.30	5.19	4.58	null	null		null	null		-1.04E-01	8.43E-01		-3.82E-01	5.50E-01		-1.56E+00	4.09E-21	Down	-1.74E+00	2.36E-25	Down	Unigene41306_All//gi|224057862|ref|XP_002299361.1|//5.00E-85//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene41306_All//4.00E-79//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene41306_All//2.00E-50//gi|73847192|gb|DT456212.1|DT456212			GO:0009314//GO:0009526//GO:0009725//GO:0016881//GO:0048878	nr +
Unigene41308_All	483	0.33	0.00	0.66	1.86	0.93	0.19	2.45	0.52	0.08	-8.34E+00	2.15E-01		1.03E+00	4.71E-01		-1.00E+00	1.61E-01		-3.31E+00	5.80E-04	Down	-2.24E+00	4.21E-04	Down	-4.89E+00	1.20E-07	Down	Unigene41308_All//gi|224141315|ref|XP_002324019.1|//2.00E-75//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222867021|gb|EEF04152.1|multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene41308_All//4.00E-67//AT3G28345| ABC transporter family protein			ko02010|ABC transporters	GO:0006810//GO:0031224//GO:0032559//GO:0042626	nr -
Unigene41309_All	511	248.81	52.85	56.69	43.97	29.04	29.87	0.99	0.74	0.47	-2.24E+00	4.32E-299	Down	-2.13E+00	3.65E-273	Down	-5.98E-01	1.46E-08		-5.58E-01	6.38E-07		-4.32E-01	6.18E-01		-1.09E+00	2.28E-01		Unigene41309_All//gi|21322711|emb|CAD22154.1|//4.00E-37//pherophorin-dz1 protein [Volvox carteri f. nagariensis]		Unigene41309_All//1.00E-128//gi|164286197|gb|ES834735.1|ES834735	ko03040|Spliceosome	GO:0016020	nr +
Unigene4131_All	2062	0.43	15.65	18.00	44.23	113.14	204.20	5.45	1.01	3.21	5.18E+00	3.32E-158	Up	5.38E+00	6.10E-182	Up	1.35E+00	0.00E+00	Up	2.21E+00	0.00E+00	Up	-2.43E+00	2.76E-36	Down	-7.66E-01	2.47E-07		Unigene4131_All//gi|30725324|gb|AAP37684.1|//1.00E-120//At3g01680 [Arabidopsis thaliana]	Unigene4131_All//4.00E-121//AT3G01680| unknown protein	Unigene4131_All//0.00E+00//ES831165				nr -
Unigene41310_All	457	0.23	0.00	0.23	6.10	2.41	5.63	2.50	0.55	0.87	-7.84E+00	3.71E-01		2.50E-02	1.00E+00		-1.34E+00	1.75E-04	Down	-1.16E-01	7.64E-01		-2.19E+00	6.83E-04	Down	-1.52E+00	7.91E-03		Unigene41310_All//gi|212717135|gb|ACJ37409.1|//7.00E-09//ATP binding/protein serine/threonine kinase [Glycine max]		Unigene41310_All//8.00E-111//TC149159			GO:0000166//GO:0004672//GO:0008152//GO:0016020	nr -
Unigene41311_All	338	3.10	3.30	0.32	1.47	0.92	2.67	0.00	0.00	0.00	9.12E-02	8.87E-01		-3.30E+00	4.58E-04	Down	-6.85E-01	5.15E-01		8.59E-01	2.70E-01		null	null		null	null									
Unigene41314_All	585	0.00	1.82	0.00	0.00	0.00	0.00	1.88	3.07	21.45	1.08E+01	3.81E-06	Up	null	null		null	null		null	null		7.09E-01	1.07E-01		3.51E+00	1.67E-59	Up	Unigene41314_All//gi|225444311|ref|XP_002263655.1|//3.00E-30//PREDICTED: similar to stigma-specific Stig1 family protein [Vitis vinifera]	Unigene41314_All//3.00E-30//AT1G11925| Encodes a Stigma-specific Stig1 family protein	Unigene41314_All//0.00E+00//TC152592				nr -
Unigene41319_All	312	231.42	39.30	83.29	758.23	524.70	248.83	593.96	729.42	206.60	-2.56E+00	1.11E-199	Down	-1.47E+00	5.76E-93	Down	-5.31E-01	2.06E-69		-1.61E+00	0.00E+00	Down	2.96E-01	3.91E-23		-1.52E+00	0.00E+00	Down	Unigene41319_All//gi|2541876|dbj|BAA22813.1|//1.00E-29//CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]	Unigene41319_All//9.00E-31//AT5G10770| chloroplast nucleoid DNA-binding protein, putative	Unigene41319_All//5.00E-176//gi|82756334|gb|DV849896.1|DV849896			GO:0004175//GO:0019538//GO:0043231	nr -
Unigene4132_All	1973	1.11	0.46	0.92	5.18	2.95	4.97	66.80	34.25	5.77	-1.27E+00	4.15E-03		-2.80E-01	5.53E-01		-8.11E-01	8.38E-07		-5.93E-02	7.69E-01		-9.64E-01	2.96E-109		-3.53E+00	0.00E+00	Down	Unigene4132_All//gi|15218579|ref|NP_175058.1|//1.00E-136//AAA-type ATPase family protein [Arabidopsis thaliana] >gi|8778680|gb|AAF79688.1|AC022314_29 F9C16.7 [Arabidopsis thaliana]	Unigene4132_All//4.00E-133//AT1G43910| AAA-type ATPase family protein	Unigene4132_All//3.00E-52//DT527654				nr +
Unigene41320_All	211	4.22	4.32	5.30	0.47	4.24	3.00	1.40	1.19	0.76	3.62E-02	9.79E-01		3.30E-01	6.40E-01		3.17E+00	8.78E-04	Up	2.67E+00	1.83E-02		-2.39E-01	8.39E-01		-8.93E-01	4.71E-01				Unigene41320_All//2.00E-07//TC158820				
Unigene41321_All	947	0.77	2.35	0.22	0.26	0.73	0.91	4.24	0.62	2.82	1.61E+00	4.50E-04	Up	-1.78E+00	6.00E-02		1.47E+00	1.16E-01		1.78E+00	3.19E-02		-2.78E+00	1.87E-15	Down	-5.90E-01	2.45E-02		Unigene41321_All//gi|15231187|ref|NP_190146.1|//1.00E-127//TET3 (TETRASPANIN3) [Arabidopsis thaliana] >gi|30023274|gb|AAP13420.1|At3g45600 [Arabidopsis thaliana]	Unigene41321_All//3.00E-109//AT3G45600| TET3 (TETRASPANIN3)	Unigene41321_All//0.00E+00//gi|78330826|gb|DT551100.1|DT551100			GO:0016020	nr +
Unigene41323_All	1185	0.00	0.00	0.00	0.00	0.00	0.00	40.92	18.55	10.79	null	null		null	null		null	null		null	null		-1.14E+00	1.91E-53	Down	-1.92E+00	1.57E-118	Down	Unigene41323_All//gi|115452153|ref|NP_001049677.1|//3.00E-87//0s03g0269100 [Oryza sativa Japonica Group] >gi|113548148|dbj|BAF11591.1|Os03g0269100 [Oryza sativa Japonica Group]	Unigene41323_All//3.00E-80//AT5G06060| tropinone reductase, putative / tropine dehydrogenase, putative	Unigene41323_All//4.00E-158//gi|164334825|gb|ES806206.1|ES806206		ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis	GO:0008152//GO:0016616	nr -
Unigene41326_All	665	0.00	0.30	0.00	0.90	1.29	2.44	3.88	0.44	1.62	8.25E+00	1.36E-01		null	null		5.26E-01	5.45E-01		1.44E+00	7.43E-03		-3.14E+00	2.22E-11	Down	-1.26E+00	3.03E-04	Down	Unigene41326_All//gi|18406084|ref|NP_565988.1|//1.00E-15//PAR1 (PHY RAPIDLY REGULATED 1) [Arabidopsis thaliana] >gi|4512668|gb|AAD21722.1|expressed protein [Arabidopsis thaliana] >gi|83776541|tpe|CAJ55345.1| TPA: helix-loop-helix protein [Arabidopsis thaliana]	Unigene41326_All//3.00E-13//AT2G42870| PAR1 (PHY RAPIDLY REGULATED 1)	Unigene41326_All//2.00E-131//TC160093			GO:0009639//GO:0043231	nr -
Unigene41327_All	291	0.00	2.09	5.49	6.50	3.79	4.19	0.73	0.72	0.27	1.10E+01	1.17E-03		1.24E+01	8.44E-09	Up	-7.81E-01	8.46E-02		-6.34E-01	1.96E-01		-1.68E-02	1.02E+00		-1.41E+00	3.80E-01		Unigene41327_All//gi|15220741|ref|NP_176416.1|//1.00E-06//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75097094|sp|Q04590.1|PPR88_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g62260, mitochondrial; Flags: Precursor >gi|2160154|gb|AAB60776.1|F19G23.18 gene product [Arabidopsis thaliana]	Unigene41327_All//5.00E-08//AT1G62260| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene41330_All	1260	0.04	0.00	0.00	0.28	0.19	0.07	3.69	0.56	3.67	-5.38E+00	6.11E-01		-5.38E+00	6.23E-01		-5.33E-01	6.46E-01		-1.95E+00	1.96E-01		-2.71E+00	2.41E-17	Down	-9.20E-03	9.64E-01		Unigene41330_All//gi|224070883|ref|XP_002303279.1|//1.00E-178//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222840711|gb|EEE78258.1|sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene41330_All//8.00E-146//AT3G15990| SULTR3;4 (SULFATE TRANSPORTER 3;4); sulfate transmembrane transporter	Unigene41330_All//0.00E+00//gi|78322830|gb|DT543104.1|DT543104			GO:0015291//GO:0015698//GO:0031224	nr -
Unigene41332_All	459	1.94	1.66	0.58	0.11	3.45	2.56	1.20	0.27	0.09	-2.27E-01	7.27E-01		-1.74E+00	3.79E-02		4.99E+00	1.40E-08	Up	4.56E+00	6.41E-06	Up	-2.13E+00	3.31E-02		-3.79E+00	2.03E-03		Unigene41332_All//gi|15235570|ref|NP_195464.1|//1.00E-43//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]	Unigene41332_All//5.00E-39//AT4G37480| DNAJ heat shock N-terminal domain-containing protein				GO:0005515//GO:0043231//GO:0044267//GO:0050896	nr +
Unigene41335_All	1177	0.04	0.09	0.00	0.47	0.38	0.23	6.18	4.33	2.88	9.52E-01	7.26E-01		-5.48E+00	6.23E-01		-2.92E-01	7.70E-01		-1.02E+00	3.29E-01		-5.12E-01	8.33E-03		-1.10E+00	1.45E-08	Down	Unigene41335_All//gi|37782214|gb|AAP55487.1|//1.00E-08//resistance protein RGC2 [Lactuca sativa]		Unigene41335_All//1.00E-164//TC179212				nr -
Unigene41339_All	1877	0.50	0.78	0.77	0.05	0.44	0.24	8.24	19.75	16.22	6.42E-01	2.37E-01		6.11E-01	2.96E-01		3.05E+00	1.99E-03		2.18E+00	1.03E-01		1.26E+00	7.99E-48	Up	9.76E-01	5.44E-27		Unigene41339_All//gi|2739004|gb|AAB94590.1|//0.00E+00//CYP82C1p [Glycine max]	Unigene41339_All//8.00E-150//AT4G31970| CYP82C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016709	nr +
Unigene41341_All	1840	0.00	0.00	0.00	0.00	0.00	0.00	1.93	12.06	1.52	null	null		null	null		null	null		null	null		2.64E+00	6.64E-78	Up	-3.49E-01	2.35E-01		Unigene41341_All//gi|110816488|sp|Q38AT2.1|YCX91_PHAAO//2.00E-09//RecName: Full=Uncharacterized protein 08F91		Unigene41341_All//2.00E-111//TC135460			GO:0009536	nr +
Unigene41342_All	414	0.13	0.49	2.19	3.49	1.33	0.11	3.37	1.82	0.00	1.95E+00	3.75E-01		4.11E+00	3.91E-04	Up	-1.39E+00	9.09E-03		-5.00E+00	7.44E-08	Down	-8.91E-01	7.94E-02		-1.17E+01	2.40E-10	Down			Unigene41342_All//3.00E-51//gi|109888942|gb|DW517911.1|DW517911				
Unigene41343_All	296	7.60	1.54	3.96	2.52	6.51	2.75	0.29	0.42	0.13	-2.30E+00	3.84E-06	Down	-9.41E-01	3.61E-02		1.37E+00	3.70E-03		1.22E-01	8.93E-01		5.68E-01	7.82E-01		-1.09E+00	6.76E-01		Unigene41343_All//gi|255555825|ref|XP_002518948.1|//3.00E-06//transcription factor, putative [Ricinus communis] >gi|223541935|gb|EEF43481.1|transcription factor, putative [Ricinus communis]		Unigene41343_All//5.00E-09//CO123445				nr -
Unigene41344_All	444	0.24	0.57	0.00	2.92	0.70	1.12	3.43	0.85	1.70	1.28E+00	4.35E-01		-7.88E+00	3.92E-01		-2.06E+00	6.01E-04	Down	-1.38E+00	2.30E-02		-2.02E+00	1.51E-04	Down	-1.01E+00	2.94E-02				Unigene41344_All//5.00E-07//ES848299				
Unigene41346_All	425	1.72	2.50	0.25	0.23	0.49	2.87	0.10	0.59	1.87	5.39E-01	4.03E-01		-2.78E+00	1.04E-02		1.05E+00	6.12E-01		3.61E+00	2.38E-05	Up	2.57E+00	1.53E-01		4.24E+00	7.42E-05	Up	Unigene41346_All//gi|15237783|ref|NP_197744.1|//3.00E-31//AtCXE18 (Arabidopsis thaliana carboxyesterase 18); carboxylesterase >gi|114050665|gb|ABI49482.1|At5g23530 [Arabidopsis thaliana]	Unigene41346_All//4.00E-23//AT5G23530| AtCXE18 (Arabidopsis thaliana carboxyesterase 18); carboxylesterase				GO:0000904//GO:0043231	nr -

Unigene41347_All	1081	0.53	12.89	1.08	1.57	0.83	1.50	0.63	4.99	0.18	4.60E+00	4.18E-64	Up	1.03E+00	1.24E-01		-9.20E-01	5.65E-02		-5.89E-02	9.21E-01		2.99E+00	4.93E-22	Up	-1.76E+00	2.80E-02		Unigene41347_All//gi|33326375|gb|AAQ08597.1|//1.00E-132//heat shock protein [Hevea brasiliensis]	Unigene41347_All//2.00E-99//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene41347_All//0.00E+00//DW501699		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene41349_All	332	5.83	7.33	6.09	3.30	7.47	8.84	17.32	13.34	8.16	3.29E-01	4.22E-01		6.39E-02	8.93E-01		1.18E+00	3.14E-03		1.42E+00	1.62E-04	Up	-3.76E-01	1.01E-01		-1.09E+00	8.32E-07	Down	Unigene41349_All//gi|79333554|ref|NP_171671.2|//1.00E-42//aspartic-type endopeptidase/ peptidase [Arabidopsis thaliana]	Unigene41349_All//4.00E-44//AT1G01650| aspartic-type endopeptidase/ peptidase	Unigene41349_All//4.00E-155//TC163032			GO:0004175//GO:0031224//GO:0031410	nr -
Unigene4135_All	1442	26.09	15.04	13.26	57.07	47.16	42.41	28.24	21.74	13.65	-7.95E-01	5.62E-19		-9.77E-01	1.42E-25		-2.75E-01	1.92E-07		-4.28E-01	7.98E-15		-3.77E-01	4.03E-07		-1.05E+00	1.74E-40	Down	Unigene4135_All//gi|133907524|gb|AB042262.1|//1.00E-157//AT-hook DNA-binding protein [Gossypium hirsutum]	Unigene4135_All//1.00E-63//AT2G45850| DNA-binding family protein	Unigene4135_All//0.00E+00//TC158736				nr -
Unigene41350_All	306	2.56	3.48	3.13	9.93	7.43	3.39	1.24	0.41	1.04	4.39E-01	5.07E-01		2.89E-01	6.65E-01		-4.19E-01	2.54E-01		-1.55E+00	2.75E-05	Down	-1.60E+00	1.81E-01		-2.56E-01	7.85E-01				Unigene41350_All//9.00E-11//gi|21092724|gb|BQ405037.1|BQ405037				
Unigene41353_All	369	68.91	191.69	138.10	46.71	48.34	62.67	42.62	98.32	42.97	1.48E+00	7.58E-94	Up	1.00E+00	4.53E-36	Up	4.95E-02	7.94E-01		4.24E-01	1.48E-04		1.21E+00	1.03E-43	Up	1.17E-02	9.56E-01		Unigene41353_All//gi|224111880|ref|XP_002316010.1|//2.00E-26//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1|cytochrome P450 [Populus trichocarpa]	Unigene41353_All//4.00E-13//AT2G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene41353_All//0.00E+00//gi|3326238|gb|AI055124.1|AI055124		ko00908|Zeatin biosynthesis//ko00591|Linoleic acid metabolism	GO:0016491//GO:0046872	nr -
Unigene41357_All	1045	0.20	0.05	0.61	14.11	14.04	9.55	0.08	0.72	0.42	-2.05E+00	3.34E-01		1.61E+00	1.11E-01		-7.40E-03	9.61E-01		-5.63E-01	7.40E-05		3.15E+00	9.54E-04	Up	2.37E+00	4.04E-02		Unigene41357_All//gi|297841511|ref|XP_002888637.1|//9.00E-68//atidd14-domain 14 [Arabidopsis lyrata subsp. lyrata] >gi|297334428|gb|EFH94896.1|atidd14-domain 14 [Arabidopsis lyrata subsp. lyrata]	Unigene41357_All//4.00E-69//AT1G68130| AtIDD14 (Arabidopsis thaliana Indeterminate(ID)-Domain 14); nucleic acid binding / transcription factor/ zinc ion binding	Unigene41357_All//0.00E+00//ES817490	C2H2		GO:0001071//GO:0009630//GO:0010468//GO:0043231//GO:0046914	nr -
Unigene41358_All	930	29.59	11.39	25.94	18.32	21.96	21.08	6.96	6.20	2.78	-1.38E+00	1.65E-33	Down	-1.90E-01	9.93E-02		2.61E-01	3.48E-02		2.02E-01	1.39E-01		-1.66E-01	4.88E-01		-1.32E+00	5.75E-10	Down	Unigene41358_All//gi|62945915|gb|AY22200.1|//1.00E-109//squalene monooxygenase [Datura inoxia]	Unigene41358_All//8.00E-104//AT1G58440| XF1; squalene monooxygenase	Unigene41358_All//0.00E+00//TC134279		ko00100|Steroid biosynthesis		nr -
Unigene41359_All	364	66.26	38.98	28.23	108.66	90.63	119.61	168.19	51.56	75.52	-7.66E-01	1.01E-11		-1.23E+00	7.25E-24	Down	-2.62E-01	1.30E-03		1.39E-01	1.26E-01		-1.71E+00	4.23E-123	Down	-1.16E+00	1.60E-70	Down	Unigene41359_All//gi|192913036|gb|ACF06626.1|//1.00E-43//S6 ribosomal protein [Elaeis guineensis]	Unigene41359_All//1.00E-44//AT5G10360| EMB3010 (embryo defective 3010); structural constituent of ribosome	Unigene41359_All//5.00E-173//gi|13247585|gb|BF271178.2|BF271178		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0019538//GO:0016020	nr -
Unigene4136_All	1175	1.69	1.94	1.90	1.78	2.05	1.50	2.73	0.82	0.54	1.98E-01	6.25E-01		1.70E-01	6.95E-01		2.04E-01	6.61E-01		-2.48E-01	6.39E-01		-1.74E+00	2.33E-07	Down	-2.33E+00	8.76E-11	Down	Unigene4136_All//gi|225445364|ref|XP_002284885.1|//1.00E-141//PREDICTED: similar to ATPDR4/PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances [Vitis vinifera]	Unigene4136_All//1.00E-128//AT2G26910| PDR4 (PLEIOTROPIC DRUG RESISTANCE 4); ATPase, coupled to transmembrane movement of substances	Unigene4136_All//0.00E+00//gi|84168904|gb|DR457552.1|DR457552		ko03040|Spliceosome//ko02010|ABC transporters		nr +
Unigene41360_All	1426	0.00	0.00	0.00	0.49	0.10	0.06	2.34	6.77	13.69	null	null		null	null		-2.34E+00	1.01E-02		-2.95E+00	5.84E-03		1.53E+00	3.08E-17	Up	2.55E+00	4.49E-67	Up	Unigene41360_All//gi|75249810|sp|Q9LB46.1|FBL74_ARATH//1.00E-40//RecName: Full=F-box/LRR-repeat protein At4g14096 >gi|14596145|gb|AAK68800.1|Unknown protein [Arabidopsis thaliana]	Unigene41360_All//4.00E-35//AT4G14103| F-box family protein	Unigene41360_All//2.00E-34//CA993092				nr +
Unigene41362_All	417	0.00	0.00	0.51	0.24	0.08	0.00	143.47	34.28	28.18	null	null		9.00E+00	1.41E-01		-1.53E+00	5.86E-01		-7.90E+00	3.99E-01		-2.07E+00	8.73E-156	Down	-2.35E+00	2.06E-188	Down	Unigene41362_All//gi|30519654|emb|CAD90835.1|//1.00E-42//(+)-delta-cadinene synthase [Gossypium arboreum]	Unigene41362_All//1.00E-25//AT3G14520| terpene synthase/cyclase family protein	Unigene41362_All//0.00E+00//TC142314		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0016829//GO:0046872	nr +
Unigene41364_All	2287	0.00	0.18	0.00	0.17	0.12	0.08	18.99	18.39	8.85	7.47E+00	1.36E-02		null	null		-5.33E-01	6.16E-01		-1.14E+00	3.79E-01		-4.64E-02	6.37E-01		-1.10E+00	1.28E-46	Down	Unigene41364_All//gi|89179406|gb|AB063142.1|//3.00E-34//Retrotransposon gag protein [Asparagus officinalis]	Unigene41364_All//1.00E-51//gi|109848628|gb|DW477608.1|DW477608				GO:0003676//GO:0043170//GO:0044238	nr +
Unigene41365_All	286	1.10	1.95	2.23	2.96	4.58	10.26	0.44	0.00	0.70	8.28E-01	3.81E-01		1.03E+00	2.81E-01		6.28E-01	3.11E-01		1.79E+00	5.03E-06	Up	-8.79E+00	2.35E-01		6.51E-01	6.65E-01				Unigene41365_All//3.00E-100//TC130526				
Unigene41367_All	1767	1.24	22.94	1.42	0.00	0.35	0.31	1.65	0.50	19.21	4.21E+00	9.52E-176	Up	1.88E-01	6.36E-01		8.45E+00	7.90E-04	Up	8.26E+00	2.45E-03		-1.73E+00	1.04E-06	Down	3.54E+00	4.60E-161	Up	Unigene41367_All//gi|76803519|gb|AB455732.1|//0.00E+00//ABA 8'-hydroxylase CYP707A1 [Solanum tuberosum]	Unigene41367_All//0.00E+00//AT4G19230| CYP707A1; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	Unigene41367_All//0.00E+00//gi|48821398|gb|CO122711.1|CO122711		ko00906|Carotenoid biosynthesis	GO:0003006//GO:0005506//GO:0006952//GO:0009416//GO:0009687//GO:0016709	nr -
Unigene41368_All	628	0.33	0.24	0.34	0.40	0.88	1.22	3.23	0.53	0.89	-4.61E-01	7.58E-01		2.53E-02	1.00E+00		1.15E+00	2.97E-01		1.62E+00	6.61E-02		-2.60E+00	1.27E-07	Down	-1.86E+00	1.51E-05	Down	Unigene41368_All//gi|224116438|ref|XP_002317301.1|//1.00E-25//outward rectifying potassium channel [Populus trichocarpa] >gi|222860366|gb|EEE57913.1|outward rectifying potassium channel [Populus trichocarpa]	Unigene41368_All//3.00E-15//AT4G18160| KC06; outward rectifier potassium channel	Unigene41368_All//1.00E-33//CO110213			GO:0005261//GO:0030001//GO:0031224//GO:0046872	nr +
Unigene41369_All	362	0.29	4.90	1.62	0.83	1.71	1.37	1.75	2.54	2.64	4.08E+00	6.27E-08	Up	2.48E+00	3.75E-02		1.05E+00	2.99E-01		7.33E-01	5.16E-01		5.36E-01	4.18E-01		5.92E-01	3.46E-01								
Unigene4137_All	1636	13.50	12.26	9.02	18.12	17.28	6.65	11.50	10.12	8.13	-1.38E-01	2.87E-01		-5.82E-01	1.28E-06		-6.82E-02	5.88E-01		-1.45E+00	7.43E-42	Down	-1.85E-01	1.38E-01		-5.00E-01	6.32E-06		Unigene4137_All//gi|18408746|ref|NP_564894.1|//1.00E-137//zinc finger (MYND type) family protein / F-box family protein [Arabidopsis thaliana] >gi|75173237|sp|Q9FVF9.1|FB76_ARATH RecName: Full=F-box protein At1g67340 >gi|9828618|gb|AAG00241.1|AC002130_6 F1N21.16 [Arabidopsis thaliana] >gi|16209726|gb|AAL14418.1|At1g67340/F1N21_16 [Arabidopsis thaliana]	Unigene4137_All//1.00E-124//AT1G67340| zinc finger (MYND type) family protein / F-box family protein	Unigene4137_All//0.00E+00//TC163331				nr +
Unigene41370_All	284	0.00	4.64	1.13	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.50E-07	Up	1.01E+01	4.51E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene41371_All	351	0.00	7.07	3.03	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	3.98E-14	Up	1.16E+01	6.62E-06	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene41372_All	602	0.00	0.17	0.00	0.00	0.00	0.30	76.76	7.50	52.68	7.39E+00	3.86E-01		null	null		null	null		8.23E+00	1.94E-01		-3.36E+00	2.39E-206	Down	-5.43E-01	2.96E-15		Unigene41372_All//gi|115471577|ref|NP_001059387.1|//6.00E-17//Os07g0287400 [Oryza sativa Japonica Group] >gi|113610923|dbj|BAF21301.1|Os07g0287400 [Oryza sativa Japonica Group]	Unigene41372_All//6.00E-13//AT5G48190| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene41372_All//0.00E+00//TC163331				nr -
Unigene41373_All	1209	0.30	0.67	0.92	0.49	1.11	0.34	1.78	0.69	0.92	1.15E+00	1.48E-01		1.61E+00	2.44E-02		1.17E+00	4.76E-02		-5.56E-01	5.76E-01		-1.37E+00	6.84E-04	Down	-9.51E-01	1.16E-02		Unigene41373_All//gi|260401919|gb|ACX37401.1|//3.00E-67//conserved telomere maintenance component 1 [Arabidopsis thaliana]	Unigene41373_All//1.00E-67//AT4G09680| unknown protein					nr +
Unigene41375_All	422	0.00	0.24	0.00	0.12	0.57	2.03	2.60	1.09	5.10	7.91E+00	3.86E-01		null	null		2.28E+00	3.05E-01		4.11E+00	3.40E-04	Up	-1.26E+00	3.46E-02		9.69E-01	1.09E-02		Unigene41375_All//gi|15450868|gb|AB96705.1|//1.00E-07//Unknown protein [Arabidopsis thaliana]	Unigene41375_All//4.00E-08//AT5G54920| unknown protein	Unigene41375_All//2.00E-31//gi|164341026|gb|EX169897.1|EX169897			GO:0043231	nr -
Unigene41377_All	243	44.14	18.77	46.68	34.64	38.26	18.40	1.39	0.52	0.82	-1.23E+00	1.64E-11	Down	8.06E-02	6.63E-01		1.43E-01	5.43E-01		-9.13E-01	3.16E-06		-1.43E+00	2.58E-01		-7.64E-01	5.01E-01		Unigene41377_All//gi|224138036|ref|XP_002326502.1|//9.00E-15//pseudo response regulator [Populus trichocarpa] >gi|222833824|gb|EEE72301.1|pseudo response regulator [Populus trichocarpa]	Unigene41377_All//3.00E-12//AT4G18020| APRR2; transcription factor/ two-component response regulator	Unigene41377_All//3.00E-130//gi|109887999|gb|DW516968.1|DW516968	ARR-B		GO:0003676//GO:0000871//GO:0006351//GO:0010468//GO:0023060//GO:0043231	nr +
Unigene4138_All	1017	5.14	10.86	5.60	2.79	1.93	2.35	2.16	1.48	3.64	1.08E+00	1.19E-09	Up	1.23E-01	6.35E-01		-5.33E-01	1.51E-01		-2.46E-01	5.62E-01		-5.47E-01	1.65E-01		7.53E-01	6.33E-03		Unigene4138_All//gi|255560481|ref|XP_002521255.1|//6.00E-24//conserved hypothetical protein [Ricinus communis] >gi|223539523|gb|EEF41111.1|conserved hypothetical protein [Ricinus communis]		Unigene4138_All//0.00E+00//gi|72283752|gb|DT054144.1|DT054144				nr +
Unigene41381_All	301	257.26	91.24	120.65	270.75	186.93	618.33	187.52	100.39	79.41	-1.50E+00	3.00E-105	Down	-1.09E+00	1.39E-62	Down	-5.34E-01	2.22E-24		1.19E+00	8.61E-191	Up	-9.01E-01	2.48E-42		-1.24E+00	1.05E-72	Down	Unigene41381_All//gi|559767189|sp|Q6UNT2.1|RL5_CUCSA//3.00E-29//RecName: Full=60S ribosomal protein L5 >gi|34484312|gb|AAQ72789.1| 60S ribosomal protein L5 [Cucumis sativus]	Unigene41381_All//2.00E-30//AT5G39740| 60S ribosomal protein L5 (RPL5B)	Unigene41381_All//2.00E-135//gi|13352810|gb|BG443158.1|BG443158		ko03010|Ribosome	GO:0003002//GO:0005198//GO:0009536//GO:0009887//GO:0010467//GO:0019538//GO:0016020//GO:0019843//GO:0022613//GO:0031981//GO:0046914//GO:0051169//GO:0065003	nr +
Unigene41383_All	630	0.91	0.00	0.00	0.00	0.00	0.00	3.62	1.66	8.92	-9.84E+00	1.52E-03		-9.84E+00	2.60E-03		null	null		null	null		-1.13E+00	3.14E-03		1.30E+00	1.73E-08	Up	Unigene41383_All//gi|255565107|ref|XP_002523546.1|//3.00E-17//conserved hypothetical protein [Ricinus communis] >gi|223537253|gb|EEF38885.1|conserved hypothetical protein [Ricinus communis]		Unigene41383_All//5.00E-17//TC165503			GO:0016853	nr -
Unigene41384_All	386	0.00	0.13	0.00	0.65	2.05	0.00	2.52	6.82	3.92	7.04E+00	6.16E-01		null	null		1.67E+00	5.20E-02		-9.33E+00	7.33E-02		1.44E+00	7.33E-05	Up	6.39E-01	1.73E-01				Unigene41384_All//8.00E-15//TC166225				
Unigene41385_All	578	3.26	2.45	2.21	7.07	5.36	5.47	7.02	8.10	2.83	-4.09E-01	3.92E-01		-5.60E-01	2.58E-01		-3.98E-01	1.95E-01		-3.70E-01	2.51E-01		2.06E-01	4.59E-01		-1.31E+00	1.59E-06	Down	Unigene41385_All//gi|15241317|ref|NP_199906.1|//1.00E-41//DNA binding [Arabidopsis thaliana]	Unigene41385_All//2.00E-34//AT5G50930| DNA binding	Unigene41385_All//0.00E+00//TC146952			GO:0003676//GO:0006351//GO:0044464	nr +
Unigene41389_All	753	1.95	0.87	1.63	0.99	2.88	1.02	0.34	0.78	0.26	-1.15E+00	3.81E-02		-2.58E-01	6.23E-01		1.54E+00	5.23E-04	Up	3.92E-02	9.59E-01		1.21E+00	1.71E-01		-3.49E-01	7.66E-01		Unigene41389_All//gi|53370641|gb|AB389136.1|//5.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene41389_All//7.00E-10//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene41389_All//0.00E+00//gi|78324210|gb|DT544484.1|DT544484			GO:0044464	nr +
Unigene4139_All	2340	3.62	2.43	1.66	8.54	5.34	5.46	10.21	6.57	5.84	-5.79E-01	3.55E-03		-1.12E+00	1.06E-07	Down	-6.76E-01	1.99E-09		-6.44E-01	7.15E-08		-6.35E-01	2.14E-10		-8.06E-01	8.21E-16		Unigene4139_All//gi|297809371|ref|XP_002872569.1|//0.00E+00//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318406|gb|EFH48828.1|transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4139_All//0.00E+00//AT4G11270| transducin family protein / WD-40 repeat family protein	Unigene4139_All//0.00E+00//TC167894				nr -
Unigene41395_All	525	1.59	4.83	3.35	0.28	0.39	0.17	0.00	0.56	1.06	1.60E+00	1.72E-04	Up	1.07E+00	4.06E-02		4.67E-01	8.25E-01		-7.26E-01	7.15E-01		9.12E+00	2.35E-02		1.01E+01	3.28E-04	Up	Unigene41395_All//gi|226532148|ref|NP_001148091.1|//2.00E-37//cytokinin-O-glucosyltransferase 2 [Zea mays] >gi|195615732|gb|ACG29696.1|cytokinin-O-glucosyltransferase 2 [Zea mays]	Unigene41395_All//1.00E-33//AT1G22380| AtUGT85A3 (UDP-glucosyl transferase 85A3); glucuronosyltransferase/ transcription factor/ transferase, transferring glycosyl groups	Unigene41395_All//0.00E+00//ES790817		ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis	GO:0035251	nr -
Unigene41396_All	331	0.63	0.61	0.97	0.75	1.46	1.50	0.89	0.00	8.43	-4.64E-02	9.88E-01		6.10E-01	6.24E-01		9.53E-01	4.24E-01		9.96E-01	3.94E-01		-9.80E+00	2.17E-02		3.24E+00	8.25E-13	Up			Unigene41396_All//4.00E-07//TC163560				
Unigene41397_All	1760	0.00	241.80	90.77	0.00	0.08	0.00	0.00	0.00	0.00	1.79E+01	0.00E+00	Up	1.65E+01	0.00E+00	Up	6.29E+00	3.18E-01		null	null		null	null		null	null									ESTscan -
Unigene41399_All	442	1.30	6.65	0.96	2.37	2.34	1.02	2.01	2.93	1.26	2.35E+00	6.50E-08	Up	-4.34E-01	6.23E-01		-1.81E-02	9.61E-01		-1.21E+00	7.81E-02		5.45E-01	3.22E-01		-6.71E-01	2.94E-01		Unigene41399_All//gi|223452369|gb|ACM89512.1|//7.00E-63//protein kinase Ptil [Glycine max]	Unigene41399_All//1.00E-63//AT3G58350| serine/threonine protein kinase, putative	Unigene41399_All//3.00E-172//gi|48827616|gb|CO126006.1|CO126006		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene41400_All	873	3.24	0.23	0.24	2.85	1.03	0.67	0.00	0.00	0.00	-3.80E+00	6.67E-12	Down	-3.73E+00	3.90E-11	Down	-1.48E+00	1.28E-04	Down	-2.08E+00	2.38E-06	Down	null	null		null	null		Unigene41400_All//gi|224109616|ref|XP_002315256.1|//1.00E-102//beta-ketoacyl-coa synthase family protein [Populus trichocarpa] >gi|222864296|gb|EEF01427.1|beta-ketoacyl-coa synthase family protein [Populus trichocarpa]	Unigene41400_All//2.00E-102//AT5G04530| KCS19 (3-KETOACYL-COA SYNTHASE 19); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene41400_All//0.00E+00//gi|78352011|gb|DT572285.1|DT572285			GO:0006631//GO:0016747//GO:0043231	nr -
Unigene41401_All	937	0.00	0.11	0.68	0.21	0.00	0.29	0.86	2.05	6.51	6.76E+00	3.86E-01		9.41E+00	1.16E-03		-7.73E+00	8.42E-02		4.43E-01	7.63E-01		1.26E+00	3.19E-03		2.92E+00	9.58E-25	Up	Unigene41401_All//gi|224062922|ref|XP_002300933.1|//4.00E-62//f-box family protein [Populus trichocarpa] >gi|222842659|gb|EEE80206.1| f-box family protein [Populus trichocarpa]	Unigene41401_All//9.00E-26//AT1G21340| Dof-type zinc finger domain-containing protein	Unigene41401_All//3.00E-158//DW504846	C2C2-Dof		GO:0001071//GO:0005488//GO:0010468	nr -
Unigene41402_All	308	0.00	2.47	0.00	1.78	0.56	1.17	2.47	1.63	0.65	1.13E+01	1.76E-04	Up	null	null		-1.67E+00	9.26E-02		-6.01E-01	5.66E-01		-6.02E-01	4.12E-01		-1.93E+00	1.14E-02								

Unigene41403_All	517	1.21	5.78	4.53	2.02	2.93	2.27	2.21	6.39	2.16	2.25E+00	1.14E-07	Up	1.90E+00	6.83E-05	Up	5.35E-01	3.52E-01		1.67E-01	7.91E-01		1.53E+00	2.10E-06	Up	-3.34E-02	9.65E-01			Unigene41403_All//gi|65541198|gb|AAF16644.1|AC011661_22//8.00E-06//T23J18.17 [Arabidopsis thaliana]		Unigene41403_All//8.00E-62//TC159277				
Unigene41405_All	383	32.10	23.68	17.38	30.30	20.14	46.46	26.94	12.11	14.67	-4.39E-01	6.80E-03		-8.85E-01	1.49E-07		-5.90E-01	1.32E-04		6.17E-01	1.50E-06		-1.15E+00	3.46E-12	Down	-8.77E-01	2.43E-08			Unigene41405_All//gi|16514198|gb|AAF16644.1|AC011661_22//8.00E-06//T23J18.17 [Arabidopsis thaliana]	Unigene41405_All//0.00E+00//gi|18101139|gb|BM360393.1|BM360393				nr -
Unigene4141_All	1005	37.12	55.16	56.91	27.21	50.57	41.75	9.72	18.76	28.98	5.71E-01	1.00E-15		6.16E-01	9.15E-18		8.94E-01	3.02E-36		6.18E-01	1.30E-14		9.49E-01	6.69E-16		1.58E+00	1.06E-53	Up	Unigene4141_All//gi|14596187|gb|AAK68821.1|//7.00E-19//Unknown protein [Arabidopsis thaliana]	Unigene4141_All//4.00E-20//AT3G07310| unknown protein	Unigene4141_All//0.00E+00//TC144343				nr +
Unigene41411_All	473	1.11	0.64	0.45	2.63	3.13	0.38	1.61	0.62	1.18	-7.83E-01	4.22E-01		-1.30E+00	2.42E-01		2.50E-01	6.91E-01		-2.79E+00	1.35E-04	Down	-1.38E+00	6.73E-02		-4.48E-01	5.31E-01			Unigene41411_All//gi|8778443|gb|AAF79451.1|AC025808_33//2.00E-48//F18O14.11 [Arabidopsis thaliana]	Unigene41411_All//1.00E-49//AT1G19390| wall-associated kinase, putative			ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0032559//GO:0046872	nr +
Unigene41412_All	618	0.85	4.59	2.67	1.05	1.00	1.68	0.75	2.10	1.87	2.44E+00	5.81E-08	Up	1.66E+00	3.57E-03		-6.32E-02	9.25E-01		6.82E-01	3.45E-01		1.48E+00	7.16E-03		1.31E+00	1.95E-02				Unigene41412_All//4.00E-73//BQ414497				
Unigene41413_All	457	0.11	1.88	2.21	4.25	3.39	0.89	0.37	0.73	0.70	4.04E+00	4.20E-04	Up	4.27E+00	1.19E-04	Up	-3.26E-01	5.20E-01		-2.26E+00	1.51E-05	Down	9.83E-01	4.24E-01		9.14E-01	4.53E-01			Unigene41413_All//gi|255547878|ref|XP_002514996.1|//9.00E-57//Ketoacyl-ACP Reductase (KAR) [Ricinus communis] >gi|223546047|gb|EEF47550.1| Ketoacyl-ACP Reductase (KAR) [Ricinus communis]	Unigene41413_All//1.00E-38//AT1G24360| 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase	Unigene41413_All//1.00E-118//TC131743	ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0000166//GO:0004312//GO:0006631//GO:0009238//GO:0009536//GO:0016128	nr -
Unigene4142_All	1546	3.55	1.57	2.65	11.47	5.48	5.49	3.28	0.68	1.65	-1.18E+00	6.99E-06	Down	-4.22E-01	1.23E-01		-1.07E+00	7.48E-18	Down	-1.06E+00	8.99E-16	Down	-2.28E+00	1.38E-15	Down	-9.93E-01	2.14E-05			Unigene4142_All//gi|224127726|ref|XP_002329162.1|//1.00E-116//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene4142_All//5.00E-81//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene4142_All//0.00E+00//TC143607	ko04626|Plant-pathogen interaction		nr -
Unigene41421_All	1226	3722.12	2222.31	3744.92	718.77	944.84	663.05	11.69	10.98	4.97	-7.44E-01	0.00E+00		8.80E-03	3.51E-01		3.95E-01	1.08E-192		-1.16E-01	4.07E-13		-9.09E-02	5.86E-01		-1.23E+00	5.54E-19	Down	Unigene41421_All//gi|119952178|dbj|BAA96385.3|//1.00E-166//oxygen evolving enhancer protein 1 precursor [Bruguiera gymnorhiza]	Unigene41421_All//1.00E-152//AT3G50820| PSBO2 (PHOTOSYSTEM II SUBUNIT O-2); oxygen evolving/poly(U) binding	Unigene41421_All//0.00E+00//TC131249	ko00195|Photosynthesis		nr -
Unigene41422_All	980	0.27	9.51	0.38	0.20	0.07	1.57	0.82	8.10	9.23	5.16E+00	1.12E-45	Up	5.11E-01	6.54E-01		-1.53E+00	4.15E-01		2.95E+00	1.22E-05	Up	3.31E+00	2.82E-35	Up	3.49E+00	7.59E-43	Up	Unigene41422_All//gi|30692434|ref|NP_195677.2|//1.00E-67//glycolipid binding / glycolipid transporter [Arabidopsis thaliana] >gi|22022510|gb|AAM83214.1| AT4g39670/T19P19_60 [Arabidopsis thaliana] >gi|23308251|gb|AAN18095.1| At4g39670/T19P19_60 [Arabidopsis thaliana]	Unigene41422_All//5.00E-69//AT4G39670| glycolipid binding / glycolipid transporter	Unigene41422_All//0.00E+00//TC168880		GO:0005319//GO:0006869//GO:0008289//GO:0044424	nr +
Unigene41423_All	339	0.46	0.00	1.41	2.35	0.20	1.87	0.75	0.99	0.82	-8.85E+00	2.15E-01		1.61E+00	1.82E-01		-3.53E+00	3.03E-04	Down	-3.34E-01	6.86E-01		3.98E-01	7.24E-01		1.37E-01	9.29E-01			Unigene41423_All//gi|124359510|gb|ABD28627.2|//8.00E-09//RNA-directed DNA polymerase (Reverse transcriptase): Ribonuclease H [Medicago truncatula]		Unigene41423_All//1.00E-158//ES815015		GO:0005488	nr -
Unigene41424_All	310	0.00	1.31	0.17	2.41	0.89	0.00	2.46	3.37	7.33	1.04E+01	1.36E-02		7.42E+00	6.35E-01		-1.44E+00	7.43E-02		-1.12E+01	9.80E-05	Down	4.57E-01	4.63E-01		1.58E+00	5.86E-05	Up								
Unigene41425_All	646	2.11	0.55	1.40	4.09	5.22	3.01	4.71	0.97	3.02	-1.94E+00	2.18E-03		-5.88E-01	3.36E-01		3.54E-01	3.27E-01		-4.43E-01	2.86E-01		-2.28E+00	1.23E-09	Down	-6.41E-01	3.69E-02			Unigene41425_All//gi|11072030|gb|AAC28909.1|AC008113_25//9.00E-47//F12A21.9 [Arabidopsis thaliana]	Unigene41425_All//5.00E-48//AT1G67780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot apex, flower, root, seed; EXPRESSED DURING: petal differentiation and expansion stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: DDT superfamily (InterPro:IPR018501), DDT subgroup (InterPro:IPR018500), Cell division cycle-associated protein (InterPro:IPR018866); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67270.1); Has 280 Blast hits to 277 proteins in 72 species: Archae - 0; Bacteria - 0; Metazoa - 114; Fungi - 47; Plants - 92; Viruses - 0; Other Eukaryotes - 27 (source: NCBI BLink).	Unigene41425_All//8.00E-10//TC160339				nr -
Unigene41426_All	580	406.57	219.63	631.84	364.16	305.88	397.91	24.20	72.85	13.33	-8.89E-01	3.25E-139		6.36E-01	1.46E-117		-2.52E-01	1.68E-15		1.28E-01	1.36E-04		1.59E+00	6.64E-77	Up	-8.61E-01	1.03E-10			Unigene41426_All//gi|3183088|sp|Q43681.1|NLTP_VIGUN//2.00E-29//RecName: Full=Probable non-specific lipid-transfer protein AKCS9; Short=LTP; Flags: Precursor >gi|499034|emb|CAA56113.1| lipid transfer like protein [Vigna unguiculata]	Unigene41426_All//7.00E-18//AT3G18280| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene41426_All//0.00E+00//gi|109835291|gb|DW233855.1|DW233855		GO:0006810	nr +
Unigene41427_All	1948	0.00	0.00	0.00	0.05	0.00	0.09	13.41	13.47	27.75	null	null		null	null		-5.68E+00	3.13E-01		8.59E-01	6.95E-01		6.50E-03	9.86E-01		1.05E+00	4.33E-53	Up	Unigene41427_All//gi|15242221|ref|NP_197017.1|//1.00E-114//WRKY72: transcription factor [Arabidopsis thaliana] >gi|29839650|sp|Q9LXG8.1|WRK72_ARATH RecName: Full=Probable WRKY transcription factor 72; AltName: Full=WRKY DNA-binding protein 72	Unigene41427_All//5.00E-62//AT5G15130| WRKY72; transcription factor	Unigene41427_All//0.00E+00//TC165579	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene41428_All	438	1.55	1.97	1.09	1.36	0.79	0.00	0.00	0.00	0.00	3.41E-01	6.17E-01		-5.05E-01	5.82E-01		-7.96E-01	3.88E-01		-1.04E+01	7.70E-04	Down	null	null		null	null			Unigene41428_All//gi|77416923|gb|AB481857.1|//1.00E-09//ripening regulated protein-like [Solanum tuberosum]	Unigene41428_All//8.00E-08//AT1G23740| oxidoreductase, zinc-binding dehydrogenase family protein				GO:0003824//GO:0005488//GO:0008152//GO:0009536//GO:0016020	nr -
Unigene41429_All	1040	2.21	0.10	0.00	2.92	6.95	1.09	0.00	0.00	0.00	-4.51E+00	6.73E-11	Down	-1.11E+01	1.38E-12	Down	1.25E+00	4.03E-09	Up	-1.43E+00	9.09E-05	Down	null	null		null	null			Unigene41429_All//gi|224101209|ref|XP_002312186.1|//1.00E-168//laccase 90a [Populus trichocarpa] >gi|222852006|gb|EEE89553.1| laccase 90a [Populus trichocarpa]	Unigene41429_All//2.00E-161//AT2G40370| LAC5 (laccase 5); laccase	Unigene41429_All//8.00E-119//gi|164246155|gb|ES821488.1|ES821488		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene4143_All	580	15.52	15.90	19.00	31.43	29.75	37.14	46.00	36.61	22.25	3.53E-02	8.65E-01		2.93E-01	1.19E-01		-7.97E-02	5.97E-01		2.41E-01	5.45E-02		-3.29E-01	5.00E-04		-1.05E+00	8.75E-27	Down			Unigene4143_All//0.00E+00//TC135400				ESTscan -
Unigene41431_All	433	0.48	0.00	0.25	1.96	1.83	0.94	2.44	0.10	1.01	-8.92E+00	1.22E-01		-9.74E-01	6.20E-01		-9.66E-02	8.77E-01		-1.06E+00	1.81E-01		-4.66E+00	1.94E-06	Down	-1.27E+00	2.97E-02			Unigene41431_All//gi|115452545|ref|NP_001049873.1|//9.00E-34//Os03g0302900 [Oryza sativa Japonica Group] >gi|108707707|gb|ABF95502.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548344|dbj|BAF11787.1| Os03g0302900 [Oryza sativa Japonica Group]	Unigene41431_All//2.00E-26//AT3G05750| unknown protein	Unigene41431_All//1.00E-07//ES822342		GO:0016787//GO:0043231	nr -
Unigene41434_All	871	2.10	1.51	1.47	3.66	0.59	0.67	1.26	0.72	0.55	-4.75E-01	3.32E-01		-5.19E-01	3.11E-01		-2.63E+00	8.34E-12	Down	-2.44E+00	1.58E-09	Down	-8.10E-01	1.69E-01		-1.20E+00	3.41E-02			Unigene41434_All//gi|18405537|ref|NP_564700.1|//3.00E-32//ATP binding / nucleotide binding / phenylalanine-tRNA ligase [Arabidopsis thaliana]	Unigene41434_All//1.00E-33//AT1G55790| ATP binding / nucleotide binding / phenylalanine-tRNA ligase	Unigene41434_All//9.00E-69//TC160819		GO:0005488//GO:0006412	nr -
Unigene41435_All	571	2.75	1.15	0.84	2.88	2.17	1.82	1.48	0.37	0.07	-1.25E+00	1.98E-02		-1.71E+00	3.82E-03		-4.07E-01	4.45E-01		-6.62E-01	2.13E-01		-2.02E+00	7.45E-03		-4.41E+00	2.37E-05	Down			Unigene41435_All//4.00E-156//gi|48797028|gb|CO098342.1|CO098342				
Unigene41437_All	1326	0.08	0.00	0.04	0.19	0.10	0.27	5.77	1.01	12.50	-6.30E+00	3.71E-01		-9.73E-01	7.20E-01		-8.54E-01	5.73E-01		5.37E-01	6.94E-01		-2.52E+00	6.22E-26	Down	1.11E+00	1.51E-18	Up	Unigene41437_All//gi|9794870|gb|AAF98369.1|AF158253.1|//1.00E-144//patatin-like protein 3 [Nicotiana tabacum]	Unigene41437_All//1.00E-108//AT4G37050| PLP4 (PATATIN-LIKE PROTEIN 4); nutrient reservoir	Unigene41437_All//4.00E-38//gi|48753539|gb|CO084058.1|CO084058				nr -
Unigene41438_All	484	1.84	0.84	2.97	7.00	5.76	3.08	4.02	4.15	6.58	-1.13E+00	1.30E-01		6.93E-01	2.40E-01		-2.80E-01	4.41E-01		-1.18E+00	4.22E-04	Down	4.48E-02	9.33E-01		7.13E-01	1.77E-02				Unigene41438_All//6.00E-07//TC162395				
Unigene41439_All	407	1.93	20.92	2.88	10.16	16.75	14.65	28.15	31.73	13.80	3.44E+00	7.80E-32	Up	5.78E-01	3.90E-01		7.22E-01	7.68E-04		5.28E-01	3.21E-02		1.73E-01	2.74E-01		-1.03E+00	1.10E-11	Down			Unigene41439_All//4.00E-63//gi|164343193|gb|EV483287.1|EV483287				
Unigene4144_All	2544	2.51	0.72	1.07	8.93	8.20	3.78	1.48	0.30	0.42	-1.81E+00	5.42E-12	Down	-1.23E+00	8.59E-07	Down	-1.22E-01	3.57E-01		-1.24E+00	1.62E-25	Down	-2.32E+00	5.39E-12	Down	-1.81E+00	3.20E-09	Down	Unigene4144_All//gi|297820234|ref|XP_002878000.1|//0.00E+00//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323838|gb|EFH54259.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4144_All//0.00E+00//AT3G54790| armadillo/beta-catenin repeat family protein / U-box domain-containing protein	Unigene4144_All//0.00E+00//DR453847	ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene41440_All	393	2.13	1.16	0.00	1.39	1.75	1.49	0.75	0.32	1.52	-8.76E-01	2.47E-01		-1.11E+01	1.19E-04	Down	3.30E-01	7.52E-01		9.96E-02	9.36E-01		-1.24E+00	3.73E-01		1.01E+00	2.18E-01		Unigene41440_All//gi|297841909|ref|XP_002888836.1|//4.00E-14//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297334677|gb|EFH65095.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene41440_All//2.00E-15//AT1G71420| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene41445_All	654	0.48	3.33	3.42	0.23	1.16	0.69	0.71	2.43	1.22	2.80E+00	3.73E-07	Up	2.83E+00	4.06E-07	Up	2.34E+00	1.36E-02		1.60E+00	2.05E-01		1.77E+00	4.38E-04	Up	7.77E-01	2.57E-01		Unigene41445_All//gi|89258512|gb|AB065465.1|//3.00E-63//protein phosphatase 2C [Gossypium hirsutum]	Unigene41445_All//2.00E-32//AT1G07430| protein phosphatase 2C, putative / PP2C, putative	Unigene41445_All//0.00E+00//ES799947		GO:0004721	nr -
Unigene41447_All	317	0.17	1.28	3.19	4.09	1.85	1.00	1.87	1.32	1.38	2.95E+00	5.91E-02		4.27E+00	1.19E-04	Up	-1.15E+00	4.27E-02		-2.03E+00	1.62E-03		-5.02E-01	5.74E-01		-4.34E-01	6.08E-01				Unigene41447_All//4.00E-07//DW518288				
Unigene4145_All	1481	11.59	8.96	10.89	2.56	2.67	1.25	3.88	2.91	2.99	-3.70E-01	6.25E-03		-8.90E-02	5.89E-01		6.49E-02	8.57E-01		-1.03E+00	9.53E-04	Down	-4.18E-01	6.60E-02		-3.79E-01	8.34E-02		Unigene4145_All//gi|297833678|ref|XP_002884721.1|//1.00E-104//PTAC13 [Arabidopsis lyrata subsp. lyrata] >gi|297330561|gb|EFH60980.1| PTAC13 [Arabidopsis lyrata subsp. lyrata]	Unigene4145_All//2.00E-88//AT3G09210| PTAC13 (PLASTID TRANSCRIPTIONALLY ACTIVE13); transcription elongation regulator	Unigene4145_All//0.00E+00//TC162970				nr -
Unigene41450_All	564	1.67	0.18	0.09	0.88	1.47	2.40	1.20	1.26	2.47	-3.22E+00	6.76E-04	Down	-4.14E+00	2.90E-04	Down	7.30E-01	3.87E-01		1.44E+00	1.69E-02		7.09E-02	9.42E-01		1.04E+00	3.40E-02		Unigene41450_All//gi|297817502|ref|XP_002876634.1|//1.00E-25//nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297322472|gb|EFH52893.1| nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene41450_All//2.00E-25//AT3G61690| unknown protein	Unigene41450_All//1.00E-11//TC169890				nr +
Unigene41452_All	720	148.32	499.02	267.88	19.03	43.19	91.96	16.32	143.38	112.21	1.75E+00	0.00E+00	Up	8.53E-01	2.94E-103		1.18E+00	6.61E-35	Up	2.27E+00	1.22E-169	Up	3.13E+00	0.00E+00	Up	2.78E+00	1.23E-303	Up	Unigene41452_All//gi|169786772|gb|ACA79924.1|//3.00E-41//chloroplast N receptor-interacting protein 1 [Nicotiana benthamiana] >gi|169786774|gb|ACA79925.1| chloroplast N receptor-interacting protein 1 [Nicotiana benthamiana]	Unigene41452_All//1.00E-37//AT4G35770| SEN1 (SENESCENCE 1)	Unigene41452_All//0.00E+00//gi|48795732|gb|CO097046.1|CO097046			GO:0004871//GO:0006950//GO:0009536//GO:0009719//GO:0016783//GO:0032502	nr +
Unigene41454_All	731	0.36	0.07	0.58	0.07	0.75	0.49	2.54	0.57	1.04	-2.37E+00	2.14E-01		7.03E-01	5.54E-01		3.47E+00	1.22E-02		2.86E+00	9.45E-02		-2.15E+00	8.47E-06	Down	-1.30E+00	2.09E-03				Unigene41454_All//6.00E-48//DT461883				

Unigene41455_All	1753	0.00	0.12	0.00	0.06	0.08	0.00	3.18	7.49	11.73	6.85E+00	1.36E-01		null	null		4.69E-01	8.76E-01		-5.83E+00	3.99E-01		1.23E+00	6.85E-17	Up	1.88E+00	1.21E-48	Up	Unigene41455_All//gi|225434959|ref|XP_002281079.1|//2.00E-22//PREDICTED: similar to GTP1/OBG family member [Vitis vinifera]	Unigene41455_All//6.00E-27//AT1G07620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: GTP-binding protein Obg/CgtA (InterPro:IPR014100); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G02390.1); Has 447 Blast hits to 405 proteins in 72 species: Archae - 0; Bacteria - 6; Metazoa - 43; Fungi - 29; Plants - 122; Viruses - 3; Other Eukaryotes - 244 (source: NCBI BLink).	Unigene41455_All//0.00E+00//DT051216				nr +
Unigene41459_All	310	0.00	1.14	4.98	2.73	0.89	0.29	0.55	2.02	1.16	1.02E+01	2.46E-02		1.23E+01	1.65E-08	Up	-1.62E+00	3.12E-02		-3.23E+00	1.04E-03		1.89E+00	3.49E-02		1.08E+00	3.50E-01									
Unigene41461_All	831	0.25	0.00	0.26	5.22	9.12	10.60	0.10	0.10	0.00	-7.98E+00	1.22E-01		2.56E-02	1.00E+00		8.06E-01	6.08E-05		1.02E+00	1.35E-07	Up	-1.71E-02	1.01E+00		-6.67E+00	3.58E-01		Unigene41461_All//gi|89276293|gb|ABD66503.1|//2.00E-74//actin depolymerizing factor 7 [Gossypium hirsutum]	Unigene41461_All//5.00E-61//AT1G01750| ADF11 (ACTIN DEPOLYMERIZING FACTOR 11); actin binding	Unigene41461_All//0.00E+00//gi|48813738|gb|CO115051.1|CO115051			GO:0008092//GO:0044464	nr -
Unigene41464_All	816	0.19	0.00	0.00	31.32	25.11	26.07	2.75	1.18	1.03	-7.59E+00	2.15E-01		-7.59E+00	2.44E-01		-3.19E-01	1.96E-03		-2.65E-01	1.69E-02		-1.22E+00	1.68E-03		-1.42E+00	2.20E-04	Down	Unigene41464_All//gi|225626259|gb|ACN97179.1|//7.00E-69//MYB transcription factor [Populus trichocarpa]	Unigene41464_All//2.00E-61//AT1G17950| MYB32 (MYB DOMAIN PROTEIN 32); DNA binding / transcription factor	Unigene41464_All//3.00E-53//BF270511	MYB		GO:0006350//GO:0009725//GO:0010468//GO:0043231	nr +
Unigene41467_All	756	0.00	0.00	0.00	0.00	0.00	0.00	47.37	84.70	12.23	null	null		null	null		null	null		null	null		8.38E-01	2.09E-42		-1.95E+00	1.30E-89	Down	Unigene41467_All//gi|124361129|gb|ABN09101.1|//8.00E-08//Ribonuclease H [Medicago truncatula]		Unigene41467_All//3.00E-31//gi|78330320|gb|DT550594.1|DT550594				nr +
Unigene4147_All	1734	18.01	60.78	40.72	17.18	6.89	12.09	51.33	236.82	20.49	1.75E+00	5.59E-179	Up	1.18E+00	1.89E-64	Up	-1.32E+00	9.73E-42	Down	-5.07E-01	1.18E-07		2.21E+00	0.00E+00	Up	-1.32E+00	1.61E-126	Down	Unigene4147_All//gi|224081773|ref|XP_002306489.1|//1.00E-167//cytochrome P450 [Populus trichocarpa] >gi|222855938|gb|EEE93485.1|cytochrome P450 [Populus trichocarpa]	Unigene4147_All//7.00E-143//AT4G37370| CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene4147_All//0.00E+00//TC130103		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene41470_All	453	757.55	808.03	612.32	36.62	75.94	84.25	10.27	23.25	13.28	9.31E-02	6.29E-04		-3.07E-01	4.61E-29		1.05E+00	4.34E-32	Up	1.20E+00	5.56E-40	Up	1.18E+00	7.88E-13	Up	3.71E-01	8.34E-02		Unigene41470_All//gi|55168340|gb|AAV44205.1|//6.00E-28//unknow protein [Oryza sativa Japonica Group]		Unigene41470_All//0.00E+00//gi|164264449|gb|ES832979.1|ES832979			GO:0009536	nr +
Unigene41472_All	880	2.79	1.21	2.06	1.19	1.10	0.31	1.39	4.18	0.41	-1.21E+00	3.44E-03		-4.42E-01	3.09E-01		-1.18E-01	8.38E-01		-1.95E+00	7.53E-03		1.58E+00	2.33E-07	Up	-1.77E+00	1.72E-03		Unigene41472_All//gi|224059590|ref|XP_002299922.1|//1.00E-45//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222847180|gb|EEE84727.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene41472_All//3.00E-11//AT5G45510| TA01 (TARGET OF AVRB OPERATION1); ATP binding / protein binding / transmembrane receptor				nr +
Unigene41473_All	662	0.00	0.15	0.00	2.48	0.52	0.14	0.77	1.83	0.30	7.26E+00	3.86E-01		null	null		-2.26E+00	2.36E-05	Down	-4.19E+00	4.25E-08	Down	1.26E+00	2.52E-02		-1.35E+00	1.40E-01								
Unigene41476_All	1546	0.07	0.13	1.07	0.90	0.22	0.61	9.79	17.19	9.07	9.53E-01	6.21E-01		3.98E+00	5.16E-07	Up	-2.02E+00	4.22E-04	Down	-5.56E-01	3.52E-01		8.12E-01	3.50E-17		-1.10E-01	4.43E-01		Unigene41476_All//gi|225425912|ref|XP_002267341.1|//1.00E-109//PREDICTED: similar to F21J9.9 [Vitis vinifera]	Unigene41476_All//2.00E-99//AT1G24430| transferase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene41476_All//3.00E-147//TC142154		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016740	nr +
Unigene41479_All	461	1.93	0.11	0.35	1.73	2.32	3.04	3.67	1.72	4.15	-4.13E+00	2.52E-04	Down	-2.48E+00	7.18E-03		4.22E-01	5.72E-01		8.13E-01	1.67E-01		-1.09E+00	1.64E-02		1.77E-01	6.68E-01		Unigene41479_All//gi|297720017|ref|NP_001172370.1|//4.00E-38//Os01g0500550 [Oryza sativa Japonica Group] >gi|56201797|dbj|BAD73247.1| bZIP protein-like [Oryza sativa Japonica Group] >gi|255673275|dbj|BAH91100.1|Os01g0500550 [Oryza sativa Japonica Group]	Unigene41479_All//9.00E-67//AT5G25590| INVOLVED IN: N-terminal protein myristoylation; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF630 (InterPro:IPR006888), Protein of unknown function DUF632 (InterPro:IPR006867), Actin-binding FH2 (InterPro:IPR015425); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52320.4); Has 31848 Blast hits to 18905 proteins in 762 species: Archae - 79; Bacteria - 761; Metazoa - 15943; Fungi - 3494; Plants - 1748; Viruses - 431; Other Eukaryotes - 9392 (source: NCBI BLink).	Unigene41479_All//0.00E+00//gi|78345386|gb|DT565660.1|DT565660			GO:0016020	nr +
Unigene4148_All	470	13.47	13.15	9.63	4.56	5.13	5.67	2.70	0.53	0.59	-3.44E-02	8.96E-01		-4.84E-01	5.03E-02		1.70E-01	7.37E-01		3.15E-01	4.71E-01		-2.34E+00	1.56E-04	Down	-2.19E+00	1.97E-04	Down	Unigene4148_All//gi|28466863|gb|AA044040.1|//1.00E-36//At4g31130 [Arabidopsis thaliana]	Unigene4148_All//9.00E-38//AT4G31130| unknown protein	Unigene4148_All//7.00E-176//gi|21092345|gb|BQ404658.1|BQ404658				nr -
Unigene41480_All	938	0.00	0.00	0.00	0.00	0.00	0.00	0.27	3.97	1.61	null	null		null	null		null	null		null	null		3.87E+00	4.23E-19	Up	2.58E+00	6.02E-06	Up	Unigene41480_All//gi|255573324|ref|XP_002527589.1|//5.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223533028|gb|EEF34791.1|conserved hypothetical protein [Ricinus communis]						nr +
Unigene41481_All	953	0.16	0.64	1.45	0.58	1.59	0.90	1.20	0.96	6.35	1.95E+00	6.03E-02		3.14E+00	4.89E-05	Up	1.47E+00	7.97E-03		6.47E-01	4.23E-01		-3.12E-01	6.25E-01		2.41E+00	4.97E-20	Up	Unigene41481_All//gi|299470556|emb|CBN78544.1|//2.00E-08//ATG2 Autophagy-related protein homolog [Ectocarpus siliculosus]	Unigene41481_All//2.00E-51//AT3G19190| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: ATG2, C-terminal (InterPro:IPR015412); Has 603 Blast hits to 514 proteins in 156 species: Archae - 0; Bacteria - 19; Metazoa - 326; Fungi - 168; Plants - 38; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene41481_All//0.00E+00//gi|109854230|gb|DW483209.1|DW483209				nr +
Unigene41483_All	686	2.36	1.18	1.24	1.02	0.65	0.40	0.99	0.91	3.43	-1.00E+00	5.37E-02		-9.29E-01	8.76E-02		-6.40E-01	4.54E-01		-1.36E+00	1.31E-01		-1.10E-01	8.90E-01		1.80E+00	5.92E-06	Up	Unigene41483_All//gi|289466341|gb|ADG94856.1|//7.00E-57//DRE transcription factor 1 [Vitis pseudoreticulata]	Unigene41483_All//3.00E-34//AT1G76890| RAP2.4 (related to AP2 4); DNA binding / transcription factor	Unigene41483_All//6.00E-88//DN803733	AP2-EREBP		GO:0006350//GO:0010468	nr +
Unigene41485_All	690	0.38	0.44	0.00	1.16	1.60	0.20	2.82	0.79	1.10	2.17E-01	8.64E-01		-8.57E+00	8.56E-02		4.67E-01	5.30E-01		-2.56E+00	6.01E-03		-1.84E+00	4.63E-05	Down	-1.36E+00	1.00E-03		Unigene41485_All//gi|297841429|ref|XP_002888596.1|//1.00E-40//exostosin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334437|gb|EFH64855.1|exostosin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene41485_All//2.00E-41//AT1G67410| exostosin family protein	Unigene41485_All//0.00E+00//gi|48813672|gb|CO114985.1|CO114985			GO:0003824//GO:0031410	nr -
Unigene41486_All	797	0.00	0.00	0.00	0.25	0.09	0.06	2.92	4.56	0.80	null	null		null	null		-1.53E+00	4.15E-01		-2.14E+00	3.47E-01		6.45E-01	2.53E-02		-1.87E+00	2.99E-06	Down								
Unigene41487_All	223	29.80	18.18	21.49	49.14	44.32	66.02	22.94	11.25	11.79	-7.13E-01	1.73E-03		-4.71E-01	5.03E-02		-1.49E-01	4.49E-01		4.26E-01	3.45E-03		-1.03E+00	1.70E-05	Down	-9.60E-01	3.44E-05		Unigene41487_All//gi|115448105|ref|NP_001047832.1|//2.00E-20//Os02g0699600 [Oryza sativa Japonica Group] >gi|113537363|dbj|BAF09746.1|Os02g0699600 [Oryza sativa Japonica Group]	Unigene41487_All//2.00E-20//AT5G60670| 60S ribosomal protein L12 (RPL12C)	Unigene41487_All//6.00E-110//gi|21089610|gb|BQ401923.1|BQ401923		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene41488_All	373	1.40	11.28	3.85	0.27	0.18	1.94	0.34	0.90	0.21	3.01E+00	3.41E-14	Up	1.46E+00	1.58E-02		-5.33E-01	8.16E-01		2.86E+00	7.12E-03		1.40E+00	2.76E-01		-6.71E-01	7.19E-01		Unigene41488_All//gi|114329246|gb|ABI64152.1|//7.00E-31//hydroxymethylbutenyl diphosphate reductase [Camptotheca acuminata]	Unigene41488_All//3.00E-23//AT4G34350| HDR (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE REDUCTASE); 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase/ 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	Unigene41488_All//4.00E-152//C0072954		ko00900|Terpenoid backbone biosynthesis	GO:0006090//GO:0006721//GO:0009532//GO:0016726//GO:0042221//GO:0052592	nr -
Unigene4149_All	788	23.11	21.86	19.33	12.14	19.71	8.60	6.60	0.95	1.67	-7.98E-02	6.10E-01		-2.58E-01	6.93E-02		6.99E-01	1.28E-07		-4.98E-01	7.06E-03		-2.79E+00	6.78E-20	Down	-1.98E+00	5.60E-14	Down	Unigene4149_All//gi|28466863|gb|AA044040.1|//1.00E-72//At4g31130 [Arabidopsis thaliana]	Unigene4149_All//7.00E-74//AT4G31130| unknown protein	Unigene4149_All//0.00E+00//gi|21092345|gb|BQ404658.1|BQ404658				nr -
Unigene41491_All	430	2.92	0.24	0.99	1.62	1.20	2.21	1.38	0.87	0.56	-3.63E+00	2.00E-05	Down	-1.56E+00	1.90E-02		-4.33E-01	6.06E-01		4.44E-01	5.74E-01		-6.54E-01	4.45E-01		-1.31E+00	1.15E-01		Unigene41491_All//gi|297851320|ref|XP_002893541.1|//8.00E-54//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297339383|gb|EFH69800.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene41491_All//4.00E-54//AT1G28690| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene41492_All	259	18.99	53.60	20.56	18.08	16.49	43.59	13.39	12.59	23.38	1.50E+00	2.36E-19	Up	1.15E-01	6.75E-01		-1.33E-01	6.71E-01		1.27E+00	3.05E-13	Up	-8.88E-02	7.83E-01		8.05E-01	1.24E-04					Unigene41492_All//8.00E-88//gi|109874367|gb|DW503341.1|DW503341					
Unigene41495_All	355	3.83	0.71	1.50	6.60	3.01	5.98	6.19	1.41	0.90	-2.42E+00	3.35E-04	Down	-1.35E+00	2.93E-02		-1.13E+00	3.99E-03		-1.41E-01	7.41E-01		-2.13E+00	1.20E-06	Down	-2.79E+00	4.04E-09	Down				Unigene41495_All//6.00E-148//gi|21101391|gb|BQ413704.1|BQ413704					
Unigene41498_All	558	2.16	0.54	2.67	5.71	4.69	1.54	1.74	0.45	0.29	-1.99E+00	3.72E-03		3.09E-01	6.01E-01		-2.85E-01	4.52E-01		-1.89E+00	4.32E-07	Down	-1.96E+00	4.44E-03		-2.61E+00	3.35E-04	Down				Unigene41498_All//0.00E+00//CO120903					
Unigene41499_All	267	5.68	7.78	5.38	14.37	6.84	4.40	2.53	1.57	1.34	4.53E-01	3.23E-01		-7.77E-02	8.89E-01		-1.07E+00	2.44E-04	Down	-1.71E+00	2.22E-07	Down	-6.95E-01	3.94E-01		-9.16E-01	2.21E-01					Unigene41499_All//3.00E-35//DW513539					
Unigene4150_All	349	2.25	1.02	0.00	8.14	7.10	5.82	0.97	0.48	1.48	-1.15E+00	1.53E-01		-1.11E+01	2.21E-04	Down	-1.96E-01	6.14E-01		-4.82E-01	2.20E-01		-1.02E+00	3.99E-01		6.15E-01	4.94E-01					Unigene4150_All//4.00E-84//DW504295					
Unigene41502_All	518	0.81	3.33	0.21	1.83	3.26	3.75	1.63	1.61	1.54	2.04E+00	2.81E-04	Up	-1.97E+00	1.51E-01		8.34E-01	1.04E-01		1.04E+00	2.88E-02		-1.66E-02	1.02E+00		-8.58E-02	9.02E-01		Unigene41502_All//gi|79441748|ref|NP_190776.2|//6.00E-17//chx28 (cation/hydrogen exchanger 28); monovalent cation:proton antiporter [Arabidopsis thaliana] >gi|298351604|sp|Q8L709.2|CHX28_ARATH RecName: Full=Cation/H(+) antiporter 28; AltName: Full=Protein CATION/H+ EXCHANGER 28; Short=AtCHX28	Unigene41502_All//4.00E-17//AT3G52080| chx28 (cation/hydrogen exchanger 28); monovalent cation:proton antiporter				GO:0006810	nr -
Unigene41504_All	701	0.45	0.00	0.15	7.11	12.08	4.70	2.59	0.83	0.11	-8.81E+00	3.65E-02		-1.56E+00	3.30E-01		7.66E-01	4.69E-05		-5.95E-01	2.72E-02		-1.64E+00	3.51E-04	Down	-4.51E+00	5.15E-11	Down	Unigene41504_All//gi|226508444|ref|NP_001148305.1|//2.00E-11//zinc finger protein 6 [Zea mays] >gi|195617338|gb|ACG30499.1| zinc finger protein 6 [Zea mays]	Unigene41504_All//5.00E-11//AT1G10480| ZFP5 (ZINC FINGER PROTEIN 5); nucleic acid binding / transcription factor/ zinc ion binding		C2H2			nr -
Unigene41506_All	835	0.25	25.61	1.79	0.60	0.95	4.06	0.56	0.85	5.73	6.68E+00	3.48E-115	Up	2.83E+00	6.17E-05	Up	6.69E-01	4.42E-01		2.77E+00	3.47E-11	Up	6.11E-01	4.27E-01		3.36E+00	3.21E-22	Up								
Unigene41508_All	616	2.46	2.14	1.90	0.16	0.00	0.59	16.95	8.62	80.00	-2.04E-01	6.81E-01		-3.73E-01	5.08E-01		-7.34E+00	3.13E-01		1.86E+00	2.19E-01		-9.76E-01	1.35E-09		2.24E+00	1.72E-144	Up	Unigene41508_All//gi|903357|gb|AAB70438.1|//2.00E-55//Strong similarity to Arabidopsis 2A6 (gb|X83096) [Arabidopsis thaliana]	Unigene41508_All//1.00E-56//AT1G04380| 2-oxoglutarate-dependent dioxygenase, putative	Unigene41508_All//0.00E+00//TC146757		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0016706	nr +

Unigene4151_All	1013	4.86	0.90	2.89	15.24	10.13	6.42	38.90	18.24	13.57	-2.43E+00	2.21E-13	Down	-7.48E-01	8.11E-03		-5.90E-01	6.36E-06		-1.25E+00	1.07E-17	Down	-1.09E+00	1.09E-40	Down	-1.52E+00	2.46E-69	Down	Unigene4151_All//gi|2370459|emb|CAA72716.1|/8.00E-29//PFF1 protein [Sinapis alba]	Unigene4151_All//1.00E-29//AT5G24860| PFF1 (FLOWERING PROMOTING FACTOR 1)	Unigene4151_All//0.00E+00//DW513005				nr +
Unigene4511_All	284	1.84	1.78	1.13	3.33	2.18	1.75	3.28	0.29	0.70	-4.63E-02	9.76E-01		-7.12E-01	4.97E-01		-6.11E-01	3.90E-01		-9.30E-01	2.06E-01		-3.48E+00	7.79E-05	Down	-2.22E+00	1.63E-03					Unigene4511_All//6.00E-52//TC177402				
Unigene4513_All	377	0.28	0.40	2.82	1.59	1.55	1.80	0.00	0.33	0.11	5.39E-01	7.79E-01		3.35E+00	3.36E-04	Up	-3.02E-02	9.50E-01		1.81E-01	8.44E-01		8.38E+00	2.40E-01		6.72E+00	6.45E-01					Unigene4513_All//3.00E-11//FL577607				
Unigene4514_All	527	2.78	0.38	0.61	2.27	0.85	1.71	0.24	0.63	0.45	-2.85E+00	3.60E-05	Down	-2.20E+00	7.90E-04	Down	-1.42E+00	1.82E-02		-4.04E-01	5.45E-01		1.40E+00	2.76E-01		9.14E-01	5.42E-01		Unigene4514_All//gi|224133044|ref|XP_002321468.1|/9.00E-10//predicted protein [Populus trichocarpa] >gi|222868464|gb|EEF05595.1| predicted protein [Populus trichocarpa]		Unigene4514_All//0.00E+00//gi|78350056|gb|DT570330.1|DT570330				nr +
Unigene4152_All	1851	5.79	5.39	4.23	14.48	11.48	11.64	19.44	11.09	6.93	-1.04E-01	6.14E-01		-4.54E-01	1.32E-02		-3.35E-01	7.41E-04		-3.15E-01	2.71E-03		-8.10E-01	7.06E-23		-1.49E+00	1.84E-61	Down	Unigene4152_All//gi|32395916|gb|AAP41818.1|/0.00E+00//PS8IPK [Solanum lycopersicum]	Unigene4152_All//6.00E-173//AT5G03160| ATPS8IPK (ARABIDOPSIS HOMOLOG OF MAMALLIAN PS8IPK); binding / heat shock protein binding	Unigene4152_All//0.00E+00//TC176004	ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene41521_All	1189	0.00	0.09	0.00	0.67	0.58	0.30	17.42	0.14	0.64	6.41E+00	3.86E-01		null	null		-2.11E-01	8.06E-01		-1.14E+00	1.63E-01		-6.95E+00	1.83E-139	Down	-4.77E+00	2.58E-124	Down	Unigene41521_All//gi|225459852|ref|XP_002284837.1|/5.00E-91//PREDICTED: similar to T23E18.17 [Vitis vinifera]	Unigene41521_All//4.00E-77//AT1G76240| unknown protein	Unigene41521_All//0.00E+00//DR453807		GO:0043231	nr -
Unigene41523_All	421	0.99	0.12	0.25	1.18	0.90	0.00	3.41	0.30	0.85	-3.05E+00	4.65E-02		-1.97E+00	1.51E-01		-3.95E-01	6.89E-01		-1.02E+01	2.97E-03		-3.52E+00	3.19E-07	Down	-2.00E+00	1.70E-04	Down				Unigene41523_All//1.00E-93//TC177477				
Unigene41524_All	319	0.00	0.00	0.00	71.36	19.21	15.29	0.00	0.52	0.25	null	null		null	null		-1.89E+00	1.69E-54	Down	-2.22E+00	3.09E-58	Down	9.03E+00	1.39E-01		7.96E+00	4.04E-01		Unigene41524_All//gi|255538400|ref|XP_002510265.1|/2.00E-10//conserved hypothetical protein [Ricinus communis] >gi|223550966|gb|EEF52452.1| conserved hypothetical protein [Ricinus communis]	Unigene41524_All//4.00E-05//AT5G66815| unknown protein				nr -
Unigene41525_All	483	0.33	1.57	2.43	0.83	0.93	0.00	0.00	0.00	0.00	2.28E+00	1.60E-02		2.90E+00	4.34E-04	Up	1.68E-01	9.04E-01		-9.69E+00	1.11E-02		null	null		null	null									ESTscan +
Unigene41528_All	439	0.48	2.42	0.49	6.47	6.28	14.09	0.00	0.00	0.00	2.35E+00	2.58E-03		2.55E-02	1.00E+00		-4.36E-02	9.06E-01		1.12E+00	2.51E-06	Up	null	null		null	null		Unigene41528_All//gi|297802294|ref|XP_002869031.1|/8.00E-27//At4g36570 [Arabidopsis lyrata subsp. lyrata] >gi|38566494|gb|AAR24137.1| At4g36570 [Arabidopsis thaliana] >gi|40823588|gb|AAR92291.1| At4g36570 [Arabidopsis thaliana] >gi|297314867|gb|EFH45290.1| At4g36570 [Arabidopsis lyrata subsp. lyrata]	Unigene41528_All//2.00E-21//AT1G75250| ATRL6 (ARABIDOPSIS RAD-LIKE 6); transcription factor	Unigene41528_All//2.00E-68//TC163219	WVB-related		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene4153_All	1721	1.16	1.30	0.53	1.91	1.86	2.15	2.65	1.55	0.39	1.65E-01	6.88E-01		-1.14E+00	1.99E-02		-3.80E-02	9.11E-01		1.72E-01	6.34E-01		-7.72E-01	2.16E-03		-2.75E+00	6.27E-18	Down	Unigene4153_All//gi|32395916|gb|AAP41818.1|/0.00E+00//PS8IPK [Solanum lycopersicum]	Unigene4153_All//0.00E+00//AT5G03160| ATPS8IPK (ARABIDOPSIS HOMOLOG OF MAMALLIAN PS8IPK); binding / heat shock protein binding	Unigene4153_All//0.00E+00//TC176004	ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene41537_All	500	1.05	4.76	0.43	1.10	2.41	0.81	2.88	2.09	2.23	2.19E+00	4.62E-06	Up	-1.30E+00	2.42E-01		1.14E+00	7.32E-02		-4.31E-01	6.67E-01		-4.60E-01	3.82E-01		-3.66E-01	4.58E-01					Unigene41537_All//0.00E+00//ES847705				
Unigene41538_All	469	0.00	0.65	0.00	0.21	0.22	3.37	22.27	55.52	217.97	9.34E+00	4.43E-02		null	null		5.27E-02	9.66E-01		3.99E+00	2.78E-07	Up	1.32E+00	3.39E-36	Up	3.29E+00	0.00E+00	Up	Unigene41538_All//gi|16118889|gb|AAL14645.1|AF417852_1//5.00E-12//AOP1 [Arabidopsis lyrata] >gi|16118984|gb|AAL14690.1| 2-oxoglutarate-dependent dioxygenase [Arabidopsis lyrata]	Unigene41538_All//8.00E-13//AT1G28030| oxidoreductase, 20G-Fe(II) oxygenase family protein	Unigene41538_All//5.00E-66//gi|73863250|gb|DT465989.1|DT465989	ko00904|Diterpenoid biosynthesis	GO:0016706//GO:0019758//GO:0044464	nr -
Unigene41543_All	317	0.33	0.00	0.00	0.94	0.33	0.00	6.67	36.52	27.90	-8.37E+00	3.71E-01		-8.37E+00	3.92E-01		-1.53E+00	2.98E-01		-9.88E+00	3.99E-02		2.45E+00	1.14E-37	Up	2.06E+00	4.50E-24	Up				Unigene41543_All//2.00E-12//TC137973				
Unigene41544_All	454	0.00	1.34	0.00	0.66	0.30	1.39	1.49	2.85	6.41	1.04E+01	1.17E-03		null	null		-1.12E+00	4.24E-01		1.08E+00	2.69E-01		9.38E-01	7.84E-02		2.10E+00	1.25E-08	Up				Unigene41544_All//5.00E-07//TC162463				
Unigene41546_All	422	0.00	1.32	0.00	5.67	2.12	2.03	0.00	1.49	0.19	1.04E+01	2.18E-03		null	null		-1.42E+00	3.12E-04	Down	-1.48E+00	4.58E-04	Down	1.05E+01	1.47E-04	Up	7.56E+00	4.04E-01									
Unigene41549_All	224	1.64	1.81	1.66	0.44	2.92	1.61	8.87	4.48	1.25	1.46E-01	8.98E-01		2.55E-02	1.00E+00		2.72E+00	1.37E-02		1.88E+00	2.19E-01		-9.86E-01	1.65E-02		-2.83E+00	1.91E-08	Down				Unigene41549_All//2.00E-72//CO075405				
Unigene4155_All	649	5.97	18.50	7.55	10.13	14.54	12.46	9.58	8.37	16.94	1.63E+00	5.25E-19	Up	3.40E-01	2.43E-01		5.21E-01	3.86E-03		2.98E-01	1.81E-01		-1.94E-01	4.08E-01		8.23E-01	5.74E-08					Unigene4155_All//1.00E-20//TC133995				
Unigene41552_All	461	0.00	0.00	0.00	0.00	0.00	0.00	71.81	133.18	29.47	null	null		null	null		null	null		null	null		8.91E-01	4.67E-45		-1.29E+00	1.88E-45	Down	Unigene41552_All//gi|255647586|gb|ACI24256.1|/8.00E-08//unknown [Glycine max]		Unigene41552_All//7.00E-28//gi|109847166|gb|DW476146.1|DW476146				nr +
Unigene41556_All	277	0.94	5.30	4.23	4.50	9.70	7.99	0.15	0.30	0.00	2.49E+00	1.51E-04	Up	2.16E+00	3.59E-03		1.11E+00	3.39E-03		8.29E-01	5.92E-02		9.84E-01	7.31E-01		-7.25E+00	6.12E-01					Unigene41556_All//3.00E-47//gi|13244391|gb|BE053318.2|BE053318				ESTscan +
Unigene41559_All	713	0.00	2.35	0.45	0.42	0.48	0.13	0.18	20.87	0.06	1.12E+01	1.54E-09	Up	8.81E+00	4.51E-02		2.04E-01	9.01E-01		-1.73E+00	2.89E-01		6.87E+00	2.23E-99	Up	-1.67E+00	4.77E-01					Unigene41559_All//0.00E+00//gi|195983439|gb|FL576413.1|FL576413				
Unigene41560_All	553	0.00	0.09	0.19	0.00	0.12	0.00	2.14	11.19	74.20	6.52E+00	6.16E-01		7.59E+00	3.98E-01		6.96E+00	6.09E-01		null	null		2.39E+00	8.29E-20	Up	5.12E+00	1.76E-249	Up	Unigene41560_All//gi|151301818|gb|ABN50365.2|/5.00E-49//ethylene responsive element binding protein 1 [Gossypium barbadense]	Unigene41560_All//4.00E-22//AT4G17500| ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene41560_All//4.00E-33//TC178747	AP2-EREBP	GO:0006351//GO:0009743//GO:0010468//GO:0030528//GO:0043231	nr +
Unigene41566_All	268	12.89	19.28	12.92	93.87	62.70	77.52	195.62	81.56	56.93	5.82E-01	2.74E-02		3.40E-03	9.90E-01		-5.82E-01	4.34E-09		-2.76E-01	1.29E-02		-1.26E+00	1.49E-67	Down	-1.78E+00	2.39E-115	Down				Unigene41566_All//3.00E-87//TC168019				
Unigene41568_All	316	4.97	1.12	4.04	0.63	1.09	0.43	0.00	0.00	0.00	-2.15E+00	3.32E-04	Down	-2.97E-01	6.10E-01		7.89E-01	5.96E-01		-5.56E-01	7.33E-01		null	null		null	null					Unigene41568_All//1.00E-43//gi|84149606|gb|DN780906.1|DN780906				
Unigene4157_All	707	16.95	3.58	4.44	23.53	14.37	25.23	29.90	10.70	13.30	-2.24E+00	8.67E-29	Down	-1.93E+00	6.82E-23	Down	-7.12E-01	1.20E-08		1.01E-01	5.40E-01		-1.48E+00	3.32E-35	Down	-1.17E+00	2.13E-25	Down	Unigene4157_All//gi|115486013|ref|NP_001068150.1|/1.00E-64//Os11g0579800 [Oryza sativa Japonica Group] >gi|113645372|dbj|BAF28513.1| Os11g0579800 [Oryza sativa Japonica Group]	Unigene4157_All//3.00E-42//AT3G03920| Gar1 RNA-binding region family protein	Unigene4157_All//2.00E-155//TC166293				nr +
Unigene41573_All	407	1.03	0.00	1.57	1.71	0.25	0.22	1.66	0.10	0.20	-1.00E+01	1.05E-02		6.10E-01	5.09E-01		-2.76E+00	3.99E-03		-2.95E+00	5.84E-03		-4.02E+00	5.36E-04	Down	-3.09E+00	1.45E-03					Unigene41573_All//5.00E-124//gi|164296010|gb|ES811161.1|ES811161				
Unigene41577_All	279	0.56	0.36	1.91	0.71	1.48	0.32	3.33	0.45	1.86	-6.31E-01	7.27E-01		1.76E+00	1.29E-01		1.05E+00	4.26E-01		-1.14E+00	5.69E-01		-2.89E+00	3.28E-04	Down	-8.45E-01	1.72E-01					Unigene41577_All//3.00E-10//gi|28347071|gb|DT567345.1|DT567345				
Unigene41578_All	311	18.00	3.26	16.61	2.56	0.89	0.44	1.22	0.94	1.28	-2.47E+00	2.20E-15	Down	-1.16E-01	6.62E-01		-1.53E+00	4.83E-02		-2.56E+00	6.01E-03		-3.79E-01	7.23E-01		6.63E-02	9.66E-01					Unigene41578_All//4.00E-19//gi|109864832|gb|DW493808.1|DW493808				
Unigene41579_All	437	3.35	1.28	8.04	7.98	5.20	2.58	0.29	0.00	0.00	-1.39E+00	1.39E-02		1.26E+00	3.30E-04	Up	-6.18E-01	5.22E-02		-1.63E+00	2.33E-06	Down	-8.18E+00	2.35E-01		-8.18E+00	2.00E-01					Unigene41579_All//4.00E-20//DW489419				
Unigene4158_All	668	59.14	39.14	63.29	105.45	87.63	107.70	54.43	35.48	25.76	-5.95E-01	2.82E-12		9.81E-02	3.19E-01		-2.67E-01	4.00E-06		3.06E-02	6.80E-01		-6.18E-01	1.11E-14		-1.08E+00	6.16E-38	Down	Unigene4158_All//4.00E-44//RecName: Full=Uncharacterized protein At5g49945; Flags: Precursor	Unigene4158_All//6.00E-38//AT5G49945| unknown protein	Unigene4158_All//0.00E+00//gi|109854377|gb|DW483356.1|DW483356			nr -
Unigene41581_All	2490	0.00	0.08	0.00	0.00	0.00	0.00	21.90	3.44	11.86	6.35E+00	1.36E-01		null	null		null	null		null	null		-2.67E+00	2.09E-193	Down	-8.86E-01	6.82E-41		Unigene41581_All//gi|224142669|ref|XP_002324677.1|/0.00E+00//auxin efflux carrier component [Populus trichocarpa] >gi|222886111|gb|EEF03242.1| auxin efflux carrier component [Populus trichocarpa]	Unigene41581_All//0.00E+00//AT5G57090| EIR1 (ETHYLENE INSENSITIVE ROOT 1); auxin efflux transmembrane transporter/ auxin:hydrogen symporter/ transporter	Unigene41581_All//1.00E-11//TC155177		GO:0005773//GO:0009630//GO:0009725//GO:0009746//GO:0015294//GO:0015562//GO:0016323//GO:0031224//GO:0031410//GO:0060918	nr -
Unigene41583_All	500	0.84	0.61	0.96	2.99	9.16	4.79	0.00	0.00	0.32	-4.61E-01	6.50E-01		1.95E-01	8.39E-01		1.62E+00	1.91E-08	Up	6.80E-01	1.10E-01		null	null		8.32E+00	1.40E-01					Unigene41583_All//7.00E-22//gi|109865518|gb|DW494494.1|DW494494				
Unigene41584_All	498	0.00	0.00	0.00	0.00	0.00	0.00	24.37	25.85	0.00	null	null		null	null		null	null		null	null		8.53E-02	6.41E-01		-1.46E+01	1.97E-89	Down	Unigene41584_All//gi|116060704|emb|CAL57182.1|/8.00E-07//unnamed protein product [Ostreococcus tauri]		Unigene41584_All//2.00E-53//TC164196				nr -
Unigene41587_All	463	14.92	38.74	10.24	19.04	17.78	51.41	19.72	36.83	20.65	1.38E+00	5.88E-22	Up	-5.43E-01	2.04E-02		-9.94E-02	6.59E-01		1.43E+00	9.60E-33	Up	9.01E-01	2.47E-13		6.62E-02	7.14E-01		Unigene41587_All//gi|227204473|dbj|BAH57088.1|/6.00E-47//AT2G25280 [Arabidopsis thaliana]	Unigene41587_All//3.00E-42//AT2G25280| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Mediator of Erb82-driven cell motility (Memo), related (InterPro:IPR002737); Has 742 Blast hits to 742 proteins in 323 species: Archae - 138; Bacteria - 240; Metazoa - 132; Fungi - 82; Plants - 26; Viruses - 0; Other Eukaryotes - 124 (source: NCBI BLink).	Unigene41587_All//0.00E+00//gi|21096835|gb|BQ409136.1|BQ409136				nr +
Unigene41590_All	243	0.43	1.67	3.94	7.38	1.70	5.76	2.09	4.99	2.95	1.95E+00	1.44E-01		3.20E+00	1.02E-03		-2.12E+00	2.16E-05	Down	-3.57E-01	4.96E-01		1.26E+00	2.52E-02		4.99E-01	5.01E-01					Unigene41590_All//5.00E-18//TC160704				ESTscan -
Unigene41593_All	384	1.36	0.53	0.42	5.84	5.92	1.76	0.22	0.11	0.31	-1.37E+00	1.97E-01		-1.71E+00	1.40E-01		1.99E-02	9.74E-01		-1.73E+00	1.22E-04	Down	-1.02E+00	7.24E-01		4.99E-01	8.07E-01		Unigene41593_All//gi|297725701|ref|NP_001173214.1|/1.00E-23//Os07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1| Os07g0501200 [Oryza sativa Japonica Group]	Unigene41593_All//2.00E-21//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene41593_All//2.00E-33//DR458540		GO:0003676//GO:0016772//GO:0044238//GO:0044260	nr -
Unigene41601_All	393	5.59	1.03	4.06	0.00	0.79	0.46	0.00	0.00	0.00	-2.44E+00	2.22E-06	Down	-4.60E-01	3.22E-01		9.62E+00	4.54E-02		8.84E+00	1.94E-01		null	null		null	null									
Unigene41602_All	372	0.00	0.00	1.86	2.81	3.24	0.36	0.34	0.11	0.00	null	null		1.09E+01	6.16E-04	Up	2.04E-01	8.01E-01		-2.95E+00	3.82E-04	Down	-1.60E+00	5.34E-01		-8.41E+00	2.00E-01		Unigene41602_All//gi|124360022|gb|ABN08038.1|/1.00E-31//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene41602_All//2.00E-30//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene41602_All//4.00E-41//TC135736		GO:0003676//GO:0006260//GO:0034061//GO:0043231	nr +
Unigene41604_All	664	0.63	0.00	0.48	0.75	2.80	1.50	0.89	0.44	0.78	-9.30E+00	1.05E-02		-3.90E-01	7.17E-01		1.90E+00	1.74E-04	Up	9.96E-01	1.72E-01		-1.02E+00	2.40E-01		-1.93E-01	7.94E-01		Unigene41604_All//gi|15218705|ref|NP_171809.1|/5.00E-88//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75200246|sp|Q9SA60.1|PPR6_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g03100, mitochondrial; Flags: Precursor >gi|4587568|gb|AAD25799.1|AC006550_7 Contains PF|00637 Clathrin 7-fold repeat. EST gb|AA721862 comes from this gene [Arabidopsis thaliana] >gi|44917465|gb|AAS49057.1| At1g03100 [Arabidopsis thaliana]	Unigene41604_All//9.00E-90//AT1G03100| pentatricopeptide (PPR) repeat-containing protein			GO:0043231	nr +
Unigene41606_All	476	0.66	5.75	0.34	0.73	0.87	2.09	0.00	0.00	0.00	3.12E+00	9.18E-10	Up	-9.75E-01	5.06E-01		2.45E-01	8.53E-01		1.51E+00	4.09E-02		null	null		null	null									
Unigene41618_All	361	0.00	0.70	0.30	0.55	1.81	0.00	1.17	2.08	5.63	9.45E+00	7.86E-02		8.20E+00	3.98E-01		1.72E+00	8.16E-02		-9.11E+00	1.33E-01		8.31E-01	2.64E-01		2.26E+00	8.89E-07	Up	Unigene41618_All//gi|297816410|ref|XP_002876088.1|/2.00E-07//phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321926|gb|EFH52347.1| phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene41618_All//8.00E-09//AT5G66020| ATSAC1B (SUPPRESSOR OF ACTIN 1B); phosphatidylinositol-4,5-bisphosphate 5-phosphatase	Unigene41618_All//2.00E-107//TC150500		GO:0000904//GO:0009826//GO:0034593//GO:0044459	nr -
Unigene41620_All	452	667.44	23.43	80.46	90.92	46.32	20.98	0.09	0.09	0.00	-4.83E+00	0.00E+00	Down	-3.05E+00	0.00E+00	Down	-9.73E-01	3.59E-35		-2.12E+00	1.63E-98	Down	-1.55E-02	1.00E+00		-6.55E+00	6.12E-01		Unigene41620_All//gi|146454676|gb|ABQ42004.1|/3.00E-34//gibberellin induced protein [Sonneratia apetala]	Unigene41620_All//3.00E-31//AT3G10185| Encodes a Gibberellin-regulated GASA/GAST/Snakin family protein	Unigene41620_All//0.00E+00//TC146782			nr -

Unigene41621_All	578	0.18	1.05	0.09	0.69	1.97	1.48	3.80	1.16	1.03	2.54E+00	2.46E-02		-9.75E-01	7.20E-01		1.51E+00	2.36E-02		1.11E+00	1.67E-01		-1.72E+00	3.46E-05	Down	-1.88E+00	5.33E-06	Down	Unigene41621_All//gi|297812057|ref|XP_002873912.1|//6.00E-80//EMB3013 [Arabidopsis lyrata subsp. lyrata] >gi|297319749|gb|EFH50171.1| EMB3013 [Arabidopsis lyrata subsp. lyrata]	Unigene41621_All//2.00E-80//AT5G18700| EMB3013 (embryo defective 3013); ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene41621_All//2.00E-161//TC136478			GO:0004674//GO:0006464//GO:0032559	nr +
Unigene41624_All	369	1.42	0.14	1.15	4.18	0.56	1.47	2.06	2.49	2.16	-3.37E+00	1.57E-02		-2.97E-01	7.50E-01		-2.90E+00	1.43E-06	Down	-1.51E+00	6.00E-03		2.73E-01	6.70E-01		6.62E-02	9.42E-01									
Unigene41630_All	582	0.00	0.00	0.00	1.71	0.71	1.32	3.34	0.22	1.99	null	null		null	null		-1.27E+00	5.75E-02		-3.76E-01	6.31E-01		-3.96E+00	2.04E-10	Down	-7.51E-01	5.89E-02		Unigene41630_All//gi|225432000|ref|XP_002273335.1|//1.00E-20//PREDICTED: similar to transcription factor/ transcription regulator [Vitis vinifera]	Unigene41630_All//3.00E-08//AT2G47270| transcription factor/ transcription regulator				GO:0010468	nr +
Unigene41634_All	572	0.73	0.00	0.00	0.52	1.57	0.79	0.52	1.10	2.72	-9.52E+00	1.05E-02		-9.52E+00	1.56E-02		1.58E+00	4.38E-02		5.96E-01	6.40E-01		1.08E+00	1.99E-01		2.39E+00	1.16E-05	Up	Unigene41634_All//gi|124359684|gb|ABD32353.2|//4.00E-74//Tetratricopeptide-like helical [Medicago truncatula]	Unigene41634_All//1.00E-73//AT2G17140| EXPRESSED IN: 7 plant structures; EXPRESSED DURING: F mature embryo stage, C globular stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT1G62910.1); Has 25910 Blast hits to 6027 proteins in 187 species: Archae - 6; Bacteria - 20; Metazoa - 625; Fungi - 635; Plants - 23410; Viruses - 0; Other Eukaryotes - 1214 (source: NCBI BLink).	Unigene41634_All//2.00E-31//TC170528				nr +
Unigene41635_All	235	55.44	51.32	40.79	89.24	54.07	125.11	137.64	123.61	49.84	-1.12E-01	5.31E-01		-4.43E-01	6.89E-03		-7.23E-01	4.83E-11		4.87E-01	4.95E-07		-1.55E-01	9.40E-02		-1.47E+00	4.10E-54	Down			Unigene41635_All//1.00E-80//gi|109870804|gb|DW499780.1|DW499780				
Unigene41636_All	443	0.00	0.00	0.72	1.12	1.71	1.84	1.34	0.00	0.18	null	null		9.49E+00	4.51E-02		6.05E-01	5.14E-01		7.07E-01	3.93E-01		-1.04E+01	2.39E-04	Down	-2.89E+00	4.53E-03		Unigene41636_All//gi|15231488|ref|NP_187419.1|//3.00E-60//exostosin family protein [Arabidopsis thaliana] >gi|75207507|sp|Q9SSE8.1|GLYT1_ARATH RecName: Full=Probable glycosyltransferase At3g07620	Unigene41636_All//2.00E-61//AT3G07620| exostosin family protein				GO:0008375//GO:0044464	nr -
Unigene41638_All	2823	0.00	31.81	24.16	0.00	0.10	0.10	0.03	0.00	0.00	1.50E+01	0.00E+00	Up	1.46E+01	0.00E+00	Up	6.61E+00	7.01E-02		6.59E+00	7.02E-02		-4.91E+00	4.03E-01		-4.91E+00	3.58E-01									
Unigene41639_All	267	13.91	13.28	21.74	4.85	5.29	2.20	1.90	0.00	0.75	-6.67E-02	8.34E-01		6.44E-01	1.23E-02		1.24E-01	8.39E-01		-1.14E+00	5.81E-02		-1.09E+01	8.89E-04	Down	-1.35E+00	1.40E-01				Unigene41639_All//3.00E-07//ES840187				
Unigene4164_All	2022	0.75	1.53	1.21	4.11	3.85	3.19	3.43	12.22	8.22	1.03E+00	4.13E-03		6.91E-01	1.04E-01		-9.62E-02	6.87E-01		-3.65E-01	7.99E-02		1.83E+00	3.78E-55	Up	1.26E+00	2.15E-22	Up	Unigene4164_All//gi|115485019|ref|NP_001067653.1|//1.00E-103//Os11g0264500 [Oryza sativa Japonica Group] >gi|113641875|dbj|BAF28016.1| Os11g0264500 [Oryza sativa Japonica Group]	Unigene4164_All//3.00E-61//AT5G67550| unknown protein					nr +
Unigene41646_All	582	0.09	0.00	0.00	0.09	0.00	0.47	3.49	0.36	39.50	-6.49E+00	6.11E-01		-6.49E+00	6.23E-01		-6.42E+00	5.55E-01		2.44E+00	2.22E-01		-3.28E+00	2.01E-09	Down	3.50E+00	3.19E-108	Up	Unigene41646_All//gi|224087611|ref|XP_002308196.1|//7.00E-65//laccase 110a [Populus trichocarpa] >gi|222854172|gb|EEE91719.1| laccase 110a [Populus trichocarpa]	Unigene41646_All//2.00E-53//AT5G01050| laccase family protein / diphenol oxidase family protein	Unigene41646_All//2.00E-41//gi|78331794|gb|DT552068.1|DT552068		ko00910|Nitrogen metabolism	GO:0003006//GO:0005576//GO:0009808//GO:0010038//GO:0016682//GO:0046914	nr +
Unigene41647_All	257	147.60	56.78	75.42	152.74	171.64	235.31	94.76	57.08	64.80	-1.38E+00	6.01E-46	Down	-9.69E-01	1.93E-25		1.68E-01	4.31E-02		6.24E-01	3.67E-21		-7.31E-01	2.50E-13		-5.48E-01	1.34E-08		Unigene41647_All//gi|115448105|ref|NP_001047832.1|//3.00E-39//Os02g0699600 [Oryza sativa Japonica Group] >gi|113537363|dbj|BAF09746.1| Os02g0699600 [Oryza sativa Japonica Group]	Unigene41647_All//4.00E-40//AT5G60670| 60S ribosomal protein L12 (RPL12C)	Unigene41647_All//3.00E-143//TC152645		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene41648_All	318	0.16	10.84	0.33	0.00	1.08	0.00	4.25	7.89	13.53	6.04E+00	4.29E-18	Up	1.03E+00	7.03E-01		1.01E+01	3.01E-02		null	null		8.90E-01	1.28E-02		1.67E+00	2.58E-09	Up								
Unigene41649_All	363	0.72	1.95	1.91	0.27	0.66	1.49	4.08	4.84	10.43	1.44E+00	1.06E-01		1.40E+00	1.39E-01		1.27E+00	5.32E-01		2.44E+00	4.41E-02		2.46E-01	6.30E-01		1.35E+00	2.45E-06	Up			Unigene41649_All//4.00E-10//EX165701				
Unigene41650_All	396	0.00	0.13	0.00	0.88	0.43	0.00	23.60	20.90	11.57	7.00E+00	6.16E-01		null	null		-1.02E+00	4.23E-01		-9.78E+00	2.12E-02		-1.75E-01	3.67E-01		-1.03E+00	1.09E-09	Down	Unigene41650_All//gi|297604052|ref|NP_001054914.2|//4.00E-17//Os05g0210400 [Oryza sativa Japonica Group] >gi|255676133|dbj|BAF16828.2| Os05g0210400 [Oryza sativa Japonica Group]	Unigene41650_All//5.00E-18//AT1G28610| GDSL-motif lipase, putative	Unigene41650_All//1.00E-07//TC136331			GO:0016787//GO:0030312//GO:0031410	nr -
Unigene41652_All	526	1.69	0.58	0.20	0.00	1.11	1.46	0.00	0.08	0.00	-1.55E+00	4.56E-02		-3.06E+00	2.25E-03		1.01E+01	1.26E-03		1.05E+01	1.27E-04	Up	6.31E+00	6.34E-01		null	null		Unigene41652_All//gi|27311791|gb|AA000861.1|//2.00E-29//expressed protein [Arabidopsis thaliana] >gi|30984528|gb|AAP42727.1| At4g14930 [Arabidopsis thaliana]	Unigene41652_All//1.00E-30//AT4G14930| acid phosphatase/ survival protein SurE, putative	Unigene41652_All//0.00E+00//TC163455		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00760|Nicotinate and nicotinamide metabolism		nr -
Unigene41653_All	354	0.15	0.57	1.20	0.00	0.78	0.26	0.72	3.31	11.25	1.95E+00	3.75E-01		3.03E+00	5.73E-02		9.60E+00	7.01E-02		8.00E+00	4.76E-01		2.21E+00	5.41E-04	Up	3.97E+00	3.41E-21	Up	Unigene41653_All//gi|225457283|ref|XP_002284415.1|//4.00E-10//PREDICTED: similar to EMB2733/ESP3 (EMBRYO DEFECTIVE 2733); ATP-dependent RNA helicase [Vitis vinifera]	Unigene41653_All//6.00E-08//AT1G32490| ESP3 (ENHANCED SILENCING PHENOTYPE 3); ATP binding / ATP-dependent RNA helicase/ ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene41653_All//1.00E-28//TC148325		ko03040|Spliceosome	GO:0000166//GO:0003006//GO:0003724//GO:0006396//GO:0016441//GO:0042623	nr +
Unigene41655_All	410	0.00	0.37	0.00	0.00	0.00	0.00	4.23	5.30	1.26	8.53E+00	2.35E-01		null	null		null	null		null	null		3.26E-01	4.30E-01		-1.74E+00	1.65E-04	Down								
Unigene41658_All	250	0.42	8.72	4.26	7.17	3.99	10.12	43.13	30.26	31.23	4.38E+00	4.79E-10	Up	3.35E+00	3.36E-04	Up	-8.45E-01	7.10E-02		4.96E-01	2.37E-01		-5.11E-01	9.55E-04		-4.66E-01	2.01E-03		Unigene41658_All//gi|224111864|ref|XP_002316007.1|//1.00E-13//cytochrome P450 [Populus trichocarpa] >gi|222865047|gb|EEF02178.1| cytochrome P450 [Populus trichocarpa]	Unigene41658_All//2.00E-07//AT2G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene41658_All//9.00E-66//gi|164326217|gb|ES827018.1|ES827018		ko00591|Linoleic acid metabolism	GO:0016491//GO:0046872	nr -
Unigene4166_All	1025	17.87	6.48	9.35	3.99	6.38	2.73	1.57	0.45	1.67	-1.46E+00	1.26E-24	Down	-9.34E-01	6.98E-12		6.80E-01	2.07E-03		-5.45E-01	7.53E-02		-1.81E+00	3.20E-04	Down	9.25E-02	8.38E-01		Unigene4166_All//gi|225460819|ref|XP_002276928.1|//9.00E-87//PREDICTED: similar to wax synthase [Vitis vinifera] >gi|27728714|gb|AAO18664.1| wax synthase isoform 1 [Vitis vinifera]	Unigene4166_All//9.00E-60//AT5G55380| membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related	Unigene4166_All//0.00E+00//gi|78351221|gb|DT571495.1|DT571495				nr +
Unigene41663_All	304	0.34	0.33	3.85	1.47	1.93	0.74	1.67	0.69	0.92	-4.60E-02	9.88E-01		3.48E+00	1.09E-04	Up	3.85E-01	7.32E-01		-9.90E-01	3.94E-01		-1.28E+00	1.86E-01		-8.64E-01	3.39E-01		Unigene41663_All//gi|297837215|ref|XP_002886489.1|//2.00E-14//AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322330|gb|EFH82748.1| AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene41663_All//2.00E-10//AT1G62130| AAA-type ATPase family protein	Unigene41663_All//4.00E-53//TC141927			GO:0000166//GO:0017111	nr -
Unigene41669_All	320	11.61	3.17	11.32	3.58	3.01	1.41	1.06	0.65	0.50	-1.87E+00	1.28E-07	Down	-3.69E-02	9.23E-01		-2.49E-01	7.04E-01		-1.34E+00	4.01E-02		-6.95E-01	5.77E-01		-1.09E+00	3.55E-01				Unigene41669_All//3.00E-23//CO069988				
Unigene4167_All	2099	0.75	1.64	2.28	5.60	6.51	8.71	15.73	21.47	29.32	1.13E+00	8.33E-04	Up	1.61E+00	1.49E-07	Up	2.18E-01	1.88E-01		6.38E-01	4.33E-07		4.48E-01	2.04E-10		8.98E-01	7.53E-47		Unigene4167_All//gi|224125984|ref|XP_002319727.1|//0.00E+00//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222858103|gb|EEE95650.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene4167_All//3.00E-111//AT5G17850| cation exchanger, putative (CAX8)	Unigene4167_All//7.00E-161//gi|54121351|gb|CO496860.1|CO496860				nr +
Unigene41670_All	371	0.71	2.32	0.86	0.67	0.37	0.49	0.91	1.24	4.72	1.72E+00	3.49E-02		2.89E-01	8.10E-01		-8.55E-01	5.73E-01		-4.64E-01	7.44E-01		4.43E-01	6.31E-01		2.37E+00	3.04E-06	Up								
Unigene41675_All	355	0.88	3.28	3.00	8.56	1.36	1.65	0.00	0.00	0.67	1.89E+00	6.32E-03		1.76E+00	1.85E-02		-2.66E+00	2.06E-11	Down	-2.37E+00	8.02E-09	Down	null	null		9.40E+00	4.39E-02		Unigene41675_All//gi|3021280|emb|CAA18475.1|//6.00E-13//serine /threonine kinase-like protein [Arabidopsis thaliana] >gi|7269176|emb|CAB79283.1| serine /threonine kinase-like protein [Arabidopsis thaliana]	Unigene41675_All//3.00E-14//AT4G23280| protein kinase, putative					nr +
Unigene41678_All	288	234.54	205.14	209.67	253.05	214.50	277.72	253.97	126.55	133.21	-1.93E-01	3.23E-03		-1.62E-01	2.08E-02		-2.38E-01	3.36E-05		1.34E-01	3.17E-02		-1.01E+00	2.42E-65	Down	-9.31E-01	3.02E-59		Unigene41678_All//gi|295687227|gb|ADG27839.1|//2.00E-20//eukaryotic translation initiation factor 5A [Gossypium hirsutum]	Unigene41678_All//3.00E-17//AT1G69410| ELF5A-3 (EUKARYOTIC ELONGATION FACTOR 5A-3); translation initiation factor	Unigene41678_All//8.00E-153//TC139232			GO:0006448//GO:0006449//GO:0008135//GO:0018205//GO:0043021	nr +
Unigene41680_All	466	22.79	5.76	10.51	44.58	43.60	41.09	83.47	38.75	42.06	-1.98E+00	5.41E-22	Down	-1.12E+00	2.23E-09	Down	-3.20E-02	8.25E-01		-1.17E-01	4.16E-01		-1.11E+00	5.18E-41	Down	-9.89E-01	3.24E-35		Unigene41680_All//gi|227202808|dbj|BAH56877.1|//3.00E-17//AT4G38680 [Arabidopsis thaliana]	Unigene41680_All//2.00E-18//AT4G38680| GRP2 (GLYCINE RICH PROTEIN 2); double-stranded DNA binding / mRNA binding / nucleic acid binding / single-stranded DNA binding	Unigene41680_All//0.00E+00//gi|78354665|gb|DT574939.1|DT574939	CSD		GO:0000502//GO:0003723//GO:0004175//GO:0006351//GO:0006508//GO:0006950//GO:0031224//GO:0031981//GO:0032392//GO:0043566//GO:0046914//GO:0048437	nr -
Unigene41681_All	248	1.48	2.25	0.86	1.81	6.80	4.37	0.34	1.52	1.12	6.06E-01	5.31E-01		-7.82E-01	5.53E-01		1.91E+00	3.81E-04	Up	1.27E+00	6.54E-02		2.15E-00	9.44E-02		1.72E+00	2.30E-01				Unigene41681_All//3.00E-07//TC147430				
Unigene41684_All	325	2.58	0.00	0.33	3.99	1.48	2.78	0.13	0.13	0.25	-1.13E+01	5.57E-05	Down	-2.97E+00	3.83E-03		-1.43E+00	1.25E-02		-5.20E-01	4.01E-01		-1.67E-02	1.00E+00		9.14E-01	7.50E-01				Unigene41684_All//4.00E-19//TC133459				
Unigene41689_All	377	99.65	22.04	74.30	14.40	10.87	3.47	0.00	0.00	0.00	-2.18E+00	8.15E-86	Down	-4.24E-01	2.43E-06		-4.06E-01	1.13E-01		-2.05E+00	6.53E-13	Down	null	null		null	null		Unigene41689_All//gi|29253565|gb|ADE34299.1|//4.00E-25//aquaporin XIP1;1 [Gossypium hirsutum]		Unigene41689_All//2.00E-105//gi|109827102|gb|DW225806.1|DW225806				nr +
Unigene41691_All	717	0.00	10.53	5.20	0.14	0.00	0.00	0.00	0.00	0.00	1.34E+01	3.63E-43	Up	1.23E+01	1.20E-20	Up	-7.12E+00	3.13E-01		-7.12E+00	3.99E-01		null	null		null	null		Unigene41691_All//gi|300261239|gb|EFJ45453.1|//1.00E-108//polyubiquitin [Volvox carteri f. nagariensis]	Unigene41691_All//3.00E-108//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene41691_All//6.00E-51//TC148105				nr -
Unigene41692_All	256	1.23	1.98	0.00	6.81	1.75	3.88	3.63	1.80	0.93	6.91E-01	4.99E-01		-1.03E+01	4.90E-02		-1.96E+00	8.20E-05	Down	-8.11E-01	1.08E-01		-1.02E+00	1.21E-01		-1.96E+00	3.98E-03									
Unigene41693_All	267	2.16	0.57	1.99	22.02	4.64	8.12	6.33	8.14	6.86	-1.92E+00	7.00E-02		-1.12E-01	9.07E-01		-2.25E+00	7.67E-18	Down	-1.44E+00	1.06E-08	Down	3.62E-01	3.92E-01		1.16E-01	7.84E-01				Unigene41693_All//2.00E-39//CO097312				
Unigene41694_All	392	2.40	0.00	3.80	0.89	0.88	0.23	0.00	0.11	0.10	-1.12E+01	1.46E-05	Down	6.63E-01	2.44E-01		-1.80E-02	9.58E-01		-1.95E+00	1.96E-01		6.74E+00	6.34E-01		6.67E+00	6.45E-01									
Unigene417_All	2794	5.32	8.94	5.22	8.08	10.43	12.74	12.29	42.33	51.52	7.49E-01	1.15E-11		-2.63E-02	8.78E-01		3.69E-01	1.00E-04		6.57E-01	7.02E-14		1.78E+00	3.13E-252	Up	2.07E+00	0.00E+00	Up	Unigene417_All//gi|30685727|ref|NP_180907.2|//1.00E-146//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|166227727|sp|Q22799.2|Y2349_ARATH RecName: Full=Uncharacterized protein At2g33590	Unigene417_All//4.00E-103//AT2G33490| hydroxyproline-rich glycoprotein family protein	Unigene417_All//0.00E+00//TC146132				nr +
Unigene4170_All	1909	0.74	0.53	0.06	2.84	3.57	6.65	28.62	24.04	33.91	-4.79E-01	3.91E-01		-3.73E+00	8.89E-06	Down	3.29E-01	1.64E-01		1.22E+00	4.87E-14	Up	-2.51E-01	9.55E-05		2.45E-01	1.98E-05		Unigene4170_All//gi|224097176|ref|XP_002310864.1|//0.00E+00//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222853767|gb|EEE91314.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene4170_All//7.00E-159//AT5G10510| AIL6 (AINTEGUMENTA-LIKE 6); DNA binding / transcription factor	Unigene4170_All//0.00E+00//TC140815	AP2-EREBP			nr +
Unigene41705_All	498	0.00	0.00	0.00	0.70	0.83	1.63	2.12	0.50	0.08	null	null		null	null		2.45E-01	8.53E-01		1.22E+00	1.40E-01		-2.08E+00	1.78E-03		-4.73E+00	8.85E-07	Down	Unigene41705_All//gi|15231488|ref|NP_187419.1|//3.00E-35//exostosin family protein [Arabidopsis thaliana] >gi|75207507|sp|Q9SSE8.1|GLYT1_ARATH RecName: Full=Probable glycosyltransferase At3g07620	Unigene41705_All//2.00E-36//AT3G07620| exostosin family protein				GO:0008375//GO:0044464	nr +

Unigene41706_All	553	0.00	0.00	0.00	0.09	0.00	0.08	2.06	3.33	26.44	null	null		null	null		-6.49E+00	5.55E-01		-1.41E-01	9.52E-01		6.88E-01	1.14E-01		3.68E+00	6.47E-72	Up	Unigene41706_All//gi|288557882|emb|CBJ49377.1|//3.00E-30//pathogenesis-related protein 10.5 [Vitis vinifera]		Unigene41706_All//6.00E-177//DR454610			GO:0006950	nr +
Unigene41707_All	293	19.11	17.47	20.54	18.02	18.57	19.27	72.58	57.20	25.29	-1.30E-01	6.03E-01		1.04E-01	6.87E-01		4.32E-02	8.93E-01		9.65E-02	7.28E-01		-3.44E-01	1.38E-03		-1.52E+00	7.10E-38	Down			Unigene41707_All//2.00E-162//TC167356				
Unigene41709_All	343	0.00	0.00	0.00	0.00	0.00	0.00	1.36	4.51	2.09	null	null		null	null		null	null		null	null		1.73E+00	6.66E-04	Up	6.25E-01	3.96E-01		Unigene41709_All//gi|224123488|ref|XP_002319090.1|//2.00E-16//predicted protein [Populus trichocarpa] >gi|222857466|gb|EEE95013.1|predicted protein [Populus trichocarpa]						nr -
Unigene4171_All	2110	3.82	1.39	1.49	10.25	6.81	2.78	11.70	3.92	5.15	-1.46E+00	3.72E-11	Down	-1.36E+00	1.19E-09	Down	-5.90E-01	4.43E-08		-1.88E+00	1.53E-44	Down	-1.58E+00	8.04E-45	Down	-1.18E+00	4.66E-30	Down	Unigene4171_All//gi|15238981|ref|NP_199656.1|//0.00E+00//sks3 (SKU5 Similar 3); copper ion binding / oxidoreductase [Arabidopsis thaliana]	Unigene4171_All//0.00E+00//AT5G48450| sks3 (SKU5 Similar 3); copper ion binding / oxidoreductase	Unigene4171_All//0.00E+00//TC149546		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene41710_All	482	0.22	2.00	1.33	0.41	1.07	0.47	1.32	0.87	2.31	3.20E+00	6.55E-04	Up	2.61E+00	2.33E-02		1.37E+00	2.26E-01		1.81E-01	9.35E-01		-6.02E-01	4.67E-01		8.15E-01	1.45E-01				Unigene41710_All//6.00E-07//TC158269				
Unigene41711_All	432	0.48	0.00	0.74	0.58	1.12	0.31	3.43	6.29	7.93	-8.92E+00	1.22E-01		6.10E-01	6.24E-01		9.53E-01	4.24E-01		-8.79E-01	6.16E-01		8.76E-01	1.03E-02		1.21E+00	4.95E-05	Up			Unigene41711_All//5.00E-07//TC154885				
Unigene41715_All	406	0.00	0.00	0.00	0.98	1.02	0.22	2.60	4.53	29.34	null	null		null	null		5.22E-02	9.89E-01		-2.14E+00	1.26E-01		7.99E-01	6.40E-02		3.49E+00	2.94E-56	Up	Unigene41715_All//gi|21537324|gb|AAM61665.1|//3.00E-46//leucoanthocyanidin dioxygenase-like protein [Arabidopsis thaliana]	Unigene41715_All//2.00E-47//AT5G05600| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene41715_All//5.00E-41//gi|48813436|gb|CO114749.1|CO114749		ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016701//GO:0016706//GO:0046914	nr +
Unigene41716_All	415	885.92	70.94	102.01	151.24	183.96	270.87	1.53	0.50	0.38	-3.64E+00	0.00E+00	Down	-3.12E+00	0.00E+00	Down	2.83E-01	3.52E-07		8.41E-01	3.89E-65		-1.60E+00	6.27E-02		-1.99E+00	2.04E-02		Unigene41716_All//gi|81230695|gb|AB059694.1|//1.00E-58//alpha-expansin 2 [Gossypium hirsutum]	Unigene41716_All//2.00E-47//AT2G40610| ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	Unigene41716_All//0.00E+00//TC136184			GO:0007047//GO:0044464	nr +
Unigene41717_All	395	74.18	318.90	191.83	238.10	237.47	299.56	174.47	271.41	190.02	2.10E+00	1.30E-272	Up	1.37E+00	1.11E-87	Up	-3.80E-03	9.52E-01		3.31E-01	3.40E-13		6.38E-01	5.44E-44		1.23E-01	2.82E-02		Unigene41717_All//gi|224130214|ref|XP_002328682.1|//4.00E-11//predicted protein [Populus trichocarpa] >gi|222838858|gb|EEE77209.1|predicted protein [Populus trichocarpa]		Unigene41717_All//0.00E+00//ES794346				nr -
Unigene41719_All	722	0.00	9.33	5.31	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.68E-38	Up	1.24E+01	3.02E-21	Up	null	null		null	null		null	null		null	null		Unigene41719_All//gi|297845958|ref|XP_002890860.1|//4.00E-52//elongation factor 1-beta [Arabidopsis lyrata subsp. lyrata] >gi|297336702|gb|EFH67119.1|elongation factor 1-beta [Arabidopsis lyrata subsp. lyrata]	Unigene41719_All//5.00E-38//AT2G18110| elongation factor 1-beta, putative / EF-1-beta, putative				GO:0006412//GO:0010038//GO:0016020	nr +
Unigene41728_All	485	86.19	20.27	69.72	26.60	28.83	14.34	0.00	0.09	0.16	-2.09E+00	1.48E-90	Down	-3.06E-01	3.78E-04		1.16E-01	5.44E-01		-8.91E-01	7.55E-09		6.43E+00	6.34E-01		7.36E+00	4.04E-01		Unigene41728_All//gi|297801768|ref|XP_002868768.1|//1.00E-37//rhomboid family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314604|gb|EFH45027.1|rhomboid family protein [Arabidopsis lyrata subsp. lyrata]	Unigene41728_All//7.00E-39//AT5G38510| rhomboid family protein	Unigene41728_All//2.00E-130//TC154843			GO:0031224//GO:0031410	nr +
Unigene41729_All	350	6.28	8.54	1.52	10.25	13.09	9.29	14.50	18.87	12.18	4.44E-01	2.28E-01		-2.05E+00	5.31E-05	Down	3.53E-01	2.43E-01		-1.41E-01	6.71E-01		3.80E-01	7.24E-02		-2.51E-01	3.13E-01				Unigene41729_All//1.00E-74//TC134238				
Unigene41734_All	330	0.00	0.00	0.00	0.00	0.00	0.55	51.25	41.67	244.95	null	null		null	null		null	null		9.10E+00	1.94E-01		-2.99E-01	1.62E-02		2.26E+00	5.05E-239	Up			Unigene41734_All//1.00E-13//TC168282				
Unigene41737_All	633	0.33	0.32	0.08	1.02	0.60	0.14	1.87	0.86	0.38	-4.61E-02	9.88E-01		-1.97E+00	3.81E-01		-7.74E-01	3.81E-01		-2.84E+00	1.02E-02		-1.12E+00	4.65E-02		-2.31E+00	2.04E-04	Down							
Unigene41741_All	454	3.23	0.45	1.64	2.74	1.67	2.49	0.75	0.37	0.79	-2.85E+00	3.60E-05	Down	-9.75E-01	9.25E-02		-7.17E-01	2.26E-01		-1.41E-01	8.11E-01		-1.02E+00	3.99E-01		8.42E-02	9.57E-01		Unigene41741_All//gi|224146656|ref|XP_002326086.1|//9.00E-14//predicted protein [Populus trichocarpa] >gi|222862961|gb|EEF00468.1|predicted protein [Populus trichocarpa]		Unigene41741_All//0.00E+00//gi|164240804|gb|ES813315.1|ES813315				nr +
Unigene41749_All	399	63.86	25.02	23.89	66.54	69.39	89.31	188.19	86.00	81.37	-1.35E+00	3.31E-30	Down	-1.42E+00	3.22E-31	Down	6.04E-02	6.33E-01		4.25E-01	1.19E-06		-1.13E+00	5.26E-81	Down	-1.21E+00	8.18E-93	Down	Unigene41749_All//gi|124360667|gb|ABN08656.1|//2.00E-41//Ribosomal protein S10, eukaryotic and archaeal form [Medicago truncatula]	Unigene41749_All//4.00E-38//AT3G47370| 40S ribosomal protein S20 (RPS20B)	Unigene41749_All//0.00E+00//gi|13356462|gb|BG446810.1|BG446810		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0003181	nr -
Unigene4175_All	1168	0.27	1.48	1.82	1.02	0.80	1.78	2.57	1.83	1.36	2.46E+00	3.84E-05	Up	2.76E+00	1.21E-06	Up	-3.63E-01	5.70E-01		7.97E-01	8.12E-02		-4.94E-01	1.34E-01		-9.14E-01	3.32E-03		Unigene4175_All//gi|8778657|gb|AAF79665.1|AC022314_6//8.00E-07//F9C16.13 [Arabidopsis thaliana]	Unigene4175_All//5.00E-65//AT5G42905| nucleic acid binding / ribonuclease H	Unigene4175_All//0.00E+00//DT464173				nr +
Unigene41753_All	751	0.00	5.94	2.48	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.10E-25	Up	1.13E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene41753_All//gi|15224174|ref|NP_179435.1|//8.00E-29//SDH1-2; succinate dehydrogenase [Arabidopsis thaliana] >gi|75216119|sp|Q9ZPX5.1|DHSA2_ARATH RecName: Full=Succinate dehydrogenase [ubiquinone] flavoprotein subunit 2, mitochondrial; AltName: Full=Flavoprotein subunit 2 of complex II; Short=FP; Flags: Precursor >gi|29028988|gb|AAO64873.1|At2g18450 [Arabidopsis thaliana]	Unigene41753_All//4.00E-30//AT2G18450| SDH1-2; succinate dehydrogenase			ko00190|Oxidative phosphorylation//ko00020|Citrate cycle (TCA cycle)	GO:0016627//GO:0022904//GO:0043231	nr +
Unigene41754_All	1815	0.00	0.00	0.00	0.11	0.00	0.00	25.44	9.28	19.45	null	null		null	null		-6.78E+00	8.42E-02		-6.78E+00	1.33E-01		-1.45E+00	7.02E-74	Down	-3.87E-01	1.33E-08		Unigene41754_All//gi|224057962|ref|XP_002299361.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene41754_All//2.00E-174//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene41754_All//4.00E-51//CO097810				nr -
Unigene41756_All	321	7.33	7.58	18.08	2.95	7.51	0.42	0.13	0.00	0.00	4.68E-02	9.20E-01		1.30E+00	9.55E-07	Up	1.35E+00	9.83E-04	Up	-2.80E+00	1.18E-03		-7.04E+00	6.57E-01		-7.04E+00	6.12E-01				Unigene41756_All//3.00E-112//TC168198				
Unigene41757_All	233	37.95	59.59	47.31	220.85	243.86	196.35	138.27	714.83	167.05	6.51E-01	1.57E-05		3.18E-01	8.56E-02		1.43E-01	5.22E-02		-1.70E-01	2.97E-02		2.37E+00	0.00E+00	Up	2.73E-01	3.06E-04		Unigene41757_All//gi|105671415|gb|ABF74683.1|//2.00E-39//caffeoyl-CoA-O-methyltransferase [Leucaena leucocephala] >gi|146335869|gb|ABE60811.2|caffeoyl coenzyme A 3-O-methyltransferase I [Leucaena leucocephala]	Unigene41757_All//2.00E-39//AT4G34050| caffeoyl-CoA 3-O-methyltransferase, putative	Unigene41757_All//5.00E-129//TC145098		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0008171//GO:0009699//GO:0010038//GO:0043169//GO:0044444	nr -
Unigene4176_All	886	12.52	6.63	5.53	18.33	16.01	14.78	7.92	3.30	4.00	-9.16E-01	1.26E-07		-1.18E+00	1.36E-10	Down	-1.95E-01	1.92E-01		-3.10E-01	2.92E-02		-1.26E+00	9.79E-10	Down	-9.85E-01	4.76E-07		Unigene4176_All//gi|15294296|gb|AAK95325.1|AF410339_1//3.00E-59//AT3g56820/T8M16_150 [Arabidopsis thaliana] >gi|23506133|gb|AAN31078.1|At3g56820/T8M16_150 [Arabidopsis thaliana]	Unigene4176_All//7.00E-41//AT3G56820| unknown protein	Unigene4176_All//0.00E+00//TC135140				nr +
Unigene41760_All	304	46.81	126.34	53.43	105.20	114.41	191.94	70.65	183.68	235.10	1.43E+00	5.11E-49	Up	1.91E-01	2.29E-01		1.21E-01	2.46E-01		8.68E-01	6.98E-36		1.38E+00	3.95E-82	Up	1.73E+00	1.25E-149	Up	Unigene41760_All//gi|116265936|gb|ABJ91216.1|//1.00E-51//CBL-interacting protein kinase 9 [Populus trichocarpa]	Unigene41760_All//1.00E-51//AT4G30960| SIP3 (SOS3-INTERACTING PROTEIN 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene41760_All//3.00E-171//gi|78324020|gb|DT544294.1|DT544294		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0006972//GO:0009926//GO:0023060//GO:0032501//GO:0032559	nr -
Unigene41764_All	801	0.46	1.01	0.80	1.80	1.63	1.35	2.27	0.73	0.85	1.15E+00	1.48E-01		8.03E-01	3.88E-01		-1.43E-01	8.15E-01		-4.14E-01	4.78E-01		-1.64E+00	3.51E-04	Down	-1.42E+00	1.00E-03		Unigene41764_All//gi|297817406|ref|XP_002876586.1|//1.00E-115//guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322424|gb|EFH52845.1|guanine nucleotide exchange family protein [Arabidopsis lyrata subsp. lyrata]	Unigene41764_All//4.00E-114//AT3G60860| guanine nucleotide exchange family protein	Unigene41764_All//0.00E+00//CO092043		ko04626|Plant-pathogen interaction	GO:0005083//GO:0009553//GO:0043231//GO:0044444	nr +
Unigene41765_All	374	0.28	2.57	1.71	1.86	1.29	1.81	4.97	7.82	8.10	3.20E+00	6.55E-04	Up	2.61E+00	2.33E-02		-5.33E-01	5.45E-01		-4.18E-02	9.44E-01		6.53E-01	4.66E-02		7.03E-01	2.33E-02		Unigene41765_All//gi|227206370|dbj|BAH57240.1|//1.00E-10//AT4G35750| Rho-GTPase-activating protein-related	Unigene41765_All//3.00E-11//AT4G35750| Rho-GTPase-activating protein-related	Unigene41765_All//5.00E-16//TC148543				nr -
Unigene41766_All	338	0.77	1.20	1.58	0.74	1.12	0.40	2.50	3.22	12.14	6.32E-01	6.01E-01		1.03E+00	3.42E-01		6.05E-01	6.59E-01		-8.78E-01	6.16E-01		3.62E-01	5.69E-01		2.28E+00	5.36E-13	Up			Unigene41766_All//1.00E-22//TC168358				
Unigene41768_All	373	0.42	0.54	0.86	0.40	0.92	1.21	0.11	1.23	1.82	3.69E-01	8.16E-01		1.03E+00	4.71E-01		1.20E+00	4.26E-01		1.60E+00	2.03E-01		3.44E+00	1.16E-02		4.00E+00	4.29E-04	Up							
Unigene4177_All	1745	3.87	2.67	2.50	9.73	11.41	9.06	11.87	6.51	5.30	-5.34E-01	1.84E-02		-6.28E-01	7.64E-03		2.29E-01	7.68E-02		-1.04E-01	5.32E-01		-8.66E-01	4.73E-15		-1.16E+00	9.25E-25	Down	Unigene4177_All//gi|145357818|ref|NP_196517.3|//0.00E+00//RAB GDP-dissociation inhibitor [Arabidopsis thaliana] >gi|7671434|emb|CAB89375.1| GDP dissociation inhibitor [Arabidopsis thaliana]	Unigene4177_All//0.00E+00//AT5G09550| RAB GDP-dissociation inhibitor	Unigene4177_All//0.00E+00//TC144124				nr +
Unigene41772_All	621	0.25	0.49	0.26	0.64	0.67	0.36	0.00	0.40	1.73	9.54E-01	5.03E-01		2.49E-02	1.00E+00		5.23E-02	9.89E-01		-8.20E-01	5.06E-01		8.66E+00	4.31E-02		1.08E+01	8.30E-08	Up	Unigene41772_All//gi|115456355|ref|NP_001051778.1|//5.00E-25//Os03g0828800 [Oryza sativa Japonica Group] >gi|108711884|gb|ABF99679.1| D-mannose binding lectin family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550249|dbj|BAF13692.1|Os03g0828800 [Oryza sativa Japonica Group]	Unigene41772_All//2.00E-11//AT1G34300| lectin protein kinase family protein				GO:0004672//GO:0005488	nr -
Unigene41774_All	486	0.22	0.21	0.00	2.46	0.00	0.00	4.96	1.72	3.12	-4.63E-02	9.88E-01		-7.75E+00	3.92E-01		-1.13E+01	7.37E-09	Down	-1.13E+01	1.76E-07	Down	-1.53E+00	7.10E-05	Down	-6.71E-01	5.69E-02		Unigene41774_All//gi|195608224|gb|ACG25942.1|//5.00E-35//brain protein 44 [Zea mays] >gi|195628422|gb|ACG36041.1| brain protein 44 [Zea mays]	Unigene41774_All//2.00E-35//AT4G05590| unknown protein	Unigene41774_All//3.00E-55//gi|73861693|gb|DT464432.1|DT464432			GO:0043231	nr +
Unigene41777_All	580	0.00	0.00	0.00	0.52	0.59	0.93	3.28	6.85	1.31	null	null		null	null		2.04E-01	9.01E-01		8.59E-01	4.23E-01		1.06E+00	1.25E-04	Up	-1.33E+00	1.45E-03		Unigene41777_All//gi|262358302|gb|ACV56756.1|//6.00E-11//ZFP1 [Chrysanthemum x morifolium]	Unigene41777_All//3.00E-11//AT5G43540| zinc finger (C2H2 type) family protein		C2H2			nr +
Unigene4178_All	832	19.56	18.21	24.77	35.86	29.47	40.33	17.89	15.82	5.17	-1.03E-01	5.11E-01		3.41E-01	7.71E-03		-2.83E-01	2.97E-03		1.69E-01	9.62E-02		-1.77E-01	2.24E-01		-1.79E+00	1.40E-33	Down			Unigene4178_All//0.00E+00//TC174455				
Unigene41783_All	273	0.00	0.74	0.39	0.00	0.00	0.99	76.51	151.26	482.59	9.54E+00	1.36E-01		8.61E+00	3.98E-01		null	null		9.96E+00	7.02E-02		9.83E-01	6.66E-36		2.66E+00	0.00E+00	Up	Unigene41783_All//gi|224092400|ref|XP_002309592.1|//2.00E-10//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222855568|gb|EEE93115.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene41783_All//2.00E-08//AT1G52810| 2-oxoglutarate-dependent dioxygenase-related	Unigene41783_All//3.00E-75//gi|73863249|gb|DT465988.1|DT465988			GO:0016491	nr +
Unigene41784_All	429	106.96	47.95	88.25	14.40	11.96	9.79	0.10	0.19	0.09	-1.16E+00	2.36E-42	Down	-2.77E-01	7.49E-04		-2.68E-01	3.01E-01		-5.56E-01	1.94E-02		9.83E-01	7.31E-01		-8.59E-02	9.71E-01		Unigene41784_All//gi|270311593|gb|ACZ72945.1|//1.00E-32//photosystem I reaction center subunit [Nicotiana tabacum]	Unigene41784_All//2.00E-30//AT5G64040| PSAN; calmodulin binding	Unigene41784_All//8.00E-83//TC148436		ko00195|Photosynthesis	GO:0005515//GO:0009522//GO:0009534//GO:0009767	nr +
Unigene41787_All	461	0.23	0.44	0.00	6.59	2.69	1.86	5.50	3.90	2.16	9.54E-01	6.21E-01		-7.83E+00	3.92E-01		-1.29E+00	1.33E-04	Down	-1.82E+00	1.74E-06	Down	-4.97E-01	1.73E-01		-1.35E+00	1.51E-04	Down			Unigene41787_All//1.00E-128//TC165151				
Unigene41790_All	396	0.92	0.00	0.67	3.65	2.52	0.68	0.21	0.21	0.00	-9.85E+00	1.96E-02		-4.60E-01	6.97E-01		-5.33E-01	3.32E-01		-2.41E+00	1.41E-04	Down	-1.63E-02	1.01E+00		-7.74E+00	3.58E-01				Unigene41790_All//5.00E-07//BE054275				
Unigene41793_All	306	0.34	0.17	0.00	8.47	3.15	1.48	0.28	0.14	0.52	-1.05E+00	6.84E-01		-8.42E+00	3.92E-01		-1.43E+00	1.45E-04	Down	-2.52E+00	4.13E-08	Down	-1.02E+00	7.24E-01		9.15E-01	6.24E-01				Unigene41793_All//9.00E-11//TC145534				

Unigene41796_All	293	0.00	0.69	0.00	1.53	3.53	4.47	1.01	6.70	7.61	9.43E+00	1.36E-01		null	null		1.20E+00	8.55E-02		1.55E+00	1.29E-02		2.73E+00	9.91E-08	Up	2.91E+00	1.81E-09	Up	Unigene41796_All//gi|297804588|ref|XP_002870178.1|//5.00E-23//calmodulin-binding transcription activator 5 [Arabidopsis lyrata subsp. lyrata] >gi|297316014|gb|EFH46437.1| calmodulin-binding transcription activator 5 [Arabidopsis lyrata subsp. lyrata]	Unigene41796_All//2.00E-24//AT4G16150| calmodulin binding / transcription regulator	Unigene41796_All//8.00E-73//CO096551	CAMTA			GO:0005515//GO:0010468//GO:0043231	nr +
Unigene41799_All	370	0.57	17.12	15.54	2.29	0.00	0.73	1.71	0.11	0.54	4.92E+00	2.19E-30	Up	4.78E+00	1.70E-26	Up	-1.12E+01	2.80E-06	Down	-1.64E+00	4.18E-02		-3.92E+00	9.80E-04	Down	-1.67E+00	4.29E-02		Unigene41799_All//gi|225454743|ref|XP_002273566.1|//3.00E-14//PREDICTED: similar to S-norcoclaurine synthase 2 [Vitis vinifera]		Unigene41799_All//0.00E+00//gi|31073143|gb|CA993422.1|CA993422			GO:0050896	nr -
Unigene4180_All	603	106.72	103.44	67.91	141.84	117.93	124.41	98.86	98.70	29.40	-4.51E-02	5.75E-01		-6.52E-01	6.24E-22		-2.66E-01	2.73E-07		-1.89E-01	8.28E-04		-2.40E-03	1.01E+00		-1.75E+00	6.94E-128	Down	Unigene4180_All//gi|150416573|gb|AB868794.1|//4.00E-19//aquaporin PIP1-2 [Gossypium hirsutum]	Unigene4180_All//2.00E-18//AT1G01620| PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1C); water channel	Unigene4180_All//0.00E+00//gi|48801262|gb|CO102576.1|CO102576				nr +
Unigene41807_All	402	0.65	0.63	2.12	0.50	0.17	1.35	0.00	0.83	1.78	-4.64E-02	9.86E-01		1.70E+00	4.53E-02		-1.53E+00	4.15E-01		1.44E+00	1.93E-01		9.70E+00	1.27E-02		1.08E+01	2.63E-05	Up	Unigene41807_All//gi|224138314|ref|XP_002322783.1|//6.00E-38//f-box family protein [Populus trichocarpa] >gi|222867413|gb|EEF04544.1| f-box family protein [Populus trichocarpa]	Unigene41807_All//6.00E-33//AT3G52440| Dof-type zinc finger domain-containing protein	Unigene41807_All//1.00E-10//TC156526	C2C2-Dof			GO:0003676//GO:0010468//GO:0046914	nr -
Unigene41808_All	309	0.00	0.00	0.00	0.00	0.00	0.00	20.93	83.32	1.03	null	null		null	null		null	null		null	null		1.99E+00	3.38E-64	Up	-4.34E+00	5.71E-37	Down								
Unigene41811_All	305	0.34	0.00	0.70	5.23	3.05	0.89	15.25	13.98	26.12	-8.42E+00	3.71E-01		1.03E+00	5.91E-01		-7.78E-01	1.24E-01		-2.56E+00	2.78E-05	Down	-1.26E-01	6.39E-01		7.77E-01	1.57E-05				Unigene41811_All//5.00E-40//gi|78330228|gb|DT550502.1|DT550502				
Unigene41812_All	250	23.23	10.54	13.63	0.20	0.41	0.18	0.00	0.00	0.00	-1.14E+00	6.43E-06	Down	-7.69E-01	2.71E-03		1.05E+00	8.08E-01		-1.41E-01	9.52E-01		null	null		null	null		Unigene41812_All//gi|268376311|gb|ACZ04921.1|//5.00E-29//actin 7-like protein [Pelargonium x hortorum]	Unigene41812_All//5.00E-30//AT5G59370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene41812_All//2.00E-122//TC135405		ko04145|Phagosome	GO:0032559//GO:0043232	nr +
Unigene41814_All	429	0.85	0.00	0.12	1.74	1.04	0.11	0.39	0.39	1.21	-9.74E+00	1.96E-02		-2.78E+00	1.03E-01		-7.39E-01	3.57E-01		-4.05E+00	7.75E-04	Down	-1.66E-02	1.02E+00		1.61E+00	8.80E-02									
Unigene41815_All	519	4.94	1.46	4.62	2.59	2.39	1.13	2.69	2.98	1.92	-1.75E+00	4.31E-05	Down	-9.74E-02	8.08E-01		-1.18E-01	8.29E-01		-1.20E+00	4.18E-02		1.49E-01	7.61E-01		-4.86E-01	3.29E-01				Unigene41815_All//1.00E-137//FL577087				
Unigene4182_All	950	22.64	9.92	20.12	8.02	8.59	7.84	1.65	0.48	0.92	-1.19E+00	4.04E-21	Down	-1.70E-01	2.12E-01		9.87E-02	6.97E-01		-3.25E-02	9.04E-01		-1.77E+00	4.93E-04	Down	-8.36E-01	6.46E-02		Unigene4182_All//gi|255566313|ref|XP_002524143.1|//4.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223536610|gb|EEF38254.1| conserved hypothetical protein [Ricinus communis]		Unigene4182_All//0.00E+00//ES832196				nr +
Unigene41823_All	399	0.52	0.25	0.53	3.62	1.12	0.45	1.27	0.84	1.30	-1.05E+00	5.64E-01		2.54E-02	1.00E+00		-1.69E+00	1.87E-03		-3.00E+00	1.34E-05	Down	-6.02E-01	5.31E-01		2.96E-02	9.70E-01		Unigene41823_All//gi|124360576|gb|ABV08575.1|//4.00E-26//Esterase/lipase/thioesterase; Lipase, active site [Medicago truncatula]	Unigene41823_All//6.00E-20//AT3G27325| hydrolase, acting on ester bonds	Unigene41823_All//4.00E-26//TC134375			GO:0031410	nr +
Unigene41825_All	299	0.00	0.00	0.00	0.00	0.00	0.15	10.18	1.12	6.26	null	null		null	null		null	null		7.24E+00	6.95E-01		-3.19E+00	1.70E-13	Down	-7.01E-01	2.23E-02									
Unigene41827_All	289	0.36	0.00	0.37	1.38	1.43	2.19	0.15	0.72	3.58	-8.50E+00	3.71E-01		2.53E-02	1.00E+00		5.23E-02	9.89E-01		6.66E-01	4.92E-01		2.31E+00	2.40E-01		4.61E+00	2.03E-06	Up								
Unigene41828_All	623	0.34	0.16	0.09	1.20	0.11	0.15	3.80	1.41	1.66	-1.05E+00	5.64E-01		-1.97E+00	3.81E-01		-3.44E+00	6.19E-04	Down	-3.05E+00	3.33E-03		-1.43E+00	1.94E-04	Down	-1.19E+00	1.05E-03									
Unigene41829_All	262	31.75	42.55	55.49	31.56	20.24	31.55	12.59	26.16	12.16	4.22E-01	1.40E-02		8.05E-01	1.31E-07		-6.41E-01	6.25E-04		-7.00E-04	9.95E-01		1.06E+00	2.38E-07	Up	-4.93E-02	8.82E-01				Unigene41829_All//2.00E-36//TC142759				
Unigene41833_All	382	0.68	5.04	3.21	0.13	0.81	2.01	0.00	0.22	0.31	2.88E+00	1.43E-06	Up	2.23E+00	2.23E-03		2.64E+00	1.61E-01		3.95E+00	1.02E-03		7.77E+00	4.01E-01		8.29E+00	2.43E-01									
Unigene41835_All	541	0.00	0.00	0.00	0.00	0.00	0.00	1.25	1.70	5.08	null	null		null	null		null	null		null	null		4.43E-01	5.19E-01		2.02E+00	7.69E-08	Up			Unigene41835_All//5.00E-23//TC171825				
Unigene41837_All	634	0.00	0.00	0.00	0.00	0.00	0.00	5.60	3.30	2.26	null	null		null	null		null	null		null	null		-7.65E-01	8.56E-03		-1.31E+00	8.64E-06	Down			Unigene41837_All//9.00E-19//TC166012				
Unigene41838_All	693	0.00	0.29	1.08	0.86	1.14	0.78	0.98	1.03	3.51	8.19E+00	1.36E-01		1.01E+01	3.27E-04	Up	4.06E-01	6.32E-01		-1.42E-01	8.79E-01		7.08E-02	9.42E-01		1.84E+00	2.54E-06	Up	Unigene41838_All//gi|225454244|ref|XP_002274479.1|//5.00E-88//PREDICTED: similar to 2-oxo acid dehydrogenase, lipoyl-binding site [Vitis vinifera]	Unigene41838_All//2.00E-63//AT4G00450| CRP (CRYPTIC PRECOCIOUS)	Unigene41838_All//0.00E+00//gi|109856529|gb|DW485508.1|DW485508			GO:0006355//GO:0016251//GO:0043234	nr -
Unigene41840_All	276	1.90	7.16	3.86	1.99	2.62	3.11	60.97	117.36	70.58	1.92E+00	1.74E-04	Up	1.03E+00	1.43E-01		4.00E-01	6.64E-01		6.47E-01	4.23E-01		9.45E-01	1.45E-26		2.11E-01	6.48E-02				Unigene41840_All//6.00E-101//gi|109837926|gb|DW236487.1|DW236487				
Unigene41841_All	369	2.55	8.38	1.59	0.54	0.28	0.00	0.00	0.00	1.73	1.71E+00	8.87E-06	Up	-6.85E-01	3.69E-01		-9.48E-01	5.88E-01		-9.08E+00	1.33E-01		null	null		1.08E+01	9.33E-05	Up	Unigene41841_All//gi|75155138|sp|Q8LC53.1|EPF2_ARATH//5.00E-21//RecName: Full=Protein EPIDERMAL PATTERNING FACTOR 2; Flags: Precursor >gi|237512857|dbj|BAH58781.1| EPF2 [Arabidopsis thaliana]	Unigene41841_All//2.00E-22//AT1G34245| FUNCTIONS IN: molecular function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: EPF1 (EPIDERMAL PATTERNING FACTOR 1) (TAIR:AT2G20875.1); Has 12 Blast hits to 12 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).				GO:0007275//GO:0031410	nr +
Unigene41844_All	401	0.13	0.00	0.13	1.86	0.69	0.34	2.64	0.52	0.00	-7.03E+00	6.11E-01		2.52E-02	9.94E-01		-1.44E+00	7.43E-02		-2.46E+00	1.02E-02		-2.34E+00	6.78E-04	Down	-1.14E+01	6.71E-08	Down								
Unigene41849_All	327	1.28	0.46	0.98	4.27	1.16	1.38	0.78	0.26	0.61	-1.46E+00	2.34E-01		-3.90E-01	7.17E-01		-1.88E+00	8.65E-04	Down	-1.63E+00	5.90E-03		-1.60E+00	3.10E-01		-3.49E-01	7.66E-01				Unigene41849_All//8.00E-30//DW506861				
Unigene41853_All	592	0.00	0.00	0.00	0.00	0.00	0.00	32.50	50.90	2.36	null	null		null	null		null	null		null	null		6.48E-01	2.64E-13		-3.79E+00	1.36E-98	Down	Unigene41853_All//gi|255081504|ref|XP_002507974.1|//3.00E-08//predicted protein [Micromonas sp. RCC299]		Unigene41853_All//2.00E-31//gi|164326977|gb|ES802237.1|ES802237				nr -
Unigene41856_All	342	0.00	0.00	0.00	8.45	5.34	3.30	0.87	0.24	0.47	null	null		null	null		-6.63E-01	6.19E-02		-1.36E+00	2.84E-04	Down	-1.82E+00	2.11E-01		-8.93E-01	4.71E-01		Unigene41856_All//gi|166203230|gb|AB918655.1|//7.00E-26//transcription factor [Glycine max]	Unigene41856_All//2.00E-22//AT2G44745| WRKY family transcription factor	Unigene41856_All//4.00E-44//TC154949	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene41857_All	650	0.24	1.33	1.47	1.99	2.49	0.21	0.72	0.45	0.67	2.46E+00	6.27E-03		2.61E+00	3.45E-03		3.21E-01	5.87E-01		-3.26E+00	1.98E-05	Down	-6.69E-01	5.08E-01		-8.58E-02	9.34E-01				Unigene41857_All//1.00E-08//TC154970				
Unigene41860_All	338	0.00	1.50	0.63	0.44	0.41	1.60	0.50	1.36	3.18	1.05E+01	4.04E-03		9.30E+00	1.41E-01		-1.18E-01	9.10E-01		1.86E+00	1.03E-01		1.44E+00	1.67E-01		2.67E+00	1.42E-04	Up								
Unigene41862_All	467	0.00	0.00	0.68	1.28	0.81	0.19	6.97	1.52	0.17	null	null		9.42E+00	4.51E-02		-6.58E-01	4.78E-01		-2.73E+00	1.74E-02		-2.20E+00	7.87E-10	Down	-5.35E+00	4.79E-21	Down	Unigene41862_All//gi|222875434|gb|ACM68923.1|//1.00E-09//gibberellin 20-oxidase [Gossypium hirsutum]	Unigene41862_All//3.00E-06//AT5G51810| GA20OX2 (GIBBERELLIN 20 OXIDASE 2); gibberellin 20-oxidase	Unigene41862_All//0.00E+00//TC134244		ko00904|Diterpenoid biosynthesis		nr -
Unigene41863_All	920	0.28	0.17	0.17	1.73	1.27	0.29	1.29	1.59	0.48	-7.84E-01	6.20E-01		-7.12E-01	6.22E-01		-4.45E-01	4.08E-01		-2.56E+00	2.78E-05	Down	3.05E-01	5.74E-01		-1.43E+00	9.72E-03				Unigene41863_All//0.00E+00//TC158165				
Unigene41865_All	336	0.16	0.00	0.79	2.52	0.31	1.21	2.27	0.37	0.59	-7.28E+00	6.11E-01		2.35E+00	2.39E-01		-3.04E+00	5.54E-04	Down	-1.06E+00	1.81E-01		-2.60E+00	2.81E-03		-1.93E+00	1.14E-02		Unigene41865_All//gi|297828041|ref|XP_002881903.1|//2.00E-21//3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327742|gb|EFH58162.1| 3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene41865_All//9.00E-23//AT2G43420| 3-beta hydroxysteroid dehydrogenase/isomerase family protein	Unigene41865_All//1.00E-25//D8456045		ko00100|Steroid biosynthesis	GO:0003676//GO:0008202//GO:0009058//GO:0016020//GO:0033764	nr +
Unigene41869_All	509	0.00	0.20	0.21	2.84	0.54	1.06	0.25	1.23	0.78	7.64E+00	3.86E-01		7.71E+00	3.98E-01		-2.39E+00	4.43E-05	Down	-1.41E+00	1.29E-02		2.31E+00	1.46E-02		1.65E+00	1.40E-01		Unigene41869_All//gi|21593272|gb|AAM65221.1|//4.00E-42//membrane related protein-like [Arabidopsis thaliana]	Unigene41869_All//3.00E-43//AT1G64720| CP5	Unigene41869_All//1.00E-180//TC159445			GO:0006950//GO:0043231	nr -
Unigene41871_All	234	0.00	5.41	0.68	1.70	1.32	6.56	0.00	0.18	0.00	1.24E+01	2.86E-07	Up	9.42E+00	2.39E-01		-3.63E-01	7.54E-01		1.95E+00	9.15E-04	Up	7.48E+00	6.34E-01		null	null		Unigene41871_All//gi|291277949|gb|ADD91442.1|//7.00E-07//cytochrome P450 [Nicotiana tabacum]	Unigene41871_All//3.00E-08//AT3G26270| CYP71B25; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene41871_All//1.00E-111//gi|48776115|gb|CO085481.1|CO085481		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016020//GO:0016491	nr +
Unigene41875_All	307	0.00	1.65	5.38	0.00	2.02	0.29	0.00	0.00	0.00	1.07E+01	4.04E-03		1.24E+01	4.30E-09	Up	1.10E+01	7.90E-04	Up	8.20E+00	4.76E-01		null	null		null	null									
Unigene41877_All	327	0.00	0.00	0.00	8.84	3.58	2.49	0.00	0.00	0.00	null	null		null	null		-1.30E+00	1.88E-04	Down	-1.83E+00	3.20E-06	Down	null	null		null	null				Unigene41877_All//4.00E-07//TC148701				
Unigene41878_All	1784	0.00	0.00	0.00	0.25	0.04	0.10	4.43	0.77	2.43	null	null		null	null		-2.70E+00	3.24E-02		-1.31E+00	2.73E-01		-2.52E+00	8.43E-27	Down	-8.65E-01	1.83E-06		Unigene41878_All//gi|15238691|ref|NP_197887.1|//1.00E-172//integral membrane transporter family protein [Arabidopsis thaliana] >gi|58331763|gb|AAW70379.1| At5g25050 [Arabidopsis thaliana]	Unigene41878_All//3.00E-146//AT5G25050| integral membrane transporter family protein	Unigene41878_All//2.00E-62//TC144233				nr +
Unigene4188_All	1417	14.47	37.30	11.69	21.87	17.59	31.08	13.55	17.82	12.71	1.37E+00	1.44E-62	Up	-3.09E-01	1.73E-02		-3.14E-01	6.39E-04		5.07E-01	6.42E-11		3.95E-01	4.41E-05		-9.22E-02	4.75E-01		Unigene4188_All//gi|42568915|ref|NP_178474.2|//1.00E-139//GEK1 (GEKO1); D-aminoacyl-tRNA deacylase [Arabidopsis thaliana] >gi|83302950|sp|Q9ZPQ3.2|GEK1_ARATH RecName: Full=D-aminoacyl-tRNA deacylase; AltName: Full=Ethanol tolerance protein GEK01 >gi|28812213|dbj|BAC65101.1| GEK01 [Arabidopsis thaliana] >gi|63025186|gb|AAY27066.1| At2g03800 [Arabidopsis thaliana]	Unigene4188_All//7.00E-119//AT2G03800| GEK1 (GEKO1); D-aminoacyl-tRNA deacylase	Unigene4188_All//0.00E+00//TC132991				nr -
Unigene41885_All	327	1.92	1.39	1.63	1.68	1.37	1.66	1.55	0.00	0.12	-4.61E-01	6.18E-01		-2.38E-01	7.75E-01		-2.92E-01	7.70E-01		-1.58E-02	9.75E-01		-1.06E+01	8.89E-04	Down	-3.67E+00	3.75E-03		Unigene41885_All//gi|297822319|ref|XP_002879042.1|//1.00E-26//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324881|gb|EFH55301.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene41885_All//1.00E-26//AT2G27060| ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene41885_All//4.00E-164//C0070724			GO:0016740//GO:0044464	nr -
Unigene41887_All	325	10.46	22.76	18.84	9.66	11.13	10.84	83.91	114.20	65.21	1.12E+00	4.12E-07	Up	8.49E-01	6.46E-04		2.04E-01	5.81E-01		1.67E-01	6.58E-01		4.45E-01	1.31E-08		-3.64E-01	6.08E-05				Unigene41887_All//2.00E-79//gi|13245403|gb|BE052252.2|BE052252				
Unigene41888_All	713	0.07	0.00	0.07	0.00	0.05	0.00	8.12	15.12	33.64	-6.20E+00	6.11E-01		2.53E-02	9.94E-01		5.59E+00	8.29E-01		null	null		8.97E-01	1.15E-08		2.05E+00	2.55E-63	Up			Unigene41888_All//2.00E-10//TC142189				
Unigene41889_All	1400	0.00	0.00	0.00	0.00	0.00	0.00	5.62	0.48	2.76	null	null		null	null		null	null		null	null		-3.56E+00	2.36E-37	Down	-1.03E+00	2.94E-08	Down	Unigene41889_All//gi|87241322|gb|ABD33180.1|//1.00E-103//TGF-beta receptor, type I/II extracellular region [Medicago truncatula]	Unigene41889_All//6.00E-88//AT1G69850| ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter				GO:0044464	nr +
Unigene4189_All	1087	4.86	0.98	1.13	11.37	5.45	6.48	40.69	36.03	50.87	-2.31E+00	1.52E-13	Down	-2.11E+00	1.40E-11	Down	-1.06E+00	1.79E-12	Down	-8.10E-01	2.54E-07		-1.75E-01	2.03E-02		3.22E-01	2.06E-07		Unigene4189_All//gi|16580130|gb|AAK92213.1|//2.00E-38//bZIP transcription factor BZI-2 [Nicotiana tabacum]	Unigene4189_All//2.00E-33//AT2G18160| ATBZIP2 (ARABIDOPSIS THALIANA BASIC LEUCINE-ZIPPER 2); DNA binding / protein heterodimerization/ transcription factor	Unigene4189_All//0.00E+00//ES843094	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene41892_All	1232	0.04	20.19	6.70	0.00	0.00	0.00	0.00	0.00	0.00	8.89E+00	6.33E-141	Up	7.30E+00	2.50E-44	Up	null	null		null	null		null	null		null	null		Unigene41892_All//gi|159479982|ref|XP_001698065.1|//1.00E-125//receptor of activated protein kinase C 1 [Chlamydomonas reinhardtii] >gi|121026|sp|P25387.1|GBLP_CHLRE RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein >gi|158273864|gb|EDO99650.1| receptor of activated protein kinase C 1 [Chlamydomonas reinhardtii]	Unigene41892_All//1.00E-116//AT1G18080| ATARCA; nucleotide binding	Unigene41892_All//2.00E-11//TC154573		ko03040|Spliceosome		nr +

Unigene41894_All	303	42.48	25.92	23.37	101.11	67.17	64.24	242.38	182.08	104.13	-7.13E-01	5.90E-06		-8.62E-01	1.49E-07		-5.90E-01	3.25E-11		-6.54E-01	4.90E-12		-4.13E-01	3.05E-14		-1.22E+00	6.90E-92	Down	Unigene41894_All//gi|75308026|sp|Q9AT56.1|METK1_ELAUM//2.00E-08//RecName: Full=S-adenosylmethionine synthase 1; Short=AdoMet synthase 1; AltName: Full=Methionine adenosyltransferase 1; Short=MAT 1 >gi|13540316|gb|AAK29409.1|AF34630 5_1 S-adenosyl-L-methionine synthetase [Elaeagnus umbellata]	Unigene41894_All//3.00E-09//AT4G01850| SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase	Unigene41894_All//7.00E-98//gi|11206846|gb|BF275776.1|BF275776		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr +
Unigene41895_All	420	0.00	0.48	1.78	2.02	0.49	0.22	6.74	2.09	2.09	8.91E+00	1.36E-01		1.08E+01	3.27E-04	Up	-2.04E+00	9.04E-03		-3.23E+00	1.04E-03		-1.69E+00	2.42E-06	Down	-1.69E+00	1.33E-06	Down										
Unigene41897_All	698	0.15	0.00	0.31	0.50	0.10	0.06	1.64	3.83	3.60	-7.23E+00	3.71E-01		1.03E+00	5.91E-01		-2.34E+00	1.01E-01		-2.95E+00	8.30E-02		1.23E+00	4.74E-04	Up	1.14E+00	1.26E-03											
Unigene4190_All	1663	1.45	1.37	0.51	3.12	4.29	2.74	5.31	1.33	1.99	-7.79E-02	8.44E-01		-1.50E+00	8.47E-04	Down	4.60E-01	3.48E-02		-1.84E-01	5.51E-01		-2.00E+00	1.30E-22	Down	-1.42E+00	1.02E-14	Down	Unigene4190_All//gi|42567496|ref|NP_195520.2|//6.00E-64//bHLH family protein [Arabidopsis thaliana]	Unigene4190_All//9.00E-54//AT4G38070| bHLH family protein	Unigene4190_All//7.00E-28//TC170437	bHLH			nr +
Unigene41901_All	881	0.00	36.92	14.20	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	1.28E-187	Up	1.38E+01	2.09E-70	Up	null	null		null	null		null	null		null	null		Unigene41901_All//gi|225448546|ref|XP_002276986.1|//1.00E-104//PREDICTED: similar to 40S ribosomal S4 protein [Vitis vinifera]	Unigene41901_All//2.00E-103//AT5G58420| 40S ribosomal protein S4 (RPS4D)			ko03010|Ribosome		nr +
Unigene41903_All	461	0.00	0.33	0.35	0.00	0.00	0.00	31.55	6.80	37.85	8.37E+00	2.35E-01		8.44E+00	2.39E-01		null	null		null	null		-2.21E+00	7.33E-42	Down	2.63E-01	2.76E-02		Unigene41903_All//gi|73624747|gb|AA279231.1|//3.00E-56//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene41903_All//6.00E-52//AT4G24000| ATCSLG2; cellulose synthase/ transferase/ transferase, transferring glycosyl groups				GO:0009250//GO:0016759//GO:0031224//GO:0045229	nr +
Unigene41906_All	713	0.00	0.00	0.00	0.00	0.00	0.00	3.80	1.17	0.17	null	null		null	null		null	null		null	null		-1.69E+00	4.12E-06	Down	-4.50E+00	4.09E-16	Down	Unigene41906_All//gi|193875702|gb|ACF24487.1|//2.00E-92//eukaryotic translation elongation factor 2 [Cyanophora paradoxa]	Unigene41906_All//2.00E-80//AT3G12915| GTP binding / GTPase	Unigene41906_All//9.00E-10//ES843714			GO:0008135//GO:0010467//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene41908_All	218	0.24	3.72	0.00	0.00	1.11	1.66	0.39	1.15	1.10	3.95E+00	7.52E-04	Up	-7.91E+00	6.23E-01		1.01E+01	1.04E-01		1.07E+01	2.37E-02		1.57E+00	3.26E-01		1.50E+00	3.39E-01											
Unigene4191_All	625	60.44	11.84	16.44	81.22	46.17	66.26	79.96	20.40	22.25	-2.35E+00	6.59E-95	Down	-1.88E+00	1.00E-68	Down	-8.15E-01	4.20E-32		-2.94E-01	5.70E-05		-1.97E+00	1.65E-122	Down	-1.85E+00	1.53E-115	Down	Unigene4191_All//gi|209967441|gb|ACJ02349.1|//3.00E-59//60S ribosomal protein L35a [Vernicia fordii]	Unigene4191_All//6.00E-58//AT1G74270| 60S ribosomal protein L35a (RPL35aC)	Unigene4191_All//0.00E+00//gi|21101410|gb|BQ413723.1|BQ413723		ko03010|Ribosome		nr +
Unigene41912_All	323	19.28	9.73	8.08	36.40	40.30	27.96	77.36	46.45	42.92	-9.87E-01	3.80E-05		-1.25E+00	8.32E-07	Down	1.47E-01	4.25E-01		-3.80E-01	2.37E-02		-7.36E-01	8.57E-14		-8.50E-01	5.51E-18		Unigene41912_All//gi|296881978|gb|ADH82414.1|//2.00E-55//actin [Jatropha curcas]	Unigene41912_All//4.00E-56//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene41912_All//0.00E+00//gi|11199604|gb|BF268609.1|BF268609		ko04145|Phagosome	GO:0032559//GO:0043232	nr -
Unigene41914_All	565	0.37	2.15	0.28	0.44	0.37	1.52	1.20	2.07	1.27	2.54E+00	5.98E-04	Up	-3.90E-01	8.07E-01		-2.70E-01	8.23E-01		1.78E+00	3.19E-02		7.91E-01	1.64E-01		8.41E-02	9.24E-01											
Unigene41915_All	1324	0.00	0.15	0.00	0.56	0.16	0.20	3.45	0.66	5.18	7.26E+00	1.36E-01		null	null		-1.85E+00	2.53E-02		-1.46E+00	9.04E-02		-2.38E+00	8.42E-15	Down	5.86E-01	2.56E-03		Unigene41915_All//gi|224113331|ref|XP_002316459.1|//1.00E-103//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222865499|gb|EEF02630.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene41915_All//2.00E-81//AT3G54320| WRI1 (WRINKLED 1); DNA binding / transcription factor	Unigene41915_All//0.00E+00//gi|109879135|gb|DW508105.1|DW508105	AP2-EREBP		GO:0006350//GO:0043231	nr -
Unigene41916_All	758	0.00	21.19	18.69	0.13	0.00	0.00	0.00	0.00	0.00	1.44E+01	2.68E-92	Up	1.42E+01	8.41E-80	Up	-7.04E+00	3.12E-01		-7.04E+00	3.99E-01		null	null		null	null		Unigene41916_All//sp|P16213|B2MG_PONPY//1.00E-63//Beta-2-microglobulin OS=Pongo pygmaeus GN=B2M PE=3 SV=2						swissprot -
Unigene41918_All	745	0.91	4.42	4.15	0.67	0.69	3.09	0.11	0.22	0.00	2.28E+00	1.78E-08	Up	2.18E+00	2.54E-07	Up	5.23E-02	9.80E-01		2.21E+00	3.75E-06	Up	9.83E-01	6.33E-01		-6.83E+00	3.58E-01		Unigene41918_All//gi|210111348|gb|ACJ07153.1|//1.00E-79//RC83 MYB transcription factor [Gossypium hirsutum]	Unigene41918_All//6.00E-69//AT3G01140| MYB106 (myb domain protein 106); DNA binding / transcription factor	Unigene41918_All//4.00E-157//gi|109884213|gb|DW513183.1|DW513183	MYB		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene4192_All	1498	13.87	4.33	10.31	19.22	12.80	18.84	12.79	6.86	6.06	-1.68E+00	7.49E-34	Down	-4.28E-01	6.46E-04		-5.86E-01	1.91E-10		-2.86E-02	8.15E-01		-8.98E-01	8.40E-15		-1.08E+00	2.52E-20	Down	Unigene4192_All//gi|161016198|gb|AB356031.1|//1.00E-152//gland development-related protein 1 [Gossypium hirsutum]	Unigene4192_All//3.00E-126//AT2G34260| transducin family protein / WD-40 repeat family protein	Unigene4192_All//0.00E+00//TC130065		ko03040|Spliceosome		nr -
Unigene41921_All	342	1.07	2.52	1.25	0.29	0.50	0.79	0.25	0.12	2.21	1.23E+00	1.12E-01		2.18E-01	8.31E-01		7.89E-01	7.70E-01		1.44E+00	4.09E-01		-1.02E+00	7.24E-01		3.16E+00	6.82E-04	Up	Unigene41921_All//gi|292668993|gb|ADE41151.1|//2.00E-08//AP2 domain class transcription factor [Malus x domestica]	Unigene41921_All//9.00E-07//AT2G20350| AP2 domain-containing transcription factor, putative	Unigene41921_All//3.00E-08//TC160311	AP2-EREBP		GO:0006350//GO:0010468	nr +
Unigene41923_All	1106	0.09	1.01	0.48	0.09	0.12	0.16	15.90	11.03	10.84	3.41E+00	1.24E-04	Up	2.35E+00	5.87E-02		4.67E-01	8.76E-01		8.58E-01	6.95E-01		-5.27E-01	7.25E-06		-5.53E-01	1.54E-06					Unigene41923_All//5.00E-40//TC158845					
Unigene41924_All	464	7.33	2.40	8.03	1.40	0.45	0.19	0.55	0.00	0.34	-1.61E+00	7.48E-06	Down	1.32E-01	6.89E-01		-1.65E+00	6.52E-02		-2.84E+00	1.02E-02		-9.09E+00	4.04E-02		-6.71E-01	6.05E-01		Unigene41924_All//gi|240255299|ref|NP_187344.4|//7.00E-25//nucleotide binding [Arabidopsis thaliana]	Unigene41924_All//2.00E-22//AT3G06880| nucleotide binding	Unigene41924_All//0.00E+00//TC146237				nr +
Unigene41925_All	767	0.00	0.26	0.00	0.13	0.00	0.12	13.06	1.53	17.66	8.05E+00	1.36E-01		null	null		-7.02E+00	3.12E-01		-1.41E-01	9.50E-01		-3.10E+00	6.37E-42	Down	4.35E-01	1.09E-03		Unigene41925_All//gi|6899646|gb|AAF31023.1|AC012189_5//4.00E-20//EST gb|AB015130 comes from this gene [Arabidopsis thaliana]	Unigene41925_All//4.00E-25//AT2G01300| unknown protein	Unigene41925_All//4.00E-09//gi|195983391|gb|FL576885.1|FL576885			GO:0006952	nr +
Unigene41926_All	347	7.84	0.58	0.31	5.17	4.76	3.51	0.61	0.48	0.46	-3.75E+00	2.32E-11	Down	-4.68E+00	2.16E-12	Down	-1.18E-01	8.38E-01		-5.56E-01	2.76E-01		-3.39E-01	8.12E-01		-4.08E-01	7.55E-01		Unigene41926_All//gi|15226146|ref|NP_178812.1|//8.00E-22//minichromosome maintenance family protein / MCM family protein [Arabidopsis thaliana]	Unigene41926_All//1.00E-20//AT2G07690| minichromosome maintenance family protein / MCM family protein	Unigene41926_All//2.00E-42//DW488641		ko03030|DNA replication	GO:0003676//GO:0006259//GO:0032559//GO:0043231	nr -
Unigene41929_All	421	0.87	2.53	0.38	1.54	2.37	0.75	2.31	0.30	0.00	1.54E+00	2.81E-02		-1.20E+00	3.96E-01		6.25E-01	4.06E-01		-1.03E+00	2.68E-01		-2.96E+00	1.89E-04	Down	-1.12E+01	2.72E-07	Down				Unigene41929_All//5.00E-84//gi|28332917|gb|DT553191.1|DT553191					
Unigene41931_All	519	9.17	3.42	9.75	0.58	0.27	0.00	0.00	0.48	0.31	-1.42E+00	1.02E-06	Down	8.75E-02	7.53E-01		-1.12E+00	4.24E-01		-9.17E+00	3.99E-02		8.92E+00	4.31E-02		8.26E+00	1.40E-01					Unigene41931_All//1.00E-11//TC160268					
Unigene41932_All	479	0.00	1.16	0.22	1.46	5.46	6.60	1.85	1.05	3.58	1.02E+01	2.18E-03		7.80E+00	3.98E-01		1.91E+00	3.76E-06	Up	2.18E+00	4.06E-08	Up	-8.24E-01	2.24E-01		9.48E-01	2.90E-02		Unigene41932_All//gi|15239795|ref|NP_199723.1|//9.00E-24//senescence-associated protein-related [Arabidopsis thaliana]	Unigene41932_All//6.00E-21//AT5G49120| senescence-associated protein-related	Unigene41932_All//0.00E+00//ES824771				nr -
Unigene41933_All	394	1.33	0.77	0.54	12.39	6.12	8.25	0.00	0.00	0.00	-7.83E-01	4.22E-01		-1.30E+00	2.42E-01		-1.02E+00	5.81E-05	Down	-5.86E-01	3.19E-02		null	null		null	null		Unigene41933_All//gi|297803014|ref|XP_002869391.1|//2.00E-13//transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata] >gi|297315227|gb|EFH45650.1| transcription factor/ transcription regulator [Arabidopsis lyrata subsp. lyrata]	Unigene41933_All//2.00E-10//AT2G18969| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: transcription factor/ transcription regulator (TAIR:AT4G30180.1); Has 49 Blast hits to 49 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 49; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene41933_All//0.00E+00//gi|84173137|gb|DR461785.1|DR461785				nr +
Unigene41934_All	544	2.79	0.09	0.10	0.27	0.32	0.42	2.72	0.08	1.32	-4.90E+00	1.22E-07	Down	-4.83E+00	3.80E-07	Down	2.04E-01	9.50E-01		5.96E-01	7.21E-01		-5.15E+00	2.98E-09	Down	-1.05E+00	2.65E-02		Unigene41934_All//gi|159025733|emb|CAN88867.1|//2.00E-64//D6-type cyclin [Populus trichocarpa]	Unigene41934_All//2.00E-20//AT4G03270| CYCD6;1 (Cyclin D6;1); cyclin-dependent protein kinase	Unigene41934_All//9.00E-31//TC174962				nr -
Unigene41936_All	353	8.89	2.73	6.34	0.42	1.56	1.41	0.00	0.00	0.00	-1.71E+00	7.36E-06	Down	-4.89E-01	1.91E-01		1.88E+00	9.41E-02		1.73E+00	1.45E-01		null	null		null	null		Unigene41936_All//gi|48310646|gb|AAT41859.1|//2.00E-13//At1g73885 [Arabidopsis thaliana]	Unigene41936_All//1.00E-13//AT1G73885| unknown protein	Unigene41936_All//5.00E-53//gi|109890882|gb|DW519845.1|DW519845			GO:0009534//GO:0031410	nr -
Unigene41937_All	741	1.98	1.09	0.50	2.62	4.46	1.22	0.46	2.65	0.97	-8.54E-01	1.22E-01		-1.97E+00	1.91E-03		7.67E-01	2.19E-02		-1.10E+00	1.82E-02		2.54E+00	3.39E-07	Up	1.08E+00	1.41E-01		Unigene41937_All//gi|223452548|gb|ACM89601.1|//1.00E-53//disease resistance protein [Glycine max]	Unigene41937_All//1.00E-25//AT4G13810| AtRLP47 (Receptor Like Protein 47); protein binding	Unigene41937_All//0.00E+00//TC166014		ko04626|Plant-pathogen interaction		nr +
Unigene41938_All	619	2.03	6.14	2.75	4.51	3.28	3.94	11.68	11.07	5.02	1.60E+00	2.39E-06	Up	4.40E-01	3.86E-01		-4.57E-01	2.29E-01		-1.94E-01	6.38E-01		-7.69E-02	7.26E-01		-1.22E+00	7.79E-10	Down	Unigene41938_All//gi|15027813|gb|AAK76732.1|//3.00E-10//3-ketoacyl-CoA thiolase [Gossypium hirsutum]	Unigene41938_All//1.00E-10//AT5G48880| PKT2 (PEROXISOMAL 3-KETO-ACYL-COA THIOLASE 2); acetyl-CoA C-acyltransferase/ catalytic	Unigene41938_All//7.00E-44//gi|21098833|gb|BQ411146.1|BQ411146		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene41943_All	243	6.67	3.13	1.31	1.64	1.98	0.93	0.00	0.34	0.66	-1.09E+00	3.63E-02		-2.34E+00	1.96E-04	Down	2.75E-01	8.20E-01		-8.20E-01	5.06E-01		8.43E+00	4.01E-01		9.36E+00	1.40E-01		Unigene41943_All//gi|15225457|ref|NP_182060.1|//1.00E-06//CRR4 (CHLORORESPIRATORY REDUCTION 4) [Arabidopsis thaliana]	Unigene41943_All//5.00E-08//AT2G45350| CRR4 (CHLORORESPIRATORY REDUCTION 4)	Unigene41943_All//2.00E-94//CO093317			GO:0009451//GO:0043231	nr +
Unigene41944_All	336	0.00	2.26	0.48	2.08	0.00	3.09	46.68	103.62	101.73	1.11E+01	1.76E-04	Up	8.89E+00	2.39E-01		-1.10E+01	3.44E-05	Down	5.75E-01	4.27E-01		1.15E+00	5.20E-39	Up	1.12E+00	8.62E-38	Up	Unigene41944_All//gi|59896631|gb|AAX11684.1|//1.00E-13//perakine reductase [Rauvolfia serpentina]	Unigene41944_All//7.00E-05//AT1G60680| aldo/keto reductase family protein	Unigene41944_All//7.00E-92//gi|48746486|gb|CO077005.1|CO077005			GO:0004033//GO:0008152	nr +
Unigene41946_All	243	8.61	22.73	14.46	5.53	10.34	10.04	6.79	11.35	13.28	1.40E+00	1.89E-07	Up	7.48E-01	2.93E-02		9.02E-01	2.23E-02		8.59E-01	3.79E-02		7.42E-01	2.83E-02		9.69E-01	1.31E-03					Unigene41946_All//2.00E-97//gi|109842245|gb|DW240805.1|DW240805					
Unigene41950_All	283	85.78	280.02	165.96	86.25	133.85	156.56	110.26	147.10	105.86	1.71E+00	1.37E-129	Up	9.52E-01	1.45E-30		6.34E-01	3.80E-15		8.60E-01	5.64E-27		4.16E-01	1.53E-08		-5.87E-02	5.78E-01		Unigene41950_All//gi|33415266|gb|AAQ18141.1|//2.00E-07//poly(A)-binding protein C-terminal interacting protein 6 [Cucumis sativus]		Unigene41950_All//3.00E-69//gi|13353348|gb|BG443696.1|BG443696				nr -
Unigene41951_All	547	0.57	0.65	0.49	1.55	2.14	0.99	2.01	1.22	0.00	1.76E-01	8.83E-01		-2.38E-01	8.50E-01		4.67E-01	5.14E-01		-6.44E-01	4.15E-01		-7.17E-01	2.30E-01		-1.10E+01	3.33E-08	Down	Unigene41951_All//gi|122209356|sp|Q2V3I3.1|EPFL4_ARATH//7.00E-29//RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 4; Short=EPF-like protein 4; Flags: Precursor	Unigene41951_All//2.00E-23//AT4G14723| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: allergen-related (TAIR:AT3G22820.1); Has 130 Blast hits to 130 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 130; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene41951_All//0.00E+00//ES823685			GO:0009791//GO:0009913	nr -
Unigene41956_All	324	2.10	0.78	2.47	4.00	1.81	0.56	1.30	0.00	0.74	-1.42E+00	1.16E-01		2.32E-01	7.49E-01		-1.15E+00	4.27E-02		-2.84E+00	7.63E-05	Down	-1.03E+01	3.25E-03		-8.23E-01	3.99E-01					Unigene41956_All//4.00E-10//FL576894					
Unigene41958_All	675	0.00	0.00	0.00	12.40	7.14	4.35	0.31	0.06	0.24	null	null		null	null		-7.96E-01	1.64E-05		-1.51E+00	5.25E-13	Down	-2.34E+00	2.37E-01		-4.08E-01	7.55E-01		Unigene41958_All//gi|254554078|gb|ACT67415.1|//1.00E-07//cellulose synthase [Shorea parvifolia subsp. parvifolia]	Unigene41958_All//3.00E-08//AT5G17420| IRX3 (IRREGULAR XYLEM 3); cellulose synthase	Unigene41958_All//9.00E-19//TC149449			GO:0007047//GO:0009832//GO:0016020//GO:0044264//GO:0046527	nr -
Unigene41959_All	673	0.00	0.00	0.00	0.00	0.00	0.00	13.76	4.60	4.50	null	null		null	null		null	null		null	null		-1.58E+00	2.30E-17	Down	-1.61E+00	2.06E-18	Down	Unigene41959_All//gi|71040679|gb|AAZ20288.1|//1.00E-44//disease resistance-responsive family protein [Arachis hypogaea]	Unigene41959_All//2.00E-41//AT5G42500| disease resistance-responsive family protein	Unigene41959_All//8.00E-47//DR454882				nr -
Unigene41960_All	797	0.00	0.00	0.00	0.00	0.00	0.00	10.08	0.31	2.30	null	null		null	null		null	null		null	null		-5.00E+00	5.66E-48	Down	-2.13E+00	3.90E-23	Down	Unigene41960_All//gi|40781598|gb|AAB89808.1|//6.00E-83//reductase 2 [Hydrangea macrophylla] >gi|40781601|gb|AAB89810.1| reductase 2 [Hydrangea macrophylla]	Unigene41960_All//0.00E+00//TC165057	Unigene41960_All//0.00E+00//TC165057		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism	GO:0008152//GO:0016747	nr +
Unigene41962_All	727	0.00	0.28	0.29	2.95	2.13	0.50	1.16	0.46	0.49	8.12E+00	1.36E-01		8.19E+00	1.41E-01		-4.67E-01	3.03E-01		-2.57E+00	6.21E-07	Down	-1.34E+00	5.68E-02		-1.24E+00	6.26E-02		Unigene41962_All//gi|18201934|gb|AK92458.3|AF398149_1//4.00E-65//kinesin-like protein heavy chain [Arabidopsis thaliana]	Unigene41962_All//2.00E-66//AT3G44730| kinesin motor protein-related	Unigene41962_All//0.00E+00//gi|109860853|gb|DW489832.1|DW489832			GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr -
Unigene41964_All	445	0.00	0.00	0.00	0.00	0.31	0.20	1.62	6.20	5.64	null	null		null	null		8.27E+00	3.18E-01		7.67E+00	4.76E-01		1.94E+00	2.70E-07	Up	1.80E+00	2.47E-06	Up	Unigene41964_All//gi|15221409|ref|NP_177012.1|//4.00E-11//VQ motif-containing protein [Arabidopsis thaliana] >gi|28372822|gb|AAO39893.1| At1g68450 [Arabidopsis thaliana]	Unigene41964_All//5.00E-10//AT1G68450| VQ motif-containing protein				GO:0043231	nr +

Unigene41966_All	572	1.37	4.69	1.30	2.18	2.05	2.29	1.63	1.46	1.32	1.77E+00	2.49E-05	Up	-7.41E-02	9.35E-01		-8.90E-02	8.70E-01		7.27E-02	9.24E-01		-1.54E-01	8.08E-01		-2.97E-01	6.31E-01		Unigene41966_All//gi|225440831|ref|XP_002282071.1|//1.00E-60//PREDICTED: similar to ubiquitin fusion protein [Vitis vinifera] >gi|71040673|gb|AAZ20285.1| ubiquitin fusion protein [Arachis hypogaea] >gi|192910738|gb|ACF06477.1| ubiquitin fusion protein [Elaeis guineensis] >gi|284433784|gb|AD885098.1| ubiquitin C variant [Jatropha curcas]	Unigene41966_All//1.00E-61//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene41966_All//0.00E+00//gi|109867178|gb|DW496154.1|DW496154		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0031981//GO:0032446	nr -
Unigene41967_All	203	34.02	71.14	47.74	56.69	75.49	88.77	19.37	37.88	35.32	1.06E+00	3.92E-12	Up	4.89E-01	1.14E-02		4.13E-01	2.65E-03		6.47E-01	3.68E-07		9.68E-01	3.58E-07		8.67E-01	6.27E-06		Unigene41967_All//gi|297829870|ref|XP_002882817.1|//6.00E-22//WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328657|gb|EFH59076.1| WD-40 repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene41967_All//2.00E-23//AT5G56190| WD-40 repeat family protein	Unigene41967_All//8.00E-109//EX172491			GO:0003676//GO:0006260//GO:0019897//GO:0031461//GO:0034061	nr +
Unigene4197_All	907	1.73	0.84	1.82	3.02	4.94	5.08	3.87	7.70	7.77	-1.05E+00	4.79E-02		7.27E-02	8.89E-01		7.08E-01	1.09E-02		7.50E-01	7.58E-03		9.92E-01	7.95E-07		1.01E+00	3.00E-07	Up	Unigene4197_All//gi|20270080|gb|AAM18168.1|AC092172_28//2.00E-39//Unknown protein [Oryza sativa Japonica Group] >gi|31430911|gb|AAP52763.1| expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene4197_All//4.00E-57//AT3G63290| unknown protein	Unigene4197_All//0.00E+00//TC178694				nr -
Unigene41975_All	608	0.34	0.25	0.35	2.05	2.66	2.08	2.09	0.14	2.23	-4.61E-01	7.58E-01		2.53E-02	1.00E+00		3.78E-01	5.26E-01		2.21E-02	9.71E-01		-3.92E+00	6.20E-07	Down	9.47E-02	8.55E-01		Unigene41975_All//gi|10176937|dbj|BAB10136.1|//7.00E-74//serine/threonine-specific kinase like protein [Arabidopsis thaliana]	Unigene41975_All//4.00E-75//AT5G55830| lectin protein kinase, putative	Unigene41975_All//0.00E+00//C0115789		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016020//GO:0030246//GO:0031410//GO:0032559//GO:0046914	nr -
Unigene41976_All	675	0.00	14.71	5.84	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	6.75E-57	Up	1.25E+01	7.61E-22	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene41977_All	466	1.80	1.09	1.94	0.00	0.00	0.87	0.00	0.27	1.28	-7.24E-01	3.48E-01		1.13E-01	8.72E-01		null	null		9.77E+00	1.36E-02		8.07E+00	2.40E-01		1.03E+01	1.75E-04	Up	Unigene41977_All//gi|149941644|dbj|BAF64844.1|//5.00E-38//aromatic L-amino acid decarboxylase [Rosa hybrid cultivar]	Unigene41977_All//5.00E-33//AT2G20340| tyrosine decarboxylase, putative			ko00360|Phenylalanine metabolism//ko00380|Tryptophan metabolism//ko00350|Tyrosine metabolism//ko00340|Histidine metabolism//ko00950|Isoquinoline alkaloid biosynthesis//ko00901|Indole alkaloid biosynthesis//ko00965|Betalain biosynthesis	GO:0016831//GO:0043436//GO:0048037	nr -
Unigene4198_All	1524	1.03	1.46	0.73	1.34	2.82	2.87	2.27	1.86	2.69	5.06E-01	2.37E-01		-4.89E-01	3.92E-01		1.08E+00	1.46E-04	Up	1.10E+00	1.51E-04	Up	-2.87E-01	3.81E-01		2.43E-01	3.85E-01		Unigene4198_All//gi|20270080|gb|AAM18168.1|AC092172_28//4.00E-90//Unknown protein [Oryza sativa Japonica Group] >gi|31430911|gb|AAP52763.1| expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene4198_All//3.00E-104//AT3G63290| unknown protein	Unigene4198_All//0.00E+00//gi|78326347|gb|DT546621.1|DT546621				nr -
Unigene41980_All	412	0.00	0.00	0.00	8.22	3.01	4.93	0.00	0.00	0.00	null	null		null	null		-1.45E+00	6.42E-06	Down	-7.37E-01	2.82E-02		null	null		null	null		Unigene41980_All//gi|186511137|ref|NP_001118849.1|//7.00E-34//metal ion binding [Arabidopsis thaliana]	Unigene41980_All//4.00E-35//AT3G56891| metal ion binding				GO:0006812//GO:0043169	nr -
Unigene41981_All	240	2.62	8.87	5.33	5.81	7.03	13.74	1.06	1.22	3.15	1.76E+00	2.38E-04	Up	1.03E+00	1.03E-01		2.75E-01	6.18E-01		1.24E+00	3.44E-04	Up	2.06E-01	8.68E-01		1.58E+00	3.40E-02									
Unigene41986_All	467	0.22	0.65	0.11	1.49	0.07	0.19	3.62	3.22	2.90	1.54E+00	3.23E-01		-9.75E-01	7.20E-01		-4.34E+00	2.80E-04	Down	-2.95E+00	5.84E-03		-1.69E-01	7.23E-01		-3.20E-01	4.77E-01		Unigene41986_All//gi|224111284|ref|XP_002332949.1|//7.00E-17//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834261|gb|EEE72738.1| cc-nbs-lrr resistance protein [Populus trichocarpa]		Unigene41986_All//2.00E-40//ES823904				nr -
Unigene41988_All	1121	0.00	16.63	3.56	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	3.09E-107	Up	1.18E+01	3.83E-22	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene4199_All	494	9.21	4.51	7.22	19.76	11.36	14.72	2.31	1.78	0.73	-1.03E+00	3.28E-04	Down	-3.52E-01	2.47E-01		-7.99E-01	2.28E-06		-4.25E-01	2.19E-02		-3.79E-01	5.32E-01		-1.67E+00	4.10E-03				Unigene4199_All//0.00E+00//DR453678				ESTscan -
Unigene41990_All	703	0.00	0.00	0.00	0.14	0.00	0.00	7.34	2.73	4.65	null	null		null	null		-7.15E+00	3.12E-01		-7.15E+00	3.99E-01		-1.42E+00	1.09E-08	Down	-6.59E-01	3.71E-03		Unigene41990_All//gi|297610175|ref|NP_001061242.2|//2.00E-07//Os10g0176300 [Oryza sativa Japonica Group] >gi|18652490|gb|AAL77124.1|AC098566_11 Unknown protein [Oryza sativa] >gi|255679246|dbj|BAF26156.2| Os10g0176300 [Oryza sativa Japonica Group]		Unigene41990_All//1.00E-14//EV492772			GO:0043231	nr +
Unigene41992_All	982	0.00	20.59	7.48	0.00	0.00	0.00	0.00	0.00	0.00	1.43E+01	2.55E-116	Up	1.29E+01	4.45E-41	Up	null	null		null	null		null	null		null	null		Unigene41992_All//sp|Q24747|EXU_DROVI//3.00E-76//Maternal protein exuperantia OS=Drosophila virilis GN=exu PE=3 SV=1						swissprot +
Unigene41996_All	450	0.23	0.56	0.00	0.55	0.69	0.30	1.60	2.51	4.43	1.28E+00	4.35E-01		-7.86E+00	3.92E-01		3.15E-01	8.38E-01		-8.78E-01	6.16E-01		6.51E-01	2.66E-01		1.47E+00	4.17E-04	Up			Unigene41996_All//5.00E-07//TC142228				
Unigene41997_All	423	0.99	3.59	0.38	1.18	0.49	0.64	1.30	2.37	5.27	1.86E+00	1.61E-03		-1.39E+00	2.80E-01		-1.27E+00	2.22E-01		-8.78E-01	4.20E-01		8.68E-01	1.64E-01		2.02E+00	1.66E-06	Up	Unigene41997_All//gi|225437941|ref|XP_002268868.1|//2.00E-40//PREDICTED: similar to Os04g0509400 [Vitis vinifera]	Unigene41997_All//7.00E-35//AT4G28703| FUNCTIONS IN: molecular_function unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Cupin, RmlC-type (InterPro:IPR011051), Protein of unknown function DUF861, cupin-3 (InterPro:IPR008579), RmlC-like jelly roll fold (InterPro:IPR014710); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G04300.1); Has 311 Blast hits to 311 proteins in 80 species: Archae - 0; Bacteria - 147; Metazoa - 0; Fungi - 0; Plants - 76; Viruses - 0; Other Eukaryotes - 88 (source: NCBI BLink).	Unigene41997_All//5.00E-44//DW510938			GO:0009536	nr +
Unigene41998_All	715	0.59	0.00	0.30	2.86	2.99	1.96	1.60	0.23	0.61	-9.19E+00	1.05E-02		-9.75E-01	4.11E-01		6.40E-02	9.06E-01		-5.45E-01	2.45E-01		-2.77E+00	7.62E-05	Down	-1.38E+00	1.42E-02		Unigene41998_All//gi|270267863|gb|ACZ65511.1|//3.00E-95//Tap46 [Nicotiana benthamiana]	Unigene41998_All//1.00E-85//AT5G53000| TAP46 (2A phosphatase associated protein of 46 kD); protein phosphatase type 2A regulator	Unigene41998_All//8.00E-146//gi|164272645|gb|ES817722.1|ES817722			GO:0006950//GO:0019888	nr -
Unigene41999_All	591	4.96	1.37	0.54	6.32	5.13	8.18	0.00	0.00	0.00	-1.85E+00	4.31E-06	Down	-3.20E+00	3.48E-10	Down	-3.02E-01	3.74E-01		3.71E-01	2.08E-01		null	null		null	null		Unigene41999_All//gi|149390803|gb|ABR25419.1|//1.00E-10//mlo like protein 4 [Oryza sativa Indica Group]	Unigene41999_All//4.00E-10//AT1G11000| MLO4 (MILDEW RESISTANCE LOCUS O 4); calmodulin binding				GO:0016020//GO:0043229	nr -
Unigene420_All	547	1.63	7.23	1.65	2.09	2.14	1.32	0.54	0.76	0.87	2.15E+00	2.04E-09	Up	2.53E-02	9.92E-01		3.12E-02	9.74E-01		-6.65E-01	3.16E-01		4.98E-01	6.33E-01		6.92E-01	4.63E-01		Unigene420_All//gi|20042920|gb|AAM08748.1|AC025098_15//3.00E-15//Unknown protein [Oryza sativa Japonica Group]	Unigene420_All//8.00E-13//AT3G18350| unknown protein	Unigene420_All//2.00E-87//BQ404320				nr +
Unigene4200_All	1102	4.46	3.13	6.04	11.66	5.66	5.49	2.95	1.21	0.90	-5.13E-01	5.97E-02		4.37E-01	7.20E-02		-1.04E+00	1.23E-12	Down	-1.09E+00	5.31E-12	Down	-1.28E+00	4.79E-05	Down	-1.71E+00	1.49E-07	Down	Unigene4200_All//gi|124359162|gb|ABN05685.1|//3.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene4200_All//0.00E+00//DR453678				nr +
Unigene42002_All	299	0.70	0.00	0.36	2.33	2.88	0.00	1.27	0.14	0.00	-9.45E+00	1.22E-01		-9.75E-01	6.20E-01		3.04E-01	7.36E-01		-1.12E+01	1.96E-04	Down	-3.19E+00	3.11E-02		-1.03E+01	4.19E-03									
Unigene42006_All	385	233.20	107.26	98.20	314.02	407.77	397.20	710.42	277.91	246.38	-1.12E+00	4.28E-78	Down	-1.25E+00	1.43E-89	Down	3.77E-01	3.59E-24		3.39E-01	1.35E-17		-1.35E+00	0.00E+00	Down	-1.53E+00	0.00E+00	Down	Unigene42006_All//gi|82621138|gb|ABB86257.1|//1.00E-23//40S ribosomal protein S15-like [Solanum tuberosum] >gi|82621162|gb|ABB86269.1| 40S ribosomal protein S15-like [Solanum tuberosum]	Unigene42006_All//9.00E-25//AT5G09510| 40S ribosomal protein S15 (RPS15D)	Unigene42006_All//0.00E+00//gi|13247106|gb|BF268614.2|BF268614		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene42007_All	468	0.67	0.22	0.46	1.28	1.32	0.97	2.62	0.36	0.85	-1.63E+00	2.76E-01		-5.60E-01	6.63E-01		5.22E-02	9.71E-01		-4.05E-01	6.73E-01		-2.87E+00	2.54E-05	Down	-1.62E+00	3.49E-03		Unigene42007_All//gi|119360031|gb|ABL66744.1|//2.00E-22//At1g54200 [Arabidopsis thaliana]	Unigene42007_All//7.00E-09//AT1G54200| unknown protein	Unigene42007_All//0.00E+00//gi|109877174|gb|DW506148.1|DW506148				nr +
Unigene4201_All	1660	9.23	4.06	4.36	16.05	11.91	22.01	17.04	8.71	9.22	-1.19E+00	3.43E-15	Down	-1.08E+00	1.25E-12	Down	-4.31E-01	9.03E-06		4.55E-01	1.21E-07		-9.68E-01	2.98E-24		-8.87E-01	1.09E-21		Unigene4201_All//gi|297811697|ref|XP_002873732.1|//0.00E+00//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319569|gb|EFH49991.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4201_All//0.00E+00//AT5G15550| transducin family protein / WD-40 repeat family protein	Unigene4201_All//0.00E+00//gi|78334216|gb|DT554490.1|DT554490		ko03040|Spliceosome		nr -
Unigene42010_All	393	0.00	5.16	1.90	0.76	1.93	0.34	0.22	0.00	0.00	1.23E+01	1.54E-11	Up	1.09E+01	3.27E-04	Up	1.34E+00	1.23E-01		-1.14E+00	4.57E-01		-7.75E+00	4.03E-01		-7.75E+00	3.58E-01		Unigene42010_All//gi|2578033|emb|CAA65744.1|//2.00E-73//omega-6 desaturase [Gossypium hirsutum]	Unigene42010_All//3.00E-60//AT3G12120| FAD2 (FATTY ACID DESATURASE 2); delta12-fatty acid dehydrogenase/ omega-6 fatty acid desaturase	Unigene42010_All//0.00E+00//TC178159		ko01040|Biosynthesis of unsaturated fatty acids	GO:0016705//GO:0044238	nr -
Unigene42012_All	409	0.38	1.98	0.65	0.12	0.67	0.88	1.76	6.34	5.65	2.37E+00	1.01E-02		7.62E-01	6.44E-01		2.47E+00	2.23E-01		2.86E+00	9.45E-02		1.85E+00	1.60E-06	Up	1.68E+00	1.93E-05	Up			Unigene42012_All//3.00E-30//TC135919				
Unigene42013_All	769	0.14	109.25	75.55	0.00	0.27	0.35	0.77	0.05	0.31	9.65E+00	0.00E+00	Up	9.12E+00	0.00E+00	Up	8.07E+00	1.57E-01		8.46E+00	7.02E-02		-3.82E+00	1.78E-03		-1.31E+00	1.15E-01		Unigene42013_All//sp|Q8IVG9|HUNTN_HUMAN//1.00E-05//Huntanin OS=Homo sapiens GN=HN PE=1 SV=1						swissprot -
Unigene42015_All	450	1.05	0.45	0.71	6.97	2.60	2.01	1.88	1.76	1.77	-1.22E+00	2.72E-01		-5.60E-01	6.28E-01		-1.42E+00	2.21E-05	Down	-1.80E+00	1.49E-06	Down	-9.06E-02	9.00E-01		-8.58E-02	9.02E-01		Unigene42015_All//gi|15236300|ref|NP_193087.1|//5.00E-57//AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter [Arabidopsis thaliana] >gi|1703292|sp|P54144.1|AMT11_ARATH RecName: Full=Ammonium transporter 1 member 1; Short=AtAMT1;1 >gi|551219|emb|CAA53473.1| amt1 [Arabidopsis thaliana] >gi|4678377|emb|CAB41109.1| ammonium transport protein (AMT1) [Arabidopsis thaliana] >gi|7268054|emb|CAB78393.1| ammonium transport protein (AMT1) [Arabidopsis thaliana]	Unigene42015_All//9.00E-48//AT4G13510| AMT1;1 (AMMONIUM TRANSPORTER 1;1); ammonium transmembrane transporter	Unigene42015_All//4.00E-94//gi|78336379|gb|DT556653.1|DT556653			GO:0015101//GO:0015695//GO:0031224//GO:0043231//GO:0043623	nr +

Unigene42016_All	321	4.07	1.58	0.33	1.71	3.00	1.27	0.66	0.26	0.50	-1.37E+00	2.40E-02		-3.62E+00	2.81E-05	Down	8.15E-01	2.80E-01		-4.31E-01	6.67E-01		-1.34E+00	4.29E-01		-4.08E-01	7.55E-01		Unigene42016_All//gi|15233144|ref|NP_191714.1|//2.00E-09//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|6856521|sp|Q9M313.1|ATL3K_ARATH RecName: Full=RING-H2 finger protein ATL3K >gi|16226239|gb|AAL16112.1|AF428280_1 AT3g61550/F2A19_150 [Arabidopsis thaliana] >gi|21436049|gb|AAM51602.1|AT3g61550/F2A19_150 [Arabidopsis thaliana]	Unigene42016_All//3.00E-09//AT3G61550| zinc finger (C3HC4-type RING finger) family protein	Unigene42016_All//9.00E-82//TC159779			GO:0046914	nr -
Unigene42017_All	1090	0.00	8.14	5.52	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	9.33E-51	Up	1.24E+01	1.52E-33	Up	null	null		null	null		null	null		null	null		Unigene42017_All//gi|145340945|ref|XP_001415577.1|//2.00E-32//Putative mitochondrial ribosomal protein L2 [Ostreococcus lucimarinus CCE9901] >gi|144575800|gb|ABO93869.1|Putative mitochondrial ribosomal protein L2 [Ostreococcus lucimarinus CCE9901]	Unigene42017_All//1.00E-26//ATCG01310| encodes a chloroplast ribosomal protein L2, a constituent of the large subunit of the ribosomal complex			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0033279	nr +
Unigene42018_All	425	24.25	15.14	10.78	77.94	56.31	67.90	210.11	173.97	55.31	-6.80E-01	1.30E-04		-1.17E+00	8.79E-10	Down	-4.69E-01	4.00E-08		-1.99E-01	4.46E-02		-2.72E-01	2.74E-08		-1.93E+00	4.46E-218	Down	Unigene42018_All//gi|211906506|gb|ACJ11746.1|//2.00E-74//luminal binding protein [Gossypium hirsutum]	Unigene42018_All//2.00E-73//AT5G42020| BIP2; ATP binding	Unigene42018_All//0.00E+00//TC134332		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0008152//GO:0016528//GO:0032559//GO:0044432//GO:0050896	nr +
Unigene42019_All	518	1.21	0.29	1.03	1.73	2.73	3.05	1.80	0.81	0.15	-2.05E+00	4.46E-02		-2.38E-01	7.75E-01		6.55E-01	2.74E-01		8.18E-01	1.31E-01		-1.15E+00	7.87E-02		-3.55E+00	3.97E-05	Down							
Unigene42020_All	820	0.57	0.12	0.00	0.85	0.88	1.32	3.30	1.99	1.07	-2.22E+00	7.76E-02		-9.17E+00	8.64E-03		5.23E-02	9.65E-01		6.36E-01	3.73E-01		-7.31E-01	3.27E-02		-1.63E+00	4.80E-06	Down							
Unigene42021_All	382	3.97	1.72	0.70	1.17	2.88	1.30	1.55	2.63	4.17	-1.20E+00	2.75E-02		-2.51E+00	1.79E-04	Down	1.30E+00	5.46E-02		1.48E-01	9.06E-01		7.61E-01	2.28E-01		1.43E+00	2.42E-03			Unigene42021_All//3.00E-14//TC130256					
Unigene42022_All	447	0.00	0.00	0.00	0.00	0.15	0.00	10.40	6.92	3.92	null	null		null	null		7.27E+00	6.09E-01		null	null		-5.89E-01	1.88E-02		-1.41E+00	4.47E-08	Down	Unigene42022_All//gi|28300299|gb|AAO37645.1|//9.00E-24//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene42022_All//7.00E-05//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene42022_All//2.00E-68//gi|164297689|gb|EX168250.1|EX168250			GO:0016787	nr -
Unigene42024_All	459	0.00	0.00	0.00	6.62	12.98	9.64	1.75	0.18	0.35	null	null		null	null		9.71E-01	2.94E-05		5.43E-01	6.67E-02		-3.26E+00	4.48E-04	Down	-2.33E+00	2.82E-03		Unigene42024_All//gi|88900424|gb|AB057524.1|//3.00E-28//At3g48550 [Arabidopsis thaliana]	Unigene42024_All//8.00E-25//AT3G48550| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: nucleic acid binding / transcription factor/ zinc ion binding (TAIR:AT3G01940.3); Has 40 Blast hits to 40 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene42024_All//0.00E+00//gi|109873257|gb|DW502232.1|DW502232				nr -
Unigene42026_All	412	2.16	2.46	0.00	5.08	3.76	0.99	0.92	0.30	0.00	1.88E-01	7.64E-01		-1.11E+01	6.30E-05	Down	-4.33E-01	3.37E-01		-2.36E+00	3.15E-06	Down	-1.60E+00	1.81E-01		-9.85E+00	4.19E-03			Unigene42026_All//3.00E-08//EX171320					
Unigene42027_All	954	0.00	0.00	0.00	0.00	0.14	0.00	4.74	3.15	0.54	null	null		null	null		7.17E+00	3.18E-01		null	null		-5.88E-01	2.09E-02		-3.13E+00	4.04E-20	Down	Unigene42027_All//gi|154163107|gb|ABS70459.1|//1.00E-121//alpha-1,2-fucosyltransferase [Populus tremula x Populus alba]	Unigene42027_All//7.00E-107//AT2G03210| FUT2 (FUCOSYLTRANSFERASE 2); fucosyltransferase/ transferase, transferring glycosyl groups	Unigene42027_All//3.00E-22//gi|164332556|gb|ES40611.1|ES40611			GO:0016757	nr +
Unigene42030_All	921	0.00	6.88	3.70	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	3.61E-36	Up	1.19E+01	7.38E-19	Up	null	null		null	null		null	null		null	null		Unigene42030_All//gi|226528551|ref|NP_001148555.1|//9.00E-23//50S ribosomal protein L6 [Zea mays] >gi|195620388|gb|ACG32024.1| 50S ribosomal protein L6 [Zea mays]	Unigene42030_All//8.00E-22//AT1G05190| emb2394 (embryo defective 2394); structural constituent of ribosome			ko03010|Ribosome	GO:0030529//GO:0043231	nr -
Unigene42033_All	778	0.00	6.45	4.65	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.34E-28	Up	1.22E+01	4.74E-20	Up	null	null		null	null		null	null		null	null		Unigene42033_All//gi|194477045|ref|YP_002049224.1|//1.00E-31//30S ribosomal protein S8 [Paulinella chromatophora] >gi|171192052|gb|ACB43014.1| 30S ribosomal protein S8 [Paulinella chromatophora]	Unigene42033_All//7.00E-23//ATCG00770| chloroplast 30S ribosomal protein S8			ko03010|Ribosome	GO:0003723//GO:0009536//GO:0030529	nr -
Unigene42036_All	575	7.46	4.93	3.61	4.94	1.14	0.94	0.00	0.00	0.00	-5.97E-01	4.20E-02		-1.05E+00	6.99E-04	Down	-2.12E+00	3.10E-08	Down	-2.39E+00	2.40E-08	Down	null	null		null	null			Unigene42036_All//1.00E-08//TC176074					
Unigene42037_All	215	4.62	1.89	2.23	1.16	0.16	0.42	11.01	4.86	2.59	-1.29E+00	6.74E-02		-1.05E+00	1.48E-01		-2.85E+00	1.37E-01		-1.46E+00	4.07E-01		-1.18E+00	1.66E-03		-2.09E+00	3.31E-07	Down		Unigene42037_All//4.00E-09//TC157946					
Unigene42038_All	498	0.95	0.00	0.00	0.90	0.69	0.54	2.72	3.44	10.32	-9.89E+00	5.55E-03		-9.89E+00	8.64E-03		-3.81E-01	7.22E-01		-7.27E-01	5.32E-01		3.41E-01	4.76E-01		1.93E+00	3.79E-13	Up	Unigene42038_All//gi|296088661|emb|CBI37652.3|//1.00E-07//unnamed protein product [Vitis vinifera]	Unigene42038_All//3.00E-06//AT3G51460| RHD4 (ROOT HAIR DEFECTIVE4); phosphatidylinositol-4,5-bisphosphate 5-phosphatase/ phosphatidylinositol-4-phosphate phosphatase	Unigene42038_All//1.00E-17//TC156264				nr -
Unigene42039_All	372	10.13	4.63	12.31	9.78	3.80	3.40	1.48	0.45	0.00	-1.13E+00	4.44E-04	Down	2.82E-01	3.75E-01		-1.36E+00	8.38E-06	Down	-1.52E+00	4.55E-06	Down	-1.72E+00	7.23E-02		-1.05E+01	2.80E-04	Down	Unigene42039_All//gi|42569541|ref|NP_180759.2|//2.00E-07//exostosin family protein [Arabidopsis thaliana] >gi|53828531|gb|AAU94375.1|At2g31990 [Arabidopsis thaliana] >gi|59958346|gb|AAX12883.1|At2g31990 [Arabidopsis thaliana]	Unigene42039_All//2.00E-08//AT2G31990| exostosin family protein				GO:0016740//GO:0030312	nr +
Unigene4204_All	1818	7.08	12.35	10.19	2.22	2.01	3.48	9.33	15.75	52.29	8.02E-01	8.75E-12		5.26E-01	7.36E-05		-1.45E-01	6.67E-01		6.48E-01	5.55E-03		7.56E-01	2.22E-16		2.49E+00	0.00E+00	Up	Unigene4204_All//gi|15241250|ref|NP_197505.1|//1.00E-157//protein kinase family protein [Arabidopsis thaliana] >gi|75332090|sp|Q94C25.1|Y5005_ARATH RecName: Full=Probable receptor-like protein kinase At5g20050; Flags: Precursor >gi|14335072|gb|AAK59800.1|AT5g20050/F28I16_200 [Arabidopsis thaliana] >gi|27363358|gb|AAO11598.1|At5g20050/F28I16_200 [Arabidopsis thaliana]	Unigene4204_All//1.00E-155//AT5G20050| protein kinase family protein	Unigene4204_All//0.00E+00//TC176962		ko04626|Plant-pathogen interaction		nr -
Unigene42041_All	1043	0.00	0.10	0.00	0.67	0.79	1.00	1.54	0.36	0.92	6.60E+00	3.86E-01		null	null		2.45E-01	8.03E-01		5.75E-01	4.27E-01		-2.09E+00	5.87E-05	Down	-7.49E-01	9.35E-02								ESTscan +
Unigene42042_All	281	299.03	266.33	465.61	124.80	89.83	68.63	284.38	260.89	99.38	-1.67E-01	4.44E-03		6.39E-01	1.56E-42		-4.74E-01	9.67E-09		-8.63E-01	8.53E-22		-1.24E-01	2.65E-02		-1.52E+00	2.11E-139	Down	Unigene42042_All//gi|224142137|ref|XP_002324415.1|//1.00E-14//predicted protein [Populus trichocarpa] >gi|222868849|gb|EEF02980.1|predicted protein [Populus trichocarpa]		Unigene42042_All//4.00E-102//gi|109889663|gb|DW518631.1|DW518631				nr +
Unigene42045_All	869	0.24	0.00	0.12	1.61	1.86	0.68	3.55	0.77	0.32	-7.91E+00	1.22E-01		-9.74E-01	6.20E-01		2.15E-01	7.32E-01		-1.25E+00	3.03E-02		-2.21E+00	2.08E-09	Down	-3.47E+00	3.01E-15	Down	Unigene42045_All//gi|8493588|gb|AAF75811.1|AC011000_14/8.00E-56//F16P17.15 [Arabidopsis thaliana]	Unigene42045_All//1.00E-53//AT4G22900| unknown protein	Unigene42045_All//2.00E-165//DW508916			GO:0044464	nr +
Unigene4205_All	1888	2.13	1.13	1.07	7.78	5.60	4.52	23.69	3.43	8.93	-9.21E-01	2.52E-03		-9.93E-01	1.86E-03		-4.75E-01	4.97E-04		-7.84E-01	3.84E-08		-2.79E+00	2.75E-166	Down	-1.41E+00	3.15E-70	Down	Unigene4205_All//gi|281332253|gb|ADA60228.1|//0.00E+00//delta-8 sphingolipid desaturase [Ribes nigrum]	Unigene4205_All//1.00E-179//AT2G46210| delta-8 sphingolipid desaturase, putative	Unigene4205_All//0.00E+00//TC152412		ko00910|Nitrogen metabolism		nr -
Unigene42050_All	826	19.19	4.42	4.58	0.12	0.00	0.00	0.00	0.00	0.00	-2.12E+00	2.31E-35	Down	-2.07E+00	6.16E-33	Down	-6.91E+00	3.12E-01		-6.91E+00	3.99E-01		null	null		null	null								
Unigene42051_All	439	3.22	0.23	0.49	1.36	2.43	2.98	0.00	0.10	0.00	-3.80E+00	3.23E-06	Down	-2.73E+00	1.56E-04	Down	8.37E-01	2.29E-01		1.13E+00	6.33E-02		6.57E+00	6.34E-01		null	null			Unigene42051_All//2.00E-132//ES825629					
Unigene42052_All	810	0.00	0.00	0.00	0.18	0.26	0.11	9.81	1.96	6.64	null	null		null	null		4.67E-01	8.25E-01		-7.27E-01	7.15E-01		-2.32E+00	1.47E-24	Down	-5.64E-01	1.55E-03		Unigene42052_All//gi|224126717|ref|XP_002319909.1|//1.00E-46//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|148572108|gb|ABQ62985.1| RAP2-like protein [Populus trichocarpa] >gi|222858285|gb|EEE95832.1|AP2/EBP domain-containing transcription factor [Populus trichocarpa]	Unigene42052_All//1.00E-29//AT2G20880| AP2 domain-containing transcription factor, putative	Unigene42052_All//3.00E-28//CO106720	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0009743//GO:0010468//GO:0043234	nr -
Unigene42055_All	352	0.15	0.00	0.00	4.53	3.91	2.57	39.04	32.30	10.98	-7.22E+00	6.11E-01		-7.22E+00	6.23E-01		-2.11E-01	7.04E-01		-8.20E-01	1.25E-01		-2.74E-01	5.39E-02		-1.83E+00	5.30E-32	Down	Unigene42055_All//gi|224111880|ref|XP_002316010.1|//7.00E-41//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1|cytochrome P450 [Populus trichocarpa]	Unigene42055_All//2.00E-31//AT3G14630| CYP72A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene42055_All//2.00E-123//gi|164260471|gb|ES824888.1|ES824888		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0008152//GO:0016491	nr +
Unigene42057_All	430	7.67	37.24	9.41	0.00	0.32	0.42	0.39	0.10	0.00	2.28E+00	9.10E-39	Up	2.96E-01	3.82E-01		8.32E+00	3.18E-01		8.71E+00	1.94E-01		-2.02E+00	3.67E-01		-8.62E+00	1.08E-01			Unigene42057_All//0.00E+00//DW506888					
Unigene42058_All	331	1.58	2.30	1.29	0.30	0.52	3.96	0.51	0.13	0.24	5.39E-01	5.02E-01		-2.97E-01	7.50E-01		7.89E-01	7.70E-01		3.72E+00	7.95E-06	Up	-2.02E+00	3.67E-01		-1.09E+00	5.52E-01		Unigene42058_All//gi|297838855|ref|XP_002887309.1|//2.00E-35//alliinase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333150|gb|EFH63568.1|alliinase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene42058_All//9.00E-37//AT1G70560| TAA1 (TRYPTOPHAN AMINOTRANSFERASE OF ARABIDOPSIS 1); L-alanine:2-oxoglutarate aminotransferase/ L-glutamine:2-oxoglutarate aminotransferase/ L-leucine:2-oxoglutarate aminotransferase/ L-methionine:2-oxoglutarate aminotransferase/ L-phenylalanine:2-oxoglut	Unigene42058_All//9.00E-147//gi|78344302|gb|DT564576.1|DT564576			GO:0009630//GO:0009639//GO:0009683//GO:0009725//GO:0009793//GO:0009888//GO:0010015//GO:0010051//GO:0010326//GO:0016846//GO:0044424//GO:0047635//GO:0048037//GO:0048438//GO:0048827//GO:0070529//GO:0070546//GO:0070547	nr +
Unigene42059_All	1089	0.00	0.00	0.00	0.00	0.00	0.00	6.79	1.73	0.95	null	null		null	null		null	null		null	null		-1.98E+00	8.16E-19	Down	-2.84E+00	1.72E-29	Down							
Unigene4206_All	1638	2.46	1.67	1.95	12.26	10.53	14.20	9.29	0.33	3.45	-5.58E-01	6.67E-02		-3.35E-01	3.15E-01		-2.19E-01	8.56E-02		2.12E-01	8.18E-02		-4.81E+00	1.03E-88	Down	-1.43E+00	5.69E-25	Down	Unigene4206_All//gi|31432130|gb|AAP53800.1|//1.00E-63//IQ calmodulin-binding motif family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene4206_All//4.00E-54//AT4G14750| IQD19 (IQ-domain 19); calmodulin binding	Unigene4206_All//0.00E+00//TC157778				nr -
Unigene42062_All	578	0.09	0.96	1.11	0.26	0.66	0.08	3.15	13.74	16.96	3.41E+00	1.24E-02		3.61E+00	6.97E-03		1.34E+00	3.40E-01		-1.73E+00	5.01E-01		2.13E+00	5.12E-22	Up	2.43E+00	2.67E-32	Up		Unigene42062_All//8.00E-167//gi|109880389|gb|DW509359.1|DW509359					
Unigene42063_All	498	0.00	1.22	0.43	0.40	0.00	0.09	1.87	22.32	5.52	1.03E+01	1.17E-03		8.74E+00	1.41E-01		-8.64E+00	8.42E-02		-2.14E+00	3.47E-01		3.58E+00	1.13E-52	Up	1.56E+00	9.05E-06	Up	Unigene42063_All//gi|224132862|ref|XP_002321428.1|//5.00E-25//predicted protein [Populus trichocarpa] >gi|222868424|gb|EEF05555.1|predicted protein [Populus trichocarpa]	Unigene42063_All//1.00E-05//AT2G36080| DNA-binding protein, putative	Unigene42063_All//6.00E-10//DT463967	ABI3VP1			nr -
Unigene42065_All	230	2.27	1.10	1.85	4.76	3.29	0.79	0.37	2.00	1.91	-1.05E+00	3.11E-01		-2.97E-01	7.50E-01		-5.33E-01	4.20E-01		-2.60E+00	7.13E-04	Down	2.44E+00	3.74E-02		2.37E+00	4.04E-02			Unigene42065_All//3.00E-53//gi|73943931|gb|DT527239.1|DT527239					

Unigene42067_All	1383	0.49	0.22	0.23	0.76	0.62	0.88	0.70	0.73	6.34	-1.16E+00	1.89E-01		-1.09E+00	2.39E-01		-2.81E-01	6.74E-01		2.21E-01	7.22E-01		4.48E-02	9.67E-01		3.17E+00	3.77E-38	Up	Unigene42067_All//gi|124360485|gb|ABN08495.1|//3.00E-93//Disease resistance protein [Medicago truncatula]	Unigene42067_All//5.00E-43//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene42067_All//0.00E+00//TC161728		ko04626|Plant-pathogen interaction	GO:0005488	nr -
Unigene4207_All	1437	0.33	0.00	0.00	1.11	1.34	0.91	1.35	0.06	0.36	-8.36E+00	5.55E-03		-8.36E+00	8.63E-03		2.75E-01	6.06E-01		-2.84E-01	6.38E-01		-4.54E+00	2.49E-11	Down	-1.91E+00	1.70E-05	Down	Unigene4207_All//gi|30682982|ref|NP_193211.2|//2.00E-84//IQD19 (IQ-domain 19); calmodulin binding [Arabidopsis thaliana]	Unigene4207_All//5.00E-63//AT4G14750| IQD19 (IQ-domain 19); calmodulin binding	Unigene4207_All//0.00E+00//gi|164348801|gb|ES791524.1|ES791524				nr +
Unigene42072_All	929	4.90	6.33	6.76	7.08	4.74	2.67	1.55	1.48	2.40	3.69E-01	1.40E-01		4.65E-01	6.20E-02		-5.77E-01	7.93E-03		-1.40E+00	2.48E-09	Down	-5.97E-02	9.19E-01		6.34E-01	8.81E-02		Unigene42072_All//gi|209970603|gb|ACJ03064.1|//3.00E-53//AM19-5p [Malus floribunda]	Unigene42072_All//4.00E-28//AT2G34930| disease resistance family protein	Unigene42072_All//0.00E+00//TC136096		ko04626|Plant-pathogen interaction		nr +
Unigene42075_All	392	0.40	0.00	0.00	0.13	0.35	0.23	9.17	29.96	16.06	-8.65E+00	2.15E-01		-8.65E+00	2.44E-01		1.47E+00	6.18E-01		8.58E-01	7.94E-01		1.71E+00	3.30E-24	Up	8.09E-01	8.13E-05				Unigene42075_All//7.00E-120//TC175130				
Unigene4208_All	1765	1.16	5.00	1.84	0.82	1.05	4.27	1.72	7.20	6.23	2.11E+00	1.03E-19	Up	6.71E-01	6.27E-02		3.64E-01	5.05E-01		2.38E+00	9.15E-21	Up	2.06E+00	1.85E-33	Up	1.85E+00	6.97E-26	Up	Unigene4208_All//gi|283800078|sp|Q9AR73.1|HGT_RAUSE/1.00E-118//RecName: Full=Hydroquinone glucosyltransferase; AltName: Full=Arbutin synthase >gi|135088844|emb|CAC35167.1| arbutin synthase [Rauvolfia serpentina]	Unigene4208_All//4.00E-103//AT4G01070| GT72B1; UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups					nr -
Unigene42083_All	579	0.81	0.53	0.55	2.75	1.78	1.09	1.24	0.00	0.69	-6.31E-01	5.54E-01		-5.60E-01	6.28E-01		-6.26E-01	2.24E-01		-1.33E+00	1.23E-02		-1.03E+01	3.26E-05	Down	-8.51E-01	2.39E-01		Unigene42083_All//gi|66261841|gb|AAF19528.1|AF215731_1//1.00E-42//Ran GTPase activating protein [Medicago sativa subsp. x varia]	Unigene42083_All//9.00E-34//AT3G63130| RANGAP1 (RAN GTPASE ACTIVATING PROTEIN 1); RAN GTPase activator/ protein binding	Unigene42083_All//3.00E-09//TC174264			GO:0005488//GO:0006605//GO:0007017//GO:0009536//GO:0012505//GO:0016020//GO:0051301	nr +
Unigene42084_All	1393	0.00	0.22	0.11	0.14	0.30	0.32	1.03	10.41	1.14	7.77E+00	4.43E-02		6.84E+00	2.39E-01		1.05E+00	4.26E-01		1.18E+00	3.38E-01		3.33E+00	1.78E-64	Up	1.49E-01	7.46E-01		Unigene42084_All//gi|124359343|gb|ABQ28505.2|//2.00E-09//RNA-directed DNA polymerase (Reverse transcriptase): Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]		Unigene42084_All//1.00E-13//FL576997				nr -
Unigene42086_All	442	0.24	0.00	0.48	3.72	3.19	2.35	22.19	39.34	49.12	-7.89E+00	3.71E-01		1.03E+00	5.91E-01		-2.20E-01	6.81E-01		-6.62E-01	2.13E-01		8.26E-01	7.91E-12		1.15E+00	4.37E-25	Up			Unigene42086_All//1.00E-90//DW477688				
Unigene42088_All	1505	0.00	181.70	74.44	0.00	0.09	0.00	0.00	0.00	0.00	1.75E+01	0.00E+00	Up	1.62E+01	0.00E+00	Up	6.52E+00	3.18E-01		null	null		null	null		null	null		Unigene42088_All//gi|171259158|ref|YP_539000.2|//0.00E+00//cytochrome c oxidase subunit I [Physcomitrella patens] >gi|186942713|dbj|BAE93071.2| cytochrome c oxidase subunit I [Physcomitrella patens]	Unigene42088_All//3.00E-138//ATMG01360| cytochrome c oxidase subunit I	Unigene42088_All//2.00E-92//gi|82756657|gb|DV850219.1|DV850219		ko00190|Oxidative phosphorylation	GO:0005506//GO:0015002//GO:0019866//GO:0031224//GO:0043231//GO:0045433//GO:0051234	nr +
Unigene42089_All	307	2.39	1.49	0.35	0.32	0.00	0.88	57.15	68.75	243.05	-6.84E-01	3.86E-01		-2.78E+00	1.04E-02		-8.34E+00	3.12E-01		1.44E+00	4.09E-01		2.67E-01	1.59E-02		2.09E+00	3.09E-200	Up			Unigene42089_All//1.00E-114//TC145240				
Unigene4209_All	222	10.37	1.37	0.48	2.02	2.17	2.44	5.90	12.61	27.82	-2.92E+00	6.54E-08	Down	-4.43E+00	3.18E-10	Down	1.05E-01	9.54E-01		2.74E-01	7.83E-01		1.10E+00	1.22E-03		2.24E+00	9.44E-19	Up	Unigene4209_All//gi|297806103|ref|XP_002870935.1|//1.00E-24//alpha 1,4-glycosyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316772|gb|EFH47194.1| alpha 1,4-glycosyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4209_All//4.00E-25//AT5G01250| alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein	Unigene4209_All//9.00E-109//DW498978				nr -
Unigene42091_All	345	0.00	0.00	0.00	0.43	1.40	0.65	1.72	0.00	1.73	null	null		null	null		1.69E+00	1.66E-01		5.95E-01	7.21E-01		-1.07E+01	2.39E-04	Down	1.37E-02	9.87E-01		Unigene42091_All//gi|296086263|emb|CBI31704.3|//8.00E-40//unnamed protein product [Vitis vinifera]	Unigene42091_All//4.00E-18//AT3G12590| unknown protein	Unigene42091_All//7.00E-52//TC162276			GO:0043231	nr +
Unigene42092_All	1005	0.00	11.50	2.76	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	2.99E-66	Up	1.14E+01	2.75E-15	Up	null	null		null	null		null	null		null	null		Unigene42092_All//sp|P27779|CUP7_DROME//3.00E-15//Pupal cuticle protein Edg-78E OS=Drosophila melanogaster GN=Edg78E PE=1 SV=1						swissprot -
Unigene42093_All	851	408.36	282.88	484.26	92.66	115.65	90.11	3.13	1.57	0.61	-5.30E-01	8.95E-83		2.46E-01	5.41E-23		3.20E-01	2.34E-11		-4.02E-02	6.25E-01		-9.94E-01	4.08E-03		-2.36E+00	3.40E-09	Down	Unigene42093_All//gi|157678962|dbj|BAF80479.1|//3.00E-91//PSI reaction center subunit II [Citrus sinensis]	Unigene42093_All//2.00E-77//AT1G30130| PSAD-2 (photosystem I subunit D-2)	Unigene42093_All//0.00E+00//TC136477		ko00195|Photosynthesis	GO:0005488//GO:0009522//GO:0009526//GO:0009534//GO:0009570//GO:0044237	nr -
Unigene42094_All	1090	0.00	0.00	0.00	0.00	0.00	0.00	15.24	5.75	13.41	null	null		null	null		null	null		null	null		-1.41E+00	8.96E-26	Down	-1.85E-01	1.48E-01		Unigene42094_All//gi|297598701|ref|NP_001046103.2|//3.00E-90//Os02g0183000 (Oryza sativa Japonica Group) >gi|255670656|dbj|BAF08017.2| Os02g0183000 (Oryza sativa Japonica Group)	Unigene42094_All//5.00E-84//AT2G12646| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF597 (InterPro:IPR006734); BEST Arabidopsis thaliana protein match is: zinc-binding protein, putative (TAIR:AT3G60670.1); Has 191 Blast hits to 191 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 191; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene42094_All//2.00E-18//gi|3325907|gb|AI054793.1|AI054793	PLATZ			nr +
Unigene42095_All	409	0.64	0.00	0.26	1.34	0.00	0.66	1.14	1.53	0.29	-9.32E+00	6.70E-02		-1.30E+00	4.36E-01		-1.04E+01	4.01E-04	Down	-1.02E+00	3.29E-01		4.31E-01	6.32E-01		-1.96E+00	5.82E-02		Unigene42095_All//gi|9502386|gb|AAF88093.1|AC025417_21//2.00E-21//T12C24.22 [Arabidopsis thaliana]	Unigene42095_All//1.00E-22//AT1G12700| helicase domain-containing protein / pentatricopeptide (PPR) repeat-containing protein	Unigene42095_All//1.00E-140//TC144858				nr -
Unigene4210_All	1723	9.81	1.59	3.25	2.52	1.66	3.20	6.16	15.11	40.46	-2.63E+00	1.58E-48	Down	-1.60E+00	9.89E-25	Down	-6.01E-01	3.15E-02		3.46E-01	2.08E-01		1.29E+00	3.07E-35	Up	2.72E+00	1.88E-255	Up	Unigene4210_All//gi|15240929|ref|NP_195745.1|//1.00E-110//alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein [Arabidopsis thaliana] >gi|51315396|gb|AAT99803.1| At5g01250 [Arabidopsis thaliana]	Unigene4210_All//4.00E-111//AT5G01250| alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein	Unigene4210_All//0.00E+00//TC163862				nr +
Unigene42100_All	362	17.92	4.62	9.71	0.41	0.95	0.25	0.00	0.00	0.00	-1.96E+00	1.81E-13	Down	-8.84E-01	2.51E-04		1.20E+00	4.26E-01		-7.26E-01	7.15E-01		null	null		null	null		Unigene42100_All//gi|15227472|ref|NP_181725.1|//2.00E-23//ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|4517524|gb|AAK62652.1| At2g19940/T6D20.16 [Arabidopsis thaliana] >gi|15810111|gb|AAL06981.1| At2g19940/T6D20.16 [Arabidopsis thaliana]	Unigene42100_All//8.00E-20//AT3G58070| GIS (GLABROUS INFLORESCENCE STEMS); nucleic acid binding / transcription factor/ zinc ion binding	Unigene42100_All//0.00E+00//ES825295	C2H2		GO:0000904//GO:0009725//GO:0010468//GO:0035315//GO:0044464//GO:0046914	nr -
Unigene42103_All	1060	1.28	0.76	0.95	6.20	3.12	1.66	0.24	0.00	0.15	-7.47E-01	1.93E-01		-4.27E-01	4.72E-01		-9.92E-01	3.16E-06		-1.90E+00	4.40E-14	Down	-7.90E+00	4.04E-02		-6.71E-01	6.05E-01		Unigene42103_All//gi|195621986|gb|ACG32823.1|//3.00E-88//BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor [Zea mays]	Unigene42103_All//2.00E-81//AT3G26700| protein kinase family protein	Unigene42103_All//0.00E+00//TC155116		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0031410	nr +
Unigene42106_All	592	0.71	0.34	0.36	1.18	0.00	0.53	1.21	1.91	0.81	-1.05E+00	3.66E-01		-9.75E-01	4.11E-01		-1.02E+01	3.44E-05	Down	-1.14E+00	2.01E-01		6.51E-01	2.66E-01		-5.88E-01	4.09E-01		Unigene42106_All//gi|24461866|gb|AAN62353.1|AF506028_20//4.00E-24//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene42106_All//2.00E-12//AT4G10780| disease resistance protein (CC-NBS-LRR class), putative			ko04626|Plant-pathogen interaction		nr +
Unigene42107_All	483	0.22	0.10	0.33	1.24	0.21	0.00	1.05	1.90	1.65	-1.05E+00	6.84E-01		6.11E-01	7.48E-01		-2.53E+00	1.36E-02		-1.03E+01	7.70E-04	Down	8.58E-01	1.95E-01		6.51E-01	3.53E-01		Unigene42107_All//gi|224122872|ref|XP_002318937.1|//9.00E-45//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222857313|gb|EEE94860.1| chromatin remodeling complex subunit [Populus trichocarpa]					GO:0003676//GO:0043231//GO:0046872	nr -
Unigene42108_All	530	0.39	2.77	0.00	0.28	0.58	0.94	0.32	1.18	3.91	2.81E+00	4.58E-05	Up	-8.63E+00	1.45E-01		1.05E+00	5.31E-01		1.73E+00	1.45E-01		1.89E+00	3.49E-02		3.61E+00	1.45E-10	Up			Unigene42108_All//7.00E-16//TC177927				
Unigene4211_All	1439	31.89	76.76	44.15	16.06	17.90	24.04	11.52	25.04	37.51	1.27E+00	4.98E-116	Up	4.69E-01	3.00E-12		1.56E-01	1.89E-01		5.82E-01	5.42E-11		1.12E+00	1.07E-38	Up	1.70E+00	2.18E-110	Up	Unigene4211_All//gi|14326541|gb|AAK60315.1|AF385724_1//1.00E-86//At1g13990/F16A14.28 [Arabidopsis thaliana] >gi|22137314|gb|AAM91502.1| AT4g27310/M4I22_120 [Arabidopsis thaliana]	Unigene4211_All//2.00E-73//AT1G13990| unknown protein	Unigene4211_All//0.00E+00//TC166971				nr -
Unigene42111_All	642	0.24	0.79	0.50	0.00	0.00	0.00	3.56	3.45	11.91	1.69E+00	1.34E-01		1.03E+00	4.71E-01		null	null		null	null		-4.36E-02	9.28E-01		1.74E+00	7.17E-17	Up	Unigene42111_All//gi|224104865|ref|XP_002333890.1|//1.00E-07//predicted protein [Populus trichocarpa] >gi|222838908|gb|EEE77259.1| predicted protein [Populus trichocarpa]		Unigene42111_All//2.00E-146//DN817187				nr -
Unigene42113_All	1539	0.07	0.26	0.00	0.06	0.13	0.41	0.96	3.42	16.36	1.95E+00	1.44E-01		-6.09E+00	3.92E-01		1.05E+00	6.12E-01		2.67E+00	1.83E-02		1.83E+00	2.47E-12	Up	4.09E+00	8.55E-134	Up	Unigene42113_All//gi|18414985|ref|NP_567544.1|//3.00E-78//UBP20 (UBIQUITIN-SPECIFIC PROTEASE 20); ubiquitin thiolesterase/ ubiquitin-specific protease [Arabidopsis thaliana] >gi|75262803|sp|Q9FFS7.1|UBP20_ARATH RecName: Full=Ubiquitin carboxyl-terminal hydrolase 20; AltName: Full=Ubiquitin thioesterase 20; AltName: Full=Ubiquitin-specific-processing protease 20; AltName: Full=Deubiquitinating enzyme 20; Short=AtUBP20 >gi|119934180|gb|AAG42758.1|AF302668_1 ubiquitin-specific protease 20 [Arabidopsis thaliana]	Unigene42113_All//3.00E-80//AT4G17895| UBP20 (UBIQUITIN-SPECIFIC PROTEASE 20); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene42113_All//9.00E-132//CO073397		ko04144|Endocytosis	GO:0008234	nr -
Unigene42116_All	491	2.56	0.21	0.65	2.13	0.84	0.74	1.98	0.00	0.32	-3.63E+00	2.00E-05	Down	-1.97E+00	4.62E-03		-1.34E+00	3.95E-02		-1.53E+00	2.88E-02		-1.10E+01	5.83E-07	Down	-2.61E+00	3.35E-04	Down			Unigene42116_All//0.00E+00//TC157963				ESTscan -
Unigene42117_All	462	0.00	1.54	2.77	0.11	0.52	0.20	2.29	1.36	0.78	1.06E+01	3.32E-04	Up	1.14E+01	4.68E-07	Up	2.27E+00	3.05E-01		8.59E-01	7.94E-01		-7.54E-01	2.17E-01		-1.56E+00	9.40E-03		Unigene42117_All//gi|15242530|ref|NP_198814.1|//7.00E-62//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75171449|sp|Q9FLD8.1|PP4O8_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g39980, chloroplastic; Flags: Precursor	Unigene42117_All//5.00E-63//AT5G39980| pentatricopeptide (PPR) repeat-containing protein	Unigene42117_All//0.00E+00//DW227921			GO:0009536	nr -

Unigene42118_All	1914	0.08	0.32	0.00	0.05	0.00	0.26	5.81	0.63	3.33	1.95E+00	6.03E-02		-6.36E+00	2.44E-01		-5.70E+00	3.12E-01		2.32E+00	6.88E-02		-3.20E+00	7.21E-48	Down	-8.03E-01	8.52E-08		Unigene42118_All//gi|115469034|ref|NP_001058116.1|//1.00E-124//Os06g0625900 [Oryza sativa Japonica Group] >gi|62900352|sp|Q67VS5.1|HAK10_ORYSJ RecName: Full=Potassium transporter 10; AltName: Full=OsHAK10 >gi|113596156|dbj|BAF20030.1|Os06g0625900 [Oryza sativa Japonica Group]	Unigene42118_All//9.00E-135//AT3G02050| KUP3 (K+ UPTAKE TRANSPORTER 3); potassium ion transmembrane transporter					nr +
Unigene42120_All	688	2.51	0.44	2.01	1.30	1.60	0.92	0.25	0.12	0.46	-2.51E+00	2.66E-05	Down	-3.19E-01	5.53E-01		2.97E-01	6.88E-01		-5.04E-01	5.11E-01		-1.02E+00	6.14E-01		9.14E-01	4.53E-01		Unigene42120_All//gi|147790551|emb|CAN76526.1|//6.00E-09//hypothetical protein [Vitis vinifera]						nr +
Unigene42121_All	609	0.00	17.81	5.16	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	3.71E-62	Up	1.23E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene42121_All//gi|301120388|ref|XP_002907921.1|//1.00E-21//polyadenylate-binding protein 1-B [Phytophthora infestans T30-4] >gi|262102952|gb|EEY61004.1| polyadenylate-binding protein 1-B [Phytophthora infestans T30-4]	Unigene42121_All//8.00E-12//AT1G49760| PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor				GO:0003676	nr +
Unigene42122_All	617	0.25	0.66	0.17	0.89	1.51	1.24	1.51	2.91	6.07	1.37E+00	2.74E-01		-5.60E-01	7.75E-01		7.63E-01	3.20E-01		4.87E-01	5.91E-01		9.50E-01	2.97E-02		2.01E+00	2.59E-10	Up			Unigene42122_All//7.00E-07//TC134528					
Unigene42123_All	582	0.00	0.78	0.00	0.60	0.65	0.78	3.05	2.51	0.41	9.61E+00	7.43E-03		null	null		1.19E-01	9.58E-01		3.73E-01	7.32E-01		-2.80E-01	5.63E-01		-2.89E+00	9.05E-08	Down								
Unigene42124_All	962	0.00	0.00	0.00	0.00	0.00	0.00	5.67	5.65	1.70	null	null		null	null		null	null		null	null		-5.50E-03	1.02E+00		-1.74E+00	2.27E-12	Down	Unigene42124_All//gi|51477387|gb|AU04760.1|//1.00E-36//MRGH12 [Curcumis melo]	Unigene42124_All//7.00E-26//AT5G17880| CSA1 (constitutive shade-avoidance1); ATP binding / transmembrane receptor	Unigene42124_All//3.00E-90//CO115409			GO:0005488	nr -
Unigene42125_All	362	0.87	0.00	0.59	0.96	1.81	1.75	5.14	0.81	1.98	-9.76E+00	3.65E-02		-5.60E-01	6.63E-01		9.08E-01	3.42E-01		8.59E-01	3.90E-01		-2.67E+00	3.21E-07	Down	-1.38E+00	1.21E-03		Unigene42125_All//gi|297727589|ref|NP_001176158.1|//3.00E-35//Os10g0422566 [Oryza sativa Japonica Group] >gi|255679411|dbj|BAH94886.1| Os10g0422566 [Oryza sativa Japonica Group]	Unigene42125_All//4.00E-34//AT1G03100| pentatricopeptide (PPR) repeat-containing protein				GO:0043231	nr -
Unigene42126_All	555	3.96	5.48	9.79	8.35	8.00	6.59	7.39	6.33	3.88	4.68E-01	2.00E-01		1.31E+00	2.21E-06	Up	-6.06E-02	8.32E-01		-3.41E-01	2.60E-01		-2.24E-01	4.47E-01		-9.31E-01	3.67E-04		Unigene42126_All//gi|224128994|ref|XP_002320474.1|//7.00E-06//predicted protein [Populus trichocarpa] >gi|222861247|gb|EEE98789.1| predicted protein [Populus trichocarpa]		Unigene42126_All//4.00E-116//gi|164253415|gb|ES803686.1|ES803686				nr -
Unigene42128_All	588	0.00	0.00	0.54	1.19	1.64	2.84	1.58	0.21	0.34	null	null		9.09E+00	4.51E-02		4.67E-01	5.47E-01		1.26E+00	1.61E-02		-2.89E+00	3.28E-04	Down	-2.22E+00	1.63E-03		Unigene42128_All//gi|32492200|emb|CAE03468.1|//2.00E-46//OSJNBa0083N12.5 [Oryza sativa (japonica cultivar-group)]	Unigene42128_All//1.00E-10//AT1G65780| tRNA-splicing endonuclease positive effector-related				GO:0003676//GO:0003678//GO:0006259//GO:0032559	nr -
Unigene4213_All	1453	11.45	4.32	5.42	19.58	15.74	17.93	22.87	9.52	10.69	-1.40E+00	3.87E-21	Down	-1.08E+00	1.40E-13	Down	-3.15E-01	1.11E-03		-1.26E-01	2.91E-01		-1.26E+00	3.19E-43	Down	-1.10E+00	1.17E-35	Down	Unigene4213_All//gi|18390448|ref|NP_563720.1|//1.00E-155//PRMT10; [myelin basic protein]-arginine N-methyltransferase/ histone-arginine N-methyltransferase/ methyltransferase/ protein-arginine omega-N asymmetric methyltransferase/ protein-arginine omega-N monomethyltransferase [Arabidopsis thaliana] >gi|75336166|sp|Q9MAT5.1|ANM42_ARATH RecName: Full=Probable protein arginine N-methyltransferase 4.2 >gi|7211979|gb|AAF40450.1|AC004809_8 Similar to protein arginine N-methyltransferase from Rattus norvegicus gb|U60882. ESTs gb|Z30908 and gb|Z29205 come from this gene [Arabidopsis thaliana] >gi|22135775|gb|AAM91044.1| At1g04870/F13M7_12 [Arabidopsis thaliana]	Unigene4213_All//4.00E-156//AT1G04870| PRMT10; methyltransferase	Unigene4213_All//0.00E+00//TC133203				nr +
Unigene42130_All	395	0.00	22.96	109.60	0.38	0.87	1.49	0.21	0.32	0.10	1.45E+01	6.32E-52	Up	1.67E+01	5.42E-246	Up	1.20E+00	4.26E-01		1.97E+00	6.99E-02		5.68E-01	7.82E-01		-1.09E+00	6.76E-01		Unigene42130_All//gi|145408591|ref|XP_001152215.1|//9.00E-10//O8F441 [Pinus koraiensis] >gi|145048840|gb|ABP35457.1| O8F441 [Pinus koraiensis]		Unigene42130_All//6.00E-22//TC149074			GO:0009536	nr +
Unigene42132_All	442	6.04	8.48	9.16	6.87	11.61	5.72	2.97	1.51	6.40	4.91E-01	1.26E-01		6.01E-01	5.86E-02		7.56E-01	3.01E-03		-2.65E-01	5.02E-01		-9.71E-01	6.64E-02		1.11E+00	7.34E-04	Up			Unigene42132_All//0.00E+00//TC142336					
Unigene42133_All	454	0.00	0.00	0.00	13.39	9.18	4.68	1.21	0.28	0.09	null	null		null	null		-5.45E-01	1.77E-02		-1.52E+00	1.17E-09	Down	-2.13E+00	3.31E-02		-3.79E+00	2.03E-03		Unigene42133_All//gi|225463464|ref|XP_002272948.1|//2.00E-51//PREDICTED: similar to cytochrome B561-related [Vitis vinifera]	Unigene42133_All//1.00E-47//AT4G18260| cytochrome B561-related	Unigene42133_All//3.00E-24//DW226589			GO:0043231	nr -
Unigene42134_All	486	0.00	0.21	0.00	0.00	0.00	0.00	1.91	5.07	5.16	7.70E+00	3.86E-01		null	null		null	null		null	null		1.41E+00	1.76E-04	Up	1.43E+00	8.46E-05	Up								
Unigene42135_All	692	0.00	0.15	0.15	0.14	0.30	0.65	35.25	18.06	12.61	7.19E+00	3.86E-01		7.27E+00	3.98E-01		1.05E+00	6.12E-01		2.18E+00	1.03E-01		-9.65E-01	6.19E-21		-1.48E+00	9.05E-42	Down			Unigene42135_All//8.00E-07//TC152333					
Unigene42137_All	498	2.00	7.33	2.25	0.40	0.35	2.09	0.34	0.17	0.16	1.88E+00	1.89E-07	Up	1.70E-01	7.78E-01		-2.11E-01	8.59E-01		2.38E+00	2.54E-03		-1.02E+00	6.14E-01		-1.09E+00	5.52E-01		Unigene42137_All//gi|75210732|sp|Q9SV72.1|EPFL9_ARATH//2.00E-25//RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 9; Short=EPF-like protein 9; Flags: Precursor	Unigene42137_All//1.00E-26//AT4G12970| unknown protein	Unigene42137_All//0.00E+00//gi|84164356|gb|DR453004.1|DR453004			GO:0031410	nr -
Unigene42139_All	631	0.00	0.00	0.00	0.00	0.00	0.00	4.82	1.92	2.27	null	null		null	null		null	null		null	null		-1.33E+00	5.51E-05	Down	-1.09E+00	5.17E-04	Down			Unigene42139_All//2.00E-10//TC163460					
Unigene42140_All	787	0.40	0.77	0.41	12.28	5.95	9.64	0.81	1.75	1.06	9.54E-01	3.14E-01		2.55E-02	1.00E+00		-1.05E+00	1.22E-09	Down	-3.49E-01	6.99E-02		1.12E+00	2.98E-02		4.00E-01	5.65E-01		Unigene42140_All//gi|1370152|emb|CAA98182.1|//4.00E-85//RAB11F [Lotus japonicus]	Unigene42140_All//2.00E-85//AT1G18200| AtRAB46b (Arabidopsis Rab GTPase homolog A6b); GTP binding / GTPase/ protein binding	Unigene42140_All//8.00E-103//DW518651			GO:0003824//GO:0006810//GO:0016020//GO:0032561//GO:0035556	nr -
Unigene42143_All	569	0.00	0.00	0.00	0.00	0.00	0.00	2.15	2.35	0.00	null	null		null	null		null	null		null	null		1.25E-01	8.14E-01		-1.11E+01	4.03E-09	Down	Unigene42143_All//gi|2500354|sp|P93847.1|RL10_SOLME//1.00E-50//RecName: Full=60S ribosomal protein L10; AltName: Full=EQM >gi|1902894|dbj|BAA19462.1| QM family protein [Solanum melongena]	Unigene42143_All//1.00E-08//AT4G26910| 60S ribosomal protein L10 (RPL10B)	Unigene42143_All//1.00E-08//ES796971		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene42146_All	807	0.00	0.00	0.00	0.00	0.09	0.00	8.75	7.67	3.75	null	null		null	null		6.41E+00	6.09E-01		null	null		-1.91E-01	4.02E-01		-1.22E+00	1.16E-09	Down	Unigene42146_All//gi|89953428|gb|AB083304.1|//3.00E-56//Fgenesh protein 125 [Beta vulgaris]	Unigene42146_All//1.00E-51//AT3G30210| MYB121 (MYB DOMAIN PROTEIN 121); DNA binding / transcription factor	Unigene42146_All//3.00E-10//TC175799	MYB		GO:0001071//GO:0003676//GO:0006351//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene42151_All	639	0.00	0.00	0.00	0.00	0.00	0.00	13.76	1.31	4.05	null	null		null	null		null	null		null	null		-3.40E+00	4.32E-40	Down	-1.76E+00	8.58E-20	Down	Unigene42151_All//gi|15236902|ref|NP_194418.1|//2.00E-41//stigma-specific Stig1 family protein [Arabidopsis thaliana] >gi|4452211|emb|CAB36534.1| STIG1 like protein [Arabidopsis thaliana] >gi|7269541|emb|CAB79543.1| STIG1 like protein [Arabidopsis thaliana]	Unigene42151_All//4.00E-42//AT4G26880| stigma-specific Stig1 family protein					nr -
Unigene42152_All	832	0.00	0.00	0.00	0.00	0.00	0.00	4.73	7.94	16.38	null	null		null	null		null	null		null	null		7.48E-01	2.43E-04		1.79E+00	1.64E-30	Up	Unigene42152_All//gi|15242624|ref|NP_201114.1|//5.00E-51//LOB (LATERAL ORGAN BOUNDARIES) [Arabidopsis thaliana] >gi|30697777|ref|NP_851252.1| LOB (LATERAL ORGAN BOUNDARIES) [Arabidopsis thaliana] >gi|30697779|ref|NP_851253.1| LOB (LATERAL ORGAN BOUNDARIES) [Arabidopsis thaliana] >gi|30697782|ref|NP_851254.1| LOB (LATERAL ORGAN BOUNDARIES) [Arabidopsis thaliana] >gi|27805499|sp|Q9FLM4.1|LOB_ARATH RecName: Full=Protein LATERAL ORGAN BOUNDARIES; AltName: Full=ASYMMETRIC LEAVES 2-like protein 4; Short=AS2-like protein 4 >gi|17484100|gb|AAL40346.1|AF447897_1 LOB6 [Arabidopsis thaliana] >gi|45330811|dbj|BAD12424.1| ASYMMETRIC LEAVES2-like gene 4 protein [Arabidopsis thaliana] >gi|107738100|gb|ABF83635.1| At5g63090 [Arabidopsis thaliana] >gi|219807084|dbj|BAH10548.1| ASYMMETRIC LEAVES2-like 4 protein [Arabidopsis thaliana]	Unigene42152_All//3.00E-52//AT5G63090| LOB (LATERAL ORGAN BOUNDARIES)	Unigene42152_All//2.00E-48//DW505234		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0043231	nr +
Unigene42154_All	618	0.00	0.00	0.00	0.00	0.00	0.15	3.42	7.71	6.83	null	null		null	null		null	null		7.19E+00	4.76E-01		1.17E+00	3.46E-06	Up	9.98E-01	1.23E-04				Unigene42154_All//1.00E-88//TC142576					
Unigene42155_All	241	5.64	1.05	7.51	3.31	2.29	5.62	0.00	0.00	0.00	-2.42E+00	3.35E-04	Down	4.12E-01	4.05E-01		-5.33E-01	5.10E-01		7.66E-01	2.05E-01		null	null		null	null		Unigene42155_All//gi|224111284|ref|XP_002332949.1|//2.00E-16//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834261|gb|EEE72738.1| cc-nbs-lrr resistance protein [Populus trichocarpa]		Unigene42155_All//1.00E-27//ES820741			GO:0016787	nr -
Unigene42156_All	809	0.00	1.57	0.00	0.86	1.57	0.17	4.70	14.57	16.30	1.06E+01	2.86E-07	Up	null	null		8.69E-01	1.60E-01		-2.36E+00	1.69E-02		1.63E+00	8.55E-23	Up	1.79E+00	1.47E-29	Up			Unigene42156_All//2.00E-69//TC166967					
Unigene42157_All	954	0.00	0.00	0.00	0.00	0.00	0.00	7.45	6.66	0.63	null	null		null	null		null	null		null	null		-1.61E-01	4.76E-01		-3.57E+00	4.28E-35	Down	Unigene42157_All//gi|145408595|ref|XP_001152219.1|//1.00E-06//O8F58F [Pinus koraiensis] >gi|145048844|gb|ABP35460.1| O8F58F [Pinus koraiensis]		Unigene42157_All//8.00E-11//TC172353			GO:0043231//GO:0044444	nr -
Unigene42158_All	262	0.20	1.16	3.25	3.04	0.79	1.72	1.78	0.48	0.30	2.54E+00	1.51E-01		4.03E+00	7.02E-04	Up	-1.95E+00	1.53E-02		-8.20E-01	3.19E-01		-1.89E+00	8.00E-02		-2.55E+00	2.35E-02									
Unigene4216_All	1079	57.85	330.41	83.26	80.61	59.71	68.56	17.83	13.48	8.90	2.51E+00	0.00E+00	Up	5.25E-01	8.25E-21		-4.33E-01	9.37E-18		-2.34E-01	2.00E-05		-4.03E-01	3.38E-04		-1.00E+00	2.89E-18	Down	Unigene4216_All//gi|15234544|ref|NP_193893.1|//2.00E-38//glycine-rich protein [Arabidopsis thaliana] >gi|16648720|gb|AAL25552.1| AT4g21620/F17L22_80 [Arabidopsis thaliana]	Unigene4216_All//4.00E-17//AT4G21620| glycine-rich protein	Unigene4216_All//0.00E+00//TC141452		ko03040|Spliceosome		nr -
Unigene42160_All	420	9.22	4.71	4.56	2.85	1.64	8.71	0.10	0.00	0.00	-9.70E-01	1.93E-03		-1.01E+00	1.94E-03		-7.96E-01	1.87E-01		1.61E+00	1.93E-06	Up	-6.65E+00	6.57E-01		-6.65E+00	6.12E-01		Unigene42160_All//gi|20149046|gb|AM12778.1|//1.00E-22//auxin-induced SAUR-like protein [Capsicum annuum]	Unigene42160_All//4.00E-22//AT4G38840| auxin-responsive protein, putative	Unigene42160_All//2.00E-170//TC167816			GO:0006950//GO:0009725//GO:0016020	nr -

Unigene42161_All	728	0.00	0.00	0.00	0.00	0.00	0.00	11.62	25.78	5.58	null	null		null	null		null	null		null	null		1.15E+00	2.16E-21	Up	-1.06E+00	3.17E-09	Down			Unigene42161_All//1.00E-76//TC166107				
Unigene42164_All	493	3.82	1.13	0.22	4.04	1.26	4.40	0.09	0.51	0.32	-1.76E+00	5.92E-04	Down	-4.14E+00	4.26E-08	Down	-1.68E+00	1.67E-04	Down	1.22E-01	7.88E-01		2.57E+00	1.53E-01		1.91E+00	3.77E-01		Unigene42164_All//gi|122236144|sp|Q0WNP3.1|PP319_ARATH//2.00E-46//RecName: Full=Pentatricopeptide repeat-containing protein At4g18520	Unigene42164_All//1.00E-47//AT4G18520| INVOLVED IN: biological_process unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT4G39530.1); Has 16698 Blast hits to 4567 proteins in 114 species: Archae - 0; Bacteria - 4; Metazoa - 97; Fungi - 32; Plants - 16266; Viruses - 0; Other Eukaryotes - 299 (source: NCBI BLink).				GO:0016787//GO:0043231	nr -
Unigene42166_All	750	0.00	0.00	0.00	0.00	0.00	0.00	1.86	4.24	3.98	null	null		null	null		null	null		null	null		1.19E+00	1.85E-04	Up	1.10E+00	5.58E-04	Up	Unigene42166_All//gi|297846292|ref|XP_002891027.1|//1.00E-90//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336869|gb|EFH67286.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene42166_All//9.00E-82//AT1G33080| MATE efflux family protein	Unigene42166_All//0.00E+00//gi|109854259|gb|DW483238.1|DW483238			GO:0015291//GO:0015893//GO:0044464	nr +
Unigene42169_All	511	1.33	0.99	0.00	1.56	3.44	1.33	1.32	0.82	1.09	-4.25E-01	5.97E-01		-1.04E+01	7.64E-04	Down	1.14E+00	2.14E-02		-2.35E-01	7.53E-01		-6.95E-01	3.94E-01		-2.78E-01	6.89E-01		Unigene42169_All//gi|15223001|ref|NP_172256.1|//8.00E-64//RPS15A (ribosomal protein s15a); structural constituent of ribosome [Arabidopsis thaliana] >gi|15238544|ref|NP_200793.1| 40S ribosomal protein S15A (RPS15aF) [Arabidopsis thaliana] >gi|42571385|ref|NP_973783.1| RPS15A (ribosomal protein s15a); structural constituent of ribosome [Arabidopsis thaliana] >gi|297796939|ref|XP_002866354.1| RPS15A [Arabidopsis lyrata subsp. lyrata] >gi|297815756|ref|XP_002875761.1| RPS15A [Arabidopsis lyrata subsp. lyrata] >gi|297849076|ref|XP_002892419.1| RPS15A [Arabidopsis lyrata subsp. lyrata] >gi|1172218|sp|P42798.2|R15A1_ARATH RecName: Full=40S ribosomal protein S15a-1 >gi|8439890|gb|AAF75076.1|AC007583_12 Strong similarity to 40S ribosomal protein S15A from Arabidopsis thaliana gb|L27461. EST gb|H30315 comes from this gene >gi|14423370|gb|AA662367.1|AF38692	Unigene42169_All//5.00E-65//AT5G59850| 40S ribosomal protein S15A (RPS15aF)	Unigene42169_All//1.00E-131//TC149695		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0043231	nr -
Unigene4217_All	828	2.21	5.57	2.70	2.05	0.87	1.75	1.99	3.18	2.94	1.33E+00	5.99E-06	Up	2.89E-01	5.32E-01		-1.23E+00	1.06E-02		-2.29E-01	6.78E-01		6.75E-01	5.31E-02		5.60E-01	1.15E-01				Unigene4217_All//0.00E+00//DR455591				
Unigene42170_All	412	0.00	0.00	0.00	0.85	0.00	0.00	4.41	14.71	6.38	null	null		null	null		-9.73E+00	9.44E-03		-9.73E+00	2.12E-02		1.74E+00	3.81E-13	Up	5.32E-01	1.16E-01				Unigene42170_All//2.00E-15//TC152959				
Unigene4218_All	803	4.24	4.23	3.51	15.01	11.84	7.09	7.11	4.06	3.82	-2.60E-03	9.91E-01		-2.69E-01	4.53E-01		-3.43E-01	3.31E-02		-1.08E+00	3.08E-11	Down	-8.08E-01	2.66E-04		-8.96E-01	3.67E-05		Unigene4218_All//gi|124359162|gb|AB005885.1|//4.00E-06//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene4218_All//5.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene4218_All//9.00E-72//TC149587				nr +
Unigene42181_All	345	2.27	6.90	2.16	7.22	6.29	4.84	0.37	1.33	0.69	1.60E+00	2.78E-04	Up	-7.41E-02	9.35E-01		-1.99E-01	6.31E-01		-5.76E-01	1.65E-01		1.86E+00	8.80E-02		9.14E-01	5.42E-01		Unigene42181_All//gi|224129950|ref|XP_002320711.1|//5.00E-07//predicted protein [Populus trichocarpa] >gi|222861484|gb|EEE99026.1| predicted protein [Populus trichocarpa]	Unigene42181_All//5.00E-07//AT4G00050| UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor	Unigene42181_All//3.00E-48//TC146895	bHLH			nr -
Unigene42182_All	520	1.61	0.58	0.00	1.44	1.06	0.96	0.00	0.00	0.00	-1.46E+00	6.69E-02		-1.07E+01	1.19E-04	Down	-4.40E-01	5.85E-01		-5.89E-01	4.87E-01		null	null		null	null		Unigene42182_All//gi|258558776|gb|ACV81697.1|//1.00E-61//MYBF1 [Vitis vinifera]	Unigene42182_All//8.00E-60//AT5G49330| AtMYB111 (myb domain protein 111); DNA binding / transcription factor	Unigene42182_All//1.00E-63//NP524481	MYB		GO:0001071//GO:0003676//GO:0006351//GO:0009699//GO:0010468//GO:0030528//GO:0043231	nr -
Unigene42186_All	538	9.73	0.75	1.29	2.78	0.64	0.50	0.16	0.00	0.30	-3.69E+00	3.83E-21	Down	-2.92E+00	2.17E-16	Down	-2.12E+00	1.37E-04	Down	-2.46E+00	8.25E-05	Down	-7.30E+00	4.03E-01		9.14E-01	6.24E-01								
Unigene42188_All	402	2.60	0.00	1.85	1.24	2.91	2.47	2.63	1.87	1.19	-1.13E+01	3.80E-06	Down	-4.89E-01	4.78E-01		1.23E+00	5.68E-02		9.96E-01	1.72E-01		-4.91E-01	4.22E-01		-1.14E+00	4.77E-02		Unigene42188_All//gi|15237421|ref|NP_197188.1|//2.00E-13//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75174141|sp|Q9LFL5.1|PP390_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g16860	Unigene42188_All//1.00E-14//AT5G16860| pentatricopeptide (PPR) repeat-containing protein				GO:0043231	nr +
Unigene4219_All	949	6.12	17.14	10.77	4.57	9.98	8.80	16.93	32.46	22.59	1.49E+00	2.65E-22	Up	8.16E-01	1.12E-05		1.13E+00	4.10E-10	Up	9.47E-01	1.87E-06		9.39E-01	4.73E-25		4.16E-01	5.82E-05		Unigene4219_All//gi|124264314|gb|AB097745.1|//4.00E-35//3-methylcrotonyl-CoA carboxylase [Solanum caripense] >gi|124264318|gb|ABM97747.1| 3-methylcrotonyl-CoA carboxylase [Solanum caripense] >gi|124264320|gb|ABM97748.1| 3-methylcrotonyl-CoA carboxylase [Solanum caripense] >gi|124264322|gb|ABM97749.1| 3-methylcrotonyl-CoA carboxylase [Solanum muricatum] >gi|124264324|gb|ABM97750.1| 3-methylcrotonyl-CoA carboxylase [Solanum fraxinifolium] >gi|124264326|gb|ABM97751.1| 3-methylcrotonyl-CoA carboxylase [Solanum fraxinifolium] >gi|124264328|gb|ABM97752.1| 3-methylcrotonyl-CoA carboxylase [Solanum fraxinifolium] >gi|124264330|gb|ABM97753.1| 3-methylcrotonyl-CoA carboxylase [Solanum fraxinifolium] >gi|124264332|gb|ABM97754.1| 3-methylcrotonyl-CoA carboxylase [Solanum heiseri] >gi|124264334|gb|ABM97755.1| 3-methylcrotonyl-CoA carboxylase	Unigene4219_All//6.00E-36//AT4G34030| MCCB (3-METHYLCROTONYL-COA CARBOXYLASE); biotin carboxylase/ methylcrotonoyl-CoA carboxylase	Unigene4219_All//0.00E+00//gi|109827842|gb|DW226503.1|DW226503		ko00280|Valine, leucine and isoleucine degradation		nr +
Unigene42190_All	381	1.10	0.00	1.54	1.44	1.45	0.47	3.55	0.99	0.73	-1.01E+01	1.05E-02		4.85E-01	6.30E-01		7.90E-03	9.83E-01		-1.60E+00	1.32E-01		-1.85E+00	9.22E-04	Down	-2.28E+00	7.13E-05	Down			Unigene42190_All//1.00E-152//gi|18099931|gb|BM359185.1|BM359185				
Unigene42191_All	755	0.00	0.13	0.00	0.00	0.00	0.00	20.10	7.69	5.22	7.07E+00	3.86E-01		null	null		null	null		null	null		-1.39E+00	4.17E-23	Down	-1.94E+00	3.33E-38	Down	Unigene42191_All//gi|238055378|sp|B9SCX0.1|U4975_RICCO//5.00E-56//RecName: Full=UPF0497 membrane protein 5	Unigene42191_All//1.00E-52//AT5G06200| integral membrane family protein					nr -
Unigene42192_All	252	3.11	0.00	0.85	5.14	5.19	3.58	42.45	3.81	20.08	-1.16E+01	1.09E-04	Down	-1.88E+00	4.13E-02		1.48E-02	9.95E-01		-5.20E-01	4.01E-01		-3.48E+00	1.20E-49	Down	-1.08E+00	8.29E-12	Down	Unigene42192_All//gi|224056577|ref|XP_002298919.1|//5.00E-06//predicted protein [Populus trichocarpa] >gi|222846177|gb|EEE83724.1| predicted protein [Populus trichocarpa]		Unigene42192_All//2.00E-116//DW507801				nr -
Unigene42194_All	304	1.38	0.33	0.35	1.31	0.79	0.45	1.95	2.89	0.00	-2.05E+00	1.20E-01		-1.97E+00	1.51E-01		-7.25E-01	5.46E-01		-1.56E+00	2.31E-01		5.68E-01	3.99E-01		-1.09E+01	1.41E-04	Down			Unigene42194_All//1.00E-161//ES807314				
Unigene42195_All	418	0.00	0.00	0.00	0.00	0.00	0.00	5.26	4.30	1.81	null	null		null	null		null	null		null	null		-2.91E-01	4.89E-01		-1.54E+00	9.61E-05	Down							
Unigene42196_All	506	0.21	0.00	0.00	1.87	0.00	0.36	0.84	2.07	1.89	-7.69E+00	3.71E-01		-7.69E+00	3.92E-01		-1.09E+01	5.17E-07	Down	-2.39E+00	3.48E-03		1.31E+00	3.44E-02		1.18E+00	5.83E-02		Unigene42196_All//gi|224086044|ref|XP_002307792.1|//5.00E-08//predicted protein [Populus trichocarpa] >gi|222857241|gb|EEE94788.1| predicted protein [Populus trichocarpa]	Unigene42196_All//3.00E-05//AT1G12680| PEPKR2 (Phosphoenolpyruvate carboxylase-related kinase 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene42196_All//6.00E-149//gi|73862930|gb|DT465669.1|DT465669				nr -
Unigene42197_All	894	0.00	0.00	0.00	0.00	0.00	0.20	17.03	5.10	25.27	null	null		null	null		null	null		7.66E+00	1.94E-01		-1.74E+00	5.07E-32	Down	5.70E-01	1.64E-08		Unigene42197_All//gi|73624747|gb|AA279231.1|//1.00E-114//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene42197_All//6.00E-112//AT4G23990| ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	Unigene42197_All//3.00E-13//ES847571				nr +
Unigene42198_All	1098	0.00	4.94	1.12	0.59	0.60	0.70	0.73	2.93	0.29	1.23E+01	6.34E-31	Up	1.01E+01	9.12E-07	Up	1.48E-02	9.91E-01		2.46E-01	7.57E-01		2.00E+00	1.03E-08	Up	-1.33E+00	5.40E-02		Unigene42198_All//gi|1708314|sp|P51819.1|HSP83_IPONI//1.00E-160//RecName: Full=Heat shock protein 83 >gi|169296|gb|AAA33748.1| heat shock protein 83 [Ipomoea nil] >gi|445625|prf||1909372A heat shock protein 83	Unigene42198_All//5.00E-133//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene42198_All//0.00E+00//gi|109874088|gb|DW503063.1|DW503063		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene42199_All	457	0.00	0.00	0.00	8.83	4.97	2.67	0.46	0.18	0.00	null	null		null	null		-8.28E-01	3.57E-03		-1.73E+00	7.70E-08	Down	-1.34E+00	4.29E-01		-8.85E+00	5.80E-02		Unigene42199_All//gi|226499540|ref|NP_001151712.1|//7.00E-20//mini zinc finger 3 [Zea mays] >gi|195649239|gb|ACG44087.1| mini zinc finger 3 [Zea mays]	Unigene42199_All//4.00E-21//AT3G28917| MIF2 (MINI ZINC FINGER 2); DNA binding	Unigene42199_All//9.00E-157//TC171328	zf-HD		GO:0003676	nr +
Unigene4220_All	978	0.43	0.62	1.09	18.90	19.86	23.55	11.72	46.03	28.92	5.39E-01	5.63E-01		1.35E+00	6.01E-02		7.16E-02	6.38E-01		3.18E-01	5.84E-03		1.97E+00	2.31E-110	Up	1.30E+00	1.77E-39	Up	Unigene4220_All//gi|6651292|gb|AAF22256.1|//1.00E-60//myb-related transcription factor [Pimpinella brachycarpa]	Unigene4220_All//3.00E-45//AT4G12350| MYB42 (myb domain protein 42); transcription factor	Unigene4220_All//7.00E-76//TC157816	MYB			nr -
Unigene42200_All	321	35.37	149.17	37.16	42.37	42.91	59.09	424.25	671.21	800.25	2.08E+00	3.74E-102	Up	7.12E-02	6.97E-01		1.84E-02	9.31E-01		4.80E-01	1.13E-04		6.62E-01	1.40E-93		9.16E-01	4.77E-199		Unigene42200_All//gi|38016531|gb|AA807601.1|//3.00E-47//fiber quinone-oxidoreductase [Gossypium barbadense]	Unigene42200_All//4.00E-35//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene42200_All//0.00E+00//gi|13352011|gb|BG442443.1|BG442443			GO:0008152//GO:0009528//GO:0009534//GO:0016655//GO:0046914	nr +
Unigene42202_All	750	0.00	2.36	2.91	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.14E-10	Up	1.15E+01	4.95E-12	Up	null	null		null	null		null	null		null	null								
Unigene42204_All	1483	0.00	0.00	0.07	0.00	0.00	0.00	14.51	2.76	5.80	null	null		6.17E+00	3.98E-01		null	null		null	null		-2.39E+00	1.14E-67	Down	-1.32E+00	3.57E-31	Down	Unigene42204_All//gi|256258961|gb|ACU64887.1|//1.00E-99//UDP-T1 [Oryza minuta]	Unigene42204_All//2.00E-44//AT3G16520| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene42204_All//0.00E+00//gi|7832474|gb|DT545021.1|DT545021		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene42206_All	318	2.47	0.00	1.51	4.39	1.52	1.70	1.60	0.79	1.50	-1.13E+01	1.09E-04	Down	-7.12E-01	3.88E-01		-1.53E+00	5.22E-03		-1.36E+00	1.87E-02		-1.02E+00	2.88E-01		-8.59E-02	9.30E-01				Unigene42206_All//4.00E-07//DW517389				

Unigene42207_All	351	0.30	0.29	0.46	0.14	2.16	2.06	1.08	1.07	0.68	-4.62E-02	9.88E-01			6.10E-01	7.48E-01			3.93E+00	9.78E-04	Up	3.86E+00	1.75E-03			-1.66E-02	1.02E+00			-6.71E-01	5.30E-01								
Unigene42209_All	561	0.09	0.00	0.00	3.02	1.17	1.37	7.84	0.45	0.78	-6.54E+00	6.11E-01			-6.54E+00	6.23E-01			-1.37E+00	4.48E-03		-1.14E+00	2.50E-02			-4.13E+00	1.27E-23	Down	-3.33E+00	1.07E-20	Down	Unigene42209_All//gi|224152830|ref|XP_002337280.1|//4.00E-35//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222838678|gb|EEE77043.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene42209_All//6.00E-27//AT5G63020| disease resistance protein (CC-NBS-LRR class), putative	Unigene42209_All//4.00E-159//DT463318		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene42211_All	751	0.00	0.00	0.00	0.00	0.00	0.00	3.94	1.28	2.28	null	null			null	null			null	null		null	null			-1.62E+00	2.89E-06	Down	-7.89E-01	1.15E-02		Unigene42211_All//gi|15226598|ref|NP_179755.1|//3.00E-67//pectinesterase family protein [Arabidopsis thaliana] >gi|75206124|sp|Q9SIJ9.1|PME11_ARATH RecName: Full=Putative pectinesterase 11; Short=PE 11; AltName: Full=Pectin methylesterase 11; Short=AtPME11	Unigene42211_All//5.00E-69//AT2G21610| pectinesterase family protein	Unigene42211_All//6.00E-11//TC179074		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0031410//GO:0071555	nr +
Unigene42212_All	245	0.85	0.00	0.00	14.84	5.06	4.42	1.55	0.17	0.33	-9.74E+00	1.22E-01			-9.74E+00	1.45E-01			-1.55E+00	6.21E-07	Down	-1.75E+00	3.13E-07	Down	-3.19E+00	3.11E-02		-2.26E+00	6.49E-02		Unigene42212_All//gi|225447209|ref|XP_002272217.1|//8.00E-14//PREDICTED: hypothetical protein [Vitis vinifera]								nr -
Unigene42215_All	617	6.36	2.30	1.38	0.00	1.56	0.59	0.00	0.00	0.00	-1.47E+00	6.73E-06	Down	-2.20E+00	3.37E-09	Down	1.06E+01	6.32E-06	Up	9.19E+00	2.37E-02		null	null			null	null		null	null		Unigene42215_All//gi|15220050|ref|NP_178125.1|//2.00E-72//TMM (TOO MANY MOUTHS); protein binding / receptor [Arabidopsis thaliana] >gi|22096215|sp|Q8GSU1.1|TMM_ARATH RecName: Full=Protein TOO MANY MOUTHS; Flags: Precursor >gi|5902366|gb|AAD55468.1|AC009322_8 Hypothetical protein [Arabidopsis thaliana]	Unigene42215_All//4.00E-70//AT1G80080| TMM (TOO MANY MOUTHS); protein binding / receptor	Unigene42215_All//0.00E+00//gi|21090377|gb|BQ402690.1|BQ402690		ko04626|Plant-pathogen interaction	GO:0004871//GO:0005488//GO:0008152//GO:0009725//GO:0009886//GO:0016628//GO:0016772//GO:0023060//GO:0031224//GO:0031410//GO:0051301	nr -
Unigene42216_All	493	0.00	1.34	0.00	1.41	1.75	4.86	0.00	0.00	0.08	1.04E+01	6.25E-04	Up	null	null		3.04E-01	7.36E-01		1.78E+00	5.60E-05	Up	null	null		6.34E+00	6.45E-01					Unigene42216_All//gi|5802250|gb|AAD51628.1|AF169025.1|//4.00E-23//seed maturation protein PM41 [Glycine max]	Unigene42216_All//4.00E-24//AT2G21820| unknown protein				GO:0043231	nr +
Unigene42223_All	482	0.00	118.58	97.33	0.52	0.43	1.59	0.09	0.00	0.33	1.69E+01	0.00E+00	Up	1.66E+01	1.14E-266	Up	-2.69E-01	8.23E-01		1.62E+00	6.61E-02		-6.45E+00	6.57E-01		1.91E+00	3.77E-01					Unigene42223_All//gi|110225675|ref|YP_665681.1|//4.00E-59//cytochrome c oxidase subunit 3 [Nephroselmis olivacea] >gi|6066190|gb|AAF03208.1|AF110138_40 cytochrome c oxidase subunit 3 [Nephroselmis olivacea]	Unigene42223_All//1.00E-45//ATMG00730| Encodes cytochrome c oxidase subunit 3.	Unigene42223_All//4.00E-08//TC154383		ko00190|Oxidative phosphorylation		nr -
Unigene42224_All	935	0.00	10.13	2.79	0.00	0.00	0.00	0.00	0.00	1.33E+01	2.89E-54	Up	1.14E+01	2.12E-14	Up	null	null		null	null		null	null			null	null					Unigene42224_All//gi|301102726|ref|XP_002900450.1|//3.00E-69//acyl-CoA desaturase 1 [Phytophthora infestans T30-4] >gi|262102191|gb|EEY60243.1| acyl-CoA desaturase 1 [Phytophthora infestans T30-4]	Unigene42224_All//1.00E-26//AT3G15850| FAD5 (FATTY ACID DESATURASE 5); 16:0 monogalactosyldiacylglycerol desaturase/ oxidoreductase			ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene42227_All	667	0.00	0.00	0.00	0.00	0.00	0.00	1.65	3.95	1.13	null	null			null	null			null	null		null	null			1.26E+00	3.97E-04	Up	-5.38E-01	3.47E-01		Unigene42227_All//gi|110816488|sp|Q3BAI2.1|YC394_PHAAO//2.00E-17//RecName: Full=Uncharacterized protein 08F91		Unigene42227_All//2.00E-35//gi|11207696|gb|BF276626.1|BF276626				nr -
Unigene42228_All	566	0.18	1.52	0.85	6.95	2.07	0.72	0.15	0.15	0.07	3.04E+00	1.94E-03		2.20E+00	9.15E-02		-1.75E+00	9.11E-09	Down	-3.28E+00	1.17E-15	Down	-1.65E-02	1.01E+00		-1.09E+00	6.76E-01		Unigene42228_All//gi|297613226|ref|NP_001066848.2|//4.00E-13//Os12g0507700 [Oryza sativa Japonica Group] >gi|77555898|gb|ABA98694.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255670332|dbj|BAF29867.2|Os12g0507700 [Oryza sativa Japonica Group]	Unigene42228_All//6.00E-17//AT3G19550| unknown protein	Unigene42228_All//0.00E+00//TC171359				nr +
Unigene4223_All	313	25.58	9.23	21.61	0.00	1.76	0.43	0.00	0.00	0.00	-1.47E+00	2.97E-11	Down	-2.43E-01	2.88E-01		1.08E+01	2.02E-03		8.76E+00	3.11E-01		null	null		null	null					Unigene4223_All//gi|296012006|gb|ADG65641.1|//4.00E-36//glycosyltransferase [Withania somnifera]	Unigene4223_All//6.00E-34//AT1G78270| AtUGT85A4 (UDP-glucosyl transferase 85A4); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring hexosyl groups	Unigene4223_All//1.00E-176//TC139985		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene42230_All	975	0.16	0.00	0.11	1.38	2.44	2.78	10.88	0.34	0.33	-7.33E+00	2.15E-01		-5.60E-01	7.75E-01		8.21E-01	4.57E-02		1.01E+00	8.83E-03		-4.99E+00	3.51E-63	Down	-5.06E+00	7.11E-66	Down	Unigene42230_All//gi|75274452|sp|Q9LW60.1|P2C44_ARATH//7.00E-67//RecName: Full=Putative protein phosphatase 2C-like protein 44; Short=AtPP2C44 >gi|11994321|dbj|BAB02280.1| protein phosphatase 2C-like protein [Arabidopsis thaliana]	Unigene42230_All//2.00E-66//AT3G23360| protein phosphatase 2C, putative / PP2C, putative	Unigene42230_All//0.00E+00//TC156829				nr -
Unigene42233_All	740	0.00	0.07	0.86	0.74	0.23	0.79	2.69	6.50	6.51	6.10E+00	6.16E-01		9.75E+00	1.16E-03		-1.67E+00	9.26E-02		9.95E-02	9.36E-01		1.27E+00	5.44E-07	Up	1.28E+00	3.01E-07	Up	Unigene42233_All//gi|89001073|gb|ABD59126.1|//1.00E-23//At1g07795 [Arabidopsis thaliana]	Unigene42233_All//1.00E-16//AT1G07795| unknown protein					nr -
Unigene42235_All	650	0.00	0.00	0.00	0.08	0.00	0.00	1.76	4.37	4.29	null	null		null	null		-6.26E+00	5.55E-01		-6.26E+00	6.35E-01		1.32E+00	1.22E-04	Up	1.29E+00	1.36E-04	Up	Unigene42235_All//gi|40822853|gb|AAR92244.1|//2.00E-20//At5g20110 [Arabidopsis thaliana] >gi|45732676|gb|AAS76236.1|At5g20110 [Arabidopsis thaliana]	Unigene42235_All//1.00E-21//AT5G20110| dynein light chain, putative	Unigene42235_All//8.00E-07//DR462237				nr +
Unigene42238_All	514	0.00	36.08	16.47	0.00	0.00	0.00	0.00	0.00	0.00	1.51E+01	1.19E-106	Up	1.40E+01	2.05E-47	Up	null	null		null	null		null	null		null	null		Unigene42238_All//gi|297832838|ref|XP_002884301.1|//2.00E-37//40S ribosomal protein S19 [Arabidopsis lyrata subsp. lyrata] >gi|297330141|gb|EFH60560.1| 40S ribosomal protein S19 [Arabidopsis lyrata subsp. lyrata]	Unigene42238_All//2.00E-34//AT3G02080| 40S ribosomal protein S19 (RPS19A)			ko03010|Ribosome		nr -
Unigene42239_All	338	3.72	1.20	0.63	8.84	10.60	7.88	1.13	0.74	0.71	-1.63E+00	1.05E-02		-2.56E+00	6.99E-04	Down	2.61E-01	4.88E-01		-1.66E-01	6.88E-01		-6.02E-01	6.12E-01		-6.71E-01	5.30E-01						Unigene42239_All//5.00E-170//TC152112					
Unigene4224_All	1657	5.18	1.71	3.15	0.18	0.15	0.11	11.87	1.16	7.69	-1.60E+00	1.90E-13	Down	-7.17E-01	4.61E-04		-3.10E-01	8.20E-01		-7.27E-01	6.38E-01		-3.35E+00	5.41E-88	Down	-6.25E-01	9.22E-09		Unigene4224_All//gi|209954703|dbj|BAG80542.1|//0.00E+00//glycosyltransferase [Lycium barbarum]	Unigene4224_All//0.00E+00//AT1G22360| AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups	Unigene4224_All//0.00E+00//TC139985		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene42241_All	388	4.32	23.11	8.10	6.03	16.24	6.87	17.54	27.68	33.47	2.42E+00	1.44E-23	Up	9.08E-01	1.36E-02		1.43E+00	1.13E-09	Up	1.87E-01	6.73E-01		6.58E-01	2.12E-05		9.32E-01	3.32E-11						Unigene42241_All//8.00E-89//gi|164309889|gb|EX164353.1|EX164353					
Unigene42242_All	433	0.00	0.23	0.25	0.00	1.35	0.52	0.68	3.96	7.54	7.87E+00	3.86E-01		7.94E+00	3.98E-01		1.04E+01	1.26E-03		9.03E+00	1.19E-01		2.53E+00	2.37E-06	Up	3.46E+00	9.03E-16	Up										
Unigene42246_All	314	0.00	0.16	0.00	2.06	0.88	2.30	9.16	0.53	0.00	7.33E+00	6.16E-01		null	null		-1.23E+00	1.60E-01		1.58E-01	8.59E-01		-4.10E+00	1.53E-15	Down	-1.32E+01	3.77E-21	Down	Unigene42246_All//gi|15232846|ref|NP_186839.1|//6.00E-25//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana]	Unigene42246_All//2.00E-26//AT3G02100| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene42246_All//9.00E-08//TC144434		ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism		nr +
Unigene4225_All	1328	20.09	13.13	20.17	0.23	0.62	0.61	0.38	0.00	0.15	-6.14E-01	5.30E-09		5.50E-03	9.87E-01		1.47E+00	7.56E-02		1.44E+00	8.45E-02		-8.58E+00	8.89E-04	Down	-1.35E+00	1.40E-01		Unigene4225_All//gi|209954703|dbj|BAG80542.1|//1.00E-155//glycosyltransferase [Lycium barbarum]	Unigene4225_All//2.00E-149//AT1G22400| UGT85A1; UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ glucuronosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene4225_All//0.00E+00//TC139985		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene42257_All	1178	0.00	17.64	8.18	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	1.52E-119	Up	1.30E+01	4.64E-54	Up	null	null		null	null		null	null		null	null											
Unigene42259_All	463	155.27	75.29	39.91	52.29	61.21	38.92	0.18	0.18	0.26	-1.04E+00	6.06E-56	Down	-1.96E+00	2.81E-138	Down	2.27E-01	2.83E-02		-4.26E-01	8.47E-05		-1.67E-02	1.01E+00		4.99E-01	8.07E-01		Unigene42259_All//gi|28569968|dbj|BAC57890.1|//7.00E-30//pherophorin [Volvox carteri f. nagariensis] >gi|300261476|gb|EFJ45689.1| extracellular matrix glycoprotein pherophorin-V9 [Volvox carteri f. nagariensis]		Unigene42259_All//9.00E-120//gi|109884138|gb|DW513108.1|DW513108		ko03040|Spliceosome		nr +
Unigene4226_All	1491	4.42	10.77	7.25	6.11	9.05	9.78	7.34	9.98	10.77	1.28E+00	7.96E-18	Up	7.13E-01	7.02E-05		5.66E-01	8.66E-05		6.78E-01	2.23E-06		4.42E-01	6.46E-04		5.52E-01	5.17E-06		Unigene4226_All//gi|15235584|ref|NP_192453.1|//1.00E-128//EDA35 (embryo sac development arrest 35) [Arabidopsis thaliana] >gi|72672304|emb|CAB81086.1| D123-like protein [Arabidopsis thaliana]	Unigene4226_All//5.00E-130//AT4G05440| EDA35 (embryo sac development arrest 35)	Unigene4226_All//0.00E+00//TC154766				nr +
Unigene42261_All	531	0.20	0.00	0.40	1.88	0.71	0.00	2.55	1.50	0.30	-7.62E+00	3.71E-01		1.03E+00	5.91E-01		-1.40E+00	3.79E-02		-1.09E-01	2.97E-06	Down	-7.69E-01	1.39E-01		-3.09E+00	1.97E-06	Down										
Unigene42262_All	415	2.02	3.54	0.13	1.44	1.16	0.65	0.82	0.81	0.38	8.12E-01	1.36E-01		-3.97E+00	9.08E-04	Down	-3.10E-01	7.41E-01		-1.14E+00	2.43E-01		-1.66E-02	1.02E+00		-1.09E+00	3.55E-01										
Unigene42269_All	470	0.56	0.43	0.00	5.72	3.52	1.06	1.80	1.33	0.68	-3.68E-01	7.78E-01		-9.12E+00	8.56E-02		-7.03E-01	5.69E-02		-2.44E+00	4.16E-08	Down	-4.32E-01	5.47E-01		-1.41E+00	3.70E-02										
Unigene4227_All	1172	3.26	1.17	1.95	2.42	2.67	1.27	8.98	2.14	1.84	-1.48E+00	7.83E-06	Down	-7.38E-01	2.45E-02		1.42E-01	7.50E-01		-9.30E-01	1.21E-02		-2.07E+00	4.65E-28	Down	-2.29E+00	8.25E-33	Down	Unigene4227_All//gi|28950899|gb|AAO63373.1|//1.00E-103//At2g27770 [Arabidopsis thaliana]	Unigene4227_All//4.00E-100//AT2G27770| unknown protein	Unigene4227_All//0.00E+00//TC142403				nr +
Unigene42270_All	337	1.71	4.51	2.21	0.30	0.51	2.28	0.13	0.37	3.43	1.40E+00	1.22E-02		3.73E-01	6.23E-01		7.89E-01	7.70E-01		2.95E+00	4.39E-03		1.57E+00	5.45E-01		4.77E+00	3.27E-07	Up										
Unigene42271_All	1574	0.43	0.58	0.74	0.44	0.26	0.66	5.94	6.77	23.87	4.23E-01	5.64E-01		7.85E-01	2.38E-01		-7.55E-01	3.69E-01		5.75E-01	4.27E-01		1.90E-01	2.77E-01		2.01E+00	3.91E-96	Up	Unigene42271_All//gi|79423995|ref|NP_188501.2|//1.00E-157//ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene42271_All//2.00E-155//AT3G28600| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene42271_All//1.00E-19//TC170632				nr -
Unigene42273_All	357	0.00	0.00	0.00	0.00	0.19	0.00	17.65	38.17	61.04	null	null		null	null		7.59E+00	6.09E-01		null	null		1.11E+00	5.52E-15	Up	1.79E+00	3.24E-48	Up	Unigene42273_All//gi|225430249|ref|XP_002282589.1|//2.00E-07//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296082019|emb|CBI21024.3| unnamed protein product [Vitis vinifera]								nr +
Unigene42275_All	359	1.02	1.13	1.04	0.83	0.48	9.06	1.53	4.31	2.55	1.46E-01	8.98E-01		2.54E-02	1.00E+00		-7.96E-01	5.57E-01		3.44E+00	3.94E-13	Up	1.49E+00	2.61E-03		7.37E-01	2.43E-01										
Unigene42276_All	861	0.00	8.12	12.25	0.00	0.08	0.10	0.05	0.00	0.00	1.30E+01	5.86E-40	Up	1.36E+01	3.32E-59	Up	6.32E+00	6.09E-01		6.71E+00	4.76E-01		-5.62E+00	6.57E-01		-5.62E+00	6.12E-01		Unigene42276_All//gi|48596901|dbj|BAD22763.1|//1.00E-108//ribosomal protein [Bromus inermis]	Unigene42276_All//1.00E-108//AT5G58420| 40S ribosomal protein S4 (RPS4D)			ko03010|Ribosome		nr -
Unigene42277_All	304	0.00	0.00	0.00	0.16	0.00	0.00	7.37	8.25	14.81	null	null		null	null		-7.36E+00	5.55E-01		-7.36E+00	6.35E-01		1.62E-01	6.65E-01		1.01E+00	6.14E-05	Up	Unigene42277_All//gi|257782114|gb|ACV65500.1|//4.00E-46//deoxyhemigossypol-6-O-methyltransferase [Gossypium hirsutum]	Unigene42277_All//2.00E-06//AT4G35160| O-methyltransferase family 2 protein	Unigene42277_All//9.00E-48//CD486066				nr -
Unigene4228_All	1184	1.90	0.64	0.45	3.74	2.53	1.83	4.21	0.60	1.38	-1.57E+00	5.19E-04	Down	-2.08E+00	3.39E-05	Down	-5.66E-01	4.16E-02		-1.03E+00	2.88E-04	Down	-2.81E+00	2.86E-19	Down	-1.61E+00	2.66E-10	Down					Unigene4228_All//0.00E+00//DW231917					
Unigene42280_All	222	7.07	11.41	12.23	6.51	7.60	14.24	2.86	6.97	10.23	6.91E-01	8.20E-02		7.91E-01	4.77E-02		2.24E-01	7.06E-01		1.13E+00	1.37E-03		1.29E+00	8.20E-03		1.84E+00	6.10E-06	Up	Unigene42280_All//gi|110931718|gb|ABH02858.1|//4.00E-17//MYB transcription factor MYB136 [Glycine max]	Unigene42280_All//3.00E-07//AT5G52660| myb family transcription factor	Unigene42280_All//8.00E-103//gi|54115364|gb|CO490873.1|CO490873	MYB-related			nr +
Unigene42282_All	309	1.35	0.00	0.00	1.77	0.00	0.44	1.64	2.43	3.22	-1.04E+01	1.05E-02		-1.04E+01	1.56E-02		-1.08E+01	4.01E-04	Down	-2.02E+00	7.05E-02		5.68E-01	4.47E-01		9.73E-01	1.06E-01										

Unigene42283_All	346	2.27	2.93	1.54	5.33	1.00	3.52	4.64	2.30	2.88	3.69E-01	6.03E-01		-5.60E-01	4.96E-01		-2.42E+00	2.00E-06	Down	-5.96E-01	2.34E-01		-1.02E+00	2.97E-02		-6.90E-01	1.21E-01				Unigene42283_All//0.00E+00//gi|21101350|gb|BQ413663.1|BQ413663				
Unigene42285_All	911	2.87	9.23	7.89	1.37	1.10	1.04	0.23	0.00	0.04	1.68E+00	4.16E-14	Up	1.46E+00	1.31E-09	Up	-3.19E-01	6.08E-01		-3.93E-01	5.49E-01		-7.86E+00	7.44E-02		-2.41E+00	1.95E-01		Unigene42285_All//gi|225447302|ref|XP_002273837.1|//5.00E-15//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297738295|emb|CBI28946.3| unnamed protein product [Vitis vinifera]		Unigene42285_All//0.00E+00//DW491309				nr -
Unigene42288_All	328	0.48	0.77	0.32	7.75	6.93	2.89	0.77	0.25	0.36	6.91E-01	6.26E-01		-5.59E-01	7.75E-01		-1.61E-01	7.18E-01		-1.42E+00	4.48E-04	Down	-1.60E+00	3.10E-01		-1.09E+00	4.28E-01		Unigene42288_All//gi|121489295|emb|CAK18868.1|//3.00E-24//type II homeodomain-leucine zipper protein precursor [Phillyrea latifolia]	Unigene42288_All//8.00E-24//AT5G06710| HAT14 (HOMEOBOX FROM ARABIDOPSIS THALIANA); DNA binding / transcription factor	Unigene42288_All//1.00E-25//gi|78340700|gb|DT560974.1|DT560974	HB			nr +
Unigene42291_All	398	72.30	34.63	44.42	242.69	231.44	222.64	80.10	54.19	64.56	-1.06E+00	1.91E-23	Down	-7.03E-01	1.71E-11		-6.84E-02	2.75E-01		-1.24E-01	2.75E-02		-5.64E-01	3.83E-11		-3.11E-01	2.02E-04		Unigene42291_All//gi|42572261|ref|NP_974226.1|//8.00E-19//heavy-metal-associated domain-containing protein [Arabidopsis thaliana]		Unigene42291_All//0.00E+00//gi|78337792|gb|DT558066.1|DT558066		ko03018|RNA degradation		nr +
Unigene42294_All	339	0.00	1.49	0.00	0.00	0.00	0.00	3.62	5.42	79.21	1.05E+01	4.04E-03		null	null		null	null		null	null		5.85E-01	1.83E-01		4.45E+00	4.78E-151	Up	Unigene42294_All//gi|255554831|ref|XP_002518453.1|//1.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223542298|gb|EEF43840.1| conserved hypothetical protein [Ricinus communis]		Unigene42294_All//1.00E-130//gi|78325351|gb|DT545625.1|DT545625				nr -
Unigene42297_All	886	0.00	0.00	0.00	0.56	0.23	0.10	2.39	8.11	6.39	null	null		null	null		-1.27E+00	2.22E-01		-2.46E+00	4.83E-02		1.77E+00	8.66E-16	Up	1.42E+00	1.18E-09	Up	Unigene42297_All//gi|224100895|ref|XP_002312057.1|//2.00E-81//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222851877|gb|EEE89424.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene42297_All//4.00E-76//AT3G55090| ATPase, coupled to transmembrane movement of substances	Unigene42297_All//0.00E+00//gi|78349095|gb|DT569369.1|DT569369		ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene42298_All	365	13.33	21.93	25.24	18.29	19.34	21.28	27.68	32.18	10.59	7.18E-01	4.66E-04		9.21E-01	3.39E-06		8.07E-02	7.91E-01		2.19E-01	3.66E-01		2.17E-01	1.79E-01		-1.39E+00	3.54E-16	Down	Unigene42298_All//gi|224111880|ref|XP_002316010.1|//8.00E-14//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]		Unigene42298_All//1.00E-112//DN801688				nr +
Unigene423_All	2776	3.96	3.94	6.48	5.78	7.29	5.09	6.21	3.10	5.75	-5.60E-03	9.89E-01		7.12E-01	1.30E-07		3.36E-01	4.83E-03		-1.82E-01	2.44E-01		-1.00E+00	5.73E-16	Down	-1.11E-01	3.99E-01		Unigene423_All//gi|115480986|ref|NP_001064086.1|//0.00E+00//Os10g0127700 [Oryza sativa Japonica Group] >gi|78707697|gb|ABB46672.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113638695|dbj|BAF26000.1| Os10g0127700 [Oryza sativa Japonica Group]	Unigene423_All//0.00E+00//AT3G18350| unknown protein	Unigene423_All//0.00E+00//ES848822				nr -
Unigene4230_All	973	5.32	3.49	4.87	14.90	8.46	7.80	4.17	4.60	1.60	-6.10E-01	2.03E-02		-1.28E-01	6.39E-01		-8.17E-01	1.59E-09		-9.34E-01	1.29E-10		1.40E-01	6.65E-01		-1.39E+00	5.24E-07	Down			Unigene4230_All//0.00E+00//TC150227				
Unigene42300_All	689	2.05	0.51	0.39	0.36	1.65	0.85	1.41	0.00	0.52	-1.99E+00	1.37E-03		-2.41E+00	4.75E-04	Down	2.19E+00	2.15E-03		1.24E+00	2.31E-01		-1.05E+01	5.83E-07	Down	-1.44E+00	2.09E-02		Unigene42300_All//gi|224107225|ref|XP_002314413.1|//2.00E-63//cytokinin biosynthetic isopentenyltransferase [Populus trichocarpa] >gi|222863453|gb|EEF00584.1| cytokinin biosynthetic isopentenyltransferase [Populus trichocarpa]	Unigene42300_All//2.00E-49//AT3G23630| ATIPT7; ATP binding / tRNA isopentenyltransferase/ transferase, transferring alkyl or aryl (other than methyl) groups			ko00908|Zeatin biosynthesis		nr -
Unigene42301_All	599	0.35	1.35	0.00	2.33	0.57	1.06	0.28	0.21	0.00	1.95E+00	2.43E-02		-8.45E+00	1.45E-01		-2.02E+00	4.22E-04	Down	-1.14E+00	4.68E-02		-4.32E-01	7.93E-01		-8.14E+00	1.08E-01		Unigene42301_All//gi|115473321|ref|NP_001060259.1|//2.00E-13//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]		Unigene42301_All//1.00E-11//DW230999				nr +
Unigene42302_All	477	0.00	0.00	0.00	0.00	0.14	0.00	3.37	11.92	6.18	null	null		null	null		7.17E+00	6.09E-01		null	null		1.82E+00	3.57E-13	Up	8.76E-01	5.52E-03				Unigene42302_All//1.00E-14//DW513532				
Unigene42304_All	1294	0.00	18.33	5.39	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	1.48E-136	Up	1.24E+01	5.73E-39	Up	null	null		null	null		null	null		null	null		Unigene42304_All//gi|115455793|ref|NP_001051497.1|//2.00E-73//Os03g0787300 [Oryza sativa Japonica Group] >gi|113549968|dbj|BAF13411.1| Os03g0787300 [Oryza sativa Japonica Group]	Unigene42304_All//7.00E-65//AT5G22060| ATJ2; protein binding			ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene42307_All	846	0.62	0.60	0.31	0.35	0.24	0.37	0.95	2.22	5.60	-4.62E-02	9.76E-01		-9.75E-01	3.76E-01		-5.33E-01	6.78E-01		8.10E-02	9.50E-01		1.23E+00	4.43E-03		2.56E+00	5.97E-17	Up			Unigene42307_All//3.00E-07//gi|164359343|gb|ES820798.1|ES820798				
Unigene4231_All	663	68.97	30.19	33.49	70.55	71.42	117.51	112.43	47.34	72.77	-1.19E+00	3.26E-44	Down	-1.04E+00	2.01E-34	Down	1.76E-02	8.59E-01		7.36E-01	4.08E-36		-1.25E+00	4.74E-94	Down	-6.28E-01	6.67E-31		Unigene4231_All//gi|55976189|sp|Q6UNT2.1|RL5_CUCSA//4.00E-98//RecName: Full=60S ribosomal protein L5 >gi|34484312|gb|AAQ72789.1| 60S ribosomal protein L5 [Cucumis sativus]	Unigene4231_All//2.00E-90//AT5G39740| 60S ribosomal protein L5 (RPL5B)	Unigene4231_All//0.00E+00//gi|21096653|gb|BQ408966.1|BQ408966		ko03010|Ribosome		nr -
Unigene42310_All	498	2520.33	1221.05	2472.38	219.26	272.02	222.28	0.00	1.68	0.16	-1.05E+00	0.00E+00	Down	-2.77E-02	9.38E-02		3.11E-01	1.03E-14		1.97E-02	7.49E-01		1.07E+01	5.53E-06	Up	7.32E+00	4.04E-01		Unigene42310_All//gi|18407178|ref|NP_566086.1|//6.00E-20//PSI-P (PHOTOSYSTEM I P SUBUNIT); DNA binding [Arabidopsis thaliana] >gi|79324933|ref|NP_001031551.1| PSI-P (PHOTOSYSTEM I P SUBUNIT); DNA binding [Arabidopsis thaliana] >gi|38503349|sp|Q8LCL1.2|TMP14_ARATH RecName: Full=Thylakoid membrane phosphoprotein 14 kDa, chloroplastic; Flags: Precursor >gi|3510256|gb|AAC33500.1| expressed protein [Arabidopsis thaliana]	Unigene42310_All//1.00E-11//AT2G46820| PSI-P (PHOTOSYSTEM I P SUBUNIT); DNA binding	Unigene42310_All//0.00E+00//TC161854				nr -
Unigene42311_All	751	0.00	0.00	0.00	0.00	0.18	0.00	19.65	7.68	4.35	null	null		null	null		7.52E+00	3.18E-01		null	null		-1.36E+00	9.14E-22	Down	-2.18E+00	7.16E-43	Down	Unigene42311_All//gi|110931814|gb|ABR02906.1|//3.00E-47//MYB transcription factor MYB161 [Glycine max]	Unigene42311_All//1.00E-47//AT5G57620| MYB36 (myb domain protein 36); DNA binding / transcription factor	Unigene42311_All//4.00E-80//TC137837	MYB			nr +
Unigene42312_All	240	145.41	12.03	126.47	0.62	2.15	0.56	0.00	0.00	0.00	-3.59E+00	1.14E-135	Down	-2.01E-01	4.44E-02		1.79E+00	1.26E-01		-1.42E-01	9.43E-01		null	null		null	null				Unigene42312_All//2.00E-119//CA992742				
Unigene42313_All	629	1.66	4.59	2.20	2.61	0.66	1.08	1.34	3.19	1.65	1.46E+00	1.63E-04	Up	4.04E-01	4.96E-01		-1.99E+00	1.18E-04	Down	-1.28E+00	1.42E-02		1.25E+00	2.74E-03		2.93E-01	6.25E-01		Unigene42313_All//gi|224135759|ref|XP_002322153.1|//3.00E-07//predicted protein [Populus trichocarpa] >gi|222869149|gb|EEF06280.1| predicted protein [Populus trichocarpa]	Unigene42313_All//9.00E-07//AT5G50090| unknown protein	Unigene42313_All//4.00E-39//EX170631				nr -
Unigene42315_All	401	0.78	0.63	0.53	2.61	0.00	1.46	0.63	1.15	0.70	-3.09E-01	7.89E-01		-5.60E-01	6.63E-01		-1.13E+01	9.43E-08	Down	-8.33E-01	2.30E-01		8.58E-01	3.96E-01		1.37E-01	9.29E-01		Unigene42315_All//gi|548488|sp|P35336.1|PGLR_ACTDE//1.00E-20//RecName: Full=Polygalacturonase; Short=PG; AltName: Full=Pectinase; Flags: Precursor >gi|166325|gb|AAC14453.1| polygalacturonase [Actinidia deliciosa var. deliciosa]	Unigene42315_All//3.00E-17//AT2G41850| PGAZAT (POLYGALACTURONASE ABSCISSION ZONE A. THALIANA); polygalacturonase	Unigene42315_All//5.00E-124//ES837961		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene42316_All	309	1.69	0.98	0.34	3.06	0.33	2.48	10.13	2.84	2.84	-7.83E-01	4.22E-01		-2.30E+00	6.76E-02		-3.20E+00	1.40E-04	Down	-3.02E-01	6.89E-01		-1.83E+00	1.17E-07	Down	-1.84E+00	5.84E-08	Down			Unigene42316_All//2.00E-95//TC175286				
Unigene42317_All	1577	0.00	0.13	0.95	0.28	0.39	0.26	1.96	1.67	6.87	7.01E+00	1.36E-01		9.88E+00	3.22E-08	Up	4.67E-01	6.34E-01		-1.42E-01	9.00E-01		-2.29E-01	5.21E-01		1.81E+00	8.84E-25	Up	Unigene42317_All//gi|1346028|sp|P49351.1|FPPS1_LUPAL//3.00E-20//RecName: Full=Farnesyl pyrophosphate synthase 1; Short=FPP synthase 1; Short=FPS 1; AltName: Full=Farnesyl diphosphate synthase 1; Includes: RecName: Full=Dimethylallyltranstransferase; Includes: RecName: Full=Geranyltranstransferase >gi|558923|gb|AAA86687.1| farnesyl pyrophosphate synthase [Lupinus albus]	Unigene42317_All//4.00E-19//AT5G47770| FPS1 (FARNESYL DIPHOSPHATE SYNTHASE 1); dimethylallyltranstransferase/ geranyltranstransferase	Unigene42317_All//0.00E+00//TC178789		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene42318_All	266	2.36	0.00	0.80	1.12	1.55	1.19	1.75	1.10	0.75	-1.12E+01	7.91E-04	Down	-1.56E+00	1.29E-01		4.67E-01	7.41E-01		8.10E-02	9.50E-01		-6.69E-01	5.08E-01		-1.22E+00	2.00E-01								
Unigene42319_All	505	0.52	0.40	0.63	0.79	1.64	0.72	1.17	3.56	3.47	-3.68E-01	7.78E-01		2.89E-01	8.10E-01		1.05E+00	1.99E-01		-1.41E-01	9.04E-01		1.60E+00	4.89E-04	Up	1.57E+00	5.53E-04	Up							
Unigene42323_All	515	0.10	0.30	0.00	1.06	1.34	0.61	2.30	0.16	0.46	1.54E+00	5.31E-01		-6.67E+00	6.23E-01		3.30E-01	7.52E-01		-7.93E-01	4.44E-01		-3.82E+00	2.12E-06	Down	-2.31E+00	2.04E-04	Down	Unigene42323_All//gi|11121449|emb|CAC14868.1|//3.00E-13//DNA Helicase [Arabidopsis thaliana]	Unigene42323_All//2.00E-14//AT1G10930| RECQ4A; ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene42323_All//3.00E-27//DN760132		ko03018|RNA degradation//ko03440|Homologous recombination		nr +
Unigene42324_All	542	0.10	0.93	0.20	1.29	0.57	0.50	4.21	0.15	3.45	3.28E+00	2.11E-02		1.03E+00	7.03E-01		-1.17E+00	1.61E-01		-1.36E+00	1.31E-01		-4.77E+00	1.41E-13	Down	-2.86E-01	4.57E-01		Unigene42324_All//gi|297828191|ref|XP_002881978.1|//6.00E-23//CYCP4_1 [Arabidopsis lyrata subsp. lyrata] >gi|297327817|gb|EFH58237.1| CYCP4_1 [Arabidopsis lyrata subsp. lyrata]	Unigene42324_All//5.00E-20//AT2G44740| CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	Unigene42324_All//0.00E+00//gi|109882516|gb|DW511486.1|DW511486				nr -
Unigene42328_All	1427	0.00	0.00	0.00	0.07	0.05	0.00	6.07	18.51	23.84	null	null		null	null		-5.31E-01	8.16E-01		-6.13E+00	3.99E-01		1.61E+00	3.98E-49	Up	1.97E+00	3.54E-85	Up	Unigene42328_All//gi|30024598|dbj|BAC75671.1|//2.00E-81//transcription factor MYB101 [Lotus japonicus]	Unigene42328_All//1.00E-72//AT3G02940| MYB107 (myb domain protein 107); DNA binding / transcription factor	Unigene42328_All//5.00E-10//gi|48747073|gb|CO077592.1|CO077592	MYB			nr +
Unigene42329_All	473	29.76	59.78	44.69	16.96	20.75	34.47	46.66	42.68	31.00	1.01E+00	4.41E-21	Up	5.87E-01	1.83E-06		2.91E-01	1.32E-01		1.02E+00	1.50E-13	Up	-1.29E-01	2.86E-01		-5.90E-01	7.27E-09		Unigene42329_All//gi|33307141|gb|AAQ2914.1|AF396464.1|//5.00E-12//C2.6 protein [Pisum sativum]	Unigene42329_All//1.00E-10//AT3G53990| universal stress protein (USP) family protein	Unigene42329_All//3.00E-64//ES847166				nr -
Unigene42333_All	594	0.53	2.05	0.36	9.64	6.49	4.79	103.57	351.46	126.22	1.95E+00	4.09E-03		-5.60E-01	6.63E-01		-5.71E-01	1.59E-02		-1.01E+00	3.81E-05	Down	1.76E+00	0.00E+00	Up	2.85E-01	6.47E-08		Unigene42333_All//gi|15451136|gb|AK96839.1|//7.00E-50//periaxin-like protein [Arabidopsis thaliana]		Unigene42333_All//0.00E+00//gi|48744532|gb|CO075051.1|CO075051		ko03040|Spliceosome		nr -
Unigene42334_All	1000	0.78	1.01	0.11	0.00	0.00	0.00	0.42	4.72	5.06	3.69E-01	6.03E-01		-2.88E+00	6.35E-03		null	null		null	null		3.48E+00	3.55E-22	Up	3.58E+00	9.61E-25	Up	Unigene42334_All//gi|224142293|ref|XP_002324493.1|//1.00E-43//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222865927|gb|EEF03058.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene42334_All//1.00E-34//AT2G29100| ATGLR2.9; intracellular ligand-gated ion channel					nr +

Unigene42335_All	766	0.00	0.00	0.00	0.00	0.00	0.00	4.58	1.80	6.09	null	null		null	null		null	null		null	null		-1.35E+00	9.92E-06	Down	4.10E-01	9.81E-02		Unigene42335_All//gi|224110992|ref|XP_002332999.1|//6.00E-38//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834484|gb|EEE72961.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene42335_All//1.00E-06//AT3G25510| disease resistance protein (TIR-NBS-LRR class), putative	Unigene42335_All//2.00E-20//TC155905				nr +
Unigene42339_All	539	0.00	0.00	0.00	0.00	0.00	0.00	6.35	10.55	1.70	null	null		null	null		null	null		null	null		7.31E-01	9.85E-04		-1.90E+00	5.12E-09	Down	Unigene42339_All//gi|015937|emb|CAA62943.1|//2.00E-58//extensin class I protein [Vigna unguiculata]		Unigene42339_All//7.00E-10//ES813279		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr +
Unigene42345_All	602	1.39	31.31	2.74	0.91	0.63	1.43	0.14	0.07	0.93	4.49E+00	1.96E-85	Up	9.80E-01	6.93E-02		-5.33E-01	5.85E-01		6.47E-01	4.23E-01		-1.02E+00	7.24E-01		2.72E+00	9.38E-03		Unigene42345_All//gi|158828162|gb|ABW81041.1|//2.00E-79//protein-phosphatase-2C [Arabidopsis lyrata subsp. lyrata]	Unigene42345_All//2.00E-80//AT1G07430| protein phosphatase 2C, putative / PP2C, putative	Unigene42345_All//1.00E-100//gi|164307548|gb|ES819433.1|ES819433				nr +
Unigene42346_All	269	0.97	0.19	1.19	3.70	2.94	3.19	2.67	1.71	0.00	-2.37E+00	2.14E-01		2.88E-01	8.10E-01		-3.31E-01	6.19E-01		-2.15E-01	7.45E-01		-6.45E-01	4.01E-01		-1.14E+01	1.78E-05	Down								nr -
Unigene42347_All	951	0.00	0.00	0.00	0.00	0.00	0.00	1.60	6.81	1.13	null	null		null	null		null	null		null	null		2.09E+00	1.04E-17	Up	-5.01E-01	2.87E-01		Unigene42347_All//gi|71041098|gb|AA220437.1|//2.00E-45//MYB21 [Malus x domestica]	Unigene42347_All//6.00E-38//AT2G31180| MYB14 (MYB DOMAIN PROTEIN 14); DNA binding / transcription factor	Unigene42347_All//5.00E-09//gi|48747073|gb|CO077592.1|CO077592	MYB			nr -
Unigene42348_All	293	0.18	1.38	0.00	0.00	0.12	0.00	161.18	30.95	53.30	2.95E+00	5.91E-02		-7.48E+00	6.23E-01		6.88E+00	8.29E-01		null	null		-2.38E+00	7.85E-147	Down	-1.60E+00	4.10E-89	Down	Unigene42348_All//gi|7105717|gb|AAB84202.2|//2.00E-45//plasma membrane proton ATPase [Kosteletzkya virginica]	Unigene42348_All//5.00E-42//AT4G30190| AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	Unigene42348_All//7.00E-64//gi|13351158|gb|BG441506.1|BG441506		ko00190|Oxidative phosphorylation		nr +
Unigene4235_All	1609	21.85	10.30	12.21	25.11	23.18	12.94	17.29	7.33	9.16	-1.09E+00	1.77E-29	Down	-8.39E-01	1.11E-18		-1.15E-01	2.26E-01		-9.56E-01	1.13E-29		-1.24E+00	3.32E-35	Down	-9.16E-01	1.63E-22		Unigene4235_All//gi|71834080|dbj|BAE16981.1|//1.00E-141//delta7 sterol C-5 desaturase [Zinnia elegans]	Unigene4235_All//1.00E-135//AT3G02580| STE1 (STEROL 1); C-5 sterol desaturase	Unigene4235_All//0.00E+00//TC130497		ko00100|Steroid biosynthesis		nr -
Unigene42353_All	1031	3.76	1.57	3.67	0.29	0.30	0.53	0.53	0.12	0.15	-1.26E+00	8.94E-05	Down	-3.43E-02	9.29E-01		5.23E-02	9.98E-01		8.59E-01	4.23E-01		-2.13E+00	3.31E-02		-1.79E+00	5.06E-02		Unigene42353_All//gi|115455105|ref|NP_001051153.1|//2.00E-28//Os03g0729200 [Oryza sativa Japonica Group] >gi|108710884|gb|ABF98679.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549624|dbj|BAF13067.1| Os03g0729200 [Oryza sativa Japonica Group]	Unigene42353_All//8.00E-34//AT5G65840| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Thioredoxin fold (InterPro:IPR012335), Thioredoxin-like fold (InterPro:IPR012336); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G37240.1); Has 167 Blast hits to 165 proteins in 51 species: Archae - 0; Bacteria - 28; Metazoa - 51; Fungi - 13; Plants - 59; Viruses - 0; Other Eukaryotes - 16 (source: NCBI BLink).						nr +
Unigene42354_All	680	0.00	10.13	6.66	0.00	0.00	0.00	0.12	0.00	0.23	1.33E+01	2.25E-39	Up	1.27E+01	3.88E-25	Up	null	null		null	null		-6.96E+00	4.03E-01		9.13E-01	6.24E-01		Unigene42354_All//gi|260401128|gb|ACX37092.1|//2.00E-69//cyclophilin [Citrus sinensis]	Unigene42354_All//1.00E-68//AT4G34870| ROC5 (ROTAMASE CYCLOPHILIN 5); peptidyl-prolyl cis-trans isomerase	Unigene42354_All//9.00E-13//gi|109832771|gb|DW231330.1|DW231330				nr +
Unigene42356_All	395	1.06	1.28	5.12	1.77	0.17	0.23	0.64	0.00	0.40	2.76E-01	7.64E-01		2.27E+00	3.13E-05	Up	-3.34E+00	1.25E-03		-2.95E+00	5.84E-03		-9.33E+00	4.04E-02		-6.71E-01	6.05E-01				Unigene42356_All//1.00E-41//BG443522				
Unigene42357_All	344	2.43	0.29	0.77	1.16	1.70	3.68	3.32	0.61	0.00	-3.05E+00	2.11E-03		-1.65E+00	5.45E-02		5.55E-01	5.99E-01		1.67E+00	9.52E-03		-2.45E+00	2.46E-04	Down	-1.17E+01	1.61E-08	Down			Unigene42357_All//4.00E-112//TC147068				
Unigene42358_All	791	4.83	1.86	3.97	9.95	4.75	2.51	0.00	0.00	0.00	-1.38E+00	2.56E-05	Down	-2.82E-01	3.94E-01		-1.07E+00	3.16E-08	Down	-1.99E+00	9.82E-18	Down	null	null		null	null									
Unigene42359_All	573	3.29	0.35	0.74	4.96	3.91	0.95	0.00	0.00	0.56	-3.22E+00	3.75E-07	Down	-2.14E+00	1.32E-04	Down	-3.43E-01	3.85E-01		-2.39E+00	2.40E-08	Down	null	null		9.12E+00	1.34E-02		Unigene42359_All//gi|297725777|ref|NP_001175252.1|//1.00E-50//Os07g0553633 [Oryza sativa Japonica Group] >gi|255677875|dbj|BAH93980.1| Os07g0553633 [Oryza sativa Japonica Group]	Unigene42359_All//7.00E-52//AT2G19130| S-locus lectin protein kinase family protein	Unigene42359_All//0.00E+00//DW498928		ko04626|Plant-pathogen interaction		nr +
Unigene42361_All	562	0.00	0.00	0.00	0.00	0.00	0.00	1.13	1.71	4.04	null	null		null	null		null	null		null	null		6.00E-01	3.67E-01		1.84E+00	6.10E-06	Up								
Unigene42364_All	1174	0.00	16.83	6.30	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	1.10E-113	Up	1.26E+01	2.22E-41	Up	null	null		null	null		null	null		null	null		Unigene42364_All//gi|1710587|sp|P50346.1|RLA0_SOYBN//3.00E-95//RecName: Full=60S acidic ribosomal protein P0 >gi|1196897|gb|AAB63814.1| acidic ribosomal protein P0 [Glycine max]	Unigene42364_All//3.00E-84//AT3G11250| 60S acidic ribosomal protein P0 (RPP0C)	Unigene42364_All//2.00E-12//DV849130		ko03010|Ribosome		nr -
Unigene42368_All	530	0.30	0.19	1.00	1.69	1.10	1.45	1.99	0.32	0.75	-6.32E-01	7.27E-01		1.76E+00	1.29E-01		-6.15E-01	4.02E-01		-2.24E-01	7.50E-01		-2.66E+00	2.25E-04	Down	-1.41E+00	1.72E-02		Unigene42368_All//gi|221272207|sp|A2A1A0.1|NCS1_COPJA//2.00E-07//RecName: Full=S-norcoclaurine synthase 1; Short=CjNCS1 >gi|123720767|dbj|BAF45337.1| norcoclaurine synthase [Coptis japonica var. dissecta] >gi|301072256|gb|ADK56103.1| 2OG/Fe(II)-dependent dioxygenase-like protein [synthetic construct]		Unigene42368_All//0.00E+00//TC152229				nr +
Unigene4237_All	2529	1.20	4.81	0.65	0.51	0.60	0.86	0.77	4.36	0.46	2.00E+00	3.28E-25	Up	-8.78E-01	1.93E-02		2.26E-01	7.27E-01		7.43E-01	9.72E-02		2.50E+00	8.84E-37	Up	-7.51E-01	5.89E-02		Unigene4237_All//gi|115477581|ref|NP_001062386.1|//1.00E-100//Os08g0541300 [Oryza sativa Japonica Group] >gi|113624355|dbj|BAF24300.1| Os08g0541300 [Oryza sativa Japonica Group]	Unigene4237_All//4.00E-77//AT4G36180| leucine-rich repeat family protein			ko04626|Plant-pathogen interaction		nr +
Unigene42370_All	548	0.76	0.18	0.58	1.36	4.02	1.73	1.23	0.69	1.24	-2.05E+00	1.20E-01		-3.90E-01	7.17E-01		1.56E+00	3.90E-04	Up	3.44E-01	6.49E-01		-8.47E-01	2.88E-01		1.60E-03	9.97E-01		Unigene42370_All//gi|15219728|ref|NP_176845.1|//2.00E-83//ATP dependent DNA ligase family protein [Arabidopsis thaliana]	Unigene42370_All//1.00E-77//AT1G66730| ATP dependent DNA ligase family protein	Unigene42370_All//1.00E-11//gi|78337916|gb|DT558190.1|DT558190				nr +
Unigene42372_All	1040	0.40	0.15	0.72	0.05	0.00	0.09	0.94	1.25	22.75	-1.46E+00	2.34E-01		8.33E-01	3.39E-01		-5.58E+00	5.55E-01		8.59E-01	7.94E-01		4.14E-01	4.51E-01		4.61E+00	6.29E-136	Up	Unigene42372_All//gi|54645911|gb|AAV36561.1|//6.00E-42//RD22-like protein [Vitis vinifera]	Unigene42372_All//2.00E-36//AT5G25610| RD22; nutrient reservoir					nr -
Unigene42373_All	651	7.31	29.27	8.18	1.61	4.02	5.27	1.10	7.83	6.06	2.00E+00	4.37E-39	Up	1.61E-01	5.90E-01		1.32E+00	6.59E-04	Up	1.71E+00	1.46E-06	Up	2.83E+00	1.01E-19	Up	2.46E+00	1.33E-13	Up	Unigene42373_All//gi|169786772|gb|ACA79924.1|//4.00E-17//chloroplast N receptor-interacting protein 1 [Nicotiana benthamiana] >gi|169786774|gb|ACA79925.1| chloroplast N receptor-interacting protein 1 [Nicotiana benthamiana]	Unigene42373_All//1.00E-15//AT4G35770| SEN1 (SENESCENCE 1)	Unigene42373_All//4.00E-36//TC135068				nr +
Unigene42376_All	372	8.58	0.82	1.86	2.28	1.57	0.97	0.00	0.00	0.00	-3.39E+00	3.02E-12	Down	-2.20E+00	1.35E-07	Down	-5.33E-01	4.90E-01		-1.23E+00	1.20E-01		null	null		null	null				Unigene42376_All//4.00E-07//TC147362				
Unigene42377_All	615	1.45	0.00	1.04	1.05	0.22	0.22	1.65	0.07	0.39	-1.05E+01	2.86E-05	Down	-4.77E-01	5.33E-01		-2.23E+00	1.79E-02		-2.26E+00	2.76E-02		-4.60E+00	3.67E-06	Down	-2.09E+00	1.52E-03		Unigene42377_All//gi|224102605|ref|XP_002312745.1|//2.00E-39//cytokinin biosynthetic isopentenyltransferase [Populus trichocarpa] >gi|222852565|gb|EEE90112.1| cytokinin biosynthetic isopentenyltransferase [Populus trichocarpa]	Unigene42377_All//5.00E-39//AT5G19040| IPT5; ATP binding / tRNA isopentenyltransferase/ transferase, transferring alkyl or aryl (other than methyl) groups			ko00908|Zeatin biosynthesis		nr -
Unigene42379_All	1125	0.37	0.00	0.09	1.64	0.58	1.61	3.65	0.89	2.02	-8.54E+00	1.05E-02		-1.97E+00	1.51E-01		-1.49E+00	1.22E-03		-2.89E-02	9.56E-01		-2.03E+00	3.98E-11	Down	-8.53E-01	1.04E-03		Unigene42379_All//gi|297824819|ref|XP_002880292.1|//5.00E-81//ribonuclease P [Arabidopsis lyrata subsp. lyrata] >gi|297326131|gb|EFH56551.1| ribonuclease P [Arabidopsis lyrata subsp. lyrata]	Unigene42379_All//4.00E-81//AT2G47300| ribonuclease P					nr +
Unigene4238_All	590	0.53	0.34	0.00	0.51	0.35	0.84	4.30	5.38	22.01	-6.31E-01	6.22E-01		-9.06E+00	4.90E-02		-5.33E-01	6.78E-01		7.33E-01	5.16E-01		3.24E-01	3.38E-01		2.36E+00	4.75E-41	Up	Unigene4238_All//gi|15240072|ref|NP_201474.1|//2.00E-07//zinc finger (C2H2 type) family protein [Arabidopsis thaliana] >gi|8843731|dbj|BAA97279.1| zinc finger protein [Arabidopsis thaliana] >gi|20466786|gb|AAM20710.1| zinc finger protein [Arabidopsis thaliana] >gi|23198204|gb|AAN15629.1| zinc finger protein [Arabidopsis thaliana]		Unigene4238_All//6.00E-38//TC158963				nr +
Unigene42385_All	1064	0.00	0.00	0.40	0.28	0.03	0.17	1.91	5.11	1.05	null	null		8.65E+00	1.38E-02		-3.12E+00	7.56E-02		-7.26E-01	6.38E-01		1.42E+00	4.55E-09	Up	-8.63E-01	2.63E-02		Unigene42385_All//gi|297822743|ref|XP_002879254.1|//1.00E-81//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325093|gb|EFH55513.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene42385_All//7.00E-83//AT2G30140| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene42385_All//0.00E+00//CO089649		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis		nr +
Unigene42386_All	496	2.22	0.00	0.86	5.83	10.00	9.38	0.85	0.17	0.88	-1.11E+01	1.95E-06	Down	-1.37E+00	5.32E-02		7.79E-01	2.70E-03		6.87E-01	1.42E-02		-2.34E+00	5.46E-02		5.17E-02	9.74E-01		Unigene42386_All//gi|22331291|ref|NP_189009.2|//6.00E-39//KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor [Arabidopsis thaliana] >gi|21703149|gb|AAM74514.1| AT3g23670/MDB19_16 [Arabidopsis thaliana] >gi|23268687|gb|AAN16470.1| phragmoplast-associated kinesin-related protein 1-like protein [Arabidopsis thaliana] >gi|23268689|gb|AAN16471.1| phragmoplast-associated kinesin-related protein 1-like protein [Arabidopsis thaliana]	Unigene42386_All//8.00E-22//AT3G23670| KINESIN-12B; microtubule motor/ plus-end-directed microtubule motor					nr -
Unigene42387_All	511	0.10	1.98	0.63	0.58	0.00	1.41	0.66	1.15	0.94	4.28E+00	7.16E-05	Up	2.61E+00	1.46E-01		-9.19E+00	2.01E-02		1.27E+00	1.56E-01		7.91E-01	3.74E-01		4.99E-01	6.12E-01				Unigene42387_All//9.00E-114//DR456498				
Unigene42389_All	471	6.33	0.86	4.41	0.42	0.58	0.00	0.45	0.00	0.93	-2.88E+00	6.29E-10	Down	-5.22E-01	1.72E-01		4.67E-01	8.16E-01		-8.72E+00	1.33E-01		-8.81E+00	7.43E-02		1.05E+00	2.98E-01		Unigene42389_All//gi|15226907|ref|NP_181038.1|//4.00E-68//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75100538|sp|Q82178.1|PP186_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g35130	Unigene42389_All//3.00E-69//AT2G35130| pentatricopeptide (PPR) repeat-containing protein	Unigene42389_All//0.00E+00//TC136642				nr -

Unigene42392_All	463	0.11	1.86	0.46	0.65	1.26	0.29	5.21	5.06	4.56	4.04E+00	4.20E-04	Up	2.03E+00	3.61E-01		9.70E-01	3.47E-01		-1.14E+00	4.57E-01		-4.22E-02	9.28E-01		-1.91E-01	6.09E-01			Unigene42392_All//8.00E-07//AT5G41080| glycerophosphoryl diester phosphodiesterase family protein	Unigene42392_All//3.00E-30//C0127462			
Unigene42396_All	361	21.31	40.14	43.66	14.90	15.93	24.65	38.88	53.26	37.41	9.14E-01	1.21E-09		1.04E+00	3.85E-12	Up	9.61E-02	7.73E-01		7.26E-01	1.35E-04		4.54E-01	5.18E-05		-5.57E-02	7.06E-01				Unigene42396_All//4.00E-118//TC134652			
Unigene42397_All	503	0.73	2.42	1.06	1.58	2.12	2.07	1.01	0.66	3.41	1.73E+00	8.94E-03		5.40E-01	6.10E-01		4.22E-01	5.72E-01		3.82E-01	6.27E-01		-6.02E-01	5.31E-01		1.76E+00	1.93E-04	Up	Unigene42397_All//gi|77745475|gb|ABB02636.1|//8.00E-07//RAD23-like [Solanum tuberosum]		Unigene42397_All//5.00E-38//TC136416		ko04141|Protein processing in endoplasmic reticulum//ko03420|Nucleotide excision repair		nr +
Unigene4240_All	962	27.85	26.34	21.20	42.67	30.57	26.29	19.07	10.60	4.76	-8.05E-02	5.07E-01		-3.93E-01	3.10E-04		-4.81E-01	2.19E-10		-6.99E-01	8.38E-18		-8.47E-01	5.63E-13		-2.00E+00	8.53E-48	Down	Unigene4240_All//gi|15217568|ref|NP_172434.1|//1.00E-104//ATRAB11C (ARABIDOPSIS RAB GTPASE 11C): GTP binding [Arabidopsis thaliana] >gi|3024516|sp|O04486.1|RAA2A_ARATH RecName: Full=Ras-related protein RABA2a; AltName: Full=Ras-related protein Rab11C >gi|21601157|gb|AAB60720.1| Strong similarity to A. thaliana ara-2 (gb|ATHARA2). ESTs gb|ATTS2483,gb|ATTS2484,gb|AA042159 come from this gene [Arabidopsis thaliana] >gi|2231303|gb|AAB61994.1| ras-related small GTPase [Arabidopsis thaliana] >gi|15010638|gb|AAK73978.1| At1g09630/F21M12_2 [Arabidopsis thaliana] >gi|22137284|gb|AAM91487.1| At1g09630/F21M12_2 [Arabidopsis thaliana]	Unigene4240_All//1.00E-101//AT1G09630| ATRAB11C (ARABIDOPSIS RAB GTPASE 11C): GTP binding	Unigene4240_All//0.00E+00//TC137934		ko04144|Endocytosis		nr +
Unigene42400_All	631	0.00	0.00	0.00	0.32	0.00	0.29	8.17	3.97	1.96	null	null		null	null		-8.30E+00	8.42E-02		-1.42E-01	9.34E-01		-1.04E+00	1.27E-05	Down	-2.06E+00	1.51E-14	Down			Unigene42400_All//7.00E-44//gi|195983984|gb|FL577607.1|FL577607			
Unigene42405_All	366	0.00	0.00	0.00	15.79	3.58	2.10	0.00	0.00	0.00	null	null		null	null		-2.14E+00	1.52E-16	Down	-2.91E+00	2.16E-20	Down	null	null		null	null			Unigene42405_All//gi|116309142|emb|CAH66244.1|//2.00E-06//OS1G0a0145C02.9 [Oryza sativa (indica cultivar-group)]	Unigene42405_All//3.00E-07//AT1G48120| calcineurin-like phosphoesterase family protein				nr -
Unigene42406_All	967	0.00	0.00	0.00	0.21	0.00	0.00	3.19	10.76	2.64	null	null		null	null		-7.69E+00	8.42E-02		-7.69E+00	1.33E-01		1.75E+00	2.60E-22	Up	-2.76E-01	3.96E-01				Unigene42406_All//8.00E-17//TC165956			
Unigene42408_All	583	0.00	0.00	0.37	0.17	0.35	0.00	8.56	41.37	16.74	null	null		8.51E+00	1.41E-01		1.05E+00	6.12E-01		-7.42E+00	3.99E-01		2.27E+00	5.15E-71	Up	9.68E-01	3.79E-09		Unigene42408_All//gi|225451659|ref|XP_002276291.1|//2.00E-35//PREDICTED: similar to protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Vitis vinifera]	Unigene42408_All//9.00E-29//AT5G13900| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene42408_All//0.00E+00//gi|109883119|gb|DW512089.1|DW512089			nr -
Unigene4241_All	2334	0.04	0.39	0.09	15.52	3.56	9.81	8.99	1.40	12.55	3.12E+00	1.14E-03		1.03E+00	5.91E-01		-2.13E+00	2.80E-101	Down	-6.61E-01	2.24E-14		-2.69E+00	3.73E-75	Down	4.82E-01	3.54E-08		Unigene4241_All//gi|115466358|ref|NP_001056778.1|//0.00E+00//Os06g0143700 [Oryza sativa Japonica Group] >gi|113594818|dbj|BAF18692.1| Os06g0143700 [Oryza sativa Japonica Group]	Unigene4241_All//0.00E+00//AT3G15990| SULTR3;4 (SULFATE TRANSPORTER 3;4): sulfate transmembrane transporter	Unigene4241_All//0.00E+00//DT467484			nr +
Unigene42412_All	311	96.23	43.66	104.10	23.71	28.79	18.59	0.00	0.00	0.00	-1.14E+00	3.23E-27	Down	1.14E-01	3.13E-01		2.80E-01	1.71E-01		-3.51E-01	1.23E-01		null	null		null	null			Unigene42412_All//gi|226358411|gb|AC051068.1|//2.00E-11//chloroplast chlorophyll A-B binding protein [Gossypium hirsutum]	Unigene42412_All//4.00E-12//AT2G40100| LHCB4.3 (light harvesting complex PSII): chlorophyll binding	Unigene42412_All//4.00E-53//TC167083		ko00196|Photosynthesis - antenna proteins		nr -
Unigene42414_All	450	0.58	1.13	0.47	3.21	2.75	0.70	1.32	1.86	1.15	9.54E-01	3.73E-01		-2.97E-01	8.32E-01		-2.21E-01	7.05E-01		-2.19E+00	3.74E-04	Down	4.98E-01	4.86E-01		-1.93E-01	7.94E-01			Unigene42414_All//gi|284026888|gb|ADB66335.1|//1.00E-18//CC-NBS-LRR protein [Quercus suber]	Unigene42414_All//4.00E-11//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene42414_All//1.00E-66//C0087346			nr +
Unigene42419_All	724	0.00	5.74	4.05	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.15E-23	Up	1.20E+01	3.52E-16	Up	null	null		null	null		null	null		null	null			Unigene42419_All//gi|297609605|ref|NP_001063421.2|//4.00E-23//Os09g0466900 [Oryza sativa Japonica Group] >gi|255678961|dbj|BAF25335.2| Os09g0466900 [Oryza sativa Japonica Group]	Unigene42419_All//4.00E-21//AT3G10660| CPK2 (CALMODULIN-DOMAIN PROTEIN KINASE CDPK ISOFORM 2): calmodulin-dependent protein kinase/ kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction	nr +
Unigene4242_All	1130	1.25	139.86	5.37	14.02	46.96	50.08	0.75	7.77	10.54	6.81E+00	0.00E+00	Up	2.10E+00	3.09E-13	Up	1.74E+00	1.93E-105	Up	1.84E+00	3.65E-110	Up	3.38E+00	1.15E-39	Up	3.82E+00	2.07E-60	Up	Unigene4242_All//gi|15218707|ref|NP_171811.1|//8.00E-33//ATRAB28 [Arabidopsis thaliana] >gi|4587565|gb|AAD25796.1|AC006550_4 Similar to rab28 protein gb|X59138 from Zea mays. EST gb|AA042774 comes from this gene [Arabidopsis thaliana]	Unigene4242_All//3.00E-28//AT1G03120| ATRAB28	Unigene4242_All//0.00E+00//gi|78334521|gb|DT554795.1|DT554795			nr +
Unigene42422_All	623	0.00	0.41	0.00	0.00	0.11	0.22	1.49	2.75	7.03	8.67E+00	7.86E-02		null	null		6.79E+00	6.09E-01		7.76E+00	3.11E-01		8.82E-01	4.98E-02		2.24E+00	1.56E-13	Up	Unigene42422_All//gi|224137458|ref|XP_002327131.1|//1.00E-06//predicted protein [Populus trichocarpa] >gi|222835446|gb|EEE73881.1| predicted protein [Populus trichocarpa]					nr -
Unigene42423_All	634	0.08	0.00	0.00	7.54	10.97	4.63	0.00	0.92	0.19	-6.37E+00	6.11E-01		-6.37E+00	6.23E-01		5.41E-01	1.26E-02		-7.04E-01	9.90E-03		9.85E+00	2.81E-04	Up	7.56E+00	2.43E-01		Unigene42423_All//gi|87240457|gb|ABD32315.1|//6.00E-29//CCT [Medicago truncatula]	Unigene42423_All//2.00E-23//AT5G59990| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot apex, stem, leaf whorl, flower; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: CCT domain (InterPro:IPR010402); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G41380.1); Has 918 Blast hits to 918 proteins in 64 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 885; Viruses - 0; Other Eukaryotes - 32 (source: NCBI BLink).	Unigene42423_All//5.00E-159//DT049048	Orphans			nr -
Unigene42426_All	610	0.43	1.50	0.00	3.27	2.09	5.55	81.93	126.48	215.46	1.80E+00	2.33E-02		-8.74E+00	8.56E-02		-6.45E-01	1.53E-01		7.66E-01	2.37E-02		6.27E-01	5.98E-31		1.40E+00	5.08E-200	Up	Unigene42426_All//gi|38016531|gb|AA007601.1|//9.00E-75//fiber quinone-oxidoreductase [Gossypium barbadense]	Unigene42426_All//6.00E-58//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene42426_All//0.00E+00//gi|31407653|gb|CD486688.1|CD486688				nr -
Unigene42427_All	383	2.05	9.53	2.78	4.55	6.47	3.54	19.65	22.48	14.35	2.22E+00	4.79E-09	Up	4.41E-01	5.22E-01		5.08E-01	2.29E-01		-3.64E-01	4.94E-01		1.94E-01	3.30E-01		-4.53E-01	1.42E-02				Unigene42427_All//2.00E-108//TC131248				
Unigene42428_All	952	0.11	0.21	0.34	0.84	1.16	0.33	1.73	0.61	10.34	9.54E-01	6.21E-01		1.61E+00	3.04E-01		4.67E-01	5.30E-01		-1.33E+00	1.06E-01		-1.49E+00	1.71E-03		2.58E+00	1.27E-34	Up							
Unigene4243_All	1227	9.72	6.28	12.67	14.66	5.39	4.79	69.67	25.14	26.07	-6.31E-01	1.13E-04		3.82E-01	1.04E-02		-1.44E+00	4.16E-29	Down	-1.61E+00	4.62E-30	Down	-1.47E+00	1.87E-138	Down	-1.42E+00	7.13E-135	Down	Unigene4243_All//gi|239909311|gb|ACS32301.1|//1.00E-153//cinnamoyl-CoA reductase [Jatropha curcas]	Unigene4243_All//3.00E-137//AT1G68540| oxidoreductase family protein	Unigene4243_All//0.00E+00//TC138041		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene42430_All	844	0.00	0.00	0.00	0.00	0.00	0.00	5.71	10.30	0.94	null	null		null	null		null	null		null	null		8.51E-01	1.32E-06		-2.60E+00	9.23E-18	Down							
Unigene42431_All	288	0.55	1.23	0.55	2.08	2.99	0.78	3.38	0.15	0.97	1.18E+00	3.72E-01		2.55E-02	1.00E+00		5.26E-01	5.45E-01		-1.40E+00	1.58E-01		-4.54E+00	6.92E-06	Down	-1.80E+00	5.53E-03								
Unigene42434_All	423	0.25	0.48	0.00	0.00	0.16	0.32	6.30	11.56	56.51	9.54E-01	6.21E-01		-7.95E+00	3.92E-01		7.35E+00	6.09E-01		8.32E+00	3.11E-01		8.77E-01	3.08E-04		3.17E+00	9.73E-103	Up	Unigene42434_All//gi|224097678|ref|XP_002334595.1|//3.00E-12//predicted protein [Populus trichocarpa] >gi|222873667|gb|EEF10798.1| predicted protein [Populus trichocarpa]		Unigene42434_All//2.00E-114//TC151238				nr +
Unigene42435_All	287	0.18	4.59	1.48	0.00	0.36	1.10	0.74	2.77	1.67	4.65E+00	1.91E-06	Up	3.03E+00	5.73E-02		8.49E+00	4.56E-01		1.01E+01	4.07E-02		1.91E+00	1.37E-02		1.18E+00	2.18E-01								
Unigene42436_All	952	0.00	10.22	6.60	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	9.96E-56	Up	1.27E+01	4.73E-35	Up	null	null		null	null		null	null		null	null		Unigene42436_All//gi|301102726|ref|XP_002900450.1|//2.00E-59//acyl-CoA desaturase 1 [Phytophthora infestans T30-4] >gi|262102191|gb|EEY60243.1| acyl-CoA desaturase 1 [Phytophthora infestans T30-4]	Unigene42436_All//8.00E-22//AT1G06080| ADS1 (DELTA 9 DESATURASE 1): oxidoreductase			ko01040|Biosynthesis of unsaturated fatty acids	nr +
Unigene42439_All	360	3.49	0.99	0.30	4.98	4.59	2.76	0.47	0.93	0.33	-1.82E+00	5.22E-03		-3.56E+00	4.96E-05	Down	-1.18E-01	8.38E-01		-8.52E-01	8.34E-02		9.83E-01	4.24E-01		-5.01E-01	7.46E-01		Unigene42439_All//gi|224132326|ref|XP_002328241.1|//1.00E-24//transcription factor E2F [Populus trichocarpa] >gi|222837756|gb|EEE76121.1| transcription factor E2F [Populus trichocarpa]	Unigene42439_All//6.00E-09//AT5G22220| E2F1; DNA binding / protein binding / transcription factor	Unigene42439_All//1.00E-93//C0114585	E2F-DP			nr -
Unigene4244_All	3053	0.82	0.41	0.30	3.70	3.82	2.99	7.37	2.01	3.78	-9.87E-01	1.38E-02		-1.47E+00	7.51E-04	Down	4.59E-02	8.23E-01		-3.10E-01	8.06E-02		-1.87E+00	7.32E-52	Down	-9.61E-01	7.87E-20		Unigene4244_All//gi|145338627|ref|NP_188362.2|//0.00E+00//POK1 (PHRAGMOPLAST ORIENTING KINESIN 1): ATP binding / microtubule motor [Arabidopsis thaliana] >gi|89160907|gb|ABD62996.1| kinesin POK1 [Arabidopsis thaliana]	Unigene4244_All//0.00E+00//AT3G17360| POK1 (PHRAGMOPLAST ORIENTING KINESIN 1): ATP binding / microtubule motor	Unigene4244_All//0.00E+00//ES792964				nr -
Unigene42440_All	1424	0.00	0.00	0.00	0.07	0.07	0.44	6.38	0.76	2.07	null	null		null	null		5.06E-02	9.66E-01		2.67E+00	1.83E-02		-3.06E+00	1.09E-37	Down	-1.62E+00	2.82E-18	Down	Unigene42440_All//gi|145333011|ref|NP_001078371.1|//2.00E-18//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene42440_All//6.00E-19//AT4G10720| ankyrin repeat family protein	Unigene42440_All//0.00E+00//ES843168				nr +
Unigene42443_All	422	4.59	1.08	1.14	2.60	2.86	1.07	1.50	0.20	0.76	-2.09E+00	7.30E-05	Down	-2.01E+00	2.05E-04	Down	1.37E-01	8.38E-01		-1.28E+00	5.68E-02		-2.92E+00	4.19E-03		-9.93E-01	2.02E-01								
Unigene42445_All	407	8.10	1.99	7.85	9.55	8.80	4.88	2.08	1.54	0.29	-2.02E+00	1.72E-07	Down	-4.50E-02	9.07E-01		-1.18E-01	7.52E-01		-9.67E-01	1.62E-03		-4.32E-01	5.47E-01		-2.82E+00	5.38E-04	Down			Unigene42445_All//3.00E-45//TC170247				
Unigene42446_All	588	0.00	14.65	4.53	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	2.69E-49	Up	1.21E+01	1.07E-14	Up	null	null		null	null		null	null		null	null		Unigene42446_All//sp|Q7M4F0|CUD9_SCHGR//9.00E-12//Endocuticle structural glycoprotein Sgkbd-9 OS=Schistocerca gregaria PE=1 SV=1					swissprot +
Unigene42447_All	724	0.07	0.77	0.29	0.76	1.09	1.06	0.41	1.85	0.50	3.41E+00	1.24E-02		2.02E+00	3.61E-01		5.32E-01	5.40E-01		4.87E-01	5.90E-01		2.18E+00	2.12E-04	Up	2.77E-01	7.87E-01								
Unigene42449_All	419	3.12	0.12	2.54	1.19	2.38	0.43	0.61	0.40	0.00	-4.69E+00	1.63E-06	Down	-2.97E-01	6.25E-01		1.00E+00	1.65E-01		-1.46E+00	1.93E-01		-6.02E-01	6.48E-01		-9.24E+00	3.04E-02		Unigene42449_All//gi|195637980|gb|ACG38458.1|//4.00E-51//polyphosphoinositide binding protein [Zea mays]	Unigene42449_All//3.00E-46//AT5G63060| transporter					nr -
Unigene4245_All	1042	2.71	1.07	0.66	4.02	3.87	2.12	4.46	2.29	2.71	-1.34E+00	5.14E-04	Down	-2.03E+00	3.46E-06	Down	-5.46E-02	8.58E-01		-9.19E-01	1.75E-03		-9.65E-01	1.21E-04		-7.18E-01	2.89E-03		Unigene4245_All//gi|18396813|ref|NP_564310.1|//1.00E-95//SYP61 (SYNTAXIN OF PLANTS 61): SNAP receptor [Arabidopsis thaliana] >gi|28380156|sp|Q946Y7.1|SYP61_ARATH RecName: Full=Syntaxin-61; Short=AtSYP61; AltName: Full=Osmotic stress-sensitive mutant 1 >gi|16041650|gb|AAK40222.2|AF355754_1 syntaxin of plants 61 [Arabidopsis thaliana]	Unigene4245_All//3.00E-70//AT1G28490| SYP61 (SYNTAXIN OF PLANTS 61): SNAP receptor	Unigene4245_All//0.00E+00//TC168331		ko04130|SNARE interactions in vesicular transport		nr -

Unigene42452_All	703	0.00	6.78	3.64	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	3.82E-27	Up	1.18E+01	4.20E-14	Up	null	null		null	null		null	null		null	null		Unigene42452_All//sp|Q9BSE4|HERP2_HUMAN//1.00E-08//Homocysteine-responsive endoplasmic reticulum-resident ubiquitin-like domain member 2 protein OS=Homo sapiens GN=HERPUD2 PE=1 SV=1						swissprot -
Unigene42453_All	257	5.09	3.94	4.97	5.43	5.23	4.39	3.13	0.33	2.95	-3.68E-01	5.31E-01		-3.35E-02	9.74E-01		-5.46E-02	9.11E-01		-3.05E-01	6.38E-01		-3.26E+00	4.48E-04	Down	-8.58E-02	9.05E-01		Unigene42453_All//gi|22328963|ref|NP_567765.2|//9.00E-21//thioredoxin family protein [Arabidopsis thaliana]	Unigene42453_All//3.00E-22//AT4G27080| thioredoxin family protein	Unigene42453_All//6.00E-95//AIT29113				nr -
Unigene42454_All	338	0.00	7.35	6.14	0.00	0.61	0.67	0.13	0.00	0.00	1.28E+01	3.98E-14	Up	1.26E+01	1.92E-11	Up	9.26E+00	1.57E-01		9.38E+00	1.19E-01		-6.97E+00	6.57E-01		-6.97E+00	6.12E-01		Unigene42454_All//gi|116222207|gb|ABJ80967.1|//5.00E-51//alpha tubulin [Entosiphon sulcatum]	Unigene42454_All//1.00E-50//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene42454_All//3.00E-11//DR460752		ko04145|Phagosome		nr +
Unigene42455_All	430	0.00	2.36	0.12	0.00	0.80	1.26	0.10	0.39	1.11	1.12E+01	7.26E-06	Up	6.95E+00	6.35E-01		9.65E+00	3.01E-02		1.03E+01	2.45E-03		1.98E+00	3.79E-01		3.50E+00	7.29E-03										
Unigene42456_All	536	0.00	0.00	0.00	0.19	0.00	0.00	5.13	34.54	48.68	null	null		null	null		-7.54E+00	3.12E-01		-7.54E+00	3.99E-01		2.75E+00	5.38E-68	Up	3.25E+00	8.51E-115	Up			Unigene42456_All//6.00E-07//DT465993					
Unigene42459_All	1229	0.00	0.00	0.00	0.00	0.00	0.00	2.44	1.70	7.00	null	null		null	null		null	null		null	null		-5.23E-01	1.12E-01		1.52E+00	1.19E-15	Up	Unigene42459_All//gi|149392583|gb|ABR26094.1|//3.00E-09//retrotransposon protein [Oryza sativa Indica Group]		Unigene42459_All//1.00E-90//DW479423				nr -
Unigene42460_All	234	2.91	2.60	0.00	3.19	1.77	0.39	1.08	0.54	0.34	-1.62E-01	8.32E-01		-1.15E+01	7.64E-04	Down	-8.55E-01	2.95E-01		-3.05E+00	3.33E-03		-1.02E+00	4.95E-01		-1.67E+00	2.56E-01				Unigene42460_All//6.00E-73//CO093194					
Unigene42461_All	692	0.00	0.00	0.00	0.00	0.10	0.00	9.29	2.78	2.53	null	null		null	null		6.64E+00	6.09E-01		null	null		-1.74E+00	5.76E-14	Down	-1.87E+00	6.80E-16	Down	Unigene42461_All//gi|71040679|gb|AAZ30288.1|//1.00E-47//disease resistance-responsive family protein [Arachis hypogaea]	Unigene42461_All//9.00E-43//AT5G42500| disease resistance-responsive family protein	Unigene42461_All//9.00E-47//DR454882				nr -
Unigene42462_All	1024	0.00	0.00	0.00	0.00	0.00	0.00	4.46	0.86	1.67	null	null		null	null		null	null		null	null		-2.38E+00	8.42E-15	Down	-1.41E+00	5.39E-08	Down	Unigene42462_All//gi|223452532|gb|ACM89593.1|//1.00E-156//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene42462_All//5.00E-133//AT1G34110| leucine-rich repeat transmembrane protein kinase, putative	Unigene42462_All//3.00E-10//TC163946				nr +
Unigene42464_All	314	0.33	1.94	3.39	1.11	1.75	0.72	1.62	1.20	1.78	2.54E+00	2.46E-02		3.35E+00	3.36E-04	Up	6.60E-01	5.44E-01		-6.27E-01	6.21E-01		-4.32E-01	6.18E-01		1.37E-01	8.76E-01										
Unigene42466_All	364	0.00	5.29	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.73E-11	Up	1.07E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene42466_All//sp|Q80X13|IF4G3_MOUSE//2.00E-15//Eukaryotic translation initiation factor 4 gamma 3 OS=Mus musculus GN=Eif4g3 PE=1 SV=2						swissprot -
Unigene42473_All	279	96.39	40.14	58.21	127.48	157.61	169.32	120.02	63.82	68.83	-1.26E+00	9.19E-29	Down	-7.28E-01	2.05E-11		3.06E-01	5.33E-05		4.10E-01	4.35E-08		-9.11E-01	6.69E-26		-8.02E-01	1.21E-21		Unigene42473_All//gi|15824574|gb|AAL09401.1|AF307336_1//9.00E-37//ribosomal protein [Petunia x hybrida]	Unigene42473_All//8.00E-37//AT1G67430| 60S ribosomal protein L17 (RPL17B)	Unigene42473_All//2.00E-156//TC163376		ko03010|Ribosome		nr +
Unigene42475_All	526	0.00	0.00	0.00	0.00	0.00	0.00	0.72	2.46	2.88	null	null		null	null		null	null		null	null		1.77E+00	1.84E-03		1.99E+00	1.35E-04	Up	Unigene42475_All//gi|224141031|ref|XP_002323878.1|//9.00E-53//AP2/EBP domain-containing transcription factor [Populus trichocarpa] >gi|222866880|gb|EEF04011.1| AP2/EBP domain-containing transcription factor [Populus trichocarpa]	Unigene42475_All//9.00E-19//AT5G19790| RAP2.11 (related to AP2 11); DNA binding / transcription factor		AP2-EREBP			nr +
Unigene42479_All	628	0.00	0.00	0.00	0.00	0.00	0.00	2.22	3.06	0.00	null	null		null	null		null	null		null	null		4.63E-01	2.89E-01		-1.11E+01	2.40E-10	Down									ESTscan +
Unigene4248_All	2006	2.35	1.64	1.25	6.83	3.95	2.72	14.23	5.54	5.10	-5.16E-01	6.53E-02		-9.12E-01	1.70E-03		-7.91E-01	1.45E-08		-1.33E+00	2.86E-17	Down	-1.36E+00	1.38E-41	Down	-1.48E+00	1.69E-48	Down	Unigene4248_All//gi|15241426|ref|NP_199229.1|//1.00E-115//NUC (nutcracker); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|75333753|sp|Q9FFH3.1|NUC_ARATH RecName: Full=Zinc finger protein NUTCRACKER >gi|14335046|gb|AAK59787.1| AT5g41160/MLN1_8 [Arabidopsis thaliana] >gi|27363364|gb|AAO11601.1| At5g41160/MLN1_8 [Arabidopsis thaliana]	Unigene4248_All//3.00E-116//AT5G41160| NUC (nutcracker); nucleic acid binding / transcription factor/ zinc ion binding	Unigene4248_All//0.00E+00//TC134372	C2H2			nr -
Unigene42481_All	288	0.36	13.72	4.44	0.00	0.00	0.00	0.00	0.00	0.00	5.24E+00	1.21E-19	Up	3.61E+00	3.41E-05	Up	null	null		null	null		null	null		null	null		Unigene42481_All//sp|Q9Z1P6|NDUA7_MOUSE//9.00E-09//NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Mus musculus GN=Ndufa7 PE=1 SV=3						swissprot -
Unigene42485_All	321	1.30	0.00	0.00	3.26	0.11	0.84	1.32	2.34	0.25	-1.03E+01	1.05E-02		-1.03E+01	1.56E-02		-4.92E+00	1.16E-06	Down	-1.95E+00	7.52E-03		8.31E-01	2.64E-01		-2.41E+00	3.93E-02										
Unigene42488_All	315	0.00	2.57	1.69	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	9.38E-05	Up	1.07E+01	4.04E-03		null	null		null	null		null	null		null	null		Unigene42488_All//gi|297723373|ref|NP_001174050.1|//6.00E-35//Os04g0566500 [Oryza sativa Japonica Group] >gi|255675697|dbj|BAH92778.1| Os04g0566500 [Oryza sativa Japonica Group]	Unigene42488_All//8.00E-35//AT1G48410| AGO1 (ARGONAUTE 1); endoribonuclease/ miRNA binding / protein binding / siRNA binding					nr +
Unigene42490_All	212	104.39	89.87	63.05	113.96	109.15	131.66	450.92	209.77	188.67	-2.16E-01	7.89E-02		-7.28E-01	1.64E-09		-6.22E-02	6.43E-01		2.08E-01	5.77E-02		-1.10E+00	3.34E-99	Down	-1.26E+00	2.87E-125	Down			Unigene42490_All//1.00E-116//TC166472					
Unigene42493_All	414	0.00	0.49	4.89	0.00	0.00	0.00	0.00	0.00	0.00	8.94E+00	1.36E-01		1.23E+01	3.79E-11	Up	null	null		null	null		null	null		null	null		Unigene42493_All//gi|148467570|gb|AB069705.2|//2.00E-43//aquaporin PIP2 [Prunus humilis]	Unigene42493_All//1.00E-41//AT4G35100| PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel	Unigene42493_All//2.00E-46//TC166797				nr -
Unigene42497_All	279	0.38	0.36	3.63	0.36	0.99	0.16	0.00	0.00	0.00	-4.65E-02	9.88E-01		3.27E+00	5.92E-04	Up	1.47E+00	4.20E-01		-1.14E+00	6.76E-01		null	null		null	null										ESTscan -
Unigene4250_All	1623	1.84	5.90	2.89	9.02	8.81	11.33	7.27	1.73	2.90	1.68E+00	6.12E-16	Up	6.52E-01	2.48E-02		-3.54E-02	8.27E-01		3.28E-01	1.27E-02		-2.07E+00	1.90E-31	Down	-1.33E+00	1.40E-17	Down	Unigene4250_All//gi|6056382|gb|AAF02846.1|AC009894_17//3.00E-86//unknown protein [Arabidopsis thaliana] >gi|8778317|gb|AAF79326.1|AC002304_19 F14J16.33 [Arabidopsis thaliana] >gi|44681358|gb|AAS47619.1| At1g56020 [Arabidopsis thaliana] >gi|45773898|gb|AAS76753.1| At1g56020 [Arabidopsis thaliana]	Unigene4250_All//7.00E-30//AT1G56020| unknown protein	Unigene4250_All//0.00E+00//TC166924				nr +
Unigene42500_All	395	0.00	10.90	5.93	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.56E-24	Up	1.25E+01	6.41E-13	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene42511_All	298	2.46	0.34	1.25	4.01	0.81	0.30	0.28	0.00	0.94	-2.85E+00	6.26E-03		-9.75E-01	2.64E-01		-2.31E+00	3.71E-04	Down	-3.73E+00	1.43E-05	Down	-8.15E+00	4.03E-01		1.72E+00	2.30E-01		Unigene42511_All//gi|124360204|gb|ABN08217.1|//4.00E-25//Tetratricopeptide-like helical [Medicago truncatula]	Unigene42511_All//2.00E-18//AT5G52630| MEF1 (MITOCHONDRIAL RNA EDITING FACTOR 1)					nr -
Unigene42512_All	275	0.00	0.37	0.00	0.18	0.00	0.16	4.00	2.89	10.87	8.53E+00	3.86E-01		null	null		-7.50E+00	5.55E-01		-1.41E-01	9.52E-01		-4.69E-01	4.31E-01		1.44E+00	1.32E-05	Up			Unigene42512_All//5.00E-52//ES790450					
Unigene42513_All	405	1.94	3.38	5.65	0.00	0.00	0.22	0.00	0.31	0.00	8.02E-01	1.60E-01		1.54E+00	8.54E-04	Up	null	null		7.80E+00	4.76E-01		8.27E+00	2.40E-01		null	null		Unigene42513_All//gi|121501699|gb|ABM55240.1|//1.00E-09//retrotransposon protein [Beta vulgaris]		Unigene42513_All//9.00E-21//FL577111				nr +
Unigene42514_All	269	2.14	0.57	1.78	3.33	1.02	0.34	0.63	1.24	1.33	-1.92E+00	7.00E-02		-2.64E-01	7.67E-01		-1.70E+00	1.98E-02		-3.31E+00	5.80E-04	Down	9.83E-01	4.24E-01		1.08E+00	3.50E-01										ESTscan -
Unigene42516_All	292	2.33	0.00	1.46	0.00	0.47	0.31	1.30	0.29	0.27	-1.12E+01	4.10E-04	Down	-6.75E-01	4.41E-01		8.88E+00	3.18E-01		8.27E+00	4.76E-01		-2.19E+00	8.75E-02		-2.26E+00	6.49E-02		Unigene42516_All//gi|11547332|ref|NP_001060259.1|//2.00E-06//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]						nr -
Unigene4252_All	1077	1.26	0.80	0.35	2.04	1.15	1.68	2.28	0.62	1.33	-6.59E-01	2.44E-01		-1.87E+00	4.39E-03		-8.22E-01	4.62E-02		-2.79E-01	5.68E-01		-1.87E+00	2.52E-06	Down	-7.74E-01	2.60E-02		Unigene4252_All//gi|87162918|gb|ABO28713.1|//7.00E-86//Pentatricopeptide repeat [Medicago truncatula]	Unigene4252_All//1.00E-60//AT1G80150| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene42520_All	200	48.92	35.98	54.58	54.30	45.97	53.52	21.77	20.06	9.56	-4.43E-01	1.62E-02		1.58E-01	4.10E-01		-2.40E-01	1.91E-01		-2.08E-02	9.34E-01		-1.18E-01	6.76E-01		-1.19E+00	4.66E-06	Down			Unigene42520_All//2.00E-109//TC155713					
Unigene42522_All	337	0.00	3.61	3.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.47E-07	Up	1.16E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene42522_All//gi|75306047|sp|Q94469.1|ALFC2_ARATH//9.00E-60//RecName: Full=Probable fructose-bisphosphate aldolase 2, chloroplastic; Flags: Precursor >gi|16226653|gb|AAL16224.1|AF428455_1 AT4g38970/F19H22_70 [Arabidopsis thaliana]	Unigene42522_All//4.00E-61//AT4G38970| fructose-bisphosphate aldolase, putative	Unigene42522_All//2.00E-49//gi|48741919|gb|C0072438.1|C0072438		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene42525_All	286	0.00	2.48	2.42	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.32E-04	Up	1.12E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene42525_All//sp|P12110|CO6A2_HUMAN//3.00E-48//Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4						swissprot +
Unigene42527_All	565	0.00	28.88	11.50	0.09	0.06	0.00	0.00	0.00	0.00	1.48E+01	9.20E-94	Up	1.35E+01	2.96E-36	Up	-5.34E-01	8.25E-01		-6.46E+00	6.35E-01		null	null		null	null		Unigene42527_All//gi|300261259|gb|EFJ45473.1|//2.00E-59//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene42527_All//2.00E-60//AT5G60670| 60S ribosomal protein L12 (RPL12C)			ko03010|Ribosome		nr +
Unigene4253_All	2137	0.20	0.28	1.00	5.90	1.29	1.97	40.14	9.31	4.55	5.38E-01	5.63E-01		2.35E+00	1.17E-05	Up	-2.19E+00	8.21E-37	Down	-1.59E+00	1.14E-20	Down	-2.11E+00	3.60E-229	Down	-3.14E+00	0.00E+00	Down	Unigene4253_All//gi|16226063|gb|AAL16065.1|AF420239_1//1.00E-110//S-adenosyl-L-methionine decarboxylase [Dendrobium crumenatum]	Unigene4253_All//1.00E-89//AT3G02470| SAMDC (S-ADENOSYLMETHIONINE DECARBOXYLASE); adenosylmethionine decarboxylase	Unigene4253_All//0.00E+00//gi|78334200|gb|DT554474.1|DT554474		ko00270|Cysteine and methionine metabolism//ko00330|Arginine and proline metabolism		nr +
Unigene42535_All	502	0.00	0.00	0.00	0.00	0.00	0.00	1.68	1.08	0.00	null	null		null	null		null	null		null	null		-6.38E-01	3.70E-01		-1.07E+01	2.21E-06	Down	Unigene42535_All//gi|115485513|ref|NP_001067900.1|//1.00E-69//Os11g0482000 [Oryza sativa Japonica Group] >gi|113645122|dbj|BAF28263.1| Os11g0482000 [Oryza sativa Japonica Group]	Unigene42535_All//1.00E-69//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	Unigene42535_All//6.00E-13//ES832899		ko03010|Ribosome		nr +
Unigene4254_All	1144	53.01	147.40	100.68	66.45	87.65	90.84	95.06	100.69	70.48	1.48E+00	6.79E-223	Up	9.26E-01	6.55E-71		4.00E-01	2.57E-17		4.51E-01	2.94E-20		8.31E-02	8.54E-02		-4.32E-01	4.87E-23		Unigene4254_All//gi|124360327|gb|ABN08340.1|//5.00E-25//ZIM [Medicago truncatula]	Unigene4254_All//2.00E-14//AT5G20900| JAZ12 (JASMONATE-ZIM-DOMAIN PROTEIN 12)	Unigene4254_All//0.00E+00//gi|164278226|gb|ES848085.1|ES848085	Tify	ko04626|Plant-pathogen interaction		nr -
Unigene42542_All	210	0.00	43.19	19.27	0.00	0.00	0.00	0.00	0.00	0.00	1.54E+01	6.32E-52	Up	1.42E+01	1.92E-22	Up	null	null		null	null		null	null		null	null		Unigene42542_All//gi|24473796|gb|AAL91663.1|//9.00E-10//60s acidic ribosomal protein [Prunus dulcis] >gi|111013714|gb|ABR03379.1| 60S acidic ribosomal protein [Prunus dulcis]				ko03010|Ribosome		nr +
Unigene42544_All	256	9.81	2.97	1.66	0.97	3.09	0.00	0.66	0.16	0.62	-1.72E+00	6.59E-05	Down	-2.56E+00	3.86E-07	Down	1.67E+00	5.20E-02		-9.93E+00	7.33E-02		-2.02E+00	3.67E-01		-8.57E-02	9.65E-01		Unigene42544_All//gi|297794569|ref|XP_002865169.1|//1.00E-13//BHLH071 [Arabidopsis lyrata subsp. lyrata] >gi|297311004|gb|EFH11428.1| BHLH071 [Arabidopsis lyrata subsp. lyrata]	Unigene42544_All//1.00E-13//AT5G46690| bHLH071 (beta HLH protein 71); DNA binding / transcription factor		bHLH			nr -
Unigene4255_All	710	0.00	0.00	0.23	24.84	21.92	10.11	10.24	10.07	5.67	null	null		7.81E+00	2.39E-01		-1.80E-01	2.14E-01		-1.30E+00	2.47E-21	Down	-2.50E-02	9.24E-01		-8.54E-01	6.55E-06		Unigene4255_All//gi|160420034|dbj|BAF93480.1|//2.00E-85//class-I knotted1-like homeobox protein IBKN3 [Ipomoea batatas]	Unigene4255_All//2.00E-55//AT4G08150| KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor	Unigene4255_All//0.00E+00//gi|164241819|gb|ES809030.1|ES809030	HB			nr -
Unigene42550_All	451	0.00	3.60	0.71	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.97E-09	Up	9.47E+00	4.51E-02		null	null		null	null		null	null		null	null		Unigene42550_All//sp|P49920|CBG_SHEEP//6.00E-07//Corticosteroid-binding globulin OS=Ovis aries GN=SERPINA6 PE=2 SV=1						swissprot -

Unigene42551_All	376	0.00	3.91	1.56	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.11E-08	Up	1.06E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene42551_All//sp|Q7M4F2|CUD8_SCHGR/2.00E-09//Endocuticle structural glycoprotein SgAbd-8 OS=Schistocerca gregaria PE=1 SV=1							swissprot -
Unigene42555_All	468	0.00	0.00	0.00	0.00	0.15	0.00	5.15	4.11	1.11	null	null		null	null		7.20E+00	6.09E-01		null	null		-3.26E-01	3.96E-01		-2.22E+00	7.72E-08	Down	Unigene42555_All//gi|11994591|dbj|BAB02646.1//6.00E-13//Ac transposase-like protein [Arabidopsis thaliana]		Unigene42555_All//1.00E-134//TC156042				nr -
Unigene42556_All	396	0.00	34.93	18.56	0.25	0.00	0.00	0.00	0.00	0.00	1.51E+01	2.03E-79	Up	1.42E+01	4.45E-41	Up	-7.98E+00	3.12E-01		-7.98E+00	3.99E-01		null	null		null	null		Unigene42556_All//gi|255071745|ref|XP_002499547.1|//3.00E-36//ribosomal protein L37e [Micromonas sp. RCC299] >gi|226514809|gb|ACO60805.1| ribosomal protein L37e [Micromonas sp. RCC299]	Unigene42556_All//1.00E-29//AT1G52300| 60S ribosomal protein L37 (RPL37B)			ko03010|Ribosome		nr -
Unigene42558_All	282	0.00	3.05	2.45	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.95E-05	Up	1.13E+01	6.16E-04	Up	null	null		null	null		null	null		null	null										
Unigene4256_All	1482	0.00	0.00	0.11	12.97	10.46	6.31	6.13	4.15	2.98	null	null		6.75E+00	2.39E-01		-3.11E-01	1.12E-02		-1.04E+00	1.72E-16	Down	-5.65E-01	8.88E-04		-1.04E+00	1.32E-09	Down	Unigene4256_All//gi|3023974|sp|Q41330.1|KN1_SOLLC//1.00E-102//RecName: Full=Homeotic protein knotted-1; Short=TKN1 >gi|1256575|gb|AAC49251.1| Knotted 1 (Tkn1) [Solanum lycopersicum] >gi|1588258|prf||2208273A Knotted-1 gene	Unigene4256_All//2.00E-40//AT4G08150| KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor	Unigene4256_All//0.00E+00//gi|164241819|gb|ES809030.1|ES809030	HB			nr -
Unigene42566_All	593	0.53	7.35	0.63	0.50	2.09	0.00	2.21	1.13	4.90	3.80E+00	7.16E-18	Up	2.48E-01	8.23E-01		2.05E+00	2.00E-03		-8.98E+00	3.99E-02		-9.71E-01	6.64E-02		1.15E+00	4.00E-04	Up			Unigene42566_All//6.00E-180//ES796239					
Unigene42568_All	276	0.57	5.51	3.09	1.26	0.87	0.65	0.00	0.00	0.43	3.28E+00	6.57E-06	Up	2.44E+00	9.09E-03		-5.33E-01	6.46E-01		-9.49E-01	4.81E-01		null	null		8.76E+00	2.43E-01				Unigene42568_All//1.00E-31//DW493972					
Unigene42570_All	221	0.47	0.92	1.45	4.73	0.93	2.04	2.10	2.27	1.44	9.54E-01	6.21E-01		1.61E+00	3.04E-01		-2.34E+00	9.24E-04	Down	-1.21E+00	7.81E-02		1.09E-01	9.14E-01		-5.45E-01	5.66E-01										
Unigene42571_All	224	46.01	11.08	10.94	35.36	36.89	18.15	29.63	14.55	6.22	-2.05E+00	2.54E-22	Down	-2.07E+00	1.24E-21	Down	6.13E-02	8.31E-01		-9.62E-01	2.22E-06		-1.03E+00	7.26E-07	Down	-2.25E+00	1.49E-20	Down	Unigene42571_All//gi|195616516|gb|ACG30088.1|//3.00E-13//histone H2A [Zea mays]	Unigene42571_All//2.00E-07//AT5G02560| HTA12; DNA binding	Unigene42571_All//4.00E-52//TC176756				nr -
Unigene42573_All	333	5.81	5.48	1.60	31.71	54.19	45.16	472.45	397.25	234.25	-8.58E-02	8.47E-01		-1.86E+00	4.64E-04	Down	7.73E-01	2.53E-10		5.10E-01	3.22E-04		-2.50E-01	5.32E-12		-1.01E+00	3.13E-145	Down	Unigene42573_All//gi|119888006|gb|ABM05955.1|//7.00E-15//proline-rich protein [Gossypium hirsutum]		Unigene42573_All//1.00E-164//TC173613				nr +
Unigene42575_All	435	0.00	7.34	3.06	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	3.64E-18	Up	1.16E+01	2.40E-07	Up	null	null		null	null		null	null		null	null		Unigene42575_All//gi|298710190|emb|CBJ26265.1|//7.00E-10//Glycosyltransferase, family GT8 [Ectocarpus siliculosus]	Unigene42575_All//5.00E-07//AT5G18480| PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups					nr +
Unigene42577_All	346	0.00	0.00	0.00	4.18	1.69	0.00	0.00	0.00	0.23	null	null		null	null		-1.30E+00	1.41E-02		-1.20E+01	4.97E-09	Down	null	null		7.85E+00	4.04E-01		Unigene42577_All//gi|11762174|gb|AAG40365.1|AF325013_1/4.00E-21//At1g17620 [Arabidopsis thaliana]	Unigene42577_All//2.00E-22//AT1G17620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G11890.1); Has 539 Blast hits to 538 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 539; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene42577_All//3.00E-162//BE054286				nr -
Unigene42584_All	475	0.22	0.64	0.11	0.10	0.94	1.05	0.71	0.35	2.94	1.54E+00	3.23E-01		-9.75E-01	7.20E-01		3.17E+00	3.95E-02		3.32E+00	2.31E-02		-1.02E+00	3.99E-01		2.04E+00	2.08E-04	Up	Unigene42584_All//gi|112280265|gb|ABI14669.1|//2.00E-42//ubiquitin-protein ligase [Aegiceras corniculatum]	Unigene42584_All//5.00E-17//AT1G55860| UPL1 (UBIQUITIN-PROTEIN LIGASE 1); ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis		nr +
Unigene42597_All	293	0.00	0.69	0.36	1.19	1.76	0.31	7.36	2.57	1.22	9.43E+00	1.36E-01		8.51E+00	3.98E-01		5.67E-01	6.04E-01		-1.95E+00	1.96E-01		-1.52E+00	2.06E-04	Down	-2.59E+00	2.46E-08	Down			Unigene42597_All//5.00E-108//gi|73859936|gb|DT462675.1|DT462675					
Unigene42599_All	257	0.00	3.15	0.00	0.39	2.28	1.41	0.00	0.49	0.78	1.16E+01	9.38E-05	Up	null	null		2.55E+00	2.84E-02		1.86E+00	2.19E-01		8.93E+00	2.40E-01		9.60E+00	7.89E-02				Unigene42599_All//9.00E-26//TC175684					
Unigene426_All	2509	98.24	55.27	95.55	5.38	7.53	4.46	0.34	0.20	1.02	-8.30E-01	1.53E-129		-4.01E-02	3.21E-01		4.86E-01	4.73E-05		-2.69E-01	9.88E-02		-7.54E-01	2.78E-01		1.59E+00	1.57E-05	Up	Unigene426_All//gi|115441603|ref|NP_001045081.1|//1.00E-128//Os01g0896500 [Oryza sativa Japonica Group] >gi|113534612|dbj|BAF06995.1| Os01g0896500 [Oryza sativa Japonica Group]	Unigene426_All//2.00E-136//AT3G59780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleus, chloroplast; EXPRESSED IN: guard cell; BEST Arabidopsis thaliana protein match is: CaS (Calcium sensing receptor) (TAIR:AT5G23060.1); Has 1338 Blast hits to 316 proteins in 95 species: Archae - 0; Bacteria - 274; Metazoa - 264; Fungi - 88; Plants - 42; Viruses - 4; Other Eukaryotes - 666 (source: NCBI BLink).	Unigene426_All//0.00E+00//TC161996				nr -
Unigene4260_All	1483	22.79	10.52	9.44	13.84	12.70	18.27	6.98	11.19	10.21	-1.11E+00	1.37E-29	Down	-1.27E+00	6.12E-35	Down	-1.24E-01	3.87E-01		4.01E-01	9.00E-05		6.80E-01	2.60E-08		5.47E-01	1.20E-05		Unigene4260_All//gi|297793895|ref|XP_002864832.1|//1.00E-108//EMB2759 [Arabidopsis lyrata subsp. lyrata] >gi|297310667|gb|EFH41091.1| EMB2759 [Arabidopsis lyrata subsp. lyrata]	Unigene4260_All//9.00E-104//AT5G63050| EMB2759 (embryo defective 2759)	Unigene4260_All//0.00E+00//DW514153				nr +
Unigene42601_All	407	0.13	0.00	0.00	3.55	0.76	0.33	1.66	0.62	0.00	-7.01E+00	6.11E-01		-7.01E+00	6.23E-01		-2.22E+00	1.08E-04	Down	-3.41E+00	3.16E-06	Down	-1.43E+00	7.83E-02		-1.07E+01	3.56E-05	Down			Unigene42601_All//5.00E-07//DW226904					
Unigene42602_All	251	0.00	3.43	5.09	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.95E-05	Up	1.23E+01	4.68E-07	Up	null	null		null	null		null	null		null	null		Unigene42602_All//gi|110738762|dbj|BAF01305.1|//8.00E-24//cytochrome c1 precursor [Arabidopsis thaliana]	Unigene42602_All//3.00E-25//AT5G40810| cytochrome c1, putative			ko00190|Oxidative phosphorylation		nr -
Unigene42609_All	673	0.16	0.00	0.32	4.15	6.40	2.21	2.51	2.98	6.45	-7.28E+00	3.71E-01		1.03E+00	5.91E-01		6.26E-01	3.01E-02		-9.04E-01	1.58E-02		2.46E-01	5.97E-01		1.36E+00	3.47E-07	Up	Unigene42609_All//gi|115484971|ref|NP_001067629.1|//1.00E-10//Os11g0252400 [Oryza sativa Japonica Group] >gi|62733020|gb|AAX95137.1| expressed protein [Oryza sativa Japonica Group] >gi|62733021|gb|AAX95138.1| expressed protein [Oryza sativa Japonica Group] >gi|77549631|gb|ABA92428.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|77549632|gb|ABA92429.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113644851|dbj|BAF27992.1| Os11g0252400 [Oryza sativa Japonica Group]		Unigene42609_All//9.00E-161//gi|109890353|gb|DW519317.1|DW519317				nr +
Unigene4261_All	971	75.44	28.91	33.34	88.14	84.23	120.05	101.59	46.53	41.97	-1.38E+00	1.15E-88	Down	-1.18E+00	8.53E-67	Down	-6.55E-02	3.25E-01		4.46E-01	3.53E-22		-1.13E+00	1.11E-105	Down	-1.28E+00	3.74E-132	Down	Unigene4261_All//gi|257219572|gb|ACV50439.1|//1.00E-114//ribosomal protein L15 [Jatropha curcas]	Unigene4261_All//9.00E-95//AT4G16720| 60S ribosomal protein L15 (RPL15A)	Unigene4261_All//0.00E+00//gi|164285628|gb|ES818851.1|ES818851		ko03010|Ribosome		nr +
Unigene42611_All	537	0.00	0.00	0.00	0.00	0.00	0.00	1.81	2.96	0.00	null	null		null	null		null	null		null	null		7.08E-01	1.35E-01		-1.08E+01	2.72E-07	Down	Unigene42611_All//gi|20139942|sp|Q9M3V8.1|RS6_ASPOF//1.00E-37//RecName: Full=40S ribosomal protein S6 >gi|7649387|emb|CAB89081.1| S6 ribosomal protein [Asparagus officinalis]	Unigene42611_All//3.00E-29//AT5G10360| EMB3010 (embryo defective 3010); structural constituent of ribosome			ko03010|Ribosome		nr -
Unigene42612_All	1242	0.00	13.26	4.76	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.22E-94	Up	1.22E+01	6.04E-33	Up	null	null		null	null		null	null		null	null		Unigene42612_All//gi|224009464|ref|XP_002293690.1|//1.00E-130//eukaryotic translation initiation factor 4A [Thalassiosira pseudonana CCMP1335] >gi|220970362|gb|EED88699.1| eukaryotic translation initiation factor 4A [Thalassiosira pseudonana CCMP1335]	Unigene42612_All//8.00E-118//AT3G13920| EIF4A1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 4A1); ATP-dependent helicase/ translation initiation factor	Unigene42612_All//3.00E-14//DT048646				nr +
Unigene42617_All	389	0.27	1.56	0.82	0.51	0.89	1.39	1.96	0.32	0.20	2.54E+00	2.46E-02		1.61E+00	3.04E-01		7.89E-01	5.96E-01		1.44E+00	1.92E-01		-2.60E+00	2.81E-03		-3.26E+00	4.48E-04	Down								
Unigene4262_All	984	2.39	2.52	2.38	2.89	2.76	1.19	2.79	0.89	1.82	7.66E-02	8.47E-01		-7.00E-03	1.00E+00		-6.18E-02	8.68E-01		-1.27E+00	6.82E-04	Down	-1.65E+00	5.56E-06	Down	-6.16E-01	5.89E-02		Unigene4262_All//gi|115468898|ref|NP_001058048.1|//2.00E-48//Os06g0609800 [Oryza sativa Japonica Group] >gi|113596088|dbj|BAF19962.1| Os06g0609800 [Oryza sativa Japonica Group]	Unigene4262_All//8.00E-41//AT5G50350| unknown protein	Unigene4262_All//6.00E-95//TC171286				nr +
Unigene42625_All	366	3.29	2.49	7.27	1.22	6.30	3.08	2.08	2.28	1.52	-4.00E-01	5.15E-01		1.15E+00	5.09E-03		2.36E+00	5.79E-07	Up	1.33E+00	4.76E-02		1.35E-01	8.42E-01		-4.48E-01	5.31E-01		Unigene42625_All//gi|115439933|ref|NP_001044246.1|//6.00E-26//Os01g0749200 [Oryza sativa Japonica Group] >gi|113533777|dbj|BAF06160.1| Os01g0749200 [Oryza sativa Japonica Group]	Unigene42625_All//3.00E-26//AT1G78630| emb1473 (embryo defective 1473); structural constituent of ribosome	Unigene42625_All//2.00E-95//TC142785		ko03010|Ribosome		nr -
Unigene42627_All	346	6.05	1.46	4.16	25.91	19.21	9.66	9.90	4.83	10.82	-2.05E+00	4.33E-05	Down	-5.42E-01	2.44E-01		-4.32E-01	2.03E-02		-1.42E+00	9.28E-13	Down	-1.03E+00	5.63E-04	Down	1.29E-01	6.56E-01		Unigene42627_All//gi|224092698|ref|XP_002309702.1|//1.00E-22//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222855678|gb|EEE93225.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene42627_All//4.00E-07//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene42627_All//1.00E-102//TC145238		ko04626|Plant-pathogen interaction		nr -
Unigene42628_All	363	0.00	0.00	0.00	0.00	0.00	0.00	9.32	18.31	41.81	null	null		null	null		null	null		null	null		9.74E-01	2.27E-06		2.17E+00	3.04E-43	Up	Unigene42628_All//gi|224054180|ref|XP_002298131.1|//2.00E-16//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845389|gb|EEE82936.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene42628_All//2.00E-12//AT4G03070| AOP1; oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene42628_All//1.00E-81//ES817500				nr +

Unigene4263_All	1282	7.22	1.98	3.99	13.87	12.06	14.48	7.26	6.19	3.67	-1.87E+00	7.33E-18	Down	-8.57E-01	1.36E-05		-2.02E-01	1.52E-01		6.18E-02	6.72E-01		-2.28E-01	2.19E-01		-9.85E-01	4.80E-09		Unigene4263_All//gi|297831660|ref|XP_002883712.1|//1.00E-105//eukaryotic translation initiation factor 2B family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329552|gb|EFH59971.1| eukaryotic translation initiation factor 2B family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4263_All//2.00E-97//AT2G05830| eukaryotic translation initiation factor 2B family protein / eIF-2B family protein	Unigene4263_All//0.00E+00//gi|21091371|gb|BQ403684.1|BQ403684				nr +
Unigene42632_All	254	0.00	0.00	1.26	0.00	0.00	0.71	17.98	30.61	79.52	null	null		1.03E+01	4.51E-02		null	null		9.47E+00	1.94E-01		7.68E-01	3.71E-05		2.15E+00	1.33E-56	Up	Unigene42632_All//gi|198449163|gb|ACH88751.1|//3.00E-21//WRKY DNA binding protein [Fragaria x ananassa]	Unigene42632_All//5.00E-18//AT5G13080| WRKY75; transcription factor	Unigene42632_All//1.00E-15//gi|73865567|gb|DT468305.1|DT468305	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene42635_All	514	0.20	0.00	0.00	0.29	0.54	0.53	1.89	0.33	0.16	-7.67E+00	3.71E-01		-7.67E+00	3.92E-01		8.83E-01	5.95E-01		8.59E-01	6.31E-01		-2.54E+00	6.41E-04	Down	-3.61E+00	2.14E-05	Down	Unigene42635_All//gi|297609225|ref|NP_001062856.2|//4.00E-43//Os09g0321200 [Oryza sativa Japonica Group] >gi|255678772|dbj|BAF24770.2| Os09g0321200 [Oryza sativa Japonica Group]	Unigene42635_All//2.00E-06//AT1G30100| NCED5 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 5); 9-cis-epoxycarotenoid dioxygenase			ko00906|Carotenoid biosynthesis		nr +
Unigene42636_All	276	0.76	1.65	9.26	1.26	1.25	0.16	0.00	0.00	0.00	1.12E+00	3.28E-01		3.61E+00	6.27E-10	Up	-1.80E-02	9.58E-01		-2.95E+00	8.30E-02		null	null		null	null									
Unigene42637_All	290	0.72	0.70	5.33	0.34	0.83	1.87	0.15	1.73	0.41	-4.63E-02	9.88E-01		2.88E+00	3.60E-05	Up	1.27E+00	5.32E-01		2.44E+00	4.41E-02		3.57E+00	6.53E-03		1.50E+00	5.58E-01					Unigene42637_All//2.00E-24//TC166260				
Unigene42640_All	844	0.00	0.00	0.00	0.00	0.04	0.27	3.11	1.39	0.66	null	null		null	null		5.35E+00	8.29E-01		8.06E+00	1.19E-01		-1.16E+00	9.86E-04	Down	-2.23E+00	1.61E-08	Down				Unigene42640_All//3.00E-99//FL576589				
Unigene42641_All	231	0.23	1.75	3.92	0.86	0.89	0.39	0.00	0.00	0.00	2.95E+00	5.91E-02		4.11E+00	3.91E-04	Up	5.22E-02	9.88E-01		-1.14E+00	5.69E-01		null	null		null	null									
Unigene42644_All	346	0.00	4.39	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.10E-08	Up	9.85E+00	4.51E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene42646_All	240	0.00	3.17	1.78	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	1.08E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene42646_All//gi|3777559|gb|AAC64934.1|//2.00E-18//collagen-like [Griffithsia japonica]								nr +
Unigene42650_All	473	0.00	0.00	0.00	0.00	0.00	0.00	1.34	1.50	0.00	null	null		null	null		null	null		null	null		1.64E-01	8.24E-01		-1.04E+01	7.11E-05	Down	Unigene42650_All//gi|297853126|ref|XP_002894444.1|//5.00E-34//mucilage-modified 4 [Arabidopsis lyrata subsp. lyrata] >gi|297340286|gb|EFH70703.1| mucilage-modified 4 [Arabidopsis lyrata subsp. lyrata]	Unigene42650_All//4.00E-35//AT1G53500| MUM4 (MUCILAGE-MODIFIED 4); UDP-4-keto-6-deoxy-glucose-3,5-epimerase/ UDP-4-keto-rhamnose-4-keto-reductase/ UDP-L-rhamnose synthase/ UDP-glucose 4,6-dehydratase/ catalytic			ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene42651_All	297	0.00	0.51	0.54	0.50	0.58	1.37	0.28	2.39	3.22	9.00E+00	2.35E-01		9.07E+00	2.39E-01		2.04E-01	9.50E-01		1.44E+00	2.82E-01		3.07E+00	1.67E-03		3.50E+00	4.29E-05	Up								
Unigene42654_All	333	49.96	106.21	76.28	2.39	4.34	11.26	0.13	0.00	0.00	1.09E+00	1.23E-29	Up	6.10E-01	3.98E-08		8.60E-01	1.31E-01		2.23E+00	8.51E-10	Up	-6.99E+00	6.56E-01		-6.99E+00	6.12E-01		Unigene42654_All//gi|114050563|gb|ABI49431.1|//2.00E-24//At3g16120 [Arabidopsis thaliana]	Unigene42654_All//5.00E-38//AT4G27360| dynein light chain, putative	Unigene42654_All//1.00E-13//TC178388				nr +
Unigene42658_All	205	0.00	3.21	4.42	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.25E-04	Up	1.21E+01	4.71E-05	Up	null	null		null	null		null	null		null	null		Unigene42658_All//sp|Q9V3U9|SLMO_DROME//1.00E-07//Protein slowmo OS=Drosophila melanogaster GN=slmo PE=1 SV=1								swissprot -
Unigene42661_All	349	0.60	0.00	0.15	0.29	0.20	0.26	1.82	1.80	8.22	-9.23E+00	1.22E-01		-1.97E+00	3.81E-01		-5.33E-01	8.16E-01		-1.42E-01	9.50E-01		-1.66E-02	1.02E+00		2.18E+00	7.38E-09	Up								
Unigene42662_All	379	0.28	0.27	0.00	0.00	0.00	0.00	1.23	8.60	24.28	-4.62E-02	9.88E-01		-8.11E+00	3.92E-01		null	null		null	null		2.81E+00	9.22E-13	Up	4.31E+00	5.74E-51	Up	Unigene42662_All//gi|297823575|ref|XP_002879670.1|//5.00E-32//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325509|gb|EFH55929.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene42662_All//1.00E-29//AT2G37430| zinc finger (C2H2 type) family protein (ZAT11)		C2H2			nr -
Unigene42663_All	797	0.07	0.00	0.00	0.13	0.17	0.00	3.34	2.20	0.15	-6.04E+00	6.11E-01		-6.04E+00	6.23E-01		4.67E-01	8.76E-01		-6.97E+00	3.99E-01		-6.02E-01	8.47E-02		-4.48E+00	7.97E-16	Down	Unigene42663_All//gi|18410575|ref|NP_565081.1|//2.00E-32//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana]	Unigene42663_All//3.00E-34//AT1G74280| hydrolase, alpha/beta fold family protein					nr +
Unigene42667_All	313	0.00	2.75	0.34	0.32	1.54	1.30	0.81	0.67	1.91	1.14E+01	4.94E-05	Up	8.41E+00	3.98E-01		2.27E+00	7.83E-02		2.03E+00	1.49E-01		-2.80E-01	8.28E-01		1.24E+00	1.39E-01		Unigene42667_All//gi|42566124|ref|NP_191727.2|//2.00E-41//lipase class 3 family protein [Arabidopsis thaliana] >gi|209529781|gb|ACI49785.1| At3g61680 [Arabidopsis thaliana]	Unigene42667_All//8.00E-43//AT3G61680| lipase class 3 family protein					nr +
Unigene4267_All	703	58.94	17.01	24.01	18.28	10.24	13.23	27.79	34.07	32.98	-1.79E+00	2.72E-73	Down	-1.30E+00	5.13E-44	Down	-8.37E-01	7.62E-09		-4.66E-01	2.77E-03		2.94E-01	3.80E-03		2.47E-01	1.52E-02		Unigene4267_All//gi|297824277|ref|XP_002880021.1|//8.00E-09//transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297325860|gb|EFH56280.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene4267_All//2.00E-09//AT2G43060| transcription factor	Unigene4267_All//0.00E+00//TC149797	bHLH			nr +
Unigene42672_All	314	0.00	3.07	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.38E-05	Up	1.06E+01	7.48E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene42676_All	240	0.00	0.00	0.00	0.21	0.00	0.38	253.86	50.85	69.22	null	null		null	null		-7.70E+00	5.55E-01		8.59E-01	7.94E-01		-2.32E+00	1.77E-183	Down	-1.87E+00	1.03E-143	Down								ESTscan -
Unigene42678_All	230	1.59	0.22	0.00	3.25	2.25	0.00	0.55	0.91	0.17	-2.85E+00	7.80E-02		-1.06E+01	2.78E-02		-5.33E-01	5.26E-01		-1.17E+01	9.80E-05	Down	7.20E-01	6.32E-01		-1.67E+00	4.77E-01									
Unigene42682_All	387	0.00	0.13	0.00	0.13	0.18	1.75	0.55	0.00	2.68	7.03E+00	6.16E-01		null	null		4.68E-01	9.58E-01		3.77E+00	2.97E-03		-9.09E+00	7.43E-02		2.29E+00	7.17E-04	Up	Unigene42682_All//gi|4559334|gb|AAD22996.1|//2.00E-37//expressed protein [Arabidopsis thaliana]	Unigene42682_All//2.00E-46//AT2G34070| unknown protein	Unigene42682_All//3.00E-39//TC133530				nr +
Unigene42684_All	255	3.69	4.57	6.89	1.76	2.03	1.59	1.99	7.21	3.91	3.07E-01	6.13E-01		9.00E-01	8.21E-02		2.04E-01	8.59E-01		-1.41E-01	9.00E-01		1.86E+00	7.25E-05	Up	9.73E-01	1.06E-01		Unigene42684_All//gi|145334271|ref|NP_001078516.1|//4.00E-15//histone H3.2 [Arabidopsis thaliana]	Unigene42684_All//2.00E-16//AT4G40030| histone H3.2	Unigene42684_All//3.00E-35//TC140747				nr -
Unigene42687_All	311	0.00	1.30	2.74	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	1.36E-02		1.14E+01	9.02E-05	Up	null	null		null	null		null	null		null	null		Unigene42687_All//sp|P12110|CO6A2_HUMAN//8.00E-56//Collagen alpha-2(VI) chain OS=Homo sapiens GN=COL6A2 PE=1 SV=4								swissprot -
Unigene4269_All	1190	16.27	3.62	6.49	42.40	46.15	48.28	11.94	7.20	6.70	-2.17E+00	2.74E-44	Down	-1.33E+00	1.46E-21	Down	1.22E-01	1.16E-01		1.87E-01	9.37E-03		-7.30E-01	4.36E-08		-8.34E-01	2.59E-10		Unigene4269_All//gi|30691739|ref|NP_198216.2|//6.00E-74//AN3 (ANGUSTIFOLIA 3); protein binding / transcription coactivator [Arabidopsis thaliana] >gi|21539890|gb|AAM52881.1| GRF1-interacting factor 1 [Arabidopsis thaliana]	Unigene4269_All//1.00E-37//AT5G28640| AN3 (ANGUSTIFOLIA 3); protein binding / transcription coactivator	Unigene4269_All//0.00E+00//TC142006		ko03040|Spliceosome		nr +
Unigene42694_All	251	0.00	5.45	0.21	0.79	1.23	0.18	0.34	0.17	0.48	1.24E+01	7.80E-08	Up	7.73E+00	6.35E-01		6.37E-01	6.95E-01		-2.14E+00	3.47E-01		-1.02E+00	7.24E-01		4.99E-01	8.07E-01					Unigene42694_All//3.00E-07//ES810920				
Unigene42695_All	474	0.00	0.00	0.00	0.00	0.00	0.00	0.54	1.76	5.38	null	null		null	null		null	null		null	null		1.72E+00	1.94E-02		3.33E+00	4.73E-12	Up				Unigene42695_All//7.00E-96//TC174042				
Unigene42696_All	422	41.04	15.49	19.05	77.79	69.85	94.71	134.35	40.71	63.82	-1.41E+00	5.45E-22	Down	-1.11E+00	1.06E-14	Down	-1.55E-01	1.24E-01		2.84E-01	7.55E-04		-1.72E+00	1.24E-115	Down	-1.07E+00	3.31E-58	Down	Unigene42696_All//gi|115475908|ref|NP_001061550.1|//3.00E-57//Os08g0326400 [Oryza sativa Japonica Group] >gi|115480049|ref|NP_001063618.1| Os09g0507800 [Oryza sativa Japonica Group] >gi|548774|sp|P35685.1|RL7A_ORYSJ RecName: Full=60S ribosomal protein L7a >gi|303855|dbj|BAA02156.1| ribosomal protein L7A [Oryza sativa Japonica Group] >gi|38423963|dbj|BAD01672.1| 60S ribosomal protein L7A [Oryza sativa Japonica Group] >gi|38837005|dbj|BAD03264.1| 60S ribosomal protein L7A [Oryza sativa Japonica Group] >gi|113623519|dbj|BAF23464.1| Os08g0326400 [Oryza sativa Japonica Group] >gi|113631851|dbj|BAF25532.1| Os09g0507800 [Oryza sativa Japonica Group]	Unigene42696_All//4.00E-32//AT3G62870| 60S ribosomal protein L7A (RPL7aB)	Unigene42696_All//0.00E+00//TC129988		ko03010|Ribosome		nr +
Unigene42698_All	527	0.00	1.54	0.00	0.19	0.20	0.09	0.56	1.11	2.19	1.06E+01	9.38E-05	Up	null	null		5.25E-02	9.66E-01		-1.14E+00	6.76E-01		9.83E-01	2.59E-01		1.96E+00	1.21E-03									
Unigene42699_All	352	3.57	0.00	0.00	3.82	7.73	5.77	1.56	1.90	3.17	-1.18E+01	2.54E-07	Down	-1.18E+01	7.11E-07	Down	1.02E+00	6.73E-03		5.96E-01	2.13E-01		2.83E-01	7.18E-01		1.02E+00	6.87E-02		Unigene42699_All//gi|22128587|gb|AAN52339.1|//6.00E-20//fertility restorer [Petunia x hybrida]	Unigene42699_All//3.00E-18//AT1G62590| pentatricopeptide (PPR) repeat-containing protein	Unigene42699_All//5.00E-133//TC144858				nr -
Unigene4270_All	3752	0.79	0.66	1.04	17.21	13.18	8.87	7.29	3.63	2.06	-2.65E-01	4.79E-01		3.82E-01	2.47E-01		-3.85E-01	9.30E-11		-9.56E-01	4.64E-47		-1.01E+00	5.81E-25	Down	-1.82E+00	1.46E-62	Down	Unigene4270_All//gi|15227816|ref|NP_179917.1|//1.00E-173//transport protein-related [Arabidopsis thaliana] >gi|75206690|sp|Q9SLN1.1|FPP7_ARATH RecName: Full=Filament-like plant protein 7; Short=AtFPP7	Unigene4270_All//8.00E-121//AT2G23360| transport protein-related	Unigene4270_All//0.00E+00//TC163259				nr -
Unigene42701_All	526	0.60	0.39	0.51	2.08	0.39	2.06	1.29	0.72	1.21	-6.31E-01	6.22E-01		-2.38E-01	8.50E-01		-2.41E+00	5.06E-04	Down	-1.59E-02	9.71E-01		-8.47E-01	2.88E-01		-8.59E-02	9.15E-01		Unigene42701_All//gi|15223099|ref|NP_172286.1|//2.00E-61//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75174869|sp|Q9LN01.1|PPR21_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g08070 >gi|8778839|gb|AAF79838.1|AC026875_18 T6D22.15 [Arabidopsis thaliana]	Unigene42701_All//1.00E-62//AT1G08070| pentatricopeptide (PPR) repeat-containing protein	Unigene42701_All//0.00E+00//TC178144				nr +
Unigene42709_All	287	0.00	0.53	0.00	2.78	1.32	0.16	0.29	0.00	0.28	9.05E+00	2.35E-01		null	null		-1.07E+00	1.62E-01		-4.14E+00	4.13E-04	Down	-8.20E+00	4.03E-01		-8.57E-02	9.71E-01									
Unigene4271_All	869	3.19	10.20	3.00	6.76	6.30	4.47	6.13	6.88	6.69	1.68E+00	9.68E-15	Up	-8.78E-02	8.19E-01		-1.02E-01	7.31E-01		-5.98E-01	1.41E-02		1.66E-01	5.10E-01		1.27E-01	5.92E-01					Unigene4271_All//1.00E-120//DW517596				
Unigene42710_All	383	1.37	1.85	1.39	1.43	4.86	1.89	0.22	0.11	0.52	4.39E-01	6.16E-01		2.53E-02	9.99E-01		1.76E+00	4.06E-04	Up	3.99E-01	6.51E-01		-1.02E+00	7.24E-01		1.24E+00	4.68E-01									
Unigene42711_All	236	0.22	0.00	0.00	5.28	1.02	0.38	2.51	0.00	0.17	-7.79E+00	6.11E-01		-7.79E+00	6.23E-01		-2.37E+00	2.03E-04	Down	-3.79E+00	7.61E-06	Down	-1.13E+01	2.39E-04	Down	-3.89E+00	1.09E-03									
Unigene42713_All	231	3.40	0.00	1.15	3.23	1.94	0.98	1.46	0.36	1.21	-1.17E+01	1.09E-04	Down	-1.56E+00	8.00E-02		-7.39E-01	3.57E-01		-1.73E+00	5.00E-02		-2.02E+00	1.36E-01		-2.78E-01	7.81E-01					Unigene42713_All//3.00E-07//EV496604				ESTscan -
Unigene42718_All	232	1.13	1.31	1.84	4.51	1.34	0.19	0.00	0.00	0.00	2.17E-01	8.64E-01		7.04E-01	5.54E-01		-1.76E+00	8.43E-03		-4.53E+00	1.60E-05	Down	null	null		null	null					Unigene42718_All//5.00E-61//TC177021				
Unigene42719_All	210	1.74	0.00	0.51	1.90	1.15	0.22	4.43	2.19	0.76	-1.08E+01	1.96E-02		-1.78E+00	2.34E-01		-7.25E-01	5.46E-01		-3.14E+00	4.88E-02		-1.02E+00	1.21E-01		-2.55E+00	5.79E-04	Down								
Unigene42720_All	248	0.00	4.70	1.72	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.05E-06	Up	1.07E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene42720_All//sp|Q9FP0U1|TOM7_HUMAN//3.00E-10//Mitochondrial import receptor subunit TOM7 homolog OS=Homo sapiens GN=TOMM7 PE=1 SV=1								swissprot -
Unigene42724_All	402	0.39	1.26	0.93	2.35	1.71	1.80	3.58	7.90	5.15	1.69E+00	1.34E-01		1.25E+00	3.66E-01		-4.59E-01	5.36E-01		-3.89E-01	6.28E-01		1.14E+00	2.98E-04	Up	5.27E-01	1.80E-01					Unigene42724_All//2.00E-49//TC136172				
Unigene4273_All	1136	4.47	0.31	1.69	6.01	4.61	6.84	17.94	5.22	4.14	-3.84E+00	3.77E-21	Down	-1.40E+00	1.30E-06	Down	-3.83E-01	8.78E-02		1.87E-01	4.47E-01		-1.78E+00	6.01E-44	Down	-2.12E+00	6.81E-57	Down	Unigene4273_All//gi|224129860|ref|XP_002320689.1|//1.00E-118//porin/voltage-dependent anion-selective channel protein [Populus trichocarpa] >gi|222861462|gb|EEE99004.1| porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	Unigene4273_All//2.00E-96//AT5G67500| VDAC2 (VOLTAGE DEPENDENT ANION CHANNEL 2); voltage-gated anion channel	Unigene4273_All//0.00E+00//TC138740				nr +

Unigene42731_All	403	0.00	2.77	1.85	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.00E-06	Up	1.09E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene42731_All//gi|115482988|ref|NP_001065087.1|//1.00E-25//Os10g0521000 [Oryza sativa Japonica Group] >gi|31433112|gb|AAP54665.1| Trehalase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639696|dbj|BAF27001.1| Os10g0521000 [Oryza sativa Japonica Group]	Unigene42731_All//2.00E-23//AT4G24040| TRE1 (TREHALASE 1); alpha,alpha-trehalase/ trehalase		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0015927	nr -
Unigene42732_All	365	0.00	1.39	0.73	0.00	0.57	1.11	2.20	6.87	6.00	1.04E+01	4.04E-03		9.51E+00	8.01E-02		9.14E+00	1.57E-01		1.01E+01	1.36E-02		1.64E+00	1.71E-05	Up	1.45E+00	2.38E-04	Up			Unigene42732_All//6.00E-68//DR453992				
Unigene42734_All	384	0.00	0.00	0.00	1.30	0.72	2.00	2.09	0.98	0.10	null	null		null	null		-8.55E-01	4.07E-01		6.24E-01	4.81E-01		-1.09E+00	1.29E-01		-4.33E+00	4.54E-05	Down	Unigene42734_All//gi|75216243|sp|Q9ZQ13.1|GDL40_ARATH//2.00E-39//RecName: Full=GDSL esterase/lipase At2g27360; AltName: Full=Extracellular lipase At2g27360; Flags: Precursor	Unigene42734_All//9.00E-41//AT2G27360| lipase, putative	Unigene42734_All//4.00E-63//gi|84171111|gb|DR459759.1|DR459759			GO:0016788//GO:0043231	nr +
Unigene42736_All	603	0.00	1.43	0.00	0.00	0.34	0.07	0.56	1.04	2.97	1.05E+01	4.94E-05	Up	null	null		8.42E+00	1.57E-01		6.23E+00	6.95E-01		8.90E-01	2.88E-01		2.41E+00	1.87E-06	Up			Unigene42736_All//0.00E+00//ES801346				
Unigene42739_All	298	0.00	1.53	4.11	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	7.43E-03		1.20E+01	9.12E-07	Up	null	null		null	null		null	null		null	null		Unigene42739_All//sp|Q5RAH0|LAP4A_PONAB//1.00E-38//Lysosomal-associated transmembrane protein 4A OS=Pongo abelii GN=LAPTM4A PE=2 SV=1						swissprot -
Unigene42740_All	522	0.40	0.00	0.00	0.86	0.00	0.26	2.02	1.28	6.87	-8.65E+00	1.22E-01		-8.65E+00	1.45E-01		-9.75E+00	2.00E-03		-1.73E+00	1.61E-01		-6.61E-01	2.78E-01		1.76E+00	1.88E-08	Up	Unigene42740_All//gi|115445023|ref|NP_001046291.1|//2.00E-29//Os02g0215700 [Oryza sativa Japonica Group] >gi|113535822|dbj|BAF08205.1| Os02g0215700 [Oryza sativa Japonica Group]	Unigene42740_All//6.00E-29//AT3G47580| leucine-rich repeat transmembrane protein kinase, putative	Unigene42740_All//1.00E-60//TC143249	ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152//GO:0016020//GO:0016491	nr -
Unigene42742_All	266	0.00	0.00	0.00	0.00	1.04	0.51	2.07	0.00	0.15	null	null		null	null		1.00E+01	7.01E-02		8.99E+00	3.11E-01		-1.10E+01	4.61E-04	Down	-3.79E+00	2.03E-03		Unigene42742_All//gi|20135538|gb|AAL25839.1|//3.00E-06//lipid transfer precursor protein [Hevea brasiliensis]		Unigene42742_All//5.00E-126//TC173012				nr -
Unigene42751_All	319	0.49	0.00	0.00	1.41	0.86	0.28	2.52	0.39	0.25	-8.94E+00	2.15E-01		-8.94E+00	2.44E-01		-7.03E-01	5.30E-01		-2.31E+00	7.81E-02		-2.68E+00	1.67E-03		-3.33E+00	2.47E-04	Down			Unigene42751_All//8.00E-178//gi|164324906|gb|ES806523.1|ES806523				
Unigene42752_All	317	0.00	0.00	0.00	16.81	1.74	2.71	1.20	0.00	0.00	null	null		null	null		-3.27E+00	1.50E-24	Down	-2.63E+00	5.66E-17	Down	-1.02E+01	6.18E-03		-1.02E+01	4.19E-03			Unigene42752_All//1.00E-05//AT3G45160| unknown protein	Unigene42752_All//4.00E-133//TC172420				
Unigene4276_All	793	2.90	3.58	1.95	23.31	21.67	23.24	16.26	11.02	5.28	3.02E-01	4.24E-01		-5.76E-01	1.97E-01		-1.05E-01	5.09E-01		-4.30E-03	9.72E-01		-5.62E-01	5.67E-05		-1.62E+00	1.46E-25	Down	Unigene4276_All//gi|15239619|ref|NP_197398.1|//9.00E-66//AWPM-19-like membrane family protein [Arabidopsis thaliana] >gi|21536663|gb|AAM60995.1| plasma membrane associated protein-like [Arabidopsis thaliana]	Unigene4276_All//8.00E-40//AT5G18970| AWPM-19-like membrane family protein	Unigene4276_All//0.00E+00//DW497266				nr +
Unigene42760_All	447	0.00	1.59	0.00	0.00	0.00	0.00	0.57	6.36	0.00	1.06E+01	3.32E-04	Up	null	null		null	null		null	null		3.49E+00	1.40E-13	Up	-9.15E+00	3.04E-02		Unigene42760_All//gi|4836473|gb|AAQ30454.1|AF123257_1//8.00E-39//17.6 kD class I small heat shock protein [Solanum lycopersicum] >gi|29547791|gb|AAN64315.1| type I small heat shock protein 17.6 kDa isoform [Solanum lycopersicum]	Unigene42760_All//4.00E-30//AT2G29500| 17.6 kDa class I small heat shock protein (HSP17.6B-CI)	Unigene42760_All//0.00E+00//TC157878				nr +
Unigene42762_All	253	8.48	0.60	3.79	5.71	3.95	4.82	0.67	0.00	0.00	-3.82E+00	3.43E-09	Down	-1.16E+00	1.29E-02		-5.33E-01	3.32E-01		-2.45E-01	6.84E-01		-9.38E+00	1.34E-01		-9.38E+00	1.08E-01				Unigene42762_All//5.00E-55//TC161602				
Unigene42765_All	358	0.00	2.12	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.76E-04	Up	1.05E+01	4.04E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene4277_All	822	94.58	122.17	147.05	226.71	255.63	220.82	238.61	211.67	93.68	3.69E-01	6.40E-13		6.37E-01	4.25E-39		1.73E-01	1.07E-07		-3.80E-02	4.28E-01		-1.73E-01	1.17E-07		-1.35E+00	7.37E-286	Down	Unigene4277_All//gi|73761685|gb|AAZ83342.1|//1.00E-132//ACC oxidase 1 [Gossypium hirsutum]	Unigene4277_All//2.00E-97//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene4277_All//0.00E+00//TC132920	ko00270|Cysteine and methionine metabolism		nr -
Unigene42770_All	360	0.00	0.42	0.00	3.46	0.29	1.51	1.06	6.85	1.33	8.72E+00	2.35E-01		null	null		-3.59E+00	1.83E-06	Down	-1.20E+00	5.16E-02		2.70E+00	2.01E-09	Up	3.29E-01	7.07E-01		Unigene42770_All//gi|92897763|gb|ABS93875.1|//3.00E-09//Leucine-rich repeat [Medicago truncatula]		Unigene42770_All//4.00E-81//TC151435		GO:0003824	nr +
Unigene42773_All	216	74.36	60.52	55.47	127.07	116.70	101.62	491.70	239.75	125.05	-2.97E-01	3.78E-02		-4.23E-01	3.66E-03		-1.23E-01	3.08E-01		-3.23E-01	1.80E-03		-1.04E+00	2.15E-99	Down	-1.98E+00	3.05E-268	Down	Unigene42773_All//gi|233955399|gb|ACQ91203.1|//2.00E-22//calreticulin [Carica papaya]		Unigene42773_All//4.00E-114//TC144291	ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	GO:0005515//GO:0030246//GO:0033554//GO:0042742//GO:0044267//GO:0044432//GO:0046872	nr +
Unigene42774_All	244	0.21	0.42	0.87	0.00	0.00	0.56	101.02	86.50	954.00	9.54E-01	7.26E-01		2.03E+00	3.61E-01		null	null		9.12E+00	3.11E-01		-2.24E-01	3.00E-02		3.24E+00	0.00E+00	Up	Unigene42774_All//gi|3287834|sp|Q39760.1|DCS2_GOSAR//2.00E-32//RecName: Full=(+)-delta-cadinene synthase isozyme XC14; Short=D-cadinene synthase XC14 >gi|1045314|gb|AAA93065.1| (+)-delta-cadinene synthase isozyme XC14 [Gossypium arboreum]	Unigene42774_All//4.00E-14//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene42774_All//9.00E-26//gi|84174242|gb|DR462890.1|DR462890	ko00904|Diterpenoid biosynthesis//ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0010334//GO:0046872	nr +
Unigene42775_All	265	0.20	0.19	0.20	2.44	0.00	0.85	0.32	0.47	0.75	-4.60E-02	9.85E-01		2.54E-02	9.94E-01		-1.13E+01	7.85E-05	Down	-1.52E+00	1.12E-01		5.68E-01	7.82E-01		1.24E+00	4.68E-01				Unigene42775_All//3.00E-35//ES842675				
Unigene42778_All	263	0.00	2.50	1.42	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.25E-04	Up	1.05E+01	2.50E-02		null	null		null	null		null	null		null	null		Unigene42778_All//sp|P27716|INX1_DROME//1.00E-43//Innexin inx1 OS=Drosophila melanogaster GN=ogre PE=1 SV=1						swissprot -
Unigene42780_All	215	17.03	6.60	26.01	67.89	73.68	53.36	11.21	4.86	5.19	-1.37E+00	4.35E-05	Down	6.10E-01	2.04E-02		1.18E-01	4.95E-01		-3.48E-01	2.00E-02		-1.21E+00	1.19E-03		-1.11E+00	1.88E-03				Unigene42780_All//6.00E-39//gi|48799448|gb|CO100762.1|CO100762				
Unigene42784_All	674	0.00	0.00	0.00	0.00	0.00	0.00	1.69	3.66	0.00	null	null		null	null		null	null		null	null		1.11E+00	2.34E-03		-1.07E+01	1.64E-08	Down	Unigene42784_All//gi|195605696|gb|ACG24678.1|//2.00E-37//elongation factor 1-delta 1 [Zea mays]	Unigene42784_All//7.00E-23//AT1G30230| elongation factor 1-beta / EF-1-beta			GO:0006412//GO:0008135//GO:0043234	nr -
Unigene42786_All	277	0.94	1.46	0.77	0.90	0.25	0.00	2.59	0.91	0.29	6.32E-01	6.01E-01		-2.96E-01	8.32E-01		-1.85E+00	2.75E-01		-9.81E+00	7.33E-02		-1.52E+00	5.42E-02		-3.17E+00	8.09E-04	Down							
Unigene42787_All	339	1.23	0.00	2.20	0.44	3.35	1.87	0.00	0.12	0.00	-1.03E+01	1.05E-02		8.33E-01	3.39E-01		2.93E+00	2.06E-04	Up	2.08E+00	4.69E-02		6.95E+00	6.34E-01		null	null				Unigene42787_All//2.00E-55//CO119918				
Unigene42789_All	312	0.00	1.95	8.88	0.00	0.00	1.01	0.00	0.00	0.00	1.09E+01	1.17E-03		1.31E+01	2.75E-15	Up	null	null		9.98E+00	4.07E-02		null	null		null	null		Unigene42789_All//gi|89542295|gb|AAD27880.2|AF139468_1//1.00E-25//photosystem I reaction center subunit III [Vigna radiata]			ko00195|Photosynthesis	GO:0009522//GO:0009526//GO:0009534//GO:0009570//GO:0044237	nr +
Unigene4279_All	1158	3.70	1.62	1.84	5.72	3.24	3.32	0.91	0.69	0.14	-1.19E+00	7.09E-05	Down	-1.01E+00	1.05E-03		-8.20E-01	1.06E-04		-7.87E-01	4.40E-04		-4.13E-01	5.15E-01		-2.73E+00	1.12E-04	Down	Unigene4279_All//gi|17381263|gb|AAL36050.1|//2.00E-98//AT4g33380/F17M5_140 [Arabidopsis thaliana] >gi|20453385|gb|AAM19931.1| AT4g33380/F17M5_140 [Arabidopsis thaliana]	Unigene4279_All//7.00E-84//AT4G33380| unknown protein	Unigene4279_All//0.00E+00//CO084319				nr -
Unigene428_All	622	1.35	2.93	1.03	4.00	4.76	3.63	3.13	0.54	1.92	1.12E+00	2.19E-02		-3.90E-01	6.41E-01		2.50E-01	5.46E-01		-1.41E-01	7.33E-01		-2.54E+00	3.67E-07	Down	-7.03E-01	7.80E-02		Unigene428_All//gi|18391394|ref|NP_563908.1|//3.00E-58//ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / binding / microtubule motor [Arabidopsis thaliana] >gi|75173334|sp|Q9FZ06.1|ARK3_ARATH RecName: Full=Armadillo repeat-containing kinesin-like protein 3; AltName: Full=Phosphatidic acid kinase >gi|9954168|gb|AAG08965.1|AF159052_1 kinesin-like protein [Arabidopsis thaliana] >gi|162958327|dbj|BAF95587.1| armadillo repeat kinesin3 [Arabidopsis thaliana]	Unigene428_All//6.00E-59//AT1G12430| ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / binding / microtubule motor	Unigene428_All//0.00E+00//gi|78335273|gb|DT555547.1|DT555547				nr +
Unigene4280_All	909	5.53	3.62	2.87	7.23	5.83	5.52	9.21	2.02	3.77	-6.09E-01	2.29E-02		-9.45E-01	7.51E-04		-3.10E-01	1.94E-01		-3.91E-01	1.02E-01		-2.19E+00	5.00E-24	Down	-1.29E+00	3.32E-12	Down	Unigene4280_All//gi|115440105|ref|NP_001044332.1|//8.00E-46//Os01g0763100 [Oryza sativa Japonica Group] >gi|57900364|dbj|BAD87354.1| rhomboid family protein-like [Oryza sativa Japonica Group] >gi|113533863|dbj|BAF06246.1| Os01g0763100 [Oryza sativa Japonica Group]	Unigene4280_All//6.00E-76//AT1G18600| RBL12 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 12)	Unigene4280_All//0.00E+00//TC149586				nr -
Unigene42802_All	295	3.19	0.17	3.43	0.17	0.93	0.61	0.00	0.00	0.00	-4.22E+00	1.36E-04	Down	1.03E-01	8.77E-01		2.47E+00	2.23E-01		1.86E+00	4.58E-01		null	null		null	null									
Unigene42804_All	243	0.00	0.00	0.00	0.00	0.00	0.00	3.83	7.74	13.28	null	null		null	null		null	null		null	null		1.02E+00	1.72E-02		1.79E+00	7.35E-08	Up								
Unigene42805_All	388	0.00	0.00	0.00	0.00	0.00	0.00	3.16	1.72	0.21	null	null		null	null		null	null		null	null		-8.75E-01	1.13E-01		-3.94E+00	4.86E-07	Down	Unigene42805_All//gi|37935558|gb|AAP46146.1|//1.00E-59//beta tubulin 2 [Pseudo-nitzschia multiseries]	Unigene42805_All//2.00E-58//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene42805_All//2.00E-09//gi|54119975|gb|CO195484.1|CO195484	ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene4281_All	2358	2.29	0.95	1.51	2.49	2.67	2.24	6.67	5.51	4.80	-1.27E+00	1.90E-06	Down	-5.95E-01	2.71E-02		1.00E-01	7.44E-01		-1.54E-01	6.13E-01		-2.75E-01	3.56E-02		-4.75E-01	9.92E-05		Unigene4281_All//gi|30681030|ref|NP_568262.2|//1.00E-157//DGS1 (DGD1 SUPPRESSOR 1) [Arabidopsis thaliana] >gi|30725404|gb|AAP37724.1| At5g12290 [Arabidopsis thaliana]	Unigene4281_All//9.00E-150//AT5G12290| DGS1 (DGD1 SUPPRESSOR 1)	Unigene4281_All//0.00E+00//DR463224				nr +
Unigene42810_All	719	0.29	0.00	0.30	0.14	0.24	0.25	2.71	0.52	1.22	-8.19E+00	1.22E-01		2.51E-02	1.00E+00		7.89E-01	7.70E-01		8.59E-01	6.95E-01		-2.37E+00	1.13E-06	Down	-1.15E+00	4.53E-03		Unigene42810_All//gi|18391228|ref|NP_563882.1|//1.00E-95//MLO4 (MILDEW RESISTANCE LOCUS O 4); calmodulin binding [Arabidopsis thaliana] >gi|33112637|sp|Q23693.2|MLO4_ARATH RecName: Full=MLO-like protein 4; Short=AtMlo4 >gi|14091578|gb|AAK53797.1|AF369565_1 membrane protein Mlo4 [Arabidopsis thaliana]	Unigene42810_All//6.00E-97//AT1G11000| MLO4 (MILDEW RESISTANCE LOCUS O 4); calmodulin binding	Unigene42810_All//6.00E-94//gi|78342090|gb|DT562364.1|DT562364			GO:0006950//GO:0009987//GO:0031224	nr -
Unigene42811_All	404	0.00	1.13	1.98	0.00	0.00	0.00	0.00	0.00	0.00	1.01E+01	7.43E-03		1.09E+01	1.72E-04	Up	null	null		null	null		null	null		null	null									
Unigene42813_All	609	5.84	2.00	5.07	3.27	2.83	2.15	11.94	8.03	5.43	-1.55E+00	8.40E-06	Down	-2.04E-01	5.84E-01		-2.11E-01	6.58E-01		-6.05E-01	2.02E-01		-5.73E-01	3.04E-03		-1.14E+00	5.94E-09	Down			Unigene42813_All//0.00E+00//gi|164366426|gb|EX170061.1|EX170061				
Unigene42816_All	263	0.00	0.00	0.00	0.00	0.00	0.00	13.34	3.34	74.53	null	null		null	null		null	null		null	null		-2.00E+00	1.92E-09	Down	2.48E+00	2.17E-65	Up	Unigene42816_All//gi|224052970|ref|XP_002297642.1|//1.00E-20//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222844900|gb|EEE82447.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene42816_All//3.00E-18//AT3G13610| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene42816_All//3.00E-38//FL577006			GO:0009699//GO:0012501//GO:0016701//GO:0016706	nr -
Unigene42819_All	283	0.00	0.00	0.00	0.00	0.00	0.00	2.39	1.62	0.00	null	null		null	null		null	null		null	null		-5.57E-01	4.89E-01		-1.12E+01	3.56E-05	Down	Unigene42819_All//gi|1173198|sp|P46298.1|RS13_PEA//1.00E-39//RecName: Full=40S ribosomal protein S13 >gi|396639|emb|CAA80974.1| ribosomal protein S13 [Pisum sativum]	Unigene42819_All//2.00E-39//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene42819_All//6.00E-21//gi|11204697|gb|BF273711.1|BF273711		ko03010|Ribosome	GO:0000904//GO:0005198//GO:0009887//GO:0010467//GO:0015935//GO:0031981//GO:0033205	nr -

Unigene4282_All	1486	0.07	1.06	0.29	5.56	4.45	6.20	1.22	3.66	2.28	3.91E+00	6.83E-07	Up	2.03E+00	1.39E-01		-3.23E-01	1.16E-01		1.56E-01	4.83E-01		1.58E+00	1.83E-10	Up	8.97E-01	2.12E-03		Unigene4282_All//gi|18415996|ref|NP_567666.1|//5.00E-76//glycine-rich protein [Arabidopsis thaliana] >gi|30685911|ref|NP_849421.1| glycine-rich protein [Arabidopsis thaliana] >gi|15809950|gb|AAL06902.1| AT4g22740/T12H17_130 [Arabidopsis thaliana]	Unigene4282_All//2.00E-71//AT4G22740| glycine-rich protein	Unigene4282_All//0.00E+00//TC138137				nr -
Unigene42822_All	385	0.00	0.26	3.04	0.52	1.61	0.23	0.00	0.00	0.00	8.04E+00	3.86E-01		1.16E+01	1.77E-06	Up	1.64E+00	1.06E-01		-1.14E+00	5.69E-01		null	null		null	null									ESTscan +
Unigene42824_All	681	0.08	0.00	0.00	0.66	0.00	0.00	0.56	0.55	4.10	-6.26E+00	6.11E-01		-6.26E+00	6.23E-01		-9.36E+00	2.00E-03		-9.36E+00	5.79E-03		-1.66E-02	1.02E+00		2.87E+00	1.65E-11	Up	Unigene42824_All//gi|226529722|ref|NP_001147789.1|//2.00E-40//symbiotic ammonium transporter [Zea mays] >gi|195613768|gb|ACG28714.1| symbiotic ammonium transporter [Zea mays]	Unigene42824_All//2.00E-41//AT2G22750| basic helix-loop-helix (bHLH) family protein	Unigene42824_All//4.00E-98//TC134717	bHLH	ko04626|Plant-pathogen interaction	GO:0008152//GO:0016491	nr +
Unigene42826_All	323	8.26	1.10	0.66	7.71	4.90	2.10	1.83	0.65	1.97	-2.91E+00	4.83E-09	Down	-3.65E+00	2.31E-10	Down	-6.53E-01	9.36E-02		-1.88E+00	1.27E-05	Down	-1.50E+00	9.13E-02		1.07E-01	9.01E-01					Unigene42826_All//6.00E-154//ES832261				ESTscan -
Unigene42827_All	455	0.00	0.00	0.00	0.00	0.00	0.00	4.83	1.93	0.88	null	null		null	null		null	null		null	null		-1.32E+00	8.35E-04	Down	-2.46E+00	4.52E-08	Down	Unigene42827_All//gi|38154485|gb|AAR12194.1|//2.00E-36//molecular chaperone HspP0-2 [Nicotiana benthamiana]	Unigene42827_All//2.00E-36//AT5G52640| AtHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559	nr -
Unigene42828_All	329	2.07	0.77	0.00	3.48	4.19	2.47	1.80	1.78	1.94	-1.42E+00	1.16E-01		-1.10E+01	7.64E-04	Down	2.66E-01	6.81E-01		-4.95E-01	4.65E-01		-1.67E-02	1.02E+00		1.07E-01	9.01E-01					Unigene42828_All//4.00E-16//ES793909				
Unigene42829_All	317	0.00	0.00	0.00	0.31	0.00	0.00	7.60	5.80	1.76	null	null		null	null		-8.30E+00	3.12E-01		-8.30E+00	3.99E-01		-3.90E-01	3.15E-01		-2.11E+00	2.02E-07	Down								
Unigene4283_All	954	81.66	40.42	60.67	20.68	23.39	24.95	3.90	5.83	3.34	-1.01E+00	8.29E-58	Down	-4.29E-01	1.15E-12		1.78E-01	1.61E-01		2.71E-01	1.91E-02		5.79E-01	1.04E-02		-2.23E-01	4.53E-01		Unigene4283_All//gi|119360097|gb|AB466777.1|//1.00E-69//At4g19100 [Arabidopsis thaliana]	Unigene4283_All//4.00E-43//AT4G19100| unknown protein	Unigene4283_All//0.00E+00//TC175579				nr +
Unigene42831_All	262	19.37	40.61	17.07	0.00	0.39	0.17	0.00	0.32	0.00	1.07E+00	3.38E-09	Up	-1.82E-01	5.46E-01		8.62E+00	4.56E-01		7.43E+00	6.95E-01		8.32E+00	4.01E-01		null	null									
Unigene42839_All	848	0.00	0.00	0.00	0.00	0.00	0.00	5.19	0.49	1.27	null	null		null	null		null	null		null	null		-3.40E+00	2.49E-20	Down	-2.03E+00	2.70E-12	Down	Unigene42839_All//gi|53370641|gb|AU89136.1|//7.00E-16//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene42839_All//2.00E-07//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative					nr +
Unigene4284_All	1273	2.51	1.87	1.09	7.00	6.57	6.14	2.62	1.08	0.91	-4.22E-01	2.34E-01		-1.20E+00	1.16E-03		-9.17E-02	6.93E-01		-1.91E-01	4.06E-01		-1.28E+00	4.07E-05	Down	-1.53E+00	9.89E-07	Down	Unigene4284_All//gi|297853304|ref|XP_002894533.1|//1.00E-20//ubiquitin-protein ligase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297340375|gb|EFH70792.1| ubiquitin-protein ligase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene4284_All//1.00E-21//AT1G55860| UPL1 (UBIQUITIN-PROTEIN LIGASE 1); ubiquitin-protein ligase	Unigene4284_All//0.00E+00//gi|78347177|gb|DT567451.1|DT567451				nr +
Unigene42842_All	438	4.90	12.61	15.80	0.80	0.63	1.03	0.00	0.00	0.00	1.36E+00	3.39E-07	Up	1.69E+00	2.42E-11	Up	-3.40E-01	7.86E-01		3.73E-01	7.32E-01		null	null		null	null		Unigene42842_All//gi|300264170|gb|EFJ48367.1|//2.00E-06//metalloproteinase, extracellular matrix glycoprotein VMP22 [Volvox carteri f. nagariensis]		Unigene42842_All//2.00E-40//gi|164327366|gb|EX165257.1|EX165257				nr +
Unigene42843_All	216	51.35	14.31	37.47	66.65	37.62	67.75	117.25	92.30	115.83	-1.84E+00	7.42E-21	Down	-4.55E-01	1.13E-02		-8.25E-01	1.28E-09		2.35E-02	9.08E-01		-3.45E-01	3.83E-04		-1.76E-02	8.84E-01		Unigene42843_All//gi|297848148|ref|XP_002891955.1|//3.00E-47//early-responsive to dehydration 2 [Arabidopsis lyrata subsp. lyrata] >gi|297337797|gb|EFH68214.1| early-responsive to dehydration 2 [Arabidopsis lyrata subsp. lyrata]	Unigene42843_All//1.00E-18//AT5G02490| heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)	Unigene42843_All//4.00E-114//gi|109854709|gb|DW483688.1|DW483688		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr -
Unigene42844_All	225	0.23	0.00	0.00	0.00	0.31	0.00	150.52	53.50	117.39	-7.86E+00	6.11E-01		-7.86E+00	6.23E-01		8.26E+00	6.09E-01		null	null		-1.49E+00	1.78E-56	Down	-3.59E-01	8.60E-06					Unigene42844_All//4.00E-83//gi|109888658|gb|DW517627.1|DW517627				
Unigene42847_All	274	0.00	1.85	2.92	1.27	0.50	1.15	0.00	0.00	0.00	1.09E+01	4.04E-03		1.15E+01	1.72E-04	Up	-1.34E+00	3.08E-01		-1.41E-01	9.12E-01		null	null		null	null					Unigene42847_All//3.00E-13//DW516915				
Unigene4285_All	805	11.24	14.79	12.04	8.60	5.18	5.16	13.03	9.50	5.00	3.96E-01	1.74E-02		9.86E-02	6.17E-01		-7.33E-01	3.93E-04		-7.37E-01	7.48E-04		-4.55E-01	3.99E-03		-1.38E+00	1.15E-16	Down	Unigene4285_All//gi|16550928|gb|AAL25647.1|AF197330_1//2.00E-75//calcineurin-like protein [Eucalyptus grandis] >gi|16550937|gb|AAL25650.1|AF197334_1 calcineurin-like protein [Eucalyptus camaldulensis]	Unigene4285_All//6.00E-73//AT3G18430| calcium-binding EF hand family protein	Unigene4285_All//0.00E+00//gi|73848662|gb|DF457682.1|DF457682		ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene42851_All	351	0.00	0.00	0.30	0.71	0.29	1.29	1.08	1.19	3.97	null	null		8.25E+00	3.98E-01		-1.27E+00	4.24E-01		8.59E-01	4.69E-01		1.35E-01	8.99E-01		1.87E+00	4.97E-04	Up				Unigene42851_All//1.00E-38//CO120826				
Unigene42855_All	369	0.57	1.65	0.72	0.00	0.28	0.98	0.34	3.40	1.94	1.54E+00	1.22E-01		3.47E-01	7.97E-01		8.13E+00	4.56E-01		9.94E+00	2.37E-02		3.31E+00	4.67E-06	Up	2.50E+00	4.03E-03					Unigene42855_All//4.00E-07//TC164412				
Unigene42856_All	401	0.65	0.25	2.12	2.48	0.17	1.13	3.80	1.67	1.29	-1.37E+00	3.83E-01		1.70E+00	4.53E-02		-3.86E+00	1.61E-05	Down	-1.14E+00	1.09E-01		-1.19E+00	1.47E-02		-1.56E+00	1.38E-03		Unigene42856_All//gi|15238313|ref|NP_201300.1|//1.00E-19//mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana]	Unigene42856_All//5.00E-21//AT5G64950| mitochondrial transcription termination factor-related / mTERF-related	Unigene42856_All//0.00E+00//ES795481				nr +
Unigene4286_All	722	6.52	2.46	5.61	7.18	6.77	8.95	1.17	3.36	1.60	-1.41E+00	1.48E-06	Down	-2.19E-01	4.73E-01		-8.34E-02	8.02E-01		3.18E-01	2.08E-01		1.52E+00	7.42E-05	Up	4.50E-01	4.17E-01		Unigene4286_All//gi|108706201|gb|ABF93996.1|//3.00E-66//Integral membrane protein DUF6 containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene4286_All//2.00E-40//AT4G08290| nodulin MtN21 family protein					nr -
Unigene42860_All	367	0.29	2.07	3.77	1.09	0.19	0.00	0.00	0.00	0.00	2.86E+00	5.51E-03		3.73E+00	1.05E-05	Up	-2.53E+00	5.79E-02		-1.01E+01	1.11E-02		null	null		null	null									ESTscan +
Unigene42863_All	611	0.00	0.00	0.00	0.33	0.28	4.14	0.55	0.34	1.43	null	null		null	null		-2.11E-01	8.59E-01		3.67E+00	8.45E-11	Up	-6.95E-01	5.77E-01		1.37E+00	3.93E-02		Unigene42863_All//gi|144905179|dbj|BAF56240.1|//5.00E-70//cytochrome P450 enzyme [Pisum sativum]	Unigene42863_All//2.00E-70//AT2G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene42863_All//6.00E-32//DR454918		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00590|Arachidonic acid metabolism	GO:0004497//GO:0005506//GO:0009314//GO:0009725//GO:0016128//GO:0016209//GO:0016634//GO:0048878	nr +
Unigene42867_All	224	8.88	6.11	3.80	4.00	6.00	7.86	36.81	17.73	13.16	-5.39E-01	2.35E-01		-1.22E+00	1.27E-02		5.83E-01	3.42E-01		9.74E-01	5.32E-02		-1.05E+00	1.12E-08	Down	-1.48E+00	1.08E-14	Down				Unigene42867_All//5.00E-101//ES824696				
Unigene4287_All	1111	8.29	2.69	1.82	7.67	3.91	9.96	1.67	2.86	1.72	-1.62E+00	1.04E-14	Down	-2.19E+00	1.10E-20	Down	-9.73E-01	1.14E-07		3.77E-01	3.17E-02		7.72E-01	1.30E-02		3.97E-02	9.46E-01		Unigene4287_All//gi|108706201|gb|ABF93996.1|//1.00E-103//Integral membrane protein DUF6 containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene4287_All//2.00E-62//AT4G08290| nodulin MtN21 family protein					nr +
Unigene42878_All	378	0.00	7.51	5.49	0.00	0.00	0.00	0.22	0.00	0.11	1.29E+01	3.83E-16	Up	1.24E+01	1.92E-11	Up	null	null		null	null		-7.81E+00	4.03E-01		-1.09E+00	6.76E-01		Unigene42878_All//gi|149391425|gb|ABR25730.1|//4.00E-47//ubiquitin fusion protein [Oryza sativa Indica Group]	Unigene42878_All//3.00E-48//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome	Unigene42878_All//4.00E-38//DW500399		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0031981//GO:0032446	nr +
Unigene42881_All	291	0.00	5.57	4.03	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.96E-09	Up	1.20E+01	1.77E-06	Up	null	null		null	null		null	null		null	null									
Unigene42883_All	254	0.62	4.99	5.45	0.78	0.81	0.00	0.67	0.49	0.78	3.01E+00	1.02E-04	Up	3.14E+00	4.89E-05	Up	5.22E-02	9.88E-01		-9.62E+00	1.33E-01		-4.32E-01	7.92E-01		2.36E-01	8.83E-01									
Unigene42885_All	352	0.59	5.33	2.12	0.00	1.76	0.90	0.12	0.12	1.36	3.16E+00	5.97E-07	Up	1.83E+00	5.05E-02		1.08E+01	7.90E-04	Up	9.81E+00	4.07E-02		-1.69E-02	1.00E+00		3.50E+00	7.29E-03									
Unigene42887_All	377	0.00	0.00	0.00	0.00	0.00	0.00	2.58	1.77	0.00	null	null		null	null		null	null		null	null		-5.40E-01	4.02E-01		-1.13E+01	2.72E-07	Down								ESTscan -
Unigene42888_All	238	0.00	0.21	0.67	0.63	2.17	1.90	0.18	0.35	11.05	7.73E+00	6.16E-01		9.39E+00	2.39E-01		1.79E+00	1.26E-01		1.60E+00	2.05E-01		9.84E-01	7.31E-01		5.96E+00	2.54E-17	Up	Unigene42888_All//gi|83316226|gb|AB302397.1|//2.00E-37//1-aminocyclopropane-1-carboxylate oxidase [Gossypium hirsutum]	Unigene42888_All//7.00E-33//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene42888_All//2.00E-116//TC134493		ko00270|Cysteine and methionine metabolism	GO:0003824//GO:0008152	nr -
Unigene42889_All	700	0.00	0.00	0.00	0.36	0.00	0.00	2.30	0.78	0.17	null	null		null	null		-8.47E+00	4.18E-02		-8.47E+00	7.33E-02		-1.56E+00	1.34E-03		-3.75E+00	9.85E-09	Down								
Unigene42894_All	239	0.00	0.00	0.00	0.00	0.00	0.00	4.25	1.40	0.00	null	null		null	null		null	null		null	null		-1.60E+00	1.27E-02		-1.21E+01	1.35E-07	Down								
Unigene42899_All	850	0.55	0.18	1.00	0.35	2.15	0.16	1.19	4.18	1.64	-1.63E+00	1.58E-01		8.56E-01	2.80E-01		2.61E+00	3.55E-06	Up	-1.14E+00	4.57E-01		1.81E+00	2.00E-08	Up	4.59E-01	3.58E-01		Unigene42899_All//gi|156103422|gb|ABU48859.1|//4.00E-75//xylosyltransferase 2 [Nicotiana benthamiana]	Unigene42899_All//2.00E-58//AT5G55500| XYLT (ARABIDOPSIS THALIANA BETA-1,2-XYLOSYLTRANSFERASE); xylosyltransferase	Unigene42899_All//4.00E-179//gi|3326536|gb|AI055422.1|AI055422		ko00510|N-Glycan biosynthesis	GO:0006486//GO:0012505//GO:0031985//GO:0042285//GO:0065002	nr +
Unigene429_All	842	1.24	0.60	0.51	4.02	3.60	3.00	2.96	0.84	1.32	-1.05E+00	1.20E-01		-1.30E+00	7.46E-02		-1.61E-01	6.59E-01		-4.22E-01	2.32E-01		-1.81E+00	3.62E-06	Down	-1.16E+00	9.80E-04	Down	Unigene429_All//gi|18391394|ref|NP_563908.1|//3.00E-79//ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / binding / microtubule motor [Arabidopsis thaliana] >gi|75173334|sp|Q9FZ06.1|ARK3_ARATH RecName: Full=Armadillo repeat-containing kinesin-like protein 3; AltName: Full=Phosphatidic acid kinase >gi|9954168|gb|AAG08965.1|AF159052_1 kinesin-like protein [Arabidopsis thaliana] >gi|162958327|dbj|BAF95587.1| armadillo repeat kinesin3 [Arabidopsis thaliana]	Unigene429_All//3.00E-60//AT1G12430| ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / microtubule motor	Unigene429_All//0.00E+00//TC139960				nr -
Unigene4290_All	1841	1.59	2.97	3.90	0.70	1.33	0.74	0.00	0.00	0.00	9.01E-01	4.43E-04		1.29E+00	3.90E-08	Up	9.17E-01	2.25E-02		6.52E-02	9.33E-01		null	null		null	null		Unigene4290_All//gi|167386715|ref|XP_001737875.1|//2.00E-08//transposase insD for insertion element IS2A/D/F/H/I/K [Entamoeba dispar SAW760] >gi|300818586|ref|ZP_07098794.1| insertion element IS2 transposase InsD [Escherichia coli MS 107-1] >gi|300916374|ref|ZP_07133115.1| insertion element IS2 transposase InsD [Escherichia coli MS 115-1] >gi|300929171|ref|ZP_07144659.1| insertion element IS2 transposase InsD [Escherichia coli MS 187-1] >gi|300416315|gb|EFJ99625.1| insertion element IS2 transposase InsD [Escherichia coli MS 115-1] >gi|300462861|gb|EFK26354.1| insertion element IS2 transposase InsD [Escherichia coli MS 187-1] >gi|300328758|gb|EFK49820.1| insertion element IS2 transposase InsD [Escherichia coli MS 107-1]						nr +
Unigene42902_All	313	4.68	0.81	0.85	5.25	2.86	4.47	4.73	1.60	1.27	-2.53E+00	1.19E-04	Down	-2.46E+00	2.95E-04	Down	-8.77E-01	7.54E-02		-2.32E-01	6.78E-01		-1.56E+00	2.28E-03		-1.89E+00	2.45E-04	Down	Unigene42902_All//gi|8778281|gb|AAF79290.1|AC068602_13//5.00E-32//F14D16.22 [Arabidopsis thaliana]	Unigene42902_All//1.00E-27//AT3G54490| CONTAINS InterPro DOMAIN/s: GINS complex, Psf3 component (InterPro:IPR010492); BEST Arabidopsis thaliana protein match is: TTN10 (TITAN 10) (TAIR:AT1G19080.1); Has 224 Blast hits to 224 proteins in 105 species: Archae - 0; Bacteria - 0; Metazoa - 105; Fungi - 76; Plants - 22; Viruses - 0; Other Eukaryotes - 21 (source: NCBI BLink).	Unigene42902_All//2.00E-144//ES824607			GO:0003006//GO:0006260//GO:0043231//GO:0043234	nr -
Unigene42903_All	269	0.00	0.19	2.77	0.00	0.90	0.84	0.79	0.47	0.89	7.56E+00	6.16E-01		1.14E+01	3.27E-04	Up	9.81E+00	1.04E-01		9.71E+00	1.19E-01		-7.54E-01	6.32E-01		1.77E-01	9.08E-01									
Unigene42904_All	288	0.36	2.29	1.66	0.00	0.60	0.16	3.23	1.45	0.14	2.65E+00	1.49E-02		2.20E+00	9.15E-02		9.22E+00	2.27E-01		7.29E+00	6.95E-01		-1.15E+00	7.87E-02		-4.55E+00	6.41E-06	Down				Unigene42904_All//7.00E-27//TC167378				
Unigene42905_All	281	0.00	5.41	2.46	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.10E-08	Up	1.13E+01	6.16E-04	Up	null	null		null	null		null	null		null	null									

Unigene42908_All	238	0.22	0.00	0.90	0.00	0.00	0.57	7.11	3.69	2.18	-7.78E+00	6.11E-01		2.03E+00	3.61E-01		null	null		9.15E+00	3.11E-01		-9.46E-01	3.66E-02		-1.71E+00	2.56E-04	Down			Unigene42908_All//3.00E-41//gi|13354419|gb|BG444767.1|BG444767				
Unigene42909_All	966	0.00	0.00	0.00	0.00	0.00	0.00	7.31	1.17	1.07	null	null		null	null		null	null		null	null		-2.65E+00	2.52E-25	Down	-2.77E+00	1.74E-27	Down	Unigene42909_All//gi|109939734|sp|P25776.2|ORYA_ORYSJ//3.00E-63//RecName: Full=Oryzain alpha chain; Flags: Precursor >gi|78192122|gb|ABR30151.1| oryzain alpha [Oryza sativa Japonica Group]	Unigene42909_All//4.00E-59//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase				GO:0004091//GO:0004175//GO:0019538//GO:0031410	nr -
Unigene42910_All	311	0.00	13.52	4.11	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	5.92E-24	Up	1.20E+01	4.68E-07	Up	null	null		null	null		null	null		null	null									
Unigene42913_All	377	13.32	15.59	17.94	14.40	21.28	18.57	12.00	15.85	28.00	2.27E-01	3.83E-01		4.29E-01	7.51E-02		5.63E-01	4.38E-03		3.67E-01	1.18E-01		4.02E-01	7.21E-02		1.22E+00	6.58E-14	Up	Unigene42913_All//4.00E-11//AT3G53500| zinc knuckle (CCHC-type) family protein	Unigene42913_All//4.00E-155//gi|78332393|gb|DT552667.1|DT552667		ko03040|Spliceosome	GO:0000398//GO:0016604//GO:0046914	nr -
Unigene42915_All	333	15.08	10.96	13.59	22.29	23.78	23.73	14.86	10.92	5.26	-4.61E-01	8.79E-02		-1.50E-01	6.39E-01		9.37E-02	7.25E-01		9.06E-02	6.94E-01		-4.44E-01	7.26E-02		-1.50E+00	2.86E-09	Down			Unigene42915_All//3.00E-85//BF275097				
Unigene4292_All	1159	2.57	0.44	0.96	4.34	2.94	2.65	1.93	1.51	2.58	-2.56E+00	7.84E-09	Down	-1.42E+00	3.22E-04	Down	-5.62E-01	2.89E-02		-7.12E-01	7.09E-03		-3.52E-01	3.98E-01		4.15E-01	1.98E-01		Unigene4292_All//gi|227438217|gb|AC930598.1|//1.00E-19//disease resistance protein [Brassica rapa subsp. pekinensis]	Unigene4292_All//1.00E-05//AT1G34070| unknown protein	Unigene4292_All//3.00E-100//gi|78351152|gb|DT571426.1|DT571426				nr -
Unigene42921_All	255	0.00	2.58	3.13	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.25E-04	Up	1.16E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene42921_All//gi|195615812|gb|AC529736.1|//5.00E-06//protein kinase [Zea mays]	Unigene42921_All//3.00E-06//AT4G35780| protein kinase family protein				GO:0016301	nr +
Unigene42928_All	592	0.18	0.43	0.00	0.08	0.35	1.68	0.43	1.41	6.12	1.28E+00	4.35E-01		-7.47E+00	3.92E-01		2.05E+00	3.94E-01		4.32E+00	6.32E-05	Up	1.72E+00	1.93E-02		3.84E+00	7.33E-19	Up			Unigene42928_All//1.00E-11//gi|48795984|gb|C0097298.1|C0097298				
Unigene4293_All	1212	3.32	2.01	1.71	11.92	17.16	15.91	6.42	1.86	3.16	-7.28E-01	1.62E-02		-9.56E-01	2.70E-03		5.26E-01	2.93E-06		4.17E-01	8.05E-04		-1.79E+00	2.58E-17	Down	-1.02E+00	3.59E-08	Down	Unigene4293_All//gi|212960297|gb|ACJ38663.1|//1.00E-46//myb-like transcription factor [Betula luminifera]	Unigene4293_All//4.00E-09//AT1G09540| MYB61 (MYB DOMAIN PROTEIN 61); DNA binding / transcription factor	Unigene4293_All//0.00E+00//TC170619	MYB			nr +
Unigene42941_All	301	0.00	6.73	2.65	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.53E-11	Up	1.14E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene42941_All//gi|71040677|gb|AZ20287.1|//4.00E-27//ubiquitin-conjugating enzyme 2 [Arachis hypogaea]	Unigene42941_All//9.00E-28//AT1G23260| MMZ1 (MMS ZWEI HOMOLOGUE 1); protein binding / ubiquitin-protein ligase				GO:0005488//GO:0006281//GO:0006464//GO:0016881//GO:0031371//GO:0060255	nr -
Unigene42945_All	380	0.41	9.60	1.54	0.26	0.91	0.00	0.22	0.00	0.10	4.54E+00	6.77E-17	Up	1.90E+00	8.48E-02		1.79E+00	2.57E-01		-8.03E+00	3.99E-01		-7.80E+00	4.03E-01		-1.09E+00	6.76E-01		Unigene42945_All//gi|30687365|ref|NP_189056.2|//5.00E-35//FMA (FAMA); DNA binding / transcription activator/ transcription factor [Arabidopsis thaliana] >gi|75293553|sp|Q56YJ8.1|FAMA_ARATH RecName: Full=Transcription factor FAMA; AltName: Full=Transcription factor EN 14; AltName: Full=bHLH transcription factor bHLH097; AltName: Full=Basic helix-loop-helix protein 97; Short=bHLH 97; Short=AtbHLH97 >gi|114213507|gb|AB154336.1| At3g24140 [Arabidopsis thaliana]	Unigene42945_All//2.00E-36//AT3G24140| FMA (FAMA); DNA binding / transcription activator/ transcription factor	Unigene42945_All//2.00E-178//TC164895	bHLH	ko04626|Plant-pathogen interaction	GO:0001071//GO:0009913//GO:0010468//GO:0010557//GO:0030528//GO:0040331//GO:0045595//GO:0048523	nr -
Unigene42947_All	225	0.00	4.05	2.60	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.62E-05	Up	1.13E+01	2.17E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene4295_All	1114	7.09	7.28	3.39	18.60	12.86	20.39	21.29	8.85	12.55	3.73E-02	8.67E-01		-1.06E+00	1.17E-06	Down	-5.33E-01	1.53E-06		1.33E-01	3.32E-01		-1.27E+00	3.92E-31	Down	-7.62E-01	2.37E-14		Unigene4295_All//gi|124360427|gb|AB008437.1|//2.00E-94//Ribosomal protein L10 [Medicago truncatula]	Unigene4295_All//1.00E-82//AT1G25260| acidic ribosomal protein P0-related	Unigene4295_All//0.00E+00//TC134892		ko03010|Ribosome		nr +
Unigene42951_All	340	0.00	0.00	0.00	0.00	0.00	0.00	3.48	1.48	0.47	null	null		null	null		null	null		null	null		-1.24E+00	2.93E-02		-2.89E+00	2.03E-05	Down	Unigene42951_All//gi|220966698|gb|ACL97363.1|//7.00E-44//elongation factor-1 alpha [Ignatius tetrasporus]	Unigene42951_All//7.00E-40//AT5G60390| elongation factor 1-alpha / EF-1-alpha				GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene42952_All	389	0.00	3.91	2.19	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.10E-08	Up	1.11E+01	9.02E-05	Up	null	null		null	null		null	null		null	null									
Unigene42955_All	237	21.19	46.61	33.03	38.46	41.99	60.03	14.09	22.40	12.27	1.14E+00	1.93E-10	Up	6.40E-01	3.03E-03		1.27E-01	5.68E-01		6.42E-01	9.99E-06		6.68E-01	3.79E-03		-2.00E-01	5.41E-01		Unigene42955_All//gi|225460841|ref|XP_002277100.1|//6.00E-06//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297737506|emb|CBI26707.3| unnamed protein product [Vitis vinifera]	Unigene42955_All//6.00E-05//AT1G76590| SVP52 (SYNTAXIN OF PLANTS 52); SNAP receptor	Unigene42955_All//1.00E-108//TC154909				nr +
Unigene42959_All	393	221.00	65.50	227.09	149.70	86.83	74.01	159.22	109.54	38.12	-1.75E+00	1.76E-148	Down	3.92E-02	5.85E-01		-7.86E-01	6.67E-35		-1.02E+00	1.71E-47	Down	-5.40E-01	1.60E-19		-2.06E+00	1.59E-167	Down	Unigene42959_All//gi|50313460|gb|AAT74600.1|//2.00E-35//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene42959_All//7.00E-21//AT3G23510| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene42959_All//1.00E-127//TC129559			GO:0006629//GO:0008757//GO:0044464	nr +
Unigene42968_All	458	0.00	0.00	0.00	0.00	0.00	0.00	2.49	0.18	3.83	null	null		null	null		null	null		null	null		-3.77E+00	3.90E-06	Down	6.19E-01	1.49E-01		Unigene42968_All//gi|42568048|ref|NP_197784.2|//1.00E-27//TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase [Arabidopsis thaliana] >gi|205785549|sp|Q84UU4.2|HUMS_ARATH RecName: Full=Alpha-humulene/(-)-(E)-beta-caryophyllene synthase	Unigene42968_All//4.00E-29//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene42968_All//9.00E-46//CO115197		ko00904|Diterpenoid biosynthesis		nr -
Unigene4297_All	951	1.16	4.80	0.84	6.39	13.61	11.26	13.12	13.76	34.23	2.05E+00	3.50E-10	Up	-4.60E-01	4.97E-01		1.09E+00	5.31E-13	Up	8.17E-01	1.91E-06		6.88E-02	6.70E-01		1.38E+00	1.53E-49	Up	Unigene4297_All//gi|224078856|ref|XP_002305655.1|//2.00E-37//f-box family protein [Populus trichocarpa] >gi|222848619|gb|EEE86166.1| f-box family protein [Populus trichocarpa]	Unigene4297_All//2.00E-31//AT4G21510| F-box family protein	Unigene4297_All//0.00E+00//TC156898				nr -
Unigene42977_All	239	4.82	2.97	1.78	23.97	6.77	11.15	11.32	24.83	12.17	-6.98E-01	2.66E-01		-1.43E+00	3.87E-02		-1.82E+00	2.82E-13	Down	-1.10E+00	7.60E-06	Down	1.13E+00	3.71E-07	Up	1.04E-01	7.51E-01				Unigene42977_All//6.00E-67//ES831261				
Unigene42986_All	400	2.35	0.25	1.33	1.00	0.60	0.79	0.32	0.21	0.30	-3.22E+00	6.76E-04	Down	-8.23E-01	2.71E-01		-7.25E-01	5.46E-01		-3.34E-01	7.56E-01		-6.01E-01	7.66E-01		-8.58E-02	9.69E-01				Unigene42986_All//5.00E-07//TC148233				
Unigene4299_All	634	16.34	9.83	8.74	21.14	20.04	30.20	63.42	31.64	25.39	-7.33E-01	3.62E-05		-9.04E-01	1.13E-06		-7.67E-02	6.81E-01		5.15E-01	2.94E-05		-1.00E+00	3.63E-36	Down	-1.32E+00	2.23E-57	Down	Unigene4299_All//gi|297795569|ref|XP_002865669.1|//2.00E-69//60S ribosomal protein L13A [Arabidopsis lyrata subsp. lyrata] >gi|297311504|gb|EFH11928.1| 60S ribosomal protein L13A [Arabidopsis lyrata subsp. lyrata]	Unigene4299_All//2.00E-63//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene4299_All//0.00E+00//gi|109826601|gb|DW225311.1|DW225311		ko03010|Ribosome		nr -
Unigene42991_All	399	0.00	0.51	0.53	2.75	1.55	0.23	4.03	3.35	1.10	8.99E+00	1.36E-01		9.06E+00	1.41E-01		-8.22E-01	1.96E-01		-3.60E+00	5.02E-05	Down	-2.65E-01	6.15E-01		-1.87E+00	1.38E-04	Down							
Unigene42992_All	319	1.48	0.32	0.67	2.65	0.22	0.85	0.66	0.39	0.50	-2.22E+00	7.76E-02		-1.14E+00	3.32E-01		-3.62E+00	1.47E-04	Down	-1.64E+00	4.18E-02		-7.54E-01	6.32E-01		-4.08E-01	7.55E-01									
Unigene42993_All	280	0.75	6.15	2.47	1.42	3.57	7.42	0.15	0.15	0.00	3.04E+00	3.13E-06	Up	1.73E+00	7.67E-02		1.33E+00	6.66E-02		2.38E+00	4.55E-06	Up	-1.63E-02	1.00E+00		-7.24E+00	6.12E-01								
Unigene42996_All	345	0.91	0.73	2.78	1.30	1.10	0.65	3.43	2.06	0.58	-3.09E-01	7.89E-01		1.61E+00	4.07E-02		-2.43E-01	8.21E-01		-9.90E-01	3.94E-01		-7.37E-01	1.94E-01		-2.57E+00	6.97E-05	Down							
Unigene42998_All	350	0.00	0.29	0.61	0.43	0.39	1.29	249.33	39.05	87.08	8.18E+00	3.86E-01		9.25E+00	1.41E-01		-1.18E-01	9.10E-01		1.60E+00	2.05E-01		-2.67E+00	0.00E+00	Down	-1.52E+00	2.56E-152	Down	Unigene42998_All//gi|461929|sp|P33560.1|TIP_ANTMA//2.00E-53//RecName: Full=Probable aquaporin TIP-type; AltName: Full=Tonoplast intrinsic protein DiP; AltName: Full=Dark intrinsic protein >gi|414088|emb|CAA48854.1| integral membrane protein [Antirrhinum majus]	Unigene42998_All//2.00E-54//AT4G17340| TIP2;2 (TONOPLAST INTRINSIC PROTEIN 2;2); water channel	Unigene42998_All//3.00E-71//gi|109838278|gb|DW236839.1|DW236839			GO:0000325//GO:0005275//GO:0005372//GO:0006810//GO:0009536//GO:0031090//GO:0031224	nr -
Unigene42999_All	236	3.33	0.00	2.26	0.63	0.29	0.19	0.00	0.00	0.00	-1.17E+01	1.09E-04	Down	-5.60E-01	4.96E-01		-1.12E+00	5.83E-01		-1.73E+00	5.01E-01		null	null		null	null									
Unigene430_All	1152	1.23	2.29	0.79	3.55	3.80	2.51	3.23	1.45	1.73	8.99E-01	2.12E-02		-6.42E-01	2.75E-01		9.85E-02	8.09E-01		-4.99E-01	1.09E-01		-1.15E+00	6.53E-05	Down	-9.01E-01	1.07E-03		Unigene430_All//gi|18391394|ref|NP_563908.1|//1.00E-149//ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / binding / microtubule motor [Arabidopsis thaliana] >gi|75173334|sp|Q9FZ06.1|ARK3_ARATH RecName: Full=Armadillo repeat-containing kinesin-like protein 3; AltName: Full=Phosphatidic acid kinase >gi|9954168|gb|AAG08965.1|AF159052_1 kinesin-like protein [Arabidopsis thaliana] >gi|162958327|dbj|BAF95587.1| armadillo repeat kinesin3 [Arabidopsis thaliana]	Unigene430_All//2.00E-150//AT1G12430| ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / binding / microtubule motor	Unigene430_All//0.00E+00//gi|78336723|gb|DT556997.1|DT556997				nr +
Unigene4300_All	808	3.24	1.51	7.71	16.34	3.58	8.05	11.93	4.14	4.19	-1.11E+00	5.16E-03		1.25E+00	8.29E-07	Up	-2.19E+00	1.82E-38	Down	-1.02E+00	3.49E-11	Down	-1.53E+00	3.46E-17	Down	-1.51E+00	1.89E-17	Down	Unigene4300_All//gi|224104361|ref|XP_002313411.1|//2.00E-32//copper transporter [Populus trichocarpa] >gi|222849819|gb|EEE87366.1| copper transporter [Populus trichocarpa]	Unigene4300_All//3.00E-21//AT5G59030| COPT1 (copper transporter 1); copper ion transmembrane transporter					nr -
Unigene43002_All	919	0.00	0.00	0.00	0.00	0.00	0.00	1.70	1.96	0.00	null	null		null	null		null	null		null	null		2.00E-01	6.50E-01		-1.07E+01	1.42E-11	Down	Unigene43002_All//gi|226505998|ref|NP_001146929.1|//7.00E-82//60S ribosomal protein L7a [Zea mays] >gi|195605318|gb|ACG24489.1| 60S ribosomal protein L7a [Zea mays]	Unigene43002_All//1.00E-76//AT3G62870| 60S ribosomal protein L7A (RPL7aB)			ko03010|Ribosome	GO:0009987//GO:0010467//GO:0015934//GO:0016020	nr +
Unigene4301_All	1492	0.56	1.22	1.04	1.27	1.75	1.06	21.40	8.96	3.15	1.12E+00	2.19E-02		8.83E-01	1.15E-01		4.67E-01	2.62E-01		-2.60E-01	6.36E-01		-1.26E+00	4.40E-41	Down	-2.76E+00	1.94E-121	Down	Unigene4301_All//gi|297851852|ref|XP_002893807.1|//1.00E-140//alliinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339649|gb|EFH70066.1| alliinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4301_All//1.00E-136//AT1G34060| alliinase family protein					nr -
Unigene43011_All	242	0.00	0.21	4.18	1.85	1.42	0.37	0.35	0.69	0.66	7.71E+00	6.16E-01		1.20E+01	1.27E-05	Up	-3.81E-01	7.22E-01		-2.31E+00	7.81E-02		9.83E-01	6.33E-01		9.14E-01	6.24E-01				Unigene43011_All//6.00E-64//TC154458				
Unigene43013_All	270	0.00	0.00	0.00	0.00	0.00	0.00	2.51	5.42	0.00	null	null		null	null		null	null		null	null		1.11E+00	2.51E-02		-1.13E+01	3.56E-05	Down								ESTscan +
Unigene43014_All	1113	0.00	10.97	3.83	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	4.70E-70	Up	1.19E+01	1.22E-23	Up	null	null		null	null		null	null		null	null		Unigene43014_All//gi|255085620|ref|XP_002505241.1|//1.00E-103//glycosyltransferase family 35 protein [Micromonas sp. RCC299] >gi|226520510|gb|AC066499.1| glycosyltransferase family 35 protein [Micromonas sp. RCC299]	Unigene43014_All//1.00E-86//AT3G29320| glucan phosphorylase, putative			ko00500|Starch and sucrose metabolism	GO:0016740	nr -
Unigene43017_All	601	0.35	1.43	0.27	0.25	0.11	0.08	0.42	1.46	3.12	2.04E+00	1.59E-02		-3.90E-01	8.07E-01		-1.12E+00	5.83E-01		-1.73E+00	5.01E-01		1.79E+00	1.27E-02		2.88E+00	5.56E-08	Up								
Unigene43018_All	318	203.03	101.02	191.23	49.81	53.39	32.24	0.53	0.53	0.63	-1.01E+00	1.94E-47	Down	-8.64E-02	2.64E-01		9.99E-02	5.45E-01		-6.28E-01	3.96E-06		-1.66E-02	1.02E+00		2.36E-01	8.83E-01				Unigene43018_All//4.00E-78//TC157601				
Unigene4302_All	794	11.80	6.19	9.12	13.49	14.96	16.44	55.97	36.22	132.21	-9.30E-01	1.03E-06		-3.71E-01	6.54E-02		1.50E-01	4.45E-01		2.85E-01	8.45E-02		-6.28E-01	2.91E-18		1.24E+00	1.63E-133	Up	Unigene4302_All//gi|92870921|gb|ABE80121.1|//1.00E-127//Pyruvate kinase [Medicago truncatula]	Unigene4302_All//2.00E-122//AT3G52990| pyruvate kinase, putative	Unigene4302_All//0.00E+00//TC177746		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene43020_All	290	0.36	0.35	0.92	0.34	3.92	3.43	1.31	0.86	0.41	-4.63E-02	9.88E-01		1.35E+00	4.09E-01		3.51E+00	4.52E-05	Up	3.32E+00	3.47E-04	Up	-6.02E-01	6.12E-01		-1.67E+00	1.40E-01		Unigene43020_All//gi|115467684|ref|NP_001657441.1|//4.00E-26//Os06g0298200 (Oryza sativa Japonica Group) >gi|113595481|dbj|BAF19355.1| Os06g0298200 (Oryza sativa Japonica Group)	Unigene43020_All//4.00E-20//AT3G07650| COL9 (CONSTANS-LIKE 9); transcription factor/ zinc ion binding	Unigene43020_All//5.00E-71//gi|109838278|gb|DW236839.1|DW236839	C2C2-CO-like		GO:0001071//GO:0010468//GO:0016020//GO:0043231//GO:0046914//GO:0048581	nr -
Unigene43021_All	310	0.00	3.60	0.69	1.45	1.11	0.73	1.09	0.81	2.31	1.18E+01	2.00E-06	Up	9.42E+00	1.41E-01		-3.81E-01	7.22E-01		-9.90E-01	3.94E-01		-4.32E-01	7.03E-01		1.08E+00	1.41E-01									

Unigene43027_All	287	0.00	6.18	1.30	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	4.14E-10	Up	1.03E+01	2.50E-02		null	null		null	null		null	null		null	null		Unigene43027_All//sp|P11424|IMAP_DROFU//2.00E-14//Male accessory gland serine protease inhibitor OS=Drosophila funebris GN=PapD PE=1 SV=1						swissprot +
Unigene43028_All	419	0.62	1.69	0.64	0.83	0.82	0.22	0.91	1.60	4.09	1.44E+00	1.06E-01		2.52E-02	1.00E+00		-1.81E-02	9.58E-01		-1.95E+00	1.96E-01		8.13E-01	3.15E-01		2.17E+00	1.39E-05	Up		Unigene43028_All//6.00E-133//C0098610				
Unigene4303_All	1603	0.62	0.89	0.47	1.18	2.60	1.94	3.27	1.20	2.58	5.13E-01	3.73E-01		-4.15E-01	5.72E-01		1.14E+00	8.57E-05	Up	7.19E-01	4.40E-02		-1.45E+00	5.10E-09	Down	-3.40E-01	1.45E-01		Unigene4303_All//gi|15240688|ref|NP_196872.1|//1.00E-163//AB01 (ABA-OVERLY SENSITIVE 1): transcription elongation regulator [Arabidopsis thaliana]	Unigene4303_All//1.00E-147//AT5G13880| AB01 (ABA-OVERLY SENSITIVE 1); transcription elongation regulator	Unigene4303_All//0.00E+00//C0111104				nr -
Unigene43031_All	294	3.03	1.38	0.00	1.02	0.82	0.61	0.00	0.00	0.00	-1.13E+00	1.30E-01		-1.16E+01	6.30E-05	Down	-3.10E-01	8.20E-01		-7.26E-01	6.38E-01		null	null		null	null		Unigene43031_All//gi|224108315|ref|XP_002314802.1|//8.00E-08//predicted protein [Populus trichocarpa] >gi|222863842|gb|EEF00973.1| predicted protein [Populus trichocarpa]						nr -
Unigene43033_All	352	0.45	0.72	3.48	2.12	1.47	1.54	0.36	0.24	0.11	6.91E-01	6.26E-01		2.96E+00	2.55E-04	Up	-5.33E-01	5.26E-01		-4.63E-01	6.06E-01		-6.01E-01	7.66E-01		-1.67E+00	4.77E-01		Unigene43033_All//gi|228535376|gb|ACQ44245.1|//2.00E-06//chlorophyll synthase [Nicotiana tabacum]	Unigene43033_All//1.00E-07//AT3G51820| G4; chlorophyll synthetase	Unigene43033_All//9.00E-30//TC137897		ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene43036_All	222	6.13	0.68	0.48	2.24	2.64	2.03	0.76	0.00	0.18	-3.16E+00	2.85E-05	Down	-3.68E+00	1.58E-05	Down	2.33E-01	8.26E-01		-1.41E-01	8.92E-01		-9.57E+00	1.34E-01		-2.09E+00	3.13E-01								
Unigene43037_All	906	0.23	0.28	0.76	0.66	0.46	0.50	0.28	1.34	6.68	2.76E-01	8.43E-01		1.73E+00	7.67E-02		-5.33E-01	5.62E-01		-4.04E-01	6.73E-01		2.26E+00	3.35E-04	Up	4.58E+00	5.47E-35	Up	Unigene43037_All//gi|15231932|ref|NP_187467.1|//1.00E-117//KOB1 (KOBITO) [Arabidopsis thaliana] >gi|23452834|gb|AAN33186.1| elongation defective 1 [Arabidopsis thaliana]	Unigene43037_All//5.00E-103//AT3G08550| KOB1 (KOBITO)	Unigene43037_All//0.00E+00//gi|78330400|gb|DT550674.1|DT550674				nr -
Unigene43039_All	253	0.00	0.00	0.00	0.00	0.00	0.00	66.34	0.17	16.85	null	null		null	null		null	null		null	null		-8.65E+00	3.32E-117	Down	-1.98E+00	4.26E-43	Down		Unigene43039_All//1.00E-09//DW236815				
Unigene43042_All	265	0.00	11.28	2.41	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	5.19E-17	Up	1.12E+01	1.16E-03		null	null		null	null		null	null		null	null								
Unigene43047_All	527	0.00	3.08	2.73	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.96E-09	Up	1.14E+01	6.30E-08	Up	null	null		null	null		null	null		null	null		Unigene43047_All//gi|134142800|gb|AB061734.1|//4.00E-81//mitochondrial glycine decarboxylase complex P-protein [Populus tremuloides]	Unigene43047_All//6.00E-74//AT4G33010| AtGLDP1 (Arabidopsis thaliana glycine decarboxylase P-protein 1); catalytic/ glycine dehydrogenase (decarboxylating)/ pyridoxal phosphate binding	Unigene43047_All//5.00E-29//TC137790		ko00260|Glycine, serine and threonine metabolism	GO:0005576//GO:0006546//GO:0009526//GO:0010038//GO:0016628//GO:00166 42//GO:0032559//GO:0043234//GO:004 8037	nr +
Unigene4305_All	1776	3.15	1.48	2.34	3.59	3.43	1.70	3.33	0.35	1.28	-1.09E+00	2.25E-05	Down	-4.31E-01	1.10E-01		-6.51E-02	8.32E-01		-1.08E+00	3.46E-06	Down	-3.24E+00	4.64E-26	Down	-1.38E+00	8.59E-10	Down	Unigene4305_All//gi|30725514|gb|AAF37779.1|//1.00E-131//At2g40980 [Arabidopsis thaliana]	Unigene4305_All//6.00E-129//AT2G40980| LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein kinase-like (InterPro:IPR011009); Has 152 Blast hits to 139 proteins in 56 species: Archae - 0; Bacteria - 74; Metazoa - 0; Fungi - 0; Plants - 60; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink).	Unigene4305_All//0.00E+00//DR456237				nr -
Unigene43052_All	219	5.26	6.25	14.83	2.96	1.57	0.41	0.00	0.00	0.00	2.49E-01	6.39E-01		1.50E+00	7.12E-05	Up	-9.11E-01	3.04E-01		-2.84E+00	1.02E-02		null	null		null	null			Unigene43052_All//2.00E-07//TC133500				
Unigene43053_All	280	3.74	1.27	2.47	6.76	2.95	1.29	1.51	0.90	0.28	-1.56E+00	2.67E-02		-5.96E-01	3.93E-01		-1.20E+00	7.69E-03		-2.39E+00	9.39E-06	Down	-7.54E-01	4.77E-01		-2.41E+00	3.93E-02			Unigene43053_All//3.00E-07//TC159198				
Unigene43054_All	290	0.00	4.37	2.02	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.86E-07	Up	1.10E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene43054_All//gi|27311771|gb|AA000851.1|//5.00E-07//Unknown protein [Arabidopsis thaliana] >gi|30725542|gb|AAP37783.1| At5g61270 [Arabidopsis thaliana]						nr +
Unigene43056_All	646	0.41	0.71	0.16	0.15	0.16	0.07	0.07	0.00	1.60	8.02E-01	4.60E-01		-1.30E+00	4.36E-01		5.24E-02	9.66E-01		-1.14E+00	6.76E-01		-6.03E+00	6.56E-01		4.62E+00	2.03E-06	Up	Unigene43056_All//gi|226724697|sp|Q6DUY3.2|PUS7_ORYSJ//1.00E-41//RecName: Full=RNA pseudourine synthase 7; AltName: Full=RNA-uridine isomerase 7; AltName: Full=RNA pseudouridylate synthase 7	Unigene43056_All//3.00E-42//AT5G51140| pseudouridine synthase family protein	Unigene43056_All//5.00E-113//TC135273			GO:0009451//GO:0016798//GO:0016866//GO:0043231	nr +
Unigene43059_All	513	0.41	0.00	0.42	2.14	2.15	0.09	0.00	0.16	0.08	-8.67E+00	1.22E-01		2.52E-02	1.00E+00		7.90E-03	9.92E-01		-4.60E+00	8.28E-06	Down	7.35E+00	4.01E-01		6.28E+00	6.44E-01								
Unigene4306_All	484	1.08	2.30	1.10	0.10	0.85	7.09	0.00	0.00	0.25	1.09E+00	9.57E-02		2.54E-02	9.99E-01		3.05E+00	5.67E-02		6.11E+00	4.30E-19	Up	null	null		7.95E+00	2.43E-01		Unigene4306_All//gi|35187464|gb|AAQ84323.1|//4.00E-45//fiber protein Fb31 [Gossypium barbadense]	Unigene4306_All//1.00E-31//AT5G13170| SAG29 (SENESCENCE-ASSOCIATED PROTEIN 29)	Unigene4306_All//0.00E+00//TC176027				nr +
Unigene43062_All	561	0.56	1.45	3.04	0.00	0.43	0.32	0.53	0.15	0.00	1.37E+00	9.21E-02		2.44E+00	7.80E-05	Up	8.75E+00	1.04E-01		8.33E+00	1.94E-01		-1.82E+00	2.11E-01		-9.04E+00	1.58E-02		Unigene43062_All//gi|300608164|emb|CAZ86692.1|//4.00E-68//epoxide hydrolase 1 [Prunus persica]	Unigene43062_All//2.00E-59//AT3G05600| epoxide hydrolase, putative	Unigene43062_All//0.00E+00//TC174965			GO:0004713	nr -
Unigene4307_All	1263	13.30	9.35	11.76	1.66	6.57	6.90	0.57	0.26	2.02	-5.09E-01	1.70E-04		-1.77E-01	2.47E-01		1.99E+00	9.98E-20	Up	2.06E+00	4.67E-20	Up	-1.10E+00	1.49E-01		1.83E+00	1.63E-06	Up	Unigene4307_All//gi|297811437|ref|XP_002873602.1|//9.00E-98//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319439|gb|EFH49861.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4307_All//7.00E-91//AT5G13170| SAG29 (SENESCENCE-ASSOCIATED PROTEIN 29)	Unigene4307_All//0.00E+00//TC131505				nr +
Unigene43070_All	213	0.25	0.00	0.00	0.00	0.16	0.00	1.79	2.35	8.98	-7.94E+00	6.11E-01		-7.94E+00	6.23E-01		7.34E+00	8.29E-01		null	null		3.98E-01	6.52E-01		2.33E+00	1.30E-06	Up		Unigene43070_All//2.00E-38//gi|84148335|gb|DN779635.1|DN779635				
Unigene43079_All	390	0.94	1.82	2.05	0.38	1.06	0.12	0.22	0.43	3.68	9.54E-01	2.62E-01		1.12E+00	1.80E-01		1.47E+00	2.79E-01		-1.73E+00	5.01E-01		9.84E-01	6.33E-01		4.08E+00	3.98E-08	Up	Unigene43079_All//gi|149944287|gb|ABR46188.1|//3.00E-26//At4g21445 [Arabidopsis thaliana]	Unigene43079_All//6.00E-24//AT4G21445| unknown protein				GO:0004871//GO:0009532	nr +
Unigene4308_All	1193	11.01	11.55	13.17	15.03	13.83	18.28	19.88	17.48	9.58	6.97E-02	6.69E-01		2.58E-01	9.30E-02		-1.21E-01	4.34E-01		2.83E-01	1.97E-02		-1.86E-01	8.71E-02		-1.05E+00	4.19E-24	Down	Unigene4308_All//gi|297826587|ref|XP_002881176.1|//1.00E-111//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297327015|gb|EFH57435.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene4308_All//1.00E-93//AT2G31440| protein binding	Unigene4308_All//0.00E+00//TC133918				nr +
Unigene43080_All	416	15.22	11.69	15.74	10.30	9.44	6.51	22.36	8.14	5.65	-3.80E-01	1.15E-01		4.90E-02	8.43E-01		-1.26E-01	7.12E-01		-6.61E-01	2.40E-02		-1.46E+00	1.48E-15	Down	-1.98E+00	2.30E-24	Down	Unigene43080_All//gi|18073820|emb|CAC84914.1|//7.00E-53//phosphoenolpyruvate carboxylase [Ginkgo biloba]	Unigene43080_All//5.00E-35//AT1G53310| ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); catalytic/ phosphoenolpyruvate carboxylase	Unigene43080_All//8.00E-157//TC137097		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0004611//GO:0009060//GO:0016628//GO:0044424//GO:0071704	nr +
Unigene43082_All	646	0.00	0.00	0.00	0.00	0.00	0.00	1.70	3.17	0.00	null	null		null	null		null	null		null	null		8.98E-01	2.61E-02		-1.07E+01	3.33E-08	Down							ESTscan -
Unigene43083_All	748	0.00	0.00	0.00	0.00	0.46	0.00	0.34	1.23	2.93	null	null		null	null		8.85E+00	3.01E-02		null	null		1.86E+00	8.33E-03		3.11E+00	7.22E-10	Up	Unigene43083_All//gi|91806075|gb|AB657766.1|//1.00E-100//mandelonitrile lyase [Arabidopsis thaliana]	Unigene43083_All//5.00E-95//AT1G72050| (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative	Unigene43083_All//0.00E+00//DT461593		ko00460|Cyanoamino acid metabolism	GO:0006950//GO:0016491//GO:0019499//GO:0030554//GO:0031410//GO:0043231	nr +
Unigene43085_All	324	0.16	1.25	0.49	0.31	0.32	0.98	8.48	0.39	1.35	2.95E+00	5.91E-02		1.61E+00	5.11E-01		5.21E-02	9.66E-01		1.67E+00	3.09E-01		-4.45E+00	1.19E-15	Down	-2.65E+00	1.15E-10	Down							
Unigene43087_All	438	0.00	1.62	3.40	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	3.32E-04	Up	1.17E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene43087_All//gi|74272635|gb|AB401113.1|//5.00E-10//calmodulin [Chlamydomonas incerta]	Unigene43087_All//5.00E-10//AT3G43810| CAM7 (CALMODULIN 7); calcium ion binding			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005488	nr +
Unigene43089_All	211	91.75	49.71	33.57	58.79	55.65	49.02	388.74	287.02	146.14	-8.84E-01	5.12E-12		-1.45E+00	1.25E-24	Down	-7.90E-02	6.85E-01		-2.62E-01	1.30E-01		-4.38E-01	1.58E-17		-1.41E+00	1.61E-128	Down		Unigene43089_All//9.00E-115//BF273663				
Unigene4309_All	554	27.77	10.79	10.96	50.80	41.52	68.64	71.13	23.39	17.62	-1.36E+00	9.33E-19	Down	-1.34E+00	1.53E-17	Down	-2.91E-01	3.09E-03		4.34E-01	2.53E-07		-1.60E+00	7.16E-73	Down	-2.01E+00	1.72E-102	Down	Unigene4309_All//gi|15229631|ref|NP_190560.1|//3.00E-31//60S ribosomal protein L26 (RPL26A) [Arabidopsis thaliana] >gi|297816242|ref|XP_002876004.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|27735242|sp|P51414.2|RL26I_ARATH RecName: Full=60S ribosomal protein L26-1 >gi|6723436|emb|CAB66929.1| 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana] >gi|297321842|gb|EFH52263.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene4309_All//9.00E-23//AT3G49910| 60S ribosomal protein L26 (RPL26A)	Unigene4309_All//3.00E-129//TC151955		ko03010|Ribosome		nr +
Unigene43091_All	599	0.00	5.16	2.13	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.38E-17	Up	1.11E+01	4.68E-07	Up	null	null		null	null		null	null		null	null		Unigene43091_All//gi|6685535|sp|P56820.1|EIF3D_ARATH//2.00E-49//RecName: Full=Eukaryotic translation initiation factor 3 subunit D; Short=eIF3d; AltName: Full=eIF-3-zeta; AltName: Full=p66 >gi|5262788|emb|CAB45893.1| translation initiation factor eIF3-like protein [Arabidopsis thaliana] >gi|7268895|emb|CAB79098.1| translation initiation factor eIF3-like protein [Arabidopsis thaliana] >gi|208879518|gb|ACI131304.1| At4g20980 [Arabidopsis thaliana] >gi|222423664|dbj|BAH19799.1| AT4G20980 [Arabidopsis thaliana]	Unigene43091_All//4.00E-51//AT4G20980| eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative				GO:0006412//GO:0008135	nr +
Unigene43092_All	252	0.00	0.00	0.00	0.00	0.00	0.00	2.18	1.99	0.00	null	null		null	null		null	null		null	null		-1.32E-01	8.80E-01		-1.11E+01	2.80E-04	Down	Unigene43092_All//gi|219112013|ref|XP_002177758.1|//6.00E-10//adenosylhomocysteinase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217410643|gb|EEC50572.1| adenosylhomocysteinase [Phaeodactylum tricornutum CCAP 1055/1]	Unigene43092_All//4.00E-09//AT4G13940| MEE58 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding			ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0016802//GO:0044237	nr -
Unigene431_All	3118	5.32	3.40	5.41	14.76	14.10	10.81	4.05	2.99	1.90	-6.47E-01	2.09E-06		2.54E-02	8.73E-01		-6.59E-02	5.13E-01		-4.50E-01	2.49E-09		-4.40E-01	1.99E-03		-1.09E+00	5.37E-14	Down	Unigene431_All//gi|18391394|ref|NP_563908.1|//0.00E+00//ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / binding / microtubule motor [Arabidopsis thaliana] >gi|75173334|sp|Q9FZ06.1|ARK3_ARATH RecName: Full=Armadillo repeat-containing kinesin-like protein 3; AltName: Full=Phosphatidic acid kinase >gi|9954168|gb|AAG08965.1|AF159052_1 kinesin-like protein [Arabidopsis thaliana] >gi|162958327|dbj|BAF95587.1| armadillo repeat kinesin3 [Arabidopsis thaliana]	Unigene431_All//0.00E+00//AT1G12430| ARK3 (ARMADILLO REPEAT KINESIN 3); ATP binding / binding / microtubule motor	Unigene431_All//0.00E+00//gi|78335273|gb|DT555547.1|DT555547				nr +

Unigene43100_All	276	0.00	0.00	0.00	0.18	0.62	0.33	3.06	8.18	0.43	null	null		null	null		1.79E+00	5.20E-01		8.59E-01	7.94E-01		1.42E+00	3.34E-04	Up	-2.82E+00	5.38E-04	Down	Unigene43100_All//gi|224121660|ref|XP_002330621.1|//4.00E-09//predicted protein [Populus trichocarpa] >gi|222872225|gb|EEF09356.1| predicted protein [Populus trichocarpa]	Unigene43100_All//5.00E-05//AT3G47580| leucine-rich repeat transmembrane protein kinase, putative	Unigene43100_All//2.00E-135//gi|109873265|gb|DW502240.1|DW502240			GO:0005488//GO:0016301	nr +
Unigene43102_All	569	0.46	0.45	3.56	0.44	0.61	0.64	0.00	0.00	0.00	-4.66E-02	9.86E-01		2.95E+00	9.74E-07	Up	4.68E-01	7.79E-01		5.37E-01	6.94E-01		null	null		null	null		Unigene43102_All//gi|255606154|ref|XP_002538514.1|//1.00E-60//Quinohemoprotein ethanol dehydrogenase, putative [Ricinus communis] >gi|223511783|gb|EEF23869.1| Quinohemoprotein ethanol dehydrogenase, putative [Ricinus communis]					GO:0016614	nr +
Unigene43106_All	275	0.00	0.00	0.00	0.00	0.00	0.00	204.94	42.71	155.15	null	null		null	null		null	null		null	null		-2.26E+00	1.10E-164	Down	-4.02E-01	6.01E-11		Unigene43106_All//gi|169349|gb|AAA33765.1|//6.00E-30//hydroxyproline-rich glycoprotein [Phaseolus vulgaris]						nr +
Unigene43107_All	250	0.00	4.26	3.20	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.81E-06	Up	1.16E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene43107_All//sp|Q9DCJ5|NDUA8_MOUSE//2.00E-08//NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Mus musculus GN=Ndufa8 PE=1 SV=3						swissprot -
Unigene43108_All	422	0.74	0.12	0.50	1.65	0.73	0.75	2.71	0.89	0.57	-2.63E+00	1.31E-01		-5.60E-01	6.63E-01		-1.17E+00	1.61E-01		-1.14E+00	2.01E-01		-1.60E+00	7.50E-03		-2.26E+00	3.40E-04	Down			Unigene43108_All//1.00E-167//TC152539				
Unigene4311_All	1618	0.23	2.32	0.13	3.73	5.45	9.60	0.73	1.42	2.04	3.36E+00	5.14E-14	Up	-7.83E-01	5.53E-01		5.49E-01	3.35E-03		1.37E+00	4.35E-20	Up	9.57E-01	1.12E-02		1.48E+00	2.50E-06	Up	Unigene4311_All//gi|209954731|dbj|BAG80556.1|//0.00E+00//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene4311_All//2.00E-158//AT4G01070| GT72B1: UDP-glucosyltransferase/ UDP-glycosyltransferase/ transferase, transferring glycosyl groups	Unigene4311_All//0.00E+00//TC178546				nr -
Unigene43113_All	597	0.00	48.55	19.71	0.00	0.00	0.00	0.00	0.00	0.00	1.56E+01	4.43E-167	Up	1.43E+01	3.66E-66	Up	null	null		null	null		null	null		null	null		Unigene43113_All//gi|301123509|ref|XP_002909481.1|//3.00E-47//60S ribosomal protein L21-1 [Phytophthora infestans T30-4] >gi|262100243|gb|EEY58295.1| 60S ribosomal protein L21-1 [Phytophthora infestans T30-4]	Unigene43113_All//3.00E-39//AT1G57860| 60S ribosomal protein L21			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene43116_All	398	0.79	0.51	1.34	5.88	3.81	1.70	3.40	0.74	1.00	-6.31E-01	6.22E-01		7.62E-01	4.52E-01		-6.28E-01	1.23E-01		-1.79E+00	5.01E-05	Down	-2.21E+00	1.58E-04	Down	-1.76E+00	9.57E-04	Down			Unigene43116_All//2.00E-64//gi|109855732|gb|DW484711.1|DW484711				
Unigene43118_All	397	1.32	19.14	1.61	1.25	3.82	6.71	79.13	138.02	124.83	3.86E+00	3.11E-31	Up	2.89E-01	7.25E-01		1.60E+00	4.07E-03		2.42E+00	9.28E-08	Up	8.03E-01	7.60E-34		6.58E-01	1.75E-22		Unigene43118_All//gi|156767195|gb|ABU95104.1|//5.00E-24//asparagine synthetase [Phaseolus vulgaris]	Unigene43118_All//5.00E-24//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene43118_All//3.00E-48//gi|109838726|gb|DW237287.1|DW237287		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0006528//GO:0009064//GO:0009267//GO:0009642//GO:0009746//GO:0016884//GO:0032559//GO:0034285	nr -
Unigene4312_All	1712	0.98	0.77	0.44	1.92	3.78	4.35	3.11	4.10	11.31	-3.46E-01	4.98E-01		-1.17E+00	3.09E-02		9.78E-01	1.01E-05		1.18E+00	4.81E-08	Up	3.98E-01	4.90E-02		1.86E+00	3.07E-45	Up	Unigene4312_All//gi|30691233|ref|NP_174300.2|//1.00E-164//glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Unigene4312_All//9.00E-150//AT1G30080| glycosyl hydrolase family 17 protein	Unigene4312_All//3.00E-132//CO117865		ko00500|Starch and sucrose metabolism		nr -
Unigene43122_All	416	0.50	0.73	3.58	0.96	0.33	0.00	0.00	0.00	0.00	5.39E-01	6.71E-01		2.83E+00	6.17E-05	Up	-1.53E+00	2.05E-01		-9.90E+00	1.11E-02		null	null		null	null								ESTscan +
Unigene43124_All	479	0.00	0.00	0.00	0.00	0.07	0.00	3.88	3.32	0.33	null	null		null	null		6.17E+00	8.29E-01		null	null		-2.28E-01	6.48E-01		-3.55E+00	1.30E-09	Down	Unigene43124_All//gi|195618614|gb|ACG31137.1|//1.00E-58//40S ribosomal protein S18 [Zea mays]	Unigene43124_All//3.00E-50//AT4G08800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006412//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr +
Unigene43128_All	505	1.86	3.41	2.95	9.67	6.07	3.76	2.60	2.57	0.95	8.71E-01	8.07E-02		6.63E-01	2.44E-01		-6.72E-01	8.92E-03		-1.36E+00	8.23E-07	Down	-1.66E-02	1.01E+00		-1.46E+00	5.49E-03		Unigene43128_All//gi|255564343|ref|XP_002523168.1|//9.00E-12//ATP binding protein, putative [Ricinus communis] >gi|223537575|gb|EEF39199.1| ATP binding protein, putative [Ricinus communis]						nr +
Unigene43131_All	410	0.64	0.62	2.60	4.50	2.77	1.10	2.37	2.24	0.10	-4.64E-02	9.86E-01		2.03E+00	8.68E-03		-6.98E-01	1.37E-01		-2.03E+00	1.02E-04	Down	-8.07E-02	9.06E-01		-4.61E+00	3.32E-06	Down	Unigene43131_All//gi|296203760|gb|AC105891.1|//2.00E-46//kinase-like protein pac.x.5.1 [Platanus x acerifolia]	Unigene43131_All//3.00E-32//AT3G47090| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0003676//GO:0004713//GO:0006464//GO:0016628//GO:0031224//GO:0032559	nr -
Unigene43135_All	443	0.00	16.36	8.41	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	2.04E-41	Up	1.30E+01	1.20E-20	Up	null	null		null	null		null	null		null	null								
Unigene43136_All	501	0.21	0.30	0.00	1.29	1.37	1.53	1.60	0.33	0.24	5.38E-01	7.79E-01		-7.71E+00	3.92E-01		8.88E-02	9.49E-01		2.46E-01	7.57E-01		-2.26E+00	4.82E-03		-2.75E+00	9.43E-04	Down							
Unigene43137_All	842	0.25	0.48	0.13	0.30	0.08	0.00	8.99	5.16	1.56	9.53E-01	4.14E-01		-9.75E-01	6.20E-01		-1.85E+00	2.75E-01		-8.21E+00	7.33E-02		-8.00E-01	2.33E-05		-2.53E+00	1.27E-26	Down	Unigene43137_All//gi|145333011|ref|NP_001078371.1|//5.00E-12//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene43137_All//2.00E-07//AT4G11000| ankyrin repeat family protein	Unigene43137_All//7.00E-48//ES843168			GO:0010033	nr +
Unigene43138_All	789	0.00	20.42	6.28	0.00	0.00	0.00	0.00	0.00	0.00	1.43E+01	1.37E-92	Up	1.26E+01	1.53E-27	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene4314_All	300	2.44	3.38	9.59	10.29	4.94	2.11	6.20	3.62	5.05	4.68E-01	4.89E-01		1.97E+00	4.12E-06	Up	-1.06E+00	1.41E-03		-2.29E+00	1.32E-08	Down	-7.76E-01	7.05E-02		-2.97E-01	4.91E-01								
Unigene43140_All	539	0.10	0.00	0.20	0.55	0.13	0.17	3.53	4.50	1.11	-6.60E+00	6.11E-01		1.03E+00	7.03E-01		-2.12E+00	1.65E-01		-1.72E+00	2.89E-01		3.50E-01	3.79E-01		-1.67E+00	1.23E-04	Down							
Unigene43148_All	561	13.71	0.18	6.83	0.00	0.00	0.00	0.68	0.00	0.36	-6.25E+00	3.43E-41	Down	-1.00E+00	5.49E-06	Down	null	null					-9.41E+00	6.18E-03		-9.34E-01	3.79E-01		Unigene43148_All//gi|224113419|ref|XP_002316491.1|//2.00E-72//cationic amino acid transporter [Populus trichocarpa] >gi|222865531|gb|EEF02662.1| cationic amino acid transporter [Populus trichocarpa]	Unigene43148_All//6.00E-56//AT5G04770| CAT6 (CATIONIC AMINO ACID TRANSPORTER 6); amino acid transmembrane transporter/ basic amino acid transmembrane transporter/ cationic amino acid transmembrane transporter	Unigene43148_All//1.00E-26//ES794141			GO:0015171//GO:0015837//GO:0031224//GO:0034110//GO:0043231//GO:0051707	nr -
Unigene43149_All	593	0.00	6.92	2.78	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.25E-23	Up	1.14E+01	4.30E-09	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene43153_All	570	0.00	0.00	0.00	0.00	0.00	0.00	6.38	6.23	0.07	null	null		null	null		null	null		null	null		-3.35E-02	9.30E-01		-6.51E+00	4.29E-25	Down	Unigene43153_All//gi|302128114|dbj|BAJ13478.1|//9.00E-79//actin 1 [Guillardia theta]	Unigene43153_All//5.00E-78//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene43153_All//5.00E-51//gi|314006833|gb|CD485868.1|CD485868			GO:0005198//GO:0006950//GO:0006996//GO:0009314//GO:0009725//GO:0009913//GO:0015629//GO:0016020//GO:0017111//GO:0030312//GO:0031981//GO:0032559//GO:0048588	nr -
Unigene43157_All	1142	0.55	0.18	0.28	0.17	0.00	0.00	8.59	9.22	3.56	-1.63E+00	9.23E-02		-9.75E-01	3.16E-01		-7.45E+00	8.42E-02		-7.45E+00	1.33E-01		1.03E-01	6.06E-01		-1.27E+00	7.19E-14	Down							
Unigene43158_All	889	0.00	0.00	0.00	0.00	0.00	0.00	3.23	1.32	0.90	null	null		null	null		null	null		null	null		-1.30E+00	1.31E-04	Down	-1.85E+00	1.86E-07	Down	Unigene43158_All//gi|224112635|ref|XP_002332743.1|//7.00E-54//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222833055|gb|EEE71532.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene43158_All//2.00E-34//AT4G27190| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction	GO:0016787	nr -
Unigene4316_All	1862	1.80	0.63	1.72	4.01	3.03	3.83	5.95	2.65	3.83	-1.52E+00	2.16E-05	Down	-6.77E-02	8.48E-01		-4.04E-01	5.53E-02		-6.65E-02	7.82E-01		-1.17E+00	2.85E-13	Down	-6.35E-01	1.84E-05		Unigene4316_All//gi|297806659|ref|XP_002871213.1|//1.00E-103//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297317050|gb|EFH47472.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene4316_All//2.00E-93//AT5G27010| binding	Unigene4316_All//1.00E-57//CK640460				nr +
Unigene43161_All	612	0.34	0.50	0.17	0.33	0.00	0.15	3.25	0.00	5.01	5.39E-01	6.71E-01		-9.75E-01	6.20E-01		-8.35E+00	8.42E-02		-1.14E+00	5.69E-01		-1.17E+01	4.61E-14	Down	6.26E-01	4.18E-02				Unigene43161_All//0.00E+00//gi|164341395|gb|ES805663.1|ES805663				
Unigene43162_All	698	0.45	0.44	0.31	0.57	4.49	3.56	0.00	0.00	0.17	-4.60E-02	9.84E-01		-5.59E-01	6.63E-01		2.98E+00	8.46E-12	Up	2.64E+00	5.97E-08	Up	null	null		7.42E+00	2.43E-01		Unigene43162_All//gi|110737098|dbj|BAF00501.1|//1.00E-89//zinc finger like protein [Arabidopsis thaliana]	Unigene43162_All//5.00E-91//AT3G57670| NTT (NO TRANSMITTING TRACT); nucleic acid binding / transcription factor/ zinc ion binding	Unigene43162_All//3.00E-46//gi|21103664|gb|BQ415977.1|BQ415977	C2H2		GO:0000904//GO:0001071//GO:0010468//GO:0031410//GO:0043231//GO:0046914	nr -
Unigene43163_All	386	3.12	0.00	0.69	1.81	1.07	1.52	0.55	0.00	0.00	-1.16E+01	5.01E-07	Down	-2.18E+00	3.05E-03		-7.55E-01	3.69E-01		-2.48E-01	7.56E-01		-9.10E+00	7.43E-02		-9.10E+00	5.79E-02		Unigene43163_All//gi|60327212|gb|AAX19029.1|//6.00E-27//Hcr2-p6 [Solanum pimpinellifolium]	Unigene43163_All//2.00E-27//AT3G24240| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0005488//GO:0044464	nr +
Unigene43164_All	629	0.00	0.00	0.00	0.00	0.00	0.00	2.76	5.45	0.06	null	null		null	null		null	null		null	null		9.83E-01	1.02E-03		-5.44E+00	1.77E-11	Down	Unigene43164_All//gi|1706586|sp|P50236.1|EF1AC_PORPU//1.00E-83//RecName: Full=Elongation factor 1-alpha C; Short=EF-1-alpha C >gi|476155|gb|AAA61793.1| EF1-alpha [Porphyra purpurea]	Unigene43164_All//2.00E-71//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene43164_All//3.00E-15//gi|13354929|gb|BG445277.1|BG445277			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene43165_All	441	0.00	6.89	7.73	0.00	0.08	0.00	0.00	0.00	0.00	1.28E+01	2.67E-17	Up	1.29E+01	7.38E-19	Up	6.29E+00	8.29E-01		null	null		null	null		null	null		Unigene43165_All//sp|P63312|TYB10_RAT//9.00E-18//Thymosin beta-10 OS=Rattus norvegicus GN=Tmsb10 PE=2 SV=2						swissprot -
Unigene43167_All	574	0.00	0.00	0.00	0.00	0.00	0.00	2.21	2.69	0.00	null	null		null	null		null	null		null	null		2.86E-01	5.92E-01		-1.11E+01	1.99E-09	Down	Unigene43167_All//gi|301108215|ref|XP_002903189.1|//1.00E-73//guanine nucleotide-binding protein subunit beta-2-like protein [Phytophthora infestans T30-4] >gi|262097361|gb|EEY55613.1| guanine nucleotide-binding protein subunit beta-2-like protein [Phytophthora infestans T30-4]	Unigene43167_All//6.00E-64//AT1G48630| RACK1B_AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding	Unigene43167_All//2.00E-07//EX168368		ko03040|Spliceosome	GO:0005840//GO:0009536//GO:0010038//GO:0031981//GO:0048513	nr -
Unigene4317_All	1269	1.03	2.48	0.88	4.95	2.93	3.10	2.80	1.78	3.30	1.26E+00	4.83E-04	Up	-2.26E-01	6.96E-01		-7.55E-01	5.60E-04		-6.76E-01	3.62E-03		-6.54E-01	2.51E-02		2.36E-01	3.97E-01		Unigene4317_All//gi|18401909|ref|NP_564657.1|//6.00E-19//spliceosome protein-related [Arabidopsis thaliana]	Unigene4317_All//2.00E-18//AT1G54380| spliceosome protein-related	Unigene4317_All//0.00E+00//ES833640				nr +
Unigene43170_All	857	0.00	0.00	0.00	0.64	0.08	0.16	0.69	2.83	1.02	null	null		null	null		-2.99E+00	9.38E-03		-2.02E+00	7.05E-02		2.03E+00	7.33E-07	Up	5.66E-01	3.85E-01				Unigene43170_All//2.00E-85//TC135236				

Unigene43172_A11	497	0.00	5.20	4.29	0.00	0.07	0.00	0.00	0.00	0.00	1.23E+01	1.06E-14	Up	1.21E+01	9.78E-12	Up	6.11E+00	8.29E-01		null	null		null	null		null	null		Unigene43172_A11//gi|4501883|ref|NP_001604.1|//8.00E-63//actin, aortic smooth muscle [Homo sapiens] >gi|6671507|ref|NP_031418.1| actin, aortic smooth muscle [Mus musculus] >gi|78045238|ref|NP_001029674.1| actin, aortic smooth muscle [Bos taurus] >gi|110625958|ref|NP_112266.1| actin, aortic smooth muscle [Rattus norvegicus] >gi|156119362|ref|NP_001095152.1| actin, aortic smooth muscle [Oryctolagus cuniculus] >gi|197097944|ref|NP_001126814.1| actin, aortic smooth muscle [Pongo abelii] >gi|213688375|ref|NP_001135417.1| actin, aortic smooth muscle [Homo sapiens] >gi|257470979|ref|NP_001158122.1| actin, aortic smooth muscle [Sus scrofa] >gi|73996085|ref|XP_534781.2| PREDICTED: similar to Actin, aortic smooth muscle (Alpha-actin 2) [Canis familiaris] >gi|114631685|ref|XP_521550.2|	Unigene43172_A11//2.00E-57//AT3G18780| ACT2 (ACTIN 2); structural constituent of cytoskeleton	Unigene43172_A11//5.00E-26//gi|31406833|gb|CD485868.1|CD485868		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008015//GO:0008092//GO:0012501//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0048747//GO:0051707//GO:0060415	nr -
Unigene43175_A11	339	0.00	2.24	0.00	0.15	0.10	1.87	0.12	0.00	0.35	1.11E+01	1.76E-04	Up	null	null		-5.32E-01	8.25E-01		3.67E+00	5.05E-03		-6.96E+00	6.56E-01		1.50E+00	5.58E-01		Unigene43175_A11//gi|68300884|gb|AY89374.1|//5.00E-50//amylase 1 [Nicotiana langsdorffii x Nicotiana sanderae]	Unigene43175_A11//1.00E-45//AT3G23920| BAM1 (BETA-AMYLASE 1); beta-amylase	Unigene43175_A11//2.00E-104//C0127468		ko00500|Starch and sucrose metabolism	GO:0003006//GO:0005982//GO:0006464//GO:0006950//GO:0007167//GO:0009933//GO:0010073//GO:0016020//GO:0016160//GO:0016772//GO:0032559//GO:0043167//GO:0043231//GO:0044444	nr -
Unigene43176_A11	407	1.54	0.00	1.57	2.20	0.68	0.00	0.10	0.31	0.00	-1.06E+01	7.91E-04	Down	2.54E-02	9.97E-01		-1.70E+00	1.98E-02		-1.11E+01	1.21E-05	Down	1.57E+00	5.45E-01		-6.70E+00	6.12E-01				Unigene43176_A11//4.00E-180//DW519466				
Unigene43178_A11	512	3.07	7.32	7.80	0.19	0.87	0.35	0.00	0.00	0.00	1.26E+00	1.24E-04	Up	1.35E+00	4.36E-05	Up	2.17E+00	1.06E-01		8.58E-01	6.95E-01		null	null		null	null		Unigene43178_A11//gi|75155138|sp|Q8LCS3.1|EPF2_ARATH|6.00E-26//RecName: Full=Protein EPIDERMAL PATTERNING FACTOR 2; Flags: Precursor >gi|237512857|dbj|BAH58781.1| EPF2 [Arabidopsis thaliana]	Unigene43178_A11//4.00E-27//AT1G34245| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabidopsis thaliana protein match is: EPF1 (EPIDERMAL PATTERNING FACTOR 1) (TAIR:AT2G20875.1); Has 12 Blast hits to 12 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).				GO:0003002//GO:0009791//GO:0031410	nr -
Unigene43182_A11	221	4.02	4.36	2.17	1.13	0.62	1.63	6.89	22.69	21.09	1.14E-01	8.65E-01		-8.92E-01	2.46E-01		-8.55E-01	5.73E-01		5.37E-01	6.94E-01		1.72E+00	7.14E-11	Up	1.61E+00	1.34E-09	Up	Unigene43182_A11//gi|11385461|gb|AG34813.1|AF243378_1//3.00E-10//glutathione S-transferase GST 23 [Glycine max]	Unigene43182_A11//2.00E-08//AT5G41240| ATGSTT2 (GLUTATHIONE S-TRANSFERASE THETA 2); glutathione transferase	Unigene43182_A11//5.00E-70//gi|48752742|gb|CO083261.1|CO083261			GO:0009404//GO:0016765//GO:0043231	nr +
Unigene43185_A11	989	0.00	0.00	0.00	0.00	0.00	0.00	6.20	5.24	0.60	null	null		null	null		null	null		null	null		-2.42E-01	3.05E-01		-3.36E+00	7.83E-29	Down			Unigene43185_A11//3.00E-10//DW479422				
Unigene43186_A11	300	0.00	4.73	2.49	0.83	1.15	1.35	1.13	0.56	0.93	1.22E+01	4.06E-08	Up	1.13E+01	3.27E-04	Up	4.67E-01	7.79E-01		7.07E-01	5.97E-01		-1.02E+00	3.99E-01		-2.78E-01	7.81E-01								
Unigene43188_A11	397	1.19	0.26	0.00	1.76	1.82	0.57	2.56	0.21	0.90	-2.22E+00	7.76E-02		-1.02E+01	8.63E-03		5.23E-02	9.65E-01		-1.63E+00	7.45E-02		-3.60E+00	2.38E-05	Down	-1.50E+00	1.41E-02		Unigene43188_A11//gi|115444287|ref|NP_001045923.1|//8.00E-43//Os02g0153000 [Oryza sativa Japonica Group] >gi|51535341|dbj|BAD38600.1| ternary complex factor MIP1-like [Oryza sativa Japonica Group] >gi|74272488|gb|ABA01090.1| ternary complex factor MIP1-like [Oryza rufipogon] >gi|76364057|gb|ABA41566.1| ternary complex factor MIP1-like [Oryza sativa Indica Group] >gi|113535454|dbj|BAF07837.1| Os02g0153000 [Oryza sativa Japonica Group]	Unigene43188_A11//8.00E-43//AT3G13000| transcription factor	Unigene43188_A11//1.00E-152//C0099117			GO:0010468//GO:0043231	nr -
Unigene43193_A11	357	6.89	2.55	7.61	0.00	0.58	0.00	0.12	0.00	0.00	-1.43E+00	6.98E-04	Down	1.43E-01	7.10E-01		9.18E+00	1.57E-01		null	null		-6.89E+00	6.56E-01		-6.89E+00	6.12E-01				Unigene43193_A11//4.00E-07//DW506513				
Unigene43195_A11	427	3.80	0.00	0.87	0.58	1.45	0.95	0.40	0.39	0.56	-1.19E+01	2.11E-09	Down	-2.12E+00	5.10E-04	Down	1.32E+00	1.88E-01		7.07E-01	5.97E-01		-1.69E-02	1.02E+00		4.99E-01	7.07E-01		Unigene43195_A11//gi|297820754|ref|XP_002878260.1|//1.00E-12//ATMRP14 [Arabidopsis lyrata subsp. lyrata] >gi|297324098|gb|EFH54519.1| ATMRP14 [Arabidopsis lyrata subsp. lyrata]	Unigene43195_A11//1.00E-13//AT3G59140| ATMRP14; ATPase, coupled to transmembrane movement of substances	Unigene43195_A11//6.00E-19//TC172337			GO:0017111	nr -
Unigene43196_A11	489	0.96	0.21	1.96	3.26	1.69	0.18	1.12	0.00	0.08	-2.22E+00	7.76E-02		1.03E+00	1.68E-01		-9.48E-01	5.80E-02		-4.14E+00	8.22E-08	Down	-1.01E+01	4.61E-04	Down	-3.79E+00	2.03E-03		Unigene43196_A11//gi|224141315|ref|XP_002324019.1|//1.00E-63//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222867021|gb|EEF04152.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene43196_A11//1.00E-55//AT3G28345| ABC transporter family protein	Unigene43196_A11//2.00E-10//DT462038		ko02010|ABC transporters	GO:0006810//GO:0015405//GO:0017111//GO:0031224//GO:0032559	nr +
Unigene43198_A11	1018	0.00	38.67	15.85	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	3.08E-227	Up	1.40E+01	5.21E-91	Up	null	null		null	null		null	null		null	null		Unigene43198_A11//sp|P11997|LSP1G_DROME//4.00E-111//Larval serum protein 1 gamma chain OS=Drosophila melanogaster GN=Lsp1gamma PE=2 SV=2						swissprot -
Unigene43199_A11	437	0.00	5.91	0.85	0.80	2.84	4.55	0.39	0.00	0.18	1.25E+01	1.06E-14	Up	9.74E+00	2.50E-02		1.83E+00	4.77E-03		2.51E+00	3.78E-06	Up	-8.60E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene43199_A11//gi|29170509|gb|AA065960.1|//8.00E-50//oleosin [Corylus avellana]	Unigene43199_A11//1.00E-20//AT4G25140| OLEO1 (OLEOSIN 1)	Unigene43199_A11//0.00E+00//TC164815			GO:0005811//GO:0031224	nr +
Unigene4320_A11	735	39.37	37.92	21.23	219.52	158.07	186.00	240.91	120.89	120.38	-5.41E-02	6.20E-01		-8.91E-01	4.61E-17		-4.74E-01	1.75E-38		-2.39E-01	7.09E-10		-9.95E-01	1.60E-154		-1.00E+00	2.22E-160	Down	Unigene4320_A11//gi|211906438|gb|ACJ11712.1|//1.00E-140//UDP-D-glucose dehydrogenase [Gossypium hirsutum]	Unigene4320_A11//4.00E-134//AT5G15490| UDP-glucose 6-dehydrogenase, putative	Unigene4320_A11//0.00E+00//TC157101		ko00500|Starch and sucrose metabolism/ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism/ko00040|Pentose and glucuronate interconversions		nr -
Unigene43200_A11	567	0.00	0.00	0.00	0.00	0.00	0.00	4.10	3.17	0.00	null	null		null	null		null	null		null	null		-3.72E-01	3.57E-01		-1.20E+01	3.99E-17	Down	Unigene43200_A11//gi|159471131|ref|XP_001693710.1|//6.00E-63//ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|269969596|sp|A8HS48.1|RS3A_CHLRE RecName: Full=40S ribosomal protein S3a >gi|158283213|gb|EDP08964.1| ribosomal protein S3a [Chlamydomonas reinhardtii]	Unigene43200_A11//8.00E-62//AT4G34670| 40S ribosomal protein S3A (RPS3aB)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030012//GO:0031981	nr +
Unigene43205_A11	371	0.85	6.56	0.57	1.07	0.56	0.24	0.00	0.00	1.29	2.95E+00	2.52E-08	Up	-5.60E-01	6.63E-01		-9.48E-01	4.21E-01		-2.14E+00	1.26E-01		null	null		1.03E+01	1.14E-03		Unigene43205_A11//gi|225447304|ref|XP_002279653.1|//7.00E-10//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene43208_A11	347	1.66	0.00	0.46	1.58	0.69	0.13	27.42	9.76	6.20	-1.07E+01	1.52E-03		-1.85E+00	9.61E-02		-1.18E+00	2.25E-01		-3.60E+00	8.97E-03		-1.49E+00	2.14E-16	Down	-2.14E+00	1.91E-27	Down	Unigene43208_A11//gi|473878|gb|AAA17742.1|//5.00E-10//calnexin homolog [Arabidopsis thaliana]		Unigene43208_A11//9.00E-107//C0083254		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	GO:0005515//GO:0009536//GO:0030246//GO:0031090//GO:0031224//GO:0044267//GO:0046872	nr +
Unigene4321_A11	1005	7.08	10.23	8.42	17.65	12.85	16.22	797.64	378.28	295.44	5.32E-01	2.90E-03		2.51E-01	2.51E-01		-4.58E-01	1.87E-04		-1.21E-01	4.48E-01		-1.08E+00	0.00E+00	Down	-1.43E+00	0.00E+00	Down	Unigene4321_A11//gi|74273314|gb|AB401325.1|//2.00E-58//VDR66 [Gossypium hirsutum] >gi|83356301|gb|ABC16635.1| bet vl [Gossypium hirsutum]	Unigene4321_A11//2.00E-50//AT1G70830| MLP28 (MLP-LIKE PROTEIN 28)	Unigene4321_A11//0.00E+00//gi|164320377|gb|ES816853.1|ES816853				nr +
Unigene43211_A11	478	0.00	72.61	31.64	0.00	0.00	0.00	0.00	0.00	0.00	1.61E+01	3.11E-200	Up	1.49E+01	3.01E-85	Up	null	null		null	null		null	null		null	null		Unigene43211_A11//gi|195623336|gb|ACG33498.1|//9.00E-29//60S ribosomal protein L34 [Zea mays]	Unigene43211_A11//7.00E-28//AT1G26880| 60S ribosomal protein L34 (RPL34A)			ko03010|Ribosome	GO:0043231	nr +
Unigene43212_A11	431	0.00	47.97	21.25	0.00	0.00	0.00	0.00	0.00	0.00	1.55E+01	5.87E-119	Up	1.44E+01	2.42E-51	Up	null	null		null	null		null	null		null	null		Unigene43212_A11//gi|161727354|dbj|BAF94304.1|//2.00E-13//lactonase [Euglena gracilis]						nr -
Unigene43214_A11	384	0.82	0.00	0.00	0.13	1.70	0.71	0.33	0.65	2.49	-9.68E+00	3.65E-02		-9.68E+00	4.90E-02		3.72E+00	3.55E-03		2.44E+00	2.22E-01		9.84E-01	5.17E-01		2.91E+00	1.88E-04	Up	Unigene43214_A11//gi|2586082|gb|AAB82754.1|//3.00E-19//retrofit [Oryza longistaminata]					GO:0003676//GO:0006259//GO:0043231	nr -
Unigene43216_A11	869	0.00	0.00	0.00	0.00	0.00	0.00	1.99	3.27	0.00	null	null		null	null		null	null		null	null		7.13E-01	3.23E-02		-1.10E+01	8.37E-13	Down	Unigene43216_A11//gi|219113969|ref|XP_002176167.1|//2.00E-07//Trustulin 5 [Phaeodactylum tricornutum CCAP 1055/1] >gi|217402880|gb|EEC42847.1| frustulin 5 [Phaeodactylum tricornutum CCAP 1055/1]				ko04141|Protein processing in endoplasmic reticulum//ko03420|Nucleotide excision repair		nr +
Unigene43217_A11	340	0.00	0.00	0.00	6.15	2.84	1.06	0.12	0.00	0.00	null	null		null	null		-1.12E+00	8.02E-03		-2.53E+00	1.08E-06	Down	-6.96E+00	6.56E-01		-6.96E+00	6.12E-01		Unigene43217_A11//gi|209954729|dbj|BAG80555.1|//5.00E-32//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene43217_A11//5.00E-28//AT2G36750| UGT73C1 (UDP-GLUCOSYL TRANSFERASE 73C1); UDP-glucosyltransferase/ UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transferring glycosyl groups			ko00908|Zeatin biosynthesis	GO:0035251	nr +
Unigene43220_A11	260	3.42	4.09	3.89	0.77	0.79	0.00	5.69	1.93	0.77	2.59E-01	6.75E-01		1.86E-01	7.75E-01		5.23E-02	9.88E-01		-9.58E+00	1.33E-01		-1.56E+00	2.28E-03		-2.89E+00	1.35E-06	Down			Unigene43220_A11//2.00E-39//ES838914				
Unigene43221_A11	1271	0.29	0.12	0.00	0.20	0.14	0.07	4.09	13.71	13.60	-1.27E+00	3.36E-01		-8.17E+00	2.78E-02		-5.33E-01	7.12E-01		-1.46E+00	4.07E-01		1.74E+00	1.33E-36	Up	1.73E+00	9.02E-37	Up	Unigene43221_A11//gi|224066615|ref|XP_002302164.1|//7.00E-57//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222843890|gb|EEE81437.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene43221_A11//9.00E-19//AT5G50080| DNA binding / transcription factor	Unigene43221_A11//0.00E+00//ES831270	AP2-EREBP		GO:0006350//GO:0006952//GO:0009738//GO:0009746//GO:0050789	nr -
Unigene43224_A11	455	0.00	0.00	0.00	0.00	0.00	0.00	3.53	4.59	0.00	null	null		null	null		null	null		null	null		3.79E-01	3.78E-01		-1.18E+01	7.00E-12	Down							

Unigene43228_All	527	0.00	0.00	0.00	0.00	0.00	0.00	5.94	5.08	0.15	null	null		null	null		null	null		null	null		-2.26E-01	5.25E-01		-5.30E+00	3.79E-20	Down	Unigene43228_All//gi|2894306|emb|CAA11268.1|//2.00E-76//ubiquitin extension protein [Nicotiana tabacum] >gi|59800131|gb|AAX07419.1| ubiquitin/s27a 40S ribosomal protein [Nicotiana benthamiana]	Unigene43228_All//1.00E-58//AT2G47710| UBQ6; protein binding	Unigene43228_All//1.00E-42//CD486028		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene43229_All	488	0.00	1.04	2.18	0.00	0.00	0.00	0.00	0.00	0.00	1.00E+01	4.04E-03		1.11E+01	6.62E-06	Up	null	null		null	null		null	null		null	null								
Unigene43232_All	709	0.00	0.00	0.00	0.00	0.00	0.00	3.70	0.94	1.63	null	null		null	null		null	null		null	null		-1.97E+00	4.08E-07	Down	-1.18E+00	5.72E-04	Down	Unigene43232_All//gi|224112158|ref|XP_002332820.1|//2.00E-07//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834208|gb|EEE72685.1| cc-nbs-lrr resistance protein [Populus trichocarpa]						nr +
Unigene43236_All	856	0.18	0.00	0.00	1.98	0.80	1.00	6.22	1.56	0.98	-7.52E+00	2.15E-01		-7.52E+00	2.44E-01		-1.30E+00	7.01E-03		-9.81E-01	5.37E-02		-1.99E+00	6.61E-14	Down	-2.67E+00	3.81E-20	Down	Unigene43236_All//gi|38454172|gb|AAR20780.1|//1.00E-34//At1g64690 [Arabidopsis thaliana] >gi|38604052|gb|AAR24769.1| At1g64690 [Arabidopsis thaliana]	Unigene43236_All//5.00E-36//AT1G64690| unknown protein	Unigene43236_All//2.00E-60//TC166656				nr -
Unigene43237_All	347	249.24	294.09	208.70	298.31	248.09	457.88	304.98	241.38	150.74	2.39E-01	3.34E-06		-2.56E-01	9.61E-06		-2.66E-01	1.12E-08		6.18E-01	6.55E-54		-3.37E-01	4.32E-14		-1.02E+00	1.14E-98	Down	Unigene43237_All//gi|224066295|ref|XP_002302069.1|//3.00E-20//histone H1 [Populus trichocarpa] >gi|222843795|gb|EEE81342.1| histone H1 [Populus trichocarpa]		Unigene43237_All//0.00E+00//gi|21094889|gb|BQ407202.1|BQ407202			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr +
Unigene43238_All	200	3.40	6.08	2.66	4.98	3.96	3.84	1.27	6.69	5.78	8.38E-01	1.73E-01		-3.53E-01	6.64E-01		-3.31E-01	6.19E-01		-3.76E-01	6.31E-01		2.40E+00	7.61E-05	Up	2.19E+00	4.81E-04	Up							
Unigene43241_All	1326	0.08	0.08	0.00	0.53	0.34	0.20	0.26	1.10	6.46	-4.65E-02	9.88E-01		-6.30E+00	3.92E-01		-6.40E-01	4.54E-01		-1.36E+00	1.31E-01		2.11E+00	1.32E-04	Up	4.66E+00	7.98E-50	Up	Unigene43241_All//gi|8469219|sp|Q42712.1|FATA_COBSA//3.00E-65//RecName: Full=Oleoyl-acyl carrier protein thioesterase, chloroplastic; AltName: Full=18:0-acyl-carrier protein thioesterase; Short=18:0-ACP thioesterase; AltName: Full=Acyl-[acyl-carrier-protein] hydrolase; Flags: Precursor >gi|511497|gb|AAA19864.1| oleoyl-acyl carrier protein thioesterase [Coriandrum sativum]	Unigene43241_All//2.00E-55//AT3G25110| AtFatA (Arabidopsis FatA acyl-ACP thioesterase); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase	Unigene43241_All//1.00E-62//gi|78349216|gb|DT569490.1|DT569490		ko00061|Fatty acid biosynthesis	GO:0004312//GO:0000631//GO:0016787	nr -
Unigene43244_All	992	0.00	9.76	3.54	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	1.96E-55	Up	1.18E+01	1.87E-19	Up	null	null		null	null		null	null		null	null								
Unigene43245_All	290	0.00	0.00	0.00	0.17	0.48	0.00	2.92	1.15	0.00	null	null		null	null		1.47E+00	6.18E-01		-7.42E+00	6.34E-01		-1.34E+00	5.68E-02		-1.15E+01	2.21E-06	Down							
Unigene43246_All	1295	0.00	0.00	0.00	0.00	0.00	0.00	56.22	91.53	5.60	null	null		null	null		null	null		null	null		7.03E-01	1.39E-57		-3.33E+00	0.00E+00	Down	Unigene43246_All//gi|297836874|ref|XP_002886319.1|//1.00E-10//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332159|gb|EFH92578.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene43246_All//3.00E-48//gi|48805733|gb|CO107047.1|CO107047				nr +
Unigene43247_All	254	2.27	9.97	3.14	0.20	2.17	5.33	0.00	1.15	0.31	2.14E+00	3.00E-06	Up	4.73E-01	5.65E-01		3.47E+00	1.22E-02		4.77E+00	6.28E-07	Up	1.02E+01	2.35E-02		8.29E+00	4.04E-01								
Unigene4325_All	958	1.86	156.24	0.67	3.64	9.13	3.91	3.31	18.85	297.33	6.39E+00	0.00E+00	Up	-1.48E+00	5.78E-03		1.33E+00	6.28E-12	Up	1.04E-01	7.60E-01		2.51E+00	6.63E-60	Up	6.49E+00	0.00E+00	Up	Unigene4325_All//gi|86155935|gb|ABC86705.1|//1.00E-110//R111 [Coffea arabica]	Unigene4325_All//4.00E-107//AT5G12010| unknown protein	Unigene4325_All//0.00E+00//gi|164336090|gb|ES816954.1|ES816954				nr +
Unigene43250_All	480	0.00	0.00	0.00	0.00	0.43	0.00	1.23	2.79	12.45	null	null		null	null		8.75E+00	1.57E-01		null	null		1.18E+00	2.54E-02		3.34E+00	1.99E-27	Up			Unigene43250_All//4.00E-17//DR461918				
Unigene43252_All	501	0.00	15.17	7.44	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	1.86E-43	Up	1.29E+01	1.20E-20	Up	null	null		null	null		null	null		null	null		Unigene43252_All//sp|P31949|S100A8_HUMAN//1.00E-54//Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2						swissprot +
Unigene43253_All	773	0.95	0.52	0.00	1.10	0.40	0.88	1.91	0.59	2.94	-8.54E-01	3.05E-01		-9.89E+00	4.13E-04	Down	-1.45E+00	5.13E-02		-3.22E-01	6.87E-01		-1.69E+00	1.15E-03		6.18E-01	9.37E-02		Unigene43253_All//gi|42569947|ref|NP_182107.3|//1.00E-34//DTA2 (DOWNSTREAM TARGET OF AGL15 2) [Arabidopsis thaliana]	Unigene43253_All//5.00E-36//AT2G45830| DTA2 (DOWNSTREAM TARGET OF AGL15 2)	Unigene43253_All//9.00E-07//TC155101				nr -
Unigene43254_All	694	0.00	3.65	2.92	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.05E-14	Up	1.15E+01	3.79E-11	Up	null	null		null	null		null	null		null	null		Unigene43254_All//sp|Q9V4M2|WECH_DROME//9.00E-21//Protein wech OS=Drosophila melanogaster GN=wech PE=1 SV=2						swissprot +
Unigene43256_All	1229	0.00	13.23	4.16	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.81E-93	Up	1.20E+01	1.92E-28	Up	null	null		null	null		null	null		null	null		Unigene43256_All//gi|211906490|gb|ACJ11738.1|//1.00E-103//malate dehydrogenase [Gossypium hirsutum]	Unigene43256_All//3.00E-95//AT1G04410| malate dehydrogenase, cytosolic, putative			ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene43257_All	560	0.00	2.08	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.05E-06	Up	1.10E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene43257_All//gi|195639160|gb|ACG39048.1|//4.00E-33//peroxisomal multifunctional enzyme type 2 [Zea mays]	Unigene43257_All//2.00E-34//AT1G76150| msoC-like dehydratase domain-containing protein				GO:0003824	nr +
Unigene43258_All	437	0.00	0.00	0.00	0.00	3.23	7.23	11.13	9.28	5.11	null	null		null	null		1.17E+01	9.78E-09	Up	1.28E+01	5.46E-19	Up	-2.62E-01	3.29E-01		-1.12E+00	3.54E-06	Down	Unigene43258_All//gi|238014838|gb|ACR38454.1|//9.00E-09//unknown [Zea mays]		Unigene43258_All//2.00E-15//DW234221				nr -
Unigene43259_All	477	0.00	1.81	0.00	0.42	0.00	0.57	2.75	0.35	1.67	1.08E+01	4.94E-05	Up	null	null		-8.71E+00	8.42E-02		4.44E-01	7.63E-01		-2.97E+00	8.34E-06	Down	-7.18E-01	1.54E-01								
Unigene43260_All	432	0.00	3.87	1.11	0.00	0.64	0.10	0.00	0.00	0.00	1.19E+01	1.54E-09	Up	1.01E+01	7.48E-03		9.32E+00	7.01E-02		6.71E+00	6.95E-01		null	null		null	null		Unigene43260_All//gi|116000763|emb|CAL50443.1|//4.00E-11//BolA (TSS) [Ostreococcus tauri]	Unigene43260_All//3.00E-09//AT4G26500| CPSUFE (CHLOROPLAST SULFUR E); enzyme activator/ transcription regulator				GO:0009532//GO:0030234//GO:0031163	nr +
Unigene43263_All	662	0.00	0.00	0.00	0.00	0.00	0.00	129.91	186.31	25.82	null	null		null	null		null	null		null	null		5.20E-01	2.79E-35		-2.33E+00	2.92E-268	Down	Unigene43263_All//gi|298713887|emb|CBJ33763.1|//1.00E-21//conserved unknown protein [Ectocarpus siliculosus]		Unigene43263_All//3.00E-49//TC146753				nr +
Unigene43264_All	452	0.00	0.00	0.00	0.11	0.30	0.00	3.65	0.74	1.32	null	null		null	null		1.47E+00	6.18E-01		-6.78E+00	6.34E-01		-2.30E+00	1.36E-05	Down	-1.46E+00	1.45E-03		Unigene43264_All//gi|224093842|ref|XP_002310016.1|//2.00E-58//cytochrome P450 [Populus trichocarpa] >gi|222852919|gb|EEE90466.1| cytochrome P450 [Populus trichocarpa]	Unigene43264_All//2.00E-36//AT4G36220| FAH1 (FERULIC ACID 5-HYDROXYLASE 1); ferulate 5-hydroxylase/ monooxygenase			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr -
Unigene43266_All	557	0.00	2.18	13.86	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	5.47E-07	Up	1.38E+01	3.43E-43	Up	null	null		null	null		null	null		null	null		Unigene43266_All//gi|90656516|gb|ABD96607.1|//3.00E-71//xyloglucan endotransglucosylase XET1 [Capsicum annuum]	Unigene43266_All//1.00E-59//AT4G14130| XTR7 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase	Unigene43266_All//4.00E-08//TC175025			GO:0005576//GO:0016758//GO:0016798//GO:0030312//GO:0031410//GO:0044042	nr -
Unigene43271_All	522	0.60	0.58	0.92	0.29	0.13	0.00	3.73	0.48	5.72	-4.63E-02	9.84E-01		6.10E-01	5.86E-01		-1.12E+00	5.83E-01		-8.16E+00	2.33E-01		-2.96E+00	2.83E-08	Down	6.19E-01	4.76E-02				Unigene43271_All//1.00E-38//TC157735				
Unigene43273_All	377	0.00	9.14	11.72	0.00	0.09	0.48	0.00	0.00	0.21	1.32E+01	1.31E-19	Up	1.35E+01	1.55E-24	Up	6.51E+00	8.29E-01		8.90E+00	1.94E-01		null	null		7.72E+00	4.04E-01				Unigene43273_All//4.00E-07//TC176820				
Unigene43274_All	405	0.00	0.00	0.00	0.25	0.00	0.00	2.30	14.86	4.82	null	null		null	null		-7.94E+00	3.12E-01		-7.94E+00	3.99E-01		2.69E+00	4.90E-22	Up	1.07E+00	8.19E-03		Unigene43274_All//gi|115446015|ref|NP_001046787.1|//1.00E-39//0s02g0460200 [Oryza sativa Japonica Group] >gi|113536318|dbj|BAF08701.1| 0s02g0460200 [Oryza sativa Japonica Group]	Unigene43274_All//1.00E-34//AT4G31380| FLP1 (PPF1-LIKE PROTEIN 1)	Unigene43274_All//4.00E-26//DW511728				nr -
Unigene43276_All	667	0.00	4.56	4.07	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.67E-17	Up	1.20E+01	5.43E-15	Up	null	null		null	null		null	null		null	null		Unigene43276_All//gi|301101616|ref|XP_002899896.1|//7.00E-07//alpha-actinin-1, putative [Phytophthora infestans T30-4] >gi|262102471|gb|EEY60523.1| alpha-actinin-1, putative [Phytophthora infestans T30-4]						nr +
Unigene43277_All	988	0.00	0.00	0.00	0.00	0.00	0.00	3.85	1.35	0.00	null	null		null	null		null	null		null	null		-1.51E+00	3.93E-07	Down	-1.19E+01	5.61E-28	Down	Unigene43277_All//gi|225435480|ref|XP_002285503.1|//4.00E-81//PREDICTED: similar to ADP,ATP carrier protein, mitochondrial [Vitis vinifera]	Unigene43277_All//9.00E-78//AT3G08580| AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/ binding	Unigene43277_All//1.00E-12//TC148194			GO:0006862//GO:0009526//GO:0015300//GO:0019866//GO:0030312//GO:0031981//GO:0046914	nr -
Unigene43287_All	552	0.09	0.83	0.48	0.00	0.62	0.33	1.91	5.75	5.92	3.12E+00	3.58E-02		2.35E+00	2.39E-01		9.28E+00	3.01E-02		8.35E+00	1.94E-01		1.59E+00	1.79E-06	Up	1.63E+00	4.77E-07	Up			Unigene43287_All//7.00E-07//CO119991				
Unigene43289_All	605	0.00	3.27	1.41	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.97E-11	Up	1.05E+01	9.02E-05	Up	null	null		null	null		null	null		null	null		Unigene43289_All//gi|2982453|emb|CAA18217.1|//2.00E-66//fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana] >gi|7269505|emb|CAB79508.1| fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana] >gi|21592977|gb|AAM64926.1| fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana] >gi|25082931|gb|AAN72017.1| fructose-bisphosphate aldolase -like protein [Arabidopsis thaliana] >gi|31711854|gb|AAP68283.1| At4g26530 [Arabidopsis thaliana]	Unigene43289_All//3.00E-60//AT4G26530| fructose-bisphosphate aldolase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway	GO:0005576//GO:0006007//GO:0006970//GO:0009536//GO:0010038//GO:0016020//GO:0016832//GO:0030312//GO:0031967//GO:0031981//GO:0046914	nr -
Unigene43291_All	313	0.17	11.98	3.23	0.32	0.22	1.01	7.97	39.53	11.33	6.16E+00	8.59E-20	Up	4.27E+00	1.19E-04	Up	-5.33E-01	8.16E-01		1.67E+00	3.09E-01		2.31E+00	1.75E-37	Up	5.07E-01	7.58E-02				Unigene43291_All//2.00E-42//TC174650				
Unigene43296_All	330	0.00	0.15	3.07	1.51	0.63	1.09	0.00	0.00	0.00	7.26E+00	6.16E-01		1.16E+01	1.27E-05	Up	-1.27E+00	2.22E-01		-4.63E-01	6.59E-01		null	null		null	null		Unigene43296_All//sp|P26397|RFBG_SALTY//2.00E-26//CDP-glucose 4,6-dehydratase OS=Salmonella typhimurium GN=rfbG PE=1 SV=1						swissprot -
Unigene43298_All	236	0.00	0.00	0.00	0.21	0.00	0.00	4.48	6.02	0.51	null	null		null	null		-7.72E+00	5.55E-01		-7.72E+00	6.34E-01		4.27E-01	4.07E-01		-3.14E+00	2.96E-05	Down			Unigene43298_All//3.00E-22//gi|109819827|gb|DW478806.1|DW478806				ESTscan -

Unigene43300_All	612	0.00	22.02	14.79	0.00	0.00	0.00	0.00	0.00	0.00	1.44E+01	2.27E-77	Up	1.39E+01	9.70E-51	Up	null	null		null	null		null	null		null	null		Unigene43300_All//gi|120609040|ref|YP_968718.1|//2.00E-37//30S ribosomal protein S10 [Acidovorax avenae subsp. citrulli AAC00-1] >gi|121592711|ref|YP_984607.1| 30S ribosomal protein S10 [Acidovorax sp. JS42] >gi|160895839|ref|YP_001561421.1| 30S ribosomal protein S10 [Delftia acidovorans SPH-1] >gi|221069451|ref|ZP_03545556.1| ribosomal protein S10 [Comamonas testosteroni KF-1] >gi|222109492|ref|YP_002551756.1| ribosomal protein S10 [Acidovorax ebreus TPSY] >gi|264667441|ref|YP_003276347.1| ribosomal protein S10 [Commamonas testosteroni CNB-2] >gi|270493757|ref|ZP_06210810.1| ribosomal protein S10 [Acidovorax avenae subsp. avenae ATCC 19860] >gi|299531237|ref|ZP_07044648.1| 30S ribosomal protein S10 [Comammonas testosteroni S44] >gi|166231229|sp|A1TJ06.1|RS10_ACIAC RecName: Full=30S ribosomal protein S10 >gi|166231233|sp|A1W2Q6.1|RS10_ACISJ RecName: Full=30S ribosomal	Unigene43300_All//4.00E-25//AT3G13120| 30S ribosomal protein S10, chloroplast, putative			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0033279	nr +
Unigene43301_All	444	0.00	4.56	3.36	0.00	0.00	0.19	0.00	0.00	1.22E+01	1.53E-11	Up	1.17E+01	3.22E-08	Up	null	null		null	null		-7.57E+00	4.03E-01		-7.57E+00	3.58E-01		Unigene43301_All//gi|40748265|gb|AB889617.1|//2.00E-68//40S ribosomal protein S5 [Capsicum annuum]	Unigene43301_All//7.00E-69//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	Unigene43301_All//1.00E-10//DT047705		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030312	nr -
Unigene43302_All	515	0.00	15.64	6.72	0.00	0.00	0.00	0.00	0.00	1.39E+01	4.38E-46	Up	1.27E+01	3.72E-19	Up	null	null		null	null		null	null		null	null		Unigene43302_All//gi|17366768|sp|Q9FVI2.1|ADF1_PETHY//5.00E-18//RecName: Full=Actin-depolymerizing factor 1; Short=ADF-1 >gi|10441256|gb|AAG16973.1|AF183903_1 actin-depolymerizing factor 1 [Petunia x hybrida] >gi|14906219|gb|AAK72617.1| actin-depolymerizing factor 1 [Petunia x hybrida]	Unigene43302_All//7.00E-19//AT5G59890| ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); actin binding				GO:0002218//GO:0008092//GO:0030036	nr +
Unigene43303_All	439	2.26	0.23	3.15	1.93	4.31	2.47	0.00	0.00	0.00	-3.29E+00	3.81E-04	Down	4.78E-01	4.06E-01		1.16E+00	1.39E-02		3.56E-01	6.40E-01		null	null		null	null		Unigene43303_All//gi|164708731|gb|AB967263.1|//8.00E-78//homeodomain protein HOX2 [Gossypium arboreum]	Unigene43303_All//6.00E-28//AT5G46880| HB-7 (HOMEOBOX-7); DNA binding / transcription factor	Unigene43303_All//0.00E+00//TC129563	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene43305_All	561	0.00	0.00	0.00	0.00	0.25	0.00	0.75	2.09	3.55	null	null		null	null		7.94E+00	3.18E-01		null	null		1.47E+00	1.19E-02		2.24E+00	1.43E-06	Up			Unigene43305_All//6.00E-152//gi|31072539|gb|CA992818.1|CA992818				
Unigene43306_All	372	0.14	0.41	0.29	2.54	0.37	0.24	1.70	1.46	2.89	1.54E+00	5.31E-01		1.03E+00	7.03E-01		-2.78E+00	4.58E-04	Down	-3.39E+00	3.17E-04	Down	-2.23E-01	7.73E-01		7.62E-01	1.85E-01		Unigene43306_All//gi|297744418|emb|CBI37680.3|//4.00E-07//unnamed protein product [Vitis vinifera]		Unigene43306_All//8.00E-126//CO096432				nr +
Unigene43309_All	333	0.00	0.00	0.00	0.00	0.00	0.00	7.75	8.91	1.08	null	null		null	null		null	null		null	null		2.02E-01	5.92E-01		-2.85E+00	8.60E-11	Down	Unigene43309_All//gi|791146|emb|CAA60020.1|//8.00E-16//extensin-like protein [Vigna unguiculata]						nr -
Unigene43310_All	699	0.00	5.22	2.97	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	9.10E-21	Up	1.15E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene43310_All//gi|298711715|emb|CBJ32762.1|//7.00E-15//membrane alanyl aminopeptidase [Ectocarpus siliculosus]	Unigene43310_All//1.00E-09//AT4G33090| APM1 (AMINOPEPTIDASE M1); aminopeptidase					nr +
Unigene43311_All	350	0.00	3.47	1.37	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.47E-07	Up	1.04E+01	7.48E-03		null	null		null	null		null	null		null	null								ESTscan +
Unigene43316_All	382	3.15	2.65	9.06	2.74	1.53	3.07	2.32	1.64	2.19	-2.48E-01	6.62E-01		1.52E+00	2.88E-05	Up	-8.38E-01	2.01E-01		1.67E-01	7.91E-01		-5.02E-01	4.60E-01		-8.58E-02	8.98E-01				Unigene43316_All//2.00E-83//TC136806					
Unigene43318_All	461	0.00	5.83	4.16	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.80E-15	Up	1.20E+01	1.47E-10	Up	null	null		null	null		null	null		null	null		Unigene43318_All//gi|159488703|ref|XP_001702342.1|//5.00E-45//ribosomal protein S7, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158271136|gb|EDO96962.1| ribosomal protein S7 [Chlamydomonas reinhardtii]	Unigene43318_All//1.00E-38//AT3G02560| 40S ribosomal protein S7 (RPS7B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0005840//GO:0009536//GO:0010467	nr -
Unigene43319_All	382	0.00	9.68	3.90	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	4.67E-21	Up	1.19E+01	3.22E-08	Up	null	null		null	null		null	null		null	null									
Unigene4332_All	546	82.22	72.94	59.69	105.92	83.82	107.53	121.96	124.77	58.37	-1.73E-01	3.93E-02		-4.62E-01	1.30E-08		-3.38E-01	1.05E-07		2.17E-02	7.96E-01		3.29E-02	6.32E-01		-1.06E+00	4.29E-67	Down	Unigene4332_All//gi|147945633|gb|AB025658.1|//4.00E-46//MnSOD [Glycine max]	Unigene4332_All//2.00E-44//AT3G10920| MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); metal ion binding / superoxide dismutase	Unigene4332_All//0.00E+00//gi|21090312|gb|BQ402625.1|BQ402625		ko04146|Peroxisome		nr -
Unigene4322_All	627	0.50	0.32	0.00	0.48	0.11	0.72	2.36	2.20	0.13	-6.31E-01	6.22E-01		-8.97E+00	4.90E-02		-2.12E+00	1.65E-01		5.96E-01	6.40E-01		-1.02E-01	8.39E-01		-4.21E+00	1.00E-08	Down	Unigene4322_All//gi|223452286|gb|ACM89471.1|//3.00E-44//PERONIA receptor-like kinase [Glycine max]	Unigene4322_All//2.00E-37//AT2G39360| protein kinase family protein			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene4323_All	357	0.00	0.00	0.00	2.51	0.29	1.77	0.00	0.00	1.34	null	null		null	null		-3.12E+00	2.80E-04	Down	-5.04E-01	5.11E-01		null	null		1.04E+01	1.14E-03									
Unigene43325_All	452	0.00	0.00	0.00	0.00	0.00	0.00	3.46	6.47	0.00	null	null		null	null		null	null		null	null		9.03E-01	5.74E-03		-1.18E+01	1.42E-11	Down	Unigene43325_All//gi|12229935|sp|Q9SM13.1|RS12_CYAPA//4.00E-42//RecName: Full=40S ribosomal protein S12 >gi|6012956|emb|CAB57311.1| 40s ribosomal protein S12 [Cyanophora paradoxa]	Unigene43325_All//3.00E-32//AT2G32060| 40S ribosomal protein S12 (RPS12C)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0005840//GO:0009536//GO:0010467	nr -
Unigene43327_All	430	0.00	0.00	0.00	0.00	0.32	0.00	0.98	2.33	5.00	null	null		null	null		8.32E+00	3.18E-01		null	null		1.25E+00	4.78E-02		2.35E+00	2.10E-07	Up								
Unigene4333_All	378	0.28	1.21	0.00	0.26	0.46	2.63	0.67	0.88	0.21	2.12E+00	9.59E-02		-8.11E+00	3.92E-01		7.89E-01	7.70E-01		3.32E+00	3.47E-04	Up	3.99E-01	7.24E-01		-1.67E+00	2.56E-01		Unigene4333_All//gi|147945633|gb|AB025658.1|//4.00E-34//MnSOD [Glycine max]	Unigene4333_All//2.00E-33//AT3G10920| MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); metal ion binding / superoxide dismutase	Unigene4333_All//1.00E-112//TC140491		ko04146|Peroxisome		nr -
Unigene43330_All	316	0.00	0.00	0.00	0.95	0.22	1.14	1.34	7.67	0.76	null	null		null	null		-2.12E+00	1.65E-01		2.74E-01	8.33E-01		2.52E+00	1.16E-08	Up	-8.23E-01	3.99E-01				Unigene43330_All//7.00E-27//BQ412901					
Unigene43331_All	545	0.00	4.00	2.35	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.11E-12	Up	1.12E+01	4.68E-07	Up	null	null		null	null		null	null		null	null		Unigene43331_All//sp|Q540K3|CDC7_DICDI//1.00E-08//Probable serine/threonine-protein kinase cdc7 OS=Dictyostelium discoideum GN=cdc7 PE=3 SV=1						swissprot +
Unigene43333_All	355	1.92	0.00	0.90	2.81	2.81	1.27	0.00	0.24	0.00	-1.09E+01	4.10E-04	Down	-1.09E+00	2.39E-01		3.40E-03	9.87E-01		-1.14E+00	1.09E-01		7.88E+00	4.01E-01		null	null		Unigene43333_All//gi|13877625|gb|AK43890.1|AF370513_1//6.00E-08//Unknown protein [Arabidopsis thaliana] >gi|23198280|gb|AAN15667.1| Unknown protein [Arabidopsis thaliana] >gi|62320689|dbj|BAD95357.1| receptor-like serine/threonine kinase [Arabidopsis thaliana]	Unigene43333_All//3.00E-09//AT1G07650| leucine-rich repeat transmembrane protein kinase, putative				GO:0004672//GO:0005488//GO:0016020	nr +
Unigene43336_All	419	0.00	43.90	22.88	0.24	0.00	0.00	0.00	0.00	0.00	1.54E+01	9.00E-106	Up	1.45E+01	9.28E-54	Up	-7.89E+00	3.12E-01		-7.89E+00	3.99E-01		null	null		null	null		Unigene43336_All//gi|116056464|emb|CAL52753.1|//2.00E-40//ribosomal protein S20 (ISS) [Ostreococcus tauri]	Unigene43336_All//2.00E-38//AT5G62300| 40S ribosomal protein S20 (RPS20C)			ko03010|Ribosome	GO:0003676//GO:0004672//GO:0005198//GO:0006464//GO:0010467//GO:0032559//GO:0033279	nr +
Unigene43337_All	1264	0.00	24.25	9.82	0.00	0.00	0.00	0.00	0.00	0.00	1.46E+01	9.16E-177	Up	1.33E+01	8.45E-70	Up	null	null		null	null		null	null		null	null		Unigene43337_All//gi|195606812|gb|ACG25236.1|//1.00E-155//60S ribosomal protein L3 [Zea mays] >gi|195619674|gb|ACG31667.1| 60S ribosomal protein L3 [Zea mays] >gi|195626206|gb|ACG34933.1| 60S ribosomal protein L3 [Zea mays] >gi|195641988|gb|ACG40462.1| 60S ribosomal protein L3 [Zea mays]	Unigene43337_All//5.00E-137//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene43337_All//1.00E-10//TC149894		ko03010|Ribosome		nr +
Unigene43340_All	384	0.00	8.84	7.77	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.55E-19	Up	1.29E+01	1.77E-16	Up	null	null		null	null		null	null		null	null		Unigene43340_All//gi|124112096|ref|YP_001019087.1|//3.00E-25//ribosomal protein L14 [Chlorokybus atmophyticus] >gi|218546907|sp|Q19VB2.2|RK14_CHLAT RecName: Full=50S ribosomal protein L14, chloroplastic >gi|124012207|gb|ABD62228.2| ribosomal protein L14 [Chlorokybus atmophyticus]	Unigene43340_All//6.00E-24//ATCG00780| encodes a chloroplast ribosomal protein L14, a constituent of the large subunit of the ribosomal complex			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0006351//GO:0009536//GO:0023060//GO:0033279//GO:0043660	nr +
Unigene43341_All	306	0.00	66.23	16.88	0.00	0.00	0.00	0.00	0.00	0.00	1.60E+01	1.30E-116	Up	1.40E+01	9.61E-29	Up	null	null		null	null		null	null		null	null		Unigene43341_All//gi|298709870|emb|CBJ26210.1|//5.00E-32//Ribosomal protein S27 [Ectocarpus siliculosus]	Unigene43341_All//5.00E-32//AT5G47930| 40S ribosomal protein S27 (RPS27B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0030312//GO:0043169	nr +
Unigene43344_All	314	0.00	0.00	0.00	0.00	0.00	0.00	16.70	7.85	3.68	null	null		null	null		null	null		null	null		-1.09E+00	4.51E-06	Down	-2.18E+00	8.26E-16	Down								
Unigene43348_All	495	0.00	0.00	0.00	0.00	0.00	0.00	1.20	8.53	18.51	null	null		null	null		null	null		null	null		2.83E+00	1.77E-16	Up	3.95E+00	7.78E-48	Up	Unigene43348_All//gi|297823575|ref|XP_002879670.1|//6.00E-41//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325509|gb|EFH55929.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene43348_All//3.00E-38//AT2G37430| zinc finger (C2H2 type) family protein (ZAT11)		C2H2		GO:0005488//GO:0009743//GO:0010468	nr +
Unigene4335_All	418	0.00	0.12	0.13	0.24	0.74	0.32	0.00	0.00	1.62	6.92E+00	6.16E-01		6.99E+00	6.35E-01		1.64E+00	3.21E-01		4.44E-01	8.61E-01		null	null		1.07E+01	4.96E-05	Up	Unigene4335_All//gi|13712623|gb|AB037118.1|//3.00E-26//cuticular water permeability [Solanum habrochaites]	Unigene4335_All//2.00E-16//AT4G38260| unknown protein					nr -
Unigene43351_All	311	0.00	0.00	0.00	0.00	0.11	0.00	2.45	7.12	3.71	null	null		null	null		6.79E+00	8.29E-01		null	null		1.54E+00	1.40E-04	Up	6.02E-01	2.77E-01									
Unigene43353_All	326	26.96	14.92	12.25	36.67	40.14	58.46	101.16	57.44	48.15	-8.54E-01	1.31E-05		-1.14E+00	4.21E-08	Down	1.30E-01	4.96E-01		6.73E-01	5.05E-08		-8.17E-01	2.55E-21		-1.07E+00	4.38E-34	Down	Unigene43353_All//gi|225462164|ref|XP_002266780.1|//3.00E-53//PREDICTED: similar to elongation factor 2 [Vitis vinifera]	Unigene43353_All//3.00E-53//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene43353_All//1.00E-179//gi|164252340|gb|ES803658.1|ES803658			GO:0006950//GO:0008135//GO:0009536//GO:0010467//GO:0016020//GO:0017111//GO:0031981//GO:0032561//GO:0046914	nr +
Unigene43354_All	534	0.00	1.61	0.10	0.37	0.13	0.68	1.43	3.05	5.37	1.07E+01	4.94E-05	Up	6.64E+00	6.35E-01		-1.53E+00	4.15E-01		8.59E-01	5.42E-01		1.10E+00	1.83E-02		1.91E+00	1.22E-07	Up	Unigene43354_All//gi|5869967|emb|CAB55555.1|//3.00E-08//auxin binding protein (ABP44); isovaleryl-CoA Dehydrogenase [Pisum sativum]	Unigene43354_All//5.00E-09//AT3G45300| IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase	Unigene43354_All//5.00E-32//ES810769		ko00280|Valine, leucine and isoleucine degradation		nr +
Unigene43355_All	734	0.00	0.00	0.22	0.00	0.00	0.00	0.17	8.83	1.90	null	null		7.77E+00	2.38E-01		null	null		null	null		5.67E+00	8.20E-41	Up	3.46E+00	4.41E-07	Up	Unigene43355_All//gi|224138226|ref|XP_002322761.1|//1.00E-119//cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa] >gi|222867391|gb|EEF04522.1| cinnamyl alcohol dehydrogenase-like protein [Populus trichocarpa]	Unigene43355_All//4.00E-76//AT4G37990| ELI3-2 (ELICITOR-ACTIVATED GENE 3-2); aryl-alcohol dehydrogenase/ mannitol dehydrogenase	Unigene43355_All//0.00E+00//TC179502		ko00940|Phenylpropanoid biosynthesis		nr -

Unigene4336_All	644	9.91	5.04	3.06	15.32	25.45	11.50	1.05	1.36	1.73	-9.77E-01	3.49E-05		-1.70E+00	1.62E-10	Down	7.33E-01	1.21E-08		-4.13E-01	2.55E-02		3.76E-01	6.10E-01		7.22E-01	2.00E-01		Unigene4336_All//gi|133712623|gb|AB037118.1|//2.00E-74//cuticular water permeability [Solanum habrochaites]	Unigene4336_All//2.00E-59//AT4G38260| unknown protein					nr -
Unigene43361_All	422	0.00	0.00	0.00	0.00	0.00	0.00	2.50	3.37	0.00	null	null		null	null		null	null		null	null		4.27E-01	4.07E-01		-1.13E+01	6.71E-08	Down	Unigene43361_All//gi|195618126|gb|ACG30893.1|//4.00E-37//40S ribosomal protein S19 [Zea mays] >gi|195640734|gb|ACG39835.1| 40S ribosomal protein S19 [Zea mays] >gi|195647028|gb|ACG42982.1| 40S ribosomal protein S19 [Zea mays]	Unigene43361_All//2.00E-30//AT3G02080| 40S ribosomal protein S19 (RPS19A)			ko03010|Ribosome	G0:0005198//G0:0010467//G0:0015935//G0:0030312//G0:0031981	nr -
Unigene43363_All	471	3.11	7.21	0.00	0.00	0.00	0.00	0.27	0.00	0.00	1.21E+00	4.37E-04	Up	-1.16E+01	5.25E-08	Down	null	null		null	null		-8.07E+00	2.35E-01		-8.07E+00	2.00E-01		Unigene43363_All//gi|115435122|ref|NP_001042319.1|//4.00E-33//Os01g0200700 [Oryza sativa Japonica Group] >gi|158512839|sp|A2WLS0.1|MT3A_ORYSI RecName: Full=Metallothionein-like protein 3A; AltName: Full=Class I metallothionein-like protein 3A; AltName: Full=OsMT-I-3a; Short=OsMT3a; Short=OsMT3 >gi|158514033|sp|A1YTN8.1|MT3A_ORYSJ RecName: Full=Metallothionein-like protein 3A; AltName: Full=Class I metallothionein-like protein 3A; AltName: Full=OsMT-I-3a; Short=OsMT3a; Short=OsMT3 >gi|2072555|gb|AAB53811.1| metallothionein-like protein [Oryza sativa Japonica Group] >gi|6103441|gb|AAF03603.1| metallothionein-like protein [Oryza sativa] >gi|53148415|dbj|BAD52235.1| metallothionein [Oryza rufipogon] >gi|53148419|dbj|BAD52237.1| metallothionein [Oryza rufipogon] >gi|53148421|dbj|BAD52238.1| metallothionein [Oryza rufipogon] >gi|53148435|dbj|BAD52245.1| metallothionein [Oryza barthii]	Unigene43363_All//4.00E-09//AT3G15353| MT3 (METALLOTHIONEIN 3); copper ion binding	Unigene43363_All//2.00E-19//TC174105				nr +
Unigene43364_All	416	0.00	0.00	0.00	0.00	0.00	0.00	11.08	3.92	2.01	null	null		null	null		null	null		null	null		-1.50E+00	2.07E-08	Down	-2.46E+00	4.67E-16	Down	Unigene43364_All//gi|220966698|gb|ACL97363.1|//1.00E-49//elongation factor-1 alpha [Ignatius tetrasporus]	Unigene43364_All//7.00E-43//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene43364_All//1.00E-10//DW516522			G0:0006412//G0:0008135//G0:0016772//G0:0017111//G0:0032561//G0:0044424	nr -
Unigene43366_All	480	2.83	7.39	2.11	4.57	3.87	3.11	1.85	3.40	1.58	1.38E+00	5.43E-05	Up	-4.27E-01	4.72E-01		-2.37E-01	6.11E-01		-5.56E-01	2.19E-01		8.76E-01	5.83E-02		-2.30E-01	7.05E-01		Unigene43366_All//gi|297607886|ref|NP_001060839.2|//9.00E-32//Os08g0113300 [Oryza sativa Japonica Group] >gi|255678105|dbj|BAF22753.2| Os08g0113300 [Oryza sativa Japonica Group]	Unigene43366_All//5.00E-32//AT3G07370| CHIP (CARBOXYL TERMINUS OF HSC70-INTERACTING PROTEIN); ubiquitin-protein ligase	Unigene43366_All//0.00E+00//TC163135		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	G0:0005515//G0:0006970//G0:0009725//G0:0019787//G0:0032446//G0:0043234	nr -
Unigene43368_All	307	0.00	4.62	3.12	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.06E-08	Up	1.16E+01	2.46E-05	Up	null	null		null	null		null	null		null	null		Unigene43368_All//sp|P11799|MYLK_CHICK//1.00E-08//Myosin light chain kinase, smooth muscle OS=Gallus gallus PE=1 SV=2						swissprot +
Unigene43369_All	380	0.00	2.40	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.62E-05	Up	1.07E+01	1.16E-03		null	null		null	null		null	null		null	null							
Unigene4337_All	1239	79.94	12.84	40.10	4.91	4.47	3.90	4.16	2.13	2.19	-2.64E+00	1.67E-283	Down	-9.95E-01	1.04E-68		-1.33E-01	6.18E-01		-3.31E-01	2.00E-01		-9.70E-01	4.22E-05		-9.29E-01	5.42E-05		Unigene4337_All//gi|157965847|gb|AB406960.1|//1.00E-113//geranylgeranyl diphosphate synthase [Corylus avellana]	Unigene4337_All//2.00E-96//AT4G36810| GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltranstransferase	Unigene4337_All//0.00E+00//TC143000		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene43372_All	389	3.77	1.56	2.33	0.26	0.27	0.58	1.30	10.96	0.72	-1.27E+00	2.39E-02		-6.95E-01	2.36E-01		5.25E-02	9.66E-01		1.18E+00	5.49E-01		3.07E+00	5.67E-18	Up	-8.63E-01	3.39E-01		Unigene43372_All//gi|115487322|ref|NP_001066148.1|//5.00E-42//Os12g0145700 [Oryza sativa Japonica Group] >gi|77553678|gb|ABA96474.1| pyruvate kinase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113648655|dbj|BAF29167.1| Os12g0145700 [Oryza sativa Japonica Group]	Unigene43372_All//3.00E-41//AT3G52990| pyruvate kinase, putative	Unigene43372_All//6.00E-173//BQ411444		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	G0:0006007//G0:0010038//G0:0016301//G0:0031420//G0:0044464	nr -
Unigene43373_All	794	0.53	0.51	0.94	1.00	0.69	0.40	6.23	0.26	0.80	-4.64E-02	9.80E-01		8.33E-01	3.39E-01		-5.33E-01	5.10E-01		-1.33E+00	1.06E-01		-4.57E+00	3.07E-28	Down	-2.96E+00	8.55E-21	Down	Unigene43373_All//gi|28466849|gb|AA044033.1|//5.00E-19//At3g50640 [Arabidopsis thaliana]	Unigene43373_All//3.00E-22//AT5G66800| unknown protein	Unigene43373_All//3.00E-130//ES799894				nr -
Unigene43375_All	376	0.56	0.13	0.00	5.03	6.32	0.72	0.22	0.00	0.00	-2.05E+00	3.34E-01		-9.12E+00	1.45E-01		3.28E-01	4.84E-01		-2.80E+00	9.57E-07	Down	-7.81E+00	4.03E-01		-7.81E+00	3.58E-01							
Unigene43376_All	530	0.00	0.00	0.00	0.00	0.07	0.00	2.87	0.16	1.35	null	null		null	null		6.02E+00	8.29E-01		null	null		-4.19E+00	1.46E-08	Down	-1.09E+00	1.94E-02		Unigene43376_All//gi|115476242|ref|NP_001061717.1|//9.00E-23//Os08g0388900 [Oryza sativa Japonica Group] >gi|113623686|dbj|BAF23631.1| Os08g0388900 [Oryza sativa Japonica Group]	Unigene43376_All//2.00E-22//AT4G23660| AtPPT1 (Arabidopsis thaliana polyprenyltransferase 1); 4-hydroxybenzoate nonaprenyltransferase	Unigene43376_All//4.00E-08//gi|109825726|gb|DW224449.1|DW224449		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	G0:0002094//G0:0006743//G0:0007275//G0:0016020//G0:0043231	nr +
Unigene43378_All	393	0.93	0.52	0.54	0.76	0.53	0.23	0.32	1.60	2.23	-8.54E-01	4.88E-01		-7.82E-01	5.53E-01		-5.33E-01	6.78E-01		-1.73E+00	2.89E-01		2.31E+00	1.46E-02		2.79E+00	5.37E-04	Up	Unigene43378_All//gi|240254187|ref|NP_174367.6|//2.00E-24//transcription factor [Arabidopsis thaliana]	Unigene43378_All//1.00E-25//AT1G30810| transcription factor	Unigene43378_All//6.00E-139//TC176923			G0:0003676//G0:0043231	nr -
Unigene43381_All	488	0.00	0.00	0.00	0.20	0.07	0.09	0.69	3.17	1.88	null	null		null	null		-1.53E+00	5.86E-01		-1.14E+00	6.76E-01		2.19E+00	5.11E-05	Up	1.44E+00	2.77E-02							
Unigene43383_All	961	0.05	0.32	0.00	0.21	0.36	0.09	13.20	1.78	0.75	2.54E+00	1.51E-01		-5.77E+00	6.23E-01		7.89E-01	5.96E-01		-1.14E+00	5.69E-01		-2.89E+00	2.43E-49	Down	-4.14E+00	9.88E-70	Down	Unigene43383_All//gi|75114455|sp|Q65200.1|GL92_ORYSJ//6.00E-34//RecName: Full=Putative germin-like protein 9-2; Flags: Precursor	Unigene43383_All//2.00E-14//AT1G10460| GLP7 (GERMIN-LIKE PROTEIN 7); manganese ion binding / nutrient reservoir				G0:0003824//G0:0005576//G0:0031410//G0:0046914	nr +
Unigene43384_All	553	0.28	0.92	0.00	2.43	6.48	4.66	0.99	0.53	1.08	1.69E+00	1.34E-01		-8.15E+00	2.44E-01		1.41E+00	1.30E-05	Up	9.37E-01	1.87E-02		-9.10E-01	3.19E-01		1.21E-01	8.88E-01			Unigene43384_All//6.00E-05//AT2G24200| cytosol aminopeptidase	Unigene43384_All//2.00E-38//DT463994		ko00480|Glutathione metabolism		kegg +
Unigene43385_All	1871	0.00	14.03	5.21	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	3.14E-151	Up	1.23E+01	1.15E-54	Up	null	null		null	null		null	null		null	null		Unigene43385_All//gi|298707121|emb|CBJ29913.1|//2.00E-89//protein disulfide isomerase [Ectocarpus siliculosus]	Unigene43385_All//8.00E-84//AT3G54960| ATPDIL1-3 (PDI-LIKE 1-3); protein disulfide isomerase			ko04141|Protein processing in endoplasmic reticulum	G0:0000322//G0:0000323//G0:0005488//G0:0005618//G0:0006970//G0:0009536//G0:0009791//G0:0010038//G0:0012501//G0:0016020//G0:0033554	nr +
Unigene43386_All	478	0.00	0.00	0.00	0.00	0.00	0.00	3.45	1.31	0.00	null	null		null	null		null	null		null	null		-1.40E+00	3.12E-03		-1.18E+01	3.45E-12	Down	Unigene43386_All//gi|15223164|ref|NP_177206.1|//2.00E-76//ARFAID; GTP binding / phospholipase activator/ protein binding [Arabidopsis thaliana] >gi|18395248|ref|NP_564195.1| ATARF1 (ADP-RIBOSYLATION FACTOR 1); GTP binding / phospholipase activator/ protein binding [Arabidopsis thaliana] >gi|30698721|ref|NP_850975.1| ARFAID; GTP binding / phospholipase activator/ protein binding [Arabidopsis thaliana] >gi|42572059|ref|NP_974120.1| ARFAID; GTP binding / phospholipase activator/ protein binding [Arabidopsis thaliana] >gi|12643250|sp|Q9SRC3.3|ARF2_ARATH RecName: Full=ADP-ribosylation factor 2; Short=AtARF2; AltName: Full=ARF1-like protein U5 >gi|116926864|gb|AAG40035.1|AF324684_1 Atlg23490 [Arabidopsis thaliana] >gi|11762198|gb|AAG40377.1|AF325025_1 Atlg70190 [Arabidopsis thaliana] >gi|13926232|gb|AAK49591.1|AF372875_1 F28C11.30/F28C11.30	Unigene43386_All//1.00E-77//AT1G70490| ARFAID; GTP binding / phospholipase activator/ protein binding	Unigene43386_All//2.00E-28//gi|50562119|gb|AI731367.1|AI731367			G0:0006464//G0:0010038//G0:0015031//G0:0016020//G0:0032561//G0:0033556//G0:0043231//G0:0060089//G0:0060229	nr -
Unigene43388_All	431	0.00	0.00	0.00	0.23	0.32	0.00	4.12	0.87	3.33	null	null		null	null		4.67E-01	8.76E-01		-7.85E+00	3.99E-01		-2.24E+00	8.44E-06	Down	-3.08E-01	4.84E-01		Unigene43388_All//gi|109946527|gb|AB648442.1|//3.00E-09//At5g05570 [Arabidopsis thaliana]	Unigene43388_All//1.00E-10//AT2G27315| unknown protein	Unigene43388_All//3.00E-76//TC153964				nr +
Unigene4339_All	1024	9.71	50.72	19.03	25.93	13.55	18.08	10.78	17.18	14.71	2.39E+00	1.86E-131	Up	9.71E-01	1.92E-13		-9.36E-01	2.01E-21		-5.20E-01	3.53E-07		6.73E-01	1.25E-08		4.49E-01	3.50E-04		Unigene4339_All//gi|115451217|ref|NP_001049209.1|//3.00E-16//Os03g0187400 [Oryza sativa Japonica Group] >gi|108706575|gb|ABF94370.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547680|dbj|BAF11123.1| Os03g0187400 [Oryza sativa Japonica Group]	Unigene4339_All//1.00E-09//AT1G02070| unknown protein	Unigene4339_All//0.00E+00//C0099486				nr +
Unigene43395_All	209	0.50	1.45	0.00	4.53	0.66	1.73	0.61	1.40	0.00	1.54E+00	3.23E-01		-8.97E+00	3.92E-01		-2.78E+00	4.58E-04	Down	-1.39E+00	6.08E-02		1.21E+00	3.92E-01		-9.25E+00	2.00E-01							

Unigene43397_All	726	0.00	56.95	22.08	0.00	0.00	0.00	0.00	0.00	0.00	1.58E+01	1.10E-238	Up	1.44E+01	2.11E-90	Up	null	null		null	null		null	null		null	null		Unigene43397_All//gi|15718687|ref|NP_000996.2|//1.00E-106//40S ribosomal protein S3 [Homo sapiens] >gi|77404290|ref|NP_001029219.1| 40S ribosomal protein S3 [Bos taurus] >gi|113205854|ref|NP_001038066.1| 40S ribosomal protein S3 [Sus scrofa] >gi|109107963|ref|XP_001086020.1| PREDICTED: 40S ribosomal protein S3 [Macaca mulatta] >gi|41771|sp|P23396.2|RS3_HUMAN RecName: Full=40S ribosomal protein S3 >gi|91207641|sp|Q3T169.1|RS3_BOVIN RecName: Full=40S ribosomal protein S3 >gi|115502828|sp|Q028U2.1|RS3_PIG RecName: Full=40S ribosomal protein S3 >gi|187609257|pdb|2ZKQ|C Chain c, Structure Of A Mammalian Ribosomal 40s Subunit Within An 80s Complex Obtained By Docking Homology Models Of The Rna And Proteins Into An 8.7 A Cryo-Em Map >gi|555941|gb|AAB60336.1| ribosomal protein S3 [Homo	Unigene43397_All//2.00E-92//AT5G35530| 40S ribosomal protein S3 (RPS3C)	Unigene43397_All//2.00E-16//gi|109891376|gb|DW520339.1|DW520339		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0033279	nr -
Unigene43399_All	362	1.73	0.00	1.18	0.14	0.29	0.25	1.05	0.23	0.66	-1.08E+01	7.91E-04	Down	-5.60E-01	5.53E-01		1.05E+00	8.08E-01		8.59E-01	7.94E-01		-2.19E+00	8.75E-02		-6.71E-01	5.30E-01									
Unigene43340_All	944	33.37	25.87	30.80	35.36	25.97	24.93	12.99	5.80	5.28	-3.67E-01	1.36E-04		-1.16E-01	3.11E-01		-4.45E-01	1.78E-07		-5.04E-01	2.09E-08		-1.16E+00	1.60E-14	Down	-1.30E+00	1.09E-17	Down		Unigene43340_All//3.00E-87//gi|164310435|gb|ES834450.1|ES834450					
Unigene43400_All	620	0.25	0.00	0.17	0.16	0.00	0.00	2.11	6.61	1.73	-7.98E+00	2.15E-01		-5.60E-01	7.75E-01		-7.33E+00	3.12E-01		-7.33E+00	3.99E-01		1.64E+00	1.66E-08	Up	-2.85E-01	6.01E-01		Unigene43400_All//gi|54397637|gb|AY338889.1|//4.00E-41//Hcr9-082A [Solanum pimpinellifolium]	Unigene43400_All//1.00E-26//AT2G15080| AtRLP19 (Receptor Like Protein 19); kinase/ protein binding	Unigene43400_All//4.00E-61//ES795055			GO:0003824	nr -
Unigene43406_All	501	0.00	0.00	0.00	0.80	0.00	0.36	17.55	10.76	4.37	null	null		null	null		-9.64E+00	4.38E-03		-1.14E+00	3.79E-01		-7.06E-01	4.57E-05		-2.00E+00	2.21E-23	Down	Unigene43406_All//gi|145408590|ref|YP_001152214.1|//3.00E-07//ORF124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| ORF124 [Pinus koraiensis]		Unigene43406_All//3.00E-24//TC142576				nr +
Unigene43407_All	267	0.00	0.00	0.00	0.00	0.00	0.00	2.38	0.94	0.00	null	null		null	null		null	null		null	null		-1.34E+00	1.13E-01		-1.12E+01	7.11E-05	Down	Unigene43407_All//gi|297829496|ref|XP_002882630.1|//2.00E-19//60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata] >gi|297328470|gb|EFH58889.1| 60S ribosomal protein L4/L1 [Arabidopsis lyrata subsp. lyrata]	Unigene43407_All//1.00E-20//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0030312//GO:0031981	nr +
Unigene43408_All	638	0.00	8.82	4.84	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	4.34E-32	Up	1.22E+01	4.51E-17	Up	null	null		null	null		null	null		null	null		Unigene43408_All//gi|2317912|gb|AAC24376.1|//7.00E-51//cathepsin B-like cysteine proteinase [Arabidopsis thaliana]	Unigene43408_All//4.00E-52//AT1G02300| cathepsin B-like cysteine protease, putative	Unigene43408_All//3.00E-09//TC165624			GO:0008233//GO:0043231	nr -
Unigene4341_All	762	12.50	16.29	11.95	10.98	21.38	18.91	9.10	38.23	64.41	3.83E-01	1.88E-02		-6.45E-02	7.50E-01		9.61E-01	2.68E-13		7.84E-01	6.45E-08		2.07E+00	3.08E-76	Up	2.82E+00	1.34E-187	Up	Unigene4341_All//gi|71041110|gb|AAZ20443.1|//3.00E-43//MYBR2 [Malus x domestica]	Unigene4341_All//2.00E-20//AT3G16350| myb family transcription factor		MYB-related			nr -
Unigene43411_All	613	0.51	0.50	0.69	2.60	0.56	0.37	2.76	2.66	1.10	-4.64E-02	9.84E-01		4.40E-01	6.77E-01		-2.21E+00	4.28E-05	Down	-2.82E+00	8.55E-06	Down	-5.32E-02	9.22E-01		-1.32E+00	3.08E-03			Unigene43411_All//3.00E-15//TC136828					
Unigene43414_All	268	0.39	0.00	0.00	0.56	1.28	1.18	0.16	0.62	2.38	-8.61E+00	3.71E-01		-8.61E+00	3.92E-01		1.20E+00	4.26E-01		1.08E+00	4.76E-01		1.98E+00	3.79E-01		3.91E+00	7.65E-04	Up	Unigene43414_All//gi|297820862|ref|XP_002878314.1|//1.00E-31//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297324152|gb|EFH54573.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene43414_All//5.00E-33//AT3G60050| pentatricopeptide (PPR) repeat-containing protein				GO:0043231	nr +
Unigene43415_All	696	0.00	7.64	2.98	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.43E-30	Up	1.15E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene43415_All//gi|79497359|ref|NP_195390.2|//4.00E-10//HVA22K (HVA22-LIKE PROTEIN K) [Arabidopsis thaliana] >gi|57012586|sp|Q6NL38.1|H22K_ARATH RecName: Full=HVA22-like protein k; Short=AtHVA22k >gi|45752772|gb|AAS76284.1| At4g36720 [Arabidopsis thaliana]	Unigene43415_All//2.00E-11//AT4G36720| HVA22K (HVA22-LIKE PROTEIN K)					nr +
Unigene43416_All	508	1.44	0.40	0.00	5.39	5.02	5.07	1.50	0.58	1.02	-1.85E+00	4.08E-02		-1.05E+01	4.13E-04	Down	-1.05E-01	8.15E-01		-8.99E-02	8.24E-01		-1.38E+00	6.73E-02		-5.55E-01	4.23E-01			Unigene43416_All//4.00E-54//gi|164345717|gb|ES826242.1|ES826242					ESTscan +
Unigene43417_All	705	0.52	0.07	0.15	0.57	1.66	2.82	0.36	0.06	0.45	-2.85E+00	7.80E-02		-1.78E+00	2.34E-01		1.55E+00	1.81E-02		2.32E+00	1.15E-05	Up	-2.60E+00	1.44E-01		3.29E-01	7.63E-01		Unigene43417_All//gi|115473385|ref|NP_001060291.1|//5.00E-52//Os07g0619100 [Oryza sativa Japonica Group] >gi|22296348|dbj|BAC10118.1| myosin heavy chain-like [Oryza sativa Japonica Group] >gi|113611827|dbj|BAF22205.1| Os07g0619100 [Oryza sativa Japonica Group]	Unigene43417_All//7.00E-48//AT3G26570| unknown protein	Unigene43417_All//7.00E-32//TC172232			GO:0016020	nr +
Unigene43419_All	379	0.00	7.89	2.53	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	5.19E-17	Up	1.13E+01	2.46E-05	Up	null	null		null	null		null	null		null	null		Unigene43419_All//gi|130751|sp|P08289.2|PPBT_RAT//1.00E-09//RecName: Full=Alkaline phosphatase, tissue-nonspecific isozyme; Short=AP-TNAP; Short=TNSALP; AltName: Full=Alkaline phosphatase liver/bone/kidney isozyme; Flags: Precursor >gi|3901092|emb|CAA34160.1| alkaline phosphatase [Rattus norvegicus] >gi|56789527|gb|AAH88399.1| Alkaline phosphatase, liver/bone/kidney [Rattus norvegicus] >gi|149024351|gb|EDL80848.1| alkaline phosphatase, tissue-nonspecific, isoform CRA_a [Rattus norvegicus] >gi|149024352|gb|EDL80849.1| alkaline phosphatase, tissue-nonspecific, isoform CRA_a [Rattus norvegicus] >gi|149024353|gb|EDL80850.1| alkaline phosphatase, tissue-nonspecific, isoform CRA_a [Rattus norvegicus]					GO:0002237//GO:0006796//GO:0016020//GO:0016791//GO:0031960//GO:0034505//GO:0044421	nr +
Unigene43422_All	606	0.00	10.70	8.00	0.00	0.00	0.00	0.14	0.00	0.00	1.34E+01	4.83E-37	Up	1.30E+01	6.11E-27	Up	null	null		null	null		-7.12E+00	4.03E-01		-7.12E+00	3.58E-01		Unigene43422_All//gi|226504938|ref|NP_001148350.1|//6.00E-63//60S ribosomal protein L12 [Zea mays] >gi|195618256|gb|ACG30958.1| 60S ribosomal protein L12 [Zea mays] >gi|195619274|gb|ACG31467.1| 60S ribosomal protein L12 [Zea mays]	Unigene43422_All//4.00E-63//AT5G60670| 60S ribosomal protein L12 (RPL12C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +
Unigene43424_All	716	0.00	99.64	80.54	0.00	0.53	0.44	0.12	0.00	0.11	1.66E+01	0.00E+00	Up	1.63E+01	0.00E+00	Up	9.05E+00	1.96E-02		8.79E+00	4.07E-02		-6.88E+00	4.03E-01		-8.56E-02	9.71E-01		Unigene43424_All//gi|1352538|sp|P48899.1|NU1M_CYACA//1.00E-50//RecName: Full=NADH-ubiquinone oxidoreductase chain 1; AltName: Full=NADH dehydrogenase subunit 1 >gi|758181|emb|CAA88775.1| NADH dehydrogenase subunit 1 [Cyanidium caldarium]	Unigene43424_All//1.00E-21//ATMG01275| Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C.			ko00190|Oxidative phosphorylation	GO:0016020	nr +
Unigene43425_All	660	0.00	24.64	9.92	0.00	0.00	0.00	0.00	0.00	0.00	1.46E+01	1.81E-93	Up	1.33E+01	1.48E-36	Up	null	null		null	null		null	null		null	null		Unigene43425_All//sp|P02516|HSP23_DROME//2.00E-45//Heat shock protein 23 OS=Drosophila melanogaster GN=Hsp23 PE=1 SV=2						swissprot +
Unigene43426_All	576	0.45	2.29	0.28	1.99	2.81	2.27	0.15	0.00	0.00	2.33E+00	6.54E-04	Up	-7.12E-01	6.22E-01		4.98E-01	3.75E-01		1.93E-01	7.47E-01		-7.20E+00	4.03E-01		-7.20E+00	3.58E-01		Unigene43426_All//gi|115440841|ref|NP_001044700.1|//2.00E-34//Os01g0831200 [Oryza sativa Japonica Group] >gi|56785178|dbj|BAD81854.1| BAG domain containing protein-like [Oryza sativa Japonica Group] >gi|113534231|dbj|BAF06614.1| Os01g0831200 [Oryza sativa Japonica Group]	Unigene43426_All//2.00E-12//AT3G51780| ATBAG4 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 4); protein binding	Unigene43426_All//4.00E-42//CO491977			GO:0005488//GO:0012501//GO:0043231	nr +
Unigene43427_All	271	0.00	22.81	8.84	0.00	0.00	0.00	0.00	0.00	0.00	1.45E+01	2.70E-35	Up	1.31E+01	3.24E-13	Up	null	null		null	null		null	null		null	null									
Unigene4343_All	935	7.50	4.77	2.62	55.83	35.50	17.05	15.83	4.51	1.83	-6.53E-01	3.09E-03		-1.52E+00	6.96E-10	Down	-6.53E-01	1.77E-22		-1.71E+00	6.67E-94	Down	-1.81E+00	7.58E-33	Down	-3.11E+00	6.54E-64	Down	Unigene4343_All//gi|115441793|ref|NP_001045176.1|//6.00E-06//Os01g0914000 [Oryza sativa Japonica Group] >gi|113534707|dbj|BAF07090.1| Os01g0914000 [Oryza sativa Japonica Group]	Unigene4343_All//1.00E-32//AT5G48500| unknown protein	Unigene4343_All//0.00E+00//TC164149				nr -
Unigene43430_All	230	143.09	38.55	103.26	71.26	63.18	30.24	1.29	0.36	0.52	-1.89E+00	9.64E-63	Down	-4.71E-01	1.06E-06		-1.74E-01	2.56E-01		-1.24E+00	1.71E-18	Down	-1.82E+00	2.11E-01		-1.31E+00	3.13E-01		Unigene43430_All//gi|116292146|dbj|BAF35580.1|//6.00E-33//multifunctional triterpene synthase [Kandelia candel]	Unigene43430_All//2.00E-30//AT1G78970| LUP1 (LUPEOL SYNTHASE 1); beta-amyrin synthase/ lupeol synthase	Unigene43430_All//1.00E-117//C0082200		ko00100|Steroid biosynthesis	GO:0031559	nr +
Unigene43434_All	778	0.13	0.13	0.07	0.38	0.44	0.17	1.03	0.70	3.69	-4.58E-02	9.88E-01		-9.76E-01	7.20E-01		2.04E-01	9.01E-01		-1.14E+00	4.57E-01		-5.64E-01	4.30E-01		1.84E+00	2.83E-07	Up	Unigene43434_All//gi|225468413|ref|XP_002263310.1|//1.00E-21//PREDICTED: similar to phosphoinositide phosphatase family protein, partial [Vitis vinifera]	Unigene43434_All//3.00E-10//AT5G66020| ATSAC1B (SUPPRESSOR OF ACTIN 1B); phosphatidylinositol-4,5-bisphosphate 5-phosphatase	Unigene43434_All//0.00E+00//AI725893			GO:0000904//GO:0009826//GO:0034593//GO:0044459	nr +
Unigene43436_All	303	0.00	24.58	13.71	0.00	0.00	0.00	0.00	0.00	0.00	1.46E+01	1.39E-42	Up	1.37E+01	4.83E-23	Up	null	null		null	null		null	null		null	null		Unigene43436_All//gi|225432388|ref|XP_002276724.1|//4.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]				ko03040|Spliceosome		nr -

Unigene4344_All	1353	4.02	2.25	2.05	3.79	4.58	5.81	8.09	4.70	3.89	-8.40E-01	1.03E-03		-9.75E-01	2.82E-04		2.73E-01	3.05E-01		6.15E-01	2.79E-03		-7.86E-01	3.47E-07		-1.06E+00	1.06E-11	Down	Unigene4344_All//gi|297802084|ref|XP_002868926.1|//3.00E-78//electron transport SCO1/SenC family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314762|gb|EFH45185.1| electron transport SCO1/SenC family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4344_All//2.00E-71//AT4G39740| electron transport SCO1/SenC family protein	Unigene4344_All//0.00E+00//TC165545				nr -
Unigene43440_All	538	1.95	0.19	1.29	0.37	0.00	0.34	0.00	0.00	0.00	-3.37E+00	2.13E-04	Down	-5.96E-01	3.93E-01		-8.53E+00	8.42E-02		-1.42E-01	9.34E-01		null	null		null	null		Unigene43440_All//sp|Q65M01|NSRR_BACLD//2.00E-26//HTH-type transcriptional regulator nsrR OS=Bacillus licheniformis (strain DSM 13 / ATCC 14580) GN=nsrR PE=3 SV=1							swissprot +
Unigene43441_All	369	0.00	0.00	0.00	0.00	0.00	0.12	27.38	8.50	11.55	null	null		null	null		null	null		6.94E+00	6.95E-01		-1.69E+00	1.18E-20	Down	-1.25E+00	7.82E-14	Down	Unigene43441_All//gi|124360970|gb|ABN08942.1|//9.00E-29//Quinonprotein alcohol dehydrogenase-like [Medicago truncatula]						GO:0008152//GO:0016491	nr +
Unigene43445_All	511	0.61	0.79	2.50	0.97	0.54	0.53	3.14	0.65	0.94	3.69E-01	7.24E-01		2.03E+00	3.44E-03		-8.55E-01	4.07E-01		-8.78E-01	4.20E-01		-2.26E+00	2.23E-05	Down	-1.75E+00	2.96E-04	Down			Unigene43445_All//2.00E-145//gi|164322106|gb|ES801472.1|ES801472				
Unigene43449_All	389	0.00	7.03	1.92	0.00	0.27	0.81	1.09	1.18	9.52	1.28E+01	1.44E-15	Up	1.09E+01	3.27E-04	Up	8.05E+00	4.56E-01		9.67E+00	4.07E-02		1.21E-01	9.07E-01		3.13E+00	2.54E-16	Up								
Unigene43453_All	803	0.00	0.00	0.00	0.00	0.00	0.00	9.11	1.20	4.47	null	null		null	null		null	null		null	null		-2.93E+00	4.09E-29	Down	-1.03E+00	8.82E-08	Down	Unigene43453_All//gi|21322711|emb|CAD22154.1|//2.00E-13//pherophorin-dr1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome	GO:0016787//GO:0044464	nr +
Unigene43454_All	850	0.00	0.00	0.00	0.00	0.00	0.00	1.64	4.82	7.73	null	null		null	null		null	null		null	null		1.55E+00	6.65E-08	Up	2.24E+00	6.52E-20	Up								
Unigene43455_All	526	0.00	8.28	4.96	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	8.00E-25	Up	1.23E+01	2.12E-14	Up	null	null		null	null		null	null		null	null		Unigene43455_All//gi|29468214|gb|AA085450.1|//2.00E-15//50S ribosomal protein L28 Rpl28 [Pyrocystis lunula]	Unigene43455_All//2.00E-08//AT2G33450| 50S ribosomal protein L28, chloroplast (CL28)			ko03010|Ribosome	GO:0009536//GO:0030529	nr +
Unigene43459_All	696	0.00	0.29	0.15	0.00	0.00	0.13	0.73	6.67	7.27	8.19E+00	1.36E-01		7.26E+00	3.97E-01		null	null		7.02E+00	4.76E-01		3.19E+00	3.23E-20	Up	3.32E+00	3.25E-23	Up	Unigene43459_All//gi|28950747|gb|AA063297.1|//6.00E-52//At2g45360 [Arabidopsis thaliana]	Unigene43459_All//3.00E-53//AT2G45360| unknown protein	Unigene43459_All//3.00E-71//TC149339				nr -
Unigene4346_All	926	1.13	0.82	0.92	3.23	3.94	2.05	3.38	0.59	2.28	-4.61E-01	4.86E-01		-2.97E-01	6.41E-01		2.88E-01	4.23E-01		-6.56E-01	7.32E-02		-2.53E+00	4.76E-11	Down	-5.67E-01	6.16E-02		Unigene4346_All//gi|17978960|gb|AAL47484.1|//1.00E-91//AT5g10020/T31P16_9 [Arabidopsis thaliana]	Unigene4346_All//4.00E-91//AT5G10020| leucine-rich repeat transmembrane protein kinase, putative	Unigene4346_All//2.00E-73//ES823369		ko04626|Plant-pathogen interaction		nr +
Unigene43460_All	231	0.23	0.00	5.07	1.51	0.60	0.59	0.00	0.00	0.69	-7.82E+00	6.11E-01		4.48E+00	1.90E-05	Up	-1.34E+00	3.08E-01		-1.36E+00	3.37E-01		null	null		9.43E+00	1.40E-01				Unigene43460_All//7.00E-08//AW187478				
Unigene43461_All	822	0.25	0.00	0.00	0.00	0.00	0.33	0.82	3.92	4.17	-7.99E+00	1.22E-01		-7.99E+00	1.45E-01		null	null		8.37E+00	7.02E-02		2.25E+00	5.72E-10	Up	2.34E+00	2.62E-11	Up	Unigene43461_All//gi|224141031|ref|XP_002323878.1|//1.00E-20//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222866880|gb|EEF04011.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]						nr -
Unigene43465_All	489	0.00	30.98	13.83	0.00	0.00	0.00	0.00	0.00	1.49E+01	5.02E-87	Up	1.38E+01	9.21E-38	Up	null	null		null	null		null	null		null	null		Unigene43465_All//sp|P61917|NPC2_PANTR//2.00E-06//Epididymal secretory protein E1 OS=Pan troglodytes GN=NPC2 PE=2 SV=1						swissprot +
Unigene43466_All	541	0.29	0.09	2.07	0.74	0.64	0.50	0.00	0.00	0.00	-1.63E+00	4.88E-01		2.83E+00	7.34E-04	Up	-2.11E-01	8.25E-01		-5.56E-01	6.38E-01		null	null		null	null		Unigene43466_All//COG3920//6.00E-18//Signal transduction histidine kinase						cog -
Unigene43469_All	295	0.89	0.69	0.18	8.44	3.85	1.53	0.00	0.43	0.27	-3.68E-01	7.78E-01		-2.30E+00	2.43E-01		-1.13E+00	2.81E-03		-2.46E+00	1.24E-07	Down	8.73E+00	2.40E-01		8.08E+00	4.04E-01				Unigene43469_All//4.00E-124//gi|78334601|gb|DT554875.1|DT554875				
Unigene4347_All	702	1.34	0.94	0.83	2.41	1.86	1.87	3.13	1.13	2.33	-5.16E-01	4.57E-01		-6.85E-01	3.69E-01		-3.72E-01	4.82E-01		-3.71E-01	4.92E-01		-1.47E+00	2.62E-04	Down	-4.29E-01	2.59E-01		Unigene4347_All//gi|217426815|gb|ACK44523.1|//4.00E-75//AT5G10020-like protein [Arabidopsis arenosa]	Unigene4347_All//2.00E-76//AT5G10020| leucine-rich repeat transmembrane protein kinase, putative	Unigene4347_All//0.00E+00//ES823369		ko04626|Plant-pathogen interaction		nr -
Unigene43470_All	569	0.92	0.00	0.00	3.76	1.27	2.14	1.26	0.15	0.70	-9.84E+00	2.92E-03		-9.84E+00	4.75E-03		-1.57E+00	2.23E-04	Down	-8.13E-01	6.70E-02		-3.10E+00	1.40E-03		-8.51E-01	2.39E-01		Unigene43470_All//gi|297814325|ref|XP_002875046.1|//2.00E-80//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320883|gb|EFH51305.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene43470_All//6.00E-73//AT4G00090| transducin family protein / WD-40 repeat family protein	Unigene43470_All//0.00E+00//gi|78345343|gb|DT565617.1|DT565617			GO:0031410	nr -
Unigene43471_All	642	0.00	0.00	0.00	0.00	0.00	0.00	19.43	22.07	0.00	null	null		null	null		null	null		null	null		1.84E-01	2.17E-01		-1.42E+01	6.17E-92	Down								
Unigene43476_All	1047	0.00	0.58	0.00	0.05	0.26	1.04	0.53	1.64	3.58	9.18E+00	1.17E-03		null	null		2.47E+00	2.23E-01		4.44E+00	2.02E-05	Up	1.64E+00	5.45E-04	Up	2.77E+00	1.15E-14	Up	Unigene43476_All//gi|224097212|ref|XP_002310878.1|//1.00E-157//1-aminocyclopropane-1-carboxylate [Populus trichocarpa] >gi|222853781|gb|EEE91328.1| 1-aminocyclopropane-1-carboxylate [Populus trichocarpa]	Unigene43476_All//5.00E-152//AT3G49700| ACS9 (1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE 9); 1-aminocyclopropane-1-carboxylate synthase			ko00270|Cysteine and methionine metabolism		nr +
Unigene43477_All	323	0.16	42.83	12.53	0.00	0.00	0.00	0.00	0.00	0.00	8.05E+00	2.69E-27	Up	6.27E+00	7.14E-21	Up	null	null		null	null		null	null		null	null									
Unigene43478_All	428	0.24	0.00	0.00	0.00	1.85	0.32	1.38	0.78	0.47	-7.93E+00	3.71E-01		-7.93E+00	3.92E-01		1.09E+01	7.26E-05	Up	8.31E+00	3.11E-01		-8.24E-01	3.48E-01		-1.57E+00	6.49E-02				Unigene43478_All//6.00E-56//TC137159				
Unigene43480_All	612	0.00	0.00	0.00	0.00	0.00	0.00	9.05	0.75	7.42	null	null		null	null		null	null		null	null		-3.59E+00	1.12E-26	Down	-2.86E-01	2.13E-01		Unigene43480_All//gi|297849944|ref|XP_002892853.1|//8.00E-38//ATPDR7/PDR7 [Arabidopsis lyrata subsp. lyrata] >gi|297338695|gb|EFH69112.1| ATPDR7/PDR7 [Arabidopsis lyrata subsp. lyrata]	Unigene43480_All//5.00E-27//AT3G16340| PDR1; ATPase, coupled to transmembrane movement of substances	Unigene43480_All//7.00E-41//TC178268			GO:0000041//GO:0009526//GO:0009814//GO:0015082//GO:0016020//GO:0016887//GO:0019762//GO:0050832//GO:0052482//GO:0071365	nr +
Unigene43483_All	335	0.00	5.60	3.66	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.11E-10	Up	1.18E+01	9.11E-07	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene43484_All	415	0.25	0.00	0.26	3.60	1.58	0.54	2.45	1.01	0.48	-7.98E+00	3.71E-01		2.55E-02	9.99E-01		-1.19E+00	2.14E-02		-2.73E+00	2.66E-05	Down	-1.28E+00	4.06E-02		-2.35E+00	5.84E-04	Down			Unigene43484_All//1.00E-07//BF274633				
Unigene43487_All	330	0.63	3.69	2.10	0.45	0.83	0.27	0.00	0.13	0.48	2.54E+00	5.98E-04	Up	1.73E+00	7.67E-02		8.82E-01	5.95E-01		-7.27E-01	7.15E-01		6.99E+00	6.34E-01		8.92E+00	1.40E-01									
Unigene43488_All	1379	0.00	5.18	1.31	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.81E-41	Up	1.04E+01	5.69E-10	Up	null	null		null	null		null	null		null	null		Unigene43488_All//gi|116060108|emb|CAL56167.1|//5.00E-06//filamin (ISS) [Ostreococcus tauri]						nr -
Unigene43490_All	493	0.00	0.00	0.00	0.00	0.00	0.00	3.17	2.54	0.00	null	null		null	null		null	null		null	null		-3.19E-01	5.33E-01		-1.16E+01	1.42E-11	Down	Unigene43490_All//gi|145351130|ref|XP_001419938.1|//3.00E-65//Heat Shock Protein 90, cytosolic [Ostreococcus lucimarinus CCE9901] >gi|145880171|gb|ABO98231.1| Heat Shock Protein 90, cytosolic [Ostreococcus lucimarinus CCE9901]	Unigene43490_All//8.00E-51//AT5G56000| heat shock protein 81-4 (HSP81-4)			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr -
Unigene43491_All	644	0.00	0.00	0.00	0.00	0.00	0.00	3.35	4.80	0.00	null	null		null	null		null	null		null	null		5.20E-01	1.07E-01		-1.17E+01	6.88E-16	Down	Unigene43491_All//gi|115484761|ref|NP_001067524.1|//1.00E-81//Os11g0220800 [Oryza sativa Japonica Group] >gi|122240410|sp|Q0ITS8.1|RL101_ORYSJ RecName: Full=60S ribosomal protein L10-1; AltName: Full=Putative tumor suppressor SC34; AltName: Full=Protein QM >gi|188513712|sp|A2ZXQ7.2|RL101_ORYSI RecName: Full=60S ribosomal protein L10-1; AltName: Full=Putative tumor suppressor SC34; AltName: Full=Protein QM >gi|113644746|dbj|BAF27887.1| Os11g0220800 [Oryza sativa Japonica Group]	Unigene43491_All//1.00E-80//AT1G66580| 60S ribosomal protein L10 (RPL10C)	Unigene43491_All//8.00E-13//BF277831		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene43492_All	319	0.00	6.35	3.67	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.53E-11	Up	1.18E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene43492_All//gi|301092583|ref|XP_002997146.1|//4.00E-07//atlastin-like protein [Phytophthora infestans T30-4] >gi|262111595|gb|EEY69647.1| atlastin-like protein [Phytophthora infestans T30-4]						nr +
Unigene43493_All	584	0.00	0.00	0.00	0.09	0.00	0.00	5.21	11.31	3.55	null	null		null	null		-6.41E+00	5.55E-01		-6.41E+00	6.34E-01		1.12E+00	1.02E-07	Up	-5.55E-01	7.20E-02									
Unigene43495_All	599	0.00	27.41	7.11	0.00	0.00	0.00	0.00	0.00	0.00	1.47E+01	2.39E-94	Up	1.28E+01	1.22E-23	Up	null	null		null	null		null	null		null	null		Unigene43495_All//gi|192910768|gb|ACF06492.1|//1.00E-56//ribosomal L9-like protein [Elaeis guineensis]	Unigene43495_All//3.00E-55//AT4G10450| 60S ribosomal protein L9 (RPL90D)	Unigene43495_All//5.00E-08//TC171167		ko03010|Ribosome	GO:0005622	nr +
Unigene43496_All	303	90.65	62.88	79.26	136.13	134.33	124.46	11.02	29.11	19.59	-5.28E-01	3.13E-07		-1.94E-01	9.24E-02		-1.91E-02	8.49E-01		-1.29E-01	1.72E-01		1.40E+00	6.05E-14	Up	8.30E-01	9.31E-05				Unigene43496_All//5.00E-65//gi|13245475|gb|BE054939.2|BE054939				
Unigene43497_All	361	0.00	3.23	5.90	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.05E-06	Up	1.25E+01	9.78E-12	Up	null	null		null	null		null	null		null	null		Unigene43497_All//gi|284807026|dbj|BAI67718.1|//9.00E-07//nuclear matrix constituent protein 2 [Daucus carota]						nr -
Unigene43499_All	518	0.00	26.70	10.69	0.00	0.00	0.00	0.00	0.00	0.00	1.47E+01	2.03E-79	Up	1.34E+01	7.61E-31	Up	null	null		null	null		null	null		null	null									
Unigene4350_All	1373	3.01	6.05	2.02	5.91	5.92	5.33	11.09	11.02	8.12	1.01E+00	9.24E-07	Up	-5.78E-01	6.69E-02		1.30E-03	9.98E-01		-1.50E-01	5.36E-01		-8.60E-03	9.85E-01		-4.48E-01	3.13E-04		Unigene4350_All//gi|18396691|ref|NP_566214.1|//5.00E-81//ATAPRL5 (APR-like 5) [Arabidopsis thaliana]	Unigene4350_All//4.00E-70//AT3G03860| ATAPRL5 (APR-like 5)	Unigene4350_All//0.00E+00//ES842886		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene43502_All	1139	0.00	13.26	2.76	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	9.81E-87	Up	1.14E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene43502_All//gi|75311246|sp|Q9LKA3.1|MDHM2_ARATH//1.00E-105//RecName: Full=Malate dehydrogenase 2, mitochondrial; AltName: Full=mNAD-MDH 2; Flags: Precursor >gi|8777485|dbj|BAA97065.1| NAD-dependent malate dehydrogenase [Arabidopsis thaliana] >gi|15010582|gb|AAK73950.1| AT3g15020/K15M2_16 [Arabidopsis thaliana] >gi|20147389|gb|AAM10404.1| AT3g15020/K15M2_16 [Arabidopsis thaliana]	Unigene43502_All//7.00E-103//AT3G15020| malate dehydrogenase (NAD), mitochondrial, putative			ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene43503_All	707	0.00	0.00	0.00	0.00	0.00	0.00	7.30	16.91	0.23	null	null		null	null		null	null		null	null		1.21E+00	4.61E-15	Up	-5.02E+00	4.11E-32	Down	Unigene43503_All//gi|42569129|ref|NP_179444.2|//2.00E-07//cupin family protein [Arabidopsis thaliana]				ko03040|Spliceosome		nr -
Unigene43507_All	850	0.00	0.00	0.00	0.00	0.00	0.21	13.68	28.08	6.19	null	null		null	null					7.73E+00	1.94E-01		1.04E+00	5.83E-23	Up	-1.14E+00	6.37E-14	Down	Unigene43507_All//gi|111379984|gb|AAQ63185.2|//7.00E-99//germin-like protein 3 [Vitis vinifera]	Unigene43507_All//2.00E-81//AT3G05950| germin-like protein, putative	Unigene43507_All//1.00E-43//gi|109873402|gb|DW502377.1|DW502377			GO:0005576//GO:0046914	nr +

Unigene43509_All	288	0.00	0.00	0.00	0.00	0.00	0.00	3.38	4.64	0.28	null	null		null	null		null	null		null	null		4.60E-01	3.93E-01		-3.61E+00	2.14E-05	Down	Unigene43509_All//gi|9256636|ref|NP_061348.1|//3.00E-06//60S ribosomal protein L41 [Mus musculus] >gi|10863875|ref|NP_066927.1| 60S ribosomal protein L41 [Homo sapiens] >gi|20806115|ref|NP_620783.1| 60S ribosomal protein L41 [Rattus norvegicus] >gi|78217384|ref|NP_001030344.1| 60S ribosomal protein L41 [Homo sapiens] >gi|114326422|ref|NP_001041622.1| 60S ribosomal protein L41 [Felis catus] >gi|197100322|ref|NP_001124641.1| 60S ribosomal protein L41 [Pongo abelii] >gi|159476032|ref|XP_001696118.1| ribosomal protein L41, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|51701777|sp|Q6YLX4.1|RL41_CYPCA RecName: Full=60S ribosomal protein L41 >gi|51701779|sp|Q7LH53.1|RL41_EPICO RecName: Full=60S ribosomal protein L41				ko03010|Ribosome		nr -
Unigene43510_All	605	0.00	0.00	0.00	0.00	0.00	0.00	8.46	1.17	14.36	null	null		null	null		null	null		null	null		-2.85E+00	5.33E-20	Down	7.64E-01	8.37E-06		Unigene43510_All//gi|226492894|ref|NP_001149512.1|//3.00E-54//Flavonol sulfotransferase-like [Zea mays] >gi|195627682|gb|ACG35671.1| flavonol sulfotransferase-like [Zea mays]	Unigene43510_All//3.00E-52//AT1G18590| SOT17 (SULFOTRANSFERASE 17); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene43510_All//2.00E-124//C0097446		ko00380|Tryptophan metabolism/ko00966|Glucosinolate biosynthesis	GO:0008146	nr -
Unigene43513_All	728	0.00	15.52	15.21	0.00	0.00	0.19	0.00	0.00	0.11	1.39E+01	8.70E-65	Up	1.39E+01	3.13E-62	Up	null	null		7.54E+00	3.11E-01		null	null		6.77E+00	4.04E-01		Unigene43513_All//gi|6978859|ref|NP_036980.1|//1.00E-96//ferritin heavy chain [Rattus norvegicus] >gi|309233|gb|AAA37612.1| ferritin heavy chain [Mus musculus] >gi|1433203|gb|AAB39890.1| ferritin-H submit [Rattus norvegicus] >gi|127799856|gb|AAH81845.2| Ferritin, heavy polypeptide 1 [Rattus norvegicus] >gi|190662360|gb|EDM12783.1| rCG47136, isoform CRA_a [Rattus norvegicus]	Unigene43513_All//7.00E-40//AT2G40300| ATFER4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal ion binding			ko00860|Porphyrin and chlorophyll metabolism	GO:0000041//GO:0002376//GO:0005506//GO:0008152//GO:0008283//GO:0010939//GO:0016724//GO:0030005//GO:0043231//GO:0044444//GO:0048193	nr +
Unigene43515_All	367	0.00	0.28	0.15	0.00	0.19	0.00	0.35	1.48	3.04	8.11E+00	3.86E-01		7.18E+00	6.35E-01		7.55E+00	6.09E-01		null	null		2.10E+00	3.71E-02		3.14E+00	2.19E-05	Up							
Unigene4352_All	906	63.47	21.36	35.91	224.60	245.49	236.68	119.33	57.76	96.17	-1.57E+00	3.78E-84	Down	-8.22E-01	3.94E-29		1.28E-01	8.76E-05		7.56E-02	4.83E-02		-1.05E+00	7.61E-103	Down	-3.11E-01	7.56E-13		Unigene4352_All//gi|46318067|gb|AAS87601.1|//1.00E-146//membrane-anchored endo-1,4-beta-glucanase [Gossypium hirsutum]	Unigene4352_All//1.00E-122//AT5G49720| ATGH9A1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9A1); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene4352_All//0.00E+00//TC161105		ko00500|Starch and sucrose metabolism		nr +
Unigene43525_All	559	0.00	5.62	3.05	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.07E-18	Up	1.16E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene43525_All//gi|293334895|ref|NP_001167666.1|//1.00E-25//calmodulin [Zea mays] >gi|195618002|gb|ACG30831.1| calmodulin [Zea mays]	Unigene43525_All//7.00E-26//AT3G43810| CAM7 (CALMODULIN 7); calcium ion binding			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005488	nr -
Unigene43526_All	712	0.00	0.00	0.00	0.00	0.00	0.00	4.81	3.23	0.84	null	null		null	null		null	null		null	null		-5.75E-01	5.57E-02		-2.52E+00	1.97E-12	Down	Unigene43526_All//gi|1015937|emb|CAA62943.1|//1.00E-09//extensin class 1 protein [Vigna unguiculata]				ko03040|Spliceosome//ko00020|Citrate cycle (TCA cycle)//ko00310|Lysine degradation		nr -
Unigene43529_All	549	0.00	17.81	6.98	0.00	0.00	0.00	0.00	0.15	0.00	1.41E+01	5.09E-56	Up	1.28E+01	3.02E-21	Up	null	null		null	null		7.25E+00	4.01E-01		null	null		Unigene43529_All//gi|1545805|dbj|BAA10929.1|//2.00E-07//cytochrome P450 like_TBP [Nicotiana tabacum]		Unigene43529_All//6.00E-32//TC137772			GO:0004497	nr -
Unigene4353_All	879	21.61	47.04	28.72	24.60	36.79	46.91	10.77	5.14	5.17	1.12E+00	2.84E-36	Up	4.10E-01	2.64E-04		5.81E-01	3.51E-11		9.32E-01	1.11E-28		-1.07E+00	4.67E-10	Down	-1.06E+00	2.87E-10	Down	Unigene4353_All//gi|18390905|ref|NP_563820.1|//1.00E-66//plastocyanin-like domain-containing protein [Arabidopsis thaliana] >gi|6664312|gb|AAF22894.1|AC006932_11 T27G7.18 [Arabidopsis thaliana] >gi|13877539|gb|AAK43847.1|AF370470_1 Unknown protein [Arabidopsis thaliana]	Unigene4353_All//5.00E-61//AT1G08500| plastocyanin-like domain-containing protein	Unigene4353_All//0.00E+00//TC132573				nr +
Unigene43532_All	700	2.69	0.72	3.04	0.43	0.89	0.52	0.00	0.00	0.00	-1.89E+00	2.73E-04	Down	1.77E-01	6.88E-01		1.05E+00	2.99E-01		2.74E-01	8.33E-01		null	null		null	null		Unigene43532_All//gi|224065781|ref|XP_002301961.1|//8.00E-89//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222843687|gb|EEE81234.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene43532_All//1.00E-80//AT1G27940| PGP13 (P-GLYCOPROTEIN 13; ATPase, coupled to transmembrane movement of substances	Unigene43532_All//1.00E-107//gi|78342920|gb|DT563194.1|DT563194		ko02010|ABC transporters	GO:0005488//GO:0042626//GO:0044464	nr +
Unigene43533_All	691	0.00	0.95	0.00	1.80	1.20	0.52	1.04	0.67	2.71	9.90E+00	6.25E-04	Up	null	null		-5.92E-01	3.18E-01		-1.79E+00	5.55E-03		-6.45E-01	4.01E-01		1.38E+00	1.22E-03		Unigene43533_All//gi|297821204|ref|XP_002878485.1|//2.00E-39//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324323|gb|EFH54744.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene43533_All//2.00E-36//AT3G62900| zinc ion binding	Unigene43533_All//9.00E-13//DW501509			GO:0044464	nr +
Unigene43537_All	294	1.96	0.52	2.54	3.73	1.05	0.61	1.15	0.43	1.49	-1.92E+00	7.00E-02		3.73E-01	6.23E-01		-1.82E+00	5.10E-03		-2.60E+00	7.13E-04	Down	-1.43E+00	2.58E-01		3.74E-01	6.82E-01								
Unigene43538_All	735	1.21	0.00	0.00	0.00	0.00	0.00	1.27	9.38	13.44	-1.02E+01	2.86E-05	Down	-1.02E+01	6.30E-05	Down	null	null		null	null		2.89E+00	4.81E-27	Up	3.41E+00	8.64E-46	Up	Unigene43538_All//gi|111379984|gb|AAQ63183.2|//1.00E-90//germin-like protein 3 [Vitis vinifera]	Unigene43538_All//6.00E-80//AT5G39110| germin-like protein, putative	Unigene43538_All//2.00E-75//gi|109873402|gb|DW502377.1|DW502377			GO:0004871//GO:0005576//GO:0008152//GO:0016623//GO:0046914	nr +
Unigene43540_All	586	3.48	0.00	1.45	0.68	0.76	0.15	0.00	0.00	0.00	-1.18E+01	8.49E-12	Down	-1.26E+00	9.17E-03		1.68E-01	9.04E-01		-2.14E+00	1.26E-01		null	null		null	null				Unigene43540_All//5.00E-20//TC162759				
Unigene43544_All	484	0.00	7.43	3.52	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.77E-20	Up	1.18E+01	2.20E-09	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene43546_All	382	0.27	0.00	0.00	4.30	4.33	0.71	0.22	0.22	0.21	-8.10E+00	3.71E-01		-8.10E+00	3.92E-01		7.90E-03	9.98E-01		-2.60E+00	1.60E-05	Down	-1.70E-02	1.01E+00		-8.59E-02	9.71E-01								
Unigene43548_All	312	1.34	0.00	0.00	0.00	0.00	3.62	0.00	0.00	0.00	-1.04E+01	1.05E-02		-1.04E+01	1.56E-02		null	null		1.18E+01	9.83E-07	Up	null	null		null	null		Unigene43548_All//gi|224127212|ref|XP_002320015.1|//5.00E-43//1-aminocyclopropane-1-carboxylate [Populus trichocarpa] >gi|222860788|gb|EEE98330.1| 1-aminocyclopropane-1-carboxylate [Populus trichocarpa]	Unigene43548_All//5.00E-42//AT3G49700| ACS9 (1-AMINACYCLOPROPANE-1-CARBOXYLATE SYNTHASE 9); 1-aminocyclopropane-1-carboxylate synthase			ko00270|Cysteine and methionine metabolism	GO:0003006//GO:0005515//GO:0006412//GO:0006555//GO:0009725//GO:0016740//GO:0016846//GO:0048037	nr -
Unigene43550_All	392	0.00	36.71	13.31	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	1.22E-82	Up	1.37E+01	4.81E-29	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene43551_All	949	0.11	103.37	81.64	0.16	0.33	0.67	0.00	0.00	0.08	9.87E+00	0.00E+00	Up	9.53E+00	0.00E+00	Up	1.05E+00	5.31E-01		2.08E+00	4.69E-02		null	null		6.39E+00	4.04E-01		Unigene43551_All//gi|299830469|ref|YP_003734840.1|//3.00E-23//NADH dehydrogenase subunit 2 [Pythium ultimum] >gi|269810846|gb|ACZ43875.1| NADH dehydrogenase subunit 2 [Pythium ultimum]				ko00190|Oxidative phosphorylation	GO:0044464	nr +
Unigene43554_All	972	0.00	0.21	0.00	0.10	0.28	0.00	5.74	2.41	0.57	7.70E+00	1.36E-01		null	null		1.47E+00	4.20E-01		-6.68E+00	3.99E-01		-1.25E+00	7.95E-08	Down	-3.32E+00	4.63E-26	Down	Unigene43554_All//gi|15237158|ref|NP_200058.1|//3.00E-98//MATE efflux protein-related [Arabidopsis thaliana]	Unigene43554_All//7.00E-90//AT5G52450| MATE efflux protein-related	Unigene43554_All//4.00E-148//TC158342			GO:0015291//GO:0015893//GO:0016020//GO:0051707	nr +
Unigene43556_All	428	0.00	0.00	0.00	0.00	0.00	0.00	5.33	5.37	0.19	null	null		null	null		null	null		null	null		9.80E-03	1.02E+00		-4.84E+00	3.22E-14	Down							
Unigene4356_All	1144	1.23	1.99	2.28	1.87	2.65	2.33	3.29	1.28	1.46	6.91E-01	1.04E-01		8.85E-01	3.06E-02		5.01E-01	1.77E-01		3.15E-01	4.71E-01		-1.36E+00	3.50E-06	Down	-1.17E+00	3.04E-05	Down	Unigene4356_All//gi|297608886|ref|NP_001062327.2|//2.00E-41//Os08g0530500 [Oryza sativa Japonica Group] >gi|255678598|dbj|BAF24241.2| Os08g0530500 [Oryza sativa Japonica Group]	Unigene4356_All//2.00E-06//AT2G27110| FRS3 (FAR1-related sequence 3); zinc ion binding	Unigene4356_All//0.00E+00//ES796265				nr +
Unigene43565_All	249	0.84	1.83	0.43	0.80	0.55	0.54	0.85	5.87	2.88	1.12E+00	3.28E-01		-9.75E-01	6.20E-01		-5.33E-01	7.48E-01		-5.57E-01	7.32E-01		2.79E+00	4.85E-06	Up	1.76E+00	2.48E-02				Unigene43565_All//5.00E-21//TC164246				
Unigene43568_All	709	0.00	18.30	13.82	0.00	0.10	0.25	0.00	0.00	0.00	1.42E+01	1.92E-74	Up	1.38E+01	5.74E-55	Up	6.60E+00	6.09E-01		7.99E+00	1.94E-01		null	null		null	null		Unigene43568_All//gi|115453873|ref|NP_001050537.1|//3.00E-58//Os03g0576700 [Oryza sativa Japonica Group] >gi|32493112|gb|AAP85547.1| ribosomal protein large subunit 13 [Oryza sativa Japonica Group] >gi|113549008|dbj|BAF12451.1| Os03g0576700 [Oryza sativa Japonica Group]	Unigene43568_All//3.00E-46//AT5G23900| 60S ribosomal protein L13 (RPL13D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr -
Unigene4357_All	1109	7.08	9.27	6.48	29.29	34.40	26.10	11.78	3.54	3.95	3.90E-01	3.13E-02		-1.27E-01	6.13E-01		2.32E-01	6.74E-03		-1.66E-01	1.12E-01		-1.73E+00	1.91E-27	Down	-1.58E+00	8.15E-25	Down	Unigene4357_All//gi|106879177|gb|ABF82618.1|//2.00E-27//At5g38300 [Arabidopsis thaliana]	Unigene4357_All//1.00E-28//AT5G38300| unknown protein	Unigene4357_All//0.00E+00//TC142799				nr -
Unigene43571_All	1150	0.05	23.92	8.80	0.00	0.00	0.00	0.00	0.00	0.00	9.04E+00	3.82E-156	Up	7.60E+00	8.26E-55	Up	null	null		null	null		null	null		null	null		Unigene43571_All//gi|15218954|ref|NP_176199.1|//1.00E-18//formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] >gi|75215697|sp|Q9XIE0.1|FH7_ARATH RecName: Full=Formin-like protein 7; Short=AtFH7; Short=AtFORMIN-7 >gi|5080823|gb|AAD39332.1|AC007258_21 Hypothetical protein [Arabidopsis thaliana] >gi|34222088|gb|AAQ62880.1| At1g59910 [Arabidopsis thaliana]				ko00230|Purine metabolism/ko00240|Pyrimidine metabolism/ko03020|RNA polymerase	GO:0044464	nr -
Unigene43572_All	486	0.00	1.36	0.22	0.41	1.28	1.58	0.96	0.69	0.90	1.04E+01	6.25E-04	Up	7.78E+00	3.97E-01		1.64E+00	1.06E-01		1.95E+00	3.23E-02		-4.76E-01	6.59E-01		-8.59E-02	9.34E-01		Unigene43572_All//gi|240255284|ref|NP_187186.5|//2.00E-55//aminopeptidase/ hydrolase [Arabidopsis thaliana] >gi|193104788|gb|AAL84973.1| AT3g05350/T12H1_32 [Arabidopsis thaliana] >gi|24111421|gb|AAN46861.1| At3g05350/T12H1_32 [Arabidopsis thaliana]	Unigene43572_All//7.00E-57//AT3G05350| aminopeptidase/ hydrolase	Unigene43572_All//2.00E-164//gi|109865062|gb|DW494038.1|DW494038			GO:0008238//GO:0009532//GO:0019538	nr +

Unigene43573_All	412	0.00	2.46	2.71	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	7.26E-06	Up	1.14E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene43573_All//gi|297837151|ref|XP_002886457.1|//6.00E-45//ATSC01/ATSC01/CPEF-G [Arabidopsis lyrata subsp. lyrata] >gi|297332298|gb|EFH62716.1| ATSC01/ATSC01/CPEF-G [Arabidopsis lyrata subsp. lyrata]	Unigene43573_All//4.00E-46//AT1G62750| SC01 (SNOWY COTYLEDON 1); ATP binding / translation elongation factor/ translation factor, nucleic acid binding				GO:0005576//GO:0006412//GO:0007275//GO:0008135//GO:0009526//GO:0009532//GO:0009657//GO:0017111//GO:0032559//GO:0032561	nr +
Unigene43574_All	330	0.00	0.00	0.32	0.00	0.52	0.68	0.38	0.63	2.66	null	null		8.33E+00	3.97E-01		9.03E+00	2.27E-01		9.42E+00	1.19E-01		7.20E-01	6.32E-01		2.79E+00	5.37E-04	Up	Unigene43574_All//gi|18379277|ref|NP_565274.1|//3.00E-36//ankyrin repeat family protein [Arabidopsis thaliana] >gi|75315914|sp|Q9ZU96.1|Y2168_ARATH RecName: Full=Ankyrin repeat-containing protein At2g01680 >gi|4220480|gb|AAD12703.1| expressed protein [Arabidopsis thaliana]	Unigene43574_All//1.00E-37//AT2G01680| ankyrin repeat family protein	Unigene43574_All//2.00E-55//gi|48777225|gb|CO086591.1|CO086591			GO:0016020//GO:0031410	nr -
Unigene43577_All	307	1.02	0.33	2.25	1.46	0.56	1.91	2.07	0.54	0.13	-1.63E+00	2.76E-01		1.14E+00	2.18E-01		-1.38E+00	2.16E-01		3.89E-01	6.77E-01		-1.92E+00	3.09E-02		-3.99E+00	5.82E-04	Down								
Unigene43578_All	693	0.00	0.00	0.00	0.00	0.00	0.00	4.27	3.44	0.00	null	null		null	null		null	null		null	null		-3.13E-01	3.78E-01		-1.21E+01	9.02E-22	Down	Unigene43578_All|gi|226454555|gb|EEH51861.1|//7.00E-73//heat shock protein 70kDa [Micromonas pusilla CCMP1545]	Unigene43578_All//5.00E-67//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene43578_All//9.00E-13//BM359807		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0000302//GO:0004672//GO:0009642//GO:0010038//GO:0016020//GO:0016887//GO:0019899//GO:0030312//GO:0032496//GO:0032559//GO:0043231//GO:0051707	nr -
Unigene43580_All	825	0.13	72.23	62.74	0.30	0.08	0.11	0.00	0.00	0.19	9.15E+00	0.00E+00	Up	8.95E+00	2.66E-289	Up	-1.85E+00	2.75E-01		-1.46E+00	4.07E-01		null	null		7.59E+00	1.40E-01		Unigene43580_All|gi|171259158|ref|YP_539000.2|//4.00E-66//cytochrome c oxidase subunit 1 [Physcomitrella patens] >gi|186942713|dbj|BAE93071.2| cytochrome c oxidase subunit 1 [Physcomitrella patens]	Unigene43580_All//6.00E-47//ATMG01360| cytochrome c oxidase subunit 1			ko00190|Oxidative phosphorylation	GO:0003676//GO:0004518//GO:0005506//GO:0006310//GO:0015002//GO:0019866//GO:0031224//GO:0043231//GO:0045333//GO:0051234	nr -
Unigene43583_All	267	0.00	0.00	0.00	0.00	0.00	0.00	2.06	4.70	0.00	null	null		null	null		null	null		null	null		1.19E+00	3.01E-02		-1.10E+01	2.80E-04	Down	Unigene43583_All//gi|115470525|ref|NP_001058861.1|//3.00E-06//0s07g0139600 [Oryza sativa Japonica Group] >gi|113610397|dbj|BAF20775.1| Os07g0139600 [Oryza sativa Japonica Group]				ko03010|Ribosome		nr +
Unigene43588_All	399	11.67	5.59	13.21	32.34	32.11	26.94	1.48	0.52	0.30	-1.06E+00	1.78E-04	Down	1.79E-01	5.44E-01		-1.03E-02	9.48E-01		-2.63E-01	1.19E-01		-1.50E+00	9.13E-02		-2.31E+00	1.36E-02				Unigene43588_All//4.00E-75//gi|13246106|gb|BE053753.2|BE053753				
Unigene43591_All	503	0.00	7.35	6.56	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	4.67E-21	Up	1.27E+01	2.92E-18	Up	null	null		null	null		null	null		null	null		Unigene43591_All//gi|189095434|ref|YP_001936147.1|//2.00E-36//ribosomal protein L3 [Heterosigma akashiwo] >gi|157694777|gb|ABV66053.1| 50S ribosomal protein L3 [Heterosigma akashiwo] >gi|157778008|gb|ABV70194.1| 50S ribosomal protein L3 [Heterosigma akashiwo]	Unigene43591_All//1.00E-34//AT3G17465| RPL3P (RIBOSOMAL PROTEIN L3 PLASTID); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231//GO:0044444	nr -
Unigene43594_All	805	0.46	0.76	0.73	0.12	0.00	0.06	0.32	2.80	2.43	7.31E-01	4.16E-01		6.77E-01	4.82E-01		-6.95E+00	3.12E-01		-1.14E+00	6.76E-01		3.15E+00	4.95E-10	Up	2.94E+00	1.90E-08	Up	Unigene43594_All//gi|224142293|ref|XP_002324493.1|//3.00E-31//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222865927|gb|EEF03058.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene43594_All//4.00E-20//AT2G29410| ATGLR2.8; intracellular ligand-gated ion channel				GO:0044464	nr +
Unigene43597_All	301	6.78	7.74	9.02	158.88	169.20	204.96	444.15	110.95	97.28	1.92E-01	6.30E-01		4.12E-01	3.16E-01		9.08E-02	3.07E-01		3.67E-01	1.37E-08		-2.00E+00	0.00E+00	Down	-2.19E+00	0.00E+00	Down	Unigene43597_All//gi|50313460|gb|AAT74600.1|//1.00E-14//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene43597_All//1.00E-05//AT3G23510| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene43597_All//2.00E-156//gi|31407520|gb|CD486555.1|CD486555			GO:0006629//GO:0008757	nr -
Unigene43599_All	636	0.00	1.35	0.00	0.00	0.16	0.00	248.30	78.73	108.55	1.04E+01	4.94E-05	Up	null	null		7.34E+00	4.55E-01		null	null		-1.66E+00	5.84E-304	Down	-1.19E+00	2.68E-190	Down	Unigene43599_All//gi|211906536|gb|ACJ11761.1|//6.00E-80//class III peroxidase [Gossypium hirsutum]	Unigene43599_All//4.00E-68//AT1G05260| RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase	Unigene43599_All//0.00E+00//gi|84156310|gb|DN817536.1|DN817536		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0005506//GO:0005618//GO:0006972//GO:0008152//GO:0009414//GO:0016209//GO:0016740//GO:0043231	nr +
Unigene43600_All	377	0.97	0.00	2.54	0.66	1.10	0.72	1.35	0.00	0.42	-9.92E+00	1.96E-02		1.39E+00	7.11E-02		7.30E-01	5.86E-01		1.22E-01	9.44E-01		-1.04E+01	8.89E-04	Down	-1.67E+00	7.78E-02									
Unigene43601_All	381	0.00	0.00	0.00	0.00	0.00	0.00	2.66	4.39	0.00	null	null		null	null		null	null		null	null		7.20E-01	1.18E-01		-1.14E+01	1.35E-07	Down	Unigene43601_All//gi|167859793|gb|ACA04850.1|//1.00E-24//senescence-associated protein [Picea abies]		Unigene43601_All//8.00E-58//gi|82755474|gb|DV849036.1|DV849036				nr +
Unigene43608_All	358	1.90	0.00	1.34	0.14	0.10	0.00	0.00	0.00	0.00	-1.09E+01	4.10E-04	Down	-5.05E-01	5.82E-01		-5.32E-01	8.25E-01		-7.12E+00	6.34E-01		null	null		null	null		Unigene43608_All//gi|194476857|ref|YP_002049036.1|//3.00E-16//CTP synthetase [Paulinella chromatophora] >gi|171191864|gb|ACB42826.1| CTP synthetase [Paulinella chromatophora]	Unigene43608_All//8.00E-14//AT4G02120| CTP synthase, putative / UTP--ammonia ligase, putative			ko00240|Pyrimidine metabolism	GO:0003824	nr -
Unigene43613_All	593	0.53	0.09	0.18	8.32	6.39	3.27	5.78	4.93	1.68	-2.63E+00	1.31E-01		-1.56E+00	3.30E-01		-3.81E-01	1.64E-01		-1.34E+00	9.70E-07	Down	-2.27E-01	4.95E-01		-1.78E+00	2.53E-08	Down	Unigene43613_All//gi|4139036|gb|AAD03671.1|//9.00E-10//resistance protein candidate RGC2J [Lactuca sativa]		Unigene43613_All//2.00E-121//CO132540				nr -
Unigene43614_All	681	0.00	23.66	12.43	0.00	0.00	0.00	0.00	0.00	0.00	1.45E+01	1.37E-92	Up	1.36E+01	2.05E-47	Up	null	null		null	null		null	null		null	null		Unigene43614_All//sp|P27779|CUP7_DROME/1.00E-45//Pupal cuticle protein Edg-78E OS=Drosophila melanogaster GN=Edg78E PE=1 SV=1						swissprot -
Unigene43616_All	523	0.00	4.36	3.97	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.64E-13	Up	1.20E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene43616_All//sp|Q05793|PGBM_MOUSE//3.00E-11//Basement membrane-specific heparan sulfate proteoglycan core protein OS=Mus musculus GN=Hspg2 PE=1 SV=1						swissprot +
Unigene43618_All	613	0.00	8.10	8.17	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	2.63E-28	Up	1.30E+01	7.66E-28	Up	null	null		null	null		null	null		null	null		Unigene43618_All//gi|15221484|ref|NP_176440.1|//5.00E-62//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|5454193|gb|AAD43608.1|AC005698_7 T3P18.7 [Arabidopsis thaliana] >gi|34365599|gb|AAQ65111.1| At1g62510 [Arabidopsis thaliana] >gi|62318622|dbj|BAD95067.1| At1g62510 [Arabidopsis thaliana] >gi|62320964|dbj|BAD93991.1| similar to 14KD proline-rich protein DC2.15 precursor [Arabidopsis thaliana] >gi|62321154|dbj|BAD94286.1| At1g62510 [Arabidopsis thaliana] >gi|110739491|dbj|BAF01655.1| similar to 14KD proline-rich protein DC2.15 precursor sp|P14009 [Arabidopsis thaliana] >gi|110741286|dbj|BAF02193.1| similar to 14KD proline-rich protein DC2.15 precursor sp|P14009 [Arabidopsis thaliana]	Unigene43618_All//1.00E-19//AT1G62510| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene43618_All//7.00E-07//BF271846			GO:0005488//GO:0006810//GO:0031224	nr +
Unigene43626_All	248	0.00	1.84	0.00	0.40	0.28	0.36	0.85	0.51	6.43	1.08E+01	7.43E-03		null	null		-5.33E-01	8.16E-01		-1.41E-01	9.49E-01		-7.54E-01	6.32E-01		2.91E+00	5.82E-07	Up			Unigene43626_All//6.00E-27//TC136747				
Unigene43629_All	389	20.56	13.73	16.88	57.24	34.34	30.72	99.57	82.35	25.91	-5.82E-01	5.83E-03		-2.84E-01	2.29E-01		-7.37E-01	1.73E-11		-8.98E-01	2.99E-14		-2.74E-01	6.16E-04		-1.94E+00	3.53E-91	Down			Unigene43629_All//2.00E-101//ES835095				
Unigene4363_All	845	8.98	4.14	5.23	7.60	4.48	4.38	3.65	2.57	8.01	-1.12E+00	2.85E-07	Down	-7.80E-01	3.95E-04		-7.63E-01	4.07E-04		-7.95E-01	4.89E-04		-5.06E-01	1.19E-01		1.13E+00	2.71E-08	Up	Unigene4363_All|gi|224094935|ref|XP_002310297.1|//5.00E-92//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222853200|gb|EEE90747.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene4363_All//9.00E-64//AT2G18060| VND1 (VASCULAR RELATED NAC-DOMAIN PROTEIN 1); transcription factor	Unigene4363_All//2.00E-20//TC145375	NAC			nr -
Unigene43630_All	326	0.00	0.00	0.00	0.00	0.00	0.00	3.50	1.41	0.37	null	null		null	null		null	null		null	null		-1.31E+00	2.45E-02		-3.26E+00	8.93E-06	Down	Unigene43630_All//gi|175363751|gb|ACB72462.1|//1.00E-07//elongation factor 1 gamma-like protein [Nicotiana tabacum]	Unigene43630_All//2.00E-07//AT1G57720| elongation factor 1B-gamma, putative / eEF-1B gamma, putative					nr +
Unigene43631_All	320	0.00	3.48	2.66	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.00E-06	Up	1.14E+01	9.02E-05	Up	null	null		null	null		null	null		null	null		Unigene43631_All|gi|159476418|ref|XP_001696308.1|//2.00E-10//ubiquinol:cytochrome c oxidoreductase 14 kDa subunit [Chlamydomonas reinhardtii] >gi|158282533|gb|EDP08285.1| ubiquinol:cytochrome c oxidoreductase 14 kDa subunit [Chlamydomonas reinhardtii]	Unigene43631_All//7.00E-07//AT4G32470| ubiquinol-cytochrome C reductase complex 14 kDa protein, putative			ko00190|Oxidative phosphorylation	GO:0005746	nr -
Unigene43632_All	491	0.00	0.00	0.00	0.00	0.00	0.00	4.91	4.17	0.32	null	null		null	null		null	null		null	null		-2.35E-01	5.70E-01		-3.92E+00	3.36E-13	Down			Unigene43632_All//6.00E-16//TC159777				
Unigene43633_All	947	0.00	0.00	0.00	0.00	0.00	0.00	2.10	1.41	0.08	null	null		null	null		null	null		null	null		-5.71E-01	1.72E-01		-4.64E+00	3.56E-12	Down	Unigene43633_All|gi|159477048|ref|XP_001696623.1|//2.00E-37//serine/threonine phosphatase, family 2C [Chlamydomonas reinhardtii] >gi|158282848|gb|EDP08600.1| serine/threonine phosphatase, family 2C [Chlamydomonas reinhardtii]	Unigene43633_All//4.00E-23//AT4G16580| catalytic					nr -
Unigene43634_All	410	0.00	0.00	0.00	0.12	0.08	0.00	127.05	68.91	328.04	null	null		null	null		-5.33E-01	8.25E-01		-6.92E+00	6.34E-01		-8.83E-01	8.79E-38		1.37E+00	8.11E-199	Up	Unigene43634_All|gi|40218371|gb|AAR83118.1|//1.00E-64//secretory laccase [Gossypium arboreum]	Unigene43634_All//1.00E-21//AT5G09360| LAC14 (laccase 14); laccase	Unigene43634_All//1.00E-170//TC137114			GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr -
Unigene43635_All	363	0.00	0.98	2.20	2.88	0.38	0.75	2.80	5.99	3.18	9.93E+00	2.46E-02		1.11E+01	1.72E-04	Up	-2.92E+00	1.21E-04	Down	-1.95E+00	7.52E-03		1.10E+00	5.13E-03		1.87E-01	7.30E-01		Unigene43635_All|gi|297849514|ref|XP_002892638.1|//5.00E-51//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338480|gb|EFH68897.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene43635_All//5.00E-52//AT1G11350| SD1-13 (S-DOMAIN-1 13); kinase/ protein kinase/ protein serine/threonine kinase	Unigene43635_All//1.00E-28//CO081718		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006468//GO:0008037//GO:0016020//GO:0030246//GO:0032559	nr -
Unigene43639_All	775	0.00	10.72	4.12	0.00	0.09	0.00	0.00	0.00	0.00	1.34E+01	1.52E-47	Up	1.20E+01	1.15E-17	Up	6.47E+00	6.09E-01		null	null		null	null		null	null		Unigene43639_All//gi|112950081|gb|ABI26645.1|//7.00E-58//aspartic proteinase [Cucumis sativus]	Unigene43639_All//8.00E-35//AT1G62290| aspartyl protease family protein				GO:0008233//GO:0044238	nr +

Unigene4364_All	841	45.04	11.63	29.70	74.10	68.30	95.00	201.60	66.15	23.59	-1.95E+00	2.80E-75	Down	-6.01E-01	1.82E-11		-1.18E-01	1.03E-01		3.58E-01	1.83E-10		-1.61E+00	0.00E+00	Down	-3.10E+00	0.00E+00	Down	Unigene4364_All//gi|18399308|ref|NP_566396.1|//3.00E-75//NHL1 [Arabidopsis thaliana] >gi|9502172|gb|AAF88021.1|AF264697_1 NDR1/HIN1-Like protein 1 [Arabidopsis thaliana] >gi|21595601|gb|AAM66116.1| harpin-induced protein-like [Arabidopsis thaliana] >gi|56381911|gb|AAV85674.1| At3g11660 [Arabidopsis thaliana] >gi|58331799|gb|AAW70397.1| At3g11660 [Arabidopsis thaliana]	Unigene4364_All//2.00E-64//AT3G11660| NHL1	Unigene4364_All//0.00E+00//TC153124				nr +
Unigene43642_All	677	2570.52	930.54	2228.48	364.23	455.24	264.58	0.62	5.80	2.77	-1.47E+00	0.00E+00	Down	-2.06E-01	4.69E-68		3.22E-01	3.72E-35		-4.61E-01	1.61E-49		3.22E+00	2.53E-17	Up	2.15E+00	5.82E-06	Up	Unigene43642_All//gi|270311593|gb|ACZ72945.1|//1.00E-62//photosystem I reaction center subunit [Nicotiana tabacum]	Unigene43642_All//3.00E-60//AT5G64040| PSAN; calmodulin binding	Unigene43642_All//0.00E+00//TC141776		ko00195|Photosynthesis	GO:0005515//GO:0009522//GO:0009534//GO:0009767	nr +
Unigene43649_All	332	0.63	0.00	0.00	0.00	0.41	0.14	2.29	0.25	2.04	-9.30E+00	1.22E-01		-9.30E+00	1.45E-01		8.70E+00	3.18E-01		7.09E+00	6.95E-01		-3.19E+00	7.92E-04	Down	-1.68E-01	7.94E-01		Unigene43649_All//gi|224126629|ref|XP_002329602.1|//4.00E-49//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222870311|gb|EEF07442.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene43649_All//3.00E-49//AT5G43530| SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein	Unigene43649_All//4.00E-07//TC143914		ko03420|Nucleotide excision repair//ko03440|Homologous recombination	GO:0003676//GO:0009292//GO:0009526//GO:0032559//GO:0042623//GO:0046914	nr +
Unigene4365_All	431	38.85	24.34	22.49	87.72	64.24	70.63	85.84	59.35	37.99	-6.75E-01	6.93E-07		-7.89E-01	2.30E-08		-4.50E-01	1.52E-08		-3.13E-01	2.73E-04		-5.32E-01	1.28E-11		-1.18E+00	3.49E-44	Down	Unigene4365_All//gi|297600676|ref|NP_001049589.2|//2.00E-54//Os03g0254900 [Oryza sativa Japonica Group] >gi|255674380|dbj|BAF11503.2| Os03g0254900 [Oryza sativa Japonica Group]	Unigene4365_All//3.00E-45//AT3G09770| zinc finger (C3HC4-type RING finger) family protein	Unigene4365_All//0.00E+00//TC146363				nr +
Unigene43650_All	729	0.00	140.47	59.90	0.00	0.14	0.00	0.00	0.00	0.00	1.71E+01	0.00E+00	Up	1.59E+01	4.04E-248	Up	7.15E+00	4.55E-01		null	null		null	null		null	null		Unigene43650_All//gi|49035520|sp|Q40302.3|CALM_MACPY//2.00E-16//RecName: Full=Calmodulin; Short=CaM >gi|728609|emb|CAA59418.1| calmodulin [Macrocystis pyrifera]	Unigene43650_All//3.00E-15//AT3G22930| calmodulin, putative			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005488	nr +
Unigene43653_All	328	0.80	1.24	1.95	1.97	2.20	1.24	2.45	0.76	0.36	6.32E-01	6.01E-01		1.29E+00	1.86E-01		1.59E-01	8.68E-01		-6.72E-01	4.78E-01		-1.68E+00	2.46E-02		-2.75E+00	9.43E-04	Down	Unigene43653_All//gi|186510818|ref|NP_190459.2|//3.00E-46//DNA binding / catalytic/ chromatin binding / nuclease [Arabidopsis thaliana]	Unigene43653_All//3.00E-47//AT3G48900| DNA binding / catalytic/ chromatin binding / nuclease	Unigene43653_All//1.00E-90//gi|11200897|gb|BF269902.1|BF269902		ko03420|Nucleotide excision repair	GO:0003676//GO:0006281//GO:0006325//GO:0009411//GO:0016788//GO:0043231//GO:0044427	nr +
Unigene43657_All	888	0.00	0.00	0.00	0.00	0.00	0.00	0.48	1.65	5.65	null	null		null	null		null	null		null	null		1.79E+00	7.25E-04	Up	3.57E+00	1.72E-24	Up	Unigene43657_All//gi|225457321|ref|XP_002284718.1|//4.00E-14//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene43658_All	406	0.13	0.00	0.00	0.12	0.00	0.11	1.46	0.93	0.00	-7.01E+00	6.11E-01		-7.01E+00	6.23E-01		-6.94E+00	5.55E-01		-1.42E-01	9.52E-01		-6.54E-01	4.45E-01		-1.05E+01	1.41E-04	Down	Unigene43658_All//gi|21592858|gb|AAM64808.1|//2.00E-41//myb-related protein M4 [Arabidopsis thaliana]	Unigene43658_All//2.00E-44//AT5G60890| MYB334 (MYB DOMAIN PROTEIN 34); DNA binding / kinase/ transcription activator/ transcription factor	Unigene43658_All//6.00E-142//C0071744	MYB		GO:0001071//GO:0006970//GO:0009725//GO:0010468	nr -
Unigene43659_All	557	0.00	0.00	0.00	0.18	0.00	0.16	6.60	11.86	21.46	null	null		null	null		-7.48E+00	3.12E-01		-1.41E-01	9.49E-01		8.44E-01	3.72E-05		1.70E+00	5.17E-25	Up	Unigene43659_All//gi|223452282|gb|ACM89469.1|//6.00E-12//serine/threonine protein kinase family protein [Glycine max]	Unigene43659_All//3.00E-06//AT1G67000| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene43659_All//7.00E-81//TC129826				nr +
Unigene43662_All	778	0.00	0.26	0.27	0.00	0.09	0.00	1.63	3.98	5.07	8.03E+00	1.36E-01		8.10E+00	1.41E-01		6.47E+00	6.09E-01		null	null		1.29E+00	7.77E-05	Up	1.64E+00	2.15E-08	Up	Unigene43662_All//gi|90900944|gb|ABE01834.1|//1.00E-78//NAK-type protein kinase [Nicotiana tabacum]	Unigene43662_All//1.00E-62//AT5G47070| protein kinase, putative	Unigene43662_All//6.00E-45//ES827016			GO:0004713//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene43665_All	535	0.00	7.67	4.18	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.25E-23	Up	1.20E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene43665_All//gi|297797389|ref|XP_002866579.1|//3.00E-13//UVB-resistance 8 [Arabidopsis lyrata subsp. lyrata] >gi|297312414|gb|EFH42838.1| UVB-resistance 8 [Arabidopsis lyrata subsp. lyrata]	Unigene43665_All//2.00E-14//AT5G63860| UVR8 (UVB-RESISTANCE 8); chromatin binding / guanyl-nucleotide exchange factor			ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0009411//GO:0044424	nr -
Unigene43667_All	473	0.00	19.28	17.90	0.00	0.15	0.00	0.00	0.00	0.17	1.42E+01	3.22E-52	Up	1.41E+01	2.05E-47	Up	7.19E+00	6.09E-01		null	null		null	null		7.40E+00	4.04E-01		Unigene43667_All//gi|301111414|ref|XP_002904786.1|//1.00E-61//ribosomal protein L27 [Phytophthora infestans T30-4] >gi|662701827|gb|AAY43423.1| ribosomal protein L27 [Phytophthora infestans] >gi|262095116|gb|EEY33168.1| ribosomal protein L27 [Phytophthora infestans T30-4]	Unigene43667_All//7.00E-41//AT1G70600| structural constituent of ribosome	Unigene43667_All//1.00E-10//TC154004		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene43668_All	703	0.00	0.00	0.00	5.74	2.50	0.64	0.00	0.00	0.00	null	null		null	null		-1.20E+00	2.59E-05	Down	-3.16E+00	1.58E-15	Down	null	null		null	null		Unigene43668_All//gi|297822233|ref|XP_002878999.1|//6.00E-55//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324838|gb|EFH55258.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene43668_All//4.00E-56//AT2G26695| binding / zinc ion binding					nr -
Unigene43669_All	718	0.00	5.01	2.82	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.77E-20	Up	1.15E+01	3.79E-11	Up	null	null		null	null		null	null		null	null		Unigene43669_All//gi|298706078|emb|CBJ29188.1|//5.00E-31//ATP synthase O subunit, mitochondrial precursor [Ectocarpus siliculosus]	Unigene43669_All//2.00E-28//AT5G13450| ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative			ko00190|Oxidative phosphorylation	GO:0006810//GO:0016020	nr +
Unigene4367_All	1761	0.83	0.40	1.24	5.43	5.24	4.98	20.12	3.18	15.43	-1.05E+00	5.84E-02		5.76E-01	2.13E-01		-5.15E-02	8.41E-01		-1.27E-01	5.81E-01		-2.66E+00	2.45E-125	Down	-3.83E-01	1.09E-06		Unigene4367_All//gi|15228789|ref|NP_191158.1|//0.00E+00//ESK1 (ESKIMO 1) [Arabidopsis thaliana]	Unigene4367_All//0.00E+00//AT3G55990| ESK1 (ESKIMO 1)	Unigene4367_All//0.00E+00//gi|48795888|gb|CO097202.1|CO097202				nr +
Unigene43672_All	595	0.00	0.00	0.00	4.86	0.81	1.59	0.14	0.00	0.54	null	null		null	null		-2.58E+00	1.52E-10	Down	-1.61E+00	2.67E-05	Down	-7.15E+00	4.03E-01		1.91E+00	1.54E-01		Unigene43672_All//gi|255552790|ref|XP_002517438.1|//5.00E-90//ER glycerol-phosphate acyltransferase [Ricinus communis] >gi|223543449|gb|EEF44980.1| ER glycerol-phosphate acyltransferase [Ricinus communis]	Unigene43672_All//2.00E-56//AT2G38110| GPAT6 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 6); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase			ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0008374//GO:0031410	nr -
Unigene43674_All	868	0.00	61.64	21.04	0.00	0.00	0.00	0.00	0.00	0.00	1.59E+01	0.00E+00	Up	1.44E+01	3.80E-103	Up	null	null		null	null		null	null		null	null		Unigene43674_All//gi|81074776|gb|AB055374.1|//1.00E-108//ribosomal protein L2-like [Solanum tuberosum]	Unigene43674_All//7.00E-104//AT2G18020| EMB2296 (embryo defective 2296); structural constituent of ribosome	Unigene43674_All//9.00E-29//gi|21101055|gb|BQ413368.1|BQ413368		ko03010|Ribosome		nr -
Unigene43676_All	275	2.28	0.00	0.00	0.18	1.50	0.49	1.38	0.46	1.30	-1.12E+01	7.91E-04	Down	-1.12E+01	1.41E-03		3.05E+00	5.67E-02		1.44E+00	6.38E-01		-1.60E+00	1.81E-01		-8.58E-02	9.43E-01										
Unigene43678_All	746	0.00	3.67	1.50	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.44E-15	Up	1.05E+01	3.43E-06	Up	null	null		null	null		null	null		null	null										
Unigene4368_All	1742	0.00	0.12	0.00	0.34	0.20	0.29	1.26	0.29	0.66	6.86E+00	1.36E-01		null	null		-7.96E-01	3.88E-01		-2.67E-01	7.57E-01		-2.13E+00	1.20E-06	Down	-9.28E-01	1.26E-02		Unigene4368_All//gi|15228789|ref|NP_191158.1|//0.00E+00//ESK1 (ESKIMO 1) [Arabidopsis thaliana]	Unigene4368_All//0.00E+00//AT3G55990| ESK1 (ESKIMO 1)	Unigene4368_All//0.00E+00//gi|48795888|gb|CO097202.1|CO097202				nr +
Unigene43680_All	401	0.00	1.77	0.80	0.00	0.17	0.23	0.74	0.31	2.48	1.08E+01	3.32E-04	Up	9.64E+00	4.51E-02		7.42E+00	6.09E-01		7.82E+00	4.76E-01		-1.24E+00	3.73E-01		1.75E+00	6.57E-03		Unigene43680_All//gi|115477334|ref|NP_001062263.1|//9.00E-07//Os08g0519900 [Oryza sativa Japonica Group] >gi|113624232|dbj|BAF24177.1| Os08g0519900 [Oryza sativa Japonica Group]	Unigene43680_All//7.00E-07//AT5G03540| ATEXO70A1 (exocyst subunit EXO70 family protein A1); protein binding	Unigene43680_All//5.00E-07//TC166787				nr +
Unigene43681_All	547	0.00	0.46	0.00	0.27	0.00	0.00	2.40	1.45	0.29	8.86E+00	7.85E-02		null	null		-8.09E+00	1.65E-01		-8.09E+00	2.33E-01		-7.23E-01	1.73E-01		-3.04E+00	3.54E-06	Down									
Unigene43685_All	504	0.00	11.66	8.14	0.30	0.21	0.00	0.25	0.00	0.08	1.35E+01	1.51E-33	Up	1.30E+01	9.64E-23	Up	-5.32E-01	7.85E-01		-8.21E+00	2.33E-01		-7.98E+00	2.35E-01		-1.67E+00	4.77E-01		Unigene43685_All//gi|247421835|gb|ACS96145.1|//1.00E-64//S18.A ribosomal protein [Jatropha curcas]	Unigene43685_All//3.00E-56//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome	Unigene43685_All//4.00E-08//EV494584		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006412//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr +
Unigene43687_All	819	0.00	0.00	0.00	0.12	0.04	0.33	6.76	0.66	10.12	null	null		null	null		-1.53E+00	5.86E-01		1.44E+00	4.09E-01		-3.35E+00	3.68E-25	Down	5.81E-01	8.69E-04		Unigene43687_All//gi|19715905|emb|CAC84140.1|//3.00E-82//NADPH oxidase [Nicotiana tabacum]	Unigene43687_All//9.00E-56//AT5G51060| RHD2 (ROOT HAIR DEFECTIVE 2); NAD(P)H oxidase	Unigene43687_All//6.00E-76//TC139823		ko04626|Plant-pathogen interaction	GO:0008152//GO:0016209//GO:0030554//GO:0031224//GO:0046914//GO:0050664	nr -
Unigene43689_All	375	0.00	0.14	0.43	2.13	0.46	0.48	106.43	614.01	75.85	7.08E+00	6.16E-01		8.73E+00	2.38E-01		-2.21E+00	7.35E-03		-2.14E+00	1.54E-02		2.53E+00	0.00E+00	Up	-4.89E-01	3.98E-11										
Unigene43693_All	466	0.00	4.68	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.11E-12	Up	1.05E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene43693_All//gi|38346643|emb|CAD40735.2|//6.00E-12//OSJNBa0072D21.13 [Oryza sativa (japonica cultivar-group)]					GO:0003824	nr -
Unigene43694_All	353	0.15	0.57	0.00	0.56	0.78	0.13	4.31	0.00	0.79	1.95E+00	3.75E-01		-7.21E+00	6.23E-01		4.67E-01	8.16E-01		-2.14E+00	3.47E-01		-1.21E+01	8.51E-11	Down	-2.45E+00	8.71E-06	Down	Unigene43694_All//gi|68566478|gb|AAN73053.2|//8.00E-51//mini-chromosome maintenance protein MCM3 [Pisum sativum]	Unigene43694_All//3.00E-33//AT5G46280| DNA replication licensing factor, putative	Unigene43694_All//5.00E-170//TC176845		ko03030|DNA replication	GO:0003676//GO:0006259//GO:0010467//GO:0016462//GO:0032559//GO:0043231	nr +
Unigene43695_All	479	0.00	0.21	0.00	0.00	0.14	0.00	221.38	49.39	107.37	7.73E+00	3.86E-01		null	null		7.17E+00	6.09E-01		null	null		-2.16E+00	9.06E-293	Down	-1.04E+00	3.12E-103	Down	Unigene43695_All//gi|15225223|ref|NP_180789.1|//2.00E-34//UCC1 (UCLACYANIN 1); copper ion binding / electron carrier [Arabidopsis thaliana] >gi|3399767|gb|AAC32038.1| uclacyanin I [Arabidopsis thaliana]	Unigene43695_All//4.00E-33//AT2G32300| UCC1 (UCLACYANIN 1); copper ion binding / electron carrier				GO:0006091//GO:0031224//GO:0031410//GO:0046914	nr -
Unigene43697_All	329	0.00	0.00	0.00	0.00	0.00	0.00	5.40	1.65	0.61	null	null		null	null		null	null		null	null		-1.71E+00	2.60E-04	Down	-3.16E+00	2.19E-08	Down	Unigene43697_All//gi|167859793|gb|AC404850.1|//5.00E-13//senescence-associated protein [Picea abies]		Unigene43697_All//3.00E-20//DN828138				nr +
Unigene43699_All	305	2.57	0.50	0.00	0.00	0.11	0.30	2.91	0.55	1.57	-2.37E+00	1.09E-02		-1.13E+01	2.21E-04	Down	6.82E+00	8.29E-01		8.21E+00	4.76E-01		-2.41E+00	1.79E-03		-8.93E-01	1.60E-01										
Unigene4370_All	203	0.52	23.21	1.05	0.74	0.00	2.67	0.00	2.68	1.77	5.49E+00	7.62E-24	Up	1.03E+00	5.91E-01		-9.52E+00	1.65E-01		1.86E+00	1.02E-01		1.14E+01	5.36E-04	Up	1.08E+01	7.28E-03										
Unigene43700_All	249	0.84	0.61	0.64	1.00	0.00	0.18	0.51	3.52	3.36	-4.61E-01	7.58E-01		-3.90E-01	8.07E-01		-9.97E+00	4.18E-02		-2.46E+00	2.23E-01		2.79E+00	6.97E-04	Up	2.72E+00	8.98E-04	Up									
Unigene43702_All	334	0.00	6.83	4.62	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	5.64E-13	Up	1.22E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene43702_All//gi|18266039|gb|AAL67432.1|AF458406_1|//2.00E-56//chlorophyll a/b binding protein [Brassica oleracea]	Unigene43702_All//2.00E-55//AT2G34430| LHB1B1; chlorophyll binding	Unigene43702_All//1.00E-25//gi|48739995|gb|CO070514.1|CO070514		ko00196|Photosynthesis - antenna proteins	GO:0005576//GO:0006091//GO:0006464//GO:0009521//GO:0009526//GO:0009534//GO:0009570//GO:0009639//GO:0031224//GO:0043169//GO:0046906	nr -
Unigene43703_All	336	2.02	0.00	1.27	0.89	1.02	0.00	0.38	0.12	1.54	-1.10E+01	4.10E-04	Down	-6.75E-01	4.41E-01		2.04E-01	9.01E-01		-9.80E+00	3.99E-02		-1.60E+00	5.34E-01		2.03E+00	4.10E-02				Unigene43703_All//6.00E-09//CO085074					
Unigene43707_All	328	0.00	15.29	5.20	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	1.34E-28	Up	1.23E+01	2.20E-09	Up	null	null		null	null		null	null		null	null										
Unigene43709_All	586	0.00	0.00	0.00	0.00	0.00	0.00	2.53	0.71	0.54	null	null		null	null		null	null		null	null		-1.82E+00	5.43E-04	Down	-2.22E+00	4.14E-05	Down	Unigene43709_All//gi|301121570|ref|XP_002908512.1|//2.00E-30//40S ribosomal protein SA [Phytophthora infestans T30-4] >gi|262103543|gb|EEY61595.1| 40S ribosomal protein SA [Phytophthora infestans T30-4]	Unigene43709_All//7.00E-27//AT1G72370| P40; structural constituent of ribosome			ko03010|Ribosome	GO:0006970//GO:0015935//GO:0016020//GO:0043231	nr -

Unigene4371_All	1694	0.43	24.17	2.29	0.74	0.33	8.45	0.70	3.38	4.70	5.80E+00	7.22E-211	Up	2.41E+00	4.02E-10	Up	-1.18E+00	4.23E-02		3.52E+00	5.24E-58	Up	2.27E+00	2.11E-17	Up	2.75E+00	3.36E-30	Up	Unigene4371_All//gi|115480349|ref|NP_001063768.1|//1.00E-110//0s09g0533300 [Oryza sativa Japonica Group] >gi|50725793|dbj|BAD33323.1| PTS protein-like [Oryza sativa Japonica Group] >gi|52075952|dbj|BAD46032.1| PTS protein-like [Oryza sativa Japonica Group] >gi|113632001|dbj|BAF25682.1|Os09g0533300 [Oryza sativa Japonica Group]	Unigene4371_All//2.00E-96//AT5G63140| ATPAP29 (ARABIDOPSIS THALIANA PURPLE ACID PHOSPHATASE 29); acid phosphatase/protein serine/threonine phosphatase	Unigene4371_All//5.00E-78//C0089895				nr +
Unigene43713_All	446	0.00	8.75	3.82	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	3.25E-22	Up	1.19E+01	2.20E-09	Up	null	null		null	null		null	null		null	null									
Unigene43714_All	410	0.64	0.99	0.26	2.67	0.50	0.00	2.06	0.00	0.00	6.32E-01	6.01E-01		-1.30E+00	4.36E-01		-2.41E+00	5.06E-04	Down	-1.14E+01	7.25E-07	Down	-1.10E+01	4.39E-06	Down	-1.10E+01	2.21E-06	Down	Unigene43714_All//gi|115455585|ref|NP_001051393.1|//2.00E-17//0s03g0769000 [Oryza sativa Japonica Group] >gi|113549864|dbj|BAF13307.1|Os03g0769000 [Oryza sativa Japonica Group]	Unigene43714_All//1.00E-19//AT2G23700| unknown protein	Unigene43714_All//3.00E-30//TC172096				nr +
Unigene43718_All	315	0.17	0.32	0.00	3.00	14.87	3.73	0.00	0.00	0.00	9.54E-01	7.26E-01		-7.38E+00	6.23E-01		2.31E+00	1.95E-13	Up	3.11E-01	6.43E-01		null	null		null	null		Unigene43718_All//gi|18390723|ref|NP_563779.1|//1.00E-08//gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein [Arabidopsis thaliana] >gi|15146334|gb|AAK83650.1|At1g07080/F10K1_15 [Arabidopsis thaliana] >gi|15809756|gb|AAL06806.1|At1g07080/F10K1_15 [Arabidopsis thaliana]	Unigene43718_All//5.00E-10//AT1G07080| gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein	Unigene43718_All//9.00E-150//ES829639				nr +
Unigene43719_All	1275	0.00	0.00	0.04	0.08	0.03	0.11	1.26	0.82	5.81	null	null		5.39E+00	6.35E-01		-1.53E+00	5.86E-01		4.45E-01	8.61E-01		-6.21E-01	1.91E-01		2.21E+00	5.50E-22	Up	Unigene43719_All//gi|57157863|dbj|BAD83884.1|//1.00E-113//FOLDED PETALS [Arabidopsis thaliana]	Unigene43719_All//1.00E-111//AT5G53390| unknown protein					nr +
Unigene43372_All	669	18.85	21.43	15.44	28.44	25.48	34.43	32.42	19.18	12.80	1.86E-01	2.44E-01		-2.88E-01	9.68E-02		-1.59E-01	2.64E-01		2.76E-01	1.92E-02		-7.57E-01	1.16E-12		-1.34E+00	4.69E-32	Down	Unigene4372_All//gi|47606183|sp|Q8LFJ5.1|T112A_ARATH//1.00E-49//RecName: Full=TRM112-like protein At1g22270 >gi|30102552|gb|AAP21194.1|At1g22270 [Arabidopsis thaliana]	Unigene4372_All//35//AT1G22270| unknown protein	Unigene4372_All//0.00E+00//gi|13248228|gb|BF274843.2|BF274843				nr -
Unigene43724_All	460	0.00	0.77	0.35	0.97	0.60	0.39	0.37	4.09	0.61	9.59E+00	2.46E-02		8.44E+00	2.38E-01		-7.03E-01	5.30E-01		-1.31E+00	2.73E-01		3.48E+00	3.72E-09	Up	7.21E-01	5.97E-01					Unigene43724_All//5.00E-07//C0080482				
Unigene43725_All	463	1.24	1.09	0.23	1.61	2.53	0.68	1.37	0.09	0.00	-1.84E-01	8.25E-01		-2.43E+00	4.40E-02		6.48E-01	3.26E-01		-1.24E+00	1.45E-01		-3.92E+00	9.80E-04	Down	-1.04E+01	7.10E-05	Down								
Unigene43726_All	940	0.00	3.83	2.04	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.77E-20	Up	1.10E+01	1.47E-10	Up	null	null		null	null		null	null		null	null		Unigene43726_All//gi|297727809|ref|NP_001176268.1|//3.00E-07//0s10g0556801 [Oryza sativa Japonica Group] >gi|255679622|dbj|BAH94996.1|Os10g0556801 [Oryza sativa Japonica Group]	Unigene43726_All//1.00E-07//AT1G02080| transcriptional regulator-related			ko03018|RNA degradation		nr -
Unigene43727_All	291	0.00	6.44	4.03	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.11E-10	Up	1.20E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene43727_All//gi|42571305|ref|NP_973743.1|//2.00E-09//IMPA-6 (IMPORTIN ALPHA ISOFORM 6); binding / protein transporter [Arabidopsis thaliana]	Unigene43727_All//6.00E-11//AT1G02690| IMPA-6 (IMPORTIN ALPHA ISOFORM 6); binding / protein transporter				GO:0005488//GO:0006950//GO:0015031//GO:0043231//GO:0051704	nr +
Unigene43728_All	388	0.40	0.00	0.96	1.41	0.44	0.93	0.00	1.51	0.62	-8.66E+00	2.15E-01		1.25E+00	3.66E-01		-1.67E+00	9.26E-02		-6.01E-01	5.66E-01		1.06E+01	2.81E-04	Up	9.27E+00	4.39E-02		Unigene43728_All//gi|116308903|emb|CAH66035.1|//2.00E-08//H0515C11.11 [Oryza sativa (indica cultivar-group)]					GO:0003676//GO:0003824//GO:0006259//GO:0043231	nr -
Unigene4373_All	1250	43.24	19.09	30.50	19.49	18.04	17.74	8.12	5.92	4.21	-1.18E+00	2.93E-51	Down	-5.03E-01	7.46E-12		-1.11E-01	3.95E-01		-1.36E-01	2.97E-01		-4.56E-01	4.66E-03		-9.48E-01	3.00E-09		Unigene4373_All//gi|15277532|gb|AAK93949.1|AF284760_1//6.00E-64//HCF106 [Pisum sativum]	Unigene4373_All//7.00E-54//AT5G52440| HCF106; proton motive force dependent protein transmembrane transporter	Unigene4373_All//0.00E+00//TC158148	ko03060|Protein export		nr +
Unigene43730_All	450	0.00	0.00	0.00	0.00	0.00	0.00	4.23	1.95	0.18	null	null		null	null		null	null		null	null		-1.12E+00	8.54E-03		-4.58E+00	1.36E-11	Down	Unigene43730_All//gi|288558954|sp|C5Z7E3.1|U497L_SOR3L//4.00E-17//RecName: Full=UPF0497 membrane protein Sb10g008220	Unigene43730_All//2.00E-15//AT5G15290| integral membrane family protein			GO:0016020	nr -
Unigene43731_All	260	0.00	3.12	1.84	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.38E-05	Up	1.08E+01	7.48E-03		null	null		null	null		null	null		null	null		Unigene43731_All//gi|13926291|gb|AK49614.1|AF372898_1//7.00E-42//AT5g66570/K1F13_25	Unigene43731_All//3.00E-43//AT3G50820| PSB02 (PHOTOSYSTEM II SUBUNIT O-2); oxygen evolving/poly(U) binding	Unigene43731_All//5.00E-12//gi|84155156|gb|DN804511.1|DN804511	ko00195|Photosynthesis		GO:0005576//GO:0006470//GO:0006952//GO:0008187//GO:0009523//GO:0009534//GO:0009570//GO:0009767//GO:0016491//GO:0042548//GO:0046872	nr +
Unigene43733_All	454	0.35	0.11	2.46	0.22	0.46	0.00	0.00	0.00	0.00	-1.63E+00	4.88E-01		2.83E+00	7.34E-04	Up	1.05E+00	6.12E-01		-7.78E+00	3.99E-01		null	null		null	null		Unigene43733_All//sp|Q52812|AAPJ_RHIL3//8.00E-34//General L-amino acid-binding periplasmic protein aapJ OS=Rhizobium leguminosarum bv. viciae (strain 3841) GN=aapJ PE=3 SV=1						swissprot +
Unigene43736_All	258	6.49	22.59	12.59	3.86	3.20	4.20	73.25	131.71	49.88	1.80E+00	7.05E-11	Up	9.56E-01	8.00E-03		-2.70E-01	7.00E-01		1.22E-01	8.66E-01		8.46E-01	3.01E-23		-5.55E-01	5.35E-07		Unigene43736_All//gi|15217844|ref|NP_174134.1|//6.00E-06//GH3.17; indole-3-acetic acid amido synthetase [Arabidopsis thaliana] >gi|62900379|sp|Q9FZ87.1|GRA17_ARATH RecName: Full=Indole-3-acetic acid-amido synthetase GH3.17; AltName: Full=Auxin-responsive GH3-like protein 17; Short=AtGH3-17 >gi|9795624|gb|AAF98442.1|AC021044_21 [unknown protein [Arabidopsis thaliana] >gi|15450365|gb|AAK96476.1|At1g28130/F3H9_19 [Arabidopsis thaliana] >gi|21360519|gb|AAM47375.1|At1g28130/F3H9_19 [Arabidopsis thaliana]	Unigene43736_All//2.00E-07//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene43736_All//5.00E-49//ES827343			GO:0009725//GO:0016881//GO:0043231//GO:0048878	nr -
Unigene43737_All	359	1.46	0.71	0.74	4.86	2.78	1.26	1.41	1.40	1.00	-1.05E+00	3.11E-01		-9.75E-01	3.76E-01		-8.04E-01	9.16E-02		-1.95E+00	2.67E-04	Down	-1.66E-02	1.02E+00		-5.01E-01	5.83E-01					Unigene43737_All//4.00E-07//TC176309				
Unigene43738_All	279	0.19	0.00	3.24	0.18	1.48	0.00	0.00	0.00	0.00	-7.55E+00	6.11E-01		4.11E+00	3.91E-04	Up	3.05E+00	5.67E-02		-7.48E+00	6.34E-01		null	null		null	null		Unigene43738_All//gi|298711459|emb|CBJ32598.1|//3.00E-23//Glutamate synthase, N-terminal fragment [Ectocarpus siliculosus]						nr -
Unigene43741_All	251	0.00	3.63	2.33	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.62E-05	Up	1.12E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene43741_All//sp|P29034|S10A2_HUMAN//8.00E-34//Protein S100-A2 OS=Homo sapiens GN=S100A2 PE=1 SV=3						swissprot -
Unigene43744_All	920	0.00	0.00	0.00	0.00	0.00	0.00	1.42	2.82	0.00	null	null		null	null		null	null		null	null		9.83E-01	5.22E-03		-1.05E+01	9.85E-10	Down	Unigene43744_All//gi|300259872|gb|EFJ44096.1|//5.00E-86//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene43744_All//8.00E-85//AT5G58420| 40S ribosomal protein S4 (RPS4D)	Unigene43744_All//5.00E-09//DW237822	ko03010|Ribosome	GO:0003723//GO:0005840//GO:0009536	nr -
Unigene43745_All	283	0.37	0.90	5.27	1.94	0.61	0.16	0.00	0.00	0.14	1.28E+00	4.35E-01		3.83E+00	3.20E-06	Up	-1.67E+00	9.26E-02		-3.60E+00	8.97E-03		null	null		7.14E+00	6.44E-01		Unigene43745_All//gi|115488294|ref|NP_001066634.1|//6.00E-17//Os12g0407500 [Oryza sativa Japonica Group] >gi|113649141|dbj|BAF29653.1|Os12g0407500 [Oryza sativa Japonica Group]	Unigene43745_All//5.00E-18//AT3G19420| ATPTN2 (ARABIDOPSIS THALIANA PTEN 2); phosphatase/protein tyrosine phosphatase	Unigene43745_All//8.00E-116//gi|78323487|gb|DT543761.1|DT543761	ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0004721//GO:0006464//GO:0006796//GO:0034594//GO:0043231	nr +
Unigene43748_All	335	0.62	4.84	3.97	0.00	0.00	0.54	0.00	0.12	0.24	2.95E+00	9.24E-06	Up	2.67E+00	3.01E-04	Up	null	null		9.07E+00	1.94E-01		6.96E+00	6.34E-01		7.89E+00	4.04E-01									
Unigene43749_All	299	3.32	1.02	0.00	2.00	1.27	0.60	1.13	0.70	2.00	-1.71E+00	2.08E-02		-1.17E+01	1.77E-05	Down	-6.58E-01	4.78E-01		-1.73E+00	9.03E-02		-6.95E-01	5.77E-01		8.21E-01	3.20E-01		Unigene43749_All//gi|30688490|ref|NP_194720.2|//4.00E-24//ORC5 (ORIGIN RECOGNITION COMPLEX PROTEIN 5); protein binding [Arabidopsis thaliana] >gi|49659272|emb|CAE01429.1|origin recognition complex 5 subunit [Arabidopsis thaliana]	Unigene43749_All//2.00E-25//AT4G29910| ORC5 (ORIGIN RECOGNITION COMPLEX PROTEIN 5); protein binding				GO:0005515//GO:0006259//GO:0043231//GO:0043234	nr +
Unigene43750_All	267	0.00	2.66	2.79	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.32E-04	Up	1.14E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene43750_All//sp|Q86CS2|ATG1_DICDI//3.00E-06//Serine/threonine-protein kinase atg1 OS=Dictyostelium discoideum GN=atg1 PE=3 SV=1						swissprot +
Unigene43751_All	369	0.00	8.51	4.62	0.00	0.00	0.00	0.00	0.00	0.22	1.31E+01	7.07E-18	Up	1.22E+01	2.20E-09	Up	null	null		null	null		null	null		7.75E+00	4.04E-01		Unigene43751_All//gi|298711973|emb|CBJ32915.1|//1.00E-27//ribosomal protein L35 [Ectocarpus siliculosus]	Unigene43751_All//5.00E-25//AT1G74270| 60S ribosomal protein L35a (RPL35aC)		ko03010|Ribosome	GO:0043231	nr +
Unigene43756_All	720	0.44	0.35	0.81	0.69	0.24	0.25	1.53	4.18	0.77	-3.09E-01	7.89E-01		9.00E-01	3.77E-01		-1.53E+00	1.45E-01		-1.46E+00	1.93E-01		1.45E+00	1.61E-05	Up	-9.79E-01	8.01E-02		Unigene43756_All//gi|38345241|emb|CAD41085.2|//3.00E-10//OSJNBa0011N17.2 [Oryza sativa (japonica cultivar-group)]		Unigene43756_All//1.00E-73//ES807842		GO:0005488	nr -
Unigene43759_All	539	1.07	1.32	0.10	0.00	0.00	0.00	0.16	2.02	2.00	3.02E-01	6.93E-01		-3.43E+00	1.41E-02		null	null		null	null		3.68E+00	9.44E-06	Up	3.67E+00	7.75E-06	Up	Unigene43759_All//gi|51477397|gb|AAU04770.1|//6.00E-56//receptor lectin protein kinase-like [Cucumis melo]	Unigene43759_All//1.00E-54//AT3G08870| lectin protein kinase, putative				GO:0004674//GO:0004871//GO:0006464//GO:0009755//GO:0016020//GO:0030246//GO:0032501//GO:0032559	nr -
Unigene43761_All	349	0.30	2.90	0.61	1.28	0.39	1.42	1.33	3.59	2.97	3.28E+00	3.79E-04	Up	1.03E+00	5.91E-01		-1.70E+00	1.35E-01		1.48E-01	9.05E-01		1.43E+00	1.04E-02		1.16E+00	5.12E-02									
Unigene43762_All	271	0.19	1.12	0.79	4.96	2.92	1.00	1.40	0.62	0.74	2.54E+00	1.51E-01		2.03E+00	3.61E-01		-7.64E-01	1.72E-01		-2.31E+00	4.01E-04	Down	-1.19E+00	3.09E-01		-9.34E-01	3.79E-01									
Unigene43764_All	445	4.59	13.66	9.93	10.97	35.13	18.07	0.48	0.56	0.54	1.58E+00	1.62E-09	Up	1.12E+00	2.52E-04	Up	1.68E+00	1.51E-29	Up	7.20E-01	3.62E-04		2.46E-01	8.53E-01		1.77E-01	9.08E-01		Unigene43764_All//gi|194466223|gb|ACF74342.1|//4.00E-29//gonadotropin beta chain [Arachis hypogaea]	Unigene43764_All//3.00E-20//AT5G14920| gibberellin-regulated family protein	Unigene43764_All//5.00E-118//ES845655				nr +
Unigene43766_All	738	0.00	0.14	0.00	0.14	0.09	0.06	1.09	0.51	3.13	7.10E+00	3.86E-01		null	null		-5.33E-01	8.16E-01		-1.14E+00	6.76E-01		-1.09E+00	1.29E-01		1.52E+00	7.84E-05	Up	Unigene43766_All//gi|140072141|gb|AB084808.1|//5.00E-91//Chaperonin Cpn60/TCP-1: Phosphatidylinositol-4-phosphate 5-kinase; Zinc finger, FYVE/PHD-type [Medicago truncatula]	Unigene43766_All//6.00E-77//AT3G14270| phosphatidylinositol-4-phosphate 5-kinase family protein	Unigene43766_All//0.00E+00//TC131881	ko04145|Phagosome//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0016307//GO:0019538//GO:0030384//GO:0032559//GO:0046914	nr -
Unigene43767_All	311	0.00	0.00	1.54	0.16	2.44	1.89	0.54	0.40	0.00	null	null		1.06E+01	7.48E-03		3.93E+00	9.78E-04	Up	3.56E+00	8.48E-03		-4.32E-01	7.92E-01		-9.09E+00	1.08E-01									
Unigene43775_All	356	0.00	5.27	4.34	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.11E-10	Up	1.21E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene43775_All//gi|38230174|gb|AR14182.1|//1.00E-13//Rho family GTPase [Fucus distichus]	Unigene43775_All//2.00E-10//AT5G45970| ARAC2 (ARABIDOPSIS RAC-LIKE 2); GTP binding		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity	GO:0043231	nr +
Unigene4378_All	743	34.36	32.39	31.18	39.09	40.09	46.62	67.15	32.35	14.91	-8.52E-02	4.90E-01		-1.41E-01	2.56E-01		3.65E-02	8.07E-01		2.54E-01	6.24E-03		-1.05E+00	2.17E-48	Down	-2.17E+00	8.75E-143	Down	Unigene4378_All//gi|10177925|dbj|BAB11336.1|//1.00E-36//NADH dehydrogenase 10.5K chain-like protein [Arabidopsis thaliana] >gi|21593502|gb|AAM65469.1| NADH dehydrogenase 10.5K chain-like protein [Arabidopsis thaliana]	Unigene4378_All//5.00E-38//AT5G47890| NADH-ubiquinone oxidoreductase B8 subunit, putative	Unigene4378_All//0.00E+00//TC158551	ko00190|Oxidative phosphorylation		nr +
Unigene43783_All	221	10.42	6.19	3.37	50.04	41.91	33.92	270.90	100.80	84.91	-7.51E-01	7.36E-02		-1.63E+00	5.02E-04	Down	-2.56E-01	1.57E-01		-5.61E-01	8.35E-04		-1.43E+00	8.29E-93	Down	-1.67E+00	1.16E-120	Down				Unigene43783_All//1.00E-114//BQ411105				

Unigene43787_All	238	1.10	0.00	0.00	0.84	0.58	0.76	5.68	0.35	1.34	-1.01E+01	6.69E-02		-1.01E+01	8.56E-02		-5.33E-01	7.48E-01		-1.42E-01	9.34E-01		-4.02E+00	1.80E-07	Down	-2.09E+00	1.85E-04	Down	Unigene43787_All//gi|221272207|sp|A2A1A0.1|NCS1_COPJA//8.00E-111//RecName: Full=S-norcoclaurine synthase 1; Short=CjNCS1 >gi|123720767|dbj|BAF45337.1| norcoclaurine synthase [Coptis japonica var. dissecta] >gi|301072256|gb|ADK56103.1| 2OG/Fe(II)-dependent dioxygenase-like protein [synthetic construct]		Unigene43787_All//1.00E-111//DW497495			GO:0008152//GO:0016491//GO:0016829	nr +
Unigene43788_All	498	1.68	0.92	0.86	2.30	2.97	1.90	1.44	1.34	3.92	-8.76E-01	2.47E-01		-9.75E-01	2.37E-01		3.70E-01	5.39E-01		-2.73E-01	6.89E-01		-1.04E-01	8.93E-01		1.44E+00	6.00E-04	Up				Unigene43788_All//1.00E-94//DR460398				
Unigene4379_All	1121	4.29	3.66	2.85	12.53	8.69	8.50	3.96	0.26	1.17	-2.30E-01	4.17E-01		-5.91E-01	4.05E-02		-5.28E-01	1.46E-04		-5.60E-01	1.27E-04		-3.92E+00	5.36E-23	Down	-1.76E+00	2.40E-10	Down	Unigene4379_All//gi|15241163|ref|NP_197474.1|//1.00E-152//pectinesterase family protein [Arabidopsis thaliana] >gi|75304460|sp|Q8YYZ3.1|PME53_ARATH RecName: Full=Probable pectinesterase 53; Short=PE 53; AltName: Full=Pectin methylesterase 53; Short=AtPME53; Flags: Precursor	Unigene4379_All//2.00E-153//AT5G19730| pectinesterase family protein	Unigene4379_All//0.00E+00//gi|164239372|gb|ES791288.1|ES791288		ko00500|Starch and sucrose metabolism/ko00040|Pentose and glucuronate interconversions		nr -
Unigene43790_All	426	0.00	5.47	2.25	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.91E-13	Up	1.11E+01	2.46E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene43792_All	269	0.00	4.52	0.00	1.30	2.69	4.03	0.47	0.62	1.04	1.21E+01	5.47E-07	Up	null	null		1.05E+00	2.40E-01		1.64E+00	2.06E-02		3.99E-01	8.14E-01		1.14E+00	3.99E-01					Unigene43792_All//3.00E-07//TC175684				
Unigene43793_All	217	0.00	3.50	0.98	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	9.94E+00	1.41E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene43796_All	406	0.00	0.50	0.26	0.86	0.00	0.11	1.67	0.93	0.00	8.96E+00	1.36E-01		8.04E+00	3.97E-01		-9.75E+00	9.44E-03		-2.95E+00	8.30E-02		-8.47E-01	2.88E-01		-1.07E+01	3.56E-05	Down								
Unigene4380_All	1253	4.38	9.87	7.10	16.82	25.23	21.66	47.85	14.01	16.66	1.17E+00	4.20E-12	Up	6.95E-01	5.30E-04		5.85E-01	4.38E-11		3.65E-01	3.92E-04		-1.77E+00	3.86E-127	Down	-1.52E+00	2.52E-105	Down	Unigene4380_All//gi|211906452|gb|ACJ11719.1|//1.00E-171//annexin [Gossypium hirsutum]	Unigene4380_All//9.00E-109//AT5G12380| annexin, putative	Unigene4380_All//0.00E+00//TC130428				nr +
Unigene43806_All	279	50.82	25.24	49.81	13.03	10.98	8.90	0.00	0.00	0.00	-1.01E+00	4.74E-11	Down	-2.88E-02	8.67E-01		-2.47E-01	4.91E-01		-5.50E-01	9.53E-02		null	null		null	null		Unigene43806_All//gi|261351266|gb|ACX71300.1|//5.00E-23//chloroplast pigment-binding protein CP26 [Capsicum annuum]	Unigene43806_All//3.00E-23//AT4G10340| LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding	Unigene43806_All//1.00E-83//gi|31074011|gb|CA994290.1|CA994290		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009503//GO:0009523//GO:0009570//GO:0009639//GO:0046906	nr -
Unigene43807_All	330	0.00	0.00	0.00	0.15	1.88	0.41	2.56	0.38	0.00	null	null		null	null		3.64E+00	5.37E-03		1.44E+00	6.38E-01		-2.75E+00	9.73E-04	Down	-1.13E+01	2.21E-06	Down								
Unigene43811_All	362	0.14	0.14	0.00	0.83	0.67	0.62	110.61	4.50	34.56	-4.56E-02	9.85E-01		-7.17E+00	6.23E-01		-3.10E-01	8.20E-01		-4.04E-01	7.51E-01		-4.62E+00	1.23E-227	Down	-1.68E+00	2.87E-81	Down				Unigene43811_All//0.00E+00//gi|109877110|gb|DW506084.1|DW506084				
Unigene43815_All	453	0.00	0.00	0.00	0.00	0.00	0.00	38.17	4.43	0.53	null	null		null	null		null	null		null	null		-3.11E+00	3.94E-72	Down	-6.18E+00	1.58E-116	Down	Unigene43815_All//gi|145408590|ref|XP_001152214.1|//5.00E-07//O8F124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| O8F124 [Pinus koraiensis]		Unigene43815_All//4.00E-26//TC142190			GO:0043231	nr -
Unigene43816_All	358	0.00	0.00	0.00	0.00	0.00	0.00	1.65	1.52	0.00	null	null		null	null		null	null		null	null		-1.24E-01	8.84E-01		-1.07E+01	1.41E-04	Down	Unigene43816_All//gi|300267444|gb|EFJ51622.1|//6.00E-43//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene43816_All//3.00E-41//AT1G72370| P40; structural constituent of ribosome	Unigene43816_All//1.00E-07//DW241132		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr +
Unigene43818_All	469	0.00	0.00	0.00	0.21	0.37	0.10	3.61	2.41	0.59	null	null		null	null		7.89E-01	7.70E-01		-1.14E+00	6.76E-01		-5.84E-01	2.08E-01		-2.60E+00	9.91E-07	Down				Unigene43818_All//2.00E-16//TC175897				
Unigene4382_All	1219	13.26	12.14	11.84	24.89	24.46	16.60	39.44	19.13	40.49	-1.28E-01	3.94E-01		-1.64E-01	3.05E-01		-2.47E-02	8.27E-01		-5.84E-01	7.39E-10		-1.04E+00	6.30E-46	Down	3.81E-02	6.41E-01		Unigene4382_All//gi|15230120|ref|NP_188691.1|//1.00E-130//leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] >gi|75334999|sp|Q9LHF1.1|LRX4_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 4; Short=LRX/EXTENSIN4; Short=AtLRX4; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|9294099|dbj|BAB01951.1| extensin-like protein [Arabidopsis thaliana]	Unigene4382_All//6.00E-129//AT3G24480| leucine-rich repeat family protein / extensin family protein	Unigene4382_All//0.00E+00//gi|78350648|gb|DT570922.1|DT570922		ko04626|Plant-pathogen interaction		nr -
Unigene43822_All	353	0.00	8.04	5.43	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	3.83E-16	Up	1.24E+01	1.47E-10	Up	null	null		null	null		null	null		null	null		Unigene43822_All//gi|124365534|gb|ABN09768.1|//4.00E-19//Cyclin-like F-box; Calcium-binding EF-hand [Medicago truncatula]				ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene43825_All	377	0.00	4.17	4.38	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.70E-09	Up	1.21E+01	4.30E-09	Up	null	null		null	null		null	null		null	null		Unigene43825_All//sp|Q4TTV7|GPL_GLOAU//2.00E-44//Lectizyme OS=Glossina austeni GN=Gpl PE=2 SV=1						swissprot +
Unigene43826_All	389	0.00	0.00	0.00	0.00	0.00	0.00	1.52	2.04	0.00	null	null		null	null		null	null		null	null		4.24E-01	5.77E-01		-1.06E+01	1.41E-04	Down								ESTscan -
Unigene43832_All	301	0.87	7.41	0.35	1.66	2.63	1.50	1.83	1.25	0.79	3.09E+00	5.42E-08	Up	-1.30E+00	4.36E-01		6.69E-01	4.42E-01		-1.42E-01	8.92E-01		-5.47E-01	5.52E-01		-1.20E+00	1.64E-01		Unigene43832_All//gi|115472787|ref|NP_001059992.1|//4.00E-15//Os07g0562800 [Oryza sativa Japonica Group] >gi|36956948|gb|AAQ87012.1| myosin heavy chain class VIII A1 protein [Oryza sativa Japonica Group] >gi|113611528|dbj|BAF21906.1| Os07g0562800 [Oryza sativa Japonica Group]	Unigene43832_All//1.00E-12//AT3G19960| ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor	Unigene43832_All//2.00E-08//TC147568			GO:0043231	nr +
Unigene43836_All	374	0.00	0.00	0.00	0.00	0.18	0.00	122.54	30.29	141.46	null	null		null	null		7.52E+00	6.09E-01		null	null		-2.02E+00	7.92E-116	Down	2.07E-01	1.41E-03		Unigene43836_All//gi|791148|emb|CAA60021.1|//4.00E-27//extensin-like protein [Vigna unguiculata]		Unigene43836_All//6.00E-31//ES813279		ko03040|Spliceosome	GO:0005198//GO:0007047	nr -
Unigene43837_All	511	0.00	9.32	4.69	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	3.82E-27	Up	1.22E+01	3.24E-13	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene43838_All	552	0.00	10.92	3.67	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.02E-34	Up	1.18E+01	3.79E-11	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene4384_All	396	5.95	1.41	4.57	5.03	2.17	4.33	0.21	1.27	1.61	-2.08E+00	9.93E-06	Down	-3.79E-01	3.92E-01		-1.21E+00	5.33E-03		-2.15E-01	6.67E-01		2.57E+00	2.28E-02		2.91E+00	3.38E-03					Unigene4384_All//0.00E+00//TC130158				ESTscan +
Unigene43840_All	261	4.81	13.59	11.43	18.70	20.98	23.19	0.16	0.00	0.00	1.50E+00	1.62E-05	Up	1.25E+00	1.23E-03		1.66E-01	5.81E-01		3.10E-01	2.35E-01		-7.34E+00	6.56E-01		-7.34E+00	6.12E-01					Unigene43840_All//4.00E-71//gi|48804230|gb|CO105544.1|CO105544				ESTscan -
Unigene43842_All	364	5.46	0.00	4.83	0.00	0.00	1.61	0.00	0.00	0.33	-1.24E+01	1.70E-11	Down	-1.78E-01	7.01E-01		null	null		1.07E+01	1.37E-03		null	null		8.36E+00	2.43E-01					Unigene43842_All//5.00E-28//TC177061				
Unigene43844_All	328	40.52	63.65	38.80	159.16	144.46	122.68	195.03	751.18	90.61	6.52E-01	6.61E-08		-6.24E-02	7.16E-01		-1.40E-01	7.11E-02		-3.76E-01	1.10E-07		1.95E+00	0.00E+00	Up	-1.11E+00	1.02E-68	Down				Unigene43844_All//1.00E-155//gi|48812091|gb|CO113404.1|CO113404				
Unigene43845_All	243	651.10	656.20	743.31	455.71	300.71	394.39	76.73	155.83	127.88	1.12E-02	8.15E-01		1.91E-01	1.08E-06		-6.00E-01	1.29E-40		-2.09E-01	1.55E-05		1.02E+00	4.13E-35	Up	7.37E-01	2.03E-17		Unigene43845_All//gi|226502997|ref|NP_001150907.1|//1.00E-09//polcalcin Jun o 2 [Zea mays] >gi|195642854|gb|ACG40895.1| polcalcin Jun o 2 [Zea mays]	Unigene43845_All//3.00E-05//AT3G25600| calcium ion binding	Unigene43845_All//1.00E-126//TC143349		ko04626|Plant-pathogen interaction/ko04070|Phosphatidylinositol signaling system	GO:0046872	nr -
Unigene43851_All	2428	0.00	0.15	0.00	0.00	0.00	0.00	9.09	17.83	22.51	7.19E+00	2.46E-02		null	null		null	null		null	null		9.72E-01	6.38E-37		1.31E+00	6.83E-76	Up	Unigene43851_All//gi|297843928|ref|XP_002888845.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335687|gb|EFH66104.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene43851_All//0.00E+00//AT1G11050| protein kinase family protein	Unigene43851_All//7.00E-75//gi|164320817|gb|ES826479.1|ES826479		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559//GO:0044464	nr -
Unigene43852_All	267	0.00	0.00	2.99	2.05	0.52	0.00	0.00	0.00	0.00	null	null		1.15E+01	1.72E-04	Up	-1.99E+00	5.12E-02		-1.10E+01	1.52E-03		null	null		null	null		Unigene43852_All//gi|11121504|emb|CAC14889.1|//4.00E-39//extensin [Nicotiana sylvestris]		Unigene43852_All//2.00E-08//gi|78338021|gb|DT558295.1|DT558295		ko03040|Spliceosome	GO:0005198//GO:0007047	nr -
Unigene43853_All	345	0.15	0.00	0.00	0.00	0.00	0.00	2.57	1.82	0.35	-7.25E+00	6.11E-01		-7.25E+00	6.23E-01		null	null		null	null		-5.02E-01	4.60E-01		-2.89E+00	3.04E-04	Down	Unigene43853_All//gi|297837435|ref|XP_002886599.1|//6.00E-22//aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332440|gb|EFH62858.1| aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene43853_All//3.00E-22//AT1G60710| ATB2; oxidoreductase	Unigene43853_All//5.00E-22//ES825842			GO:0004033//GO:0008152	nr +
Unigene4386_All	875	2.27	1.91	2.37	27.10	26.29	12.54	5.94	2.44	3.10	-2.50E-01	6.11E-01		6.29E-02	8.93E-01		-4.38E-02	7.80E-01		-1.11E+00	1.93E-22	Down	-1.29E+00	1.29E-07	Down	-9.41E-01	4.09E-05		Unigene4386_All//gi|115334948|gb|AB194060.1|//1.00E-120//ripening-related expansin [Cucumis melo]	Unigene4386_All//2.00E-118//AT2G39700| ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	Unigene4386_All//0.00E+00//gi|109827613|gb|DW226288.1|DW226288				nr +
Unigene43862_All	323	19.92	21.02	20.77	32.85	22.49	21.95	70.29	36.88	24.05	7.73E-02	7.37E-01		6.02E-02	8.05E-01		-5.46E-01	8.38E-04		-5.82E-01	7.07E-04		-9.31E-01	1.95E-18		-1.55E+00	2.21E-41	Down				Unigene43862_All//8.00E-67//TC136016				
Unigene43863_All	234	0.00	11.69	4.32	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	1.44E-15	Up	1.21E+01	1.27E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene43866_All	295	9.05	2.75	7.76	10.13	9.34	6.58	0.00	0.00	0.00	-1.72E+00	3.82E-05	Down	-2.21E-01	6.16E-01		-1.18E-01	7.87E-01		-6.22E-01	9.03E-02		null	null		null	null		Unigene43866_All//gi|225434311|ref|XP_002264896.1|//8.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene43866_All//7.00E-07//AT2G30520| RPT2 (ROOT PHOTOTROPISM 2); protein binding	Unigene43866_All//1.00E-90//gi|48790532|gb|CO091846.1|CO091846				nr -
Unigene4387_All	974	2.47	6.92	7.33	17.64	16.26	19.10	12.24	14.89	12.07	1.49E+00	1.14E-09	Up	1.57E+00	1.51E-10	Up	-1.18E-01	4.56E-01		1.15E-01	4.67E-01		2.83E-01	3.92E-02		-2.08E-02	9.13E-01		Unigene4387_All//gi|110931672|gb|ABH02835.1|//3.00E-39//MYB transcription factor MYB75 [Glycine max]	Unigene4387_All//2.00E-33//AT5G05790| myb family transcription factor	Unigene4387_All//0.00E+00//gi|109853776|gb|DW482755.1|DW482755	MYB			nr +
Unigene43874_All	256	1.64	1.19	0.42	0.00	1.61	0.00	1.32	5.55	0.93	-4.61E-01	6.50E-01		-1.97E+00	1.51E-01		1.07E+01	1.25E-02		null	null		2.07E+00	2.12E-04	Up	-5.01E-01	6.49E-01									
Unigene43876_All	649	0.00	7.10	4.27	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.84E-26	Up	1.21E+01	2.75E-15	Up	null	null		null	null		null	null		null	null		Unigene43876_All//sp|P54385|DHE3_DROME//6.00E-15//Glutamate dehydrogenase, mitochondrial OS=Drosophila melanogaster GN=Gdh PE=1 SV=2						swissprot +
Unigene43877_All	314	0.00	27.59	11.36	0.00	0.00	0.00	0.00	0.00	0.00	1.48E+01	1.38E-49	Up	1.35E+01	9.41E-20	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene43879_All	425	0.00	0.00	0.00	0.23	0.16	0.11	3.58	3.84	0.47	null	null		null	null		-5.33E-01	8.16E-01		-1.14E+00	6.76E-01		9.89E-02	8.36E-01		-2.93E+00	7.58E-07	Down	Unigene43879_All//gi|42573527|ref|NP_974860.1|//1.00E-06//peptidyl-tRNA hydrolase family protein [Arabidopsis thaliana]	Unigene43879_All//8.00E-08//AT5G38290| peptidyl-tRNA hydrolase family protein	Unigene43879_All//7.00E-37//DT468122			GO:0004091//GO:0010467//GO:0044424	nr +
Unigene43882_All	736	0.14	0.07	0.51	1.35	0.14	0.06	5.86	0.80	1.19	-1.05E+00	6.84E-01		1.83E+00	2.13E-01		-3.27E+00	6.96E-05	Down	-4.46E+00	3.09E-05	Down	-2.88E+00	3.70E-17	Down	-2.30E+00	5.81E-14	Down	Unigene43882_All//gi|38566598|gb|AAR24189.1|//9.00E-30//At5g14690 [Arabidopsis thaliana] >gi|40824071|gb|AAR92338.1| At5g14690 [Arabidopsis thaliana]	Unigene43882_All//8.00E-13//AT3G01516| unknown protein	Unigene43882_All//7.00E-26//DW009333				nr -
Unigene4389_All	1605	1.11	1.36	1.79	3.45	1.80	1.91	5.29	2.50	1.27	2.93E-01	5.14E-01		6.93E-01	7.43E-02		-9.35E-01	6.99E-05		-8.48E-01	6.58E-04		-1.08E+00	2.80E-09	Down	-2.06E+00	1.80E-23	Down	Unigene4389_All//gi|224133496|ref|XP_002321582.1|//1.00E-170//rna-dependent RNA polymerase [Populus trichocarpa] >gi|222868578|gb|EEF05709.1| rna-dependent RNA polymerase [Populus trichocarpa]	Unigene4389_All//3.00E-155//AT4G11130| RDR2 (RNA-DEPENDENT RNA POLYMERASE 2); RNA-directed RNA polymerase	Unigene4389_All//0.00E+00//DT047092				nr +
Unigene43890_All	986	0.00	0.00	0.00	0.00	0.00	0.00	1.80	25.94	0.44	null	null		null	null		null	null		null	null		3.85E+00	7.83E-128	Up	-2.02E+00	2.07E-05	Down				Unigene43890_All//3.00E-19//gi|109844272|gb|DW242830.1|DW242830				
Unigene43891_All	268	2.34	0.00	0.79	7.44	1.28	1.35	0.32	0.00	0.30	-1.12E+01	7.91E-04	Down	-1.56E+00	1.29E-01		-2.53E+00	2.94E-07	Down	-2.46E+00	3.20E-06	Down	-8.30E+00	4.03E-01		-8.57E-02	9.71E-01									
Unigene43893_All	458	0.00	0.00	0.00	0.00	0.00	0.00	1.85	1.64	0.00	null	null		null	null		null	null		null	null		-1.69E-01	7.99E-01		-1.09E+01	2.21E-06	Down	Unigene43893_All//gi|255074491|ref|XP_002500920.1|//3.00E-09//predicted protein [Micromonas sp. RCC299] >gi|226516183|gb|ACO62178.1| predicted protein [Micromonas sp. RCC299]						nr -
Unigene43896_All	390	0.00	0.00	0.00	0.00	0.00	0.00	1.63	1.71	0.00	null	null		null	null		null	null		null	null		7.65E-02	9.37E-01		-1.07E+01	7.10E-05	Down	Unigene43896_All//gi|270303614|gb|ACZ71035.1|//2.00E-42//eukaryotic release factor 1-3 [Brassica oleracea var. botrytis]	Unigene43896_All//4.00E-41//AT1G12920| ERF1-2 (EUKARYOTIC RELEASE FACTOR 1-2); translation release factor				GO:0003747//GO:0006412//GO:0016020//GO:0043234//GO:0044424	nr -
Unigene439_All	1828	33.00	19.82	18.12	53.44	48.68	44.13	65.18	28.83	77.50	-7.36E-01	2.63E-26		-8.65E-01	2.71E-33		-1.35E-01	1.10E-02		-2.76E-01	5.10E-08		-1.18E+00	1.04E-136	Down	2.50E-01	3.55E-11		Unigene439_All//gi|211906526|gb|ACJ11756.1|//0.00E+00//rhamnose synthase [Gossypium hirsutum]	Unigene439_All//0.00E+00//AT1G78570| RHM1 (RHAMNOSE BIOSYNTHESIS 1); UDP-L-rhamnose synthase/ UDP-glucose 4,6-dehydratase/ catalytic	Unigene439_All//0.00E+00//TC145500		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene43900_All	411	0.25	0.49	0.00	0.85	1.01	0.00	0.93	1.42	4.27	9.54E-01	6.21E-01		-7.99E+00	3.92E-01		2.45E-01	8.53E-01		-9.73E+00	2.12E-02		6.21E-01	4.78E-01		2.20E+00	8.71E-06	Up				Unigene43900_All//5.00E-07//CO498117				

Unigene43905_All	346	0.00	17.57	2.46	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	1.03E-34	Up	1.13E+01	9.02E-05	Up	null	null		null	null		null	null		null	null									
Unigene4391_All	967	275.56	132.83	187.50	84.69	72.75	67.96	66.37	52.99	25.30	-1.05E+00	1.77E-208	Down	-5.56E-01	4.27E-67		-2.19E-01	5.35E-05		-3.18E-01	1.07E-08		-3.25E-01	2.55E-08		-1.39E+00	1.30E-98	Down	Unigene4391_All//gi|211906470|gb|ACJ11728.1|//2.00E-78//glyceraldehyde-3-phosphate dehydrogenase [Gossypium hirsutum]	Unigene4391_All//9.00E-69//AT3G04120| GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)//glyceraldehyde-3-phosphate dehydrogenase	Unigene4391_All//0.00E+00//TC153528		ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene43913_All	266	0.00	4.38	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	1.10E+01	4.04E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene43915_All	468	0.78	7.25	0.23	0.11	0.15	1.06	0.00	0.18	0.34	3.21E+00	2.83E-12	Up	-1.78E+00	2.34E-01		4.68E-01	9.58E-01		3.32E+00	2.31E-02		7.48E+00	4.01E-01		8.41E+00	1.40E-01		Unigene43915_All//gi|38566580|gb|AAR24180.1|//6.00E-30//At4g31830 [Arabidopsis thaliana] >gi|40824020|gb|AAR92326.1| At4g31830 [Arabidopsis thaliana]	Unigene43915_All//4.00E-31//AT4G31830| unknown protein					nr +
Unigene43919_All	349	3.30	0.58	0.31	0.86	1.18	1.04	0.36	1.08	0.46	-2.51E+00	8.99E-04	Down	-3.43E+00	1.54E-04	Down	4.67E-01	7.41E-01		2.74E-01	8.33E-01		1.57E+00	1.95E-01		3.29E-01	8.51E-01			Unigene43919_All//0.00E+00//TC150476					ESTscan -
Unigene4392_All	1124	23.60	12.35	14.40	61.65	58.82	30.18	18.70	5.80	12.69	-9.34E-01	1.13E-17		-7.13E-01	6.89E-11		-6.77E-02	3.78E-01		-1.03E+00	3.78E-57	Down	-1.69E+00	4.08E-42	Down	-5.59E-01	8.84E-08		Unigene4392_All//gi|225426536|ref|XP_002278895.1|//2.00E-11//PREDICTED: hypothetical protein isoform 2 [Vitis vinifera]		Unigene4392_All//0.00E+00//gi|164342110|gb|ES802973.1|ES802973				nr +
Unigene43921_All	325	0.97	4.37	0.66	0.92	1.91	2.22	2.34	0.77	3.31	2.18E+00	6.83E-04	Up	-5.60E-01	6.63E-01		1.05E+00	2.99E-01		1.27E+00	1.56E-01		-1.60E+00	3.70E-02		4.99E-01	3.90E-01		Unigene43921_All//gi|297833598|ref|XP_002884681.1|//2.00E-49//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330521|gb|EFH60940.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene43921_All//2.00E-38//AT3G08505| zinc finger (CCCH-type/C3HC4-type RING finger) family protein	Unigene43921_All//3.00E-106//TC146069	C3H		GO:0046914	nr +
Unigene43922_All	271	0.00	28.05	16.51	0.00	0.00	0.00	0.00	0.00	0.00	1.48E+01	1.86E-43	Up	1.40E+01	7.75E-25	Up	null	null		null	null		null	null		null	null									
Unigene43923_All	447	2.22	0.00	2.74	0.11	0.31	0.10	0.00	0.00	0.00	-1.11E+01	7.45E-06	Down	3.01E-01	6.32E-01		1.47E+00	6.18E-01		-1.41E-01	9.52E-01		null	null		null	null		Unigene43923_All//gi|115466472|ref|NP_001056835.1|//8.00E-18//Os06g0152300 [Oryza sativa Japonica Group] >gi|113594875|dbj|BAF18749.1| Os06g0152300 [Oryza sativa Japonica Group]	Unigene43923_All//4.00E-17//AT2G30920| ATCOQ3 (ARABIDOPSIS THALIANA COENZYME Q 3); hexaprenyldihydroxybenzoate methyltransferase/polyprenyldihydroxybenzoate methyltransferase			ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0006743//GO:0010420//GO:0031967//GO:0043231	nr -
Unigene43926_All	392	0.27	0.00	0.27	0.64	0.53	0.46	2.05	0.32	0.20	-8.06E+00	3.71E-01		2.57E-02	9.99E-01		-2.70E-01	8.23E-01		-4.63E-01	7.44E-01		-2.68E+00	1.67E-03		-3.33E+00	2.47E-04	Down	Unigene43926_All//gi|240255733|ref|NP_192232.4|//2.00E-43//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene43926_All//9.00E-45//AT4G03230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding				GO:0004672//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene43930_All	335	0.47	4.84	3.34	0.00	1.03	0.00	0.00	0.37	0.36	3.37E+00	2.12E-06	Up	2.83E+00	7.34E-04	Up	1.00E+01	3.01E-02		null	null		8.55E+00	2.40E-01		8.48E+00	2.43E-01		Unigene43930_All//gi|5902404|gb|AAD55506.1|AC008148_16//3.00E-09//Unknown protein [Arabidopsis thaliana]	Unigene43930_All//3.00E-11//AT1G23110| unknown protein	Unigene43930_All//5.00E-105//TC134909				nr +
Unigene43936_All	441	0.00	0.00	0.00	0.00	0.00	0.00	2.59	0.95	0.00	null	null		null	null		null	null		null	null		-1.45E+00	1.40E-02		-1.13E+01	1.64E-08	Down	Unigene43936_All//gi|2894308|emb|CAA11269.1|//1.00E-29//polyubiquitin [Nicotiana tabacum]	Unigene43936_All//2.00E-27//AT4G05320| UBQ10 (POLYUBIQUITIN 10); protein binding	Unigene43936_All//2.00E-31//gi|164339609|gb|ES793180.1|ES793180			GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene43937_All	402	0.00	0.00	0.00	0.00	0.00	290.91	996.13	153.21	null	null			null	null		null	null		null	null		1.78E+00	0.00E+00	Up	-9.25E-01	3.27E-93		Unigene43937_All//gi|71534908|gb|AAZ32858.1|//9.00E-21//BURP domain-containing protein [Medicago sativa]	Unigene43937_All//6.00E-15//AT1G49320| BURP domain-containing protein	Unigene43937_All//2.00E-68//ES840078				nr +
Unigene43939_All	540	1.16	0.00	0.20	0.37	1.21	2.34	0.00	0.00	0.00	-1.02E+01	7.91E-04	Down	-2.56E+00	2.72E-02		1.72E+00	8.16E-02		2.67E+00	2.42E-04	Up	null	null		null	null		Unigene43939_All//gi|224062041|ref|XP_002300725.1|//3.00E-61//cytochrome P450 [Populus trichocarpa] >gi|222842451|gb|EEE79998.1| cytochrome P450 [Populus trichocarpa]	Unigene43939_All//2.00E-49//AT5G26210| CYP71B23; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene43939_All//4.00E-113//C0095080		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr -
Unigene4394_All	1011	17.70	37.34	19.49	19.96	21.97	13.27	28.73	26.79	25.30	1.08E+00	4.42E-31	Up	1.39E-01	3.45E-01		1.39E-01	3.08E-01		-5.89E-01	7.25E-07		-1.01E-01	3.50E-01		-1.84E-01	4.65E-02		Unigene4394_All//gi|27311565|gb|AAO00748.1|//3.00E-45//Unknown protein [Arabidopsis thaliana] >gi|30102820|gb|AAP21328.1| At3g09085 [Arabidopsis thaliana]	Unigene4394_All//1.00E-46//AT3G09085| unknown protein	Unigene4394_All//0.00E+00//TC177716				nr -
Unigene43942_All	317	3.47	2.24	0.34	1.41	2.06	0.57	0.00	0.00	0.13	-6.31E-01	3.35E-01		-3.37E+00	2.67E-04	Down	5.45E-01	5.86E-01		-1.31E+00	2.73E-01		null	null		6.97E+00	6.44E-01		Unigene43942_All//gi|115479043|ref|NP_001063115.1|//2.00E-19//Os09g0400500 [Oryza sativa Japonica Group] >gi|113631348|dbj|BAF25029.1| Os09g0400500 [Oryza sativa Japonica Group]	Unigene43942_All//6.00E-16//AT2G26730| leucine-rich repeat transmembrane protein kinase, putative				GO:0006464//GO:0016301//GO:0031410//GO:0032559	nr -
Unigene43944_All	399	0.13	0.00	0.00	0.75	0.26	0.11	27.13	0.84	0.00	-7.03E+00	6.11E-01		-7.03E+00	6.22E-01		-1.53E+00	2.98E-01		-2.73E+00	1.37E-01		-5.02E+00	1.27E-64	Down	-1.47E+01	9.68E-80	Down	Unigene43944_All//gi|14334057|gb|AK60517.1|AF332974_1//3.00E-26//P450 monooxygenase [Gossypium arboreum]	Unigene43944_All//2.00E-21//AT1G33730| CYP76C5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene43944_All//2.00E-108//TC137030		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506	nr +
Unigene43946_All	319	0.00	2.70	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.94E-05	Up	9.38E+00	1.41E-01		null	null		null	null		null	null		null	null		Unigene43946_All//gi|168041828|ref|XP_001773392.1|//6.00E-06//predicted protein [Physcomitrella patens subsp. patens] >gi|162675268|gb|EDQ61765.1| predicted protein [Physcomitrella patens subsp. patens]						nr +
Unigene43949_All	292	0.00	3.82	3.83	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.00E-06	Up	1.19E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene43949_All//sp|P01023|A2MG_HUMAN//9.00E-49//Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2						swissprot +
Unigene43950_All	456	0.23	2.33	0.35	0.66	1.51	0.59	0.93	1.19	0.70	3.35E+00	2.17E-04	Up	6.10E-01	7.48E-01		1.20E+00	1.94E-01		-1.41E-01	9.20E-01		3.62E-01	6.73E-01		-4.08E-01	6.54E-01		Unigene43950_All//gi|224119836|ref|XP_002331173.1|//1.00E-08//predicted protein [Populus trichocarpa] >gi|222873256|gb|EEF10387.1| predicted protein [Populus trichocarpa]						nr -
Unigene43951_All	267	0.00	10.82	4.59	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.97E-16	Up	1.22E+01	9.11E-07	Up	null	null		null	null		null	null		null	null		Unigene43951_All//gi|300259547|gb|EFJ43774.1|//2.00E-27//ribosomal protein S6 component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene43951_All//1.00E-27//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome	Unigene43951_All//8.00E-11//BF268962		ko03010|Ribosome	GO:0004872//GO:0005198//GO:0006952//GO:0009536//GO:0010467//GO:0015935//GO:0016462//GO:0031981//GO:0032559//GO:0044425	nr +
Unigene43953_All	374	0.00	0.00	0.00	2.00	2.67	1.45	1.81	1.45	15.77	null	null		null	null		4.18E-01	5.85E-01		-4.63E-01	6.06E-01		-3.16E-01	6.74E-01		3.12E+00	1.61E-25	Up							
Unigene43957_All	351	0.00	0.00	0.00	3.55	4.81	0.00	0.60	0.71	0.57	null	null		null	null		4.38E-01	4.27E-01		-1.18E+01	8.64E-08	Down	2.47E-01	8.53E-01		-8.59E-02	9.61E-01		Unigene43957_All//gi|115463117|ref|NP_001055158.1|//1.00E-07//Os05g0310600 [Oryza sativa Japonica Group] >gi|113578709|dbj|BAF17072.1| Os05g0310600 [Oryza sativa Japonica Group]	Unigene43957_All//8.00E-08//AT5G06370| NC domain-containing protein	Unigene43957_All//9.00E-33//TC155458				nr -
Unigene43958_All	463	0.45	1.31	0.81	0.97	0.60	7.32	0.73	0.00	0.43	1.54E+00	1.22E-01		8.33E-01	5.16E-01		-7.03E-01	5.30E-01		2.92E+00	8.73E-12	Up	-9.51E+00	1.17E-02		-7.64E-01	5.01E-01		Unigene43958_All//gi|28302070|gb|AAM09514.2|AF489874.1|//8.00E-47//zeatin O-glucosyltransferase [Glycine max]	Unigene43958_All//1.00E-04//AT1G22370| AtUGT85A5 (UDP-glucosyl transferase 85A5); glucuronosyltransferase/ transferase, transferring glycosyl groups	Unigene43958_All//0.00E+00//TC163771		ko00908|Zeatin biosynthesis	GO:0005635//GO:0008194//GO:0016758//GO:0051234	nr -
Unigene43961_All	408	0.00	0.00	0.00	0.24	0.34	1.33	0.00	0.31	3.81	null	null		null	null		4.67E-01	8.76E-01		2.44E+00	4.41E-02		8.26E+00	2.40E-01		1.19E+01	3.54E-11	Up							
Unigene43963_All	427	0.00	2.37	4.86	0.00	0.16	0.00	0.00	0.00	0.00	1.12E+01	7.26E-06	Up	1.22E+01	1.92E-11	Up	7.33E+00	6.09E-01		null	null		null	null		null	null		Unigene43963_All//gi|297847300|ref|XP_002891531.1|//4.00E-41//PAB8 binding protein 8 [Arabidopsis lyrata subsp. lyrata] >gi|297337373|gb|EFH67790.1| PAB8 binding protein 8 [Arabidopsis lyrata subsp. lyrata]	Unigene43963_All//3.00E-42//AT1G49760| PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor			ko03040|Spliceosome	GO:0003676//GO:0010038	nr +
Unigene43964_All	859	0.00	0.00	0.00	0.06	0.00	0.00	1.18	2.29	11.22	null	null		null	null		-5.86E+00	5.55E-01		-5.86E+00	6.34E-01		9.53E-01	2.15E-02		3.25E+00	8.04E-43	Up	Unigene43964_All//gi|55168340|gb|AAV44205.1|//3.00E-30//unknow protein [Oryza sativa Japonica Group]		Unigene43964_All//3.00E-118//TC149394			GO:0009536	nr +
Unigene43965_All	331	0.00	3.52	7.88	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.05E-06	Up	1.29E+01	2.12E-14	Up	null	null		null	null		null	null		null	null		Unigene43965_All//gi|226462534|gb|EEH59826.1|//5.00E-17//ribosomal protein S28e [Micromonas pusilla CCMP1545]	Unigene43965_All//1.00E-07//AT5G64140| RPS28 (RIBOSOMAL PROTEIN S28); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene43970_All	290	2.35	0.70	1.10	0.17	0.48	0.00	2.19	0.14	0.27	-1.75E+00	6.23E-02		-1.09E+00	2.39E-01		1.47E+00	6.18E-01		-7.42E+00	6.34E-01		-3.92E+00	9.80E-04	Down	-2.99E+00	2.58E-03		Unigene43970_All//gi|297798236|ref|XP_002867002.1|//6.00E-38//SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312838|gb|EFH43261.1| SEC14 cytosolic factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene43970_All//8.00E-38//AT4G36640| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene43970_All//1.00E-160//gi|78338531|gb|DT558805.1|DT558805			GO:0044464//GO:0051234	nr -
Unigene43976_All	264	9.12	6.14	7.87	0.00	0.26	0.34	0.00	0.00	1.96	-5.70E-01	1.64E-01		-2.13E-01	6.28E-01		8.03E+00	6.08E-01		8.42E+00	4.76E-01		null	null		1.09E+01	6.13E-04	Up	Unigene43976_All//gi|224122320|ref|XP_002330594.1|//9.00E-12//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222872152|gb|EEF09283.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene43976_All//8.00E-11//AT5G46730| disease resistance protein (CC-NBS class), putative			ko04626|Plant-pathogen interaction		nr -
Unigene43977_All	320	0.00	6.97	4.66	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.09E-12	Up	1.22E+01	3.22E-08	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene43978_All	375	36.00	107.42	42.17	45.83	49.77	98.03	58.63	63.98	60.34	1.58E+00	3.73E-59	Up	2.29E-01	1.41E-01		1.19E-01	4.41E-01		1.10E+00	2.28E-33	Up	1.26E-01	2.73E-01		4.16E-02	7.20E-01		Unigene43978_All//gi|269999990|gb|ACZ57923.1|//9.00E-58//DnaJ-like protein [Glycine max]	Unigene43978_All//2.00E-52//AT1G56300| DNAJ heat shock N-terminal domin-containing protein	Unigene43978_All//0.00E+00//gi|109874367|gb|DW503341.1|DW503341			GO:0005515//GO:0044267//GO:0050896	nr -
Unigene43981_All	324	0.00	0.00	0.00	0.00	0.00	0.00	2.22	4.13	0.00	null	null		null	null		null	null		null	null		8.96E-01	8.68E-02		-1.11E+01	1.78E-05	Down	Unigene43981_All//gi|297847742|ref|XP_002891752.1|//1.00E-15//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337594|gb|EFH68011.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene43981_All//3.00E-11//AT1G53410| leucine-rich repeat family protein / protein kinase family protein			ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488//GO:0016020	nr +
Unigene43986_All	393	0.00	4.38	1.08	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.99E-10	Up	1.01E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene43986_All//sp|Q07984|SSRD_RAT//4.00E-15//Translocon-associated protein subunit delta OS=Rattus norvegicus GN=Ssr4 PE=2 SV=1						swissprot +
Unigene43988_All	462	0.00	7.90	1.84	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	9.10E-21	Up	1.08E+01	9.02E-05	Up	null	null		null	null		null	null		null	null									ESTscan -

Unigene43989_All	419	0.00	0.36	0.25	0.00	0.00	0.00	4.54	1.40	0.00	8.50E+00	2.35E-01		7.99E+00	3.97E-01		null	null		null	null		-1.70E+00	1.53E-04	Down	-1.21E+01	4.91E-14	Down	Unigene43989_All//gi|297810207|ref|XP_002872987.1|//3.00E-18//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318824|gb|EFH49246.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene43989_All//3.00E-13//AT5G01880| zinc finger (C3HC4-type RING finger) family protein				GO:0046872	nr +
Unigene43991_All	347	0.00	6.86	3.22	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.50E-13	Up	1.17E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene43991_All//gi|4501883|ref|NP_001604.1|//2.00E-55//actin, aortic smooth muscle [Homo sapiens] >gi|6671507|ref|NP_031418.1| actin, aortic smooth muscle [Mus musculus] >gi|78045238|ref|NP_001029674.1| actin, aortic smooth muscle [Bos taurus] >gi|110625958|ref|NP_112266.1| actin, aortic smooth muscle [Rattus norvegicus] >gi|156119362|ref|NP_001095152.1| actin, aortic smooth muscle [Oryctolagus cuniculus] >gi|197097944|ref|NP_001126814.1| actin, aortic smooth muscle [Pongo abelii] >gi|213688375|ref|NP_001135417.1| actin, aortic smooth muscle [Homo sapiens] >gi|257470979|ref|NP_001158122.1| actin, aortic smooth muscle [Sus scrofa] >gi|73996085|ref|XP_534781.2| PREDICTED: similar to Actin, aortic smooth muscle (Alpha-actin 2) [Canis familiaris] >gi|114631685|ref|XP_521550.2|	Unigene43991_All//6.00E-49//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene43991_All//2.00E-24//TC153744		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008015//GO:0008092//GO:0012501//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0042995//GO:0048747//GO:0051707//GO:0060415	nr -
Unigene43992_All	500	0.00	0.00	0.00	0.50	0.00	0.36	2.79	5.52	7.49	null	null		null	null		-8.96E+00	4.18E-02		-4.63E-01	7.44E-01		9.83E-01	3.75E-03		1.42E+00	1.06E-06	Up	Unigene43992_All//gi|4008010|gb|AAC95353.1|//8.00E-34//receptor-like protein kinase [Arabidopsis thaliana]	Unigene43992_All//6.00E+00//CO081718			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0009987	nr -
Unigene43993_All	327	0.00	0.00	0.98	0.00	0.00	0.00	13.96	27.48	73.46	null	null		9.93E+00	4.51E-02		null	null		null	null		9.77E-01	2.31E-08		2.40E+00	9.14E-77	Up	Unigene43993_All//3.00E-35//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase				ko00480|Glutathione metabolism	GO:0004672//GO:0006464//GO:0016765//GO:0016846//GO:0032559//GO:0044424	nr -
Unigene43995_All	517	0.00	0.00	0.00	0.00	0.00	0.00	2.45	1.70	0.08	null	null		null	null		null	null		null	null		-5.31E-01	3.43E-01		-4.99E+00	3.13E-08	Down	Unigene43995_All//gi|298714763|emb|CBJ25662.1|//4.00E-48//60S ribosomal protein L13a [Ectocarpus siliculosus]	Unigene43995_All//6.00E-44//AT3G07110| 60S ribosomal protein L13A (RPL13aA)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr +
Unigene43996_All	348	0.75	0.00	1.22	4.58	1.29	0.78	1.09	0.00	0.11	-9.55E+00	6.69E-02		7.04E-01	5.54E-01		-1.83E+00	4.08E-04	Down	-2.56E+00	2.78E-05	Down	-1.01E+01	6.18E-03		-3.26E+00	2.22E-02		Unigene43996_All//gi|19310401|gb|AAL84940.1|//8.00E-08//At2g46980/F14M4.19 [Arabidopsis thaliana]	Unigene43996_All//3.00E-09//AT2G46980| unknown protein					nr +
Unigene43997_All	409	0.00	0.00	0.00	0.00	0.00	0.00	11.06	2.25	2.53	null	null		null	null		null	null		null	null		-2.30E+00	4.15E-14	Down	-2.13E+00	2.43E-13	Down								
Unigene43998_All	409	0.00	5.82	4.56	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.50E-13	Up	1.22E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene43998_All//gi|299530380|ref|YP_003734595.1|//3.00E-41//50S ribosomal protein L2 [Kryptoperidinium foliaceum] >gi|297385082|gb|ADI40380.1| 50S ribosomal protein L2 [Kryptoperidinium foliaceum]	Unigene43998_All//3.00E-29//ATCG01310| encodes a chloroplast ribosomal protein L2, a constituent of the large subunit of the ribosomal complex			ko03010|Ribosome	GO:0005840//GO:0009536	nr +
Unigene43999_All	489	0.00	0.00	0.00	0.00	0.00	0.00	3.11	1.97	0.73	null	null		null	null		null	null		null	null		-6.63E-01	1.73E-01		-2.09E+00	6.46E-05	Down		Unigene43999_All//6.00E-07//FL576573					
Unigene4400_All	1258	11.65	3.83	2.79	13.70	14.89	13.61	10.35	3.62	5.32	-1.61E+00	1.26E-22	Down	-2.06E+00	2.59E-30	Down	1.20E-01	4.33E-01		-1.00E-02	9.56E-01		-1.52E+00	1.11E-22	Down	-9.60E-01	7.66E-12		Unigene4400_All//gi|297827893|ref|XP_002881829.1|//2.00E-52//polychome, UV-B-insensitive 4 [Arabidopsis lyrata subsp. lyrata] >gi|297327668|gb|EFH58088.1| polychome, UV-B-insensitive 4 [Arabidopsis lyrata subsp. lyrata]	Unigene4400_All//5.00E-46//AT2G42260| UVI4 (UV-B-INSENSITIVE 4)	Unigene4400_All//0.00E+00//TC162416				nr -
Unigene44001_All	474	0.00	2.14	1.46	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	7.25E-06	Up	1.05E+01	6.16E-04	Up	null	null		null	null		null	null		null	null		Unigene44001_All//gi|291246022|gb|ADO85140.1|//3.00E-16//calmodulin [Triticum aestivum]	Unigene44001_All//8.00E-16//AT5G37780| CAM6 (CALMODULIN 1); calcium ion binding			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene44002_All	539	1.55	1.03	0.49	0.74	3.51	2.93	0.94	0.00	0.00	-5.87E-01	4.26E-01		-1.65E+00	5.45E-02		2.25E+00	1.74E-05	Up	1.99E+00	6.07E-04	Up	-9.88E+00	8.89E-04	Down	-9.88E+00	5.54E-04	Down	Unigene44002_All//gi|224078652|ref|XP_002305592.1|//2.00E-76//cytochrome P450 [Populus trichocarpa] >gi|222848556|gb|EEE86103.1| cytochrome P450 [Populus trichocarpa]	Unigene44002_All//9.00E-68//AT1G11600| CYP77B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene44002_All//8.00E-102//TC158594		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016712//GO:0043231	nr -
Unigene44003_All	1415	0.00	0.00	0.04	0.00	0.17	0.10	1.17	0.59	7.12	null	null		5.23E+00	6.35E-01		7.41E+00	1.04E-01		6.58E+00	3.11E-01		-9.80E-01	3.31E-02		2.61E+00	5.75E-36	Up	Unigene44003_All//gi|209954715|dbj|BAG80548.1|//1.00E-144//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene44003_All//4.00E-140//AT2G28080| glycosyltransferase family protein	Unigene44003_All//2.00E-175//BQ410213		ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0016757	nr +
Unigene44005_All	551	0.00	0.55	0.00	0.81	0.56	2.13	0.31	3.87	10.48	9.11E+00	4.42E-02		null	null		-5.33E-01	5.96E-01		1.39E+00	3.52E-02		3.66E+00	1.04E-10	Up	5.09E+00	2.39E-35	Up							
Unigene44007_All	354	0.89	1.15	3.16	5.77	2.14	5.61	0.12	0.24	0.68	3.69E-01	7.24E-01		1.83E+00	1.24E-02		-1.43E+00	9.35E-04	Down	-3.95E-02	9.42E-01		9.84E-01	7.31E-01		2.50E+00	1.59E-01		Unigene44007_All//gi|225456020|ref|XP_002279587.1|//5.00E-35//PREDICTED: similar to inositol polyphosphate multikinase [Vitis vinifera]	Unigene44007_All//2.00E-31//AT5G61760| ATIPK2BETA: inositol or phosphatidylinositol kinase/ inositol trisphosphate 6-kinase	Unigene44007_All//1.00E-13//TC130598			GO:0000904//GO:0009856//GO:0016020//GO:0043231//GO:0051766	nr -
Unigene4401_All	1808	4.51	8.02	9.66	5.01	6.69	5.77	0.28	0.02	0.09	8.28E-01	2.75E-08		1.10E+00	1.16E-14	Up	4.15E-01	9.13E-03		2.03E-01	3.18E-01		-3.60E+00	5.77E-03		-1.67E+00	7.78E-02		Unigene4401_All//gi|18652398|gb|AAL77102.1|AF472608_1//1.00E-177//carbohydrate oxidase [Lactuca sativa]	Unigene4401_All//0.00E+00//AT1G30700| FAD-binding domain-containing protein	Unigene4401_All//0.00E+00//gi|164343807|gb|ES793461.1|ES793461				nr -
Unigene44011_All	315	0.00	1.93	0.00	1.42	0.22	0.00	30.47	63.56	22.01	1.09E+01	1.17E-03		null	null		-2.70E+00	3.24E-02		-1.05E+01	5.78E-03		1.06E+00	4.43E-20	Up	-4.69E-01	3.51E-03				Unigene44011_All//1.00E-158//gi|109875411|gb|DW504385.1|DW504385				
Unigene44014_All	372	0.00	11.99	5.73	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	2.10E-25	Up	1.25E+01	9.77E-12	Up	null	null		null	null		null	null		null	null		Unigene44014_All//gi|115461973|ref|NP_001054586.1|//8.00E-25//Os05g0137400 [Oryza sativa Japonica Group] >gi|78599760|sp|P42211.2|ASPRX_ORYSJ RecName: Full=Aspartic proteinase; Flags: Precursor >gi|46485798|gb|AAS98423.1| aspartic proteinase [Oryza sativa Japonica Group] >gi|113578137|dbj|BAF16500.1| Os05g0137400 [Oryza sativa Japonica Group]	Unigene44014_All//5.00E-22//AT1G62290| aspartyl protease family protein				GO:0004175//GO:0019538//GO:0031410//GO:0043231	nr -
Unigene44015_All	321	0.00	0.00	0.00	0.00	0.00	0.00	3.16	2.47	0.00	null	null		null	null		null	null		null	null		-3.54E-01	5.99E-01		-1.16E+01	1.35E-07	Down	Unigene44015_All//gi|76160933|gb|ABA40430.1|//8.00E-35//ribosomal protein L27a-like protein [Solanum tuberosum] >gi|76160998|gb|ABA40462.1| ribosomal protein L27a-like protein [Solanum tuberosum]	Unigene44015_All//1.00E-33//AT1G70600| structural constituent of ribosome	Unigene44015_All//2.00E-09//CD486164		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene44019_All	409	0.00	3.10	1.95	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.86E-07	Up	1.09E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene44019_All//gi|300255800|gb|EFJ40085.1|//2.00E-10//eukaryotic translation initiation factor 3d [Volvox carteri f. nagariensis]						nr +
Unigene4402_All	866	22.60	58.98	38.31	31.46	41.47	42.35	28.12	37.50	27.69	1.38E+00	9.82E-62	Up	7.62E-01	4.68E-15		3.99E-01	1.72E-06		4.29E-01	6.19E-07		4.15E-01	7.98E-07		-2.21E-02	8.51E-01		Unigene4402_All//gi|18405485|ref|NP_564699.1|//1.00E-102//WD-40 repeat family protein [Arabidopsis thaliana]	Unigene4402_All//3.00E-103//AT1G55880| WD-40 repeat family protein	Unigene4402_All//0.00E+00//TC167042		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis//ko03018|RNA degradation//ko03022|Basal transcription factors		nr -
Unigene44020_All	379	0.00	0.00	0.00	0.00	0.00	0.00	2.01	2.76	0.00	null	null		null	null		null	null		null	null		4.57E-01	4.63E-01		-1.10E+01	8.87E-06	Down	Unigene44020_All//gi|116782446|gb|ABK22509.1|//9.00E-07//unknown [Picea sitchensis] >gi|116782553|gb|ABK22550.1| unknown [Picea sitchensis] >gi|116782724|gb|ABK22629.1| unknown [Picea sitchensis] >gi|116790392|gb|ABK25597.1| unknown [Picea sitchensis] >gi|224284911|gb|ACN40185.1| unknown [Picea sitchensis] >gi|224285835|gb|ACN40631.1| unknown [Picea sitchensis] >gi|224286582|gb|ACN40996.1| unknown [Picea sitchensis]	Unigene44020_All//2.00E-05//AT3G05540| INVOLVED IN: biological_process unknown; LOCATED IN: cytoplasm; CONTAINS InterPro DOMAIN/s: Translationally controlled tumour protein (InterPro:IPR018105), Translationally controlled tumour-associated TCTP (InterPro:IPR001983), Mss4/translationally controlled tumour-associated TCTP (InterPro:IPR011323), Translationally controlled tumour protein, conserved site (InterPro:IPR018103), Mss4-like (InterPro:IPR011657); BEST Arabidopsis thaliana protein match is: TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN) (TAIR:AT3G16640.1); Has 640 Blast hits to 640 proteins in 231 species: Archae - 0; Bacteria - 0; Metazoa - 343; Fungi - 110; Plants - 105; Viruses - 0; Other Eukaryotes - 82 (source: NCBI BLink).					nr +
Unigene44021_All	403	3.12	1.51	0.53	2.10	0.68	0.90	1.78	1.04	3.16	-1.05E+00	8.27E-02		-2.56E+00	6.99E-04	Down	-1.62E+00	3.12E-02		-1.23E+00	1.20E-01		-7.82E-01	3.10E-01		8.27E-01	1.08E-01		Unigene44021_All//gi|44917429|gb|AS49039.1|//2.00E-25//At3g46810 [Arabidopsis thaliana]	Unigene44021_All//8.00E-27//AT3G46810| DC1 domain-containing protein	Unigene44021_All//3.00E-70//DR458371			GO:0044464	nr -
Unigene44024_All	360	0.00	8.87	5.77	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	3.64E-18	Up	1.25E+01	1.92E-11	Up	null	null		null	null		null	null		null	null									ESTscan -

Unigene4403_All	693	4.23	4.83	3.00	6.69	3.13	4.50	2.93	2.29	3.16	1.91E-01	6.12E-01		-4.97E-01	2.04E-01		-1.09E+00	2.91E-05	Down	-5.72E-01	4.27E-02		-3.54E-01	4.02E-01		1.11E-01	7.73E-01		Unigene4403_All//gi|32815875|gb|AAP88334.1|//3.00E-58//At1g15860 [Arabidopsis thaliana]	Unigene4403_All//2.00E-59//AT1G15860| INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Defective in cullin neddylation (InterPro:IPR014764), Protein of unknown function DUF298 (InterPro:IPR005176); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G12760.1); Has 576 Blast hits to 576 proteins in 121 species: Archae - 0; Bacteria - 0; Metazoa - 403; Fungi - 78; Plants - 51; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink).	Unigene4403_All//0.00E+00//gi|48878944|gb|CO129966.1|CO129966				nr -
Unigene44030_All	292	0.00	0.00	0.00	1.02	0.47	0.00	0.00	0.00	1.77	null	null		null	null		-1.12E+00	4.24E-01		-1.00E+01	3.99E-02		null	null		1.08E+01	6.13E-04	Up							
Unigene44033_All	374	0.28	0.00	0.00	2.26	0.92	0.12	0.34	0.00	0.00	-8.13E+00	3.71E-01		-8.13E+00	3.92E-01		-1.30E+00	8.00E-02		-4.23E+00	2.18E-04	Down	-8.41E+00	2.35E-01		-8.41E+00	2.00E-01								
Unigene44037_All	371	0.00	0.00	0.00	0.00	0.00	0.00	7.98	4.84	0.64	null	null		null	null		null	null		null	null		-7.20E-01	2.65E-02		-3.63E+00	3.43E-15	Down		Unigene44037_All//3.00E-14//TC137772					
Unigene44038_All	387	0.00	3.14	2.06	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.47E-07	Up	1.10E+01	1.72E-04	Up	null	null		null	null		null	null		null	null								
Unigene4404_All	1277	4.92	29.80	4.38	4.80	9.92	11.25	7.28	11.29	36.66	2.60E+00	1.80E-106	Up	-1.67E-01	5.32E-01		1.05E+00	5.75E-12	Up	1.23E+00	6.80E-16	Up	6.33E-01	1.50E-06		2.33E+00	3.21E-144	Up	Unigene4404_All//gi|12003394|gb|AAG43554.1|AF211536_1//1.00E-133//Avr9/Cf-9 rapidly elicited protein 231 [Nicotiana tabacum]	Unigene4404_All//7.00E-132//AT3G28340| GATL10 (Galacturonosyltransferase-like 10); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring hexosyl groups	Unigene4404_All//0.00E+00//TC163241				nr -
Unigene44040_All	411	0.00	0.00	0.00	0.00	0.00	0.00	2.16	4.68	0.00	null	null		null	null		null	null		null	null		1.11E+00	8.32E-03		-1.11E+01	1.10E-06	Down	Unigene44040_All//gi|5706704|gb|AAD47346.1|AF112440_1//1.00E-33//ribosomal protein S26 [Pisum sativum]	Unigene44040_All//8.00E-21//AT3G56340| 40S ribosomal protein S26 (RPS26C)		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene44042_All	322	3.57	4.72	0.50	2.01	1.18	6.73	7.62	9.35	8.29	4.01E-01	4.53E-01		-2.85E+00	6.02E-04	Down	-7.74E-01	3.81E-01		1.74E+00	1.85E-04	Up	2.95E-01	3.95E-01		1.22E-01	7.25E-01			Unigene44042_All//5.00E-65//DW516589					
Unigene44043_All	386	0.00	0.00	0.00	0.00	0.00	0.00	10.73	12.34	0.00	null	null		null	null		null	null		null	null		2.02E-01	4.66E-01		-1.34E+01	1.83E-30	Down		Unigene44043_All//2.00E-12//TC133518					
Unigene44045_All	363	0.00	3.07	1.76	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.00E-06	Up	1.08E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene44045_All//gi|16930763|gb|AAL32041.1|AF439282_1//3.00E-37//chl a/b-binding protein [Retama raetam]	Unigene44045_All//5.00E-26//AT4G10340| LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding	Unigene44045_All//4.00E-07//EX167600		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009503//GO:0009523//GO:0009570//GO:0009639//GO:0046906	nr -
Unigene44046_All	258	2.64	0.79	0.00	0.39	0.13	0.00	0.00	0.00	0.00	-1.75E+00	6.23E-02		-1.14E+01	7.63E-04	Down	-1.53E+00	5.86E-01		-8.59E+00	3.99E-01		null	null		null	null								
Unigene4405_All	1157	104.37	84.04	96.37	37.85	36.01	40.56	17.03	13.58	7.37	-3.13E-11	1.82E-11		-1.15E-01	2.75E-02		-7.16E-02	4.73E-01		9.99E-02	2.81E-01		-3.26E-01	3.76E-03		-1.21E+00	5.67E-25	Down	Unigene4405_All//gi|6554182|gb|AAF16628.1|AC011661_6//7.00E-77//T23J18.10 [Arabidopsis thaliana]	Unigene4405_All//1.00E-70//AT1G11430| plastid developmental protein DAG, putative	Unigene4405_All//0.00E+00//TC146252				nr -
Unigene44051_All	382	1.51	1.19	0.14	2.22	1.62	1.18	3.21	0.33	1.04	-3.36E-01	6.90E-01		-3.43E+00	1.41E-02		-4.50E-01	5.52E-01		-9.07E-01	2.47E-01		-3.29E+00	6.14E-06	Down	-1.62E+00	3.49E-03			Unigene44051_All//1.00E-176//ES829359					
Unigene44052_All	863	0.00	62.53	21.53	0.00	0.00	0.00	0.00	0.00	0.00	1.59E+01	0.00E+00	Up	1.44E+01	5.78E-105	Up	null	null		null	null		null	null		null	null		Unigene44052_All//gi|115475427|ref|NP_001061310.1|//2.00E-72//Os08g0234000 [Oryza sativa Japonica Group] >gi|113623279|dbj|BAF23224.1|Os08g0234000 [Oryza sativa Japonica Group]	Unigene44052_All//6.00E-73//AT3G13580| 60S ribosomal protein L7 (RPL7D)		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene44054_All	383	25.14	45.11	39.21	35.77	64.82	87.50	49.68	28.92	270.34	8.44E-01	5.16E-10		6.41E-01	1.66E-05		8.58E-01	1.09E-16		1.29E+00	3.09E-39	Up	-7.81E-01	9.09E-12		2.44E+00	0.00E+00	Up	Unigene44054_All//gi|16416376|dbj|BAB21610.2|//2.00E-34//mangrin [Bruguiera sexangula]	Unigene44054_All//3.00E-26//AT3G25760| AOC1 (ALLENE OXIDE CYCLASE 1); allene-oxide cyclase	Unigene44054_All//0.00E+00//gi|164302638|gb|ES824091.1|ES824091		ko00592|alpha-Linolenic acid metabolism	GO:0009536//GO:0009694//GO:0009975	nr +
Unigene44058_All	340	0.00	0.00	0.00	0.00	0.00	0.00	8.08	11.68	0.70	null	null		null	null		null	null		null	null		5.31E-01	5.53E-02		-3.52E+00	8.04E-14	Down							ESTscan +
Unigene4406_All	1066	0.83	1.71	4.70	3.32	3.71	4.96	0.12	0.39	0.00	1.04E+00	3.37E-02		2.49E+00	2.17E-13	Up	1.63E-01	6.41E-01		5.79E-01	2.76E-02		1.72E+00	1.35E-01		-6.89E+00	2.00E-01		Unigene4406_All//gi|115446781|ref|NP_001047120.1|//7.00E-07//Os02g0566300 [Oryza sativa Japonica Group] >gi|113536701|dbj|BAF09084.1|Os02g0566300 [Oryza sativa Japonica Group]						nr +
Unigene44060_All	403	0.00	0.00	0.00	0.00	0.00	0.00	5.04	7.26	0.69	null	null		null	null		null	null		null	null		5.28E-01	1.15E-01		-2.86E+00	1.08E-08	Down							
Unigene44061_All	618	0.00	0.00	0.00	0.00	0.00	0.00	2.19	1.69	0.13	null	null		null	null		null	null		null	null		-3.73E-01	4.95E-01		-4.09E+00	7.07E-08	Down	Unigene44061_All//gi|57118009|gb|AAW34136.1|//1.00E-36//cysteine protease gp3a [Zingiber officinale]	Unigene44061_All//5.00E-35//AT4G16190| cysteine proteinase, putative				GO:0016787	nr +
Unigene44062_All	480	0.00	0.00	0.00	0.00	0.00	0.00	1.76	2.09	0.00	null	null		null	null		null	null		null	null		2.46E-01	6.89E-01		-1.08E+01	2.21E-06	Down	Unigene44062_All//gi|301117182|ref|XP_002906319.1|//8.00E-41//60S ribosomal protein L27 [Phytophthora infestans T30-4] >gi|262107668|gb|EE165720.1| 60S ribosomal protein L27 [Phytophthora infestans T30-4]	Unigene44062_All//6.00E-34//AT2G32220| 60S ribosomal protein L27 (RPL27A)		ko03010|Ribosome	GO:0030529	nr -
Unigene44063_All	401	0.91	0.00	1.20	3.98	2.49	0.90	0.53	0.83	0.99	-9.83E+00	1.96E-02		3.88E-01	6.97E-01		-6.75E-01	1.88E-01		-2.14E+00	2.07E-04	Down	6.61E-01	6.09E-01		9.14E-01	3.86E-01		Unigene44063_All//gi|15232059|ref|NP_189337.1|//1.00E-12//AT-TCP20; transcription factor [Arabidopsis thaliana] >gi|75273954|sp|Q9LSD5.1|TCP20_ARATH RecName: Full=Transcription factor TCP20	Unigene44063_All//6.00E-14//AT3G27010| AT-TCP20; transcription factor	Unigene44063_All//2.00E-154//TC177765	TCP			nr -
Unigene44064_All	1001	0.26	0.10	0.11	0.20	0.21	0.27	0.63	1.88	20.85	-1.37E+00	3.83E-01		-1.30E+00	4.36E-01		5.19E-02	9.88E-01		4.43E-01	7.63E-01		1.57E+00	4.37E-04	Up	5.04E+00	4.34E-126	Up	Unigene44064_All//gi|212717129|gb|ACJ37406.1|//2.00E-14//stress-induced receptor-like kinase [Glycine max]		Unigene44064_All//1.00E-126//TC138707			GO:0016740	nr -
Unigene44065_All	524	0.00	0.00	0.00	0.00	0.00	0.00	1.86	3.27	0.08	null	null		null	null		null	null		null	null		8.17E-01	6.98E-02		-4.61E+00	3.32E-06	Down	Unigene44065_All//gi|6094086|sp|O65353.1|RL5_HELAN//1.00E-31//RecName: Full=60S ribosomal protein L5 >gi|3153904|gb|AAC17448.1| RPL5A-related protein [Helianthus annuus]	Unigene44065_All//3.00E-22//AT3G25520| ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); 5S rRNA binding / structural constituent of ribosome		ko03010|Ribosome	GO:0019843//GO:0030529//GO:0043229//GO:0044444	nr -
Unigene44068_All	298	0.00	11.05	5.72	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	9.63E-19	Up	1.25E+01	2.20E-09	Up	null	null		null	null		null	null		null	null								
Unigene4407_All	367	2.42	7.18	6.96	6.11	3.57	2.95	2.65	2.28	1.95	1.57E+00	1.55E-04	Up	1.52E+00	4.46E-04	Up	-7.77E-01	5.80E-02		-1.05E+00	1.43E-02		-2.18E-01	7.24E-01		-4.40E-01	4.73E-01				Unigene4407_All//7.00E-154//gi|78350978|gb|DT571252.1|DT571252				
Unigene44073_All	814	0.00	6.35	2.94	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.81E-29	Up	1.15E+01	3.24E-13	Up	null	null		null	null		null	null		null	null		Unigene44073_All//gi|255085620|ref|XP_002505241.1|//6.00E-84//glycosyltransferase family 35 protein [Micromonas sp. RCC299] >gi|226520510|gb|ACO66499.1| glycosyltransferase family 35 protein [Micromonas sp. RCC299]	Unigene44073_All//2.00E-72//AT3G46970| PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups		ko00500|Starch and sucrose metabolism	GO:0005488//GO:0008152//GO:0016757	nr +
Unigene44075_All	395	0.00	0.00	0.00	0.00	0.00	0.00	4.71	20.42	16.44	null	null		null	null		null	null		null	null		2.12E+00	3.23E-22	Up	1.80E+00	4.35E-15	Up	Unigene44075_All//gi|255647586|gb|ACU24256.1|//1.00E-12//unknown [Glycine max]		Unigene44075_All//7.00E-43//gi|109858081|gb|DW487060.1|DW487060				nr +
Unigene44077_All	342	1.07	33.93	8.10	4.95	24.17	11.36	5.07	4.28	6.87	4.99E+00	7.18E-56	Up	2.92E+00	6.14E-09	Up	2.29E+00	2.62E-23	Up	1.20E+00	1.36E-04	Up	-2.45E-01	6.31E-01		4.39E-01	2.34E-01		Unigene44077_All//gi|86755972|gb|ABD15130.1|//2.00E-06//cold-acclimation protein COR413-PM1 [Chimonanthus praecox]	Unigene44077_All//3.00E-06//AT3G50830| COR413-PM2 (COLD-REGULATED 413-PLASMA MEMBRANE 2)	Unigene44077_All//2.00E-33//TC140066				nr +
Unigene44078_All	716	0.00	0.00	0.00	0.00	0.00	0.00	61.35	26.33	8.35	null	null		null	null		null	null		null	null		-1.22E+00	7.23E-54	Down	-2.88E+00	3.03E-174	Down	Unigene44078_All//gi|255081504|ref|XP_002507974.1|//2.00E-10//predicted protein [Micromonas sp. RCC299]		Unigene44078_All//4.00E-61//ES810763				nr +
Unigene44079_All	856	0.00	6.57	2.43	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	4.34E-32	Up	1.12E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene44079_All//gi|298714208|emb|CBJZ7344.1|//2.00E-09//similar to Mucin-1 precursor (MUC-1) (Polymorphic epithelial mucin) (PEM) (PEMT) (Episialin) (Tumor-associated mucin) (Carcinoma-associated mucin) (Tumor-associated epithelial membrane antigen) (EMA) [Ectocarpus siliculosus]				ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism/ko00520|Amino sugar and nucleotide sugar metabolism//ko00020|Citrate cycle (TCA cycle)		nr +
Unigene44082_All	353	0.15	0.43	0.00	2.68	0.29	0.13	1.08	1.42	1.13	1.54E+00	5.31E-01		-7.21E+00	6.22E-01		-3.20E+00	1.40E-04	Down	-4.39E+00	5.96E-05	Down	3.98E-01	6.52E-01		6.62E-02	9.66E-01								
Unigene44083_All	348	0.00	0.73	2.14	3.15	1.39	0.52	0.12	0.12	0.80	9.51E+00	7.85E-02		1.11E+01	3.27E-04	Up	-1.18E+00	5.94E-02		-2.60E+00	7.13E-04	Down	-1.67E-02	1.00E+00		2.72E+00	9.93E-02		Unigene44083_All//gi|297849064|ref|XP_002892413.1|//2.00E-06//endoplasmic reticulum-type calcium-transporting ATPase 4 [Arabidopsis lyrata subsp. lyrata] >gi|297338255|gb|EFH68672.1| endoplasmic reticulum-type calcium-transporting ATPase 4 [Arabidopsis lyrata subsp. lyrata]	Unigene44083_All//1.00E-07//AT1G07670| calcium-transporting ATPase			GO:0000041//GO:0009206//GO:0010038//GO:0019829//GO:0030005//GO:0003227//GO:0032559//GO:0070838	nr +
Unigene44084_All	355	0.00	0.43	0.00	3.79	3.59	2.29	0.36	10.83	1.68	8.74E+00	2.35E-01		null	null		-7.81E-02	8.79E-01		-7.26E-01	2.23E-01		4.92E+00	7.44E-23	Up	2.24E+00	1.67E-02		Unigene44084_All//gi|297794047|ref|XP_002864908.1|//1.00E-17//ANAC104/XND1 [Arabidopsis lyrata subsp. lyrata] >gi|297310743|gb|EFH41167.1| ANAC104/XND1 [Arabidopsis lyrata subsp. lyrata]	Unigene44084_All//5.00E-19//AT5G64530| XND1; transcription factor	Unigene44084_All//7.00E-83//TC139014	NAC		GO:0001071//GO:0003676//GO:0010087//GO:0010468//GO:0012501//GO:0048513	nr -
Unigene44085_All	791	0.00	0.13	0.20	0.00	0.13	0.91	0.00	0.00	0.30	7.00E+00	3.86E-01		7.66E+00	2.38E-01		7.03E+00	4.55E-01		9.84E+00	2.31E-04	Up	null	null		8.24E+00	4.39E-02								kegg -
Unigene44086_All	521	0.60	0.19	0.20	0.00	0.07	0.52	8.28	1.68	17.51	-1.63E+00	2.76E-01		-1.56E+00	3.30E-01		6.05E+00	8.29E-01		9.02E+00	7.02E-02		-2.30E+00	1.80E-13	Down	1.08E+00	3.91E-10	Up	Unigene44086_All//gi|115432146|gb|AB197350.1|//6.00E-13//cold-induced wall associated kinase [Ammopiptanthus mongolicus]	Unigene44086_All//1.00E-11//AT1G79670| RF01 (RESISTANCE TO FUSARIUM OXYSPORUM 1); kinase	Unigene44086_All//6.00E-47//DT462732			GO:0004674//GO:0006464//GO:0032559	nr +
Unigene44087_All	330	0.00	0.00	0.00	0.00	0.00	0.00	2.05	3.42	0.00	null	null		null	null		null	null		null	null		7.38E-01	2.09E-01		-1.10E+01	3.56E-05	Down	Unigene44087_All//gi|159483157|ref|XP_001699629.1|//2.00E-15//acidic ribosomal protein P1 [Chlamydomonas reinhardtii] >gi|266947|sp|P29763.1|RLA1_CHLRE RecName: Full=60S acidic ribosomal protein P1 >gi|18211|emb|CAA47042.1| ribosomal protein P1 [Chlamydomonas reinhardtii] >gi|158272734|gb|EDO98531.1| acidic ribosomal protein P1 [Chlamydomonas reinhardtii]			ko03010|Ribosome	GO:0005840//GO:0006412//GO:0016020//GO:0043231	nr -
Unigene44089_All	341	0.00	6.98	2.97	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.50E-13	Up	1.15E+01	1.27E-05	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene44093_All	449	0.23	0.45	0.24	1.00	0.23	0.60	2.26	0.28	0.27	9.54E-01	6.21E-01		2.52E-02	9.99E-01		-2.12E+00	7.27E-02		-7.26E-01	5.32E-01		-3.02E+00	1.08E-04	Down	-3.09E+00	5.36E-05	Down							
Unigene44096_All	422	0.00	29.54	9.72	0.00	0.00	0.00	0.00	0.00	0.00	1.49E+01	1.63E-71	Up	1.32E+01	9.64E-23	Up	null	null		null	null		null	null		null	null		Unigene44096_All//gi|81076822|gb|AB855398.1|//2.00E-23//40S ribosomal protein S10-like [Solanum tuberosum]	Unigene44096_All//2.00E-19//AT5G41520| 40S ribosomal protein S10 (RPS10B)		ko03010|Ribosome		nr +

Unigene44099_All	322	0.00	5.98	1.65	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.73E-11	Up	1.07E+01	4.03E-03		null	null		null	null		null	null		null	null		Unigene44099_All//gi|1657851|gb|AAB18205.1|//5.00E-07//cold acclimation protein WCOR518 [Triticum aestivum]							nr +
Unigene4410_All	877	73.62	70.83	82.64	68.16	57.29	31.26	1.88	2.62	1.77	-5.57E-02	4.68E-01		1.67E-01	1.26E-02		-2.51E-01	9.24E-05		-1.12E+00	7.42E-57	Down	4.79E-01	2.23E-01		-8.58E-02	8.50E-01		Unigene4410_All//gi|224131668|ref|XP_002321148.1|//1.00E-133//nitrate transporter, H+/oligopeptide symporter POT family [Populus trichocarpa] >gi|222861921|gb|EEE99463.1| nitrate transporter, H+/oligopeptide symporter POT family [Populus trichocarpa]	Unigene4410_All//1.00E-103//AT3G21670| nitrate transporter (NTP3)	Unigene4410_All//0.00E+00//gi|78337050|gb|DT557324.1|DT557324				nr -
Unigene44100_All	272	2.50	1.49	0.00	2.38	1.27	1.00	0.78	0.61	0.15	-7.47E-01	3.80E-01		-1.13E+01	7.63E-04	Down	-9.11E-01	3.04E-01		-1.26E+00	1.83E-01		-3.39E-01	8.11E-01		-2.41E+00	1.95E-01				Unigene44100_All//6.00E-64//DT468324				
Unigene44104_All	490	0.21	0.83	0.54	0.51	2.53	1.75	0.52	0.51	0.89	1.95E+00	1.44E-01		1.35E+00	4.09E-01		2.32E+00	7.36E-04	Up	1.78E+00	3.19E-02		-1.65E-02	1.02E+00		7.89E-01	4.23E-01									ESTscan +
Unigene4411_All	943	17.14	21.06	7.00	32.96	35.20	67.05	173.11	129.78	229.82	2.97E-01	1.93E-02		-1.29E+00	2.10E-17	Down	9.48E-02	4.04E-01		1.02E+00	4.41E-51	Up	-4.16E-01	4.91E-31		4.09E-01	1.12E-40		Unigene4411_All//gi|281485191|gb|ADA70361.1|//1.00E-114//actin [Persea americana]	Unigene4411_All//5.00E-113//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene4411_All//0.00E+00//TC140485		ko04145|Phagosome		nr -
Unigene44111_All	741	0.00	0.00	0.00	0.00	0.00	0.00	1.88	2.48	0.00	null	null		null	null		null	null		null	null		3.98E-01	3.89E-01		-1.09E+01	2.40E-10	Down	Unigene44111_All//gi|301105319|ref|XP_002901743.1|//7.00E-92//elongation factor 2 [Phytophthora infestans T30-4] >gi|262099081|gb|EEY57133.1| elongation factor 2 [Phytophthora infestans T30-4]	Unigene44111_All//7.00E-78//AT3G12915| GTP binding / GTPase				GO:0008135//GO:0017111//GO:0032561	nr +
Unigene44112_All	786	0.00	0.00	0.00	0.00	0.00	0.00	0.38	3.72	2.69	null	null		null	null		null	null		null	null		3.31E+00	2.31E-13	Up	2.83E+00	8.98E-09	Up	Unigene44112_All//gi|15226598|ref|NP_179755.1|//4.00E-93//pectinesterase family protein [Arabidopsis thaliana] >gi|75206124|sp|Q9SIJ9.1|PME11_ARATH RecName: Full=Putative pectinesterase 11; Short=PE 11; AltName: Full=Pectin methylesterase 11; Short=AtPME11	Unigene44112_All//2.00E-94//AT2G21610| pectinesterase family protein	Unigene44112_All//7.00E-23//TC179074	ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		GO:0004091//GO:0005618//GO:0044424	nr -
Unigene44114_All	482	0.00	0.00	0.44	0.31	0.29	0.37	3.33	3.47	0.83	null	null		8.79E+00	1.41E-01		-1.17E-01	9.10E-01		2.74E-01	9.04E-01		5.74E-02	9.15E-01		-2.01E+00	5.95E-05	Down	Unigene44114_All//gi|29119653|emb|CAD79350.1|//1.00E-23//LRR receptor-like kinase 2 [Arabidopsis thaliana]	Unigene44114_All//7.00E-25//AT3G24240| leucine-rich repeat transmembrane protein kinase, putative	Unigene44114_All//0.00E+00//DT464025	ko04626|Plant-pathogen interaction	GO:0016301		nr +
Unigene44116_All	364	0.00	3.76	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.80E-08	Up	1.00E+01	2.50E-02		null	null		null	null		null	null		null	null		Unigene44116_All//sp|P35579|MYH9_HUMAN//3.00E-14//Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4							swissprot +
Unigene44118_All	453	0.00	0.00	0.00	0.00	0.00	3.83	6.00	0.18	null	null	null		null	null		null	null		null	null		6.48E-01	5.90E-02		-4.44E+00	1.94E-10	Down								
Unigene44119_All	749	0.00	5.89	2.99	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	4.10E-25	Up	1.15E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene44119_All//gi|42569129|ref|NP_179444.2|//6.00E-22//cupin family protein [Arabidopsis thaliana]	Unigene44119_All//4.00E-11//AT4G11420| EIF3A (EUKARYOTIC TRANSLATION INITIATION FACTOR 3A); translation initiation factor					nr -
Unigene44122_All	716	0.73	0.21	0.67	0.49	1.64	0.00	3.48	1.23	0.22	-1.78E+00	1.08E-01		-1.27E-01	8.98E-01		1.75E+00	8.89E-03		-8.93E+00	2.12E-02		-1.51E+00	6.17E-05	Down	-3.97E+00	9.21E-14	Down			Unigene44122_All//3.00E-80//ES825531				
Unigene44125_All	281	61.82	69.78	46.05	163.80	115.68	196.89	345.31	922.78	561.71	1.75E-01	1.98E-01		-4.25E-01	2.23E-03		-5.02E-01	1.75E-12		2.65E-01	1.58E-04		1.42E+00	0.00E+00	Up	7.02E-01	5.86E-78		Unigene44125_All//6.00E-46//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene44125_All//1.00E-157//gi|13353009|gb|BG443357.1|BG443357		ko00190|Oxidative phosphorylation	GO:0006570//GO:0006818//GO:0015405//GO:0016462//GO:0016628//GO:0031410	nr -
Unigene44126_All	657	0.00	0.00	0.00	0.00	0.00	0.00	0.51	1.34	2.00	null	null		null	null		null	null		null	null		1.38E+00	4.62E-02		1.96E+00	5.04E-04	Up			Unigene44126_All//5.00E-14//FL577415				
Unigene44127_All	308	0.00	0.49	0.35	0.00	0.00	0.00	8.37	24.83	65.32	8.95E+00	2.35E-01		8.43E+00	3.97E-01		null	null		null	null		1.57E+00	2.81E-14	Up	2.96E+00	3.54E-81	Up			Unigene44127_All//1.00E-124//TC144528				
Unigene4413_All	1688	0.40	2.55	0.63	5.11	1.88	2.30	2.68	5.82	3.42	2.66E+00	6.95E-13	Up	6.47E-01	3.62E-01		-1.44E+00	3.71E-14	Down	-1.15E+00	5.57E-09	Down	1.12E+00	4.14E-11	Up	3.53E-01	1.09E-01		Unigene4413_All//gi|15235990|ref|NP_196682.1|//8.00E-14//VQ motif-containing protein [Arabidopsis thaliana] >gi|40823004|gb|AAR92252.1| At4g39720 [Arabidopsis thaliana] >gi|45752688|gb|AAS76242.1| At4g39720 [Arabidopsis thaliana]		Unigene4413_All//0.00E+00//TC170163				nr +
Unigene44130_All	427	1.23	0.59	4.36	0.35	0.32	0.00	0.00	0.00	0.00	-1.05E+00	3.11E-01		1.83E+00	6.91E-04	Up	-1.18E-01	9.10E-01		-8.45E+00	2.33E-01		null	null		null	null									
Unigene44133_All	501	0.31	0.20	0.43	17.80	19.80	5.59	0.25	0.67	0.56	-6.31E-01	7.27E-01		4.40E-01	7.75E-01		1.53E-01	4.82E-01		-1.67E+00	6.63E-16	Down	1.40E+00	2.76E-01		1.14E+00	3.99E-01				Unigene44133_All//4.00E-17//TC153539				
Unigene44134_All	597	0.00	0.00	0.00	0.00	0.00	0.00	1.56	1.61	0.00	null	null		null	null		null	null		null	null		4.75E-02	9.64E-01		-1.06E+01	5.47E-07	Down								ESTscan -
Unigene44137_All	359	0.00	0.00	0.00	0.00	0.00	0.00	2.12	0.23	4.11	null	null		null	null		null	null		null	null		-3.19E+00	7.92E-04	Down	9.54E-01	4.41E-02		Unigene44137_All//gi|224123518|ref|XP_002319099.1|//1.00E-36//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222857475|gb|EEE95022.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene44137_All//3.00E-15//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene44137_All//5.00E-56//CO091061	AP2-EREBP		GO:0000160//GO:0000171//GO:0003676//GO:0006351//GO:0006950//GO:0010468//GO:0023033//GO:0030528//GO:0043231	nr -
Unigene44138_All	451	0.12	0.90	0.00	0.00	0.00	0.00	0.75	0.74	2.92	2.95E+00	5.91E-02		-6.86E+00	6.22E-01		null	null		null	null		-1.66E-02	1.02E+00		1.96E+00	5.04E-04	Up								
Unigene44141_All	677	0.08	0.67	0.47	0.74	0.71	0.07	0.31	0.74	1.65	3.12E+00	3.58E-02		2.61E+00	1.46E-01		-4.72E-02	9.49E-01		-3.46E+00	1.61E-02		1.25E+00	2.04E-01		2.40E+00	2.76E-04	Up			Unigene44141_All//2.00E-20//CO097337				
Unigene44144_All	351	0.00	0.00	0.00	3.55	1.77	0.39	0.12	0.24	0.00	null	null		null	null		-1.01E+00	8.39E-02		-3.20E+00	3.61E-05	Down	9.83E-01	7.31E-01		-6.91E+00	6.12E-01								
Unigene4415_All	1271	9.76	6.26	7.67	9.05	12.49	11.02	14.67	8.12	7.33	-6.40E-01	6.32E-05		-3.48E-01	4.39E-02		4.64E-01	4.78E-04		2.83E-01	7.42E-02		-8.53E-01	2.63E-13		-1.00E+00	1.16E-17	Down	Unigene4415_All//gi|225428904|ref|XP_002285375.1|//8.00E-77//PREDICTED: similar to reticulon family protein (RTNLB11) [Vitis vinifera]	Unigene4415_All//1.00E-45//AT3G19460| reticulon family protein (RTNLB11)	Unigene4415_All//0.00E+00//TC147808				nr +
Unigene44158_All	353	2.08	0.00	1.51	2.68	1.46	0.26	1.32	0.83	0.79	-1.10E+01	2.11E-04	Down	-4.60E-01	6.02E-01		-8.74E-01	2.10E-01		-3.39E+00	3.17E-04	Down	-6.69E-01	5.08E-01		-7.38E-01	4.26E-01								
Unigene44159_All	730	0.29	0.69	0.07	0.48	1.23	2.23	0.35	1.26	15.34	1.28E+00	2.31E-01		-1.98E+00	3.81E-01		1.36E+00	8.05E-02		2.22E+00	1.55E-04	Up	1.86E+00	8.33E-03		5.46E+00	2.33E-70	Up	Unigene44159_All//gi|225428015|ref|XP_002278452.1|//2.00E-88//PREDICTED: similar to KAK (KAKTUS) isoform 2 [Vitis vinifera]	Unigene44159_All//6.00E-80//AT4G38600| KAK (KAKTUS); ubiquitin-protein ligase	Unigene44159_All//9.00E-121//TC163055		ko04120|Ubiquitin mediated proteolysis	GO:0000904//GO:0006261//GO:0016020//GO:0016879//GO:0043412	nr -
Unigene4416_All	3052	4.94	1.74	0.72	9.76	10.54	10.51	15.10	7.34	7.13	-1.50E+00	3.73E-21	Down	-2.79E+00	2.16E-44	Down	1.11E-01	3.20E-01		1.06E-01	3.59E-01		-1.04E+00	7.25E-44	Down	-1.08E+00	3.96E-48	Down	Unigene4416_All//gi|224140989|ref|XP_002323859.1|//0.00E+00//condens in complex components subunit [Populus trichocarpa] >gi|222866861|gb|EEF03992.1| condensin complex components subunit [Populus trichocarpa]	Unigene4416_All//0.00E+00//AT5G48600| ATSMC3 (ARABIDOPSIS THALIANA STRUCTURAL MAINTENANCE OF CHROMOSOME 3); ATP binding / transporter	Unigene4416_All//0.00E+00//TC161336				nr +
Unigene44162_All	411	128.70	365.78	154.18	257.56	188.68	227.36	777.30	1351.80	835.25	1.51E+00	4.51E-205	Up	2.61E-01	1.54E-04		-4.49E-01	5.38E-23		-1.80E-01	3.50E-04		7.98E-01	0.00E+00		1.04E-01	1.99E-05		Unigene44162_All//gi|91992506|gb|AB672969.1|//6.00E-38//ATPase [Camellia sinensis]	Unigene44162_All//2.00E-16//ATMG01080| subunit 9 of mitochondrial F0-ATPase	Unigene44162_All//0.00E+00//gi|13246285|gb|BE053392.2|BE053392		ko00190|Oxidative phosphorylation	GO:0003676//GO:0005740//GO:0006260//GO:0006754//GO:0006818//GO:0015078//GO:0031224//GO:0031410//GO:0032559//GO:0033177//GO:0034061	nr -
Unigene44165_All	306	0.00	4.80	0.00	0.49	1.69	0.30	0.41	0.27	0.26	1.22E+01	2.11E-08	Up	null	null		1.79E+00	1.26E-01		-7.26E-01	7.15E-01		-6.01E-01	7.66E-01		-6.71E-01	7.19E-01				Unigene44165_All//2.00E-08//TC162967				
Unigene44166_All	344	0.00	1.33	0.00	4.63	1.30	0.53	0.00	0.00	0.00	1.04E+01	7.43E-03		null	null		-1.83E+00	4.08E-04	Down	-3.14E+00	2.23E-06	Down	null	null		null	null				Unigene44166_All//8.00E-132//TC153320				
Unigene44168_All	292	0.00	15.96	9.48	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	1.46E-26	Up	1.32E+01	2.75E-15	Up	null	null		null	null		null	null		null	null		Unigene44168_All//gi|11465771|ref|NP_053915.1|//9.00E-10//ribosomal protein S17 [Porphyra purpurea] >gi|1710696|sp|P51305.1|RS17_PORPU RecName: Full=30S ribosomal protein S17, chloroplastic >gi|1276771|gb|AAC08191.1| 30S ribosomal protein S17 [Porphyra purpurea]	Unigene44168_All//7.00E-10//AT1G49400| emb1129 (embryo defective 1129); structural constituent of ribosome		ko03010|Ribosome	GO:0010467//GO:0030529//GO:0043229//GO:0044444	nr +
Unigene44169_All	332	0.00	8.70	3.37	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	1.97E-16	Up	1.17E+01	3.43E-06	Up	null	null		null	null		null	null		null	null		Unigene44169_All//gi|159462944|ref|XP_001689702.1|//8.00E-35//aconitate hydratase [Chlamydomonas reinhardtii] >gi|158283690|gb|EDP09440.1| aconitate hydratase [Chlamydomonas reinhardtii]			ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0000166//GO:0004448//GO:0009060//GO:0016836//GO:0043231//GO:0046872//GO:0051536	nr -
Unigene4417_All	1656	2.31	15.70	1.83	5.23	3.74	6.90	12.87	27.66	13.88	2.77E+00	5.29E-78	Up	-3.32E-01	3.38E-01		-4.84E-01	9.76E-03		3.99E-01	1.98E-02		1.10E+00	7.15E-48	Up	1.09E-01	3.43E-01		Unigene4417_All//gi|259121427|gb|ACY92033.1|//2.00E-94//WRKY transcription factor 31 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene4417_All//6.00E-52//AT5G48520| WRKY48; transcription factor	Unigene4417_All//0.00E+00//TC144070	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene44173_All	290	0.00	0.00	0.00	0.00	0.00	0.00	2.48	1.15	0.00	null	null		null	null		null	null		null	null		-1.10E+00	1.49E-01		-1.13E+01	1.78E-05	Down	Unigene44173_All//gi|15242434|ref|NP_196512.1|//5.00E-23//40S ribosomal protein S15 (RPS15C) [Arabidopsis thaliana] >gi|297811045|ref|XP_002873406.1| 40S ribosomal protein S15 [Arabidopsis lyrata subsp. lyrata] >gi|27923839|sp|Q9FY65.1|RS153_ARATH RecName: Full=40S ribosomal protein S15-3 >gi|9955537|emb|CAC05476.1| ribosomal protein S15-like [Arabidopsis thaliana] >gi|33589676|gb|AAQ22604.1| At5g09500 [Arabidopsis thaliana] >gi|110735784|dbj|BAE99869.1| ribosomal protein S15-like [Arabidopsis thaliana] >gi|297319243|gb|EFH49665.1| 40S ribosomal protein S15 [Arabidopsis lyrata subsp. lyrata]	Unigene44173_All//1.00E-16//AT5G09500| 40S ribosomal protein S15 (RPS15C)		ko03010|Ribosome	GO:0010467//GO:0015935	nr -
Unigene44176_All	202	0.00	0.00	0.00	0.00	0.00	0.00	36.00	43.86	0.20	null	null		null	null		null	null		null	null		2.85E-01	1.22E-01		-7.51E+00	1.42E-51	Down			Unigene44176_All//9.00E-10//TC148521				ESTscan -
Unigene44179_All	323	0.00	0.00	0.00	0.00	0.00	0.00	2.88	2.46	39.96	null	null		null	null		null	null		null	null		-2.28E-01	7.18E-01		3.79E+00	3.98E-65	Up			Unigene44179_All//3.00E-100//DT462103				
Unigene4418_All	301	4.17	5.72	4.25	7.61	8.81	10.50	7.73	21.11	36.13	4.56E-01	3.78E-01		2.54E-02	9.86E-01		2.11E-01	6.21E-01		4.64E-01	2.14E-01		1.45E+00	9.06E-11	Up	2.23E+00	2.97E-32	Up			Unigene4418_All//9.00E-122//gi|18098602|gb|BM357856.1|BM357856				
Unigene44180_All	388	0.94	0.26	0.27	1.03	2.57	1.63	5.78	3.66	2.26	-1.85E+00	1.87E-01		-1.78E+00	2.34E-01		1.33E+00	6.66E-02		6.66E-01	4.92E-01		-6.57E-01	8.79E-02		-1.35E+00	3.87E-04	Down	Unigene44180_All//gi|115466360|ref|NP_001056779.1|//2.00E-60//Os06g0143900 [Oryza sativa Japonica Group] >gi|75109943|sp|Q5VQ78.1|COB21_ORYSJ RecName: Full=Coatomer subunit beta'-1; AltName: Full=Beta'-coat protein 1; Short=Beta'-COP 1 >gi|113594819|dbj|BAF18693.1| Os06g0143900 [Oryza sativa Japonica Group]	Unigene44180_All//6.00E-61//AT1G79990| LOCATED IN: endomembrane system, COPI vesicle coat, Golgi membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SYS1 homologue (InterPro:IPR016973); Has 55556 Blast hits to 24059 proteins in 620 species: Archae - 38; Bacteria - 5697; Metazoa - 25539; Fungi - 10898; Plants - 5309; Viruses - 0; Other Eukaryotes - 8075 (source: NCBI BLink).	Unigene44180_All//7.00E-114//TC178243			GO:0004683//GO:0005488//GO:0015031//GO:0030120	nr +
Unigene44186_All	357	0.00	0.28	0.90	0.70	0.87	0.89	0.00	1.52	1.67	8.15E+00	3.86E-01		9.81E+00	4.51E-02		3.15E-01	8.38E-01		3.44E-01	7.96E-01		1.06E+01	5.36E-04	Up	1.07E+01	1.75E-04	Up	Unigene44186_All//gi|297805090|ref|XP_002870429.1|//2.00E-53//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316265|gb|EFH46688.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44186_All//3.00E-53//AT2G24370| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene44186_All//2.00E-21//gi|193217955|gb|EY197162.1|EY197162		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism	GO:0004713//GO:0006464//GO:0032559//GO:0050896	nr -

Unigene44191_All	270	1.55	0.75	0.39	0.37	0.00	0.84	2.04	1.08	0.00	-1.05E+00	3.66E-01		-1.97E+00	1.51E-01		-8.53E+00	3.12E-01		1.18E+00	5.49E-01		-9.10E-01	3.19E-01		-1.10E+01	2.80E-04	Down		Unigene44191_All//1.00E-05//AT2G35750| unknown protein	Unigene44191_All//2.00E-110//DW517015				
Unigene44192_All	489	0.00	0.00	0.00	0.00	0.00	0.00	2.08	2.39	0.00	null	null		null	null		null	null		null	null		2.06E-01	7.23E-01		-1.10E+01	1.35E-07	Down	Unigene44192_All//gi|159465507|ref|XP_001690964.1|//8.00E-49//E3 ubiquitin ligase [Chlamydomonas reinhardtii] >gi|158279650|gb|EDP05410.1| E3 ubiquitin ligase [Chlamydomonas reinhardtii]	Unigene44192_All//3.00E-46//AT1G75950| SKP1 (S PHASE KINASE-ASSOCIATED PROTEIN 1); protein binding / ubiquitin-protein ligase	Unigene44192_All//2.00E-12//TC174480		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0003824//GO:0005488//GO:0019941	nr -
Unigene44195_All	441	0.47	0.69	0.36	2.82	1.72	0.51	0.19	0.95	0.18	5.39E-01	6.71E-01		-3.90E-01	8.07E-01		-7.17E-01	2.26E-01		-2.46E+00	4.15E-04	Down	2.31E-00	5.99E-02		-8.53E-02	9.71E-01									
Unigene44196_All	335	0.00	0.00	0.00	1.04	0.62	0.00	4.42	1.75	0.36	null	null		null	null		-7.55E-01	5.67E-01		-1.00E+01	2.12E-02		-1.34E+00	7.48E-03		-3.63E+00	6.55E-08	Down								
Unigene44199_All	368	0.00	2.75	1.30	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	7.25E-06	Up	1.03E+01	7.47E-03		null	null		null	null		null	null		null	null		Unigene44199_All//gi|464595|sp|Q02980.1|RBS_MALSP//3.00E-58//RecName: Full=Ribulose bisphosphate carboxylase small chain, chloroplastic; Short=RuBisCO small subunit; Flags: Precursor >gi|19581|emb|CAA46475.1| ribulose bisphosphate carboxylase [Malus sp.]	Unigene44199_All//2.00E-57//AT1G67090| RBCS1A (RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A); copper ion binding / ribulose-bisphosphate carboxylase	Unigene44199_All//1.00E-31//EX169366		ko00710|Carbon fixation in photosynthetic organisms//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005576//GO:0005840//GO:0006950//GO:0009526//GO:0009532//GO:0009534//GO:0009639//GO:0015977//GO:0016491//GO:0016831//GO:0030312//GO:0043094//GO:0044436//GO:0046914	nr -
Unigene4420_All	717	29.04	23.67	24.14	34.04	30.64	34.39	14.80	12.47	7.39	-2.95E-01	1.67E-02		-2.67E-01	4.13E-02		-1.52E-01	2.16E-01		1.47E-02	9.31E-01		-2.47E-01	1.41E-01		-1.00E+00	1.81E-10	Down			Unigene4420_All//0.00E+00//TC168318				
Unigene44200_All	422	1.36	2.04	1.89	1.77	1.22	0.11	0.20	0.00	0.28	5.82E-01	4.27E-01		4.73E-01	5.65E-01		-5.33E-01	5.26E-01		-4.05E+00	7.75E-04	Down	-7.65E+00	4.03E-01		4.99E-01	8.07E-01									
Unigene44203_All	413	0.00	5.64	3.48	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.91E-13	Up	1.18E+01	6.30E-08	Up	null	null		null	null		null	null		null	null		Unigene44203_All//sp|P22736|NR4A1_HUMAN//3.00E-22//Nuclear receptor subfamily 4 group A member 1 OS=Homo sapiens GN=NR4A1 PE=1 SV=1						swissprot +
Unigene44205_All	303	0.00	0.00	0.00	0.00	0.00	0.00	3.77	9.10	0.00	null	null		null	null		null	null		null	null		1.27E+00	2.43E-04	Up	-1.19E+01	1.64E-08	Down								
Unigene44206_All	600	0.00	8.36	1.07	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.34E-28	Up	1.01E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene44206_All//gi|255593650|ref|XP_002535920.1|//5.00E-09//alpha-amylase, putative [Ricinus communis] >gi|223521525|gb|EEF26463.1| alpha-amylase, putative [Ricinus communis]						nr -
Unigene4421_All	471	2.44	2.37	4.41	2.43	2.19	2.01	3.14	2.84	0.93	-4.63E-02	9.53E-01		8.51E-01	6.95E-02		-1.49E-01	8.32E-01		-2.73E-01	6.89E-01		-1.46E-01	7.67E-01		-1.76E+00	5.33E-04	Down			Unigene4421_All//2.00E-87//TC168318				
Unigene44210_All	388	0.27	0.13	0.00	1.03	1.15	0.35	4.03	1.51	0.72	-1.05E+00	6.84E-01		-8.08E+00	3.92E-01		1.68E-01	9.04E-01		-1.56E+00	2.31E-01		-1.42E+00	3.64E-03		-2.49E+00	5.08E-06	Down								
Unigene44212_All	320	0.65	0.32	0.00	0.00	2.04	0.71	2.51	0.00	0.62	-1.05E+00	5.64E-01		-9.35E+00	1.45E-01		1.10E+01	4.92E-04	Up	9.46E+00	1.19E-01		-1.13E+01	8.57E-06	Down	-2.01E+00	7.11E-03		Unigene44212_All//gi|224056467|ref|XP_002298871.1|//2.00E-14//predicted protein [Populus trichocarpa] >gi|222846129|gb|EEE83676.1| predicted protein [Populus trichocarpa]	Unigene44212_All//2.00E-13//AT5G55820| unknown protein					nr -
Unigene44213_All	413	0.13	0.98	0.39	0.84	0.25	0.22	0.61	2.33	3.18	2.95E+00	5.91E-02		1.61E+00	5.11E-01		-1.76E+00	1.90E-01		-1.95E+00	1.96E-01		1.92E+00	5.42E-03		2.37E+00	7.20E-05	Up			Unigene44213_All//4.00E-26//TC136315				
Unigene44216_All	258	0.00	6.87	3.92	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	4.14E-10	Up	1.19E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene44216_All//gi|164605523|dbj|BAF98589.1|//4.00E-12//GM0216.550.nc [Lotus japonicus]	Unigene44216_All//4.00E-13//AT1G73230| nascent polypeptide-associated complex (NAC) domain-containing protein				GO:0006970	nr +
Unigene44218_All	631	0.00	0.00	0.00	0.00	0.00	0.00	2.68	1.59	0.00	null	null		null	null		null	null		null	null		-7.54E-01	9.64E-02		-1.14E+01	1.70E-12	Down	Unigene44218_All//gi|301091801|ref|XP_002896076.1|//6.00E-39//ras protein let-60 [Phytophthora infestans T30-4] >gi|301118482|ref|XP_002906969.1| ras protein let-60 [Phytophthora infestans T30-4] >gi|262094999|gb|EEY53051.1| ras protein let-60 [Phytophthora infestans T30-4] >gi|262108318|gb|EEY66370.1| ras protein let-60 [Phytophthora infestans T30-4]	Unigene44218_All//2.00E-17//AT4G35860| ATGB2 (GTP-BINDING 2); GTP binding				GO:0006810//GO:0009536//GO:0017111//GO:0031410//GO:0032561//GO:0035556	nr -
Unigene44219_All	275	0.00	0.00	0.00	0.00	0.25	0.66	1.23	5.47	7.68	null	null		null	null		7.97E+00	6.08E-01		9.36E+00	1.94E-01		2.15E+00	8.23E-05	Up	2.64E+00	3.33E-08	Up			Unigene44219_All//5.00E-49//TC177917				
Unigene4422_All	747	33.76	15.13	21.03	40.75	36.23	39.60	79.86	30.21	32.53	-1.16E+00	1.25E-23	Down	-6.83E-01	1.10E-09		-1.69E-01	1.04E-01		-4.11E-02	7.23E-01		-1.40E+00	3.65E-90	Down	-1.30E+00	3.06E-82	Down	Unigene4422_All//gi|5706704|gb|AAD47346.1|AF112440_1//1.00E-63//ribosomal protein S26 [Pisum sativum]	Unigene4422_All//0.00E+00//gi|109881770|gb|DW510740.1|DW510740	Unigene4422_All//0.00E+00//gi|109881770|gb|DW510740.1|DW510740		ko03010|Ribosome		nr -
Unigene44222_All	584	0.00	19.26	4.01	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	1.70E-64	Up	1.20E+01	6.41E-13	Up	null	null		null	null		null	null		null	null		Unigene44222_All//gi|156554296|ref|XP_001602465.1|//8.00E-72//PREDICTED: similar to S14e ribosomal protein [Nasonia vitripennis]	Unigene44222_All//2.00E-43//AT2G36160| 40S ribosomal protein S14 (RPS14A)	Unigene44222_All//4.00E-08//CD485874		ko03010|Ribosome		nr +
Unigene44223_All	587	0.00	0.00	0.00	0.00	0.00	0.00	2.95	0.57	2.31	null	null		null	null		null	null		null	null		-2.37E+00	4.93E-06	Down	-3.56E-01	4.17E-01		Unigene44223_All//gi|301120388|ref|XP_002907921.1|//2.00E-23//polyadenylate-binding protein 1-B [Phytophthora infestans T30-4] >gi|262102952|gb|EEY61004.1| polyadenylate-binding protein 1-B [Phytophthora infestans T30-4]	Unigene44223_All//4.00E-07//AT1G49760| PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor					nr +
Unigene44225_All	252	0.00	3.02	2.54	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	1.13E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene44225_All//gi|194476545|ref|XP_002048724.1|//5.00E-14//DNA binding protein HU [Paulinella chromatophora] >gi|171191552|gb|ACB42514.1| DNA binding protein HU [Paulinella chromatophora]						nr -
Unigene44226_All	1352	3.21	2.92	3.66	3.68	3.01	3.51	1.06	1.36	2.45	-1.36E-01	6.36E-01		1.90E-01	5.33E-01		-2.94E-01	3.12E-01		-7.10E-02	8.08E-01		3.55E-01	4.30E-01		1.20E+00	7.74E-05	Up	Unigene44226_All//gi|15228596|ref|NP_187013.1|//4.00E-77//CS26; cysteine synthase [Arabidopsis thaliana] >gi|11131558|sp|O22682.1|CYSK4_ARATH RecName: Full=Probable cysteine synthase, chloroplastic; Short=CSase; AltName: Full=O-acetylserine sulfhydrylase; AltName: Full=O-acetylserine (thiol)-lyase; Short=OAS-TL; AltName: Full=CS26; Flags: Precursor >gi|6091759|gb|AAF03469.1|AC009327_8 O-acetylserine (thiol) lyase [Arabidopsis thaliana] >gi|2281780|dbj|BAA21628.1| O-acetylserine (thiol) lyase [Arabidopsis thaliana] >gi|20466215|gb|AAM20425.1| O-acetylserine (thiol) lyase [Arabidopsis thaliana] >gi|25084065|gb|AAN72166.1| O-acetylserine (thiol) lyase [Arabidopsis thaliana]	Unigene44226_All//1.00E-69//AT3G03630| CS26; cysteine synthase	Unigene44226_All//4.00E-155//C0117114		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr +
Unigene44227_All	504	0.00	3.42	1.69	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.99E-10	Up	1.07E+01	9.02E-05	Up	null	null		null	null		null	null		null	null		Unigene44227_All//gi|224552425|gb|ACN54549.1|//1.00E-19//mother of FT and TFL1-like protein [Selaginella erythropus]	Unigene44227_All//2.00E-16//AT2G27550| ATC (ARABIDOPSIS THALIANA CENTRORADIALIS); phosphatidylethanolamine binding					nr -
Unigene44229_All	1067	0.00	0.00	0.00	0.00	0.00	0.00	1.31	3.09	0.07	null	null		null	null		null	null		null	null		1.24E+00	6.89E-05	Up	-4.13E+00	3.70E-08	Down								ESTscan -
Unigene4423_All	299	0.00	1.02	0.00	0.50	1.50	4.38	1.41	2.52	0.13	9.99E+00	4.42E-02		null	null		1.58E+00	2.17E-01		3.13E+00	3.90E-05	Up	8.31E-01	2.64E-01		-3.41E+00	1.24E-02		Unigene4423_All//gi|255545450|ref|XP_002513785.1|//3.00E-12//zinc finger protein, putative [Ricinus communis] >gi|223546871|gb|EEF48368.1| zinc finger protein, putative [Ricinus communis]						nr -
Unigene44231_All	226	8.57	0.90	2.59	22.70	15.69	6.39	2.99	1.48	0.88	-3.26E+00	2.09E-07	Down	-1.72E+00	9.79E-04	Down	-5.33E-01	3.72E-02		-1.83E+00	1.45E-10	Down	-1.02E+00	2.04E-01		-1.76E+00	2.80E-02				Unigene44231_All//2.00E-66//CO089888				
Unigene4424_All	1401	1.79	1.63	1.10	3.66	6.00	5.51	2.66	2.77	7.11	-1.39E-01	7.21E-01		-7.02E-01	9.42E-02		7.12E-01	1.71E-04		5.90E-01	4.64E-03		6.31E-02	8.36E-01		1.42E+00	2.34E-16	Up	Unigene4424_All//gi|297846702|ref|XP_002891232.1|//6.00E-70//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337074|gb|EFH67491.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4424_All//1.00E-65//AT1G60360| zinc finger (C3HC4-type RING finger) family protein	Unigene4424_All//4.00E-29//DT465859				nr -
Unigene44240_All	549	0.00	5.63	4.27	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.38E-17	Up	1.21E+01	6.41E-13	Up	null	null		null	null		null	null		null	null		Unigene44240_All//gi|116056635|emb|CAL52924.1|//1.00E-24//CCCH-type Zn-finger protein (ISS) [Ostreococcus tauri]	Unigene44240_All//5.00E-18//AT1G66810| zinc finger (CCCH-type) family protein		C3H			nr +
Unigene44242_All	239	0.00	13.36	4.23	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	3.64E-18	Up	1.20E+01	1.27E-05	Up	null	null		null	null		null	null		null	null										
Unigene44243_All	403	2.34	0.25	1.98	0.62	0.51	0.00	3.67	1.76	0.30	-3.22E+00	6.76E-04	Down	-2.38E-01	7.23E-01		-2.70E-01	8.23E-01		-9.27E+00	7.33E-02		-1.06E+00	3.15E-02		-3.63E+00	6.55E-08	Down	Unigene44243_All//gi|24461866|gb|AAN62353.1|AF506028_20//9.00E-07//NBS-LRR type disease resistance protein [Citrus trifoliata]						nr -
Unigene44248_All	360	0.00	0.00	0.15	1.38	0.29	0.63	3.76	0.58	0.22	null	null		7.21E+00	6.35E-01		-2.27E+00	4.22E-02		-1.14E+00	3.07E-01		-2.69E+00	1.77E-05	Down	-4.09E+00	7.07E-08	Down			Unigene44248_All//4.00E-07//gi|13248059|gb|BF273904.2|BF273904				
Unigene4425_All	667	8.94	100.88	47.66	14.26	20.34	26.68	5.32	7.83	27.53	3.50E+00	1.42E-252	Up	2.41E+00	6.95E-80	Up	5.12E-01	4.06E-04		9.03E-01	4.36E-12		5.57E-01	1.78E-02		2.37E+00	3.77E-58	Up	Unigene4425_All//gi|105829424|gb|AB74693.1|//1.00E-27//At1g52855 [Arabidopsis thaliana]	Unigene4425_All//7.00E-29//AT1G52855| unknown protein	Unigene4425_All//0.00E+00//BG446184				nr +
Unigene44250_All	334	0.16	0.00	2.87	0.60	1.65	0.54	0.00	0.00	0.00	-7.29E+00	6.11E-01		4.20E+00	2.16E-04	Up	1.47E+00	1.77E-01		-1.41E-01	9.34E-01		null	null		null	null		Unigene44250_All//CO617022//7.00E-15//Phosphate starvation-inducible protein PhoH, predicted ATPase						cog +
Unigene44251_All	502	0.00	35.02	16.55	0.00	0.00	0.00	0.00	0.00	0.00	1.51E+01	4.38E-101	Up	1.40E+01	1.64E-46	Up	null	null		null	null		null	null		null	null										
Unigene44252_All	530	0.00	13.10	2.91	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.15E-39	Up	1.15E+01	1.65E-08	Up	null	null		null	null		null	null		null	null										
Unigene44253_All	292	0.00	0.00	0.00	0.00	0.00	0.00	0.72	17.75	11.46	null	null		null	null		null	null		null	null		4.62E+00	1.26E-29	Up	3.98E+00	6.32E-18	Up								
Unigene44254_All	621	0.00	0.00	0.00	0.00	0.00	0.00	1.77	2.15	0.00	null	null		null	null		null	null		null	null		2.83E-01	6.34E-01		-1.08E+01	3.33E-08	Down	Unigene44254_All//gi|224118402|ref|XP_002331473.1|//3.00E-30//ABC transporter family protein [Populus trichocarpa] >gi|222873351|gb|EEF10682.1| ABC transporter family protein [Populus trichocarpa]	Unigene44254_All//9.00E-26//AT5G60790| ATGCN1; transporter					nr -
Unigene44255_All	469	0.00	38.57	15.44	0.21	0.00	0.00	0.00	0.00	0.00	1.52E+01	5.13E-104	Up	1.39E+01	1.78E-40	Up	-7.73E+00	3.12E-01		-7.73E+00	3.99E-01		null	null		null	null		Unigene44255_All//gi|115471123|ref|NP_001059160.1|//2.00E-55//Os07g0208000 [Oryza sativa Japonica Group] >gi|28411802|dbj|BAC57277.1| ribosomal protein S15 [Oryza sativa Japonica Group] >gi|113610696|dbj|BAF21074.1| Os07g0208000 [Oryza sativa Japonica Group]	Unigene44255_All//6.00E-56//AT5G59850| 40S ribosomal protein S15A (RPS15aF)			ko03010|Ribosome		nr +

Unigene44256_All	228	8.49	7.56	5.37	13.98	6.65	8.91	3.52	2.20	5.24	-1.68E-01	7.03E-01			-6.61E-01	1.77E-01			-1.07E+00	9.98E-04	Down	-6.50E-01	6.53E-02		-6.80E-01	3.53E-01		5.73E-01	2.93E-01				Unigene44256_All//8.00E-94//TC158558				
Unigene44257_All	321	1.14	0.47	1.33	3.10	0.86	0.42	1.45	2.21	0.62	-1.27E+00	3.36E-01			2.18E-01	8.31E-01			-1.85E+00	7.41E-03		-2.88E+00	6.76E-04	Down	6.11E-01	4.27E-01		-1.22E+00	2.00E-01								
Unigene44259_All	997	0.00	0.00	0.00	0.20	0.21	0.23	1.53	4.78	4.08	null	null			null	null			5.17E-02	9.88E-01		1.80E-01	9.35E-01		1.65E+00	8.64E-10	Up	1.42E+00	3.76E-07	Up	Unigene44259_All//gi|224096718|ref|XP_002310710.1|//1.00E-120//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222853613|gb|EEE91160.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene44259_All//1.00E-115//AT3G50210| 2-oxoacid-dependent oxidase, putative					nr -
Unigene44261_All	359	0.00	16.80	7.56	0.28	0.00	0.00	0.00	0.00	0.00	1.40E+01	2.02E-34	Up		1.29E+01	5.42E-15	Up		-8.12E+00	3.12E-01		-8.12E+00	3.99E-01		null	null		null	null								ESTscan +
Unigene44262_All	438	0.00	3.12	3.04	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.80E-08	Up		1.16E+01	2.40E-07	Up		null	null		null	null		null	null		null	null		Unigene44262_All//sp|P02452|CO1A1_HUMAN//2.00E-64//Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=4						swissprot +
Unigene44264_All	523	0.00	2.42	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.86E-07	Up		9.99E+00	4.03E-03			null	null		null	null		null	null		null	null		Unigene44264_All//gi|12231176|dbj|BAB20971.1|//5.00E-10//aspartic proteinase 3 [Nepenthes alata]	Unigene44264_All//2.00E-07//AT5G01800| saposin B domain-containing protein					nr +
Unigene44266_All	399	0.00	8.13	7.47	0.00	0.00	0.23	1.80	1.47	0.10	1.30E+01	1.87E-18	Up		1.29E+01	1.77E-16	Up		null	null		7.82E+00	4.76E-01		-2.97E-01	6.85E-01		-4.17E+00	1.64E-04	Down	Unigene44266_All//gi|288300146|gb|ADC45376.1|//2.00E-59//actin [Cleistogenes songorica]	Unigene44266_All//4.00E-56//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene44266_All//2.00E-83//TC153744		ko04145|Phagosome		nr +
Unigene44268_All	422	0.00	0.48	0.13	0.59	3.18	2.25	0.30	0.30	0.09	8.91E+00	1.36E-01			6.98E+00	6.35E-01			2.43E+00	2.42E-04	Up	1.93E+00	1.48E-02		-1.69E-02	1.02E+00		-1.67E+00	4.77E-01				Unigene44268_All//1.00E-07//TC143273				
Unigene4427_All	1297	11.38	10.78	6.86	19.70	29.82	29.11	38.37	61.78	97.03	-7.73E-02	6.13E-01			-7.30E-01	1.30E-06			5.98E-01	5.80E-14		5.63E-01	2.70E-11		6.87E-01	1.15E-37		1.34E+00	6.44E-180	Up	Unigene4427_All//gi|215789967|gb|AC J70053.1|//5.00E-76//RIN4-like protein [Malus x domestica]	Unigene4427_All//7.00E-41//AT3G25070| RIN4 (RPM1 INTERACTING PROTEIN 4); protein binding	Unigene4427_All//0.00E+00//TC151627		ko04626|Plant-pathogen interaction		nr -
Unigene44270_All	411	0.76	0.99	1.30	1.58	2.35	1.54	7.00	2.14	4.07	3.69E-01	7.24E-01			7.62E-01	4.52E-01			5.74E-01	4.52E-01		-3.45E-02	9.53E-01		-1.71E+00	1.59E-06	Down	-7.81E-01	1.38E-02		Unigene44270_All//gi|1335862|gb|AAC49294.1|//1.00E-68//clathrin heavy chain [Glycine max]	Unigene44270_All//2.00E-71//AT3G08530| clathrin heavy chain, putative			ko04144|Endocytosis		nr -
Unigene44272_All	595	25.06	14.99	11.01	52.49	38.89	41.52	75.32	53.46	43.66	-7.42E-01	3.40E-07			-1.19E+00	3.58E-14	Down	-4.33E-01	1.06E-06		-3.38E-01	3.85E-04		-4.95E-01	2.90E-12		-7.87E-01	9.56E-28		Unigene44272_All//gi|20453062|gb|AAM19776.1|//3.00E-106//AT3g08530/T8G24_1 [Arabidopsis thaliana] >gi|21928019|gb|AAM78038.1| AT3g08530/T8G24_1 [Arabidopsis thaliana]	Unigene44272_All//6.00E-108//AT3G11130| clathrin heavy chain, putative	Unigene44272_All//0.00E+00//gi|78327913|gb|DT548187.1|DT548187		ko04144|Endocytosis		nr -
Unigene44273_All	552	16.21	12.94	6.27	22.02	16.84	18.82	52.93	43.46	33.49	-3.25E-01	1.03E-01			-1.37E+00	8.90E-11	Down	-3.87E-01	1.38E-02		-2.27E-01	2.08E-01		-2.84E-01	1.77E-03		-6.60E-01	8.85E-14		Unigene44273_All//gi|20453062|gb|AAM19776.1|//3.00E-93//AT3g08530/T8G24_1 [Arabidopsis thaliana] >gi|21928019|gb|AAM78038.1| AT3g08530/T8G24_1 [Arabidopsis thaliana]	Unigene44273_All//5.00E-87//AT3G08530| clathrin heavy chain, putative	Unigene44273_All//0.00E+00//gi|164342622|gb|ES824593.1|ES824593		ko04144|Endocytosis		nr +
Unigene44274_All	697	6.23	4.00	2.83	27.59	20.45	20.93	29.30	14.57	17.89	-6.40E-01	2.74E-02			-1.14E+00	2.22E-04	Down	-4.32E-01	2.38E-04		-3.99E-01	1.38E-03		-1.01E+00	6.59E-19	Down	-7.12E-01	3.57E-11		Unigene44274_All//gi|20453062|gb|AAM19776.1|//1.00E-114//AT3g08530/T8G24_1 [Arabidopsis thaliana] >gi|21928019|gb|AAM78038.1| AT3g08530/T8G24_1 [Arabidopsis thaliana]	Unigene44274_All//3.00E-116//AT3G11130| clathrin heavy chain, putative	Unigene44274_All//0.00E+00//CD486598		ko04144|Endocytosis		nr -
Unigene4428_All	1305	8.78	8.81	6.12	12.29	12.30	10.59	9.88	10.99	4.49	5.50E-03	9.90E-01			-5.21E-01	2.88E-03			6.00E-04	9.98E-01		-2.15E-01	1.59E-01		1.53E-01	3.16E-01		-1.14E+00	3.16E-15	Down	Unigene4428_All//gi|153850916|gb|ABS52645.1|//1.00E-108//GEM-like 1 [Vitis vinifera]	Unigene4428_All//1.00E-84//AT1G28200| FIP1 (FH INTERACTING PROTEIN 1)	Unigene4428_All//0.00E+00//gi|164288102|gb|ES798397.1|ES798397				nr +
Unigene44280_All	630	4.32	3.54	1.86	13.44	7.32	4.30	41.74	24.75	16.44	-2.87E-01	4.60E-01			-1.22E+00	2.83E-03			-8.76E-01	1.80E-06		-1.64E+00	8.55E-15	Down	-7.54E-01	4.46E-15		-1.34E+00	7.62E-39	Down			Unigene44280_All//3.00E-151//TC152684				
Unigene44285_All	1799	1.69	1.13	0.41	2.41	2.45	1.66	4.96	1.60	3.43	-5.82E-01	1.03E-01			-2.03E+00	1.39E-06	Down	2.44E-02	9.61E-01		-5.40E-01	6.94E-02		-1.63E+00	1.88E-17	Down	-5.31E-01	1.48E-03		Unigene44285_All//gi|30695804|ref|NP_851024.1|//0.00E+00//WD-40 repeat family protein [Arabidopsis thaliana] >gi|30725544|gb|AAP37794.1| At3g63460 [Arabidopsis thaliana]	Unigene44285_All//0.00E+00//AT3G63460| WD-40 repeat family protein	Unigene44285_All//0.00E+00//gi|164352517|gb|ES800313.1|ES800313				nr +
Unigene44288_All	2393	3.74	2.71	3.23	9.08	8.84	9.70	17.46	8.47	11.09	-4.64E-01	1.66E-02			-2.13E-01	3.35E-01		-3.88E-02	8.19E-01		9.60E-02	4.90E-01		-1.04E+00	5.43E-40	Down	-6.55E-01	4.91E-19		Unigene44288_All//gi|30695804|ref|NP_851024.1|//0.00E+00//WD-40 repeat family protein [Arabidopsis thaliana] >gi|30725544|gb|AAP37794.1| At3g63460 [Arabidopsis thaliana]	Unigene44288_All//0.00E+00//AT3G63460| WD-40 repeat family protein	Unigene44288_All//0.00E+00//TC141178				nr +
Unigene44289_All	2387	5.41	3.48	3.41	11.48	8.89	8.72	12.89	6.18	5.27	-6.37E-01	4.67E-05			-6.66E-01	4.13E-05		-3.69E-01	1.39E-04		-3.96E-01	9.44E-05		-1.06E+00	1.74E-30	Down	-1.29E+00	1.46E-42	Down	Unigene44289_All//gi|30695804|ref|NP_851024.1|//0.00E+00//WD-40 repeat family protein [Arabidopsis thaliana] >gi|30725544|gb|AAP37794.1| At3g63460 [Arabidopsis thaliana]	Unigene44289_All//0.00E+00//AT3G63460| WD-40 repeat family protein	Unigene44289_All//0.00E+00//gi|78325323|gb|DT545597.1|DT545597		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene4429_All	548	8.59	1.66	4.08	7.09	7.67	3.46	0.62	0.00	0.29	-2.37E+00	1.79E-12	Down		-1.07E+00	2.52E-04	Down	1.13E-01	7.76E-01		-1.03E+00	7.71E-04	Down	-9.27E+00	1.17E-02		-1.09E+00	3.55E-01		Unigene4429_All//gi|224118590|ref|XP_002317858.1|//6.00E-07//predicted protein [Populus trichocarpa] >gi|222858531|gb|EEE96078.1| predicted protein [Populus trichocarpa]		Unigene4429_All//6.00E-35//gi|210989993|gb|BQ411306.1|BQ411306				nr +
Unigene44290_All	1777	18.81	12.49	12.17	44.12	33.56	35.00	35.81	22.23	16.86	-5.91E-01	2.16E-10			-6.29E-01	5.29E-11		-3.95E-01	1.41E-13		-3.34E-01	3.88E-09		-6.88E-01	3.55E-30		-1.09E+00	1.82E-66	Down	Unigene44290_All//gi|30695804|ref|NP_851024.1|//1.00E-135//WD-40 repeat family protein [Arabidopsis thaliana] >gi|30725544|gb|AAP37794.1| At3g63460 [Arabidopsis thaliana]	Unigene44290_All//1.00E-121//AT3G63460| WD-40 repeat family protein	Unigene44290_All//0.00E+00//TC152684		ko03040|Spliceosome//ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene44294_All	658	0.80	0.31	1.13	1.74	3.14	2.47	1.99	2.22	4.66	-1.37E+00	1.97E-01			5.11E-01	5.47E-01		8.51E-01	5.85E-02		5.05E-01	3.72E-01		1.59E-01	7.51E-01		1.23E+00	1.14E-04	Up	Unigene44294_All//gi|42565171|ref|NP_189132.2|//2.00E-36//DNA binding [Arabidopsis thaliana]	Unigene44294_All//1.00E-37//AT3G24880| DNA binding					nr +
Unigene44299_All	949	0.33	0.37	0.00	0.52	0.29	0.86	6.24	1.10	4.03	1.76E-01	8.83E-01			-8.37E+00	4.90E-02		-8.55E-01	4.07E-01		7.07E-01	3.93E-01		-2.50E+00	4.36E-20	Down	-6.30E-01	2.69E-03		Unigene44299_All//gi|11994595|dbj|BAB02650.1|//3.00E-51//receptor-like serine/threonine kinase [Arabidopsis thaliana]	Unigene44299_All//5.00E-51//AT1G53420| serine/threonine protein kinase-related	Unigene44299_All//3.00E-16//TC133547				nr +
Unigene443_All	1891	58.85	26.69	31.54	25.42	28.59	28.28	5.14	4.53	2.42	-1.14E+00	1.78E-99	Down		-9.00E-01	2.97E-65		1.70E-01	2.08E-02		1.54E-01	4.82E-02		-1.83E-01	3.29E-01		-1.09E+00	6.71E-11	Down	Unigene443_All//gi|30679912|ref|NP_195935.2|//1.00E-107//JKD (JACKDAW); nucleic acid binding / protein binding / protein homodimerization/ transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|75325688|sp|Q700D2.1|JKD_ARATH RecName: Full=Zinc finger protein JACKDAW; AltName: Full=ID1-like zinc finger protein 3 >gi|41059985|emb|CAF18563.1| ID1-like zinc finger protein 3 [Arabidopsis thaliana] >gi|45935041|gb|AAS79555.1| C2H2 type zinc finger family protein [Arabidopsis thaliana]	Unigene443_All//2.00E-91//AT3G45260| zinc finger (C2H2 type) family protein	Unigene443_All//0.00E+00//TC159397	C2H2			nr +
Unigene4430_All	1494	5.88	1.63	4.74	4.90	5.28	2.42	0.51	0.36	0.29	-1.85E+00	8.53E-17	Down		-3.12E-01	1.41E-01		1.07E-01	6.70E-01		-1.02E+00	1.79E-06	Down	-4.86E-01	5.25E-01		-7.96E-01	2.52E-01		Unigene4430_All//gi|53370641|gb|AAU89136.1|//1.00E-19//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene4430_All//1.00E-07//AT3G25270| nucleic acid binding	Unigene4430_All//2.00E-71//TC159813				nr +
Unigene44301_All	702	5.89	0.65	2.12	10.93	3.38	3.47	6.08	5.66	1.93	-3.18E+00	7.62E-15	Down		-1.47E+00	7.39E-06	Down	-1.69E+00	6.98E-16	Down	-1.65E+00	1.47E-13	Down	-1.05E-01	7.23E-01		-1.66E+00	2.87E-09	Down	Unigene44301_All//gi|226498624|ref|NP_001147903.1|//8.00E-63//protein kinase [Zea mays] >gi|195614480|gb|ACG29070.1| protein kinase [Zea mays]	Unigene44301_All//8.00E-62//AT5G65600| legume lectin family protein / protein kinase family protein	Unigene44301_All//4.00E-49//TC159627		ko04626|Plant-pathogen interaction		nr +
Unigene44302_All	1465	5.64	1.04	3.49	13.70	5.50	5.55	2.05	2.74	0.76	-2.44E+00	3.54E-22	Down		-6.93E-01	9.20E-04		-1.32E+00	3.41E-28	Down	-1.30E+00	1.94E-24	Down	4.19E-01	1.37E-01		-1.43E+00	1.28E-05	Down	Unigene44302_All//gi|212717161|gb|ACJ37422.1|//4.00E-93//receptor-like serine/threonine kinase [Glycine max]	Unigene44302_All//1.00E-85//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene44302_All//7.00E-74//TC142773		ko04626|Plant-pathogen interaction		nr +
Unigene44303_All	2219	3.61	4.34	3.86	7.79	6.01	8.79	3.30	4.11	9.30	2.66E-01	1.71E-01			9.89E-02	6.39E-01		-3.75E-01	3.21E-03		1.75E-01	2.20E-01		3.17E-01	7.50E-02		1.50E+00	1.47E-35	Up	Unigene44303_All//gi|11994595|dbj|BAB02650.1|//0.00E+00//receptor-like serine/threonine kinase [Arabidopsis thaliana]	Unigene44303_All//0.00E+00//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene44303_All//4.00E-175//TC144463		ko04626|Plant-pathogen interaction		nr -
Unigene44304_All	1865	8.84	1.66	2.20	33.73	13.96	22.98	45.02	60.08	61.14	-2.41E+00	5.03E-43	Down		-2.01E+00	6.17E-33	Down	-1.27E+00	2.77E-83	Down	-5.54E-01	5.20E-18		4.16E-01	1.31E-21		4.41E-01	5.07E-25		Unigene44304_All//gi|240255348|ref|NP_188102.4|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana]	Unigene44304_All//0.00E+00//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene44304_All//0.00E+00//TC163165		ko04626|Plant-pathogen interaction		nr -
Unigene44306_All	2307	7.03	12.43	7.96	8.68	6.66	9.77	6.32	12.90	5.25	8.22E-01	1.92E-15			1.80E-01	2.26E-01		-3.83E-01	9.86E-04		1.71E-01	1.94E-01		1.03E+00	4.77E-28	Up	-2.68E-01	4.14E-02		Unigene44306_All//gi|224589567|gb|ACN39317.1|//1.00E-134//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene44306_All//2.00E-135//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene44306_All//1.00E-97//TC159627		ko04626|Plant-pathogen interaction		nr +
Unigene44309_All	9405	64.39	186.05	110.98	40.51	34.09	33.48	83.05	70.94	71.27	1.53E+00	0.00E+00	Up		7.85E-01	0.00E+00		-2.49E-01	4.64E-27		-2.75E-01	3.40E-29		-2.27E-01	5.39E-47		-2.21E-01	1.56E-45		Unigene44309_All//gi|91208933|ref|YP_538968.1|//0.00E+00//RNA polymerase alpha subunit [Gossypium hirsutum] >gi|109900621|sp|Q2L938.1|RPOA_GOSHI RecName: Full=DNA-directed RNA polymerase subunit alpha; Short=PEP; AltName: Full=Plastid-encoded RNA polymerase subunit alpha; Short=RNA polymerase subunit alpha >gi|85687447|gb|ABC73659.1| RNA polymerase alpha subunit [Gossypium hirsutum]	Unigene44309_All//4.00E-143//ATCG00740| RNA polymerase alpha subunit	Unigene44309_All//0.00E+00//TC148301		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene4431_All	883	5.39	3.79	9.65	5.87	3.35	3.68	5.12	4.97	2.17	-5.10E-01	6.71E-02			8.40E-01	4.66E-05		-8.07E-01	9.77E-04		-6.72E-01	9.99E-03		-4.39E-02	8.83E-01		-1.24E+00	1.18E-06	Down							
Unigene44312_All	1682	0.65	0.81	1.14	2.25	1.11	1.15	4.55	3.53	2.53	3.16E-01	5.98E-01			8.03E-01	1.02E-01		-1.03E+00	4.89E-04	Down	-9.63E-01	2.01E-03		-3.67E-01	5.85E-02		-8.44E-01	4.51E-06		Unigene44312_All//gi|186501175|ref|NP_179383.2|//0.00E+00//binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor [Arabidopsis thaliana]	Unigene44312_All//0.00E+00//AT2G17930| binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor	Unigene44312_All//0.00E+00//gi|31073617|gb|CA993896.1|CA993896				nr +
Unigene44313_All	3754	3.92	3.50	3.15	5.91	5.83	4.66	17.57	7.55	5.64	-1.64E-01	3.11E-01			-3.15E-01	4.49E-02		-1.75E-02	9.02E-01		-3.43E-01	3.22E-03		-1.22E+00	2.64E-80	Down	-1.64E+00	4.18E-129	Down	Unigene44313_All//gi|115473707|ref|NP_001060452.1|//0.00E+00//Os07g0645100 [Oryza sativa Japonica Group] >gi|113611988|dbj|BAF22366.1| Os07g0645100 [Oryza sativa Japonica Group]	Unigene44313_All//0.00E+00//AT2G17930| binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor	Unigene44313_All//0.00E+00//TC168720				nr -

Unigene44315_All	773	0.81	3.08	2.27	3.35	3.74	4.50	4.27	2.81	5.51	1.92E+00	2.85E-05	Up	1.48E+00	5.78E-03		1.59E-01	7.26E-01		4.25E-01	2.32E-01		-6.02E-01	4.98E-02		3.70E-01	1.59E-01		Unigene44315_All//gi|297820744|ref|XP_002878255.1|//1.00E-117//protein transporter [Arabidopsis lyrata subsp. lyrata] >gi|297324093|gb|EFH54514.1|protein transporter [Arabidopsis lyrata subsp. lyrata]	Unigene44315_All//5.00E-115//AT3G59020| binding / protein transporter	Unigene44315_All//6.00E-159//DW478267				nr +
Unigene44316_All	1702	3.14	2.02	2.97	7.40	6.92	7.67	7.45	2.97	6.13	-6.31E-01	1.43E-02		-7.72E-02	7.75E-01		-9.78E-02	6.12E-01		5.05E-02	7.84E-01		-1.33E+00	3.05E-18	Down	-2.81E-01	4.78E-02		Unigene44316_All//gi|30685014|ref|NP_180724.2|//0.00E+00//SAD2 (SUPER SENSITIVE TO ABA AND DROUGHT2); binding / protein transporter [Arabidopsis thaliana]	Unigene44316_All//0.00E+00//AT2G31660| SAD2 (SUPER SENSITIVE TO ABA AND DROUGHT2); binding / protein transporter	Unigene44316_All//2.00E-117//DW478267				nr +
Unigene44319_All	1793	4.41	2.83	2.76	8.75	11.12	11.66	8.06	3.24	7.73	-6.41E-01	1.90E-03		-6.74E-01	1.71E-03		3.46E-01	3.96E-03		4.14E-01	4.83E-04		-1.32E+00	1.98E-20	Down	-6.07E-02	6.77E-01		Unigene44319_All//gi|30685014|ref|NP_180724.2|//0.00E+00//SAD2 (SUPER SENSITIVE TO ABA AND DROUGHT2); binding / protein transporter [Arabidopsis thaliana]	Unigene44319_All//0.00E+00//AT2G31660| SAD2 (SUPER SENSITIVE TO ABA AND DROUGHT2); binding / protein transporter	Unigene44319_All//1.00E-121//DW478267				nr +
Unigene44322_All	692	1.36	1.46	1.31	1.87	2.59	4.05	1.04	1.15	3.05	1.06E-01	8.72E-01		-5.70E-02	9.49E-01		4.67E-01	3.80E-01		1.11E+00	3.36E-03		1.44E-01	8.36E-01		1.55E+00	1.37E-04	Up	Unigene44322_All//gi|240255922|ref|NP_193364.5|//4.00E-33//LDL3 (LSD1-LIKE3); amine oxidase/ electron carrier/ oxidoreductase [Arabidopsis thaliana]	Unigene44322_All//2.00E-34//AT4G16310| LDL3 (LSD1-LIKE3); amine oxidase/ electron carrier/ oxidoreductase					nr -
Unigene44323_All	863	0.36	0.53	1.73	2.42	1.52	1.94	2.25	2.13	3.60	5.39E-01	6.02E-01		2.25E+00	5.49E-04	Up	-6.77E-01	1.17E-01		-3.24E-01	4.99E-01		-8.07E-02	8.53E-01		6.76E-01	2.66E-02		Unigene44323_All//gi|297610832|ref|NP_001065146.2|//4.00E-43//Os10g0532100 [Oryza sativa Japonica Group] >gi|255679583|dbj|BAF27060.2|Os10g0532100 [Oryza sativa Japonica Group]	Unigene44323_All//2.00E-39//AT4G16310| LDL3 (LSD1-LIKE3); amine oxidase/ electron carrier/ oxidoreductase					nr +
Unigene44324_All	2025	0.31	0.75	0.05	0.89	0.97	0.40	2.63	2.25	1.28	1.28E+00	2.09E-02		-2.56E+00	2.72E-02		1.30E-01	8.35E-01		-1.14E+00	2.04E-02		-2.26E-01	3.89E-01		-1.04E+00	5.26E-06	Down	Unigene44324_All//gi|240255922|ref|NP_193364.5|//1.00E-23//LDL3 (LSD1-LIKE3); amine oxidase/ electron carrier/ oxidoreductase [Arabidopsis thaliana]	Unigene44324_All//7.00E-25//AT4G16310| LDL3 (LSD1-LIKE3); amine oxidase/ electron carrier/ oxidoreductase	Unigene44324_All//0.00E+00//gi|164343673|gb|ES843911.1|ES843911				nr -
Unigene44328_All	444	4.12	5.59	1.08	4.71	3.80	5.70	5.14	3.77	3.95	4.39E-01	2.84E-01		-1.93E+00	4.88E-04	Down	-3.10E-01	5.23E-01		2.74E-01	5.49E-01		-4.50E-01	2.50E-01		-3.81E-01	3.13E-01		Unigene44328_All//gi|224067588|ref|XP_002302510.1|//2.00E-47//histone ubiquitination proteins group [Populus trichocarpa] >gi|222844236|gb|EEE81783.1|histone ubiquitination proteins group [Populus trichocarpa]	Unigene44328_All//1.00E-38//AT2G44950| HUB1 (HISTONE MONO-UBIQUITINATION 1); protein binding / protein homodimerization/ ubiquitin-protein ligase/ zinc ion binding	Unigene44328_All//2.00E-111//TC164850				nr -
Unigene4433_All	1207	6.50	1.76	4.85	5.12	3.48	3.82	1.30	0.35	0.23	-1.88E+00	2.24E-15	Down	-4.22E-01	5.59E-02		-5.56E-01	1.41E-02		-4.23E-01	8.45E-02		-1.90E+00	2.24E-04	Down	-2.49E+00	5.08E-06	Down	Unigene4433_All//gi|29028856|gb|AA064807.1|//1.00E-100//At5g22340 [Arabidopsis thaliana]	Unigene4433_All//2.00E-89//AT5G22340| unknown protein	Unigene4433_All//0.00E+00//TC165308				nr -
Unigene44330_All	712	2.50	2.85	0.45	3.64	3.53	2.85	2.61	1.82	3.64	1.88E-01	6.66E-01		-2.48E+00	4.58E-05	Down	-4.33E-02	9.11E-01		-3.50E-01	4.08E-01		-5.22E-01	2.33E-01		4.77E-01	1.68E-01		Unigene44330_All//gi|224067588|ref|XP_002302510.1|//7.00E-88//histone ubiquitination proteins group [Populus trichocarpa] >gi|222844236|gb|EEE81783.1|histone ubiquitination proteins group [Populus trichocarpa]	Unigene44330_All//2.00E-67//AT2G44950| HUB1 (HISTONE MONO-UBIQUITINATION 1); protein binding / protein homodimerization/ ubiquitin-protein ligase/ zinc ion binding	Unigene44330_All//0.00E+00//TC164850				nr +
Unigene44338_All	901	3.14	0.84	0.65	3.59	4.28	2.91	7.56	7.89	6.37	-1.89E+00	4.74E-06	Down	-2.27E+00	5.16E-07	Down	2.52E-01	4.83E-01		-3.06E-01	4.19E-01		6.18E-02	7.83E-01		-2.47E-01	2.36E-01		Unigene44338_All//gi|9759187|dbj|BAB09724.1|//3.00E-18//importin beta [Arabidopsis thaliana]	Unigene44338_All//2.00E-19//AT5G53480| importin beta-2, putative	Unigene44338_All//0.00E+00//TC145452				nr +
Unigene44343_All	358	1.46	1.13	1.04	4.17	5.68	0.76	3.42	3.04	7.79	-3.68E-01	6.83E-01		-4.89E-01	6.32E-01		4.43E-01	3.67E-01		-2.46E+00	8.25E-05	Down	-1.74E-01	7.49E-01		1.19E+00	3.83E-04	Up	Unigene44343_All//gi|190148353|gb|ACE63259.1|//5.00E-38//cytokinin receptor 1 [Betula pendula]	Unigene44343_All//3.00E-30//AT2G01830| WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase	Unigene44343_All//9.00E-73//gi|78335654|gb|DT555928.1|DT555928	Orphans			nr -
Unigene44344_All	1712	4.95	2.72	4.26	11.70	12.43	12.85	21.71	8.13	6.28	-8.63E-01	1.60E-05		-2.16E-01	3.41E-01		8.77E-02	5.54E-01		1.35E-01	3.29E-01		-1.42E+00	2.48E-57	Down	-1.79E+00	1.70E-82	Down	Unigene44344_All//gi|190148363|gb|ACE63264.1|//0.00E+00//cytokinin receptor 1A [Populus trichocarpa]	Unigene44344_All//0.00E+00//AT2G01830| WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase	Unigene44344_All//0.00E+00//gi|78348342|gb|DT568616.1|DT568616	Orphans	ko04712|Circadian rhythm - plant		nr -
Unigene44345_All	4066	4.88	1.79	2.84	13.18	12.09	10.62	24.13	12.24	6.11	-1.44E+00	4.93E-26	Down	-7.79E-01	1.37E-09		-1.24E-01	1.11E-01		-3.12E-01	9.28E-06		-9.79E-01	9.57E-84		-1.98E+00	7.87E-249	Down	Unigene44345_All//gi|225424440|ref|XP_002285117.1|//0.00E+00//PREDICTED: similar to cytokinin receptor 1 [Vitis vinifera]	Unigene44345_All//0.00E+00//AT2G01830| WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase	Unigene44345_All//0.00E+00//TC136880	Orphans			nr -
Unigene44346_All	3145	4.38	4.51	4.23	8.16	9.71	7.64	4.36	4.57	14.64	4.41E-02	7.81E-01		-4.77E-02	7.74E-01		2.52E-01	9.40E-03		-9.46E-02	4.84E-01		6.98E-02	6.45E-01		1.75E+00	7.94E-98	Up	Unigene44346_All//gi|225424440|ref|XP_002285117.1|//0.00E+00//PREDICTED: similar to cytokinin receptor 1 [Vitis vinifera]	Unigene44346_All//0.00E+00//AT2G01830| WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase	Unigene44346_All//0.00E+00//gi|78348342|gb|DT568616.1|DT568616	Orphans	ko04712|Circadian rhythm - plant		nr +
Unigene44347_All	4199	5.08	1.07	1.88	17.51	13.54	12.20	23.85	9.72	14.56	-2.24E+00	7.36E-51	Down	-1.44E+00	9.40E-27	Down	-3.71E-01	2.05E-11		-5.22E-01	7.40E-19		-1.29E+00	1.48E-133	Down	-7.12E-01	2.87E-51		Unigene44347_All//gi|190148353|gb|ACE63259.1|//0.00E+00//cytokinin receptor 1 [Betula pendula]	Unigene44347_All//0.00E+00//AT2G01830| WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase	Unigene44347_All//0.00E+00//TC152619	Orphans	ko04712|Circadian rhythm - plant		nr -
Unigene4435_All	1461	2.04	2.39	2.41	3.78	3.30	3.15	4.28	4.35	1.88	2.29E-01	5.10E-01		2.37E-01	5.09E-01		-1.98E-01	4.95E-01		-2.63E-01	3.55E-01		2.19E-02	9.47E-01		-1.19E+00	2.57E-08	Down	Unigene4435_All//gi|85719360|gb|AB075365.1|//1.00E-155//RNA polymerase, dimerisation [Medicago truncatula]	Unigene4435_All//7.00E-153//AT2G15430| NRPB3; DNA binding / DNA-directed RNA polymerase/ protein dimerization	Unigene4435_All//0.00E+00//TC138255		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene44353_All	603	2.60	1.85	0.18	3.22	2.97	3.07	8.41	3.60	3.70	-4.94E-01	3.61E-01		-3.88E+00	1.55E-06	Down	-1.18E-01	8.28E-01		-6.93E-02	8.97E-01		-1.22E+00	6.06E-07	Down	-1.19E+00	6.74E-07	Down	Unigene44353_All//gi|297834554|ref|XP_002885159.1|//4.00E-23//ATKINESIN-13A/KINESIN-13A [Arabidopsis lyrata subsp. lyrata] >gi|297309999|gb|EFH61418.1|ATKINESIN-13A/KINESIN-13A [Arabidopsis lyrata subsp. lyrata]	Unigene44353_All//2.00E-24//AT3G16630| KINESIN-13A; ATP binding / microtubule motor	Unigene44353_All//0.00E+00//CB066374				nr -
Unigene44357_All	3035	7.31	5.28	6.53	21.42	21.48	16.44	19.94	10.85	8.91	-4.70E-01	4.99E-05		-1.63E-01	2.25E-01		4.00E-03	9.65E-01		-3.81E-01	1.16E-09		-8.77E-01	2.49E-43		-1.16E+00	2.71E-70	Down	Unigene44357_All//gi|33439496|gb|AAQ18797.1|//0.00E+00//central motor kinesin 1 [Gossypium hirsutum]	Unigene44357_All//0.00E+00//AT3G16630| KINESIN-13A; ATP binding / microtubule motor	Unigene44357_All//0.00E+00//TC151867				nr +
Unigene44358_All	1091	3.31	9.52	6.69	1.78	3.54	4.14	3.53	9.39	7.34	1.52E+00	4.84E-15	Up	1.01E+00	8.09E-06	Up	9.89E-01	1.05E-03		1.22E+00	2.38E-05	Up	1.41E+00	2.95E-16	Up	1.06E+00	1.02E-08	Up	Unigene44358_All//gi|94503774|gb|ABF29696.1|//9.00E-18//abscisic acid responsive element-binding protein 2 [Populus suaveolens]		Unigene44358_All//0.00E+00//gi|164315221|gb|ES827446.1|ES827446				nr +
Unigene44359_All	1162	34.58	145.64	65.81	27.99	87.13	147.58	33.84	113.45	103.06	2.07E+00	0.00E+00	Up	9.28E-01	1.96E-47		1.64E+00	1.87E-184	Up	2.40E+00	0.00E+00	Up	1.75E+00	1.83E-272	Up	1.61E+00	1.45E-224	Up	Unigene44359_All//gi|225458627|ref|XP_002284791.1|//1.00E-116//PREDICTED: ripening-related bZIP protein-like isoform 2 [Vitis vinifera] >gi|225458629|ref|XP_002284785.1|PREDICTED: ripening-related bZIP protein-like isoform 1 [Vitis vinifera]	Unigene44359_All//2.00E-75//AT1G45249| ABF2 (ABSCISIC ACID RESPONSIVE ELEMENTS-BINDING FACTOR 2); DNA binding / protein binding / transcription activator/ transcription factor	Unigene44359_All//0.00E+00//TC150495	bZIP			nr +
Unigene4436_All	905	15.15	22.23	14.47	33.41	30.21	30.44	17.89	8.82	12.59	5.53E-01	6.37E-06		-6.55E-02	7.03E-01		-1.45E-01	1.77E-01		-1.34E-01	2.31E-01		-1.02E+00	1.85E-15	Down	-5.07E-01	2.42E-05		Unigene4436_All//gi|3702345|gb|AAC62902.1|//2.00E-51//expressed protein [Arabidopsis thaliana] >gi|20197205|gb|AAM14970.1|expressed protein [Arabidopsis thaliana] >gi|90568016|gb|ABD94078.1|At2g46000 [Arabidopsis thaliana]	Unigene4436_All//5.00E-44//AT2G46000| unknown protein	Unigene4436_All//0.00E+00//TC168251				nr +
Unigene44360_All	1642	3.19	13.82	9.31	3.82	6.52	8.22	2.55	8.27	10.38	2.12E+00	6.13E-50	Up	1.55E+00	1.66E-21	Up	7.71E-01	2.62E-06		1.11E+00	9.51E-13	Up	1.70E+00	1.18E-27	Up	2.03E+00	1.36E-44	Up	Unigene44360_All//gi|225458627|ref|XP_002284791.1|//1.00E-125//PREDICTED: ripening-related bZIP protein-like isoform 2 [Vitis vinifera] >gi|225458629|ref|XP_002284785.1|PREDICTED: ripening-related bZIP protein-like isoform 1 [Vitis vinifera]	Unigene44360_All//3.00E-47//AT1G45249| ABF2 (ABSCISIC ACID RESPONSIVE ELEMENTS-BINDING FACTOR 2); DNA binding / protein binding / transcription activator/ transcription factor	Unigene44360_All//1.00E-168//ES827446	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene44362_All	3282	3.40	20.07	9.26	3.66	6.52	9.22	42.63	50.39	54.30	2.56E+00	3.85E-181	Up	1.45E+00	1.99E-38	Up	8.33E-01	9.52E-14		1.33E+00	2.73E-37	Up	2.41E-01	8.49E-12		3.49E-01	2.96E-25		Unigene44362_All//gi|240256390|ref|NP_199107.5|//1.00E-146//triacylglycerol lipase [Arabidopsis thaliana]	Unigene44362_All//2.00E-140//AT5G42930| triacylglycerol lipase	Unigene44362_All//0.00E+00//TC146285		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene44367_All	2203	7.84	7.04	6.21	17.71	15.37	11.34	16.52	9.64	6.02	-1.55E-01	2.92E-01		-3.35E-01	1.83E-02		-2.05E-01	1.72E-02		-6.43E-01	1.02E-14		-7.78E-01	1.25E-21		-1.46E+00	3.10E-60	Down	Unigene44367_All//gi|165905462|dbj|BAF98996.1|//0.00E+00//nucleoporin 98 [Daucus carota]	Unigene44367_All//2.00E-149//AT1G10390| nucleoporin family protein	Unigene44367_All//0.00E+00//TC152462		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene44368_All	573	1.37	1.59	4.65	3.65	4.69	5.99	3.39	2.33	1.74	2.17E-01	7.42E-01		1.76E+00	5.21E-05	Up	3.60E-01	3.95E-01		7.14E-01	3.42E-02		-5.40E-01	2.08E-01		-9.66E-01	1.58E-02		Unigene44368_All//gi|165905462|dbj|BAF98996.1|//4.00E-69//nucleoporin 98 [Daucus carota]	Unigene44368_All//4.00E-30//AT1G59660| nucleoporin family protein	Unigene44368_All//0.00E+00//TC141755		ko03040|Spliceosome//ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene4437_All	1314	3.30	2.85	1.62	8.11	5.90	9.56	5.66	4.74	4.06	-2.12E-01	4.90E-01		-1.03E+00	7.90E-04	Down	-4.60E-01	5.57E-03		2.36E-01	1.81E-01		-2.57E-01	2.18E-01		-4.79E-01	9.80E-03		Unigene4437_All//gi|12539611|gb|AAG59585.1|AF229927_1//1.00E-106//threonine deaminase [Nicotiana attenuata] >gi|60502212|gb|AAX22214.1|threonine deaminase [Nicotiana attenuata]	Unigene4437_All//3.00E-135//AT3G10050| OMR1 (L-O-METHYLTHREONINE RESISTANT 1); L-threonine ammonia-lyase	Unigene4437_All//0.00E+00//TC148948		ko00260|Glycine, serine and threonine metabolism//ko00290|Valine, leucine and isoleucine biosynthesis		nr +
Unigene44371_All	1894	2.90	1.44	4.92	7.73	8.51	6.53	4.24	2.14	2.82	-1.01E+00	9.32E-05	Down	7.62E-01	9.53E-05		1.38E-01	4.02E-01		-2.43E-01	1.26E-01		-9.87E-01	1.10E-07		-5.90E-01	8.63E-04		Unigene44371_All//gi|22329468|ref|NP_172510.2|//1.00E-111//nucleoporin family protein [Arabidopsis thaliana] >gi|79317517|ref|NP_001031018.1|nucleoporin family protein [Arabidopsis thaliana] >gi|19310423|gb|AAL84948.1|At1g10390/F14N23_29 [Arabidopsis thaliana] >gi|27764948|gb|AAO23595.1|At1g10390/F14N23_29 [Arabidopsis thaliana]	Unigene44371_All//5.00E-58//AT1G59660| nucleoporin family protein	Unigene44371_All//0.00E+00//TC147797		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene44389_All	1704	1.87	1.61	0.97	2.48	4.43	3.05	4.81	1.37	3.95	-2.22E-01	5.47E-01		-9.51E-01	9.11E-03		8.33E-01	3.60E-05		2.95E-01	3.12E-01		-1.81E+00	1.55E-18	Down	-2.85E-01	1.19E-01		Unigene44389_All//gi|15222554|ref|NP_176570.1|//1.00E-173//PRLI-interacting factor-related [Arabidopsis thaliana]	Unigene44389_All//2.00E-167//AT1G63850| PRLI-interacting factor-related	Unigene44389_All//0.00E+00//gi|164364866|gb|EX167525.1|EX167525				nr +
Unigene4439_All	970	17.15	26.43	15.87	38.05	48.39	40.04	22.36	50.20	44.97	6.24E-01	7.04E-09		-1.13E-01	4.80E-01		3.47E-01	1.54E-06		7.35E-02	4.94E-01		1.17E+00	1.83E-55	Up	1.01E+00	2.35E-40	Up	Unigene4439_All//gi|297795247|ref|XP_002865508.1|//1.00E-09//abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311343|gb|EFH41767.1|abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4439_All//6.00E-09//AT5G42560| abscisic acid-responsive HVA22 family protein	Unigene4439_All//0.00E+00//TC148631				nr +

Unigene44392_All	2717	3.16	1.51	2.74	14.96	9.90	6.20	8.50	1.65	2.39	-1.06E+00	1.47E-07	Down	-2.03E-01	3.75E-01		-5.96E-01	5.55E-15		-1.27E+00	4.82E-47	Down	-2.37E+00	1.27E-71	Down	-1.83E+00	3.54E-53	Down	Unigene44392_All//gi|15222554|ref|NP_176570.1|//0.00E+00//PRLI-interacting factor-related [Arabidopsis thaliana]	Unigene44392_All//0.00E+00//AT1G63850| PRLI-interacting factor-related	Unigene44392_All//0.00E+00//TC161690				nr +
Unigene44393_All	2786	2.54	2.02	2.77	4.04	4.93	2.97	1.64	0.53	1.83	-3.29E-01	1.47E-01		1.29E-01	6.09E-01		2.87E-01	6.57E-02		-4.46E-01	8.48E-03		-1.64E+00	2.10E-09	Down	1.59E-01	5.47E-01		Unigene44393_All//gi|15222554|ref|NP_176570.1|//0.00E+00//PRLI-interacting factor-related [Arabidopsis thaliana]	Unigene44393_All//0.00E+00//AT1G63850| PRLI-interacting factor-related	Unigene44393_All//0.00E+00//TC133853				nr -
Unigene44401_All	296	0.00	0.34	2.52	0.00	0.00	0.00	0.57	1.69	0.81	8.42E+00	3.86E-01		1.13E+01	3.27E-04	Up	null	null		null	null		1.57E+00	1.18E-01		4.99E-01	7.07E-01		Unigene44401_All//gi|79405297|ref|NP_188346.2|//1.00E-20//UPL6 (UBIQUITIN PROTEIN LIGASE 6); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75247591|sp|Q8RH88.1|UPL6_ARATH RecName: Full=E3 ubiquitin-protein ligase UPL6; Short=Ubiquitin-protein ligase 6 >gi|37202000|gb|AAQ89615.1| At3g17205 [Arabidopsis thaliana]	Unigene44401_All//9.00E-18//AT3G17205| UPL6 (UBIQUITIN PROTEIN LIGASE 6); ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene44404_All	1826	1.06	2.72	1.98	3.00	3.87	4.80	5.05	4.19	7.00	1.36E+00	1.63E-06	Up	9.03E-01	7.44E-03		3.65E-01	1.08E-01		6.77E-01	4.22E-04		-2.69E-01	1.37E-01		4.72E-01	5.78E-04		Unigene44404_All//gi|115462227|ref|NP_001054713.1|//1.00E-126//0s05g0159000 [Oryza sativa Japonica Group] >gi|113578264|dbj|BAF16627.1| Os05g0159000 [Oryza sativa Japonica Group]	Unigene44404_All//1.00E-92//AT3G17205| UPL6 (UBIQUITIN PROTEIN LIGASE 6); ubiquitin-protein ligase	Unigene44404_All//1.00E-152//gi|109859689|gb|DW488668.1|DW488668		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene4441_All	1097	0.14	0.97	0.19	2.00	2.26	1.81	1.50	2.36	4.54	2.76E+00	8.45E-04	Up	4.41E-01	7.75E-01		1.78E-01	7.14E-01		-1.41E-01	7.49E-01		6.52E-01	6.51E-02		1.59E+00	4.93E-10	Up	Unigene4441_All//gi|106647236|gb|AB782271.1|//1.00E-107//class III chitinase [Panax ginseng]	Unigene4441_All//2.00E-85//AT5G24090| acidic endochitinase (CHIB1)	Unigene4441_All//1.00E-145//DN800027		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene44413_All	236	3.99	4.08	2.26	8.02	3.36	2.11	8.78	10.09	9.12	3.17E-02	9.83E-01		-8.23E-01	2.71E-01		-1.26E+00	5.12E-03		-1.93E+00	1.45E-04	Down	2.02E-01	6.46E-01		5.44E-02	9.05E-01		Unigene44413_All//gi|186510627|ref|NP_189916.4|//2.00E-13//ATMIN7 (ARABIDOPSIS THALIANA HOPM INTERACTOR 7); guanyl-nucleotide exchange factor/ protein binding [Arabidopsis thaliana]	Unigene44413_All//9.00E-15//AT3G43300| ATMIN7 (ARABIDOPSIS THALIANA HOPM INTERACTOR 7); guanyl-nucleotide exchange factor/ protein binding	Unigene44413_All//8.00E-131//TC172821		ko04626|Plant-pathogen interaction		nr +
Unigene44414_All	1783	2.99	2.56	3.52	8.05	8.23	7.85	8.09	3.84	7.15	-2.27E-01	3.94E-01		2.36E-01	3.80E-01		3.21E-02	8.59E-01		-3.52E-02	8.47E-01		-1.07E+00	5.79E-15	Down	-1.78E-01	2.02E-01		Unigene44414_All//gi|186510627|ref|NP_189916.4|//0.00E+00//ATMIN7 (ARABIDOPSIS THALIANA HOPM INTERACTOR 7); guanyl-nucleotide exchange factor/ protein binding [Arabidopsis thaliana]	Unigene44414_All//0.00E+00//AT3G43300| ATMIN7 (ARABIDOPSIS THALIANA HOPM INTERACTOR 7); guanyl-nucleotide exchange factor/ protein binding	Unigene44414_All//0.00E+00//TC144939		ko04626|Plant-pathogen interaction		nr -
Unigene44421_All	731	12.96	7.28	7.21	22.69	27.79	26.13	11.34	4.97	5.45	-8.32E-01	9.29E-06		-8.45E-01	1.38E-05		2.93E-01	1.62E-02		2.04E-01	1.42E-01		-1.19E+00	2.13E-10	Down	-1.06E+00	4.74E-09	Down	Unigene44421_All//gi|297604347|ref|NP_001055269.2|//1.00E-113//0s05g0349200 [Oryza sativa Japonica Group] >gi|255676283|dbj|BAF17183.2| Os05g0349200 [Oryza sativa Japonica Group]	Unigene44421_All//2.00E-102//AT2G38280| FAC1 (EMBRYONIC FACTOR1); AMP deaminase	Unigene44421_All//0.00E+00//gi|48828853|gb|C0127243.1|C0127243		ko00230|Purine metabolism		nr -
Unigene44423_All	2826	3.28	7.78	4.03	5.78	4.62	10.10	11.15	10.93	13.59	1.25E+00	4.38E-23	Up	2.99E-01	1.02E-01		-3.24E-01	1.62E-02		8.05E-01	9.34E-16		-2.83E-02	7.86E-01		2.86E-01	1.66E-04		Unigene44423_All//gi|18404701|ref|NP_565886.1|//0.00E+00//FAC1 (EMBRYONIC FACTOR1); AMP deaminase [Arabidopsis thaliana] >gi|30687456|ref|NP_850294.1| FAC1 (EMBRYONIC FACTOR1); AMP deaminase [Arabidopsis thaliana] >gi|75223196|sp|Q80452.2|AMPD_ARATH RecName: Full=AMP deaminase; Short=AtAMPD; AltName: Full=Protein EMBRYONIC FACTOR 1	Unigene44423_All//0.00E+00//AT2G38280| FAC1 (EMBRYONIC FACTOR1); AMP deaminase	Unigene44423_All//0.00E+00//TC138616		ko00230|Purine metabolism		nr +
Unigene44424_All	1780	7.35	4.87	8.35	11.73	21.51	16.06	10.45	3.92	7.56	-5.94E-01	1.30E-04		1.84E-01	2.62E-01		8.76E-01	1.98E-26		4.54E-01	4.21E-06		-1.41E+00	5.25E-29	Down	-4.66E-01	2.82E-05		Unigene44424_All//gi|18404701|ref|NP_565886.1|//0.00E+00//FAC1 (EMBRYONIC FACTOR1); AMP deaminase [Arabidopsis thaliana] >gi|30687456|ref|NP_850294.1| FAC1 (EMBRYONIC FACTOR1); AMP deaminase [Arabidopsis thaliana] >gi|75223196|sp|Q80452.2|AMPD_ARATH RecName: Full=AMP deaminase; Short=AtAMPD; AltName: Full=Protein EMBRYONIC FACTOR 1	Unigene44424_All//0.00E+00//AT2G38280| FAC1 (EMBRYONIC FACTOR1); AMP deaminase	Unigene44424_All//0.00E+00//TC150453		ko00230|Purine metabolism		nr -
Unigene44426_All	1180	5.28	1.29	2.84	9.92	8.14	6.39	10.10	10.38	8.24	-2.03E+00	1.35E-13	Down	-8.92E-01	3.11E-04		-2.85E-01	9.21E-02		-6.34E-01	8.69E-05		3.86E-02	8.20E-01		-2.95E-01	4.42E-02		Unigene44426_All//gi|115445271|ref|NP_001046415.1|//3.00E-67//0s02g0244300 [Oryza sativa Japonica Group] >gi|113535946|dbj|BAF08329.1| Os02g0244300 [Oryza sativa Japonica Group]	Unigene44426_All//1.00E-68//AT1G17110| UBP15 (UBIQUITIN-SPECIFIC PROTEASE 15); ubiquitin-specific protease	Unigene44426_All//0.00E+00//TC155194				nr -
Unigene44432_All	1692	5.13	4.67	3.56	36.68	34.90	28.51	26.61	20.21	11.30	-1.36E-01	5.31E-01		-5.30E-01	9.77E-03		-7.18E-02	3.76E-01		-3.64E-01	1.58E-08		-3.97E-01	1.70E-08		-1.24E+00	6.97E-58	Down	Unigene44432_All//gi|297818750|ref|XP_002877258.1|//1.00E-170//glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] >gi|297336164|gb|EFH66581.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	Unigene44432_All//9.00E-171//AT3G42950| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene44432_All//0.00E+00//gi|164315106|gb|ES803406.1|ES803406		ko00500|Starch and sucrose metabolism/ko00040|Pentose and glucuronate interconversions		nr +
Unigene44433_All	1871	0.98	1.27	1.28	17.55	16.40	11.37	5.20	1.65	4.09	3.79E-01	3.64E-01		3.88E-01	3.90E-01		-9.75E-02	3.87E-01		-6.26E-01	6.32E-12		-1.65E+00	2.49E-19	Down	-3.46E-01	3.30E-02		Unigene44433_All//gi|297844882|ref|XP_002890322.1|//0.00E+00//glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] >gi|297336164|gb|EFH66581.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]	Unigene44433_All//0.00E+00//AT1G19170| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene44433_All//0.00E+00//ES817974		ko00500|Starch and sucrose metabolism/ko00040|Pentose and glucuronate interconversions		nr -
Unigene44434_All	1269	2.97	13.26	3.94	10.64	11.97	12.60	14.29	19.70	21.10	2.16E+00	4.49E-38	Up	4.10E-01	1.50E-01		1.70E-01	3.05E-01		2.44E-01	1.05E-01		4.63E-01	1.85E-06		5.62E-01	1.07E-09		Unigene44434_All//gi|15230025|ref|NP_187218.1|//2.00E-56//PHD finger family protein [Arabidopsis thaliana]	Unigene44434_All//2.00E-11//AT3G05670| PHD finger family protein	Unigene44434_All//6.00E-74//TC173148		ko03040|Spliceosome		nr +
Unigene44437_All	2681	0.80	2.12	0.79	1.45	1.64	1.58	2.71	3.63	4.96	1.40E+00	1.17E-07	Up	-1.01E-02	1.00E+00		1.82E-01	5.88E-01		1.28E-01	6.85E-01		4.21E-01	1.13E-02		8.72E-01	2.47E-10		Unigene44437_All//gi|15230025|ref|NP_187218.1|//1.00E-156//PHD finger family protein [Arabidopsis thaliana]	Unigene44437_All//3.00E-121//AT3G05670| PHD finger family protein	Unigene44437_All//0.00E+00//TC173148				nr -
Unigene44439_All	3145	1.36	6.83	1.63	4.28	5.21	4.54	7.76	11.06	12.12	2.32E+00	5.09E-53	Up	2.53E-01	3.85E-01		2.85E-01	4.13E-02		8.56E-02	6.34E-01		5.11E-01	3.02E-10		6.44E-01	6.70E-17		Unigene44439_All//gi|15230025|ref|NP_187218.1|//1.00E-162//PHD finger family protein [Arabidopsis thaliana]	Unigene44439_All//7.00E-122//AT3G05670| PHD finger family protein	Unigene44439_All//0.00E+00//TC175596		ko03040|Spliceosome		nr +
Unigene44442_All	721	8.64	2.74	5.61	2.14	2.67	2.63	0.70	0.29	0.94	-1.66E+00	1.87E-10	Down	-6.22E-01	1.20E-02		3.21E-01	5.66E-01		2.97E-01	5.85E-01		-1.28E+00	1.86E-01		4.17E-01	6.01E-01		Unigene44442_All//gi|297834278|ref|XP_002885021.1|//5.00E-89//phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330861|gb|EFH61280.1| phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44442_All//1.00E-89//AT3G14205| phosphoinositide phosphatase family protein	Unigene44442_All//0.00E+00//gi|48830126|gb|C0128516.1|C0128516				nr +
Unigene44445_All	3135	5.72	5.35	7.78	5.10	5.26	6.73	7.27	9.40	19.79	-9.76E-02	5.13E-01		4.43E-01	1.07E-04		4.48E-02	8.18E-01		3.99E-01	7.48E-04		3.71E-01	3.11E-05		1.44E+00	7.11E-100	Up	Unigene44445_All//gi|18400310|ref|NP_566481.1|//0.00E+00//phosphoinositide phosphatase family protein [Arabidopsis thaliana] >gi|15215806|gb|AAK91448.1| At3g14201 [Arabidopsis thaliana] >gi|20334798|gb|AAM16260.1| at3g14201/at3g14201 [Arabidopsis thaliana] >gi|31415721|gb|AAP49835.1| SAC domain protein 2 [Arabidopsis thaliana]	Unigene44445_All//0.00E+00//AT3G14205| phosphoinositide phosphatase family protein	Unigene44445_All//0.00E+00//TC175485				nr -
Unigene44447_All	3486	4.68	4.68	3.12	7.82	7.50	5.82	12.29	7.83	5.55	-8.00E-04	9.95E-01		-5.88E-01	3.64E-05		-6.01E-02	6.29E-01		-4.26E-01	2.57E-05		-6.50E-01	1.06E-18		-1.15E+00	6.06E-49	Down	Unigene44447_All//gi|9759112|dbj|BAB09597.1|//0.00E+00//low density lipoprotein B-like protein [Arabidopsis thaliana]	Unigene44447_All//0.00E+00//AT5G16300| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Vps51/Vps67 (InterPro:IPR014812); Has 204 Blast hits to 183 proteins in 76 species: Archae - 0; Bacteria - 0; Metazoa - 127; Fungi - 34; Plants - 24; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink).	Unigene44447_All//0.00E+00//TC143320				nr +
Unigene44448_All	4192	1.69	1.43	2.07	3.54	3.99	3.21	4.14	2.10	1.50	-2.41E-01	3.09E-01		2.97E-01	1.63E-01		1.73E-01	2.61E-01		-1.41E-01	4.07E-01		-9.75E-01	2.35E-15		-1.46E+00	2.72E-29	Down	Unigene44448_All//gi|9759112|dbj|BAB09597.1|//0.00E+00//low density lipoprotein B-like protein [Arabidopsis thaliana]	Unigene44448_All//0.00E+00//AT5G16300| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Vps51/Vps67 (InterPro:IPR014812); Has 204 Blast hits to 183 proteins in 76 species: Archae - 0; Bacteria - 0; Metazoa - 127; Fungi - 34; Plants - 24; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink).	Unigene44448_All//0.00E+00//TC143320				nr +

Unigene44449_All	3573	3.18	2.04	3.29	8.96	7.44	7.57	9.86	5.86	4.46	-6.38E-01	1.48E-04		5.18E-02	7.76E-01		-2.69E-01	3.51E-03		-2.44E-01	1.28E-02		-7.50E-01	9.95E-20		-1.14E+00	2.46E-40	Down	Unigene44449_All//gi|9759112|dbj|BAB09597.1|//0.00E+00//low density lipoprotein B-like protein [Arabidopsis thaliana]	Unigene44449_All//0.00E+00//AT5G16300| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Vps51/Vps67 (InterPro:IPR014812); Has 204 Blast hits to 183 proteins in 76 species: Archae - 0; Bacteria - 0; Metazoa - 127; Fungi - 34; Plants - 24; Viruses - 0; Other Eukaryotes - 19 (source: NCBI BLink).	Unigene44449_All//0.00E+00//TC176528				nr +
Unigene44450_All	468	7.83	11.80	1.71	7.77	5.30	5.98	7.05	11.34	9.79	5.93E-01	1.95E-02		-2.20E+00	1.35E-08	Down	-5.53E-01	7.93E-02		-3.77E-01	2.78E-01		6.87E-01	2.94E-03		4.74E-01	5.49E-02				Unigene44450_All//4.00E-131//gi|109825612|gb|DW224337.1|DW224337				
Unigene44453_All	1835	3.39	3.59	1.63	3.15	5.09	4.41	4.75	5.90	6.69	8.13E-02	7.26E-01		-1.06E+00	2.16E-05	Down	6.92E-01	1.03E-04		4.84E-01	1.89E-02		3.14E-01	5.12E-02		4.95E-01	4.27E-04		Unigene44453_All//gi|49523571|emb|CAF18247.1|//0.00E+00//SEU1 protein [Antirrhinum majus]	Unigene44453_All//3.00E-94//AT5G62090| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arabidopsis thaliana protein match is: SLK1 (SEUSS-LIKE 1); transcription regulator (TAIR:AT4G25520.1); Has 38202 Blast hits to 15459 proteins in 742 species: Archae - 6; Bacteria - 1392; Metazoa - 14682; Fungi - 3752; Plants - 2341; Viruses - 407; Other Eukaryotes - 15622 (source: NCBI BLink).	Unigene44453_All//0.00E+00//TC169810				nr +
Unigene44459_All	215	0.49	1.65	2.48	0.93	0.80	0.42	0.39	5.44	2.04	1.76E+00	2.18E-01		2.35E+00	5.87E-02		-2.11E-01	8.59E-01		-1.14E+00	5.68E-01		3.79E+00	2.86E-06	Up	2.37E+00	4.04E-02		Unigene44459_All//gi|4585991|gb|AAD25627.1|AC005287_29//2.00E-25//Dma1- and Dma2-like protein [Arabidopsis thaliana]	Unigene44459_All//6.00E-27//AT1G54490| XEN4 (EXORIBONUCLEASE 4); 5'-3' exonuclease/ 5'-3' exoribonuclease/ nucleic acid binding	Unigene44459_All//6.00E-116//TC178862		ko03018|RNA degradation		nr -
Unigene4446_All	817	6.79	7.38	6.45	11.40	9.82	12.94	9.94	5.78	3.12	1.21E-01	6.20E-01		-7.32E-02	7.83E-01		-2.15E-01	3.05E-01		1.82E-01	3.82E-01		-7.81E-01	1.70E-05		-1.67E+00	4.74E-17	Down	Unigene4446_All//gi|158828223|gb|AB981101.1|//3.00E-42//RNApol24 [Cleome spinosa]	Unigene4446_All//2.00E-34//AT2G29540| ATRPC14 (RNA POLYMERASE 14 KDA SUBUNIT); DNA binding / DNA-directed RNA polymerase/ protein dimerization	Unigene4446_All//0.00E+00//TC162911		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene44465_All	1542	1.93	0.99	1.48	2.33	2.37	0.73	7.73	3.98	4.65	-9.72E-01	7.36E-03		-3.81E-01	3.34E-01		2.53E-02	9.49E-01		-1.67E+00	9.86E-07	Down	-9.57E-01	1.67E-10		-7.34E-01	3.18E-07		Unigene44465_All//gi|42567409|ref|NP_195253.3|//1.00E-113//RWP-RK domain-containing protein [Arabidopsis thaliana]	Unigene44465_All//2.00E-90//AT4G35270| RWP-RK domain-containing protein	Unigene44465_All//0.00E+00//TC162202	RWP-RK			nr +
Unigene44466_All	2071	1.47	2.59	1.16	4.38	3.82	2.01	12.82	4.40	1.31	8.24E-01	1.43E-03		-3.41E-01	3.92E-01		-1.95E-01	3.59E-01		-1.13E+00	4.03E-09	Down	-1.54E+00	1.18E-46	Down	-3.29E+00	1.66E-120	Down	Unigene44466_All//gi|6448579|emb|CAB61243.1|//1.00E-146//nodule inception protein [Lotus japonicus] >gi|6453569|emb|CAB61338.1| nodule inception protein [Lotus japonicus]	Unigene44466_All//2.00E-129//AT4G35270| RWP-RK domain-containing protein	Unigene44466_All//6.00E-78//DT464338	RWP-RK			nr +
Unigene4447_All	760	23.54	9.93	35.59	39.00	24.78	22.76	15.13	11.05	6.13	-1.25E+00	5.96E-19	Down	5.96E-01	2.77E-08		-6.54E-01	5.63E-13		-7.77E-01	1.48E-15		-4.53E-01	2.52E-03		-1.30E+00	1.06E-16	Down	Unigene4447_All//gi|115441931|ref|NP_001045245.1|//1.00E-07//Os01g0924200 [Oryza sativa Japonica Group] >gi|113534776|dbj|BAF07159.1|Os01g0924200 [Oryza sativa Japonica Group]		Unigene4447_All//1.00E-175//gi|164355355|gb|ES834576.1|ES834576				nr +
Unigene44472_All	532	2.95	3.05	2.00	7.96	8.35	7.39	4.45	1.81	5.39	4.69E-02	9.41E-01		-5.60E-01	3.18E-01		6.92E-02	8.31E-01		-1.08E-01	7.33E-01		-1.30E+00	6.01E-04	Down	2.77E-01	4.11E-01		Unigene44472_All//sp|Q02817|MUC2_HUMAN//1.00E-06//Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2		Unigene44472_All//0.00E+00//TC160396				swissprot +
Unigene44476_All	1070	2.54	0.38	2.19	5.87	4.15	2.70	7.59	2.11	2.27	-2.75E+00	1.03E-08	Down	-2.16E-01	6.19E-01		-4.99E-01	2.84E-02		-1.12E+00	1.86E-06	Down	-1.85E+00	7.46E-19	Down	-1.74E+00	5.27E-18	Down	Unigene44476_All//gi|152413312|ref|NP_196916.1|//1.00E-118//nodulin family protein [Arabidopsis thaliana] >gi|9757793|dbj|BAB08291.1|nodulin-like protein [Arabidopsis thaliana]	Unigene44476_All//7.00E-112//AT5G14120| nodulin family protein	Unigene44476_All//6.00E-89//DW231799				nr +
Unigene44477_All	1365	4.18	2.30	4.45	8.50	5.85	3.94	10.78	5.60	2.86	-8.60E-01	5.63E-04		9.01E-02	7.20E-01		-5.39E-01	5.16E-04		-1.11E+00	2.85E-11	Down	-9.44E-01	1.64E-12		-1.91E+00	2.65E-36	Down	Unigene44477_All//gi|297807437|ref|XP_002871602.1|//1.00E-147//nodulin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317439|gb|EFH47861.1|nodulin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44477_All//1.00E-133//AT5G14120| nodulin family protein	Unigene44477_All//0.00E+00//DW517717				nr -
Unigene44479_All	2271	7.17	11.33	10.53	19.57	39.42	29.31	27.20	18.02	18.14	6.62E-01	8.43E-10		5.55E-01	1.35E-06		1.01E+00	5.62E-78	Up	5.83E-01	1.09E-20		-5.94E-01	8.77E-23		-5.85E-01	8.57E-23		Unigene44479_All//gi|297828556|ref|XP_002882160.1|//0.00E+00//nodulin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328000|gb|EFH58419.1|nodulin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44479_All//0.00E+00//AT5G14120| nodulin family protein	Unigene44479_All//0.00E+00//TC150316				nr +
Unigene4448_All	602	12.43	8.84	18.93	16.47	22.19	37.74	36.94	31.66	44.40	-4.92E-01	2.17E-02		6.07E-01	4.95E-04		4.31E-01	3.81E-03		1.20E+00	7.97E-24	Up	-2.23E-01	4.20E-02		2.65E-01	4.46E-03		Unigene4448_All//gi|75250205|sp|Q9 41D7.1|GGPPS_HEVBR//9.00E-26//RecName: Full=Geranylgeranyl pyrophosphate synthase, chloroplastic; Short=GGPP synthase; Includes: RecName: Full=Dimethylallyltranstransferase; Includes: RecName: Full=Geranyltranstransferase; Includes: RecName: Full=Farnesyltranstransferase; Flags: Precursor >gi|14325238|dbj|BAB60678.1|geranylgeranyl diphosphate synthase [Hevea brasiliensis]	Unigene4448_All//3.00E-13//AT4G36810| GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltranstransferase	Unigene4448_All//0.00E+00//TC130518		ko00900|Terpenoid backbone biosynthesis		nr +
Unigene44486_All	2331	11.47	5.09	11.33	7.24	6.53	7.73	11.34	13.93	14.49	-1.17E+00	1.68E-25	Down	-1.76E-02	8.92E-01		-1.50E-01	3.21E-01		9.37E-02	5.71E-01		2.97E-01	4.90E-04		3.54E-01	1.17E-05		Unigene44486_All//gi|224060213|ref|XP_002300088.1|//1.00E-164//cytochrome P450 [Populus trichocarpa] >gi|222847346|gb|EEE84893.1|cytochrome P450 [Populus trichocarpa]	Unigene44486_All//7.00E-128//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene44486_All//0.00E+00//TC141877		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene44487_All	969	26.19	10.25	12.53	35.68	29.46	26.24	37.61	16.22	13.32	-1.35E+00	3.93E-30	Down	-1.06E+00	5.73E-20	Down	-2.76E-01	1.61E-03		-4.43E-01	5.41E-07		-1.21E+00	2.00E-44	Down	-1.50E+00	7.82E-63	Down	Unigene44487_All//gi|224065409|ref|XP_002301803.1|//1.00E-157//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222843529|gb|EEE81076.1|glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene44487_All//2.00E-156//AT3G25140| QUA1 (QUASIMODO 1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene44487_All//0.00E+00//TC141605				nr -
Unigene44488_All	2096	24.81	9.55	17.25	48.32	27.73	32.21	25.17	11.73	10.68	-1.38E+00	1.02E-62	Down	-5.24E-01	2.88E-12		-8.01E-01	6.39E-62		-5.85E-01	1.49E-31		-1.10E+00	5.83E-55	Down	-1.24E+00	8.78E-68	Down	Unigene44488_All//gi|224065409|ref|XP_002301803.1|//0.00E+00//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222843529|gb|EEE81076.1|glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene44488_All//0.00E+00//AT3G25140| QUA1 (QUASIMODO 1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene44488_All//0.00E+00//TC141605				nr -
Unigene44489_All	4240	27.01	15.07	20.40	37.00	35.96	29.93	23.10	10.37	12.19	-8.42E-01	4.61E-62		-4.05E-01	1.39E-16		-4.09E-02	4.26E-01		-3.06E-01	5.31E-15		-1.16E+00	2.38E-109	Down	-9.23E-01	6.55E-78		Unigene44489_All//gi|224065409|ref|XP_002301803.1|//0.00E+00//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222843529|gb|EEE81076.1|glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene44489_All//0.00E+00//AT3G25140| QUA1 (QUASIMODO 1); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene44489_All//0.00E+00//TC143726		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene4449_All	667	4.86	11.62	5.75	14.12	13.42	13.54	108.58	84.66	37.93	1.26E+00	1.01E-08	Up	2.41E-01	4.78E-01		-7.26E-02	7.69E-01		-5.98E-02	7.79E-01		-3.59E-01	4.87E-11		-1.52E+00	1.62E-126	Down			Unigene4449_All//0.00E+00//gi|13349784|gb|BG440134.1|BG440134				
Unigene44492_All	3546	5.46	4.37	4.96	11.00	11.97	13.58	8.35	11.23	19.40	-3.20E-01	1.22E-02		-1.40E-01	3.48E-01		1.22E-01	1.81E-01		3.04E-01	5.34E-05		4.29E-01	1.26E-08		1.22E+00	3.11E-85	Up	Unigene44492_All//gi|226509827|ref|NP_001151544.1|//6.00E-62//transposon protein [Zea mays] >gi|195647582|gb|ACG43259.1|transposon protein [Zea mays]	Unigene44492_All//4.00E-39//AT3G42170| DNA binding	Unigene44492_All//0.00E+00//TC137986				nr +
Unigene44493_All	1005	10.88	39.28	24.53	8.72	12.57	16.45	9.72	7.65	6.90	1.85E+00	1.60E-72	Up	1.17E+00	1.08E-22	Up	5.28E-01	4.66E-04		9.15E-01	1.68E-11		-3.45E-01	4.10E-02		-4.95E-01	1.87E-03		Unigene44493_All//gi|59668642|emb|CAI53675.1|//1.00E-134//pyruvate kinase [Glycine max]	Unigene44493_All//8.00E-134//AT5G56350| pyruvate kinase, putative	Unigene44493_All//0.00E+00//TC131052		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene44494_All	427	0.37	4.63	3.99	0.58	1.05	0.85	3.37	3.03	3.17	3.65E+00	3.76E-08	Up	3.44E+00	1.59E-06	Up	8.46E-01	5.14E-01		5.37E-01	6.94E-01		-1.50E-01	7.64E-01		-8.58E-02	8.60E-01		Unigene44494_All//gi|10177833|dbj|BAB11262.1|//9.00E-10//pyruvate kinase [Arabidopsis thaliana] >gi|15450942|gb|AAK96742.1|pyruvate kinase [Arabidopsis thaliana] >gi|17978781|gb|AAL47384.1|pyruvate kinase [Arabidopsis thaliana] >gi|21592702|gb|AAM64651.1|pyruvate kinase [Arabidopsis thaliana]	Unigene44494_All//6.00E-11//AT5G56350| pyruvate kinase, putative	Unigene44494_All//3.00E-48//DR463157		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene44495_All	1183	4.33	4.07	3.60	6.36	6.11	6.41	18.69	16.22	73.45	-9.11E-02	7.28E-01		-2.67E-01	3.71E-01		-5.68E-02	8.11E-01		1.25E-02	9.53E-01		-2.05E-01	6.59E-02		1.97E+00	1.12E-216	Up	Unigene44495_All//gi|4033431|sp|O65595.1|KPYC_ARATH//6.00E-57//RecName: Full=Probable pyruvate kinase, cytosolic isozyme; Short=PK >gi|2982467|emb|CAA18231.1|pyruvate kinase like protein [Arabidopsis thaliana] >gi|7269491|emb|CAB79494.1|pyruvate kinase like protein [Arabidopsis thaliana]	Unigene44495_All//3.00E-58//AT4G26390| pyruvate kinase, putative	Unigene44495_All//0.00E+00//ES816356		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -

Unigene44496_All	1091	0.72	2.60	1.66	0.27	0.82	1.32	1.24	1.26	0.44	1.85E+00	7.02E-06	Up	1.21E+00	1.95E-02		1.58E+00	4.38E-02		2.27E+00	3.41E-04	Up	2.78E-02	9.89E-01		-1.50E+00	3.72E-03		Unigene44496_All//gi|59668642|emb|CAI53675.1|//1.00E-106//pyruvate kinase [Glycine max]	Unigene44496_All//1.00E-105//AT4G26390| pyruvate kinase, putative	Unigene44496_All//0.00E+00//TC131052		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene44497_All	1682	23.02	21.99	15.01	26.00	24.75	26.29	94.54	92.41	197.04	-6.59E-02	5.15E-01		-6.17E-01	3.02E-12		-7.12E-02	4.78E-01		1.57E-02	8.89E-01		-3.28E-02	4.83E-01		1.06E+00	0.00E+00	Up	Unigene44497_All//gi|59668642|emb|CAI53675.1|//0.00E+00//pyruvate kinase [Glycine max]	Unigene44497_All//0.00E+00//AT5G56350| pyruvate kinase, putative	Unigene44497_All//0.00E+00//TC161023		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene44498_All	1319	10.23	35.07	18.85	8.54	8.90	10.68	15.26	13.88	12.05	1.78E+00	2.98E-80	Up	8.81E-01	1.60E-14		6.08E-02	7.98E-01		3.24E-01	3.68E-02		-1.37E-01	2.77E-01		-3.40E-01	1.56E-03		Unigene44498_All//gi|59668642|emb|CAI53675.1|//1.00E-132//pyruvate kinase [Glycine max]	Unigene44498_All//2.00E-129//AT5G56350| pyruvate kinase, putative	Unigene44498_All//0.00E+00//gi|193219644|gb|EY198106.1|EY198106		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene44499_All	875	0.30	0.58	1.46	2.16	1.69	1.70	2.37	1.00	0.91	9.54E-01	3.73E-01		2.29E+00	1.40E-03		-3.54E-01	4.76E-01		-3.45E-01	4.99E-01		-1.24E+00	2.35E-03		-1.38E+00	5.68E-04	Down	Unigene44499_All//gi|75335380|sp|Q9LR20.1|TPR2_ARATH//1.00E-115//RecName: Full=Topless-related protein 2	Unigene44499_All//2.00E-177//AT3G16830| TPR2 (TOPLESS-RELATED 2)	Unigene44499_All//2.00E-177//gi|78344654|gb|DT564928.1|DT564928				nr +
Unigene4450_All	882	1.48	5.46	3.44	6.33	5.11	6.35	39.02	33.74	16.94	1.88E+00	1.27E-09	Up	1.21E+00	1.43E-03		-3.07E-01	2.48E-01		5.40E-03	9.85E-01		-2.10E-01	1.40E-02		-1.20E+00	1.06E-42	Down			Unigene4450_All//0.00E+00//DR459996				
Unigene44501_All	3720	2.73	5.61	3.05	3.66	3.10	4.19	3.67	8.04	4.09	1.04E+00	1.32E-16	Up	1.60E-01	3.91E-01		-2.37E-01	1.39E-01		1.96E-01	2.20E-01		1.13E+00	8.41E-33	Up	1.56E-01	2.56E-01		Unigene44501_All//gi|22331124|ref|NP_188306.2|//0.00E+00//TPR2 (TOPLESS-RELATED 2) [Arabidopsis thaliana]	Unigene44501_All//0.00E+00//AT3G16830| TPR2 (TOPLESS-RELATED 2)	Unigene44501_All//0.00E+00//gi|82756102|gb|DV849664.1|DV849664		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene44502_All	878	8.58	5.19	4.12	14.92	14.35	13.58	41.41	15.95	15.93	-7.24E-01	6.31E-04		-1.06E+00	2.50E-06	Down	-5.59E-02	7.93E-01		-1.36E-01	4.70E-01		-1.38E+00	9.53E-54	Down	-1.38E+00	1.91E-55	Down	Unigene44502_All//gi|17979243|gb|AAL49938.1|//1.00E-155//AT3g11830/F26K24_12 [Arabidopsis thaliana] >gi|20857172|gb|AAM26704.1| AT3g11830/F26K24_12 [Arabidopsis thaliana]	Unigene44502_All//2.00E-143//AT3G11830| chaperonin, putative	Unigene44502_All//0.00E+00//TC156493				nr -
Unigene44503_All	2199	28.05	15.23	14.53	43.13	39.34	38.67	34.17	16.84	15.58	-8.81E-01	2.09E-36		-9.49E-01	1.04E-39		-1.33E-01	1.39E-02		-1.57E-01	4.02E-03		-1.02E+00	8.18E-69	Down	-1.13E+00	1.04E-83	Down	Unigene44503_All//gi|17979243|gb|AAL49938.1|//0.00E+00//AT3g11830/F26K24_12 [Arabidopsis thaliana] >gi|20857172|gb|AAM26704.1| AT3g11830/F26K24_12 [Arabidopsis thaliana]	Unigene44503_All//0.00E+00//AT3G11830| chaperonin, putative	Unigene44503_All//0.00E+00//TC137870				nr -
Unigene44504_All	2082	15.78	9.22	6.42	32.28	29.51	40.33	33.95	16.98	17.49	-7.75E-01	5.39E-16		-1.30E+00	4.49E-35	Down	-1.29E-01	5.44E-02		3.21E-01	4.83E-09		-1.00E+00	1.30E-62		-9.57E-01	5.72E-60		Unigene44504_All//gi|17979243|gb|AAL49938.1|//0.00E+00//AT3g11830/F26K24_12 [Arabidopsis thaliana] >gi|20857172|gb|AAM26704.1| AT3g11830/F26K24_12 [Arabidopsis thaliana]	Unigene44504_All//0.00E+00//AT3G11830| chaperonin, putative	Unigene44504_All//0.00E+00//TC156493				nr -
Unigene44505_All	610	3.60	2.82	5.06	4.82	5.19	5.11	11.30	4.52	5.09	-3.51E-01	4.14E-01		4.91E-01	1.93E-01		1.08E-01	8.13E-01		8.45E-02	8.32E-01		-1.32E+00	3.27E-10	Down	-1.15E+00	1.16E-08	Down	Unigene44505_All//gi|224069844|ref|XP_002326428.1|//2.00E-83//ZIP transporter [Populus trichocarpa] >gi|222833621|gb|EEE72098.1| ZIP transporter [Populus trichocarpa]	Unigene44505_All//9.00E-43//AT3G08650| metal transporter family protein	Unigene44505_All//1.00E-162//BP274567				nr -
Unigene44508_All	2518	7.19	6.24	5.96	8.72	10.12	8.99	15.06	8.33	6.52	-2.05E-01	1.37E-01		-2.70E-01	5.65E-02		2.14E-01	5.61E-02		4.26E-02	7.56E-01		-8.54E-01	2.85E-26		-1.21E+00	3.15E-47	Down	Unigene44508_All//gi|224069844|ref|XP_002326428.1|//0.00E+00//ZIP transporter [Populus trichocarpa] >gi|222833621|gb|EEE72098.1| ZIP transporter [Populus trichocarpa]	Unigene44508_All//0.00E+00//AT3G08650| metal transporter family protein	Unigene44508_All//0.00E+00//TC157326				nr -
Unigene4451_All	724	8.53	7.28	4.34	12.52	9.04	4.37	7.83	6.75	4.18	-2.29E-01	3.61E-01		-9.75E-01	9.44E-05		-4.71E-01	1.01E-02		-1.52E+00	3.72E-14	Down	-2.12E-01	4.08E-01		-9.04E-01	3.40E-05		Unigene4451_All//gi|224131422|ref|XP_002328535.1|//2.00E-67//histone 2 [Populus trichocarpa] >gi|222838250|gb|EEE76615.1| histone 2 [Populus trichocarpa]	Unigene4451_All//8.00E-50//AT1G54690| GAMMA-H2AX (GAMMA HISTONE VARIANT H2AX); DNA binding	Unigene4451_All//0.00E+00//gi|13244901|gb|BE054618.2|BE054618				nr -
Unigene44515_All	775	2.50	0.78	1.79	2.31	3.87	1.98	6.55	5.55	4.88	-1.67E+00	7.92E-04	Down	-4.84E-01	3.33E-01		7.40E-01	3.89E-02		-2.24E-01	6.74E-01		-2.37E-01	3.76E-01		-4.23E-01	6.95E-02		Unigene44515_All//gi|15222516|ref|NP_174475.1|//1.00E-53//XLG3 (extra-large GTP-binding protein 3); guanyl nucleotide binding / signal transducer [Arabidopsis thaliana] >gi|30692624|ref|NP_849737.1| XLG3 (extra-large GTP-binding protein 3); guanyl nucleotide binding / signal transducer [Arabidopsis thaliana] >gi|222423921|dbj|BAH19924.1| AT1G31930 [Arabidopsis thaliana] >gi|222424740|dbj|BAH20323.1| AT1G31930 [Arabidopsis thaliana] >gi|251737921|gb|ACT10805.1| extra-large GTP-binding protein 3 [Arabidopsis thaliana]	Unigene44515_All//4.00E-16//AT1G31930| XLG3 (extra-large GTP-binding protein 3); guanyl nucleotide binding / signal transducer	Unigene44515_All//0.00E+00//TC169297				nr +
Unigene44452_All	595	26.82	19.67	8.86	21.94	20.89	26.04	102.25	56.20	29.46	-4.47E-01	1.37E-03		-1.60E+00	1.99E-23	Down	-7.02E-02	7.23E-01		2.47E-01	1.07E-01		-8.64E-01	1.96E-42		-1.80E+00	2.95E-135	Down	Unigene4452_All//gi|76573339|gb|AB046774.1|//4.00E-72//ribosomal protein L25-like protein [Solanum tuberosum]	Unigene4452_All//4.00E-46//AT3G55280| RPL23AB (RIBOSOMAL PROTEIN L23AB); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene4452_All//0.00E+00//TC159650		ko03010|Ribosome		nr +
Unigene44522_All	1518	3.17	1.74	2.70	9.06	8.92	5.00	5.54	2.59	2.65	-8.69E-01	1.55E-03		-2.31E-01	4.36E-01		-2.28E-02	8.99E-01		-8.58E-01	7.85E-09		-1.10E+00	2.14E-09	Down	-1.06E+00	2.84E-09	Down	Unigene44522_All//gi|297806617|ref|XP_002871192.1|//0.00E+00//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317029|gb|EFH47451.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44522_All//2.00E-180//AT5G65970| NED01 (NEURAL PRECURSOR CELL EXPRESSED, DEVELOPMENTALLY DOWN-REGULATED GENE 1); nucleotide binding	Unigene44522_All//0.00E+00//D8462431		ko03040|Spliceosome		nr +
Unigene44524_All	2504	4.99	2.49	2.57	17.61	16.64	11.09	8.24	4.76	3.23	-1.00E+00	9.09E-10	Down	-9.57E-01	1.24E-08		-8.14E-02	4.02E-01		-6.67E-01	1.33E-17		-7.93E-01	5.24E-13		-1.35E+00	6.66E-31	Down	Unigene44524_All//gi|297806617|ref|XP_002871192.1|//4.00E-72//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317029|gb|EFH47451.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44524_All//2.00E-59//AT5G65970| NED01 (NEURAL PRECURSOR CELL EXPRESSED, DEVELOPMENTALLY DOWN-REGULATED GENE 1); nucleotide binding	Unigene44524_All//0.00E+00//AI729429				nr -
Unigene44525_All	3140	2.98	7.75	5.82	9.80	12.25	13.06	12.37	17.48	17.13	1.38E+00	1.65E-29	Up	9.64E-01	1.76E-12		3.21E-01	8.11E-05		4.14E-01	3.12E-07		4.98E-01	5.43E-15		4.69E-01	1.25E-13		Unigene44525_All//gi|297806423|ref|XP_002871095.1|//0.00E+00//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297316932|gb|EFH47354.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene44525_All//0.00E+00//AT5G04460| protein binding / zinc ion binding	Unigene44525_All//0.00E+00//TC141937				nr +
Unigene4453_All	1897	34.97	14.48	17.63	46.09	34.42	41.47	41.30	20.12	18.40	-1.27E+00	1.09E-70	Down	-9.88E-01	1.29E-45		-4.21E-01	5.62E-17		-1.52E-01	8.47E-03		-1.04E+00	1.09E-73	Down	-1.17E+00	1.94E-91	Down	Unigene4453_All//gi|225435082|ref|XP_002284448.1|//3.00E-73//PREDICTED: similar to 60S ribosomal protein L23A isoform 2 [Vitis vinifera] >gi|225435084|ref|XP_002284445.1| PREDICTED: similar to 60S ribosomal protein L23A isoform 1 [Vitis vinifera]	Unigene4453_All//5.00E-46//AT2G39460| RPL23AA (RIBOSOMAL PROTEIN L23AA); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene4453_All//0.00E+00//gi|31074008|gb|CA994287.1|CA994287		ko03010|Ribosome		nr -
Unigene44532_All	475	0.33	2.56	1.23	0.63	0.29	1.52	2.31	1.32	2.18	2.95E+00	1.75E-04	Up	1.90E+00	8.47E-02		-1.12E+00	4.24E-01		1.27E+00	1.56E-01		-8.10E-01	1.69E-01		-8.59E-02	8.84E-01				Unigene44532_All//6.00E-07//CO128532				
Unigene44538_All	1199	2.09	1.65	1.91	6.81	4.65	5.09	5.50	2.51	6.31	-3.46E-01	3.82E-01		-1.33E-01	7.41E-01		-5.50E-01	4.02E-03		-4.22E-01	4.11E-02		-1.13E+00	7.20E-08	Down	1.99E-01	3.28E-01		Unigene44538_All//gi|15237894|ref|NP_197204.1|//0.00E+00//XPO1A; protein binding / protein transporter/ receptor [Arabidopsis thaliana] >gi|5931694|emb|CAB56597.1| Exportin1 (XPO1) protein [Arabidopsis thaliana] >gi|7671510|emb|CAB89280.1| Exportin1 (XPO1) protein [Arabidopsis thaliana] >gi|9755703|emb|CAC01715.1| Exportin1 (XPO1) protein [Arabidopsis thaliana]	Unigene44538_All//0.00E+00//AT5G17020| XPO1A; protein binding / protein transporter/ receptor	Unigene44538_All//0.00E+00//gi|78331121|gb|DT551395.1|DT551395				nr +
Unigene44540_All	885	2.31	1.83	4.99	2.53	3.00	3.67	3.58	3.26	2.30	-3.32E-01	4.66E-01		1.12E+00	2.52E-04	Up	2.42E-01	5.85E-01		5.37E-01	1.33E-01		-1.37E-01	6.81E-01		-6.42E-01	3.22E-02		Unigene44540_All//gi|115489788|ref|NP_001067381.1|//2.00E-61//Os12g0638600 [Oryza sativa Japonica Group] >gi|77556810|gb|ABA99606.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649888|dbj|BAF30400.1| Os12g0638600 [Oryza sativa Japonica Group]	Unigene44540_All//6.00E-74//AT5G20170| unknown protein	Unigene44540_All//0.00E+00//TC139477				nr -
Unigene44549_All	6093	0.39	0.37	0.79	0.58	0.36	0.49	0.95	0.36	0.50	-4.63E-02	9.20E-01		1.03E+00	3.87E-04	Up	-7.05E-01	2.35E-02		-2.47E-01	5.02E-01		-1.39E+00	2.56E-09	Down	-9.17E-01	2.12E-05		Unigene44549_All//gi|15451044|gb|AAK96793.1|//1.00E-165//Unknown protein [Arabidopsis thaliana] >gi|30725532|gb|AAP37788.1| At5g53620 [Arabidopsis thaliana]	Unigene44549_All//2.00E-158//AT5G53620| unknown protein	Unigene44549_All//0.00E+00//TC157827		ko03022|Basal transcription factors		nr +
Unigene4455_All	792	1.72	5.82	5.72	3.02	3.13	3.54	9.66	7.02	18.56	1.76E+00	1.58E-08	Up	1.73E+00	6.90E-08	Up	5.23E-02	9.19E-01		2.28E-01	6.17E-01		-4.61E-01	1.50E-02		9.42E-01	9.01E-13		Unigene4455_All//gi|21693562|gb|AAW75346.1|AF520810_1//7.00E-21//DNA-binding protein phosphatase 2C [Nicotiana tabacum]	Unigene4455_All//5.00E-07//AT3G17250| protein phosphatase 2C-related / PP2C-related	Unigene4455_All//0.00E+00//TC158389				nr +
Unigene44550_All	282	1.67	0.00	1.51	2.47	0.73	4.48	3.15	5.93	8.05	-1.07E+01	5.55E-03		-1.45E-01	8.90E-01		-1.76E+00	4.11E-02		8.59E-01	1.71E-01		9.13E-01	4.52E-02		1.35E+00	3.86E-04	Up	Unigene44550_All//gi|23306434|gb|AAN17444.1|//7.00E-23//eukaryotic initiation factor 4, eIF4-like protein [Arabidopsis thaliana] >gi|28059736|gb|AAO30087.1| eukaryotic initiation factor 4, eIF4-like protein [Arabidopsis thaliana]	Unigene44550_All//5.00E-21//AT5G57870| eukaryotic translation initiation factor 4F, putative / eIF-4F, putative	Unigene44550_All//3.00E-38//ES831546				nr -
Unigene44553_All	3109	15.20	11.59	7.33	25.36	23.20	32.61	29.47	21.48	24.94	-3.91E-01	3.60E-07		-1.05E+00	4.47E-36	Down	-1.28E-01	3.56E-02		3.63E-01	2.18E-13		-4.56E-01	5.89E-21		-2.41E-01	4.01E-07		Unigene44553_All//gi|23306434|gb|AAN17444.1|//0.00E+00//eukaryotic initiation factor 4, eIF4-like protein [Arabidopsis thaliana] >gi|28059736|gb|AAO30087.1| eukaryotic initiation factor 4, eIF4-like protein [Arabidopsis thaliana]	Unigene44553_All//0.00E+00//AT5G57870| eukaryotic translation initiation factor 4F, putative / eIF-4F, putative	Unigene44553_All//0.00E+00//TC168395				nr -

Unigene44555_All	682	3.76	2.30	0.47	4.97	4.29	3.97	5.15	1.78	4.15	-7.07E-01	7.30E-02		-3.00E+00	1.73E-08	Down	-2.11E-01	5.74E-01		-3.22E-01	3.93E-01		-1.53E+00	8.80E-07	Down	-3.11E-01	3.00E-01		Unigene44555_All//gi|18400779|ref|NP_566515.1|//5.00E-88//WD-40 repeat family protein [Arabidopsis thaliana] >gi|13937211|gb|AAK50098.1|AF372960_1 AT3g15470/MJK13_13 [Arabidopsis thaliana] >gi|15795112|dbj|BAB02376.1| WD-40 repeat protein-like [Arabidopsis thaliana] >gi|19548013|gb|AAL87370.1|AT3g15470/MJK13_13 [Arabidopsis thaliana]	Unigene44555_All//2.00E-70//AT1G34200| WD-40 repeat family protein	Unigene44555_All//1.00E-132//gi|164366551|gb|ES842803.1|ES842803				nr -
Unigene44556_All	3306	1.52	1.27	1.21	3.30	3.01	2.12	6.47	2.93	4.84	-2.56E-01	3.76E-01		-3.31E-01	2.52E-01		-1.33E-01	5.26E-01		-6.40E-01	1.42E-04		-1.14E+00	4.93E-24	Down	-4.18E-01	5.24E-05		Unigene44556_All//gi|18400779|ref|NP_566515.1|//0.00E+00//WD-40 repeat family protein [Arabidopsis thaliana] >gi|13937211|gb|AAK50098.1|AF372960_1 AT3g15470/MJK13_13 [Arabidopsis thaliana] >gi|15795112|dbj|BAB02376.1| WD-40 repeat protein-like [Arabidopsis thaliana] >gi|19548013|gb|AAL87370.1|AT3g15470/MJK13_13 [Arabidopsis thaliana]	Unigene44556_All//0.00E+00//AT3G15470| WD-40 repeat family protein	Unigene44556_All//0.00E+00//TC162598		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene44566_All	1388	30.42	14.35	33.34	16.83	20.74	10.90	6.40	3.91	3.79	-1.08E+00	3.33E-35	Down	1.32E-01	1.39E-01		3.01E-01	2.05E-03		-6.27E-01	1.08E-08		-7.09E-01	3.90E-05		-7.56E-01	7.38E-06		Unigene44566_All//gi|124359162|gb|ABN05685.1|//1.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene44566_All//7.00E-10//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene44566_All//2.00E-107//TC173067				nr -
Unigene44567_All	1958	10.72	4.04	7.97	6.74	5.40	3.41	3.13	2.67	1.30	-1.41E+00	1.48E-26	Down	-4.27E-01	6.15E-04		-3.20E-01	3.78E-02		-9.82E-01	1.63E-10		-2.31E-01	3.33E-01		-1.27E+00	6.09E-09	Down	Unigene44567_All//gi|124359191|gb|ABR32189.2|//2.00E-07//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]		Unigene44567_All//2.00E-65//TC173067				nr +
Unigene44573_All	1027	3.92	1.18	5.03	6.84	7.54	4.57	5.89	3.17	6.01	-1.73E+00	2.02E-07	Down	3.59E-01	2.13E-01		1.42E-01	5.78E-01		-5.81E-01	8.13E-03		-8.91E-01	3.55E-05		3.04E-02	9.09E-01		Unigene44573_All//gi|115459268|ref|NP_001053234.1|//1.00E-106//Os04g0502200 [Oryza sativa Japonica Group] >gi|113564805|dbj|BAF15148.1|Os04g0502200 [Oryza sativa Japonica Group]	Unigene44573_All//8.00E-134//AT5G11040| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Transport protein Trs120 (InterPro:IPR013935); Has 230 Blast hits to 190 proteins in 91 species: Archae - 0; Bacteria - 0; Metazoa - 128; Fungi - 64; Plants - 15; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).					nr -
Unigene44574_All	508	1.85	2.59	6.71	6.28	5.02	2.31	12.32	7.40	8.47	4.84E-01	3.94E-01		1.86E+00	1.28E-06	Up	-3.23E-01	3.85E-01		-1.44E+00	5.02E-05	Down	-7.34E-01	4.68E-04		-5.40E-01	8.05E-03		Unigene44574_All//gi|32479981|emb|CAE01639.1|//1.00E-33//OSJNBa0029802.30 [Oryza sativa (japonica cultivar-group)]	Unigene44574_All//3.00E-38//AT5G11040| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Transport protein Trs120 (InterPro:IPR013935); Has 230 Blast hits to 190 proteins in 91 species: Archae - 0; Bacteria - 0; Metazoa - 128; Fungi - 64; Plants - 15; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).	Unigene44574_All//2.00E-83//TC151872				nr -
Unigene44575_All	2205	0.71	1.79	0.99	1.36	1.33	1.37	4.85	2.88	2.46	1.33E+00	3.24E-05	Up	4.76E-01	3.04E-01		-3.02E-02	9.37E-01		1.78E-02	9.60E-01		-7.52E-01	1.39E-06		-9.81E-01	3.23E-10		Unigene44575_All//gi|115459268|ref|NP_001053234.1|//0.00E+00//Os04g0502200 [Oryza sativa Japonica Group] >gi|113564805|dbj|BAF15148.1|Os04g0502200 [Oryza sativa Japonica Group]	Unigene44575_All//0.00E+00//AT5G11040| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Transport protein Trs120 (InterPro:IPR013935); Has 230 Blast hits to 190 proteins in 91 species: Archae - 0; Bacteria - 0; Metazoa - 128; Fungi - 64; Plants - 15; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).					nr +
Unigene44589_All	3288	5.92	12.91	6.06	13.21	13.10	17.43	19.60	22.36	28.67	1.13E+00	2.16E-37	Up	3.31E-02	8.12E-01		-1.20E-02	9.07E-01		4.00E-01	2.78E-09		1.90E-01	6.48E-04		5.49E-01	1.39E-30		Unigene44589_All//gi|115474841|ref|NP_001061017.1|//0.00E+00//Os08g0154900 [Oryza sativa Japonica Group] >gi|113622986|dbj|BAF22931.1|Os08g0154900 [Oryza sativa Japonica Group]	Unigene44589_All//0.00E+00//AT4G08180| OBP1C (OSBP(OXYSTEROL BINDING PROTEIN)-RELATED PROTEIN 1C); oxysterol binding / phosphoinositide binding	Unigene44589_All//0.00E+00//ES818632				nr -
Unigene4459_All	975	0.38	0.94	0.82	19.72	13.74	13.20	4.99	0.94	1.27	1.32E+00	7.93E-02		1.13E+00	1.80E-01		-5.22E-01	6.68E-06		-5.79E-01	2.11E-06		-2.40E+00	6.86E-16	Down	-1.98E+00	4.56E-13	Down	Unigene4459_All//gi|56797970|emb|CAI39214.1|//2.00E-46//BCL-2 binding anthanogene-1 [Hordeum vulgare subsp. vulgare]	Unigene4459_All//1.00E-24//AT3G51780| ATBAG4 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 4); protein binding	Unigene4459_All//2.00E-144//gi|54118652|gb|CO494161.1|CO494161				nr -
Unigene44593_All	3790	2.39	0.91	1.36	3.48	3.33	2.41	5.97	7.19	16.90	-1.39E+00	1.05E-11	Down	-8.09E-01	4.83E-05		-6.29E-02	7.59E-01		-5.33E-01	4.46E-04		2.69E-01	4.75E-03		1.50E+00	3.29E-109	Up	Unigene44593_All//gi|300168191|gb|EFJ34795.1|//1.00E-105//ubiquitin-protein ligase, PUB13 [Selaginella moellendorffii]	Unigene44593_All//3.00E-93//AT1G20780| SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein ligase	Unigene44593_All//0.00E+00//TC165447				nr +
Unigene44594_All	3297	3.17	2.21	1.97	3.76	4.59	4.27	6.53	7.33	15.18	-5.20E-01	3.21E-03		-6.88E-01	1.72E-04		2.85E-01	5.20E-02		1.84E-01	2.85E-01		1.67E-01	1.29E-01		1.22E+00	3.08E-62	Up	Unigene4594_All//gi|300168191|gb|EFJ34795.1|//1.00E-104//ubiquitin-protein ligase, PUB13 [Selaginella moellendorffii]	Unigene4594_All//3.00E-87//AT1G20780| SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein ligase	Unigene44594_All//0.00E+00//TC178545				nr +
Unigene44596_All	2367	5.95	6.08	2.59	9.49	11.52	9.81	26.74	30.14	25.31	3.20E-02	8.43E-01		-1.20E+00	1.21E-13	Down	2.80E-01	6.19E-03		4.72E-02	7.25E-01		1.73E-01	2.59E-03		-7.91E-02	2.32E-01		Unigene44596_All//gi|115461575|ref|NP_001051387.1|//0.00E+00//Os05g0102600 [Oryza sativa Japonica Group] >gi|113577938|dbj|BAF16301.1|Os05g0102600 [Oryza sativa Japonica Group]	Unigene44596_All//0.00E+00//AT1G57820| VIM1 (VARIANT IN METHYLATION 1); DNA binding / chromatin binding / double-stranded methylated DNA binding / histone binding / methyl-CpG binding / methyl-CpNpG binding / methyl-CpNpN binding / ubiquitin-protein ligase	Unigene44596_All//0.00E+00//gi|164338676|gb|ES814429.1|ES814429				nr +
Unigene4460_All	1111	0.38	0.41	0.29	19.82	17.02	10.57	2.44	0.23	1.00	1.24E-01	9.11E-01		-3.89E-01	7.17E-01		-2.20E-01	6.84E-02		-9.07E-01	4.47E-15		-3.43E+00	7.61E-13	Down	-1.28E+00	1.75E-04	Down	Unigene4460_All//gi|56797970|emb|CAI39214.1|//1.00E-20//BCL-2 binding anthanogene-1 [Hordeum vulgare subsp. vulgare]	Unigene4460_All//2.00E-08//AT3G51780| ATBAG4 (ARABIDOPSIS THALIANA BCL-2-ASSOCIATED ATHANOGENE 4); protein binding	Unigene4460_All//1.00E-173//gi|164312991|gb|EX168912.1|EX168912				nr +
Unigene44607_All	702	4.99	16.31	7.51	11.78	17.46	17.24	11.56	12.56	29.06	1.71E+00	2.68E-19	Up	5.89E-01	3.07E-02		5.68E-01	1.99E-04		5.50E-01	6.08E-04		1.20E-01	5.73E-01		1.33E+00	1.49E-29	Up	Unigene44607_All//gi|124360769|gb|ABR03426.2|//3.00E-55//C2 [Medicago truncatula]	Unigene44607_All//1.00E-50//AT4G11610| C2 domain-containing protein	Unigene44607_All//4.00E-175//ES800656				nr +
Unigene44608_All	1037	1.61	2.79	5.55	1.15	2.79	3.09	71.19	153.52	80.98	7.87E-01	3.32E-02		1.78E+00	3.42E-10	Up	1.27E+00	4.65E-04	Up	1.42E+00	7.00E-05	Up	1.11E+00	1.20E-165	Up	1.86E-01	2.35E-04		Unigene44608_All//gi|90399215|emb|CAJ58177.1|//1.00E-147//H0306F12.8 [Oryza sativa (indica cultivar-group)]	Unigene44608_All//5.00E-147//AT4G11610| C2 domain-containing protein	Unigene44608_All//0.00E+00//TC144652				nr +
Unigene44609_All	3354	9.44	42.16	14.61	19.09	26.25	24.63	30.38	46.59	55.23	2.16E+00	0.00E+00	Up	6.30E-01	6.77E-16		4.60E-01	1.18E-19		3.68E-01	2.65E-11		6.17E-01	3.39E-60		8.62E-01	5.20E-130		Unigene44609_All//gi|115461410|ref|NP_001051305.1|//0.00E+00//Os04g0683800 [Oryza sativa Japonica Group] >gi|32488702|emb|CAE03445.1|OSJNBa0088809.3 [Oryza sativa (japonica cultivar-group)] >gi|113565876|dbj|BAF16219.1|Os04g0683800 [Oryza sativa Japonica Group]	Unigene44609_All//0.00E+00//AT4G11610| C2 domain-containing protein	Unigene44609_All//0.00E+00//TC143264				nr -
Unigene4461_All	1095	25.04	244.60	73.67	37.39	194.85	149.31	336.70	872.48	1239.44	3.29E+00	0.00E+00	Up	1.56E+00	6.89E-113	Up	2.38E+00	0.00E+00	Up	2.00E+00	0.00E+00	Up	1.37E+00	0.00E+00	Up	1.88E+00	0.00E+00	Up	Unigene4461_All//gi|14030723|gb|AAK53036.1|AF375452_1//9.00E-92//AT4g27450/F27G19_50 [Arabidopsis thaliana]	Unigene4461_All//6.00E-80//AT4G27450| unknown protein	Unigene4461_All//0.00E+00//DW499679		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene44611_All	1339	15.24	21.46	18.21	29.28	35.18	41.52	96.88	155.85	226.09	4.94E-01	9.71E-07		2.57E-01	3.12E-02		2.65E-01	3.39E-04		5.04E-01	1.77E-13		6.86E-01	1.55E-96		1.22E+00	0.00E+00	Up	Unigene44611_All//gi|58531948|gb|AAW78689.1|//0.00E+00//peroxisomal acyl-CoA oxidase 1A [Solanum lycopersicum]	Unigene44611_All//0.00E+00//AT4G16760| ACX1 (ACYL-COA OXIDASE 1); acyl-CoA oxidase	Unigene44611_All//0.00E+00//TC137718		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene44612_All	2476	7.10	8.08	8.69	17.12	19.12	26.92	54.63	83.81	142.15	1.87E-01	1.56E-01		2.91E-01	2.17E-02		1.60E-01	4.77E-02		6.53E-01	3.24E-25		6.18E-01	8.44E-80		1.38E+00	0.00E+00	Up	Unigene44612_All//gi|15553480|gb|AAL01888.1|AF404404_1//0.00E+00//acyl-CoA oxidase [Glycine max]	Unigene44612_All//0.00E+00//AT4G16760| ACX1 (ACYL-COA OXIDASE 1); acyl-CoA oxidase	Unigene44612_All//0.00E+00//TC137718		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene44615_All	888	0.53	1.43	0.72	1.80	1.78	0.71	3.48	2.64	0.99	1.43E+00	2.23E-02		4.40E-01	6.23E-01		-9.10E-03	9.69E-01		-1.33E+00	1.23E-02		-3.99E-01	2.34E-01		-1.82E+00	9.22E-08	Down			Unigene44615_All//0.00E+00//BF270631				
Unigene44618_All	5337	11.14	61.26	23.01	14.70	20.45	43.14	35.02	80.34	52.50	2.46E+00	0.00E+00	Up	1.05E+00	1.21E-92	Up	4.77E-01	7.28E-26		1.55E+00	0.00E+00	Up	1.20E+00	0.00E+00	Up	5.84E-01	1.39E-99		Unigene44618_All//gi|23193174|gb|AAN14410.1|//0.00E+00//bifunctional lysine-ketoglutarate reductase/saccharopine dehydrogenase [Gossypium hirsutum]	Unigene44618_All//0.00E+00//AT4G33150| lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme	Unigene44618_All//0.00E+00//TC139036		ko00310|Lysine degradation//ko00300|Lysine biosynthesis		nr +
Unigene44620_All	1525	1.89	1.66	2.03	3.53	6.50	8.06	4.82	7.48	6.03	-1.84E-01	6.23E-01		1.02E-01	7.74E-01		8.82E-01	2.96E-07		1.19E+00	4.77E-13	Up	6.33E-01	2.31E-05		3.23E-01	5.70E-02		Unigene44620_All//gi|3819699|emb|CAA08758.1|//1.00E-130//BnMAP4K alpha2 [Brassica napus]	Unigene44620_All//2.00E-120//AT3G15220| protein kinase, putative	Unigene44620_All//0.00E+00//ES827440				nr +
Unigene44623_All	2001	12.24	16.16	16.13	39.96	44.40	37.78	34.99	25.13	17.18	4.01E-01	2.30E-05		3.98E-01	4.82E-05		1.52E-01	5.78E-03		-8.07E-02	2.41E-01		-4.78E-01	1.40E-17		-1.03E+00	1.45E-66	Down	Unigene44623_All//gi|297823295|ref|XP_002879530.1|//0.00E+00//UTP--glucose-1-phosphate uridylyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325369|gb|EFH55789.1| UTP--glucose-1-phosphate uridylyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44623_All//0.00E+00//AT1G31070| UDP-N-acetylglucosamine pyrophosphorylase-related	Unigene44623_All//0.00E+00//gi|78342114|gb|DT562388.1|DT562388		ko00520|Amino sugar and nucleotide sugar metabolism		nr -

Unigene44626_All	1253	2.67	3.84	3.23	10.10	11.60	11.82	8.44	3.54	2.93	5.24E-01	5.84E-02		2.73E-01	3.93E-01		2.00E-01	2.21E-01		2.28E-01	1.53E-01		-1.25E+00	3.97E-14	Down	-1.53E+00	2.20E-19	Down	Unigene44626_All//gi|297823295|ref|XP_002879530.1|//1.00E-133//UTP--glucose-1-phosphate uridylyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325369|gb|EFH55789.1| UTP--glucose-1-phosphate uridylyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44626_All//2.00E-123//AT1G31070| UDP-N-acetylglucosamine pyrophosphorylase-related	Unigene44626_All//0.00E+00//gi|78342114|gb|DT562388.1|DT562388		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene4463_All	821	17.46	52.89	20.88	221.89	239.54	203.87	166.44	189.84	105.59	1.60E+00	5.69E-65	Up	2.58E-01	7.95E-02		1.10E-01	2.22E-03		-1.22E-01	1.58E-03		1.90E-01	2.49E-07		-6.57E-01	1.79E-60		Unigene4463_All//gi|135916116|db|BAB40967.1|//1.00E-120//UDP-D-glucuronate carboxy-lyase [Pisum sativum]	Unigene4463_All//1.00E-110//AT2G28760| NAD-dependent epimerase/dehydratase family protein	Unigene4463_All//0.00E+00//TC143716		ko00523|Polyketide sugar unit biosynthesis		nr -
Unigene44634_All	2368	8.09	2.38	4.45	15.71	13.18	6.20	12.00	6.23	4.66	-1.77E+00	1.51E-33	Down	-8.61E-01	6.83E-11		-2.54E-01	2.74E-03		-1.34E+00	7.03E-47	Down	-9.45E-01	1.87E-23		-1.36E+00	7.62E-43	Down	Unigene44634_All//gi|224074675|ref|XP_002304419.1|//1.00E-134//GRAS family transcription factor [Populus trichocarpa] >gi|222841851|gb|EEE79398.1| GRAS family transcription factor [Populus trichocarpa]	Unigene44634_All//1.00E-98//AT2G45160| scarecrow transcription factor family protein	Unigene44634_All//0.00E+00//TC169654	GRAS			nr +
Unigene44638_All	650	0.08	0.08	0.49	1.07	0.37	0.00	0.52	0.06	0.61	-4.55E-02	9.85E-01		2.61E+00	1.46E-01		-1.53E+00	7.01E-02		-1.01E+01	1.96E-04	Down	-3.02E+00	5.30E-02		2.36E-01	8.04E-01					Unigene44638_All//9.00E-56//TC174171				
Unigene4464_All	584	31.89	26.20	32.73	45.63	81.72	90.64	97.09	124.46	209.97	-2.84E-01	3.16E-02		3.75E-02	7.93E-01		8.41E-01	1.01E-30		9.90E-01	1.59E-40		3.58E-01	5.01E-11		1.11E+00	2.71E-131	Up	Unigene4464_All//gi|15450691|gb|AAK96617.1|//3.00E-89//AT3g04350/T6K12_3 [Arabidopsis thaliana] >gi|21360521|gb|AAM47376.1| AT3g04350/T6K12_3 [Arabidopsis thaliana]	Unigene4464_All//2.00E-90//AT3G04350| unknown protein	Unigene4464_All//0.00E+00//TC179392				nr -
Unigene44640_All	2276	6.16	2.69	4.16	14.69	13.54	8.85	6.85	7.91	9.82	-1.19E+00	4.26E-14	Down	-5.65E-01	2.74E-04		-1.17E-01	2.75E-01		-7.31E-01	9.34E-16		2.07E-01	9.86E-02		5.19E-01	2.95E-07		Unigene44640_All//gi|115473321|ref|NP_001060259.1|//2.00E-13//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene44640_All//5.00E-06//AT3G25270| nucleic acid binding	Unigene44640_All//0.00E+00//gi|13356329|gb|BG446677.1|BG446677				nr +
Unigene44646_All	2344	9.75	8.24	5.27	13.11	11.31	11.35	17.35	8.40	6.31	-2.44E-01	4.02E-02		-8.88E-01	1.53E-13		-2.13E-01	3.06E-02		-2.08E-01	4.27E-02		-1.05E+00	3.47E-39	Down	-1.46E+00	1.76E-67	Down	Unigene44646_All//gi|18411430|ref|NP_567184.1|//0.00E+00//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75163241|sp|Q93095.1|PMTD_ARATH RecName: Full=Probable methyltransferase PMT13 >gi|16648931|gb|AAL24317.1| Unknown protein [Arabidopsis thaliana] >gi|16649087|gb|AAL24395.1| Unknown protein [Arabidopsis thaliana] >gi|23197886|gb|AAN15470.1| Unknown protein [Arabidopsis thaliana] >gi|30725428|gb|AAP37736.1| At4g00740 [Arabidopsis thaliana]	Unigene44646_All//0.00E+00//AT4G00740| dehydration-responsive protein-related	Unigene44646_All//0.00E+00//TC158016				nr +
Unigene44647_All	785	2.93	3.55	3.32	7.42	5.70	5.47	5.55	2.66	2.79	2.76E-01	4.79E-01		1.81E-01	6.43E-01		-3.81E-01	1.26E-01		-4.42E-01	8.03E-02		-1.06E+00	5.40E-05	Down	-9.91E-01	9.59E-05		Unigene44647_All//gi|162463122|ref|NP_001105631.1|//1.00E-06//histone deacetylase HDT2 [Zea mays] >gi|73919941|sp|Q9M4U5.1|HDT2_MAIZE RecName: Full=Histone deacetylase HDT2; AltName: Full=Histone deacetylase 2b; Short=HD2b; AltName: Full=Zm-HD2b >gi|7716948|gb|AAF68824.1|AF254072_1 histone deacetylase 2 isoform b [Zea mays]		Unigene44647_All//0.00E+00//gi|78345356|gb|DT565630.1|DT565630				nr +
Unigene44649_All	2468	10.47	11.70	8.98	14.98	13.51	13.91	12.85	11.30	6.34	1.60E-01	1.40E-01		-2.23E-01	5.79E-02		-1.49E-01	1.15E-01		-1.07E-01	3.13E-01		-1.86E-01	4.12E-02		-1.02E+00	2.91E-30	Down	Unigene44649_All//gi|38345789|emb|CAE03561.2|//5.00E-51//OSJNBa0085I10.6 [Oryza sativa (japonica cultivar-group)] >gi|90265080|emb|CAH67753.1| H0702G05.12 [Oryza sativa (indica cultivar-group)] >gi|116309963|emb|CAH66992.1| OSIGBa0152L12.1 [Oryza sativa (indica cultivar-group)]	Unigene44649_All//1.00E-36//AT1G58025| DNA binding	Unigene44649_All//0.00E+00//gi|109848306|gb|DW477286.1|DW477286				nr -
Unigene44653_All	1965	2.90	6.50	3.14	4.99	4.78	6.30	12.14	14.06	13.69	1.16E+00	2.34E-12	Up	1.15E-01	6.45E-01		-6.20E-02	8.06E-01		3.35E-01	4.46E-02		2.12E-01	2.88E-02		1.73E-01	7.48E-02		Unigene44653_All//gi|297852504|ref|XP_002894133.1|//0.00E+00//mov34 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339975|gb|EFH70392.1| mov34 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44653_All//2.00E-175//AT1G48790| mov34 family protein	Unigene44653_All//0.00E+00//D8462843		ko04144|Endocytosis		nr +
Unigene44658_All	2285	5.68	2.31	4.22	11.01	10.43	8.93	6.64	4.43	3.59	-1.30E+00	7.19E-15	Down	-4.29E-01	9.04E-03		-7.82E-02	5.61E-01		-3.01E-01	5.99E-03		-5.86E-01	4.40E-06		-8.87E-01	4.58E-12		Unigene44658_All//gi|20856498|gb|AAM26669.1|//0.00E+00//AT4g16650/dl4350w [Arabidopsis thaliana] >gi|233084145|gb|ANN18192.1| At4g16650/dl4350w [Arabidopsis thaliana] >gi|51969788|dbj|BAD43586.1| growth regulator like protein [Arabidopsis thaliana]	Unigene44658_All//0.00E+00//AT4G16650| unknown protein	Unigene44658_All//0.00E+00//TC152234				nr -
Unigene4466_All	1004	0.31	2.17	2.12	2.28	3.22	1.66	2.36	2.16	1.79	2.79E+00	3.73E-07	Up	2.76E+00	1.21E-06	Up	4.98E-01	1.63E-01		-4.56E-01	3.09E-01		-1.24E-01	7.49E-01		-4.01E-01	2.74E-01									
Unigene44660_All	639	1.97	0.40	0.17	3.82	2.59	2.26	5.49	0.98	2.49	-2.31E+00	9.22E-04	Down	-3.56E+00	4.96E-05	Down	-5.62E-01	1.62E-01		-7.56E-01	6.57E-02		-2.48E+00	4.26E-12	Down	-1.14E+00	8.79E-05	Down	Unigene44660_All//gi|15223458|ref|NP_176007.1|//1.00E-65//NOP56 (Arabidopsis homolog of nucleolar protein Nop56) [Arabidopsis thaliana] >gi|6056371|gb|AAF02835.1|AC009894_6 nucleolar protein [Arabidopsis thaliana] >gi|11878189|gb|AAG40838.1|AF302492_1 NOP56-like protein [Arabidopsis thaliana] >gi|14517412|gb|AAK62596.1| At1g56110/T6H22_9 [Arabidopsis thaliana] >gi|20857405|gb|AAM26718.1| At1g56110/T6H22_9 [Arabidopsis thaliana]	Unigene44660_All//7.00E-67//AT1G56110| NOP56 (Arabidopsis homolog of nucleolar protein Nop56)	Unigene44660_All//0.00E+00//gi|13247149|gb|BF268804.2|BF268804				nr +
Unigene44661_All	1641	9.15	8.61	8.50	6.34	5.41	6.74	4.43	3.87	1.89	-8.71E-02	6.16E-01		-1.06E-01	5.36E-01		-2.29E-01	2.29E-01		8.79E-02	6.79E-01		-1.95E-01	3.79E-01		-1.23E+00	5.51E-10	Down	Unigene44661_All//gi|18397896|ref|NP_565377.1|//1.00E-109//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75216221|sp|Q9ZQE5.2|PP153_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g15690 >gi|14335136|gb|AAK59848.1| At2g15690/F9013.24 [Arabidopsis thaliana] >gi|20197709|gb|AAD17413.2| Expressed protein [Arabidopsis thaliana] >gi|29028728|gb|AAO64743.1| At2g15690/F9013.24 [Arabidopsis thaliana]	Unigene44661_All//7.00E-93//AT2G15690| pentatricopeptide (PPR) repeat-containing protein	Unigene44661_All//0.00E+00//TC167233				nr -
Unigene44662_All	2092	5.53	1.62	2.98	13.29	7.57	11.53	21.32	5.47	7.52	-1.77E+00	1.54E-20	Down	-8.92E-01	3.16E-07		-8.11E-01	1.27E-17		-2.05E-01	6.27E-02		-1.96E+00	1.00E-108	Down	-1.50E+00	3.89E-77	Down	Unigene44662_All//gi|15223458|ref|NP_176007.1|//0.00E+00//NOP56 (Arabidopsis homolog of nucleolar protein Nop56) [Arabidopsis thaliana] >gi|6056371|gb|AAF02835.1|AC009894_6 nucleolar protein [Arabidopsis thaliana] >gi|11878189|gb|AAG40838.1|AF302492_1 NOP56-like protein [Arabidopsis thaliana] >gi|14517412|gb|AAK62596.1| At1g56110/T6H22_9 [Arabidopsis thaliana] >gi|20857405|gb|AAM26718.1| At1g56110/T6H22_9 [Arabidopsis thaliana]	Unigene44662_All//0.00E+00//AT1G56110| NOP56 (Arabidopsis homolog of nucleolar protein Nop56)	Unigene44662_All//0.00E+00//TC167263		ko03040|Spliceosome		nr +
Unigene44663_All	2743	12.84	4.19	4.60	27.95	18.19	27.86	42.13	14.22	17.88	-1.61E+00	7.77E-54	Down	-1.48E+00	8.87E-46	Down	-6.20E-01	6.70E-30		-4.70E-03	9.57E-01		-1.57E+00	2.89E-205	Down	-1.24E+00	2.10E-147	Down	Unigene44663_All//gi|15223458|ref|NP_176007.1|//0.00E+00//NOP56 (Arabidopsis homolog of nucleolar protein Nop56) [Arabidopsis thaliana] >gi|6056371|gb|AAF02835.1|AC009894_6 nucleolar protein [Arabidopsis thaliana] >gi|11878189|gb|AAG40838.1|AF302492_1 NOP56-like protein [Arabidopsis thaliana] >gi|14517412|gb|AAK62596.1| At1g56110/T6H22_9 [Arabidopsis thaliana] >gi|20857405|gb|AAM26718.1| At1g56110/T6H22_9 [Arabidopsis thaliana]	Unigene44663_All//0.00E+00//AT1G56110| NOP56 (Arabidopsis homolog of nucleolar protein Nop56)	Unigene44663_All//0.00E+00//TC167263		ko03040|Spliceosome		nr +
Unigene44669_All	3047	2.35	2.61	3.90	8.40	8.92	7.92	8.95	4.61	4.29	1.50E-01	5.06E-01		7.28E-01	1.89E-05		8.56E-02	5.22E-01		-8.63E-02	5.17E-01		-9.58E-01	5.21E-23		-1.06E+00	6.15E-28	Down	Unigene44669_All//gi|18416416|ref|NP_568242.1|//0.00E+00//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene44669_All//0.00E+00//AT5G10940| transducin family protein / WD-40 repeat family protein	Unigene44669_All//0.00E+00//gi|18099799|gb|BM359053.1|BM359053				nr +

Unigene4467_All	887	6.02	47.24	10.21	37.63	24.19	17.57	50.24	48.96	66.61	2.97E+00	3.30E-135	Up	7.62E-01	1.24E-04		-6.38E-01	6.31E-14		-1.10E+00	8.28E-31	Down	-3.73E-02	6.66E-01		4.07E-01	1.17E-11		Unigene4467_All//gi|297802270|ref|XP_002869019.1|//5.00E-55//transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297314855|gb|EFH45278.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene4467_All//6.00E-50//AT2G23790| unknown protein	Unigene4467_All//0.00E+00//gi|48743732|gb|CO074251.1|CO074251				nr +
Unigene44678_All	727	0.14	0.70	0.88	0.75	0.90	0.37	0.76	3.10	2.47	2.28E+00	6.23E-02		2.61E+00	2.33E-02		2.56E-01	8.21E-01		-1.02E+00	3.29E-01		2.04E+00	1.89E-06	Up	1.71E+00	1.83E-04	Up	Unigene44678_All//gi|19699290|gb|AL91256.1|//1.00E-100//At1g15070/F9L1_1 [Arabidopsis thaliana] >gi|24111379|gb|AAN46813.1| At1g15070/F9L1_1 [Arabidopsis thaliana]	Unigene44678_All//5.00E-102//AT1G15060| LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031088, alpha/beta hydrolase, At1g15070 (InterPro:IPR016969); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73750.1); Has 120 Blast hits to 104 proteins in 29 species: Archae - 0; Bacteria - 61; Metazoa - 1; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene44678_All//0.00E+00//ES835925				nr -
Unigene44679_All	589	4.44	7.40	7.41	3.98	5.67	9.12	1.58	3.41	1.56	7.36E-01	1.13E-02		7.39E-01	1.44E-02		5.13E-01	1.43E-01		1.20E+00	4.11E-06	Up	1.11E+00	7.07E-03		-2.16E-02	9.60E-01		Unigene44679_All//gi|5103806|gb|AAD39636.1|AC007591_1//3.00E-46//EST gb|F14271 comes from this gene [Arabidopsis thaliana]	Unigene44679_All//2.00E-44//AT1G15060| LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031088, alpha/beta hydrolase, At1g15070 (InterPro:IPR016969); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73750.1); Has 120 Blast hits to 104 proteins in 29 species: Archae - 0; Bacteria - 61; Metazoa - 1; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene44679_All//0.00E+00//gi|78333069|gb|DT553343.1|DT553343				nr -
Unigene4468_All	677	5.26	4.34	6.45	6.11	5.65	7.67	13.12	6.30	8.94	-2.76E-01	4.04E-01		2.96E-01	3.61E-01		-1.13E-01	7.54E-01		3.29E-01	2.49E-01		-1.06E+00	2.44E-09	Down	-5.52E-01	9.74E-04		Unigene4468_All//gi|18400083|ref|NP_564470.1|//2.00E-29//methyltransferase [Arabidopsis thaliana] >gi|79319214|ref|NP_001031144.1| methyltransferase [Arabidopsis thaliana] >gi|222423891|dbj|BAH19909.1| AT1G36310 [Arabidopsis thaliana]	Unigene4468_All//2.00E-23//AT1G36310| methyltransferase	Unigene4468_All//0.00E+00//TC147549				nr -
Unigene44681_All	1618	3.95	11.21	4.34	5.02	7.00	8.63	7.03	12.86	10.66	1.51E+00	2.69E-25	Up	1.39E-01	5.94E-01		4.81E-01	3.11E-03		7.81E-01	1.19E-07		8.72E-01	2.85E-15		6.01E-01	2.68E-07		Unigene44681_All//gi|19699290|gb|AL91256.1|//1.00E-151//At1g15070/F9L1_1 [Arabidopsis thaliana] >gi|24111379|gb|AAN46813.1| At1g15070/F9L1_1 [Arabidopsis thaliana]	Unigene44681_All//3.00E-152//AT1G15060| LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031088, alpha/beta hydrolase, At1g15070 (InterPro:IPR016969); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73750.1); Has 120 Blast hits to 104 proteins in 29 species: Archae - 0; Bacteria - 61; Metazoa - 1; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene44681_All//0.00E+00//ES835925				nr -
Unigene44682_All	2226	2.35	4.92	4.31	4.05	3.45	3.55	5.76	6.97	6.96	1.06E+00	2.15E-09	Up	8.73E-01	6.21E-06		-2.32E-01	2.69E-01		-1.90E-01	4.04E-01		2.76E-01	3.70E-02		2.75E-01	3.06E-02		Unigene44682_All//gi|19699290|gb|AL91256.1|//0.00E+00//At1g15070/F9L1_1 [Arabidopsis thaliana] >gi|24111379|gb|AAN46813.1| At1g15070/F9L1_1 [Arabidopsis thaliana]	Unigene44682_All//0.00E+00//AT1G15060| LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031088, alpha/beta hydrolase, At1g15070 (InterPro:IPR016969); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73750.1); Has 120 Blast hits to 104 proteins in 29 species: Archae - 0; Bacteria - 61; Metazoa - 1; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene44682_All//0.00E+00//TC179108				nr +
Unigene44683_All	1078	4.95	27.31	6.87	13.12	12.01	14.83	38.75	38.73	32.41	2.46E+00	1.32E-77	Up	4.72E-01	3.74E-02		-1.28E-01	4.66E-01		1.77E-01	2.70E-01		-7.00E-04	9.92E-01		-2.58E-01	3.96E-04		Unigene44683_All//gi|15218566|ref|NP_174686.1|//4.00E-92//phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] >gi|5091620|gb|AAD39608.1|AC007454_7 Contains similarity to gi|836774 FAB1 protein from Saccharomyces cerevisiae genome gb|D50617 [Arabidopsis thaliana]	Unigene44683_All//9.00E-94//AT1G34260| phosphatidylinositol-4-phosphate 5-kinase family protein	Unigene44683_All//0.00E+00//TC155630		ko04145|Phagosome//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene44684_All	1224	0.90	5.13	1.48	3.13	3.88	2.69	2.52	1.09	1.50	2.52E+00	2.02E-17	Up	7.21E-01	1.52E-01		3.09E-01	3.14E-01		-2.18E-01	5.44E-01		-1.21E+00	1.87E-04	Down	-7.52E-01	1.35E-02		Unigene44684_All//gi|15218566|ref|NP_174686.1|//5.00E-86//phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] >gi|5091620|gb|AAD39608.1|AC007454_7 Contains similarity to gi|836774 FAB1 protein from Saccharomyces cerevisiae genome gb|D50617 [Arabidopsis thaliana]	Unigene44684_All//9.00E-88//AT1G34260| phosphatidylinositol-4-phosphate 5-kinase family protein	Unigene44684_All//0.00E+00//ES803116		ko04144|Endocytosis//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene44685_All	4756	1.34	6.49	2.06	3.93	4.75	5.48	17.53	11.45	21.45	2.27E+00	6.41E-74	Up	6.18E-01	1.14E-03		2.74E-01	1.75E-02		4.80E-01	3.67E-06		-6.14E-01	2.71E-32		2.91E-01	8.14E-11		Unigene44685_All//gi|15218566|ref|NP_174686.1|//0.00E+00//phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] >gi|5091620|gb|AAD39608.1|AC007454_7 Contains similarity to gi|836774 FAB1 protein from Saccharomyces cerevisiae genome gb|D50617 [Arabidopsis thaliana]	Unigene44685_All//0.00E+00//AT1G34260| phosphatidylinositol-4-phosphate 5-kinase family protein	Unigene44685_All//0.00E+00//TC175290		ko04145|Phagosome//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene44686_All	682	4.91	2.53	2.42	6.06	4.90	5.56	6.14	1.53	3.62	-9.59E-01	4.72E-03		-1.02E+00	4.12E-03		-3.08E-01	3.24E-01		-1.24E-01	6.94E-01		-2.00E+00	3.84E-11	Down	-7.61E-01	2.94E-03		Unigene44686_All//gi|15236004|ref|NP_194887.1|//9.00E-82//ATCSLC5 (CELLULOSE-SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75201904|sp|Q9SB75.1|CSLC5_ARATH RecName: Full=Probable xyloglucan glycosyltransferase 5; AltName: Full=Cellulose synthase-like protein C5; Short=AtCslC5 >gi|30725520|gb|AAP37782.1| At4g31590 [Arabidopsis thaliana]	Unigene44686_All//2.00E-76//AT4G31590| ATCSLC5 (CELLULOSE-SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups	Unigene44686_All//0.00E+00//TC165083				nr +
Unigene44687_All	3053	6.12	1.86	3.72	13.77	13.50	11.14	7.82	1.40	4.54	-1.72E+00	1.67E-31	Down	-7.20E-01	5.41E-08		-2.86E-02	8.14E-01		-3.06E-01	1.58E-04		-2.49E+00	1.91E-78	Down	-7.85E-01	3.75E-15		Unigene44687_All//gi|15236004|ref|NP_194887.1|//0.00E+00//ATCSLC5 (CELLULOSE-SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75201904|sp|Q9SB75.1|CSLC5_ARATH RecName: Full=Probable xyloglucan glycosyltransferase 5; AltName: Full=Cellulose synthase-like protein C5; Short=AtCslC5 >gi|30725520|gb|AAP37782.1| At4g31590 [Arabidopsis thaliana]	Unigene44687_All//0.00E+00//AT4G31590| ATCSLC5 (CELLULOSE-SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups	Unigene44687_All//0.00E+00//TC165083				nr -
Unigene44688_All	2905	9.33	4.57	7.68	15.67	15.10	15.62	6.21	1.19	3.95	-1.03E+00	4.57E-21	Down	-2.81E-01	1.18E-02		-5.36E-02	5.89E-01		-4.50E-03	9.56E-01		-2.38E+00	1.73E-56	Down	-6.54E-01	1.00E-08		Unigene44688_All//gi|15236004|ref|NP_194887.1|//0.00E+00//ATCSLC5 (CELLULOSE-SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75201904|sp|Q9SB75.1|CSLC5_ARATH RecName: Full=Probable xyloglucan glycosyltransferase 5; AltName: Full=Cellulose synthase-like protein C5; Short=AtCslC5 >gi|30725520|gb|AAP37782.1| At4g31590 [Arabidopsis thaliana]	Unigene44688_All//0.00E+00//AT4G31590| ATCSLC5 (CELLULOSE-SYNTHASE LIKE C5); cellulose synthase/ transferase, transferring glycosyl groups	Unigene44688_All//0.00E+00//TC165083				nr -
Unigene44690_All	923	8.56	14.16	11.77	9.88	14.51	19.96	40.54	15.76	22.57	7.27E-01	3.40E-06		4.59E-01	1.13E-02		5.55E-01	1.30E-04		1.02E+00	4.79E-15	Up	-1.36E+00	1.81E-54	Down	-8.45E-01	3.23E-26		Unigene44690_All//gi|71493366|gb|AA232787.1|//5.00E-95//cellulose synthase-like protein CslE [Nicotiana tabacum]	Unigene44690_All//4.00E-84//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene44690_All//3.00E-115//gi|73863433|gb|DT466172.1|DT466172				nr -
Unigene44691_All	1307	11.21	10.86	15.03	1.18	6.19	6.19	0.68	2.69	2.07	-4.63E-02	7.68E-01		4.24E-01	1.07E-03		2.39E+00	5.10E-24	Up	2.39E+00	2.87E-22	Up	1.98E+00	2.48E-09	Up	1.61E+00	6.67E-06	Up	Unigene44691_All//gi|71493366|gb|AA232787.1|//1.00E-137//cellulose synthase-like protein CslE [Nicotiana tabacum]	Unigene44691_All//3.00E-123//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene44691_All//0.00E+00//TC163664				nr -
Unigene44692_All	1528	0.72	1.76	1.64	6.46	5.45	6.00	28.03	17.07	207.64	1.29E+00	1.16E-03		1.19E+00	5.24E-03		-2.43E-01	2.14E-01		-1.05E-01	6.20E-01		-7.16E-01	5.35E-22		2.89E+00	0.00E+00	Up	Unigene44692_All//gi|71493366|gb|AA232787.1|//1.00E-161//cellulose synthase-like protein CslE [Nicotiana tabacum]	Unigene44692_All//1.00E-146//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene44692_All//0.00E+00//TC163664				nr +

Unigene44693_All	1889	2.27	3.35	3.75	11.26	12.60	11.62	136.67	41.26	52.70	5.62E-01	1.68E-02		7.23E-01	1.54E-03		1.62E-01	1.93E-01		4.53E-02	7.44E-01		-1.73E+00	0.00E+00	Down	-1.37E+00	0.00E+00	Down	Unigene44693_All//gi|226502156|ref|NP_001147894.1|//1.00E-167//CSLE6 - cellulose synthase-like family E [Zea mays] >gi|195614436|gb|ACG29048.1| CSLE6 - cellulose synthase-like family E [Zea mays]	Unigene44693_All//2.00E-164//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene44693_All//0.00E+00//BF268325				nr -
Unigene44695_All	2096	11.63	24.37	16.26	18.30	30.43	31.48	47.36	40.82	48.51	1.07E+00	3.50E-41	Up	4.83E-01	3.15E-07		7.34E-01	1.70E-32		7.83E-01	4.76E-34		-2.15E-01	4.42E-06		3.44E-02	5.53E-01		Unigene44695_All//gi|18087627|gb|AAL58943.1|AF462857_1//1.00E-124//At1g29350/F15D2_27 [Arabidopsis thaliana]	Unigene44695_All//1.00E-91//AT1G29350| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, guard cell, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1296 (InterPro:IPR009719); BEST Arabidopsis thaliana protein match is: kinase-related (TAIR:AT1G29370.1); Has 13611 Blast hits to 7582 proteins in 387 species: Archae - 0; Bacteria - 354; Metazoa - 5683; Fungi - 1538; Plants - 892; Viruses - 68; Other Eukaryotes - 5076 (source: NCBI BLink).	Unigene44695_All//0.00E+00//gi|78332359|gb|DT552633.1|DT552633				nr -
Unigene44698_All	3454	4.89	12.22	5.49	7.50	7.05	9.14	9.77	16.69	20.81	1.32E+00	1.27E-47	Up	1.66E-01	2.48E-01		-8.95E-02	5.02E-01		2.85E-01	3.21E-03		7.73E-01	2.42E-33		1.09E+00	7.29E-75	Up	Unigene44698_All//gi|30684887|ref|NP_850164.1|//0.00E+00//APG9 (autophagy 9) [Arabidopsis thaliana] >gi|19715618|gb|AAL91630.1| At2g31260/F16D14.10 [Arabidopsis thaliana] >gi|19912149|dbj|BAB88386.1| autophagy 9 [Arabidopsis thaliana] >gi|23463043|gb|AAX33191.1| At2g31260/F16D14.10 [Arabidopsis thaliana]	Unigene44698_All//0.00E+00//AT2G31260| APG9 (autophagy 9)	Unigene44698_All//0.00E+00//DW504983				nr -
Unigene44699_All	1867	5.91	4.40	5.48	5.15	6.82	5.85	5.91	2.22	2.07	-4.28E-01	1.34E-02		-1.11E-01	5.93E-01		4.06E-01	8.53E-03		1.85E-01	3.58E-01		-1.42E+00	1.52E-17	Down	-1.51E+00	6.20E-20	Down	Unigene44699_All//gi|164564335|gb|ABY61050.1|//0.00E+00//5-enolpyruvylshikimate-3-phosphate synthase [Gossypium hirsutum] >gi|193230774|gb|ACF16410.1| 5-enolpyruvylshikimate-3-phosphate synthase [Gossypium hirsutum]	Unigene44699_All//0.00E+00//AT2G45300| 3-phosphoshikimate 1-carboxyvinyltransferase / 5-enolpyruvylshikimate-3-phosphate / EPSP synthase	Unigene44699_All//0.00E+00//TC141971	ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis			nr +
Unigene447_All	997	2.57	1.68	1.87	5.70	6.08	7.34	12.09	5.99	4.32	-6.17E-01	1.21E-01		-4.60E-01	2.73E-01		9.39E-02	7.71E-01		3.66E-01	1.10E-01		-1.01E+00	1.47E-11	Down	-1.49E+00	4.05E-21	Down	Unigene447_All//gi|30693010|ref|NP_174675.2|//1.00E-172//STT3B (staurosporin and temperature sensitive 3-like b); oligosaccharyl transferase [Arabidopsis thaliana] >gi|10086464|gb|AAG12524.1|AC015446_5 Putative integral membrane protein [Arabidopsis thaliana]	Unigene447_All//4.00E-165//AT1G34130| STT3B (staurosporin and temperature sensitive 3-like b); oligosaccharyl transferase	Unigene447_All//0.00E+00//TC147182	ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis			nr -
Unigene44705_All	986	15.92	65.01	27.87	5.51	8.03	14.66	15.48	39.29	16.81	2.03E+00	1.22E-132	Up	8.08E-01	7.40E-14		5.45E-01	6.44E-03		1.41E+00	1.16E-19	Up	1.34E+00	4.47E-55	Up	1.19E-01	3.80E-01		Unigene44705_All//gi|193848548|gb|ACF22735.1|//4.00E-62//beta-glycosidase [Brachypodium distachyon]	Unigene44705_All//5.00E-56//AT3G06510| SFR2 (SENSITIVE TO FREEZING 2); beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene44705_All//0.00E+00//gi|48789671|gb|CO090985.1|CO090985	ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism			nr +
Unigene44706_All	2902	12.93	37.43	28.97	5.65	7.86	16.05	8.25	15.04	10.61	1.53E+00	2.98E-152	Up	1.16E+00	2.06E-75	Up	4.76E-01	8.93E-06		1.51E+00	1.54E-68	Up	8.67E-01	8.36E-31		3.64E-01	1.87E-05		Unigene44706_All//gi|195612308|gb|ACG27984.1|//0.00E+00//SFR2 [Zea mays]	Unigene44706_All//0.00E+00//AT3G06510| SFR2 (SENSITIVE TO FREEZING 2); beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene44706_All//0.00E+00//TC152311	ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism			nr +
Unigene44707_All	2253	22.29	24.27	26.57	30.07	38.26	78.00	31.96	36.32	35.35	1.22E-01	1.20E-01		2.53E-01	3.86E-04		3.47E-01	1.30E-11		1.38E+00	5.56E-225	Up	1.85E-01	4.53E-04		1.45E-01	6.30E-03		Unigene44707_All//gi|226532064|ref|NP_001148579.1|//1.00E-171//SCPL33 [Zea mays] >gi|195620848|gb|ACG32104.1| SCPL33 [Zea mays]	Unigene44707_All//3.00E-167//AT3G17180| scpl33 (serine carboxypeptidase-like 33); serine-type carboxypeptidase	Unigene44707_All//0.00E+00//TC157824	ko00460|Cyanoamino acid metabolism			nr +
Unigene44708_All	329	13.68	4.77	12.30	18.93	14.13	31.16	5.53	4.83	0.97	-1.52E+00	6.01E-07	Down	-1.53E-01	6.30E-01		-4.22E-01	7.23E-02		7.19E-01	4.03E-05		-1.95E-01	6.57E-01		-2.51E+00	6.12E-07	Down	Unigene44708_All//gi|15220099|ref|NP_178146.1|//3.00E-11//NTT1 (NUCLEOTIDE TRANSPORTER 1); ATP:ADP antiporter [Arabidopsis thaliana] >gi|21264532|sp|Q39002.2|TLC1_ARATH RecName: Full=ADP,ATP carrier protein 1, chloroplastic; AltName: Full=ADP/ATP translocase 1; AltName: Full=Adenine nucleotide translocase 1; Flags: Precursor >gi|12324978|gb|AAG52434.1|AC018848_5 adenine nucleotide translocase; 19474-21800 [Arabidopsis thaliana] >gi|16226734|gb|AAL16246.1|AF428316_1 At1g80300/F516_5 [Arabidopsis thaliana] >gi|10741072|dbj|BAE98630.1| adenine nucleotide translocase [Arabidopsis thaliana]	Unigene44708_All//1.00E-12//AT1G80300| NTT1 (NUCLEOTIDE TRANSPORTER 1); ATP:ADP antiporter	Unigene44708_All//2.00E-169//gi|78338575|gb|DT558849.1|DT558849				nr -
Unigene44709_All	2291	14.91	6.97	7.93	20.87	20.46	26.10	23.47	17.92	13.18	-1.10E+00	3.43E-29	Down	-9.12E-01	8.12E-21		-2.91E-02	7.96E-01		3.22E-01	1.13E-06		-3.90E-01	1.14E-09		-8.33E-01	2.12E-36		Unigene44709_All//gi|224070859|ref|XP_002303268.1|//0.00E+00//ATP/ADP transporter [Populus trichocarpa] >gi|222840700|gb|EEE78247.1| ATP/ADP transporter [Populus trichocarpa]	Unigene44709_All//0.00E+00//AT1G80300| NTT1 (NUCLEOTIDE TRANSPORTER 1); ATP:ADP antiporter	Unigene44709_All//0.00E+00//TC157677				nr +
Unigene4471_All	1147	13.55	48.20	30.04	1.91	4.26	5.04	1.18	0.98	0.80	1.83E+00	8.82E-100	Up	1.15E+00	1.72E-30	Up	1.16E+00	1.15E-05	Up	1.40E+00	4.25E-08	Up	-2.62E-01	6.63E-01		-5.62E-01	2.58E-01		Unigene4471_All//gi|98960861|gb|AB058914.1|//4.00E-14//At5g14410 [Arabidopsis thaliana]	Unigene4471_All//1.00E-10//AT5G14410| unknown protein	Unigene4471_All//0.00E+00//gi|21093126|gb|BQ405439.1|BQ405439				nr -
Unigene44710_All	2612	3.87	1.77	2.02	7.34	3.98	4.93	24.33	52.32	73.96	-1.13E+00	1.40E-09	Down	-9.38E-01	6.79E-07		-8.83E-01	3.68E-14		-5.75E-01	2.55E-06		1.10E+00	1.74E-141	Up	1.60E+00	0.00E+00	Up	Unigene44710_All//gi|71068360|gb|AZ23107.1|//0.00E+00//plastid ATP/ADP transport protein 2 [Manihot esculenta]	Unigene44710_All//0.00E+00//AT1G80300| NTT1 (NUCLEOTIDE TRANSPORTER 1); ATP:ADP antiporter	Unigene44710_All//0.00E+00//TC157677				nr +
Unigene44712_All	2865	5.39	1.98	3.90	10.35	8.86	5.66	5.59	2.31	3.14	-1.44E+00	1.89E-20	Down	-4.65E-01	1.68E-03		-2.24E-01	2.48E-02		-8.70E-01	8.89E-19		-1.28E+00	1.27E-21	Down	-8.32E-01	1.84E-11		Unigene44712_All//gi|297827451|ref|XP_002881608.1|//0.00E+00//GAUT7/LGT7 [Arabidopsis lyrata subsp. lyrata] >gi|297327447|gb|EFH57867.1| GAUT7/LGT7 [Arabidopsis lyrata subsp. lyrata]	Unigene44712_All//6.00E-174//AT2G38650| GAUT7 (GALACTURONOSYLTRANSFERASE 7); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups	Unigene44712_All//0.00E+00//gi|48750564|gb|CO081083.1|CO081083				nr -
Unigene44714_All	725	2.96	2.45	2.20	4.81	3.85	3.99	7.17	1.90	3.79	-2.75E-01	5.46E-01		-4.25E-01	3.74E-01		-3.22E-01	3.54E-01		-2.71E-01	4.67E-01		-1.91E+00	6.31E-13	Down	-9.20E-01	5.88E-05		Unigene44714_All//gi|42563074|ref|NP_177101.2|//1.00E-81//zinc finger (DHHC type) family protein [Arabidopsis thaliana] >gi|42572047|ref|NP_974114.1| zinc finger (DHHC type) family protein [Arabidopsis thaliana] >gi|223635846|sp|Q9C533.2|ZDHC1_ARATH RecName: Full=Probable S-acyltransferase At1g69420; AltName: Full=Probable palmitoyltransferase At1g69420; AltName: Full=Zinc finger DHHC domain-containing protein At1g69420	Unigene44714_All//5.00E-74//AT1G69420| zinc finger (DHHC type) family protein	Unigene44714_All//0.00E+00//TC140763				nr -
Unigene44715_All	1859	7.09	4.39	4.27	8.74	8.47	6.73	8.76	2.81	4.80	-6.93E-01	7.92E-06		-7.33E-01	5.15E-06		-4.53E-02	8.15E-01		-3.76E-01	6.59E-03		-1.64E+00	1.75E-31	Down	-8.67E-01	2.03E-12		Unigene44715_All//gi|297838707|ref|XP_002887235.1|//1.00E-174//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333076|gb|EFH63494.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44715_All//3.00E-139//AT1G69420| zinc finger (DHHC type) family protein	Unigene44715_All//0.00E+00//TC140763				nr +
Unigene44716_All	1374	2.89	2.80	1.63	12.00	9.00	5.16	6.68	1.37	4.26	-4.62E-02	8.87E-01		-8.30E-01	9.42E-03		-4.16E-01	1.30E-03		-1.22E+00	3.65E-18	Down	-2.29E+00	1.04E-27	Down	-6.48E-01	8.31E-05		Unigene44716_All//gi|42563074|ref|NP_177101.2|//6.00E-89//zinc finger (DHHC type) family protein [Arabidopsis thaliana] >gi|42572047|ref|NP_974114.1| zinc finger (DHHC type) family protein [Arabidopsis thaliana] >gi|223635846|sp|Q9C533.2|ZDHC1_ARATH RecName: Full=Probable S-acyltransferase At1g69420; AltName: Full=Probable palmitoyltransferase At1g69420; AltName: Full=Zinc finger DHHC domain-containing protein At1g69420	Unigene44716_All//2.00E-69//AT1G69420| zinc finger (DHHC type) family protein	Unigene44716_All//0.00E+00//gi|78326455|gb|DT546729.1|DT546729				nr -
Unigene44717_All	2124	6.13	4.60	3.79	17.12	13.68	7.65	12.88	4.21	6.64	-4.14E-01	8.54E-03		-6.96E-01	1.65E-05		-3.23E-01	1.03E-04		-1.16E+00	1.35E-36	Down	-1.61E+00	3.52E-51	Down	-9.56E-01	1.04E-23		Unigene44717_All//gi|226496834|ref|NP_001148046.1|//1.00E-166//LOC100281655 [Zea mays] >gi|195615492|gb|ACG29576.1| metal ion binding protein [Zea mays]	Unigene44717_All//3.00E-105//AT1G69420| zinc finger (DHHC type) family protein	Unigene44717_All//0.00E+00//TC152683				nr +
Unigene44718_All	582	2.34	0.35	1.10	6.25	5.68	3.88	3.05	2.23	4.24	-2.75E+00	1.08E-04	Down	-1.09E+00	7.47E-02		-1.38E-01	7.10E-01		-6.87E-01	3.33E-02		-4.55E-01	3.24E-01		4.76E-01	1.82E-01		Unigene44718_All//gi|227202670|dbj|BAH56898.1|//4.00E-15//AT1G79090 [Arabidopsis thaliana]	Unigene44718_All//7.00E-08//AT3G22270| unknown protein	Unigene44718_All//6.00E-69//ES842926	ko03018|RNA degradation			nr -
Unigene44725_All	1844	0.45	1.35	0.64	1.22	1.14	1.20	2.84	4.56	4.90	1.57E+00	2.51E-04	Up	4.85E-01	4.47E-01		-9.38E-02	8.26E-01		-1.85E-02	9.56E-01		6.80E-01	1.29E-04		7.87E-01	2.82E-06		Unigene44725_All//gi|8843739|dbj|BAA97287.1|//1.00E-122//retroelement pol polyprotein-like [Arabidopsis thaliana]	Unigene44725_All//2.00E-112//AT4G23160| protein kinase family protein	Unigene44725_All//0.00E+00//TC160991				nr -
Unigene44728_All	1427	0.44	0.11	0.07	2.48	5.07	3.48	1.27	3.72	4.10	-2.05E+00	4.46E-02		-2.56E+00	2.72E-02		1.03E+00	7.28E-07	Up	4.90E-01	7.73E-02		1.55E+00	5.99E-10	Up	1.69E+00	1.48E-12	Up	Unigene44728_All//gi|164605535|dbj|BAF98601.1|//5.00E-32//CM0545.290.nc [Lotus japonicus]	Unigene44728_All//8.00E-32//AT5G06600| UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene44728_All//0.00E+00//ES823536				nr -

Unigene4473_All	800	2.49	3.36	3.20	2.68	4.95	8.58	16.07	17.03	106.22	4.34E-01	2.68E-01		3.63E-01	3.90E-01		8.87E-01	2.86E-03		1.68E+00	3.18E-12	Up	8.42E-02	6.34E-01		2.72E+00	0.00E+00	Up	Unigene4473_All//gi|9743343|gb|AAF97967.1|AC000103.17//1.00E-11//F21J9.24 [Arabidopsis thaliana]	Unigene4473_All//5.00E-13//AT1G24580| zinc finger (C3HC4-type RING finger) family protein	Unigene4473_All//0.00E+00//gi|164344362|gb|ES807898.1|ES807898				nr -
Unigene44730_All	1568	6.64	6.72	9.24	40.82	16.67	20.74	11.92	17.59	21.65	1.76E-02	9.43E-01		4.76E-01	1.88E-03		-1.29E+00	9.38E-87	Down	-9.77E-01	2.12E-48		5.62E-01	1.09E-09		8.61E-01	1.76E-24		Unigene44730_All//gi|164605535|dbj|BAF98601.1|//3.00E-30//CM0545.290.nc [Lotus japonicus]	Unigene44730_All//3.00E-29//AT5G06600| UBP12 (UBIQUITIN-SPECIFIC PROTEASE 12); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene44730_All//0.00E+00//TC138013				nr +
Unigene44732_All	634	12.13	9.19	5.38	18.31	29.98	18.45	6.67	7.45	9.11	-4.01E-01	6.10E-02		-1.17E+00	1.66E-07	Down	7.12E-01	1.77E-09		1.12E-02	9.48E-01		1.60E-01	5.90E-01		4.50E-01	3.73E-02		Unigene44732_All//gi|5080778|gb|AAD39288.1|AC007576.11//6.00E-51//Similar to auxin-independent growth promoter protein [Arabidopsis thaliana]	Unigene44732_All//3.00E-52//AT1G14020| unknown protein	Unigene44732_All//0.00E+00//TC154110				nr +
Unigene44734_All	1476	4.32	4.26	1.15	4.25	3.64	4.19	6.79	6.40	9.42	-2.28E-02	9.41E-01		-1.91E+00	3.13E-12	Down	-2.25E-01	3.89E-01		-2.06E-02	9.51E-01		-8.52E-02	6.37E-01		4.73E-01	3.11E-04		Unigene44734_All//gi|37202038|gb|AAQ89634.1|//0.00E+00//At1g14020 [Arabidopsis thaliana] >gi|110739513|dbj|BAF01665.1| growth regulator like protein [Arabidopsis thaliana] >gi|110739824|dbj|BAF01818.1| growth regulator like protein [Arabidopsis thaliana]	Unigene44734_All//0.00E+00//AT1G14020| unknown protein	Unigene44734_All//0.00E+00//gi|21103030|gb|BQ415343.1|BQ415343				nr -
Unigene44737_All	803	2.87	1.14	3.85	6.20	5.19	3.04	5.16	5.83	3.13	-1.34E+00	2.11E-03		4.24E-01	2.59E-01		-2.58E-01	3.81E-01		-1.03E+00	1.07E-04	Down	1.76E-01	5.42E-01		-7.23E-01	4.89E-03		Unigene44737_All//gi|146424382|emb|CAM97883.1|//3.00E-46//actin-related protein 3 [Nicotiana tabacum]	Unigene44737_All//9.00E-46//AT1G13180| DIS1 (DISTORTED TRICHOMES 1); ATP binding / actin binding / protein binding / structural constituent of cytoskeleton	Unigene44737_All//2.00E-156//gi|78337946|gb|DT558220.1|DT558220		ko04145|Phagosome		nr +
Unigene4474_All	1012	4.03	4.06	1.21	19.94	16.13	9.82	3.51	3.63	1.73	8.20E-03	9.85E-01		-1.74E+00	3.71E-07	Down	-3.06E-01	1.05E-02		-1.02E+00	8.70E-17	Down	5.05E-02	8.78E-01		-1.02E+00	3.53E-04	Down	Unigene4474_All//gi|115441397|ref|NP_001014978.1|//6.00E-29//Os01g0878000 [Oryza sativa Japonica Group] >gi|113534509|dbj|BAF06892.1| Os01g0878000 [Oryza sativa Japonica Group]	Unigene4474_All//2.00E-25//AT1G09812| unknown protein	Unigene4474_All//0.00E+00//TC149235				nr -
Unigene44741_All	337	0.78	0.45	2.69	2.96	0.31	0.54	0.75	0.50	1.06	-7.83E-01	6.20E-01		1.79E+00	3.07E-02		-3.27E+00	6.96E-05	Down	-2.46E+00	2.07E-03		-6.02E-01	6.47E-01		4.99E-01	6.27E-01		Unigene44741_All//gi|147856633|emb|CAN82456.1|//1.00E-07//hypothetical protein [Vitis vinifera]		Unigene44741_All//2.00E-18//gi|109851095|gb|DW480074.1|DW480074				nr +
Unigene44743_All	963	0.71	0.32	2.49	1.81	2.79	2.06	1.89	2.56	3.02	-1.16E+00	1.89E-01		1.82E+00	9.66E-05	Up	6.24E-01	1.10E-01		1.89E-01	6.88E-01		4.40E-01	2.40E-01		6.78E-01	3.24E-02		Unigene44743_All//gi|297793271|ref|XP_002864520.1|//1.00E-112//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310355|gb|EFH40779.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44743_All//3.00E-112//AT5G57610| protein kinase family protein	Unigene44743_All//0.00E+00//TC140985				nr -
Unigene44746_All	675	10.08	10.13	10.57	22.95	37.75	59.88	7.52	7.18	8.26	8.20E-03	9.89E-01		6.91E-02	7.70E-01		7.18E-01	9.81E-13		1.38E+00	1.74E-52	Up	-6.55E-02	8.04E-01		1.37E-01	5.97E-01		Unigene44746_All//gi|31711716|gb|AAP68214.1|//3.00E-91//At4g24530 [Arabidopsis thaliana] >gi|110743919|dbj|BAE99793.1| PsRT17-1 like protein [Arabidopsis thaliana]	Unigene44746_All//4.00E-86//AT5G65470| unknown protein	Unigene44746_All//0.00E+00//TC164016				nr +
Unigene44748_All	2141	13.22	19.41	17.46	59.42	101.81	132.18	10.43	17.14	11.59	5.54E-01	2.28E-11		4.01E-01	8.63E-06		7.77E-01	3.67E-122		1.15E+00	2.01E-275	Up	7.17E-01	5.18E-19		1.53E-01	1.40E-01		Unigene44748_All//gi|31711716|gb|AAP68214.1|//0.00E+00//At4g24530 [Arabidopsis thaliana] >gi|110743919|dbj|BAE99793.1| PsRT17-1 like protein [Arabidopsis thaliana]	Unigene44748_All//0.00E+00//AT5G65470| unknown protein	Unigene44748_All//0.00E+00//TC171159				nr +
Unigene44749_All	1798	24.09	7.05	12.71	17.62	17.79	14.97	20.83	5.90	15.71	-1.77E+00	1.77E-75	Down	-9.23E-01	8.57E-27		1.40E-02	9.11E-01		-2.35E-01	1.76E-02		-1.82E+00	1.32E-82	Down	-4.07E-01	9.22E-08		Unigene44749_All//gi|255671797|gb|ACU26531.1|//0.00E+00//diaminopimelate decarboxylase [Glycine max]	Unigene44749_All//0.00E+00//AT5G11880| diaminopimelate decarboxylase, putative / DAP carboxylase, putative	Unigene44749_All//0.00E+00//TC151434		ko00300|Lysine biosynthesis		nr +
Unigene4475_All	852	0.86	2.02	1.38	4.33	2.10	2.60	2.33	1.08	0.65	1.23E+00	1.58E-02		6.78E-01	3.04E-01		-1.04E+00	4.93E-04	Down	-7.36E-01	2.10E-02		-1.11E+00	7.17E-03		-1.83E+00	2.39E-05	Down	Unigene4475_All//gi|115441397|ref|NP_001014978.1|//1.00E-22//Os01g0878000 [Oryza sativa Japonica Group] >gi|113534509|dbj|BAF06892.1| Os01g0878000 [Oryza sativa Japonica Group]	Unigene4475_All//4.00E-22//AT1G09812| unknown protein	Unigene4475_All//0.00E+00//TC149235				nr +
Unigene44750_All	2060	22.83	7.08	12.23	22.63	22.15	22.14	44.48	19.82	24.79	-1.69E+00	1.91E-76	Down	-9.01E-01	6.63E-28		-3.13E-02	7.80E-01		-3.16E-02	7.37E-01		-1.17E+00	9.54E-104	Down	-8.43E-01	1.12E-62		Unigene44750_All//gi|255671797|gb|ACU26531.1|//0.00E+00//diaminopimelate decarboxylase [Glycine max]	Unigene44750_All//0.00E+00//AT5G11880| diaminopimelate decarboxylase, putative / DAP carboxylase, putative	Unigene44750_All//0.00E+00//TC131339		ko00300|Lysine biosynthesis		nr -
Unigene44751_All	1173	3.26	3.11	2.41	7.26	3.23	1.31	5.73	3.06	3.12	-6.62E-02	8.33E-01		-4.37E-01	1.95E-01		-1.17E+00	3.52E-10	Down	-2.47E+00	5.16E-25	Down	-9.03E-01	8.93E-06		-8.75E-01	9.95E-06		Unigene44751_All//gi|19698981|gb|AAL91226.1|//1.00E-82//similar to phosphatidylserine synthase-2 [Arabidopsis thaliana] >gi|22136302|gb|AAM91229.1| similar to phosphatidylserine synthase-2 [Arabidopsis thaliana]	Unigene44751_All//7.00E-84//AT1G15110| phosphatidyl serine synthase family protein	Unigene44751_All//0.00E+00//TC151623		ko00564|Glycerophospholipid metabolism		nr -
Unigene44752_All	1627	2.48	3.24	2.00	4.99	2.16	1.80	4.52	2.18	3.13	3.87E-01	1.44E-01		-3.11E-01	3.61E-01		-1.21E+00	3.08E-10	Down	-1.47E+00	4.01E-12	Down	-1.05E+00	8.76E-08	Down	-5.29E-01	4.49E-03		Unigene44752_All//gi|297844412|ref|XP_002890087.1|//0.00E+00//phosphatidyl serine synthase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335929|gb|EFH66346.1| phosphatidyl serine synthase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44752_All//0.00E+00//AT1G15110| phosphatidyl serine synthase family protein	Unigene44752_All//0.00E+00//TC151623		ko00564|Glycerophospholipid metabolism		nr -
Unigene44756_All	618	4.06	8.20	6.29	3.87	3.34	4.68	3.69	3.52	6.58	1.01E+00	1.77E-04	Up	6.30E-01	5.20E-02		-2.11E-01	6.15E-01		2.74E-01	5.07E-01		-7.11E-02	8.62E-01		8.32E-01	1.52E-03		Unigene44756_All//gi|75333448|sp|Q9C718.1|RH20_ARATH//3.00E-52//RecName: Full=DEAD-box ATP-dependent RNA helicase 20 >gi|17065338|gb|AAL32823.1| Unknown protein [Arabidopsis thaliana]	Unigene44756_All//5.00E-43//AT1G55150| DEAD box RNA helicase, putative (RH20)	Unigene44756_All//0.00E+00//gi|78353619|gb|DT573893.1|DT573893		ko03040|Spliceosome		nr -
Unigene44759_All	2263	3.26	2.66	2.12	9.40	7.43	4.77	8.03	2.51	5.09	-2.91E-01	1.97E-01		-6.22E-01	5.43E-03		-3.40E-01	2.83E-03		-9.79E-01	1.74E-16		-1.68E+00	3.29E-36	Down	-6.59E-01	6.86E-09		Unigene44759_All//gi|217426815|gb|ACK44523.1|//0.00E+00//AT5G10020-like protein [Arabidopsis arenosa]	Unigene44759_All//0.00E+00//AT5G10020| leucine-rich repeat transmembrane protein kinase, putative	Unigene44759_All//0.00E+00//TC147648				nr -
Unigene4476_All	506	0.93	1.40	1.58	1.28	0.75	0.62	3.59	1.90	1.10	5.91E-01	4.78E-01		7.62E-01	3.62E-01		-7.74E-01	3.81E-01		-1.03E+00	2.68E-01		-9.19E-01	3.38E-02		-1.70E+00	1.42E-04	Down			Unigene4476_All//2.00E-136//TC153974				
Unigene44760_All	2293	3.79	2.92	2.04	7.06	5.77	5.00	7.30	2.70	4.59	-3.77E-01	5.96E-02		-8.90E-01	1.36E-05		-2.92E-01	3.44E-02		-4.97E-01	2.41E-04		-1.44E+00	8.68E-27	Down	-6.71E-01	1.72E-08		Unigene44760_All//gi|217426815|gb|ACK44523.1|//0.00E+00//AT5G10020-like protein [Arabidopsis arenosa]	Unigene44760_All//7.00E-156//AT5G10020| leucine-rich repeat transmembrane protein kinase, putative	Unigene44760_All//0.00E+00//gi|5048487|gb|AI729635.1|AI729635				nr +
Unigene44761_All	4031	71.28	34.48	64.11	44.06	54.21	38.00	40.41	45.69	41.01	-1.05E+00	4.82E-223	Down	-1.53E-01	6.80E-07		2.99E-01	7.21E-22		-2.13E-01	8.48E-09		1.77E-01	1.47E-07		2.13E-02	6.28E-01		Unigene44761_All//gi|183239014|gb|ACC60965.1|//0.00E+00//phytochrome A [Vitis vinifera]	Unigene44761_All//0.00E+00//AT1G09570| PHYA (PHYTOCHROME A); G-protein coupled photoreceptor/ protein histidine kinase/ red or far-red light photoreceptor/ signal transducer	Unigene44761_All//0.00E+00//TC145086		ko04712|Circadian rhythm - plant		nr -
Unigene44762_All	1762	165.93	154.97	168.76	87.36	76.75	84.18	8.64	6.31	4.02	-9.86E-02	1.32E-03		2.44E-02	5.17E-01		-1.87E-01	1.13E-06		-5.36E-02	2.92E-01		-4.53E-01	3.91E-04		-1.10E+00	6.16E-17	Down	Unigene44762_All//gi|2494076|sp|P93338.1|GAPN_NICPL//0.00E+00//RecName: Full=NADP-dependent glyceraldehyde-3-phosphate dehydrogenase; AltName: Full=Non-phosphorylating glyceraldehyde 3-phosphate dehydrogenase; AltName: Full=Glyceraldehyde-3-phosphate dehydrogenase [NADP+]; AltName: Full=Triosephosphate dehydrogenase >gi|1842115|gb|AAB47571.1| non-phosphorylating glyceraldehyde dehydrogenase [Nicotiana plumbaginifolia]	Unigene44762_All//0.00E+00//AT2G24270| ALDH11A3; 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydrogenase (NADP+)	Unigene44762_All//0.00E+00//TC158564		ko00010|Glycolysis / Gluconeogenesis//ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00650|Butanoate metabolism		nr -
Unigene44764_All	2022	80.27	234.80	178.66	24.41	31.80	78.15	25.47	2.56	16.31	1.55E+00	0.00E+00	Up	1.15E+00	0.00E+00	Up	3.81E-01	2.37E-10		1.68E+00	4.02E-271	Up	-3.31E+00	3.17E-227	Down	-6.43E-01	1.60E-22		Unigene44764_All//gi|3913711|sp|P81406.1|GAPA_PEA//0.00E+00//RecName: Full=NADP-dependent glyceraldehyde-3-phosphate dehydrogenase; AltName: Full=Non-phosphorylating glyceraldehyde 3-phosphate dehydrogenase; AltName: Full=Glyceraldehyde-3-phosphate dehydrogenase [NADP+]; AltName: Full=Triosephosphate dehydrogenase >gi|4379384|emb|CAA53076.1| glyceraldehyde-3-phosphate dehydrogenase (nonphosphorylating,NADP+) [Pisum sativum] >gi|28274680|gb|AAO38512.1| non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase [Pisum sativum]	Unigene44764_All//0.00E+00//AT2G24270| ALDH11A3; 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydrogenase (NADP+)	Unigene44764_All//0.00E+00//TC153274		ko00010|Glycolysis / Gluconeogenesis//ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00650|Butanoate metabolism		nr +
Unigene44765_All	407	2.06	4.23	0.92	3.43	2.28	1.78	11.53	9.04	4.70	1.04E+00	3.90E-02		-1.17E+00	1.52E-01		-5.85E-01	3.07E-01		-9.49E-01	9.91E-02		-3.52E-01	1.80E-01		-1.30E+00	2.83E-07	Down	Unigene44765_All//gi|297803612|ref|XP_002869690.1|//1.00E-27//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297315526|gb|EFH45949.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	Unigene44765_All//9.00E-29//AT4G25070| unknown protein	Unigene44765_All//1.00E-127//ES812887				nr +
Unigene44769_All	953	13.51	12.39	15.09	17.09	21.17	16.78	29.55	13.82	21.15	-1.25E-01	4.76E-01		1.60E-01	3.60E-01		3.09E-01	1.07E-02		-2.69E-02	8.80E-01		-1.10E+00	1.82E-29	Down	-4.82E-01	6.08E-08		Unigene44769_All//gi|119866037|gb|ABM05488.1|//1.00E-107//Impa2 [Nicotiana benthamiana]	Unigene44769_All//8.00E-102//AT4G16143| IMPA-2 (IMPORTIN ALPHA ISOFORM 2); binding / protein transporter	Unigene44769_All//0.00E+00//gi|109849465|gb|DW478444.1|DW478444		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene4477_All	757	10.02	12.72	11.54	17.44	12.01	8.53	32.12	29.48	19.26	3.44E-01	7.06E-02		2.03E-01	3.68E-01		-5.38E-01	1.83E-04		-1.03E+00	2.35E-11	Down	-1.23E-01	2.81E-01		-7.38E-01	6.47E-14		Unigene4477_All//gi|14030733|gb|AAK53041.1|AF375457.1//5.00E-18//AT5g01350/T1008_60 [Arabidopsis thaliana] >gi|15010720|gb|AAK74019.1| AT5g01350/T1008_60 [Arabidopsis thaliana] >gi|16974531|gb|AAL31175.1| AT5g01350/T1008_60 [Arabidopsis thaliana]	Unigene4477_All//3.00E-19//AT5G01350| unknown protein	Unigene4477_All//0.00E+00//TC153974				nr -

Unigene4478_All	825	30.19	31.38	34.92	49.69	45.41	40.13	46.74	40.38	21.34	5.61E-02	6.27E-01		2.10E-01	5.81E-02		-1.30E-01	1.56E-01		-3.09E-01	1.72E-04		-2.11E-01	8.23E-03		-1.13E+00	2.87E-43	Down	Unigene4478_All//gi|42572379|ref|NP_974285.1|//2.00E-61//vacuolar protein sorting 55 family protein / VPS55 family protein [Arabidopsis thaliana] >gi|16648828|gb|AAL25604.1| AT3g11530/F24K9_21 [Arabidopsis thaliana] >gi|20466135|gb|AAM19989.1| AT3g11530/F24K9_21 [Arabidopsis thaliana]	Unigene4478_All//1.00E-62//AT3G11530| vacuolar protein sorting 55 family protein / VPS55 family protein	Unigene4478_All//0.00E+00//TC154233				nr +
Unigene44781_All	1362	24.59	15.92	20.49	22.02	17.85	19.37	14.28	6.54	7.46	-6.27E-01	1.83E-11		-2.63E-01	7.93E-03		-3.03E-01	1.29E-03		-1.85E-01	8.27E-02		-1.13E+00	1.68E-21	Down	-9.37E-01	1.39E-16		Unigene44781_All//gi|145359623|ref|NP_201203.2|//1.00E-137//SAL1; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase [Arabidopsis thaliana]	Unigene44781_All//4.00E-122//AT5G63980| SAL1; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase	Unigene44781_All//0.00E+00//TC142430		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism		nr +
Unigene44782_All	2011	0.26	1.06	0.21	0.89	0.60	2.43	13.43	27.18	48.40	2.02E+00	4.61E-05	Up	-2.97E-01	7.50E-01		-5.73E-01	2.36E-01		1.44E+00	3.15E-07	Up	1.02E+00	6.53E-50	Up	1.85E+00	2.95E-222	Up	Unigene44782_All//gi|267631202|gb|ACY78677.1|//0.00E+00//fatty acid elongase [Pistacia chinensis]	Unigene44782_All//0.00E+00//AT2G26640| KCS11 (3-KETOACYL-COA SYNTHASE 11); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene44782_All//0.00E+00//TC140366				nr -
Unigene44784_All	1699	8.96	17.71	3.01	15.51	10.15	9.01	49.02	50.95	48.84	9.83E-01	1.42E-21		-1.57E+00	6.52E-22	Down	-6.11E-01	2.56E-10		-7.83E-01	4.35E-14		5.55E-02	3.76E-01		-5.30E-03	9.51E-01		Unigene44784_All//gi|267631202|gb|ACY78677.1|//0.00E+00//fatty acid elongase [Pistacia chinensis]	Unigene44784_All//0.00E+00//AT2G26640| KCS11 (3-KETOACYL-COA SYNTHASE 11); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene44784_All//0.00E+00//TC140366				nr +
Unigene44785_All	427	0.61	3.44	0.00	0.47	1.61	1.90	5.84	6.07	6.90	2.49E+00	1.51E-04	Up	-9.26E+00	8.56E-02		1.79E+00	6.10E-02		2.03E+00	2.17E-02		5.49E-02	8.91E-01		2.41E-01	4.76E-01		Unigene44785_All//gi|109676368|gb|ABG37666.1|//1.00E-19//CCHC-type integrase [Populus trichocarpa]		Unigene44785_All//5.00E-112//DW501456				nr -
Unigene44786_All	3804	7.08	2.04	2.31	8.90	6.31	10.58	11.49	6.19	14.50	-1.80E+00	4.98E-48	Down	-1.62E+00	6.67E-40	Down	-4.97E-01	3.60E-09		2.49E-01	3.59E-03		-8.94E-01	1.66E-32		3.36E-01	6.39E-08		Unigene44786_All//gi|133711804|gb|ABO36622.1|//0.00E+00//copia LTR rider [Solanum lycopersicum] >gi|133711819|gb|ABO36636.1| copia LTR rider [Solanum lycopersicum]	Unigene44786_All//9.00E-72//AT4G23160| protein kinase family protein	Unigene44786_All//0.00E+00//TC163233				nr +
Unigene44787_All	4324	8.81	2.04	1.88	9.34	5.69	9.69	7.57	3.88	9.34	-2.11E+00	1.03E-83	Down	-2.23E+00	2.62E-86	Down	-7.16E-01	1.56E-20		5.30E-02	6.39E-01		-9.65E-01	8.17E-28		3.04E-01	3.72E-05		Unigene44787_All//gi|133711804|gb|ABO36622.1|//0.00E+00//copia LTR rider [Solanum lycopersicum] >gi|133711819|gb|ABO36636.1| copia LTR rider [Solanum lycopersicum]	Unigene44787_All//8.00E-82//AT4G23160| protein kinase family protein	Unigene44787_All//0.00E+00//TC163233				nr -
Unigene44789_All	5517	3.91	2.58	2.47	10.28	7.14	7.83	13.33	4.46	5.12	-5.98E-01	3.97E-07		-6.61E-01	5.95E-08		-5.26E-01	1.23E-16		-3.93E-01	5.94E-09		-1.58E+00	3.29E-132	Down	-1.38E+00	1.90E-111	Down	Unigene44789_All//gi|110741802|dbj|BAE98844.1|//0.00E+00//formin-like protein AHF1 [Arabidopsis thaliana]	Unigene44789_All//3.00E-179//AT3G25500| AFH1 (FORMIN HOMOLOGY 1); actin binding / actin filament binding / protein binding	Unigene44789_All//0.00E+00//TC160643				nr -
Unigene4479_All	1135	3.46	2.68	1.45	3.42	4.07	2.35	6.30	2.43	2.11	-3.68E-01	2.40E-01		-1.25E+00	1.57E-04	Down	2.48E-01	4.40E-01		-5.44E-01	8.53E-02		-1.37E+00	3.73E-11	Down	-1.58E+00	5.25E-14	Down	Unigene4479_All//gi|192910708|gb|ACF06462.1|//1.00E-94//24 kDa seed maturation protein [Elaeis guineensis]	Unigene4479_All//2.00E-66//AT1G64090| reticulon family protein (RTNLB3)	Unigene4479_All//0.00E+00//gi|109879320|gb|DW508290.1|DW508290				nr -
Unigene44792_All	3433	0.59	0.34	0.79	1.39	1.01	0.97	2.03	1.13	0.96	-8.08E-01	7.29E-02		4.12E-01	3.16E-01		-4.59E-01	9.10E-02		-5.17E-01	6.59E-02		-8.44E-01	2.11E-05		-1.08E+00	5.63E-08	Down	Unigene44792_All//0.00E+00//CDC5-like protein [Solanum lycopersicum] >gi|156106718|gb|ABU49592.1| CDC5-like protein [Solanum lycopersicum]	Unigene44792_All//0.00E+00//AT1G09770| ATCDC5 (ARABIDOPSIS THALIANA CELL DIVISION CYCLE 5); DNA binding / transcription factor	Unigene44792_All//0.00E+00//TC142939	MYB	ko03040|Spliceosome		nr +
Unigene44794_All	1976	3.20	1.82	2.08	3.91	4.18	2.65	3.57	0.95	1.47	-8.15E-01	5.10E-04		-6.27E-01	1.04E-02		9.81E-02	6.97E-01		-5.60E-01	7.09E-03		-1.91E+00	3.28E-17	Down	-1.28E+00	2.52E-10	Down	Unigene44794_All//gi|240255306|ref|NP_187508.5|//0.00E+00//binding / protein transporter [Arabidopsis thaliana]	Unigene44794_All//0.00E+00//AT3G08960| binding / protein transporter	Unigene44794_All//0.00E+00//TC164022				nr -
Unigene44795_All	3716	1.84	0.75	1.88	4.62	3.87	3.32	7.77	3.36	4.52	-1.30E+00	3.34E-08	Down	2.54E-02	9.28E-01		-2.56E-01	6.05E-02		-4.79E-01	2.57E-04		-1.21E+00	3.94E-35	Down	-7.81E-01	5.91E-18		Unigene44795_All//gi|240255306|ref|NP_187508.5|//0.00E+00//binding / protein transporter [Arabidopsis thaliana]	Unigene44795_All//0.00E+00//AT3G08960| binding / protein transporter	Unigene44795_All//0.00E+00//TC147376				nr -
Unigene44796_All	1122	8.63	7.36	6.64	11.10	11.17	9.74	8.06	6.00	3.94	-2.29E-01	2.39E-01		-3.77E-01	5.59E-02		9.30E-03	9.67E-01		-1.88E-01	3.08E-01		-4.27E-01	1.35E-02		-1.03E+00	1.79E-09	Down	Unigene44796_All//gi|297851322|ref|XP_002893542.1|//3.00E-92//F1K23.5 [Arabidopsis lyrata subsp. lyrata] >gi|297339384|gb|EFH69801.1| F1K23.5 [Arabidopsis lyrata subsp. lyrata]	Unigene44796_All//1.00E-83//AT1G28960| ATNUDX15 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 15); hydrolase	Unigene44796_All//0.00E+00//TC131104				nr -
Unigene448_All	802	10.57	1.64	8.50	33.91	29.20	21.51	10.39	2.92	5.86	-2.69E+00	3.23E-25	Down	-3.14E-01	1.46E-01		-2.16E-01	4.16E-02		-6.57E-01	8.00E-11		-1.83E+00	4.08E-19	Down	-8.25E-01	2.58E-06		Unigene448_All//gi|298713412|emb|CBJ33619.1|//1.00E-58//Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A, N-terminal fragment, family GT66 [Ectocarpus siliculosus]	Unigene448_All//6.00E-59//AT5G19690| STT3A (STAUROSPORIN AND TEMPERATURE SENSITIVE 3-LIKE A); oligosaccharyl transferase	Unigene448_All//0.00E+00//gi|78335133|gb|DT555407.1|DT555407		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis		nr +
Unigene4480_All	693	23.48	76.63	59.70	26.45	65.84	79.64	9.27	28.29	32.48	1.71E+00	5.49E-87	Up	1.35E+00	9.82E-47	Up	1.32E+00	2.94E-60	Up	1.59E+00	8.66E-88	Up	1.61E+00	1.09E-36	Up	1.81E+00	1.88E-50	Up	Unigene4480_All//gi|42561991|gb|AAS20434.1|//3.00E-07//AREB-like protein [Solanum lycopersicum]		Unigene4480_All//2.00E-155//gi|78324427|gb|DT544701.1|DT544701				nr +
Unigene44800_All	722	0.65	0.56	0.44	1.38	2.81	2.13	2.23	0.46	2.48	-2.16E-01	8.17E-01		-5.60E-01	6.28E-01		1.03E+00	2.26E-02		6.24E-01	2.70E-01		-2.26E+00	2.23E-05	Down	1.58E-01	7.12E-01		Unigene44800_All//gi|19570247|dbj|BAB86283.1|//1.00E-112//kinesin-like protein NACK1 [Nicotiana tabacum]	Unigene44800_All//5.00E-112//AT1G18370| HIK (HINKEL); ATP binding / microtubule motor	Unigene44800_All//6.00E-128//TC146839				nr -
Unigene44801_All	2086	1.78	1.07	0.41	4.75	5.50	3.90	8.15	1.20	3.82	-7.37E-01	2.03E-02		-2.12E+00	2.22E-08	Down	2.10E-01	2.63E-01		-2.86E-01	1.41E-01		-2.76E+00	7.11E-63	Down	-1.09E+00	1.43E-18	Down	Unigene44801_All//gi|19570247|dbj|BAB86283.1|//0.00E+00//kinesin-like protein NACK1 [Nicotiana tabacum]	Unigene44801_All//0.00E+00//AT1G18370| HIK (HINKEL); ATP binding / microtubule motor	Unigene44801_All//0.00E+00//TC141853				nr +
Unigene44802_All	3551	2.40	2.15	1.39	7.86	8.89	7.29	10.87	2.31	4.99	-1.57E-01	4.66E-01		-7.84E-01	1.40E-04		1.79E-01	7.86E-02		-1.08E-01	3.92E-01		-2.24E+00	2.37E-111	Down	-1.12E+00	8.02E-43	Down	Unigene44802_All//gi|19570247|dbj|BAB86283.1|//0.00E+00//kinesin-like protein NACK1 [Nicotiana tabacum]	Unigene44802_All//0.00E+00//AT1G18370| HIK (HINKEL); ATP binding / microtubule motor	Unigene44802_All//0.00E+00//TC135134				nr +
Unigene44803_All	1807	13.43	9.53	16.36	5.57	6.12	3.50	2.53	1.48	0.88	-4.95E-01	7.27E-06		2.84E-01	7.31E-03		1.36E-01	5.23E-01		-6.70E-01	1.41E-04		-7.72E-01	2.16E-03		-1.52E+00	8.61E-09	Down	Unigene44803_All//gi|120820085|dbj|BAB20760.1|//0.00E+00//ferrochelatase [Cucumis sativus]	Unigene44803_All//0.00E+00//AT2G30390| FC2 (FERROCHELATASE 2); ferrochelatase	Unigene44803_All//0.00E+00//TC161846		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene44806_All	4138	13.52	7.21	13.04	58.02	45.16	37.97	106.21	369.90	683.25	-9.06E-01	1.19E-34		-5.22E-02	5.57E-01		-3.62E-01	1.26E-34		-6.12E-01	2.56E-80		1.80E+00	0.00E+00	Up	2.69E+00	0.00E+00	Up	Unigene44806_All//gi|224130858|ref|XP_002320942.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222861715|gb|EEE99257.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene44806_All//0.00E+00//AT2G47000| ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase	Unigene44806_All//0.00E+00//TC145075		ko02010|ABC transporters		nr +
Unigene44808_All	1114	8.41	5.32	4.59	14.89	12.21	13.62	26.61	11.74	16.34	-6.60E-01	4.28E-04		-8.73E-01	8.33E-06		-2.86E-01	3.60E-02		-1.29E-01	4.31E-01		-1.18E+00	9.98E-35	Down	-7.03E-01	1.72E-15		Unigene44808_All//gi|115474339|ref|NP_001060766.1|//1.00E-102//Os08g0102100 [Oryza sativa Japonica Group] >gi|113622735|dbj|BAF22680.1| Os08g0102100 [Oryza sativa Japonica Group]	Unigene44808_All//4.00E-101//AT3G44330| INVOLVED IN: protein processing; LOCATED IN: mitochondrion, endoplasmic reticulum, plasma membrane, vacuole; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Nicalin (InterPro:IPR016574), EF-HAND 1 (InterPro:IPR018247), Nicastrin (InterPro:IPR008710); Has 192 Blast hits to 192 proteins in 79 species: Archae - 6; Bacteria - 5; Metazoa - 124; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink).	Unigene44808_All//0.00E+00//TC159189				nr +
Unigene4481_All	667	56.79	64.50	64.91	107.47	123.08	172.05	52.11	81.59	118.38	1.84E-01	3.16E-02		1.93E-01	2.93E-02		1.96E-01	4.15E-04		6.79E-01	4.80E-46		6.47E-01	2.58E-23		1.18E+00	1.44E-93	Up	Unigene4481_All//gi|21069016|dbj|BAB03108.1|//4.00E-53//betaine/proline transporter [Avicennia marina]	Unigene4481_All//1.00E-42//AT3G55740| PROT2 (PROLINE TRANSPORTER 2); L-proline transmembrane transporter/ amino acid transmembrane transporter	Unigene4481_All//0.00E+00//TC141717				nr -
Unigene44810_All	376	7.51	1.48	3.97	4.90	8.33	6.73	5.85	3.11	6.25	-2.34E+00	1.15E-07	Down	-9.22E-01	1.86E-02		7.66E-01	2.73E-02		4.57E-01	2.88E-01		-9.10E-01	1.86E-02		9.64E-02	7.94E-01		Unigene44810_All//gi|13605605|gb|AK32796.1|AF361628_1/1.00E-25//AT3g57980/T10K17_190 [Arabidopsis thaliana] >gi|21360543|gb|AAM47468.1| AT3g57980/T10K17_190 [Arabidopsis thaliana]	Unigene44810_All//6.00E-15//AT2G42150| DNA-binding bromodomain-containing protein	Unigene44810_All//2.00E-179//ES840708	MYB-related			nr -
Unigene44821_All	1018	5.86	6.62	8.68	4.80	6.87	8.03	1.99	0.62	1.33	1.76E-01	4.70E-01		5.68E-01	4.93E-03		5.18E-01	1.73E-02		7.44E-01	1.96E-04		-1.69E+00	8.97E-05	Down	-5.83E-01	1.37E-01		Unigene44821_All//gi|129770485|gb|AB033358.1|//1.00E-110//starch branching enzyme II-1 [Malus x domestica]	Unigene44821_All//3.00E-92//AT5G03650| SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme	Unigene44821_All//0.00E+00//gi|109866213|gb|DW495189.1|DW495189		ko00500|Starch and sucrose metabolism		nr -
Unigene44822_All	808	9.32	10.35	8.96	9.37	10.02	9.61	2.67	1.76	0.84	1.50E-01	4.94E-01		-5.71E-02	8.04E-01		9.59E-02	7.12E-01		3.69E-02	8.93E-01		-6.02E-01	1.32E-01		-1.67E+00	3.80E-05	Down	Unigene44822_All//gi|15553091|dbj|BAB64912.1|//1.00E-147//starch branching enzyme II [Ipomoea batatas]	Unigene44822_All//3.00E-146//AT5G03650| SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme	Unigene44822_All//0.00E+00//gi|164263237|gb|ES806393.1|ES806393		ko00500|Starch and sucrose metabolism		nr -
Unigene44823_All	1857	4.99	4.31	3.99	4.16	4.38	3.31	2.60	1.06	2.23	-2.10E-01	3.05E-01		-3.23E-01	1.17E-01		7.39E-02	7.97E-01		-3.30E-01	1.37E-01		-1.30E+00	3.54E-07	Down	-2.18E-01	3.96E-01		Unigene44823_All//gi|1345570|emb|CAA56319.1|//0.00E+00//starch branching enzyme I [Pisum sativum]	Unigene44823_All//0.00E+00//AT5G03650| SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme	Unigene44823_All//0.00E+00//TC166196		ko00500|Starch and sucrose metabolism		nr -
Unigene44829_All	2305	0.59	1.17	1.57	1.73	1.49	1.84	5.74	7.11	3.47	9.81E-01	1.13E-02		1.41E+00	5.68E-05	Up	-2.11E-01	5.54E-01		9.13E-02	7.80E-01		3.08E-01	1.46E-02		-7.25E-01	8.97E-08		Unigene44829_All//gi|108861895|sp|QS80U8.2|RH42_ARATH//8.00E-58//RecName: Full=DEAD-box ATP-dependent RNA helicase 42 >gi|4836896|gb|AAD30599.1|AC007369_9 Similar to RNA helicases [Arabidopsis thaliana]	Unigene44829_All//4.00E-49//AT1G20920| DEAD box RNA helicase, putative	Unigene44829_All//0.00E+00//ES809359		ko03040|Spliceosome		nr +
Unigene4483_All	814	75.20	94.18	87.07	28.09	15.40	13.21	22.65	27.32	22.81	3.25E-01	4.53E-08		2.11E-01	1.31E-03		-8.67E-01	2.69E-16		-1.09E+00	5.69E-21	Down	2.71E-01	1.16E-02		1.02E-02	9.59E-01		Unigene4483_All//gi|224349|prf||1102209C//9.00E-24//ORF 3	Unigene4483_All//3.00E-18//ATCG00130| ATPase F subunit.	Unigene4483_All//0.00E+00//TC176666		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr +
Unigene44832_All	485	0.65	0.10	1.10	2.36	2.84	3.72	3.57	2.15	1.07	-2.63E+00	1.31E-01		7.62E-01	4.52E-01		2.66E-01	6.81E-01		6.57E-01	1.96E-01		-7.30E-01	1.03E-01		-1.74E+00	1.65E-04	Down	Unigene44832_All//gi|22331140|ref|NP_188368.2|//1.00E-80//GPK1; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|11994680|dbj|BAB02918.1| serine/threonine protein kinase-like protein [Arabidopsis thaliana]	Unigene44832_All//8.00E-82//AT3G17420| GPK1; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene44832_All//2.00E-96//DR457299		ko04626|Plant-pathogen interaction		nr -
Unigene44833_All	2300	1.77	0.84	2.29	9.92	12.64	10.27	8.93	5.76	5.92	-1.08E+00	3.98E-04	Down	3.69E-01	1.89E-01		3.49E-01	2.49E-04		5.01E-02	7.08E-01		-6.33E-01	5.20E-09		-5.93E-01	2.24E-08		Unigene44833_All//gi|42561860|ref|NP_172415.2|//1.00E-155//protein kinase family protein [Arabidopsis thaliana]	Unigene44833_All//4.00E-149//AT1G09440| protein kinase family protein	Unigene44833_All//0.00E+00//TC163427		ko04626|Plant-pathogen interaction		nr +

Unigene44834_All	2194	3.08	1.92	2.33	9.85	7.69	5.13	9.06	4.00	3.12	-6.83E-01	2.47E-03		-4.01E-01	9.74E-02		-3.58E-01	1.40E-03		-9.43E-01	8.87E-16		-1.18E+00	1.62E-23	Down	-1.54E+00	5.97E-36	Down	Unigene44834_All//gi|297807871|ref|XP_002871819.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317656|gb|EFH48078.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44834_All//0.00E+00//AT5G18500| protein kinase family protein	Unigene44834_All//0.00E+00//TC153357		ko04626|Plant-pathogen interaction		nr +
Unigene44836_All	773	45.35	17.63	28.45	57.93	49.85	54.04	45.62	16.92	22.06	-1.36E+00	8.39E-42	Down	-6.73E-01	7.04E-13		-2.17E-01	5.37E-03		-1.00E-01	2.91E-01		-1.43E+00	3.26E-55	Down	-1.05E+00	3.74E-35	Down	Unigene44836_All//gi|8919178|emb|CAB96077.1|//1.00E-137//alpha-glucosidase [Solanum tuberosum]	Unigene44836_All//2.00E-137//AT1G68560| XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Unigene44836_All//0.00E+00//TC139829		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene44837_All	908	18.67	8.15	12.49	16.35	18.81	20.94	37.58	9.25	13.56	-1.20E+00	6.05E-17	Down	-5.80E-01	3.17E-05		2.02E-01	1.66E-01		3.57E-01	5.08E-03		-2.02E+00	1.08E-86	Down	-1.47E+00	2.42E-57	Down	Unigene44837_All//gi|8919178|emb|CAB96077.1|//1.00E-163//alpha-glucosidase [Solanum tuberosum]	Unigene44837_All//2.00E-161//AT1G68560| XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Unigene44837_All//0.00E+00//TC142464		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr +
Unigene44838_All	3092	4.65	7.18	4.75	6.27	7.26	4.95	6.56	4.04	2.77	6.25E-01	8.00E-08		3.06E-02	8.54E-01		2.12E-01	8.08E-02		-3.40E-01	7.10E-03		-7.00E-01	1.82E-10		-1.24E+00	7.18E-27	Down	Unigene44838_All//gi|5725356|emb|CAA10382.2|//0.00E+00//alpha-D-xylosidase [Tropaeolum majus]	Unigene44838_All//0.00E+00//AT1G68560| XYL1 (ALPHA-XYLOSIDASE 1); alpha-N-arabinofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds / xylan 1,4-beta-xylosidase	Unigene44838_All//0.00E+00//TC156289		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene44839_All	725	1.73	2.24	0.88	2.20	2.66	3.24	2.57	5.65	2.97	3.69E-01	4.80E-01		-9.75E-01	1.29E-01		2.75E-01	6.06E-01		5.59E-01	2.02E-01		1.14E+00	3.21E-05	Up	2.10E-01	6.00E-01		Unigene44839_All//gi|31980091|emb|CAD98760.1|//3.00E-17//MYB transcription factor R3 type [Populus tremula x Populus tremuloides]		Unigene44839_All//0.00E+00//gi|13244882|gb|BE053045.2|BE053045				nr +
Unigene44841_All	2171	2.41	6.70	2.35	5.00	5.74	4.68	9.21	9.97	11.23	1.47E+00	8.32E-20	Up	-3.35E-02	9.14E-01		1.99E-01	2.71E-01		-9.58E-02	6.41E-01		1.15E-01	3.67E-01		2.86E-01	3.49E-03		Unigene44841_All//gi|31980091|emb|CAD98760.1|//0.00E+00//MYB transcription factor R3 type [Populus tremula x Populus tremuloides]	Unigene44841_All//3.00E-133//AT5G02320| MYB3R-5 (MYB DOMAIN PROTEIN 3R-5); DNA binding / transcription factor	Unigene44841_All//0.00E+00//gi|164247332|gb|ES830113.1|ES830113	MYB			nr -
Unigene44842_All	2096	1.25	2.30	2.31	1.73	1.56	2.63	1.92	3.47	4.03	8.80E-01	1.41E-03		8.89E-01	1.81E-03		-1.53E-01	6.66E-01		6.00E-01	1.89E-02		8.57E-01	1.03E-05		1.07E+00	2.46E-09	Up	Unigene44842_All//gi|31980091|emb|CAD98760.1|//0.00E+00//MYB transcription factor R3 type [Populus tremula x Populus tremuloides]	Unigene44842_All//1.00E-121//AT5G02320| MYB3R-5 (MYB DOMAIN PROTEIN 3R-5); DNA binding / transcription factor	Unigene44842_All//0.00E+00//gi|13244882|gb|BE053045.2|BE053045	MYB			nr +
Unigene44843_All	2259	3.38	2.58	3.70	8.80	8.17	7.00	7.92	6.14	3.72	-3.91E-01	6.88E-02		1.30E-01	5.86E-01		-1.07E-01	4.72E-01		-3.30E-01	8.11E-03		-3.66E-01	1.92E-03		-1.09E+00	2.16E-19	Down	Unigene44843_All//gi|30686165|ref|NP_181014.2|//1.00E-140//proline-rich family protein [Arabidopsis thaliana]	Unigene44843_All//3.00E-103//AT2G34670| proline-rich family protein	Unigene44843_All//0.00E+00//CO084285				nr +
Unigene44845_All	2302	7.59	4.18	4.63	25.77	23.58	17.40	18.86	16.59	8.93	-8.60E-01	1.84E-10		-7.15E-01	1.94E-07		-1.29E-01	7.77E-02		-5.67E-01	1.04E-17		-1.85E-01	1.47E-02		-1.08E+00	4.16E-45	Down	Unigene44845_All//gi|30686165|ref|NP_181014.2|//1.00E-138//proline-rich family protein [Arabidopsis thaliana]	Unigene44845_All//2.00E-111//AT2G34670| proline-rich family protein	Unigene44845_All//0.00E+00//TC142784				nr +
Unigene44846_All	1794	0.53	0.20	0.21	0.50	0.84	0.53	0.75	0.47	0.20	-1.41E+00	5.70E-02		-1.34E+00	8.48E-02		7.57E-01	1.71E-01		8.11E-02	9.31E-01		-6.95E-01	1.84E-01		-1.92E+00	4.37E-04	Down	Unigene44846_All//gi|30686165|ref|NP_181014.2|//1.00E-144//proline-rich family protein [Arabidopsis thaliana]	Unigene44846_All//6.00E-102//AT2G34670| proline-rich family protein	Unigene44846_All//0.00E+00//EX168678				nr -
Unigene44847_All	2580	0.41	0.39	0.39	1.41	1.44	0.70	1.88	0.83	0.91	-4.63E-02	9.57E-01		-4.85E-02	9.57E-01		3.24E-02	9.47E-01		-1.01E+00	1.59E-03		-1.19E+00	1.95E-06	Down	-1.05E+00	1.29E-05	Down	Unigene44847_All//gi|30686165|ref|NP_181014.2|//1.00E-138//proline-rich family protein [Arabidopsis thaliana]	Unigene44847_All//3.00E-111//AT2G34670| proline-rich family protein	Unigene44847_All//0.00E+00//TC142784				nr +
Unigene44848_All	2224	21.76	10.50	20.73	11.87	14.85	11.09	14.58	14.94	9.44	-1.05E+00	2.78E-38	Down	-6.97E-02	4.43E-01		3.23E-01	2.93E-04		-9.85E-02	4.51E-01		3.51E-02	7.31E-01		-6.27E-01	6.04E-14		Unigene44848_All//gi|297791073|ref|XP_002863421.1|//1.00E-159//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309256|gb|EFH39680.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44848_All//1.00E-145//AT5G46170| F-box family protein	Unigene44848_All//0.00E+00//DW497140				nr -
Unigene44851_All	2078	3.88	1.34	2.33	8.10	6.86	6.43	7.75	4.24	4.91	-1.53E+00	5.64E-12	Down	-7.34E-01	5.55E-04		-2.40E-01	8.46E-02		-3.33E-01	1.57E-02		-8.69E-01	5.82E-12		-6.60E-01	5.50E-08		Unigene44851_All//gi|22329767|ref|NP_173822.2|//1.00E-175//ARL1 (ARG1-LIKE 1); heat shock protein binding / unfolded protein binding [Arabidopsis thaliana] >gi|67462409|sp|Q8VXV4.1|DNJ16_ARATH RecName: Full=Chaperone protein dnaJ 16; Short=AtJ16; Short=AtDjB16; AltName: Full=Protein ARG1-LIKE 1; Short=AtARL1 >gi|18377835|gb|AAL67104.1| At1g24120/F316_4 [Arabidopsis thaliana] >gi|345834419|gb|AAP49704.1| ARG1-like protein 1 [Arabidopsis thaliana] >gi|109134177|gb|AB625086.1| At1g24120 [Arabidopsis thaliana]	Unigene44851_All//3.00E-161//AT1G24120| ARL1 (ARG1-LIKE 1); heat shock protein binding / unfolded protein binding	Unigene44851_All//0.00E+00//TC149813		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene44854_All	2043	15.24	26.71	14.65	16.04	17.53	32.78	14.61	18.21	37.52	8.10E-01	5.78E-28		-5.69E-02	6.30E-01		1.28E-01	2.08E-01		1.03E+00	1.21E-54	Up	3.18E-01	5.50E-05		1.36E+00	1.27E-112	Up	Unigene44854_All//gi|115452853|ref|NP_001050027.1|//0.00E+00//Os03g0334000 [Oryza sativa Japonica Group] >gi|113548498|dbj|BAF11941.1| Os03g0334000 [Oryza sativa Japonica Group]	Unigene44854_All//4.00E-173//AT3G08720| S6K2 (ARABIDOPSIS THALIANA SERINE/THREONINE PROTEIN KINASE 2); kinase/ protein kinase	Unigene44854_All//0.00E+00//TC140680				nr -
Unigene44855_All	2446	3.17	2.03	1.89	16.84	15.29	9.12	12.22	5.88	4.90	-6.41E-01	2.13E-03		-7.41E-01	6.44E-04		-1.40E-01	1.19E-01		-8.85E-01	1.34E-26		-1.06E+00	2.08E-29	Down	-1.32E+00	9.95E-43	Down	Unigene44855_All//gi|25140423|gb|AAN71616.1|//0.00E+00//PIN-like protein [Gossypium hirsutum]	Unigene44855_All//0.00E+00//AT1G73590| PIN1 (PIN-FORMED 1); transporter	Unigene44855_All//0.00E+00//TC142535				nr +
Unigene44856_All	2347	6.67	2.89	3.09	53.02	47.45	31.52	27.69	24.22	23.17	-1.20E+00	7.51E-16	Down	-1.11E+00	2.04E-13	Down	-1.60E-01	3.03E-04		-7.50E-01	7.96E-60		-1.93E-01	1.22E-03		-2.57E-01	6.79E-06		Unigene44856_All//gi|224118654|ref|XP_002317874.1|//0.00E+00//auxin efflux carrier component [Populus trichocarpa] >gi|222858547|gb|EEE96094.1| auxin efflux carrier component [Populus trichocarpa]	Unigene44856_All//0.00E+00//AT1G73590| PIN1 (PIN-FORMED 1); transporter	Unigene44856_All//0.00E+00//TC177696				nr +
Unigene44859_All	834	3.70	3.83	6.07	5.91	7.43	7.85	7.66	3.41	7.93	4.83E-02	8.99E-01		7.13E-01	1.03E-02		3.30E-01	1.91E-01		4.09E-01	8.79E-02		-1.17E+00	5.48E-08	Down	5.08E-02	8.16E-01		Unigene44859_All//gi|297839899|ref|XP_002887831.1|//2.00E-72//EMB2753 [Arabidopsis lyrata subsp. lyrata] >gi|297333672|gb|EFH64090.1| EMB2753 [Arabidopsis lyrata subsp. lyrata]	Unigene44859_All//5.00E-72//AT1G80410| EMB2753 (EMBRYO DEFECTIVE 2753); binding	Unigene44859_All//2.00E-35//TC134685				nr +
Unigene4486_All	489	74.68	41.76	63.49	117.35	88.73	110.46	159.87	102.31	70.88	-8.39E-01	3.69E-20		-2.34E-01	1.40E-02		-4.03E-01	1.82E-10		-8.73E-02	2.99E-01		-6.44E-01	6.67E-33		-1.17E+00	4.37E-92	Down	Unigene4486_All//gi|288311314|gb|ADC45396.1|//1.00E-48//HSP90-2 [Glycine max]	Unigene4486_All//6.00E-49//AT5G56010| HSP81-3; ATP binding / unfolded protein binding	Unigene4486_All//0.00E+00//TC136470		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene44860_All	1424	7.31	5.73	7.22	15.64	15.43	17.70	22.00	8.83	16.67	-3.52E-01	5.16E-02		-1.88E-02	9.39E-01		-1.94E-02	8.91E-01		1.79E-01	1.36E-01		-1.32E+00	2.23E-43	Down	-4.00E-01	1.90E-06		Unigene44860_All//gi|297839899|ref|XP_002887831.1|//0.00E+00//EMB2753 [Arabidopsis lyrata subsp. lyrata] >gi|297333672|gb|EFH64090.1| EMB2753 [Arabidopsis lyrata subsp. lyrata]	Unigene44860_All//0.00E+00//AT1G80410| EMB2753 (EMBRYO DEFECTIVE 2753); binding	Unigene44860_All//2.00E-144//gi|73861312|gb|DT464051.1|DT464051				nr -
Unigene44864_All	491	4.58	5.26	4.01	0.51	3.23	3.77	3.36	0.60	2.92	2.00E-01	6.15E-01		-1.91E-01	6.53E-01		2.67E+00	1.61E-05	Up	2.89E+00	1.35E-06	Up	-2.49E+00	4.58E-06	Down	-2.01E-01	6.43E-01		Unigene44864_All//gi|224133450|ref|XP_002328045.1|//1.00E-37//aminotransferase family protein [Populus trichocarpa] >gi|222837454|gb|EEE78833.1| aminotransferase family protein [Populus trichocarpa]	Unigene44864_All//4.00E-32//AT5G36160| aminotransferase-related	Unigene44864_All//0.00E+00//TC132675		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene44865_All	562	4.65	4.24	5.59	1.60	5.70	4.18	3.31	0.52	3.76	-1.36E-01	7.23E-01		2.64E-01	4.86E-01		1.84E+00	4.28E-07	Up	1.39E+00	1.21E-03		-2.67E+00	3.21E-07	Down	1.83E-01	6.37E-01		Unigene44865_All//gi|224133454|ref|XP_002328046.1|//8.00E-79//aminotransferase family protein [Populus trichocarpa] >gi|222837455|gb|EEE78834.1| aminotransferase family protein [Populus trichocarpa]	Unigene44865_All//5.00E-71//AT5G53970| aminotransferase, putative	Unigene44865_All//0.00E+00//TC132675		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr +
Unigene44866_All	1101	3.52	4.97	4.21	1.45	2.50	3.24	1.23	0.38	0.51	4.99E-01	5.20E-02		2.59E-01	3.82E-01		7.89E-01	3.58E-02		1.16E+00	4.12E-04	Up	-1.69E+00	1.96E-03		-1.28E+00	1.14E-02		Unigene44866_All//gi|224133454|ref|XP_002328046.1|//1.00E-122//aminotransferase family protein [Populus trichocarpa] >gi|222837455|gb|EEE78834.1| aminotransferase family protein [Populus trichocarpa]	Unigene44866_All//1.00E-93//AT2G20610| SUR1 (SUPERROOT 1); S-alkylthiohydroximate lyase/ carbon-sulfur lyase/ transaminase	Unigene44866_All//0.00E+00//TC132675		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene44867_All	1678	11.23	10.30	16.47	8.34	8.78	7.21	6.32	3.14	2.07	-1.25E-01	3.80E-01		5.53E-01	1.80E-07		7.44E-02	6.87E-01		-2.10E-01	2.11E-01		-1.01E+00	2.89E-10	Down	-1.61E+00	5.18E-21	Down	Unigene44867_All//gi|224133454|ref|XP_002328046.1|//1.00E-174//aminotransferase family protein [Populus trichocarpa] >gi|222837455|gb|EEE78834.1| aminotransferase family protein [Populus trichocarpa]	Unigene44867_All//1.00E-142//AT5G36160| aminotransferase-related	Unigene44867_All//0.00E+00//TC159199		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene44868_All	2600	15.52	64.10	23.57	15.94	17.80	21.30	10.02	13.00	12.72	2.05E+00	0.00E+00	Up	6.04E-01	2.59E-18		1.59E-01	5.16E-02		4.18E-01	1.06E-09		3.77E-01	4.92E-06		3.44E-01	2.60E-05		Unigene44868_All//gi|224080658|ref|XP_002306199.1|//0.00E+00//neutral amino acid transport protein [Populus trichocarpa] >gi|222849163|gb|EEE86710.1| neutral amino acid transport protein [Populus trichocarpa]	Unigene44868_All//0.00E+00//AT1G31830| amino acid permease family protein	Unigene44868_All//0.00E+00//gi|78339316|gb|DT559590.1|DT559590				nr +

Unigene4487_All	728	16.75	9.67	14.34	4.45	3.17	2.61	4.01	8.67	5.03	-7.92E-01	1.18E-06		-2.24E-01	2.22E-01		-4.89E-01	1.56E-01		-7.71E-01	2.49E-02		1.11E+00	2.26E-07	Up	3.29E-01	2.56E-01		Unigene4487_All//gi|115470679|ref|NP_001058938.1|//5.00E-49//0s07g0160300 [Oryza sativa Japonica Group] >gi|113610474|dbj|BAF20852.1|Os07g0160300 [Oryza sativa Japonica Group]		Unigene4487_All//0.00E+00//gi|109883820|gb|DW512790.1|DW512790				nr -
Unigene44870_All	1211	1.69	8.08	4.71	0.99	2.56	1.79	5.87	19.64	16.35	2.26E+00	1.13E-23	Up	1.48E+00	6.40E-08	Up	1.37E+00	9.45E-05	Up	8.59E-01	5.30E-02		1.74E+00	1.29E-49	Up	1.48E+00	1.40E-33	Up	Unigene44870_All//gi|297604274|ref|NP_001055194.2|//2.00E-08//Os05g0323800 [Oryza sativa Japonica Group] >gi|255676246|dbj|BAF17108.2|Os05g0323800 [Oryza sativa Japonica Group]		Unigene44870_All//2.00E-132//DT463741				nr +
Unigene44871_All	2453	29.58	103.12	64.10	13.12	25.27	29.88	20.74	69.19	61.15	1.80E+00	0.00E+00	Up	1.12E+00	1.84E-131	Up	9.46E-01	1.90E-48		1.19E+00	5.92E-75	Up	1.74E+00	0.00E+00	Up	1.56E+00	2.09E-269	Up	Unigene44871_All//gi|18412437|ref|NP_565214.1|//0.00E+00//ABC1 family protein [Arabidopsis thaliana] >gi|75191793|sp|Q9MA15.1|Y1960_ARATH RecName: Full=Uncharacterized aarF domain-containing protein kinase At1g79600, chloroplastic; Flags: Precursor >gi|7715610|gb|AAF68128.1|AC010793_23 F20B17.3 [Arabidopsis thaliana] >gi|18086325|gb|AAL57626.1|At1g79600/F20B17_3 [Arabidopsis thaliana] >gi|22655328|gb|AAM98256.1|At1g79600/F20B17_3 [Arabidopsis thaliana]	Unigene44871_All//0.00E+00//AT1G79600| ABC1 family protein	Unigene44871_All//0.00E+00//TC134830				nr -
Unigene44877_All	485	0.00	0.52	0.22	0.10	0.50	0.37	6.97	15.43	7.64	9.03E+00	7.85E-02		7.78E+00	3.97E-01		2.27E+00	3.05E-01		1.86E+00	4.58E-01		1.15E+00	5.89E-09	Up	1.31E-01	6.51E-01		Unigene44877_All//gi|227053553|gb|ACP18875.1|//6.00E-39//beta-galactosidase pBG(a) [Carica papaya]	Unigene44877_All//2.00E-36//AT3G13750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene44877_All//2.00E-123//TC168338		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation		nr -
Unigene44878_All	1435	0.88	0.92	0.15	4.44	4.18	3.65	8.13	9.96	9.74	6.92E-02	9.12E-01		-2.56E+00	6.99E-04	Down	-8.97E-02	7.61E-01		-2.84E-01	2.70E-01		2.93E-01	3.34E-02		2.61E-01	5.47E-02		Unigene44878_All//gi|157313304|gb|ABV32545.1|//0.00E+00//beta-galactosidase protein 2 [Prunus persica]	Unigene44878_All//0.00E+00//AT3G13750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene44878_All//0.00E+00//TC140935		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series		nr +
Unigene4488_All	562	5.31	5.95	5.97	5.05	4.41	11.09	18.43	37.18	29.06	1.65E-01	6.16E-01		1.70E-01	6.17E-01		-1.96E-01	6.14E-01		1.13E+00	1.88E-06	Up	1.01E+00	1.89E-19	Up	6.57E-01	5.34E-08		Unigene4488_All//gi|148750945|gb|ABR10070.1|//5.00E-58//MAPK [Malus hupehensis]	Unigene4488_All//9.00E-57//AT4G01370| ATMPK4 (ARABIDOPSIS THALIANA MAP KINASE 4); MAP kinase/ kinase	Unigene4488_All//0.00E+00//gi|109851164|gb|DW480143.1|DW480143		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene44882_All	2305	5.95	30.01	7.74	17.46	17.34	18.65	33.37	9.99	49.72	2.34E+00	1.53E-170	Up	3.80E-01	5.85E-03		-9.70E-03	9.31E-01		9.52E-02	3.35E-01		-1.74E+00	8.45E-159	Down	5.76E-01	3.11E-40		Unigene44882_All//gi|124359946|gb|ABN07962.1|//0.00E+00//ATP-citrate lyase/succinyl-CoA ligase [Medicago truncatula]	Unigene44882_All//0.00E+00//AT5G49460| ACLB-2 (ATP CITRATE LYASE SUBUNIT B 2); ATP citrate synthase	Unigene44882_All//0.00E+00//TC158676		ko00020|Citrate cycle (TCA cycle)		nr -
Unigene44883_All	1184	4.91	0.86	1.71	1.94	2.01	1.56	24.46	26.16	11.57	-2.52E+00	2.59E-16	Down	-1.52E+00	2.52E-08	Down	5.23E-02	9.22E-01		-3.07E-01	5.02E-01		9.67E-02	3.57E-01		-1.08E+00	2.04E-30	Down	Unigene44883_All//gi|51536432|gb|AU05454.1|//1.00E-123//At1g61820 [Arabidopsis thaliana] >gi|52421273|gb|AU45206.1|At1g61820 [Arabidopsis thaliana]	Unigene44883_All//1.00E-124//AT1G61820| BGLU46 (BETA GLUCOSIDASE 46); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene44883_All//0.00E+00//EX165210		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr -
Unigene44885_All	1946	1.32	2.86	5.12	17.33	18.49	21.84	98.18	27.92	25.30	1.12E+00	1.48E-05	Up	1.96E+00	1.61E-19	Up	9.36E-02	3.86E-01		3.34E-01	3.12E-05		-1.81E+00	0.00E+00	Down	-1.96E+00	0.00E+00	Down	Unigene44885_All//gi|306996622|ref|NP_850968.1|//0.00E+00//BGLU46 (BETA GLUCOSIDASE 46); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|281312216|sp|Q80690.2|BGL46_ARATH RecName: Full=Beta-glucosidase 46; Short=AtBGLU46; Flags: Precursor	Unigene44885_All//8.00E-177//AT1G61820| BGLU46 (BETA GLUCOSIDASE 46); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene44885_All//0.00E+00//TC155588		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr -
Unigene44886_All	1236	13.97	12.46	8.66	17.13	12.15	18.31	29.18	19.11	12.41	-1.65E-01	2.57E-01		-6.90E-01	5.83E-07		-4.96E-01	6.41E-06		9.59E-02	4.99E-01		-6.11E-01	2.66E-14		-1.23E+00	2.03E-46	Down	Unigene44886_All//gi|15237303|ref|NP_200104.1|//1.00E-149//PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1); pyruvate kinase [Arabidopsis thaliana] >gi|10177106|dbj|BAB10440.1|pyruvate kinase [Arabidopsis thaliana] >gi|21536743|gb|AAM61075.1|pyruvate kinase [Arabidopsis thaliana]	Unigene44886_All//1.00E-150//AT5G52920| PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1); pyruvate kinase	Unigene44886_All//0.00E+00//TC132317		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene44887_All	2218	4.81	1.67	2.71	14.33	12.37	11.48	10.03	3.96	6.07	-1.53E+00	1.39E-15	Down	-8.27E-01	5.35E-06		-2.12E-01	2.86E-02		-3.19E-01	7.66E-04		-1.34E+00	6.58E-32	Down	-7.24E-01	2.00E-12		Unigene44887_All//gi|15237303|ref|NP_200104.1|//0.00E+00//PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1); pyruvate kinase [Arabidopsis thaliana] >gi|10177106|dbj|BAB10440.1|pyruvate kinase [Arabidopsis thaliana] >gi|21536743|gb|AAM61075.1|pyruvate kinase [Arabidopsis thaliana]	Unigene44887_All//0.00E+00//AT5G52920| PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1); pyruvate kinase	Unigene44887_All//0.00E+00//TC163371		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene44898_All	3586	12.07	4.32	7.20	15.99	12.76	9.17	10.88	2.06	4.04	-1.48E+00	3.20E-58	Down	-7.45E-01	1.08E-18		-3.25E-01	3.72E-07		-8.02E-01	3.26E-31		-2.40E+00	1.49E-122	Down	-1.43E+00	1.14E-62	Down	Unigene44898_All//gi|195612300|gb|ACG27980.1|//0.00E+00//receptor protein kinase TMK1 precursor [Zea mays]	Unigene44898_All//6.00E-138//AT2G01820| leucine-rich repeat protein kinase, putative	Unigene44898_All//0.00E+00//ES847940				nr -
Unigene44899_All	384	5.04	0.26	0.97	1.43	0.99	1.41	2.42	1.09	0.31	-4.26E+00	6.09E-09	Down	-2.38E+00	3.07E-05	Down	-5.33E-01	5.85E-01		-1.59E-02	9.75E-01		-1.15E+00	7.87E-02		-2.96E+00	1.72E-04	Down	Unigene44899_All//gi|33945885|emb|CAE45595.1|//7.00E-21//S-receptor kinase-like protein 2 [Lotus japonicus] >gi|164605526|dbj|BAF98592.1|CM0216.580.nc [Lotus japonicus]	Unigene44899_All//3.00E-18//AT1G11330| S-locus lectin protein kinase family protein	Unigene44899_All//4.00E-07//TC154318		ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism		nr +
Unigene449_All	2485	1.12	0.53	0.77	2.25	1.75	2.05	5.34	2.30	2.71	-1.07E+00	4.84E-03		-5.33E-01	1.82E-01		-3.63E-01	1.59E-01		-1.29E-01	6.60E-01		-1.21E+00	1.10E-16	Down	-9.80E-01	1.98E-12		Unigene449_All//gi|30693010|ref|NP_174675.2|//0.00E+00//STT3B (staurosporin and temperature sensitive 3-like b); oligosaccharyl transferase [Arabidopsis thaliana] >gi|10086464|gb|AAG12524.1|AC015446_5 Putative integral membrane protein [Arabidopsis thaliana]	Unigene449_All//0.00E+00//AT1G33130| STT3B (staurosporin and temperature sensitive 3-like b); oligosaccharyl transferase	Unigene449_All//0.00E+00//TC147182		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis		nr -
Unigene4490_All	616	60.81	61.36	74.95	79.01	71.95	89.96	96.37	66.63	44.37	1.29E-02	9.07E-01		3.02E-01	2.14E-04		-1.35E-01	9.74E-02		1.87E-01	1.09E-02		-5.32E-01	3.89E-18		-1.12E+00	4.86E-65	Down	Unigene4490_All//gi|106879141|gb|ABF82600.1|//2.00E-30//At1g76200 [Arabidopsis thaliana]	Unigene4490_All//3.00E-26//AT1G76200| unknown protein	Unigene4490_All//0.00E+00//TC165908				nr -
Unigene44900_All	1842	15.59	1.68	8.96	0.84	0.80	0.39	0.07	0.02	0.00	-3.22E+00	3.74E-101	Down	-7.99E-01	3.52E-14		-6.05E-02	9.01E-01		-1.10E+00	4.18E-02		-1.60E+00	5.34E-01		-6.11E+00	2.00E-01		Unigene44900_All//gi|240256087|ref|NP_194459.4|//1.00E-118//ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene44900_All//2.00E-118//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene44900_All//0.00E+00//TC142819				nr +
Unigene44902_All	2543	4.26	2.05	3.79	3.29	5.43	3.20	1.76	2.20	1.52	-1.05E+00	3.41E-09	Down	-1.68E-01	3.96E-01		7.23E-01	3.39E-07		-4.19E-02	8.61E-01		3.22E-01	1.77E-01		-2.14E-01	4.22E-01		Unigene44902_All//gi|240256087|ref|NP_194459.4|//0.00E+00//ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene44902_All//0.00E+00//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene44902_All//0.00E+00//TC142819		ko04626|Plant-pathogen interaction		nr +
Unigene4491_All	908	78.54	185.32	107.73	223.29	243.85	289.18	82.65	252.89	318.80	1.24E+00	2.85E-170	Up	4.56E-01	1.38E-17		1.27E-01	1.08E-04		3.73E-01	1.45E-35		1.61E+00	0.00E+00	Up	1.95E+00	0.00E+00	Up	Unigene4491_All//gi|116265936|gb|AB191216.1|//1.00E-92//CRL-interacting protein kinase 9 [Populus trichocarpa]	Unigene4491_All//2.00E-58//AT4G30960| SIP3 (SOS3-INTERACTING PROTEIN 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene4491_All//0.00E+00//gi|73860966|gb|DT463705.1|DT463705		ko04626|Plant-pathogen interaction		nr +
Unigene44910_All	1321	0.75	0.08	0.52	0.79	0.55	0.34	1.70	1.65	0.97	-3.29E+00	3.81E-04	Down	-5.22E-01	4.60E-01		-5.33E-01	4.27E-01		-1.21E+00	7.81E-02		-4.40E-02	9.27E-01		-8.14E-01	2.64E-02		Unigene44910_All//gi|211906526|gb|ACJ11756.1|//0.00E+00//rhamnose synthase [Gossypium hirsutum]	Unigene44910_All//0.00E+00//AT1G78570| RHM1 (RHAMNOSE BIOSYNTHESIS 1); UDP-L-rhamnose synthase/ UDP-glucose 4,6-dehydratase/ catalytic	Unigene44910_All//0.00E+00//TC135633		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene44912_All	280	7.29	11.76	6.09	7.65	9.84	7.74	23.86	16.87	7.54	6.91E-01	4.36E-02		-2.60E-01	6.05E-01		3.63E-01	3.83E-01		1.73E-02	9.69E-01		-5.00E-01	1.43E-02		-1.66E+00	4.46E-14	Down		Unigene44912_All//1.00E-142//gi|13246194|gb|BE052034.2|BE052034					nr -
Unigene44913_All	2512	3.27	4.24	2.78	1.65	1.51	1.83	5.13	8.37	12.75	3.73E-01	3.66E-02		-2.36E-01	3.00E-01		-1.26E-01	7.17E-01		1.56E-01	6.24E-01		7.05E-01	6.06E-11		1.31E+00	4.75E-45	Up	Unigene44913_All//gi|224077016|ref|XP_002305094.1|//1.00E-171//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222848058|gb|EEE85605.1|glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene44913_All//7.00E-70//AT2G29120| ATGLR2.7; intracellular ligand-gated ion channel	Unigene44913_All//0.00E+00//TC138885				nr -
Unigene44914_All	3017	2.39	3.64	3.55	0.56	0.29	0.73	0.94	5.33	5.94	6.07E-01	4.02E-04		5.68E-01	1.69E-03		-9.77E-01	4.19E-02		3.86E-01	4.10E-01		2.51E+00	2.25E-53	Up	2.66E+00	9.88E-65	Up	Unigene44914_All//gi|224077014|ref|XP_002305093.1|//0.00E+00//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222848057|gb|EEE85604.1|glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene44914_All//1.00E-129//AT2G29120| ATGLR2.7; intracellular ligand-gated ion channel	Unigene44914_All//0.00E+00//gi|109849245|gb|DW478224.1|DW478224				nr -
Unigene44916_All	1913	4.62	3.50	4.68	8.20	8.86	10.03	12.20	11.65	4.12	-4.03E-01	4.09E-02		1.68E-02	9.53E-01		1.11E-01	5.15E-01		2.91E-01	2.57E-02		-6.72E-02	6.15E-01		-1.57E+00	3.24E-43	Down	Unigene44916_All//gi|74231016|gb|AB006652.1|//0.00E+00//mitogen-activated protein kinase [Gossypium hirsutum]	Unigene44916_All//3.00E-170//AT1G59580| ATMPK2 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 2); MAP kinase/ kinase/ protein kinase	Unigene44916_All//0.00E+00//TC153416		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene44919_All	1850	9.59	32.37	8.29	14.43	13.89	21.41	31.65	37.44	26.90	1.76E+00	5.28E-102	Up	-2.10E-01	1.51E-01		-5.57E-02	6.71E-01		5.69E-01	5.00E-12		2.42E-01	1.90E-05		-2.35E-01	1.09E-04		Unigene44919_All//gi|224066759|ref|XP_002302201.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222843927|gb|EEE81474.1| GRAS family transcription factor [Populus trichocarpa]	Unigene44919_All//2.00E-180//AT1G21450| SCL1 (SCARECROW-LIKE 1); transcription factor	Unigene44919_All//0.00E+00//ES812809	GRAS			nr +
Unigene44921_All	5158	2.15	3.68	1.98	3.70	2.19	2.22	20.02	16.46	9.59	7.77E-01	1.38E-09		-1.18E-01	5.64E-01		-7.56E-01	6.93E-11		-7.34E-01	2.51E-09		-2.83E-01	4.45E-10		-1.06E+00	1.89E-103	Down	Unigene44921_All//gi|147225251|dbj|BAA36471.2|//1.00E-134//F0-ATPase subunit 6 [Beta vulgaris]	Unigene44921_All//4.00E-104//ATMG01170| ATPase subunit 6	Unigene44921_All//0.00E+00//gi|164272788|gb|ESR26872.1|ESR26872		ko00190|Oxidative phosphorylation		nr +

Unigene44923_All	3279	28.42	14.12	25.58	22.36	21.27	14.19	7.21	2.88	3.18	-1.01E+00	2.36E-68	Down	-1.52E-01	9.25E-03		-7.25E-02	3.15E-01		-6.57E-01	3.75E-28		-1.32E+00	3.56E-33	Down	-1.18E+00	1.15E-28	Down	Unigene44923_All//gi|15220579|ref|NP_176957.1|//0.00E+00//phototropic-responsive NPH3 family protein [Arabidopsis thaliana] >gi|42572025|ref|NP_974103.1| phototropic-responsive NPH3 family protein [Arabidopsis thaliana] >gi|31711740|gb|AAP68226.1| At1g67900 [Arabidopsis thaliana]	Unigene44923_All//0.00E+00//AT1G67900| phototropic-responsive NPH3 family protein	Unigene44923_All//0.00E+00//DW506233				nr -
Unigene44924_All	1354	7.92	7.15	5.82	7.84	8.21	7.14	12.49	10.16	5.62	-1.48E-01	4.31E-01		-4.45E-01	1.52E-02		6.80E-02	7.73E-01		-1.35E-01	5.19E-01		-2.99E-01	1.62E-02		-1.15E+00	4.77E-20	Down	Unigene44924_All//gi|16326135|dbj|BAB70511.1|//6.00E-64//Myb [Nicotiana tabacum]	Unigene44924_All//6.00E-40//AT4G32730| PC-MYB1; DNA binding / transcription coactivator/ transcription factor	Unigene44924_All//0.00E+00//ES837901	MYB			nr -
Unigene44928_All	2322	5.34	8.62	4.59	11.39	9.92	11.03	13.24	7.24	4.74	6.91E-01	2.37E-08		-2.20E-01	2.29E-01		-1.99E-01	6.97E-02		-4.68E-02	7.09E-01		-8.71E-01	3.63E-22		-1.48E+00	2.20E-52	Down	Unigene44928_All//gi|297816238|ref|XP_002876002.1|//0.00E+00//glycosyl hydrolase family protein 43 [Arabidopsis lyrata subsp. lyrata] >gi|297321840|gb|EFH52261.1| glycosyl hydrolase family protein 43 [Arabidopsis lyrata subsp. lyrata]	Unigene44928_All//0.00E+00//AT3G49880| glycosyl hydrolase family protein 43	Unigene44928_All//0.00E+00//TC165169				nr +
Unigene4493_All	768	50.21	18.41	24.54	52.80	43.72	67.86	102.95	40.11	43.42	-1.45E+00	2.96E-50	Down	-1.03E+00	1.12E-28	Down	-2.72E-01	6.40E-04		3.62E-01	3.52E-07		-1.36E+00	7.55E-114	Down	-1.25E+00	2.83E-102	Down	Unigene4493_All//gi|15229845|ref|NP_187143.1|//5.00E-64//40S ribosomal protein S24 (RPS24A) [Arabidopsis thaliana] >gi|11134742|sp|Q8RS17.1|RS241_ARATH RecName: Full=40S ribosomal protein S24-1 >gi|15215672|gb|AAK91381.1| AT3g04920/T9J14_13 [Arabidopsis thaliana] >gi|20334888|gb|AAM16200.1| AT3g04920/T9J14_13 [Arabidopsis thaliana]	Unigene4493_All//4.00E-60//AT3G04920| 40S ribosomal protein S24 (RPS24A)	Unigene4493_All//0.00E+00//TC149886		ko03010|Ribosome		nr +
Unigene44931_All	818	9.40	7.74	8.46	2.74	5.73	2.60	2.53	2.04	3.60	-2.80E-01	2.07E-01		-1.52E-01	5.30E-01		1.06E+00	7.84E-05	Up	-7.87E-02	8.66E-01		-3.09E-01	4.71E-01		5.09E-01	1.09E-01		Unigene44931_All//gi|224071632|ref|XP_002303546.1|//5.00E-66//cytochrome P450 [Populus trichocarpa] >gi|222840978|gb|EEE78525.1| cytochrome P450 [Populus trichocarpa]	Unigene44931_All//6.00E-46//AT2G45550| CYP76C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene44931_All//3.00E-179//C0071836		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene44933_All	1861	17.54	14.46	13.53	10.44	12.16	8.86	4.84	2.25	6.81	-2.79E-01	3.63E-03		-3.74E-01	1.29E-04		2.20E-01	6.77E-02		-2.37E-01	7.46E-02		-1.11E+00	4.05E-10	Down	4.92E-01	3.55E-04		Unigene44933_All//gi|224071632|ref|XP_002303546.1|//1.00E-164//cytochrome P450 [Populus trichocarpa] >gi|222840978|gb|EEE78525.1| cytochrome P450 [Populus trichocarpa]	Unigene44933_All//2.00E-121//AT2G45550| CYP76C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene44933_All//0.00E+00//C0071836		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene44941_All	1667	34.18	28.69	31.91	50.98	45.84	44.59	86.51	51.57	36.73	-2.52E-01	3.47E-04		-9.91E-02	2.36E-01		-1.53E-01	6.34E-03		-1.93E-01	6.61E-04		-7.46E-01	1.51E-77		-1.24E+00	1.16E-183	Down	Unigene44941_All//gi|55979111|gb|AAV69019.1|//9.00E-69//NADH:cytochrome b5 reductase [Vernicia fordii] >gi|55979115|gb|AAV69021.1| NADH:cytochrome b5 reductase [Vernicia fordii]	Unigene44941_All//2.00E-66//AT5G17770| ATCBR (ARABIDOPSIS THALIANA NADH:CYTOCHROME B5 REDUCTASE 1); cytochrome-b5 reductase	Unigene44941_All//0.00E+00//TC161330		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene44942_All	462	0.45	0.00	0.00	2.80	0.37	0.59	48.32	36.55	24.75	-8.82E+00	1.22E-01		-8.82E+00	1.45E-01		-2.91E+00	1.33E-05	Down	-2.26E+00	6.70E-04	Down	-4.03E-01	9.97E-05		-9.65E-01	8.01E-20		Unigene44942_All//gi|33636090|emb|CAD91338.1|//9.00E-36//beta-fructofuranosidase [Glycine max]	Unigene44942_All//5.00E-32//AT3G13790| ATBFRUCT1; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene44942_All//0.00E+00//ES796097		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene44944_All	981	0.53	0.31	0.33	1.47	1.05	0.46	43.66	20.41	19.21	-7.83E-01	4.22E-01		-7.11E-01	4.97E-01		-4.84E-01	3.91E-01		-1.68E+00	3.92E-03		-1.10E+00	1.99E-44	Down	-1.18E+00	1.35E-51	Down	Unigene44944_All//gi|21322516|emb|CAD19323.1|//1.00E-123//exocellular acid invertase 2 [Beta vulgaris]	Unigene44944_All//6.00E-115//AT3G13790| ATBFRUCT1; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene44944_All//0.00E+00//C0095726		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr +
Unigene44945_All	2656	1.95	1.83	2.41	1.93	2.72	1.75	5.87	12.67	8.88	-9.07E-02	7.28E-01		3.03E-01	2.34E-01		4.95E-01	2.06E-02		-1.41E-01	6.38E-01		1.11E+00	1.32E-35	Up	5.96E-01	1.59E-09		Unigene44945_All//gi|11967654|emb|CAC19366.1|//1.00E-177//fructan 1-exohydrolase I [Cichorium intybus]	Unigene44945_All//1.00E-148//AT3G13784| AtcwINV5 (Arabidopsis thaliana cell wall invertase 5); hydrolase, hydrolyzing O-glycosyl compounds	Unigene44945_All//0.00E+00//C0095726		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr -
Unigene44946_All	5274	3.03	5.85	2.42	5.48	5.61	5.69	13.83	21.79	85.80	9.51E-01	5.76E-21		-3.20E-01	3.22E-02		3.39E-02	8.11E-01		5.37E-02	6.73E-01		6.56E-01	1.51E-49		2.63E+00	0.00E+00	Up	Unigene44946_All//gi|297849340|ref|XP_002892551.1|//0.00E+00//NF-X1 type zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338393|gb|EFH68810.1| NF-X1 type zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene44946_All//0.00E+00//AT1G10170| ATNFXL1 (ARABIDOPSIS THALIANA NF-X-LIKE 1); protein binding / transcription factor/ zinc ion binding	Unigene44946_All//0.00E+00//TC150697				nr -
Unigene44948_All	3777	8.05	17.25	8.87	10.33	12.51	14.71	15.84	26.16	25.96	1.10E+00	5.47E-55	Up	1.40E-01	1.92E-01		2.77E-01	1.66E-04		5.10E-01	9.31E-14		7.24E-01	1.35E-50		7.13E-01	4.74E-50		Unigene44948_All//gi|42573473|ref|NP_974833.1|//0.00E+00//transcription elongation factor-related [Arabidopsis thaliana]	Unigene44948_All//3.00E-166//AT5G25520| transcription elongation factor-related	Unigene44948_All//0.00E+00//TC178114				nr +
Unigene44949_All	305	1.72	0.00	0.00	1.31	1.13	0.30	6.24	4.39	0.00	-1.07E+01	2.92E-03		-1.07E+01	4.75E-03		-2.11E-01	8.25E-01		-2.14E+00	1.26E-01		-5.09E-01	2.40E-01		-1.26E+01	4.91E-14	Down	Unigene44949_All//gi|60327196|gb|AAX19021.1|//4.00E-11//Cf-2.3 [Solanum pimpinellifolium]	Unigene44949_All//3.00E-10//AT3G11080| AtRLP35 (Receptor Like Protein 35); kinase/ protein binding					nr +
Unigene4495_All	637	13.72	8.35	13.04	32.69	25.79	23.40	32.86	19.88	13.01	-7.16E-01	2.42E-04		-7.29E-02	7.29E-01		-3.42E-01	2.99E-03		-4.82E-01	3.92E-05		-7.25E-01	2.09E-11		-1.34E+00	7.86E-31	Down	Unigene4495_All//gi|28416749|gb|AA042905.1|//1.00E-22//At5g53650 [Arabidopsis thaliana]	Unigene4495_All//1.00E-14//AT5G53650| unknown protein	Unigene4495_All//0.00E+00//TC166390				nr -
Unigene44950_All	548	4.49	2.40	3.60	1.09	1.19	0.25	5.25	4.35	0.29	-9.00E-01	2.59E-02		-3.20E-01	4.54E-01		1.30E-01	9.05E-01		-2.14E+00	4.39E-02		-2.71E-01	4.47E-01		-4.17E+00	2.58E-16	Down	Unigene44950_All//gi|224112233|ref|XP_002332812.1|//7.00E-45//leucine rich repeat family protein with ABC domain [Populus trichocarpa] >gi|222833206|gb|EEE71683.1| leucine rich repeat family protein with ABC domain [Populus trichocarpa]	Unigene44950_All//3.00E-40//AT1G07390| protein binding	Unigene44950_All//3.00E-138//DT465312				nr +
Unigene44951_All	1337	17.96	6.22	18.84	12.89	5.56	3.07	17.58	7.66	2.38	-1.53E+00	3.11E-34	Down	6.87E-02	6.21E-01		-1.21E+00	2.55E-21	Down	-2.07E+00	2.38E-40	Down	-1.20E+00	2.11E-28	Down	-2.88E+00	1.08E-93	Down	Unigene44951_All//gi|224112233|ref|XP_002332812.1|//7.00E-37//leucine rich repeat family protein with ABC domain [Populus trichocarpa] >gi|222833206|gb|EEE71683.1| leucine rich repeat family protein with ABC domain [Populus trichocarpa]	Unigene44951_All//7.00E-177//AT1G74180| AtRLP14 (Receptor Like Protein 14); protein binding with ABC domain	Unigene44951_All//2.00E-61//gi|3326612|gb|AI055498.1|AI055498		ko04626|Plant-pathogen interaction		nr +
Unigene44952_All	3161	2.75	2.32	4.65	4.60	2.17	0.80	15.61	8.85	1.39	-2.41E-01	2.41E-01		7.59E-01	5.26E-07		-1.09E+00	3.65E-15	Down	-2.52E+00	1.85E-43	Down	-8.19E-01	1.15E-31		-3.49E+00	1.05E-235	Down	Unigene44952_All//gi|223452526|gb|ACM89590.1|//1.00E-169//disease resistance protein [Glycine max]	Unigene44952_All//3.00E-117//AT1G07390| protein binding	Unigene44952_All//0.00E+00//TC175191				nr +
Unigene44955_All	966	4.82	139.05	7.99	16.09	53.26	88.97	256.00	625.34	642.94	4.85E+00	0.00E+00	Up	7.30E-01	7.85E-04		1.73E+00	7.60E-101	Up	2.47E+00	9.89E-243	Up	1.29E+00	0.00E+00	Up	1.33E+00	0.00E+00	Up	Unigene44955_All//gi|3132675|gb|AAC16325.1|//1.00E-120//asparagine synthetase [Elaeagnus umbellata]	Unigene44955_All//3.00E-117//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene44955_All//0.00E+00//gi|48823415|gb|C0124728.1|C0124728		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene44956_All	1910	1.81	5.94	1.51	4.04	3.06	1.89	138.77	562.51	119.35	1.72E+00	2.87E-19	Up	-2.64E-01	4.60E-01		-3.99E-01	5.33E-02		-1.10E+00	1.48E-07	Down	2.02E+00	0.00E+00	Up	-2.18E-01	1.15E-15		Unigene44956_All//gi|156767195|gb|ABU95104.1|//0.00E+00//asparagine synthetase [Phaseolus vulgaris]	Unigene44956_All//0.00E+00//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene44956_All//0.00E+00//TC131580		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene44957_All	2387	6.97	10.53	3.88	7.14	5.93	4.58	138.85	578.00	115.41	5.95E-01	4.43E-08		-8.45E-01	2.91E-09		-2.68E-01	4.86E-02		-6.40E-01	9.50E-07		2.06E+00	0.00E+00	Up	-2.67E-01	3.50E-28		Unigene44957_All//gi|16226759|gb|AAL16254.1|AF428324_1/1.00E-128//At2g30010/F23F1.7 [Arabidopsis thaliana] >gi|34200050|gb|AAC31851.1| expressed protein [Arabidopsis thaliana] >gi|56382013|gb|AAV85725.1| At2g30010 [Arabidopsis thaliana]	Unigene44957_All//3.00E-132//AT5G58600| PMR5 (POWDERY MILDEW RESISTANT 5)	Unigene44957_All//0.00E+00//TC162045		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene44958_All	360	3.78	5.07	5.03	10.52	4.69	6.15	3.99	2.09	2.32	4.23E-01	3.85E-01		4.12E-01	4.05E-01		-1.17E+00	7.96E-05	Down	-7.75E-01	1.33E-02		-9.34E-01	6.12E-02		-7.81E-01	1.01E-01		Unigene44958_All//gi|297833446|ref|XP_002884605.1|//2.00E-18//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297330445|gb|EFH60864.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene44958_All//1.00E-19//AT3G06670| binding	Unigene44958_All//2.00E-74//TC176982				nr -
Unigene4496_All	820	2.04	2.29	1.56	4.62	3.95	3.08	6.24	5.81	2.92	1.63E-01	7.23E-01		-3.90E-01	4.60E-01		-2.26E-01	5.30E-01		-5.82E-01	6.95E-02		-1.03E-01	6.98E-01		-1.10E+00	3.02E-06	Down	Unigene4496_All//gi|224122872|ref|XP_002318937.1|//9.00E-15//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222857313|gb|EEE94860.1| chromatin remodeling complex subunit [Populus trichocarpa]		Unigene4496_All//0.00E+00//TC161031				nr -
Unigene44961_All	793	1.98	1.28	1.88	11.87	11.07	7.69	8.26	7.38	3.92	-6.31E-01	2.31E-01		-7.42E-02	8.92E-01		-1.01E-01	6.38E-01		-6.27E-01	6.35E-04		-1.64E-01	4.92E-01		-1.08E+00	1.53E-07	Down	Unigene44961_All//gi|223452315|gb|ACM89485.1|//8.00E-70//receptor-like kinase [Glycine max]	Unigene44961_All//8.00E-59//AT5G38990| protein kinase family protein	Unigene44961_All//1.00E-24//TC160726		ko04626|Plant-pathogen interaction		nr +
Unigene44962_All	533	1.87	2.38	1.90	17.29	10.08	8.05	3.65	3.69	1.12	3.50E-01	5.68E-01		2.54E-02	9.90E-01		-7.79E-01	8.28E-06		-1.10E+00	5.56E-09	Down	1.44E-02	1.01E+00		-1.70E+00	7.95E-05	Down	Unigene44962_All//gi|255587611|ref|XP_002534329.1|//7.00E-10//Serine/threonine-protein kinase PBS1, putative [Ricinus communis] >gi|223525483|gb|EEF28053.1| Serine/threonine-protein kinase PBS1, putative [Ricinus communis]	Unigene44962_All//2.00E-05//AT5G54380| THE1 (THESEUS1); kinase/ protein kinase	Unigene44962_All//0.00E+00//gi|109877402|gb|DW506375.1|DW506375				nr +
Unigene44963_All	2963	3.67	2.55	4.17	23.37	18.22	10.26	9.85	11.62	3.78	-5.28E-01	2.22E-03		1.83E-01	3.23E-01		-3.59E-01	3.73E-10		-1.19E+00	8.69E-72	Down	2.39E-01	4.42E-03		-1.38E+00	8.17E-45	Down	Unigene44963_All//gi|223452393|gb|ACM89524.1|//0.00E+00//FERONIA receptor-like kinase [Glycine max]	Unigene44963_All//0.00E+00//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene44963_All//0.00E+00//TC160726		ko04626|Plant-pathogen interaction		nr -
Unigene44967_All	499	1.26	3.55	0.96	2.80	1.52	2.72	4.24	1.26	2.55	1.50E+00	3.72E-03		-3.90E-01	6.46E-01		-8.81E-01	1.06E-01		-4.19E-02	9.52E-01		-1.75E+00	3.84E-05	Down	-7.30E-01	5.46E-02		Unigene44967_All//gi|42571665|ref|NP_973923.1|//3.00E-14//interferon-related developmental regulator family protein / IFRD protein family [Arabidopsis thaliana]	Unigene44967_All//2.00E-15//AT1G27760| interferon-related developmental regulator family protein / IFRD protein family	Unigene44967_All//6.00E-13//DR458524				nr -
Unigene4497_All	1497	3.11	8.39	7.29	40.66	41.57	27.39	2.29	3.94	0.56	1.43E+00	1.64E-16	Up	1.23E+00	3.94E-11	Up	3.17E-02	7.35E-01		-5.70E-01	2.42E-18		7.83E-01	3.20E-04		-2.03E+00	9.11E-10	Down	Unigene4497_All//gi|297832904|ref|XP_002884334.1|//1.00E-26//NC domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297330174|gb|EFH60593.1| NC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene4497_All//4.00E-27//AT3G02700| NC domain-containing protein	Unigene4497_All//0.00E+00//gi|109878307|gb|DW507278.1|DW507278				nr +
Unigene44971_All	1740	2.80	2.30	1.87	9.02	5.92	9.53	15.38	6.10	31.64	-2.82E-01	3.31E-01		-5.83E-01	4.23E-02		-6.08E-01	2.57E-06		7.90E-02	6.35E-01		-1.33E+00	6.30E-38	Down	1.04E+00	2.27E-53	Up	Unigene44971_All//gi|189163920|gb|ACD77110.1|//1.00E-165//protein kinase 1b [Solanum lycopersicum]	Unigene44971_All//7.00E-151//AT1G07570| APK1A; kinase/ protein serine/threonine kinase	Unigene44971_All//0.00E+00//DW511782		ko04626|Plant-pathogen interaction		nr -

Unigene44972_All	1502	7.56	19.94	9.75	11.44	10.25	12.90	31.87	88.13	140.23	1.40E+00	4.66E-37	Up	3.67E-01	1.79E-02		-1.59E-01	2.97E-01		1.73E-01	2.25E-01		1.47E+00	5.58E-213	Up	2.14E+00	0.00E+00	Up	Unigene44972_All//gi|189163920|gb|ACD77110.1|//1.00E-156//protein kinase 1b [Solanum lycopersicum]	Unigene44972_All//2.00E-147//AT1G07570| APK1A: kinase/ protein serine/threonine kinase	Unigene44972_All//0.00E+00//TC147502		ko04626|Plant-pathogen interaction		nr -
Unigene44976_All	458	5.14	1.11	4.19	5.66	6.54	4.14	10.89	6.48	10.18	-2.22E+00	3.85E-06	Down	-2.97E-01	5.08E-01		2.10E-01	5.98E-01		-4.50E-01	2.83E-01		-7.50E-01	1.71E-03		-9.81E-02	6.91E-01				Unigene44976_All//0.00E+00//gi|164277103|gb|ES809468.1|ES809468				nr -
Unigene44977_All	366	4.00	0.00	2.04	4.63	3.20	0.62	6.70	1.94	2.94	-1.20E+01	1.65E-08	Down	-9.75E-01	9.25E-02		-5.33E-01	3.00E-01		-2.91E+00	2.69E-06	Down	-1.79E+00	5.61E-06	Down	-1.19E+00	8.55E-04	Down	Unigene44977_All//gi|92893678|gb|AES91856.1|//3.00E-12//hypothetical protein MtrDRAFT_AC140551g6v2 [Medicago truncatula]		Unigene44977_All//2.00E-107//C0104733				nr -
Unigene44978_All	1832	19.13	5.53	6.25	28.33	20.96	13.78	30.88	17.04	31.25	-1.79E+00	5.64E-62	Down	-1.61E+00	1.08E-51	Down	-4.35E-01	7.09E-11		-1.04E+00	1.48E-43	Down	-8.58E-01	4.74E-39		1.72E-02	8.14E-01		Unigene44978_All//gi|115441485|ref|NP_001045022.1|//3.00E-84//Os01g0885200 [Oryza sativa Japonica Group] >gi|113534553|dbj|BAF06936.1|Os01g0885200 [Oryza sativa Japonica Group]	Unigene44978_All//3.00E-78//AT1G57680| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031277 (InterPro:IPR016971); Has 35 Blast hits to 35 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene44978_All//0.00E+00//TC173383				nr -
Unigene44979_All	1823	17.05	4.98	6.13	18.91	17.42	11.74	36.18	22.88	33.28	-1.78E+00	1.94E-54	Down	-1.47E+00	3.19E-40	Down	-1.19E-01	2.57E-01		-6.87E-01	1.24E-14		-6.61E-01	3.54E-29		-1.20E-01	4.65E-02		Unigene44979_All//gi|115441485|ref|NP_001045022.1|//3.00E-77//Os01g0885200 [Oryza sativa Japonica Group] >gi|113534553|dbj|BAF06936.1|Os01g0885200 [Oryza sativa Japonica Group]	Unigene44979_All//5.00E-79//AT1G57680| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031277 (InterPro:IPR016971); Has 35 Blast hits to 35 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 33; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene44979_All//0.00E+00//TC145495				nr +
Unigene44980_All	861	1.34	1.29	0.56	2.66	3.40	1.94	7.46	4.51	3.70	-4.63E-02	9.53E-01		-1.26E+00	6.41E-02		3.53E-01	3.84E-01		-4.56E-01	3.09E-01		-7.25E-01	4.49E-04		-1.01E+00	8.78E-07	Down	Unigene44980_All//gi|15219406|ref|NP_178071.1|//1.00E-104//GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana] >gi|4835756|gb|AAD00223.1|AC007202_5 Is a member of the PF|00044 glyceraldehyde 3-phosphate dehydrogenase family, ESTs gb|T43985, gb|N38867, gb|N65037, gb|AA713069 and gb|AI099548 come from this gene [Arabidopsis thaliana]	Unigene44980_All//1.00E-105//AT1G79530| GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene44980_All//0.00E+00//TC150281		ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene44982_All	1276	9.76	4.69	3.00	51.26	33.57	52.03	154.84	53.10	88.76	-1.06E+00	1.58E-10	Down	-1.70E+00	4.92E-20	Down	-6.11E-01	6.64E-25		2.15E-02	7.93E-01		-1.54E+00	0.00E+00	Down	-8.03E-01	2.13E-123		Unigene44982_All//gi|226528826|ref|NP_001149357.1|//1.00E-170//LOC100282981 [Zea mays] >gi|195626622|gb|ACG35141.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Zea mays] >gi|195641440|gb|ACG40188.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Zea mays]	Unigene44982_All//1.00E-162//AT1G16300| GAPCP-2; NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene44982_All//0.00E+00//TC130515		ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene44983_All	1662	2.64	1.16	2.69	5.51	2.86	3.18	5.37	2.39	3.50	-1.19E+00	5.90E-05	Down	2.54E-02	9.48E-01		-9.48E-01	7.13E-08		-7.95E-01	1.89E-05		-1.17E+00	7.51E-11	Down	-6.17E-01	2.20E-04		Unigene44983_All//gi|18072805|emb|CAC80372.1|//1.00E-174//glyceraldehyde-3-phosphate dehydrogenase [Capsicum annuum] >gi|269867729|emb|CAC88118.1| glyceraldehyde-3-phosphate dehydrogenase [Capsicum annuum]	Unigene44983_All//7.00E-144//AT1G16300| GAPCP-2; NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene44983_All//0.00E+00//TC152338		ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene4499_All	759	100.16	40.46	63.98	121.75	123.00	98.00	107.46	90.47	73.85	-1.31E+00	2.02E-84	Down	-6.47E-01	2.03E-25		1.47E-02	8.24E-01		-3.13E-01	1.76E-09		-2.48E-01	1.56E-06		-5.41E-01	4.90E-26		Unigene4499_All//gi|115474123|ref|NP_001060660.1|//1.00E-29//Os07g0682400 [Oryza sativa Japonica Group] >gi|122166929|sp|Q6H3J9.1|CH053_ORYSJ RecName: Full=Zinc finger CCCH domain-containing protein 53; Short=OsC3H53 >gi|113612196|dbj|BAF22574.1|Os07g0682400 [Oryza sativa Japonica Group]	Unigene4499_All//2.00E-119//AT3G51950| zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein	Unigene4499_All//0.00E+00//gi|78326250|gb|DT546524.1|DT546524	C3H			nr -
Unigene44990_All	285	2.20	0.36	1.31	37.75	23.08	13.79	9.05	2.79	0.84	-2.63E+00	1.78E-02		-7.52E-01	4.11E-01		-7.10E-01	9.00E-06		-1.45E+00	1.18E-15	Down	-1.70E+00	7.01E-06	Down	-3.43E+00	9.72E-13	Down	Unigene44990_All//gi|110432095|gb|ABG73621.1|//3.00E-38//leucine-rich repeat receptor-like kinase [Populus tomentosa]	Unigene44990_All//2.00E-23//AT3G25560| NIK2 (NSP-INTERACTING KINASE 2); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene44990_All//5.00E-43//gi|48817142|gb|CO118455.1|CO118455		ko04626|Plant-pathogen interaction		nr +
Unigene44991_All	958	2.73	1.06	2.00	3.02	2.88	2.45	4.19	3.36	1.91	-1.37E+00	7.23E-04	Down	-4.49E-01	2.81E-01		-6.87E-02	8.51E-01		-2.99E-01	4.67E-01		-3.20E-01	2.71E-01		-1.13E+00	2.63E-05	Down	Unigene44991_All//gi|110432095|gb|ABG73621.1|//1.00E-116//leucine-rich repeat receptor-like kinase [Populus tomentosa]	Unigene44991_All//9.00E-82//AT5G16000| NIK1 (NSP-INTERACTING KINASE 1); kinase	Unigene44991_All//1.00E-37//TC141331				nr +
Unigene44992_All	2456	2.34	1.77	2.08	41.68	28.04	17.16	39.41	9.85	6.83	-4.01E-01	1.13E-01		-1.71E-01	5.45E-01		-5.72E-01	1.72E-34		-1.28E+00	2.85E-119	Down	-2.00E+00	2.56E-241	Down	-2.53E+00	0.00E+00	Down	Unigene44992_All//gi|110432095|gb|ABG73621.1|//0.00E+00//leucine-rich repeat receptor-like kinase [Populus tomentosa]	Unigene44992_All//0.00E+00//AT3G25560| NIK2 (NSP-INTERACTING KINASE 2); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene44992_All//0.00E+00//TC141331		ko04626|Plant-pathogen interaction		nr +
Unigene44994_All	977	0.48	2.18	0.33	1.73	1.27	0.79	1.73	2.78	0.69	2.18E+00	1.82E-05	Up	-5.60E-01	6.28E-01		-4.50E-01	3.87E-01		-1.14E+00	2.50E-02		6.84E-01	4.58E-02		-1.32E+00	3.08E-03										
Unigene44996_All	2061	11.47	9.61	10.62	13.90	13.33	9.60	14.40	6.92	9.90	-2.55E-01	2.77E-02		-1.12E-01	3.99E-01		-5.98E-02	6.20E-01		-5.34E-01	4.85E-08		-1.06E+00	2.59E-29	Down	-5.41E-01	4.65E-10		Unigene44996_All//gi|15224120|ref|NP_179409.1|//0.00E+00//ATMPK7 (ARABIDOPSIS THALIANA MAP KINASE 7); MAP kinase/ kinase [Arabidopsis thaliana] >gi|21431797|sp|Q39027.2|MPK7_ARATH RecName: Full=Mitogen-activated protein kinase 7; Short=MAP kinase 7; Short=AtMPK7 >gi|4874286|gb|AAD31349.1| MAP kinase (ATMPK7) [Arabidopsis thaliana] >gi|110739420|dbj|BAF01620.1| MAP kinase [Arabidopsis thaliana]	Unigene44996_All//0.00E+00//AT2G18170| ATMPK7 (ARABIDOPSIS THALIANA MAP KINASE 7); MAP kinase/ kinase	Unigene44996_All//0.00E+00//TC156132		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene45_All	1402	0.26	0.18	0.80	1.39	1.89	1.22	2.20	0.80	2.50	-5.32E-01	6.27E-01		1.61E+00	2.44E-02		4.49E-01	2.82E-01		-1.79E-01	7.02E-01		-1.45E+00	1.20E-05	Down	1.84E-01	5.68E-01		Unigene45_All//gi|186489926|ref|NP_001117459.1|//0.00E+00//TOR (TARGET OF RAPAMYCIN); 1-phosphatidylinositol-3-kinase/ protein binding [Arabidopsis thaliana]	Unigene45_All//0.00E+00//AT1G50030| TOR (TARGET OF RAPAMYCIN); 1-phosphatidylinositol-3-kinase/ protein binding					nr -
Unigene450_All	2630	6.19	2.77	4.84	12.84	10.12	10.42	18.76	7.06	8.07	-1.16E+00	1.71E-15	Down	-3.55E-01	1.54E-02		-3.44E-01	6.99E-05		-3.01E-01	1.09E-03		-1.41E+00	2.25E-75	Down	-1.22E+00	8.06E-62	Down	Unigene450_All//gi|30693010|ref|NP_174675.2|//0.00E+00//STT3B (staurosporin and temperature sensitive 3-like b); oligosaccharyl transferase [Arabidopsis thaliana] >gi|10086464|gb|AAG12524.1|AC015446_5 Putative integral membrane protein [Arabidopsis thaliana]	Unigene450_All//0.00E+00//AT1G34130| STT3B (staurosporin and temperature sensitive 3-like b); oligosaccharyl transferase	Unigene450_All//0.00E+00//TC147182		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis		nr +
Unigene45000_All	1530	29.85	20.67	28.47	50.24	42.18	57.83	39.93	19.48	26.64	-5.31E-01	1.39E-11		-6.85E-02	4.70E-01		-2.52E-01	5.20E-06		2.03E-01	2.31E-04		-1.04E+00	1.90E-57	Down	-5.84E-01	1.59E-22		Unigene45000_All//gi|115315698|gb|ABI93948.1|//0.00E+00//methylputrescine oxidase [Nicotiana tabacum] >gi|134048906|dbj|BAF49519.1| N-methylputrescine oxidase [Nicotiana tabacum]	Unigene45000_All//0.00E+00//AT2G42490| copper amine oxidase, putative	Unigene45000_All//0.00E+00//ES848781		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene45006_All	506	1.14	0.00	1.05	2.36	2.99	1.43	3.59	0.50	1.81	-1.02E+01	1.52E-03		-1.12E-01	9.07E-01		3.42E-01	5.76E-01		-7.26E-01	2.56E-01		-2.86E+00	1.53E-07	Down	-9.89E-01	1.76E-02		Unigene45006_All//gi|68566478|gb|AAN73053.2|//5.00E-87//mini-chromosome maintenance protein MCM3 [Pisum sativum]	Unigene45006_All//2.00E-83//AT5G46280| DNA replication licensing factor, putative	Unigene45006_All//0.00E+00//ES828888		ko03030|DNA replication		nr -
Unigene45007_All	527	1.29	0.00	0.20	0.95	2.61	1.63	1.68	0.32	0.83	-1.03E+01	4.10E-04	Down	-2.67E+00	1.69E-02		1.47E+00	1.25E-02		7.85E-01	3.33E-01		-2.41E+00	1.79E-03		-1.02E+00	1.09E-01		Unigene45007_All//gi|3036819|emb|CAA03887.1|//2.00E-75//MCM3 homolog [Arabidopsis thaliana]	Unigene45007_All//1.00E-76//AT5G46280| DNA replication licensing factor, putative	Unigene45007_All//0.00E+00//ES849916		ko03030|DNA replication		nr -
Unigene45008_All	1098	2.48	0.83	0.19	4.76	2.98	3.50	8.12	1.98	2.21	-1.58E+00	1.00E-04	Down	-3.68E+00	1.28E-10	Down	-6.77E-01	5.89E-03		-4.46E-01	9.90E-02		-2.04E+00	2.03E-23	Down	-1.88E+00	9.05E-22	Down	Unigene45008_All//gi|68566478|gb|AAN73053.2|//1.00E-90//mini-chromosome maintenance protein MCM3 [Pisum sativum]	Unigene45008_All//2.00E-60//AT5G46280| DNA replication licensing factor, putative	Unigene45008_All//0.00E+00//gi|73847613|gb|DT456633.1|DT456633		ko03030|DNA replication		nr +
Unigene45009_All	3306	5.06	1.81	1.53	8.33	6.54	3.84	16.75	1.90	3.95	-1.49E+00	4.66E-23	Down	-1.73E+00	2.30E-27	Down	-3.49E-01	3.26E-04		-1.12E+00	3.12E-26	Down	-3.14E+00	1.48E-232	Down	-2.08E+00	2.60E-150	Down	Unigene45009_All//gi|68566478|gb|AAN73053.2|//0.00E+00//mini-chromosome maintenance protein MCM3 [Pisum sativum]	Unigene45009_All//0.00E+00//AT5G46280| DNA replication licensing factor, putative	Unigene45009_All//0.00E+00//gi|164359039|gb|ES828888.1|ES828888		ko03030|DNA replication		nr +
Unigene45010_All	340	0.62	3.13	1.88	0.88	1.32	1.46	2.24	0.49	0.23	2.35E+00	2.58E-03		1.61E+00	1.11E-01		5.83E-01	6.26E-01		7.33E-01	5.16E-01		-2.19E+00	7.77E-03		-3.26E+00	4.48E-04	Down	Unigene45010_All//gi|211906436|gb|ACJ11711.1|//2.00E-07//UDP-D-glucose pyrophosphorylase [Gossypium hirsutum]		Unigene45010_All//6.00E-148//gi|13248697|gb|BF276869.2|BF276869				nr -
Unigene45011_All	1749	0.36	1.16	0.64	10.22	11.56	11.10	9.60	1.29	2.44	1.69E+00	5.40E-04	Up	8.33E-01	2.23E-01		1.77E-01	1.91E-01		1.19E-01	4.32E-01		-2.89E+00	2.97E-65	Down	-1.98E+00	4.26E-43	Down	Unigene45011_All//gi|211906434|gb|ACJ11710.1|//0.00E+00//UDP-D-glucose pyrophosphorylase [Gossypium hirsutum]	Unigene45011_All//0.00E+00//AT3G03250| UGP (UDP-glucose pyrophosphorylase); UTP:glucose-1-phosphate uridylyltransferase/ nucleotidyltransferase	Unigene45011_All//0.00E+00//TC149915		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00040|Pentose and glucuronate interconversions//ko00052|Galactose metabolism		nr -

Unigene45012_All	1778	78.10	35.48	55.59	108.31	91.76	93.76	119.30	49.60	45.80	-1.14E+00	1.57E-123	Down	-4.91E-01	3.59E-28		-2.39E-01	6.57E-13		-2.08E-01	4.29E-09		-1.27E+00	1.12E-272	Down	-1.38E+00	0.00E+00	Down	Unigene45014_All//gi|211906436|gb|ACJ11711.1|//0.00E+00//UDP-D-glucose pyrophosphorylase [Gossypium hirsutum]	Unigene45012_All//0.00E+00//AT5G17310| UTP--glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, putative	Unigene45012_All//0.00E+00//TC151444		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00040|Pentose and glucuronate interconversions//ko00052|Galactose metabolism		nr -
Unigene45014_All	5222	3.78	8.81	5.63	5.24	4.58	5.66	11.12	13.15	8.83	1.22E+00	5.09E-46	Up	5.76E-01	1.96E-08		-1.93E-01	7.55E-02		1.11E-01	3.57E-01		2.41E-01	2.21E-05		-3.34E-01	3.14E-08		Unigene45014_All//gi|225445069|ref|XP_002280317.1|//0.00E+00//PREDICTED: similar to protein kinase family protein / WD-40 repeat family protein [Vitis vinifera]	Unigene45014_All//0.00E+00//AT4G29380| protein kinase family protein / WD-40 repeat family protein	Unigene45014_All//0.00E+00//TC143006		ko04140|Regulation of autophagy		nr +
Unigene45015_All	1346	6.88	6.81	4.71	20.06	9.77	11.01	9.08	5.50	3.29	-1.40E-02	9.64E-01		-5.47E-01	5.48E-03		-1.04E+00	8.28E-26	Down	-8.66E-01	5.14E-17		-7.24E-01	5.50E-07		-1.47E+00	5.27E-21	Down			Unigene45015_All//4.00E-155//C0118675					
Unigene45016_All	3020	8.25	2.72	5.34	6.37	6.09	6.18	3.78	1.99	2.49	-1.60E+00	7.86E-38	Down	-6.26E-01	2.60E-08		-6.44E-02	6.79E-01		-4.39E-02	7.64E-01		-9.24E-01	1.45E-09		-6.00E-01	3.79E-05		Unigene45016_All//gi|30698050|ref|NP_201263.2|//0.00E+00//AAA-type ATPase family protein [Arabidopsis thaliana]	Unigene45016_All//0.00E+00//AT5G64580| AAA-type ATPase family protein	Unigene45016_All//0.00E+00//C0118676				nr +
Unigene45018_All	2108	8.34	2.33	3.76	16.40	10.42	10.50	18.77	3.59	3.33	-1.84E+00	1.53E-32	Down	-1.15E+00	9.04E-16	Down	-6.54E-01	4.66E-15		-6.44E-01	3.95E-13		-2.39E+00	1.57E-123	Down	-2.50E+00	2.95E-134	Down	Unigene45018_All//gi|283488499|gb|ADB24771.1|//0.00E+00//UDP-D-glucuronic acid 4-epimerase [Gossypium hirsutum]	Unigene45018_All//0.00E+00//AT4G00110| GAE3 (UDP-D-GLUCURONATE 4-EPIMERASE 3); UDP-glucuronate 4-epimerase/ catalytic	Unigene45018_All//0.00E+00//TC174703		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene4502_All	560	135.85	120.97	141.02	125.60	139.28	152.02	105.70	52.39	41.33	-1.67E-01	7.18E-03		5.39E-02	4.49E-01		1.49E-01	1.29E-02		2.75E-01	5.16E-07		-1.01E+00	1.12E-53	Down	-1.35E+00	2.32E-87	Down	Unigene4502_All//gi|22296820|gb|AAM94349.1|//2.00E-95//pyruvate kinase [Glycine max]	Unigene4502_All//4.00E-94//AT5G08570| pyruvate kinase, putative	Unigene4502_All//0.00E+00//gi|164243944|gb|ES809658.1|ES809658		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene45020_All	1798	14.75	16.12	12.50	20.67	25.20	20.22	29.72	24.83	60.89	1.28E-01	2.50E-01		-2.39E-01	3.73E-02		2.86E-01	1.34E-04		-3.16E-02	7.63E-01		-2.60E-01	6.56E-05		1.03E+00	2.81E-104	Up	Unigene45020_All//gi|15528441|emb|CAC69138.1|//1.00E-156//MAP kinase kinase [Medicago sativa subsp. x varia]	Unigene45020_All//6.00E-134//AT4G26810| ATMKK2 (ARABIDOPSIS THALIANA MAP KINASE KINASE 2); MAP kinase kinase/ kinase	Unigene45020_All//0.00E+00//TC141809		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene45025_All	3125	8.04	10.77	10.10	10.01	10.59	11.16	18.27	16.10	8.75	4.22E-01	5.10E-06		3.30E-01	9.98E-04		8.11E-02	4.94E-01		1.56E-01	1.23E-01		-1.82E-01	5.03E-03		-1.06E+00	1.39E-57	Down	Unigene45025_All//gi|224106165|ref|XP_002314067.1|//0.00E+00//xanthine dehydrogenase [Populus trichocarpa] >gi|222850475|gb|EEE88022.1| xanthine dehydrogenase [Populus trichocarpa]	Unigene45025_All//0.00E+00//AT4G34890| XDH1 (XANTHINE DEHYDROGENASE 1); xanthine dehydrogenase	Unigene45025_All//0.00E+00//gi|164274771|gb|ES801161.1|ES801161		ko00230|Purine metabolism//ko04146|Peroxisome//ko00232|Caffeine metabolism		nr -
Unigene45026_All	4511	0.71	1.20	1.72	1.39	1.83	1.68	2.57	1.71	1.58	7.65E-01	2.88E-03		1.28E+00	1.21E-08	Up	3.97E-01	5.05E-02		2.74E-01	2.38E-01		-5.83E-01	8.25E-05		-7.00E-01	1.46E-06		Unigene45026_All//gi|224106165|ref|XP_002314067.1|//0.00E+00//xanthine dehydrogenase [Populus trichocarpa] >gi|222850475|gb|EEE88022.1| xanthine dehydrogenase [Populus trichocarpa]	Unigene45026_All//0.00E+00//AT4G34890| XDH1 (XANTHINE DEHYDROGENASE 1); xanthine dehydrogenase	Unigene45026_All//0.00E+00//gi|164274771|gb|ES801161.1|ES801161		ko00230|Purine metabolism//ko04146|Peroxisome//ko00232|Caffeine metabolism		nr +
Unigene45027_All	3684	246.19	577.03	380.02	95.33	85.27	72.32	19.59	25.12	13.71	1.23E+00	0.00E+00	Up	6.26E-01	0.00E+00		-1.61E-01	5.31E-11		-3.99E-01	8.95E-54		3.59E-01	7.99E-14		-5.15E-01	3.22E-21		Unigene45027_All//gi|297837989|ref|XP_002886876.1|//0.00E+00//H+-transporting two-sector ATPase, alpha/beta subunit, central region [Arabidopsis lyrata subsp. lyrata] >gi|297332717|gb|EFH63135.1| H+-transporting two-sector ATPase, alpha/beta subunit, central region [Arabidopsis lyrata subsp. lyrata]	Unigene45027_All//0.00E+00//ATCG00480| chloroplast-encoded gene for beta subunit of ATP synthase	Unigene45027_All//0.00E+00//TC176987		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr +
Unigene4503_All	981	0.80	2.22	2.50	4.42	4.70	5.20	3.97	4.52	2.44	1.47E+00	1.25E-03		1.64E+00	2.69E-04	Up	9.05E-02	8.18E-01		2.36E-01	4.38E-01		1.88E-01	5.28E-01		-7.03E-01	8.31E-03		Unigene4503_All//gi|30690020|ref|NP_850436.1|//2.00E-89//LBD18 (LOB DOMAIN-CONTAINING PROTEIN 18) [Arabidopsis thaliana] >gi|27885494|sp|Q22131.2|LBD18_ARATH RecName: Full=LOB domain-containing protein 18; AltName: Full=ASYMMETRIC LEAVES 2-like protein 20; Short=AS2-like protein 20 >gi|17227164|gb|AAL38036.1|AF447891_1 LOB DOMAIN 18 [Arabidopsis thaliana] >gi|20196916|gb|AAB82622.2| expressed protein [Arabidopsis thaliana] >gi|106879179|gb|ABF82619.1| At2g45420 [Arabidopsis thaliana] >gi|219907116|dbj|BAH10564.1| ASYMMETRIC LEAVES2-like 20 protein [Arabidopsis thaliana]	Unigene4503_All//1.00E-68//AT2G45420| LBD18 (LOB DOMAIN-CONTAINING PROTEIN 18)			ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene45030_All	1978	4.68	7.61	5.49	7.86	7.31	6.69	4.04	8.33	5.38	7.00E-01	1.26E-06		2.30E-01	2.40E-01		-1.04E-01	5.66E-01		-2.32E-01	1.33E-01		1.04E+00	3.11E-16	Up	4.13E-01	7.02E-03		Unigene45030_All//gi|15240256|ref|NP_200953.1|//1.00E-152//2-phosphoglycerate kinase-related [Arabidopsis thaliana]	Unigene45030_All//6.00E-154//AT5G61450| 2-phosphoglycerate kinase-related	Unigene45030_All//0.00E+00//ES849408				nr +
Unigene45032_All	775	5.47	6.60	5.08	7.20	4.62	6.18	6.87	4.91	3.39	2.72E-01	3.36E-01		-1.05E-01	7.31E-01		-6.40E-01	7.14E-03		-2.21E-01	4.45E-01		-4.86E-01	3.79E-02		-1.02E+00	7.90E-06	Down	Unigene45032_All//gi|58618123|gb|AR88628.1|//4.00E-76//phosphoinositide 3-kinase [Nicotiana tabacum]	Unigene45032_All//1.00E-75//AT1G60490| ATVPS34; 1-phosphatidylinositol-3-kinase/ binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor	Unigene45032_All//0.00E+00//TC151619		ko04145|Phagosome//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko04140|Regulation of autophagy		nr +
Unigene45036_All	686	1.53	2.36	1.71	1.89	1.76	2.50	3.14	0.67	2.03	6.32E-01	2.23E-01		1.63E-01	7.82E-01		-1.04E-01	8.43E-01		4.06E-01	4.62E-01		-2.23E+00	7.33E-07	Down	-6.29E-01	9.53E-02		Unigene45036_All//gi|18766642|gb|AAL79042.1|AF469649_1//1.00E-101//NIMA-related protein kinase [Populus tremula x Populus alba]	Unigene45036_All//8.00E-83//AT1G54510| ATNEK1 (ARABIDOPSIS THALIANA NIMA-RELATED SERINE/THREONINE KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene45036_All//0.00E+00//TC130121				nr -
Unigene45037_All	2381	2.64	1.83	1.10	7.18	6.80	7.66	10.49	1.88	5.72	-5.27E-01	2.55E-02		-1.27E+00	5.95E-07	Down	-7.82E-02	6.16E-01		9.47E-02	5.65E-01		-2.48E+00	7.23E-82	Down	-8.75E-01	7.48E-19		Unigene45037_All//gi|18766642|gb|AAL79042.1|AF469649_1//0.00E+00//NIMA-related protein kinase [Populus tremula x Populus alba]	Unigene45037_All//0.00E+00//AT1G54510| ATNEK1 (ARABIDOPSIS THALIANA NIMA-RELATED SERINE/THREONINE KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene45037_All//0.00E+00//TC166864				nr +
Unigene45038_All	2170	6.37	5.60	5.89	3.54	5.93	3.58	2.55	0.48	1.51	-1.84E-01	2.60E-01		-1.12E-01	5.32E-01		7.47E-01	4.02E-07		1.81E-02	9.46E-01		-2.41E+00	4.90E-18	Down	-7.62E-01	4.97E-04		Unigene45038_All//gi|18766642|gb|AAL79042.1|AF469649_1//0.00E+00//NIMA-related protein kinase [Populus tremula x Populus alba]	Unigene45038_All//1.00E-178//AT1G54510| ATNEK1 (ARABIDOPSIS THALIANA NIMA-RELATED SERINE/THREONINE KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene45038_All//0.00E+00//TC130121				nr -
Unigene4504_All	746	11.22	10.53	7.07	21.77	24.19	20.40	12.36	2.35	7.10	-9.21E-02	6.57E-01		-6.67E-01	1.32E-03		1.52E-01	3.18E-01		-9.35E-02	6.00E-01		-2.39E+00	2.34E-29	Down	-7.99E-01	1.45E-06		Unigene4504_All//gi|15241525|ref|NP_199269.1|//3.00E-96//VPS2.2 [Arabidopsis thaliana] >gi|226698193|sp|Q9RTY4.2|VPS2B_ARATH RecName: Full=Vacuolar protein sorting-associated protein 2 homolog 2; Short=AtVPS2-2; AltName: Full=Charged multivesicular body protein 2 homolog 2; AltName: Full=ESCRT-III complex subunit VPS2 homolog 2	Unigene4504_All//5.00E-86//AT5G44560| VPS2.2	Unigene4504_All//0.00E+00//gi|84163918|gb|DR452566.1|DR452566		ko04144|Endocytosis		nr -
Unigene45040_All	2149	2.00	1.63	1.34	12.52	10.22	5.15	7.48	4.36	4.23	-2.95E-01	3.41E-01		-5.77E-01	6.09E-02		-2.92E-01	3.86E-03		-1.28E+00	1.04E-31	Down	-7.79E-01	4.93E-10		-8.23E-01	2.70E-11		Unigene45040_All//gi|15238082|ref|NP_198961.1|//0.00E+00//fringe-related protein [Arabidopsis thaliana] >gi|53828537|gb|AAU94378.1| At5g41460 [Arabidopsis thaliana] >gi|57444904|gb|AAW50706.1| At5g41460 [Arabidopsis thaliana]	Unigene45040_All//0.00E+00//AT5G41460| fringe-related protein	Unigene45040_All//0.00E+00//TC173388				nr -
Unigene45041_All	1997	15.04	10.20	10.05	14.87	19.80	16.94	4.72	1.59	2.57	-5.60E-01	1.27E-08		-5.81E-01	9.95E-09		4.13E-01	1.53E-07		1.88E-01	5.80E-02		-1.57E+00	1.78E-17	Down	-8.76E-01	1.11E-07		Unigene45041_All//gi|15238082|ref|NP_198961.1|//0.00E+00//fringe-related protein [Arabidopsis thaliana] >gi|53828537|gb|AAU94378.1| At5g41460 [Arabidopsis thaliana] >gi|57444904|gb|AAW50706.1| At5g41460 [Arabidopsis thaliana]	Unigene45041_All//0.00E+00//AT5G41460| fringe-related protein	Unigene45041_All//0.00E+00//TC162393				nr -
Unigene45045_All	1791	8.15	9.08	4.43	13.71	22.76	9.48	5.29	11.81	7.30	1.56E-01	3.10E-01		-8.80E-01	9.52E-09		7.31E-01	8.76E-21		-5.32E-01	5.94E-07		1.16E+00	2.72E-24	Up	4.64E-01	6.18E-04		Unigene45045_All//gi|224092067|ref|XP_002309461.1|//1.00E-110//leucine-rich repeat protein kinase [Populus trichocarpa] >gi|222855437|gb|EEE92984.1| leucine-rich repeat protein kinase [Populus trichocarpa]	Unigene45045_All//2.00E-99//AT2G26330| ER (ERECTA); transmembrane receptor protein kinase	Unigene45045_All//0.00E+00//gi|164366012|gb|ES828435.1|ES828435		ko04626|Plant-pathogen interaction		nr -
Unigene45046_All	3338	6.27	3.11	5.15	9.79	18.49	6.59	0.05	0.20	0.67	-1.01E+00	5.71E-16	Down	-2.83E-01	2.83E-02		9.17E-01	7.54E-46		-5.71E-01	3.60E-10		1.98E+00	2.25E-02		3.72E+00	1.41E-11	Up	Unigene45046_All//gi|15225286|ref|NP_180201.1|//0.00E+00//ER (ERECTA); transmembrane receptor protein kinase [Arabidopsis thaliana] >gi|75319658|sp|Q42371.1|ERECT_ARATH RecName: Full=LRR receptor-like serine/threonine-protein kinase ERECTA; AltName: Full=Protein QUANTITATIVE RESISTANCE TO PLECTOSPHAERELLA 1; AltName: Full=Protein QUANTITATIVE RESISTANCE TO RALSTONIA SOLANACEARUM 1; AltName: Full=Protein TRANSPIRATION EFFICIENCY 1; Flags: Precursor >gi|1345132|gb|AAC49302.1| ERECTA [Arabidopsis thaliana] >gi|1389566|dbj|BAA11869.1| receptor protein kinase [Arabidopsis thaliana] >gi|224589525|gb|ACN59296.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene45046_All//0.00E+00//AT2G26330| ER (ERECTA); transmembrane receptor protein kinase	Unigene45046_All//0.00E+00//TC149534				nr +
Unigene45047_All	3379	3.65	3.91	3.55	127.45	119.54	94.12	27.25	13.92	12.21	9.90E-02	5.85E-01		-4.35E-02	8.07E-01		-9.24E-02	6.99E-05		-4.37E-01	3.98E-78		-9.70E-01	2.20E-77		-1.16E+00	4.89E-106	Down	Unigene45047_All//gi|1706958|gb|AAB37767.1|//0.00E+00//cellulose synthase [Gossypium hirsutum]	Unigene45047_All//0.00E+00//AT5G05170| CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene45047_All//0.00E+00//TC129590				nr -

Unigene45048_All	783	2.14	6.92	3.06	6.43	8.22	7.90	5.89	6.83	10.48	1.70E+00	2.00E-09	Up	5.17E-01	2.32E-01		3.56E-01	1.44E-01		2.98E-01	2.52E-01		2.15E-01	4.03E-01		8.33E-01	2.82E-06		Unigene45048_All//gi|5734788|gb|AAD50053.1|AC007980.18//2.00E-82//Similar to RNA-binding proteins [Arabidopsis thaliana]	Unigene45048_All//2.00E-60//AT1G50300| TAF15 (TBP-associated factor 15); RNA binding / nucleic acid binding / nucleotide binding / zinc ion binding	Unigene45048_All//0.00E+00//gi|73860850|gb|DT463589.1|DT463589				nr +
Unigene4505_All	960	4.36	6.28	2.50	7.68	7.93	8.56	7.40	2.09	2.49	5.27E-01	2.97E-02		-8.05E-01	9.50E-03		4.58E-02	8.57E-01		1.57E-01	5.11E-01		-1.82E+00	2.52E-16	Down	-1.57E+00	7.94E-14	Down	Unigene4505_All//gi|15241525|ref|NP_199269.1|//8.00E-99//VPS2.2 [Arabidopsis thaliana] >gi|226698193|sp|Q0WTY4.2|VPS2B_ARATH RecName: Full=Vacuolar protein sorting-associated protein 2 homolog 2; Short=AtVPS2-2; AltName: Full=Charged multivesicular body protein 2 homolog 2; AltName: Full=ESCRT-III complex subunit VPS2 homolog 2	Unigene4505_All//1.00E-88//AT5G41560| VPS2.2	Unigene4505_All//0.00E+00//gi|84163918|gb|DR452566.1|DR452566		ko04144|Endocytosis		nr -
Unigene45051_All	1053	1.14	1.49	1.21	4.92	6.18	4.76	9.24	23.50	29.13	3.84E-01	4.66E-01		8.68E-02	8.84E-01		3.29E-01	1.77E-01		-4.74E-02	8.81E-01		1.35E+00	1.37E-35	Up	1.66E+00	1.07E-60	Up	Unigene45051_All//gi|18414504|ref|NP_568136.1|//2.00E-85//OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|186520008|ref|NP_001119168.1| OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|90093272|gb|ABD85149.1| At5g04250 [Arabidopsis thaliana]	Unigene45051_All//6.00E-82//AT5G04250| OTU-like cysteine protease family protein	Unigene45051_All//1.00E-148//ES791705				nr +
Unigene45052_All	1351	1.32	3.75	2.96	1.18	1.99	2.27	2.47	3.16	5.46	1.51E+00	1.27E-07	Up	1.17E+00	3.21E-04	Up	7.53E-01	4.91E-02		9.46E-01	8.12E-03		3.52E-01	2.08E-01		1.14E+00	4.85E-09	Up	Unigene45052_All//gi|18414504|ref|NP_568136.1|//1.00E-107//OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|186520008|ref|NP_001119168.1| OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|90093272|gb|ABD85149.1| At5g04250 [Arabidopsis thaliana]	Unigene45052_All//5.00E-101//AT5G04250| OTU-like cysteine protease family protein	Unigene45052_All//0.00E+00//CO127834				nr +
Unigene45057_All	3425	5.80	3.86	2.77	17.32	13.23	23.02	40.32	28.56	43.36	-5.88E-01	1.83E-06		-1.07E+00	6.81E-16	Down	-3.89E-01	4.10E-10		4.11E-01	3.97E-13		-4.98E-01	2.01E-36		1.05E-01	6.67E-03		Unigene45057_All//gi|21929220|dbj|BAC06184.1|//0.00E+00//110 kDa 4SNc-Tudor domain protein [Pisum sativum]	Unigene45057_All//0.00E+00//AT5G07350| tudor domain-containing protein / nuclease family protein	Unigene45057_All//0.00E+00//TC165348				nr +
Unigene4506_All	643	22.21	26.87	38.01	39.20	11.73	9.41	5.39	6.11	43.93	2.75E-01	4.67E-02		7.75E-01	1.38E-11		-1.74E+00	1.25E-53	Down	-2.06E+00	1.89E-58	Down	1.80E-01	5.76E-01		3.03E+00	4.06E-116	Up	Unigene4506_All//gi|224137758|ref|XP_002322644.1|//2.00E-06//predicted protein [Populus trichocarpa] >gi|222867274|gb|EEF04405.1| predicted protein [Populus trichocarpa]		Unigene4506_All//0.00E+00//TC159688				nr +
Unigene45061_All	849	0.49	2.15	0.75	3.87	5.52	3.51	1.79	2.95	1.97	2.12E+00	1.13E-04	Up	6.10E-01	5.09E-01		5.10E-01	6.97E-02		-1.41E-01	6.89E-01		7.20E-01	4.44E-02		1.37E-01	7.54E-01		Unigene45061_All//gi|224086052|ref|XP_002307796.1|//6.00E-13//bromodomain protein [Populus trichocarpa] >gi|222857245|gb|EEE94792.1| bromodomain protein [Populus trichocarpa]		Unigene45061_All//0.00E+00//gi|109878861|gb|DW507831.1|DW507831				nr +
Unigene45065_All	3753	23.55	19.85	26.28	4.17	4.80	4.12	6.48	3.71	1.86	-2.47E-01	8.59E-06		1.58E-01	4.84E-03		2.03E-01	1.51E-01		-1.82E-02	9.30E-01		-8.05E-01	1.48E-15		-1.80E+00	8.39E-55	Down	Unigene45065_All//gi|30679171|ref|NP_567242.2|//0.00E+00//TOC159 (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 159); transmembrane receptor [Arabidopsis thaliana] >gi|75100143|sp|Q81283.1|TC159_ARATH RecName: Full=Translocase of chloroplast 159, chloroplastic; Short=AtToc159; AltName: Full=Translocase of chloroplast 160, chloroplastic; Short=AtToc160; AltName: Full=Translocase of chloroplast 86, chloroplastic; Short=AtToc86; AltName: Full=159 kDa chloroplast outer envelope protein; AltName: Full=Plastid protein import 2 >gi|3193301|gb|AAC19285.1| T14P8.24 [Arabidopsis thaliana]	Unigene45065_All//0.00E+00//AT4G02510| TOC159 (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 159); transmembrane receptor	Unigene45065_All//0.00E+00//TC147323		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene45066_All	1988	1.71	1.99	0.70	3.98	3.81	2.45	4.59	1.24	4.63	2.17E-01	5.05E-01		-1.30E+00	3.23E-04	Down	-6.42E-02	8.18E-01		-6.99E-01	5.44E-04		-1.89E+00	9.53E-22	Down	1.10E-02	9.68E-01		Unigene45066_All//gi|5305100|emb|CAB46083.1|//1.00E-138//cyclin A2 [Medicago sativa subsp. x varia]	Unigene45066_All//2.00E-117//AT1G80370| CYCA2;4 (Cyclin A2;4); cyclin-dependent protein kinase regulator	Unigene45066_All//0.00E+00//TC135970				nr -
Unigene45067_All	1793	4.14	2.23	1.10	3.08	4.09	2.24	9.31	1.19	2.89	-8.92E-01	3.48E-05		-1.91E+00	3.10E-14	Down	4.08E-01	6.16E-02		-4.60E-01	7.63E-02		-2.97E+00	1.22E-66	Down	-1.69E+00	1.07E-34	Down	Unigene45067_All//gi|297842829|ref|XP_002889296.1|//1.00E-146//CYCA2_4 [Arabidopsis lyrata subsp. lyrata] >gi|297335137|gb|EFH65555.1| CYCA2_4 [Arabidopsis lyrata subsp. lyrata]	Unigene45067_All//2.00E-132//AT1G80370| CYCA2;4 (Cyclin A2;4); cyclin-dependent protein kinase regulator	Unigene45067_All//0.00E+00//gi|78342879|gb|DT563153.1|DT563153				nr +
Unigene45068_All	640	2.62	5.86	7.82	2.49	5.92	6.07	5.29	5.49	7.72	1.16E+00	3.35E-04	Up	1.58E+00	1.15E-07	Up	1.25E+00	5.34E-05	Up	1.28E+00	4.81E-05	Up	5.38E-02	8.72E-01		5.47E-01	1.98E-02		Unigene45068_All//gi|115450285|ref|NP_001048743.1|//5.00E-65//Os03g0114300 [Oryza sativa Japonica Group] >gi|113547214|dbj|BAF10657.1| Os03g0114300 [Oryza sativa Japonica Group]	Unigene45068_All//1.00E-64//AT4G10730| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene45068_All//0.00E+00//DT054210		ko04626|Plant-pathogen interaction		nr +
Unigene45076_All	498	14.18	14.45	16.57	17.51	21.64	13.88	11.55	16.95	24.80	2.67E-02	9.21E-01		2.25E-01	3.26E-01		3.06E-01	8.76E-02		-3.35E-01	1.04E-01		5.54E-01	1.80E-03		1.10E+00	8.08E-14	Up	Unigene45076_All//gi|51490665|emb|CAG26903.1|//3.00E-44//ALY protein [Nicotiana benthamiana]	Unigene45076_All//6.00E-30//AT5G59950| RNA and export factor-binding protein, putative	Unigene45076_All//5.00E-103//gi|78340221|gb|DT560495.1|DT560495		ko03040|Spliceosome		nr -
Unigene45078_All	1804	4.90	2.25	3.22	9.22	7.50	8.26	6.47	3.41	3.03	-1.13E+00	2.00E-08	Down	-6.07E-01	2.60E-03		-2.98E-01	2.76E-02		-1.59E-01	3.16E-01		-9.26E-01	8.64E-10		-1.10E+00	4.33E-13	Down	Unigene45078_All//gi|115489492|ref|NP_001067233.1|//0.00E+00//Os12g0607100 [Oryza sativa Japonica Group] >gi|113649740|dbj|BAF30252.1| Os12g0607100 [Oryza sativa Japonica Group]	Unigene45078_All//0.00E+00//AT1G04170| EIF2 GAMMA; translation factor, nucleic acid binding / translation initiation factor	Unigene45078_All//0.00E+00//TC177403				nr +
Unigene45080_All	590	2.75	5.84	1.90	6.42	11.15	33.30	24.51	64.25	48.82	1.09E+00	1.30E-03		-5.37E-01	3.31E-01		7.97E-01	2.67E-04		2.38E+00	3.03E-53	Up	1.39E+00	9.77E-57	Up	9.94E-01	2.33E-26		Unigene45080_All//gi|68271836|gb|AY89231.1|//1.00E-97//hexose transporter 1 [Juglans regia]	Unigene45080_All//7.00E-71//AT1G11260| STP1 (SUGAR TRANSPORTER 1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene45080_All//0.00E+00//gi|73866250|gb|DT468988.1|DT468988				nr +
Unigene45081_All	1736	0.27	0.93	0.15	6.31	3.87	2.50	5.02	1.93	1.01	1.78E+00	1.52E-03		-8.22E-01	4.57E-01		-7.07E-01	7.99E-06		-1.34E+00	4.07E-14	Down	-1.38E+00	1.55E-13	Down	-2.31E+00	1.36E-27	Down	Unigene45081_All//gi|215271818|emb|CAN87006.1|//0.00E+00//hexose transporter 1 [Hevea brasiliensis]	Unigene45081_All//0.00E+00//AT1G11260| STP1 (SUGAR TRANSPORTER 1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene45081_All//0.00E+00//TC139797				nr -
Unigene45082_All	1767	15.72	33.87	20.01	33.52	58.83	99.37	121.41	299.31	241.02	1.11E+00	4.64E-51	Up	3.48E-01	2.08E-04		8.12E-01	7.96E-63		1.57E+00	3.58E-273	Up	1.30E+00	0.00E+00	Up	9.89E-01	0.00E+00		Unigene45082_All//gi|57283538|emb|CAG27609.1|//0.00E+00//monosaccharide transporter [Populus tremula x Populus tremuloides]	Unigene45082_All//0.00E+00//AT1G11260| STP1 (SUGAR TRANSPORTER 1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene45082_All//0.00E+00//TC139797				nr -
Unigene45083_All	1813	13.33	11.88	6.46	12.12	11.98	12.23	15.32	14.82	13.54	-1.67E-01	1.64E-01		-1.05E+00	1.59E-18	Down	-1.58E-02	9.10E-01		1.35E-02	9.40E-01		-4.77E-02	6.63E-01		-1.79E-01	5.96E-02		Unigene45083_All//gi|28950997|gb|AA063422.1|//1.00E-151//At1g03457 [Arabidopsis thaliana]	Unigene45083_All//8.00E-135//AT1G03457| RNA-binding protein, putative	Unigene45083_All//0.00E+00//TC134227				nr -
Unigene45086_All	935	3.41	9.59	5.13	4.85	5.38	8.11	18.59	21.28	25.82	1.49E+00	1.10E-12	Up	5.87E-01	4.26E-02		1.49E-01	6.22E-01		7.43E-01	3.68E-04		1.95E-01	1.03E-01		4.74E-01	9.77E-07		Unigene45086_All//gi|224144877|ref|XP_002325447.1|//2.00E-69//f-box family protein [Populus trichocarpa] >gi|222862322|gb|EEE99828.1| f-box family protein [Populus trichocarpa]	Unigene45086_All//3.00E-41//AT5G60570| kelch repeat-containing F-box family protein	Unigene45086_All//0.00E+00//TC161678				nr -
Unigene45088_All	1871	6.91	6.36	5.78	9.85	8.72	7.19	12.00	8.56	5.71	-1.18E-01	5.02E-01		-2.58E-01	1.41E-01		-1.75E-01	2.17E-01		-4.54E-01	3.31E-04		-4.88E-01	2.06E-06		-1.07E+00	1.56E-23	Down	Unigene45088_All//gi|224144877|ref|XP_002325447.1|//0.00E+00//f-box family protein [Populus trichocarpa] >gi|222862322|gb|EEE99828.1| f-box family protein [Populus trichocarpa]	Unigene45088_All//3.00E-119//AT5G60570| kelch repeat-containing F-box family protein	Unigene45088_All//0.00E+00//TC146420				nr +
Unigene45090_All	4852	0.88	1.78	1.50	1.70	1.75	2.00	1.81	1.40	1.82	1.01E+00	5.81E-07	Up	7.66E-01	6.47E-04		4.06E-02	8.67E-01		2.32E-01	2.61E-01		-3.77E-01	3.41E-02		8.20E-03	9.76E-01		Unigene45090_All//gi|42564075|ref|NP_187802.2|//0.00E+00//cleavage and polyadenylation specificity factor (CPSF) A subunit C-terminal domain-containing protein [Arabidopsis thaliana]	Unigene45090_All//0.00E+00//AT3G11960| cleavage and polyadenylation specificity factor (CPSF) A subunit C-terminal domain-containing protein	Unigene45090_All//0.00E+00//TC168960		ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair		nr +
Unigene45091_All	1530	1.95	0.99	1.01	15.69	10.20	6.61	6.25	1.15	1.22	-9.72E-01	7.36E-03		-9.50E-01	1.25E-02		-6.22E-01	9.65E-10		-1.25E+00	3.46E-27	Down	-2.44E+00	3.59E-31	Down	-2.35E+00	8.73E-31	Down	Unigene45091_All//gi|30692267|ref|NP_190059.3|//0.00E+00//kinesin motor protein-related [Arabidopsis thaliana]	Unigene45091_All//0.00E+00//AT3G44730| kinesin motor protein-related	Unigene45091_All//2.00E-151//CO086398				nr -
Unigene45092_All	3659	1.13	1.00	1.24	18.04	10.43	6.13	6.91	1.17	0.89	-1.80E-01	5.82E-01		1.31E-01	6.57E-01		-7.91E-01	1.51E-39		-1.56E+00	1.95E-103	Down	-2.57E+00	4.11E-86	Down	-2.95E+00	3.20E-103	Down	Unigene45092_All//gi|30692267|ref|NP_190059.3|//0.00E+00//kinesin motor protein-related [Arabidopsis thaliana]	Unigene45092_All//0.00E+00//AT3G44730| kinesin motor protein-related	Unigene45092_All//0.00E+00//TC146112				nr +
Unigene45096_All	4520	2.04	8.87	6.07	15.55	19.42	42.29	19.16	20.46	31.60	2.12E+00	5.52E-88	Up	1.57E+00	3.26E-39	Up	3.21E-01	3.12E-10		1.44E+00	3.67E-263	Up	9.52E-02	7.67E-02		7.22E-01	3.83E-74		Unigene45096_All//gi|57012985|sp|Q8LPT9.1|GWD1_CITRE//0.00E+00//RecName: Full=Alpha-glucan water dikinase, chloroplastic; AltName: Full=Starch-related protein R1; Flags: Precursor >gi|20384925|gb|AAM18228.1| R1 [Citrus reticulata]	Unigene45096_All//0.00E+00//AT1G10760| SEX1 (STARCH EXCESS 1); alpha-glucan, water dikinase	Unigene45096_All//0.00E+00//TC147028				nr +
Unigene45097_All	612	3.59	13.58	5.66	15.71	9.51	20.37	20.79	21.92	31.83	1.92E+00	1.58E-16	Up	6.56E-01	5.89E-02		-7.24E-01	2.19E-05		3.75E-01	2.19E-02		7.62E-02	6.23E-01		6.14E-01	2.05E-08		Unigene45097_All//gi|186886420|gb|ACC93586.1|//5.00E-27//starch-granule-bound R1 protein [Solanum tuberosum]	Unigene45097_All//2.00E-22//AT1G10760| SEX1 (STARCH EXCESS 1); alpha-glucan, water dikinase	Unigene45097_All//5.00E-162//gi|73860834|gb|DT463573.1|DT463573				nr -
Unigene45098_All	4875	0.34	1.18	0.64	2.15	2.08	4.12	3.17	2.22	4.68	1.79E+00	1.08E-10	Up	9.08E-01	1.36E-02		-4.23E-02	8.24E-01		9.42E-01	1.61E-14		-5.12E-01	5.17E-05		5.65E-01	1.77E-08		Unigene45098_All//gi|57012985|sp|Q8LPT9.1|GWD1_CITRE//0.00E+00//RecName: Full=Alpha-glucan water dikinase, chloroplastic; AltName: Full=Starch-related protein R1; Flags: Precursor >gi|20384925|gb|AAM18228.1| R1 [Citrus reticulata]	Unigene45098_All//0.00E+00//AT1G10760| SEX1 (STARCH EXCESS 1); alpha-glucan, water dikinase	Unigene45098_All//0.00E+00//TC147028				nr -

Unigene4510_All	940	0.83	0.97	0.57	9.86	7.51	2.83	1.21	0.76	0.25	2.17E-01	7.42E-01		-5.60E-01	4.96E-01		-3.92E-01	3.42E-02		-1.80E+00	3.08E-18	Down	-6.84E-01	2.37E-01		-2.26E+00	3.40E-04	Down	Unigene4510_All//gi|29027737|dbj|BAC65867.1|//1.00E-35//bZIP transcription factor [Arabidopsis thaliana] >gi|29027747|dbj|BAC65872.1| bZIP transcription factor [Arabidopsis thaliana]	Unigene4510_All//2.00E-20//AT4G35900| FD; DNA binding / protein binding / transcription activator/ transcription factor	Unigene4510_All//5.00E-95//DW504907	bZIP				nr +
Unigene45100_All	5231	2.88	8.20	3.96	3.58	3.50	4.20	7.70	17.66	14.33	1.51E+00	3.99E-59	Up	4.59E-01	2.43E-04		-3.20E-02	8.23E-01		2.32E-01	6.30E-02		1.20E+00	7.56E-109	Up	8.95E-01	1.68E-56		Unigene45100_All//gi|183239018|gb|ACC60967.1|//0.00E+00//phytochrome C [Vitis vinifera]	Unigene45100_All//0.00E+00//AT5G35840| PHYC (phytochrome defective c); protein histidine kinase	Unigene45100_All//0.00E+00//TC172734		ko04712|Circadian rhythm - plant		nr -
Unigene45101_All	554	1.13	6.68	2.02	5.04	2.61	2.93	2.67	0.91	6.40	2.56E+00	1.05E-10	Up	8.33E-01	2.23E-01		-9.48E-01	7.45E-03		-7.79E-01	3.91E-02		-1.56E+00	2.28E-03		1.26E+00	1.87E-05	Up	Unigene45101_All//gi|121501706|gb|ABM55247.1|//2.00E-83//calmodulin-binding protein [Beta vulgaris]	Unigene45101_All//7.00E-84//AT2G26190| calmodulin-binding family protein	Unigene45101_All//0.00E+00//gi|78351959|gb|DT572233.1|DT572233				nr +
Unigene45102_All	1459	4.23	3.82	4.67	3.69	3.49	1.58	0.52	1.12	0.79	-1.48E-01	5.78E-01		1.43E-01	5.93E-01		-7.81E-02	8.16E-01		-1.22E+00	2.15E-06	Down	1.10E+00	1.83E-02		6.02E-01	2.77E-01		Unigene45102_All//gi|18401055|ref|NP_565618.1|//1.00E-165//calmodulin-binding family protein [Arabidopsis thaliana] >gi|169304469|gb|AAL31920.1|AF419588_1 At2g26190/T1D16.17 [Arabidopsis thaliana] >gi|3075398|gb|AAC14530.1| expressed protein [Arabidopsis thaliana] >gi|20453237|gb|AAM19857.1| At2g26190/T1D16.17 [Arabidopsis thaliana] >gi|22135809|gb|AAM91091.1| At2g26190/T1D16.17 [Arabidopsis thaliana]	Unigene45102_All//2.00E-166//AT2G26190| calmodulin-binding family protein	Unigene45102_All//0.00E+00//TC172511				nr +
Unigene45104_All	3353	0.47	2.48	1.13	0.65	1.04	3.35	6.15	11.63	3.84	2.40E+00	1.04E-21	Up	1.27E+00	1.72E-04	Up	6.66E-01	4.21E-02		2.36E+00	2.19E-30	Up	9.18E-01	2.25E-30		-6.81E-01	1.65E-10		Unigene45104_All//gi|224092168|ref|XP_002309491.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222855467|gb|EEE93014.1| cytochrome P450 [Populus trichocarpa]	Unigene45104_All//0.00E+00//AT2G26170| CYP71A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene45104_All//0.00E+00//TC172511		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis;/ko00903|Limonene and pinene degradation		nr +
Unigene45105_All	1741	4.33	20.90	2.60	6.35	8.39	5.24	9.20	4.35	21.67	2.27E+00	5.62E-87	Up	-7.35E-01	8.64E-04		4.01E-01	4.83E-03		-2.78E-01	1.32E-01		-1.08E+00	8.77E-17	Down	1.24E+00	3.17E-48	Up	Unigene45105_All//gi|121501706|gb|ABM55247.1|//1.00E-169//calmodulin-binding protein [Beta vulgaris]	Unigene45105_All//2.00E-158//AT2G26190| calmodulin-binding family protein	Unigene45105_All//0.00E+00//gi|78351959|gb|DT572233.1|DT572233				nr -
Unigene45107_All	1128	4.73	2.16	3.73	12.85	9.77	13.29	9.22	7.15	9.25	-1.13E+00	1.83E-05	Down	-3.43E-01	2.28E-01		-3.96E-01	4.90E-03		4.88E-02	7.74E-01		-3.67E-01	2.32E-02		5.10E-03	9.73E-01		Unigene45107_All//gi|224110590|ref|XP_002315568.1|//1.00E-160//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222864608|gb|EEF01739.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene45107_All//3.00E-138//AT3G06400| CHR11 (CHROMATIN-REMODELING PROTEIN 11); ATP binding / DNA binding / DNA-dependent ATPase/ helicase/ hydrolase, acting on acid anhydrides, in phosphorus-containing anhydrides / nucleic acid binding / nucleosome binding	Unigene45107_All//0.00E+00//TC169115				nr -
Unigene45108_All	1266	2.48	1.40	1.89	10.70	8.05	7.92	12.66	4.42	7.87	-8.24E-01	1.87E-02		-3.90E-01	3.04E-01		-4.11E-01	4.85E-03		-4.35E-01	4.26E-03		-1.52E+00	9.18E-28	Down	-6.86E-01	1.85E-08		Unigene45108_All//gi|14091823|gb|AAK53826.1|AC011806_3/1.00E-163//Putative SWI/SNF related, matrix associated, actin dependent regulator of chromatin [Oryza sativa]	Unigene45108_All//1.00E-80//AT3G06400| CHR11 (CHROMATIN-REMODELING PROTEIN 11); ATP binding / DNA binding / DNA-dependent ATPase/ helicase/ hydrolase, acting on acid anhydrides, in phosphorus-containing anhydrides / nucleic acid binding / nucleosome binding	Unigene45108_All//2.00E-39//TC169115				nr +
Unigene45109_All	634	5.86	2.64	7.81	3.61	4.29	2.56	0.27	0.00	0.00	-1.15E+00	3.89E-04	Down	4.15E-01	1.47E-01		2.48E-01	5.76E-01		-4.95E-01	2.65E-01		-8.06E+00	1.34E-01		-8.06E+00	1.08E-01		Unigene45109_All//gi|225445222|ref|XP_002280919.1|//3.00E-06//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297738818|emb|CBI28063.3| unnamed protein product [Vitis vinifera]		Unigene45109_All//3.00E-68//TC142769				nr -
Unigene4511_All	1092	1.34	1.30	0.20	7.85	9.93	5.54	1.01	1.84	0.36	-4.63E-02	9.43E-01		-2.78E+00	9.28E-05	Down	3.40E-01	5.24E-02		-5.02E-01	1.10E-02		8.68E-01	3.38E-02		-1.46E+00	1.18E-02		Unigene4511_All//gi|29027737|dbj|BAC65867.1|//7.00E-29//bZIP transcription factor [Arabidopsis thaliana] >gi|29027747|dbj|BAC65872.1| bZIP transcription factor [Arabidopsis thaliana]	Unigene4511_All//5.00E-15//AT4G35900| FD; DNA binding / protein binding / transcription activator/ transcription factor	Unigene4511_All//0.00E+00//DW504907	bZIP			nr +
Unigene45110_All	2545	181.02	130.55	216.60	72.09	109.08	70.34	5.35	3.81	1.96	-4.72E-01	1.10E-88		2.59E-01	1.13E-33		5.98E-01	2.48E-98		-3.53E-02	4.78E-01		-4.90E-01	3.10E-04		-1.45E+00	5.95E-23	Down	Unigene45110_All//gi|3107905|dbj|BAA25906.1|//0.00E+00//leaf protein [Ipomoea nil]	Unigene45110_All//0.00E+00//AT5G21222| protein kinase family protein	Unigene45110_All//0.00E+00//gi|109861447|gb|DW490424.1|DW490424				nr -
Unigene45111_All	589	0.36	2.24	2.17	3.21	3.39	2.15	2.58	1.49	2.10	2.65E+00	2.16E-04	Up	2.61E+00	5.00E-04	Up	7.74E-02	8.87E-01		-5.82E-01	2.31E-01		-7.94E-01	1.00E-01		-3.02E-01	5.42E-01										
Unigene45114_All	1114	9.25	11.69	4.45	12.52	10.94	11.80	16.17	17.86	15.66	3.37E-01	3.53E-02		-1.06E+00	2.06E-08	Down	-1.94E-01	2.35E-01		-8.58E-02	6.34E-01		1.44E-01	2.51E-01		-4.57E-02	7.25E-01		Unigene45114_All//gi|15239132|ref|NP_199109.1|//3.00E-76//GYF domain-containing protein [Arabidopsis thaliana]	Unigene45114_All//4.00E-59//AT5G42950| GYF domain-containing protein	Unigene45114_All//0.00E+00//gi|48752953|gb|C0083472.1|C0083472				nr -
Unigene45116_All	762	1.65	2.93	4.75	4.64	4.34	4.33	3.72	3.84	2.88	8.28E-01	5.37E-02		1.53E+00	1.71E-05	Up	-9.75E-02	8.12E-01		-1.01E-01	7.69E-01		4.66E-02	9.06E-01		-3.71E-01	2.64E-01				Unigene45116_All//9.00E-07//TC135971				
Unigene45118_All	1166	0.09	0.09	0.18	1.32	1.45	1.20	18.89	11.43	7.11	-4.58E-02	9.88E-01		1.03E+00	5.91E-01		1.28E-01	8.26E-01		-1.42E-01	7.94E-01		-7.24E-01	5.96E-12		-1.41E+00	4.18E-35	Down	Unigene45118_All//gi|224122284|ref|XP_002330585.1|//1.00E-112//amino acid permease [Populus trichocarpa] >gi|222872143|gb|EEF09274.1| amino acid permease [Populus trichocarpa]	Unigene45118_All//1.00E-93//AT5G23810| AAP7; amino acid transmembrane transporter	Unigene45118_All//0.00E+00//CO108113				nr -
Unigene45120_All	3968	5.58	4.75	6.58	44.20	44.12	41.59	38.20	42.93	16.94	-2.32E-01	5.76E-02		2.38E-01	4.09E-02		-2.70E-03	9.55E-01		-8.79E-02	3.65E-02		1.69E-01	1.77E-06		-1.17E+00	8.91E-178	Down	Unigene45120_All//gi|60327629|gb|AX190054.1|//0.00E+00//class III HD-Zip protein 5 [Populus trichocarpa]	Unigene45120_All//0.00E+00//AT1G52150| ATHB-15; DNA binding / transcription factor	Unigene45120_All//0.00E+00//ES810681	HB			nr -
Unigene45121_All	909	3.17	8.70	3.92	6.08	5.53	6.76	9.35	8.78	7.67	1.46E+00	6.31E-11	Up	3.10E-01	3.96E-01		-1.37E-01	6.17E-01		1.52E-01	6.14E-01		-9.02E-02	6.47E-01		-2.86E-01	1.10E-01		Unigene45121_All//gi|68053506|gb|AAY85174.1|//1.00E-107//alpha-amylase 2 [Manihot esculenta]	Unigene45121_All//2.00E-100//AT1G76130| AMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase/ calcium ion binding / catalytic/ cation binding	Unigene45121_All//0.00E+00//gi|78342347|gb|DT562621.1|DT562621		ko00500|Starch and sucrose metabolism		nr -
Unigene45122_All	1038	23.14	18.89	24.11	12.09	5.37	6.83	0.73	1.05	0.42	-2.92E-01	1.02E-02		5.96E-02	6.23E-01		-1.17E+00	8.57E-15	Down	-8.24E-01	1.25E-07		5.14E-01	3.96E-01		-7.96E-01	2.52E-01		Unigene45122_All//gi|60652323|gb|AX33234.1|//1.00E-152//cytosolic alpha-amylase [Malus x domestica]	Unigene45122_All//1.00E-146//AT1G76130| AMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase/ calcium ion binding / catalytic/ cation binding	Unigene45122_All//0.00E+00//gi|48793233|gb|C0094547.1|C0094547		ko00500|Starch and sucrose metabolism		nr -
Unigene45123_All	1540	11.65	25.04	15.39	26.17	21.76	22.32	16.56	18.73	17.31	1.10E+00	5.60E-33	Up	4.01E-01	5.92E-04		-2.66E-01	9.09E-04		-2.30E-01	7.60E-03		1.78E-01	6.75E-02		6.40E-02	5.76E-01		Unigene45123_All//gi|60652323|gb|AX33234.1|//0.00E+00//cytosolic alpha-amylase [Malus x domestica]	Unigene45123_All//0.00E+00//AT1G76130| AMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase/ calcium ion binding / catalytic/ cation binding	Unigene45123_All//0.00E+00//TC158600		ko00500|Starch and sucrose metabolism		nr +
Unigene45124_All	1694	17.61	14.84	14.59	10.97	5.16	5.92	1.15	1.46	0.78	-2.47E-01	1.55E-02		-2.71E-01	1.02E-02		-1.09E+00	2.75E-19	Down	-8.90E-01	1.96E-12		3.43E-01	3.84E-01		-5.65E-01	1.60E-01		Unigene45124_All//gi|60652323|gb|AX33234.1|//0.00E+00//cytosolic alpha-amylase [Malus x domestica]	Unigene45124_All//0.00E+00//AT1G76130| AMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase/ calcium ion binding / catalytic/ cation binding	Unigene45124_All//0.00E+00//TC142007		ko00500|Starch and sucrose metabolism		nr +
Unigene45127_All	4858	3.26	2.36	1.35	6.20	4.27	4.53	7.89	4.77	4.26	-4.69E-01	7.98E-04		-1.28E+00	9.42E-17	Down	-5.40E-01	1.80E-09		-4.54E-01	1.91E-06		-7.26E-01	2.95E-20		-8.90E-01	3.33E-29		Unigene45127_All//gi|114149987|gb|ABI51615.1|//3.00E-98//RPG [Medicago truncatula]	Unigene45127_All//8.00E-22//AT1G22060| LOCATED IN: vacuole; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT1G22000.1); Has 67094 Blast hits to 30189 proteins in 1408 species: Archae - 880; Bacteria - 6261; Metazoa - 35085; Fungi - 5326; Plants - 2622; Viruses - 293; Other Eukaryotes - 16627 (source: NCBI BLink).	Unigene45127_All//0.00E+00//gi|164315696|gb|ES817893.1|ES817893				nr +
Unigene45128_All	1437	7.50	10.01	9.19	15.60	13.11	16.28	12.83	5.99	11.01	4.17E-01	5.09E-03		2.93E-01	8.16E-02		-2.51E-01	3.05E-02		6.16E-02	6.68E-01		-1.10E+00	1.29E-19	Down	-2.21E-01	5.97E-02		Unigene45128_All//gi|34222066|gb|AAQ62869.1|//5.00E-93//At1g12450 [Arabidopsis thaliana]	Unigene45128_All//1.00E-90//AT4G22850| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (InterPro:IPR015414); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12000.1); Has 1331 Blast hits to 1328 proteins in 349 species: Archae - 4; Bacteria - 600; Metazoa - 103; Fungi - 64; Plants - 162; Viruses - 0; Other Eukaryotes - 398 (source: NCBI BLink).	Unigene45128_All//0.00E+00//TC158645				nr +
Unigene45129_All	1477	10.45	78.56	10.60	8.77	18.00	19.08	4.81	4.70	6.07	2.91E+00	0.00E+00	Up	2.05E-02	9.06E-01		1.04E+00	2.65E-24	Up	1.12E+00	1.30E-26	Up	-3.39E-02	8.87E-01		3.36E-01	5.03E-02		Unigene45129_All//gi|34222066|gb|AAQ62869.1|//1.00E-89//At1g12450 [Arabidopsis thaliana]	Unigene45129_All//9.00E-88//AT4G22850| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (InterPro:IPR015414); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12000.1); Has 1331 Blast hits to 1328 proteins in 349 species: Archae - 4; Bacteria - 600; Metazoa - 103; Fungi - 64; Plants - 162; Viruses - 0; Other Eukaryotes - 398 (source: NCBI BLink).	Unigene45129_All//0.00E+00//gi|21095057|gb|BQ407370.1|BQ407370				nr -
Unigene4513_All	1299	23.40	15.56	32.63	1.96	4.00	1.15	1.37	0.32	0.37	-5.88E-01	1.89E-09		4.80E-01	1.04E-08		1.03E+00	4.31E-05	Up	-7.70E-01	5.39E-02		-2.09E+00	2.21E-05	Down	-1.89E+00	4.84E-05	Down	Unigene4513_All//gi|159025735|emb|CAN88868.1|//3.00E-94//D6-type cyclin [Populus trichocarpa]	Unigene4513_All//2.00E-52//AT4G03270| CYCD6;1 (Cyclin D6;1); cyclin-dependent protein kinase	Unigene4513_All//0.00E+00//TC169408				nr -

Unigene45131_All	2029	1.52	6.67	2.41	3.61	3.75	4.59	4.96	3.98	5.22	2.13E+00	2.93E-30	Up	6.66E-01	1.87E-02		5.56E-02	8.28E-01		3.45E-01	8.05E-02		-3.19E-01	5.68E-02		7.47E-02	6.62E-01		Unigene45131_All//gi|297792417|ref|XP_002864093.1|//0.00E+00//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309928|gb|EFH40352.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45131_All//0.00E+00//AT5G51050| mitochondrial substrate carrier family protein	Unigene45131_All//0.00E+00//DW504693				nr +
Unigene45134_All	349	0.75	17.57	2.75	1.00	4.05	3.36	2.79	3.35	2.74	4.55E+00	3.44E-28	Up	1.87E+00	2.06E-02		2.02E+00	9.22E-04	Up	1.75E+00	9.86E-03		2.67E-01	6.28E-01		-2.44E-02	9.71E-01					Unigene45134_All//2.00E-61//TC149943				
Unigene45135_All	397	4.22	16.59	4.43	3.26	4.25	6.71	6.71	10.42	10.54	1.98E+00	9.71E-14	Up	6.98E-02	8.91E-01		3.82E-01	5.10E-01		1.04E+00	7.64E-03		6.35E-01	1.76E-02		6.51E-01	1.13E-02		Unigene45135_All//gi|226508354|ref|NP_001149285.1|//1.00E-06//lectin-like protein [Zea mays] >gi|195626052|gb|ACG34856.1| lectin-like protein [Zea mays]		Unigene45135_All//1.00E-130//TC149943				nr +
Unigene45136_All	468	16.66	113.68	25.83	13.73	23.84	29.63	12.65	18.22	14.81	2.77E+00	1.83E-159	Up	6.33E-01	1.71E-04		7.96E-01	6.90E-07		1.11E+00	3.78E-13	Up	5.27E-01	2.93E-03		2.28E-01	2.75E-01		Unigene45136_All//gi|226508354|ref|NP_001149285.1|//3.00E-32//lectin-like protein [Zea mays] >gi|195626052|gb|ACG34856.1| lectin-like protein [Zea mays]	Unigene45136_All//6.00E-32//AT4G19840| ATPP2-A1; carbohydrate binding	Unigene45136_All//0.00E+00//TC149943				nr +
Unigene45137_All	5174	6.23	36.78	8.71	3.80	7.97	7.93	13.92	15.95	25.50	2.56E+00	0.00E+00	Up	4.83E-01	2.51E-09		1.07E+00	2.33E-39	Up	1.06E+00	3.75E-35	Up	1.96E-01	1.65E-04		8.73E-01	9.28E-95		Unigene45137_All//gi|224053298|ref|XP_002297751.1|//0.00E+00//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222845009|gb|EEE82556.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene45137_All//4.00E-123//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene45137_All//0.00E+00//TC175330		ko04626|Plant-pathogen interaction		nr -
Unigene4514_All	675	4.50	3.23	4.65	5.46	6.89	6.02	9.08	4.27	4.90	-4.78E-01	1.88E-01		5.00E-02	8.95E-01		3.35E-01	2.74E-01		1.41E-01	6.93E-01		-1.09E+00	5.80E-07	Down	-8.91E-01	1.96E-05					Unigene4514_All//3.00E-111//gi|78339454|gb|DT559728.1|DT559728				
Unigene45148_All	3894	0.77	1.16	0.67	1.01	1.00	1.03	0.81	1.47	2.68	5.97E-01	3.66E-02		-1.93E-01	6.22E-01		-1.62E-02	9.50E-01		3.05E-02	9.43E-01		8.53E-01	1.22E-04		1.72E+00	2.81E-22	Up	Unigene45148_All//gi|297613455|ref|NP_001067177.2|//0.00E+00//Os12g0594200 [Oryza sativa Japonica Group] >gi|255670445|dbj|BAF30196.2| Os12g0594200 [Oryza sativa Japonica Group]	Unigene45148_All//0.00E+00//AT3G50380| INVOLVED IN: protein localization; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Vacuolar protein sorting-associated protein (InterPro:IPR009543); Has 239 Blast hits to 235 proteins in 73 species: Archae - 0; Bacteria - 0; Metazoa - 130; Fungi - 71; Plants - 23; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink).	Unigene45148_All//0.00E+00//CO131085				nr -
Unigene4515_All	291	8.09	4.88	2.20	5.48	7.57	6.05	1.89	3.73	3.97	-7.31E-01	7.80E-02		-1.88E+00	7.74E-05	Down	4.67E-01	3.07E-01		1.44E-01	7.81E-01		9.83E-01	9.75E-02		1.07E+00	5.22E-02		Unigene4515_All//gi|9989055|gb|AAG10818.1|AC011808_6//9.00E-20//Hypothetical protein [Arabidopsis thaliana]	Unigene4515_All//9.00E-13//AT1G16650| unknown protein	Unigene4515_All//5.00E-117//TC173092				nr -
Unigene45152_All	2856	3.46	10.43	12.64	5.30	6.80	6.06	3.36	3.73	3.52	1.59E+00	1.81E-44	Up	1.87E+00	1.80E-65	Up	3.59E-01	3.06E-03		1.92E-01	2.01E-01		1.51E-01	4.00E-01		6.49E-02	7.13E-01		Unigene45152_All//gi|226497604|ref|NP_001148089.1|//0.00E+00//ubiquinone biosynthesis protein ubiB [Zea mays] >gi|195615724|gb|ACG29692.1| ubiquinone biosynthesis protein ubiB [Zea mays]	Unigene45152_All//5.00E-156//AT5G24970| ABC1 family protein	Unigene45152_All//0.00E+00//TC179302				nr -
Unigene45157_All	812	9.92	7.05	9.25	20.98	25.40	23.36	33.90	15.60	28.06	-4.93E-01	1.63E-02		-1.02E-01	6.41E-01		2.76E-01	2.34E-02		1.55E-01	2.96E-01		-1.12E+00	8.78E-30	Down	-2.73E-01	2.91E-03		Unigene45157_All//gi|109729860|gb|ABG46343.1|//2.00E-61//transport inhibitor response 1 [Gossypium hirsutum]	Unigene45157_All//2.00E-56//AT3G62980| TIR1 (TRANSPORT INHIBITOR RESPONSE 1); auxin binding / protein binding / ubiquitin-protein ligase	Unigene45157_All//0.00E+00//gi|164248961|gb|ES796019.1|ES796019		ko04626|Plant-pathogen interaction		nr -
Unigene45158_All	2462	4.76	3.77	4.50	10.44	16.14	9.83	7.21	8.42	19.30	-3.38E-01	4.58E-02		-8.15E-02	6.53E-01		6.29E-01	1.23E-15		-8.65E-02	5.14E-01		2.23E-01	5.07E-02		1.42E+00	8.39E-75	Up	Unigene45158_All//gi|109729860|gb|ABG46343.1|//0.00E+00//transport inhibitor response 1 [Gossypium hirsutum]	Unigene45158_All//0.00E+00//AT3G62980| TIR1 (TRANSPORT INHIBITOR RESPONSE 1); auxin binding / protein binding / ubiquitin-protein ligase	Unigene45158_All//0.00E+00//gi|164248961|gb|ES796019.1|ES796019		ko04626|Plant-pathogen interaction		nr +
Unigene45159_All	3044	3.94	2.98	1.71	17.64	13.43	8.96	11.24	3.24	4.07	-4.02E-01	1.51E-02		-1.20E+00	1.10E-11	Down	-3.94E-01	2.05E-09		-9.77E-01	1.09E-40		-1.79E+00	4.58E-74	Down	-1.47E+00	3.75E-57	Down	Unigene45159_All//gi|115439815|ref|NP_001044187.1|//1.00E-178//Os01g0738300 [Oryza sativa Japonica Group] >gi|113533718|dbj|BAF06101.1| Os01g0738300 [Oryza sativa Japonica Group]	Unigene45159_All//3.00E-134//AT1G70460| protein kinase, putative	Unigene45159_All//0.00E+00//DR462160		ko00270|Cysteine and methionine metabolism		nr +
Unigene45160_All	1284	84.80	64.05	72.16	40.58	41.70	38.37	28.98	18.33	12.32	-4.05E-01	1.98E-16		-2.33E-01	5.50E-06		3.94E-02	6.78E-01		-8.06E-02	3.78E-01		-6.61E-01	8.08E-17		-1.23E+00	6.71E-48	Down	Unigene45160_All//gi|18378982|ref|NP_563657.1|//1.00E-141//CLPP5 (NUCLEAR ENCODED CLP PROTEASE 5); serine-type endopeptidase [Arabidopsis thaliana] >gi|75313059|sp|Q9SS34.1|CLPP5_ARATH RecName: Full=ATP-dependent Clp protease proteolytic subunit 5, chloroplastic; AltName: Full=Endopeptidase ClpP5; Short=nClpP5; AltName: Full=nClpP1; Flags: Precursor >gi|9972387|gb|AAG10637.1|AC022521_15 ATP-dependent Clp protease subunit ClpP [Arabidopsis thaliana] >gi|4887543|emb|CAB43488.1| ATP-dependent Clp protease subunit ClpP [Arabidopsis thaliana] >gi|5360579|dbj|BAA82065.1| nClpP1 [Arabidopsis thaliana] >gi|21536639|gb|AAM60971.1| ATP-dependent Clp protease proteolytic subunit ClpP5 [Arabidopsis thaliana] >gi|89274139|gb|ABD65590.1| At1g02560 [Arabidopsis thaliana]	Unigene45160_All//4.00E-137//AT1G02560| CLPP5 (NUCLEAR ENCODED CLP PROTEASE 5); serine-type endopeptidase	Unigene45160_All//0.00E+00//TC133024				nr -
Unigene45162_All	2745	13.29	24.37	9.16	36.20	98.64	99.54	86.19	258.46	205.22	8.75E-01	7.80E-39		-5.37E-01	3.73E-09		1.45E+00	0.00E+00	Up	1.46E+00	0.00E+00	Up	1.58E+00	0.00E+00	Up	1.25E+00	0.00E+00	Up	Unigene45162_All//gi|23452226|gb|AAN32954.1|//0.00E+00//alkaline alpha-galactosidase seed imbibition protein [Solanum lycopersicum]	Unigene45162_All//0.00E+00//AT1G55740| AtSIP1 (Arabidopsis thaliana seed imbibition 1); hydrolase, hydrolyzing O-glycosyl compounds	Unigene45162_All//1.00E-11//EX164522		ko00052|Galactose metabolism		nr +
Unigene45165_All	1803	17.47	14.00	14.68	25.09	21.64	20.92	30.65	16.60	15.27	-3.20E-01	9.63E-04		-2.51E-01	1.49E-02		-2.13E-01	6.02E-03		-2.62E-01	8.83E-04		-8.85E-01	3.30E-40		-1.01E+00	5.25E-51	Down	Unigene45165_All//gi|21537290|gb|AAM61631.1|//0.00E+00//aspartyl aminopeptidase-like protein [Arabidopsis thaliana]	Unigene45165_All//0.00E+00//AT5G60160| aspartyl aminopeptidase, putative	Unigene45165_All//0.00E+00//ES795033				nr +
Unigene45166_All	3962	1.25	1.69	1.21	6.36	6.69	4.01	5.12	2.03	2.74	4.28E-01	6.41E-02		-5.26E-02	8.56E-01		7.31E-02	5.81E-01		-6.65E-01	2.75E-10		-1.34E+00	4.26E-29	Down	-9.05E-01	2.40E-16		Unigene45166_All//gi|42570286|ref|NP_849997.2|//0.00E+00//CLASP (CLIP-ASSOCIATED PROTEIN); binding [Arabidopsis thaliana]	Unigene45166_All//2.00E-120//AT2G20190| CLASP (CLIP-ASSOCIATED PROTEIN); binding	Unigene45166_All//0.00E+00//TC163001				nr -
Unigene45167_All	2954	112.52	41.84	27.80	186.98	95.74	32.63	48.94	38.09	17.21	-1.43E+00	0.00E+00	Down	-2.02E+00	0.00E+00	Down	-9.66E-01	0.00E+00		-2.52E+00	0.00E+00	Down	-3.62E-01	1.90E-21		-1.51E+00	1.94E-249	Down	Unigene45167_All//gi|24474446|gb|AN15927.1|//0.00E+00//nitrate reductase [Tilia platyphyllos]	Unigene45167_All//0.00E+00//AT1G37130| NIA2 (NITRATE REDUCTASE 2); nitrate reductase (NADH)/ nitrate reductase	Unigene45167_All//0.00E+00//TC159858		ko00910|Nitrogen metabolism//ko00920|Sulfur metabolism		nr +
Unigene45168_All	805	0.26	23.92	2.18	1.11	3.38	5.39	2.00	15.37	2.13	6.52E+00	4.68E-103	Up	3.07E+00	3.99E-06	Up	1.60E+00	3.85E-05	Up	2.27E+00	1.74E-11	Up	2.94E+00	6.11E-49	Up	9.25E-02	8.38E-01		Unigene45168_All//gi|15225258|ref|NP_180187.1|//5.00E-44//IQD6 (IQ-domain 6); calmodulin binding [Arabidopsis thaliana] >gi|119935823|gb|ABM06004.1| At2g26180 [Arabidopsis thaliana]	Unigene45168_All//8.00E-34//AT2G26180| IQD6 (IQ-domain 6); calmodulin binding	Unigene45168_All//0.00E+00//gi|21101018|gb|BQ413331.1|BQ413331				nr -
Unigene45169_All	3122	1.06	30.79	3.34	3.33	6.12	9.27	4.63	21.09	3.90	4.87E+00	0.00E+00	Up	1.66E+00	1.94E-16	Up	8.76E-01	2.15E-13		1.48E+00	1.74E-41	Up	2.19E+00	8.51E-184	Up	-2.46E-01	6.50E-02		Unigene45169_All//gi|297825759|ref|XP_002880762.1|//1.00E-110//IQ-domain 6 [Arabidopsis lyrata subsp. lyrata] >gi|297326601|gb|EFH57021.1| IQ-domain 6 [Arabidopsis lyrata subsp. lyrata]	Unigene45169_All//6.00E-82//AT2G26150| ATHSFA2; DNA binding / transcription factor	Unigene45169_All//0.00E+00//TC165110	HSF			nr -
Unigene4517_All	971	12.99	29.38	18.97	17.85	25.00	20.33	13.06	13.04	18.18	1.18E+00	3.28E-27	Up	5.47E-01	3.87E-05		4.86E-01	2.52E-06		1.87E-01	1.79E-01		-2.30E-03	1.02E+00		4.77E-01	3.36E-05		Unigene4517_All//gi|297598779|ref|NP_001046223.2|//4.00E-28//Os02g0201000 [Oryza sativa Japonica Group] >gi|255670693|dbj|BAF08137.2| Os02g0201000 [Oryza sativa Japonica Group]	Unigene4517_All//7.00E-26//AT5G25360| unknown protein	Unigene4517_All//0.00E+00//ES801524				nr +
Unigene45172_All	512	32.39	43.25	22.78	179.80	163.57	85.56	171.76	135.35	151.18	4.17E-01	3.51E-04		-5.08E-01	3.28E-04		-1.37E-01	1.26E-02		-1.07E+00	9.94E-81	Down	-3.44E-01	3.01E-12		-1.84E-01	1.86E-04		Unigene45172_All//gi|124360798|gb|ABN08770.1|//6.00E-51//Galactose-binding like [Medicago truncatula]	Unigene45172_All//3.00E-47//AT3G52840| BGAL2 (beta-galactosidase 2); beta-galactosidase/ catalytic/ cation binding	Unigene45172_All//0.00E+00//TC132714		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation		nr +
Unigene45174_All	459	0.91	1.99	1.74	8.47	8.18	2.85	4.42	1.27	1.82	1.12E+00	1.30E-01		9.32E-01	2.56E-01		-4.99E-02	8.73E-01		-1.57E+00	1.09E-06	Down	-1.79E+00	4.24E-05	Down	-1.28E+00	1.41E-03		Unigene45174_All//gi|15224360|ref|NP_181908.1|//2.00E-12//formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] >gi|75097595|sp|Q22824.1|FH2_ARATH RecName: Full=Formin-like protein 2; Short=AtFH2; Short=AtFORMIN-2; Flags: Precursor	Unigene45174_All//9.00E-06//AT2G43800| formin homology 2 domain-containing protein / FH2 domain-containing protein	Unigene45174_All//5.00E-149//ES823812				nr +
Unigene45175_All	3290	5.28	2.83	4.34	25.15	23.62	15.28	10.81	2.22	1.93	-8.98E-01	3.97E-11		-2.84E-01	4.91E-02		-9.03E-02	1.60E-01		-7.19E-01	4.03E-37		-2.28E+00	3.73E-105	Down	-2.49E+00	2.94E-120	Down	Unigene45175_All//gi|15224360|ref|NP_181908.1|//0.00E+00//formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] >gi|75097595|sp|Q22824.1|FH2_ARATH RecName: Full=Formin-like protein 2; Short=AtFH2; Short=AtFORMIN-2; Flags: Precursor	Unigene45175_All//2.00E-160//AT3G25500| AFH1 (FORMIN HOMOLOGY 1); actin binding / actin filament binding / protein binding	Unigene45175_All//0.00E+00//gi|164339679|gb|ES815317.1|ES815317				nr +
Unigene45189_All	422	4.34	2.52	2.90	11.57	6.69	6.96	6.71	8.42	185.41	-7.83E-01	1.03E-01		-5.80E-01	2.47E-01		-7.90E-01	1.87E-03		-7.34E-01	6.34E-03		3.27E-01	2.99E-01		4.79E+00	0.00E+00	Up	Unigene45189_All//gi|89357199|gb|AB072482.1|//7.00E-63//MRP-like ABC transporter protein [Gossypium barbadense]	Unigene45189_All//8.00E-55//AT3G13080| ATMRP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase	Unigene45189_All//6.00E-167//TC138277		ko02010|ABC transporters		nr -

Unigene45190_All	4297	1.42	0.87	1.25	5.65	2.20	2.82	11.29	10.57	260.88	-7.07E-01	3.02E-03		-1.87E-01	4.85E-01		-1.36E+00	1.25E-35	Down	-1.00E+00	1.74E-19	Down	-9.42E-02	2.34E-01		4.53E+00	0.00E+00	Up	Unigene45190_All//gi|224061172|ref|XP_002300362.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222847620|gb|EEE85167.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene45190_All//0.00E+00//AT3G13080| ATMDP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase	Unigene45190_All//0.00E+00//TC138277		ko02010|ABC transporters		nr +
Unigene45196_All	416	0.63	0.00	0.64	4.91	2.81	1.41	0.00	0.30	0.00	-9.30E+00	6.69E-02		2.52E-02	1.00E+00		-8.03E-01	6.37E-02		-1.80E+00	1.71E-04	Down	8.24E+00	2.40E-01		null	null		Unigene45196_All//gi|19698446|gb|AL93151.1|AF485265.1//2.00E-25//class III peroxidase [Gossypium hirsutum]	Unigene45196_All//2.00E-16//AT5G58390| peroxidase, putative	Unigene45196_All//2.00E-86//TC138284		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene45197_All	519	2.02	0.20	1.64	49.43	36.09	51.43	9.86	10.23	5.83	-3.37E+00	2.13E-04	Down	-2.97E-01	6.41E-01		-4.54E-01	4.51E-06		5.72E-02	6.71E-01		5.32E-02	8.39E-01		-7.57E-01	9.32E-04		Unigene45197_All//gi|19698446|gb|AL93151.1|AF485265.1//7.00E-25//class III peroxidase [Gossypium hirsutum]	Unigene45197_All//5.00E-08//AT5G05340| peroxidase, putative	Unigene45197_All//6.00E-155//gi|3326040|gb|AI054926.1|AI054926		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene45199_All	1276	45.43	9.97	38.56	189.46	157.93	118.15	1.09	6.58	1.06	-2.19E+00	4.69E-133	Down	-2.37E-01	1.19E-03		-2.63E-01	3.70E-19		-6.81E-01	7.38E-98		2.59E+00	3.12E-29	Up	-4.28E-02	9.47E-01		Unigene45199_All//gi|19698446|gb|AL93151.1|AF485265.1//1.00E-174//class III peroxidase [Gossypium hirsutum]	Unigene45199_All//5.00E-121//AT5G05340| peroxidase, putative	Unigene45199_All//0.00E+00//TC138284		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene4520_All	733	38.62	452.98	36.69	39.35	62.25	109.49	22.73	58.33	81.31	3.55E+00	0.00E+00	Up	-7.40E-02	5.56E-01		6.62E-01	1.47E-19		1.48E+00	1.94E-114	Up	1.36E+00	8.57E-62	Up	1.84E+00	2.33E-135	Up	Unigene4520_All//gi|753348873|sp|Q9LE22.1|CML27_ARATH//4.00E-50//RecName: Full=Probable calcium-binding protein CML27; AltName: Full=Calmodulin-like protein 27 >gi|8671778|gb|AAF78384.1|AC069551_17 T10022.19 [Arabidopsis thaliana] >gi|9719735|gb|AAF97837.1|AC034107_20 Strong similarity to calcium-binding protein (PC423) from Olea europaea gb|AF078680 and contains multiple EF-hand PF|00036 domains. ESTs gb|T21585, gb|T21589, gb|T41586, gb|Z37721, gb|Z29218, gb|AI100607, gb|AI997012, gb|AV540453, gb|AV544989, gb|AV544993, gb|AV554674 come from this gene [Arabidopsis thaliana]	Unigene4520_All//2.00E-47//AT1G18210| calcium-binding protein, putative	Unigene4520_All//0.00E+00//TC130328		ko04626|Plant-pathogen interaction		nr -
Unigene45200_All	1485	15.96	4.67	12.94	264.07	204.99	269.06	50.54	40.39	26.02	-1.77E+00	1.69E-41	Down	-3.02E-01	1.15E-02		-3.65E-01	1.69E-57		2.71E-02	4.03E-01		-3.23E-01	1.63E-09		-9.58E-01	1.18E-63		Unigene45200_All//gi|19698446|gb|AL93151.1|AF485265.1//1.00E-151//class III peroxidase [Gossypium hirsutum]	Unigene45200_All//4.00E-117//AT5G58390| peroxidase, putative	Unigene45200_All//0.00E+00//TC133157		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene45204_All	2860	14.80	18.44	16.29	30.52	29.23	31.87	46.63	30.73	21.95	3.18E-01	1.30E-05		1.39E-01	1.19E-01		-6.19E-02	3.57E-01		6.25E-02	3.58E-01		-6.01E-01	2.97E-49		-1.09E+00	2.26E-138	Down	Unigene45204_All//gi|15222380|ref|NP_172218.1|//0.00E+00//ceramidase family protein [Arabidopsis thaliana]	Unigene45204_All//0.00E+00//AT1G07380| ceramidase family protein	Unigene45204_All//0.00E+00//TC149144				nr +
Unigene45215_All	1351	3.41	3.49	0.67	3.58	4.44	5.38	7.57	2.04	2.95	3.35E-02	9.20E-01		-2.35E+00	1.69E-11	Down	3.10E-01	2.34E-01		5.90E-01	6.33E-03		-1.89E+00	2.60E-24	Down	-1.36E+00	6.25E-16	Down	Unigene45215_All//gi|297840641|ref|XP_002888202.1|//0.00E+00//ZCF125 [Arabidopsis lyrata subsp. lyrata] >gi|297334043|gb|EFH64461.1| ZCF125 [Arabidopsis lyrata subsp. lyrata]	Unigene45215_All//3.00E-167//AT1G59540| ZCF125; ATP binding / microtubule motor					nr +
Unigene45216_All	2115	4.25	1.94	1.31	7.35	7.73	5.94	5.48	0.95	2.64	-1.13E+00	1.21E-08	Down	-1.70E+00	1.22E-14	Down	7.37E-02	6.67E-01		-3.08E-01	3.55E-02		-2.53E+00	3.84E-39	Down	-1.05E+00	2.92E-12	Down	Unigene45216_All//gi|22330953|ref|NP_187629.2|//1.00E-127//kinesin motor protein-related [Arabidopsis thaliana]	Unigene45216_All//0.00E+00//AT1G59540| ZCF125; ATP binding / microtubule motor	Unigene45216_All//4.00E-107//DR452783				nr +
Unigene45230_All	4074	13.43	7.89	8.74	13.43	13.85	8.08	8.20	3.66	9.20	-7.69E-01	9.07E-26		-6.19E-01	3.77E-17		4.53E-02	6.04E-01		-7.32E-01	1.64E-25		-1.16E+00	3.82E-38	Down	1.67E-01	3.90E-02		Unigene45230_All//gi|223452389|gb|ACM89522.1|//0.00E+00//brassinosteroid receptor [Glycine max] >gi|223452566|gb|ACM89610.1| brassinosteroid receptor [Glycine max]	Unigene45230_All//0.00E+00//AT4G39400| BRI1 (BRASSINOSTEROID INSENSITIVE 1); kinase/ protein binding / protein heterodimerization/ protein homodimerization/ protein kinase/ protein serine/threonine kinase	Unigene45230_All//0.00E+00//TC166811			GO:0000226//GO:0004672//GO:0004896//GO:0006464//GO:0009411//GO:0009646//GO:0009720//GO:0009908//GO:0010208//GO:0016020//GO:0031410//GO:0032559//GO:0032991//GO:0042802//GO:0043231//GO:0043401//GO:0046983//GO:0048827//GO:0048878	nr +
Unigene45238_All	3702	1.40	3.04	2.46	3.50	3.55	3.27	2.87	3.65	2.14	1.12E+00	2.28E-10	Up	8.14E-01	4.07E-05		2.24E-02	9.10E-01		-9.77E-02	6.37E-01		3.47E-01	1.28E-02		-4.21E-01	5.83E-03		Unigene45238_All//gi|297848666|ref|XP_002892214.1|//4.00E-83//F19P19.16 [Arabidopsis lyrata subsp. lyrata] >gi|297338056|gb|EFH68473.1| F19P19.16 [Arabidopsis lyrata subsp. lyrata]	Unigene45238_All//4.00E-58//AT1G04390| protein binding	Unigene45238_All//0.00E+00//TC144516			GO:0005488	nr -
Unigene45239_All	1132	22.23	10.30	13.78	21.83	19.74	20.55	24.39	16.43	11.37	-1.11E+00	4.30E-22	Down	-6.90E-01	7.96E-10		-1.45E-01	2.36E-01		-8.72E-02	5.22E-01		-5.70E-01	6.19E-10		-1.10E+00	5.73E-30	Down	Unigene45239_All//gi|1050840|emb|CAA90282.1|//1.00E-105//U1snRNP-specific protein, U1A [Solanum tuberosum]	Unigene45239_All//2.00E-83//AT2G47580| U1A (SPLICEOSOMAL PROTEIN U1A); RNA binding / nucleic acid binding / nucleotide binding	Unigene45239_All//0.00E+00//TC142267		ko03040|Spliceosome	GO:0000377//GO:0003676//GO:0006970//GO:0030532//GO:0031981	nr +
Unigene4524_All	1290	1.34	1.10	0.91	2.43	2.38	2.10	3.67	1.30	2.35	-2.83E-01	5.86E-01		-5.60E-01	2.87E-01		-3.42E-02	9.24E-01		-2.12E-01	6.15E-01		-1.50E+00	1.22E-08	Down	-6.45E-01	6.80E-03		Unigene4524_All//gi|62733423|gb|AAX95540.1|//1.00E-167//Putative C2 protein [Oryza sativa Japonica Group]	Unigene4524_All//5.00E-179//AT3G03680| C2 domain-containing protein	Unigene4524_All//2.00E-86//gi|78328591|gb|DT548865.1|DT548865				nr -
Unigene45240_All	1323	9.37	4.79	8.61	9.30	8.56	9.66	10.45	6.95	4.70	-9.69E-01	3.51E-09		-1.22E-01	5.16E-01		-1.19E-01	5.52E-01		5.49E-02	7.62E-01		-5.88E-01	1.18E-05		-1.15E+00	1.40E-16	Down	Unigene45240_All//gi|15226631|ref|NP_182280.1|//2.00E-90//U1A (SPLICEOSOMAL PROTEIN U1A); RNA binding / nucleic acid binding / nucleotide binding [Arabidopsis thaliana] >gi|1050430|emb|CAA90283.1| U1snRNP-specific protein [Arabidopsis thaliana] >gi|2529669|gb|AAC62852.1| small nuclear ribonucleoprotein U1A [Arabidopsis thaliana] >gi|15450591|gb|AAK96567.1| At2g47580/T30B22.12 [Arabidopsis thaliana] >gi|16649011|gb|AAL24357.1| small nuclear ribonucleoprotein U1A [Arabidopsis thaliana] >gi|20259986|gb|AAM13340.1| small nuclear ribonucleoprotein U1A [Arabidopsis thaliana] >gi|22655484|gb|AAO98334.1| At2g47580/T30B22.12 [Arabidopsis thaliana]	Unigene45240_All//1.00E-91//AT2G47580| U1A (SPLICEOSOMAL PROTEIN U1A); RNA binding / nucleic acid binding / nucleotide binding	Unigene45240_All//0.00E+00//TC143772		ko03040|Spliceosome	GO:0000377//GO:0003676//GO:0006970//GO:0030532//GO:0031981	nr +
Unigene45245_All	1063	0.84	5.67	0.75	9.37	7.81	8.12	1.79	4.17	12.48	2.76E+00	1.78E-18	Up	-1.55E-01	8.24E-01		-2.64E-01	1.67E-01		-2.08E-01	3.12E-01		1.22E+00	3.97E-06	Up	2.80E+00	8.97E-51	Up	Unigene45245_All//gi|15222311|ref|NP_172195.1|//2.00E-61//MAPKKK13; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|8954031|gb|AAF82205.1|AC067971_13 Strong similarity to a protein kinase homolog F23F1.4 gi|7488253 from Arabidopsis thaliana BAC F23F1 gb|AC004680. It contains a eukaryotic protein kinase domain PF|00069. ESTs gb|F13903 and gb|F13904 come from this gene	Unigene45245_All//4.00E-62//AT1G07150| MAPKKK13; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene45245_All//0.00E+00//TC160564		ko04626|Plant-pathogen interaction	GO:0016301	nr -
Unigene45246_All	1294	1.01	1.14	0.00	2.73	2.82	3.00	1.11	1.55	7.64	1.68E-01	7.42E-01		-9.98E+00	3.71E-07	Down	4.55E-02	9.11E-01		1.35E-01	6.81E-01		4.81E-01	2.53E-01		2.78E+00	1.05E-37	Up	Unigene45246_All//gi|297822725|ref|XP_002879245.1|//1.00E-112//MAPKKK14 [Arabidopsis lyrata subsp. lyrata] >gi|297325084|gb|EFH55504.1| MAPKKK14 [Arabidopsis lyrata subsp. lyrata]	Unigene45246_All//5.00E-110//AT2G30040| MAPKKK14; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene45246_All//0.00E+00//TC172589		ko04626|Plant-pathogen interaction	GO:0004672	nr +
Unigene45247_All	1524	3.47	18.59	1.40	2.61	2.78	7.62	2.19	2.93	14.85	2.42E+00	3.17E-73	Up	-1.31E+00	3.04E-06	Down	8.79E-02	8.29E-01		1.54E+00	4.98E-18	Up	4.21E-01	1.11E-01		2.76E+00	9.10E-85	Up	Unigene45247_All//gi|297822725|ref|XP_002879245.1|//1.00E-102//MAPKKK14 [Arabidopsis lyrata subsp. lyrata] >gi|297325084|gb|EFH55504.1| MAPKKK14 [Arabidopsis lyrata subsp. lyrata]	Unigene45247_All//4.00E-103//AT1G07150| MAPKKK13; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene45247_All//0.00E+00//TC161841		ko04626|Plant-pathogen interaction		nr -
Unigene45248_All	3546	16.48	91.37	23.91	21.72	64.34	54.58	116.31	143.82	210.62	2.47E+00	0.00E+00	Up	5.37E-01	2.00E-20		1.57E+00	0.00E+00	Up	1.33E+00	2.87E-235	Up	3.06E-01	5.14E-54		8.57E-01	0.00E+00		Unigene45248_All//gi|55792822|gb|AAV65494.1|//0.00E+00//trehalose 6-phosphate synthase [Gossypium hirsutum]	Unigene45248_All//0.00E+00//AT1G23870| ATTPS9; transferase, transferring glycosyl groups / trehalose-phosphatase	Unigene45248_All//0.00E+00//TC168377		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0019203//GO:0035251	nr -
Unigene45252_All	2647	5.83	5.36	6.58	14.43	13.02	5.95	12.44	7.26	3.66	-1.22E-01	4.36E-01		1.74E-01	2.46E-01		-1.49E-01	1.09E-01		-1.28E+00	1.33E-44	Down	-7.77E-01	1.34E-19		-1.77E+00	5.97E-72	Down	Unigene45252_All//gi|15218422|ref|NP_177979.1|//0.00E+00//ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE); alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75213463|sp|Q9SYM4.1|TPS1_ARATH RecName: Full=Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1; AltName: Full=Trehalose-6-phosphate synthase 1; Short=AtTPS1 >gi|4836875|gb|AAD30578.1|AC007260_9 trehalose-6-phosphate synthase [Arabidopsis thaliana]	Unigene45252_All//0.00E+00//AT1G78580| ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE); alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups	Unigene45252_All//0.00E+00//gi|48800579|gb|CO101893.1|CO101893		ko00500|Starch and sucrose metabolism	GO:0003006//GO:0005991//GO:0007275//GO:0009756//GO:0019203//GO:0035251//GO:0042546	nr -
Unigene45253_All	3520	13.15	7.80	9.23	24.85	16.93	10.11	12.55	9.46	3.10	-7.54E-01	3.26E-21		-5.12E-01	1.56E-10		-5.53E-01	7.93E-28		-1.30E+00	4.67E-104	Down	-4.08E-01	1.03E-08		-2.02E+00	4.24E-115	Down	Unigene45253_All//gi|15218422|ref|NP_177979.1|//0.00E+00//ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE); alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75213463|sp|Q9SYM4.1|TPS1_ARATH RecName: Full=Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1; AltName: Full=Trehalose-6-phosphate synthase 1; Short=AtTPS1 >gi|4836875|gb|AAD30578.1|AC007260_9 trehalose-6-phosphate synthase [Arabidopsis thaliana]	Unigene45253_All//0.00E+00//AT1G78580| ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE); alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups	Unigene45253_All//0.00E+00//TC156366		ko00500|Starch and sucrose metabolism	GO:0003006//GO:0005991//GO:0007275//GO:0009756//GO:0019203//GO:0035251//GO:0042546	nr +

Unigene45256_All	718	13.48	42.70	23.14	34.90	51.61	81.14	30.97	49.95	29.91	1.66E+00	1.08E-48	Up	7.79E-01	3.63E-08		5.64E-01	3.89E-12		1.22E+00	5.21E-62	Up	6.89E-01	2.08E-17		-5.06E-02	6.65E-01		Unigene45256_All|gi|224120508|ref|XP_002331065.1||2.00E-40||plant synaptotagmin [Populus trichocarpa] >gi|222872995|gb|EEF10126.1| plant synaptotagmin [Populus trichocarpa]	Unigene45256_All||4.00E-39||AT1G05500| NTMC2T2.1	Unigene45256_All||0.00E+00||DW501748			GO:0016020	nr +
Unigene45258_All	1605	6.10	12.50	6.30	12.51	11.71	15.95	9.56	9.53	11.37	1.04E+00	6.85E-16	Up	4.84E-02	8.07E-01		-9.46E-02	5.42E-01		3.51E-01	1.03E-03		-4.70E-03	1.01E+00		2.50E-01	3.25E-02		Unigene45258_All|gi|195639514|gb|ACG39225.1||0.00E+00||COP9 signalosome complex subunit 4 [Zea mays]	Unigene45258_All||0.00E+00||AT5G42970| COP8 (CONSTITUTIVE PHOTOMORPHOGENIC 8); protein binding	Unigene45258_All||0.00E+00||TC170573			GO:0000338||GO:0005488||GO:0009639||GO:0043234||GO:0051319	nr +
Unigene45260_All	2445	0.43	0.33	0.57	12.90	3.61	3.20	20.34	22.99	11.21	-3.68E-01	5.90E-01		4.04E-01	4.96E-01		-1.84E+00	1.96E-72	Down	-2.01E+00	6.14E-71	Down	1.77E-01	6.92E-03		-8.59E-01	1.57E-35		Unigene45260_All|gi|224081114|ref|XP_002306299.1||0.00E+00||white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222855748|gb|EEE93295.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene45260_All||0.00E+00||AT1G17840| WBC11 (WHITE-BROWN COMPLEX HOMOLOG PROTEIN 11); ATPase, coupled to transmembrane movement of substances / fatty acid transporter	Unigene45260_All||0.00E+00||TC176061		ko03040|Spliceosome||ko02010|ABC transporters	GO:0015604||GO:0017111||GO:0032559||GO:0044464	nr -
Unigene45261_All	2298	4.58	8.73	6.28	16.58	18.28	16.80	0.04	0.35	0.03	9.32E-01	1.85E-13		4.57E-01	3.00E-03		1.41E-01	1.15E-01		1.91E-02	8.68E-01		3.23E+00	5.44E-04	Up	-8.48E-02	9.71E-01		Unigene45261_All|gi|224081114|ref|XP_002306299.1||0.00E+00||white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222855748|gb|EEE93295.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene45261_All||0.00E+00||AT1G17840| WBC11 (WHITE-BROWN COMPLEX HOMOLOG PROTEIN 11); ATPase, coupled to transmembrane movement of substances / fatty acid transporter	Unigene45261_All||0.00E+00||TC176061		ko03040|Spliceosome||ko02010|ABC transporters	GO:0015604||GO:0017111||GO:0032559||GO:0044464	nr -
Unigene45262_All	622	5.05	3.42	4.62	9.29	7.20	4.36	13.80	14.18	2.95	-5.61E-01	1.13E-01		-1.27E-01	7.21E-01		-3.68E-01	1.44E-01		-1.09E+00	8.42E-06	Down	3.91E-02	8.48E-01		-2.23E+00	5.18E-26	Down	Unigene45262_All|gi|79495605|ref|NP_195054.2||6.00E-13||DNA binding / transcription factor [Arabidopsis thaliana] >gi|75159005|sp|Q8RYD1.1|REM16_ARATH RecName: Full=B3 domain-containing protein REM16; AltName: Full=Protein REPRODUCTIVE MERISTEM 16; AltName: Full=Auxin response factor 36 >gi|20145851|emb|CAD29616.1| auxin response factor 36 [Arabidopsis thaliana]	Unigene45262_All||1.00E-12||AT4G33280| DNA binding / transcription factor	Unigene45262_All||0.00E+00||TC160237	ABI3VP1		GO:0006350||GO:0043231	nr +
Unigene45263_All	866	25.50	9.07	19.25	3.74	3.94	4.17	23.14	13.08	6.81	-1.49E+00	2.40E-30	Down	-4.06E-01	8.38E-04		7.43E-02	8.46E-01		1.58E-01	6.75E-01		-8.23E-01	1.87E-13		-1.77E+00	4.60E-44	Down	Unigene45263_All|gi|3927834|gb|AAC79591.1||2.00E-07||expressed protein [Arabidopsis thaliana] >gi|89861099|gb|ABF59033.1| At2g28870 [Arabidopsis thaliana]	Unigene45263_All||8.00E-10||AT5G02420| unknown protein	Unigene45263_All||4.00E-43||DW504073				nr -
Unigene45265_All	1348	6.95	5.26	7.94	12.08	12.90	10.29	5.14	4.96	2.33	-4.01E-01	3.58E-02		1.93E-01	3.37E-01		9.43E-02	5.72E-01		-2.33E-01	1.20E-01		-5.23E-02	8.15E-01		-1.14E+00	1.32E-08	Down	Unigene45265_All|gi|79495605|ref|NP_195054.2||3.00E-40||DNA binding / transcription factor [Arabidopsis thaliana] >gi|75159005|sp|Q8RYD1.1|REM16_ARATH RecName: Full=B3 domain-containing protein REM16; AltName: Full=Protein REPRODUCTIVE MERISTEM 16; AltName: Full=Auxin response factor 36 >gi|20145851|emb|CAD29616.1| auxin response factor 36 [Arabidopsis thaliana]	Unigene45265_All||1.00E-41||AT4G33280| DNA binding / transcription factor	Unigene45265_All||0.00E+00||TC167793	ABI3VP1		GO:0001071||GO:0003676||GO:0006351||GO:0010468||GO:0043231	nr -
Unigene45269_All	3777	3.01	2.94	2.28	8.07	8.08	8.78	9.21	4.50	5.17	-3.31E-02	8.57E-01		-3.96E-01	2.66E-02		1.10E-03	9.96E-01		1.21E-01	2.72E-01		-1.03E+00	6.68E-33	Down	-8.34E-01	6.20E-24		Unigene45269_All|gi|115449999|ref|NP_001048603.1||0.00E+00||Os02g0828900 [Oryza sativa Japonica Group] >gi|113538134|dbj|BAF10517.1| Os02g0828900 [Oryza sativa Japonica Group]	Unigene45269_All||0.00E+00||AT1G62310| transcription factor jumonji (jmjC) domain-containing protein	Unigene45269_All||0.00E+00||TC168567		ko00230|Purine metabolism||ko00240|Pyrimidine metabolism||ko03020|RNA polymerase	GO:0005488	nr +
Unigene4527_All	831	28.90	70.36	28.84	8.51	7.50	10.82	1.07	2.77	1.92	1.28E+00	6.00E-63	Up	-3.20E-03	1.00E+00		-1.83E-01	4.64E-01		3.46E-01	8.73E-02		1.37E+00	4.17E-04	Up	8.44E-01	6.15E-02		Unigene4527_All|gi|91208930|ref|YP_538965.1||3.00E-31||photosystem II protein H [Gossypium hirsutum] >gi|119368528|ref|YP_913216.1| PSII 10kD phosphoprotein [Gossypium barbadense] >gi|122201409|sp|Q2L934.1|PSBH_GOSHI RecName: Full=Photosystem II reaction center protein H; Short=PSII-H; AltName: Full=Photosystem II 10 kDa phosphoprotein >gi|129971532|sp|A0ZZ64.1|PSBH_GOSBA RecName: Full=Photosystem II reaction center protein H; Short=PSII-H; AltName: Full=Photosystem II 10 kDa phosphoprotein >gi|85687444|gb|ABC73656.1| photosystem II phosphoprotein [Gossypium hirsutum] >gi|119224890|dbj|BAF41276.1| PSII 10kD phosphoprotein [Gossypium barbadense]	Unigene4527_All||7.00E-29||ATCG00710| Encodes a 8 kD phosphoprotein that is a component of the photosystem II oxygen evolving core. Its exact molecular function has not been determined but it may play a role in mediating electron transfer between the secondary quinone acceptors, QA and QB, associated with the acceptor side of PSII.	Unigene4527_All||0.00E+00||TC176547		ko00195|Photosynthesis		nr -
Unigene45275_All	997	2.89	3.35	1.01	6.35	8.43	5.07	2.12	1.43	1.36	2.17E-01	5.50E-01		-1.51E+00	1.99E-04	Down	4.09E-01	4.09E-02		-3.23E-01	2.02E-01		-5.73E-01	1.53E-01		-6.42E-01	9.20E-02		Unigene45275_All|gi|147859240|emb|CAN79695.1||2.00E-14||hypothetical protein [Vitis vinifera]		Unigene45275_All||0.00E+00||TC150041				nr -
Unigene45277_All	1128	2.04	1.62	2.83	2.43	1.59	1.32	1.87	2.19	0.57	-3.36E-01	4.24E-01		4.73E-01	2.04E-01		-6.14E-01	9.73E-02		-8.78E-01	2.06E-02		2.22E-01	5.94E-01		-1.73E+00	2.86E-05	Down		Unigene45277_All||5.00E-105||TC150041				
Unigene45279_All	517	8.40	8.43	2.88	6.94	7.46	7.77	4.42	2.26	5.32	5.00E-03	9.85E-01		-1.54E+00	1.67E-06	Down	1.05E-01	8.10E-01		1.64E-01	6.34E-01		-9.64E-01	1.09E-02		2.68E-01	4.44E-01		Unigene45279_All|gi|56126414|gb|AAY76001.1||7.00E-46||cyclin dependent kinase inhibitor [Euphorbia esula]	Unigene45279_All||4.00E-27||AT2G32710| KRP4; cyclin binding / cyclin-dependent protein kinase inhibitor	Unigene45279_All||0.00E+00||TC138998			GO:0000079||GO:0005515||GO:0016538||GO:0022402||GO:0043231	nr -
Unigene45280_All	1221	1.84	4.27	1.44	4.94	3.58	2.89	3.43	3.39	5.94	1.21E+00	7.47E-06	Up	-3.57E-01	4.20E-01		-4.63E-01	4.92E-02		-7.75E-01	1.07E-03		-1.66E-02	9.85E-01		7.93E-01	2.91E-05		Unigene45280_All|gi|56126414|gb|AAY76001.1||3.00E-54||cyclin dependent kinase inhibitor [Euphorbia esula]	Unigene45280_All||2.00E-37||AT2G32710| KRP4; cyclin binding / cyclin-dependent protein kinase inhibitor	Unigene45280_All||0.00E+00||TC138998			GO:0000079||GO:0005515||GO:0043231	nr +
Unigene45281_All	913	2.06	4.72	2.86	5.57	4.56	4.20	0.88	1.46	0.96	1.19E+00	7.34E-05	Up	4.70E-01	2.53E-01		-2.86E-01	3.08E-01		-4.04E-01	1.46E-01		7.35E-01	1.60E-01		1.26E-01	8.48E-01		Unigene45281_All|gi|56126414|gb|AAY76001.1||2.00E-56||cyclin dependent kinase inhibitor [Euphorbia esula]	Unigene45281_All||4.00E-26||AT2G32710| KRP4; cyclin binding / cyclin-dependent protein kinase inhibitor	Unigene45281_All||0.00E+00||DT462384			GO:0005515||GO:0044424||GO:0051726	nr +
Unigene45284_All	1719	132.61	205.60	174.59	45.79	58.51	156.17	4.75	16.70	15.37	6.33E-01	2.35E-115		3.97E-01	6.14E-41		3.54E-01	6.12E-14		1.77E+00	0.00E+00	Up	1.82E+00	3.77E-63	Up	1.69E+00	5.06E-54	Up	Unigene45284_All|gi|60459560|gb|AAX18166.2||0.00E+00||CNGC2 [Gossypium hirsutum]	Unigene45284_All||0.00E+00||AT5G15410| DND1 (DEFENSE NO DEATH 1); calcium channel/ calmodulin binding / cation channel/ cyclic nucleotide binding / intracellular cAMP activated cation channel/ intracellular cyclic nucleotide activated cation channel/ inward rectifier potassium channel	Unigene45284_All||0.00E+00||TC129570		ko04626|Plant-pathogen interaction	GO:0006810||GO:0015075||GO:0031224	nr +
Unigene45285_All	2564	40.38	65.06	70.59	14.01	17.42	48.49	2.14	3.80	4.04	6.88E-01	1.88E-63		8.06E-01	6.09E-88		3.14E-01	2.67E-05		1.79E+00	1.17E-233	Up	8.25E-01	5.68E-07		9.14E-01	7.45E-09		Unigene45285_All|gi|60459560|gb|AAX18166.2||0.00E+00||CNGC2 [Gossypium hirsutum]	Unigene45285_All||0.00E+00||AT5G15410| DND1 (DEFENSE NO DEATH 1); calcium channel/ calmodulin binding / cation channel/ cyclic nucleotide binding / intracellular cAMP activated cation channel/ intracellular cyclic nucleotide activated cation channel/ inward rectifier potassium channel	Unigene45285_All||0.00E+00||TC129570		ko04626|Plant-pathogen interaction	GO:0000166||GO:0005221||GO:0005249||GO:0005515||GO:0006810||GO:0023033||GO:0031224||GO:0033554||GO:0043231	nr +
Unigene4529_All	768	27.93	22.30	36.05	1.36	0.94	0.00	2.70	3.27	2.39	-3.25E-01	6.97E-03		3.68E-01	6.05E-04		-5.33E-01	4.27E-01		-1.04E+01	1.47E-06	Down	2.76E-01	4.80E-01		-1.77E-01	6.47E-01		Unigene4529_All|gi|89258498|gb|ABD65462.1||3.00E-68||short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene4529_All||7.00E-47||AT1G52340| ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase	Unigene4529_All||0.00E+00||TC136345		ko00906|Carotenoid biosynthesis		nr -
Unigene45291_All	2321	0.00	0.17	0.18	0.32	0.91	2.63	3.84	21.20	15.81	7.45E+00	1.36E-02		7.52E+00	1.38E-02		1.49E+00	9.31E-04	Up	3.03E+00	1.08E-21	Up	2.46E+00	9.59E-159	Up	2.04E+00	6.79E-96	Up	Unigene45291_All|gi|223452548|gb|ACM89601.1||1.00E-112||disease resistance protein [Glycine max]	Unigene45291_All||1.00E-93||AT3G05660| ArRLP33 (Receptor Like Protein 33); kinase/ protein binding	Unigene45291_All||6.00E-106||BF275400				nr +
Unigene45292_All	335	2.19	0.61	6.04	3.87	1.44	0.00	0.00	0.00	0.00	-1.85E+00	4.08E-02		1.47E+00	3.00E-03		-1.43E+00	1.25E-02		-1.19E+01	4.24E-08	Down	null	null		null	null		Unigene45292_All|gi|223452508|gb|ACM89581.1||2.00E-08||disease resistance protein [Glycine max]	Unigene45292_All||2.00E-08||ATIG45616| ArRLP6 (Receptor Like Protein 6); protein binding				GO:0003824	nr -
Unigene45293_All	906	0.00	0.22	0.71	0.22	1.79	1.30	3.31	25.93	18.73	7.81E+00	1.36E-01		9.46E+00	1.16E-03		3.02E+00	2.63E-06	Up	2.56E+00	6.34E-04	Up	2.97E+00	3.96E-93	Up	2.50E+00	3.58E-57	Up	Unigene45293_All|gi|15240433|ref|NP_198058.1||8.00E-16||ArRLP53 (Receptor Like Protein 53); kinase/ protein binding [Arabidopsis thaliana] >gi|5732036|gb|AAD48937.1|AF160760_5 similar to disease resistance proteins; contains similarity ot Pfam family PF00560 - Leucine Rich Repeat; score=166.7, E-4e-46, N-24 [Arabidopsis thaliana]	Unigene45293_All||1.00E-13||AT5G27060| ArRLP53 (Receptor Like Protein 53); kinase/ protein binding	Unigene45293_All||3.00E-170||TC148848		ko04626|Plant-pathogen interaction	GO:0003824	nr -
Unigene45294_All	2418	0.02	0.04	0.26	1.55	0.70	0.28	1.64	3.27	1.98	9.56E-01	7.25E-01		3.61E+00	6.97E-03		-1.15E+00	1.16E-04	Down	-2.46E+00	3.44E-11	Down	9.91E-01	1.31E-07		2.67E-01	2.98E-01		Unigene45294_All|gi|164605529|dbj|BAF98595.1||7.00E-124||CM0545.400.nc [Lotus japonicus]	Unigene45294_All||1.00E-105||AT3G24982| protein binding	Unigene45294_All||2.00E-155||BF275400		ko04626|Plant-pathogen interaction		nr -
Unigene45295_All	2139	0.32	0.50	0.57	7.01	3.03	2.98	7.49	16.26	6.74	6.46E-01	3.37E-01		8.49E-01	1.85E-01		-1.21E+00	1.39E-18	Down	-1.24E+00	6.08E-17	Down	1.12E+00	3.01E-37	Up	-1.52E-01	2.56E-01		Unigene45295_All|gi|223452548|gb|ACM89601.1||1.00E-101||disease resistance protein [Glycine max]	Unigene45295_All||2.00E-83||AT2G33060| ArRLP27 (Receptor Like Protein 27); kinase/ protein binding	Unigene45295_All||2.00E-108||gi|164270527|gb|EV491261.1|EV491261				nr -

Unigene45297_All	1006	2.91	21.05	4.50	9.26	7.98	9.11	15.09	32.20	31.80	2.85E+00	9.54E-66	Up	6.27E-01	3.50E-02		-2.15E-01	3.05E-01		-2.30E-02	9.32E-01		1.09E+00	1.42E-33	Up	1.08E+00	4.57E-33	Up	Unigene45297_All//gi|5080804|gb|AAD39313.1|AC007258_2//5.00E-67//Hypothetical protein [Arabidopsis thaliana] >gi|15010642|gb|AAK73980.1| At1g59710/T30E16_31 [Arabidopsis thaliana] >gi|22137290|gb|AAM91490.1| At1g59710/T30E16_31 [Arabidopsis thaliana]	Unigene45297_All//2.00E-66//AT1G59710| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27100.1); Has 119 Blast hits to 107 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 119; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene45297_All//0.00E+00//TC155105				nr -
Unigene45298_All	2719	5.04	26.37	5.27	12.37	10.85	12.36	22.14	38.72	40.82	2.39E+00	1.77E-181	Up	6.34E-02	6.98E-01		-1.88E-01	4.84E-02		-1.00E-03	9.91E-01		8.06E-01	8.78E-65		8.82E-01	2.69E-81		Unigene45298_All//gi|190016000|gb|ACE62888.1|//1.00E-155//At1g27100 [Arabidopsis thaliana]	Unigene45298_All//9.00E-110//AT1G59710| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27100.1); Has 119 Blast hits to 107 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 119; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene45298_All//0.00E+00//TC155105				nr +
Unigene4530_All	1007	19.43	19.67	31.94	0.59	0.31	0.31	3.69	3.98	1.46	1.79E-02	9.08E-01		7.17E-01	3.21E-13		-9.48E-01	3.09E-01		-9.19E-01	3.51E-01		1.09E-01	7.22E-01		-1.34E+00	3.42E-06	Down	Unigene4530_All//gi|89258498|gb|ABD65462.1|//5.00E-90//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene4530_All//2.00E-51//AT4G03140| binding / catalytic/ oxidoreductase	Unigene4530_All//0.00E+00//TC136345		ko00906|Carotenoid biosynthesis		nr -
Unigene45302_All	2679	7.13	14.53	3.34	9.84	11.27	12.48	20.91	19.13	40.18	1.03E+00	1.11E-29	Up	-1.09E+00	7.38E-16	Down	1.97E-01	5.49E-02		3.43E-01	1.88E-04		-1.29E-01	6.15E-02		9.42E-01	5.81E-88		Unigene45302_All//gi|30678365|ref|NP_850592.1|//0.00E+00//DRH1 (DEAD BOX RNA HELICASE 1); ATP-dependent RNA helicase/ ATPase [Arabidopsis thaliana] >gi|42572223|ref|NP_974206.1| DRH1 (DEAD BOX RNA HELICASE 1); ATP-dependent RNA helicase/ ATPase [Arabidopsis thaliana] >gi|79295442|ref|NP_001030619.1| DRH1 (DEAD BOX RNA HELICASE 1); ATP-dependent RNA helicase/ ATPase [Arabidopsis thaliana] >gi|108861885|sp|Q8RH36.2|RH14_ARATH RecName: Full=DEAD-box ATP-dependent RNA helicase 14 >gi|6016713|gb|AAF01539.1|AC009325_9 RNA helicase, DRH1 [Arabidopsis thaliana] >gi|3149952|dbj|BAA28347.1| DRH1 [Arabidopsis thaliana]	Unigene45302_All//0.00E+00//AT3G01540| DRH1 (DEAD BOX RNA HELICASE 1); ATP-dependent RNA helicase/ ATPase	Unigene45302_All//0.00E+00//TC155883		ko03040|Spliceosome	GO:0003676//GO:0032559//GO:0042623	nr -
Unigene45303_All	2232	0.38	0.86	0.33	0.47	0.65	0.36	1.48	0.69	1.37	1.20E+00	1.19E-02		-1.67E-01	8.16E-01		4.67E-01	4.44E-01		-3.64E-01	6.33E-01		-1.09E+00	3.88E-04	Down	-1.04E-01	7.36E-01		Unigene45303_All//gi|7573310|emb|CAB87628.1|//0.00E+00//DRH1 DEAD box protein-like [Arabidopsis thaliana]	Unigene45303_All//9.00E-177//AT5G14610| ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding / protein binding	Unigene45303_All//0.00E+00//TC155883		ko03040|Spliceosome	GO:0003676//GO:0032559//GO:0042623	nr +
Unigene45306_All	2823	0.69	1.62	1.60	2.03	2.92	1.10	1.21	1.30	2.48	1.24E+00	2.44E-05	Up	1.23E+00	5.33E-05	Up	5.23E-01	7.70E-03		-8.78E-01	3.18E-04		1.03E-01	7.36E-01		1.03E+00	1.71E-07	Up	Unigene45306_All//gi|42568139|ref|NP_568527.2|//0.00E+00//DENN (AEX-3) domain-containing protein [Arabidopsis thaliana]	Unigene45306_All//0.00E+00//AT5G35560| DENN (AEX-3) domain-containing protein	Unigene45306_All//0.00E+00//TC165549				nr +
Unigene4531_All	1737	0.81	1.95	0.98	3.50	1.98	1.90	5.79	3.61	3.78	1.26E+00	2.63E-04	Up	2.71E-01	6.27E-01		-8.20E-01	2.30E-04		-8.82E-01	1.82E-04		-6.83E-01	2.11E-05		-6.14E-01	8.44E-05		Unigene4531_All//gi|240254318|ref|NP_176659.6|//0.00E+00//binding [Arabidopsis thaliana]	Unigene4531_All//1.00E-174//AT1G64790| binding					nr +
Unigene45314_All	2982	1.05	1.12	0.43	3.83	3.30	2.62	4.11	4.86	4.53	9.13E-02	7.83E-01		-1.30E+00	5.92E-04	Down	-2.12E-01	2.46E-01		-5.46E-01	9.44E-04		2.42E-01	8.31E-02		1.39E-01	3.61E-01		Unigene45314_All//gi|225016138|gb|ACN78962.1|//0.00E+00//methyltransferase [Glycine max]	Unigene45314_All//0.00E+00//AT2G45750| dehydration-responsive family protein	Unigene45314_All//0.00E+00//ES801170			GO:0016741//GO:0043231	nr +
Unigene45315_All	3839	1.16	0.67	0.36	2.76	3.30	2.44	1.52	1.30	1.63	-7.83E-01	6.26E-03		-1.68E+00	1.92E-07	Down	2.56E-01	1.28E-01		-1.83E-01	3.75E-01		-2.30E-01	3.51E-01		1.00E-01	6.51E-01		Unigene45315_All//gi|124360854|gb|ABN08826.1|//0.00E+00//Generic methyltransferase [Medicago truncatula]	Unigene45315_All//0.00E+00//AT4G00750| dehydration-responsive family protein	Unigene45315_All//0.00E+00//TC163242			GO:0016741//GO:0043231	nr +
Unigene45316_All	2527	7.64	28.65	26.72	21.29	30.78	42.95	25.72	53.59	87.31	1.91E+00	6.18E-138	Up	1.81E+00	1.02E-116	Up	5.32E-01	1.47E-22		1.01E+00	1.04E-85	Up	1.06E+00	5.82E-131	Up	1.76E+00	0.00E+00	Up	Unigene45316_All//gi|297845328|ref|XP_002890545.1|//0.00E+00//T-complex protein 11 [Arabidopsis lyrata subsp. lyrata] >gi|297336387|gb|EFH66804.1| T-complex protein 11 [Arabidopsis lyrata subsp. lyrata]	Unigene45316_All//2.00E-169//AT1G22930| T-complex protein 11	Unigene45316_All//0.00E+00//gi|78336347|gb|DT556621.1|DT556621				nr +
Unigene45317_All	1978	1.88	1.13	0.75	4.91	5.19	4.45	10.47	5.62	7.33	-7.37E-01	2.03E-02		-1.32E+00	1.24E-04	Down	7.92E-02	7.38E-01		-1.41E-01	5.17E-01		-8.98E-01	5.86E-16		-5.15E-01	9.74E-07		Unigene45317_All//gi|297806263|ref|XP_002871015.1|//1.00E-130//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316852|gb|EFH47274.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45317_All//8.00E-105//AT5G03150| JKD (JACKDAW); nucleic acid binding / protein binding / protein homodimerization/ transcription factor/ zinc ion binding	Unigene45317_All//0.00E+00//C0086205	C2H2			nr +
Unigene45318_All	2183	2.64	2.58	1.88	28.30	21.04	11.88	7.63	6.03	7.77	-3.32E-02	9.06E-01		-4.89E-01	6.17E-02		-4.27E-01	1.91E-12		-1.25E+00	1.12E-69	Down	-3.40E-01	6.07E-03		2.68E-02	8.51E-01		Unigene45318_All//gi|297806263|ref|XP_002871015.1|//1.00E-132//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316852|gb|EFH47274.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45318_All//4.00E-106//AT5G03150| JKD (JACKDAW); nucleic acid binding / protein binding / protein homodimerization/ transcription factor/ zinc ion binding	Unigene45318_All//0.00E+00//TC134374	C2H2			nr -
Unigene4532_All	691	26.05	14.81	13.18	29.92	31.69	38.50	41.91	17.06	17.87	-8.14E-01	7.30E-10		-9.83E-01	1.13E-12		8.32E-02	5.74E-01		3.64E-01	4.87E-04		-1.30E+00	2.86E-39	Down	-1.23E+00	2.85E-37	Down	Unigene4532_All//gi|297829086|ref|XP_002882425.1|//2.00E-55//60S ribosomal protein L22-2 [Arabidopsis lyrata subsp. lyrata] >gi|297328265|gb|EFH58684.1| 60S ribosomal protein L22-2 [Arabidopsis lyrata subsp. lyrata]	Unigene4532_All//3.00E-46//AT3G05560| 60S ribosomal protein L22-2 (RPL22B)	Unigene4532_All//0.00E+00//TC146241		ko03010|Ribosome		nr -
Unigene45320_All	808	5.63	5.20	5.07	13.62	9.50	6.37	5.91	3.47	2.07	-1.14E-01	6.85E-01		-1.51E-01	6.33E-01		-5.20E-01	1.22E-03		-1.10E+00	1.64E-10	Down	-7.71E-01	1.67E-03		-1.51E+00	4.06E-09	Down	Unigene45320_All//gi|124359162|gb|ABN05685.1|//4.00E-09//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene45320_All//2.00E-09//AT3G25270| nucleic acid binding	Unigene45320_All//2.00E-165//gi|13246243|gb|BE052538.2|BE052538			GO:0005488	nr -
Unigene45321_All	301	2.96	0.17	1.59	4.14	3.43	2.40	1.26	0.14	1.46	-4.13E+00	2.52E-04	Down	-8.92E-01	2.46E-01		-2.70E-01	6.54E-01		-7.85E-01	2.08E-01		-3.19E+00	3.11E-02		2.04E-01	8.26E-01		Unigene45321_All//gi|53370641|gb|AAB89136.1|//2.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene45321_All//3.00E-05//AT5G65005| nucleic acid binding	Unigene45321_All//4.00E-22//DW509391				nr -
Unigene45323_All	718	1.68	3.03	3.34	9.64	7.10	4.28	1.41	1.57	1.11	8.56E-01	4.88E-02		9.94E-01	2.16E-02		-4.42E-01	4.19E-02		-1.17E+00	1.47E-07	Down	1.53E-01	7.89E-01		-3.49E-01	5.71E-01		Unigene45323_All//gi|15230827|ref|NP_189164.1|//4.00E-12//nucleic acid binding [Arabidopsis thaliana] >gi|9294184|dbj|BAB02086.1| reverse transcriptase-like protein [Arabidopsis thaliana]	Unigene45323_All//2.00E-13//AT3G25270| nucleic acid binding	Unigene45323_All//7.00E-134//gi|164309269|gb|ES848422.1|ES848422				nr -
Unigene45325_All	1111	4.99	4.79	4.22	10.76	7.50	5.00	4.72	2.14	0.90	-6.00E-02	8.15E-01		-2.43E-01	4.04E-01		-5.21E-01	6.63E-04		-1.11E+00	1.64E-11	Down	-1.14E+00	1.83E-06	Down	-2.40E+00	1.28E-17	Down	Unigene45325_All//gi|15230827|ref|NP_189164.1|//5.00E-11//nucleic acid binding [Arabidopsis thaliana] >gi|9294184|dbj|BAB02086.1| reverse transcriptase-like protein [Arabidopsis thaliana]	Unigene45325_All//3.00E-13//AT3G25270| nucleic acid binding	Unigene45325_All//0.00E+00//DW509391				nr +
Unigene45326_All	1593	27.85	37.18	38.84	12.63	11.15	8.65	15.71	6.93	3.05	4.17E-01	9.21E-10		4.80E-01	2.05E-12		-1.80E-01	1.74E-01		-5.47E-01	4.39E-06		-1.18E+00	1.61E-29	Down	-2.36E+00	6.69E-80	Down	Unigene45326_All//gi|87162706|gb|ABD28501.1|//2.00E-39//Zinc finger, C2H2-type [Medicago truncatula]	Unigene45326_All//1.00E-12//AT3G13810| AtIDD11 (Arabidopsis thaliana Indeterminate(ID)-Domain 11); nucleic acid binding / transcription factor/ zinc ion binding	Unigene45326_All//0.00E+00//TC137344	C2H2			nr +
Unigene45327_All	2064	16.60	16.52	22.01	6.44	5.02	3.35	7.48	4.54	2.20	-7.20E-03	9.65E-01		4.06E-01	5.02E-07		-3.60E-01	1.68E-02		-9.45E-01	5.72E-10		-7.21E-01	1.48E-08		-1.76E+00	4.09E-34	Down	Unigene45327_All//gi|87162706|gb|ABD28501.1|//1.00E-125//Zinc finger, C2H2-type [Medicago truncatula]	Unigene45327_All//5.00E-100//AT1G55110| AtIDD7 (Arabidopsis thaliana Indeterminate(ID)-Domain 7); nucleic acid binding / transcription factor/ zinc ion binding	Unigene45327_All//0.00E+00//TC137344	C2H2			nr +
Unigene45328_All	790	0.93	1.48	1.35	2.27	4.18	2.92	0.91	1.48	3.88	6.70E-01	2.88E-01		5.40E-01	4.18E-01		8.82E-01	7.99E-03		3.61E-01	4.38E-01		7.03E-01	2.23E-01		2.09E+00	5.22E-09	Up	Unigene45328_All//gi|9280693|gb|AAF86562.1|AC069252_21//1.00E-69//F2E2.8 [Arabidopsis thaliana]	Unigene45328_All//3.00E-48//AT1G22030| unknown protein	Unigene45328_All//0.00E+00//TC151778				nr -
Unigene45329_All	1321	2.02	5.33	2.66	10.18	9.33	4.51	3.65	1.49	1.75	1.40E+00	2.74E-09	Up	3.97E-01	2.55E-01		-1.26E-01	4.96E-01		-1.17E+00	4.10E-14	Down	-1.29E+00	3.54E-07	Down	-1.06E+00	1.16E-05	Down	Unigene45329_All//gi|9280693|gb|AAF86562.1|AC069252_21//2.00E-95//F2E2.8 [Arabidopsis thaliana]	Unigene45329_All//6.00E-84//AT1G22030| unknown protein	Unigene45329_All//0.00E+00//gi|48802618|gb|CO103932.1|CO103932				nr -
Unigene4533_All	1198	3.32	2.75	1.96	6.74	7.50	3.51	2.44	1.12	1.43	-2.72E-01	3.79E-01		-7.63E-01	1.70E-02		1.55E-01	5.09E-01		-9.42E-01	2.77E-06		-1.13E+00	6.78E-04	Down	-7.68E-01	1.46E-02		Unigene4533_All//gi|225130299|ref|XP_002285150.1|//3.00E-75//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene4533_All//6.00E-41//AT4G32295| unknown protein	Unigene4533_All//0.00E+00//TC137158				nr +
Unigene45330_All	1355	6.29	3.59	4.44	21.21	13.85	9.47	6.15	2.19	1.94	-8.10E-01	4.51E-05		-5.03E-01	1.54E-02		-6.15E-01	2.49E-11		-1.16E+00	3.84E-29	Down	-1.49E+00	1.98E-14	Down	-1.66E+00	2.28E-17	Down	Unigene45330_All//gi|9280693|gb|AAF86562.1|AC069252_21//1.00E-105//F2E2.8 [Arabidopsis thaliana]	Unigene45330_All//2.00E-82//AT1G22030| unknown protein	Unigene45330_All//0.00E+00//gi|78343566|gb|DT563840.1|DT563840				nr +

Unigene45331_All	4438	2.61	2.23	1.62	6.42	6.83	4.94	6.20	2.84	5.09	-2.27E-01	2.05E-01			-6.86E-01	7.31E-05		8.88E-02	4.61E-01			-3.79E-01	1.37E-04		-1.12E+00	5.54E-30	Down	-2.85E-01	1.78E-03		Unigene45331_All//gi|224141893|ref|XP_002324295.1|//0.00E+00//rna-dependent RNA polymerase [Populus trichocarpa] >gi|222865729|gb|EEF02860.1| rna-dependent RNA polymerase [Populus trichocarpa]	Unigene45331_All//0.00E+00//AT3G49500| RDR6 (RNA-DEPENDENT RNA POLYMERASE 6); RNA-directed RNA polymerase/ nucleic acid binding	Unigene45331_All//0.00E+00//TC179533			GO:0002252//GO:0005488//GO:0008037//GO:0030422//GO:0034062//GO:0035195//GO:0043231//GO:0045087//GO:0048437//GO:0048438//GO:0048827	nr +
Unigene45333_All	1045	3.71	1.16	0.97	2.81	2.83	2.85	3.40	2.28	2.59	-1.67E+00	7.24E-07	Down	-1.94E+00	8.43E-08	Down	1.09E-02	9.89E-01			2.03E-02	9.53E-01		-5.76E-01	5.03E-02		-3.91E-01	1.78E-01		Unigene45333_All//gi|42569151|ref|NP_179539.2|//7.00E-81//recA family protein [Arabidopsis thaliana] >gi|209572665|sp|Q9ZUP2.2|RECA3_ARATH RecName: Full=DNA repair protein recA homolog 3, mitochondrial; AltName: Full=Recombinase A homolog 3; Flags: Precursor >gi|199935859|gb|ABM06015.1| At2g19490 [Arabidopsis thaliana]	Unigene45333_All//8.00E-57//AT2G19490| recA family protein	Unigene45333_All//0.00E+00//TC139777		ko03440|Homologous recombination	GO:0006259//GO:0031668//GO:0032559//GO:0033554//GO:0042623//GO:0043231//GO:0043566	nr -
Unigene45334_All	1898	3.09	1.31	3.84	4.65	3.97	6.12	6.55	3.19	3.78	-1.24E+00	1.10E-06	Down	3.16E-01	1.80E-01		-2.26E-01	2.94E-01			3.97E-01	1.93E-02		-1.04E+00	2.39E-12	Down	-7.94E-01	1.85E-08		Unigene45334_All//gi|42569151|ref|NP_179539.2|//1.00E-164//recA family protein [Arabidopsis thaliana] >gi|209572665|sp|Q9ZUP2.2|RECA3_ARATH RecName: Full=DNA repair protein recA homolog 3, mitochondrial; AltName: Full=Recombinase A homolog 3; Flags: Precursor >gi|199935859|gb|ABM06015.1| At2g19490 [Arabidopsis thaliana]	Unigene45334_All//6.00E-147//AT2G19490| recA family protein	Unigene45334_All//0.00E+00//ES803232		ko03440|Homologous recombination	GO:0005488//GO:0006259	nr -
Unigene45337_All	2269	5.88	2.77	6.50	9.15	7.83	4.08	4.06	3.17	1.97	-1.09E+00	1.12E-11	Down	1.45E-01	3.89E-01		-2.25E-01	6.99E-02		-1.17E+00	2.91E-21	Down	-3.59E-01	3.96E-02		-1.05E+00	7.94E-10	Down	Unigene45337_All//gi|224112164|ref|XP_002332822.1|//2.00E-66//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834210|gb|EEE72687.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene45337_All//1.00E-32//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene45337_All//0.00E+00//DT457825		ko04626|Plant-pathogen interaction		nr +
Unigene45339_All	556	8.47	4.28	9.67	11.02	10.65	4.71	2.97	4.21	2.79	-9.84E-01	4.43E-04		1.92E-01	5.07E-01		-4.89E-02	8.47E-01		-1.23E+00	3.31E-07	Down	5.05E-01	1.88E-01		-8.58E-02	8.50E-01		Unigene45339_All//gi|15230827|ref|NP_189164.1|//3.00E-07//nucleic acid binding [Arabidopsis thaliana] >gi|9294184|dbj|BAB02086.1| reverse transcriptase-like protein [Arabidopsis thaliana]	Unigene45339_All//2.00E-08//AT3G25270| nucleic acid binding	Unigene45339_All//1.00E-128//TC137783				nr +
Unigene4534_All	918	11.40	10.27	7.02	12.21	12.98	11.56	7.42	15.21	9.50	-1.51E-01	4.27E-01			-7.00E-01	1.32E-04		8.82E-02	6.59E-01		-7.87E-02	6.74E-01		1.04E+00	9.66E-14	Up	3.58E-01	3.87E-02		Unigene4534_All//gi|9802527|gb|AAF99729.1|AC004557_8//7.00E-22//F17L21.9 [Arabidopsis thaliana] >gi|15450914|gb|AAK96728.1| Unknown protein [Arabidopsis thaliana]	Unigene4534_All//1.00E-17//AT1G27300| unknown protein	Unigene4534_All//0.00E+00//C0097590				nr +
Unigene45341_All	1872	6.32	2.95	6.57	7.08	6.40	4.66	2.53	2.08	1.34	-1.10E+00	1.31E-10	Down	5.70E-02	7.47E-01		-1.45E-01	4.21E-01		-6.04E-01	6.07E-05		-2.85E-01	2.88E-01		-9.16E-01	1.44E-04		Unigene45341_All//gi|124360549|gb|ABD33126.2|//2.00E-47//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene45341_All//8.00E-25//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene45341_All//5.00E-177//TC144144			GO:0003676//GO:0016772//GO:0044238//GO:0044260	nr -
Unigene45346_All	753	13.48	7.07	12.80	6.35	5.58	9.18	4.89	1.44	1.01	-9.32E-01	3.14E-07		-7.47E-02	7.04E-01		-1.87E-01	5.41E-01		5.31E-01	1.82E-02		-1.76E+00	1.99E-08	Down	-2.28E+00	6.41E-12	Down			Unigene45346_All//5.00E-175//gi|13248268|gb|BF275009.2|BF275009					
Unigene45347_All	1656	99.65	49.26	57.59	133.41	111.25	74.40	87.57	111.00	35.20	-1.02E+00	4.55E-122	Down	-7.91E-01	1.37E-77		-2.62E-01	1.78E-17		-8.43E-01	2.53E-129		3.42E-01	1.93E-24		-1.32E+00	1.91E-203	Down	Unigene45347_All//gi|263202219|gb|ACT70395.1|//0.00E+00//heterotrophic ferredoxin NADP+ oxidoreductase [Populus tremula x Populus tremuloides]	Unigene45347_All//1.00E-171//AT1G30510| ATRFNR2 (ROOT FNR 2); FAD binding / NADP or NADPH binding / electron carrier/ ferredoxin-NADP+ reductase/ oxidoreductase	Unigene45347_All//0.00E+00//TC150723		ko00195|Photosynthesis	GO:0008152//GO:0008937//GO:0030554//GO:0034357	nr +
Unigene45348_All	567	28.42	10.72	15.97	15.99	10.51	5.89	7.76	5.90	6.67	-1.41E+00	1.60E-20	Down	-8.32E-01	8.75E-09		-6.06E-01	6.70E-04		-1.44E+00	4.21E-13	Down	-3.95E-01	1.40E-01		-2.16E-01	4.20E-01		Unigene45348_All//gi|297796399|ref|XP_002866084.1|//4.00E-60//ftsz1-1 [Arabidopsis lyrata subsp. lyrata] >gi|297311919|gb|EFH42343.1| ftsz1-1 [Arabidopsis lyrata subsp. lyrata]	Unigene45348_All//2.00E-56//AT5G55280| FTSZ1-1; protein binding / structural molecule	Unigene45348_All//0.00E+00//TC131361			GO:0005515//GO:0009532//GO:0009658//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623//GO:0048285	nr -
Unigene45349_All	1182	11.29	4.54	6.26	5.06	3.64	2.48	5.04	1.98	2.93	-1.31E+00	1.73E-15	Down	-8.50E-01	1.22E-07		-4.74E-01	4.44E-02		-1.03E+00	1.83E-05	Down	-1.35E+00	3.32E-09	Down	-7.82E-01	1.97E-04		Unigene45349_All//gi|283993128|gb|ADB57040.1|//1.00E-153//plastid-dividing ring protein [Solanum lycopersicum]	Unigene45349_All//6.00E-120//AT5G55280| FTSZ1-1; protein binding / structural molecule	Unigene45349_All//0.00E+00//TC131361				nr +
Unigene45350_All	1731	5.89	3.40	4.15	3.48	2.73	2.95	1.95	1.38	0.76	-7.96E-01	9.49E-06		-5.05E-01	6.98E-03		-3.54E-01	1.54E-01		-2.40E-01	3.87E-01		-5.06E-01	9.85E-02		-1.36E+00	7.36E-06	Down	Unigene45350_All//gi|15240490|ref|NP_200339.1|//0.00E+00//FTSZ1-1; protein binding / structural molecule [Arabidopsis thaliana] >gi|21903428|sp|Q42545.2|FTSZ_ARATH RecName: Full=Cell division protein ftsZ homolog, chloroplastic; Flags: Precursor >gi|9758125|dbj|BAB08597.1| cell division protein FtsZ chloroplast homolog precursor [Arabidopsis thaliana]	Unigene45350_All//6.00E-146//AT5G55280| FTSZ1-1; protein binding / structural molecule	Unigene45350_All//0.00E+00//TC131361			GO:0005515//GO:0009532//GO:0009658//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623//GO:0048285	nr +
Unigene45351_All	1746	11.00	3.63	6.22	5.39	7.10	4.60	4.14	2.20	2.51	-1.60E+00	2.73E-29	Down	-8.22E-01	3.88E-10		3.97E-01	1.18E-02		-2.28E-01	2.79E-01		-9.11E-01	3.16E-06		-7.22E-01	1.25E-04		Unigene45351_All//gi|297796399|ref|XP_002866084.1|//0.00E+00//ftsz1-1 [Arabidopsis lyrata subsp. lyrata] >gi|297311919|gb|EFH42343.1| ftsz1-1 [Arabidopsis lyrata subsp. lyrata]	Unigene45351_All//4.00E-136//AT5G55280| FTSZ1-1; protein binding / structural molecule	Unigene45351_All//0.00E+00//TC141123			GO:0005515//GO:0009532//GO:0009658//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623//GO:0048285	nr +
Unigene45352_All	2188	14.42	108.26	36.31	33.97	87.39	130.85	91.98	168.71	165.67	2.91E+00	0.00E+00	Up	1.33E+00	5.25E-88	Up	1.36E+00	1.34E-266	Up	1.95E+00	0.00E+00	Up	8.75E-01	3.61E-259		8.49E-01	4.87E-247		Unigene45352_All//gi|32364482|gb|AAO61674.1|//1.00E-83//AKIN gamma [Medicago truncatula]	Unigene45352_All//1.00E-67//AT3G48530| KING1 (SNF1-RELATED PROTEIN KINASE REGULATORY SUBUNIT GAMMA 1)	Unigene45352_All//0.00E+00//TC130551			GO:0005618//GO:0016772	nr +
Unigene45353_All	1577	1.69	5.82	3.58	5.24	4.11	3.15	3.91	3.63	3.81	1.78E+00	1.71E-16	Up	1.08E+00	4.32E-05	Up	-3.53E-01	8.16E-02		-7.35E-01	1.91E-04		-1.08E-01	6.40E-01		-3.72E-02	8.79E-01		Unigene45353_All//gi|18406854|ref|NP_566051.1|//1.00E-108//calcineurin B subunit-related [Arabidopsis thaliana]	Unigene45353_All//1.00E-109//AT2G45670| calcineurin B subunit-related	Unigene45353_All//0.00E+00//C0129543		ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism	GO:0003824	nr +
Unigene45355_All	688	15.21	16.06	20.97	5.29	5.76	4.33	3.81	2.79	0.58	7.81E-02	6.68E-01		4.64E-01	2.55E-03		1.23E-01	7.57E-01		-2.87E-01	4.20E-01		-4.47E-01	2.20E-01		-2.72E+00	1.79E-10	Down	Unigene45355_All//gi|22328777|ref|NP_193616.2|//5.00E-20//binding / catalytic/ transcription repressor [Arabidopsis thaliana] >gi|30725402|gb|AP37723.1| At4g18810 [Arabidopsis thaliana]	Unigene45355_All//8.00E-20//AT4G18810| binding / catalytic/ transcription repressor	Unigene45355_All//0.00E+00//gi|164281005|gb|ES828512.1|ES828512			GO:0009536//GO:0019740//GO:0030528	nr -
Unigene45356_All	2165	106.62	92.28	116.29	52.41	51.01	40.47	6.37	4.54	2.80	-2.08E-01	3.37E-10		1.25E-01	2.13E-04		-3.92E-02	5.48E-01		-3.73E-01	9.16E-16		-4.89E-01	2.87E-04		-1.19E+00	2.97E-17	Down	Unigene45356_All//gi|297800180|ref|XP_002867974.1|//0.00E+00//transcriptional repressor [Arabidopsis lyrata subsp. lyrata] >gi|297313810|gb|EFH44233.1| transcriptional repressor [Arabidopsis lyrata subsp. lyrata]	Unigene45356_All//0.00E+00//AT4G18810| binding / catalytic/ transcription repressor	Unigene45356_All//0.00E+00//TC145307			GO:0009536//GO:0019740//GO:0030528	nr -
Unigene45358_All	824	5.21	4.06	6.07	9.73	19.52	19.84	15.55	6.14	13.20	-3.59E-01	2.35E-01		2.22E-01	4.44E-01		1.00E+00	4.41E-14	Up	1.03E+00	1.14E-13	Up	-1.34E+00	1.04E-18	Down	-2.36E-01	1.02E-01		Unigene45358_All//gi|224110774|ref|XP_002315633.1|//7.00E-48//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222861673|gb|EEF01804.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene45358_All//1.00E-31//AT3G13100| ATMRP7; ATPase, coupled to transmembrane movement of substances			ko02010|ABC transporters	GO:0005576//GO:0005773//GO:0006810//GO:0009607//GO:0016491//GO:0022891//GO:0031090//GO:0031224//GO:0031410//GO:0032559//GO:0071997	nr +
Unigene45359_All	2139	1.76	1.80	2.32	4.17	5.91	7.24	6.70	2.21	7.67	3.18E-02	9.36E-01		3.95E-01	1.72E-01		5.03E-01	8.86E-04		7.97E-01	1.08E-08		-1.60E+00	6.46E-27	Down	1.96E-01	1.26E-01		Unigene45359_All//gi|224102345|ref|XP_002312645.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222852465|gb|EEE90012.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene45359_All//0.00E+00//AT3G13080| ATMRP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase	Unigene45359_All//2.00E-179//gi|3326796|gb|AI055682.1|AI055682		ko02010|ABC transporters	GO:0005576//GO:0005773//GO:0006810//GO:0016491//GO:0022891//GO:0031090//GO:0031410//GO:0032559//GO:0043234//GO:0044425//GO:0071997	nr +
Unigene45360_All	4387	1.55	1.44	2.16	2.19	4.87	4.47	5.73	2.16	5.52	-1.03E-01	6.55E-01		4.79E-01	1.43E-02		1.15E+00	3.63E-23	Up	1.03E+00	2.81E-16	Up	-1.41E+00	1.20E-38	Down	-5.46E-02	6.30E-01		Unigene45360_All//gi|224102345|ref|XP_002312645.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222852465|gb|EEE90012.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene45360_All//0.00E+00//AT3G13080| ATMRP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase	Unigene45360_All//0.00E+00//gi|109850911|gb|DW479890.1|DW479890		ko02010|ABC transporters	GO:0004888//GO:0005773//GO:0006810//GO:0006875//GO:0006970//GO:0015405//GO:0016491//GO:0017111//GO:0031090//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene45361_All	3532	0.65	0.39	0.72	0.93	1.67	1.59	1.83	0.43	1.02	-7.51E-01	7.36E-02		1.51E-01	7.03E-01		8.41E-01	3.16E-04		7.69E-01	2.07E-03		-2.10E+00	7.00E-18	Down	-8.51E-01	2.48E-05		Unigene45361_All//gi|224102345|ref|XP_002312645.1|//0.00E+00//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222852465|gb|EEE90012.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene45361_All//0.00E+00//AT3G13080| ATMRP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase	Unigene45361_All//0.00E+00//gi|109850911|gb|DW479890.1|DW479890		ko02010|ABC transporters	GO:0005576//GO:0005773//GO:0006810//GO:0008152//GO:0016628//GO:0022891//GO:0031090//GO:0031224//GO:0031410//GO:0032559//GO:0043234//GO:0071997	nr +
Unigene45363_All	3109	7.07	6.21	4.06	13.48	12.02	12.16	8.62	3.79	6.07	-1.87E-01	1.36E-01		-8.00E-01	5.09E-11		-1.65E-01	5.37E-02		-1.48E-01	1.03E-01		-1.19E+00	1.03E-31	Down	-5.05E-01	3.31E-08		Unigene45363_All//gi|15240762|ref|NP_201548.1|//0.00E+00//formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] >gi|75171125|sp|Q9FJX6.1|FH6_ARATH RecName: Full=Formin-like protein 6; Short=AtFH6; Short=AtFORMIN-6; Flags: Precursor >gi|9757868|dbj|BAB08455.1| formin-like protein [Arabidopsis thaliana] >gi|37694426|gb|AAQ99143.1| formin-like protein AtFH6 [Arabidopsis thaliana]	Unigene45363_All//0.00E+00//AT5G67470| formin homology 2 domain-containing protein / FH2 domain-containing protein	Unigene45363_All//0.00E+00//TC137197		ko03040|Spliceosome	GO:0016043//GO:0031410	nr -

Unigene45364_All	2343	3.71	1.17	2.39	6.70	10.76	6.48	8.84	3.32	11.75	-1.67E+00	2.03E-14	Down	-6.35E-01	1.81E-03		6.84E-01	1.31E-11		-4.83E-02	7.66E-01		-1.41E+00	3.29E-32	Down	4.10E-01	5.46E-06		Unigene45364_All//gi|15223460|ref|NP_176009.1|//0.00E+00//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|263711285|sp|Q8LGH2.2|Y1561_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g56130; Flags: Precursor	Unigene45364_All//0.00E+00//AT1G56130| leucine-rich repeat family protein / protein kinase family protein	Unigene45364_All//0.00E+00//ES811663		ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0016020//GO:0016491//GO:0032559	nr -
Unigene45365_All	2030	4.20	1.37	2.28	6.13	10.86	6.23	11.43	6.69	13.58	-1.61E+00	1.45E-13	Down	-8.80E-01	2.05E-05		8.24E-01	6.79E-14		2.21E-02	9.24E-01		-7.73E-01	6.00E-14		2.48E-01	7.18E-03		Unigene45365_All//gi|6056376|gb|AAF02840.1|AC009894_11//0.00E+00//Similar to serine/threonine kinases [Arabidopsis thaliana]	Unigene45365_All//0.00E+00//AT1G56140| leucine-rich repeat family protein / protein kinase family protein	Unigene45365_All//0.00E+00//gi|164345274|gb|ES815163.1|ES815163		ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0016628//GO:0032559	nr +
Unigene45369_All	1169	2.28	0.91	2.10	3.41	3.62	3.90	7.13	5.26	3.78	-1.33E+00	8.72E-04	Down	-1.24E-01	7.50E-01		8.79E-02	8.29E-01		1.95E-01	5.62E-01		-4.39E-01	1.54E-02		-9.14E-01	2.47E-07		Unigene45369_All//gi|110741068|dbj|BAE98628.1|//4.00E-80//Calmodulin-binding transcription activator 3 [Arabidopsis thaliana]	Unigene45369_All//2.00E-81//AT3G22300| SR1 (SIGNAL RESPONSIVE 1); calmodulin binding / transcription regulator	Unigene45369_All//0.00E+00//DT466629	CAMTA		GO:0003676//GO:0005515//GO:0016604//GO:0050896	nr +
Unigene45370_All	3976	4.62	2.75	3.52	9.32	7.76	6.40	14.32	11.45	6.80	-7.47E-01	9.17E-09		-3.91E-01	3.90E-03		-2.65E-01	1.76E-03		-5.44E-01	1.60E-10		-3.23E-01	2.03E-07		-1.07E+00	1.81E-58	Down	Unigene45370_All//gi|110741068|dbj|BAE98628.1|//0.00E+00//Calmodulin-binding transcription activator 3 [Arabidopsis thaliana]	Unigene45370_All//0.00E+00//AT2G22300| SR1 (SIGNAL RESPONSIVE 1); calmodulin binding / transcription regulator	Unigene45370_All//0.00E+00//TC145979	CAMTA		GO:0003676//GO:0005515//GO:0016604//GO:0050896	nr -
Unigene45371_All	1441	12.42	121.80	23.95	26.48	26.24	34.95	10.71	22.30	14.93	3.29E+00	0.00E+00	Up	9.47E-01	2.05E-22		-1.32E-02	9.04E-01		4.00E-01	3.01E-08		1.06E+00	1.23E-31	Up	4.79E-01	3.36E-06		Unigene45371_All//gi|158828228|gb|ABW81106.1|//1.00E-94//putRNAbp29 [Cleome spinosa]	Unigene45371_All//4.00E-30//AT1G07350| transformer serine/arginine-rich ribonucleoprotein, putative	Unigene45371_All//0.00E+00//DR458996		ko03040|Spliceosome	GO:0005488//GO:0044424	nr -
Unigene45372_All	1154	1.31	37.06	7.94	4.96	5.43	7.08	3.81	8.95	5.80	4.82E+00	9.29E-202	Up	2.59E+00	3.28E-25	Up	1.30E-01	6.35E-01		5.13E-01	1.18E-02		1.23E+00	2.02E-13	Up	6.06E-01	2.07E-03		Unigene45372_All//gi|158828228|gb|ABW81106.1|//2.00E-53//putRNAbp29 [Cleome spinosa]	Unigene45372_All//0.00E+00//DR458996		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0005488	nr +
Unigene45373_All	968	1.57	20.62	4.18	5.40	4.91	7.88	2.88	4.58	4.53	3.72E+00	4.35E-79	Up	1.42E+00	1.74E-05	Up	-1.38E-01	6.27E-01		5.45E-01	9.84E-03		6.67E-01	9.36E-03		6.51E-01	9.23E-03		Unigene45373_All//gi|158828228|gb|ABW81106.1|//1.00E-37//putRNAbp29 [Cleome spinosa]	Unigene45373_All//1.00E-27//AT1G07350| transformer serine/arginine-rich ribonucleoprotein, putative	Unigene45373_All//0.00E+00//CO105581		ko03040|Spliceosome	GO:0003676//GO:0006396	nr -
Unigene45374_All	741	3.95	3.83	4.24	4.97	3.49	5.18	11.98	33.34	27.04	-4.63E-02	9.07E-01		1.01E-01	7.75E-01		-5.13E-01	1.03E-01		5.85E-02	8.78E-01		1.48E+00	1.14E-40	Up	1.17E+00	4.27E-24	Up	Unigene45374_All//gi|74474913|dbj|BAE44440.1|//2.00E-15//MAP kinase phosphatase 1 [Solanum tuberosum]		Unigene45374_All//0.00E+00//DT462961				nr +
Unigene45375_All	1816	3.51	6.61	4.08	4.50	3.53	4.55	10.85	27.69	25.05	9.12E-01	4.23E-08		2.14E-01	3.88E-01		-3.51E-01	8.40E-02		1.68E-02	9.49E-01		1.35E+00	7.29E-72	Up	1.21E+00	5.95E-56	Up	Unigene45375_All//gi|74474913|dbj|BAE44440.1|//2.00E-85//MAP kinase phosphatase 1 [Solanum tuberosum]	Unigene45375_All//2.00E-05//AT3G55270| MKP1 (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 1); MAP kinase tyrosine/serine/threonine phosphatase	Unigene45375_All//0.00E+00//DT462961			GO:0016791	nr -
Unigene45376_All	3147	0.98	1.98	2.34	2.09	1.42	2.21	5.13	9.59	11.62	1.01E+00	2.55E-05	Up	1.25E+00	6.59E-08	Up	-5.55E-01	1.10E-02		8.10E-02	7.45E-01		9.02E-01	5.33E-23		1.18E+00	1.60E-43	Up	Unigene45376_All//gi|74474913|dbj|BAE44440.1|//0.00E+00//MAP kinase phosphatase 1 [Solanum tuberosum]	Unigene45376_All//2.00E-143//AT3G55270| MKP1 (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 1); MAP kinase tyrosine/serine/threonine phosphatase	Unigene45376_All//0.00E+00//DT462961			GO:0004721	nr +
Unigene45379_All	2138	17.23	36.81	20.05	28.80	28.14	28.98	36.07	54.09	42.73	1.10E+00	8.48E-66	Up	2.19E-01	1.26E-02		-3.35E-02	7.11E-01		9.20E-03	9.31E-01		5.85E-01	1.03E-40		2.44E-01	2.95E-07		Unigene45379_All//gi|167178795|gb|ABZ11028.1|//0.00E+00//Potyvirus VPg interacting protein [Arachis hypogaea]	Unigene45379_All//0.00E+00//AT5G48160| OBE2 (OBERON2); protein binding / zinc ion binding	Unigene45379_All//0.00E+00//ES816623			GO:0003006//GO:0010015//GO:0010074//GO:0010467//GO:0042802//GO:0043231//GO:0046739//GO:0046914//GO:0046983	nr +
Unigene45380_All	673	3.50	1.96	1.03	2.22	1.54	2.62	75.14	90.36	80.33	-8.38E-01	4.35E-02		-1.77E+00	1.68E-04	Down	-5.33E-01	3.21E-01		2.37E-01	6.65E-01		2.66E-01	1.09E-05		9.64E-02	1.71E-01		Unigene45380_All//gi|15240929|ref|NP_195745.1|//1.00E-86//alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein [Arabidopsis thaliana] >gi|51315396|gb|AAT99803.1|At5g01250 [Arabidopsis thaliana]	Unigene45380_All//6.00E-88//AT5G01250| alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein	Unigene45380_All//3.00E-108//TC163862			GO:0035250//GO:0044431	nr -
Unigene45381_All	2167	5.17	0.65	0.88	2.78	2.75	0.75	22.73	19.29	13.11	-2.98E+00	6.70E-37	Down	-2.55E+00	5.67E-30	Down	-1.69E-02	9.56E-01		-1.89E+00	7.26E-13	Down	-2.37E-01	5.51E-04		-7.94E-01	7.13E-31		Unigene45381_All//gi|15240929|ref|NP_195745.1|//1.00E-111//alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein [Arabidopsis thaliana] >gi|51315396|gb|AAT99803.1|At5g01250 [Arabidopsis thaliana]	Unigene45381_All//5.00E-112//AT5G01250| alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein	Unigene45381_All//1.00E-128//TC163862			GO:0008378	nr -
Unigene45382_All	1694	0.77	0.06	1.13	0.76	1.30	0.96	21.44	21.32	18.46	-3.69E+00	1.09E-05	Down	5.52E-01	2.59E-01		7.67E-01	7.80E-02		3.28E-01	5.75E-01		-8.30E-03	9.56E-01		-2.16E-01	6.86E-03		Unigene45382_All//gi|15240929|ref|NP_195745.1|//1.00E-113//alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein [Arabidopsis thaliana] >gi|51315396|gb|AAT99803.1|At5g01250 [Arabidopsis thaliana]	Unigene45382_All//2.00E-114//AT5G01250| alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein	Unigene45382_All//9.00E-123//TC163862			GO:0016740	nr -
Unigene4539_All	1682	0.37	0.54	0.00	1.42	1.68	0.56	8.55	3.53	3.22	5.39E-01	4.49E-01		-8.54E+00	1.41E-03		2.40E-01	5.83E-01		-1.33E+00	1.38E-03		-1.28E+00	2.02E-19	Down	-1.41E+00	3.79E-23	Down	Unigene4539_All//gi|42562741|ref|NP_175789.2|//1.00E-107//remorin family protein [Arabidopsis thaliana] >gi|60253498|gb|AAT71951.1|At1g53860 [Arabidopsis thaliana] >gi|53850525|gb|AAU95439.1|At1g53860 [Arabidopsis thaliana]	Unigene4539_All//1.00E-102//AT1G53860| remorin family protein	Unigene4539_All//0.00E+00//gi|78348479|gb|DT568753.1|DT568753				nr +
Unigene45390_All	2819	14.01	37.82	50.95	27.96	40.57	61.07	14.38	9.86	14.16	1.43E+00	5.55E-135	Up	1.86E+00	8.51E-259	Up	5.37E-01	1.36E-33		1.13E+00	1.19E-161	Up	-5.45E-01	3.71E-13		-2.25E-02	7.94E-01		Unigene45390_All//gi|129563703|gb|AB031100.1|//0.00E+00//ovule receptor-like kinase 28 [Solanum chacoense]	Unigene45390_All//0.00E+00//AT3G14350| SRF7 (STRUBBELIG-RECEPTOR FAMILY 7); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene45390_All//0.00E+00//ES829960		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004871//GO:0006464//GO:0007167//GO:0031224//GO:0031410//GO:0032559//GO:0043231	nr +
Unigene45397_All	1079	24.29	13.62	13.37	45.38	36.45	36.83	92.63	39.98	30.50	-8.35E-01	1.38E-14		-8.61E-01	1.11E-14		-3.16E-01	6.57E-06		-3.01E-01	5.06E-05		-1.21E+00	2.49E-120	Down	-1.60E+00	7.81E-189	Down	Unigene45397_All//gi|115456045|ref|NP_001051623.1|//1.00E-116//Os03g0804800 [Oryza sativa Japonica Group] >gi|113550094|dbj|BAF13537.1|Os03g0804800 [Oryza sativa Japonica Group]	Unigene45397_All//2.00E-102//AT3G03960| chaperonin, putative	Unigene45397_All//0.00E+00//TC160761			GO:0005515//GO:0032559//GO:0044267//GO:0044424	nr -
Unigene4540_All	884	121.27	165.71	123.25	51.67	33.58	24.52	11.29	28.79	11.13	4.50E-01	2.26E-26		2.33E-02	6.99E-01		-6.22E-01	4.36E-18		-1.08E+00	1.55E-40	Down	1.35E+00	9.72E-37	Up	-2.01E-02	9.28E-01		Unigene4540_All//gi|15234544|ref|NP_193893.1|//9.00E-39//glycine-rich protein [Arabidopsis thaliana] >gi|16648720|gb|AAL25552.1|AT4g21620/F17L22_80 [Arabidopsis thaliana]	Unigene4540_All//2.00E-16//AT4G21620| glycine-rich protein	Unigene4540_All//0.00E+00//TC147939				nr -
Unigene45400_All	3311	23.13	14.40	27.84	28.98	41.73	51.33	20.98	36.17	50.40	-6.84E-01	2.67E-29		2.67E-01	1.61E-06		5.26E-01	5.00E-39		8.25E-01	3.86E-95		7.86E-01	2.22E-70		1.26E+00	2.54E-218	Up	Unigene45400_All//gi|261664473|sp|C0LGK4.1|Y2165_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At2g16250; Flags: Precursor >gi|224589511|gb|ACN59289.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene45400_All//0.00E+00//AT2G16250| leucine-rich repeat transmembrane protein kinase, putative	Unigene45400_All//0.00E+00//TC147717			GO:0004672//GO:0005488//GO:0005618//GO:0008152//GO:0016020//GO:0016491	nr -
Unigene45401_All	3952	1.23	0.81	0.27	1.87	2.40	2.78	5.93	2.50	3.59	-6.08E-01	2.53E-02		-2.19E+00	3.31E-11	Down	3.66E-01	5.16E-02		5.74E-01	7.06E-04		-1.25E+00	4.37E-30	Down	-7.24E-01	4.90E-13		Unigene45401_All//gi|5042431|gb|AA038270.1|AC006193_26//0.00E+00//Hypothetical Protein [Arabidopsis thaliana]	Unigene45401_All//0.00E+00//AT1G64960| binding	Unigene45401_All//0.00E+00//gi|164288860|gb|ES844156.1|ES844156				nr +
Unigene45403_All	2368	49.38	86.08	67.10	30.92	19.70	15.33	34.83	40.01	23.99	8.02E-01	7.85E-101		4.42E-01	1.04E-26		-6.50E-01	4.00E-31		-1.01E+00	1.38E-58	Down	2.00E-01	3.33E-05		-5.38E-01	4.55E-26		Unigene45403_All//gi|91208904|ref|YP_538937.1|//1.00E-110//ribosomal protein S4 [Gossypium hirsutum] >gi|119368501|ref|YP_913189.1|ribosomal protein S4 [Gossypium barbadense] >gi|90101660|sp|Q2L908.1|RR4_GOSHI RecName: Full=30S ribosomal protein S4, chloroplastic >gi|125598751|sp|A0ZZ37.1|RR4_GOSBA RecName: Full=30S ribosomal protein S4, chloroplastic >gi|85687418|gb|ABC73630.1|ribosomal protein S4 [Gossypium hirsutum] >gi|119224863|dbj|BAF41249.1|Ribosomal protein S4 [Gossypium barbadense]	Unigene45403_All//3.00E-97//ATCG00380| Chloroplast encoded ribosomal protein S4	Unigene45403_All//0.00E+00//TC136682		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0033279	nr -
Unigene45408_All	3140	18.41	4.31	3.48	19.28	22.61	13.25	32.90	9.21	20.15	-2.10E+00	1.41E-125	Down	-2.41E+00	7.33E-144	Down	2.30E-01	9.59E-05		-5.41E-01	1.17E-16		-1.84E+00	1.09E-229	Down	-7.07E-01	2.97E-52		Unigene45408_All//gi|224057130|ref|XP_002299134.1|//0.00E+00//DNA methyltransferase [Populus trichocarpa] >gi|222846392|gb|EEE83939.1| DNA methyltransferase [Populus trichocarpa]	Unigene45408_All//6.00E-162//AT1G69770| CMT3 (chromomethylase 3); DNA (cytosine-5-)-methyltransferase	Unigene45408_All//0.00E+00//gi|164340043|gb|ES821771.1|ES821771		ko00270|Cysteine and methionine metabolism	GO:0005488//GO:0008757//GO:0009793//GO:0016458//GO:0032776//GO:0034968//GO:0043231	nr -
Unigene45409_All	1791	4.09	7.70	3.81	5.26	5.81	7.16	18.06	25.62	49.60	9.12E-01	3.52E-09		-1.04E-01	6.52E-01		1.44E-01	5.11E-01		4.46E-01	4.60E-03		5.05E-01	5.78E-13		1.46E+00	1.21E-144	Up	Unigene45409_All//gi|115467680|ref|NP_001057439.1|//0.00E+00//Os06g0297800 [Oryza sativa Japonica Group] >gi|113595479|dbj|BAF19353.1|Os06g0297800 [Oryza sativa Japonica Group]	Unigene45409_All//8.00E-148//AT5G50170| C2 domain-containing protein / GRAM domain-containing protein	Unigene45409_All//0.00E+00//TC147239				nr -
Unigene4541_All	985	2.66	5.56	4.27	17.14	18.25	25.08	74.64	57.50	35.88	1.06E+00	4.21E-05	Up	6.85E-01	2.68E-02		9.01E-02	5.88E-01		5.49E-01	2.67E-07		-3.77E-01	3.71E-12		-1.06E+00	2.59E-73	Down	Unigene4541_All//gi|82581142|emb|CAJ43712.1|//2.00E-83//caffeoyl-CoA O-methyltransferase [Plantago major]	Unigene4541_All//1.00E-78//AT1G67980| CCoAMT; caffeoyl-CoA O-methyltransferase	Unigene4541_All//0.00E+00//TC158103		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene45410_All	2915	0.88	2.26	1.06	1.91	1.77	2.08	5.79	6.84	15.81	1.36E+00	2.09E-08	Up	2.69E-01	4.81E-01		-1.11E-01	7.09E-01		1.17E-01	6.88E-01		2.41E-01	3.74E-02		1.45E+00	7.70E-75	Up	Unigene45410_All//gi|115467680|ref|NP_001057439.1|//0.00E+00//Os06g0297800 [Oryza sativa Japonica Group] >gi|113595479|dbj|BAF19353.1|Os06g0297800 [Oryza sativa Japonica Group]	Unigene45410_All//0.00E+00//AT1G03370| protein binding / zinc ion binding	Unigene45410_All//0.00E+00//TC170885			GO:0009555//GO:0019932	nr +

Unigene45411_All	4354	0.59	0.93	0.95	1.09	1.10	1.64	2.65	3.29	9.24	6.61E-01	2.91E-02		6.96E-01	2.54E-02		1.64E-02	9.67E-01		5.93E-01	6.66E-03		3.13E-01	2.18E-02		1.80E+00	4.25E-89	Up	Unigene45411_All//gi|297843150|ref|XP_002889456.1|//0.00E+00//C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335298|gb|EFH65715.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene45411_All//0.00E+00//AT1G03370| protein binding / zinc ion binding	Unigene45411_All//0.00E+00//TC170885			GO:0009555//GO:0019932	nr -
Unigene45412_All	1833	20.49	10.14	15.19	9.57	12.76	10.10	2.31	5.13	2.43	-1.01E+00	3.15E-28	Down	-4.32E-01	1.52E-06		4.15E-01	9.91E-05		7.86E-02	6.09E-01		1.15E+00	3.62E-11	Up	7.77E-02	7.69E-01		Unigene45412_All//gi|226377504|gb|ACO52508.1|//1.00E-152//transcription factor APETALA2 [Vitis vinifera]	Unigene45412_All//1.00E-80//AT4G36920| AP2 (APETALA 2); transcription factor	Unigene45412_All//0.00E+00//TC167185	AP2-EREBP		GO:0006350	nr +
Unigene45417_All	1740	3.58	8.12	2.39	5.04	4.06	8.54	7.68	14.44	17.36	1.18E+00	5.90E-14	Up	-5.84E-01	1.84E-02		-3.13E-01	1.16E-01		7.61E-01	8.91E-08		9.11E-01	1.35E-19		1.18E+00	5.78E-36	Up	Unigene45417_All//gi|119935896|gb|ABM06027.1|//1.00E-102//At4g24460 [Arabidopsis thaliana]	Unigene45417_All//2.00E-84//AT4G24460| unknown protein	Unigene45417_All//0.00E+00//TC178083				nr -
Unigene45422_All	3141	2.12	0.98	0.83	3.43	3.07	2.49	2.96	1.41	1.50	-1.10E+00	2.31E-06	Down	-1.35E+00	5.46E-08	Down	-1.58E-01	4.25E-01		-4.62E-01	7.76E-03		-1.07E+00	6.63E-10	Down	-9.85E-01	4.80E-09		Unigene45422_All//gi|225446819|ref|XP_002279329.1|//0.00E+00//PREDICTED: similar to Golgi transport complex protein-related [Vitis vinifera]	Unigene45422_All//0.00E+00//AT1G67930| Golgi transport complex protein-related	Unigene45422_All//0.00E+00//TC142003		ko03040|Spliceosome	GO:0006810//GO:0043231	nr +
Unigene45423_All	2403	17.68	14.36	11.92	41.42	41.79	35.01	64.24	44.67	28.23	-3.00E-01	2.63E-04		-5.69E-01	1.26E-11		1.28E-02	8.47E-01		-2.42E-01	1.68E-06		-5.24E-01	1.38E-44		-1.19E+00	3.71E-184	Down	Unigene45423_All//gi|297804040|ref|XP_002869904.1|//0.00E+00//ribophorin II family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315740|gb|EFH46163.1| ribophorin II family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45423_All//0.00E+00//AT4G21150| HAP6 (HAPLESS 6); dolichyl-diphosphooligosaccharide-protein glycotransferase	Unigene45423_All//0.00E+00//TC151414		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0004576//GO:0005618//GO:0005789//GO:0006487//GO:0006950//GO:0031410	nr +
Unigene45426_All	565	0.93	0.90	0.75	5.29	3.23	3.12	5.69	8.36	1.69	-4.62E-02	9.76E-01		-2.96E-01	7.50E-01		-7.12E-01	3.96E-02		-7.63E-01	3.51E-02		5.56E-01	2.57E-02		-1.75E+00	1.11E-07	Down	Unigene45426_All//gi|9965899|gb|AAG10197.1|//5.00E-12//cinnamate-4-hydroxylase [Gossypium arboreum]	Unigene45426_All//1.00E-11//AT2G30490| C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	Unigene45426_All//0.00E+00//gi|78322906|gb|DT543180.1|DT543180		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene45427_All	1868	65.85	74.84	91.45	196.43	223.83	247.02	236.25	236.54	67.50	1.85E-01	2.55E-05		4.74E-01	1.84E-32		1.88E-01	2.36E-17		3.31E-01	1.31E-49		1.80E-03	9.79E-01		-1.81E+00	0.00E+00	Down	Unigene45427_All//gi|9965899|gb|AAG10197.1|//0.00E+00//cinnamate-4-hydroxylase [Gossypium arboreum]	Unigene45427_All//0.00E+00//AT2G30490| C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	Unigene45427_All//0.00E+00//TC130013		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0005506//GO:0008152//GO:0016709	nr -
Unigene45429_All	3090	6.43	7.12	6.60	34.72	27.89	23.96	9.56	4.36	3.80	1.45E-01	2.57E-01		3.67E-02	7.90E-01		-3.16E-01	2.87E-12		-5.36E-01	1.45E-28		-1.13E+00	1.37E-32	Down	-1.33E+00	7.19E-43	Down	Unigene45429_All//gi|297804404|ref|XP_002870086.1|//0.00E+00//ATTPS5 [Arabidopsis lyrata subsp. lyrata] >gi|297315922|gb|EFH46345.1| ATTPS5 [Arabidopsis lyrata subsp. lyrata]	Unigene45429_All//0.00E+00//AT4G17770| ATTPS5; protein binding / transferase, transferring glycosyl groups / trehalose-phosphatase	Unigene45429_All//0.00E+00//TC141217		ko00500|Starch and sucrose metabolism	GO:0005488//GO:0005991//GO:0019203//GO:0035251//GO:0043231	nr -
Unigene4543_All	766	63.39	59.00	75.77	39.41	66.89	44.46	35.99	17.13	63.87	-1.03E-01	2.26E-01		2.58E-01	3.75E-04		7.63E-01	5.26E-28		1.74E-01	8.29E-02		-1.07E+00	8.65E-28	Down	8.28E-01	1.14E-32		Unigene4543_All//gi|171452356|dbj|BAG15869.1|//1.00E-58//ankyrin repeat protein [Bruguiera gymnorhiza]	Unigene4543_All//9.00E-60//AT4G10720| ankyrin repeat family protein	Unigene4543_All//0.00E+00//TC175160				nr +
Unigene45430_All	660	0.40	6.68	2.82	0.00	0.63	2.12	3.91	6.90	161.47	4.07E+00	5.22E-19	Up	2.83E+00	5.06E-06	Up	9.29E+00	1.25E-02		1.11E+01	2.43E-08	Up	8.21E-01	1.14E-03		5.37E+00	0.00E+00	Up		Unigene45430_All//1.00E-05//AT5G17530| phosphoglucosamine mutase family protein	Unigene45430_All//0.00E+00//TC159434				ESTscan -
Unigene45431_All	2112	4.24	24.90	4.41	0.97	1.26	1.35	5.14	16.01	24.80	2.56E+00	3.32E-144	Up	5.88E-02	7.74E-01		3.77E-01	3.77E-01		4.78E-01	2.27E-01		1.64E+00	2.39E-64	Up	2.27E+00	3.65E-156	Up			Unigene45431_All//0.00E+00//TC175163				ESTscan -
Unigene45436_All	734	1.28	0.14	0.73	1.56	0.99	0.49	9.16	5.98	4.02	-3.22E+00	6.76E-04	Down	-8.23E-01	2.71E-01		-6.64E-01	2.98E-01		-1.67E+00	1.29E-02		-6.15E-01	2.28E-03		-1.19E+00	6.77E-09	Down	Unigene45436_All//gi|255549230|ref|XP_002515669.1|//4.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223545212|gb|EEF46721.1| conserved hypothetical protein [Ricinus communis]		Unigene45436_All//2.00E-128//gi|109847108|gb|DW476088.1|DW476088				nr -
Unigene45437_All	2906	5.10	4.83	3.61	7.20	8.01	4.31	23.08	11.29	10.94	-7.72E-02	6.13E-01		-4.97E-01	1.00E-03		1.54E-01	2.25E-01		-7.42E-01	2.39E-10		-1.03E+00	1.54E-62	Down	-1.08E+00	5.84E-69	Down	Unigene45437_All//gi|15912253|gb|AAL08260.1|//3.00E-56//AT4g27870/T2T E11_110 [Arabidopsis thaliana]	Unigene45437_All//6.00E-51//AT4G27870| integral membrane family protein	Unigene45437_All//0.00E+00//TC146123			GO:0044464	nr +
Unigene45438_All	3200	10.56	8.15	7.52	26.31	25.34	19.29	15.93	6.23	4.84	-3.73E-01	5.38E-05		-4.90E-01	2.48E-07		-5.40E-02	4.52E-01		-4.47E-01	2.28E-16		-1.35E+00	2.96E-73	Down	-1.72E+00	9.45E-107	Down	Unigene45438_All//gi|116309852|emb|CAH66887.1|//6.00E-88//OSIGBa0099L20.2 [Oryza sativa (indica cultivar-group)]	Unigene45438_All//3.00E-47//AT1G19870| iqg32 (IQ-domain 32); calmodulin binding	Unigene45438_All//0.00E+00//TC171803			GO:0043231//GO:0044444	nr -
Unigene45439_All	2253	37.88	46.76	30.58	53.84	49.17	62.10	87.98	218.68	167.10	3.04E-01	1.30E-09		-3.09E-01	8.89E-08		-1.31E-01	5.02E-03		2.06E-01	1.19E-06		1.31E+00	0.00E+00	Up	9.26E-01	8.95E-297		Unigene45439_All//gi|297850558|ref|XP_002893160.1|//1.00E-158//VHS domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297339002|gb|EFH69419.1| VHS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene45439_All//8.00E-139//AT1G21380| VHS domain-containing protein / GAT domain-containing protein	Unigene45439_All//0.00E+00//TC136609			GO:0015031//GO:0044464	nr -
Unigene4544_All	731	4.37	4.02	4.74	19.63	15.78	14.33	4.22	2.74	1.80	-1.19E-01	7.24E-01		1.17E-01	7.28E-01		-3.15E-01	3.21E-02		-4.53E-01	1.95E-03		-6.22E-01	5.11E-02		-1.23E+00	9.25E-05	Down	Unigene4544_All//gi|225436069|ref|XP_002272311.1|//2.00E-18//PREDICTED: similar to Hsp20/alpha crystallin family protein [Vitis vinifera]	Unigene4544_All//1.00E-17//AT2G27140| heat shock family protein					nr +
Unigene45444_All	3039	0.59	1.47	1.16	9.41	9.44	8.01	3.20	1.60	1.32	1.33E+00	9.63E-06	Up	9.82E-01	4.36E-03		4.60E-03	9.71E-01		-2.32E-01	2.81E-02		-1.00E+00	2.22E-09	Down	-1.27E+00	8.74E-14	Down	Unigene45444_All//gi|115463087|ref|NP_001055143.1|//1.00E-154//Os05g0304600 [Oryza sativa Japonica Group] >gi|113578694|dbj|BAF17057.1| Os05g0304600 [Oryza sativa Japonica Group]	Unigene45444_All//2.00E-140//AT3G22400| LOX5; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene45444_All//0.00E+00//CO128352		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0008152	nr +
Unigene45445_All	2731	4.46	2.04	2.69	59.90	47.23	24.21	12.60	3.89	4.58	-1.13E+00	2.25E-11	Down	-7.30E-01	1.36E-05		-3.43E-01	1.80E-21		-1.31E+00	1.41E-196	Down	-1.70E+00	5.53E-69	Down	-1.46E+00	3.26E-57	Down	Unigene45445_All//gi|18400323|ref|NP_566483.1|//0.00E+00//subtilase family protein [Arabidopsis thaliana] >gi|9279572|dbj|BAB01030.1| subtilisin proteinase-like protein [Arabidopsis thaliana]	Unigene45445_All//0.00E+00//AT3G14240| subtilase family protein	Unigene45445_All//0.00E+00//TC142348		ko04141|Protein processing in endoplasmic reticulum	GO:0004175//GO:0005515//GO:0009664//GO:0019538//GO:0030312//GO:0031410//GO:0044092	nr -
Unigene45449_All	1957	5.80	1.94	2.72	6.87	5.72	6.32	5.60	3.27	4.56	-1.58E+00	2.71E-17	Down	-1.09E+00	1.17E-09	Down	-2.65E-01	9.20E-02		-1.20E-01	5.15E-01		-7.76E-01	4.70E-07		-2.95E-01	5.55E-02		Unigene45449_All//gi|76880152|dbj|BAE45851.1|//1.00E-148//DNA polymerase [Nicotiana tabacum]	Unigene45449_All//6.00E-138//AT3G20540| POLGAMMA1 (polymerase gamma 1); 3'-5' exonuclease/ DNA binding / DNA-directed DNA polymerase/ nucleic acid binding	Unigene45449_All//9.00E-37//TC156781		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination		nr +
Unigene4545_All	737	6.39	1.51	2.96	9.53	5.56	5.58	1.95	0.68	2.54	-2.08E+00	9.94E-11	Down	-1.11E+00	1.64E-04	Down	-7.77E-01	1.45E-04		-7.73E-01	3.57E-04		-1.52E+00	3.35E-03		3.81E-01	3.71E-01		Unigene4545_All//gi|42569545|ref|NP_180761.2|//2.00E-33//endonuclease/exonuclease/phosphatase family protein [Arabidopsis thaliana]	Unigene4545_All//3.00E-26//AT2G32010| endonuclease/exonuclease/phosphatase family protein					nr -
Unigene45450_All	4083	4.64	1.76	2.57	3.93	3.54	3.65	5.01	2.69	3.07	-1.40E+00	9.55E-24	Down	-8.52E-01	1.31E-10		-1.49E-01	3.41E-01		-1.06E-01	5.37E-01		-8.97E-01	9.85E-16		-7.06E-01	4.89E-11		Unigene45450_All//gi|18087568|gb|AAL58915.1|AF462826_1//0.00E+00//At1g50840/F8A12_8 [Arabidopsis thaliana] >gi|71013470|dbj|BAE10873.1| PolI-like A DNA polymerase [Arabidopsis thaliana]	Unigene45450_All//0.00E+00//AT1G50840| POLGAMMA2 (polymerase gamma 2); DNA binding / DNA-directed DNA polymerase	Unigene45450_All//0.00E+00//TC156781		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination	GO:0003676//GO:0004527//GO:0006259//GO:0009536//GO:0034061//GO:0043632	nr +
Unigene45451_All	2023	27.67	13.17	14.11	56.19	46.16	50.77	75.68	33.22	25.97	-1.07E+00	1.61E-45	Down	-9.72E-01	1.62E-37		-2.84E-01	1.21E-10		-1.47E-01	3.20E-03		-1.19E+00	4.21E-178	Down	-1.54E+00	3.08E-273	Down	Unigene45451_All//gi|115468554|ref|NP_001057876.1|//0.00E+00//Os06g0562600 [Oryza sativa Japonica Group] >gi|113595916|dbj|BAF19790.1| Os06g0562600 [Oryza sativa Japonica Group]	Unigene45451_All//0.00E+00//AT1G24510| T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative	Unigene45451_All//0.00E+00//TC155817			GO:0005515//GO:0016020//GO:0032559//GO:0044267//GO:0044424	nr +
Unigene45453_All	797	1.51	1.46	2.47	2.75	2.85	2.21	4.19	1.26	1.75	-4.63E-02	9.51E-01		7.11E-01	1.40E-01		5.23E-02	9.25E-01		-3.15E-01	5.00E-01		-1.74E+00	1.37E-07	Down	-1.26E+00	3.09E-05	Down	Unigene45453_All//gi|113205236|gb|AAT39308.2|//3.00E-72//V-type ATPase 116kDa subunit family protein [Solanum demissum]	Unigene45453_All//9.00E-71//AT2G28520| VHA-A1 (VACUOLAR PROTON ATPASE A 1); ATPase	Unigene45453_All//0.00E+00//CO108097		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0006754//GO:0015077//GO:0016469//GO:0017111//GO:0030658	nr +
Unigene45456_All	611	6.17	3.73	4.27	7.91	4.73	3.92	8.30	5.68	4.43	-7.24E-01	2.14E-02		-5.30E-01	1.14E-01		-7.40E-01	3.90E-03		-1.01E+00	1.80E-04	Down	-5.49E-01	2.17E-02		-9.05E-01	9.39E-05				Unigene45456_All//0.00E+00//TC178226				nr +
Unigene4546_All	740	8.56	6.98	7.84	10.30	13.12	8.18	30.11	14.35	18.09	-2.93E-01	2.34E-01		-1.25E-01	6.08E-01		3.50E-01	6.22E-02		-3.33E-01	1.36E-01		-1.07E+00	1.40E-22	Down	-7.35E-01	9.19E-13		Unigene4546_All//gi|30814148|gb|AAP34362.1|//1.00E-45//fiber protein Fb15 [Gossypium barbadense]	Unigene4546_All//1.00E-31//AT4G30010| unknown protein	Unigene4546_All//0.00E+00//BF274779				nr +
Unigene45460_All	1965	19.86	33.78	19.43	35.69	55.99	52.40	67.17	97.54	166.27	7.66E-01	7.86E-31		-3.18E-02	7.48E-01		6.50E-01	3.08E-45		5.54E-01	6.06E-29		5.38E-01	9.26E-58		1.31E+00	0.00E+00	Up	Unigene45460_All//gi|188509939|gb|ACD56625.1|//0.00E+00//trehalose synthase/phosphatase-like protein [Gossypium raimondii]	Unigene45460_All//3.00E-170//AT1G06410| ATTPS7; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase	Unigene45460_All//0.00E+00//TC161848		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0019203//GO:0035251	nr -
Unigene45462_All	1753	0.84	0.92	0.21	1.65	3.75	6.36	15.39	32.95	61.97	1.46E-01	7.64E-01		-1.97E+00	1.91E-03		1.19E+00	9.97E-08	Up	1.95E+00	8.07E-24	Up	1.10E+00	1.14E-59	Up	2.01E+00	3.32E-277	Up	Unigene45462_All//gi|224091028|ref|XP_002309151.1|//0.00E+00//ammonium transporter [Populus trichocarpa] >gi|222855127|gb|EEE92674.1| ammonium transporter [Populus trichocarpa]	Unigene45462_All//0.00E+00//AT2G38290| ATAMT2 (AMMONIUM TRANSPORTER 2); ammonium transmembrane transporter/ high affinity secondary active ammonium transmembrane transporter	Unigene45462_All//0.00E+00//TC165875			GO:0015101//GO:0015291//GO:0015695//GO:0031224//GO:0051707	nr -
Unigene45463_All	3697	5.69	11.09	8.70	4.12	5.69	6.36	8.39	20.38	15.17	9.63E-01	3.89E-28		6.13E-01	3.58E-10		4.65E-01	3.57E-05		6.26E-01	1.13E-08		1.28E+00	9.72E-99	Up	8.54E-01	2.49E-39		Unigene45463_All//gi|29029052|gb|AA064905.1|//1.00E-146//At5g13950 [Arabidopsis thaliana]	Unigene45463_All//3.00E-106//AT5G13950| unknown protein	Unigene45463_All//0.00E+00//TC172727				nr +
Unigene45465_All	590	123.18	65.87	67.96	168.61	158.17	175.07	142.25	55.47	68.33	-9.03E-01	1.51E-44		-8.58E-01	1.84E-39		-9.22E-02	1.05E-01		5.42E-02	3.93E-01		-1.36E+00	1.21E-120	Down	-1.06E+00	1.19E-83	Down	Unigene45465_All//gi|224121558|ref|XP_002318614.1|//2.00E-61//autoinhibited H+ ATPase [Populus trichocarpa] >gi|222859287|gb|EEE96834.1| autoinhibited H+ ATPase [Populus trichocarpa]	Unigene45465_All//2.00E-52//AT3G47960| AHA4; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	Unigene45465_All//0.00E+00//gi|164242840|gb|ES805728.1|ES805728		ko00190|Oxidative phosphorylation	GO:0006811//GO:0006818//GO:0006970//GO:0009206//GO:0015662//GO:0031224//GO:0032559//GO:0043169	nr +
Unigene45466_All	2742	66.21	24.89	40.67	89.07	101.64	93.44	97.19	32.82	47.18	-1.41E+00	1.19E-225	Down	-7.03E-01	1.35E-69		1.90E-01	6.12E-12		6.90E-02	4.84E-02		-1.57E+00	0.00E+00	Down	-1.04E+00	7.57E-258	Down	Unigene45466_All//gi|6759599|emb|CAB69824.1|//0.00E+00//plasma membrane H+ ATPase [Prunus persica]	Unigene45466_All//0.00E+00//AT5G62670| AHA11 (Arabidopsis H(+)-ATPase 11); ATPase	Unigene45466_All//0.00E+00//TC147276		ko00190|Oxidative phosphorylation	GO:0006811//GO:0006818//GO:0006970//GO:0009206//GO:0015662//GO:0031224//GO:0032559//GO:0043169	nr +
Unigene45467_All	2873	20.36	14.87	11.34	15.71	19.74	56.86	32.85	41.81	74.52	-4.54E-01	3.67E-11		-8.44E-01	5.42E-31		3.30E-01	3.89E-07		1.86E+00	0.00E+00	Up	3.48E-01	8.78E-17		1.18E+00	9.82E-252	Up	Unigene45467_All//gi|124360857|gb|ABN08829.1|//0.00E+00//Armadillo [Medicago truncatula]	Unigene45467_All//0.00E+00//AT2G45720| armadillo/beta-catenin repeat family protein	Unigene45467_All//0.00E+00//TC153955			GO:0003824	nr +

Unigene45469_All	3314	64.30	29.71	50.66	20.26	19.69	17.77	9.94	6.21	4.82	-1.11E+00	7.12E-183	Down	-3.44E-01	1.77E-22		-4.13E-02	6.00E-01		-1.89E-01	3.75E-03		-6.80E-01	1.08E-15		-1.04E+00	1.13E-32	Down	Unigene45469_All//gi|15239874|ref|NP_196771.1|//1.00E-161//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75171712|sp|Q9FWQ1.1|PP376_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g12100, mitochondrial; Flags: Precursor	Unigene45469_All//6.00E-157//AT5G12100| pentatricopeptide (PPR) repeat-containing protein	Unigene45469_All//0.00E+00//ES803238		ko04146|Peroxisome	GO:0003824//GO:0019725	nr +
Unigene4547_All	732	20.80	22.91	16.51	146.52	107.49	99.33	57.82	9.54	8.33	1.40E-01	3.69E-01		-3.33E-01	2.95E-02		-4.47E-01	4.28E-23		-5.61E-01	5.64E-31		-2.60E+00	8.53E-146	Down	-2.80E+00	8.18E-163	Down	Unigene4547_All//gi|21703131|gb|AAM74506.1|//3.00E-54//AT5g16250/T21H19_170 [Arabidopsis thaliana] >gi|23505791|gb|AAN28755.1| At5g16250/T21H19_170 [Arabidopsis thaliana]	Unigene4547_All//3.00E-47//AT5G16250| unknown protein	Unigene4547_All//0.00E+00//TC151508				nr -
Unigene45471_All	682	3.61	10.55	6.71	3.65	2.68	5.23	4.40	2.02	3.68	1.55E+00	7.08E-11	Up	8.97E-01	2.31E-03		-4.49E-01	2.78E-01		5.19E-01	1.28E-01		-1.12E+00	5.69E-04	Down	-2.58E-01	4.33E-01		Unigene45471_All//gi|297610841|ref|NP_001065174.2|//3.00E-33//Os10g0537500 [Oryza sativa Japonica Group] >gi|255676588|dbj|BAF27088.2| Os10g0537500 [Oryza sativa Japonica Group]	Unigene45471_All//5.00E-34//AT1G14530| THB1 (TOM THREE HOMOLOG 1); virion binding	Unigene45471_All//5.00E-76//gi|48830175|gb|C0128565.1|C0128565			GO:0005488//GO:0044464	nr -
Unigene45472_All	557	3.01	7.10	2.96	6.71	5.32	3.49	7.06	5.48	9.44	1.24E+00	9.39E-05	Up	-2.04E-02	9.91E-01		-3.35E-01	3.10E-01		-9.44E-01	2.66E-03		-3.66E-01	2.10E-01		4.19E-01	6.75E-02		Unigene45472_All//gi|297610841|ref|NP_001065174.2|//1.00E-34//Os10g0537500 [Oryza sativa Japonica Group] >gi|255676588|dbj|BAF27088.2| Os10g0537500 [Oryza sativa Japonica Group]	Unigene45472_All//4.00E-34//AT1G14530| THB1 (TOM THREE HOMOLOG 1); virion binding	Unigene45472_All//5.00E-88//gi|48830175|gb|C0128565.1|C0128565			GO:0044464	nr -
Unigene45475_All	3691	2.61	1.30	2.21	6.07	5.88	5.29	8.28	4.68	2.78	-1.00E+00	1.19E-07	Down	-2.41E-01	2.43E-01		-4.73E-02	7.68E-01		-2.00E-01	1.13E-01		-8.25E-01	3.87E-20		-1.57E+00	1.01E-56	Down	Unigene45475_All//gi|115436148|ref|NP_001042832.1|//0.00E+00//Os01g0303200 [Oryza sativa Japonica Group] >gi|52077473|dbj|BAD45037.1| transmembrane domain, a coiled coil-4 domain, of eukaryotic origin (91.3 kD) -like protein [Oryza sativa Japonica Group] >gi|113532363|dbj|BAF04746.1| Os01g0303200 [Oryza sativa Japonica Group]	Unigene45475_All//0.00E+00//AT1G35220| unknown protein	Unigene45475_All//0.00E+00//TC166500			GO:0031410	nr +
Unigene45477_All	398	23.66	17.19	13.11	27.79	26.30	32.23	81.59	57.13	35.53	-4.61E-01	1.42E-02		-8.52E-01	1.27E-05		-7.92E-02	7.09E-01		2.14E-01	2.26E-01		-5.14E-01	1.02E-09		-1.20E+00	4.35E-40	Down	Unigene45477_All//gi|3914467|sp|P93768.1|PSMD3_TOBAC//4.00E-65//RecName: Full=Probable 26S proteasome non-ATPase regulatory subunit 3; Short=26S proteasome subunit S3; AltName: Full=26S proteasome regulatory subunit RPN3; AltName: Full=Nuclear antigen 21D7 >gi|1864003|dbj|BAA19252.1| 21D7 [Nicotiana tabacum]	Unigene45477_All//7.00E-66//AT1G20200| EMB2719 (EMBRYO DEFECTIVE 2719); enzyme regulator	Unigene45477_All//0.00E+00//gi|13351505|gb|BG441853.1|BG441853		ko03050|Proteasome	GO:0003006//GO:0005488//GO:0009894//GO:0016020//GO:0019941//GO:0043231//GO:0043234	nr -
Unigene45482_All	4455	0.43	1.36	1.21	3.51	3.32	3.87	8.92	5.42	2.99	1.65E+00	3.99E-10	Up	1.47E+00	1.84E-07	Up	-7.91E-02	6.31E-01		1.41E-01	3.81E-01		-7.18E-01	1.35E-20		-1.58E+00	6.57E-74	Down	Unigene45482_All//gi|225443168|ref|XP_002264313.1|//0.00E+00//PREDICTED: similar to Multidrug Resistance associated Protein 1 [Vitis vinifera]	Unigene45482_All//0.00E+00//AT2G07680| ATMRP11; ATPase, coupled to transmembrane movement of substances	Unigene45482_All//3.00E-57//TC166829		ko02010|ABC transporters	GO:0000166//GO:0006810//GO:0016020//GO:0016491//GO:0017111//GO:0031410	nr -
Unigene45483_All	287	5.47	5.30	4.45	10.07	7.08	9.13	8.99	3.64	3.05	-4.63E-02	9.40E-01		-2.97E-01	6.10E-01		-5.08E-01	1.63E-01		-1.41E-01	7.14E-01		-1.30E+00	3.05E-04	Down	-1.56E+00	1.68E-05	Down	Unigene45483_All//gi|297831152|ref|XP_002883458.1|//5.00E-23//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329298|gb|EFH59717.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45483_All//2.00E-24//AT3G23750| leucine-rich repeat family protein / protein kinase family protein	Unigene45483_All//1.00E-139//gi|48751559|gb|C0082078.1|C0082078			GO:0004702//GO:0006464//GO:0031224//GO:0032559	nr +
Unigene45487_All	3373	2.28	6.93	2.26	5.55	5.47	4.03	4.11	36.79	4.38	1.60E+00	2.30E-35	Up	-1.44E-02	9.70E-01		-2.12E-02	8.90E-01		-4.62E-01	2.16E-04		3.16E+00	0.00E+00	Up	9.19E-02	5.49E-01		Unigene45487_All//gi|216296850|gb|ACJ72158.1|//1.00E-126//UGT1 [Pueraria montana var. lobata]	Unigene45487_All//2.00E-96//AT1G73880| UGT89B1 (UDP-GLUCOSYL TRANSFERASE 89B1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl group	Unigene45487_All//0.00E+00//TC153523		ko00908|Zeatin biosynthesis	GO:0016740	nr +
Unigene4549_All	751	126.38	19.16	30.84	24.01	22.15	17.62	32.99	20.31	25.30	-2.72E+00	3.47E-281	Down	-2.03E+00	8.81E-192	Down	-1.17E-01	4.57E-01		-4.47E-01	4.91E-04		-7.00E-01	1.34E-12		-3.83E-01	6.11E-05		Unigene4549_All//gi|297807463|ref|XP_002871615.1|//3.00E-43//ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317452|gb|EFH47874.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4549_All//2.00E-39//AT5G14360| ubiquitin family protein	Unigene4549_All//0.00E+00//gi|109877833|gb|DW506806.1|DW506806				nr +
Unigene45491_All	1038	5.24	2.98	2.26	14.59	11.15	4.35	14.58	67.16	22.15	-8.16E-01	1.41E-03		-1.22E+00	8.78E-06	Down	-3.88E-01	4.68E-03		-1.75E+00	2.58E-28	Down	2.20E+00	1.73E-196	Up	6.03E-01	1.79E-09		Unigene45491_All//gi|6573762|gb|AAF17682.1|AC009243.9//7.00E-46//F28K19.13 [Arabidopsis thaliana] >gi|14586402|emb|CAC42910.1| bZIP50 protein [Arabidopsis thaliana]	Unigene45491_All//4.00E-47//AT1G77920| bZIP family transcription factor	Unigene45491_All//0.00E+00//TC149374	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0009627//GO:0043231	nr +
Unigene45492_All	1603	5.25	2.88	4.32	17.31	15.38	7.10	12.42	52.96	19.83	-8.69E-01	1.48E-05		-2.83E-01	2.00E-01		-1.70E-01	1.21E-01		-1.29E+00	7.48E-33	Down	2.09E+00	6.51E-224	Up	6.75E-01	2.18E-15		Unigene45492_All//gi|6573762|gb|AAF17682.1|AC009243.9//1.00E-123//F28K19.13 [Arabidopsis thaliana] >gi|14586402|emb|CAC42910.1| bZIP50 protein [Arabidopsis thaliana]	Unigene45492_All//3.00E-114//AT1G77920| bZIP family transcription factor	Unigene45492_All//0.00E+00//TC149374	bZIP			nr -
Unigene45496_All	1938	18.09	15.79	12.39	16.99	21.80	27.03	2.53	1.88	6.00	-1.96E-01	3.97E-02		-5.46E-01	4.56E-09		3.60E-01	2.50E-06		6.70E-01	7.84E-21		-4.32E-01	8.25E-02		1.25E+00	1.14E-15	Up	Unigene45496_All//gi|15241759|ref|NP_201028.1|//0.00E+00//exostosin family protein [Arabidopsis thaliana]	Unigene45496_All//0.00E+00//AT5G62220| exostosin family protein	Unigene45496_All//0.00E+00//DW234685			GO:0016740//GO:0044464	nr -
Unigene45497_All	1962	1.84	3.00	3.72	6.35	6.65	5.66	2.05	1.02	1.64	7.03E-01	4.01E-03		1.01E+00	8.09E-06	Up	6.76E-02	7.48E-01		-1.65E-01	3.88E-01		-1.00E+00	2.49E-04	Down	-3.16E-01	2.50E-01		Unigene45497_All//gi|297797191|ref|XP_002866480.1|//0.00E+00//exostosin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312315|gb|EFH42739.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45497_All//0.00E+00//AT5G62220| exostosin family protein	Unigene45497_All//7.00E-167//DW234685			GO:0016740//GO:0044464	nr +
Unigene45499_All	1711	3.09	1.42	1.68	10.28	11.41	6.47	9.79	8.50	6.40	-1.12E+00	2.52E-05	Down	-8.78E-01	1.22E-03		1.51E-01	2.98E-01		-6.68E-01	1.95E-07		-2.03E-01	1.25E-01		-6.12E-01	2.39E-07		Unigene45499_All//gi|224121164|ref|XP_002330759.1|//7.00E-16//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222872561|gb|EEF09692.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene45499_All//1.00E-11//AT4G26090| RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding	Unigene45499_All//0.00E+00//ES843115		ko04626|Plant-pathogen interaction		nr -
Unigene4550_All	1780	0.12	0.40	0.42	3.22	2.63	4.16	4.39	30.76	36.17	1.76E+00	5.60E-02		1.83E+00	5.05E-02		-2.91E-01	2.75E-01		3.71E-01	1.01E-01		2.81E+00	2.56E-204	Up	3.04E+00	2.77E-265	Up	Unigene4550_All//gi|15224473|ref|NP_181360.1|//4.00E-82//DNA-binding protein-related [Arabidopsis thaliana] >gi|179810140|gb|AAL50816.1|AF453582_1 GT-1 like transcription factor [Arabidopsis thaliana]	Unigene4550_All//5.00E-39//AT2G38250| DNA-binding protein-related	Unigene4550_All//0.00E+00//DW513921	Trihelix			nr +
Unigene45500_All	3806	1.18	0.41	0.67	3.97	4.97	3.44	3.78	3.38	2.99	-1.52E+00	6.01E-07	Down	-8.16E-01	6.13E-03		3.25E-01	9.39E-03		-2.05E-01	2.02E-01		-1.59E-01	2.90E-01		-3.35E-01	1.00E-02		Unigene45500_All//gi|224124220|ref|XP_002319275.1|//3.00E-66//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222857651|gb|EEE95198.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene45500_All//2.00E-52//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene45500_All//0.00E+00//ES843115		ko04626|Plant-pathogen interaction		nr +
Unigene45501_All	777	13.40	7.37	6.31	15.45	13.52	12.73	4.08	3.50	4.56	-8.63E-01	1.36E-06		-1.09E+00	7.45E-09	Down	-1.93E-01	2.92E-01		-2.80E-01	1.09E-01		-2.23E-01	5.29E-01		1.61E-01	6.01E-01		Unigene45501_All//gi|15242784|ref|NP_201152.1|//1.00E-90//NF-YC4 (NUCLEAR FACTOR Y, SUBUNIT C4); DNA binding / transcription factor [Arabidopsis thaliana] >gi|79332019|ref|NP_001032130.1| NF-YC4 (NUCLEAR FACTOR Y, SUBUNIT C4); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75262732|sp|Q9FWN3.1|NFYC4_ARATH RecName: Full=Nuclear transcription factor Y subunit C-4; Short=AtNF-YC-4 >gi|9758288|dbj|BAB08812.1| transcription factor Hap5a-like protein [Arabidopsis thaliana] >gi|18252935|gb|AAL62394.1| transcription factor Hap5a-like protein [Arabidopsis thaliana] >gi|23198020|gb|AAN15537.1| transcription factor Hap5a-like protein [Arabidopsis thaliana] >gi|222423523|dbj|BAH19731.1| AT5G63470 [Arabidopsis thaliana]	Unigene45501_All//7.00E-66//AT3G48590| NF-YC1 (NUCLEAR FACTOR Y, SUBUNIT C1); DNA binding / transcription activator/ transcription factor	Unigene45501_All//0.00E+00//TC136458	CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication	GO:0001071//GO:0003677//GO:0005667//GO:0030528//GO:0032583	nr -
Unigene45504_All	272	1.92	1.86	2.35	0.73	0.25	2.66	5.91	17.36	6.74	-4.63E-02	9.76E-01		2.88E-01	7.25E-01		-1.53E+00	4.15E-01		1.86E+00	4.71E-02		1.56E+00	5.16E-09	Up	1.90E-01	6.51E-01		Unigene45504_All//gi|15225315|ref|NP_176558.1|//4.00E-06//CYP86A7; fatty acid (omega-1)-hydroxylase/ oxygen binding [Arabidopsis thaliana]	Unigene45504_All//1.00E-07//AT1G63710| CYP86A7; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene45504_All//5.00E-126//ES831245			GO:0005488//GO:0016713//GO:0032787	nr +
Unigene45505_All	595	2.81	0.51	0.72	0.92	0.81	2.58	0.64	1.12	4.69	-2.46E+00	4.49E-05	Down	-1.97E+00	7.74E-04	Down	-1.85E-01	8.25E-01		1.49E+00	7.99E-03		8.14E-01	3.15E-01		2.87E+00	1.65E-11	Up	Unigene45505_All//gi|224130296|ref|XP_002320802.1|//2.00E-91//cytochrome P450 [Populus trichocarpa] >gi|222861575|gb|EEE99117.1| cytochrome P450 [Populus trichocarpa]	Unigene45505_All//8.00E-81//AT1G01600| CYP86A4; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene45505_All//0.00E+00//gi|78347528|gb|DT567802.1|DT567802		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0016712//GO:0016713//GO:0032787	nr -

Unigene45506_All	2151	2.12	1.88	0.59	1.13	1.81	0.92	5.66	11.68	6.63	-1.67E-01	5.95E-01		-1.83E+00	1.82E-08	Down	6.73E-01	2.77E-02		-2.97E-01	5.03E-01		1.04E+00	2.17E-24	Up	2.28E-01	9.49E-02		Unigene45506_All//gi|224130296|ref|XP_002320802.1|//0.00E+00//cytochrome P450 [Populus trichocarpa]>gi|222861575|gb|EEE99117.1|cytochrome P450 [Populus trichocarpa]	Unigene45506_All//0.00E+00//ES813176	Unigene45506_All//0.00E+00//ES813176		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0016712//GO:0016713//GO:0032787	nr -
Unigene45507_All	2096	5.24	2.90	2.52	5.61	4.78	4.55	0.87	1.24	10.83	-8.54E-01	8.40E-07		-1.06E+00	6.01E-09	Down	-2.30E-01	1.91E-01		-3.03E-01	8.12E-02		5.11E-01	1.53E-01		3.64E+00	1.65E-110	Up	Unigene45507_All//gi|224130296|ref|XP_002320802.1|//0.00E+00//cytochrome P450 [Populus trichocarpa]>gi|222861575|gb|EEE99117.1|cytochrome P450 [Populus trichocarpa]	Unigene45507_All//0.00E+00//AT2G45970| CYP86A8; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene45507_All//0.00E+00//gi|78347528|gb|DT567802.1|DT567802	Unigene45507_All//0.00E+00//gi|78347528|gb|DT567802.1|DT567802	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0016712//GO:0016713//GO:0032787	nr -
Unigene45510_All	1376	3.19	3.90	6.89	5.00	5.76	4.89	11.37	8.14	7.30	2.89E-01	2.85E-01		1.11E+00	2.24E-08	Up	2.04E-01	3.89E-01		-3.08E-02	9.18E-01		-4.82E-01	1.24E-04		-6.40E-01	2.01E-07		Unigene45510_All//gi|124359649|gb|AB032334.2|//2.00E-37//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene45510_All//6.00E-11//AT1G21280| unknown protein	Unigene45510_All//3.00E-137//gi|13245564|gb|BE052981.2|BE052981	Unigene45510_All//3.00E-137//gi|13245564|gb|BE052981.2|BE052981		GO:0005488	nr +
Unigene45511_All	2185	24.64	62.17	40.19	11.97	20.30	14.59	5.19	10.06	5.56	1.34E+00	1.58E-154	Up	7.06E-01	3.89E-34		7.62E-01	3.22E-24		2.86E-01	2.97E-03		9.56E-01	1.20E-18		1.01E-01	5.53E-01		Unigene45511_All//gi|255552335|ref|XP_002517212.1|//0.00E+00//Acyl-CoA synthetase [Ricinus communis]>gi|83320525|gb|ABC02881.1| ACS2 [Ricinus communis]>gi|223543847|gb|EEF45375.1| Acyl-CoA synthetase [Ricinus communis]	Unigene45511_All//0.00E+00//AT3G05970| LACS6 (long-chain acyl-CoA synthetase 6); long-chain-fatty-acid-CoA ligase	Unigene45511_All//0.00E+00//TC138878	Unigene45511_All//0.00E+00//TC138878	ko04146|Peroxisome//ko00071|Fatty acid metabolism	GO:0015645//GO:0044464	nr -
Unigene45519_All	836	11.33	5.70	8.28	5.54	6.18	3.73	3.69	0.60	1.05	-9.92E-01	1.90E-07		-4.52E-01	2.18E-02		1.57E-01	5.98E-01		-5.72E-01	4.27E-02		-2.62E+00	2.43E-11	Down	-1.82E+00	9.22E-08	Down	Unigene45519_All//gi|6689892|gb|AAF23892.1|AF152172.1|//3.00E-42//pectin methyl esterase [Solanum tuberosum]	Unigene45519_All//2.00E-38//AT1G53830| ATPME2; pectinesterase	Unigene45519_All//1.00E-178//TC161288	Unigene45519_All//1.00E-178//TC161288	ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0030234//GO:0045229//GO:0071555	nr -
Unigene4552_All	920	3.98	8.10	5.15	11.15	11.34	11.19	3.95	6.27	8.23	1.02E+00	2.72E-06	Up	3.72E-01	2.18E-01		2.40E-02	9.17E-01		5.00E-03	9.79E-01		6.66E-01	2.50E-03		1.06E+00	2.72E-08	Up	Unigene4552_All//gi|15228190|ref|NP_191137.1|//5.00E-12//glycosyl hydrolase family 17 protein [Arabidopsis thaliana]>gi|7263566|emb|CAB81603.1| beta-1, 3-glucanase-like protein [Arabidopsis thaliana]		Unigene4552_All//0.00E+00//gi|164312969|gb|ES803342.1|ES803342			nr -
Unigene45520_All	2063	163.40	72.04	112.36	89.08	109.80	79.67	39.47	5.09	15.62	-1.18E+00	0.00E+00	Down	-5.40E-01	1.12E-80		3.02E-01	5.28E-23		-1.61E-01	1.44E-05		-2.96E+00	0.00E+00	Down	-1.34E+00	1.56E-117	Down	Unigene45520_All//gi|6689892|gb|AAF23892.1|AF152172.1|//0.00E+00//pectin methyl esterase [Solanum tuberosum]	Unigene45520_All//0.00E+00//AT3G14310| ATPME3; pectinesterase	Unigene45520_All//0.00E+00//gi|78340552|gb|DT560826.1|DT560826	Unigene45520_All//0.00E+00//gi|78340552|gb|DT560826.1|DT560826	ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005576//GO:0030234//GO:0030312//GO:0044424//GO:0045229//GO:0051707//GO:0071555	nr +
Unigene45522_All	1163	27.89	13.77	27.01	39.71	34.02	32.08	17.23	16.75	11.89	-1.02E+00	1.23E-24	Down	-4.62E-02	6.72E-01		-2.23E-01	3.40E-03		-3.08E-01	5.96E-05		-4.12E-02	7.53E-01		-5.36E-01	5.63E-07		Unigene45522_All//gi|1620970|emb|CAA70100.1|//1.00E-171//L-lactate dehydrogenase [Solanum lycopersicum]>gi|1806117|emb|CAA71611.1| L-lactate dehydrogenase [Solanum lycopersicum]	Unigene45522_All//2.00E-155//AT4G17260| L-lactate dehydrogenase, putative	Unigene45522_All//0.00E+00//gi|78340203|gb|DT560477.1|DT560477		ko00010|Glycolysis / Gluconeogenesis//ko00270|Cysteine and methionine metabolism//ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism		nr -
Unigene45523_All	1303	1.73	2.96	4.50	3.78	5.26	5.34	4.15	8.08	26.02	7.75E-01	1.30E-02		1.38E+00	2.24E-07	Up	4.75E-01	3.30E-02		4.96E-01	2.80E-02		9.61E-01	2.01E-09		2.65E+00	4.42E-121	Up	Unigene45523_All//gi|1620970|emb|CAA70100.1|//1.00E-172//L-lactate dehydrogenase [Solanum lycopersicum]>gi|1806117|emb|CAA71611.1| L-lactate dehydrogenase [Solanum lycopersicum]	Unigene45523_All//2.00E-160//AT4G17260| L-lactate dehydrogenase, putative	Unigene45523_All//0.00E+00//TC139352	Unigene45523_All//0.00E+00//TC139352	ko00010|Glycolysis / Gluconeogenesis//ko00270|Cysteine and methionine metabolism//ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism		nr -
Unigene45524_All	1375	8.33	3.98	8.64	9.60	8.06	7.75	23.80	18.42	5.65	-1.07E+00	7.42E-10	Down	5.15E-02	7.76E-01		-2.52E-01	1.18E-01		-3.09E-01	5.63E-02		-3.70E-01	1.07E-05		-2.07E+00	1.28E-88	Down	Unigene45524_All//gi|1620970|emb|CAA70100.1|//1.00E-172//L-lactate dehydrogenase [Solanum lycopersicum]>gi|1806117|emb|CAA71611.1| L-lactate dehydrogenase [Solanum lycopersicum]	Unigene45524_All//1.00E-161//AT4G17260| L-lactate dehydrogenase, putative	Unigene45524_All//0.00E+00//TC139810	Unigene45524_All//0.00E+00//TC139810	ko00010|Glycolysis / Gluconeogenesis//ko00270|Cysteine and methionine metabolism//ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism		nr -
Unigene45526_All	1497	22.37	11.78	15.69	22.99	21.69	19.64	21.46	11.84	8.28	-9.25E-01	9.11E-22		-5.12E-01	8.08E-08		-8.41E-02	4.57E-01		-2.27E-01	1.63E-02		-8.59E-01	1.40E-22		-1.37E+00	6.71E-49	Down	Unigene45526_All//gi|115488654|ref|NP_001066814.1|//6.00E-84//Os12g0498800 [Oryza sativa Japonica Group]>gi|77555808|gb|ABA98604.1| expressed protein [Oryza sativa (japonica cultivar-group)]>gi|113649321|dbj|BAF29833.1|Os12g0498800 [Oryza sativa Japonica Group]	Unigene45526_All//3.00E-85//AT5G55610| unknown protein	Unigene45526_All//0.00E+00//TC176830			GO:0043231	nr +
Unigene45528_All	506	3.41	2.90	1.89	7.68	5.24	2.95	0.42	0.33	0.71	-2.33E-01	6.14E-01		-8.49E-01	1.05E-01		-5.51E-01	6.86E-02		-1.38E+00	1.17E-05	Down	-3.39E-01	8.11E-01		7.62E-01	4.99E-01		Unigene45528_All//gi|168988195|gb|ACA33266.1|//5.00E-15//nuclear transport family protein [Cucumis sativus]	Unigene45528_All//7.00E-07//AT5G43960| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene45528_All//2.00E-176//TC177756	Unigene45528_All//2.00E-176//TC177756		GO:0003676//GO:0006810//GO:0044464	nr +
Unigene4553_All	886	9.45	11.61	7.87	5.40	9.02	3.82	11.21	8.63	4.36	2.97E-01	1.10E-01		-2.63E-01	2.34E-01		7.40E-01	1.45E-04		-4.98E-01	7.67E-02		-3.77E-01	2.26E-02		-1.36E+00	1.60E-15	Down			Unigene4553_All//0.00E+00//gi|164251407|gb|ES814289.1|ES814289				
Unigene45537_All	2719	5.62	5.39	3.94	31.35	19.00	17.44	26.05	18.95	11.05	-6.12E-02	6.88E-01		-5.13E-01	5.35E-04		-7.23E-01	1.43E-43		-8.46E-01	1.72E-50		-4.59E-01	1.51E-16		-1.24E+00	9.45E-91	Down	Unigene45537_All//gi|108710112|gb|ABF97907.1|//0.00E+00//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene45537_All//0.00E+00//AT3G11760| unknown protein	Unigene45537_All//0.00E+00//ES813969			GO:0043231	nr -
Unigene45540_All	285	5.14	2.31	2.06	1.22	0.00	2.06	7.86	5.57	2.66	-1.15E+00	3.81E-02		-1.32E+00	2.55E-02		-1.03E+01	9.44E-03		7.52E-01	4.67E-01		-4.97E-01	2.11E-01		-1.57E+00	6.40E-05	Down	Unigene45540_All//gi|224137522|ref|XP_002327147.1|//2.00E-16//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]>gi|222835462|gb|EEE73897.1|glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene45540_All//7.00E-05//AT2G17260| GLR2 (GLUTAMATE RECEPTOR 2); intracellular ligand-gated ion channel	Unigene45540_All//5.00E-49//CO069891			GO:0005215//GO:0044464	nr +
Unigene45543_All	1154	3.63	10.23	7.52	15.37	14.65	13.15	23.16	25.24	20.37	1.50E+00	1.51E-16	Up	1.05E+00	3.73E-07	Up	-6.88E-02	6.68E-01		-2.25E-01	1.16E-01		1.25E-01	2.28E-01		-1.85E-01	5.61E-02		Unigene45543_All//gi|145567026|gb|ABP81863.1|//1.00E-103//LATE BLOOMER 1 [Pisum sativum]	Unigene45543_All//4.00E-95//AT1G22770| GI (GIGANTEA)	Unigene45543_All//0.00E+00//TC136948	Unigene45543_All//0.00E+00//TC136948	ko04712|Circadian rhythm - plant	GO:0000302//GO:0005488//GO:0009266//GO:0009639//GO:0010468//GO:0031981//GO:0048511//GO:0048582	nr +
Unigene45544_All	1731	2.12	7.05	3.32	5.18	6.54	6.78	34.07	36.82	24.72	1.74E+00	5.17E-21	Up	6.51E-01	1.17E-02		3.37E-01	4.82E-02		3.89E-01	2.12E-02		1.12E-01	8.66E-02		-4.63E-01	1.38E-14		Unigene45544_All//gi|145567026|gb|ABP81863.1|//0.00E+00//LATE BLOOMER 1 [Pisum sativum]	Unigene45544_All//3.00E-179//AT1G22770| GI (GIGANTEA)	Unigene45544_All//0.00E+00//TC171969	Unigene45544_All//0.00E+00//TC171969	ko04712|Circadian rhythm - plant		nr +
Unigene4555_All	1121	2.66	30.96	15.91	2.18	8.05	12.89	11.58	46.08	38.06	3.54E+00	7.85E-132	Up	2.58E+00	1.65E-48	Up	1.89E+00	5.00E-20	Up	2.57E+00	7.12E-43	Up	1.99E+00	3.79E-128	Up	1.72E+00	2.31E-88	Up			Unigene4555_All//0.00E+00//CA994161				
Unigene45550_All	2863	4.26	2.42	4.50	3.69	3.24	1.51	3.22	1.65	1.38	-8.12E-01	6.39E-07		8.01E-02	6.40E-01		-1.89E-01	3.26E-01		-1.28E+00	7.92E-13	Down	-9.65E-01	2.07E-08		-1.22E+00	2.17E-12	Down	Unigene45550_All//14149112|dbj|BAB53653.1|//7.00E-94//bp55 [Brugsiera gymnorhiza]	Unigene45550_All//1.00E-40//AT4G36550| binding / ubiquitin-protein ligase	Unigene45550_All//0.00E+00//gi|109849994|gb|DW478973.1|DW478973		ko01141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene45552_All	493	0.64	0.41	2.05	1.11	1.12	1.28	2.66	2.80	7.52	-6.31E-01	6.22E-01		1.69E+00	2.74E-02		7.90E-03	9.83E-01		2.07E-01	8.23E-01		7.36E-02	8.96E-01		1.50E+00	4.29E-07	Up	Unigene45552_All//gi|115441287|ref|NP_001044923.1|//2.00E-27//Os01g0869000 [Oryza sativa Japonica Group]>gi|113534454|dbj|BAF06837.1|Os01g0869000 [Oryza sativa Japonica Group]	Unigene45552_All//3.00E-23//AT1G71240| unknown protein	Unigene45552_All//1.00E-32//gi|109882244|gb|DW511214.1|DW511214			GO:0043231	nr +
Unigene45553_All	2891	3.22	4.15	2.12	3.27	3.53	4.16	7.39	11.93	22.31	3.67E-01	2.74E-02		-6.05E-01	2.02E-03		1.07E-01	6.13E-01		3.44E-01	4.18E-02		6.92E-01	7.37E-17		1.59E+00	5.47E-120	Up	Unigene45553_All//gi|115441287|ref|NP_001044923.1|//0.00E+00//Os01g0869000 [Oryza sativa Japonica Group]>gi|113534454|dbj|BAF06837.1|Os01g0869000 [Oryza sativa Japonica Group]	Unigene45553_All//0.00E+00//AT1G71240| unknown protein	Unigene45553_All//4.00E-154//TC173352			GO:0043231	nr -
Unigene45554_All	3763	5.23	10.61	5.28	10.72	12.29	16.36	12.64	30.42	49.36	1.02E+00	3.68E-30	Up	1.38E-02	9.36E-01		1.97E-01	1.22E-02		6.09E-01	1.08E-20		1.27E+00	2.45E-147	Up	1.97E+00	0.00E+00	Up	Unigene45554_All//gi|115480511|ref|NP_001063849.1|//1.00E-135//Os09g0547300 [Oryza sativa Japonica Group]>gi|113632082|dbj|BAF25763.1|Os09g0547300 [Oryza sativa Japonica Group]	Unigene45554_All//6.00E-163//AT4G35240| unknown protein	Unigene45554_All//0.00E+00//gi|164353365|gb|ES795047.1|ES795047				nr +
Unigene45556_All	3198	8.62	4.01	5.23	24.70	17.99	15.11	10.81	8.98	5.13	-1.10E+00	6.14E-24	Down	-7.22E-01	1.57E-11		-4.57E-01	7.45E-18		-7.09E-01	1.23E-34		-2.68E-01	1.22E-03		-1.08E+00	6.37E-36	Down	Unigene45556_All//gi|225424570|ref|XP_002282089.1|//0.00E+00//PREDICTED: similar to oxysterol-binding family protein [Vitis vinifera]	Unigene45556_All//0.00E+00//AT1G13170| ORP1D (OSBP(OXYSTEROL BINDING PROTEIN)-RELATED PROTEIN 1D); oxysterol binding	Unigene45556_All//0.00E+00//TC140202			GO:0005543//GO:0006629//GO:0023060//GO:0032934	nr -
Unigene45558_All	2350	1.83	3.36	4.62	2.73	3.85	2.98	4.23	6.79	5.53	8.82E-01	2.39E-05		1.34E+00	1.39E-12	Up	4.95E-01	7.79E-03		1.24E-01	6.33E-01		6.84E-01	4.10E-08		3.86E-01	4.79E-03		Unigene45558_All//gi|240256055|ref|NP_194189.5|//0.00E+00//RES1 (ROP1 ENHANCER 1); Rho GTPase activator/ Rho GTPase binding / phosphoinositide binding [Arabidopsis thaliana]	Unigene45558_All//4.00E-156//AT4G24580| RES1 (ROP1 ENHANCER 1); Rho GTPase activator/ Rho GTPase binding / phosphoinositide binding	Unigene45558_All//4.00E-178//CO078906				nr +
Unigene45559_All	1668	18.32	43.71	20.30	60.57	61.52	40.34	47.53	19.59	57.11	1.25E+00	1.30E-75	Up	1.49E-01	1.56E-01		2.26E-02	7.66E-01		-5.86E-01	1.34E-31		-1.28E+00	8.44E-104	Down	2.65E-01	1.24E-08		Unigene45559_All//gi|226425257|gb|ACO53628.1|//0.00E+00//bHLH domain protein [Gossypium hirsutum]	Unigene45559_All//2.00E-76//AT1G32640| MYC2; DNA binding / transcription activator/ transcription factor	Unigene45559_All//0.00E+00//gi|78338664|gb|DT558938.1|DT558938	Unigene45559_All//0.00E+00//gi|78338664|gb|DT558938.1|DT558938	bHLH	ko04626|Plant-pathogen interaction	GO:0010468//GO:0043231	nr +
Unigene4556_All	687	13.25	8.04	8.76	15.15	14.94	18.14	27.51	13.32	12.93	-7.21E-01	1.55E-04		-5.97E-01	2.60E-03		-2.09E-02	9.19E-01		2.60E-01	1.32E-01		-1.05E+00	1.29E-18	Down	-1.09E+00	1.95E-20	Down	Unigene4556_All//gi|195604664|gb|ACG24162.1|//4.00E-55//small nuclear ribonucleoprotein Sm D1 [Zea mays]	Unigene4556_All//2.00E-44//AT4G02840| small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative	Unigene4556_All//0.00E+00//gi|164307931|gb|ES819441.1|ES819441	Unigene4556_All//0.00E+00//gi|164307931|gb|ES819441.1|ES819441		ko03040|Spliceosome		nr +
Unigene45563_All	708	2.59	7.01	1.81	0.42	0.10	0.77	0.30	2.72	1.91	1.44E+00	5.00E-07	Up	-5.19E-01	3.11E-01		-2.12E+00	1.65E-01		8.59E-01	4.23E-01		3.18E+00	1.04E-08	Up	2.68E+00	1.36E-05	Up	Unigene45563_All//gi|297847712|ref|XP_002891737.1|//3.00E-25//sodium/calcium exchanger family protein [Arabidopsis lyrata subsp. lyrata]>gi|297337579|gb|EFH67996.1|sodium/calcium exchanger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45563_All//2.00E-26//AT1G53210| sodium/calcium exchanger family protein / calcium-binding EF hand family protein	Unigene45563_All//3.00E-117//TC132319			GO:0005773//GO:0006810//GO:0031090//GO:0031224//GO:0046872	nr +
Unigene45564_All	2079	61.61	45.94	49.59	7.57	8.41	44.27	15.25	122.65	80.54	-4.23E-01	9.02E-21		-3.13E-01	1.25E-11		1.52E-01	3.15E-01		2.55E+00	1.10E-269	Up	3.01E+00	0.00E+00	Up	2.40E+00	0.00E+00	Up	Unigene45564_All//gi|30695448|ref|NP_564623.2|//0.00E+00//sodium/calcium exchanger family protein / calcium-binding EF hand family protein [Arabidopsis thaliana]	Unigene45564_All//0.00E+00//AT1G53210| sodium/calcium exchanger family protein / calcium-binding EF hand family protein	Unigene45564_All//0.00E+00//TC155990			GO:0005773//GO:0006810//GO:0031090//GO:0031224//GO:0046872	nr +
Unigene45565_All	1440	7.30	8.06	6.29	14.94	11.98	11.82	12.83	6.59	6.06	1.42E-01	4.34E-01		-2.16E-01	2.73E-01		-3.19E-01	5.21E-03		-3.38E-01	4.41E-03		-9.62E-01	5.83E-16		-1.08E+00	8.16E-20	Down	Unigene45565_All//gi|224068797|ref|XP_002326202.1|//0.00E+00//s-adenosylmethionine synthetase 6 [Populus trichocarpa]>gi|223635286|sp|A9FK5.1|METK4_POPTR RecName: Full=S-adenosylmethionine synthetase 4; Short=AdoMet synthase 4; AltName: Full=Methionine adenosyltransferase 4; Short=MAT 4>gi|222833395|gb|EEE71872.1| s-adenosylmethionine synthetase 6 [Populus trichocarpa]	Unigene45565_All//0.00E+00//AT2G36880| MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase	Unigene45565_All//0.00E+00//TC135867		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0000097//GO:0016020//GO:0016765//GO:0032559//GO:0044424//GO:0046914	nr +

Unigene45566_All	1506	0.24	0.37	0.71	1.29	1.60	0.87	2.84	1.58	1.40	6.06E-01	5.31E-01			1.54E+00	3.53E-02		3.11E-01	5.14E-01			-5.69E-01	2.36E-01			-8.42E-01	1.30E-03		-1.02E+00	7.90E-05	Down	Unigene45566_All//gi|224068797|ref|XP_002326202.1|//0.00E+00//s-adenosylmethionine synthetase 6 [Populus trichocarpa] >gi|223635286|sp|A9FPK5.1|METK4_POPTR RecName: Full=S-adenosylmethionine synthase 4; Short=AdoMet synthase 4; AltName: Full=Methionine adenosyltransferase 4; Short=MAT 4 >gi|222833395|gb|EEE71872.1| s-adenosylmethionine synthetase 6 [Populus trichocarpa]	Unigene45566_All//0.00E+00//AT2G36880| MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase	Unigene45566_All//0.00E+00//TC135867		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0000097//GO:0016020//GO:0016765//GO:0032559//GO:0044424//GO:0046914	nr -
Unigene45567_All	1557	2.76	2.73	0.62	3.71	3.56	3.48	5.16	1.29	3.79	-1.15E-02	9.87E-01			-2.16E+00	8.67E-10	Down	-5.98E-02	8.25E-01			-9.25E-02	7.32E-01			-2.00E+00	1.07E-20	Down	-4.46E-01	1.24E-02		Unigene45567_All//gi|1709004|sp|P50302.1|METK2_ACTCH//0.00E+00//RecName: Full=S-adenosylmethionine synthase 2; Short=AdoMet synthase 2; AltName: Full=Methionine adenosyltransferase 2; Short=MAT 2 >gi|726028|gb|AAA81377.1| S-adenosylmethionine synthetase [Actinidia chinensis]	Unigene45567_All//0.00E+00//AT2G36880| MAT3 (methionine adenosyltransferase 3); copper ion binding / methionine adenosyltransferase	Unigene45567_All//0.00E+00//TC168110		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0000097//GO:0016020//GO:0016765//GO:0032559//GO:0044424//GO:0046914	nr +
Unigene45568_All	3040	4.39	6.42	5.33	10.54	14.20	13.68	4.02	2.12	13.14	5.48E-01	1.10E-05			2.79E-01	6.34E-02		4.31E-01	8.27E-09			3.77E-01	2.84E-06			-9.25E-01	3.36E-10		1.71E+00	2.67E-82	Up	Unigene45568_All//gi|282161430|gb|ADA79674.1|//0.00E+00//shaker-like potassium channel 1 [Populus euphratica]	Unigene45568_All//0.00E+00//AT2G26650| AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel	Unigene45568_All//0.00E+00//TC167010		ko04626|Plant-pathogen interaction	GO:0000166//GO:0005249//GO:0006970//GO:0030001//GO:0031224//GO:0048588	nr -
Unigene4557_All	1489	1.55	2.38	0.50	9.60	6.24	5.94	4.60	2.16	1.58	6.24E-01	5.75E-02			-1.63E+00	5.02E-04	Down	-6.21E-01	5.23E-06			-6.92E-01	1.62E-06			-1.09E+00	1.05E-07	Down	-1.54E+00	4.89E-13	Down	Unigene4557_All//gi|87240813|gb|AB032671.1|//1.00E-127//RhoGAP; Wiscott-Aldrich syndrome, C-terminal [Medicago truncatula]	Unigene4557_All//3.00E-120//AT5G22400| rac GTPase activating protein, putative	Unigene4557_All//0.00E+00//gi|78350200|gb|DT570474.1|DT570474				nr +
Unigene45570_All	1176	2.49	3.02	2.08	1.36	2.05	2.23	0.79	2.99	4.98	2.76E-01	4.08E-01			-2.58E-01	5.16E-01		5.97E-01	1.58E-01			7.17E-01	7.27E-02			1.92E+00	5.94E-09	Up	2.65E+00	1.42E-21	Up	Unigene45570_All//gi|224132476|ref|XP_002328289.1|//7.00E-83//Cl-channel clc-7 [Populus trichocarpa] >gi|222837804|gb|EEE76169.1| Cl-channel clc-7 [Populus trichocarpa]	Unigene45570_All//3.00E-63//AT4G35440| CLC-E (CHLORIDE CHANNEL E); ion channel/ voltage-gated chloride channel	Unigene45570_All//1.00E-43//TC171818			GO:0003676//GO:0005254//GO:0006260//GO:0009534//GO:0015698//GO:0032124//GO:0034061	nr +
Unigene45571_All	1618	4.04	5.17	2.90	1.69	2.28	3.01	2.59	5.58	6.50	3.54E-01	8.44E-02			-4.81E-01	4.80E-02		4.27E-01	2.06E-01			8.32E-01	2.10E-03			1.11E+00	3.81E-10	Up	1.33E+00	1.17E-15	Up	Unigene45571_All//gi|224132476|ref|XP_002328289.1|//4.00E-95//Cl-channel clc-7 [Populus trichocarpa] >gi|222837804|gb|EEE76169.1| Cl-channel clc-7 [Populus trichocarpa]	Unigene45571_All//6.00E-80//AT4G35440| CLC-E (CHLORIDE CHANNEL E); ion channel/ voltage-gated chloride channel	Unigene45571_All//0.00E+00//TC171818			GO:0003824//GO:0005254//GO:0008152//GO:0009534//GO:0009987//GO:0015698//GO:0031224	nr +
Unigene45573_All	2613	2.06	2.44	1.10	3.91	3.82	3.01	4.30	3.17	2.13	2.45E-01	3.32E-01			-9.06E-01	7.45E-04		-3.23E-02	8.75E-01			-3.78E-01	3.97E-02			-4.43E-01	3.62E-03		-1.01E+00	3.32E-11	Down	Unigene45573_All//gi|10177186|dbj|BAB10320.1|//1.00E-178//mutator-like transposase-like protein [Arabidopsis thaliana]	Unigene45573_All//5.00E-33//AT1G49920| zinc finger protein-related	Unigene45573_All//0.00E+00//ES834616				nr +
Unigene45574_All	2948	25.79	8.32	10.78	143.26	100.09	53.74	81.28	12.50	20.45	-1.63E+00	2.23E-117	Down		-1.26E+00	7.54E-77	Down	-5.17E-01	5.31E-118			-1.41E+00	0.00E+00	Down		-2.70E+00	0.00E+00	Down	-1.99E+00	0.00E+00	Down	Unigene45574_All//gi|18396193|ref|NP_565330.1|//0.00E+00//subtilase family protein [Arabidopsis thaliana]	Unigene45574_All//0.00E+00//AT2G05920| subtilase family protein	Unigene45574_All//0.00E+00//TC138728			GO:0004175//GO:0005515//GO:0005618//GO:0019538//GO:0031410//GO:0044092	nr +
Unigene45577_All	2483	45.89	32.51	38.50	41.15	57.62	60.48	16.04	7.59	11.30	-4.98E-01	1.00E-24			-2.54E-01	3.27E-07		4.86E-01	5.04E-35			5.56E-01	3.43E-42			-1.08E+00	2.68E-40	Down	-5.06E-01	8.96E-12		Unigene45577_All//gi|116268422|gb|ABJ96379.1|//0.00E+00//expressed protein [Prunus persica]	Unigene45577_All//0.00E+00//AT5G65470| unknown protein	Unigene45577_All//0.00E+00//TC166352				nr +
Unigene45579_All	2241	4.72	12.12	4.66	15.74	18.90	36.48	37.19	98.42	288.84	1.36E+00	2.46E-32	Up		-1.81E-02	9.41E-01		2.64E-01	8.08E-04			1.21E+00	2.43E-86	Up		1.40E+00	0.00E+00	Up	2.96E+00	0.00E+00	Up	Unigene45579_All//gi|297814588|ref|XP_002875177.1|//1.00E-153//kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321015|gb|EFH51436.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45579_All//2.00E-146//AT2G02870| kelch repeat-containing F-box family protein	Unigene45579_All//0.00E+00//CO071922				nr -
Unigene4558_All	1896	4.75	2.24	2.30	7.54	5.68	7.55	9.23	8.60	7.44	-1.08E+00	4.57E-08	Down		-1.04E+00	2.76E-07	Down	-4.08E-01	3.92E-03			2.00E-03	9.91E-01			-1.03E-01	4.67E-01		-3.12E-01	7.75E-03		Unigene4558_All//gi|75336890|sp|Q9SA27.1|RH36_ARATH//0.00E+00//RecName: Full=DEAD-box ATP-dependent RNA helicase 36 >gi|4966350|gb|AAD31681.1|AC006341_9 Similar to gb|L13612 DEAD-box protein (dbp45A) from Drosophila melanogaster and is a member of PF|00270 DEAD/DEAH box helicase family [Arabidopsis thaliana]	Unigene4558_All//2.00E-156//AT1G16280| DEAD/DEAH box helicase, putative	Unigene4558_All//0.00E+00//gi|78326381|gb|DT546655.1|DT546655				nr -
Unigene45580_All	364	4.02	30.21	7.31	8.35	13.62	29.53	1.74	23.65	2.30	2.91E+00	4.90E-35	Up		8.62E-01	3.32E-02		7.07E-01	6.84E-03			1.82E+00	4.87E-21	Up		3.76E+00	1.38E-42	Up	4.00E-01	5.65E-01		Unigene45580_All//gi|11561806|gb|AAC83688.2|//1.00E-59//101 kDa heat shock protein [Nicotiana tabacum]	Unigene45580_All//5.00E-58//AT1G74310| AT HSP101 (ARABIDOPSIS THALIANA HEAT SHOCK PROTEIN 101); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding	Unigene45580_All//2.00E-09//gi|78348579|gb|DT568853.1|DT568853			GO:0016462//GO:0032559//GO:0043170//GO:0050896	nr +
Unigene45581_All	3208	4.32	28.90	7.14	6.41	9.84	18.43	3.69	52.54	6.54	2.74E+00	1.60E-274	Up		7.24E-01	9.52E-10		6.18E-01	3.68E-12			1.52E+00	2.64E-88	Up		3.83E+00	0.00E+00	Up	8.27E-01	1.67E-14		Unigene45581_All//gi|530207|gb|AAA66338.1|//0.00E+00//heat shock protein [Glycine max]	Unigene45581_All//5.00E-58//AT1G74310| AT HSP101 (ARABIDOPSIS THALIANA HEAT SHOCK PROTEIN 101); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding	Unigene45581_All//0.00E+00//gi|78328369|gb|DT548643.1|DT548643			GO:0016462//GO:0032559//GO:0043170//GO:0050896	nr +
Unigene45582_All	222	0.00	0.00	0.00	1.35	0.31	0.00	3.05	0.19	1.79	null	null			null	null		-2.12E+00	1.65E-01			-1.04E+01	3.99E-02			-4.02E+00	5.36E-04	Down	-7.64E-01	3.12E-01		Unigene45582_All//gi|297793859|ref|XP_002864814.1|//3.00E-19//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310649|gb|EFH41073.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45582_All//1.00E-15//AT5G62710| leucine-rich repeat family protein / protein kinase family protein	Unigene45582_All//8.00E-29//TC170945			GO:0004702//GO:0006464//GO:0031224//GO:0032559	nr -
Unigene45583_All	2209	1.59	0.55	0.84	9.58	5.86	2.35	7.79	0.98	1.98	-1.53E+00	1.25E-05	Down		-9.11E-01	8.25E-03		-7.09E-01	8.55E-11			-2.03E+00	3.39E-48	Down		-2.99E+00	5.35E-69	Down	-1.97E+00	4.80E-44	Down	Unigene45583_All//gi|297793859|ref|XP_002864814.1|//0.00E+00//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310649|gb|EFH41073.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45583_All//0.00E+00//AT5G62710| leucine-rich repeat family protein / protein kinase family protein	Unigene45583_All//0.00E+00//TC170945			GO:0004702//GO:0006464//GO:0031224//GO:0032559	nr +
Unigene45584_All	2177	2.11	1.51	0.29	2.04	4.57	2.99	7.81	1.15	3.84	-4.83E-01	8.83E-02			-2.85E+00	3.90E-14	Down	1.17E+00	3.67E-11	Up		5.53E-01	1.74E-02			-2.76E+00	7.10E-63	Down	-1.02E+00	9.45E-17	Down	Unigene45584_All//gi|297793859|ref|XP_002864814.1|//0.00E+00//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310649|gb|EFH41073.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45584_All//0.00E+00//AT5G62710| leucine-rich repeat family protein / protein kinase family protein	Unigene45584_All//3.00E-154//gi|164269218|gb|ES808492.1|ES808492			GO:0004702//GO:0006464//GO:0031224//GO:0032559	nr -
Unigene45585_All	4225	2.50	1.74	1.60	6.52	6.38	4.23	7.97	3.69	4.27	-5.25E-01	2.80E-03			-6.44E-01	3.99E-04		-3.10E-02	8.38E-01			-6.23E-01	4.93E-10			-1.11E+00	9.61E-36	Down	-8.99E-01	3.22E-26		Unigene45585_All//gi|224138276|ref|XP_002326562.1|//5.00E-62//nbs-lrr resistance protein [Populus trichocarpa] >gi|105922886|gb|ABF81442.1| NBS-LRR type disease resistance protein [Populus trichocarpa] >gi|222833884|gb|EEE72361.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene45585_All//5.00E-26//AT3G46710| disease resistance protein (CC-NBS-LRR class), putative	Unigene45585_All//0.00E+00//TC178696		ko04626|Plant-pathogen interaction		nr -
Unigene45586_All	2461	7.33	18.55	8.78	8.99	16.04	17.98	30.72	51.00	109.40	1.34E+00	1.56E-52	Up		2.60E-01	4.26E-02		8.35E-01	3.49E-25			1.00E+00	1.42E-34	Up		7.31E-01	3.15E-65		1.83E+00	0.00E+00	Up	Unigene45586_All//gi|224064181|ref|XP_002301399.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222843125|gb|EEE80672.1| GH3 family protein [Populus trichocarpa]	Unigene45586_All//2.00E-154//AT2G46370| JAR1 (JASMONATE RESISTANT 1); ATP binding / adenylyltransferase/ catalytic/ jasmonate-amino synthetase	Unigene45586_All//0.00E+00//TC144227				nr +
Unigene45588_All	2016	11.08	9.05	6.34	11.00	19.56	22.27	8.62	12.79	9.62	-2.93E-01	1.34E-02			-8.06E-01	2.53E-11		8.31E-01	6.16E-25			1.02E+00	4.81E-36	Up		5.70E-01	2.57E-09		1.59E-01	1.84E-01		Unigene45588_All//gi|3695061|gb|AAC62625.1|//1.00E-150//rac GTPase activating protein 2 [Lotus japonicus]	Unigene45588_All//3.00E-124//AT2G46710| rac GTPase activating protein, putative	Unigene45588_All//0.00E+00//TC137600				nr +
Unigene45589_All	497	0.00	1.33	0.64	9.02	7.48	12.99	0.51	3.78	0.40	1.04E+01	6.25E-04	Up		9.33E+00	4.51E-02		-2.70E-01	3.87E-01			5.27E-01	2.46E-02			2.89E+00	7.82E-08	Up	-3.49E-01	7.66E-01		Unigene45589_All//gi|33149681|gb|AP96920.1|//1.00E-58//pyruvate decarboxylase [Dianthus caryophyllus]	Unigene45589_All//1.00E-48//AT5G54960| PDC2 (pyruvate decarboxylase-2); carboxy-lyase/ catalytic/ magnesium ion binding / pyruvate decarboxylase/ thiamin pyrophosphate binding	Unigene45589_All//0.00E+00//gi|109834947|gb|DW233512.1|DW233512		ko00010|Glycolysis / Gluconeogenesis//ko00380|Tryptophan metabolism	GO:0016831//GO:0019842//GO:0043231//GO:0046872	nr -
Unigene4559_All	1033	2.58	2.26	0.67	0.29	0.00	0.00	55.21	73.84	125.73	-1.95E-01	6.15E-01			-1.95E+00	1.31E-05	Down	-8.18E+00	2.01E-02			-8.18E+00	3.99E-02			4.19E-01	3.58E-15		1.19E+00	4.64E-154	Up	Unigene4559_All//gi|300498294|gb|AD623849.1|//4.00E-68//WRKY72 [Solanum lycopersicum]	Unigene4559_All//2.00E-39//AT1G18860| WRKY61; transcription factor	Unigene4559_All//3.00E-16//CO123903	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene45593_All	2734	4.61	2.26	2.96	2.93	3.01	2.44	3.56	1.45	1.95	-1.03E+00	3.38E-10	Down		-6.40E-01	1.02E-04		3.73E-02	8.80E-01			-2.63E-01	2.40E-01			-1.29E+00	1.22E-13	Down	-8.65E-01	9.39E-08		Unigene45593_All//gi|4678317|emb|CAB41128.1|//0.00E+00//aminoacyl-tRNA synthetase [Arabidopsis thaliana]	Unigene45593_All//0.00E+00//AT3G48110| EDD1 (EMBRYO-DEFECTIVE-DEVELOPMENT 1); glycine-tRNA ligase	Unigene45593_All//0.00E+00//TC164341		ko00970|Aminoacyl-tRNA biosynthesis	GO:0003006//GO:0004812//GO:0006418//GO:0009532//GO:0032559//GO:0020026	nr +
Unigene45595_All	214	0.98	2.84	0.25	0.23	0.48	0.21	0.79	7.62	0.00	1.54E+00	1.22E-01			-1.97E+00	3.81E-01		1.05E+00	8.07E-01			-1.42E-01	9.52E-01			3.27E+00	1.24E-07	Up	-9.63E+00	1.08E-01				Unigene45595_All//9.00E-44//gi|13245180|gb|BE052868.2|BE052868				
Unigene45596_All	2371	37.27	175.73	39.55	60.07	39.53	57.66	24.52	201.63	6.72	2.24E+00	0.00E+00	Up		8.56E-02	1.73E-01		-6.04E-01	9.42E-53			-5.90E-02	2.54E-01			3.04E+00	0.00E+00	Up	-1.87E+00	2.06E-136	Down	Unigene45596_All//gi|115486793|ref|NP_001068540.1|//0.00E+00//Os11g0703900 [Oryza sativa Japonica Group] >gi|62733235|gb|AAX95352.1| dnaK-type molecular chaperone hsp70 - rice (fragment) [Oryza sativa Japonica Group] >gi|113645762|dbj|BAF28903.1| Os11g0703900 [Oryza sativa Japonica Group]	Unigene45596_All//0.00E+00//AT5G02500| HSC70-1 (HEAT SHOCK COGNATE PROTEIN 70-1); ATP binding	Unigene45596_All//0.00E+00//TC171696		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr +
Unigene45597_All	2341	8.07	16.17	6.80	16.41	24.18	23.00	18.86	26.33	35.21	1.00E+00	8.29E-28	Up		-2.47E-01	7.83E-02		5.60E-01	4.65E-18			4.87E-01	2.53E-12			4.82E-01	8.26E-16		9.01E-01	9.85E-63		Unigene45597_All//gi|30678998|ref|NP_563716.3|//0.00E+00//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene45597_All//0.00E+00//AT1G04780| ankyrin repeat family protein	Unigene45597_All//0.00E+00//TC173952			GO:0016020	nr -
Unigene45598_All	3114	4.12	5.78	4.70	6.72	8.07	10.11	8.89	9.81	20.80	4.89E-01	1.78E-04			1.92E-01	2.41E-01		2.65E-01	1.46E-02			5.89E-01	2.81E-10			1.42E-01	1.45E-01		1.23E+00	3.24E-81	Up	Unigene45598_All//gi|22325475|ref|NP_178539.2|//0.00E+00//cation efflux family protein [Arabidopsis thaliana]	Unigene45598_All//9.00E-141//AT2G01620| cation efflux family protein	Unigene45598_All//0.00E+00//CO127660			GO:0006811//GO:0015075//GO:0044464	nr +

Unigene4560_All	1291	6.08	3.96	6.31	3.59	2.99	2.03	1.90	1.42	0.65	-6.17E-01	2.90E-03		5.40E-02	8.07E-01		-2.65E-01	3.84E-01		-8.23E-01	2.94E-03		-4.15E-01	2.74E-01		-1.55E+00	3.01E-05	Down	Unigene4560_All//gi|18406750|ref|NP_566039.1|//1.00E-156//glycoprotease M22 family protein [Arabidopsis thaliana] >gi|18460924|gb|AAK00530.1| sialoglycoprotease GCP1 [Arabidopsis thaliana]	Unigene4560_All//5.00E-158//AT2G45270| glycoprotease M22 family protein	Unigene4560_All//0.00E+00//gi|48804853|gb|CO106167.1|CO106167				nr -
Unigene45601_All	2355	4.55	8.86	3.87	3.60	2.84	2.63	5.24	2.95	2.55	9.61E-01	1.17E-14		-2.36E-01	2.31E-01		-3.42E-01	8.68E-02		-4.53E-01	2.40E-02		-8.31E-01	9.78E-09		-1.04E+00	1.10E-12	Down	Unigene45601_All|gi|75115359|sp|Q66Q2.1|Y5162_ARATH|3.00E-96//RecName: Full=Uncharacterized protein At5g41620 >gi|51536470|gb|AAU05473.1| At5g41620 [Arabidopsis thaliana] >gi|53850503|gb|AAU95428.1| At5g41620 [Arabidopsis thaliana]	Unigene45601_All//2.00E-97//AT5G41620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, plasma membrane; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: intracellular protein transport protein USO1-related (TAIR:AT1G64180.1); Has 2568 Blast hits to 2157 proteins in 267 species: Archae - 27; Bacteria - 258; Metazoa - 955; Fungi - 181; Plants - 134; Viruses - 0; Other Eukaryotes - 1013 (source: NCBI BLink).	Unigene45601_All//0.00E+00//TC142544			GO:0009536//GO:0016020	nr +
Unigene45609_All	924	4.36	3.95	3.92	11.05	10.14	6.70	2.52	0.77	1.68	-1.43E-01	6.31E-01		-1.54E-01	6.20E-01		-1.25E-01	5.54E-01		-7.23E-01	3.43E-05		-1.71E+00	2.03E-05	Down	-5.82E-01	1.08E-01		Unigene45609_All//gi|224589493|gb|ACN59280.1|//2.00E-96//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene45609_All//7.00E-97//AT2G01210| leucine-rich repeat transmembrane protein kinase, putative	Unigene45609_All//0.00E+00//gi|109863205|gb|DW492182.1|DW492182		ko04626|Plant-pathogen interaction	GO:0004672//GO:0005618//GO:0006464//GO:0007167//GO:0009532//GO:0016020//GO:0016491//GO:0031410//GO:0032559	nr +
Unigene45610_All	2742	7.42	5.80	6.82	15.70	16.85	14.08	9.16	3.55	4.75	-3.55E-01	3.97E-03		-1.23E-01	3.89E-01		1.03E-01	2.60E-01		-1.57E-01	7.60E-02		-1.37E+00	5.86E-37	Down	-9.47E-01	1.61E-21		Unigene45610_All|gi|15912327|gb|AL08297.1|//0.00E+00//At1g25320/F4F7_17 [Arabidopsis thaliana] >gi|34365565|gb|AAQ65091.1| At1g25320/F4F7_17 [Arabidopsis thaliana] >gi|224589398|gb|ACN59233.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene45610_All//0.00E+00//AT1G25320| leucine-rich repeat transmembrane protein kinase, putative	Unigene45610_All//0.00E+00//TC155349			GO:0004672//GO:0005618//GO:0006464//GO:0007167//GO:0009532//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene45611_All	393	2.53	0.90	0.27	2.28	2.89	3.45	0.65	1.17	1.42	-1.49E+00	3.93E-02		-3.22E+00	7.83E-04	Down	3.42E-01	6.20E-01		5.96E-01	3.36E-01		8.58E-01	3.96E-01		1.14E+00	1.91E-01					Unigene45611_All//6.00E-22//ES806214				
Unigene45612_All	599	1.75	5.16	2.04	2.91	3.91	3.17	6.99	8.30	4.66	1.56E+00	3.62E-05	Up	2.27E-01	7.03E-01		4.26E-01	3.40E-01		1.22E-01	8.06E-01		2.49E-01	3.56E-01		-5.86E-01	2.22E-02					Unigene45612_All//4.00E-147//ES798467				
Unigene4562_All	1270	6.92	4.07	4.44	36.44	48.02	17.25	0.90	1.42	0.44	-7.66E-01	8.38E-05		-6.39E-01	1.57E-03		3.98E-01	1.23E-10		-1.08E+00	2.72E-41	Down	6.55E-01	1.38E-01		-1.03E+00	5.95E-02		Unigene4562_All|gi|297609840|ref|NP_001063742.2|//4.00E-07//Os09g0529300 [Oryza sativa Japonica Group] >gi|255679079|dbj|BAF25656.2| Os09g0529300 [Oryza sativa Japonica Group]	Unigene4562_All//2.00E-26//AT2G46640| unknown protein	Unigene4562_All//0.00E+00//TC152254				nr +
Unigene45620_All	2243	85.79	116.52	106.57	53.68	88.12	47.30	4.35	9.35	10.41	4.42E-01	7.46E-45		3.13E-01	3.88E-21		7.15E-01	4.88E-96		-1.83E-01	9.04E-05		1.10E+00	2.49E-22	Up	1.26E+00	5.47E-31	Up	Unigene45620_All|gi|15219408|ref|NP_175088.1|//0.00E+00//CH1 (CHLORINA 1); chlorophyllide a oxygenase [Arabidopsis thaliana] >gi|75264959|sp|Q9MBA1.1|CAO_ARATH RecName: Full=Chlorophyllide a oxygenase, chloroplastic; Short=Chlorophyll a oxygenase; AltName: Full=Chlorophyll b synthase; Short=AtCAO; Flags: Precursor >gi|13876511|gb|AAK43487.1|AC08480_12 chlorophyll a oxygenase [Arabidopsis thaliana] >gi|6853279|dbj|BAB90462.1| chlorophyll a oxygenase [Arabidopsis thaliana] >gi|22135956|gb|AAM91560.1| chlorophyll a oxygenase [Arabidopsis thaliana] >gi|25083487|gb|AAN72086.1| chlorophyll a oxygenase [Arabidopsis thaliana] >gi|110737210|dbj|BAF00553.1| chlorophyll a oxygenase [Arabidopsis thaliana]	Unigene45620_All//0.00E+00//AT1G44446| CH1 (CHLORINA 1); chlorophyllide a oxygenase	Unigene45620_All//0.00E+00//DR454218		ko00860|Porphyrin and chlorophyll metabolism	GO:0006779//GO:0009528//GO:0016703//GO:0034357//GO:0046914//GO:0051536	nr -
Unigene45621_All	467	5.60	3.47	6.16	11.73	10.18	6.48	14.67	10.20	3.41	-6.90E-01	7.70E-02		1.36E-01	7.17E-01		-2.06E-01	4.72E-01		-8.57E-01	6.22E-04		-5.24E-01	9.12E-03		-2.10E+00	1.60E-19	Down	Unigene45621_All|gi|30683873|ref|NP_196756.2|//9.00E-52//protein homodimerization [Arabidopsis thaliana] >gi|42573343|ref|NP_974768.1| protein homodimerization [Arabidopsis thaliana] >gi|75147169|sp|Q84WC2.1|LOG8_ARATH RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG8; AltName: Full=Protein LONELY GUY 8; AltName: Full=LOG family protein At5g11950 >gi|30102598|gb|AAP21217.1| At5g11950 [Arabidopsis thaliana] >gi|110743604|dbj|BAE99639.1| lysine decarboxylase - like protein [Arabidopsis thaliana]	Unigene45621_All//6.00E-53//AT5G11950| protein homodimerization	Unigene45621_All//0.00E+00//gi|164260417|gb|ES819569.1|ES819569			GO:0003824//GO:0043231//GO:0044444	nr -
Unigene45622_All	917	18.43	16.19	16.84	36.07	28.43	21.33	75.11	41.52	16.29	-1.87E-01	2.03E-01		-1.30E-01	3.93E-01		-3.44E-01	8.52E-05		-7.58E-01	1.35E-16		-8.55E-01	3.84E-47		-2.20E+00	1.10E-200	Down	Unigene45622_All//gi|30683873|ref|NP_196756.2|//3.00E-95//protein homodimerization [Arabidopsis thaliana] >gi|42573343|ref|NP_974768.1| protein homodimerization [Arabidopsis thaliana] >gi|75147169|sp|Q84WC2.1|LOG8_ARATH RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG8; AltName: Full=Protein LONELY GUY 8; AltName: Full=LOG family protein At5g11950 >gi|30102598|gb|AAP21217.1| At5g11950 [Arabidopsis thaliana] >gi|110743604|dbj|BAE99639.1| lysine decarboxylase - like protein [Arabidopsis thaliana]	Unigene45622_All//2.00E-96//AT5G11950| protein homodimerization	Unigene45622_All//0.00E+00//TC137512			GO:0003824//GO:0043231//GO:0044444	nr -
Unigene45623_All	1099	9.76	5.72	6.93	11.51	10.03	5.05	18.35	11.64	7.79	-7.72E-01	9.81E-06		-4.94E-01	6.65E-03		-1.99E-01	2.52E-01		-1.19E+00	1.50E-13	Down	-6.57E-01	2.09E-09		-1.24E+00	2.06E-26	Down	Unigene45623_All|gi|30683873|ref|NP_196756.2|//1.00E-100//protein homodimerization [Arabidopsis thaliana] >gi|42573343|ref|NP_974768.1| protein homodimerization [Arabidopsis thaliana] >gi|75147169|sp|Q84WC2.1|LOG8_ARATH RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG8; AltName: Full=Protein LONELY GUY 8; AltName: Full=LOG family protein At5g11950 >gi|30102598|gb|AAP21217.1| At5g11950 [Arabidopsis thaliana] >gi|110743604|dbj|BAE99639.1| lysine decarboxylase - like protein [Arabidopsis thaliana]	Unigene45623_All//3.00E-101//AT5G11950| protein homodimerization	Unigene45623_All//0.00E+00//gi|164260417|gb|ES819569.1|ES819569			GO:0003824	nr +
Unigene45625_All	1246	12.26	11.96	9.40	12.63	11.03	13.41	40.38	24.08	15.79	-3.64E-02	8.15E-01		-3.83E-01	1.12E-02		-1.96E-01	1.97E-01		8.62E-02	6.38E-01		-7.46E-01	1.54E-27		-1.35E+00	2.41E-74	Down	Unigene45625_All|gi|297828988|ref|XP_002882376.1|//1.00E-140//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297328216|gb|EFH58635.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene45625_All//7.00E-141//AT3G04830| binding	Unigene45625_All//0.00E+00//TC132385				nr -
Unigene45629_All	1994	51.06	38.22	58.32	60.73	58.66	52.75	0.47	3.75	1.14	-4.18E-01	2.63E-16		1.92E-01	1.30E-04		-5.00E-02	3.90E-01		-2.03E-01	9.83E-06		3.01E+00	1.83E-30	Up	1.29E+00	6.77E-04	Up	Unigene45629_All|gi|79579427|ref|NP_680473.2|//0.00E+00//protein binding / signal transducer [Arabidopsis thaliana]	Unigene45629_All//0.00E+00//AT5G67385| protein binding / signal transducer	Unigene45629_All//0.00E+00//gi|78343740|gb|DT564014.1|DT564014			GO:0005488//GO:0009314//GO:0060089	nr +
Unigene4563_All	630	0.25	0.72	2.03	0.71	0.93	0.79	4.63	4.05	3.41	1.54E+00	1.96E-01		3.03E+00	1.48E-04	Up	3.85E-01	7.32E-01		1.48E-01	9.05E-01		-1.94E-01	6.12E-01		-4.40E-01	1.73E-01		Unigene4563_All|gi|240255979|ref|NP_193525.5|//6.00E-07//transferase, transferring acyl groups [Arabidopsis thaliana]	Unigene4563_All//3.00E-08//AT4G17910| transferase, transferring acyl groups	Unigene4563_All//0.00E+00//TC164734				nr +
Unigene45636_All	674	1.94	0.30	1.98	1.77	1.89	0.74	2.82	2.73	3.90	-2.69E+00	1.84E-04	Down	2.53E-02	9.85E-01		9.18E-02	9.00E-01		-1.27E+00	4.58E-02		-4.91E-02	9.25E-01		4.67E-01	1.74E-01		Unigene45636_All|gi|115475850|ref|NP_001061521.1|//3.00E-13//Os08g0318500 [Oryza sativa Japonica Group] >gi|50508194|dbj|BAD31511.1| exocyst complex component Sec8-like [Oryza sativa Japonica Group] >gi|113623490|dbj|BAF23435.1| Os08g0318500 [Oryza sativa Japonica Group] >gi|258644591|dbj|BAI39842.1| exocyst complex component Sec8-like [Oryza sativa Indica Group]	Unigene45636_All//2.00E-08//AT3G10380| SEC8 (SUBUNIT OF EXOCYST COMPLEX 8)				GO:0000904//GO:0009856//GO:0043234//GO:0044444//GO:0048278	nr +
Unigene45642_All	2742	2.25	2.75	2.27	4.07	3.37	4.64	5.20	10.38	16.30	2.90E-01	1.94E-01		1.31E-02	9.80E-01		-2.74E-01	1.19E-01		1.91E-01	2.95E-01		9.98E-01	1.32E-25		1.65E+00	1.79E-87	Up	Unigene45642_All//gi|9294678|dbj|BAB03027.1|//0.00E+00//glutamine-fructose-6-phosphate transaminase 2 [Arabidopsis thaliana]	Unigene45642_All//0.00E+00//AT3G24090| glutamine-fructose-6-phosphate transaminase (isomerizing)/ sugar binding / transaminase	Unigene45642_All//0.00E+00//ES790962		ko00520|Amino sugar and nucleotide sugar metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0005975//GO:0008483//GO:0030246//GO:0043231	nr +
Unigene45643_All	707	4.07	10.18	7.98	11.27	13.83	11.12	7.00	9.52	6.59	1.32E+00	9.51E-09	Up	9.72E-01	2.10E-04		2.95E-01	1.26E-01		-2.04E-02	9.42E-01		4.44E-01	3.09E-02		-8.58E-02	7.33E-01		Unigene45643_All|gi|56461760|gb|AAV91336.1|//1.00E-45//At1g74530 [Arabidopsis thaliana] >gi|58331809|gb|AAT70402.1| At1g74530 [Arabidopsis thaliana]	Unigene45643_All//2.00E-36//AT1G74530| unknown protein	Unigene45643_All//0.00E+00//TC140826				nr +

Unigene45647_All	1244	7.36	17.84	14.81	19.14	29.15	41.39	19.98	24.16	19.34	1.28E+00	3.93E-24	Up	1.01E+00	1.58E-13	Up	6.07E-01	1.83E-13		1.11E+00	1.36E-47	Up	2.74E-01	2.32E-03		-4.71E-02	6.69E-01		Unigene45647_All//gi|224144112|ref|XP_002325190.1|//1.00E-174//plant synaptotagmin [Populus trichocarpa] >gi|222866624|gb|EEF03755.1| plant synaptotagmin [Populus trichocarpa]	Unigene45647_All//1.00E-161//AT1G05500| NTM2T2.1	Unigene45647_All//0.00E+00//TC166332				nr -
Unigene4565_All	1932	0.79	0.00	0.14	1.32	1.57	1.75	5.36	2.03	6.31	-9.62E+00	8.33E-09	Down	-2.51E+00	1.79E-04	Down	2.54E-01	5.56E-01		4.15E-01	2.48E-01		-1.40E+00	3.06E-16	Down	2.35E-01	1.14E-01		Unigene4565_All//gi|297827501|ref|XP_002881633.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327472|gb|EFH57892.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4565_All//0.00E+00//AT3G09780| CCR1 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ receptor	Unigene4565_All//0.00E+00//TC152114				nr -
Unigene45652_All	1171	4.87	7.10	7.00	11.53	25.20	18.94	13.00	20.27	6.70	5.43E-01	7.04E-03		5.24E-01	1.36E-02		1.13E+00	8.65E-31	Up	7.16E-01	3.22E-10		6.41E-01	1.73E-10		-9.56E-01	1.38E-13		Unigene45652_All//gi|115440493|ref|NP_001044526.1|//1.00E-15//Os01g0799000 [Oryza sativa Japonica Group] >gi|20804725|dbj|BAB92411.1| NBS-LRR resistance protein RGH1-like [Oryza sativa Japonica Group] >gi|113534057|dbj|BAF06440.1| Os01g0799000 [Oryza sativa Japonica Group]	Unigene45652_All//8.00E-25//AT5G45520| unknown protein	Unigene45652_All//0.00E+00//gi|109865256|gb|DW494232.1|DW494232				nr +
Unigene45653_All	2855	7.07	8.54	6.25	13.45	20.67	22.26	30.14	44.59	11.01	2.71E-01	1.70E-02		-1.79E-01	2.01E-01		6.20E-01	1.69E-22		7.26E-01	6.77E-29		5.65E-01	3.70E-42		-1.45E+00	9.72E-141	Down	Unigene45653_All//gi|115440493|ref|NP_001044526.1|//8.00E-71//Os01g0799000 [Oryza sativa Japonica Group] >gi|20804725|dbj|BAB92411.1| NBS-LRR resistance protein RGH1-like [Oryza sativa Japonica Group] >gi|113534057|dbj|BAF06440.1| Os01g0799000 [Oryza sativa Japonica Group]	Unigene45653_All//1.00E-91//AT5G45500| unknown protein	Unigene45653_All//0.00E+00//TC140450				nr +
Unigene45654_All	510	0.82	30.90	3.86	13.19	21.67	15.94	3.40	3.69	2.73	5.23E+00	1.17E-77	Up	2.23E+00	5.06E-05	Up	7.17E-01	8.54E-06		2.74E-01	2.24E-01		1.18E-01	7.88E-01		-3.14E-01	4.81E-01		Unigene45654_All//gi|18403453|ref|NP_566712.1|//1.00E-34//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|15010698|gb|AAK74008.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] >gi|18958062|gb|AAL79604.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] >gi|84778474|dbj|BAE73264.1| xylogen like protein 8 [Arabidopsis thaliana]	Unigene45654_All//2.00E-21//AT3G22600| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene45654_All//0.00E+00//gi|54117053|gb|CO492562.1|CO492562		GO:0005488//GO:0006810//GO:0031224	nr -
Unigene45655_All	1874	12.20	26.20	13.13	21.21	21.90	20.10	12.86	12.67	10.42	1.10E+00	9.40E-42	Up	1.06E-01	4.03E-01		4.63E-02	6.65E-01		-7.77E-02	4.66E-01		-2.17E-02	8.61E-01		-3.04E-01	1.91E-03		Unigene45655_All//gi|224111144|ref|XP_002315762.1|//1.00E-165//PAF1 complex component [Populus trichocarpa] >gi|222864802|gb|EEF01933.1| PAF1 complex component [Populus trichocarpa]	Unigene45655_All//3.00E-153//AT3G22590| RNA pol II accessory factor Cdc73 family protein	Unigene45655_All//0.00E+00//TC139278				nr +
Unigene45656_All	1448	0.76	13.96	1.10	4.99	9.23	8.39	1.66	2.60	2.64	4.20E+00	1.07E-87	Up	5.40E-01	3.30E-01		8.87E-01	1.10E-09		7.50E-01	2.45E-06		6.42E-01	2.31E-02		6.66E-01	1.37E-02		Unigene45656_All//gi|18403453|ref|NP_566712.1|//8.00E-41//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|15010698|gb|AAK74008.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] >gi|18958062|gb|AAL79604.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] >gi|84778474|dbj|BAE73264.1| xylogen like protein 8 [Arabidopsis thaliana]	Unigene45656_All//8.00E-24//AT3G22600| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene45656_All//0.00E+00//TC173223		GO:0005488//GO:0006810//GO:0031224	nr +
Unigene45659_All	3356	0.83	1.68	0.83	1.48	1.49	1.74	2.86	2.43	2.01	1.02E+00	6.28E-05	Up	-2.10E-03	9.96E-01		3.40E-03	9.99E-01		2.26E-01	4.21E-01		-2.36E-01	1.91E-01		-5.11E-01	1.43E-03		Unigene45659_All//gi|15242310|ref|NP_196472.1|//0.00E+00//ILP1 (increased level of polyploidy1-1D); translation repressor [Arabidopsis thaliana] >gi|117412996|dbj|BAF36503.1| transcriptional repressor ILP1 [Arabidopsis thaliana]	Unigene45659_All//0.00E+00//AT5G08550| ILP1 (increased level of polyploidy1-1D); translation repressor	Unigene45659_All//0.00E+00//TC136623		GO:0006261//GO:0006350//GO:0010468//GO:0043231//GO:0044444//GO:0045182	nr +
Unigene45660_All	554	27.01	72.89	46.04	9.44	8.70	15.90	9.01	17.65	12.22	1.43E+00	1.66E-51	Up	7.69E-01	6.39E-12		-1.18E-01	6.99E-01		7.52E-01	8.48E-05		9.71E-01	5.93E-09		4.41E-01	2.55E-02		Unigene45660_All//gi|18414821|ref|NP_568150.1|//1.00E-66//ABC1 family protein [Arabidopsis thaliana] >gi|75261770|sp|Q9ASX5.1|Y5520_ARATH RecName: Full=Uncharacterized aarF domain-containing protein kinase At5g05200, chloroplastic; Flags: Precursor >gi|13605575|gb|AAK32781.1|AF36161_3_1 AT5g05200/K2A11_7 [Arabidopsis thaliana] >gi|16648993|gb|AAL24348.1| Unknown protein [Arabidopsis thaliana] >gi|22137078|gb|AAM91384.1| At5g05200/K2A11_7 [Arabidopsis thaliana]	Unigene45660_All//6.00E-59//AT5G05200| ABC1 family protein	Unigene45660_All//0.00E+00//TC147550		GO:0006464//GO:0009570//GO:0016301//GO:0032559	nr +
Unigene45661_All	322	3.09	8.18	6.28	3.09	1.82	2.95	0.66	2.08	2.97	1.41E+00	5.42E-04	Up	1.03E+00	3.20E-02		-7.67E-01	2.60E-01		-7.11E-02	9.28E-01		1.66E+00	4.76E-02		2.18E+00	1.83E-03		Unigene45661_All//gi|18414821|ref|NP_568150.1|//2.00E-15//ABC1 family protein [Arabidopsis thaliana] >gi|75261770|sp|Q9ASX5.1|Y5520_ARATH RecName: Full=Uncharacterized aarF domain-containing protein kinase At5g05200, chloroplastic; Flags: Precursor >gi|13605575|gb|AAK32781.1|AF36161_3_1 AT5g05200/K2A11_7 [Arabidopsis thaliana] >gi|16648993|gb|AAL24348.1| Unknown protein [Arabidopsis thaliana] >gi|22137078|gb|AAM91384.1| At5g05200/K2A11_7 [Arabidopsis thaliana]	Unigene45661_All//1.00E-16//AT5G05200| ABC1 family protein	Unigene45661_All//2.00E-64//gi|48821290|gb|CO122603.1|CO122603		GO:0006464//GO:0009570//GO:0016301//GO:0032559	nr +
Unigene45662_All	2046	35.47	104.91	67.49	13.32	13.16	22.91	12.01	23.80	17.12	1.56E+00	0.00E+00	Up	9.28E-01	2.52E-85		-1.70E-02	8.95E-01		7.83E-01	2.37E-24		9.87E-01	1.89E-42		5.12E-01	1.30E-10		Unigene45662_All//gi|18414821|ref|NP_568150.1|//0.00E+00//ABC1 family protein [Arabidopsis thaliana] >gi|75261770|sp|Q9ASX5.1|Y5520_ARATH RecName: Full=Uncharacterized aarF domain-containing protein kinase At5g05200, chloroplastic; Flags: Precursor >gi|13605575|gb|AAK32781.1|AF36161_3_1 AT5g05200/K2A11_7 [Arabidopsis thaliana] >gi|16648993|gb|AAL24348.1| Unknown protein [Arabidopsis thaliana] >gi|22137078|gb|AAM91384.1| At5g05200/K2A11_7 [Arabidopsis thaliana]	Unigene45662_All//0.00E+00//AT5G05200| ABC1 family protein	Unigene45662_All//0.00E+00//TC147550		GO:0006464//GO:0009570//GO:0032559	nr -
Unigene45663_All	1900	31.59	7.04	10.17	7.63	8.17	3.90	1.31	0.09	1.07	-2.17E+00	6.55E-136	Down	-1.63E+00	7.38E-90	Down	9.94E-02	5.73E-01		-9.69E-01	3.02E-11		-3.90E+00	4.34E-13	Down	-2.96E-01	4.11E-01		Unigene45663_All//gi|18410417|ref|NP_567032.1|//1.00E-166//glucose-methanol-choline (GMC) oxidoreductase family protein [Arabidopsis thaliana] >gi|15982755|gb|AAL09718.1| AT3g56060/F18O21_20 [Arabidopsis thaliana]	Unigene45663_All//2.00E-168//AT3G56060| glucose-methanol-choline (GMC) oxidoreductase family protein	Unigene45663_All//0.00E+00//ES791677		ko00460|Cyanoamino acid metabolism	GO:0016829	nr -
Unigene45664_All	1658	1.07	69.56	16.44	0.33	2.99	17.00	0.61	1.51	9.27	6.02E+00	0.00E+00	Up	3.94E+00	1.54E-110	Up	3.18E+00	9.29E-20	Up	5.68E+00	1.03E-153	Up	1.31E+00	3.82E-04	Up	3.92E+00	1.89E-79	Up	Unigene45664_All//gi|226496133|ref|NP_001151589.1|//7.00E-50//protein phosphatase 2C ABI1 [Zea mays] >gi|195647972|gb|ACG43454.1| protein phosphatase 2C ABI1 [Zea mays]	Unigene45664_All//2.00E-35//AT5G59220| protein phosphatase 2C, putative / PP2C, putative			GO:0004721//GO:0006464//GO:0043169//GO:0043234	nr -
Unigene45665_All	1374	0.99	182.21	36.31	1.92	9.50	47.83	1.66	2.59	17.40	7.52E+00	0.00E+00	Up	5.20E+00	1.09E-240	Up	2.31E+00	4.41E-37	Up	4.64E+00	0.00E+00	Up	6.38E-01	2.95E-02		3.39E+00	2.49E-109	Up	Unigene45665_All//gi|115438949|ref|NP_001043754.1|//6.00E-79//Os01g0656200 [Oryza sativa Japonica Group] >gi|75286811|sp|Q5SN75.1|P2C08_ORYSJ RecName: Full=Probable protein phosphatase 2C 8; Short=OsPP2C08 >gi|55773943|dbj|BAD72331.1| protein phosphatase 2C-like [Oryza sativa Japonica Group] >gi|113533285|dbj|BAF05668.1| Os01g0656200 [Oryza sativa Japonica Group]	Unigene45665_All//4.00E-59//AT3G11410| PP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA); protein binding / protein serine/threonine phosphatase	Unigene45665_All//0.00E+00//TC164924		GO:0004721	nr +
Unigene45669_All	3823	3.44	3.38	1.67	5.85	7.64	4.62	7.89	7.92	9.26	-2.35E-02	8.98E-01		-1.04E+00	2.92E-10	Down	3.85E-01	4.44E-05		-3.41E-01	3.25E-03		5.50E-03	9.92E-01		2.33E-01	3.90E-03		Unigene45669_All//gi|224098441|ref|XP_002311175.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222850995|gb|EEE88542.1| GRAS family transcription factor [Populus trichocarpa]	Unigene45669_All//0.00E+00//AT5G13840| FZR3 (FIZZY-RELATED 3); signal transducer	Unigene45669_All//0.00E+00//TC175537		ko04120|Ubiquitin mediated proteolysis	GO:0010468	nr -

Unigene4567_All	639	2.37	3.41	2.08	41.78	29.26	20.92	8.47	2.62	1.93	5.22E-01	2.36E-01		-1.89E-01	7.21E-01		-5.14E-01	8.87E-08		-9.98E-01	3.23E-21		-1.69E+00	1.79E-11	Down	-2.13E+00	7.62E-16	Down	Unigene4567_All//gi|124360804|gb|ABN08776.1|//1.00E-24//Wiscott-Aldrich syndrome, C-terminal [Medicago truncatula]	Unigene4567_All//2.00E-18//AT5G16190| RIC4 (ROP-INTERACTIVE CRIB MOTIF-CONTAINING PROTEIN 4); protein binding	Unigene4567_All//0.00E+00//gi|109885983|gb|DW514953.1|DW514953				nr -
Unigene45670_All	4764	1.22	1.22	0.61	2.81	3.43	2.63	1.74	0.82	1.16	4.70E-03	9.83E-01		-9.88E-01	1.35E-04		2.85E-01	4.19E-02		-9.91E-02	6.21E-01		-1.08E+00	5.38E-09	Down	-5.82E-01	8.25E-04		Unigene45670_All//gi|224098441|ref|XP_002311175.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222850995|gb|EEE88542.1| GRAS family transcription factor [Populus trichocarpa]	Unigene45670_All//0.00E+00//AT5G13840| FZR3 (FIZZY-RELATED 3); signal transducer	Unigene45670_All//0.00E+00//TC175537		ko04120|Ubiquitin mediated proteolysis	GO:0009536//GO:0010468//GO:0019897//GO:0023060	nr -
Unigene45672_All	1580	12.72	22.74	10.11	27.81	29.64	29.56	41.61	79.33	107.34	8.38E-01	9.10E-20		-3.31E-01	1.12E-02		9.21E-02	3.13E-01		8.80E-02	3.57E-01		9.31E-01	4.56E-98		1.37E+00	3.72E-250	Up	Unigene45672_All//gi|224124058|ref|XP_002330094.1|//1.00E-125//f-box family protein [Populus trichocarpa] >gi|222871228|gb|EEF08359.1| f-box family protein [Populus trichocarpa]	Unigene45672_All//8.00E-116//AT2G02870| kelch repeat-containing F-box family protein	Unigene45672_All//0.00E+00//gi|164280324|gb|ES835185.1|ES835185				nr +
Unigene45674_All	993	1.00	1.17	0.21	2.26	3.71	1.82	5.58	8.08	15.57	2.29E-01	6.94E-01		-2.22E+00	7.48E-03		7.17E-01	2.25E-02		-3.11E-01	5.01E-01		5.35E-01	3.47E-03		1.48E+00	1.90E-26	Up			Unigene45674_All//4.00E-179//gi|21102017|gb|BQ414330.1|BQ414330				
Unigene45675_All	1497	8.07	10.29	8.96	31.58	34.16	30.20	31.63	45.37	93.38	3.50E-01	1.56E-02		1.51E-01	3.94E-01		1.13E-01	1.70E-01		-6.44E-02	5.06E-01		5.20E-01	8.28E-20		1.56E+00	1.71E-251	Up	Unigene45675_All//gi|301073323|gb|ADK56149.1|//5.00E-46//acyl-CoA-binding protein [Vitis vinifera]	Unigene45675_All//2.00E-35//AT4G24230| ACBP3 (ACYL-COA-BINDING DOMAIN 3); acyl-CoA binding	Unigene45675_All//0.00E+00//TC159636			GO:0005488//GO:0005576	nr -
Unigene45682_All	1211	1.81	4.35	2.29	7.98	9.30	6.71	6.88	5.94	4.44	1.26E+00	3.25E-06	Up	3.34E-01	3.94E-01		2.21E-01	2.36E-01		-2.49E-01	2.22E-01		-2.12E-01	2.87E-01		-6.31E-01	2.77E-04		Unigene45682_All//gi|259121425|gb|ACV92032.1|//1.00E-113//WRKY transcription factor 30 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene45682_All//1.00E-86//AT4G30935| WRKY32; transcription factor	Unigene45682_All//0.00E+00//TC135098	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene45688_All	2550	1.31	2.70	2.15	3.79	2.81	3.06	9.14	7.11	6.76	1.04E+00	5.09E-06	Up	7.12E-01	7.24E-03		-4.32E-01	1.52E-02		-3.07E-01	1.18E-01		-3.61E-01	3.82E-04		-4.34E-01	1.08E-05		Unigene45688_All//gi|134103847|gb|AB060876.1|//0.00E+00//auxin response factor 3 [Gossypium hirsutum]	Unigene45688_All//0.00E+00//AT2G28350| ARF10 (AUXIN RESPONSE FACTOR 10); miRNA binding / transcription factor	Unigene45688_All//0.00E+00//TC132206	ARF		GO:0003676//GO:0005515//GO:0006351//GO:0009718//GO:0009755//GO:0010468//GO:0040007//GO:0043231//GO:0048437//GO:0048822	nr +
Unigene4569_All	585	25.67	20.70	11.65	37.04	22.37	28.49	40.40	41.08	23.77	-3.10E-01	3.65E-02		-1.14E+00	2.07E-13	Down	-7.28E-01	1.61E-11		-3.79E-01	1.17E-03		2.41E-02	8.44E-01		-7.65E-01	2.13E-14		Unigene4569_All//gi|238481261|ref|NP_001154712.1|//6.00E-06//ATGSL12 (glucan synthase-like 12); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene4569_All//3.00E-07//AT5G13000| ATGSL12 (glucan synthase-like 12); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups	Unigene4569_All//0.00E+00//gi|109877025|gb|DW505999.1|DW505999				nr +
Unigene45690_All	2698	14.41	35.46	18.79	18.46	24.03	23.34	24.01	31.32	27.83	1.30E+00	1.74E-104	Up	3.83E-01	5.09E-07		3.80E-01	2.12E-10		3.38E-01	1.42E-07		3.84E-01	2.66E-14		2.13E-01	6.31E-05		Unigene45690_All//gi|255559820|ref|XP_002520929.1|//0.00E+00//bromodomain-containing protein [Ricinus communis] >gi|223539895|gb|EEF41474.1| bromodomain-containing protein [Ricinus communis]	Unigene45690_All//1.00E-102//AT1G20670| DNA-binding bromodomain-containing protein	Unigene45690_All//0.00E+00//TC173692		ko03022|Basal transcription factors	GO:0016740	nr +
Unigene45692_All	1343	1.48	2.68	3.89	4.49	4.08	3.97	1.45	1.74	3.06	8.56E-01	8.54E-03		1.39E+00	1.01E-06	Up	-1.39E-01	5.99E-01		-1.78E-01	5.28E-01		2.67E-01	5.17E-01		1.08E+00	5.21E-05	Up	Unigene45692_All//gi|115442463|ref|NP_001045511.1|//1.00E-19//Os01g0967700 (Oryza sativa Japonica Group) >gi|113535042|dbj|BAF07425.1|Os01g0967700 (Oryza sativa Japonica Group)	Unigene45692_All//7.00E-20//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene45692_All//0.00E+00//ES798104				nr +
Unigene45694_All	3361	1.26	1.70	1.51	21.14	20.24	11.37	10.08	2.97	3.47	4.34E-01	8.49E-02		2.55E-01	4.02E-01		-6.28E-02	4.16E-01		-8.95E-01	2.45E-46		-1.76E+00	1.63E-71	Down	-1.54E+00	1.07E-60	Down	Unigene45694_All//gi|224589491|gb|ACN59279.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene45694_All//0.00E+00//AT1G79620| leucine-rich repeat transmembrane protein kinase, putative	Unigene45694_All//0.00E+00//gi|48745059|gb|CO075578.1|CO075578		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004871//GO:0006464//GO:0007167//GO:0016491//GO:0031224//GO:0031410//GO:0032259//GO:0043231	nr -
Unigene45701_All	1279	0.04	0.63	1.00	3.08	0.78	5.61	7.34	31.40	6.51	3.95E+00	7.52E-04	Up	4.61E+00	5.51E-06	Up	-1.98E+00	2.65E-10	Down	8.68E-01	5.74E-05		2.10E+00	1.36E-106	Up	-1.73E-01	3.42E-01		Unigene45701_All//gi|124365249|gb|ABN09653.1|//1.00E-132//beta-1,3-glucanase [Hevea brasiliensis]	Unigene45701_All//2.00E-114//AT4G16260| catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene45701_All//0.00E+00//TC142668		ko00500|Starch and sucrose metabolism		nr -
Unigene45702_All	1256	3.21	12.75	7.72	38.95	21.60	97.99	264.12	342.35	124.53	1.99E+00	9.69E-33	Up	1.27E+00	2.13E-10	Up	-8.50E-01	2.75E-33		1.33E+00	5.56E-150	Up	3.74E-01	3.04E-66		-1.08E+00	0.00E+00	Down	Unigene45702_All//gi|110085241|gb|ABG49148.1|//1.00E-135//beta-1,3-glucanase [Hevea brasiliensis] >gi|124294783|gb|ABN03965.1| beta-1,3-glucanase [Hevea brasiliensis]	Unigene45702_All//2.00E-113//AT4G16260| catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene45702_All//0.00E+00//TC175473		ko00500|Starch and sucrose metabolism		nr -
Unigene45703_All	3262	17.50	8.48	14.71	9.90	13.14	7.71	1.18	0.90	1.25	-1.04E+00	1.30E-44	Down	-2.51E-01	6.23E-04		4.09E-01	5.22E-08		-3.60E-01	1.09E-04		-3.95E-01	1.74E-01		7.88E-02	7.77E-01		Unigene45703_All//gi|15234045|ref|NP_192012.1|//1.00E-177//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene45703_All//3.00E-178//AT4G01030| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene45707_All	3010	0.52	1.60	0.90	2.48	2.32	2.46	3.88	3.96	4.43	1.62E+00	5.93E-08	Up	7.91E-01	4.77E-02		-9.61E-02	7.09E-01		-1.27E-02	9.49E-01		2.96E-02	8.68E-01		1.94E-01	1.82E-01		Unigene45707_All//gi|297839985|ref|XP_002887874.1|//1.00E-108//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297333715|gb|EFH64133.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene45707_All//6.00E-72//AT1G64570| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Homeodomain-like (InterPro:IPR009057); Has 1675 Blast hits to 1424 proteins in 225 species: Archae - 2; Bacteria - 192; Metazoa - 559; Fungi - 257; Plants - 67; Viruses - 46; Other Eukaryotes - 552 (source: NCBI BLink).	Unigene45707_All//1.00E-27//TC137251		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr -
Unigene45708_All	3112	2.07	0.78	1.32	1.81	2.24	1.89	3.70	2.30	4.22	-1.40E+00	1.24E-08	Down	-6.50E-01	7.28E-03		3.05E-01	1.99E-01		6.08E-02	8.32E-01		-6.86E-01	4.19E-06		1.93E-01	1.88E-01		Unigene45708_All//gi|297836398|ref|XP_002886081.1|//1.00E-158//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331921|gb|EFH62340.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene45708_All//1.00E-90//AT2G16880| pentatricopeptide (PPR) repeat-containing protein	Unigene45708_All//0.00E+00//CO071439				nr +
Unigene4571_All	1304	0.48	0.70	1.76	0.84	0.61	0.45	1.13	0.83	1.56	5.39E-01	4.49E-01		1.87E+00	1.06E-04	Up	-4.68E-01	4.82E-01		-9.01E-01	1.81E-01		-4.45E-01	3.92E-01		4.57E-01	2.53E-01		Unigene4571_All//gi|224093142|ref|XP_002309806.1|//4.00E-09//predicted protein [Populus trichocarpa] >gi|222852709|gb|EEE90256.1| predicted protein [Populus trichocarpa]		Unigene4571_All//0.00E+00//FL576792				nr +
Unigene45710_All	1345	13.27	26.63	23.72	63.26	68.74	76.39	45.05	197.88	58.77	1.01E+00	1.78E-26	Up	8.38E-01	5.43E-17		1.20E-01	3.37E-02		2.72E-01	3.74E-08		2.14E+00	0.00E+00	Up	3.84E-01	8.56E-14		Unigene45710_All//gi|294514718|gb|ADE95828.1|//1.00E-178//4-coumarate:CoA ligase 1 [Corchorus capsularis]	Unigene45710_All//1.00E-164//AT1G65880| 4CL1 (4-COUMARATE:COA LIGASE 1); 4-coumarate-CoA ligase	Unigene45710_All//0.00E+00//TC146625		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene45712_All	2874	5.68	18.56	13.77	17.87	15.82	22.33	23.41	37.17	42.04	1.71E+00	1.47E-87	Up	1.28E+00	3.10E-41	Up	-1.76E-01	1.81E-02		3.22E-01	4.45E-07		6.67E-01	1.76E-47		8.45E-01	3.24E-82		Unigene45712_All//gi|84453182|dbj|BAE71188.1|//1.00E-155//BEL1-like homeodomain transcription factor [Trifolium pratense]	Unigene45712_All//5.00E-104//AT2G35940| BLH1 (BEL1-LIKE HOMEODOMAIN 1); DNA binding / protein heterodimerization/ protein homodimerization/ transcription factor	Unigene45712_All//0.00E+00//TC162985	HB			nr +
Unigene45714_All	511	45.67	22.01	44.81	29.83	25.41	18.56	7.45	4.66	3.12	-1.05E+00	6.81E-19	Down	-2.73E-02	8.34E-01		-2.32E-01	1.22E-01		-6.85E-01	8.62E-07		-6.76E-01	1.59E-02		-1.26E+00	8.09E-06	Down			Unigene45714_All//0.00E+00//TC159813				
Unigene45716_All	1724	70.56	36.62	65.02	68.74	69.45	34.45	10.03	4.41	6.75	-9.46E-01	4.10E-80		-1.18E-01	2.29E-02		1.48E-02	8.10E-01		-9.97E-01	3.24E-92		-1.18E+00	9.98E-21	Down	-5.72E-01	8.45E-07		Unigene45716_All//gi|124359162|gb|ABN05685.1|//1.00E-18//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene45716_All//4.00E-05//AT3G09510| nucleic acid binding	Unigene45716_All//0.00E+00//TC149105				nr -
Unigene45717_All	1069	6.12	3.27	5.38	12.77	10.18	9.72	8.27	3.17	4.10	-9.04E-01	9.51E-05		-1.86E-01	4.70E-01		-3.27E-01	2.98E-02		-3.94E-01	1.00E-02		-1.38E+00	9.20E-14	Down	-1.01E+00	5.39E-09	Down			Unigene45717_All//9.00E-165//DR462464				
Unigene45718_All	500	3.87	0.81	1.70	5.98	5.58	3.61	7.53	1.34	1.20	-2.26E+00	2.83E-05	Down	-1.18E+00	1.70E-02		-9.97E-02	8.16E-01		-7.26E-01	4.49E-02		-2.49E+00	5.78E-13	Down	-2.65E+00	2.33E-14	Down			Unigene45718_All//0.00E+00//DR462464				
Unigene45720_All	1584	53.74	25.94	45.85	61.58	53.91	94.32	94.92	29.95	30.28	-1.05E+00	8.59E-67	Down	-2.29E-01	1.01E-04		-1.92E-01	1.20E-04		6.15E-01	2.73E-50		-1.66E+00	4.00E-291	Down	-1.65E+00	2.08E-295	Down	Unigene45720_All//gi|224142069|ref|XP_002324381.1|//0.00E+00//sarcosine oxidase [Populus trichocarpa] >gi|222868815|gb|EEF02946.1| sarcosine oxidase [Populus trichocarpa]	Unigene45720_All//8.00E-174//AT2G24580| sarcosine oxidase family protein	Unigene45720_All//0.00E+00//TC142130			GO:0006760//GO:0016647	nr +
Unigene45721_All	2943	9.28	8.87	6.39	24.66	24.92	23.05	20.36	6.21	7.09	-6.57E-02	6.04E-01		-5.39E-01	4.48E-07		1.52E-02	8.44E-01		-9.75E-02	1.68E-01		-1.71E+00	2.92E-121	Down	-1.52E+00	3.78E-105	Down	Unigene45721_All//gi|18414189|ref|NP_567426.1|//0.00E+00//phragmoplast-associated kinesin-related protein 2 (PAKRP2) [Arabidopsis thaliana] >gi|16973451|gb|AAL32293.1|AF320248_1 phragmoplast-associated kinesin-related protein 2 [Arabidopsis thaliana] >gi|16973453|gb|AAL32294.1|AF320249_1 phragmoplast-associated kinesin-related protein 2 [Arabidopsis thaliana]	Unigene45721_All//0.00E+00//AT4G14330| phragmoplast-associated kinesin-related protein 2 (PAKRP2)	Unigene45721_All//0.00E+00//TC152770			GO:0000166//GO:0003774//GO:0043229//GO:0044444	nr -
Unigene45725_All	1916	3.28	8.67	5.84	10.45	13.34	21.71	21.29	7.00	11.04	1.40E+00	5.40E-21	Up	8.33E-01	2.50E-06		3.52E-01	6.33E-04		1.05E+00	2.18E-35	Up	-1.60E+00	2.03E-75	Down	-9.48E-01	1.97E-34		Unigene45725_All//gi|189503705|gb|ACE06982.1|//0.00E+00//obtusifolio 1-14alpha-demethylase [Gossypium hirsutum]	Unigene45725_All//0.00E+00//AT1G11680| CYP51G1 (CYTOCHROME P450 51G1); oxygen binding / sterol 14-demethylase	Unigene45725_All//0.00E+00//TC151579		ko00100|Steroid biosynthesis		nr +
Unigene45730_All	977	0.43	1.24	1.36	1.58	2.36	2.27	1.34	0.13	0.08	1.54E+00	1.75E-02		1.67E+00	9.89E-03		5.79E-01	1.82E-01		5.19E-01	2.56E-01		-3.39E+00	1.90E-06	Down	-4.04E+00	1.35E-07	Down			Unigene45730_All//2.00E-94//ES799343				
Unigene45732_All	2813	0.65	0.58	0.85	0.62	0.88	0.72	0.30	0.04	0.06	-1.76E-01	6.99E-01		3.88E-01	3.90E-01		5.08E-01	2.29E-01		2.21E-01	6.61E-01		-2.75E+00	9.73E-04	Down	-2.41E+00	1.68E-03		Unigene45732_All//gi|139867053|dbj|BAF52941.1|//0.00E+00//isoamylase-type starch-debranching enzyme 1 [Phaseolus vulgaris]	Unigene45732_All//0.00E+00//AT2G39930| ISA1 (ISOAMYLASE 1); alpha-amylase/ isoamylase	Unigene45732_All//0.00E+00//TC145593				nr +
Unigene45733_All	539	96.39	111.49	137.03	25.32	29.13	32.68	1.02	3.33	1.11	2.10E-01	2.55E-03		5.08E-01	3.29E-16		2.02E-01	1.89E-01		3.68E-01	5.68E-03		1.71E+00	2.41E-04	Up	1.21E-01	8.88E-01		Unigene45733_All//gi|157863714|gb|ABV90878.1|//2.00E-58//inositol-1,4,5-triphosphate-5-phosphatase [Solanum lycopersicum]	Unigene45733_All//5.00E-37//AT2G32010| endonuclease/exonuclease/phosphatase family protein	Unigene45733_All//0.00E+00//gi|164357961|gb|ES804120.1|ES804120				nr -
Unigene45734_All	1696	34.52	40.06	62.45	7.37	12.08	11.66	0.37	1.65	0.82	2.15E-01	9.11E-04		8.55E-01	4.09E-57		7.13E-01	3.38E-10		6.62E-01	4.39E-08		2.14E+00	2.69E-08	Up	1.14E+00	2.18E-02		Unigene45734_All//gi|157863714|gb|ABV90878.1|//2.00E-92//inositol-1,4,5-triphosphate-5-phosphatase [Solanum lycopersicum]	Unigene45734_All//1.00E-45//AT2G37440| endonuclease/exonuclease/phosphatase family protein	Unigene45734_All//0.00E+00//TC169894				nr +
Unigene45735_All	2276	27.70	60.44	31.75	48.02	51.29	110.75	63.66	129.89	146.77	1.13E+00	1.01E-119	Up	1.97E-01	2.69E-03		9.51E-02	6.49E-02		1.21E+00	3.64E-263	Up	1.03E+00	6.66E-272	Up	1.21E+00	0.00E+00	Up	Unigene45735_All//gi|229335617|gb|ACQ57001.1|//0.00E+00//PAD4 [Glycine max]	Unigene45735_All//2.00E-86//AT3G32430| PAD4 (PHYTOALEXIN DEFICIENT 4); lipase/ protein binding / triacylglycerol lipase	Unigene45735_All//0.00E+00//TC150064				nr +
Unigene45739_All	1608	7.48	19.57	14.64	2.14	3.79	1.77	0.05	0.26	0.15	1.39E+00	2.17E-38	Up	9.68E-01	5.16E-16		8.27E-01	3.02E-04		-2.73E-01	4.67E-01		2.30E+00	5.99E-02		1.50E+00	3.39E-01		Unigene45739_All//gi|186478150|ref|NP_001117231.1|//0.00E+00//HDG2 (HOMEODOMAIN GLABROUS 2); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene45739_All//0.00E+00//AT1G05230| HDG2 (HOMEODOMAIN GLABROUS 2); DNA binding / transcription factor	Unigene45739_All//0.00E+00//gi|78331094|gb|DT551368.1|DT551368	HB			nr +
Unigene4574_All	821	6.31	4.75	4.61	11.22	7.84	17.11	6.33	2.24	2.14	-4.09E-01	1.27E-01		-4.54E-01	1.05E-01		-5.17E-01	3.88E-03		6.08E-01	3.32E-05		-1.50E+00	2.15E-09	Down	-1.57E+00	2.48E-10	Down			Unigene4574_All//2.00E-82//TC169165				

Unigene45742_All	343	1.68	3.69	0.16	1.45	1.81	5.00	12.45	4.14	6.39	1.14E+00	6.20E-02		-3.43E+00	1.41E-02		3.15E-01	7.84E-01		1.78E+00	9.22E-04	Up	-1.59E+00	1.84E-08	Down	-9.63E-01	1.72E-04			Unigene45745_All//5.00E-110//AT4G08390| SAPX (STROMAL ASCORBATE PEROXIDASE); L-ascorbate peroxidase	Unigene42742_All//2.00E-92//gi|3326158|gb|AI055044.1|AI055044				
Unigene45745_All	1053	168.54	97.78	179.78	52.84	49.64	38.99	1.77	0.48	1.14	-7.86E-01	4.22E-85		9.31E-02	2.47E-02		-9.01E-02	2.78E-01		-4.39E-01	1.17E-10		-1.89E+00	5.01E-05	Down	-6.38E-01	1.19E-01		Unigene45745_All//gi|211906478|gb|ACJ11732.1|//1.00E-130//stromal ascorbate peroxidase [Gossypium hirsutum]	Unigene45745_All//0.00E+00//TC171389		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene45747_All	2751	7.15	4.40	5.88	11.46	12.81	7.63	7.19	4.80	3.30	-7.00E-01	2.02E-08		-2.81E-01	3.63E-02		1.60E-01	1.00E-01		-5.86E-01	2.79E-10		-5.83E-01	1.25E-07		-1.12E+00	2.08E-22	Down	Unigene45747_All//gi|115460452|ref|NP_001053826.1|//1.00E-61//Os04g0610000 [Oryza sativa Japonica Group] >gi|113565397|dbj|BAF15740.1|Os04g0610000 [Oryza sativa Japonica Group]	Unigene45747_All//3.00E-28//AT1G58025| DNA binding	Unigene45747_All//0.00E+00//C0106085				nr +
Unigene4575_All	1683	11.53	8.58	11.77	13.20	13.26	7.59	14.55	12.32	4.81	-4.27E-01	6.60E-04		2.93E-02	8.36E-01		6.30E-03	9.64E-01		-7.98E-01	2.48E-12		-2.40E-01	1.95E-02		-1.60E+00	1.18E-46	Down	Unigene4575_All//gi|297839453|ref|XP_002887608.1|//1.00E-163//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333449|gb|EFH63867.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4575_All//2.00E-147//AT1G75710| zinc finger (C2H2 type) family protein	Unigene4575_All//0.00E+00//TC155439	C2H2			nr +
Unigene45750_All	1767	26.62	12.73	19.11	304.81	281.68	204.12	42.16	17.13	9.56	-1.06E+00	5.69E-38	Down	-4.78E-01	1.54E-09		-1.14E-01	1.09E-08		-5.79E-01	1.44E-162		-1.30E+00	3.93E-100	Down	-2.14E+00	4.18E-209	Down	Unigene45750_All//gi|223453022|gb|ACM89775.1|//0.00E+00//beta-tubulin 3 [Gossypium hirsutum]	Unigene45750_All//0.00E+00//AT5G12250| TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton	Unigene45750_All//0.00E+00//TC172504		ko04145|Phagosome		nr +
Unigene45751_All	2572	41.66	259.89	172.86	21.96	64.77	62.04	1.86	4.45	6.23	2.64E+00	0.00E+00	Up	2.05E+00	0.00E+00	Up	1.56E+00	2.54E-283	Up	1.50E+00	3.11E-232	Up	1.26E+00	2.47E-15	Up	1.75E+00	1.94E-34	Up	Unigene45751_All//gi|18397470|ref|NP_564354.1|//0.00E+00//ERD4 (early-responsive to dehydration 4) [Arabidopsis thaliana]	Unigene45751_All//0.00E+00//AT1G30360| ERD4 (early-responsive to dehydration 4)	Unigene45751_All//0.00E+00//TC166562				nr -
Unigene45753_All	1609	3.61	0.50	1.13	2.07	2.03	4.07	2.08	2.34	2.72	-2.84E+00	1.65E-18	Down	-1.68E+00	1.63E-09	Down	-2.89E-02	9.37E-01		9.72E-01	2.08E-05		1.72E-01	6.14E-01		3.92E-01	1.27E-01		Unigene45753_All//gi|297815926|ref|XP_002875846.1|//1.00E-87//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321684|gb|EFH52105.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45753_All//1.00E-73//AT1G14260| zinc finger (C3HC4-type RING finger) family protein	Unigene45753_All//0.00E+00//gi|78327565|gb|DT547839.1|DT547839		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene45755_All	1423	11.51	6.62	8.01	14.21	21.13	29.36	11.77	9.49	12.18	-7.97E-01	9.43E-09		-5.23E-01	2.39E-04		5.72E-01	3.70E-10		1.05E+00	4.17E-35	Up	-3.11E-01	1.25E-02		4.97E-02	7.09E-01		Unigene45755_All//gi|16604523|gb|AL242267.1|//0.00E+00//At2g31810/F20M17.15 [Arabidopsis thaliana] >gi|21653295|gb|AAM65359.1|At2g31810/F20M17.15 [Arabidopsis thaliana]	Unigene45755_All//2.00E-174//AT2G31810| acetolactate synthase small subunit, putative	Unigene45755_All//0.00E+00//gi|78344310|gb|DT564584.1|DT564584		ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis//ko00660|C5-Branched dibasic acid metabolism		nr -
Unigene45757_All	2083	3.99	8.17	6.75	21.26	12.27	28.66	35.05	18.44	130.88	1.03E+00	1.54E-13	Up	7.57E-01	1.05E-06		-7.93E-01	8.46E-27		4.31E-01	5.47E-11		-9.27E-01	4.31E-57		1.90E+00	0.00E+00	Up	Unigene45757_All//gi|115459830|ref|NP_001053515.1|//0.00E+00//Os04g0555300 [Oryza sativa Japonica Group] >gi|38345584|emb|CAD41637.2|OSJNBb0012E24.2 [Oryza sativa (japonica cultivar-group)] >gi|113565086|dbj|BAF15429.1|Os04g0555300 [Oryza sativa Japonica Group]	Unigene45757_All//0.00E+00//AT3G47420| glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative	Unigene45757_All//0.00E+00//TC156621				nr -
Unigene45759_All	970	0.76	2.09	0.33	1.75	2.95	0.84	16.08	88.46	21.27	1.47E+00	2.05E-03		-1.20E+00	1.80E-01		7.55E-01	4.06E-02		-1.06E+00	3.78E-02		2.46E+00	4.40E-276	Up	4.04E-01	1.34E-04		Unigene45759_All//gi|84514177|gb|ABC59097.1|//1.00E-114//cytochrome P450 monooxygenase CYP710A15 [Medicago truncatula]	Unigene45759_All//4.00E-102//AT2G34500| CYP710A1 (cytochrome P450, family 710, subfamily A, polypeptide 1); C-22 sterol desaturase/ oxygen binding	Unigene45759_All//0.00E+00//gi|78329990|gb|DT550264.1|DT550264		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00100|Steroid biosynthesis		nr +
Unigene4576_All	1046	62.22	20.64	32.07	113.34	95.27	78.80	83.91	30.57	26.70	-1.59E+00	4.64E-97	Down	-9.56E-01	2.17E-42		-2.51E-01	7.45E-09		-5.25E-01	2.41E-30		-1.46E+00	3.77E-140	Down	-1.65E+00	2.61E-173	Down	Unigene4576_All//gi|57222168|gb|AAW38991.1|//1.00E-127//At1g55360 [Arabidopsis thaliana] >gi|111074434|gb|ABH04590.1|At1g55360 [Arabidopsis thaliana]	Unigene4576_All//1.00E-128//AT1G55360| unknown protein	Unigene4576_All//0.00E+00//TC132669				nr -
Unigene45760_All	2198	1.38	2.42	0.85	3.90	5.04	4.83	18.62	67.35	24.09	8.10E-01	1.81E-03		-7.03E-01	6.08E-02		3.72E-01	2.94E-02		3.09E-01	9.67E-02		1.85E+00	0.00E+00	Up	3.72E-01	4.87E-09		Unigene45760_All//gi|84514177|gb|ABC59097.1|//0.00E+00//cytochrome P450 monooxygenase CYP710A15 [Medicago truncatula]	Unigene45760_All//0.00E+00//AT2G34500| CYP710A1 (cytochrome P450, family 710, subfamily A, polypeptide 1); C-22 sterol desaturase/ oxygen binding	Unigene45760_All//0.00E+00//TC160375		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00100|Steroid biosynthesis		nr +
Unigene45765_All	1260	2.91	0.88	3.55	4.86	4.56	2.11	2.11	1.23	0.60	-1.72E+00	9.36E-07	Down	2.88E-01	3.68E-01		-9.15E-02	7.61E-01		-1.20E+00	5.32E-07	Down	-7.85E-01	2.28E-02		-1.82E+00	8.29E-07	Down	Unigene45765_All//gi|82697951|gb|AB889010.1|//1.00E-107//CXE carboxylesterase [Malus pumila]	Unigene45765_All//1.00E-89//AT3G48690| CXE12; carboxylesterase	Unigene45765_All//0.00E+00//TC172470				nr -
Unigene45766_All	1244	132.91	87.16	102.22	94.34	73.30	84.92	6.05	2.89	1.02	-6.09E-01	7.39E-51		-3.79E-01	6.28E-21		-3.64E-01	2.43E-17		-1.52E-01	1.74E-03		-1.07E+00	4.01E-08	Down	-2.56E+00	6.70E-27	Down	Unigene45766_All//gi|82697943|gb|AB889006.1|//1.00E-104//CXE carboxylesterase [Malus pumila]	Unigene45766_All//4.00E-92//AT3G48690| CXE12; carboxylesterase	Unigene45766_All//0.00E+00//TC145192			GO:0044424	nr -
Unigene45772_All	927	3.05	1.09	1.26	13.17	8.17	7.60	2.87	4.42	4.81	-1.48E+00	1.63E-04	Down	-1.27E+00	1.49E-03		-6.88E-01	3.78E-06		-7.93E-01	5.34E-07		6.21E-01	2.12E-02		7.44E-01	2.67E-03		Unigene45772_All//gi|157849752|gb|ABV89659.1|//1.00E-143//dehydration-responsive protein-related [Brassica rapa]	Unigene45772_All//0.00E+00//AT1G78240| TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase	Unigene45772_All//0.00E+00//gi|164290763|gb|ES794921.1|ES794921				nr -
Unigene45773_All	2606	2.19	1.28	0.69	12.08	7.19	6.17	3.65	4.89	5.11	-7.70E-01	1.95E-03		-1.66E+00	3.67E-09	Down	-7.49E-01	2.29E-17		-9.69E-01	9.14E-24		4.22E-01	2.95E-03		4.84E-01	3.10E-04		Unigene45773_All//gi|42563316|ref|NP_177948.3|//0.00E+00//TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase [Arabidopsis thaliana] >gi|238479105|ref|NP_001154475.1|TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase [Arabidopsis thaliana] >gi|292630946|sp|Q9C9Q8.2|PMTT_ARATH RecName: Full=Probable pectin methyltransferase QUA2; AltName: Full=Protein QUASIMODO 2; AltName: Full=Protein OVERSENSITIVE TO SUGAR 1; AltName: Full=Protein TUMOROUS SHOOT DEVELOPMENT 2	Unigene45773_All//0.00E+00//AT1G78240| TSD2 (TUMOROUS SHOOT DEVELOPMENT 2); methyltransferase	Unigene45773_All//0.00E+00//TC136974			GO:0016741//GO:0043231//GO:0045489//GO:0048513	nr +
Unigene45774_All	1863	2.39	5.90	4.00	3.26	3.18	4.61	3.09	4.24	3.57	1.31E+00	9.82E-13	Up	7.45E-01	7.75E-04		-3.71E-02	8.86E-01		4.98E-01	1.21E-02		4.58E-01	1.40E-02		2.10E-01	3.35E-01		Unigene45774_All//gi|30680137|ref|NP_849969.1|//1.00E-180//SDG37; zinc ion binding [Arabidopsis thaliana] >gi|94707144|sp|Q7XJS0.2|ASHR1_ARATH RecName: Full=Histone-lysine N-methyltransferase ASHR1; AltName: Full=ASH1-related protein 1; AltName: Full=Protein SET DOMAIN GROUP 37 >gi|145651792|gb|ABP88121.1|At2g17900 [Arabidopsis thaliana]	Unigene45774_All//0.00E+00//AT2G17900| SDG37; zinc ion binding	Unigene45774_All//0.00E+00//TC173854			GO:0046914	nr -
Unigene45775_All	2824	4.43	3.44	2.77	11.43	12.44	9.60	13.73	5.64	5.12	-3.62E-01	2.56E-02		-6.76E-01	4.39E-05		1.22E-01	2.38E-01		-2.52E-01	9.17E-03		-1.28E+00	1.74E-51	Down	-1.42E+00	6.48E-62	Down	Unigene45775_All//gi|30725674|gb|AK237859.1|//7.00E-29//At5g40040 [Arabidopsis thaliana]	Unigene45775_All//2.00E-14//AT2G33400| unknown protein	Unigene45775_All//0.00E+00//TC153108				nr -
Unigene45781_All	2414	5.74	9.24	14.10	8.42	10.74	19.59	3.26	7.77	9.79	6.85E-01	4.30E-09		1.30E+00	2.70E-36	Up	3.51E-01	5.70E-04		1.22E+00	1.82E-50	Up	1.25E+00	1.98E-24	Up	1.59E+00	3.78E-44	Up	Unigene45781_All//gi|9759309|dbj|BAB09815.1|//4.00E-12//non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	Unigene45781_All//2.00E-08//AT5G42905| nucleic acid binding / ribonuclease H	Unigene45781_All//0.00E+00//TC161411				nr +
Unigene45782_All	939	1.62	1.24	1.30	2.76	3.89	2.79	27.42	12.15	7.26	-3.81E-01	4.78E-01		-3.09E-01	5.99E-01		4.95E-01	1.36E-01		1.61E-02	9.67E-01		-1.17E+00	4.79E-30	Down	-1.92E+00	4.34E-63	Down	Unigene45782_All//gi|23477636|gb|AN34791.1|//1.00E-110//Grp94 [Xerophyta viscosa]	Unigene45782_All//4.00E-72//AT4G24190| SHD (SHEPHERD); ATP binding / unfolded protein binding	Unigene45782_All//1.00E-151//TC152949		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene45783_All	1543	83.21	102.36	71.82	193.35	168.99	234.80	362.79	253.92	134.83	2.99E-01	1.37E-13		-2.13E-01	6.27E-06		-1.94E-01	2.28E-13		2.80E-01	1.04E-28		-5.15E-01	1.86E-154		-1.43E+00	0.00E+00	Down	Unigene45783_All//gi|462013|sp|P35016.1|ENPL_CATRO//0.00E+00//RecName: Full=Endoplasmin homolog; AltName: Full=Glucose-regulated protein 94 homolog; Short=GRP-94 homolog; Flags: Precursor >gi|348696|gb|AAA16785.1| heat shock protein 90 [Catharanthus roseus]	Unigene45783_All//8.00E-110//AT4G24190| SHD (SHEPHERD); ATP binding / unfolded protein binding	Unigene45783_All//0.00E+00//TC152949		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005198//GO:0005515//GO:0006970//GO:0009536//GO:0009933//GO:0010038//GO:0010073//GO:0010467//GO:0015031//GO:0016020//GO:0030529//GO:0031410//GO:0032559//GO:0044267//GO:0044432	nr +
Unigene45784_All	3759	18.73	7.40	16.96	2.73	2.72	1.73	1.87	0.39	1.18	-1.34E+00	3.24E-81	Down	-1.44E-01	3.81E-02		-4.90E-03	9.73E-01		-6.58E-01	1.59E-04		-2.26E+00	4.21E-21	Down	-6.66E-01	4.84E-04		Unigene45784_All//gi|240255299|ref|NP_187344.4|//0.00E+00//nucleotide binding [Arabidopsis thaliana]	Unigene45784_All//0.00E+00//AT3G06880| nucleotide binding	Unigene45784_All//0.00E+00//TC150094			GO:0044424	nr -
Unigene45790_All	306	0.00	0.00	0.00	0.00	0.00	0.00	4.42	0.68	5.60	null	null		null	null		null	null		null	null		-2.69E+00	1.77E-05	Down	3.40E-01	4.52E-01		Unigene45790_All//gi|224133270|ref|XP_002328002.1|//5.00E-07//predicted protein [Populus trichocarpa] >gi|222837411|gb|EEE75790.1|predicted protein [Populus trichocarpa]	Unigene45790_All//5.00E-07//AT3G47210| unknown protein	Unigene45790_All//9.00E-48//DW497012				nr +
Unigene45791_All	738	0.43	0.48	1.37	10.93	10.69	5.08	7.28	7.82	3.13	1.76E-01	8.83E-01		1.69E+00	2.74E-02		-3.33E-02	8.83E-01		-1.11E+00	5.56E-08	Down	1.03E-01	6.75E-01		-1.22E+00	1.63E-07	Down			Unigene45791_All//3.00E-31//gi|109859862|gb|DW488841.1|DW488841				
Unigene45792_All	1574	1.86	4.60	2.37	29.72	34.09	23.24	51.74	35.50	17.82	1.31E+00	1.17E-08	Up	3.47E-01	3.16E-01		1.98E-01	5.68E-03		-3.55E-01	2.55E-06		-5.43E-01	1.89E-25		-1.54E+00	5.91E-145	Down	Unigene45792_All//gi|115459306|ref|NP_001053253.1|//6.00E-53//Os04g0505400 [Oryza sativa Japonica Group] >gi|32490273|emb|CAE05562.1|OSJNBb0116K07.15 [Oryza sativa (japonica cultivar-group)] >gi|113564824|dbj|BAF15167.1|Os04g0505400 [Oryza sativa Japonica Group] >gi|116310257|emb|CAH67264.1|OSIGBa0145C12.1 [Oryza sativa (indica cultivar-group)]	Unigene45792_All//5.00E-65//AT3G50170| unknown protein	Unigene45792_All//0.00E+00//DW497013				nr +
Unigene45793_All	3297	8.63	8.10	7.24	15.21	12.19	11.71	34.44	20.25	16.54	-9.21E-02	4.18E-01		-2.55E-01	1.99E-02		-3.20E-01	3.71E-06		-3.78E-01	1.78E-07		-7.67E-01	3.86E-64		-1.06E+00	5.72E-113	Down	Unigene45793_All//gi|145357905|ref|NP_196717.3|//0.00E+00//catalytic [Arabidopsis thaliana]	Unigene45793_All//0.00E+00//AT5G11560| catalytic	Unigene45793_All//0.00E+00//TC161470			GO:0031410	nr +
Unigene45797_All	2392	4.92	4.02	3.76	7.14	6.13	4.55	6.96	4.30	3.35	-2.90E-01	9.04E-02		-3.88E-01	2.71E-02		-2.20E-01	1.18E-01		-6.51E-01	6.11E-07		-6.96E-01	1.13E-08		-1.06E+00	2.68E-17	Down	Unigene45797_All//gi|18419973|ref|NP_568378.1|//0.00E+00//OEP80 (OUTER ENVELOPE PROTEIN OF 80 KDA) [Arabidopsis thaliana] >gi|75168961|sp|Q9C5J8.1|OEP80_ARATH RecName: Full=Outer envelope protein of 80 kDa, chloroplastic; Short=AtOEP80; AltName: Full=Protein TOC75-V; Short=AtToc75-V	Unigene45797_All//0.00E+00//AT5G19620| OEP80 (OUTER ENVELOPE PROTEIN OF 80 KDA)	Unigene45797_All//0.00E+00//TC166340			GO:0003006//GO:0009526//GO:0016020	nr -

Unigene4580_All	920	5.80	2.26	1.85	67.52	42.33	32.65	11.21	21.40	16.84	-1.36E+00	5.39E-07	Down	-1.65E+00	1.48E-08	Down	-6.74E-01	3.78E-28		-1.05E+00	9.80E-53	Down	9.32E-01	4.06E-16		5.87E-01	2.06E-06		Unigene4580_All//gi|297844396|ref|XP_002890079.1|//8.00E-56//invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335921|gb|EFH66338.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4580_All//1.00E-55//AT1G14890| enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor	Unigene4580_All//0.00E+00//TC156663		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene45800_All	692	1.21	1.10	2.69	1.15	1.59	1.70	13.08	9.36	2.53	-1.39E-01	8.39E-01		1.15E+00	2.26E-02		4.67E-01	5.30E-01		5.59E-01	4.04E-01		-4.82E-01	4.98E-03		-2.37E+00	1.97E-29	Down	Unigene45800_All//gi|283132359|dbj|BAI63585.1|//8.00E-96//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene45800_All//7.00E-88//AT4G38470| protein kinase family protein	Unigene45800_All//1.00E-58//TC176323			GO:0004713//GO:0006464//GO:0031406//GO:0032559//GO:0043231	nr +
Unigene45801_All	1092	1.39	2.32	2.83	1.28	1.55	0.99	12.43	5.59	1.86	7.40E-01	6.36E-02		1.03E+00	5.92E-03		2.75E-01	6.18E-01		-3.64E-01	5.56E-01		-1.15E+00	8.80E-16	Down	-2.74E+00	1.47E-51	Down	Unigene45801_All//gi|283132359|dbj|BAI63585.1|//2.00E-37//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene45801_All//9.00E-33//AT4G35780| protein kinase family protein	Unigene45801_All//2.00E-178//C0126597			GO:0004713//GO:0006464//GO:0031406//GO:0032559	nr +
Unigene45802_All	2197	1.86	1.18	2.33	2.00	1.91	1.58	10.22	5.02	3.92	-6.59E-01	2.83E-02		3.25E-01	2.55E-01		-6.14E-02	8.35E-01		-3.34E-01	2.90E-01		-1.02E+00	2.90E-21	Down	-1.38E+00	9.43E-35	Down	Unigene45802_All//gi|283132359|dbj|BAI63585.1|//0.00E+00//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene45802_All//2.00E-175//AT4G38470| protein kinase family protein	Unigene45802_All//0.00E+00//C0126596			GO:0004672//GO:0005488//GO:0008152//GO:0044444	nr -
Unigene45804_All	236	30.82	28.77	23.92	13.93	11.67	13.97	3.40	1.59	0.51	-9.91E-02	6.56E-01		-3.66E-01	1.19E-01		-2.55E-01	5.03E-01		4.00E-03	9.93E-01		-1.09E+00	1.29E-01		-2.75E+00	9.42E-04	Down			Unigene45804_All//9.00E-66//TC146486				
Unigene45805_All	732	15.15	22.98	13.46	17.83	14.30	8.58	4.74	5.88	1.69	6.01E-01	9.05E-06		-1.71E-01	3.96E-01		-3.18E-01	4.06E-02		-1.06E+00	1.19E-11	Down	3.12E-01	2.63E-01		-1.49E+00	1.04E-06	Down	Unigene45805_All//gi|297725701|ref|NP_001175214.1|//2.00E-122//Os07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1| Os07g0501200 [Oryza sativa Japonica Group]	Unigene45805_All//9.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene45805_All//0.00E+00//D#225938				nr +
Unigene45806_All	1108	7.84	13.67	13.79	10.25	8.27	5.42	3.28	2.07	0.72	8.03E-01	3.22E-08		8.15E-01	4.04E-08		-3.10E-01	6.87E-02		-9.19E-01	3.01E-08		-6.62E-01	2.17E-02		-2.19E+00	2.94E-11	Down	Unigene45806_All//gi|53370641|gb|AU89136.1|//2.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene45806_All//2.00E-05//AT3G25270| nucleic acid binding	Unigene45806_All//0.00E+00//TC146486				nr +
Unigene45807_All	1284	10.76	11.21	8.88	6.79	4.77	2.36	2.31	1.07	0.47	5.91E-02	7.12E-01		-2.78E-01	9.23E-02		-5.08E-01	6.16E-03		-1.53E+00	1.02E-13	Down	-1.10E+00	7.79E-04	Down	-2.31E+00	7.12E-10	Down	Unigene45807_All//gi|124359162|gb|ABW05685.1|//5.00E-19//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene45807_All//3.00E-10//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene45807_All//0.00E+00//gi|73861341|gb|DT464080.1|DT464080				nr -
Unigene45809_All	2776	0.79	0.44	0.88	5.33	4.85	3.45	6.46	5.63	2.41	-8.54E-01	4.74E-02		1.57E-01	6.98E-01		-1.36E-01	4.24E-01		-6.28E-01	9.02E-06		-1.98E-01	1.21E-01		-1.42E+00	4.66E-29	Down	Unigene45809_All//gi|259016184|sp|Q9FL10.2|BH120_ARATH//2.00E-23//RecName: Full=Transcription factor bHLH120; AltName: Full=Transcription factor EN 4; AltName: Full=bHLH transcription factor bHLH120; AltName: Full=Basic helix-loop-helix protein 120; Short=bHLH 120; Short=AtbHLH120	Unigene45809_All//1.00E-24//AT4G25410| DNA binding / transcription factor	Unigene45809_All//0.00E+00//ES805839	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene4581_All	1424	5.00	4.70	4.60	8.26	10.18	7.58	14.01	9.39	6.60	-8.93E-02	6.91E-01		-1.20E-01	6.34E-01		3.02E-01	4.25E-02		-1.23E-01	5.42E-01		-5.77E-01	1.45E-07		-1.09E+00	1.97E-21	Down	Unigene4581_All//gi|297834432|ref|XP_002885098.1|//1.00E-165//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330938|gb|EFH61357.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4581_All//3.00E-166//AT3G15610| transducin family protein / WD-40 repeat family protein	Unigene4581_All//0.00E+00//TC156326				nr +
Unigene45814_All	1920	6.68	35.05	9.24	13.47	16.03	30.93	99.09	65.33	53.78	2.39E+00	8.64E-171	Up	4.68E-01	6.10E-04		2.52E-01	9.10E-03		1.20E+00	8.66E-62	Up	-6.01E-01	7.14E-70		-8.82E-01	2.07E-139		Unigene45814_All//gi|15224499|ref|NP_181374.1|//0.00E+00//AGT3 (ALANINE:GLYOXYLATE AMINOTRANSFERASE 3); alanine-glyoxylate transaminase/ catalytic/ pyridoxal phosphate binding / transaminase [Arabidopsis thaliana] >gi|85683263|sp|Q94AL9.2|AGT22_ARATH RecName: Full=Alanine--glyoxylate aminotransferase 2 homolog 2, mitochondrial; AltName: Full=Beta-alanine-pyruvate aminotransferase 2; Flags: Precursor >gi|5731261|gb|AAD48838.1|AF166352_1 alanine:glyoxylate aminotransferase 2 homolog [Arabidopsis thaliana]	Unigene45814_All//0.00E+00//AT2G38400| AGT3 (ALANINE:GLYOXYLATE AMINOTRANSFERASE 3); alanine-glyoxylate transaminase/ catalytic/ pyridoxal phosphate binding / transaminase	Unigene45814_All//0.00E+00//TC1511105		ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism	GO:0008483//GO:0043231//GO:0048037	nr -
Unigene45815_All	2984	19.94	2.34	2.89	17.31	11.96	10.19	15.88	2.24	3.11	-3.09E+00	3.93E-201	Down	-2.79E+00	9.55E-175	Down	-5.34E-01	1.39E-15		-7.65E-01	5.33E-26		-2.83E+00	1.08E-178	Down	-2.35E+00	9.97E-150	Down	Unigene45815_All//gi|15239630|ref|NP_200249.1|//0.00E+00//THE1 (THESEUS1); kinase/ protein kinase [Arabidopsis thaliana] >gi|75335100|sp|Q9LK35.1|THE1_ARATH RecName: Full=Receptor-like protein kinase THESEUS 1; Flags: Precursor >gi|8953753|dbj|BAA98098.1| receptor-protein kinase-like protein [Arabidopsis thaliana]	Unigene45815_All//0.00E+00//AT5G54380| THE1 (THESEUS1); kinase/ protein kinase	Unigene45815_All//0.00E+00//TC149670			GO:0000902//GO:0001558//GO:0004672//GO:0006468//GO:0007275//GO:0016020//GO:0032559//GO:0043231//GO:0043401	nr +
Unigene45816_All	752	2.78	2.16	0.14	5.63	3.75	1.38	6.24	9.34	3.23	-3.68E-01	4.01E-01		-4.30E+00	3.74E-09	Down	-5.85E-01	4.01E-02		-2.03E+00	4.88E-10	Down	5.81E-01	3.20E-03		-9.50E-01	9.26E-05		Unigene45816_All//gi|217075448|gb|ACJ86084.1|//8.00E-08//unknown [Medicago truncatula]	Unigene45816_All//1.00E-05//AT3G14200| DNAJ heat shock N-terminal domain-containing protein	Unigene45816_All//1.00E-76//TC167318			GO:0005515	nr -
Unigene45817_All	658	6.44	7.16	2.99	11.89	6.49	3.71	15.49	26.55	7.63	1.53E-01	5.94E-01		-1.11E+00	4.03E-04	Down	-8.73E-01	5.47E-06		-1.68E+00	3.92E-14	Down	7.78E-01	8.46E-11		-1.02E+00	2.21E-10	Down	Unigene45817_All//gi|225442030|ref|XP_002269039.1|//1.00E-08//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene45817_All//0.00E+00//D#510743				nr +
Unigene45818_All	1353	4.64	5.65	2.83	13.18	9.01	3.30	16.69	16.93	7.21	2.85E-01	1.99E-01		-7.12E-01	3.73E-03		-5.49E-01	5.35E-06		-2.00E+00	7.52E-40	Down	2.07E-02	8.73E-01		-1.21E+00	1.56E-28	Down	Unigene45818_All//gi|297834276|ref|XP_002885020.1|//5.00E-50//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297330860|gb|EFH61279.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene45818_All//3.00E-40//AT3G14200| DNAJ heat shock N-terminal domain-containing protein	Unigene45818_All//0.00E+00//TC140767		ko04141|Protein processing in endoplasmic reticulum	GO:0005515	nr -
Unigene4582_All	1181	2.53	3.90	0.99	16.07	18.19	13.38	3.08	1.34	1.65	6.29E-01	2.53E-02		-1.35E+00	5.59E-04	Down	1.79E-01	1.64E-01		-2.64E-01	4.66E-02		-1.20E+00	4.81E-05	Down	-8.97E-01	1.29E-03		Unigene4582_All//gi|134035510|gb|AB047743.1|//7.00E-82//homeobox protein [Gossypium hirsutum]	Unigene4582_All//3.00E-55//AT5G15150| ATHB-3 (ARABIDOPSIS THALIANA HOMEOBOX 3); DNA binding / sequence-specific DNA binding / transcription factor	Unigene4582_All//0.00E+00//TC136688	HB			nr -
Unigene45825_All	1367	0.69	0.78	0.23	1.89	1.64	0.93	4.95	2.14	2.24	1.76E-01	7.74E-01		-1.56E+00	4.90E-02		-2.11E-01	6.04E-01		-1.03E+00	8.32E-03		-1.21E+00	7.48E-09	Down	-1.14E+00	1.97E-08	Down	Unigene45825_All//gi|224072103|ref|XP_002303625.1|//2.00E-65//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222841057|gb|EEE78604.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene45825_All//1.00E-35//AT4G23750| CRF2 (CYTOKININ RESPONSE FACTOR 2); DNA binding / transcription factor	Unigene45825_All//0.00E+00//TC169398	AP2-EREBP		GO:0005488//GO:0006350//GO:0006606//GO:0009793//GO:0043231//GO:0048827	nr -
Unigene45827_All	914	1.09	4.66	0.82	1.25	1.51	1.48	1.67	0.87	1.83	2.10E+00	8.49E-10	Up	-4.15E-01	5.72E-01		2.66E-01	6.81E-01		2.42E-01	6.70E-01		-9.39E-01	5.17E-02		1.37E-01	7.54E-01		Unigene45827_All//gi|224072103|ref|XP_002303625.1|//1.00E-53//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222841057|gb|EEE78604.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene45827_All//6.00E-32//AT4G23750| CRF2 (CYTOKININ RESPONSE FACTOR 2); DNA binding / transcription factor	Unigene45827_All//0.00E+00//TC130404	AP2-EREBP		GO:0005488//GO:0009987//GO:0048827	nr +
Unigene45829_All	1418	1.55	5.40	1.24	4.22	4.98	3.60	1.91	0.83	2.78	1.80E+00	4.58E-14	Up	-3.23E-01	4.83E-01		2.40E-01	3.22E-01		-2.28E-01	4.04E-01		-1.21E+00	5.14E-04	Down	5.44E-01	4.19E-02		Unigene45829_All//gi|224072103|ref|XP_002303625.1|//3.00E-53//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222841057|gb|EEE78604.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene45829_All//2.00E-35//AT4G23750| CRF2 (CYTOKININ RESPONSE FACTOR 2); DNA binding / transcription factor	Unigene45829_All//0.00E+00//TC130404	AP2-EREBP		GO:0005488//GO:0006350//GO:0006606//GO:0009793//GO:0043231//GO:0048513	nr -
Unigene45830_All	2502	3.76	8.81	5.13	7.92	7.14	8.81	39.68	68.37	68.83	1.23E+00	1.50E-22	Up	4.46E-01	6.82E-03		-1.50E-01	2.90E-01		1.53E-01	2.56E-01		7.85E-01	4.05E-100		7.95E-01	2.82E-105		Unigene45830_All//gi|223452426|gb|ACM89540.1|//0.00E+00//protein kinase family protein [Glycine max]	Unigene45830_All//0.00E+00//AT1G70520| protein kinase family protein	Unigene45830_All//0.00E+00//TC148709		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene45832_All	524	5.79	5.71	11.99	2.28	1.18	1.98	0.16	0.24	0.53	-2.16E-02	9.71E-01		1.05E+00	2.32E-05	Up	-9.48E-01	1.12E-01		-2.03E-01	7.36E-01		5.68E-01	7.81E-01		1.72E+00	2.30E-01		Unigene45832_All//gi|13346190|gb|AK19617.1|AF336284_1//7.00E-76//GHMYB36 [Gossypium hirsutum]	Unigene45832_All//5.00E-48//AT5G35550| TT2 (TRANSPARENT TESTA 2); DNA binding / transcription factor	Unigene45832_All//0.00E+00//ES849185	MYB		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene45833_All	864	3.82	0.06	3.33	1.10	0.88	2.82	1.37	0.82	3.60	-6.02E+00	1.52E-17	Down	-1.97E-01	6.17E-01		-3.21E-01	6.38E-01		1.37E+00	1.11E-03		-7.37E-01	1.94E-01		1.39E+00	1.53E-05	Up	Unigene45833_All//gi|13346190|gb|AK19617.1|AF336284_1//2.00E-77//GHMYB36 [Gossypium hirsutum]	Unigene45833_All//9.00E-35//AT5G35550| TT2 (TRANSPARENT TESTA 2); DNA binding / transcription factor	Unigene45833_All//0.00E+00//TC132726	MYB			nr -
Unigene45834_All	857	3.24	5.97	7.46	1.16	1.25	1.48	0.10	0.00	0.00	8.84E-01	8.99E-04		1.20E+00	1.35E-06	Up	9.96E-02	9.02E-01		3.44E-01	6.24E-01		-6.63E+00	4.03E-01		-6.63E+00	3.58E-01		Unigene45834_All//gi|13346190|gb|AK19617.1|AF336284_1//1.00E-86//GHMYB36 [Gossypium hirsutum]	Unigene45834_All//2.00E-35//AT5G35550| TT2 (TRANSPARENT TESTA 2); DNA binding / transcription factor	Unigene45834_All//0.00E+00//TC140530	MYB			nr +
Unigene45835_All	979	5.72	6.73	14.69	15.42	17.80	37.83	16.15	2.60	2.81	2.35E-01	3.46E-01		1.36E+00	7.82E-17	Up	2.07E-01	1.51E-01		1.29E+00	1.57E-43	Up	-2.63E+00	1.31E-55	Down	-2.52E+00	9.29E-55	Down	Unigene45835_All//gi|13346190|gb|AK19617.1|AF336284_1//1.00E-156//GHMYB36 [Gossypium hirsutum]	Unigene45835_All//3.00E-52//AT5G35550| TT2 (TRANSPARENT TESTA 2); DNA binding / transcription factor	Unigene45835_All//0.00E+00//TC157497	MYB		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene45836_All	1450	15.91	29.70	19.83	21.99	21.28	34.54	34.17	32.49	15.00	9.00E-01	1.78E-26		3.18E-01	2.79E-03		-4.72E-02	7.04E-01		6.52E-01	5.13E-19		-7.31E-02	3.78E-01		-1.19E+00	8.19E-60	Down	Unigene45836_All//gi|162458637|ref|NP_001105506.1|//1.00E-172//pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays] >gi|3851001|gb|AAC72193.1| pyruvate dehydrogenase E1 beta subunit isoform 2 [Zea mays]	Unigene45836_All//6.00E-169//AT5G50850| MAB1 (MACC1-BOU); catalytic/ pyruvate dehydrogenase (acetyl-transferring)	Unigene45836_All//0.00E+00//TC148578		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)//ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis		nr +
Unigene45837_All	3723	2.49	3.21	1.63	9.54	8.79	8.02	24.59	17.58	59.91	3.69E-01	2.69E-02		-6.09E-01	1.93E-03		-1.19E-01	2.46E-01		-2.51E-01	6.17E-03		-4.84E-01	3.01E-23		1.29E+00	5.53E-299	Up	Unigene45837_All//gi|224123504|ref|XP_002319094.1|//0.00E+00//ethylene receptor 6 [Populus trichocarpa] >gi|222857470|gb|EEE95017.1| ethylene receptor 6 [Populus trichocarpa]	Unigene45837_All//0.00E+00//AT3G04580| EIN4 (ETHYLENE INSENSITIVE 4); ethylene binding / glycogen synthase kinase 3/ protein histidine kinase/ receptor	Unigene45837_All//0.00E+00//TC174875	Orphans	ko04712|Circadian rhythm - plant	GO:0004673//GO:0004871//GO:0006351//GO:0006468//GO:0009873//GO:0031090//GO:0032559//GO:0042562	nr +

Unigene45842_All	781	1.81	6.94	3.00	2.49	3.79	3.82	8.50	8.51	7.14	1.94E+00	3.54E-11	Up	7.30E-01	9.36E-02		6.08E-01	9.85E-02		6.18E-01	9.76E-02		1.60E-03	9.93E-01		-2.51E-01	2.33E-01		Unigene45842_All//gi|21537297|gb|AAM61638.1|//4.00E-11//DNA-damage inducible protein DDI1-like [Arabidopsis thaliana]	Unigene45842_All//2.00E-12//AT3G13235| ubiquitin family protein	Unigene45842_All//4.00E-166//gi|164342139|gb|ES810427.1|ES810427			GO:0004175//GO:0010038//GO:0019538//GO:0043231//GO:0044444	nr -
Unigene45845_All	1178	4.93	14.45	10.71	6.09	9.06	10.62	14.86	21.86	11.36	1.55E+00	8.46E-25	Up	1.12E+00	4.24E-11	Up	5.74E-01	5.40E-04		8.02E-01	3.20E-07		5.57E-01	5.81E-09		-3.87E-01	8.17E-04		Unigene45845_All//gi|182407840|gb|ACB37911.1|//1.00E-103//F-box-containing protein 1 [Malus x domestica]	Unigene45845_All//4.00E-78//AT1G15740| leucine-rich repeat family protein	Unigene45845_All//0.00E+00//TC141291				nr -
Unigene45846_All	2495	14.62	45.98	30.61	24.10	33.17	35.61	29.23	41.58	21.97	1.65E+00	3.84E-179	Up	1.07E+00	1.75E-59	Up	4.61E-01	1.52E-18		5.63E-01	8.74E-26		5.08E-01	1.33E-28		-4.12E-01	1.58E-14		Unigene45846_All//gi|182407840|gb|ACB37911.1|//0.00E+00//F-box-containing protein 1 [Malus x domestica]	Unigene45846_All//0.00E+00//AT1G15740| leucine-rich repeat family protein	Unigene45846_All//0.00E+00//TC140424		ko04626|Plant-pathogen interaction		nr +
Unigene45849_All	790	2.52	3.27	3.91	4.73	3.57	4.34	7.65	5.56	3.68	3.78E-01	3.59E-01		6.36E-01	8.68E-02		-4.04E-01	2.15E-01		-1.22E-01	7.14E-01		-4.62E-01	3.41E-02		-1.06E+00	7.78E-07	Down	Unigene45849_All//gi|297815088|ref|XP_002875427.1|//1.00E-74//calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297321265|gb|EFH51686.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene45849_All//1.00E-67//AT5G40190| calmodulin-binding protein	Unigene45849_All//0.00E+00//TC159180			GO:0005515//GO:0044260//GO:0044464	nr -
Unigene45850_All	1100	1.86	1.20	1.69	3.31	2.75	1.23	2.81	2.55	3.22	-6.31E-01	1.60E-01		-1.31E-01	7.73E-01		-2.63E-01	4.48E-01		-1.42E+00	1.49E-05	Down	-1.40E-01	6.78E-01		2.00E-01	5.27E-01		Unigene45850_All//gi|297815088|ref|XP_002875427.1|//3.00E-74//calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297321265|gb|EFH51686.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene45850_All//6.00E-67//AT5G40190| calmodulin-binding protein	Unigene45850_All//0.00E+00//TC159180			GO:0005515//GO:0044260//GO:0044464	nr +
Unigene45851_All	1410	4.12	4.28	4.12	4.31	8.28	4.71	6.93	8.15	20.17	5.41E-02	8.29E-01		-8.00E-04	9.97E-01		9.42E-01	2.34E-09		1.28E-01	6.30E-01		2.35E-01	1.44E-01		1.54E+00	7.31E-51	Up	Unigene45851_All//gi|297815088|ref|XP_002875427.1|//2.00E-70//calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297321265|gb|EFH51686.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene45851_All//2.00E-63//AT5G40190| calmodulin-binding protein	Unigene45851_All//0.00E+00//TC158930			GO:0005515//GO:0044260//GO:0044464	nr +
Unigene45852_All	1685	2.58	3.85	2.88	9.22	12.00	6.65	5.65	2.36	4.18	5.79E-01	1.25E-02		1.58E-01	6.22E-01		3.79E-01	1.24E-03		-4.73E-01	6.83E-04		-1.26E+00	6.90E-13	Down	-4.32E-01	7.73E-03		Unigene45852_All|gi|15221563|ref|NP_177058.1|//2.00E-47//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|79590003|ref|NP_849863.2| basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75333634|sp|Q9CAA9.1|BH049_ARATH RecName: Full=Transcription factor bHLH49; AltName: Full=Transcription factor EN 82; AltName: Full=bHLH transcription factor bHLH049; AltName: Full=Basic helix-loop-helix protein 49; Short=bHLH 49; Short=AtbHLH49 >gi|22135841|gb|AAM91106.1| At1g68920/T6L1_10 [Arabidopsis thaliana] >gi|25090290|gb|AAN72270.1| At1g68920/T6L1_10 [Arabidopsis thaliana]	Unigene45852_All//3.00E-39//AT1G68920| basic helix-loop-helix (bHLH) family protein	Unigene45852_All//0.00E+00//TC152699	bHLH			nr -
Unigene45853_All	2534	3.06	4.30	3.91	8.43	11.21	6.54	6.24	2.08	3.87	4.93E-01	4.41E-03		3.55E-01	6.95E-02		4.11E-01	1.61E-05		-3.67E-01	1.90E-03		-1.59E+00	3.23E-29	Down	-6.90E-01	1.94E-08		Unigene45853_All|gi|79320926|ref|NP_001031255.1|//1.00E-105//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|227204401|dbj|BAH57052.1| AT1G68920 [Arabidopsis thaliana]	Unigene45853_All//7.00E-99//AT1G68920| basic helix-loop-helix (bHLH) family protein	Unigene45853_All//0.00E+00//gi|109842660|gb|DW241220.1|DW241220	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0010468//GO:0043231	nr -
Unigene45855_All	475	0.11	0.32	1.35	2.73	2.83	4.09	3.12	0.88	0.92	1.54E+00	5.31E-01		3.61E+00	6.97E-03		5.23E-02	9.57E-01		5.84E-01	2.29E-01		-1.82E+00	5.43E-04	Down	-1.76E+00	5.33E-04	Down	Unigene45855_All|gi|255578386|ref|XP_002530059.1|//2.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223520436|gb|EEF32321.1| conserved hypothetical protein [Ricinus communis]		Unigene45855_All//3.00E-110//TC161555				nr +
Unigene45856_All	1994	2.23	2.13	2.48	6.77	7.36	5.91	8.86	5.09	3.54	-6.33E-02	8.26E-01		1.55E-01	6.26E-01		1.20E-01	5.12E-01		-1.96E-01	2.56E-01		-7.99E-01	2.07E-11		-1.33E+00	7.50E-26	Down	Unigene45856_All|gi|84102164|ref|NP_564526.1|//9.00E-81//RHL1 (ROOT HAIRLESS 1); DNA binding / protein binding [Arabidopsis thaliana] >gi|75100120|sp|Q81242.1|RHL1_ARATH RecName: Full=DNA-binding protein RHL1; AltName: Full=Protein ROOT HAIRLESS 1; AltName: Full=Protein ELONGATED HYPOCOTYL 7 >gi|5733871|gb|AAD49759.1|AC007932_7 Identical to root hairless 1 (RHL1) from Arabidopsis thaliana gb|Z29767. EST gb|AI995014 comes from this gene >gi|3219355|gb|AAC23500.1| ROOT HAIRLESS 1 [Arabidopsis thaliana] >gi|16323206|gb|AAL15337.1| At1g68380/F11A17_7 [Arabidopsis thaliana] >gi|22137216|gb|AAM91453.1| At1g68380/F11A17_7 [Arabidopsis thaliana]	Unigene45856_All//4.00E-70//AT1G68380| RHL1 (ROOT HAIRLESS 1); DNA binding / protein binding	Unigene45856_All//0.00E+00//gi|164255063|gb|ES849607.1|ES849607			GO:0000904//GO:0005488//GO:0006261//GO:0031981	nr +
Unigene45857_All	1490	1.30	0.88	0.93	1.94	1.71	1.15	2.84	2.16	1.02	-5.55E-01	2.36E-01		-4.84E-01	3.33E-01		-1.81E-01	6.41E-01		-7.52E-01	4.17E-02		-3.94E-01	1.50E-01		-1.48E+00	6.12E-08	Down	Unigene45857_All|gi|3811320|gb|AAC69460.1|//5.00E-60//ROOT HAIRLESS 1 [Arabidopsis thaliana]	Unigene45857_All//4.00E-56//AT1G48380| RHL1 (ROOT HAIRLESS 1); DNA binding / protein binding	Unigene45857_All//0.00E+00//gi|164255063|gb|ES849607.1|ES849607			GO:0000904//GO:0005488//GO:0006261//GO:0031981	nr -
Unigene45858_All	2653	8.26	4.20	4.17	23.30	28.04	31.78	25.50	11.15	9.28	-9.76E-01	8.59E-16		-9.85E-01	2.39E-15		2.67E-01	2.39E-06		4.48E-01	2.48E-16		-1.19E+00	1.30E-79	Down	-1.46E+00	1.93E-111	Down	Unigene45858_All|gi|225445252|ref|XP_002284512.1|//0.00E+00//PREDICTED: similar to BY-2 kinesin-like protein 10 [Vitis vinifera]	Unigene45858_All//0.00E+00//AT3G16060| kinesin motor family protein	Unigene45858_All//0.00E+00//TC176613			GO:0003774//GO:0007017//GO:0015630//GO:0016020//GO:0032559//GO:0043231	nr -
Unigene45859_All	1474	8.98	9.52	13.01	9.12	17.59	55.31	74.61	46.96	42.65	8.45E-02	6.09E-01		5.34E-01	4.00E-05		9.47E-01	1.79E-20		2.60E+00	2.45E-244	Up	-6.68E-01	5.60E-49		-8.07E-01	1.19E-69		Unigene45859_All|gi|297832266|ref|XP_002884015.1|//1.00E-122//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329855|gb|EFH60274.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45859_All//1.00E-118//AT2G16750| protein kinase family protein	Unigene45859_All//0.00E+00//DR453396		ko04626|Plant-pathogen interaction		nr +
Unigene45862_All	1769	52.47	12.26	32.12	81.44	60.42	25.30	22.59	5.03	5.61	-2.10E+00	1.30E-201	Down	-7.08E-01	3.30E-36		-4.31E-01	7.22E-29		-1.69E+00	2.39E-253	Down	-2.17E+00	9.68E-111	Down	-2.01E+00	1.11E-103	Down	Unigene45862_All|gi|173386118|gb|AAL38605.1|AF446872_1|//0.00E+00//AT5g50150/MPF21_17 [Arabidopsis thaliana] >gi|15529145|gb|AAK97667.1| AT5g50150/MPF21_17 [Arabidopsis thaliana]	Unigene45862_All//1.00E-176//AT5G50150| unknown protein	Unigene45862_All//0.00E+00//TC151865				nr +
Unigene45863_All	1071	8.50	5.49	6.41	4.93	4.82	5.27	3.28	1.13	1.41	-6.31E-01	9.10E-04		-4.06E-01	4.51E-02		-3.18E-02	9.10E-01		9.65E-02	7.28E-01		-1.53E+00	8.80E-07	Down	-1.21E+00	3.43E-05	Down	Unigene45863_All|gi|14485577|gb|AK63013.1|AF320029_1|//4.00E-63//heme oxygenase 2 [Solanum lycopersicum]	Unigene45863_All//1.00E-56//AT2G26550| HO2 (HEME OXYGENASE 2); heme oxygenase (decyclizing)	Unigene45863_All//0.00E+00//TC133789		ko00860|Porphyrin and chlorophyll metabolism	GO:0006787//GO:0016705//GO:0043231	nr +
Unigene45864_All	1575	18.40	11.94	14.37	13.79	15.41	12.85	5.61	1.62	3.49	-6.25E-01	5.59E-10		-3.57E-01	6.60E-04		1.61E-01	1.91E-01		-1.02E-01	4.70E-01		-1.79E+00	1.11E-19	Down	-6.85E-01	4.74E-05		Unigene45864_All|gi|42569350|ref|NP_180223.2|//1.00E-59//HO2 (HEME OXYGENASE 2); heme oxygenase (decyclizing) [Arabidopsis thaliana]	Unigene45864_All//1.00E-53//AT2G26550| HO2 (HEME OXYGENASE 2); heme oxygenase (decyclizing)	Unigene45864_All//0.00E+00//TC133789		ko00860|Porphyrin and chlorophyll metabolism	GO:0008152//GO:0043231	nr -
Unigene45869_All	2640	6.06	7.89	8.61	8.57	6.09	4.72	6.10	3.99	2.67	3.79E-01	1.77E-03		5.06E-01	1.88E-05		-4.92E-01	3.34E-06		-8.59E-01	3.58E-14		-6.13E-01	7.01E-07		-1.19E+00	3.78E-20	Down	Unigene45869_All|gi|115451203|ref|NP_001049202.1|//1.00E-114//Os03g0186500 [Oryza sativa Japonica Group] >gi|108706564|gb|ABF94359.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547673|dbj|BAF11116.1| Os03g0186500 [Oryza sativa Japonica Group]	Unigene45869_All//8.00E-24//AT5G66820| unknown protein	Unigene45869_All//0.00E+00//TC139350				nr +
Unigene4587_All	944	13.75	4.83	3.33	7.86	9.89	7.75	14.56	4.03	8.82	-1.51E+00	1.96E-18	Down	-2.05E+00	1.13E-26	Down	3.30E-01	8.80E-02		-2.07E-02	9.44E-01		-1.85E+00	1.54E-31	Down	-7.23E-01	5.30E-08		Unigene4587_All|gi|145322900|ref|NP_001030726.2|//4.00E-75//DNA binding [Arabidopsis thaliana] >gi|122178676|sp|Q1G3M3.1|Y3918_ARATH RecName: Full=B3 domain-containing protein At3g19184	Unigene4587_All//8.00E-59//AT3G19184| DNA binding	Unigene4587_All//0.00E+00//gi|78331234|gb|DT551508.1|DT551508	ABI3VP1			nr -
Unigene45870_All	3196	13.36	7.67	12.25	14.39	18.32	11.05	1.75	0.52	0.95	-8.00E-01	1.16E-21		-1.25E-01	1.83E-01		3.49E-01	4.26E-08		-3.81E-01	5.27E-07		-1.74E+00	3.26E-12	Down	-8.82E-01	5.85E-05		Unigene45870_All|gi|1730557|sp|P53535.1|PHSL2_SOLTU//0.00E+00//RecName: Full=Alpha-1,4 glucan phosphorylase L-2 isozyme, chloroplastic/amyloplastic; AltName: Full=Starch phosphorylase L-2; Flags: Precursor >gi|313349|emb|CAA52036.1| starch phosphorylase [Solanum tuberosum]	Unigene45870_All//0.00E+00//AT3G29320| glucan phosphorylase, putative	Unigene45870_All//0.00E+00//TC150291		ko00500|Starch and sucrose metabolism	GO:0005515//GO:0006950//GO:0009532//GO:0009628//GO:0016758//GO:0044238//GO:0048037	nr -
Unigene45871_All	1923	21.00	27.11	34.95	120.04	61.22	43.31	75.61	33.01	47.40	3.68E-01	4.51E-07		7.34E-01	4.12E-28		-9.71E-01	3.42E-196		-1.47E+00	0.00E+00	Down	-1.20E+00	6.24E-171	Down	-6.74E-01	2.98E-67		Unigene45871_All|gi|224141637|ref|XP_002324173.1|//1.00E-173//ZIP transporter [Populus trichocarpa] >gi|222865607|gb|EEF02738.1| ZIP transporter [Populus trichocarpa]	Unigene45871_All//2.00E-128//AT1G10970| ZIP4 (ZINC TRANSPORTER 4 PRECURSOR); cation transmembrane transporter/ copper ion transmembrane transporter	Unigene45871_All//0.00E+00//TC137962			GO:0000041//GO:0008152//GO:0015082//GO:0016628//GO:0031224	nr -
Unigene45874_All	1636	3.33	5.42	7.29	3.01	3.12	2.98	4.78	7.61	6.53	7.05E-01	2.77E-04		1.13E+00	1.05E-10	Up	4.75E-02	8.83E-01		-1.59E-02	9.47E-01		6.71E-01	2.57E-06		4.49E-01	3.17E-03		Unigene45874_All|gi|82791812|gb|AB906835.1|//0.00E+00//VHS and GAT domain protein [Glycine max]	Unigene45874_All//4.00E-159//AT4G32760| protein transporter	Unigene45874_All//0.00E+00//CO087530			GO:0015031//GO:0044464	nr -
Unigene45879_All	1712	20.51	29.92	24.20	12.98	18.28	19.94	4.40	12.79	10.52	5.45E-01	1.81E-13		2.39E-01	6.99E-03		4.95E-01	3.03E-08		6.20E-01	4.37E-12		1.54E+00	1.82E-38	Up	1.26E+00	3.82E-24	Up	Unigene45879_All|gi|2292917|emb|CAA68163.1|//0.00E+00//galactokinase [Arabidopsis thaliana]	Unigene45879_All//6.00E-120//AT3G06580| GALK; ATP binding / galactokinase	Unigene45879_All//0.00E+00//TC172500		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism	GO:0016310//GO:0016773//GO:0019318//GO:0032559//GO:0044424	nr -
Unigene45880_All	820	6.57	3.83	4.87	4.07	1.72	2.81	1.70	1.12	1.70	-7.79E-01	2.42E-03		-4.32E-01	1.17E-01		-1.24E+00	1.02E-04	Down	-5.35E-01	1.26E-01		-6.02E-01	2.40E-01		-9.00E-04	9.95E-01		Unigene45880_All|gi|240256063|ref|NP_194259.4|//1.00E-53//DNA photolyase [Arabidopsis thaliana]	Unigene45880_All//4.00E-54//AT4G25290| DNA photolyase	Unigene45880_All//0.00E+00//TC170137			GO:0006259//GO:0016830//GO:0043231	nr -
Unigene45881_All	1263	4.02	1.48	2.53	1.42	1.58	1.22	2.68	1.09	1.55	-1.44E+00	3.43E-07	Down	-6.68E-01	1.62E-02		1.55E-01	7.98E-01		-2.24E-01	6.74E-01		-1.29E+00	2.88E-05	Down	-7.93E-01	6.10E-03		Unigene45881_All|gi|240256063|ref|NP_194259.4|//4.00E-90//DNA photolyase [Arabidopsis thaliana]	Unigene45881_All//6.00E-91//AT4G25290| DNA photolyase	Unigene45881_All//0.00E+00//TC170137			GO:0005488//GO:0006259//GO:0016830//GO:0043231	nr +
Unigene45882_All	1596	4.13	0.83	4.10	3.37	2.16	1.64	1.91	1.20	1.05	-2.32E+00	7.98E-17	Down	-9.40E-03	9.93E-01		-6.44E-01	8.04E-03		-1.04E+00	4.52E-05	Down	-6.63E-01	3.84E-02		-8.63E-01	5.01E-03		Unigene45882_All|gi|240256063|ref|NP_194259.4|//1.00E-172//DNA photolyase [Arabidopsis thaliana]	Unigene45882_All//1.00E-158//AT4G25290| DNA photolyase	Unigene45882_All//2.00E-129//TC150413			GO:0006259//GO:0016830	nr -

Unigene45884_All	1583	12.20	4.71	6.83	15.70	11.94	10.61	7.61	5.91	4.88	-1.37E+00	1.26E-23	Down	-8.37E-01	1.73E-10		-3.95E-01	1.07E-04		-5.65E-01	9.31E-08		-3.64E-01	1.41E-02		-6.41E-01	6.16E-06		Unigene45884_All//gi|42567296|ref|NP_194849.2|//1.00E-173//DNA topoisomerase family protein [Arabidopsis thaliana]	Unigene45884_All//1.00E-174//AT4G31210| DNA topoisomerase family protein	Unigene45884_All//1.00E-44//ES802677			GO:0003916//GO:0006261//GO:0043231//GO:0043232	nr -
Unigene45885_All	2119	1.36	0.19	1.43	1.74	1.22	1.64	1.64	0.75	0.96	-2.83E+00	1.94E-09	Down	7.70E-02	8.32E-01		-5.13E-01	1.03E-01		-8.41E-02	8.03E-01		-1.13E+00	1.75E-04	Down	-7.71E-01	6.84E-03		Unigene45885_All//gi|42567296|ref|NP_194849.2|//0.00E+00//DNA topoisomerase family protein [Arabidopsis thaliana]	Unigene45885_All//0.00E+00//AT4G31210| DNA topoisomerase family protein	Unigene45885_All//2.00E-44//ES802677			GO:0003916//GO:0006261//GO:0043232	nr -
Unigene45889_All	2249	2.44	3.58	4.17	4.70	5.39	2.99	2.59	1.21	0.76	5.52E-01	7.05E-03		7.71E-01	7.66E-05		1.99E-01	2.79E-01		-6.50E-01	1.48E-04		-1.10E+00	8.54E-07	Down	-1.77E+00	1.86E-13	Down	Unigene45889_All//gi|115455417|ref|NP_001051309.1|//1.00E-151//0s03g0754900 (Oryza sativa Japonica Group) >gi|113549780|dbj|BAF13223.1| Os03g0754900 (Oryza sativa Japonica Group)	Unigene45889_All//2.00E-148//AT5G60940| transducin family protein / WD-40 repeat family protein	Unigene45889_All//0.00E+00//TC151697		ko03022|Basal transcription factors	nr +
Unigene4589_All	1342	2.18	1.59	2.78	5.53	5.13	3.03	7.53	4.58	3.59	-4.61E-01	2.17E-01		3.47E-01	3.16E-01		-1.08E-01	6.60E-01		-8.69E-01	3.51E-05		-7.18E-01	7.63E-06		-1.07E+00	5.17E-11	Down	Unigene4589_All//gi|145327193|ref|NP_001077798.1|//2.00E-59//transcription factor [Arabidopsis thaliana]	Unigene4589_All//1.00E-56//AT1G69580| transcription factor	Unigene4589_All//0.00E+00//ES806166	G2-like		nr -
Unigene45892_All	965	0.70	0.11	0.55	0.41	0.71	0.89	1.62	0.74	3.43	-2.75E+00	1.06E-02		-3.53E-01	6.64E-01		7.89E-01	4.04E-01		1.11E+00	1.67E-01		-1.14E+00	1.72E-02		1.08E+00	3.22E-04	Up	Unigene45892_All//gi|297830654|ref|XP_002883209.1|//2.00E-95//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297329049|gb|EFH59468.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene45892_All//5.00E-82//AT3G19870| binding	Unigene45892_All//5.00E-18//TC145225			nr +
Unigene45898_All	2328	0.61	0.81	0.27	0.81	1.01	1.16	1.14	0.41	0.60	4.08E-01	3.81E-01		-1.14E+00	5.55E-02		3.07E-01	5.29E-01		5.18E-01	2.00E-01		-1.47E+00	4.62E-05	Down	-9.34E-01	5.07E-03		Unigene45898_All//gi|15230124|ref|NP_189092.1|//6.00E-68//transcription factor [Arabidopsis thaliana]	Unigene45898_All//2.00E-59//AT3G24490| transcription factor	Unigene45898_All//0.00E+00//TC141819	Trihelix	ko04120|Ubiquitin mediated proteolysis	GO:0010468	nr -
Unigene45900_All	1876	107.07	127.65	76.24	39.25	40.53	53.18	24.99	68.22	60.23	2.54E-01	5.36E-15		-4.90E-01	2.05E-40		4.64E-02	5.46E-01		4.38E-01	1.69E-18		1.45E+00	5.81E-202	Up	1.27E+00	8.22E-149	Up	Unigene45900_All//gi|300507125|gb|ADK23938.1|//0.00E+00//GPAT [Gossypium hirsutum]	Unigene45900_All//0.00E+00//AT4G00400| GPAT8 (glycerol-3-phosphate acyltransferase 8); acyltransferase/ glycerol-3-phosphate O-acyltransferase	Unigene45900_All//0.00E+00//TC154812		ko00564|Glycerophospholipid metabolism/ko00561|Glycerolipid metabolism	GO:0006633//GO:0009791//GO:0016411//GO:0043231	nr -
Unigene45908_All	540	0.00	1.41	0.10	0.37	0.51	0.75	26.93	266.18	6.20	1.05E+01	1.76E-04	Up	6.62E+00	6.35E-01		4.67E-01	8.16E-01		1.03E+00	4.28E-01		3.30E+00	0.00E+00	Up	-2.12E+00	6.31E-41	Down	Unigene45908_All//gi|29419702|gb|AO61854.1|//5.00E-47//glutathione S-transferase U1 [Malva pusilla]	Unigene45908_All//0.00E+00//AT5G17220| GSTU19 (GLUTATHIONE S-TRANSFERASE TAU 19); glutathione binding / glutathione transferase	Unigene45908_All//0.00E+00//gi|48775312|gb|CO084678.1|CO084678		ko00480|Glutathione metabolism	GO:0009755//GO:0016765	nr +
Unigene45909_All	1074	67.72	69.78	53.70	93.04	77.37	74.56	81.61	108.30	31.90	4.33E-02	5.60E-01		-3.35E-01	9.87E-08		-2.66E-01	2.08E-08		-3.20E-01	1.40E-10		4.08E-01	1.23E-21		-1.36E+00	4.78E-129	Down	Unigene45909_All//gi|29419702|gb|AO61854.1|//1.00E-89//glutathione S-transferase U1 [Malva pusilla]	Unigene45909_All//0.00E+00//AT5G17220| GSTU19 (GLUTATHIONE S-TRANSFERASE TAU 19); glutathione binding / glutathione transferase	Unigene45909_All//0.00E+00//TC132680		ko00480|Glutathione metabolism	GO:0016765//GO:0016846	nr +
Unigene45910_All	2990	3.46	4.37	4.47	6.85	6.75	14.68	26.24	28.89	26.12	3.36E-01	3.58E-02		3.68E-01	2.48E-02		-2.09E-02	8.86E-01		1.10E+00	5.99E-40	Up	1.39E-01	8.53E-03		-7.20E-03	9.28E-01		Unigene45910_All//gi|15239586|ref|NP_197387.1|//0.00E+00//inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis thaliana] >gi|19310427|gb|AAL84950.1| AT5g18860/F17K4_110 [Arabidopsis thaliana] >gi|22137232|gb|AAM91461.1| AT5g18860/F17K4_110 [Arabidopsis thaliana]	Unigene45910_All//0.00E+00//AT5G18860| inosine-uridine preferring nucleoside hydrolase family protein	Unigene45910_All//0.00E+00//TC160849			GO:0003824//GO:0030312//GO:0031410//GO:0043231	nr -
Unigene45912_All	1775	272.54	73.99	150.60	22.51	24.81	25.29	4.10	2.43	1.64	-1.88E+00	0.00E+00	Down	-8.56E-01	9.45E-260		1.41E-01	1.05E-01		1.68E-01	4.81E-02		-7.56E-01	8.83E-05		-1.32E+00	4.10E-11	Down	Unigene45912_All//gi|15229349|ref|NP_187130.1|//1.00E-107//ribose 5-phosphate isomerase-related [Arabidopsis thaliana]	Unigene45912_All//1.00E-101//AT3G04790| ribose 5-phosphate isomerase-related	Unigene45912_All//0.00E+00//TC138392		ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway	GO:0006098//GO:0016861//GO:0043231	nr +
Unigene45914_All	462	2.15	2.41	1.38	5.93	4.40	2.15	16.75	18.55	52.26	1.65E-01	7.79E-01		-6.38E-01	3.90E-01		-4.31E-01	2.71E-01		-1.46E+00	1.68E-04	Down	1.47E-01	4.72E-01		1.64E+00	2.61E-47	Up	Unigene45914_All//gi|62857014|dbj|BAD95892.1|//1.00E-20//Ser/Thr protein kinase [Lotus japonicus]	Unigene45914_All//3.00E-20//AT3G05840| ATSK12; protein kinase/ protein serine/threonine kinase	Unigene45914_All//1.00E-75//TC178024			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene45917_All	2212	19.44	5.84	4.21	40.09	30.73	59.35	80.72	22.05	24.51	-1.73E+00	1.18E-72	Down	-2.21E+00	2.04E-96	Down	-3.83E-01	1.64E-14		5.66E-01	3.21E-38		-1.87E+00	0.00E+00	Down	-1.72E+00	0.00E+00	Down	Unigene45917_All//gi|295291644|gb|ADF87507.1|//0.00E+00//ketol-acid reductoisomerase [Catharanthus roseus]	Unigene45917_All//0.00E+00//AT3G58610| ketol-acid reductoisomerase	Unigene45917_All//0.00E+00//TC140362		ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis	GO:0005576//GO:0008652//GO:0009526//GO:0009532//GO:0010038//GO:0016616//GO:0030312//GO:0042802//GO:0046914//GO:0050661	nr +
Unigene45919_All	1134	3.69	4.96	4.74	10.41	11.27	9.36	18.94	10.43	8.36	4.26E-01	9.53E-02		3.62E-01	1.95E-01		1.14E-01	5.55E-01		-1.54E-01	4.28E-01		-8.61E-01	2.00E-15		-1.18E+00	3.73E-26	Down	Unigene45919_All//gi|115454911|ref|NP_001051056.1|//1.00E-153//0s03g0711400 (Oryza sativa Japonica Group) >gi|75333115|sp|Q9AUR8.1|COPA1_ORYSJ RecName: Full=Coatomer subunit alpha-1; AltName: Full=Alpha-coat protein 1; Short=Alpha-COP 1 >gi|113549527|dbj|BAF12970.1| Os03g0711400 (Oryza sativa Japonica Group)	Unigene45919_All//1.00E-154//AT2G21390| coatomer protein complex, subunit alpha, putative	Unigene45919_All//0.00E+00//gi|13355067|gb|BG445499.1|BG445499			nr -
Unigene4592_All	1762	0.86	1.38	1.42	50.44	31.45	20.68	10.97	1.85	2.10	6.81E-01	9.55E-02		7.22E-01	8.55E-02		-6.82E-01	5.51E-41		-1.29E+00	2.99E-104	Down	-2.57E+00	6.27E-66	Down	-2.38E+00	2.04E-62	Down	Unigene4592_All//gi|224083500|ref|XP_002307053.1|//0.00E+00//amino acid permease [Populus trichocarpa] >gi|222856502|gb|EEE94049.1| amino acid permease [Populus trichocarpa]	Unigene4592_All//0.00E+00//AT5G09220| AAP2 (AMINO ACID PERMEASE 2); amino acid transmembrane transporter	Unigene4592_All//0.00E+00//TC138457			nr -
Unigene45921_All	1857	195.76	127.83	166.69	53.27	60.27	50.66	16.69	10.33	6.74	-6.15E-01	4.75E-113		-2.32E-01	3.06E-18		1.78E-01	1.42E-04		-7.26E-02	2.39E-01		-6.92E-01	2.88E-15		-1.31E+00	8.15E-44	Down	Unigene45921_All//gi|297816078|ref|XP_002875922.1|//0.00E+00//glutamate-1-semialdehyde 2,1-aminomutase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297321760|gb|EFH52181.1| glutamate-1-semialdehyde 2,1-aminomutase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene45921_All//0.00E+00//AT3G48730| GSA2 (glutamate-1-semialdehyde 2,1-aminomutase 2); catalytic/ glutamate-1-semialdehyde 2,1-aminomutase/ pyridoxal phosphate binding / transaminase	Unigene45921_All//0.00E+00//TC135121		ko00860|Porphyrin and chlorophyll metabolism	GO:0005576//GO:0006779//GO:0009314//GO:0009526//GO:0009532//GO:0016769//GO:0016869//GO:0048037	nr -
Unigene45923_All	765	1.85	2.85	2.99	1.95	2.03	2.89	3.10	2.08	0.73	6.25E-01	1.50E-01		6.97E-01	1.17E-01		5.23E-02	9.50E-01		5.66E-01	2.14E-01		-5.76E-01	1.27E-01		-2.09E+00	3.31E-07	Down			Unigene45923_All//0.00E+00//ES799164				
Unigene45924_All	948	24.28	33.30	43.81	10.14	12.02	12.96	7.94	5.51	3.61	4.56E-01	1.96E-06		8.51E-01	1.59E-22		2.46E-01	1.73E-01		3.54E-01	3.35E-02		-5.27E-01	5.60E-03		-1.14E+00	3.26E-09	Down	Unigene45924_All//gi|226498094|ref|NP_001148441.1|//8.00E-65//cyclase/dehydrase [Zea mays] >gi|195619296|gb|ACG31478.1| cyclase/dehydrase [Zea mays]	Unigene45924_All//9.00E-68//AT1G02475| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Streptomyces cyclase/dehydrase (InterPro:IPR005031); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01883.1); Has 350 Blast hits to 350 proteins in 105 species: Archae - 0; Bacteria - 211; Metazoa - 0; Fungi - 0; Plants - 29; Viruses - 0; Other Eukaryotes - 110 (source: NCBI BLink).	Unigene45924_All//0.00E+00//TC135651			GO:0009536	nr +
Unigene45926_All	1278	1.39	2.34	2.46	1.75	3.53	2.26	5.66	6.57	5.49	7.49E-01	3.83E-02		8.21E-01	2.50E-02		1.01E+00	2.39E-04	Up	3.67E-01	3.73E-01		2.17E-01	2.72E-01		-4.42E-02	8.34E-01				Unigene45926_All//0.00E+00//TC172903				
Unigene45927_All	886	0.59	0.23	0.00	0.90	1.32	0.82	4.29	7.69	11.38	-1.37E+00	1.97E-01		-9.21E+00	4.75E-03		5.55E-01	4.19E-01		-1.41E-01	8.60E-01		8.40E-01	2.95E-05		1.41E+00	2.72E-16	Up	Unigene45927_All//gi|18404020|ref|NP_565832.1|//5.00E-56//HVA22J (HVA22-LIKE PROTEIN J) [Arabidopsis thaliana] >gi|57012598|sp|Q8GXE9.2|HA22J_ARATH RecName: Full=HVA22-like protein j; Short=AtHVA22j >gi|20197992|gb|AAD21455.2| expressed protein [Arabidopsis thaliana] >gi|91806321|gb|ABE65888.1| abscisic acid-responsive HVA22 family protein [Arabidopsis thaliana]	Unigene45927_All//2.00E-57//AT2G36020| HVA22J (HVA22-LIKE PROTEIN J)	Unigene45927_All//7.00E-119//ES833630			nr -
Unigene45928_All	1023	2.56	8.52	3.18	16.60	14.17	11.04	39.80	61.57	94.55	1.74E+00	3.47E-15	Up	3.12E-01	3.83E-01		-2.29E-01	1.04E-01		-5.89E-01	6.74E-06		6.29E-01	1.28E-25		1.25E+00	2.42E-124	Up	Unigene45928_All//gi|297827079|ref|XP_002881422.1|//2.00E-52//abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327261|gb|EFH57681.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45928_All//9.00E-54//AT2G36020| HVA22J (HVA22-LIKE PROTEIN J)	Unigene45928_All//3.00E-38//D8456804			GO:0044464	nr +
Unigene4593_All	1301	1.85	1.52	1.19	2.34	4.90	1.39	6.99	1.96	5.54	-2.84E-01	4.99E-01		-6.40E-01	1.37E-01		1.07E+00	2.00E-06	Up	-7.50E-01	3.65E-02		-1.83E+00	7.81E-21	Down	-3.34E-01	4.87E-02		Unigene4593_All//gi|257831433|gb|ACV71017.1|//9.00E-71//UPA17 [Capsicum annuum]	Unigene4593_All//8.00E-28//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene4593_All//0.00E+00//TC169730	GRF			nr -
Unigene45930_All	808	13.21	18.69	13.91	13.62	15.00	14.70	22.76	15.41	10.16	5.01E-01	5.02E-04		7.41E-02	6.95E-01		1.39E-01	4.79E-01		1.10E-01	6.05E-01		-5.62E-01	9.53E-07		-1.16E+00	4.50E-22	Down	Unigene45930_All//gi|192910858|gb|ACF06537.1|//3.00E-34//24 kDa seed maturation protein [Elaeis guineensis]	Unigene45930_All//1.00E-18//AT1G64090| reticulon family protein (RTNLB3)	Unigene45930_All//4.00E-148//TC138538			GO:0031090//GO:0043231	nr -
Unigene45935_All	2129	42.66	69.99	42.77	50.68	39.71	142.43	104.88	193.37	234.30	7.14E-01	1.38E-60		3.60E-03	9.77E-01		-3.52E-01	5.13E-15		1.49E+00	0.00E+00	Up	8.83E-01	3.27E-293		1.16E+00	0.00E+00	Up	Unigene45935_All//gi|224105433|ref|XP_002313809.1|//0.00E+00//polyol transporter [Populus trichocarpa] >gi|222850217|gb|EEE87764.1| polyol transporter [Populus trichocarpa]	Unigene45935_All//0.00E+00//AT3G18830| ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann	Unigene45935_All//0.00E+00//TC138874			GO:0006810//GO:0008152//GO:0016628//GO:0022857//GO:0031224	nr +
Unigene45937_All	3735	1.33	0.57	0.44	3.36	3.61	2.89	12.44	10.13	14.39	-1.22E+00	1.06E-05	Down	-1.59E+00	1.18E-07	Down	1.05E-01	5.86E-01		-2.18E-01	2.22E-01		-2.97E-01	2.11E-05		2.10E-01	1.09E-03		Unigene45937_All//gi|300253180|gb|ADJ96592.1|//0.00E+00//auxin response factor 5 [Solanum lycopersicum]	Unigene45937_All//0.00E+00//AT1G19850| MP (MONOPTEROS); transcription factor	Unigene45937_All//0.00E+00//TC158795	ARF		GO:0000578//GO:0001071//GO:0005515//GO:0006351//GO:0009755//GO:0009791//GO:0009888//GO:0010051//GO:0010468//GO:0043231//GO:0043565//GO:0048513	nr -

Unigene45938_All	2406	19.88	40.39	19.03	29.42	26.13	49.87	45.27	72.60	73.85	1.02E+00	1.19E-72	Up	-6.25E-02	5.10E-01		-1.71E-01	5.48E-03		7.62E-01	1.06E-58		6.81E-01	5.60E-80		7.06E-01	1.47E-88		Unigene45938_All//gi|558545|emb|CAA85321.1|//0.00E+00//protein containing C-terminal RING-finger [Lotus japonicus] >gi|1771195|emb|CAA70734.1| RING-finger protein [Lotus japonicus]	Unigene45938_All//2.00E-118//AT2G37150| zinc finger (C3HC4-type RING finger) family protein	Unigene45938_All//0.00E+00//TC142119		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0046914	nr -
Unigene45944_All	470	44.19	34.61	26.96	86.27	91.58	102.63	40.66	77.81	101.72	-3.53E-01	3.81E-03		-7.13E-01	1.12E-08		8.62E-02	3.85E-01		2.50E-01	1.08E-03		9.36E-01	1.88E-29		1.32E+00	1.32E-67	Up	Unigene45944_All|gi|75312311|sp|Q99PZ2.1|TPP2_ARATH|/6.00E-06//RecName: Full=Probable thylakoidal processing peptidase 2, chloroplastic; AltName: Full=Signal peptidase I-2; Flags: Precursor >gi|89000987|gb|ABD59083.1| At1g06870 [Arabidopsis thaliana]	Unigene45944_All//4.00E-102//AT1G06870| signal peptidase, putative	Unigene45944_All//0.00E+00//gi|78332736|gb|DT553010.1|DT553010		ko03060|Protein export	GO:0019538//GO:0031224//GO:0070011	nr -
Unigene45949_All	1688	1.95	3.99	2.02	6.76	7.30	7.41	5.71	8.42	10.69	1.03E+00	7.84E-06	Up	4.82E-02	8.95E-01		1.12E-01	5.73E-01		1.33E-01	4.84E-01		5.60E-01	2.32E-05		9.05E-01	1.59E-14		Unigene45949_All//gi|18412073|ref|NP_565187.1|//1.00E-128//brassinosteroid signalling positive regulator-related [Arabidopsis thaliana] >gi|61211694|sp|Q9ZV88.1|BEH4_ARATH RecName: Full=BES1/BZR1 homolog protein 4 >gi|3834322|gb|AAC83038.1| EST gb|R30300 comes from this gene [Arabidopsis thaliana] >gi|15215802|gb|AAK91446.1| At1g78700/F9K20_26 [Arabidopsis thaliana] >gi|19699252|gb|AAL90992.1| At1g78700/F9K20_26 [Arabidopsis thaliana]	Unigene45949_All//3.00E-99//AT1G78700| brassinosteroid signalling positive regulator-related	Unigene45949_All//0.00E+00//TC142658	BES1			nr +
Unigene4595_All	529	4.06	1.63	2.62	4.80	2.08	0.77	2.24	0.32	1.13	-1.32E+00	3.56E-03		-6.32E-01	1.70E-01		-1.21E+00	1.31E-03		-2.64E+00	2.26E-08	Down	-2.82E+00	4.41E-05	Down	-9.86E-01	6.53E-02		Unigene4595_All//gi|291622148|emb|CBJ23784.1|//6.00E-26//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene4595_All//5.00E-27//AT1G62910| pentatricopeptide (PPR) repeat-containing protein	Unigene4595_All//0.00E+00//C0111817				nr +
Unigene45951_All	1991	115.65	76.91	104.90	66.05	82.10	67.26	7.07	4.62	3.46	-5.89E-01	1.68E-66		-1.41E-01	6.10E-05		3.14E-01	5.91E-18		2.61E-02	6.58E-01		-6.15E-01	3.83E-06		-1.03E+00	3.38E-14	Down	Unigene45951_All//gi|4102582|gb|AAD01509.1|//1.00E-108//CAO [Arabidopsis thaliana]	Unigene45951_All//9.00E-98//AT2G47450| CAO (CHAOS); chromatin binding	Unigene45951_All//0.00E+00//gi|164334418|gb|ES814023.1|ES814023			GO:0043231	nr -
Unigene45954_All	1010	3.94	4.16	1.90	5.97	7.06	5.01	12.89	2.15	5.60	8.08E-02	7.84E-01		-1.05E+00	1.12E-03		2.42E-01	3.13E-01		-2.53E-01	3.52E-01		-2.58E+00	5.94E-45	Down	-1.20E+00	1.10E-16	Down	Unigene45954_All//gi|9989057|gb|AAG10820.1|AC011808_8|/4.00E-12//Hypothetical protein [Arabidopsis thaliana] >gi|38603812|gb|AAR24651.1| At1g16630 [Arabidopsis thaliana] >gi|11073871|dbj|BAF01309.1| Hypothetical protei [Arabidopsis thaliana]	Unigene45954_All//6.00E-13//AT2G16270| unknown protein	Unigene45954_All//0.00E+00//TC170561				nr +
Unigene45955_All	2608	2.29	2.41	0.86	7.09	8.04	7.55	9.74	2.16	4.02	7.50E-02	7.57E-01		-1.42E+00	9.81E-08	Down	1.82E-01	1.65E-01		9.15E-02	5.63E-01		-2.17E+00	7.30E-71	Down	-1.28E+00	8.32E-35	Down	Unigene45955_All//gi|9989057|gb|AAG10820.1|AC011808_8|/3.00E-53//Hypothetical protein [Arabidopsis thaliana] >gi|38603812|gb|AAR24651.1| At1g16630 [Arabidopsis thaliana] >gi|11073871|dbj|BAF01309.1| Hypothetical protei [Arabidopsis thaliana]	Unigene45955_All//2.00E-52//AT2G16270| unknown protein	Unigene45955_All//0.00E+00//TC179246				nr +
Unigene45958_All	1412	17.90	19.74	13.16	25.01	27.53	19.96	31.32	18.91	13.85	1.41E-01	2.16E-01		-4.43E-01	7.58E-05		1.39E-01	1.44E-01		-3.26E-01	2.55E-04		-7.28E-01	2.49E-23		-1.18E+00	1.04E-52	Down	Unigene45958_All//gi|27728731|gb|AA018639.1|//1.00E-116//galactose dehydrogenase [Actinidia deliciosa]	Unigene45958_All//5.00E-108//AT4G33670| L-galactose dehydrogenase (L-GalDH)	Unigene45958_All//0.00E+00//gi|164334293|gb|ES793076.1|ES793076		ko00053|Ascorbate and aldarate metabolism		nr +
Unigene45961_All	3427	4.43	2.26	3.60	13.10	11.88	6.47	5.72	3.40	3.01	-9.69E-01	4.77E-11		-2.97E-01	5.59E-02		-1.41E-01	9.66E-02		-1.02E+00	2.08E-36	Down	-7.51E-01	2.30E-11		-9.27E-01	1.93E-16		Unigene45961_All//gi|49523817|emb|CAF18249.1|//0.00E+00//SEU3A protein [Antirrhinum majus]	Unigene45961_All//1.00E-123//AT1G43850| SEU (seuss); DNA binding / protein binding / protein heterodimerization/ transcription cofactor	Unigene45961_All//0.00E+00//TC153685		ko03022|Basal transcription factors	GO:0003676//GO:0046983//GO:0048438	nr +
Unigene45962_All	2016	8.41	4.83	8.03	31.95	33.99	53.07	6.59	3.01	4.05	-8.01E-01	4.21E-09		-6.65E-02	6.59E-01		8.94E-02	2.23E-01		7.32E-01	5.79E-49		-1.13E+00	5.17E-15	Down	-7.01E-01	2.10E-07		Unigene45962_All//gi|15242959|ref|NP_197666.1|//0.00E+00//ATCSLA02; mannan synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75171864|sp|Q9FNI7.1|CSLA2_ARATH RecName: Full=Glucomannan 4-beta-mannosyltransferase 2; AltName: Full=Glucomannan synthase; AltName: Full=Mannan synthase 2; AltName: Full=Cellulose synthase-like protein A2; Short=AtCslA2 >gi|10178248|dbj|BAB11680.1| glucosyltransferase-like protein [Arabidopsis thaliana] >gi|16648764|gb|AAL25573.1| AT5g22740/MDJ22_16 [Arabidopsis thaliana] >gi|16648965|gb|AAL24334.1| glucosyltransferase-like protein [Arabidopsis thaliana] >gi|20259890|gb|AAM13292.1| glucosyltransferase-like protein [Arabidopsis thaliana]	Unigene45962_All//0.00E+00//AT5G22740| ATCSLA02; mannan synthase/ transferase, transferring glycosyl groups	Unigene45962_All//0.00E+00//TC155802			GO:0016759	nr -
Unigene45963_All	2717	1.02	4.87	1.53	1.91	1.27	1.05	1.73	1.78	9.68	2.25E+00	1.13E-31	Up	5.83E-01	6.31E-02		-5.89E-01	1.89E-02		-8.65E-01	8.31E-04		4.69E-02	8.68E-01		2.49E+00	1.18E-87	Up	Unigene45963_All|gi|212717149|gb|ACJ37416.1|//1.00E-143//stress-induced receptor-like kinase [Glycine max]	Unigene45963_All//1.00E-85//AT5G38280| PRSK; kinase/ transmembrane receptor protein serine/threonine kinase	Unigene45963_All//0.00E+00//BG440069		ko04626|Plant-pathogen interaction		nr -
Unigene45967_All	3258	0.50	3.25	1.83	1.16	1.86	3.11	2.52	5.21	7.61	2.71E+00	2.40E-31	Up	1.88E+00	2.65E-11	Up	6.79E-01	3.34E-03		1.42E+00	5.27E-14	Up	1.05E+00	7.63E-17	Up	1.60E+00	1.33E-46	Up	Unigene45967_All//gi|30680213|ref|NP_849971.1|//1.00E-74//PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein [Arabidopsis thaliana] >gi|13877655|gb|AAK43905.1|AF370586_1 Unknown protein [Arabidopsis thaliana]	Unigene45967_All//5.00E-76//AT2G18090| PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein	Unigene45967_All//0.00E+00//CO103466				nr +
Unigene45968_All	913	2.18	2.61	1.40	4.15	5.24	4.85	8.85	12.59	25.00	2.60E-01	5.48E-01		-6.38E-01	1.87E-01		3.38E-01	2.56E-01		2.25E-01	4.93E-01		5.09E-01	6.47E-04		1.50E+00	2.38E-39	Up	Unigene45968_All//gi|145357850|ref|NP_196588.3|//4.00E-64//AtRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding [Arabidopsis thaliana] >gi|8953407|emb|CAB96682.1| GTP-binding protein [Arabidopsis thaliana]	Unigene45968_All//2.00E-65//AT5G10260| AtRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding	Unigene45968_All//0.00E+00//TC169246				nr -
Unigene45969_All	856	11.92	11.13	7.90	14.90	16.73	15.04	6.22	6.93	15.59	-9.90E-02	6.10E-01		-5.93E-01	1.41E-03		1.68E-01	3.21E-01		1.34E-02	9.49E-01		1.56E-01	5.42E-01		1.32E+00	1.52E-19	Up	Unigene45969_All//gi|145357850|ref|NP_196588.3|//1.00E-100//AtRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding [Arabidopsis thaliana] >gi|8953407|emb|CAB96682.1| GTP-binding protein [Arabidopsis thaliana]	Unigene45969_All//5.00E-101//AT5G10260| AtRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding	Unigene45969_All//0.00E+00//TC165054				nr -
Unigene4597_All	1286	8.30	17.30	8.53	11.00	14.30	10.01	10.03	8.26	9.14	1.06E+00	3.76E-18	Up	3.95E-02	8.36E-01		3.78E-01	2.36E-03		-1.36E-01	4.47E-01		-2.81E-01	5.59E-02		-1.34E-01	3.84E-01		Unigene4597_All//gi|22330531|ref|NP_177122.2|//1.00E-123//SBH1 (SPHINGOID BASE HYDROXYLASE 1); catalytic/ sphingosine hydroxylase [Arabidopsis thaliana] >gi|17979635|gb|AAL50102.1| At1g69640/F24J1.22 [Arabidopsis thaliana] >gi|23505995|gb|AAN28857.1| At1g69640/F24J1.22 [Arabidopsis thaliana]	Unigene4597_All//3.00E-108//AT1G69640| SBH1 (SPHINGOID BASE HYDROXYLASE 1); catalytic/ sphingosine hydroxylase	Unigene4597_All//0.00E+00//gi|109878682|gb|DW507652.1|DW507652		ko00100|Steroid biosynthesis		nr -
Unigene45974_All	1114	2.11	0.91	0.86	4.47	5.35	4.74	2.69	0.34	1.75	-1.22E+00	4.07E-03		-1.30E+00	3.68E-03		2.58E-01	3.34E-01		8.51E-02	7.67E-01		-3.00E+00	1.35E-12	Down	-6.21E-01	4.50E-02		Unigene45974_All|gi|297818318|ref|XP_002877042.1|//5.00E-71//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322880|gb|EFH53301.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45974_All//3.00E-66//AT3G27330| zinc finger (C3HC4-type RING finger) family protein	Unigene45974_All//2.00E-101//gi|48740302|gb|CO070821.1|CO070821				nr +
Unigene45975_All	1276	2.67	2.30	1.63	4.41	5.91	6.02	5.83	0.59	2.84	-2.11E-01	5.56E-01		-7.12E-01	4.34E-02		4.22E-01	4.74E-02		4.48E-01	3.75E-02		-3.31E+00	3.21E-33	Down	-1.04E+00	5.33E-08	Down	Unigene45975_All|gi|297818318|ref|XP_002877042.1|//4.00E-79//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322880|gb|EFH53301.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45975_All//1.00E-69//AT3G27330| zinc finger (C3HC4-type RING finger) family protein	Unigene45975_All//0.00E+00//TC169631				nr +
Unigene45984_All	4547	0.56	1.16	0.82	5.32	5.68	4.87	3.63	1.91	4.85	1.04E+00	8.73E-05	Up	5.40E-01	1.08E-01		9.33E-02	4.84E-01		-1.30E-01	3.24E-01		-9.24E-01	1.88E-13		4.21E-01	3.57E-05		Unigene45984_All|gi|15222153|ref|NP_177653.1|//1.00E-119//SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|79321292|ref|NP_001031283.1| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana]	Unigene45984_All//9.00E-121//AT1G75170| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene45984_All//0.00E+00//ES800991				nr +
Unigene45985_All	3187	199.55	234.70	287.17	41.87	77.09	57.83	6.08	7.38	22.96	2.34E-01	7.20E-39		5.25E-01	7.63E-208		8.81E-01	2.34E-170		4.66E-01	1.25E-37		2.81E-01	6.39E-03		1.92E+00	9.45E-176	Up	Unigene45985_All|gi|87241270|gb|ABD33128.1|//1.00E-92//Zinc finger, RING-type; Thioredoxin-related [Medicago truncatula]	Unigene45985_All//1.00E-75//AT5G39550| zinc finger (C3HC4-type RING finger) family protein	Unigene45985_All//0.00E+00//TC165642				nr +
Unigene45991_All	424	0.99	5.86	1.26	3.41	4.87	5.11	17.75	36.47	30.16	2.57E+00	1.98E-07	Up	3.47E-01	7.05E-01		5.16E-01	2.83E-01		5.86E-01	2.02E-01		1.04E+00	3.37E-15	Up	7.65E-01	3.78E-08		Unigene45991_All|gi|224053533|ref|XP_002297860.1|//3.00E-34//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222845118|gb|EEE82665.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene45991_All//4.00E-31//AT5G13180| ANAC083 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 83); transcription factor	Unigene45991_All//1.00E-152//ES806311	NAC			nr +

Unigene45992_All	1748	5.48	12.26	3.26	42.23	38.65	26.43	132.16	175.65	147.62	1.16E+00	3.20E-20	Up	-7.49E-01	1.01E-04		-1.28E-01	4.40E-02		-6.76E-01	7.93E-30		4.10E-01	2.86E-56		1.60E-01	8.69E-09		Unigene45992_All//gi|224075517|ref|XP_002304662.1|//1.00E-107//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842094|gb|EEE79641.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene45992_All//6.00E-80//AT5G13180| ANAC083 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 83); transcription factor	Unigene45992_All//0.00E+00//TC136326	NAC			nr -
Unigene45997_All	1389	6.63	2.77	8.97	19.55	23.30	11.45	8.77	10.38	5.28	-1.26E+00	2.84E-10	Down	4.36E-01	9.35E-03		2.54E-01	6.63E-03		-7.72E-01	3.77E-14		2.44E-01	8.16E-02		-7.32E-01	2.45E-07		Unigene45997_All//gi|297838497|ref|XP_002887130.1|//1.00E-167//lipoxygenase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332971|gb|EFH63389.1| lipoxygenase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene45997_All//2.00E-162//AT1G67560| lipoxygenase family protein	Unigene45997_All//0.00E+00//TC167089		ko00592|alpha-Linolenic acid metabolism/ko00591|Linoleic acid metabolism		nr +
Unigene45998_All	3157	10.87	4.37	10.54	27.71	26.43	14.62	10.83	11.78	5.87	-1.32E+00	7.49E-39	Down	-4.45E-02	6.76E-01		-6.82E-02	3.10E-01		-9.22E-01	6.26E-60		1.21E-01	1.73E-01		-8.85E-01	6.09E-26		Unigene45998_All//gi|10505183|gb|AAG18376.1|AF283894_1|/0.00E+00//lipoxygenase [Zantedeschia aethiopica]	Unigene45998_All//0.00E+00//AT1G67560| lipoxygenase family protein	Unigene45998_All//0.00E+00//TC167089		ko00592|alpha-Linolenic acid metabolism/ko00591|Linoleic acid metabolism		nr +
Unigene4600_All	957	9.08	6.14	10.85	13.12	17.60	16.90	3.23	2.31	1.29	-5.63E-01	4.05E-03		2.58E-01	1.89E-01		4.24E-01	1.06E-03		3.65E-01	9.16E-03		-4.79E-01	1.40E-01		-1.32E+00	3.29E-05	Down	Unigene4600_All//gi|115453499|ref|NP_001050350.1|//4.00E-28//Os03g0411600 [Oryza sativa Japonica Group] >gi|28209490|gb|AAO37508.1| expressed protein [Oryza sativa Japonica Group] >gi|108708775|gb|ABF96570.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548821|dbj|BAF12264.1| Os03g0411600 [Oryza sativa Japonica Group]	Unigene4600_All//5.00E-19//AT1G19380| unknown protein	Unigene4600_All//0.00E+00//gi|164241591|gb|ES795909.1|ES795909				nr -
Unigene46003_All	2463	13.77	23.93	10.05	14.70	17.98	17.09	24.87	33.96	60.25	7.98E-01	2.23E-29		-4.53E-01	1.79E-06		2.90E-01	1.31E-04		2.17E-01	1.05E-02		4.49E-01	1.13E-18		1.28E+00	4.68E-197	Up	Unigene46003_All//gi|30697711|ref|NP_177025.2|//1.00E-136//agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein [Arabidopsis thaliana] >gi|30725466|gb|AAP37755.1| At1g68580 [Arabidopsis thaliana]	Unigene46003_All//3.00E-127//AT1G68580| agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein	Unigene46003_All//0.00E+00//TC174998				nr -
Unigene46007_All	1309	19.95	8.67	13.79	18.19	18.91	13.28	22.03	7.25	11.08	-1.20E+00	7.23E-26	Down	-5.32E-01	1.17E-06		5.63E-02	6.93E-01		-4.54E-01	3.17E-05		-1.60E+00	1.77E-53	Down	-9.92E-01	1.84E-26		Unigene46007_All//gi|224081597|ref|XP_002306462.1|//1.00E-165//CPK related kinase 5 [Populus trichocarpa] >gi|222855911|gb|EEE93458.1| CPK related kinase 5 [Populus trichocarpa]	Unigene46007_All//6.00E-159//AT3G50530| CRK (CDPK-related kinase); ATP binding / calcium ion binding / calcium-dependent protein serine/threonine phosphatase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene46007_All//0.00E+00//gi|109840091|gb|DW238652.1|DW238652		ko04626|Plant-pathogen interaction		nr +
Unigene46008_All	2197	20.05	7.29	7.88	19.61	17.76	13.53	9.53	2.68	6.96	-1.46E+00	4.64E-58	Down	-1.35E+00	1.09E-49	Down	-1.43E-01	9.90E-02		-5.36E-01	7.66E-12		-1.83E+00	8.57E-47	Down	-4.52E-01	1.49E-05		Unigene46008_All//gi|1706130|sp|P53681.1|CRK_DAUCA//0.00E+00//RecName: Full=CDPK-related protein kinase; AltName: Full=PK421 >gi|1103386|emb|CAA58750.1| CDPK-related protein kinase [Daucus carota]	Unigene46008_All//0.00E+00//AT3G50530| CRK (CDPK-related kinase); ATP binding / calcium ion binding / calcium-dependent protein serine/threonine phosphatase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene46008_All//0.00E+00//TC155697				nr -
Unigene4601_All	1405	1.23	0.07	1.63	1.88	1.15	9.42	81.28	24.48	33.63	-4.09E+00	7.75E-08	Down	4.07E-01	3.76E-01		-7.06E-01	5.83E-02		2.33E+00	4.33E-35	Up	-1.73E+00	6.15E-234	Down	-1.27E+00	1.66E-152	Down	Unigene4601_All//gi|7770345|gb|AAF69715.1|AC016041_20//6.00E-50//F27J15.18 [Arabidopsis thaliana] >gi|38602922|gb|AAR24706.1| At1g49030 [Arabidopsis thaliana] >gi|44681424|gb|AAS47652.1| At1g49030 [Arabidopsis thaliana]	Unigene4601_All//2.00E-46//AT1G49030| unknown protein	Unigene4601_All//0.00E+00//TC152452		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism/ko00565|Ether lipid metabolism		nr +
Unigene46013_All	995	1.31	2.44	3.21	2.35	2.56	2.13	2.59	2.65	3.72	8.95E-01	2.85E-02		1.29E+00	5.42E-04	Up	1.22E-01	8.12E-01		-1.41E-01	7.41E-01		2.99E-02	9.59E-01		5.23E-01	5.98E-02		Unigene46013_All//gi|297795189|ref|XP_002865479.1|//2.00E-46//inositol-pentakisphosphate 2-kinase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297311314|gb|EFH41738.1| inositol-pentakisphosphate 2-kinase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene46013_All//3.00E-45//AT5G42810| ATIPK1 (Inositol-pentakisphosphate 2-kinase 1); inositol pentakisphosphate 2-kinase/ inositol tetrakisphosphate 2-kinase	Unigene46013_All//0.00E+00//TC138769				nr -
Unigene46017_All	3734	0.39	0.71	0.17	0.75	0.65	0.52	0.46	0.31	0.15	8.47E-01	2.96E-02		-1.20E+00	4.21E-02		-1.90E-01	6.26E-01		-5.23E-01	1.84E-01		-5.67E-01	2.16E-01		-1.64E+00	3.35E-04	Down	Unigene46017_All//gi|297809743|ref|XP_002872755.1|//0.00E+00//UV-damaged DNA-binding protein 1A [Arabidopsis lyrata subsp. lyrata] >gi|297318592|gb|EFH49014.1| UV-damaged DNA-binding protein 1A [Arabidopsis lyrata subsp. lyrata]	Unigene46017_All//0.00E+00//AT4G05420| DDB1A (DAMAGED DNA BINDING PROTEIN 1A); DNA binding / protein binding	Unigene46017_All//0.00E+00//TC152860		ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair		nr -
Unigene46018_All	2448	4.38	5.22	3.72	2.20	2.45	4.50	18.27	41.20	47.28	2.52E-01	1.30E-01		-2.36E-01	2.31E-01		1.55E-01	5.85E-01		1.03E+00	1.67E-09	Up	1.17E+00	4.87E-115	Up	1.37E+00	1.00E-171	Up	Unigene46018_All//gi|145340395|ref|NP_193399.3|//1.00E-145//MRH1 (morphogenesis of root hair 1); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|263505146|sp|C0LGQ4.1|MRH1_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase MRH1; AltName: Full=Protein MORPHOGENESIS OF ROOT HAIR 1; Flags: Precursor >gi|224589612|gb|ACN59339.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene46018_All//1.00E-110//AT3G56050| protein kinase family protein	Unigene46018_All//0.00E+00//TC143149		ko04626|Plant-pathogen interaction		nr -
Unigene46019_All	769	35.86	17.53	16.34	71.84	66.81	65.19	85.55	30.44	31.96	-1.03E+00	1.61E-21	Down	-1.13E+00	6.09E-24	Down	-1.05E-01	1.90E-01		-1.40E-01	7.09E-02		-1.49E+00	7.14E-109	Down	-1.42E+00	3.26E-104	Down	Unigene46019_All//gi|247421866|gb|ACS96446.1|//5.00E-97//60S ribosomal protein L18a [Jatropha curcas]	Unigene46019_All//4.00E-94//AT2G34480| 60S ribosomal protein L18A (RPL18aB)	Unigene46019_All//0.00E+00//TC146130		ko03010|Ribosome		nr +
Unigene4602_All	824	2.92	3.57	2.52	4.35	4.35	2.52	3.75	0.41	1.31	2.88E-01	4.38E-01		-2.13E-01	6.28E-01		-2.20E-03	9.86E-01		-7.88E-01	1.47E-02		-3.21E+00	9.47E-14	Down	-1.52E+00	3.15E-06	Down	Unigene4602_All//gi|255551819|ref|XP_002516955.1|//3.00E-56//conserved hypothetical protein [Ricinus communis] >gi|223544043|gb|EEF45569.1| conserved hypothetical protein [Ricinus communis]	Unigene4602_All//1.00E-31//AT5G49170| unknown protein	Unigene4602_All//0.00E+00//TC136278				nr -
Unigene46020_All	1070	13.84	6.68	8.06	13.36	9.78	12.58	23.63	14.49	12.70	-1.05E+00	3.03E-12	Down	-7.79E-01	2.43E-07		-4.50E-01	1.26E-03		-8.71E-02	6.21E-01		-7.05E-01	5.15E-13		-8.96E-01	8.09E-20		Unigene46020_All//gi|225462960|ref|XP_002268750.1|//5.00E-97//PREDICTED: similar to RPL18AA (60S RIBOSOMAL PROTEIN L18A-1); structural constituent of ribosome [Vitis vinifera]	Unigene46020_All//2.00E-93//AT2G34480| 60S ribosomal protein L18A (RPL18aB)	Unigene46020_All//0.00E+00//TC160468		ko03010|Ribosome		nr +
Unigene46021_All	2660	3.01	2.50	3.08	12.49	7.48	16.15	10.52	4.49	5.24	-2.70E-01	2.14E-01		3.48E-02	8.80E-01		-7.39E-01	6.73E-18		3.70E-01	2.87E-06		-1.23E+00	6.58E-35	Down	-1.01E+00	2.80E-26	Down	Unigene46021_All//gi|297803912|ref|XP_002869840.1|//0.00E+00//kinase [Arabidopsis lyrata subsp. lyrata] >gi|297315676|gb|EFH46099.1| kinase [Arabidopsis lyrata subsp. lyrata]	Unigene46021_All//0.00E+00//AT4G22130| SRF8 (STRUBBELIG-RECEPTOR FAMILY 8); ATP binding / kinase/ protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene46021_All//0.00E+00//TC160756		ko04626|Plant-pathogen interaction		nr +
Unigene46022_All	1339	33.45	29.59	27.96	21.43	20.73	25.47	19.23	12.95	9.46	-1.77E-01	3.50E-02		-2.59E-01	2.07E-03		-4.80E-02	7.18E-01		2.49E-01	8.23E-03		-5.70E-01	2.53E-09		-1.02E+00	6.11E-25	Down	Unigene46022_All//gi|115444621|ref|NP_001046090.1|//1.00E-58//Os02g0180200 [Oryza sativa Japonica Group] >gi|113535621|dbj|BAF08004.1| Os02g0180200 [Oryza sativa Japonica Group]	Unigene46022_All//1.00E-51//AT2G24020| unknown protein	Unigene46022_All//0.00E+00//TC138488				nr -
Unigene46023_All	290	3.07	2.27	2.20	8.76	9.14	4.67	1.75	0.00	2.20	-4.33E-01	5.56E-01		-4.77E-01	5.33E-01		6.17E-02	8.97E-01		-9.07E-01	2.23E-02		-1.08E+01	8.89E-04	Down	3.29E-01	6.60E-01		Unigene46023_All//gi|24418033|gb|AAN60483.1|//9.00E-18//Hypothetical protein [Oryza sativa Japonica Group]	Unigene46023_All//1.00E-26//AT4G11450| unknown protein	Unigene46023_All//6.00E-49//CO079332				nr -
Unigene46025_All	2327	1.06	0.50	0.73	3.87	2.29	2.45	2.36	0.61	1.30	-1.08E+00	8.37E-03		-5.29E-01	2.23E-01		-7.56E-01	1.92E-05		-6.64E-01	4.06E-04		-1.95E+00	6.02E-14	Down	-8.60E-01	9.91E-05		Unigene46025_All//gi|115450161|ref|NP_001048681.1|//9.00E-83//Os03g0105800 [Oryza sativa Japonica Group] >gi|113547152|dbj|BAF10595.1| Os03g0105800 [Oryza sativa Japonica Group]	Unigene46025_All//8.00E-111//AT4G11450| unknown protein	Unigene46025_All//0.00E+00//TC178197				nr -
Unigene46029_All	2454	71.81	21.51	55.98	6.70	6.20	5.54	0.07	1.14	0.10	-1.74E+00	5.25E-297	Down	-3.59E-01	3.25E-20		-1.11E-01	5.11E-01		-2.74E-01	5.71E-02		4.05E+00	5.95E-15	Up	4.99E-01	7.07E-01		Unigene46029_All//gi|87240554|gb|AB032412.1|//0.00E+00//Cellulose synthase [Medicago truncatula]	Unigene46029_All//0.00E+00//AT2G32540| ATCSLB04; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	Unigene46029_All//0.00E+00//DW508053				nr -
Unigene4603_All	713	3.67	2.56	1.57	8.59	9.42	10.77	2.85	1.58	0.89	-5.20E-01	1.87E-01		-1.23E+00	3.28E-03		1.32E-01	6.13E-01		3.26E-01	1.47E-01		-8.47E-01	3.68E-02		-1.67E+00	6.85E-05	Down	Unigene4603_All//gi|20378863|gb|AAM21012.1|AF469074_1|/3.00E-10//NBS resistance protein-like protein [Gossypium hirsutum]		Unigene4603_All//1.00E-18//NP508212				nr +
Unigene46030_All	2411	14.54	5.42	6.74	5.66	6.03	3.92	3.89	3.21	3.07	-1.42E+00	1.35E-44	Down	-1.11E+00	2.60E-29	Down	9.04E-02	6.05E-01		-5.32E-01	3.54E-04		-2.80E-01	1.17E-01		-3.41E-01	3.99E-02		Unigene46030_All//gi|295322838|gb|ADG01868.1|//0.00E+00//plastid RNA-binding protein [Nicotiana benthamiana]	Unigene46030_All//4.00E-174//AT3G48500| RNA binding	Unigene46030_All//0.00E+00//TC142848				nr +
Unigene46038_All	3906	9.54	13.47	16.09	23.56	31.32	23.61	15.48	17.30	5.85	4.98E-01	8.09E-12		7.54E-01	1.53E-27		4.11E-01	3.59E-22		3.40E-03	9.54E-01		1.61E-01	7.07E-03		-1.40E+00	4.68E-94	Down	Unigene46038_All//gi|90823307|gb|ABE01124.1|//0.00E+00//RNA-dependent RNA polymerase [Gossypium hirsutum]	Unigene46038_All//0.00E+00//AT1G14790| RDR1 (RNA-DEPENDENT RNA POLYMERASE 1); RNA-directed RNA polymerase/ nucleic acid binding	Unigene46038_All//0.00E+00//TC155442				nr +
Unigene46039_All	2158	6.55	3.87	5.75	13.18	10.74	8.60	11.52	3.56	4.02	-7.57E-01	4.49E-07		-1.87E-01	2.67E-01		-2.96E-01	2.44E-03		-6.16E-01	3.91E-10		-1.69E+00	7.23E-50	Down	-1.52E+00	5.71E-44	Down	Unigene46039_All//gi|30696733|ref|NP_568840.3|//1.00E-179//calmodulin-binding protein [Arabidopsis thaliana]	Unigene46039_All//9.00E-142//AT5G56360| calmodulin-binding protein	Unigene46039_All//0.00E+00//TC147702		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene4604_All	1444	2.17	1.44	0.92	4.14	3.93	3.63	0.91	0.43	0.22	-5.96E-01	8.99E-02		-1.24E+00	9.77E-04	Down	-7.32E-02	8.19E-01		-1.90E-01	4.94E-01		-1.06E+00	4.42E-02		-2.04E+00	3.01E-04	Down	Unigene4604_All//gi|20378863|gb|AAM21012.1|AF469074_1|/8.00E-10//NBS resistance protein-like protein [Gossypium hirsutum]		Unigene4604_All//2.00E-18//NP508212				nr +
Unigene46043_All	2282	63.51	52.85	61.79	23.27	22.24	18.92	1.74	0.75	0.56	-2.65E-01	3.61E-10		-3.96E-02	4.51E-01		-6.51E-02	4.71E-01		-2.99E-01	2.60E-05		-1.21E+00	1.49E-05	Down	-1.64E+00	1.41E-08	Down	Unigene46043_All//gi|269819302|gb|ACZ44841.1|//1.00E-160//glycosyltransferase [Malus x domestica]	Unigene46043_All//4.00E-107//AT3G16520| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene46043_All//0.00E+00//TC163425				nr +
Unigene46045_All	1808	42.66	15.75	23.80	58.27	60.03	63.15	23.97	7.17	10.00	-1.44E+00	8.09E-99	Down	-8.42E-01	1.53E-40		4.29E-02	5.15E-01		1.16E-01	2.49E-02		-1.74E+00	6.41E-90	Down	-1.26E+00	1.67E-57	Down	Unigene46045_All//gi|124360348|gb|ABN08361.1|//1.00E-118//Hypothetical plant protein [Medicago truncatula]	Unigene46045_All//2.00E-163//AT3G21190| unknown protein	Unigene46045_All//0.00E+00//TC146170				nr +

Unigene46046_All	987	7.85	2.98	5.72	8.53	11.41	7.69	5.05	4.95	5.81	-1.40E+00	3.64E-10	Down	-4.56E-01	3.97E-02		4.20E-01	1.14E-02		-1.50E-01	5.26E-01		-2.89E-02	9.29E-01		2.02E-01	3.92E-01		Unigene46046_All//gi|75150653|sp|Q8GUM4.1|Y3739_ARATH//9.00E-64//RecName: Full=Uncharacterized membrane protein At3g27390 >gi|27311557|gb|AAO00744.1| Unknown protein [Arabidopsis thaliana]	Unigene46046_All//6.00E-47//AT5G40640| unknown protein	Unigene46046_All//0.00E+00//gi|48795441|gb|CO096755.1|CO096755				nr -
Unigene46049_All	1653	42.19	88.25	55.25	105.35	154.09	146.66	99.98	211.66	137.11	1.06E+00	5.11E-116	Up	3.89E-01	2.01E-12		5.49E-01	2.04E-77		4.77E-01	1.47E-51		1.08E+00	0.00E+00	Up	4.56E-01	1.04E-51		Unigene46049_All//gi|15224501|ref|NP_181375.1|//1.00E-157//VHS domain-containing protein / GAT domain-containing protein [Arabidopsis thaliana] >gi|209529799|gb|ACI49794.1| At2g38410 [Arabidopsis thaliana]	Unigene46049_All//6.00E-127//AT2G38410| VHS domain-containing protein / GAT domain-containing protein	Unigene46049_All//0.00E+00//TC160462		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene46054_All	2070	11.96	25.95	11.42	20.48	17.57	18.59	30.35	68.10	39.43	1.12E+00	1.28E-46	Up	-6.59E-02	6.43E-01		-2.21E-01	5.82E-03		-1.40E-01	1.27E-01		1.17E+00	4.65E-159	Up	3.78E-01	7.74E-14		Unigene46054_All//gi|87240487|gb|AB032345.1|//1.00E-110//Octicosapeptide/Phox/BemIp [Medicago truncatula]	Unigene46054_All//9.00E-86//AT4G05150| octicosapeptide/Phox/BemIp (PB1) domain-containing protein	Unigene46054_All//0.00E+00//TC166731				nr +
Unigene46055_All	2248	2.02	1.37	0.95	7.02	5.42	4.68	6.28	3.63	4.52	-5.59E-01	4.86E-02		-1.10E+00	2.56E-04	Down	-3.73E-01	5.51E-03		-5.86E-01	1.77E-05		-7.93E-01	3.60E-09		-4.75E-01	2.45E-04		Unigene46055_All//gi|297829060|ref|XP_002882412.1|//0.00E+00//acyl-CoA binding protein 4, acyl-CoA-binding domain 4 [Arabidopsis lyrata subsp. lyrata] >gi|297328252|gb|EFH58671.1| acyl-CoA binding protein 4, acyl-CoA-binding domain 4 [Arabidopsis lyrata subsp. lyrata]	Unigene46055_All//0.00E+00//AT3G05420| ACBP4 (ACYL-COA BINDING PROTEIN 4); acyl-CoA binding	Unigene46055_All//0.00E+00//ES841668		ko04712|Circadian rhythm - plant		nr -
Unigene46056_All	595	25.06	6.13	15.39	59.61	53.19	31.12	15.78	12.64	10.58	-2.03E+00	1.50E-31	Down	-7.03E-01	2.73E-06		-1.65E-01	8.41E-02		-9.38E-01	2.76E-25		-3.19E-01	6.79E-02		-5.76E-01	3.81E-04		Unigene46056_All//gi|240255733|ref|NP_192232.4|//3.00E-55//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene46056_All//2.00E-56//AT4G03230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene46056_All//0.00E+00//gi|164286549|gb|ES806016.1|ES806016				nr +
Unigene46058_All	3242	11.86	4.05	9.26	19.70	20.55	9.39	9.32	10.39	9.46	-1.55E+00	1.85E-55	Down	-3.57E-01	6.54E-05		6.13E-02	4.51E-01		-1.07E+00	6.16E-56	Down	1.56E-01	8.38E-02		2.11E-02	8.39E-01		Unigene46058_All//gi|240255733|ref|NP_192232.4|//0.00E+00//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene46058_All//6.00E-00//AT4G03230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene46058_All//0.00E+00//TC151245		ko04626|Plant-pathogen interaction		nr +
Unigene46059_All	439	0.72	1.85	3.03	9.19	4.47	3.91	1.83	1.43	2.00	1.37E+00	9.21E-02		2.08E+00	2.18E-03		-1.04E+00	2.43E-04	Down	-1.23E+00	5.12E-05	Down	-3.58E-01	6.48E-01		1.26E-01	8.48E-01		Unigene46059_All//gi|24636978|gb|AA063500.1|AF317558.1//2.00E-09//lysine ketoglutarate reductase trans-splicing related 1 [Arabidopsis thaliana]	Unigene46059_All//1.00E-10//AT1G61240| unknown protein	Unigene46059_All//1.00E-60//gi|84163791|gb|DR452439.1|DR452439				nr +
Unigene46060_All	1526	7.03	7.40	5.16	32.68	25.14	24.33	24.30	10.85	18.35	7.51E-02	6.77E-01		-4.45E-01	1.52E-02		-3.78E-01	3.43E-08		-4.26E-01	3.95E-09		-1.16E+00	2.54E-42	Down	-4.05E-01	1.29E-07		Unigene46060_All//gi|109946455|gb|ABG48406.1|//1.00E-162//At1g61240 [Arabidopsis thaliana]	Unigene46060_All//6.00E-158//AT1G61240| unknown protein	Unigene46060_All//0.00E+00//TC171710				nr -
Unigene46063_All	2544	1.36	1.02	0.71	2.10	1.61	0.92	4.40	4.68	4.76	-4.18E-01	2.16E-01		-9.32E-01	7.43E-03		-3.79E-01	1.51E-01		-1.18E+00	4.84E-06	Down	8.83E-02	6.43E-01		1.12E-01	4.94E-01		Unigene46063_All//gi|224059584|ref|XP_002299919.1|//1.00E-107//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222847177|gb|EEE84724.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene46063_All//7.00E-35//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene46063_All//0.00E+00//DR452686		ko04626|Plant-pathogen interaction		nr +
Unigene46067_All	2050	2.19	1.83	1.12	4.71	3.11	4.03	5.84	2.34	5.42	-2.63E-01	3.76E-01		-9.75E-01	1.13E-03		-6.01E-01	4.58E-04		-2.26E-01	2.76E-01		-1.32E+00	4.77E-17	Down	-1.06E-01	5.27E-01		Unigene46067_All//gi|238480861|ref|NP_001154255.1|//1.00E-58//metalloendopeptidase [Arabidopsis thaliana]	Unigene46067_All//8.00E-53//AT4G20310| metalloendopeptidase	Unigene46067_All//0.00E+00//gi|78350139|gb|DT570413.1|DT570413		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene46069_All	605	1.04	3.60	1.85	3.46	1.31	1.87	6.36	6.49	2.37	1.80E+00	1.58E-04	Up	8.33E-01	2.23E-01		-1.40E+00	9.86E-04	Down	-8.90E-01	4.64E-02		3.02E-02	9.38E-01		-1.42E+00	6.23E-07	Down			Unigene46069_All//4.00E-61//gi|164290962|gb|ES826103.1|ES826103				
Unigene46071_All	1816	15.59	8.20	15.31	5.51	7.22	13.18	5.38	19.47	19.92	-9.26E-01	1.52E-18		-2.62E-02	8.25E-01		3.90E-01	1.05E-02		1.26E+00	4.57E-27	Up	1.86E+00	5.44E-80	Up	1.89E+00	1.81E-85	Up	Unigene46071_All//gi|14030731|gb|AAK53040.1|AF375156_1//1.00E-180//AT5g65380/MNA5_11 [Arabidopsis thaliana] >gi|23506079|gb|AAN28899.1| At5g65380/MNA5_11 [Arabidopsis thaliana]	Unigene46071_All//9.00E-162//AT5G65380| ripening-responsive protein, putative	Unigene46071_All//0.00E+00//TC133605				nr -
Unigene46072_All	1870	10.41	5.83	8.26	2.93	3.33	8.43	2.17	7.78	7.90	-8.37E-01	4.44E-11		-3.34E-01	1.19E-02		1.86E-01	5.17E-01		1.52E+00	6.72E-24	Up	1.84E+00	5.57E-33	Up	1.86E+00	8.49E-35	Up	Unigene46072_All//gi|14030731|gb|AAK53040.1|AF375156_1//0.00E+00//AT5g65380/MNA5_11 [Arabidopsis thaliana] >gi|23506079|gb|AAN28899.1| At5g65380/MNA5_11 [Arabidopsis thaliana]	Unigene46072_All//0.00E+00//AT5G65380| ripening-responsive protein, putative	Unigene46072_All//0.00E+00//TC141625				nr +
Unigene46073_All	637	1.31	0.95	0.25	1.72	0.54	0.43	1.39	2.36	5.88	-4.61E-01	5.43E-01		-2.39E+00	1.14E-02		-1.67E+00	9.38E-03		-2.02E+00	4.74E-03		7.61E-01	1.21E-01		2.08E+00	1.01E-10	Up	Unigene46073_All//gi|297818120|ref|XP_002876943.1|//7.00E-27//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322781|gb|EFH53202.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46073_All//2.00E-27//AT3G26000| F-box family protein	Unigene46073_All//2.00E-180//TC150145				nr +
Unigene46074_All	3209	4.16	3.30	3.62	1.97	2.78	2.01	3.54	4.17	16.61	-3.33E-01	3.48E-02		-2.01E-01	2.43E-01		4.95E-01	8.31E-03		2.98E-02	9.29E-01		2.34E-01	1.14E-01		2.23E+00	2.18E-155	Up	Unigene46074_All//gi|297818120|ref|XP_002876943.1|//1.00E-110//F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322781|gb|EFH53202.1| F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46074_All//5.00E-103//AT3G26000| F-box family protein	Unigene46074_All//0.00E+00//TC150145				nr +
Unigene46075_All	710	6.04	1.28	4.88	8.70	6.89	4.13	4.64	3.30	5.11	-2.23E+00	1.07E-10	Down	-3.10E-01	3.41E-01		-3.37E-01	1.65E-01		-1.07E+00	5.35E-06	Down	-4.95E-01	1.13E-01		1.37E-01	6.40E-01		Unigene46075_All//gi|297849978|ref|XP_002892870.1|//5.00E-47//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338712|gb|EFH69129.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46075_All//5.00E-48//AT1G15490| hydrolase, alpha/beta fold family protein	Unigene46075_All//0.00E+00//ES792388				nr -
Unigene46076_All	2841	6.21	2.03	5.02	17.76	10.57	8.87	7.69	5.08	7.22	-1.61E+00	3.47E-27	Down	-3.05E-01	3.13E-02		-7.49E-01	1.36E-27		-1.00E+00	7.37E-40	Down	-6.00E-01	9.66E-09		-9.14E-02	4.43E-01		Unigene46076_All//gi|297849978|ref|XP_002892870.1|//0.00E+00//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338712|gb|EFH69129.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46076_All//0.00E+00//AT1G15490| hydrolase, alpha/beta fold family protein	Unigene46076_All//0.00E+00//TC143267				nr +
Unigene46077_All	486	3.45	1.98	3.18	10.66	10.49	3.07	14.01	6.19	32.13	-7.98E-01	1.16E-01		-1.17E-01	8.14E-01		-2.36E-02	9.37E-01		-1.80E+00	1.97E-10	Down	-1.18E+00	1.43E-08	Down	1.20E+00	1.50E-19	Up	Unigene46077_All//gi|15223428|ref|NP_171661.1|//1.00E-11//protein kinase family protein [Arabidopsis thaliana] >gi|158561340|sp|Q3EDL4.2|Y1154_ARATH RecName: Full=Probable serine/threonine-protein kinase At1g01540	Unigene46077_All//6.00E-13//AT1G01540| protein kinase family protein	Unigene46077_All//5.00E-63//TC156908				nr +
Unigene46078_All	1755	25.34	10.77	20.36	43.60	45.33	25.68	23.99	12.72	57.45	-1.23E+00	1.98E-45	Down	-3.16E-01	1.41E-04		5.60E-02	4.51E-01		-7.64E-01	4.15E-38		-9.16E-01	1.23E-32		1.26E+00	2.05E-131	Up	Unigene46078_All//gi|240255713|ref|NP_192042.5|//0.00E+00//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene46078_All//0.00E+00//AT4G01330| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene46078_All//0.00E+00//TC156908		ko04626|Plant-pathogen interaction		nr -
Unigene4608_All	2079	7.37	2.44	1.92	8.43	8.02	5.50	13.00	3.98	5.86	-1.60E+00	1.82E-23	Down	-1.94E+00	2.36E-29	Down	-7.32E-02	6.41E-01		-6.18E-01	1.54E-06		-1.71E+00	9.15E-55	Down	-1.15E+00	2.57E-31	Down	Unigene4608_All//gi|20147346|gb|AAM10386.1|//1.00E-83//AT5g38690/MEB18_24 [Arabidopsis thaliana] >gi|23463059|gb|AAN33199.1| At5g38690/MEB18_24 [Arabidopsis thaliana]	Unigene4608_All//4.00E-80//AT5G38690| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: DDT superfamily (InterPro:IPR018501), DDT subgroup (InterPro:IPR018500), Cell division cycle-associated protein (InterPro:IPR018866); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67780.1); Has 492 Blast hits to 468 proteins in 97 species: Archae - 9; Bacteria - 41; Metazoa - 179; Fungi - 19; Plants - 99; Viruses - 2; Other Eukaryotes - 143 (source: NCBI BLink).	Unigene4608_All//0.00E+00//TC140295				nr +
Unigene46080_All	734	1.21	0.76	1.16	1.15	1.13	1.17	1.04	1.77	7.98	-6.74E-01	3.69E-01		-6.20E-02	9.45E-01		-3.52E-02	9.55E-01		1.91E-02	9.82E-01		7.68E-01	1.50E-01		2.94E+00	5.80E-24	Up	Unigene46080_All//gi|15234128|ref|NP_195053.1|//1.00E-68//CDC20.1; signal transducer [Arabidopsis thaliana] >gi|4490294|emb|CAB38785.1| WD-repeat protein-like protein [Arabidopsis thaliana] >gi|7270275|emb|CAB80044.1| WD-repeat protein-like protein [Arabidopsis thaliana] >gi|109946631|gb|ABG48494.1| At4g33270 [Arabidopsis thaliana]	Unigene46080_All//7.00E-70//AT4G33270| CDC20.1; signal transducer	Unigene46080_All//2.00E-78//gi|78346900|gb|DT567174.1|DT567174		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene46081_All	1021	30.80	29.08	37.97	24.69	42.39	32.69	1.28	8.56	4.37	-8.27E-02	4.49E-01		3.02E-01	7.80E-04		7.80E-01	1.35E-24		4.05E-01	8.24E-06		2.74E+00	3.21E-32	Up	1.77E+00	2.35E-10	Up	Unigene46081_All//gi|283837097|emb|CBH19893.1|//1.00E-113//cell division control 20 [Solanum lycopersicum var. cerasiforme]	Unigene46081_All//3.00E-111//AT4G33270| CDC20.1; signal transducer	Unigene46081_All//0.00E+00//TC161778		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene46083_All	2778	25.65	31.76	26.47	55.79	59.21	79.53	40.56	31.50	20.25	3.08E-01	2.27E-08		4.54E-02	5.58E-01		8.61E-02	4.22E-02		5.12E-01	2.51E-53		-3.65E-01	3.74E-17		-1.00E+00	1.41E-102	Down	Unigene46083_All//gi|15232841|ref|NP_186854.1|//0.00E+00//KUP3 (K+ UPTAKE TRANSPORTER 3); potassium ion transmembrane transporter [Arabidopsis thaliana] >gi|38560197|sp|Q9LD18.2|POT4_ARATH RecName: Full=Potassium transporter 4; Short=AtPOT4; Short=AtKUP3; Short=AtKT4	Unigene46083_All//0.00E+00//AT3G02050| KUP3 (K+ UPTAKE TRANSPORTER 3); potassium ion transmembrane transporter	Unigene46083_All//0.00E+00//TC162532				nr +

Unigene46084_All	2633	7.71	10.14	9.20	16.21	14.63	13.93	12.46	7.98	3.87	3.96E-01	1.73E-04		2.55E-01	3.36E-02		-1.48E-01	8.72E-02		-2.19E-01	8.81E-03		-6.42E-01	3.19E-14		-1.69E+00	3.76E-67	Down	Unigene46084_All//gi|15225518|ref|NP_182083.1|//0.00E+00//protein kinase family protein [Arabidopsis thaliana]	Unigene46084_All//5.00E-158//AT2G45590| protein kinase family protein	Unigene46084_All//0.00E+00//gi|78348308|gb|DT568582.1|DT568582		ko04626|Plant-pathogen interaction		nr +
Unigene46092_All	1973	162.72	21.32	41.83	67.59	26.56	30.63	21.71	172.54	23.64	-2.93E+00	0.00E+00	Down	-1.96E+00	0.00E+00	Down	-1.35E+00	6.08E-193	Down	-1.14E+00	1.71E-129	Down	2.99E+00	0.00E+00	Up	1.23E-01	9.60E-02		Unigene46092_All//gi|18252504|gb|AAL66290.1|AF452450_1//0.00E+00//adenosine 5'-phosphosulfate reductase [Glycine max]	Unigene46092_All//0.00E+00//AT4G04610| APR1 (APS REDUCTASE 1); adenylyl-sulfate reductase	Unigene46092_All//0.00E+00//TC155594				nr +
Unigene46093_All	1497	18.63	945.83	112.80	48.05	274.88	816.98	55.55	626.43	208.96	5.67E+00	0.00E+00	Up	2.60E+00	0.00E+00	Up	2.52E+00	0.00E+00	Up	4.09E+00	0.00E+00	Up	3.50E+00	0.00E+00	Up	1.91E+00	0.00E+00	Up	Unigene46093_All//gi|15217709|ref|NP_176647.1|//0.00E+00//ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase [Arabidopsis thaliana] >gi|6633821|gb|AAF19680.1|AC009519_14 F1N19.23 [Arabidopsis thaliana] >gi|16226491|gb|AAL16181.1|AF428413_1 At1g64660/F1N19_22 [Arabidopsis thaliana] >gi|15450932|gb|AAK96737.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana] >gi|30387533|gb|AAP31932.1| At1g64660 [Arabidopsis thaliana] >gi|110740851|dbj|BAE98522.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana]	Unigene46093_All//0.00E+00//AT1G64660| ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase	Unigene46093_All//0.00E+00//TC138839		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -
Unigene46094_All	1494	0.32	23.23	3.21	1.43	5.69	16.72	2.75	22.94	8.29	6.20E+00	4.75E-183	Up	3.35E+00	3.54E-17	Up	1.99E+00	3.11E-20	Up	3.54E+00	1.32E-101	Up	3.06E+00	5.54E-140	Up	1.60E+00	1.00E-23	Up	Unigene46094_All//gi|15217709|ref|NP_176647.1|//3.00E-77//ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase [Arabidopsis thaliana] >gi|6633821|gb|AAF19680.1|AC009519_14 F1N19.23 [Arabidopsis thaliana] >gi|16226491|gb|AAL16181.1|AF428413_1 At1g64660/F1N19_22 [Arabidopsis thaliana] >gi|15450932|gb|AAK96737.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana] >gi|30387533|gb|AAP31932.1| At1g64660 [Arabidopsis thaliana] >gi|110740851|dbj|BAE98522.1| similar to O-succinylhomoserine sulfhydrylase [Arabidopsis thaliana]	Unigene46094_All//2.00E-72//AT1G64660| ATMGL (ARABIDOPSIS THALIANA METHIONINE GAMMA-LYASE); catalytic/ methionine gamma-lyase	Unigene46094_All//0.00E+00//gi|48799994|gb|CO101308.1|CO101308		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr +
Unigene46095_All	1907	5.27	6.38	4.75	78.26	60.74	46.02	21.26	9.62	11.28	2.76E-01	1.04E-01		-1.50E-01	4.64E-01		-3.66E-01	4.21E-22		-7.66E-01	2.58E-74		-1.14E+00	5.62E-45	Down	-9.14E-01	2.78E-32		Unigene46095_All//gi|60657602|gb|AA33322.1|//0.00E+00//secondary cell wall-related glycosyltransferase family 47 [Populus tremula x Populus tremuloides]	Unigene46095_All//8.00E-163//AT2G28110| FRA8 (FRAGILE FIBER 8); glucuronosyltransferase/ transferase	Unigene46095_All//0.00E+00//TC147160				nr -
Unigene46096_All	1504	3.13	1.38	2.83	5.00	3.53	3.81	3.18	1.70	2.15	-1.18E+00	3.44E-05	Down	-1.45E-01	6.12E-01		-5.04E-01	1.30E-02		-3.91E-01	7.48E-02		-9.06E-01	2.34E-04		-5.66E-01	1.71E-02		Unigene46096_All//gi|297826567|ref|XP_002881166.1|//0.00E+00//tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327005|gb|EFH57425.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46096_All//0.00E+00//AT2G31240| tetratricopeptide repeat (TPR)-containing protein	Unigene46096_All//2.00E-123//TC153652				nr -
Unigene46097_All	1854	3.25	1.53	2.07	5.72	4.68	4.80	6.07	3.11	3.52	-1.08E+00	1.08E-05	Down	-6.50E-01	9.80E-03		-2.90E-01	1.06E-01		-2.54E-01	1.87E-01		-9.63E-01	4.60E-10		-7.84E-01	1.37E-07		Unigene46097_All//gi|297826567|ref|XP_002881166.1|//0.00E+00//tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327005|gb|EFH57425.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46097_All//0.00E+00//AT2G31240| tetratricopeptide repeat (TPR)-containing protein	Unigene46097_All//0.00E+00//gi|21096154|gb|BQ408467.1|BQ408467				nr -
Unigene46098_All	1386	0.15	0.44	0.58	5.28	2.61	3.91	42.95	42.61	15.64	1.54E+00	1.22E-01		1.93E+00	3.42E-02		-1.02E+00	3.79E-07	Down	-4.34E-01	4.87E-02		-1.15E-02	8.89E-01		-1.46E+00	4.01E-98	Down	Unigene46098_All//gi|158706508|sp|Q56XQ0.2|U4961_ARATH//9.00E-37//RecName: Full=UPF0496 protein At2g18630	Unigene46098_All//2.00E-26//AT2G18630| unknown protein	Unigene46098_All//2.00E-160//TC166593				nr -
Unigene46099_All	1912	0.05	0.21	0.06	4.04	3.46	2.15	20.79	18.89	6.75	1.95E+00	1.44E-01		2.61E-02	9.99E-01		-2.24E-01	3.22E-01		-9.10E-01	9.74E-06		-1.38E-01	9.74E-02		-1.62E+00	7.07E-77	Down	Unigene46099_All//gi|158706508|sp|Q56XQ0.2|U4961_ARATH//1.00E-38//RecName: Full=UPF0496 protein At2g18630	Unigene46099_All//3.00E-38//AT2G18630| unknown protein	Unigene46099_All//0.00E+00//TC166593				nr +
Unigene4610_All	566	10.54	9.58	6.12	32.92	32.25	27.69	37.13	17.35	17.24	-1.38E-01	6.21E-01		-7.85E-01	1.89E-03		-2.97E-02	8.39E-01		-2.50E-01	6.63E-02		-1.10E+00	3.29E-22	Down	-1.11E+00	3.48E-23	Down	Unigene4610_All//gi|225453502|ref|XP_002277890.1|//3.00E-28//PREDICTED: similar to sec61beta family protein [Vitis vinifera]	Unigene4610_All//7.00E-15//AT3G60540| sec61beta family protein	Unigene4610_All//1.00E-140//BG442620		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export		nr -
Unigene46102_All	2969	5.46	15.41	6.67	11.85	9.99	4.62	8.91	8.25	7.98	1.50E+00	3.76E-62	Up	2.88E-01	3.02E-02		-2.46E-01	5.27E-03		-1.36E+00	4.38E-45	Down	-1.12E-01	3.14E-01		-1.59E-01	1.08E-01		Unigene46102_All//gi|14149112|dbj|BAB55653.1|//0.00E+00//bg55 [Bruguiera gymnorhiza]	Unigene46102_All//2.00E-120//AT4G36550| binding / ubiquitin-protein ligase	Unigene46102_All//0.00E+00//gi|109857330|gb|DW486309.1|DW486309				nr +
Unigene46103_All	1929	10.96	5.75	9.72	24.22	15.99	17.28	18.89	8.04	6.24	-9.30E-01	3.92E-14		-1.73E-01	2.05E-01		-5.99E-01	2.67E-17		-4.87E-01	7.50E-11		-1.23E+00	1.59E-45	Down	-1.60E+00	4.17E-69	Down	Unigene46103_All//gi|18402672|ref|NP_566664.1|//0.00E+00//ATPDIL5-3 (PDI-LIKE 5-3); protein disulfide isomerase [Arabidopsis thaliana] >gi|15215847|gb|AAS91468.1| AT3g20560/K10D20_9 [Arabidopsis thaliana]	Unigene46103_All//0.00E+00//AT3G20560| ATPDIL5-3 (PDI-LIKE 5-3); protein disulfide isomerase	Unigene46103_All//0.00E+00//TC134955		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene46107_All	616	3.06	0.41	3.20	18.20	18.89	12.90	4.74	5.63	2.98	-2.89E+00	1.55E-06	Down	6.49E-02	8.92E-01		5.44E-02	8.14E-01		-4.96E-01	3.18E-03		2.50E-01	4.38E-01		-6.71E-01	3.29E-02		Unigene46107_All//gi|192764525|gb|ACF05806.1|//3.00E-29//PAE [Litchi chinensis]	Unigene46107_All//8.00E-28//AT4G19420| pectinacetylesterase family protein	Unigene46107_All//4.00E-147//TC148155				nr -
Unigene46108_All	1712	7.37	0.98	3.55	26.62	27.40	16.44	11.68	12.35	10.70	-2.91E+00	1.42E-40	Down	-1.05E+00	4.22E-10	Down	4.12E-02	6.87E-01		-6.96E-01	1.41E-19		8.07E-02	5.43E-01		-1.26E-01	3.00E-01		Unigene46108_All//gi|192764525|gb|ACF05806.1|//1.00E-180//PAE [Litchi chinensis]	Unigene46108_All//2.00E-176//AT4G19420| pectinacetylesterase family protein	Unigene46108_All//0.00E+00//TC148155				nr +
Unigene46109_All	1448	35.63	31.42	35.67	39.29	40.36	42.17	52.03	29.67	23.33	-1.81E-01	1.86E-02		1.80E-03	1.00E+00		3.88E-02	6.64E-01		1.02E-01	1.95E-01		-8.10E-01	4.93E-47		-1.16E+00	7.88E-87	Down	Unigene46109_All//gi|22947842|gb|AAN07899.1|//1.00E-130//20S proteasome alpha 6 subunit [Nicotiana benthamiana]	Unigene46109_All//2.00E-120//AT5G42790| PAF1; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene46109_All//0.00E+00//TC129849		ko03050|Proteasome		nr +
Unigene4611_All	1159	1.76	1.40	1.19	3.83	6.18	4.01	9.81	5.81	4.19	-3.32E-01	4.66E-01		-5.60E-01	2.40E-01		6.92E-01	9.06E-04		6.94E-02	8.29E-01		-7.57E-01	5.03E-07		-1.23E+00	4.06E-15	Down	Unigene4611_All//gi|225453502|ref|XP_002277890.1|//1.00E-27//PREDICTED: similar to sec61beta family protein [Vitis vinifera]	Unigene4611_All//2.00E-14//AT3G60540| sec61beta family protein	Unigene4611_All//2.00E-129//BG442620		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export		nr +
Unigene46113_All	1388	40.48	140.91	81.56	55.13	75.37	85.80	88.00	90.25	73.94	1.80E+00	0.00E+00	Up	1.01E+00	1.22E-80	Up	4.51E-01	1.71E-22		6.38E-01	6.96E-43		3.63E-02	4.95E-01		-2.51E-01	7.01E-10		Unigene46113_All//gi|297822777|ref|XP_002879271.1|//1.00E-170//BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325110|gb|EFH55530.1| BTB/POZ domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46113_All//1.00E-167//AT2G30600| BTB/POZ domain-containing protein	Unigene46113_All//6.00E-145//DT469030				nr +
Unigene46114_All	1693	7.48	124.20	14.00	20.80	28.52	30.81	20.43	44.19	67.82	4.05E+00	0.00E+00	Up	9.04E-01	1.89E-14		4.55E-01	9.25E-11		5.67E-01	1.52E-15		1.11E+00	1.04E-78	Up	1.73E+00	2.43E-239	Up	Unigene46114_All//gi|75223238|sp|Q80871.1|P2C25_ARATH//1.00E-145//RecName: Full=Probable protein phosphatase 2C 25; Short=AtPP2C25; AltName: Full=Protein phosphatase AP2C1	Unigene46114_All//1.00E-121//AT2G30020| protein phosphatase 2C, putative / PP2C, putative	Unigene46114_All//0.00E+00//TC153130				nr -
Unigene46117_All	1672	1.75	53.18	3.41	5.66	15.98	19.96	21.44	106.36	250.59	4.92E+00	0.00E+00	Up	9.60E-01	2.33E-04		1.50E+00	8.06E-43	Up	1.82E+00	3.38E-64	Up	2.31E+00	0.00E+00	Up	3.55E+00	0.00E+00	Up	Unigene46117_All//gi|27311581|gb|AA000756.1|//1.00E-147//Unknown protein [Arabidopsis thaliana]	Unigene46117_All//1.00E-132//AT2G40000| HSP80Z (ARABIDOPSIS ORTHOLOG OF SUGAR BEET HS1 PRO-1 2)	Unigene46117_All//0.00E+00//gi|78352297|gb|DT572571.1|DT572571				nr -
Unigene46119_All	502	1.46	1.21	2.97	3.87	5.56	2.61	0.76	2.33	5.16	-2.69E-01	7.19E-01		1.03E+00	7.47E-02		5.22E-01	1.80E-01		-5.69E-01	2.36E-01		1.62E+00	6.24E-03		2.77E+00	2.35E-10	Up		Unigene46119_All//3.00E-52//TC166299					
Unigene46120_All	1411	25.99	31.35	25.40	45.26	60.50	56.40	20.26	38.69	57.01	2.70E-01	8.49E-04		-3.34E-02	7.46E-01		4.19E-01	4.23E-16		3.17E-01	1.99E-08		9.33E-01	2.44E-43		1.49E+00	1.04E-135	Up	Unigene46120_All//gi|229609889|gb|ACQ83560.1|//2.00E-92//calcineurin B-like protein 06 [Vitis vinifera]	Unigene46120_All//2.00E-74//AT4G33000| CBL10 (CALCINEURIN B-LIKE 10); calcium ion binding	Unigene46120_All//0.00E+00//gi|109878852|gb|DW507822.1|DW507822		ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene46122_All	617	2.29	3.86	1.12	1.45	1.79	1.83	1.51	3.05	4.65	7.53E-01	6.78E-02		-1.03E+00	8.34E-02		2.97E-01	6.88E-01		3.33E-01	6.21E-01		1.02E+00	1.72E-02		1.62E+00	2.84E-06	Up		Unigene46122_All//7.00E-72//DT462451					
Unigene46123_All	2089	0.43	1.16	0.92	0.24	0.08	0.13	0.28	0.18	0.17	1.45E+00	6.88E-04	Up	1.11E+00	2.53E-02		-1.53E+00	1.45E-01		-8.79E-01	4.20E-01		-6.54E-01	4.45E-01		-7.24E-01	3.71E-01		Unigene46123_All//gi|240254055|ref|NP_563875.6|//0.00E+00//polygalacturonase [Arabidopsis thaliana]	Unigene46123_All//0.00E+00//AT1G10640| polygalacturonase	Unigene46123_All//0.00E+00//TC162376		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene46124_All	1579	16.87	18.00	14.47	23.85	23.71	27.89	62.31	37.30	30.40	9.41E-02	4.07E-01		-2.21E-01	5.53E-02		-8.80E-03	9.44E-01		2.26E-01	5.91E-03		-7.40E-01	1.92E-52		-1.04E+00	1.49E-94	Down	Unigene46124_All//gi|15223830|ref|NP_172914.1|//2.00E-86//DECOY (DECOY) [Arabidopsis thaliana] >gi|20022540|gb|AAM83228.1| At1g14620/T5E21_15 [Arabidopsis thaliana] >gi|24111323|gb|AAN46785.1| At1g14620/T5E21_15 [Arabidopsis thaliana]	Unigene46124_All//9.00E-88//AT1G14620| DECOY (DECOY)	Unigene46124_All//0.00E+00//TC175286				nr -
Unigene46125_All	1707	16.46	9.14	15.29	40.83	37.46	35.08	6.76	2.69	2.89	-8.48E-01	5.58E-16		-1.07E-01	3.93E-01		-1.24E-01	6.16E-02		-2.19E-01	4.80E-04		-1.33E+00	1.07E-16	Down	-1.22E+00	2.74E-15	Down	Unigene46125_All//gi|18400116|ref|NP_565544.1|//1.00E-174//galactosyl transferase GMA12/MNN10 family protein [Arabidopsis thaliana] >gi|46576210|sp|Q81007.1|GT7_ARATH RecName: Full=Putative glycosyltransferase 7; Short=AtGT7 >gi|3445207|gb|AAC32437.1| Expressed protein [Arabidopsis thaliana]	Unigene46125_All//2.00E-175//AT2G22900| galactosyl transferase GMA12/MNN10 family protein	Unigene46125_All//0.00E+00//TC131260				nr +

Unigene46127_All	2340	1.77	2.32	1.62	5.43	4.68	3.65	6.70	3.47	3.20	3.91E-01	1.36E-01			-1.29E-01	6.81E-01			-2.14E-01	2.11E-01			-5.74E-01	2.09E-04			-9.52E-01	1.84E-13			-1.07E+00	1.43E-16	Down	Unigene46127_All//gi|116310758|emb|CAH67552.1|//3.00E-53//H0031C003.6 [Oryza sativa (indica cultivar-group)]	Unigene46127_All//5.00E-30//AT4G31880| LOCATED IN: cytosol, chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: binding (TAIR:AT1G15940.1); Has 114836 Blast hits to 56273 proteins in 1914 species: Archae - 187; Bacteria - 15478; Metazoa - 53116; Fungi - 16017; Plants - 4342; Viruses - 719; Other Eukaryotes - 24977 (source: NCBI BLink).	Unigene46127_All//0.00E+00//ES797123				nr +
Unigene46129_All	1997	6.50	5.81	5.12	3.69	5.83	6.72	2.56	4.81	6.66	-1.61E-01	3.59E-01			-3.44E-01	4.07E-02			6.59E-01	2.57E-05			8.63E-01	1.24E-08			9.10E-01	5.45E-08			1.38E+00	1.17E-20	Up	Unigene46129_All//gi|297798508|ref|XP_002867138.1|//1.00E-140//DJ-1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312974|gb|EFH43397.1| DJ-1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46129_All//3.00E-131//AT4G34020| DJ-1 family protein	Unigene46129_All//0.00E+00//TC162450				nr +
Unigene46130_All	419	3.12	2.78	3.94	7.13	6.99	2.69	2.52	1.60	1.90	-1.67E-01	7.57E-01			3.36E-01	5.35E-01			-3.02E-02	9.37E-01			-1.40E+00	1.33E-04	Down	-6.61E-01	2.78E-01				-4.08E-01	4.85E-01		Unigene46130_All||gi|183604855|gb|ACC64525.1|//1.00E-29//GAGA-binding transcriptional activator BBR/BPC1-like [Vitis vinifera] >gi|183604857|gb|ACC64526.1| GAGA-binding transcriptional activator BBR/BPC1-like [Vitis vinifera]	Unigene46130_All//1.00E-17//AT2G01930| BPC1 (BASIC PENTACYSTEINE1); DNA binding / specific transcriptional repressor/ transcription factor	Unigene46130_All//0.00E+00//ES817684	BBR/BPC			nr -
Unigene46132_All	2656	4.06	2.65	3.35	12.02	13.11	12.63	23.81	25.63	7.15	-6.14E-01	3.90E-04			-2.77E-01	1.46E-01			1.25E-01	2.27E-01			7.16E-02	5.50E-01			1.06E-01	9.30E-02			-1.73E+00	4.84E-134	Down	Unigene46132_All//gi|30690045|ref|NP_177617.2|//0.00E+00//catalytic [Arabidopsis thaliana] >gi|34395733|sp|Q9SSG3.2|HIPL1_ARATH RecName: Full=HIPL1 protein; Flags: Precursor	Unigene46132_All//0.00E+00//AT1G74790| catalytic	Unigene46132_All//0.00E+00//TC172030				nr -
Unigene46133_All	1215	3.01	1.33	1.31	8.49	10.68	9.07	13.40	16.03	4.00	-1.18E+00	3.36E-04	Down	-1.20E+00	4.68E-04	Down	3.32E-01	3.49E-02			9.58E-02	6.42E-01			2.59E-01	2.59E-02			-1.74E+00	2.33E-35	Down	Unigene46133_All||gi|5882745|gb|AAD55298.1|AC008263_29//1.00E-125//F25A4.24 [Arabidopsis thaliana]	Unigene46133_All//3.00E-117//AT1G74790| catalytic	Unigene46133_All//0.00E+00//DT466508				nr -
Unigene46134_All	1080	6.25	14.92	7.40	12.73	8.13	6.40	9.94	12.96	4.57	1.26E+00	2.83E-17	Up	2.43E-01	2.89E-01		-6.47E-01	3.36E-06			-9.93E-01	4.10E-11			3.83E-01	4.73E-03			-1.12E+00	1.62E-12	Down	Unigene46134_All//gi|225626255|gb|ACN97177.1|//1.00E-103//MYB transcription factor [Populus trichocarpa]	Unigene46134_All//9.00E-85//AT4G38620| MYB4; DNA binding / transcription factor	Unigene46134_All//0.00E+00//TC139976	MYB			nr +
Unigene46135_All	1307	50.36	21.98	33.12	52.44	35.41	25.85	12.23	12.82	8.44	-1.20E+00	1.13E-63	Down	-6.04E-01	1.19E-19		-5.67E-01	7.81E-23			-1.02E+00	1.17E-55	Down	6.86E-02	6.20E-01		-5.34E-01	1.01E-05						Unigene46135_All||gi|13346194|gb|AAK19619.1|AF336286_1|/1.00E-154//GHMYB9 [Gossypium hirsutum] >gi|207298825|gb|ACI23564.1| MYB-like protein 3 [Gossypium barbadense]	Unigene46135_All//2.00E-87//AT4G38620| MYB4; DNA binding / transcription factor	Unigene46135_All//0.00E+00//TC145663	MYB			nr +
Unigene46137_All	983	4.10	11.91	3.09	5.17	11.67	5.51	70.02	67.26	82.84	1.54E+00	4.47E-17	Up	-4.09E-01	2.15E-01		1.17E+00	6.22E-13	Up	9.31E-02	7.44E-01		-5.80E-02	3.96E-01						2.43E-01	1.74E-06		Unigene46137_All||gi|15237552|ref|NP_198924.1|//7.00E-85//glycerophosphoryl diester phosphodiesterase family protein [Arabidopsis thaliana] >gi|124301014|gb|ABN04759.1| At5g41080 [Arabidopsis thaliana]	Unigene46137_All//3.00E-79//AT5G41080| glycerophosphoryl diester phosphodiesterase family protein	Unigene46137_All//0.00E+00//TC178926				nr -
Unigene46138_All	1662	3.87	8.17	2.15	4.68	7.15	3.29	66.98	72.20	73.25	1.08E+00	1.14E-11	Up	-8.51E-01	4.43E-04		6.12E-01	7.79E-05			-5.08E-01	1.50E-02			1.08E-01	1.64E-02			1.29E-01	2.30E-03		Unigene46138_All||gi|15237552|ref|NP_198924.1|//1.00E-134//glycerophosphoryl diester phosphodiesterase family protein [Arabidopsis thaliana] >gi|124301014|gb|ABN04759.1| At5g41080 [Arabidopsis thaliana]	Unigene46138_All//3.00E-128//AT5G41080| glycerophosphoryl diester phosphodiesterase family protein	Unigene46138_All//0.00E+00//CO127462				nr +
Unigene46139_All	2117	7.02	4.95	3.37	12.52	10.26	16.66	13.68	21.18	31.22	-5.03E-01	5.23E-04		-1.06E+00	7.51E-12	Down	-2.87E-01	5.10E-03			4.13E-01	2.75E-06			6.31E-01	1.49E-18			1.19E+00	4.06E-79	Up	Unigene46139_All||gi|224118412|ref|XP_002317812.1|//0.00E+00//CPK related kinase 4 [Populus trichocarpa] >gi|222858485|gb|EEE96032.1| CPK related kinase 4 [Populus trichocarpa]	Unigene46139_All//5.00E-151//AT5G24430| calcium-dependent protein kinase, putative / CDPK, putative	Unigene46139_All//0.00E+00//gi|78339338|gb|DT559612.1|DT559612				nr -
Unigene46141_All	2824	0.32	0.48	0.36	1.06	0.99	0.56	0.75	0.30	0.52	6.21E-01	2.77E-01		1.86E-01	7.75E-01		-9.97E-02	8.16E-01			-9.19E-01	1.05E-02			-1.34E+00	9.81E-04	Down	-5.20E-01	1.77E-01		Unigene46141_All||gi|225444543|ref|XP_002275664.1|//0.00E+00//PREDICTED; similar to glycoside hydrolase family 47 protein [Vitis vinifera]	Unigene46141_All//0.00E+00//AT1G30000| glycoside hydrolase family 47 protein	Unigene46141_All//0.00E+00//TC167979		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	nr +
Unigene46143_All	1415	9.80	9.35	9.48	3.87	5.33	3.29	0.45	2.04	0.73	-6.82E-02	6.72E-01		-4.72E-02	7.76E-01		4.61E-01	2.86E-02			-2.36E-01	4.09E-01			2.19E+00	1.03E-08	Up	7.08E-01	2.28E-01		Unigene46143_All||gi|19699285|gb|AAL91254.1|//8.00E-62//AT5g52030/MSG15_11 [Arabidopsis thaliana] >gi|23308347|gb|AAN18143.1| At5g52030/MSG15_11 [Arabidopsis thaliana]	Unigene46143_All//5.00E-53//AT5G52030| TraB protein-related	Unigene46143_All//0.00E+00//gi|78334732|gb|DT555006.1|DT555006				nr +
Unigene46144_All	1660	5.23	2.87	4.14	2.49	2.66	1.71	0.43	1.96	0.89	-8.67E-01	1.12E-05		-3.38E-01	1.11E-01		9.23E-02	8.19E-01			-5.39E-01	7.67E-02			2.18E+00	9.69E-10	Up	1.04E+00	2.97E-02		Unigene46144_All||gi|19699285|gb|AAL91254.1|//6.00E-43//AT5g52030/MSG15_11 [Arabidopsis thaliana] >gi|23308347|gb|AAN18143.1| At5g52030/MSG15_11 [Arabidopsis thaliana]	Unigene46144_All//3.00E-44//AT5G52030| TraB protein-related	Unigene46144_All//6.00E-173//gi|78334732|gb|DT555006.1|DT555006				nr +
Unigene46148_All	1797	43.38	9.14	15.59	64.92	41.37	22.19	14.05	3.84	1.84	-2.25E+00	7.99E-185	Down	-1.48E+00	1.31E-100	Down	-6.50E-01	2.16E-49			-1.55E+00	2.45E-181	Down	-1.87E+00	4.28E-58	Down	-2.93E+00	2.43E-102	Down	Unigene46148_All||gi|166343827|gb|AB986656.1|//0.00E+00//beta-tubulin 8 [Gossypium hirsutum]	Unigene46148_All//0.00E+00//AT1G75780| TUB1; GTP binding / GTPase/ structural molecule	Unigene46148_All//0.00E+00//TC160056		ko04145|Phagosome		nr -
Unigene46154_All	3575	3.85	4.58	2.58	5.18	3.12	4.41	8.87	19.26	8.48	2.50E-01	8.15E-02		-5.79E-01	2.22E-04		-7.32E-01	5.03E-10			-2.34E-01	8.97E-02			1.12E+00	5.22E-73	Up	-6.48E-02	5.27E-01		Unigene46154_All||gi|297846442|ref|XP_002891102.1|//0.00E+00//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336944|gb|EFH67361.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46154_All//0.00E+00//AT1G34420| leucine-rich repeat family protein / protein kinase family protein	Unigene46154_All//0.00E+00//TC143101				nr +
Unigene46155_All	1765	21.88	19.46	15.45	30.76	25.09	28.28	33.56	24.98	14.90	-1.69E-01	6.64E-02		-5.02E-01	1.27E-08		-2.94E-01	1.01E-05			-1.22E-01	1.33E-01			-4.26E-01	2.67E-12			-1.17E+00	8.20E-70	Down	Unigene46155_All||gi|224106141|ref|XP_002314058.1|//1.00E-106//silencing group B protein [Populus trichocarpa] >gi|222850466|gb|EEE88013.1| silencing group B protein [Populus trichocarpa]	Unigene46155_All//5.00E-83//AT5G13780| GCN5-related N-acetyltransferase, putative	Unigene46155_All//0.00E+00//TC166635				nr -
Unigene46156_All	1298	23.54	23.34	22.69	36.00	27.94	37.86	44.07	39.93	17.10	-1.21E-02	9.26E-01		-5.33E-02	6.28E-01		-3.66E-01	2.84E-07			7.26E-02	4.47E-01			-1.42E-01	3.33E-02			-1.37E+00	1.48E-85	Down	Unigene46156_All||gi|18421420|ref|NP_568525.1|//1.00E-89//protein binding [Arabidopsis thaliana]	Unigene46156_All//7.00E-91//AT5G35080| protein binding	Unigene46156_All//0.00E+00//TC161362		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene46157_All	915	2.69	6.31	6.63	0.49	1.17	0.69	2.54	11.28	5.92	1.23E+00	1.62E-06	Up	1.30E+00	4.86E-07	Up	1.25E+00	6.99E-02			4.96E-01	6.37E-01			2.15E+00	8.61E-29	Up	1.22E+00	1.54E-07	Up	Unigene46157_All||gi|74229863|gb|AB400460.1|//4.00E-32//serine-glyoxylate aminotransferase [Spirodela polyrhiza]	Unigene46157_All//1.00E-25//AT2G13360| AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE); alanine-glyoxylate transaminase/ serine-glyoxylate transaminase/ serine-pyruvate transaminase	Unigene46157_All//1.00E-126//gi|48742049|gb|CO072568.1|CO072568		ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism		nr -
Unigene46158_All	1956	180.77	240.27	257.18	19.69	29.98	24.50	32.57	130.77	55.30	4.11E-01	4.75E-70		5.09E-01	7.03E-108		6.07E-01	1.53E-21			3.16E-01	2.68E-05			2.01E+00	0.00E+00	Up	7.64E-01	4.93E-62		Unigene46158_All||gi|74229863|gb|AB400460.1|//0.00E+00//serine-glyoxylate aminotransferase [Spirodela polyrhiza]	Unigene46158_All//0.00E+00//AT2G13360| AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE); alanine-glyoxylate transaminase/ serine-glyoxylate transaminase/ serine-pyruvate transaminase	Unigene46158_All//0.00E+00//TC139658		ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism		nr +
Unigene46163_All	3180	3.65	3.55	5.04	2.96	4.88	8.14	1.24	1.22	1.37	-3.98E-02	8.23E-01		4.65E-01	1.32E-03		7.22E-01	5.05E-08			1.46E+00	1.61E-36	Up	-1.67E-02	9.87E-01		1.43E-01	6.05E-01		Unigene46163_All||gi|110630091|gb|ABD64063.1|//0.00E+00//copper P1B-ATPase [Glycine max]	Unigene46163_All//0.00E+00//AT5G21930| PAA2 (P-TYPE ATPASE OF ARABIDOPSIS 2); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / copper ion transmembrane transporter	Unigene46163_All//0.00E+00//CO088887				nr +
Unigene46164_All	2697	3.61	1.58	2.53	5.12	3.61	6.18	8.07	3.52	5.05	-1.19E+00	5.15E-10	Down	-5.14E-01	7.44E-03		-5.02E-01	3.70E-04			2.72E-01	5.81E-02			-1.20E+00	2.37E-26	Down	-6.76E-01	6.46E-11		Unigene46164_All||gi|145337741|ref|NP_178036.2|//0.00E+00//binding [Arabidopsis thaliana]	Unigene46164_All//0.00E+00//AT1G79150| binding	Unigene46164_All//0.00E+00//TC179192				nr +
Unigene46166_All	2634	13.85	9.79	9.93	397.44	374.70	295.50	74.26	31.43	30.72	-5.00E-01	1.60E-08		-4.80E-01	1.35E-07		-8.50E-02	1.89E-09			-4.28E-01	1.09E-181			-1.24E+00	2.04E-243	Down	-1.27E+00	8.85E-261	Down	Unigene46166_All||gi|6683114|dbj|BAA89049.1|//0.00E+00//sucrose synthase [Citrus unshiu]	Unigene46166_All//0.00E+00//AT5G20830| SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase	Unigene46166_All//0.00E+00//TC171724		ko00500|Starch and sucrose metabolism		nr -
Unigene46170_All	1256	2.21	5.61	3.14	4.16	3.95	4.03	1.31	1.13	0.67	1.34E+00	8.75E-09	Up	5.07E-01	1.22E-01		-7.70E-02	8.12E-01			-4.83E-02	8.77E-01			-2.15E-01	6.40E-01		-9.79E-01	2.63E-02		Unigene46170_All||gi|106880168|emb|CAJ80766.1|//9.00E-94//red chlorophyll catabolite reductase [Solanum lycopersicum]	Unigene46170_All//9.00E-78//AT4G37000| ACD2 (ACCELERATED CELL DEATH 2); red chlorophyll catabolite reductase	Unigene46170_All//0.00E+00//TC134783				nr +
Unigene46172_All	907	28.44	103.52	77.38	81.83	95.64	130.46	77.47	112.12	73.48	1.86E+00	2.58E-173	Up	1.44E+00	7.09E-88	Up	2.25E-01	1.98E-05			6.73E-01	1.00E-46			5.33E-01	1.58E-30		-7.63E-02	2.22E-01		Unigene46172_All||gi|9958057|gb|AAG05646.1|AC011810_5|/6.00E-21//Unknown Protein [Arabidopsis thaliana]	Unigene46172_All//3.00E-22//AT1G13360| unknown protein	Unigene46172_All//0.00E+00//ES808066				nr -
Unigene46173_All	1072	7.27	39.23	15.99	20.26	21.94	52.62	4.18	34.74	14.72	2.43E+00	5.72E-109	Up	1.14E+00	3.26E-15	Up	1.15E-01	3.93E-01			1.38E+00	1.45E-72	Up	3.05E+00	1.16E-151	Up	1.82E+00	8.46E-36	Up	Unigene46173_All||gi|9958057|gb|AAG05646.1|AC011810_5|/4.00E-21//Unknown Protein [Arabidopsis thaliana]	Unigene46173_All//2.00E-22//AT1G13360| unknown protein	Unigene46173_All//0.00E+00//TC173354				nr -
Unigene46174_All	2064	3.22	1.96	1.60	6.18	4.32	6.46	11.06	5.55	7.78	-7.13E-01	1.73E-03		-1.01E+00	2.61E-05	Down	-5.16E-01	4.63E-04			6.32E-02	7.22E-01			-9.95E-01	1.23E-20		-5.08E-01	3.50E-07		Unigene46174_All||gi|75337761|sp|Q93K44.1|RH16_ARATH|/0.00E+00//RecN ame: Full=DEAD-box ATP-dependent RNA helicase 16 >gi|5123708|emb|CAB45452.1| RNA helicase (RH16) [Arabidopsis thaliana] >gi|7270442|emb|CAB80208.1| RNA helicase (RH16) [Arabidopsis thaliana]	Unigene46174_All//0.00E+00//AT4G34910| DEAD/DEAH box helicase, putative (RH16)	Unigene46174_All//0.00E+00//TC179284				nr -
Unigene4618_All	1164	1.66	3.40	4.03	12.80	25.44	32.90	50.56	72.21	37.51	1.03E+00	9.42E-04	Up	1.28E+00	1.97E-05	Up	9.92E-01	3.86E-25			1.36E+00	1.28E-48	Up	5.14E-01	8.32E-24		-4.31E-01	7.54E-13		Unigene4618_All||gi|4808126|emb|CAB42793.1|//1.00E-153//phenylalanine-ammonia lyase [Citrus clementina x Citrus reticulata]	Unigene4618_All//4.00E-148//AT3G53260| PAL2; phenylalanine ammonia-lyase	Unigene4618_All//0.00E+00//TC144609		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00910|Nitrogen metabolism		nr +

Unigene46180_All	1169	2.69	2.69	2.73	2.00	8.90	9.70	0.00	0.00	0.17	1.00E-03	9.99E-01		2.54E-02	9.61E-01		2.15E+00	3.26E-27	Up	2.28E+00	2.40E-29	Up	null	null		7.41E+00	7.88E-02		Unigene46180_All//gi|15230370|ref|NP_191326.1|//1.00E-105//NTT (NO TRANSMITTING TRACT); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|18027012|gb|AAL55722.1|AF254447_1 WIP2 protein [Arabidopsis thaliana] >gi|4678280|emb|CAB41188.1| zinc finger-like protein [Arabidopsis thaliana] >gi|59958298|gb|AAX12859.1|At3g57670 [Arabidopsis thaliana]	Unigene46180_All//3.00E-97//AT3G57670| NTT (NO TRANSMITTING TRACT); nucleic acid binding / transcription factor/ zinc ion binding	Unigene46180_All//1.00E-154//ES797352	C2H2			nr +
Unigene46181_All	3311	2.91	5.51	3.43	7.36	5.75	6.37	7.33	15.78	14.55	9.22E-01	4.23E-12		2.37E-01	2.13E-01		-3.55E-01	6.62E-04		-2.08E-01	7.96E-02		1.11E+00	1.20E-54	Up	9.89E-01	4.19E-43		Unigene46181_All//gi|18398454|ref|NP_565419.1|//1.00E-120//IRE1A; endoribonuclease/ kinase [Arabidopsis thaliana] >gi|13194578|gb|AAK15470.1|AF308596_1 endoribonuclease/protein kinase IRE1-like protein [Arabidopsis thaliana] >gi|15277139|dbj|BAB63367.1| Ire1 homolog-2 [Arabidopsis thaliana]	Unigene46181_All//1.00E-114//AT2G17520| IRE1A; endoribonuclease/ kinase	Unigene46181_All//0.00E+00//DW226604		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene46182_All	3084	0.17	0.49	0.28	0.81	0.41	0.26	0.85	1.29	1.85	1.54E+00	6.71E-03		7.03E-01	3.83E-01		-9.67E-01	1.07E-02		-1.62E+00	1.09E-04	Down	5.99E-01	2.94E-02		1.12E+00	5.42E-07	Up	Unigene46182_All//gi|18398454|ref|NP_565419.1|//0.00E+00//IRE1A; endoribonuclease/ kinase [Arabidopsis thaliana] >gi|13194578|gb|AAK15470.1|AF308596_1 endoribonuclease/protein kinase IRE1-like protein [Arabidopsis thaliana] >gi|15277139|dbj|BAB63367.1| Ire1 homolog-2 [Arabidopsis thaliana]	Unigene46182_All//1.00E-176//AT2G17520| IRE1A; endoribonuclease/ kinase	Unigene46182_All//0.00E+00//DW226604		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene46185_All	357	3.22	9.94	3.28	5.02	10.13	8.22	17.41	9.83	9.49	1.62E+00	4.26E-06	Up	2.54E-02	9.87E-01		1.01E+00	1.28E-03		7.11E-01	5.57E-02		-8.24E-01	9.68E-05		-8.76E-01	2.27E-05		Unigene46185_All//gi|22329097|ref|NP_194968.2|//5.00E-51//peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis thaliana]	Unigene46185_All//2.00E-52//AT4G32420| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	Unigene46185_All//7.00E-160//gi|78334264|gb|DT554538.1|DT554538				nr +
Unigene46187_All	1843	7.35	11.30	13.23	24.35	27.06	28.99	11.31	23.86	18.29	6.20E-01	2.72E-07		8.48E-01	2.20E-13		1.52E-01	5.46E-02		2.51E-01	4.89E-04		1.08E+00	3.47E-44	Up	6.93E-01	5.29E-17		Unigene46187_All//gi|297836406|ref|XP_002886085.1|//4.00E-53//Ar2g16900/F12A24.8 [Arabidopsis lyrata subsp. lyrata] >gi|297331925|gb|EFH62344.1|At2g16900/F12A24.8 [Arabidopsis lyrata subsp. lyrata]	Unigene46187_All//2.00E-48//AT2G16900| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Phospholipase-like, arabidopsis (InterPro:IPR007942); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G35110.4); Has 353 Blast hits to 254 proteins in 60 species: Archae - 2; Bacteria - 4; Metazoa - 73; Fungi - 16; Plants - 115; Viruses - 51; Other Eukaryotes - 92 (source: NCBI BLink).	Unigene46187_All//0.00E+00//gi|48811754|gb|CO113067.1|CO113067		ko03040|Spliceosome		nr +
Unigene46188_All	1885	0.92	1.99	2.06	2.48	3.38	4.15	2.38	5.37	4.08	1.12E+00	5.36E-04	Up	1.17E+00	3.77E-04	Up	4.44E-01	5.90E-02		7.39E-01	3.16E-04		1.17E+00	2.82E-12	Up	7.79E-01	2.17E-05		Unigene46188_All//gi|297836406|ref|XP_002886085.1|//3.00E-56//Ar2g16900/F12A24.8 [Arabidopsis lyrata subsp. lyrata] >gi|297331925|gb|EFH62344.1|At2g16900/F12A24.8 [Arabidopsis lyrata subsp. lyrata]	Unigene46188_All//4.00E-52//AT2G16900| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Phospholipase-like, arabidopsis (InterPro:IPR007942); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G35110.4); Has 353 Blast hits to 254 proteins in 60 species: Archae - 2; Bacteria - 4; Metazoa - 73; Fungi - 16; Plants - 115; Viruses - 51; Other Eukaryotes - 92 (source: NCBI BLink).	Unigene46188_All//0.00E+00//TC151175		ko03040|Spliceosome		nr +
Unigene46190_All	2188	15.02	8.36	8.64	5.83	4.22	4.11	13.06	4.18	3.75	-8.45E-01	1.93E-18		-7.98E-01	4.44E-16		-4.67E-01	1.72E-03		-5.05E-01	1.17E-03		-1.64E+00	7.41E-55	Down	-1.80E+00	3.42E-64	Down	Unigene46190_All//gi|22121982|gb|AAM89397.1|//0.00E+00//glutamate/malate translocator [Nicotiana tabacum]	Unigene46190_All//0.00E+00//AT5G64290| DIT2.1 (DICARBOXYLATE TRANSPORT 2.1); oxoglutarate:malate antiporter	Unigene46190_All//0.00E+00//TC134576				nr -
Unigene46191_All	2556	26.65	17.17	22.13	26.10	28.17	20.60	29.94	13.20	12.41	-6.35E-01	5.46E-23		-2.69E-01	4.67E-05		1.10E-01	1.01E-01		-3.41E-01	3.80E-08		-1.18E+00	1.13E-88	Down	-1.27E+00	3.51E-102	Down	Unigene46191_All//gi|2829868|gb|AAC00576.1|//1.00E-71//Unknown protein [Arabidopsis thaliana]	Unigene46191_All//5.00E-60//AT1G24160| unknown protein	Unigene46191_All//0.00E+00//TC147006				nr +
Unigene46192_All	2015	12.49	5.05	6.08	6.33	4.97	7.17	1.87	1.45	2.14	-1.31E+00	2.66E-28	Down	-1.04E+00	4.35E-19	Down	-3.48E-01	2.50E-02		1.81E-01	2.89E-01		-3.63E-01	2.26E-01		1.93E-01	4.89E-01		Unigene46192_All//gi|186494070|ref|NP_177080.2|//0.00E+00//kinase [Arabidopsis thaliana]	Unigene46192_All//7.00E-168//AT1G69200| kinase	Unigene46192_All//2.00E-90//ES847448		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene46195_All	2515	42.11	184.28	82.09	31.93	34.67	55.31	20.29	16.32	12.02	2.13E+00	0.00E+00	Up	9.63E-01	1.39E-135		1.19E-01	4.27E-02		7.93E-01	7.98E-73		-3.14E-01	2.01E-06		-7.55E-01	2.36E-29		Unigene46195_All//gi|18418376|ref|NP_567952.1|//2.00E-74//LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1) [Arabidopsis thaliana]	Unigene46195_All//1.00E-75//AT4G34120| LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1)	Unigene46195_All//0.00E+00//gi|164343236|gb|ES848570.1|ES848570				nr +
Unigene46196_All	214	0.00	0.00	0.25	0.00	0.00	0.63	17.58	5.47	14.89	null	null		7.96E+00	6.35E-01		null	null		9.31E+00	3.11E-01		-1.69E+00	3.80E-08	Down	-2.40E-01	4.08E-01					Unigene46196_All//4.00E-15//TC173675				
Unigene46197_All	713	1.91	2.98	4.11	2.93	1.88	7.35	255.40	130.84	238.31	6.46E-01	1.41E-01		1.11E+00	4.13E-03		-6.40E-01	1.44E-01		1.32E+00	7.40E-07	Up	-9.65E-01	4.18E-151		-1.00E-01	3.95E-03		Unigene46197_All//gi|15811629|gb|AAL09033.1|AF416652_1//3.00E-75//ribonuclease-like PR-10 [Gossypium arboreum]		Unigene46197_All//2.00E-152//TC172987				nr -
Unigene46198_All	753	2.92	6.53	13.93	1.26	1.37	1.98	118.47	43.13	68.04	1.16E+00	3.07E-05	Up	2.26E+00	1.64E-24	Up	1.26E-01	8.71E-01		6.55E-01	2.52E-01		-1.46E+00	1.41E-142	Down	-8.00E-01	6.92E-56		Unigene46198_All//gi|15811629|gb|AAL09033.1|AF416652_1//4.00E-77//ribonuclease-like PR-10 [Gossypium arboreum]		Unigene46198_All//9.00E-152//TC173675				nr +
Unigene46199_All	834	9.35	7.47	14.24	29.86	13.96	19.33	1101.72	785.85	859.92	-3.23E-01	1.34E-01		6.07E-01	3.59E-04		-1.10E+00	3.98E-26	Down	-6.27E-01	3.08E-09		-4.87E-01	3.69E-229		-3.58E-01	1.55E-132		Unigene46199_All//gi|15811629|gb|AAL09033.1|AF416652_1//6.00E-87//ribonuclease-like PR-10 [Gossypium arboreum]	Unigene46199_All//8.00E-07//AT1G24020| MLP423 (MLP-LIKE PROTEIN 423)	Unigene46199_All//0.00E+00//TC172987				nr -
Unigene462_All	938	1.00	1.46	1.53	1.75	2.64	2.02	1.49	2.54	4.33	5.39E-01	3.59E-01		6.10E-01	2.96E-01		5.93E-01	1.55E-01		2.07E-01	7.00E-01		7.72E-01	3.67E-02		1.54E+00	5.48E-08	Up	Unigene462_All//gi|15229748|ref|NP_187751.1|//9.00E-28//MYB65 (MYB DOMAIN PROTEIN 65); DNA binding / transcription factor [Arabidopsis thaliana] >gi|12003234|gb|AAG43496.1|AF048840_1 MYB65 [Arabidopsis thaliana] >gi|41619234|gb|AAS10055.1| MYB transcription factor [Arabidopsis thaliana]	Unigene462_All//2.00E-28//AT3G11440| MYB65 (MYB DOMAIN PROTEIN 65); DNA binding / transcription factor	Unigene462_All//4.00E-108//CO104468	MYB		GO:0009725//GO:0009987//GO:0010468	nr -
Unigene46200_All	3658	1.12	0.72	0.22	2.55	1.39	1.51	4.11	3.18	3.99	-6.31E-01	3.65E-02		-2.35E+00	2.77E-10	Down	-8.70E-01	5.50E-07		-7.58E-01	3.81E-05		-3.73E-01	4.10E-03		-4.58E-02	7.51E-01		Unigene46200_All//gi|115452551|ref|NP_001049876.1|//1.00E-111//0s03g0304400 [Oryza sativa Japonica Group] >gi|108707717|gb|ABF95512.1| BRCA1 C Terminus domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548347|dbj|BAF11790.1|Os03g0304400 [Oryza sativa Japonica Group]	Unigene46200_All//7.00E-103//AT4G02110| transcription coactivator	Unigene46200_All//0.00E+00//gi|109827710|gb|DW226376.1|DW226376				nr -
Unigene46201_All	2033	5.22	3.84	4.90	8.97	7.32	8.44	15.87	17.82	138.33	-4.45E-01	1.16E-02		-9.30E-02	6.21E-01		-2.94E-01	2.18E-02		-8.72E-02	6.06E-01		1.68E-01	4.99E-02		3.12E+00	0.00E+00	Up	Unigene46201_All//gi|18086395|gb|AAL57656.1|//0.00E+00//AT5g13210/T31B5_30 [Arabidopsis thaliana]	Unigene46201_All//0.00E+00//AT5G13210| CONTAINS InterPro DOMAIN/s: Uncharacterized conserved protein UCP015417, vWA (InterPro:IPR011205), von Willebrand factor, type A (InterPro:IPR002035); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G24780.1); Has 250 Blast hits to 233 proteins in 28 species: Archae - 0; Bacteria - 8; Metazoa - 0; Fungi - 23; Plants - 45; Viruses - 15; Other Eukaryotes - 159 (source: NCBI BLink).	Unigene46201_All//0.00E+00//TC132948				nr -
Unigene46202_All	654	3.20	10.54	4.15	5.18	6.32	4.14	6.08	10.23	8.41	1.72E+00	5.31E-12	Up	3.76E-01	3.69E-01		2.87E-01	3.94E-01		-3.22E-01	3.93E-01		7.51E-01	2.08E-04		4.68E-01	3.50E-02		Unigene46202_All//gi|224066961|ref|XP_002302300.1|//9.00E-07//predicted protein [Populus trichocarpa] >gi|222844026|gb|EEE81573.1|predicted protein [Populus trichocarpa]		Unigene46202_All//2.00E-167//ES842962				nr +
Unigene46205_All	2800	4.84	3.58	3.82	8.18	7.54	9.66	8.68	5.15	4.30	-4.34E-01	4.70E-03		-3.40E-01	3.76E-02		-1.18E-01	3.78E-01		2.40E-01	2.82E-02		-7.54E-01	5.61E-14		-1.01E+00	2.72E-23	Down	Unigene46205_All//gi|38345802|emb|CAE03574.2|//0.00E+00//OSJNBa0085I10.19 [Oryza sativa (japonica cultivar-group)] >gi|38568013|emb|CAE05198.3|OSJNBa0070C17.5 [Oryza sativa (japonica cultivar-group)]	Unigene46205_All//0.00E+00//AT4G19610| RNA binding / nucleic acid binding / nucleotide binding	Unigene46205_All//0.00E+00//AI725650				nr +
Unigene46210_All	3260	0.45	0.64	0.67	0.66	1.32	1.15	1.57	0.38	2.13	5.04E-01	2.63E-01		5.76E-01	2.13E-01		1.01E+00	3.64E-04	Up	8.07E-01	1.10E-02		-2.03E+00	1.14E-13	Down	4.38E-01	2.45E-02		Unigene46210_All//gi|212717123|gb|ACJ37403.1|//0.00E+00//CC-NBS-LRR class disease resistance protein [Glycine max]	Unigene46210_All//3.00E-168//AT1G50180| disease resistance protein (CC-NBS-LRR class), putative	Unigene46210_All//0.00E+00//gi|11210015|gb|BF278945.1|BF278945		ko04626|Plant-pathogen interaction		nr -
Unigene46211_All	2985	7.48	15.62	8.22	13.78	15.14	15.51	12.71	23.85	15.01	1.06E+00	2.51E-37	Up	1.36E-01	2.89E-01		1.35E-01	1.17E-01		1.70E-01	4.13E-02		9.08E-01	8.83E-54		2.41E-01	6.17E-04		Unigene46211_All//gi|42565106|ref|NP_188849.3|//3.00E-77//phototropic-responsive NPH3 protein-related [Arabidopsis thaliana]	Unigene46211_All//7.00E-71//AT3G22104| phototropic-responsive NPH3 protein-related	Unigene46211_All//0.00E+00//CO072895				nr -

Unigene46215_All	1532	23.36	19.12	19.26	30.53	26.70	17.86	22.00	19.51	6.87	-2.89E-01	1.44E-03		-2.79E-01	3.30E-03		-1.93E-01	1.25E-02		-7.73E-01	5.12E-24		-1.73E-01	5.12E-02		-1.68E+00	1.31E-68	Down	Unigene46215_All//gi|13605601|gb|AK32794.1|AF361626_1/1.00E-50//At1g54460/F20D21_28 [Arabidopsis thaliana] >gi|15777865|gb|AAL05893.1| At1g54460/F20D21_28 [Arabidopsis thaliana]	Unigene46215_All//2.00E-46//AT1G54460| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: WDL1 (TAIR:AT3G04630.3); Has 393 Blast hits to 375 proteins in 76 species: Archae - 0; Bacteria - 3; Metazoa - 143; Fungi - 38; Plants - 160; Viruses - 0; Other Eukaryotes - 49 (source: NCBI BLink).	Unigene46215_All//0.00E+00//TC139120				nr -
Unigene46217_All	2472	16.49	4.84	4.65	11.08	10.03	5.77	20.75	17.79	12.12	-1.77E+00	8.87E-71	Down	-1.83E+00	2.57E-71	Down	-1.44E-01	2.13E-01		-9.41E-01	9.02E-20		-2.22E-01	9.91E-04		-7.76E-01	7.42E-31		Unigene46217_All//gi|53828635|gb|AY94427.1|/5.00E-97//At1g58110 [Arabidopsis thaliana]	Unigene46217_All//9.00E-80//AT1G58110| bZIP family transcription factor	Unigene46217_All//0.00E+00//TC136690				nr -
Unigene4622_All	1307	16.69	11.98	10.47	21.57	15.52	23.26	28.18	12.86	13.84	-4.79E-01	4.33E-05		-6.73E-01	2.84E-08		-4.75E-01	3.71E-07		1.08E-01	3.64E-01		-1.13E+00	2.94E-40	Down	-1.03E+00	2.01E-35	Down	Unigene4622_All//gi|13631844|sp|P92792.1|TOM20_SOLTU//1.00E-71//RecName: Full=Mitochondrial import receptor subunit TOM20; AltName: Full=Translocase of outer membrane 20 kDa subunit >gi|1524370|emb|CAA63223.1| TOM20 [Solanum tuberosum]	Unigene4622_All//2.00E-54//AT1G27390| TOM20-2 (TRANSLOCASE OUTER MEMBRANE 20-2); P-P-bond-hydrolysis-driven protein transmembrane transporter/ metal ion binding	Unigene4622_All//0.00E+00//TC138108				nr -
Unigene46222_All	414	1.64	3.18	0.77	2.77	1.25	0.65	5.21	2.12	1.64	9.54E-01	1.06E-01		-1.09E+00	2.39E-01		-1.15E+00	6.01E-02		-2.08E+00	2.95E-03		-1.30E+00	1.18E-03		-1.67E+00	3.80E-05	Down			Unigene46222_All//1.00E-78//TC146894				
Unigene46224_All	1118	2.76	0.45	0.67	11.09	6.62	38.90	7.03	81.12	13.93	-2.61E+00	2.67E-09	Down	-2.05E+00	8.87E-07	Down	-7.45E-01	4.36E-07		1.81E+00	4.82E-83	Up	3.53E+00	0.00E+00	Up	9.86E-01	1.78E-14		Unigene46224_All//gi|297830862|ref|XP_002883313.1|//1.00E-103//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329153|gb|EFH59572.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46224_All//3.00E-100//AT3G21690| MATE efflux family protein	Unigene46224_All//0.00E+00//TC150630				nr -
Unigene46225_All	1888	1.39	0.70	1.10	7.70	3.39	20.57	5.60	43.10	9.64	-9.90E-01	1.16E-02		-3.33E-01	4.12E-01		-1.18E+00	2.22E-17	Down	1.42E+00	2.78E-52	Up	2.94E+00	0.00E+00	Up	7.85E-01	1.10E-11		Unigene46225_All//gi|297830862|ref|XP_002883313.1|//0.00E+00//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329153|gb|EFH59572.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46225_All//0.00E+00//AT3G21690| MATE efflux family protein	Unigene46225_All//0.00E+00//CO113031				nr +
Unigene46227_All	3148	1.86	1.58	1.35	24.75	21.35	15.15	10.18	5.30	3.29	-2.39E-01	3.72E-01		-4.60E-01	7.85E-02		-2.13E-01	1.46E-04		-7.08E-01	4.59E-34		-9.42E-01	3.23E-26		-1.63E+00	1.55E-62	Down	Unigene46227_All//gi|15227816|ref|NP_179917.1|//3.00E-34//transport protein-related [Arabidopsis thaliana] >gi|75206690|sp|Q9SLN1.1|FPP7_ARATH RecName: Full=Filament-like plant protein 7; Short=AtFPP7	Unigene46227_All//2.00E-31//AT2G23360| transport protein-related	Unigene46227_All//1.00E-135//gi|164244179|gb|ES832918.1|ES832918				nr -
Unigene46230_All	1605	1.27	5.30	2.46	5.49	4.48	3.52	4.06	4.09	2.36	2.06E+00	1.70E-18	Up	9.50E-01	3.21E-03		-2.93E-01	1.47E-01		-6.43E-01	7.33E-04		1.12E-02	9.95E-01		-7.83E-01	9.24E-05		Unigene46230_All//gi|297838467|ref|XP_002887115.1|//1.00E-143//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332956|gb|EFH63374.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46230_All//4.00E-135//AT1G67340| zinc finger (MYND type) family protein / F-box family protein	Unigene46230_All//0.00E+00//TC152629				nr +
Unigene46231_All	1058	0.45	0.53	1.56	1.60	2.38	5.29	14.19	14.38	31.78	2.43E-01	7.77E-01		1.81E+00	1.76E-03		5.70E-01	1.65E-01		1.73E+00	1.98E-10	Up	1.95E-02	9.10E-01		1.16E+00	2.86E-39	Up	Unigene46231_All//gi|229609885|gb|ACQ83558.1|//3.00E-46//calcineurin B-like protein 04 [Vitis vinifera]	Unigene46231_All//9.00E-43//AT5G24270| SOS3 (SALT OVERLY SENSITIVE 3); calcium ion binding / calcium-dependent protein serine/threonine phosphatase	Unigene46231_All//0.00E+00//TC158548		ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene46232_All	1323	0.75	0.61	0.52	3.01	4.35	6.93	23.33	30.45	61.91	-2.94E-01	6.37E-01		-5.22E-01	4.60E-01		5.29E-01	3.08E-02		1.20E+00	5.11E-10	Up	3.85E-01	2.82E-07		1.41E+00	1.09E-126	Up	Unigene46232_All//gi|133925821|gb|AB043663.1|//2.00E-93//calcineurin B-like protein 4-1 [Populus trichocarpa]	Unigene46232_All//6.00E-85//AT5G24270| SOS3 (SALT OVERLY SENSITIVE 3); calcium ion binding / calcium-dependent protein serine/threonine phosphatase	Unigene46232_All//0.00E+00//TC158548		ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene46236_All	1107	4.68	7.23	5.58	5.08	7.50	12.24	10.47	27.60	52.33	6.28E-01	2.19E-03		2.54E-01	3.43E-01		5.60E-01	3.84E-03		1.27E+00	9.83E-16	Up	1.40E+00	2.66E-46	Up	2.32E+00	1.80E-177	Up	Unigene46236_All//gi|195650981|gb|ACG44958.1|//1.00E-133//iron ion binding protein [Zea mays]	Unigene46236_All//1.00E-132//AT1G35190| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene46236_All//0.00E+00//gi|164283105|gb|ES818763.1|ES818763				nr +
Unigene46237_All	1475	1.92	3.61	2.45	1.72	3.34	4.04	5.05	16.21	33.65	9.13E-01	4.65E-04		3.58E-01	3.07E-01		9.55E-01	2.42E-04		1.23E+00	5.84E-07	Up	1.68E+00	1.56E-47	Up	2.74E+00	1.27E-183	Up	Unigene46237_All//gi|195650981|gb|ACG44958.1|//1.00E-148//iron ion binding protein [Zea mays]	Unigene46237_All//6.00E-150//AT1G35190| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene46237_All//0.00E+00//TC160727				nr -
Unigene46238_All	1462	18.93	20.79	60.83	29.95	17.97	28.48	166.08	20.24	40.77	1.35E-01	2.14E-01		1.68E+00	2.83E-139	Up	-7.37E-01	2.49E-23		-7.25E-02	4.80E-01		-3.04E+00	0.00E+00	Down	-2.03E+00	0.00E+00	Down	Unigene46238_All//gi|153805696|gb|ABS52573.1|//0.00E+00//chalcone synthase [Gossypium hirsutum]	Unigene46238_All//0.00E+00//AT5G13930| TT4 (TRANSPARENT TESTA 4); naringenin-chalcone synthase	Unigene46238_All//0.00E+00//TC139851		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr +
Unigene46240_All	1914	15.03	35.02	19.75	50.62	59.66	89.19	23.44	79.49	62.65	1.22E+00	1.34E-66	Up	3.94E-01	1.13E-05		2.37E-01	1.19E-07		8.17E-01	4.61E-94		1.76E+00	0.00E+00	Up	1.42E+00	3.25E-187	Up	Unigene46240_All//gi|15229809|ref|NP_188316.1|//0.00E+00//AAE7 (ACYL-ACTIVATING ENZYME 7); AMP binding / acetate-CoA ligase [Arabidopsis thaliana] >gi|20799723|gb|AAM28624.1|AF503766_1 adenosine monophosphate binding protein 7 AMPBP7 [Arabidopsis thaliana] >gi|18086379|gb|AAL57649.1| AT3g16910/K14A17_3 [Arabidopsis thaliana] >gi|19699128|gb|AAL90930.1| AT3g16910/K14A17_3 [Arabidopsis thaliana]	Unigene46240_All//0.00E+00//AT3G16910| AAE7 (ACYL-ACTIVATING ENZYME 7); AMP binding / acetate-CoA ligase	Unigene46240_All//0.00E+00//TC144868		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene46242_All	1433	30.05	258.97	39.50	79.40	194.91	180.91	74.74	96.60	135.92	3.11E+00	0.00E+00	Up	3.95E-01	3.69E-08		1.30E+00	0.00E+00	Up	1.19E+00	1.75E-264	Up	3.70E-01	1.83E-21		8.63E-01	8.72E-137		Unigene46242_All//gi|194475604|gb|ACF74549.1|//1.00E-112//RAV [Nicotiana tabacum]	Unigene46242_All//1.00E-98//AT1G13260| RAV1; DNA binding / transcription factor/ transcription repressor	Unigene46242_All//0.00E+00//TC151984	AP2-EREBP			nr +
Unigene46243_All	658	3.02	3.23	1.78	2.12	3.24	3.02	6.10	18.36	31.85	9.81E-02	8.17E-01		-7.63E-01	1.14E-01		6.14E-01	1.75E-01		5.11E-01	3.03E-01		1.59E+00	1.70E-22	Up	2.38E+00	1.16E-66	Up	Unigene46243_All//gi|151934217|gb|ABS18446.1|//9.00E-41//WRKY50 [Glycine max]	Unigene46243_All//2.00E-39//AT4G31550| WRKY11; calmodulin binding / transcription factor	Unigene46243_All//1.00E-159//TC162370	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene46244_All	1596	3.84	9.78	4.17	7.02	14.91	9.88	9.59	21.68	51.90	1.35E+00	1.18E-18	Up	1.21E-01	6.12E-01		1.09E+00	1.98E-23	Up	4.92E-01	3.75E-04		1.18E+00	3.36E-40	Up	2.44E+00	2.24E-268	Up	Unigene46244_All//gi|259121413|gb|ACV92026.1|//1.00E-108//WRKY transcription factor 24 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene46244_All//0.00E+00//AT2G24570| WRKY17; calmodulin binding / transcription factor	Unigene46244_All//0.00E+00//gi|78353572|gb|DT573846.1|DT573846	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene4625_All	552	9.00	4.22	9.26	16.88	20.52	17.59	15.01	16.43	12.20	-1.09E+00	6.73E-05	Down	4.05E-02	8.91E-01		2.82E-01	1.10E-01		5.99E-02	7.79E-01		1.30E-01	5.26E-01		-3.00E-01	9.84E-02				Unigene4625_All//1.00E-131//TC152460				
Unigene46253_All	2746	9.79	17.97	11.21	16.87	21.14	19.64	39.08	94.25	27.33	8.76E-01	6.91E-29		1.95E-01	7.13E-02		3.26E-01	3.85E-07		2.19E-01	2.69E-03		1.27E+00	0.00E+00	Up	-5.16E-01	3.34E-31		Unigene46253_All//gi|115477128|ref|NP_001062160.1|//1.00E-177//Os08g0500800 [Oryza sativa Japonica Group] >gi|42407752|dbj|BAD08898.1| zinc metalloproteinase-like [Oryza sativa Japonica Group] >gi|113624129|dbj|BAF24074.1| Os08g0500800 [Oryza sativa Japonica Group]	Unigene46253_All//3.00E-168//AT5G35690| LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: WLM (InterPro:IPR013536), PUG (InterPro:IPR006567); BEST Arabidopsis thaliana protein match is: zinc ion binding (TAIR:AT1G55915.1); Has 335 Blast hits to 326 proteins in 115 species: Archae - 0; Bacteria - 24; Metazoa - 37; Fungi - 138; Plants - 58; Viruses - 2; Other Eukaryotes - 76 (source: NCBI BLink).	Unigene46253_All//0.00E+00//TC177549				nr -
Unigene46258_All	2149	8.67	8.94	6.89	11.20	13.12	19.19	8.68	13.32	18.15	4.40E-02	7.47E-01		-3.31E-01	1.49E-02		2.29E-01	2.72E-02		7.77E-01	3.13E-21		6.19E-01	9.21E-12		1.06E+00	1.77E-39	Up	Unigene46258_All//gi|225438229|ref|XP_002264391.1|//0.00E+00//PREDICTED: similar to GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein [Vitis vinifera]	Unigene46258_All//0.00E+00//AT4G37670| GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein	Unigene46258_All//0.00E+00//ES822546		ko00330|Arginine and proline metabolism		nr +
Unigene46259_All	1799	30.54	8.03	15.42	151.55	147.29	92.76	32.32	30.41	15.75	-1.93E+00	5.42E-107	Down	-9.86E-01	1.11E-37		-4.11E-02	2.68E-01		-7.08E-01	4.55E-118		-8.76E-02	2.28E-01		-1.04E+00	2.08E-56	Down	Unigene46259_All//gi|297822685|ref|XP_002879225.1|//1.00E-108//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325064|gb|EFH55484.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46259_All//6.00E-101//AT2G29660| zinc finger (C2H2 type) family protein	Unigene46259_All//0.00E+00//TC132533	C2H2			nr +
Unigene46261_All	2297	12.14	11.63	12.05	13.32	14.66	28.23	15.96	26.29	37.69	-6.26E-02	6.23E-01		-1.02E-02	9.48E-01		1.39E-01	1.76E-01		1.08E+00	2.01E-57	Up	7.20E-01	5.42E-31		1.24E+00	3.55E-110	Up	Unigene46261_All//gi|212717149|gb|ACJ37416.1|//1.00E-150//stress-induced receptor-like kinase [Glycine max]	Unigene46261_All//2.00E-90//AT5G38280| PR5K; kinase/ transmembrane receptor protein serine/threonine kinase	Unigene46261_All//0.00E+00//TC151650		ko04626|Plant-pathogen interaction		nr +
Unigene46266_All	2868	2.70	2.40	3.40	10.33	7.85	5.83	3.72	0.57	3.04	-1.68E-01	4.53E-01		3.32E-01	9.42E-02		-3.96E-01	1.64E-05		-8.27E-01	3.01E-17		-2.71E+00	7.43E-39	Down	-2.88E-01	6.56E-02		Unigene46266_All//gi|115480511|ref|NP_001063849.1|//1.00E-117//Os09g0547300 [Oryza sativa Japonica Group] >gi|113632082|dbj|BAF25763.1| Os09g0547300 [Oryza sativa Japonica Group]	Unigene46266_All//4.00E-170//AT4G35240| unknown protein	Unigene46266_All//0.00E+00//TC177695		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene4627_All	1238	1.35	4.13	8.22	17.02	12.04	7.15	2.12	0.81	0.23	1.61E+00	2.23E-08	Up	2.60E+00	4.54E-28	Up	-4.99E-01	5.89E-06		-1.25E+00	4.73E-24	Down	-1.39E+00	1.23E-04	Down	-3.23E+00	2.64E-12	Down	Unigene4627_All//gi|166418779|gb|AAL25580.1|//6.00E-47//At1g69160/F4N2_9 [Arabidopsis thaliana]	Unigene4627_All//1.00E-26//AT1G69160| unknown protein	Unigene4627_All//3.00E-85//TC132810				nr -
Unigene46272_All	2926	5.61	2.63	3.82	9.02	7.93	9.76	15.94	7.39	8.28	-1.09E+00	2.48E-14	Down	-5.55E-01	9.18E-05		-1.86E-01	9.46E-02		1.13E-01	3.60E-01		-1.11E+00	3.41E-49	Down	-9.45E-01	4.70E-39		Unigene46272_All//gi|30681697|ref|NP_850024.1|//0.00E+00//NOL1/NOP2/sun family protein [Arabidopsis thaliana]	Unigene46272_All//0.00E+00//AT2G22400| NOL1/NOP2/sun family protein	Unigene46272_All//0.00E+00//TC161552		ko00350|Tyrosine metabolism//ko00450|Selenoamino acid metabolism//ko00340|Histidine metabolism		nr +
Unigene46275_All	2288	15.80	43.25	27.35	10.06	25.19	19.09	9.33	27.77	27.23	1.45E+00	5.35E-128	Up	7.91E-01	9.33E-30		1.32E+00	6.62E-77	Up	9.24E-01	5.87E-30		1.57E+00	1.62E-113	Up	1.55E+00	9.78E-111	Up	Unigene46275_All//gi|62286587|sp|Q64894.1|ACOX2_CUCMA//0.00E+00//RecName: Full=Acyl-coenzyme A oxidase, peroxisomal; Short=AOX; AltName: Full=Long-chain acyl-CoA oxidase; Flags: Precursor >gi|7431668|pir||T07901 acyl CoA oxidase homolog - cucurbit >gi|3115374|gb|AAC15870.1| acyl CoA oxidase homolog [Cucurbita cv. Kurokawa Amakuri]	Unigene46275_All//0.00E+00//AT5G65110| ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase	Unigene46275_All//0.00E+00//TC152865		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr +

Unigene46276_All	2199	5.16	5.60	3.75	48.46	35.69	23.37	19.25	7.49	7.03	1.17E-01	5.21E-01			-4.60E-01	9.23E-03		-4.41E-01	2.00E-22		-1.05E+00	1.26E-90	Down	-1.36E+00	2.08E-61	Down	-1.45E+00	1.16E-69	Down	Unigene46276_All//gi|15232012|ref|NP_187519.1|//1.00E-133//glycine-rich protein [Arabidopsis thaliana] >gi|75207465|sp|Q9SS80.1|US03A_ARATH RecName: Full=UPF0503 protein At3g09070, chloroplastic; Flags: Precursor	Unigene46276_All//7.00E-92//AT3G09070| glycine-rich protein	Unigene46276_All//0.00E+00//TC148966				nr -
Unigene46279_All	1123	4.52	5.14	5.03	5.86	5.21	4.67	9.15	4.47	4.43	1.87E-01	4.83E-01			1.53E-01	6.01E-01		-1.68E-01	5.37E-01		-3.28E-01	1.85E-01		-1.03E+00	2.56E-10	Down	-1.04E+00	8.00E-11	Down	Unigene46279_All//gi|30686755|ref|NP_850263.1|//1.00E-143//kelch repeat-containing protein [Arabidopsis thaliana] >gi|79324451|ref|NP_001031493.1| kelch repeat-containing protein [Arabidopsis thaliana] >gi|222423480|dbj|BAH19710.1| AT2G36360 [Arabidopsis thaliana]	Unigene46279_All//9.00E-131//AT2G36360| kelch repeat-containing protein	Unigene46279_All//0.00E+00//gi|78326389|gb|DT546663.1|DT546663		ko04712|Circadian rhythm - plant		nr -
Unigene4628_All	887	2.24	5.48	5.28	2.98	12.66	8.30	7.25	3.30	3.64	1.29E+00	5.63E-06	Up	1.24E+00	3.26E-05	Up	2.09E+00	2.62E-28	Up	1.48E+00	5.62E-11	Up	-1.14E+00	1.02E-07	Down	-9.94E-01	1.30E-06		Unigene4628_All//gi|224095810|ref|XP_002310488.1|//4.00E-52//MIKC mads-box transcription factor [Populus trichocarpa] >gi|222853391|gb|EEE90938.1| MIKC mads-box transcription factor [Populus trichocarpa]	Unigene4628_All//3.00E-42//AT2G22540| SVP (SHORT VEGETATIVE PHASE); transcription factor/ translation repressor, nucleic acid binding	Unigene4628_All//5.00E-27//TC143124	MADS			nr +
Unigene46280_All	1989	1.42	2.47	1.55	2.78	2.16	1.39	5.14	3.13	2.64	7.99E-01	3.27E-03		1.29E-01	7.17E-01		-3.61E-01	1.63E-01		-1.01E+00	5.86E-05	Down	-7.16E-01	6.89E-06		-9.60E-01	1.70E-09		Unigene46280_All//gi|297827115|ref|XP_002881440.1|//0.00E+00//kelch repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327279|gb|EFH57699.1| kelch repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46280_All//0.00E+00//AT2G36360| kelch repeat-containing protein	Unigene46280_All//0.00E+00//gi|78326389|gb|DT546663.1|DT546663		ko04712|Circadian rhythm - plant		nr -
Unigene46281_All	1973	3.63	5.55	3.62	8.48	13.32	7.46	11.49	38.55	24.45	6.11E-01	3.82E-04		-6.50E-03	1.00E+00		6.51E-01	4.12E-11		-1.85E-01	2.28E-01		1.75E+00	1.17E-157	Up	1.09E+00	1.75E-50	Up	Unigene46281_All//gi|297827895|ref|XP_002881830.1|//3.00E-78//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327669|gb|EFH58089.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46281_All//1.00E-79//AT2G42280| basic helix-loop-helix (bHLH0 family protein	Unigene46281_All//0.00E+00//DT464872	bHLH	ko04712|Circadian rhythm - plant		nr +
Unigene46282_All	1610	0.71	1.45	1.29	2.54	2.44	0.84	3.20	9.45	5.82	1.02E+00	1.57E-02		8.51E-01	6.95E-02		-5.73E-02	8.53E-01		-1.59E+00	3.89E-07	Down	1.56E+00	1.95E-27	Up	8.60E-01	2.21E-07		Unigene46282_All//gi|297827895|ref|XP_002881830.1|//2.00E-82//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327669|gb|EFH58089.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46282_All//1.00E-83//AT2G42280| basic helix-loop-helix (bHLH0 family protein	Unigene46282_All//3.00E-175//DT464872	bHLH	ko04712|Circadian rhythm - plant		nr -
Unigene46283_All	2401	16.63	7.20	9.40	25.79	22.65	13.43	30.61	17.93	6.79	-1.21E+00	1.67E-39	Down	-8.22E-01	2.05E-20		-1.88E-01	4.31E-03		-9.41E-01	5.05E-44		-7.71E-01	3.17E-42		-2.17E+00	3.32E-210	Down	Unigene46283_All//gi|22327934|ref|NP_200617.2|//0.00E+00//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|38257732|sp|Q93208.2|E136_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 6; AltName: Full=(1->3)-beta-glucan endohydrolase 6; Short=(1->3)-beta-glucanase 6; AltName: Full=Beta-1,3-endoglucanase 6; Short=Beta-1,3-glucanase 6; Flags: Precursor >gi|9759535|dbj|BAB11001.1| glucanase; glucan endo-1,3-beta-glucosidase [Arabidopsis thaliana]	Unigene46283_All//0.00E+00//AT5G58090| glycosyl hydrolase family 17 protein	Unigene46283_All//0.00E+00//TC135805		ko00500|Starch and sucrose metabolism		nr +
Unigene46284_All	1135	10.65	12.68	9.85	8.65	9.68	10.58	11.77	10.50	5.62	2.52E-01	1.05E-01		-1.12E-01	5.65E-01		1.63E-01	4.19E-01		2.92E-01	9.31E-02		-1.66E-01	2.89E-01		-1.07E+00	2.86E-14	Down	Unigene46284_All//gi|15240586|ref|NP_198696.1|//2.00E-20//embryogenesis-associated protein-related [Arabidopsis thaliana]	Unigene46284_All//8.00E-22//AT5G49950| embryogenesis-associated protein-related	Unigene46284_All//0.00E+00//TC172098				nr +
Unigene46286_All	2161	12.30	7.88	5.57	13.90	12.54	13.50	14.46	12.15	9.75	-6.43E-01	1.19E-09		-1.14E+00	2.11E-23	Down	-1.49E-01	1.65E-01		-4.20E-02	7.19E-01		-2.51E-01	4.49E-03		-5.68E-01	1.99E-11		Unigene46286_All//gi|297850394|ref|XP_002893078.1|//0.00E+00//regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338920|gb|EFH69337.1| regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46286_All//0.00E+00//AT1G19880| regulator of chromosome condensation (RCC1) family protein	Unigene46286_All//0.00E+00//gi|78351950|gb|DT572224.1|DT572224		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene46287_All	1952	1.13	3.30	3.33	3.98	4.55	4.37	5.05	4.75	6.71	1.55E+00	8.14E-10	Up	1.56E+00	1.27E-09	Up	1.93E-01	3.86E-01		1.35E-01	5.80E-01		-8.64E-02	6.34E-01		4.12E-01	2.44E-03		Unigene46287_All//gi|297832096|ref|XP_002883930.1|//1.00E-173//phox domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329770|gb|EFH60189.1| phox domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46287_All//1.00E-146//AT2G15900| phox (PX) domain-containing protein	Unigene46287_All//0.00E+00//TC175189				nr -
Unigene46288_All	1350	33.52	48.19	14.12	29.93	67.44	46.27	63.67	80.59	172.16	5.24E-01	9.29E-16		-1.25E+00	2.67E-45	Down	1.17E+00	1.47E-100	Up	6.29E-01	3.76E-22		3.40E-01	1.19E-14		1.44E+00	0.00E+00	Up	Unigene46288_All//gi|124359681|gb|ABD32347.2|//5.00E-79//Uncharacterized Cys-rich domain [Medicago truncatula]	Unigene46288_All//6.00E-79//AT1G11380| unknown protein	Unigene46288_All//0.00E+00//TC141610				nr -
Unigene46289_All	2765	2.12	1.41	1.52	6.43	3.92	6.75	6.04	2.66	4.26	-5.87E-01	1.65E-02		-4.78E-01	6.55E-02		-7.13E-01	3.10E-09		6.88E-02	6.70E-01		-1.18E+00	5.35E-20	Down	-5.02E-01	2.13E-05		Unigene46289_All//gi|75333533|sp|Q9CSS9.1|RH48_ARATH//0.00E+00//RecName: Full=Probable DEAD-box ATP-dependent RNA helicase 48	Unigene46289_All//0.00E+00//AT1G63250| DEAD box RNA helicase, putative	Unigene46289_All//0.00E+00//gi|78332680|gb|DT552954.1|DT552954				nr +
Unigene4629_All	1349	0.62	2.37	1.93	1.07	3.24	2.48	3.10	1.61	2.04	1.93E+00	7.71E-07	Up	1.64E+00	1.60E-04	Up	1.60E+00	5.75E-08	Up	1.21E+00	4.20E-04	Up	-9.46E-01	3.80E-04		-6.07E-01	1.77E-02		Unigene4629_All//gi|224095810|ref|XP_002310488.1|//2.00E-57//MIKC mads-box transcription factor [Populus trichocarpa] >gi|222853391|gb|EEE90938.1| MIKC mads-box transcription factor [Populus trichocarpa]	Unigene4629_All//1.00E-47//AT2G22540| SVP (SHORT VEGETATIVE PHASE); transcription factor/ translation repressor, nucleic acid binding	Unigene4629_All//8.00E-27//TC143124	MADS			nr -
Unigene46291_All	946	2.65	4.77	2.48	6.58	3.49	6.59	9.92	19.93	11.62	8.45E-01	3.11E-03		-1.00E-01	8.04E-01		-9.14E-01	3.11E-05		1.30E-03	9.98E-01		1.01E+00	1.92E-17	Up	2.28E-01	1.50E-01		Unigene46291_All//gi|15239759|ref|NP_200294.1|//2.00E-57//DOMON domain-containing protein / dopamine beta-monooxygenase N-terminal domain-containing protein [Arabidopsis thaliana] >gi|19699059|gb|AAL90897.1| At5g54830/MDG8_9 [Arabidopsis thaliana] >gi|27363250|gb|AAO11544.1| At5g54830/MDG8_9 [Arabidopsis thaliana]	Unigene46291_All//4.00E-40//AT5G54830| DOMON domain-containing protein / dopamine beta-monooxygenase N-terminal domain-containing protein	Unigene46291_All//8.00E-165//TC175794				nr -
Unigene46293_All	1100	1.81	0.60	0.29	2.13	1.69	1.93	4.11	1.56	2.10	-1.59E+00	1.04E-03		-2.64E+00	6.10E-06	Down	-3.32E-01	4.57E-01		-1.41E-01	7.41E-01		-1.40E+00	1.51E-07	Down	-9.69E-01	9.45E-05		Unigene46293_All//gi|72255611|gb|AA266929.1|//2.00E-40//117M18_10 [Brassica rapa]	Unigene46293_All//3.00E-41//AT5G10110| unknown protein	Unigene46293_All//1.00E-145//TC150880				nr -
Unigene46294_All	1166	3.99	2.13	2.06	7.09	5.76	4.73	6.96	2.37	2.77	-9.07E-01	1.21E-03		-9.59E-01	1.08E-03		-3.00E-01	1.52E-01		-5.86E-01	3.22E-03		-1.56E+00	5.47E-15	Down	-1.33E+00	2.03E-12	Down	Unigene46294_All//gi|72255611|gb|AA266929.1|//6.00E-39//117M18_10 [Brassica rapa]	Unigene46294_All//4.00E-37//AT5G10110| unknown protein	Unigene46294_All//0.00E+00//gi|78341800|gb|DT562074.1|DT562074				nr -
Unigene46296_All	2467	1.59	3.82	1.49	2.36	2.85	4.19	4.71	3.24	8.98	1.26E+00	1.61E-10	Up	-9.48E-02	7.68E-01		2.69E-01	2.70E-01		8.27E-01	2.23E-06		-5.43E-01	2.47E-04		9.30E-01	2.05E-18		Unigene46296_All//gi|186499124|ref|NP_001077875.2|//0.00E+00//asparagine synthase (glutamine-hydrolyzing) [Arabidopsis thaliana]	Unigene46296_All//0.00E+00//AT2G03667| asparagine synthase (glutamine-hydrolyzing)	Unigene46296_All//6.00E-131//gi|73859293|gb|DT462032.1|DT462032				nr +
Unigene46298_All	565	5.00	7.35	4.90	6.52	11.64	9.99	9.58	6.81	4.51	5.56E-01	6.43E-02		-2.91E-02	9.57E-01		8.35E-01	1.32E-04		6.15E-01	1.43E-02		-4.93E-01	3.34E-02		-1.09E+00	1.86E-06	Down	Unigene46298_All//gi|184214200|ref|NP_568525.1|//7.00E-44//protein binding [Arabidopsis thaliana]	Unigene46298_All//4.00E-45//AT5G35080| protein binding	Unigene46298_All//0.00E+00//TC147984		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene46299_All	1560	2.82	5.72	3.69	6.90	6.84	6.46	6.29	7.10	5.41	1.02E+00	2.45E-07	Up	3.88E-01	1.44E-01		-1.14E-02	9.63E-01		-9.54E-02	6.46E-01		1.75E-01	3.13E-01		-2.16E-01	2.04E-01		Unigene46299_All//gi|184214200|ref|NP_568525.1|//6.00E-90//protein binding [Arabidopsis thaliana]	Unigene46299_All//3.00E-91//AT5G35080| protein binding	Unigene46299_All//0.00E+00//TC147984		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene4630_All	1668	5.08	3.55	2.36	6.57	6.44	5.23	13.79	6.82	3.46	-5.16E-01	9.59E-03		-1.11E+00	1.66E-07	Down	-2.86E-02	8.84E-01		-3.30E-01	6.59E-02		-1.02E+00	1.72E-21	Down	-1.99E+00	2.27E-59	Down	Unigene4630_All//gi|225423595|ref|XP_002273965.1|//1.00E-130//PREDICTED: similar to Os06g0665100 isoform 2 [Vitis vinifera] >gi|225423597|ref|XP_002273939.1| PREDICTED: similar to Os06g0665100 isoform 1 [Vitis vinifera]	Unigene4630_All//4.00E-121//AT5G44730| haloacid dehalogenase-like hydrolase family protein	Unigene4630_All//0.00E+00//TC146185				nr +
Unigene46300_All	1190	4.18	3.02	0.81	3.22	3.07	2.39	2.66	1.33	1.71	-4.66E-01	8.60E-02		-2.37E+00	1.53E-12	Down	-7.16E-02	8.29E-01		-4.31E-01	1.95E-01		-9.98E-01	1.43E-03		-6.42E-01	3.22E-02		Unigene46300_All//gi|38345778|emb|CAD41819.2|//8.00E-51//OSJNBa0083N12.16 [Oryza sativa (japonica cultivar-group)]	Unigene46300_All//2.00E-21//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene46300_All//0.00E+00//TC158460	GRF			nr +
Unigene46301_All	1074	4.09	4.15	2.33	6.08	4.46	4.29	2.52	1.63	0.96	2.09E-02	9.64E-01		-8.12E-01	7.14E-03		-4.47E-01	4.70E-02		-5.02E-01	3.07E-02		-6.24E-01	7.08E-02		-1.39E+00	5.90E-05	Down	Unigene46301_All//gi|115466038|ref|NP_001056618.1|//3.00E-55//Os06g0116200 [Oryza sativa Japonica Group] >gi|51038839|tpg|DAA05209.1| TPA_exp: growth-regulating factor 5 [Oryza sativa (japonica cultivar-group)] >gi|113594658|dbj|BAF18532.1| Os06g0116200 [Oryza sativa Japonica Group]	Unigene46301_All//4.00E-23//AT2G36400| AtGRF3 (GROWTH-REGULATING FACTOR 3); transcription activator	Unigene46301_All//0.00E+00//gi|78344253|gb|DT564527.1|DT564527	GRF			nr +
Unigene46302_All	591	2.12	8.75	1.80	1.43	2.39	2.29	3.93	3.11	4.52	2.04E+00	2.29E-11	Up	-2.38E-01	6.85E-01		7.37E-01	2.09E-01		6.78E-01	2.65E-01		-3.39E-01	3.94E-01		1.99E-01	5.99E-01		Unigene46302_All//gi|55793838|gb|AAV65493.1|//1.00E-88//calmodulin-binding heat shock protein [Gossypium hirsutum]	Unigene46302_All//4.00E-78//AT3G49050| lipase class 3 family protein / calmodulin-binding heat-shock protein, putative	Unigene46302_All//0.00E+00//TC173452				nr +
Unigene46303_All	2251	2.28	6.96	2.70	2.72	3.04	3.29	3.40	2.41	3.54	1.61E+00	4.31E-24	Up	2.44E-01	3.73E-01		1.61E-01	5.39E-01		2.74E-01	2.46E-01		-4.94E-01	8.89E-03		5.82E-02	7.66E-01		Unigene46303_All//gi|55793838|gb|AAV65493.1|//1.00E-180//calmodulin-binding heat shock protein [Gossypium hirsutum]	Unigene46303_All//2.00E-166//AT4G00500| lipase class 3 family protein / calmodulin-binding heat-shock protein-related	Unigene46303_All//0.00E+00//TC173452				nr -
Unigene46304_All	1915	21.01	20.40	13.32	32.57	19.80	11.41	13.25	8.38	6.01	-4.25E-02	6.49E-01		-6.58E-01	3.91E-14		-7.18E-01	1.27E-31		-1.51E+00	9.33E-94	Down	-6.61E-01	1.02E-11		-1.14E+00	3.98E-29	Down	Unigene46304_All//gi|124360549|gb|ABD33126.2|//8.00E-97//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene46304_All//3.00E-28//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene46304_All//0.00E+00//TC163202				nr +
Unigene46305_All	2028	7.35	2.87	4.57	8.57	8.03	8.71	6.90	3.96	4.40	-1.36E+00	4.69E-18	Down	-6.87E-01	4.61E-06		-9.41E-02	5.62E-01		2.25E-02	9.05E-01		-8.02E-01	2.90E-09		-6.49E-01	6.89E-07		Unigene46305_All//gi|51091163|dbj|BAD35858.1|//1.00E-136//lustrin A-like [Oryza sativa Japonica Group] >gi|51091192|dbj|BAD35885.1| lustrin A-like [Oryza sativa Japonica Group]	Unigene46305_All//4.00E-132//AT5G06700| unknown protein	Unigene46305_All//0.00E+00//C0074046				nr +

Unigene46306_All	1548	15.48	15.09	15.51	170.26	91.38	48.23	29.66	6.05	9.26	-3.69E-02	7.63E-01		3.20E-03	1.00E+00		-8.98E-01	5.38E-196		-1.82E+00	0.00E+00	Down	-2.29E+00	1.49E-136	Down	-1.68E+00	4.14E-93	Down	Unigene46306_All//gi|38046726|gb|AB09168.1|//1.00E-142//alpha-expansin 1 [Populus tremula x Populus tremuloides]	Unigene46306_All//2.00E-134//AT2G39700| ATEXPA4 (ARABIDOPSIS THALIANA EXPANSIN A4)	Unigene46306_All//0.00E+00//TC146043				nr -
Unigene46307_All	357	7.62	2.84	4.18	10.33	5.98	3.80	10.42	23.88	69.97	-1.42E+00	3.45E-04	Down	-8.68E-01	3.01E-02		-7.88E-01	8.91E-03		-1.44E+00	1.01E-05	Down	1.20E+00	9.22E-11	Up	2.75E+00	4.92E-93	Up	Unigene46307_All//gi|121501706|gb|ABM55247.1|//2.00E-21//calmodulin-binding protein [Beta vulgaris]	Unigene46307_All//4.00E-20//AT2G26190| calmodulin-binding family protein	Unigene46307_All//0.00E+00//TC167041				nr +
Unigene46308_All	2164	4.38	1.83	1.33	4.49	3.12	1.23	9.50	20.03	59.96	-1.26E+00	1.40E-10	Down	-1.72E+00	1.30E-15	Down	-5.25E-01	2.41E-03		-1.87E+00	4.55E-20	Down	1.08E+00	1.47E-43	Up	2.66E+00	0.00E+00	Up	Unigene46308_All//gi|79610240|ref|NP_974673.2|//1.00E-156//EDA39 (embryo sac development arrest 39); calmodulin binding [Arabidopsis thaliana]	Unigene46308_All//2.00E-141//AT4G33050| EDA39 (embryo sac development arrest 39); calmodulin binding	Unigene46308_All//0.00E+00//gi|73863570|gb|DT466309.1|DT466309				nr +
Unigene4631_All	1628	1.77	0.56	1.24	11.81	11.40	4.77	2.49	1.44	0.86	-1.66E+00	2.95E-05	Down	-5.08E-01	1.97E-01		-5.10E-02	7.68E-01		-1.31E+00	1.60E-23	Down	-7.94E-01	3.19E-03		-1.54E+00	4.60E-08	Down	Unigene4631_All//gi|297851290|ref|XP_002893526.1|//1.00E-116//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339368|gb|EFH69785.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4631_All//1.00E-102//AT1G28390| protein kinase family protein	Unigene4631_All//0.00E+00//gi|78333286|gb|DT553560.1|DT553560				nr -
Unigene46311_All	1537	9.63	9.40	16.84	14.88	17.25	21.60	2.94	3.05	6.09	-3.61E-02	8.17E-01		8.06E-01	4.95E-13		2.14E-01	5.02E-02		5.38E-01	2.92E-09		4.92E-02	8.63E-01		1.05E+00	6.28E-10	Up	Unigene46311_All//gi|77553760|gb|AB096556.1|//1.00E-116//Sodium Bile acid symporter family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene46311_All//4.00E-62//AT1G78560| bile acid:sodium symporter family protein	Unigene46311_All//0.00E+00//TC146701				nr -
Unigene46313_All	1435	27.45	11.65	28.80	7.08	7.06	3.71	0.44	0.50	0.56	-1.24E+00	2.03E-40	Down	6.88E-02	4.97E-01		-5.40E-03	9.71E-01		-9.31E-01	1.33E-07		1.64E-01	8.24E-01		3.29E-01	6.33E-01		Unigene46313_All//gi|4008008|gb|AAC95352.1|//1.00E-126//receptor-like protein kinase [Arabidopsis thaliana]	Unigene46313_All//2.00E-123//AT1G11410| S-locus protein kinase, putative	Unigene46313_All//3.00E-20//TC179543		ko04626|Plant-pathogen interaction		nr +
Unigene46314_All	2280	0.11	116.32	3.18	6.23	27.29	44.39	2.54	13.24	48.54	9.99E+00	0.00E+00	Up	4.79E+00	2.22E-33	Up	2.13E+00	6.78E-161	Up	2.83E+00	0.00E+00	Up	2.38E+00	8.62E-94	Up	4.26E+00	0.00E+00	Up	Unigene46314_All//gi|38112198|gb|AAR11193.1|//0.00E+00//9-cis-epoxycarotenoid dioxygenase 1 [Vitis vinifera]	Unigene46314_All//0.00E+00//AT3G14440| NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	Unigene46314_All//0.00E+00//TC175846		ko00906|Carotenoid biosynthesis		nr -
Unigene46316_All	3478	1.14	2.07	1.00	3.15	2.78	4.36	8.68	22.58	14.72	8.56E-01	9.60E-05		-2.00E-01	5.63E-01		-1.80E-01	3.48E-01		4.70E-01	9.29E-04		1.38E+00	2.39E-115	Up	7.62E-01	9.74E-30		Unigene46316_All//gi|224057465|ref|XP_002299234.1|//0.00E+00//heavy metal ATPase [Populus trichocarpa] >gi|222846492|gb|EEE84039.1| heavy metal ATPase [Populus trichocarpa]	Unigene46316_All//0.00E+00//AT1G63440| HMA5 (HEAVY METAL ATPASE 5); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	Unigene46316_All//0.00E+00//ES814967				nr -
Unigene46317_All	2083	9.90	11.31	13.04	7.94	8.53	6.42	3.43	1.67	1.87	1.93E-01	1.10E-01		3.98E-01	2.33E-04		1.04E-01	5.36E-01		-3.07E-01	2.93E-02		-1.04E+00	1.68E-07	Down	-8.72E-01	5.30E-06		Unigene46317_All//gi|90341123|gb|ACE74720.1|//0.00E+00//At3g27180 [Arabidopsis thaliana]	Unigene46317_All//6.00E-174//AT3G27180| unknown protein	Unigene46317_All//0.00E+00//CO099515		ko00350|Tyrosine metabolism//ko00450|Selenoamino acid metabolism//ko00340|Histidine metabolism		nr -
Unigene4632_All	754	78.76	262.49	82.28	103.26	236.53	306.92	28.99	110.25	82.42	1.74E+00	0.00E+00	Up	6.30E-02	4.29E-01		1.20E+00	3.08E-203	Up	1.57E+00	0.00E+00	Up	1.93E+00	5.84E-197	Up	1.51E+00	1.47E-106	Up	Unigene4632_All//gi|297839669|ref|XP_002887716.1|//2.00E-84//Atlg78070/F28K19_28 [Arabidopsis lyrata subsp. lyrata] >gi|297333557|gb|EFH63975.1| Atlg78070/F28K19_28 [Arabidopsis lyrata subsp. lyrata]	Unigene4632_All//2.00E-55//AT1G78070| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: CUL4 RING ubiquitin ligase complex; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), WD40 repeat, region (InterPro:IPR017986), WD40/YVTN repeat-like (InterPro:IPR015943), WD40 repeat (InterPro:IPR001680); BEST Arabidopsis thaliana protein match is: WD-40 repeat family protein (TAIR:AT1G36070.1); Has 110 Blast hits to 110 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 28; Plants - 80; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene4632_All//0.00E+00//TC157100		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis//ko03022|Basal transcription factors		nr +
Unigene46320_All	464	0.11	0.22	0.00	0.00	0.22	0.00	2.00	4.23	8.33	9.53E-01	7.25E-01		-6.82E+00	6.22E-01		7.80E+00	4.55E-01		null	null		1.08E+00	9.60E-03		2.05E+00	6.68E-11	Up	Unigene46320_All//gi|15222593|ref|NP_174496.1|//3.00E-20//XTR4 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 4); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase [Arabidopsis thaliana] >gi|38605150|sp|Q38908.2|XTH30_ARATH RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 30; Short=At-XTH30; Short=XTH-30; Flags: Precursor	Unigene46320_All//3.00E-21//AT1G32170| XTR4 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 4); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase	Unigene46320_All//2.00E-93//TC147487				nr +
Unigene46321_All	1324	2.96	8.92	2.57	15.80	17.22	12.14	62.75	93.57	168.41	1.59E+00	5.25E-18	Up	-2.03E-01	5.57E-01		1.24E-01	3.57E-01		-3.80E-01	1.43E-03		5.76E-01	1.76E-42		1.42E+00	0.00E+00	Up	Unigene46321_All//gi|124109189|gb|ABM91070.1|//1.00E-101//xyloglucan endotransglycosylase/hydrolase precursor XTH-3 [Populus tremula x Populus tremuloides]	Unigene46321_All//5.00E-97//AT1G32170| XTR4 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 4); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase	Unigene46321_All//0.00E+00//EV493197				nr -
Unigene46323_All	2000	16.59	14.54	12.22	10.21	11.74	9.42	5.35	2.45	3.65	-1.90E-01	5.46E-02		-4.41E-01	4.63E-06		2.02E-01	9.09E-02		-1.17E-01	4.23E-01		-1.13E+00	3.20E-12	Down	-5.53E-01	2.47E-04		Unigene46323_All//gi|15231097|ref|NP_190767.1|//1.00E-103//protein kinase family protein [Arabidopsis thaliana] >gi|75337704|sp|Q9SV05.1|CCR35_ARATH RecName: Full=Serine/threonine-protein kinase-like protein At3g51990; AltName: Full=CRINKLY 4-related kinase; Flags: Precursor	Unigene46323_All//6.00E-103//AT3G51990| protein kinase family protein	Unigene46323_All//0.00E+00//TC171512		ko04626|Plant-pathogen interaction		nr +
Unigene46325_All	2831	11.44	12.03	12.25	28.40	39.60	35.29	24.66	21.33	9.30	7.22E-02	5.02E-01		9.81E-02	3.80E-01		4.80E-01	6.83E-27		3.13E-01	3.55E-10		-2.09E-01	2.44E-04		-1.41E+00	6.66E-109	Down	Unigene46325_All//gi|115470203|ref|NP_001058700.1|//1.00E-122//Os07g0105800 [Oryza sativa (japonica Group)] >gi|113610236|dbj|BAF20614.1| Os07g0105800 [Oryza sativa (japonica Group)]	Unigene46325_All//0.00E+00//AT5G45530| unknown protein	Unigene46325_All//0.00E+00//gi|78347607|gb|DT567881.1|DT567881				nr -
Unigene46329_All	2679	13.46	6.47	9.70	46.19	39.44	37.04	15.85	6.44	7.70	-1.06E+00	6.01E-29	Down	-4.72E-01	2.58E-07		-2.28E-01	8.77E-08		-3.19E-01	7.01E-13		-1.30E+00	2.87E-57	Down	-1.04E+00	1.22E-41	Down	Unigene46329_All//gi|15236611|ref|NP_192621.1|//0.00E+00//SUB1; calcium ion binding [Arabidopsis thaliana] >gi|15912229|gb|AAL08248.1| AT4g08810/T32A17_120 [Arabidopsis thaliana] >gi|27363304|gb|AAO11571.1| At4g08810/T32A17_120 [Arabidopsis thaliana]	Unigene46329_All//0.00E+00//AT4G08810| SUB1; calcium ion binding	Unigene46329_All//0.00E+00//gi|78330639|gb|DT550913.1|DT550913				nr -
Unigene4633_All	1160	20.61	14.07	25.84	16.92	13.45	17.21	22.56	6.02	7.11	-5.51E-01	7.35E-07		3.26E-01	1.61E-03		-3.31E-01	5.74E-03		2.44E-02	8.83E-01		-1.91E+00	1.04E-61	Down	-1.67E+00	7.32E-53	Down	Unigene4633_All//gi|224058527|ref|XP_002299535.1|//5.00E-80//glutathione peroxidase [Populus trichocarpa] >gi|222846793|gb|EEE84340.1| glutathione peroxidase [Populus trichocarpa]	Unigene4633_All//4.00E-73//AT1G63460| glutathione peroxidase, putative	Unigene4633_All//0.00E+00//gi|164240834|gb|ES817485.1|ES817485		ko00480|Glutathione metabolism//ko00590|Arachidonic acid metabolism		nr +
Unigene46330_All	806	0.32	2.45	1.26	9.64	5.21	4.09	19.62	34.59	29.31	2.92E+00	8.36E-07	Up	1.95E+00	1.37E-02		-8.87E-01	4.17E-06		-1.24E+00	4.37E-09	Down	8.18E-01	3.49E-18		5.79E-01	4.19E-09		Unigene46330_All//gi|297799730|ref|XP_002867749.1|//1.00E-102//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313585|gb|EFH44008.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46330_All//2.00E-87//AT4G22790| MATE efflux family protein	Unigene46330_All//0.00E+00//TC136459				nr -
Unigene46331_All	1624	0.48	2.22	1.02	7.52	4.20	4.53	25.41	35.36	28.70	2.20E+00	7.71E-09	Up	1.07E+00	4.72E-02		-8.40E-01	1.75E-08		-7.29E-01	3.76E-06		4.77E-01	1.64E-14		1.76E-01	1.30E-02		Unigene46331_All//gi|297799730|ref|XP_002867749.1|//1.00E-130//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313585|gb|EFH44008.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46331_All//2.00E-118//AT4G22790| MATE efflux family protein	Unigene46331_All//0.00E+00//TC166534				nr +
Unigene46332_All	1400	12.52	44.70	38.91	19.82	15.03	27.61	72.81	37.53	66.96	1.84E+00	2.57E-113	Up	1.64E+00	5.80E-82	Up	-3.99E-01	2.91E-05		4.79E-01	9.26E-09		-9.56E-01	1.25E-83		-1.21E-01	1.03E-02		Unigene46332_All//gi|4559334|gb|AAD22996.1|//1.00E-148//expressed protein [Arabidopsis thaliana]	Unigene46332_All//8.00E-149//AT2G42570| unknown protein	Unigene46332_All//0.00E+00//TC171811				nr +
Unigene46333_All	870	9.98	5.36	7.83	11.85	8.67	6.75	7.44	6.25	3.34	-8.98E-01	5.69E-06		-3.50E-01	9.78E-02		-4.51E-01	7.96E-03		-8.13E-01	2.97E-06		-2.52E-01	2.63E-01		-1.15E+00	3.17E-08	Down	Unigene46333_All//gi|225442523|ref|XP_002278786.1|//1.00E-67//PREDICTED: similar to cell division protein FtsH-like [Vitis vinifera]	Unigene46333_All//8.00E-63//AT3G16290| EMB2083 (embryo defective 2083); ATP binding / ATP-dependent peptidase/ ATPase/ metalloendopeptidase/ metallopeptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase	Unigene46333_All//0.00E+00//TC142998				nr -
Unigene46334_All	2926	12.71	6.63	7.43	12.56	11.44	10.14	7.73	4.80	3.58	-9.39E-01	1.14E-24		-7.76E-01	2.61E-17		-1.35E-01	1.64E-01		-3.09E-01	4.07E-04		-6.88E-01	2.95E-11		-1.11E+00	4.97E-25	Down	Unigene46334_All//gi|18401080|ref|NP_566541.1|//0.00E+00//EMB2083 (embryo defective 2083); ATP binding / ATP-dependent peptidase/ ATPase/ metalloendopeptidase/ metallopeptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase [Arabidopsis thaliana]	Unigene46334_All//0.00E+00//AT3G16290| EMB2083 (embryo defective 2083); ATP binding / ATP-dependent peptidase/ ATPase/ metalloendopeptidase/ metallopeptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase	Unigene46334_All//0.00E+00//TC142998				nr +
Unigene46337_All	2106	3.55	5.03	1.72	16.04	21.71	25.13	23.01	30.15	24.23	5.01E-01	4.32E-03		-1.05E+00	3.34E-06	Down	4.37E-01	1.56E-09		6.48E-01	7.01E-20		3.90E-01	2.93E-11		7.48E-02	3.27E-01		Unigene46337_All//gi|115441063|ref|NP_001044811.1|//4.00E-44//Os01g0850000 [Oryza sativa (japonica Group)] >gi|113534342|dbj|BAF06725.1| Os01g0850000 [Oryza sativa (japonica Group)]	Unigene46337_All//6.00E-42//AT3G54000| unknown protein	Unigene46337_All//0.00E+00//TC137750				nr +
Unigene46338_All	1708	16.17	12.73	11.63	11.29	10.79	9.12	7.55	3.47	3.99	-3.46E-01	8.65E-04		-4.76E-01	7.52E-06		-6.55E-02	6.71E-01		-3.07E-01	1.68E-02		-1.12E+00	2.24E-14	Down	-9.21E-01	5.37E-11		Unigene46338_All//gi|18424393|ref|NP_568928.1|//1.00E-137//CAAX amino terminal protease family protein [Arabidopsis thaliana]	Unigene46338_All//2.00E-136//AT5G60750| CAAX amino terminal protease family protein	Unigene46338_All//0.00E+00//TC153072				nr -
Unigene46341_All	2309	10.08	9.63	17.34	10.16	10.48	7.84	6.68	1.76	2.42	-6.58E-02	6.04E-01		7.82E-01	7.08E-19		4.51E-02	7.78E-01		-3.74E-01	8.10E-04		-1.93E+00	3.06E-37	Down	-1.47E+00	2.38E-26	Down	Unigene46341_All//gi|15217901|ref|NP_174156.1|//0.00E+00//AtRLP4 (Receptor Like Protein 4); protein binding [Arabidopsis thaliana]	Unigene46341_All//0.00E+00//AT1G28340| AtRLP4 (Receptor Like Protein 4); protein binding	Unigene46341_All//0.00E+00//TC177434				nr -

Unigene46342_All	2495	1.41	0.91	0.94	0.54	0.86	0.51	1.58	0.39	0.65	-6.21E-01	5.96E-02		-5.81E-01	9.34E-02		6.67E-01	1.40E-01		-8.91E-02	8.87E-01		-2.03E+00	1.06E-10	Down	-1.27E+00	4.66E-06	Down	Unigene46342_All//gi|15217901|ref|NP_174156.1|//0.00E+00//AtRLP4 (Receptor Like Protein 4); protein binding [Arabidopsis thaliana]	Unigene46342_All//0.00E+00//AT1G28340| AtRLP4 (Receptor Like Protein 4); protein binding	Unigene46342_All//0.00E+00//TC177434				nr +
Unigene46344_All	2236	2.25	1.93	1.91	1.60	1.26	1.56	1.53	3.08	5.74	-2.22E-01	4.25E-01		-2.38E-01	4.09E-01		-3.45E-01	3.18E-01		-4.45E-02	9.12E-01		1.01E+00	6.24E-07	Up	1.91E+00	3.54E-31	Up	Unigene46344_All//gi|15222532|ref|NP_173893.1|//1.00E-39//ASB1 (ANTHRANILATE SYNTHASE BETA SUBUNIT 1); anthranilate synthase [Arabidopsis thaliana] >gi|11067285|gb|AAG28813.1|AC07937 4.16 anthranilate synthase beta subunit [Arabidopsis thaliana] >gi|403434|gb|AAA32742.1| anthranilate synthase beta subunit [Arabidopsis thaliana] >gi|20466736|gb|AAM20685.1| anthranilate synthase beta subunit [Arabidopsis thaliana] >gi|30023756|gb|AAP13411.1| At1g25220 [Arabidopsis thaliana]	Unigene46344_All//6.00E-41//AT1G25220| ASB1 (ANTHRANILATE SYNTHASE BETA SUBUNIT 1); anthranilate synthase	Unigene46344_All//0.00E+00//TC175849		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr +
Unigene46345_All	1145	5.99	4.56	5.72	8.83	6.74	9.31	10.60	5.58	3.48	-3.93E-01	8.46E-02		-6.55E-02	7.84E-01		-3.91E-01	2.62E-02		7.59E-02	7.03E-01		-9.24E-01	3.99E-10		-1.61E+00	9.54E-24	Down	Unigene46345_All//gi|297819626|ref|XP_002877696.1|//4.00E-55//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297323534|gb|EFH53955.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46345_All//3.00E-54//AT3G49725| GTP binding	Unigene46345_All//0.00E+00//ES794372				nr +
Unigene46347_All	956	4.98	4.40	8.02	6.88	8.50	7.70	1.06	0.09	0.58	-1.79E-01	5.51E-01		6.88E-01	1.63E-03		3.06E-01	1.56E-01		1.63E-01	5.23E-01		-3.60E+00	2.38E-05	Down	-8.63E-01	1.40E-01		Unigene46347_All//gi|15228789|ref|NP_191158.1|//6.00E-50//ESK1 (ESKIMO 1) [Arabidopsis thaliana]	Unigene46347_All//8.00E-41//AT3G55990| ESK1 (ESKIMO 1)	Unigene46347_All//0.00E+00//TC170083				nr -
Unigene46348_All	1279	9.00	4.48	11.99	11.57	10.07	10.17	2.81	0.52	1.81	-1.01E+00	4.30E-09	Down	4.14E-01	5.62E-03		-2.00E-01	2.05E-01		-1.86E-01	2.59E-01		-2.43E+00	4.70E-12	Down	-6.37E-01	2.24E-02		Unigene46348_All//gi|115464415|ref|NP_001055807.1|//1.00E-98//Os05g0470000 (Oryza sativa Japonica Group) >gi|113579358|dbj|BAF17721.1| Os05g0470000 (Oryza sativa Japonica Group)	Unigene46348_All//1.00E-86//AT2G40150| INVOLVED IN: biological_process unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: L3 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF231, plant (InterPro:IPR004235); BEST Arabidopsis thaliana protein match is: ESK1 (ESKIMO 1) (TAIR:AT3G55990.1); Has 712 Blast hits to 693 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 712; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene46348_All//0.00E+00//TC170083				nr +
Unigene46349_All	2901	5.52	13.36	6.87	7.52	8.97	10.32	12.13	11.89	12.51	1.28E+00	1.53E-41	Up	3.15E-01	1.66E-02		2.55E-01	1.72E-02		4.57E-01	2.02E-06		-2.88E-02	7.70E-01		4.50E-02	6.35E-01		Unigene46349_All//gi|297827261|ref|XP_002881513.1|//0.00E+00//PHD finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327352|gb|EFH57772.1| PHD finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46349_All//0.00E+00//AT3G53680| PHD finger transcription factor, putative	Unigene46349_All//0.00E+00//ES829807				nr -
Unigene46351_All	556	0.19	0.46	0.77	1.61	1.73	5.69	3.65	2.18	26.58	1.28E+00	4.35E-01		2.03E+00	1.39E-01		1.05E-01	9.03E-01		1.82E+00	1.51E-06	Up	-7.44E-01	6.77E-02		2.86E+00	8.56E-58	Up	Unigene46351_All//gi|297817536|ref|XP_002876651.1|//1.00E-64//metal ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322489|gb|EFH52910.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene46351_All//3.00E-65//AT3G62010| unknown protein	Unigene46351_All//4.00E-107//TC135109				nr -
Unigene46352_All	775	0.00	0.13	0.21	1.67	2.27	1.92	4.09	1.40	34.49	7.03E+00	3.86E-01		7.69E+00	2.38E-01		4.39E-01	4.18E-01		2.03E-01	7.14E-01		-1.55E+00	2.93E-06	Down	3.08E+00	1.12E-111	Up	Unigene46352_All//gi|297817536|ref|XP_002876651.1|//3.00E-62//metal ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322489|gb|EFH52910.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene46352_All//2.00E-63//AT3G62010| unknown protein	Unigene46352_All//1.00E-120//TC135109				nr +
Unigene46353_All	792	0.33	0.58	0.47	0.94	1.17	0.91	2.99	2.01	6.19	8.02E-01	4.60E-01		5.11E-01	6.54E-01		3.15E-01	7.04E-01		-4.84E-02	9.50E-01		-5.76E-01	1.27E-01		1.05E+00	1.30E-05	Up	Unigene46353_All//gi|297817536|ref|XP_002876651.1|//1.00E-55//metal ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322489|gb|EFH52910.1| metal ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene46353_All//4.00E-56//AT3G62010| unknown protein	Unigene46353_All//0.00E+00//TC135109				nr +
Unigene46355_All	1338	0.12	6.63	1.23	0.63	0.93	5.81	2.75	23.08	30.82	5.82E+00	9.76E-46	Up	3.39E+00	2.86E-06	Up	5.50E-01	4.06E-01		3.20E+00	5.41E-29	Up	3.07E+00	1.78E-126	Up	3.49E+00	5.06E-193	Up	Unigene46355_All//gi|297242515|gb|ADI24921.1|//1.00E-11//L-allo-threonine aldolase [Carica papaya]		Unigene46355_All//2.00E-110//gi|84150628|gb|DN799983.1|DN799983		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene46356_All	1782	4.58	107.25	23.94	12.08	22.47	238.95	29.92	165.21	206.44	4.55E+00	0.00E+00	Up	2.39E+00	1.28E-105	Up	8.96E-01	1.02E-28		4.31E+00	0.00E+00	Up	2.47E+00	0.00E+00	Up	2.79E+00	0.00E+00	Up	Unigene46356_All//gi|297242515|gb|ADI24921.1|//1.00E-159//L-allo-threonine aldolase [Carica papaya]	Unigene46356_All//1.00E-151//AT1G08630| THA1 (Threonine Aldolase 1); aldehyde-lyase/threonine aldolase	Unigene46356_All//0.00E+00//TC139061		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene46359_All	2547	3.08	33.70	5.44	15.35	11.26	17.43	29.56	204.02	12.51	3.45E+00	0.00E+00	Up	8.19E-01	1.79E-07		-4.47E-01	9.87E-09		1.83E-01	3.01E-02		2.79E+00	0.00E+00	Up	-1.24E+00	8.07E-97	Down	Unigene46359_All//gi|33326375|gb|AAQ08597.1|//0.00E+00//heat shock protein [Hevea brasiliensis]	Unigene46359_All//0.00E+00//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene46359_All//0.00E+00//TC167157		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene4636_All	1230	19.40	6.30	13.59	16.69	22.42	17.96	12.79	4.62	9.94	-1.62E+00	6.25E-37	Down	-5.13E-01	8.49E-06		4.27E-01	1.01E-05		1.06E-01	4.62E-01		-1.47E+00	5.02E-26	Down	-3.63E-01	3.21E-03		Unigene4636_All//gi|18087521|gb|AAL58895.1|AF462799_1//6.00E-29//AT3g17120/K14A17_24 [Arabidopsis thaliana]	Unigene4636_All//2.00E-13//AT3G17120| unknown protein	Unigene4636_All//0.00E+00//ES821599				nr +
Unigene46362_All	1837	22.84	14.67	7.48	116.44	72.88	32.03	22.49	7.96	12.36	-6.38E-01	1.30E-14		-1.61E+00	1.28E-61	Down	-6.76E-01	6.17E-97		-1.86E+00	0.00E+00	Down	-1.50E+00	4.47E-69	Down	-8.63E-01	6.71E-30		Unigene46362_All//gi|269819290|gb|ACZ44835.1|//1.00E-139//glycosyltransferase [Malus x domestica]	Unigene46362_All//1.00E-128//AT1G07250| UGT71C4 (UDP-GLUCOSYL TRANSFERASE 71C4); quercetin 3-O-glucosyltransferase/quercetin 7-O-glucosyltransferase/transferase, transferring glycosyl groups	Unigene46362_All//0.00E+00//TC169837		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene46364_All	2302	3.41	1.89	1.92	17.61	16.19	9.30	27.33	7.81	17.76	-8.49E-01	4.66E-05		-8.28E-01	1.27E-04		-1.22E-01	1.91E-01		-9.22E-01	5.12E-28		-1.81E+00	4.20E-137	Down	-6.22E-01	7.82E-26		Unigene46364_All//gi|225452330|ref|XP_002272711.1|//0.00E+00//PREDICTED: similar to stpk1 protein kinase [Vitis vinifera]	Unigene46364_All//1.00E-172//AT5G47750| D6PKL2 (D6 PROTEIN KINASE LIKE 2); kinase	Unigene46364_All//0.00E+00//gi|13246747|gb|BE054074.2|BE054074				nr +
Unigene46366_All	2101	10.73	4.65	7.76	47.35	39.42	24.31	22.16	7.68	13.79	-1.21E+00	1.51E-22	Down	-4.69E-01	8.46E-05		-2.65E-01	2.82E-08		-9.62E-01	5.21E-73		-1.53E+00	3.96E-80	Down	-6.85E-01	9.15E-23		Unigene46366_All//gi|30694458|ref|NP_191207.2|//0.00E+00//myosin heavy chain-related [Arabidopsis thaliana] >gi|29028898|gb|AAO64828.1| At3g56480 [Arabidopsis thaliana]	Unigene46366_All//0.00E+00//AT3G56480| myosin heavy chain-related	Unigene46366_All//0.00E+00//TC144075				nr -
Unigene46367_All	2192	14.35	46.14	11.76	8.02	14.80	25.82	23.65	154.77	118.70	1.69E+00	2.38E-162	Up	-2.87E-01	4.82E-03		8.83E-01	8.86E-23		1.69E+00	7.32E-98	Up	2.71E+00	0.00E+00	Up	2.33E+00	0.00E+00	Up	Unigene46367_All//gi|224131790|ref|XP_002321179.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222861952|gb|EEE99494.1| GRAS family transcription factor [Populus trichocarpa]	Unigene46367_All//2.00E-170//AT1G50600| SCL5; transcription factor	Unigene46367_All//0.00E+00//TC153894	GRAS			nr +
Unigene4637_All	1175	3.70	2.76	1.59	8.78	9.29	4.27	5.33	4.06	2.03	-4.21E-01	1.52E-01		-1.22E+00	8.75E-05	Down	8.22E-02	7.11E-01		-1.04E+00	3.96E-09	Down	-3.93E-01	7.08E-02		-1.39E+00	2.29E-10	Down	Unigene4637_All//gi|87162688|gb|AB028483.1|//2.00E-79//Alkaline phytoceramidase [Medicago truncatula]	Unigene4637_All//1.00E-80//AT4G22330| ATCES1; catalytic/hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in linear amides	Unigene4637_All//0.00E+00//TC179037		ko00600|Sphingolipid metabolism		nr +
Unigene46373_All	2245	2.45	10.11	2.66	2.44	1.96	2.86	5.89	17.87	38.88	2.05E+00	7.67E-48	Up	1.19E-01	6.41E-01		-3.14E-01	2.38E-01		2.27E-01	3.88E-01		1.60E+00	9.65E-74	Up	2.72E+00	0.00E+00	Up	Unigene46373_All//gi|224091046|ref|XP_002309158.1|//2.00E-48//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222855134|gb|EEE92681.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene46373_All//6.00E-30//AT3G11020| DREB2B (DRE/CRT-BINDING PROTEIN 2B); DNA binding / transcription activator/transcription factor	Unigene46373_All//0.00E+00//TC145747	AP2-EREBP			nr +
Unigene46374_All	956	7.39	14.63	4.62	20.11	21.43	47.15	37.77	48.31	32.80	9.85E-01	1.79E-10		-6.76E-01	3.16E-03		9.16E-02	5.39E-01		1.23E+00	8.61E-49	Up	3.55E-01	3.37E-07		-2.04E-01	1.14E-02		Unigene46374_All//gi|119657095|gb|ABL86672.1|//1.00E-98//ERS1 [Gossypium barbadense]	Unigene46374_All//8.00E-62//AT2G40940| ERS1 (ETHYLENE RESPONSE SENSOR 1); ethylene binding / protein histidine kinase/ receptor	Unigene46374_All//0.00E+00//TC175008				nr -
Unigene46376_All	548	2.29	2.13	4.86	3.36	4.71	3.30	3.86	8.47	1.24	-1.08E-01	8.46E-01		1.08E+00	7.80E-03		4.87E-01	2.40E-01		-2.89E-02	9.56E-01		1.13E+00	8.95E-06	Up	-1.64E+00	5.85E-05	Down			Unigene46376_All//3.00E-117//TC169728				
Unigene46377_All	765	6.77	7.95	7.31	12.70	15.98	14.58	5.14	17.65	2.86	2.31E-01	3.61E-01		1.10E-01	6.79E-01		3.32E-01	4.22E-02		2.00E-01	3.10E-01		1.78E+00	2.70E-29	Up	-8.44E-01	1.52E-03		Unigene46377_All//gi|186508557|ref|NP_001118534.1|//9.00E-07//ABIL1 (Abi-1-like 1) [Arabidopsis thaliana]	Unigene46377_All//5.00E-08//AT2G46225| ABIL1 (Abi-1-like 1)	Unigene46377_All//9.00E-149//TC169728				nr +
Unigene46378_All	1558	8.97	10.76	11.24	22.92	29.75	22.61	7.38	25.03	3.99	2.64E-01	6.23E-02		3.27E-01	2.08E-02		3.76E-01	1.95E-07		-1.99E-02	8.65E-01		1.76E+00	4.51E-82	Up	-8.88E-01	2.27E-09		Unigene46378_All//gi|18407012|ref|NP_566067.1|//9.00E-62//ABIL1 (Abi-1-like 1) [Arabidopsis thaliana] >gi|75160480|sp|Q8S8M5.1|ABIL1_ARATH RecName: Full=Protein ABIL1; AltName: Full=Abl interactor-like protein 1; Short=AtABIL1 >gi|20197375|gb|AAM15048.1| expressed protein [Arabidopsis thaliana] >gi|57240092|gb|AAW49256.1| Abl interactor-like protein-1 [Arabidopsis thaliana] >gi|108385243|gb|ABF85765.1| At2g46225 [Arabidopsis thaliana]	Unigene46378_All//2.00E-63//AT2G46225| ABIL1 (Abi-1-like 1)	Unigene46378_All//0.00E+00//TC169728				nr +

Unigene46379_All	1597	59.36	27.38	36.28	85.40	56.77	28.79	1.48	1.13	2.02	-1.12E+00	5.93E-82	Down	-7.11E-01	3.39E-37		-5.89E-01	2.24E-48		-1.57E+00	5.04E-216	Down	-3.98E-01	3.10E-01		4.47E-01	1.42E-01		Unigene46379_All//gi|15232847|ref|NP_186860.1|//0.00E+00//scpl25 (serine carboxypeptidase-like 25); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|125987777|sp|Q8L9T0.2|SCP25_ARATH RecName: Full=Serine carboxypeptidase-like 25; Flags: Precursor >gi|14335062|gb|AAK59795.1|AT3g02110/F1C9_10 [Arabidopsis thaliana] >gi|27363308|gb|AAO11573.1|At3g02110/F1C9_10 [Arabidopsis thaliana]	Unigene46379_All//0.00E+00//AT3G02110| scpl25 (serine carboxypeptidase-like 25); serine-type carboxypeptidase	Unigene46379_All//0.00E+00//TC151487				nr -
Unigene4638_All	2112	5.25	4.08	3.93	8.75	8.10	9.88	17.50	8.63	9.96	-3.65E-01	3.64E-02		-4.17E-01	2.10E-02		-1.11E-01	4.72E-01		1.75E-01	1.97E-01		-1.02E+00	3.27E-34	Down	-8.13E-01	2.59E-24		Unigene4638_All//gi|15232945|ref|NP_186914.1|//1.00E-150//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene4638_All//3.00E-149//AT3G02850| pentatricopeptide (PPR) repeat-containing protein	Unigene4638_All//0.00E+00//gi|109863593|gb|DW492570.1|DW492570				nr -
Unigene46382_All	3070	9.83	8.48	13.25	4.09	5.26	3.24	2.88	2.38	1.21	-2.13E-01	3.83E-02		4.30E-01	5.33E-07		3.64E-01	7.33E-03		-3.37E-01	4.00E-02		-2.73E-01	1.39E-01		-1.25E+00	2.47E-12	Down	Unigene46382_All//gi|22330276|ref|NP_175996.2|//1.00E-110//amine oxidase-related [Arabidopsis thaliana] >gi|179789776|gb|AAL47449.1|T6H22.19/T6H22.19 [Arabidopsis thaliana] >gi|22655396|gb|AAM98290.1|At1g55980/T6H22.19 [Arabidopsis thaliana] >gi|222423033|dbj|BAH19499.1|AT1G56000 [Arabidopsis thaliana]	Unigene46382_All//4.00E-111//AT1G56000| amine oxidase-related	Unigene46382_All//0.00E+00//TC154469				nr +
Unigene46383_All	1611	5.03	10.35	13.22	25.29	28.75	75.22	53.41	46.00	114.79	1.04E+00	2.13E-13	Up	1.39E+00	1.49E-25	Up	1.85E-01	2.00E-02		1.57E+00	2.43E-189	Up	-2.16E-01	2.03E-05		1.10E+00	4.42E-195	Up	Unigene46383_All//gi|82568691|dbj|BAE48659.1|//1.00E-116//2-oxoacid-dependent dioxygenase [Prunus mume]	Unigene46383_All//9.00E-94//AT1G14130| 2-oxoglutarate-dependent dioxygenase, putative	Unigene46383_All//0.00E+00//TC130329		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr -
Unigene46388_All	2299	0.61	0.95	1.44	1.13	1.27	1.36	2.80	0.82	0.92	6.25E-01	1.50E-01		1.22E+00	7.48E-04	Up	1.76E-01	6.80E-01		2.67E-01	4.98E-01		-1.77E+00	2.66E-14	Down	-1.61E+00	5.74E-13	Down	Unigene46388_All//gi|115463725|ref|NP_001055462.1|//0.00E+00//Os05g0395300 [Oryza sativa Japonica Group] >gi|113579013|dbj|BAF17376.1|Os05g0395300 [Oryza sativa Japonica Group]	Unigene46388_All//5.00E-169//AT4G14240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF21 (InterPro:IPR002550), Cystathionine beta-synthase, core (InterPro:IPR000644); BEST Arabidopsis thaliana protein match is: CBS domain-containing protein-related (TAIR:AT4G14230.1); Has 6770 Blast hits to 6657 proteins in 1347 species: Archae - 62; Bacteria - 4461; Metazoa - 254; Fungi - 179; Plants - 121; Viruses - 0; Other Eukaryotes - 1693 (source: NCBI BLink).	Unigene46388_All//0.00E+00//TC147791				nr -
Unigene46389_All	1800	16.45	39.78	16.27	15.03	31.30	35.96	10.57	19.92	21.20	1.27E+00	5.40E-76	Up	-1.60E-02	8.97E-01		1.06E+00	6.44E-53	Up	1.26E+00	1.65E-72	Up	9.14E-01	8.41E-28		1.00E+00	3.32E-35	Up	Unigene46389_All//gi|60617303|gb|AX31279.1|//1.00E-163//phosphomannose isomerase [Cyamopsis tetragonoloba]	Unigene46389_All//3.00E-150//AT1G67070| DIN9 (DARK INDUCIBLE 9); mannose-6-phosphate isomerase	Unigene46389_All//0.00E+00//TC152247		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr +
Unigene4639_All	1465	0.18	23.03	1.82	0.48	1.41	2.71	2.68	2.94	29.61	7.01E+00	3.57E-184	Up	3.35E+00	1.01E-09	Up	1.57E+00	6.25E-04	Up	2.51E+00	8.48E-12	Up	1.31E-01	6.39E-01		3.46E+00	6.46E-202	Up	Unigene4639_All//gi|15222311|ref|NP_172195.1|//1.00E-102//MAPKKK13; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|8954031|gb|AAF82205.1|AC067971_13 Strong similarity to a protein kinase homolog F23F1.4 gi|7482253 from Arabidopsis thaliana BAC F23F1 gb|AC004680. It contains a eukaryotic protein kinase domain PF|00069. ESTs gb|F13903 and gb|F13904 come from this gene	Unigene4639_All//5.00E-104//AT1G07150| MAPKKK13; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene4639_All//0.00E+00//TC131655		ko04626|Plant-pathogen interaction		nr +
Unigene46394_All	2220	19.91	13.88	15.23	33.99	38.06	27.77	34.95	13.03	17.84	-5.21E-01	6.70E-11		-3.87E-01	2.61E-06		1.63E-01	3.66E-03		-2.92E-01	5.67E-07		-1.42E+00	9.93E-120	Down	-9.70E-01	3.19E-67		Unigene46394_All//gi|297822137|ref|XP_002878951.1|//0.00E+00//3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 2 [Arabidopsis lyrata subsp. lyrata] >gi|297324790|gb|EFH55210.1|3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 2 [Arabidopsis lyrata subsp. lyrata]	Unigene46394_All//0.00E+00//AT2G26260| ATSBETAHSD/D2 (3BETA-HYDROXYSTEROID-DEHYDROGENASE/DECARBOXYLASE ISOFORM 2); 3-beta-hydroxy-delta5-steroid dehydrogenase/ sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating)	Unigene46394_All//0.00E+00//TC140175		ko00100|Steroid biosynthesis		nr -
Unigene46395_All	422	0.25	0.36	2.65	6.49	4.81	3.00	1.40	1.49	0.66	5.39E-01	7.79E-01		3.42E+00	1.92E-04	Up	-4.31E-01	2.71E-01		-1.12E+00	3.31E-03		8.28E-02	9.32E-01		-1.09E+00	1.86E-01				Unigene46395_All//1.00E-66//TC144932				
Unigene46397_All	3348	23.57	10.44	13.52	22.17	20.85	19.34	15.02	7.38	7.64	-1.17E+00	5.03E-74	Down	-8.02E-01	3.62E-38		-8.86E-02	1.99E-01		-1.97E-01	1.31E-03		-1.03E+00	1.24E-46	Down	-9.75E-01	3.23E-44		Unigene46397_All//gi|15221009|ref|NP_172176.1|//0.00E+00//TIC110 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 110) [Arabidopsis thaliana] >gi|20453114|gb|AAM19799.1|At1g06940/F24H5_1 [Arabidopsis thaliana]	Unigene46397_All//0.00E+00//AT1G06950| TIC110 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 110)	Unigene46397_All//0.00E+00//TC174706				nr +
Unigene46398_All	773	0.00	0.00	0.21	0.13	0.09	0.18	0.11	1.62	49.22	null	null		7.69E+00	2.38E-01		-5.33E-01	8.16E-01		4.44E-01	8.61E-01		3.89E+00	8.57E-07	Up	8.81E+00	4.62E-269	Up	Unigene46398_All//gi|30725574|gb|AP37809.1|//5.00E-07//At3g57190 [Arabidopsis thaliana]	Unigene46398_All//8.00E-11//AT3G57190| peptide chain release factor, putative	Unigene46398_All//4.00E-77//ES823103				nr -
Unigene464_All	1901	0.83	2.03	1.48	1.83	1.61	1.31	3.60	3.45	11.38	1.29E+00	6.40E-05	Up	8.46E-01	3.02E-02		-1.86E-01	6.15E-01		-4.89E-01	1.53E-01		-6.18E-02	7.82E-01		1.66E+00	4.11E-43	Up	Unigene464_All//gi|121281634|gb|ABM53274.1|//1.00E-114//GAMYB-like2 [Solanum lycopersicum]	Unigene464_All//1.00E-104//AT3G11440| MYB65 (MYB DOMAIN PROTEIN 65); DNA binding / transcription factor	Unigene464_All//0.00E+00//TC178444	MYB		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene46400_All	1047	13.19	39.83	36.52	23.31	42.10	46.80	17.89	15.69	29.15	1.59E+00	3.74E-62	Up	1.47E+00	3.00E-49	Up	8.53E-01	4.50E-29		1.01E+00	1.64E-38	Up	-1.89E-01	1.30E-01		7.04E-01	6.90E-16		Unigene46400_All//gi|225446362|ref|XP_002273215.1|//7.00E-83//PREDICTED: two pore channel 1 [Vitis vinifera]	Unigene46400_All//4.00E-77//AT4G03560| ATTPC1 (TWO-PORE CHANNEL 1); calcium channel/ voltage-gated calcium channel	Unigene46400_All//0.00E+00//TC158888				nr -
Unigene46401_All	1897	3.83	1.63	2.39	15.23	15.70	5.36	3.95	0.62	2.94	-1.23E+00	4.60E-08	Down	-6.84E-01	2.38E-03		4.40E-02	7.51E-01		-1.51E+00	1.93E-43	Down	-2.68E+00	3.83E-27	Down	-4.24E-01	2.27E-02		Unigene46401_All//gi|15227816|ref|NP_179917.1|//2.00E-42//transport protein-related [Arabidopsis thaliana] >gi|75206690|sp|Q9SLN1.1|FPP7_ARATH RecName: Full=Filament-like plant protein 7; Short=AtFPP7	Unigene46401_All//6.00E-41//AT2G23360| transport protein-related	Unigene46401_All//0.00E+00//TC144748				nr -
Unigene46408_All	2237	0.68	0.43	1.17	0.82	1.46	2.14	1.47	1.05	0.89	-6.56E-01	2.20E-01		7.82E-01	5.59E-02		8.28E-01	1.37E-02		1.38E+00	1.15E-06	Up	-4.95E-01	1.13E-01		-7.27E-01	1.31E-02		Unigene46408_All//gi|9454546|gb|AAF87869.1|AC012561_2//0.00E+00//Unknown protein [Arabidopsis thaliana]	Unigene46408_All//0.00E+00//AT1G50660| unknown protein	Unigene46408_All//0.00E+00//TC163919				nr -
Unigene4641_All	677	6.03	6.74	7.39	9.71	13.73	17.34	3.06	6.85	2.12	1.60E-01	6.18E-01		2.95E-01	3.21E-01		5.00E-01	6.23E-03		8.37E-01	2.85E-07		1.16E+00	5.59E-06	Up	-5.31E-01	1.73E-01		Unigene4641_All//gi|115474397|ref|NP_001060795.1|//1.00E-46//Os08g0107100 [Oryza sativa Japonica Group] >gi|113622764|dbj|BAF22709.1|Os08g0107100 [Oryza sativa Japonica Group]	Unigene4641_All//4.00E-34//AT4G19950| unknown protein	Unigene4641_All//0.00E+00//gi|48739789|gb|CO070308.1|CO070308				nr +
Unigene46413_All	1738	12.43	14.31	10.57	20.55	17.51	21.62	14.84	31.58	65.67	2.03E-01	7.79E-02		-2.34E-01	7.13E-02		-2.31E-01	9.19E-03		7.32E-02	5.01E-01		1.09E+00	5.64E-56	Up	2.15E+00	0.00E+00	Up	Unigene46413_All//gi|224109864|ref|XP_002315336.1|//1.00E-144//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222864376|gb|EEF01507.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene46413_All//2.00E-113//AT3G10480| no apical meristem (NAM) family protein	Unigene46413_All//0.00E+00//TC143837	NAC			nr +
Unigene46415_All	610	1.97	3.07	3.23	2.29	7.68	8.29	0.97	1.37	1.50	6.40E-01	1.80E-01		7.11E-01	1.40E-01		1.75E+00	1.47E-09	Up	1.86E+00	2.00E-10	Up	4.98E-01	4.86E-01		6.30E-01	3.24E-01		Unigene46415_All//gi|15227958|ref|NP_179397.1|//6.00E-87//VND1 (VASCULAR RELATED NAC-DOMAIN PROTEIN 1); transcription factor [Arabidopsis thaliana]	Unigene46415_All//9.00E-89//AT2G18060| VND1 (VASCULAR RELATED NAC-DOMAIN PROTEIN 1); transcription factor	Unigene46415_All//3.00E-12//CO075517	NAC			nr +
Unigene4642_All	1188	2.20	2.09	2.38	2.60	4.43	5.09	3.88	3.83	1.41	-7.54E-02	8.43E-01		1.09E-01	7.74E-01		7.71E-01	2.09E-03		9.71E-01	4.93E-05		-1.66E-02	9.82E-01		-1.46E+00	2.00E-08	Down	Unigene4642_All//gi|115474397|ref|NP_001060795.1|//2.00E-76//Os08g0107100 [Oryza sativa Japonica Group] >gi|113622764|dbj|BAF22709.1|Os08g0107100 [Oryza sativa Japonica Group]	Unigene4642_All//6.00E-44//AT4G19950| unknown protein	Unigene4642_All//0.00E+00//TC143454				nr +
Unigene46420_All	1978	2.80	3.07	4.42	6.45	6.22	5.16	4.23	1.46	2.70	1.33E-01	5.99E-01		6.55E-01	1.22E-03		-5.29E-02	8.06E-01		-3.21E-01	4.97E-02		-1.54E+00	3.67E-15	Down	-6.49E-01	1.77E-04		Unigene46420_All//gi|224105833|ref|XP_002313948.1|//1.00E-138//sugar transporter/spinster transmembrane protein [Populus trichocarpa] >gi|222850356|gb|EEE87903.1| sugar transporter/spinster transmembrane protein [Populus trichocarpa]	Unigene46420_All//3.00E-122//AT5G64500| membrane protein-related	Unigene46420_All//0.00E+00//TC149005				nr +

Unigene46421_All	1305	2.00	1.16	1.88	8.59	9.05	6.40	4.92	3.20	2.17	-7.83E-01	4.36E-02		-9.49E-02	8.09E-01		7.56E-02	7.28E-01		-4.24E-01	1.31E-02		-6.21E-01	2.71E-03		-1.18E+00	1.73E-08	Down	Unigene46421_All//gi|75156737|sp|Q8LEE5.1|FPP_SOLLC//3.00E-77//RecName: Full=Filament-like plant protein; Short=LeFPP >gi|22652089|gb|AAN03605.1|AF405309_1 coiled-coil protein [Solanum lycopersicum]	Unigene46421_All//4.00E-48//AT1G21810| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF869, plant (InterPro:IPR008587); BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT1G77580.2); Has 62951 Blast hits to 33517 proteins in 1593 species: Archae - 800; Bacteria - 6354; Metazoa - 33836; Fungi - 4765; Plants - 2651; Viruses - 311; Other Eukaryotes - 14234 (source: NCBI BLink).	Unigene46421_All//0.00E+00//ES797342				nr -
Unigene46422_All	2468	5.55	2.92	2.63	17.10	19.44	13.87	8.36	4.91	2.55	-9.30E-01	1.90E-09		-1.08E+00	2.75E-11	Down	1.85E-01	1.73E-02		-3.02E-01	1.95E-04		-7.67E-01	2.39E-12		-1.71E+00	1.69E-43	Down	Unigene46422_All//gi|75156737|sp|Q8LEE5.1|FPP_SOLLC//1.00E-151//RecName: Full=Filament-like plant protein; Short=LeFPP >gi|22652089|gb|AAN03605.1|AF405309_1 coiled-coil protein [Solanum lycopersicum]	Unigene46422_All//2.00E-69//AT3G05270| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF869, plant (InterPro:IPR008587); BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT1G77580.2); Has 97002 Blast hits to 49715 proteins in 2003 species: Archae - 1158; Bacteria - 12418; Metazoa - 49297; Fungi - 7501; Plants - 3801; Viruses - 453; Other Eukaryotes - 22374 (source: NCBI BLink).	Unigene46422_All//0.00E+00//ES797342				nr -
Unigene46423_All	2217	71.34	29.16	55.65	42.71	42.87	28.60	4.96	2.66	2.07	-1.29E+00	1.85E-171	Down	-3.58E-01	3.93E-18		5.20E-03	9.53E-01		-5.79E-01	5.52E-29		-8.99E-01	7.12E-09		-1.26E+00	2.78E-15	Down	Unigene46423_All//gi|260594177|gb|ACX46383.1|//0.00E+00//isochorismate synthase [Populus trichocarpa] >gi|269851435|gb|ACZ50509.1| isochorismate synthase [Populus fremontii x Populus angustifolia] >gi|269851437|gb|ACZ50510.1| isochorismate synthase [Populus fremontii x Populus angustifolia]	Unigene46423_All//0.00E+00//AT1G18870| ICS2 (ISOCHORISMATE SYNTHASE 2); isochorismate synthase	Unigene46423_All//0.00E+00//TC160101		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene46426_All	736	2.70	7.85	7.45	37.36	39.63	52.10	0.00	0.11	0.00	1.54E+00	8.42E-09	Up	1.46E+00	1.58E-07	Up	8.50E-02	5.06E-01		4.80E-01	9.93E-09		6.83E+00	4.01E-01		null	null		Unigene46426_All//gi|45934586|gb|AS79352.1|//1.00E-43//(-)-a-terpineol synthase [Vitis vinifera]	Unigene46426_All//1.00E-27//AT4G16740| ATTPS03; (E)-beta-ocimene synthase/ myrcene synthase	Unigene46426_All//0.00E+00//gi|164264970|gb|ES796248.1|ES796248		ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis		nr -
Unigene46427_All	1654	8.54	9.50	4.93	4.79	6.33	6.83	2.02	0.38	0.48	1.53E-01	3.32E-01		-7.94E-01	3.06E-07		4.02E-01	2.11E-02		5.12E-01	2.31E-03		-2.41E+00	3.44E-11	Down	-2.07E+00	9.79E-10	Down	Unigene46427_All//gi|225470869|ref|XP_002269732.1|//1.00E-169//PREDICTED: (-)-a-terpineol synthase [Vitis vinifera]	Unigene46427_All//4.00E-120//AT3G25810| myrcene/ocimene synthase, putative	Unigene46427_All//0.00E+00//gi|164264970|gb|ES796248.1|ES796248		ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis		nr -
Unigene46429_All	1991	1.45	1.71	1.07	6.31	4.12	4.58	3.36	2.33	1.44	2.39E-01	4.99E-01		-4.34E-01	2.69E-01		-6.15E-01	2.86E-05		-4.61E-01	3.59E-03		-5.26E-01	9.85E-03		-1.22E+00	3.61E-09	Down	Unigene46429_All//gi|90265237|emb|CAH67772.1|//5.00E-15//H0322F07.9 [Oryza sativa (indica cultivar-group)] >gi|90399190|emb|CAH68177.1| H0403D02.5 [Oryza sativa (indica cultivar-group)]					nr -
Unigene46430_All	2408	7.08	15.19	13.80	23.89	33.55	30.52	16.49	30.62	20.04	1.10E+00	3.30E-31	Up	9.62E-01	3.76E-22		4.90E-01	3.38E-20		3.53E-01	2.04E-09		8.93E-01	3.92E-54		2.81E-01	2.74E-05		Unigene46430_All//gi|30725324|gb|AE037684.1|//1.00E-140//At3g01680 [Arabidopsis thaliana]	Unigene46430_All//2.00E-136//AT3G01680| unknown protein	Unigene46430_All//0.00E+00//TC134810				nr +
Unigene46431_All	1702	22.50	9.74	14.64	6.18	9.02	5.68	52.49	27.70	30.41	-1.21E+00	5.87E-38	Down	-6.20E-01	3.28E-12		5.47E-01	4.43E-05		-1.21E-01	5.78E-01		-9.22E-01	4.22E-69		-7.88E-01	1.72E-54		Unigene46431_All//gi|224092091|ref|XP_002309468.1|//0.00E+00//cytokinin oxidase [Populus trichocarpa] >gi|222855444|gb|EEE92991.1| cytokinin oxidase [Populus trichocarpa]	Unigene46431_All//0.00E+00//AT5G21482| CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase	Unigene46431_All//0.00E+00//TC166894		ko00908|Zeatin biosynthesis		nr -
Unigene46432_All	1101	48.85	78.65	63.21	50.45	53.48	95.58	50.04	134.12	30.03	6.87E-01	3.32E-33		3.72E-01	6.62E-09		8.43E-02	3.08E-01		9.22E-01	3.27E-71		1.42E+00	1.14E-226	Up	-7.37E-01	2.62E-30					Unigene46432_All//0.00E+00//TC136010				ESTscan -
Unigene46433_All	1328	5.28	6.07	10.31	6.83	7.55	12.18	5.79	4.06	2.52	2.01E-01	3.76E-01		9.65E-01	1.56E-09		1.44E-01	5.19E-01		8.35E-01	9.82E-10		-5.13E-01	6.28E-03		-1.20E+00	3.34E-10	Down	Unigene46433_All//gi|41469187|gb|AS07116.1|//1.00E-55//expressed protein [Oryza sativa Japonica Group]	Unigene46433_All//2.00E-46//AT4G15545| unknown protein	Unigene46433_All//0.00E+00//gi|11206095|gb|BF275025.1|BF275025				nr -
Unigene46435_All	2193	5.08	3.23	2.70	9.95	12.06	12.40	5.55	4.42	1.65	-6.52E-01	1.25E-04		-9.15E-01	2.91E-07		2.78E-01	7.81E-03		3.17E-01	2.37E-03		-3.29E-01	2.75E-02		-1.75E+00	9.46E-27	Down	Unigene46435_All//gi|71905585|gb|AZS2770.1|//1.00E-141//expressed protein [Arabidopsis thaliana]	Unigene46435_All//4.00E-112//AT5G42690| unknown protein	Unigene46435_All//0.00E+00//TC140406				nr +
Unigene46436_All	2835	0.92	0.32	0.73	3.23	2.90	2.85	0.67	0.65	0.41	-1.52E+00	2.21E-04	Down	-3.33E-01	4.12E-01		-1.55E-01	4.84E-01		-1.81E-01	4.08E-01		-4.90E-02	9.25E-01		-7.20E-01	7.44E-02		Unigene46436_All//gi|71905585|gb|AZS2770.1|//1.00E-158//expressed protein [Arabidopsis thaliana]	Unigene46436_All//1.00E-121//AT5G42690| unknown protein	Unigene46436_All//0.00E+00//TC140406				nr -
Unigene46437_All	2684	2.26	0.60	1.11	5.59	4.44	2.74	9.88	2.21	4.71	-1.90E+00	3.17E-12	Down	-1.03E+00	5.04E-05	Down	-3.32E-01	1.93E-02		-1.03E+00	1.02E-12	Down	-2.16E+00	2.14E-73	Down	-1.07E+00	1.60E-27	Down	Unigene46437_All//gi|224094755|ref|XP_002310223.1|//0.00E+00//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222853126|gb|EEE90673.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene46437_All//0.00E+00//AT5G66750| CHR1 (CHROMATIN REMODELING 1); ATPase/ helicase	Unigene46437_All//0.00E+00//BF279204				nr -
Unigene46438_All	2778	1.66	0.64	0.58	4.21	2.69	1.02	3.49	0.90	1.94	-1.38E+00	3.10E-06	Down	-1.53E+00	9.09E-07	Down	-6.48E-01	2.24E-05		-2.04E+00	4.48E-27	Down	-1.95E+00	5.81E-24	Down	-8.48E-01	1.69E-07		Unigene46438_All//gi|224094755|ref|XP_002310223.1|//1.00E-179//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222853126|gb|EEE90673.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene46438_All//7.00E-162//AT5G66750| CHR1 (CHROMATIN REMODELING 1); ATPase/ helicase	Unigene46438_All//0.00E+00//TC164914				nr -
Unigene4644_All	1030	21.94	4.97	4.55	6.77	6.35	9.43	1.77	1.26	2.24	-2.14E+00	7.40E-51	Down	-2.27E+00	1.37E-52	Down	-9.21E-02	7.38E-01		4.78E-01	9.81E-03		-4.89E-01	2.74E-01		3.46E-01	3.61E-01		Unigene4644_All//gi|6573743|gb|AAF17663.1|AC009398_12//5.00E-49//F20B24.22 [Arabidopsis thaliana]	Unigene4644_All//4.00E-09//AT1G10800| unknown protein					nr +
Unigene46442_All	2113	3.59	7.27	5.29	5.66	10.19	12.53	4.30	5.76	3.51	1.02E+00	5.46E-12	Up	5.60E-01	1.51E-03		8.48E-01	2.98E-14		1.15E+00	6.73E-26	Up	4.20E-01	4.00E-03		-2.95E-01	8.61E-02					Unigene46442_All//5.00E-174//AJ514118				
Unigene46446_All	1528	125.60	105.85	126.92	17.05	11.29	8.81	7.22	7.25	3.08	-2.47E-01	1.30E-11		1.51E-02	7.32E-01		-5.95E-01	9.62E-10		-9.53E-01	3.21E-19		5.30E-03	1.01E+00		-1.23E+00	8.96E-15	Down	Unigene46446_All//gi|42795544|gb|AAS46110.1|//2.00E-10//photosystem II M protein [Oryza sativa Japonica Group] >gi|42795608|gb|AAS46173.1| photosystem II M protein [Oryza sativa Japonica Group]	Unigene46446_All//1.00E-09//ATCG00220| PSII low MW protein	Unigene46446_All//0.00E+00//TC178759		ko00195|Photosynthesis		nr +
Unigene46449_All	1011	5.18	5.26	2.42	11.68	12.16	8.49	3.55	3.18	2.21	2.41E-02	9.46E-01		-1.09E+00	7.61E-05	Down	5.84E-02	8.03E-01		-4.60E-01	5.03E-03		-1.59E-01	6.56E-01		-6.88E-01	1.36E-02		Unigene46449_All//gi|38345009|emb|CAE01608.2|//7.00E-65//OSJNBa0052021.12 [Oryza sativa (japonica cultivar-group)]	Unigene46449_All//1.00E-24//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene46449_All//6.00E-61//gi|21100782|gb|BQ413095.1|BQ413095				nr +
Unigene46451_All	2116	16.59	7.16	10.80	29.83	21.17	25.68	26.00	11.30	15.49	-1.21E+00	5.14E-35	Down	-6.20E-01	3.03E-11		-4.95E-01	1.67E-16		-2.16E-01	1.15E-03		-1.20E+00	1.13E-65	Down	-7.47E-01	5.82E-31		Unigene46451_All//gi|255291798|dbj|BAH89252.1|//0.00E+00//protein disulfide isomerase L-3b [Glycine max]	Unigene46451_All//0.00E+00//AT3G16110| ATPDIL1-6 (PDI-LIKE 1-6); protein disulfide isomerase	Unigene46451_All//0.00E+00//ES798882		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene46453_All	1142	3.80	3.42	4.06	7.33	5.58	5.38	5.04	1.87	2.30	-1.55E-01	6.06E-01		9.33E-02	7.48E-01		-3.94E-01	4.54E-02		-4.46E-01	2.77E-02		-1.43E+00	1.14E-09	Down	-1.13E+00	3.44E-07	Down	Unigene46453_All//gi|30677982|ref|NP_178323.2|//2.00E-83//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene46453_All//1.00E-78//AT2G02150| pentatricopeptide (PPR) repeat-containing protein	Unigene46453_All//0.00E+00//TC149865				nr +
Unigene4646_All	1213	24.80	14.20	17.52	10.47	9.03	10.20	4.67	2.31	1.12	-8.04E-01	1.23E-15		-5.02E-01	7.24E-07		-2.14E-01	2.11E-01		-3.77E-02	8.46E-01		-1.02E+00	6.69E-06	Down	-2.06E+00	6.43E-16	Down	Unigene4646_All//gi|18416739|ref|NP_567745.1|//2.00E-92//antitermination NusB domain-containing protein [Arabidopsis thaliana] >gi|30984514|gb|AAP42720.1| At4g26370 [Arabidopsis thaliana]	Unigene4646_All//4.00E-93//AT4G26370| antitermination NusB domain-containing protein	Unigene4646_All//0.00E+00//TC139308				nr +
Unigene46464_All	2675	6.69	5.61	4.56	12.07	8.68	8.19	14.83	12.61	6.75	-2.55E-01	6.23E-02		-5.53E-01	4.31E-05		-4.76E-01	3.92E-08		-5.59E-01	1.05E-09		-2.34E-01	2.65E-03		-1.14E+00	8.57E-45	Down	Unigene46464_All//gi|77403667|dbj|BAE46412.1|//0.00E+00//Pre-mRNA splicing factor [Solanum tuberosum]	Unigene46464_All//4.00E-172//AT4G31200| SWAP (Suppressor-of-White-APricot)/surp domain-containing protein	Unigene46464_All//0.00E+00//TC167746			GO:0003676//GO:0010467	nr -
Unigene46465_All	1980	4.86	11.77	9.39	9.99	12.47	11.77	8.48	10.55	9.58	1.28E+00	2.95E-25	Up	9.49E-01	2.20E-12		3.20E-01	2.61E-03		2.37E-01	4.76E-02		3.16E-01	3.78E-03		1.76E-01	1.39E-01		Unigene46465_All//gi|15220440|ref|NP_172009.1|//0.00E+00//galactosyltransferase family protein [Arabidopsis thaliana] >gi|14488078|gb|AAK63859.1|AF389287_1 At1g05170/YUP8H12_22 [Arabidopsis thaliana] >gi|2388580|gb|AAB71461.1| Similar to Sequence 10 from patent 5477002 (gb|1253956) [Arabidopsis thaliana] >gi|21360399|gb|AAM47315.1| At1g05170/YUP8H12_22 [Arabidopsis thaliana]	Unigene46465_All//0.00E+00//AT1G05170| galactosyltransferase family protein	Unigene46465_All//0.00E+00//TC150405			GO:0006464//GO:0031224//GO:0035250//GO:0043231	nr +
Unigene46467_All	1614	57.15	20.81	29.07	34.69	23.38	30.75	17.42	15.20	9.08	-1.46E+00	1.58E-120	Down	-9.75E-01	6.44E-62		-5.69E-01	7.22E-19		-1.74E-01	1.86E-02		-1.97E-01	4.27E-02		-9.40E-01	1.12E-23		Unigene46467_All//gi|224102663|ref|XP_002312769.1|//6.00E-72//type-a response regulator [Populus trichocarpa] >gi|222852589|gb|EEE90136.1| type-a response regulator [Populus trichocarpa]	Unigene46467_All//3.00E-57//AT1G10470| ARR4 (RESPONSE REGULATOR 4); protein binding / transcription regulator/ two-component response regulator	Unigene46467_All//0.00E+00//TC132952	ARR-B	ko04712|Circadian rhythm - plant	GO:0003006//GO:0004871//GO:0005488//GO:0009755//GO:0010017//GO:0020360//GO:0043231//GO:0048511//GO:0050789	nr +
Unigene46472_All	1610	1.04	1.35	0.50	1.67	1.45	2.22	4.15	3.79	2.05	3.80E-01	3.91E-01		-1.07E+00	4.69E-02		-2.00E-01	6.17E-01		4.08E-01	2.42E-01		-1.31E-01	6.02E-01		-1.01E+00	4.82E-07	Down	Unigene46472_All//gi|15229132|ref|NP_190508.1|//1.00E-108//CID10; RNA binding / protein binding [Arabidopsis thaliana] >gi|79314662|ref|NP_001030833.1| CID10; RNA binding / protein binding [Arabidopsis thaliana] >gi|6723409|emb|CAB66418.1| RNA-binding-like protein [Arabidopsis thaliana] >gi|222424104|dbj|BAH20012.1| AT3G49390 [Arabidopsis thaliana]	Unigene46472_All//7.00E-110//AT3G49390| CID10; RNA binding / protein binding	Unigene46472_All//0.00E+00//TC166914		ko03040|Spliceosome		nr +

Unigene46477_All	1490	205.49	118.41	206.75	47.61	86.25	831.55	114.84	252.74	311.22	-7.95E-01	1.59E-149		8.80E-03	8.05E-01		8.57E-01	3.48E-85		4.13E+00	0.00E+00	Up	1.14E+00	0.00E+00	Up	1.44E+00	0.00E+00	Up	Unigene46477_All//gi|37719662|gb|AF41851.1|//0.00E+00//beta-cyanoalanine synthase [Hevea brasiliensis]	Unigene46477_All//2.00E-159//AT3G61440| CYSC1 (CYSTEINE SYNTHASE C1); L-3-cyanoalanine synthase/ cysteine synthase	Unigene46477_All//0.00E+00//TC132216		ko00270|Cysteine and methionine metabolism//ko00460|Cyanoamino acid metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0000097//GO:0006563//GO:0016835//GO:0048037	nr -
Unigene46479_All	2012	7.39	3.43	9.34	19.16	16.50	14.46	18.03	8.85	13.70	-1.11E+00	2.56E-13	Down	3.39E-01	1.21E-02		-2.16E-01	1.15E-02		-4.07E-01	1.10E-06		-1.03E+00	5.82E-34	Down	-3.96E-01	3.31E-07		Unigene46479_All//gi|79318876|ref|NP_001031111.1|//0.00E+00//acetyltransferase-related [Arabidopsis thaliana]	Unigene46479_All//0.00E+00//AT1G29890| acetyltransferase-related	Unigene46479_All//3.00E-141//ES797373			GO:0044464	nr -
Unigene4648_All	1515	2.73	1.57	3.48	9.17	11.98	6.98	4.49	1.57	3.29	-7.96E-01	7.73E-03		3.51E-01	2.18E-01		3.85E-01	2.10E-03		-3.95E-01	8.98E-03		-1.51E+00	3.18E-12	Down	-4.51E-01	2.14E-02		Unigene4648_All//gi|115486173|ref|NP_001068230.1|//5.00E-25//Os11g0602300 [Oryza sativa Japonica Group] >gi|77551799|gb|ABA94596.1|TB2/DP1, HVA22 family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113645452|dbj|BAF28593.1|Os11g0602300 [Oryza sativa Japonica Group]	Unigene4648_All//4.00E-24//AT1G74520| ATHVA22A	Unigene4648_All//0.00E+00//TC176514				nr -
Unigene46484_All	610	1.54	0.50	0.09	5.23	3.16	6.52	2.91	2.95	2.87	-1.63E+00	3.13E-02		-4.14E+00	2.90E-04	Down	-7.25E-01	2.86E-02		3.18E-01	3.52E-01		1.73E-02	1.01E+00		-1.87E-02	9.70E-01		Unigene46484_All//gi|115473125|ref|NP_001060161.1|//8.00E-86//Os07g0592200 [Oryza sativa Japonica Group] >gi|113611697|dbj|BAF22075.1|Os07g0592200 [Oryza sativa Japonica Group]	Unigene46484_All//2.00E-86//AT3G50050| aspartyl protease family protein	Unigene46484_All//3.00E-114//BG442097			GO:0004175//GO:0019538//GO:0044464	nr -
Unigene46486_All	994	14.00	27.58	35.84	3.31	4.02	5.54	1.62	2.44	1.96	9.78E-01	1.50E-19		1.36E+00	9.91E-41	Up	2.81E-01	4.14E-01		7.45E-01	3.12E-03		5.94E-01	1.10E-01		2.81E-01	5.13E-01		Unigene46486_All//gi|222618468|gb|EE354600.1|//1.00E-08//hypothetical protein Os3_01823 [Oryza sativa Japonica Group]		Unigene46486_All//7.00E-70//DR462298				nr -
Unigene46487_All	842	11.56	36.59	37.82	2.01	5.07	8.37	2.01	3.38	3.97	1.66E+00	6.64E-49	Up	1.71E+00	3.72E-51	Up	1.33E+00	4.21E-06	Up	2.06E+00	2.81E-16	Up	7.49E-01	2.41E-02		9.85E-01	8.72E-04				Unigene46487_All//8.00E-66//TC138748				
Unigene46488_All	1673	19.92	34.53	20.18	78.34	57.43	41.71	26.81	22.63	13.05	7.93E-01	1.46E-28		1.86E-02	8.67E-01		-4.48E-01	2.83E-28		-9.09E-01	1.73E-87		-2.45E-01	7.01E-04		-1.04E+00	7.58E-44	Down	Unigene46488_All//gi|18398566|ref|NP_564408.1|//1.00E-72//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene46488_All//6.00E-51//AT1G32740| protein binding / zinc ion binding	Unigene46488_All//0.00E+00//TC152641			GO:0046872	nr +
Unigene46489_All	1939	1.57	3.48	1.84	3.44	3.92	3.94	3.97	5.91	7.40	1.15E+00	8.55E-07	Up	2.34E-01	5.13E-01		1.89E-01	4.44E-01		1.93E-01	4.30E-01		5.74E-01	1.21E-04		8.98E-01	1.34E-11		Unigene46489_All//gi|12322008|gb|AAG51046.1|AC069473.8/7.00E-84//gypsy/Ty-3 retroelement polyprotein; 69969-74404 [Arabidopsis thaliana] >gi|10998138|dbj|BAB03109.1|retroelement pol polyprotein [Arabidopsis thaliana]		Unigene46489_All//4.00E-48//TC138833			GO:0003676//GO:0009987//GO:0043170//GO:0044238	nr +
Unigene4649_All	1970	10.54	3.42	4.41	23.77	17.03	20.29	20.45	7.36	9.99	-1.62E+00	2.67E-32	Down	-1.26E+00	2.38E-21	Down	-4.81E-01	8.62E-12		-2.28E-01	3.71E-03		-1.47E+00	7.52E-66	Down	-1.03E+00	3.71E-39	Down	Unigene4649_All//gi|18408151|ref|NP_564842.1|//1.00E-178//ribosomal protein S5 family protein [Arabidopsis thaliana] >gi|48958531|gb|AAT47818.1|At1g64880 [Arabidopsis thaliana]	Unigene4649_All//1.00E-152//AT1G64880| ribosomal protein S5 family protein	Unigene4649_All//0.00E+00//TC143896		ko03010|Ribosome		nr +
Unigene46490_All	1330	7.55	6.25	7.85	1.35	0.41	1.53	2.45	4.21	2.22	-2.74E-01	1.45E-01		5.51E-02	7.75E-01		-1.70E+00	3.60E-04	Down	1.81E-01	7.01E-01		7.83E-01	4.75E-04		-1.43E-01	6.39E-01				Unigene46490_All//3.00E-85//DT457854				
Unigene46492_All	2583	15.66	6.04	7.07	41.71	31.68	22.00	19.86	7.01	6.79	-1.37E+00	1.03E-48	Down	-1.15E+00	1.56E-35	Down	-3.97E-01	1.05E-18		-9.23E-01	7.43E-74		-1.50E+00	5.13E-86	Down	-1.55E+00	1.52E-92	Down	Unigene46492_All//gi|224065140|ref|XP_002301687.1|//0.00E+00//leucine-rich repeat transmembrane protein [Populus trichocarpa] >gi|222843413|gb|EEE80960.1|leucine-rich repeat transmembrane protein [Populus trichocarpa]	Unigene46492_All//0.00E+00//AT3G17840| RLK902; ATP binding / kinase/ protein serine/threonine kinase	Unigene46492_All//0.00E+00//TC131225			GO:0004672//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene46493_All	2458	59.90	16.06	13.89	151.06	84.88	64.64	79.76	14.45	25.58	-1.90E+00	2.63E-280	Down	-2.11E+00	0.00E+00	Down	-8.32E-01	4.54E-242		-1.22E+00	0.00E+00	Down	-2.46E+00	0.00E+00	Down	-1.64E+00	0.00E+00	Down	Unigene46493_All//gi|15234558|ref|NP_192979.1|//0.00E+00//SKU5; copper ion binding / oxidoreductase [Arabidopsis thaliana] >gi|38258655|sp|Q9SU40.1|SKU5_ARATH RecName: Full=Monocopper oxidase-like protein SKU5; AltName: Full=Skewed roots; Flags: Precursor >gi|18158154|gb|AAL62306.1|AF439406_1 multi-copper oxidase-related protein [Arabidopsis thaliana]	Unigene46493_All//0.00E+00//AT4G12420| SKU5; copper ion binding / oxidoreductase	Unigene46493_All//0.00E+00//TC156991		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0005618//GO:0008152//GO:0009826//GO:0016682//GO:0031225//GO:0043412//GO:0048914	nr +
Unigene46496_All	829	0.63	1.65	0.45	2.40	1.66	0.44	2.35	1.66	1.39	1.39E+00	1.95E-02		-4.89E-01	6.32E-01		-5.33E-01	2.46E-01		-2.46E+00	3.20E-06	Down	-4.96E-01	2.44E-01		-7.51E-01	5.89E-02		Unigene46496_All//gi|115445439|ref|NP_001046499.1|//3.00E-47//Os02g0265400 [Oryza sativa Japonica Group] >gi|113536030|dbj|BAF08413.1|Os02g0265400 [Oryza sativa Japonica Group]	Unigene46496_All//6.00E-46//AT3G47810| MAG1 (MAIGO 1); hydrolase/ protein serine/threonine phosphatase	Unigene46496_All//0.00E+00//TC171106			GO:0044464	nr +
Unigene46497_All	1694	25.17	15.76	23.89	10.85	12.34	10.56	3.37	2.32	1.60	-6.75E-01	2.64E-16		-7.54E-02	4.36E-01		1.85E-01	1.57E-01		-3.95E-02	7.91E-01		-5.39E-01	1.57E-02		-1.08E+00	1.14E-06	Down	Unigene46497_All//gi|186492055|ref|NP_001117518.1|//1.00E-117//ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4); 1,4-dihydroxy-2-naphthoate octaprenyltransferase/ prenyltransferase [Arabidopsis thaliana]	Unigene46497_All//8.00E-105//AT1G60600| ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4); 1,4-dihydroxy-2-naphthoate octaprenyltransferase/ prenyltransferase	Unigene46497_All//0.00E+00//gi|11200125|gb|BF269130.1|BF269130		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0016765//GO:0031224//GO:0043231	nr -
Unigene46498_All	1610	9.46	4.25	9.06	3.99	4.66	3.56	0.60	0.16	0.30	-1.15E+00	1.71E-14	Down	-6.14E-02	7.00E-01		2.24E-01	3.47E-01		-1.64E-01	5.53E-01		-1.95E+00	4.44E-03		-1.02E+00	9.02E-02		Unigene46498_All//gi|186492055|ref|NP_001117518.1|//1.00E-122//ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4); 1,4-dihydroxy-2-naphthoate octaprenyltransferase/ prenyltransferase [Arabidopsis thaliana]	Unigene46498_All//2.00E-110//AT1G60600| ABC4 (ABERRANT CHLOROPLAST DEVELOPMENT 4); 1,4-dihydroxy-2-naphthoate octaprenyltransferase/ prenyltransferase	Unigene46498_All//0.00E+00//gi|11200125|gb|BF269130.1|BF269130		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0016765//GO:0031224//GO:0043231	nr +
Unigene465_All	1541	0.95	2.50	1.11	2.88	2.37	2.70	1.84	2.47	2.61	1.39E+00	2.09E-05	Up	2.18E-01	6.56E-01		-2.81E-01	3.63E-01		-9.36E-02	7.60E-01		4.25E-01	1.43E-01		5.06E-01	5.66E-02		Unigene465_All//gi|297806629|ref|XP_002871198.1|//9.00E-65//ATMYB33/MYB33 [Arabidopsis lyrata subsp. lyrata] >gi|297317035|gb|EFH47457.1|ATMYB33/MYB33 [Arabidopsis lyrata subsp. lyrata]	Unigene465_All//3.00E-65//AT5G06100| MYB33 (MYB DOMAIN PROTEIN 33); DNA binding / transcription factor	Unigene465_All//3.00E-88//TC178444	MYB			nr -
Unigene4650_All	1930	0.33	0.03	0.19	1.11	1.25	1.50	1.82	0.43	0.68	-3.63E+00	5.07E-03		-7.52E-01	4.11E-01		1.70E-01	7.37E-01		4.32E-01	2.77E-01		-2.07E+00	7.72E-10	Down	-1.42E+00	2.35E-06	Down	Unigene4650_All//gi|18408151|ref|NP_564842.1|//1.00E-179//ribosomal protein S5 family protein [Arabidopsis thaliana] >gi|48958531|gb|AAT47818.1|At1g64880 [Arabidopsis thaliana]	Unigene4650_All//3.00E-154//AT1G64880| ribosomal protein S5 family protein	Unigene4650_All//0.00E+00//TC143896		ko03010|Ribosome		nr -
Unigene46500_All	659	5.72	8.53	5.82	2.65	7.47	3.97	3.08	2.79	1.93	5.78E-01	2.15E-02		2.54E-02	9.54E-01		1.50E+00	3.61E-08	Up	5.87E-01	1.47E-01		-1.42E-01	7.30E-01		-6.71E-01	8.49E-02								
Unigene46502_All	2312	1.47	2.56	1.31	2.35	1.76	2.42	2.74	3.58	5.94	8.02E-01	1.02E-03		-1.64E-01	6.27E-01		-4.18E-01	1.02E-01		4.46E-02	8.90E-01		3.84E-01	3.74E-02		1.12E+00	1.49E-15	Up	Unigene46502_All//gi|33355392|gb|AAQ16126.1|//0.00E+00//homeodomain protein BNLGHI6313 [Gossypium hirsutum]	Unigene46502_All//0.00E+00//AT4G00730| ANL2 (ANTHOCYANINLESS 2); transcription factor/ transcription regulator	Unigene46502_All//0.00E+00//TC172946	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231//GO:0043629//GO:0048513	nr -
Unigene46504_All	1193	18.86	15.63	18.21	44.51	41.65	36.12	31.40	15.77	10.62	-2.71E-01	2.27E-02		-5.04E-02	7.00E-01		-9.58E-02	2.53E-01		-3.02E-01	2.12E-05		-9.94E-01	2.92E-33		-1.56E+00	8.72E-69	Down	Unigene46504_All//gi|91107145|gb|BE11602.1|//1.00E-117//COV1-like protein [Solanum chacoense]	Unigene46504_All//5.00E-103//AT1G43130| LCV2 (LIKE COV 2)	Unigene46504_All//0.00E+00//TC159289				nr +
Unigene46505_All	798	1.70	2.60	3.87	4.62	9.62	32.88	15.47	54.84	263.94	6.11E-01	1.73E-01		1.18E+00	1.67E-03		1.06E+00	1.51E-07	Up	2.83E+00	2.39E-86	Up	1.83E+00	1.23E-96	Up	4.09E+00	0.00E+00	Up	Unigene46505_All//gi|116672836|gb|ABK15560.1|//1.00E-34//gibberellin 2-oxidase 2 [Solanum lycopersicum]	Unigene46505_All//3.00E-26//AT1G78440| ATGA2OX1 (gibberellin 2-oxidase 1); gibberellin 2-beta-dioxygenase	Unigene46505_All//0.00E+00//TC168258		ko00008|Ca2+	GO:0008152//GO:0016701//GO:0016706//GO:0046914	nr -
Unigene46506_All	1353	6.46	22.28	19.48	25.99	57.39	265.34	35.34	140.28	771.16	1.79E+00	6.68E-53	Up	1.59E+00	2.38E-38	Up	1.14E+00	2.20E-82	Up	3.35E+00	0.00E+00	Up	1.99E+00	0.00E+00	Up	4.45E+00	0.00E+00	Up	Unigene46506_All//gi|224061332|ref|XP_002300030.1|//1.00E-143//gibberellin 2-oxidase [Populus trichocarpa] >gi|222847688|gb|EEE85235.1|gibberellin 2-oxidase [Populus trichocarpa]	Unigene46506_All//1.00E-108//AT1G78440| ATGA2OX1 (gibberellin 2-oxidase 1); gibberellin 2-beta-dioxygenase	Unigene46506_All//0.00E+00//TC168258		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene46507_All	2128	20.78	12.76	9.43	3.02	4.71	8.47	0.50	2.99	1.18	-7.03E-01	4.67E-18		-1.14E+00	2.22E-38	Down	6.41E-01	1.79E-04		1.49E+00	2.59E-26	Up	2.59E+00	3.03E-22	Up	1.25E+00	4.67E-04	Up	Unigene46507_All//gi|268526570|gb|ACZ05614.1|//0.00E+00//vacuolar invertase 2 [Gossypium hirsutum]	Unigene46507_All//7.00E-134//AT1G12240| ATBETAFRUCT4; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene46507_All//0.00E+00//DT469011		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism	GO:0004553//GO:0016757//GO:0044238	nr -
Unigene46508_All	1339	5.20	5.22	23.19	23.21	54.06	141.53	4.67	23.54	4.28	7.00E-03	9.91E-01		2.16E+00	5.30E-68	Up	1.22E+00	4.86E-85	Up	2.61E+00	0.00E+00	Up	2.33E+00	1.57E-95	Up	-1.25E-01	6.05E-01		Unigene46508_All//gi|194136583|gb|ACF33514.1|//1.00E-140//salicylic acid methyl transferase-like protein [Glycine max]	Unigene46508_All//9.00E-77//AT3G11480| BSMT1; S-adenosylmethionine-dependent methyltransferase	Unigene46508_All//0.00E+00//TC153265		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene46509_All	1132	1.39	37.11	13.45	21.74	26.40	43.01	13.30	18.83	16.01	4.74E+00	1.97E-196	Up	3.28E+00	5.80E-53	Up	2.81E-01	3.67E-03		9.84E-01	5.70E-37		5.02E-01	2.08E-06		2.68E-01	2.14E-02		Unigene46509_All//gi|18405204|ref|NP_565918.1|//2.00E-84//acid phosphatase class B family protein [Arabidopsis thaliana] >gi|75096954|sp|Q94195.2|Y2992_ARATH RecName: Full=Uncharacterized protein At2g39920 >gi|20198305|gb|AAB95277.2|expressed protein [Arabidopsis thaliana] >gi|90962976|gb|ABE02412.1|At2g39920 [Arabidopsis thaliana]	Unigene46509_All//6.00E-33//AT2G39920| acid phosphatase class B family protein	Unigene46509_All//0.00E+00//TC149558		ko03010|Ribosome	GO:0010038//GO:0044464	nr +
Unigene4651_All	1149	0.68	4.45	0.19	2.21	4.35	9.32	3.61	29.03	54.85	2.71E+00	1.91E-15	Up	-1.88E+00	4.13E-02		9.75E-01	1.59E-04		2.07E+00	9.03E-25	Up	3.01E+00	7.43E-134	Up	3.93E+00	0.00E+00	Up	Unigene4651_All//gi|70609694|gb|AAZ05072.1|//2.00E-35//hypoxia-responsive family protein [Citrus sinensis]	Unigene4651_All//1.00E-24//AT3G56550| hypoxia-responsive family protein	Unigene4651_All//0.00E+00//TC155766				nr +
Unigene46510_All	1575	0.23	7.69	5.38	4.68	6.49	11.76	3.92	7.64	7.77	5.05E+00	1.15E-58	Up	4.53E+00	8.89E-38	Up	4.72E-01	6.47E-03		1.33E+00	7.05E-23	Up	9.64E-01	1.06E-10		9.87E-01	1.45E-11		Unigene46510_All//gi|18405204|ref|NP_565918.1|//5.00E-52//acid phosphatase class B family protein [Arabidopsis thaliana] >gi|75096954|sp|Q94195.2|Y2992_ARATH RecName: Full=Uncharacterized protein At2g39920 >gi|20198305|gb|AAB95277.2|expressed protein [Arabidopsis thaliana] >gi|90962976|gb|ABE02412.1|At2g39920 [Arabidopsis thaliana]	Unigene46510_All//2.00E-40//AT2G39920| acid phosphatase class B family protein	Unigene46510_All//0.00E+00//TC149558		ko03010|Ribosome	GO:0010038//GO:0044464	nr -
Unigene46513_All	1056	4.31	1.44	1.31	5.71	3.78	7.01	10.77	3.40	3.66	-1.58E+00	2.10E-07	Down	-1.72E+00	8.47E-08	Down	-5.94E-01	9.38E-03		2.97E-01	2.05E-01		-1.66E+00	1.20E-22	Down	-1.56E+00	2.34E-21	Down	Unigene46513_All//gi|190609947|dbj|BAG49074.1|//1.00E-58//30S ribosomal protein S16 [Populus alba]	Unigene46513_All//3.00E-56//AT5G56940| ribosomal protein S16 family protein	Unigene46513_All//0.00E+00//TC130920		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0009526//GO:0010467//GO:0022613//GO:0030529	nr -

Unigene46514_All	1369	2.71	3.48	5.60	7.02	4.48	3.00	6.95	6.05	4.51	3.59E-01	2.13E-01		1.05E+00	2.42E-06	Up	-6.49E-01	1.50E-04		-1.23E+00	5.98E-11	Down	-2.01E-01	2.77E-01		-6.24E-01	1.10E-04		Unigene46514_All//gi|255555555|ref|XP_002518814.1|//4.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223542195|gb|EEF43739.1| conserved hypothetical protein [Ricinus communis]	Unigene46514_All//2.00E-06//AT1G60670| INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Homeodomain-like (InterPro:IPR009057); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10820.2); Has 83 Blast hits to 83 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 77; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink).	Unigene46514_All//2.00E-40//C0079177				nr +
Unigene46515_All	2238	146.58	96.54	150.02	96.18	66.13	119.08	93.87	38.02	47.07	-6.03E-01	1.78E-98		3.34E-02	3.37E-01		-5.40E-01	3.47E-65		3.08E-01	2.33E-25		-1.30E+00	1.18E-282	Down	-9.96E-01	1.21E-188		Unigene46515_All//gi|225443790|ref|XP_002266308.1|//0.00E+00//PREDICTED: similar to cysteine protease Cp5 [Vitis vinifera]	Unigene46515_All//1.00E-103//AT1G69850| XBCP3 (xylem bark cysteine peptidase 3); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene46515_All//0.00E+00//TC152020			GO:0004175//GO:0019538	nr +
Unigene46517_All	1676	4.93	21.86	7.31	19.23	22.70	27.57	10.22	29.10	62.87	2.15E+00	1.03E-81	Up	5.67E-01	7.04E-04		2.40E-01	5.07E-03		5.20E-01	6.50E-12		1.51E+00	2.82E-82	Up	2.62E+00	0.00E+00	Up	Unigene46517_All//gi|195654299|gb|ACG46617.1|//3.00E-39//DNA binding protein [Zea mays]	Unigene46517_All//4.00E-33//AT1G68670| myb family transcription factor	Unigene46517_All//0.00E+00//TC167784	G2-like			nr +
Unigene4652_All	1398	0.79	0.40	2.89	1.10	1.63	3.52	25.65	9.57	12.80	-9.79E-01	1.34E-01		1.88E+00	7.07E-08	Up	5.58E-01	2.09E-01		1.67E+00	7.20E-09	Up	-1.42E+00	1.15E-55	Down	-1.00E+00	2.70E-33	Down	Unigene4652_All//gi|9794870|gb|AAF98369.1|AF158253.1|//1.00E-130//patatin-like protein 3 [Nicotiana tabacum]	Unigene4652_All//2.00E-109//AT4G37050| PLP4 (PATATIN-LIKE PROTEIN 4); nutrient reservoir	Unigene4652_All//0.00E+00//TC138520				nr +
Unigene46521_All	1106	5.16	3.85	1.59	10.36	14.23	10.94	5.35	11.68	8.07	-4.22E-01	9.52E-02		-1.70E+00	1.78E-09	Down	4.58E-01	6.19E-04		7.92E-02	6.98E-01		1.13E+00	1.72E-14	Up	5.92E-01	4.04E-04		Unigene46521_All//gi|297794383|ref|XP_002865076.1|//3.00E-66//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310911|gb|EFH41335.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46521_All//6.00E-59//AT5G66320| zinc finger (GATA type) family protein	Unigene46521_All//0.00E+00//TC131334	C2C2-GATA			GO:0046872	nr +
Unigene46522_All	1441	7.70	5.87	3.73	22.82	25.81	12.88	12.50	13.95	13.19	-3.91E-01	2.43E-02		-1.04E+00	7.84E-09	Down	1.78E-01	5.24E-02		-8.25E-01	5.43E-19		1.59E-01	1.99E-01		7.73E-02	5.66E-01		Unigene46522_All//gi|297794383|ref|XP_002865076.1|//3.00E-94//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310911|gb|EFH41335.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46522_All//2.00E-77//AT5G66320| zinc finger (GATA type) family protein	Unigene46522_All//0.00E+00//gi|78331843|gb|DT552117.1|DT552117	C2C2-GATA			GO:0005488	nr +
Unigene46524_All	1934	18.18	8.07	15.97	1786.18	1072.73	274.95	54.98	172.30	15.80	-1.17E+00	2.97E-33	Down	-1.87E-01	6.21E-02		-7.36E-01	0.00E+00		-2.70E+00	0.00E+00	Down	1.65E+00	0.00E+00	Up	-1.80E+00	1.39E-236	Down	Unigene46524_All//gi|74273619|gb|AB01477.1|//0.00E+00//cytochrome P450 DDWF1 [Gossypium hirsutum]	Unigene46524_All//3.00E-109//AT5G07990| TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	Unigene46524_All//0.00E+00//TC147281		ko00941|Flavonoid biosynthesis||ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr -
Unigene46526_All	862	3.64	1.65	3.09	13.52	8.95	10.43	4.32	2.81	10.49	-1.15E+00	1.33E-03		-2.38E-01	5.38E-01		-5.96E-01	1.07E-04		-3.75E-01	2.68E-02		-6.18E-01	3.02E-02		1.28E+00	6.94E-13	Up	Unigene46526_All//gi|15217871|ref|NP_174142.1|//2.00E-69//ATJ1; heat shock protein binding / nucleic acid binding / unfolded protein binding / zinc ion binding [Arabidopsis thaliana] >gi|9795616|gb|AAP98434.1|AC021044_13 Putative dnaJ protein [Arabidopsis thaliana]	Unigene46526_All//4.00E-48//AT1G28210| ATJ1; heat shock protein binding / unfolded protein binding	Unigene46526_All//0.00E+00//gi|48821788|gb|C0123101.1|C0123101			GO:0005515//GO:0006950//GO:0032559//GO:0043231//GO:0044267//GO:0046914	nr +
Unigene46529_All	1811	3.61	14.19	5.41	16.72	13.04	17.18	35.14	46.00	41.44	1.97E+00	1.39E-51	Up	5.83E-01	2.15E-03		-3.59E-01	9.17E-05		3.90E-02	7.37E-01		3.89E-01	2.02E-14		2.38E-01	7.09E-06		Unigene46529_All//gi|75735996|dbj|BAA94509.1|//1.00E-174//protein kinase 1 [Populus nigra]	Unigene46529_All//9.00E-167//AT1G07870| protein kinase family protein	Unigene46529_All//0.00E+00//TC149053		ko04626|Plant-pathogen interaction		nr +
Unigene46532_All	2169	6.83	1.47	3.34	5.83	5.29	6.56	4.68	2.10	2.85	-2.21E+00	6.74E-35	Down	-1.03E+00	2.32E-11	Down	-1.42E-01	4.44E-01		1.69E-01	3.30E-01		-1.16E+00	4.88E-12	Down	-7.17E-01	4.56E-06		Unigene46532_All//gi|297580367|ref|XP_002872067.1|//0.00E+00//polynucleotide adenylyltransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317904|gb|EFH48326.1| polynucleotide adenylyltransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46532_All//1.00E-174//AT5G23690| polynucleotide adenylyltransferase family protein	Unigene46532_All//0.00E+00//TC131308			GO:0003676//GO:0010467//GO:0070566	nr -
Unigene46535_All	2229	3.00	6.14	5.14	4.83	5.25	5.75	4.06	1.59	2.14	1.03E+00	5.48E-11	Up	7.74E-01	8.76E-06		1.22E-01	5.41E-01		2.54E-01	1.36E-01		-1.35E+00	1.47E-13	Down	-9.20E-01	5.59E-08		Unigene46535_All//gi|225459207|ref|XP_002284042.1|//0.00E+00//PREDICTED: similar to isoamylase-type starch-debranching enzyme 3 [Vitis vinifera]	Unigene46535_All//0.00E+00//AT4G09020| ISA3 (ISOAMYLASE 3); alpha-amylase/ isoamylase	Unigene46535_All//0.00E+00//TC156237			GO:0004133//GO:0005982//GO:0009532//GO:0016798//GO:0043036//GO:0043167	nr +
Unigene46537_All	2032	3.30	1.57	2.23	7.60	7.07	6.82	6.24	6.13	4.02	-1.07E+00	4.02E-06	Down	-5.65E-01	1.74E-02		-1.05E-01	5.61E-01		-1.55E-01	3.52E-01		-2.63E-02	8.81E-01		-6.35E-01	4.03E-06		Unigene46537_All//gi|223452436|gb|ACN89545.1|//1.00E-162//calmodulin-binding receptor-like cytoplasmic kinase [Glycine max]	Unigene46537_All//2.00E-142//AT2G11520| CRCK3; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene46537_All//0.00E+00//TC176229		ko04626|Plant-pathogen interaction		nr +
Unigene46539_All	2402	2.13	1.03	1.75	3.28	2.29	2.93	6.74	3.58	5.94	-1.05E+00	9.60E-05	Down	-2.86E-01	3.33E-01		-5.15E-01	9.10E-03		-1.60E-01	5.08E-01		-9.11E-01	5.94E-13		-1.83E-01	1.59E-01		Unigene46539_All//gi|92870993|gb|ABE80154.1|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene46539_All//6.00E-155//AT1G73660| protein kinase family protein	Unigene46539_All//6.00E-171//DW518755			GO:0000166//GO:0004672	nr -
Unigene46543_All	1452	1.08	2.13	1.87	5.01	3.18	2.43	3.64	2.96	2.72	9.78E-01	6.22E-03		7.91E-01	4.77E-02		-6.56E-01	1.16E-03		-1.05E+00	1.11E-06	Down	-2.96E-01	2.34E-01		-4.22E-01	6.37E-02		Unigene46543_All//gi|225442633|ref|XP_002284593.1|//7.00E-77//PREDICTED: similar to BY-2 kinesin-like protein 10 [Vitis vinifera]	Unigene46543_All//6.00E-60//AT3G16060| kinesin motor family protein	Unigene46543_All//0.00E+00//gi|164308434|gb|ES841588.1|ES841588			GO:0000166//GO:0003774//GO:0016020//GO:0043231	nr +
Unigene46545_All	1808	17.71	10.15	12.10	14.35	14.15	13.21	4.42	1.80	2.29	-8.04E-01	1.41E-16		-5.49E-01	1.99E-08		-2.06E-02	8.74E-01		-1.19E-01	3.50E-01		-1.29E+00	2.28E-11	Down	-9.48E-01	1.83E-07		Unigene46545_All//gi|75162595|sp|Q8VS93.1|LGUC_ARATH|/1.00E-159//RecName: Full=Probable lactoylglutathione lyase, chloroplast; AltName: Full=Glyoxalase I; Flags: Precursor >gi|16930396|gb|AAL31884.1|AF419651_1 At1g67280/F1N21_10 [Arabidopsis thaliana] >gi|19316505|gb|AAL84986.1| At1g67280/F1N21_10 [Arabidopsis thaliana]	Unigene46545_All//1.00E-157//AT1G67280| lactoylglutathione lyase, putative / glyoxalase I, putative	Unigene46545_All//0.00E+00//TC139355		ko00620|Pyruvate metabolism		nr +
Unigene46546_All	501	0.73	1.31	0.11	13.32	9.97	8.92	1.18	6.01	1.83	8.47E-01	3.48E-01		-2.78E+00	1.03E-01		-4.19E-01	6.22E-02		-5.78E-01	1.06E-02		2.35E+00	8.26E-10	Up	6.30E-01	3.24E-01				Unigene46546_All//0.00E+00//gi|78335226|gb|DT555500.1|DT555500				ESTscan +
Unigene46549_All	1184	7.47	6.08	6.48	9.55	8.84	6.52	3.96	1.20	1.75	-2.97E-01	1.38E-01		-2.06E-01	3.60E-01		-1.11E-01	5.88E-01		-5.50E-01	9.12E-04		-1.72E+00	2.86E-10	Down	-1.18E+00	2.10E-06	Down	Unigene46549_All//gi|9280650|gb|AAF86519.1|AC002560_12//6.00E-68//F21B7.29 [Arabidopsis thaliana]	Unigene46549_All//6.00E-62//AT1G03687| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: DTW (InterPro:IPR005636); Has 347 Blast hits to 347 proteins in 176 species: Archae - 0; Bacteria - 320; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink).	Unigene46549_All//0.00E+00//gi|78337796|gb|DT558070.1|DT558070				nr +
Unigene46550_All	1059	3.56	1.58	2.87	2.49	3.45	2.86	0.96	0.51	0.68	-1.17E+00	2.82E-04	Down	-3.12E-01	3.77E-01		4.67E-01	1.62E-01		1.97E-01	6.19E-01		-9.01E-01	1.44E-01		-5.01E-01	3.99E-01		Unigene46550_All//gi|124300982|gb|ABN04743.1|//5.00E-78//At1g03687 [Arabidopsis thaliana]	Unigene46550_All//3.00E-78//AT1G03687| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: DTW (InterPro:IPR005636); Has 347 Blast hits to 347 proteins in 176 species: Archae - 0; Bacteria - 320; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink).	Unigene46550_All//0.00E+00//TC165560				nr -
Unigene46553_All	1731	34.79	20.96	35.16	291.00	224.56	143.66	72.84	32.50	16.75	-7.31E-01	5.50E-26		1.53E-02	8.50E-01		-3.74E-01	4.31E-77		-1.02E+00	0.00E+00	Down	-1.16E+00	3.40E-142	Down	-2.12E+00	0.00E+00	Down	Unigene46553_All//gi|225428877|ref|XP_002282482.1|//1.00E-112//PREDICTED: similar to leucine-rich repeat family protein [Vitis vinifera]	Unigene46553_All//8.00E-93//AT3G19320| leucine-rich repeat family protein	Unigene46553_All//0.00E+00//gi|78339888|gb|DT560162.1|DT560162		ko04626|Plant-pathogen interaction	GO:0031410	nr -
Unigene46554_All	1547	52.96	93.38	66.81	45.08	84.27	80.75	1.45	22.07	2.32	8.18E-01	3.70E-74		3.35E-01	9.87E-11		9.03E-01	3.37E-94		8.41E-01	2.24E-72		3.93E+00	2.68E-173	Up	6.78E-01	1.57E-02		Unigene46554_All//gi|34260064|emb|CAA07575.1|//1.00E-128//monooxygenase [Arabidopsis thaliana] >gi|4467141|emb|CAB37510.1| monooxygenase 2 (MO2) [Arabidopsis thaliana] >gi|7270837|emb|CAB80518.1| monooxygenase 2 (MO2) [Arabidopsis thaliana]	Unigene46554_All//4.00E-122//AT4G38540| monooxygenase, putative (MO2)	Unigene46554_All//0.00E+00//TC146874		ko00906|Carotenoid biosynthesis		nr -
Unigene46560_All	2453	4.12	3.39	2.30	8.10	7.79	9.54	7.98	3.95	2.79	-2.81E-01	1.35E-01		-8.39E-01	7.63E-06		-5.66E-02	7.26E-01		2.35E-01	4.87E-02		-1.01E+00	2.53E-18	Down	-1.51E+00	1.03E-34	Down	Unigene46560_All//gi|297792335|ref|XP_002864052.1|//0.00E+00//kelch repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297309887|gb|EFH40311.1| kelch repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46560_All//0.00E+00//AT5G50310| kelch repeat-containing protein	Unigene46560_All//0.00E+00//gi|164359997|gb|ES804787.1|ES804787		ko04712|Circadian rhythm - plant	GO:0005488	nr +
Unigene46562_All	513	6.94	7.01	2.08	0.78	4.50	13.47	3.21	11.65	10.79	1.60E-02	9.82E-01		-1.74E+00	2.45E-06	Down	2.53E+00	1.72E-07	Up	4.12E+00	1.26E-31	Up	1.86E+00	3.75E-14	Up	1.75E+00	1.79E-12	Up	Unigene46562_All//gi|1345776|sp|P29031.2|CHIB_POPTR//7.00E-51//RecName: Full=Acidic endochitinase WIN6.2B; Flags: Precursor >gi|1197373|emb|CAA42612.1| gwin6.2b [Populus trichocarpa]	Unigene46562_All//6.00E-34//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene46562_All//1.00E-20//BF276148		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0004568//GO:0006026//GO:0009607//GO:0030247//GO:0031410	nr +
Unigene46563_All	1153	29.81	124.94	35.33	13.00	35.96	168.51	15.58	12.90	50.03	2.07E+00	8.17E-305	Up	2.45E-01	5.99E-03		1.47E+00	1.92E-64	Up	3.70E+00	0.00E+00	Up	-2.72E-01	2.45E-02		1.68E+00	6.80E-116	Up	Unigene46563_All//gi|38261495|gb|AAR15893.1|//1.00E-121//chitinase [Oryza sativa]	Unigene46563_All//3.00E-103//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene46563_All//1.00E-22//BF276148		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene46564_All	664	4.81	4.27	5.77	12.53	3.99	1.56	27.00	6.42	2.22	-1.70E-01	6.12E-01		2.65E-01	4.26E-01		-1.65E+00	1.35E-16	Down	-3.00E+00	4.28E-30	Down	-2.07E+00	2.41E-47	Down	-3.60E+00	2.70E-88	Down	Unigene46564_All//gi|225440392|ref|XP_002267559.1|//5.00E-21//PREDICTED: ripening-related protein-like [Vitis vinifera]	Unigene46564_All//6.00E-16//AT5G02230| haloacid dehalogenase-like hydrolase family protein	Unigene46564_All//0.00E+00//gi|109879065|gb|DW508035.1|DW508035				nr +

Unigene46565_All	487	12.36	7.49	12.90	21.48	14.78	8.90	70.41	15.02	12.11	-7.22E-01	2.72E-03		6.26E-02	8.04E-01		-5.40E-01	1.08E-03		-1.27E+00	1.65E-12	Down	-2.23E+00	1.41E-98	Down	-2.54E+00	9.84E-119	Down	Unigene46565_All//gi|15241720|ref|NP_195843.1|//5.00E-37//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|30679562|ref|NP_850754.1|haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|107738426|gb|ABF83695.1|At5g02230 [Arabidopsis thaliana]	Unigene46565_All//3.00E-38//AT5G02230| haloacid dehalogenase-like hydrolase family protein	Unigene46565_All//1.00E-149//gi|48748176|gb|C0078695.1|C0078695			GO:0003824	nr +
Unigene46566_All	1391	32.16	22.00	33.27	54.86	29.48	16.04	72.04	32.51	13.98	-5.48E-01	5.58E-12		4.88E-02	6.34E-01		-8.96E-01	1.27E-56		-1.77E+00	2.88E-144	Down	-1.15E+00	1.29E-110	Down	-2.37E+00	0.00E+00	Down	Unigene46566_All//gi|225440392|ref|XP_002267559.1|//1.00E-117//PREDICTED: ripening-related protein-like [Vitis vinifera]	Unigene46566_All//3.00E-93//AT5G02230| haloacid dehalogenase-like hydrolase family protein	Unigene46566_All//0.00E+00//TC169722				nr +
Unigene46567_All	1485	3.52	4.03	3.41	9.09	7.95	6.78	8.17	5.77	3.54	1.93E-01	4.55E-01		-4.86E-02	8.65E-01		-1.93E-01	2.52E-01		-4.23E-01	5.68E-03		-5.02E-01	5.24E-04		-1.21E+00	1.12E-15	Down	Unigene46567_All//gi|15219953|ref|NP_173694.1|//1.00E-131//methyltransferase [Arabidopsis thaliana] >gi|84028281|sp|O80543.2|Y1280_ARATH RecName: Full=Uncharacterized protein At1g22800 >gi|30102638|gb|AAP21237.1|At1g22800 [Arabidopsis thaliana]	Unigene46567_All//6.00E-133//AT1G22800| methyltransferase	Unigene46567_All//0.00E+00//TC164096			GO:0016741	nr +
Unigene46572_All	387	0.00	0.79	1.79	1.16	0.62	0.70	1.20	1.08	1.13	9.62E+00	4.42E-02		1.08E+01	6.15E-04	Up	-8.95E-01	4.13E-01		-7.26E-01	5.32E-01		-1.54E-01	8.70E-01		-8.58E-02	9.34E-01					Unigene46572_All//1.00E-07//TC175527				
Unigene46575_All	849	12.57	9.49	14.05	14.67	16.71	12.93	15.14	10.09	5.91	-4.06E-01	2.15E-02		1.60E-01	3.94E-01		1.88E-01	2.62E-01		-1.82E-01	3.23E-01		-5.85E-01	2.86E-05		-1.36E+00	1.08E-19	Down	Unigene46575_All//gi|30678076|ref|NP_178473.2|//2.00E-99//translin family protein [Arabidopsis thaliana] >gi|87116652|gb|ABD19690.1|At2g03780 [Arabidopsis thaliana]	Unigene46575_All//1.00E-85//AT2G03780| translin family protein	Unigene46575_All//0.00E+00//TC142080			GO:0003677	nr -
Unigene46576_All	1427	7.41	3.69	11.16	8.10	9.12	10.16	4.15	3.13	3.10	-1.00E+00	2.25E-08	Down	5.91E-01	4.14E-05		1.72E-01	3.32E-01		3.27E-01	3.14E-02		-4.05E-01	7.14E-02		-4.21E-01	4.87E-02		Unigene46576_All//gi|30678076|ref|NP_178473.2|//1.00E-107//translin family protein [Arabidopsis thaliana] >gi|87116652|gb|ABD19690.1|At2g03780 [Arabidopsis thaliana]	Unigene46576_All//1.00E-90//AT2G03780| translin family protein	Unigene46576_All//0.00E+00//ES846606			GO:0003677	nr +
Unigene46577_All	1834	15.29	8.23	15.19	46.09	37.80	40.83	4.59	0.59	0.98	-8.93E-01	2.42E-17		-1.00E-02	9.50E-01		-2.86E-01	3.43E-08		-1.75E-01	2.41E-03		-2.95E+00	1.10E-33	Down	-2.23E+00	1.48E-25	Down	Unigene46577_All//gi|224131672|ref|XP_002321149.1|//0.00E+00//glycosyl hydrolase family 9 [Populus trichocarpa] >gi|222861922|gb|EEE99464.1|glycosyl hydrolase family 9 [Populus trichocarpa]	Unigene46577_All//0.00E+00//AT2G32990| AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene46577_All//0.00E+00//gi|164251628|gb|ES834212.1|ES834212		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0031410//GO:0044238	nr -
Unigene46578_All	1893	1.41	9.15	4.05	1.82	2.04	2.43	7.64	8.30	12.94	2.70E+00	8.38E-51	Up	1.52E+00	7.60E-11	Up	1.66E-01	6.39E-01		4.23E-01	1.55E-01		1.20E-01	4.10E-01		7.61E-01	1.15E-14		Unigene46578_All//gi|115311477|gb|AB193919.1|//1.00E-129//At1g10040 [Arabidopsis thaliana]	Unigene46578_All//4.00E-129//AT1G10040| unknown protein	Unigene46578_All//4.00E-91//D8459091			GO:0043231	nr +
Unigene46579_All	1716	4.79	12.40	7.98	7.75	9.79	13.03	14.86	52.61	29.07	1.37E+00	8.19E-26	Up	7.36E-01	2.84E-06		3.37E-01	1.16E-02		7.49E-01	4.33E-11		1.82E+00	1.59E-198	Up	9.68E-01	4.23E-43		Unigene46579_All//gi|289466351|gb|ADC94861.1|//1.00E-102//HSF transcription factor [Vitis pseudoreticulata]	Unigene46579_All//4.00E-76//AT4G11660| AT-HSFB2B; transcription factor/ transcription repressor	Unigene46579_All//0.00E+00//TC168462	HSF		GO:0009743//GO:0030528	nr -
Unigene46582_All	877	2.09	2.43	1.58	2.22	2.16	1.96	7.62	15.49	17.13	2.17E-01	6.23E-01		-4.04E-01	4.14E-01		-3.67E-02	9.36E-01		-1.79E-01	7.02E-01		1.02E+00	3.76E-13	Up	1.17E+00	3.79E-18	Up	Unigene46582_All//gi|79387510|ref|NP_186929.2|//9.00E-46//phosphatase/ phosphoprotein phosphatase/ protein tyrosine phosphatase [Arabidopsis thaliana]	Unigene46582_All//5.00E-47//AT3G02800| phosphatase/ phosphoprotein phosphatase/ protein tyrosine phosphatase	Unigene46582_All//0.00E+00//TC144241			GO:0004721//GO:0006796	nr -
Unigene46583_All	1132	5.36	7.48	3.95	6.12	7.39	7.42	17.26	34.26	43.75	4.80E-01	1.66E-02		-4.40E-01	8.54E-02		2.73E-01	2.07E-01		2.79E-01	2.03E-01		9.90E-01	4.05E-34		1.34E+00	1.51E-71	Up	Unigene46583_All//gi|87162589|gb|AB028384.1|//1.00E-79//Tyrosine specific protein phosphatase and dual specificity protein phosphatase; Putative tyrosine phosphatase [Medicago truncatula]	Unigene46583_All//2.00E-79//AT3G02800| phosphatase/ phosphoprotein phosphatase/ protein tyrosine phosphatase	Unigene46583_All//0.00E+00//gi|73864218|gb|DT466957.1|DT466957			GO:0004721//GO:0006796	nr +
Unigene46584_All	2132	3.09	13.21	3.57	2.69	3.83	5.63	13.13	17.53	55.59	2.10E+00	4.90E-61	Up	2.08E-01	3.96E-01		5.11E-01	9.74E-03		1.07E+00	7.90E-11	Up	4.17E-01	8.90E-08		2.08E+00	0.00E+00	Up	Unigene46584_All//gi|226532648|ref|NP_001148060.1|//0.00E+00//MAC/Perforin domain containing protein [Zea mays] >gi|195615364|gb|ACG29612.1|MAC/Perforin domain containing protein [Zea mays]	Unigene46584_All//1.00E-145//AT1G14780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G14290.2); Has 119 Blast hits to 118 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 14; Fungi - 0; Plants - 105; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene46584_All//0.00E+00//TC155025				nr -
Unigene46585_All	1273	2.88	5.17	3.85	29.86	41.39	33.03	56.10	16.45	1.53	8.47E-01	2.37E-04		4.20E-01	1.45E-01		4.71E-01	1.94E-12		1.46E-01	1.12E-01		-1.77E+00	4.44E-151	Down	-5.19E+00	0.00E+00	Down	Unigene46585_All//gi|15294284|gb|AAK95319.1|AF410333_1//9.00E-92//AT3g62730/F26K9_160 [Arabidopsis thaliana] >gi|20147275|gb|AAM10351.1|AT3g62730/F26K9_160 [Arabidopsis thaliana]	Unigene46585_All//2.00E-84//AT3G62730| unknown protein				GO:0005488//GO:0031410	nr +
Unigene46586_All	2174	3.63	1.82	1.94	11.78	9.74	6.98	6.22	2.63	2.53	-9.99E-01	2.01E-06		-9.09E-01	2.60E-05		-2.74E-01	9.31E-03		-7.55E-01	6.95E-13		-1.24E+00	1.45E-17	Down	-1.30E+00	2.07E-19	Down	Unigene46586_All//gi|18076679|emb|CAC84774.1|//1.00E-178//P70 protein [Nicotiana tabacum]	Unigene46586_All//2.00E-115//AT2G37080| myosin heavy chain-related	Unigene46586_All//0.00E+00//TC177697				nr +
Unigene46588_All	1234	19.46	9.40	9.06	42.91	30.86	24.23	39.16	7.15	13.79	-1.05E+00	2.53E-19	Down	-1.10E+00	4.89E-20	Down	-4.76E-01	5.53E-13		-8.25E-01	3.06E-30		-2.45E+00	9.75E-156	Down	-1.51E+00	9.13E-84	Down	Unigene46588_All//gi|18141198|ref|NP_567427.1|//1.00E-109//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|79325109|ref|NP_001031639.1|dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75249435|sp|Q93V7.1|PMT3_ARATH RecName: Full=Probable methyltransferase PMT3	Unigene46588_All//8.00E-108//AT4G14360| dehydration-responsive protein-related	Unigene46588_All//0.00E+00//TC139117				nr -
Unigene46590_All	2418	0.67	0.65	0.66	0.91	0.58	0.47	1.29	0.80	0.64	-4.63E-02	9.39E-01		-2.19E-02	9.89E-01		-6.35E-01	1.35E-01		-9.57E-01	2.75E-02		-7.03E-01	2.52E-02		-1.01E+00	9.66E-04	Down	Unigene46590_All//gi|18411376|ref|NP_565150.1|//0.00E+00//VPS45 (VACUOLAR PROTEIN SORTING 45); protein transporter [Arabidopsis thaliana] >gi|28201912|sp|O49048.2|VPS45_ARATH RecName: Full=Vacuolar protein sorting-associated protein 45 homolog; Short=AtVPS45 >gi|3540194|gb|AAC34344.1|AtVPS45p [Arabidopsis thaliana] >gi|15215684|gb|AAK93388.1|At1g77140/T14N5_2 [Arabidopsis thaliana] >gi|20835922|gb|AAM26638.1|At1g77140/T14N5_2 [Arabidopsis thaliana]	Unigene46590_All//0.00E+00//AT1G77140| VPS45 (VACUOLAR PROTEIN SORTING 45); protein transporter	Unigene46590_All//0.00E+00//ES820298		ko03040|Spliceosome	GO:0000325//GO:0005488//GO:0015031//GO:0022892//GO:0044431//GO:0048278	nr -
Unigene46592_All	2570	0.69	0.47	0.44	3.14	2.87	1.88	4.10	4.78	1.49	-5.49E-01	2.61E-01		-6.70E-01	1.95E-01		-1.31E-01	5.89E-01		-7.40E-01	2.14E-04		2.23E-01	1.52E-01		-1.46E+00	4.05E-18	Down	Unigene46592_All//gi|75115359|sp|Q66Q42.1|Y5162_ARATH//1.00E-142//RecName: Full=Uncharacterized protein At5g41620 >gi|51536470|gb|AAU05473.1|At5g41620 [Arabidopsis thaliana] >gi|53850503|gb|AAU95428.1|At5g41620 [Arabidopsis thaliana]	Unigene46592_All//9.00E-142//AT5G41620| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, plasma membrane; EXPRESSED IN: 9 plant structures; EXPRESSED DURING: 6 growth stages; BEST Arabidopsis thaliana protein match is: intracellular protein transport protein USO1-related (TAIR:AT1G41180.1); Has 2568 Blast hits to 2157 proteins in 267 species: Archae - 27; Bacteria - 258; Metazoa - 955; Fungi - 181; Plants - 134; Viruses - 0; Other Eukaryotes - 1013 (source: NCBI BLink).	Unigene46592_All//0.00E+00//TC157400				nr -
Unigene46596_All	1988	2.53	6.88	3.13	4.26	6.63	7.25	7.83	5.34	1.90	1.45E+00	3.75E-18	Up	3.11E-01	2.37E-01		6.39E-01	1.13E-05		7.67E-01	1.20E-07		-5.52E-01	1.16E-05		-2.04E+00	1.22E-41	Down				Unigene46596_All//0.00E+00//TC156668				
Unigene46597_All	2337	6.31	3.66	3.30	27.45	23.75	16.10	13.98	6.15	7.50	-7.85E-01	8.86E-08		-9.34E-01	1.05E-09		-2.09E-01	9.24E-04		-7.70E-01	1.61E-32		-1.18E+00	1.87E-38	Down	-8.99E-01	1.79E-25		Unigene46597_All//gi|121308607|dbj|BAF43699.1|//0.00E+00//PERK1-like protein kinase [Nicotiana tabacum]	Unigene46597_All//9.00E-164//AT3G24550| ATPERK1 (PROLINE EXTENSIN-LIKE RECEPTOR KINASE 1); ATP binding / protein kinase	Unigene46597_All//0.00E+00//TC147070		ko00270|Cysteine and methionine metabolism	GO:0004672//GO:0004871//GO:0006464//GO:0006950//GO:0016021//GO:0032559//GO:0043231//GO:0051707	nr -
Unigene46599_All	1781	2.23	38.44	16.21	4.75	30.45	49.14	2.64	4.32	11.39	4.11E+00	9.56E-292	Up	2.86E+00	1.30E-87	Up	2.68E+00	8.84E-183	Up	3.37E+00	0.00E+00	Up	7.13E-01	1.37E-04		2.11E+00	1.05E-55	Up	Unigene46599_All//gi|15242182|ref|NP_199989.1|//1.00E-115//ABG1 (ABA-hypersensitive germination 1); catalytic/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75309185|sp|Q9FLI3.1|P2C75_ARATH RecName: Full=Probable protein phosphatase 2C 75; Short=AtP2C75; AltName: Full=Protein phosphatase 2C ABG1; Short=PP2C ABG1; AltName: Full=Protein ABA-HYPERSENSITIVE GERMINATION 1 >gi|10177875|dbj|BAB11245.1|protein phosphatase-2C; PP2C-like protein [Arabidopsis thaliana]	Unigene46599_All//8.00E-101//AT5G51760| ABG1 (ABA-hypersensitive germination 1); catalytic/ protein serine/threonine phosphatase	Unigene46599_All//0.00E+00//ES808392			GO:0003824	nr -

Unigene466_All	2320	0.90	1.46	2.11	1.31	1.47	1.07	2.53	2.76	6.18	6.98E-01	3.76E-02		1.23E+00	2.34E-05	Up	1.66E-01	6.71E-01		-2.91E-01	4.68E-01		1.22E-01	6.41E-01		1.29E+00	4.63E-20	Up	Unigene466_All//gi|115440625|ref|NP_001044592.1|//1.00E-118//Os01g0812000 [Oryza sativa Japonica Group] >gi|122241089|sp|Q0JIC2.1|GAM1_ORYSJ RecName: Full=Transcription factor GAMYB; AltName: Full=OsGAMyb >gi|18844771|dbj|BAB85242.1| transcription factor GAMyb [Oryza sativa Japonica Group] >gi|113534123|dbj|BAF06506.1| Os01g0812000 [Oryza sativa Japonica Group]	Unigene466_All//1.00E-116//AT5G06100| MYB33 (MYB DOMAIN PROTEIN 33); DNA binding / transcription factor	Unigene466_All//0.00E+00//TC178444	MYB			GO:0003676//GO:0010468//GO:0043231	nr -
Unigene4660_All	409	683.50	55.75	99.08	131.05	149.61	226.37	0.83	0.20	1.07	-3.62E+00	0.00E+00	Down	-2.79E+00	0.00E+00	Down	1.91E-01	4.04E-03		7.89E-01	3.45E-48		-2.02E+00	1.36E-01		3.74E-01	6.82E-01		Unigene4660_All//gi|29467501|dbj|BAC67189.1|//4.00E-38//expansin [Pyrus communis]	Unigene4660_All//2.00E-15//AT5G02260| ATEXPA9 (ARABIDOPSIS THALIANA EXPANSIN A9)	Unigene4660_All//8.00E-157//gi|164242973|gb|ES821101.1|ES821101				nr +
Unigene46601_All	395	10.33	8.34	8.36	6.94	3.92	1.94	0.96	2.12	1.11	-3.09E-01	3.31E-01		-3.06E-01	3.63E-01		-8.22E-01	2.23E-02		-1.84E+00	5.93E-06	Down	1.14E+00	1.06E-01		2.04E-01	8.26E-01		Unigene46601_All//gi|297797974|ref|XP_002866871.1|//6.00E-06//EMB2453 [Arabidopsis lyrata subsp. lyrata] >gi|297312707|gb|EFH43130.1| EMB2453 [Arabidopsis lyrata subsp. lyrata]	Unigene46601_All//1.00E-05//AT4G39620| EMB2453 (embryo defective 2453)	Unigene46601_All//7.00E-154//DT052329				nr -
Unigene46606_All	670	1.17	0.00	0.24	1.56	1.70	1.69	2.02	1.93	2.02	-1.02E+01	1.09E-04	Down	-2.30E+00	1.79E-02		1.20E-01	8.71E-01		1.10E-01	8.80E-01		-6.25E-02	9.17E-01		1.60E-03	1.00E+00		Unigene46606_All//gi|212717123|gb|ACJ37403.1|//1.00E-51//CC-NBS-LRR class disease resistance protein [Glycine max]	Unigene46606_All//3.00E-49//AT1G50180| disease resistance protein (CC-NBS-LRR class), putative	Unigene46606_All//2.00E-90//TC153347		ko04626|Plant-pathogen interaction	GO:0016787	nr +
Unigene46609_All	3390	1.45	1.88	0.86	8.13	5.37	4.57	7.76	4.80	2.99	3.76E-01	1.18E-01		-7.48E-01	8.11E-03		-5.97E-01	2.49E-10		-8.31E-01	3.42E-16		-6.94E-01	3.86E-13		-1.38E+00	2.60E-40	Down	Unigene46609_All//gi|225454979|ref|XP_002278113.1|//0.00E+00//PREDICTED: similar to MIM (HYPERSENSITIVE TO MMS, IRRADIATION AND MMC) ; ATP binding [Vitis vinifera]	Unigene46609_All//0.00E+00//AT5G07660| structural maintenance of chromosomes (SMC) family protein	Unigene46609_All//0.00E+00//gi|164275645|gb|ES813846.1|ES813846			GO:0000725//GO:0007059//GO:0010212//GO:0032259//GO:0043231//GO:0043232	nr -
Unigene4661_All	607	73.27	6.09	14.21	49.24	27.17	56.92	2.37	1.10	0.79	-3.59E+00	1.51E-172	Down	-2.37E+00	1.43E-108	Down	-8.58E-01	8.80E-21		2.09E-01	2.96E-02		-1.10E+00	2.77E-02		-1.59E+00	1.64E-03		Unigene4661_All//gi|81230695|gb|ABB59694.1|//6.00E-95//alpha-expansin 2 [Goossypium hirsutum]	Unigene4661_All//3.00E-73//AT2G40610| ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	Unigene4661_All//0.00E+00//gi|78338558|gb|DT558832.1|DT558832				nr -
Unigene46610_All	1168	12.32	29.07	19.51	14.12	18.37	16.39	17.41	19.90	10.33	1.24E+00	7.45E-35	Up	6.64E-01	1.98E-08		3.80E-01	8.01E-04		2.16E-01	1.18E-01		1.92E-01	7.82E-02		-7.53E-01	3.53E-12		Unigene46610_All//gi|22326767|ref|NP_196828.2|//9.00E-91//transcription regulator [Arabidopsis thaliana]	Unigene46610_All//4.00E-92//AT5G13240| transcription regulator	Unigene46610_All//0.00E+00//TC174067			GO:0006359//GO:0043231	nr +
Unigene46611_All	1434	15.43	34.84	24.77	81.18	48.92	46.27	226.94	216.12	152.16	1.17E+00	6.14E-47	Up	6.82E-01	2.22E-13		-7.31E-01	1.21E-60		-8.11E-01	4.65E-64		-7.05E-02	8.69E-03		-5.77E-01	1.94E-113		Unigene46611_All//gi|51564277|gb|ABS17589.1|//8.00E-78//SKP1 component-like 1 [Humulus lupulus]	Unigene46611_All//2.00E-66//AT5G42190| ASK2 (ARABIDOPSIS SKP1-LIKE 2); protein binding / ubiquitin-protein ligase	Unigene46611_All//0.00E+00//TC155125		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0003006//GO:0005488//GO:0019941//GO:0031461	nr -
Unigene46613_All	1450	4.51	2.41	3.82	3.33	2.94	3.61	2.27	0.86	1.79	-9.04E-01	9.51E-05		-2.40E-01	3.59E-01		-1.78E-01	5.65E-01		1.17E-01	6.77E-01		-1.40E+00	1.11E-05	Down	-3.49E-01	2.53E-01		Unigene46613_All//gi|108861900|sp|Q2E9C3.1|RH58_ARATH//1.00E-157//RecName: Full=DEAD-box ATP-dependent RNA helicase 58, chloroplastic; Flags: Precursor	Unigene46613_All//7.00E-159//AT5G19210| DEAD/DEAH box helicase, putative	Unigene46613_All//0.00E+00//gi|164310451|gb|ES835531.1|ES835531		ko03040|Spliceosome		nr +
Unigene46617_All	877	26.79	10.23	20.89	1.25	1.45	0.46	0.00	0.00	0.36	-1.39E+00	4.67E-29	Down	-3.59E-01	2.39E-03		2.17E-01	7.73E-01		-1.43E+00	3.46E-02		null	null		8.51E+00	1.34E-02		Unigene46617_All//gi|15227684|ref|NP_180560.1|//1.00E-115//NDA2 (ALTERNATIVE NAD(P)H DEHYDROGENASE 2); FAD binding / NADH dehydrogenase/ oxidoreductase [Arabidopsis thaliana]	Unigene46617_All//1.00E-116//AT2G29990| NDA2 (ALTERNATIVE NAD(P)H DEHYDROGENASE 2); FAD binding / NADH dehydrogenase/ oxidoreductase	Unigene46617_All//0.00E+00//gi|109883746|gb|DW512716.1|DW512716		ko00190|Oxidative phosphorylation		nr +
Unigene4662_All	1496	2.34	0.20	1.10	7.46	4.35	8.03	15.86	5.81	21.28	-3.53E+00	7.80E-14	Down	-1.09E+00	1.80E-03		-7.78E-01	6.73E-07		1.07E-01	6.16E-01		-1.45E+00	4.52E-38	Down	4.24E-01	3.60E-07		Unigene4662_All//gi|15239000|ref|NP_199665.1|//6.00E-88//33 kDa secretory protein-related [Arabidopsis thaliana] >gi|75180590|sp|Q9LV60.1|CRR55_ARATH RecName: Full=Cysteine-rich repeat secretory protein 55; Flags: Precursor >gi|8777384|dbj|BAA96974.1| 33 kDa secretory protein-like [Arabidopsis thaliana]	Unigene4662_All//8.00E-81//AT5G48540| 33 kDa secretory protein-related	Unigene4662_All//0.00E+00//DW234197				nr +
Unigene46620_All	2295	20.50	12.14	15.38	28.76	24.17	14.05	24.35	16.48	11.04	-7.55E-01	1.31E-21		-4.14E-01	1.82E-07		-2.51E-01	3.44E-05		-1.03E+00	1.06E-54	Down	-5.63E-01	7.01E-19		-1.14E+00	3.00E-63	Down	Unigene46620_All//gi|75171749|sp|Q9FMX2.1|TCP7_ARATH//2.00E-76//RecName: Full=Transcription factor TCP7	Unigene46620_All//7.00E-53//AT5G23280| TCP family transcription factor, putative	Unigene46620_All//0.00E+00//TC168939	TCP		GO:0001071//GO:0005488//GO:0010468//GO:0043231//GO:0043392	nr +
Unigene46621_All	1816	3.34	0.39	1.73	7.74	3.45	6.62	3.73	2.42	1.86	-3.10E+00	5.19E-21	Down	-9.50E-01	1.61E-04		-1.16E+00	2.24E-16	Down	-2.26E-01	1.71E-01		-6.24E-01	1.88E-03		-9.98E-01	5.85E-07		Unigene46621_All//gi|15240232|ref|NP_200945.1|//1.00E-149//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75171474|sp|Q9FLJ6.1|PP439_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g61370, mitochondrial; Flags: Precursor	Unigene46621_All//1.00E-146//AT5G61370| pentatricopeptide (PPR) repeat-containing protein	Unigene46621_All//0.00E+00//gi|13351167|gb|BG441515.1|BG441515			GO:0043231	nr -
Unigene46624_All	860	4.50	9.96	7.37	11.01	10.29	14.60	9.14	6.17	4.86	1.15E+00	2.34E-08	Up	7.11E-01	3.53E-03		-9.69E-02	6.55E-01		4.08E-01	1.13E-02		-5.67E-01	2.14E-03		-9.11E-01	6.05E-07		Unigene46624_All//gi|87162873|gb|ABD28668.1|//1.00E-21//Peptidase C14, caspase catalytic subunit p20 [Medicago truncatula]	Unigene46624_All//5.00E-22//AT5G04200| AtMC9 (metacaspase 9); cysteine-type peptidase	Unigene46624_All//0.00E+00//TC158381			GO:0005576//GO:0070011	nr -
Unigene46626_All	1696	26.90	30.62	31.62	37.18	32.30	46.63	22.19	14.98	9.98	1.87E-01	1.44E-02		2.33E-01	2.29E-03		-2.03E-01	1.52E-03		3.27E-01	8.41E-09		-5.66E-01	4.22E-13		-1.15E+00	1.65E-43	Down	Unigene46626_All//gi|87162873|gb|ABM63441.1|//1.00E-06//latex-abundant protein-like [Arabidopsis thaliana]	Unigene46626_All//6.00E-08//AT5G04200| AtMC9 (metacaspase 9); cysteine-type peptidase	Unigene46626_All//6.00E-133//gi|13246286|gb|BE053394.2|BE053394			GO:0005576//GO:0070011	nr -
Unigene46627_All	2220	17.32	12.58	14.18	15.80	12.83	20.43	29.50	19.96	13.78	-4.62E-01	7.50E-08		-2.89E-01	1.42E-03		-3.00E-01	4.65E-04		3.71E-01	1.38E-06		-5.64E-01	5.14E-22		-1.10E+00	1.62E-69	Down	Unigene46627_All//gi|1723182|sp|Q10710.1|STA_RICCO//0.00E+00//RecName: Full=Sugar carrier protein A >gi|169736|gb|AAA79769.1| sugar carrier protein [Ricinus communis]	Unigene46627_All//0.00E+00//AT4G02050| sugar transporter, putative	Unigene46627_All//0.00E+00//TC154898			GO:0006810//GO:0008152//GO:0015291//GO:0016628//GO:0031224	nr -
Unigene46628_All	2248	0.93	0.97	1.97	1.11	0.81	1.73	0.66	0.67	0.43	5.80E-02	9.01E-01		1.08E+00	3.84E-04	Up	-4.49E-01	2.78E-01		6.41E-01	4.14E-02		2.39E-02	9.95E-01		-6.30E-01	1.82E-01		Unigene46628_All//gi|1723182|sp|Q10710.1|STA_RICCO//0.00E+00//RecName: Full=Sugar carrier protein A >gi|169736|gb|AAA79769.1| sugar carrier protein [Ricinus communis]	Unigene46628_All//0.00E+00//AT4G02050| sugar transporter, putative	Unigene46628_All//0.00E+00//TC154898			GO:0006810//GO:0008152//GO:0015291//GO:0016628//GO:0031224	nr +
Unigene46632_All	1360	4.73	3.50	4.15	59.96	62.29	63.76	7.37	2.67	3.43	-4.34E-01	6.57E-02		-1.89E-01	4.63E-01		5.49E-02	4.42E-01		8.86E-02	1.72E-01		-1.46E+00	9.05E-17	Down	-1.10E+00	1.72E-11	Down	Unigene46632_All//gi|297834368|ref|XP_002885066.1|//4.00E-72//IQ-domain 10 [Arabidopsis lyrata subsp. lyrata] >gi|297330906|gb|EFH61325.1| IQ-domain 10 [Arabidopsis lyrata subsp. lyrata]	Unigene46632_All//1.00E-71//AT3G15050| IQD10 (IQ-domain 10); calmodulin binding	Unigene46632_All//0.00E+00//TC166349			GO:0016020	nr +
Unigene46637_All	1786	17.58	38.47	10.70	7.67	4.57	6.30	4.45	154.36	5.49	1.13E+00	1.73E-60	Up	-7.16E-01	7.37E-13		-7.47E-01	8.14E-08		-2.85E-01	7.43E-02		5.12E+00	0.00E+00	Up	3.02E-01	6.57E-02		Unigene46637_All//gi|119640513|gb|ABL85473.1|//1.00E-145//glycosyltransferase UGT71A13 [Maclura pomifera]	Unigene46637_All//5.00E-125//AT3G21760| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene46637_All//0.00E+00//TC158155				nr -
Unigene46639_All	1706	5.58	3.65	3.25	20.38	16.09	8.74	6.67	4.09	4.72	-6.12E-01	9.84E-04		-7.82E-01	5.24E-05		-3.41E-01	5.91E-05		-1.22E+00	6.11E-38	Down	-7.04E-01	2.72E-06		-4.99E-01	6.27E-04		Unigene46639_All//gi|38346716|emb|CAE04866.2|//1.00E-40//OSJNBa0086006.14 [Oryza sativa (japonica cultivar-group)]	Unigene46639_All//6.00E-29//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene46639_All//0.00E+00//BQ409652			GO:0005488//GO:0016772	nr -
Unigene46641_All	1276	16.11	14.81	21.95	38.14	52.33	50.97	8.62	12.55	22.32	-1.22E-01	3.66E-01		4.46E-01	2.43E-05		4.56E-01	8.88E-15		4.18E-01	2.68E-11		5.42E-01	1.20E-05		1.37E+00	5.44E-43	Up	Unigene46641_All//gi|297796807|ref|XP_002866288.1|//1.00E-108//pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312123|gb|EFH42547.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46641_All//1.00E-101//AT5G38730| pfkB-type carbohydrate kinase family protein	Unigene46641_All//0.00E+00//gi|164348923|gb|ES815680.1|ES815680		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene46643_All	1780	9.67	11.41	13.37	14.69	11.94	11.90	20.10	15.90	51.30	2.39E-01	6.15E-02		4.68E-01	5.19E-05		-3.00E-01	3.42E-03		-3.04E-01	4.51E-03		-3.38E-01	2.48E-05		1.35E+00	9.47E-133	Up	Unigene46643_All//gi|15232853|ref|NP_186865.1|//2.00E-60//DNA binding [Arabidopsis thaliana] >gi|53749144|gb|AAU90057.1| At3g02160 [Arabidopsis thaliana] >gi|55167884|gb|AAY43774.1| At3g02160 [Arabidopsis thaliana]	Unigene46643_All//2.00E-61//AT3G02160| DNA binding	Unigene46643_All//0.00E+00//TC135706				nr -
Unigene46645_All	2604	27.99	31.02	31.98	5.26	3.37	3.28	80.78	29.65	23.99	1.48E-01	1.49E-02		1.92E-01	1.49E-03		-6.42E-01	4.24E-06		-6.82E-01	3.81E-06		-1.45E+00	0.00E+00	Down	-1.75E+00	0.00E+00	Down	Unigene46645_All//gi|240255790|ref|NP_192966.5|//0.00E+00//amine oxidase/ copper ion binding / quinone binding [Arabidopsis thaliana] >gi|22654995|gb|AAM88089.1| AT4g12290/T4C9_130 [Arabidopsis thaliana] >gi|28416507|gb|AAO42784.1| AT4g12290/T4C9_130 [Arabidopsis thaliana]	Unigene46645_All//0.00E+00//AT4G12290| amine oxidase/ copper ion binding / quinone binding	Unigene46645_All//0.00E+00//TC144348		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0006807//GO:0016641//GO:0031410//GO:0043231//GO:0046914//GO:0048037	nr +
Unigene46646_All	1529	52.18	41.69	45.38	109.96	107.18	84.21	69.10	60.44	31.63	-3.24E-01	2.39E-08		-2.02E-01	1.12E-03		-3.69E-02	4.63E-01		-3.85E-01	2.08E-24		-1.93E-01	2.12E-05		-1.13E+00	1.74E-116	Down	Unigene46646_All//gi|115484337|ref|NP_001065830.1|//0.00E+00//Os11g0163100 [Oryza sativa Japonica Group] >gi|34851127|gb|AAO62546.1| actin [Oryza sativa Japonica Group] >gi|62732979|gb|AAX95098.1| actin [Oryza sativa Japonica Group] >gi|62732980|gb|AAX95099.1| actin [Oryza sativa Japonica Group] >gi|62732981|gb|AAX95100.1| actin [Oryza sativa Japonica Group] >gi|113644534|dbj|BAF27675.1| Os11g0163100 [Oryza sativa Japonica Group]	Unigene46646_All//0.00E+00//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene46646_All//0.00E+00//TC133433		ko04145|Phagosome	GO:0005198//GO:0006950//GO:0009314//GO:0009725//GO:0009913//GO:0016020//GO:0030312//GO:0031981//GO:0032559//GO:0043232//GO:0048588	nr -
Unigene4665_All	1249	3.10	2.80	1.71	5.58	3.69	4.85	5.59	2.34	2.90	-1.47E-01	6.28E-01		-8.62E-01	8.00E-03		-5.96E-01	4.35E-03		-2.05E-01	4.19E-01		-1.25E+00	1.38E-09	Down	-9.44E-01	1.35E-06		Unigene4665_All//gi|297597082|ref|NP_001043416.2|//3.00E-64//Os01g0583200 [Oryza sativa Japonica Group] >gi|53793441|dbj|BAD53164.1| RNA-binding protein-like [Oryza sativa Japonica Group] >gi|255673398|dbj|BAF05330.2| Os01g0583200 [Oryza sativa Japonica Group]	Unigene4665_All//2.00E-44//AT2G19385| zinc ion binding	Unigene4665_All//0.00E+00//TC179006				nr +
Unigene46653_All	2272	6.40	12.09	8.53	10.61	11.11	13.68	10.72	22.83	17.52	9.17E-01	1.14E-17		4.14E-01	1.51E-03		6.61E-02	6.18E-01		3.66E-01	1.22E-04		1.09E+00	4.68E-53	Up	7.09E-01	1.17E-20		Unigene46653_All//gi|219291116|gb|ACL13991.1|//1.00E-103//At2g33360 [Arabidopsis thaliana]	Unigene46653_All//3.00E-98//AT2G33360| unknown protein	Unigene46653_All//0.00E+00//TC167200			GO:0043231	nr -

Unigene46654_All	2636	19.49	32.02	26.26	17.78	17.40	21.85	12.99	27.19	18.86	7.16E-01	8.53E-35		4.30E-01	2.07E-11		-3.13E-02	7.80E-01		2.97E-01	1.27E-05		1.07E+00	2.48E-70	Up	5.38E-01	5.30E-16		Unigene46654_All//gi|226425257|gb|AC053628.1|//0.00E+00//bHLH domain protein [Gossypium hirsutum]	Unigene46654_All//1.00E-153//AT1G32640| MYC2; DNA binding / transcription activator/ transcription factor	Unigene46654_All//0.00E+00//TC159939	bHLH	ko04626|Plant-pathogen interaction	GO:0003676//GO:0009414//GO:0009725//GO:0009743//GO:0009813//GO:0010552//GO:0016491//GO:0023033//GO:0030528//GO:0034599//GO:0043231//GO:0045449	nr +
Unigene46656_All	1749	3.47	3.85	2.65	3.79	3.41	2.53	5.42	3.75	2.69	1.51E-01	5.48E-01		-3.90E-01	1.35E-01		-1.53E-01	5.61E-01		-5.82E-01	1.04E-02		-5.29E-01	1.47E-03		-1.01E+00	1.47E-09	Down	Unigene46656_All//gi|226457847|gb|EU635145.1|//1.00E-166//glycosyltransferase family 35 protein [Micromonas pusilla CCMP1545]	Unigene46656_All//1.00E-139//AT3G46970| PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups	Unigene46656_All//0.00E+00//TC162611		ko00500|Starch and sucrose metabolism	GO:0016758//GO:0044238//GO:0048037	nr +
Unigene46660_All	2617	11.16	28.36	20.33	42.16	54.15	56.78	13.26	6.77	10.06	1.35E+00	9.19E-86	Up	8.66E-01	1.65E-29		3.61E-01	3.46E-20		4.29E-01	2.84E-26		-9.70E-01	1.11E-29		-3.99E-01	5.25E-07		Unigene46660_All//gi|163889361|gb|ABY48131.1|//0.00E+00//zinc finger protein [Medicago truncatula]	Unigene46660_All//2.00E-149//AT4G37890| EDA40 (embryo sac development arrest 40); protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene46660_All//0.00E+00//TC176803			GO:0000741//GO:0005886//GO:0007155//GO:0046872	nr +
Unigene46661_All	1416	11.49	6.44	3.50	14.63	16.12	15.44	17.23	6.11	8.30	-8.35E-01	2.34E-09		-1.72E+00	2.19E-26	Down	1.40E-01	2.97E-01		7.70E-02	6.27E-01		-1.50E+00	5.00E-41	Down	-1.05E+00	8.44E-25	Down	Unigene46661_All//gi|229890018|dbj|BAH58382.1|//1.00E-119//AtEB1c-like protein [Nicotiana tabacum]	Unigene46661_All//1.00E-108//AT5G67270| ATEB1C (microtubule end binding protein 1); microtubule binding	Unigene46661_All//0.00E+00//TC138626				nr -
Unigene46663_All	2613	46.91	7.06	18.38	24.19	40.17	37.83	28.67	6.51	14.16	-2.73E+00	0.00E+00	Down	-1.35E+00	2.57E-138	Down	7.32E-01	4.37E-53		6.45E-01	2.32E-36		-2.14E+00	6.72E-204	Down	-1.02E+00	3.42E-70	Down	Unigene46663_All//gi|15218202|ref|NP_177929.1|//0.00E+00//glycosyl hydrolase family 3 protein [Arabidopsis thaliana] >gi|259585708|sp|Q9SGZ5.2|BXL7_ARATH RecName: Full=Probable beta-D-xylosidase 7; Short=AtBXL7; Flags: Precursor >gi|18086336|gb|AAL57631.1|At1g78060/F28K19_32 [Arabidopsis thaliana]	Unigene46663_All//0.00E+00//AT1G78060| glycosyl hydrolase family 3 protein	Unigene46663_All//0.00E+00//TC147850		ko00500|Starch and sucrose metabolism/ko00940|Phenylpropanoid biosynthesis/ko00460|Cyanoamino acid metabolism	GO:0005576//GO:0005618//GO:0009536//GO:0015926//GO:0031410//GO:0004338	nr -
Unigene46664_All	1035	2.38	2.25	1.54	9.91	5.22	1.40	4.58	3.96	3.66	-7.73E-02	8.44E-01		-6.22E-01	1.44E-01		-9.25E-01	2.07E-08		-2.83E+00	7.48E-35	Down	-2.09E-01	4.46E-01		-3.23E-01	1.96E-01		Unigene46664_All//gi|297805364|ref|XP_002870566.1|//5.00E-37//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316402|gb|EFH46825.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46664_All//1.00E-32//AT5G37790| protein kinase family protein	Unigene46664_All//0.00E+00//DT459468			GO:0004672//GO:0006464//GO:0032559	nr +
Unigene46665_All	1969	7.07	5.04	3.57	25.75	18.24	6.51	8.89	5.01	6.21	-4.87E-01	1.20E-03		-9.86E-01	5.54E-10		-4.98E-01	1.66E-13		-1.98E+00	1.13E-111	Down	-8.28E-01	5.92E-12		-5.17E-01	7.07E-06		Unigene46665_All//gi|297805364|ref|XP_002870566.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316402|gb|EFH46825.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46665_All//0.00E+00//AT5G37790| protein kinase family protein	Unigene46665_All//0.00E+00//TC140490		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr -
Unigene46668_All	1741	19.41	23.57	21.10	15.28	14.52	11.44	13.92	12.80	6.59	2.80E-01	8.91E-04		1.21E-01	2.43E-01		-7.37E-02	5.77E-01		-4.18E-01	4.90E-05		-1.21E-01	2.94E-01		-1.08E+00	1.52E-25	Down	Unigene46668_All//gi|15240954|ref|NP_195754.1|//1.00E-147//mitochondrial substrate carrier family protein [Arabidopsis thaliana] >gi|15450697|gb|AAK96620.1|AT5g01340/T1008_50 [Arabidopsis thaliana] >gi|20466091|gb|AAM19967.1|AT5g01340/T1008_50 [Arabidopsis thaliana]	Unigene46668_All//5.00E-149//AT5G01340| mitochondrial substrate carrier family protein	Unigene46668_All//0.00E+00//TC170272			GO:0006810//GO:0016020	nr -
Unigene46669_All	1362	15.67	10.42	11.65	27.21	20.78	16.88	14.47	6.44	9.65	-5.89E-01	6.70E-07		-4.28E-01	5.32E-04		-3.89E-01	1.56E-06		-6.89E-01	9.27E-16		-1.17E+00	5.98E-23	Down	-5.84E-01	7.17E-08		Unigene46669_All//gi|297819904|ref|XP_002892833.1|//7.00E-90//atmap70-4 [Arabidopsis lyrata subsp. lyrata] >gi|297338675|gb|EFH69092.1|atmap70-4 [Arabidopsis lyrata subsp. lyrata]	Unigene46669_All//2.00E-71//AT1G14840| ATMAP70-4 (microtubule-associated proteins 70-4); microtubule binding	Unigene46669_All//0.00E+00//TC133384			GO:0003002//GO:0006996//GO:0015631//GO:0016020//GO:0042546//GO:0043231//GO:0055028	nr +
Unigene46667_All	1183	15.61	19.92	60.36	185.99	250.33	375.17	18.19	20.28	19.94	3.51E-01	2.00E-03		1.95E+00	5.08E-137	Up	4.29E-01	1.81E-57		1.01E+00	0.00E+00	Up	1.57E-01	1.55E-01		1.32E-01	2.27E-01		Unigene46667_All//gi|295917225|gb|ADG59899.1|//7.00E-82//annexin 11 [Glycine max]	Unigene46667_All//8.00E-72//AT2G38750| ANNAT4 (ANNEXIN ARABIDOPSIS 4); calcium ion binding / calcium-dependent phospholipid binding	Unigene46667_All//0.00E+00//TC138161				nr +
Unigene46670_All	369	9.07	9.61	8.37	12.01	10.73	16.89	8.48	13.71	20.41	8.30E-02	7.99E-01		-1.17E-01	7.36E-01		-1.63E-01	5.96E-01		4.91E-01	4.16E-02		6.93E-01	3.51E-03		1.27E+00	1.06E-10	Up	Unigene46670_All//gi|297799382|ref|XP_002867575.1|//1.00E-07//hypothetical protein ARALYDRAFT_492193 [Arabidopsis lyrata subsp. lyrata] >gi|297313411|gb|EFH13834.1|hypothetical protein ARALYDRAFT_492193 [Arabidopsis lyrata subsp. lyrata]	Unigene46670_All//2.00E-08//AT4G26190| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: NLI interacting factor (InterPro:IPR004274); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G36550.1); Has 24148 Blast hits to 14674 proteins in 713 species: Archae - 56; Bacteria - 1518; Metazoa - 9576; Fungi - 1916; Plants - 955; Viruses - 87; Other Eukaryotes - 10040 (source: NCBI BLink).	Unigene46670_All//5.00E-127//TC154886				nr -
Unigene46671_All	388	0.00	0.91	0.41	0.77	0.80	0.81	0.22	0.43	2.16	9.84E+00	2.46E-02		8.69E+00	2.38E-01		5.24E-02	9.98E-01		8.10E-02	9.50E-01		9.84E-01	6.33E-01		3.31E+00	2.30E-04	Up	Unigene46671_All//gi|30689737|ref|NP_189619.2|//5.00E-21//NLI interacting factor (NIF) family protein [Arabidopsis thaliana]	Unigene46671_All//3.00E-22//AT3G29760| NLI interacting factor (NIF) family protein	Unigene46671_All//2.00E-98//DT455631				nr +
Unigene46672_All	1557	1.95	2.34	1.64	3.62	2.83	3.31	4.78	6.09	10.93	2.66E-01	4.20E-01		-2.48E-01	5.28E-01		-3.53E-01	1.66E-01		-1.29E-01	6.58E-01		3.51E-01	4.09E-02		1.19E+00	4.41E-21	Up	Unigene46672_All//gi|20473411|gb|AM22488.1|//3.00E-63//3615.7 [Oryza sativa Japonica Group]	Unigene46672_All//6.00E-55//AT3G29760| NLI interacting factor (NIF) family protein	Unigene46672_All//0.00E+00//TC154886				nr +
Unigene46673_All	2074	10.52	32.69	17.97	27.02	23.74	35.54	42.87	47.98	59.82	1.64E+00	1.86E-104	Up	7.73E-01	2.97E-17		-1.87E-01	7.57E-03		3.95E-01	1.61E-11		1.63E-01	6.62E-04		4.81E-01	1.41E-31		Unigene46673_All//gi|224080620|ref|XP_002306182.1|//0.00E+00//plant synaptotagmin [Populus trichocarpa] >gi|222849146|gb|EEE86693.1| plant synaptotagmin [Populus trichocarpa]	Unigene46673_All//0.00E+00//AT2G20990| SYTA (SYNAPTOTAGMIN A)	Unigene46673_All//0.00E+00//gi|109847828|gb|DW476808.1|DW476808			GO:0006605//GO:0006950//GO:0007009//GO:0016020//GO:0016197//GO:0031410//GO:0043231//GO:0046739//GO:0051707	nr +
Unigene46675_All	1582	1.06	2.11	1.92	0.85	1.74	1.54	1.58	4.91	4.26	9.98E-01	3.52E-03		8.58E-01	2.21E-02		1.03E+00	5.41E-03		8.59E-01	3.79E-02		1.64E+00	2.08E-15	Up	1.43E+00	1.82E-11	Up	Unigene46675_All//gi|14517538|gb|AK62659.1|//8.00E-42//AT4g25670/L73G19_50 [Arabidopsis thaliana] >gi|18700212|gb|AAL77716.1|AT4g25670/L73G19_50 [Arabidopsis thaliana]	Unigene46675_All//3.00E-30//AT4G25670| unknown protein	Unigene46675_All//0.00E+00//TC169576			GO:0005488	nr +
Unigene46676_All	1228	51.38	74.11	184.77	33.47	83.37	159.87	61.97	25.77	251.55	5.28E-01	4.54E-22		1.85E+00	0.00E+00	Up	1.32E+00	2.19E-135	Up	2.26E+00	0.00E+00	Up	-1.27E+00	3.15E-98	Down	2.02E+00	0.00E+00	Up	Unigene46676_All//gi|196259696|dbj|BAG68856.1|//2.00E-39//jasmonate ZIM-domain protein 2 [Nicotiana tabacum]	Unigene46676_All//5.00E-29//AT3G17860| JAZ3 (JASMONATE-ZIM-DOMAIN PROTEIN 3)	Unigene46676_All//0.00E+00//TC1316 89	Tify	ko04626|Plant-pathogen interaction		nr -
Unigene46677_All	1424	102.66	49.85	81.52	42.22	46.43	35.55	48.04	36.95	21.82	-1.04E+00	1.00E-112	Down	-3.33E-01	1.07E-14		1.37E-01	4.24E-02		-2.48E-01	2.27E-04		-3.79E-01	1.79E-11		-1.14E+00	6.72E-77	Down	Unigene46677_All//gi|259496080|gb|ACW82829.1|//1.00E-109//F-box/kelch protein [Vitis vinifera]	Unigene46677_All//8.00E-75//AT1G23390| kelch repeat-containing F-box family protein	Unigene46677_All//0.00E+00//gi|78332957|gb|DT553231.1|DT553231				nr +
Unigene46678_All	1879	7.13	2.67	6.21	28.98	20.89	13.15	5.65	1.45	0.93	-1.42E+00	2.25E-17	Down	-2.00E-01	2.45E-01		-4.72E-01	3.68E-13		-1.14E+00	5.71E-53	Down	-1.97E+00	1.74E-26	Down	-2.60E+00	3.27E-38	Down	Unigene46678_All//gi|297819968|ref|XP_002877867.1|//3.00E-95//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323705|gb|EFH54126.1|aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46678_All//2.00E-81//AT3G32500| aspartyl protease family protein	Unigene46678_All//0.00E+00//TC135339			GO:0005618	nr +
Unigene46679_All	1438	10.15	4.58	7.89	5.54	6.82	4.96	2.91	2.91	4.07	-1.15E+00	8.22E-14	Down	-3.64E-01	1.94E-02		3.00E-01	1.16E-01		-1.60E-01	5.05E-01		-2.10E-03	1.01E+00		4.85E-01	2.34E-02		Unigene46679_All//gi|15081620|gb|AK82465.1|//3.00E-46//AT5g59400/f2o15_60 [Arabidopsis thaliana] >gi|15777877|gb|AAL05899.1|AT5g59400/f2o15_60 [Arabidopsis thaliana]	Unigene46679_All//4.00E-90//AT5G59400| unknown protein	Unigene46679_All//0.00E+00//gi|78335145|gb|DT555419.1|DT555419			GO:0031410//GO:0043231	nr +
Unigene46680_All	1747	4.52	5.16	6.55	1.71	3.00	4.03	2.25	3.59	4.65	1.91E-01	3.73E-01		5.35E-01	2.16E-03		8.08E-01	1.27E-03		1.24E+00	3.58E-08	Up	6.73E-01	1.34E-03		1.05E+00	1.03E-08	Up	Unigene46680_All//gi|145334337|ref|NP_001078550.1|//1.00E-150//SRT2 (SIRTUIN 2); DNA binding / NAD or NADH binding / NAD-dependent histone deacetylase/ zinc ion binding [Arabidopsis thaliana]	Unigene46680_All//4.00E-138//AT5G09230| SRT2 (SIRTUIN 2); DNA binding / NAD or NADH binding / NAD-dependent histone deacetylase/ zinc ion binding	Unigene46680_All//0.00E+00//gi|78334117|gb|DT554391.1|DT554391			GO:0006464//GO:0016458//GO:0016810//GO:0044424//GO:0046914//GO:0051287	nr +
Unigene46681_All	513	1.84	1.48	0.93	11.65	7.32	5.19	14.67	26.23	2.87	-3.09E-01	6.29E-01		-9.75E-01	2.00E-01		-6.71E-01	3.10E-03		-1.17E+00	1.48E-06	Down	8.39E-01	1.45E-09		-2.35E+00	2.00E-24	Down	Unigene46681_All//gi|4097571|gb|AAD09514.1|//1.00E-09//GMF75 [Glycine max]	Unigene46681_All//1.00E-08//AT2G36950| heavy-metal-associated domain-containing protein	Unigene46681_All//3.00E-58//TC145830			GO:0006812//GO:0046914	nr -
Unigene46682_All	595	2.29	4.51	2.95	29.05	20.37	11.77	15.42	41.23	4.29	9.81E-01	1.13E-02		3.69E-01	4.72E-01		-5.12E-01	3.30E-05		-1.30E+00	4.08E-21	Down	1.42E+00	3.99E-38	Up	-1.85E+00	6.46E-22	Down	Unigene46682_All//gi|15242741|ref|NP_195958.1|//1.00E-07//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|7378619|emb|CAB83295.1|farnesylated protein-like [Arabidopsis thaliana] >gi|16604513|gb|AAL24262.1|At5g03380/C160EPL23M [Arabidopsis thaliana] >gi|21591780|gb|AAM64219.1|cadmium induced protein CdI19 [Arabidopsis thaliana] >gi|21655291|gb|AAM65357.1|At5g03380/C160EPL23M [Arabidopsis thaliana]	Unigene46682_All//4.00E-07//AT2G36950| heavy-metal-associated domain-containing protein	Unigene46682_All//3.00E-71//TC145830			GO:0006812//GO:0046872	nr +

Unigene46683_All	1147	34.39	54.91	33.05	294.50	282.69	173.84	149.03	314.87	61.51	6.75E-01	1.26E-23		-5.73E-02	5.99E-01		-5.91E-02	4.46E-02		-7.61E-01	1.35E-165		1.08E+00	0.00E+00	Up	-1.28E+00	6.53E-229	Down	Unigene46683_All//gi|15242741|ref|NP_195958.1|//4.00E-88//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|7378619|emb|CAB83295.1|farnesylated protein-like [Arabidopsis thaliana] >gi|16604513|gb|AAL24262.1|At5g03380/C160EPL23M [Arabidopsis thaliana] >gi|21591780|gb|AAM64219.1|cadmium induced protein CdI19 [Arabidopsis thaliana] >gi|21655291|gb|AAM65357.1|At5g03380/C160EPL23M [Arabidopsis thaliana]	Unigene46683_All//1.00E-43//AT2G36950| heavy-metal-associated domain-containing protein	Unigene46683_All//0.00E+00//TC145830		ko03040|Spliceosome	GO:0046914	nr +
Unigene46688_All	2274	5.98	5.64	5.64	11.52	9.25	7.79	7.83	3.25	3.89	-8.56E-02	6.09E-01		-8.41E-02	6.11E-01		-3.17E-01	1.81E-03		-5.66E-01	3.76E-08		-1.27E+00	1.38E-23	Down	-1.01E+00	3.86E-17	Down	Unigene46688_All//gi|17065500|gb|AL32904.1|//2.00E-40//Unknown protein [Arabidopsis thaliana]	Unigene46688_All//1.00E-35//AT1G78810| unknown protein	Unigene46688_All//0.00E+00//gi|21097296|gb|BQ409609.1|BQ409609				nr +
Unigene46689_All	2357	3.04	2.15	2.96	4.84	4.70	3.99	3.80	1.76	1.28	-5.01E-01	2.26E-02		-3.92E-02	8.73E-01		-4.09E-02	8.22E-01		-2.80E-01	1.20E-01		-1.12E+00	3.52E-10	Down	-1.57E+00	3.85E-17	Down	Unigene46689_All//gi|17065500|gb|AL32904.1|//6.00E-43//Unknown protein [Arabidopsis thaliana]	Unigene46689_All//5.00E-38//AT1G78810| unknown protein	Unigene46689_All//0.00E+00//gi|21097296|gb|BQ409609.1|BQ409609				nr +
Unigene46690_All	2105	5.74	4.24	4.68	7.27	7.66	5.11	8.92	2.82	3.75	-4.39E-01	7.44E-03		-2.95E-01	9.57E-02		7.56E-02	6.59E-01		-5.09E-01	2.73E-04		-1.66E+00	7.25E-37	Down	-1.25E+00	4.09E-25	Down	Unigene46690_All//gi|224137640|ref|XP_002327176.1|//0.00E+00//f-box family protein [Populus trichocarpa] >gi|222835491|gb|EEE73926.1| f-box family protein [Populus trichocarpa]	Unigene46690_All//2.00E-159//AT1G47056| VFB1 (VIER F-BOX PROTEINE 1); ubiquitin-protein ligase	Unigene46690_All//0.00E+00//TC158328		ko04626|Plant-pathogen interaction//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene46691_All	3379	1.64	2.13	1.48	7.15	4.70	3.56	13.10	3.65	4.42	3.76E-01	9.27E-02		-1.48E-01	6.21E-01		-6.06E-01	2.29E-09		-1.01E+00	1.47E-19	Down	-1.84E+00	2.51E-99	Down	-1.57E+00	2.31E-81	Down	Unigene46691_All//gi|224589616|gb|ACN38341.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene46691_All//0.00E+00//AT4G20270| BAM3 (BARELY ANY MERISTEM 3); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene46691_All//0.00E+00//gi|72276428|gb|DT050630.1|DT050630			GO:0003006//GO:0004672//GO:0005488//GO:0006952//GO:0006950//GO:0009536//GO:0009933//GO:0010073//GO:0016020//GO:0016160	nr +
Unigene46692_All	2496	10.12	4.41	5.27	12.85	8.39	13.82	17.55	7.60	12.24	-1.20E+00	5.05E-25	Down	-9.42E-01	2.16E-16		-6.16E-01	1.29E-12		1.05E-01	3.43E-01		-1.21E+00	8.94E-53	Down	-5.20E-01	1.90E-13		Unigene46692_All//gi|186478661|ref|NP_564088.2|//0.00E+00//NFD5 (NUCLEAR FUSION DEFECTIVE 5) [Arabidopsis thaliana] >gi|8778424|gb|AAF79432.1|AC025808_14 F18014.27 [Arabidopsis thaliana]	Unigene46692_All//0.00E+00//AT1G19520| NFD5 (NUCLEAR FUSION DEFECTIVE 5)	Unigene46692_All//0.00E+00//gi|164337725|gb|ES814392.1|ES814392				nr -
Unigene46693_All	1502	24.80	53.54	34.57	25.84	46.68	42.67	45.32	64.47	39.97	1.11E+00	1.06E-68	Up	4.79E-01	1.73E-10		8.53E-01	3.63E-46		7.24E-01	5.88E-29		5.09E-01	8.79E-27		-1.81E-01	1.44E-03				Unigene46693_All//0.00E+00//TC164583					
Unigene46696_All	2910	2.75	2.79	1.56	7.53	8.66	8.30	9.14	2.27	4.49	1.82E-02	9.51E-01		-8.23E-01	1.19E-04		2.02E-01	7.75E-02		1.41E-01	2.79E-01		-2.01E+00	3.44E-67	Down	-1.03E+00	8.30E-26	Down	Unigene46696_All//gi|225462236|ref|XP_002270779.1|//0.00E+00//PREDICTED: similar to kinesin motor protein-related [Vitis vinifera]	Unigene46696_All//0.00E+00//AT1G72250| kinesin motor protein-related				GO:0003774//GO:0007017//GO:0015630//GO:0032559	nr +
Unigene46697_All	1828	24.50	61.51	14.89	10.71	13.09	20.88	16.56	24.46	17.33	1.33E+00	6.55E-127	Up	-7.19E-01	3.23E-18		2.90E-01	8.50E-03		9.63E-01	4.54E-28		5.63E-01	3.05E-15		6.52E-02	5.26E-01		Unigene46697_All//gi|15229865|ref|NP_187788.1|//1.00E-136//SYP121 (SYNTAXIN OF PLANTS 121); SNAP receptor/ protein anchor [Arabidopsis thaliana] >gi|28380149|sp|Q9ZS94.1|SY121_ARATH RecName: Full=Syntaxin-121; Short=AtSYP121; AltName: Full=Syntaxin-related protein At-Syr1 >gi|4206789|gb|AAD11809.1|syntaxin-related protein At-SYR1 [Arabidopsis thaliana]	Unigene46697_All//4.00E-127//AT3G11820| SYP121 (SYNTAXIN OF PLANTS 121); SNAP receptor/ protein anchor	Unigene46697_All//0.00E+00//TC133206		ko04130|SNARE interactions in vesicular transport		nr -
Unigene46698_All	1913	9.52	15.26	11.13	5.16	7.63	7.89	8.09	16.60	17.06	6.81E-01	1.57E-11		2.26E-01	8.46E-02		5.66E-01	4.00E-05		6.13E-01	1.31E-05		1.04E+00	2.69E-30	Up	1.08E+00	9.73E-34	Up	Unigene46698_All//gi|110825715|sp|Q38JU2.2|CRYD_SOLLC//0.00E+00//RecName: Full=Cryptochrome DASH, chloroplastic/mitochondrial; AltName: Full=Cryptochrome-3; Flags: Precursor >gi|98467788|gb|ABB01166.2|cryptochrome 3 [Solanum lycopersicum]	Unigene46698_All//1.00E-166//AT5G24850| CRY3 (cryptochrome 3); DNA binding / DNA photolyase/ FMN binding	Unigene46698_All//0.00E+00//CO120624			GO:0003676//GO:0006259//GO:0006464//GO:0009536//GO:0016830	nr +
Unigene46699_All	1995	1.65	4.34	2.67	1.20	1.16	1.90	1.57	4.65	3.63	1.39E+00	3.47E-11	Up	6.92E-01	1.03E-02		-5.15E-02	8.99E-01		6.66E-01	3.68E-02		1.57E+00	3.71E-17	Up	1.21E+00	1.04E-09	Up	Unigene46699_All//gi|110825715|sp|Q38JU2.2|CRYD_SOLLC//0.00E+00//RecName: Full=Cryptochrome DASH, chloroplastic/mitochondrial; AltName: Full=Cryptochrome-3; Flags: Precursor >gi|98467788|gb|ABB01166.2|cryptochrome 3 [Solanum lycopersicum]	Unigene46699_All//0.00E+00//AT5G24850| CRY3 (cryptochrome 3); DNA binding / DNA photolyase/ FMN binding	Unigene46699_All//0.00E+00//gi|21095955|gb|BQ408268.1|BQ408268			GO:0000166//GO:0003676//GO:0003913//GO:0006259//GO:0009536	nr +
Unigene46702_All	2148	14.54	9.67	12.47	15.79	16.51	13.20	20.16	8.97	9.22	-5.88E-01	1.10E-09		-2.22E-01	3.53E-02		6.42E-02	5.82E-01		-2.58E-01	5.84E-03		-1.17E+00	1.44E-49	Down	-1.13E+00	2.49E-48	Down	Unigene46702_All//gi|124359955|gb|ABN07971.1|//0.00E+00//Aldehyde dehydrogenase [Medicago truncatula]	Unigene46702_All//0.00E+00//AT3G66658| ALDH22a1 (Aldehyde Dehydrogenase 22a1); 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Unigene46702_All//0.00E+00//ES816316		ko00260|Glycine, serine and threonine metabolism	GO:0004030//GO:0008152//GO:0031410//GO:0043231	nr -
Unigene46703_All	1706	3.16	1.60	2.12	7.97	6.78	3.49	5.53	2.23	1.75	-9.78E-01	1.64E-04		-5.74E-01	3.37E-02		-2.33E-01	1.49E-01		-1.19E+00	1.47E-14	Down	-1.31E+00	1.64E-13	Down	-1.66E+00	1.85E-19	Down	Unigene46703_All//gi|18417879|ref|NP_567883.1|//1.00E-08//WRKY family transcription factor [Arabidopsis thaliana] >gi|34365741|gb|AAQ65182.1|At4g31805 [Arabidopsis thaliana]	Unigene46703_All//3.00E-34//AT3G09730| unknown protein	Unigene46703_All//0.00E+00//TC136941			GO:0005488	nr +
Unigene46705_All	1354	44.48	131.13	113.42	89.07	90.44	86.22	145.61	22.29	83.86	1.56E+00	1.12E-254	Up	1.35E+00	1.68E-173	Up	2.20E-02	7.44E-01		-4.68E-02	4.34E-01		-2.71E+00	0.00E+00	Down	-7.96E-01	2.14E-121		Unigene46705_All//gi|3158476|gb|AAC17529.1|//1.00E-138//aquaporin 2 [Samanea saman]	Unigene46705_All//1.00E-133//AT3G54820| PIP2;5 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;5); water channel	Unigene46705_All//0.00E+00//TC139746				nr +
Unigene46710_All	1499	17.38	11.46	10.52	23.69	21.46	22.66	20.76	19.18	10.31	-6.01E-01	1.66E-08		-7.25E-01	5.10E-11		-1.43E-01	1.46E-01		-6.46E-02	5.85E-01		-1.14E-01	2.52E-01		-1.01E+00	2.62E-29	Down	Unigene46710_All//gi|20197959|gb|AAD21739.2|//1.00E-107//expressed protein [Arabidopsis thaliana] >gi|20198080|gb|AAM15389.1|expressed protein [Arabidopsis thaliana] >gi|88196755|gb|ABD43020.1|At2g42670 [Arabidopsis thaliana]	Unigene46710_All//7.00E-109//AT3G58670| unknown protein	Unigene46710_All//0.00E+00//TC163712			GO:0008152//GO:0016702//GO:0043231	nr -
Unigene46712_All	641	0.73	1.82	3.32	0.31	1.02	0.78	0.40	0.07	0.00	1.31E+00	4.44E-02		2.18E+00	3.14E-05	Up	1.72E+00	8.16E-02		1.32E+00	2.52E-01		-2.60E+00	1.44E-01		-8.63E+00	3.04E-02		Unigene46712_All//gi|18414386|ref|NP_568128.1|//4.00E-45//electron carrier [Arabidopsis thaliana] >gi|15451054|gb|AAK96798.1|Unknown protein [Arabidopsis thaliana]	Unigene46712_All//7.00E-46//AT5G03880| electron carrier	Unigene46712_All//4.00E-144//TC167071			GO:0009534//GO:0015036//GO:0019725	nr +
Unigene46714_All	338	0.93	0.60	2.52	6.34	5.40	0.40	3.50	0.12	0.59	-6.31E-01	6.22E-01		1.44E+00	8.22E-02		-2.31E-01	6.06E-01		-3.98E+00	4.09E-10	Down	-4.82E+00	2.83E-07	Down	-2.57E+00	6.97E-05	Down	Unigene46714_All//gi|297800188|ref|XP_002867978.1|//1.00E-22//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313814|gb|EFH44237.1|leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46714_All//2.00E-10//AT4G18760| AtRLP51 (Receptor Like Protein 51); protein binding	Unigene46714_All//1.00E-176//TC129648			GO:0005488//GO:0016020//GO:0016772//GO:0023060	nr -
Unigene46715_All	1827	4.27	1.83	1.02	6.24	6.14	4.28	4.24	1.28	3.49	-1.22E+00	1.87E-08	Down	-2.06E+00	2.14E-16	Down	-2.32E-02	9.05E-01		-5.46E-01	9.44E-04		-1.73E+00	1.86E-16	Down	-2.80E-01	1.40E-01		Unigene46715_All//gi|297800188|ref|XP_002867978.1|//1.00E-116//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313814|gb|EFH44237.1|leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46715_All//2.00E-82//AT4G18760| AtRLP51 (Receptor Like Protein 51); protein binding	Unigene46715_All//0.00E+00//AI729616		ko04626|Plant-pathogen interaction		nr +
Unigene46718_All	1328	11.15	25.83	16.36	33.31	28.03	44.52	28.27	33.58	29.46	1.21E+00	4.63E-34	Up	5.53E-01	5.00E-06		-2.49E-01	1.18E-03		4.18E-01	2.45E-10		2.48E-01	5.94E-04		5.93E-02	5.18E-01		Unigene46718_All//gi|224482657|gb|ACN50185.1|//1.00E-112//syntaxin-71 [Annona cherimola]	Unigene46718_All//5.00E-76//AT3G09740| SYP71 (SYNTAXIN OF PLANTS 71); protein transporter	Unigene46718_All//0.00E+00//TC137748		ko04130|SNARE interactions in vesicular transport	GO:0022892//GO:0031224	nr +
Unigene46719_All	1524	4.12	10.04	4.79	4.97	6.12	5.51	9.52	16.02	16.68	1.29E+00	5.00E-17	Up	2.17E-01	3.84E-01		3.02E-01	1.27E-01		1.50E-01	5.32E-01		7.51E-01	6.10E-14		8.10E-01	8.56E-17		Unigene46719_All//gi|124359981|gb|ABN07997.1|//6.00E-08//contains similarity to reverse trancriptase, related [Medicago truncatula]	Unigene46719_All//5.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene46719_All//4.00E-174//TC171395				nr -
Unigene4672_All	1020	8.98	1.94	6.21	6.35	5.03	5.67	3.94	1.39	1.60	-2.21E+00	8.36E-22	Down	-5.31E-01	7.49E-03		-3.36E-01	1.58E-01		-1.64E-01	5.51E-01		-1.50E+00	2.00E-07	Down	-1.30E+00	2.28E-06	Down	Unigene4672_All//gi|297399774|ref|NP_001047798.2|//3.00E-51//Os02g0692700 [Oryza sativa Japonica Group] >gi|255671178|dbj|BAF09712.2|Os02g0692700 [Oryza sativa Japonica Group]	Unigene4672_All//5.00E-51//AT2G27930| binding	Unigene4672_All//2.00E-61//TC179204	PLATZ			nr -
Unigene46722_All	1082	47.05	47.91	39.17	38.07	40.96	41.16	18.60	15.18	8.28	2.60E-02	7.54E-01		-2.64E-01	6.87E-04		1.05E-01	2.57E-01		1.12E-01	2.28E-01		-2.93E-01	9.14E-03		-1.17E+00	3.74E-24	Down	Unigene46722_All//gi|258644638|dbj|BAI39887.1|//1.00E-100//cyclase-like protein [Oryza sativa Indica Group]	Unigene46722_All//4.00E-97//AT4G35220| cyclase family protein	Unigene46722_All//0.00E+00//TC178055			GO:0031410	nr +
Unigene46724_All	2378	2.44	1.90	1.97	2.09	1.46	1.03	2.10	0.90	1.12	-3.65E-01	1.47E-01		-3.10E-01	2.45E-01		-5.18E-01	4.66E-02		-1.03E+00	1.07E-04	Down	-1.23E+00	7.17E-07	Down	-9.02E-01	1.14E-04		Unigene46724_All//gi|13605829|gb|AAK32900.1|AF367313_1//1.00E-117//AT5g04550/T32M21_140 [Arabidopsis thaliana]	Unigene46724_All//1.00E-111//AT5G04550| unknown protein	Unigene46724_All//0.00E+00//TC153174				nr +
Unigene46726_All	1154	0.45	0.66	0.83	0.43	0.36	2.47	4.80	15.65	8.87	5.39E-01	5.02E-01		8.73E-01	2.38E-01		-2.70E-01	8.02E-01		2.51E+00	1.36E-08	Up	1.70E+00	1.05E-36	Up	8.86E-01	2.30E-08		Unigene46726_All//gi|1263291|gb|AAA97409.1|//0.00E+00//alcohol dehydrogenase 2b [Gossypium hirsutum]	Unigene46726_All//6.00E-157//AT1G77120| ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase	Unigene46726_All//0.00E+00//TC135397		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism	GO:0008152//GO:0016616//GO:0046914	nr -
Unigene46727_All	1256	17.91	5.85	15.39	51.60	82.39	111.47	64.30	117.87	79.04	-1.61E+00	1.21E-34	Down	-2.19E-01	8.52E-02		6.75E-01	1.56E-45		1.11E+00	1.67E-128	Up	8.74E-01	3.74E-104		2.98E-01	5.67E-11		Unigene46727_All//gi|1220196|gb|AAA91811.1|//0.00E+00//alcohol dehydrogenase 2a [Gossypium hirsutum]	Unigene46727_All//1.00E-165//AT1G77120| ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase	Unigene46727_All//0.00E+00//TC131586		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism	GO:0008152//GO:0016616//GO:0046914	nr -
Unigene46728_All	1403	19.50	44.39	23.38	36.18	31.37	41.49	26.10	34.82	22.40	1.19E+00	2.94E-59	Up	2.62E-01	9.10E-03		-2.06E-01	4.70E-03		1.98E-01	5.24E-03		4.16E-01	6.83E-10		-2.20E-01	5.47E-03		Unigene46728_All//gi|115459576|ref|NP_001053388.1|//1.00E-105//Os04g0530300 [Oryza sativa Japonica Group] >gi|38346625|emb|CAD41208.2|OSJNBa0074L08.19 [Oryza sativa (japonica cultivar-group)] >gi|38346756|emb|CAE03864.2|OSJNBa0081C01.7 [Oryza sativa (japonica cultivar-group)] >gi|113564959|dbj|BAF15302.1|Os04g0530300 [Oryza sativa Japonica Group]	Unigene46728_All//7.00E-71//AT5G53800| unknown protein	Unigene46728_All//0.00E+00//gi|21095884|gb|BQ408197.1|BQ408197		ko03040|Spliceosome		nr +
Unigene46729_All	934	50.19	40.42	44.41	55.68	39.63	58.36	81.12	39.25	32.67	-3.13E-01	5.73E-05		-1.77E-01	3.93E-02		-4.91E-01	1.75E-13		6.79E-02	4.56E-01		-1.05E+00	2.24E-72	Down	-1.31E+00	2.93E-106	Down	Unigene46729_All//gi|13774348|gb|AAK38843.1|AF346308_1//3.00E-65//histidine-containing phosphotransfer protein [Catharanthus roseus]	Unigene46729_All//8.00E-56//AT3G21510| AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 1); histidine phosphotransfer kinase	Unigene46729_All//0.00E+00//TC159895			GO:0004871//GO:0008152//GO:0009736//GO:0016628//GO:0019901//GO:0023060//GO:0040007//GO:0043231//GO:0048229	nr +

Unigene4673_All	975	3.11	4.99	5.73	11.96	18.40	8.89	20.77	19.46	154.29	6.81E-01	1.26E-02		8.82E-01	7.78E-04		6.22E-01	3.36E-07		-4.27E-01	1.04E-02		-9.40E-02	4.77E-01		2.89E+00	0.00E+00	Up	Unigene4673_All//gi|124359396|gb|AB058859.1|//1.00E-88//Glutamine amidotransferase class-I [Medicago truncatula]	Unigene4673_All//1.00E-61//AT2G23970| defense-related protein, putative	Unigene4673_All//0.00E+00//TC149460		ko00230|Purine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene46730_All	2160	39.97	20.85	31.93	20.59	17.30	17.21	11.78	5.86	7.47	-9.39E-01	2.79E-56		-3.24E-01	1.48E-08		-2.52E-01	9.76E-04		-2.59E-01	1.16E-03		-1.01E+00	2.43E-23	Down	-6.58E-01	4.85E-12		Unigene46730_All|gi|15237183|ref|NP_200065.1|//0.00E+00//OVA6 (OVULE ABORTION 6); ATP binding / aminoacyl-tRNA ligase/ nucleotide binding / proline-tRNA ligase [Arabidopsis thaliana] >gi|10177035|dbj|BAB10183.1| prolyl tRNA synthetase [Arabidopsis thaliana] >gi|34365755|gb|AAQ65189.1| At5g52520 [Arabidopsis thaliana] >gi|51970984|dbj|BAD44184.1| prolyl tRNA synthetase [Arabidopsis thaliana]	Unigene46730_All//0.00E+00//AT5G52520| OVA6 (OVULE ABORTION 6); ATP binding / aminoacyl-tRNA ligase/ nucleotide binding / proline-tRNA ligase	Unigene46730_All//0.00E+00//TC152121		ko00970|Aminoacyl-tRNA biosynthesis	GO:0003006//GO:0004812//GO:0006418//GO:0009532//GO:0009791//GO:0015979//GO:0032559//GO:0048229	nr +
Unigene46731_All	2012	3.28	1.16	2.14	10.92	7.29	6.64	13.89	7.19	5.80	-1.50E+00	1.17E-09	Down	-6.12E-01	1.05E-02		-5.83E-01	5.07E-08		-7.17E-01	3.12E-10		-9.51E-01	2.76E-23		-1.26E+00	2.38E-37	Down	Unigene46731_All//gi|8979726|emb|CAB96847.1|//0.00E+00//argininosuccinate lyase (AtArgH) [Arabidopsis thaliana] >gi|24030227|gb|AAN41291.1| argininosuccinate lyase (AtArgH) [Arabidopsis thaliana]	Unigene46731_All//0.00E+00//AT5G10920| argininosuccinate lyase, putative / arginosuccinase, putative	Unigene46731_All//0.00E+00//ES809903		ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006526//GO:0009532//GO:0016842	nr +
Unigene46732_All	1913	236.22	160.67	193.85	25.96	23.83	22.26	9.99	6.07	4.56	-5.56E-01	2.81E-117		-2.85E-01	3.47E-33		-1.23E-01	1.35E-01		-2.22E-01	3.66E-03		-7.18E-01	2.52E-10		-1.13E+00	6.56E-22	Down	Unigene46732_All//gi|3915699|sp|P49364.2|GCST_PEA//0.00E+00//RecName: Full=Aminomethyltransferase, mitochondrial; AltName: Full=Glycine cleavage system T protein; Short=GCVT; Flags: Precursor >gi|438217|emb|CAA81080.1| T-protein [Pisum sativum] >gi|3021553|emb|CAA10976.1| T protein [Pisum sativum]	Unigene46732_All//0.00E+00//AT1G11860| aminomethyltransferase, putative	Unigene46732_All//0.00E+00//TC133075		ko00910|Nitrogen metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate	GO:0006544//GO:0008168//GO:0016769//GO:0043231//GO:0043234	nr +
Unigene46734_All	2127	37.91	15.10	22.68	57.75	58.06	49.03	19.78	18.92	14.44	-1.33E+00	1.44E-91	Down	-7.41E-01	4.50E-34		7.50E-03	9.05E-01		-2.36E-01	1.59E-07		-6.38E-02	4.87E-01		-4.54E-01	2.62E-10		Unigene46734_All|gi|42563995|ref|NP_187692.2|//1.00E-135//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|145651778|gb|ABP88114.1| At3g10810 [Arabidopsis thaliana]	Unigene46734_All//3.00E-104//AT3G56590| hydroxyproline-rich glycoprotein family protein	Unigene46734_All//0.00E+00//TC170868				nr +
Unigene46735_All	1624	270.11	184.18	221.23	194.93	202.48	149.03	12.76	8.98	3.14	-5.53E-01	1.52E-112		-2.88E-01	8.04E-33		5.48E-02	7.37E-02		-3.87E-01	4.97E-46		-5.06E-01	2.44E-06		-2.02E+00	1.42E-54	Down	Unigene46735_All|gi|197266026|gb|ACH73166.1|//1.00E-129//CONSTANS-like protein [Prunus persica]	Unigene46735_All//3.00E-107//AT5G24930| zinc finger (B-box type) family protein	Unigene46735_All//0.00E+00//TC133393	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr -
Unigene46736_All	1904	8.19	7.50	5.17	14.21	14.34	13.05	13.32	5.97	7.01	-1.26E-01	4.14E-01		-6.62E-01	5.76E-06		1.37E-02	9.24E-01		-1.23E-01	3.21E-01		-1.16E+00	5.54E-29	Down	-9.27E-01	5.55E-21		Unigene46736_All|gi|30680066|ref|NP_187349.2|//0.00E+00//protein arginine N-methyltransferase family protein [Arabidopsis thaliana] >gi|51536598|gb|AAU05537.1| At3g06930 [Arabidopsis thaliana]	Unigene46736_All//0.00E+00//AT3G06930| protein arginine N-methyltransferase family protein	Unigene46736_All//0.00E+00//TC136916			GO:0009908//GO:0016274//GO:0034969//GO:0035247//GO:0042802//GO:0043231//GO:0046983	nr +
Unigene46739_All	1980	23.94	32.01	28.16	14.97	21.97	26.94	20.69	9.69	9.11	4.19E-01	1.72E-10		2.34E-01	1.74E-03		5.53E-01	1.09E-13		8.48E-01	1.37E-31		-1.09E+00	2.24E-42	Down	-1.18E+00	2.79E-49	Down	Unigene46739_All|gi|229814830|gb|ACQ85264.1|//0.00E+00//pectin methylesterase [Musa acuminata AAA Group]	Unigene46739_All//2.00E-161//AT4G02320| pectinesterase family protein	Unigene46739_All//0.00E+00//ES833456		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0030234//GO:0030312//GO:0071555	nr -
Unigene4674_All	800	6.15	5.51	6.12	7.16	6.71	8.24	5.02	4.96	2.34	-1.58E-01	6.03E-01		-5.60E-03	1.00E+00		-9.28E-02	7.69E-01		2.03E-01	4.49E-01		-1.66E-02	9.86E-01		-1.10E+00	4.11E-05	Down	Unigene4674_All|gi|29839555|sp|Q8LS08.1|X5486_ARATH/4.00E-61//RecName: Full=Uncharacterized protein At5g64816; Flags: Precursor >gi|98861067|gb|ABF59017.1| At5g64816 [Arabidopsis thaliana] >gi|222424148|dbj|BAH20033.1| AT5G64816 [Arabidopsis thaliana]	Unigene4674_All//2.00E-62//AT5G64816| unknown protein	Unigene4674_All//0.00E+00//TC154366				nr +
Unigene46740_All	1408	10.03	8.38	13.84	10.61	11.42	10.39	26.24	6.26	14.66	-2.59E-01	9.68E-02		4.64E-01	3.34E-04		1.06E-01	5.55E-01		-3.04E-02	8.67E-01		-2.07E+00	1.51E-96	Down	-8.41E-01	1.08E-25		Unigene46740_All|gi|57283532|emb|CAG27606.1|//0.00E+00//monosaccharide transporter [Populus tremula x Populus tremuloides]	Unigene46740_All//3.00E-169//AT1G34580| monosaccharide transporter, putative	Unigene46740_All//0.00E+00//TC155259			GO:0006810//GO:0008152//GO:0016020//GO:0022857//GO:0031224	nr +
Unigene46741_All	2187	0.81	1.88	2.61	1.07	1.54	1.36	4.08	0.82	2.20	1.21E+00	9.76E-05	Up	1.68E+00	2.31E-09	Up	5.28E-01	1.26E-01		3.49E-01	3.94E-01		-2.31E+00	2.58E-27	Down	-8.88E-01	1.80E-07		Unigene46741_All|gi|57283532|emb|CAG27606.1|//1.00E-168//monosaccharide transporter [Populus tremula x Populus tremuloides]	Unigene46741_All//4.00E-135//AT1G34580| monosaccharide transporter, putative	Unigene46741_All//0.00E+00//gi|78341149|gb|DT561423.1|DT561423				nr -
Unigene46742_All	2216	2.83	2.97	2.16	0.85	0.64	2.71	4.04	6.45	3.04	6.92E-02	7.70E-01		-3.90E-01	1.27E-01		-4.23E-01	3.84E-01		1.67E+00	1.21E-10	Up	6.73E-01	3.65E-07		-4.13E-01	1.41E-02		Unigene46742_All|gi|4530126|gb|AAD21872.1|//1.00E-174//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene46742_All//2.00E-109//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene46742_All//0.00E+00//DN816929		ko04626|Plant-pathogen interaction		nr -
Unigene46743_All	1714	15.81	7.42	9.01	5.96	6.43	6.03	5.13	1.71	2.56	-1.09E+00	4.27E-23	Down	-8.12E-01	9.34E-14		1.10E-01	6.01E-01		1.83E-02	9.44E-01		-1.59E+00	1.29E-16	Down	-1.00E+00	7.27E-09	Down	Unigene46743_All|gi|115436768|ref|NP_001043131.1|//1.00E-177//Os01g0500900 [Oryza sativa Japonica Group] >gi|113532662|dbj|BAF05045.1| Os01g0500900 [Oryza sativa Japonica Group]	Unigene46743_All//0.00E+00//AT3G02660| emb2768 (EMBRYO DEFECTIVE 2768); ATP binding / RNA binding / aminoacyl-tRNA ligase/ nucleotide binding / tyrosine-tRNA ligase	Unigene46743_All//0.00E+00//TC170388		ko00970|Aminoacyl-tRNA biosynthesis	GO:0003676//GO:0004812//GO:0006260//GO:0006418//GO:0032559//GO:0034061//GO:0044424	nr -
Unigene46746_All	1848	6.34	3.98	4.84	12.83	10.45	9.70	8.63	2.87	3.86	-6.74E-01	4.62E-05		-3.90E-01	2.66E-02		-2.96E-01	6.64E-03		-4.03E-01	2.50E-04		-1.59E+00	1.90E-29	Down	-1.16E+00	3.76E-19	Down	Unigene46746_All|gi|3600054|gb|AAC35541.1|//1.00E-162//P2P3.4 gene product [Arabidopsis thaliana] >gi|71143056|gb|AAZ23919.1| At4g11090 [Arabidopsis thaliana]	Unigene46746_All//6.00E-153//AT4G11090| unknown protein	Unigene46746_All//0.00E+00//TC153113				nr +
Unigene46747_All	1450	4.40	7.13	5.66	1.20	0.62	1.90	6.53	28.42	16.98	6.95E-01	9.21E-05		3.61E-01	9.65E-02		-9.61E-01	4.14E-02		6.60E-01	8.96E-02		2.12E+00	5.97E-111	Up	1.38E+00	1.83E-37	Up	Unigene46747_All|gi|30696620|ref|NP_200367.2|//1.00E-133//protein kinase family protein [Arabidopsis thaliana] >gi|75323650|sp|Q6ICW6.1|WNK11_ARATH RecName: Full=Probable serine/threonine-protein kinase WNK11; Short=AtWNK11; AltName: Full=Protein kinase with no lysine 11 >gi|48596991|gb|AAT46036.1| At5g55560 [Arabidopsis thaliana] >gi|50198956|gb|AAT70481.1| At5g55560 [Arabidopsis thaliana]	Unigene46747_All//3.00E-134//AT5G55560| protein kinase family protein	Unigene46747_All//0.00E+00//CO089516		ko04712|Circadian rhythm - plant		nr +
Unigene46748_All	1612	0.23	1.63	1.75	0.25	0.24	0.34	1.08	4.51	2.77	2.85E+00	1.15E-08	Up	2.95E+00	3.52E-09	Up	-7.30E-02	9.25E-01		4.44E-01	6.78E-01		2.07E+00	1.51E-19	Up	1.36E+00	2.19E-07	Up	Unigene46748_All|gi|30696620|ref|NP_200367.2|//1.00E-133//protein kinase family protein [Arabidopsis thaliana] >gi|75323650|sp|Q6ICW6.1|WNK11_ARATH RecName: Full=Probable serine/threonine-protein kinase WNK11; Short=AtWNK11; AltName: Full=Protein kinase with no lysine 11 >gi|48596991|gb|AAT46036.1| At5g55560 [Arabidopsis thaliana] >gi|50198956|gb|AAT70481.1| At5g55560 [Arabidopsis thaliana]	Unigene46748_All//2.00E-134//AT5G55560| protein kinase family protein	Unigene46748_All//0.00E+00//CO089516		ko04712|Circadian rhythm - plant		nr +
Unigene4675_All	1660	9.64	7.48	10.30	9.72	7.38	8.43	10.77	9.22	4.85	-3.67E-01	9.21E-03		9.44E-02	5.62E-01		-3.97E-01	2.59E-03		-2.05E-01	1.84E-01		-2.25E-01	7.10E-02		-1.15E+00	3.79E-21	Down	Unigene4675_All|gi|42567769|ref|NP_196608.2|//1.00E-119//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|50198963|gb|AAT70484.1| At5g10460 [Arabidopsis thaliana]	Unigene4675_All//4.00E-121//AT5G10460| haloacid dehalogenase-like hydrolase family protein	Unigene4675_All//0.00E+00//TC166510				nr -
Unigene46752_All	3471	11.95	5.88	12.24	20.91	15.32	12.91	22.23	28.86	25.97	-1.02E+00	1.64E-31	Down	3.45E-02	7.18E-01		-4.49E-01	6.70E-16		-6.96E-01	7.67E-31		3.77E-01	2.94E-16		2.25E-01	3.09E-06		Unigene46752_All|gi|155242124|gb|ABT18098.1|//0.00E+00//FERONIA receptor-like kinase [Arabidopsis lyrata]	Unigene46752_All//0.00E+00//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene46752_All//0.00E+00//TC133874		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006468//GO:0007275//GO:0009856//GO:0016020//GO:0044426	nr -
Unigene46755_All	1087	5.49	2.94	6.12	4.08	3.99	2.24	5.95	2.61	1.54	-9.02E-01	2.15E-04		1.58E-01	5.45E-01		-3.11E-02	9.18E-01		-8.62E-01	2.37E-03		-1.19E+00	2.84E-08	Down	-1.95E+00	7.90E-17	Down	Unigene46755_All|gi|226500026|ref|NP_001149746.1|//3.00E-47//peptidase C45, acyl-coenzyme A/6-aminopenicillanic acid acyl-transferase [Zea mays] >gi|195630677|gb|ACG36645.1| peptidase C45, acyl-coenzyme A/6-aminopenicillanic acid acyl-transferase [Zea mays]	Unigene46755_All//2.00E-47//AT5G41650| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene46755_All//0.00E+00//TC150836			GO:0016701//GO:0030654	nr +
Unigene46756_All	404	5.05	2.88	7.12	30.95	24.04	14.31	0.94	0.10	0.59	-8.08E-01	7.28E-02		4.95E-01	2.11E-01		-3.65E-01	1.95E-02		-1.11E+00	3.93E-12	Down	-3.19E+00	3.11E-02		-6.71E-01	5.30E-01		Unigene46756_All|gi|34452360|gb|AAQ72578.1|//2.00E-06//resistance protein RGC2 [Lactuca sativa]		Unigene46756_All//1.00E-75//ES850138				nr +
Unigene46758_All	859	4.99	2.83	3.53	8.87	8.30	4.21	2.21	2.53	1.11	-8.19E-01	5.15E-03		-4.99E-01	1.09E-01		-9.66E-02	7.04E-01		-1.08E+00	2.81E-07	Down	1.92E-01	6.29E-01		-9.93E-01	1.44E-02		Unigene46758_All|gi|224117086|ref|XP_002331783.1|//1.00E-12//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222832242|gb|EEE70719.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene46758_All//4.00E-07//AT4G33300| ADR1-L1 (ADR1-like 1); ATP binding / protein binding	Unigene46758_All//3.00E-90//ES850138				nr -
Unigene4676_All	876	163.23	747.09	449.52	210.86	348.24	349.19	39.92	101.29	94.64	2.19E+00	0.00E+00	Up	1.46E+00	0.00E+00	Up	7.24E-01	2.32E-151		7.28E-01	9.17E-138		1.34E+00	3.93E-125	Up	1.25E+00	2.63E-106	Up	Unigene4676_All|gi|77741869|gb|AB802388.1|//1.00E-104//temperature-induced lipocalin' [Gossypium arboreum]	Unigene4676_All//1.00E-73//AT5G58070| TIL (TEMPERATURE-INDUCED LIPOCALIN); binding / transporter	Unigene4676_All//0.00E+00//TC160055				nr -
Unigene46760_All	1038	2.82	1.56	0.72	4.46	2.79	1.61	3.34	0.56	2.03	-8.54E-01	1.94E-02		-1.97E+00	3.42E-06	Down	-6.80E-01	1.02E-02		-1.47E+00	3.34E-07	Down	-2.57E+00	2.22E-12	Down	-7.16E-01	1.20E-02		Unigene46760_All|gi|71480741|gb|AAK85402.2|//1.00E-168//beta-1,3-glucanase [Camellia sinensis]	Unigene46760_All//3.00E-154//AT2G01630| glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative	Unigene46760_All//0.00E+00//TC145789		ko00500|Starch and sucrose metabolism	GO:0008422//GO:0043167//GO:0044238	nr +
Unigene46761_All	1894	3.37	2.17	2.84	2.71	2.91	1.34	5.34	1.43	3.66	-6.37E-01	6.23E-03		-2.47E-01	3.51E-01		1.03E-01	7.59E-01		-1.02E+00	9.42E-05	Down	-1.90E+00	4.37E-24	Down	-5.44E-01	4.81E-04		Unigene46761_All|gi|71480741|gb|AAK85402.2|//0.00E+00//beta-1,3-glucanase [Camellia sinensis]	Unigene46761_All//0.00E+00//AT2G01630| glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative	Unigene46761_All//0.00E+00//TC145789		ko00500|Starch and sucrose metabolism	GO:0008422//GO:0031225//GO:0031410//GO:0043167//GO:0044238	nr +

Unigene46764_All	1104	27.72	8.44	12.44	35.87	26.39	44.80	61.62	25.59	27.75	-1.72E+00	4.67E-51	Down	-1.16E+00	2.44E-27	Down	-4.43E-01	1.07E-08		3.21E-01	1.38E-05		-1.27E+00	4.91E-88	Down	-1.15E+00	8.26E-78	Down	Unigene46764_All//gi|18416588|ref|NP_567724.1|//1.00E-141//FIB2 (FIBRILLARIN 2); snoRNA binding [Arabidopsis thaliana] >gi|67461067|sp|Q94AH9.2|FBRL2_ARATH RecName: Full=rRNA 2'-O-methyltransferase fibrillarin 2; AltName: Full=Fibrillarin-like protein 2 >gi|9965655|gb|AAG10104.1|AF233444_1 fibrillarin 2 [Arabidopsis thaliana] >gi|4914455|emb|CAB43694.1| fibrillarin-like protein [Arabidopsis thaliana] >gi|7269413|emb|CAB81373.1| fibrillarin-like protein [Arabidopsis thaliana] >gi|9965796|gb|AAG10153.1| fibrillarin 2 [Arabidopsis thaliana] >gi|21536840|gb|AAM61172.1| fibrillarin 2 (AtFib2) [Arabidopsis thaliana] >gi|23297150|gb|AAN13105.1| fibrillarin 2 (AtFib2) [Arabidopsis thaliana]	Unigene46764_All//3.00E-129//AT4G25630| FIB2 (FIBRILLARIN 2); snoRNA binding	Unigene46764_All//0.00E+00//TC144974		ko03040|Spliceosome		nr +
Unigene46765_All	863	11.64	9.81	7.90	19.57	15.80	20.99	57.96	26.20	26.96	-2.48E-01	1.97E-01		-5.60E-01	2.91E-03		-3.09E-01	2.04E-02		1.01E-01	5.33E-01		-1.15E+00	2.09E-55	Down	-1.10E+00	8.71E-54	Down	Unigene46765_All//gi|161377377|gb|ABX71676.1|//1.00E-21//60S ribosomal protein L6-like protein [Panax quinquefolius]	Unigene46765_All//2.00E-13//AT1G18540| 60S ribosomal protein L6 (RPL6A)	Unigene46765_All//0.00E+00//gi|21100528|gb|BQ412841.1|BQ412841		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene46766_All	308	2.89	5.43	9.34	0.81	1.57	1.47	12.90	12.89	12.29	9.11E-01	7.45E-02		1.69E+00	4.22E-05	Up	9.53E-01	4.23E-01		8.59E-01	4.69E-01		-1.40E-03	9.95E-01		-7.05E-02	8.00E-01		Unigene46766_All//gi|16118889|gb|AAL14645.1|AF417857_1//6.00E-07//AOP1 [Arabidopsis lyrata] >gi|16118984|gb|AAL14690.1| 2-oxoglutarate-dependent dioxygenase [Arabidopsis lyrata]	Unigene46766_All//5.00E-06//AT4G03070| AOP1; oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene46766_All//2.00E-104//ES826231			GO:0016491	nr -
Unigene46767_All	1286	8.06	22.18	30.77	5.35	1.69	6.46	75.12	86.74	55.79	1.46E+00	1.13E-37	Up	1.93E+00	4.27E-75	Up	-1.66E+00	5.87E-14	Down	2.74E-01	2.19E-01		2.08E-01	2.33E-06		-4.29E-01	2.24E-20		Unigene46767_All//gi|224092400|ref|XP_002309592.1|//3.00E-61//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222855568|gb|EEE93115.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene46767_All//5.00E-48//AT4G03070| AOP1; oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene46767_All//0.00E+00//ES826231		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis	GO:0016491	nr +
Unigene46769_All	258	1.01	0.59	2.27	5.79	4.67	1.40	0.00	1.13	0.00	-7.83E-01	6.20E-01		1.16E+00	2.47E-01		-3.10E-01	5.87E-01		-2.05E+00	5.54E-04	Down	1.01E+01	2.35E-02		null	null		Unigene46769_All//gi|255581160|ref|XP_002531393.1|//8.00E-11//Auxin-induced protein 5NG4, putative [Ricinus communis] >gi|223528986|gb|EEF30977.1| Auxin-induced protein 5NG4, putative [Ricinus communis]	Unigene46769_All//2.00E-06//AT1G60050| nodulin-related				GO:0044464	nr -
Unigene46677_All	953	2.25	1.81	1.68	2.20	2.67	2.32	1.29	2.37	2.93	-3.16E-01	4.77E-01		-4.25E-01	3.74E-01		2.85E-01	5.45E-01		8.09E-02	8.72E-01		8.80E-01	2.08E-02		1.19E+00	3.83E-04	Up								
Unigene46770_All	568	4.97	1.78	4.78	11.58	7.58	7.08	4.32	1.84	0.42	-1.48E+00	1.63E-04	Down	-5.71E-02	8.87E-01		-6.11E-01	4.64E-03		-7.10E-01	1.64E-03		-1.23E+00	8.56E-04	Down	-3.36E+00	6.21E-12	Down	Unigene46770_All//gi|42568214|ref|NP_198840.2|//2.00E-27//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|10177511|dbj|BAB10905.1| nodulin-like protein [Arabidopsis thaliana] >gi|30725298|gb|AAP37671.1| At5g40240 [Arabidopsis thaliana]	Unigene46770_All//1.00E-28//AT5G40240| nodulin MtN21 family protein				GO:0044464	nr +
Unigene46771_All	1118	4.59	1.41	4.19	9.09	7.95	4.69	2.76	1.05	1.43	-1.71E+00	4.31E-09	Down	-1.30E-01	6.36E-01		-1.94E-01	3.22E-01		-9.56E-01	6.53E-08		-1.40E+00	2.18E-05	Down	-9.54E-01	1.90E-03		Unigene46771_All//gi|10177510|dbj|BAB10904.1|//6.00E-60//nodulin-like protein [Arabidopsis thaliana]	Unigene46771_All//1.00E-64//AT5G40240| nodulin MtN21 family protein					nr +
Unigene46773_All	1521	1.62	3.46	3.33	3.86	3.71	3.03	3.47	2.20	4.19	1.10E+00	3.66E-05	Up	1.04E+00	2.06E-04	Up	-5.78E-02	8.17E-01		-3.52E-01	1.79E-01		-6.61E-01	4.30E-03		2.70E-01	2.06E-01		Unigene46773_All//gi|115455525|ref|NP_001051363.1|//2.00E-31//Os03g0762900 [Oryza sativa Japonica Group] >gi|108711227|gb|ABF99022.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549834|dbj|BAF13277.1| Os03g0762900 [Oryza sativa Japonica Group]	Unigene46773_All//1.00E-55//AT1G49890| unknown protein	Unigene46773_All//0.00E+00//TC156441				nr +
Unigene46774_All	860	3.10	2.83	2.48	35.04	20.98	11.34	5.06	2.04	1.25	-1.34E-01	7.24E-01		-3.25E-01	4.20E-01		-7.40E-01	2.65E-16		-1.63E+00	1.29E-50	Down	-1.31E+00	1.14E-06	Down	-2.02E+00	4.40E-12	Down	Unigene46774_All//gi|242056489|ref|XP_002457390.1|//2.00E-08//hypothetical protein SORBIDRAFT_03g006560 [Sorghum bicolor] >gi|241929365|gb|EES02510.1| hypothetical protein SORBIDRAFT_03g006560 [Sorghum bicolor]		Unigene46774_All//7.00E-119//gi|21095732|gb|BQ408045.1|BQ408045				nr +
Unigene46775_All	1357	4.43	3.77	2.67	39.87	22.28	10.62	8.76	3.30	1.56	-2.34E-01	3.74E-01		-7.33E-01	3.57E-03		-8.39E-01	5.54E-36		-1.91E+00	3.61E-113	Down	-1.41E+00	1.01E-18	Down	-2.49E+00	9.63E-41	Down	Unigene46775_All//gi|124359981|gb|ABN07997.1|//5.00E-29//contains similarity to reverse trancriptase, related [Medicago truncatula]	Unigene46775_All//9.00E-17//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene46775_All//3.00E-177//gi|21095732|gb|BQ408045.1|BQ408045				nr -
Unigene46776_All	910	3.68	1.73	1.35	2.19	1.97	2.43	12.08	6.34	6.39	-1.09E+00	1.43E-03		-1.45E+00	8.55E-05	Down	-1.54E-01	7.69E-01		1.51E-01	7.38E-01		-9.31E-01	2.40E-09		-9.18E-01	1.80E-09		Unigene46776_All//gi|30685150|ref|NP_188529.2|//7.00E-53//VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor [Arabidopsis thaliana] >gi|75153628|sp|Q8L3W1.1|VRN1_ARATH RecName: Full=B3 domain-containing transcription factor VRN1; AltName: Full=Protein VERNALIZATION 1 >gi|21734794|gb|AAM76972.1|AF289051_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|21734796|gb|AAM76973.1|AF289052_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|89000959|gb|ABD59069.1| At3g18990 [Arabidopsis thaliana]	Unigene46776_All//6.00E-50//AT3G18990| VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor	Unigene46776_All//0.00E+00//TC162992	ABI3VP1		GO:0001071//GO:0003676//GO:0006351//GO:0009409//GO:0009908//GO:0010468//GO:0031981	nr -
Unigene46777_All	1617	2.17	0.85	1.35	2.74	2.26	2.29	13.23	6.15	5.94	-1.36E+00	7.41E-05	Down	-6.83E-01	4.77E-02		-2.81E-01	3.63E-01		-2.60E-01	4.18E-01		-1.10E+00	7.71E-23	Down	-1.16E+00	2.99E-25	Down	Unigene46777_All//gi|30685150|ref|NP_188529.2|//1.00E-105//VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor [Arabidopsis thaliana] >gi|75153628|sp|Q8L3W1.1|VRN1_ARATH RecName: Full=B3 domain-containing transcription factor VRN1; AltName: Full=Protein VERNALIZATION 1 >gi|21734794|gb|AAM76972.1|AF289051_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|21734796|gb|AAM76973.1|AF289052_1 reduced vernalization response 1 [Arabidopsis thaliana] >gi|89000959|gb|ABD59069.1| At3g18990 [Arabidopsis thaliana]	Unigene46777_All//2.00E-59//AT3G18990| VRN1 (REDUCED VERNALIZATION RESPONSE 1); transcription repressor	Unigene46777_All//0.00E+00//TC132946	ABI3VP1		GO:0001071//GO:0003676//GO:0006351//GO:0009908//GO:0010468//GO:0043231	nr -
Unigene46778_All	1575	10.36	19.24	5.95	7.78	11.08	19.27	11.36	13.77	17.71	8.92E-01	1.40E-18		-8.01E-01	2.29E-08		5.11E-01	4.25E-05		1.31E+00	2.49E-36	Up	2.78E-01	1.01E-02		6.41E-01	1.69E-12		Unigene46778_All//gi|15222993|ref|NP_172250.1|//1.00E-154//ankyrin repeat family protein [Arabidopsis thaliana] >gi|8439897|gb|AAF75083.1|AC007583_19 It contains Ank repeat PF|00023. EST gb|AI996003 comes from this gene [Arabidopsis thaliana]	Unigene46778_All//7.00E-144//AT1G07710| ankyrin repeat family protein	Unigene46778_All//0.00E+00//TC158209				nr +
Unigene46779_All	2251	3.00	7.52	2.98	3.67	5.00	5.24	6.09	7.37	7.52	1.33E+00	1.22E-19	Up	-8.50E-03	9.96E-01		4.46E-01	6.81E-03		5.12E-01	1.77E-03		2.77E-01	2.92E-02		3.06E-01	1.07E-02		Unigene46779_All//gi|15222993|ref|NP_172250.1|//0.00E+00//ankyrin repeat family protein [Arabidopsis thaliana] >gi|8439897|gb|AAF75083.1|AC007583_19 It contains Ank repeat PF|00023. EST gb|AI996003 comes from this gene [Arabidopsis thaliana]	Unigene46779_All//0.00E+00//AT1G07710| ankyrin repeat family protein	Unigene46779_All//0.00E+00//TC158209				nr -
Unigene46678_All	1394	5.40	1.71	3.25	20.90	14.80	7.91	2.58	0.06	0.17	-1.66E+00	1.48E-12	Down	-7.35E-01	8.64E-04		-4.99E-01	5.21E-08		-1.40E+00	2.25E-39	Down	-5.43E+00	1.83E-22	Down	-3.91E+00	2.32E-19	Down	Unigene46678_All//gi|222822566|gb|ACM68432.1|//1.00E-103//xyloglucanase-specific endoglucanase inhibitor protein [Petunia x hybrida]	Unigene46678_All//3.00E-87//AT1G03220| extracellular dermal glycoprotein, putative / EDGP, putative	Unigene46678_All//0.00E+00//TC135152				nr +
Unigene46782_All	1531	2.32	5.39	2.61	5.21	5.02	4.31	2.54	0.76	2.34	1.22E+00	8.36E-09	Up	1.67E-01	6.43E-01		-5.37E-02	8.19E-01		-2.74E-01	2.25E-01		-1.73E+00	1.06E-08	Down	-1.18E-01	6.71E-01		Unigene46782_All//gi|224125528|ref|XP_002329827.1|//4.00E-75//f-box family protein [Populus trichocarpa] >gi|222870889|gb|EEF08020.1| f-box family protein [Populus trichocarpa]	Unigene46782_All//3.00E-38//AT1G28310| Dof-type zinc finger domain-containing protein	Unigene46782_All//0.00E+00//CO070529	C2C2-Dof		GO:0005488	nr +
Unigene46784_All	2277	1.49	5.32	1.96	3.02	2.53	2.54	4.61	7.75	3.90	1.83E+00	2.24E-22	Up	3.95E-01	2.01E-01		-2.57E-01	2.91E-01		-2.50E-01	3.19E-01		7.50E-01	2.77E-10		-2.39E-01	1.40E-01		Unigene46784_All//gi|115472857|ref|NP_001060027.1|//1.00E-87//Os07g0568200 [Oryza sativa Japonica Group] >gi|113611563|dbj|BAF21941.1| Os07g0568200 [Oryza sativa Japonica Group]	Unigene46784_All//3.00E-70//AT2G47820| unknown protein	Unigene46784_All//3.00E-83//DR463022				nr +
Unigene46786_All	2035	8.33	4.86	5.70	23.40	21.20	17.87	34.86	12.86	19.69	-7.79E-01	1.04E-08		-5.46E-01	9.02E-05		-1.42E-01	8.16E-02		-3.89E-01	1.61E-07		-1.44E+00	2.43E-111	Down	-8.24E-01	6.87E-47		Unigene46786_All//gi|289721336|gb|ADO17678.1|//0.00E+00//squalene epoxidase [Withania somnifera]	Unigene46786_All//0.00E+00//AT1G58440| XF1; squalene monooxygenase	Unigene46786_All//0.00E+00//TC147537		ko00100|Steroid biosynthesis	GO:0004497//GO:0008152//GO:0030554//GO:0031224//GO:0031410//GO:0043231	nr -

Unigene46788_A11	1249	15.92	7.87	9.25	62.74	55.75	51.60	33.31	20.81	16.39	-1.02E+00	2.43E-15	Down	-7.83E-01	1.09E-09		-1.70E-01	3.25E-03		-2.82E-01	8.44E-07		-6.78E-01	1.51E-19		-1.02E+00	1.05E-39	Down	Unigene46788_A11//gi|224082836|ref|XP_002306860.1|//1.00E-112//ABC transporter family protein [Populus trichocarpa] >gi|222856309|gb|EEE93856.1| ABC transporter family protein [Populus trichocarpa]	Unigene46788_A11//3.00E-99//AT1G03900| ATNAP4 (Arabidopsis thaliana non-intrinsic ABC protein 4); ATPase, coupled to transmembrane movement of substances / transporter	Unigene46788_A11//0.00E+00//TC131238			GO:0016192//GO:0044464	nr -
Unigene46790_A11	1860	2.64	2.62	1.98	3.35	3.37	2.38	5.55	4.34	2.74	-1.59E-02	9.74E-01		-4.21E-01	1.44E-01		9.40E-03	9.78E-01		-4.93E-01	3.98E-02		-3.55E-01	2.96E-02		-1.02E+00	2.00E-10	Down	Unigene46790_A11//gi|296040739|gb|ADG85337.1|//2.00E-89//NADH dehydrogenase subunit 7 [Silene latifolia]	Unigene46790_A11//4.00E-84//ATMG00510| NADH dehydrogenase subunit 7	Unigene46790_A11//0.00E+00//TC139290		ko00190|Oxidative phosphorylation	GO:0000166//GO:0005746//GO:0015980//GO:0016491//GO:0030964//GO:0048037	nr -
Unigene46791_A11	2173	5.73	2.87	3.95	9.70	8.34	5.07	5.88	1.12	1.89	-9.99E-01	1.22E-09		-5.39E-01	1.20E-03		-2.18E-01	7.84E-02		-9.35E-01	3.45E-15		-2.40E+00	1.70E-40	Down	-1.64E+00	1.30E-25	Down	Unigene46791_A11//gi|19699077|gb|AAL90906.1|//1.00E-114//AT5g28150/T24G3_80 [Arabidopsis thaliana] >gi|23308357|gb|AAN18148.1| At5g28150/T24G3_80 [Arabidopsis thaliana]	Unigene46791_A11//3.00E-115//AT5G28150| unknown protein	Unigene46791_A11//0.00E+00//TC135242				nr -
Unigene46793_A11	2306	5.08	3.47	4.36	11.95	14.10	7.85	4.42	0.87	4.20	-5.50E-01	8.77E-04		-2.20E-01	2.36E-01		2.39E-01	1.12E-02		-6.05E-01	1.49E-09		-2.34E+00	1.26E-31	Down	-7.39E-02	6.69E-01		Unigene46793_A11//gi|225445059|ref|XP_002283473.1|//0.00E+00//PREDICTED: similar to beta-1,3-glucanase [Vitis vinifera]	Unigene46793_A11//0.00E+00//AT5G56590| glycosyl hydrolase family 17 protein	Unigene46793_A11//0.00E+00//TC139705		ko00500|Starch and sucrose metabolism	GO:0005618//GO:0008422//GO:0031225//GO:0031410//GO:0043167//GO:0044238	nr -
Unigene46794_A11	1845	1.96	2.31	1.93	7.34	8.53	4.28	3.19	0.29	0.78	2.38E-01	4.37E-01		-1.71E-02	9.82E-01		2.16E-01	1.55E-01		-7.78E-01	1.81E-07		-3.44E+00	3.00E-27	Down	-2.03E+00	3.43E-16	Down	Unigene46794_A11//gi|225445059|ref|XP_002283473.1|//0.00E+00//PREDICTED: similar to beta-1,3-glucanase [Vitis vinifera]	Unigene46794_A11//0.00E+00//AT5G56590| glycosyl hydrolase family 17 protein	Unigene46794_A11//0.00E+00//TC139705		ko00500|Starch and sucrose metabolism	GO:0005618//GO:0008422//GO:0031225//GO:0031410//GO:0043167//GO:0044238	nr -
Unigene46795_A11	2119	15.80	11.81	15.81	21.46	18.61	18.01	24.52	11.89	11.11	-4.20E-01	5.87E-06		4.00E-04	9.96E-01		-2.06E-01	8.19E-03		-2.53E-01	1.36E-03		-1.04E+00	1.33E-49	Down	-1.14E+00	6.47E-59	Down	Unigene46795_A11//gi|18414910|ref|NP_568157.1|//1.00E-163//outer membrane OMP85 family protein [Arabidopsis thaliana] >gi|16648863|gb|AAL24283.1| Unknown protein [Arabidopsis thaliana]	Unigene46795_A11//6.00E-160//AT5G05520| outer membrane OMP85 family protein	Unigene46795_A11//0.00E+00//ES792815				nr +
Unigene46797_A11	3114	2.08	0.96	1.56	21.66	19.83	7.83	11.51	2.12	2.90	-1.12E+00	2.44E-06	Down	-4.21E-01	8.73E-02		-1.28E-01	5.82E-02		-1.47E+00	6.48E-97	Down	-2.44E+00	6.13E-115	Down	-1.99E+00	9.89E-92	Down	Unigene46797_A11//gi|225441716|ref|XP_002283010.1|//0.00E+00//PREDICTED: similar to Protein kinase [Vitis vinifera]	Unigene46797_A11//0.00E+00//AT5G06940| leucine-rich repeat family protein	Unigene46797_A11//0.00E+00//TC175507		ko04626|Plant-pathogen interaction	GO:0016772//GO:0044464	nr +
Unigene46798_A11	1564	8.33	6.80	8.31	8.06	6.89	4.27	8.43	3.39	2.98	-2.92E-01	7.08E-02		-3.90E-03	1.00E+00		-2.26E-01	1.82E-01		-9.15E-01	5.10E-09		-1.31E+00	1.16E-18	Down	-1.50E+00	2.25E-23	Down	Unigene46798_A11//gi|42564175|ref|NP_188107.3|//1.00E-108//phosphoesterase [Arabidopsis thaliana]	Unigene46798_A11//5.00E-106//AT3G14890| phosphoesterase	Unigene46798_A11//0.00E+00//TC145219			GO:0043231	nr +
Unigene46801_A11	273	6.32	2.41	1.17	1.46	2.78	3.31	2.17	1.22	2.33	-1.39E+00	7.05E-03		-2.43E+00	7.48E-05	Down	9.27E-01	2.97E-01		1.18E+00	1.29E-01		-8.24E-01	3.48E-01		1.07E-01	9.01E-01		Unigene46801_A11//gi|89357201|gb|ABD72483.1|//2.00E-15//ABC transporter II-like protein [Gossypium barbadense]	Unigene46801_A11//3.00E-27//AT1G65410| ATNAP11 (ARABIDOPSIS THALIANA NON-INTRINSIC ABC PROTEIN 11); transporter	Unigene46801_A11//7.00E-67//gi|48743237|gb|C0073756.1|C0073756			GO:0006810//GO:0009536//GO:0015116//GO:0017111//GO:0032559	nr -
Unigene46807_A11	1678	43.65	30.86	15.74	26.33	44.04	22.61	2.29	4.83	3.66	-5.00E-01	2.47E-16		-1.47E+00	4.72E-94	Down	7.42E-01	2.31E-38		-2.20E-01	7.26E-03		1.08E+00	8.64E-09	Up	6.73E-01	1.13E-03		Unigene46807_A11//gi|253560642|gb|ACT32043.1|//1.00E-116//RAV transcription factor [Camellia sinensis]	Unigene46807_A11//4.00E-103//AT1G13260| RAV1; DNA binding / transcription factor/ transcription repressor	Unigene46807_A11//0.00E+00//TC146095	AP2-EREBP		GO:0000160//GO:0001071//GO:0006350//GO:0009648//GO:0043231	nr -
Unigene4681_A11	1085	5.69	4.39	3.93	8.26	7.81	11.16	8.07	3.54	4.66	-3.74E-01	1.24E-01		-5.35E-01	3.24E-02		-8.20E-02	7.34E-01		4.33E-01	8.12E-03		-1.19E+00	6.53E-11	Down	-7.91E-01	3.47E-06		Unigene4681_A11//gi|229890016|dbj|BAH58381.1|//1.00E-109//AtERH1-like protein [Nicotiana tabacum]	Unigene4681_A11//5.00E-101//AT3G47690| ATERH1; microtubule binding	Unigene4681_A11//0.00E+00//TC135895				nr +
Unigene46810_A11	1200	16.74	16.64	11.14	18.39	12.25	9.97	50.24	21.28	41.86	-9.20E-03	9.66E-01		-5.88E-01	3.43E-06		-5.86E-01	3.97E-08		-8.83E-01	1.85E-14		-1.24E+00	2.06E-75	Down	-2.63E-01	9.47E-06		Unigene46810_A11//gi|224094290|ref|XP_002310127.1|//2.00E-59//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|148372118|gb|ABQ62960.1| RAP2-like protein [Populus trichocarpa] >gi|222853030|gb|EEE90577.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene46810_A11//8.00E-46//AT5G67190| AP2 domain-containing transcription factor, putative	Unigene46810_A11//0.00E+00//gi|78332301|gb|DT552575.1|DT552575	AP2-EREBP		GO:0001071//GO:0003676//GO:0006350//GO:0010468	nr +
Unigene46812_A11	1495	41.05	40.47	30.13	63.68	55.37	78.85	97.88	81.69	47.89	-2.07E-02	7.85E-01		-4.46E-01	7.60E-11		-2.02E-01	5.99E-05		3.08E-01	1.48E-11		-2.61E-01	4.33E-12		-1.03E+00	2.18E-139	Down	Unigene46812_A11//gi|18411408|ref|NP_567089.1|//0.00E+00//MAP2B (METHIONINE AMINOPEPTIDASE 2B); aminopeptidase/ metalloexopeptidase [Arabidopsis thaliana] >gi|30696106|ref|NP_850725.1| MAP2B (METHIONINE AMINOPEPTIDASE 2B); aminopeptidase/ metalloexopeptidase [Arabidopsis thaliana] >gi|79315754|ref|NP_001030898.1| MAP2B (METHIONINE AMINOPEPTIDASE 2B); aminopeptidase/ metalloexopeptidase [Arabidopsis thaliana] >gi|85700451|sp|Q56185.2|AMP2B_ARATH RecName: Full=Methionine aminopeptidase 2B; Short=MetAP 2B; Short=MAP 2B; AltName: Full=Peptidase M 2B	Unigene46812_A11//0.00E+00//AT3G59990| MAP2B (METHIONINE AMINOPEPTIDASE 2B); aminopeptidase/ metalloexopeptidase	Unigene46812_A11//0.00E+00//TC151255			GO:0008237//GO:0008238//GO:0043169//GO:0044424//GO:0051604	nr -
Unigene46813_A11	1822	20.45	3.92	2.13	17.63	14.67	8.90	8.84	1.15	2.47	-2.38E+00	4.92E-95	Down	-3.26E+00	4.68E-128	Down	-2.66E-01	3.90E-03		-9.87E-01	5.98E-25		-2.95E+00	8.70E-64	Down	-1.84E+00	1.27E-37	Down	Unigene46813_A11//gi|15240743|ref|NP_201547.1|//1.00E-83//glycosyl hydrolase family protein 17 [Arabidopsis thaliana]	Unigene46813_A11//3.00E-80//AT5G67460| glycosyl hydrolase family protein 17	Unigene46813_A11//0.00E+00//TC163438			GO:0016787//GO:0044464	nr -
Unigene46816_A11	1620	38.92	150.79	24.00	39.51	96.08	78.28	98.55	69.17	92.37	1.95E+00	0.00E+00	Up	-6.98E-01	3.86E-24		1.28E+00	1.38E-197	Up	9.86E-01	6.62E-96		-5.11E-01	5.62E-44		-9.35E-02	1.30E-02		Unigene46816_A11//gi|222822564|gb|ACM68431.1|//2.00E-81//xyloglucan-specific endoglucanase inhibitor protein [Capsicum annuum]	Unigene46816_A11//2.00E-65//AT5G19120| aspartic-type endopeptidase	Unigene46816_A11//0.00E+00//TC135762				nr +
Unigene46818_A11	2633	4.53	0.65	2.41	11.22	7.56	8.42	9.91	3.19	4.10	-2.79E+00	9.66E-37	Down	-9.13E-01	1.07E-07		-5.70E-01	3.41E-10		-4.14E-01	1.96E-05		-1.63E+00	8.69E-50	Down	-1.27E+00	1.75E-35	Down	Unigene46818_A11//gi|115447813|ref|NP_001047686.1|//1.00E-157//Os02g0668400 [Oryza sativa Japonica Group] >gi|113537217|dbj|BAF09600.1| Os02g0668400 [Oryza sativa Japonica Group]	Unigene46818_A11//7.00E-153//AT1G20370| tRNA pseudouridine synthase family protein	Unigene46818_A11//0.00E+00//TC143826			GO:0003676//GO:0006399//GO:0009451//GO:0016866	nr +
Unigene46819_A11	2742	27.27	11.81	25.52	12.92	12.66	4.33	8.77	4.69	12.57	-1.21E+00	2.51E-73	Down	-9.56E-02	1.75E-01		-2.91E-02	8.21E-01		-1.58E+00	9.90E-57	Down	-9.02E-01	1.54E-18		5.19E-01	1.07E-10		Unigene46819_A11//gi|15224480|ref|NP_178588.1|//1.00E-152//zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|75337298|sp|Q9SJ41.1|C3H18_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 18; Short=AtC3H18	Unigene46819_A11//8.00E-143//AT2G05160| zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein	Unigene46819_A11//0.00E+00//ES850185	C3H		GO:0003676//GO:0005618//GO:0046914	nr +
Unigene46829_A11	1142	17.87	17.79	16.18	28.31	31.03	34.53	12.66	17.60	28.75	-6.10E-03	9.84E-01		-1.43E-01	3.16E-01		1.32E-01	1.90E-01		2.86E-01	7.44E-04		4.75E-01	1.36E-05		1.18E+00	2.38E-39	Up	Unigene46829_A11//gi|255568313|ref|XP_002525131.1|//3.00E-11//bromodomain-containing protein, putative [Ricinus communis] >gi|223535590|gb|EEF37258.1| bromodomain-containing protein, putative [Ricinus communis]		Unigene46829_A11//4.00E-87//gi|78333180|gb|DT553454.1|DT553454				nr -
Unigene4683_A11	673	13.53	18.14	8.55	42.41	39.96	36.10	55.66	93.65	126.44	4.24E-01	9.51E-03		-6.63E-01	8.18E-04		-8.59E-02	4.96E-01		-2.32E-01	2.81E-02		7.51E-01	1.18E-34		1.18E+00	9.45E-101	Up	Unigene4683_A11//gi|15277225|ref|NP_178836.1|//1.00E-16//UCP5 (UNCOUPLING PROTEIN 5); binding [Arabidopsis thaliana] >gi|90567689|emb|CAJ86454.1| mitochondrial dicarboxylate carrier [Arabidopsis thaliana]	Unigene4683_A11//3.00E-13//AT2G22500| UCP5 (UNCOUPLING PROTEIN 5); binding	Unigene4683_A11//3.00E-148//gi|11203641|gb|BF272571.1|BF272571				nr +
Unigene46832_A11	1555	3.84	8.34	2.98	6.18	6.53	14.00	19.22	39.78	45.30	1.12E+00	7.21E-12	Up	-3.65E-01	1.61E-01		7.94E-02	7.38E-01		1.18E+00	2.41E-22	Up	1.05E+00	2.65E-59	Up	1.24E+00	2.00E-89	Up	Unigene46832_A11//gi|4580461|gb|AAD24385.1|//1.00E-112//expressed protein [Arabidopsis thaliana]	Unigene46832_A11//2.00E-106//AT2G20120| COV1 (CONTINUOUS VASCULAR RING)	Unigene46832_A11//0.00E+00//gi|164348112|gb|ES801311.1|ES801311				nr +
Unigene46834_A11	1416	2.88	7.34	5.60	5.10	3.31	5.58	4.72	7.05	6.36	1.35E+00	1.24E-12	Up	9.59E-01	9.01E-06		-6.25E-01	2.14E-03		1.30E-01	6.26E-01		5.81E-01	3.16E-04		4.31E-01	1.03E-02		Unigene46834_A11//gi|15236781|ref|NP_194965.1|//1.00E-158//phosphate translocator-related [Arabidopsis thaliana]	Unigene46834_A11//2.00E-138//AT4G32390| phosphate translocator-related	Unigene46834_A11//0.00E+00//TC137680				nr +
Unigene46835_A11	1924	4.38	1.00	1.83	9.48	6.10	6.55	2.02	2.48	8.80	-2.13E+00	3.31E-19	Down	-1.26E+00	4.83E-09	Down	-6.35E-01	8.67E-08		-5.33E-01	2.35E-05		2.93E-01	2.70E-01		2.12E+00	6.14E-47	Up	Unigene46835_A11//gi|224133860|ref|XP_002327698.1|//1.00E-151//GRAS family transcription factor [Populus trichocarpa] >gi|222836783|gb|EEE75176.1| GRAS family transcription factor [Populus trichocarpa]	Unigene46835_A11//9.00E-125//AT4G36710| transcription factor	Unigene46835_A11//0.00E+00//TC131932	GRAS			nr +
Unigene46837_A11	2046	0.49	0.82	0.75	0.95	1.01	0.73	3.49	1.65	1.97	7.50E-01	1.37E-01		6.35E-01	2.49E-01		8.88E-02	8.63E-01		-3.82E-01	4.51E-01		-1.08E+00	7.12E-08	Down	-8.29E-01	1.42E-05		Unigene46837_A11//gi|30681070|ref|NP_172401.2|//0.00E+00//metallopeptidase M24 family protein [Arabidopsis thaliana]	Unigene46837_A11//0.00E+00//AT1G09300| metallopeptidase M24 family protein	Unigene46837_A11//0.00E+00//TC168058			GO:0008237//GO:0008238//GO:0019538//GO:0043231//GO:0046914	nr +
Unigene46838_A11	3004	0.31	0.24	0.51	0.50	0.70	0.62	0.45	0.14	1.02	-4.09E-01	5.66E-01		7.14E-01	2.04E-01		4.91E-01	3.07E-01		3.09E-01	5.68E-01		-1.70E+00	1.96E-03		1.18E+00	1.89E-04	Up	Unigene46838_A11//gi|186478297|ref|NP_001117254.1|//1.00E-137//metallopeptidase M24 family protein [Arabidopsis thaliana]	Unigene46838_A11//2.00E-138//AT1G09300| metallopeptidase M24 family protein	Unigene46838_A11//0.00E+00//TC171890			GO:0043231	nr +
Unigene46839_A11	1536	82.43	16.89	24.13	322.40	155.27	50.60	30.42	3.10	1.71	-2.29E+00	0.00E+00	Down	-1.77E+00	2.04E-212	Down	-1.05E+00	0.00E+00	Down	-2.67E+00	0.00E+00	Down	-3.29E+00	4.58E-205	Down	-4.15E+00	6.17E-256	Down	Unigene46839_A11//gi|15242118|ref|NP_199968.1|//1.00E-162//EXL3 (EXORDIUM LIKE 3) [Arabidopsis thaliana] >gi|16226762|gb|AAL16255.1|AF42832_5_1 AT5g51550/K17N15_10 [Arabidopsis thaliana]	Unigene46839_A11//6.00E-151//AT5G51550| EXL3 (EXORDIUM LIKE 3)	Unigene46839_A11//0.00E+00//TC169496				nr +
Unigene4684_A11	1453	4.36	6.45	7.44	2.78	5.52	10.23	29.91	20.51	23.50	5.66E-01	2.57E-03		7.72E-01	1.75E-05		9.92E-01	4.01E-07		1.88E+00	3.88E-30	Up	-5.45E-01	4.99E-14		-3.48E-01	7.65E-07		Unigene4684_A11//gi|87240694|gb|ABD32552.1|//1.00E-102//Short-chain dehydrogenase/reductase SDR [Medicago truncatula]	Unigene4684_A11//7.00E-101//AT3G26760| short-chain dehydrogenase/reductase (SDR) family protein	Unigene4684_A11//0.00E+00//TC158468		ko00906|Carotenoid biosynthesis		nr -
Unigene46840_A11	1133	20.73	12.03	11.84	35.74	37.57	30.61	22.73	9.92	10.55	-7.85E-01	6.46E-12		-8.08E-01	6.38E-12		7.17E-02	4.90E-01		-2.24E-01	9.45E-03		-1.20E+00	6.80E-31	Down	-1.11E+00	3.02E-28	Down	Unigene46840_A11//gi|195613194|gb|ACG28427.1|//1.00E-101//vesicle-associated membrane protein 725 [Zea mays]	Unigene46840_A11//9.00E-88//AT1G04750| VAMP721 (VESICLE-ASSOCIATED MEMBRANE PROTEIN 721)	Unigene46840_A11//0.00E+00//TC174098		ko04130|SNARE interactions in vesicular transport	GO:0006810//GO:0031224	nr -
Unigene46841_A11	3007	0.66	3.62	1.29	2.00	3.81	4.03	4.13	2.02	3.07	2.45E+00	6.22E-29	Up	9.67E-01	2.91E-03		9.28E-01	5.45E-09		1.01E+00	6.12E-10	Up	-1.04E+00	2.39E-12	Down	-4.28E-01	2.16E-03		Unigene46841_A11//gi|187370620|dbj|BAG31926.1|//0.00E+00//alpha-1,4-glucan phosphorylase H isozyme [Cucurbita maxima]	Unigene46841_A11//0.00E+00//AT3G46970| PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups	Unigene46841_A11//0.00E+00//TC135255		ko00500|Starch and sucrose metabolism	GO:0006950//GO:0009536//GO:0010038//GO:0016758//GO:0044238//GO:0048037	nr -

Unigene46842_All	1001	3.08	0.71	1.28	2.09	2.89	1.49	1.69	0.71	0.92	-2.12E+00	1.89E-07	Down	-1.27E+00	8.14E-04	Down	4.67E-01	2.27E-01		-4.89E-01	3.03E-01		-1.25E+00	6.43E-03		-8.84E-01	4.08E-02		Unigene46842_All//gi|297796595|ref|XP_002866182.1|//2.00E-19//At5g57100 [Arabidopsis lyrata subsp. lyrata] >gi|297312017|gb|EFH42441.1|At5g57100 [Arabidopsis lyrata subsp. lyrata]	Unigene46842_All//9.00E-13//AT5G57100| transporter-related	Unigene46842_All//3.00E-29//gi|5047860|gb|AI729008.1|AI729008			GO:0006810//GO:0031224	nr -
Unigene46843_All	1394	1.65	2.58	1.80	2.29	1.24	1.04	11.37	28.60	12.03	6.44E-01	4.70E-02		1.21E-01	7.65E-01		-8.89E-01	6.56E-03		-1.14E+00	1.01E-03		1.33E+00	8.46E-56	Up	8.11E-02	5.75E-01		Unigene46843_All//gi|297796595|ref|XP_002866182.1|//1.00E-127//At5g57100 [Arabidopsis lyrata subsp. lyrata] >gi|297312017|gb|EFH42441.1|At5g57100 [Arabidopsis lyrata subsp. lyrata]	Unigene46843_All//9.00E-113//AT5G57100| transporter-related	Unigene46843_All//1.00E-136//TC162443				nr +
Unigene46846_All	2520	3.63	2.29	3.51	24.79	20.91	11.67	20.42	14.48	9.06	-6.65E-01	4.60E-04		-5.08E-02	8.06E-01		-2.46E-01	8.81E-05		-1.09E+00	3.03E-56	Down	-4.96E-01	5.18E-14		-1.17E+00	7.97E-61	Down	Unigene46846_All//gi|79379437|ref|NP_177526.2|//1.00E-134//structural constituent of ribosome [Arabidopsis thaliana] >gi|40823465|gb|AAR92284.1|At1g73850 [Arabidopsis thaliana] >gi|46518405|gb|AAS99684.1|At1g73850 [Arabidopsis thaliana]	Unigene46846_All//2.00E-100//AT1G73850| structural constituent of ribosome	Unigene46846_All//2.00E-90//DR460862				nr +
Unigene46847_All	1959	8.68	6.49	7.77	12.71	14.45	10.58	9.00	3.84	6.47	-4.19E-01	1.94E-03		-1.59E-01	3.08E-01		1.85E-01	8.68E-02		-2.65E-01	1.85E-02		-1.23E+00	2.56E-22	Down	-4.77E-01	3.21E-05		Unigene46847_All//gi|37359277|gb|AAN85416.1|//0.00E+00//purple acid phosphatase-like protein [Glycine max] >gi|37359279|gb|AAN85417.1|purple acid phosphatase-like protein [Glycine max] >gi|37359281|gb|AAN85418.1| purple acid phosphatase-like protein [Glycine max] >gi|37359283|gb|AAN85419.1| purple acid phosphatase-like protein [Glycine max] >gi|37359285|gb|AAN85420.1| purple acid phosphatase-like protein [Glycine max]	Unigene46847_All//0.00E+00//AT5G34850| PAP26 (PURPLE ACID PHOSPHATASE 26); acid phosphatase/ protein serine/threonine phosphatase	Unigene46847_All//0.00E+00//DR457381			GO:0004721//GO:0005618//GO:0006464//GO:0043169//GO:0043231//GO:0043234//GO:0055061	nr -
Unigene46848_All	447	9.83	8.96	13.58	12.37	16.18	30.72	5.96	4.11	4.46	-1.35E-01	6.37E-01		4.66E-01	6.72E-02		3.87E-01	8.16E-02		1.31E+00	8.79E-17	Up	-5.35E-01	1.31E-01		-4.19E-01	2.19E-01		Unigene46848_All//gi|186513977|ref|NP_567763.2|//8.00E-20//aconitate hydratase/ copper ion binding [Arabidopsis thaliana]	Unigene46848_All//1.00E-18//AT4G26970| aconitate hydratase/ copper ion binding	Unigene46848_All//0.00E+00//DW479350		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene4685_All	1418	0.37	0.54	0.11	1.72	4.40	14.01	31.10	56.56	67.57	5.39E-01	5.02E-01		-1.71E+00	1.40E-01		1.35E+00	7.32E-09	Up	3.03E+00	5.58E-70	Up	8.63E-01	1.50E-55		1.12E+00	9.74E-104	Up	Unigene4685_All//gi|283132365|dbj|BAI63588.1|//1.00E-144//leucine rich repeat protein [Lotus japonicus]	Unigene4685_All//2.00E-134//AT2G19330| leucine-rich repeat family protein			ko04626|Plant-pathogen interaction		nr +
Unigene46851_All	2802	3.03	1.45	1.77	7.84	4.33	3.90	7.70	3.51	7.35	-1.06E+00	1.76E-07	Down	-7.75E-01	1.74E-04		-8.58E-01	2.16E-15		-1.01E+00	8.17E-18	Down	-1.13E+00	5.56E-24	Down	-6.61E-02	6.11E-01		Unigene46851_All//gi|15226012|ref|NP_179089.1|//0.00E+00//NPY2 (NAKED PINS IN YUC MUTANTS 2); protein binding / signal transducer [Arabidopsis thaliana]	Unigene46851_All//0.00E+00//AT2G14820| NPY2 (NAKED PINS IN YUC MUTANTS 2); protein binding / signal transducer	Unigene46851_All//0.00E+00//gi|164259394|gb|ES812161.1|ES812161			GO:0005488//GO:0009314//GO:0060089	nr -
Unigene46853_All	1861	10.49	11.73	10.24	4.18	6.86	8.49	1.79	2.90	1.99	1.62E-01	2.09E-01		-3.38E-02	8.10E-01		7.17E-01	1.28E-06		1.02E+00	3.58E-13	Up	6.91E-01	2.53E-03		1.50E-01	6.23E-01		Unigene46853_All//gi|15239022|ref|NP_196694.1|//1.00E-112//monooxygenase family protein [Arabidopsis thaliana] >gi|28950969|gb|AAO63408.1|At5g11330 [Arabidopsis thaliana]	Unigene46853_All//2.00E-113//AT5G11330| monooxygenase family protein	Unigene46853_All//0.00E+00//gi|109876999|gb|DW505973.1|DW505973			GO:0008152//GO:0016491//GO:0031410	nr +
Unigene46854_All	1538	18.71	9.95	10.11	70.61	3.54	6.40	48.00	13.32	10.21	-9.11E-01	2.36E-18		-8.88E-01	6.97E-17		-4.32E+00	0.00E+00	Down	-3.46E+00	0.00E+00	Down	-1.85E+00	6.12E-166	Down	-2.23E+00	1.44E-218	Down	Unigene46854_All//gi|89243481|gb|AB064879.1|//1.00E-126//nicotianamine synthase [Malus xiaojinensis]	Unigene46854_All//6.00E-113//AT1G09240| NAS3 (NICOTIANAMINE SYNTHASE 3); nicotianamine synthase	Unigene46854_All//0.00E+00//TC157313				nr -
Unigene46855_All	1505	22.25	49.46	18.33	22.08	24.05	25.45	88.63	133.61	134.60	1.15E+00	1.53E-67	Up	-2.80E-01	4.50E-03		1.23E-01	2.26E-01		2.05E-01	2.37E-02		5.92E-01	8.68E-72		6.03E-01	2.05E-76		Unigene46855_All//gi|15240163|ref|NP_200929.1|//1.00E-107//SNAP33 (SOLUBLE N-ETHYLMALEIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding [Arabidopsis thaliana] >gi|27806727|sp|Q96279.1|SNP33_ARATH RecName: Full=SNAP25 homologous protein SNAP33; Short=AtSNAP33; AltName: Full=Synaptosomal-associated protein SNAP25-like 1; Short=SNAP-25-like protein 1; AltName: Full=Snap25a >gi|5731763|emb|CAB52582.1| SNAP33 protein [Arabidopsis thaliana] >gi|5731764|emb|CAB52583.1|SNAP33B protein [Arabidopsis thaliana] >gi|9759467|dbj|BAB10383.1|SNAP25A protein [Arabidopsis thaliana] >gi|16332047|gb|AAL15258.1|AT5g61210/maf19_210 [Arabidopsis thaliana] >gi|18072736|emb|CAC79615.1| SNAP-25 like protein [Arabidopsis thaliana] >gi|22655332|gb|AAM98258.1|At5g61210/maf19_210 [Arabidopsis thaliana]	Unigene46855_All//4.00E-97//AT5G61210| SNAP33 (SOLUBLE N-ETHYLMALEIMIDE-SENSITIVE FACTOR ADAPTOR PROTEIN 33); SNAP receptor/ protein binding	Unigene46855_All//0.00E+00//TC146462		ko04130|SNARE interactions in vesicular transport		nr +
Unigene46856_All	1119	78.04	84.00	99.70	25.29	44.87	47.91	17.65	4.89	19.65	1.06E-01	6.79E-02		3.53E-01	1.14E-12		8.27E-01	1.88E-31		9.22E-01	1.64E-36		-1.85E+00	6.57E-45	Down	1.55E-01	1.63E-01		Unigene46856_All//gi|34550779|gb|AAQ74955.1|//4.00E-72//Gbiaa-Re [Gossypium barbadense]	Unigene46856_All//4.00E-67//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene46856_All//5.00E-145//gi|21101546|gb|BQ413859.1|BQ413859			GO:0001071//GO:0003676//GO:0005515//GO:0006412//GO:0009755//GO:0010468//GO:0043231	nr +
Unigene46858_All	2965	25.53	7.66	18.68	1.43	1.80	1.58	0.17	0.14	0.24	-1.74E+00	9.34E-128	Down	-4.51E-01	1.74E-13		3.34E-01	2.26E-01		1.50E-01	6.40E-01		-2.79E-01	7.49E-01		5.00E-01	5.01E-01		Unigene46858_All//gi|49388598|dbj|BAD25713.1|//0.00E+00//transducin-like [Oryza sativa Japonica Group]	Unigene46858_All//4.00E-97//AT3G06880| nucleotide binding	Unigene46858_All//5.00E-110//TC133583			GO:0044424	nr +
Unigene46859_All	1701	9.90	69.14	21.38	31.69	57.37	48.35	13.82	10.89	19.04	2.80E+00	0.00E+00	Up	1.11E+00	1.79E-30	Up	8.57E-01	1.37E-64		6.10E-01	1.78E-27		-3.44E-01	6.81E-04		4.62E-01	2.27E-08		Unigene46859_All//gi|63054325|gb|AY289930.1|//2.00E-98//sucrose responsive element binding protein [Vitis vinifera]	Unigene46859_All//7.00E-57//AT4G37260| MYB73 (MYB DOMAIN PROTEIN 73); DNA binding / transcription factor	Unigene46859_All//0.00E+00//TC135318	MYB		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene4686_All	1080	6.98	1.50	3.70	8.12	7.91	5.52	10.92	2.36	2.91	-2.22E+00	4.22E-18	Down	-9.16E-01	3.76E-05		-3.79E-02	8.60E-01		-5.56E-01	3.88E-03		-2.21E+00	5.23E-34	Down	-1.91E+00	4.10E-29	Down	Unigene4686_All//gi|16323095|gb|AAL15282.1|//6.00E-56//AT4g39900/T5J17_70 [Arabidopsis thaliana]	Unigene4686_All//1.00E-56//AT4G39900| unknown protein	Unigene4686_All//0.00E+00//gi|164360366|gb|ES807371.1|ES807371				nr -
Unigene46860_All	577	5.80	4.48	1.48	8.37	5.61	6.73	5.42	2.39	2.07	-3.74E-01	2.80E-01		-1.97E+00	5.44E-07	Down	-5.78E-01	2.77E-02		-3.15E-01	2.95E-01		-1.18E+00	2.19E-04	Down	-1.39E+00	1.30E-05	Down	Unigene46860_All//gi|31790111|gb|AP58374.1|//9.00E-18//RPA 32kDa [Pisum sativum]	Unigene46860_All//7.00E-16//AT2G24490| RPA2 (REPLICON PROTEIN A2); protein binding	Unigene46860_All//0.00E+00//TC174109		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair	GO:0003676//GO:0006259//GO:0043231	nr -
Unigene46861_All	1199	7.16	1.35	1.91	4.90	5.92	2.56	11.04	1.25	2.06	-2.40E+00	1.42E-22	Down	-1.91E+00	2.94E-16	Down	2.71E-01	2.62E-01		-9.37E-01	9.98E-05		-3.14E+00	7.82E-56	Down	-2.42E+00	8.06E-44	Down	Unigene46861_All//gi|31790111|gb|AP58374.1|//9.00E-78//RPA 32kDa [Pisum sativum]	Unigene46861_All//1.00E-72//AT2G24490| RPA2 (REPLICON PROTEIN A2); protein binding	Unigene46861_All//0.00E+00//TC133410		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair	GO:0005488//GO:0006259//GO:0043231	nr -
Unigene46862_All	1834	9.98	2.54	5.23	6.44	1.86	2.61	10.56	21.06	11.01	-1.97E+00	3.33E-37	Down	-9.34E-01	6.98E-12		-1.79E+00	2.61E-26	Down	-1.30E+00	1.44E-14	Down	9.96E-01	2.51E-34		6.08E-02	6.33E-01		Unigene46862_All//gi|297811403|ref|XP_002873585.1|//1.00E-152//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319422|gb|EFH49844.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46862_All//3.00E-151//AT5G12890| UDP-glucoronosyl/UDP-glucosyl transferase family protein			ko00908|Zeatin biosynthesis	GO:0035251	nr +
Unigene46863_All	2426	156.14	158.55	185.72	27.10	45.78	74.58	0.16	0.41	0.07	2.20E-02	4.86E-01		2.50E-01	6.47E-26		7.56E-01	1.87E-59		1.46E+00	1.70E-253	Up	1.40E+00	2.82E-02		-1.26E+00	2.48E-01		Unigene46863_All//gi|15239581|ref|NP_200236.1|//0.00E+00//ATCNGC4 (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL 4); calmodulin binding / cation channel/ cation transmembrane transporter/ cyclic nucleotide binding [Arabidopsis thaliana] >gi|30696428|ref|NP_851188.1|ATCNGC4 (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL 4); calmodulin binding / cation channel/ cation transmembrane transporter/ cyclic nucleotide binding [Arabidopsis thaliana] >gi|38503128|sp|Q94AS9.2|CNGC4_ARATH RecName: Full=Cyclic nucleotide-gated ion channel 4; Short=AtCNGC4; AltName: Full=Cyclic nucleotide- and calmodulin-regulated ion channel 4; Short=AtHLM1 >gi|4581203|emb|CAB40129.1| cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana] >gi|9759498|dbj|BAB10748.1| cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]	Unigene46863_All//0.00E+00//AT5G54250| ATCNGC4 (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL 4); calmodulin binding / cation channel/ cation transmembrane transporter/ cyclic nucleotide binding	Unigene46863_All//0.00E+00//TC158705		ko04626|Plant-pathogen interaction	GO:0006810//GO:0015075//GO:0031224//GO:0043231	nr -
Unigene46865_All	1513	7.68	5.86	6.83	4.54	3.66	6.15	18.30	27.60	168.49	-3.90E-01	2.09E-02		-1.69E-01	3.89E-01		-3.10E-01	1.80E-01		4.37E-01	2.27E-02		5.92E-01	1.42E-15		3.20E+00	0.00E+00	Up	Unigene46865_All//gi|297831428|ref|XP_002883596.1|//1.00E-135//oxidative signal-inducible1 [Arabidopsis lyrata subsp. lyrata] >gi|297329436|gb|EFH59855.1|oxidative signal-inducible1 [Arabidopsis lyrata subsp. lyrata]	Unigene46865_All//2.00E-123//AT3G25250| AGC2-1 (OXIDATIVE SIGNAL-INDUCIBLE1); kinase	Unigene46865_All//0.00E+00//TC153441			GO:0016772	nr -
Unigene46868_All	1910	51.94	176.65	35.21	14.84	18.97	25.47	10.82	14.66	14.54	1.77E+00	0.00E+00	Up	-5.61E-01	1.06E-25		3.54E-01	2.33E-05		7.79E-01	4.77E-25		4.38E-01	1.58E-06		4.26E-01	2.14E-06		Unigene46868_All//gi|157673576|gb|ABV60087.1|//0.00E+00//beta-ketoacyl-CoA synthase [Gossypium hirsutum]	Unigene46868_All//0.00E+00//AT5G43760| KCS20 (3-KETOACYL-COA SYNTHASE 20); fatty acid elongase	Unigene46868_All//0.00E+00//TC175097			GO:0004312//GO:0006631//GO:0006950//GO:0009314//GO:0044464	nr -

Unigene46869_All	1601	31.31	23.55	36.02	132.52	160.73	116.62	17.72	41.22	13.04	-4.11E-01	3.33E-08		2.02E-01	6.61E-03		2.79E-01	1.83E-22		-1.84E-01	5.25E-08		1.22E+00	3.86E-80	Up	-4.43E-01	5.81E-07		Unigene46869_All//gi|15242769|ref|NP_195969.1|//1.00E-140//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|7378633|emb|CAB83309.1| UDPG glucosyltransferase-like protein [Arabidopsis thaliana] >gi|111074184|gb|ABH04465.1| At5g03190 [Arabidopsis thaliana]	Unigene46869_All//2.00E-123//AT5G03490| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene46869_All//0.00E+00//TC168403		ko00908|Zeatin biosynthesis		nr -
Unigene4687_All	1408	28.80	81.04	42.85	14.05	21.20	31.15	4.11	18.58	4.67	1.49E+00	1.34E-153	Up	5.73E-01	1.67E-16		5.94E-01	8.98E-11		1.15E+00	9.92E-43	Up	2.18E+00	6.19E-73	Up	1.83E-01	3.99E-01		Unigene4687_All//gi|18409339|ref|NP_566951.1|//1.00E-104//YLS2; strictosidine synthase [Arabidopsis thaliana] >gi|18087629|gb|AAL58944.1|AF462858_1 AT3g51430/F26O13_70 [Arabidopsis thaliana] >gi|13122282|dbj|BAB32882.1| strictosidine synthase-like protein [Arabidopsis thaliana] >gi|18086443|gb|AAL57676.1| AT3g51430/F26O13_70 [Arabidopsis thaliana] >gi|21592926|gb|AAM64876.1| mucin-like protein [Arabidopsis thaliana] >gi|38564288|gb|AAR23723.1| At3g51430 [Arabidopsis thaliana]	Unigene4687_All//1.00E-101//AT3G51430| YLS2; strictosidine synthase	Unigene4687_All//0.00E+00//TC149741		ko00901|Indole alkaloid biosynthesis		nr -
Unigene46870_All	2017	18.44	39.62	35.24	27.04	40.21	39.57	36.70	37.40	25.32	1.10E+00	1.42E-67	Up	9.34E-01	1.31E-44		5.72E-01	9.84E-27		5.49E-01	3.37E-22		2.72E-02	6.85E-01		-5.36E-01	2.64E-23		Unigene46870_All//gi|297850392|ref|XP_002893077.1|//7.00E-79//protein IQ-DOMAIN 32 [Arabidopsis lyrata subsp. lyrata] >gi|297338919|gb|EFH69336.1| protein IQ-DOMAIN 32 [Arabidopsis lyrata subsp. lyrata]	Unigene46870_All//2.00E-65//AT1G19870| iqd32 (IQ-domain 32); calmodulin binding	Unigene46870_All//0.00E+00//TC152553			GO:0044424	nr +
Unigene46872_All	2075	0.50	0.81	1.59	1.58	1.86	1.74	1.65	0.54	0.79	6.76E-01	1.85E-01		1.66E+00	1.30E-05	Up	2.30E-01	5.36E-01		1.36E-01	6.93E-01		-1.60E+00	5.15E-07	Down	-1.07E+00	2.59E-04	Down	Unigene46872_All//gi|94442455|gb|AAF19015.1|//2.00E-35//At4g02715 [Arabidopsis thaliana]	Unigene46872_All//1.00E-21//AT4G02715| unknown protein	Unigene46872_All//0.00E+00//gi|109842501|gb|DW241061.1|DW241061				nr +
Unigene46873_All	3669	334.72	179.34	292.36	22.14	28.62	20.45	5.59	1.93	1.47	-9.00E-01	0.00E+00		-1.95E-01	1.96E-43		3.70E-01	9.53E-16		-1.15E-01	7.06E-02		-1.54E+00	5.09E-36	Down	-1.93E+00	7.49E-51	Down	Unigene46873_All//gi|18391021|ref|NP_563844.1|//0.00E+00//G6PD4 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 4); glucose-6-phosphate dehydrogenase [Arabidopsis thaliana] >gi|25452977|sp|Q93ZW0.1|G6PD4_ARATH RecName: Full=Glucose-6-phosphate 1-dehydrogenase 4, chloroplastic; Short=G6PD4; Short=G6PD4; Flags: Precursor	Unigene46873_All//0.00E+00//AT1G09420| G6PD4 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 4); glucose-6-phosphate dehydrogenase	Unigene46873_All//0.00E+00//TC134589		ko00480|Glutathione metabolism//ko00030|Pentose phosphate pathway	GO:0005576//GO:0006952//GO:0009526//GO:0009570//GO:0009657//GO:0016616//GO:0019318//GO:0030529//GO:0042254//GO:0042579//GO:0048037//GO:0048511	nr +
Unigene46874_All	1844	9.65	4.53	6.15	5.84	4.56	3.62	4.20	2.29	1.73	-1.09E+00	2.25E-15	Down	-6.49E-01	1.70E-06		-3.57E-01	3.78E-02		-6.87E-01	5.02E-05		-8.74E-01	3.23E-06		-1.28E+00	3.14E-11	Down	Unigene46874_All//gi|226501514|ref|NP_001150630.1|//1.00E-154//pseudouridylate synthase/ transporter [Zea mays] >gi|195640714|gb|ACG39825.1| pseudouridylate synthase/ transporter [Zea mays]	Unigene46874_All//4.00E-108//AT5G14460| pseudouridine synthase/ transporter	Unigene46874_All//0.00E+00//CO085608			GO:0009451	nr -
Unigene46876_All	1426	1.65	2.20	2.13	5.62	7.32	5.99	1.07	0.29	0.45	4.16E-01	2.41E-01		3.66E-01	3.51E-01		3.80E-01	3.16E-02		8.99E-02	6.81E-01		-1.86E+00	3.50E-04	Down	-1.26E+00	7.68E-03		Unigene46876_All//gi|60657602|gb|AAX33322.1|//1.00E-104//secondary cell wall-related glycosyltransferase family 47 [Populus tremula x Populus tremuloides]	Unigene46876_All//9.00E-84//AT5G22940| FSH (FRA8 HOMOLOG); catalytic	Unigene46876_All//7.00E-86//gi|109837912|gb|DW236473.1|DW236473			GO:0009832//GO:0010413//GO:0043231	nr +
Unigene46877_All	1572	2.36	1.97	1.25	3.23	4.58	5.29	1.26	0.21	0.18	-2.65E-01	4.14E-01		-9.15E-01	6.10E-03		5.02E-01	1.92E-02		7.10E-01	3.36E-04		-2.57E+00	2.16E-07	Down	-2.83E+00	1.91E-08	Down	Unigene46877_All//gi|114325715|gb|ABI64067.1|//1.00E-155//glycosyltransferase GT47C [Populus tremula x Populus alba]	Unigene46877_All//1.00E-135//AT2G28110| FRA8 (FRAGILE FIBER 8); glucuronosyltransferase/ transferase	Unigene46877_All//0.00E+00//TC147160				nr +
Unigene4688_All	1790	13.33	9.20	14.96	22.10	19.49	15.44	22.51	11.88	9.50	-5.35E-01	1.59E-06		1.67E-01	1.58E-01		-1.81E-01	3.76E-02		-5.17E-01	2.87E-10		-9.21E-01	1.44E-31		-1.24E+00	1.92E-52	Down	Unigene4688_All//gi|145348919|ref|NP_194678.2|//0.00E+00//aminopeptidase/ manganese ion binding [Arabidopsis thaliana]	Unigene4688_All//0.00E+00//AT4G29490| aminopeptidase/ manganese ion binding	Unigene4688_All//0.00E+00//TC130990				nr -
Unigene46882_All	803	3.06	0.63	0.27	2.42	3.09	2.76	4.32	1.20	1.79	-2.28E+00	1.43E-06	Down	-3.53E+00	2.42E-09	Down	3.52E-01	4.30E-01		1.88E-01	6.76E-01		-1.85E+00	1.67E-08	Down	-1.27E+00	1.78E-05	Down	Unigene46882_All//gi|119935825|gb|ABM06005.1|//4.00E-23//At5g04320 [Arabidopsis thaliana]	Unigene46882_All//2.00E-28//AT5G04320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: meiotic chromosome segregation; LOCATED IN: chromosome, centromeric region, nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Shugoshin, C-terminal (InterPro:IPR011515); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G10440.1); Has 951 Blast hits to 743 proteins in 147 species: Archae - 0; Bacteria - 61; Metazoa - 474; Fungi - 60; Plants - 48; Viruses - 0; Other Eukaryotes - 308 (source: NCBI BLink).	Unigene46882_All//3.00E-105//ES850076			GO:0007049//GO:0007059//GO:0043229	nr -
Unigene46883_All	1189	1.14	0.47	0.27	1.47	2.37	3.49	4.02	2.04	2.71	-1.29E+00	2.82E-02		-2.09E+00	1.95E-03		6.96E-01	6.27E-02		1.25E+00	3.57E-05	Up	-9.79E-01	7.63E-05		-5.66E-01	1.71E-02		Unigene46883_All//gi|115482338|ref|NP_001064762.1|//2.00E-25//Os10g0457400 [Oryza sativa Japonica Group] >gi|110289183|gb|AAP54098.2| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113639371|dbj|BAF26676.1| Os10g0457400 [Oryza sativa Japonica Group]	Unigene46883_All//4.00E-19//AT5G04320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: meiotic chromosome segregation; LOCATED IN: chromosome, centromeric region, nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Shugoshin, C-terminal (InterPro:IPR011515); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G10440.1); Has 951 Blast hits to 743 proteins in 147 species: Archae - 0; Bacteria - 61; Metazoa - 474; Fungi - 60; Plants - 48; Viruses - 0; Other Eukaryotes - 308 (source: NCBI BLink).	Unigene46883_All//0.00E+00//ES850076				nr -
Unigene46885_All	798	7.08	2.60	4.54	5.18	4.40	2.60	3.18	1.15	0.90	-1.44E+00	5.74E-08	Down	-6.42E-01	1.39E-02		-2.35E-01	4.78E-01		-9.93E-01	7.98E-04		-1.46E+00	7.83E-05	Down	-1.82E+00	1.48E-06	Down	Unigene46885_All//gi|226529026|ref|NP_001148165.1|//1.00E-34//beta-glucosidase [Zea mays] >gi|195616320|gb|ACG29990.1| beta-glucosidase [Zea mays]	Unigene46885_All//5.00E-35//AT4G21760| BGLU47 (Beta-glucosidase 47); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene46885_All//1.00E-126//TC155706		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0008152//GO:0016798//GO:0031410//GO:0043231	nr +
Unigene46886_All	946	6.03	1.98	3.94	3.11	1.64	0.57	1.39	0.62	0.76	-1.61E+00	2.97E-09	Down	-6.14E-01	1.84E-02		-9.24E-01	7.14E-03		-2.44E+00	8.12E-09	Down	-1.16E+00	2.87E-02		-8.70E-01	8.35E-02		Unigene46886_All//gi|75296459|sp|Q75XS2.2|BGL16_ORYSJ//7.00E-41//RecName: Full=Beta-glucosidase 16; Short=Os4bglu16; Flags: Precursor >gi|38345327|emb|CAE54544.1| OSJNBa0004N05.24 [Oryza sativa (japonica cultivar-group)] >gi|38345685|emb|CAE01908.2| OSJNBb0070J16.1 [Oryza sativa (japonica cultivar-group)]	Unigene46886_All//5.00E-35//AT4G21760| BGLU47 (Beta-glucosidase 47); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene46886_All//0.00E+00//TC155706		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0008152//GO:0016798//GO:0031410//GO:0043231	nr +
Unigene46887_All	1921	1.53	1.08	0.97	2.02	3.14	3.90	3.15	3.07	6.43	-4.96E-01	1.79E-01		-6.53E-01	8.87E-02		6.33E-01	6.67E-03		9.48E-01	7.16E-06		-3.70E-02	8.86E-01		1.03E+00	1.81E-12	Up	Unigene46887_All//gi|18424537|ref|NP_568948.1|//1.00E-116//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75170898|sp|Q9FT77.1|PP442_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g61990, mitochondrial; Flags: Precursor	Unigene46887_All//9.00E-116//AT5G61990| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene46888_All	590	11.71	3.44	6.50	2.87	2.10	0.46	0.79	0.14	0.27	-1.77E+00	1.46E-12	Down	-8.49E-01	2.64E-04		-4.50E-01	3.87E-01		-2.64E+00	9.23E-06	Down	-2.48E+00	3.38E-02		-1.55E+00	1.16E-01		Unigene46888_All//gi|115471667|ref|NP_001059432.1|//3.00E-35//Os07g0406800 [Oryza sativa Japonica Group] >gi|113610968|dbj|BAF21346.1| Os07g0406800 [Oryza sativa Japonica Group]	Unigene46888_All//8.00E-36//AT1G67320| DNA primase, large subunit family			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03030|DNA replication	GO:0003899//GO:0006259	nr +
Unigene46889_All	1758	2.50	1.73	1.30	3.43	2.74	1.95	3.20	0.90	1.41	-5.32E-01	6.67E-02		-9.41E-01	1.90E-03		-3.22E-01	1.98E-01		-8.12E-01	6.01E-04		-1.82E+00	4.41E-13	Down	-1.19E+00	1.46E-07	Down	Unigene46889_All//gi|115471667|ref|NP_001059432.1|//0.00E+00//Os07g0406800 [Oryza sativa Japonica Group] >gi|113610968|dbj|BAF21346.1| Os07g0406800 [Oryza sativa Japonica Group]	Unigene46889_All//1.00E-178//AT1G67320| DNA primase, large subunit family	Unigene46889_All//0.00E+00//CO122569		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03030|DNA replication	GO:0003899//GO:0006259	nr +
Unigene4689_All	846	1.55	1.68	2.39	4.24	5.25	4.91	2.30	3.95	6.97	1.17E-01	8.24E-01		6.30E-01	1.87E-01		3.09E-01	3.20E-01		2.12E-01	5.43E-01		7.82E-01	9.62E-03		1.60E+00	8.85E-12	Up	Unigene4689_All//gi|226505928|ref|NP_001152052.1|//2.00E-59//RNA-binding protein [Zea mays] >gi|195652155|gb|ACG45545.1| RNA-binding protein [Zea mays]	Unigene4689_All//3.00E-46//AT1G24440| protein binding / zinc ion binding			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene46892_All	1344	5.72	9.01	6.02	2.93	5.28	6.65	92.74	197.81	383.42	6.55E-01	5.59E-05		7.36E-02	7.37E-01		8.50E-01	4.75E-05		1.18E+00	1.42E-09	Up	1.09E+00	6.51E-270	Up	2.05E+00	0.00E+00	Up	Unigene46892_All//gi|18402992|ref|NP_566685.1|//5.00E-86//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|29029088|gb|AAO64923.1| At3g21420 [Arabidopsis thaliana]	Unigene46892_All//2.00E-87//AT3G21420| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene46892_All//0.00E+00//TC137113		ko00941|Flavonoid biosynthesis	GO:0003824	nr +
Unigene46893_All	838	1.25	2.00	3.30	5.77	1.64	4.15	10.90	214.12	2.90	6.76E-01	1.85E-01		1.40E+00	6.00E-04	Up	-1.81E+00	3.69E-11	Down	-4.75E-01	9.17E-02		4.30E+00	0.00E+00	Up	-1.91E+00	8.69E-23	Down	Unigene46893_All//gi|59896631|gb|AAX11684.1|//6.00E-89//perakine reductase [Rauvolfia serpentina]	Unigene46893_All//2.00E-72//AT1G60690| aldo/keto reductase family protein	Unigene46893_All//4.00E-114//gi|78340622|gb|DT560896.1|DT560896			GO:0004033//GO:0008152	nr -

Unigene46894_All	1304	26.36	14.77	27.77	13.45	24.08	14.17	0.42	4.55	0.18	-8.36E-01	6.30E-19		7.50E-02	4.85E-01		8.41E-01	2.49E-20		7.51E-02	6.33E-01		3.43E+00	2.15E-27	Up	-1.20E+00	1.64E-01		Unigene46894_All//gi|297610489|ref|NP_001061615.2|//6.00E-81//Os10g0419100 [Oryza sativa Japonica Group] >gi|255679407|dbj|BAF26529.2|Os10g0419100 [Oryza sativa Japonica Group]	Unigene46894_All//3.00E-71//AT1G60690| aldo/keto reductase family protein	Unigene46894_All//6.00E-148//gi|78340622|gb|DT560896.1|DT560896		ko00053|Ascorbate and aldarate metabolism	GO:0004033//GO:0008152	nr +
Unigene46895_All	2129	1.47	0.33	0.55	1.59	4.56	9.78	76.68	73.81	65.23	-2.15E+00	1.16E-07	Down	-1.42E+00	1.97E-04	Down	1.52E+00	4.72E-16	Up	2.62E+00	4.52E-63	Up	-5.49E-02	1.96E-01		-2.33E-01	2.65E-11					Unigene46895_All//0.00E+00//DT463830					ESTscan -
Unigene46897_All	317	3.30	3.36	4.03	1.57	2.72	5.56	0.40	0.79	0.50	2.41E-02	9.89E-01		2.88E-01	6.09E-01		7.89E-01	3.21E-01		1.82E+00	6.24E-04	Up	9.84E-01	5.17E-01		3.29E-01	8.51E-01					Unigene46897_All//2.00E-61//CO073130					
Unigene46898_All	1871	4.53	2.84	5.52	10.84	15.33	12.24	7.93	6.14	19.82	-6.72E-01	6.96E-04		2.86E-01	1.42E-01		5.01E-01	9.23E-08		1.76E-01	1.72E-01		-3.69E-01	4.99E-03		1.32E+00	1.45E-52	Up	Unigene46898_All//gi|115487968|ref|NP_001066471.1|//8.00E-98//Os12g0239000 [Oryza sativa Japonica Group] >gi|77554064|gb|ABA96860.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113648978|dbj|BAF29490.1|Os12g0239000 [Oryza sativa Japonica Group]	Unigene46898_All//2.00E-97//AT1G27850| unknown protein	Unigene46898_All//0.00E+00//CO073130		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene46899_All	1416	9.64	11.13	17.56	51.93	33.37	27.56	83.25	75.44	36.04	2.07E-01	1.69E-01		8.65E-01	4.41E-14		-6.38E-01	3.16E-30		-9.14E-01	1.08E-49		-1.42E-01	1.24E-03		-1.21E+00	6.65E-145	Down	Unigene46899_All//gi|211853240|emb|CAP16664.1|//2.00E-91//homeodomain leucine zipper protein [Solanum lycopersicum]	Unigene46899_All//1.00E-72//AT3G01470| ATHB-1 (ARABIDOPSIS THALIANA HOMEOBOX 1); DNA binding / protein homodimerization/ sequence-specific DNA binding / transcription activator/ transcription factor	Unigene46899_All//0.00E+00//TC152268	HB		GO:0001071//GO:0003677//GO:0006351//GO:0006970//GO:0009416//GO:0009887//GO:0010468//GO:0010557//GO:0030528//GO:0042802//GO:0043231	nr +
Unigene46903_All	1760	3.75	3.69	3.87	8.21	7.81	15.47	9.95	6.53	4.73	-2.35E-02	9.36E-01		4.81E-02	8.43E-01		-7.23E-02	6.91E-01		9.15E-01	1.44E-18		-6.07E-01	2.75E-07		-1.07E+00	1.56E-18	Down	Unigene46903_All//gi|15223426|ref|NP_174029.1|//1.00E-120//glycine-rich protein [Arabidopsis thaliana] >gi|8778876|gb|AAF79875.1|AC000348_28_T7N9.15 [Arabidopsis thaliana]	Unigene46903_All//1.00E-101//AT1G27090| glycine-rich protein	Unigene46903_All//0.00E+00//gi|78335866|gb|DT556140.1|DT556140				nr +
Unigene46904_All	1432	11.03	6.79	6.73	37.15	33.31	12.71	43.46	22.56	17.30	-7.00E-01	6.36E-07		-7.13E-01	9.02E-07		-1.58E-01	3.45E-02		-1.55E+00	9.21E-83	Down	-9.46E-01	1.90E-50		-1.33E+00	3.91E-89	Down	Unigene46904_All//gi|306856412|ref|NP_850205.1|//2.00E-71//IAA13; transcription factor [Arabidopsis thaliana] >gi|38504400|sp|Q38831.2|IAA13_ARATH RecName: Full=Auxin-responsive protein IAA13; AltName: Full=Indoleacetic acid-induced protein 13 >gi|29028860|gb|AAO64809.1|At2g33310 [Arabidopsis thaliana] >gi|110742999|dbj|BAE99393.1|auxin regulated protein [Arabidopsis thaliana]	Unigene46904_All//3.00E-63//AT2G33310| IAA13; transcription factor	Unigene46904_All//0.00E+00//CO084858			GO:0003002//GO:0005515//GO:0009725//GO:0009790//GO:0009987//GO:0010467//GO:0030528//GO:0048513	nr +
Unigene46906_All	1443	29.99	68.51	77.97	45.50	45.94	60.25	211.46	29.08	42.57	1.19E+00	2.12E-94	Up	1.38E+00	3.25E-131	Up	1.38E-02	8.69E-01		4.05E-01	4.45E-14		-2.86E+00	0.00E+00	Down	-2.31E+00	0.00E+00	Down	Unigene46906_All//gi|74273631|gb|AB401883.1|//0.00E-00//gibberellin 3-hydroxylase 1 [Gossypium hirsutum] >gi|121755807|gb|ABM64801.1|anthocyanidin synthase [Gossypium hirsutum]	Unigene46906_All//3.00E-143//AT4G22880| LDOX (LEUCOANTHOCYANIDIN DIOXYGENASE); leucocyanidin oxygenase	Unigene46906_All//0.00E+00//TC168804		ko00941|Flavonoid biosynthesis	GO:0008152//GO:0016701//GO:0016706	nr +
Unigene46909_All	1764	8.28	7.01	3.05	8.10	13.41	10.55	12.10	7.98	14.93	-2.40E-01	1.20E-01		-1.44E+00	1.65E-18	Down	7.27E-01	4.31E-12		3.80E-01	3.01E-03		-6.00E-01	1.48E-08		3.03E-01	1.19E-03		Unigene46909_All//gi|224072103|ref|XP_002303625.1|//2.00E-72//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222841057|gb|EEE78604.1|AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene46909_All//1.00E-47//AT4G23750| CRF2 (CYTOKININ RESPONSE FACTOR 2); DNA binding / transcription factor	Unigene46909_All//0.00E+00//TC168627	AP2-EREBP		GO:0005488//GO:0006606//GO:0009793//GO:0048827	nr +
Unigene4691_All	1444	9.38	4.25	7.97	49.71	43.43	31.09	48.75	32.88	49.22	-1.14E+00	8.22E-13	Down	-2.37E-01	1.60E-01		-1.95E-01	1.07E-03		-6.77E-01	4.31E-29		-5.68E-01	6.51E-24		1.38E-02	8.40E-01		Unigene4691_All//gi|301119757|ref|XP_002907606.1|//1.00E-10//NUK6 [Phytophthora infestans T30-4] >gi|262106118|gb|EEY64170.1| NUK6 [Phytophthora infestans T30-4]	Unigene4691_All//1.00E-14//AT2G22795| unknown protein	Unigene4691_All//0.00E+00//ES826110				nr +
Unigene46910_All	1632	43.02	18.35	32.43	67.27	65.03	48.73	10.08	5.22	7.93	-1.23E+00	7.00E-71	Down	-4.08E-01	1.59E-10		-4.89E-02	4.25E-01		-4.65E-01	1.07E-22		-9.48E-01	5.61E-14		-3.45E-01	4.16E-03		Unigene46910_All//gi|157273652|gb|ABV27480.1|//0.00E+00//fasciclin-like arabinogalactan protein 9 [Gossypium hirsutum]	Unigene46910_All//7.00E-107//AT3G46550| SOS5 (salt overly sensitive 5); polysaccharide binding / protein binding	Unigene46910_All//0.00E+00//TC130452		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene46912_All	1327	2.76	3.28	4.33	2.33	2.23	3.47	2.84	3.59	1.23	2.51E-01	4.00E-01		6.51E-01	1.17E-02		-6.06E-02	8.65E-01		5.77E-01	4.35E-02		3.41E-01	1.93E-01		-1.20E+00	1.88E-05	Down	Unigene46912_All//gi|115473321|ref|NP_001060259.1|//3.00E-12//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene46912_All//1.00E-07//AT3G25270| nucleic acid binding	Unigene46912_All//2.00E-113//DW497751				nr +
Unigene46915_All	785	2.00	3.23	2.98	11.30	7.28	4.66	8.08	6.71	2.74	6.91E-01	8.20E-02		5.78E-01	1.88E-01		-6.33E-01	4.31E-04		-1.28E+00	8.89E-11	Down	-2.68E-01	2.34E-01		-1.56E+00	2.58E-12	Down	Unigene46915_All//gi|115479811|ref|NP_001063499.1|//3.00E-21//Os09g0482000 [Oryza sativa Japonica Group] >gi|50725876|dbj|BAD33405.1| ETEA protein -like [Oryza sativa Japonica Group] >gi|113631732|dbj|BAF25413.1|Os09g0482000 [Oryza sativa Japonica Group]	Unigene46915_All//2.00E-19//AT4G10790| UBX domain-containing protein	Unigene46915_All//0.00E+00//DW500828				nr +
Unigene46916_All	1533	13.75	12.46	18.55	69.38	35.18	30.58	13.21	8.56	4.83	-1.43E-01	2.81E-01		4.32E-01	3.88E-05		-9.80E-01	9.81E-92		-1.18E+00	3.51E-109	Down	-6.26E-01	9.93E-09		-1.45E+00	1.06E-33	Down	Unigene46916_All//gi|86438623|emb|CAJ26580.1|//5.00E-86//ETEA-like (expressed in T-cells and eosinophils in atopic dermatitis) protein [Brachypodium sylvaticum]	Unigene46916_All//1.00E-59//AT4G10790| UBX domain-containing protein	Unigene46916_All//0.00E+00//ES791513			GO:0043231	nr +
Unigene46917_All	2596	0.10	1.41	0.57	1.69	2.64	3.51	6.19	1.66	12.86	3.80E+00	4.68E-15	Up	2.51E+00	1.98E-04	Up	6.45E-01	2.76E-03		1.06E+00	3.05E-08	Up	-1.90E+00	5.46E-38	Down	1.06E+00	1.95E-33	Up	Unigene46917_All//gi|297811107|ref|XP_002873437.1|//1.00E-127//tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319274|gb|EFH49696.1|tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46917_All//9.00E-121//AT5G10090| tetratricopeptide repeat (TPR)-containing protein				GO:0019725	nr +
Unigene46918_All	1870	57.86	73.65	78.91	7.91	14.11	9.18	0.25	0.65	2.22	3.48E-01	1.12E-15		4.48E-01	2.28E-25		8.34E-01	6.54E-17		2.14E-01	1.45E-01		1.38E+00	1.48E-02		3.16E+00	2.69E-18	Up	Unigene46918_All//gi|186478068|ref|NP_849578.5|//1.00E-180//BGLU11 (BETA GLUCOSIDASE 11); hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]	Unigene46918_All//4.00E-174//AT1G62850| BGLU11 (BETA GLUCOSIDASE 11); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene46918_All//0.00E+00//CO079114		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0015926//GO:0043167//GO:0044238	nr -
Unigene46919_All	2186	10.99	4.20	6.99	5.24	4.10	3.10	1.64	0.52	0.66	-1.39E+00	1.13E-29	Down	-6.52E-01	1.39E-08		-3.56E-01	3.11E-02		-7.58E-01	3.57E-06		-1.67E+00	9.88E-08	Down	-1.33E+00	6.00E-06	Down	Unigene46919_All//gi|15218422|ref|NP_177979.1|//0.00E+00//ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE): alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75213463|sp|Q9SYM4.1|TPS1_ARATH RecName: Full=Alpha,alpha-trehalose-phosphate synthase [UDP-forming] 1; AltName: Full=Trehalose-6-phosphate synthase 1; Short=AtTPS1 >gi|4836875|gb|AAD30578.1|AC007260_9 trehalose-6-phosphate synthase [Arabidopsis thaliana]	Unigene46919_All//0.00E+00//AT1G78580| ATTPS1 (TREHALOSE-6-PHOSPHATE SYNTHASE); alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups	Unigene46919_All//0.00E+00//TC167455		ko00500|Starch and sucrose metabolism	GO:0003006//GO:0005991//GO:0007275//GO:0009756//GO:0019203//GO:0035251//GO:0042546	nr +
Unigene46921_All	2971	2.66	0.97	1.20	7.44	6.24	6.40	6.38	1.84	3.33	-1.45E+00	6.40E-11	Down	-1.15E+00	1.97E-07	Down	-2.56E-01	2.85E-02		-2.18E-01	8.03E-02		-1.79E+00	3.07E-41	Down	-9.39E-01	3.13E-16		Unigene46921_All//gi|17064874|gb|AAL32591.1|//3.00E-15//Unknown protein [Arabidopsis thaliana] >gi|27311933|gb|AA000932.1|Unknown protein [Arabidopsis thaliana]	Unigene46921_All//1.00E-15//AT4G14200| unknown protein	Unigene46921_All//0.00E+00//TC168121				nr +
Unigene46925_All	577	1.63	2.28	3.32	1.21	2.27	1.96	6.23	2.83	4.00	4.84E-01	3.94E-01		1.03E+00	3.81E-02		9.08E-01	1.35E-01		6.95E-01	3.13E-01		-1.14E+00	1.07E-04	Down	-6.37E-01	2.24E-02		Unigene46925_All//gi|297816792|ref|XP_002876279.1|//6.00E-54//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297322117|gb|EFH52538.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46925_All//8.00E-54//AT3G54980| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene46927_All	1689	7.25	2.40	4.82	4.60	6.36	19.52	0.50	0.82	2.88	-1.59E+00	7.56E-19	Down	-5.88E-01	4.53E-04		4.67E-01	5.51E-03		2.08E+00	5.89E-76	Up	7.06E-01	1.71E-01		2.52E+00	4.40E-17	Up	Unigene46927_All//gi|224123490|ref|XP_002330327.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222871362|gb|EEF08493.1|cytochrome P450 [Populus trichocarpa]	Unigene46927_All//8.00E-148//AT4G19230| CYP707A1; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	Unigene46927_All//0.00E+00//TC154536		ko00906|Carotenoid biosynthesis	GO:0005506//GO:0008152//GO:0016491	nr +
Unigene46928_All	1836	46.99	19.43	48.99	28.05	28.88	17.61	0.44	0.50	0.11	-1.27E+00	6.18E-92	Down	6.00E-02	3.84E-01		4.20E-02	6.49E-01		-6.72E-01	9.70E-21		1.95E-01	7.62E-01		-2.01E+00	7.11E-03		Unigene46928_All//gi|297726167|ref|NP_001175447.1|//6.00E-95//Os08g0230800 [Oryza sativa Japonica Group] >gi|255678252|dbj|BAH94175.1|Os08g0230800 [Oryza sativa Japonica Group]	Unigene46928_All//3.00E-41//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene46928_All//2.00E-83//ES849970		ko04626|Plant-pathogen interaction		nr -
Unigene4693_All	948	6.95	2.99	2.75	5.83	5.96	4.48	5.00	1.50	1.05	-1.22E+00	3.12E-07	Down	-1.34E+00	7.72E-08	Down	3.05E-02	9.28E-01		-3.81E-01	1.53E-01		-1.74E+00	1.86E-10	Down	-2.25E+00	7.09E-15	Down	Unigene4693_All//gi|213495894|gb|ACJ49167.1|//8.00E-99//protection of telomeres 1 protein [Gossypium hirsutum]	Unigene4693_All//7.00E-34//AT2G05210| AtPOT1a (Protection of Telomeres 1a); telomeric DNA binding	Unigene4693_All//0.00E+00//ES800052				nr -
Unigene46931_All	1202	38.91	57.71	47.00	57.81	56.90	57.90	65.32	42.21	31.42	5.69E-01	2.60E-19		2.73E-01	1.97E-04		-2.31E-02	8.02E-01		2.20E-03	9.75E-01		-6.30E-01	8.54E-32		-1.06E+00	4.44E-78	Down	Unigene46931_All//gi|85701293|sp|Q9SQ29.2|Y3478_ARATH//3.00E-81//RecName: Full=UPF0424 protein At3g04780 >gi|16648681|gb|AAL25533.1|AT3g04780/F7O18_27 [Arabidopsis thaliana] >gi|20147247|gb|AAM10337.1|AT3g04780/F7O18_27 [Arabidopsis thaliana]	Unigene46931_All//2.00E-80//AT3G04780| Encodes a protein with little sequence identity with any other protein of known structure or function. Part of this protein shows a 42% sequence identity with the C-terminal domain of the 32-kD human thioredoxin-like protein.	Unigene46931_All//0.00E+00//TC143733			GO:0019725	nr -

Unigene46932_All	2601	2.78	2.63	1.47	4.10	3.27	2.66	9.66	4.11	3.43	-7.80E-02	7.26E-01		-9.13E-01	5.99E-05		-3.26E-01	6.32E-02		-6.26E-01	2.47E-04		-1.23E+00	1.53E-31	Down	-1.49E+00	2.27E-43	Down	Unigene46932_All//gi|60543313|gb|AAX22254.1|/1.00E-103//At4g21890 [Arabidopsis thaliana] >gi|106879183|gb|ABF82621.1| At4g21890 [Arabidopsis thaliana]	Unigene46932_All//4.00E-89//AT4G21890| unknown protein	Unigene46932_All//0.00E+00//TC178723			GO:0046914	nr -
Unigene46933_All	575	20.38	9.34	14.54	7.71	5.75	3.38	3.90	3.49	2.84	-1.13E+00	6.44E-11	Down	-4.87E-01	4.81E-03		-4.23E-01	1.45E-01		-1.19E+00	3.43E-05	Down	-1.60E-01	6.91E-01		-4.56E-01	2.24E-01		Unigene46933_All//gi|30023660|gb|AAP13363.1|/3.00E-47//At5g55710 [Arabidopsis thaliana]	Unigene46933_All//9.00E-44//AT5G55710| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: tic20 protein-related (TAIR:AT2G47840.1); Has 268 Blast hits to 268 proteins in 76 species: Archae - 0; Bacteria - 107; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 124 (source: NCBI BLink).				GO:0009534//GO:0031224	nr +
Unigene46935_All	579	5.87	1.58	4.51	11.53	7.91	4.29	6.21	1.16	0.41	-1.90E+00	3.78E-07	Down	-3.82E-01	2.91E-01		-5.44E-01	1.21E-02		-1.43E+00	1.14E-09	Down	-2.43E+00	4.69E-12	Down	-3.91E+00	2.32E-19	Down	Unigene46935_All//gi|124359162|gb|ABN05885.1|//2.00E-07//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene46935_All//2.00E-05//AT3G09510| nucleic acid binding	Unigene46935_All//9.00E-176//TC149593				nr -
Unigene46936_All	2295	8.50	3.47	8.40	30.97	19.25	10.59	4.97	0.82	0.54	-1.29E+00	7.53E-22	Down	-1.78E-02	9.10E-01		-6.86E-01	3.11E-33		-1.55E+00	1.33E-110	Down	-2.60E+00	8.39E-40	Down	-3.21E+00	6.18E-51	Down	Unigene46936_All//gi|124360549|gb|ABB33126.2|/1.00E-82//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene46936_All//7.00E-26//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene46936_All//0.00E+00//DW485722			GO:0003676//GO:0016772//GO:0044238//GO:0044260	nr -
Unigene46937_All	1976	3.79	3.28	1.99	6.25	7.51	3.63	1.97	1.80	4.74	-2.06E-01	3.63E-01		-9.25E-01	3.40E-05		2.65E-01	8.00E-02		-7.83E-01	6.13E-07		-1.31E-01	6.59E-01		1.27E+00	4.27E-13	Up	Unigene46937_All//gi|9295691|gb|AAF86997.1|AC005292_6//1.00E-34//F26F24.8 [Arabidopsis thaliana]	Unigene46937_All//5.00E-36//AT1G23230| unknown protein	Unigene46937_All//0.00E+00//gi|164321172|gb|ES791754.1|ES791754			GO:0044464	nr +
Unigene46938_All	1982	17.32	7.26	12.73	81.26	75.30	72.28	29.46	7.11	12.20	-1.25E+00	4.43E-36	Down	-4.43E-01	2.61E-06		-1.10E-01	6.84E-03		-1.69E-01	2.23E-05		-2.05E+00	9.74E-151	Down	-1.27E+00	3.15E-78	Down	Unigene46938_All//gi|157273664|gb|ABV27486.1|//0.00E+00//fasciclin-like arabinogalactan protein 15 [Gossypium hirsutum]	Unigene46938_All//2.00E-153//AT5G06390| FLA17 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 17 PRECURSOR)	Unigene46938_All//0.00E+00//TC130215			GO:0009987//GO:0043231	nr +
Unigene46939_All	2186	1.96	1.27	1.27	2.46	1.76	2.89	3.35	1.43	2.64	-6.23E-01	3.37E-02		-6.32E-01	4.03E-02		-4.80E-01	5.64E-02		2.33E-01	3.95E-01		-1.22E+00	1.17E-09	Down	-3.41E-01	7.63E-02		Unigene46939_All//gi|297848576|ref|XP_002892169.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297338011|gb|EFH68428.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene46939_All//0.00E+00//AT1G03560| pentatricopeptide (PPR) repeat-containing protein	Unigene46939_All//0.00E+00//gi|21102468|gb|BQ414781.1|BQ414781				nr -
Unigene4694_All	1302	8.04	24.13	17.75	14.12	65.19	143.36	0.13	0.45	0.80	1.59E+00	1.23E-46	Up	1.14E+00	1.82E-20	Up	2.21E+00	3.75E-229	Up	3.34E+00	0.00E+00	Up	1.79E+00	5.30E-02		2.61E+00	2.37E-04	Up	Unigene4694_All//gi|75297894|sp|Q84MB3.1|ACCH1_ARATH//1.00E-113//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene4694_All//2.00E-114//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene4694_All//0.00E+00//TC130370		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene46943_All	1117	55.46	63.64	63.40	40.72	43.50	32.99	18.43	14.71	5.46	1.99E-01	1.79E-03		1.93E-01	3.69E-03		9.54E-02	2.92E-01		-3.03E-01	8.94E-05		-3.26E-01	3.00E-03		-1.76E+00	6.16E-45	Down	Unigene46943_All//gi|4835787|gb|AAD30253.1|AC007296_14//1.00E-50//ESTs gb|R65381 and gb|T44635 come from this gene [Arabidopsis thaliana] >gi|27808534|gb|AAO24547.1| At1g11700 [Arabidopsis thaliana]	Unigene46943_All//7.00E-52//AT1G11700| unknown protein	Unigene46943_All//0.00E+00//DW517610			GO:0009536	nr -
Unigene46945_All	837	0.69	1.88	2.04	3.87	2.76	7.12	7.48	17.28	18.75	1.45E+00	8.58E-03		1.57E+00	4.57E-03		-4.89E-01	1.56E-01		8.81E-01	2.48E-04		1.21E+00	5.72E-18	Up	1.33E+00	7.00E-23	Up	Unigene46945_All//gi|224061505|ref|XP_002300513.1|//8.00E-68//caffeic acid 3-O-methyltransferase [Populus trichocarpa] >gi|222847771|gb|EEE85318.1| caffeic acid 3-O-methyltransferase [Populus trichocarpa]	Unigene46945_All//2.00E-52//AT1G33030| O-methyltransferase family 2 protein	Unigene46945_All//4.00E-126//TC164875		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0008171	nr -
Unigene46947_All	607	4.14	2.34	4.04	4.92	5.11	3.42	5.57	5.44	2.49	-8.24E-01	3.90E-02		-3.60E-02	9.45E-01		5.23E-02	9.05E-01		-5.25E-01	1.61E-01		-3.48E-02	9.30E-01		-1.16E+00	9.44E-05	Down	Unigene46947_All//gi|186506099|ref|NP_181263.2|//3.00E-16//TTG2 (TRANSPARENT TESTA GLABRA 2); transcription factor [Arabidopsis thaliana] >gi|29839696|sp|Q9ZUU0.2|WRK44_ARATH RecName: Full=WRKY transcription factor 44; AltName: Full=WRKY DNA-binding protein 44; AltName: Full=Protein TRANSPARENT TESTA GLABRA 2 >gi|154996558|dbj|BAF74397.1| WRKY transcription factor [Arabidopsis thaliana]	Unigene46947_All//3.00E-16//AT2G37260| TTG2 (TRANSPARENT TESTA GLABRA 2); transcription factor	Unigene46947_All//0.00E+00//TC132413	WRKY		GO:0001071//GO:0001708//GO:0003006//GO:0003677//GO:0006350//GO:0010468//GO:0043231	nr +
Unigene4695_All	1790	0.23	0.51	0.42	3.06	3.16	2.27	1.96	0.93	0.67	1.12E+00	1.30E-01		8.33E-01	3.39E-01		4.35E-02	8.88E-01		-4.31E-01	1.03E-01		-1.07E+00	3.11E-04	Down	-1.55E+00	3.68E-07	Down	Unigene4695_All//gi|297843100|ref|XP_002889431.1|//0.00E+00//phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335273|gb|EFH65690.1| phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4695_All//0.00E+00//AT1G03010| phototropic-responsive NPH3 family protein	Unigene4695_All//0.00E+00//DW517629				nr -
Unigene46951_All	1578	28.98	55.07	34.42	21.53	30.22	27.70	10.53	22.65	17.70	9.26E-01	3.08E-55		2.48E-01	1.00E-03		4.89E-01	4.43E-12		3.64E-01	3.50E-06		1.10E+00	1.48E-37	Up	7.49E-01	3.56E-16		Unigene46951_All//gi|9958056|gb|AAG09545.1|AC011810_4//5.00E-84//Unknown protein [Arabidopsis thaliana]	Unigene46951_All//4.00E-67//AT1G13340| unknown protein	Unigene46951_All//0.00E+00//TC157246			GO:0043231	nr +
Unigene46953_All	814	2.57	0.62	1.11	1.96	2.58	2.16	1.87	3.29	1.81	-2.05E+00	4.33E-05	Down	-1.21E+00	1.09E-02		3.98E-01	4.17E-01		1.44E-01	7.81E-01		8.14E-01	1.82E-02		-4.63E-02	9.37E-01		Unigene46953_All//gi|297824099|ref|XP_002879932.1|//4.00E-39//apurinic endonuclease-redox protein [Arabidopsis lyrata subsp. lyrata] >gi|297325771|gb|EFH56191.1| apurinic endonuclease-redox protein [Arabidopsis lyrata subsp. lyrata]	Unigene46953_All//1.00E-39//AT2G41460| ARP; DNA-(apurinic or apyrimidinic site) lyase	Unigene46953_All//2.00E-143//TC172908		ko03410|Base excision repair	GO:0003676//GO:0004518//GO:0006259//GO:0010557//GO:0016835//GO:0043231	nr -
Unigene46959_All	740	0.99	1.99	1.37	2.89	2.42	2.99	1.71	3.28	5.55	1.00E+00	6.92E-02		4.66E-01	5.11E-01		-2.59E-01	5.87E-01		4.70E-02	9.34E-01		9.34E-01	1.06E-02		1.69E+00	4.34E-09	Up	Unigene46959_All//gi|195627412|gb|ACG35536.1|//3.00E-08//retrotransposon protein [Zea mays]	Unigene46959_All//1.00E-06//AT1G15215| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: sequence-specific DNA binding / transcription factor (TAIR:AT5G18380.1); Has 41 Blast hits to 40 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene46959_All//0.00E+00//ES829220				nr -
Unigene4696_All	1409	0.56	1.91	0.91	3.11	2.86	3.37	3.24	4.06	3.25	1.77E+00	2.49E-05	Up	7.03E-01	2.54E-01		-1.22E-01	7.20E-01		1.13E-01	7.09E-01		3.27E-01	1.63E-01		4.80E-03	9.84E-01		Unigene4696_All//gi|224124996|ref|XP_002328665.1|//1.00E-158//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222871102|gb|EEF08233.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene4696_All//3.00E-115//AT1G12260| ANAC007 (ARABIDOPSIS NAC 007); transcription factor	Unigene4696_All//1.00E-35//gi|109882837|gb|DW511807.1|DW511807	NAC			nr +
Unigene46960_All	1345	5.87	7.23	6.81	10.56	7.09	11.79	5.31	12.06	6.49	3.00E-01	1.19E-01		2.13E-01	3.25E-01		-5.74E-01	2.94E-05		1.59E-01	3.34E-01		1.18E+00	2.13E-19	Up	2.88E-01	1.04E-01		Unigene46960_All//gi|195627412|gb|ACG35536.1|//3.00E-57//retrotransposon protein [Zea mays]	Unigene46960_All//4.00E-49//AT3G18380| sequence-specific DNA binding / transcription factor	Unigene46960_All//0.00E+00//TC160629			GO:0005488//GO:0009987	nr +
Unigene46961_All	2123	47.32	23.17	20.82	83.74	115.50	131.72	29.26	11.20	14.88	-1.03E+00	3.56E-76	Down	-1.18E+00	2.57E-92	Down	4.64E-01	4.99E-55		6.54E-01	2.48E-104		-1.39E+00	4.28E-92	Down	-9.75E-01	1.90E-54		Unigene46961_All//gi|224064460|ref|XP_002301487.1|//0.00E+00//glycosyl hydrolase family 9 [Populus trichocarpa] >gi|222843213|gb|EEE80760.1| glycosyl hydrolase family 9 [Populus trichocarpa]	Unigene46961_All//0.00E+00//AT4G02290| AtGH9B13 (Arabidopsis thaliana glycosyl hydrolase 9B13); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene46961_All//0.00E+00//TC153206		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0007275//GO:0044238//GO:0044464//GO:0051707	nr -
Unigene46963_All	1456	9.52	5.53	5.96	3.87	3.78	2.61	1.48	3.36	3.94	-7.83E-01	2.47E-07		-6.76E-01	1.48E-05		-3.09E-02	9.10E-01		-5.69E-01	2.34E-02		1.18E+00	2.14E-06	Up	1.41E+00	1.06E-09	Up	Unigene46963_All//gi|15238474|ref|NP_200769.1|//2.00E-67//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|124300972|gb|ABN04738.1| At5g59610 [Arabidopsis thaliana]	Unigene46963_All//1.00E-68//AT5G59610| DNAJ heat shock N-terminal domain-containing protein	Unigene46963_All//0.00E+00//gi|48789780|gb|CO091094.1|CO091094				nr -
Unigene46964_All	2017	142.57	101.39	94.91	34.63	43.19	52.57	11.80	28.70	13.51	-4.92E-01	5.34E-60		-5.87E-01	6.45E-80		3.19E-01	4.51E-10		6.03E-01	1.47E-34		1.28E+00	3.29E-76	Up	1.95E-01	4.03E-02		Unigene46964_All//gi|15228395|ref|NP_187702.1|//6.00E-49//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565331|sp|Q9SG96.1|ATL3C_ARATH RecName: Full=RING-H2 finger protein ATL3C >gi|28466857|gb|AAO44037.1| At3g10910 [Arabidopsis thaliana]	Unigene46964_All//2.00E-36//AT3G10910| zinc finger (C3HC4-type RING finger) family protein	Unigene46964_All//0.00E+00//gi|164296865|gb|ES811188.1|ES811188				nr -
Unigene46965_All	846	7.67	4.97	4.78	17.55	13.39	23.86	4.50	1.14	2.31	-6.25E-01	6.74E-03		-6.81E-01	4.67E-03		-3.90E-01	5.00E-03		4.44E-01	2.33E-04		-1.98E+00	4.34E-10	Down	-9.63E-01	4.22E-04		Unigene46965_All//gi|297842803|ref|XP_002889283.1|//9.00E-09//ribosomal protein S15 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335124|gb|EFH65542.1| ribosomal protein S15 family protein [Arabidopsis lyrata subsp. lyrata]		Unigene46965_All//0.00E+00//TC174710				nr +

Unigene46966_All	1598	27.63	6.37	10.86	42.49	31.61	60.14	34.08	11.22	14.76	-2.12E+00	2.91E-97	Down	-1.35E+00	9.46E-50	Down	-4.27E-01	1.36E-13		5.01E-01	1.16E-22		-1.60E+00	2.94E-100	Down	-1.21E+00	2.43E-67	Down	Unigene46966_All//gi|30699526|ref|NP_849914.1|/8.00E-88//ribosomal protein S15 family protein [Arabidopsis thaliana]	Unigene46966_All//2.00E-79//AT1G80620| ribosomal protein S15 family protein	Unigene46966_All//0.00E+00//TC174710		ko03010|Ribosome		nr +
Unigene46967_All	1894	9.06	6.98	3.80	7.39	7.85	7.06	3.93	2.67	3.45	-3.76E-01	5.47E-03		-1.26E+00	1.17E-17	Down	8.78E-02	6.11E-01		-6.64E-02	6.98E-01		-5.57E-01	3.49E-03		-1.88E-01	3.53E-01		Unigene46967_All//gi|18397669|ref|NP_566289.1|//1.00E-89//PAPA-1-like family protein / zinc finger (HIT type) family protein [Arabidopsis thaliana]	Unigene46967_All//9.00E-77//AT3G06660| PAPA-1-like family protein / zinc finger (HIT type) family protein	Unigene46967_All//0.00E+00//gi|78331036|gb|DT551310.1|DT551310				nr +
Unigene4697_All	1547	9.13	36.68	15.52	10.69	14.40	14.80	26.59	49.71	37.83	2.01E+00	1.03E-115	Up	7.66E-01	3.60E-11		4.30E-01	8.50E-05		4.69E-01	2.66E-05		9.03E-01	1.95E-57		5.09E-01	5.89E-17		Unigene4697_All//gi|297802604|ref|XP_002869186.1|/1.00E-146//phosphatase 2C family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315022|gb|EFH45445.1| phosphatase 2C family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4697_All//2.00E-137//AT4G33920| protein phosphatase 2C family protein / PP2C family protein	Unigene4697_All//0.00E+00//TC145065				nr -
Unigene46971_All	1160	4.83	10.05	6.47	16.10	24.43	12.50	38.02	37.58	43.55	1.06E+00	7.49E-10	Up	4.24E-01	6.10E-02		6.01E-01	1.85E-10		-3.66E-01	4.25E-03		-1.66E-02	8.54E-01		1.96E-01	3.38E-03		Unigene46971_All//gi|195655535|gb|ACG47083.1|/4.00E-57//zinc finger protein [Zea mays]	Unigene46971_All//7.00E-36//AT5G62460| zinc finger (C3HC4-type RING finger) family protein	Unigene46971_All//0.00E+00//gi|164256507|gb|ES811872.1|ES811872		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene46972_All	2071	0.30	0.27	0.69	7.53	3.69	8.13	37.89	16.63	12.81	-1.72E-01	8.29E-01		1.20E+00	4.42E-02		-1.03E+00	7.31E-15	Down	1.12E-01	4.99E-01		-1.19E+00	1.18E-91	Down	-1.56E+00	2.88E-143	Down	Unigene46972_All//gi|117940159|sp|P93051.2|EXDL7_ARATH//1.00E-155//RecName: Full=Sugar transporter ERD6-like 7	Unigene46972_All//4.00E-157//AT2G48020| sugar transporter, putative	Unigene46972_All//0.00E+00//CO081832				nr +
Unigene46973_All	1840	0.06	0.17	0.00	1.60	0.75	1.79	10.73	3.68	2.25	1.54E+00	3.23E-01		-5.83E+00	3.92E-01		-1.09E+00	1.41E-03		1.66E-01	6.76E-01		-1.54E+00	6.38E-35	Down	-2.25E+00	1.32E-59	Down	Unigene46973_All//gi|118572295|sp|Q8LB19.2|EDL16_ARATH//0.00E+00//RecName: Full=Sugar transporter ERD6-like 16 >gi|17381265|gb|AAL36051.1| AT5g18840/F17K1_90 [Arabidopsis thaliana] >gi|23309019|gb|AAN18269.1| At5g18840/F17K1_90 [Arabidopsis thaliana]	Unigene46973_All//7.00E+00//AT5G18840| sugar transporter, putative	Unigene46973_All//0.00E+00//CO081832				nr -
Unigene46974_All	2257	5.59	4.00	3.80	7.31	5.87	2.52	5.19	0.81	2.26	-4.83E-01	2.38E-03		-5.57E-01	7.38E-04		-3.15E-01	1.96E-02		-1.53E+00	1.15E-25	Down	-2.67E+00	5.22E-42	Down	-1.20E+00	4.92E-15	Down	Unigene46974_All//gi|261664505|sp|C0LGQ9.1|Y4294_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At4g20940 >gi|224589622|gb|ACN59344.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene46974_All//1.00E-135//AT4G20940| leucine-rich repeat family protein	Unigene46974_All//0.00E+00//TC140082				nr +
Unigene46977_All	1621	3.94	2.28	1.94	9.10	7.14	6.88	13.02	16.32	17.06	-7.87E-01	7.37E-04		-1.02E+00	3.17E-05	Down	-3.50E-01	1.36E-02		-4.03E-01	5.76E-03		3.27E-01	6.02E-04		3.90E-01	1.48E-05		Unigene46977_All//gi|32483159|emb|CAE02147.1|//2.00E-60//OSJNBa0081G05.2 [Oryza sativa (japonica cultivar-group)] >gi|116309213|emb|CAH66305.1| OSIGBa0135K14.2 [Oryza sativa (indica cultivar-group)] >gi|116309230|emb|CAH66320.1| OSIGBa0150M16.3 [Oryza sativa (indica cultivar-group)]	Unigene46977_All//9.00E-43//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene46977_All//0.00E+00//TC133982				nr -
Unigene46978_All	2009	127.46	636.41	303.46	44.01	40.93	60.54	1.94	0.89	2.10	2.32E+00	0.00E+00	Up	1.25E+00	0.00E+00	Up	-1.05E-01	7.86E-02		4.60E-01	1.87E-24		-1.11E+00	7.32E-05	Down	1.19E-01	6.65E-01		Unigene46978_All//gi|74273645|gb|AB401490.1|//0.00E+00//3-ketoacyl-CoA synthase [Gossypium hirsutum]	Unigene46978_All//0.00E+00//AT1G68530| KCS6 (3-KETOACYL-COA SYNTHASE 6); catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene46978_All//0.00E+00//TC130908				nr +
Unigene46980_All	1511	4.22	4.46	4.51	8.21	9.39	10.58	3.67	11.89	5.70	7.83E-02	7.34E-01		9.47E-02	6.97E-01		1.94E-01	2.41E-01		3.66E-01	9.41E-03		1.70E+00	2.42E-36	Up	6.36E-01	2.02E-04		Unigene46980_All//gi|195655031|gb|ACG46983.1|/1.00E-19//HVA22-like protein a [Zea mays]	Unigene46980_All//5.00E-19//AT1G74520| ATHVA22A	Unigene46980_All//0.00E+00//CO069886				nr +
Unigene46982_All	2019	8.55	3.89	5.12	12.68	8.82	11.61	13.40	7.45	9.00	-1.14E+00	6.01E-16	Down	-7.41E-01	8.55E-08		-5.24E-01	9.70E-08		-1.27E-01	3.15E-01		-8.47E-01	1.02E-18		-5.75E-01	3.26E-10		Unigene46982_All//gi|297801970|ref|XP_002868869.1|//0.00E+00//dihydrouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314705|gb|EFH45128.1| dihydrouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46982_All//0.00E+00//AT4G38890| dihydrouridine synthase family protein	Unigene46982_All//0.00E+00//gi|164337652|gb|ES798179.1|ES798179				nr +
Unigene46983_All	2229	0.70	0.89	1.15	1.81	1.58	1.38	3.43	1.01	1.89	3.32E-01	4.78E-01		7.03E-01	8.93E-02		-2.00E-01	5.53E-01		-3.94E-01	2.23E-01		-1.76E+00	9.57E-17	Down	-8.58E-01	3.26E-06		Unigene46983_All//gi|297801970|ref|XP_002868869.1|//0.00E+00//dihydrouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314705|gb|EFH45128.1| dihydrouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46983_All//0.00E+00//AT4G38890| dihydrouridine synthase family protein	Unigene46983_All//0.00E+00//ES842532				nr -
Unigene46984_All	2217	73.02	394.34	394.39	143.35	173.82	276.28	32.36	11.88	20.67	2.43E+00	0.00E+00	Up	2.43E+00	0.00E+00	Up	2.78E-01	2.29E-33		9.47E-01	0.00E+00		-1.45E+00	2.03E-113	Down	-6.47E-01	2.14E-31		Unigene46984_All//gi|15218445|ref|NP_175036.1|//0.00E+00//emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana] >gi|7523682|gb|AAF63121.1|AC009526_6 Putative histidine decarboxylase [Arabidopsis thaliana] >gi|15011302|gb|AAK77493.1|AF389349_1 serine decarboxylase [Arabidopsis thaliana] >gi|17907848|dbj|BAB79456.1| histidine decarboxylase [Arabidopsis thaliana] >gi|17907853|dbj|BAB79457.1| histidine decarboxylase [Arabidopsis thaliana]	Unigene46984_All//0.00E+00//AT1G43710| emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding	Unigene46984_All//0.00E+00//TC133682		ko00340|Histidine metabolism		nr -
Unigene46986_All	2269	6.39	9.69	8.50	6.50	8.92	12.04	6.71	12.53	16.24	6.02E-01	2.69E-07		4.12E-01	1.69E-03		4.58E-01	7.11E-05		8.90E-01	8.16E-18		9.01E-01	1.13E-21		1.28E+00	1.67E-49	Up	Unigene46986_All//gi|44681378|gb|AS47629.1|/4.00E-56//At1g26580 [Arabidopsis thaliana] >gi|45773908|gb|AAS76758.1| At1g26580 [Arabidopsis thaliana]	Unigene46986_All//9.00E-53//AT2G03470| myb family transcription factor / ELM2 domain-containing protein	Unigene46986_All//0.00E+00//TC174177	MYB-related			nr -
Unigene46987_All	1899	19.23	6.70	14.97	45.30	46.62	44.95	36.76	25.29	23.37	-1.52E+00	2.94E-51	Down	-3.61E-01	8.64E-05		4.14E-02	5.68E-01		-1.13E-02	8.86E-01		-5.40E-01	1.11E-21		-6.53E-01	4.42E-31		Unigene46987_All//gi|42568828|ref|NP_201506.2|//1.00E-145//lipase class 3 family protein [Arabidopsis thaliana]	Unigene46987_All//8.00E-139//AT5G67050| lipase class 3 family protein	Unigene46987_All//0.00E+00//gi|109861877|gb|DW490854.1|DW490854				nr +
Unigene4699_All	1395	13.39	4.32	6.34	7.43	4.52	5.57	4.49	6.23	1.77	-1.63E+00	2.71E-29	Down	-1.08E+00	3.37E-15	Down	-7.17E-01	1.13E-05		-4.16E-01	2.07E-02		4.74E-01	6.99E-03		-1.34E+00	7.06E-10	Down	Unigene4699_All//gi|30688695|ref|NP_172815.2|//1.00E-88//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|30688704|ref|NP_849703.1| GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|9369403|gb|AAF87151.1|AC002423_16 T23E23.19 [Arabidopsis thaliana] >gi|38603846|gb|AAR24668.1| At1g24040 [Arabidopsis thaliana]	Unigene4699_All//7.00E-83//AT1G24040| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene4699_All//0.00E+00//TC175509				nr -
Unigene46991_All	2147	10.43	3.49	3.67	8.42	7.23	6.42	7.64	2.96	5.85	-1.58E+00	2.18E-33	Down	-1.51E+00	4.93E-30	Down	-2.20E-01	1.06E-01		-3.93E-01	2.42E-03		-1.37E+00	1.84E-24	Down	-3.87E-01	1.26E-03		Unigene46991_All//gi|297827897|ref|XP_002881831.1|//0.00E+00//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327670|gb|EFH58090.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene46991_All//8.00E-172//AT3G57830| leucine-rich repeat transmembrane protein kinase, putative	Unigene46991_All//0.00E+00//TC133938				nr -
Unigene46993_All	1200	70.46	35.05	54.05	24.04	27.46	24.88	5.88	4.84	1.96	-1.01E+00	5.80E-62	Down	-3.83E-01	3.30E-11		1.92E-01	4.80E-02		4.97E-02	7.02E-01		-2.81E-01	1.82E-01		-1.59E+00	6.17E-14	Down	Unigene46993_All//gi|15234010|ref|NP_195580.1|//1.00E-48//GRP2 (GLYCINE RICH PROTEIN 2); double-stranded DNA binding / mRNA binding / nucleic acid binding / single-stranded DNA binding [Arabidopsis thaliana] >gi|14326487|gb|AAK60289.1|AF385696_1 AT4g38680/F20M13_240 [Arabidopsis thaliana] >gi|259445|gb|AAB24074.1| glycine-rich protein [Arabidopsis thaliana] >gi|4467155|emb|CAB37524.1| glycine-rich protein 2 (GRP2) [Arabidopsis thaliana] >gi|7270851|emb|CAB80532.1| glycine-rich protein 2 (GRP2) [Arabidopsis thaliana] >gi|22137152|gb|AAM91421.1| AT4g38680/F20M13_240 [Arabidopsis thaliana]	Unigene46993_All//3.00E-19//AT4G36020| CSDP1 (cold shock domain protein 1); RNA binding / double-stranded DNA binding / nucleic acid binding / single-stranded DNA binding	Unigene46993_All//0.00E+00//TC158202	CSD			nr -
Unigene46996_All	1718	3.53	1.98	0.96	5.28	4.19	2.94	7.24	3.11	2.90	-8.38E-01	4.92E-04		-1.88E+00	1.90E-11	Down	-3.33E-01	8.47E-02		-8.42E-01	6.90E-06		-1.22E+00	9.89E-16	Down	-1.32E+00	2.54E-18	Down	Unigene46996_All//gi|42573790|ref|NP_974991.1|//0.00E+00//FAS2 (FASCIATA 2); nucleotide binding / protein binding [Arabidopsis thaliana] >gi|4884488|dbj|BAA77766.1| FAS2 [Arabidopsis thaliana] >gi|10178066|dbj|BAB11430.1| FAS2 [Arabidopsis thaliana]	Unigene46996_All//0.00E+00//AT5G64630| FAS2 (FASCIATA 2); nucleotide binding / protein binding	Unigene46996_All//0.00E+00//gi|78343476|gb|DT563750.1|DT563750				nr -
Unigene46999_All	1691	22.25	25.29	18.99	56.91	67.77	53.47	41.93	54.10	96.64	1.85E-01	3.06E-02		-2.28E-01	1.51E-02		2.52E-01	1.48E-08		-9.01E-02	1.34E-01		3.68E-01	2.67E-14		1.20E+00	3.50E-198	Up	Unigene46999_All//gi|63029722|gb|AY227752.1|//0.00E+00//12-oxophytodienoate reductase [Hevea brasiliensis]	Unigene46999_All//1.00E-172//AT3G06050| OPR3 (OPDA-REDUCTASE 3); 12-oxophytodienoate reductase	Unigene46999_All//0.00E+00//TC136760		ko00592|alpha-Linolenic acid metabolism		nr -
Unigene470_All	846	0.49	0.24	0.13	7.54	3.34	6.35	2.30	1.88	1.60	-1.05E+00	3.65E-01		-1.97E+00	1.51E-01		-1.18E+00	8.09E-08	Down	-2.47E-01	3.49E-01		-2.92E-01	5.22E-01		-5.22E-01	1.98E-01		Unigene470_All//1.00E-78//AT1G27440| GUT2; catalytic/ glucuronoxylan glucuronosyltransferase	Unigene470_All//0.00E+00//gi|109877559|gb|DW506532.1|DW506532			GO:0009832//GO:0010413//GO:0015020//GO:0031410//GO:0043231	nr -
Unigene4700_All	1122	11.05	6.19	8.02	89.15	67.77	65.13	89.01	24.03	25.32	-8.37E-01	2.38E-07		-4.63E-01	5.90E-03		-3.96E-01	2.80E-17		-4.53E-01	9.04E-20		-1.89E+00	7.97E-231	Down	-1.81E+00	9.38E-225	Down	Unigene4700_All//gi|85719356|gb|AB075361.1|/8.00E-70//2-oxo acid dehydrogenase, lipoyl-binding site [Medicago truncatula]	Unigene4700_All//6.00E-67//AT2G35120| glycine cleavage system H protein, mitochondrial, putative	Unigene4700_All//0.00E+00//TC139413				nr -

Unigene47001_All	1645	3.09	3.97	2.30	3.45	2.95	1.29	2.93	2.06	2.37	3.65E-01	1.23E-01		-4.25E-01	1.40E-01		-2.26E-01	4.13E-01		-1.42E+00	2.87E-08	Down	-5.10E-01	3.96E-02		-3.04E-01	2.21E-01		Unigene47001_All//gi|18410540|ref|NP_565080.1|//1.00E-121//mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana]	Unigene47001_All//6.00E-112//AT1G74120| mitochondrial transcription termination factor-related / mTERF-related					nr -
Unigene47003_All	1646	2.07	8.56	3.24	4.93	10.48	11.50	3.83	2.23	3.15	2.05E+00	5.55E-30	Up	6.47E-01	1.65E-02		1.09E+00	4.19E-17	Up	1.22E+00	1.47E-20	Up	-7.76E-01	2.09E-04		-2.83E-01	1.88E-01		Unigene47003_All//gi|15238082|ref|NP_198961.1|//1.00E-179//fringe-related protein [Arabidopsis thaliana] >gi|53828537|gb|AAU94378.1|At5g41460 [Arabidopsis thaliana] >gi|57441904|gb|AAW50706.1|At5g41460 [Arabidopsis thaliana]	Unigene47003_All//2.00E-175//AT4G23490| fringe-related protein	Unigene47003_All//0.00E+00//gi|164274865|gb|ES809430.1|ES809430				nr -
Unigene47006_All	2110	2.45	2.83	4.57	2.41	2.35	1.13	2.69	2.48	3.76	2.07E-01	4.14E-01		8.96E-01	3.43E-06		-3.52E-02	9.02E-01		-1.09E+00	3.85E-05	Down	-1.17E-01	6.28E-01		4.85E-01	6.96E-03		Unigene47006_All//gi|15228865|ref|NP_188922.1|//1.00E-96//AT-HSFA6B; DNA binding / transcription factor [Arabidopsis thaliana] >gi|75311595|sp|Q9LUH8.1|HFA6B_ARATH RecName: Full=Heat stress transcription factor A-6b; Short=AtHsfA6b; AltName: Full=AtHsf-07 >gi|9279701|dbj|BAB01258.1| heat shock transcription factor-like protein [Arabidopsis thaliana]	Unigene47006_All//2.00E-93//AT3G22830| AT-HSFA6B; DNA binding / transcription factor	Unigene47006_All//9.00E-145//gi|78341176|gb|DT561450.1|DT561450	HSF			nr +
Unigene47007_All	1353	35.77	53.59	47.19	43.96	61.92	93.50	41.41	92.18	244.24	5.83E-01	4.64E-21		4.00E-01	2.57E-09		4.94E-01	2.76E-21		1.09E+00	2.24E-112	Up	1.15E+00	1.28E-138	Up	2.56E+00	0.00E+00	Up	Unigene47007_All//gi|297843432|ref|XP_002889597.1|//0.00E+00//acyl-CoA oxidase ACX3 [Arabidopsis lyrata subsp. lyrata] >gi|297335439|gb|EFH65856.1| acyl-CoA oxidase ACX3 [Arabidopsis lyrata subsp. lyrata]	Unigene47007_All//2.00E-179//AT1G06290| ACX3 (ACYL-COA OXIDASE 3); acyl-CoA oxidase	Unigene47007_All//0.00E+00//TC155839		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene47009_All	2174	1.42	9.95	3.09	3.92	7.78	15.66	26.22	22.92	65.59	2.81E+00	4.64E-66	Up	1.12E+00	3.23E-06	Up	9.89E-01	1.92E-14		2.00E+00	2.60E-74	Up	-1.94E-01	2.58E-03		1.32E+00	4.10E-200	Up	Unigene47009_All//gi|115459830|ref|NP_001053515.1|//0.00E+00//Os04g0555300 [Oryza sativa Japonica Group] >gi|38345584|emb|CAD41637.2|OSJNBb0012E24.2 [Oryza sativa (japonica cultivar-group)] >gi|113565086|dbj|BAF15429.1|Os04g0555300 [Oryza sativa Japonica Group]	Unigene47009_All//0.00E+00//AT3G47420| glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative	Unigene47009_All//0.00E+00//gi|73862616|gb|DT465355.1|DT465355				nr +
Unigene4701_All	933	12.56	9.45	15.98	8.86	11.22	30.25	11.69	11.56	19.86	-4.11E-01	1.39E-02		3.47E-01	2.45E-02		3.40E-01	5.80E-02		1.77E+00	1.90E-52	Up	-1.66E-02	9.46E-01		7.64E-01	2.19E-11		Unigene4701_All//gi|117168213|gb|AB322189.1|//1.00E-76//At3g60810 [Arabidopsis thaliana]	Unigene4701_All//2.00E-75//AT3G60810| unknown protein	Unigene4701_All//0.00E+00//gi|109885226|gb|DW514196.1|DW514196				nr -
Unigene47010_All	1404	3.28	2.56	1.56	3.58	4.49	3.41	2.71	3.10	2.81	-3.56E-01	2.19E-01		-1.08E+00	2.94E-04	Down	3.25E-01	1.94E-01		-7.17E-02	8.04E-01		1.92E-01	5.21E-01		5.17E-02	8.65E-01		Unigene47010_All//gi|18415647|ref|NP_568185.1|//1.00E-52//mitochondrial transcription termination factor family protein / mTERF family protein [Arabidopsis thaliana]	Unigene47010_All//7.00E-54//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene47010_All//0.00E+00//TC166339				nr -
Unigene47011_All	1161	7.03	15.19	10.64	10.64	11.30	10.39	8.56	11.99	9.75	1.11E+00	1.18E-15	Up	5.98E-01	3.26E-04		8.68E-02	6.44E-01		-3.49E-02	8.58E-01		4.86E-01	2.90E-04		1.87E-01	2.42E-01		Unigene47011_All//gi|297820780|ref|XP_002878273.1|//3.00E-84//far-red impaired responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324111|gb|EFH54532.1| far-red impaired responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47011_All//8.00E-85//AT3G59470| far-red impaired responsive family protein / FAR1 family protein	Unigene47011_All//0.00E+00//TC139194				nr -
Unigene47012_All	1775	3.98	4.62	1.86	4.24	4.68	6.26	6.19	8.97	9.94	2.17E-01	3.25E-01		-1.10E+00	2.65E-06	Down	1.42E-01	5.57E-01		5.63E-01	8.29E-04		5.35E-01	1.68E-05		6.83E-01	4.10E-09		Unigene47012_All//gi|115473793|ref|NP_001060495.1|//1.00E-172//Os07g0655300 [Oryza sativa Japonica Group] >gi|113612031|dbj|BAF22409.1|Os07g0655300 [Oryza sativa Japonica Group]	Unigene47012_All//2.00E-164//AT3G06190| BPM2 (BTB-POZ AND MATH DOMAIN 2); protein binding	Unigene47012_All//0.00E+00//gi|78349723|gb|DT569997.1|DT569997				nr +
Unigene47014_All	1351	13.79	15.86	20.57	16.78	27.25	21.76	18.09	21.56	47.89	2.03E-01	1.10E-01		5.78E-01	4.62E-08		7.00E-01	1.95E-17		3.75E-01	1.31E-04		2.54E-01	5.94E-03		1.40E+00	7.28E-100	Up	Unigene47014_All//gi|62319903|dbj|BAD93968.1|//3.00E-89//ARF1-binding protein [Arabidopsis thaliana]	Unigene47014_All//1.00E-90//AT5G62000| ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Unigene47014_All//0.00E+00//ES815710	ARF			nr +
Unigene47015_All	1917	4.94	1.35	1.78	10.00	10.33	6.36	17.95	12.75	2.04	-1.87E+00	2.70E-18	Down	-1.47E+00	1.27E-12	Down	4.60E-02	8.01E-01		-6.53E-01	9.29E-08		-4.93E-01	1.46E-09		-3.14E+00	3.74E-149	Down	Unigene47015_All//gi|224114479|ref|XP_002332364.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222874681|gb|EEF11812.1| GRAS family transcription factor [Populus trichocarpa]	Unigene47015_All//9.00E-149//AT4G37650| SHR (SHORT ROOT); protein binding / sequence-specific DNA binding / transcription factor	Unigene47015_All//0.00E+00//gi|109827571|gb|DW226247.1|DW226247	GRAS			nr -
Unigene47016_All	1578	8.69	18.88	8.77	9.34	18.20	10.30	37.99	96.68	100.86	1.12E+00	3.01E-26	Up	1.43E-02	9.49E-01		9.62E-01	3.23E-23		1.41E-01	4.04E-01		1.35E+00	1.16E-215	Up	1.41E+00	1.21E-245	Up	Unigene47016_All//gi|297821154|ref|XP_002878460.1|//6.00E-45//ATBZIP53 [Arabidopsis lyrata subsp. lyrata] >gi|297324298|gb|EFH54719.1|ATBZIP53 [Arabidopsis lyrata subsp. lyrata]	Unigene47016_All//3.00E-42//AT3G62420| ATBZIP53 (BASIC REGION/LEUCINE ZIPPER MOTIF 53); DNA binding / protein heterodimerization/ sequence-specific DNA binding / transcription factor	Unigene47016_All//0.00E+00//TC151051	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene4702_All	1307	1.08	38.61	2.24	0.88	1.69	4.39	4.11	10.36	11.52	5.16E+00	7.92E-247	Up	1.05E+00	6.29E-03		9.44E-01	2.80E-02		2.32E+00	1.97E-15	Up	1.33E+00	1.47E-19	Up	1.49E+00	5.77E-26	Up			Unigene4702_All//0.00E+00//TC155380				
Unigene47021_All	1050	7.57	2.12	2.23	15.85	12.04	8.86	6.89	3.74	3.15	-1.83E+00	4.63E-15	Down	-1.76E+00	1.20E-13	Down	-3.97E-01	2.15E-03		-8.39E-01	3.52E-10		-8.80E-01	6.41E-06		-1.13E+00	8.24E-09	Down	Unigene47021_All//gi|15238833|ref|NP_200187.1|//1.00E-135//MLO11 (MILDEW RESISTANCE LOCUS O 11); calmodulin binding [Arabidopsis thaliana] >gi|79330795|ref|NP_001032070.1|MLO11 (MILDEW RESISTANCE LOCUS O 11); calmodulin binding [Arabidopsis thaliana] >gi|33112394|sp|Q9FI00.1|MLO11_ARATH RecName: Full=MLO-like protein 11; Short=AtMlo11 >gi|14091592|gb|AAK53804.1|AF369572_1 membrane protein Mlo11 [Arabidopsis thaliana] >gi|15982791|gb|AAL09743.1|AT5g53760/MGN6_12 [Arabidopsis thaliana] >gi|222423988|dbj|BAH19955.1|AT5G53760 [Arabidopsis thaliana]	Unigene47021_All//3.00E-130//AT5G53760| MLO11 (MILDEW RESISTANCE LOCUS O 11); calmodulin binding	Unigene47021_All//0.00E+00//ES834383				nr +
Unigene47022_All	1723	1.58	0.76	0.80	3.61	2.70	1.47	2.43	1.12	1.36	-1.05E+00	6.56E-03		-9.75E-01	1.51E-02		-4.22E-01	7.23E-02		-1.30E+00	5.96E-08	Down	-1.12E+00	3.18E-05	Down	-8.33E-01	1.18E-03		Unigene47022_All//gi|15238833|ref|NP_200187.1|//0.00E+00//MLO11 (MILDEW RESISTANCE LOCUS O 11); calmodulin binding [Arabidopsis thaliana] >gi|79330795|ref|NP_001032070.1|MLO11 (MILDEW RESISTANCE LOCUS O 11); calmodulin binding [Arabidopsis thaliana] >gi|33112394|sp|Q9FI00.1|MLO11_ARATH RecName: Full=MLO-like protein 11; Short=AtMlo11 >gi|14091592|gb|AAK53804.1|AF369572_1 membrane protein Mlo11 [Arabidopsis thaliana] >gi|15982791|gb|AAL09743.1|AT5g53760/MGN6_12 [Arabidopsis thaliana] >gi|222423988|dbj|BAH19955.1|AT5G53760 [Arabidopsis thaliana]	Unigene47022_All//0.00E+00//AT5G53760| MLO11 (MILDEW RESISTANCE LOCUS O 11); calmodulin binding	Unigene47022_All//0.00E+00//TC177477				nr +
Unigene47024_All	1842	2.53	2.04	1.19	7.22	5.81	2.92	4.36	3.20	6.25	-3.13E-01	2.82E-01		-1.09E+00	2.19E-04	Down	-3.13E-01	4.19E-02		-1.31E+00	1.96E-16	Down	-4.47E-01	1.56E-02		5.19E-01	3.53E-04		Unigene47024_All//gi|18328941|ref|NP_563646.1|//1.00E-171//endonuclease/exonuclease/phosphatase family protein / calcium-binding EF hand family protein [Arabidopsis thaliana] >gi|148887024|sp|Q81916.2|YC22_ARATH RecName: Full=Uncharacterized calcium-binding protein At1g02270 >gi|15450673|gb|AAK96608.1|At1g02270/T6A9_9 [Arabidopsis thaliana] >gi|17380606|gb|AAL36066.1|At1g02270/T6A9_9 [Arabidopsis thaliana]	Unigene47024_All//7.00E-173//AT1G02270| endonuclease/exonuclease/phosphatase family protein / calcium-binding EF hand family protein	Unigene47024_All//0.00E+00//TC173904		ko03018|RNA degradation		nr +
Unigene47027_All	1223	2.31	1.41	4.66	9.41	5.83	6.98	20.74	19.31	16.03	-7.14E-01	5.52E-02		1.01E+00	1.09E-04	Up	-6.91E-01	7.18E-06		-4.31E-01	1.02E-02		-1.03E-01	3.76E-01		-3.72E-01	7.94E-05		Unigene47027_All//gi|88010865|gb|ABD38865.1|//1.00E-15//At4g23885 [Arabidopsis thaliana]	Unigene47027_All//6.00E-17//AT4G23885| unknown protein	Unigene47027_All//4.00E-07//ES835257				nr -
Unigene47028_All	1574	2.93	9.27	3.42	8.64	8.27	7.98	6.07	5.47	5.14	1.66E+00	1.51E-23	Up	2.24E-01	4.19E-01		-6.32E-02	7.52E-01		-1.15E-01	5.37E-01		-1.50E-01	4.28E-01		-2.41E-01	1.59E-01		Unigene47028_All//gi|297817552|ref|XP_002876659.1|//1.00E-116//SNF7 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322497|gb|EFH52918.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47028_All//1.00E-100//AT3G62080| SNF7 family protein	Unigene47028_All//0.00E+00//ES798338		ko04144|Endocytosis		nr +
Unigene47029_All	1868	11.79	3.36	4.50	27.12	16.37	22.24	33.84	11.10	11.75	-1.81E+00	9.45E-40	Down	-1.39E+00	3.31E-26	Down	-7.28E-01	2.15E-26		-2.86E-01	9.32E-05		-1.61E+00	7.42E-117	Down	-1.53E+00	2.09E-111	Down	Unigene47029_All//gi|18416534|ref|NP_567717.1|//9.00E-57//immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related [Arabidopsis thaliana] >gi|15982872|gb|AAL09783.1|AT4g25340/T30C3_20 [Arabidopsis thaliana] >gi|23506415|gb|AAN28917.1|At4g25340/T30C3_20 [Arabidopsis thaliana]	Unigene47029_All//1.00E-61//AT3G12340| FKS06 binding / peptidyl-prolyl cis-trans isomerase	Unigene47029_All//0.00E+00//gi|109877024|gb|DW505998.1|DW505998				nr +
Unigene4703_All	713	2.50	7.04	5.15	5.17	5.94	4.81	5.04	4.28	2.68	1.50E+00	1.84E-07	Up	1.05E+00	1.91E-03		2.00E-01	5.62E-01		-1.03E-01	7.59E-01		-2.36E-01	4.58E-01		-9.10E-01	1.19E-03				Unigene4703_All//2.00E-10//C0105483				

Unigene47030_All	1253	16.16	85.93	26.56	68.70	121.80	151.57	7.19	30.29	37.49	2.41E+00	1.41E-275	Up	7.17E-01	1.17E-13		8.26E-01	5.12E-95		1.14E+00	6.77E-182	Up	2.08E+00	2.17E-99	Up	2.38E+00	1.59E-148	Up	Unigene47030_All//gi|224073168|ref|XP_002304005.1|//1.00E-127//f-box family protein [Populus trichocarpa] >gi|222841437|gb|EEE78984.1| f-box family protein [Populus trichocarpa]	Unigene47030_All//2.00E-45//AT2G44130| kelch repeat-containing F-box family protein	Unigene47030_All//0.00E+00//gi|78325198|gb|DT545472.1|DT545472				nr +
Unigene47032_All	1694	13.03	5.77	8.80	6.88	7.14	7.86	4.22	1.78	2.23	-1.17E+00	3.05E-21	Down	-5.66E-01	2.44E-06		5.23E-02	8.20E-01		1.93E-01	2.73E-01		-1.25E+00	9.88E-10	Down	-9.17E-01	1.88E-06		Unigene47032_All//gi|222423169|dbj|BAH19562.1|//1.00E-101//AT5G18590|[Arabidopsis thaliana]	Unigene47032_All//1.00E-126//AT5G18590| kelch repeat-containing protein	Unigene47032_All//0.00E+00//gi|109881536|gb|DW510506.1|DW510506				nr +
Unigene47033_All	2257	5.40	4.20	5.36	9.93	7.45	8.66	12.38	9.83	5.45	-3.64E-01	2.73E-02		-1.22E-02	9.66E-01		-4.16E-01	1.14E-04		-1.97E-01	1.20E-01		-3.33E-01	3.07E-04		-1.18E+00	6.66E-34	Down	Unigene47033_All//gi|15219020|ref|NP_175661.1|//1.00E-171//FRS6 (FAR1-related sequence 6); zinc ion binding [Arabidopsis thaliana] >gi|75207551|sp|Q9SSQ4.1|FRS6_ARATH RecName: Full=Protein FAR1-RELATED SEQUENCE 6 >gi|5903066|gb|AAD55625.1|AC008016_35 F6D8_26 [Arabidopsis thaliana]	Unigene47033_All//2.00E-172//AT1G52520| FRS6 (FAR1-related sequence 6); zinc ion binding	Unigene47033_All//0.00E+00//DW236708				nr -
Unigene47036_All	1596	3.34	19.78	6.27	41.23	50.47	73.63	44.66	84.85	47.45	2.56E+00	4.58E-87	Up	9.08E-01	1.58E-06		2.92E-01	5.59E-08		8.37E-01	1.66E-67		9.26E-01	6.58E-105		8.73E-02	1.37E-01		Unigene47036_All//gi|4098172|gb|AAD00239.1|//1.00E-159//PK11-C1 [Nicotiana tabacum]	Unigene47036_All//1.00E-137//AT4G33950| OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase	Unigene47036_All//0.00E+00//TC150385				nr -
Unigene47038_All	1647	5.05	6.83	14.32	8.68	3.35	6.86	16.89	7.64	10.52	4.35E-01	1.09E-02		1.50E+00	1.29E-31	Up	-1.38E+00	1.40E-21	Down	-3.41E-01	2.46E-02		-1.15E+00	3.74E-31	Down	-6.83E-01	6.51E-14		Unigene47038_All//gi|224121000|ref|XP_002318472.1|//0.00E+00//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222859145|gb|EEE96692.1|oligopeptide transporter OPT family [Populus trichocarpa]	Unigene47038_All//2.00E-165//AT5G53550| YSL3 (YELLOW STRIPE LIKE 3); oligopeptide transporter	Unigene47038_All//5.00E-112//TC178963				nr -
Unigene47039_All	1215	11.97	7.88	11.00	24.19	16.78	16.13	9.33	5.16	3.84	-6.03E-01	3.83E-05		-1.22E-01	4.73E-01		-5.28E-01	6.71E-09		-5.84E-01	1.42E-09		-8.54E-01	2.01E-08		-1.28E+00	4.50E-16	Down	Unigene47039_All//gi|15809944|gb|AAL06899.1|//1.00E-109//AT5g21070/T10F18_100 [Arabidopsis thaliana] >gi|18958048|gb|AAL79597.1|AT5g21070/T10F18_100 [Arabidopsis thaliana]	Unigene47039_All//4.00E-110//AT5G21070| unknown protein	Unigene47039_All//0.00E+00//TC154518				nr -
Unigene4704_All	1488	16.03	10.59	7.77	10.78	10.90	9.68	12.64	4.47	7.92	-5.98E-01	8.42E-08		-1.05E+00	2.56E-18	Down	1.60E-02	9.37E-01		-1.55E-01	3.44E-01		-1.50E+00	5.36E-32	Down	-6.74E-01	1.67E-09		Unigene4704_All//gi|222154050|gb|ACM47215.1|//1.00E-160//plastid aspartate carbamoyltransferase [Medicago truncatula]	Unigene4704_All//3.00E-148//AT3G20330| aspartate carabmoyltransferase, chloroplast / aspartate transcarbamylase / ATCase (PYRB)	Unigene4704_All//0.00E+00//TC163588		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene47040_All	1452	3.28	1.50	2.82	2.98	3.42	4.98	2.68	1.90	3.68	-1.13E+00	6.24E-05	Down	-2.16E-01	4.78E-01		1.94E-01	5.59E-01		7.38E-01	5.92E-04		-4.96E-01	7.85E-02		4.57E-01	4.35E-02		Unigene47040_All//gi|297793271|ref|XP_002864520.1|//7.00E-27//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310355|gb|EFH40779.1|kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47040_All//8.00E-44//AT5G57610| protein kinase family protein	Unigene47040_All//2.00E-15//gi|164328745|gb|EX163894.1|EX163894				nr +
Unigene47042_All	1725	5.64	9.58	5.59	6.01	4.29	2.07	5.83	4.97	3.97	7.63E-01	3.24E-08		-1.39E-02	9.65E-01		-4.85E-01	3.90E-03		-1.54E+00	2.26E-16	Down	-2.32E-01	1.86E-01		-5.54E-01	3.83E-04		Unigene47042_All//gi|22329119|ref|NP_195070.2|//0.00E+00//glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	Unigene47042_All//1.00E-179//AT4G33440| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene47042_All//0.00E+00//gi|13244885|gb|BE053247.2|BE053247		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene47043_All	1479	5.87	12.20	8.32	9.83	10.90	12.98	12.15	19.41	16.73	1.05E+00	9.35E-15	Up	5.02E-01	2.77E-03		1.48E-01	3.58E-01		4.00E-01	1.40E-03		6.76E-01	1.16E-13		4.61E-01	1.39E-06		Unigene47043_All//gi|79596815|ref|NP_850557.2|//5.00E-44//reticulon family protein [Arabidopsis thaliana]	Unigene47043_All//1.00E-34//AT3G10915| reticulon family protein	Unigene47043_All//0.00E+00//TC171744				nr +
Unigene47044_All	1590	3.13	9.05	5.86	7.61	11.20	3.41	7.50	3.31	2.31	1.53E+00	9.96E-21	Up	9.07E-01	4.04E-06		5.57E-01	5.84E-06		-1.16E+00	1.60E-12	Down	-1.18E+00	1.97E-14	Down	-1.70E+00	2.83E-25	Down	Unigene47044_All//gi|224092091|ref|XP_002309468.1|//0.00E+00//cytokinin oxidase [Populus trichocarpa] >gi|222855444|gb|EEE92991.1|cytokinin oxidase [Populus trichocarpa]	Unigene47044_All//0.00E+00//AT5G21482| CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase	Unigene47044_All//3.00E-144//TC166894		ko00908|Zeatin biosynthesis		nr -
Unigene47047_All	1620	4.33	12.54	7.56	14.21	30.21	21.49	15.24	19.58	43.36	1.54E+00	5.16E-29	Up	8.05E-01	1.63E-06		1.09E+00	4.51E-48	Up	5.97E-01	1.45E-11		3.62E-01	2.36E-05		1.51E+00	2.10E-120	Up	Unigene47047_All//gi|18394770|ref|NP_564093.1|//1.00E-31//wound-responsive family protein [Arabidopsis thaliana] >gi|79318202|ref|NP_001031068.1|wound-responsive family protein [Arabidopsis thaliana] >gi|222424435|dbj|BAH20173.1|AT1G19660 [Arabidopsis thaliana]	Unigene47047_All//6.00E-74//AT5G66050| LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF151 (InterPro:IPR003729); BEST Arabidopsis thaliana protein match is: wound-responsive family protein (TAIR:AT1G19660.2); Has 338 Blast hits to 338 proteins in 128 species: Archae - 11; Bacteria - 214; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryotes - 46 (source: NCBI BLink).	Unigene47047_All//0.00E+00//CO128218				nr +
Unigene47048_All	2302	2.70	1.17	1.11	21.36	16.38	13.97	14.38	4.99	6.35	-1.21E+00	7.51E-07	Down	-1.28E+00	4.91E-07	Down	-3.83E-01	2.98E-08		-6.13E-01	6.48E-17		-1.53E+00	4.63E-57	Down	-1.18E+00	8.54E-40	Down	Unigene47048_All//gi|15230141|ref|NP_189109.1|//0.00E+00//TMKL1 (transmembrane kinase-like 1); ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|464900|sp|P33543.1|TMKL1_ARATH RecName: Full=Putative kinase-like protein TMKL1; Flags: Precursor >gi|313190|emb|CAA51385.1| TMKL1 [Arabidopsis thaliana] >gi|92759794|dbj|BAB01215.1|receptor kinase [Arabidopsis thaliana]	Unigene47048_All//0.00E+00//AT3G24660| TMKL1 (transmembrane kinase-like 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene47048_All//0.00E+00//gi|164292076|gb|ES833455.1|ES833455				nr +
Unigene4705_All	791	1.39	1.47	3.10	4.16	2.00	1.77	4.28	6.97	5.44	8.50E-02	8.94E-01		1.16E+00	7.22E-03		-1.05E+00	9.97E-04	Down	-1.23E+00	3.30E-04	Down	7.06E-01	1.77E-03		3.47E-01	1.89E-01		Unigene4705_All//gi|224112939|ref|XP_002332682.1|//3.00E-87//cytochrome P450 [Populus trichocarpa] >gi|222838808|gb|EEE77159.1|cytochrome P450 [Populus trichocarpa]	Unigene4705_All//8.00E-66//AT4G31950| CYP82C3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene4705_All//0.00E+00//TC152580		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene47051_All	1625	17.64	8.08	27.98	3.46	4.66	5.25	1.61	0.59	0.69	-1.13E+00	1.16E-25	Down	6.66E-01	3.05E-16		4.29E-01	4.29E-02		6.01E-01	2.18E-03		-1.45E+00	6.76E-05	Down	-1.23E+00	3.51E-04	Down	Unigene47051_All//gi|11074178|gb|AB004462.1|//1.00E-64//At5g22090 [Arabidopsis thaliana]	Unigene47051_All//6.00E-55//AT5G22090| unknown protein	Unigene47051_All//4.00E-35//DW239830				nr -
Unigene47055_All	1266	0.91	2.40	1.43	2.91	2.45	1.53	2.64	2.41	2.01	1.40E+00	1.82E-04	Up	6.53E-01	2.02E-01		-2.50E-01	4.77E-01		-9.25E-01	3.49E-03		-1.31E-01	6.89E-01		-3.90E-01	1.96E-01		Unigene47055_All//gi|61611694|gb|AAX47176.1|//3.00E-90//expressed protein [Pisum sativum]	Unigene47055_All//8.00E-58//AT2G25920| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: 3'-5' exonuclease domain-containing protein / K homology domain-containing protein / KH domain-containing protein (TAIR:AT2G25910.2); Has 84 Blast hits to 79 proteins in 34 species: Archae - 0; Bacteria - 23; Metazoa - 11; Fungi - 12; Plants - 23; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink).	Unigene47055_All//0.00E+00//DT527323				nr +
Unigene47057_All	2328	0.52	1.04	1.56	1.33	1.32	1.65	0.91	0.75	0.96	1.02E+00	1.34E-02		1.59E+00	8.97E-06	Up	-1.11E-02	9.68E-01		3.14E-01	3.75E-01		-2.68E-01	5.40E-01		7.76E-02	8.46E-01		Unigene47057_All//gi|224122408|ref|XP_002318826.1|//2.00E-52//methyl binding domain protein [Populus trichocarpa] >gi|222859499|gb|EEE97046.1|methyl binding domain protein [Populus trichocarpa]	Unigene47057_All//6.00E-15//AT5G52230| MBD13; methyl-CpG binding	Unigene47057_All//0.00E+00//TC139382				nr +
Unigene47058_All	2282	5.23	4.82	6.93	7.57	5.42	3.86	39.58	14.14	9.83	-1.18E-01	5.26E-01		4.07E-01	5.66E-03		-4.84E-01	9.40E-05		-9.73E-01	2.20E-13		-1.48E+00	2.56E-148	Down	-2.01E+00	2.04E-233	Down	Unigene47058_All//gi|15233493|ref|NP_194650.1|//0.00E+00//GGT4 (GAMMA-GLUTAMYL TRANSPEPTIDASE 4); gamma-glutamyltransferase/ glutathione gamma-glutamylcysteinyltransferase [Arabidopsis thaliana] >gi|7269819|emb|CAB79679.1| gamma-glutamyltransferase-like protein [Arabidopsis thaliana] >gi|110737078|dbj|BAF00192.1|gamma-glutamyltransferase-like protein [Arabidopsis thaliana]	Unigene47058_All//0.00E+00//AT4G29210| GGT4 (GAMMA-GLUTAMYL TRANSPEPTIDASE 4); gamma-glutamyltransferase/ glutathione gamma-glutamylcysteinyltransferase	Unigene47058_All//0.00E+00//TC149844		ko00480|Glutathione metabolism//ko00460|Cyanoamino acid metabolism//ko00450|Selenoamino acid metabolism//ko00590|Arachidonic acid metabolism//ko00430|Taurine and hypotaurine metabolism		nr +
Unigene47060_All	1531	6.22	5.33	4.66	6.34	6.21	5.34	8.01	4.91	2.47	-2.23E-01	2.60E-01		-4.16E-01	3.51E-02		-3.15E-02	8.78E-01		-2.49E-01	2.22E-01		-7.05E-01	1.01E-06		-1.70E+00	7.65E-26	Down	Unigene47060_All//gi|297799000|ref|XP_002867384.1|//1.00E-140//EMB2757 [Arabidopsis lyrata subsp. lyrata] >gi|297313220|gb|EFH43643.1|EMB2757 [Arabidopsis lyrata subsp. lyrata]	Unigene47060_All//1.00E-139//AT4G28860| EMB2757 (EMBRYO DEFECTIVE 2757); nucleotide binding	Unigene47060_All//0.00E+00//TC161932		ko03040|Spliceosome//ko03022|Basal transcription factors		nr +
Unigene47061_All	550	341.61	132.39	240.88	98.54	107.19	109.46	23.75	14.97	19.77	-1.37E+00	1.46E-222	Down	-5.04E-01	7.97E-40		1.21E-01	1.04E-01		1.52E-01	3.71E-02		-6.66E-01	1.63E-06		-2.65E-01	5.97E-02		Unigene47061_All//gi|15294254|gb|AA935304.1|AF410318_1|//5.00E-15//AT4g24770/F22K18_30 [Arabidopsis thaliana] >gi|23505889|gb|AAN28804.1|At4g24770/F22K18_30 [Arabidopsis thaliana]		Unigene47061_All//0.00E+00//TC151038				nr +
Unigene47062_All	474	107.95	50.78	68.53	32.37	33.93	35.54	9.46	4.76	6.05	-1.09E+00	9.37E-43	Down	-6.56E-01	1.03E-17		6.78E-02	7.08E-01		1.35E-01	4.01E-01		-9.90E-01	1.16E-04		-6.44E-01	8.77E-03		Unigene47062_All//gi|681906|dbj|BAA06520.1|//4.00E-15//RNA-binding protein cp31 [Arabidopsis thaliana]		Unigene47062_All//0.00E+00//gi|82756071|gb|DV849633.1|DV849633				nr +

Unigene47063_All	2298	1.21	0.29	0.39	1.32	1.65	1.49	2.39	1.75	2.34	-2.07E+00	1.34E-06	Down	-1.62E+00	1.17E-04	Down	3.18E-01	3.58E-01		1.76E-01	6.41E-01		-4.54E-01	4.94E-02		-3.13E-02	9.10E-01		Unigene47063_All//gi|115443625|ref|NP_001045592.1|//1.00E-107//0s02g0101800 [Oryza sativa Japonica Group] >gi|113535123|dbj|BAF07506.1| Os02g0101800 [Oryza sativa Japonica Group]	Unigene47063_All//1.00E-49//AT1G20060| ATP binding / microtubule motor	Unigene47063_All//0.00E+00//gi|164301855|gb|ES833656.1|ES833656				nr +
Unigene47065_All	2601	5.63	1.13	1.66	10.50	8.41	13.21	17.88	6.62	10.34	-2.32E+00	1.68E-36	Down	-1.76E+00	1.04E-24	Down	-3.20E-01	1.20E-03		3.32E-01	2.43E-04		-1.43E+00	8.45E-73	Down	-7.90E-01	5.73E-29		Unigene47065_All//gi|75338927|sp|Q92RZ8.1|RH28_ARATH//0.00E+00//RecName: Full=DEAD-box ATP-dependent RNA helicase 28 >gi|3776027|emb|CAA09214.1| RNA helicase [Arabidopsis thaliana] >gi|110736657|dbj|BAF00292.1| RNA helicase like protein [Arabidopsis thaliana]	Unigene47065_All//1.00E+00//AT4G16630| DEAD/DEAH box helicase, putative (RH28)	Unigene47065_All//0.00E+00//ES846293				nr -
Unigene47066_All	1714	11.39	21.23	18.45	20.29	26.54	22.21	9.03	4.44	9.62	8.99E-01	2.08E-22		6.97E-01	2.09E-12		3.88E-01	1.05E-07		1.31E-01	1.91E-01		-1.02E+00	6.66E-15	Down	9.20E-02	5.18E-01		Unigene47066_All//gi|18404252|ref|NP_690235.1|//1.00E-133//ACT domain-containing protein [Arabidopsis thaliana] >gi|4883601|gb|AAD31570.1| expressed protein [Arabidopsis thaliana]	Unigene47066_All//1.00E-134//AT2G36840| ACT domain-containing protein	Unigene47066_All//2.00E-09//ES850135				nr -
Unigene47068_All	1472	1.46	0.96	0.94	1.42	1.24	1.44	3.96	1.85	2.68	-5.97E-01	1.74E-01		-6.32E-01	1.70E-01		-1.97E-01	6.76E-01		2.09E-02	9.62E-01		-1.10E+00	8.54E-07	Down	-5.65E-01	7.70E-03		Unigene47068_All//gi|19310497|gb|AAL84982.1|//8.00E-84//AT3g08780/F17O14_25 [Arabidopsis thaliana] >gi|20908088|gb|AAM26727.1| AT3g08780/F17O14_25 [Arabidopsis thaliana]	Unigene47068_All//2.00E-79//AT3G08780| unknown protein	Unigene47068_All//0.00E+00//TC140171				nr +
Unigene47072_All	2533	2.23	2.20	1.20	11.68	8.33	6.45	6.13	4.24	3.05	-1.98E-02	9.57E-01		-8.97E-01	6.08E-04		-4.87E-01	8.20E-08		-8.56E-01	3.09E-18		-5.31E-01	2.52E-05		-1.01E+00	5.65E-15	Down	Unigene47072_All//gi|297814706|ref|XP_002875236.1|//0.00E+00//phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321074|gb|EFH51495.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47072_All//0.00E+00//AT2G03890| phosphatidylinositol 3- and 4-kinase family protein	Unigene47072_All//0.00E+00//TC149021				nr +
Unigene47073_All	1413	1.15	4.70	1.51	2.26	3.31	2.27	6.82	17.54	9.78	2.03E+00	2.47E-14	Up	3.93E-01	4.00E-01		5.55E-01	4.52E-02		8.40E-03	9.83E-01		1.36E+00	3.04E-36	Up	5.20E-01	7.53E-05		Unigene47073_All//gi|88196763|gb|AB043024.1|//1.00E-29//At4g01960 [Arabidopsis thaliana]	Unigene47073_All//6.00E-09//AT4G01960| unknown protein	Unigene47073_All//0.00E+00//gi|78332101|gb|DT552375.1|DT552375				nr -
Unigene47075_All	1065	3.59	3.47	2.55	22.59	14.91	15.78	13.97	6.99	3.29	-4.63E-02	8.90E-01		-4.92E-01	1.39E-01		-6.00E-01	3.55E-09		-5.18E-01	1.56E-06		-1.00E+00	7.68E-14	Down	-2.09E+00	5.13E-41	Down	Unigene47075_All//gi|15232501|ref|NP_191007.1|//1.00E-21//transcription factor [Arabidopsis thaliana] >gi|30023794|gb|AAP13430.1| At3g54390 [Arabidopsis thaliana]	Unigene47075_All//7.00E-19//AT3G54390| transcription factor	Unigene47075_All//0.00E+00//gi|11209142|gb|BF277976.1|BF277976	Trihelix			nr -
Unigene47076_All	1609	16.19	12.00	9.33	96.10	72.55	59.25	30.85	20.18	9.76	-4.33E-01	4.71E-05		-7.95E-01	8.16E-13		-4.06E-01	1.02E-27		-6.98E-01	2.13E-65		-6.12E-01	1.96E-19		-1.66E+00	4.41E-99	Down	Unigene47076_All//gi|297820184|ref|XP_002877975.1|//7.00E-86//transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297323813|gb|EFH54234.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene47076_All//1.00E-73//AT3G54390| transcription factor	Unigene47076_All//0.00E+00//gi|11209142|gb|BF277976.1|BF277976	Trihelix	ko03040|Spliceosome		nr +
Unigene47077_All	2123	6.60	3.60	15.75	12.93	14.92	22.04	0.00	0.08	0.26	-8.74E-01	9.10E-09		1.25E+00	6.09E-34	Up	2.07E-01	3.56E-02		7.70E-01	1.29E-23		6.30E+00	1.39E-01		8.04E+00	3.28E-04	Up	Unigene47077_All//gi|291167241|gb|ADD81294.1|//1.00E-180//linalool synthase [Actinidia arguta]	Unigene47077_All//6.00E-128//AT1G61680| TPS14 (TERPENE SYNTHASE 14); S-linalool synthase	Unigene47077_All//0.00E+00//TC155873		ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis		nr -
Unigene47078_All	3424	27.69	19.22	20.48	28.02	26.87	21.84	26.40	11.17	13.47	-5.27E-01	7.26E-23		-4.35E-01	1.12E-15		-6.04E-02	3.42E-01		-3.59E-01	1.51E-12		-1.24E+00	6.04E-113	Down	-9.70E-01	3.36E-78		Unigene47078_All//gi|2970447|gb|AAC05981.1|//0.00E+00//aspartokinase-homoserine dehydrogenase [Glycine max]	Unigene47078_All//0.00E+00//AT4G19710| bifunctional aspartate kinase/homoserine dehydrogenase, putative / AK-HSDH, putative	Unigene47078_All//0.00E+00//TC173171		ko00270|Cysteine and methionine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00300|Lysine biosynthesis		nr +
Unigene47079_All	1966	1.38	0.26	0.92	47.08	49.27	42.82	14.41	5.10	4.48	-2.43E+00	1.10E-07	Down	-5.88E-01	1.44E-01		6.57E-02	3.05E-01		-1.37E-01	1.61E-02		-1.50E+00	1.29E-47	Down	-1.69E+00	4.20E-58	Down	Unigene47079_All//gi|224109236|ref|XP_002315131.1|//0.00E+00//laccase 90c [Populus trichocarpa] >gi|222864171|gb|EEF01302.1| laccase 90c [Populus trichocarpa]	Unigene47079_All//0.00E+00//AT2G40370| LAC5 (laccase 5); laccase	Unigene47079_All//0.00E+00//TC147312		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene4708_All	1583	38.37	18.53	32.06	16.46	13.68	5.68	1.79	0.21	0.05	-1.05E+00	8.43E-48	Down	-2.59E-01	2.36E-04		-2.66E-01	1.09E-02		-1.54E+00	2.73E-40	Down	-3.08E+00	3.10E-12	Down	-5.15E+00	4.64E-18	Down	Unigene4708_All//gi|115467270|ref|NP_001057234.1|//2.00E-69//0s06g0233800 [Oryza sativa Japonica Group] >gi|113395274|dbj|BAF19148.1| Os06g0233800 [Oryza sativa Japonica Group]	Unigene4708_All//8.00E-66//AT1G60060| unknown protein	Unigene4708_All//0.00E+00//TC145565				nr -
Unigene47080_All	1575	6.21	2.93	6.25	14.04	14.89	6.80	2.47	1.22	1.19	-1.09E+00	9.23E-09	Down	9.90E-03	9.83E-01		8.44E-02	5.47E-01		-1.05E+00	4.44E-19	Down	-1.02E+00	2.64E-04	Down	-1.05E+00	1.06E-04	Down	Unigene47080_All//gi|13937141|gb|AAK50064.1|AF372924_1/2.00E-70//At1g69210/F4N2_11 [Arabidopsis thaliana] >gi|22137004|gb|AAM91347.1| At1g69210/F4N2_11 [Arabidopsis thaliana]	Unigene47080_All//1.00E-57//AT1G69210| unknown protein	Unigene47080_All//0.00E+00//TC166329				nr -
Unigene47081_All	1979	1.96	1.72	2.45	7.05	7.66	3.17	1.13	0.84	0.20	-1.90E-01	5.73E-01		3.24E-01	2.75E-01		1.19E-01	5.03E-01		-1.15E+00	3.40E-14	Down	-4.23E-01	2.92E-01		-2.49E+00	2.63E-08	Down	Unigene47081_All//gi|13937141|gb|AAK50064.1|AF372924_1/4.00E-73//At1g69210/F4N2_11 [Arabidopsis thaliana] >gi|22137004|gb|AAM91347.1| At1g69210/F4N2_11 [Arabidopsis thaliana]	Unigene47081_All//1.00E-66//AT1G69210| unknown protein	Unigene47081_All//0.00E+00//TC166329				nr +
Unigene47084_All	2309	1.54	2.33	1.50	9.56	9.98	6.57	3.99	1.30	2.33	5.94E-01	2.13E-02		-3.97E-02	9.17E-01		6.20E-02	6.66E-01		-5.40E-01	1.80E-06		-1.61E+00	8.67E-18	Down	-7.77E-01	2.64E-06		Unigene47084_All//gi|15724288|gb|AAL06537.1|AF412084_1/1.00E-124//AT3g11590/F24K9_26 [Arabidopsis thaliana]	Unigene47084_All//2.00E-96//AT3G11590| unknown protein	Unigene47084_All//0.00E+00//gi|78351778|gb|DT572052.1|DT572052				nr +
Unigene47085_All	510	0.62	2.98	3.34	5.86	3.51	4.25	4.06	5.08	1.80	2.28E+00	2.68E-04	Up	2.44E+00	7.80E-05	Up	-7.39E-01	3.17E-02		-4.63E-01	2.23E-01		3.23E-01	4.05E-01		-1.18E+00	2.66E-03		Unigene47085_All//gi|145330328|ref|NP_001077989.1|//2.00E-32//TEJ (Sanskrit for "bright"); poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana]	Unigene47085_All//1.00E-24//AT2G31870| TEJ (Sanskrit for "bright"); poly(ADP-ribose) glycohydrolase	Unigene47085_All//0.00E+00//ES831486				nr -
Unigene47090_All	2135	0.51	3.30	1.62	1.49	0.65	1.54	3.19	3.41	4.11	2.68E+00	7.94E-21	Up	1.66E+00	7.71E-06	Up	-1.21E+00	2.19E-04	Down	4.84E-02	9.14E-01		9.54E-02	6.58E-01		3.65E-01	3.44E-02		Unigene47090_All//gi|79529581|ref|NP_199288.4|//1.00E-143//REV1; DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|59796995|dbj|BAD89586.1| deoxycytidyl transferase [Arabidopsis thaliana]	Unigene47090_All//1.00E-132//AT5G44750| REV1; DNA-directed DNA polymerase	Unigene47090_All//0.00E+00//DT527096				nr +
Unigene47091_All	2115	38.27	43.22	42.27	16.30	29.65	27.46	0.20	0.75	0.11	1.76E-01	1.66E-03		1.44E-01	1.72E-02		8.63E-01	4.08E-42		7.53E-01	4.17E-28		1.91E+00	1.97E-04	Up	-8.23E-01	3.99E-01		Unigene47091_All//gi|297802558|ref|XP_002869163.1|//0.00E+00//ALDH3I1 [Arabidopsis lyrata subsp. lyrata] >gi|297314999|gb|EFH45422.1| ALDH3I1 [Arabidopsis lyrata subsp. lyrata]	Unigene47091_All//0.00E+00//AT4G34240| ALDH3I1 (ALDEHYDE DEHYDROGENASE 3	Unigene47091_All//0.00E+00//TC160994		ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism/ko00250|Alanine, aspartate and glutamate metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00350|Tyrosine metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr -
Unigene47092_All	2488	3.09	6.68	4.02	6.41	8.95	8.71	7.95	8.97	11.67	1.11E+00	8.33E-15	Up	3.80E-01	4.87E-02		4.83E-01	8.56E-06		4.44E-01	1.26E-04		1.74E-01	1.29E-01		5.54E-01	3.38E-10		Unigene47092_All//gi|108862821|gb|ABA98936.2|//4.00E-71//PAPA-1-like conserved region family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene47092_All//3.00E-55//AT1G56460| PAPA-1-like family protein / zinc finger (HIT type) family protein	Unigene47092_All//0.00E+00//gi|164281707|gb|ES820896.1|ES820896				nr +
Unigene47093_All	2293	2.21	0.97	0.72	7.89	6.86	4.35	11.76	3.01	4.33	-1.19E+00	1.44E-05	Down	-1.62E+00	5.38E-08	Down	-2.01E-01	1.51E-01		-8.57E-01	2.08E-11		-1.97E+00	2.76E-66	Down	-1.44E+00	2.87E-44	Down	Unigene47093_All//gi|297841559|ref|XP_002888661.1|//0.00E+00//At1g68400/T2E12_5 [Arabidopsis lyrata subsp. lyrata] >gi|297334502|gb|EFH64920.1| At1g68400/T2E12_5 [Arabidopsis lyrata subsp. lyrata]	Unigene47093_All//0.00E+00//AT1G68400| leucine-rich repeat transmembrane protein kinase, putative	Unigene47093_All//0.00E+00//TC150467		ko04626|Plant-pathogen interaction		nr -
Unigene47095_All	820	3.45	8.22	7.53	2.86	3.53	2.09	2.01	2.04	1.07	1.25E+00	1.17E-07	Up	1.13E+00	7.60E-06	Up	3.05E-01	4.60E-01		-4.48E-01	3.12E-01		1.99E-02	1.00E+00		-9.12E-01	3.80E-02		Unigene47095_All//gi|125557660|gb|EAZ03196.1|//1.00E-07//hypothetical protein Os1_25347 [Oryza sativa Indica Group]		Unigene47095_All//1.00E-27//D8457132				nr -
Unigene47096_All	1133	3.74	5.55	3.10	3.17	3.59	1.08	2.91	1.03	0.53	5.68E-01	1.60E-02		-2.70E-01	3.86E-01		1.80E-01	5.94E-01		-1.56E+00	3.67E-06	Down	-1.49E+00	3.28E-06	Down	-2.46E+00	1.01E-11	Down	Unigene47096_All//gi|124359981|gb|ABN07997.1|//1.00E-14//contains similarity to reverse trancriptase, related [Medicago truncatula]	Unigene47096_All//2.00E-08//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene47096_All//2.00E-27//D8457132				nr -
Unigene47099_All	405	0.65	2.63	3.29	1.11	1.28	0.56	1.57	1.03	1.67	2.02E+00	6.57E-03		2.35E+00	8.68E-04	Up	2.04E-01	8.59E-01		-9.89E-01	3.94E-01		-6.02E-01	4.67E-01		9.48E-02	9.12E-01		Unigene47099_All//gi|102139963|gb|ABF70103.1|//1.00E-58//glucose-inhibited division A family protein [Musa balbisiana]	Unigene47099_All//3.00E-59//AT2G13440| glucose-inhibited division family A protein	Unigene47099_All//2.00E-179//TC141823				nr -
Unigene471_All	1541	4.11	2.70	4.28	107.58	86.52	102.64	21.78	18.44	6.80	-6.08E-01	9.46E-03		6.07E-02	8.05E-01		-3.14E-01	1.63E-18		-6.79E-02	1.38E-01		-2.40E-01	4.87E-03		-1.68E+00	2.35E-68	Down	Unigene471_All//gi|60657598|gb|AAX33320.1|//0.00E+00//secondary cell wall-related glycosyltransferase family 47 [Populus tremula x Populus tremuloides]	Unigene471_All//0.00E+00//AT1G27440| GUT2; catalytic/ glucuronoxylan glucuronosyltransferase	Unigene471_All//0.00E+00//TC157630			GO:0009832//GO:0010413//GO:0015020//GO:0031410//GO:0043231	nr -
Unigene47100_All	412	6.35	1.48	1.68	3.14	1.59	1.10	0.72	0.91	0.97	-2.11E+00	2.26E-06	Down	-1.92E+00	2.03E-05	Down	-9.85E-01	8.32E-02		-1.52E+00	1.32E-02		3.46E-01	7.38E-01		4.29E-01	6.61E-01		Unigene47100_All//gi|104295013|gb|ABF72028.1|//2.00E-70//glucose-inhibited division A family protein [Musa acuminata]	Unigene47100_All//5.00E-70//AT2G13440| glucose-inhibited division family A protein	Unigene47100_All//0.00E+00//gi|164349531|gb|ES803988.1|ES803988				nr +
Unigene47101_All	2605	13.26	6.30	9.87	6.12	6.65	4.37	6.78	6.03	5.47	-1.07E+00	1.98E-28	Down	-4.25E-01	6.35E-06		1.20E-01	4.52E-01		-4.86E-01	3.82E-04		-1.69E-01	1.99E-01		-3.09E-01	7.91E-03		Unigene47101_All//gi|102139963|gb|ABF70103.1|//0.00E+00//glucose-inhibited division A family protein [Musa balbisiana]	Unigene47101_All//0.00E+00//AT2G13440| glucose-inhibited division family A protein	Unigene47101_All//0.00E+00//TC141823				nr +

Unigene47102_All	2043	4.46	4.02	4.46	39.21	45.21	27.01	12.87	2.46	3.12	-1.49E-01	4.74E-01		3.00E-04	9.98E-01		2.05E-01	6.36E-05		-5.37E-01	1.34E-21		-2.39E+00	2.00E-82	Down	-2.04E+00	4.88E-70	Down	Unigene47102_All//gi|82592920|sp|P92990.2|JP650_ARATH//0.00E+00//RecName: Full=Probable polygalacturonase non-catalytic subunit JP650; AltName: Full=Aromatic-rich glycoprotein JP650; Flags: Precursor >gi|3176680|gb|AAC18803.1| Identical to polygalacuronase isoenzyme 1 beta subunit homolog mRNA gb|163373. EST gb|AA404828 comes from this gene [Arabidopsis thaliana]	Unigene47102_All//0.00E+00//AT1G70370| BURP domain-containing protein / polygalacturonase, putative	Unigene47102_All//0.00E+00//TC145124				nr +
Unigene47105_All	2201	2.64	4.24	3.65	32.32	7.01	5.54	14.64	2.22	12.05	6.83E-01	2.87E-04		4.69E-01	2.94E-02		-2.21E+00	1.07E-208	Down	-2.54E+00	1.88E-213	Down	-2.72E+00	9.19E-117	Down	-2.80E-01	8.13E-04		Unigene47105_All//gi|224141637|ref|XP_002324173.1|//1.00E-159//ZIP transporter [Populus trichocarpa] >gi|222865607|gb|EEF02738.1| ZIP transporter [Populus trichocarpa]	Unigene47105_All//2.00E-134//AT1G10970| ZIP4 (ZINC TRANSPORTER 4 PRECURSOR); cation transmembrane transporter/ copper ion transmembrane transporter	Unigene47105_All//0.00E+00//TC144077				nr -
Unigene47113_All	1677	7.39	0.88	3.49	4.49	1.11	24.43	10.99	148.42	179.48	-3.08E+00	4.12E-42	Down	-1.08E+00	2.44E-10	Down	-2.02E+00	8.34E-20	Down	2.45E+00	1.48E-114	Up	3.76E+00	0.00E+00	Up	4.03E+00	0.00E+00	Up	Unigene47113_All//gi|209954703|dbj|BAG80542.1|//0.00E+00//glycosyltransferase [Lycium barbarum]	Unigene47113_All//0.00E+00//AT1G22360| AtUGT85A2 (UDP-glucosyl transferase 85A2); UDP-glycosyltransferase/ glucuronosyltransferase/ transferase, transferring glycosyl groups	Unigene47113_All//0.00E+00//EX164578		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene47114_All	1837	3.30	1.08	0.99	4.66	4.78	4.60	5.04	3.14	4.23	-1.62E+00	6.54E-10	Down	-1.75E+00	2.07E-10	Down	3.54E-02	8.83E-01		-2.08E-02	9.41E-01		-6.83E-01	4.86E-05		-2.53E-01	1.42E-01		Unigene47114_All//gi|224101385|ref|XP_002312257.1|//0.00E+00//SET domain protein [Populus trichocarpa] >gi|222852077|gb|EEE89624.1| SET domain protein [Populus trichocarpa]	Unigene47114_All//0.00E+00//AT1G26760| SDG25 (SET DOMAIN PROTEIN 35); binding	Unigene47114_All//0.00E+00//ES846028				nr +
Unigene47115_All	1151	14.00	15.89	14.53	16.66	15.98	22.41	10.91	6.94	5.30	1.83E-01	1.93E-01		5.32E-02	7.24E-01		-6.07E-02	7.04E-01		4.27E-01	4.65E-05		-6.54E-01	4.10E-06		-1.04E+00	5.45E-13	Down	Unigene47115_All//gi|224118092|ref|XP_002331556.1|//1.00E-108//ebs-bah-phd domain-containing protein [Populus trichocarpa] >gi|222873780|gb|EEF10911.1| ebs-bah-phd domain-containing protein [Populus trichocarpa]	Unigene47115_All//4.00E-108//AT4G22140| DNA binding / protein binding / zinc ion binding	Unigene47115_All//0.00E+00//TC142343				nr -
Unigene47116_All	1547	15.39	10.15	10.71	59.86	61.95	60.84	54.44	23.78	20.45	-6.00E-01	8.12E-08		-5.24E-01	5.62E-06		4.94E-02	4.61E-01		2.34E-02	7.23E-01		-1.20E+00	2.96E-99	Down	-1.41E+00	3.89E-132	Down	Unigene47116_All//gi|211906446|gb|ACJ11716.1|//1.00E-177//adenosine kinase [Gossypium hirsutum]	Unigene47116_All//6.00E-172//AT5G03300| ADK2 (ADENOSINE KINASE 2); adenosine kinase/ copper ion binding / kinase	Unigene47116_All//0.00E+00//TC156691		ko00230|Purine metabolism		nr +
Unigene47117_All	2264	4.46	4.39	1.43	11.68	10.19	20.05	44.22	26.27	57.47	-2.40E-02	9.12E-01		-1.64E+00	1.60E-15	Down	-1.97E-01	7.28E-02		7.79E-01	2.09E-23		-7.51E-01	1.03E-54		3.78E-01	1.49E-21		Unigene47117_All//gi|42570907|ref|NP_973527.1|//0.00E+00//calmodulin-binding protein [Arabidopsis thaliana]	Unigene47117_All//0.00E+00//AT2G24300| calmodulin-binding protein	Unigene47117_All//0.00E+00//TC139006		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene47118_All	1599	185.76	196.18	171.87	38.79	77.29	108.15	64.28	253.60	421.96	7.88E-02	9.31E-03		-1.12E-01	3.27E-04		9.95E-01	7.25E-105		1.48E+00	4.68E-247	Up	1.98E+00	0.00E+00	Up	2.71E+00	0.00E+00	Up	Unigene47118_All//gi|116804319|gb|AB827327.1|//0.00E+00//vacuolar citrate/H+ symporter [Citrus sinensis]	Unigene47118_All//0.00E+00//AT5G47560| TDT (TONOPLAST DICARBOXYLATE TRANSPORTER); malate transmembrane transporter/ sodium:dicarboxylate symporter	Unigene47118_All//0.00E+00//C0118203				nr +
Unigene47120_All	1692	1.39	1.92	1.07	4.06	4.25	4.46	2.00	3.43	5.02	4.62E-01	1.89E-01		-3.79E-01	3.92E-01		6.61E-02	8.30E-01		1.34E-01	6.23E-01		7.80E-01	3.75E-04		1.33E+00	9.09E-13	Up	Unigene47120_All//gi|21593647|gb|AM65614.1|//2.00E-48//replication protein A1-like [Arabidopsis thaliana]	Unigene47120_All//1.00E-49//AT5G60990| DEAD/DEAH box helicase, putative (RH10)	Unigene47120_All//1.00E-57//TC143969		ko03040|Spliceosome		nr -
Unigene47121_All	1672	2.79	2.18	1.59	2.35	3.87	3.24	4.75	2.02	3.38	-3.52E-01	2.22E-01		-8.07E-01	5.69E-03		7.18E-01	1.18E-03		4.62E-01	8.15E-02		-1.23E+00	1.55E-10	Down	-4.91E-01	6.02E-03		Unigene47121_All//gi|224105109|ref|XP_002313690.1|//2.00E-12//f-box family protein [Populus trichocarpa] >gi|222850098|gb|EEE87645.1| f-box family protein [Populus trichocarpa]	Unigene47121_All//9.00E-06//AT4G17565| F-box family protein	Unigene47121_All//3.00E-11//TC150402				nr +
Unigene47125_All	1361	141.89	83.21	123.75	27.74	29.15	29.83	6.93	4.85	1.81	-7.70E-01	2.01E-89		-1.97E-01	1.64E-07		7.12E-02	5.19E-01		1.05E-01	2.97E-01		-5.14E-01	2.10E-03		-1.93E+00	7.38E-24	Down	Unigene47125_All//gi|40781598|gb|AA88988.1|//1.00E-117//reductase 2 [Hydrangea macrophylla] >gi|40781601|gb|AA889810.1| reductase 2 [Hydrangea macrophylla]	Unigene47125_All//1.00E-106//AT1G59950| aldo/keto reductase, putative	Unigene47125_All//0.00E+00//ES840399		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr -
Unigene47127_All	1539	19.38	17.12	20.10	10.39	14.59	23.95	9.95	17.65	13.02	-1.79E-01	9.04E-02		5.30E-02	6.27E-01		4.90E-01	5.76E-06		1.20E+00	9.44E-39	Up	8.28E-01	4.34E-18		3.89E-01	2.99E-04		Unigene47127_All//gi|42561724|ref|NP_172060.2|//1.00E-120//BT3 (BTB AND TAZ DOMAIN PROTEIN 3); protein binding / transcription regulator [Arabidopsis thaliana]	Unigene47127_All//5.00E-108//AT5G05690| BT3 (BTB AND TAZ DOMAIN PROTEIN 3); protein binding / transcription regulator	Unigene47127_All//0.00E+00//DR456750	TAZ	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene47129_All	2344	1.56	1.32	1.57	15.81	12.66	5.49	3.41	1.82	2.14	-2.45E-01	4.61E-01		4.60E-03	9.95E-01		-3.20E-01	1.02E-04		-1.53E+00	1.37E-56	Down	-9.06E-01	9.54E-07		-6.71E-01	1.61E-04		Unigene47129_All//gi|75180396|sp|Q9LSS5.1|CR3_ARATH//1.00E-124//RecName: Full=Interactor of constitutive active ROPs 3 >gi|8885572|dbj|BAB97502.1| myosin heavy chain-like [Arabidopsis thaliana]	Unigene47129_All//1.00E-92//AT5G60210| LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: myosin heavy chain-related (TAIR:AT2G37080.1); Has 77946 Blast hits to 39215 proteins in 1793 species: Archae - 845; Bacteria - 8877; Metazoa - 39997; Fungi - 6049; Plants - 2988; Viruses - 248; Other Eukaryotes - 18942 (source: NCBI BLink).	Unigene47129_All//0.00E+00//TC139634				nr -
Unigene47130_All	1808	1.50	0.78	0.80	4.82	8.55	5.50	5.50	2.03	3.35	-9.39E-01	1.38E-02		-9.20E-01	2.18E-02		8.27E-01	6.12E-10		1.89E-01	3.79E-01		-1.43E+00	3.59E-16	Down	-7.14E-01	6.23E-06		Unigene47130_All//gi|115460150|ref|NP_001053675.1|//1.00E-147//Os04g0585100 [Oryza sativa Japonica Group] >gi|38344276|emb|CAE03758.2|OSJNBa0013K16.7 [Oryza sativa (japonica cultivar-group)] >gi|113565246|dbj|BAF15589.1| Os04g0585100 [Oryza sativa Japonica Group]	Unigene47130_All//2.00E-108//AT2G33640| zinc finger (DHHC type) family protein	Unigene47130_All//0.00E+00//ES815072				nr -
Unigene47131_All	1738	7.86	5.13	4.87	19.40	16.09	15.70	15.57	9.23	6.53	-6.15E-01	5.03E-05		-6.90E-01	1.18E-05		-2.70E-01	2.44E-03		-3.06E-01	8.86E-04		-7.54E-01	1.83E-15		-1.25E+00	6.73E-36	Down	Unigene47131_All//gi|30387529|gb|AAP31930.1|//1.00E-147//At3g09570 [Arabidopsis thaliana]	Unigene47131_All//4.00E-160//AT5G18520| LOCATED IN: endomembrane system, integral to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Transmembrane receptor, eukaryota (InterPro:IPR009637); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G09570.1); Has 385 Blast hits to 381 proteins in 83 species: Archae - 0; Bacteria - 2; Metazoa - 213; Fungi - 14; Plants - 131; Viruses - 0; Other Eukaryotes - 25 (source: NCBI BLink).	Unigene47131_All//0.00E+00//TC159290				nr -
Unigene47132_All	998	28.52	23.05	27.48	40.38	24.77	20.64	21.44	7.96	5.99	-3.07E-01	2.84E-03		-5.36E-02	6.41E-01		-7.05E-01	6.56E-20		-9.69E-01	3.20E-30		-1.43E+00	8.86E-34	Down	-1.84E+00	1.03E-49	Down	Unigene47132_All//gi|30682545|ref|NP_850057.1|//1.00E-92//ARF3 (ADP-RIBOSYLATION FACTOR 3); protein binding [Arabidopsis thaliana] >gi|297821835|ref|XP_002878800.1| ADP-ribosylation factor 3 [Arabidopsis lyrata subsp. lyrata] >gi|728882|sp|P40940.2|ARF3_ARATH RecName: Full=ADP-ribosylation factor 3; Short=AtARF3; AltName: Full=Protein ARF-LIKE 1; Short=AtARL1 >gi|453191|emb|CAA54564.1| ADP-ribosylation factor 3 [Arabidopsis thaliana] >gi|23297380|gb|AAN12955.1| ADP-ribosylation factor 3 [Arabidopsis thaliana] >gi|297324639|gb|EFH55059.1| ADP-ribosylation factor 3 [Arabidopsis lyrata subsp. lyrata]	Unigene47132_All//6.00E-94//AT2G24765| ARF3 (ADP-RIBOSYLATION FACTOR 3); protein binding	Unigene47132_All//0.00E+00//TC171731				nr -
Unigene47133_All	1362	71.30	32.51	55.99	46.01	45.74	52.82	21.82	13.78	10.30	-1.13E+00	6.68E-86	Down	-3.49E-01	7.47E-11		-8.60E-03	9.22E-01		1.99E-01	1.40E-03		-6.63E-01	1.10E-13		-1.08E+00	2.19E-31	Down	Unigene47133_All//gi|297824281|ref|XP_002880023.1|//5.00E-71//aconitase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297323862|gb|EFH56282.1| aconitase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene47133_All//6.00E-62//AT2G43090| aconitase C-terminal domain-containing protein	Unigene47133_All//0.00E+00//TC138430		ko00290|Valine, leucine and isoleucine biosynthesis//ko00660|C5-Branched dibasic acid metabolism		nr -
Unigene47139_All	821	32.76	21.54	25.04	45.93	41.78	41.53	43.36	29.73	19.31	-6.05E-01	7.70E-09		-3.88E-01	3.68E-04		-1.37E-01	1.54E-01		-1.45E-01	1.34E-01		-5.45E-01	1.21E-11		-1.17E+00	4.87E-42	Down	Unigene47139_All//gi|194708824|gb|ACF88496.1|//2.00E-73//At4g29870 [Arabidopsis thaliana]	Unigene47139_All//6.00E-62//AT4G29870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: membrane protein, putative (TAIR:AT2G19340.2); Has 163 Blast hits to 163 proteins in 56 species: Archae - 0; Bacteria - 0; Metazoa - 127; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink).	Unigene47139_All//0.00E+00//TC146916				nr -

Unigene47140_All	2410	27.16	13.79	26.36	3.06	3.10	1.80	1.75	0.36	0.86	-9.78E-01	8.32E-46		-4.31E-02	6.13E-01		1.94E-02	9.56E-01		-7.66E-01	2.75E-04		-2.27E+00	4.93E-13	Down	-1.03E+00	7.14E-05	Down	Unigene47140_All//gi|300680944|sp|B5W7Z8.1|FAO1_LOTJA//0.00E+00//RecName: Full=Long-chain-alcohol oxidase FAO1; AltName: Full=Long-chain fatty alcohol oxidase 1 >gi|209570220|emb|CAP15762.1| long chain fatty alcohol oxidase FAO1 [Lotus japonicus]	Unigene47140_All//0.00E+00//AT3G23410| alcohol oxidase-related	Unigene47140_All//0.00E+00//TC136607				nr -
Unigene47141_All	1894	3.98	3.69	1.63	5.94	5.56	6.53	7.01	5.38	5.93	-1.08E-01	6.17E-01		-1.29E+00	2.16E-08	Down	-9.54E-02	6.20E-01		1.37E-01	4.73E-01		-3.81E-01	6.44E-03		-2.41E-01	8.74E-02		Unigene47141_All//gi|115483971|ref|NP_001065647.1|//3.00E-19//Os11g0129800 [Oryza sativa Japonica Group] >gi|113644351|dbj|BAF27492.1| Os11g0129800 [Oryza sativa Japonica Group]	Unigene47141_All//5.00E-11//AT5G50350| unknown protein	Unigene47141_All//0.00E+00//TC175152				nr +
Unigene47142_All	1848	10.48	17.85	13.83	19.22	24.62	23.73	3.07	3.14	13.21	7.69E-01	8.35E-16		4.01E-01	3.34E-04		3.57E-01	1.11E-06		3.04E-01	1.25E-04		3.62E-02	8.92E-01		2.11E+00	8.64E-67	Up	Unigene47142_All//gi|115448753|ref|NP_001048156.1|//2.00E-54//Os02g0754600 [Oryza sativa Japonica Group] >gi|113537687|dbj|BAF10070.1| Os02g0754600 [Oryza sativa Japonica Group]	Unigene47142_All//4.00E-73//AT5G64230| unknown protein	Unigene47142_All//4.00E-54//TC164255				nr -
Unigene47143_All	2264	1.41	0.65	1.67	6.95	5.64	2.49	5.17	1.44	0.65	-1.12E+00	1.52E-03		2.44E-01	4.74E-01		-3.01E-01	3.10E-02		-1.48E+00	3.01E-23	Down	-1.84E+00	7.84E-27	Down	-2.99E+00	8.43E-49	Down	Unigene47143_All//gi|14005317|gb|ABE39572.2|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene47143_All//8.00E-147//AT4G20270| BAM3 (BARELY ANY MERISTEM 3); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene47143_All//2.00E-105//gi|48793101|gb|CO094415.1|CO094415		ko04626|Plant-pathogen interaction		nr +
Unigene47144_All	1704	34.27	17.16	16.47	34.73	36.05	38.56	32.65	20.68	18.59	-9.98E-01	2.44E-42		-1.06E+00	7.51E-45	Down	5.39E-02	5.48E-01		1.51E-01	2.83E-02		-6.59E-01	1.27E-24		-8.13E-01	3.79E-36		Unigene47144_All//gi|166203413|gb|ABI84675.1|//0.00E+00//multicopy suppressor of IRA1 [Nicotiana tabacum]	Unigene47144_All//0.00E+00//AT5G58230| MS11 (MULTICOPY SUPRESSOR OF IRA1); protein binding	Unigene47144_All//0.00E+00//TC168152				nr +
Unigene47145_All	2492	2.14	1.67	2.18	50.85	34.30	14.23	50.15	18.57	17.76	-3.61E-01	1.74E-01		2.54E-02	9.40E-01		-5.68E-01	3.84E-42		-1.84E+00	1.97E-251	Down	-1.43E+00	1.49E-194	Down	-1.50E+00	1.38E-213	Down	Unigene47145_All//gi|30678198|ref|NP_563639.2|//0.00E+00//SBT11.1; serine-type endopeptidase [Arabidopsis thaliana]	Unigene47145_All//0.00E+00//AT1G01900| SBT11.1; serine-type endopeptidase	Unigene47145_All//0.00E+00//gi|109850569|gb|DW479548.1|DW479548				nr +
Unigene47147_All	846	4.33	5.39	8.25	5.59	4.93	8.54	4.25	3.71	1.93	3.16E-01	2.83E-01		9.30E-01	6.12E-05		-1.84E-01	5.56E-01		6.11E-01	4.77E-03		-1.97E-01	5.52E-01		-1.14E+00	7.20E-05	Down			Unigene47147_All//3.00E-127//TC164807				
Unigene47148_All	1198	1.44	3.60	1.51	3.62	3.05	3.51	3.92	3.42	1.80	1.32E+00	1.54E-05	Up	6.85E-02	8.91E-01		-2.48E-01	4.38E-01		-4.52E-02	9.01E-01		-1.96E-01	4.86E-01		-1.13E+00	5.38E-06	Down			Unigene47148_All//0.00E+00//TC164807				
Unigene47149_All	1519	1.45	5.84	1.68	9.12	5.98	6.93	4.20	4.51	2.96	2.01E+00	1.10E-18	Up	2.18E-01	6.28E-01		-6.07E-01	1.24E-05		-3.96E-01	8.96E-03		1.03E-01	6.41E-01		-5.04E-01	1.27E-02		Unigene47149_All//gi|224075521|ref|XP_002304664.1|//1.00E-133//serine/threonine protein kinase PBS1 [Populus trichocarpa] >gi|222842096|gb|EEE79643.1| serine/threonine protein kinase PBS1 [Populus trichocarpa]	Unigene47149_All//4.00E-132//AT5G13160| PBS1 (avrPphB susceptible 1); kinase/ protein serine/threonine kinase	Unigene47149_All//0.00E+00//TC178888		ko04626|Plant-pathogen interaction		nr +
Unigene4715_All	1468	1.78	2.28	2.36	5.26	2.53	1.32	0.43	0.46	0.84	3.54E-01	3.17E-01		4.04E-01	2.51E-01		-1.05E+00	6.44E-08	Down	-1.99E+00	1.81E-17	Down	7.64E-02	9.37E-01		9.62E-01	6.77E-02		Unigene4715_All//gi|223452302|gb|ACM89479.1|//1.00E-171//cysteine-rich protein [Glycine max]	Unigene4715_All//2.00E-145//AT4G11530| kinase	Unigene4715_All//9.00E-24//TC165530		ko04626|Plant-pathogen interaction		nr +
Unigene47150_All	1899	4.88	9.87	5.83	6.22	8.38	9.58	5.57	4.73	18.25	1.02E+00	1.75E-14	Up	2.58E-01	1.70E-01		4.30E-01	1.29E-03		6.25E-01	7.97E-07		-2.34E-01	1.67E-01		1.71E+00	1.02E-71	Up	Unigene47150_All//gi|13605503|gb|AAK32745.1|AF361577_1/1.00E-176//AT5g44670/K15C23_12 [Arabidopsis thaliana] >gi|259901660|gb|ANT22243.1| At5g44670/K15C23_12 [Arabidopsis thaliana]	Unigene47150_All//4.00E-165//AT4G20170| unknown protein	Unigene47150_All//0.00E+00//TC169660		ko00270|Cysteine and methionine metabolism		nr +
Unigene47152_All	1961	0.69	2.30	1.14	8.26	5.53	4.74	5.24	2.92	2.50	1.73E+00	3.64E-08	Up	7.17E-01	1.11E-01		-5.78E-01	5.59E-06		-7.99E-01	3.47E-09		-8.43E-01	1.44E-07		-1.07E+00	3.46E-11	Down	Unigene47152_All//gi|20197184|gb|AAC16076.2|//1.00E-175//expressed protein [Arabidopsis thaliana]	Unigene47152_All//1.00E-172//AT2G44260| unknown protein	Unigene47152_All//0.00E+00//CO109883				nr +
Unigene47153_All	1564	3.21	3.73	0.65	2.64	9.18	1.70	5.27	2.81	13.86	2.14E-01	4.02E-01		-2.31E+00	2.75E-12	Down	1.80E+00	9.20E-30	Up	-6.34E-01	3.50E-02		-9.10E-01	5.68E-07		1.39E+00	1.19E-33	Up	Unigene47153_All//gi|3540181|gb|AAC34331.1|//3.00E-70//Unknown protein [Arabidopsis thaliana] >gi|40823449|gb|AAR92283.1| At1g10020 [Arabidopsis thaliana] >gi|46184221|gb|AAS99692.1| At1g10020 [Arabidopsis thaliana]	Unigene47153_All//2.00E-92//AT4G29310| unknown protein	Unigene47153_All//0.00E+00//TC157459				nr -
Unigene47156_All	1819	2.99	3.57	4.57	7.04	9.86	8.49	5.09	2.00	2.63	2.53E-01	3.06E-01		6.10E-01	3.49E-03		4.87E-01	7.68E-05		2.71E-01	7.26E-02		-1.35E+00	7.46E-14	Down	-9.54E-01	1.37E-08		Unigene47156_All//gi|217038859|gb|ACJ76786.1|//1.00E-155//tyrosinase polyphenol oxidase [Argemone mexicana]		Unigene47156_All//0.00E+00//TC145743		ko00350|Tyrosine metabolism//ko00950|Isoquinoline alkaloid biosynthesis		nr +
Unigene47157_All	2174	2.91	1.40	0.71	8.32	5.24	8.75	7.66	3.11	5.24	-1.06E+00	9.46E-06	Down	-2.04E+00	3.49E-13	Down	-6.66E-01	2.29E-08		7.25E-02	6.43E-01		-1.30E+00	5.69E-23	Down	-5.48E-01	3.67E-06		Unigene47157_All//gi|297799634|ref|XP_002867701.1|//1.00E-128//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297313537|gb|EFH43960.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene47157_All//4.00E-119//AT4G23540| binding	Unigene47157_All//0.00E+00//TC133888				nr +
Unigene47158_All	817	22.48	12.96	18.90	16.10	17.15	16.81	12.68	15.71	42.76	-7.94E-01	1.16E-09		-2.50E-01	7.84E-02		9.18E-02	6.06E-01		6.21E-02	7.22E-01		3.09E-01	3.40E-02		1.75E+00	1.12E-74	Up	Unigene47158_All//gi|116265922|gb|ABJ91209.1|//2.00E-65//CBL-interacting protein kinase 1 [Populus trichocarpa]	Unigene47158_All//6.00E-57//AT3G17510| CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding	Unigene47158_All//0.00E+00//EX164882		ko04140|Regulation of autophagy		nr +
Unigene47159_All	1294	19.25	9.01	13.42	13.32	15.83	16.26	9.64	15.67	32.63	-1.10E+00	2.07E-21	Down	-5.21E-01	3.64E-06		2.49E-01	4.49E-02		2.88E-01	1.96E-02		7.01E-01	1.79E-10		1.76E+00	1.73E-90	Up	Unigene47159_All//gi|116265922|gb|ABJ91209.1|//1.00E-147//CBL-interacting protein kinase 1 [Populus trichocarpa]	Unigene47159_All//3.00E-131//AT3G17510| CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding	Unigene47159_All//0.00E+00//TC160134		ko04140|Regulation of autophagy		nr +
Unigene47160_All	1151	1.82	3.04	0.46	1.69	1.11	1.81	5.25	5.59	1.52	7.40E-01	2.46E-02		-1.97E+00	1.29E-04	Down	-6.09E-01	1.84E-01		9.68E-02	8.48E-01		9.03E-02	7.03E-01		-1.79E+00	4.24E-14	Down	Unigene47160_All//gi|224057376|ref|XP_002299218.1|//1.00E-128//GRAS family transcription factor [Populus trichocarpa] >gi|222846476|gb|EEE84023.1| GRAS family transcription factor [Populus trichocarpa]	Unigene47160_All//7.00E-89//AT1G50420| SCL3; transcription factor	Unigene47160_All//7.00E-21//ES815142	GRAS			nr +
Unigene47161_All	1785	1.96	1.85	2.71	3.77	3.13	2.58	12.29	2.90	2.39	-9.00E-02	7.78E-01		4.67E-01	1.08E-01		-2.70E-01	2.69E-01		-5.46E-01	1.59E-02		-2.08E+00	3.85E-58	Down	-2.36E+00	4.05E-70	Down	Unigene47161_All//gi|3913711|sp|P81406.1|GAPN_PEA//0.00E+00//RecName: Full=NADP-dependent glyceraldehyde-3-phosphate dehydrogenase; AltName: Full=Non-phosphorylating glyceraldehyde 3-phosphate dehydrogenase; AltName: Full=Glyceraldehyde-3-phosphate dehydrogenase [NADP+]; AltName: Full=Triosephosphate dehydrogenase >gi|4379384|emb|CAA53076.1| glyceraldehyde-3-phosphate dehydrogenase (nonphosphorylating,NADP+) [Pisum sativum] >gi|28274680|gb|AAO38512.1| non-phosphorylating glyceraldehyde-3-phosphate dehydrogenase [Pisum sativum]	Unigene47161_All//7.00E-177//AT2G24270| ALDH11A3; 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydrogenase (NADP+)	Unigene47161_All//0.00E+00//TC172306		ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene47162_All	1338	5.40	22.23	8.40	4.32	5.25	8.74	11.41	32.24	23.67	2.04E+00	2.46E-62	Up	6.38E-01	2.80E-04		2.82E-01	2.39E-01		1.02E+00	8.48E-10	Up	1.50E+00	4.90E-72	Up	1.05E+00	1.14E-31	Up	Unigene47162_All//gi|51315784|sp|Q7Y1X1.1|EST_HEVBR//1.00E-142//RecName: Full=Esterase; AltName: Full=Early nodule-specific protein homolog; AltName: Full=Latex allergen Hev b 13; AltName: Allergen=Hev b 13; Flags: Precursor >gi|30909057|gb|AAP37470.1| ENSP-like protein [Hevea brasiliensis]	Unigene47162_All//4.00E-113//AT3G26430| GDSL-motif lipase/hydrolase family protein	Unigene47162_All//0.00E+00//TC149543				nr +
Unigene47163_All	1353	15.70	33.97	17.20	18.45	20.77	24.77	12.47	29.01	28.97	1.11E+00	9.83E-40	Up	1.32E-01	3.26E-01		1.71E-01	1.21E-01		4.25E-01	2.58E-06		1.22E+00	5.57E-48	Up	1.22E+00	6.73E-49	Up	Unigene47163_All//gi|14190517|gb|AAK55739.1|AF380658_1//9.00E-47//At1g53031 [Arabidopsis thaliana] >gi|15809782|gb|AAL06819.1| At1g53031 [Arabidopsis thaliana]	Unigene47163_All//5.00E-39//AT1G53035| unknown protein	Unigene47163_All//0.00E+00//TC158322				nr +
Unigene47165_All	944	1.66	4.24	1.97	3.22	3.21	3.64	8.38	10.67	9.45	1.35E+00	2.31E-05	Up	2.48E-01	6.18E-01		-3.90E-03	9.80E-01		1.76E-01	6.41E-01		3.49E-01	3.50E-02		1.75E-01	3.55E-01		Unigene47165_All//gi|297843584|ref|XP_002889673.1|//3.00E-39//ATRNL [Arabidopsis lyrata subsp. lyrata] >gi|297335515|gb|EFH65932.1| ATRNL [Arabidopsis lyrata subsp. lyrata]	Unigene47165_All//4.00E-40//AT1G07910| RNL (RNA LIGASE); 2',3'-cyclic-nucleotide 3'-phosphodiesterase/ RNA ligase (ATP)/ polynucleotide kinase	Unigene47165_All//2.00E-168//gi|164311984|gb|EX165133.1|EX165133				nr +
Unigene47167_All	1635	2.46	1.46	1.63	76.50	70.89	32.04	2.74	1.97	2.17	-7.58E-01	1.24E-02		-5.98E-01	6.12E-02		-1.10E-01	2.04E-02		-1.26E+00	3.20E-141	Down	-4.78E-01	6.63E-02		-3.38E-01	1.89E-01		Unigene47167_All//gi|224133250|ref|XP_002327997.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222837406|gb|EEE75785.1| GRAS family transcription factor [Populus trichocarpa]	Unigene47167_All//9.00E-113//AT4G37650| SHR (SHORT ROOT); protein binding / sequence-specific DNA binding / transcription factor	Unigene47167_All//0.00E+00//TC136335	GRAS			nr -
Unigene47168_All	1767	0.68	1.35	1.30	6.06	7.25	5.67	7.18	20.65	12.20	9.85E-01	1.78E-02		9.28E-01	3.63E-02		2.58E-01	1.20E-01		-9.52E-02	6.47E-01		1.52E+00	1.39E-62	Up	7.65E-01	4.03E-13		Unigene47168_All//gi|223452470|gb|ACM89562.1|//1.00E-157//calmodulin-binding receptor-like cytoplasmic kinase [Glycine max]	Unigene47168_All//7.00E-121//AT4G00330| CRCK2; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene47168_All//0.00E+00//TC164647		ko04626|Plant-pathogen interaction		nr +
Unigene47169_All	1198	2.58	1.99	1.07	4.78	4.31	4.56	5.01	1.50	2.83	-3.74E-01	3.07E-01		-1.27E+00	8.14E-04	Down	-1.49E-01	5.98E-01		-6.80E-02	8.01E-01		-1.74E+00	4.33E-13	Down	-8.26E-01	8.33E-05		Unigene47169_All//gi|297801902|ref|XP_002868835.1|//1.00E-87//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297314671|gb|EFH45094.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene47169_All//7.00E-88//AT4G38150| pentatricopeptide (PPR) repeat-containing protein	Unigene47169_All//0.00E+00//TC160606				nr +
Unigene4717_All	1039	50.21	5.75	11.12	6.52	7.19	10.56	14.24	22.21	24.42	-3.13E+00	1.92E-178	Down	-2.17E+00	8.44E-115	Down	1.41E-01	5.87E-01		6.96E-01	3.62E-05		6.41E-01	3.35E-10		7.78E-01	1.00E-15		Unigene4717_All//gi|15241290|ref|NP_197519.1|//6.00E-64//binding [Arabidopsis thaliana]	Unigene4717_All//1.00E-44//AT5G20190| binding	Unigene4717_All//0.00E+00//TC141161				nr -
Unigene47171_All	1478	7.68	5.45	9.08	12.94	9.48	15.10	4.52	2.38	1.94	-4.95E-01	3.37E-03		2.41E-01	1.53E-01		-4.49E-01	1.32E-04		2.22E-01	7.35E-02		-9.28E-01	5.66E-06		-1.22E+00	3.61E-09	Down	Unigene47171_All//gi|297807269|ref|XP_002871518.1|//1.00E-160//beta subunit of rab geranylgeranyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297317355|gb|EFH47777.1| beta subunit of rab geranylgeranyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene47171_All//2.00E-152//AT5G12210| geranylgeranyl transferase type II beta subunit, putative / RAB geranylgeranyltransferase beta subunit, putative	Unigene47171_All//0.00E+00//TC146552				nr +

Unigene47172_All	1270	6.72	1.99	4.82	2.16	3.55	2.77	3.33	2.40	2.70	-1.75E+00	3.84E-15	Down	-4.78E-01	2.21E-02		7.19E-01	9.37E-03		3.63E-01	3.13E-01		-4.71E-01	8.05E-02		-3.03E-01	2.56E-01		Unigene47172_All//gi|297799354|ref|XP_002867561.1|//1.00E-131//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313397|gb|EFH43820.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47172_All//1.00E-122//AT4G26540| kinase			ko04626|Plant-pathogen interaction		nr -
Unigene47174_All	1443	3.19	1.86	2.25	10.53	7.56	6.23	4.51	4.49	2.02	-7.78E-01	5.60E-03		-5.03E-01	9.10E-02		-4.77E-01	3.60E-04		-7.57E-01	5.94E-08		-7.30E-03	1.01E+00		-1.16E+00	2.27E-08	Down	Unigene47174_All//gi|15241025|ref|NP_198121.1|//3.00E-48//heavy-metal-associated domain-containing protein [Arabidopsis thaliana]	Unigene47174_All//8.00E-22//AT5G27690| heavy-metal-associated domain-containing protein	Unigene47174_All//0.00E+00//DW506635		ko03018|RNA degradation		nr +
Unigene47177_All	1440	7.67	9.04	4.59	13.08	16.21	16.37	11.33	7.00	5.45	2.38E-01	1.47E-01		-7.42E-01	2.99E-05		3.10E-01	5.03E-03		3.24E-01	4.25E-03		-6.96E-01	1.63E-08		-1.06E+00	5.98E-17	Down	Unigene47177_All//gi|9294423|dbj|BAB02543.1|//1.00E-174//mitotic checkpoint protein [Arabidopsis thaliana]	Unigene47177_All//6.00E-169//AT1G49910| WD-40 repeat family protein / mitotic checkpoint_protein, putative	Unigene47177_All//0.00E+00//gi|78354467|gb|DT574741.1|DT574741				nr -
Unigene47178_All	1901	2.31	1.09	1.32	3.17	4.42	2.42	1.31	1.19	1.55	-1.08E+00	2.29E-04	Down	-8.12E-01	7.14E-03		4.79E-01	1.43E-02		-3.88E-01	1.26E-01		-1.44E-01	7.06E-01		2.41E-01	4.76E-01		Unigene47178_All//gi|82749768|gb|ABB88771.1|//1.00E-111//At3g12540-like protein [Boechera stricta]	Unigene47178_All//8.00E-118//AT2G39690| unknown protein	Unigene47178_All//0.00E+00//AI731575				nr -
Unigene47179_All	1797	15.52	8.66	11.76	39.36	30.09	30.18	34.30	16.86	12.22	-8.42E-01	1.11E-15		-4.00E-01	1.74E-04		-3.88E-01	6.54E-12		-3.83E-01	1.55E-10		-1.02E+00	5.98E-57	Down	-1.49E+00	6.73E-105	Down	Unigene47179_All//gi|255572737|ref|XP_002527301.1|//3.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223533301|gb|EEF35053.1| conserved hypothetical protein [Ricinus communis]	Unigene47179_All//6.00E-06//AT3G58320| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: meprin and TRAF homology domain-containing protein / MATH domain-containing protein (TAIR:AT3G58270.2); Has 134 Blast hits to 120 proteins in 3 species: Archae - 0; Bacteria - 2; Metazoa - 0; Fungi - 0; Plants - 132; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene47179_All//0.00E+00//TC146674				nr -
Unigene47180_All	1395	7.09	14.24	11.18	18.07	18.09	17.22	15.61	15.43	13.37	1.01E+00	4.94E-15	Up	6.58E-01	6.46E-06		2.00E-03	9.90E-01		-6.91E-02	6.35E-01		-1.66E-02	9.08E-01		-2.24E-01	3.56E-02		Unigene47180_All//gi|31711832|gb|AAP68272.1|//1.00E-114//At5g15880 [Arabidopsis thaliana]	Unigene47180_All//2.00E-95//AT5G15880| unknown protein	Unigene47180_All//0.00E+00//TC136628				nr -
Unigene47182_All	2180	2.45	2.77	3.22	1.60	2.29	1.47	1.20	1.15	0.42	1.76E-01	4.99E-01		3.97E-01	9.23E-02		5.18E-01	5.39E-02		-1.21E-01	7.28E-01		-6.40E-02	8.68E-01		-1.52E+00	2.13E-05	Down	Unigene47182_All//gi|227202520|dbj|BAB56733.1|//0.00E+00//AT4G30310 [Arabidopsis thaliana]	Unigene47182_All//0.00E+00//AT4G30310| ribitol kinase, putative	Unigene47182_All//0.00E+00//TC164773		ko04626|Plant-pathogen interaction//ko00040|Pentose and glucuronate interconversions//ko00561|Glycerolipid metabolism		nr -
Unigene47183_All	1352	0.70	1.50	2.44	5.08	3.72	2.54	18.86	22.97	13.29	1.11E+00	1.62E-02		1.81E+00	3.06E-06	Up	-4.51E-01	3.88E-02		-1.00E+00	5.72E-06	Down	2.85E-01	1.19E-03		-5.05E-01	7.78E-08		Unigene47183_All//gi|224096656|ref|XP_002310688.1|//4.00E-86//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222853591|gb|EEE91138.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene47183_All//2.00E-73//AT1G56010| NAC1; transcription factor	Unigene47183_All//0.00E+00//DW243243	NAC			nr -
Unigene47185_All	1432	168.22	67.02	84.63	37.81	58.29	52.23	10.69	6.01	7.18	-1.33E+00	1.47E-272	Down	-9.91E-01	1.58E-165		6.24E-01	4.36E-32		4.66E-01	1.30E-15		-8.30E-01	1.32E-10		-5.74E-01	3.66E-06		Unigene47185_All//gi|12230584|sp|Q08935.1|ROC1_NICSY//9.00E-83//RecName: Full=29 kDa ribonucleoprotein A, chloroplastic; AltName: Full=CP29A; Flags: Precursor >gi|19754|emb|CAA43427.1| 29kD A ribonucleoprotein [Nicotiana sylvestris]	Unigene47185_All//3.00E-74//AT2G37220| 29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative	Unigene47185_All//0.00E+00//TC135872		ko03040|Spliceosome		nr -
Unigene47186_All	2007	5.71	4.70	4.17	21.32	12.46	6.84	14.33	10.00	4.23	-2.82E-01	1.08E-01		-4.55E-01	9.77E-03		-7.75E-01	6.65E-25		-1.64E+00	1.68E-72	Down	-5.19E-01	7.73E-09		-1.76E+00	1.28E-62	Down	Unigene47186_All//gi|124360549|gb|ABO33126.2|//3.00E-54//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene47186_All//2.00E-37//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene47186_All//0.00E+00//gi|13248822|gb|BF278592.2|BF278592				nr -
Unigene47188_All	1909	15.10	11.09	11.69	20.90	19.99	13.41	16.99	8.69	7.45	-4.45E-01	9.59E-06		-3.70E-01	4.27E-04		-6.46E-02	5.66E-01		-6.40E-01	6.52E-15		-9.67E-01	1.24E-27		-1.19E+00	1.61E-39	Down	Unigene47188_All//gi|297792977|ref|XP_002864373.1|//1.00E-171//2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis lyrata subsp. lyrata] >gi|297310208|gb|EFH40632.1| 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis lyrata subsp. lyrata]	Unigene47188_All//6.00E-142//AT5G55070| 2-oxoacid dehydrogenase family protein	Unigene47188_All//0.00E+00//TC134326		ko00020|Citrate cycle (TCA cycle)//ko00310|Lysine degradation		nr -
Unigene47189_All	2141	5.87	4.97	2.41	11.05	9.57	11.39	12.18	9.21	8.19	-2.39E-01	1.54E-01		-1.28E+00	1.72E-13	Down	-2.08E-01	7.50E-02		4.36E-02	7.41E-01		-4.03E-01	2.17E-05		-5.74E-01	7.64E-10		Unigene47189_All//gi|145357578|ref|NP_195927.2|//0.00E+00//IMPA-9 (IMPORTIN ALPHA ISOFORM 9); binding [Arabidopsis thaliana]	Unigene47189_All//0.00E+00//AT5G03070| IMPA-9 (IMPORTIN ALPHA ISOFORM 9); binding	Unigene47189_All//0.00E+00//TC166017				nr -
Unigene47192_All	2014	0.21	1.11	0.95	2.00	0.92	4.22	23.70	15.15	29.69	2.41E+00	2.46E-06	Up	2.20E+00	8.21E-05	Up	-1.12E+00	8.34E-05	Down	1.07E+00	6.88E-08	Up	-6.46E-01	1.65E-20		3.25E-01	4.67E-08		Unigene47192_All//gi|224482639|gb|ACN50176.1|//0.00E+00//pectinesterase [Annona cherimola]	Unigene47192_All//0.00E+00//AT1G76160| sks5 (SKU5 Similar 5); copper ion binding / oxidoreductase	Unigene47192_All//0.00E+00//TC138027		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene47194_All	1900	19.80	11.47	21.75	10.62	14.10	5.94	5.21	2.97	2.22	-7.88E-01	1.04E-18		1.36E-01	1.51E-01		4.09E-01	3.32E-05		-8.37E-01	3.50E-12		-8.10E-01	6.93E-07		-1.23E+00	2.72E-13	Down	Unigene47194_All//gi|15233707|ref|NP_194145.1|//1.00E-152//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|19699292|gb|AAL91257.1| AT4g24140/T19F6_130 [Arabidopsis thaliana] >gi|25090311|gb|AAN72274.1| At4g24140/T19F6_130 [Arabidopsis thaliana]	Unigene47194_All//3.00E-149//AT4G24140| hydrolase, alpha/beta fold family protein	Unigene47194_All//0.00E+00//TC170405				nr +
Unigene47197_All	1393	3.61	2.84	2.71	15.56	26.80	14.43	57.24	70.84	161.44	-3.46E-01	2.15E-01		-4.10E-01	1.50E-01		7.85E-01	1.83E-21		-1.09E-01	4.53E-01		3.07E-01	3.33E-11		1.50E+00	0.00E+00	Up	Unigene47197_All//gi|28558782|gb|AAO45753.1|//1.00E-100//RING/C3HC4/PHD zinc finger-like protein [Cucumis melo]	Unigene47197_All//3.00E-54//AT3G05200| ATL6; protein binding / zinc ion binding	Unigene47197_All//0.00E+00//TC166962				nr +
Unigene47199_All	2696	7.43	4.10	5.08	15.34	15.72	13.59	21.92	8.36	9.44	-8.59E-01	7.32E-12		-5.50E-01	1.45E-05		3.60E-02	7.58E-01		-1.75E-01	4.84E-02		-1.39E+00	2.57E-88	Down	-1.22E+00	8.88E-74	Down	Unigene47199_All//gi|222423617|dbj|BAH19777.1|//0.00E+00//AT5G66420 [Arabidopsis thaliana]	Unigene47199_All//0.00E+00//AT5G66420| LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP033271 (InterPro:IPR008322), TIM-barrel signal transduction protein, predicted (InterPro:IPR009215); Has 809 Blast hits to 807 proteins in 200 species: Archae - 4; Bacteria - 603; Metazoa - 0; Fungi - 61; Plants - 24; Viruses - 0; Other Eukaryotes - 117 (source: NCBI BLink).	Unigene47199_All//0.00E+00//TC141407				nr +
Unigene472_All	3485	17.63	10.32	11.32	33.79	31.30	22.43	34.90	16.25	20.01	-7.72E-01	4.93E-29		-6.39E-01	3.33E-20		-1.10E-01	2.49E-02		-5.91E-01	2.72E-37		-1.10E+00	8.04E-126	Down	-8.03E-01	2.45E-76		Unigene472_All//gi|189503705|gb|ACE06982.1|//0.00E+00//obtusifoliol-14alpha-demethylase [Gossypium hirsutum]	Unigene472_All//0.00E+00//AT1G11680| CYP51G1 (CYTOCHROME P450 51G1); oxygen binding / sterol 14-demethylase	Unigene472_All//0.00E+00//TC146822		ko00100|Steroid biosynthesis	GO:0005506//GO:0006694//GO:0016709//GO:0016741//GO:0031224//GO:0043231	nr +
Unigene47203_All	2277	2.83	2.96	3.55	10.11	10.36	7.36	7.56	6.68	3.60	6.65E-02	7.78E-01		3.31E-01	1.39E-01		3.55E-02	8.32E-01		-4.58E-01	3.76E-05		-1.78E-01	1.80E-01		-1.07E+00	3.89E-18	Down	Unigene47203_All//gi|15219165|ref|NP_175710.1|//1.00E-109//UBC26 (UBIQUITIN-CONJUGATING ENZYME 26); ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene47203_All//3.00E-110//AT1G53020| UBC26 (UBIQUITIN-CONJUGATING ENZYME 26); ubiquitin-protein ligase	Unigene47203_All//0.00E+00//gi|164296144|gb|ES840913.1|ES840913		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene47204_All	1628	12.05	9.80	11.12	15.27	15.53	18.09	7.53	3.36	5.38	-2.98E-01	1.96E-02		-1.16E-01	4.14E-01		2.41E-02	8.58E-01		2.44E-01	1.79E-02		-1.16E+00	1.60E-14	Down	-4.84E-01	5.45E-04		Unigene47204_All//gi|85541788|sp|Q56Y1.2|DDPS2_ARATH//7.00E-52//RecName: Full=Dehydrodolichyl diphosphate synthase 2; Short=Dedol-PP synthase 2 >gi|208879536|gb|ACI31313.1| At5g58770 [Arabidopsis thaliana]	Unigene47204_All//3.00E-53//AT5G58770| dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative	Unigene47204_All//0.00E+00//gi|78351667|gb|DT571941.1|DT571941		ko00900|Terpenoid backbone biosynthesis		nr +
Unigene47205_All	757	1.38	11.78	4.50	6.32	33.07	31.20	2.51	4.20	1.16	3.09E+00	2.90E-30	Up	1.70E+00	5.79E-06	Up	2.39E+00	4.15E-74	Up	2.30E+00	1.11E-61	Up	7.39E-01	1.76E-02		-1.12E+00	6.32E-03		Unigene47205_All//gi|22333|emb|CAA44844.1|//8.00E-08//hydroxyproline-rich glycoprotein [Zea mays] >gi|228936|prf||1814452A Hyp-rich glycoprotein						nr +
Unigene47206_All	868	0.00	8.11	0.86	2.41	8.33	13.84	2.00	2.89	2.62	1.30E+01	3.00E-40	Up	9.75E+00	3.27E-04	Up	1.79E+00	4.93E-15	Up	2.52E+00	5.19E-35	Up	5.33E-01	1.44E-01		3.90E-01	3.11E-01		Unigene47206_All//gi|53370641|gb|AAU89136.1|//3.00E-06//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene47206_All//3.00E-07//TC168701				nr -
Unigene47207_All	1240	0.13	1.68	0.77	0.72	2.92	2.73	0.92	1.45	0.90	3.73E+00	1.15E-08	Up	2.61E+00	3.45E-03		2.01E+00	6.75E-09	Up	1.92E+00	1.92E-07	Up	6.55E-01	1.38E-01		-3.33E-02	9.65E-01		Unigene47207_All//gi|124359162|gb|ABN05685.1|//1.00E-07//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene47207_All//4.00E-07//TC168701				nr -
Unigene47210_All	1791	6.19	3.54	2.20	9.32	7.90	7.77	13.74	4.53	7.25	-8.08E-01	2.52E-06		-1.49E+00	5.99E-15	Down	-2.38E-01	9.09E-02		-2.63E-01	6.86E-02		-1.60E+00	1.16E-45	Down	-9.22E-01	3.26E-20		Unigene47210_All//gi|7769865|gb|AAF69543.1|AC008007.18//1.00E-147//F12M16.27 [Arabidopsis thaliana] >gi|49858495|gb|AAT47800.1| At1g53380 [Arabidopsis thaliana] >gi|53828581|gb|AAU94400.1| At1g53380 [Arabidopsis thaliana]	Unigene47210_All//3.00E-148//AT1G53380| unknown protein	Unigene47210_All//0.00E+00//TC153689				nr -
Unigene47211_All	1228	123.22	53.06	80.96	175.28	169.88	227.95	306.22	158.74	152.22	-1.22E+00	2.39E-149	Down	-6.06E-01	1.09E-44		-4.52E-02	2.83E-01		3.79E-01	5.38E-39		-9.48E-01	2.62E-302		-1.01E+00	0.00E+00	Down	Unigene47211_All//gi|211906502|gb|ACJ11744.1|//0.00E+00//Isocitrate dehydrogenase [Gossypium hirsutum]	Unigene47211_All//0.00E+00//AT1G65930| isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	Unigene47211_All//0.00E+00//TC133862		ko04146|Peroxisome//ko00480|Glutathione metabolism//ko00020|Citrate cycle (TCA cycle)		nr -
Unigene47214_All	903	9.68	1.74	3.66	1.32	1.30	2.40	12.27	12.40	3.71	-2.48E+00	9.30E-24	Down	-1.40E+00	6.51E-11	Down	-3.02E-02	9.58E-01		8.59E-01	5.30E-02		1.60E-02	9.49E-01		-1.73E+00	5.14E-24	Down	Unigene47214_All//gi|4105798|gb|AAD02556.1|//1.00E-100//PGPD14 [Petunia x hybrida]	Unigene47214_All//3.00E-98//AT5G22920| zinc finger (C3HC4-type RING finger) family protein	Unigene47214_All//0.00E+00//TC177586		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene47215_All	1296	5.73	1.25	3.41	1.35	0.90	1.64	7.18	4.45	1.81	-2.20E+00	1.15E-17	Down	-7.49E-01	7.57E-04		-5.75E-01	2.44E-01		2.84E-01	5.75E-01		-6.90E-01	3.95E-05		-1.98E+00	2.30E-24	Down	Unigene47215_All//gi|4105798|gb|AAD02556.1|//1.00E-127//PGPD14 [Petunia x hybrida]	Unigene47215_All//1.00E-123//AT5G22920| zinc finger (C3HC4-type RING finger) family protein	Unigene47215_All//0.00E+00//TC177586		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene47216_All	2172	3.42	3.55	2.28	7.04	6.12	5.59	16.23	5.77	3.34	5.19E-02	8.15E-01		-5.85E-01	8.75E-03		-2.02E-01	1.88E-01		-3.32E-01	2.31E-02		-1.49E+00	9.82E-59	Down	-2.28E+00	1.52E-107	Down	Unigene47216_All//gi|22330247|ref|NP_683432.1|//1.00E-171//binding [Arabidopsis thaliana] >gi|79319936|ref|NP_001031189.1| binding [Arabidopsis thaliana]	Unigene47216_All//8.00E-162//AT1G54385| binding	Unigene47216_All//0.00E+00//TC163882				nr +

Unigene47217_All	1474	7.17	3.27	4.23	8.21	6.49	11.80	8.35	6.07	4.78	-1.13E+00	4.88E-10	Down	-7.62E-01	2.84E-05		-3.39E-01	3.56E-02		5.23E-01	6.00E-05		-4.60E-01	1.42E-03		-8.03E-01	1.55E-08		Unigene47217_All//gi|22022566|gb|AAM83240.1|//1.00E-116//AT5g13610/MSH12_7 [Arabidopsis thaliana] >gi|23308429|gb|AAN18184.1| At5g13610/MSH12_7 [Arabidopsis thaliana]	Unigene47217_All//6.00E-117//AT5G13610| unknown protein	Unigene47217_All//0.00E+00//gi|78335310|gb|DT555584.1|DT555584				nr +
Unigene47219_All	1628	9.83	16.18	14.16	11.02	8.95	17.81	1.04	2.52	2.28	7.19E-01	1.87E-11		5.26E-01	7.20E-06		-3.00E-01	2.00E-02		6.93E-01	1.76E-12		1.28E+00	4.37E-06	Up	1.13E+00	6.52E-05	Up	Unigene47219_All//gi|297822743|ref|XP_002879254.1|//1.00E-140//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325093|gb|EFH55513.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47219_All//2.00E-140//AT2G30140| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene47219_All//0.00E+00//TC151373		ko00940|Phenylpropanoid biosynthesis//ko00380|Tryptophan metabolism//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00966|Glucosinolate biosynthesis		nr -
Unigene47220_All	2491	6.55	4.09	6.26	9.62	7.59	4.84	17.35	7.85	8.81	-6.81E-01	7.98E-07		-6.53E-02	6.73E-01		-3.42E-01	1.24E-03		-9.91E-01	7.21E-19		-1.14E+00	7.58E-48	Down	-9.77E-01	2.84E-38		Unigene47220_All//gi|15240012|ref|NP_201457.1|//0.00E+00//phototropic-responsive NPH3 family protein [Arabidopsis thaliana]	Unigene47220_All//0.00E+00//AT5G66560| phototropic-responsive NPH3 family protein	Unigene47220_All//0.00E+00//TC162625				nr -
Unigene47221_All	1382	3.03	49.94	20.69	184.41	287.84	1016.83	34.51	57.64	196.89	4.04E+00	6.75E-291	Up	2.77E+00	5.38E-84	Up	6.42E-01	3.69E-160		2.46E+00	0.00E+00	Up	7.40E-01	1.50E-42		2.51E+00	0.00E+00	Up	Unigene47221_All//gi|297827611|ref|XP_002881688.1|//1.00E-152//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327527|gb|EFH57947.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47221_All//4.00E-146//AT2G39980| transferase family protein	Unigene47221_All//0.00E+00//DN780134		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene47223_All	1251	2.51	7.94	6.26	8.32	11.40	18.05	19.53	18.64	76.14	1.66E+00	3.22E-16	Up	1.32E+00	5.02E-09	Up	4.53E-01	1.42E-03		1.12E+00	2.72E-21	Up	-6.74E-02	6.02E-01		1.96E+00	1.21E-235	Up	Unigene47223_All//gi|30690409|ref|NP_850456.1|//5.00E-13//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene47223_All//4.00E-16//AT5G53110| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: zinc finger (C3HC4-type RING finger) family protein (TAIR:AT2G46195.1); Has 118 Blast hits to 116 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 118; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene47223_All//0.00E+00//DN507088				nr +
Unigene47227_All	528	96.91	169.19	100.65	132.84	155.61	150.97	114.27	231.38	163.35	8.04E-01	9.17E-45		5.46E-02	5.48E-01		2.28E-01	2.62E-05		1.85E-01	1.86E-03		1.02E+00	9.06E-111	Up	5.16E-01	3.69E-25		Unigene47227_All//gi|4589726|dbj|BAA76883.1|//4.00E-65//DnaJ homolog protein [Salix gilgiana] >gi|4589739|dbj|BAA76888.1| DnaJ homolog protein [Salix gilgiana]	Unigene47227_All//1.00E-44//AT3G44110| ATJ3; protein binding	Unigene47227_All//0.00E+00//TC149999		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene47228_All	1366	109.70	181.16	119.52	145.25	164.66	160.35	103.60	208.95	209.23	7.24E-01	1.69E-102		1.24E-01	4.30E-03		1.81E-01	7.01E-09		1.43E-01	2.82E-05		1.01E+00	1.26E-255	Up	1.01E+00	2.59E-262	Up	Unigene47228_All//gi|4589726|dbj|BAA76883.1|//1.00E-150//DnaJ homolog protein [Salix gilgiana] >gi|4589739|dbj|BAA76888.1| DnaJ homolog protein [Salix gilgiana]	Unigene47228_All//2.00E-105//AT3G44110| ATJ3; protein binding	Unigene47228_All//0.00E+00//TC132826		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene47234_All	418	2.63	1.94	1.27	0.83	1.40	1.40	5.06	2.90	0.67	-4.39E-01	4.95E-01		-1.05E+00	1.35E-01		7.48E-01	4.81E-01		7.52E-01	4.67E-01		-8.03E-01	4.24E-02		-2.92E+00	3.37E-09	Down	Unigene47234_All//gi|297812451|ref|XP_002874109.1|//2.00E-38//acyl-activating enzyme 17 [Arabidopsis lyrata subsp. lyrata] >gi|297319946|gb|EFH50368.1| acyl-activating enzyme 17 [Arabidopsis lyrata subsp. lyrata]	Unigene47234_All//3.00E-39//AT5G23050| AAE17 (ACYL-ACTIVATING ENZYME 17); catalytic/ligase	Unigene47234_All//3.00E-150//TC158870		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism		nr +
Unigene47236_All	1947	1.26	0.88	0.93	6.98	6.37	4.11	4.39	1.35	1.15	-5.13E-01	2.12E-01		-4.42E-01	3.09E-01		-1.34E-01	4.50E-01		-7.67E-01	2.52E-07		-1.70E+00	1.06E-17	Down	-1.94E+00	9.45E-22	Down	Unigene47236_All//gi|28200788|emb|CAD45375.1|//1.00E-171//potyviral helper component protease-interacting protein 2 [Solanum tuberosum subsp. andigena]	Unigene47236_All//1.00E-146//AT4G27060| TOR1 (TORTIFOLIA 1); microtubule binding	Unigene47236_All//0.00E+00//TC148726				nr +
Unigene47237_All	1617	2.69	9.34	6.78	6.56	7.71	7.82	2.17	5.25	1.55	1.80E+00	4.90E-27	Up	1.34E+00	1.19E-12	Up	2.33E-01	1.78E-01		2.53E-01	1.41E-01		1.27E+00	9.78E-12	Up	-4.84E-01	9.22E-02		Unigene47237_All//gi|15241393|ref|NP_199929.1|//6.00E-31//ankyrin repeat family protein [Arabidopsis thaliana] >gi|45825143|gb|AAS77479.1| At5g51160 [Arabidopsis thaliana]	Unigene47237_All//4.00E-32//AT5G51160| ankyrin repeat family protein	Unigene47237_All//0.00E+00//ES831259				nr +
Unigene47239_All	2765	1.49	2.25	2.06	5.10	3.03	2.50	5.54	3.48	3.18	5.92E-01	1.24E-02		4.63E-01	7.91E-02		-7.53E-01	4.07E-08		-1.03E+00	4.92E-12	Down	-6.71E-01	1.40E-07		-7.98E-01	2.72E-10		Unigene47239_All//gi|79562781|ref|NP_180102.3|//1.00E-151//transferase, transferring glycosyl groups / transferase, transferring hexosyl groups [Arabidopsis thaliana] >gi|75110959|sp|Q9XEZ1.1|B3GT9_ARATH RecName: Full=Probable beta-1,3-galactosyltransferase 9 >gi|53828557|gb|AAU94388.1| At2g25300 [Arabidopsis thaliana] >gi|57444893|gb|AAW50705.1| At2g25300 [Arabidopsis thaliana]	Unigene47239_All//7.00E-144//AT2G25300| transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene47239_All//0.00E+00//TC160254				nr +
Unigene47240_All	1500	4.29	2.03	3.41	6.48	7.02	5.99	7.61	2.45	3.03	-1.08E+00	5.16E-06	Down	-3.32E-01	1.90E-01		1.17E-01	5.82E-01		-1.12E-01	6.35E-01		-1.63E+00	3.32E-22	Down	-1.33E+00	4.36E-17	Down	Unigene47240_All//gi|18412023|ref|NP_565182.1|//1.00E-141//bile acid:sodium symporter family protein [Arabidopsis thaliana] >gi|16648877|gb|AAL24290.1| Unknown protein [Arabidopsis thaliana] >gi|23197632|gb|AAN15343.1| Unknown protein [Arabidopsis thaliana]	Unigene47240_All//5.00E-121//AT1G78560| bile acid:sodium symporter family protein	Unigene47240_All//0.00E+00//CO115327				nr +
Unigene47241_All	1718	13.46	6.28	7.81	14.85	11.30	19.16	22.84	11.63	11.34	-1.10E+00	4.81E-20	Down	-7.85E-01	3.24E-11		-3.93E-01	9.06E-05		3.68E-01	6.31E-05		-9.74E-01	1.17E-33		-1.01E+00	9.31E-37	Down	Unigene47241_All//gi|297795569|ref|XP_002865669.1|//1.00E-105//60S ribosomal protein L13A [Arabidopsis lyrata subsp. lyrata] >gi|297311504|gb|EFH41928.1| 60S ribosomal protein L13A [Arabidopsis lyrata subsp. lyrata]	Unigene47241_All//3.00E-106//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene47241_All//0.00E+00//TC139550		ko03010|Ribosome		nr +
Unigene47242_All	1582	6.65	10.41	6.16	10.64	8.82	7.62	20.87	32.36	46.21	6.47E-01	2.41E-06		-1.10E-01	6.09E-01		-2.72E-01	4.59E-02		-4.82E-01	2.82E-04		6.33E-01	3.57E-21		1.15E+00	2.06E-82	Up	Unigene47242_All//gi|224129122|ref|XP_002320506.1|//1.00E-168//f-box family protein [Populus trichocarpa] >gi|222861279|gb|EEE98821.1| f-box family protein [Populus trichocarpa]	Unigene47242_All//3.00E-138//AT3G07870| F-box family protein	Unigene47242_All//0.00E+00//TC157064				nr +
Unigene47243_All	1692	12.43	14.73	12.65	9.83	14.59	17.27	34.06	60.25	240.11	2.45E-01	3.04E-02		2.54E-02	8.53E-01		5.70E-01	2.24E-08		8.13E-01	2.28E-16		8.23E-01	5.88E-65		2.82E+00	0.00E+00	Up	Unigene47243_All//gi|115477188|ref|NP_001062190.1|//3.00E-45//Os08g0506700 [Oryza sativa Japonica Group] >gi|113624159|dbj|BAF24104.1| Os08g0506700 [Oryza sativa Japonica Group]	Unigene47243_All//6.00E-30//AT2G42280| basic helix-loop-helix (bHLH0) family protein	Unigene47243_All//0.00E+00//TC132550	bHLH	ko04712|Circadian rhythm - plant		nr +
Unigene47246_All	2215	4.49	2.22	3.80	11.72	8.05	6.87	11.59	8.30	3.06	-1.02E+00	4.58E-08	Down	-2.41E-01	2.33E-01		-5.41E-01	2.91E-08		-7.70E-01	1.72E-13		-4.81E-01	4.83E-07		-1.92E+00	4.79E-63	Down	Unigene47246_All//gi|18075958|emb|CAD12836.1|//0.00E+00//diphosphonucleotide phosphatase 1 [Lupinus luteus]	Unigene47246_All//0.00E+00//AT1G13750| calcineurin-like phosphoesterase family protein	Unigene47246_All//0.00E+00//TC150872				nr -
Unigene47247_All	1523	0.89	22.79	4.76	5.27	2.85	5.43	5.58	7.90	2.07	4.67E+00	5.84E-161	Up	2.41E+00	1.85E-18	Up	-8.86E-01	2.85E-06		4.34E-02	8.60E-01		5.02E-01	5.55E-04		-1.43E+00	2.13E-14	Down	Unigene47247_All//gi|11386775|sp|O65781.1|GALE2_CYATE//1.00E-172//RecName: Full=UDP-glucose 4-epimerase GEPI48; AltName: Full=UDP-galactose 4-epimerase; AltName: Full=Galactowaldenase >gi|3021357|emb|CAA06339.1| UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]	Unigene47247_All//1.00E-163//AT4G23920| UGE2 (UDP-D-glucose/UDP-D-galactose 4-epimerase 2); UDP-glucose 4-epimerase/ protein dimerization	Unigene47247_All//0.00E+00//TC141432		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism		nr -
Unigene47248_All	1775	8.11	4.22	7.65	9.04	7.26	10.58	7.93	2.64	2.06	-9.40E-01	4.83E-10		-8.35E-02	6.33E-01		-3.17E-01	2.05E-02		2.28E-01	9.76E-02		-1.59E+00	3.74E-26	Down	-1.94E+00	1.97E-35	Down	Unigene47248_All//gi|297852474|ref|XP_002894118.1|//7.00E-81//zinc finger (Ran-binding) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339960|gb|EFH70377.1| zinc finger (Ran-binding) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47248_All//5.00E-75//AT1G48570| zinc finger (Ran-binding) family protein	Unigene47248_All//0.00E+00//D8452705				nr -
Unigene47249_All	1050	5.68	19.16	7.61	9.77	10.33	15.31	25.33	22.53	22.04	1.75E+00	1.28E-34	Up	4.21E-01	5.33E-02		8.00E-02	7.22E-01		6.48E-01	1.80E-06		-1.69E-01	1.00E-01		-2.00E-01	3.70E-02		Unigene47249_All//gi|71041098|gb|AAZ20437.1|//1.00E-47//MYB21 [Malus x domestica]	Unigene47249_All//2.00E-42//AT2G31180| MYB14 (MYB DOMAIN PROTEIN 14); DNA binding / transcription factor	Unigene47249_All//7.00E-67//NP524439	MYB			nr +
Unigene4725_All	1178	17.85	7.83	13.34	62.97	43.73	41.10	4.49	1.21	1.45	-1.19E+00	1.17E-20	Down	-4.21E-01	7.27E-04		-5.26E-01	1.37E-21		-6.15E-01	1.96E-25		-1.90E+00	5.92E-13	Down	-1.63E+00	5.45E-11	Down	Unigene4725_All//gi|124300986|gb|AB04745.1|//1.00E-54//At2g26110 [Arabidopsis thaliana]	Unigene4725_All//8.00E-33//AT2G26110| unknown protein	Unigene4725_All//0.00E+00//gi|109850665|gb|DW479644.1|DW479644				nr -
Unigene47250_All	937	0.22	1.30	1.08	0.80	0.77	1.21	2.30	0.76	1.36	2.54E+00	5.98E-04	Up	2.27E+00	5.76E-03		-4.73E-02	9.43E-01		5.96E-01	3.98E-01		-1.60E+00	1.06E-04	Down	-7.58E-01	4.29E-02		Unigene47250_All//2.00E-42//AT2G31180| MYB14 (MYB DOMAIN PROTEIN 14); DNA binding / transcription factor	Unigene47250_All//6.00E-67//NP524439	MYB			nr -
Unigene47252_All	1561	5.53	4.93	6.31	2.97	2.34	1.45	1.68	0.40	0.69	-1.65E-01	4.35E-01		1.91E-01	3.69E-01		-3.44E-01	2.36E-01		-1.04E+00	1.88E-04	Down	-2.06E+00	1.66E-07	Down	-1.29E+00	2.12E-04	Down	Unigene47252_All//gi|18399058|ref|NP_566383.1|//6.00E-75//protein phosphatase-related [Arabidopsis thaliana] >gi|87116654|gb|ABD19691.1| At3g10940 [Arabidopsis thaliana]	Unigene47252_All//6.00E-73//AT3G10940| protein phosphatase-related	Unigene47252_All//0.00E+00//TC146836				nr -

Unigene47254_All	1980	48.65	47.29	43.57	19.12	20.50	16.49	13.67	11.10	6.72	-4.08E-02	5.26E-01		-1.59E-01	5.21E-03		1.01E-01	3.14E-01		-2.13E-01	1.82E-02		-3.00E-01	1.54E-03		-1.02E+00	3.39E-26	Down	Unigene47254_All//gi|18407701|ref|NP_564804.1|//0.00E+00//ACS10 (ACC SYNTHASE 10); 1-aminocyclopropane-1-carboxylate synthase/ L-aspartate:2-oxoglutarate aminotransferase/ aromatic-amino-acid:2-oxoglutarate aminotransferase [Arabidopsis thaliana] >gi|50100664|sp|Q9LQ10.1|1A110_ARATH RecName: Full=Probable aminotransferase ACS10 >gi|8493584|gb|AAF75807.1|AC011000_10 Strong similarity to ACS5 from Lupinus albus gb|AF119414, and contains an Aminotransferase-classI domain PF|00155 [Arabidopsis thaliana] >gi|13194768|gb|AAK15546.1|AF348575_1 aminotransferase [Arabidopsis thaliana] >gi|15451222|gb|AAK96882.1| Strong similarity to ACS5 from Lupinus albus gb|AF119414, and contains an Aminotransferase-classI domain PF|00155 [Arabidopsis thaliana] >gi|31711978|gb|AAP68345.1|At1g62960 [Arabidopsis thaliana]	Unigene47254_All//0.00E+00//AT1G62960| ACS10 (ACC SYNTHASE 10); 1-aminocyclopropane-1-carboxylate synthase/ L-aspartate:2-oxoglutarate aminotransferase/ aromatic-amino-acid:2-oxoglutarate aminotransferase	Unigene47254_All//0.00E+00//TC153485		ko00270|Cysteine and methionine metabolism		nr -
Unigene47255_All	1871	10.51	34.20	9.71	10.09	20.43	16.37	22.06	24.86	95.26	1.70E+00	2.54E-104	Up	-1.16E-01	4.16E-01		1.02E+00	9.28E-34	Up	6.98E-01	2.73E-13		1.73E-01	1.87E-02		2.11E+00	0.00E+00	Up	Unigene47255_All//gi|87241412|gb|AB033270.1|//1.00E-96//t-snare [Medicago truncatula]	Unigene47255_All//9.00E-74//AT1G27700| protein binding	Unigene47255_All//0.00E+00//TC142143		ko04130|SNARE interactions in vesicular transport		nr -
Unigene47256_All	900	2.03	2.03	2.72	4.04	3.37	8.88	10.19	5.90	17.79	-5.60E-03	9.86E-01		4.20E-01	3.39E-01		-2.63E-01	4.48E-01		1.14E+00	4.06E-08	Up	-7.90E-01	3.36E-06		8.04E-01	8.66E-11				Unigene47256_All//0.00E+00//ES816657				
Unigene47257_All	1546	8.93	8.46	10.95	19.37	21.20	51.79	16.27	11.00	38.11	-7.94E-02	6.16E-01		2.94E-01	4.43E-02		1.31E-01	2.22E-01		1.42E+00	1.13E-107	Up	-5.65E-01	5.50E-09		1.23E+00	3.98E-74	Up	Unigene47257_All//gi|297381026|gb|ADI39634.1|//2.00E-26//plastid jasmonates ZIM-domain protein [Hevea brasiliensis]	Unigene47257_All//2.00E-27//AT4G24450| JAZ6 (JASMONATE-ZIM-DOMAIN PROTEIN 6)	Unigene47257_All//0.00E+00//TC156247	Tify			nr -
Unigene47258_All	1363	10.56	3.72	2.66	39.33	33.25	9.68	3.91	1.87	1.08	-1.51E+00	2.64E-20	Down	-1.99E+00	1.67E-28	Down	-2.42E-01	4.22E-04		-2.02E+00	3.63E-121	Down	-1.06E+00	5.84E-06	Down	-1.85E+00	3.94E-13	Down	Unigene47258_All//gi|124359162|gb|ABN05685.1|//3.00E-11//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene47258_All//0.00E+00//gi|164259275|gb|ES800903.1|ES800903				nr -
Unigene47259_All	1826	3.01	1.55	2.54	6.96	5.70	8.29	32.42	8.49	9.77	-9.53E-01	1.98E-04		-2.46E-01	3.99E-01		-2.89E-01	7.28E-02		2.52E-01	1.03E-01		-1.93E+00	2.94E-141	Down	-1.73E+00	5.81E-125	Down	Unigene47259_All//gi|18405098|ref|NP_565908.1|//1.00E-157//ACT domain-containing protein [Arabidopsis thaliana] >gi|3355486|gb|AAC27848.1| expressed protein [Arabidopsis thaliana]	Unigene47259_All//9.00E-159//AT2G39570| ACT domain-containing protein	Unigene47259_All//0.00E+00//DW515153				nr +
Unigene4726_All	1150	7.19	1.23	2.18	7.58	5.18	7.30	7.90	2.94	4.92	-2.54E+00	3.43E-23	Down	-1.72E+00	9.62E-14	Down	-5.49E-01	2.83E-03		-5.34E-02	8.08E-01		-1.43E+00	9.83E-15	Down	-6.84E-01	3.63E-05		Unigene4726_All//gi|18417696|ref|NP_567861.1|//6.00E-65//NFD1 (NUCLEAR FUSION DEFECTIVE 1); RNA binding / structural constituent of ribosome [Arabidopsis thaliana] >gi|29839556|sp|Q8LN40.1|RM21_ARATH RecName: Full=50S ribosomal protein L21, mitochondrial; Flags: Precursor >gi|29028852|gb|AAO64805.1|At4g30930 [Arabidopsis thaliana]	Unigene4726_All//1.00E-43//AT4G30930| NFD1 (NUCLEAR FUSION DEFECTIVE 1); RNA binding / structural constituent of ribosome	Unigene4726_All//0.00E+00//gi|78350470|gb|DT570744.1|DT570744		ko03010|Ribosome		nr +
Unigene47264_All	2688	2.82	5.99	3.53	4.80	7.15	6.12	6.64	6.25	8.74	1.09E+00	6.88E-14	Up	3.21E-01	1.13E-01		5.75E-01	9.82E-07		3.50E-01	1.22E-02		-8.67E-02	5.51E-01		3.98E-01	5.31E-05		Unigene47264_All//gi|297724965|ref|NP_001174846.1|//0.00E+00//Os06g0558700 [Oryza sativa Japonica Group] >gi|255677141|dbj|BAH93574.1|Os06g0558700 [Oryza sativa Japonica Group]	Unigene47264_All//0.00E+00//AT4G32850| mPAP (NUCLEAR POLY(A) POLYMERASE); nucleotidyltransferase/ protein binding	Unigene47264_All//0.00E+00//gi|164339779|gb|ES841143.1|ES841143		ko03018|RNA degradation		nr -
Unigene4727_All	1256	5.04	10.33	6.49	5.24	6.50	7.34	11.71	12.88	9.58	1.03E+00	1.59E-10	Up	3.64E-01	9.52E-02		3.12E-01	1.47E-01		4.87E-01	1.06E-02		1.37E-01	3.48E-01		-2.90E-01	2.54E-02		Unigene4727_All//gi|297801870|ref|XP_002868819.1|//1.00E-58//seven in absentia family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316655|gb|EFH45078.1| seven in absentia family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4727_All//6.00E-48//AT5G37930| seven in absentia (SINA) family protein	Unigene4727_All//0.00E+00//TC169388		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene47270_All	1689	2.60	2.19	1.29	22.41	14.88	9.92	13.34	4.50	2.50	-2.49E-01	3.99E-01		-1.01E+00	8.93E-04	Down	-5.91E-01	8.92E-14		-1.18E+00	7.66E-39	Down	-1.57E+00	1.36E-40	Down	-2.42E+00	7.24E-74	Down	Unigene47270_All//gi|75208205|sp|Q9SK39.1|GPI7_ARATH//1.00E-107//RecName: Full=Uncharacterized GPI-anchored protein At4g28100; Flags: Precursor	Unigene47270_All//3.00E-106//AT4G28100| unknown protein	Unigene47270_All//0.00E+00//gi|11200710|gb|BF269715.1|BF269715				nr +
Unigene47272_All	1369	9.17	9.96	3.89	17.03	10.34	17.35	18.93	8.15	9.60	1.18E-01	4.88E-01		-1.24E+00	8.27E-13	Down	-7.20E-01	3.86E-12		2.71E-02	8.52E-01		-1.22E+00	6.61E-32	Down	-9.79E-01	2.12E-23		Unigene47272_All//gi|115485041|ref|NP_001067664.1|//2.00E-52//Os11g0266000 [Oryza sativa Japonica Group] >gi|113644886|dbj|BAF28027.1|Os11g0266000 [Oryza sativa Japonica Group]	Unigene47272_All//8.00E-58//AT5G48240| unknown protein	Unigene47272_All//0.00E+00//TC148904				nr -
Unigene47274_All	401	0.00	0.25	0.00	1.12	0.17	4.05	81.71	78.59	98.16	7.98E+00	3.86E-01		null	null		-2.70E+00	3.24E-02		1.86E+00	9.27E-04	Up	-5.63E-02	6.14E-01		2.65E-01	4.37E-04		Unigene47274_All//gi|48310199|gb|AAT41773.1|//7.00E-52//At5g24600 [Arabidopsis thaliana] >gi|50198891|gb|AAT70465.1|At5g24600 [Arabidopsis thaliana]	Unigene47274_All//4.00E-53//AT5G24600| unknown protein	Unigene47274_All//0.00E+00//TC141294				nr -
Unigene47275_All	1306	0.32	14.98	1.47	4.01	2.35	5.91	19.72	25.35	16.56	5.55E+00	6.99E-99	Up	2.20E+00	8.21E-05	Up	-7.71E-01	1.56E-03		5.62E-01	7.17E-03		3.62E-01	1.43E-05		-2.51E-01	8.54E-03		Unigene47275_All//gi|48310199|gb|AAT41773.1|//4.00E-84//At5g24600 [Arabidopsis thaliana] >gi|50198891|gb|AAT70465.1|At5g24600 [Arabidopsis thaliana]	Unigene47275_All//2.00E-85//AT5G24600| unknown protein	Unigene47275_All//0.00E+00//TC176860				nr +
Unigene47277_All	828	6.00	12.48	12.99	2.95	2.99	2.13	2.81	1.01	1.11	1.06E+00	8.23E-09	Up	1.11E+00	1.77E-09	Up	2.26E-02	9.65E-01		-4.71E-01	2.74E-01		-1.48E+00	1.54E-04	Down	-1.34E+00	3.20E-04	Down	Unigene47277_All//gi|15450439|gb|AAK96513.1|//2.00E-16//AT3g52230/F4F15_340 [Arabidopsis thaliana] >gi|16974441|gb|AAL31224.1|AT3g52230/F4F15_340 [Arabidopsis thaliana]	Unigene47277_All//1.00E-17//AT3G52230| unknown protein	Unigene47277_All//0.00E+00//TC151404				nr -
Unigene47279_All	2161	19.25	7.50	21.78	19.16	16.08	8.65	14.97	5.98	7.63	-1.36E+00	2.83E-49	Down	1.79E-01	3.62E-02		-2.53E-01	1.51E-03		-1.15E+00	9.27E-41	Down	-1.32E+00	3.52E-45	Down	-9.72E-01	1.29E-28		Unigene47279_All//gi|2497542|sp|Q40546.1|KPYG_TOBAC//0.00E+00//RecName: Full=Pyruvate kinase isozyme G, chloroplastic; Flags: Precursor >gi|482938|emb|CAA82223.1| Pyruvate kinase; plastid isozyme [Nicotiana tabacum] >gi|12054705|emb|CAA49996.1| pyruvate kinase [Nicotiana tabacum]	Unigene47279_All//0.00E+00//AT1G32440| PKpG3 (plastidial pyruvate kinase 3); pyruvate kinase	Unigene47279_All//0.00E+00//ES833370		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene47280_All	879	18.04	40.01	32.23	13.60	13.40	16.65	8.47	6.66	6.57	1.15E+00	3.96E-32	Up	8.38E-01	3.87E-15		-2.17E-02	9.10E-01		2.92E-01	5.83E-02		-3.47E-01	8.04E-02		-3.65E-01	5.34E-02		Unigene47280_All//gi|195622354|gb|ACG33007.1|//8.00E-72//palmitoyl-protein thioesterase 1 precursor [Zea mays]	Unigene47280_All//1.00E-63//AT3G60340| palmitoyl protein thioesterase family protein	Unigene47280_All//0.00E+00//TC157782		ko00062|Fatty acid elongation in mitochondria		nr +
Unigene47281_All	1609	36.16	95.89	56.76	34.52	30.97	32.90	14.37	10.47	12.36	1.41E+00	5.66E-190	Up	6.50E-01	8.51E-31		-1.57E-01	3.11E-02		-6.95E-02	4.32E-01		-4.57E-01	6.15E-06		-2.18E-01	3.42E-02		Unigene47281_All//gi|195622354|gb|ACG33007.1|//1.00E-127//palmitoyl-protein thioesterase 1 precursor [Zea mays]	Unigene47281_All//2.00E-121//AT3G60340| palmitoyl protein thioesterase family protein	Unigene47281_All//0.00E+00//TC157782		ko00062|Fatty acid elongation in mitochondria		nr +
Unigene47282_All	709	6.05	26.44	10.14	4.92	17.19	15.80	3.22	11.50	10.90	2.13E+00	1.34E-41	Up	7.45E-01	1.01E-03		1.81E+00	1.79E-25	Up	1.68E+00	1.13E-19	Up	1.84E+00	9.78E-19	Up	1.76E+00	3.13E-17	Up	Unigene47282_All//gi|255538684|ref|XP_002510407.1|//5.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223551108|gb|EEF52594.1| conserved hypothetical protein [Ricinus communis]		Unigene47282_All//2.00E-66//TC161986				nr -
Unigene47283_All	1602	23.45	143.88	42.55	25.96	80.31	103.52	18.90	117.56	149.61	2.62E+00	0.00E+00	Up	8.60E-01	3.22E-37		1.63E+00	1.34E-232	Up	2.00E+00	0.00E+00	Up	2.64E+00	0.00E+00	Up	2.99E+00	0.00E+00	Up	Unigene47283_All//gi|193872612|gb|ACF23034.1|//1.00E-12//ST225 [Thellungiella halophila]	Unigene47283_All//4.00E-12//AT1G19530| unknown protein	Unigene47283_All//0.00E+00//TC161986				nr +
Unigene47284_All	1341	15.18	8.46	9.57	32.32	18.08	13.00	11.76	6.83	4.52	-8.43E-01	1.15E-11		-6.65E-01	1.26E-07		-8.38E-01	8.16E-29		-1.31E+00	9.00E-53	Down	-7.85E-01	5.58E-10		-1.38E+00	1.32E-24	Down	Unigene47284_All//gi|30693130|ref|NP_188582.2|//2.00E-96//PDLP7 (PLASMODESMATA-LOCATED PROTEIN 7) [Arabidopsis thaliana] >gi|63025162|gb|AAY27054.1|At5g37660 [Arabidopsis thaliana]	Unigene47284_All//3.00E-71//AT5G37660| PDLP7 (PLASMODESMATA-LOCATED PROTEIN 7)	Unigene47284_All//0.00E+00//gi|78336855|gb|DT557129.1|DT557129				nr -
Unigene47285_All	2147	3.00	2.88	1.84	0.79	2.49	0.93	10.48	5.84	14.88	-5.80E-02	8.09E-01		-7.08E-01	3.43E-03		1.66E+00	4.25E-10	Up	2.31E-01	6.48E-01		-8.43E-01	1.38E-15		5.06E-01	1.33E-09		Unigene47285_All//gi|297823583|ref|XP_002879674.1|//1.00E-169//endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325513|gb|EFH55933.1| endonuclease/exonuclease/phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47285_All//6.00E-170//AT2G37440| endonuclease/exonuclease/phosphatase family protein	Unigene47285_All//4.00E-08//TC159707				nr +
Unigene47286_All	694	0.00	0.15	0.31	0.22	0.00	0.07	5.30	2.89	0.69	7.19E+00	3.86E-01		8.26E+00	1.41E-01		-7.75E+00	1.65E-01		-1.73E+00	5.01E-01		-8.75E-01	2.19E-03		-2.94E+00	1.39E-15	Down	Unigene47286_All//gi|113367150|gb|AB134632.1|//4.00E-10//bZIP transcription factor bZIP90 [Glycine max]	Unigene47286_All//1.00E-09//AT1G08320| bZIP family transcription factor	Unigene47286_All//3.00E-136//CO085603	bZIP			nr +
Unigene47287_All	1670	0.50	0.70	0.19	2.51	2.62	1.22	45.04	40.84	18.27	4.77E-01	4.39E-01		-1.39E+00	9.66E-02		6.37E-02	8.50E-01		-1.04E+00	4.05E-04	Down	-1.41E-01	1.33E-02		-1.30E+00	3.38E-104	Down	Unigene47287_All//gi|151347477|gb|ABS01351.1|//1.00E-170//basic leucine zipper protein [Carica papaya]	Unigene47287_All//1.00E-145//AT1G08320| bZIP family transcription factor	Unigene47287_All//0.00E+00//gi|48827973|gb|CO126363.1|CO126363	bZIP			nr +
Unigene4729_All	1609	8.03	5.45	3.28	15.82	13.01	8.08	25.83	11.12	8.39	-5.60E-01	3.41E-04		-1.29E+00	4.64E-14	Down	-2.82E-01	7.35E-03		-9.69E-01	2.68E-19		-1.22E+00	1.02E-50	Down	-1.62E+00	2.65E-80	Down	Unigene4729_All//gi|22328578|ref|NP_192945.2|//2.00E-76//DNA-binding family protein [Arabidopsis thaliana] >gi|79294885|gb|AAL50079.1|AT4g12080/F16J13_150 [Arabidopsis thaliana] >gi|23506149|gb|AAX31086.1|At4g12080/F16J13_150 [Arabidopsis thaliana] >gi|118420990|dbj|BAF37220.1| AT-hook motif nuclear localized protein 1 [Arabidopsis thaliana]	Unigene4729_All//5.00E-57//AT4G00200| DNA binding	Unigene4729_All//0.00E+00//TC159201				nr +

Unigene47290_All	2414	4.07	2.27	3.02	9.82	9.23	4.92	5.20	1.68	1.09	-8.46E-01	4.25E-06		-4.31E-01	2.54E-02		-8.99E-02	5.24E-01		-9.97E-01	6.99E-19		-1.63E+00	2.76E-24	Down	-2.26E+00	2.91E-38	Down	Unigene47290_All//gi|15233845|ref|NP_195556.1|//0.00E+00//ROPGEF1; Rho guanyl-nucleotide exchange factor/ protein binding [Arabidopsis thaliana] >gi|94730494|sp|Q93Z72.2|ROGF1_ARATH RecName: Full=Rop guanine nucleotide exchange factor 1; Short=RopGEF1; AltName: Full=Kinase partner protein-like; Short=KPP-like >gi|15912195|gb|AAL08231.1|AT4g38430/F22I13_200 [Arabidopsis thaliana] >gi|22137268|gb|AAM91479.1|AT4g38430/F22I13_200 [Arabidopsis thaliana] >gi|23306424|gb|AAN17439.1|Unknown protein [Arabidopsis thaliana]	Unigene47290_All//0.00E+00//AT4G38430| ROPGEF1; Rho guanyl-nucleotide exchange factor/ protein binding	Unigene47290_All//0.00E+00//TC140078				nr -
Unigene47292_All	2619	3.52	1.22	2.72	5.19	3.52	2.69	3.41	2.55	4.65	-1.53E+00	1.53E-13	Down	-3.68E-01	7.10E-02		-5.59E-01	7.29E-05		-9.49E-01	3.01E-10		-4.16E-01	1.75E-02		4.51E-01	1.42E-03		Unigene47292_All//gi|12043533|emb|CAC19789.1|//1.00E-134//MYB-like DNA-binding protein [Catharanthus roseus]	Unigene47292_All//6.00E-128//AT1G07540| TRFL2 (TRF-LIKE 2); DNA binding	Unigene47292_All//0.00E+00//gi|78336766|gb|DT557040.1|DT557040	MYB-related			nr -
Unigene47293_All	1113	4.61	4.64	3.44	8.59	9.03	14.49	12.80	6.20	5.58	1.14E-02	9.87E-01		-4.19E-01	1.38E-01		7.22E-02	7.71E-01		7.53E-01	3.01E-08		-1.05E+00	2.97E-14	Down	-1.20E+00	4.85E-18	Down	Unigene47293_All//gi|75327220|sp|Q7XJN0.1|RH17_ARATH//1.00E-127//RecName: Full=DEAD-box ATP-dependent RNA helicase 17	Unigene47293_All//1.00E-122//AT2G40700| DEAD/DEAH box helicase, putative (RH17)					nr +
Unigene47294_All	2113	1.73	1.34	1.61	2.69	2.56	4.06	5.12	2.04	2.90	-3.68E-01	2.62E-01		-1.04E-01	7.52E-01		-7.10E-02	8.23E-01		5.96E-01	2.32E-03		-1.33E+00	9.63E-16	Down	-8.19E-01	7.57E-08		Unigene47294_All//gi|75327220|sp|Q7XJN0.1|RH17_ARATH//0.00E+00//RecName: Full=DEAD-box ATP-dependent RNA helicase 17	Unigene47294_All//0.00E+00//AT2G40700| DEAD/DEAH box helicase, putative (RH17)					nr -
Unigene47299_All	288	0.00	0.00	0.00	0.69	0.24	0.63	3.52	2.03	30.16	null	null		null	null		-1.53E+00	4.15E-01		-1.41E-01	9.34E-01		-7.94E-01	2.03E-01		3.10E+00	5.64E-37	Up	Unigene47299_All//gi|113722135|gb|AAW51924.2|//9.00E-44//phenylalanine ammonia-lyase [Rhizophora mangle]	Unigene47299_All//9.00E-39//AT3G53260| PAL2; phenylalanine ammonia-lyase	Unigene47299_All//1.00E-123//DT465176		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00910|Nitrogen metabolism		nr -
Unigene47300_All	2349	0.31	0.93	0.23	2.95	2.70	5.10	8.82	14.32	98.03	1.57E+00	6.61E-04	Up	-4.60E-01	6.02E-01		-1.28E-01	6.04E-01		7.90E-01	9.14E-07		7.00E-01	8.57E-17		3.47E+00	0.00E+00	Up	Unigene47300_All//gi|113722135|gb|AAW51924.2|//0.00E+00//phenylalanine ammonia-lyase [Rhizophora mangle]	Unigene47300_All//0.00E+00//AT3G53260| PAL2; phenylalanine ammonia-lyase	Unigene47300_All//0.00E+00//gi|73862437|gb|DT465176.1|DT465176		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00910|Nitrogen metabolism		nr -
Unigene47301_All	1846	0.88	2.25	1.47	5.59	6.68	4.77	4.72	1.38	4.90	1.36E+00	1.42E-05	Up	7.44E-01	6.28E-02		2.58E-01	1.33E-01		-2.28E-01	2.49E-01		-1.77E+00	4.13E-19	Down	5.42E-02	7.68E-01		Unigene47301_All//gi|297843100|ref|XP_002889431.1|//0.00E+00//phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335273|gb|EFH65690.1|phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47301_All//0.00E+00//AT1G03010| phototropic-responsive NPH3 family protein	Unigene47301_All//0.00E+00//TC153715				nr +
Unigene47302_All	457	0.57	0.44	0.00	4.25	1.81	1.38	0.46	0.82	1.48	-3.68E-01	7.78E-01		-9.16E+00	8.56E-02		-1.23E+00	5.24E-03		-1.62E+00	8.10E-04	Down	8.31E-01	4.67E-01		1.68E+00	3.70E-02		Unigene47302_All//gi|224141349|ref|XP_002324035.1|//9.00E-27//porin/voltage-dependent anion-selective channel protein [Populus trichocarpa] >gi|222867037|gb|EEF04168.1|porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	Unigene47302_All//2.00E-23//AT3G01280| VDAC1 (VOLTAGE DEPENDENT ANION CHANNEL 1); voltage-gated anion channel	Unigene47302_All//1.00E-134//TC149604				nr +
Unigene47303_All	910	67.79	33.69	45.29	57.48	45.64	54.05	77.31	44.23	33.71	-1.01E+00	1.74E-45	Down	-5.82E-01	2.84E-17		-3.33E-01	7.57E-07		-8.88E-02	3.13E-01		-8.06E-01	1.50E-43		-1.20E+00	1.19E-85	Down	Unigene47303_All//gi|161788876|dbj|BAF95072.1|//1.00E-106//voltage-dependent anion channel [Nicotiana tabacum]	Unigene47303_All//1.00E-90//AT3G01280| VDAC1 (VOLTAGE DEPENDENT ANION CHANNEL 1); voltage-gated anion channel	Unigene47303_All//0.00E+00//gi|78329294|gb|DT549568.1|DT549568				nr +
Unigene47304_All	346	3.78	3.95	4.00	11.23	4.98	12.66	3.79	6.89	2.99	6.48E-02	9.17E-01		8.20E-02	8.86E-01		-1.17E+00	5.52E-05	Down	1.73E-01	6.35E-01		8.62E-01	1.95E-02		-3.40E-01	5.21E-01		Unigene47304_All//gi|295291644|gb|ADF87507.1|//4.00E-53//ketol-acid reductoisomerase [Catharanthus roseus]	Unigene47304_All//6.00E-54//AT3G58610| ketol-acid reductoisomerase	Unigene47304_All//6.00E-145//gi|54118894|gb|CO494403.1|CO494403		ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene47307_All	486	0.97	1.04	0.66	2.46	1.28	2.23	6.52	1.55	2.95	1.06E-01	9.22E-01		-5.60E-01	6.28E-01		-9.48E-01	1.12E-01		-1.41E-01	8.16E-01		-2.08E+00	5.45E-09	Down	-1.14E+00	1.96E-04	Down			Unigene47307_All//2.00E-90//TC179173				
Unigene4731_All	896	70.36	23.36	38.10	64.77	60.34	45.01	26.47	11.80	11.87	-1.59E+00	6.25E-94	Down	-8.85E-01	3.83E-36		-1.02E-01	1.89E-01		-5.25E-01	3.55E-15		-1.17E+00	2.00E-27	Down	-1.16E+00	6.17E-28	Down	Unigene4731_All//gi|53370641|gb|AAU89136.1|//1.00E-08//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene4731_All//3.00E-99//TC149674				nr +
Unigene47311_All	1470	2.63	1.03	2.03	6.27	7.87	5.68	5.15	1.99	2.98	-1.35E+00	3.09E-05	Down	-3.77E-01	2.57E-01		3.28E-01	5.28E-02		-1.41E-01	5.34E-01		-1.37E+00	9.57E-12	Down	-7.88E-01	1.91E-05		Unigene47311_All//gi|297610205|ref|NP_001064277.2|//6.00E-10//Os10g0191000 [Oryza sativa Japonica Group] >gi|255679263|dbj|BAF26191.2|Os10g0191000 [Oryza sativa Japonica Group]	Unigene47311_All//5.00E-06//AT3G25270| nucleic acid binding	Unigene47311_All//6.00E-142//DW496703				nr +
Unigene47314_All	1451	1.12	163.78	10.31	10.75	42.34	58.24	6.29	60.98	50.27	7.19E+00	0.00E+00	Up	3.21E+00	5.82E-51	Up	1.98E+00	1.80E-144	Up	2.44E+00	2.23E-235	Up	3.28E+00	0.00E+00	Up	3.00E+00	2.92E-296	Up	Unigene47314_All//gi|297822725|ref|XP_002879245.1|//1.00E-108//MAPKKK14 [Arabidopsis lyrata subsp. lyrata] >gi|297325084|gb|EFH55504.1|MAPKKK14 [Arabidopsis lyrata subsp. lyrata]	Unigene47314_All//2.00E-107//AT2G30040| MAPKKK14; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene47314_All//0.00E+00//TC135952		ko04626|Plant-pathogen interaction		nr +
Unigene47315_All	1354	26.70	25.93	27.77	22.41	24.14	22.21	23.92	40.13	48.96	-4.21E-02	6.72E-01		5.64E-02	6.19E-01		1.07E-01	3.27E-01		-1.23E-02	9.34E-01		7.47E-01	1.05E-29		1.03E+00	2.33E-63	Up	Unigene47315_All//gi|297805606|ref|XP_002870687.1|//1.00E-121//PQ-loop repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316523|gb|EFH46946.1| PQ-loop repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47315_All//4.00E-121//AT5G40670| PQ-loop repeat family protein / transmembrane family protein	Unigene47315_All//0.00E+00//TC168772				nr -
Unigene47316_All	1178	1.20	4.95	3.39	2.41	3.86	3.49	3.66	2.73	3.86	2.04E+00	9.44E-13	Up	1.50E+00	7.63E-06	Up	6.79E-01	1.41E-02		5.34E-01	8.44E-02		-4.22E-01	1.18E-01		7.47E-02	7.76E-01		Unigene47316_All//gi|115453623|ref|NP_001050412.1|//4.00E-82//Os03g0427100 [Oryza sativa Japonica Group] >gi|37718893|gb|AAR01764.1|expressed protein [Oryza sativa Japonica Group] >gi|113548883|dbj|BAF12326.1|Os03g0427100 [Oryza sativa Japonica Group]	Unigene47316_All//4.00E-76//AT3G29270| ubiquitin-protein ligase	Unigene47316_All//2.00E-42//ES840820				nr -
Unigene47318_All	1676	4.21	3.87	2.70	23.81	16.09	9.27	10.70	8.10	21.20	-1.23E-01	5.96E-01		-6.42E-01	5.10E-03		-5.66E-01	2.01E-13		-1.36E+00	2.61E-51	Down	-4.00E-01	6.36E-04		9.87E-01	6.03E-32		Unigene47318_All//gi|7620007|gb|AAF64547.1|AF078531_1//1.00E-108//purine permease [Arabidopsis thaliana]	Unigene47318_All//4.00E-93//AT1G28230| PUP1 (PURINE PERMEASE 1); purine nucleoside transmembrane transporter/ purine transmembrane transporter	Unigene47318_All//0.00E+00//TC170546				nr +
Unigene47319_All	1690	3.16	1.86	0.95	1.74	2.55	2.06	1.60	1.31	1.01	-7.65E-01	3.05E-03		-1.74E+00	3.43E-09	Down	5.51E-01	6.02E-02		2.43E-01	5.19E-01		-2.89E-01	4.29E-01		-6.60E-01	4.46E-02		Unigene47319_All//gi|297816786|ref|XP_002876276.1|//1.00E-156//morphogenesis of root hair 2 [Arabidopsis lyrata subsp. lyrata] >gi|297322114|gb|EFH52535.1|morphogenesis of root hair 2 [Arabidopsis lyrata subsp. lyrata]	Unigene47319_All//3.00E-102//AT3G54870| MRH2 (MORPHOGENESIS OF ROOT HAIR 2); actin binding / microtubule binding / microtubule motor	Unigene47319_All//0.00E+00//C0095913				nr +
Unigene4732_All	1150	1.91	1.19	0.37	6.63	4.31	2.08	9.19	6.00	10.43	-6.84E-01	1.15E-01		-2.37E+00	7.70E-06	Down	-6.20E-01	1.67E-03		-1.67E+00	1.13E-13	Down	-6.16E-01	7.79E-05		1.82E-01	2.41E-01		Unigene4732_All//gi|9755454|gb|AAF98215.1|AC007152_1//2.00E-28//Unknown protein [Arabidopsis thaliana]	Unigene4732_All//1.00E-18//AT1G67050| unknown protein	Unigene4732_All//0.00E+00//TC168236				nr -
Unigene47320_All	2584	15.13	12.28	24.46	55.50	35.94	28.65	4.68	2.28	2.22	-3.01E-01	4.71E-04		6.94E-01	5.45E-24		-6.27E-01	7.27E-57		-9.54E-01	1.01E-103		-1.04E+00	4.80E-12	Down	-1.08E+00	3.77E-13	Down	Unigene47320_All//gi|15451020|gb|AB36781.1|//0.00E+00//Unknown protein [Arabidopsis thaliana]	Unigene47320_All//0.00E+00//AT4G16370| ATOPT3 (OLIGOPEPTIDE TRANSPORTER); oligopeptide transporter	Unigene47320_All//0.00E+00//TC140924				nr -
Unigene47326_All	1955	0.67	0.31	1.58	13.63	13.46	9.17	3.44	1.09	1.79	-1.11E+00	6.24E-02		1.24E+00	1.05E-03		-1.86E-02	8.84E-01		-5.72E-01	1.98E-08		-1.66E+00	1.20E-13	Down	-9.39E-01	2.44E-06		Unigene47326_All//gi|30696817|ref|NP_200517.2|//2.00E-61//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	Unigene47326_All//2.00E-14//AT5G57070| hydroxyproline-rich glycoprotein family protein	Unigene47326_All//0.00E+00//TC176184				nr +
Unigene47328_All	2155	0.34	1.86	0.77	1.11	3.28	2.24	2.96	4.79	4.71	2.45E+00	5.16E-11	Up	1.17E+00	3.12E-02		1.56E+00	3.20E-12	Up	1.02E+00	2.01E-04	Up	6.93E-01	1.21E-05		6.70E-01	1.81E-05				Unigene47328_All//9.00E-139//DR453907				
Unigene47329_All	762	5.63	6.58	5.52	11.77	9.44	8.30	3.66	3.07	7.89	2.26E-01	4.18E-01		-2.84E-02	9.42E-01		-3.17E-01	1.05E-01		-5.04E-01	8.58E-03		-2.54E-01	4.95E-01		1.11E+00	3.15E-07	Up							
Unigene4733_All	798	1.57	145.85	21.49	2.56	13.46	27.62	0.74	2.51	5.44	6.53E+00	0.00E+00	Up	3.77E+00	3.17E-67	Up	2.40E+00	6.26E-32	Up	3.43E+00	3.07E-87	Up	1.76E+00	6.27E-05	Up	2.87E+00	1.54E-17	Up	Unigene4733_All//gi|115502910|gb|AB199469.1|//9.00E-66//MFT-like protein [Vitis vinifera]	Unigene4733_All//4.00E-60//AT1G18100| E12A11; phosphatidylethanolamine binding	Unigene4733_All//0.00E+00//TC170840				nr -
Unigene47333_All	1792	13.49	9.67	10.25	28.74	27.11	19.23	13.50	5.32	8.27	-4.80E-01	1.42E-05		-3.96E-01	6.15E-04		-8.42E-02	3.28E-01		-5.80E-01	4.33E-16		-1.34E+00	1.01E-34	Down	-7.07E-01	6.54E-13		Unigene47333_All//gi|297796595|ref|XP_002866182.1|//1.00E-158//At5g57100 [Arabidopsis lyrata subsp. lyrata] >gi|297312017|gb|EFH42441.1|At5g57100 [Arabidopsis lyrata subsp. lyrata]	Unigene47333_All//3.00E-149//AT5G57100| transporter-related	Unigene47333_All//0.00E+00//TC162443				nr +
Unigene47334_All	2009	7.32	5.80	6.87	1.22	0.89	1.28	7.18	14.17	46.10	-3.35E-01	2.46E-02		-9.22E-02	6.11E-01		-4.47E-01	2.87E-01		7.68E-02	8.66E-01		9.81E-01	6.53E-25		2.68E+00	0.00E+00	Up	Unigene47334_All//gi|9758799|dbj|BAB09252.1|//1.00E-149//serine/threonine protein kinase-like [Arabidopsis thaliana]	Unigene47334_All//1.00E-150//AT5G35960| protein kinase, putative	Unigene47334_All//0.00E+00//gi|109874924|gb|DW503898.1|DW503898		ko04626|Plant-pathogen interaction		nr +
Unigene47335_All	2340	11.72	11.02	12.65	15.77	13.89	11.23	12.90	6.82	5.89	-8.82E-02	4.53E-01		1.11E-01	3.56E-01		-1.83E-01	4.26E-02		-4.90E-01	8.73E-09		-9.19E-01	9.40E-24		-1.13E+00	4.46E-34	Down	Unigene47335_All//gi|226500876|ref|NP_001149790.1|//1.00E-177//LOC100283417 [Zea mays] >gi|195634685|gb|ACG36811.1|peptidyl-prolyl isomerase [Zea mays]	Unigene47335_All//7.00E-151//AT5G48570| peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative	Unigene47335_All//0.00E+00//TC165108				nr +
Unigene47336_All	1486	36.51	96.26	82.67	18.97	18.47	14.10	7.03	6.67	3.19	1.40E+00	1.44E-174	Up	1.18E+00	2.90E-112	Up	-3.89E-02	7.86E-01		-4.28E-01	1.62E-05		-7.63E-02	6.74E-01		-1.14E+00	1.66E-12	Down	Unigene47336_All//gi|18406052|ref|NP_565982.1|//1.00E-136//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|17978968|gb|AAL47445.1|At2g42750/F7D19.25 [Arabidopsis thaliana] >gi|20197961|gb|AAD21732.2|expressed protein [Arabidopsis thaliana] >gi|20453337|gb|AAM19907.1|At2g42750/F7D19.25 [Arabidopsis thaliana]	Unigene47336_All//4.00E-120//AT2G42750| DNAJ heat shock N-terminal domain-containing protein	Unigene47336_All//0.00E+00//TC139607		ko04141|Protein processing in endoplasmic reticulum		nr +

Unigene47339_All	1208	14.47	20.51	23.23	67.05	81.76	67.63	2.63	5.67	0.99	5.04E-01	4.01E-06		6.83E-01	9.86E-11		2.86E-01	2.47E-09		1.25E-02	8.77E-01		1.11E+00	6.30E-08	Up	-1.41E+00	8.85E-06	Down	Unigene47339_All//gi|18379273|ref|NP_565272.1|//2.00E-95//PDLP6 (PLASMODESMATA-LOCATED PROTEIN 6) [Arabidopsis thaliana] >gi|75216738|sp|Q9ZU94.2|CRR12_ARATH RecName: Full=Cysteine-rich repeat secretory protein 12; Flags: Precursor >gi|17065482|gb|AAL32895.1| Unknown protein [Arabidopsis thaliana] >gi|20197542|gb|AAD12705.2| expressed protein [Arabidopsis thaliana] >gi|30023778|gb|AAP13422.1| At2g01660 [Arabidopsis thaliana]	Unigene47339_All//3.00E-80//AT2G01660| PDLP6 (PLASMODESMATA-LOCATED PROTEIN 6)	Unigene47339_All//0.00E+00//TC138285				nr -
Unigene4734_All	1056	1.68	0.77	1.87	6.65	4.83	3.68	3.84	1.70	1.36	-1.13E+00	2.21E-02		1.47E-01	7.47E-01		-4.63E-01	3.09E-02		-8.55E-01	7.99E-05		-1.18E+00	2.05E-05	Down	-1.50E+00	8.70E-08	Down	Unigene4734_All//gi|226495333|ref|NP_001150432.1|//1.00E-147//LOC100284062 [Zea mays] >gi|195639212|gb|ACG39074.1| lysine ketoglutarate reductase trans-splicing related 1 [Zea mays]	Unigene4734_All//9.00E-144//AT3G27470| unknown protein	Unigene4734_All//0.00E+00//TC143143				nr -
Unigene47340_All	2111	24.49	34.95	36.90	74.36	52.33	34.34	31.85	8.81	7.15	5.13E-01	3.73E-17		5.92E-01	2.44E-22		-5.07E-01	2.36E-42		-1.11E+00	1.58E-146	Down	-1.85E+00	1.33E-151	Down	-2.15E+00	2.77E-190	Down	Unigene47340_All//gi|75335557|sp|Q9LVM0.1|Y5830_ARATH//0.00E+00//RecName: Full=Probable inactive receptor kinase At5g58300; Flags: Precursor >gi|8777331|dbj|BAA96921.1| receptor-like protein kinase [Arabidopsis thaliana] >gi|24797034|gb|AAN64529.1| At5g58299/At5g58299 [Arabidopsis thaliana] >gi|224589729|gb|ACN59396.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene47340_All//0.00E+00//AT5G58300| leucine-rich repeat transmembrane protein kinase, putative	Unigene47340_All//0.00E+00//TC156016		ko04626|Plant-pathogen interaction		nr -
Unigene47342_All	1162	7.79	3.88	11.78	125.22	65.37	87.76	126.59	107.47	90.65	-1.01E+00	2.68E-07	Down	5.96E-01	1.47E-04		-9.38E-01	1.59E-116		-5.13E-01	1.18E-35		-2.36E-01	3.49E-10		-4.82E-01	1.42E-37		Unigene47342_All//gi|225626263|gb|ACN97181.1|//1.00E-152//peroxidase [Populus trichocarpa]	Unigene47342_All//2.00E-129//AT2G37130| peroxidase 21 (PER21) (P21) (PRX35)	Unigene47342_All//0.00E+00//TC149657		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene47344_All	1776	7.81	19.74	9.74	12.57	11.50	18.49	15.86	22.85	25.71	1.34E+00	1.71E-40	Up	3.20E-01	2.45E-02		-1.28E-01	3.31E-01		5.57E-01	1.00E-09		5.27E-01	1.88E-12		6.97E-01	6.24E-23		Unigene47344_All//gi|75100042|sp|Q81027.2|HMGCL_ARATH//1.00E-180//RecName: Full=Hydroxymethylglutaryl-CoA lyase, mitochondrial; Short=HMG-CoA lyase; Short=HL; AltName: Full=3-hydroxy-3-methylglutarate-CoA lyase	Unigene47344_All//1.00E-169//AT2G26800| hydroxymethylglutaryl-CoA lyase, putative / 3-hydroxy-3-methylglutarate-CoA lyase, putative / HMG-CoA lyase, putative	Unigene47344_All//0.00E+00//TC143504		ko04146|Peroxisome//ko00280|Valine, leucine and isoleucine degradation//ko00650|Butanoate metabolism//ko00072|Synthesis and degradation of ketone bodies		nr +
Unigene47347_All	1905	1.43	0.93	1.23	1.83	2.21	2.16	15.91	5.70	6.36	-6.18E-01	1.06E-01		-2.16E-01	6.19E-01		2.69E-01	4.24E-01		2.37E-01	4.86E-01		-1.48E+00	5.04E-50	Down	-1.32E+00	1.28E-43	Down	Unigene47347_All//gi|5080773|gb|AAD39283.1|AC007576_6//1.00E-148//Hypothetical protein [Arabidopsis thaliana]	Unigene47347_All//8.00E-150//AT1G13970| unknown protein	Unigene47347_All//0.00E+00//BF278858				nr -
Unigene47348_All	2230	9.76	16.22	7.76	11.04	9.77	10.94	21.03	48.47	24.94	7.33E-01	5.99E-16		-3.31E-01	7.82E-03		-1.75E-01	1.39E-01		-1.30E-02	9.36E-01		1.20E+00	1.37E-128	Up	2.46E-01	7.93E-05		Unigene47348_All//gi|164605542|dbj|BAP98608.1|//0.00E+00//CM0545.430.nc [Lotus japonicus]	Unigene47348_All//0.00E+00//AT4G15420| PRL1-interacting factor K	Unigene47348_All//0.00E+00//TC164093		ko03022|Basal transcription factors		nr +
Unigene4735_All	990	34.62	16.17	12.37	23.25	21.25	27.55	75.29	69.79	74.45	-1.10E+00	2.85E-29	Down	-1.48E+00	9.49E-45	Down	-1.29E-01	3.14E-01		2.45E-01	2.33E-02		-1.10E-01	6.64E-02		-1.63E-02	7.98E-01		Unigene4735_All//gi|149350003|gb|AB824134.1|//2.00E-93//protein phosphatase 2c [Medicago truncatula]	Unigene4735_All//3.00E-78//AT3G02750| protein phosphatase 2C family protein / PP2C family protein	Unigene4735_All//0.00E+00//TC134337				nr -
Unigene47350_All	765	4.17	0.79	1.11	2.02	2.52	1.36	0.44	0.22	0.05	-2.39E+00	9.11E-09	Down	-1.91E+00	2.05E-06	Down	3.21E-01	5.66E-01		-5.72E-01	3.09E-01		-1.02E+00	3.99E-01		-3.09E+00	3.92E-02		Unigene47350_All//gi|297836838|ref|XP_002886301.1|//2.00E-46//CAAX amino terminal protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332141|gb|EFH62560.1| CAAX amino terminal protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47350_All//6.00E-35//AT2G20725| CAAX amino terminal protease family protein					nr +
Unigene47351_All	1679	5.02	2.05	2.32	4.93	4.02	1.99	4.94	0.57	0.88	-1.29E+00	8.25E-10	Down	-1.12E+00	1.43E-07	Down	-2.93E-01	1.62E-01		-1.31E+00	1.95E-10	Down	-3.11E+00	7.06E-35	Down	-2.49E+00	1.23E-28	Down	Unigene47351_All//gi|30697080|ref|NP_200656.2|//0.00E+00//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|75170428|sp|Q9FGH4.1|E139_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 9; AltName: Full=(1->3)-beta-glucan endohydrolase 9; Short=(1->3)-beta-glucanase 9; AltName: Full=Beta-1,3-endoglucanase 9; Short=Beta-1,3-glucanase 9; Flags: Precursor >gi|10177025|dbj|BAB10263.1| beta-1,3-glucanase-like [Arabidopsis thaliana]	Unigene47351_All//0.00E+00//AT5G58480| glycosyl hydrolase family 17 protein	Unigene47351_All//0.00E+00//TC164135		ko00500|Starch and sucrose metabolism		nr -
Unigene47353_All	1767	3.58	2.06	1.93	6.99	9.88	10.38	7.80	3.52	3.25	-7.95E-01	6.90E-04		-8.94E-01	2.66E-04		4.99E-01	6.48E-05		5.70E-01	6.16E-06		-1.15E+00	7.23E-16	Down	-1.26E+00	5.56E-19	Down	Unigene47353_All//gi|18766642|gb|AAL79042.1|AF469649_1//1.00E-153//NIMA-related protein kinase [Populus tremula x Populus alba]	Unigene47353_All//2.00E-108//AT3G63280| ATNEK4 (NIMA-RELATED KINASE 4); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene47353_All//0.00E+00//TC140239				nr -
Unigene47357_All	1292	1.70	2.39	1.48	2.54	3.81	4.40	2.85	7.57	8.11	4.92E-01	1.70E-01		-1.97E-01	6.46E-01		5.83E-01	2.93E-02		7.92E-01	1.35E-03		1.41E+00	1.54E-15	Up	1.51E+00	1.03E-18	Up	Unigene47357_All//gi|18410195|ref|NP_565049.1|//5.00E-61//NF-YA3 (NUCLEAR FACTOR Y, SUBUNIT A3); transcription factor [Arabidopsis thaliana] >gi|81174954|sp|Q93ZH2.2|NFYA3_ARATH RecName: Full=Nuclear transcription factor Y subunit A-3; Short=AtNF-YA-3; AltName: Full=Transcriptional activator HAP2C >gi|5903072|gb|AAD55630.1|AC008017_3 Transcription Factor [Arabidopsis thaliana] >gi|31711816|gb|AAP68264.1| At1g72830 [Arabidopsis thaliana]	Unigene47357_All//2.00E-47//AT1G72830| NF-YA3 (NUCLEAR FACTOR Y, SUBUNIT A3); transcription factor	Unigene47357_All//0.00E+00//TC139504	CCAAT			nr +
Unigene47360_All	1530	167.63	58.09	35.43	176.43	84.36	195.53	237.38	254.74	190.97	-1.53E+00	0.00E+00	Down	-2.24E+00	0.00E+00	Down	-1.06E+00	2.49E-267	Down	1.48E-01	1.98E-07		1.02E-01	1.17E-05		-3.14E-01	1.30E-41		Unigene47360_All//gi|211906496|gb|ACJ11741.1|//0.00E+00//heat shock protein 70 [Gossypium hirsutum]	Unigene47360_All//5.00E-162//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene47360_All//0.00E+00//TC136616		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -
Unigene47362_All	1262	0.83	1.12	1.05	1.30	1.23	0.89	3.25	0.93	1.39	4.39E-01	4.25E-01		3.47E-01	5.78E-01		-8.52E-02	8.59E-01		-5.42E-01	3.16E-01		-1.81E+00	1.21E-09	Down	-1.23E+00	5.20E-06	Down	Unigene47362_All//gi|27447974|gb|AA013749.1|AF268257_1//2.00E-53//PTEN-like protein [Arabidopsis thaliana]	Unigene47362_All//4.00E-51//AT3G19420| ATPEN2 (ARABIDOPSIS THALIANA PTEN 2); phosphatase/ protein tyrosine phosphatase	Unigene47362_All//0.00E+00//TC161863		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr +
Unigene47363_All	2068	6.53	13.03	6.80	14.77	7.31	12.69	7.11	3.94	3.06	9.98E-01	7.32E-20		5.86E-02	7.22E-01		-1.01E+00	4.36E-28	Down	-2.19E-01	3.29E-02		-8.52E-01	1.16E-10		-1.22E+00	4.80E-19	Down	Unigene47363_All//gi|48310551|gb|AAT41837.1|//0.00E+00//At5g23850 [Arabidopsis thaliana]	Unigene47363_All//2.00E-173//AT5G23850| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Lipopolysaccharide-modifying protein (InterPro:IPR006598), Protein of unknown function DUF521, CAP10-like (InterPro:IPR008539); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48980.1); Has 588 Blast hits to 567 proteins in 103 species: Archae - 2; Bacteria - 34; Metazoa - 301; Fungi - 69; Plants - 115; Viruses - 3; Other Eukaryotes - 64 (source: NCBI BLink).	Unigene47363_All//0.00E+00//TC138450				nr +
Unigene47366_All	1167	3.59	2.95	3.42	39.57	33.31	38.31	9.24	8.88	4.51	-2.81E-01	3.60E-01		-6.77E-02	8.29E-01		-2.48E-01	9.02E-04		-4.65E-02	6.38E-01		-5.68E-02	7.50E-01		-1.04E+00	3.63E-11	Down			Unigene47366_All//0.00E+00//DN503626				
Unigene47369_All	1679	1.65	33.20	6.72	1.78	4.55	12.19	0.73	4.73	7.88	4.33E+00	2.28E-246	Up	2.03E+00	4.71E-23	Up	1.35E+00	8.48E-11	Up	2.78E+00	5.79E-66	Up	2.70E+00	7.01E-29	Up	3.43E+00	1.97E-61	Up	Unigene47369_All//gi|116008246|gb|ABJ51933.1|//0.00E+00//sucrose transporter 1 [Hevea brasiliensis]	Unigene47369_All//5.00E-168//AT1G22710| SUC2 (SUCROSE-PROTON SYMPORTER 2); carbohydrate transmembrane transporter/ sucrose transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter	Unigene47369_All//0.00E+00//EE593220				nr +
Unigene47372_All	1368	2.14	0.78	0.86	3.28	1.74	2.05	10.48	4.22	5.53	-1.46E+00	1.38E-04	Down	-1.32E+00	7.76E-04	Down	-9.16E-01	5.73E-04		-6.79E-01	1.69E-02		-1.31E+00	3.31E-20	Down	-9.21E-01	3.92E-12		Unigene47372_All//gi|24461865|gb|AAN62352.1|AF506028_19//1.00E-105//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene47372_All//3.00E-75//AT5G63020| disease resistance protein (CC-NBS-LRR class), putative	Unigene47372_All//0.00E+00//ES852122		ko04626|Plant-pathogen interaction		nr +
Unigene47375_All	1080	1.94	2.25	2.22	8.39	7.49	6.86	5.17	4.37	2.51	2.17E-01	5.93E-01		1.95E-01	6.29E-01		-1.64E-01	4.51E-01		-2.92E-01	1.56E-01		-2.41E-01	3.37E-01		-1.04E+00	2.89E-06	Down	Unigene47375_All//gi|224062371|ref|XP_002300824.1|//1.00E-136//homocysteine s-methyltransferase [Populus trichocarpa] >gi|222842550|gb|EEE80097.1| homocysteine s-methyltransferase [Populus trichocarpa]	Unigene47375_All//2.00E-128//AT3G63250| HMT2 (HOMOCYSTEINE METHYLTRANSFERASE 2); homocysteine S-methyltransferase	Unigene47375_All//0.00E+00//gi|78333788|gb|DT554062.1|DT554062		ko00270|Cysteine and methionine metabolism		nr +
Unigene47380_All	1607	55.71	79.65	100.20	21.14	36.00	43.87	1.18	0.34	0.52	5.16E-01	1.91E-29		8.47E-01	3.04E-85		7.68E-01	6.55E-32		1.05E+00	1.60E-59	Up	-1.81E+00	7.18E-05	Down	-1.19E+00	3.99E-03		Unigene47380_All//gi|297599681|ref|NP_001047583.2|//1.00E-133//Os02g0649400 [Oryza sativa Japonica Group] >gi|255671132|dbj|BAF09497.2| Os02g0649400 [Oryza sativa Japonica Group]	Unigene47380_All//3.00E-129//AT3G50790| late embryogenesis abundant protein, putative / LEA protein, putative	Unigene47380_All//0.00E+00//TC152765				nr +

Unigene47381_All	878	18.18	18.52	20.74	19.35	29.14	17.64	51.91	40.42	23.87	2.75E-02	8.59E-01		1.91E-01	1.95E-01		5.91E-01	3.24E-09		-1.33E-01	4.05E-01		-3.61E-01	2.55E-07		-1.12E+00	2.76E-50	Down	Unigene47381_All//gi|17978974|gb|AAL47448.1|//3.00E-50//At1g31940/F5M6.6 [Arabidopsis thaliana] >gi|20334862|gb|AAM16187.1|At1g31940/F5M6.6 [Arabidopsis thaliana]	Unigene47381_All//1.00E-47//AT1G31940| unknown protein	Unigene47381_All//0.00E+00//TC158347				nr -
Unigene47384_All	1408	108.36	34.08	95.27	195.40	174.84	68.39	9.85	4.63	3.51	-1.67E+00	1.14E-242	Down	-1.86E-01	1.68E-05		-1.60E-01	1.12E-08		-1.51E+00	0.00E+00	Down	-1.09E+00	9.32E-15	Down	-1.49E+00	2.97E-24	Down	Unigene47384_All//gi|297720249|ref|NP_001172486.1|//1.00E-116//0s01g0652800 [Oryza sativa Japonica Group] >gi|19571153|dbj|BAB86576.1| leaf senescence protein-like [Oryza sativa Japonica Group] >gi|20161502|dbj|BAB90425.1| leaf senescence protein-like [Oryza sativa Japonica Group] >gi|255673513|dbj|BAH91216.1|Os01g0652800 [Oryza sativa Japonica Group]	Unigene47384_All//3.00E-144//AT5G15900| unknown protein	Unigene47384_All//0.00E+00//TC135673				nr +
Unigene47385_All	1167	419.10	33.17	83.41	193.79	130.51	363.32	27.50	33.77	34.82	-3.66E+00	0.00E+00	Down	-2.33E+00	0.00E+00	Down	-5.70E-01	1.57E-75		9.07E-01	4.20E-278		2.97E-01	1.07E-04		3.41E-01	3.28E-06		Unigene47385_All//gi|21314553|gb|AAM47002.1|AF512544_1/1.00E-137//alpha-expansin precursor [Gossypium hirsutum]	Unigene47385_All//3.00E-123//AT1G26770| ATEXPA10 (ARABIDOPSIS THALIANA EXPANSIN A 10); structural constituent of cell wall	Unigene47385_All//0.00E+00//TC136518				nr +
Unigene47387_All	1940	4.85	12.07	4.39	7.57	8.01	8.50	11.20	11.14	13.41	1.31E+00	1.66E-26	Up	-1.45E-01	5.05E-01		7.97E-02	6.42E-01		1.66E-01	3.00E-01		-8.20E-03	9.77E-01		2.60E-01	6.33E-03		Unigene47387_All//gi|108711913|gb|ABF99708.1|//6.00E-89//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene47387_All//7.00E-90//AT4G16100| unknown protein	Unigene47387_All//0.00E+00//TC150310				nr +
Unigene47388_All	710	0.66	0.00	0.00	7.65	5.43	7.32	24.71	5.18	12.23	-9.37E+00	5.55E-03		-9.37E+00	8.63E-03		-4.94E-01	4.72E-02		-6.41E-02	8.23E-01		-2.25E+00	1.81E-51	Down	-1.01E+00	4.71E-17	Down	Unigene47388_All//gi|6983690|emb|CAB75356.1|//1.00E-89//AE9 stearoyl-ACP desaturase [Gossypium hirsutum]	Unigene47388_All//2.00E-75//AT2G43710| SSI2; acyl-[acyl-carrier-protein] desaturase/ stearoyl-CoA 9-desaturase	Unigene47388_All//0.00E+00//gi|164267952|gb|ES796299.1|ES796299		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis		nr -
Unigene47389_All	1012	79.67	61.99	82.51	126.31	128.42	285.17	186.33	217.07	187.62	-3.62E-01	3.38E-10		5.05E-02	4.70E-01		2.39E-02	6.99E-01		1.17E+00	2.93E-289	Up	2.20E-01	4.74E-13		9.90E-03	8.07E-01		Unigene47389_All//gi|6983690|emb|CAB75356.1|//1.00E-128//AE9 stearoyl-ACP desaturase [Gossypium hirsutum]	Unigene47389_All//1.00E-105//AT2G43710| SSI2; acyl-[acyl-carrier-protein] desaturase/ stearoyl-CoA 9-desaturase	Unigene47389_All//0.00E+00//TC134210		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis		nr -
Unigene4739_All	1058	40.11	13.36	12.43	9.70	7.36	9.14	4.36	14.77	3.05	-1.59E+00	4.14E-63	Down	-1.69E+00	1.07E-66	Down	-3.99E-01	2.13E-02		-8.64E-02	6.93E-01		1.76E+00	2.36E-33	Up	-5.14E-01	3.48E-02		Unigene4739_All//gi|28950899|gb|AA063373.1|//5.00E-57//At2g27770 [Arabidopsis thaliana]	Unigene4739_All//3.00E-58//AT2G27770| unknown protein	Unigene4739_All//0.00E+00//TC178015				nr +
Unigene47390_All	665	2.44	3.05	1.60	3.82	5.18	3.80	1.40	4.34	5.27	3.22E-01	4.89E-01		-6.07E-01	2.61E-01		4.39E-01	2.12E-01		-6.50E-03	9.82E-01		1.63E+00	3.70E-06	Up	1.91E+00	3.68E-09	Up	Unigene47390_All//gi|255573054|ref|XP_002527457.1|//4.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223533192|gb|EEF34949.1| conserved hypothetical protein [Ricinus communis]	Unigene47390_All//9.00E-07//AT3G03272| Encodes a ECA1 gametogenesis related family protein					nr +
Unigene47391_All	1445	2.50	1.51	2.87	3.55	5.48	4.97	0.91	3.44	1.43	-7.29E-01	2.42E-02		2.02E-01	5.45E-01		6.26E-01	1.51E-03		4.85E-01	2.87E-02		1.92E+00	1.94E-12	Up	6.61E-01	8.87E-02		Unigene47391_All//gi|255573054|ref|XP_002527457.1|//1.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223533192|gb|EEF34949.1| conserved hypothetical protein [Ricinus communis]	Unigene47391_All//3.00E-06//AT3G03272| Encodes a ECA1 gametogenesis related family protein					nr +
Unigene47392_All	2123	0.71	1.55	2.41	5.07	4.09	14.08	2.35	8.23	30.32	1.12E+00	1.30E-03		1.75E+00	6.06E-09	Up	-3.10E-01	7.79E-02		1.47E+00	8.75E-43	Up	1.81E+00	1.64E-38	Up	3.69E+00	0.00E+00	Up	Unigene47392_All//gi|66271061|gb|AY438068.1|//3.00E-13//Pb17 [Gossypium hirsutum]		Unigene47392_All//0.00E+00//TC140728				nr +
Unigene47396_All	1034	128.78	309.11	165.93	37.48	49.92	42.89	45.63	106.11	65.88	1.26E+00	0.00E+00	Up	3.66E-01	2.26E-20		4.14E-01	1.07E-09		1.95E-01	2.01E-02		1.22E+00	1.16E-132	Up	5.30E-01	4.88E-21		Unigene47396_All//gi|222423754|dbj|BAH19843.1|//6.00E-79//AT1G75180 [Arabidopsis thaliana]	Unigene47396_All//2.00E-63//AT1G75180| unknown protein	Unigene47396_All//0.00E+00//TC133306				nr +
Unigene47397_All	2727	11.72	5.83	7.36	19.93	16.14	12.26	14.03	11.88	4.82	-1.01E+00	7.73E-24	Down	-6.71E-01	9.32E-12		-3.04E-01	4.45E-06		-7.01E-01	1.51E-23		-2.40E-01	2.39E-03		-1.54E+00	9.24E-69	Down	Unigene47397_All//gi|57168303|gb|AAW38935.1|//0.00E+00//AvrPto-dependent Pto-interacting protein 3 [Solanum lycopersicum]	Unigene47397_All//0.00E+00//AT2G44830| protein kinase, putative	Unigene47397_All//0.00E+00//TC166615				nr +
Unigene47398_All	1143	141.49	58.87	150.11	71.95	73.90	45.01	7.14	8.70	2.44	-1.27E+00	6.14E-170	Down	8.53E-02	5.45E-02		3.85E-02	6.05E-01		-6.77E-01	3.07E-33		2.86E-01	9.48E-02		-1.55E+00	1.89E-15	Down	Unigene47398_All//gi|297795877|ref|XP_002865823.1|//1.00E-83//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311658|gb|EFH42082.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47398_All//2.00E-77//AT5G50790| nodulin MtN3 family protein	Unigene47398_All//0.00E+00//TC132705				nr +
Unigene47399_All	811	37.42	15.49	20.49	57.74	44.20	42.66	62.40	24.02	23.24	-1.27E+00	1.11E-32	Down	-8.69E-01	3.73E-17		-3.85E-01	5.56E-08		-4.37E-01	5.30E-09		-1.38E+00	1.41E-74	Down	-1.43E+00	8.87E-81	Down	Unigene47399_All//gi|78191458|gb|ABB29950.1|//2.00E-91//succinyl-CoA ligase alpha I subunit-like [Solanum tuberosum]	Unigene47399_All//1.00E-80//AT5G23250| succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative	Unigene47399_All//0.00E+00//TC131503		ko00020|Citrate cycle (TCA cycle)//ko00640|Propanoate metabolism		nr -
Unigene4740_All	1418	2.18	3.50	1.43	3.48	4.78	8.89	4.38	1.56	4.21	6.86E-01	1.09E-02		-6.09E-01	1.03E-01		4.60E-01	4.11E-02		1.35E+00	3.60E-16	Up	-1.49E+00	5.81E-11	Down	-5.67E-02	7.99E-01		Unigene4740_All//gi|57222120|gb|AAW38967.1|//1.00E-143//At5g65140 [Arabidopsis thaliana] >gi|57222226|gb|AAW39020.1|At5g65140 [Arabidopsis thaliana] >gi|62320350|dbj|BAD94722.1| trehalose-6-phosphate phosphatase [Arabidopsis thaliana]	Unigene4740_All//4.00E-144//AT5G65140| trehalose-6-phosphate phosphatase, putative	Unigene4740_All//0.00E+00//TC135974		ko00500|Starch and sucrose metabolism		nr -
Unigene47401_All	1836	1.37	0.58	0.58	2.79	1.69	1.87	5.90	2.62	3.15	-1.24E+00	2.46E-03		-1.24E+00	3.81E-03		-7.27E-01	3.30E-03		-5.80E-01	2.88E-02		-1.17E+00	4.77E-13	Down	-9.06E-01	3.79E-09		Unigene47401_All//gi|15237943|ref|NP_197229.1|//0.00E+00//tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	Unigene47401_All//0.00E+00//AT5G17270| tetratricopeptide repeat (TPR)-containing protein	Unigene47401_All//0.00E+00//TC145404				nr -
Unigene47403_All	1061	9.91	19.96	17.82	9.91	12.95	9.28	1.91	1.14	2.10	1.01E+00	4.48E-16	Up	8.46E-01	1.75E-10		3.87E-01	9.23E-03		-9.43E-02	6.55E-01		-7.44E-01	6.77E-02		1.37E-01	7.19E-01		Unigene47403_All//gi|7682789|gb|AAF67369.1|//5.00E-24//Hypothetical protein T15F17.a [Arabidopsis thaliana]		Unigene47403_All//1.00E-114//TC135287				nr +
Unigene47404_All	822	5.60	11.53	13.02	14.54	10.56	6.70	3.81	5.19	3.05	1.04E+00	5.68E-08	Up	1.22E+00	9.08E-11	Up	-4.62E-01	2.85E-03		-1.12E+00	1.06E-11	Down	4.46E-01	9.80E-02		-3.18E-01	3.21E-01		Unigene47404_All//gi|115473321|ref|NP_001060259.1|//4.00E-09//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene47404_All//2.00E-65//AT3G25270| nucleic acid binding	Unigene47404_All//5.00E-101//TC163297				nr +
Unigene47406_All	1907	9.60	2.15	1.79	16.06	9.70	3.29	19.18	0.15	8.96	-2.16E+00	1.14E-41	Down	-2.43E+00	3.57E-46	Down	-7.28E-01	4.04E-16		-2.29E+00	4.55E-81	Down	-6.97E+00	1.95E-246	Down	-1.10E+00	3.43E-39	Down	Unigene47406_All//gi|297820612|ref|XP_002878189.1|//2.00E-88//bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324027|gb|EFH54448.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47406_All//1.00E-74//AT2G42380| bZIP transcription factor family protein	Unigene47406_All//0.00E+00//TC132107	bZIP			nr -
Unigene47407_All	1490	2.63	1.80	1.07	6.32	5.08	8.58	15.01	8.36	8.40	-5.47E-01	7.77E-02		-1.30E+00	9.35E-05	Down	-3.14E-01	1.01E-01		4.41E-01	5.24E-03		-8.45E-01	1.51E-15		-8.38E-01	7.69E-16		Unigene47407_All//gi|140052431|gb|ABE38131.2|//7.00E-57//HMG-I and HMG-Y, DNA-binding [Medicago truncatula]	Unigene47407_All//1.00E-47//AT4G12080| DNA-binding family protein	Unigene47407_All//0.00E+00//gi|78340548|gb|DT560822.1|DT560822				nr +
Unigene47410_All	511	15.87	12.79	12.09	13.45	13.28	5.30	3.72	2.70	3.27	-3.11E-01	1.38E-01		-3.93E-01	7.20E-02		-1.92E-02	9.45E-01		-1.34E+00	3.96E-09	Down	-4.64E-01	2.90E-01		-1.85E-01	6.46E-01		Unigene47410_All//gi|115463777|ref|NP_001055488.1|//2.00E-11//Os05g0401300 [Oryza sativa Japonica Group] >gi|113579039|dbj|BAF17402.1|Os05g0401300 [Oryza sativa Japonica Group]	Unigene47410_All//2.00E-10//AT5G27390| LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Mog1/PsbP/DUF1795, alpha/beta/alpha sandwich (InterPro:IPR016124); Has 11 Blast hits to 11 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene47410_All//5.00E-72//C0123311				nr -
Unigene47411_All	1203	42.10	26.75	39.09	20.37	16.14	8.33	5.17	2.95	4.17	-6.55E-01	3.16E-18		-1.07E-01	2.25E-01		-3.36E-01	1.35E-03		-1.29E+00	3.29E-29	Down	-8.07E-01	1.33E-04		-3.08E-01	1.49E-01		Unigene47411_All//gi|115463777|ref|NP_001055488.1|//3.00E-67//Os05g0401300 [Oryza sativa Japonica Group] >gi|113579039|dbj|BAF17402.1|Os05g0401300 [Oryza sativa Japonica Group]	Unigene47411_All//3.00E-72//AT5G27390| LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Mog1/PsbP/DUF1795, alpha/beta/alpha sandwich (InterPro:IPR016124); Has 11 Blast hits to 11 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene47411_All//0.00E+00//C0101457				nr -
Unigene47412_All	1147	17.61	5.96	13.46	12.94	14.20	10.91	2.14	1.86	1.46	-1.56E+00	9.88E-30	Down	-3.87E-01	2.53E-03		1.34E-01	4.16E-01		-2.47E-01	1.16E-01		-2.02E-01	6.35E-01		-5.52E-01	1.15E-01		Unigene47412_All//gi|30696750|ref|NP_176463.2|//1.00E-07//invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana] >gi|6630459|gb|AAF19547.1|AC007190_15 F22N19.12 [Arabidopsis thaliana]		Unigene47412_All//0.00E+00//TC162724				nr +
Unigene47415_All	206	1.52	1.23	4.14	3.87	2.34	4.38	3.90	11.77	0.77	-3.09E-01	7.89E-01		1.44E+00	8.22E-02		-7.25E-01	3.46E-01		1.81E-01	8.07E-01		1.59E+00	3.82E-05	Up	-2.33E+00	2.82E-03		Unigene47415_All//gi|18397705|ref|NP_564367.1|//5.00E-22//integral membrane HRF1 family protein [Arabidopsis thaliana] >gi|145324088|ref|NP_001077633.1| integral membrane HRF1 family protein [Arabidopsis thaliana]	Unigene47415_All//2.00E-23//AT1G30890| integral membrane HRF1 family protein	Unigene47415_All//2.00E-103//TC173933				nr +
Unigene47417_All	1687	19.17	6.40	12.69	5.64	6.41	4.85	5.94	2.23	2.74	-1.58E+00	4.01E-48	Down	-5.95E-01	1.02E-09		1.85E-01	3.48E-01		-2.19E-01	3.01E-01		-1.41E+00	5.64E-16	Down	-1.12E+00	1.11E-11	Down	Unigene47417_All//gi|42562778|ref|NP_176001.2|//0.00E+00//GTP-binding protein-related [Arabidopsis thaliana]	Unigene47417_All//2.00E-177//AT1G56050| GTP-binding protein-related	Unigene47417_All//0.00E+00//TC160555				nr -
Unigene4742_All	1036	61.26	3.37	12.95	67.36	18.78	11.64	34.12	9.96	17.50	-4.18E+00	3.79E-277	Down	-2.24E+00	4.94E-145	Down	-1.84E+00	8.65E-161	Down	-2.53E+00	2.43E-208	Down	-1.78E+00	1.94E-75	Down	-9.64E-01	9.18E-31		Unigene4742_All//gi|9650828|emb|CAC00658.1|//2.00E-39//common plant regulatory factor 7 [Petroselinum crispum]	Unigene4742_All//9.00E-32//AT4G34590| GBF6 (G-BOX BINDING FACTOR 6); DNA binding / protein heterodimerization/ transcription factor	Unigene4742_All//0.00E+00//gi|164336044|gb|ES806243.1|ES806243	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene47426_All	294	0.53	1.38	1.27	1.02	0.59	1.69	3.60	7.96	10.30	1.37E+00	2.74E-01		1.25E+00	3.66E-01		-7.96E-01	5.57E-01		7.33E-01	5.16E-01		1.15E+00	2.37E-03		1.52E+00	4.79E-06	Up									
Unigene47427_All	2066	6.00	9.61	7.22	7.98	12.82	9.40	12.14	32.11	83.09	6.80E-01	4.37E-08		2.66E-01	9.30E-02		6.84E-01	3.61E-12		2.36E-01	7.76E-02		1.40E+00	4.01E-100	Up	2.78E+00	0.00E+00	Up	Unigene47427_All//gi|224082190|ref|XP_002306596.1|//1.00E-179//f-box family protein [Populus trichocarpa]	Unigene47427_All//5.00E-167//AT1G22040| kelch repeat-containing F-box family protein	Unigene47427_All//0.00E+00//DW496633				nr +

Unigene47428_All	1971	0.21	0.77	0.89	0.38	0.38	0.30	1.33	2.78	4.87	1.86E+00	1.61E-03		2.07E+00	3.29E-04	Up	2.00E-02	1.00E+00		-3.48E-01	6.84E-01		1.06E+00	4.34E-06	Up	1.87E+00	5.02E-23	Up	Unigene47428_All//gi|224082190|ref|XP_002306596.1|//1.00E-179//f-box family protein [Populus trichocarpa] >gi|222856045|gb|EEE93592.1| f-box family protein [Populus trichocarpa]	Unigene47428_All//4.00E-167//AT1G22040| kelch repeat-containing F-box family protein	Unigene47428_All//0.00E+00//DW496633				nr +
Unigene4743_All	1120	7.52	4.12	3.52	3.02	3.01	1.94	5.55	0.97	1.28	-8.69E-01	1.48E-05		-1.10E+00	2.24E-07	Down	-5.40E-03	9.77E-01		-6.44E-01	5.76E-02		-2.52E+00	3.48E-21	Down	-2.12E+00	6.55E-18	Down	Unigene4743_All//gi|16648746|gb|AAL25565.1|//5.00E-80//AT5g19750/T29J13_170 [Arabidopsis thaliana] >gi|24111335|gb|AAN46791.1| At5g19750/T29J13_170 [Arabidopsis thaliana]	Unigene4743_All//3.00E-57//AT5G19750| peroxisomal membrane 22 kDa family protein	Unigene4743_All//0.00E+00//TC139644		ko04146|Peroxisome		nr -
Unigene47430_All	1099	3.48	4.79	3.78	4.71	5.33	4.85	2.31	3.99	5.11	4.64E-01	7.74E-02		1.21E-01	7.01E-01		1.76E-01	5.66E-01		4.08E-02	9.04E-01		7.91E-01	2.15E-03		1.15E+00	3.85E-07	Up	Unigene47430_All//gi|124359978|gb|ABN07994.1|//2.00E-52//Protein kinase [Medicago truncatula]	Unigene47430_All//3.00E-40//AT3G57090| BIOTIN; binding	Unigene47430_All//0.00E+00//ES822974				nr +
Unigene47431_All	1429	10.22	4.68	5.66	7.67	7.64	6.42	4.38	2.52	2.51	-1.13E+00	2.06E-13	Down	-8.51E-01	2.63E-08		-5.70E-03	9.69E-01		-2.57E-01	1.69E-01		-8.00E-01	1.43E-04		-8.03E-01	8.81E-05		Unigene47431_All//gi|115459540|ref|NP_001053370.1|//4.00E-66//Os04g0527800 [Oryza sativa Japonica Group] >gi|38344450|emb|CAE05656.2| OSJNBa0038010.22 [Oryza sativa (japonica cultivar-group)] >gi|113564941|dbj|BAF15284.1| Os04g0527800 [Oryza sativa Japonica Group] >gi|116310971|emb|CAH67907.1| OSIGBa0115K01-H0319F09.13 [Oryza sativa (indica cultivar-group)]	Unigene47431_All//5.00E-67//AT5G08540| unknown protein	Unigene47431_All//0.00E+00//TC161114				nr -
Unigene47435_All	1483	8.47	2.97	7.18	6.79	5.92	7.67	1.48	0.68	2.63	-1.51E+00	6.84E-18	Down	-2.38E-01	1.80E-01		-1.97E-01	3.17E-01		1.78E-01	3.73E-01		-1.13E+00	3.71E-03		8.29E-01	2.02E-03		Unigene47435_All//gi|42573594|ref|NP_974893.1|//1.00E-137//peptidase S41 family protein [Arabidopsis thaliana]	Unigene47435_All//3.00E-127//AT5G46390| peptidase S41 family protein	Unigene47435_All//0.00E+00//CO111749				nr +
Unigene47436_All	1892	2.18	1.53	1.01	10.53	9.23	10.03	9.05	18.36	22.28	-5.17E-01	8.53E-02		-1.11E+00	4.70E-04	Down	-1.91E-01	1.51E-01		-7.10E-02	6.38E-01		1.02E+00	3.53E-32	Up	1.30E+00	4.07E-58	Up	Unigene47436_All//gi|297851244|ref|XP_002893503.1|//3.00E-99//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339345|gb|EFH69762.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47436_All//2.00E-89//AT2G33500| zinc finger (B-box type) family protein	Unigene47436_All//0.00E+00//gi|78346602|gb|DT566876.1|DT566876	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr -
Unigene47437_All	1775	1.18	1.60	1.20	19.14	16.12	13.89	7.00	1.93	1.80	4.39E-01	2.43E-01		2.53E-02	9.74E-01		-2.48E-01	5.98E-03		-4.62E-01	2.20E-07		-1.86E+00	1.03E-28	Down	-1.96E+00	7.69E-32	Down	Unigene47437_All//gi|15228789|ref|NP_191158.1|//0.00E+00//ESK1 (ESKIMO 1) [Arabidopsis thaliana]	Unigene47437_All//8.00E-158//AT2G40150| INVOLVED IN: biological_process unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF231, plant (InterPro:IPR004253); BEST Arabidopsis thaliana protein match is: ESK1 (ESKIMO 1) (TAIR:AT3G55990.1); Has 712 Blast hits to 693 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 712; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene47437_All//2.00E-65//ES795179				nr -
Unigene47439_All	1417	9.23	20.88	9.13	13.11	9.60	6.09	5.64	5.34	4.41	1.18E+00	3.38E-28	Up	-1.56E-02	9.45E-01		-4.50E-01	1.64E-04		-1.11E+00	1.35E-17	Down	-7.90E-02	7.09E-01		-3.53E-01	5.20E-02		Unigene47439_All//gi|115441063|ref|NP_001044811.1|//1.00E-46//Os01g0850000 [Oryza sativa Japonica Group] >gi|113534342|dbj|BAF06725.1| Os01g0850000 [Oryza sativa Japonica Group]	Unigene47439_All//3.00E-33//AT3G54000| unknown protein	Unigene47439_All//0.00E+00//TC136406				nr -
Unigene47443_All	1767	26.92	12.10	21.52	14.97	15.06	15.08	10.67	2.55	6.40	-1.15E+00	1.25E-43	Down	-3.23E-01	5.10E-05		9.10E-03	9.61E-01		1.06E-02	9.50E-01		-2.06E+00	1.80E-49	Down	-7.37E-01	5.53E-11		Unigene47443_All//gi|15221516|ref|NP_176448.1|//0.00E+00//flavin-containing monooxygenase family protein / FMO family protein [Arabidopsis thaliana] >gi|145324274|gb|AAK63965.1| At1g62600/T3P18_16 [Arabidopsis thaliana] >gi|23308211|gb|AAN18075.1| At1g62600/T3P18_16 [Arabidopsis thaliana]	Unigene47443_All//2.00E-171//AT1G62600| flavin-containing monooxygenase family protein / FMO family protein	Unigene47443_All//0.00E+00//TC131243		ko00380|Tryptophan metabolism		nr -
Unigene47444_All	2110	3.52	3.03	3.36	14.47	13.73	17.04	2.32	0.97	0.70	-2.19E-01	3.48E-01		-6.91E-02	7.66E-01		-7.64E-02	5.43E-01		2.36E-01	1.05E-02		-1.26E+00	5.09E-07	Down	-1.73E+00	3.64E-11	Down	Unigene47444_All//gi|115463731|ref|NP_001055165.1|//1.00E-171//Os05g0396900 [Oryza sativa Japonica Group] >gi|113579016|dbj|BAF17379.1| Os05g0396900 [Oryza sativa Japonica Group]	Unigene47444_All//0.00E+00//AT3G06150| unknown protein	Unigene47444_All//0.00E+00//TC178371				nr -
Unigene47445_All	1416	3.70	6.55	7.48	9.57	9.56	14.13	7.11	2.92	21.24	8.26E-01	1.42E-05		1.02E+00	3.58E-08	Up	-1.80E-03	9.88E-01		5.62E-01	2.79E-06		-1.28E+00	6.33E-14	Down	1.58E+00	1.29E-55	Up	Unigene47445_All//gi|42573822|ref|NP_975007.1|//1.00E-123//BT4 (BTB AND TAZ DOMAIN PROTEIN 4); protein binding / transcription regulator [Arabidopsis thaliana]	Unigene47445_All//3.00E-124//AT5G67480| BT4 (BTB AND TAZ DOMAIN PROTEIN 4); protein binding / transcription regulator	Unigene47445_All//0.00E+00//TC158001	TAZ	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene47446_All	1426	0.22	0.00	0.78	0.24	0.65	0.44	1.04	0.41	2.29	-7.78E+00	3.65E-02		1.83E+00	1.24E-02		1.42E+00	6.25E-02		8.59E-01	3.90E-01		-1.34E+00	7.48E-03		1.14E+00	1.73E-04	Up	Unigene47446_All//gi|42573822|ref|NP_975007.1|//1.00E-135//BT4 (BTB AND TAZ DOMAIN PROTEIN 4); protein binding / transcription regulator [Arabidopsis thaliana]	Unigene47446_All//1.00E-129//AT5G67480| BT4 (BTB AND TAZ DOMAIN PROTEIN 4); protein binding / transcription regulator	Unigene47446_All//0.00E+00//TC158001	TAZ	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene47447_All	1709	2.82	5.84	2.96	2.86	2.16	2.70	8.46	15.90	13.80	1.05E+00	1.73E-08	Up	7.17E-02	7.97E-01		-4.06E-01	1.40E-01		-8.37E-02	7.77E-01		9.10E-01	4.34E-21		7.06E-01	1.58E-12		Unigene47447_All//gi|297814846|ref|XP_002875306.1|//1.00E-170//regulator of G-protein signaling 1 [Arabidopsis lyrata subsp. lyrata] >gi|297321144|gb|EFH51565.1| regulator of G-protein signaling 1 [Arabidopsis lyrata subsp. lyrata]	Unigene47447_All//4.00E-171//AT3G26090| RGS1 (REGULATOR OF G-PROTEIN SIGNALING 1); G-protein coupled receptor	Unigene47447_All//0.00E+00//TC169006				nr -
Unigene47449_All	742	64.52	30.18	38.75	116.28	84.97	146.87	126.61	61.91	53.64	-1.10E+00	1.66E-40	Down	-7.35E-01	3.40E-20		-4.53E-01	4.37E-19		3.37E-01	1.41E-12		-1.03E+00	1.88E-87	Down	-1.24E+00	2.16E-120	Down	Unigene47449_All//gi|192913036|gb|ACF06626.1|//1.00E-122//S6 ribosomal protein [Elaeis guineensis]	Unigene47449_All//8.00E-95//AT5G10360| EMB3010 (embryo defective 3010); structural constituent of ribosome	Unigene47449_All//0.00E+00//gi|78344766|gb|DT565040.1|DT565040		ko03010|Ribosome		nr +
Unigene4745_All	856	11.74	30.54	19.97	12.16	19.11	31.50	18.72	52.54	40.77	1.38E+00	8.82E-32	Up	7.67E-01	3.60E-08		6.52E-01	3.95E-07		1.37E+00	9.35E-35	Up	1.49E+00	2.41E-74	Up	1.12E+00	1.61E-38	Up	Unigene4745_All//gi|224129190|ref|XP_002320523.1|//5.00E-10//predicted protein [Populus trichocarpa] >gi|222861296|gb|EEE98838.1| predicted protein [Populus trichocarpa]						nr -
Unigene47452_All	856	50.98	24.92	25.75	127.85	86.01	89.69	96.27	48.34	26.20	-1.03E+00	1.29E-33	Down	-9.85E-01	5.31E-30		-5.72E-01	7.31E-37		-5.11E-01	8.11E-27		-9.94E-01	3.48E-72		-1.88E+00	1.66E-194	Down	Unigene47452_All//gi|163930028|dbj|BAF95902.1|//1.00E-109//protein disulfide isomerase family [Glycine max] >gi|163930094|dbj|BAD42856.2| protein disulfide isomerse like protein [Glycine max]	Unigene47452_All//1.00E-99//AT1G04980| ATPDIL2-2 (PDI-LIKE 2-2); protein disulfide isomerase	Unigene47452_All//0.00E+00//TC132570		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene47453_All	1659	9.18	2.20	3.66	15.19	8.36	6.37	4.79	0.78	1.25	-2.06E+00	8.23E-33	Down	-1.33E+00	4.37E-17	Down	-8.61E-01	1.04E-17		-1.25E+00	9.14E-29	Down	-2.62E+00	4.28E-28	Down	-1.94E+00	2.42E-20	Down	Unigene47453_All//gi|21911135|gb|AAB61022.1|//1.00E-130//A_IG002N01.14 gene product [Arabidopsis thaliana] >gi|51608852|gb|AAV34774.1| At4g01080 [Arabidopsis thaliana]	Unigene47453_All//4.00E-134//AT1G01430| unknown protein	Unigene47453_All//0.00E+00//TC138597				nr -
Unigene47457_All	1281	8.70	11.35	6.90	13.26	31.88	36.49	18.62	52.07	179.35	3.84E-01	9.86E-03		-3.34E-01	6.90E-02		1.27E+00	7.59E-51	Up	1.46E+00	1.00E-65	Up	1.48E+00	2.03E-109	Up	3.27E+00	0.00E+00	Up	Unigene47457_All//gi|57117314|gb|AW33880.1|//1.00E-67//RING-H2 subgroup RHE protein [Populus tremula x Populus alba]	Unigene47457_All//9.00E-51//AT3G16720| ATL2; protein binding / zinc ion binding	Unigene47457_All//0.00E+00//gi|78340883|gb|DT561157.1|DT561157				nr -
Unigene4746_All	1011	134.40	208.94	143.21	34.34	73.50	42.89	0.04	0.25	0.32	6.37E-01	5.51E-70		9.16E-02	5.86E-02		1.10E+00	5.83E-74	Up	3.21E-01	5.52E-05		2.57E+00	1.53E-01		2.91E+00	5.99E-02		Unigene4746_All//gi|41323976|gb|AAS00054.1|//1.00E-109//CONSTANS-like protein CO1 [Populus deltoides]	Unigene4746_All//1.00E-59//AT5G15840| CO (CONSTANS); transcription factor/ transcription regulator/ zinc ion binding	Unigene4746_All//0.00E+00//gi|164296370|gb|EX168210.1|EX168210	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr -
Unigene47460_All	1049	24.94	58.01	38.99	53.04	45.37	68.54	51.67	80.64	33.95	1.22E+00	2.33E-60	Up	6.45E-01	6.73E-14		-2.26E-01	8.94E-04		3.70E-01	5.19E-10		6.42E-01	2.46E-35		-6.06E-01	2.18E-21		Unigene47460_All//gi|15218575|ref|NP_175056.1|//1.00E-101//ATRAB18 (ARABIDOPSIS RAB GTPASE HOMOLOG B18); GTP binding [Arabidopsis thaliana] >gi|145324172|ref|NP_001077675.1| ATRAB18 (ARABIDOPSIS RAB GTPASE HOMOLOG B18); GTP binding [Arabidopsis thaliana] >gi|186488925|ref|NP_001117435.1| ATRAB18 (ARABIDOPSIS RAB GTPASE HOMOLOG B18); GTP binding [Arabidopsis thaliana] >gi|7523663|gb|AAF63103.1|AC006423_4 AtRab18 [Arabidopsis thaliana] >gi|2231312|gb|AAB61997.1| AtRab18 [Arabidopsis thaliana]	Unigene47460_All//4.00E-102//AT1G43890| ATRAB18 (ARABIDOPSIS RAB GTPASE HOMOLOG B18); GTP binding	Unigene47460_All//0.00E+00//TC132652				nr -
Unigene47461_All	775	43.88	31.19	20.34	18.32	12.44	11.13	5.40	6.63	3.50	-4.93E-01	8.05E-08		-1.11E+00	1.97E-28	Down	-5.58E-01	4.93E-05		-7.19E-01	7.00E-07		2.97E-01	2.39E-01		-6.28E-01	1.41E-02		Unigene47461_All//gi|115480279|ref|NP_001063733.1|//2.00E-18//Os09g0527900 [Oryza sativa Japonica Group] >gi|113631966|dbj|BAF25647.1| Os09g0527900 [Oryza sativa Japonica Group]	Unigene47461_All//3.00E-10//AT4G38960| zinc finger (B-box type) family protein	Unigene47461_All//0.00E+00//TC142376	Orphans			nr -
Unigene47462_All	2090	19.40	8.85	11.75	19.16	14.14	14.46	10.36	5.00	9.78	-1.13E+00	2.98E-36	Down	-7.24E-01	9.39E-17		-4.39E-01	1.20E-08		-4.07E-01	6.50E-07		-1.05E+00	2.32E-21	Down	-8.30E-02	4.96E-01		Unigene47462_All//gi|224125528|ref|XP_002329827.1|//1.00E-110//f-box family protein [Populus trichocarpa] >gi|222870889|gb|EEF08020.1| f-box family protein [Populus trichocarpa]	Unigene47462_All//2.00E-48//AT1G28310| Dof-type zinc finger domain-containing protein	Unigene47462_All//0.00E+00//TC152631	C2C2-Dof			nr +
Unigene47465_All	994	17.58	11.06	9.64	41.80	33.81	37.12	9.40	5.72	3.81	-6.68E-01	4.79E-07		-8.66E-01	4.25E-10		-3.06E-01	7.93E-05		-1.71E-01	5.38E-02		-7.17E-01	1.86E-05		-1.30E+00	9.51E-14	Down			Unigene47465_All//2.00E-134//gi|73851353|gb|DT460373.1|DT460373				

Unigene47466_All	1239	2.15	1.80	1.98	3.30	1.56	2.62	3.51	1.89	1.64	-2.59E-01	5.18E-01		-1.23E-01	7.50E-01		-1.08E+00	1.20E-04	Down	-3.29E-01	3.18E-01		-8.96E-01	5.53E-04		-1.10E+00	1.84E-05	Down	Unigene47466_All//gi|122230198|sp|Q0WVU0.1|PP278_ARATH//2.00E-64//RecName: Full=Pentatricopeptide repeat-containing protein At3g51320	Unigene47466_All//1.00E-65//AT3G51320| INVOLVED IN: biological_process unknown; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: binding (TAIR:AT3G62890.1); Has 12158 Blast hits to 4373 proteins in 95 species: Archae - 0; Bacteria - 0; Metazoa - 23; Fungi - 18; Plants - 12009; Viruses - 0; Other Eukaryotes - 108 (source: NCBI BLink).	Unigene47466_All//0.00E+00//TC136823				nr +
Unigene47468_All	2144	1.83	1.28	0.87	2.32	1.24	0.88	4.40	2.30	1.77	-5.20E-01	9.36E-02		-1.07E+00	9.77E-04	Down	-9.10E-01	2.71E-04		-1.39E+00	3.84E-07	Down	-9.35E-01	3.45E-08		-1.32E+00	4.59E-14	Down	Unigene47468_All//gi|30687514|ref|NP_850630.1|//0.00E+00//MSH7 (MUTS HOMOLOG 7); ATP binding / damaged DNA binding / mismatched DNA binding [Arabidopsis thaliana] >gi|126438489|sp|Q9SM97.1|MSH7_ARATH RecName: Full=DNA mismatch repair protein Msh6-2; Short=AtMsh6-2; AltName: Full=MutS homolog 7 >gi|3757550|emb|CAA07685.1| Msh6-2 protein [Arabidopsis thaliana] >gi|9294039|dbj|BAB01996.1| DNA repair protein MutS [Arabidopsis thaliana]	Unigene47468_All//0.00E+00//AT3G24495| MSH7 (MUTS HOMOLOG 7); ATP binding / damaged DNA binding / mismatched DNA binding	Unigene47468_All//3.00E-117//DT049355		ko03430|Mismatch repair		nr -
Unigene47471_All	1715	9.15	14.60	15.18	8.10	7.47	9.14	25.94	4.58	9.01	6.73E-01	7.99E-10		7.30E-01	3.70E-11		-1.18E-01	5.24E-01		1.73E-01	2.89E-01		-2.50E+00	1.46E-146	Down	-1.52E+00	1.49E-78	Down	Unigene47471_All//gi|260401276|gb|ACX37118.1|//0.00E+00//MATE transporter [Medicago truncatula]	Unigene47471_All//0.00E+00//AT3G59030| TT12 (TRANSPARENT TESTA 12): antiporter/ solute:hydrogen antiporter/ transmembrane transporter/ transporter	Unigene47471_All//0.00E+00//TC132535				nr -
Unigene47474_All	1989	9.39	9.07	8.14	6.56	7.24	6.79	16.73	6.05	7.61	-5.03E-02	7.20E-01		-2.06E-01	1.45E-01		1.41E-01	4.20E-01		4.92E-02	7.87E-01		-1.47E+00	4.06E-54	Down	-1.14E+00	9.64E-38	Down	Unigene47474_All//gi|300507131|gb|ADK23941.1|//0.00E+00//KASIII [Gossypium hirsutum]	Unigene47474_All//2.00E-167//AT1G62640| KAS III (3-KETOACYL-ACYL CARRIER PROTEIN SYNTHASE III); 3-oxoacyl-[acyl-carrier-protein] synthase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene47474_All//0.00E+00//TC152518		ko00061|Fatty acid biosynthesis		nr +
Unigene4748_All	1343	2.88	1.62	1.78	7.49	6.77	4.34	1.57	0.37	0.92	-8.30E-01	7.51E-03		-6.92E-01	3.36E-02		-1.47E-01	4.92E-01		-7.88E-01	7.62E-06		-2.08E+00	3.13E-06	Down	-7.75E-01	4.06E-02		Unigene4748_All//gi|15239123|ref|NP_201371.1|//1.00E-175//BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|2827715|emb|CAA16688.1| receptor protein kinase - like protein [Arabidopsis thaliana] >gi|10177328|dbj|BAB10677.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|20466696|gb|AAM20665.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|31711786|gb|AAP68249.1| At5g65700 [Arabidopsis thaliana] >gi|110741066|dbj|BAE98627.1| receptor protein kinase like protein [Arabidopsis thaliana] >gi|224589751|gb|ACN59407.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene4748_All//1.00E-174//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene4748_All//0.00E+00//TC149157				nr -
Unigene47480_All	1598	16.50	11.16	15.90	29.40	29.93	29.99	14.05	7.35	5.63	-5.64E-01	9.26E-08		-5.40E-02	6.53E-01		2.60E-02	8.17E-01		2.87E-02	7.57E-01		-9.35E-01	2.26E-18		-1.32E+00	2.50E-32	Down	Unigene47480_All//gi|297610489|ref|NP_001061615.2|//1.00E-143//Os10g0419100 (Oryza sativa Japonica Group) >gi|255679407|dbj|BAF26529.2| Os10g0419100 [Oryza sativa Japonica Group]	Unigene47480_All//9.00E-112//AT1G60690| aldo/keto reductase family protein	Unigene47480_All//0.00E+00//TC134621		ko00010|Glycolysis / Gluconeogenesis//ko00053|Ascorbate and aldarate metabolism//ko00561|Glycerolipid metabolism		nr -
Unigene47483_All	646	4.29	1.73	3.13	1.31	2.45	3.57	0.85	1.62	1.79	-1.31E+00	7.32E-04	Down	-4.55E-01	2.54E-01		9.03E-01	8.93E-02		1.44E+00	9.32E-04	Up	9.27E-01	1.30E-01		1.07E+00	5.22E-02		Unigene47483_All//gi|297186087|gb|ADI24331.1|//1.00E-05//glucose-6-phosphate isomerase [Miscanthus sinensis]	Unigene47483_All//2.00E-06//AT5G42740| glucose-6-phosphate isomerase, cytosolic (PGIC)	Unigene47483_All//1.00E-54//TC162222		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene47484_All	928	1.01	0.05	0.92	0.27	0.37	0.83	1.28	1.40	1.76	-4.22E+00	1.36E-04	Down	-1.45E-01	8.31E-01		4.67E-01	7.79E-01		1.62E+00	6.61E-02		1.30E-01	8.09E-01		4.64E-01	3.13E-01		Unigene47484_All//gi|9279779|dbj|BAB01431.1|//1.00E-06//non-LTR retroelement reverse transcriptase-like protein [Arabidopsis thaliana]	Unigene47484_All//4.00E-07//AT1G43730| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G04650.1); Has 562 Blast hits to 549 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 562; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene47484_All//3.00E-10//ES842288		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene47487_All	1686	2.23	1.62	1.01	1.45	2.74	3.24	2.88	2.36	2.58	-4.61E-01	1.47E-01		-1.14E+00	6.36E-04	Down	9.19E-01	6.82E-04		1.16E+00	6.07E-06	Up	-2.92E-01	2.63E-01		-1.63E-01	5.44E-01		Unigene47487_All//gi|224126633|ref|XP_002329603.1|//1.00E-126//SET domain protein [Populus trichocarpa] >gi|222870312|gb|EEF07443.1| SET domain protein [Populus trichocarpa]	Unigene47487_All//5.00E-106//AT2G35160| SUVH5 (SU(VAR)3-9 HOMOLOG 5); histone methyltransferase	Unigene47487_All//0.00E+00//gi|164269482|gb|ES848992.1|ES848992		ko00310|Lysine degradation		nr -
Unigene47488_All	1628	2.41	2.46	2.16	5.51	4.78	5.08	2.52	4.26	6.09	2.87E-02	9.43E-01		-1.59E-01	6.12E-01		-2.04E-01	3.30E-01		-1.18E-01	6.37E-01		7.59E-01	1.31E-04		1.27E+00	6.14E-14	Up	Unigene47488_All//gi|116310937|emb|CAH67874.1|//3.00E-34//OSIGBa0153E02-OSIGBa0093I20.3 [Oryza sativa (indica cultivar-group)]	Unigene47488_All//2.00E-24//AT4G23160| protein kinase family protein	Unigene47488_All//2.00E-21//gi|78342702|gb|DT562976.1|DT562976				nr +
Unigene47489_All	1117	13.77	21.00	26.70	7.31	16.22	13.46	0.53	2.99	1.07	6.09E-01	7.00E-08		9.55E-01	1.06E-19		1.15E+00	1.52E-19	Up	8.80E-01	6.70E-10		2.50E+00	1.38E-11	Up	1.01E+00	5.98E-02		Unigene47489_All//gi|297850564|ref|XP_002893163.1|//1.00E-104//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339005|gb|EFH69422.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47489_All//2.00E-97//AT1G21460| nodulin MtN3 family protein	Unigene47489_All//0.00E+00//TC162583				nr -
Unigene4749_All	495	1.59	0.61	0.86	5.53	6.68	2.65	4.44	0.93	1.37	-1.37E+00	9.59E-02		-8.82E-01	2.95E-01		2.71E-01	4.91E-01		-1.06E+00	4.98E-03		-2.26E+00	4.47E-07	Down	-1.70E+00	2.47E-05	Down	Unigene4749_All//gi|9502419|gb|AAF88118.1|AC021043_11//4.00E-42//Hypothetical protein [Arabidopsis thaliana]	Unigene4749_All//2.00E-39//AT1G29200| unknown protein	Unigene4749_All//5.00E-180//TC129589				nr +
Unigene47490_All	1861	12.23	4.90	5.41	22.11	17.71	23.32	43.80	21.02	15.50	-1.32E+00	4.40E-26	Down	-1.18E+00	4.68E-21	Down	-3.20E-01	3.62E-05		7.70E-02	4.50E-01		-1.06E+00	3.26E-79	Down	-1.50E+00	1.01E-139	Down	Unigene47490_All//gi|99083509|gb|AB566654.1|//2.00E-99//EBP1 [Ammopiptanthus mongolicus] >gi|146336945|gb|ABQ23586.1| EBP1 [Ammopiptanthus mongolicus]	Unigene47490_All//2.00E-78//AT3G51800| ATG2; aminopeptidase/ metalloexopeptidase	Unigene47490_All//0.00E+00//gi|48784187|gb|CO090065.1|CO090065				nr +
Unigene47491_All	1780	13.64	15.74	16.45	16.06	25.54	20.04	4.56	3.05	2.15	2.07E-01	5.50E-02		2.71E-01	1.13E-02		6.69E-01	7.62E-20		3.19E-01	3.31E-04		-5.79E-01	1.40E-03		-1.09E+00	3.02E-09	Down	Unigene47491_All//gi|83853834|gb|AB647866.1|//1.00E-78//remorin [Glycine max]	Unigene47491_All//3.00E-70//AT4G36970| remorin family protein	Unigene47491_All//0.00E+00//TC130003				nr +
Unigene47495_All	1474	3.73	1.58	1.91	3.92	4.37	6.07	2.50	2.07	5.32	-1.24E+00	2.64E-06	Down	-9.61E-01	3.15E-04		1.56E-01	5.76E-01		6.30E-01	9.27E-04		-2.70E-01	3.99E-01		1.09E+00	5.49E-09	Up	Unigene47495_All//gi|226495371|ref|NP_001149043.1|//1.00E-60//LOC100282663 [Zea mays] >gi|195624240|gb|ACG33950.1| kinesin heavy chain isolog [Zea mays]	Unigene47495_All//6.00E-58//AT4G24175| unknown protein	Unigene47495_All//0.00E+00//gi|78337390|gb|DT557664.1|DT557664				nr +
Unigene47496_All	1225	1.88	1.20	0.61	0.73	1.46	2.51	1.14	0.65	1.85	-6.48E-01	1.23E-01		-1.63E+00	5.02E-04	Down	9.98E-01	4.19E-02		1.78E+00	3.35E-06	Up	-8.13E-01	1.11E-01		7.03E-01	5.55E-02		Unigene47496_All//gi|226495371|ref|NP_001149043.1|//7.00E-57//LOC100282663 [Zea mays] >gi|195624240|gb|ACG33950.1| kinesin heavy chain isolog [Zea mays]	Unigene47496_All//2.00E-46//AT4G24175| unknown protein	Unigene47496_All//0.00E+00//gi|78337390|gb|DT557664.1|DT557664				nr +
Unigene4750_All	1324	0.87	0.00	1.33	4.89	3.54	3.31	4.15	0.63	1.81	-9.76E+00	9.91E-07	Down	6.10E-01	2.38E-01		-4.68E-01	3.81E-02		-5.64E-01	1.46E-02		-2.72E+00	1.98E-20	Down	-1.20E+00	1.54E-07	Down	Unigene4750_All//gi|115468436|ref|NP_001057817.1|//1.00E-152//Os06g0545900 (Oryza sativa Japonica Group) >gi|113595857|dbj|BAF19731.1| Os06g0545900 [Oryza sativa Japonica Group]	Unigene4750_All//1.00E-164//AT1G29200| unknown protein	Unigene4750_All//0.00E+00//TC129589				nr +
Unigene47500_All	218	0.00	0.00	0.00	0.00	0.63	0.41	1.16	0.38	6.76	null	null		null	null		9.30E+00	3.18E-01		8.69E+00	4.76E-01		-1.60E+00	3.10E-01		2.54E+00	9.95E-06	Up	Unigene47500_All//gi|124359531|gb|ABN05953.1|//2.00E-17//nodulin-like protein, related [Medicago truncatula]	Unigene47500_All//9.00E-18//AT5G45275| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Nodulin-like (InterPro:IPR010658), Major facilitator superfamily, general substrate transporter (InterPro:IPR011701); BEST Arabidopsis thaliana protein match is: nodulin-related (TAIR:AT4G19450.1); Has 697 Blast hits to 659 proteins in 149 species: Archae - 19; Bacteria - 126; Metazoa - 5; Fungi - 146; Plants - 324; Viruses - 0; Other Eukaryotes - 77 (source: NCBI BLink).	Unigene47500_All//8.00E-106//TC151591				nr -

Unigene47501_All	2036	1.26	1.19	0.94	4.26	3.74	3.35	11.59	10.12	40.11	-7.60E-02	8.43E-01		-4.19E-01	3.27E-01		-1.88E-01	3.95E-01		-3.46E-01	9.22E-02		-1.95E-01	7.09E-02		1.79E+00	1.01E-178	Up	Unigene47501_All//gi|56236086|gb|AAV84499.1|/0.00E+00//At5g45275 [Arabidopsis thaliana] >gi|56790236|gb|AAW30035.1| At5g45275 [Arabidopsis thaliana]	Unigene47501_All//6.00E-170//AT5G45275| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Nodulin-like (InterPro:IPR010658), Major facilitator superfamily, general substrate transporter (InterPro:IPR001761); BEST Arabidopsis thaliana protein match is: nodulin-related (TAIR:AT4G19450.1); Has 697 Blast hits to 659 proteins in 149 species: Archae - 19; Bacteria - 126; Metazoa - 5; Fungi - 146; Plants - 324; Viruses - 0; Other Eukaryotes - 77 (source: NCBI BLink).	Unigene47501_All//0.00E+00//TC147002					nr +
Unigene47502_All	1277	16.06	42.18	19.35	18.84	14.10	15.53	29.17	18.82	14.85	1.39E+00	1.08E-65	Up	2.69E-01	2.30E-02		-4.18E-01	5.25E-05		-2.79E-01	1.42E-02		-6.32E-01	1.28E-15		-9.74E-01	6.03E-33		Unigene47502_All//gi|2493895|sp|Q43317.1|CYSK_CITLA//1.00E-159//RecName: Full=Cysteine synthase; Short=CSase; AltName: Full=O-acetylserine sulfhydrylase; AltName: Full=O-acetylserine (thiol)-lyase; Short=OAS-TL; AltName: Full=Beta-pyrazolylalanine synthase; AltName: Full=Beta-PA/CSase; AltName: Full=L-mimosine synthase >gi|540497|dbj|BAA05965.1| cysteine synthase [Citrullus lanatus subsp. vulgaris]	Unigene47502_All//9.00E-128//AT4G14880| OAS1 (O-ACETYLSERINE (THIOL) LYASE (OAS-TL) ISOFORM A1); cysteine synthase	Unigene47502_All//0.00E+00//TC165309		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr -
Unigene47503_All	1120	2.76	16.78	8.94	11.12	6.09	15.08	3.74	21.49	18.43	2.61E+00	5.28E-53	Up	1.70E+00	3.07E-16	Up	-8.69E-01	3.92E-09		4.40E-01	1.02E-03		2.52E+00	3.49E-80	Up	2.30E+00	5.29E-63	Up	Unigene47503_All//gi|294847482|gb|ADF43752.1|/2.00E-74//MYB [Camellia sinensis]	Unigene47503_All//3.00E-62//AT1G68320| MYB62 (myb domain protein 62); DNA binding / transcription factor	Unigene47503_All//0.00E+00//TC131540	MYB			nr +
Unigene47504_All	1007	25.51	9.46	10.15	25.28	20.00	10.14	24.14	16.73	10.05	-1.43E+00	3.83E-33	Down	-1.33E+00	1.50E-28	Down	-3.38E-01	9.67E-04		-1.32E+00	2.30E-31	Down	-5.29E-01	7.61E-08		-1.26E+00	8.42E-33	Down			Unigene47504_All//4.00E-148//ES815847				
Unigene47506_All	1207	2.99	0.76	1.68	3.38	3.82	3.59	5.85	3.98	2.87	-1.98E+00	5.98E-08	Down	-8.35E-01	1.39E-02		1.76E-01	5.94E-01		8.60E-02	7.94E-01		-5.55E-01	4.79E-03		-1.03E+00	1.60E-07	Down	Unigene47506_All//gi|224132326|ref|XP_002328241.1|/1.00E-109//transcription factor E2F [Populus trichocarpa] >gi|222837756|gb|EEE76121.1| transcription factor E2F [Populus trichocarpa]	Unigene47506_All//1.00E-87//AT2G36010| E2F3 (E2F TRANSCRIPTION FACTOR 3); DNA binding / transcription factor	Unigene47506_All//0.00E+00//TC149035	E2F-DP			nr +
Unigene47507_All	1609	1.20	0.82	0.70	2.54	1.26	1.35	1.81	1.22	1.61	-5.55E-01	2.36E-01		-7.92E-01	1.06E-01		-1.01E+00	3.37E-04	Down	-9.14E-01	2.15E-03		-5.71E-01	8.53E-02		-1.72E-01	6.11E-01		Unigene47507_All//gi|79322370|ref|NP_001031359.1|/1.00E-167//TRN1 (TRANSPORTIN 1); protein transporter [Arabidopsis thaliana] >gi|317111774|gb|AAP68243.1| At2g16950 [Arabidopsis thaliana]	Unigene47507_All//2.00E-155//AT2G16950| TRN1 (TRANSPORTIN 1); protein transporter	Unigene47507_All//5.00E-121//gi|109854524|gb|DW483503.1|DW483503				nr -
Unigene47509_All	937	6.03	0.92	3.07	22.97	14.70	9.21	11.96	3.84	11.22	-2.71E+00	3.33E-17	Down	-9.75E-01	2.05E-04		-6.44E-01	2.63E-09		-1.32E+00	1.31E-26	Down	-1.64E+00	6.37E-22	Down	-9.13E-02	6.16E-01		Unigene47509_All//gi|224069266|ref|XP_002302941.1|/7.00E-50//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222844667|gb|EEE82214.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene47509_All//6.00E-33//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene47509_All//2.00E-110//TC177573		ko04626|Plant-pathogen interaction		nr +
Unigene47510_All	953	1.98	1.44	3.30	9.20	6.32	3.93	4.84	3.60	4.85	-4.61E-01	3.40E-01		7.38E-01	4.51E-02		-5.41E-01	3.22E-03		-1.23E+00	4.92E-10	Down	-4.27E-01	9.81E-02		4.00E-03	9.87E-01		Unigene47510_All//gi|28300299|gb|AA037645.1|/2.00E-79//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene47510_All//6.00E-61//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene47510_All//6.00E-61//TC177573		ko04626|Plant-pathogen interaction		nr -
Unigene47512_All	552	4.74	0.73	1.35	10.47	8.48	4.42	11.80	12.87	24.75	-2.69E+00	3.11E-08	Down	-1.81E+00	4.52E-05	Down	-3.03E-01	2.43E-01		-1.24E+00	5.56E-07	Down	1.26E-01	6.05E-01		1.07E+00	1.67E-14	Up	Unigene47512_All//gi|224076725|ref|XP_002304987.1|/4.00E-37//equilibrative nucleoside transporter [Populus trichocarpa] >gi|222847951|gb|EEE85498.1| equilibrative nucleoside transporter [Populus trichocarpa]	Unigene47512_All//1.00E-36//AT4G05120| FUR1 (FUDR RESISTANT 1); nucleoside transmembrane transporter					nr -
Unigene47514_All	1580	3.38	0.48	1.89	6.81	3.79	3.40	18.44	20.58	26.93	-2.81E+00	6.95E-17	Down	-8.40E-01	1.85E-03		-8.45E-01	1.30E-07		-1.00E+00	5.88E-09	Down	1.59E-01	8.49E-02		5.47E-01	3.32E-14		Unigene47514_All//gi|224076725|ref|XP_002304987.1|/0.00E+00//equilibrative nucleoside transporter [Populus trichocarpa] >gi|222847951|gb|EEE85498.1| equilibrative nucleoside transporter [Populus trichocarpa]	Unigene47514_All//3.00E-167//AT4G05120| FUR1 (FUDR RESISTANT 1); nucleoside transmembrane transporter					nr -
Unigene47515_All	1465	2.71	2.28	3.53	36.28	31.24	30.58	24.33	4.96	6.85	-2.50E-01	4.27E-01		3.77E-01	1.83E-01		-2.16E-01	2.13E-03		-2.47E-01	6.53E-04		-2.29E+00	4.59E-106	Down	-1.83E+00	1.54E-81	Down	Unigene47515_All//gi|60922273|gb|AAX37336.1|/0.00E+00//UDP-glucuronic acid decarboxylase 3 [Populus tomentosa]	Unigene47515_All//3.00E-179//AT2G28760| NAD-dependent epimerase/dehydratase family protein	Unigene47515_All//0.00E+00//TC141088		ko00523|Polyketide sugar unit biosynthesis		nr -
Unigene47523_All	2219	15.18	11.69	17.11	14.37	17.05	15.24	6.34	2.98	3.57	-3.77E-01	4.61E-05		1.72E-01	7.66E-02		2.47E-01	3.73E-03		8.55E-02	4.60E-01		-1.09E+00	4.84E-15	Down	-8.29E-01	4.04E-10		Unigene47523_All//gi|225462225|ref|XP_002271727.1|/0.00E+00//PREDICTED: similar to replicase [Vitis vinifera]	Unigene47523_All//6.00E-173//AT1G79050| DNA repair protein recA	Unigene47523_All//0.00E+00//TC171802		ko03440|Homologous recombination		nr -
Unigene47524_All	2432	4.37	2.79	3.48	15.32	16.20	12.78	12.48	4.19	7.21	-6.46E-01	2.16E-04		-3.27E-01	8.41E-02		8.03E-02	4.49E-01		-2.62E-01	3.05E-03		-1.57E+00	9.23E-55	Down	-7.92E-01	2.66E-19		Unigene47524_All//gi|18076679|emb|CAC84774.1|/0.00E+00//P70 protein [Nicotiana tabacum]	Unigene47524_All//1.00E-136//AT2G37080| myosin heavy chain-related	Unigene47524_All//0.00E+00//TC142405				nr +
Unigene47525_All	2194	3.51	40.05	3.59	7.65	13.83	9.59	3.87	8.48	9.48	3.51E+00	0.00E+00	Up	3.52E-02	8.81E-01		8.54E-01	3.74E-20		3.26E-01	7.15E-03		1.13E+00	1.22E-20	Up	1.29E+00	7.88E-29	Up	Unigene47525_All//gi|297796919|ref|XP_002866344.1|/1.00E-166//ATEXO70H7 [Arabidopsis lyrata subsp. lyrata] >gi|297312179|gb|EFH42603.1| ATEXO70H7 [Arabidopsis lyrata subsp. lyrata]	Unigene47525_All//1.00E-149//AT5G59730| ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H7); protein binding	Unigene47525_All//0.00E+00//TC146321				nr +
Unigene47526_All	1226	5.80	25.33	7.12	3.49	6.52	5.64	3.31	3.82	6.11	2.13E+00	1.75E-68	Up	2.96E-01	1.64E-01		8.99E-01	4.08E-06		6.90E-01	1.79E-03		2.06E-01	4.59E-01		8.84E-01	2.50E-06				Unigene47526_All//0.00E+00//gi|164358790|gb|ES847061.1|ES847061				
Unigene4753_All	841	9.39	7.17	9.37	5.03	5.00	7.41	28.66	79.17	37.80	-3.90E-01	6.46E-02		-3.60E-03	9.95E-01		-1.13E-02	9.64E-01		5.58E-01	1.93E-02		1.47E+00	2.91E-107	Up	4.00E-01	1.68E-06		Unigene4753_All//gi|115446137|ref|NP_001046848.1|//7.00E-45//0s02g0479300 [Oryza sativa Japonica Group] >gi|47848144|dbj|BAD21925.1| XTP3-transactivated protein A-like [Oryza sativa Japonica Group] >gi|47848239|dbj|BAD22064.1| XTP3-transactivated protein A-like [Oryza sativa Japonica Group] >gi|113536379|dbj|BAF08762.1| 0s02g0479300 [Oryza sativa Japonica Group]	Unigene4753_All//2.00E-39//AT3G25400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: NTP Pyrophosphohydrolase MazG-related, RS21-C6 (InterPro:IPR011394), EAR (InterPro:IPR009039), NTP pyrophosphohydrolase MazG, putative catalytic core (InterPro:IPR004518); Has 572 Blast hits to 572 proteins in 181 species: Archae - 11; Bacteria - 286; Metazoa - 71; Fungi - 1; Plants - 31; Viruses - 0; Other Eukaryotes - 172 (source: NCBI BLink).	Unigene4753_All//3.00E-68//DW519333				nr -
Unigene47530_All	1892	6.25	11.19	7.46	8.08	10.41	16.52	17.12	33.93	32.87	8.41E-01	4.97E-12		2.55E-01	1.23E-01		3.65E-01	2.32E-03		1.03E+00	9.02E-26	Up	9.87E-01	1.02E-55		9.41E-01	4.23E-51		Unigene47530_All//gi|75154127|sp|Q8L7A4.1|AGD11_ARATH//1.00E-136//RecName: Full=Probable ADP-ribosylation factor GTPase-activating protein AGD11; Short=ARF GAP AGD11; AltName: Full=Protein ARF-GAP DOMAIN 11; Short=AtAGD11	Unigene47530_All//2.00E-127//AT3G07940| zinc finger and C2 domain protein, putative	Unigene47530_All//0.00E+00//TC163093		ko04144|Endocytosis		nr +
Unigene47531_All	2196	1.88	2.49	2.86	9.21	8.45	3.56	9.53	6.89	10.21	4.05E-01	1.23E-01		6.04E-01	1.38E-02		-1.24E-01	3.87E-01		-1.37E+00	1.40E-26	Down	-4.68E-01	1.19E-05		9.99E-02	3.92E-01		Unigene47531_All//gi|224134707|ref|XP_002327470.1|/0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222836024|gb|EEE74445.1| GRAS family transcription factor [Populus trichocarpa]	Unigene47531_All//5.00E-143//AT5G52510| scarecrow-like transcription factor 8 (SCL8)	Unigene47531_All//0.00E+00//ES817887	GRAS			nr +
Unigene47532_All	1835	5.13	5.85	5.46	13.87	11.30	10.73	11.27	5.53	6.64	1.90E-01	3.22E-01		8.81E-02	6.53E-01		-2.96E-01	4.48E-03		-3.70E-01	5.01E-04		-1.03E+00	1.14E-19	Down	-7.62E-01	1.28E-12		Unigene47532_All//gi|225445559|ref|XP_002282272.1|/1.00E-161//PREDICTED: similar to beta-1,3-glucanase 1 [Vitis vinifera]	Unigene47532_All//1.00E-133//AT2G26600| glycosyl hydrolase family 17 protein	Unigene47532_All//0.00E+00//TC169477		ko00500|Starch and sucrose metabolism		nr +
Unigene47536_All	1384	6.65	4.91	5.35	38.73	30.13	20.13	2.57	1.66	0.58	-4.40E-01	2.15E-02		-3.15E-01	1.30E-01		-3.62E-01	4.09E-08		-9.44E-01	2.39E-38		-6.28E-01	3.22E-02		-2.16E+00	8.10E-11	Down	Unigene47536_All//gi|3152589|gb|AAC17070.1|/1.00E-144//Strong similarity to lupeol synthase gb|U49919 from A. thaliana (second gene in a series of three with similar homologies) [Arabidopsis thaliana]	Unigene47536_All//2.00E-96//AT1G78955| CAMS1 (Camelliol C synthase 1); beta-amyrin synthase	Unigene47536_All//0.00E+00//C0114162		ko00100|Steroid biosynthesis		nr +
Unigene47537_All	1266	3.47	20.53	3.70	5.51	7.32	17.80	36.50	112.58	60.99	2.56E+00	8.91E-72	Up	9.25E-02	7.49E-01		4.10E-01	2.97E-02		1.69E+00	2.14E-39	Up	1.62E+00	3.81E-266	Up	7.41E-01	2.77E-42		Unigene47537_All//gi|270308994|dbj|BAI52950.1|/2.00E-95//GRAM domain-containing protein [Citrullus lanatus subsp. vulgaris]	Unigene47537_All//2.00E-88//AT5G13200| GRAM domain-containing protein / ABA-responsive protein-related	Unigene47537_All//0.00E+00//TC147530				nr +
Unigene47538_All	597	0.44	0.68	0.18	4.42	7.84	2.80	2.20	0.14	0.00	6.32E-01	6.01E-01		-1.30E+00	4.36E-01		8.27E-01	2.07E-03		-6.60E-01	9.44E-02		-3.97E+00	3.34E-07	Down	-1.11E+01	9.85E-10	Down			Unigene47538_All//0.00E+00//TC133770				
Unigene47539_All	1065	6.63	2.90	4.45	38.26	35.18	14.16	20.72	2.28	9.28	-1.19E+00	1.76E-07	Down	-5.76E-01	1.25E-02		-1.21E-01	1.94E-01		-1.43E+00	1.11E-56	Down	-3.19E+00	3.76E-94	Down	-1.16E+00	3.81E-26	Down			Unigene47539_All//0.00E+00//DW503513				
Unigene47540_All	1486	52.95	38.29	48.02	97.18	96.26	104.92	60.63	34.43	29.70	-4.68E-01	1.50E-15		-1.41E-01	3.00E-02		-1.37E-02	8.36E-01		1.11E-01	1.06E-02		-8.17E-01	8.06E-57		-1.03E+00	7.35E-86	Down	Unigene47540_All//gi|3353335|gb|AAC2713T.1|/1.00E-111//ESTs gb|F14113 and gb|T42122 come from this region [Arabidopsis thaliana] >gi|27311649|gb|AAO00790.1| expressed protein [Arabidopsis thaliana] >gi|30023788|gb|AAP13427.1| At1g65270 [Arabidopsis thaliana] >gi|222423330|dbj|BAH19640.1| AT1G65270 [Arabidopsis thaliana] >gi|222423443|dbj|BAH19692.1| AT1G65270 [Arabidopsis thaliana]	Unigene47540_All//2.00E-109//AT1G65270| unknown protein	Unigene47540_All//0.00E+00//TC153481				nr -

Unigene47541_All	1486	2.08	4.30	1.86	12.60	10.13	8.15	5.32	2.14	2.84	1.05E+00	1.08E-05	Up	-1.57E-01	6.64E-01		-3.16E-01	1.12E-02		-6.30E-01	3.69E-07		-1.32E+00	1.56E-11	Down	-9.05E-01	6.54E-07		Unigene47541_All//gi|13605601|gb|AK32794.1|AF361626_1/1.00E-46//At1g54460/F20D21_28 [Arabidopsis thaliana] >gi|15777865|gb|AL053893.1| At1g54460/F20D21_28 [Arabidopsis thaliana]	Unigene47541_All//2.00E-34//AT1G54460| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: WDL1 (TAIR:AT3G04630.3); Has 393 Blast hits to 375 proteins in 76 species: Archae - 0; Bacteria - 3; Metazoa - 143; Fungi - 38; Plants - 160; Viruses - 0; Other Eukaryotes - 49 (source: NCBI BLink).	Unigene47541_All//0.00E+00//TC177866				nr -
Unigene47548_All	1456	14.81	9.12	11.96	27.75	26.80	25.00	14.98	5.51	5.86	-6.99E-01	3.89E-09		-3.08E-01	1.44E-02		-5.03E-02	6.20E-01		-1.50E-01	1.06E-01		-1.44E+00	6.76E-35	Down	-1.36E+00	8.77E-33	Down	Unigene47548_All//gi|2760835|gb|AA895303.1|//1.00E-126//expressed protein [Arabidopsis thaliana]	Unigene47548_All//5.00E-119//AT2G26680| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Methyltransferase FkbM (InterPro:IPR006342); Has 827 Blast hits to 827 proteins in 145 species: Archae - 22; Bacteria - 329; Metazoa - 0; Fungi - 2; Plants - 28; Viruses - 2; Other Eukaryotes - 444 (source: NCBI BLink).	Unigene47548_All//0.00E+00//TC141957				nr +
Unigene4755_All	1716	0.21	1.12	0.12	1.54	1.22	1.79	4.98	4.63	6.41	2.39E+00	1.59E-05	Up	-7.82E-01	5.53E-01		-3.30E-01	4.24E-01		2.18E-01	6.14E-01		-1.05E-01	6.41E-01		3.65E-01	1.59E-02		Unigene4755_All//gi|15221327|ref|NP_172704.1|//1.00E-166//ACR8; amino acid binding [Arabidopsis thaliana] >gi|8778647|gb|AAF79655.1|AC025416_29 F5O11.14 [Arabidopsis thaliana] >gi|22138106|gb|AAM93433.1| ACR8 [Arabidopsis thaliana] >gi|111074504|gb|ABH04625.1| At1g12420 [Arabidopsis thaliana]	Unigene4755_All//1.00E-163//AT1G12420| ACR8; amino acid binding	Unigene4755_All//0.00E+00//gi|164264304|gb|ES813541.1|ES813541				nr -
Unigene47550_All	1000	26.06	15.30	23.16	10.36	9.50	9.44	9.77	2.22	6.33	-7.68E-01	1.17E-12		-1.70E-01	1.57E-01		-1.25E-01	5.50E-01		-1.35E-01	5.28E-01		-2.14E+00	3.40E-27	Down	-6.25E-01	8.44E-05		Unigene47550_All//gi|297796609|ref|XP_002866189.1|//2.00E-49//macrophage migration inhibitory factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312024|gb|EFH42448.1| macrophage migration inhibitory factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47550_All//3.00E-45//AT5G57170| macrophage migration inhibitory factor family protein / MIF family protein	Unigene47550_All//0.00E+00//gi|164257454|gb|ES810943.1|ES810943	ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism			nr +
Unigene47551_All	2179	1.34	0.84	1.25	2.45	3.79	3.21	20.66	6.66	4.11	-6.84E-01	6.11E-02		-1.10E-01	7.70E-01		6.33E-01	9.95E-04		3.93E-01	8.94E-02		-1.63E+00	2.19E-85	Down	-2.33E+00	1.45E-140	Down	Unigene47551_All//gi|15236223|ref|NP_192203.1|//1.00E-167//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	Unigene47551_All//7.00E-153//AT4G02940| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene47551_All//0.00E+00//TC175182				nr -
Unigene47552_All	1306	12.22	11.37	11.74	23.92	19.43	17.84	20.85	16.42	10.16	-1.04E-01	5.11E-01		-5.74E-02	7.15E-01		-3.00E-01	1.13E-03		-4.23E-01	6.64E-06		-3.45E-01	2.21E-04		-1.04E+00	6.70E-27	Down	Unigene47552_All//gi|18398108|ref|NP_566326.1|//1.00E-126//rhomboid protein-related [Arabidopsis thaliana] >gi|25083369|gb|AAN72066.1| expressed protein [Arabidopsis thaliana] >gi|31711794|gb|AAP68253.1| At3g07950 [Arabidopsis thaliana]	Unigene47552_All//3.00E-114//AT3G07950| rhomboid protein-related	Unigene47552_All//0.00E+00//gi|164274142|gb|ES815961.1|ES815961				nr +
Unigene47555_All	1291	17.06	8.63	10.35	291.86	298.37	155.08	43.13	18.26	24.87	-9.83E-01	4.85E-16		-7.21E-01	2.52E-09		3.18E-02	3.10E-01		-9.12E-01	2.88E-252		-1.24E+00	9.02E-70	Down	-7.94E-01	8.69E-35		Unigene47555_All//gi|29420787|dbj|BAC66615.1|//1.00E-156//L-asparaginase [Glycine max]	Unigene47555_All//4.00E-157//AT3G16150| L-asparaginase, putative / L-asparagine amidohydrolase, putative	Unigene47555_All//0.00E+00//TC134580				nr -
Unigene47557_All	967	10.77	12.63	12.45	3.81	1.78	2.76	1.57	3.59	2.93	2.30E-01	1.83E-01		2.09E-01	2.51E-01		-1.10E+00	2.43E-04	Down	-4.68E-01	1.60E-01		1.19E+00	8.32E-05	Up	8.94E-01	5.71E-03		Unigene47557_All//gi|91208911|ref|YP_538944.1|//1.00E-174//acetyl-CoA carboxylase carboxyltransferase beta subunit [Gossypium hirsutum] >gi|122201397|sp|Q2L915.1|ACCD_GOSHI RecName: Full=Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta, chloroplastic; Short=Acetyl-CoA carboxylase carboxyltransferase subunit beta; Short=ACCase subunit beta >gi|85687425|gb|ABC73637.1| acetyl-CoA carboxylase carboxyltransferase beta subunit [Gossypium hirsutum]	Unigene47557_All//7.00E-126//ATCG00500| Encodes the carboxytransferase beta subunit of the Acetyl-CoA carboxylase (ACCase) complex in plastids. This complex catalyzes the carboxylation of acetyl-CoA to produce malonyl-CoA, the first committed step in fatty acid synthesis.	Unigene47557_All//0.00E+00//TC129620		ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism		nr +
Unigene47558_All	1695	10.56	8.67	6.69	18.16	15.56	18.17	12.12	8.14	5.66	-2.84E-01	3.56E-02		-6.58E-01	1.15E-06		-2.23E-01	2.22E-02		8.00E-04	9.95E-01		-5.75E-01	1.02E-07		-1.10E+00	2.03E-22	Down	Unigene47558_All//gi|115464829|ref|NP_001056014.1|//1.00E-162//Os05g0511300 [Oryza sativa Japonica Group] >gi|113579565|dbj|BAF17928.1| Os05g0511300 [Oryza sativa Japonica Group]	Unigene47558_All//2.00E-174//AT2G32170| LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: N2227-like (InterPro:IPR012901); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G32160.3); Has 362 Blast hits to 319 proteins in 141 species: Archae - 0; Bacteria - 0; Metazoa - 132; Fungi - 130; Plants - 25; Viruses - 0; Other Eukaryotes - 75 (source: NCBI BLink).	Unigene47558_All//0.00E+00//TC174795				nr -
Unigene47561_All	563	42.93	50.76	43.79	73.17	59.76	53.99	41.08	27.84	18.68	2.42E-01	2.13E-02		2.85E-02	8.22E-01		-2.92E-01	1.89E-04		-4.39E-01	4.62E-08		-5.61E-01	3.00E-08		-1.14E+00	1.58E-26	Down	Unigene47561_All//gi|238692413|sp|B3H7G2.1|UBM12_ARATH//5.00E-42//RecName: Full=Ubiquitin-related modifier 1 homolog 2	Unigene47561_All//5.00E-35//AT3G61113| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Ubiquitin related modifier 1 (InterPro:IPR015221), Ubiquitin-related modifier 1 (InterPro:IPR017188), Molybdopterin synthase/thiamin biosynthesis sulphur carrier, beta-grasp (InterPro:IPR016155); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G45695.1); Has 242 Blast hits to 242 proteins in 127 species: Archae - 2; Bacteria - 0; Metazoa - 93; Fungi - 74; Plants - 18; Viruses - 0; Other Eukaryotes - 55 (source: NCBI BLink).	Unigene47561_All//0.00E+00//TC165244				nr -
Unigene47562_All	1183	47.63	280.80	104.79	95.88	217.67	330.50	36.20	79.39	67.96	2.56E+00	0.00E+00	Up	1.14E+00	5.62E-107	Up	1.18E+00	1.47E-288	Up	1.79E+00	0.00E+00	Up	1.13E+00	2.11E-101	Up	9.09E-01	4.69E-62		Unigene47562_All//gi|255546295|ref|XP_002514207.1|//6.00E-25//conserved hypothetical protein [Ricinus communis] >gi|223546663|gb|EEF48161.1| conserved hypothetical protein [Ricinus communis]		Unigene47562_All//0.00E+00//TC168709				nr -
Unigene47563_All	1007	43.64	163.73	99.84	32.06	61.35	77.99	41.44	89.11	84.23	1.91E+00	0.00E+00	Up	1.19E+00	9.28E-94	Up	9.36E-01	1.64E-47		1.28E+00	1.54E-90	Up	1.10E+00	4.26E-93	Up	1.02E+00	1.55E-79	Up	Unigene47563_All//gi|145334895|ref|NP_001078793.1|//6.00E-28//dentin sialophosphoprotein-related [Arabidopsis thaliana]	Unigene47563_All//3.00E-29//AT5G64170| dentin sialophosphoprotein-related	Unigene47563_All//0.00E+00//TC176231				nr +
Unigene47564_All	1157	45.04	25.53	19.61	100.92	62.50	65.07	203.98	173.72	61.19	-8.19E-01	2.51E-27		-1.20E+00	4.88E-49	Down	-6.91E-01	3.94E-55		-6.33E-01	9.26E-42		-2.32E-01	2.71E-15		-1.74E+00	0.00E+00	Down	Unigene47564_All//gi|3334138|sp|Q39817.1|CALX_SOYBN//1.00E-123//RecName: Full=Calnexin homolog; Flags: Precursor >gi|669003|gb|AAA80588.1| calnexin [Glycine max]	Unigene47564_All//8.00E-83//AT5G61790| calnexin 1 (CNX1)	Unigene47564_All//0.00E+00//TC138911		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr -
Unigene47565_All	1533	5.80	3.97	4.65	131.08	93.02	69.79	25.98	10.61	4.13	-5.49E-01	4.49E-03		-3.18E-01	1.35E-01		-4.95E-01	7.47E-52		-9.09E-01	6.28E-134		-1.29E+00	1.99E-53	Down	-2.65E+00	1.02E-144	Down	Unigene47565_All//gi|115452393|ref|NP_001049797.1|//7.00E-72//Os03g0290900 [Oryza sativa Japonica Group] >gi|108707604|gb|ABF95399.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548268|dbj|BAF11711.1| Os03g0290900 [Oryza sativa Japonica Group]	Unigene47565_All//1.00E-147//AT3G54260| unknown protein	Unigene47565_All//0.00E+00//TC165028				nr +
Unigene47566_All	640	0.16	0.00	0.00	1.87	1.88	0.49	10.11	9.21	4.98	-7.35E+00	3.71E-01		-7.35E+00	3.92E-01		1.17E-02	9.99E-01		-1.92E+00	4.14E-03		-1.35E-01	5.94E-01		-1.02E+00	6.49E-07	Down	Unigene47566_All//gi|240254132|ref|NP_173358.4|//1.00E-08//GLTP2 (glycolipid transfer protein 2); glycolipid binding / glycolipid transporter [Arabidopsis thaliana] >gi|45773920|gb|AAS76764.1| At1g21360 [Arabidopsis thaliana]	Unigene47566_All//6.00E-10//AT1G21360| GLTP2 (glycolipid transfer protein 2); glycolipid binding / glycolipid transporter					nr +
Unigene47567_All	976	1.39	2.96	0.71	8.93	4.90	3.05	123.94	131.47	76.13	1.09E+00	3.72E-03		-9.75E-01	1.09E-01		-8.65E-01	1.63E-06		-1.55E+00	5.40E-14	Down	8.51E-02	5.88E-02		-7.03E-01	2.00E-60		Unigene47567_All//gi|238479842|ref|NP_001154632.1|//4.00E-67//glycolipid transfer protein-related [Arabidopsis thaliana]	Unigene47567_All//2.00E-68//AT3G21260| glycolipid transfer protein-related					nr +

Unigene47568_All	1366	60.29	29.53	44.36	57.62	53.01	61.03	59.43	42.07	28.20	-1.03E+00	1.44E-62	Down	-4.43E-01	3.97E-14		-1.20E-01	5.24E-02		8.31E-02	2.19E-01		-4.98E-01	8.31E-22		-1.08E+00	3.99E-83	Down	Unigene47568_All//gi|206748343|gb|ACI22358.1|//1.00E-104//5'-methylthioadenosine nucleosidase [Lupinus luteus] >gi|216360974|gb|ACJ72491.1| 5'-methylthioadenosine nucleosidase [Lupinus luteus]	Unigene47568_All//5.00E-100//AT4G34840| ATMTN2; methylthioadenosine nucleosidase	Unigene47568_All//0.00E+00//TC129799		ko00270|Cysteine and methionine metabolism		nr +
Unigene47569_All	1707	1.93	0.56	1.15	5.69	4.42	4.13	7.16	4.99	1.33	-1.78E+00	2.03E-06	Down	-7.43E-01	3.81E-02		-3.65E-01	4.45E-02		-4.63E-01	1.19E-02		-5.19E-01	3.13E-04		-2.43E+00	1.22E-40	Down	Unigene47569_All//gi|15242536|ref|NP_198817.1|//1.00E-158//AATP1 (AAA-ATPase 1): ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene47569_All//5.00E-152//AT5G40010| AATP1 (AAA-ATPase 1); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene47569_All//0.00E+00//ES794711				nr +
Unigene4757_All	1283	2.24	1.54	0.21	7.69	14.36	6.62	4.35	1.34	3.01	-5.42E-01	1.41E-01		-3.43E+00	1.24E-10	Down	9.01E-01	1.57E-13		-2.16E-01	2.97E-01		-1.70E+00	6.91E-12	Down	-5.30E-01	1.49E-02		Unigene4757_All//gi|115463683|ref|NP_001055441.1|//2.00E-57//Os05g0390600 [Oryza sativa Japonica Group] >gi|113578992|dbj|BAF17355.1| Os05g0390600 [Oryza sativa Japonica Group]	Unigene4757_All//2.00E-24//AT5G26230| unknown protein	Unigene4757_All//0.00E+00//gi|78328928|gb|DT549202.1|DT549202				nr -
Unigene47570_All	1224	16.03	7.99	9.75	37.36	36.40	29.41	18.10	23.15	10.94	-1.00E+00	7.04E-15	Down	-7.18E-01	2.49E-08		-3.74E-02	7.25E-01		-3.45E-01	6.30E-06		3.55E-01	9.75E-05		-7.27E-01	1.82E-12		Unigene47570_All//gi|108385354|gb|ABF85773.1|//1.00E-111//At5g13890 [Arabidopsis thaliana]	Unigene47570_All//2.00E-73//AT5G13890| unknown protein	Unigene47570_All//0.00E+00//TC138008		ko03040|Spliceosome//ko04144|Endocytosis//ko03018|RNA degradation		nr -
Unigene47571_All	1110	20.88	11.73	16.41	14.81	15.67	5.78	20.91	21.50	47.45	-8.32E-01	6.60E-13		-3.48E-01	3.60E-03		8.12E-02	6.13E-01		-1.36E+00	2.27E-21	Down	4.01E-02	7.35E-01		1.18E+00	1.57E-62	Up	Unigene47571_All//gi|38566628|gb|AAR24204.1|//1.00E-42//At1g32690 [Arabidopsis thaliana] >gi|40824115|gb|AAR92349.1| At1g32690 [Arabidopsis thaliana]	Unigene47571_All//2.00E-29//AT1G32690| unknown protein	Unigene47571_All//2.00E-178//C0087009				nr +
Unigene47575_All	662	12.65	28.78	13.03	16.18	13.42	13.03	23.44	36.24	31.11	1.19E+00	1.26E-18	Up	4.33E-02	8.41E-01		-2.70E-01	1.37E-01		-3.12E-01	8.85E-02		6.29E-01	2.98E-10		4.09E-01	1.12E-04		Unigene47575_All//gi|297604119|ref|NP_001055012.2|//6.00E-19//Os05g0244600 [Oryza sativa Japonica Group] >gi|255676168|dbj|BAF16926.2| Os05g0244600 [Oryza sativa Japonica Group]	Unigene47575_All//5.00E-19//AT2G33845| DNA-binding protein-related	Unigene47575_All//0.00E+00//gi|109884859|gb|DW513829.1|DW513829		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +
Unigene47576_All	823	55.56	88.23	58.10	60.53	68.83	79.52	36.83	47.13	86.70	6.67E-01	1.41E-26		6.45E-02	4.92E-01		1.85E-01	8.13E-03		3.94E-01	3.18E-10		3.56E-01	3.44E-06		1.23E+00	2.15E-90	Up	Unigene47576_All//gi|297604119|ref|NP_001055012.2|//7.00E-46//Os05g0244600 [Oryza sativa Japonica Group] >gi|255676168|dbj|BAF16926.2| Os05g0244600 [Oryza sativa Japonica Group]	Unigene47576_All//8.00E-47//AT4G28440| DNA-binding protein-related	Unigene47576_All//0.00E+00//TC140060		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr -
Unigene47577_All	1940	4.94	7.10	4.75	2.54	1.56	2.58	1.16	1.81	2.59	5.26E-01	5.12E-04		-5.57E-02	7.82E-01		-7.03E-01	5.68E-03		2.36E-02	9.45E-01		6.48E-01	2.79E-02		1.16E+00	1.33E-06	Up	Unigene47577_All//gi|225438229|ref|XP_002264391.1|//1.00E-138//PREDICTED: similar to GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein [Vitis vinifera]	Unigene47577_All//2.00E-129//AT2G22910| GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein	Unigene47577_All//0.00E+00//gi|78346529|gb|DT566803.1|DT566803		ko00330|Arginine and proline metabolism		nr -
Unigene47578_All	1457	10.77	25.87	19.48	8.82	14.98	16.09	4.85	3.61	1.37	1.26E+00	7.34E-40	Up	8.55E-01	1.12E-15		7.64E-01	3.55E-12		8.67E-01	1.01E-14		-4.23E-01	3.49E-02		-1.83E+00	8.48E-17	Down	Unigene47578_All//gi|224057134|ref|XP_002299136.1|//1.00E-166//metal tolerance protein [Populus trichocarpa] >gi|222846394|gb|EEE83941.1| metal tolerance protein [Populus trichocarpa]	Unigene47578_All//2.00E-146//AT3G58060| cation efflux family protein / metal tolerance protein, putative (MTPc3)					nr -
Unigene47579_All	2380	7.69	0.96	0.81	5.02	3.70	2.52	16.45	3.07	5.93	-3.01E+00	1.52E-60	Down	-3.26E+00	6.67E-63	Down	-4.40E-01	4.81E-03		-9.93E-01	9.43E-10		-2.42E+00	3.16E-124	Down	-1.47E+00	8.01E-66	Down	Unigene47579_All//gi|257831433|gb|ACV71017.1|//1.00E-161//UPA17 [Capsicum annuum]	Unigene47579_All//6.00E-99//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene47579_All//0.00E+00//TC178779	GRF			nr -
Unigene4758_All	1696	1.23	0.75	0.91	4.96	3.09	6.92	15.71	24.47	31.48	-7.24E-01	1.03E-01		-4.39E-01	3.64E-01		-6.86E-01	2.06E-04		4.80E-01	3.57E-03		6.40E-01	1.19E-17		1.00E+00	8.75E-49	Up	Unigene4758_All//gi|18415319|ref|NP_567589.1|//0.00E+00//glycosyl transferase family 1 protein [Arabidopsis thaliana]	Unigene4758_All//0.00E+00//AT4G19460| glycosyl transferase family 1 protein			ko00561|Glycerolipid metabolism//ko00563|Glycosylphosphatidylinositol (GPI)-anchor biosynthesis		nr -
Unigene47581_All	1952	5.74	14.64	5.70	11.38	10.88	13.23	30.41	40.75	51.12	1.35E+00	1.27E-33	Up	-8.70E-03	9.86E-01		-6.44E-02	6.46E-01		2.18E-01	5.66E-02		4.22E-01	5.75E-16		7.50E-01	1.60E-55		Unigene47581_All//gi|1170239|sp|P42044.1|HEMH_CUCSA//1.00E-179//RecName: Full=Ferrochelatase-2, chloroplastic; AltName: Full=Ferrochelatase II; AltName: Full=Protoheme ferro-lyase 2; AltName: Full=Heme synthase 2; Flags: Precursor >gi|474968|dbj|BAA05102.1| ferrochelatase [Cucumis sativus]	Unigene47581_All//2.00E-165//AT5G26030| FC1 (ferrochelatase 1); ferrochelatase	Unigene47581_All//0.00E+00//TC133696		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene47582_All	1218	3.61	4.49	2.62	6.95	5.09	5.08	2.08	2.51	4.55	3.16E-01	2.35E-01		-4.60E-01	1.40E-01		-4.50E-01	1.91E-02		-4.53E-01	2.40E-02		2.66E-01	4.41E-01		1.13E+00	7.08E-07	Up	Unigene47582_All//gi|15241903|ref|NP_201070.1|//2.00E-83//proline-rich family protein [Arabidopsis thaliana] >gi|136656675|gb|AAK32831.1|AF361818_1 AT5g62640/MRG21_6 [Arabidopsis thaliana] >gi|27363410|gb|AAO11624.1| At5g62640/MRG21_6 [Arabidopsis thaliana]	Unigene47582_All//2.00E-40//AT5G62640| proline-rich family protein	Unigene47582_All//4.00E-22//TC135715		ko03040|Spliceosome		nr +
Unigene47583_All	529	2.18	6.32	6.34	1.04	2.02	2.22	7.27	4.90	2.71	1.54E+00	2.01E-05	Up	1.54E+00	3.32E-05	Up	9.62E-01	1.64E-01		1.10E+00	9.17E-02		-5.70E-01	4.20E-02		-1.42E+00	6.23E-07	Down			Unigene47583_All//2.00E-173//DW226008				
Unigene47586_All	1577	1064.70	78.72	233.33	241.93	190.10	104.53	3.22	1.67	0.35	-3.76E+00	0.00E+00	Down	-2.19E+00	0.00E+00	Down	-3.48E-01	5.20E-51		-1.21E+00	0.00E+00	Down	-9.46E-01	7.35E-05		-3.19E+00	7.20E-23	Down	Unigene47586_All//gi|166343775|gb|ABV88635.1|//1.00E-154//xyloglucan endotransglycosylase/hydrolase [Gossypium raimondii]	Unigene47586_All//1.00E-136//AT5G65730| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene47586_All//0.00E+00//TC153886				nr +
Unigene47588_All	1270	51.74	36.07	25.79	35.54	43.36	38.05	30.06	26.53	93.89	-5.21E-01	8.64E-16		-1.00E+00	1.98E-46	Down	2.87E-01	1.78E-05		9.86E-02	2.79E-01		-1.81E-01	2.77E-02		1.64E+00	7.32E-231	Up	Unigene47588_All//gi|224459179|gb|ACN43325.1|//2.00E-41//bZIP transcription factor [Solanum lycopersicum]	Unigene47588_All//3.00E-32//AT4G34590| GBF6 (G-BOX BINDING FACTOR 6); DNA binding / protein heterodimerization/ transcription factor	Unigene47588_All//0.00E+00//TC140006	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene47589_All	1220	13.42	9.93	6.15	82.85	64.61	57.19	14.17	14.35	24.85	-4.35E-01	1.58E-03		-1.13E+00	2.75E-14	Down	-3.59E-01	1.36E-14		-5.35E-01	7.58E-27		1.82E-02	9.10E-01		8.10E-01	7.08E-20		Unigene47589_All//gi|18424977|ref|NP_569016.1|//3.00E-45//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|751803377|sp|Q9LS89.1|Y5566_ARATH RecName: Full=Uncharacterized protein At5g65660 >gi|30102568|gb|AAP21202.1| At5g65660 [Arabidopsis thaliana]	Unigene47589_All//7.00E-32//AT5G65660| hydroxyproline-rich glycoprotein family protein	Unigene47589_All//0.00E+00//gi|164242918|gb|ES813336.1|ES813336				nr +
Unigene47590_All	1541	6.86	4.47	3.32	9.67	10.15	6.54	5.16	3.44	3.65	-6.17E-01	4.20E-04		-1.05E+00	1.72E-08	Down	6.99E-02	7.01E-01		-5.65E-01	6.39E-05		-5.83E-01	1.50E-03		-5.01E-01	4.99E-03		Unigene47590_All//gi|92870991|gb|ABE80152.1|//6.00E-51//High mobility group proteins HMG-I and HMG-Y; Linker histone, N-terminal [Medicago truncatula]	Unigene47590_All//1.00E-25//AT1G48620| HON3 (High Mobility Group Family A 5); DNA binding	Unigene47590_All//0.00E+00//TC150267				nr -
Unigene47591_All	494	0.53	4.92	0.32	3.73	2.86	2.10	1.88	1.35	0.81	3.22E+00	5.76E-09	Up	-7.12E-01	6.22E-01		-3.85E-01	4.43E-01		-8.27E-01	8.81E-02		-4.76E-01	4.76E-01		-1.22E+00	5.14E-02		Unigene47591_All//gi|211906444|gb|ACJ11715.1|//3.00E-13//Fructokinase [Gossypium hirsutum]	Unigene47591_All//2.00E-11//AT3G59480| pfkB-type carbohydrate kinase family protein	Unigene47591_All//1.00E-60//TC136577		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene47593_All	1550	9.08	7.00	11.68	18.42	19.37	22.90	33.72	9.63	15.91	-3.76E-01	1.30E-02		3.63E-01	8.08E-03		7.31E-02	5.57E-01		3.15E-01	4.30E-04		-1.81E+00	4.83E-114	Down	-1.08E+00	1.77E-54	Down	Unigene47593_All//gi|30679729|ref|NP_172142.2|//1.00E-161//enoyl-CoA hydratase/isomerase family protein [Arabidopsis thaliana] >gi|292630834|sp|Q9SHJ8.2|HIBC8_ARATH RecName: Full=3-hydroxyisobutyryl-CoA hydrolase-like protein 5 >gi|62320504|dbj|BAD95058.1| 3-hydroxyisobutyryl-coenzyme A hydrolase [Arabidopsis thaliana] >gi|630003868|gb|AAY25463.1| At1g06550 [Arabidopsis thaliana] >gi|109946425|gb|ABG48391.1| At1g06550 [Arabidopsis thaliana]	Unigene47593_All//7.00E-159//AT1G06550| enoyl-CoA hydratase/isomerase family protein	Unigene47593_All//0.00E+00//TC135506		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism		nr -
Unigene47597_All	1900	4.30	3.97	2.21	4.75	3.15	3.80	17.07	6.73	4.32	-1.13E-01	6.03E-01		-9.56E-01	7.06E-06		-5.90E-01	9.93E-04		-3.19E-01	1.18E-01		-1.34E+00	3.20E-46	Down	-1.98E+00	8.88E-83	Down	Unigene47597_All//gi|52627103|gb|AAU84678.1|//1.00E-136//At4g11120 [Arabidopsis thaliana] >gi|55167888|gb|AAV43776.1| At4g11120 [Arabidopsis thaliana]	Unigene47597_All//9.00E-133//AT4G11120| translation elongation factor Ts (EF-Ts), putative	Unigene47597_All//0.00E+00//TC150020				nr -
Unigene47601_All	1060	15.75	36.19	16.73	18.23	18.48	20.20	13.36	18.33	15.15	1.20E+00	1.93E-37	Up	8.74E-02	5.89E-01		1.97E-02	9.04E-01		1.47E-01	2.89E-01		4.56E-01	4.21E-05		1.81E-01	1.68E-01		Unigene47601_All//gi|284433796|gb|ADB85104.1|//1.00E-106//vacuolar protein sorting-associated protein VPS28 [Jatropha curcas]	Unigene47601_All//2.00E-97//AT4G05000| VPS28-2; transporter	Unigene47601_All//0.00E+00//TC130858		ko04144|Endocytosis		nr +
Unigene47602_All	1298	44.50	37.90	24.41	74.11	47.25	75.09	19.93	5.38	10.34	-2.32E-01	1.03E-03		-8.66E-01	5.52E-32		-6.49E-01	1.09E-40		1.89E-02	7.74E-01		-1.89E+00	2.54E-60	Down	-9.47E-01	3.95E-22		Unigene47602_All//gi|21314553|gb|AAM47002.1|AF512544_1//1.00E-146//alpha-expansin precursor [Gossypium hirsutum]	Unigene47602_All//4.00E-122//AT1G26770| ATEXPA10 (ARABIDOPSIS THALIANA EXPANSIN A 10); structural constituent of cell wall	Unigene47602_All//0.00E+00//TC143501				nr +
Unigene47603_All	1418	14.13	8.61	10.10	42.12	33.54	39.94	74.06	54.59	28.26	-7.15E-01	7.55E-09		-4.84E-01	1.43E-04		-3.29E-01	1.41E-07		-7.67E-02	3.64E-01		-4.40E-01	1.93E-22		-1.39E+00	1.49E-160	Down	Unigene47603_All//gi|115466448|ref|NP_001056823.1|//8.00E-97//Os06g0150400 [Oryza sativa Japonica Group] >gi|113594863|dbj|BAF18737.1| Os06g0150400 [Oryza sativa Japonica Group]	Unigene47603_All//9.00E-98//AT4G26520| LOCATED IN: endoplasmic reticulum, plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Saposin B (InterPro:IPR008139); Has 120 Blast hits to 120 proteins in 43 species: Archae - 2; Bacteria - 0; Metazoa - 42; Fungi - 10; Plants - 19; Viruses - 0; Other Eukaryotes - 47 (source: NCBI BLink).	Unigene47603_All//0.00E+00//TC160072				nr -
Unigene47605_All	1169	6.49	5.98	6.70	8.39	7.36	7.38	2.89	1.47	0.99	-1.18E-01	6.00E-01		4.51E-02	8.42E-01		-1.89E-01	3.52E-01		-1.86E-01	3.88E-01		-9.81E-01	1.12E-03		-1.55E+00	6.56E-07	Down	Unigene47605_All//gi|124359162|gb|ABN05685.1|//2.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]						nr +

Unigene47606_All	2817	1.95	0.77	1.38	6.86	5.87	6.08	1.79	0.47	0.83	-1.33E+00	5.47E-07	Down	-4.99E-01	6.35E-02		-2.26E-01	8.26E-02		-1.75E-01	2.19E-01		-1.91E+00	1.67E-12	Down	-1.10E+00	3.69E-06	Down	Unigene47606_All//gi|224082644|ref|XP_002306777.1|//0.00E+00//copaly l diphosphate synthase [Populus trichocarpa] >gi|222856226|gb|EEE93773.1| copalyl diphosphate synthase [Populus trichocarpa]	Unigene47606_All//0.00E+00//AT4G02780| GA1 (GA REQUIRING 1); ent-copalyl diphosphate synthase/ magnesium ion binding			ko00904|Diterpenoid biosynthesis		nr -
Unigene47607_All	567	3.97	9.74	6.57	7.82	6.26	4.30	4.47	3.69	3.02	1.30E+00	1.04E-06	Up	7.28E-01	2.79E-02		-3.22E-01	2.95E-01		-8.62E-01	2.37E-03		-2.80E-01	4.67E-01		-5.66E-01	9.98E-02			Unigene47607_All//0.00E+00//TC144393					
Unigene47609_All	1436	7.25	6.42	7.05	12.14	14.15	9.09	4.27	1.40	2.39	-1.75E-01	3.76E-01		-4.14E-02	8.32E-01		2.21E-01	8.42E-02		-4.18E-01	1.48E-03		-1.61E+00	4.67E-12	Down	-8.39E-01	5.34E-05		Unigene47609_All//gi|15223367|ref|NP_171636.1|//4.00E-74//CNX3 (COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 3); catalytic [Arabidopsis thaliana] >gi|238478311|ref|NP_001154299.1| CNX3 (COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 3); catalytic [Arabidopsis thaliana] >gi|2497964|sp|Q39056.1|CNX3_ARATH RecName: Full=Molybdopterin biosynthesis protein CNX3; AltName: Full=Molybdenum cofactor biosynthesis enzyme CNX3 >gi|9665143|gb|AAF97327.1|AC023628 _8 Molybdopterin Biosythesis CNX3 protein [Arabidopsis thaliana] >gi|662873|emb|CAA88106.1| Cnx3 [Arabidopsis thaliana] >gi|105829726|gb|ABF74702.1| At1g01290 [Arabidopsis thaliana]	Unigene47609_All//2.00E-75//AT1G01290| CNX3 (COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 3); catalytic	Unigene47609_All//0.00E+00//TC151601				nr -
Unigene4761_All	1167	11.97	5.43	6.07	22.07	17.08	29.80	24.13	10.57	10.96	-1.14E+00	3.94E-13	Down	-9.80E-01	6.21E-10		-3.69E-01	2.38E-04		4.33E-01	9.85E-07		-1.19E+00	1.55E-33	Down	-1.14E+00	3.44E-32	Down	Unigene4761_All//gi|115472049|ref|NP_001039623.1|//1.00E-105//0s07g0475800 [Oryza sativa Japonica Group] >gi|113611159|dbj|BAF21537.1| Os07g0475800 [Oryza sativa Japonica Group]	Unigene4761_All//5.00E-71//AT3G22660| rRNA processing protein-related	Unigene4761_All//0.00E+00//TC133793				nr -
Unigene47611_All	2097	1.72	1.04	1.19	1.83	1.05	1.62	5.20	2.03	2.81	-7.29E-01	2.42E-02		-5.29E-01	1.26E-01		-7.99E-01	6.47E-03		-1.79E-01	6.38E-01		-1.36E+00	2.66E-16	Down	-8.88E-01	6.26E-09		Unigene47611_All//gi|10176976|dbj|BAB10208.1|//0.00E+00//mitochondri al RNA helicase-like protein [Arabidopsis thaliana]	Unigene47611_All//0.00E+00//AT5G39840| ATP-dependent RNA helicase, mitochondrial, putative	Unigene47611_All//0.00E+00//CO498938				nr -
Unigene47612_All	1470	1.07	0.34	0.07	1.63	3.98	26.64	28.04	34.72	53.71	-1.63E+00	3.58E-03		-3.88E+00	1.55E-06	Down	1.29E+00	7.95E-08	Up	4.03E+00	2.36E-176	Up	3.08E-01	3.28E-06		9.38E-01	3.10E-64		Unigene47612_All//gi|74273615|gb|AB01475.1|//1.00E-176//1-aminocyclopropane-1-carboxylate synthase ACS6 [Gossypium hirsutum]	Unigene47612_All//2.00E-123//AT4G11280| ACS6 (1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID (ACC) SYNTHASE 6); 1-aminocyclopropane-1-carboxylate synthase	Unigene47612_All//0.00E+00//TC129594		ko00270|Cysteine and methionine metabolism		nr -
Unigene47613_All	626	1.00	0.24	2.21	1.11	5.50	0.58	0.00	0.00	0.00	-2.05E+00	4.46E-02		1.14E+00	5.84E-02		2.30E+00	6.12E-10	Up	-9.49E-01	2.88E-01		null	null		null	null		Unigene47613_All//gi|115456355|ref|NP_001051778.1|//6.00E-24//Os03g0828800 [Oryza sativa Japonica Group] >gi|108711884|gb|ABF99679.1| D-mannose binding lectin family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550249|dbj|BAF13692.1| Os03g0828800 [Oryza sativa Japonica Group]	Unigene47613_All//7.00E-11//AT1G34300| lectin protein kinase family protein					nr +
Unigene47614_All	1278	3.44	8.88	3.08	2.34	3.66	1.66	0.86	0.33	0.47	1.37E+00	4.81E-14	Up	-1.58E-01	6.22E-01		6.48E-01	1.77E-02		-4.94E-01	1.95E-01		-1.40E+00	2.04E-02		-8.79E-01	1.15E-01		Unigene47614_All//gi|115456355|ref|NP_001051778.1|//8.00E-42//Os03g0828800 [Oryza sativa Japonica Group] >gi|108711884|gb|ABF99679.1| D-mannose binding lectin family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550249|dbj|BAF13692.1| Os03g0828800 [Oryza sativa Japonica Group]	Unigene47614_All//4.00E-21//AT1G34300| lectin protein kinase family protein					nr +
Unigene47615_All	1865	1.94	1.06	3.60	4.27	4.38	9.23	3.83	12.39	5.90	-8.69E-01	7.29E-03		8.94E-01	1.59E-04		3.42E-02	8.95E-01		1.11E+00	3.35E-16	Up	1.69E+00	2.37E-46	Up	6.22E-01	3.13E-05		Unigene47615_All//gi|15218070|ref|NP_172969.1|//1.00E-177//MATE efflux family protein [Arabidopsis thaliana] >gi|30387589|gb|AAP31960.1| At1g15170 [Arabidopsis thaliana]	Unigene47615_All//7.00E-164//AT1G15170| MATE efflux family protein	Unigene47615_All//0.00E+00//TC178513				nr -
Unigene4762_All	1220	1.20	4.07	2.10	9.43	7.99	1.85	3.60	0.96	1.27	1.76E+00	3.97E-09	Up	8.03E-01	5.20E-02		-2.40E-01	1.74E-01		-2.35E+00	1.07E-31	Down	-1.91E+00	5.22E-11	Down	-1.50E+00	2.30E-08	Down	Unigene4762_All//gi|15724286|gb|AAL06536.1|AF412083_1//3.00E-77//AT4g35240/F23E12_200 [Arabidopsis thaliana] >gi|23308207|gb|AAN18073.1| At4g35240/F23E12_200 [Arabidopsis thaliana]	Unigene4762_All//2.00E-77//AT4G35240| unknown protein	Unigene4762_All//0.00E+00//TC159371				nr -
Unigene47620_All	992	9.18	33.25	22.60	4.02	2.95	7.65	1.07	2.15	1.41	1.86E+00	6.06E-61	Up	1.30E+00	3.23E-24	Up	-4.45E-01	1.48E-01		9.29E-01	9.29E-06		1.01E+00	1.05E-02		4.00E-01	4.25E-01		Unigene47620_All//gi|225441740|ref|XP_002277512.1|//2.00E-86//PREDICTED: similar to peptidase S41 family protein [Vitis vinifera]	Unigene47620_All//1.00E-79//AT3G57680| peptidase S41 family protein	Unigene47620_All//0.00E+00//TC145060				nr -
Unigene47621_All	1973	6.28	37.34	18.70	2.83	3.51	5.56	0.99	1.42	0.95	2.57E+00	3.25E-203	Up	1.57E+00	1.38E-52	Up	3.11E-01	1.90E-01		9.76E-01	1.15E-08		5.26E-01	1.27E-01		-5.49E-02	9.05E-01		Unigene47621_All//gi|225441740|ref|XP_002277512.1|//0.00E+00//PREDICTED: similar to peptidase S41 family protein [Vitis vinifera]	Unigene47621_All//0.00E+00//AT3G57680| peptidase S41 family protein	Unigene47621_All//0.00E+00//TC145060				nr -
Unigene47622_All	1168	13.39	7.42	7.80	23.16	16.86	16.70	17.38	4.72	8.29	-8.52E-01	2.56E-09		-7.81E-01	9.78E-08		-4.58E-01	1.83E-06		-4.71E-01	3.24E-06		-1.88E+00	4.26E-47	Down	-1.07E+00	3.19E-21	Down	Unigene47622_All//gi|75183398|sp|Q9MZY6.1|Y3972_ARATH|/1.00E-108//RecName: Full=Uncharacterized protein At3g49720 >gi|222424727|dbj|BAH20317.1| AT3G49720 [Arabidopsis thaliana]	Unigene47622_All//2.00E-101//AT3G49720| unknown protein	Unigene47622_All//0.00E+00//TC135901				nr -
Unigene47623_All	2071	16.22	25.57	27.97	1.13	5.42	3.99	0.00	0.00	0.00	6.57E-01	4.49E-19		7.86E-01	2.63E-27		2.26E+00	3.40E-31	Up	1.82E+00	2.98E-16	Up	null	null		null	null		Unigene47623_All//gi|115465213|ref|NP_001056206.1|//1.00E-114//Os05g0543700 [Oryza sativa Japonica Group] >gi|113579757|dbj|BAF18120.1| Os05g0543700 [Oryza sativa Japonica Group]	Unigene47623_All//7.00E-83//AT1G21080| DNAJ heat shock N-terminal domain-containing protein	Unigene47623_All//5.00E-128//TC143044		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene47624_All	2002	8.26	7.19	6.25	9.26	10.89	15.86	30.05	42.34	61.05	-2.00E-01	1.71E-01		-4.02E-01	5.09E-03		2.34E-01	5.34E-02		7.77E-01	1.84E-16		4.95E-01	2.06E-22		1.02E+00	3.94E-114	Up	Unigene47624_All//gi|115440523|ref|NP_001044541.1|//0.00E+00//Os01g0801600 [Oryza sativa Japonica Group] >gi|15570996|dbj|BAB86423.1| glycerol-3-phosphate dehydrogenase-like protein [Oryza sativa Japonica Group] >gi|113534072|dbj|BAF06455.1| Os01g0801600 [Oryza sativa Japonica Group]	Unigene47624_All//0.00E+00//AT2G41540| GPDHC1; NAD or NADH binding / glycerol-3-phosphate dehydrogenase (NAD+)	Unigene47624_All//0.00E+00//TC150577		ko00564|Glycerophospholipid metabolism		nr -
Unigene47625_All	2053	12.69	6.84	6.28	16.89	15.05	15.80	15.94	9.43	7.65	-8.93E-01	3.80E-16		-1.02E+00	4.82E-19	Down	-1.67E-01	8.35E-02		-9.65E-02	3.95E-01		-7.58E-01	1.04E-18		-1.06E+00	2.85E-33	Down	Unigene47625_All//gi|15238380|ref|NP_196418.1|//1.00E-112//sad1/unc-84 protein-related [Arabidopsis thaliana] >gi|15912311|gb|AAL08289.1| AT5g04990/MEG13_15 [Arabidopsis thaliana] >gi|21360559|gb|AAM47476.1| AT5g04990/MEG13_15 [Arabidopsis thaliana]	Unigene47625_All//2.00E-109//AT5G04990| sad1/unc-84 protein-related	Unigene47625_All//0.00E+00//TC136914				nr -
Unigene4763_All	697	16.06	4.07	6.72	62.96	55.48	39.59	4.55	3.66	3.26	-1.98E+00	4.24E-23	Down	-1.26E+00	9.53E-12	Down	-1.83E-01	2.51E-02		-6.69E-01	1.18E-17		-3.15E-01	3.57E-01		-4.82E-01	1.13E-01		Unigene4763_All//gi|15238328|ref|NP_199039.1|//5.00E-43//scp142 (serine carboxypeptidase-like 42); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75170531|sp|Q9FH05.1|SCP42_ARATH RecName: Full=Serine carboxypeptidase-like 42; Flags: Precursor >gi|13665557|gb|AAK32772.1|AF361604_1 AT5g42240/K5J14_4 [Arabidopsis thaliana] >gi|10177009|dbj|BAB10197.1| serine carboxypeptidase II-like [Arabidopsis thaliana] >gi|23505957|gb|AAN28838.1| At5g42240/K5J14_4 [Arabidopsis thaliana]	Unigene4763_All//3.00E-44//AT5G42240| scp142 (serine carboxypeptidase-like 42); serine-type carboxypeptidase	Unigene4763_All//0.00E+00//gi|109886741|gb|DW515710.1|DW515710				nr +
Unigene47631_All	2256	6.10	1.21	0.94	7.02	7.43	5.69	16.74	4.13	5.32	-2.33E+00	1.52E-34	Down	-2.69E+00	4.47E-39	Down	8.22E-02	6.13E-01		-3.05E-01	3.57E-02		-2.02E+00	1.24E-95	Down	-1.65E+00	3.76E-75	Down	Unigene47631_All//gi|13560783|gb|AK30205.1|AF349964_1//0.00E+00//poly(A)-binding protein [Daucus carota]	Unigene47631_All//0.00E+00//AT2G23350| PAB4 (POLY(A) BINDING PROTEIN 4); RNA binding / translation initiation factor	Unigene47631_All//0.00E+00//TC149350		ko03040|Spliceosome		nr -
Unigene47633_All	1177	24.27	8.05	12.80	39.95	26.74	42.06	33.23	10.30	11.47	-1.59E+00	6.06E-43	Down	-9.23E-01	7.75E-18		-5.79E-01	2.03E-16		7.40E-02	4.31E-01		-1.69E+00	7.50E-78	Down	-1.53E+00	8.90E-70	Down	Unigene47633_All//gi|15229675|ref|NP_188488.1|//3.00E-67//single-strand-binding family protein [Arabidopsis thaliana]	Unigene47633_All//1.00E-64//AT3G18580| single-strand-binding family protein	Unigene47633_All//0.00E+00//TC149301		ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +
Unigene47635_All	1362	50.36	56.44	43.59	72.75	68.69	69.27	73.54	33.97	31.15	1.64E-01	8.00E-03		-2.08E-01	1.95E-03		-8.27E-02	1.59E-01		-7.06E-02	2.57E-01		-1.11E+00	1.92E-105	Down	-1.24E+00	2.52E-128	Down	Unigene47635_All//gi|226493796|ref|NP_001147401.1|//3.00E-38//tubulin alpha-6 chain [Zea mays] >gi|195611052|gb|ACG27356.1| tubulin alpha-6 chain [Zea mays]	Unigene47635_All//6.00E-48//AT1G50020| unknown protein	Unigene47635_All//0.00E+00//TC157897		ko04145|Phagosome		nr -
Unigene47637_All	1486	6.44	3.21	6.41	33.52	35.22	24.77	9.16	21.71	12.81	-1.01E+00	1.07E-07	Down	-6.50E-03	9.98E-01		7.14E-02	4.28E-01		-4.37E-01	1.58E-09		1.24E+00	6.15E-41	Up	4.84E-01	1.12E-05		Unigene47637_All//gi|224113471|ref|XP_002332583.1|//1.00E-102//f-box family protein [Populus trichocarpa] >gi|222832921|gb|EEE71398.1| f-box family protein [Populus trichocarpa]	Unigene47637_All//9.00E-40//AT3G55370| OBP3 (OBF-BINDING PROTEIN 3); DNA binding / transcription factor	Unigene47637_All//0.00E+00//TC149697	C2C2-Dof			nr +

Unigene4764_All	1200	1.22	0.38	1.11	66.75	55.53	43.96	4.90	4.84	2.29	-1.68E+00	4.05E-03		-1.38E-01	7.97E-01		-2.66E-01	7.95E-07		-6.03E-01	1.99E-26		-1.67E-02	9.73E-01		-1.10E+00	4.95E-07	Down	Unigene4764_All//gi|18402578|ref|NP_565716.1|//1.00E-75//LSH3 (LIGHT SENSITIVE HYPOCOTYLS 3) [Arabidopsis thaliana] >gi|3746060|gb|AAC63835.1| expressed protein [Arabidopsis thaliana] >gi|15912211|gb|AAL08239.1| At2g31160/T16B12.3 [Arabidopsis thaliana] >gi|19547989|gb|AAL87358.1| At2g31160/T16B12.3 [Arabidopsis thaliana]	Unigene4764_All//8.00E-60//AT2G31160| LSH3 (LIGHT SENSITIVE HYPOCOTYLS 3)	Unigene4764_All//0.00E+00//TC149589				nr -
Unigene47640_All	1169	158.31	159.85	115.88	64.64	71.26	84.49	37.90	26.60	17.55	1.40E-02	7.46E-01		-4.50E-01	5.73E-32		1.41E-01	1.59E-02		3.86E-01	1.29E-14		-5.11E-01	8.10E-13		-1.11E+00	3.33E-48	Down	Unigene47640_All//gi|21780187|gb|AAM7651.1|AF522274_1//1.00E-124//cp10-like protein [Gossypium hirsutum]	Unigene47640_All//8.00E-98//AT5G20720| CPN20 (CHAPERONIN 20); calmodulin binding	Unigene47640_All//0.00E+00//TC147992				nr -
Unigene47645_All	869	32.15	10.96	12.68	59.44	38.56	33.11	164.55	108.36	43.32	-1.55E+00	1.62E-40	Down	-1.34E+00	1.88E-31	Down	-6.25E-01	1.47E-20		-8.45E-01	1.02E-30		-6.03E-01	5.92E-53		-1.93E+00	0.00E+00	Down	Unigene47645_All//gi|56744207|dbj|BAD81043.1|//1.00E-126//calnexin [Glycine max]	Unigene47645_All//2.00E-108//AT5G61790| calnexin 1 (CNX1)	Unigene47645_All//0.00E+00//gi|78336141|gb|DT556415.1|DT556415		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr +
Unigene47646_All	1391	10.46	11.62	9.69	27.72	29.91	22.96	2.61	1.17	0.80	1.52E-01	3.26E-01		-1.11E-01	5.25E-01		1.10E-01	2.52E-01		-2.72E-01	1.61E-03		-1.16E+00	7.76E-05	Down	-1.70E+00	2.59E-08	Down	Unigene47646_All//gi|297840355|ref|XP_002888059.1|//1.00E-150//patatin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333900|gb|EFH64318.1| patatin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47646_All//4.00E-151//AT1G61850| galactolipase/phospholipase	Unigene47646_All//0.00E+00//gi|84174529|gb|DR463177.1|DR463177				nr -
Unigene47649_All	1031	9.34	9.34	8.57	14.11	10.55	13.97	13.12	11.27	6.22	0.00E+00	9.99E-01		-1.23E-01	5.78E-01		-4.19E-01	2.64E-03		-1.38E-02	9.50E-01		-2.20E-01	1.37E-01		-1.08E+00	1.25E-14	Down	Unigene47649_All//gi|297832346|ref|XP_002884055.1|//4.00E-62//ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328995|gb|EFH60314.1| ARID/BRIGHT DNA-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene47649_All//5.00E-56//AT2G17410| ARID/BRIGHT DNA-binding domain-containing protein	Unigene47649_All//0.00E+00//gi|21103471|gb|BQ415784.1|BQ415784				nr -
Unigene4765_All	966	6.99	7.19	5.95	6.81	6.35	25.11	2.01	3.25	2.72	4.05E-02	8.66E-01		-2.31E-01	3.72E-01		-1.01E-01	7.12E-01		1.88E+00	5.26E-49	Up	6.89E-01	2.86E-02		4.35E-01	2.06E-01		Unigene4765_All|gi|298108575|gb|ADB93673.2|//8.00E-30//indole-3-acetic acid inducible 29 [Arabidopsis thaliana]	Unigene4765_All//8.00E-30//AT4G32280| IAA29 (INDOLE-3-ACETIC ACID INDUCIBLE 29); transcription factor	Unigene4765_All//0.00E+00//TC153725				nr +
Unigene47651_All	1239	33.32	26.87	24.28	42.66	37.60	41.41	71.93	51.54	26.01	-3.10E-01	1.98E-04		-4.56E-01	8.19E-08		-1.82E-01	1.24E-02		-4.29E-02	6.44E-01		-4.81E-01	2.09E-22		-1.47E+00	5.66E-148	Down	Unigene47651_All//gi|58652054|gb|AW80852.1|//1.00E-133//At4g24330 [Arabidopsis thaliana]	Unigene47651_All//1.00E-106//AT4G24330| unknown protein	Unigene47651_All//0.00E+00//gi|164370396|gb|ES850728.1|ES850728				nr +
Unigene47652_All	616	1.87	1.65	1.82	2.83	0.84	1.39	1.51	1.22	0.78	-1.84E-01	7.48E-01		-4.17E-02	9.65E-01		-1.76E+00	3.19E-04	Down	-1.02E+00	4.05E-02		-3.06E-01	6.21E-01		-9.60E-01	1.20E-01		Unigene47652_All//gi|15241926|ref|NP_200486.1|//3.00E-28//Ndr family protein [Arabidopsis thaliana] >gi|10176779|dbj|BAB09893.1| pollen specific protein SF21 [Arabidopsis thaliana] >gi|15215798|gb|AAK91444.1| AT5g56750/MIK19_22 [Arabidopsis thaliana] >gi|19699254|gb|AAL90993.1| AT5g56750/MIK19_22 [Arabidopsis thaliana] >gi|21590137|gb|AAM65086.1| pollen specific protein SF21 [Arabidopsis thaliana]	Unigene47652_All//2.00E-29//AT5G56750| Ndr family protein	Unigene47652_All//2.00E-66//TC163978				nr +
Unigene47653_All	1024	1.64	1.39	2.91	3.16	3.26	6.35	1.69	1.84	0.97	-2.39E-01	6.10E-01		8.33E-01	2.76E-02		4.49E-02	9.17E-01		1.01E+00	1.21E-05	Up	1.18E-01	7.88E-01		-8.00E-01	6.02E-02		Unigene47653_All//gi|297793185|ref|XP_002864477.1|//1.00E-118//ndr family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310312|gb|EFH40736.1| ndr family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47653_All//3.00E-119//AT5G56750| Ndr family protein	Unigene47653_All//0.00E+00//CO100181				nr +
Unigene47655_All	431	2.79	4.94	0.74	4.85	1.76	5.45	3.04	2.33	1.57	8.23E-01	6.26E-02		-1.91E+00	7.10E-03		-1.47E+00	6.00E-04	Down	1.67E-01	7.02E-01		-3.86E-01	4.87E-01		-9.53E-01	5.85E-02		Unigene47655_All//gi|50253576|gb|AAT71960.1|//1.00E-12//At1g12020 [Arabidopsis thaliana]	Unigene47655_All//1.00E-13//AT5G64010| unknown protein	Unigene47655_All//2.00E-111//DR459226				nr -
Unigene47657_All	1308	125.64	65.20	90.01	300.03	171.10	184.97	86.73	89.73	21.47	-9.47E-01	4.72E-108		-4.81E-01	4.27E-32		-8.10E-01	1.42E-244		-6.98E-01	1.77E-165		4.91E-02	3.60E-01		-2.01E+00	6.73E-294	Down	Unigene47657_All//gi|9838492|ref|NP_064104.1|//5.00E-19//orf110b [Beta vulgaris subsp. vulgaris] >gi|9087354|dbj|BAA99498.1| orf110b [Beta vulgaris subsp. vulgaris]		Unigene47657_All//0.00E+00//TC163522				nr +
Unigene47658_All	1659	13.34	12.13	16.37	17.96	20.55	18.95	22.94	13.58	7.40	-1.38E-01	2.87E-01		2.95E-01	7.52E-03		1.95E-01	4.09E-02		7.75E-02	5.22E-01		-7.56E-01	1.55E-21		-1.63E+00	2.60E-74	Down	Unigene47658_All//gi|17064942|gb|AAL32625.1|//1.00E-168//Unknown protein [Arabidopsis thaliana] >gi|24899799|gb|AAN65114.1| Unknown protein [Arabidopsis thaliana]	Unigene47658_All//1.00E-133//AT5G52540| unknown protein	Unigene47658_All//0.00E+00//TC146957				nr -
Unigene47660_All	1037	4.24	12.22	9.40	14.75	19.43	19.29	1.71	0.89	0.31	1.53E+00	3.17E-18	Up	1.15E+00	4.68E-09	Up	3.98E-01	6.81E-04		3.88E-01	1.56E-03		-9.50E-01	3.09E-02		-2.48E+00	1.05E-06	Down	Unigene47660_All//gi|18409649|ref|NP_564995.1|//7.00E-62//caleosin-related family protein [Arabidopsis thaliana] >gi|15810177|gb|AAL06990.1| At1g70670/F5A18_15 [Arabidopsis thaliana] >gi|23505789|gb|AAN28754.1| At1g70670/F5A18_15 [Arabidopsis thaliana]	Unigene47660_All//4.00E-63//AT1G70670| caleosin-related family protein	Unigene47660_All//0.00E+00//CO114849				nr +
Unigene47662_All	1822	2.04	5.51	2.78	1.97	1.89	1.59	4.43	4.68	3.17	1.43E+00	2.40E-13	Up	4.46E-01	1.18E-01		-5.87E-02	8.58E-01		-3.11E-01	3.95E-01		7.84E-02	7.02E-01		-4.83E-01	6.37E-03		Unigene47662_All//gi|91208892|ref|YP_538925.1|//0.00E+00//RNA polymerase beta'' subunit [Gossypium hirsutum] >gi|122201383|sp|Q2L825.1|RPOC2_GOSHI RecName: Full=DNA-directed RNA polymerase subunit beta''; AltName: Full=PEP; AltName: Full=Plastid-encoded RNA polymerase subunit beta''; Short=RNA polymerase subunit beta'' >gi|85687406|gb|ABC73618.1| RNA polymerase beta' subunit [Gossypium hirsutum]	Unigene47662_All//0.00E+00//ATCG00170| RNA polymerase beta' subunit-2	Unigene47662_All//0.00E+00//TC163163		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene47663_All	1043	5.12	4.47	2.96	9.36	6.93	6.80	9.61	5.45	3.74	-1.95E-01	4.79E-01		-7.89E-01	3.42E-03		-4.33E-01	1.42E-02		-4.62E-01	1.20E-02		-8.18E-01	4.60E-07		-1.36E+00	1.33E-15	Down			Unigene47663_All//1.00E-09//FL576597				
Unigene47664_All	1417	11.45	4.47	7.97	22.29	13.92	16.29	17.54	7.14	7.28	-1.36E+00	1.36E-19	Down	-5.23E-01	2.62E-04		-6.79E-01	1.06E-14		-4.53E-01	1.13E-06		-1.30E+00	7.74E-34	Down	-1.27E+00	1.09E-33	Down	Unigene47664_All//gi|115440525|ref|NP_001044542.1|//1.00E-109//Os01g0801700 [Oryza sativa Japonica Group] >gi|19570997|dbj|BAB86424.1| mucin-like protein [Oryza sativa Japonica Group] >gi|113534073|dbj|BAF06456.1| Os01g0801700 [Oryza sativa Japonica Group]	Unigene47664_All//4.00E-84//AT5G62270| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: mucin-related (TAIR:AT2G02880.1); Has 48 Blast hits to 48 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 4; Plants - 40; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene47664_All//0.00E+00//TC139527				nr -
Unigene47665_All	931	10.17	3.86	7.04	14.71	8.62	18.97	5.81	2.33	1.84	-1.40E+00	3.02E-12	Down	-5.32E-01	6.35E-03		-7.72E-01	3.10E-08		3.66E-01	5.80E-03		-1.32E+00	3.80E-08	Down	-1.66E+00	1.51E-11	Down			Unigene47665_All//4.00E-31//TC162857				
Unigene47666_All	1235	8.22	83.53	18.11	2.02	2.68	4.06	3.18	3.08	6.74	3.35E+00	0.00E+00	Up	1.14E+00	9.82E-20	Up	4.08E-01	2.65E-01		1.01E+00	1.59E-04	Up	-4.80E-02	8.81E-01		1.08E+00	2.42E-09	Up	Unigene47666_All//gi|75154955|sp|Q8LBB7.1|LOG5_ARATH//1.00E-92//RecName: Full=Cytokinin riboside 5'-monophosphate phosphoribohydrolase LOG5; AltName: Full=Protein LONELY GUY 5 >gi|21592909|gb|AAM64859.1| lysine decarboxylase-like protein [Arabidopsis thaliana] >gi|111074284|gb|ABH04515.1| At4g35190 [Arabidopsis thaliana]	Unigene47666_All//3.00E-84//AT4G35190| unknown protein	Unigene47666_All//0.00E+00//D#519735				nr +
Unigene47669_All	1768	14.00	7.91	9.13	17.78	14.88	19.57	14.97	7.38	7.53	-8.23E-01	1.66E-13		-6.17E-01	4.55E-08		-2.57E-01	6.24E-03		1.38E-01	1.87E-01		-1.02E+00	8.77E-25	Down	-9.92E-01	2.21E-24		Unigene47669_All|gi|297837423|ref|XP_002886593.1|//0.00E+00//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297332434|gb|EFH62852.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene47669_All//1.00E-164//AT1G60720| pentatricopeptide (PPR) repeat-containing protein	Unigene47669_All//0.00E+00//TC163408				nr +
Unigene4767_All	1178	0.89	2.88	0.99	3.64	3.68	2.15	0.90	1.06	1.86	1.70E+00	3.39E-06	Up	1.63E-01	7.82E-01		1.83E-02	9.63E-01		-7.60E-01	8.87E-03		2.46E-01	6.45E-01		1.05E+00	5.43E-03		Unigene4767_All|gi|297610528|ref|NP_001064665.2|//1.00E-10//Os10g0431000 [Oryza sativa Japonica Group] >gi|255679428|dbj|BAF26579.2| Os10g0431000 [Oryza sativa Japonica Group]	Unigene4767_All//1.00E-10//AT4G17410| zinc ion binding	Unigene4767_All//3.00E-174//gi|164239409|gb|ES793530.1|ES793530		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene47670_All	1027	2.39	2.71	3.01	46.32	35.81	68.69	19.23	42.73	16.41	1.81E-01	6.19E-01		3.29E-01	3.88E-01		-3.71E-01	1.37E-07		5.68E-01	6.29E-21		1.15E+00	4.23E-49	Up	-2.29E-01	4.19E-02		Unigene47670_All//gi|30102914|gb|AAP21375.1|//1.00E-40//At3g61920 [Arabidopsis thaliana]	Unigene47670_All//1.00E-40//AT3G61920| unknown protein	Unigene47670_All//0.00E+00//TC158697				nr +
Unigene4768_All	739	114.77	68.15	134.53	7.35	16.64	9.41	1.32	0.45	5.18	-7.52E-01	4.47E-38		2.29E-01	2.14E-05		1.18E+00	6.38E-14	Up	3.57E-01	1.32E-01		-1.54E+00	1.90E-02		1.98E+00	2.64E-10	Up	Unigene4768_All|gi|225461183|ref|XP_002283133.1|//3.00E-14//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene4768_All//0.00E+00//CO075589				nr -
Unigene47684_All	1510	2.32	2.85	2.12	24.78	33.30	30.93	9.86	2.93	7.41	2.97E-01	3.38E-01		-1.34E-01	6.97E-01		4.26E-01	5.53E-10		3.20E-01	2.66E-05		-1.75E+00	1.61E-31	Down	-4.11E-01	1.14E-03		Unigene47684_All|gi|15240866|ref|NP_196397.1|//0.00E+00//flavin-containing monooxygenase family protein / FMO family protein [Arabidopsis thaliana] >gi|10176714|dbj|BAB09944.1| dimethylaniline monooxygenase-like protein [Arabidopsis thaliana]	Unigene47684_All//8.00E-180//AT5G07800| flavin-containing monooxygenase family protein / FMO family protein	Unigene47684_All//0.00E+00//TC169146				nr +

Unigene47685_All	1081	0.24	0.56	0.00	0.55	0.89	2.55	0.70	11.87	22.00	1.22E+00	2.07E-01		-7.92E+00	8.56E-02		6.90E-01	3.61E-01		2.20E+00	3.13E-07	Up	4.08E+00	4.07E-67	Up	4.97E+00	1.65E-142	Up	Unigene47685_All//gi|18416717|ref|NP_567742.1|//1.00E-171//PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase [Arabidopsis thaliana] >gi|75164938|sp|Q94AA4.1|K6PF3_ARATH RecName: Full=6-phosphofructokinase 3; AltName: Full=Phosphofructokinase 3; AltName: Full=Phosphohexokinase 3 >gi|15146208|gb|AAK83587.1|AT4g26270/T25K17_80 [Arabidopsis thaliana] >gi|19699124|gb|AAL90928.1|AT4g26270/T25K17_80 [Arabidopsis thaliana]	Unigene47685_All//4.00E-172//AT4G26270| PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase	Unigene47685_All//0.00E+00//TC169193		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene47686_All	1891	1.19	0.91	0.42	6.56	5.14	6.54	13.66	5.68	6.49	-3.85E-01	3.69E-01		-1.49E+00	1.37E-03		-3.53E-01	2.49E-02		-3.40E-03	9.82E-01		-1.27E+00	7.60E-34	Down	-1.07E+00	5.18E-27	Down	Unigene47686_All//gi|18416717|ref|NP_567742.1|//0.00E+00//PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase [Arabidopsis thaliana] >gi|75164938|sp|Q94AA4.1|K6PF3_ARATH RecName: Full=6-phosphofructokinase 3; AltName: Full=Phosphofructokinase 3; AltName: Full=Phosphohexokinase 3 >gi|15146208|gb|AAK83587.1|AT4g26270/T25K17_80 [Arabidopsis thaliana] >gi|19699124|gb|AAL90928.1|AT4g26270/T25K17_80 [Arabidopsis thaliana]	Unigene47686_All//0.00E+00//AT4G26270| PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase	Unigene47686_All//0.00E+00//gi|164253482|gb|ES809798.1|ES809798		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene47688_All	982	14.33	12.38	13.12	13.59	16.34	14.90	6.37	4.30	2.47	-2.11E-01	1.89E-01		-1.27E-01	4.60E-01		2.65E-01	6.48E-02		1.32E-01	4.59E-01		-5.68E-01	7.04E-03		-1.36E+00	4.04E-10	Down	Unigene47688_All//gi|18399536|ref|NP_566413.1|//1.00E-73//sequence-specific DNA binding [Arabidopsis thaliana]	Unigene47688_All//5.00E-52//AT3G12210| sequence-specific DNA binding	Unigene47688_All//0.00E+00//gi|109834348|gb|DW232913.1|DW232913				nr +
Unigene47689_All	1063	5.32	4.05	10.47	12.09	9.07	7.56	2.78	0.51	0.75	-3.92E-01	1.25E-01		9.78E-01	4.85E-08		-4.15E-01	5.79E-03		-6.77E-01	9.82E-06		-2.45E+00	3.91E-10	Down	-1.89E+00	7.36E-08	Down	Unigene47689_All//gi|18399536|ref|NP_566413.1|//9.00E-79//sequence-specific DNA binding [Arabidopsis thaliana]	Unigene47689_All//2.00E-57//AT3G12210| sequence-specific DNA binding	Unigene47689_All//0.00E+00//gi|109834348|gb|DW232913.1|DW232913				nr +
Unigene4769_All	1013	17.87	20.61	12.25	25.82	16.59	18.41	20.37	10.23	8.34	2.06E-01	1.09E-01		-5.45E-01	4.99E-05		-6.38E-01	4.95E-11		-4.88E-01	2.25E-06		-9.93E-01	1.16E-18		-1.29E+00	8.81E-29	Down	Unigene4769_All//gi|115466536|ref|NP_001056867.1|//2.00E-95//Os06g0158600 [Oryza sativa Japonica Group] >gi|113594907|dbj|BAF18781.1|Os06g0158600 [Oryza sativa Japonica Group]	Unigene4769_All//2.00E-93//AT2G46230| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF652 (InterPro:IPR006984), Nucleotide binding protein, PINc (InterPro:IPR006596); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G26530.1); Has 493 Blast hits to 493 proteins in 165 species: Archae - 21; Bacteria - 0; Metazoa - 192; Fungi - 143; Plants - 53; Viruses - 0; Other Eukaryotes - 84 (source: NCBI BLink).	Unigene4769_All//0.00E+00//TC153082				nr +
Unigene47690_All	1470	3.84	2.48	2.97	16.33	10.45	17.17	12.94	4.98	2.71	-6.31E-01	1.15E-02		-3.72E-01	1.66E-01		-6.45E-01	2.40E-10		7.24E-02	6.20E-01		-1.38E+00	1.43E-28	Down	-2.26E+00	1.47E-57	Down	Unigene47690_All//gi|297849186|ref|XP_002892474.1|//5.00E-68//VAMP/synaptobrevin-associated protein 27-2 [Arabidopsis lyrata subsp. lyrata] >gi|297338316|gb|EFH68733.1|VAMP/synaptobrevin-associated protein 27-2 [Arabidopsis lyrata subsp. lyrata]	Unigene47690_All//9.00E-61//AT1G08820| VAP27-2 (VAMP/SYNAPTOBREVIN-ASSOCIATED PROTEIN 27-2); structural molecule	Unigene47690_All//0.00E+00//TC169628				nr +
Unigene47691_All	328	5.42	4.17	1.46	11.09	7.98	5.78	15.60	11.47	15.55	-3.79E-01	4.35E-01		-1.89E+00	7.43E-04	Down	-4.75E-01	1.41E-01		-9.39E-01	3.27E-03		-4.44E-01	6.69E-02		-4.70E-03	9.80E-01		Unigene47691_All//gi|9759187|dbj|BAB09724.1|//1.00E-45//importin beta [Arabidopsis thaliana]	Unigene47691_All//5.00E-47//AT5G53480| importin beta-2, putative	Unigene47691_All//7.00E-169//TC175708				nr +
Unigene47693_All	1480	10.29	5.48	6.80	8.25	11.21	8.39	7.63	3.50	5.79	-9.09E-01	4.78E-10		-5.97E-01	5.44E-05		4.44E-01	6.41E-04		2.52E-02	9.10E-01		-1.12E+00	9.52E-13	Down	-3.98E-01	7.05E-03		Unigene47693_All//gi|15227607|ref|NP_181165.1|//1.00E-119//APG10 (ALBINO AND PALE GREEN 10); 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4- carboxamide isomerase [Arabidopsis thaliana] >gi|52000658|sp|082782.1|HIS4_ARATH RecName: Full=1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase, chloroplastic; AltName: Full=Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase; AltName: Full=5-proFAR isomerase; AltName: Full=HBM I1; Flags: Precursor >gi|3449282|dbj|BAA32456.1|phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase [Arabidopsis thaliana] >gi|3449284|dbj|BAA32457.1| N"-5"-phosphoribosyl-formimino-5-aminoimidazole- 4-carboxamide ribonucleotide isomerase [Arabidopsis thaliana] >gi|4510353|gb|AAD21442.1|phosphoribosylformimino-5-	Unigene47693_All//6.00E-121//AT2G36230| APG10 (ALBINO AND PALE GREEN 10); 1-(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase	Unigene47693_All//0.00E+00//TC142077		ko00340|Histidine metabolism		nr +
Unigene47694_All	1713	2.99	1.86	1.80	0.20	0.16	0.08	5.16	1.83	3.63	-6.84E-01	9.57E-03		-7.31E-01	7.99E-03		-3.41E-01	7.85E-01		-1.36E+00	3.37E-01		-1.50E+00	2.38E-15	Down	-5.08E-01	2.51E-03		Unigene47694_All//gi|9759111|dbj|BAB09596.1|//1.00E-176//acetolactate synthase-like protein [Arabidopsis thaliana] >gi|63003744|gb|AAY25401.1|At5g16290 [Arabidopsis thaliana] >gi|110742103|dbj|BAE98982.1|acetolactate synthase-like protein [Arabidopsis thaliana]	Unigene47694_All//2.00E-177//AT5G16290| acetolactate synthase small subunit, putative	Unigene47694_All//0.00E+00//TC172007		ko00650|Butanoate metabolism//ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis//ko00660|C5-Branched dibasic acid metabolism		nr +
Unigene47697_All	1021	65.85	42.18	69.63	22.54	38.25	20.70	2.82	2.46	0.78	-6.43E-01	3.45E-23		8.05E-02	2.78E-01		7.63E-01	2.15E-21		-1.23E-01	3.75E-01		-1.97E-01	6.13E-01		-1.85E+00	1.86E-07	Down	Unigene47697_All//gi|297812303|ref|XP_002874035.1|//1.00E-60//YGGT family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319872|gb|EFH50294.1| YGGT family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47697_All//1.00E-59//AT5G21920| YGGT family protein	Unigene47697_All//0.00E+00//TC133223				nr -
Unigene47698_All	1346	1.79	0.90	1.98	3.52	2.33	3.02	3.83	1.86	3.08	-9.85E-01	1.66E-02		1.46E-01	7.08E-01		-5.95E-01	2.47E-02		-2.19E-01	4.80E-01		-1.04E+00	1.27E-05	Down	-3.16E-01	1.85E-01		Unigene47698_All//gi|15219974|ref|NP_173709.1|//9.00E-70//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|193806406|sp|P0C7Q9.1|PPR56_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g22960, mitochondrial; Flags: Precursor	Unigene47698_All//4.00E-71//AT1G22960| pentatricopeptide (PPR) repeat-containing protein	Unigene47698_All//0.00E+00//ES839995				nr +
Unigene477_All	569	0.09	0.45	0.56	1.05	0.30	0.16	1.41	1.10	4.13	2.27E+00	2.34E-01		2.61E+00	1.46E-01		-1.80E+00	5.86E-02		-2.73E+00	1.74E-02		-3.58E-01	6.48E-01		1.55E+00	5.38E-05	Up	Unigene477_All//gi|32815816|gb|AAP88291.1|//1.00E-41//protein kinase [Cucumis sativus]	Unigene477_All//2.00E-41//AT3G27560| ATN1; kinase/ protein serine/threonine kinase/ protein serine/threonine/tyrosine kinase/ protein tyrosine kinase	Unigene477_All//1.00E-91//TC157350			GO:0004702//GO:0006464//GO:0032559//GO:0043231	nr +
Unigene4770_All	647	14.07	23.96	28.31	105.71	117.84	93.89	11.83	18.02	15.21	7.68E-01	7.72E-08		1.01E+00	1.89E-13	Up	1.57E-01	9.35E-03		-1.71E-01	9.12E-03		6.08E-01	3.90E-05		3.63E-01	2.45E-02		Unigene4770_All//gi|255557991|ref|XP_002520024.1|//7.00E-09//conserved hypothetical protein [Ricinus communis] >gi|223540788|gb|EEF42348.1|conserved hypothetical protein [Ricinus communis]		Unigene4770_All//0.00E+00//DW496631				nr -
Unigene47701_All	1972	1.57	17.96	4.62	7.55	8.89	21.05	35.87	86.92	69.80	3.52E+00	7.47E-134	Up	1.56E+00	3.29E-13	Up	2.35E-01	9.09E-02		1.48E+00	1.79E-59	Up	1.28E+00	5.64E-223	Up	9.60E-01	7.29E-116		Unigene47701_All//gi|223452400|gb|ACM89527.1|//0.00E+00//protein kinase-related protein [Glycine max]	Unigene47701_All//0.00E+00//AT5G02070| protein kinase-related	Unigene47701_All//0.00E+00//TC176021		ko04626|Plant-pathogen interaction		nr +
Unigene47702_All	1748	2.27	1.77	0.91	6.27	6.17	5.09	7.30	1.15	3.26	-3.64E-01	2.44E-01		-1.32E+00	6.70E-05	Down	-2.40E-02	9.04E-01		-3.01E-01	9.86E-02		-2.67E+00	1.00E-45	Down	-1.16E+00	1.34E-15	Down	Unigene47702_All//gi|108706818|gb|ABF94613.1|//4.00E-77//Targeting protein for Xklp2 containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene47702_All//2.00E-100//AT3G01015| EXPRESSED IN: 8 plant structures; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis, F mature embryo stage, D bilateral stage; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G15510.1); Has 341 Blast hits to 320 proteins in 58 species: Archae - 0; Bacteria - 0; Metazoa - 122; Fungi - 12; Plants - 165; Viruses - 0; Other Eukaryotes - 42 (source: NCBI BLink).			ko04141|Protein processing in endoplasmic reticulum		nr +

Unigene47703_All	1118	39.45	13.96	23.34	32.39	43.40	16.00	6.50	0.07	2.07	-1.50E+00	2.04E-60	Down	-7.57E-01	1.34E-19		4.22E-01	1.77E-09		-1.02E+00	1.66E-29	Down	-6.44E+00	5.12E-48	Down	-1.65E+00	3.71E-15	Down	Unigene47703_All//gi|33468424|emb|CAD67694.1|//1.00E-107//Nod26-like protein [Cucurbita pepo]	Unigene47703_All//2.00E-59//AT5G37820| NIP4;2 (NOD26-LIKE INTRINSIC PROTEIN 4;2); water channel	Unigene47703_All//0.00E+00//TC142738				nr -
Unigene47704_All	1535	3.92	3.27	1.80	11.26	9.24	10.89	8.07	7.54	5.24	-2.62E-01	3.07E-01		-1.12E+00	1.24E-05	Down	-2.85E-01	3.23E-02		-4.88E-02	7.54E-01		-9.76E-02	5.88E-01		-6.22E-01	8.12E-06		Unigene47704_All//gi|145338625|ref|NP_188360.3|//1.00E-115//binding / protein transporter [Arabidopsis thaliana]	Unigene47704_All//2.00E-94//AT3G17340| binding / protein transporter	Unigene47704_All//0.00E+00//gi|13353021|gb|BG443369.1|BG443369				nr -
Unigene47705_All	1720	2.01	2.68	1.27	6.92	4.56	5.07	8.48	6.20	3.17	4.17E-01	1.44E-01		-6.62E-01	5.75E-02		-6.01E-01	7.57E-05		-4.50E-01	5.94E-03		-4.53E-01	5.43E-04		-1.42E+00	9.90E-24	Down	Unigene47705_All//gi|145338625|ref|NP_188360.3|//1.00E-133//binding / protein transporter [Arabidopsis thaliana]	Unigene47705_All//8.00E-106//AT3G17340| binding / protein transporter	Unigene47705_All//0.00E+00//TC173247				nr -
Unigene47706_All	1286	4.27	5.91	5.34	3.56	3.21	2.99	2.40	0.59	1.15	4.68E-01	2.80E-02		3.22E-01	1.86E-01		-1.49E-01	6.22E-01		-2.56E-01	4.17E-01		-2.04E+00	1.41E-08	Down	-1.07E+00	5.76E-04	Down	Unigene47706_All//gi|42567513|ref|NP_195577.2|//1.00E-157//glycosyl hydrolase family 10 protein [Arabidopsis thaliana] >gi|28416709|gb|AAO42885.1|At4g38650 [Arabidopsis thaliana]	Unigene47706_All//1.00E-158//AT4G38650| glycosyl hydrolase family 10 protein	Unigene47706_All//0.00E+00//ES803339				nr -
Unigene4771_All	1255	9.09	5.49	6.70	4.60	6.04	5.11	39.38	13.75	28.47	-7.27E-01	1.55E-05		-4.39E-01	1.33E-02		3.91E-01	6.96E-02		1.50E-01	6.06E-01		-1.52E+00	3.93E-84	Down	-4.68E-01	1.36E-12		Unigene4771_All//gi|225429418|ref|XP_002278546.1|//3.00E-68//PREDICTED: similar to Os05g0553400 [Vitis vinifera]	Unigene4771_All//3.00E-56//AT3G49690| MYB84 (MYB DOMAIN PROTEIN 84); DNA binding / transcription factor	Unigene4771_All//3.00E-72//NP524476	MYB			nr -
Unigene47710_All	1463	120.45	185.15	240.81	22.75	29.09	49.76	0.72	3.74	1.82	6.20E-01	1.52E-85		1.00E+00	5.48E-246		3.55E-01	3.12E-06		1.13E+00	9.22E-69	Up	2.37E+00	1.66E-17	Up	1.34E+00	1.23E-04	Up	Unigene47710_All//gi|115450643|ref|NP_001048922.1|//2.00E-59//Os03g0140700 [Oryza sativa Japonica Group] >gi|108706105|gb|ABF93900.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547393|dbj|BAF10836.1|Os03g0140700 [Oryza sativa Japonica Group]	Unigene47710_All//1.00E-29//AT4G17940| binding	Unigene47710_All//0.00E+00//TC178605				nr +
Unigene47716_All	1668	16.22	17.13	10.25	20.46	16.54	21.69	26.51	46.33	83.14	7.93E-02	5.00E-01		-6.62E-01	7.90E-10		-3.07E-01	4.16E-04		8.43E-02	4.51E-01		8.05E-01	1.16E-47		1.65E+00	9.19E-270	Up	Unigene47716_All//gi|75163673|sp|Q93W5.1|P2C58_ARATH//1.00E-116//RecName: Full=Probable protein phosphatase 2C 58; Short=AtPP2C58	Unigene47716_All//5.00E-118//AT4G28400| protein phosphatase 2C, putative / PP2C, putative	Unigene47716_All//0.00E+00//ES806717				nr -
Unigene4772_All	1180	640.75	231.28	386.96	189.34	161.12	151.03	4.73	4.46	3.44	-1.47E+00	0.00E+00	Down	-7.28E-01	0.00E+00		-2.33E-01	3.60E-14		-3.26E-01	8.79E-24		-8.37E-02	7.34E-01		-4.58E-01	3.70E-02		Unigene4772_All//gi|45773780|gb|AAS76694.1|//2.00E-62//At5g58250 [Arabidopsis thaliana] >gi|46539839|gb|AAS88783.1|At5g58250 [Arabidopsis thaliana]	Unigene4772_All//2.00E-61//AT5G58250| unknown protein	Unigene4772_All//0.00E+00//TC135432				nr +
Unigene47720_All	2014	2.70	4.00	0.87	3.51	4.24	3.74	11.17	13.01	18.06	5.66E-01	5.68E-03		-1.63E+00	1.34E-08	Down	2.72E-01	2.04E-01		9.26E-02	6.95E-01		2.20E-01	2.70E-02		6.93E-01	2.78E-18		Unigene47720_All//gi|297719995|ref|NP_001172359.1|//1.00E-168//Os01g0388566 [Oryza sativa Japonica Group] >gi|255673262|dbj|BAH91089.1|Os01g0388566 [Oryza sativa Japonica Group]	Unigene47720_All//0.00E+00//AT2G48060| unknown protein	Unigene47720_All//0.00E+00//EX172533				nr -
Unigene47721_All	1418	6.79	9.54	9.46	5.45	4.54	4.75	4.59	1.95	1.85	4.91E-01	1.34E-03		4.79E-01	2.75E-03		-2.62E-01	2.40E-01		-1.98E-01	4.06E-01		-1.24E+00	7.50E-09	Down	-1.31E+00	6.83E-10	Down	Unigene47721_All//gi|224126779|ref|XP_002329471.1|//7.00E-97//mtn21-like protein [Populus trichocarpa] >gi|222870151|gb|EEF07282.1|mtn21-like protein [Populus trichocarpa]	Unigene47721_All//3.00E-47//AT2G39510| nodulin MtN21 family protein					nr +
Unigene47723_All	917	3.14	2.49	4.99	4.45	3.23	2.02	3.97	1.87	2.39	-3.36E-01	3.72E-01		6.70E-01	2.32E-02		-4.64E-01	1.22E-01		-1.14E+00	1.44E-04	Down	-1.09E+00	1.93E-04	Down	-7.31E-01	8.27E-03			Unigene47723_All//0.00E+00//CO097388					
Unigene47725_All	1160	4.56	3.58	5.33	2.19	5.85	4.24	1.86	1.30	1.89	-3.47E-01	1.98E-01		2.25E-01	3.95E-01		1.42E+00	2.91E-10	Up	9.54E-01	3.97E-04		-5.19E-01	1.98E-01		2.31E-02	9.69E-01		Unigene47725_All//gi|85701293|sp|Q9SQ29.2|Y3478_ARATH//1.00E-50//RecName: Full=UPF0424 protein At3g04780 >gi|16648681|gb|AAL25533.1|AT3g04780/F7018_27 [Arabidopsis thaliana] >gi|20147247|gb|AAM10337.1|AT3g04780/F7018_27 [Arabidopsis thaliana]	Unigene47725_All//8.00E-52//AT3G04780| Encodes a protein with little sequence identity with any other protein of known structure or function. Part of this protein shows a 42% sequence identity with the C-terminal domain of the 32-kD human thioredoxin-like protein.	Unigene47725_All//2.00E-126//BG446251				nr +
Unigene47727_All	1496	2.48	9.11	0.64	3.96	5.00	44.20	3.45	27.80	119.17	1.88E+00	7.01E-26	Up	-1.95E+00	1.35E-07	Down	3.34E-01	1.36E-01		3.48E+00	7.78E-265	Up	3.01E+00	6.44E-167	Up	5.11E+00	0.00E+00	Up	Unigene47727_All//gi|224083841|ref|XP_002307142.1|//6.00E-61//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222856591|gb|EEE94138.1|AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene47727_All//2.00E-27//AT5G64750| ABR1 (ABA REPRESSOR1); DNA binding / transcription factor	Unigene47727_All//0.00E+00//TC151663	AP2-EREBP			nr -
Unigene4773_All	645	0.57	6.91	2.23	2.24	4.80	3.29	2.03	2.66	2.72	3.61E+00	1.42E-17	Up	1.97E+00	2.09E-03		1.10E+00	1.46E-03		5.55E-01	2.29E-01		3.87E-01	4.05E-01		4.19E-01	3.48E-01				Unigene4773_All//8.00E-07//DW516027				
Unigene47731_All	1368	0.96	1.67	1.56	3.57	4.58	4.95	3.65	1.65	1.69	8.02E-01	5.88E-02		7.03E-01	1.31E-01		3.60E-01	1.45E-01		4.73E-01	4.02E-02		-1.14E+00	3.07E-06	Down	-1.11E+00	3.27E-06	Down		Unigene47731_All//3.00E-57//ES836194				
Unigene47732_All	2114	4.88	10.23	2.47	9.24	7.77	7.69	14.06	17.34	53.48	1.07E+00	6.04E-18	Up	-9.82E-01	1.58E-07		-2.50E-01	4.82E-02		-2.64E-01	4.24E-02		3.02E-01	1.45E-04		1.93E+00	5.84E-273	Up	Unigene47732_All//gi|18425169|ref|NP_569047.1|//1.00E-178//SKIP2 (SKP1/ASK1 INTERACTING PROTEIN 2); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75272932|sp|Q9FE83.1|SKIP2_ARATH RecName: Full=F-box protein SKIP2; AltName: Full=SKP1-interacting partner 2 >gi|10716949|gb|AAG21977.1| SKP1 interacting partner 2 [Arabidopsis thaliana] >gi|27311735|gb|AAO00833.1| SKP1 interacting partner 2 (SKIP2) [Arabidopsis thaliana] >gi|31711938|gb|AAP68325.1|At5g67250 [Arabidopsis thaliana]	Unigene47732_All//8.00E-177//AT5G67250| SKIP2 (SKP1/ASK1 INTERACTING PROTEIN 2); ubiquitin-protein ligase	Unigene47732_All//0.00E+00//TC133439		ko04626|Plant-pathogen interaction		nr -
Unigene47734_All	1456	640.21	290.44	607.11	73.46	69.53	61.20	2.79	6.23	3.17	-1.14E+00	0.00E+00	Down	-7.66E-02	7.06E-06		-7.92E-02	1.61E-01		-2.63E-01	5.17E-08		1.16E+00	6.85E-11	Up	1.87E-01	4.86E-01		Unigene47734_All//gi|32746733|gb|AP87140.1|//1.00E-177//mRNA-binding protein precursor [Nicotiana tabacum]	Unigene47734_All//3.00E-165//AT3G63140| CSP41A (CHLOROPLAST STEM-LOOP BINDING PROTEIN OF 41 KDA); mRNA binding / poly(U) binding	Unigene47734_All//0.00E+00//TC166709				nr -
Unigene47735_All	1201	1.57	1.27	0.58	2.99	3.10	2.03	0.99	1.91	2.32	-3.09E-01	5.23E-01		-1.44E+00	5.08E-03		5.23E-02	8.95E-01		-5.56E-01	9.39E-02		9.57E-01	1.12E-02		1.24E+00	2.31E-04	Up	Unigene47735_All//gi|75336836|sp|Q9SZ16.1|RPK2_ARATH//1.00E-96//RecName: Full=LRR receptor-like serine/threonine-protein kinase RPK2; AltName: Full=Receptor-like protein kinase 2; AltName: Full=Protein TOADSTOOL 2; Flags: Precursor	Unigene47735_All//7.00E-116//AT3G02130| RPK2 (RECEPTOR-LIKE PROTEIN KINASE 2); ATP binding / kinase/ protein serine/threonine kinase	Unigene47735_All//0.00E+00//ES823054				nr +
Unigene47736_All	1060	107.85	81.88	95.10	84.40	84.69	71.88	44.08	22.87	19.17	-3.97E-01	1.19E-16		-1.82E-01	3.61E-04		4.90E-03	9.58E-01		-2.32E-01	1.73E-05		-9.47E-01	4.04E-38		-1.20E+00	1.89E-57	Down	Unigene47736_All//gi|224144638|ref|XP_002325358.1|//2.00E-79//type IIIF peroxiredoxin [Populus trichocarpa] >gi|222862233|gb|EEE99739.1| type IIF peroxiredoxin [Populus trichocarpa]	Unigene47736_All//6.00E-79//AT3G06050| PRXIIF (PEROXIREDOXIN IIF); antioxidant/ peroxidase	Unigene47736_All//0.00E+00//TC132090		ko04146|Peroxisome		nr +
Unigene47739_All	966	6.39	27.28	15.66	15.42	23.03	49.60	8.93	15.01	11.92	2.09E+00	4.68E-57	Up	1.29E+00	2.25E-16	Up	5.79E-01	8.31E-08		1.69E+00	7.01E-83	Up	7.50E-01	1.36E-08		4.17E-01	4.35E-03		Unigene47739_All//gi|9958057|gb|AAG09546.1|AC011810_5//8.00E-17//Unknown Protein [Arabidopsis thaliana]	Unigene47739_All//2.00E-15//AT1G13360| unknown protein	Unigene47739_All//0.00E+00//TC134780				nr +
Unigene4774_All	932	6.62	17.67	7.71	10.96	12.93	13.81	5.35	5.20	7.14	1.42E+00	4.79E-21	Up	2.20E-01	3.80E-01		2.39E-01	1.71E-01		3.34E-01	4.03E-02		-4.13E-02	8.84E-01		4.15E-01	3.82E-02		Unigene4774_All//gi|75334522|sp|Q9FYK2.1|CML25_ARATH//5.00E-55//RecName: Full=Probable calcium-binding protein CML25; AltName: Full=Calmodulin-like protein 25 >gi|9743349|gb|AAF97973.1|AC000103_23 F21J9.28 [Arabidopsis thaliana] >gi|91805849|gb|ABE65653.1|polcalcin [Arabidopsis thaliana]	Unigene4774_All//3.00E-56//AT1G24620| polcalcin, putative / calcium-binding pollen allergen, putative	Unigene4774_All//0.00E+00//TC156088		ko04626|Plant-pathogen interaction		nr +
Unigene47740_All	1288	6.74	13.53	12.40	10.87	12.91	9.89	9.72	14.41	10.08	1.01E+00	2.92E-13	Up	8.79E-01	1.61E-09		2.49E-01	8.06E-02		-1.36E-01	4.51E-01		5.68E-01	6.54E-07		5.35E-02	7.30E-01		Unigene47740_All//gi|4455156|emb|CAA16784.1|//1.00E-172//CDP-diacylglycerol synthetase-like protein [Arabidopsis thaliana] >gi|7269080|emb|CAB79189.1| CDP-diacylglycerol synthetase-like protein [Arabidopsis thaliana] >gi|21536804|gb|AAM61136.1| CDP-diacylglycerol synthetase-like protein [Arabidopsis thaliana]	Unigene47740_All//7.00E-174//AT4G22340| phosphatidate cytidylyltransferase, putative / CDP-diglyceride synthetase, putative	Unigene47740_All//0.00E+00//gi|48818879|gb|CO120192.1|CO120192		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism		nr -
Unigene47741_All	1013	23.60	24.36	25.18	41.75	39.77	35.49	43.03	32.06	16.48	4.55E-02	7.08E-01		9.32E-02	4.63E-01		-7.00E-02	5.00E-01		-2.34E-01	4.92E-03		-4.25E-01	3.14E-09		-1.38E+00	9.58E-67	Down	Unigene47741_All//gi|259130182|gb|ACV95534.1|//1.00E-101//protein L-isoaspartyl methyltransferase [Cicer arietinum] >gi|282761987|gb|ADA84676.1|protein L-isoaspartyl methyltransferase 1 [Cicer arietinum]	Unigene47741_All//5.00E-96//AT5G50240| PIMT2 (PROTEIN-L-ISOASPARTATE METHYLTRANSFERASE 2); protein-L-isoaspartate (D-aspartate) O-methyltransferase	Unigene47741_All//0.00E+00//TC140762				nr +
Unigene47744_All	1278	4.59	3.21	3.83	60.14	50.09	26.86	311.58	279.06	134.01	-5.14E-01	3.67E-02		-2.58E-01	3.51E-01		-2.64E-01	1.69E-06		-1.16E+00	5.11E-77	Down	-1.59E-01	1.28E-12		-1.22E+00	0.00E+00	Down	Unigene47744_All//gi|211906536|gb|ACJ11761.1|//0.00E+00//class III peroxidase [Gossypium hirsutum]	Unigene47744_All//4.00E-124//AT1G05260| RCI3 (RARE COLD INDUCIBLE GENE 3); peroxidase	Unigene47744_All//0.00E+00//TC143685		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene47745_All	265	3.16	4.21	4.42	5.64	3.25	3.92	29.36	42.58	9.77	4.13E-01	5.26E-01		4.85E-01	4.47E-01		-7.96E-01	1.31E-01		-5.25E-01	3.66E-01		5.37E-01	3.68E-04		-1.59E+00	2.86E-15	Down	Unigene47745_All//2.00E-16//AT2G39940| COI1 (CORONATINE INSENSITIVE 1); protein binding / ubiquitin-protein ligase	Unigene47745_All//2.00E-131//gi|109879708|gb|DW508678.1|DW508678		ko04626|Plant-pathogen interaction		nr -
Unigene47747_All	1408	49.65	124.95	147.69	31.77	35.51	38.40	0.60	1.10	1.39	1.33E+00	4.00E-199	Up	1.57E+00	3.41E-295	Up	1.61E-01	3.96E-02		2.73E-01	1.19E-04		8.71E-01	6.92E-02		1.21E+00	3.22E-03		Unigene47747_All//gi|22331680|ref|NP_680110.1|//1.00E-120//CYP71A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|13878403|sp|Q9STL1.1|C71AM_ARATH RecName: Full=Cytochrome P450 71A22 >gi|4678357|emb|CAB41167.1|cytochrome P450-like protein [Arabidopsis thaliana]	Unigene47747_All//1.00E-113//AT3G48310| CYP71A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene47747_All//0.00E+00//TC174831		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism		nr +
Unigene47749_All	1464	0.64	0.76	0.91	1.12	1.29	1.42	1.82	1.23	0.52	2.43E-01	6.82E-01		4.99E-01	3.93E-01		2.04E-01	7.18E-01		3.38E-01	4.92E-01		-5.68E-01	1.06E-01		-1.82E+00	8.29E-07	Down	Unigene47749_All//gi|289466339|gb|ADC94855.1|//3.00E-98//B-zip transcription factor [Vitis pseudoreticulata]	Unigene47749_All//1.00E-55//AT1G24267| unknown protein	Unigene47749_All//0.00E+00//TC178698				nr +

Unigene4775_All	974	3.55	13.11	6.45	1.59	3.71	5.61	2.87	3.69	4.05	1.89E+00	1.77E-24	Up	8.64E-01	4.31E-04		1.23E+00	1.09E-04	Up	1.82E+00	5.99E-11	Up	3.65E-01	2.37E-01		4.99E-01	6.29E-02									
Unigene47751_All	2091	13.24	6.47	9.83	32.16	31.49	23.78	10.07	3.22	4.13	-1.03E+00	1.34E-21	Down	-4.29E-01	5.61E-05		-3.05E-02	7.29E-01		-4.36E-01	1.37E-12		-1.65E+00	1.02E-40	Down	-1.28E+00	3.33E-29	Down	Unigene47751_All//gi|225007946|gb|ACN78665.1|//1.00E-165//endo-beta-mannanase [Malus x domestica]	Unigene47751_All//1.00E-148//AT2G20680| glycosyl hydrolase family 5 protein / cellulase family protein	Unigene47751_All//0.00E+00//TC143532				nr -
Unigene47753_All	1669	0.60	3.49	1.95	0.69	1.57	1.08	0.53	3.08	5.30	2.55E+00	1.89E-16	Up	1.71E+00	9.75E-06	Up	1.19E+00	2.00E-03		6.57E-01	1.96E-01		2.53E+00	1.01E-17	Up	3.32E+00	4.47E-40	Up	Unigene47753_All//gi|124359941|gb|ABW07857.1|//7.00E-27//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene47753_All//1.00E-22//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene47753_All//0.00E+00//C0071475				nr -
Unigene47754_All	1415	0.52	2.47	0.87	0.39	0.54	0.67	0.45	1.24	2.25	2.25E+00	7.25E-09	Up	7.41E-01	2.46E-01		4.68E-01	6.07E-01		7.92E-01	2.99E-01		1.47E+00	1.38E-03		2.33E+00	1.62E-10	Up	Unigene47754_All//gi|115473321|ref|NP_001060259.1|//2.00E-24//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene47754_All//1.00E-22//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene47754_All//3.00E-131//C0071475				nr -
Unigene47755_All	1651	0.35	2.49	0.19	2.11	1.56	1.94	2.79	3.57	1.09	2.83E+00	4.21E-13	Up	-8.49E-01	3.97E-01		-4.33E-01	1.95E-01		-1.21E-01	7.28E-01		3.55E-01	1.21E-01		-1.36E+00	1.16E-07	Down	Unigene47755_All//gi|15225187|ref|NP_180771.1|//0.00E+00//HSP70T-2 (HEAT-SHOCK PROTEIN 70T-2); ATP binding [Arabidopsis thaliana] >gi|30685183|ref|NP_850183.1| HSP70T-2 (HEAT-SHOCK PROTEIN 70T-2); ATP binding [Arabidopsis thaliana] >gi|4263707|gb|AAD15393.1| 70kD heat shock protein [Arabidopsis thaliana] >gi|21703121|gb|AAM74502.1| At2g32120/F22D22.13 [Arabidopsis thaliana] >gi|24111419|gb|AAN46859.1| At2g32120/F22D22.13 [Arabidopsis thaliana]	Unigene47755_All//0.00E+00//AT2G32120| HSP70T-2 (HEAT-SHOCK PROTEIN 70T-2); ATP binding	Unigene47755_All//0.00E+00//TC137216		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr +
Unigene47758_All	1873	1.01	5.38	1.14	5.61	4.67	19.15	5.82	132.86	24.80	2.42E+00	2.09E-26	Up	1.77E-01	6.88E-01		-2.65E-01	1.52E-01		1.77E+00	1.73E-66	Up	4.51E+00	0.00E+00	Up	2.09E+00	4.77E-125	Up	Unigene47758_All//gi|38194913|gb|AAR13301.1|//1.00E-89//anthocyanin acyltransferase [Phaseolus vulgaris]	Unigene47758_All//4.00E-86//AT1G03940| transferase family protein	Unigene47758_All//0.00E+00//gi|109851541|gb|DW480520.1|DW480520		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene47760_All	1422	7.47	7.59	12.62	3.05	2.93	1.37	5.92	3.67	3.67	2.31E-02	9.14E-01		7.57E-01	2.32E-08		-5.68E-02	8.51E-01		-1.16E+00	6.73E-05	Down	-6.88E-01	1.07E-04		-6.89E-01	6.79E-05		Unigene47760_All//gi|115447703|ref|NP_001047631.1|//4.00E-14//Os02g0657700 [Oryza sativa Japonica Group] >gi|113537162|dbj|BAF09545.1| Os02g0657700 [Oryza sativa Japonica Group]	Unigene47760_All//5.00E-34//AT4G25170| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP012943 (InterPro:IPR016606); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61490.1); Has 87 Blast hits to 86 proteins in 16 species: Archae - 0; Bacteria - 4; Metazoa - 15; Fungi - 3; Plants - 63; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene47760_All//5.00E-90//DW516116				nr -
Unigene47761_All	1624	3.67	5.58	6.03	1.99	0.89	0.47	6.48	3.89	3.46	6.05E-01	1.56E-03		7.16E-01	1.61E-04		-1.16E+00	3.31E-04	Down	-2.08E+00	4.89E-08	Down	-7.38E-01	2.57E-06		-9.06E-01	6.30E-09		Unigene47761_All//gi|116310130|emb|CAH67146.1|//5.00E-23//OS1GB4012223.3 [Oryza sativa (indica cultivar-group)]	Unigene47761_All//3.00E-37//AT4G25170| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP012943 (InterPro:IPR016606); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61490.1); Has 87 Blast hits to 86 proteins in 16 species: Archae - 0; Bacteria - 4; Metazoa - 15; Fungi - 3; Plants - 63; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene47761_All//0.00E+00//TC169584				nr -
Unigene47766_All	1075	15.53	10.09	6.14	16.08	16.27	37.18	20.49	14.85	10.67	-6.22E-01	4.63E-06		-1.34E+00	6.56E-19	Down	1.72E-02	9.25E-01		1.21E+00	3.04E-42	Up	-4.64E-01	7.86E-06		-9.41E-01	8.58E-19		Unigene47766_All//gi|224135721|ref|XP_002322144.1|//8.00E-61//type-a response regulator [Populus trichocarpa] >gi|222869140|gb|EEF06271.1| type-a response regulator [Populus trichocarpa]	Unigene47766_All//2.00E-53//AT5G62920| ARR6 (RESPONSE REGULATOR 6); transcription regulator/ two-component response regulator	Unigene47766_All//2.00E-162//TC155509	ARR-B	ko04712|Circadian rhythm - plant		nr +
Unigene47767_All	1116	33.94	30.87	34.64	69.50	68.50	80.33	21.29	34.34	99.49	-1.37E-01	1.48E-01		2.94E-02	7.71E-01		-2.09E-02	8.16E-01		2.09E-01	1.27E-04		6.90E-01	1.44E-18		2.22E+00	0.00E+00	Up	Unigene47767_All//gi|145323948|ref|NP_001077563.1|//8.00E-81//HhH-GPD base excision DNA repair family protein [Arabidopsis thaliana]	Unigene47767_All//2.00E-81//AT1G19480| HhH-GPD base excision DNA repair family protein	Unigene47767_All//0.00E+00//gi|164366870|gb|ES802625.1|ES802625		ko03410|Base excision repair		nr +
Unigene47769_All	993	53.48	46.69	34.00	182.25	131.60	157.32	74.98	17.34	22.87	-1.96E-01	9.08E-03		-6.54E-01	2.91E-18		-4.70E-01	1.86E-42		-2.12E-01	7.03E-09		-2.11E+00	1.97E-199	Down	-1.71E+00	6.82E-155	Down	Unigene47769_All//gi|256010124|gb|ACU55135.1|//1.00E-100//dirigent-like protein 1 [Gossypium hirsutum]	Unigene47769_All//2.00E-58//AT1G58170| disease resistance-responsive protein-related / dirigent protein-related	Unigene47769_All//0.00E+00//TC152224				nr +
Unigene4777_All	1681	15.03	11.30	6.11	39.59	37.24	25.39	22.26	10.37	15.50	-4.11E-01	1.45E-04		-1.30E+00	4.21E-27	Down	-8.82E-02	2.32E-01		-6.41E-01	1.49E-24		-1.10E+00	3.35E-39	Down	-5.22E-01	1.01E-11		Unigene4777_All//gi|38194913|gb|AAR13301.1|//1.00E-109//anthocyanin acyltransferase [Phaseolus vulgaris]	Unigene4777_All//7.00E-83//AT1G03940| transferase family protein	Unigene4777_All//0.00E+00//gi|78338891|gb|DT559165.1|DT559165				nr -
Unigene47770_All	1543	40.35	188.56	116.99	10.07	20.24	20.43	0.82	0.24	1.60	2.22E+00	0.00E+00	Up	1.54E+00	2.10E-247	Up	1.01E+00	3.68E-27	Up	1.02E+00	1.49E-25	Up	-1.75E+00	2.19E-03		9.62E-01	6.17E-03		Unigene47770_All//gi|124360082|gb|ABN08098.1|//1.00E-102//Transferase [Medicago truncatula]	Unigene47770_All//4.00E-78//AT4G24510| CER2 (ECERIFERUM 2); transferase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene47770_All//0.00E+00//TC174036		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene47772_All	1368	0.08	0.00	0.00	41.07	28.24	9.74	21.08	8.77	5.18	-6.26E+00	3.71E-01		-6.26E+00	3.92E-01		-5.40E-01	2.85E-17		-2.08E+00	2.13E-131	Down	-1.27E+00	1.18E-37	Down	-2.02E+00	1.06E-75	Down	Unigene47772_All//gi|161778780|gb|ABX79341.1|//1.00E-160//cysteine protease [Vitis vinifera]	Unigene47772_All//1.00E-149//AT4G29090| RD19 (RESPONSIVE TO DEHYDRATION 19); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene47772_All//0.00E+00//TC177893				nr -
Unigene47774_All	828	5.69	8.08	3.86	7.70	6.53	8.56	17.11	13.63	8.04	5.06E-01	2.67E-02		-5.60E-01	5.56E-02		-2.38E-01	3.46E-01		1.53E-01	5.68E-01		-3.28E-01	1.63E-02		-1.09E+00	1.45E-15	Down	Unigene47774_All//gi|115482288|ref|NP_001064737.1|//5.00E-28//Os10g0452800 [Oryza sativa Japonica Group] >gi|113639346|dbj|BAF26651.1| Os10g0452800 [Oryza sativa Japonica Group]	Unigene47774_All//3.00E-11//AT5G08420| RNA binding	Unigene47774_All//0.00E+00//gi|164280787|gb|ES798322.1|ES798322				nr +
Unigene47776_All	2078	2.14	1.22	1.26	5.54	2.75	2.24	10.87	15.39	12.15	-8.12E-01	4.61E-03		-7.69E-01	1.02E-02		-1.01E+00	9.04E-11	Down	-1.31E+00	2.76E-14	Down	5.02E-01	3.34E-09		1.62E-01	1.12E-01		Unigene47776_All//gi|224104811|ref|XP_002313574.1|//0.00E+00//calcium dependent protein kinase 5 [Populus trichocarpa] >gi|222849982|gb|EEE87529.1| calcium dependent protein kinase 5 [Populus trichocarpa]	Unigene47776_All//0.00E+00//AT2G17290| CPK6 (CALCIUM-DEPENDENT PROTEIN KINASE 6); ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase	Unigene47776_All//0.00E+00//TC174287		ko04626|Plant-pathogen interaction		nr +
Unigene47777_All	1797	2.07	2.82	1.24	3.55	8.95	9.98	2.07	7.14	10.84	4.48E-01	9.76E-02		-7.32E-01	2.77E-02		1.33E+00	7.66E-22	Up	1.49E+00	2.77E-26	Up	1.79E+00	5.13E-28	Up	2.39E+00	3.50E-62	Up	Unigene47777_All//gi|22331831|ref|NP_191271.2|//1.00E-137//protein kinase family protein [Arabidopsis thaliana]	Unigene47777_All//1.00E-124//AT3G57120| protein kinase family protein	Unigene47777_All//0.00E+00//TC174667		ko04626|Plant-pathogen interaction		nr +
Unigene47778_All	1779	2.50	1.77	2.36	3.44	3.06	2.46	5.32	2.30	2.66	-5.02E-01	8.18E-02		-8.02E-02	7.89E-01		-1.71E-01	5.46E-01		-4.84E-01	4.58E-02		-1.21E+00	4.48E-12	Down	-9.98E-01	2.18E-09		Unigene47778_All//gi|224053781|ref|XP_002297976.1|//1.00E-134//inner membrane protein [Populus trichocarpa] >gi|222845234|gb|EEE82781.1| inner membrane protein [Populus trichocarpa]	Unigene47778_All//3.00E-97//AT5G62050| OXA1; P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene47778_All//0.00E+00//DW503930		ko03060|Protein export		nr -
Unigene4778_All	751	38.74	11.27	10.92	40.46	35.08	37.10	128.14	32.28	40.90	-1.78E+00	3.51E-51	Down	-1.83E+00	4.81E-51	Down	-2.06E-01	3.95E-02		-1.25E-01	2.77E-01		-1.99E+00	2.93E-238	Down	-1.65E+00	3.55E-189	Down	Unigene4778_All//gi|6984134|gb|AAF34767.1|AF227622_1//3.00E-88//60S acidic ribosomal protein P0 [Euphorbia esula]	Unigene4778_All//3.00E-89//AT2G40010| 60S acidic ribosomal protein P0 (RPP0A)	Unigene4778_All//0.00E+00//TC171572		ko03010|Ribosome		nr -
Unigene47783_All	1018	18.50	22.70	8.16	37.34	23.71	25.73	30.28	28.53	35.93	2.95E-01	1.13E-02		-1.18E+00	1.31E-17	Down	-6.55E-01	1.50E-16		-5.37E-01	1.49E-10		-8.55E-02	4.07E-01		2.47E-01	1.72E-03		Unigene47783_All//gi|164564732|dbj|BAF98214.1|//1.00E-91//CM02216.300.nc [Lotus japonicus]	Unigene47783_All//5.00E-89//AT2G26640| KCS11 (3-KETOACYL-COA SYNTHASE 11); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene47783_All//0.00E+00//gi|73865664|gb|DT468402.1|DT468402				nr +
Unigene47784_All	606	5.44	3.26	2.20	2.88	1.76	11.03	15.21	23.66	55.22	-7.38E-01	3.00E-02		-1.31E+00	3.67E-04	Down	-7.08E-01	1.44E-01		1.94E+00	2.30E-14	Up	6.37E-01	1.36E-06		1.86E+00	1.62E-77	Up	Unigene47784_All//gi|226494043|ref|NP_001150498.1|//3.00E-27//LOC100284129 [Zea mays] >gi|195639632|gb|ACG39284.1| pathogen-related protein [Zea mays]	Unigene47784_All//7.00E-22//AT1G78780| pathogenesis-related family protein					nr -
Unigene47785_All	1086	12.82	8.21	9.37	6.56	3.61	19.46	16.31	22.13	83.20	-6.42E-01	1.91E-05		-4.53E-01	3.99E-03		-8.60E-01	2.23E-05		1.57E+00	3.07E-33	Up	4.40E-01	9.10E-06		2.35E+00	1.30E-280	Up	Unigene47785_All//gi|226494043|ref|NP_001150498.1|//7.00E-39//LOC100284129 [Zea mays] >gi|195639632|gb|ACG39284.1| pathogen-related protein [Zea mays]	Unigene47785_All//2.00E-31//AT1G78780| pathogenesis-related family protein					nr -
Unigene47787_All	929	28.67	26.67	32.39	47.40	42.15	42.64	14.34	9.40	5.19	-1.04E-01	3.81E-01		1.76E-01	1.13E-01		-1.70E-01	4.04E-02		-1.53E-01	8.03E-02		-6.09E-01	9.13E-06		-1.47E+00	8.21E-23	Down			Unigene47787_All//0.00E+00//gi|21098090|gb|BQ410403.1|BQ410403				
Unigene47788_All	988	98.76	45.08	74.16	69.48	53.88	79.58	32.91	23.14	11.65	-1.13E+00	3.67E-86	Down	-4.13E-01	1.01E-14		-3.67E-01	1.81E-10		1.96E-01	9.55E-04		-5.08E-01	1.54E-09		-1.50E+00	3.68E-56	Down	Unigene47788_All//gi|107738205|gb|ABF83661.1|//2.00E-35//At4g38100 [Arabidopsis thaliana]	Unigene47788_All//7.00E-32//AT4G38100| unknown protein	Unigene47788_All//0.00E+00//gi|78336679|gb|DT556953.1|DT556953				nr -
Unigene47789_All	3042	7.43	6.60	7.30	12.82	10.49	11.68	18.55	10.15	9.12	-1.72E-01	1.67E-01		-2.56E-02	8.49E-01		-2.89E-01	3.55E-04		-1.34E-01	1.67E-01		-8.70E-01	6.71E-40		-1.03E+00	8.73E-54	Down	Unigene47789_All//gi|224160069|gb|ACN43585.1|//0.00E+00//nuclear cap-binding protein [Solanum tuberosum] >gi|224160071|gb|ACN43586.1| nuclear cap-binding protein [Solanum tuberosum]	Unigene47789_All//0.00E+00//AT2G13540| ABH1 (ABA HYPERSENSITIVE 1); RNA cap binding	Unigene47789_All//0.00E+00//TC162130		ko03040|Spliceosome		nr -

Unigene4779_All	249	0.42	0.41	1.28	0.00	0.55	0.00	0.68	1.51	4.64	-4.60E-02	9.88E-01		1.61E+00	3.04E-01		9.11E+00	3.18E-01		null	null		1.15E+00	3.27E-01		2.77E+00	5.09E-05	Up	Unigene4779_All//gi|297836416|ref|XP_002886090.1|//4.00E-33//mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331930|gb|EFH62349.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene4779_All//2.00E-34//AT2G17010| mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein	Unigene4779_All//1.00E-40//gi|78323148|gb|DT543422.1|DT543422				nr +
Unigene47790_All	1358	14.18	19.96	29.45	32.28	60.78	49.02	0.19	0.40	0.09	4.94E-01	2.08E-06		1.05E+00	8.22E-31	Up	9.13E-01	8.04E-61		6.03E-01	6.54E-22		1.10E+00	2.36E-01		-1.09E+00	4.28E-01		Unigene47790_All//gi|297798270|ref|XP_002867019.1|//1.00E-135//cytochrome P450 [Arabidopsis lyrata subsp. lyrata] >gi|297312855|gb|EFH43278.1| cytochrome P450 [Arabidopsis lyrata subsp. lyrata]	Unigene47790_All//2.00E-135//AT4G36380| ROT3 (ROTUNDIFOLIA 3); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding / steroid hydroxylase	Unigene47790_All//2.00E-98//gi|78353187|gb|DT573461.1|DT573461		ko00905|Brassinosteroid biosynthesis		nr +
Unigene47791_All	1404	17.10	17.43	16.99	38.39	35.34	30.69	29.12	19.98	9.51	2.73E-02	8.24E-01		-9.60E-03	9.59E-01		-1.19E-01	1.30E-01		-3.23E-01	3.92E-06		-5.44E-01	3.21E-13		-1.62E+00	1.49E-78	Down	Unigene47791_All//gi|15228926|ref|NP_191205.1|//1.00E-150//oxidoreductase, zinc-binding dehydrogenase family protein [Arabidopsis thaliana] >gi|7594524|emb|CAB88049.1| quinone reductase-like protein [Arabidopsis thaliana] >gi|62320240|dbj|BAD94498.1| quinone reductase-like protein [Arabidopsis thaliana]	Unigene47791_All//9.00E-132//AT3G56460| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene47791_All//0.00E+00//TC143867				nr -
Unigene47792_All	1341	47.13	20.06	28.07	47.14	57.44	44.19	7.25	3.18	4.40	-1.23E+00	4.38E-64	Down	-7.47E-01	3.12E-27		2.85E-01	2.31E-07		-9.33E-02	2.31E-01		-1.19E+00	4.40E-12	Down	-7.22E-01	6.48E-06		Unigene47792_All//gi|124365580|gb|ABN09814.1|//2.00E-71//Zinc finger, GATA-type [Medicago truncatula]	Unigene47792_All//5.00E-28//AT3G60530| zinc finger (GATA type) family protein	Unigene47792_All//0.00E+00//gi|48791889|gb|CO093203.1|CO093203	C2C2-GATA			nr +
Unigene47793_All	1242	2.57	4.53	4.37	11.07	9.90	5.02	4.43	1.92	0.96	8.17E-01	1.16E-03		7.67E-01	3.98E-03		-1.61E-01	3.42E-01		-1.14E+00	8.31E-14	Down	-1.21E+00	2.60E-07	Down	-2.20E+00	1.04E-16	Down	Unigene47793_All//gi|115435408|ref|NP_001042462.1|//8.00E-10//Os01g0226200 [Oryza sativa Japonica Group] >gi|113531993|dbj|BAF04376.1| Os01g0226200 [Oryza sativa Japonica Group]	Unigene47793_All//8.00E-17//AT5G52870| unknown protein	Unigene47793_All//0.00E+00//ES804775				nr +
Unigene47794_All	913	20.52	9.27	8.05	55.22	42.77	31.36	47.70	14.33	9.34	-1.15E+00	1.81E-17	Down	-1.35E+00	1.93E-21	Down	-3.69E-01	6.66E-08		-8.16E-01	2.59E-28		-1.74E+00	7.37E-90	Down	-2.35E+00	1.14E-137	Down	Unigene47794_All//gi|298362843|gb|ADI78873.1|//5.00E-68//actin-depolymerizing factor [Hevea brasiliensis]	Unigene47794_All//6.00E-64//AT5G59890| ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); actin binding	Unigene47794_All//0.00E+00//TC137651				nr -
Unigene47796_All	2309	32.86	11.26	20.53	7.64	7.34	3.64	0.09	0.04	0.24	-1.55E+00	3.25E-108	Down	-6.79E-01	1.32E-27		-5.78E-02	7.40E-01		-1.07E+00	7.41E-16	Down	-1.34E+00	4.29E-01		1.40E+00	1.12E-01		Unigene47796_All//gi|283488505|gb|ADB24774.1|//0.00E+00//rhamnose synthase [Gossypium hirsutum]	Unigene47796_All//0.00E+00//AT1G78570| RHM1 (RHAMNOSE BIOSYNTHESIS 1); UDP-L-rhamnose synthase/ UDP-glucose 4,6-dehydratase/ catalytic	Unigene47796_All//0.00E+00//gi|164266233|gb|ES809150.1|ES809150		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene47797_All	2040	0.13	0.35	0.10	1.25	0.86	1.17	25.62	46.36	61.61	1.44E+00	1.06E-01		-2.96E-01	8.32E-01		-5.33E-01	1.75E-01		-8.59E-02	8.42E-01		8.56E-01	1.80E-64		1.27E+00	6.13E-165	Up	Unigene47797_All//gi|8778214|gb|AAF79223.1|AC006917_8//0.00E+00//F10B6.18 [Arabidopsis thaliana]	Unigene47797_All//1.00E-179//AT1G14780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24290.2); Has 119 Blast hits to 118 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 14; Fungi - 0; Plants - 105; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene47797_All//0.00E+00//gi|11209830|gb|BF278664.1|BF278664				nr -
Unigene478_All	706	1.19	4.88	0.60	4.02	4.63	8.64	5.45	10.12	7.11	2.04E+00	8.15E-08	Up	-9.75E-01	2.37E-01		2.04E-01	6.11E-01		1.10E+00	4.45E-06	Up	8.93E-01	5.52E-06		3.84E-01	1.07E-01		Unigene478_All//gi|9758080|dbj|BAB08324.1|//5.00E-60//protein kinase AIN1 [Arabidopsis thaliana] >gi|110738180|dbj|BAF01021.1| protein kinase like protein [Arabidopsis thaliana]	Unigene478_All//2.00E-61//AT5G40540| protein kinase, putative	Unigene478_All//0.00E+00//C0123225		ko04140|Regulation of autophagy	GO:0004702//GO:0006464//GO:0032559//GO:0043231	nr -
Unigene4780_All	796	1.91	1.97	1.61	2.32	2.94	3.74	3.88	7.77	3.80	4.99E-02	9.37E-01		-2.48E-01	6.33E-01		3.45E-01	4.53E-01		6.94E-01	6.03E-02		1.00E+00	3.08E-06	Up	-2.77E-02	9.50E-01		Unigene4780_All//gi|297842639|ref|XP_002889201.1|//1.00E-74//mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335042|gb|EFH65460.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene4780_All//2.00E-55//AT1G78610| MSL6 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 6)	Unigene4780_All//2.00E-82//gi|78323148|gb|DT543422.1|DT543422				nr +
Unigene47800_All	1079	12.51	3.62	4.98	87.67	81.60	75.97	11.79	105.90	4.87	-1.79E+00	2.86E-24	Down	-1.33E+00	3.13E-15	Down	-1.04E-01	7.05E-02		-2.07E-01	9.17E-05		3.17E+00	0.00E+00	Up	-1.28E+00	8.28E-18	Down	Unigene47800_All//gi|151303115|gb|ABR92760.1|//1.00E-153//transcription factor TF1 [Gossypium hirsutum]	Unigene47800_All//8.00E-69//AT4G22680| MYB85 (myb domain protein 85); DNA binding / transcription activator/ transcription factor	Unigene47800_All//0.00E+00//TC135046	MYB			nr -
Unigene47801_All	1698	0.62	0.18	0.16	4.69	4.54	3.14	1.92	0.86	1.45	-1.78E+00	1.36E-02		-1.97E+00	1.13E-02		-4.72E-02	8.29E-01		-5.81E-01	4.30E-03		-1.15E+00	2.15E-04	Down	-3.99E-01	1.93E-01		Unigene47801_All//gi|227053577|gb|ACP18876.1|//0.00E+00//subtilisin-like serine protease [Carica papaya]	Unigene47801_All//3.00E-165//AT5G59810| SBT5.4; identical protein binding / serine-type endopeptidase	Unigene47801_All//9.00E-49//CO069790				nr +
Unigene47806_All	1798	1.92	4.88	1.54	2.55	2.49	3.84	3.72	5.35	6.74	1.34E+00	9.77E-11	Up	-3.19E-01	3.91E-01		-3.38E-02	9.10E-01		5.92E-01	7.81E-03		5.25E-01	1.48E-03		8.58E-01	2.89E-09		Unigene47806_All//gi|225451585|ref|XP_002275581.1|//1.00E-127//PREDICTED: similar to Tetratricopeptide-like helical [Vitis vinifera]	Unigene47806_All//2.00E-119//AT4G30700| pentatricopeptide (PPR) repeat-containing protein	Unigene47806_All//0.00E+00//TC138734				nr +
Unigene47807_All	1199	20.64	62.67	32.73	8.39	9.65	14.69	36.78	57.03	45.29	1.60E+00	2.38E-112	Up	6.65E-01	4.27E-14		2.01E-01	2.88E-01		8.08E-01	5.22E-10		6.33E-01	5.33E-28		3.00E-01	1.71E-06		Unigene47807_All//gi|225446337|ref|XP_002272136.1|//9.00E-72//PREDICTED: similar to ring domain containing protein isoform 2 [Vitis vinifera] >gi|225446339|ref|XP_002272107.1| PREDICTED: similar to ring domain containing protein isoform 1 [Vitis vinifera]	Unigene47807_All//1.00E-50//AT4G03510| RMA1; protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene47807_All//0.00E+00//TC154063		ko04146|Peroxisome		nr -
Unigene47808_All	949	16.54	12.17	6.57	21.21	16.62	25.03	48.38	70.78	47.81	-4.42E-01	1.72E-03		-1.33E+00	1.01E-17	Down	-3.52E-01	2.69E-03		2.39E-01	4.24E-02		5.49E-01	1.70E-21		-1.71E-02	8.40E-01		Unigene47808_All//gi|223452311|gb|ACM89483.1|//1.00E-82//leucine-rich repeat family protein [Glycine max]	Unigene47808_All//1.00E-73//AT5G48380| leucine-rich repeat family protein / protein kinase family protein	Unigene47808_All//0.00E+00//TC156101		ko04626|Plant-pathogen interaction		nr +
Unigene47809_All	1721	3.68	1.74	2.91	6.11	5.06	4.64	5.65	4.32	4.24	-1.08E+00	6.22E-06	Down	-3.39E-01	1.83E-01		-2.71E-01	1.40E-01		-3.95E-01	2.76E-02		-3.86E-01	2.10E-02		-4.16E-01	9.56E-03		Unigene47809_All//gi|15450868|gb|AAB96705.1|//6.00E-81//Unknown protein [Arabidopsis thaliana]	Unigene47809_All//7.00E-84//AT5G54920| unknown protein	Unigene47809_All//0.00E+00//gi|164341026|gb|EX169897.1|EX169897				nr -
Unigene4781_All	1419	6.56	2.14	4.20	22.92	24.22	11.17	0.00	0.03	0.00	-1.62E+00	9.11E-15	Down	-6.43E-01	1.01E-03		7.93E-02	4.96E-01		-1.04E+00	2.27E-27	Down	4.88E+00	6.34E-01		null	null		Unigene4781_All//gi|2865437|gb|AAC02672.1|//7.00E-11//polyprotein [Arabidopsis arenosa]						nr +
Unigene47812_All	1085	35.06	17.09	12.37	13.08	10.16	54.24	555.45	243.80	178.67	-1.04E+00	1.44E-29	Down	-1.50E+00	1.52E-50	Down	-3.66E-01	1.12E-02		2.05E+00	1.39E-132	Up	-1.19E+00	0.00E+00	Down	-1.64E+00	0.00E+00	Down	Unigene47812_All//gi|292653531|gb|ADE34283.1|//1.00E-132//aquaporin TIP1;7 [Gossypium hirsutum]	Unigene47812_All//2.00E-99//AT4G01470| TIP1;3 (TONOPLAST INTRINSIC PROTEIN 1;3); urea transmembrane transporter/ water channel	Unigene47812_All//0.00E+00//TC152003				nr +
Unigene47813_All	1731	0.06	1.29	0.37	1.01	3.24	6.11	2.61	31.03	34.84	4.41E+00	2.58E-10	Up	2.61E+00	2.33E-02		1.69E+00	7.30E-11	Up	2.60E+00	6.69E-32	Up	3.57E+00	3.31E-252	Up	3.74E+00	5.93E-299	Up	Unigene47813_All//gi|224126261|ref|XP_002319796.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222858172|gb|EEE95719.1| GRAS family transcription factor [Populus trichocarpa]	Unigene47813_All//6.00E-110//AT5G48150| PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor	Unigene47813_All//0.00E+00//TC173319	GRAS			nr +
Unigene47816_All	1828	2.66	7.96	0.90	3.24	3.09	3.68	16.38	43.60	105.37	1.58E+00	7.94E-22	Up	-1.56E+00	2.56E-07	Down	-6.99E-02	8.22E-01		1.83E-01	4.86E-01		1.41E+00	2.24E-121	Up	2.69E+00	0.00E+00	Up	Unigene47816_All//gi|15231625|ref|NP_191467.1|//0.00E+00//aspartyl protease family protein [Arabidopsis thaliana] >gi|15983376|gb|AAL11556.1|AF424562_1 AT3g59080/F17J16_130 [Arabidopsis thaliana]	Unigene47816_All//0.00E+00//AT3G59080| aspartyl protease family protein	Unigene47816_All//0.00E+00//FL684443				nr -
Unigene47818_All	1367	10.14	5.63	5.10	11.37	9.90	7.30	11.13	3.21	5.16	-8.48E-01	2.74E-08		-9.91E-01	4.92E-10		-2.00E-01	1.90E-01		-6.39E-01	3.39E-06		-1.79E+00	2.23E-33	Down	-1.11E+00	3.96E-17	Down	Unigene47818_All//gi|42565781|ref|NP_190512.3|//1.00E-100//SRp34a (Ser/Arg-rich protein 34a); RNA binding / nucleic acid binding / nucleotide binding [Arabidopsis thaliana] >gi|124301106|gb|ABN04805.1| At3g49430 [Arabidopsis thaliana]	Unigene47818_All//8.00E-70//AT3G49430| SRp34a (Ser/Arg-rich protein 34a); RNA binding / nucleic acid binding / nucleotide binding	Unigene47818_All//0.00E+00//gi|78334945|gb|DT555219.1|DT555219		ko03040|Spliceosome		nr -
Unigene47819_All	1989	0.18	0.89	0.32	4.63	3.76	2.95	9.74	7.46	3.16	2.28E+00	6.80E-05	Up	8.03E-01	3.88E-01		-3.03E-01	1.19E-01		-6.50E-01	4.54E-04		-3.84E-01	6.33E-04		-1.62E+00	7.43E-38	Down	Unigene47819_All//gi|224127726|ref|XP_002329162.1|//5.00E-40//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870943|gb|EEF08074.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene47819_All//2.00E-12//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene47819_All//0.00E+00//TC145516		ko04626|Plant-pathogen interaction		nr +
Unigene4782_All	747	46.16	57.25	51.68	46.01	51.68	67.29	19.13	42.36	45.60	3.11E-01	1.47E-04		1.63E-01	9.11E-02		1.67E-01	6.55E-02		5.48E-01	3.59E-14		1.15E+00	2.39E-35	Up	1.25E+00	1.37E-44	Up	Unigene4782_All//gi|297799708|ref|XP_002867738.1|//3.00E-87//SPX domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297313574|gb|EFH43997.1| SPX domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene4782_All//2.00E-88//AT4G22990| SPX (SYG1/Pho81/XPR1) domain-containing protein	Unigene4782_All//0.00E+00//gi|78352026|gb|DT572300.1|DT572300				nr +
Unigene47820_All	1466	4.78	2.25	4.14	10.26	9.28	10.04	13.44	12.89	9.51	-1.09E+00	1.52E-06	Down	-2.08E-01	3.85E-01		-1.45E-01	3.84E-01		-3.11E-02	8.62E-01		-6.06E-02	6.36E-01		-4.99E-01	3.82E-06		Unigene47820_All//gi|223452365|gb|ACM89510.1|//1.00E-175//serine/threonine protein kinase [Glycine max]	Unigene47820_All//9.00E-157//AT2G47060| serine/threonine protein kinase, putative	Unigene47820_All//0.00E+00//TC172155		ko04626|Plant-pathogen interaction		nr +

Unigene47821_All	1773	9.68	3.63	5.71	14.39	11.21	12.18	11.16	4.57	4.52	-1.42E+00	5.20E-22	Down	-7.62E-01	4.16E-08		-3.60E-01	3.78E-04		-2.41E-01	3.27E-02		-1.29E+00	9.10E-27	Down	-1.31E+00	3.58E-28	Down	Unigene47821_All//gi|30697455|ref|NP_200906.2|//1.00E-91//nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|17063173|gb|AAL32982.1| AT5g60980/MSL3_100 [Arabidopsis thaliana] >gi|27764908|gb|AAO23575.1| At5g60980/MSL3_100 [Arabidopsis thaliana]	Unigene47821_All//9.00E-85//AT5G60980| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene47821_All//1.00E-149//gi|109858643|gb|DW487622.1|DW487622		ko03040|Spliceosome		nr +
Unigene47822_All	1897	2.92	4.38	4.86	9.11	9.69	7.50	49.61	15.86	9.07	5.83E-01	3.73E-03		7.32E-01	1.95E-04		8.92E-02	5.86E-01		-2.81E-01	4.31E-02		-1.65E+00	2.00E-179	Down	-2.45E+00	0.00E+00	Down	Unigene47822_All//gi|15242672|ref|NP_195939.1|//1.00E-108//CPU0RF47 (CONSERVED PEPTIDE UPSTREAM OPEN READING FRAME 47) [Arabidopsis thaliana]	Unigene47822_All//7.00E-112//AT3G53400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; BEST Arabidopsis thaliana protein match is: CPU0RF47 (CONSERVED PEPTIDE UPSTREAM OPEN READING FRAME 47) (TAIR:AT5G03190.1); Has 120 Blast hits to 120 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 115; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene47822_All//0.00E+00//TC170817				nr -
Unigene47826_All	1696	8.05	10.52	9.76	15.13	11.31	15.42	9.00	13.60	21.09	3.85E-01	3.62E-03		2.78E-01	6.03E-02		-4.20E-01	2.49E-05		2.76E-02	8.38E-01		5.96E-01	4.54E-09		1.23E+00	2.07E-45	Up	Unigene47826_All//gi|79323080|ref|NP_001031419.1|//1.00E-148//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|50253504|gb|AAT71954.1| At2g26000 [Arabidopsis thaliana] >gi|53850529|gb|AAU95441.1| At2g26000 [Arabidopsis thaliana]	Unigene47826_All//3.00E-137//AT2G26000| zinc finger (C3HC4-type RING finger) family protein	Unigene47826_All//0.00E+00//ES832128				nr -
Unigene47827_All	3315	11.71	4.49	3.36	21.68	19.72	27.64	15.15	9.12	8.15	-1.38E+00	3.37E-47	Down	-1.80E+00	8.74E-67	Down	-1.37E-01	3.12E-02		3.50E-01	1.97E-11		-7.33E-01	1.01E-26		-8.95E-01	2.15E-38		Unigene47827_All//gi|61162196|dbj|BAD91080.1|//0.00E+00//beta-D-galactosidase [Pyrus pyrifolia]	Unigene47827_All//0.00E+00//AT5G63810| BGAL10 (beta-galactosidase 10); beta-galactosidase/ catalytic/ cation binding	Unigene47827_All//0.00E+00//TC162243		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series		nr -
Unigene47829_All	1725	5.82	1.82	1.64	3.87	2.58	4.71	4.19	8.38	16.70	-1.68E+00	1.04E-16	Down	-1.83E+00	5.57E-18	Down	-5.88E-01	6.23E-03		2.84E-01	2.02E-01		1.00E+00	1.89E-13	Up	1.99E+00	3.00E-73	Up	Unigene47829_All//gi|115459306|ref|NP_001053253.1|//4.00E-64//Os04g0505400 [Oryza sativa Japonica Group] >gi|32490273|emb|CAE05562.1| OSJNBa0116K07.15 [Oryza sativa (japonica cultivar-group)] >gi|113564824|dbj|BAF15167.1| Os04g0505400 [Oryza sativa Japonica Group] >gi|116310257|emb|CAH67264.1| OS1GBa0145C12.1 [Oryza sativa (indica cultivar-group)]	Unigene47829_All//gi|115459306|ref|NP_001053253.1|//4.00E-64//Os04g0505400 [Oryza sativa Japonica Group] >gi|32490273|emb|CAE05562.1| OSJNBa0116K07.15 [Oryza sativa (japonica cultivar-group)] >gi|113564824|dbj|BAF15167.1| Os04g0505400 [Oryza sativa Japonica Group] >gi|116310257|emb|CAH67264.1| OS1GBa0145C12.1 [Oryza sativa (indica cultivar-group)]	Unigene47829_All//1.00E-68//AT3G50170| unknown protein				nr -
Unigene4783_All	1002	0.89	1.16	0.64	8.15	6.46	2.93	1.65	0.17	0.91	3.90E-01	5.39E-01		-4.77E-01	5.33E-01		-3.36E-01	1.03E-01		-1.48E+00	2.68E-12	Down	-3.30E+00	8.30E-08	Down	-8.48E-01	5.37E-02		Unigene4783_All//gi|188509950|gb|ACD56636.1|//2.00E-09//disease resistance related protein [Gossypium raimondii]	Unigene4783_All//4.00E-08//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene4783_All//4.00E-167//TC176729		ko04626|Plant-pathogen interaction		nr -
Unigene47832_All	1385	3.89	1.21	0.88	6.47	7.31	3.00	1.86	0.75	0.98	-1.69E+00	2.20E-09	Down	-2.14E+00	5.43E-12	Down	1.75E-01	4.04E-01		-1.11E+00	7.75E-09	Down	-1.30E+00	3.05E-04	Down	-9.29E-01	6.22E-03		Unigene47832_All//gi|224092067|ref|XP_002309461.1|//1.00E-165//leucine-rich repeat protein kinase [Populus trichocarpa] >gi|222855437|gb|EEE92984.1| leucine-rich repeat protein kinase [Populus trichocarpa]	Unigene47832_All//5.00E-152//AT2G26330| ER (ERECTA); transmembrane receptor protein kinase	Unigene47832_All//0.00E+00//TC141967				nr +
Unigene47834_All	1282	32.98	6.21	19.85	16.05	16.87	16.98	5.21	1.99	1.15	-2.41E+00	2.95E-109	Down	-7.32E-01	9.29E-18		7.20E-02	6.15E-01		8.15E-02	5.97E-01		-1.39E+00	1.17E-10	Down	-2.18E+00	6.66E-20	Down	Unigene47834_All//gi|9502420|gb|AAF88119.1|AC021043_12//1.00E-50//Unknown protein [Arabidopsis thaliana] >gi|15529248|gb|AAK97718.1| At1g29190/F28N24_12 [Arabidopsis thaliana] >gi|16974401|gb|AAL31126.1| At1g29190/F28N24_12 [Arabidopsis thaliana]	Unigene47834_All//6.00E-40//AT1G29195| unknown protein	Unigene47834_All//0.00E+00//gi|48811319|gb|CO112632.1|CO112632				nr -
Unigene47837_All	1592	15.41	8.63	7.43	32.10	23.17	25.11	20.69	9.29	14.29	-8.38E-01	9.02E-14		-1.05E+00	4.82E-19	Down	-4.71E-01	2.50E-12		-3.55E-01	7.65E-07		-1.15E+00	3.23E-37	Down	-5.34E-01	8.08E-11		Unigene47837_All//gi|193885155|gb|ACF28391.1|//1.00E-170//At4g01220 [Arabidopsis thaliana]	Unigene47837_All//9.00E-168//AT4G01220| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Reticulon (InterPro:IPR003388); BEST Arabidopsis thaliana protein match is: RGXT1 (rhamnogalacturonan xylosyltransferase 1); UDP-xylosyltransferase (TAIR:AT4G01770.1); Has 188 Blast hits to 185 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 165; Viruses - 0; Other Eukaryotes - 21 (source: NCBI BLink).	Unigene47837_All//0.00E+00//TC161554				nr -
Unigene47839_All	738	4.18	2.88	3.75	7.76	4.85	5.02	12.72	4.53	4.64	-5.37E-01	1.32E-01		-1.57E-01	6.64E-01		-6.78E-01	3.59E-03		-6.29E-01	1.07E-02		-1.49E+00	3.64E-16	Down	-1.45E+00	3.85E-16	Down	Unigene47839_All//gi|3024501|sp|Q40193.1|RB11C_LOTJA//4.00E-79//RecName: Full=Ras-related protein Rab11C >gi|1370146|emb|CAA98179.1| RAB11C [Lotus japonicus]	Unigene47839_All//4.00E-67//AT1G07410| ATRABA2B (ARABIDOPSIS RAB GTPASE HOMOLOG A2B); GTP binding / GTPase/ protein binding	Unigene47839_All//0.00E+00//TC148486				nr -
Unigene4784_All	792	1.98	1.86	1.08	9.81	10.61	7.36	14.36	5.70	11.52	-9.52E-02	8.47E-01		-8.81E-01	1.13E-01		1.13E-01	6.28E-01		-4.16E-01	5.17E-02		-1.33E+00	1.47E-16	Down	-3.18E-01	3.34E-02		Unigene4784_All//gi|29695320|gb|AAO89147.1|//1.00E-63//NBS-type resistance protein [Gossypium barbadense]	Unigene4784_All//3.00E-32//AT1G61300| disease resistance protein (NBS-LRR class), putative	Unigene4784_All//0.00E+00//TC176729		ko04626|Plant-pathogen interaction		nr +
Unigene47840_All	1115	7.93	4.77	3.73	16.08	11.89	10.00	12.48	4.87	6.54	-7.33E-01	1.56E-04		-1.09E+00	1.20E-07	Down	-4.36E-01	3.65E-04		-6.85E-01	7.08E-08		-1.36E+00	1.38E-20	Down	-9.32E-01	5.09E-12		Unigene47840_All//gi|3024501|sp|Q40193.1|RB11C_LOTJA//1.00E-105//RecName: Full=Ras-related protein Rab11C >gi|1370146|emb|CAA98179.1| RAB11C [Lotus japonicus]	Unigene47840_All//2.00E-92//AT3G46830| ATRABA2C (ARABIDOPSIS RAB GTPASE HOMOLOG A2C); GTP binding	Unigene47840_All//0.00E+00//TC148486				nr -
Unigene47843_All	1033	61.24	35.95	27.84	64.33	55.40	43.76	66.26	29.50	28.69	-7.68E-01	1.22E-29		-1.14E+00	1.31E-54	Down	-2.16E-01	4.57E-04		-5.56E-01	4.17E-19		-1.17E+00	6.88E-78	Down	-1.21E+00	1.86E-84	Down	Unigene47843_All//gi|145334271|ref|NP_001078516.1|//1.00E-70//histone H3.2 [Arabidopsis thaliana]	Unigene47843_All//5.00E-72//AT4G40030| histone H3.2	Unigene47843_All//0.00E+00//TC151963				nr +
Unigene47844_All	1361	1.15	5.44	2.35	1.76	1.75	3.42	0.87	2.27	4.71	2.24E+00	7.67E-18	Up	1.03E+00	4.96E-03		-9.10E-03	9.68E-01		9.60E-01	5.71E-04		1.39E+00	2.55E-05	Up	2.44E+00	1.79E-21	Up	Unigene47844_All//gi|12325224|gb|AAG52554.1|AC010675_2//1.00E-157//nitrate transporter (NTL1); 53025-56402 [Arabidopsis thaliana]	Unigene47844_All//4.00E-143//AT1G69850| ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter	Unigene47844_All//0.00E+00//gi|3325962|gb|AI054848.1|AI054848				nr -
Unigene47845_All	995	17.56	12.32	17.71	16.97	15.05	10.30	14.62	11.05	7.13	-5.11E-01	1.11E-04		1.24E-02	9.51E-01		-1.73E-01	2.47E-01		-7.20E-01	4.44E-08		-4.04E-01	2.20E-03		-1.04E+00	9.18E-15	Down	Unigene47845_All//gi|284433764|gb|ADB85088.1|//1.00E-68//actin-depolymerizing factor 6 [Jatropha curcas]	Unigene47845_All//2.00E-63//AT2G31200| ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); actin binding	Unigene47845_All//0.00E+00//TC150472				nr +
Unigene47849_All	1504	4.31	2.12	3.40	5.33	4.51	3.75	3.04	2.17	3.44	-1.02E+00	1.33E-05	Down	-3.44E-01	1.69E-01		-2.42E-01	2.80E-01		-5.07E-01	1.35E-02		-4.86E-01	5.79E-02		1.82E-01	4.74E-01		Unigene47849_All//gi|34365753|gb|AAQ65188.1|//1.00E-176//At3g26950 [Arabidopsis thaliana]	Unigene47849_All//5.00E-161//AT3G26950| unknown protein	Unigene47849_All//0.00E+00//DT463768				nr -
Unigene47853_All	701	1.64	2.17	1.22	1.14	2.60	3.61	1.03	1.01	1.19	4.01E-01	4.53E-01		-4.34E-01	5.09E-01		1.20E+00	1.36E-02		1.67E+00	7.87E-05	Up	-1.66E-02	1.02E+00		2.19E-01	7.35E-01		Unigene47853_All//gi|297820914|ref|XP_002878340.1|//2.00E-31//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324178|gb|EFH54599.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene47853_All//2.00E-32//AT3G60520| unknown protein	Unigene47853_All//0.00E+00//TC156040				nr +
Unigene47854_All	818	10.62	16.23	18.16	5.42	9.93	31.19	10.08	19.77	55.23	6.12E-01	7.29E-05		7.75E-01	2.65E-07		8.74E-01	5.96E-06		2.53E+00	4.00E-74	Up	9.72E-01	2.67E-14		2.45E+00	6.70E-148	Up	Unigene47854_All//gi|297820914|ref|XP_002878340.1|//3.00E-32//zinc ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324178|gb|EFH54599.1| zinc ion binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene47854_All//2.00E-27//AT3G60520| unknown protein	Unigene47854_All//1.00E-113//gi|109881523|gb|DW510493.1|DW510493				nr +
Unigene47858_All	2484	4.74	3.28	4.97	5.13	6.18	6.96	7.56	6.49	17.21	-5.29E-01	1.34E-03		6.96E-02	6.99E-01		2.68E-01	6.94E-02		4.40E-01	8.62E-04		-2.19E-01	7.29E-02		1.19E+00	2.87E-51	Up	Unigene47858_All//gi|25992001|gb|AAN77002.1|//0.00E+00//lecithine cholesterol acyltransferase-like protein [Medicago truncatula]	Unigene47858_All//0.00E+00//AT1G04010| phosphatidate-sterol O-acyltransferase/ phosphatidylcholine-sterol O-acyltransferase/ phosphatidylethanolamine-sterol O-acyltransferase	Unigene47858_All//7.00E-32//TC175758		ko00561|Glycerolipid metabolism		nr -
Unigene4786_All	1733	7.16	8.22	7.93	13.77	7.97	5.55	3.73	1.11	0.23	1.99E-01	2.17E-01		1.48E-01	3.98E-01		-7.89E-01	1.70E-14		-1.31E+00	3.64E-29	Down	-1.75E+00	3.74E-14	Down	-4.02E+00	4.37E-35	Down	Unigene4786_All//gi|224057048|ref|XP_002299117.1|//1.00E-118//neutral amino acid transport protein [Populus trichocarpa] >gi|222846375|gb|EEE83922.1| neutral amino acid transport protein [Populus trichocarpa]	Unigene4786_All//3.00E-92//AT3G13620| amino acid permease family protein	Unigene4786_All//2.00E-80//gi|13246732|gb|BE054055.2|BE054055				nr -

Unigene47861_All	563	5.95	2.52	6.43	1.77	3.24	2.09	0.23	0.15	0.14	-1.24E+00	3.57E-04	Down	1.13E-01	7.32E-01		8.73E-01	7.31E-02		2.37E-01	7.09E-01		-6.01E-01	7.66E-01		-6.71E-01	7.19E-01		Unigene47861_All//gi|22329863|ref|NP_174340.2|//6.00E-53//AAE14 (Acyl-Activating Enzyme 14); AMP binding / o-succinylbenzoate-CoA ligase [Arabidopsis thaliana] >gi|17979487|gb|AAL50080.1|At1g30520/F26G16_3 [Arabidopsis thaliana] >gi|29893264|gb|AAP03026.1| acyl-activating enzyme 14 [Arabidopsis thaliana] >gi|34365547|gb|AAQ65085.1|At1g30520/F26G16_3 [Arabidopsis thaliana]	Unigene47861_All//3.00E-54//AT1G30520| AAE14 (Acyl-Activating Enzyme 14); AMP binding / o-succinylbenzoate-CoA ligase	Unigene47861_All//0.00E+00//TC135030		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene47863_All	934	2.58	5.32	2.91	12.75	11.24	11.32	8.74	6.26	5.20	1.04E+00	1.36E-04	Up	1.74E-01	6.49E-01		-1.81E-01	3.15E-01		-1.72E-01	3.75E-01		-4.80E-01	8.47E-03		-7.48E-01	2.27E-05		Unigene47863_All//gi|18414255|ref|NP_568121.1|//3.00E-87//RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding [Arabidopsis thaliana] >gi|2723477|dbj|BAA24074.1| GTP-binding protein [Arabidopsis thaliana] >gi|7378638|emb|CAB83314.1| AtRab GTP-binding protein [Arabidopsis thaliana]	Unigene47863_All//6.00E-81//AT5G05530| RABC2A (RAB GTPASE HOMOLOG C2A); GTP binding / GTP-dependent protein binding / myosin XI tail binding	Unigene47863_All//7.00E-156//TC161007				nr +
Unigene47865_All	611	7.11	11.36	15.43	7.66	7.55	10.72	9.69	7.87	19.82	6.77E-01	2.35E-03		1.12E+00	1.96E-08	Up	-2.12E-02	9.50E-01		4.84E-01	3.96E-02		-3.00E-01	1.98E-01		1.03E+00	2.74E-12	Up	Unigene47865_All//gi|27720499|dbj|BAB56951.1|//6.00E-49//AT4G10430 [Arabidopsis thaliana]	Unigene47865_All//1.00E-39//AT1G33230| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: TMPIT-like (InterPro:IPR012926); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10430.3); Has 198 Blast hits to 198 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 148; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink).	Unigene47865_All//0.00E+00//gi|78323741|gb|DT544015.1|DT544015				nr +
Unigene47866_All	659	1.19	5.38	2.83	2.95	2.98	7.61	4.36	4.25	6.11	2.18E+00	1.24E-08	Up	1.25E+00	1.41E-02		1.48E-02	9.89E-01		1.37E+00	6.92E-07	Up	-3.80E-02	9.30E-01		4.85E-01	6.76E-02		Unigene47866_All//gi|27720499|dbj|BAB56951.1|//5.00E-34//AT4G10430 [Arabidopsis thaliana]	Unigene47866_All//8.00E-27//AT1G33230| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: TMPIT-like (InterPro:IPR012926); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10430.3); Has 198 Blast hits to 198 proteins in 60 species: Archae - 0; Bacteria - 0; Metazoa - 148; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink).	Unigene47866_All//0.00E+00//gi|78347303|gb|DT567577.1|DT567577				nr +
Unigene47867_All	1865	13.30	10.81	6.08	3.04	2.66	4.31	0.00	0.04	0.17	-2.98E-01	7.39E-03		-1.13E+00	1.93E-21	Down	-1.96E-01	4.93E-01		5.02E-01	1.50E-02		5.49E+00	4.01E-01		7.42E+00	1.34E-02		Unigene47867_All//gi|217038859|gb|ACJ76786.1|//0.00E+00//tyrosinase polyphenol oxidase [Argemone mexicana]		Unigene47867_All//0.00E+00//gi|78347690|gb|DT567964.1|DT567964		ko00350|Tyrosine metabolism//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene47868_All	1080	9.83	5.72	8.18	11.21	11.38	9.95	13.39	6.35	6.53	-7.81E-01	8.65E-06		-2.65E-01	1.68E-01		2.23E-02	9.16E-01		-1.71E-01	3.72E-01		-1.08E+00	4.28E-15	Down	-1.04E+00	1.12E-14	Down	Unigene47868_All//gi|124360902|gb|ABN08874.1|//1.00E-51//RNA polymerase Rpb4 [Medicago truncatula]	Unigene47868_All//2.00E-18//AT5G09920| NRPB4; DNA-directed RNA polymerase	Unigene47868_All//0.00E+00//TC169770		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene47872_All	1522	0.45	0.67	1.47	5.27	6.99	5.25	2.11	1.35	1.78	5.75E-01	3.83E-01		1.72E+00	3.36E-04	Up	4.08E-01	1.82E-02		-4.70E-03	9.79E-01		-6.50E-01	3.63E-02		-2.46E-01	4.40E-01		Unigene47872_All//gi|18416311|ref|NP_567697.1|//1.00E-153//MLO13 (MILDEW RESISTANCE LOCUS O 13); calmodulin binding [Arabidopsis thaliana] >gi|33112389|sp|Q94KB2.1|MLO13_ARATH RecName: Full=MLO-like protein 13; Short=AtMlo13; Short=AtMlo20 >gi|14091596|gb|AAK53806.1|AF36957 4_1 membrane protein Mlo13 [Arabidopsis thaliana] >gi|62320884|dbj|BAD95219.1| membrane protein Mlo13 [Arabidopsis thaliana] >gi|11107421 4|gb|ABR04480.1| At4g24250 [Arabidopsis thaliana]	Unigene47872_All//3.00E-148//AT4G24250| MLO13 (MILDEW RESISTANCE LOCUS O 13); calmodulin binding	Unigene47872_All//0.00E+00//CO113311				nr -
Unigene47873_All	1085	117.90	88.92	98.55	102.84	102.35	212.50	71.08	91.26	57.79	-4.07E-01	2.39E-19		-2.59E-01	2.74E-08		-6.90E-03	9.15E-01		1.05E+00	5.15E-192	Up	3.61E-01	7.07E-15		-2.99E-01	8.94E-09		Unigene47873_All//gi|297824281|ref|XP_002880023.1|//5.00E-87//aconitase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325862|gb|EFH56282.1| aconitase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene47873_All//3.00E-78//AT2G43090| aconitase C-terminal domain-containing protein	Unigene47873_All//0.00E+00//TC132512		ko00290|Valine, leucine and isoleucine biosynthesis//ko00660|C5-Branched dibasic acid metabolism		nr +
Unigene47874_All	1246	9.32	7.32	12.01	398.23	356.43	305.20	43.23	42.50	21.20	-3.49E-01	4.03E-02		3.65E-01	1.70E-02		-1.60E-01	3.53E-15		-3.84E-01	1.08E-70		-2.46E-02	7.59E-01		-1.03E+00	1.40E-51	Down	Unigene47874_All//gi|34016877|gb|AAQ56599.1|//0.00E+00//chitinase-like protein [Gossypium hirsutum]	Unigene47874_All//8.00E-156//AT3G16920| chitinase	Unigene47874_All//0.00E+00//TC130079		ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene47875_All	934	15.69	9.77	16.93	46.99	51.36	45.31	13.40	4.47	4.65	-6.84E-01	2.97E-06		1.10E-01	5.06E-01		1.28E-01	1.27E-01		-5.25E-02	6.39E-01		-1.58E+00	3.35E-23	Down	-1.53E+00	8.98E-23	Down	Unigene47875_All//gi|18398882|ref|NP_565443.1|//4.00E-43//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|16649043|gb|AAL24373.1| Unknown protein [Arabidopsis thaliana] >gi|20197034|gb|AAC09038.2| expressed protein [Arabidopsis thaliana]	Unigene47875_All//1.00E-20//AT2G18910| hydroxyproline-rich glycoprotein family protein	Unigene47875_All//0.00E+00//gi|109823394|gb|DW008254.1|DW008254				nr +
Unigene47878_All	1289	7.71	12.85	8.34	10.70	11.86	10.34	7.15	5.84	3.03	7.37E-01	8.38E-08		1.14E-01	5.89E-01		1.48E-01	3.78E-01		-5.06E-02	7.72E-01		-2.93E-01	1.01E-01		-1.24E+00	1.32E-12	Down	Unigene47878_All//gi|115447621|ref|NP_001047590.1|//3.00E-57//Os02g0651000 [Oryza sativa Japonica Group] >gi|113537121|dbj|BAF09504.1| Os02g0651000 [Oryza sativa Japonica Group]	Unigene47878_All//8.00E-91//AT5G51170| unknown protein	Unigene47878_All//0.00E+00//TC151420				nr +
Unigene47881_All	3202	9.17	1.12	0.80	13.01	9.35	11.44	24.81	6.91	15.00	-3.03E+00	1.70E-97	Down	-3.52E+00	4.21E-108	Down	-4.77E-01	2.29E-10		-1.85E-01	3.42E-02		-1.85E+00	6.16E-178	Down	-7.26E-01	3.28E-42		Unigene47881_All//gi|15235420|ref|NP_192999.1|//0.00E+00//ORC1B (ORIGIN OF REPLICATION COMPLEX 1B); DNA binding / double-stranded methylated DNA binding / protein binding [Arabidopsis thaliana] >gi|5823573|emb|CAB53755.1| origin recognition complex subunit 1-like protein [Arabidopsis thaliana] >gi|7267964|emb|CAB78305.1| origin recognition complex subunit 1-like protein [Arabidopsis thaliana] >gi|38567376|emb|CAD20132.1| origin recognition complex 1b protein [Arabidopsis thaliana]	Unigene47881_All//0.00E+00//AT4G12620| ORC1B (ORIGIN OF REPLICATION COMPLEX 1B); DNA binding / double-stranded methylated DNA binding / protein binding	Unigene47881_All//0.00E+00//TC173765				nr +
Unigene47882_All	1167	10.89	43.98	49.14	6.62	17.41	27.63	4.85	6.34	5.33	2.01E+00	3.41E-105	Up	2.17E+00	1.28E-126	Up	1.40E+00	2.03E-29	Up	2.06E+00	2.89E-73	Up	3.85E-01	5.08E-02		1.34E-01	5.80E-01		Unigene47882_All//gi|225453843|ref|XP_002277773.1|//1.00E-82//PREDICTED: MADS-box protein [Vitis vinifera] >gi|95116634|gb|ABF56527.1| MADS-box protein [Vitis vinifera]	Unigene47882_All//5.00E-61//AT2G45660| AGL20 (AGAMOUS-LIKE 20); transcription factor	Unigene47882_All//1.00E-80//ES835572	MADS			nr +
Unigene47885_All	1402	1.94	2.17	3.04	6.61	3.24	1.90	3.98	4.17	2.07	1.60E-01	6.47E-01		6.47E-01	3.58E-02		-1.03E+00	5.04E-09	Down	-1.80E+00	3.08E-18	Down	6.83E-02	7.83E-01		-9.40E-01	2.02E-05		Unigene47885_All//gi|16323172|gb|AAL15320.1|AT5g06850/MQJ9_2 [Arabidopsis thaliana] >gi|22137214|gb|AAM91452.1|AT5g06850/MQJ9_2 [Arabidopsis thaliana]	Unigene47885_All//0.00E+00//AT5G06850| C2 domain-containing protein	Unigene47885_All//0.00E+00//gi|48812277|gb|CO113590.1|CO113590				nr -
Unigene47886_All	1286	0.94	1.34	0.99	15.80	8.11	8.01	2.01	7.90	4.99	5.18E-01	3.08E-01		8.68E-02	8.84E-01		-9.62E-01	2.96E-17		-9.81E-01	7.67E-16		1.98E+00	1.65E-25	Up	1.31E+00	9.91E-10	Up	Unigene47886_All//gi|224079161|ref|XP_002305774.1|//1.00E-122//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222848738|gb|EEE86285.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene47886_All//1.00E-93//AT4G28500| ANAC073 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 73); transcription activator/ transcription factor	Unigene47886_All//0.00E+00//DT464670	NAC			nr -
Unigene47889_All	1107	5.34	7.78	6.21	3.11	4.23	2.86	8.56	3.06	2.23	5.43E-01	5.92E-03		2.16E-01	3.85E-01		4.46E-01	1.19E-01		-1.21E-01	7.31E-01		-1.48E+00	3.15E-16	Down	-1.94E+00	4.58E-24	Down	Unigene47889_All//gi|258523310|gb|ACV73676.1|//1.00E-123//lysophosphatidic acid acyltransferase 2 [Tropaeolum majus]	Unigene47889_All//5.00E-116//AT3G57650| LPAT2; 1-acylglycerol-3-phosphate O-acyltransferase	Unigene47889_All//0.00E+00//TC177232		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr +
Unigene47890_All	1022	1.69	1.59	1.88	3.80	2.66	1.37	3.85	2.54	2.30	-9.07E-02	8.47E-01		1.51E-01	7.44E-01		-5.14E-01	9.09E-02		-1.47E+00	3.73E-06	Down	-6.02E-01	2.95E-02		-7.42E-01	5.07E-03		Unigene47890_All//gi|15241015|ref|NP_195778.1|//1.00E-56//OSH1 (OAS HIGH ACCUMULATION 1); catalytic [Arabidopsis thaliana]	Unigene47890_All//5.00E-58//AT5G01580| OSH1 (OAS HIGH ACCUMULATION 1); catalytic				nr +

Unigene47892_All	809	8.47	9.33	4.61	8.74	13.58	7.82	1.78	2.74	6.16	1.40E-01	5.58E-01		-8.79E-01	1.72E-04		6.35E-01	8.96E-05		-1.62E-01	5.34E-01		6.24E-01	1.10E-01		1.79E+00	1.14E-11	Up	Unigene47892_All//gi|297596391|ref|NP_001042511.2|//1.00E-45//Os01g0233400 [Oryza sativa Japonica Group] >gi|77555036|gb|ABA97832.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255673031|dbj|BAF04425.2| Os01g0233400 [Oryza sativa Japonica Group]	Unigene47892_All// 1.00E-47//AT4G14385| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Histone H4 acetyltransferase, Nat4 complex, Esa6 (InterPro:IPR001487); Has 245 Blast hits to 245 proteins in 100 species: Archae - 0; Bacteria - 0; Metazoa - 126; Fungi - 60; Plants - 29; Viruses - 0; Other Eukaryotes - 30 (source: NCBI BLink).	Unigene47892_All//0.00E+00//TC157628				nr +
Unigene47893_All	702	1.04	5.27	5.84	5.32	4.81	3.54	1.63	1.73	1.36	2.34E+00	1.03E-09	Up	2.48E+00	5.07E-11	Up	-1.47E-01	6.78E-01		-5.89E-01	6.81E-02		8.64E-02	8.83E-01		-2.56E-01	6.49E-01		Unigene47893_All//gi|124359981|gb|ABN07997.1|//3.00E-10//contains similarity to reverse trancriptase, related [Medicago truncatula]	Unigene47893_All// 2.00E-05//AT3G26855| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: reverse transcriptase-related (TAIR:AT2G02650.1); Has 97 Blast hits to 97 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 97; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene47893_All//0.00E+00//gi|13247852|gb|BF272728.2|BF272728				nr +
Unigene47894_All	1064	1.67	6.33	6.16	5.76	6.12	3.78	1.23	0.90	1.46	1.92E+00	1.48E-13	Up	1.88E+00	2.25E-12	Up	8.71E-02	7.85E-01		-6.08E-01	1.04E-02		-4.47E-01	4.05E-01		2.46E-01	6.06E-01		Unigene47894_All//gi|124359162|gb|ABN06685.1|//4.00E-14//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene47894_All// 9.00E-09//AT3G09510| nucleic acid binding	Unigene47894_All//2.00E-147//gi|13247852|gb|BF272728.2|BF272728				nr -
Unigene47895_All	817	4.55	6.76	3.39	29.63	32.71	28.80	32.09	83.54	171.40	5.72E-01	2.46E-02		-4.24E-01	2.19E-01		1.42E-01	2.30E-01		-4.11E-02	7.55E-01		1.38E+00	1.82E-100	Up	2.42E+00	0.00E+00	Up	Unigene47895_All//gi|30844109|gb|AF36697.1|//2.00E-67//MAP kinase-like protein [Gossypium hirsutum]	Unigene47895_All// 0.00E-51//AT5G55560| protein kinase family protein	Unigene47895_All//0.00E+00//TC138635		ko04712|Circadian rhythm - plant		nr +
Unigene47896_All	1038	4.89	10.25	6.31	22.60	26.90	32.11	34.91	82.63	227.75	1.07E+00	3.38E-09	Up	3.68E-01	1.37E-01		2.51E-01	1.42E-02		5.07E-01	2.10E-08		1.24E+00	2.71E-107	Up	2.71E+00	0.00E+00	Up	Unigene47896_All//gi|30844109|gb|AF36697.1|//1.00E-169//MAP kinase-like protein [Gossypium hirsutum]	Unigene47896_All// 3.00E-136//AT5G55560| protein kinase family protein	Unigene47896_All//0.00E+00//TC138635		ko04712|Circadian rhythm - plant		nr +
Unigene47897_All	813	0.51	1.00	0.13	2.08	2.12	3.56	9.57	10.18	76.20	9.54E-01	2.26E-01		-1.97E+00	1.51E-01		2.37E-02	9.74E-01		7.71E-01	3.91E-02		8.92E-02	6.58E-01		2.99E+00	2.66E-251	Up	Unigene47897_All//gi|225441862|ref|XP_002284216.1|//3.00E-08//PREDICTED: similar to AT-HSFB3 (Arabidopsis thaliana heat shock transcription factor B3); DNA binding / transcription factor [Vitis vinifera]						nr +
Unigene47898_All	734	1.43	1.38	1.16	2.10	2.25	5.54	8.81	12.81	128.31	-4.63E-02	9.56E-01		-2.96E-01	6.41E-01		9.81E-02	8.68E-01		1.40E+00	7.29E-06	Up	5.40E-01	1.23E-03		3.86E+00	0.00E+00	Up	Unigene47898_All//gi|30697614|ref|NP_201008.2|//8.00E-31//AT-HSFB2A; DNA binding / transcription factor [Arabidopsis thaliana] >gi|11386851|sp|Q9SCW4.1|HFB2A_ARATH RecName: Full=Heat stress transcription factor B-2a; Short=AtHsfB2a; AltName: Full=Heat shock factor protein 6; Short=HSF 6; AltName: Full=Heat shock transcription factor 6; Short=HSTF 6; AltName: Full=AtHsf-22 >gi|6624616|emb|CAB63802.1| heat shock factor 6 [Arabidopsis thaliana] >gi|10176919|dbj|BAB10163.1| heat shock factor 6 [Arabidopsis thaliana] >gi|110739232|dbj|BAF01530.1| heat shock factor 6 [Arabidopsis thaliana]	Unigene47898_All// 4.00E-27//AT4G36990| HSF4 (HEAT SHOCK FACTOR 4) ; DNA binding / transcription factor/ transcription repressor	Unigene47898_All//6.00E-51//DN802166	HSF			nr +
Unigene479_All	1352	0.70	0.22	0.35	0.66	0.84	0.80	1.78	2.81	4.33	-1.63E+00	3.13E-02		-9.75E-01	2.00E-01		3.42E-01	6.20E-01		2.74E-01	6.70E-01		6.58E-01	1.92E-02		1.28E+00	1.21E-08	Up	Unigene479_All//gi|15232197|ref|NP_189393.1|//1.00E-160//ATN1; kinase/ protein serine/threonine kinase/ protein serine/threonine/tyrosine kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|11994183|dbj|BAB01286.1| nearly identical to protein kinase ATN1 [Arabidopsis thaliana] >gi|16604328|gb|AAL24170.1| AT3g27560/MMJ24_11 [Arabidopsis thaliana] >gi|19699190|gb|AAL90961.1| AT3g27560/MMJ24_11 [Arabidopsis thaliana]	Unigene479_All// 6.00E-154//AT3G27560| ATN1; kinase/ protein serine/threonine kinase/ protein serine/threonine/tyrosine kinase/ protein tyrosine kinase	Unigene479_All//0.00E+00//TC157350				nr +
Unigene4790_All	749	2.38	0.34	1.42	5.32	2.02	2.83	17.33	25.56	16.06	-2.81E+00	4.70E-06	Down	-7.40E-01	1.46E-01		-1.40E+00	1.67E-06	Down	-9.09E-01	2.65E-03		5.61E-01	6.01E-07		-1.10E-01	4.86E-01		Unigene4790_All//gi|119360053|gb|AB|66755.1|//1.00E-35//At5g65030 [Arabidopsis thaliana]	Unigene4790_All// 4.00E-34//AT5G65030| unknown protein	Unigene4790_All//3.00E-59//DW237862				nr -
Unigene47902_All	2313	4.00	1.58	1.11	9.48	6.86	11.13	26.40	7.35	12.59	-1.34E+00	2.34E-11	Down	-1.86E+00	6.31E-17	Down	-4.65E-01	1.68E-05		2.32E-01	3.99E-02		-1.84E+00	1.04E-136	Down	-1.07E+00	4.86E-62	Down	Unigene47902_All//gi|75262222|sp|Q9C977.1|PP135_ARATH//1.00E-104//RecName: Full=Pentatricopeptide repeat-containing protein At1g80270, mitochondrial; Flags: Precursor >gi|17064898|gb|AAL32603.1| Unknown protein [Arabidopsis thaliana]	Unigene47902_All// 3.00E-105//AT1G80270| DNA-binding protein, putative	Unigene47902_All//0.00E+00//TC143948				nr -
Unigene47903_All	917	21.74	8.34	9.58	35.26	28.54	24.87	17.01	12.22	5.39	-1.38E+00	1.46E-24	Down	-1.18E+00	1.26E-18	Down	-3.05E-01	6.95E-04		-5.03E-01	3.87E-08		-4.78E-01	1.45E-04		-1.66E+00	1.14E-31	Down	Unigene47903_All//gi|14596227|gb|AK68841.1|//6.00E-72//Unknown protein [Arabidopsis thaliana]	Unigene47903_All// 1.00E-64//AT1G68220| unknown protein	Unigene47903_All//0.00E+00//TC151517				nr -
Unigene47904_All	1391	31.26	15.55	22.28	36.56	24.73	23.93	23.22	14.09	8.53	-1.01E+00	3.64E-32	Down	-4.88E-01	3.49E-09		-5.64E-01	6.49E-17		-6.12E-01	1.97E-17		-7.21E-01	5.46E-17		-1.44E+00	6.95E-53	Down	Unigene47904_All//gi|115477226|ref|NP_001062209.1|//4.00E-50//Os08g0510800 [Oryza sativa Japonica Group] >gi|113624178|dbj|BAF24123.1| Os08g0510800 [Oryza sativa Japonica Group]	Unigene47904_All// 9.00E-89//AT3G57990| unknown protein	Unigene47904_All//0.00E+00//TC169659				nr -
Unigene47906_All	1402	59.71	34.04	18.76	22.78	20.68	14.14	9.02	9.93	7.27	-8.11E-01	1.03E-42		-1.67E+00	3.53E-129	Down	-1.39E-01	1.86E-01		-6.88E-01	1.31E-13		1.39E-01	3.83E-01		-3.10E-01	2.81E-02		Unigene47906_All//gi|15237783|ref|NP_197744.1|//1.00E-125//AtCXE18 (Arabidopsis thaliana carboxyesterase 18); carboxylesterase >gi|114050665|gb|ABI49482.1| At5g23530 [Arabidopsis thaliana]	Unigene47906_All// 4.00E-108//AT5G23530| AtCXE18 (Arabidopsis thaliana carboxyesterase 18); carboxylesterase	Unigene47906_All//0.00E+00//TC1131883				nr +
Unigene47907_All	1493	61.19	39.67	36.09	78.64	73.67	95.80	51.29	18.22	15.88	-6.25E-01	8.95E-30		-7.62E-01	2.12E-40		-9.43E-02	6.51E-02		2.85E-01	4.91E-12		-1.49E+00	7.99E-127	Down	-1.69E+00	1.90E-156	Down	Unigene47907_All//gi|297842071|ref|XP_002888917.1|//1.00E-153//GDP-4-keto-6-deoxymannose-3,5-epimerase-4-reductase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297334758|gb|EFH65176.1| GDP-4-keto-6-deoxymannose-3,5-epimerase-4-reductase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene47907_All// 3.00E-149//AT1G17890| GER2; binding / catalytic/ coenzyme binding	Unigene47907_All//0.00E+00//TC156142		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene47908_All	1848	4.16	45.95	19.80	6.60	7.51	15.03	6.93	11.42	11.12	3.46E+00	0.00E+00	Up	2.25E+00	2.15E-84	Up	1.85E-01	2.79E-01		1.19E+00	1.22E-28	Up	7.20E-01	2.26E-11		6.82E-01	1.90E-10		Unigene47908_All//gi|145105398|gb|ABP35583.1|//0.00E+00//CBL-interacting protein kinase [Gossypium hirsutum]	Unigene47908_All// 3.00E-159//AT5G25110| CIPK25 (CBL-INTERACTING PROTEIN KINASE 25); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene47908_All//0.00E+00//gi|78328522|gb|DT548796.1|DT548796		ko04140|Regulation of autophagy		nr -
Unigene47910_All	1502	0.38	0.44	0.35	16.32	28.47	19.18	3.52	2.00	1.72	1.95E-01	8.07E-01		-1.12E-01	9.07E-01		8.03E-01	1.56E-25		2.34E-01	2.68E-02		-8.13E-01	4.50E-04		-1.03E+00	7.15E-06	Down	Unigene47910_All//gi|297813085|ref|XP_002874426.1|//3.00E-72//light-dependent short hypocotyls 1 [Arabidopsis lyrata subsp. lyrata] >gi|297320263|gb|EFH50685.1| light-dependent short hypocotyls 1 [Arabidopsis lyrata subsp. lyrata]	Unigene47910_All// 7.00E-55//AT5G28490| LSH1 (LIGHT-DEPENDENT SHORT HYPOCOTYLS 1)	Unigene47910_All//0.00E+00//ES837930				nr +
Unigene47911_All	1347	30.61	19.30	22.61	18.08	18.99	14.92	15.51	5.99	4.91	-6.66E-01	2.08E-15		-4.37E-01	2.97E-07		7.09E-02	6.04E-01		-2.77E-01	1.42E-02		-1.37E+00	4.62E-31	Down	-1.66E+00	4.12E-42	Down	Unigene47911_All//gi|297794353|ref|XP_002865061.1|//1.00E-133//aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310896|gb|EFH41320.1| aldose 1-epimerase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47911_All// 8.00E-133//AT5G66530| aldose 1-epimerase family protein	Unigene47911_All//0.00E+00//TC141034				nr +
Unigene47912_All	1500	2.37	0.71	0.99	5.71	5.85	5.39	4.34	4.12	4.28	-1.74E+00	1.05E-06	Down	-1.25E+00	3.32E-04	Down	3.54E-02	8.83E-01		-8.38E-02	7.03E-01		-7.40E-02	7.48E-01		-2.17E-02	9.40E-01		Unigene47912_All//gi|9759187|dbj|BAB09724.1|//0.00E+00//importin beta [Arabidopsis thaliana]	Unigene47912_All// 0.00E+00//AT5G53480| importin beta-2, putative	Unigene47912_All//0.00E+00//TC155834				nr -
Unigene4792_All	1219	6.14	6.07	2.27	8.46	5.71	3.08	6.17	6.69	9.35	-1.63E-02	9.61E-01		-1.43E+00	1.03E-09	Down	-5.68E-01	6.13E-04		-1.46E+00	4.02E-15	Down	1.15E-01	6.15E-01		5.98E-01	4.33E-05		Unigene4792_All//gi|15237049|ref|NP_194461.1|//2.00E-40//zinc finger (B-box type) family protein [Arabidopsis thaliana]	Unigene4792_All// 2.00E-30//AT4G27310| zinc finger (B-box type) family protein	Unigene4792_All//0.00E+00//TC173280	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene47922_All	1034	21.86	17.74	8.70	24.62	18.48	23.67	53.03	54.53	16.88	-3.01E-01	1.04E-02		-1.33E+00	3.70E-25	Down	-4.14E-01	3.60E-05		-5.64E-02	6.84E-01		4.01E-02	6.45E-01		-1.65E+00	1.54E-108	Down	Unigene47922_All//gi|288311314|gb|ADC45396.1|//1.00E-149//HSP90-2 [Glycine max]	Unigene47922_All// 7.00E-118//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Unigene47922_All//0.00E+00//TC143331		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene47923_All	2013	12.87	12.76	8.86	22.59	24.19	7.74	12.52	3.53	4.22	-1.17E-02	9.38E-01		-5.38E-01	1.00E-06		9.84E-02	2.71E-01		-1.55E+00	1.13E-70	Down	-1.83E+00	4.17E-56	Down	-1.57E+00	8.10E-47	Down	Unigene47923_All//gi|257219873|gb|ACU52014.1|//0.00E+00//GAI/RGA-like 3-b [Gossypium hirsutum] >gi|296398839|gb|ADH10267.1| GAI3b [Gossypium hirsutum]	Unigene47923_All// 3.00E-116//AT1G14920| GAI (GIBBERELLIC ACID INSENSITIVE); transcription factor	Unigene47923_All//0.00E+00//gi|78327194|gb|DT547468.1|DT547468	GRAS			nr +

Unigene47924_All	915	4.63	2.99	1.86	7.19	8.88	6.56	4.48	1.28	2.87	-6.31E-01	3.23E-02		-1.31E+00	3.61E-05	Down	3.06E-01	1.56E-01		-1.31E-01	6.16E-01		-1.81E+00	1.21E-09	Down	-6.41E-01	1.32E-02		Unigene47924_All//gi|15220440|ref|NP_172009.1|//6.00E-97//galactosyltransferase family protein [Arabidopsis thaliana] >gi|14488078|gb|AAK63859.1|AF389287_1 At1g05170/YUP8H12_22 [Arabidopsis thaliana] >gi|2388580|gb|AAB71461.1| Similar to Sequence 10 from patent 5477002 (gb|1253956) [Arabidopsis thaliana] >gi|21360399|gb|AAM47315.1| At1g05170/YUP8H12_22 [Arabidopsis thaliana]	Unigene47924_All//4.00E-98//AT1G05170| galactosyltransferase family protein	Unigene47924_All//9.00E-63//C0127395				nr -
Unigene47925_All	1659	2.71	1.07	1.70	2.88	3.24	1.93	3.72	0.86	1.49	-1.34E+00	6.42E-06	Down	-6.73E-01	2.42E-02		1.68E-01	5.88E-01		-5.77E-01	3.78E-02		-2.12E+00	3.04E-17	Down	-1.32E+00	1.48E-09	Down	Unigene47925_All//gi|15220440|ref|NP_172009.1|//1.00E-158//galactosyltransferase family protein [Arabidopsis thaliana] >gi|14488078|gb|AAK63859.1|AF389287_1 At1g05170/YUP8H12_22 [Arabidopsis thaliana] >gi|2388580|gb|AAB71461.1| Similar to Sequence 10 from patent 5477002 (gb|1253956) [Arabidopsis thaliana] >gi|21360399|gb|AAM47315.1| At1g05170/YUP8H12_22 [Arabidopsis thaliana]	Unigene47925_All//6.00E-160//AT1G05170| galactosyltransferase family protein	Unigene47925_All//3.00E-73//DT458137				nr -
Unigene47927_All	1630	5.36	2.39	0.62	6.42	6.89	5.60	7.94	2.72	3.03	-1.16E+00	9.57E-09	Down	-3.11E+00	7.20E-29	Down	1.02E-01	6.13E-01		-1.98E-01	3.30E-01		-1.55E+00	3.42E-23	Down	-1.39E+00	1.62E-20	Down	Unigene47927_All//gi|297841461|ref|XP_002888612.1|//1.00E-133//DNA polymerase alpha subunit B family [Arabidopsis lyrata subsp. lyrata] >gi|297334453|gb|EFH64871.1| DNA polymerase alpha subunit B family [Arabidopsis lyrata subsp. lyrata]	Unigene47927_All//4.00E-133//AT1G67630| POLA2 (DNA POLYMERASE ALPHA 2); DNA binding / DNA-directed DNA polymerase	Unigene47927_All//0.00E+00//TC157529		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03030|DNA replication		nr +
Unigene47928_All	561	50.64	26.10	24.39	52.83	46.28	50.56	69.71	62.28	83.30	-9.56E-01	1.37E-19		-1.05E+00	5.76E-22	Down	-1.91E-01	6.39E-02		-6.35E-02	6.37E-01		-1.63E-01	4.76E-02		2.57E-01	1.77E-04		Unigene47928_All//gi|79305850|ref|NP_001030625.1|//1.00E-29//protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana]	Unigene47928_All//2.00E-23//AT3G02750| protein phosphatase 2C family protein / PP2C family protein	Unigene47928_All//0.00E+00//TC164108				nr -
Unigene47931_All	1391	20.88	5.65	10.80	31.37	26.74	14.55	6.78	5.80	3.64	-1.89E+00	3.22E-55	Down	-9.51E-01	4.82E-19		-2.31E-01	3.23E-03		-1.11E+00	1.05E-40	Down	-2.25E-01	2.23E-01		-8.98E-01	5.61E-08		Unigene47931_All//gi|297834100|ref|XP_002884932.1|//1.00E-67//protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297330772|gb|EFH61191.1| protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene47931_All//2.00E-62//AT3G12920| protein binding / zinc ion binding	Unigene47931_All//0.00E+00//TC153579				nr -
Unigene47932_All	1279	29.45	70.48	48.67	122.37	119.59	213.14	55.40	58.53	61.86	1.26E+00	8.64E-94	Up	7.25E-01	1.77E-25		-3.31E-02	5.53E-01		8.01E-01	8.87E-145		7.91E-02	2.12E-01		1.59E-01	2.65E-03		Unigene47932_All//gi|4440602|emb|CAA54393.1|//1.00E-137//HSR203J [Nicotiana tabacum]	Unigene47932_All//6.00E-45//AT5G06570| hydrolase	Unigene47932_All//0.00E+00//TC138153				nr -
Unigene47933_All	1064	15.10	21.05	16.27	12.83	7.41	4.24	6.64	3.61	4.46	4.80E-01	3.31E-05		1.08E-01	4.95E-01		-7.92E-01	1.49E-08		-1.60E+00	1.50E-22	Down	-8.77E-01	9.03E-06		-5.75E-01	2.51E-03		Unigene47933_All//gi|224127334|ref|XP_002320048.1|//7.00E-57//SAUR family protein [Populus trichocarpa] >gi|222860821|gb|EEE98363.1| SAUR family protein [Populus trichocarpa]	Unigene47933_All//7.00E-40//AT3G60690| auxin-responsive family protein	Unigene47933_All//0.00E+00//DW503754				nr +
Unigene47934_All	887	67.19	124.07	53.13	147.03	87.16	94.60	46.24	119.03	42.49	8.85E-01	1.14E-64		-3.39E-01	1.36E-06		-7.54E-01	8.78E-72		-6.36E-01	5.69E-47		1.36E+00	2.84E-152	Up	-1.22E-01	1.26E-01		Unigene47934_All//gi|89258500|gb|AB065463.1|//7.00E-94//DNA binding/zinc ion binding protein [Gossypium hirsutum]	Unigene47934_All//2.00E-49//AT4G12040| zinc finger (AN1-like) family protein	Unigene47934_All//0.00E+00//TC135185				nr +
Unigene47935_All	382	72.18	41.12	41.40	56.46	46.79	65.62	12.84	8.10	4.17	-8.12E-01	1.29E-14		-8.02E-01	1.03E-13		-2.71E-01	2.04E-02		2.17E-01	6.27E-02		-6.65E-01	5.91E-03		-1.62E+00	3.13E-10	Down				Unigene47935_All//6.00E-37//gi|13353264|gb|BG443612.1|BG443612				
Unigene47936_All	781	6.90	10.58	10.64	14.16	11.68	10.52	10.02	7.55	4.69	6.16E-01	2.24E-03		6.24E-01	2.78E-03		-2.77E-01	1.16E-01		-4.28E-01	1.28E-02		-4.09E-01	3.11E-02		-1.09E+00	4.91E-09	Down				Unigene47936_All//3.00E-50//TC169144				
Unigene47938_All	1038	2.27	2.44	3.64	4.61	7.90	8.53	5.70	7.37	2.57	1.06E-01	7.82E-01		6.83E-01	3.85E-02		7.77E-01	5.10E-05		8.88E-01	3.52E-06		3.70E-01	5.65E-02		-1.15E+00	1.46E-07	Down	Unigene47938_All//gi|68124015|emb|CAJ01915.1|//7.00E-06//DNA-directed RNA polymerase [Solanum tuberosum]		Unigene47938_All//4.00E-105//EV490378		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene4794_All	728	8.98	10.09	5.56	17.72	20.95	12.41	40.60	13.61	15.38	1.68E-01	4.72E-01		-6.93E-01	3.87E-03		2.42E-01	1.09E-01		-5.14E-01	8.51E-04		-1.58E+00	1.71E-53	Down	-1.40E+00	2.63E-46	Down	Unigene4794_All//gi|192910792|gb|ACF06504.1|//1.00E-07//60S ribosomal protein L28 [Elaeis guineensis]		Unigene4794_All//2.00E-161//TC155115		ko03010|Ribosome		nr -
Unigene47940_All	2201	0.67	3.64	1.14	2.87	4.47	3.43	22.67	13.54	13.09	2.45E+00	2.18E-21	Up	7.73E-01	6.55E-02		6.39E-01	2.21E-04		2.54E-01	2.89E-01		-7.43E-01	3.49E-27		-7.93E-01	3.76E-31		Unigene47940_All//gi|51655577|gb|ABS18382.1|//0.00E+00//3-ketoacyl-CoA synthase [Eranthis hyemalis]	Unigene47940_All//0.00E+00//AT1G19440| KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene47940_All//0.00E+00//gi|78348340|gb|DT568614.1|DT568614		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr -
Unigene47941_All	1401	6.57	17.83	5.32	9.74	8.33	7.48	6.67	6.56	7.31	1.44E+00	2.34E-32	Up	-3.05E-01	1.40E-01		-2.26E-01	1.63E-01		-3.82E-01	1.30E-02		-2.32E-02	9.19E-01		1.32E-01	4.57E-01		Unigene47941_All//gi|115436240|ref|NP_001042878.1|//1.00E-37//Os01g0316500 [Oryza sativa Japonica Group] >gi|113532409|dbj|BAF04792.1| Os01g0316500 [Oryza sativa Japonica Group]	Unigene47941_All//3.00E-41//AT4G02425| unknown protein	Unigene47941_All//0.00E+00//TC143939				nr +
Unigene47942_All	1980	0.53	1.71	0.67	5.06	6.30	5.43	2.86	1.08	0.72	1.70E+00	3.39E-06	Up	3.47E-01	5.78E-01		3.16E-01	5.21E-02		1.02E-01	6.17E-01		-1.41E+00	2.40E-09	Down	-1.98E+00	3.88E-15	Down	Unigene47942_All//gi|75333601|sp|Q9C9T8.1|Y3868_ARATH|/0.00E+00//Rec Name: Full=Probable inactive receptor kinase At3g08680; Flags: Precursor >gi|224589559|gb|ACN59313.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene47942_All//0.00E+00//AT3G08680| leucine-rich repeat transmembrane protein kinase, putative	Unigene47942_All//0.00E+00//TC141679		ko04626|Plant-pathogen interaction		nr -
Unigene47945_All	405	4.91	2.00	3.68	17.96	18.20	6.69	1.04	1.65	0.79	-1.29E+00	5.96E-03		-4.15E-01	3.93E-01		1.90E-02	9.58E-01		-1.42E+00	1.83E-10	Down	6.61E-01	4.02E-01		-4.08E-01	6.54E-01		Unigene47945_All//gi|9280681|gb|AAF86550.1|AC069252_9//2.00E-21//F2E2.14 [Arabidopsis thaliana]	Unigene47945_All//1.00E-22//AT1G22070| TGA3; DNA binding / calmodulin binding / protein binding / transcription factor	Unigene47945_All//3.00E-113//TC175221	bZIP			nr +
Unigene47946_All	1666	1.44	0.21	0.74	6.04	2.36	1.46	20.48	10.74	3.35	-2.76E+00	7.95E-08	Down	-9.75E-01	2.41E-02		-1.36E+00	5.17E-15	Down	-2.04E+00	2.12E-23	Down	-9.32E-01	2.43E-27		-2.61E+00	5.24E-122	Down	Unigene47946_All//gi|15148922|gb|AK84888.1|AF402607_1//1.00E-143//TGA-type basic leucine zipper protein TGA1.1 [Phaseolus vulgaris]	Unigene47946_All//2.00E-133//AT5G65210| TGA1; DNA binding / calmodulin binding / transcription factor	Unigene47946_All//3.00E-85//TC148920	bZIP			nr +
Unigene47949_All	1719	7.37	3.39	5.61	6.52	8.85	7.67	9.62	2.29	3.64	-1.12E+00	1.23E-11	Down	-3.94E-01	1.91E-02		4.41E-01	1.27E-03		2.35E-01	1.70E-01		-2.07E+00	9.72E-44	Down	-1.40E+00	2.46E-26	Down	Unigene47949_All//gi|38260619|gb|AR15437.1|//0.00E+00//WD-repeat protein [Sisymbrium irio]	Unigene47949_All//0.00E+00//AT5G07590| WD-40 repeat protein family	Unigene47949_All//0.00E+00//TC141661				nr +
Unigene4795_All	767	171.29	169.32	227.65	101.25	118.35	137.20	57.22	91.22	150.68	-1.67E-02	7.47E-01		4.10E-01	1.46E-25		2.25E-01	1.16E-05		4.38E-01	1.78E-19		6.73E-01	7.93E-32		1.40E+00	2.40E-176	Up	Unigene4795_All//gi|260513716|gb|AC342570.1|//2.00E-52//CONSTANS-like zinc finger protein [Glycine max]	Unigene4795_All//7.00E-49//AT5G57660| zinc finger (B-box type) family protein	Unigene4795_All//0.00E+00//gi|78323120|gb|DT543394.1|DT543394	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +
Unigene47951_All	1560	1.48	1.33	2.15	3.00	1.90	2.81	3.23	1.58	1.97	-1.48E-01	7.16E-01		5.43E-01	1.31E-01		-6.61E-01	1.22E-02		-9.61E-02	7.49E-01		-1.03E+00	2.03E-05	Down	-7.14E-01	1.95E-03		Unigene47951_All//gi|297824945|ref|XP_002880355.1|//1.00E-174//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297326194|gb|EFH56614.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene47951_All//3.00E-166//AT2G21090| pentatricopeptide (PPR) repeat-containing protein	Unigene47951_All//0.00E+00//ES806297				nr -
Unigene47952_All	1327	5.76	5.61	9.63	7.66	6.64	9.12	9.56	5.57	4.44	-3.64E-02	8.74E-01		7.42E-01	5.56E-06		-2.05E-01	3.06E-01		2.52E-01	1.55E-01		-7.78E-01	4.51E-08		-1.11E+00	2.52E-14	Down	Unigene47952_All//gi|225468598|ref|XP_002264581.1|//1.00E-111//PREDICTED: similar to Os03g0235100 [Vitis vinifera]	Unigene47952_All//2.00E-90//AT1G61150| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: LisH dimerisation motif, subgroup (InterPro:IPR013720), CTLH, C-terminal to LisH motif (InterPro:IPR006595), LisH dimerisation motif (InterPro:IPR006594), CT11-RanBPM (InterPro:IPR013144); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G11110.1); Has 740 Blast hits to 708 proteins in 137 species: Archae - 0; Bacteria - 0; Metazoa - 401; Fungi - 144; Plants - 139; Viruses - 0; Other Eukaryotes - 56 (source: NCBI BLink).	Unigene47952_All//0.00E+00//TC159537				nr -
Unigene47954_All	2354	28.96	15.61	19.27	41.48	49.63	30.75	33.96	10.80	17.14	-8.92E-01	5.41E-41		-5.88E-01	2.36E-19		2.59E-01	3.69E-09		-4.32E-01	1.05E-17		-1.65E+00	1.20E-153	Down	-9.86E-01	3.86E-71		Unigene47954_All//gi|145357576|ref|NP_568110.2|//1.00E-120//iqd2 (IQ-domain 2); calmodulin binding [Arabidopsis thaliana] >gi|238481199|ref|NP_001154693.1| iqd2 (IQ-domain 2); calmodulin binding [Arabidopsis thaliana] >gi|15982840|gb|AAL09767.1| AT5g03040/F15A17_70 [Arabidopsis thaliana] >gi|23506103|gb|AAN28911.1| At5g03040/F15A17_70 [Arabidopsis thaliana]	Unigene47954_All//3.00E-96//AT5G03040| iqd2 (IQ-domain 2); calmodulin binding	Unigene47954_All//0.00E+00//TC133834				nr -
Unigene47955_All	679	101.10	58.43	53.17	177.54	173.65	179.46	189.86	59.83	95.23	-7.91E-01	9.86E-34		-9.27E-01	1.89E-42		-3.20E-02	6.04E-01		1.55E-02	7.89E-01		-1.67E+00	4.69E-250	Down	-9.96E-01	6.07E-116		Unigene47955_All//gi|242205330|gb|ACS88359.1|//1.00E-130//cellulose synthase catalytic subunit [Gossypium hirsutum]	Unigene47955_All//8.00E-107//AT4G32410| CESA1 (CELLULOSE SYNTHASE 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene47955_All//0.00E+00//TC132034				nr +
Unigene47956_All	1130	9.21	0.90	1.84	12.92	8.35	3.04	3.48	0.67	0.39	-3.36E+00	1.84E-38	Down	-2.33E+00	3.89E-25	Down	-6.29E-01	2.92E-06		-2.09E+00	1.17E-34	Down	-2.39E+00	6.96E-13	Down	-3.17E+00	8.91E-18	Down	Unigene47956_All//gi|9743345|gb|AAF97969.1|AC000103_19//1.00E-39//F21J9.30 [Arabidopsis thaliana]	Unigene47956_All//3.00E-28//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene47956_All//2.00E-91//C0109006				nr -

Unigene47957_All	734	32.01	8.97	8.92	52.12	38.42	14.71	8.24	1.99	1.52	-1.83E+00	3.89E-43	Down	-1.84E+00	8.91E-42	Down	-4.40E-01	2.56E-08		-1.83E+00	2.14E-75	Down	-2.05E+00	3.32E-16	Down	-2.44E+00	1.33E-20	Down	Unigene47957_All//gi|222625788|gb|EEE59920.1|//3.00E-06//hypothetical protein Os_I_12548 [Oryza sativa Japonica Group]		Unigene47957_All//2.00E-143//ES796024				nr +
Unigene4796_All	1147	8.35	8.17	9.15	18.89	17.53	10.75	18.39	15.38	7.64	-3.06E-02	8.83E-01		1.32E-01	5.20E-01		-1.08E-01	4.46E-01		-8.14E-01	1.94E-12		-2.58E-01	1.99E-02		-1.27E+00	1.12E-28	Down	Unigene4796_All//gi|13877549|gb|AAK43852.1|AF370475_1//2.00E-75//Unknown protein [Arabidopsis thaliana]	Unigene4796_All//2.00E-45//AT3G07510| unknown protein	Unigene4796_All//0.00E+00//TC134634				nr -
Unigene47960_All	1530	6.26	5.50	4.42	17.94	22.30	13.70	1.41	2.95	5.44	-1.87E-01	3.65E-01		-5.02E-01	9.79E-03		3.14E-01	3.41E-04		-3.89E-01	1.25E-04		1.07E+00	3.50E-05	Up	1.95E+00	3.96E-21	Up	Unigene47960_All//gi|297810781|ref|XP_002873274.1|//2.00E-79//homeobox-leucine zipper protein 14 [Arabidopsis lyrata subsp. lyrata] >gi|297319111|gb|EFH49533.1| homeobox-leucine zipper protein 14 [Arabidopsis lyrata subsp. lyrata]	Unigene47960_All//1.00E-59//AT5G06710| HAT14 (HOMEOBOX FROM ARABIDOPSIS THALIANA); DNA binding / transcription factor	Unigene47960_All//0.00E+00//gi|78340700|gb|DT560974.1|DT560974	HB			nr -
Unigene47961_All	553	16.08	6.96	16.47	16.84	17.62	6.78	5.12	2.42	1.15	-1.21E+00	2.20E-09	Down	3.39E-02	8.76E-01		6.51E-02	8.07E-01		-1.31E+00	9.22E-12	Down	-1.08E+00	1.26E-03		-2.15E+00	9.02E-09	Down			Unigene47961_All//1.00E-113//gi|09850554|gb|DW479533.1|DW479533				
Unigene47962_All	1015	23.35	7.39	24.45	25.28	18.66	13.79	5.87	2.43	1.33	-1.66E+00	6.35E-38	Down	6.62E-02	6.40E-01		-4.38E-01	1.01E-05		-8.74E-01	1.96E-16		-1.27E+00	1.71E-08	Down	-2.14E+00	1.96E-17	Down			Unigene47962_All//3.00E-152//TC147703				
Unigene47963_All	1429	16.22	7.27	14.16	4.71	5.18	3.48	3.08	2.02	1.03	-1.16E+00	9.07E-22	Down	-1.96E-01	1.26E-01		1.39E-01	5.87E-01		-4.37E-01	6.02E-02		-6.09E-01	1.86E-02		-1.58E+00	6.31E-09	Down	Unigene47963_All//gi|297814844|ref|XP_002875305.1|//5.00E-81//CAAX amino terminal protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321143|gb|EFH51564.1| CAAX amino terminal protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47963_All//3.00E-81//AT3G26085| CAAX amino terminal protease family protein	Unigene47963_All//0.00E+00//TC165933				nr -
Unigene47965_All	545	13.34	33.10	22.57	23.67	22.37	30.91	40.34	47.39	25.07	1.31E+00	1.60E-20	Up	7.58E-01	5.68E-06		-8.19E-02	6.61E-01		3.85E-01	4.62E-03		2.33E-01	2.00E-02		-6.86E-01	2.85E-11		Unigene47965_All//gi|15229253|ref|NP_187074.1|//3.00E-55//SEC (secret agent); transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75336082|sp|Q9M8Y0.1|SEC_ARATH RecName: Full=Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC; AltName: Full=Protein SECRET AGENT >gi|18139887|gb|AAL60196.1|AF441079_1 O-linked N-acetyl glucosamine transferase [Arabidopsis thaliana] >gi|110742062|dbj|BAE98963.1| O-linked GlcNAc transferase like protein [Arabidopsis thaliana]	Unigene47965_All//2.00E-56//AT3G04240| SEC (secret agent); transferase, transferring glycosyl groups	Unigene47965_All//0.00E+00//gi|73848682|gb|DT457702.1|DT457702				nr -
Unigene47968_All	2091	2.33	1.16	0.89	2.43	2.03	3.02	6.69	3.66	4.25	-1.00E+00	2.79E-04	Down	-1.38E+00	3.03E-06	Down	-2.63E-01	3.59E-01		3.16E-01	2.20E-01		-8.72E-01	1.52E-10		-6.56E-01	5.41E-07		Unigene47968_All//gi|115474983|ref|NP_001061088.1|//1.00E-102//Os08g0169700 [Oryza sativa Japonica Group] >gi|113623057|dbj|BAF23002.1| Os08g0169700 [Oryza sativa Japonica Group]	Unigene47968_All//1.00E-144//AT3G55160| EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: HEAT (InterPro:IPR000357); Has 244 Blast hits to 237 proteins in 110 species: Archae - 0; Bacteria - 0; Metazoa - 124; Fungi - 72; Plants - 17; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink).	Unigene47968_All//0.00E+00//DW238174				nr +
Unigene47969_All	1101	1.19	15.23	4.26	4.80	7.60	8.08	2.65	3.83	2.57	3.68E+00	5.82E-66	Up	1.84E+00	8.79E-09	Up	6.64E-01	4.82E-04		7.53E-01	7.54E-05		5.33E-01	4.59E-02		-4.46E-02	9.06E-01		Unigene47969_All//gi|63025168|gb|AY227057.1|//1.00E-105//At5g40550 [Arabidopsis thaliana] >gi|87116622|gb|ABD19675.1| At5g40550 [Arabidopsis thaliana]	Unigene47969_All//2.00E-90//AT3G27460| unknown protein	Unigene47969_All//0.00E+00//gi|164256354|gb|ES798622.1|ES798622				nr +
Unigene4797_All	1073	45.98	13.60	12.95	76.00	61.59	36.16	49.33	7.44	31.41	-1.76E+00	8.90E-85	Down	-1.83E+00	1.91E-86	Down	-3.03E-01	8.82E-09		-1.07E+00	1.32E-71	Down	-2.73E+00	2.92E-192	Down	-6.51E-01	1.16E-23		Unigene4797_All//gi|87240662|gb|ABD32520.1|//1.00E-65//Blue (type 1) copper domain [Medicago truncatula]	Unigene4797_All//8.00E-45//AT5G15350| plastocyanin-like domain-containing protein	Unigene4797_All//0.00E+00//TC131610				nr -
Unigene47970_All	1939	2.00	1.52	0.33	0.80	1.14	5.99	2.90	12.33	28.15	-3.98E-01	2.15E-01		-2.60E+00	6.80E-11	Down	5.13E-01	2.64E-01		2.91E+00	2.00E-39	Up	2.09E+00	2.38E-63	Up	3.28E+00	9.78E-242	Up	Unigene47970_All//gi|224105651|ref|XP_002313887.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222850295|gb|EEE87842.1| GH3 family protein [Populus trichocarpa]	Unigene47970_All//0.00E+00//AT2G14960| GH3.1	Unigene47970_All//0.00E+00//TC160929				nr -
Unigene47971_All	1804	14.76	23.45	9.48	14.64	35.91	18.98	0.05	0.02	0.00	6.68E-01	7.61E-16		-6.40E-01	3.75E-09		1.29E+00	1.82E-83	Up	3.75E-01	3.07E-05		-1.02E+00	7.24E-01		-5.55E+00	3.58E-01		Unigene47971_All//gi|18410804|ref|NP_565106.1|//4.00E-72//AtHB33 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 33); DNA binding / transcription factor [Arabidopsis thaliana] >gi|114050583|gb|ABI49441.1| At1g75240 [Arabidopsis thaliana]	Unigene47971_All//8.00E-51//AT1G75240| AtHB33 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 33); DNA binding / transcription factor	Unigene47971_All//0.00E+00//TC140360	zf-HD			nr +
Unigene47972_All	868	20.92	20.61	22.33	19.46	27.97	18.16	38.92	24.51	15.83	-2.15E-02	8.87E-01		9.44E-02	5.31E-01		5.24E-01	3.63E-07		-9.95E-02	5.57E-01		-6.67E-01	1.38E-15		-1.30E+00	4.80E-47	Down	Unigene47972_All//gi|15224138|ref|NP_179417.1|//5.00E-70//ATCOAD (4-phosphopantetheine adenylyltransferase); nucleotidyltransferase/ pantetheine-phosphate adenylyltransferase [Arabidopsis thaliana] >gi|75267775|sp|Q9ZPV8.1|COAD_ARATH RecName: Full=Phosphopantetheine adenylyltransferase; AltName: Full=Pantetheine-phosphate adenylyltransferase; AltName: Full=Dephospho-CoA pyrophosphorylase; Short=AtCoaD >gi|34365611|gb|AAQ65117.1| At2g18250 [Arabidopsis thaliana]	Unigene47972_All//3.00E-71//AT2G18250| ATCOAD (4-phosphopantetheine adenylyltransferase); nucleotidyltransferase/ pantetheine-phosphate adenylyltransferase	Unigene47972_All//0.00E+00//TC138674				nr -
Unigene47973_All	1111	127.15	65.17	23.96	92.23	92.55	43.66	60.66	14.33	14.34	-9.64E-01	7.01E-96		-2.41E+00	0.00E+00	Down	5.00E-03	9.53E-01		-1.08E+00	7.37E-91	Down	-2.08E+00	3.46E-177	Down	-2.08E+00	2.11E-182	Down	Unigene47973_All//gi|15214035|sp|O65758.1|H2AX_CICAR//1.00E-60//RecName: Full=Histone H2AX >gi|3204129|emb|CAA07234.1| histone H2A [Cicer arietinum]	Unigene47973_All//8.00E-42//AT1G54690| GAMMA-H2AX (GAMMA HISTONE VARIANT H2AX); DNA binding	Unigene47973_All//0.00E+00//gi|109829396|gb|DW227982.1|DW227982				nr +
Unigene47975_All	1556	2.79	5.50	5.03	18.63	20.34	8.56	9.81	6.98	9.11	9.80E-01	1.14E-06		8.50E-01	8.58E-05		1.26E-01	2.50E-01		-1.12E+00	1.02E-27	Down	-4.90E-01	1.18E-04		-1.06E-01	4.64E-01		Unigene47975_All//gi|15229731|ref|NP_187742.1|//1.00E-133//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|111074382|gb|ABH04564.1| At3g11340 [Arabidopsis thaliana]	Unigene47975_All//6.00E-126//AT3G11340| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene47975_All//0.00E+00//TC145385		ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene47981_All	1960	20.93	4.89	10.00	23.28	12.00	9.03	9.10	6.29	2.99	-2.10E+00	1.98E-89	Down	-1.07E+00	4.63E-32	Down	-9.56E-01	6.85E-38		-1.37E+00	6.07E-59	Down	-5.33E-01	4.82E-06		-1.61E+00	1.60E-34	Down	Unigene47981_All//gi|18874283|gb|AAL78741.1|//1.00E-114//MYB-like transcription factor DIVARICATA [Antirrhinum majus]	Unigene47981_All//2.00E-82//AT2G38090| myb family transcription factor	Unigene47981_All//0.00E+00//TC157633	MYB	ko04712|Circadian rhythm - plant		nr +
Unigene47982_All	1723	1.46	3.71	2.23	3.79	4.32	3.80	4.37	7.16	5.90	1.35E+00	4.79E-08	Up	6.10E-01	6.27E-02		1.89E-01	4.54E-01		5.10E-03	9.84E-01		7.12E-01	7.35E-07		4.33E-01	5.74E-03		Unigene47982_All//gi|224081036|ref|XP_002306272.1|//4.00E-27//predicted protein [Populus trichocarpa] >gi|222855721|gb|EEE93268.1| predicted protein [Populus trichocarpa]		Unigene47982_All//0.00E+00//gi|78352072|gb|DT572346.1|DT572346				nr -
Unigene47984_All	866	28.76	10.77	13.96	22.09	26.12	21.23	10.69	4.20	9.89	-1.42E+00	1.07E-31	Down	-1.04E+00	5.24E-19	Down	2.42E-01	4.01E-02		-5.75E-02	6.92E-01		-1.35E+00	7.46E-14	Down	-1.12E-01	5.59E-01		Unigene47984_All//gi|18397703|ref|NP_566290.1|//5.00E-34//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|71660789|sp|Q8LG10.2|GAT15_ARATH RecName: Full=GATA transcription factor 15	Unigene47984_All//2.00E-32//AT3G06740| zinc finger (GATA type) family protein	Unigene47984_All//0.00E+00//ES804921	C2C2-GATA			nr +
Unigene47985_All	1563	17.71	8.56	11.52	26.74	22.78	19.01	24.62	18.96	16.06	-1.05E+00	3.85E-22	Down	-6.21E-01	4.97E-09		-2.31E-01	4.03E-03		-4.92E-01	6.23E-10		-3.77E-01	9.28E-07		-6.16E-01	6.72E-16		Unigene47985_All//gi|18407372|ref|NP_566102.1|//1.00E-141//mitochondrial substrate carrier family protein [Arabidopsis thaliana] >gi|13937206|gb|AAK50096.1|AF372957_1 At2g47490/T30B22.21 [Arabidopsis thaliana] >gi|18491125|gb|AAL69531.1| At2g47490/T30B22.21 [Arabidopsis thaliana] >gi|73531025|emb|CAI38582.1| mitochondrial carrier like protein [Arabidopsis thaliana] >gi|222423082|dbj|BAH19521.1| AT2G47490 [Arabidopsis thaliana] >gi|283482334|emb|CAR70090.1| chloroplastic nicotinamide adenine dinucleotide transporter 1 [Arabidopsis thaliana]	Unigene47985_All//2.00E-127//AT2G47490| mitochondrial substrate carrier family protein	Unigene47985_All//0.00E+00//TC152319		ko04146|Peroxisome		nr +
Unigene47990_All	1559	21.48	16.67	25.17	7.19	9.72	10.66	2.96	1.50	1.41	-3.65E-01	8.56E-05		2.29E-01	1.27E-02		4.35E-01	1.57E-03		5.68E-01	2.00E-05		-9.78E-01	1.08E-04		-1.07E+00	1.55E-05	Down	Unigene47990_All//gi|16209661|gb|AAL14390.1|//1.00E-134//At1g26760/T24P13_13 [Arabidopsis thaliana] >gi|22653318|gb|AAM88251.1| At1g26760/T24P13_13 [Arabidopsis thaliana]	Unigene47990_All//4.00E-133//AT1G26761| unknown protein	Unigene47990_All//0.00E+00//CO110064				nr -
Unigene47991_All	1076	2.14	4.85	2.08	3.06	2.14	1.80	3.18	4.47	2.85	1.18E+00	1.23E-05	Up	-4.17E-02	9.36E-01		-5.11E-01	1.32E-01		-7.60E-01	2.60E-02		4.89E-01	4.95E-02		-1.59E-01	6.10E-01		Unigene47991_All//gi|224115568|ref|XP_002317068.1|//5.00E-55//jumonji domain protein [Populus trichocarpa] >gi|222860133|gb|EEE97680.1| jumonji domain protein [Populus trichocarpa]	Unigene47991_All//4.00E-48//AT1G30810| transcription factor	Unigene47991_All//0.00E+00//gi|5044371|gb|AI725439.1|AI725439				nr -

Unigene47992_A11	3877	3.67	0.42	0.95	0.73	0.29	0.07	13.42	5.15	10.70	-3.13E+00	4.09E-49	Down	-1.95E+00	1.60E-27	Down	-1.32E+00	1.81E-04	Down	-3.39E+00	9.61E-12	Down	-1.38E+00	5.45E-77	Down	-3.28E-01	3.04E-07		Unigene47992_A11//gi|297799354|ref|XP_002867561.1|//0.00E+00//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313397|gb|EFH43820.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene47992_A11//0.00E+00//AT5G56040| leucine-rich repeat protein kinase, putative	Unigene47992_A11//0.00E+00//TC171196				nr +
Unigene47994_A11	915	65.76	28.85	28.69	69.85	60.67	78.78	45.75	37.91	36.49	-1.19E+00	1.07E-57	Down	-1.20E+00	2.60E-56	Down	-2.03E-01	1.36E-03		1.74E-01	6.32E-03		-2.71E-01	2.71E-04		-3.26E-01	5.82E-06		Unigene47994_A11//gi|297792921|ref|XP_002864345.1|//2.00E-40//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297310180|gb|EFH40604.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene47994_A11//3.00E-38//AT5G54580| RNA recognition motif (RRM)-containing protein	Unigene47994_A11//0.00E+00//TC136529		ko03040|Spliceosome		nr +
Unigene47996_A11	798	2.10	7.62	5.74	5.37	7.16	6.34	3.44	2.10	3.15	1.86E+00	8.21E-12	Up	1.45E+00	2.54E-06	Up	4.16E-01	1.03E-01		2.40E-01	4.30E-01		-7.17E-01	3.45E-02		-1.31E-01	6.97E-01		Unigene47996_A11//gi|145049690|gb|ABF35526.1|//8.00E-14//CCR4-associated factor [Ipomoea batatas]	Unigene47996_A11//2.00E-12//AT5G22250| CCR4-NOT transcription complex protein, putative	Unigene47996_A11//0.00E+00//gi|13351860|gb|BG442208.1|BG442208		ko03018|RNA degradation		nr -
Unigene48_A11	696	5.26	2.04	6.73	11.17	11.43	9.47	8.38	2.52	16.31	-1.37E+00	4.35E-05	Down	3.56E-01	2.37E-01		3.37E-02	8.98E-01		-2.37E-01	3.11E-01		-1.73E+00	1.13E-12	Down	9.61E-01	2.27E-10		Unigene48_A11//gi|47078500|gb|AAT09898.1|//1.00E-84//cellulose synthase [Populus tremula x Populus tremuloides]	Unigene48_A11//1.00E-65//AT4G39350| CESA2 (CELLULOSE SYNTHASE A2); cellulose synthase/ transferase, transferring glycosyl groups	Unigene48_A11//0.00E+00//DW485908				nr -
Unigene480_A11	2226	4.58	17.78	9.86	18.86	21.29	38.73	13.87	21.39	29.03	1.96E+00	3.42E-78	Up	1.10E+00	1.92E-18	Up	1.74E-01	2.80E-02		1.04E+00	5.50E-71	Up	6.25E-01	2.41E-19		1.07E+00	6.01E-65	Up	Unigene480_A11//gi|32815816|gb|AAP88291.1|//1.00E-160//protein kinase [Cucumis sativus]	Unigene480_A11//4.00E-151//AT5G40540| protein kinase, putative	Unigene480_A11//0.00E+00//TC147234				nr -
Unigene48000_A11	1936	2.76	1.86	1.38	8.41	8.31	8.09	10.07	4.53	4.42	-5.69E-01	2.77E-02		-1.00E+00	2.23E-04	Down	-1.86E-02	9.11E-01		-5.58E-02	7.26E-01		-1.15E+00	3.01E-22	Down	-1.19E+00	5.08E-24	Down	Unigene48000_A11//gi|42568131|ref|NP_198315.2|//2.00E-78//chromosome-associated kinesin-related [Arabidopsis thaliana] >gi|53850475|gb|AAU95414.1| At5g33300 [Arabidopsis thaliana] >gi|55733741|gb|AAV59267.1| At5g33300 [Arabidopsis thaliana]	Unigene48000_A11//5.00E-53//AT5G33300| chromosome-associated kinesin-related	Unigene48000_A11//0.00E+00//TC141042				nr +
Unigene48001_A11	1423	44.08	45.61	30.46	40.36	45.76	36.91	25.58	19.83	10.53	4.92E-02	5.30E-01		-5.33E-01	4.27E-15		1.81E-01	5.06E-03		-1.29E-01	9.40E-02		-3.68E-01	3.42E-06		-1.28E+00	1.17E-49	Down	Unigene48001_A11//gi|12711645|gb|AK01931.1|AF329816_1|1.00E-124//Cu/Zn-superoxide dismutase copper chaperone precursor [Glycine max]	Unigene48001_A11//5.00E-109//AT1G12520| ATCCS (COPPER CHAPERONE FOR SOD1); superoxide dismutase/ superoxide dismutase copper chaperone	Unigene48001_A11//0.00E+00//gi|78348486|gb|DT568760.1|DT568760		ko04146|Peroxisome		nr -
Unigene48002_A11	1615	5.93	13.46	8.01	13.73	13.92	15.63	18.72	23.50	15.57	1.18E+00	4.76E-21	Up	4.35E-01	8.21E-03		2.06E-02	8.91E-01		1.88E-01	1.16E-01		3.28E-01	2.43E-05		-2.66E-01	2.20E-03		Unigene48002_A11//gi|115462059|ref|NP_001054629.1|//1.00E-168//Os05g0145000 [Oryza sativa Japonica Group] >gi|51038194|gb|AAT93997.1| unknow protein [Oryza sativa Japonica Group] >gi|113578180|dbj|BAF16543.1| Os05g0145000 [Oryza sativa Japonica Group]	Unigene48002_A11//4.00E-166//AT3G47990| zinc finger (C3HC4-type RING finger) family protein	Unigene48002_A11//0.00E+00//TC162614				nr +
Unigene48004_A11	1844	4.60	6.51	10.11	3.19	3.62	3.23	0.44	0.39	0.15	5.03E-01	2.15E-03		1.14E+00	1.78E-16	Up	1.85E-01	4.97E-01		2.04E-02	9.48E-01		-1.77E-01	7.93E-01		-1.53E+00	3.04E-02		Unigene48004_A11//gi|115445371|ref|NP_001046465.1|//1.00E-141//Os02g0255700 [Oryza sativa Japonica Group] >gi|113535996|dbj|BAF08379.1| Os02g0255700 [Oryza sativa Japonica Group]	Unigene48004_A11//2.00E-104//AT1G15290| binding	Unigene48004_A11//8.00E-111//CA994256				nr -
Unigene48007_A11	1459	0.36	1.29	2.23	7.72	11.38	10.12	5.07	6.93	6.23	1.84E+00	4.09E-04	Up	2.63E+00	2.14E-09	Up	5.60E-01	1.19E-05		3.92E-01	7.61E-03		4.51E-01	5.27E-03		2.96E-01	8.61E-02		Unigene48007_A11//gi|30678252|ref|NP_171719.2|//4.00E-67//AMC1 (METACASPASE 1); cysteine-type endopeptidase [Arabidopsis thaliana] >gi|75232683|sp|Q7XJE6.1|MCA1_ARATH RecName: Full=Metacaspase-1; Short=AtMCP1b; Short=AtMC1; AltName: Full=Protein LSD ONE LIKE 3 >gi|32482812|gb|AAP84706.1| metacaspase 1 [Arabidopsis thaliana] >gi|37788545|gb|AAP44514.1| metacaspase 1 [Arabidopsis thaliana]	Unigene48007_A11//5.00E-62//AT1G02170| AMC1 (METACASPASE 1); cysteine-type endopeptidase	Unigene48007_A11//3.00E-08//TC178900				nr -
Unigene48008_A11	1477	4.71	10.43	5.62	7.08	14.13	11.86	8.65	9.62	9.71	1.15E+00	1.95E-14	Up	2.56E-01	2.46E-01		9.96E-01	6.05E-18		7.44E-01	9.77E-09		1.54E-01	3.12E-01		1.68E-01	2.38E-01		Unigene48008_A11//gi|226505048|ref|NP_001151501.1|//5.00E-59//DNA binding protein [Zea mays]	Unigene48008_A11//1.00E-41//AT4G13040| AP2 domain-containing transcription factor family protein	Unigene48008_A11//0.00E+00//TC140660	AP2-EREBP			nr +
Unigene48009_A11	1447	9.18	10.05	9.90	13.87	13.71	12.17	15.69	10.60	6.33	1.30E-01	4.18E-01		1.08E-01	5.38E-01		-1.74E-02	9.07E-01		-1.89E-01	1.67E-01		-5.66E-01	3.21E-08		-1.31E+00	2.41E-32	Down	Unigene48009_A11//gi|297831530|ref|XP_002883647.1|//5.00E-92//indole-3-butyric acid response 5 [Arabidopsis lyrata subsp. lyrata] >gi|297329487|gb|EFH59906.1| indole-3-butyric acid response 5 [Arabidopsis lyrata subsp. lyrata]	Unigene48009_A11//5.00E-88//AT2G04550| IBR5 (INDOLE-3-BUTYRIC ACID RESPONSE 5); MAP kinase phosphatase/ protein tyrosine/serine/threonine phosphatase	Unigene48009_A11//0.00E+00//TC159292				nr -
Unigene4801_A11	630	6.98	1.93	6.93	9.41	7.71	11.33	3.02	2.32	6.89	-1.85E+00	9.28E-09	Down	-9.40E-03	9.99E-01		-2.88E-01	2.69E-01		2.68E-01	2.73E-01		-3.79E-01	4.07E-01		1.19E+00	5.19E-06	Up	Unigene4801_A11//gi|37202038|gb|AAQ89634.1|//5.00E-35//At1g14020 [Arabidopsis thaliana] >gi|110739513|dbj|BAF01665.1| growth regulator like protein [Arabidopsis thaliana] >gi|110739824|dbj|BAF01818.1| growth regulator like protein [Arabidopsis thaliana]	Unigene4801_A11//2.00E-29//AT1G14020| unknown protein	Unigene4801_A11//0.00E+00//TC154665				nr -
Unigene48010_A11	1796	1.81	5.50	4.92	4.91	9.07	12.05	0.49	0.67	0.09	1.61E+00	2.02E-15	Up	1.45E+00	1.54E-11	Up	8.85E-01	1.15E-11		1.29E+00	1.25E-25	Up	4.49E-01	4.29E-01		-2.48E+00	9.93E-04	Down	Unigene48010_A11//gi|82623417|gb|AB88123.1|//1.00E-167//aspartic protease precursor-like [Solanum tuberosum]	Unigene48010_A11//3.00E-144//AT1G62290| aspartyl protease family protein	Unigene48010_A11//0.00E+00//C0126166				nr +
Unigene48012_A11	1598	18.27	16.11	19.63	83.17	57.13	57.83	14.53	6.93	3.84	-1.82E-01	8.84E-02		1.03E-01	3.79E-01		-5.42E-01	1.50E-40		-5.24E-01	6.12E-34		-1.07E+00	2.05E-23	Down	-1.92E+00	5.17E-57	Down	Unigene48012_A11//gi|300608164|emb|CAZ88692.1|//1.00E-141//epoxide hydrolase 1 [Prunus persica]	Unigene48012_A11//9.00E-115//AT4G15960| catalytic/ epoxide hydrolase	Unigene48012_A11//0.00E+00//gi|78335353|gb|DT555627.1|DT555627				nr +
Unigene48013_A11	2272	1.29	1.72	1.31	1.86	4.12	6.14	7.44	24.08	19.08	4.13E-01	1.94E-01		2.54E-02	9.63E-01		1.15E+00	3.03E-10	Up	1.72E+00	3.88E-25	Up	1.69E+00	9.61E-109	Up	1.36E+00	7.65E-64	Up	Unigene48013_A11//gi|223452282|gb|ACM89469.1|//1.00E-153//serine/threonine protein kinase family protein [Glycine max]	Unigene48013_A11//2.00E-147//AT1G18390| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene48013_A11//8.00E-16//TC177699				nr +
Unigene48019_A11	979	11.22	4.81	5.38	16.03	9.15	15.27	16.20	8.71	5.29	-1.22E+00	1.34E-11	Down	-1.06E+00	6.01E-09	Down	-8.10E-01	4.06E-10		-6.99E-02	6.96E-01		-8.95E-01	2.43E-12		-1.61E+00	5.85E-31	Down	Unigene48019_A11//gi|18417773|ref|NP_568321.1|//2.00E-86//RNA-binding S4 domain-containing protein [Arabidopsis thaliana] >gi|51968508|dbj|BAD42946.1| ribosomal protein-like [Arabidopsis thaliana] >gi|107738200|gb|ABF83660.1| At5g15750 [Arabidopsis thaliana]	Unigene48019_A11//4.00E-80//AT5G15750| RNA-binding S4 domain-containing protein	Unigene48019_A11//0.00E+00//TC139471		ko03010|Ribosome		nr -
Unigene4802_A11	728	4.02	6.75	5.27	14.10	18.97	26.06	3.83	2.81	60.74	7.46E-01	5.91E-03		3.88E-01	2.42E-01		4.28E-01	3.33E-03		8.86E-01	1.84E-12		-4.46E-01	2.03E-01		3.99E+00	1.97E-230	Up	Unigene4802_A11//gi|18397376|ref|NP_564349.1|//2.00E-20//JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8) [Arabidopsis thaliana] >gi|75155014|sp|Q8LEM2.1|TIF5A_ARATH RecName: Full=Protein TIFY 5A; AltName: Full=Jasmonate ZIM domain-containing protein 8 >gi|109946551|gb|ABG48454.1| At1g30135 [Arabidopsis thaliana]	Unigene4802_A11//3.00E-18//AT1G30135| JAZ8 (JASMONATE-ZIM-DOMAIN PROTEIN 8)	Unigene4802_A11//0.00E+00//TC163560	Tify			nr +
Unigene48020_A11	714	33.93	29.59	33.34	44.93	53.05	56.80	28.31	28.39	64.33	-1.97E-01	9.40E-02		-2.53E-02	8.44E-01		2.40E-01	5.14E-03		3.38E-01	3.88E-05		4.40E-03	1.01E+00		1.18E+00	7.93E-55	Up	Unigene48020_A11//gi|297829912|ref|XP_002882838.1|//4.00E-31//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329878|gb|EFH59097.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48020_A11//2.00E-32//AT3G13670| protein kinase family protein	Unigene48020_A11//0.00E+00//gi|78348380|gb|DT568654.1|DT568654				nr +
Unigene48021_A11	1063	17.08	50.76	20.04	39.22	72.43	66.53	42.00	53.04	98.04	1.57E+00	1.26E-78	Up	2.31E-01	7.97E-02		8.85E-01	7.16E-54		7.62E-01	7.18E-35		3.37E-01	7.29E-08		1.22E+00	1.11E-129	Up	Unigene48021_A11//gi|20269057|emb|CAC84709.1|//1.00E-67//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene48021_A11//2.00E-39//AT4G28640| IAA11 (INDOLE-3-ACETIC ACID INDUCIBLE 11); transcription factor	Unigene48021_A11//0.00E+00//TC160945				nr -
Unigene48022_A11	1141	11.33	12.52	8.49	28.29	30.39	51.14	6.19	22.45	3.53	1.45E-01	3.74E-01		-4.15E-01	1.20E-02		1.03E-01	3.33E-01		8.54E-01	5.87E-35		1.86E+00	2.71E-58	Up	-8.11E-01	2.35E-05		Unigene48022_A11//gi|259121385|gb|ACV92012.1|//2.00E-81//WRKY transcription factor 10 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene48022_A11//4.00E-36//AT4G39410| WRKY13; transcription factor	Unigene48022_A11//0.00E+00//TC177377	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene48023_A11	868	31.59	58.67	71.59	46.08	49.95	44.38	8.77	10.11	8.31	8.93E-01	9.15E-31		1.18E+00	4.62E-57	Up	1.16E-01	2.06E-01		-5.43E-02	6.40E-01		2.06E-01	2.89E-01		-7.78E-02	6.97E-01					Unigene48023_A11//5.00E-18//gi|78333552|gb|DT553826.1|DT553826				
Unigene48025_A11	1128	5.89	12.08	8.69	6.85	7.91	7.73	10.50	10.78	7.52	1.04E+00	4.79E-11	Up	5.60E-01	3.26E-03		2.08E-01	3.36E-01		1.75E-01	4.51E-01		3.90E-02	8.18E-01		-4.80E-01	7.71E-04		Unigene48025_A11//gi|225435733|ref|XP_002285704.1|//5.00E-85//PREDICTED: similar to TAF7 (TBP-ASSOCIATED FACTOR 7); general RNA polymerase II transcription factor [Vitis vinifera]	Unigene48025_A11//2.00E-63//AT1G55300| TAF7 (TBP-ASSOCIATED FACTOR 7); general RNA polymerase II transcription factor	Unigene48025_A11//0.00E+00//TC167053		ko03022|Basal transcription factors		nr +
Unigene48027_A11	1021	3.48	20.30	4.28	6.59	6.48	5.13	1.04	2.05	1.29	2.54E+00	8.84E-57	Up	2.96E-01	3.61E-01		-2.45E-02	9.23E-01		-3.60E-01	1.33E-01		9.83E-01	1.38E-02		3.15E-01	5.59E-01		Unigene48027_A11//gi|225459358|ref|XP_002284225.1|//1.00E-09//PREDICTED: similar to F28K19.26 [Vitis vinifera]	Unigene48027_A11//6.00E-09//AT4G08685| SAH7	Unigene48027_A11//0.00E+00//gi|78338909|gb|DT559183.1|DT559183				nr -
Unigene48029_A11	859	60.12	10.15	15.31	113.31	82.26	112.41	101.79	38.68	44.06	-2.57E+00	1.67E-143	Down	-1.97E+00	2.84E-100	Down	-4.62E-01	2.55E-22		-1.16E-02	8.73E-01		-1.40E+00	6.48E-131	Down	-1.21E+00	1.00E-107	Down	Unigene48029_A11//gi|115457852|ref|NP_001052526.1|//1.00E-106//Os04g0349500 [Oryza sativa Japonica Group] >gi|32489919|emb|CAE05511.1| OSJNBa0038P21.4 [Oryza sativa (japonica cultivar-group)] >gi|113564097|dbj|BAF14440.1| Os04g0349500 [Oryza sativa Japonica Group]	Unigene48029_A11//9.00E-78//AT5G39240| 40S ribosomal protein S8 (RPS8B)	Unigene48029_A11//0.00E+00//TC131031		ko03010|Ribosome		nr +

Unigene4803_All	1075	1.36	0.66	1.59	1.76	2.08	2.31	2.01	0.89	4.22	-1.05E+00	5.84E-02		2.18E-01	6.56E-01		2.42E-01	6.06E-01		3.92E-01	3.82E-01		-1.17E+00	3.23E-03		1.07E+00	1.95E-05	Up	Unigene4803_All//gi|224126033|ref|XP_002319739.1|//1.00E-117//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222858115|gb|EEE95662.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene4803_All//3.00E-104//AT3G54280| BG03 (ROOT GROWTH DEFECTIVE 3); ATP binding / DNA binding / binding / helicase/ nucleic acid binding	Unigene4803_All//6.00E-135//DW484463				nr -
Unigene48030_All	1138	16.09	4.50	10.20	42.90	36.04	15.36	26.49	17.74	13.37	-1.84E+00	6.93E-34	Down	-6.58E-01	8.40E-07		-2.51E-01	5.02E-04		-1.48E+00	2.87E-71	Down	-5.79E-01	4.81E-11		-9.86E-01	2.23E-27		Unigene48030_All//gi|15228391|ref|NP_187698.1|//8.00E-92//MES17 (METHYL ESTERASE 17); hydrolase/ hydrolase, acting on ester bonds / methyl indole-3-acetate esterase [Arabidopsis thaliana]	Unigene48030_All//4.00E-93//AT3G10870| MES17 (METHYL ESTERASE 17); hydrolase/ hydrolase, acting on ester bonds / methyl indole-3-acetate esterase	Unigene48030_All//0.00E+00//TC132961		ko00901|Indole alkaloid biosynthesis		nr +
Unigene48038_All	1564	9.94	9.78	11.58	5.48	5.59	3.64	1.35	0.29	0.87	-2.22E-02	8.94E-01		2.21E-01	1.30E-01		2.97E-02	9.05E-01		-5.90E-01	2.41E-03		-2.20E+00	1.20E-06	Down	-6.42E-01	9.20E-02		Unigene48038_All//gi|45752622|gb|AS76209.1|//3.00E-31//At4g13140 [Arabidopsis thaliana] >gi|46359781|gb|AAS88754.1| At4g13140 [Arabidopsis thaliana]	Unigene48038_All//1.00E-112//AT4G13150| unknown protein	Unigene48038_All//0.00E+00//DW009255				nr +
Unigene48040_All	891	11.16	4.95	1.67	69.49	22.53	35.84	70.70	83.17	79.59	-1.17E+00	5.78E-10	Down	-2.74E+00	7.75E-29	Down	-1.62E+00	4.65E-119	Down	-9.55E-01	3.93E-45		2.34E-01	1.81E-05		1.71E-01	2.25E-03		Unigene48040_All//gi|113367218|gb|AB134666.1|//2.00E-49//bZIP transcription factor bZIP124 [Glycine max]	Unigene48040_All//8.00E-34//AT4G34590| GBF6 (G-BOX BINDING FACTOR 6); DNA binding / protein heterodimerization/ transcription factor	Unigene48040_All//0.00E+00//EX170178	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene48041_All	1317	0.72	2.04	2.67	1.70	1.67	2.67	5.97	5.81	4.84	1.51E+00	2.03E-04	Up	1.90E+00	5.26E-07	Up	-2.45E-02	9.58E-01		6.52E-01	5.04E-02		-4.01E-02	8.54E-01		-3.03E-01	1.05E-01		Unigene48041_All//gi|115465355|ref|NP_001056277.1|//1.00E-142//0s05g0556000 [Oryza sativa Japonica Group] >gi|113579828|dbj|BAF18191.1| 0s05g0556000 [Oryza sativa Japonica Group]	Unigene48041_All//5.00E-129//AT4G13400| unknown protein					nr -
Unigene48043_All	1824	5.94	3.97	3.44	14.75	12.91	8.96	0.53	0.02	0.26	-5.80E-01	7.83E-04		-7.85E-01	1.26E-05		-1.92E-01	8.01E-02		-7.18E-01	1.94E-12		-4.54E+00	6.92E-06	Down	-1.02E+00	9.02E-02		Unigene48043_All//gi|17978954|gb|AAL47442.1|//1.00E-151//At1g22570/T12C24_9 [Arabidopsis thaliana]	Unigene48043_All//6.00E-105//AT3G56060| glucose-methanol-choline (GMC) oxidoreductase family protein	Unigene48043_All//0.00E+00//gi|54121698|gb|CO497207.1|CO497207		ko00460|Cyanoamino acid metabolism		nr -
Unigene48045_All	1305	0.56	129.95	7.39	2.79	8.42	28.62	9.53	89.96	53.64	7.86E+00	0.00E+00	Up	3.72E+00	2.06E-37	Up	1.59E+00	2.13E-19	Up	3.36E+00	4.55E-145	Up	3.24E+00	0.00E+00	Up	2.49E+00	4.18E-233	Up	Unigene48045_All//gi|4666360|gb|AAD26942.1|AF119050|1/5.00E-37//zinc-finger protein 1 [Datisca glomerata]	Unigene48045_All//1.00E-20//AT5G04340| ZAT6 (ZINC FINGER OF ARABIDOPSIS THALIANA 6); nucleic acid binding / transcription factor/ zinc ion binding	Unigene48045_All//0.00E+00//TC139442	C2H2			nr +
Unigene48048_All	967	10.06	2.99	8.32	3.45	4.91	3.97	0.92	1.73	0.78	-1.75E+00	3.38E-17	Down	-2.75E-01	1.72E-01		5.10E-01	6.71E-02		2.02E-01	5.91E-01		9.13E-01	4.52E-02		-2.30E-01	7.05E-01		Unigene48048_All//gi|50253440|gb|AAT71922.1|//5.00E-11//At4g09970 [Arabidopsis thaliana] >gi|58331783|gb|AAR70089.1| At4g09970 [Arabidopsis thaliana]	Unigene48048_All//5.00E-13//AT4G09970| unknown protein					nr -
Unigene48051_All	1170	4.52	8.32	3.19	4.51	4.39	4.94	8.85	5.18	4.05	8.81E-01	2.21E-06		-5.04E-01	6.73E-02		-4.14E-02	8.80E-01		1.31E-01	6.51E-01		-7.73E-01	1.11E-06		-1.13E+00	3.18E-12	Down	Unigene48051_All//gi|15229569|ref|NP_188430.1|//1.00E-93//ATHAL3A; FMN binding / phosphopantothenoylcysteine decarboxylase [Arabidopsis thaliana] >gi|13124313|sp|Q9SWE5.1|HAL3A_ARATH RecName: Full=Phosphopantothenoylcysteine decarboxylase; Short=PPCDC; AltName: Full=Halotolerance protein Hal3a; Short=AtHal3a; Short=AtCoaC >gi|108358869|pdb|1E20|A Chain A, The Fmn Binding Protein Athal3 >gi|5802225|gb|AAD51616.1|AF166262_1 HAL3A protein [Arabidopsis thaliana] >gi|11994209|dbj|BAB01331.1| HAL3A protein [Arabidopsis thaliana] >gi|48310154|gb|AAT41764.1| At3g18030 [Arabidopsis thaliana] >gi|52218792|gb|AAU29466.1| At3g18030 [Arabidopsis thaliana] >gi|110737049|dbj|BAF00478.1| HAL3A protein [Arabidopsis thaliana]	Unigene48051_All//7.00E-95//AT3G18030| ATHAL3A; FMN binding / phosphopantothenoylcysteine decarboxylase	Unigene48051_All//0.00E+00//TC152152		ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene48052_All	1052	73.86	13.87	12.50	66.81	45.40	25.24	37.78	3.66	5.76	-2.41E+00	1.02E-200	Down	-2.56E+00	3.78E-208	Down	-5.57E-01	9.89E-23		-1.40E+00	1.75E-94	Down	-3.37E+00	3.57E-178	Down	-2.71E+00	3.97E-148	Down	Unigene48052_All//gi|15232681|ref|NP_190278.1|//2.00E-66//deoxyuridine 5'-triphosphate nucleotidohydrolase family [Arabidopsis thaliana] >gi|5541665|emb|CAB51171.1| dUTP pyrophosphatase-like protein [Arabidopsis thaliana]	Unigene48052_All//1.00E-67//AT3G46940| deoxyuridine 5'-triphosphate nucleotidohydrolase family	Unigene48052_All//0.00E+00//TC139113		ko00240|Pyrimidine metabolism		nr -
Unigene48053_All	1214	7.63	17.07	13.73	4.19	8.20	5.92	0.10	0.28	0.53	1.16E+00	1.45E-19	Up	8.48E-01	2.36E-09		9.70E-01	2.01E-08		4.99E-01	2.39E-02		1.40E+00	2.76E-01		2.33E+00	1.05E-02		Unigene48053_All//gi|224099887|ref|XP_002311660.1|//1.00E-123//magnesium transporter [Populus trichocarpa] >gi|222851480|gb|EEE89027.1| magnesium transporter [Populus trichocarpa]	Unigene48053_All//4.00E-106//AT5G64560| magnesium transporter CorA-like family protein (MRS2-2)	Unigene48053_All//0.00E+00//TC177709				nr +
Unigene48054_All	1330	5.59	15.35	8.37	3.75	3.86	3.60	0.06	0.38	0.57	1.46E+00	4.39E-27	Up	5.83E-01	9.74E-04		4.27E-02	8.98E-01		-5.73E-02	8.56E-01		2.57E+00	2.28E-02		3.16E+00	6.82E-04	Up	Unigene48054_All//gi|224099887|ref|XP_002311660.1|//1.00E-135//magnesium transporter [Populus trichocarpa] >gi|222851480|gb|EEE89027.1| magnesium transporter [Populus trichocarpa]	Unigene48054_All//4.00E-121//AT5G64560| magnesium transporter CorA-like family protein (MRS2-2)	Unigene48054_All//0.00E+00//TC171755				nr +
Unigene48055_All	1426	15.56	3.80	5.60	26.62	15.41	20.68	2.82	2.26	0.47	-2.03E+00	1.11E-46	Down	-1.47E+00	8.13E-29	Down	-7.89E-01	8.40E-23		-3.64E-01	1.71E-05		-3.20E-01	2.71E-01		-2.57E+00	9.42E-15	Down	Unigene48055_All//gi|15220550|ref|NP_176949.1|//1.00E-134//ATFXG1 (alpha-fucosidase 1); alpha-L-fucosidase/ carboxylesterase [Arabidopsis thaliana] >gi|75173075|sp|Q9FXE5.1|FUCO3_ARATH RecName: Full=Alpha-L-fucosidase 3; AltName: Full=Alpha-L-fucoside fucohydrolase 3; AltName: Full=Alpha-1,2-fucosidase; Short=AtFXG1; Flags: Precursor >gi|11072007|gb|AAG28886.1|AC008113_2 F12A21.4 [Arabidopsis thaliana]	Unigene48055_All//1.00E-135//AT1G67830| ATFXG1 (alpha-fucosidase 1); alpha-L-fucosidase/ carboxylesterase	Unigene48055_All//0.00E+00//TC166297				nr -
Unigene48057_All	2076	8.17	10.37	6.52	13.51	11.84	13.68	16.09	21.18	34.20	3.45E-01	3.97E-03		-3.26E-01	2.39E-02		-1.90E-01	7.53E-02		1.85E-02	8.98E-01		3.97E-01	2.76E-08		1.09E+00	1.28E-73	Up	Unigene48057_All//gi|75274192|sp|Q9LU89.1|2A5N_ARATH//0.00E+00//RecName: Full=Serine/threonine protein phosphatase 2A 59 kDa regulatory subunit B' eta isoform; Short=PP2A, B' subunit, eta isoform; Short=AtB' eta >gi|14194123|gb|AAK56256.1|AF36726_7_1 AT3g26020/MPE11_17 [Arabidopsis thaliana] >gi|9279607|dbj|BAB01065.1| protein phosphatase 2A regulatory subunit B' [Arabidopsis thaliana] >gi|16323340|gb|AAL15383.1| AT3g26020/MPE11_17 [Arabidopsis thaliana] >gi|222424130|dbj|BAH20024.1| AT3G26020 [Arabidopsis thaliana]	Unigene48057_All//0.00E+00//AT3G26020| serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative	Unigene48057_All//0.00E+00//TC142610				nr +
Unigene48060_All	1956	16.42	1.66	2.97	25.98	18.40	33.09	57.54	14.74	23.08	-3.31E+00	4.25E-116	Down	-2.47E+00	1.74E-82	Down	-4.98E-01	1.55E-13		3.49E-01	3.25E-08		-1.96E+00	4.75E-274	Down	-1.32E+00	1.28E-158	Down	Unigene48060_All//gi|225433375|ref|XP_002285608.1|//0.00E+00//PREDICTED: similar to GroEL-like chaperone, ATPase [Vitis vinifera]	Unigene48060_All//0.00E+00//AT3G23990| HSP60 (HEAT SHOCK PROTEIN 60); ATP binding	Unigene48060_All//0.00E+00//gi|78336593|gb|DT556867.1|DT556867		ko03018|RNA degradation		nr -
Unigene48061_All	1268	9.86	4.32	5.67	260.94	155.91	194.12	371.02	62.63	141.89	-1.19E+00	1.24E-12	Down	-7.99E-01	1.51E-06		-7.43E-01	3.23E-177		-4.27E-01	1.70E-57		-2.57E+00	0.00E+00	Down	-1.39E+00	0.00E+00	Down	Unigene48061_All//gi|21390654\0|gb|AGJ11763.1|//1.00E-156//class III peroxidase [Gossypium hirsutum]	Unigene48061_All//2.00E-135//AT4G37530| peroxidase, putative	Unigene48061_All//0.00E+00//TC133431		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene48067_All	1034	2.38	2.60	1.60	4.19	4.63	4.59	3.31	1.46	1.19	1.27E-01	7.30E-01		-5.75E-01	1.78E-01		1.43E-01	6.55E-01		1.30E-01	6.94E-01		-1.19E+00	9.42E-05	Down	-1.47E+00	1.55E-06	Down	Unigene48067_All//gi|16323095|gb|AAL15282.1|//6.00E-51//AT4g39900/T5J17_70 [Arabidopsis thaliana]	Unigene48067_All//1.00E-51//AT4G39900| unknown protein	Unigene48067_All//0.00E+00//DT466301				nr -
Unigene48069_All	1000	16.43	5.62	27.00	34.97	23.93	15.13	0.59	4.18	2.15	-1.55E+00	5.60E-24	Down	7.17E-01	3.42E-11		-5.47E-01	3.67E-11		-1.21E+00	1.69E-37	Down	2.82E+00	3.07E-16	Up	1.86E+00	9.53E-06	Up	Unigene48069_All//gi|133712623|gb|AB037118.1|//2.00E-94//cuticular water permeability [Solanum habrochaites]	Unigene48069_All//4.00E-77//AT4G38260| unknown protein					nr -
Unigene48070_All	1153	29.59	24.48	23.23	42.77	40.11	41.44	67.55	32.01	22.22	-2.74E-01	3.53E-03		-3.49E-01	2.69E-04		-9.27E-02	2.99E-01		-4.56E-02	6.32E-01		-1.08E+00	7.84E-78	Down	-1.60E+00	1.80E-147	Down	Unigene48070_All//gi|87240804|gb|ABD32662.1|//2.00E-94//Pyrophosphate-dependent phosphofructokinase PfpB [Medicago truncatula]	Unigene48070_All//2.00E-93//AT1G12000| pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative	Unigene48070_All//0.00E+00//TC144026		ko00051|Fructose and mannose metabolism		nr +
Unigene48071_All	2172	0.22	0.40	0.86	2.64	1.38	1.04	4.36	2.27	7.63	8.71E-01	2.45E-01		1.98E+00	3.17E-04	Up	-9.35E-01	4.87E-05		-1.34E+00	1.03E-07	Down	-9.41E-01	2.62E-08		8.07E-01	3.27E-11		Unigene48071_All//gi|158827646|gb|ABR81000.1|//0.00E+00//PI-phospholipase C PLC4 [Solanum lycopersicum]	Unigene48071_All//1.00E-153//AT2G40116| phosphoinositide-specific phospholipase C family protein	Unigene48071_All//0.00E+00//CO123746		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene48073_All	958	40.85	19.68	20.46	55.48	43.10	39.98	28.95	13.57	10.77	-1.05E+00	3.11E-31	Down	-9.98E-01	1.54E-27		-3.64E-01	3.87E-08		-4.73E-01	1.26E-11		-1.09E+00	6.78E-29	Down	-1.43E+00	1.02E-44	Down	Unigene48073_All//gi|18398882|ref|NP_565443.1|//1.00E-41//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|166490043|gb|AAL24373.1| Unknown protein [Arabidopsis thaliana] >gi|20197034|gb|AAC09038.2| expressed protein [Arabidopsis thaliana]	Unigene48073_All//2.00E-19//AT2G18910| hydroxyproline-rich glycoprotein family protein	Unigene48073_All//0.00E+00//TC138779				nr +

Unigene48074_All	847	3.09	3.95	4.90	5.00	6.22	5.65	2.95	6.56	11.99	3.54E-01	3.17E-01			6.67E-01	3.27E-02		3.15E-01	2.68E-01		1.77E-01	5.99E-01		1.16E+00	6.02E-07	Up	2.03E+00	6.92E-27	Up	Unigene48074_All//gi|38603876|gb|AAR24683.1|//1.00E-47//At2g31670 [Arabidopsis thaliana] >gi|38638692|gb|AAR25640.1| At2g31670 [Arabidopsis thaliana]	Unigene48074_All//2.00E-47//AT2G31670| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: peroxisome, chloroplast stroma, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 16 growth stages; CONTAINS InterPro DOMAIN/s: Stress responsive alpha-beta barrel (InterPro:IPR013097), Dimeric alpha-beta barrel (InterPro:IPR011008); BEST Arabidopsis thaliana protein match is: DABB1 (DIMERIC A/B BARREL DOMAINS-PROTEIN 1) (TAIR:AT1G51360.1); Has 138 Blast hits to 135 proteins in 38 species: Archae - 0; Bacteria - 51; Metazoa - 0; Fungi - 4; Plants - 74; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene48074_All//0.00E+00//gi|164322074|gb|ES791780.1|ES791780				nr -
Unigene48075_All	1220	0.73	2.95	1.13	1.84	1.81	1.48	3.85	5.00	9.14	2.02E+00	5.20E-08	Up	6.38E-01	2.82E-01		-2.45E-02	9.58E-01		-3.11E-01	5.01E-01		3.79E-01	8.76E-02		1.25E+00	4.07E-15	Up	Unigene48075_All//gi|38603876|gb|AAR24683.1|//2.00E-51//At2g31670 [Arabidopsis thaliana] >gi|38638692|gb|AAR25640.1| At2g31670 [Arabidopsis thaliana]	Unigene48075_All//1.00E-46//AT2G31670| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: peroxisome, chloroplast stroma, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 16 growth stages; CONTAINS InterPro DOMAIN/s: Stress responsive alpha-beta barrel (InterPro:IPR013097), Dimeric alpha-beta barrel (InterPro:IPR011008); BEST Arabidopsis thaliana protein match is: DABB1 (DIMERIC A/B BARREL DOMAINS-PROTEIN 1) (TAIR:AT1G51360.1); Has 138 Blast hits to 135 proteins in 38 species: Archae - 0; Bacteria - 51; Metazoa - 0; Fungi - 4; Plants - 74; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene48075_All//0.00E+00//TC168655				nr +
Unigene48076_All	548	43.44	29.22	27.21	72.09	54.29	70.55	39.35	22.35	19.63	-5.72E-01	3.00E-07		-6.75E-01	5.21E-09		-4.09E-01	1.48E-07		-3.11E-02	7.60E-01		-8.16E-01	3.25E-14		-1.00E+00	2.17E-20	Down	Unigene48076_All//gi|88010973|gb|AB038881.1|//9.00E-27//At3g52030 [Arabidopsis thaliana] >gi|90962950|gb|ABE02399.1| At3g52040 [Arabidopsis thaliana]	Unigene48076_All//5.00E-28//AT3G52040| unknown protein	Unigene48076_All//0.00E+00//TC163816				nr -
Unigene48077_All	820	3.06	0.87	3.77	5.89	4.20	5.34	2.84	2.29	1.70	-1.82E+00	3.10E-05	Down	2.98E-01	4.22E-01		-4.89E-01	6.91E-02		-1.41E-01	6.51E-01		-3.06E-01	4.43E-01		-7.38E-01	3.95E-02		Unigene48077_All//gi|224104105|ref|XP_002313321.1|//4.00E-10//predicted protein [Populus trichocarpa] >gi|222849729|gb|EEE87276.1| predicted protein [Populus trichocarpa]	Unigene48077_All//1.00E-06//AT3G52040| unknown protein	Unigene48077_All//0.00E+00//TC163816				nr +
Unigene48079_All	1157	1.94	2.45	1.20	4.31	2.71	1.95	3.87	2.75	4.86	3.35E-01	3.81E-01		-7.01E-01	1.20E-01		-6.69E-01	8.40E-03		-1.14E+00	2.04E-05	Down	-4.97E-01	5.50E-02		3.26E-01	1.50E-01		Unigene48079_All//gi|95147298|gb|AB757284.1|//1.00E-120//At4g17430 [Arabidopsis thaliana]	Unigene48079_All//9.00E-102//AT4G17430| unknown protein	Unigene48079_All//3.00E-78//gi|78341833|gb|DT562107.1|DT562107				nr +
Unigene4808_All	1143	19.77	22.21	24.83	11.16	12.11	14.50	15.17	17.11	6.83	1.68E-01	1.50E-01		3.29E-01	2.10E-03		1.18E-01	5.32E-01		3.78E-01	5.89E-03		1.74E-01	1.54E-01		-1.15E+00	1.76E-20	Down	Unigene4808_All//gi|20138099|sp|O24296.1|GPX1_PEA//4.00E-91//RecName: Full=Phospholipid hydroperoxide glutathione peroxidase, chloroplastic; Short=PHGPx; Flags: Precursor >gi|2632109|emb|CAA04142.1| phospholipid glutathione peroxidase [Pisum sativum]	Unigene4808_All//4.00E-86//AT2G25080| ATGPX1 (GLUTATHIONE PEROXIDASE 1); glutathione peroxidase	Unigene4808_All//0.00E+00//TC133408		ko00480|Glutathione metabolism//ko00590|Arachidonic acid metabolism		nr +
Unigene48081_All	1350	2.09	2.06	3.27	3.73	2.19	4.65	3.10	1.95	6.82	-1.98E-02	9.76E-01		6.46E-01	3.21E-02		-7.65E-01	2.20E-03		3.19E-01	2.15E-01		-6.69E-01	1.17E-02		1.14E+00	5.36E-11	Up	Unigene48081_All//gi|297799384|ref|XP_002867576.1|//2.00E-63//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313412|gb|EFH43835.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48081_All//3.00E-45//AT4G26180| mitochondrial substrate carrier family protein	Unigene48081_All//0.00E+00//gi|13356927|gb|BG447275.1|BG447275				nr +
Unigene48083_All	1325	12.24	9.71	9.69	20.19	17.00	20.18	9.38	8.01	4.18	-3.34E-01	1.78E-02		-3.38E-01	2.21E-02		-2.48E-01	1.74E-02		-7.00E-04	9.93E-01		-2.28E-01	1.40E-01		-1.17E+00	2.98E-15	Down	Unigene48083_All//gi|224083666|ref|XP_002307082.1|//1.00E-116//tubulin folding cofactor [Populus trichocarpa] >gi|222856531|gb|EEE94078.1| tubulin folding cofactor [Populus trichocarpa]	Unigene48083_All//1.00E-106//AT4G39920| PQR (PORCINO); binding	Unigene48083_All//0.00E+00//TC144046				nr -
Unigene48084_All	1296	3.71	6.06	6.12	15.99	15.84	29.31	29.04	52.76	101.07	7.06E-01	6.61E-04		7.21E-01	7.51E-04		-1.39E-02	9.27E-01		8.74E-01	7.83E-24		8.62E-01	2.34E-47		1.80E+00	4.69E-288	Up	Unigene48084_All//gi|225440392|ref|XP_002267559.1|//2.00E-98//PREDICTED: ripening-related protein-like [Vitis vinifera]	Unigene48084_All//8.00E-97//AT5G02230| haloacid dehalogenase-like hydrolase family protein	Unigene48084_All//0.00E+00//TC147456				nr +
Unigene48086_All	1283	95.55	50.27	59.60	34.75	36.61	27.88	23.10	10.03	12.61	-9.26E-01	6.16E-78		-6.81E-01	1.53E-44		7.52E-02	4.31E-01		-3.18E-01	4.65E-05		-1.20E+00	8.58E-36	Down	-8.74E-01	3.81E-22		Unigene48086_All//gi|60145889|sp|Q41651.1|CYP8_VICFA//2.00E-84//RecName: Full=Peptidyl-prolyl cis-trans isomerase, chloroplastic; Short=PPIase; AltName: Full=Rotamase; AltName: Full=Cyclophilin; AltName: Full=Cyclosporin A-binding protein; Short=CYP B; Flags: Precursor >gi|499693|gb|AAA64430.1| cyclophilin [Vicia faba]	Unigene48086_All//8.00E-76//AT3G62030| peptidyl-prolyl cis-trans isomerase, chloroplast / cyclophilin / rotamase / cyclosporin A-binding protein (ROC4)	Unigene48086_All//0.00E+00//TC134542				nr +
Unigene48087_All	1059	17.49	11.29	7.49	40.83	30.27	20.60	18.53	12.63	11.02	-6.31E-01	8.80E-07		-1.22E+00	2.82E-18	Down	-4.32E-01	5.04E-09		-9.87E-01	2.07E-33		-5.53E-01	6.00E-07		-7.49E-01	1.08E-11		Unigene48087_All//gi|21780187|gb|AAM77651.1|AF522274_1/3.00E-17//cp10-like protein [Gossypium hirsutum]	Unigene48087_All//2.00E-09//AT5G20720| CPN20 (CHAPERONIN 20); calmodulin binding	Unigene48087_All//0.00E+00//TC161144				nr -
Unigene48089_All	1903	0.33	2.21	1.34	5.29	2.90	3.35	153.75	3.56	2.03	2.74E+00	5.51E-13	Up	2.03E+00	1.13E-05	Up	-8.69E-01	1.74E-07		-6.60E-01	1.80E-04		-5.43E+00	0.00E+00	Down	-6.24E+00	0.00E+00	Down	Unigene48089_All//gi|37903683|gb|AAP46144.1|//0.00E+00//ferric-chelate reductase [Solanum lycopersicum]	Unigene48089_All//2.00E-139//AT1G01580| FRO2 (FERRIC REDUCTION OXIDASE 2); ferric-chelate reductase	Unigene48089_All//0.00E+00//gi|48748152|gb|CO078671.1|CO078671		ko04626|Plant-pathogen interaction		nr -
Unigene4809_All	747	2.31	1.90	3.78	8.14	9.17	6.11	9.79	3.47	0.96	-2.83E-01	5.85E-01		7.09E-01	7.03E-02		1.73E-01	5.26E-01		-4.14E-01	9.66E-02		-1.50E+00	7.24E-13	Down	-3.35E+00	3.38E-34	Down	Unigene4809_All//gi|15229342|ref|NP_187123.1|//2.00E-85//PR4 (PATHOGENESIS-RELATED 4); chitin binding [Arabidopsis thaliana] >gi|1170247|sp|P43082.1|HEVL_ARATH RecName: Full=Hevein-like protein; Flags: Precursor >gi|6175186|gb|AAF04912.1|AC011437_27 hevein-like protein precursor [Arabidopsis thaliana] >gi|13899683|gb|AAK48963.1|AF370536_1 hevein-like protein precursor [Arabidopsis thaliana] >gi|407248|gb|AAA20642.1| pre-hevein-like protein [Arabidopsis thaliana] >gi|21617916|gb|AAM66966.1| hevein-like protein precursor PR-4 [Arabidopsis thaliana] >gi|23197676|gb|AAN15365.1| hevein-like protein precursor [Arabidopsis thaliana]	Unigene4809_All//6.00E-80//AT3G04720| PR4 (PATHOGENESIS-RELATED 4); chitin binding			ko00520|Amino sugar and nucleotide sugar metabolism		nr +
Unigene48090_All	1364	19.52	22.07	31.15	16.40	21.18	30.26	3.91	9.35	15.83	1.77E-01	9.38E-02		6.74E-01	1.48E-15		3.69E-01	1.04E-04		8.84E-01	2.41E-26		1.26E+00	6.25E-17	Up	2.02E+00	5.37E-56	Up	Unigene48090_All//gi|115311433|gb|AB193897.1|//1.00E-38//At1g65690 [Arabidopsis thaliana] >gi|222422971|dbj|BAH19470.1| AT4G01670 [Arabidopsis thaliana]	Unigene48090_All//1.00E-29//AT2G46940| unknown protein	Unigene48090_All//2.00E-114//DW504838				nr +
Unigene48091_All	1132	1.66	3.00	3.43	1.41	1.40	1.99	1.16	2.40	2.96	8.50E-01	1.15E-02		1.05E+00	1.35E-03		-9.10E-03	9.69E-01		5.02E-01	2.69E-01		1.05E+00	2.22E-03		1.35E+00	1.09E-05	Up	Unigene48091_All//gi|115311433|gb|AB193897.1|//5.00E-43//At1g65690 [Arabidopsis thaliana] >gi|222422971|dbj|BAH19470.1| AT4G01670 [Arabidopsis thaliana]	Unigene48091_All//3.00E-34//AT2G46940| unknown protein	Unigene48091_All//0.00E+00//DW504838				nr +
Unigene48093_All	1983	7.70	0.51	2.34	13.99	4.10	2.12	6.57	2.44	0.76	-3.91E+00	9.12E-64	Down	-1.72E+00	6.65E-25	Down	-1.77E+00	1.66E-60	Down	-2.72E+00	5.37E-90	Down	-1.43E+00	8.90E-21	Down	-3.10E+00	3.22E-56	Down	Unigene48093_All//gi|18265373|dbj|BAB84015.1|//3.00E-65//polyprotein [Arabidopsis thaliana]	Unigene48093_All//1.00E-43//AT5G40210| nodulin MtN21 family protein	Unigene48093_All//0.00E+00//TC148144				nr -
Unigene48095_All	695	32.52	15.31	19.00	59.06	53.46	62.51	98.61	35.66	37.20	-1.09E+00	2.92E-19	Down	-7.75E-01	9.37E-11		-1.44E-01	1.07E-01		8.20E-02	4.08E-01		-1.47E+00	9.57E-111	Down	-1.41E+00	6.15E-107	Down	Unigene48095_All//gi|34098897|gb|AAG56831.1|//1.00E-110//At3g03960 [Arabidopsis thaliana]	Unigene48095_All//2.00E-111//AT3G03960| chaperonin, putative	Unigene48095_All//0.00E+00//TC133446				nr +
Unigene48096_All	1299	56.71	121.39	106.42	108.60	198.34	220.71	29.68	24.49	19.29	1.10E+00	9.17E-132	Up	9.08E-01	2.33E-82		8.69E-01	1.05E-174		1.02E+00	7.54E-230	Up	-2.78E-01	3.56E-04		-6.22E-01	3.59E-16		Unigene48096_All//gi|9828617|gb|AAG00240.1|AC002130_5//1.00E-103//F1N21.15 [Arabidopsis thaliana] >gi|40823166|gb|AAR92263.1| At1g67330 [Arabidopsis thaliana] >gi|45752704|gb|AAS76250.1| At1g67330 [Arabidopsis thaliana]	Unigene48096_All//1.00E-104//AT1G67330| unknown protein	Unigene48096_All//0.00E+00//TC134341				nr +
Unigene48098_All	3405	0.46	0.45	1.00	3.70	1.40	1.53	15.12	10.00	7.77	-4.64E-02	9.40E-01		1.12E+00	1.56E-03		-1.41E+00	9.82E-20	Down	-1.28E+00	4.26E-15	Down	-5.96E-01	3.00E-19		-9.61E-01	3.15E-44		Unigene48098_All//gi|224128410|ref|XP_002329155.1|//1.00E-153//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222869824|gb|EEF06955.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene48098_All//2.00E-85//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene48098_All//0.00E+00//gi|13352677|gb|BG443025.1|BG443025		ko04626|Plant-pathogen interaction		nr +
Unigene4810_All	908	13.31	7.14	4.05	2.69	4.82	4.97	20.40	33.33	54.45	-8.98E-01	5.45E-08		-1.72E+00	9.52E-20	Down	8.41E-01	2.65E-03		8.88E-01	1.72E-03		7.08E-01	1.66E-15		1.42E+00	1.75E-77	Up	Unigene4810_All//gi|6692128|gb|AAF24593.1|AC007654_9//2.00E-60//T19G23.14 [Arabidopsis thaliana]	Unigene4810_All//9.00E-62//AT1G31350| F-box family protein	Unigene4810_All//0.00E+00//ES835281				nr +

Unigene48101_All	1084	25.24	12.20	15.47	11.26	11.12	9.83	3.39	3.35	2.24	-1.05E+00	6.71E-22	Down	-7.06E-01	4.82E-11		-1.81E-02	9.25E-01		-1.95E-01	2.90E-01		-1.66E-02	9.89E-01		-5.98E-01	3.03E-02		Unigene48101_All//gi|13899075|gb|AAK48959.1|AF370532_1//1.00E-77//unknown protein [Arabidopsis thaliana] >gi|20196922|gb|AAC31837.2|expressed protein [Arabidopsis thaliana]	Unigene48101_All//8.00E-71//AT2G44870| unknown protein	Unigene48101_All//0.00E+00//TC132721				nr +
Unigene48104_All	1439	2.69	1.83	4.33	45.00	9.24	12.08	5.88	3.28	3.71	-5.55E-01	7.54E-02		6.86E-01	5.26E-03		-2.28E+00	9.16E-199	Down	-1.90E+00	2.83E-134	Down	-8.40E-01	2.45E-06		-6.64E-01	1.17E-04		Unigene48104_All//gi|51557078|gb|AAU06309.1|/1.00E-114//MYB transcription factor [Hevea brasiliensis]	Unigene48104_All//6.00E-94//AT2G38090| myb family transcription factor	Unigene48104_All//0.00E+00//TC143880	MYB	ko04712|Circadian rhythm - plant		nr -
Unigene48105_All	1879	0.95	0.35	0.54	2.49	2.62	1.80	3.04	0.96	1.55	-1.43E+00	4.85E-03		-8.14E-01	1.15E-01		7.26E-02	8.22E-01		-4.67E-01	1.05E-01		-1.67E+00	8.44E-12	Down	-9.73E-01	8.56E-06		Unigene48105_All//gi|168481664|gb|ACA25009.1|//1.00E-09//polyadenylation factor I complex subunit FIP1 [Populus tremula]		Unigene48105_All//0.00E+00//DR458252				nr +
Unigene48107_All	1351	1.78	5.40	2.17	5.75	7.54	8.42	13.96	10.64	25.60	1.60E+00	1.64E-11	Up	2.83E-01	4.68E-01		3.91E-01	2.84E-02		5.51E-01	9.25E-04		-3.91E-01	5.98E-04		8.75E-01	1.39E-25		Unigene48107_All//gi|148595722|emb|CAM12540.1|//7.00E-39//YA2 [Antirrhinum majus]	Unigene48107_All//4.00E-35//AT1G72830| NF-YA3 (NUCLEAR FACTOR Y, SUBUNIT A3); transcription factor	Unigene48107_All//0.00E+00//TC168682	CCAAT			nr +
Unigene4811_All	1675	12.46	3.48	5.25	2.65	3.00	4.13	11.18	17.14	26.02	-1.84E+00	1.37E-38	Down	-1.25E+00	3.47E-21	Down	1.81E-01	5.67E-01		6.40E-01	3.86E-03		6.16E-01	1.01E-11		1.22E+00	2.11E-54	Up	Unigene4811_All//gi|6692128|gb|AAF24593.1|AC007654_9//1.00E-103//T19E23.14 [Arabidopsis thaliana]	Unigene4811_All//3.00E-97//AT1G31350| F-box family protein	Unigene4811_All//0.00E+00//ES835281				nr -
Unigene48112_All	1250	145.74	455.86	324.87	110.99	344.85	299.05	126.50	63.70	64.51	1.65E+00	0.00E+00	Up	1.16E+00	0.00E+00	Up	1.64E+00	0.00E+00	Up	1.43E+00	0.00E+00	Up	-9.90E-01	5.95E-137		-9.72E-01	1.86E-136		Unigene48112_All//gi|115453689|ref|NP_001050445.1|//1.00E-129//Os03g0437600 [Oryza sativa Japonica Group] >gi|108709023|gb|ABF96818.1|hydrolase, alpha/beta fold family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548916|dbj|BAF12359.1|Os03g0437600 [Oryza sativa Japonica Group]	Unigene48112_All//3.00E-130//AT4G37470| hydrolase, alpha/beta fold family protein	Unigene48112_All//0.00E+00//TC145000				nr -
Unigene48117_All	607	5.26	13.77	8.16	8.04	9.47	6.92	9.47	9.16	7.88	1.39E+00	9.12E-11	Up	6.34E-01	2.48E-02		2.36E-01	4.03E-01		-2.17E-01	4.78E-01		-4.88E-02	8.47E-01		-2.66E-01	2.43E-01		Unigene48117_All//gi|18410907|ref|NP_565115.1|//4.00E-30//DNA-directed RNA polymerase/ RNA binding [Arabidopsis thaliana] >gi|42572115|ref|NP_974148.1| DNA-directed RNA polymerase/ RNA binding [Arabidopsis thaliana]	Unigene48117_All//2.00E-31//AT1G75670| DNA-directed RNA polymerase/ RNA binding	Unigene48117_All//0.00E+00//TC175223		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene4812_All	826	20.59	14.17	9.67	25.27	20.59	27.72	33.02	18.22	11.62	-5.39E-01	5.95E-05		-1.09E+00	4.17E-14	Down	-2.95E-01	1.22E-02		1.34E-01	3.23E-01		-8.58E-01	2.89E-19		-1.51E+00	1.25E-47	Down	Unigene4812_All//gi|297830548|ref|XP_002883156.1|//1.00E-39//ribosomal protein S17 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328996|gb|EFH59415.1|ribosomal protein S17 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4812_All//1.00E-40//AT1G49400| emb1129 (embryo defective 1129); structural constituent of ribosome	Unigene4812_All//0.00E+00//TC154305		ko03010|Ribosome		nr -
Unigene48121_All	1007	10.24	21.23	12.69	13.70	19.25	11.89	39.72	55.08	35.49	1.05E+00	2.62E-17	Up	3.10E-01	6.93E-02		4.91E-01	3.03E-05		-2.05E-01	2.25E-01		4.72E-01	8.79E-14		-1.63E-01	3.66E-02		Unigene48121_All//gi|7635492|emb|CAB88665.1|//6.00E-74//tubby-like protein [Cicer arietinum]	Unigene48121_All//1.00E-57//AT1G47270| AtTLP6 (TUBBY LIKE PROTEIN 6); phosphoric diester hydrolase/ transcription factor	Unigene48121_All//0.00E+00//TC157555	TUB			nr +
Unigene48122_All	1359	4.47	1.27	2.39	7.62	6.18	5.28	2.58	1.11	2.40	-1.82E+00	1.62E-11	Down	-9.02E-01	3.26E-04		-3.02E-01	9.41E-02		-5.29E-01	2.53E-03		-1.22E+00	4.85E-05	Down	-1.03E-01	7.29E-01		Unigene48122_All//gi|92893902|gb|AB691952.1|//1.00E-24//Zinc finger, CCHC-type [Medicago truncatula]	Unigene48122_All//8.00E-13//AT2G01050| nucleic acid binding / zinc ion binding	Unigene48122_All//0.00E+00//DT047555				nr -
Unigene48124_All	1774	0.59	9.48	2.28	2.81	3.96	21.44	92.07	596.10	766.19	4.01E+00	1.28E-70	Up	1.95E+00	3.08E-08	Up	4.96E-01	2.27E-02		2.93E+00	1.16E-129	Up	2.69E+00	0.00E+00	Up	3.06E+00	0.00E+00	Up	Unigene48124_All//gi|285741|dbj|BAA03413.1|//1.00E-173//EDGP precursor [Daucus carota]	Unigene48124_All//7.00E-151//AT1G03220| extracellular dermal glycoprotein, putative / EDGP, putative	Unigene48124_All//0.00E+00//TC164192				nr -
Unigene48125_All	1631	0.71	17.93	4.60	1.28	1.12	0.94	4.07	0.46	1.78	4.67E+00	1.77E-135	Up	2.71E+00	1.05E-21	Up	-1.97E-01	6.76E-01		-4.46E-01	3.50E-01		-3.14E+00	2.43E-28	Down	-1.19E+00	8.26E-09	Down	Unigene48125_All//gi|115485651|ref|NP_001067969.1|//1.00E-121//Os11g0514800 [Oryza sativa Japonica Group] >gi|77551091|gb|ABA93888.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113645191|dbj|BAF28332.1|Os11g0514800 [Oryza sativa Japonica Group]	Unigene48125_All//1.00E-141//AT5G14020| INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: vacuole; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: BR01 (InterPro:IPR004328); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73390.3); Has 53 Blast hits to 53 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 53; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr +
Unigene48126_All	642	24.78	7.58	12.69	8.69	5.79	6.68	18.18	19.99	28.92	-1.71E+00	1.01E-26	Down	-9.65E-01	5.91E-11		-5.85E-01	1.47E-02		-3.79E-01	1.54E-01		1.37E-01	4.02E-01		6.70E-01	2.99E-09		Unigene48126_All//gi|116309754|emb|CAH66797.1|//3.00E-31//H0215F08.8 [Oryza sativa (indica cultivar-group)]	Unigene48126_All//2.00E-32//AT3G14130| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene48126_All//0.00E+00//TC172637		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene48127_All	1323	18.35	130.64	29.87	33.85	69.91	45.71	89.77	167.34	370.44	2.83E+00	0.00E+00	Up	7.03E-01	1.46E-15		1.05E+00	3.17E-85	Up	4.33E-01	3.17E-11		8.99E-01	9.96E-163		2.05E+00	0.00E+00	Up	Unigene48127_All//gi|18378853|ref|NP_563630.1|//8.00E-16//BPS1 (BYPASS 1) [Arabidopsis thaliana] >gi|79316260|ref|NP_001030929.1|BPS1 (BYPASS 1) [Arabidopsis thaliana] >gi|75174796|sp|Q9LM06.1|BPS1_ARATH RecName: Full=Protein BPS1, chloroplastic; AltName: Full=Protein BYPASS 1; Flags: Precursor >gi|16648871|gb|AAL24287.1|Unknown protein [Arabidopsis thaliana] >gi|23197666|gb|AAN15360.1|Unknown protein [Arabidopsis thaliana]	Unigene48127_All//3.00E-12//AT1G01550| BPS1 (BYPASS 1)	Unigene48127_All//0.00E+00//TC131129				nr +
Unigene48128_All	755	1.80	4.76	1.76	1.85	2.14	0.60	1.79	0.89	2.06	1.40E+00	3.83E-05	Up	-3.12E-02	9.77E-01		2.15E-01	7.32E-01		-1.63E+00	5.90E-03		-1.02E+00	4.99E-02		2.00E-01	6.65E-01		Unigene48128_All//gi|255579841|ref|XP_002530757.1|//4.00E-26//hypothetical protein RCOM_0003370 [Ricinus communis] >gi|223529673|gb|EEF31617.1|hypothetical protein RCOM_0003370 [Ricinus communis]	Unigene48128_All//8.00E-143//DN801588					nr +
Unigene48130_All	1291	14.14	30.61	19.06	22.03	22.99	22.63	10.45	10.75	8.89	1.11E+00	2.69E-34	Up	4.30E-01	1.58E-04		6.15E-02	6.11E-01		3.89E-02	7.47E-01		4.10E-02	7.94E-01		-2.33E-01	9.63E-02		Unigene48130_All//gi|18401872|ref|NP_564514.1|//5.00E-93//PEX11A (PEROXIN 11A) [Arabidopsis thaliana] >gi|75173415|sp|Q9FZF1.1|PX11A_ARATH RecName: Full=Peroxisomal membrane protein 11A; AltName: Full=Peroxin-11A; Short=AtPEX11a >gi|9802590|gb|AAF99792.1|AC012463_9 T25E.18 [Arabidopsis thaliana] >gi|87116582|gb|ABD19655.1|At1g47750 [Arabidopsis thaliana]	Unigene48130_All//2.00E-87//AT1G47750| PEX11A (PEROXIN 11A)	Unigene48130_All//0.00E+00//gi|78350128|gb|DT570402.1|DT570402				nr +
Unigene48132_All	1898	0.50	2.48	0.62	1.84	1.40	1.33	5.26	4.40	4.43	2.32E+00	4.10E-12	Up	3.15E-01	6.23E-01		-3.95E-01	2.44E-01		-4.63E-01	1.83E-01		-2.55E-01	1.40E-01		-2.47E-01	1.36E-01		Unigene48132_All//gi|224122872|ref|XP_002318937.1|//2.00E-34//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222857313|gb|EEE94860.1|chromatin remodeling complex subunit [Populus trichocarpa]	Unigene48132_All//2.00E-08//AT2G43900| inositol or phosphatidylinositol phosphatase/ inositol-polyphosphate 5-phosphatase	Unigene48132_All//0.00E+00//TC138758		ko03040|Spliceosome		nr +
Unigene48135_All	1400	1.72	1.45	1.79	2.35	1.43	1.68	6.67	8.45	26.81	-2.48E-01	5.63E-01		5.65E-02	8.94E-01		-7.19E-01	2.71E-02		-4.85E-01	1.74E-01		3.40E-01	2.43E-02		2.01E+00	6.14E-96	Up	Unigene48135_All//gi|297799384|ref|XP_002867576.1|//1.00E-131//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313412|gb|EFH43835.1|mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48135_All//8.00E-125//AT4G26180| mitochondrial substrate carrier family protein	Unigene48135_All//0.00E+00//TC149482				nr +
Unigene48136_All	907	60.11	45.81	50.55	102.81	93.13	115.17	67.83	30.41	33.51	-3.92E-01	3.59E-08		-2.50E-01	8.99E-04		-1.43E-01	8.05E-03		1.64E-01	1.46E-03		-1.16E+00	4.52E-69	Down	-1.02E+00	9.22E-58	Down	Unigene48136_All//gi|194462395|gb|ACF72672.1|//2.00E-80//ribosomal protein L24 [Cucumis melo var. cantalupensis]	Unigene48136_All//9.00E-73//AT5G23535| KOW domain-containing protein	Unigene48136_All//0.00E+00//TC140104		ko03010|Ribosome		nr -
Unigene48137_All	1097	33.77	19.21	31.16	142.04	81.58	43.39	88.38	47.93	9.66	-8.13E-01	1.97E-19		-1.16E-01	2.58E-01		-8.00E-01	5.46E-95		-1.71E+00	1.20E-279	Down	-8.83E-01	1.19E-69		-3.19E+00	0.00E+00	Down	Unigene48137_All//gi|7362791|emb|CAB83067.1|//2.00E-72//nodulin-like protein [Arabidopsis thaliana] >gi|34365643|gb|AAQ65133.1|At3g43660 [Arabidopsis thaliana] >gi|51970300|dbj|BAD43842.1|nodulin - like protein [Arabidopsis thaliana]	Unigene48137_All//5.00E-58//AT1G76800| nodulin, putative	Unigene48137_All//0.00E+00//gi|78330376|gb|DT550650.1|DT550650				nr -
Unigene48138_All	794	17.66	9.44	23.74	17.69	11.58	5.18	2.77	1.00	2.21	-9.03E-01	3.22E-09		4.27E-01	1.26E-03		-6.12E-01	9.02E-06		-1.77E+00	7.10E-27	Down	-1.47E+00	2.62E-04	Down	-3.27E-01	4.01E-01					Unigene48138_All//2.00E-162//TC149505				
Unigene48139_All	1573	18.76	9.57	10.29	40.66	36.34	22.91	6.10	2.90	3.65	-9.72E-01	7.62E-21		-8.66E-01	1.31E-16		-1.62E-01	1.42E-02		-8.28E-01	1.22E-36		-1.08E+00	2.89E-10	Down	-7.43E-01	4.24E-06		Unigene48139_All//gi|115483965|ref|NP_001065644.1|//8.00E-29//Os11g0129500 [Oryza sativa Japonica Group] >gi|113644348|dbj|BAF27489.1|Os11g0129500 [Oryza sativa Japonica Group]	Unigene48139_All//3.00E-25//AT4G10950| GDSL-motif lipase/hydrolase family protein	Unigene48139_All//0.00E+00//gi|164354334|gb|ES805255.1|ES805255				nr +
Unigene4814_All	1343	12.51	5.70	5.71	25.04	17.13	22.87	30.60	11.27	14.74	-1.13E+00	1.73E-15	Down	-1.13E+00	9.30E-15	Down	-5.48E-01	8.99E-11		-1.31E-01	2.23E-01		-1.44E+00	5.79E-65	Down	-1.05E+00	3.78E-41	Down	Unigene4814_All//gi|297834412|ref|XP_002885088.1|//1.00E-158//brix domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297330928|gb|EFH61347.1| brix domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene4814_All//2.00E-143//AT3G15460| brix domain-containing protein	Unigene4814_All//0.00E+00//TC155961				nr +
Unigene48140_All	389	9.28	4.56	7.12	3.07	4.43	1.28	7.39	2.15	2.56	-1.03E+00	1.69E-03		-3.83E-01	2.71E-01		5.26E-01	3.15E-01		-1.27E+00	4.58E-02		-1.78E+00	7.42E-07	Down	-1.53E+00	6.68E-06	Down	Unigene48140_All//gi|157812633|gb|ABV80356.1|//8.00E-59//phosphoenolpyruvate carboxylase [Gossypium hirsutum]	Unigene48140_All//3.00E-55//AT3G14940| ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase	Unigene48140_All//2.00E-117//TC131208		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -

Unigene48141_All	570	11.93	6.93	13.64	7.43	5.98	3.17	17.21	6.01	3.84	-7.83E-01	4.99E-04		1.93E-01	3.97E-01		-3.13E-01	3.13E-01		-1.23E+00	3.31E-05	Down	-1.52E+00	2.63E-17	Down	-2.16E+00	1.47E-28	Down	Unigene48141_All//gi|157812633|gb|ABV80356.1|//6.00E-93//phosphoenolpyruvate carboxylase [Gossypium hirsutum]	Unigene48141_All//8.00E-93//AT1G53310| ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); catalytic/ phosphoenolpyruvate carboxylase	Unigene48141_All//0.00E+00//gi|164259655|gb|ES838731.1|ES838731		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene48142_All	810	3.42	2.19	3.22	4.12	5.57	4.63	11.90	3.82	5.71	-6.45E-01	8.65E-02		-8.78E-02	8.19E-01		4.35E-01	1.41E-01		1.68E-01	6.42E-01		-1.64E+00	5.73E-19	Down	-1.06E+00	1.92E-10	Down	Unigene48142_All//gi|157812633|gb|ABV80356.1|//1.00E-112//phosphoenolpyruvate carboxylase [Gossypium hirsutum]	Unigene48142_All//2.00E-100//AT1G53310| ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); catalytic/ phosphoenolpyruvate carboxylase	Unigene48142_All//0.00E+00//TC137097		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene48143_All	1257	34.13	20.52	29.87	8.44	11.37	3.49	1.51	0.67	0.16	-7.34E-01	7.15E-19		-1.93E-01	3.04E-02		4.30E-01	2.63E-03		-1.28E+00	9.18E-13	Down	-1.19E+00	5.40E-03		-3.26E+00	3.59E-09	Down	Unigene48143_All//gi|145359559|ref|NP_201049.3|//4.00E-40//CDF1 (CYCLING DOF FACTOR 1); DNA binding / protein binding / transcription factor [Arabidopsis thaliana] >gi|55583963|sp|QEW1E3.2|DOF55_ARATH RecName: Full=Dof zinc finger protein DOF5.5; Short=AtDOF5.5 >gi|10178074|dbj|BAB11493.1| H-protein promoter binding factor-like protein [Arabidopsis thaliana] >gi|71833953|dbj|BAE16983.1| cyclic dof factor 1 [Arabidopsis thaliana]	Unigene48143_All//2.00E-41//AT5G62430| CDF1 (CYCLING DOF FACTOR 1); DNA binding / protein binding / transcription factor	Unigene48143_All//0.00E+00//TC150325	C2C2-Dof			nr +
Unigene48145_All	973	3.07	1.56	2.19	7.22	4.71	5.71	2.69	1.85	0.70	-9.72E-01	7.36E-03		-4.86E-01	2.11E-01		-6.17E-01	2.93E-03		-3.39E-01	1.48E-01		-5.45E-01	1.27E-01		-1.95E+00	2.58E-07	Down	Unigene48145_All//gi|15222460|ref|NP_174459.1|//1.00E-70//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75169166|sp|Q9C689.1|PPR66_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g31790 >gi|11074348|gb|AH00454|7.1| At1g31790 [Arabidopsis thaliana]	Unigene48145_All//6.00E-72//AT1G31790| pentatricopeptide (PPR) repeat-containing protein	Unigene48145_All//0.00E+00//CO090017				nr +
Unigene48147_All	1158	2.94	1.09	3.31	5.85	6.51	7.72	7.34	5.85	6.19	-1.42E+00	4.93E-05	Down	1.73E-01	6.37E-01		1.55E-01	5.65E-01		4.01E-01	4.34E-02		-3.28E-01	7.60E-02		-2.45E-01	1.81E-01		Unigene48147_All//gi|126508782|gb|AB015566.1|//1.00E-133//cysteine synthase [Glycine max]	Unigene48147_All//1.00E-115//AT3G04940| CYSD1 (CYSTEINE SYNTHASE D1); cysteine synthase	Unigene48147_All//0.00E+00//TC178496		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr +
Unigene48815_All	723	38.06	38.26	25.93	32.87	33.48	34.48	35.85	32.32	17.14	7.60E-03	9.69E-01		-5.54E-01	1.87E-07		2.69E-02	8.43E-01		6.93E-02	6.40E-01		-1.50E-01	1.58E-01		-1.06E+00	9.91E-27	Down	Unigene4815_All//gi|224143081|ref|XP_002324843.1|//6.00E-61//histone 2 [Populus trichocarpa] >gi|222866277|gb|EEF03408.1| histone 2 [Populus trichocarpa]	Unigene4815_All//1.00E-51//AT1G52740| HTA9 (HISTONE H2A PROTEIN 9); DNA binding	Unigene4815_All//0.00E+00//TC148962				nr +
Unigene48150_All	1273	0.04	0.08	0.00	4.42	3.44	5.43	5.75	4.99	2.72	9.54E-01	7.25E-01		-5.36E+00	6.22E-01		-3.64E-01	1.57E-01		2.96E-01	2.27E-01		-2.03E-01	3.55E-01		-1.08E+00	2.52E-08	Down	Unigene48150_All//gi|119331576|gb|ABL63114.1|//1.00E-54//DNA-binding protein [Catharanthus roseus]	Unigene48150_All//1.00E-30//AT3G51060| STY1 (STYLISH 1); protein heterodimerization/ transcription factor	Unigene48150_All//0.00E+00//gi|109879303|gb|DW508273.1|DW508273	SRS			nr -
Unigene48151_All	1530	1.37	0.89	0.66	1.14	0.81	0.12	1.41	3.41	2.21	-6.13E-01	1.67E-01		-1.05E+00	2.56E-02		-4.92E-01	3.18E-01		-3.27E+00	3.65E-07	Down	1.28E+00	1.50E-07	Up	6.51E-01	2.49E-02		Unigene48151_All//gi|50234592|gb|AAT70497.1|//9.00E-90//S-locus-like receptor protein kinase [Prunus persica]	Unigene48151_All//9.00E-64//AT1G34300| lectin protein kinase family protein	Unigene48151_All//5.00E-158//TC168727		ko04626|Plant-pathogen interaction		nr +
Unigene48153_All	1086	16.62	108.76	9.95	22.11	48.26	23.08	18.65	13.39	60.31	2.71E+00	0.00E+00	Up	-7.40E-01	4.28E-08		1.13E+00	2.31E-54	Up	6.20E-02	6.49E-01		-4.78E-01	1.14E-05		1.69E+00	1.20E-132	Up	Unigene48153_All//gi|145049690|gb|ABP35526.1|//1.00E-117//CCR4-associated factor [Ipomoea batatas]	Unigene48153_All//2.00E-111//AT5G22250| CCR4-NOT transcription complex protein, putative	Unigene48153_All//0.00E+00//gi|109838839|gb|DW237400.1|DW237400		ko03018|RNA degradation		nr -
Unigene48154_All	403	0.39	3.39	0.26	1.24	0.51	1.01	1.68	5.08	4.25	3.12E+00	3.45E-05	Up	-5.59E-01	7.75E-01		-1.27E+00	2.22E-01		-2.93E-01	7.57E-01		1.60E+00	1.77E-04	Up	1.34E+00	2.74E-03				Unigene48154_All//2.00E-55//gi|73944011|gb|DT527319.1|DT527319				
Unigene48155_All	1299	16.80	78.91	18.41	82.22	63.94	87.89	58.00	182.63	221.40	2.23E+00	5.03E-239	Up	1.32E-01	3.15E-01		-3.63E-01	1.04E-15		9.63E-02	7.32E-02		1.65E+00	0.00E+00	Up	1.93E+00	0.00E+00	Up	Unigene48155_All//gi|16648923|gb|AAL24313.1|//2.00E-49//Unknown protein [Arabidopsis thaliana]		Unigene48155_All//3.00E-177//TC170943		ko03040|Spliceosome		nr +
Unigene48156_All	855	13.16	34.91	22.17	15.50	13.61	16.38	25.81	38.23	22.69	1.41E+00	2.88E-37	Up	7.53E-01	1.01E-08		-1.87E-01	2.78E-01		7.94E-02	6.71E-01		5.67E-01	1.74E-11		-1.86E-01	8.54E-02		Unigene48156_All//gi|301601264|dbj|BAJ13304.1|//1.00E-44//autophagy 8 [Ipomoea nil]	Unigene48156_All//6.00E-45//AT3G15580| APG8H (AUTOPHAGY 8H); APG8 activating enzyme/ APG8-specific protease/ Atg8 ligase/ microtubule binding	Unigene48156_All//0.00E+00//TC175259		ko04140|Regulation of autophagy		nr +
Unigene48158_All	1179	2.17	0.86	3.34	28.01	11.33	5.63	1.61	5.78	1.25	-1.34E+00	1.04E-03		6.20E-01	5.44E-02		-1.31E+00	1.41E-45	Down	-2.31E+00	1.14E-88	Down	1.84E+00	7.84E-16	Up	-3.68E-01	3.79E-01		Unigene48158_All//gi|15225480|ref|NP_181483.1|//1.00E-120//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|3355480|gb|AAC27842.1| nodulin-like protein [Arabidopsis thaliana] >gi|30017241|gb|AAP12854.1| At2g39510 [Arabidopsis thaliana] >gi|110743791|dbj|BAE99731.1| nodulin-like protein [Arabidopsis thaliana]	Unigene48158_All//3.00E-121//AT2G39510| nodulin MtN21 family protein	Unigene48158_All//0.00E+00//CO111368				nr -
Unigene48159_All	1311	12.49	94.23	10.48	44.87	88.49	23.63	45.57	40.90	412.21	2.92E+00	0.00E+00	Up	-2.53E-01	9.29E-02		9.80E-01	5.29E-96		-9.25E-01	1.13E-40		-1.56E-01	1.54E-02		3.18E+00	0.00E+00	Up	Unigene48159_All//gi|151301818|gb|ABN50365.2|//1.00E-107//ethylene responsive element binding protein 1 [Gossypium barbadense]	Unigene48159_All//1.00E-59//AT4G17500| ATERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene48159_All//0.00E+00//gi|78351204|gb|DT571478.1|DT571478	AP2-EREBP			nr -
Unigene4816_All	1333	16.52	7.53	13.02	142.90	106.82	29.92	0.00	0.06	0.06	-1.13E+00	4.40E-20	Down	-3.44E-01	5.25E-03		-4.20E-01	2.48E-36		-2.26E+00	0.00E+00	Down	5.97E+00	4.01E-01		5.90E+00	4.04E-01		Unigene4816_All//gi|161610920|gb|ABX75139.1|//1.00E-176//lipase [Gossypium hirsutum]	Unigene4816_All//1.00E-139//AT5G53370| GDSL-motif lipase/hydrolase family protein	Unigene4816_All//0.00E+00//gi|78335816|gb|DT556090.1|DT556090				nr -
Unigene48160_All	860	1.89	4.54	3.84	22.42	22.74	25.73	4.92	1.90	2.36	1.27E+00	7.80E-05	Up	1.03E+00	4.18E-03		2.09E-02	8.99E-01		1.99E-01	1.20E-01		-1.38E+00	6.24E-07	Down	-1.06E+00	4.74E-05	Down	Unigene48160_All//gi|9295718|gb|AAF87024.1|AC006535_2//3.00E-113//T24P13.3 [Arabidopsis thaliana]	Unigene48160_All//1.00E-14//AT1G26650| unknown protein					nr -
Unigene48161_All	1007	1.77	4.38	5.02	4.40	5.44	3.90	1.60	2.37	1.58	1.31E+00	1.36E-05	Up	1.51E+00	2.83E-07	Up	3.05E-01	2.77E-01		-1.74E-01	6.22E-01		5.68E-01	1.33E-01		-1.18E-02	9.71E-01				Unigene48161_All//5.00E-86//gi|6462028|gb|AW187592.1|AW187592				
Unigene48162_All	851	17.40	13.28	8.20	22.19	23.19	15.28	16.49	7.02	4.26	-3.90E-01	7.84E-03		-1.09E+00	2.73E-12	Down	6.37E-02	6.90E-01		-5.38E-01	1.35E-05		-1.23E+00	5.30E-18	Down	-1.95E+00	1.34E-35	Down	Unigene48162_All//gi|115488936|ref|NP_001066955.1|//4.00E-29//Os12g0541400 [Oryza sativa Japonica Group] >gi|113649462|dbj|BAF29974.1| Os12g0541400 [Oryza sativa Japonica Group]	Unigene48162_All//3.00E-34//AT4G15790| unknown protein	Unigene48162_All//0.00E+00//TC144125				nr +
Unigene48166_All	1417	10.12	162.56	24.73	47.70	56.21	38.02	45.17	37.87	100.03	4.01E+00	0.00E+00	Up	1.29E+00	4.21E-37	Up	2.37E-01	1.72E-05		-3.27E-01	1.11E-07		-2.54E-01	1.60E-05		1.15E+00	4.02E-159	Up	Unigene48166_All//gi|292668913|gb|ADE41111.1|//4.00E-63//AP2 domain class transcription factor [Malus x domestica]	Unigene48166_All//2.00E-20//AT1G28370| ERF11 (ERF DOMAIN PROTEIN 11); DNA binding / transcription factor/ transcription repressor	Unigene48166_All//0.00E+00//TC130282	AP2-EREBP			nr -
Unigene48167_All	1029	7.07	3.30	6.05	4.21	3.55	5.93	2.38	0.89	1.36	-1.10E+00	7.70E-07	Down	-2.23E-01	3.69E-01		-2.48E-01	4.38E-01		4.93E-01	4.39E-02		-1.42E+00	1.67E-04	Down	-8.14E-01	1.92E-02		Unigene48167_All//gi|30686896|ref|NP_197360.2|//1.00E-137//kelch repeat-containing protein [Arabidopsis thaliana] >gi|30686901|ref|NP_850846.1| kelch repeat-containing protein [Arabidopsis thaliana] >gi|110740537|dbj|BAE98374.1| RanGAP1 interacting protein [Arabidopsis thaliana]	Unigene48167_All//9.00E-139//AT5G18590| kelch repeat-containing protein	Unigene48167_All//0.00E+00//gi|109854587|gb|DW483566.1|DW483566		ko04712|Circadian rhythm - plant		nr -
Unigene48168_All	1901	3.08	0.88	0.98	5.84	4.89	7.60	7.65	2.95	3.86	-1.81E+00	4.36E-11	Down	-1.65E+00	2.23E-09	Down	-2.57E-01	1.53E-01		3.80E-01	1.10E-02		-1.38E+00	5.70E-22	Down	-9.89E-01	1.01E-13		Unigene48168_All//gi|297843032|ref|XP_002889397.1|//1.00E-141//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335239|gb|EFH65656.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene48168_All//1.00E-133//AT1G02370| pentatricopeptide (PPR) repeat-containing protein	Unigene48168_All//0.00E+00//gi|78350706|gb|DT570980.1|DT570980				nr -
Unigene48171_All	978	61.63	56.99	58.75	38.35	38.48	30.76	9.47	26.62	43.42	-1.13E-01	1.30E-01		-6.90E-02	3.84E-01		4.90E-03	9.69E-01		-3.19E-01	2.18E-04		1.49E+00	1.74E-43	Up	2.20E+00	8.55E-122	Up	Unigene48171_All//gi|297614156|gb|ADI48416.1|//1.00E-56//cell number regulator 2 [Zea mays]	Unigene48171_All//8.00E-54//AT1G14870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: plasma membrane; EXPRESSED IN: callus; CONTAINS InterPro DOMAIN/s: EGF-type aspartate/asparagine hydroxylation conserved site (InterPro:IPR000152), Protein of unknown function Cys-rich (InterPro:IPR006461); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35525.1); Has 492 Blast hits to 491 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 93; Fungi - 76; Plants - 297; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink).	Unigene48171_All//0.00E+00//TC132166				nr +
Unigene48172_All	1605	1.79	3.69	2.39	3.91	4.53	3.66	2.56	1.77	2.06	1.04E+00	2.63E-05	Up	4.14E-01	2.22E-01		2.11E-01	3.95E-01		-9.63E-02	7.10E-01		-5.29E-01	5.16E-02		-3.11E-01	2.53E-01		Unigene48172_All//gi|225445549|ref|XP_002282244.1|//1.00E-114//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene48172_All//7.00E-69//AT3G24150| unknown protein	Unigene48172_All//0.00E+00//TC150981				nr -

Unigene48174_All	1904	0.99	1.94	1.09	1.70	2.08	1.09	3.22	1.71	1.26	9.74E-01	2.50E-03		1.41E-01	7.48E-01		2.91E-01	3.98E-01		-6.40E-01	6.71E-02		-9.11E-01	2.10E-05		-1.36E+00	7.12E-10	Down	Unigene48174_All//gi|30698733|ref|NP_177218.3|//1.00E-125//ATTAP1; ATPase, coupled to transmembrane movement of substances / transporter [Arabidopsis thaliana] >gi|75330788|sp|Q8RY46.1|AB26B_ARATH RecName: Full=ABC transporter B family member 26, chloroplastic; Short=ABC transporter ABCB.26; Short=AtABCB26; AltName: Full=Antigen peptide transporter-like 1; AltName: Full=Transporter associated with antigen processing-like protein 1; Short=AtTAP1; Flags: Precursor >gi|19335722|gb|AAL85485.1| transporter associated with antigen processing-like protein [Arabidopsis thaliana] >gi|110737412|dbj|BAF00650.1| transporter associated with antigen processing-like protein [Arabidopsis thaliana]	Unigene48174_All//4.00E-119//AT1G70610| ATTAP1; ATPase, coupled to transmembrane movement of substances / transporter	Unigene48174_All//0.00E+00//TC176451		ko02010|ABC transporters		nr +
Unigene48175_All	1329	1.93	1.68	1.72	3.97	3.19	1.67	3.56	2.89	2.91	-2.02E-01	6.10E-01		-1.63E-01	6.85E-01		-3.18E-01	2.42E-01		-1.25E+00	1.65E-06	Down	-3.00E-01	2.56E-01		-2.93E-01	2.44E-01		Unigene48175_All|gi|224106505|ref|XP_002314189.1|/1.00E-108//f-box family protein [Populus trichocarpa] >gi|222850597|gb|EEE88144.1| f-box family protein [Populus trichocarpa]	Unigene48175_All//5.00E-44//AT2G28810| Dof-type zinc finger domain-containing protein	Unigene48175_All//0.00E+00//DW520385	C2C2-Dof			nr +
Unigene48179_All	1499	3.35	6.12	1.56	6.15	6.62	4.25	3.10	12.66	3.88	8.69E-01	6.07E-06		-1.10E+00	1.03E-04	Down	1.06E-01	6.16E-01		-5.33E-01	4.50E-03		2.03E+00	1.32E-48	Up	3.23E-01	1.45E-01		Unigene48179_All//gi|224054472|ref|XP_002298277.1|//3.00E-85//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|224149083|ref|XP_002336754.1| NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222836661|gb|EEE75054.1| NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222845535|gb|EEE83082.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene48179_All//1.00E-67//AT3G44350| anac061 (Arabidopsis NAC domain containing protein 61); transcription factor	Unigene48179_All//0.00E+00//TC160180	NAC			nr +
Unigene48180_All	1594	0.46	0.70	0.40	2.44	1.25	1.87	0.61	2.60	0.65	6.06E-01	3.59E-01		-1.97E-01	7.99E-01		-9.60E-01	9.13E-04		-3.82E-01	2.46E-01		2.09E+00	1.43E-11	Up	9.10E-02	8.86E-01		Unigene48180_All//gi|224054472|ref|XP_002298277.1|//3.00E-80//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|224149083|ref|XP_002336754.1| NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222836661|gb|EEE75054.1| NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222845535|gb|EEE83082.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene48180_All//1.00E-62//AT3G44350| anac061 (Arabidopsis NAC domain containing protein 61); transcription factor	Unigene48180_All//0.00E+00//TC160180	NAC			nr +
Unigene48183_All	1408	65.96	31.60	42.96	55.86	46.81	50.71	19.16	10.75	10.58	-1.06E+00	4.66E-74	Down	-6.19E-01	1.25E-28		-2.55E-01	2.95E-06		-1.40E-01	2.55E-02		-8.34E-01	3.25E-18		-8.56E-01	1.39E-19		Unigene48183_All//gi|297820558|ref|XP_002878162.1|//1.00E-130//aspartate/glutamate/uridylate kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324000|gb|EFH54421.1| aspartate/glutamate/uridylate kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48183_All//2.00E-119//AT3G57560| aspartate/glutamate/uridylate kinase family protein	Unigene48183_All//0.00E+00//TC153628		ko00330|Arginine and proline metabolism		nr -
Unigene48184_All	439	0.24	0.12	0.00	0.11	0.00	0.00	38.81	18.66	85.30	-1.05E+00	6.84E-01		-7.90E+00	3.92E-01		-6.83E+00	5.55E-01		-6.83E+00	6.34E-01		-1.06E+00	3.95E-17	Down	1.14E+00	4.95E-42	Up	Unigene48184_All//gi|15239947|ref|NP_199182.1|//9.00E-38//sulfotransferase family protein [Arabidopsis thaliana] >gi|10177937|dbj|BAB11296.1| steroid sulfotransferase-like [Arabidopsis thaliana] >gi|38566684|gb|AAR24232.1| At5g43690 [Arabidopsis thaliana] >gi|51536530|gb|AAU05503.1| At5g43690 [Arabidopsis thaliana]	Unigene48184_All//4.00E-38//AT5G43690| sulfotransferase family protein	Unigene48184_All//1.00E-100//TC178273		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr +
Unigene48185_All	498	0.00	0.00	0.11	0.60	0.07	0.00	55.10	16.87	33.60	null	null		6.74E+00	6.35E-01		-3.12E+00	7.56E-02		-9.23E+00	3.99E-02		-1.71E+00	1.21E-55	Down	-7.14E-01	9.09E-15		Unigene48185_All//gi|297810811|ref|XP_002873289.1|//3.00E-29//sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319126|gb|EFH49548.1| sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48185_All//3.00E-30//AT5G07000| ST2B (SULFOTRANSFERASE 2B); hydroxyjasmonate sulfotransferase/ sulfotransferase	Unigene48185_All//3.00E-166//TC178273		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr +
Unigene48186_All	1192	16.86	0.38	6.43	49.23	13.75	29.74	21.10	9.36	23.23	-5.46E+00	3.33E-102	Down	-1.39E+00	5.66E-24	Down	-1.84E+00	6.41E-135	Down	-7.27E-01	5.47E-27		-1.17E+00	2.57E-29	Down	1.38E-01	1.62E-01		Unigene48186_All//gi|15230602|ref|NP_190093.1|//5.00E-72//sulfotransferase family protein [Arabidopsis thaliana] >gi|6911845|emb|CAB72145.1| sulfotransferase-like protein [Arabidopsis thaliana] >gi|44917543|gb|AAS49696.1| At3g45070 [Arabidopsis thaliana]	Unigene48186_All//7.00E-70//AT5G07000| ST2B (SULFOTRANSFERASE 2B); hydroxyjasmonate sulfotransferase/ sulfotransferase	Unigene48186_All//0.00E+00//TC178273		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr +
Unigene48188_All	825	24.61	23.40	29.43	27.05	29.89	34.00	6.92	3.24	4.10	-7.25E-02	5.92E-01		2.58E-01	3.07E-02		1.44E-01	2.50E-01		3.30E-01	1.24E-03		-1.09E+00	1.39E-06	Down	-7.53E-01	4.58E-04		Unigene48188_All//gi|40806814|gb|AB92206.1|//2.00E-80//MADS box transcription factor [Populus tomentosa]	Unigene48188_All//3.00E-58//AT2G22540| SVP (SHORT VEGETATIVE PHASE); transcription factor/ translation repressor, nucleic acid binding	Unigene48188_All//3.00E-10//TC143124	MADS			nr +
Unigene48189_All	875	9.81	6.37	5.72	19.47	19.32	10.43	4.06	1.58	1.09	-6.23E-01	1.56E-03		-7.78E-01	1.51E-04		-1.09E-02	9.54E-01		-9.01E-01	1.12E-11		-1.36E+00	6.91E-06	Down	-1.89E+00	2.88E-09	Down	Unigene48189_All//gi|115489196|ref|NP_001067085.1|//2.00E-60//Os12g0571300 [Oryza sativa Japonica Group] >gi|77556867|gb|ABA99663.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649592|dbj|BAF30104.1| Os12g0571300 [Oryza sativa Japonica Group]	Unigene48189_All//2.00E-67//AT3G55420| unknown protein	Unigene48189_All//0.00E+00//gi|109868109|gb|DW497085.1|DW497085				nr -
Unigene4819_All	743	33.94	18.82	40.21	43.31	41.85	63.34	36.36	75.83	58.50	-8.51E-01	1.73E-14		2.44E-01	2.23E-02		-4.95E-02	6.81E-01		5.48E-01	2.64E-13		1.06E+00	5.20E-55	Up	6.86E-01	2.77E-21		Unigene4819_All//gi|261876231|emb|CAZ15549.1|//4.00E-44//phloem protein 2 [Malus x domestica]	Unigene4819_All//7.00E-28//AT1G10155| ATPP2-A10 (PHLOEM PROTEIN 2-A10)	Unigene4819_All//0.00E+00//gi|109872422|gb|DW501397.1|DW501397				nr +
Unigene48191_All	1054	19.41	93.84	15.01	15.08	34.93	45.55	19.86	35.21	71.66	2.27E+00	6.48E-236	Up	-3.71E-01	3.66E-03		1.21E+00	7.00E-43	Up	1.60E+00	9.23E-77	Up	8.27E-01	2.41E-24		1.85E+00	5.68E-173	Up	Unigene48191_All//gi|156145802|gb|ABU53677.1|//1.00E-122//ethylene-responsive element binding protein [Gossypium barbadense]	Unigene48191_All//1.00E-29//AT5G44210| EEP9 (ERF DOMAIN PROTEIN 9); DNA binding / transcription factor/ transcription repressor	Unigene48191_All//0.00E+00//TC129747	AP2-EREBP			nr -
Unigene48195_All	338	0.00	0.00	0.00	0.29	0.71	0.40	0.25	0.62	2.36	null	null		null	null		1.27E+00	5.31E-01		4.44E-01	8.61E-01		1.31E+00	4.47E-01		3.24E+00	3.96E-04	Up	Unigene48195_All//gi|18411319|ref|NP_565147.1|//5.00E-08//SKP2B; ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75318353|sp|Q49286.1|FBL5_ARATH RecName: Full=F-box/LRR-repeat protein 5 >gi|2829911|gb|AAC00619.1| Unknown protein [Arabidopsis thaliana] >gi|21592038|gb|AAM64987.1| F-box protein family, AtFBL5 [Arabidopsis thaliana] >gi|89000991|gb|ABD59085.1| At1g77000 [Arabidopsis thaliana]	Unigene48195_All//6.00E-08//AT1G77000| SKP2B; ubiquitin-protein ligase	Unigene48195_All//2.00E-49//gi|48819134|gb|CO120447.1|CO120447		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene48196_All	1322	1.54	3.60	2.46	5.28	5.76	5.47	11.16	22.76	17.78	1.22E+00	1.83E-05	Up	6.71E-01	6.27E-02		1.26E-01	6.07E-01		5.13E-02	8.46E-01		1.03E+00	2.48E-28	Up	6.72E-01	1.59E-11		Unigene48196_All|gi|18394987|ref|NP_564139.1|//1.00E-157//SKP2A [Arabidopsis thaliana] >gi|9454572|gb|AAF87895.1|AC015447_5 Unknown protein [Arabidopsis thaliana] >gi|16604366|gb|AAL24189.1| At1g21410/F24J8_17 [Arabidopsis thaliana] >gi|19699206|gb|AAL90969.1| At1g21410/F24J8_17 [Arabidopsis thaliana]	Unigene48196_All//1.00E-158//AT1G21410| SKP2A	Unigene48196_All//0.00E+00//TC143731		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene48197_All	834	16.81	12.70	13.09	12.72	14.29	19.17	26.51	15.64	12.42	-4.05E-01	7.40E-03		-3.61E-01	2.36E-02		1.67E-01	3.84E-01		5.92E-01	1.39E-05		-7.62E-01	5.09E-13		-1.09E+00	6.20E-24	Down	Unigene48197_All//gi|21542239|sp|Q9432X.1|SRP19_ARATH//1.00E-52//RecName: Full=Signal recognition particle 19 kDa protein; Short=SRP19 >gi|16612311|gb|AAL27515.1|AF439847_1 At1g48160/F21D18_11 [Arabidopsis thaliana] >gi|21928099|gb|AAN78078.1| At1g48160/F21D18_11 [Arabidopsis thaliana]	Unigene48197_All//1.00E-48//AT1G48160| signal recognition particle 19 kDa protein, putative / SRP19, putative	Unigene48197_All//0.00E+00//TC140880		ko03060|Protein export		nr +
Unigene48198_All	1404	2.91	2.53	4.21	3.73	3.78	2.99	6.63	1.07	3.83	-2.02E-01	5.32E-01		5.34E-01	3.73E-02		1.99E-02	9.51E-01		-3.17E-01	2.66E-01		-2.63E+00	6.46E-33	Down	-7.90E-01	1.63E-06		Unigene48198_All|gi|224102751|ref|XP_002334132.1|//2.00E-99//glycinamide ribonucleotide transformylase [Populus trichocarpa] >gi|222869679|gb|EEF06810.1| glycinamide ribonucleotide transformylase [Populus trichocarpa]	Unigene48198_All//8.00E-86//AT1G31220| phosphoribosylglycinamide formyltransferase	Unigene48198_All//0.00E+00//ES797314		ko00230|Purine metabolism//ko00670|One carbon pool by folate		nr +

Unigene48201_All	844	31.93	34.88	29.21	27.45	29.95	37.35	83.86	40.06	33.42	1.28E-01	2.45E-01		-1.28E-01	2.97E-01		1.26E-01	3.15E-01		4.45E-01	1.96E-06		-1.07E+00	1.44E-69	Down	-1.33E+00	4.19E-101	Down	Unigene48201_All//gi|110740918|dbj|BAE98555.1|//4.00E-28//ubiquinol-cytochrome-c reductase like protein [Arabidopsis thaliana] >gi|114050691|gb|ABI49495.1| Atlg15120 [Arabidopsis thaliana] >gi|227204459|dbj|BAH57081.1| AT1G15120 [Arabidopsis thaliana]	Unigene48201_All//2.00E-29//AT1G15120| ubiquinol-cytochrome C reductase complex 7.8 kDa protein, putative / mitochondrial hinge protein, putative	Unigene48201_All//0.00E+00//TC160488		ko00190|Oxidative phosphorylation		nr -
Unigene48203_All	1021	7.38	18.16	23.37	11.76	14.06	32.07	10.73	7.74	9.68	1.30E+00	8.16E-21	Up	1.66E+00	6.22E-37	Up	2.58E-01	9.49E-02		1.45E+00	1.45E-45	Up	-4.71E-01	2.20E-03		-1.48E-01	3.76E-01		Unigene48203_All//gi|224103611|ref|XP_002313121.1|//1.00E-48//thioredoxin m [Populus trichocarpa] >gi|222849529|gb|EEE87076.1| thioredoxin m [Populus trichocarpa]	Unigene48203_All//2.00E-48//AT2G15570| thioredoxin M-type 3, chloroplast (TRX-M3)	Unigene48203_All//0.00E+00//TC154263				nr -
Unigene48204_All	1112	1.13	2.55	3.26	15.99	15.36	35.54	50.61	52.28	76.49	1.18E+00	2.02E-03		1.53E+00	1.71E-05	Up	-5.83E-02	7.35E-01		1.15E+00	1.03E-38	Up	4.70E-02	5.60E-01		5.96E-01	5.76E-32		Unigene48204_All//gi|110931672|gb|AB802835.1|//4.00E-87//MYB transcription factor MYB75 [Glycine max]	Unigene48204_All//2.00E-72//AT5G05790| myb family transcription factor	Unigene48204_All//0.00E+00//TC137059	MYB	ko04712|Circadian rhythm - plant		nr -
Unigene48206_All	1808	1.39	0.22	0.12	4.71	2.61	1.80	7.83	2.70	1.41	-2.63E+00	9.22E-08	Down	-3.56E+00	1.35E-09	Down	-8.53E-01	3.10E-06		-1.39E+00	9.99E-12	Down	-1.53E+00	4.84E-25	Down	-2.47E+00	5.18E-48	Down	Unigene48206_All//gi|60657600|gb|AAX33321.1|//1.00E-175//secondary cell wall-related glycosyltransferase family 47 [Populus tremula x Populus tremuloides]	Unigene48206_All//1.00E-162//AT3G45400| exostosin family protein	Unigene48206_All//0.00E+00//TC145091				nr -
Unigene48208_All	2895	1.17	0.39	0.40	8.66	5.91	6.18	22.02	15.65	27.58	-1.61E+00	7.48E-06	Down	-1.54E+00	3.17E-05	Down	-5.50E-01	3.18E-08		-4.87E-01	4.09E-06		-4.93E-01	5.54E-17		3.24E-01	2.04E-10		Unigene48208_All//gi|15234429|ref|NP_193870.1|//0.00E+00//B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding [Arabidopsis thaliana] >gi|3402758|emb|CAA20204.1| serine/threonine kinase-like protein [Arabidopsis thaliana] >gi|7268936|emb|CAB81246.1| serine/threonine kinase-like protein [Arabidopsis thaliana] >gi|157086543|gb|ABV21215.1| At4g21390 [Arabidopsis thaliana]	Unigene48208_All//0.00E+00//AT4G21390| B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding	Unigene48208_All//0.00E+00//gi|54121249|gb|CO496758.1|CO496758		ko04626|Plant-pathogen interaction		nr +
Unigene48209_All	863	2.43	1.88	0.99	5.25	1.52	3.72	3.63	2.08	1.52	-3.68E-01	4.01E-01		-1.30E+00	6.74E-03		-1.79E+00	2.34E-10	Down	-5.00E-01	8.55E-02		-8.00E-01	1.08E-02		-1.25E+00	6.54E-05	Down			Unigene48209_All//1.00E-111//DW235983				
Unigene4821_All	1597	0.82	0.63	0.87	18.62	16.78	15.27	6.43	2.38	5.54	-3.68E-01	5.31E-01		8.20E-02	8.86E-01		-1.51E-01	1.64E-01		-2.86E-01	4.21E-03		-1.43E+00	1.08E-16	Down	-2.16E-01	1.95E-01		Unigene4821_All//gi|115452395|ref|NP_001049798.1|//1.00E-129//0s03g0291200 [Oryza sativa Japonica Group] >gi|108707605|gb|ABF95400.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548269|dbj|BAF11712.1| Os03g0291200 [Oryza sativa Japonica Group]	Unigene4821_All//2.00E-166//AT5G01360| EXPRESSED IN: 13 plant structures: EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF231, plant (InterPro:IPR004253); BEST Arabidopsis thaliana protein match is: ESK1 (ESKIMO 1) (TAIR:AT3G55990.1); Has 710 Blast hits to 702 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 2; Plants - 705; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene4821_All//0.00E+00//TC174498				nr -
Unigene48211_All	730	6.88	4.86	5.98	3.82	6.60	4.70	4.05	5.67	23.85	-5.02E-01	6.27E-02		-2.02E-01	4.99E-01		7.89E-01	2.81E-03		2.99E-01	4.21E-01		4.83E-01	7.63E-02		2.56E+00	3.83E-60	Up	Unigene48211_All//gi|18394385|ref|NP_564003.1|//4.00E-60//protein kinase family protein [Arabidopsis thaliana] >gi|16649103|gb|AAL24403.1| Unknown protein [Arabidopsis thaliana] >gi|23197888|gb|AAN15471.1| Unknown protein [Arabidopsis thaliana]	Unigene48211_All//7.00E-62//AT1G16670| protein kinase family protein	Unigene48211_All//2.00E-128//TC158335				nr -
Unigene48212_All	1583	9.88	17.22	7.30	9.57	13.03	11.38	7.53	9.48	40.34	8.01E-01	4.14E-14		-4.37E-01	3.02E-03		4.46E-01	9.41E-05		2.51E-01	7.09E-02		3.32E-01	1.18E-02		2.42E+00	1.44E-205	Up	Unigene48212_All//gi|18394385|ref|NP_564003.1|//1.00E-131//protein kinase family protein [Arabidopsis thaliana] >gi|16649103|gb|AAL24403.1| Unknown protein [Arabidopsis thaliana] >gi|23197888|gb|AAN15471.1| Unknown protein [Arabidopsis thaliana]	Unigene48212_All//8.00E-132//AT1G16670| protein kinase family protein	Unigene48212_All//0.00E+00//TC158335		ko04626|Plant-pathogen interaction		nr -
Unigene48214_All	660	39.08	28.02	30.42	45.81	47.22	51.94	89.75	55.98	43.04	-4.80E-01	6.94E-06		-3.62E-01	1.24E-03		4.36E-02	7.48E-01		1.81E-01	6.88E-02		-6.81E-01	1.17E-27		-1.06E+00	1.59E-59	Down	Unigene48214_All//gi|190895764|gb|ACE96395.1|//1.00E-124//esterase/lipase/thioesterase [Populus tremula] >gi|190895766|gb|ACE96396.1| esterase/lipase/thioesterase [Populus tremula] >gi|190895768|gb|ACE96397.1| esterase/lipase/thioesterase [Populus tremula] >gi|190895770|gb|ACE96398.1| esterase/lipase/thioesterase [Populus tremula]	Unigene48214_All//1.00E-121//AT5G08530| CI51 (51 kDa subunit of complex I); 4 iron, 4 sulfur cluster binding / FMN binding / NAD or NADH binding / NADH dehydrogenase (ubiquinone)/ oxidoreductase, acting on NADH or NADPH	Unigene48214_All//0.00E+00//gi|48822899|gb|CO124212.1|CO124212		ko00190|Oxidative phosphorylation		nr -
Unigene48215_All	2599	2.64	1.46	3.40	0.04	0.13	0.07	7.84	5.00	17.74	-8.51E-01	1.54E-04		3.67E-01	7.93E-02		1.79E+00	2.57E-01		8.60E-01	6.95E-01		-6.49E-01	2.65E-09		1.18E+00	1.66E-54	Up	Unigene48215_All//gi|79570100|ref|NP_181364.2|//1.00E-58//DNA binding / transcription factor [Arabidopsis thaliana]	Unigene48215_All//8.00E-50//AT2G38300| DNA binding / transcription factor	Unigene48215_All//3.00E-09//TC148270	G2-like			nr -
Unigene48216_All	1575	8.04	6.53	7.07	1.20	1.14	4.59	1.42	4.35	15.08	-3.00E-01	6.72E-02		-1.86E-01	3.05E-01		-8.02E-02	8.58E-01		1.93E+00	1.99E-15	Up	1.61E+00	2.24E-13	Up	3.41E+00	4.28E-109	Up	Unigene48216_All//gi|225434642|ref|XP_002279786.1|//1.00E-105//PREDICTED: similar to binding [Vitis vinifera]	Unigene48216_All//7.00E-67//AT3G47080| binding	Unigene48216_All//0.00E+00//TC169063				nr +
Unigene48219_All	860	1.40	1.06	1.80	0.87	2.48	2.05	2.16	1.17	0.93	-4.00E-01	5.15E-01		3.60E-01	5.20E-01		1.51E+00	7.00E-04	Up	1.24E+00	1.46E-02		-8.91E-01	3.70E-02		-1.22E+00	3.47E-03		Unigene48219_All//gi|18396541|ref|NP_566205.1|//6.00E-77//Ku70-binding family protein [Arabidopsis thaliana]	Unigene48219_All//2.00E-78//AT3G03420| Ku70-binding family protein	Unigene48219_All//0.00E+00//D8453325				nr +
Unigene4822_All	790	8.68	3.27	3.51	9.27	12.34	8.29	17.39	9.26	6.61	-1.41E+00	3.57E-09	Down	-1.31E+00	7.13E-08	Down	4.12E-01	2.35E-02		-1.61E-01	5.26E-01		-9.10E-01	4.39E-11		-1.40E+00	6.51E-22	Down	Unigene4822_All//gi|225437368|ref|XP_002268744.1|//2.00E-37//PREDICTED: similar to complex I family protein / LVR family protein [Vitis vinifera]	Unigene4822_All//2.00E-36//AT3G62810| complex I family protein / LVR family protein	Unigene4822_All//0.00E+00//TC165144				nr -
Unigene48220_All	1145	22.57	3.81	19.67	8.35	4.06	2.45	5.21	1.93	3.76	-2.57E+00	4.18E-72	Down	-1.99E-01	9.51E-02		-1.04E+00	1.74E-09	Down	-1.77E+00	1.91E-18	Down	-1.43E+00	5.78E-10	Down	-4.71E-01	2.56E-02		Unigene48220_All//gi|116265922|gb|AB191209.1|//1.00E-141//CBL-interacting protein kinase 1 [Populus trichocarpa]	Unigene48220_All//9.00E-127//AT3G17510| CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding	Unigene48220_All//0.00E+00//TC133196		ko04140|Regulation of autophagy		nr +
Unigene48221_All	2526	1.20	0.88	0.32	3.18	7.91	6.56	11.73	27.45	14.73	-4.45E-01	2.20E-01		-1.93E+00	3.31E-06	Down	1.32E+00	1.68E-26	Up	1.05E+00	2.87E-14	Up	1.23E+00	4.74E-85	Up	3.28E-01	1.96E-05		Unigene48221_All//gi|224059472|ref|XP_002299863.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222847121|gb|EEE84668.1| GRAS family transcription factor [Populus trichocarpa]	Unigene48221_All//2.00E-152//AT2G29060| scarecrow transcription factor family protein	Unigene48221_All//0.00E+00//DT465657	GRAS			nr +
Unigene48222_All	942	15.50	6.45	13.34	24.38	20.98	22.73	11.58	7.37	3.81	-1.26E+00	6.04E-16	Down	-2.16E-01	1.89E-01		-2.16E-01	6.63E-02		-1.01E-01	4.76E-01		-6.53E-01	2.07E-05		-1.61E+00	2.10E-21	Down			Unigene48222_All//9.00E-60//ES813303				
Unigene48223_All	1877	5.30	3.40	5.16	7.48	5.17	4.04	4.39	0.87	1.42	-6.39E-01	4.19E-04		-3.67E-02	8.57E-01		-5.33E-01	1.24E-04		-8.89E-01	1.57E-09		-2.34E+00	1.21E-25	Down	-1.63E+00	1.08E-16	Down	Unigene48223_All//gi|297842799|ref|XP_002889281.1|//1.00E-136//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335122|gb|EFH65540.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48223_All//5.00E-129//AT4G32000| protein kinase family protein	Unigene48223_All//0.00E+00//gi|21100056|gb|BQ412369.1|BQ412369		ko04626|Plant-pathogen interaction		nr -
Unigene48224_All	1493	29.58	65.81	41.52	22.76	18.08	19.42	13.06	22.03	26.15	1.15E+00	4.19E-89	Up	4.89E-01	7.37E-13		-3.32E-01	1.24E-04		-2.29E-01	1.66E-02		7.55E-01	1.17E-18		1.00E+00	7.15E-36	Up	Unigene48224_All//gi|15234236|ref|NP_192894.1|//1.00E-124//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|30681816|ref|NP_849359.1| haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|166487889|gb|AAL23585.1| AT4g11570/F23E4_190 [Arabidopsis thaliana] >gi|20466125|gb|AAM19984.1| AT4g11570/F23E4_190 [Arabidopsis thaliana]	Unigene48224_All//8.00E-121//AT4G11570| haloacid dehalogenase-like hydrolase family protein	Unigene48224_All//0.00E+00//TC135164		ko00740|Riboflavin metabolism		nr -
Unigene48226_All	1469	14.00	9.11	9.79	25.87	27.43	26.01	10.97	2.50	4.31	-6.20E-01	3.09E-07		-5.16E-01	3.76E-05		8.41E-02	4.15E-01		7.60E-03	9.50E-01		-2.13E+00	3.85E-44	Down	-1.35E+00	3.37E-24	Down	Unigene48226_All//gi|115480509|ref|NP_001063848.1|//7.00E-94//0s09g0547200 [Oryza sativa Japonica Group] >gi|113632081|dbj|BAF25762.1| Os09g0547200 [Oryza sativa Japonica Group]	Unigene48226_All//4.00E-100//AT4G35730| unknown protein	Unigene48226_All//0.00E+00//gi|78340647|gb|DT560921.1|DT560921				nr -
Unigene48227_All	1602	2.25	0.70	1.36	5.41	3.63	3.95	6.68	3.65	4.45	-1.70E+00	1.43E-06	Down	-7.26E-01	3.23E-02		-5.75E-01	1.77E-03		-4.55E-01	2.14E-02		-8.70E-01	3.12E-08		-5.85E-01	1.07E-04		Unigene48227_All//gi|116309786|emb|CAH66826.1|//3.00E-60//OS10GB0148A10.3 [Oryza sativa (indica cultivar-group)]	Unigene48227_All//4.00E-73//AT4G27010| unknown protein	Unigene48227_All//0.00E+00//ES811860				nr -
Unigene48228_All	1100	2.71	1.15	2.28	2.81	1.41	1.72	3.65	2.74	1.81	-1.24E+00	8.57E-04	Down	-2.53E-01	5.22E-01		-9.95E-01	2.76E-03		-7.03E-01	4.82E-02		-4.17E-01	1.39E-01		-1.01E+00	1.44E-04	Down	Unigene48228_All//gi|115452463|ref|NP_001049832.1|//4.00E-71//0s03g0296700 [Oryza sativa Japonica Group] >gi|108707651|gb|ABF95446.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548303|dbj|BAF11746.1| Os03g0296700 [Oryza sativa Japonica Group]	Unigene48228_All//3.00E-85//AT2G40316| unknown protein					nr -
Unigene4823_All	722	56.60	36.28	54.36	207.95	168.03	139.99	139.67	42.95	47.56	-6.41E-01	2.31E-14		-5.83E-02	5.85E-01		-3.08E-01	3.78E-16		-5.71E-01	1.48E-44		-1.70E+00	1.37E-201	Down	-1.55E+00	3.98E-182	Down	Unigene4823_All//gi|297831418|ref|XP_002883591.1|//1.00E-62//FK506-binding protein 15 kD-1 [Arabidopsis lyrata subsp. lyrata] >gi|297329431|gb|EFH59850.1| FK506-binding protein 15 kD-1 [Arabidopsis lyrata subsp. lyrata]	Unigene4823_All//3.00E-61//AT3G25220| FKBP15-1; FK506 binding / peptidyl-prolyl cis-trans isomerase	Unigene4823_All//0.00E+00//TC175727				nr -

Unigene48230_All	806	2.21	0.88	1.06	8.16	12.39	17.65	49.05	46.15	73.30	-1.33E+00	8.42E-03		-1.06E+00	4.11E-02		6.03E-01	4.57E-04		1.11E+00	1.50E-13	Up	-8.78E-02	3.39E-01		5.80E-01	1.93E-21		Unigene48230_All//gi|224075627|ref|XP_002304713.1|//9.00E-69//pleiotropic drug resistance protein [Populus trichocarpa] >gi|222842145|gb|EEE79692.1| pleiotropic drug resistance protein [Populus trichocarpa]	Unigene48230_All//4.00E-47//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene48230_All//0.00E+00//DT464626				nr -
Unigene48231_All	1690	1.11	0.69	1.42	4.27	1.06	4.12	6.30	5.69	8.46	-6.93E-01	1.39E-01		3.47E-01	4.14E-01		-2.01E+00	5.57E-19	Down	-5.45E-02	8.27E-01		-1.48E-01	4.01E-01		4.25E-01	1.02E-03		Unigene48231_All//gi|193878344|gb|ACF25912.1|//0.00E+00//MLO-like protein 7 [Vitis vinifera]	Unigene48231_All//4.00E-174//AT4G02600| MLO1; calmodulin binding	Unigene48231_All//0.00E+00//TC152564				nr +
Unigene48233_All	2250	7.84	7.90	9.28	13.57	14.14	16.92	25.03	21.36	11.62	1.24E-02	9.50E-01		2.44E-01	6.43E-02		5.93E-02	6.12E-01		3.18E-01	2.04E-04		-2.29E-01	3.39E-04		-1.11E+00	9.53E-61	Down	Unigene48233_All//gi|3080740|gb|AAC39415.1|//0.00E-00//pasticcino 1-D [Arabidopsis thaliana]	Unigene48233_All//0.00E+00//AT3G54010| PAS1 (PASTICCINO 1); FK506 binding / binding / peptidyl-prolyl cis-trans isomerase	Unigene48233_All//0.00E+00//TC158566				nr -
Unigene48234_All	1386	14.31	3.95	5.49	1.01	1.69	2.35	31.48	10.43	10.20	-1.86E+00	3.98E-37	Down	-1.38E+00	1.91E-23	Down	7.48E-01	7.48E-02		1.22E+00	4.66E-04	Up	-1.59E+00	8.68E-80	Down	-1.63E+00	1.54E-84	Down	Unigene48234_All//gi|27464177|gb|AA015998.1|AF516879_1/1.00E-131//expansin [Glycine max]	Unigene48234_All//6.00E-106//AT1G20190| ATEXPA11 (ARABIDOPSIS THALIANA EXPANSIN 11)	Unigene48234_All//0.00E+00//TC160817				nr +
Unigene48235_All	1245	11.98	6.84	7.74	16.00	12.39	15.16	26.49	17.19	12.38	-8.09E-01	3.19E-08		-6.30E-01	2.60E-05		-3.69E-01	1.61E-03		-7.79E-02	6.35E-01		-6.24E-01	1.27E-13		-1.10E+00	2.13E-35	Down	Unigene48235_All//gi|224108213|ref|XP_002314761.1|//1.00E-112//anthranilate synthase, beta subunit, ASB1 [Populus trichocarpa] >gi|222863801|gb|EEF00932.1| anthranilate synthase, beta subunit, ASB1 [Populus trichocarpa]	Unigene48235_All//5.00E-112//AT1G25220| ASB1 (ANTHRANILATE SYNTHASE BETA SUBUNIT 1); anthranilate synthase	Unigene48235_All//0.00E+00//gi|109871922|gb|DW500898.1|DW500898		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene48237_All	1463	5.54	11.78	5.06	8.75	7.53	12.19	16.70	34.68	25.87	1.09E+00	8.38E-15	Up	-1.32E-01	5.89E-01		-2.16E-01	2.02E-01		4.79E-01	2.04E-04		1.05E+00	3.79E-49	Up	6.31E-01	3.25E-16		Unigene48237_All//gi|124359825|gb|ABD32921.2|//1.00E-126//F5011.19, related [Medicago truncatula]	Unigene48237_All//5.00E-114//AT2G02370| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (InterPro:IPR015114); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G12450.1); Has 1745 Blast hits to 1745 proteins in 446 species: Archae - 2; Bacteria - 792; Metazoa - 108; Fungi - 97; Plants - 119; Viruses - 0; Other Eukaryotes - 627 (source: NCBI BLink).	Unigene48237_All//0.00E+00//ES814359				nr +
Unigene48238_All	946	0.33	0.11	0.23	7.85	8.77	5.30	2.77	3.27	6.19	-1.63E+00	2.76E-01		-5.59E-01	6.63E-01		1.61E-01	5.13E-01		-5.66E-01	7.76E-03		2.39E-01	4.99E-01		1.16E+00	1.59E-07	Up	Unigene48238_All//gi|186511471|ref|NP_001118919.1|//1.00E-64//UNE12 (unfertilized embryo sac 12); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene48238_All//1.00E-55//AT4G02590| UNE12 (unfertilized embryo sac 12); DNA binding / transcription factor	Unigene48238_All//2.00E-141//gi|78352442|gb|DT572716.1|DT572716	bHLH	ko04712|Circadian rhythm - plant		nr -
Unigene48239_All	1822	0.46	0.50	0.20	5.55	4.27	1.41	1.76	0.71	3.08	1.24E-01	8.56E-01		-1.17E+00	1.52E-01		-3.78E-01	3.24E-02		-1.97E+00	1.81E-22	Down	-1.31E+00	3.98E-05	Down	8.06E-01	2.27E-04		Unigene48239_All//gi|18411987|ref|NP_567245.1|//3.00E-64//UNE12 (unfertilized embryo sac 12); DNA binding / transcription factor [Arabidopsis thaliana] >gi|79324985|ref|NP_001031577.1| UNE12 (unfertilized embryo sac 12); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75277341|sp|Q22768.2|UNE12_ARATH RecName: Full=Transcription factor UNE12; AltName: Full=Protein UNFERTILIZED EMBRYO SAC 12; AltName: Full=Transcription factor EN 93; AltName: Full=bHLH transcription factor bHLH059; AltName: Full=Basic helix-loop-helix protein 59; Short=bHLH 59; Short=AtbHLH59 >gi|13605859|gb|AAK32915.1|AF367328_1 AT4g02590/T10P11_13 [Arabidopsis thaliana] >gi|23506061|gb|AAN28890.1| At4g02590/T10P11_13 [Arabidopsis thaliana] >gi|222422973|dbj|BAH19471.1| AT4G02590 [Arabidopsis thaliana]	Unigene48239_All//2.00E-33//AT4G02590| UNE12 (unfertilized embryo sac 12); DNA binding / transcription factor	Unigene48239_All//5.00E-137//gi|164353448|gb|ES805229.1|ES805229	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant		nr -
Unigene4824_All	1012	3.46	5.11	4.31	15.01	11.40	15.71	6.64	4.50	2.68	5.60E-01	3.44E-02		3.17E-01	3.21E-01		-3.97E-01	3.63E-03		6.54E-02	6.82E-01		-5.61E-01	5.53E-03		-1.31E+00	3.22E-10	Down	Unigene4824_All//gi|226508366|ref|NP_001151358.1|//9.00E-09//hsp20/alpha crystallin family protein [Zea mays] >gi|195646116|gb|ACG42526.1| hsp20/alpha crystallin family protein [Zea mays]						nr -
Unigene48241_All	799	26.98	35.07	35.99	40.09	31.76	56.24	16.03	10.88	6.23	3.78E-01	2.28E-04		4.16E-01	6.80E-05		-3.36E-01	1.70E-04		4.89E-01	1.95E-10		-5.59E-01	6.52E-05		-1.36E+00	8.93E-20	Down			Unigene48241_All//0.00E+00//TC161771				
Unigene48242_All	1032	0.05	0.29	0.00	0.10	0.03	0.00	0.20	0.04	1.85	2.54E+00	1.51E-01		-5.66E+00	6.22E-01		-1.53E+00	5.86E-01		-6.59E+00	3.99E-01		-2.34E+00	2.37E-01		3.18E+00	7.45E-09	Up	Unigene48242_All//gi|89953446|gb|AB083318.1|//6.00E-38//Fgenesh protein 88 [Beta vulgaris]	Unigene48242_All//3.00E-26//AT3G06950| tRNA pseudouridine synthase family protein					nr +
Unigene48245_All	913	3.95	5.55	9.57	87.08	56.12	55.01	17.41	25.00	5.02	4.89E-01	6.91E-02		1.27E+00	1.61E-09	Up	-6.34E-01	2.89E-32		-6.63E-01	5.60E-31		5.22E-01	3.12E-07		-1.79E+00	6.17E-36	Down	Unigene48245_All//gi|14326489|gb|AAK60290.1|AF385697_1/5.00E-82//AT5g10580/F12B17_70 [Arabidopsis thaliana] >gi|18700208|gb|AAL77714.1| AT5g10580/F12B17_70 [Arabidopsis thaliana]	Unigene48245_All//2.00E-86//AT4G31330| unknown protein	Unigene48245_All//0.00E+00//TC155985				nr +
Unigene48246_All	1860	8.07	4.96	8.73	3.11	3.05	1.09	0.41	0.11	1.03	-7.03E-01	1.13E-06		1.13E-01	4.84E-01		-2.44E-02	9.30E-01		-1.51E+00	3.94E-09	Down	-1.86E+00	1.82E-02		1.33E+00	1.54E-03		Unigene48246_All//gi|223452508|gb|ACM89581.1|//1.00E-146//disease resistance protein [Glycine max]	Unigene48246_All//2.00E-88//AT1G47890| AtRLP7 (Receptor Like Protein 7); kinase/ protein binding	Unigene48246_All//2.00E-53//TC130243		ko04626|Plant-pathogen interaction		nr +
Unigene48248_All	601	1.92	1.52	3.37	5.72	4.07	4.13	4.71	2.57	1.06	-3.36E-01	6.09E-01		8.14E-01	8.61E-02		-4.91E-01	1.39E-01		-4.69E-01	1.81E-01		-8.73E-01	8.62E-03		-2.15E+00	9.02E-09	Down			Unigene48248_All//8.00E-56//DR463255				
Unigene48249_All	756	1.31	1.47	2.39	3.49	2.73	1.37	2.57	2.21	0.79	1.65E-01	7.79E-01		8.65E-01	8.81E-02		-3.54E-01	3.86E-01		-1.35E+00	6.28E-04	Down	-2.18E-01	6.58E-01		-1.70E+00	7.95E-05	Down			Unigene48249_All//1.00E-55//DR463255				
Unigene4825_All	1248	29.22	27.24	33.79	27.82	30.77	26.16	62.37	43.70	27.93	-1.01E-01	3.22E-01		2.10E-01	1.83E-02		1.45E-01	1.23E-01		-8.86E-02	4.28E-01		-5.13E-01	4.80E-22		-1.16E+00	6.75E-90	Down	Unigene4825_All//gi|297833908|ref|XP_002884836.1|//1.00E-108//CPRD49 [Arabidopsis lyrata subsp. lyrata] >gi|297330676|gb|EFH61095.1| CPRD49 [Arabidopsis lyrata subsp. lyrata]	Unigene4825_All//4.00E-108//AT3G11210| GDSL-motif lipase/hydrolase family protein	Unigene4825_All//0.00E+00//TC134222				nr +
Unigene48250_All	2040	2.08	9.98	2.79	5.23	6.63	5.96	6.90	12.97	11.97	2.27E+00	9.20E-49	Up	4.27E-01	1.09E-01		3.44E-01	2.40E-02		1.89E-01	3.12E-01		9.10E-01	1.44E-20		7.95E-01	1.09E-15		Unigene48250_All//gi|30698743|ref|NP_177231.2|//1.00E-152//protein kinase family protein [Arabidopsis thaliana] >gi|193870477|gb|ACF22895.1| At1g70740 [Arabidopsis thaliana]	Unigene48250_All//7.00E-150//AT1G70740| protein kinase family protein	Unigene48250_All//0.00E+00//TC173427		ko04626|Plant-pathogen interaction		nr +
Unigene48251_All	1971	5.15	3.98	5.19	1.95	2.04	0.89	5.43	1.74	2.24	-3.70E-01	4.35E-02		1.04E-02	9.79E-01		7.09E-02	8.37E-01		-1.12E+00	3.10E-04	Down	-1.64E+00	5.35E-21	Down	-1.27E+00	4.25E-15	Down	Unigene48251_All//gi|183904104|ref|NP_563709.1|//1.00E-42//binding [Arabidopsis thaliana]	Unigene48251_All//2.00E-42//AT1G04530| binding	Unigene48251_All//0.00E+00//TC153580				nr +
Unigene48253_All	868	2.23	1.34	0.67	6.83	4.52	3.90	3.26	1.11	1.24	-7.32E-01	1.17E-01		-1.72E+00	9.79E-04	Down	-5.95E-01	9.92E-03		-8.07E-01	7.33E-04		-1.56E+00	9.71E-06	Down	-1.40E+00	3.34E-05	Down			Unigene48253_All//5.00E-15//CO109829				
Unigene48254_All	1203	85.59	26.03	73.30	42.36	25.36	15.47	17.85	6.81	5.96	-1.72E+00	9.86E-171	Down	-2.24E-01	2.44E-05		-7.40E-01	2.71E-27		-1.45E+00	2.90E-72	Down	-1.39E+00	1.51E-32	Down	-1.58E+00	1.75E-40	Down	Unigene48254_All//gi|18398566|ref|NP_564408.1|//4.00E-71//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene48254_All//2.00E-56//AT1G32740| protein binding / zinc ion binding	Unigene48254_All//0.00E+00//TC176697				nr -
Unigene48255_All	863	20.13	11.86	12.34	14.89	17.36	13.71	7.50	16.61	3.69	-7.63E-01	1.27E-08		-7.06E-01	2.95E-07		2.21E-01	1.56E-01		-1.19E-01	5.34E-01		1.15E+00	1.74E-16	Up	-1.02E+00	6.49E-07	Down	Unigene48255_All//gi|15234010|ref|NP_195580.1|//1.00E-45//GRP2 (GLYCINE RICH PROTEIN 2); double-stranded DNA binding / mRNA binding / nucleic acid binding / single-stranded DNA binding [Arabidopsis thaliana] >gi|14326487|gb|AAK60289.1|AF385696_1 AT4g38680/F20M13_240 [Arabidopsis thaliana] >gi|259445|gb|AAB24074.1| glycine-rich protein [Arabidopsis thaliana] >gi|4467155|emb|CAB37524.1| glycine-rich protein 2 (GRP2) [Arabidopsis thaliana] >gi|7270851|emb|CAB80532.1| glycine-rich protein 2 (GRP2) [Arabidopsis thaliana] >gi|22137152|gb|AAM91421.1| AT4g38680/F20M13_240 [Arabidopsis thaliana]	Unigene48255_All//7.00E-24//AT2G17870| cold-shock DNA-binding family protein	Unigene48255_All//0.00E+00//TC173502	CSD			nr +
Unigene48256_All	1022	28.05	41.60	37.78	12.43	19.41	18.60	0.74	2.54	2.57	5.68E-01	3.96E-12		4.29E-01	1.20E-06		6.43E-01	2.41E-08		5.82E-01	2.43E-06		1.77E+00	3.55E-06	Up	1.79E+00	1.58E-06	Up	Unigene48256_All//gi|18390799|ref|NP_563794.1|//9.00E-62//thioredoxin family protein [Arabidopsis thaliana] >gi|75168930|sp|Q9C5C5.1|TRL4_ARATH RecName: Full=Thioredoxin-like 4, chloroplastic; AltName: Full=Lilium-type thioredoxin 3; Flags: Precursor	Unigene48256_All//5.00E-63//AT1G07700| thioredoxin family protein	Unigene48256_All//0.00E+00//TC172785				nr -
Unigene48258_All	2420	1.84	3.83	4.44	24.60	25.29	24.00	14.05	9.59	9.80	1.06E+00	5.00E-08	Up	1.27E+00	1.42E-11	Up	3.98E-02	6.40E-01		-3.55E-02	6.95E-01		-5.51E-01	2.16E-11		-5.20E-01	1.16E-10		Unigene48258_All//gi|30725324|gb|AAP37684.1|//1.00E-147//At3g01680 [Arabidopsis thaliana]	Unigene48258_All//5.00E-128//AT3G01680| unknown protein	Unigene48258_All//0.00E+00//TC147150				nr +
Unigene48259_All	1495	17.64	5.80	10.19	1.77	1.89	1.54	1.02	0.17	0.77	-1.61E+00	3.56E-40	Down	-7.92E-01	7.01E-13		9.70E-02	8.25E-01		-1.97E-01	6.43E-01		-2.60E+00	6.96E-06	Down	-3.98E-01	4.02E-01		Unigene48259_All//gi|115480061|ref|NP_001063624.1|//1.00E-128//Os09g0508900 [Oryza sativa Japonica Group] >gi|113631857|dbj|BAF25538.1| Os09g0508900 [Oryza sativa Japonica Group]	Unigene48259_All//1.00E-98//AT2G39970| peroxisomal membrane protein (PMP36)	Unigene48259_All//0.00E+00//TC143105		ko04146|Peroxisome		nr +

Unigene4826_All	1428	0.22	0.82	0.63	4.78	3.69	2.09	24.90	18.26	13.75	1.89E+00	6.32E-03		1.53E+00	5.77E-02		-3.73E-01	9.85E-02		-1.20E+00	1.16E-07	Down	-4.47E-01	2.29E-08		-8.56E-01	1.58E-25		Unigene4826_All//gi|297821617|ref|XP_002878691.1|//1.00E-168//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324530|gb|EFH54950.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4826_All//1.00E-168//AT2G23540| GDSL-motif lipase/hydrolase family protein	Unigene4826_All//0.00E+00//TC167644				nr -
Unigene48260_All	1138	4.18	15.76	11.32	2.63	6.14	5.24	4.98	4.15	5.60	1.91E+00	9.10E-35	Up	1.44E+00	2.17E-16	Up	1.23E+00	1.41E-08	Up	9.96E-01	3.71E-05		-2.63E-01	2.80E-01		1.70E-01	4.52E-01		Unigene48260_All//gi|18414994|ref|NP_567545.1|//7.00E-96//binding [Arabidopsis thaliana]	Unigene48260_All//1.00E-47//AT4G17940| binding	Unigene48260_All//0.00E+00//gi|73851685|gb|DT460705.1|DT460705				nr +
Unigene48262_All	888	30.40	88.10	50.85	90.04	116.57	119.57	43.23	53.19	50.07	1.54E+00	6.92E-110	Up	7.42E-01	2.09E-19		3.73E-01	9.77E-16		4.09E-01	2.23E-17		2.99E-01	1.55E-05		2.12E-01	3.01E-03		Unigene48262_All//gi|224102883|ref|XP_002312841.1|//7.00E-38//ethylene-insensitive 3a [Populus trichocarpa] >gi|222849249|gb|EEE86796.1| ethylene-insensitive 3a [Populus trichocarpa]	Unigene48262_All//3.00E-24//AT3G20770| EIN3 (ETHYLENE-INSENSITIVE3); transcription factor	Unigene48262_All//0.00E+00//gi|78341981|gb|DT562255.1|DT562255	EIL			nr +
Unigene48263_All	779	2.89	2.21	0.82	21.04	20.51	15.54	24.64	38.52	28.64	-3.85E-01	3.69E-01		-1.82E+00	1.79E-04	Down	-3.66E-02	8.24E-01		-4.37E-01	1.27E-03		6.45E-01	3.72E-13		2.17E-01	3.98E-02		Unigene48263_All//gi|227204257|dbj|BAH56980.1|//2.00E-80//AT1G75800 [Arabidopsis thaliana]	Unigene48263_All//9.00E-82//AT1G75800| pathogenesis-related thaumatin family protein	Unigene48263_All//0.00E+00//gi|78349559|gb|DT569833.1|DT569833				nr +
Unigene48265_All	1383	6.70	8.32	8.05	15.85	12.52	14.66	31.95	69.42	56.81	3.13E-01	7.06E-02		2.65E-01	1.54E-01		-3.40E-01	2.39E-03		-1.12E-01	4.27E-01		1.12E+00	9.90E-102	Up	8.30E-01	3.29E-52		Unigene48265_All//gi|55978461|gb|AAV68714.1|//5.00E-96//3-beta hydroxysteroid dehydrogenase [Digitalis ferrugines] >gi|55978465|gb|AAV68716.1| 3-beta hydroxysteroid dehydrogenase [Digitalis purpurea]	Unigene48265_All//1.00E-91//AT2G47140| short-chain dehydrogenase/reductase (SDR) family protein	Unigene48265_All//0.00E+00//TC145281		ko00906|Carotenoid biosynthesis		nr -
Unigene48266_All	1497	3.29	2.00	1.64	0.93	0.99	1.66	1.89	1.59	12.08	-7.18E-01	7.81E-03		-1.01E+00	4.13E-04	Down	8.63E-02	8.96E-01		8.33E-01	4.12E-02		-2.50E-01	4.98E-01		2.67E+00	1.22E-65	Up	Unigene48266_All//gi|18405138|ref|NP_565911.1|//1.00E-134//aspartyl protease family protein [Arabidopsis thaliana] >gi|20196976|gb|AAD87120.2| expressed protein [Arabidopsis thaliana] >gi|20197046|gb|AAM14894.1| expressed protein [Arabidopsis thaliana]	Unigene48266_All//1.00E-133//AT2G39710| aspartyl protease family protein	Unigene48266_All//2.00E-15//TC146281				nr +
Unigene48267_All	840	2.18	3.92	5.07	4.57	3.20	1.13	4.83	59.11	4.79	8.47E-01	1.34E-02		1.22E+00	1.04E-04	Up	-5.14E-01	9.40E-02		-2.02E+00	4.39E-09	Down	3.61E+00	1.45E-235	Up	-1.26E-02	9.70E-01		Unigene48267_All//gi|159138935|gb|ABR89867.1|//6.00E-65//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene48267_All//3.00E-51//AT1G53540| 17.6 kDa class I small heat shock protein (HSP17.6C-CI) (AA 1-156)	Unigene48267_All//0.00E+00//gi|109867681|gb|DW496657.1|DW496657				nr -
Unigene48268_All	1820	1.06	2.45	1.55	3.89	3.14	2.46	5.18	2.60	2.93	1.20E+00	4.63E-05	Up	5.44E-01	1.65E-01		-3.07E-01	1.77E-01		-6.62E-01	2.25E-03		-9.97E-01	5.01E-09		-8.21E-01	5.68E-07		Unigene48268_All//gi|30686295|ref|NP_850237.1|//3.00E-42//MEE22 (MATERNAL EFFECT EMBRYO ARREST 22) [Arabidopsis thaliana]	Unigene48268_All//1.00E-30//AT2G34780| MEE22 (MATERNAL EFFECT EMBRYO ARREST 22)	Unigene48268_All//8.00E-77//CA993965		ko03040|Spliceosome		nr +
Unigene48272_All	938	6.69	9.94	6.98	22.78	15.31	16.13	5.27	3.30	2.63	5.70E-01	2.46E-03		6.10E-02	8.04E-01		-5.74E-01	1.28E-07		-4.98E-01	1.59E-05		-6.78E-01	4.81E-03		-1.00E+00	2.37E-05	Down			Unigene48272_All//0.00E+00//gi|11200087|gb|BF269092.1|BF269092				
Unigene48273_All	968	5.84	12.93	6.27	7.46	7.93	8.86	7.69	15.72	9.38	1.15E+00	6.95E-12	Up	1.03E-01	6.87E-01		8.83E-02	7.51E-01		2.49E-01	2.58E-01		1.03E+00	8.36E-15	Up	2.88E-01	9.67E-02		Unigene48273_All//gi|18411133|ref|NP_567078.1|//1.00E-40//TXR1 (THAXTOMIN A RESISTANT 1) [Arabidopsis thaliana] >gi|14190487|gb|AAK55724.1|AF380643_1 AT3g59280/F25L23_140 [Arabidopsis thaliana] >gi|15809738|gb|AAL06797.1| AT3g59280/F25L23_140 [Arabidopsis thaliana] >gi|32306447|gb|AAM63549.1| thaxtomin resistance protein TXR1 [Arabidopsis thaliana]	Unigene48273_All//5.00E-42//AT3G59280| TXR1 (THAXTOMIN A RESISTANT 1)	Unigene48273_All//0.00E+00//TC153240				nr -
Unigene48274_All	1502	7.98	10.15	5.74	52.93	42.76	34.58	27.45	9.02	13.82	3.48E-01	1.68E-02		-4.74E-01	5.60E-03		-3.08E-01	8.30E-09		-6.14E-01	3.99E-27		-1.61E+00	2.72E-76	Down	-9.90E-01	2.45E-37		Unigene48274_All//gi|15240888|ref|NP_195729.1|//9.00E-41//legume lectin family protein [Arabidopsis thaliana] >gi|6759432|emb|CAB69837.1| lectin-like protein [Arabidopsis thaliana] >gi|110736881|dbj|BAF00398.1| lectin - like protein [Arabidopsis thaliana]	Unigene48274_All//3.00E-32//AT5G01090| legume lectin family protein	Unigene48274_All//0.00E+00//TC138141				nr +
Unigene48276_All	1725	2.03	2.06	1.17	4.65	4.95	3.19	1.86	2.83	4.27	1.69E-02	9.80E-01		-7.93E-01	2.15E-02		9.06E-02	7.22E-01		-5.42E-01	7.83E-03		6.06E-01	1.26E-02		1.20E+00	1.11E-09	Up	Unigene48276_All//gi|22331831|ref|NP_191271.2|//1.00E-145//protein kinase family protein [Arabidopsis thaliana]	Unigene48276_All//6.00E-125//AT3G57120| protein kinase family protein	Unigene48276_All//0.00E+00//TC153303		ko04626|Plant-pathogen interaction		nr -
Unigene48277_All	1263	15.04	14.16	11.00	26.15	20.37	27.07	23.83	10.89	14.86	-8.66E-02	5.59E-01		-4.51E-01	6.17E-04		-3.61E-01	3.47E-05		4.99E-02	6.76E-01		-1.13E+00	5.61E-33	Down	-6.82E-01	6.02E-15		Unigene48277_All//gi|14626935|gb|AAX08805.1|//1.00E-122//leucine-rich repeat resistance protein-like protein [Gossypium hirsutum]	Unigene48277_All//8.00E-134//AT5G61240| protein binding	Unigene48277_All//0.00E+00//TC137694		ko04626|Plant-pathogen interaction		nr +
Unigene48278_All	1780	3.76	6.58	5.44	0.76	1.06	5.63	0.14	0.19	0.09	8.06E-01	1.43E-06		5.33E-01	5.48E-03		4.94E-01	3.21E-01		2.90E+00	5.89E-34	Up	3.98E-01	7.24E-01		-6.71E-01	6.05E-01		Unigene48278_All//gi|18409649|ref|NP_198854.2|//0.00E+00//protein kinase family protein [Arabidopsis thaliana]	Unigene48278_All//0.00E+00//AT5G40380| protein kinase family protein	Unigene48278_All//2.00E-25//DT462977		ko04626|Plant-pathogen interaction		nr +
Unigene48828_All	1010	12.59	17.51	25.41	254.50	154.14	222.55	32.11	15.85	12.07	4.76E-01	3.04E-04		1.01E+00	9.67E-19	Up	-7.23E-01	2.32E-131		-1.94E-01	1.98E-10		-1.02E+00	4.71E-30	Down	-1.41E+00	2.54E-51	Down	Unigene4828_All//gi|18409649|ref|NP_564995.1|//3.00E-64//caleosin-related family protein [Arabidopsis thaliana] >gi|15810177|gb|AAL06990.1| At1g70670/F5A18_15 [Arabidopsis thaliana] >gi|23565789|gb|AAN28754.1| At1g70670/F5A18_15 [Arabidopsis thaliana]	Unigene4828_All//1.00E-65//AT1G70670| caleosin-related family protein	Unigene4828_All//0.00E+00//gi|164258484|gb|ES817967.1|ES817967				nr +
Unigene48281_All	1184	18.43	13.01	11.06	28.06	28.85	32.16	15.75	7.73	7.10	-5.02E-01	1.77E-05		-7.36E-01	1.46E-09		4.00E-02	7.60E-01		1.96E-01	3.20E-02		-1.03E+00	7.62E-18	Down	-1.15E+00	6.28E-22	Down	Unigene48281_All//gi|40233087|gb|AAR83341.1|//2.00E-80//homeodomain protein HB2 [Populus tomentosa]	Unigene48281_All//1.00E-64//AT4G35550| WOX13 (WUSCHEL-RELATED HOMEOBOX 13); DNA binding / transcription factor	Unigene48281_All//0.00E+00//TC133701	HB			nr +
Unigene48282_All	1472	2.45	2.55	2.53	12.72	10.76	12.64	22.89	12.89	8.93	5.47E-02	8.69E-01		4.62E-02	8.94E-01		-2.42E-01	6.44E-02		-9.50E-03	9.56E-01		-8.29E-01	2.71E-22		-1.36E+00	2.73E-50	Down	Unigene48282_All//gi|193237557|dbj|BAG50055.1|//4.00E-81//transcription factor CCAAT [Lotus japonicus]	Unigene48282_All//6.00E-38//AT5G06510| NF-YA10 (NUCLEAR FACTOR Y, SUBUNIT A10); transcription factor	Unigene48282_All//0.00E+00//TC177407	CCAAT			nr -
Unigene48285_All	1295	13.74	12.76	11.27	17.35	18.35	17.33	16.98	9.91	7.08	-1.07E-01	4.69E-01		-2.86E-01	4.48E-02		8.08E-02	5.69E-01		-1.30E-03	9.90E-01		-7.77E-01	2.30E-13		-1.26E+00	1.11E-29	Down	Unigene48285_All//gi|224118092|ref|XP_002331556.1|//1.00E-115//ebs-bah-phd domain-containing protein [Populus trichocarpa] >gi|222873780|gb|EEF10911.1| ebs-bah-phd domain-containing protein [Populus trichocarpa]	Unigene48285_All//2.00E-109//AT4G22140| DNA binding / protein binding / zinc ion binding	Unigene48285_All//0.00E+00//TC166123				nr +
Unigene48287_All	1256	1.75	2.14	0.85	3.69	2.77	2.70	3.53	1.70	2.32	2.89E-01	4.63E-01		-1.05E+00	2.24E-02		-4.14E-01	1.45E-01		-4.52E-01	1.22E-01		-1.06E+00	4.54E-05	Down	-6.10E-01	1.36E-02		Unigene48287_All//gi|62287141|sp|Q58845.1|POLLU_LOTJA//2.00E-46//RecName: Full=Ion channel POLLUX >gi|58430445|dbj|BAD89020.1| ion channel [Lotus japonicus] >gi|58430449|dbj|BAD89022.1| POLLUX [Lotus japonicus]	Unigene48287_All//3.00E-29//AT5G49960| binding / catalytic					nr -
Unigene48288_All	1545	5.93	3.31	4.58	8.19	9.99	6.93	6.08	4.65	2.78	-8.39E-01	1.15E-05		-3.71E-01	6.97E-02		2.86E-01	4.84E-02		-2.41E-01	1.63E-01		-3.85E-01	2.43E-02		-1.13E+00	3.98E-11	Down	Unigene48288_All//gi|124360303|gb|ABN08316.1|//4.00E-95//NAD-dependent epimerase/dehydratase [Medicago truncatula]	Unigene48288_All//5.00E-70//AT2G45400| BEN1; binding / catalytic/ coenzyme binding / oxidoreductase, acting on CH-OH group of donors	Unigene48288_All//0.00E+00//TC177014		ko00941|Flavonoid biosynthesis		nr +
Unigene4829_All	1199	11.04	7.69	6.53	28.54	43.57	51.98	14.39	29.07	18.57	-5.22E-01	7.35E-04		-7.58E-01	2.35E-06		6.10E-01	2.07E-19		8.65E-01	4.29E-38		1.01E+00	5.13E-32	Up	3.69E-01	2.86E-04		Unigene4829_All//gi|224064466|ref|XP_002301490.1|//2.00E-78//AP2/EREBP domain-containing transcription factor [Populus trichocarpa] >gi|222843216|gb|EEE80763.1| AP2/EREBP domain-containing transcription factor [Populus trichocarpa]	Unigene4829_All//3.00E-27//AT3G16770| ATERF (ETHYLENE-RESPONSIVE ELEMENT BINDING PROTEIN); DNA binding / protein binding / transcription activator/ transcription factor	Unigene4829_All//0.00E+00//TC135659	AP2-EREBP			nr -
Unigene48296_All	1609	2.80	14.17	8.11	7.59	22.11	19.17	0.21	0.16	0.17	2.34E+00	9.79E-57	Up	1.54E+00	2.96E-18	Up	1.54E+00	1.62E-59	Up	1.34E+00	3.55E-38	Up	-4.31E-01	7.03E-01		-2.79E-01	7.81E-01		Unigene48296_All//gi|124360795|gb|ABN08767.1|//1.00E-178//Amine oxidase [Medicago truncatula]	Unigene48296_All//0.00E+00//AT4G29720| ATPA05 (Polyamine oxidase 5); amine oxidase/ electron carrier/ oxidoreductase	Unigene48296_All//0.00E+00//gi|109861102|gb|DW490080.1|DW490080				nr +
Unigene48298_All	729	3.59	9.59	2.56	15.58	25.60	27.63	59.33	63.52	64.49	1.42E+00	2.16E-09	Up	-4.89E-01	2.38E-01		7.17E-01	2.02E-09		8.27E-01	8.62E-12		9.85E-02	2.27E-01		1.20E-01	1.05E-01		Unigene48298_All//gi|297852976|ref|XP_002894369.1|//3.00E-42//dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340211|gb|EFH70628.1| dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48298_All//3.00E-43//AT1G52240| ROPGEF11 (ROH GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor	Unigene48298_All//1.00E-166//CO494646				nr +
Unigene483_All	2364	6.17	13.42	7.48	9.36	10.50	9.90	13.54	15.68	21.76	1.12E+00	6.98E-28	Up	2.76E-01	5.28E-02		1.67E-01	1.66E-01		8.10E-02	5.79E-01		2.12E-01	9.50E-03		6.84E-01	6.43E-25		Unigene483_All//gi|222422845|dbj|BAH19109.1|//1.00E-115//AT5G19900 [Arabidopsis thaliana]	Unigene483_All//5.00E-75//AT5G19900| PRL1-interacting factor, putative	Unigene483_All//0.00E+00//CO105658				nr -
Unigene4830_All	1260	34.67	26.74	34.23	35.46	26.97	24.91	16.34	11.88	7.78	-3.75E-01	3.05E-06		-1.85E-02	8.48E-01		-3.95E-01	5.77E-08		-5.10E-01	3.12E-11		-4.61E-01	1.95E-05		-1.07E+00	1.28E-21	Down	Unigene4830_All//gi|7671502|emb|CAB89343.1|//1.00E-112//ids-4 protein-like [Arabidopsis thaliana]	Unigene4830_All//2.00E-107//AT5G15330| SPX4 (SPX DOMAIN GENE 4)	Unigene4830_All//0.00E+00//TC134167				nr +
Unigene48300_All	1282	1.51	2.06	3.53	7.23	5.29	5.71	5.31	5.57	4.60	4.45E-01	2.59E-01		1.23E+00	5.33E-05	Up	-4.50E-01	1.32E-02		-3.41E-01	8.43E-02		7.03E-02	7.49E-01		-2.07E-01	3.34E-01		Unigene48300_All//gi|150036255|gb|ABR67418.1|//1.00E-136//mitochondrial FAD carrier [Cucumis melo]	Unigene48300_All//2.00E-113//AT3G05290| PNC1 (PEROXISOMAL ADENINE NUCLEOTIDE CARRIER 1); ADP transmembrane transporter/ ATP transmembrane transporter/ binding	Unigene48300_All//0.00E+00//gi|78351408|gb|DT571682.1|DT571682		ko04146|Peroxisome		nr -
Unigene48302_All	1197	2.58	4.02	2.58	4.54	6.21	4.34	2.97	2.62	1.20	6.41E-01	1.97E-02		7.00E-04	9.97E-01		4.54E-01	3.28E-02		-6.41E-02	8.23E-01		-1.80E-01	6.04E-01		-1.31E+00	8.64E-06	Down	Unigene48302_All//gi|224137268|ref|XP_002322515.1|//1.00E-30//predicted protein [Populus trichocarpa] >gi|222867145|gb|EEF04276.1| predicted protein [Populus trichocarpa]		Unigene48302_All//0.00E+00//TC141710				nr -

Unigene48303_All	1573	5.59	4.41	4.54	10.55	8.89	9.02	17.36	7.04	5.67	-3.41E-01	8.86E-02		-3.01E-01	1.54E-01		-2.47E-01	7.91E-02		-2.26E-01	1.29E-01		-1.30E+00	2.65E-37	Down	-1.61E+00	1.07E-52	Down	Unigene48303_All//gi|18399097|ref|NP_564433.1|//1.00E-158//transporter-related [Arabidopsis thaliana] >gi|10086480|gb|AAG12540.1|AC015446_21 Unknown protein [Arabidopsis thaliana] >gi|193788740|gb|ACF20469.1|At1g34020 [Arabidopsis thaliana]	Unigene48303_All//3.00E-140//AT1G34020| transporter-related	Unigene48303_All//0.00E+00//TC176616				nr +
Unigene48305_All	498	29.00	23.81	28.34	27.31	27.04	35.82	44.06	31.89	21.20	-2.84E-01	6.28E-02		-3.33E-02	8.42E-01		-1.44E-02	9.43E-01		3.92E-01	2.81E-03		-4.66E-01	7.49E-06		-1.06E+00	1.84E-22	Down	Unigene48305_All//gi|21592398|gb|AAM64349.1|//2.00E-68//26S proteasome non-ATPase regulatory subunit [Arabidopsis thaliana]	Unigene48305_All//2.00E-66//AT5G23540| 26S proteasome regulatory subunit, putative	Unigene48305_All//0.00E+00//TC147556		ko03050|Proteasome		nr -
Unigene48309_All	1339	12.50	5.30	5.81	18.97	17.87	13.49	10.33	3.96	4.22	-1.24E+00	1.19E-17	Down	-1.11E+00	3.15E-14	Down	-8.62E-02	5.29E-01		-4.92E-01	2.66E-06		-1.38E+00	5.08E-21	Down	-1.29E+00	1.37E-19	Down	Unigene48309_All//gi|270342120|gb|ACZ74703.1|//7.00E-95//carboxilic ester hydrolase [Phaseolus vulgaris]	Unigene48309_All//8.00E-85//AT3G27950| early nodule-specific protein, putative	Unigene48309_All//0.00E+00//gi|78326453|gb|DT546727.1|DT546727				nr -
Unigene48310_All	1661	10.17	3.33	4.68	11.52	8.15	10.06	4.94	8.33	4.82	-1.61E+00	3.64E-26	Down	-1.12E+00	1.26E-14	Down	-4.99E-01	1.81E-05		-1.95E-01	1.63E-01		7.54E-01	2.61E-08		-3.47E-02	8.66E-01		Unigene48310_All//gi|115464761|ref|NP_001055980.1|//1.00E-104//Os05g0506000 [Oryza sativa Japonica Group] >gi|113576531|dbj|BAF17894.1|Os05g0506000 [Oryza sativa Japonica Group]	Unigene48310_All//1.00E-101//AT1G04770| male sterility MS5 family protein	Unigene48310_All//0.00E+00//TC156859				nr -
Unigene48311_All	729	27.34	72.15	44.19	37.58	51.02	61.02	45.76	40.42	136.07	1.40E+00	1.26E-64	Up	6.93E-01	1.69E-12		4.41E-01	5.78E-08		6.99E-01	4.06E-19		-1.79E-01	4.38E-02		1.57E+00	2.19E-180	Up	Unigene48311_All//gi|18390998|ref|NP_563839.1|//2.00E-38//transcription factor [Arabidopsis thaliana] >gi|75278846|sp|Q80482.1|BHLH149_ARATH RecName: Full=Transcription factor bHLH149; AltName: Full=Transcription factor EN 144; AltName: Full=bHLH transcription factor bHLH149; AltName: Full=Basic helix-loop-helix protein 149; Short=bHLH 149; Short=AtbHLH149 >gi|3249098|gb|AAC24081.1| ESTs gb|T04610, gb|N38459, gb|T45174, gb|R30481 and gb|N64971 come from this gene [Arabidopsis thaliana] >gi|27764992|gb|AAO23617.1|At1g09250 [Arabidopsis thaliana]	Unigene48311_All//2.00E-35//AT1G09250| transcription factor	Unigene48311_All//0.00E+00//gi|13246764|gb|BE054359.2|BE054359	bHLH			nr -
Unigene48314_All	2271	1.94	0.18	0.00	3.99	3.82	1.33	13.27	3.17	6.82	-3.44E+00	7.43E-17	Down	-1.09E+01	3.37E-24	Down	-6.32E-02	8.03E-01		-1.58E+00	5.42E-15	Down	-2.07E+00	6.15E-79	Down	-9.60E-01	3.23E-26		Unigene48314_All//gi|224137566|ref|XP_002322614.1|//0.00E+00//auxin efflux carrier component [Populus trichocarpa] >gi|222867244|gb|EEF04375.1| auxin efflux carrier component [Populus trichocarpa]	Unigene48314_All//0.00E+00//AT1G73590| PIN1 (PIN-FORMED 1); transporter	Unigene48314_All//9.00E-142//gi|21101190|gb|BQ413503.1|BQ413503				nr -
Unigene48315_All	823	5.59	3.76	2.52	7.08	8.87	7.90	6.01	3.05	4.65	-5.75E-01	4.13E-02		-1.15E+00	1.22E-04	Down	3.25E-01	1.57E-01		1.58E-01	5.71E-01		-9.80E-01	5.37E-05		-3.71E-01	1.20E-01		Unigene48315_All//gi|15231723|ref|NP_191522.1|//1.00E-65//diphthamide synthesis DPH2 family protein [Arabidopsis thaliana] >gi|19715609|gb|AAL91627.1|AT3g59630/T16L24_180 [Arabidopsis thaliana] >gi|53749154|gb|AAU90062.1|At3g59630 [Arabidopsis thaliana]	Unigene48315_All//1.00E-66//AT3G59630| diphthamide synthesis DPH2 family protein	Unigene48315_All//0.00E+00//gi|48813979|gb|CO115292.1|CO115292				nr -
Unigene48317_All	1000	1.78	8.21	3.09	6.48	6.13	8.04	6.85	1.50	2.83	2.21E+00	2.11E-19	Up	7.96E-01	3.17E-02		-7.93E-02	7.92E-01		3.12E-01	1.57E-01		-2.19E+00	8.60E-20	Down	-1.28E+00	5.32E-10	Down	Unigene48317_All//gi|15239503|ref|NP_197955.1|//1.00E-67//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|71660770|sp|P69781.1|GAT12_ARATH RecName: Full=GATA transcription factor 12	Unigene48317_All//4.00E-52//AT5G25830| zinc finger (GATA type) family protein	Unigene48317_All//0.00E+00//gi|78333320|gb|DT553594.1|DT553594	C2C2-GATA			nr +
Unigene48318_All	1408	0.45	3.42	0.42	1.42	1.71	0.90	3.36	0.53	2.04	2.94E+00	8.16E-16	Up	-1.00E-01	9.15E-01		2.75E-01	5.56E-01		-6.56E-01	1.63E-01		-2.65E+00	2.90E-17	Down	-7.23E-01	2.41E-03		Unigene48318_All//gi|15239503|ref|NP_197955.1|//2.00E-77//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|71660770|sp|P69781.1|GAT12_ARATH RecName: Full=GATA transcription factor 12	Unigene48318_All//2.00E-63//AT5G25830| zinc finger (GATA type) family protein	Unigene48318_All//0.00E+00//gi|78333320|gb|DT553594.1|DT553594	C2C2-GATA			nr -
Unigene48319_All	1328	78.80	38.99	46.59	40.59	35.16	44.25	15.15	11.05	12.72	-1.01E+00	1.90E-77	Down	-7.58E-01	7.46E-46		-2.07E-01	3.19E-03		1.25E-01	1.05E-01		-4.56E-01	2.99E-05		-2.53E-01	2.17E-02		Unigene48319_All//gi|283484355|gb|ADB23407.1|//2.00E-64//chloroplast CGE1 [Physcomitrella patens]	Unigene48319_All//1.00E-46//AT1G36390| co-chaperone grpE family protein	Unigene48319_All//0.00E+00//TC137108				nr +
Unigene48321_All	1274	20.21	5.81	9.91	18.14	12.22	9.93	58.44	20.87	43.03	-1.80E+00	5.70E-46	Down	-1.03E+00	3.40E-19	Down	-5.71E-01	4.08E-08		-8.70E-01	9.14E-15		-1.49E+00	1.63E-122	Down	-4.42E-01	9.84E-17		Unigene48321_All//gi|40781599|gb|AAB89809.1|//1.00E-118//reductase 1 [Hydrangea macrophylla] >gi|40781603|gb|AAB89811.1| reductase 1 [Hydrangea macrophylla]	Unigene48321_All//6.00E-108//AT1G59950| aldo/keto reductase, putative	Unigene48321_All//0.00E+00//TC165057		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene48322_All	1207	11.18	5.46	4.10	7.14	8.67	6.85	7.22	2.77	3.60	-1.04E+00	5.71E-11	Down	-1.45E+00	2.88E-17	Down	2.81E-01	1.33E-01		-6.03E-02	7.89E-01		-1.38E+00	1.55E-13	Down	-1.00E+00	8.86E-09	Down	Unigene48322_All//gi|15236999|ref|NP_192004.1|//1.00E-30//MEE47 (maternal effect embryo arrest 47); transcription factor [Arabidopsis thaliana] >gi|55583995|sp|Q9M160.1|Y4095_ARATH RecName: Full=Uncharacterized protein At4g00950	Unigene48322_All//2.00E-26//AT4G00950| MEE47 (maternal effect embryo arrest 47); transcription factor	Unigene48322_All//0.00E+00//ES829415				nr -
Unigene48324_All	1565	7.42	2.65	2.14	4.04	3.43	1.85	10.97	1.58	22.83	-1.48E+00	3.48E-16	Down	-1.79E+00	4.12E-20	Down	-2.36E-01	3.55E-01		-1.13E+00	1.34E-06	Down	-2.80E+00	1.96E-64	Down	1.06E+00	7.15E-36	Up	Unigene48324_All//gi|301133576|gb|ADK63410.1|//8.00E-11//C3HC4 type zinc finger protein [Brassica rapa]	Unigene48324_All//5.00E-12//AT1G26800| zinc finger (C3HC4-type RING finger) family protein	Unigene48324_All//3.00E-125//DW497343				nr -
Unigene48325_All	1430	2.16	1.13	1.23	6.69	3.73	2.37	15.58	5.11	2.62	-9.29E-01	8.94E-03		-8.13E-01	2.83E-02		-8.42E-01	8.65E-07		-1.50E+00	1.37E-14	Down	-1.61E+00	1.27E-41	Down	-2.57E+00	1.55E-78	Down	Unigene48325_All//gi|297805668|ref|XP_002870718.1|//1.00E-122//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316554|gb|EFH46977.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48325_All//3.00E-96//AT5G40250| zinc finger (C3HC4-type RING finger) family protein	Unigene48325_All//0.00E+00//TC174246				nr -
Unigene48326_All	1656	1.30	1.50	2.28	1.96	7.53	4.47	3.86	1.49	2.89	2.11E-01	6.00E-01		8.18E-01	1.31E-02		1.94E+00	1.03E-28	Up	1.19E+00	3.95E-08	Up	-1.37E+00	4.84E-10	Down	-4.17E-01	4.09E-02		Unigene48326_All//gi|297603691|ref|NP_001054442.2|//4.00E-35//Os03g0110700 [Oryza sativa Japonica Group] >gi|255675950|dbj|BAF16356.2|Os03g0110700 [Oryza sativa Japonica Group]	Unigene48326_All//1.00E-63//AT3G48210| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Kinetochore-Ndc80 complex, subunit Spc25 (InterPro:IPR013225); Has 142 Blast hits to 142 proteins in 51 species: Archae - 0; Bacteria - 2; Metazoa - 61; Fungi - 34; Plants - 34; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).					nr +
Unigene48327_All	490	0.00	0.00	0.00	0.20	0.00	0.18	0.86	3.84	2.93	null	null		null	null		-7.67E+00	3.12E-01		-1.42E-01	9.49E-01		2.15E+00	7.79E-06	Up	1.76E+00	7.26E-04	Up									
Unigene48328_All	1564	0.64	1.43	1.12	1.43	0.55	0.72	14.84	30.28	17.40	1.17E+00	7.67E-03		8.22E-01	1.13E-01		-1.38E+00	7.07E-04	Down	-9.90E-01	2.09E-02		1.03E+00	3.71E-44	Up	2.29E-01	1.43E-02		Unigene48328_All//gi|224139090|ref|XP_002326765.1|//1.00E-20//predicted protein [Populus trichocarpa] >gi|222834087|gb|EEE72564.1| predicted protein [Populus trichocarpa]		Unigene48328_All//9.00E-172//gi|109872057|gb|DW501033.1|DW501033				nr +
Unigene48332_All	1524	12.19	6.22	10.27	4.64	5.20	3.26	1.47	0.47	0.71	-9.71E-01	2.14E-13		-2.47E-01	7.93E-02		1.63E-01	5.20E-01		-5.10E-01	2.12E-02		-1.66E+00	4.68E-05	Down	-1.06E+00	4.30E-03		Unigene48332_All//gi|115455185|ref|NP_001051193.1|//2.00E-90//Os03g0736400 [Oryza sativa Japonica Group] >gi|108710953|gb|ABF98748.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108710954|gb|ABF98749.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549664|dbj|BAF13107.1|Os03g0736400 [Oryza sativa Japonica Group]	Unigene48332_All//2.00E-105//AT3G28460| unknown protein	Unigene48332_All//0.00E+00//TC141657				nr +
Unigene48336_All	790	13.78	7.70	11.32	16.39	15.78	14.24	10.12	4.55	2.98	-8.40E-01	1.39E-06		-2.83E-01	1.40E-01		-5.52E-02	7.99E-01		-2.04E-01	2.43E-01		-1.15E+00	1.29E-09	Down	-1.77E+00	4.41E-18	Down	Unigene48336_All//gi|29839555|sp|Q8L8Q8.1|Y5486_ARATH//4.00E-61//RecName: Full=Uncharacterized protein At5g64816; Flags: Precursor >gi|98961067|gb|ABF59017.1|At5g64816 [Arabidopsis thaliana] >gi|222424148|dbj|BAH20033.1|AT5G64816 [Arabidopsis thaliana]	Unigene48336_All//2.00E-62//AT5G64816| unknown protein	Unigene48336_All//0.00E+00//TC143063				nr -
Unigene4834_All	894	0.70	1.30	1.55	3.29	3.89	4.60	3.17	1.31	1.83	8.92E-01	1.56E-01		1.14E+00	5.84E-02		2.43E-01	5.37E-01		4.84E-01	1.24E-01		-1.28E+00	1.86E-04	Down	-7.94E-01	1.31E-02		Unigene4834_All//gi|240256240|ref|NP_195691.4|//1.00E-84//exonuclease/ nucleic acid binding [Arabidopsis thaliana]	Unigene4834_All//5.00E-81//AT4G39810| exonuclease/ nucleic acid binding					nr -
Unigene48340_All	805	120.96	408.63	207.18	154.21	156.65	162.03	196.90	318.48	156.68	1.76E+00	0.00E+00	Up	7.76E-01	4.73E-76		2.27E-02	7.28E-01		7.14E-02	1.78E-01		6.94E-01	9.00E-121		-3.30E-01	2.08E-20		Unigene48340_All//gi|87240982|gb|AB032840.1|//1.00E-111//Peptidase C1A, papain; Somatotropin hormone; Peptidase C1, propeptide [Medicago truncatula]	Unigene48340_All//4.00E-94//AT1G02305| cathepsin B-like cysteine protease, putative	Unigene48340_All//0.00E+00//gi|13356171|gb|BG446519.1|BG446519				nr +
Unigene48341_All	394	74.50	42.18	79.74	23.90	23.60	18.46	8.16	3.82	3.54	-8.21E-01	8.75E-16		9.81E-02	3.91E-01		-1.81E-02	9.37E-01		-3.73E-01	5.34E-02		-1.09E+00	4.62E-04	Down	-1.20E+00	8.77E-05	Down	Unigene48341_All//gi|297810295|ref|XP_002873031.1|//1.00E-07//legume lectin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318868|gb|EFH49290.1| legume lectin family protein [Arabidopsis lyrata subsp. lyrata]		Unigene48341_All//0.00E+00//gi|13245882|gb|BE054695.2|BE054695				nr +

Unigene48342_All	1533	25.87	14.68	16.78	6.40	4.69	5.74	8.22	4.25	2.55	-8.18E-01	6.13E-21		-6.25E-01	8.69E-13		-4.47E-01	1.07E-02		-1.56E-01	4.77E-01		-9.50E-01	6.03E-11		-1.69E+00	2.06E-26	Down	Unigene48342_All//gi|15240888|ref|NP_195729.1|//5.00E-69//legume lectin family protein [Arabidopsis thaliana] >gi|6759432|emb|CAB69837.1| lectin-like protein [Arabidopsis thaliana] >gi|110736881|dbj|BAF00398.1| lectin - like protein [Arabidopsis thaliana]	Unigene48342_All//3.00E-61//AT5G01090| legume lectin family protein	Unigene48342_All//0.00E+00//TC166717				nr -
Unigene48344_All	1272	20.53	16.33	9.80	96.93	114.54	80.99	23.53	27.11	80.65	-3.30E-01	2.18E-03		-1.07E+00	1.23E-20	Down	2.41E-01	6.70E-10		-2.59E-01	7.03E-09		2.04E-01	1.73E-02		1.78E+00	8.00E-222	Up	Unigene48344_All//gi|224131780|ref|XP_002328106.1|//1.00E-103//f-box family protein [Populus trichocarpa] >gi|22283762|gb|EEE75986.1| f-box family protein [Populus trichocarpa]	Unigene48344_All//3.00E-64//AT2G27310| F-box family protein	Unigene48344_All//8.00E-33//TC144688				nr +
Unigene48346_All	639	31.85	35.13	34.08	52.00	44.19	44.60	90.45	58.02	40.40	1.41E-01	2.69E-01		9.77E-02	4.82E-01		-2.35E-01	1.09E-02		-2.21E-01	2.27E-02		-6.41E-01	2.53E-24		-1.16E+00	2.56E-67	Down	Unigene48346_All//gi|282848216|gb|AB802889.1|//5.00E-42//small nuclear ribonucleoprotein polypeptide [Jatropha curcas]	Unigene48346_All//1.00E-40//AT4G30330| small nuclear ribonucleoprotein E, putative / snRNP-E, putative / Sm protein E, putative	Unigene48346_All//0.00E+00//gi|164314344|gb|ES848836.1|ES848836		ko03040|Spliceosome		nr -
Unigene48347_All	1956	9.31	5.03	4.93	8.38	7.36	8.34	6.85	3.21	3.54	-8.89E-01	1.87E-11		-9.18E-01	1.71E-11		-1.87E-01	2.13E-01		-7.50E-03	9.55E-01		-1.10E+00	1.95E-14	Down	-9.51E-01	5.51E-12		Unigene48347_All//gi|8886946|gb|AAF80632.1|AC069251_25/1.00E-42//F2D10.26 [Arabidopsis thaliana] >gi|38454150|gb|AAR20769.1| At1g20770 [Arabidopsis thaliana] >gi|41349930|gb|AAO90350.1| At1g20770 [Arabidopsis thaliana]	Unigene48347_All//4.00E-43//AT1G20770| unknown protein	Unigene48347_All//0.00E+00//TC149434				nr -
Unigene48348_All	1187	3.31	6.06	4.08	3.27	4.41	2.78	2.46	3.49	5.81	8.75E-01	6.84E-05		3.04E-01	3.11E-01		4.30E-01	1.08E-01		-2.37E-01	4.96E-01		5.04E-01	6.35E-02		1.24E+00	1.42E-09	Up	Unigene48348_All//gi|30695663|ref|NP_199751.2|//4.00E-31//zinc knuckle (CCHC-type) family protein [Arabidopsis thaliana] >gi|38603954|gb|AAR24722.1| At5g49400 [Arabidopsis thaliana] >gi|44681446|gb|AAS47663.1| At5g49400 [Arabidopsis thaliana]	Unigene48348_All//1.00E-14//AT5G49400| zinc knuckle (CCHC-type) family protein	Unigene48348_All//4.00E-130//DW242358				nr +
Unigene48349_All	866	92.14	61.67	45.99	221.92	234.13	149.57	78.36	15.11	20.93	-5.79E-01	7.15E-23		-1.00E+00	4.66E-56	Down	7.73E-02	4.26E-02		-5.69E-01	1.33E-56		-2.38E+00	3.51E-210	Down	-1.90E+00	1.99E-163	Down	Unigene48349_All//gi|21703131|gb|AAM74506.1|//1.00E-57//AT5g16250/T21H19_170 [Arabidopsis thaliana] >gi|23505791|gb|AAN28755.1| At5g16250/T21H19_170 [Arabidopsis thaliana]	Unigene48349_All//2.00E-59//AT5G16250| unknown protein	Unigene48349_All//0.00E+00//gi|109887612|gb|DW516581.1|DW516581				nr +
Unigene4835_All	1332	0.00	0.08	0.00	17.32	9.62	7.60	1.59	0.63	0.36	6.25E+00	3.86E-01		null	null		-8.48E-01	7.66E-16		-1.19E+00	2.81E-24	Down	-1.34E+00	9.81E-04	Down	-2.14E+00	1.01E-06	Down	Unigene4835_All//gi|224062135|ref|XP_002300772.1|//2.00E-97//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842498|gb|EEE80045.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene4835_All//8.00E-68//AT4G28530| anac074 (Arabidopsis NAC domain containing protein 74); transcription factor	Unigene4835_All//0.00E+00//TC145142	NAC			nr +
Unigene48350_All	1059	13.73	2.30	4.17	17.69	13.23	8.53	16.53	7.30	3.31	-2.58E+00	5.04E-41	Down	-1.72E+00	1.12E-23	Down	-4.18E-01	4.74E-04		-1.05E+00	2.29E-16	Down	-1.18E+00	8.30E-21	Down	-2.32E+00	7.59E-55	Down	Unigene48350_All//gi|10946427|gb|AAG24908.1|AF305075_1/1.00E-137//proliferating cell nuclear antigen [Nicotiana benthamiana]	Unigene48350_All//3.00E-125//AT2G29570| PCNA2 (PROLIFERATING CELL NUCLEAR ANTIGEN 2); DNA binding / DNA polymerase processivity factor	Unigene48350_All//0.00E+00//TC151943		ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03430|Mismatch repair		nr -
Unigene48351_All	1711	1.53	8.35	1.53	4.72	7.37	4.80	9.44	11.73	15.67	2.45E+00	1.08E-37	Up	-3.80E-03	9.92E-01		6.43E-01	1.68E-05		2.65E-02	9.29E-01		3.13E-01	5.20E-03		7.31E-01	5.82E-15		Unigene48351_All//gi|18408953|ref|NP_566927.1|//1.00E-156//U-box domain-containing protein [Arabidopsis thaliana] >gi|122163922|sp|Q6S8P4.1|PUB30_ARATH RecName: Full=U-box domain-containing protein 30; AltName: Full=Plant U-box protein 30 >gi|115646761|gb|ABJ17109.1| At5g49810 [Arabidopsis thaliana]	Unigene48351_All//7.00E-134//AT5G65920| U-box domain-containing protein	Unigene48351_All//0.00E+00//TC134039				nr -
Unigene48352_All	1586	11.88	15.56	9.47	13.79	15.39	15.46	22.47	9.59	17.01	3.90E-01	4.01E-04		-3.27E-01	1.57E-02		1.59E-01	1.95E-01		1.65E-01	1.86E-01		-1.23E+00	2.81E-44	Down	-4.02E-01	2.81E-07		Unigene48352_All//gi|225444450|ref|XP_002271487.1|//1.00E-146//PREDICTED: similar to tobamovirus multiplication 1 [Vitis vinifera]	Unigene48352_All//4.00E-121//AT4G21790| TOM1 (TOBAMOVIRUS MULTIPLICATION 1); protein binding	Unigene48352_All//0.00E+00//TC142126				nr -
Unigene48354_All	1211	2.94	2.30	0.70	3.70	5.54	4.36	7.26	2.38	4.84	-3.52E-01	2.97E-01		-2.06E+00	8.90E-08	Down	5.83E-01	8.05E-03		2.37E-01	4.23E-01		-1.61E+00	6.48E-17	Down	-5.87E-01	4.90E-04		Unigene48354_All//gi|15223725|ref|NP_173427.1|//6.00E-60//cytomatrix protein-related [Arabidopsis thaliana]	Unigene48354_All//1.00E-56//AT1G19980| cytomatrix protein-related	Unigene48354_All//0.00E+00//TC141870				nr +
Unigene48357_All	1726	7.94	7.49	3.70	4.79	5.55	3.51	0.73	0.22	0.67	-8.53E-02	6.09E-01		-1.10E+00	1.14E-11	Down	2.11E-01	3.06E-01		-4.50E-01	2.72E-02		-1.75E+00	2.19E-03		-1.35E-01	7.87E-01		Unigene48357_All//gi|4903018|dbj|BAA77842.1|//0.00E+00//ACE [Arabidopsis thaliana]	Unigene48357_All//0.00E+00//AT1G72970| HTH (HOTHEAD); FAD binding / aldehyde-lyase/ mandelonitrile lyase	Unigene48357_All//0.00E+00//TC137800		ko00460|Cyanoamino acid metabolism		nr +
Unigene48359_All	1519	11.33	7.21	8.45	15.18	12.51	12.73	16.51	9.58	6.79	-6.53E-01	1.04E-06		-4.24E-01	2.42E-03		-2.79E-01	1.26E-02		-2.55E-01	3.16E-02		-7.86E-01	2.12E-15		-1.28E+00	1.81E-34	Down	Unigene48359_All//gi|224106087|ref|XP_002314038.1|//1.00E-173//actin related protein [Populus trichocarpa] >gi|222850446|gb|EEE87993.1| actin related protein [Populus trichocarpa]	Unigene48359_All//1.00E-172//AT3G60830| ATARP7 (ACTIN-RELATED PROTEIN 7); structural constituent of cytoskeleton	Unigene48359_All//0.00E+00//TC140769		ko04145|Phagosome		nr -
Unigene48361_All	1184	22.27	16.82	15.65	11.78	12.22	11.82	2.82	0.74	0.74	-4.05E-01	1.28E-04		-5.09E-01	3.00E-06		5.23E-02	8.03E-01		5.40E-03	9.73E-01		-1.93E+00	1.22E-08	Down	-1.93E+00	5.68E-09	Down	Unigene48361_All//gi|224119114|ref|XP_002331328.1|//1.00E-85//chalcone isomerase-like protein [Populus trichocarpa] >gi|22873991|gb|EEF11042.1| chalcone isomerase-like protein [Populus trichocarpa]	Unigene48361_All//8.00E-73//AT1G53520| chalcone-flavanone isomerase-related	Unigene48361_All//0.00E+00//TC170630		ko00941|Flavonoid biosynthesis		nr +
Unigene48364_All	1157	0.63	3.59	2.62	1.98	2.08	1.01	1.50	2.42	0.72	2.50E+00	1.12E-11	Up	2.05E+00	1.04E-06	Up	7.31E-02	8.78E-01		-9.65E-01	2.24E-02		6.92E-01	3.98E-02		-1.05E+00	1.45E-02		Unigene48364_All//gi|19698448|gb|AAL93152.1|AF485266_1/0.00E+00//gaiacol peroxidase [Gossypium hirsutum]	Unigene48364_All//1.00E-140//AT2G22420| peroxidase 17 (PER17) (P17)	Unigene48364_All//0.00E+00//TC133852		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene48365_All	1130	2.13	2.33	1.13	3.26	1.74	2.20	3.11	1.33	2.96	1.31E-01	7.25E-01		-9.13E-01	3.42E-02		-9.09E-01	2.37E-03		-5.70E-01	7.96E-02		-1.22E+00	4.85E-05	Down	-6.85E-02	8.17E-01		Unigene48365_All//gi|62734377|gb|AAX96486.1|//1.00E-51//expressed protein [Oryza sativa Japonica Group] >gi|77548902|gb|ABA91699.1| expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene48365_All//2.00E-69//AT5G09580| unknown protein	Unigene48365_All//6.00E-120//ES835743				nr -
Unigene48366_All	1360	87.95	32.75	67.11	19.12	16.03	11.92	4.41	1.38	2.72	-1.43E+00	5.16E-151	Down	-3.90E-01	3.84E-16		-2.55E-01	1.60E-02		-6.82E-01	4.91E-11		-1.67E+00	1.92E-12	Down	-6.96E-01	8.40E-04		Unigene48366_All//gi|30696124|ref|NP_564718.2|//2.00E-98//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana]	Unigene48366_All//9.00E-100//AT1G56500| haloacid dehalogenase-like hydrolase family protein	Unigene48366_All//0.00E+00//TC154714		ko00740|Riboflavin metabolism		nr -
Unigene48368_All	1792	30.80	25.50	29.77	32.52	28.36	25.58	32.23	18.99	15.65	-2.72E-01	1.39E-04		-4.90E-02	5.92E-01		-1.98E-01	3.43E-03		-3.46E-01	2.11E-07		-7.64E-01	8.74E-33		-1.04E+00	1.83E-56	Down	Unigene48368_All//gi|210110272|gb|ACJ07139.1|//1.00E-168//malonyl-CoA:ACP transacylase 1-3 [Arachis hypogaea]	Unigene48368_All//8.00E-165//AT2G30200| [acyl-carrier-protein] S-malonyltransferase/ binding / catalytic/ transferase	Unigene48368_All//0.00E+00//TC141737		ko00061|Fatty acid biosynthesis		nr +
Unigene48370_All	1411	2.56	3.91	4.68	10.73	9.79	11.49	67.75	143.63	108.25	6.13E-01	1.56E-02		8.71E-01	2.62E-04		-1.33E-01	4.25E-01		9.85E-02	5.73E-01		1.08E+00	3.37E-203	Up	6.76E-01	1.05E-70		Unigene48370_All//gi|259121381|gb|ACV92010.1|//7.00E-82//WRKY transcription factor 8 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene48370_All//1.00E-61//AT1G29280| WRKY65; transcription factor	Unigene48370_All//0.00E+00//TC136977	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene48371_All	1753	6.36	8.35	4.83	6.31	7.39	3.30	18.02	5.91	17.91	3.94E-01	7.67E-03		-3.96E-01	2.81E-02		2.28E-01	1.79E-01		-9.36E-01	2.82E-08		-1.61E+00	1.07E-58	Down	-8.70E-03	9.50E-01		Unigene48371_All//gi|297825631|ref|XP_002880698.1|//1.00E-176//sulfate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326537|gb|EFH56957.1| sulfate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene48371_All//4.00E-168//AT2G25680| MOT1 (molybdate transporter 1); molybdate ion transmembrane transporter/ sulfate transmembrane transporter	Unigene48371_All//2.00E-111//TC165538				nr +
Unigene48373_All	663	13.57	41.96	24.34	48.46	39.53	32.63	130.03	98.22	75.29	1.63E+00	6.15E-43	Up	8.42E-01	5.54E-09		-2.94E-01	1.18E-03		-5.71E-01	5.39E-10		-4.05E-01	5.11E-16		-7.88E-01	1.11E-52		Unigene48373_All//gi|129613|sp|P05993.1|PAPA5_CARPA//3.00E-25//RecName: Full=Cysteine proteinase; AltName: Full=Clone PLBPC13 >gi|18098|emb|CAA27609.1| pot. cysteine proteinase [Carica papaya]	Unigene48373_All//4.00E-23//AT4G39090| RD19 (RESPONSIVE TO DEHYDRATION 19); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene48373_All//0.00E+00//TC131520				nr -
Unigene48379_All	1470	4.77	4.27	2.72	15.93	17.76	24.76	2.19	0.91	4.39	-1.58E-01	5.13E-01		-8.12E-01	4.24E-04		1.57E-01	1.83E-01		6.37E-01	1.94E-13		-1.26E+00	6.77E-05	Down	1.01E+00	1.06E-06	Up	Unigene48379_All//gi|15225663|ref|NP_181552.1|//1.00E-163//transferase family protein [Arabidopsis thaliana]	Unigene48379_All//4.00E-151//AT2G40230| transferase family protein	Unigene48379_All//0.00E+00//gi|78338918|gb|DT559192.1|DT559192		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene4838_All	1278	5.77	2.78	4.13	8.93	7.76	13.78	9.16	3.53	4.27	-1.06E+00	1.51E-06	Down	-4.85E-01	3.25E-02		-2.02E-01	2.78E-01		6.27E-01	1.15E-06		-1.38E+00	8.03E-18	Down	-1.10E+00	3.14E-13	Down	Unigene4838_All//gi|18416821|ref|NP_567757.1|//6.00E-75//AR192; adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization [Arabidopsis thaliana] >gi|21593024|gb|AAM64973.1| grpE like protein [Arabidopsis thaliana]	Unigene4838_All//3.00E-76//AT4G26780| AR192; adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization	Unigene4838_All//0.00E+00//TC140730				nr -
Unigene48380_All	1170	111.84	50.50	105.41	30.48	30.43	12.24	0.00	0.04	0.00	-1.15E+00	6.69E-118	Down	-8.55E-02	9.99E-02		-2.50E-03	9.78E-01		-1.32E+00	1.15E-43	Down	5.16E+00	6.34E-01		null	null		Unigene48380_All//gi|15228157|ref|NP_178536.1|//1.00E-135//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75206255|sp|Q9SJB4.1|GDL34_ARATH RecName: Full=GDSL esterase/lipase At2g04570; AltName: Full=Extracellular lipase At2g04570; Flags: Precursor	Unigene48380_All//2.00E-136//AT2G04570| GDSL-motif lipase/hydrolase family protein	Unigene48380_All//0.00E+00//TC133133				nr -

Unigene48381_All	1225	0.85	14.68	4.13	3.94	2.92	4.76	1.69	2.66	4.72	4.10E+00	8.63E-77	Up	2.27E+00	3.43E-12	Up	-4.32E-01	1.13E-01		2.70E-01	3.29E-01		6.54E-01	3.37E-02		1.48E+00	2.11E-10	Up	Unigene48381_All//gi|15219028|ref|NP_175665.1|//2.00E-65//26.5 kDa class I small heat shock protein-like (HSP26.5-P) [Arabidopsis thaliana] >gi|75313824|sp|Q9SSQ8.1|HS26M_ARATH RecName: Full=26.5 kDa heat shock protein, mitochondrial; Short=AtHsp26.5; Flags: Precursor >gi|5903049|gb|AAD55608.1|AC008016_18 Similar to gb|X07187 heat shock protein 21 precursor from Pisum sativum and is a member of the PF|00011 HSP20|alpha crystallin family [Arabidopsis thaliana] >gi|38566632|gb|AAR24206.1|At1g52560 [Arabidopsis thaliana] >gi|40824092|gb|AAR92344.1|At1g52560 [Arabidopsis thaliana]	Unigene48381_All//1.00E-62//AT1G52560| 26.5 kDa class I small heat shock protein-like (HSP26.5-P)	Unigene48381_All//0.00E+00//DW235723				nr +
Unigene48383_All	2145	1.71	1.28	0.12	7.80	4.54	3.56	16.70	13.78	3.81	-4.21E-01	2.01E-01		-3.78E+00	1.75E-14	Down	-7.80E-01	4.01E-10		-1.13E+00	1.73E-16	Down	-2.77E-01	6.31E-04		-2.13E+00	2.24E-100	Down	Unigene48383_All//gi|15232315|ref|NP_188700.1|//3.00E-90//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|75299591|sp|Q8GX73.1|BH123_ARATH RecName: Full=Transcription factor bHLH123; AltName: Full=Transcription factor EN 63; AltName: Full=bHLH transcription factor bHLH123; AltName: Full=Basic helix-loop-helix protein 123; Short=bHLH 123; Short=AtbHLH123	Unigene48383_All//3.00E-76//AT3G20640| ethylene-responsive protein -related	Unigene48383_All//0.00E+00//TC167595	bHLH			nr -
Unigene48384_All	2046	7.11	4.11	2.37	21.21	18.46	7.88	7.19	1.12	1.64	-7.90E-01	9.27E-08		-1.59E+00	3.62E-21	Down	-2.00E-01	1.32E-02		-1.43E+00	5.57E-60	Down	-2.68E+00	9.19E-53	Down	-2.14E+00	8.40E-42	Down	Unigene48384_All//gi|297798774|ref|XP_002867271.1|//1.00E-174//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313107|gb|EFH43530.1|armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48384_All//8.00E-159//AT4G31890| armadillo/beta-catenin repeat family protein	Unigene48384_All//0.00E+00//TC171693				nr +
Unigene48385_All	966	11.37	11.28	3.80	14.70	13.69	19.26	16.24	16.10	42.02	-1.23E-02	9.66E-01		-1.58E+00	4.79E-16	Down	-1.03E-01	5.71E-01		3.90E-01	2.27E-03		-1.27E-02	9.54E-01		1.37E+00	8.78E-61	Up	Unigene48385_All//gi|222423782|dbj|BAH19857.1|//7.00E-26//AT5G18310 [Arabidopsis thaliana]	Unigene48385_All//8.00E-22//AT5G18310| unknown protein	Unigene48385_All//0.00E+00//gi|164263297|gb|ES811388.1|ES811388				nr -
Unigene48386_All	2382	0.64	0.55	0.58	7.61	5.81	3.15	8.79	1.40	1.56	-2.04E-01	6.81E-01		-1.32E-01	8.01E-01		-3.89E-01	1.55E-03		-1.27E+00	2.33E-21	Down	-2.65E+00	8.50E-74	Down	-2.50E+00	2.28E-71	Down	Unigene48386_All//gi|2911040|emb|CAA17550.1|//0.00E+00//receptor protein kinase-like protein [Arabidopsis thaliana] >gi|7270372|emb|CAB80139.1|receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene48386_All//0.00E+00//AT4G34220| leucine-rich repeat transmembrane protein kinase, putative	Unigene48386_All//0.00E+00//gi|78336484|gb|DT556758.1|DT556758		ko04626|Plant-pathogen interaction		nr -
Unigene48387_All	1447	0.90	2.91	0.74	0.83	0.71	0.94	29.07	71.81	25.88	1.68E+00	2.01E-07	Up	-2.97E-01	6.25E-01		-2.11E-01	7.52E-01		1.81E-01	7.57E-01		1.30E+00	6.17E-140	Up	-1.68E-01	2.57E-02		Unigene48387_All//gi|15228909|ref|NP_188316.1|//0.00E+00//AAE7 (ACYL-ACTIVATING ENZYME 7); AMP binding / acetate-CoA ligase [Arabidopsis thaliana] >gi|20799723|gb|AAM28624.1|AF503766_1 adenosine monophosphate binding protein 7 AMPBP7 [Arabidopsis thaliana] >gi|18086379|gb|AAL57649.1|AT3g16910/K14A17_3 [Arabidopsis thaliana] >gi|19699128|gb|AAL90930.1|AT3g16910/K14A17_3 [Arabidopsis thaliana]	Unigene48387_All//0.00E+00//AT3G16910| AAE7 (ACYL-ACTIVATING ENZYME 7); AMP binding / acetate-CoA ligase	Unigene48387_All//0.00E+00//gi|78342648|gb|DT562922.1|DT562922		ko00940|Phenylpropanoid biosynthesis//ko04146|Peroxisome//ko00360|Phenylalanine metabolism//ko00071|Fatty acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene48388_All	849	21.69	49.06	21.07	48.58	72.48	131.07	39.64	65.38	68.88	1.18E+00	2.21E-39	Up	-4.17E-02	7.74E-01		5.77E-01	1.10E-20		1.43E+00	1.69E-151	Up	7.22E-01	1.20E-28		7.97E-01	1.61E-36				Unigene48388_All//0.00E+00//TC153565				ESTscan +
Unigene48389_All	1980	1.06	0.82	0.56	1.06	0.77	2.26	1.58	3.34	5.73	-3.68E-01	4.01E-01		-9.04E-01	5.29E-02		-4.66E-01	3.11E-01		1.10E+00	1.35E-04	Up	1.08E+00	2.52E-07	Up	1.86E+00	7.92E-27	Up	Unigene48389_All//gi|290766481|gb|ADD60243.1|//0.00E+00//rubisco activase [Glycine max]	Unigene48389_All//0.00E+00//AT2G39730| RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	Unigene48389_All//0.00E+00//TC161473		ko03050|Proteasome		nr -
Unigene4839_All	594	2.03	2.30	2.42	1.01	2.03	3.57	2.92	1.97	3.35	1.85E-01	7.28E-01		2.57E-01	6.27E-01		1.01E+00	1.11E-01		1.83E+00	1.26E-04	Up	-5.67E-01	2.16E-01		2.01E-01	6.34E-01		Unigene4839_All//gi|9955581|emb|CAC05508.1|//3.00E-49//thioredoxin-like protein [Arabidopsis thaliana]	Unigene4839_All//4.00E-48//AT5G04260| WCRKC2 (WCRKC THIOREDOXIN 2)	Unigene4839_All//0.00E+00//gi|13356226|gb|BG446574.1|BG446574				nr +
Unigene48390_All	4184	0.16	0.41	0.38	1.27	1.52	1.24	1.62	5.46	11.48	1.34E+00	9.43E-03		1.23E+00	2.70E-02		2.57E-01	3.20E-01		-3.74E-02	9.09E-01		1.76E+00	3.07E-48	Up	2.83E+00	5.50E-184	Up	Unigene48390_All//gi|124359162|gb|ABN05685.1|//2.00E-61//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene48390_All//1.00E-18//AT1G43760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706), Endonuclease/exonuclease/phosphatase (InterPro:IPR005135); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40390.1); Has 2614 Blast hits to 2551 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 1517; Fungi - 2; Plants - 1086; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene48390_All//5.00E-37//ES792704				nr -
Unigene48392_All	734	155.68	111.90	186.01	130.17	205.81	154.56	137.96	51.08	42.17	-4.76E-01	5.90E-23		2.57E-01	1.08E-08		6.61E-01	5.56E-64		2.48E-01	1.39E-07		-1.43E+00	1.02E-157	Down	-1.71E+00	7.65E-210	Down	Unigene48392_All//gi|221271520|dbj|BAH15071.1|//3.00E-67//indole-3-acetic acid 14 transcription factor like [Malus prunifolia]	Unigene48392_All//3.00E-56//AT4G14550| IAA14 (INDOLE-3-ACETIC ACID INDUCIBLE 14); protein binding / transcription factor/ transcription repressor	Unigene48392_All//0.00E+00//TC150099				nr -
Unigene48394_All	2044	1.56	1.71	0.65	6.73	5.07	7.53	5.46	5.23	11.01	1.32E-01	6.86E-01		-1.26E+00	7.05E-04	Down	-4.08E-01	4.84E-03		1.64E-01	3.24E-01		-6.10E-02	7.30E-01		1.01E+00	2.21E-21	Up	Unigene48394_All//gi|297720585|ref|NP_001172654.1|//2.00E-27//Os01g0850200 [Oryza sativa Japonica Group] >gi|20166570|dbj|BAB89518.1| zinc finger protein-like [Oryza sativa Japonica Group] >gi|20805170|dbj|BAB92839.1| zinc finger protein-like [Oryza sativa Japonica Group] >gi|255673877|dbj|BAH91384.1|Os01g0850200 [Oryza sativa Japonica Group]	Unigene48394_All//2.00E-23//AT2G34200| zinc finger (C3HC4-type RING finger) family protein	Unigene48394_All//0.00E+00//DW511249				nr +
Unigene48401_All	1032	41.62	92.45	102.42	66.56	99.97	130.19	99.10	132.15	87.48	1.15E+00	2.90E-86	Up	1.30E+00	1.62E-112	Up	5.87E-01	1.75E-35		9.68E-01	1.84E-98		4.15E-01	5.42E-26		-1.80E-01	7.33E-05		Unigene48401_All//gi|4666311|dbj|BAA77218.1|//1.00E-98//LON protease homologue [Lithospermum erythrorhizon]	Unigene48401_All//3.00E-99//AT5G47040| LON2 (LON PROTEASE 2); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase	Unigene48401_All//0.00E+00//TC163653				nr -
Unigene48403_All	1338	15.56	7.12	12.14	6.11	7.15	5.30	0.98	0.75	1.40	-1.13E+00	7.24E-19	Down	-3.59E-01	4.66E-03		2.29E-01	2.70E-01		-2.04E-01	3.89E-01		-3.86E-01	4.87E-01		5.15E-01	2.17E-01		Unigene48403_All//gi|115482594|ref|NP_001064890.1|//1.00E-151//Os10g0484700 [Oryza sativa Japonica Group] >gi|110289290|gb|AAP54338.2|aminotransferase, classes I and II family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639499|dbj|BAF26804.1|Os10g0484700 [Oryza sativa Japonica Group]	Unigene48403_All//6.00E-69//AT1G77670| aminotransferase class I and II family protein	Unigene48403_All//0.00E+00//TC179514				nr +
Unigene48406_All	1676	3.34	6.23	3.27	8.71	6.02	7.73	9.79	14.44	24.22	8.99E-01	5.39E-07		-2.96E-02	9.24E-01		-5.33E-01	8.70E-05		-1.71E-01	3.10E-01		5.61E-01	1.41E-08		1.31E+00	1.64E-56	Up	Unigene48406_All//gi|87240364|gb|ABD32222.1|//1.00E-126//Thioredoxin fold [Medicago truncatula]	Unigene48406_All//6.00E-104//AT5G39865| glutaredoxin family protein	Unigene48406_All//0.00E+00//TC169726				nr +
Unigene48407_All	909	60.55	85.56	65.73	87.08	76.75	80.54	178.42	117.43	85.68	4.99E-01	3.56E-17		1.18E-01	1.34E-01		-1.82E-01	1.35E-03		-1.13E-01	8.26E-02		-6.04E-01	4.25E-60		-1.06E+00	5.02E-161	Down	Unigene48407_All//gi|297841401|ref|XP_002888582.1|//2.00E-58//proteasome maturation factor UMP1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334423|gb|EFH64841.1|proteasome maturation factor UMP1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48407_All//9.00E-57//AT1G67250| proteasome maturation factor UMP1 family protein	Unigene48407_All//0.00E+00//TC157784		ko03050|Proteasome		nr -
Unigene48409_All	986	14.86	44.66	15.34	27.69	23.61	34.67	22.30	39.63	36.81	1.59E+00	3.27E-65	Up	4.59E-02	7.75E-01		-2.30E-01	2.79E-02		3.25E-01	3.63E-04		8.30E-01	9.27E-26		7.23E-01	1.44E-19		Unigene48409_All//gi|4104242|gb|AAD01982.1|//1.00E-107//palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]	Unigene48409_All//1.00E-74//AT1G08510| FATB (fatty acyl-ACP thioesterases B); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase	Unigene48409_All//0.00E+00//TC129652		ko00061|Fatty acid biosynthesis		nr -
Unigene48411_All	1023	4.71	9.61	6.77	6.67	6.83	6.84	6.49	5.97	4.63	1.03E+00	4.11E-08	Up	5.24E-01	2.47E-02		3.46E-02	9.02E-01		3.67E-02	9.02E-01		-1.21E-01	6.33E-01		-4.86E-01	1.41E-02		Unigene48411_All//gi|297822505|ref|XP_002879135.1|//2.00E-73//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324974|gb|EFH55394.1|nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene48411_All//1.00E-72//AT2G27790| nucleic acid binding / nucleotide binding	Unigene48411_All//0.00E+00//TC140645				nr +
Unigene48413_All	963	5.54	7.31	5.53	9.83	7.29	4.55	12.64	12.15	9.39	4.00E-01	7.60E-02		-3.20E-03	9.89E-01		-4.30E-01	1.72E-02		-1.11E+00	2.59E-09	Down	-5.73E-02	7.28E-01		-4.29E-01	2.34E-03				Unigene48413_All//0.00E+00//gi|193218011|gb|EY197188.1|EY197188				
Unigene48414_All	1630	19.48	17.87	10.23	4.68	10.82	5.98	1.35	0.74	6.04	-1.24E-01	2.37E-01		-9.30E-01	5.01E-20		1.21E+00	1.27E-20	Up	3.56E-01	6.32E-02		-8.59E-01	2.61E-02		2.16E+00	2.99E-28	Up	Unigene48414_All//gi|15219594|ref|NP_171890.1|//2.00E-88//transferase family protein [Arabidopsis thaliana] >gi|4204295|gb|AAD10676.1|Hypothetical protein [Arabidopsis thaliana]	Unigene48414_All//1.00E-83//AT1G03940| transferase family protein	Unigene48414_All//0.00E+00//ES828069				nr +

Unigene48416_All	1021	1.43	2.43	1.20	2.10	2.33	1.42	3.64	1.11	1.13	7.61E-01	5.91E-02		-2.58E-01	6.23E-01		1.50E-01	7.83E-01		-5.68E-01	2.16E-01		-1.72E+00	2.77E-08	Down	-1.69E+00	2.23E-08	Down	Unigene48416_All//gi|62816284|emb|CAD47810.2|//1.00E-124//hydroxypheny|pyruvate reductase (HPPR) [Solenostemon scutellarioides]	Unigene48416_All//1.00E-113//AT1G79870| oxidoreductase family protein	Unigene48416_All//0.00E+00//TC173357		ko00620|Pyruvate metabolism//ko00260|Glycine, serine and threonine metabolism//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene48417_All	834	11.86	5.59	11.62	47.90	45.38	38.77	12.47	6.77	5.06	-1.09E+00	7.67E-09	Down	-2.91E-02	8.92E-01		-7.82E-02	4.55E-01		-3.05E-01	2.56E-04		-8.82E-01	3.39E-08		-1.30E+00	3.81E-15	Down	Unigene48417_All//gi|3319353|gb|AAC26242.1|//7.00E-94//contains similarity to copper-binding proteins [Arabidopsis thaliana] >gi|45732728|gb|AAS76262.1| At5g26330 [Arabidopsis thaliana]	Unigene48417_All//1.00E-46//AT5G26330| plastocyanin-like domain-containing protein / mavicyanin, putative	Unigene48417_All//0.00E+00//TC176438				nr -
Unigene48419_All	589	19.63	50.50	36.89	2.11	2.63	7.97	2.58	2.77	5.34	1.36E+00	2.10E-35	Up	9.10E-01	1.94E-13		3.15E-01	5.97E-01		1.92E+00	4.32E-10	Up	9.89E-02	8.36E-01		1.05E+00	6.60E-04	Up	Unigene48419_All//gi|28372884|gb|AO39924.1|//1.00E-22//At4g04630 [Arabidopsis thaliana]	Unigene48419_All//3.00E-18//AT4G04630| unknown protein					nr +
Unigene4842_All	716	21.26	44.09	23.28	31.93	30.97	67.81	48.72	73.32	58.03	1.05E+00	3.71E-25	Up	1.31E-01	3.95E-01		-4.41E-02	7.84E-01		1.09E+00	3.14E-43	Up	5.90E-01	3.18E-19		2.53E-01	5.61E-04			Unigene4842_All//0.00E+00//gi|21089207|gb|BQ401520.1|BQ401520					
Unigene48420_All	1241	4.60	12.82	13.90	0.48	0.44	1.64	1.57	0.40	1.61	1.48E+00	1.03E-21	Up	1.60E+00	2.38E-25	Up	-1.18E-01	8.76E-01		1.77E+00	2.78E-04	Up	-1.96E+00	2.03E-05	Down	3.45E-02	9.55E-01		Unigene48420_All//gi|28372884|gb|AO39924.1|//1.00E-30//At4g04630 [Arabidopsis thaliana]	Unigene48420_All//3.00E-26//AT4G04630| unknown protein					nr -
Unigene48426_All	1089	6.58	14.47	8.12	13.86	14.04	13.48	13.32	11.74	11.05	1.14E+00	1.47E-14	Up	3.02E-01	1.50E-01		1.86E-02	9.24E-01		-4.03E-02	8.11E-01		-1.81E-01	2.18E-01		-2.70E-01	4.11E-02		Unigene48426_All//gi|225427310|ref|XP_002282053.1|//8.00E-61//PREDICTED: similar to pentatricopeptide repeat-containing protein At1g32415 [Vitis vinifera]	Unigene48426_All//9.00E-46//AT1G32410| vacuolar protein sorting 55 family protein / VPS55 family protein	Unigene48426_All//0.00E+00//TC155686				nr +
Unigene48427_All	1402	1.49	0.72	0.19	3.62	2.26	2.00	4.92	1.52	3.18	-1.05E+00	1.96E-02		-2.97E+00	5.84E-07	Down	-6.82E-01	6.44E-03		-8.60E-01	1.02E-03		-1.69E+00	2.23E-14	Down	-6.27E-01	1.14E-03		Unigene48427_All//gi|65736533|dbj|BAD98515.1|//4.00E-91//TONSOKU protein [Nicotiana tabacum]	Unigene48427_All//6.00E-67//AT3G18730| TSK (TONSOKU); protein binding	Unigene48427_All//4.00E-118//CA994064				nr +
Unigene48429_All	897	2.74	9.04	4.10	8.44	5.11	3.88	6.88	5.36	3.11	1.72E+00	5.17E-14	Up	5.79E-01	8.59E-02		-7.25E-01	2.17E-04		-1.12E+00	1.08E-07	Down	-3.61E-01	1.03E-01		-1.15E+00	8.03E-08	Down	Unigene48429_All//gi|115464585|ref|NP_001055892.1|//3.00E-89//Os05g0489600 [Oryza sativa Japonica Group] >gi|1703380|sp|P51823.2|ARF2_ORYSJ RecName: Full=ADP-ribosylation factor 2 >gi|1132483|dbj|BAA04607.1| ADP-ribosylation factor [Oryza sativa Japonica Group] >gi|13646976|dbj|BAB41081.1| ADP-ribosylation factor [Triticum aestivum] >gi|23304413|emb|CAD48129.2| ADP-ribosylation factor 1-like protein [Hordeum vulgare subsp. vulgare] >gi|50511366|gb|AAT77289.1| ADP-ribosylation factor [Oryza sativa Japonica Group] >gi|113579443|dbj|BAF17806.1| Os05g0489600 [Oryza sativa Japonica Group]	Unigene48429_All//2.00E-88//AT1G70490| ARFA1D; GTP binding / phospholipase activator/ protein binding	Unigene48429_All//0.00E+00//TC172643				nr +
Unigene48433_All	384	5.18	6.47	8.60	31.91	14.44	7.41	12.99	11.32	5.19	3.21E-01	4.31E-01		7.32E-01	4.06E-02		-1.14E+00	5.89E-14	Down	-2.11E+00	1.70E-29	Down	-1.99E-01	4.59E-01		-1.32E+00	6.47E-08	Down	Unigene48433_All//gi|115470305|ref|NP_001058751.1|//8.00E-35//Os07g0114300 [Oryza sativa Japonica Group] >gi|113610287|dbj|BAF20665.1| Os07g0114300 [Oryza sativa Japonica Group]	Unigene48433_All//2.00E-32//AT2G23090| unknown protein	Unigene48433_All//2.00E-120//DW235569				nr -
Unigene48434_All	811	1.68	2.62	1.38	9.70	3.40	0.84	10.84	8.25	3.09	6.46E-01	1.41E-01		-2.83E-01	6.05E-01		-1.51E+00	6.57E-14	Down	-3.54E+00	3.68E-33	Down	-3.95E-01	2.57E-02		-1.81E+00	1.82E-20	Down	Unigene48434_All//gi|75099212|sp|Q6481 8.1|Y2309_ARATH//1.00E-115//RecName: Full=Uncharacterized protein At2g23090 >gi|3169182|gb|AAC17825.1| Expressed protein [Arabidopsis thaliana] >gi|15450484|gb|AAK96535.1| At2g23090/F21P24.15 [Arabidopsis thaliana] >gi|15912199|gb|AAL08233.1| At2g23090/F21P24.15 [Arabidopsis thaliana] >gi|23565759|gb|AAN28739.1| At2g23090/F21P24.15 [Arabidopsis thaliana]	Unigene48434_All//6.00E-17//AT2G23090| unknown protein	Unigene48434_All//6.00E-79//DW235569				nr -
Unigene48435_All	1563	0.74	2.46	2.56	0.96	0.29	0.66	15.66	24.01	566.94	1.74E+00	3.77E-07	Up	1.79E+00	2.42E-07	Up	-1.74E+00	1.14E-03		-5.25E-01	3.66E-01		6.17E-01	4.56E-15		5.18E+00	0.00E+00	Up	Unigene48435_All//gi|82409049|gb|AB573306.1|//0.00E+00//alternative oxidase [Gossypium hirsutum]	Unigene48435_All//4.00E-142//AT3G22370| AOX1A (ALTERNATIVE OXIDASE 1A); alternative oxidase	Unigene48435_All//0.00E+00//TC133844				nr -
Unigene48437_All	1758	18.15	32.48	16.08	23.80	30.48	38.72	14.29	24.16	28.94	8.39E-01	4.95E-31		-1.75E-01	1.03E-01		3.57E-01	9.08E-08		7.02E-01	3.89E-29		7.58E-01	5.44E-24		1.02E+00	1.08E-47	Up	Unigene48437_All//gi|224054732|ref|XP_002298356.1|//0.00E+00//glycoside hydrolase [Populus trichocarpa] >gi|222845614|gb|EEE83161.1| glycoside hydrolase [Populus trichocarpa]	Unigene48437_All//4.00E-135//AT5G24318| catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene48437_All//0.00E+00//TC151447		ko00500|Starch and sucrose metabolism		nr +
Unigene48438_All	1792	37.28	18.97	25.38	37.69	36.88	31.10	18.83	6.74	7.98	-9.75E-01	1.63E-46		-5.55E-01	3.42E-17		-3.17E-02	7.13E-01		-2.77E-01	8.43E-06		-1.48E+00	1.08E-55	Down	-1.24E+00	9.68E-44	Down	Unigene48438_All//gi|297839243|ref|XP_002887503.1|//1.00E-123//glycosyl transferase family 28 protein [Arabidopsis lyrata subsp. lyrata] >gi|297333344|gb|EFH63762.1| glycosyl transferase family 28 protein [Arabidopsis lyrata subsp. lyrata]	Unigene48438_All//9.00E-122//AT1G73740| glycosyl transferase family 28 protein	Unigene48438_All//0.00E+00//TC148693				nr -
Unigene48439_All	956	3.56	1.75	4.29	4.79	4.11	3.73	2.03	0.96	0.67	-1.02E+00	2.43E-03		2.70E-01	3.96E-01		-2.23E-01	4.78E-01		-3.61E-01	2.35E-01		-1.08E+00	9.78E-03		-1.61E+00	1.60E-04	Down	Unigene48439_All//gi|297726827|ref|NP_001175777.1|//1.00E-24//Os09g0326850 [Oryza sativa Japonica Group] >gi|255678784|dbj|BAH94505.1| Os09g0326850 [Oryza sativa Japonica Group]	Unigene48439_All//3.00E-20//AT2G37975| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Yos1-like (InterPro:IPR013880); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54085.2); Has 146 Blast hits to 146 proteins in 66 species: Archae - 0; Bacteria - 0; Metazoa - 89; Fungi - 25; Plants - 26; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink).	Unigene48439_All//0.00E+00//TC131851				nr +
Unigene48440_All	1808	9.43	27.44	10.40	9.42	11.31	15.76	6.66	12.09	10.66	1.54E+00	3.07E-70	Up	1.40E-01	3.55E-01		2.64E-01	3.25E-02		7.42E-01	9.33E-14		8.59E-01	1.27E-15		6.78E-01	9.16E-10		Unigene48440_All//gi|14517540|gb|AAK62660.1|//1.00E-109//AT3g50910/F18B3_190 [Arabidopsis thaliana] >gi|27764930|gb|AAO23586.1| At3g50910/F18B3_190 [Arabidopsis thaliana]	Unigene48440_All//3.00E-79//AT3G50910| unknown protein	Unigene48440_All//0.00E+00//gi|78346551|gb|DT566825.1|DT566825				nr -
Unigene48441_All	1382	26.16	10.74	23.85	8.47	7.18	4.31	0.70	0.24	0.49	-1.28E+00	2.28E-39	Down	-1.33E-01	1.98E-01		-2.39E-01	1.70E-01		-9.74E-01	2.84E-09		-1.54E+00	1.90E-02		-5.22E-01	3.89E-01		Unigene48441_All//gi|115447063|ref|NP_001047311.1|//7.00E-16//Os02g0595200 [Oryza sativa Japonica Group] >gi|113536842|dbj|BAF09225.1| Os02g0595200 [Oryza sativa Japonica Group]	Unigene48441_All//3.00E-19//AT4G24700| unknown protein	Unigene48441_All//0.00E+00//TC176871				nr -
Unigene48442_All	1873	6.56	1.97	5.80	11.20	7.24	7.93	34.83	28.88	8.17	-1.73E+00	3.26E-21	Down	-1.79E-01	3.40E-01		-6.28E-01	1.01E-08		-4.97E-01	2.04E-05		-2.71E-01	3.28E-06		-2.09E+00	6.72E-178	Down	Unigene48442_All//gi|9838391|ref|NP_064003.1|//2.00E-86//orf300 [Beta vulgaris subsp. vulgaris] >gi|9049305|dbj|BAA99315.1| orf300 [Beta vulgaris subsp. vulgaris]	Unigene48442_All//2.00E-62//AT2G07689| NADH-ubiquinone oxidoreductase, putative	Unigene48442_All//0.00E+00//TC150129		ko00190|Oxidative phosphorylation		nr -
Unigene48443_All	1543	1.25	1.51	0.72	2.81	3.15	3.45	13.97	51.98	179.11	2.68E-01	5.39E-01		-7.92E-01	1.06E-01		1.64E-01	6.17E-01		2.98E-01	3.03E-01		1.90E+00	7.96E-186	Up	3.68E+00	0.00E+00	Up	Unigene48443_All//gi|14582202|gb|AAK69402.1|AF274565_1 immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum] >gi|14582202|gb|AAK69402.1|AF274565_1 immediate-early fungal elicitor protein CMPG1 [Petroselinum crispum]	Unigene48443_All//1.00E-97//AT5G37490| U-box domain-containing protein	Unigene48443_All//2.00E-138//TC150442				nr -
Unigene48444_All	1864	0.06	0.22	0.00	6.57	6.58	3.90	28.60	2.71	5.09	1.95E+00	1.44E-01		-5.81E+00	3.92E-01		5.00E-04	9.98E-01		-7.53E-01	1.74E-06		-3.40E+00	9.81E-241	Down	-2.49E+00	3.30E-180	Down	Unigene48444_All//gi|15231199|ref|NP_190151.1|//1.00E-164//NAXT1 (NITRATE EXCRETION TRANSPORTER1); nitrate efflux transmembrane transporter/ transporter [Arabidopsis thaliana]	Unigene48444_All//2.00E-147//AT3G45650| NAXT1 (NITRATE EXCRETION TRANSPORTER1); nitrate efflux transmembrane transporter/ transporter	Unigene48444_All//0.00E+00//CO077072				nr +
Unigene48448_All	2183	7.33	4.85	5.83	9.86	8.03	6.66	17.76	8.75	6.81	-5.96E-01	1.75E-05		-3.31E-01	2.59E-02		-2.96E-01	1.04E-02		-5.65E-01	8.21E-07		-1.02E+00	6.18E-36	Down	-1.38E+00	2.23E-59	Down	Unigene48448_All//gi|6573719|gb|AAF17639.1|AC009978_15//4.00E-96//T23818.18 [Arabidopsis thaliana]	Unigene48448_All//2.00E-97//AT1G76250| unknown protein	Unigene48448_All//0.00E+00//TC135157				nr +
Unigene48449_All	949	6.01	4.86	7.74	46.51	41.29	32.12	11.05	5.81	3.44	-3.07E-01	2.32E-01		3.66E-01	1.16E-01		-1.72E-01	3.73E-02		-5.34E-01	4.98E-12		-9.26E-01	6.81E-09		-1.68E+00	5.52E-22	Down	Unigene48449_All//gi|4835761|gb|AAD30228.1|AC007202_10//6.00E-41//T8K14.10 [Arabidopsis thaliana]	Unigene48449_All//8.00E-35//AT1G79480| LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: X8 (InterPro:IPR012946); BEST Arabidopsis thaliana protein match is: glycosyl hydrolase family protein 17 (TAIR:AT5G67460.1); Has 136128 Blast hits to 57102 proteins in 1817 species: Archae - 165; Bacteria - 17617; Metazoa - 56967; Fungi - 20796; Plants - 12784; Viruses - 3661; Other Eukaryotes - 24138 (source: NCBI BLink).	Unigene48449_All//0.00E+00//TC132902		ko04144|Endocytosis//ko00270|Cysteine and methionine metabolism		nr -
Unigene48845_All	817	15.05	13.15	13.88	27.32	20.44	17.80	15.11	10.54	6.88	-1.95E-01	2.61E-01		-1.16E-01	5.41E-01		-4.18E-01	1.07E-04		-6.18E-01	3.88E-08		-5.20E-01	2.82E-04		-1.14E+00	1.46E-14	Down			Unigene4845_All//2.00E-125//gi|21094259|gb|BQ406572.1|BQ406572				
Unigene48450_All	954	27.70	15.40	26.23	4.44	5.56	5.59	1.46	1.93	4.68	-8.47E-01	5.05E-15		-7.82E-02	5.46E-01		3.25E-01	2.46E-01		3.32E-01	2.34E-01		3.98E-01	3.89E-01		1.68E+00	1.09E-09	Up	Unigene48450_All//gi|90200410|gb|ABD92707.1|//4.00E-85//solanesyl diphosphate synthase [Hevea brasiliensis]	Unigene48450_All//2.00E-74//AT1G17050| SPS2 (Solanesyl diphosphate synthase 2); trans-octaprenyltranstransferase	Unigene48450_All//0.00E+00//TC172967		ko00900|Terpenoid backbone biosynthesis		nr -

Unigene48453_All	2374	0.82	1.86	0.92	2.46	1.70	2.49	9.05	13.84	54.00	1.19E+00	6.34E-05	Up	1.74E-01	6.91E-01		-5.33E-01	2.40E-02		2.17E-02	9.45E-01		6.13E-01	3.61E-13		2.58E+00	0.00E+00	Up	Unigene48453_All//gi|92870237|gb|ABE79564.1|//0.00E+00//Membrane attack complex component/perforin/complement C9 [Medicago truncatula]	Unigene48453_All//0.00E+00//AT4G24290| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Membrane attack complex component/perforin/complement C9 (InterPro:IPR001862); BEST Arabidopsis thaliana protein match is: NSL1 (necrotic spotted lesions 1) (TAIR:AT1G28380.1); Has 124 Blast hits to 124 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 41; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene48453_All//0.00E+00//TC172019				nr +
Unigene48454_All	612	29.15	62.67	42.20	27.67	46.98	43.10	62.11	58.32	335.37	1.10E+00	7.55E-33	Up	5.34E-01	1.25E-06		7.64E-01	7.08E-16		6.39E-01	5.76E-10		-9.07E-02	3.30E-01		2.43E+00	0.00E+00	Up	Unigene48454_All//gi|67483357|gb|AY68034.1|//1.00E-74//3-hydroxy-methylglutaryl coenzyme A reductase [Tilia miqueliana]	Unigene48454_All//3.00E-24//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene48454_All//0.00E+00//TC149825		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene48455_All	1481	11.52	3.22	3.13	23.88	20.95	15.00	17.04	8.86	23.13	-1.84E+00	1.25E-31	Down	-1.88E+00	2.79E-31	Down	-1.89E-01	4.12E-02		-6.71E-01	2.19E-14		-9.44E-01	7.26E-21		4.41E-01	3.88E-08		Unigene48455_All//gi|42561693|ref|NP_171946.2|//1.00E-121//PDLP2 (PLASMODESMATA-LOCATED PROTEIN 2) [Arabidopsis thaliana] >gi|75127023|sp|Q6NM23.1|CRR3_ARATH RecName: Full=Cysteine-rich repeat secretory protein 3; Flags: Precursor >gi|385666686|gb|AAR24233.1| At1g04520 [Arabidopsis thaliana] >gi|45592918|gb|AAS68113.1| At1g04520 [Arabidopsis thaliana]	Unigene48455_All//2.00E-109//AT1G04520| PDLP2 (PLASMODESMATA-LOCATED PROTEIN 2)	Unigene48455_All//0.00E+00//TC139402				nr +
Unigene48456_All	1662	37.05	80.82	52.74	30.63	31.10	28.61	30.40	58.09	32.72	1.13E+00	7.87E-117	Up	5.09E-01	3.09E-19		2.19E-02	8.20E-01		-9.83E-02	2.62E-01		9.34E-01	3.72E-76		1.06E-01	1.24E-01		Unigene48456_All//gi|42563541|ref|NP_187268.2|//0.00E+00//TMS membrane family protein / tumour differentially expressed (TDE) family protein [Arabidopsis thaliana] >gi|71143054|gb|AAZ23918.1| At3g06170 [Arabidopsis thaliana]	Unigene48456_All//2.00E-162//AT3G06170| TMS membrane family protein / tumour differentially expressed (TDE) family protein	Unigene48456_All//0.00E+00//TC143547				nr -
Unigene48459_All	947	3.15	1.82	1.18	21.25	45.13	59.90	21.30	16.37	5.72	-7.92E-01	2.80E-02		-1.42E+00	3.22E-04	Down	1.09E+00	6.88E-42	Up	1.50E+00	1.76E-82	Up	-3.79E-01	5.61E-04		-1.90E+00	7.69E-49	Down	Unigene48459_All//gi|30698967|ref|NP_177524.2|//3.00E-39//BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75299562|sp|Q8GWK7.1|BEE3_ARATH RecName: Full=Transcription factor BEE 3; AltName: Full=Protein Brassinosteroid enhanced expression 3; AltName: Full=Transcription factor EN 76; AltName: Full=bHLH transcription factor bHLH050; AltName: Full=Basic helix-loop-helix protein 50; Short=bHLH 50; Short=AtbHLH50	Unigene48459_All//2.00E-36//AT1G72830| BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor	Unigene48459_All//2.00E-39//TC141393	bHLH	ko04712|Circadian rhythm - plant		nr +
Unigene48460_All	418	7.76	4.12	2.42	8.34	3.13	8.97	5.26	2.30	2.48	-9.13E-01	8.10E-03		-1.68E+00	1.34E-05	Down	-1.41E+00	7.20E-06	Down	1.04E-01	7.60E-01		-1.19E+00	2.33E-03		-1.09E+00	3.88E-03					Unigene48460_All//9.00E-126//BF275593					
Unigene48462_All	2104	2.16	1.06	1.37	3.98	5.48	3.76	5.83	0.79	2.63	-1.03E+00	3.26E-04	Down	-6.63E-01	2.51E-02		4.63E-01	4.13E-03		-8.25E-02	7.13E-01		-2.87E+00	1.71E-47	Down	-1.15E+00	1.13E-14	Down	Unigene48462_All//gi|115464301|ref|NP_001055750.1|//1.00E-165//Os05g0459400 [Oryza sativa Japonica Group] >gi|113579301|dbj|BAF17664.1| Os05g0459400 [Oryza sativa Japonica Group]	Unigene48462_All//3.00E-157//AT5G02370| kinesin motor protein-related	Unigene48462_All//0.00E+00//TC139700				nr +
Unigene48465_All	328	5.90	4.63	5.52	9.26	6.09	9.78	2.96	11.21	3.40	-3.49E-01	4.53E-01		-9.66E-02	8.35E-01		-6.05E-01	8.19E-02		7.76E-02	8.47E-01		1.92E+00	2.31E-09	Up	1.98E-01	7.17E-01		Unigene48465_All//gi|53828515|gb|AY94367.1|//2.00E-14//At1g65020 [Arabidopsis thaliana] >gi|55167914|gb|AAV43789.1| At1g65020 [Arabidopsis thaliana]	Unigene48465_All//8.00E-16//AT1G65020| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum, plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: NERD (InterPro:IPR011528); Has 53 Blast hits to 53 proteins in 19 species: Archae - 0; Bacteria - 18; Metazoa - 9; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	Unigene48465_All//1.00E-145//BQ402213			GO:0016020//GO:0043231	nr -
Unigene48467_All	1395	3.30	7.63	4.73	6.00	5.36	7.35	9.30	12.04	8.80	1.21E+00	4.94E-11	Up	5.20E-01	3.05E-02		-1.63E-01	4.81E-01		2.93E-01	1.28E-01		3.72E-01	2.32E-03		-8.11E-02	6.06E-01		Unigene48467_All//gi|53828515|gb|AY94367.1|//1.00E-112//At1g65020 [Arabidopsis thaliana] >gi|55167914|gb|AAV43789.1| At1g65020 [Arabidopsis thaliana]	Unigene48467_All//7.00E-111//AT1G65020| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endoplasmic reticulum, plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: NERD (InterPro:IPR011528); Has 53 Blast hits to 53 proteins in 19 species: Archae - 0; Bacteria - 18; Metazoa - 9; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	Unigene48467_All//0.00E+00//gi|54116994|gb|CO492503.1|CO492503				nr +
Unigene48469_All	1431	5.16	14.13	7.59	7.80	6.74	5.24	11.08	7.51	6.88	1.45E+00	1.04E-26	Up	5.58E-01	1.87E-03		-2.11E-01	2.58E-01		-5.74E-01	5.84E-04		-5.62E-01	6.39E-06		-6.88E-01	2.02E-08		Unigene48469_All//gi|75244377|sp|Q8GWR3.1|QKIL5_ARATH//1.00E-105//RecName: Full=KH domain-containing protein At1g09660; AltName: Full=Quaking-like protein 5	Unigene48469_All//5.00E-100//AT1G09660| KH domain-containing quaking protein, putative	Unigene48469_All//0.00E+00//gi|54123147|gb|CO498656.1|CO498656			GO:0003676//GO:0043231	nr -
Unigene4847_All	763	1.92	2.99	1.40	3.33	4.11	3.37	5.15	2.25	5.64	6.38E-01	1.33E-01		-4.60E-01	4.10E-01		3.03E-01	4.46E-01		1.90E-02	9.61E-01		-1.20E+00	2.08E-05	Down	1.30E-01	6.48E-01		Unigene4847_All//gi|147855998|emb|CAN82820.1|//3.00E-08//hypothetical protein [Vitis vinifera]	Unigene4847_All//4.00E-05//AT2G30710| RabGAP/TBC domain-containing protein	Unigene4847_All//0.00E+00//gi|164285930|gb|ES793839.1|ES793839				nr -
Unigene48470_All	734	42.20	75.18	93.66	26.47	43.44	59.75	50.81	78.75	62.47	8.33E-01	1.23E-29		1.15E+00	1.58E-60	Up	7.15E-01	1.02E-15		1.17E+00	3.08E-44	Up	6.32E-01	9.11E-24		2.98E-01	1.45E-05		Unigene48470_All//gi|219547603|gb|ABR04092.2|//1.00E-38//cytochrome b5 [Malus x domestica]	Unigene48470_All//3.00E-38//AT5G53560| CB5-E (CYTOCHROME B5 ISOFORM E); heme binding	Unigene48470_All//0.00E+00//gi|109877229|gb|DW506203.1|DW506203		ko00910|Nitrogen metabolism	GO:0006091//GO:0009534//GO:0016491//GO:0031090//GO:0042598//GO:0044425//GO:0046872	nr -
Unigene48472_All	975	22.81	9.30	23.21	28.51	16.63	15.38	27.71	36.39	22.68	-1.29E+00	9.15E-25	Down	2.54E-02	8.49E-01		-7.77E-01	2.21E-16		-8.91E-01	2.53E-18		3.93E-01	9.42E-07		-2.89E-01	1.70E-03		Unigene48472_All//gi|3157952|gb|AAC17635.1|//2.00E-42//F12F1.11 [Arabidopsis thaliana]	Unigene48472_All//4.00E-32//AT1G12020| unknown protein	Unigene48472_All//0.00E+00//gi|13248676|gb|BF276840.2|BF276840				nr +
Unigene48474_All	1146	3.56	2.43	2.37	8.22	16.29	31.96	9.04	9.99	27.85	-5.50E-01	6.88E-02		-5.88E-01	6.42E-02		9.87E-01	7.40E-16		1.96E+00	7.36E-78	Up	1.45E-01	4.04E-01		1.62E+00	2.82E-61	Up	Unigene48474_All//gi|16648748|gb|AAL25566.1|//4.00E-22//AT5g02020/T7H20_70 [Arabidopsis thaliana] >gi|20334906|gb|AAM16209.1| AT5g02020/T7H20_70 [Arabidopsis thaliana]	Unigene48474_All//1.00E-14//AT3G55646| unknown protein	Unigene48474_All//0.00E+00//TC175458				nr -
Unigene48475_All	1682	0.12	0.06	0.00	16.97	6.98	7.25	16.31	10.69	1.97	-1.05E+00	5.64E-01		-6.96E+00	1.45E-01		-1.28E+00	2.74E-38	Down	-1.23E+00	1.99E-31	Down	-6.11E-01	4.53E-11		-3.05E+00	8.36E-116	Down	Unigene48475_All//gi|224117652|ref|XP_002317634.1|//1.00E-115//auxin efflux carrier family protein [Populus trichocarpa] >gi|222860699|gb|EEE98246.1| auxin efflux carrier family protein [Populus trichocarpa]	Unigene48475_All//8.00E-111//AT1G20925| auxin efflux carrier family protein	Unigene48475_All//1.00E-20//EE592691				nr +
Unigene48476_All	876	10.39	45.81	11.43	4.32	5.74	9.74	111.49	269.24	264.00	2.14E+00	4.68E-89	Up	1.37E-01	5.11E-01		4.09E-01	1.42E-01		1.17E+00	4.88E-09	Up	1.27E+00	5.86E-305	Up	1.24E+00	1.48E-294	Up	Unigene48476_All//gi|115474397|ref|NP_001060795.1|//1.00E-53//Os08g0107100 [Oryza sativa Japonica Group] >gi|113622764|dbj|BAF22709.1| Os08g0107100 [Oryza sativa Japonica Group]	Unigene48476_All//3.00E-37//AT4G19950| unknown protein	Unigene48476_All//0.00E+00//TC132068			GO:0044464	nr -
Unigene48477_All	1894	18.29	11.50	8.88	15.73	12.07	15.36	25.81	10.39	10.90	-6.69E-01	3.54E-13		-1.04E+00	3.60E-26	Down	-3.82E-01	3.35E-05		-3.45E-02	7.70E-01		-1.31E+00	6.75E-67	Down	-1.24E+00	2.06E-63	Down	Unigene48477_All//gi|225423947|ref|XP_002282287.1|//0.00E+00//PREDICTED: similar to LTA2 (PLASTID E2 SUBUNIT OF PYRUVATE DECARBOXYLASE): dihydrolipoyllysine-residue acetyltransferase [Vitis vinifera]	Unigene48477_All//6.00E-166//AT3G25860| LTA2; dihydrolipoyllysine-residue acetyltransferase	Unigene48477_All//0.00E+00//TC136550		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)	GO:0005488//GO:0005840//GO:0006085//GO:0009526//GO:0009532//GO:0016418	nr +
Unigene48479_All	761	3.30	1.20	2.17	2.29	3.53	5.82	4.56	2.31	3.66	-1.46E+00	4.79E-04	Down	-6.05E-01	1.47E-01		6.23E-01	1.10E-01		1.34E+00	5.18E-06	Up	-9.82E-01	9.45E-04		-3.14E-01	2.98E-01		Unigene48479_All//gi|297820930|ref|XP_002878348.1|//4.00E-24//40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata] >gi|297324186|gb|EFH54607.1| 40S ribosomal protein S13 [Arabidopsis lyrata subsp. lyrata]	Unigene48479_All//2.00E-25//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene48479_All//0.00E+00//CO093316		ko03010|Ribosome	GO:0000904//GO:0005198//GO:0009536//GO:0009887//GO:0010467//GO:0015935//GO:0030312//GO:0031410//GO:0031981//GO:0033205	nr -
Unigene48480_All	1271	35.36	19.06	20.57	43.11	37.12	47.90	38.52	15.78	16.89	-8.92E-01	2.92E-27		-7.82E-01	4.81E-21		-2.16E-01	1.74E-03		1.52E-01	3.52E-02		-1.29E+00	4.44E-65	Down	-1.19E+00	3.29E-59	Down	Unigene48480_All//gi|82621170|gb|AB88273.1|//1.00E-70//cytoplasmic ribosomal protein S13-like [Solanum tuberosum]	Unigene48480_All//9.00E-78//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene48480_All//0.00E+00//TC150369		ko03010|Ribosome	GO:0000904//GO:0005198//GO:0009536//GO:0009887//GO:0010467//GO:0015935//GO:0030312//GO:0031981//GO:0033205	nr -
Unigene48481_All	1475	13.41	18.58	8.30	9.08	5.86	7.75	3.67	26.38	3.13	4.71E-01	5.23E-06		-6.91E-01	6.70E-08		-6.33E-01	7.64E-06		-2.30E-01	1.74E-01		2.85E+00	1.92E-147	Up	-2.28E-01	3.48E-01		Unigene48481_All//gi|16323087|gb|AAL15278.1|//0.00E+00//AT3g01490/F4F13_4 [Arabidopsis thaliana] >gi|110742522|dbj|BAE99178.1| protein kinase like protein [Arabidopsis thaliana]	Unigene48481_All//0.00E+00//AT3G01490| protein kinase, putative	Unigene48481_All//0.00E+00//TC179076			GO:0004713//GO:0006464//GO:0032559	nr +
Unigene48482_All	1754	0.89	2.66	0.91	3.10	5.20	4.35	14.97	21.16	55.96	1.57E+00	1.92E-07	Up	2.54E-02	9.81E-01		7.49E-01	3.22E-05		4.91E-01	2.13E-02		4.99E-01	1.88E-10		1.90E+00	5.69E-233	Up	Unigene48482_All//gi|6573719|gb|AAF17639.1|AC009978_15//1.00E-137//T23E18.18 [Arabidopsis thaliana]	Unigene48482_All//1.00E-136//AT1G76250| unknown protein	Unigene48482_All//0.00E+00//TC159603				nr -
Unigene48485_All	1548	5.64	8.84	9.36	5.15	1.85	5.89	9.83	11.99	7.08	6.47E-01	2.07E-05		7.29E-01	1.70E-06		-1.48E+00	1.32E-13	Down	1.95E-01	3.87E-01		2.86E-01	1.56E-02		-4.74E-01	1.36E-04		Unigene48485_All//gi|30962522|dbj|BAC76729.1|//0.00E+00//alpha-amylase [Vigna angularis]	Unigene48485_All//1.00E-164//AT4G25000| AMY1 (ALPHA-AMYLASE-LIKE); alpha-amylase	Unigene48485_All//4.00E-131//TC134812		ko00500|Starch and sucrose metabolism	GO:0016160//GO:0044238//GO:0046872	nr +

Unigene48486_All	1672	6.60	6.91	6.53	9.98	8.40	7.10	12.62	9.55	5.89	6.55E-02	7.15E-01		-1.62E-02	9.49E-01		-2.48E-01	7.54E-02		-4.91E-01	2.30E-04			-4.02E-01	1.68E-04		-1.10E+00	4.42E-23	Down	Unigene48486_All//gi|29029106|gb|AA064932.1|//1.00E-28//At2g17540 [Arabidopsis thaliana]	Unigene48486_All//1.00E-22//AT4G35510| unknown protein	Unigene48486_All//0.00E+00//gi|13354576|gb|BG444924.1|BG444924				nr +
Unigene48487_All	1757	46.16	33.80	26.82	35.30	25.03	18.79	8.59	6.23	3.70	-4.50E-01	6.23E-15		-7.83E-01	1.11E-37		-4.96E-01	2.55E-16		-9.10E-01	1.17E-41			-4.63E-01	3.08E-04		-1.22E+00	1.54E-19	Down	Unigene48487_All//gi|262410511|gb|ACY66803.1|//1.00E-165//myb family transcription factor [Castanea mollissima]	Unigene48487_All//3.00E-116//AT2G37630| AS1 (ASYMMETRIC LEAVES 1); DNA binding / protein homodimerization/ transcription factor	Unigene48487_All//0.00E+00//TC148343	MYB			nr -
Unigene48488_All	967	7.79	7.81	5.73	17.21	12.04	19.34	11.81	5.14	6.51	3.00E-03	9.88E-01		-4.44E-01	4.87E-02		-5.16E-01	4.32E-05		1.68E-01	2.47E-01			-1.20E+00	3.37E-14	Down	-8.59E-01	7.57E-09		Unigene48488_All//gi|28372864|gb|AA039914.1|//3.00E-35//At1g71430 [Arabidopsis thaliana]	Unigene48488_All//3.00E-26//AT1G71430| unknown protein	Unigene48488_All//0.00E+00//TC139582				nr -
Unigene48489_All	635	50.10	37.50	32.62	72.01	59.92	72.47	152.81	111.17	73.72	-4.18E-01	1.17E-05		-6.19E-01	3.18E-10		-2.65E-01	3.73E-04		9.20E-03	9.41E-01			-4.59E-01	2.16E-22		-1.05E+00	1.11E-95	Down	Unigene48489_All//gi|297849408|ref|XP_002892585.1|//2.00E-57//ADP-ribosylation factor [Arabidopsis lyrata subsp. lyrata] >gi|297338427|gb|EFH68844.1| ADP-ribosylation factor [Arabidopsis lyrata subsp. lyrata]	Unigene48489_All//1.00E-58//AT3G62290| ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding	Unigene48489_All//0.00E+00//TC152476				nr +
Unigene48491_All	1487	0.21	188.43	9.70	0.37	1.02	11.24	4.46	28.64	83.70	9.80E+00	0.00E+00	Up	5.52E+00	2.30E-71	Up	1.47E+00	7.97E-03		4.93E+00	2.91E-85	Up		2.68E+00	2.29E-151	Up	4.23E+00	0.00E+00	Up	Unigene48491_All//gi|4336434|gb|AAD17804.1|//4.00E-81//nodule-enhanced protein phosphatase type 2C [Lotus japonicus]	Unigene48491_All//3.00E-60//AT5G59220| protein phosphatase 2C, putative / PP2C, putative	Unigene48491_All//9.00E-24//TC164924			GO:0004721	nr -
Unigene48492_All	2403	3.37	1.81	1.15	9.22	10.96	7.35	9.36	2.16	4.21	-8.96E-01	1.29E-05		-1.55E+00	1.11E-11	Down	2.49E-01	1.95E-02		-3.28E-01	5.06E-03			-2.12E+00	7.03E-61	Down	-1.15E+00	2.24E-26	Down	Unigene48492_All//gi|224589551|gb|ACN59309.1|//0.00E+00//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene48492_All//0.00E+00//AT2G45340| leucine-rich repeat transmembrane protein kinase, putative	Unigene48492_All//0.00E+00//TC140635			GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0003410//GO:0032559	nr -
Unigene48493_All	581	6.66	4.88	4.49	12.43	10.55	10.57	37.33	11.44	15.09	-4.48E-01	1.53E-01		-5.69E-01	8.23E-02		-2.37E-01	3.13E-01		-2.34E-01	3.44E-01			-1.71E+00	4.23E-44	Down	-1.31E+00	7.16E-31	Down	Unigene48493_All//gi|683502|emb|CAA57528.1|//7.00E-41//protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]	Unigene48493_All//4.00E-42//AT3G25800| PP2AA2 (PROTEIN PHOSPHATASE 2A SUBUNIT A2); protein phosphatase type 2A regulator	Unigene48493_All//0.00E+00//gi|13245461|gb|BE052658.2|BE052658			GO:0008287//GO:0010038//GO:0016020//GO:0016310//GO:0019888//GO:0030312	nr +
Unigene48494_All	2180	5.57	3.30	3.81	10.03	7.77	8.06	21.63	6.65	11.13	-7.55E-01	3.62E-06		-5.47E-01	1.17E-03		-3.68E-01	8.88E-04		-3.16E-01	7.73E-03			-1.70E+00	1.56E-94	Down	-9.58E-01	2.24E-40		Unigene48494_All//gi|15230896|ref|NP_188208.1|//0.00E+00//PP2AA2 (PROTEIN PHOSPHATASE 2A SUBUNIT A2); protein phosphatase type 2A regulator [Arabidopsis thaliana] >gi|83287930|sp|Q38950.2|2AAB_ARATH RecName: Full=Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform; Short=PP2A, subunit A, beta isoform; Short=AtA beta >gi|7939566|dbj|BAA95767.1| protein phosphotase 2a 65kd regulatory subunit [Arabidopsis thaliana] >gi|27311765|gb|AAO00848.1| protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana] >gi|30725386|gb|AAP37715.1| At3g25800 [Arabidopsis thaliana]	Unigene48494_All//0.00E+00//AT3G25800| PP2AA2 (PROTEIN PHOSPHATASE 2A SUBUNIT A2); protein phosphatase type 2A regulator	Unigene48494_All//0.00E+00//TC131383			GO:0008287//GO:0010038//GO:0016020//GO:0016310//GO:0019888//GO:0030312	nr +
Unigene48496_All	1758	1.19	2.19	1.18	6.94	4.68	3.24	10.77	6.16	6.07	8.80E-01	4.96E-03		-1.12E-02	1.00E+00		-5.68E-01	1.52E-04		-1.10E+00	1.17E-11	Down	-8.07E-01	2.29E-12		-8.27E-01	2.90E-13		Unigene48496_All//gi|60327635|gb|AAX19057.1|//0.00E+00//class III HD-Zip protein 8 [Populus trichocarpa]	Unigene48496_All//2.00E-177//AT1G52150| ATHB-15; DNA binding / transcription factor	Unigene48496_All//0.00E+00//TC173324	HB		GO:0001071//GO:0003006//GO:0003677//GO:0006351//GO:0009799//GO:0009887//GO:0009933//GO:0009953//GO:0010073//GO:0010468//GO:0043231	nr +
Unigene48497_All	1179	0.71	19.51	1.67	5.62	13.49	19.12	1.22	5.85	1.93	4.78E+00	4.18E-108	Up	1.23E+00	1.21E-02		1.26E+00	6.52E-20	Up	1.77E+00	8.62E-42	Up	2.26E+00	1.09E-20	Up	6.60E-01	7.20E-02		Unigene48497_All//gi|297843190|ref|XP_002889476.1|//7.00E-75//zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335318|gb|EFH65735.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48497_All//2.00E-55//AT1G03790| SOM (SOMNUS); nucleic acid binding / transcription factor	Unigene48497_All//0.00E+00//TC129629	C3H		GO:0010029//GO:0043231//GO:0046914	nr -
Unigene485_All	510	1.85	3.38	1.46	3.32	5.54	3.72	6.22	4.92	13.05	8.71E-01	8.07E-02		-3.37E-01	6.16E-01		7.38E-01	4.68E-02		1.64E-01	7.39E-01		-3.39E-01	3.12E-01		1.07E+00	1.66E-07	Up	Unigene485_All//gi|20466770|gb|AAM20702.1|//2.00E-33//receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene485_All//3.00E-30//AT4G39270| leucine-rich repeat transmembrane protein kinase, putative	Unigene485_All//0.00E+00//gi|73943901|gb|DT527209.1|DT527209		ko00270|Cysteine and methionine metabolism	GO:0004672//GO:0005488//GO:0005618//GO:0008152//GO:0016020//GO:0016491	nr +
Unigene4850_All	891	1.17	5.18	0.60	4.03	2.40	4.51	8.02	9.33	10.19	2.14E+00	8.41E-11	Up	-9.75E-01	1.67E-01		-7.48E-01	1.49E-02		1.64E-01	6.34E-01		2.19E-01	2.68E-01		3.46E-01	4.11E-02		Unigene4850_All//gi|297810367|ref|XP_002873067.1|//9.00E-34//pseudo-response regulator 7 [Arabidopsis lyrata subsp. lyrata] >gi|297318904|gb|EFH49326.1| pseudo-response regulator 7 [Arabidopsis lyrata subsp. lyrata]	Unigene4850_All//2.00E-31//AT5G02810| PRR7 (PSEUDO-RESPONSE REGULATOR 7); transcription regulator/ two-component response regulator	Unigene4850_All//0.00E+00//gi|78347322|gb|DT567596.1|DT567596		ko04712|Circadian rhythm - plant		nr -
Unigene48500_All	1023	13.60	14.61	19.10	30.97	27.77	22.47	13.31	8.62	2.73	1.03E-01	5.32E-01		4.90E-01	1.47E-04		-1.57E-01	1.27E-01		-4.63E-01	6.04E-07		-6.26E-01	3.82E-06		-2.29E+00	4.05E-42	Down	Unigene48500_All//gi|124359981|gb|ABN07997.1|//1.00E-10//contains similarity to reverse trancriptase, related [Medicago truncatula]	Unigene48500_All//2.00E-08//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene48500_All//2.00E-57//BF275150				nr -
Unigene48502_All	523	0.00	0.00	0.00	1.43	1.91	0.43	0.65	2.80	0.53	null	null		null	null		4.18E-01	5.85E-01		-1.73E+00	5.00E-02		2.11E+00	1.32E-04	Up	-2.78E-01	7.81E-01		Unigene48502_All//gi|224101819|ref|XP_002312432.1|//3.00E-12//predicted protein [Populus trichocarpa] >gi|222852252|gb|EEE89799.1| predicted protein [Populus trichocarpa]					GO:0005488//GO:0016301	nr +
Unigene48505_All	1634	15.56	7.44	7.59	19.76	18.97	20.43	21.32	11.48	8.56	-1.06E+00	7.19E-21	Down	-1.04E+00	3.61E-19	Down	-5.87E-02	6.07E-01		4.82E-02	6.95E-01		-8.93E-01	5.13E-26		-1.32E+00	1.31E-49	Down	Unigene48505_All//gi|186511991|ref|NP_193540.3|//1.00E-159//clathrin binding [Arabidopsis thaliana] >gi|219281239|gb|AAM78997.1| AT4g18060/F15J5_30 [Arabidopsis thaliana] >gi|25090269|gb|AAN72266.1| At4g18060/F15J5_30 [Arabidopsis thaliana]	Unigene48505_All//2.00E-144//AT4G18060| clathrin binding	Unigene48505_All//0.00E+00//TC146619		ko04144|Endocytosis		nr -
Unigene48506_All	2066	0.99	0.61	1.62	0.55	0.42	1.33	7.41	12.16	67.61	-6.88E-01	1.27E-01		7.17E-01	4.30E-02		-4.12E-01	5.39E-01		1.27E+00	1.05E-03		7.15E-01	3.32E-13		3.19E+00	0.00E+00	Up	Unigene48506_All//gi|212717149|gb|ACJ37416.1|//1.00E-151//stress-induced receptor-like kinase [Glycine max]	Unigene48506_All//2.00E-88//AT1G66920| serine/threonine protein kinase, putative	Unigene48506_All//0.00E+00//DT462619		ko04626|Plant-pathogen interaction		nr -
Unigene48507_All	1791	3.39	3.96	1.61	5.37	4.96	5.35	7.96	7.72	5.41	2.25E-01	3.48E-01		-1.08E+00	2.20E-05	Down	-1.14E-01	6.03E-01		-5.90E-03	9.71E-01		-4.25E-02	7.84E-01		-5.58E-01	1.52E-05		Unigene48507_All//gi|115464153|ref|NP_001055676.1|//4.00E-36//Os05g0443700 [Oryza sativa Japonica Group] >gi|113579227|dbj|BAF17590.1| Os05g0443700 [Oryza sativa Japonica Group]	Unigene48507_All//3.00E-21//AT4G30240| protein binding	Unigene48507_All//0.00E+00//TC150181				nr +
Unigene48509_All	1077	4.86	2.92	2.67	8.70	12.37	4.86	1.73	0.19	1.07	-7.36E-01	4.76E-03		-8.64E-01	1.55E-03		5.09E-01	5.09E-04		-8.38E-01	5.12E-06		-3.15E+00	2.08E-08	Down	-6.87E-01	9.37E-02		Unigene48509_All//gi|20197906|gb|AAF18656.2|//2.00E-73//expressed protein [Arabidopsis thaliana]	Unigene48509_All//6.00E-51//AT2G01080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54200.1); Has 388 Blast hits to 387 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 386; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene48509_All//0.00E+00//gi|48753481|gb|CO084000.1|CO084000			GO:0016020	nr +
Unigene48510_All	934	40.45	46.22	30.50	64.16	70.90	59.14	64.24	28.77	28.92	1.93E-01	2.31E-02		-4.07E-01	5.65E-06		1.44E-01	3.12E-02		-1.18E-01	1.26E-01		-1.16E+00	1.61E-67	Down	-1.15E+00	9.21E-69	Down	Unigene48510_All//gi|195612686|gb|ACG28173.1|//3.00E-90//pleckstrin homology domain containing, family A [Zea mays] >gi|195657457|gb|ACG48196.1| pleckstrin homology domain containing, family A [Zea mays]	Unigene48510_All//3.00E-85//AT2G33470| GLTP1 (glycolipid transfer protein 1); glycolipid binding / glycolipid transporter	Unigene48510_All//0.00E+00//TC176352			GO:0005319//GO:0006869//GO:0008289//GO:0043231	nr -
Unigene48513_All	817	5.12	4.40	4.82	5.85	4.43	2.49	9.88	12.69	15.07	-2.19E-01	4.87E-01		-8.71E-02	7.75E-01		-4.03E-01	1.49E-01		-1.23E+00	7.91E-06	Down	3.60E-01	2.65E-02		6.08E-01	1.46E-05		Unigene48513_All//gi|297521186|ref|XP_002878476.1|//3.00E-07//AT3g62770/F26K9_200 [Arabidopsis lyrata subsp. lyrata] >gi|297324314|gb|EFH54735.1| AT3g62770/F26K9_200 [Arabidopsis lyrata subsp. lyrata]	Unigene48513_All//1.00E-08//AT3G62770| AtATG18a	Unigene48513_All//0.00E+00//CO114184			GO:0006950//GO:0009536//GO:0010260//GO:0044248	nr -
Unigene48515_All	1141	5.59	18.07	12.32	90.50	101.98	91.36	0.67	0.33	0.87	1.69E+00	9.22E-34	Up	1.14E+00	1.29E-12	Up	1.72E-01	1.76E-04		1.35E-02	8.42E-01		-1.02E+00	1.69E-01		3.88E-01	5.38E-01		Unigene48515_All//gi|225470869|ref|XP_002269732.1|//1.00E-110//PREDICTED: (-)-a-terpineol synthase [Vitis vinifera]	Unigene48515_All//1.00E-89//AT3G25810| myrcene/ocimene synthase, putative	Unigene48515_All//0.00E+00//gi|109888657|gb|DW517626.1|DW517626		ko00902|Monoterpenoid biosynthesis		nr -
Unigene48516_All	1310	11.46	7.31	9.63	14.15	15.67	25.10	20.79	13.66	10.01	-6.49E-01	6.70E-06		-2.51E-01	1.16E-01		1.47E-01	2.98E-01		8.27E-01	6.65E-19		-6.06E-01	7.37E-11		-1.05E+00	1.28E-27	Down	Unigene48516_All//gi|38238855|sp|Q81769.1|DPH5_ARATH//1.00E-129//RecName: Full=Probable diphthine synthase; AltName: Full=Diphthamide biosynthesis methyltransferase >gi|13605813|gb|AAX32892.1|AF367305.1 AT4g31790/F28M20_20 [Arabidopsis thaliana] >gi|3281849|emb|CAA19744.1| methyltransferase - like protein [Arabidopsis thaliana] >gi|7270082|emb|CAB79897.1| methyltransferase-like protein [Arabidopsis thaliana] >gi|23505927|gb|AAN28823.1| At4g31790/F28M20_20 [Arabidopsis thaliana]	Unigene48516_All//7.00E-131//AT4G31790| diphthine synthase, putative (DPH5)	Unigene48516_All//0.00E+00//TC135778			GO:0008152//GO:0008168	nr -
Unigene48518_All	983	0.37	1.65	1.35	1.47	2.66	1.33	2.28	3.66	2.55	2.15E+00	2.79E-04	Up	1.86E+00	4.86E-03		8.57E-01	2.65E-02		-1.41E-01	7.93E-01		6.82E-01	1.88E-02		1.64E-01	6.44E-01					Unigene48518_All//0.00E+00//TC152200				
Unigene4852_All	1588	1.58	3.38	2.18	7.00	11.10	11.15	7.45	2.45	4.59	1.10E+00	3.14E-05	Up	4.63E-01	1.91E-01		6.66E-01	6.25E-08		6.72E-01	1.71E-07		-1.61E+00	1.82E-22	Down	-6.99E-01	1.12E-06		Unigene4852_All//gi|211906524|gb|ACJ11755.1|//1.00E-146//UDP-D-xylose 4-epimerase [Gossypium hirsutum]	Unigene4852_All//3.00E-142//AT5G44480| DUR (DEFECTIVE UGE IN ROOT); UDP-glucose 4-epimerase/ binding / catalytic/ coenzyme binding	Unigene4852_All//0.00E+00//TC169571		ko00520|Amino sugar and nucleotide sugar metabolism		nr +

Unigene48520_All	1771	8.09	33.30	9.86	9.79	9.86	22.52	14.18	18.90	8.80	2.04E+00	6.32E-123	Up	2.85E-01	4.68E-02		1.02E-02	9.51E-01		1.20E+00	9.50E-42	Up	4.15E-01	5.39E-07		-6.89E-01	7.75E-13		Unigene48520_All//gi|14600257|gb|AK71314.1|AF388175_1/1.00E-178//papain-like cysteine peptidase XBCP3 [Arabidopsis thaliana]	Unigene48520_All//1.00E-164//AT1G69850| XBCP3 (xylem bark cysteine peptidase 3); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene48520_All//0.00E+00//TC167751			GO:0004175//GO:0016628//GO:0019538	nr +
Unigene48521_All	1828	7.07	9.62	4.92	13.93	10.85	9.26	8.65	20.26	13.14	4.44E-01	7.99E-04		-5.22E-01	1.35E-03		-3.60E-01	3.90E-04		-5.88E-01	1.84E-08		1.23E+00	7.26E-46	Up	6.03E-01	7.12E-10		Unigene48521_All//gi|297793215|ref|XP_002864492.1|//0.00E+00//N-myristoyltransferase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297310327|gb|EFH40751.1| N-myristoyltransferase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene48521_All//0.00E+00//AT5G57020| NMT1 (MYRISTOYL-COA:PROTEIN N-MYRISTOYLTRANSFERASE1); glycylpeptide N-tetradecanoyltransferase/ myristoyltransferase	Unigene48521_All//0.00E+00//TC153777			GO:0006498//GO:0010016//GO:0016410//GO:0016741//GO:0030529//GO:0043231//GO:0044444	nr -
Unigene48525_All	1477	1.20	0.89	0.22	3.24	5.11	4.62	11.28	14.43	26.08	-4.33E-01	3.75E-01		-2.48E+00	4.58E-05	Down	6.57E-01	1.19E-03		5.12E-01	2.43E-02		3.56E-01	8.90E-04		1.21E+00	1.21E-47	Up	Unigene48525_All//gi|16226275|gb|AAL16121.1|AF428289_1/2.00E-27//AT5g57340/MJB24_15 [Arabidopsis thaliana]	Unigene48525_All//1.00E-29//AT5G57340| unknown protein	Unigene48525_All//0.00E+00//TC153777				nr -
Unigene48527_All	826	9.44	19.94	3.42	33.47	17.18	34.88	95.77	148.46	123.28	1.08E+00	5.07E-14	Up	-1.47E+00	2.06E-10	Down	-9.63E-01	2.37E-23		5.97E-02	6.35E-01		6.32E-01	1.64E-49		3.64E-01	5.54E-16		Unigene48527_All//gi|7770334|gb|AAF69704.1|AC016041_9//5.00E-31//F27J15.21 [Arabidopsis thaliana] >gi|45476547|gb|AAS65939.1| At1g49000 [Arabidopsis thaliana] >gi|46359837|gb|AAS88782.1| At1g49000 [Arabidopsis thaliana]	Unigene48527_All//5.00E-28//AT1G49000| unknown protein	Unigene48527_All//1.00E-30//ES849926				nr +
Unigene48528_All	1897	288.85	119.61	177.41	18.17	18.23	8.31	14.53	6.61	10.35	-1.27E+00	0.00E+00	Down	-7.03E-01	1.51E-209		4.20E-03	9.70E-01		-1.13E+00	3.38E-33	Down	-1.14E+00	1.60E-30	Down	-4.89E-01	5.62E-08		Unigene48528_All//gi|5733730|gb|AAD49734.1|AF169795_1//0.00E+00//glutamine synthetase precursor [Juglans nigra]	Unigene48528_All//0.00E+00//AT5G35630| GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase	Unigene48528_All//0.00E+00//TC157418		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006541//GO:0009536//GO:0016211//GO:0032599//GO:0071941	nr +
Unigene48529_All	1132	12.85	8.01	14.72	11.84	15.85	8.42	5.94	2.84	2.01	-6.81E-01	3.50E-06		1.97E-01	2.04E-01		4.21E-01	7.34E-04		-4.92E-01	1.15E-03		-1.06E+00	2.64E-07	Down	-1.57E+00	4.53E-13	Down	Unigene48529_All//gi|15230729|ref|NP_187298.1|//3.00E-90//GNS1/SUR4 membrane family protein [Arabidopsis thaliana]	Unigene48529_All//2.00E-65//AT3G06470| GNS1/SUR4 membrane family protein	Unigene48529_All//6.00E-89//gi|164295942|gb|EX168196.1|EX168196			GO:0031224//GO:0043231	nr -
Unigene48530_All	719	21.18	24.67	28.88	134.27	121.22	118.47	86.21	337.97	79.46	2.20E-01	1.16E-01		4.48E-01	3.40E-04		-1.48E-01	4.86E-03		-1.81E-01	6.67E-04		1.97E+00	0.00E+00	Up	-1.18E-01	6.15E-02		Unigene48530_All//gi|124488474|gb|ABN12321.1|//3.00E-83//benzoquinone reductase [Gossypium hirsutum]	Unigene48530_All//3.00E-70//AT4G27270| quinone reductase family protein	Unigene48530_All//0.00E+00//TC155409			GO:0000166//GO:0006350//GO:0016020//GO:0016655	nr -
Unigene48533_All	756	9.41	15.21	9.44	9.55	10.75	15.83	88.92	201.18	106.24	6.93E-01	3.54E-05		4.00E-03	1.00E+00		1.70E-01	4.83E-01		7.29E-01	5.61E-06		1.18E+00	2.36E-174	Up	2.57E-01	4.86E-07		Unigene48533_All//gi|297790792|ref|XP_002863281.1|//2.00E-79//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297309115|gb|EFH39540.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene48533_All//3.00E-80//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene48533_All//0.00E+00//TC147786			GO:0008152//GO:0009528//GO:0009534//GO:0016655//GO:0046914	nr +
Unigene48537_All	1706	18.83	6.86	15.61	43.51	34.09	43.81	23.15	12.15	15.39	-1.46E+00	2.31E-42	Down	-2.71E-01	7.38E-03		-3.52E-01	1.81E-10		1.01E-02	9.11E-01		-9.30E-01	2.06E-31		-5.89E-01	4.31E-15		Unigene48537_All//gi|15218889|ref|NP_174226.1|//1.00E-139//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|111074196|gb|ABH04471.1| At1g29320 [Arabidopsis thaliana]	Unigene48537_All//2.00E-133//AT1G29320| transducin family protein / WD-40 repeat family protein	Unigene48537_All//0.00E+00//gi|164299163|gb|ES828566.1|ES828566				nr -
Unigene48538_All	763	7.82	7.64	6.98	8.42	5.64	5.98	2.88	1.86	1.10	-3.37E-02	9.02E-01		-1.64E-01	5.57E-01		-5.78E-01	8.69E-03		-4.94E-01	3.57E-02		-6.30E-01	1.07E-01		-1.39E+00	3.22E-04	Down			Unigene48538_All//2.00E-131//gi|21094479|gb|BQ406804.1|BQ406804				
Unigene48539_All	1016	10.04	8.78	5.14	84.87	81.82	50.41	50.85	11.64	19.80	-1.94E-01	3.23E-01		-9.67E-01	2.72E-07		-5.29E-02	4.58E-01		-7.52E-01	9.77E-42		-2.13E+00	8.79E-140	Down	-1.36E+00	7.05E-77	Down	Unigene48539_All//gi|297797992|ref|XP_002866880.1|//1.00E-52//lipid-associated family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312716|gb|EFH43139.1| lipid-associated family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48539_All//4.00E-52//AT2G22170| lipid-associated family protein	Unigene48539_All//0.00E+00//ES806793			GO:0009534//GO:0016020	nr +
Unigene48541_All	778	31.34	203.79	117.38	40.72	85.91	78.02	89.83	235.89	217.58	2.70E+00	0.00E+00	Up	1.91E+00	9.60E-170	Up	1.08E+00	1.58E-64	Up	9.38E-01	1.81E-42		1.39E+00	8.61E-273	Up	1.28E+00	1.19E-224	Up			Unigene48541_All//0.00E+00//TC133226				
Unigene48542_All	1016	5.97	2.89	2.15	9.56	14.95	8.98	3.33	2.55	0.90	-1.05E+00	1.84E-05	Down	-1.48E+00	2.57E-08	Down	6.45E-01	1.54E-06		-9.05E-02	6.89E-01		-3.84E-01	2.26E-01		-1.88E+00	8.17E-09	Down	Unigene48542_All//gi|37051131|dbj|BAC81662.1|//2.00E-65//DNA binding with one finger 5 protein [Pisum sativum]	Unigene48542_All//5.00E-51//AT3G50410| OBP1 (OBF BINDING PROTEIN 1); DNA binding / protein binding / transcription factor	Unigene48542_All//0.00E+00//TC147757	C2C2-Dof		GO:0003676//GO:0009725//GO:0010468//GO:0010556//GO:0048518//GO:0051726//GO:0071555	nr +
Unigene48543_All	1887	0.39	1.77	0.45	19.61	65.75	22.21	30.58	4.85	2.79	2.19E+00	3.06E-08	Up	2.18E-01	7.57E-01		1.75E+00	6.49E-247	Up	1.79E-01	4.07E-02		-2.66E+00	1.86E-203	Down	-3.46E+00	4.61E-273	Down	Unigene48543_All//gi|224057703|ref|XP_002299298.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222846556|gb|EEE84103.1| cytochrome P450 [Populus trichocarpa]	Unigene48543_All//5.00E-144//AT1G74110| CYP78A10; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene48543_All//0.00E+00//TC175301		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506	nr -
Unigene48545_All	1758	3.69	2.39	4.94	16.83	16.47	15.16	22.68	6.23	9.06	-6.25E-01	6.74E-03		4.20E-01	4.43E-02		-3.10E-02	8.28E-01		-1.51E-01	1.80E-01		-1.86E+00	7.39E-91	Down	-1.32E+00	4.81E-57	Down	Unigene48545_All//gi|82568706|dbj|BAE48666.1|//0.00E+00//Serine carboxypeptidase [Prunus mume]	Unigene48545_All//0.00E+00//AT3G45010| scp148 (serine carboxypeptidase-like 48); serine-type carboxypeptidase	Unigene48545_All//1.00E-171//TC139716		ko00940|Phenylpropanoid biosynthesis	GO:0004180//GO:0019538	nr +
Unigene48546_All	1430	3.66	69.45	8.53	5.99	14.79	19.68	4.55	9.27	23.57	4.25E+00	0.00E+00	Up	1.22E+00	3.09E-12	Up	1.30E+00	1.28E-27	Up	1.72E+00	5.08E-50	Up	1.02E+00	7.22E-13	Up	2.37E+00	3.45E-106	Up	Unigene48546_All//gi|14210079|gb|AAK56924.1|AF368227_1/1.00E-105//circadian clock coupling factor ZGT [Nicotiana tabacum]	Unigene48546_All//9.00E-92//AT3G63060| EDL3 (EID1-like 3)	Unigene48546_All//0.00E+00//gi|78329780|gb|DT550054.1|DT550054				nr -
Unigene48548_All	3353	0.55	1.33	1.32	0.74	1.37	0.55	2.51	3.32	6.72	1.28E+00	1.65E-05	Up	1.27E+00	3.85E-05	Up	8.79E-01	1.22E-03		-4.28E-01	3.21E-01		4.02E-01	9.17E-03		1.42E+00	5.21E-36	Up	Unigene48548_All//gi|224127917|ref|XP_002329209.1|//1.00E-100//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870990|gb|EEF08121.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene48548_All//1.00E-87//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene48548_All//0.00E+00//gi|109857553|gb|DW486532.1|DW486532		ko04626|Plant-pathogen interaction		nr -
Unigene48549_All	1144	2.79	4.96	5.03	5.66	6.32	3.83	8.28	9.39	3.52	8.30E-01	9.12E-04		8.50E-01	9.93E-04		1.59E-01	5.60E-01		-5.64E-01	1.46E-02		1.82E-01	3.03E-01		-1.24E+00	7.28E-13	Down	Unigene48549_All//gi|161789859|gb|ABX79677.1|//3.00E-85//GT-1 [Glycine max]	Unigene48549_All//2.00E-79//AT1G13450| DNA binding protein GT-1	Unigene48549_All//0.00E+00//ES826831	Trihelix		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene48855_All	1678	0.16	25.46	0.19	0.27	1.62	2.15	4.84	19.18	259.05	7.35E+00	1.31E-235	Up	2.88E-01	8.10E-01		2.60E+00	5.15E-09	Up	3.01E+00	6.31E-13	Up	1.99E+00	8.90E-80	Up	5.74E+00	0.00E+00	Up	Unigene48855_All//gi|30686609|ref|NP_181137.2|//1.00E-139//PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75148205|sp|Q84TG3.1|PUB23_ARATH RecName: Full=U-box domain-containing protein 23; AltName: Full=Plant U-box protein 23 >gi|29028770|gb|AAO64764.1| At2g35930 [Arabidopsis thaliana]	Unigene4855_All//4.00E-142//AT2G35930| PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase	Unigene4855_All//0.00E+00//TC143982		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene48550_All	1643	1.59	1.79	1.43	3.58	2.05	1.51	4.55	3.13	5.33	1.68E-01	6.35E-01		-1.59E-01	6.90E-01		-8.01E-01	4.22E-04		-1.24E+00	4.48E-07	Down	-5.42E-01	4.43E-03		2.28E-01	2.08E-01		Unigene48550_All//gi|225436998|ref|XP_002277508.1|//1.00E-180//PREDICTED: similar to bHLH-like DNA binding protein [Vitis vinifera]	Unigene48550_All//4.00E-87//AT4G09820| TT8 (TRANSPARENT TESTA 8); DNA binding / transcription factor	Unigene48550_All//0.00E+00//TC155117	bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene48551_All	1091	1.82	2.14	2.44	1.60	2.56	0.99	2.64	0.88	1.57	2.29E-01	6.15E-01		4.21E-01	3.10E-01		6.78E-01	7.29E-02		-6.86E-01	1.80E-01		-1.58E+00	6.51E-06	Down	-7.47E-01	1.84E-02				Unigene48551_All//0.00E+00//DW480723				
Unigene48554_All	1237	11.12	4.26	9.69	15.99	10.80	6.57	2.50	0.64	0.71	-1.38E+00	3.02E-17	Down	-2.00E-01	2.43E-01		-5.66E-01	6.27E-07		-1.28E+00	1.77E-23	Down	-1.96E+00	3.44E-08	Down	-1.82E+00	9.21E-08	Down	Unigene48554_All//gi|18405204|ref|NP_565918.1|//1.00E-96//acid phosphatase class B family protein [Arabidopsis thaliana] >gi|75096954|sp|Q94195.2|Y2992_ARATH RecName: Full=Uncharacterized protein At2g39920 >gi|20198305|gb|AAB95277.2| expressed protein [Arabidopsis thaliana] >gi|90962976|gb|ABE02412.1| At2g39920 [Arabidopsis thaliana]	Unigene48554_All//8.00E-39//AT2G39920| acid phosphatase class B family protein	Unigene48554_All//0.00E+00//TC140501		ko03010|Ribosome	GO:0010038	nr +
Unigene48555_All	1287	4.11	1.02	3.23	5.61	3.42	2.42	0.33	0.19	0.28	-2.00E+00	1.95E-11	Down	-3.47E-01	2.24E-01		-7.13E-01	4.15E-04		-1.21E+00	3.00E-08	Down	-7.53E-01	4.77E-01		-2.38E-01	7.88E-01		Unigene48555_All//gi|18405204|ref|NP_565918.1|//1.00E-89//acid phosphatase class B family protein [Arabidopsis thaliana] >gi|75096954|sp|Q94195.2|Y2992_ARATH RecName: Full=Uncharacterized protein At2g39920 >gi|20198305|gb|AAB95277.2| expressed protein [Arabidopsis thaliana] >gi|90962976|gb|ABE02412.1| At2g39920 [Arabidopsis thaliana]	Unigene48555_All//8.00E-42//AT2G39920| acid phosphatase class B family protein	Unigene48555_All//0.00E+00//gi|78336475|gb|DT556749.1|DT556749		ko03010|Ribosome	GO:0010038	nr -
Unigene48556_All	385	1.90	1.84	0.83	5.05	3.94	5.40	36.02	4.56	9.73	-4.63E-02	9.68E-01		-1.20E+00	1.80E-01		-3.59E-01	4.59E-01		9.67E-02	8.48E-01		-2.98E+00	1.16E-55	Down	-1.89E+00	1.14E-33	Down	Unigene48556_All//gi|224056579|ref|XP_002298920.1|//2.00E-122//predicted protein [Populus trichocarpa] >gi|222846178|gb|EEE83725.1| predicted protein [Populus trichocarpa]		Unigene48556_All//0.00E+00//gi|109881768|gb|DW510738.1|DW510738				nr -
Unigene48557_All	597	4.38	2.21	0.98	21.36	7.73	3.03	20.96	9.31	7.81	-9.90E-01	1.16E-02		-2.16E+00	3.44E-06	Down	-1.47E+00	3.05E-21	Down	-2.82E+00	4.35E-43	Down	-1.17E+00	5.94E-15	Down	-1.42E+00	1.27E-20	Down	Unigene48557_All//gi|224056579|ref|XP_002298920.1|//9.00E-13//predicted protein [Populus trichocarpa] >gi|222846178|gb|EEE83725.1| predicted protein [Populus trichocarpa]		Unigene48557_All//0.00E+00//TC156509				nr -
Unigene48559_All	1262	9.45	8.99	9.28	31.74	41.88	80.59	1.47	0.56	0.41	-7.18E-02	6.82E-01		-2.61E-02	8.93E-01		4.00E-01	2.26E-09		1.34E+00	6.27E-126	Up	-1.39E+00	1.59E-03		-1.84E+00	4.29E-05	Down	Unigene48559_All//gi|21314549|gb|AAM47000.1|AF512542_1/1.00E-141//alpha-expansin precursor [Gossypium hirsutum]	Unigene48559_All//1.00E-131//AT2G28950| ATEXPA6 (ARABIDOPSIS THALIANA EXPANSIN A6)	Unigene48559_All//0.00E+00//gi|78340464|gb|DT560738.1|DT560738				nr +
Unigene48562_All	1930	0.41	0.18	0.06	2.04	1.93	1.57	2.08	2.14	5.43	-1.15E+00	1.53E-01		-2.88E+00	6.35E-03		-8.16E-02	8.35E-01		-3.79E-01	2.47E-01		4.29E-02	8.93E-01		1.38E+00	1.60E-16	Up	Unigene48562_All//gi|224127426|ref|XP_002320071.1|//1.00E-162//cytochrome P450 [Populus trichocarpa] >gi|222860844|gb|EEE98386.1| cytochrome P450 [Populus trichocarpa]	Unigene48562_All//5.00E-145//AT2G45510| CYP704A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene48562_All//0.00E+00//TC160989		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene48563_All	839	25.76	65.77	39.22	20.72	19.74	25.25	23.13	24.06	30.91	1.35E+00	2.33E-64	Up	6.07E-01	3.16E-10		-6.99E-02	6.65E-01		2.85E-01	2.08E-02		5.69E-02	6.57E-01		4.18E-01	7.11E-06		Unigene48563_All//gi|30689144|ref|NP_194903.2|//2.00E-26//WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75302285|sp|Q8RUX3.1|P2C59_ARATH RecName: Full=Probable protein phosphatase 2C 59; Short=AtPP2C59; AltName: Full=Protein phosphatase 2C WIN2; Short=PP2C WIN2; AltName: Full=HopW1-1-interacting protein 2	Unigene48563_All//8.00E-28//AT4G31750| WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase	Unigene48563_All//0.00E+00//gi|48783721|gb|CO089994.1|CO089994			GO:0004721//GO:0006464//GO:0006952//GO:0016020//GO:0031410//GO:0043169//GO:0043231//GO:0043234	nr +

Unigene48564_All	869	7.04	82.04	20.59	2.75	3.25	9.41	44.71	105.67	29.29	3.54E+00	1.31E-270	Up	1.55E+00	4.12E-25	Up	2.40E-01	5.83E-01		1.77E+00	1.52E-15	Up	1.24E+00	1.69E-114	Up	-6.10E-01	8.97E-16		Unigene48564_All//gi|1778823|gb|AAC16403.1|//3.00E-56//early light-induced protein [Glycine max]	Unigene48564_All//7.00E-41//AT3G22840| ELIP1 (EARLY LIGHT-INDUCABLE PROTEIN); chlorophyll binding	Unigene48564_All//0.00E+00//TC137566			GO:0006950	nr +
Unigene48565_All	991	206.33	195.67	224.55	36.59	36.24	30.76	7.76	2.74	2.17	-7.65E-02	4.85E-02		1.22E-01	7.82E-04		-1.39E-02	9.01E-01		-2.51E-01	5.65E-03		-1.50E+00	1.48E-13	Down	-1.84E+00	2.11E-18	Down	Unigene48565_All//gi|15222063|ref|NP_177635.1|//4.00E-78//RPS9 (RIBOSOMAL PROTEIN S9); structural constituent of ribosome [Arabidopsis thaliana] >gi|48428563|sp|Q9XJZ7.1|RR9_ARATH RecName: Full=30S ribosomal protein S9, chloroplastic; Flags: Precursor >gi|5883726|gb|AAD55279.1|AC008263_10 Identical to gb|AB022676 ribosomal protein S9 from Arabidopsis thaliana. ESTs gb|T13861, gb|AA389790, gb|T42539, gb|AA586013, gb|AA395093 and gb|AA041154 come from this gene >gi|5456946|dbj|BAA82396.1| ribosomal protein S9 [Arabidopsis thaliana] >gi|15010598|gb|AAK73958.1| AT2G74970/F25A4.6 [Arabidopsis thaliana]	Unigene48565_All//1.00E-71//AT1G74970| RPS9 (RIBOSOMAL PROTEIN S9); structural constituent of ribosome	Unigene48565_All//0.00E+00//TC143509		ko03010|Ribosome	GO:0000314//GO:0003723//GO:0005198//GO:0009526//GO:0009532//GO:0010467	nr -
Unigene48566_All	1726	0.42	0.59	0.12	3.49	3.55	2.43	2.30	0.92	3.55	4.68E-01	4.89E-01		-1.78E+00	6.00E-02		2.42E-02	9.48E-01		-5.21E-01	3.21E-02		-1.32E+00	3.10E-06	Down	6.26E-01	2.43E-03		Unigene48566_All//gi|264664501|sp|C0LGK9.1|Y2242_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At2g24230; Flags: Precursor >gi|224589521|gb|ACN59294.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene48566_All//2.00E-96//AT2G24230| leucine-rich repeat transmembrane protein kinase, putative	Unigene48566_All//0.00E+00//ES827240			GO:0004713//GO:0006464//GO:0007167//GO:0016787//GO:0032559	nr +
Unigene48567_All	1021	16.09	19.75	29.36	5.61	6.51	15.92	25.26	15.39	25.75	2.96E-01	1.87E-02		8.68E-01	6.06E-17		2.14E-01	4.14E-01		1.51E+00	3.44E-24	Up	-7.15E-01	1.51E-13		2.78E-02	7.97E-01		Unigene48567_All//gi|84619272|emb|CAJ41404.1|//2.00E-97//soluble inorganic pyrophosphatase [Papaver rhoeas]	Unigene48567_All//2.00E-96//AT3G53620| AtPPa4 (Arabidopsis thaliana pyrophosphorylase 4); inorganic diphosphatase	Unigene48567_All//0.00E+00//TC147933		ko00190|Oxidative phosphorylation	GO:0006793//GO:0016462//GO:0044424//GO:0046872	nr +
Unigene48568_All	1381	94.45	539.75	253.76	126.43	222.42	233.37	167.44	519.34	354.68	2.51E+00	0.00E+00	Up	1.43E+00	0.00E+00	Up	8.15E-01	7.28E-187		8.84E-01	1.02E-202		1.63E+00	0.00E+00	Up	1.08E+00	0.00E+00	Up	Unigene48568_All//gi|297808579|ref|XP_002872173.1|//1.00E-111//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318010|gb|EFH48432.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48568_All//3.00E-111//AT5G25560| zinc finger (C3HC4-type RING finger) family protein	Unigene48568_All//0.00E+00//TC135794		ko04120|Ubiquitin mediated proteolysis	GO:0046914	nr -
Unigene48569_All	811	0.65	0.56	1.58	2.21	2.08	1.56	4.54	3.09	1.87	-1.98E-01	8.20E-01		1.29E+00	4.48E-02		-8.78E-02	8.47E-01		-5.04E-01	3.30E-01		-5.53E-01	5.57E-02		-1.28E+00	8.40E-06	Down		Unigene48569_All//1.00E-05//AT3G28770| unknown protein					
Unigene4857_All	1346	2.25	0.98	0.32	2.44	1.84	3.83	2.48	1.52	3.40	-1.20E+00	1.00E-03		-2.83E+00	2.02E-09	Down	-4.07E-01	2.45E-01		6.47E-01	1.44E-02		-7.06E-01	1.97E-02		4.56E-01	6.50E-02		Unigene4857_All//gi|226496697|ref|NP_001147836.1|//1.00E-129//vegetative storage protein [Zea mays] >gi|195614038|gb|ACG28849.1| vegetative storage protein [Zea mays]	Unigene4857_All//1.00E-83//AT4G33170| pentatricopeptide (PPR) repeat-containing protein	Unigene4857_All//0.00E+00//gi|164281658|gb|ES814907.1|ES814907				nr +
Unigene48570_All	635	1.98	3.35	3.27	2.04	0.98	1.49	0.07	0.92	3.76	7.61E-01	8.36E-02		7.26E-01	1.24E-01		-1.06E+00	6.06E-02		-4.50E-01	4.83E-01		3.79E+00	2.07E-03		5.82E+00	1.17E-15	Up	Unigene48570_All//gi|115469258|ref|NP_001058228.1|//5.00E-13//Os06g0651300 [Oryza sativa Japonica Group] >gi|113596268|dbj|BAF20142.1| Os06g0651300 [Oryza sativa Japonica Group]	Unigene48570_All//1.00E-07//AT2G24030| nucleic acid binding / zinc ion binding					nr -
Unigene48571_All	778	1.82	0.39	3.76	3.07	4.16	3.37	2.07	2.69	2.71	-2.22E+00	5.59E-04	Down	1.05E+00	6.29E-03		4.37E-01	2.30E-01		1.32E-01	7.51E-01		3.79E-01	3.78E-01		3.94E-01	3.24E-01				Unigene48571_All//9.00E-07//TC147717				
Unigene48572_All	1471	4.91	10.64	5.03	3.18	1.73	3.07	10.81	30.12	29.90	1.12E+00	4.34E-14	Up	3.58E-02	8.83E-01		-8.78E-01	7.12E-04		-5.21E-02	8.74E-01		1.48E+00	1.63E-72	Up	1.47E+00	9.22E-73	Up	Unigene48572_All//gi|115476708|ref|NP_001061950.1|//6.00E-61//Os08g0451800 [Oryza sativa Japonica Group] >gi|113623919|dbj|BAF23864.1| Os08g0451800 [Oryza sativa Japonica Group]	Unigene48572_All//7.00E-55//AT3G53690| zinc finger (C3HC4-type RING finger) family protein	Unigene48572_All//0.00E+00//TC142508			GO:0005488	nr -
Unigene48573_All	1371	5.11	10.27	6.41	8.28	6.43	8.40	7.52	9.72	10.34	1.01E+00	6.80E-11	Up	3.26E-01	1.26E-01		-3.66E-01	2.71E-02		2.01E-02	9.34E-01		3.70E-01	8.10E-03		4.59E-01	3.97E-04		Unigene48573_All//gi|22329188|ref|NP_195278.2|//9.00E-37//phosphatidylinositolglycan-related [Arabidopsis thaliana]	Unigene48573_All//3.00E-34//AT4G35530| phosphatidylinositolglycan-related	Unigene48573_All//0.00E+00//TC176579		ko00563|Glycosylphosphatidylinositol(GPI)-anchor biosynthesis		nr -
Unigene48574_All	2128	15.29	10.95	11.74	25.73	21.85	17.51	11.82	5.34	4.08	-4.82E-01	3.03E-07		-3.82E-01	9.40E-05		-2.36E-01	5.30E-04		-5.55E-01	8.13E-16		-1.15E+00	2.77E-28	Down	-1.53E+00	3.29E-45	Down	Unigene48574_All//gi|297808029|ref|XP_002871898.1|//0.00E+00//exostosin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317735|gb|EFH48157.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48574_All//0.00E+00//AT5G19670| exostosin family protein	Unigene48574_All//0.00E+00//TC141914			GO:0044464	nr -
Unigene48575_All	968	2.38	1.26	1.32	5.51	3.84	2.94	3.49	0.04	0.78	-9.21E-01	2.85E-02		-8.49E-01	5.44E-02		-5.19E-01	3.83E-02		-9.06E-01	3.75E-04		-6.34E+00	2.53E-22	Down	-2.16E+00	2.32E-10	Down	Unigene48575_All//gi|242075750|ref|XP_002447811.1|//8.00E-07//hypothetical protein SORBIDRAFT_06g016240 [Sorghum bicolor] >gi|241938994|gb|EES12139.1| hypothetical protein SORBIDRAFT_06g016240 [Sorghum bicolor]		Unigene48575_All//0.00E+00//gi|164311754|gb|ES846234.1|ES846234				nr +
Unigene48576_All	1128	5.52	3.91	4.48	9.14	10.65	8.01	2.32	1.26	0.92	-4.98E-01	3.62E-02		-3.00E-01	2.43E-01		2.21E-01	2.21E-01		-1.91E-01	3.53E-01		-8.83E-01	1.12E-02		-1.34E+00	1.25E-04	Down	Unigene48576_All//gi|124359162|gb|ABN05685.1|//6.00E-09//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene48576_All//2.00E-47//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene48576_All//0.00E+00//DW243499				nr +
Unigene48577_All	1151	3.09	3.08	2.64	4.59	5.65	3.96	0.62	0.54	0.07	-4.50E-03	9.86E-01		-2.29E-01	5.25E-01		3.02E-01	2.28E-01		-2.11E-01	4.70E-01		-1.97E-01	7.84E-01		-3.17E+00	8.09E-04	Down	Unigene48577_All//gi|297725701|ref|NP_001175214.1|//1.00E-17//Os07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1| Os07g0501200 [Oryza sativa Japonica Group]	Unigene48577_All//1.00E-08//AT3G25270| nucleic acid binding	Unigene48577_All//0.00E+00//DW243499				nr +
Unigene48578_All	1410	2.97	0.79	1.02	2.54	1.88	2.88	2.13	2.22	2.32	-1.91E+00	1.10E-08	Down	-1.54E+00	2.74E-06	Down	-4.36E-01	1.84E-01		1.81E-01	6.33E-01		6.25E-02	8.57E-01		1.22E-01	6.95E-01		Unigene48578_All//gi|297792853|ref|XP_002864311.1|//1.00E-124//PTAC15 [Arabidopsis lyrata subsp. lyrata] >gi|297310146|gb|EFH40570.1| PTAC15 [Arabidopsis lyrata subsp. lyrata]	Unigene48578_All//2.00E-124//AT5G54180| PTAC15 (PLASTID TRANSCRIPTIONALLY ACTIVE15)	Unigene48578_All//0.00E+00//TC179085				nr -
Unigene48579_All	945	0.89	7.77	1.24	1.58	3.46	12.86	23.18	34.59	28.84	3.13E+00	2.39E-25	Up	4.85E-01	4.47E-01		1.13E+00	7.46E-04	Up	3.02E+00	7.62E-43	Up	5.78E-01	7.29E-12		3.15E-01	5.62E-04		Unigene48579_All//gi|283135896|gb|ADB11339.1|//3.00E-79//zeta class glutathione transferase GSTZ1 [Populus trichocarpa]	Unigene48579_All//2.00E-53//AT2G02390| ATGSTZ1 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE ZETA 1); catalytic/ glutathione transferase	Unigene48579_All//0.00E+00//gi|109881188|gb|DW510158.1|DW510158		ko00350|Tyrosine metabolism	GO:0006520//GO:0016740//GO:0016859//GO:0044424	nr -
Unigene48580_All	1604	3.72	1.61	0.80	6.89	5.20	2.42	0.95	1.41	0.92	-1.21E+00	1.51E-06	Down	-2.22E+00	7.64E-14	Down	-4.08E-01	1.34E-02		-1.51E+00	5.62E-17	Down	5.68E-01	1.42E-01		-4.62E-02	9.37E-01		Unigene48580_All//gi|193734712|gb|ACF19982.1|//1.00E-146//MYC2 [Hevea brasiliensis]	Unigene48580_All//1.00E-65//AT4G17880| basic helix-loop-helix (bHLH) family protein	Unigene48580_All//0.00E+00//TC151639	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene48581_All	802	14.42	8.72	15.80	36.46	32.07	29.56	18.50	7.45	9.54	-7.26E-01	1.38E-05		1.32E-01	4.67E-01		-1.85E-01	7.73E-02		-3.02E-01	2.56E-03		-1.31E+00	7.26E-21	Down	-9.56E-01	2.79E-13		Unigene48581_All//gi|297818246|ref|XP_002877006.1|//3.00E-68//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322844|gb|EFH53265.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48581_All//2.00E-63//AT3G26935| zinc finger (DHHC type) family protein	Unigene48581_All//0.00E+00//gi|78328429|gb|DT548703.1|DT548703			GO:0008152//GO:0016020//GO:0016628//GO:0032501//GO:0046914	nr +
Unigene48582_All	1292	0.32	0.67	0.66	2.20	1.89	4.61	58.77	43.96	64.51	1.04E+00	1.72E-01		1.03E+00	2.04E-01		-2.16E-01	5.92E-01		1.07E+00	1.04E-05	Up	-4.19E-01	4.38E-15		1.34E-01	1.02E-02		Unigene48582_All//gi|48431269|gb|AAT44124.1|//2.00E-84//F3H-like protein [Saussurea medusa]	Unigene48582_All//3.00E-60//AT4G10500| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene48582_All//0.00E+00//TC150457		ko00941|Flavonoid biosynthesis/ko00904|Diterpenoid biosynthesis	GO:0016491	nr -
Unigene48585_All	1359	13.24	10.51	8.42	21.81	20.42	15.29	11.51	7.32	5.01	-3.33E-01	1.22E-02		-6.53E-01	1.28E-06		-9.48E-02	4.25E-01		-5.13E-01	9.46E-08		-6.53E-01	2.08E-07		-1.20E+00	8.84E-20	Down	Unigene48585_All//gi|15215713|gb|AAB91402.1|//1.00E-102//At1g27930/F13K9_4 [Arabidopsis thaliana] >gi|21700811|gb|AAM70529.1| At1g27930/F13K9_4 [Arabidopsis thaliana]	Unigene48585_All//7.00E-104//AT1G27930| unknown protein	Unigene48585_All//0.00E+00//TC162871			GO:0031410	nr -
Unigene48587_All	280	0.00	0.00	0.95	0.00	0.00	2.26	0.00	0.30	0.14	null	null		9.89E+00	8.01E-02		null	null		1.11E+01	7.60E-04	Up	8.22E+00	4.00E-01		7.15E+00	6.44E-01		Unigene48587_All//gi|297801284|ref|XP_002868526.1|//3.00E-36//thiF family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314362|gb|EFH44785.1| thiF family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48587_All//5.00E-22//AT5G37530| thiF family protein	Unigene48587_All//7.00E-70//DW517396			GO:0043231	nr -
Unigene48588_All	1407	2.42	2.38	1.82	3.93	3.70	4.37	5.14	2.85	2.18	-2.43E-02	9.60E-01		-4.12E-01	2.47E-01		-8.87E-02	7.86E-01		1.52E-01	6.14E-01		-8.50E-01	1.27E-05		-1.24E+00	4.73E-10	Down	Unigene48588_All//gi|297801284|ref|XP_002868526.1|//0.00E+00//thiF family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314362|gb|EFH44785.1| thiF family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48588_All//9.00E-179//AT5G37530| thiF family protein	Unigene48588_All//0.00E+00//gi|21097490|gb|BQ409803.1|BQ409803			GO:0044464	nr -
Unigene48589_All	884	94.28	26.37	192.58	31.78	67.55	30.91	3.59	22.74	11.00	-1.84E+00	5.40E-152	Down	1.03E+00	4.90E-125	Up	1.09E+00	1.39E-58	Up	-4.02E-02	7.42E-01		2.66E+00	3.10E-71	Up	1.62E+00	3.90E-19	Up	Unigene48589_All//gi|254692064|emb|CBA10126.1|//1.00E-48//PME inhibitor [Nicotiana benthamiana]	Unigene48589_All//2.00E-47//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene48589_All//0.00E+00//TC144097		ko00500|Starch and sucrose metabolism/ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0030234	nr -
Unigene48591_All	1170	123.33	35.77	96.71	143.10	132.36	131.75	210.35	95.06	101.61	-1.79E+00	1.72E-252	Down	-3.51E-01	5.68E-16		-1.13E-01	4.35E-03		-1.19E-01	3.48E-03		-1.15E+00	4.22E-270	Down	-1.05E+00	7.84E-241	Down	Unigene48591_All//gi|151347486|gb|ABS01352.1|//0.00E+00//methionine synthase [Carica papaya]	Unigene48591_All//2.00E-179//AT5G17920| ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase	Unigene48591_All//0.00E+00//gi|48812015|gb|CO113328.1|CO113328		ko00270|Cysteine and methionine metabolism	GO:0000097//GO:0008172//GO:0044424//GO:0046914	nr +
Unigene48592_All	974	56.78	34.18	46.53	44.03	43.20	27.68	85.04	56.99	35.09	-7.32E-01	5.43E-24		-2.87E-01	9.90E-05		-2.75E-02	8.20E-01		-6.70E-01	2.79E-17		-5.78E-01	8.55E-29		-1.28E+00	2.54E-111	Down	Unigene48592_All//gi|30725530|gb|AAP37787.1|//3.00E-37//At4g30200 [Arabidopsis thaliana]	Unigene48592_All//2.00E-38//AT4G30200| Encodes a protein with similarity to VRN5 and VIN3.Contains both a fibronectin III and PHD finger domain. VEL1 is a part of a polycomb repressive complex (PRC2) that is involved in epigenetic silencing of the FLC flowering locus.	Unigene48592_All//0.00E+00//TC162582			GO:0003006//GO:0043234	nr +

Unigene48593_All	612	18.64	27.16	27.76	2.36	6.98	8.93	2.63	0.55	1.17	5.43E-01	6.64E-05		5.75E-01	3.59E-05		1.56E+00	1.44E-07	Up	1.92E+00	1.09E-11	Up	-2.26E+00	2.23E-05	Down	-1.16E+00	1.02E-02		Unigene48593_All//gi|124360239|gb|ABN08252.1|//1.00E-45//Zinc finger, RING-type [Medicago truncatula] >gi|124360861|gb|ABN08833.1| Zinc finger, RING-type [Medicago truncatula]	Unigene48593_All//3.00E-18//AT4G33565| protein binding / zinc ion binding	Unigene48593_All//8.00E-130//ESS30919			GO:0031410//GO:0046914	nr +
Unigene48594_All	764	27.26	57.77	53.53	7.89	16.41	13.12	1.11	1.20	1.77	1.08E+00	1.40E-36	Up	9.74E-01	1.10E-27		1.06E+00	5.58E-12	Up	7.34E-01	3.52E-05		1.21E-01	8.54E-01		6.80E-01	1.74E-01		Unigene48594_All//gi|124360239|gb|ABN08252.1|//1.00E-49//Zinc finger, RING-type [Medicago truncatula] >gi|124360861|gb|ABN08833.1| Zinc finger, RING-type [Medicago truncatula]	Unigene48594_All//2.00E-18//AT4G33565| protein binding / zinc ion binding	Unigene48594_All//1.00E-138//ESS30919			GO:0031410//GO:0046914	nr +
Unigene48595_All	1141	3.16	2.22	3.31	6.59	6.37	4.55	2.33	0.81	1.85	-5.11E-01	1.19E-01		6.66E-02	8.39E-01		-5.00E-02	8.22E-01		-5.34E-01	1.17E-02		-1.53E+00	2.46E-05	Down	-3.35E-01	3.41E-01		Unigene48595_All//gi|15226168|ref|NP_178215.1|//4.00E-17//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene48595_All//2.00E-18//AT2G01050| nucleic acid binding / zinc ion binding				nr +
Unigene48597_All	1344	1.71	0.23	0.40	1.07	0.90	1.51	7.14	2.55	4.33	-2.92E+00	6.54E-08	Down	-2.11E+00	2.16E-05	Down	-2.61E-01	6.33E-01		4.92E-01	3.11E-01		-1.49E+00	1.86E-16	Down	-7.23E-01	7.39E-06		Unigene48597_All//gi|224071947|ref|XP_002303599.1|//0.00E+00//tir-nbs resistance protein [Populus trichocarpa] >gi|222841031|gb|EEE78578.1| tir-nbs resistance protein [Populus trichocarpa]	Unigene48597_All//0.00E+00//AT4G23440| nucleoside-triphosphatase/ nucleotide binding / transmembrane receptor	Unigene48597_All//4.00E-10//DR453777			GO:0004872//GO:0006952//GO:0012501//GO:0016462//GO:0023060//GO:0032559//GO:0044425	nr -
Unigene48599_All	1238	2.07	2.95	1.46	6.68	11.54	7.92	2.60	5.91	2.99	5.09E-01	1.20E-01		-5.02E-01	2.39E-01		7.89E-01	1.45E-08		2.45E-01	2.30E-01		1.19E+00	3.09E-09	Up	2.05E-01	5.00E-01		Unigene48599_All//gi|158706508|sp|Q56XQ0.2|U4961_ARATH//5.00E-23//RecName: Full=UPF0496 protein At2g18630	Unigene48599_All//1.00E-17//AT2G18630| unknown protein	Unigene48599_All//1.00E-13//gi|109889545|gb|DW518513.1|DW518513			GO:0042579	nr +
Unigene48600_All	1052	2.98	8.09	2.58	2.84	3.21	4.25	4.82	3.93	3.29	1.44E+00	1.68E-11	Up	-2.09E-01	6.00E-01		1.75E-01	6.48E-01		5.81E-01	4.57E-02		-2.94E-01	2.47E-01		-5.50E-01	1.67E-02		Unigene48600_All//gi|115468582|ref|NP_001057890.1|//1.00E-31//Os06g0565300 (Oryza sativa Japonica Group) >gi|113565930|dbj|BAF19804.1| Os06g0565300 (Oryza sativa Japonica Group)	Unigene48600_All//5.00E-46//AT3G13780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: SMAD/FHA domain (InterPro:IPR008984); Has 14184 Blast hits to 8674 proteins in 364 species: Archae - 7; Bacteria - 1751; Metazoa - 6167; Fungi - 1701; Plants - 645; Viruses - 191; Other Eukaryotes - 3722 (source: NCBI BLink).					nr +
Unigene48601_All	830	69.03	72.16	74.87	166.13	117.58	106.27	160.16	112.45	60.77	6.40E-02	4.11E-01		1.17E-01	1.29E-01		-4.99E-01	3.66E-36		-6.45E-01	8.41E-51		-5.10E-01	1.08E-36		-1.40E+00	7.19E-205	Down	Unigene48601_All//gi|1360725|emb|CAA87068.1|//1.00E-52//non-photosynthetic ferredoxin [Citrus sinensis]	Unigene48601_All//4.00E-50//AT2G27510| AIF103 (ferredoxin 3); 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding	Unigene48601_All//0.00E+00//TC146166		ko00195|Photosynthesis	GO:0006091//GO:0009536//GO:0043169//GO:0051536	nr -
Unigene48602_All	1494	1.54	1.97	1.92	5.23	4.84	5.62	7.50	7.47	3.33	3.52E-01	3.60E-01		3.21E-01	4.05E-01		-1.13E-01	6.27E-01		1.03E-01	6.71E-01		-5.80E-03	1.01E+00		-1.17E+00	6.81E-14	Down	Unigene48602_All//gi|297824457|ref|XP_002880111.1|//1.00E-126//N-terminal asparagine amidohydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325950|gb|EFH56370.1| N-terminal asparagine amidohydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48602_All//9.00E-114//AT2G44420| protein N-terminal asparagine amidohydrolase family protein	Unigene48602_All//0.00E+00//TC173999			GO:0043231	nr +
Unigene48604_All	1353	1.89	0.56	0.55	1.55	1.37	1.34	1.81	1.85	2.77	-1.75E+00	4.31E-05	Down	-1.78E+00	6.83E-05	Down	-1.70E-01	7.32E-01		-2.12E-01	6.63E-01		3.23E-02	9.55E-01		6.11E-01	2.59E-02		Unigene48604_All//gi|15237034|ref|NP_195279.1|//6.00E-80//transcription regulator/ zinc ion binding [Arabidopsis thaliana]	Unigene48604_All//2.00E-65//AT4G35540| transcription regulator/ zinc ion binding	Unigene48604_All//1.00E-34//gi|109856429|gb|DW485408.1|DW485408			GO:0005488//GO:0006350	nr +
Unigene48606_All	673	0.93	0.38	0.95	5.55	5.32	2.01	2.64	0.37	0.71	-1.31E+00	1.61E-01		2.54E-02	9.97E-01		-6.10E-02	8.50E-01		-1.46E+00	6.80E-06	Down	-2.82E+00	2.67E-07	Down	-1.89E+00	4.84E-05	Down	Unigene48606_All//gi|42568402|ref|NP_199685.2|//3.00E-38//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|261664537|sp|C0LGV0.1|Y5487_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At5g48740; Flags: Precursor >gi|224589707|gb|ACN59385.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene48606_All//8.00E-39//AT5G48740| leucine-rich repeat family protein / protein kinase family protein	Unigene48606_All//1.00E-73//ESS35766			GO:0004672//GO:0005488//GO:0044464	nr -
Unigene48607_All	264	0.20	0.00	1.61	4.72	1.43	4.79	3.20	0.32	0.60	-7.63E+00	6.11E-01		3.03E+00	5.73E-02		-1.72E+00	3.99E-03		2.21E-02	9.71E-01		-3.34E+00	2.51E-04	Down	-2.41E+00	1.68E-03				Unigene48607_All//4.00E-68//gi|54119356|gb|CO494865.1|CO494865				
Unigene48608_All	1637	0.51	0.31	0.62	3.93	3.98	3.61	3.33	0.77	1.07	-7.25E-01	3.48E-01		2.73E-01	6.75E-01		1.83E-02	9.48E-01		-1.19E-01	6.62E-01		-2.12E+00	2.46E-15	Down	-1.64E+00	1.99E-11	Down	Unigene48608_All//gi|42568402|ref|NP_199685.2|//5.00E-96//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|261664537|sp|C0LGV0.1|Y5487_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At5g48740; Flags: Precursor >gi|224589707|gb|ACN59385.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene48608_All//1.00E-89//AT5G48740| leucine-rich repeat family protein / protein kinase family protein	Unigene48608_All//0.00E+00//TC161479		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559//GO:0044464	nr +
Unigene48609_All	942	2.89	3.82	2.88	14.28	14.04	9.25	1.97	1.24	0.25	4.03E-01	2.26E-01		-2.60E-03	9.94E-01		-2.45E-02	8.92E-01		-6.26E-01	2.76E-05		-6.69E-01	1.22E-01		-2.96E+00	2.82E-08	Down	Unigene48609_All//gi|115446781|ref|NP_001047170.1|//1.00E-07//Os02g0566300 (Oryza sativa Japonica Group) >gi|113536701|dbj|BAF09084.1| Os02g0566300 (Oryza sativa Japonica Group)		Unigene48609_All//0.00E+00//TC165739				nr +
Unigene48611_All	543	16.28	34.99	17.26	10.83	17.19	15.30	2.57	2.31	2.27	1.10E+00	1.24E-16	Up	8.40E-02	6.82E-01		6.67E-01	1.82E-04		5.00E-01	1.35E-02		-1.54E-01	7.65E-01		-1.76E-01	7.13E-01				Unigene48611_All//1.00E-146//gi|3325364|gb|AI054150.1|AI054150				
Unigene48613_All	989	6.88	4.15	7.43	4.43	4.74	4.43	5.17	2.32	2.74	-7.29E-01	1.17E-03		1.12E-01	6.23E-01		9.54E-02	8.07E-01		-9.00E-04	9.94E-01		-1.15E+00	1.88E-06	Down	-9.17E-01	7.14E-05	Down	Unigene48613_All//gi|226502060|ref|NP_00115011 7.1|//5.00E-78//LOC100283746 [Zea mays] >gi|195636860|gb|ACG37888.1| catalytic/ hydrolase [Zea mays]	Unigene48613_All//5.00E-76//AT1G79790| haloacid dehalogenase-like hydrolase family protein	Unigene48613_All//0.00E+00//TC169213			GO:0009536//GO:0016787	nr +
Unigene48614_All	1091	3.50	236.12	27.19	5.57	15.31	22.64	83.86	374.74	414.05	6.08E+00	0.00E+00	Up	2.96E+00	3.32E-93	Up	1.46E+00	7.81E-26	Up	2.02E+00	7.62E-55	Up	2.16E+00	0.00E+00	Up	2.30E+00	0.00E+00	Up	Unigene48614_All//gi|187940301|gb|ACD39381.1|//3.00E-86//NAC domain protein [Glycine max]	Unigene48614_All//1.00E-58//AT1G69490| NAP (NAC-like, activated by AP3/PI); transcription factor	Unigene48614_All//0.00E+00//TC170351	NAC		GO:0001071//GO:0003676//GO:0009791//GO:0010260//GO:0010468//GO:0016149//GO:0043231	nr +
Unigene48615_All	878	10.01	4.33	5.94	25.08	12.98	9.72	2.02	1.67	1.00	-1.21E+00	2.64E-09	Down	-7.52E-01	1.99E-04		-9.50E-01	2.84E-18		-1.37E+00	9.93E-29	Down	-2.80E-01	5.63E-01		-1.02E+00	1.59E-02		Unigene48615_All//gi|195655707|gb|ACG47321.1|//2.00E-29//negatively light-regulated protein [Zea mays]	Unigene48615_All//2.00E-21//AT1G69510| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Lg106-like (InterPro:IPR012482); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64120.1); Has 92 Blast hits to 92 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 92; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene48615_All//8.00E-131//DR461420				nr +
Unigene48616_All	941	16.35	9.80	10.53	40.60	35.35	42.24	35.00	18.65	15.16	-7.38E-01	2.43E-07		-6.35E-01	1.57E-05		-2.00E-01	2.17E-02		5.69E-02	6.27E-01		-9.08E-01	2.47E-25		-1.21E+00	4.34E-41	Down	Unigene48616_All//gi|17065324|gb|AAL32816.1|//8.00E-41//unknown protein [Arabidopsis thaliana]	Unigene48616_All//7.00E-20//AT1G11240| unknown protein	Unigene48616_All//0.00E+00//gi|84168007|gb|DR456655.1|DR456655				nr +
Unigene48617_All	2343	0.04	0.13	0.14	1.70	1.18	1.14	14.87	2.52	24.74	1.54E+00	3.23E-01		1.61E+00	3.04E-01		-5.33E-01	7.48E-02		-5.81E-01	6.10E-02		-2.56E+00	3.38E-118	Down	7.35E-01	1.56E-31		Unigene48617_All//gi|28268880|dbj|BAC56865.1|//0.00E+00//respiratory burst oxidase homolog [Nicotiana benthamiana]	Unigene48617_All//0.00E+00//AT5G51060| RHD2 (ROOT HAIR DEFECTIVE 2); NAD(P)H oxidase	Unigene48617_All//0.00E+00//DT459768		ko04626|Plant-pathogen interaction	GO:0006950//GO:0008152//GO:0009913//GO:0010033//GO:0016021//GO:0016209//GO:0030554//GO:0046914//GO:0050664	nr -
Unigene4862_All	1393	94.99	118.69	100.19	34.08	23.53	18.90	4.37	1.41	1.49	3.21E-01	3.60E-16		7.69E-02	1.34E-01		-5.34E-01	2.30E-14		-8.50E-01	1.32E-28		-1.63E+00	3.49E-12	Down	-1.56E+00	8.24E-12	Down	Unigene4862_All//gi|82568711|dbj|BAE48668.1|//1.00E-127//Alcohol acyl-transferase [Prunus mume]	Unigene4862_All//3.00E-118//AT5G48930| HCT (HYDROXYCINNAMOYL-COA SHIKIMATE/QUINATE HYDROXYCINNAMOYL TRANSFERASE); quinate O-hydroxycinnamoyltransferase/ shikimate O-hydroxycinnamoyltransferase/ transferase	Unigene4862_All//0.00E+00//TC132479		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene48621_All	636	8.06	2.55	1.51	99.71	76.07	123.63	49.53	71.76	83.37	-1.66E+00	8.86E-09	Down	-2.42E+00	3.38E-13	Down	-3.90E-01	7.42E-11		3.10E-01	5.16E-08		5.35E-01	3.02E-14		7.51E-01	4.69E-30		Unigene48621_All//gi|22947852|gb|AAN07898.1|//2.00E-75//xyloglucan endotransglycosylase [Malus x domestica] >gi|187372984|gb|ACD03226.1| xyloglucan endotransglucosylase/hydrolase 2 [Malus x domestica]	Unigene48621_All//4.00E-67//AT5G57560| TCH4 (Touch 4); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene48621_All//0.00E+00//TC134464			GO:0005576//GO:0016758//GO:0016798//GO:0030312//GO:0044042	nr +
Unigene48622_All	562	25.97	2.61	1.80	119.75	107.41	90.57	69.97	35.03	76.77	-3.31E+00	4.85E-53	Down	-3.85E+00	7.83E-58	Down	-1.57E-01	1.51E-02		-4.03E-01	5.46E-11		-9.98E-01	4.16E-35		1.34E-01	7.96E-02		Unigene48622_All//gi|187372996|gb|ACD03232.1|//3.00E-61//xyloglucan endotransglucosylase/hydrolase 8 [Malus x domestica]	Unigene48622_All//2.00E-53//AT5G57560| TCH4 (Touch 4); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene48622_All//0.00E+00//TC138737			GO:0005576//GO:0016758//GO:0016798//GO:0030312//GO:0044042	nr +
Unigene48623_All	704	11.07	19.00	11.57	17.90	19.22	19.76	5.59	11.52	13.36	7.79E-01	5.04E-07		6.36E-02	7.74E-01		1.03E-01	5.84E-01		1.42E-01	4.27E-01		1.04E+00	2.05E-08	Up	1.26E+00	5.25E-13	Up	Unigene48623_All//gi|255581966|ref|XP_002531781.1|//7.00E-19//conserved hypothetical protein [Ricinus communis] >gi|223528574|gb|EEF30595.1| conserved hypothetical protein [Ricinus communis]	Unigene48623_All//2.00E-12//AT2G35658| unknown protein	Unigene48623_All//0.00E+00//gi|73863937|gb|DT466676.1|DT466676			GO:0043231	nr +

Unigene48624_All	773	4.60	17.04	5.65	12.24	15.86	18.17	28.77	39.36	37.78	1.89E+00	2.87E-25	Up	2.96E-01	3.61E-01		3.73E-01	1.99E-02		5.70E-01	1.04E-04		4.52E-01	2.09E-07		3.93E-01	6.92E-06		Unigene48624_All//gi|227202782|dbj|BAH56864.1|//2.00E-35//AT2G18670 [Arabidopsis thaliana]	Unigene48624_All//3.00E-25//AT2G18670| zinc finger (C3HC4-type RING finger) family protein	Unigene48624_All//0.00E+00//TC164965		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0009743//GO:0046872	nr +
Unigene48625_All	946	31.41	99.46	24.09	35.49	25.15	35.62	46.39	107.32	70.33	1.66E+00	3.32E-148	Up	-3.83E-01	2.00E-04		-4.97E-01	4.39E-09		5.00E-03	9.59E-01		1.21E+00	1.26E-121	Up	6.00E-01	1.61E-25		Unigene48625_All//gi|224123924|ref|XP_002330243.1|//3.00E-18//predicted protein [Populus trichocarpa] >gi|222871699|gb|EEF08830.1| predicted protein [Populus trichocarpa]		Unigene48625_All//0.00E+00//TC138777				nr +
Unigene48628_All	991	4.33	2.15	3.65	4.47	5.52	4.74	6.36	2.40	4.82	-1.01E+00	6.24E-04	Down	-2.45E-01	4.37E-01		3.05E-01	2.77E-01		8.33E-02	7.91E-01		-1.40E+00	3.15E-10	Down	-3.98E-01	5.43E-02		Unigene48628_All//gi|297792573|ref|XP_002864171.1|//3.00E-10//oxidoreductase/ transition metal ion binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297310006|gb|EFH10430.1| oxidoreductase/ transition metal ion binding protein [Arabidopsis lyrata subsp. lyrata]		Unigene48628_All//3.00E-19//CO104866				nr -
Unigene48630_All	1713	3.91	3.61	3.98	4.86	4.06	2.00	0.12	0.10	0.09	-1.16E-01	6.13E-01		2.54E-02	9.29E-01		-2.58E-01	2.26E-01		-1.28E+00	3.80E-10	Down	-3.38E-01	8.11E-01		-4.08E-01	7.55E-01		Unigene48630_All//gi|51849627|dbj|BAD42345.1|//0.00E+00//sorbitol transporter [Malus x domestica]	Unigene48630_All//4.00E-162//AT3G18830| ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann	Unigene48630_All//0.00E+00//gi|164343060|gb|ES824599.1|ES824599			GO:0006810//GO:0008152//GO:0016628//GO:0022857//GO:0031224	nr -
Unigene48631_All	861	66.66	50.61	47.25	155.05	155.46	128.88	39.53	11.12	8.10	-3.97E-01	9.18E-09		-4.97E-01	2.96E-12		3.80E-03	9.62E-01		-2.67E-01	4.60E-10		-1.83E+00	9.55E-76	Down	-2.29E+00	3.88E-104	Down	Unigene48631_All//gi|21703131|gb|AAM14506.1|//4.00E-70//AT5g16250/T21H19_170 [Arabidopsis thaliana] >gi|23505791|gb|AAN28755.1| At5g16250/T21H19_170 [Arabidopsis thaliana]	Unigene48631_All//5.00E-63//AT5G16250| unknown protein	Unigene48631_All//0.00E+00//gi|13349543|gb|BG439886.1|BG439886				nr -
Unigene48633_All	787	5.98	6.82	7.92	51.21	42.09	29.15	41.69	18.32	19.74	1.90E-01	4.91E-01		4.04E-01	1.12E-01		-2.83E-01	3.84E-04		-8.13E-01	1.38E-22		-1.19E+00	1.13E-38	Down	-1.08E+00	2.78E-34	Down		Unigene48633_All//5.00E-05//AT5G09463| CPuORF41 (Conserved peptide upstream open reading frame 41)	Unigene48633_All//0.00E+00//gi|73863011|gb|DT465750.1|DT465750				
Unigene48634_All	1004	29.55	65.41	42.96	35.77	46.20	48.49	33.56	40.59	38.05	1.15E+00	3.61E-59	Up	5.40E-01	8.03E-11		3.69E-01	3.33E-07		4.39E-01	2.32E-09		2.74E-01	2.81E-04		1.81E-01	2.19E-02		Unigene48634_All//gi|145334895|ref|NP_001078793.1|//7.00E-19//dentin sialophosphoprotein-related [Arabidopsis thaliana]	Unigene48634_All//4.00E-20//AT5G64170| dentin sialophosphoprotein-related	Unigene48634_All//0.00E+00//gi|78331057|gb|DT551331.1|DT551331				nr -
Unigene48636_All	852	45.57	11.24	10.88	48.82	30.39	55.50	89.92	31.64	30.44	-2.02E+00	1.47E-80	Down	-2.07E+00	3.82E-80	Down	-6.84E-01	1.77E-19		1.85E-01	2.26E-02		-1.51E+00	1.13E-128	Down	-1.56E+00	1.17E-139	Down	Unigene48636_All//gi|82623403|gb|AB887116.1|//2.00E-69//40S ribosomal protein S19-like [Solanum tuberosum]	Unigene48636_All//1.00E-69//AT5G61170| 40S ribosomal protein S19 (RPS19C)	Unigene48636_All//0.00E+00//TC149868		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0031981	nr +
Unigene48638_All	1061	17.70	43.22	25.40	22.30	22.30	26.14	22.00	22.26	19.22	1.29E+00	9.87E-50	Up	5.21E-01	1.30E-06		-3.00E-04	9.94E-01		2.29E-01	3.46E-02		1.70E-02	8.99E-01		-1.94E-01	6.15E-02		Unigene48638_All//gi|13926327|gb|AK49628.1|AF372912_1//1.00E-73//At1g26660/T24P13_4 [Arabidopsis thaliana] >gi|16323258|gb|AAL15363.1| At1g26660/T24P13_4 [Arabidopsis thaliana]	Unigene48638_All//1.00E-70//AT1G26665| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: RNA polymerase II mediator complex protein-related (TAIR:AT5G41910.1); Has 223 Blast hits to 223 proteins in 105 species: Archae - 0; Bacteria - 0; Metazoa - 112; Fungi - 83; Plants - 24; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene48638_All//0.00E+00//gi|164354504|gb|ES839670.1|ES839670			GO:0006355//GO:0016251//GO:0043234	nr +
Unigene48639_All	784	28.30	32.38	27.64	43.52	37.16	36.64	47.03	26.66	21.09	1.95E-01	9.04E-02		-3.36E-02	8.00E-01		-2.28E-01	1.24E-02		-2.49E-01	8.16E-03		-8.19E-01	7.46E-24		-1.16E+00	6.24E-43	Down	Unigene48639_All//gi|18402340|ref|NP_565699.1|//1.00E-48//KIS (KIESEL); unfolded protein binding [Arabidopsis thaliana] >gi|21542453|sp|O04350.2|TBCA_ARATH RecName: Full=Tubulin-specific chaperone A; AltName: Full=Tubulin-folding cofactor A; Short=CFA; AltName: Full=TCP1-chaperonin cofactor A >gi|20514257|gb|AAM22957.1|AF486848_1 tubulin folding cofactor A [Arabidopsis thaliana] >gi|20196887|gb|AAM14821.1| TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] >gi|20198325|gb|AAB63093.2| TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana] >gi|21553949|gb|AAM63030.1| TCP1-chaperonin cofactor A isolog [Arabidopsis thaliana]	Unigene48639_All//7.00E-50//AT2G30410| KIS (KIESEL); unfolded protein binding	Unigene48639_All//0.00E+00//gi|164250803|gb|ES848349.1|ES848349			GO:0005515//GO:0015630//GO:0043623//GO:0051301	nr -
Unigene48864_All	875	0.90	0.23	0.24	6.26	7.44	3.10	42.33	1.72	14.39	-1.95E+00	2.62E-02		-1.88E+00	4.13E-02		2.48E-01	3.28E-01		-1.02E+00	5.39E-05	Down	-4.62E+00	1.17E-210	Down	-1.56E+00	1.46E-67	Down	Unigene4864_All//gi|15242112|ref|NP_199965.1|//3.00E-35//invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana] >gi|9758194|dbj|BAB08668.1| ripening-related protein-like [Arabidopsis thaliana] >gi|67633876|gb|AAY78862.1| invertase [Arabidopsis thaliana]	Unigene4864_All//1.00E-36//AT5G51520| invertase/pectin methylesterase inhibitor family protein			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene48642_All	1289	3.90	2.99	3.06	5.68	6.14	6.55	7.05	3.53	3.43	-3.83E-01	1.60E-01		-3.50E-01	2.35E-01		1.13E-01	6.42E-01		2.06E-01	3.78E-01		-9.97E-01	1.01E-08		-1.04E+00	1.32E-09	Down	Unigene48642_All//gi|297538283|ref|XP_002887023.1|//1.00E-103//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297332864|gb|EFH63282.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene48642_All//1.00E-101//AT1G66345| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene48646_All	1021	0.51	0.99	0.00	2.39	4.45	2.03	9.36	4.09	18.73	9.54E-01	1.65E-01		-9.00E+00	4.75E-03		8.97E-01	1.01E-03		-2.33E-01	6.31E-01		-1.19E+00	6.19E-12	Down	1.00E+00	5.51E-18	Up	Unigene48646_All//gi|124109195|gb|ABM91073.1|//1.00E-139//xyloglucan endotransglycosylase/hydrolase precursor XTH-17 [Populus tremula x Populus tremuloides]	Unigene48646_All//4.00E-122//AT4G25810| XTR6 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6); hydrolase, acting on glycosyl bonds / hydrolase, hydrolyzing O-glycosyl compounds / xyloglucan:xyloglucosyl transferase	Unigene48646_All//0.00E+00//TC134856				nr +
Unigene48647_All	422	0.25	2.52	2.15	0.24	0.41	0.86	3.21	5.05	2.83	3.35E+00	2.17E-04	Up	3.11E+00	1.76E-03		7.89E-01	7.70E-01		1.86E+00	2.19E-01		6.56E-01	9.89E-02		-1.79E-01	7.13E-01		Unigene48647_All//gi|34925093|sp|P93788.1|REMO_SOLTU//4.00E-07//RecName: Full=Remorin; AltName: Full=pg34 >gi|1881585|gb|AAB49425.1| remorin [Solanum tuberosum]		Unigene48647_All//1.00E-66//DW233029			GO:0016020//GO:0043168	nr +
Unigene48648_All	634	34.25	105.65	51.40	41.80	47.85	47.59	22.81	21.49	12.57	1.63E+00	2.82E-102	Up	5.86E-01	1.49E-09		1.95E-01	5.67E-02		1.87E-01	7.87E-02		-8.57E-02	6.14E-01		-8.60E-01	5.50E-11		Unigene48648_All//gi|259490269|ref|NP_001159012.1|//6.00E-26//remorin [Zea mays] >gi|195628632|gb|ACG36146.1| remorin [Zea mays]	Unigene48648_All//8.00E-26//AT5G23750| remorin family protein	Unigene48648_All//4.00E-141//TC170476			GO:0007154//GO:0016020//GO:0043168//GO:0043231//GO:0051234	nr -
Unigene48649_All	1311	1.12	0.39	0.81	2.20	1.08	1.72	2.90	0.86	1.55	-1.53E+00	7.80E-03		-4.60E-01	4.10E-01		-1.03E+00	2.84E-03		-3.56E-01	3.84E-01		-1.75E+00	1.17E-08	Down	-9.05E-01	8.75E-04		Unigene48649_All//gi|115476752|ref|NP_001061972.1|//1.00E-104//Os08g0459100 [Oryza sativa Japonica Group] >gi|113623941|dbj|BAF23886.1| Os08g0459100 [Oryza sativa Japonica Group]	Unigene48649_All//2.00E-128//AT2G06040| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: Leucine-rich repeat, cysteine-containing subtype (InterPro:IPR006553); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G21900.1); Has 3642 Blast hits to 1885 proteins in 175 species: Archae - 0; Bacteria - 109; Metazoa - 2066; Fungi - 492; Plants - 697; Viruses - 0; Other Eukaryotes - 278 (source: NCBI BLink).	Unigene48649_All//2.00E-117//TC173193		ko04626|Plant-pathogen interaction//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene4865_All	649	2.74	30.53	2.79	1.46	3.08	4.04	3.91	17.77	2.21	3.48E+00	3.06E-74	Up	2.54E-02	9.78E-01		1.08E+00	1.83E-02		1.47E+00	2.87E-04	Up	2.19E+00	1.00E-32	Up	-8.23E-01	1.58E-02		Unigene4865_All//gi|167962173|dbj|BAG09537.1|//5.00E-56//peroxisomal small heat shock protein [Glycine max]	Unigene4865_All//1.00E-45//AT5G37670| 15.7 kDa class I-related small heat shock protein-like (HSP15.7-CI)	Unigene4865_All//0.00E+00//TC162233				nr -
Unigene48650_All	1435	0.29	0.07	0.15	7.57	4.75	2.52	2.50	2.97	2.89	-2.05E+00	1.20E-01		-9.75E-01	4.11E-01		-6.72E-01	2.51E-05		-1.59E+00	6.36E-18	Down	2.46E-01	4.09E-01		2.05E-01	4.71E-01		Unigene48650_All//gi|297818318|ref|XP_002877042.1|//3.00E-73//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322880|gb|EFH53300.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48650_All//4.00E-131//AT4G37420| unknown protein					nr -
Unigene48651_All	1687	0.93	0.99	0.88	0.71	1.55	1.98	5.99	3.30	7.96	9.13E-02	8.53E-01		-7.41E-02	8.92E-01		1.13E+00	3.31E-03		1.48E+00	2.46E-05	Up	-8.62E-01	1.04E-07		4.10E-01	2.24E-03		Unigene48651_All//gi|75151444|sp|Q8GJ2.1|Y2608_ARATH//1.00E-61//RecName: Full=B3 domain-containing protein At2g36080; AltName: Full=Protein AUXIN RESPONSIVE FACTOR 31	Unigene48651_All//5.00E-57//AT2G36080| DNA-binding protein, putative	Unigene48651_All//3.00E-107//gi|78341852|gb|DT562126.1|DT562126	ABI3VP1		GO:0006350//GO:0010468//GO:0030528	nr +

Unigene48653_All	1344	6.23	10.93	5.90	53.26	74.53	47.31	21.05	7.74	9.19	8.12E-01	3.91E-08		-7.74E-02	7.17E-01		4.85E-01	1.62E-24		-1.71E-01	7.50E-03		-1.44E+00	5.40E-45	Down	-1.20E+00	7.10E-35	Down	Unigene48653_All//gi|22327990|ref|NP_200888.2|//3.00E-73//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|28416657|gb|AAO42859.1|At5g60800 [Arabidopsis thaliana]	Unigene48653_All//6.00E-32//AT5G60800| heavy-metal-associated domain-containing protein	Unigene48653_All//0.00E+00//DW513794		ko03040|Spliceosome		nr -
Unigene48654_All	675	28.06	38.51	34.08	40.00	38.67	37.67	82.56	51.21	34.41	4.57E-01	1.79E-05		2.80E-01	2.21E-02		-4.88E-02	7.24E-01		-8.66E-02	4.99E-01		-6.89E-01	1.35E-26		-1.26E+00	7.22E-74	Down	Unigene48654_All//gi|224117802|ref|XP_002331635.1|//3.00E-63//methylenetetrahydrofolate reductase [Populus trichocarpa] >gi|222874031|gb|EEF11162.1| methylenetetrahydrofolate reductase [Populus trichocarpa]	Unigene48654_All//6.00E-63//AT3G59970| MTHFR1 (METHYLENETETRAHYDROFOLATE REDUCTASE 1); methylenetetrahydrofolate reductase (NADPH)	Unigene48654_All//0.00E+00//gi|5044966|gb|AI726114.1|AI726114		ko00670|One carbon pool by folate	GO:0000096//GO:0016646	nr +
Unigene48655_All	380	6.20	2.40	1.12	4.46	5.89	4.28	6.12	0.88	1.47	-1.37E+00	1.46E-03		-2.47E+00	1.77E-06	Down	4.02E-01	3.92E-01		-5.90E-02	9.21E-01		-2.80E+00	2.78E-09	Down	-2.06E+00	5.41E-07	Down	Unigene48655_All//gi|8778729|gb|AAF79737.1|AC005106_18//3.00E-32//T25N20.9 [Arabidopsis thaliana]	Unigene48655_All//1.00E-33//AT1G05440| unknown protein	Unigene48655_All//1.00E-127//ES820715			GO:0008204//GO:0016863//GO:0043231	nr -
Unigene48656_All	1354	3.44	1.61	2.52	5.22	6.79	4.60	5.34	0.34	2.03	-1.10E+00	1.17E-04	Down	-4.50E-01	1.35E-01		3.78E-01	4.77E-02		-1.83E-01	4.66E-01		-3.97E+00	1.69E-37	Down	-1.40E+00	6.36E-12	Down	Unigene48656_All//gi|8778729|gb|AAF79737.1|AC005106_18//7.00E-73//T25N20.9 [Arabidopsis thaliana]	Unigene48656_All//2.00E-63//AT1G05440| unknown protein	Unigene48656_All//0.00E+00//ES820715			GO:0043231	nr +
Unigene48657_All	1071	49.34	44.14	56.93	68.33	80.96	93.53	93.28	47.84	31.51	-1.61E-01	3.67E-02		2.06E-01	4.08E-03		2.45E-01	2.77E-06		4.53E-01	1.07E-19		-9.63E-01	5.65E-83		-1.57E+00	1.74E-182	Down	Unigene48657_All//gi|25091506|sp|Q9SX77.1|UMP6_ARATH//2.00E-71//RecName: Full=Uncharacterized protein At1g47420, mitochondrial; Flags: Precursor >gi|5668814|gb|AAD46040.1|AC007519_25 ESTs gb|H36253 and gb|AA04251 come from this gene [Arabidopsis thaliana] >gi|15450966|gb|AAK96754.1| Unknown protein [Arabidopsis thaliana] >gi|23198274|gb|AAN15664.1| Unknown protein [Arabidopsis thaliana]	Unigene48657_All//9.00E-73//AT1G47420| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, nucleus; EXPRESSED IN: 26 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: GAMMA CA2 (GAMMA CARBONIC ANHYDRASE 2); carbonate dehydratase (TAIR:AT1G47260.1); Has 85 Blast hits to 85 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 84; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene48657_All//0.00E+00//TC1311197			GO:0043231	nr +
Unigene48659_All	2635	4.84	0.23	1.76	9.68	5.87	3.39	0.13	8.22	6.27	-4.39E+00	8.38E-58	Down	-1.46E+00	1.28E-16	Down	-7.22E-01	2.67E-13		-1.51E+00	1.42E-38	Down	6.00E+00	7.59E-139	Up	5.61E+00	5.95E-105	Up	Unigene48659_All//gi|224090288|ref|XP_002308966.1|//0.00E+00//cation proton exchanger [Populus trichocarpa] >gi|222854942|gb|EEE92489.1| cation proton exchanger [Populus trichocarpa]	Unigene48659_All//0.00E+00//AT3G53720| ATCHX20 (CATION/H+ EXCHANGER 20); monovalent cation:proton antiporter/ sodium:hydrogen antiporter	Unigene48659_All//3.00E-74//gi|48830746|gb|CO129136.1|CO129136			GO:0006811//GO:0015298//GO:0031224//GO:0050896	nr +
Unigene4866_All	812	1.42	0.12	0.39	2.33	1.65	1.28	2.97	1.70	2.06	-3.51E+00	6.57E-05	Down	-1.85E+00	1.07E-02		-4.95E-01	3.07E-01		-8.66E-01	7.02E-02		-8.05E-01	2.78E-02		-5.26E-01	1.40E-01		Unigene4866_All//gi|15239254|ref|NP_196202.1|//4.00E-34//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|30102534|gb|AAP21185.1| At5g05830 [Arabidopsis thaliana]	Unigene4866_All//3.00E-30//AT5G05830| zinc finger (C3HC4-type RING finger) family protein	Unigene4866_All//0.00E+00//gi|78339965|gb|DT560239.1|DT560239	NAC			nr +
Unigene48663_All	870	82.39	65.70	81.47	117.72	105.72	172.56	82.08	212.73	106.56	-3.27E-01	1.09E-07		-1.63E-02	8.27E-01		-1.55E-01	1.96E-03		5.52E-01	1.20E-41		1.37E+00	2.05E-269	Up	3.77E-01	1.66E-15		Unigene48663_All//gi|18404500|ref|NP_566763.1|//8.00E-88//auxin-responsive family protein [Arabidopsis thaliana] >gi|79313415|ref|NP_001030764.1| auxin-responsive family protein [Arabidopsis thaliana] >gi|16323200|gb|AAL15334.1| AT3g25290/MJL12_25 [Arabidopsis thaliana] >gi|25090093|gb|AAN72226.1| At3g25290/MJL12_25 [Arabidopsis thaliana]	Unigene48663_All//3.00E-86//AT3G25290| auxin-responsive family protein	Unigene48663_All//0.00E+00//gi|78342687|gb|DT562961.1|DT562961			GO:0016020	nr -
Unigene48668_All	1362	3.19	3.65	2.38	4.06	5.01	3.51	9.19	4.66	4.12	1.93E-01	5.03E-01		-4.19E-01	1.79E-01		3.02E-01	2.13E-01		-2.08E-01	4.83E-01		-9.78E-01	2.26E-11		-1.16E+00	3.90E-15	Down	Unigene48668_All//gi|7527722|gb|AAF63171.1|AC010657_7//4.00E-70//T5E21.16 [Arabidopsis thaliana] >gi|8778209|gb|AAF79218.1|AC006917_3 F10B6.4 [Arabidopsis thaliana]	Unigene48668_All//2.00E-77//AT4G09060| unknown protein	Unigene48668_All//0.00E+00//DW500134				nr -
Unigene48669_All	1265	75.98	64.85	57.38	154.60	203.48	302.61	238.11	58.81	64.66	-2.29E-01	1.70E-05		-4.05E-01	5.21E-14		3.96E-01	2.87E-43		9.69E-01	1.63E-280		-2.02E+00	0.00E+00	Down	-1.88E+00	0.00E+00	Down	Unigene48669_All//gi|14031049|gb|AK52084.1|//1.00E-146//peroxidase [Nicotiana tabacum]	Unigene48669_All//2.00E-124//AT1G71695| peroxidase 12 (PER12) (P12) (PRXR6)	Unigene48669_All//0.00E+00//TC160796		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene4867_All	1004	0.73	0.50	0.11	0.74	2.20	0.54	0.72	0.75	0.75	-5.32E-01	5.13E-01		-2.78E+00	1.04E-02		1.56E+00	3.90E-04	Up	-4.63E-01	6.06E-01		6.58E-02	9.46E-01		7.46E-02	9.33E-01		Unigene4867_All//gi|15239254|ref|NP_196202.1|//2.00E-51//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|30102534|gb|AAP21185.1| At5g05830 [Arabidopsis thaliana]	Unigene4867_All//3.00E-47//AT5G05830| zinc finger (C3HC4-type RING finger) family protein	Unigene4867_All//0.00E+00//TC163633				nr +
Unigene48670_All	840	41.36	26.48	24.34	59.72	66.82	67.37	61.36	28.61	28.41	-6.43E-01	2.18E-12		-7.65E-01	8.06E-16		1.62E-01	2.50E-02		1.74E-01	1.81E-02		-1.10E+00	1.43E-53	Down	-1.11E+00	6.27E-56	Down	Unigene48670_All//gi|33667910|gb|AAQ42534.1|//4.00E-30//SWIb domain-containing protein [Solanum chacoense]	Unigene48670_All//2.00E-27//AT2G35605| SWIB complex BAF60b domain-containing protein	Unigene48670_All//0.00E+00//gi|13247322|gb|BF269830.2|BF269830			GO:0043231//GO:0044444	nr -
Unigene48671_All	1100	3.71	5.53	2.76	21.06	18.88	22.01	87.90	140.32	353.15	5.75E-01	1.67E-02		-4.27E-01	1.86E-01		-1.58E-01	2.09E-01		6.36E-02	6.47E-01		6.75E-01	1.47E-69		2.01E+00	0.00E+00	Up	Unigene48671_All//gi|224120972|ref|XP_002318465.1|//6.00E-44//SAUR family protein [Populus trichocarpa] >gi|222859138|gb|EEE96685.1| SAUR family protein [Populus trichocarpa]	Unigene48671_All//1.00E-29//AT4G00880| auxin-responsive family protein	Unigene48671_All//0.00E+00//TC158008			GO:0009725	nr +
Unigene48672_All	785	24.33	28.79	40.57	26.14	69.09	38.83	0.22	0.43	0.00	2.43E-01	4.33E-02		7.38E-01	9.94E-14		1.40E+00	8.44E-79	Up	5.71E-01	1.87E-09		9.84E-01	4.24E-01		-7.75E+00	1.08E-01		Unigene48672_All//gi|114786427|gb|AB178942.1|//5.00E-56//aspartic protease [Ipomoea batatas]	Unigene48672_All//5.00E-38//AT4G04460| aspartyl protease family protein	Unigene48672_All//0.00E+00//TC157826			GO:0004175//GO:0019538//GO:0031410	nr -
Unigene48673_All	1453	0.58	0.77	0.22	15.87	10.33	8.49	7.97	1.09	4.22	4.13E-01	5.26E-01		-1.39E+00	9.66E-02		-6.19E-01	2.62E-09		-9.04E-01	1.14E-15		-2.87E+00	8.81E-45	Down	-9.17E-01	6.54E-10		Unigene48673_All//gi|177417106|gb|AK68745.2|//1.00E-45//Unknown protein [Arabidopsis thaliana]	Unigene48673_All//5.00E-35//AT5G61340| unknown protein	Unigene48673_All//0.00E+00//gi|54121787|gb|CO497296.1|CO497296				nr +
Unigene48677_All	1258	9.69	5.28	3.01	14.49	11.63	17.30	16.20	4.75	7.47	-8.77E-01	9.05E-08		-1.69E+00	1.86E-19	Down	-3.17E-01	1.22E-02		2.56E-01	3.82E-02		-1.77E+00	1.32E-43	Down	-1.12E+00	8.03E-23	Down	Unigene48677_All//gi|18398306|ref|NP_566339.1|//1.00E-107//electron transport SCO1/SenC family protein [Arabidopsis thaliana]	Unigene48677_All//6.00E-101//AT3G08950| electron transport SCO1/SenC family protein				GO:0019725//GO:0043231	nr -
Unigene48678_All	1630	2.05	0.25	0.72	43.40	24.00	7.84	25.68	10.62	7.77	-3.05E+00	1.13E-11	Down	-1.52E+00	4.63E-05	Down	-8.55E-01	1.98E-48		-2.47E+00	6.70E-205	Down	-1.27E+00	6.62E-55	Down	-1.72E+00	3.36E-88	Down	Unigene48678_All//gi|50346664|gb|AAT75042.1|//0.00E+00//Ce19B [Populus tremula x Populus tremuloides]	Unigene48678_All//0.00E+00//AT1G71380| ATCEL3 (ARABIDOPSIS THALIANA CELLULASE 3); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene48678_All//0.00E+00//TC133668		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0005618//GO:0016020//GO:0044238	nr -
Unigene48679_All	1003	28.12	65.27	51.18	13.11	10.27	9.14	8.26	1.96	2.86	1.22E+00	1.24E-64	Up	8.64E-01	2.05E-28		-3.53E-01	2.02E-02		-5.21E-01	6.38E-04		-2.08E+00	2.46E-22	Down	-1.53E+00	2.03E-15	Down	Unigene48679_All//gi|115441397|ref|NP_001044978.1|//8.00E-13//Os01g0878000 [Oryza sativa Japonica Group] >gi|113534509|dbj|BAF06892.1| Os01g0878000 [Oryza sativa Japonica Group]	Unigene48679_All//7.00E-34//AT1G11120| unknown protein					nr +
Unigene4868_All	1384	2.34	0.15	1.46	4.10	1.24	1.63	7.64	1.75	4.89	-4.00E+00	4.29E-14	Down	-6.81E-01	5.92E-02		-1.72E+00	3.60E-12	Down	-1.33E+00	1.50E-07	Down	-2.12E+00	4.23E-29	Down	-6.42E-01	2.46E-05		Unigene4868_All//gi|300392782|gb|ADK11431.1|//1.00E-126//trehalose-6-phosphate phosphatase [Medicago sativa]	Unigene4868_All//3.00E-136//AT1G35910| trehalose-6-phosphate phosphatase, putative	Unigene4868_All//8.00E-18//TC135974		ko00500|Starch and sucrose metabolism		nr +
Unigene48682_All	803	92.26	42.34	45.82	129.53	130.49	147.58	178.70	92.44	83.89	-1.12E+00	7.47E-65	Down	-1.01E+00	1.04E-52	Down	1.07E-02	8.73E-01		1.88E-01	6.15E-05		-9.51E-01	2.35E-116		-1.09E+00	9.05E-150	Down	Unigene48682_All//gi|3023847|sp|O24076.1|GBLP_MEDSA//1.00E-122//RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein >gi|2385376|emb|CAA69934.1| G protein beta subunit-like [Medicago sativa subsp. x varia]	Unigene48682_All//3.00E-115//AT1G18080| ATARCA; nucleotide binding	Unigene48682_All//0.00E+00//TC133545		ko03040|Spliceosome		nr -
Unigene48683_All	1396	3.94	2.07	4.23	3.60	3.85	3.46	3.39	1.47	1.17	-9.28E-01	2.87E-04		1.06E-01	6.85E-01		9.45E-02	7.86E-01		-5.81E-02	8.52E-01		-1.21E+00	1.97E-06	Down	-1.54E+00	3.21E-09	Down	Unigene48683_All//gi|7406456|emb|CAB85558.1|//3.00E-35//3-oxoacyl-[acyl-carrier-protein] synthase-like protein [Arabidopsis thaliana]	Unigene48683_All//8.00E-131//AT1G06240| unknown protein	Unigene48683_All//0.00E+00//DT460099				nr +
Unigene48684_All	962	7.83	31.66	11.18	28.01	53.41	55.73	17.80	42.49	30.02	2.02E+00	1.05E-62	Up	5.14E-01	4.55E-03		9.31E-01	3.69E-39		9.92E-01	3.46E-41		1.26E+00	2.58E-52	Up	7.54E-01	6.91E-17		Unigene48684_All//gi|116310760|emb|CAH67554.1|//8.00E-36//H0311C03.8 [Oryza sativa (indica cultivar-group)]	Unigene48684_All//3.00E-33//AT2G32580| unknown protein	Unigene48684_All//0.00E+00//gi|78333281|gb|DT553555.1|DT553555				nr -
Unigene48686_All	572	10.79	20.46	7.17	20.38	12.58	23.92	9.90	9.65	4.46	9.23E-01	4.64E-08		-5.91E-01	1.76E-02		-6.96E-01	5.28E-06		2.31E-01	1.67E-01		-3.83E-02	8.86E-01		-1.15E+00	2.67E-07	Down			Unigene48686_All//3.00E-129//TC147155				
Unigene48687_All	448	1.17	4.98	3.09	3.34	3.46	1.92	3.30	3.27	2.40	2.09E+00	1.86E-05	Up	1.40E+00	2.28E-02		5.23E-02	9.50E-01		-8.00E-01	1.48E-01		-1.66E-02	1.01E+00		-4.60E-01	3.42E-01				Unigene48687_All//7.00E-65//TC147155				
Unigene48688_All	533	19.93	30.04	9.79	17.85	16.67	18.30	68.06	98.18	55.98	5.92E-01	2.06E-05		-1.03E+00	2.96E-08	Down	-9.89E-02	6.44E-01		3.61E-02	8.79E-01		5.29E-01	7.10E-16		-2.82E-01	3.18E-04		Unigene48688_All//gi|89000969|gb|AB059074.1|//1.00E-19//At4g25030 [Arabidopsis thaliana] >gi|222424032|dbj|BAH19977.1| AT4G25030 [Arabidopsis thaliana]	Unigene48688_All//8.00E-21//AT4G25030| unknown protein	Unigene48688_All//0.00E+00//TC174367				nr -
Unigene48691_All	1276	26.32	8.34	11.94	14.60	11.25	11.43	7.32	4.68	2.03	-1.66E+00	2.13E-53	Down	-1.14E+00	2.30E-29	Down	-3.76E-01	2.02E-03		-3.53E-01	6.05E-03		-6.45E-01	1.15E-04		-1.85E+00	2.28E-22	Down	Unigene48691_All//gi|297849170|ref|XP_002892466.1|//1.00E-99//heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297338308|gb|EFH68725.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene48691_All//1.00E-83//AT1G08640| unknown protein	Unigene48691_All//0.00E+00//TC149931			GO:0005515//GO:0043231	nr +
Unigene48692_All	1450	5.74	3.25	2.83	2.44	1.99	3.30	0.52	0.63	0.77	-8.20E-01	4.69E-05		-1.02E+00	1.43E-06	Down	-2.90E-01	4.15E-01		4.37E-01	1.32E-01		2.73E-01	6.70E-01		5.52E-01	3.37E-01		Unigene48692_All//gi|297849170|ref|XP_002892466.1|//4.00E-98//heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297338308|gb|EFH68725.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene48692_All//1.00E-82//AT1G08640| unknown protein	Unigene48692_All//0.00E+00//TC149931			GO:0005515//GO:0043231	nr +
Unigene48693_All	1127	1.16	1.48	1.37	4.55	2.54	2.04	3.94	2.56	1.63	3.54E-01	4.89E-01		2.40E-01	6.41E-01		-8.44E-01	5.94E-04		-1.16E+00	1.18E-05	Down	-6.22E-01	1.53E-02		-1.28E+00	8.59E-07	Down							
Unigene48696_All	2076	9.12	6.37	7.00	19.58	21.08	14.64	11.51	3.32	3.93	-5.18E-01	4.19E-05		-3.82E-01	4.14E-03		1.07E-01	2.53E-01		-4.19E-01	2.22E-07		-1.79E+00	6.94E-52	Down	-1.55E+00	1.52E-43	Down	Unigene48696_All//gi|5734587|emb|CAB52797.1|//0.00E+00//external rotenone-insensitive NADPH dehydrogenase [Solanum tuberosum]	Unigene48696_All//0.00E+00//AT4G28220| NDB1 (NAD(P)H dehydrogenase B1); NADH dehydrogenase/ disulfide oxidoreductase	Unigene48696_All//0.00E+00//TC162415		ko00190|Oxidative phosphorylation	GO:0005743//GO:0008152//GO:0016667//GO:0030554//GO:0046872//GO:0050136	nr -
Unigene48697_All	875	13.33	17.84	14.30	23.68	20.19	25.81	13.67	11.99	6.69	4.20E-01	3.16E-03		1.01E-01	6.06E-01		-2.30E-01	6.31E-02		1.24E-01	3.77E-01		-1.90E-01	2.40E-01		-1.03E+00	3.33E-12	Down			Unigene48697_All//1.00E-77//BG447013				
Unigene48698_All	1141	2.48	3.86	3.13	19.34	12.10	20.74	5.48	16.12	15.26	6.42E-01	2.61E-02		3.37E-01	3.50E-01		-6.76E-01	2.32E-10		1.01E-01	4.71E-01		1.56E+00	7.49E-33	Up	1.48E+00	1.50E-29	Up	Unigene48698_All//gi|60459387|gb|AX200039.1|//4.00E-81//tyrosine specific protein phosphatase family protein [Capsicum annuum]	Unigene48698_All//4.00E-79//AT4G03960| tyrosine specific protein phosphatase family protein	Unigene48698_All//0.00E+00//TC150986			GO:0004721//GO:0006796	nr +

Unigene48699_All	1163	7.60	5.53	6.73	20.77	13.24	17.94	4.58	5.71	1.03	-4.59E-01	1.90E-02		-1.76E-01	4.11E-01		-6.50E-01	1.45E-10		-2.12E-01	7.48E-02		3.19E-01	1.38E-01		-2.16E+00	7.96E-16	Down	Unigene48699_All||gi|224066817|ref|XP_002302230.1|//6.00E-69//type-a response regulator [Populus trichocarpa] >gi|222843956|gb|EEE81503.1| type-a response regulator [Populus trichocarpa]	Unigene48699_All//1.00E-36//AT3G57040| ARR9 (RESPONSE REGULATOR 9); transcription regulator/ two-component response regulator	Unigene48699_All//0.00E+00//TC130862	ARR-B	ko04712|Circadian rhythm - plant	GO:0004871//GO:0006351//GO:0009725//GO:0023060	nr +
Unigene48701_All	1686	0.50	0.66	1.58	3.28	6.07	6.78	1.91	2.50	2.69	4.13E-01	5.26E-01		1.67E+00	1.07E-04	Up	8.87E-01	1.57E-07		1.05E+00	5.13E-10	Up	3.94E-01	1.51E-01		4.99E-01	4.35E-02		Unigene48701_All||gi|224138036|ref|XP_002326502.1|//1.00E-129//pseudo response regulator [Populus trichocarpa] >gi|222833824|gb|EEE72301.1| pseudo response regulator [Populus trichocarpa]	Unigene48701_All//1.00E-87//AT4G18020| APRR2; transcription factor/ two-component response regulator	Unigene48701_All//3.00E-110//gi|109838940|gb|DW237501.1|DW237501	ARR-B	ko04712|Circadian rhythm - plant	GO:0006355	nr -
Unigene48706_All	1020	0.82	23.30	8.67	8.25	6.95	15.01	49.24	39.46	17.07	4.83E+00	2.78E-112	Up	3.40E+00	7.38E-32	Up	-2.47E-01	2.49E-01		8.63E-01	9.43E-10		-3.20E-01	1.64E-06		-1.53E+00	6.24E-89	Down	Unigene48706_All//gi|15227574|ref|NP_181153.1|//3.00E-73//F-box family protein [Arabidopsis thaliana]	Unigene48706_All//6.00E-55//AT2G36090| F-box family protein	Unigene48706_All//0.00E+00//TC174799				nr +
Unigene48707_All	1399	0.07	6.56	0.61	1.50	1.21	0.94	35.54	17.63	7.18	6.45E+00	6.41E-49	Up	3.03E+00	3.01E-03		-3.10E-01	5.23E-01		-6.76E-01	1.36E-01		-1.01E+00	3.68E-45	Down	-2.31E+00	1.71E-153	Down	Unigene48707_All//gi|15227574|ref|NP_181153.1|//5.00E-88//F-box family protein [Arabidopsis thaliana]	Unigene48707_All//2.00E-69//AT2G36090| F-box family protein	Unigene48707_All//0.00E+00//TC174799				nr -
Unigene48708_All	938	44.12	11.72	22.99	153.27	138.77	71.98	18.35	14.75	9.34	-1.91E+00	6.94E-80	Down	-9.40E-01	2.11E-26		-1.43E-01	5.35E-04		-1.09E+00	1.59E-129	Down	-3.15E-01	1.01E-02		-9.73E-01	1.09E-15		Unigene48708_All//gi|89274163|gb|AB065602.1|//3.00E-40//At1g06980 [Arabidopsis thaliana]	Unigene48708_All//1.00E-40//AT2G30230| unknown protein	Unigene48708_All//0.00E+00//gi|54115512|gb|CO491021.1|CO491021				nr -
Unigene48710_All	1485	7.33	1.84	0.54	4.86	6.86	4.38	5.07	1.41	2.39	-1.99E+00	1.23E-22	Down	-3.77E+00	2.03E-42	Down	4.97E-01	4.04E-03		-1.51E-01	5.64E-01		-1.85E+00	1.48E-17	Down	-1.09E+00	1.23E-08	Down	Unigene48710_All//gi|115474509|ref|NP_001060851.1|//1.00E-104//Os08g0115200 [Oryza sativa Japonica Group] >gi|42409298|dbj|BAD10560.1| calmodulin-binding protein family-like [Oryza sativa Japonica Group] >gi|113622820|dbj|BAF22765.1| Os08g0115200 [Oryza sativa Japonica Group]	Unigene48710_All//5.00E-62//AT4G00820| iqd17 (IQ-domain 17); calmodulin binding	Unigene48710_All//0.00E+00//TC151065				nr -
Unigene48711_All	1080	2.91	3.80	1.23	16.28	12.91	8.61	9.12	2.05	3.43	3.87E-01	2.15E-01		-1.24E+00	9.77E-04	Down	-3.34E-01	9.10E-03		-9.18E-01	2.08E-12		-2.15E+00	1.28E-27	Down	-1.41E+00	3.45E-16	Down	Unigene48711_All//gi|115459076|ref|NP_001053138.1|//2.00E-95//Os04g0486500 [Oryza sativa Japonica Group] >gi|113564709|dbj|BAF15052.1| Os04g0486500 [Oryza sativa Japonica Group]	Unigene48711_All//2.00E-96//AT3G25980| mitotic spindle checkpoint protein, putative (MAD2)	Unigene48711_All//0.00E+00//TC137863			GO:0000087//GO:0043231	nr +
Unigene48712_All	612	9.75	35.19	14.36	16.77	19.36	29.00	23.28	33.94	23.96	1.85E+00	7.52E-40	Up	5.59E-01	5.87E-03		2.07E-01	2.61E-01		7.91E-01	9.74E-10		5.44E-01	4.07E-07		4.11E-02	7.76E-01		Unigene48712_All//gi|15235657|ref|NP_195483.1|//1.00E-102//HHP4 (heptahelical protein 4); receptor [Arabidopsis thaliana]	Unigene48712_All//5.00E-103//AT4G37680| HHP4 (heptahelical protein 4); receptor	Unigene48712_All//0.00E+00//gi|164359295|gb|ES804175.1|ES804175			GO:0004871//GO:0009719//GO:0031224//GO:0034285	nr +
Unigene48714_All	1512	0.97	0.10	0.00	1.81	1.46	0.99	6.12	1.71	3.79	-3.27E+00	8.97E-06	Down	-9.92E+00	5.25E-08	Down	-3.14E-01	4.39E-01		-8.78E-01	2.06E-02		-1.84E+00	2.96E-21	Down	-6.91E-01	2.56E-05		Unigene48714_All//gi|87240518|gb|AB032376.1|//1.00E-159//Lipolytic enzyme, G-D-S-L [Medicago truncatula] >gi|124361052|gb|ABN09024.1| Lipolytic enzyme, G-D-S-L [Medicago truncatula]	Unigene48714_All//1.00E-140//AT1G54790| GDSL-motif lipase/hydrolase family protein	Unigene48714_All//0.00E+00//DN802060				nr +
Unigene48716_All	1246	1.76	29.65	9.10	0.88	0.77	0.94	12.56	0.37	1.89	4.07E+00	1.49E-156	Up	2.37E+00	4.64E-28	Up	-1.85E-01	8.01E-01		9.97E-02	8.93E-01		-5.09E+00	5.92E-94	Down	-2.73E+00	3.41E-59	Down	Unigene48716_All//gi|37202078|gb|AAQ89654.1|//1.00E-14//At3g24750 [Arabidopsis thaliana]	Unigene48716_All//3.00E-16//AT3G24750| unknown protein					nr -
Unigene48717_All	854	14.89	6.59	11.10	32.96	26.09	36.01	31.29	9.01	32.98	-1.18E+00	1.39E-12	Down	-4.24E-01	1.10E-02		-3.37E-01	4.67E-04		1.28E-01	2.59E-01		-1.80E+00	3.81E-58	Down	7.60E-02	4.76E-01		Unigene48717_All//gi|15233117|ref|NP_191705.1|//6.00E-53//BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|297820998|ref|XP_002878382.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata] >gi|4689366|gb|AAD27870.1|AF134155_1 BRH1 RING finger protein [Arabidopsis thaliana] >gi|6850837|emb|CAB71076.1| RING finger protein [Arabidopsis thaliana] >gi|21554590|gb|AAM63625.1| RING finger protein [Arabidopsis thaliana] >gi|297324220|gb|EFH54641.1| brassinosteroid-responsive ring-H2 [Arabidopsis lyrata subsp. lyrata]	Unigene48717_All//3.00E-47//AT3G61460| BRH1 (BRASSINOSTEROID-RESPONSIVE RING-H2); protein binding / zinc ion binding	Unigene48717_All//0.00E+00//TC148169			GO:0009725//GO:0009743//GO:0046914	nr -
Unigene48718_All	1631	3.11	0.93	0.56	2.05	1.33	1.74	1.81	1.36	6.38	-1.74E+00	3.15E-09	Down	-2.49E+00	1.80E-13	Down	-6.22E-01	5.74E-02		-2.30E-01	5.53E-01		-4.18E-01	2.21E-01		1.81E+00	7.92E-24	Up	Unigene48718_All//gi|288558799|gb|ACW87202.2|//1.00E-135//glycosyltransferase [Populus deltoides]	Unigene48718_All//5.00E-102//AT3G16520| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene48718_All//0.00E+00//ES806532				nr +
Unigene48719_All	1112	33.55	114.23	17.34	7.88	8.18	27.70	37.95	355.19	108.37	1.77E+00	7.09E-218	Up	-9.53E-01	2.37E-24		5.23E-02	8.24E-01		1.81E+00	4.92E-59	Up	3.23E+00	0.00E+00	Up	1.51E+00	2.92E-207	Up	Unigene48719_All//gi|156118336|gb|ABU49726.1|//8.00E-26//ferritin [Solanum tuberosum]	Unigene48719_All//8.00E-21//AT3G11050| ATFER2 (ferritin 2); binding / ferric iron binding / oxidoreductase/ transition metal ion binding	Unigene48719_All//0.00E+00//TC133120		ko00860|Porphyrin and chlorophyll metabolism	GO:0000041//GO:0005506//GO:0008152//GO:0009536//GO:0016724//GO:0030005	nr -
Unigene48725_All	822	1.85	1.11	1.30	1.03	2.14	0.99	1.39	0.10	0.53	-7.34E-01	1.70E-01		-5.11E-01	3.80E-01		1.05E+00	3.38E-02		-5.89E-02	9.44E-01		-3.77E+00	3.90E-06	Down	-1.38E+00	1.42E-02		Unigene48725_All//gi|42567681|ref|NP_196213.2|//7.00E-59//ROPGEF5 (ROP GUANINE NUCLEOTIDE EXCHANGE FACTOR 5); Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana]	Unigene48725_All//3.00E-51//AT5G05940| ROPGEF5 (ROP GUANINE NUCLEOTIDE EXCHANGE FACTOR 5); Rho guanyl-nucleotide exchange factor	Unigene48725_All//1.00E-95//gi|48744102|gb|CO074621.1|CO074621			GO:0005088	nr +
Unigene48726_All	822	1.40	2.65	3.17	2.30	1.21	2.91	1.18	0.00	0.68	9.21E-01	3.53E-02		1.18E+00	4.44E-03		-9.23E-01	4.06E-02		3.39E-01	4.61E-01		-1.02E+01	5.83E-07	Down	-8.02E-01	1.83E-01		Unigene48726_All//gi|42567681|ref|NP_196213.2|//1.00E-49//ROPGEF5 (ROP GUANINE NUCLEOTIDE EXCHANGE FACTOR 5); Rho guanyl-nucleotide exchange factor [Arabidopsis thaliana]	Unigene48726_All//5.00E-43//AT5G05940| ROPGEF5 (ROP GUANINE NUCLEOTIDE EXCHANGE FACTOR 5); Rho guanyl-nucleotide exchange factor	Unigene48726_All//2.00E-79//gi|48744102|gb|CO074621.1|CO074621			GO:0005088	nr +
Unigene48727_All	1035	4.95	3.52	2.11	5.73	4.59	3.71	2.53	1.25	1.42	-4.91E-01	6.60E-02		-1.23E+00	1.37E-05	Down	-3.19E-01	2.10E-01		-6.27E-01	9.46E-03		-1.02E+00	3.65E-03		-8.31E-01	1.32E-02		Unigene48727_All//gi|15234795|ref|NP_194790.1|//1.00E-140//BRS1 (BRI1 SUPPRESSOR 1); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|57012621|sp|Q9M099.1|SCP24_ARATH RecName: Full=Serine carboxypeptidase 24; AltName: Full=Serine carboxypeptidase II; AltName: Full=Carboxypeptidase D; AltName: Full=Bri1 suppressor 1; Contains: RecName: Full=Serine carboxypeptidase 24 chain A; AltName: Full=Serine carboxypeptidase II chain A; Contains: RecName: Full=Serine carboxypeptidase 24 chain B; AltName: Full=Serine carboxypeptidase II chain B; Flags: Precursor >gi|7269962|emb|CAB79779.1| SERINE CARBOXYPEPTIDASE II-like protein [Arabidopsis thaliana]	Unigene48727_All//1.00E-141//AT4G30610| BRS1 (BRI1 SUPPRESSOR 1); serine-type carboxypeptidase	Unigene48727_All//3.00E-10//TC151487		ko00460|Cyanoamino acid metabolism		nr -
Unigene48728_All	650	21.65	7.87	9.01	30.81	20.93	32.10	40.91	19.03	16.43	-1.46E+00	5.16E-19	Down	-1.26E+00	9.40E-15	Down	-5.58E-01	7.52E-07		5.93E-02	7.04E-01		-1.10E+00	3.63E-28	Down	-1.32E+00	4.61E-38	Down	Unigene48728_All//gi|115451827|ref|NP_001049514.1|//1.00E-58//Os03g0241200 [Oryza sativa Japonica Group] >gi|113547985|dbj|BAF11428.1| Os03g0241200 [Oryza sativa Japonica Group]	Unigene48728_All//2.00E-50//AT5G20160| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	Unigene48728_All//0.00E+00//gi|84148411|gb|DN779711.1|DN779711		ko03040|Spliceosome	GO:0022613//GO:0030529	nr +
Unigene48732_All	1344	7.63	3.81	6.78	4.56	3.23	1.98	1.38	0.87	0.59	-1.00E+00	3.94E-08	Down	-1.72E-01	4.00E-01		-4.98E-01	3.10E-02		-1.20E+00	5.32E-07	Down	-6.69E-01	1.22E-01		-1.22E+00	3.47E-03		Unigene48732_All//gi|297834116|ref|XP_002884940.1|//5.00E-48//CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297330780|gb|EFH61199.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene48732_All//3.00E-40//AT1G55930| CBS domain-containing protein / transporter associated domain-containing protein	Unigene48732_All//4.00E-109//TC171712			GO:0008152//GO:0009536//GO:0030554	nr +
Unigene48733_All	1280	1.35	2.49	1.54	0.39	0.13	0.92	17.74	63.25	27.11	8.87E-01	1.10E-02		1.91E-01	6.77E-01		-1.53E+00	1.45E-01		1.24E+00	5.89E-02		1.83E+00	2.00E-179	Up	6.12E-01	3.41E-14		Unigene48733_All//gi|115469074|ref|NP_001058136.1|//3.00E-92//Os06g0634300 [Oryza sativa Japonica Group] >gi|51535777|dbj|BAD37816.1| MutT domain protein-like [Oryza sativa Japonica Group] >gi|51535894|dbj|BAD37977.1| MutT domain protein-like [Oryza sativa Japonica Group] >gi|113596176|dbj|BAF20050.1| Os06g0634300 [Oryza sativa Japonica Group]	Unigene48733_All//8.00E-82//AT4G12720| NUDT7; ADP-ribose diphosphatase/ NAD or NADH binding / hydrolase/ nucleoside-diphosphatase/ protein homodimerization	Unigene48733_All//2.00E-169//DN818046		ko03018|RNA degradation	GO:0016787//GO:0043231	nr -
Unigene48735_All	637	63.74	65.07	53.75	91.89	95.63	119.32	204.76	96.12	115.89	2.98E-02	7.48E-01		-2.46E-01	5.91E-03		5.76E-02	5.15E-01		3.77E-01	6.55E-11		-1.09E+00	1.56E-132	Down	-8.21E-01	5.60E-85		Unigene48735_All//gi|192910736|gb|ACF06476.1|//3.00E-37//mitochondrial F0 ATP synthase D chain [Elaeis guineensis]	Unigene48735_All//2.00E-38//AT3G52300| ATPQ (ATP SYNTHASE D CHAIN, MITOCHONDRIAL); hydrogen ion transmembrane transporter	Unigene48735_All//0.00E+00//gi|21102667|gb|BQ414980.1|BQ414980		ko00190|Oxidative phosphorylation	GO:0003824//GO:0005753//GO:0005840//GO:0006754//GO:0006970//GO:0009534//GO:0015077//GO:0031981//GO:0046914	nr -

Unigene48736_All	765	12.99	5.89	4.11	14.85	8.24	17.42	20.34	10.00	6.61	-1.14E+00	1.47E-09	Down	-1.66E+00	1.28E-15	Down	-8.50E-01	4.40E-08		2.30E-01	1.78E-01		-1.02E+00	5.60E-15	Down	-1.62E+00	1.43E-30	Down	Unigene48736_All//gi|15233044|ref|NP_191670.1|//6.00E-43//ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome [Arabidopsis thaliana] >gi|73917991|sp|Q9M2F1.2|RS272_ARATH RecName: Full=40S ribosomal protein S27-2 >gi|15724226|gb|AAL06506.1|AF412053_1 AT3g61110/T27I15_200 [Arabidopsis thaliana] >gi|4193382|gb|AAD10029.1| ribosomal protein S27 [Arabidopsis thaliana] >gi|4193384|gb|AAD10030.1| ribosomal protein S27 [Arabidopsis thaliana] >gi|8388627|emb|CAB94147.1| ribosomal protein S27 [Arabidopsis thaliana] >gi|19699108|gb|AAL90920.1| AT3g61110/T27I15_200 [Arabidopsis thaliana]	Unigene48736_All//2.00E-37//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome	Unigene48736_All//0.00E+00//gi|109872408|gb|DW501383.1|DW501383		ko03010|Ribosome	GO:0005198//GO:0003735//GO:0015935//GO:0022613//GO:0030312//GO:0043169	nr +
Unigene48737_All	1439	2.62	0.60	0.74	3.05	1.96	4.14	3.76	2.61	1.66	-2.13E+00	5.70E-09	Down	-1.82E+00	4.58E-07	Down	-6.35E-01	2.12E-02		4.44E-01	7.73E-02		-5.25E-01	2.27E-02		-1.18E+00	3.04E-07	Down	Unigene48737_All//gi|297811669|ref|XP_002873318.1|//1.00E-143//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319555|gb|EFH49977.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene48737_All//9.00E-143//AT5G15300| pentatricopeptide (PPR) repeat-containing protein	Unigene48737_All//1.00E-102//ES819912				nr -
Unigene48874_All	1032	2.64	0.98	1.91	2.32	1.64	1.44	4.71	4.01	3.32	-1.42E+00	3.45E-04	Down	-4.66E-01	2.47E-01		-5.03E-01	2.26E-01		-6.82E-01	1.04E-01		-2.33E-01	4.00E-01		-5.05E-01	3.25E-02		Unigene48874_All//gi|226510240|ref|NP_001148845.1|//1.00E-70//inhibitor of growth protein 5 [Zea mays] >gi|195622570|gb|ACG33115.1| inhibitor of growth protein 5 [Zea mays]	Unigene48874_All//6.00E-71//AT3G24010| ING1 (INHIBITOR OF GROWTH 1); DNA binding / methylated histone residue binding	Unigene48874_All//0.00E+00//gi|78351887|gb|DT572161.1|DT572161				nr -
Unigene48740_All	239	0.44	0.64	1.78	0.21	1.15	1.51	2.30	5.60	10.33	5.39E-01	7.79E-01		2.03E+00	1.39E-01		2.47E+00	2.23E-01		2.86E+00	9.44E-02		1.28E+00	1.56E-02		2.17E+00	1.07E-07	Up	Unigene48740_All//gi|297799262|ref|XP_002867515.1|//1.00E-09//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313351|gb|EFH43774.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48740_All//6.00E-10//AT4G27280| calcium-binding EF hand family protein	Unigene48740_All//1.00E-111//DR455311			GO:0009725//GO:0043231//GO:0044267//GO:0044444//GO:0046914	nr +
Unigene48741_All	776	3.10	9.47	1.24	6.42	8.03	8.03	15.47	31.02	58.06	1.61E+00	1.10E-11	Up	-1.33E+00	2.62E-03		3.23E-01	2.01E-01		3.23E-01	2.10E-01		1.00E+00	5.72E-22	Up	1.91E+00	1.08E-107	Up	Unigene48741_All//gi|56542451|gb|AAV92890.1|//1.00E-34//Avr9/Cf-9 rapidly elicited protein 20 [Nicotiana tabacum]	Unigene48741_All//2.00E-29//AT4G27280| calcium-binding EF hand family protein	Unigene48741_All//0.00E+00//DR455311		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0046872	nr +
Unigene48742_All	1523	1.82	1.00	0.52	3.30	3.14	3.47	8.25	2.85	3.03	-8.67E-01	2.14E-02		-1.80E+00	2.78E-05	Down	-7.19E-02	8.36E-01		7.07E-02	8.07E-01		-1.53E+00	3.27E-22	Down	-1.44E+00	4.71E-21	Down	Unigene48742_All//gi|240254508|ref|NP_179804.5|//1.00E-137//ATEME1B (ARABIDOPSIS ESSENTIAL MEIOTIC ENDONUCLEASE 1B); endonuclease [Arabidopsis thaliana] >gi|223930680|gb|ACN24999.1| essential meiotic endonuclease 1B [Arabidopsis thaliana]	Unigene48742_All//1.00E-122//AT2G22140| ATEME1B (ARABIDOPSIS ESSENTIAL MEIOTIC ENDONUCLEASE 1B); endonuclease	Unigene48742_All//0.00E+00//CO120773			GO:0003676//GO:0016788//GO:0043231//GO:0044260	nr -
Unigene48743_All	304	2.07	5.50	5.61	7.54	16.65	21.39	2.36	7.01	5.11	1.41E+00	7.54E-03		1.44E+00	8.27E-03		1.14E+00	9.61E-06	Up	1.51E+00	5.38E-10	Up	1.57E+00	1.57E-04	Up	1.11E+00	1.64E-02		Unigene48743_All//gi|255576115|ref|XP_002528952.1|//6.00E-16//Dual specificity protein phosphatase, putative [Ricinus communis] >gi|223531598|gb|EEF33426.1| Dual specificity protein phosphatase, putative [Ricinus communis]		Unigene48743_All//3.00E-100//gi|109847105|gb|DW476085.1|DW476085			GO:0016791	nr -
Unigene48744_All	904	0.41	7.01	1.06	7.66	11.92	10.24	3.41	17.34	6.61	4.11E+00	2.69E-27	Up	1.39E+00	7.11E-02		6.38E-01	9.83E-05		4.19E-01	3.00E-02		2.34E+00	3.91E-48	Up	9.53E-01	8.23E-06		Unigene48744_All//gi|255576115|ref|XP_002528952.1|//5.00E-19//Dual specificity protein phosphatase, putative [Ricinus communis] >gi|223531598|gb|EEF33426.1| Dual specificity protein phosphatase, putative [Ricinus communis]		Unigene48744_All//0.00E+00//gi|109847105|gb|DW476085.1|DW476085			GO:0016791	nr -
Unigene48745_All	1284	0.37	0.91	0.33	1.55	3.11	2.39	1.35	3.48	6.76	1.31E+00	4.44E-02		-1.44E-01	8.90E-01		1.00E+00	6.86E-04	Up	6.24E-01	8.71E-02		1.37E+00	3.24E-07	Up	2.32E+00	2.79E-27	Up	Unigene48745_All//gi|124359162|gb|ABN05685.1|//2.00E-65//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene48745_All//2.00E-27//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene48745_All//3.00E-45//TC153494				nr -
Unigene48746_All	829	4.67	10.57	7.58	30.04	30.70	18.25	10.56	7.26	5.43	1.18E+00	6.67E-09	Up	6.99E-01	4.29E-03		3.10E-02	8.23E-01		-7.19E-01	1.38E-11		-5.40E-01	1.90E-03		-9.59E-01	3.09E-08		Unigene48746_All//gi|149944379|gb|ABR46232.1|//3.00E-20//At5g42146 [Arabidopsis thaliana]	Unigene48746_All//3.00E-09//AT5G42146| unknown protein					nr +
Unigene48747_All	1419	1.47	1.39	1.13	4.91	5.58	4.97	1.70	2.86	7.52	-8.28E-02	8.46E-01		-3.90E-01	3.94E-01		1.84E-01	4.50E-01		1.47E-02	9.48E-01		7.50E-01	5.41E-03		2.15E+00	2.48E-30	Up	Unigene48747_All//gi|28950925|gb|AA063386.1|//4.00E-28//At5g58630 [Arabidopsis thaliana]	Unigene48747_All//9.00E-31//AT5G58630| unknown protein	Unigene48747_All//0.00E+00//ES802158				nr +
Unigene48748_All	2093	0.30	0.22	0.56	1.57	1.65	0.93	0.30	0.30	1.87	-4.61E-01	6.18E-01		9.00E-01	1.70E-01		6.69E-02	8.64E-01		-7.60E-01	2.60E-02		-1.68E-02	1.02E+00		2.62E+00	1.94E-14	Up	Unigene48748_All//gi|28950925|gb|AA063386.1|//4.00E-28//At5g58630 [Arabidopsis thaliana]	Unigene48748_All//1.00E-28//AT5G58630| unknown protein	Unigene48748_All//0.00E+00//ES802158				nr -
Unigene48751_All	1044	2.41	1.99	4.74	5.34	6.76	5.28	7.90	3.28	2.52	-2.74E-01	5.06E-01		9.80E-01	5.33E-04		3.39E-01	1.43E-01		-1.80E-02	9.53E-01		-1.27E+00	2.37E-11	Down	-1.65E+00	5.39E-17	Down	Unigene48751_All//gi|32815875|gb|AP88334.1|//4.00E-82//At1g15860 [Arabidopsis thaliana]	Unigene48751_All//3.00E-70//AT1G15860| INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Defective in cullin neddylation (InterPro:IPR014764), Protein of unknown function DUF298 (InterPro:IPR005176); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G12760.1); Has 576 Blast hits to 576 proteins in 121 species: Archae - 0; Bacteria - 0; Metazoa - 403; Fungi - 78; Plants - 51; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink).	Unigene48751_All//0.00E+00//gi|48878944|gb|CO129966.1|CO129966			GO:0046872	nr +
Unigene48753_All	525	7.67	5.12	3.14	0.38	2.36	1.46	0.24	0.16	0.00	-5.85E-01	5.44E-02		-1.29E+00	8.16E-05	Down	2.64E+00	2.32E-04	Up	1.95E+00	3.23E-02		-6.02E-01	7.66E-01		-7.92E+00	2.00E-01		Unigene48753_All//gi|224070774|ref|XP_002303230.1|//8.00E-70//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222840662|gb|EEE78209.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene48753_All//9.00E-54//AT2G02450| ANAC035 (Arabidopsis NAC domain containing protein 35); transcription factor	Unigene48753_All//2.00E-176//CO096386	NAC		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene48754_All	1113	19.65	11.24	9.43	2.01	4.27	2.52	0.72	0.00	0.00	-8.05E-01	1.32E-11		-1.06E+00	3.38E-17	Down	1.08E+00	4.95E-05	Up	3.21E-01	4.46E-01		-9.50E+00	8.57E-06	Down	-9.50E+00	4.43E-06	Down	Unigene48754_All//gi|224129830|ref|XP_002328813.1|//1.00E-116//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222839111|gb|EEE77462.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene48754_All//1.00E-72//AT2G02450| ANAC035 (Arabidopsis NAC domain containing protein 35); transcription factor	Unigene48754_All//3.00E-177//CO096386	NAC		GO:0003676//GO:0010468	nr -
Unigene48755_All	1194	1.05	3.99	1.43	3.13	3.55	3.40	1.88	2.07	3.70	1.92E+00	8.43E-10	Up	4.40E-01	3.86E-01		1.81E-01	6.02E-01		1.22E-01	7.13E-01		1.38E-01	7.26E-01		9.81E-01	1.06E-04		Unigene48755_All//gi|224146960|ref|XP_002336373.1|//6.00E-07//predicted protein [Populus trichocarpa] >gi|222834836|gb|EEE73285.1| predicted protein [Populus trichocarpa]		Unigene48755_All//0.00E+00//DT463870				nr +
Unigene48756_All	1060	12.93	4.78	6.03	21.19	20.89	19.30	18.23	7.65	8.12	-1.44E+00	4.16E-18	Down	-1.10E+00	1.14E-11	Down	-2.10E-02	8.78E-01		-1.35E-01	3.21E-01		-1.25E+00	4.13E-25	Down	-1.17E+00	3.14E-23	Down	Unigene48756_All//gi|193290377|gb|AB165001.1|//1.00E-122//14-3-3b protein [Gossypium hirsutum]	Unigene48756_All//4.00E-110//AT1G78300| GRF2 (GENERAL REGULATORY FACTOR 2); protein binding / protein phosphorylated amino acid binding	Unigene48756_All//0.00E+00//TC176897				nr -
Unigene48757_All	941	9.06	19.06	10.24	8.79	12.99	12.53	21.70	35.93	24.77	1.07E+00	4.55E-15	Up	1.77E-01	3.83E-01		5.64E-01	2.29E-04		5.12E-01	1.77E-03		7.28E-01	5.19E-18		1.91E-01	6.77E-02		Unigene48757_All//gi|30682195|ref|NP_187834.2|//4.00E-08//NF-YC11 (NUCLEAR FACTOR Y, SUBUNIT C11); DNA binding / transcription factor [Arabidopsis thaliana] >gi|18087592|gb|AAL58929.1|AF462841_1 At3g12480/MQC3.32 [Arabidopsis thaliana] >gi|23505853|gb|AAN28786.1| At3g12480/MQC3.32 [Arabidopsis thaliana]		Unigene48757_All//0.00E+00//TC147033			GO:0003677//GO:0043231	nr -
Unigene48758_All	566	22.46	5.64	9.69	54.65	49.40	46.68	5.83	4.28	6.55	-1.99E+00	2.31E-26	Down	-1.21E+00	1.41E-12	Down	-1.46E-01	1.67E-01		-2.28E-01	2.42E-02		-4.44E-01	1.57E-01		1.68E-01	5.98E-01		Unigene48758_All//gi|21554844|gb|AAM63706.1|//5.00E-20//arabinogalactan-protein homolog [Arabidopsis thaliana]		Unigene48758_All//1.00E-113//gi|78330117|gb|DT550391.1|DT550391		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene48759_All	821	5.80	4.44	2.79	17.54	13.21	19.69	4.79	4.84	2.23	-3.84E-01	1.74E-01		-1.06E+00	2.88E-04	Down	-4.08E-01	3.68E-03		1.68E-01	2.99E-01		1.41E-02	9.96E-01		-1.10E+00	5.03E-05	Down			Unigene48759_All//1.00E-110//gi|21101993|gb|BQ414306.1|BQ414306				
Unigene4876_All	1563	0.13	0.97	0.27	0.61	0.37	0.35	9.39	23.13	14.20	2.86E+00	2.69E-05	Up	1.03E+00	3.96E-01		-6.93E-01	3.15E-01		-8.04E-01	2.77E-01		1.30E+00	5.59E-49	Up	5.97E-01	4.93E-09		Unigene4876_All//gi|224109632|ref|XP_002315262.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222864302|gb|EEF01433.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene4876_All//0.00E+00//AT5G13580| ABC transporter family protein	Unigene4876_All//0.00E+00//CA994013		ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene48760_All	821	10.32	7.65	6.88	5.64	4.66	4.18	4.79	4.17	1.55	-4.32E-01	3.15E-02		-5.87E-01	4.58E-03		-2.77E-01	3.54E-01		-4.33E-01	1.37E-01		-1.98E-01	5.32E-01		-1.63E+00	2.16E-08	Down	Unigene48760_All//gi|224121584|ref|XP_002318620.1|//6.00E-20//5-formyltetrahydrofolate cyclo-ligase [Populus trichocarpa] >gi|222859293|gb|EEE96840.1| 5-formyltetrahydrofolate cyclo-ligase [Populus trichocarpa]	Unigene48760_All//4.00E-18//AT5G13050| 5-FCL (5-FORMYLTETRAHYDROFOLATE CYCLOLIGASE); 5-formyltetrahydrofolate cyclo-ligase			ko00670|One carbon pool by folate	GO:0006760//GO:0016882//GO:0032559//GO:0043231	nr +
Unigene48761_All	1098	1.48	1.11	2.62	1.77	2.60	1.23	4.12	1.14	2.39	-4.16E-01	4.12E-01		8.26E-01	3.26E-02		5.57E-01	1.45E-01		-5.20E-01	2.89E-01		-1.85E+00	7.13E-11	Down	-7.83E-01	1.40E-03		Unigene48761_All//gi|75337365|sp|Q9SKZ2.2|CAF1G_ARATH//1.00E-114//RecName: Full=Probable CCR4-associated factor 1 homolog 7	Unigene48761_All//3.00E-115//AT2G32070| CCR4-NOT transcription complex protein, putative	Unigene48761_All//0.00E+00//TC144287		ko03018|RNA degradation		nr -

Unigene48762_All	1439	0.00	0.46	0.67	3.08	2.92	2.67	1.15	1.83	3.74	8.84E+00	6.25E-04	Up	9.38E+00	2.46E-05	Up	-7.76E-02	8.32E-01		-2.08E-01	5.29E-01		6.75E-01	5.31E-02		1.71E+00	9.22E-12	Up	Unigene48762_All//gi|115473321|ref|NP_001060259.1|//2.00E-20//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]	Unigene48762_All//1.00E-14//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative				GO:0043231	nr +
Unigene48763_All	752	34.37	43.53	41.35	83.20	64.29	102.34	48.13	72.98	21.99	3.41E-01	3.16E-04		2.67E-01	9.74E-03		-3.72E-01	7.77E-10		2.99E-01	2.34E-07		6.01E-01	1.08E-20		-1.13E+00	1.22E-40	Down	Unigene48763_All//gi|110737195|dbj|BAF00546.1|//3.00E-73//TPR-repeat protein [Arabidopsis thaliana]	Unigene48763_All//4.00E-68//AT1G62740| stress-inducible protein, putative	Unigene48763_All//0.00E+00//TC139921			GO:0000302//GO:0009642//GO:0010038//GO:0016020//GO:0043231//GO:0044444	nr +
Unigene48764_All	782	1.14	54.17	6.47	4.91	4.93	3.06	17.57	43.29	153.19	5.57E+00	1.25E-214	Up	2.51E+00	1.29E-13	Up	7.90E-03	9.89E-01		-6.80E-01	2.95E-02		1.30E+00	6.71E-46	Up	3.12E+00	0.00E+00	Up	Unigene48764_All//gi|115467000|ref|NP_001057099.1|//4.00E-122//Os06g0207200 [Oryza sativa Japonica Group] >gi|113595139|dbj|BAF19013.1| Os06g0207200 [Oryza sativa Japonica Group]	Unigene48764_All//2.00E-122//AT1G05575| unknown protein	Unigene48764_All//0.00E+00//TC173724			GO:0045333	nr -
Unigene48769_All	808	1.75	4.26	2.17	2.90	1.66	1.40	2.93	6.72	2.17	1.29E+00	1.88E-04	Up	3.15E-01	5.52E-01		-8.02E-01	4.33E-02		-1.05E+00	1.16E-02		1.20E+00	3.68E-07	Up	-4.34E-01	2.35E-01		Unigene48769_All//gi|224135135|ref|XP_002321992.1|//2.00E-45//predicted protein [Populus trichocarpa] >gi|222868988|gb|EEF06119.1| predicted protein [Populus trichocarpa]	Unigene48769_All//4.00E-27//AT4G27810| unknown protein	Unigene48769_All//0.00E+00//gi|78346827|gb|DT567101.1|DT567101				nr +
Unigene48771_All	708	67.10	67.49	64.31	74.93	76.94	94.22	94.17	61.28	43.44	8.30E-03	9.42E-01		-6.14E-02	5.17E-01		3.82E-02	6.87E-01		3.30E-01	1.10E-07		-6.20E-01	2.13E-26		-1.12E+00	1.17E-72	Down	Unigene48771_All//gi|3915165|sp|O50046.1|TRP8_CAMMC//5.00E-81//RecName: Full=Tryptophan synthase beta chain 2, chloroplastic; Flags: Precursor >gi|2792520|gb|AAB97087.1| tryptophan synthase beta subunit [Camptotheca acuminata] >gi|2801771|gb|AAB97526.1| tryptophan synthase beta [Camptotheca acuminata]	Unigene48771_All//5.00E-78//AT4G27070| TSB2 (TRYPTOPHAN SYNTHASE BETA-SUBUNIT 2); tryptophan synthase	Unigene48771_All//0.00E+00//TC131701		ko00260|Glycine, serine and threonine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0004672//GO:0006464//GO:0006568//GO:0006970//GO:0008652//GO:0009532//GO:0009683//GO:0016836//GO:0032559//GO:0048037	nr +
Unigene48772_All	707	35.60	17.99	12.05	116.61	22.26	21.14	58.01	40.61	44.35	-9.85E-01	2.82E-18		-1.56E+00	1.61E-35	Down	-2.39E+00	1.33E-267	Down	-2.46E+00	3.34E-238	Down	-5.14E-01	4.62E-12		-3.87E-01	9.62E-08		Unigene48772_All//gi|14030677|gb|AK53013.1|AF375429_1//3.00E-38//AT4g18280/T9A21_130 [Arabidopsis thaliana] >gi|19548065|gb|AAL87396.1| AT4g18280/T9A21_130 [Arabidopsis thaliana]		Unigene48772_All//2.00E-121//C0075046		ko03040|Spliceosome	GO:0043229	nr +
Unigene48773_All	629	8.15	5.08	8.30	6.26	7.94	5.53	2.08	6.31	1.90	-6.84E-01	9.57E-03		2.54E-02	9.42E-01		3.44E-01	2.32E-01		-1.78E-01	6.40E-01		1.60E+00	5.60E-08	Up	-1.33E-01	7.86E-01									
Unigene48775_All	951	14.91	11.40	8.96	12.05	10.61	12.77	7.65	3.30	4.99	-3.87E-01	1.02E-02		-7.35E-01	1.92E-06		-1.83E-01	3.19E-01		8.46E-02	6.75E-01		-1.21E+00	1.64E-09	Down	-6.17E-01	9.71E-04		Unigene48775_All//gi|297802186|ref|XP_002868977.1|//1.00E-44//ribosomal protein L12 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314813|gb|EFH45236.1| ribosomal protein L12 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48775_All//3.00E-16//AT4G37660| ribosomal protein L12 family protein	Unigene48775_All//0.00E+00//TC156875		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279//GO:0043231	nr +
Unigene48777_All	1003	3.13	3.54	1.22	3.03	4.36	3.83	7.88	9.71	10.21	1.76E-01	5.97E-01		-1.36E+00	3.44E-04	Down	5.25E-01	7.23E-02		3.37E-01	3.29E-01		3.01E-01	8.05E-02		3.73E-01	1.77E-02		Unigene48777_All//gi|82570061|gb|ABB83615.1|//8.00E-74//CA-responsive protein [Brassica oleracea]	Unigene48777_All//1.00E-74//AT1G17665| unknown protein	Unigene48777_All//0.00E+00//TC178954			GO:0044464	nr +
Unigene48779_All	745	13.91	8.91	9.79	27.48	20.71	24.13	8.51	4.66	3.10	-6.42E-01	2.85E-04		-5.06E-01	6.38E-03		-4.08E-01	3.34E-04		-1.88E-01	1.64E-01		-8.70E-01	3.27E-05		-1.46E+00	3.24E-11	Down			Unigene48779_All//0.00E+00//gi|13356123|gb|BG446471.1|BG446471				
Unigene4878_All	1346	10.65	0.30	2.65	0.52	0.46	0.47	2.86	1.99	1.18	-5.14E+00	5.86E-71	Down	-2.01E+00	1.06E-28	Down	-1.70E-01	8.21E-01		-1.41E-01	8.66E-01		-5.24E-01	6.35E-02		-1.27E+00	5.67E-06	Down	Unigene4878_All//gi|115488046|ref|NP_001066510.1|//1.00E-173//Os12g0257000 [Oryza sativa Japonica Group] >gi|584892|sp|P37890.1|CBP1_ORYSJ RecName: Full=Serine carboxypeptidase 1; AltName: Full=Serine carboxypeptidase I; AltName: Full=Carboxypeptidase C; Contains: RecName: Full=Serine carboxypeptidase 1 chain A; AltName: Full=Serine carboxypeptidase 1 chain A; Contains: RecName: Full=Serine carboxypeptidase 1 chain B; AltName: Full=Serine carboxypeptidase 1 chain B; Flags: Precursor >gi|409580|dbj|BAA04510.1| serine carboxypeptidase I [Oryza sativa Japonica Group] >gi|113649017|dbj|BAF29529.1| Os12g0257000 [Oryza sativa Japonica Group]	Unigene4878_All//2.00E-164//AT4G12910| scp120 (serine carboxypeptidase-like 20); serine-type carboxypeptidase	Unigene4878_All//0.00E+00//TC132342				nr -
Unigene48781_All	1722	3.07	3.30	4.11	0.72	0.80	0.58	1.96	0.66	0.25	1.03E-01	6.84E-01		4.22E-01	7.17E-02		1.45E-01	8.22E-01		-3.26E-01	6.41E-01		-1.58E+00	7.71E-07	Down	-2.95E+00	2.09E-14	Down	Unigene48781_All//gi|97052021|sp|Q2MHE4.1|HT1_ARATH//1.00E-175//RecName: Full=Serine/threonine-protein kinase HT1; AltName: Full=High leaf temperature protein 1 >gi|84875482|dbj|BAE75921.1| HT1 protein kinase [Arabidopsis thaliana]	Unigene48781_All//5.00E-172//AT1G62400| HT1 (high leaf temperature 1); kinase/ protein serine/threonine/tyrosine kinase	Unigene48781_All//3.00E-98//GE653379			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene48782_All	678	109.58	23.09	58.12	48.49	45.71	45.16	30.24	35.75	9.87	-2.25E+00	4.60E-176	Down	-9.15E-01	6.45E-45		-8.52E-02	4.52E-01		-1.03E-01	3.73E-01		2.41E-01	1.93E-02		-1.62E+00	7.89E-40	Down	Unigene48782_All//gi|224111062|ref|XP_002332994.1|//1.00E-09//predicted protein [Populus trichocarpa] >gi|224113049|ref|XP_002332662.1| predicted protein [Populus trichocarpa] >gi|222833142|gb|EEE71619.1| predicted protein [Populus trichocarpa] >gi|222834356|gb|EEE72833.1| predicted protein [Populus trichocarpa]		Unigene48782_All//0.00E+00//TC157619				nr +
Unigene48784_All	803	26.26	18.30	19.83	27.73	28.09	29.87	64.24	29.88	24.21	-5.21E-01	1.25E-05		-4.05E-01	1.15E-03		1.86E-02	9.03E-01		1.07E-01	4.30E-01		-1.10E+00	6.66E-54	Down	-1.41E+00	8.52E-81	Down	Unigene48784_All//gi|242129052|gb|ACS83605.1|//1.00E-33//ATP synthase epsilon subunit 1 [Gossypium hirsutum]	Unigene48784_All//9.00E-31//AT1G51650| ATP synthase epsilon chain, mitochondrial	Unigene48784_All//0.00E+00//DW516466		ko00190|Oxidative phosphorylation	GO:0005753//GO:0006754//GO:0006818//GO:0015078//GO:0019829//GO:0033178	nr -
Unigene48786_All	1510	127.51	745.24	165.89	37.44	201.89	94.01	18.96	59.32	73.32	2.55E+00	0.00E+00	Up	3.80E-01	1.40E-31		2.43E+00	0.00E+00	Up	1.33E+00	2.28E-172	Up	1.65E+00	1.53E-170	Up	1.95E+00	9.67E-272	Up	Unigene48786_All//gi|225431128|ref|XP_002265844.1|//1.00E-37//PREDICTED: similar to DnaJ-like protein [Vitis vinifera]	Unigene48786_All//8.00E-28//AT2G17880| DNAJ heat shock protein, putative	Unigene48786_All//0.00E+00//TC140944			GO:0005515//GO:0043231//GO:0050896	nr -
Unigene48787_All	1395	0.56	2.94	0.23	1.64	4.52	2.20	4.36	5.87	40.21	2.39E+00	5.84E-11	Up	-1.30E+00	1.38E-01		1.46E+00	5.73E-10	Up	4.23E-01	2.71E-01		4.28E-01	1.98E-02		3.20E+00	4.05E-243	Up	Unigene48787_All//gi|19911585|dbj|BAB86896.1|//1.00E-132//syringolide-induced protein 13-1-1 [Glycine max]	Unigene48787_All//5.00E-109//AT5G37490| U-box domain-containing protein	Unigene48787_All//0.00E+00//TC159214		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene48788_All	760	51.43	39.34	31.88	50.27	39.56	71.07	138.86	78.97	49.64	-3.87E-01	5.76E-06		-6.90E-01	6.61E-15		-3.46E-01	1.67E-05		5.00E-01	6.52E-13		-8.14E-01	4.32E-66		-1.48E+00	4.96E-178	Down	Unigene48788_All//gi|40287504|gb|AR83866.1|//2.00E-58//40S ribosomal protein S17 [Capsicum annuum]	Unigene48788_All//7.00E-55//AT5G04800| 40S ribosomal protein S17 (RPS17D)	Unigene48788_All//0.00E+00//gi|109871664|gb|DW500640.1|DW500640		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene48789_All	656	20.58	18.38	18.83	64.09	48.98	20.59	17.02	8.98	5.65	-1.63E-01	3.40E-01		-1.28E-01	4.69E-01		-3.88E-01	2.62E-07		-1.64E+00	3.77E-71	Down	-9.22E-01	2.44E-09		-1.59E+00	1.30E-21	Down	Unigene48789_All//gi|124359162|gb|ABN05685.1|//7.00E-20//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene48789_All//0.00E+00//TC176721			GO:0003676//GO:0003824	nr +
Unigene4879_All	1176	0.27	4.27	1.13	8.13	13.15	12.48	16.25	32.34	75.44	4.00E+00	2.73E-21	Up	2.08E+00	2.18E-03		6.93E-01	1.78E-07		6.18E-01	1.51E-05		9.93E-01	1.18E-33		2.21E+00	2.72E-256	Up	Unigene4879_All//gi|30841458|gb|AAP34366.1|//3.00E-53//fiber protein Fb19 [Gossypium barbadense]	Unigene4879_All//3.00E-52//AT4G40080| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	Unigene4879_All//0.00E+00//TC131773				nr -
Unigene48791_All	925	4.41	10.08	7.37	40.39	44.90	31.49	30.81	15.14	16.32	1.19E+00	1.44E-09	Up	7.40E-01	1.52E-03		1.53E-01	8.48E-02		-3.59E-01	2.70E-05		-1.03E+00	8.71E-27	Down	-9.16E-01	4.86E-23		Unigene48791_All//gi|18402674|ref|NP_566665.1|//1.00E-46//plastocyanin-like domain-containing protein [Arabidopsis thaliana] >gi|32815931|gb|AAP88350.1| At3g20570 [Arabidopsis thaliana]	Unigene48791_All//9.00E-41//AT3G20570| plastocyanin-like domain-containing protein	Unigene48791_All//0.00E+00//TC165041			GO:0006091//GO:0031410//GO:0046914	nr -
Unigene48792_All	707	48.03	20.00	20.64	56.30	56.45	52.70	172.53	51.08	52.24	-1.26E+00	3.80E-36	Down	-1.22E+00	6.88E-33	Down	3.90E-03	9.69E-01		-9.52E-02	3.56E-01		-1.76E+00	6.79E-255	Down	-1.72E+00	1.48E-255	Down	Unigene48792_All//gi|3334115|sp|O22342.1|ADT1_GOSHI//1.00E-127//RecName: Full=ADP,ATP carrier protein 1, mitochondrial; AltName: Full=ADP/ATP translocase 1; AltName: Full=Adenine nucleotide translocator 1; Short=ANT 1; Flags: Precursor >gi|2463664|gb|AAB72047.1| adenine nucleotide translocator 1 [Gossypium hirsutum]	Unigene48792_All//6.00E-118//AT3G08580| AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/ binding	Unigene48792_All//0.00E+00//TC149761				nr -
Unigene48793_All	498	0.21	0.20	0.64	4.60	5.53	3.90	0.85	53.29	4.48	-4.60E-02	9.88E-01		1.61E+00	3.04E-01		2.66E-01	5.61E-01		-2.39E-01	6.35E-01		5.97E+00	6.44E-170	Up	2.40E+00	7.90E-08	Up	Unigene48793_All//gi|187940291|gb|ACD39376.1|//1.00E-34//NAC domain protein [Glycine max]	Unigene48793_All//2.00E-23//AT5G64530| XND1; transcription factor	Unigene48793_All//6.00E-158//TC139014	NAC		GO:0001071//GO:0003676//GO:0010087//GO:0010468//GO:0012501//GO:0048513	nr -
Unigene48794_All	1183	1.90	1.58	2.34	27.12	27.80	22.33	2.82	106.06	10.78	-2.63E-01	5.55E-01		3.00E-01	4.53E-01		3.58E-02	7.99E-01		-2.80E-01	3.48E-03		5.23E+00	0.00E+00	Up	1.93E+00	1.46E-31	Up	Unigene48794_All//gi|30698042|ref|NP_201258.2|//2.00E-78//XND1; transcription factor [Arabidopsis thaliana] >gi|107738104|gb|ABF83636.1| At5g64530 [Arabidopsis thaliana]	Unigene48794_All//2.00E-72//AT5G64530| XND1; transcription factor	Unigene48794_All//0.00E+00//TC139014	NAC		GO:0001071//GO:0003676//GO:0010087//GO:0010468//GO:0012501//GO:0048513	nr +
Unigene48795_All	499	5.24	1.52	3.63	5.49	5.18	6.88	1.95	1.01	2.00	-1.78E+00	2.79E-05	Down	-5.31E-01	2.02E-01		-8.52E-02	8.26E-01		3.25E-01	3.90E-01		-9.55E-01	1.35E-01		3.45E-02	9.70E-01		Unigene48795_All//gi|196052752|gb|ABY48757.4|//7.00E-40//iron-superoxide dismutase [Dimocarpus longan] >gi|210112069|gb|ACJ07160.1| chloroplast iron superoxide dismutase [Dimocarpus longan]	Unigene48795_All//3.00E-25//AT5G51100| FSD2 (FE SUPEROXIDE DISMUTASE 2); superoxide dismutase	Unigene48795_All//5.00E-106//TC135628		ko04146|Peroxisome	GO:0003824//GO:0006800//GO:0009416//GO:0009536//GO:0016209//GO:0043269//GO:0043232	nr -

Unigene48798_All	1613	4.12	0.97	2.94	2.41	2.67	1.57	1.55	0.52	0.32	-2.08E+00	7.16E-15	Down	-4.88E-01	4.38E-02		1.48E-01	6.67E-01		-6.19E-01	4.72E-02		-1.58E+00	3.22E-05	Down	-2.27E+00	2.76E-08	Down	Unigene48798_All//gi|30687061|ref|NP_197392.2|//1.00E-138//protein kinase family protein [Arabidopsis thaliana] >gi|29028912|gb|AA064835.1|At5g18910 [Arabidopsis thaliana]	Unigene48798_All//1.00E-140//AT5G18910| protein kinase family protein	Unigene48798_All//4.00E-69//CO076063		ko04626|Plant-pathogen interaction		nr -
Unigene488_All	2016	0.55	0.23	0.08	0.84	0.27	1.57	1.17	1.41	1.38	-1.27E+00	5.68E-02		-2.78E+00	1.00E-03		-1.62E+00	9.57E-04	Down	9.01E-01	1.04E-02		2.64E-01	4.67E-01		2.36E-01	5.04E-01		Unigene488_All//gi|264664473|sp|CO LGK4.1|Y2165_ARATH//1.00E-175//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At2g16250; Flags: Precursor >gi|224589511|gb|ACN59289.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene488_All//4.00E-135//AT2G16250| leucine-rich repeat transmembrane protein kinase, putative	Unigene488_All//0.00E+00//TC154092		ko04626|Plant-pathogen interaction	GO:0004871//GO:0006464//GO:0016301//GO:0016628//GO:0031224//GO:0032559	nr +
Unigene4880_All	1330	1.65	9.22	11.97	0.97	10.98	6.38	3.05	6.69	4.70	2.48E+00	6.84E-33	Up	2.86E+00	2.28E-48	Up	3.49E+00	3.06E-63	Up	2.71E+00	6.66E-27	Up	1.13E+00	2.43E-10	Up	6.24E-01	2.26E-03		Unigene4880_All//gi|1483232|emb|CA A67869.1|//2.00E-98//MADS3 protein [Betula pendula]	Unigene4880_All//1.00E-73//AT5G60910| AGL8 (agamous-like 8); transcription factor	Unigene4880_All//0.00E+00//gi|48880611|gb|CO131633.1|CO131633	MADS			nr -
Unigene48800_All	915	4.29	10.80	5.88	2.99	4.82	2.81	0.83	1.10	0.87	1.33E+00	7.45E-12	Up	4.55E-01	9.59E-02		6.86E-01	1.49E-02		-8.99E-02	8.24E-01		3.99E-01	5.45E-01		6.63E-02	9.42E-01		Unigene48800_All//gi|224104401|ref|XP_002313425.1|//1.00E-115//cytochrome P450 [Populus trichocarpa] >gi|222849833|gb|EEE87380.1|cytochrome P450 [Populus trichocarpa]	Unigene48800_All//4.00E-102//AT2G29090| CYP707A2; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	Unigene48800_All//6.00E-138//C0107319		ko00906|Carotenoid biosynthesis	GO:0003006//GO:0005506//GO:0006714//GO:0006952//GO:0009416//GO:0016709	nr +
Unigene48801_All	713	22.45	20.89	26.74	15.16	15.31	5.83	3.20	2.58	0.61	-1.04E-01	5.11E-01		2.52E-01	6.86E-02		1.41E-02	9.63E-01		-1.38E+00	1.43E-14	Down	-3.12E-01	4.37E-01		-2.38E+00	4.65E-08	Down	Unigene48801_All//gi|15242739|ref|NP_195957.1|//9.00E-40//acylphosphatase family [Arabidopsis thaliana]	Unigene48801_All//7.00E-38//AT5G03370| acylphosphatase family	Unigene48801_All//0.00E+00//TC154406		ko00620|Pyruvate metabolism	GO:0016818//GO:0043231	nr -
Unigene48802_All	840	129.31	51.57	25.61	84.74	94.37	46.13	75.20	18.16	15.98	-1.33E+00	6.15E-123	Down	-2.34E+00	4.48E-261	Down	1.55E-01	8.45E-03		-8.77E-01	6.17E-45		-2.05E+00	7.45E-163	Down	-2.23E+00	3.62E-187	Down	Unigene48802_All//gi|15232146|ref|NP_189372.1|//1.00E-69//histone H3 [Arabidopsis thaliana] >gi|15238433|ref|NP_201339.1|histone H3 [Arabidopsis thaliana] >gi|18390992|ref|NP_563838.1|histone H3 [Arabidopsis thaliana] >gi|18416261|ref|NP_568227.1|histone H3 [Arabidopsis thaliana] >gi|18416264|ref|NP_568228.1|histone H3 [Arabidopsis thaliana] >gi|115441249|ref|NP_001044904.1|Os01g0866200 [Oryza sativa Japonica Group] >gi|115458332|ref|NP_001052776.1|Os04g0419600 [Oryza sativa Japonica Group] >gi|115464121|ref|NP_001055660.1|Os05g0438700 [Oryza sativa Japonica Group] >gi|115466556|ref|NP_001056877.1|Os06g0160100 [Oryza sativa Japonica Group] >gi|115484259|ref|NP_001065791.1|Os11g0155900 [Oryza sativa Japonica Group] >gi|212721652|ref|NP_001131276.1|histone H3.2 [Zea mays] >gi|297724495|ref|NP_001174611.1|Os06g0159501 [Oryza sativa	Unigene48802_All//2.00E-60//AT4G40030| histone H3.2	Unigene48802_All//0.00E+00//TC153301			GO:0000785//GO:0003676//GO:0009536//GO:0031981//GO:0034728	nr -
Unigene48803_All	1204	3.39	1.26	1.28	4.43	1.92	3.11	4.78	2.22	1.06	-1.42E+00	7.13E-06	Down	-1.40E+00	1.92E-05	Down	-1.21E+00	6.70E-07	Down	-5.08E-01	5.31E-02		-1.10E+00	1.02E-06	Down	-2.17E+00	3.53E-17	Down	Unigene48803_All//gi|15231160|ref|NP_187922.1|//2.00E-88//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75311241|sp|Q9LK58.1|PP225_ARA TH RecName: Full=Pentatricopeptide repeat-containing protein At3g13150 >gi|66792658|gb|AAY56431.1|At3g13150 [Arabidopsis thaliana]	Unigene48803_All//1.00E-86//AT3G13150| pentatricopeptide (PPR) repeat-containing protein	Unigene48803_All//0.00E+00//TC135553			GO:0043231	nr +
Unigene48805_All	1086	7.66	4.20	2.55	12.20	6.88	8.73	7.05	4.43	5.54	-8.67E-01	1.77E-05		-1.59E+00	2.32E-12	Down	-8.26E-01	6.35E-09		-4.82E-01	1.56E-03		-6.71E-01	3.35E-04		-3.47E-01	6.27E-02		Unigene48805_All//gi|194708822|gb|ACF88495.1|//2.00E-20//At5g55210 [Arabidopsis thaliana]	Unigene48805_All//8.00E-39//AT4G22320| unknown protein	Unigene48805_All//0.00E+00//TC136501			GO:0043231	nr -
Unigene4881_All	1169	6.85	2.21	5.42	8.44	8.28	6.57	9.58	3.25	3.17	-1.63E+00	5.72E-13	Down	-3.37E-01	1.33E-01		-2.76E-02	8.94E-01		-3.61E-01	5.53E-02		-1.56E+00	2.02E-20	Down	-1.60E+00	8.52E-22	Down	Unigene4881_All//gi|112972|sp|P287 34.1|AATC_DAUCA//1.00E-139//RecName: Full=Aspartate aminotransferase, cytoplasmic; AltName: Full=Transaminase A >gi|167546|gb|AAA33134.1|aspartate aminotransferase [Daucus carota] >gi|445587|prf||1909339A Asp aminotransferase	Unigene4881_All//7.00E-138//AT5G11520| ASP3 (ASPARTATE AMINOTRANSFERASE 3); L-aspartate:2-oxoglutarate aminotransferase	Unigene4881_All//0.00E+00//TC158740		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism//ko00350|Tyrosine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr +
Unigene48811_All	947	2.87	5.51	1.35	7.05	6.98	6.92	42.82	94.80	107.15	9.40E-01	3.75E-04		-1.09E+00	6.96E-03		-1.38E-02	9.51E-01		-2.76E-02	9.30E-01		1.15E+00	6.90E-99	Up	1.32E+00	1.09E-142	Up	Unigene48811_All//gi|259121421|gb|ACV92030.1|//4.00E-85//WRKY transcription factor 28 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene48811_All//5.00E-33//AT4G22070| WRKY31; transcription factor	Unigene48811_All//5.00E-83//C0071372	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0003677//GO:0010468//GO:0043231	nr +
Unigene48813_All	770	38.87	9.15	7.88	55.25	45.21	67.86	74.73	18.40	35.23	-2.09E+00	6.08E-65	Down	-2.30E+00	9.95E-71	Down	-2.89E-01	1.70E-04		2.97E-01	3.65E-05		-2.02E+00	8.77E-146	Down	-1.08E+00	5.19E-60	Down	Unigene48813_All//gi|24473796|gb|AAL91663.1|//5.00E-44//60s acidic ribosomal protein [Prunus dulcis] >gi|111013714|gb|ABH03379.1|60S acidic ribosomal protein [Prunus dulcis]	Unigene48813_All//6.00E-19//AT3G44590| 60S acidic ribosomal protein P2 (RPP2D)	Unigene48813_All//0.00E+00//gi|109886023|gb|DW514993.1|DW514993		ko03010|Ribosome	GO:0005198//GO:0006412//GO:0030529//GO:0043231	nr -
Unigene48814_All	660	34.17	50.13	33.32	48.98	36.16	51.39	61.24	48.89	29.64	5.53E-01	3.34E-09		-3.62E-02	7.82E-01		-4.38E-01	4.57E-07		6.92E-02	5.64E-01		-3.25E-01	1.50E-05		-1.05E+00	4.30E-40	Down	Unigene48814_All//gi|66096352|gb|AAV42864.1|//4.00E-49//thioredoxin H [Nicotiana alata]	Unigene48814_All//1.00E-41//AT5G39950| ATTRX2 (THIOREDOXIN 2); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	Unigene48814_All//0.00E+00//gi|109889421|gb|DW518389.1|DW518389			GO:0015036//GO:0016020//GO:0018904//GO:0019725//GO:0043231//GO:0044464	nr -
Unigene48815_All	2019	0.80	1.10	1.16	0.44	1.04	0.65	2.14	4.51	2.76	4.59E-01	2.94E-01		5.31E-01	2.35E-01		1.23E+00	5.57E-03		5.47E-01	3.98E-01		1.08E+00	7.94E-10	Up	3.71E-01	9.88E-02		Unigene48815_All//gi|2792188|emb|CA A05276.1|//1.00E-75//Hcr9-9E [Solanum pimpinellifolium]	Unigene48815_All//7.00E-45//AT1G45616| AtRLP6 (Receptor Like Protein 6); protein binding	Unigene48815_All//1.00E-17//ES836854		ko04626|Plant-pathogen interaction		nr +
Unigene48817_All	1103	2.94	1.52	0.97	4.70	6.37	6.18	1.65	3.07	2.09	-9.56E-01	5.68E-03		-1.61E+00	2.68E-05	Down	4.39E-01	4.70E-02		3.97E-01	9.15E-02		8.97E-01	2.82E-03		3.46E-01	3.61E-01		Unigene48817_All//gi|15217506|ref|NP_172410.1|//1.00E-111//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75099786|sp|Q80522.1|GDL2_ARAT H RecName: Full=GDSL esterase/lipase AtLg09390; AltName: Full=Extracellular lipase At1g09390; Flags: Precursor >gi|3482914|gb|AAC33199.1| Similar to nodulins and lipase [Arabidopsis thaliana]	Unigene48817_All//3.00E-102//AT1G09390| GDSL-motif lipase/hydrolase family protein	Unigene48817_All//0.00E+00//gi|109840163|gb|DW238724.1|DW238724			GO:0043231	nr +
Unigene48818_All	1149	1.64	5.38	4.22	2.04	2.64	3.07	2.32	1.71	2.53	1.71E+00	8.38E-11	Up	1.36E+00	4.09E-06	Up	3.72E-01	3.34E-01		5.89E-01	7.98E-02		-4.39E-01	2.24E-01		1.27E-01	7.03E-01		Unigene48818_All//gi|124359941|gb|ABN07957.1|//1.00E-10//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene48818_All//5.00E-08//AT2G33160| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene48818_All//5.00E-74//gi|21089498|gb|BQ401811.1|BQ401811				nr -
Unigene48819_All	1521	6.91	9.66	8.68	19.88	24.90	58.88	541.00	1397.97	2283.83	4.83E-01	9.64E-04		3.29E-01	4.83E-02		3.25E-01	7.61E-05		1.57E+00	3.09E-139	Up	1.37E+00	0.00E+00	Up	2.07E+00	0.00E+00	Up	Unigene48819_All//gi|149938956|gb|ABR45723.1|//0.00E+00//GDH1 [Actinidia chinensis]	Unigene48819_All//0.00E+00//AT3G03910| GDH3 (GLUTAMATE DEHYDROGENASE 3); binding / catalytic/ oxidoreductase/ oxidoreductase, acting on the CH-NH2 group of donors, NAD or NADP as acceptor	Unigene48819_All//0.00E+00//TC143512		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006519//GO:0006970//GO:0009642//GO:0010038//GO:0016639//GO:0019222//GO:0031980//GO:0032559//GO:0046914	nr -
Unigene4882_All	1596	0.20	0.19	0.17	3.53	3.71	6.99	14.73	5.66	8.74	-4.62E-02	9.84E-01		-2.38E-01	8.50E-01		7.34E-02	8.29E-01		9.87E-01	6.05E-09		-1.38E+00	3.59E-35	Down	-7.54E-01	5.77E-14		Unigene4882_All//gi|297845716|ref|XP_002890739.1|//1.00E-177//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336581|gb|EFH66998.1|transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4882_All//8.00E-175//AT1G27620| transferase family protein	Unigene4882_All//0.00E+00//gi|13350833|gb|BG441181.1|BG441181		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene48820_All	1108	1.79	2.47	1.59	10.75	7.18	7.54	6.37	4.15	31.10	4.61E-01	2.35E-01		-1.78E-01	7.01E-01		-5.82E-01	1.30E-04		-5.11E-01	1.58E-03		-6.19E-01	1.60E-03		2.29E+00	6.31E-104	Up	Unigene48820_All//gi|297845654|ref|XP_002890708.1|//4.00E-90//F21J9.14 [Arabidopsis lyrata subsp. lyrata] >gi|297336550|gb|EFH66967.1|F21J9.14 [Arabidopsis lyrata subsp. lyrata]	Unigene48820_All//1.00E-84//AT1G24480| methyltransferase	Unigene48820_All//0.00E+00//gi|78342286|gb|DT562560.1|DT562560			GO:0016741//GO:0043231	nr +
Unigene48821_All	958	34.84	22.58	33.30	53.82	44.18	58.46	68.28	42.97	31.27	-6.26E-01	2.14E-11		-6.56E-02	5.76E-01		-2.85E-01	3.54E-05		1.19E-01	1.33E-01		-6.68E-01	1.86E-29		-1.13E+00	2.48E-72	Down	Unigene48821_All//gi|18425101|ref|NP_569038.1|//1.00E-117//DGL1; dolichyl-diphosphooligosaccharide-protein glycotransferase [Arabidopsis thaliana] >gi|16226812|gb|AAL16268.1|AF42833 8_1 AT5g66680/MSN2_7 [Arabidopsis thaliana]	Unigene48821_All//2.00E-118//AT5G66680| DGL1; dolichyl-diphosphooligosaccharide-protein glycotransferase	Unigene48821_All//0.00E+00//gi|78327832|gb|DT548106.1|DT548106		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis		nr -
Unigene48822_All	841	3.36	2.95	3.74	4.62	2.66	4.83	2.31	3.28	0.81	-1.87E-01	6.22E-01		1.53E-01	6.67E-01		-7.96E-01	6.32E-03		6.51E-02	8.58E-01		5.04E-01	1.44E-01		-1.52E+00	3.06E-04	Down							

Unigene48824_All	656	77.68	37.77	14.53	31.74	41.05	18.59	60.13	14.08	7.35	-1.04E+00	1.27E-39	Down	-2.42E+00	1.15E-127	Down	3.71E-01	1.82E-04		-7.72E-01	5.41E-11		-2.09E+00	8.86E-105	Down	-3.03E+00	3.96E-165	Down	Unigene48824_All//gi|15232146|ref|NP_189372.1|//1.00E-69//histone H3 [Arabidopsis thaliana] >gi|15238433|ref|NP_201339.1| histone H3 [Arabidopsis thaliana] >gi|18390992|ref|NP_563838.1| histone H3 [Arabidopsis thaliana] >gi|18416261|ref|NP_568227.1| histone H3 [Arabidopsis thaliana] >gi|18416264|ref|NP_568228.1| histone H3 [Arabidopsis thaliana] >gi|115441249|ref|NP_001044904.1| Os01g0866200 [Oryza sativa Japonica Group] >gi|115458352|ref|NP_001052776.1| Os04g0419600 [Oryza sativa Japonica Group] >gi|115464121|ref|NP_001055660.1| Os05g0438700 [Oryza sativa Japonica Group] >gi|115466556|ref|NP_001056877.1| Os06g0160100 [Oryza sativa Japonica Group] >gi|115484259|ref|NP_001065791.1| Os11g0155900 [Oryza sativa Japonica Group] >gi|212721652|ref|NP_001131276.1| histone H3.2 [Zea mays] >gi|297724495|ref|NP_001174611.1| Os06g0159501 [Oryza sativa	Unigene48824_All//3.00E-60//AT5G65360| histone H3	Unigene48824_All//0.00E+00//TC155451			GO:0000785//GO:0003676//GO:0009536 //GO:0031981//GO:0034728	nr -
Unigene48825_All	1668	9.72	10.42	10.98	13.92	11.95	13.46	13.97	8.52	6.16	9.97E-02	5.12E-01		1.76E-01	2.40E-01		-2.19E-01	5.96E-02		-4.85E-02	7.14E-01		-7.13E-01	2.83E-12		-1.18E+00	2.54E-28	Down	Unigene48825_All//gi|18397556|ref|NP_564358.1|//1.00E-138//ATPase, BadF/BadG/BcrA/BcrD-type family [Arabidopsis thaliana] >gi|30102644|gb|AAP21240.1| At1g30540 [Arabidopsis thaliana]	Unigene48825_All//5.00E-134//AT1G30540| ATPase, BadF/BadG/BcrA/BcrD-type family	Unigene48825_All//0.00E+00//TC133552				nr +
Unigene48826_All	1951	4.53	3.56	2.98	8.89	7.47	6.99	10.77	4.97	4.96	-3.49E-01	7.82E-02		-6.07E-01	2.60E-03		-2.51E-01	6.53E-02		-3.46E-01	1.02E-02		-1.12E+00	8.55E-23	Down	-1.12E+00	1.43E-23	Down	Unigene48826_All//gi|15241122|ref|NP_200420.1|//0.00E+00//COX15 (cytochrome c oxidase 15) [Arabidopsis thaliana]	Unigene48826_All//0.00E+00//AT5G56090| COX15 (cytochrome c oxidase 15)	Unigene48826_All//0.00E+00//TC163173		ko00190|Oxidative phosphorylation//ko00860|Porphyrin and chlorophyll metabolism	GO:0006783//GO:0016020//GO:0065003	nr +
Unigene48828_All	1046	0.20	12.74	5.40	10.52	9.25	10.58	5.42	7.87	5.52	5.99E+00	1.97E-69	Up	4.75E+00	6.34E-26	Up	-1.86E-01	3.22E-01		7.30E-03	9.68E-01		5.39E-01	2.79E-03		2.80E-02	9.24E-01		Unigene48828_All//gi|162135178|gb|ABX82698.1|//1.00E-102//stay green protein [Capsicum annuum] >gi|170947249|emb|CAN88917.2| chlorophyll retainer (stay green) [Capsicum annuum] >gi|171903868|gb|ACB56586.1| chlorophyll retainer [Capsicum annuum]	Unigene48828_All//8.00E-100//AT4G22920| NYE1 (NON-YELLOWING 1)	Unigene48828_All//0.00E+00//TC149223			GO:0006787	nr +
Unigene48829_All	301	1.22	24.75	4.42	2.32	4.46	9.45	6.32	15.41	16.54	4.35E+00	3.12E-33	Up	1.86E+00	4.86E-03		9.45E-01	1.10E-01		2.03E+00	8.90E-07	Up	1.29E+00	7.34E-07	Up	1.39E+00	2.43E-08	Up	Unigene48829_All//gi|225437941|ref|XP_002268868.1|//2.00E-21//PREDICTED: similar to Os04g0509400 [Vitis vinifera]	Unigene48829_All//2.00E-17//AT4G28703| FUNCTIONS IN: molecular_function unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Cupin, RmlC-type (InterPro:IPR011051), Protein of unknown function DUF861, cupin-3 (InterPro:IPR008579), RmlC-like jelly roll fold (InterPro:IPR014710); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G04300.1); Has 311 Blast hits to 311 proteins in 80 species: Archae - 0; Bacteria - 147; Metazoa - 0; Fungi - 0; Plants - 76; Viruses - 0; Other Eukaryotes - 88 (source: NCBI BLink).	Unigene48829_All//1.00E-167//BE054198				nr -
Unigene48830_All	556	3.76	34.45	7.66	3.49	7.56	6.58	15.21	35.03	41.70	3.19E+00	1.69E-66	Up	1.03E+00	9.08E-04	Up	1.11E+00	1.11E-04	Up	9.13E-01	4.50E-03		1.20E+00	8.95E-24	Up	1.46E+00	2.88E-38	Up	Unigene48830_All//gi|225437941|ref|XP_002268868.1|//1.00E-44//PREDICTED: similar to Os04g0509400 [Vitis vinifera]	Unigene48830_All//1.00E-37//AT3G04300| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Cupin, RmlC-type (InterPro:IPR011051), Protein of unknown function DUF861, cupin-3 (InterPro:IPR008579), RmlC-like jelly roll fold (InterPro:IPR014710); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G10300.1); Has 364 Blast hits to 364 proteins in 91 species: Archae - 0; Bacteria - 191; Metazoa - 0; Fungi - 0; Plants - 78; Viruses - 0; Other Eukaryotes - 95 (source: NCBI BLink).	Unigene48830_All//0.00E+00//gi|109881968|gb|DW510938.1|DW510938			GO:0009536	nr -
Unigene48832_All	966	8.88	20.56	5.57	4.85	3.74	3.97	12.34	31.67	31.05	1.21E+00	5.37E-20	Up	-6.74E-01	1.01E-03		-3.73E-01	1.91E-01		-2.87E-01	3.57E-01		1.36E+00	2.04E-44	Up	1.33E+00	3.76E-43	Up	Unigene48832_All//gi|75180217|sp|Q9LQU4.1|Y1487_ARATH//4.00E-54//RecName: Full=Uncharacterized protein At1g14870 >gi|8778226|gb|AAF79235.1|AC006917_20 F10B6.27 [Arabidopsis thaliana]	Unigene48832_All//7.00E-47//AT1G14870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: plasma membrane; EXPRESSED IN: callus; CONTAINS InterPro DOMAIN/s: EGF-type aspartate/asparagine hydroxylation conserved site (InterPro:IPR000152), Protein of unknown function Cys-rich (InterPro:IPR006461); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35525.1); Has 492 Blast hits to 491 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 93; Fungi - 76; Plants - 297; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink).	Unigene48832_All//0.00E+00//TC138589				nr +
Unigene48833_All	800	0.00	0.00	0.00	0.00	0.22	0.00	3.70	1.41	3.83	null	null		null	null		7.75E+00	2.27E-01		null	null		-1.39E+00	3.67E-05	Down	5.17E-02	8.85E-01		Unigene48833_All//gi|297833348|ref|XP_002884556.1|//2.00E-26//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330396|gb|EFH60815.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48833_All//1.00E-23//AT5G19200| short-chain dehydrogenase/reductase (SDR) family protein	Unigene48833_All//0.00E+00//TC158649			GO:0003824//GO:0008152	nr -
Unigene48838_All	1224	12.10	10.93	10.09	17.54	14.69	20.00	25.35	20.32	12.63	-1.47E-01	3.74E-01		-2.61E-01	1.02E-01		-2.56E-01	3.08E-02		1.89E-01	1.19E-01		-3.20E-01	2.43E-04		-1.01E+00	4.75E-29	Down	Unigene48838_All//gi|297828079|ref|XP_002881922.1|//2.00E-45//signal recognition particle 14 kDa family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327761|gb|EFH58181.1| signal recognition particle 14 kDa family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48838_All//9.00E-37//AT2G43640| signal recognition particle 14 kDa family protein / SRP14 family protein	Unigene48838_All//0.00E+00//gi|13351996|gb|BG442428.1|BG442428		ko03060|Protein export	GO:0003723//GO:0005048//GO:0006448 //GO:0006613//GO:0048500	nr -
Unigene48840_All	1432	6.17	5.84	2.57	40.39	50.04	27.22	0.12	0.06	0.03	-8.08E-02	6.88E-01		-1.27E+00	1.60E-09	Down	3.09E-01	6.19E-08		-5.69E-01	1.99E-17		-1.02E+00	6.14E-01		-2.09E+00	3.13E-01		Unigene48840_All//gi|45649132|gb|AAS75127.1|//1.00E-156//GSDL-motif lipase [Agave americana]	Unigene48840_All//1.00E-148//AT4G28780| GDSL-motif lipase/hydrolase family protein	Unigene48840_All//0.00E+00//TC174355				nr -
Unigene48843_All	688	23.96	56.78	24.92	61.47	87.99	72.54	103.98	125.93	143.55	1.25E+00	2.47E-40	Up	5.71E-02	7.04E-01		5.17E-01	8.58E-17		2.39E-01	1.57E-03		2.76E-01	2.86E-08		4.65E-01	6.38E-24		Unigene48843_All//gi|15227350|ref|NP_181673.1|//1.00E-36//proline-rich family protein [Arabidopsis thaliana] >gi|75160475|sp|Q8SSM0.1|U647A_ARATH RecName: Full=UPF0467 protein At2g41420 >gi|27808506|gb|AAO24533.1| At2g41420 [Arabidopsis thaliana]		Unigene48843_All//0.00E+00//TC160213		ko03040|Spliceosome	GO:0016020	nr -
Unigene48844_All	1188	14.93	6.23	12.46	15.56	11.39	15.47	22.56	9.75	6.98	-1.26E+00	3.60E-19	Down	-2.61E-01	6.98E-02		-4.50E-01	1.75E-04		-7.80E-03	9.50E-01		-1.21E+00	8.70E-33	Down	-1.69E+00	2.20E-55	Down	Unigene48844_All//gi|300392452|dbj|BAJ10726.1|//1.00E-131//WD40 repeat nucleoporin similar to SEH1 [Lotus japonicus]	Unigene48844_All//3.00E-124//AT1G64350| SEH1H; nucleotide binding	Unigene48844_All//0.00E+00//BG440257				nr +
Unigene48845_All	908	0.40	1.95	2.29	1.21	3.34	1.99	1.40	2.53	2.15	2.28E+00	6.80E-05	Up	2.50E+00	6.61E-06	Up	1.47E+00	4.54E-05	Up	7.21E-01	1.51E-01		8.58E-01	2.27E-02		6.22E-01	1.21E-01		Unigene48845_All//gi|13676415|dbj|BAB41198.1|//7.00E-18//hypothetical protein [Glycine max]		Unigene48845_All//0.00E+00//TC151174				nr -
Unigene48846_All	1325	0.87	1.61	1.69	1.24	1.69	2.25	1.47	1.48	3.10	8.87E-01	4.43E-02		9.58E-01	3.31E-02		4.45E-01	3.26E-01		8.59E-01	1.85E-02		1.45E-02	1.01E+00		1.08E+00	5.21E-05	Up	Unigene48846_All//gi|297601813|ref|NP_001051548.2|//3.00E-37//Os03g0795400 (Oryza sativa Japonica Group) >gi|255674962|dbj|BAF13462.2| Os03g0795400 [Oryza sativa Japonica Group]	Unigene48846_All//4.00E-23//AT3G53700| MEE40 (maternal effect embryo arrest 40)					nr -
Unigene48848_All	1303	48.71	34.03	50.76	62.32	65.20	56.64	27.29	17.48	10.15	-5.18E-01	4.10E-15		5.95E-02	4.43E-01		6.52E-02	3.36E-01		-1.38E-01	2.48E-02		-6.43E-01	2.33E-15		-1.43E+00	4.31E-57	Down	Unigene48848_All//gi|13161912|emb|CAC33003.1|//1.00E-144//urease accessory protein G [Solanum tuberosum]	Unigene48848_All//3.00E-128//AT2G34470| UREG (UREASE ACCESSORY PROTEIN G); ATP binding / metal ion binding / nickel ion binding / nucleotide binding	Unigene48848_All//0.00E+00//TC130672				nr -

Unigene48849_All	1559	1.14	6.70	1.84	1.95	3.51	4.49	0.98	2.57	2.91	2.55E+00	5.31E-29	Up	6.93E-01	7.43E-02		8.50E-01	4.96E-04		1.20E+00	8.18E-08	Up	1.40E+00	9.40E-07	Up	1.58E+00	4.30E-09	Up	Unigene48849_All//gi|75313300|sp|Q9SD02.1|P2C47_ARATH//1.00E-151//RecName: Full=Probable protein phosphatase 2C 47; Short=AtPP2C47 >gi|6572068|emb|CAB63011.1| protein phosphatase 2C-like protein [Arabidopsis thaliana] >gi|51536524|gb|AAU05500.1| At3g51470 [Arabidopsis thaliana] >gi|51972144|gb|AAU15176.1| At3g51470 [Arabidopsis thaliana]	Unigene48849_All//5.00E-142//AT3G51470| protein phosphatase 2C, putative / PP2C, putative	Unigene48849_All//0.00E+00//TC165314	DBP			nr +
Unigene48850_All	1722	5.71	2.80	3.77	6.80	6.62	5.95	4.25	1.94	2.20	-1.03E+00	3.68E-08	Down	-5.99E-01	1.61E-03		-3.85E-02	8.33E-01		-1.91E-01	3.12E-01		-1.13E+00	1.30E-08	Down	-9.51E-01	6.12E-07		Unigene48850_All//gi|115441491|ref|XP_001045025.1|//1.00E-129//Os01g0885600 [Oryza sativa Japonica Group] >gi|56784309|dbj|BAD82235.1| hydrolase-like protein [Oryza sativa Japonica Group] >gi|113534556|dbj|BAF06939.1| Os01g0885600 [Oryza sativa Japonica Group]	Unigene48850_All//2.00E-124//AT4G10030| hydrolase, alpha/beta fold family protein	Unigene48850_All//0.00E+00//gi|78337034|gb|DT557308.1|DT557308				nr -
Unigene48851_All	2114	6.71	5.46	7.41	11.26	14.53	12.71	10.92	4.84	5.50	-2.96E-01	5.47E-02		1.43E-01	3.98E-01		3.67E-01	6.32E-05		1.75E-01	1.31E-01		-1.17E+00	5.70E-27	Down	-9.89E-01	2.89E-21		Unigene48851_All//gi|224134308|ref|XP_002327806.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222836891|gb|EEE75284.1| GRAS family transcription factor [Populus trichocarpa]	Unigene48851_All//3.00E-155//AT5G66770| scarecrow transcription factor family protein	Unigene48851_All//0.00E+00//TC168345	GRAS		GO:0010467	nr +
Unigene48852_All	1066	1.13	1.66	1.90	3.08	2.81	1.53	3.65	1.57	1.08	5.59E-01	2.54E-01		7.50E-01	1.16E-01		-1.34E-01	7.37E-01		-1.02E+00	2.77E-03		-1.22E+00	1.77E-05	Down	-1.75E+00	3.85E-09	Down	Unigene48852_All//gi|15235023|ref|NP_194262.1|//7.00E-65//DNA-binding protein-related [Arabidopsis thaliana] >gi|119657350|tpd|FAA00274.1| TPA: AT-hook motif nuclear localized protein 3 [Arabidopsis thaliana]	Unigene48852_All//1.00E-55//AT4G25320| DNA-binding protein-related	Unigene48852_All//0.00E+00//gi|164287078|gb|EX165723.1|EX165723			GO:0003676//GO:0006351//GO:0043231	nr -
Unigene48853_All	1775	1.27	0.74	1.26	3.70	3.47	5.24	4.05	1.34	3.39	-7.72E-01	6.92E-02		-8.60E-03	1.00E+00		-9.33E-02	7.44E-01		5.01E-01	8.00E-03		-1.59E+00	8.77E-14	Down	-2.57E-01	1.98E-01		Unigene48853_All//gi|79356046|ref|NP_564341.2|//0.00E+00//NRPA2; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding [Arabidopsis thaliana]	Unigene48853_All//0.00E+00//AT1G29940| NRPA2; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding	Unigene48853_All//1.00E-26//DR452437		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0001882//GO:0003676//GO:0010467//GO:0034062//GO:0043231	nr -
Unigene48854_All	1324	12.65	10.75	12.19	15.65	14.85	15.49	34.97	11.59	13.51	-2.34E-01	1.03E-01		-5.34E-02	7.24E-01		-7.58E-02	6.16E-01		-1.53E-02	9.33E-01		-1.59E+00	1.19E-84	Down	-1.37E+00	7.67E-70	Down	Unigene48854_All//gi|82621186|gb|AB886281.1|//1.00E-132//transcription factor APF1-like [Solanum tuberosum]	Unigene48854_All//8.00E-132//AT1G19580| GAMMA CA1 (GAMMA CARBONIC ANHYDRASE 1); carbonate dehydratase	Unigene48854_All//0.00E+00//gi|78325205|gb|DT545479.1|DT545479				nr -
Unigene48856_All	1364	8.02	11.85	8.47	15.74	8.00	6.82	18.35	17.44	14.57	5.64E-01	4.57E-05		7.96E-02	6.63E-01		-9.76E-01	1.22E-18		-1.21E+00	3.71E-23	Down	-7.38E-02	5.45E-01		-3.32E-01	4.94E-04		Unigene48856_All//gi|1346029|sp|P49352.1|FPPS2_LUPAL//1.00E-134//RecName: Full=Farnesyl pyrophosphate synthase 2; Short=FPP synthase 2; Short=FPS 2; AltName: Full=Farnesyl diphosphate synthase 2; Includes: RecName: Full=Dimethylallyltranstransferase; Includes: RecName: Full=Geranyltranstransferase >gi|710350|gb|AAA87729.1| farnesyl pyrophosphate synthase [Lupinus albus]	Unigene48856_All//1.00E-131//AT5G47770| FPS1 (FARNESYL DIPHOSPHATE SYNTHASE 1); dimethylallyltranstransferase/ geranyltranstransferase	Unigene48856_All//1.00E-152//TC174405		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene4886_All	1238	30.18	22.84	23.31	13.96	12.41	6.27	1.26	0.14	0.80	-4.02E-01	4.16E-06		-3.72E-01	3.99E-05		-1.71E-01	2.49E-01		-1.15E+00	1.66E-17	Down	-3.23E+00	2.68E-07	Down	-6.51E-01	1.52E-01		Unigene4886_All//gi|225451974|ref|XP_002279826.1|//1.00E-80//PREDICTED: hypothetical protein [Vitis vinifera] >gi|298204374|emb|CBI16854.3| unnamed protein product [Vitis vinifera]	Unigene4886_All//8.00E-52//AT5G16030| unknown protein	Unigene4886_All//0.00E+00//CO127793				nr +
Unigene48860_All	998	14.42	57.42	19.53	11.18	15.49	15.48	82.78	112.03	60.36	1.99E+00	6.67E-116	Up	4.38E-01	7.42E-04		4.71E-01	4.85E-04		4.69E-01	8.31E-04		4.37E-01	1.84E-23		-4.56E-01	1.64E-19		Unigene48860_All//gi|225446337|ref|XP_002272136.1|//4.00E-82//PREDICTED: similar to ring domain containing protein isoform 2 [Vitis vinifera] >gi|225446339|ref|XP_002272107.1| PREDICTED: similar to ring domain containing protein isoform 1 [Vitis vinifera]	Unigene48860_All//2.00E-49//AT4G03510| RMA1; protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene48860_All//7.00E-153//gi|54120743|gb|CO496252.1|CO496252		ko04146|Peroxisome	GO:0006511//GO:0006886//GO:0006950//GO:0009725//GO:0019787//GO:0031090//GO:0032446//GO:0043231//GO:0046872//GO:0046903	nr +
Unigene48863_All	1195	3.68	14.97	7.89	3.38	4.12	4.35	12.60	1.85	5.13	2.02E+00	2.61E-37	Up	1.10E+00	3.04E-08	Up	2.87E-01	3.30E-01		3.64E-01	1.97E-01		-2.76E+00	7.88E-56	Down	-1.29E+00	2.18E-21	Down	Unigene48863_All//gi|14916566|sp|Q92WQ9.1|FLS_CITUN//1.00E-149//RecName: Full=Flavonol synthase/flavanone 3-hydroxylase; AltName: Full=CitFLS; Short=FLS >gi|4126403|dbj|BAA36554.1| flavonol synthase [Citrus unshiu]	Unigene48863_All//4.00E-124//AT5G08640| FLS (FLAVONOL SYNTHASE); flavonol synthase	Unigene48863_All//0.00E+00//TC152773		ko00941|Flavonoid biosynthesis		nr -
Unigene48864_All	1063	15.60	30.22	18.03	20.62	21.93	24.05	16.59	39.12	26.61	9.54E-01	6.97E-22		2.09E-01	1.37E-01		8.90E-02	5.44E-01		2.22E-01	5.21E-02		1.24E+00	4.38E-52	Up	6.82E-01	4.98E-14		Unigene48864_All//gi|297825287|ref|XP_002880526.1|//2.00E-87//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326365|gb|EFH56785.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48864_All//5.00E-75//AT2G23280| zinc finger (C3HC4-type RING finger) family protein	Unigene48864_All//0.00E+00//gi|164258198|gb|ES793917.1|ES793917		ko04146|Peroxisome	GO:0046914	nr +
Unigene48865_All	1071	1.32	4.64	2.09	3.02	1.83	5.78	4.11	15.06	15.03	1.81E+00	1.80E-09	Up	6.63E-01	1.39E-01		-7.22E-01	2.79E-02		9.34E-01	7.35E-05		1.88E+00	2.11E-37	Up	1.87E+00	5.09E-38	Up	Unigene48865_All//gi|115438827|ref|NP_001043693.1|//1.00E-69//Os01g0643600 [Oryza sativa Japonica Group] >gi|75315200|sp|Q9XU38.1|HOX3_ORYSI RecName: Full=Homeobox-leucine zipper protein HOX3; AltName: Full=Homeodomain transcription factor HOX3; AltName: Full=HD-ZIP protein HOX3; AltName: Full=OsHox3 >gi|122228648|sp|Q0JKX1.1|HOX3_ORYSJ RecName: Full=Homeobox-leucine zipper protein HOX3; AltName: Full=Homeodomain transcription factor HOX3; AltName: Full=HD-ZIP protein HOX3; AltName: Full=OsHox3 >gi|5006851|gb|AAD37696.1|AF145727_1 homeodomain leucine zipper protein [Oryza sativa Indica Group] >gi|113533224|dbj|BAF05607.1| Os01g0643600 [Oryza sativa Japonica Group]	Unigene48865_All//4.00E-52//AT2G01430| ATHB17 (ARABIDOPSIS THALIANA HOMEOBOX-LEUCINE ZIPPER PROTEIN 17); transcription factor	Unigene48865_All//0.00E+00//DR452294	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene48866_All	1168	1.88	1.78	1.50	14.03	9.58	3.13	4.45	3.54	3.07	8.11E-02	8.45E-01		-3.23E-01	4.83E-01		-5.50E-01	1.39E-05		-2.16E+00	1.19E-40	Down	-3.30E-01	1.84E-01		-5.37E-01	1.79E-02		Unigene48866_All//gi|295917227|gb|ADG59900.1|//9.00E-73//annexin 14 [Glycine max]	Unigene48866_All//2.00E-26//AT5G12380| annexin, putative	Unigene48866_All//0.00E+00//DT457896				nr +
Unigene48869_All	871	12.98	7.85	15.96	18.24	18.11	18.36	28.01	9.98	14.87	-7.24E-01	1.84E-05		2.98E-01	6.76E-02		-1.09E-02	9.56E-01		8.80E-03	9.51E-01		-1.49E+00	9.48E-41	Down	-9.14E-01	9.07E-20		Unigene48869_All//gi|145334127|ref|NP_001078444.1|//1.00E-106//PGI1 (PHOSPHOGLUCOSE ISOMERASE 1); glucose-6-phosphate isomerase [Arabidopsis thaliana]	Unigene48869_All//1.00E-107//AT4G24620| PGI1 (PHOSPHOGLUCOSE ISOMERASE 1); glucose-6-phosphate isomerase	Unigene48869_All//0.00E+00//TC135710		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway	GO:0006007//GO:0016861//GO:0043231	nr -
Unigene4887_All	1552	15.00	6.33	15.20	5.75	6.32	5.91	0.71	0.32	0.44	-1.24E+00	2.11E-24	Down	1.89E-02	8.90E-01		1.38E-01	5.47E-01		4.01E-02	8.65E-01		-1.13E+00	5.52E-02		-6.99E-01	2.11E-01		Unigene4887_All//gi|297833172|ref|XP_002884468.1|//1.00E-130//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297330308|gb|EFH60727.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene4887_All//1.00E-126//AT3G04760| pentatricopeptide (PPR) repeat-containing protein	Unigene4887_All//4.00E-140//DW500497				nr +
Unigene48870_All	1259	2.74	1.41	1.61	1.78	0.90	0.93	2.08	0.33	1.71	-9.61E-01	3.99E-03		-7.71E-01	2.64E-02		-9.80E-01	1.54E-02		-9.33E-01	2.93E-02		-2.65E+00	7.81E-10	Down	-2.85E-01	4.18E-01		Unigene48870_All//gi|109946601|gb|ABG48479.1|//1.00E-132//At5g18460 [Arabidopsis thaliana]	Unigene48870_All//7.00E-134//AT5G18460| unknown protein	Unigene48870_All//2.00E-166//gi|78344721|gb|DT564995.1|DT564995				nr +
Unigene48871_All	1215	2.20	9.26	4.38	3.36	9.98	37.77	9.71	51.19	88.30	2.08E+00	1.90E-24	Up	9.97E-01	2.42E-04		1.57E+00	6.78E-21	Up	3.49E+00	3.00E-184	Up	2.40E+00	2.21E-194	Up	3.19E+00	0.00E+00	Up	Unigene48871_All//gi|224109958|ref|XP_002313369.1|//1.00E-25//f-box family protein [Populus trichocarpa] >gi|222864409|gb|EEF01540.1| f-box family protein [Populus trichocarpa]	Unigene48871_All//2.00E-18//AT5G07610| F-box family protein	Unigene48871_All//6.00E-43//CD485784				nr -
Unigene48872_All	838	71.99	154.55	102.81	70.26	125.95	111.18	36.58	48.08	57.57	1.10E+00	5.22E-109	Up	5.14E-01	3.01E-19		8.42E-01	7.25E-68		6.62E-01	6.97E-36		3.94E-01	1.37E-07		6.54E-01	1.02E-21		Unigene48872_All//gi|7768151|emb|CAB90633.1|//2.00E-63//protein phpsphatase 2C (PP2C) [Fagus sylvatica]	Unigene48872_All//1.00E-52//AT3G11410| PP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA); protein binding / protein serine/threonine phosphatase	Unigene48872_All//0.00E+00//gi|164299986|gb|ES806063.1|ES806063			GO:0004721//GO:0006464//GO:0006950//GO:0009738//GO:0010118//GO:0043169//GO:0043234	nr -
Unigene48873_All	926	4.24	1.48	1.09	1.83	2.12	2.49	3.84	1.22	2.11	-1.52E+00	3.62E-06	Down	-1.96E+00	5.42E-08	Down	2.13E-01	6.94E-01		4.44E-01	3.33E-01		-1.65E+00	1.50E-07	Down	-8.63E-01	2.19E-03		Unigene48873_All//gi|102139988|gb|ABF70123.1|//4.00E-36//DNA-binding protein-related [Musa balbisiana]	Unigene48873_All//4.00E-23//AT1G06190| ATP binding / ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism	Unigene48873_All//0.00E+00//TC161181			GO:0005488//GO:0006139//GO:0009536//GO:0044249	nr -
Unigene48874_All	1049	127.09	55.50	76.40	30.15	34.37	24.84	6.65	12.95	6.57	-1.20E+00	3.34E-128	Down	-7.34E-01	3.54E-55		1.89E-01	4.12E-02		-2.80E-01	3.82E-03		9.61E-01	6.22E-12		-1.75E-02	9.54E-01		Unigene48874_All//gi|115441201|ref|NP_001044880.1|//2.00E-46//Os01g0862200 [Oryza sativa Japonica Group] >gi|113534411|dbj|BAF06794.1| Os01g0862200 [Oryza sativa Japonica Group]	Unigene48874_All//2.00E-43//AT2G36145| unknown protein	Unigene48874_All//0.00E+00//TC152465			GO:0009532//GO:0009534	nr +
Unigene48875_All	1119	41.80	29.16	31.84	57.43	43.51	56.22	35.93	16.40	10.79	-5.20E-01	2.01E-11		-3.93E-01	8.30E-07		-4.00E-01	1.70E-11		-3.06E-02	7.01E-01		-1.13E+00	7.24E-44	Down	-1.74E+00	1.46E-85	Down	Unigene48875_All//gi|15226875|ref|NP_181046.1|//2.00E-31//AT01 (Arabidopsis thioredoxin 01) [Arabidopsis thaliana] >gi|145330362|ref|NP_001078006.1| AT01 (Arabidopsis thioredoxin 01) [Arabidopsis thaliana] >gi|75099186|sp|O64764.1|TRX01_ARATH RecName: Full=Thioredoxin 01, mitochondrial; Short=AtTrxo1; Flags: Precursor >gi|107738216|gb|ABF83663.1| At2g35010 [Arabidopsis thaliana]	Unigene48875_All//9.00E-28//AT2G35010| AT01 (Arabidopsis thioredoxin 01)	Unigene48875_All//0.00E+00//TC155079			GO:0016667//GO:0031980	nr -

Unigene48877_All	2005	0.81	0.58	1.49	1.84	1.91	1.06	1.43	9.48	2.11	-4.77E-01	3.71E-01		8.79E-01	2.04E-02		5.23E-02	8.93E-01		-7.96E-01	1.21E-02		2.73E+00	4.24E-69	Up	5.55E-01	3.05E-02		Unigene48877_All//gi|156103422|gb|ABU48859.1|//1.00E-172//xylosyltransferase 2 [Nicotiana benthamiana]	Unigene48877_All//9.00E-150//AT5G55500| XYLT (ARABIDOPSIS THALIANA BETA-1,2-XYLOSYLTRANSFERASE); xylosyltransferase	Unigene48877_All//0.00E+00//gi|3326536|gb|AI055422.1|AI055422		ko00510|N-Glycan biosynthesis		nr +
Unigene48878_All	775	29.10	6.54	14.43	63.51	26.13	26.05	54.45	37.70	22.00	-2.15E+00	4.56E-51	Down	-1.01E+00	1.83E-16	Down	-1.28E+00	7.65E-66	Down	-1.29E+00	6.78E-58	Down	-5.30E-01	4.75E-13		-1.31E+00	3.19E-59	Down	Unigene48878_All//gi|11367218|gb|AB134666.1|//3.00E-40//bZIP transcription factor bZIP124 [Glycine max]	Unigene48878_All//3.00E-31//AT4G34590| GBF6 (G-BOX BINDING FACTOR 6); DNA binding / protein heterodimerization/ transcription factor	Unigene48878_All//0.00E+00//TC162194	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0003677//GO:0006351//GO:0006412//GO:0034285//GO:0043231//GO:0046983	nr +
Unigene48879_All	1187	22.57	8.20	8.70	37.73	25.99	38.43	30.88	19.37	15.54	-1.46E+00	1.32E-35	Down	-1.37E+00	2.71E-31	Down	-5.38E-01	1.00E-13		2.66E-02	7.87E-01		-6.73E-01	4.21E-17		-9.91E-01	2.39E-33		Unigene48879_All//gi|15239505|ref|NP_200911.1|//2.00E-61//GR-RBP3 (glycine-rich RNA-binding protein 3); ATP binding / RNA binding [Arabidopsis thaliana] >gi|16974556|gb|AAL31194.1|AT5g61030/maf19_30 [Arabidopsis thaliana] >gi|21928059|gb|AAM78058.1|AT5g61030/maf19_30 [Arabidopsis thaliana]	Unigene48879_All//8.00E-41//AT5G61030| GR-RBP3 (glycine-rich RNA-binding protein 3); ATP binding / RNA binding	Unigene48879_All//0.00E+00//gi|78331601|gb|DT551875.1|DT551875		ko03040|Spliceosome	GO:0032559//GO:0043231//GO:0046914	nr -
Unigene48880_All	703	7.07	2.59	3.18	12.40	9.06	6.30	5.11	2.32	1.25	-1.45E+00	4.04E-07	Down	-1.15E+00	5.68E-05	Down	-4.53E-01	1.63E-02		-9.78E-01	4.02E-07		-1.14E+00	1.07E-04	Down	-2.04E+00	3.18E-10	Down			Unigene48880_All//0.00E+00//TC153940				
Unigene48881_All	864	24.83	9.21	12.63	31.83	21.28	16.20	12.14	3.82	5.58	-1.43E+00	8.76E-28	Down	-9.75E-01	8.77E-15		-5.81E-01	7.71E-10		-9.74E-01	5.56E-21		-1.67E+00	4.97E-21	Down	-1.12E+00	2.95E-12	Down			Unigene48881_All//0.00E+00//TC153940				
Unigene48882_All	1286	2.40	0.28	1.28	4.65	2.62	2.70	3.58	1.82	1.43	-3.12E+00	4.78E-11	Down	-9.03E-01	1.51E-02		-8.25E-01	2.41E-04		-7.82E-01	1.02E-03		-9.78E-01	1.08E-04		-1.33E+00	2.01E-07	Down	Unigene48882_All//gi|115452569|ref|NP_001049885.1|//1.00E-154//0s03g0305700 [Oryza sativa Japonica Group] >gi|108707729|gb|ABF95524.1|peptide chain release factor 2 family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548356|dbj|BAF11799.1|0s03g0305700 [Oryza sativa Japonica Group]	Unigene48882_All//2.00E-160//AT1G56350| peptide chain release factor, putative	Unigene48882_All//0.00E+00//gi|164249986|gb|ES793670.1|ES793670			GO:0003747	nr +
Unigene48884_All	531	1.38	0.19	0.00	1.97	3.57	1.53	0.24	0.71	0.68	-2.85E+00	6.26E-03		-1.04E+01	4.13E-04	Down	8.56E-01	7.22E-02		-3.64E-01	6.33E-01		1.57E+00	1.95E-01		1.50E+00	2.03E-01		Unigene48884_All//gi|206204560|gb|AC105918.1|//4.00E-43//kinase-like protein pac.x.7.4 [Platanus x acerifolia]	Unigene48884_All//7.00E-32//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0016628//GO:0031224//GO:0032559	nr +
Unigene48886_All	1174	19.88	15.06	14.61	20.03	16.10	16.70	20.89	10.82	7.74	-4.00E-01	4.14E-04		-4.45E-01	1.49E-04		-3.15E-01	3.71E-03		-2.63E-01	2.43E-02		-9.49E-01	1.81E-20		-1.43E+00	6.77E-40	Down	Unigene48886_All//gi|30688336|ref|NP_030605.2|//1.00E-81//appr-1-p processing enzyme family protein [Arabidopsis thaliana]	Unigene48886_All//9.00E-82//AT2G40600| appr-1-p processing enzyme family protein	Unigene48886_All//0.00E+00//TC139656			GO:0009523//GO:0016779//GO:0044237//GO:0046872	nr +
Unigene48889_All	1163	20.87	24.27	16.94	10.28	12.44	36.50	14.91	35.43	28.98	2.17E-01	4.21E-02		-3.01E-01	1.06E-02		2.75E-01	7.16E-02		1.83E+00	3.50E-82	Up	1.25E+00	2.37E-52	Up	9.59E-01	5.64E-29		Unigene48889_All//gi|297796999|ref|XP_002866384.1|//1.00E-112//ATPDX2/EMB2407/PDX2 [Arabidopsis lyrata subsp. lyrata] >gi|297312219|gb|EFH42643.1|ATPDX2/EMB2407/PDX2 [Arabidopsis lyrata subsp. lyrata]	Unigene48889_All//1.00E-109//AT5G60540| PDX2 (PYRIDOXINE BIOSYNTHESIS 2); glutaminase/ glutamine[-tRNA synthase (glutamine-hydrolyzing)/ protein heterodimerization	Unigene48889_All//0.00E+00//CO078033		ko00750|Vitamin B6 metabolism	GO:0003824//GO:0006541//GO:0009108	nr -
Unigene4889_All	1730	0.88	1.49	1.11	0.43	0.88	1.28	1.86	1.84	3.02	7.68E-01	5.06E-02		3.37E-01	4.97E-01		1.02E+00	6.18E-02		1.57E+00	5.28E-04	Up	-1.66E-02	9.93E-01		7.00E-01	2.02E-03		Unigene4889_All//gi|115473217|ref|NP_001060207.1|//1.00E-153//0s07g0602700 [Oryza sativa Japonica Group] >gi|113611743|dbj|BAF22121.1|0s07g0602700 [Oryza sativa Japonica Group]	Unigene4889_All//3.00E-136//AT3G02130| RPK2 (RECEPTOR-LIKE PROTEIN KINASE 2); ATP binding / kinase/ protein serine/threonine kinase	Unigene4889_All//0.00E+00//TC166252		ko04626|Plant-pathogen interaction		nr -
Unigene48890_All	480	107.91	43.49	45.37	158.37	133.94	138.69	175.37	75.15	91.79	-1.31E+00	6.18E-58	Down	-1.25E+00	5.92E-52	Down	-2.42E-01	1.59E-05		-1.91E-01	1.58E-03		-1.22E+00	8.36E-103	Down	-9.34E-01	2.07E-68		Unigene48890_All//gi|21617886|gb|AM66936.1|//5.00E-41//40S ribosomal protein S5 [Arabidopsis thaliana]	Unigene48890_All//3.00E-42//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	Unigene48890_All//0.00E+00//TC163109		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030312	nr +
Unigene48892_All	1104	56.06	32.68	85.95	20.30	30.41	9.90	1.07	0.64	1.66	-7.79E-01	1.07E-29		6.16E-01	4.11E-29		5.83E-01	1.16E-11		-1.04E+00	5.16E-19	Down	-7.37E-01	1.94E-01		6.30E-01	1.31E-01		Unigene48892_All//gi|30678541|ref|NP_191916.3|//6.00E-65//UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75299638|sp|Q8GZ38.1|UNE10_ARATH RecName: Full=Transcription factor UNE10; AltName: Full=Protein UNFERTILIZED EMBRYO SAC 10; AltName: Full=Transcription factor EN 108; AltName: Full=bHLH transcription factor bHLH016; AltName: Full=Basic helix-loop-helix protein 16; Short=bHLH 16; Short=AtbHLH16 >gi|109134123|gb|ABG25060.1|At4g00050 [Arabidopsis thaliana]	Unigene48892_All//1.00E-62//AT4G00050| UNE10 (unfertilized embryo sac 10); DNA binding / transcription factor	Unigene48892_All//0.00E+00//TC157319	bHLH	ko04626|Plant-pathogen interaction//ko04712|Circadian rhythm - plant	GO:0001071//GO:0003676//GO:0005515//GO:0006779//GO:0009566//GO:0009630//GO:0009640//GO:0010017//GO:0010029//GO:0010468//GO:0010476//GO:0043231	nr -
Unigene48896_All	930	3.49	2.89	1.26	51.90	43.32	35.89	10.18	17.17	9.51	-2.73E-01	4.37E-01		-1.47E+00	9.62E-05	Down	-2.61E-01	3.13E-04		-5.32E-01	4.91E-13		7.53E-01	1.89E-09		-9.87E-02	6.20E-01		Unigene48896_All//gi|89111872|gb|ABD60708.1|//5.00E-27//At5g47635 [Arabidopsis thaliana]	Unigene48896_All//2.00E-28//AT5G47635| unknown protein	Unigene48896_All//0.00E+00//TC160455				nr -
Unigene48899_All	2072	3.13	2.62	4.29	12.04	10.95	13.23	21.10	5.71	6.71	-2.59E-01	2.90E-01		4.55E-01	2.55E-02		-1.37E-01	2.70E-01		1.36E-01	2.61E-01		-1.89E+00	3.99E-101	Down	-1.65E+00	9.61E-87	Down	Unigene48899_All//gi|15242672|ref|NP_195939.1|//1.00E-102//CPU0RF47 (CONSERVED PEPTIDE UPSTREAM OPEN READING FRAME 47) [Arabidopsis thaliana]	Unigene48899_All//2.00E-109//AT3G53400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; BEST Arabidopsis thaliana protein match is: CPU0RF47 (CONSERVED PEPTIDE UPSTREAM OPEN READING FRAME 47) (TAIR:AT5G03190.1); Has 120 Blast hits to 120 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 115; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene48899_All//0.00E+00//TC170795				nr -
Unigene48900_All	1634	1.67	0.87	0.95	9.57	4.95	3.07	2.48	0.87	1.15	-9.39E-01	1.38E-02		-8.17E-01	4.17E-02		-9.51E-01	3.94E-13		-1.64E+00	7.91E-27	Down	-1.51E+00	1.36E-07	Down	-1.12E+00	2.99E-05	Down	Unigene48900_All//gi|82469976|gb|AB877236.1|//1.00E-122//patellin 1 [Cucurbita pepo]	Unigene48900_All//1.00E-90//AT1G72160| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene48900_All//2.00E-139//gi|109838891|gb|DW237452.1|DW237452			GO:0000904//GO:0005576//GO:0009536//GO:0016020//GO:0019899	nr -
Unigene48901_All	1263	1.28	1.56	1.14	6.86	3.98	3.25	21.83	32.27	13.00	2.85E-01	5.53E-01		-1.74E-01	7.29E-01		-7.86E-01	1.41E-05		-1.08E+00	3.49E-08	Down	5.64E-01	5.30E-14		-7.48E-01	5.01E-16		Unigene48901_All//gi|115311477|gb|AB193919.1|//2.00E-82//At1g10040 [Arabidopsis thaliana]	Unigene48901_All//8.00E-84//AT1G10040| unknown protein	Unigene48901_All//0.00E+00//TC168779			GO:0043231	nr +
Unigene48902_All	1266	0.74	2.32	1.26	3.58	2.99	2.60	4.48	5.48	3.27	1.64E+00	2.96E-05	Up	7.62E-01	1.60E-01		-2.59E-01	4.04E-01		-4.59E-01	1.19E-01		2.92E-01	1.67E-01		-4.52E-01	3.82E-02		Unigene48902_All//gi|1293690|gb|AA842054.1|//1.00E-90//STA1-12 [Silene latifolia subsp. alba]	Unigene48902_All//3.00E-79//AT3G42960| ATA1 (ARABIDOPSIS TAPETUM 1); binding / catalytic/ oxidoreductase	Unigene48902_All//8.00E-104//gi|3326779|gb|AI055665.1|AI055665		ko00906|Carotenoid biosynthesis	GO:0003824//GO:0008152//GO:0009791	nr +
Unigene48903_All	681	0.00	1.71	0.63	0.00	0.20	1.06	1.86	1.90	9.54	1.07E+01	1.05E-06	Up	9.29E+00	1.38E-02		7.66E+00	3.18E-01		1.01E+01	2.31E-04	Up	3.07E-02	9.85E-01		2.36E+00	6.56E-21	Up	Unigene48903_All//gi|125630795|gb|ABN47005.1|//9.00E-39//early nodulin 93 protein [Populus alba x Populus tremula var. glandulosa]	Unigene48903_All//8.00E-12//AT5G25940| early nodulin-related	Unigene48903_All//0.00E+00//gi|109843868|gb|DW242426.1|DW242426			GO:0031224//GO:0044403	nr +
Unigene48904_All	785	0.07	0.32	0.47	1.33	3.55	2.30	0.75	2.08	4.87	2.27E+00	2.34E-01		2.83E+00	9.30E-02		1.41E+00	1.70E-04	Up	7.88E-01	1.17E-01		1.46E+00	2.29E-03		2.69E+00	1.51E-14	Up	Unigene48904_All//gi|125630795|gb|ABN47005.1|//2.00E-39//early nodulin 93 protein [Populus alba x Populus tremula var. glandulosa]	Unigene48904_All//2.00E-13//AT5G25940| early nodulin-related	Unigene48904_All//0.00E+00//TC166254			GO:0031224//GO:0044403	nr +
Unigene48905_All	2028	18.03	7.67	10.00	15.18	14.55	11.65	3.61	2.64	0.83	-1.23E+00	2.01E-37	Down	-8.50E-01	8.13E-20		-6.10E-02	6.00E-01		-3.82E-01	5.86E-05		-4.51E-01	2.08E-02		-2.13E+00	4.34E-21	Down	Unigene48905_All//gi|76880174|dbj|BAE45859.1|//2.00E-94//MurF synthetase [Physcomitrella patens subsp. patens]		Unigene48905_All//0.00E+00//TC178385			GO:0008152//GO:0009987//GO:0016881	nr +
Unigene48906_All	752	35.34	12.94	12.53	125.73	99.78	47.81	28.45	4.67	5.67	-1.45E+00	6.22E-35	Down	-1.50E+00	3.50E-35	Down	-3.34E-01	5.58E-12		-1.40E+00	1.01E-125	Down	-2.61E+00	3.33E-74	Down	-2.33E+00	4.05E-67	Down	Unigene48906_All//gi|18394637|ref|NP_564059.1|//3.00E-38//PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding [Arabidopsis thaliana] >gi|9795591|gb|AAF98409.1|AC026238_1 Hypothetical protein [Arabidopsis thaliana] >gi|30017221|gb|AAP12844.1|At1g18650 [Arabidopsis thaliana]	Unigene48906_All//1.00E-36//AT1G18650| PDCB3 (PLASMODESMATA CALLOSE-BINDING PROTEIN 3); callose binding / polysaccharide binding	Unigene48906_All//0.00E+00//TC140304			GO:0003824//GO:0005911//GO:0030247//GO:0031224	nr -
Unigene48907_All	960	3.38	3.59	1.44	1.87	4.16	3.39	3.08	3.13	11.91	8.70E-02	7.91E-01		-1.23E+00	8.40E-04	Down	1.16E+00	1.03E-04	Up	8.59E-01	1.29E-02		2.40E-02	9.72E-01		1.95E+00	1.01E-28	Up	Unigene48907_All//gi|224082982|ref|XP_002306917.1|//2.00E-56//SAUR family protein [Populus trichocarpa] >gi|222856366|gb|EEE93913.1| SAUR family protein [Populus trichocarpa]	Unigene48907_All//8.00E-56//AT1G75590| auxin-responsive family protein	Unigene48907_All//6.00E-98//TC173565			GO:0009725	nr +
Unigene48909_All	1513	0.55	1.57	1.34	2.04	2.14	1.37	2.24	2.02	3.32	1.51E+00	5.37E-04	Up	1.27E+00	8.67E-03		6.77E-02	8.68E-01		-5.72E-01	1.17E-01		-1.49E-01	6.36E-01		5.70E-01	1.41E-02		Unigene48909_All//gi|15241481|ref|NP_196415.1|//2.00E-57//dentin sialophosphoprotein-related [Arabidopsis thaliana]	Unigene48909_All//2.00E-53//AT5G07980| dentin sialophosphoprotein-related	Unigene48909_All//2.00E-80//TC143292				nr +
Unigene4891_All	1228	6.86	3.88	3.21	5.68	4.43	6.73	3.51	1.57	2.14	-8.23E-01	3.93E-05		-1.10E+00	2.24E-07	Down	-3.58E-01	1.10E-01		2.45E-01	2.80E-01		-1.17E+00	1.22E-05	Down	-7.14E-01	4.49E-03		Unigene4891_All//gi|62149356|dbj|BAD93478.1|//1.00E-117//phytochromobilin synthase [Solanum lycopersicum] >gi|62149358|dbj|BAD93479.1|phytochromobilin synthase [Solanum lycopersicum]	Unigene4891_All//2.00E-109//AT3G09150| HY2 (ELONGATED HYPOCOTYL 2); phytochromobilin:ferredoxin oxidoreductase			ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene48910_All	1640	1.21	0.80	0.78	12.82	7.12	6.03	7.84	2.96	3.43	-5.94E-01	1.98E-01		-6.38E-01	1.87E-01		-8.49E-01	1.74E-14		-1.09E+00	2.73E-19	Down	-1.41E+00	3.98E-20	Down	-1.19E+00	2.64E-16	Down	Unigene48910_All//gi|15240904|ref|NP_195737.1|//5.00E-79//glycine-rich protein [Arabidopsis thaliana] >gi|63850563|gb|AAU95458.1|At5g01170 [Arabidopsis thaliana]	Unigene48910_All//2.00E-35//AT3G09070| glycine-rich protein	Unigene48910_All//0.00E+00//TC175433				nr +
Unigene48911_All	1579	29.03	19.99	18.11	35.59	28.00	42.25	30.47	14.48	13.75	-5.38E-01	6.86E-12		-6.81E-01	5.57E-17		-3.46E-01	8.04E-08		2.48E-01	9.76E-05		-1.07E+00	4.16E-48	Down	-1.15E+00	4.57E-55	Down	Unigene48911_All//gi|297827107|ref|XP_002881436.1|//1.00E-139//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327275|gb|EFH57695.1|hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48911_All//1.00E-138//AT2G36290| hydrolase, alpha/beta fold family protein	Unigene48911_All//0.00E+00//TC137178				nr -
Unigene48912_All	935	30.89	81.23	35.48	64.63	60.69	76.42	55.39	79.12	62.34	1.40E+00	1.38E-92	Up	2.00E-01	5.13E-02		-9.05E-02	2.46E-01		2.42E-01	7.80E-05		5.14E-01	4.53E-21		1.70E-01	6.43E-03		Unigene48912_All//gi|289540943|gb|ADD09614.1|//7.00E-58//zinc ion binding protein [Trifolium repens]	Unigene48912_All//5.00E-48//AT4G39140| protein binding / zinc ion binding	Unigene48912_All//0.00E+00//gi|48778786|gb|CO088152.1|CO088152			GO:0003824//GO:0016020//GO:0046914	nr -

Unigene48913_All	847	13.53	13.76	21.94	3.12	7.81	2.40	0.40	0.39	0.19	2.44E-02	9.02E-01		6.98E-01	1.38E-07		1.32E+00	4.27E-09	Up	-3.78E-01	3.78E-01		-1.64E-02	1.02E+00		-1.09E+00	3.55E-01		Unigene48913_All//gi|18403077|ref|NP_564570.1|//4.00E-97//binding / catalytic [Arabidopsis thaliana] >gi|14517416|gb|AAK62598.1| At1g50450/F11F12_20 [Arabidopsis thaliana] >gi|20453277|gb|AAM19877.1| At1g50450/F11F12_20 [Arabidopsis thaliana]	Unigene48913_All//3.00E-87//AT1G50450| binding / catalytic	Unigene48913_All//3.00E-59//CA992633			GO:0009536	nr +
Unigene48914_All	1222	5.65	8.29	9.24	1.88	3.86	2.88	0.24	0.17	0.13	5.53E-01	2.11E-03		7.09E-01	5.13E-05		1.04E+00	9.98E-05	Up	6.20E-01	6.50E-02		-5.02E-01	6.77E-01		-8.93E-01	4.71E-01		Unigene48914_All//gi|18403077|ref|NP_564570.1|//3.00E-61//binding / catalytic [Arabidopsis thaliana] >gi|14517416|gb|AAK62598.1| At1g50450/F11F12_20 [Arabidopsis thaliana] >gi|20453277|gb|AAM19877.1| At1g50450/F11F12_20 [Arabidopsis thaliana]	Unigene48914_All//2.00E-48//AT1G50450| binding / catalytic	Unigene48914_All//3.00E-97//CA992633			GO:0009536	nr -
Unigene48917_All	561	9.33	19.15	10.06	4.08	6.26	5.96	6.03	9.09	11.50	1.04E+00	6.87E-09	Up	1.10E-01	6.80E-01		6.16E-01	6.10E-02		5.45E-01	1.23E-01		5.92E-01	1.26E-02		9.32E-01	5.18E-06		Unigene48917_All//gi|297800772|ref|XP_002868270.1|//5.00E-26//RNA polymerase Rpb7 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297314106|gb|EFH44529.1| RNA polymerase Rpb7 N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene48917_All//2.00E-22//AT4G14660| NRPE7; DNA-directed RNA polymerase	Unigene48917_All//0.00E+00//gi|48752748|gb|C0083267.1|C0083267		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0055029	nr +
Unigene48920_All	1974	6.33	3.98	2.97	10.88	10.43	12.70	20.11	12.70	13.82	-6.71E-01	2.60E-05		-1.09E+00	1.34E-10	Down	-6.02E-02	6.84E-01		2.23E-01	5.32E-02		-6.63E-01	5.65E-18		-5.41E-01	3.91E-13		Unigene48920_All//gi|45476407|dbj|BAD12556.1|//0.00E+00//RIO kinase [Nicotiana tabacum]	Unigene48920_All//0.00E+00//AT5G37350| RIO1 family protein	Unigene48920_All//0.00E+00//gi|78339372|gb|DT559646.1|DT559646			GO:0004672//GO:0032559//GO:0044464	nr -
Unigene48921_All	1016	1.80	0.30	1.57	3.78	3.52	2.49	8.70	5.92	3.84	-2.59E+00	9.26E-06	Down	-1.97E-01	6.80E-01		-9.90E-02	8.04E-01		-6.01E-01	5.74E-02		-5.54E-01	1.35E-03		-1.18E+00	2.90E-11	Down	Unigene48921_All//gi|297803592|ref|XP_002869680.1|//2.00E-96//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297315516|gb|EFH45939.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene48921_All//5.00E-96//AT1G17020| SRG1 (SENESCENCE-RELATED GENE 1); oxidoreductase, acting on diphenols and related substances as donors, oxygen as acceptor / oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and inc	Unigene48921_All//0.00E+00//TC138716		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis	GO:0007568//GO:0009699//GO:0016679//GO:0016706	nr +
Unigene48922_All	755	5.20	3.42	3.74	8.18	9.58	12.38	2.74	0.94	2.59	-6.03E-01	5.05E-02		-4.76E-01	1.44E-01		2.27E-01	3.50E-01		5.98E-01	1.29E-03		-1.54E+00	2.37E-04	Down	-8.58E-02	8.26E-01		Unigene48922_All//gi|297803408|ref|XP_002869588.1|//4.00E-89//AT-HF [Arabidopsis lyrata subsp. lyrata] >gi|297315424|gb|EFH45847.1| AT-HF [Arabidopsis lyrata subsp. lyrata]	Unigene48922_All//1.00E-89//AT4G26900| AT-HF (HIS HF); imidazoleglycerol-phosphate synthase	Unigene48922_All//3.00E-167//gi|48753697|gb|C0084216.1|C0084216		ko00340|Histidine metabolism	GO:0006547//GO:0009536//GO:0016763//GO:0016861	nr +
Unigene48925_All	1160	53.13	18.65	26.03	18.77	10.33	14.56	16.91	13.15	11.47	-1.51E+00	4.00E-85	Down	-1.03E+00	2.47E-45	Down	-8.61E-01	2.35E-15		-3.66E-01	1.73E-03		-3.63E-01	1.19E-03		-5.60E-01	2.41E-07		Unigene48925_All//gi|297824277|ref|XP_002880021.1|//4.00E-14//transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297325860|gb|EFH56280.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene48925_All//3.00E-11//AT2G43060| transcription factor	Unigene48925_All//2.00E-92//TC162763	bHLH			nr -
Unigene48927_All	942	153.80	96.87	113.57	150.71	190.38	157.74	31.51	35.81	14.00	-6.67E-01	2.03E-52		-4.38E-01	6.83E-24		3.37E-01	1.91E-22		6.57E-02	1.88E-01		1.85E-01	3.61E-02		-1.17E+00	2.29E-35	Down	Unigene48927_All//gi|15220010|ref|NP_173718.1|//7.00E-29//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|28299006|gb|AAC00614.1| Hypothetical protein [Arabidopsis thaliana] >gi|38454056|gb|AAR20722.1| At1g23050 [Arabidopsis thaliana] >gi|386023998|gb|AAR24742.1| At1g23050 [Arabidopsis thaliana]		Unigene48927_All//0.00E+00//TC140819		ko04626|Plant-pathogen interaction//ko04144|Endocytosis		nr -
Unigene48928_All	974	12.03	9.26	7.49	48.64	40.48	42.75	112.56	106.63	32.56	-3.78E-01	2.43E-02		-6.84E-01	6.69E-05		-2.65E-01	2.85E-04		-1.86E-01	2.12E-02		-7.80E-02	1.23E-01		-1.79E+00	4.03E-242	Down	Unigene48928_All//gi|211906506|gb|ACJ11746.1|//1.00E-132//luminal binding protein [Gossypium hirsutum]	Unigene48928_All//7.00E-122//AT5G42020| BIP2; ATP binding	Unigene48928_All//0.00E+00//TC179313		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr -
Unigene48929_All	984	50.03	21.47	54.98	352.85	283.85	93.03	57.79	7.18	10.12	-1.22E+00	2.51E-49	Down	1.36E-01	9.37E-02		-3.14E-01	2.62E-38		-1.92E+00	0.00E+00	Down	-3.01E+00	1.01E-228	Down	-2.51E+00	3.83E-194	Down	Unigene48929_All//gi|300793618|tpg|DAA33872.1|//1.00E-138//TPA: TPA_inf: aquaporin TIP4;1 [Gossypium hirsutum] >gi|300793626|tpg|DAA33873.1| TPA_inf: aquaporin TIP4;2 [Gossypium hirsutum]	Unigene48929_All//1.00E-95//AT2G25810| TIP4;1 (tonoplast intrinsic protein 4;1); water channel	Unigene48929_All//0.00E+00//TC130058			GO:0000322//GO:0000325//GO:0005372//GO:0009526//GO:0010476//GO:00312 24//GO:0042044//GO:0042886//GO:0042887	nr -
Unigene48930_All	1598	3.08	0.98	0.23	3.83	4.59	3.45	4.60	1.67	3.14	-1.65E+00	2.33E-08	Down	-3.72E+00	4.17E-19	Down	2.60E-01	2.79E-01		-1.53E-01	6.02E-01		-1.46E+00	1.73E-12	Down	-5.52E-01	3.02E-03		Unigene48930_All//gi|15231815|ref|NP_190912.1|//3.00E-61//DNA binding [Arabidopsis thaliana] >gi|30693817|ref|NP_850691.1| DNA binding [Arabidopsis thaliana] >gi|29028920|gb|AAO64839.1| At3g53440 [Arabidopsis thaliana]	Unigene48930_All//9.00E-56//AT3G53440| DNA binding	Unigene48930_All//0.00E+00//ES844440				nr -
Unigene48934_All	1623	2.71	21.35	6.50	19.95	13.49	10.52	20.92	15.61	32.33	2.98E+00	3.97E-112	Up	1.26E+00	3.32E-11	Up	-5.64E-01	6.15E-11		-9.24E-01	1.47E-22		-4.23E-01	2.60E-07		6.28E-01	6.02E-22		Unigene48934_All//gi|30023704|gb|AAP13385.1|//4.00E-39//At3g56360 [Arabidopsis thaliana]	Unigene48934_All//4.00E-38//AT5G05250| unknown protein	Unigene48934_All//0.00E+00//gi|78329384|gb|DT549658.1|DT549658				nr -
Unigene48937_All	2246	3.68	0.95	2.11	6.59	7.39	4.99	0.79	0.52	0.32	-1.96E+00	5.46E-17	Down	-8.03E-01	1.29E-04		1.66E-01	2.92E-01		-4.02E-01	5.79E-03		-6.01E-01	1.78E-01		-1.31E+00	2.53E-03		Unigene48937_All//gi|6224712|gb|AAF50694.1|//0.00E+00//non-phototropic hypocotyl 3 [Arabidopsis thaliana]	Unigene48937_All//0.00E+00//AT5G64330| NPH3 (NON-PHOTOTROPIC HYPOCOTYL 3); protein binding / signal transducer	Unigene48937_All//0.00E+00//TC170260			GO:0005488//GO:0009314//GO:0009606//GO:0016020//GO:0030522//GO:0060089	nr +
Unigene48938_All	1816	2.07	0.45	1.41	6.42	5.04	4.00	4.19	15.21	0.86	-2.22E+00	2.16E-09	Down	-5.60E-01	9.29E-02		-3.48E-01	3.40E-02		-6.81E-01	2.58E-05		1.86E+00	7.86E-63	Up	-2.29E+00	5.89E-24	Down	Unigene48938_All//gi|224138076|ref|XP_002326512.1|//1.00E-123//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222833834|gb|EEE72311.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene48938_All//6.00E-86//AT4G17980| anac071 (Arabidopsis NAC domain containing protein 71); transcription factor	Unigene48938_All//0.00E+00//TC170198	NAC		GO:0001071//GO:0005488//GO:0010468	nr +
Unigene48939_All	1193	7.41	7.69	5.85	25.89	23.26	16.77	36.54	14.71	7.18	5.27E-02	7.91E-01		-3.42E-01	1.03E-01		-1.54E-01	1.45E-01		-6.26E-01	2.86E-11		-1.31E+00	9.17E-60	Down	-2.35E+00	1.99E-137	Down	Unigene48939_All//gi|115441313|ref|NP_001044936.1|//1.00E-161//Os01g0871300 [Oryza sativa Japonica Group] >gi|113534467|dbj|BAF06850.1| Os01g0871300 [Oryza sativa Japonica Group]	Unigene48939_All//2.00E-150//AT2G22250| aminotransferase class I and II family protein	Unigene48939_All//0.00E+00//TC155123				nr +
Unigene48940_All	1470	2.67	7.10	3.37	3.42	4.29	4.15	4.34	9.61	9.57	1.41E+00	1.48E-13	Up	3.36E-01	2.47E-01		3.25E-01	1.94E-01		2.77E-01	3.04E-01		1.15E+00	3.28E-16	Up	1.14E+00	2.10E-16	Up	Unigene48940_All//gi|4530126|gb|AAD21872.1|//1.00E-98//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene48940_All//3.00E-93//AT4G21390| B120; ATP binding / protein kinase/ protein serine/threonine kinase/ sugar binding	Unigene48940_All//0.00E+00//TC144445		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr +
Unigene48941_All	1482	1.20	1.09	2.62	51.43	45.17	42.57	18.80	3.02	5.32	-1.34E-01	7.71E-01		1.13E+00	5.93E-04	Up	-1.87E-01	1.23E-03		-2.73E-01	2.89E-06		-2.64E+00	8.88E-98	Down	-1.82E+00	1.44E-63	Down	Unigene48941_All//gi|33771692|gb|AAQ54338.1|//0.00E+00//glycuronosyl transferase-like protein [Gossypium hirsutum]	Unigene48941_All//3.00E-122//AT2G37090| IRX9 (IRREGULAR XYLEM 9); transferase, transferring glycosyl groups / xylosyltransferase	Unigene48941_All//0.00E+00//TC161701			GO:0015020//GO:0043231	nr +
Unigene48942_All	1991	0.32	1.12	0.80	3.93	3.67	2.93	2.57	0.86	0.34	1.83E+00	1.03E-04	Up	1.35E+00	1.65E-02		-9.94E-02	6.86E-01		-4.25E-01	4.53E-02		-1.58E+00	6.61E-10	Down	-2.92E+00	3.34E-21	Down	Unigene48942_All//gi|11320514 5|gb|AAT40494.2|//1.00E-149//Putative microtubule-associated protein, identical [Solanum demissum]	Unigene48942_All//7.00E-123//AT3G60840| MAP65-4 (MICROTUBULE-ASSOCIATED PROTEIN 65-4)	Unigene48942_All//0.00E+00//TC175387				nr -
Unigene48943_All	887	14.27	14.28	16.09	26.68	29.47	29.02	50.19	32.94	23.85	6.00E-04	9.97E-01		1.73E-01	3.13E-01		1.44E-01	2.32E-01		1.22E-01	3.46E-01		-6.08E-01	2.62E-17		-1.07E+00	7.24E-46	Down	Unigene48943_All//gi|115453939|ref|NP_001050570.1|//3.00E-62//Os03g0586600 [Oryza sativa Japonica Group] >gi|113549041|dbj|BAF12484.1| Os03g0586600 [Oryza sativa Japonica Group]	Unigene48943_All//1.00E-43//AT5G51940| NRPB6A; DNA binding / DNA-directed RNA polymerase	Unigene48943_All//0.00E+00//D9236378		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003676//GO:0006350//GO:0016591//GO:0034062//GO:0055029	nr +
Unigene48945_All	1356	4.40	19.58	7.11	14.51	12.77	10.89	1.62	1.17	1.00	2.15E+00	1.34E-59	Up	6.92E-01	3.02E-04		-1.84E-01	1.67E-01		-4.14E-01	7.27E-04		-4.69E-01	2.41E-01		-6.99E-01	5.93E-02		Unigene48945_All//gi|255689399|gb|ACU30051.1|//1.00E-124//branched-chain amino acid aminotransferase [Glycine max]	Unigene48945_All//8.00E-125//AT3G49680| BCAT3 (BRANCHED-CHAIN AMINOTRANSFERASE 3); branched-chain-amino-acid transaminase/ catalytic	Unigene48945_All//6.00E-111//gi|73851037|gb|DT460057.1|DT460057		ko00280|Valine, leucine and isoleucine degradation//ko00290|Valine, leucine and isoleucine biosynthesis//ko00966|Glucosinolate biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene48950_All	1297	0.24	1.21	0.82	33.26	15.08	7.97	4.07	3.54	4.27	2.32E+00	1.67E-04	Up	1.76E+00	1.85E-02		-1.14E+00	5.69E-48	Down	-2.06E+00	6.20E-100	Down	-2.01E-01	4.35E-01		6.73E-02	7.76E-01		Unigene48950_All//gi|9759561|dbj|BAB11163.1|//1.00E-149//MtN21 nodulin protein-like [Arabidopsis thaliana]	Unigene48950_All//2.00E-142//AT5G07050| LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF6, transmembrane (InterPro:IPR000620); BEST Arabidopsis thaliana protein match is: nodulin MtN21 family protein (TAIR:AT2G40900.1); Has 2288 Blast hits to 2270 proteins in 280 species: Archae - 23; Bacteria - 774; Metazoa - 5; Fungi - 0; Plants - 641; Viruses - 0; Other Eukaryotes - 845 (source: NCBI BLink).	Unigene48950_All//0.00E+00//TC159804				nr +
Unigene48951_All	1383	173.61	53.67	44.28	451.53	748.29	1614.32	77.90	466.46	299.01	-1.69E+00	0.00E+00	Down	-1.97E+00	0.00E+00	Down	7.29E-01	0.00E+00		1.84E+00	0.00E+00	Up	2.58E+00	0.00E+00	Up	1.94E+00	0.00E+00	Up	Unigene48951_All//gi|283131283|dbj|BAI63297.1|//1.00E-119//thaumatin-like protein [Citrus jambhiri]	Unigene48951_All//2.00E-108//AT2G28790| osmotin-like protein, putative	Unigene48951_All//0.00E+00//gi|78323880|gb|DT544154.1|DT544154			GO:0031410	nr -
Unigene48955_All	1480	4.35	12.12	1.15	31.44	45.95	41.99	53.16	238.91	115.99	1.48E+00	2.34E-24	Up	-1.92E+00	2.01E-12	Down	5.48E-01	8.26E-21		4.18E-01	8.53E-11		2.17E+00	0.00E+00	Up	1.13E+00	7.56E-187	Up	Unigene48955_All//gi|14970839|emb|CAC44500.1|//1.00E-156//beta-galactosidase [Fragaria x ananassa]	Unigene48955_All//3.00E-112//AT3G13750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene48955_All//0.00E+00//TC130564		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation		nr -
Unigene48957_All	1419	20.35	23.42	17.04	38.09	34.14	32.31	24.31	22.24	12.02	2.03E-01	3.84E-02		-2.57E-01	1.78E-02		-1.58E-01	3.26E-02		-2.38E-01	9.55E-04		-1.29E-01	1.60E-01		-1.02E+00	8.96E-33	Down	Unigene48957_All//gi|225424442|ref|XP_002285121.1|//2.00E-83//PREDICTED: similar to ZFP4 (ZINC FINGER PROTEIN 4); nucleic acid binding / transcription factor/ zinc ion binding [Vitis vinifera]	Unigene48957_All//2.00E-35//AT1G66140| ZFP4 (ZINC FINGER PROTEIN 4); nucleic acid binding / transcription factor/ zinc ion binding	Unigene48957_All//0.00E+00//TC151709	C2H2		GO:0005488	nr +
Unigene4896_All	1090	4.66	2.18	3.71	4.80	2.56	1.74	1.94	0.73	1.32	-1.09E+00	5.58E-05	Down	-3.27E-01	2.55E-01		-9.07E-01	1.87E-04		-1.46E+00	5.42E-08	Down	-1.41E+00	5.54E-04	Down	-5.60E-01	1.43E-01		Unigene4896_All//gi|92893902|gb|ABE91952.1|//4.00E-12//Zinc finger, CCHC-type [Medicago truncatula]	Unigene4896_All//3.00E-11//AT2G01050| nucleic acid binding / zinc ion binding					nr +

Unigene48960_All	560	2.34	1.00	0.29	2.22	2.09	1.05	1.81	0.97	0.57	-1.23E+00	3.96E-02			-3.03E+00	1.24E-04	Down	-8.90E-02	8.70E-01			-1.08E+00	7.79E-02			-9.01E-01	1.44E-01		-1.67E+00	7.35E-03		Unigene48960_All//gi|89001037|gb|AB059108.1|//2.00E-60//At3g18800 [Arabidopsis thaliana]	Unigene48960_All//2.00E-49//AT3G18800| unknown protein	Unigene48960_All//0.00E+00//TC168850			GO:0016020	nr -
Unigene48961_All	635	2.88	0.72	1.26	1.96	1.46	0.57	1.33	0.07	0.06	-2.01E+00	1.86E-04	Down	-1.20E+00	1.99E-02		-4.22E-01	5.06E-01			-1.79E+00	5.55E-03			-4.34E+00	4.55E-05	Down	-4.41E+00	2.37E-05	Down	Unigene48961_All//gi|89001037|gb|AB059108.1|//7.00E-67//At3g18800 [Arabidopsis thaliana]	Unigene48961_All//6.00E-59//AT3G18800| unknown protein	Unigene48961_All//0.00E+00//DW498406			GO:0016020	nr +
Unigene48962_All	1075	6.23	2.26	2.48	10.24	10.09	9.20	9.71	4.63	5.19	-1.46E+00	1.86E-09	Down	-1.33E+00	6.70E-08	Down	-2.14E-02	9.13E-01			-1.55E-01	4.49E-01			-1.07E+00	5.03E-11	Down	-9.05E-01	7.66E-09		Unigene48962_All//gi|195655667|gb|ACG47301.1|//1.00E-92//adenylyl-sulfate kinase [Zea mays]	Unigene48962_All//2.00E-101//AT3G03900| adenylylsulfate kinase, putative	Unigene48962_All//0.00E+00//TC136463		ko00230|Purine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0006520//GO:0006790//GO:0016301//GO:0031406//GO:0032559//GO:0043234	nr +
Unigene48964_All	1309	1.48	3.95	1.75	2.78	2.84	2.79	5.56	5.94	5.48	1.42E+00	3.92E-07	Up	2.42E-01	6.08E-01		3.24E-02	9.47E-01			8.60E-03	9.80E-01			9.63E-02	6.41E-01		-2.02E-02	9.42E-01		Unigene48964_All//gi|145323808|ref|NP_001077493.1|//2.00E-62//F-box family protein [Arabidopsis thaliana] >gi|238055474|sp|Q9CAZ0.2|SK12_ARATH RecName: Full=F-box protein SKIP24; AltName: Full=SKP1-interacting partner 24	Unigene48964_All//1.00E-62//AT1G08710| F-box family protein					nr -
Unigene48965_All	1475	26.21	15.70	19.46	34.68	33.41	39.87	59.77	34.03	24.79	-7.40E-01	2.69E-17		-4.30E-01	1.15E-06		-5.41E-02	5.68E-01			2.01E-01	4.22E-03			-8.12E-01	3.87E-55		-1.27E+00	2.44E-117	Down	Unigene48965_All//gi|297824001|ref|XP_002879883.1|//1.00E-141//tRNA-binding region domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297325722|gb|EFH56142.1| tRNA-binding region domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene48965_All//3.00E-122//AT2G40060| tRNA-binding region domain-containing protein	Unigene48965_All//0.00E+00//TC149830		ko00450|Selenoamino acid metabolism//ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene48966_All	740	3.18	5.48	2.16	3.03	2.84	3.42	2.34	4.80	3.28	7.84E-01	9.73E-03		-5.60E-01	2.06E-01		-9.38E-02	8.26E-01			1.74E-01	6.78E-01			1.04E+00	4.34E-04	Up	4.87E-01	1.74E-01		Unigene48966_All//gi|145330697|ref|NP_001078024.1|//4.00E-44//integral membrane Yip1 family protein [Arabidopsis thaliana]	Unigene48966_All//2.00E-45//AT2G39805| integral membrane Yip1 family protein	Unigene48966_All//0.00E+00//CO077864				nr -
Unigene48967_All	856	0.00	1.18	0.81	0.99	0.68	0.74	1.38	1.56	1.26	1.02E+01	7.25E-06	Up	9.66E+00	6.15E-04	Up	-5.33E-01	4.90E-01			-4.21E-01	6.18E-01			1.76E-01	7.33E-01		-1.38E-01	7.88E-01		Unigene48967_All//gi|145330697|ref|NP_001078024.1|//6.00E-48//integral membrane Yip1 family protein [Arabidopsis thaliana]	Unigene48967_All//3.00E-49//AT2G39805| integral membrane Yip1 family protein	Unigene48967_All//0.00E+00//CO077864				nr -
Unigene48968_All	1044	25.06	23.15	28.31	23.71	20.19	14.84	5.71	2.08	1.79	-1.14E-01	3.49E-01		1.76E-01	1.17E-01		-2.32E-01	3.60E-02			-6.76E-01	2.09E-10			-1.46E+00	3.14E-10	Down	-1.67E+00	9.54E-13	Down	Unigene48968_All//gi|149944309|gb|ABR46197.1|//1.00E-25//At1g69760 [Arabidopsis thaliana]	Unigene48968_All//9.00E-14//AT1G26920| unknown protein	Unigene48968_All//0.00E+00//TC138246				nr +
Unigene4897_All	500	5.76	6.59	1.17	4.78	6.96	5.96	23.85	24.16	12.27	1.95E-01	6.05E-01		-2.30E+00	3.18E-07	Down	5.41E-01	1.08E-01			3.18E-01	4.29E-01			1.87E-02	9.29E-01		-9.59E-01	6.89E-11				Unigene4897_All//0.00E+00//TC145274				
Unigene48970_All	823	1.59	5.60	4.27	1.03	1.17	2.20	0.00	0.00	0.24	1.82E+00	7.16E-09	Up	1.43E+00	6.61E-05	Up	1.87E-01	8.11E-01			1.09E+00	2.78E-02			null	null		7.92E+00	7.88E-02		Unigene48970_All//gi|6671365|gb|AAF23176.1|AF216497_1//1.00E-132//P-glycoprotein [Gossypium hirsutum]	Unigene48970_All//2.00E-113//AT4G25960| PGP2 (P-GLYCOPROTEIN 2); ATPase, coupled to transmembrane movement of substances	Unigene48970_All//0.00E+00//TC141861		ko02010|ABC transporters		nr +
Unigene48972_All	401	10.83	9.22	10.49	7.95	8.33	5.74	8.75	3.86	3.68	-2.32E-01	4.43E-01		-4.59E-02	8.87E-01		6.72E-02	8.66E-01			-4.69E-01	1.99E-01			-1.18E+00	7.92E-05	Down	-1.25E+00	2.08E-05	Down			Unigene48972_All//2.00E-89//gi|13244470|gb|BE054416.2|BE054416				
Unigene48973_All	809	11.64	8.83	12.51	9.85	11.11	12.11	9.09	6.56	2.86	-3.99E-01	3.63E-02		1.03E-01	6.43E-01		1.73E-01	4.44E-01			2.98E-01	1.31E-01			-4.71E-01	1.51E-02		-1.67E+00	1.57E-15	Down			Unigene48973_All//0.00E+00//TC165272				
Unigene48974_All	1502	11.63	13.66	12.59	12.27	10.78	11.58	9.99	7.26	4.62	2.32E-01	6.89E-02		1.13E-01	4.38E-01		-1.88E-01	1.76E-01			-8.41E-02	6.23E-01			-4.60E-01	3.49E-04		-1.11E+00	5.23E-17	Down	Unigene48974_All//gi|18406073|ref|NP_564725.1|//7.00E-80//F-box family protein [Arabidopsis thaliana] >gi|75172668|sp|Q9FVS1.1|FBK23_ARATH RecName: Full=F-box/kelch-repeat protein At1g57790 >gi|30984578|gb|AAP42752.1|At1g57790 [Arabidopsis thaliana]	Unigene48974_All//5.00E-76//AT1G57790| F-box family protein	Unigene48974_All//0.00E+00//TC167474				nr +
Unigene48975_All	1381	16.44	9.03	7.87	31.49	27.23	25.31	24.03	11.35	15.15	-8.65E-01	1.73E-13		-1.06E+00	6.23E-18	Down	-2.10E-01	8.61E-03			-3.15E-01	6.97E-05			-1.08E+00	7.10E-34	Down	-6.66E-01	9.27E-16		Unigene48975_All//gi|195609778|gb|ACG26719.1|//1.00E-110//protein SUR2 [Zea mays]	Unigene48975_All//7.00E-97//AT1G69640| SBH1 (SPHINGOID BASE HYDROXYLASE 1); catalytic/ sphingosine hydroxylase	Unigene48975_All//0.00E+00//TC138933		ko00100|Steroid biosynthesis		nr +
Unigene48976_All	1161	5.59	1.35	4.45	2.53	2.02	2.45	18.14	13.79	20.49	-2.05E+00	3.05E-14	Down	-3.29E-01	1.93E-01		-3.28E-01	3.96E-01			-4.68E-02	9.18E-01			-3.95E-01	2.22E-04		1.76E-01	9.27E-02		Unigene48976_All//gi|224075846|ref|XP_002304794.1|//2.00E-63//type-a response regulator [Populus trichocarpa] >gi|222842226|gb|EEE79773.1| type-a response regulator [Populus trichocarpa]	Unigene48976_All//5.00E-48//AT3G57040| ARR9 (RESPONSE REGULATOR 9); transcription regulator/ two-component response regulator	Unigene48976_All//0.00E+00//gi|109826106|gb|DW224827.1|DW224827	ARR-B	ko04712|Circadian rhythm - plant		nr -
Unigene48978_All	867	5.55	10.99	2.40	5.17	21.88	12.76	23.90	22.32	324.64	9.85E-01	2.21E-07		-1.21E+00	3.50E-05	Down	2.08E+00	1.41E-47	Up	1.30E+00	1.69E-13	Up	-9.84E-02	4.43E-01		3.76E+00	0.00E+00	Up	Unigene48978_All//gi|15225174|ref|NP_180763.1|//1.00E-55//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|89111890|gb|ABD60717.1|At2g32030 [Arabidopsis thaliana]	Unigene48978_All//7.00E-57//AT2G32030| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene48978_All//0.00E+00//TC144122				nr -
Unigene48979_All	1165	6.60	3.31	5.53	7.06	10.37	6.01	11.50	6.60	3.32	-9.98E-01	2.92E-06		-2.55E-01	2.71E-01		5.56E-01	3.08E-04			-2.32E-01	3.13E-01			-8.01E-01	6.87E-09		-1.79E+00	2.05E-30	Down	Unigene48979_All//gi|297790937|ref|XP_002863353.1|//9.00E-65//vesicle-associated membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309188|gb|EFH39612.1| vesicle-associated membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48979_All//1.00E-65//AT5G47180| vesicle-associated membrane family protein / VAMP family protein	Unigene48979_All//3.00E-109//gi|54119462|gb|CO494971.1|CO494971				nr -
Unigene4898_All	1282	2.49	1.11	1.99	4.47	5.83	3.03	1.19	1.08	0.31	-1.17E+00	9.68E-04	Down	-3.20E-01	3.94E-01		3.83E-01	7.86E-02			-5.61E-01	2.42E-02			-1.42E-01	7.70E-01		-1.93E+00	1.54E-04	Down	Unigene4898_All//gi|124359162|gb|AB005685.1|//6.00E-75//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene4898_All//2.00E-29//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene4898_All//1.00E-170//DW241491				nr -
Unigene48981_All	1098	2.48	1.02	1.89	10.80	4.64	5.26	3.62	1.07	2.29	-1.29E+00	1.04E-03		-3.90E-01	3.51E-01		-1.22E+00	6.68E-15	Down	-1.04E+00	2.46E-10	Down	-1.76E+00	4.48E-09	Down	-6.63E-01	1.18E-02		Unigene48981_All//gi|15241069|ref|NP_195804.1|//1.00E-32//OFP1 (OVATE FAMILY PROTEIN 1); protein binding / transcription repressor [Arabidopsis thaliana]	Unigene48981_All//2.00E-24//AT5G01840| OFP1 (OVATE FAMILY PROTEIN 1); protein binding / transcription repressor	Unigene48981_All//0.00E+00//TC178201				nr -
Unigene48982_All	1155	19.21	3.55	3.00	23.55	16.19	6.53	14.42	4.20	4.48	-2.43E+00	2.87E-58	Down	-2.68E+00	1.48E-62	Down	-5.41E-01	1.26E-08			-1.85E+00	1.02E-54	Down	-1.78E+00	4.37E-36	Down	-1.69E+00	1.65E-34	Down	Unigene48982_All//gi|33325041|gb|AQ08180.1|//4.00E-89//TK1-like deoxyribonucleoside kinase [Solanum lycopersicum]	Unigene48982_All//1.00E-83//AT1G07800| thymidine kinase, putative	Unigene48982_All//0.00E+00//TC142330		ko00240|Pyrimidine metabolism		nr +
Unigene48983_All	1006	23.46	19.09	27.15	31.59	30.88	25.81	34.00	17.41	13.27	-2.97E-01	9.62E-03		2.11E-01	6.48E-02		-3.31E-02	8.12E-01			-2.91E-01	2.38E-03			-9.66E-01	4.66E-29		-1.36E+00	5.02E-51	Down	Unigene48983_All//gi|124359979|gb|ABN07995.1|//1.00E-83//RNA polymerase subunit, RPB5; RNA polymerase Rpb5, N-terminal [Medicago truncatula]	Unigene48983_All//2.00E-79//AT3G57080| NRPE5; DNA binding / DNA-directed RNA polymerase	Unigene48983_All//0.00E+00//TC149775		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene48984_All	1151	14.96	4.49	7.36	18.09	15.02	9.53	13.52	3.67	5.88	-1.74E+00	1.76E-29	Down	-1.02E+00	6.05E-13	Down	-2.69E-01	2.52E-02			-9.24E-01	1.00E-14			-1.88E+00	2.37E-36	Down	-1.20E+00	1.08E-19	Down	Unigene48984_All//gi|255564345|ref|XP_002523169.1|//1.00E-121//sphingolipid fatty acid alpha hydroxylase [Ricinus communis] >gi|223537576|gb|EEF39200.1|sphingolipid fatty acid alpha hydroxylase [Ricinus communis]	Unigene48984_All//1.00E-114//AT2G34770| FAH1 (FATTY ACID HYDROXYLASE 1); catalytic/ fatty acid alpha-hydroxylase	Unigene48984_All//0.00E+00//TC165889				nr +
Unigene48986_All	972	5.33	4.17	3.45	9.38	8.47	4.04	9.53	3.70	4.63	-3.54E-01	1.94E-01		-6.27E-01	2.30E-02		-1.48E-01	5.20E-01			-1.21E+00	2.90E-10	Down	-1.37E+00	4.23E-14	Down	-1.04E+00	8.84E-10	Down	Unigene48986_All//gi|15219850|ref|NP_176717.1|//4.00E-70//CLV2 (clavata 2); protein binding / receptor signaling protein [Arabidopsis thaliana] >gi|3333351|gb|AAC27153.1| Similar to ERECTA receptor protein kinase gb|D83257 from A. thaliana. ESTs gb|T41629 and gb|AA586072 come from this gene [Arabidopsis thaliana] >gi|6049566|gb|AAF02654.1|receptor-like protein CLAVATA2 [Arabidopsis thaliana]	Unigene48986_All//3.00E-71//AT1G65480| CLV2 (clavata 2); protein binding / receptor signaling protein	Unigene48986_All//0.00E+00//gi|48829505|gb|CO127895.1|CO127895				nr -
Unigene48987_All	822	26.03	45.74	35.11	37.15	43.74	76.65	22.48	31.37	28.74	8.13E-01	1.24E-19		4.32E-01	3.32E-05		2.36E-01	8.01E-03			1.04E+00	1.46E-52	Up	4.81E-01	4.52E-07		3.55E-01	3.15E-04		Unigene48987_All//gi|297817634|ref|XP_002876700.1|//4.00E-99//NPL4 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322538|gb|EFH52959.1| NPL4 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene48987_All//2.00E-99//AT3G63000| NPL41 (NPL4-LIKE PROTEIN 1)	Unigene48987_All//0.00E+00//gi|78341500|gb|DT561774.1|DT561774				nr +
Unigene48992_All	1897	78.61	9.91	25.68	14.10	10.22	8.29	1.34	0.62	0.36	-2.99E+00	0.00E+00	Down	-1.61E+00	5.18E-219	Down	-4.64E-01	1.46E-06			-7.67E-01	8.34E-14			-1.12E+00	1.86E-03		-1.91E+00	6.61E-07	Down	Unigene48992_All//gi|297830450|ref|XP_002883107.1|//0.00E+00//glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata] >gi|297328947|gb|EFH59366.1|glycosyl hydrolase family 1 protein [Arabidopsis lyrata subsp. lyrata]	Unigene48992_All//0.00E+00//AT3G18080| BGLU44 (B-S GLUCOSIDASE 44); (R)-amygdalin beta-glucosidase/ 4-methylumbelliferyl-beta-D-glucopyranoside beta-glucosidase/ beta-gentiobiose beta-glucosidase/ cellobiose glucosidase/ esculin beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene48992_All//0.00E+00//gi|78348781|gb|DT569055.1|DT569055		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism		nr -
Unigene48993_All	617	6.70	7.39	13.03	63.05	40.46	32.43	56.60	74.38	8.14	1.42E-01	6.12E-01		9.60E-01	7.57E-06		-6.40E-01	2.91E-16			-9.59E-01	9.57E-29			3.94E-01	1.61E-08		-2.80E+00	1.33E-134	Down	Unigene48993_All//gi|224122808|ref|XP_002318921.1|//4.00E-06//stress-induced hydrophobic peptide [Populus trichocarpa] >gi|222857297|gb|EEE94844.1|stress-induced hydrophobic peptide [Populus trichocarpa]		Unigene48993_All//0.00E+00//gi|109876801|gb|DW505775.1|DW505775				nr -
Unigene48994_All	1397	1.46	0.44	0.27	2.18	1.21	1.36	2.42	1.50	5.96	-1.75E+00	3.40E-04	Down	-2.45E+00	1.15E-05	Down	-8.49E-01	1.19E-02			-6.80E-01	5.99E-02			-6.95E-01	2.07E-02		1.30E+00	3.54E-12	Up	Unigene48994_All//gi|18394846|ref|NP_564110.1|//1.00E-161//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75174883|sp|Q9LN22.1|PPR54_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g20300, mitochondrial; Flags: Precursor >gi|17386104|gb|AAL38598.1|AF446865_1 At1g20300/F14O10_8 [Arabidopsis thaliana] >gi|15450347|gb|AAK96467.1|At1g20300/F14O10_8 [Arabidopsis thaliana]	Unigene48994_All//2.00E-162//AT1G20300| pentatricopeptide (PPR) repeat-containing protein	Unigene48994_All//0.00E+00//gi|78350847|gb|DT571121.1|DT571121				nr +
Unigene48995_All	996	2.84	2.39	2.25	94.08	92.73	86.43	17.70	11.62	4.64	-2.47E-01	5.29E-01		-3.37E-01	3.83E-01		-2.09E-02	7.96E-01			-1.22E-01	3.38E-02			-6.07E-01	2.48E-07		-1.93E+00	7.25E-44	Down	Unigene48995_All//gi|158979021|gb|ABW86883.1|//5.00E-75//isopiperitenol dehydrogenase [Mentha x piperita]	Unigene48995_All//1.00E-72//AT2G47140| short-chain dehydrogenase/reductase (SDR) family protein	Unigene48995_All//0.00E+00//TC144614		ko00906|Carotenoid biosynthesis		nr +

Unigene48996_All	879	31.31	19.02	26.96	37.40	33.42	30.93	27.51	19.35	10.65	-7.19E-01	5.76E-12		-2.16E-01	5.73E-02		-1.63E-01	1.04E-01		-2.74E-01	3.80E-03		-5.08E-01	2.71E-07		-1.37E+00	8.62E-37	Down	Unigene48996_All//gi|15233053|ref|NP_191679.1|//7.00E-36//thioesterase family protein [Arabidopsis thaliana] >gi|18650609|gb|AAL75904.1|AT3g61200/T20K12_100 [Arabidopsis thaliana] >gi|21700815|gb|AAM70531.1|AT3g61200/T20K12_100 [Arabidopsis thaliana]	Unigene48996_All//4.00E-30//AT3G61200| thioesterase family protein	Unigene48996_All//0.00E+00//TC136599				nr +
Unigene48997_All	1114	12.40	8.01	11.33	76.73	70.51	53.96	16.17	4.91	8.69	-6.31E-01	2.83E-05		-1.30E-01	4.52E-01		-1.22E-01	3.78E-02		-5.08E-01	8.08E-21		-1.72E+00	4.35E-37	Down	-8.96E-01	2.30E-14		Unigene48997_All//gi|157273640|gb|ABV27474.1|//1.00E-107//fasciclin-like arabinogalactan protein 3 [Gossypium hirsutum]	Unigene48997_All//4.00E-55//AT2G04780| FLAT (FASCICLIN-LIKE ARABINOOGALACTAN 7)	Unigene48997_All//0.00E+00//gi|78324625|gb|DT544899.1|DT544899				nr +
Unigene49_All	949	1.60	0.96	0.56	4.20	3.08	1.24	2.49	1.32	3.57	-7.34E-01	1.70E-01		-1.51E+00	1.05E-02		-4.45E-01	1.48E-01		-1.76E+00	5.81E-08	Down	-9.17E-01	1.31E-02		5.16E-01	7.83E-02		Unigene49_All//gi|242205328|gb|ACS88338.1|//1.00E-131//cellulose synthase catalytic subunit [Gossypium hirsutum]	Unigene49_All//4.00E-106//AT2G21770| CESA9 (CELLULOSE SYNTHASE A9); cellulose synthase/ transferase, transferring glycosyl groups	Unigene49_All//0.00E+00//TC137429				nr -
Unigene490_All	2951	1.28	1.80	1.17	3.39	4.11	3.46	8.07	8.02	23.25	4.98E-01	5.69E-02		-1.22E-01	7.08E-01		2.76E-01	1.05E-01		2.77E-02	9.11E-01		-9.00E-03	9.67E-01		1.53E+00	8.76E-120	Up	Unigene490_All//gi|264664473|sp|C0LGK4.1|Y2165_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At2g16250; Flags: Precursor >gi|224589511|gb|ACN59289.1|leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene490_All//0.00E+00//AT2G16250| leucine-rich repeat transmembrane protein kinase, putative	Unigene490_All//0.00E+00//TC176578			GO:0004672//GO:0005618//GO:0006464//GO:0007167//GO:0016020//GO:0016491//GO:0032559	nr -
Unigene49000_All	1503	17.82	40.32	24.59	8.72	8.80	12.71	12.69	13.46	11.80	1.18E+00	4.94E-57	Up	4.64E-01	2.80E-07		1.34E-02	9.60E-01		5.44E-01	1.01E-05		8.53E-02	5.35E-01		-1.05E-01	4.00E-01		Unigene49000_All//gi|18399067|ref|NP_566385.1|//1.00E-148//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana]	Unigene49000_All//5.00E-145//AT3G10970| haloacid dehalogenase-like hydrolase family protein	Unigene49000_All//0.00E+00//TC155521				nr +
Unigene49001_All	875	10.94	12.33	5.05	12.75	10.90	5.63	12.51	6.59	5.78	1.73E-01	3.74E-01		-1.12E+00	1.66E-08	Down	-2.26E-01	2.18E-01		-1.18E+00	6.51E-12	Down	-9.25E-01	3.14E-09		-1.11E+00	1.23E-12	Down	Unigene49001_All//gi|15237011|ref|NP_195272.1|//3.00E-67//leucine-rich repeat family protein [Arabidopsis thaliana] >gi|57868150|gb|AM57413.1| plant intracellular Ras-group-related LRR protein 4 [Arabidopsis thaliana]	Unigene49001_All//1.00E-68//AT4G35470| leucine-rich repeat family protein	Unigene49001_All//0.00E+00//TC172887		ko04626|Plant-pathogen interaction		nr +
Unigene49005_All	748	28.26	23.98	19.36	45.15	46.82	51.02	22.61	16.20	8.57	-2.37E-01	5.81E-02		-5.45E-01	9.51E-06		5.23E-02	6.45E-01		1.76E-01	5.92E-02		-4.81E-01	6.40E-05		-1.40E+00	7.98E-27	Down			Unigene49005_All//0.00E+00//TC177655				
Unigene49007_All	651	22.58	19.85	26.42	33.97	32.90	38.09	43.45	27.48	11.08	-1.86E-01	2.33E-01		2.26E-01	1.31E-01		-4.63E-02	7.74E-01		1.65E-01	1.84E-01		-6.61E-01	5.48E-13		-1.97E+00	8.55E-72	Down	Unigene49007_All//gi|15239564|ref|NP_197381.1|//2.00E-42//NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein [Arabidopsis thaliana] >gi|30687007|ref|NP_850849.1|NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein [Arabidopsis thaliana] >gi|297807915|ref|XP_002871841.1|NADH-ubiquinone oxidoreductase 19 kDa subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|21536569|gb|AAM60901.1|NADH:ubiquinone oxidoreductase-like protein [Arabidopsis thaliana] >gi|28466879|gb|AAO44048.1|At5g18800 [Arabidopsis thaliana] >gi|110735767|dbj|BAE99861.1|NADH:ubiquinone oxidoreductase like protein [Arabidopsis thaliana] >gi|297317678|gb|EFH48100.1| NADH-ubiquinone oxidoreductase 19 kDa subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49007_All//9.00E-44//AT5G18800| NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein	Unigene49007_All//0.00E+00//gi|84169446|gb|DR458094.1|DR458094		ko00190|Oxidative phosphorylation		nr +
Unigene49012_All	1195	3.46	1.53	1.74	3.67	3.60	2.31	3.47	3.18	5.93	-1.18E+00	1.18E-04	Down	-9.93E-01	1.59E-03		-2.63E-02	9.35E-01		-6.70E-01	2.03E-02		-1.24E-01	6.70E-01		7.75E-01	5.26E-05		Unigene49012_All//gi|227463012|gb|ACP39958.1|//1.00E-143//pentatricopeptide repeat protein [Gossypium hirsutum] >gi|227463014|gb|ACP39959.1|pentatricopeptide repeat protein [Gossypium hirsutum]	Unigene49012_All//2.00E-84//AT5G47360| pentatricopeptide (PPR) repeat-containing protein	Unigene49012_All//0.00E+00//TC159923				nr +
Unigene49014_All	1954	1.10	0.34	0.25	1.96	2.70	1.92	3.48	1.20	2.55	-1.70E+00	3.02E-04	Down	-2.16E+00	3.37E-05	Down	4.58E-01	8.37E-02		-3.32E-02	9.33E-01		-1.54E+00	1.66E-12	Down	-4.51E-01	2.14E-02		Unigene49014_All//gi|224089995|ref|XP_002308898.1|//0.00E+00//condensin complex components subunit [Populus trichocarpa] >gi|222854874|gb|EEE92421.1|condensin complex components subunit [Populus trichocarpa]	Unigene49014_All//0.00E+00//AT3G57060| binding	Unigene49014_All//0.00E+00//TC172918				nr +
Unigene49017_All	1121	2.89	10.85	4.51	7.91	12.87	8.34	11.65	25.13	45.10	1.91E+00	1.15E-23	Up	6.41E-01	2.14E-02		7.02E-01	3.65E-07		7.64E-02	7.21E-01		1.11E+00	6.23E-30	Up	1.95E+00	1.73E-124	Up	Unigene49017_All//gi|4666360|gb|AAD26942.1|AF119050_1//3.00E-70//zinc-finger protein I [Datisca glomerata]	Unigene49017_All//1.00E-42//AT1G27730| STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding	Unigene49017_All//0.00E+00//gi|164266073|gb|EX164958.1|EX164958	C2H2			nr +
Unigene49019_All	947	3.43	1.87	1.07	4.16	4.00	3.43	1.65	1.15	2.02	-8.71E-01	1.14E-02		-1.68E+00	1.34E-05	Down	-5.51E-02	8.61E-01		-2.75E-01	4.20E-01		-5.26E-01	2.81E-01		2.90E-01	5.02E-01		Unigene49019_All//gi|15233088|ref|NP_191695.1|//4.00E-98//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75264589|sp|Q9MZX8.1|PP291_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g61360	Unigene49019_All//3.00E-93//AT3G61360| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene49020_All	1261	6.51	3.86	7.47	5.14	2.79	2.15	4.39	1.89	1.07	-7.56E-01	1.84E-04		1.98E-01	3.61E-01		-8.83E-01	3.80E-05		-1.26E+00	7.41E-08	Down	-1.22E+00	1.86E-07	Down	-2.03E+00	2.81E-15	Down	Unigene49020_All//gi|115486791|ref|NP_001068539.1|//2.00E-33//Os11g0703600 [Oryza sativa Japonica Group] >gi|77552699|gb|ABA95496.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|77552700|gb|ABA95497.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113645761|dbj|BAF28902.1|Os11g0703600 [Oryza sativa Japonica Group]	Unigene49020_All//6.00E-44//AT5G59350| unknown protein	Unigene49020_All//0.00E+00//gi|48783747|gb|CO090020.1|CO090020				nr +
Unigene49022_All	1552	4.38	1.83	1.03	0.13	0.09	0.06	5.88	2.61	2.44	-1.26E+00	7.96E-08	Down	-2.09E+00	1.36E-14	Down	-5.32E-01	7.48E-01		-1.14E+00	5.68E-01		-1.17E+00	3.84E-11	Down	-1.27E+00	5.76E-13	Down	Unigene49022_All//gi|224074241|ref|XP_002304316.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222841748|gb|EEE79295.1| GRAS family transcription factor [Populus trichocarpa]	Unigene49022_All//5.00E-142//AT3G49950| scarecrow transcription factor family protein	Unigene49022_All//2.00E-111//CA992599	GRAS			nr -
Unigene49023_All	1596	0.69	0.95	1.90	1.44	0.78	1.13	6.01	18.12	20.89	4.68E-01	3.85E-01		1.47E+00	1.73E-04	Up	-8.86E-01	2.70E-02		-3.43E-01	4.58E-01		1.59E+00	6.04E-53	Up	1.80E+00	1.07E-73	Up	Unigene49023_All//gi|14484938|gb|AAK62821.1|AF332960_1//1.00E-150//auxin-regulated dual specificity cytosolic kinase [Solanum lycopersicum] >gi|270303597|gb|ACZ71039.1|auxin-regulated dual specificity cytosolic kinase [Solanum lycopersicum]	Unigene49023_All//1.00E-141//AT1G72540| protein kinase, putative	Unigene49023_All//2.00E-15//TC154062		ko04626|Plant-pathogen interaction		nr +
Unigene49024_All	1224	3.55	0.99	1.48	4.52	2.95	2.44	0.97	25.95	0.23	-1.84E+00	1.45E-08	Down	-1.26E+00	5.27E-05	Down	-6.13E-01	1.06E-02		-8.91E-01	3.46E-04		4.75E+00	9.59E-183	Up	-2.09E+00	5.32E-04	Down	Unigene49024_All//gi|297829824|ref|XP_002882794.1|//1.00E-143//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328634|gb|EFH59053.1|oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene49024_All//1.00E-143//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene49024_All//4.00E-16//TC134433		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene49025_All	821	1.66	3.58	4.09	2.55	3.06	2.97	2.99	4.68	3.30	1.11E+00	2.76E-03		1.30E+00	3.27E-04	Up	2.65E-01	5.63E-01		2.21E-01	6.18E-01		6.49E-01	2.02E-02		1.44E-01	6.70E-01				Unigene49025_All//4.00E-89//gi|78325783|gb|DT546057.1|DT546057				
Unigene49026_All	750	2.37	0.34	0.71	2.26	1.84	1.57	0.90	4.07	6.53	-2.81E+00	4.70E-06	Down	-1.74E+00	1.58E-03		-2.98E-01	5.76E-01		-5.28E-01	3.21E-01		2.17E+00	4.01E-09	Up	2.86E+00	1.41E-19	Up	Unigene49026_All//gi|187940289|gb|ACD39375.1|//1.00E-35//NAC domain protein [Glycine max]	Unigene49026_All//2.00E-30//AT5G64530| XND1; transcription factor		NAC			nr +
Unigene49027_All	605	6.92	1.26	1.85	3.87	2.50	3.06	1.05	1.38	6.72	-2.46E+00	1.21E-11	Down	-1.90E+00	3.23E-08	Down	-6.28E-01	1.23E-01		-3.38E-01	4.60E-01		3.98E-01	5.94E-01		2.68E+00	2.43E-15	Up	Unigene49027_All//gi|187940289|gb|ACD39375.1|//1.00E-38//NAC domain protein [Glycine max]	Unigene49027_All//4.00E-30//AT5G64530| XND1; transcription factor		NAC			nr +
Unigene49028_All	837	34.38	187.91	66.86	38.74	21.80	57.68	16.82	53.88	53.83	2.45E+00	0.00E+00	Up	9.60E-01	8.36E-37		-8.29E-01	2.85E-21		5.74E-01	9.32E-15		1.68E+00	1.09E-88	Up	1.68E+00	2.40E-90	Up			Unigene49028_All//0.00E+00//TC169008				
Unigene49029_All	814	2.31	0.56	1.18	1.84	3.43	3.77	4.78	1.64	3.96	-2.05E+00	1.17E-04	Down	-9.75E-01	5.03E-02		9.00E-01	1.50E-02		1.04E+00	3.68E-03		-1.54E+00	1.79E-07	Down	-2.70E-01	3.51E-01		Unigene49029_All//gi|20466790|gb|AAM20712.1|//1.00E-83//26S proteasome regulatory subunit [Arabidopsis thaliana]	Unigene49029_All//1.00E-73//AT2G32730| 26S proteasome regulatory subunit, putative	Unigene49029_All//0.00E+00//DT468571		ko03050|Proteasome		nr -
Unigene4903_All	794	5.86	5.55	8.18	10.16	7.72	8.30	16.77	49.80	30.41	-7.91E-02	7.78E-01		4.80E-01	4.90E-02		-3.97E-01	4.85E-02		-2.91E-01	1.91E-01		1.57E+00	1.06E-70	Up	8.58E-01	1.41E-17		Unigene4903_All//gi|115446965|ref|NP_001047262.1|//3.00E-19//Os02g0584800 [Oryza sativa Japonica Group] >gi|113536793|dbj|BAF09176.1|Os02g0584800 [Oryza sativa Japonica Group]	Unigene4903_All//3.00E-14//AT5G48290| heavy-metal-associated domain-containing protein	Unigene4903_All//0.00E+00//TC164033				nr +
Unigene49030_All	666	10.21	1.67	6.32	17.20	10.34	9.83	2.29	7.47	6.94	-2.61E+00	9.72E-20	Down	-6.93E-01	3.07E-03		-7.34E-01	1.91E-06		-8.07E-01	8.48E-07		1.71E+00	1.09E-10	Up	1.60E+00	1.98E-09	Up			Unigene49030_All//1.00E-135//gi|109883187|gb|DW512157.1|DW512157				ESTscan -
Unigene49031_All	901	241.69	143.01	350.53	22.89	26.91	13.99	5.87	3.85	1.15	-7.57E-01	7.76E-98		5.36E-01	1.08E-74		2.33E-01	4.04E-02		-7.11E-01	1.62E-09		-6.07E-01	8.83E-03		-2.35E+00	2.23E-17	Down	Unigene49031_All//gi|19699178|gb|AAL90955.1|//2.00E-47//At2g04039/At2g04039 [Arabidopsis thaliana]	Unigene49031_All//8.00E-40//AT2G04039| unknown protein	Unigene49031_All//0.00E+00//TC146275				nr +
Unigene49032_All	1867	25.36	0.98	5.59	1.41	1.29	0.31	0.48	0.27	0.04	-4.70E+00	6.98E-223	Down	-2.18E+00	1.18E-104	Down	-1.31E-01	7.77E-01		-2.17E+00	5.29E-07	Down	-8.24E-01	2.24E-01		-3.48E+00	7.33E-05	Down	Unigene49032_All//gi|18409382|ref|NP_564978.1|//0.00E+00//ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter [Arabidopsis thaliana]	Unigene49032_All//0.00E+00//AT1G69850| ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter					nr +

Unigene49034_All	1151	1.09	0.97	0.42	1.90	1.47	5.49	158.32	185.74	485.30	-1.72E-01	7.55E-01		-1.39E+00	3.39E-02		-3.77E-01	4.06E-01		1.53E+00	6.08E-10	Up	2.30E-01	8.58E-14		1.62E+00	0.00E+00	Up	Unigene49034_All//gi|225442485|ref|XP_002278313.1|//1.00E-156//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene49034_All//1.00E-131//AT1G59870| PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	Unigene49034_All//0.00E+00//gi|78354132|gb|DT574406.1|DT574406		ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene49035_All	1091	2.06	1.49	0.20	2.79	3.22	3.10	3.26	1.38	2.56	-4.73E-01	2.72E-01		-3.40E+00	2.44E-08	Down	2.09E-01	5.83E-01		1.57E-01	6.92E-01		-1.24E+00	3.47E-05	Down	-3.49E-01	2.35E-01		Unigene49035_All//gi|224088410|ref|XP_002308444.1|//1.00E-110//transcription factor E2F [Populus trichocarpa] >gi|222854420|gb|EEE91967.1| transcription factor E2F [Populus trichocarpa]	Unigene49035_All//4.00E-98//AT2G36010| E2F3 (E2F TRANSCRIPTION FACTOR 3); DNA binding / transcription factor	Unigene49035_All//9.00E-159//gi|78338523|gb|DT558797.1|DT558797	E2F-DP			nr -
Unigene49036_All	886	3.48	8.98	5.41	11.47	10.34	14.07	9.97	12.17	6.61	1.37E+00	4.89E-10	Up	6.35E-01	2.72E-02		-1.50E-01	4.73E-01		2.95E-01	8.18E-02		2.87E-01	7.84E-02		-5.94E-01	4.04E-04					Unigene49036_All//2.00E-26//gi|164364157|gb|ES846671.1|ES846671				
Unigene49037_All	620	11.39	7.36	11.25	6.91	9.44	3.42	40.23	9.10	24.29	-6.31E-01	4.05E-03		-1.80E-02	9.58E-01		4.51E-01	7.00E-02		-1.01E+00	4.81E-04	Down	-2.14E+00	1.63E-68	Down	-7.28E-01	5.84E-14					Unigene49037_All//2.00E-62//gi|13244969|gb|BE053310.2|BE053310				
Unigene49039_All	835	9.02	4.19	4.08	18.14	11.13	16.28	57.37	112.37	46.28	-1.11E+00	3.89E-07	Down	-1.14E+00	4.26E-07	Down	-7.04E-01	8.90E-08		-1.56E-01	3.57E-01		9.70E-01	9.10E-79		-3.10E-01	3.72E-06		Unigene49039_All//gi|27808522|gb|AA024541.1|//1.00E-22//At4g33985 [Arabidopsis thaliana]	Unigene49039_All//1.00E-19//AT4G33985| unknown protein	Unigene49039_All//0.00E+00//gi|164301404|gb|ES833629.1|ES833629				nr +
Unigene49041_All	833	3.45	11.01	16.62	36.78	59.45	90.06	3.35	17.96	16.40	1.67E+00	3.66E-15	Up	2.27E+00	2.03E-32	Up	6.93E-01	6.12E-23		1.29E+00	1.88E-87	Up	2.42E+00	8.59E-48	Up	2.29E+00	9.07E-42	Up				Unigene49041_All//0.00E+00//TC160836				ESTscan +
Unigene49043_All	1719	7.91	9.70	3.78	3.07	2.34	1.50	0.00	0.00	0.00	2.93E-01	3.66E-02		-1.07E+00	4.98E-11	Down	-3.90E-01	1.39E-01		-1.04E+00	5.62E-05	Down	null	null		null	null		Unigene49043_All//gi|224078652|ref|XP_002305592.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222848556|gb|EEE86103.1| cytochrome P450 [Populus trichocarpa]	Unigene49043_All//0.00E+00//TC147778	Unigene49043_All//0.00E+00//TC147778		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene49044_All	807	1.43	44.89	1.85	1.79	3.33	7.28	18.81	86.85	82.05	4.98E+00	5.61E-174	Up	3.73E-01	5.11E-01		8.95E-01	1.83E-02		2.02E+00	2.27E-13	Up	2.21E+00	5.78E-198	Up	2.13E+00	9.76E-182	Up	Unigene49044_All//gi|5702231|gb|AAD17213.1|AF145386_1//3.00E-48//hypersensitive reaction associated Ca2+-binding protein [Phaseolus vulgaris]	Unigene49044_All//6.00E-44//AT5G49480| ATCP1 (Ca2+-binding protein 1); calcium ion binding	Unigene49044_All//0.00E+00//DW494657		ko04626|Plant-pathogen interaction		nr +
Unigene49045_All	1278	1.23	0.52	3.04	2.22	1.29	2.30	3.04	1.50	0.97	-1.25E+00	1.98E-02		1.31E+00	8.74E-05	Up	-7.81E-01	2.74E-02		4.80E-02	9.22E-01		-1.02E+00	2.64E-04	Down	-1.66E+00	1.65E-08	Down				Unigene49045_All//5.00E-62//AI054841				
Unigene49046_All	1175	326.70	113.11	320.95	292.14	182.49	160.28	21.77	33.12	27.67	-1.53E+00	0.00E+00	Down	-2.56E-02	4.17E-01		-6.79E-01	1.05E-156		-8.66E-01	1.82E-210		6.05E-01	4.14E-15		3.46E-01	2.85E-05		Unigene49046_All//gi|186510343|ref|NP_001078202.2|//9.00E-48//LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4) [Arabidopsis thaliana]	Unigene49046_All//3.00E-41//AT3G22290| LSH4 (LIGHT SENSITIVE HYPOCOTYLS 4)	Unigene49046_All//0.00E+00//TC134674				nr -
Unigene49047_All	698	44.30	167.54	132.74	130.10	198.03	288.19	53.55	116.64	190.40	1.92E+00	2.11E-224	Up	1.58E+00	8.27E-133	Up	6.06E-01	2.92E-50		1.15E+00	3.22E-194	Up	1.12E+00	7.85E-87	Up	1.83E+00	4.22E-299	Up	Unigene49047_All//gi|1399307|gb|AAB03259.1|//3.00E-97//phosphoinositide-specific phospholipase C PZS [Glycine max]	Unigene49047_All//2.00E-75//AT3G08510| ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C	Unigene49047_All//0.00E+00//TC133093		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene49048_All	633	4.38	2.00	4.21	2.28	2.07	3.92	4.27	1.32	1.20	-1.13E+00	3.16E-03		-5.86E-02	8.85E-01		-1.43E-01	8.15E-01		7.82E-01	5.65E-02		-1.69E+00	4.12E-06	Down	-1.84E+00	5.25E-07	Down	Unigene49048_All//gi|2921334|ref|AAC04717.1|//1.00E-111//MYB-like DNA-binding domain protein [Gossypium hirsutum]	Unigene49048_All//9.00E-44//AT5G35550| TT2 (TRANSPARENT TESTA 2); DNA binding / transcription factor	Unigene49048_All//0.00E+00//TC135442	MYB			nr +
Unigene49049_All	1662	34.41	8.32	13.36	41.33	28.32	20.84	41.47	20.24	17.59	-2.05E+00	1.43E-120	Down	-1.36E+00	1.28E-65	Down	-5.45E-01	2.30E-21		-9.88E-01	7.68E-53		-1.03E+00	1.42E-64	Down	-1.24E+00	2.81E-88	Down	Unigene49049_All//gi|15241571|ref|NP_196443.1|//0.00E+00//scpl35 (serine carboxypeptidase-like 35); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75334909|sp|Q9LEY1.1|SCP35_ARATH RecName: Full=Serine carboxypeptidase-like 35; Flags: Precursor >gi|8346563|emb|CAB93727.1| serine-type carboxypeptidase II-like protein [Arabidopsis thaliana]	Unigene49049_All//0.00E+00//AT5G08260| scpl35 (serine carboxypeptidase-like 35); serine-type carboxypeptidase	Unigene49049_All//0.00E+00//gi|78339617|gb|DT559891.1|DT559891				nr +
Unigene49050_All	1145	2.65	2.74	2.70	17.53	10.14	7.38	7.35	2.01	0.97	5.00E-02	8.96E-01		2.54E-02	9.62E-01		-7.91E-01	2.60E-12		-1.25E+00	6.99E-23	Down	-1.87E+00	7.31E-20	Down	-2.92E+00	2.23E-34	Down	Unigene49050_All//gi|56461774|gb|AAV91343.1|//7.00E-48//At2g01990 [Arabidopsis thaliana]	Unigene49050_All//1.00E-41//AT1G14630| unknown protein	Unigene49050_All//0.00E+00//gi|48746869|gb|CO077388.1|CO077388				nr -
Unigene49051_All	1080	3.05	7.27	2.22	5.90	8.39	10.45	4.62	6.54	7.05	1.25E+00	8.80E-09	Up	-4.60E-01	2.11E-01		5.06E-01	6.33E-03		8.24E-01	7.32E-07		5.02E-01	1.13E-02		6.09E-01	8.81E-04		Unigene49051_All//gi|224131652|ref|XP_002328075.1|//2.00E-19//predicted protein [Populus trichocarpa] >gi|222837590|gb|EEE75955.1| predicted protein [Populus trichocarpa]		Unigene49051_All//0.00E+00//TC152136				nr +
Unigene49052_All	737	5.32	3.64	4.05	9.26	4.86	4.96	52.38	12.99	14.76	-5.47E-01	7.77E-02		-3.96E-01	2.39E-01		-9.30E-01	7.72E-06		-9.00E-01	4.54E-05		-2.01E+00	2.34E-97	Down	-1.83E+00	3.22E-88	Down	Unigene49052_All//gi|115470525|ref|NP_001058861.1|//8.00E-07//Os07g0139600 [Oryza sativa Japonica Group] >gi|113610397|dbj|BAF20775.1| Os07g0139600 [Oryza sativa Japonica Group]		Unigene49052_All//1.00E-85//TC173194		ko03010|Ribosome		nr -
Unigene49053_All	734	113.55	18.91	14.80	128.20	71.45	32.61	26.84	0.91	2.39	-2.59E+00	2.65E-233	Down	-2.94E+00	4.76E-259	Down	-8.43E-01	6.57E-63		-1.98E+00	6.81E-206	Down	-4.88E+00	1.04E-115	Down	-3.49E+00	2.27E-94	Down	Unigene49053_All//gi|105829831|gb|ABF74705.1|//6.00E-19//At4g28310 [Arabidopsis thaliana]		Unigene49053_All//0.00E+00//TC159012				nr -
Unigene49054_All	1913	4.46	1.59	2.03	0.00	0.27	0.05	27.30	27.03	40.59	-1.49E+00	3.89E-12	Down	-1.13E+00	7.79E-08	Down	8.08E+00	3.21E-03		5.56E+00	4.76E-01		-1.43E-02	8.66E-01		5.72E-01	2.75E-27		Unigene49054_All//gi|15223699|ref|NP_173419.1|//0.00E+00//glyoxal oxidase-related [Arabidopsis thaliana] >gi|16604507|gb|AAL24259.1| At1g19900/F6F9_4 [Arabidopsis thaliana]	Unigene49054_All//0.00E+00//AT1G19900| glyoxal oxidase-related	Unigene49054_All//8.00E-145//TC177936				nr +
Unigene49057_All	990	82.13	32.24	38.94	63.80	56.94	56.07	18.79	16.42	14.00	-1.35E+00	1.33E-94	Down	-1.08E+00	3.62E-64	Down	-1.64E-01	1.36E-02		-1.87E-01	5.98E-03		-1.94E-01	1.20E-01		-4.24E-01	1.42E-04		Unigene49057_All//gi|297799182|ref|XP_002867475.1|//7.00E-61//YGGT family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313311|gb|EFH43734.1| YGGT family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49057_All//2.00E-60//AT4G27990| YGGT family protein	Unigene49057_All//0.00E+00//TC137983				nr -
Unigene49058_All	1065	3.44	1.19	2.40	4.44	1.68	1.70	7.90	2.71	3.93	-1.53E+00	7.22E-06	Down	-5.19E-01	1.30E-01		-1.40E+00	1.13E-07	Down	-1.39E+00	8.58E-07	Down	-1.54E+00	2.46E-15	Down	-1.01E+00	1.46E-08	Down	Unigene49058_All//gi|15228120|ref|NP_181270.1|//1.00E-112//ALS3 (ALUMINUM SENSITIVE 3) [Arabidopsis thaliana] >gi|75216846|sp|Q9ZUT3.1|ALS3_ARATH RecName: Full=Protein ALUMINUM SENSITIVE 3; AltName: Full=ABC transporter I family member 16; Short=ABC transporter ABCI.16; Short=AtABCI16; AltName: Full=ybbM homolog protein >gi|53275047|gb|AAV49319.1| aluminum sensitive 3 [Arabidopsis thaliana]	Unigene49058_All//2.00E-108//AT2G37330| ALS3 (ALUMINUM SENSITIVE 3)	Unigene49058_All//0.00E+00//TC167439				nr -
Unigene49059_All	869	25.95	7.11	23.78	16.80	21.64	24.06	1.31	0.63	1.47	-1.87E+00	2.00E-42	Down	-1.26E-01	3.60E-01		3.65E-01	3.06E-03		5.19E-01	9.67E-06		-1.07E+00	6.31E-02		1.59E-01	7.53E-01		Unigene49059_All//gi|224142968|ref|XP_002324799.1|//9.00E-78//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372075|gb|ABQ62969.1| TINY-like protein [Populus trichocarpa] >gi|222866233|gb|EEF03364.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene49059_All//4.00E-51//AT5G11590| TINY2 (TINY2); DNA binding / transcription factor	Unigene49059_All//0.00E+00//DW517601	AP2-EREBP			nr -
Unigene4906_All	706	3.56	9.26	2.49	0.28	2.05	1.66	8.14	11.01	12.53	1.38E+00	1.67E-08	Up	-5.15E-01	2.31E-01		2.86E+00	2.11E-05	Up	2.56E+00	6.34E-04	Up	4.35E-01	2.14E-02		6.21E-01	2.26E-04		Unigene4906_All//gi|115145141|ref|NP_001046350.1|//9.00E-22//Os02g0227100 [Oryza sativa Japonica Group] >gi|113535881|dbj|BAF08264.1| Os02g0227100 [Oryza sativa Japonica Group]	Unigene4906_All//6.00E-17//AT5G56550| OXS3 (OXIDATIVE STRESS 3)					nr +
Unigene49061_All	766	8.74	0.86	1.46	11.84	6.61	13.27	7.07	3.49	2.03	-3.35E+00	8.18E-25	Down	-2.58E+00	2.29E-18	Down	-8.41E-01	1.86E-06		1.65E-01	4.39E-01		-1.02E+00	1.13E-05	Down	-1.80E+00	7.72E-13	Down	Unigene49061_All//gi|37202058|gb|AAQ89644.1|//4.00E-22//At4g17310 [Arabidopsis thaliana]	Unigene49061_All//5.00E-10//AT4G17310| unknown protein	Unigene49061_All//9.00E-118//CO086005				nr -
Unigene49063_All	1022	3.79	0.69	1.98	34.17	19.44	14.32	63.38	9.32	24.95	-2.45E+00	9.27E-11	Down	-9.36E-01	4.03E-03		-8.14E-01	3.85E-22		-1.25E+00	1.06E-39	Down	-2.76E+00	1.65E-238	Down	-1.35E+00	1.69E-94	Down	Unigene49063_All//gi|186491088|ref|NP_564682.2|//5.00E-38//lipid binding [Arabidopsis thaliana]	Unigene49063_All//5.00E-32//AT2G44300| lipid transfer protein-related	Unigene49063_All//0.00E+00//TC137076				nr +
Unigene49064_All	943	3.44	4.03	4.69	6.76	4.78	5.36	8.83	5.27	3.72	2.28E-01	4.89E-01		4.46E-01	1.46E-01		-4.99E-01	2.68E-02		-3.34E-01	1.84E-01		-7.44E-01	3.17E-05		-1.25E+00	1.33E-11	Down	Unigene49064_All//gi|297792921|ref|XP_002864345.1|//5.00E-25//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297310180|gb|EFH40604.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene49064_All//2.00E-26//AT5G54580| RNA recognition motif (RRM)-containing protein					nr -
Unigene49066_All	933	6.39	1.74	2.34	1.76	1.44	1.16	2.40	3.45	5.12	-1.88E+00	7.94E-12	Down	-1.45E+00	5.38E-08	Down	-2.92E-01	5.85E-01		-6.01E-01	2.60E-01		5.22E-01	9.70E-02		1.09E+00	8.21E-06	Up	Unigene49066_All//gi|224075092|ref|XP_002304554.1|//1.00E-73//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222841986|gb|EEE79533.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene49066_All//5.00E-53//AT1G64380| AP2 domain-containing transcription factor, putative	Unigene49066_All//6.00E-73//gi|78338627|gb|DT558901.1|DT558901	AP2-EREBP			nr +
Unigene49068_All	1232	1.40	2.14	3.11	7.72	5.70	5.17	2.33	4.38	1.68	6.10E-01	1.21E-01		1.15E+00	5.15E-04	Up	-4.38E-01	1.46E-02		-5.79E-01	1.55E-03		9.07E-01	8.14E-05		-4.73E-01	1.42E-01		Unigene49068_All//gi|225468955|ref|XP_002272008.1|//1.00E-46//PREDICTED: similar to nucleic acid binding , related [Vitis vinifera]	Unigene49068_All//4.00E-40//AT1G55790| ATP binding / nucleotide binding / phenylalanine-tRNA ligase	Unigene49068_All//0.00E+00//gi|78339096|gb|DT559370.1|DT559370				nr +
Unigene49069_All	1971	0.53	0.57	0.89	8.97	5.56	6.16	5.53	3.75	2.67	9.13E-02	8.87E-01		7.48E-01	1.45E-01		-6.92E-01	1.00E-08		-5.42E-01	2.38E-05		-5.60E-01	2.58E-04		-1.05E+00	1.45E-11	Down	Unigene49069_All//gi|15230158|ref|NP_188497.1|//5.00E-38//ankyrin repeat family protein [Arabidopsis thaliana]	Unigene49069_All//2.00E-28//AT3G18670| ankyrin repeat family protein	Unigene49069_All//0.00E+00//DN758589				nr +
Unigene4907_All	1291	1.78	13.78	3.30	4.01	13.90	27.71	8.42	13.66	104.70	2.95E+00	3.50E-57	Up	8.88E-01	3.87E-03		1.79E+00	5.01E-37	Up	2.79E+00	9.94E-116	Up	6.99E-01	3.50E-09		3.64E+00	0.00E+00	Up	Unigene4907_All//gi|15225692|ref|NP_180810.1|//7.00E-81//MAPKKK17; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Unigene4907_All//2.00E-82//AT2G32510| MAPKKK17; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene4907_All//0.00E+00//TC132037		ko04626|Plant-pathogen interaction		nr -

Unigene49071_A11	1122	16.69	26.78	46.70	19.45	33.21	42.31	2.56	16.69	4.58	6.82E-01	7.09E-12		1.48E+00	2.09E-68	Up	7.72E-01	7.56E-21		1.12E+00	1.83E-44	Up	2.70E+00	1.91E-67	Up	8.38E-01	2.71E-04		Unigene49071_A11//gi|18422246|ref|NP_568610.1|//2.00E-46//BK11 (BRI1 kinase inhibitor 1); protein heterodimerization [Arabidopsis thaliana] >gi|192571736|gb|ACF04813.1|At5g42750 [Arabidopsis thaliana]	Unigene49071_A11//2.00E-22//AT5G42750| BK11 (BRI1 kinase inhibitor 1); protein heterodimerization	Unigene49071_A11//1.00E-40//gi|164274164|gb|ES817753.1|ES817753				nr +
Unigene49076_A11	730	5.52	11.18	5.76	8.33	6.60	6.19	19.58	28.40	21.77	1.02E+00	9.45E-07	Up	6.24E-02	8.40E-01		-3.34E-01	1.75E-01		-4.28E-01	8.33E-02		5.37E-01	5.90E-07		1.54E-01	2.54E-01		Unigene49076_A11//gi|18650616|gb|AAL75907.1|//1.00E-46//AT4g03420/F9H3_4 [Arabidopsis thaliana] >gi|20453247|gb|AAM19862.1|AT4g03420/F9H3_4 [Arabidopsis thaliana]	Unigene49076_A11//7.00E-48//AT4G03420| unknown protein	Unigene49076_A11//0.00E+00//TC166652				nr -
Unigene49079_A11	338	209.59	40.48	53.72	201.17	151.80	236.77	197.64	76.17	77.91	-2.37E+00	1.97E-179	Down	-1.96E+00	1.22E-136	Down	-4.06E-01	1.81E-12		2.35E-01	4.35E-05		-1.38E+00	5.51E-98	Down	-1.34E+00	3.30E-97	Down	Unigene49079_A11//gi|3334320|sp|O22518.1|RSSA_SOYBN//8.00E-59//RecName: Full=40S ribosomal protein SA; AltName: Full=p40 >gi|2444420|gb|AAB82659.1|ribosome-associated protein p40 [Glycine max]	Unigene49079_A11//7.00E-57//AT1G72370| P40; structural constituent of ribosome	Unigene49079_A11//0.00E+00//ES809734		ko03010|Ribosome		nr +
Unigene4908_A11	905	2.02	2.52	3.65	2.31	3.16	1.75	1.96	0.88	0.26	3.16E-01	4.62E-01		8.50E-01	1.69E-02		4.50E-01	2.54E-01		-4.04E-01	3.93E-01		-1.16E+00	8.83E-03		-2.89E+00	9.05E-08	Down	Unigene4908_A11//gi|30698040|ref|NP_201257.2|//9.00E-34//XRCC2 [Arabidopsis thaliana]	Unigene4908_A11//4.00E-35//AT5G64520| XRCC2	Unigene4908_A11//0.00E+00//TC138184		ko03440|Homologous recombination		nr +
Unigene49080_A11	419	82.29	33.74	35.58	133.75	102.73	146.05	216.95	97.76	88.42	-1.29E+00	1.12E-37	Down	-1.21E+00	5.37E-33	Down	-3.81E-01	3.10E-09		1.27E-01	8.77E-02		-1.15E+00	9.91E-101	Down	-1.29E+00	8.97E-125	Down	Unigene49080_A11//gi|3334320|sp|O22518.1|RSSA_SOYBN//9.00E-76//RecName: Full=40S ribosomal protein SA; AltName: Full=p40 >gi|2444420|gb|AAB82659.1|ribosome-associated protein p40 [Glycine max]	Unigene49080_A11//1.00E-73//AT1G72370| P40; structural constituent of ribosome	Unigene49080_A11//0.00E+00//TC131519		ko03010|Ribosome		nr +
Unigene49081_A11	1427	15.73	28.97	17.99	7.23	11.29	23.42	0.15	0.23	0.08	8.81E-01	1.43E-24		1.94E-01	1.07E-01		6.44E-01	6.70E-07		1.70E+00	2.00E-58	Up	6.62E-01	6.09E-01		-8.22E-01	5.99E-01		Unigene49081_A11//gi|71143481|gb|AAZ23955.1|//1.00E-163//GDSL-lipase 1 [Capsicum annuum]	Unigene49081_A11//8.00E-155//AT1G29670| GDSL-motif lipase/hydrolase family protein	Unigene49081_A11//0.00E+00//TC141685				nr -
Unigene49083_A11	1388	15.08	17.41	32.76	50.35	71.77	70.32	25.13	17.01	14.32	2.08E-01	7.74E-02		1.12E+00	1.71E-38	Up	5.11E-01	7.87E-27		4.82E-01	1.96E-21		-5.63E-01	4.47E-12		-8.11E-01	6.42E-23		Unigene49083_A11//gi|229458366|gb|ACQ65866.1|//1.00E-109//annexin 3 [Brassica juncea] >gi|251747933|gb|ABD47520.2|annexin 3 [Brassica juncea]	Unigene49083_A11//1.00E-105//AT2G38760| ANNAT3 (ANNEXIN ARABIDOPSIS 3); calcium ion binding / calcium-dependent phospholipid binding	Unigene49083_A11//0.00E+00//TC141982				nr +
Unigene49084_A11	1307	7.77	24.50	24.00	20.28	41.94	35.11	0.00	0.00	0.06	1.66E+00	1.34E-50	Up	1.63E+00	5.55E-47	Up	1.05E+00	9.95E-51	Up	7.92E-01	2.54E-24		null	null		5.93E+00	4.04E-01		Unigene49084_A11//gi|30683951|ref|NP_172923.3|//1.00E-116//PAP3 (PURPLE ACID PHOSPHATASE 3); acid phosphatase/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75244598|sp|Q8HI29.1|PPA3_ARATH RecName: Full=Purple acid phosphatase 3; Flags: Precursor	Unigene49084_A11//7.00E-115//AT1G14700| PAP3 (PURPLE ACID PHOSPHATASE 3); acid phosphatase/ protein serine/threonine phosphatase			ko00740|Riboflavin metabolism		nr -
Unigene49085_A11	1297	0.08	3.52	2.34	3.42	1.01	9.99	12.84	9.86	6.67	5.45E+00	5.30E-23	Up	4.86E+00	3.55E-14	Up	-1.76E+00	6.72E-10	Down	1.55E+00	3.56E-20	Up	-3.81E-01	1.86E-03		-9.46E-01	1.47E-14		Unigene49085_A11//gi|32351452|gb|AAP76387.1|//1.00E-112//class III peroxidase [Gossypium hirsutum]	Unigene49085_A11//1.00E-83//AT1G14550| anionic peroxidase, putative	Unigene49085_A11//0.00E+00//TC163871		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene49086_A11	863	6.37	13.68	7.77	8.43	11.85	10.20	14.31	20.15	22.48	1.10E+00	1.26E-10	Up	2.88E-01	2.42E-01		4.92E-01	4.37E-03		2.76E-01	1.94E-01		4.94E-01	3.02E-05		6.52E-01	3.18E-09		Unigene49086_A11//gi|297802630|ref|XP_002869199.1|//3.00E-43//AT4g33690/T16L1_180 [Arabidopsis lyrata subsp. lyrata] >gi|297315035|gb|EFH45458.1|AT4g33690/T16L1_180 [Arabidopsis lyrata subsp. lyrata]	Unigene49086_A11//1.00E-23//AT4G33690| unknown protein	Unigene49086_A11//0.00E+00//ES823355				nr +
Unigene49089_A11	1856	0.45	0.93	0.86	10.49	5.25	3.55	23.85	49.93	9.53	1.04E+00	3.90E-02		9.32E-01	8.84E-02		-9.99E-01	1.30E-17		-1.56E+00	5.11E-31	Down	1.07E+00	1.02E-90	Up	-1.32E+00	2.90E-63	Down	Unigene49089_A11//gi|297607204|ref|NP_001059610.2|//1.00E-58//Os07g0471900 [Oryza sativa Japonica Group] >gi|255677757|dbj|BAF21524.2|Os07g0471900 [Oryza sativa Japonica Group]	Unigene49089_A11//2.00E-26//AT1G31050| transcription factor	Unigene49089_A11//2.00E-09//ES818883	bHLH			nr -
Unigene4909_A11	1132	0.00	0.45	0.00	0.70	0.49	0.88	1.16	1.48	2.96	8.81E+00	4.04E-03		null	null		-5.33E-01	5.10E-01		3.18E-01	6.73E-01		3.51E-01	4.66E-01		1.35E+00	1.09E-05	Up	Unigene4909_A11//gi|240255415|ref|NP_189131.4|//5.00E-19//DNA binding [Arabidopsis thaliana]	Unigene4909_A11//1.00E-09//AT3G24880| DNA binding					nr -
Unigene49092_A11	848	19.93	20.97	13.94	31.49	36.83	39.52	65.76	49.34	31.66	7.37E-02	6.17E-01		-5.16E-01	2.29E-04		2.26E-01	2.03E-02		3.28E-01	3.70E-04		-4.15E-01	4.16E-11		-1.05E+00	1.35E-55	Down	Unigene49092_A11//gi|225425690|ref|XP_002273676.1|//4.00E-28//PREDICTED: similar to 60S ribosomal protein L34 [Vitis vinifera] >gi|225452827|ref|XP_002283595.1|PREDICTED: similar to 60S ribosomal protein L34 [Vitis vinifera]	Unigene49092_A11//3.00E-16//AT1G26880| 60S ribosomal protein L34 (RPL34A)	Unigene49092_A11//0.00E+00//gi|164284586|gb|ES814628.1|ES814628		ko03010|Ribosome		nr -
Unigene49093_A11	1118	1.87	0.00	0.10	2.32	1.85	2.95	5.26	5.46	16.36	-1.09E+01	4.25E-12	Down	-4.30E+00	3.74E-09	Down	-3.26E-01	4.33E-01		3.48E-01	3.59E-01		5.42E-02	8.22E-01		1.64E+00	6.51E-36	Up	Unigene49093_A11//gi|4510404|gb|AAD21491.1|//6.00E-07//expressed protein [Arabidopsis thaliana] >gi|89111822|gb|ABD60683.1|At2g28570 [Arabidopsis thaliana]		Unigene49093_A11//0.00E+00//TC151565				nr -
Unigene49096_A11	368	6.11	16.25	6.37	2.44	3.28	9.94	9.42	9.65	7.36	1.41E+00	4.44E-08	Up	5.85E-02	8.94E-01		4.27E-01	5.52E-01		2.03E+00	1.49E-08	Up	3.52E-02	9.27E-01		-3.56E-01	2.30E-01				Unigene49096_A11//1.00E-112//DW232648						
Unigene49097_A11	819	11.63	24.50	14.04	2.49	8.24	14.72	9.91	4.64	5.89	1.08E+00	7.83E-17	Up	2.73E-01	1.38E-01		1.72E+00	2.21E-13	Up	2.56E+00	9.07E-36	Up	-1.09E+00	4.92E-09	Down	-7.52E-01	2.15E-05		Unigene49097_A11//gi|224081427|ref|XP_002306405.1|//1.00E-40//SAUR family protein [Populus trichocarpa] >gi|222855854|gb|EEE93401.1| SAUR family protein [Populus trichocarpa]	Unigene49097_A11//4.00E-41//AT3G12830| auxin-responsive family protein	Unigene49097_A11//0.00E+00//gi|78348721|gb|DT568995.1|DT568995				nr -
Unigene49098_A11	1098	16.39	9.18	9.89	31.26	29.61	15.30	26.30	20.29	20.61	-8.36E-01	2.80E-10		-7.29E-01	7.03E-08		-7.84E-02	4.95E-01		-1.03E+00	1.46E-28	Down	-3.74E-01	3.15E-05		-3.52E-01	6.37E-05		Unigene49098_A11//gi|15238798|ref|NP_199586.1|//1.00E-156//D6PKL2 (D6 PROTEIN KINASE LIKE 2); kinase [Arabidopsis thaliana] >gi|217861|dbj|BAA01715.1|serine/threonine protein kinase [Arabidopsis thaliana] >gi|10177911|dbj|BAB11322.1|protein kinase (EC 2.7.1.37) 5 [Arabidopsis thaliana] >gi|15809919|gb|AAL06887.1|AT5g47750/MCA23_7 [Arabidopsis thaliana] >gi|21360567|gb|AAM47480.1|AT5g47750/MCA23_7 [Arabidopsis thaliana]	Unigene49098_A11//2.00E-142//AT5G47750| D6PKL2 (D6 PROTEIN KINASE LIKE 2); kinase	Unigene49098_A11//0.00E+00//gi|164342145|gb|ES810433.1|ES810433				nr +
Unigene49100_A11	769	33.95	18.05	16.13	51.50	40.75	44.58	80.55	62.29	41.19	-9.11E-01	1.00E-16		-1.07E+00	7.93E-21	Down	-3.38E-01	1.85E-05		-2.08E-01	1.83E-02		-3.71E-01	4.18E-10		-9.68E-01	1.30E-53		Unigene49100_A11//gi|7528270|gb|AAF63202.1|AF240679_1//1.00E-50//poly(A)-binding protein [Cucumis sativus]	Unigene49100_A11//1.00E-37//AT1G49760| PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor	Unigene49100_A11//0.00E+00//TC161909				nr -
Unigene49103_A11	1286	6.96	2.96	2.82	14.68	11.41	8.29	12.76	6.40	8.02	-1.24E+00	9.52E-10	Down	-1.31E+00	4.77E-10	Down	-3.64E-01	2.67E-03		-8.25E-01	3.65E-11		-9.95E-01	4.92E-15		-6.69E-01	2.66E-08		Unigene49103_A11//gi|49659431|dbj|BAD27254.1|//3.00E-61//SlHDL1 [Silene latifolia]	Unigene49103_A11//2.00E-26//AT2G22430| ATHB6; DNA binding / protein binding / sequence-specific DNA binding / transcription activator/ transcription factor	Unigene49103_A11//0.00E+00//TC147009	HB			nr -
Unigene49105_A11	560	3.64	1.45	0.86	7.03	6.21	6.61	5.29	2.16	2.63	-1.33E+00	4.16E-03		-2.09E+00	8.44E-05	Down	-1.78E-01	6.05E-01		-8.76E-02	7.95E-01		-1.29E+00	1.12E-04	Down	-1.01E+00	1.44E-03				Unigene49105_A11//6.00E-69//ES850459						
Unigene49106_A11	1218	1.55	1.50	0.61	3.56	3.53	2.34	2.43	1.37	0.92	-4.63E-02	9.32E-01		-1.34E+00	8.77E-03		-9.80E-03	9.62E-01		-6.07E-01	3.85E-02		-8.24E-01	1.10E-02		-1.41E+00	1.89E-05	Down	Unigene49106_A11//gi|224132326|ref|XP_002328241.1|//1.00E-75//transcription factor E2F [Populus trichocarpa] >gi|222837756|gb|EEE76121.1|transcription factor E2F [Populus trichocarpa]	Unigene49106_A11//5.00E-42//AT5G22220| E2F1; DNA binding / protein binding / transcription factor	Unigene49106_A11//0.00E+00//TC169347	E2F-DP			nr +
Unigene49108_A11	903	4.23	0.79	2.12	3.81	2.56	0.30	3.75	1.06	1.15	-2.43E+00	1.57E-10	Down	-9.95E-01	2.52E-03		-5.75E-01	7.60E-02		-3.66E+00	4.47E-15	Down	-1.82E+00	4.07E-08	Down	-1.71E+00	8.33E-08	Down	Unigene49108_A11//gi|15240888|ref|NP_195729.1|//1.00E-64//legume lectin family protein [Arabidopsis thaliana] >gi|6759432|emb|CAB69837.1|lectin-like protein [Arabidopsis thaliana] >gi|110736881|dbj|BAF00398.1|lectin - like protein [Arabidopsis thaliana]	Unigene49108_A11//7.00E-59//AT5G01090| legume lectin family protein	Unigene49108_A11//3.00E-167//C0124401				nr -
Unigene49109_A11	946	9.90	2.84	6.25	6.42	4.70	2.20	3.53	0.40	0.76	-1.80E+00	3.34E-17	Down	-6.64E-01	6.52E-04		-4.52E-01	5.47E-02		-1.55E+00	6.23E-10	Down	-3.15E+00	1.34E-14	Down	-2.22E+00	1.45E-10	Down	Unigene49109_A11//gi|15240888|ref|NP_195729.1|//8.00E-67//legume lectin family protein [Arabidopsis thaliana] >gi|6759432|emb|CAB69837.1|lectin-like protein [Arabidopsis thaliana] >gi|110736881|dbj|BAF00398.1|lectin - like protein [Arabidopsis thaliana]	Unigene49109_A11//5.00E-61//AT5G01090| legume lectin family protein	Unigene49109_A11//0.00E+00//TC147153				nr -
Unigene49110_A11	1332	78.68	66.57	75.24	15.37	14.45	15.36	3.43	2.89	1.05	-2.41E-01	1.85E-06		-6.45E-02	2.94E-01		-8.90E-02	5.46E-01		-1.00E-03	9.92E-01		-2.48E-01	3.81E-01		-1.71E+00	2.82E-10	Down	Unigene49110_A11//gi|115453075|ref|NP_001050138.1|//1.00E-110//0s03g0355900 [Oryza sativa Japonica Group] >gi|108708218|gb|ABF96013.1| NAD dependent epimerase/dehydratase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548609|dbj|BAF12052.1|0s03g0355900 [Oryza sativa Japonica Group]	Unigene49110_A11//4.00E-79//AT4G31530| binding / catalytic	Unigene49110_A11//0.00E+00//gi|48741150|gb|C0071669.1|C0071669				nr +
Unigene49111_A11	415	12.73	5.86	10.78	15.60	14.52	19.15	5.50	6.85	3.36	-1.12E+00	2.52E-05	Down	-2.41E-01	3.86E-01		-1.04E-01	7.07E-01		2.96E-01	1.91E-01		3.16E-01	3.87E-01		-7.11E-01	4.99E-02				Unigene49111_A11//2.00E-37//DN803587						
Unigene49114_A11	1209	32.15	46.86	15.72	19.37	27.12	20.06	37.35	52.96	41.39	5.43E-01	1.01E-14		-1.03E+00	6.96E-29	Down	4.86E-01	2.39E-08		5.09E-02	6.97E-01		5.04E-01	1.05E-17		1.48E-01	3.23E-02		Unigene49114_A11//gi|108743310|dbj|BAE95414.1|//1.00E-136//mitogen-activated protein kinase kinase [Nicotiana benthamiana]	Unigene49114_A11//1.00E-110//AT1G73500| MKK9 (MAP KINASE KINASE 9); MAP kinase kinase/ kinase/ protein kinase activator	Unigene49114_A11//0.00E+00//TC139083		ko04626|Plant-pathogen interaction		nr -
Unigene49116_A11	714	2.86	3.90	4.25	95.93	99.06	77.87	25.17	37.87	11.55	4.50E-01	2.34E-01		5.73E-01	1.32E-01		4.63E-02	5.69E-01		-3.01E-01	9.74E-07		5.90E-01	2.65E-10		-1.12E+00	1.93E-20	Down	Unigene49116_A11//gi|25992549|gb|AAN77154.1|//8.00E-58//fiber protein FbI0 [Gossypium barbadense]		Unigene49116_A11//0.00E+00//gi|11199681|gb|BF268686.1|BF268686				nr -

Unigene49117_All	1178	2.31	2.15	1.45	3.51	4.30	2.45	4.63	0.78	1.45	-1.03E-01	7.77E-01			-6.75E-01	9.18E-02		2.92E-01	3.17E-01		-5.16E-01	9.21E-02		-2.57E+00	4.22E-19	Down	-1.67E+00	9.81E-12	Down	Unigene49117_All//gi|15228224|ref|NP_188270.1|//6.00E-87//IQD26 (IQ-domain 26); calmodulin binding [Arabidopsis thaliana] >gi|54606842|gb|AAV34769.1|At3g16490 [Arabidopsis thaliana] >gi|58531348|gb|AAM78596.1|At3g16490 [Arabidopsis thaliana]	Unigene49117_All//3.00E-80//AT3G16490| IQD26 (IQ-domain 26); calmodulin binding	Unigene49117_All//2.00E-30//TC135160				nr +
Unigene4912_All	931	4.61	17.85	11.21	15.57	13.57	91.73	100.64	364.58	299.20	1.95E+00	3.81E-33	Up	1.28E+00	2.33E-11	Up	-1.98E-01	2.18E-01		2.56E+00	1.86E-251	Up	1.86E+00	0.00E+00	Up	1.57E+00	0.00E+00	Up			Unigene4912_All//0.00E+00//TC139401				ESTscan -
Unigene49120_All	972	1.13	3.60	3.67	1.49	2.09	2.69	2.96	2.32	1.97	1.67E+00	3.13E-06	Up	1.70E+00	3.43E-06	Up	4.92E-01	3.16E-01		8.59E-01	2.96E-02		-3.49E-01	3.25E-01		-5.88E-01	6.47E-02				Unigene49120_All//6.00E-107//gi|109861617|gb|DW490594.1|DW490594				nr +
Unigene49121_All	1612	20.25	11.25	8.65	31.95	32.26	33.00	21.14	14.78	9.47	-8.48E-01	1.98E-18		-1.23E+00	5.82E-32	Down	1.36E-02	8.88E-01		4.67E-02	6.42E-01		-5.16E-01	3.12E-10		-1.16E+00	7.21E-40	Down	Unigene49121_All//gi|297810979|ref|XP_002873373.1|//1.00E-170//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319210|gb|EFH49632.1|calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49121_All//1.00E-141//AT5G08580| calcium-binding EF hand family protein	Unigene49121_All//0.00E+00//TC175340		ko04626|Plant-pathogen interaction		nr +
Unigene49124_All	657	12.42	64.32	16.21	6.52	10.17	5.43	10.30	12.34	5.09	2.37E+00	2.38E-106	Up	3.84E-01	3.95E-02		6.41E-01	3.39E-03		-2.64E-01	4.19E-01		2.61E-01	1.83E-01		-1.02E+00	3.95E-07	Down			Unigene49124_All//9.00E-96//ES837204				
Unigene49126_All	737	92.22	347.19	126.95	188.17	230.63	254.13	115.42	181.59	108.00	1.91E+00	0.00E+00	Up	4.61E-01	3.46E-17		2.94E-01	1.72E-16		4.34E-01	1.49E-33		6.54E-01	3.55E-57		-9.59E-02	7.54E-02		Unigene49126_All//gi|224131746|ref|XP_002328098.1|//8.00E-40//ethylene-insensitive 3b [Populus trichocarpa] >gi|222837613|gb|EEE75978.1|ethylene-insensitive 3b [Populus trichocarpa]	Unigene49126_All//8.00E-18//AT3G20770| EIN3 (ETHYLENE-INSENSITIVE3); transcription factor	Unigene49126_All//0.00E+00//TC151023	EIL			nr +
Unigene49129_All	1782	1.32	2.76	1.17	0.62	0.85	0.46	2.37	2.70	6.28	1.06E+00	1.19E-04	Up	-1.81E-01	6.63E-01		4.67E-01	4.26E-01		-4.31E-01	5.37E-01		1.85E-01	5.13E-01		1.40E+00	5.48E-18	Up	Unigene49129_All//gi|22329119|ref|NP_195070.2|//0.00E+00//glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana]	Unigene49129_All//0.00E+00//AT4G33440| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene49129_All//0.00E+00//TC131788		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene4913_All	796	128.30	52.39	80.41	203.45	180.83	180.60	159.93	79.39	83.33	-1.29E+00	4.09E-111	Down	-6.74E-01	1.54E-36		-1.70E-01	6.45E-06		-1.72E-01	1.44E-05		-1.01E+00	3.58E-114	Down	-9.41E-01	3.09E-104		Unigene4913_All//gi|40287504|gb|AA88866.1|//3.00E-60//40S ribosomal protein S17 [Capsicum annuum]	Unigene4913_All//4.00E-57//AT5G04800| 40S ribosomal protein S17 (RPS17D)	Unigene4913_All//0.00E+00//TC145776		ko03010|Ribosome		nr -
Unigene49130_All	1413	23.70	5.81	5.84	12.55	8.46	9.27	5.00	1.18	2.37	-2.03E+00	5.71E-70	Down	-2.02E+00	3.80E-67	Down	-5.70E-01	2.41E-06		-4.37E-01	7.41E-04		-2.08E+00	3.69E-19	Down	-1.08E+00	4.60E-08	Down	Unigene49130_All//gi|298569778|gb|AD187417.1|//0.00E+00//fructokinase-like protein 1 [Gossypium hirsutum]	Unigene49130_All//6.00E-162//AT3G54090| pfkB-type carbohydrate kinase family protein	Unigene49130_All//0.00E+00//gi|164240512|gb|ES795193.1|ES795193		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr +
Unigene49131_All	628	86.56	53.41	81.32	132.47	126.06	123.19	113.91	50.25	55.06	-6.97E-01	1.11E-21		-9.02E-02	2.92E-01		-7.15E-02	2.98E-01		-1.05E-01	1.02E-01		-1.18E+00	8.27E-83	Down	-1.05E+00	1.89E-70	Down	Unigene49131_All//gi|18401423|ref|NP_566569.1|//5.00E-47//HS1 (HEAT STABLE PROTEIN 1) [Arabidopsis thaliana] >gi|51316534|sp|Q9LUV2.1|POP3_ARATH RecName: Full=Probable protein Pop3 >gi|13877523|gb|AAK43839.1|AF370462_1 [Unknown protein [Arabidopsis thaliana]	Unigene49131_All//2.00E-39//AT3G17210| HS1 (HEAT STABLE PROTEIN 1)	Unigene49131_All//0.00E+00//gi|109836208|gb|DW234769.1|DW234769				nr -
Unigene49137_All	647	92.51	50.59	58.52	86.92	69.62	96.54	46.40	76.03	119.39	-8.71E-01	1.17E-34		-6.61E-01	6.68E-21		-3.20E-01	7.55E-07		1.51E-01	3.31E-02		7.13E-01	6.16E-25		1.36E+00	7.00E-114	Up	Unigene49137_All//gi|73761699|gb|AZ83349.1|//1.00E-71//MAP kinase [Gossypium hirsutum]	Unigene49137_All//3.00E-47//AT3G14720| ATMPK19; MAP kinase	Unigene49137_All//0.00E+00//gi|73862348|gb|DT465087.1|DT465087				nr -
Unigene49140_All	889	0.00	0.11	0.00	2.91	2.21	1.37	35.24	27.41	15.86	6.83E+00	3.86E-01		null	null		-4.00E-01	3.14E-01		-1.09E+00	5.63E-03		-3.63E-01	2.52E-05		-1.15E+00	2.41E-36	Down	Unigene49140_All//gi|75337341|sp|Q9SK86.1|ADH_1_ARATH//1.00E-108//RecName: Full=Alcohol dehydrogenase-like 1 >gi|6587845|gb|AAF18534.1|AC006551_20 Very similar to alcohol dehydrogenase [Arabidopsis thaliana]	Unigene49140_All//2.00E-86//AT1G22430| alcohol dehydrogenase, putative	Unigene49140_All//0.00E+00//gi|78338450|gb|DT558724.1|DT558724		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr +
Unigene49141_All	1479	0.07	0.21	0.11	0.51	0.49	0.37	15.32	9.35	7.11	1.54E+00	3.23E-01		6.09E-01	7.48E-01		-4.73E-02	9.43E-01		-4.63E-01	6.06E-01		-7.12E-01	6.21E-12		-1.11E+00	5.61E-25	Down	Unigene49141_All//gi|21618210|gb|AM67260.1|//1.00E-135//alcohol dehydrogenase-like protein [Arabidopsis thaliana]	Unigene49141_All//2.00E-125//AT1G22430| alcohol dehydrogenase, putative	Unigene49141_All//0.00E+00//gi|164355661|gb|ES805292.1|ES805292		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr -
Unigene49142_All	895	2.40	1.19	0.77	2.89	1.81	3.94	5.53	2.99	4.18	-1.01E+00	2.17E-02		-1.63E+00	8.10E-04	Down	-6.79E-01	7.37E-02		4.44E-01	2.05E-01		-8.87E-01	2.36E-04		-4.02E-01	9.18E-02		Unigene49142_All//gi|75127120|sp|Q6NPG7.1|Y5382_ARATH//1.00E-45//RecName: Full=Uncharacterized protein At5g43822 >gi|38454054|gb|AAR20721.1|At5g43820 [Arabidopsis thaliana] >gi|38603984|gb|AAR24735.1|At5g43820 [Arabidopsis thaliana]	Unigene49142_All//3.00E-40//AT5G43822| unknown protein	Unigene49142_All//0.00E+00//gi|109888161|gb|DW517130.1|DW517130				nr +
Unigene49143_All	1507	9.51	6.76	4.38	12.53	11.61	10.34	7.21	6.43	6.37	-4.93E-01	8.52E-04		-1.12E+00	1.81E-12	Down	-1.10E-01	4.69E-01		-2.77E-01	3.63E-02		-1.64E-01	3.61E-01		-1.79E-01	2.79E-01		Unigene49143_All//gi|18391032|ref|NP_563845.1|//3.00E-32//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|3482927|gb|AAC33212.1| Unknown protein [Arabidopsis thaliana] >gi|15529272|gb|AAK97730.1|At1g09520/F14J9_18 [Arabidopsis thaliana] >gi|25141213|gb|AAN73301.1|At1g09520/F14J9_18 [Arabidopsis thaliana]	Unigene49143_All//7.00E-11//AT1G09520| protein binding / zinc ion binding	Unigene49143_All//0.00E+00//gi|78333661|gb|DT553935.1|DT553935				nr -
Unigene49144_All	1356	1.47	1.01	1.49	1.21	2.34	2.00	3.02	1.05	2.20	-5.39E-01	2.35E-01		2.55E-02	9.75E-01		9.47E-01	5.49E-03		7.21E-01	6.52E-02		-1.53E+00	9.15E-08	Down	-4.57E-01	8.18E-02		Unigene49144_All//gi|32250969|gb|AAP74222.1|//1.00E-146//RST1 [Arabidopsis thaliana]	Unigene49144_All//4.00E-146//AT3G27670| RST1 (RESURRECTION1); binding					nr -
Unigene49146_All	682	33.68	37.22	27.48	38.49	34.18	31.19	77.43	53.44	29.97	1.44E-01	2.26E-01		-2.93E-01	1.61E-02		-1.71E-01	1.33E-01		-3.04E-01	4.51E-03		-5.35E-01	2.31E-16		-1.37E+00	2.46E-79	Down	Unigene49146_All//gi|17064906|gb|AAL32607.1|//1.00E-15//Unknown protein [Arabidopsis thaliana] >gi|231978400|gb|ANN15447.1|Unknown protein [Arabidopsis thaliana]	Unigene49146_All//8.00E-17//AT5G19010| MPK16; MAP kinase	Unigene49146_All//0.00E+00//TC145924				nr +
Unigene49148_All	1010	0.83	3.51	2.85	1.04	1.43	1.34	1.13	1.41	1.50	2.08E+00	3.27E-08	Up	1.78E+00	2.03E-05	Up	4.67E-01	4.44E-01		3.73E-01	5.63E-01		3.16E-01	5.63E-01		4.07E-01	3.97E-01				Unigene49148_All//0.00E+00//CO123807				ESTscan +
Unigene49149_All	987	4.24	1.28	2.70	3.53	0.45	2.70	1.88	4.32	1.98	-1.72E+00	1.17E-07	Down	-6.53E-01	3.64E-02		-2.96E+00	1.24E-14	Down	-3.88E-01	2.74E-01		1.20E+00	8.93E-06	Up	6.95E-02	8.77E-01									
Unigene4915_All	1216	5.94	12.17	7.79	12.78	13.82	13.48	16.34	17.77	14.68	1.04E+00	6.75E-12	Up	3.93E-01	4.81E-02		1.13E-01	5.07E-01		7.70E-02	6.49E-01		1.21E-01	3.30E-01		-1.55E-01	1.90E-01		Unigene4915_All//gi|115455053|ref|NP_001051127.1|//2.00E-33//Os03g0725100 [Oryza sativa Japonica Group] >gi|113549598|dbj|BAF13041.1|Os03g0725100 [Oryza sativa Japonica Group]	Unigene4915_All//2.00E-25//AT5G58040| ATFIP1[V] (Arabidopsis homolog of yeast Fip1 [V]); RNA binding / protein binding	Unigene4915_All//0.00E+00//TC149136				nr -
Unigene49151_All	627	0.17	2.51	0.17	2.15	3.73	3.75	0.88	0.13	0.64	3.91E+00	6.83E-07	Up	2.57E-02	9.99E-01		8.00E-01	5.49E-02		8.04E-01	5.79E-02		-2.72E+00	1.22E-02		-4.64E-01	5.97E-01		Unigene49151_All//gi|18417474|ref|NP_567835.1|//5.00E-46//CFIM-25 [Arabidopsis thaliana] >gi|15081674|gb|AAK82492.1|AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|20147173|gb|AAM10303.1|AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|21554114|gb|AAM63194.1| mRNA cleavage factor subunit-like protein [Arabidopsis thaliana]	Unigene49151_All//8.00E-47//AT4G29820| CFIM-25	Unigene49151_All//1.00E-60//TC161737				nr +
Unigene49152_All	1065	1.38	5.04	0.90	4.68	9.54	12.38	1.19	1.10	1.08	1.87E+00	1.29E-10	Up	-6.12E-01	2.90E-01		1.03E+00	2.16E-09	Up	1.40E+00	7.64E-18	Up	-1.16E-01	8.30E-01		-1.35E-01	7.87E-01		Unigene49152_All//gi|18417474|ref|NP_567835.1|//2.00E-79//CFIM-25 [Arabidopsis thaliana] >gi|15081674|gb|AAK82492.1|AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|20147173|gb|AAM10303.1|AT4g29820/F27B13_60 [Arabidopsis thaliana] >gi|21554114|gb|AAM63194.1| mRNA cleavage factor subunit-like protein [Arabidopsis thaliana]	Unigene49152_All//1.00E-80//AT4G29820| CFIM-25	Unigene49152_All//2.00E-144//TC161737				nr +
Unigene49153_All	1413	0.93	0.18	0.98	15.93	10.82	7.86	15.05	1.86	2.28	-2.37E+00	5.60E-04	Down	8.19E-02	8.86E-01		-5.58E-01	1.21E-07		-1.02E+00	1.37E-18	Down	-3.01E+00	5.91E-86	Down	-2.72E+00	9.21E-80	Down	Unigene49153_All//gi|15237744|ref|NP_200683.1|//1.00E-117//wound-responsive protein-related [Arabidopsis thaliana] >gi|8843795|dbj|BAA97343.1|induced upon wounding stress-like protein [Arabidopsis thaliana] >gi|119360131|gb|ABL66794.1|At5g58750 [Arabidopsis thaliana]	Unigene49153_All//3.00E-118//AT5G58750| wound-responsive protein-related	Unigene49153_All//0.00E+00//CO119137				nr -
Unigene49154_All	693	1.06	2.63	1.54	3.23	2.14	1.56	5.67	3.74	2.36	1.32E+00	8.22E-03		5.40E-01	4.18E-01		-5.98E-01	1.55E-01		-1.05E+00	1.43E-02		-6.02E-01	2.95E-02		-1.27E+00	4.66E-06	Down	Unigene49154_All//gi|224054140|ref|XP_002298111.1|//8.00E-06//predicted protein [Populus trichocarpa] >gi|222845369|gb|EEE82916.1|predicted protein [Populus trichocarpa]	Unigene49154_All//2.00E-05//AT4G29900| ACA10 (AUTOINHIBITED CA(2+)-ATPASE 10); calcium-transporting ATPase/calmodulin binding	Unigene49154_All//4.00E-89//DW239604				nr +

Unigene49156_All	1531	318.91	164.45	238.98	5.50	7.60	4.04	1.88	7.02	2.91	-9.56E-01	0.00E+00		-4.16E-01	1.90E-72		4.67E-01	3.57E-03		-4.44E-01	2.79E-02		1.90E+00	1.31E-25	Up	6.34E-01	1.05E-02		Unigene49156_All//gi|15242466|ref|NP_196528.1|//1.00E-168//PMDH2 (peroxisomal NAD-malate dehydrogenase 2); malate dehydrogenase [Arabidopsis thaliana] >gi|11133713|sp|Q9ZP05.1|MDHG1_ARATH RecName: Full=Malate dehydrogenase, glyoxysomal; AltName: Full=mbNAD-MDH; Flags: Precursor >gi|16226937|gb|AAL16303.1|AF428373_1 AT5g09660/F17I14_150 [Arabidopsis thaliana] >gi|3929651|emb|CAA10321.1| microbody NAD-dependent malate dehydrogenase [Arabidopsis thaliana] >gi|7671423|emb|CAB89364.1| microbody NAD-dependent malate dehydrogenase [Arabidopsis thaliana] >gi|9758994|dbj|BAB09521.1| microbody NAD-dependent malate dehydrogenase [Arabidopsis thaliana] >gi|14335146|gb|AAK59853.1| AT5g09660/F17I14_150 [Arabidopsis thaliana] >gi|18655351|gb|AAL76131.1|	Unigene49156_All//4.00E-169//AT5G09660| PMDH2 (peroxisomal NAD-malate dehydrogenase 2); malate dehydrogenase	Unigene49156_All//0.00E+00//TC133256		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene49158_All	1496	0.59	1.66	0.85	1.07	1.10	1.09	4.15	3.58	3.06	1.48E+00	4.79E-04	Up	5.23E-01	3.99E-01		5.24E-02	9.47E-01		2.86E-02	9.53E-01		-2.16E-01	3.68E-01		-4.40E-01	3.32E-02		Unigene49158_All//gi|94033212|ref|YP_002000549.1|//1.00E-121//cytochrome c oxidase subunit 3 [Oryza sativa Japonica Group] >gi|60498734|dbj|BAC19853.2| Cytochrome c oxidase subunit 3 [Oryza sativa Japonica Group]	Unigene49158_All//1.00E-110//ATMG00730| Encodes cytochrome c oxidase subunit 3.	Unigene49158_All//0.00E+00//TC141632		ko00190|Oxidative phosphorylation		nr +
Unigene49159_All	1113	1.74	1.73	1.63	2.51	1.36	1.34	1.25	5.75	0.14	-7.70E-03	9.81E-01		-9.66E-02	8.35E-01		-8.81E-01	1.31E-02		-9.04E-01	1.58E-02		2.20E+00	1.42E-18	Up	-3.13E+00	1.09E-06	Down	Unigene49159_All//gi|38112427|gb|AR11299.1|//1.00E-150//lectin-like receptor kinase 7;2 [Medicago truncatula]	Unigene49159_All//1.00E-126//AT2G37710| RLK (receptor lectin kinase); kinase	Unigene49159_All//0.00E+00//CO081089		ko04626|Plant-pathogen interaction		nr +
Unigene4916_All	703	2.83	7.06	3.56	9.07	4.41	10.02	13.71	13.85	7.54	1.32E+00	2.85E-06	Up	3.32E-01	4.26E-01		-1.04E+00	1.64E-06	Down	1.44E-01	6.02E-01		1.47E-02	9.64E-01		-8.63E-01	1.14E-07		Unigene4916_All//gi|15219078|ref|NP_175683.1|//4.00E-60//HTA9 (HISTONE H2A PROTEIN 9); DNA binding [Arabidopsis thaliana] >gi|75308904|sp|Q9C944.1|H2AV3_ARATH RecName: Full=Probable histone H2A variant 3; AltName: Full=H2A.F/Z 3; AltName: Full=HTA9 >gi|16648742|gb|AAL25563.1| At1g52740/F14G24_1 [Arabidopsis thaliana]	Unigene4916_All//3.00E-54//AT1G52740| HTA9 (HISTONE H2A PROTEIN 9); DNA binding	Unigene4916_All//0.00E+00//gi|164254606|gb|ES814573.1|ES814573				nr +
Unigene49161_All	720	8.07	9.15	8.21	10.45	11.67	9.79	19.55	11.32	8.19	1.82E-01	4.59E-01		2.54E-02	9.36E-01		1.60E-01	5.14E-01		-9.44E-02	6.82E-01		-7.89E-01	4.57E-09		-1.26E+00	3.63E-19	Down	Unigene49161_All//gi|15242365|ref|NP_196487.1|//5.00E-38//KIWI; DNA binding / protein binding / transcription coactivator [Arabidopsis thaliana] >gi|37079587|sp|O65154.1|KIWI_ARATH RecName: Full=RNA polymerase II transcriptional coactivator KIWI >gi|28466805|gb|AAO44011.1| At5g09250 [Arabidopsis thaliana]	Unigene49161_All//2.00E-33//AT5G09250| KIWI; DNA binding / protein binding / transcription coactivator	Unigene49161_All//0.00E+00//TC154504				nr -
Unigene49164_All	1655	23.39	22.53	34.43	0.72	1.35	0.46	0.97	0.25	0.60	-5.41E-02	6.14E-01		5.57E-01	7.00E-15		9.05E-01	3.36E-02		-6.39E-01	3.24E-01		-1.94E+00	1.42E-04	Down	-6.90E-01	1.21E-01		Unigene49164_All//gi|223452406|gb|ACM89530.1|//1.00E-151//protein kinase [Glycine max]	Unigene49164_All//4.00E-117//AT2G45820| protein kinase family protein	Unigene49164_All//0.00E+00//TC158860		ko04626|Plant-pathogen interaction		nr +
Unigene49165_All	1403	4.77	10.18	5.20	9.02	8.20	6.89	6.48	10.49	17.66	1.09E+00	1.62E-12	Up	1.23E-01	6.40E-01		-1.38E-01	4.54E-01		-3.89E-01	1.54E-02		6.95E-01	1.02E-07		1.45E+00	1.72E-40	Up	Unigene49165_All//gi|30680596|ref|NP_849613.1|//3.00E-92//armadillo/beta-catenin repeat family protein [Arabidopsis thaliana]	Unigene49165_All//3.00E-88//AT1G08315| armadillo/beta-catenin repeat family protein	Unigene49165_All//0.00E+00//TC175401				nr +
Unigene49167_All	582	2.52	2.70	2.29	5.48	7.10	7.29	9.08	14.36	23.55	1.01E-01	8.43E-01		-1.38E-01	7.97E-01		3.74E-01	2.41E-01		4.13E-01	1.92E-01		6.61E-01	2.05E-04		1.37E+00	3.72E-21	Up			Unigene49167_All//7.00E-07//TC166801				
Unigene49168_All	1395	11.33	14.38	15.08	6.00	7.60	5.63	3.00	0.87	0.51	3.45E-01	5.67E-03		4.13E-01	9.33E-04		3.42E-01	5.48E-02		-9.08E-02	6.76E-01		-1.79E+00	1.11E-09	Down	-2.55E+00	3.40E-15	Down	Unigene49168_All//gi|6587849|gb|AAF18538.1|AC006551_24//2.00E-42//Very similar to retrotransposon reverse transcriptase [Arabidopsis thaliana]	Unigene49168_All//8.00E-40//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene49168_All//6.00E-40//gi|13245268|gb|BE053245.2|BE053245				nr +
Unigene49171_All	824	81.15	325.42	126.08	73.21	96.33	99.86	244.60	228.25	132.33	2.00E+00	0.00E+00	Up	6.36E-01	1.39E-33		3.96E-01	1.44E-13		4.48E-01	5.83E-16		-9.98E-02	3.12E-03		-8.86E-01	6.08E-149		Unigene49171_All//gi|297841421|ref|XP_002888592.1|//9.00E-32//rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334433|gb|EFH64851.1| rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49171_All//6.00E-30//AT1G67360| rubber elongation factor (REF) family protein	Unigene49171_All//0.00E+00//TC168855				nr +
Unigene49174_All	849	38.27	84.15	27.03	37.38	68.91	41.17	51.54	122.93	186.57	1.14E+00	1.84E-63	Up	-5.02E-01	2.36E-07		8.83E-01	8.50E-41		1.40E-01	1.78E-01		1.25E+00	3.29E-132	Up	1.86E+00	0.00E+00	Up	Unigene49174_All//gi|18391499|ref|NP_563926.1|//2.00E-20//myb family transcription factor [Arabidopsis thaliana] >gi|9958063|gb|AAG09552.1|AC011810_11 Unknown Protein [Arabidopsis thaliana] >gi|136058575|gb|AAK32923.1|AF367336_1 At1g13300/T6J4_6 [Arabidopsis thaliana] >gi|21700900|gb|AAM70574.1| At1g13300/T6J4_6 [Arabidopsis thaliana]	Unigene49174_All//8.00E-10//AT1G13300| myb family transcription factor	Unigene49174_All//0.00E+00//TC153086	G2-like			nr +
Unigene49175_All	742	29.55	17.62	6.89	41.36	45.11	26.17	8.66	4.56	6.50	-7.46E-01	2.76E-10		-2.10E+00	2.56E-46	Down	1.25E-01	2.36E-01		-6.60E-01	3.12E-12		-9.25E-01	9.54E-06		-4.15E-01	4.15E-02		Unigene49175_All//gi|2980891|dbj|BAA25203.1|//6.00E-23//histone H1 [Triticum aestivum]	Unigene49175_All//1.00E-12//AT2G30620| histone H1.2	Unigene49175_All//0.00E+00//TC171753				nr -
Unigene49176_All	1197	3.67	1.95	0.98	23.22	21.03	9.28	20.49	2.72	3.59	-9.15E-01	1.60E-03		-1.91E+00	1.30E-08	Down	-1.43E-01	2.12E-01		-1.32E+00	2.19E-34	Down	-2.91E+00	1.27E-95	Down	-2.51E+00	5.36E-84	Down	Unigene49176_All//gi|15239503|ref|NP_197955.1|//1.00E-59//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|71660770|sp|P69781.1|GAT12_ARATH RecName: Full=GATA transcription factor 12	Unigene49176_All//1.00E-58//AT5G25830| zinc finger (GATA type) family protein	Unigene49176_All//0.00E+00//TC171245	C2C2-GATA			nr -
Unigene49177_All	1047	1.95	0.77	0.20	3.24	2.24	2.63	1.13	1.36	0.57	-1.33E+00	4.16E-03		-3.26E+00	2.37E-07	Down	-5.33E-01	1.06E-01		-2.98E-01	4.20E-01		2.64E-01	6.49E-01		-9.86E-01	6.53E-02		Unigene49177_All//gi|224134186|ref|XP_002327777.1|//3.00E-84//short internodes 2 [Populus trichocarpa] >gi|222836862|gb|EEE75255.1| short internodes 2 [Populus trichocarpa]	Unigene49177_All//4.00E-51//AT5G66350| SHI (SHORT INTERNODES): protein binding / protein heterodimerization/ transcription factor	Unigene49177_All//3.00E-41//gi|78332396|gb|DT552670.1|DT552670	SRS			nr -
Unigene49178_All	1138	59.49	67.54	63.73	13.96	15.19	17.10	3.60	9.00	9.66	1.83E-01	2.82E-03		9.93E-02	1.62E-01		1.22E-01	4.55E-01		2.93E-01	2.34E-02		1.32E+00	9.53E-15	Up	1.42E+00	5.22E-18	Up	Unigene49178_All//gi|116310889|emb|CAH67829.1|//2.00E-74//B0616E02-H0507E05.5 [Oryza sativa (indica cultivar-group)]	Unigene49178_All//3.00E-69//AT1G62780| unknown protein	Unigene49178_All//0.00E+00//gi|78342203|gb|DT562477.1|DT562477				nr -
Unigene49179_All	1320	7.49	7.02	4.11	9.36	12.00	8.35	4.58	1.65	4.95	-9.28E-02	6.22E-01		-8.64E-01	5.41E-06		3.59E-01	9.08E-03		-1.65E-01	3.90E-01		-1.48E+00	1.46E-10	Down	1.12E-01	6.22E-01		Unigene49179_All//gi|2443885|gb|AAB71478.1|//2.00E-22//Unknown protein [Arabidopsis thaliana] >gi|30017227|gb|AAP12847.1| At1g61170 [Arabidopsis thaliana]	Unigene49179_All//3.00E-16//AT1G11120| unknown protein	Unigene49179_All//0.00E+00//TC160540				nr +
Unigene49180_All	883	16.83	9.87	10.73	15.29	11.54	15.91	29.88	13.35	10.65	-7.70E-01	1.35E-07		-6.49E-01	1.53E-05		-4.05E-01	5.59E-03		5.72E-02	7.44E-01		-1.16E+00	2.72E-30	Down	-1.49E+00	2.50E-45	Down	Unigene49180_All//gi|297725267|ref|NP_001174997.1|//3.00E-15//Os06g0717300 [Oryza sativa Japonica Group] >gi|255677399|dbj|BAH93725.1| Os06g0717300 [Oryza sativa Japonica Group]	Unigene49180_All//1.00E-10//AT1G47820| unknown protein	Unigene49180_All//0.00E+00//gi|164262694|gb|ES849731.1|ES849731				nr -
Unigene49182_All	800	21.39	39.52	27.22	25.22	25.18	27.27	20.08	40.65	21.81	8.86E-01	3.91E-19		3.48E-01	4.85E-03		-2.20E-03	9.84E-01		1.13E-01	4.28E-01		1.02E+00	5.00E-30	Up	1.19E-01	3.66E-01		Unigene49182_All//gi|149391537|gb|ABR25786.1|//1.00E-26//pi starvation-induced protein [Oryza sativa Indica Group]	Unigene49182_All//9.00E-16//AT1G71950| identical protein binding / serine-type endopeptidase	Unigene49182_All//0.00E+00//gi|13244854|gb|BE052175.2|BE052175				nr -
Unigene49186_All	1340	45.68	39.74	40.30	48.81	58.85	59.69	10.76	11.79	5.32	-2.01E-01	3.64E-03		-1.81E-01	1.32E-02		2.70E-01	7.95E-07		2.90E-01	2.96E-07		1.32E-01	3.75E-01		-1.02E+00	3.41E-14	Down	Unigene49186_All//gi|18405251|ref|NP_565921.1|//6.00E-67//protein binding / structural molecule [Arabidopsis thaliana] >gi|20886662|gb|AAM95291.1| expressed protein [Arabidopsis thaliana]	Unigene49186_All//9.00E-46//AT2G40060| protein binding / structural molecule	Unigene49186_All//0.00E+00//TC131707				nr +
Unigene49187_All	817	26.38	131.29	59.70	42.07	40.59	38.47	36.17	74.54	66.56	2.32E+00	1.52E-261	Up	1.18E+00	9.97E-45	Up	-5.17E-02	6.46E-01		-1.29E-01	2.22E-01		1.04E+00	7.74E-58	Up	8.80E-01	4.42E-40		Unigene49187_All//gi|301601262|dbj|BAJ13303.1|//2.00E-53//autophagy 8 [Ipomoea nil]	Unigene49187_All//2.00E-53//AT4G16520| ATG8F (autophagy 8f); microtubule binding	Unigene49187_All//0.00E+00//gi|109876487|gb|DW505461.1|DW505461		ko04140|Regulation of autophagy		nr -
Unigene49188_All	1819	7.68	3.70	3.60	0.58	0.21	0.10	4.35	0.11	0.04	-1.05E+00	1.33E-11	Down	-1.09E+00	9.63E-12	Down	-1.47E+00	2.48E-02		-2.53E+00	1.22E-03		-5.24E+00	2.59E-48	Down	-6.63E+00	1.55E-54	Down	Unigene49188_All//gi|224093250|ref|XP_002309852.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222852755|gb|EEE90302.1| GRAS family transcription factor [Populus trichocarpa]	Unigene49188_All//1.00E-94//AT3G49950| scarecrow transcription factor family protein		GRAS			nr -
Unigene49189_All	1413	4.44	4.37	5.09	1.52	2.39	0.99	0.63	3.73	0.65	-2.24E-02	9.43E-01		1.95E-01	4.12E-01		6.56E-01	5.03E-02		-6.14E-01	1.77E-01		2.57E+00	2.08E-18	Up	4.54E-02	9.62E-01		Unigene49189_All//gi|15232280|ref|NP_191581.1|//2.00E-84//ATL4; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|68565314|sp|Q9LY41.1|ATL3J_ARATH RecName: Full=RING-H2 finger protein ATL3J; AltName: Full=RING-H2 finger protein ATL4; AltName: Full=RING-H2 finger protein RHKla >gi|7576198|emb|CAB87859.1| RING-H2 zinc finger protein ATL4 [Arabidopsis thaliana] >gi|66865934|gb|AAY57601.1| RING finger family protein [Arabidopsis thaliana] >gi|114050661|gb|ABI49480.1| At3g60220 [Arabidopsis thaliana]	Unigene49189_All//2.00E-53//AT3G60220| ATL4; protein binding / zinc ion binding	Unigene49189_All//0.00E+00//gi|78338789|gb|DT559063.1|DT559063		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +

Unigene49191_All	887	3.60	1.37	2.28	8.48	8.62	6.82	8.39	3.96	3.23	-1.39E+00	1.23E-04	Down	-6.57E-01	7.25E-02			2.33E-02	9.40E-01		-3.14E-01	1.70E-01			-1.08E+00	3.09E-08	Down	-1.38E+00	5.30E-12	Down	Unigene49191_All//gi|15231858|ref|NP_188063.1|//1.00E-109//CID9 (CTC-Interacting Domain 9); RNA binding / protein binding [Arabidopsis thaliana]	Unigene49191_All//6.00E-101//AT3G14450| CID9 (CTC-Interacting Domain 9); RNA binding / protein binding	Unigene49191_All//0.00E+00//gi|73850970|gb|DT459990.1|DT459990			nr +
Unigene49192_All	1256	0.67	0.65	0.72	2.58	1.84	2.37	4.01	2.46	1.55	-4.62E-02	9.64E-01		1.13E-01	8.72E-01			-4.89E-01	1.55E-01		-1.19E-01	7.42E-01			-7.02E-01	3.17E-03		-1.37E+00	2.56E-08	Down	Unigene49192_All//gi|15231858|ref|NP_188063.1|//1.00E-109//CID9 (CTC-Interacting Domain 9); RNA binding / protein binding [Arabidopsis thaliana]	Unigene49192_All//1.00E-94//AT3G14450| CID9 (CTC-Interacting Domain 9); RNA binding / protein binding	Unigene49192_All//0.00E+00//TC164043			nr +
Unigene49193_All	1176	0.40	1.98	0.59	5.55	5.62	7.34	1.98	1.21	1.32	2.31E+00	2.70E-06	Up	5.56E-01	5.28E-01			1.89E-02	9.62E-01		4.03E-01	4.69E-02			-7.11E-01	5.79E-02		-5.82E-01	1.08E-01		Unigene49193_All//gi|18401489|ref|NP_566576.1|//8.00E-47//meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana]	Unigene49193_All//4.00E-48//AT3G17380| meprin and TRAF homology domain-containing protein / MATH domain-containing protein				nr +
Unigene49195_All	668	4.70	9.56	6.70	7.53	11.44	12.71	7.22	8.57	9.42	1.02E+00	1.64E-05	Up	5.11E-01	9.08E-02			6.04E-01	2.86E-03		7.55E-01	1.11E-04			2.49E-01	3.10E-01		3.85E-01	6.42E-02		Unigene49195_All//gi|9910632|sp|Q9SM29.1|Y4331_ARATH//4.00E-27//RecName: Full=Uncharacterized protein At4g33100 >gi|37202052|gb|AAQ89641.1|At4g33100 [Arabidopsis thaliana]	Unigene49195_All//2.00E-28//AT4G33100| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Mitochondrial distribution and morphology family 35/apoptosis (InterPro:IPR007918); Has 160 Blast hits to 160 proteins in 70 species: Archae - 0; Bacteria - 0; Metazoa - 95; Fungi - 46; Plants - 13; Viruses - 0; Other Eukaryotes - 6 (source: NCBI BLink).	Unigene49195_All//0.00E+00//TC154584			nr -
Unigene49196_All	1083	170.34	564.34	440.55	88.45	141.08	134.32	68.24	97.91	63.34	1.73E+00	0.00E+00	Up	1.37E+00	0.00E+00	Up	6.74E-01	6.99E-67		6.03E-01	3.03E-47			5.21E-01	1.67E-30		-1.07E-01	6.19E-02		Unigene49196_All//gi|21553731|gb|AM62824.1|//4.00E-96//cytochrome b561 [Arabidopsis thaliana]	Unigene49196_All//3.00E-97//AT4G25570| ACYB-2; carbon-monoxide oxygenase	Unigene49196_All//0.00E+00//gi|109871287|gb|DW500263.1|DW500263			nr -
Unigene49197_All	1182	13.55	8.57	11.44	21.49	15.06	23.08	20.07	9.12	11.56	-6.60E-01	2.13E-06		-2.43E-01	1.15E-01			-5.13E-01	2.09E-07		1.03E-01	4.15E-01			-1.14E+00	2.12E-26	Down	-7.96E-01	2.20E-15		Unigene49197_All//gi|15237466|ref|NP_198882.1|//1.00E-112//ATP12 protein-related [Arabidopsis thaliana] >gi|14517426|gb|AAK62603.1|AT5g40660/MNF13_180 [Arabidopsis thaliana] >gi|22655442|gb|AAM98313.1|At5g40660/MNF13_180 [Arabidopsis thaliana]	Unigene49197_All//1.00E-83//AT5G40660| ATP12 protein-related	Unigene49197_All//0.00E+00//gi|78336124|gb|DT556398.1|DT556398			nr -
Unigene49198_All	1965	1.33	2.48	0.49	2.31	3.10	2.21	4.15	7.47	3.95	8.95E-01	1.11E-03		-1.45E+00	6.62E-04	Down	4.27E-01	8.00E-02		-6.42E-02	8.42E-01			8.46E-01	1.68E-10		-7.09E-02	7.16E-01		Unigene49198_All//gi|224128576|ref|XP_002320366.1|//0.00E+00//sodium proton exchanger [Populus trichocarpa] >gi|222861139|gb|EEE98681.1|sodium proton exchanger [Populus trichocarpa]	Unigene49198_All//1.00E-180//AT3G05030| NHX2 (SODIUM HYDROGEN EXCHANGER 2); sodium ion transmembrane transporter/ sodium:hydrogen antiporter	Unigene49198_All//8.00E-34//TC179101			nr +
Unigene49200_All	316	2.48	4.97	6.24	10.88	7.85	5.57	6.02	6.08	1.77	1.00E+00	5.98E-02		1.33E+00	7.43E-03			-4.71E-01	1.58E-01		-9.65E-01	3.49E-03			1.51E-02	1.01E+00		-1.77E+00	5.92E-05	Down	Unigene49200_All//gi|3776578|gb|AAC64895.1|//4.00E-11//ESTs gb|F13915 and gb|F13916 come from this gene [Arabidopsis thaliana]	Unigene49200_All//9.00E-12//AT1G54860| unknown protein				nr -
Unigene49201_All	772	1.29	5.25	3.24	13.42	9.55	11.12	10.08	5.47	5.06	2.03E+00	5.38E-09	Up	1.33E+00	1.99E-03			-4.92E-01	3.37E-03		-2.72E-01	1.55E-01			-8.82E-01	2.49E-06		-9.95E-01	7.95E-08		Unigene49201_All//gi|3776578|gb|AAC64895.1|//5.00E-39//ESTs gb|F13915 and gb|F13916 come from this gene [Arabidopsis thaliana]	Unigene49201_All//3.00E-40//AT1G54860| unknown protein	Unigene49201_All//1.00E-150//DW233971			nr -
Unigene49202_All	1373	6.86	3.10	6.01	5.01	4.51	3.06	1.29	0.49	0.73	-1.15E+00	3.67E-09	Down	-1.90E-01	3.83E-01			-1.49E-01	5.65E-01		-7.11E-01	1.21E-03			-1.41E+00	1.85E-03		-8.34E-01	4.69E-02		Unigene49202_All//gi|15228596|ref|NP_187013.1|//1.00E-145//CS26; cysteine synthase [Arabidopsis thaliana] >gi|11131558|sp|Q22682.1|CYSK4_ARATH RecName: Full=Probable cysteine synthase, chloroplastic; Short=CSase; AltName: Full=O-acetylserine sulfhydrylase; AltName: Full=O-acetylserine (thiol)-lyase; Short=OAS-TL; AltName: Full=CS26; Flags: Precursor >gi|6091759|gb|AAF03469.1|AC009327_8 O-acetylserine (thiol) lyase [Arabidopsis thaliana] >gi|2281780|dbj|BAA21628.1| O-acetylserine (thiol) lyase [Arabidopsis thaliana] >gi|20466215|gb|AAM20425.1| O-acetylserine (thiol) lyase [Arabidopsis thaliana] >gi|25084065|gb|AAN72166.1| O-acetylserine (thiol) lyase [Arabidopsis thaliana]	Unigene49202_All//3.00E-118//AT3G03630| CS26; cysteine synthase	Unigene49202_All//0.00E+00//CO117114		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr +
Unigene49203_All	1851	1.41	0.52	0.17	1.00	0.82	0.73	0.55	0.14	0.52	-1.44E+00	4.08E-04	Down	-3.03E+00	9.96E-09	Down	-2.83E-01	5.82E-01		-4.44E-01	3.98E-01			-2.02E+00	2.83E-03		-8.59E-02	8.88E-01		Unigene49203_All//gi|15228596|ref|NP_187013.1|//1.00E-139//CS26; cysteine synthase [Arabidopsis thaliana] >gi|11131558|sp|Q22682.1|CYSK4_ARATH RecName: Full=Probable cysteine synthase, chloroplastic; Short=CSase; AltName: Full=O-acetylserine sulfhydrylase; AltName: Full=O-acetylserine (thiol)-lyase; Short=OAS-TL; AltName: Full=CS26; Flags: Precursor >gi|6091759|gb|AAF03469.1|AC009327_8 O-acetylserine (thiol) lyase [Arabidopsis thaliana] >gi|2281780|dbj|BAA21628.1| O-acetylserine (thiol) lyase [Arabidopsis thaliana] >gi|20466215|gb|AAM20425.1| O-acetylserine (thiol) lyase [Arabidopsis thaliana] >gi|25084065|gb|AAN72166.1| O-acetylserine (thiol) lyase [Arabidopsis thaliana]	Unigene49203_All//5.00E-113//AT3G03630| CS26; cysteine synthase	Unigene49203_All//0.00E+00//CO117114		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr +
Unigene49204_All	468	4.92	7.36	5.69	3.73	4.64	3.57	5.42	1.88	1.28	5.82E-01	8.08E-02		2.10E-01	6.35E-01		3.15E-01	5.34E-01		-6.12E-02	9.17E-01			-1.53E+00	4.18E-05	Down	-2.09E+00	1.16E-07	Down	Unigene49204_All//gi|8469220|sp|Q9SQ13.1|FATB_GOSHI//3.00E-32//RecName: Full=Myristoyl-acyl carrier protein thioesterase, chloroplastic; AltName: Full=16:0-acyl-carrier protein thioesterase; Short=16:0-ACP thioesterase; AltName: Full=Acyl-[acyl-carrier-protein] hydrolase; AltName: Full=PATE; Flags: Precursor >gi|6048397|gb|AAF02215.1|AF076535_1 palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]	Unigene49204_All//2.00E-18//AT1G08510| FATB (fatty acyl-ACP thioesterases B); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase	Unigene49204_All//1.00E-146//gi|78329293|gb|DT549567.1|DT549567		ko00061|Fatty acid biosynthesis		nr +
Unigene49205_All	595	20.40	18.48	11.81	24.20	24.65	21.03	4.48	1.83	3.55	-1.43E-01	4.16E-01		-7.88E-01	3.00E-06		2.71E-02	8.83E-01		-2.03E-01	2.22E-01			-1.29E+00	2.59E-04	Down	-3.35E-01	3.41E-01		Unigene49205_All//gi|8469220|sp|Q9SQ13.1|FATB_GOSHI//1.00E-33//RecName: Full=Myristoyl-acyl carrier protein thioesterase, chloroplastic; AltName: Full=16:0-acyl-carrier protein thioesterase; Short=16:0-ACP thioesterase; AltName: Full=Acyl-[acyl-carrier-protein] hydrolase; AltName: Full=PATE; Flags: Precursor >gi|6048397|gb|AAF02215.1|AF076535_1 palmitoyl-acyl carrier protein thioesterase [Gossypium hirsutum]	Unigene49205_All//8.00E-20//AT1G08510| FATB (fatty acyl-ACP thioesterases B); acyl carrier/ acyl-[acyl-carrier-protein] hydrolase	Unigene49205_All//0.00E+00//gi|78333610|gb|DT553884.1|DT553884		ko00061|Fatty acid biosynthesis		nr +
Unigene49207_All	619	33.64	14.24	6.88	35.81	32.99	73.18	34.36	16.61	18.34	-1.24E+00	8.52E-22	Down	-2.29E+00	5.65E-49	Down	-1.18E-01	3.86E-01		1.03E+00	4.06E-37	Up	-1.05E+00	6.30E-21	Down	-9.05E-01	4.31E-17		Unigene49207_All//gi|1173209|sp|P46293.1|RS16_GOSHI//4.00E-75//RecName: Full=40S ribosomal protein S16 >gi|439654|emb|CAA53567.1| RS16 protein, 40S subunit [Gossypium hirsutum]	Unigene49207_All//9.00E-70//AT2G09990| 40S ribosomal protein S16 (RPS16A)	Unigene49207_All//0.00E+00//TC154346		ko03010|Ribosome		nr +
Unigene49208_All	1211	0.78	1.17	2.07	5.64	8.64	6.41	46.23	12.08	7.63	5.91E-01	2.94E-01		1.41E+00	1.15E-03		6.17E-01	2.19E-04		1.87E-01	4.47E-01			-1.94E+00	6.01E-134	Down	-2.60E+00	1.56E-198	Down	Unigene49208_All//gi|224138336|ref|XP_002326577.1|//1.00E-116//phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa] >gi|222833899|gb|EEE72376.1|phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa]	Unigene49208_All//5.00E-100//AT1G32100| PBR1 (PINORESINOL REDUCTASE 1); pinoresinol reductase	Unigene49208_All//0.00E+00//TC169993		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism		nr -
Unigene49209_All	1047	0.00	0.68	0.05	3.52	6.38	3.36	2.06	1.48	4.07	9.40E+00	3.32E-04	Up	5.67E+00	6.35E-01		8.58E-01	7.46E-05		-6.55E-02	8.60E-01			-4.80E-01	2.34E-01		9.83E-01	1.41E-04		Unigene49209_All//gi|15218093|ref|NP_173523.1|//2.00E-75//DC1 domain-containing protein [Arabidopsis thaliana]	Unigene49209_All//2.00E-68//AT1G20990| DC1 domain-containing protein	Unigene49209_All//2.00E-39//ES821810				nr -
Unigene4921_All	1663	7.24	2.89	3.30	14.29	9.36	7.58	9.58	2.69	5.34	-1.32E+00	3.47E-14	Down	-1.13E+00	8.71E-11	Down	-6.10E-01	2.45E-09		-9.15E-01	1.84E-16			-1.83E+00	5.94E-36	Down	-8.43E-01	1.17E-11		Unigene4921_All//gi|15221371|ref|NP_172712.1|//1.00E-151//phosphate translocator-related [Arabidopsis thaliana] >gi|8778643|gb|AAF79651.1|AC025416_25 F5O11.25 [Arabidopsis thaliana] >gi|9502394|gb|AAF88101.1|AC025417_29 T12C24.5 [Arabidopsis thaliana]	Unigene4921_All//4.00E-140//AT1G12500| phosphate translocator-related	Unigene4921_All//0.00E+00//TC148253				nr -

Unigene49213_All	1243	16.33	34.89	13.41	17.75	22.00	23.14	23.57	32.52	30.96	1.10E+00	1.41E-36	Up	-2.85E-01	3.05E-02		3.09E-01	2.09E-03		3.83E-01	1.16E-04		4.64E-01	5.42E-10		3.93E-01	1.75E-07		Unigene49213_All//gi|92948810|gb|AAF86687.1|//7.00E-25//MTD1 [Medicago truncatula]	Unigene49213_All//3.00E-17//AT5G21940| unknown protein	Unigene49213_All//0.00E+00//gi|48777652|gb|CO087018.1|CO087018				nr -
Unigene49217_All	946	66.92	52.28	102.45	12.74	17.69	21.63	3.49	3.36	1.26	-3.56E-01	5.78E-08		6.14E-01	1.53E-29		4.73E-01	2.32E-04		7.63E-01	1.64E-10		-5.41E-02	8.76E-01		-1.46E+00	2.75E-06	Down	Unigene49217_All//gi|15236688|ref|NP_191914.1|//1.00E-74//plastid-lipid associated protein PAP / fibrillin family protein [Arabidopsis thaliana] >gi|75100154|sp|Q81304.1|PAP11_ARATH RecName: Full=Probable plastid-lipid-associated protein 11, chloroplastic; AltName: Full=Fibrillin-11; Flags: Precursor >gi|3193328|gb|AAC19310.1| F6N15.13 gene product [Arabidopsis thaliana] >gi|15899917|gb|AAL06886.1| AT4g00030/F6N15_13 [Arabidopsis thaliana] >gi|18377823|gb|AAL67098.1| AT4g00030/F6N15_13 [Arabidopsis thaliana]	Unigene49217_All//7.00E-76//AT4G00030| plastid-lipid associated protein PAP / fibrillin family protein	Unigene49217_All//0.00E+00//TC157042				nr -
Unigene4922_All	1257	19.56	15.16	20.88	22.95	27.29	24.94	16.18	7.45	7.10	-3.68E-01	8.58E-04		9.43E-02	4.48E-01		2.50E-01	5.69E-03		1.20E-01	2.95E-01		-1.12E+00	3.42E-22	Down	-1.19E+00	4.31E-25	Down	Unigene4922_All//gi|15225693|ref|NP_180811.1|//1.00E-112//dienelactone hydrolase family protein [Arabidopsis thaliana] >gi|30102612|gb|AAP21224.1| At2g32520 [Arabidopsis thaliana]	Unigene4922_All//2.00E-100//AT2G32520| dienelactone hydrolase family protein	Unigene4922_All//0.00E+00//TC137179				nr -
Unigene49222_All	811	19.48	75.29	12.28	13.21	27.26	22.28	33.26	45.92	48.04	1.95E+00	6.70E-120	Up	-6.66E-01	4.33E-06		1.05E+00	1.62E-20	Up	7.54E-01	3.52E-09		4.65E-01	2.58E-09		5.31E-01	1.91E-12		Unigene49222_All//gi|56542451|gb|AAV92890.1|//1.00E-42//Avr9/Cf-9 rapidly elicited protein 20 [Nicotiana tabacum]	Unigene49222_All//6.00E-33//AT4G27280| calcium-binding EF hand family protein	Unigene49222_All//0.00E+00//gi|84157005|gb|DN818231.1|DN818231		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr +
Unigene49224_All	296	0.71	14.04	1.80	3.37	4.65	7.93	0.57	0.00	0.00	4.31E+00	1.31E-18	Up	1.35E+00	2.25E-01		4.67E-01	4.51E-01		1.24E+00	3.56E-03		-9.16E+00	1.34E-01		-9.16E+00	1.08E-01		Unigene49224_All//gi|16648748|gb|AAL25566.1|//1.00E-06//AT5g02020/T7H20_70 [Arabidopsis thaliana] >gi|20334906|gb|AAM16209.1| AT5g02020/T7H20_70 [Arabidopsis thaliana]	Unigene49224_All//5.00E-08//AT5G02020| unknown protein	Unigene49224_All//8.00E-153//ES851721				nr +
Unigene49225_All	931	2.25	30.37	3.15	4.07	10.65	8.49	0.86	1.03	0.73	3.76E+00	8.80E-113	Up	4.85E-01	2.16E-01		1.39E+00	2.05E-14	Up	1.06E+00	2.85E-07	Up	2.59E-01	6.78E-01		-2.46E-01	7.00E-01		Unigene49225_All//gi|16648748|gb|AAL25566.1|//7.00E-32//AT5g02020/T7H20_70 [Arabidopsis thaliana] >gi|20334906|gb|AAM16209.1| AT5g02020/T7H20_70 [Arabidopsis thaliana]	Unigene49225_All//3.00E-33//AT5G02020| unknown protein	Unigene49225_All//0.00E+00//TC136399				nr +
Unigene49229_All	1318	3.33	2.65	1.86	16.33	20.82	8.98	1.12	0.79	0.06	-3.30E-01	2.69E-01		-8.43E-01	5.18E-03		3.51E-01	3.72E-04		-8.63E-01	1.33E-13		-5.02E-01	3.26E-01		-4.21E+00	1.00E-08	Down	Unigene49229_All//gi|15229741|ref|NP_187746.1|//8.00E-48//DC1 domain-containing protein [Arabidopsis thaliana]	Unigene49229_All//4.00E-49//AT3G11390| DC1 domain-containing protein	Unigene49229_All//6.00E-37//CO092998				nr -
Unigene4923_All	852	30.89	28.55	26.88	32.33	30.60	34.67	43.77	25.90	21.65	-1.14E-01	3.50E-01		-2.01E-01	8.71E-02		-7.97E-02	5.49E-01		1.01E-01	4.05E-01		-7.57E-01	3.75E-21		-1.02E+00	2.75E-35	Down	Unigene4923_All//gi|195604664|gb|AGZ4162.1|//2.00E-58//small nuclear ribonucleoprotein Sm D1 [Zea mays]	Unigene4923_All//9.00E-48//AT4G02840| small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative	Unigene4923_All//0.00E+00//TC145706		ko03040|Spliceosome		nr +
Unigene49232_All	2224	1.51	0.14	0.93	0.38	0.39	1.04	8.38	5.26	1.58	-3.46E+00	4.89E-13	Down	-6.89E-01	5.14E-02		2.37E-02	9.92E-01		1.44E+00	9.32E-04	Up	-6.72E-01	4.44E-09		-2.41E+00	4.20E-61	Down	Unigene49232_All//gi|223452302|gb|ACM89479.1|//1.00E-141//cysteine-rich protein [Glycine max]	Unigene49232_All//2.00E-132//AT4G23180| CRK10 (CYSTEINE-RICH RLK(10): ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene49232_All//1.00E-08//TC154318		ko04626|Plant-pathogen interaction		nr +
Unigene49233_All	1231	1.91	1.07	0.13	0.77	0.95	1.28	1.20	13.68	6.57	-8.38E-01	4.35E-02		-3.88E+00	1.31E-09	Down	3.07E-01	6.58E-01		7.40E-01	1.79E-01		3.51E+00	3.27E-78	Up	2.45E+00	4.93E-27	Up	Unigene49233_All//gi|224075092|ref|XP_002304554.1|//3.00E-88//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222841986|gb|EEE79533.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene49233_All//4.00E-33//AT1G64380| AP2 domain-containing transcription factor, putative	Unigene49233_All//0.00E+00//gi|78334234|gb|DT554508.1|DT554508	AP2-EREBP			nr -
Unigene49235_All	582	0.81	0.87	0.37	0.60	0.95	1.24	2.47	3.45	11.36	1.06E-01	9.22E-01		-1.14E+00	3.32E-01		6.60E-01	5.44E-01		1.05E+00	2.35E-01		4.81E-01	2.53E-01		2.20E+00	1.15E-19	Up	Unigene49235_All//gi|297794409|ref|XP_002865089.1|//3.00E-09//phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310924|gb|EFH41348.1| phosphoinositide phosphatase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49235_All//2.00E-10//AT5G66020| ATSAC1B (SUPPRESSOR OF ACTIN 1B); phosphatidylinositol-4,5-bisphosphate 5-phosphatase	Unigene49235_All//0.00E+00//TC150500				nr -
Unigene49236_All	785	5.53	8.00	3.87	6.16	7.90	9.72	9.80	15.39	28.57	5.33E-01	2.45E-02		-5.17E-01	9.31E-02		3.59E-01	1.50E-01		6.60E-01	1.56E-03		6.51E-01	7.27E-06		1.54E+00	2.50E-40	Up	Unigene49236_All//gi|145359710|ref|NP_201403.2|//2.00E-80//ATSAC1B (SUPPRESSOR OF ACTIN 1B); phosphatidylinositol-4,5-bisphosphate 5-phosphatase [Arabidopsis thaliana] >gi|30840665|gb|AAP41367.1|AF266458_1 SAC1-like protein AtSAC1b [Arabidopsis thaliana] >gi|31415729|gb|AAP49839.1| SAC domain protein 6 [Arabidopsis thaliana]	Unigene49236_All//4.00E-76//AT5G66020| ATSAC1B (SUPPRESSOR OF ACTIN 1B); phosphatidylinositol-4,5-bisphosphate 5-phosphatase	Unigene49236_All//5.00E-110//DV848639				nr +
Unigene4924_All	1159	3.21	1.22	1.56	3.57	6.51	5.18	0.66	0.07	0.14	-1.39E+00	3.01E-05	Down	-1.04E+00	2.00E-03		8.67E-01	1.71E-05		5.39E-01	2.77E-02		-3.19E+00	7.92E-04	Down	-2.26E+00	4.68E-03		Unigene4924_All//gi|55375996|gb|AAV50009.1|//1.00E-84//anthranilate N-hydroxycinnamoyl/benzoyltransferase [Malus x domestica]	Unigene4924_All//3.00E-57//AT5G67150| transferase family protein	Unigene4924_All//0.00E+00//TC150605		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene49240_All	922	3.86	2.86	1.50	4.97	4.26	2.20	4.04	0.59	0.60	-4.33E-01	1.94E-01		-1.36E+00	1.17E-04	Down	-2.23E-01	4.78E-01		-1.17E+00	3.11E-05	Down	-2.78E+00	2.40E-14	Down	-2.74E+00	1.16E-14	Down	Unigene49240_All//gi|30678256|ref|NP_171720.2|//3.00E-71//ferredoxin-related [Arabidopsis thaliana]	Unigene49240_All//1.00E-71//AT1G02180| ferredoxin-related	Unigene49240_All//0.00E+00//TC157026				nr +
Unigene49241_All	238	20.66	51.52	90.39	6.70	1.16	4.17	2.49	4.04	0.00	1.32E+00	2.62E-14	Up	2.13E+00	1.98E-46	Up	-2.53E+00	6.66E-06	Down	-6.82E-01	2.07E-01		7.00E-01	2.78E-01		-1.13E+01	1.41E-04	Down	Unigene49241_All//gi|238055376|sp|B9RT03.1|U4974_RICCO//8.00E-09//RecName: Full=UPF0497 membrane protein 4	Unigene49241_All//3.00E-06//AT4G15610| integral membrane family protein	Unigene49241_All//1.00E-129//TC175023				nr +
Unigene49242_All	893	43.94	141.57	187.72	13.72	8.95	10.12	10.27	12.03	6.83	1.69E+00	3.19E-203	Up	2.09E+00	0.00E+00	Up	-6.17E-01	3.45E-05		-4.40E-01	6.30E-03		2.28E-01	1.79E-01		-5.90E-01	3.29E-04		Unigene49242_All//gi|238055376|sp|B9RT03.1|U4974_RICCO//5.00E-58//RecName: Full=UPF0497 membrane protein 4	Unigene49242_All//2.00E-27//AT3G06390| integral membrane family protein	Unigene49242_All//0.00E+00//TC175023				nr +
Unigene49245_All	847	4.82	13.82	6.41	32.23	43.58	62.87	24.51	31.04	10.16	1.52E+00	8.71E-17	Up	4.12E-01	1.36E-01		4.35E-01	9.61E-08		9.64E-01	5.04E-39		3.41E-01	3.49E-04		-1.27E+00	2.44E-28	Down	Unigene49245_All//gi|18395194|ref|NP_564187.1|//3.00E-21//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|2829907|gb|AAC00615.1| Unknown protein [Arabidopsis thaliana] >gi|98960877|gb|ABF58922.1| At1g23040 [Arabidopsis thaliana]		Unigene49245_All//0.00E+00//gi|164334763|gb|ES799827.1|ES799827		ko03040|Spliceosome		nr +
Unigene49249_All	1539	1.87	1.25	0.45	6.21	6.15	9.07	3.19	6.65	10.51	-5.80E-01	1.19E-01		-2.06E+00	2.21E-06	Down	-1.43E-02	9.54E-01		5.45E-01	2.21E-04		1.06E+00	1.10E-10	Up	1.72E+00	3.89E-34	Up	Unigene49249_All//gi|15229832|ref|NP_190639.1|//4.00E-98//AtIDD2 (Arabidopsis thaliana Indeterminate(ID)-Domain 2); nucleic acid binding / transcription factor/ zinc ion binding >gi|6561973|emb|CAB62439.1| zinc finger protein [Arabidopsis thaliana] >gi|89858491|gb|AAT47798.1| At3g50700 [Arabidopsis thaliana] >gi|53828579|gb|AAU94399.1| At3g50700 [Arabidopsis thaliana] >gi|110742152|dbj|BAE99004.1| zinc finger protein [Arabidopsis thaliana]	Unigene49249_All//8.00E-79//AT3G50700| AtIDD2 (Arabidopsis thaliana Indeterminate(ID)-Domain 2); nucleic acid binding / transcription factor/ zinc ion binding	Unigene49249_All//0.00E+00//TC178143	C2H2			nr +
Unigene49250_All	2029	0.00	0.05	0.05	9.92	21.74	27.22	10.54	17.84	20.16	5.64E+00	3.86E-01		5.71E+00	3.97E-01		1.13E+00	3.69E-46	Up	1.46E+00	2.70E-77	Up	7.59E-01	1.30E-20		9.35E-01	1.39E-33		Unigene49250_All//gi|186511048|ref|NP_974431.2|//0.00E+00//transporter [Arabidopsis thaliana] >gi|72583348|emb|CAB77565.1| oligopeptide transporter-like protein [Arabidopsis thaliana]	Unigene49250_All//0.00E+00//AT3G54450| transporter	Unigene49250_All//1.00E-149//gi|78341949|gb|DT562223.1|DT562223				nr -
Unigene49252_All	3944	0.00	0.26	0.34	0.39	0.23	0.37	8.20	47.89	32.61	8.01E+00	7.25E-06	Up	8.40E+00	2.40E-07	Up	-7.86E-01	1.28E-01		-9.56E-02	8.64E-01		2.55E+00	0.00E+00	Up	1.99E+00	0.00E+00	Up	Unigene49252_All//gi|225437164|ref|XP_002274787.1|//0.00E+00//PREDICTED: similar to type IIB calcium ATPase [Vitis vinifera]	Unigene49252_All//0.00E+00//AT3G63380| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12)	Unigene49252_All//0.00E+00//ES840734				nr -
Unigene49253_All	464	0.79	1.20	2.07	1.72	1.19	0.58	4.37	3.42	1.55	6.06E-01	5.31E-01		1.39E+00	7.11E-02		-5.33E-01	5.10E-01		-1.56E+00	6.26E-02		-3.54E-01	4.02E-01		-1.50E+00	2.57E-04	Down	Unigene49253_All//gi|195627022|gb|ACG35341.1|//4.00E-28//ATP binding protein [Zea mays]	Unigene49253_All//6.00E-29//AT3G01490| protein kinase, putative	Unigene49253_All//4.00E-119//TC179076				nr +
Unigene49254_All	922	1.65	3.19	3.87	0.70	1.83	1.52	1.70	0.82	0.39	9.54E-01	9.42E-03		1.23E+00	3.90E-04	Up	1.38E+00	7.12E-03		1.11E+00	5.66E-02		-1.06E+00	2.63E-02		-2.13E+00	3.93E-05	Down	Unigene49254_All//gi|16323087|gb|AAL15278.1|//1.00E-56//AT3g01490/F4P13_4 [Arabidopsis thaliana] >gi|110742522|dbj|BAE99178.1| protein kinase like protein [Arabidopsis thaliana]	Unigene49254_All//6.00E-58//AT3G01490| protein kinase, putative	Unigene49254_All//0.00E+00//DW232922				nr +
Unigene49255_All	1195	0.00	1.06	0.45	2.83	22.53	35.79	2.94	17.38	10.80	1.00E+01	2.86E-07	Up	8.80E+00	4.03E-03		2.99E+00	1.90E-101	Up	3.66E+00	1.13E-178	Up	2.57E+00	1.47E-70	Up	1.88E+00	8.38E-31	Up	Unigene49255_All//gi|110737096|dbj|BAF00500.1|//1.00E-95//thaumatin-like protein [Arabidopsis thaliana]	Unigene49255_All//2.00E-96//AT4G38660| thaumatin, putative	Unigene49255_All//1.00E-105//gi|78346648|gb|DT566922.1|DT566922				nr -
Unigene49256_All	1784	1.00	4.83	0.24	4.24	4.56	3.01	6.23	7.59	41.51	2.28E+00	4.32E-21	Up	-2.06E+00	3.27E-04	Down	1.02E-01	6.83E-01		-4.95E-01	2.02E-02		2.84E-01	4.59E-02		2.74E+00	1.79E-273	Up	Unigene49256_All//gi|75223238|sp|Q80871.1|P2C25_ARATH//1.00E-129//RecName: Full=Probable protein phosphatase 2C 25; Short=AtPP2C25; AltName: Full=Protein phosphatase AP2C1	Unigene49256_All//2.00E-106//AT2G30020| protein phosphatase 2C, putative / PP2C, putative	Unigene49256_All//0.00E+00//TC145094				nr -
Unigene49258_All	870	8.78	25.10	14.26	58.00	59.25	64.16	21.92	26.57	15.94	1.52E+00	1.46E-30	Up	7.00E-01	2.47E-05		3.08E-02	7.77E-01		1.46E-01	5.75E-02		2.78E-01	7.79E-03		-4.60E-01	2.85E-05		Unigene49258_All//gi|225457681|ref|XP_002276622.1|//2.00E-11//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene49258_All//2.00E-06//AT1G76560| CP12-3	Unigene49258_All//6.00E-141//gi|109831625|gb|DW230184.1|DW230184				nr -

Unigene49260_All	1055	3.22	2.83	0.45	1.89	2.97	1.80	6.01	3.41	2.87	-1.86E-01	6.17E-01		-2.83E+00	1.76E-10	Down	6.53E-01	6.35E-02		-7.10E-02	8.92E-01		-8.19E-01	8.81E-05		-1.07E+00	3.13E-07	Down	Unigene49260_All//gi|18396383|ref|NP_566188.1|//1.00E-68//replication protein-related [Arabidopsis thaliana] >gi|90186248|gb|ABD91500.1|At3g02920 [Arabidopsis thaliana]	Unigene49260_All//8.00E-58//AT3G02920| replication protein-related	Unigene49260_All//0.00E+00//gi|78343070|gb|DT563344.1|DT563344		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +
Unigene49261_All	588	39.15	26.46	22.46	82.09	63.42	47.47	29.05	12.44	12.81	-5.66E-01	6.59E-07		-8.02E-01	1.49E-11		-3.72E-01	1.00E-07		-7.90E-01	1.06E-25		-1.22E+00	1.64E-21	Down	-1.18E+00	4.86E-21	Down	Unigene49261_All//gi|18403359|ref|NP_564591.1|//5.00E-15//Y14; RNA binding / protein binding [Arabidopsis thaliana]	Unigene49261_All//4.00E-09//AT1G51510| Y14; RNA binding / protein binding	Unigene49261_All//0.00E+00//DW513067		ko03040|Spliceosome		nr −
Unigene49262_All	874	1.80	3.71	4.26	9.12	9.97	8.42	19.21	22.81	20.69	1.05E+00	2.71E-03		1.25E+00	2.39E-04	Up	1.28E-01	5.82E-01		-1.15E-01	6.31E-01		2.48E-01	3.14E-02		1.08E-01	4.03E-01		Unigene49262_All|gi|164564739|dbj|BAF98220.1|//1.00E-19//CM02216.380.nc [Lotus japonicus]	Unigene49262_All//6.00E-26//AT4G34560| unknown protein	Unigene49262_All//2.00E-137//gi|109890961|gb|DW519924.1|DW519924				nr +
Unigene49265_All	1612	0.55	0.66	0.07	0.93	0.75	0.76	6.24	12.24	28.07	2.59E-01	6.75E-01		-3.06E+00	2.25E-03		-3.10E-01	5.87E-01		-2.93E-01	6.38E-01		9.71E-01	3.10E-17		2.17E+00	1.13E-127	Up	Unigene49265_All//gi|297817714|ref|XP_002876740.1|//2.00E-71//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322578|gb|EFH52999.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49265_All//3.00E-66//AT2G01275| zinc finger (C3HC4-type RING finger) family protein	Unigene49265_All//0.00E+00//TC157689		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene49267_All	1237	4.19	16.63	11.11	1.81	4.18	4.71	0.07	0.10	1.99E+00	7.32E-42	Up	1.41E+00	6.35E-17	Up	1.20E+00	2.66E-06	Up	1.38E+00	5.50E-08	Up	-1.70E-02	1.01E+00		4.98E-01	8.07E-01		Unigene49267_All//gi|6671365|gb|AAF23176.1|AF216497_1//1.00E-162//P-glycoprotein [Gossypium hirsutum]	Unigene49267_All//3.00E-138//AT4G25960| PGP2 (P-GLYCOPROTEIN 2); ATPase, coupled to transmembrane movement of substances	Unigene49267_All//0.00E+00//TC176290		ko02010|ABC transporters		nr +
Unigene49269_All	1438	0.22	0.70	0.26	3.91	2.56	2.73	2.65	1.05	2.94	1.69E+00	2.14E-02		2.48E-01	8.22E-01		-6.11E-01	9.99E-03		-5.19E-01	4.07E-02		-1.34E+00	4.28E-06	Down	1.50E-01	6.20E-01		Unigene49269_All|gi|38566688|gb|AAR24234.1|//1.00E-123//At5g62960 [Arabidopsis thaliana] >gi|38604058|gb|AAR24772.1|At5g62960 [Arabidopsis thaliana]	Unigene49269_All//1.00E-111//AT5G62960| unknown protein	Unigene49269_All//2.00E-15//TC172964				nr +
Unigene4927_All	957	13.39	10.48	8.79	33.26	27.35	17.93	8.84	3.67	4.33	-3.54E-01	2.74E-02		-6.08E-01	1.96E-04		-2.83E-01	2.08E-03		-8.91E-01	6.28E-21		-1.27E+00	1.20E-11	Down	-1.03E+00	7.25E-09	Down	Unigene4927_All|gi|2673910|gb|AAB88614.1|//3.00E-34//expressed protein [Arabidopsis thaliana]	Unigene4927_All//2.00E-24//AT2G42190| unknown protein	Unigene4927_All//0.00E+00//gi|164251257|gb|ES803157.1|ES803157				nr −
Unigene49271_All	979	1.76	5.59	5.98	36.18	38.66	29.62	1034.94	217.94	306.83	1.66E+00	2.78E-09	Up	1.76E+00	3.10E-10	Up	9.56E-02	3.56E-01		-2.89E-01	1.35E-03		-2.25E+00	0.00E+00	Down	-1.75E+00	0.00E+00	Down	Unigene49271_All|gi|283132357|dbj|BAI63584.1|//1.00E-68//component of high affinity nitrate transporter [Lotus japonicus]	Unigene49271_All//1.00E-44//AT5G50200| WR3 (WOUND-RESPONSIVE 3); nitrate transmembrane transporter	Unigene49271_All//0.00E+00//gi|78352940|gb|DT573214.1|DT573214				nr +
Unigene49272_All	593	2.74	12.39	10.78	1.43	0.81	0.99	3.35	3.10	17.13	2.18E+00	3.46E-17	Up	1.98E+00	6.89E-13	Up	-8.13E-01	2.80E-01		-5.29E-01	5.02E-01		-1.12E-01	7.93E-01		2.35E+00	3.04E-32	Up	Unigene49272_All|gi|3337365|gb|AAC27410.1|//6.00E-22//expressed protein [Arabidopsis thaliana] >gi|28416871|gb|AAO42966.1|At2g34340 [Arabidopsis thaliana]	Unigene49272_All//4.00E-19//AT1G29640| unknown protein					nr −
Unigene49277_All	1051	6.52	33.51	6.89	7.25	9.17	13.28	49.88	80.41	93.40	2.36E+00	3.25E-88	Up	7.94E-02	7.31E-01		3.39E-01	7.34E-02		8.73E-01	4.18E-09		6.89E-01	7.46E-40		9.05E-01	4.48E-75		Unigene49277_All|gi|116643154|gb|ABK06394.1|//5.00E-61//Ca2+-binding protein [Citrus sinensis]	Unigene49277_All//1.00E-46//AT5G44460| calcium-binding protein, putative	Unigene49277_All//0.00E+00//TC168789		ko04626|Plant-pathogen interaction		nr −
Unigene4928_All	395	14.04	7.18	12.40	1.01	4.01	6.86	0.00	0.00	0.40	-9.67E-01	1.51E-04		-1.79E-01	5.33E-01		1.99E+00	4.24E-04	Up	2.77E+00	4.90E-09	Up	null	null		8.66E+00	1.40E-01		Unigene4928_All|gi|38346337|emb|CAD40655.2|//3.00E-37//OSJNBa0073L04.8 [Oryza sativa (japonica cultivar-group)]	Unigene4928_All//4.00E-37//AT2G27500| glycosyl hydrolase family 17 protein	Unigene4928_All//9.00E-169//DR456934		ko00500|Starch and sucrose metabolism		nr +
Unigene49281_All	944	2.11	0.97	0.79	11.56	13.72	6.12	5.11	2.17	3.33	-1.12E+00	1.53E-02		-1.42E+00	4.48E-03		2.47E-01	1.40E-01		-9.16E-01	6.53E-08		-1.23E+00	1.01E-06	Down	-6.15E-01	9.13E-03		Unigene49281_All|gi|5902371|gb|AAD55473.1|AC009322|3/2.00E-71//Hypothetical protein [Arabidopsis thaliana]	Unigene49281_All//4.00E-69//AT1G80160| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene49281_All//0.00E+00//TC137625				nr −
Unigene49282_All	795	19.88	20.08	20.63	21.93	21.83	24.48	4.73	3.84	1.80	1.45E-02	9.41E-01		5.38E-02	7.24E-01		-6.60E-03	9.63E-01		1.59E-01	2.72E-01		-3.03E-01	3.25E-01		-1.39E+00	1.34E-06	Down	Unigene49282_All//gi|2288994|gb|AAB64323.1|//1.00E-40//expressed protein [Arabidopsis thaliana] >gi|194708808|gb|ACF88488.1|At2g43540 [Arabidopsis thaliana]	Unigene49282_All//1.00E-29//AT2G43540| unknown protein	Unigene49282_All//2.00E-171//ES814895				nr −
Unigene49284_All	1517	0.41	3.34	3.09	9.26	6.13	6.70	0.78	0.00	0.26	3.01E+00	5.12E-17	Up	2.90E+00	1.04E-14	Up	-5.95E-01	1.58E-05		-4.67E-01	1.57E-03		-9.61E+00	1.97E-08	Down	-1.57E+00	5.26E-03		Unigene49284_All//gi|15221078|ref|NP_175244.1|//0.00E+00//glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana] >gi|75306312|sp|Q94921.1|PGLR4_ARATH RecName: Full=Polygalacturonase At1g48100; Short=PG; AltName: Full=Pectinase At1g48100; Flags: Precursor	Unigene49284_All//0.00E+00//AT1G48100| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene49284_All//0.00E+00//TC131867		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr −
Unigene49285_All	797	25.54	33.44	28.26	56.69	59.19	81.83	254.21	574.86	202.24	3.89E-01	2.24E-04		1.46E-01	2.71E-01		6.23E-02	5.41E-01		5.30E-01	3.98E-17		1.18E+00	0.00E+00	Up	-3.30E-01	7.17E-26		Unigene49285_All|gi|146432261|gb|ABQ41114.1|//1.00E-86//monodehydroascorbate reductase [Vitis vinifera]	Unigene49285_All//8.00E-81//AT5G03630| ATMDAR2; monodehydroascorbate reductase (NADH)	Unigene49285_All//0.00E+00//gi|164307925|gb|ES807660.1|ES807660		ko00053|Ascorbate and aldarate metabolism		nr +
Unigene49286_All	914	1.43	4.44	3.61	2.73	3.05	2.22	2.73	2.29	1.31	1.63E+00	6.72E-07	Up	1.34E+00	2.75E-04	Up	1.63E-01	7.23E-01		-2.93E-01	5.03E-01		-2.55E-01	5.23E-01		-1.06E+00	2.35E-03		Unigene49286_All//gi|58532129|emb|CAE04131.3|//2.00E-52//OSJNBa0009P12.18 [Oryza sativa (japonica cultivar-group)]		Unigene49286_All//0.00E+00//gi|21101178|gb|BQ413491.1|BQ413491				nr +
Unigene49288_All	925	1.24	0.44	0.58	2.53	1.90	2.49	3.84	1.40	1.46	-1.51E+00	2.31E-02		-1.11E+00	9.93E-02		-4.15E-01	3.25E-01		-2.36E-02	9.45E-01		-1.45E+00	2.12E-06	Down	-1.39E+00	2.86E-06	Down	Unigene49288_All//gi|15221232|ref|NP_172058.1|//2.00E-94//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|238478356|ref|NP_001154307.1|UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|4836917|gb|AAD30619.1|AC007153_11 similar to indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]	Unigene49288_All//1.00E-95//AT1G05670| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene49288_All//0.00E+00//ES801156				nr −
Unigene49289_All	478	18.17	3.39	10.14	6.15	3.53	2.65	1.06	1.66	0.25	-2.42E+00	4.95E-23	Down	-8.42E-01	3.74E-05		-8.01E-01	2.04E-02		-1.22E+00	8.86E-04	Down	6.46E-01	3.83E-01		-2.09E+00	3.64E-02		Unigene49289_All|gi|294992077|gb|ABG90381.2|//7.00E-57//glutathione S-transferase [Caragana korshinskii]	Unigene49289_All//3.00E-52//AT1G78380| ATGSTU19 (GLUTATHIONE S-TRANSFERASE TAU 19); glutathione binding / glutathione transferase	Unigene49289_All//1.00E-162//TC154023		ko00480|Glutathione metabolism		nr +
Unigene4929_All	1281	16.13	10.48	15.42	1.83	2.39	5.43	0.00	0.52	1.21	-6.22E-01	2.66E-07		-6.50E-02	6.27E-01		3.89E-01	3.08E-01		1.57E+00	2.68E-11	Up	9.03E+00	7.64E-05	Up	1.02E+01	3.54E-11	Up	Unigene4929_All|gi|18401444|ref|NP_565652.1|//1.00E-148//glycosyl hydrolase family 17 protein [Arabidopsis thaliana] >gi|75216237|sp|Q9ZQG9.2|E1314_ARATH RecName: Full=Glucan endo-1,3-beta-glucosidase 14; AltName: Full=(1->3)-beta-glucan endohydrolase 14; Short=(1->3)-beta-glucanase 14; AltName: Full=Beta-1,3-endoglucanase 14; Short=Beta-1,3-glucanase 14; Flags: Precursor	Unigene4929_All//4.00E-148//AT2G27500| glycosyl hydrolase family 17 protein	Unigene4929_All//0.00E+00//DR456934		ko00500|Starch and sucrose metabolism		nr +
Unigene49290_All	781	170.03	85.57	130.77	59.13	43.17	38.17	84.89	53.30	29.74	-9.91E-01	2.89E-94		-3.79E-01	6.30E-17		-4.54E-01	1.73E-10		-6.32E-01	8.85E-17		-6.71E-01	4.14E-30		-1.51E+00	2.19E-115	Down	Unigene49290_All//gi|29419702|gb|AA061854.1|//3.00E-80//glutathione S-transferase U1 [Malva pusilla]	Unigene49290_All//8.00E-72//AT1G17180| ATGSTU25 (GLUTATHIONE S-TRANSFERASE TAU 25); glutathione transferase	Unigene49290_All//0.00E+00//TC146318		ko00480|Glutathione metabolism		nr +
Unigene49291_All	851	14.08	36.26	27.09	12.53	33.50	41.34	14.81	5.35	17.60	1.36E+00	8.89E-37	Up	9.44E-01	4.26E-15		1.42E+00	3.09E-42	Up	1.72E+00	8.24E-63	Up	-1.47E+00	5.43E-21	Down	2.50E-01	5.72E-02		Unigene49291_All//gi|115477795|ref|NP_001062493.1|//4.00E-51//Os08g0558300 [Oryza sativa Japonica Group] >gi|113624462|dbj|BAF24407.1|Os08g0558300 [Oryza sativa Japonica Group]	Unigene49291_All//2.00E-62//AT3G44380| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Water Stress and Hypersensitive response (InterPro:IPR013990), Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G52330.1); Has 88 Blast hits to 87 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 88; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene49291_All//0.00E+00//TC149288				nr −
Unigene49293_All	762	11.12	5.79	4.96	14.19	21.38	12.15	11.93	1.32	1.93	-9.43E-01	2.79E-06		-1.16E+00	4.18E-08	Down	5.92E-01	4.55E-06		-2.24E-01	2.44E-01		-3.18E+00	4.90E-39	Down	-2.62E+00	3.30E-33	Down	Unigene49293_All//gi|13926242|gb|AAK49595.1|AF372879_1//2.00E-25//AT4g15140/d13815c [Arabidopsis thaliana] >gi|27764958|gb|AAO23600.1|At4g15140/d13815c [Arabidopsis thaliana]	Unigene49293_All//9.00E-20//AT4G15140| unknown protein	Unigene49293_All//0.00E+00//gi|109842161|gb|DW240721.1|DW240721				nr +
Unigene49294_All	1382	1.70	3.56	0.96	4.22	4.58	4.02	1.41	1.09	2.80	1.06E+00	1.19E-04	Up	-8.23E-01	5.86E-02		1.21E-01	6.67E-01		-6.93E-02	7.95E-01		-3.70E-01	3.99E-01		9.91E-01	2.84E-04		Unigene49294_All//gi|2765442|emb|CAA75349.1|//1.00E-21//ERT2 [Arabidopsis thaliana]	Unigene49294_All//7.00E-20//AT4G20880| ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2)	Unigene49294_All//0.00E+00//ES802090				nr +
Unigene49295_All	1259	21.78	6.92	21.49	8.59	7.71	3.30	1.58	0.76	0.16	-1.65E+00	1.64E-43	Down	-1.93E-02	8.78E-01		-1.55E-01	4.40E-01		-1.38E+00	1.43E-14	Down	-1.05E+00	1.11E-02		-3.32E+00	1.06E-09	Down	Unigene49295_All|gi|18417976|ref|NP_567891.1|//2.00E-18//IAA29 (INDOLE-3-ACETIC ACID INDUCIBLE 29); transcription factor [Arabidopsis thaliana] >gi|46395937|sp|Q93MC4.2|IAA29_ARATH RecName: Full=Auxin-responsive protein IAA29; AltName: Full=Indoleacetic acid-induced protein 29 >gi|49616375|gb|AAT67084.1| IAA29 [Arabidopsis thaliana]	Unigene49295_All//1.00E-18//AT4G32280| IAA29 (INDOLE-3-ACETIC ACID INDUCIBLE 29); transcription factor	Unigene49295_All//0.00E+00//gi|164367280|gb|ES791206.1|ES791206				nr +
Unigene49296_All	573	13.61	24.94	51.86	47.73	51.50	21.75	81.83	65.14	32.68	8.74E-01	6.85E-09		1.93E+00	2.37E-56	Up	1.10E-01	3.48E-01		-1.13E+00	1.29E-26	Down	-3.29E-01	1.94E-06		-1.32E+00	4.96E-67	Down	Unigene49296_All//gi|224088316|ref|XP_002308410.1|//4.00E-34//stress-induced hydrophobic peptide [Populus trichocarpa] >gi|222854386|gb|EEE91933.1|stress-induced hydrophobic peptide [Populus trichocarpa]	Unigene49296_All//1.00E-22//AT4G28088| hydrophobic protein, putative / low temperature and salt responsive protein, putative	Unigene49296_All//0.00E+00//gi|21092082|gb|BQ404395.1|BQ404395				nr +
Unigene49297_All	1380	0.30	0.15	0.00	22.81	13.50	7.69	2.60	28.23	1.41	-1.05E+00	3.65E-01		-8.24E+00	1.56E-02		-7.57E-01	1.10E-17		-1.57E+00	3.96E-50	Down	3.44E+00	3.65E-177	Up	-8.80E-01	1.69E-03		Unigene49297_All//gi|6651292|gb|AAF22256.1|//1.00E-96//myb-related transcription factor [Pimpinella brachycarpa]	Unigene49297_All//7.00E-87//AT4G12350| MYB42 (myb domain protein 42); transcription factor	Unigene49297_All//0.00E+00//gi|78325016|gb|DT545290.1|DT545290	MYB			nr −

Unigene49300_All	1076	10.89	5.37	6.53	2.96	5.09	5.54	0.16	0.08	0.19	-1.02E+00	1.99E-09	Down	-7.38E-01	1.75E-05		7.80E-01	1.40E-03		9.03E-01	1.74E-04		-1.02E+00	6.14E-01		2.36E-01	8.83E-01		Unigene49300_All//gi|15221010|ref|NP_175225.1|//1.00E-61//AtRLP7 (Receptor Like Protein 7); kinase/ protein binding [Arabidopsis thaliana]	Unigene49300_All//2.00E-48//AT1G47890| AtRLP7 (Receptor Like Protein 7); kinase/ protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene49303_All	1469	0.43	2.76	1.16	2.81	1.95	1.66	0.72	1.93	1.11	2.69E+00	2.71E-12	Up	1.44E+00	8.27E-03		-5.33E-01	6.87E-02		-7.62E-01	1.03E-02		1.43E+00	3.86E-05	Up	6.28E-01	1.61E-01		Unigene49303_All//gi|29028930|gb|AO64814.1|//2.00E-07//At3g53320 [Arabidopsis thaliana]	Unigene49303_All//1.00E-07//AT3G53320| unknown protein	Unigene49303_All//0.00E+00//ES843966				nr +
Unigene49306_All	1190	0.48	0.68	0.45	7.53	3.47	8.84	236.38	42.08	10.95	4.95E-01	5.26E-01		-1.12E-01	9.07E-01		-1.12E+00	5.69E-10	Down	2.31E-01	2.36E-01		-2.49E+00	0.00E+00	Down	-4.43E+00	0.00E+00	Down	Unigene49306_All//gi|1706918|sp|P52838.1|FSTL_FLABI//1.00E-90//RecName: Full=Flavonol sulfotransferase-like >gi|498647|gb|AAA87399.1| sulfotransferase-like flavonol [Flaveria bidentis]	Unigene49306_All//2.00E-89//AT1G74090| SOT18 (DESULFO-GLUCOSINOLATE SULFOTRANSFERASE 18); 3-methylthiopropyl-desulfoglucosinolate sulfotransferase/ 4-methylthiobutyl-desulfoglucosinolate sulfotransferase/ 5-methylthiopentyl-desulfoglucosinolate sulfotransferase/ 7-methylthioheptyl-desulfogluco	Unigene49306_All//0.00E+00//gi|109839541|gb|DW238102.1|DW238102		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism		nr -
Unigene49308_All	506	7.86	3.60	5.37	14.08	18.17	12.94	0.75	0.00	0.71	-1.12E+00	3.10E-04	Down	-5.50E-01	8.81E-02		3.68E-01	5.57E-02		-1.21E-01	6.31E-01		-9.55E+00	6.17E-03		-8.58E-02	9.43E-01		Unigene49308_All//gi|115459086|ref|NP_001053143.1|//1.00E-34//Os04g0487100 [Oryza sativa Japonica Group] >gi|38344229|emb|CAE02056.2| Q1991113_30.6 [Oryza sativa (japonica cultivar-group)] >gi|90265262|emb|CAH67662.1| H0302E05.10 [Oryza sativa (indica cultivar-group)] >gi|113564714|dbj|BAF15057.1| Os04g0487100 [Oryza sativa Japonica Group]	Unigene49308_All//1.00E-34//AT1G51540| INVOLVED IN: biological_process unknown; LOCATED IN: Golgi apparatus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Galactose oxidase/kelch, beta-propeller (InterPro:IPR011043), Kelch repeat type 1 (InterPro:IPR006652), Kelch repeat type 2 (InterPro:IPR011498), Kelch related (InterPro:IPR013089), Kelch-type beta propeller (InterPro:IPR015915); BEST Arabidopsis thaliana protein match is: kelch repeat-containing protein (TAIR:AT3G27220.1); Has 1571 Blast hits to 1365 proteins in 151 species: Archae - 11; Bacteria - 200; Metazoa - 1128; Fungi - 24; Plants - 53; Viruses - 41; Other Eukaryotes - 114 (source: NCBI BLink).	Unigene49308_All//1.00E-100//DT465749				nr +
Unigene49309_All	1134	2.58	0.76	1.50	4.04	5.59	2.67	0.37	0.15	1.16	-1.77E+00	9.37E-06	Down	-7.82E-01	4.17E-02		4.67E-01	4.56E-02		-5.99E-01	3.47E-02		-1.34E+00	2.24E-01		1.64E+00	2.41E-03		Unigene49309_All//gi|115459086|ref|NP_001053143.1|//2.00E-56//Os04g0487100 [Oryza sativa Japonica Group] >gi|38344229|emb|CAE02056.2| Q1991113_30.6 [Oryza sativa (japonica cultivar-group)] >gi|90265262|emb|CAH67662.1| H0302E05.10 [Oryza sativa (indica cultivar-group)] >gi|113564714|dbj|BAF15057.1| Os04g0487100 [Oryza sativa Japonica Group]	Unigene49309_All//3.00E-51//AT1G51540| INVOLVED IN: biological_process unknown; LOCATED IN: Golgi apparatus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Galactose oxidase/kelch, beta-propeller (InterPro:IPR011043), Kelch repeat type 1 (InterPro:IPR006652), Kelch repeat type 2 (InterPro:IPR011498), Kelch related (InterPro:IPR013089), Kelch-type beta propeller (InterPro:IPR015915); BEST Arabidopsis thaliana protein match is: kelch repeat-containing protein (TAIR:AT3G27220.1); Has 1571 Blast hits to 1365 proteins in 151 species: Archae - 11; Bacteria - 200; Metazoa - 1128; Fungi - 24; Plants - 53; Viruses - 41; Other Eukaryotes - 114 (source: NCBI BLink).	Unigene49309_All//1.00E-108//DT465749				nr -
Unigene49311_All	1246	1.43	0.04	0.38	2.44	1.38	0.62	3.73	1.58	3.10	-5.13E+00	4.61E-09	Down	-1.89E+00	7.43E-04	Down	-8.20E-01	1.54E-02		-1.98E+00	3.50E-07	Down	-1.24E+00	1.41E-06	Down	-2.67E-01	3.02E-01		Unigene49311_All//gi|15219798|ref|NP_171966.1|//8.00E-74//AAA-type ATPase family protein [Arabidopsis thaliana]	Unigene49311_All//7.00E-66//AT1G04730| AAA-type ATPase family protein	Unigene49311_All//0.00E+00//ES850798				nr +
Unigene49312_All	682	81.93	43.91	32.25	183.19	197.62	145.22	35.21	9.50	12.44	-9.00E-01	3.18E-34		-1.35E+00	9.71E-63	Down	1.09E-01	1.64E-02		-3.35E-01	3.08E-14		-1.89E+00	4.92E-56	Down	-1.50E+00	7.76E-42	Down	Unigene49312_All//gi|145332667|ref|NP_001078199.1|//6.00E-27//structural constituent of cell wall [Arabidopsis thaliana]		Unigene49312_All//0.00E+00//BF268717		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene49313_All	945	27.02	10.51	5.75	41.49	29.70	60.31	10.34	8.76	11.89	-1.36E+00	1.30E-30	Down	-2.23E+00	3.49E-58	Down	-4.82E-01	5.50E-10		5.40E-01	1.47E-15		-2.39E-01	1.79E-01		2.02E-01	2.03E-01		Unigene49313_All//gi|15232612|ref|NP_188173.1|//3.00E-50//IAA19 (INDOLE-3-ACETIC ACID INDUCIBLE 19); transcription factor [Arabidopsis thaliana] >gi|17365900|sp|Q24409.2|IAA19_ARATH RecName: Full=Auxin-responsive protein IAA19; AltName: Full=Indoleacetic acid-induced protein 19; AltName: Full=Protein MASSUGU 2 >gi|7021739|gb|AAF35420.1| early auxin-induced protein, IAA19 [Arabidopsis thaliana] >gi|15795119|dbj|BAB02383.1| auxin-regulated protein, IAA19 [Arabidopsis thaliana] >gi|49616371|gb|AAT67082.1| IAA19 [Arabidopsis thaliana] >gi|88193790|gb|ABD42984.1| At3g15540 [Arabidopsis thaliana]	Unigene49313_All//3.00E-50//AT3G15540| IAA19 (INDOLE-3-ACETIC ACID INDUCIBLE 19); transcription factor	Unigene49313_All//0.00E+00//gi|109890808|gb|DW519772.1|DW519772				nr -
Unigene49314_All	1000	19.10	23.00	16.93	13.50	14.19	20.46	6.43	14.46	10.88	2.69E-01	2.25E-02		-1.74E-01	2.36E-01		7.17E-02	7.12E-01		6.00E-01	4.14E-07		1.17E+00	4.13E-17	Up	7.59E-01	5.54E-07		Unigene49314_All//gi|108706319|gb|ABF94114.1|//5.00E-33//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene49314_All//1.00E-51//AT4G14746| INVOLVED IN: biological_process unknown; LOCATED IN: anchored to membrane; CONTAINS InterPro DOMAIN/s: EGF (InterPro:IPR006210); Has 201 Blast hits to 179 proteins in 41 species: Archae - 0; Bacteria - 0; Metazoa - 168; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene49314_All//0.00E+00//TC148001				nr -
Unigene49315_All	1184	14.01	7.92	14.21	8.20	8.14	5.26	1.93	0.14	0.00	-8.23E-01	2.61E-09		2.08E-02	8.99E-01		-1.07E-02	9.53E-01		-6.40E-01	3.76E-04		-3.77E+00	9.58E-12	Down	-1.09E+01	8.15E-17	Down	Unigene49315_All//gi|15237245|ref|NP_197105.1|//6.00E-79//3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein [Arabidopsis thaliana] >gi|14190513|gb|AAK55737.1|AF38065 6_1 AT5g16010/F1N13_150 [Arabidopsis thaliana] >gi|9755647|emb|CAC01800.1| steroid 5alpha-reductase-like protein [Arabidopsis thaliana] >gi|24797018|gb|AAN64521.1| At5g16010/F1N13_150 [Arabidopsis thaliana]	Unigene49315_All//3.00E-80//AT5G16010| 3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein	Unigene49315_All//5.00E-108//ES794235		ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene49317_All	845	22.35	11.75	8.70	27.00	25.63	32.92	74.65	61.88	42.67	-9.27E-01	1.16E-12		-1.36E+00	6.63E-22	Down	-7.50E-02	5.95E-01		2.86E-01	6.07E-03		-2.71E-01	4.83E-06		-8.07E-01	2.30E-40		Unigene49317_All//gi|76161014|gb|AB440740.1|//2.00E-42//ribosomal protein S6-like protein [Solanum tuberosum]	Unigene49317_All//2.00E-29//AT5G10360| EMB3010 (embryo defective 3010); structural constituent of ribosome	Unigene49317_All//1.00E-120//gi|48793639|gb|CO094953.1|CO094953		ko03010|Ribosome		nr +
Unigene49318_All	1716	1.89	2.13	0.59	5.08	3.01	4.37	3.72	9.01	6.69	1.70E-01	6.08E-01		-1.68E+00	1.34E-05	Down	-7.55E-01	2.87E-05		-2.18E-01	3.28E-01		1.28E+00	8.49E-21	Up	8.46E-01	1.26E-08		Unigene49318_All//gi|105830274|gb|ABF74719.1|//2.00E-98//At4g11300 [Arabidopsis thaliana]	Unigene49318_All//2.00E-89//AT4G23530| unknown protein	Unigene49318_All//0.00E+00//gi|78325986|gb|DT546260.1|DT546260				nr +
Unigene49322_All	1182	10.67	3.86	9.96	493.93	312.95	265.59	25.68	18.88	11.06	-1.47E+00	3.04E-17	Down	-9.96E-02	6.12E-01		-6.58E-01	2.23E-252		-8.95E-01	0.00E+00		-4.44E-01	3.59E-07		-1.22E+00	2.31E-38	Down	Unigene49322_All//gi|157273648|gb|ABV27478.1|//1.00E-137//fasciclin-like arabinogalactan protein 7 [Gossypium hirsutum]	Unigene49322_All//1.00E-55//AT5G60490| FLA12	Unigene49322_All//0.00E+00//DW507038				nr +
Unigene49323_All	785	7.80	15.68	10.92	2.22	6.23	10.18	3.72	3.41	6.70	1.01E+00	1.21E-09	Up	4.86E-01	1.91E-02		1.49E+00	4.84E-08	Up	2.20E+00	5.83E-20	Up	-1.25E-01	7.19E-01		8.50E-01	1.85E-04		Unigene49323_All//gi|15234319|ref|NP_192088.1|//6.00E-38//ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein / ribonuclease P-related [Arabidopsis thaliana] >gi|89001035|gb|ABD59107.1| At4g01790 [Arabidopsis thaliana]	Unigene49323_All//3.00E-39//AT4G01790| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein / ribonuclease P-related	Unigene49323_All//2.00E-128//TC159304				nr +
Unigene49325_All	999	302.40	170.32	246.05	56.75	58.63	69.40	14.52	15.23	6.86	-8.28E-01	3.54E-158		-2.98E-01	3.46E-24		4.72E-02	5.96E-01		2.90E-01	2.21E-06		6.91E-02	6.36E-01		-1.08E+00	1.00E-15	Down	Unigene49325_All//gi|15241386|ref|NP_199924.1|//3.00E-64//4-alpha-hydroxytetrahydrobiopterin dehydratase [Arabidopsis thaliana] >gi|15529258|gb|AAK97723.1| AT5g51110/MWD22_5 [Arabidopsis thaliana] >gi|23505809|gb|AAN28764.1| At5g51110/MWD22_5 [Arabidopsis thaliana] >gi|42794935|gb|AAS45833.1| PCD/DCoH-like protein 1 [Arabidopsis thaliana]	Unigene49325_All//2.00E-65//AT5G51110| 4-alpha-hydroxytetrahydrobiopterin dehydratase	Unigene49325_All//0.00E+00//gi|164366423|gb|EX169263.1|EX169263				nr -
Unigene49326_All	793	169.89	64.85	72.99	219.92	199.62	299.57	256.35	114.95	114.94	-1.39E+00	1.26E-163	Down	-1.22E+00	2.01E-129	Down	-1.40E-01	1.64E-04		4.46E-01	1.19E-44		-1.16E+00	1.15E-226	Down	-1.16E+00	5.67E-233	Down	Unigene49326_All//gi|76161000|gb|AB440653.1|//7.00E-93//elongation factor-like protein [Solanum tuberosum]	Unigene49326_All//2.00E-38//AT5G19510| elongation factor 1B alpha-subunit 2 (eEF1Balpha2)	Unigene49326_All//0.00E+00//gi|109862252|gb|DW491229.1|DW491229				nr -
Unigene49329_All	1174	1.69	1.90	1.13	1.61	2.70	3.85	73.79	199.37	680.92	1.65E-01	6.88E-01		-5.79E-01	2.40E-01		7.43E-01	3.13E-02		1.25E+00	1.41E-05	Up	1.43E+00	0.00E+00	Up	3.21E+00	0.00E+00	Up	Unigene49329_All//gi|224103111|ref|XP_002312929.1|//1.00E-123//lysine/histidine transporter [Populus trichocarpa] >gi|222849337|gb|EEE86884.1| lysine/histidine transporter [Populus trichocarpa]	Unigene49329_All//2.00E-103//AT1G47670| amino acid transporter family protein	Unigene49329_All//0.00E+00//TC174042				nr +

Unigene49933_All	1324	4.66	4.36	4.26	22.91	16.93	13.10	25.90	88.11	16.31	-9.60E-02	6.91E-01		-1.29E-01	6.32E-01		-4.37E-01	1.27E-06		-8.07E-01	6.19E-17		1.77E+00	3.08E-245	Up	-6.67E-01	2.71E-16		Unigene4933_All//gi|212960522|gb|ACJ38670.1|//6.00E-16//cinnamoyl CoA reductase [Betula luminifera]	Unigene4933_All//1.00E-14//AT1G80820| CCR2 (CINNAMOYL COA REDUCTASE); cinnamoyl-CoA reductase	Unigene4933_All//4.00E-75//DN818000		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene49330_All	837	1.25	1.21	0.95	3.69	2.35	2.10	3.99	1.00	0.86	-4.63E-02	9.56E-01		-3.90E-01	5.89E-01		-6.54E-01	5.53E-02		-8.10E-01	2.18E-02		-2.00E+00	5.10E-09	Down	-2.22E+00	1.45E-10	Down			Unigene49330_All//0.00E+00//gi|109855376|gb|DW484355.1|DW484355				nr -
Unigene49331_All	787	4.25	4.57	5.62	2.03	2.14	4.65	4.03	8.76	7.44	1.04E-01	7.47E-01		4.00E-01	1.98E-01		8.20E-02	8.94E-01		1.20E+00	2.27E-04	Up	1.12E+00	4.62E-08	Up	8.85E-01	3.79E-05		Unigene49331_All//gi|283135852|gb|ADB11317.1|//9.00E-69//tau class glutathione transferase GSTU14 [Populus trichocarpa]	Unigene49331_All//4.00E-45//AT3G09270| ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	Unigene49331_All//0.00E+00//TC143158		ko00480|Glutathione metabolism		nr -
Unigene49332_All	754	20.75	111.08	28.32	39.90	40.51	48.64	51.70	111.42	94.79	2.42E+00	1.80E-215	Up	4.49E-01	2.67E-04		2.17E-02	8.59E-01		2.86E-01	1.27E-03		1.11E+00	1.33E-87	Up	8.75E-01	6.99E-52		Unigene49332_All//gi|297845328|ref|XP_002890545.1|//2.00E-59//T-complex protein 11 [Arabidopsis lyrata subsp. lyrata] >gi|297336387|gb|EFH66804.1| T-complex protein 11 [Arabidopsis lyrata subsp. lyrata]	Unigene49332_All//2.00E-43//AT1G22930| T-complex protein 11	Unigene49332_All//0.00E+00//ES822903				nr +
Unigene49333_All	868	21.82	50.55	16.99	63.70	53.40	26.69	97.76	42.08	103.13	1.21E+00	2.23E-43	Up	-3.61E-01	7.08E-03		-2.55E-01	1.45E-04		-1.25E+00	1.36E-62	Down	-1.22E+00	9.87E-103	Down	7.71E-02	1.54E-01		Unigene49333_All//gi|226425257|gb|ACO53628.1|//3.00E-68//bHLH domain protein [Gossypium hirsutum]	Unigene49333_All//2.00E-58//AT4G17880| basic helix-loop-helix (bHLH) family protein	Unigene49333_All//0.00E+00//TC141829	bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene49336_All	3025	17.78	9.77	13.50	22.08	19.78	13.94	17.75	7.72	7.86	-8.65E-01	7.61E-31		-3.97E-01	7.24E-08		-1.59E-01	1.43E-02		-6.63E-01	3.74E-26		-1.20E+00	5.45E-64	Down	-1.17E+00	1.25E-63	Down	Unigene49336_All//gi|30684197|ref|NP_196800.2|//0.00E+00//catalytic [Arabidopsis thaliana]	Unigene49336_All//0.00E+00//AT5G12960| catalytic	Unigene49336_All//0.00E+00//TC151659				nr -
Unigene49337_All	675	57.28	43.24	53.09	54.39	39.13	62.02	10.84	30.15	10.80	-4.06E-01	2.17E-06		-1.10E-01	2.79E-01		-4.75E-01	3.80E-09		1.90E-01	2.93E-02		1.48E+00	1.16E-33	Up	-4.70E-03	9.76E-01		Unigene49337_All//gi|226531011|ref|NP_001147608.1|//3.00E-21//lipid binding protein [Zea mays] >gi|195612468|gb|ACG28064.1| lipid binding protein [Zea mays]	Unigene49337_All//7.00E-15//AT1G70250| receptor serine/threonine kinase, putative	Unigene49337_All//0.00E+00//gi|109883091|gb|DW512061.1|DW512061				nr +
Unigene49338_All	1213	0.30	1.34	0.35	4.35	3.09	3.50	12.16	12.68	20.13	2.15E+00	2.79E-04	Up	2.18E-01	8.31E-01		-4.92E-01	5.19E-02		-3.15E-01	2.67E-01		5.99E-02	6.90E-01		7.27E-01	1.42E-13		Unigene49338_All//gi|223276668|ref|NP_199758.2|//1.00E-103//protein kinase family protein [Arabidopsis thaliana]	Unigene49338_All//2.00E-100//AT5G49470| protein kinase family protein	Unigene49338_All//0.00E+00//gi|48746634|gb|C0077153.1|C0077153				nr +
Unigene49340_All	798	110.35	57.02	37.50	63.98	76.68	55.52	66.33	21.26	33.40	-9.53E-01	8.11E-59		-1.56E+00	8.18E-123	Down	2.61E-01	3.92E-05		-2.05E-01	7.05E-03		-1.64E+00	7.43E-101	Down	-9.90E-01	1.09E-47		Unigene49340_All//gi|224085557|ref|XP_002307619.1|//1.00E-67//histone 2 [Populus trichocarpa] >gi|222857068|gb|EEE94615.1| histone 2 [Populus trichocarpa]	Unigene49340_All//3.00E-52//AT3G54560| HTA11; DNA binding	Unigene49340_All//0.00E+00//gi|164258212|gb|ES794501.1|ES794501				nr +
Unigene49343_All	1202	1.13	0.67	0.27	2.78	2.06	3.08	23.36	9.11	70.07	-7.47E-01	1.93E-01		-2.09E+00	1.95E-03		-4.29E-01	2.15E-01		1.50E-01	6.91E-01		-1.36E+00	7.73E-41	Down	1.58E+00	4.93E-155	Up	Unigene49343_All//gi|15241377|ref|NP_196938.1|//5.00E-75//AtMYB40 (myb domain protein 40; DNA binding / transcription factor [Arabidopsis thaliana] >gi|41619392|gb|AAS10092.1| MYB transcription factor [Arabidopsis thaliana]	Unigene49343_All//6.00E-70//AT5G14340| AtMYB40 (myb domain protein 40; DNA binding / transcription factor	Unigene49343_All//3.00E-14//DW519609	MYB			nr -
Unigene49344_All	539	12.23	58.66	19.76	29.48	24.79	32.43	6.67	8.06	7.32	2.26E+00	2.90E-75	Up	6.92E-01	1.31E-04		-2.50E-01	8.21E-02		1.37E-01	3.95E-01		2.74E-01	3.39E-01		1.34E-01	6.29E-01				Unigene49344_All//2.00E-167//gi|199884721|gb|DW513691.1|DW513691				
Unigene49345_All	2220	1.30	0.89	1.30	3.50	3.01	2.48	8.30	2.39	7.48	-5.42E-01	1.41E-01		-1.00E-03	9.98E-01		-2.18E-01	3.36E-01		-4.96E-01	1.78E-02		-1.80E+00	2.53E-40	Down	-1.50E-01	2.25E-01		Unigene49345_All//gi|30684540|ref|NP_193617.2|//0.00E+00//ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene49345_All//4.00E-176//AT4G18820| ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding	Unigene49345_All//0.00E+00//TC171199		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03430|Mismatch repair		nr +
Unigene49346_All	2049	0.03	0.87	0.00	0.32	1.01	1.10	5.30	2.73	4.16	5.09E+00	7.04E-09	Up	-4.67E+00	6.22E-01		1.67E+00	2.99E-04	Up	1.80E+00	8.39E-05	Up	-9.56E-01	1.22E-09		-3.50E-01	2.16E-02		Unigene49346_All//gi|224105651|ref|XP_002313887.1|//0.00E+00//GH3 family protein [Populus trichocarpa] >gi|222850295|gb|EEE87412.1| GH3 family protein [Populus trichocarpa]	Unigene49346_All//0.00E+00//AT2G14960| GH3.1	Unigene49346_All//0.00E+00//gi|78329328|gb|DT549602.1|DT549602				nr +
Unigene4935_All	1524	4.12	8.41	5.21	7.45	6.12	6.82	11.85	6.12	9.12	1.03E+00	2.46E-10	Up	3.38E-01	1.34E-01		-2.83E-01	1.01E-01		-1.29E-01	5.26E-01		-9.54E-01	2.05E-15		-3.77E-01	9.29E-04		Unigene4935_All//gi|42563882|ref|NP_187552.3|//1.00E-161//pectinacetylesterase family protein [Arabidopsis thaliana] >gi|119035842|gb|ABM96009.1| At3g09410 [Arabidopsis thaliana]	Unigene4935_All//6.00E-159//AT3G09410| pectinacetylesterase family protein	Unigene4935_All//0.00E+00//TC149305				nr -
Unigene49351_All	639	0.33	3.01	0.67	6.00	4.53	1.55	34.74	58.80	46.01	3.20E+00	3.42E-07	Up	1.03E+00	3.96E-01		-4.07E-01	2.02E-01		-1.95E+00	1.02E-08	Down	7.59E-01	2.11E-21		4.06E-01	3.19E-06		Unigene49351_All//gi|18403453|ref|NP_566712.1|//7.00E-36//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|15010698|gb|AAK74008.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] >gi|18958062|gb|AAL79604.1| AT3g22600/F16J14_17 [Arabidopsis thaliana] >gi|84778474|dbj|BAE73264.1| xylogen like protein 8 [Arabidopsis thaliana]	Unigene49351_All//2.00E-27//AT3G22600| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene49351_All//0.00E+00//TC147934				nr -
Unigene49354_All	512	1.02	4.26	0.83	1.17	1.41	0.97	3.96	7.76	3.50	2.06E+00	2.93E-05	Up	-2.97E-01	7.50E-01		2.75E-01	8.00E-01		-2.67E-01	7.57E-01		9.68E-01	4.28E-04		-1.79E-01	6.47E-01										
Unigene49357_All	651	92.83	46.08	21.68	54.02	45.17	40.38	68.84	15.54	19.34	-1.01E+00	1.08E-44	Down	-2.10E+00	4.39E-127	Down	-2.58E-01	3.22E-03		-4.20E-01	1.70E-06		-2.15E+00	8.19E-123	Down	-1.83E+00	1.23E-102	Down	Unigene49357_All//gi|7387726|sp|O2 2582.3|H2B_GOSHI//2.00E-66//RecName: Full=Histone H2B >gi|25589962|gb|AAB97163.1| histone H2B1 [Gossypium hirsutum]	Unigene49357_All//1.00E-44//AT5G59910| HTB4; DNA binding	Unigene49357_All//0.00E+00//gi|164345269|gb|ES810538.1|ES810538				nr +
Unigene49358_All	1303	7.55	7.97	5.27	14.22	10.25	6.45	5.52	5.23	6.15	7.86E-02	6.76E-01		-5.18E-01	6.70E-03		-4.72E-01	7.44E-05		-1.14E+00	2.07E-18	Down	-7.73E-02	7.26E-01		1.56E-01	4.33E-01		Unigene49358_All//gi|15232059|ref|NP_189337.1|//3.00E-63//AT-TCP20; transcription factor [Arabidopsis thaliana] >gi|75273954|sp|Q9LSD5.1|TCP20_ARATH RecName: Full=Transcription factor TCP20	Unigene49358_All//6.00E-60//AT3G27010| AT-TCP20; transcription factor	Unigene49358_All//0.00E+00//TC131626	TCP			nr -
Unigene49360_All	497	2.00	6.52	4.50	5.21	6.51	5.82	14.46	18.25	14.83	1.71E+00	5.49E-06	Up	1.17E+00	1.00E-02		3.22E-01	4.04E-01		1.58E-01	6.80E-01		3.36E-01	5.81E-02		3.62E-02	8.72E-01				Unigene49360_All//2.00E-120//gi|21096352|gb|BQ408665.1|BQ408665				
Unigene49361_All	1335	12.23	37.04	12.25	8.96	11.99	12.69	6.68	8.89	8.27	1.60E+00	6.34E-74	Up	2.10E-03	9.96E-01		4.22E-01	1.59E-03		5.02E-01	1.48E-04		4.12E-01	5.46E-03		3.07E-01	4.49E-02		Unigene49361_All//gi|5263332|gb|AAD41434.1|AC007727_23//1.00E-106//F38J7.23 [Arabidopsis thaliana] >gi|6552728|gb|AAF16527.1|AC013482_1 T26F17.1 [Arabidopsis thaliana]	Unigene49361_All//2.00E-98//AT1G21790| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TRAM, LAG1 and CLN8 homology (InterPro:IPR006634); Has 127 Blast hits to 127 proteins in 26 species: Archae - 0; Bacteria - 0; Metazoa - 84; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene49361_All//0.00E+00//TC171435				nr -
Unigene49362_All	424	2.34	6.69	4.65	6.70	8.37	3.52	8.18	11.04	7.05	1.51E+00	1.25E-04	Up	9.87E-01	4.25E-02		3.21E-01	3.77E-01		-9.30E-01	1.21E-02		4.33E-01	9.01E-02		-2.15E-01	4.90E-01				Unigene49362_All//2.00E-163//ES809789				
Unigene49363_All	901	0.00	0.00	0.47	1.49	1.15	1.85	2.63	4.59	1.02	null	null		8.89E+00	1.38E-02		-3.81E-01	5.36E-01		3.13E-01	5.94E-01		8.05E-01	2.53E-03		-1.37E+00	2.21E-04	Down										
Unigene49364_All	846	10.95	7.61	9.44	8.24	8.39	6.14	9.80	4.25	4.71	-5.23E-01	5.50E-03		-2.13E-01	3.22E-01		2.46E-02	9.39E-01		-4.25E-01	6.24E-02		-1.21E+00	1.30E-10	Down	-1.06E+00	4.74E-09	Down			Unigene49364_All//5.00E-55//TC176799				
Unigene49365_All	810	20.15	14.07	12.49	28.35	21.34	29.16	34.66	19.76	14.02	-5.18E-01	1.63E-04		-6.90E-01	1.27E-06		-4.10E-01	1.17E-04		4.06E-02	7.60E-01		-8.11E-01	4.76E-18		-1.31E+00	1.21E-39	Down	Unigene49365_All//gi|164605530|dbj|BAF98596.1|//7.00E-45//CM0545.370.nc [Lotus japonicus]	Unigene49365_All//6.00E-36//AT5G35140| ribosomal protein L30 family protein	Unigene49365_All//0.00E+00//TC155181		ko03010|Ribosome		nr -
Unigene49369_All	1225	1.54	0.50	0.78	3.33	1.88	2.36	1.52	3.14	2.93	-1.63E+00	1.19E-03		-9.75E-01	5.03E-02		-8.24E-01	3.50E-03		-4.99E-01	1.09E-01		1.05E+00	1.99E-04	Up	9.47E-01	8.46E-04		Unigene49369_All//gi|115434700|ref|NP_001042108.1|//1.00E-125//Os01g0165100 [Oryza sativa Japonica Group] >gi|113531639|dbj|BAF04022.1| Os01g0165100 [Oryza sativa Japonica Group]	Unigene49369_All//8.00E-131//AT2G40390| unknown protein	Unigene49369_All//2.00E-95//DR459519				nr +
Unigene49371_All	618	40.89	106.26	55.15	90.92	114.45	90.69	61.37	133.30	128.54	1.38E+00	1.22E-78	Up	4.31E-01	5.26E-06		3.32E-01	7.02E-09		-3.70E-03	9.60E-01		1.12E+00	2.47E-87	Up	1.07E+00	9.94E-80	Up	Unigene49371_All//gi|15724184|gb|AAL06484.1|AF411794_1//1.00E-18//At2g24550/F25P17.15 [Arabidopsis thaliana]	Unigene49371_All//1.00E-07//AT2G24550| unknown protein	Unigene49371_All//0.00E+00//BF269937				nr +
Unigene49372_All	1036	0.96	1.27	2.26	42.89	27.46	34.31	9.39	1.98	1.69	4.06E-01	4.87E-01		1.24E+00	5.33E-03		-6.44E-01	1.07E-18		-3.22E-01	3.72E-05		-2.25E+00	9.82E-29	Down	-2.47E+00	3.54E-33	Down	Unigene49372_All//gi|2500197|sp|Q41253.1|RAC13_GOSHI//1.00E-110//RecName: Full=Rac-like GTP-binding protein RAC13; Flags: Precursor >gi|1087111|gb|AAB35093.1| pea Rho1 protein homolog/mammalian rac protein homolog [Gossypium hirsutum]	Unigene49372_All//3.00E-91//AT5G45970| ARAC2 (ARABIDOPSIS RAC-LIKE 2); GTP binding	Unigene49372_All//0.00E+00//TC169212		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene49373_All	1866	0.11	0.11	0.00	0.00	0.11	0.02	4.10	0.74	7.22	-4.70E-02	9.88E-01		-6.81E+00	1.45E-01		6.79E+00	1.57E-01		4.60E+00	6.95E-01		-2.47E+00	2.02E-25	Down	8.15E-01	2.03E-09		Unigene49373_All//gi|224058595|ref|XP_002299857.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222846815|gb|EEE83462.1| cytochrome P450 [Populus trichocarpa]	Unigene49373_All//0.00E+00//AT1G12740| CYP97A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene49373_All//3.00E-76//gi|3326060|gb|AI054946.1|AI054946		ko00905|Brassinosteroid biosynthesis		nr +
Unigene49377_All	1325	30.13	12.70	28.90	1.99	2.91	0.65	0.03	0.06	1.23	-1.25E+00	1.78E-41	Down	-6.03E-02	5.73E-01		5.47E-01	8.26E-02		-1.62E+00	5.94E-05	Down	9.84E-01	7.31E-01		5.27E+00	1.93E-10	Up	Unigene49377_All//gi|124365567|gb|ABN09801.1|//1.00E-128//Galactose mutarotase-like [Medicago truncatula]	Unigene49377_All//3.00E-115//AT1G64770| NDF2 (NDH-DEPENDENT CYCLIC ELECTRON FLOW 1); carbohydrate binding / catalytic	Unigene49377_All//0.00E+00//TC141792				nr -
Unigene49378_All	675	7.52	4.95	4.50	3.84	2.81	2.81	4.51	2.54	1.77	-6.02E-01	2.38E-02		-7.42E-01	7.45E-03		-4.52E-01	2.60E-01		-4.50E-01	2.83E-01		-8.29E-01	9.27E-03		-1.35E+00	2.75E-05	Down			Unigene49378_All//7.00E-106//DW490925				
Unigene49379_All	1355	0.54	5.76	1.10	0.48	1.19	0.60	1.50	6.39	2.50	3.41E+00	4.97E-29	Up	1.03E+00	7.47E-02		1.32E+00	1.19E-02		3.28E-01	7.01E-01		2.09E+00	1.95E-23	Up	7.39E-01	1.09E-02				Unigene49379_All//0.00E+00//DT466932				
Unigene4938_All	2058	0.03	4.33	0.62	0.99	0.55	0.24	2.30	10.24	192.79	7.41E+00	4.07E-49	Up	4.61E+00	5.51E-06	Up	-8.46E-01	4.95E-02		-2.04E+00	3.45E-05	Down	2.15E+00	4.12E-58	Up	6.39E+00	0.00E+00	Up	Unigene4938_All//gi|164604828|dbj|BAF98466.1|//1.00E-163//cytochrome P450 [Coptis japonica var. dissecta]	Unigene4938_All//9.00E-141//AT3G14660| CYP72A13; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene4938_All//0.00E+00//TC167649		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +

Unigene49380_All	848	3.46	3.29	4.14	17.80	25.75	15.34	1.50	0.00	0.19	-7.23E-02	8.42E-01		2.63E-01	4.56E-01		5.33E-01	1.11E-06		-2.15E-01	1.78E-01		-1.05E+01	5.06E-09	Down	-2.99E+00	6.36E-06	Down	Unigene49380_All//gi|75174184|sp|Q9LFT5.1|EPFL1_ARATH//1.00E-25//RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 1; Short=EPF-like protein 1; Flags: Precursor >gi|38566574|gb|AAR24177.1| At5g10310 [Arabidopsis thaliana] >gi|40823959|gb|AAR92318.1| At5g10310 [Arabidopsis thaliana]	Unigene49380_All//8.00E-25//AT5G10310| unknown protein	Unigene49380_All//1.00E-15//DW503287				nr +
Unigene49381_All	430	28.11	33.82	24.02	68.58	57.50	71.21	69.61	42.57	34.37	2.67E-01	8.07E-02		-2.26E-01	2.19E-01		-2.54E-01	9.34E-03		5.43E-02	6.63E-01		-7.09E-01	2.12E-15		-1.02E+00	1.29E-28	Down	Unigene49381_All//gi|2511592|emb|CAA74027.1|//1.00E-06//multicatalytic endopeptidase complex, proteasome component, alpha subunit [Arabidopsis thaliana]	Unigene49381_All//8.00E-08//AT2G27020| PAG1; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene49381_All//0.00E+00//TC167018		ko03050|Proteasome		nr -
Unigene49382_All	675	9.38	9.61	12.62	25.76	21.73	19.27	47.85	33.31	23.90	3.49E-02	8.94E-01		4.29E-01	4.19E-02		-2.45E-01	7.28E-02		-4.19E-01	1.47E-03		-5.23E-01	6.16E-10		-1.00E+00	5.28E-30	Down	Unigene49382_All//gi|224123910|ref|XP_002319194.1|//6.00E-11//predicted protein [Populus trichocarpa] >gi|118481251|gb|ABK92575.1| unknown [Populus trichocarpa] >gi|222857570|gb|EEE95117.1| predicted protein [Populus trichocarpa]		Unigene49382_All//6.00E-97//CO491349				nr -
Unigene49383_All	585	120.74	299.17	144.37	52.37	43.15	30.57	30.43	41.94	18.59	1.31E+00	5.87E-193	Up	2.58E-01	1.08E-05		-2.79E-01	2.98E-03		-7.77E-01	4.83E-16		4.63E-01	2.30E-06		-7.11E-01	7.80E-10					Unigene49383_All//7.00E-155//DW234720				
Unigene49384_All	1300	0.32	5.50	0.74	1.03	0.58	1.01	3.51	6.08	42.84	4.09E+00	1.21E-30	Up	1.20E+00	1.15E-01		-8.28E-01	1.40E-01		-3.83E-02	9.48E-01		7.91E-01	1.86E-05		3.61E+00	2.67E-268	Up	Unigene49384_All//gi|15225398|ref|NP_182030.1|//3.00E-87//matrix metalloproteinase [Arabidopsis thaliana] >gi|31711730|gb|AAP68221.1| At2g45040 [Arabidopsis thaliana]	Unigene49384_All//1.00E-88//AT2G45040| matrix metalloproteinase	Unigene49384_All//4.00E-07//CA992801				nr +
Unigene49386_All	677	2.40	1.95	3.22	6.33	6.56	2.80	5.00	3.09	2.06	-3.00E-01	5.73E-01		4.29E-01	3.62E-01		5.23E-02	8.78E-01		-1.18E+00	5.99E-05	Down	-6.95E-01	2.07E-02		-1.28E+00	2.16E-05	Down	Unigene49386_All//gi|15239619|ref|NP_197398.1|//2.00E-63//AWPM-19-like membrane family protein [Arabidopsis thaliana] >gi|21536663|gb|AAM60995.1| plasma membrane associated protein-like [Arabidopsis thaliana]	Unigene49386_All//1.00E-45//AT5G18970| AWPM-19-like membrane family protein	Unigene49386_All//3.00E-123//DW497266				nr -
Unigene49388_All	518	20.10	16.82	23.95	26.35	61.09	45.69	92.56	84.88	157.74	-2.57E-01	1.68E-01		2.53E-01	1.50E-01		1.21E+00	5.91E-37	Up	7.94E-01	7.11E-13		-1.25E-01	9.98E-02		7.69E-01	1.12E-47		Unigene49388_All//gi|74476783|gb|AB048442.1|//2.00E-44//neutral/alkaline invertase [Manihot esculenta]	Unigene49388_All//2.00E-28//AT1G35580| CINV1 (cytosolic invertase 1); beta-fructofuranosidase	Unigene49388_All//0.00E+00//gi|78350775|gb|DT571049.1|DT571049				nr +
Unigene49389_All	748	12.24	4.27	6.05	8.52	6.63	8.15	2.26	1.51	4.53	-1.52E+00	2.29E-13	Down	-1.02E+00	4.06E-07	Down	-3.63E-01	1.26E-01		-6.46E-02	8.00E-01		-5.84E-01	2.08E-01		1.00E+00	6.60E-04	Up	Unigene49389_All//gi|225423983|ref|XP_002282631.1|//6.00E-24//PREDICTED: similar to CLE27 (CLAVATA3/ESR-RELATED 27); receptor binding [Vitis vinifera]	Unigene49389_All//6.00E-10//AT3G25905| CLE27 (CLAVATA3/ESR-RELATED 27); protein binding / receptor binding	Unigene49389_All//0.00E+00//DN802828				nr +
Unigene4939_All	2121	6.54	2.17	3.79	21.00	9.32	21.49	26.91	6.82	9.49	-1.59E+00	3.96E-21	Down	-7.86E-01	5.22E-07		-1.17E+00	1.09E-51	Down	3.32E-02	7.29E-01		-1.98E+00	9.33E-141	Down	-1.50E+00	1.31E-98	Down	Unigene4939_All//gi|115473407|ref|NP_001060302.1|//7.00E-34//Os07g0620600 [Oryza sativa Japonica Group] >gi|113611838|dbj|BAF22216.1| Os07g0620600 [Oryza sativa Japonica Group]	Unigene4939_All//8.00E-54//AT1G58120| unknown protein	Unigene4939_All//0.00E+00//gi|164303190|gb|ES850523.1|ES850523				nr +
Unigene49390_All	584	6.90	4.16	9.39	8.36	5.84	2.32	1.45	1.36	0.34	-7.28E-01	1.62E-02		4.45E-01	1.00E-01		-5.18E-01	4.97E-02		-1.85E+00	3.12E-10	Down	-9.07E-02	9.00E-01		-2.09E+00	4.37E-03					Unigene49390_All//5.00E-51//gi|21093552|gb|BQ405865.1|BQ405865				
Unigene49391_All	413	7.22	1.23	13.54	14.23	14.42	6.78	1.02	1.62	0.87	-2.56E+00	7.83E-09	Down	9.07E-01	5.61E-04		1.93E-02	9.48E-01		-1.07E+00	1.03E-05	Down	6.62E-01	4.02E-01		-2.38E-01	7.88E-01					Unigene49391_All//7.00E-179//gi|21093552|gb|BQ405865.1|BQ405865				
Unigene49392_All	1151	15.32	7.04	11.15	2.94	3.17	0.90	0.07	0.15	0.21	-1.12E+00	6.24E-16	Down	-4.58E-01	8.36E-04		1.08E-01	8.02E-01		-1.71E+00	1.41E-06	Down	9.83E-01	6.33E-01		1.50E+00	3.39E-01		Unigene49392_All//gi|15235203|ref|NP_193718.1|//2.00E-73//immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana] >gi|6686800|emb|CAB64722.1| FKBP like protein [Arabidopsis thaliana] >gi|88196737|gb|ABD43011.1| At4g19830 [Arabidopsis thaliana]	Unigene49392_All//4.00E-68//AT4G19830| immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein					nr -
Unigene49394_All	1740	6.68	4.19	6.37	0.40	0.38	0.39	1.80	1.30	4.60	-6.71E-01	5.39E-05		-6.86E-02	7.09E-01		-9.21E-02	8.94E-01		-4.20E-02	9.44E-01		-4.71E-01	1.44E-01		1.36E+00	1.80E-12	Up	Unigene49394_All//gi|297723391|ref|NP_001174059.1|//3.00E-55//Os04g0581400 [Oryza sativa Japonica Group] >gi|239983845|sp|Q7F9W2.2|Y4814_ORYSJ RecName: Full=B3 domain-containing protein Os04g0581400 >gi|255675715|dbj|BAH92787.1| Os04g0581400 [Oryza sativa Japonica Group]	Unigene49394_All//4.00E-54//AT2G46870| NGA1 (NGATHA1); transcription factor	Unigene49394_All//0.00E+00//gi|48806430|gb|CO107744.1|CO107744	ABI3VP1			nr +
Unigene49395_All	1235	7.88	1.23	3.67	2.30	2.73	1.94	0.41	0.07	0.00	-2.68E+00	8.76E-29	Down	-1.10E+00	1.65E-08	Down	2.49E-01	5.31E-01		-2.46E-01	5.62E-01		-2.60E+00	2.05E-02		-8.68E+00	5.54E-04	Down	Unigene49395_All//gi|224095730|ref|XP_002310455.1|//1.00E-134//phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa] >gi|222853338|gb|EEE90905.1| phenylcoumaran benzylic ether reductase -like protein [Populus trichocarpa]	Unigene49395_All//2.00E-67//AT1G75290| oxidoreductase, acting on NADH or NADPH			ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism		nr +
Unigene49396_All	532	0.39	2.67	0.80	1.87	3.75	2.97	0.08	0.71	2.17	2.76E+00	7.72E-05	Up	1.03E+00	3.96E-01		1.00E+00	2.81E-02		6.66E-01	2.29E-01		3.15E+00	3.41E-02		4.77E+00	3.27E-07	Up	Unigene49396_All//gi|225431806|ref|XP_002272864.1|//1.00E-64//PREDICTED: similar to PLDP1 (PHOSPHOLIPASE D ZETA1); phospholipase D [Vitis vinifera]	Unigene49396_All//2.00E-52//AT3G16785| PLDP1 (PHOSPHOLIPASE D P1); phospholipase D	Unigene49396_All//4.00E-125//TC164151		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr +
Unigene49397_All	698	0.15	0.29	0.31	2.64	2.57	2.72	2.24	1.92	6.91	9.54E-01	6.21E-01		1.03E+00	5.91E-01		-4.17E-02	9.26E-01		4.15E-02	9.51E-01		-2.26E-01	6.32E-01		1.62E+00	5.70E-10	Up	Unigene49397_All//gi|225431806|ref|XP_002272864.1|//1.00E-83//PREDICTED: similar to PLDP1 (PHOSPHOLIPASE D ZETA1); phospholipase D [Vitis vinifera]	Unigene49397_All//2.00E-64//AT3G16785| PLDP1 (PHOSPHOLIPASE D P1); phospholipase D	Unigene49397_All//0.00E+00//TC164151		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr -
Unigene49398_All	1240	1.35	0.78	0.43	2.41	1.86	1.97	5.11	3.37	1.86	-7.98E-01	1.16E-01		-1.65E+00	3.47E-03		-3.74E-01	3.17E-01		-2.93E-01	4.68E-01		-6.02E-01	3.93E-03		-1.46E+00	3.24E-11	Down				Unigene49398_All//0.00E+00//CO131256				
Unigene494_All	1178	21.50	11.23	13.52	18.65	15.49	15.91	15.22	9.30	6.70	-9.37E-01	5.35E-17		-6.70E-01	2.07E-09		-2.68E-01	2.11E-02		-2.29E-01	6.62E-02		-7.11E-01	1.36E-09		-1.18E+00	4.12E-22	Down	Unigene494_All//gi|18420643|ref|NP_568427.1|//1.00E-107//NCLPP7 (NUCLEAR-ENCODED CLP PROTEASE P7); serine-type endopeptidase [Arabidopsis thaliana] >gi|75309225|sp|Q9FN42.1|CLPP2_ARATH RecName: Full=ATP-dependent Clp protease proteolytic subunit 2, mitochondrial; AltName: Full=Endopeptidase ClpP2; AltName: Full=nClpP7; Flags: Precursor >gi|9759272|dbj|BAB09831.1| ATP-dependent protease proteolytic subunit ClpP-like protein [Arabidopsis thaliana] >gi|289568603|gb|AAO63325.1| At5g23140 [Arabidopsis thaliana]	Unigene494_All//1.00E-96//AT5G23140| NCLPP7 (NUCLEAR-ENCODED CLP PROTEASE P7); serine-type endopeptidase	Unigene494_All//0.00E+00//TC150828			GO:0004175//GO:0019538//GO:0043231	nr +
Unigene4940_All	719	1.82	4.86	3.18	2.98	1.92	3.45	1.29	2.79	2.55	1.42E+00	4.33E-05	Up	8.08E-01	6.77E-02		-6.37E-01	1.39E-01		2.14E-01	6.29E-01		1.11E+00	7.07E-03		9.78E-01	1.92E-02		Unigene4940_All//gi|89953403|gb|AB083295.1|//1.00E-65//Fgenesh protein 81 [Beta vulgaris]	Unigene4940_All//1.00E-41//AT3G62940| OTU-like cysteine protease family protein	Unigene4940_All//5.00E-150//TC131497				nr +
Unigene49400_All	1434	4.74	4.24	4.68	5.56	6.94	2.02	0.27	0.00	0.50	-1.62E-01	5.09E-01		-1.97E-02	9.53E-01		3.20E-01	8.64E-02		-1.46E+00	7.37E-12	Down	-8.05E+00	6.17E-03		9.14E-01	2.12E-01		Unigene49400_All//gi|122162768|sp|Q01JD1.1|SPL7_ORYSI//1.00E-49//RecName: Full=Squamosa promoter-binding-like protein 7 >gi|116310136|emb|CAH67152.1| OSIGBa0122F23.9 [Oryza sativa (indica cultivar-group)]	Unigene49400_All//2.00E-33//AT1G27370| squamosa promoter-binding protein-like 10 (SPL10)	Unigene49400_All//0.00E+00//gi|78332943|gb|DT553217.1|DT553217	SBP			nr +
Unigene49401_All	1065	27.02	16.41	21.15	17.45	19.43	12.85	7.62	3.89	1.83	-7.19E-01	1.75E-12		-3.53E-01	7.95E-04		1.56E-01	2.58E-01		-4.41E-01	4.61E-04		-9.72E-01	1.37E-07		-2.06E+00	2.42E-22	Down	Unigene49401_All//gi|224069292|ref|XP_002302948.1|//9.00E-71//high mobility group family [Populus trichocarpa] >gi|222844674|gb|EEE82221.1| high mobility group family [Populus trichocarpa]	Unigene49401_All//5.00E-29//AT1G14900| HMGA (HIGH MOBILITY GROUP A); DNA binding	Unigene49401_All//0.00E+00//DR463068				nr +
Unigene49402_All	5931	0.04	111.70	43.25	0.00	0.08	0.00	0.00	0.00	0.00	1.16E+01	0.00E+00	Up	1.03E+01	0.00E+00	Up	6.35E+00	5.07E-03		null	null		null	null		null	null		Unigene49402_All//sp|Q91PP5|POLG_RTSVT//6.00E-49//Genome polyprotein OS=Rice tungro spherical virus (strain Vt6) PE=1 SV=1						swissprot -
Unigene49403_All	812	232.03	293.35	455.38	151.04	225.36	198.40	73.57	299.52	184.52	3.38E-01	3.37E-25		9.73E-01	7.77E-247		5.77E-01	5.56E-61		3.94E-01	2.87E-24		2.03E+00	0.00E+00	Up	1.33E+00	3.85E-211	Up	Unigene49403_All//gi|5263319|gb|AAD41421.1|AC007727_10//2.00E-85//ESTs gb|N96028, gb|F14286, gb|T20680, gb|F14443, gb|AA657300 and gb|N65244 come from this gene [Arabidopsis thaliana]	Unigene49403_All//1.00E-73//AT1G21680| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole, plant-type cell wall; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40-like Beta Propeller (InterPro:IPR011659), Six-bladed beta-propeller, TolB-like (InterPro:IPR011042); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21670.1); Has 6869 Blast hits to 3873 proteins in 790 species: Archae - 41; Bacteria - 3697; Metazoa - 41; Fungi - 29; Plants - 64; Viruses - 0; Other Eukaryotes - 2987 (source: NCBI BLink).	Unigene49403_All//0.00E+00//gi|164333668|gb|ES816150.1|ES816150				nr +
Unigene49407_All	797	2.43	2.16	3.41	5.31	5.62	4.87	3.24	1.42	1.65	-1.68E-01	7.03E-01		4.88E-01	2.35E-01		8.03E-02	8.11E-01		-1.25E-01	6.88E-01		-1.19E+00	8.48E-04	Down	-9.72E-01	4.26E-03		Unigene49407_All//gi|13486669|dbj|BAB39906.1|//2.00E-06//P0028E10.10 [Oryza sativa Japonica Group]	Unigene49407_All//8.00E-16//AT2G30480| unknown protein	Unigene49407_All//7.00E-57//TC164456				nr -
Unigene49408_All	1161	1.17	1.70	0.37	3.05	7.47	6.26	1.35	6.23	6.93	5.39E-01	2.41E-01		-1.68E+00	8.96E-03		1.29E+00	2.02E-11	Up	1.04E+00	1.54E-06	Up	2.21E+00	4.78E-21	Up	2.36E+00	8.13E-26	Up				Unigene49408_All//1.00E-12//BQ403264				
Unigene49409_All	903	2.43	8.75	5.25	2.98	1.68	3.10	3.28	2.96	2.47	1.85E+00	5.32E-15	Up	1.11E+00	1.51E-04	Up	-8.28E-01	2.29E-02		5.79E-02	9.05E-01		-1.46E-01	6.73E-01		-4.08E-01	2.03E-01		Unigene49409_All//gi|183393002|gb|ACC61674.1|//5.00E-54//mitochondrial cytochrome c [Vitis vinifera]	Unigene49409_All//3.00E-54//AT4G10040| CYTC-2 (cytochrome c-2); electron carrier/ heme binding / iron ion binding	Unigene49409_All//0.00E+00//gi|109869694|gb|DW498670.1|DW498670				nr -

Unigene4941_All	1103	3.75	3.68	1.69	3.66	4.37	2.13	4.33	7.12	4.19	-2.81E-02	9.41E-01			-1.15E+00	3.03E-04	Down	2.57E-01	4.10E-01		-7.81E-01	9.47E-03		7.18E-01	1.01E-04		-4.80E-02	8.56E-01		Unigene4941_All//gi|297804406|ref|XP_002870087.1|//1.00E-135//damaged DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297315923|gb|EFH46346.1| damaged DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene4941_All//8.00E-133//AT4G17760| damaged DNA binding / exodeoxyribonuclease III	Unigene4941_All//0.00E+00//TC151993				nr +
Unigene49410_All	1181	2.13	1.20	0.68	7.47	10.67	7.11	2.94	1.20	2.33	-8.24E-01	3.90E-02			-1.65E+00	2.09E-04	Down	5.15E-01	6.55E-04		-6.99E-02	7.49E-01		-1.29E+00	2.44E-05	Down	-3.35E-01	2.60E-01		Unigene49410_All//gi|15225377|ref|NP_179646.1|//1.00E-139//DNAJ heat shock family protein [Arabidopsis thaliana] >gi|15982895|gb|AAL09794.1| At2g20560/T13C7.15 [Arabidopsis thaliana] >gi|22137258|gb|AAM91474.1| At2g20560/T13C7.15 [Arabidopsis thaliana]	Unigene49410_All//3.00E-132//AT2G20560| DNAJ heat shock family protein	Unigene49410_All//2.00E-08//TC142357				nr -
Unigene49413_All	716	24.04	10.90	19.26	88.71	93.59	86.67	193.04	54.46	60.93	-1.14E+00	5.23E-16	Down		-3.20E-01	2.52E-02		7.73E-02	3.07E-01		-3.35E-02	7.05E-01		-1.83E+00	8.77E-305	Down	-1.66E+00	2.78E-275	Down	Unigene49413_All//gi|297807807|ref|XP_002871787.1|//1.00E-113//cobalamin-independent methionine synthase [Arabidopsis lyrata subsp. lyrata] >gi|297317624|gb|EFH48046.1| cobalamin-independent methionine synthase [Arabidopsis lyrata subsp. lyrata]	Unigene49413_All//8.00E-105//AT5G17920| ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase	Unigene49413_All//0.00E+00//TC140693		ko00270|Cysteine and methionine metabolism		nr -
Unigene49417_All	821	2.04	0.93	1.75	0.85	2.77	1.27	1.96	1.53	1.70	-1.14E+00	2.63E-02			-2.20E-01	6.59E-01		1.70E+00	1.01E-04	Up	5.75E-01	4.26E-01		-3.58E-01	4.67E-01		-2.04E-01	6.42E-01									
Unigene49418_All	996	14.87	7.78	8.13	12.70	10.48	8.03	19.57	5.71	9.96	-9.34E-01	3.36E-10			-8.71E-01	9.82E-09		-2.78E-01	8.52E-02		-6.63E-01	1.79E-05		-1.78E+00	5.30E-42	Down	-9.74E-01	1.11E-17		Unigene49418_All//gi|115485231|ref|NP_001067759.1|//1.00E-120//Os11g0312400 [Oryza sativa Japonica Group] >gi|585338|sp|Q08480.1|KAD2_ORYSJ RecName: Full=Adenylate kinase B; Short=AK B; AltName: Full=ATP-AMP transphosphorylase B >gi|391879|dbj|BAA01181.1| adenylate kinase-b [Oryza sativa] >gi|62734015|gb|AAX96124.1| adenylate kinase b (ec 2.7.4.3) (atp-amp transphosphorylase) [Oryza sativa Japonica Group] >gi|113644981|dbj|BAF28122.1| Os11g0312400 [Oryza sativa Japonica Group]	Unigene49418_All//1.00E-110//AT5G50370| adenylate kinase, putative	Unigene49418_All//0.00E+00//DW504486		ko00230|Purine metabolism		nr -
Unigene49422_All	1595	1.02	0.44	1.10	13.55	12.89	6.09	38.07	17.22	34.39	-1.19E+00	2.32E-02			1.16E-01	8.09E-01		-7.26E-02	6.02E-01		-1.15E+00	8.85E-22	Down	-1.14E+00	5.01E-67	Down	-1.46E-01	1.81E-02		Unigene49422_All//gi|28949891|emb|CAD70622.1|//1.00E-142//1-aminocyclopropane-1-carboxylic acid oxidase [Cicer arietinum]	Unigene49422_All//2.00E-123//AT1G77330| 1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative			ko00270|Cysteine and methionine metabolism		nr -
Unigene49423_All	1251	16.31	8.55	8.22	2.23	7.68	5.99	0.00	0.00	0.00	-9.33E-01	9.80E-14			-9.90E-01	1.96E-14		1.78E+00	8.30E-20	Up	1.43E+00	1.31E-10	Up	null	null		null	null		Unigene49423_All//gi|297801024|ref|XP_002868396.1|//1.00E-148//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314232|gb|EFH44655.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49423_All//1.00E-145//AT5G33370| GDSL-motif lipase/hydrolase family protein	Unigene49423_All//0.00E+00//TC166006				nr -
Unigene49424_All	1051	12.40	9.88	7.35	5.83	6.82	5.97	2.05	6.76	2.88	-3.27E-01	4.13E-02			-7.55E-01	3.17E-06		2.25E-01	3.61E-01		3.50E-02	9.12E-01		1.72E+00	4.38E-15	Up	4.90E-01	1.18E-01		Unigene49424_All//gi|297796031|ref|XP_002865900.1|//3.00E-71//sugar isomerase domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297311735|gb|EFH42159.1| sugar isomerase domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene49424_All//1.00E-70//AT5G52190| sugar isomerase (SIS) domain-containing protein	Unigene49424_All//0.00E+00//TC139478				nr +
Unigene49426_All	820	2.87	2.90	1.49	15.67	8.57	8.48	26.55	11.52	15.45	1.64E-02	9.87E-01			-9.43E-01	3.08E-02		-8.72E-01	1.89E-09		-8.86E-01	9.88E-09		-1.20E+00	1.44E-26	Down	-7.81E-01	8.69E-14		Unigene49426_All//gi|115473585|ref|NP_001060391.1|//3.00E-113//Os07g0636000 [Oryza sativa Japonica Group] >gi|113611927|dbj|BAF22305.1| Os07g0636000 [Oryza sativa Japonica Group]		Unigene49426_All//1.00E-163//TC177607				nr +
Unigene49429_All	985	0.90	3.29	1.62	0.86	2.10	4.40	2.19	4.20	23.05	1.87E+00	1.15E-06	Up		8.45E-01	1.25E-01		1.29E+00	4.17E-03		2.36E+00	5.82E-12	Up	9.40E-01	4.51E-04		3.40E+00	4.01E-104	Up	Unigene49429_All//gi|224055785|ref|XP_002298652.1|//4.00E-47//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222845910|gb|EEE83457.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene49429_All//7.00E-31//AT5G13180| ANAC083 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 83); transcription factor	Unigene49429_All//0.00E+00//TC172236	NAC			nr -
Unigene49430_All	754	8.19	7.19	5.37	5.55	4.75	4.61	5.94	2.99	1.85	-1.87E-01	4.58E-01			-6.09E-01	1.41E-02		-2.25E-01	5.06E-01		-2.67E-01	4.20E-01		-9.90E-01	1.16E-04		-1.68E+00	6.76E-10	Down	Unigene49430_All//gi|225433788|ref|XP_002272866.1|//1.00E-28//PREDICTED: similar to FAD-binding domain-containing protein [Vitis vinifera]	Unigene49430_All//1.00E-26//AT1G32310| unknown protein	Unigene49430_All//1.00E-52//ES790537				nr +
Unigene49431_All	750	12.56	19.05	11.57	23.78	20.34	25.83	13.30	10.31	5.95	6.01E-01	4.92E-05			-1.18E-01	6.03E-01		-2.25E-01	9.94E-02		1.20E-01	4.29E-01		-3.68E-01	2.63E-02		-1.16E+00	2.48E-12	Down	Unigene49431_All//gi|28207685|gb|AA032066.1|//7.00E-41//Erwinia induced protein 2 [Solanum tuberosum]	Unigene49431_All//6.00E-41//AT5G17190| unknown protein	Unigene49431_All//0.00E+00//TC151781				nr -
Unigene49432_All	688	48.67	98.17	38.39	74.36	79.98	85.01	112.58	136.63	95.14	1.01E+00	7.93E-50	Up		-3.42E-01	4.10E-04		1.05E-01	1.93E-01		1.93E-01	6.40E-03		2.79E-01	4.60E-09		-2.43E-01	3.05E-06		Unigene49432_All//gi|89258500|gb|AB065463.1|//2.00E-48//DNA binding/zinc ion binding protein [Gossypium hirsutum]	Unigene49432_All//1.00E-29//AT1G12440| zinc finger (AN1-like) family protein	Unigene49432_All//0.00E+00//gi|78352380|gb|DT572654.1|DT572654				nr -
Unigene49434_All	833	89.19	27.55	75.24	49.22	31.67	20.06	7.51	5.77	3.44	-1.69E+00	5.11E-121	Down		-2.45E-01	1.04E-04		-6.36E-01	6.11E-17		-1.29E+00	7.80E-49	Down	-3.81E-01	8.03E-02		-1.13E+00	1.04E-07	Down	Unigene49434_All//gi|5902368|gb|AAD55470.1|AC009322_10//2.00E-54//Unknown protein [Arabidopsis thaliana]	Unigene49434_All//5.00E-54//AT3G15810| unknown protein	Unigene49434_All//0.00E+00//TC135288				nr +
Unigene49435_All	1083	1.98	0.33	0.64	3.04	1.78	3.04	3.94	3.47	2.91	-2.60E+00	1.21E-06	Down		-1.63E+00	8.10E-04	Down	-7.70E-01	1.75E-02		4.00E-03	9.93E-01		-1.83E-01	5.43E-01		-4.40E-01	8.74E-02					Unigene49435_All//0.00E+00//D8453543					
Unigene49436_All	507	2.37	1.60	1.16	64.36	24.59	15.14	38.69	21.19	8.01	-5.70E-01	3.65E-01			-1.04E+00	1.14E-01		-1.39E+00	1.56E-49	Down	-2.09E+00	6.05E-77	Down	-8.69E-01	2.22E-14		-2.27E+00	7.92E-60	Down				Unigene49436_All//0.00E+00//TC144946					
Unigene49439_All	918	10.37	6.73	10.85	11.23	11.44	11.91	19.99	12.11	9.37	-6.23E-01	7.82E-04			6.45E-02	7.46E-01		2.65E-02	9.07E-01		8.40E-02	6.96E-01		-7.23E-01	4.65E-10		-1.09E+00	5.76E-20	Down	Unigene49439_All//gi|73921112|sp|Q61D70.1|Y3377_ARATH//5.00E-62//RecName: Full=Uncharacterized protein At3g03773 >gi|48310264|gb|AAT41786.1| At3g03773 [Arabidopsis thaliana] >gi|50198936|gb|AAT70471.1| At3g03773 [Arabidopsis thaliana]	Unigene49439_All//1.00E-57//AT3G03773| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; CONTAINS InterPro DOMAIN/s: CS domain (InterPro:IPR007052), HSP20-like chaperone (InterPro:IPR008978), CS (InterPro:IPR017447); BEST Arabidopsis thaliana protein match is: glycine-rich protein (TAIR:AT4G02450.2); Has 482 Blast hits to 482 proteins in 157 species: Archae - 0; Bacteria - 0; Metazoa - 241; Fungi - 87; Plants - 64; Viruses - 0; Other Eukaryotes - 90 (source: NCBI BLink).	Unigene49439_All//0.00E+00//TC168459				nr -
Unigene4944_All	1201	1.70	1.18	1.91	2.99	2.55	2.29	2.32	0.84	2.79	-5.24E-01	2.43E-01			1.66E-01	6.97E-01		-2.27E-01	5.42E-01		-3.81E-01	2.77E-01		-1.48E+00	2.73E-05	Down	2.62E-01	4.04E-01		Unigene4944_All//gi|15242791|ref|NP_200569.1|//1.00E-103//protein kinase family protein [Arabidopsis thaliana]	Unigene4944_All//1.00E-97//AT5G57610| protein kinase family protein	Unigene4944_All//6.00E-151//TC159955				nr -
Unigene49440_All	776	0.88	3.40	2.54	2.31	2.66	4.31	10.19	10.23	128.24	1.95E+00	7.44E-06	Up		1.53E+00	2.38E-03		2.04E-01	6.98E-01		8.98E-01	8.17E-03		6.30E-03	1.01E+00		3.65E+00	0.00E+00	Up	Unigene49440_All//gi|297851116|ref|XP_002890439.1|//6.00E-12//F21J9.24 [Arabidopsis lyrata subsp. lyrata] >gi|297339281|gb|EFH69698.1| F21J9.24 [Arabidopsis lyrata subsp. lyrata]	Unigene49440_All//3.00E-13//AT1G24580| zinc finger (C3HC4-type RING finger) family protein	Unigene49440_All//0.00E+00//gi|109880739|gb|DW509709.1|DW509709				nr +
Unigene49442_All	880	2.79	2.30	0.73	2.04	5.95	2.72	0.29	0.19	0.23	-2.79E-01	5.03E-01			-1.94E+00	3.26E-05	Down	1.55E+00	4.95E-09	Up	4.17E-01	3.56E-01		-6.02E-01	6.47E-01		-3.49E-01	7.66E-01		Unigene49442_All//gi|46518427|gb|AAS99695.1|//6.00E-77//At5g47530 [Arabidopsis thaliana]	Unigene49442_All//3.00E-78//AT5G47530| auxin-responsive protein, putative	Unigene49442_All//1.00E-09//TC146754				nr +
Unigene49444_All	981	3275.89	1117.21	2234.55	260.45	362.75	200.86	5.22	7.54	4.14	-1.55E+00	0.00E+00	Down		-5.52E-01	0.00E+00		4.78E-01	2.85E-84		-3.75E-01	4.67E-35		5.32E-01	5.59E-03		-3.32E-01	1.62E-01		Unigene49444_All//gi|1709651|sp|P00299.2|PLAS1_POPNI//1.00E-70//RecName: Full=Plastocyanin A, chloroplastic; Flags: Precursor >gi|929813|emb|CAA90564.1| plastocyanin a [Populus nigra]	Unigene49444_All//5.00E-51//AT1G20340| DRT112; copper ion binding / electron carrier	Unigene49444_All//0.00E+00//TC175783		ko00195|Photosynthesis		nr -
Unigene49445_All	776	1.35	1.83	0.62	3.79	1.60	1.05	1.85	1.62	2.93	4.39E-01	4.25E-01			-1.13E+00	1.17E-01		-1.25E+00	2.98E-04	Down	-1.85E+00	2.03E-06	Down	-1.97E-01	6.99E-01		6.60E-01	7.20E-02		Unigene49445_All//gi|115455231|ref|NP_001051216.1|//4.00E-122//Os03g0739700 [Oryza sativa Japonica Group] >gi|108710985|gb|ABF98780.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549687|dbj|BAF13130.1| Os03g0739700 [Oryza sativa Japonica Group]	Unigene49445_All//3.00E-10//AT4G19090| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP022348 (InterPro:IPR016804), Uncharacterised protein family UPF0114 (InterPro:IPR005134); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13720.1); Has 553 Blast hits to 553 proteins in 219 species: Archae - 18; Bacteria - 407; Metazoa - 0; Fungi - 0; Plants - 54; Viruses - 0; Other Eukaryotes - 74 (source: NCBI BLink).	Unigene49445_All//0.00E+00//BF276023				nr +
Unigene49446_All	1001	17.93	12.81	8.67	25.43	20.50	31.13	16.05	8.64	7.44	-4.85E-01	1.98E-04			-1.05E+00	5.70E-14	Down	-3.11E-01	2.69E-03		2.92E-01	2.70E-03		-8.93E-01	1.88E-12		-1.11E+00	5.36E-18	Down	Unigene49446_All//gi|77999307|gb|AB817000.1|//7.00E-53//ribosomal protein L23 family protein [Solanum tuberosum]	Unigene49446_All//6.00E-39//AT4G39880| ribosomal protein L23 family protein	Unigene49446_All//0.00E+00//TC146980				nr -

Unigene49447_All	1372	0.65	0.66	0.12	0.87	1.41	1.05	2.59	1.22	1.48	3.63E-02	9.79E-01			-2.48E+00	7.18E-03		6.90E-01	1.53E-01		2.74E-01	6.49E-01		-1.09E+00	2.30E-04	Down	-8.06E-01	4.19E-03		Unigene49447_All//gi|297838453|ref|XP_002887108.1|//6.00E-28//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332949|gb|EFH63367.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49447_All//3.00E-29//AT1G67180| zinc finger (C3HC4-type RING finger) family protein / BRCT domain-containing protein	Unigene49447_All//0.00E+00//TC165296				nr -
Unigene49448_All	525	31.69	53.56	81.35	88.24	83.63	104.87	94.39	76.59	71.41	7.57E-01	2.97E-13			1.36E+00	5.74E-49	Up	-7.75E-02	4.16E-01		2.49E-01	4.48E-04		-3.02E-01	7.50E-06		-4.03E-01	8.92E-10		Unigene49448_All//gi|224128011|ref|XP_002320219.1|//3.00E-46//SAUR family protein [Populus trichocarpa] >gi|222860992|gb|EEE98534.1| SAUR family protein [Populus trichocarpa]	Unigene49448_All//5.00E-33//AT2G46690| auxin-responsive family protein	Unigene49448_All//1.00E-69//DT047283				nr -
Unigene49449_All	1324	16.36	3.75	9.69	21.03	8.82	4.40	5.65	11.11	0.99	-2.13E+00	2.99E-48	Down	-7.55E-01	6.67E-10		-1.25E+00	4.04E-36	Down	-2.26E+00	1.58E-72	Down	9.75E-01	3.82E-13		-2.51E+00	3.81E-26	Down	Unigene49449_All//gi|2688828|gb|AAB88878.1|//6.00E-89//ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]	Unigene49449_All//5.00E-76//AT1G49390| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene49449_All//0.00E+00//TC145714		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis		nr +
Unigene49451_All	1077	4.66	4.75	5.69	5.55	7.23	7.72	4.08	0.93	3.74	2.70E-02	9.38E-01			2.86E-01	2.75E-01		3.81E-01	7.36E-02		4.75E-01	1.94E-02		-2.13E+00	1.39E-12	Down	-1.28E-01	6.46E-01		Unigene49451_All//gi|5454194|gb|AAD43609.1|AC005698_8//2.00E-83//T3F18.8 [Arabidopsis thaliana]	Unigene49451_All//6.00E-67//AT1G62520| unknown protein	Unigene49451_All//0.00E+00//TC159891				nr -
Unigene49453_All	857	41.39	413.22	167.52	77.25	249.89	180.76	14.06	72.23	78.19	3.32E+00	0.00E+00	Up	2.02E+00	7.04E-288	Up	1.69E+00	0.00E+00	Up	1.23E+00	2.99E-166	Up	2.36E+00	7.12E-190	Up	2.48E+00	2.62E-221	Up	Unigene49453_All//gi|225431128|ref|XP_002265844.1|//6.00E-29//PREDICTED: similar to DnaJ-like protein [Vitis vinifera]	Unigene49453_All//1.00E-25//AT2G17880| DNAJ heat shock protein, putative	Unigene49453_All//0.00E+00//TC130603				nr +
Unigene49454_All	1225	3.25	3.76	2.83	8.21	7.36	7.34	2.62	1.26	0.94	2.14E-01	4.73E-01		-2.00E-01	5.63E-01		-1.58E-01	4.54E-01		-1.63E-01	4.44E-01		-1.06E+00	7.09E-04	Down	-1.48E+00	3.30E-06	Down	Unigene49454_All//gi|42566766|ref|NP_193135.2|//0.00E+00//exostosin family protein [Arabidopsis thaliana]	Unigene49454_All//0.00E+00//AT4G13990| exostosin family protein	Unigene49454_All//0.00E+00//ES802449				nr -
Unigene49457_All	628	7.17	35.99	14.41	4.05	14.91	21.14	7.54	3.59	4.69	2.33E+00	7.21E-56	Up	1.01E+00	5.56E-07	Up	1.88E+00	9.92E-21	Up	2.39E+00	2.75E-36	Up	-1.07E+00	1.99E-05	Down	-6.84E-01	4.12E-03		Unigene49457_All//gi|300608164|emb|CAZ86692.1|//5.00E-52//epoxide hydrolase 1 [Prunus persica]	Unigene49457_All//4.00E-49//AT2G26740| ATSEH (Arabidopsis thaliana soluble epoxide hydrolase); epoxide hydrolase	Unigene49457_All//0.00E+00//gi|48805472|gb|CO106786.1|CO106786				nr -
Unigene49459_All	836	1.38	0.06	1.21	1.91	1.85	2.59	3.14	2.10	2.05	-4.51E+00	1.11E-05	Down	-1.86E-01	7.59E-01		-4.08E-02	9.33E-01		4.44E-01	3.51E-01		-5.79E-01	1.02E-01		-6.14E-01	6.72E-02		Unigene49459_All//gi|15226583|ref|NP_179165.1|//3.00E-76//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75216226|sp|Q9ZQF1.1|PP152_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g15630, mitochondrial; Flags: Precursor	Unigene49459_All//1.00E-77//AT2G15630| pentatricopeptide (PPR) repeat-containing protein	Unigene49459_All//0.00E+00//CO121919				nr -
Unigene49460_All	914	10.93	24.61	4.25	24.20	16.01	22.83	4.95	187.67	1.74	1.17E+00	2.04E-21	Up	-1.36E+00	7.28E-12	Down	-5.96E-01	2.21E-08		-8.41E-02	5.70E-01		5.24E+00	0.00E+00	Up	-1.51E+00	1.29E-08	Down	Unigene49460_All//gi|123580|sp|P05477.1|HSP21_SOYBN//2.00E-60//RecName: Full=17.9 kDa class II heat shock protein	Unigene49460_All//5.00E-32//AT5G12020| HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN)	Unigene49460_All//0.00E+00//gi|109835449|gb|DW234012.1|DW234012				nr +
Unigene49462_All	758	54.74	84.29	37.16	172.58	175.36	665.06	180.61	302.05	516.59	6.23E-01	6.96E-21		-5.59E-01	4.86E-11		2.31E-02	7.10E-01		1.95E+00	0.00E+00	Up	7.42E-01	2.54E-121		1.52E+00	0.00E+00	Up	Unigene49462_All//gi|225466053|ref|XP_002263278.1|//7.00E-68//PREDICTED: ripening-related protein-like [Vitis vinifera]	Unigene49462_All//1.00E-57//AT5G62350| invertase/pectin methylesterase inhibitor family protein / DC 1.2 homolog (PL5-2122)	Unigene49462_All//0.00E+00//gi|73864057|gb|DT466796.1|DT466796		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene49464_All	1000	1.41	1.93	0.32	1.89	3.37	1.90	2.07	1.76	7.29	4.47E-01	3.56E-01		-2.14E+00	1.24E-03		8.34E-01	1.12E-02		3.00E-03	9.99E-01		-2.39E-01	6.04E-01		1.82E+00	5.57E-17	Up	Unigene49464_All//gi|212717196|gb|ACJ37439.1|//5.00E-59//AP2 domain-containing transcription factor 5 [Glycine max]	Unigene49464_All//8.00E-25//AT1G44830| AP2 domain-containing transcription factor TINY, putative	Unigene49464_All//0.00E+00//TC157922	AP2-EREBP			nr +
Unigene49465_All	591	5.22	2.57	2.79	8.68	9.15	9.09	32.48	12.45	17.32	-1.02E+00	4.17E-03		-9.03E-01	1.51E-02		7.54E-02	8.36E-01		6.69E-02	8.20E-01		-1.38E+00	5.88E-29	Down	-9.07E-01	1.50E-15		Unigene49465_All//gi|18402631|ref|NP_564545.1|//3.00E-17//TOM6 (translocase of the outer mitochondrial membrane 6) [Arabidopsis thaliana] >gi|46577137|sp|Q9XIA7.1|TOM6_ARATH RecName: Full=Mitochondrial import receptor subunit TOM6 homolog; AltName: Full=Translocase of outer membrane 6 kDa subunit homolog >gi|5430759|gb|AAD43159.1|AC007504_14 Unknown Protein [Arabidopsis thaliana] >gi|11692924|gb|AAG40065.1|AF324714_1 At1g49410 [Arabidopsis thaliana] >gi|17622380|gb|AAG40411.1|AF325059_1 At1g49410 [Arabidopsis thaliana] >gi|14335020|gb|AAK59774.1|At1g49410/F13F21_16 [Arabidopsis thaliana] >gi|27363338|gb|AAO11588.1|At1g49410/F13F21_16 [Arabidopsis thaliana]	Unigene49465_All//2.00E-18//AT1G49410| TOM6 (translocase of the outer mitochondrial membrane 6)	Unigene49465_All//0.00E+00//gi|164326696|gb|ES838511.1|ES838511				nr +
Unigene49466_All	243	2.15	0.42	2.19	0.00	0.00	4.09	0.35	1.38	0.49	-2.37E+00	4.75E-02		2.54E-02	9.99E-01		null	null		1.20E+01	6.14E-06	Up	1.98E+00	1.44E-01		4.99E-01	8.07E-01					Unigene49466_All//7.00E-14//TC147599				
Unigene49467_All	630	2.57	3.86	6.68	3.08	3.61	5.02	1.28	0.80	0.38	5.85E-01	1.51E-01		1.38E+00	1.83E-05	Up	2.26E-01	6.27E-01		7.03E-01	4.76E-02		-6.80E-01	3.53E-01		-1.75E+00	1.55E-02					Unigene49467_All//4.00E-110//BF278573				
Unigene49468_All	505	35.85	26.69	18.56	69.64	58.03	82.28	66.81	33.52	26.74	-4.26E-01	1.10E-03		-9.50E-01	4.52E-12		-2.63E-01	2.59E-03		2.41E-01	4.25E-03		-9.95E-01	4.33E-30		-1.32E+00	2.74E-48	Down	Unigene49468_All//gi|115447237|ref|XP_001047398.1|//3.00E-13//Os02g0610400 (Oryza sativa Japonica Group) >gi|113536929|dbj|BAF09312.1|Os02g0610400 (Oryza sativa Japonica Group)	Unigene49468_All//2.00E-07//AT4G32720| AtLa1 (Arabidopsis thaliana La protein 1); RNA binding	Unigene49468_All//0.00E+00//gi|21103386|gb|BQ415699.1|BQ415699				nr -
Unigene49470_All	940	0.78	0.92	2.89	1.75	1.83	0.77	4.77	2.36	1.95	2.34E-01	7.28E-01		1.89E+00	1.57E-05	Up	6.68E-02	9.14E-01		-1.19E+00	2.25E-02		-1.02E+00	7.74E-05	Down	-1.29E+00	5.99E-07	Down									
Unigene49472_All	1213	2.76	2.13	2.81	0.86	1.22	3.87	6.38	4.96	114.62	-3.74E-01	2.80E-01		2.54E-02	9.59E-01		5.01E-01	3.99E-01		2.17E+00	1.00E-11	Up	-3.62E-01	6.02E-02		4.17E+00	0.00E+00	Up	Unigene49472_All//gi|297850166|ref|XP_002892964.1|//7.00E-97//phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297338806|gb|EFH69223.1| phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene49472_All//5.00E-93//AT1G73010| phosphatase	Unigene49472_All//0.00E+00//TC143830				nr -
Unigene49473_All	484	5.41	2.83	4.84	8.85	5.55	4.11	35.12	12.09	10.12	-9.35E-01	1.67E-02		-1.59E-01	6.90E-01		-6.74E-01	1.54E-02		-1.11E+00	1.44E-04	Down	-1.54E+00	5.21E-30	Down	-1.79E+00	2.39E-38	Down				Unigene49473_All//0.00E+00//TC144291				
Unigene49474_All	669	32.22	37.57	40.83	64.41	62.23	68.86	77.04	46.86	36.74	2.21E-01	5.18E-02		3.42E-01	1.68E-03		-4.96E-02	6.17E-01		9.64E-02	3.09E-01		-7.17E-01	2.08E-26		-1.07E+00	1.57E-52	Down	Unigene49474_All//gi|122194126|sp|Q1W376.1|PMM_SOYBN//6.00E-57//RecName: Full=Phosphomannomutase; AltName: Full=GmPMM >gi|90762150|gb|ABD97873.1| phosphomannomutase [Glycine max]	Unigene49474_All//1.00E-51//AT2G45790| PMM (PHOSPHOMANNOMUTASE); phosphomannomutase	Unigene49474_All//0.00E+00//gi|21102499|gb|BQ414812.1|BQ414812		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene49475_All	449	8.39	18.51	2.02	9.65	5.75	4.33	5.65	3.72	3.11	1.14E+00	4.28E-08	Up	-2.06E+00	3.54E-08	Down	-7.47E-01	6.37E-03		-1.16E+00	6.72E-05	Down	-6.02E-01	9.38E-02		-8.63E-01	1.15E-02					Unigene49475_All//0.00E+00//TC162455				
Unigene49476_All	635	2.97	4.07	3.10	6.75	1.90	1.64	2.00	1.78	1.19	4.56E-01	2.50E-01		6.50E-02	8.92E-01		-1.83E+00	4.36E-10	Down	-2.04E+00	2.97E-10	Down	-1.69E-01	7.53E-01		-7.45E-01	1.46E-01					Unigene49476_All//2.00E-96//TC162455				
Unigene49477_All	635	5.03	23.54	4.86	14.98	45.01	33.78	16.05	31.99	62.74	2.23E+00	3.17E-35	Up	-4.74E-02	9.02E-01		1.59E+00	8.90E-50	Up	1.17E+00	7.50E-22	Up	9.95E-01	2.01E-18		1.97E+00	3.08E-99	Up	Unigene49477_All//gi|255583867|ref|XP_002532684.1|//2.00E-25//conserved hypothetical protein [Ricinus communis] >gi|223527581|gb|EEF29697.1| conserved hypothetical protein [Ricinus communis]	Unigene49477_All//1.00E-14//AT3G15518| unknown protein					nr -
Unigene49478_All	822	1.78	1.79	0.78	6.67	8.13	21.32	43.41	167.18	235.83	4.40E-03	9.94E-01		-1.20E+00	4.21E-02		2.86E-01	2.48E-01		1.68E+00	2.38E-30	Up	1.95E+00	0.00E+00	Up	2.44E+00	0.00E+00	Up	Unigene49478_All//gi|290578583|gb|ADD51186.1|//2.00E-79//tumor-related protein [Vitis berlandieri x Vitis riparia]	Unigene49478_All//7.00E-64//AT1G17860| trypsin and protease inhibitor family protein / Kunitz family protein	Unigene49478_All//0.00E+00//TC154740				nr +
Unigene49479_All	967	47.51	49.10	43.78	2.88	8.48	6.40	0.17	0.99	0.25	4.76E-02	6.23E-01		-1.18E-01	1.98E-01		1.55E+00	4.79E-14	Up	1.15E+00	1.56E-06	Up	2.51E+00	7.99E-04	Up	4.99E-01	7.07E-01		Unigene49479_All//gi|15238143|ref|NP_199572.1|//2.00E-41//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565286|sp|Q9FGJ6.1|ATL5M_ARATH RecName: Full=RING-H2 finger protein ATL5M; Flags: Precursor >gi|98960905|gb|ABF58936.1| At5g47610 [Arabidopsis thaliana]	Unigene49479_All//9.00E-37//AT5G47610| zinc finger (C3HC4-type RING finger) family protein	Unigene49479_All//2.00E-26//CA994184		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene4948_All	791	19.71	16.85	15.42	14.80	15.80	19.07	28.06	10.78	9.37	-2.27E-01	1.30E-01		-3.55E-01	1.81E-02		9.46E-02	6.19E-01		3.66E-01	1.22E-02		-1.38E+00	3.04E-33	Down	-1.58E+00	8.12E-42	Down	Unigene4948_All//gi|297811663|ref|XP_002873715.1|//7.00E-56//ribosomal protein L27 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319552|gb|EFH49974.1| ribosomal protein L27 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4948_All//9.00E-52//AT5G15220| ribosomal protein L27 family protein	Unigene4948_All//0.00E+00//TC146021		ko03010|Ribosome		nr -
Unigene49480_All	558	29.91	7.54	18.04	63.12	51.04	68.72	74.33	31.61	26.27	-1.99E+00	2.71E-34	Down	-7.30E-01	2.23E-07		-3.07E-01	3.30E-04		1.23E-01	2.22E-01		-1.23E+00	9.53E-52	Down	-1.50E+00	1.37E-71	Down	Unigene49480_All//gi|116292768|gb|ABJ97690.1|//5.00E-55//EBP1 [Solanum tuberosum]	Unigene49480_All//4.00E-51//AT3G51800| ATG2; aminopeptidase/ metalloexopeptidase	Unigene49480_All//0.00E+00//gi|21090037|gb|BQ402350.1|BQ402350				nr +
Unigene49481_All	822	10.63	32.86	17.62	34.79	46.54	43.68	9.46	18.00	8.38	1.63E+00	1.06E-41	Up	7.29E-01	1.70E-06		4.20E-01	1.58E-07		3.29E-01	2.02E-04		9.27E-01	3.21E-12		-1.75E-01	3.80E-01		Unigene49481_All//gi|6721099|gb|AAF26753.1|AC007396_2//2.00E-31//T4012.4 [Arabidopsis thaliana] >gi|37202064|gb|AAQ83647.1|At1g75810 [Arabidopsis thaliana]	Unigene49481_All//8.00E-33//AT1G75810| unknown protein	Unigene49481_All//0.00E+00//DW496777				nr -
Unigene49482_All	557	3.01	9.73	3.25	6.53	10.02	3.89	18.90	100.70	109.36	1.70E+00	2.00E-09	Up	1.13E-01	8.10E-01		6.17E-01	1.19E-02		-7.46E-01	2.02E-02		2.41E+00	1.15E-176	Up	2.53E+00	1.43E-206	Up	Unigene49482_All//gi|2346978|dbj|BAA21923.1|//1.00E-49//ZPT2-14 [Petunia x hybrida]	Unigene49482_All//2.00E-29//AT2G28710| zinc finger (C2H2 type) family protein	Unigene49482_All//2.00E-22//DW501288	C2H2			nr +
Unigene49483_All	703	1.86	5.33	2.80	6.73	5.83	9.19	4.03	6.18	6.91	1.52E+00	6.88E-06	Up	5.91E-01	2.29E-01		-2.08E-01	5.15E-01		4.49E-01	6.08E-02		6.18E-01	1.77E-02		7.79E-01	9.95E-04		Unigene49483_All//gi|300161172|gb|EFJ27788.1|//6.00E-09//rab family GTPase [Selaginella moellendorffii] >gi|300170271|gb|EFJ36872.1| rab family GTPase [Selaginella moellendorffii]	Unigene49483_All//3.00E-10//AT5G59840| Ras-related GTP-binding family protein	Unigene49483_All//5.00E-42//TC131134				nr -
Unigene49484_All	978	0.80	86.63	0.71	2.39	3.87	5.36	0.56	5.00	2.73	6.75E+00	0.00E+00	Up	-1.81E-01	8.07E-01		6.94E-01	2.51E-02		1.16E+00	1.02E-05	Up	3.15E+00	4.89E-21	Up	2.28E+00	9.98E-09	Up	Unigene49484_All//gi|78499707|gb|ABB45860.1|//1.00E-123//DRE-binding protein 3a [Gossypium hirsutum]	Unigene49484_All//8.00E-30//AT1G12630| DNA binding / transcription activator/ transcription factor	Unigene49484_All//0.00E+00//TC131768	AP2-EREBP			nr -
Unigene49485_All	749	5.38	15.15	5.90	10.77	8.78	12.90	8.47	19.08	21.91	1.49E+00	6.51E-16	Up	1.34E-01	6.54E-01		-2.95E-01	1.65E-01		2.60E-01	2.00E-01		1.17E+00	5.67E-17	Up	1.37E+00	4.31E-25	Up				Unigene49485_All//2.00E-85//ES795392				

Unigene49486_All	1419	0.81	0.07	0.41	8.78	1.46	2.64	10.10	1.65	2.50	-3.51E+00	6.57E-05	Down	-9.75E-01	1.46E-01		-2.59E+00	1.39E-44	Down	-1.73E+00	3.97E-23	Down	-2.61E+00	4.48E-50	Down	-2.02E+00	7.75E-38	Down	Unigene49486_All//gi|38344063|emb|CAE02744.2|//4.00E-18//OSJNBa0006820.7 [Oryza sativa (japonica cultivar-group)] >gi|116310779|emb|CAH67571.1|H0315A08.1 [Oryza sativa (indica cultivar-group)]		Unigene49486_All//0.00E+00//D8461919				nr -
Unigene49487_All	1494	1.05	1.05	0.86	1.23	0.97	3.75	4.61	5.18	3.47	1.10E-03	1.00E+00		-2.97E-01	6.10E-01		-3.50E-01	4.93E-01		1.60E+00	1.83E-09	Up	1.66E-01	4.32E-01		-4.12E-01	3.51E-02		Unigene49487_All//gi|224106229|ref|XP_002314093.1|//0.00E+00//GRAS family transcription factor [Populus trichocarpa] >gi|222850501|gb|EEE88048.1| GRAS family transcription factor [Populus trichocarpa]	Unigene49487_All//3.00E-162//AT1G50420| SCL3; transcription factor	Unigene49487_All//0.00E+00//CO103008	GRAS			nr +
Unigene4949_All	964	16.99	12.14	13.70	25.53	22.22	19.44	16.23	9.19	6.78	-4.85E-01	4.17E-04		-3.10E-01	3.59E-02		-2.00E-01	8.08E-02		-3.93E-01	2.76E-04		-8.20E-01	1.28E-10		-1.26E+00	2.67E-21	Down	Unigene4949_All//gi|79497359|ref|NP_195390.2|//1.00E-61//HVA22K (HVA22-LIKE PROTEIN K) [Arabidopsis thaliana] >gi|57012586|sp|Q6NL18.1|HA22K_ARATH RecName: Full=HVA22-like protein k; Short=AtHVA22k >gi|45752772|gb|AAS76284.1|At4g36720 [Arabidopsis thaliana]	Unigene4949_All//7.00E-63//AT4G36720| HVA22K (HVA22-LIKE PROTEIN K)	Unigene4949_All//0.00E+00//TC165238				nr -
Unigene49490_All	1509	0.90	1.95	2.08	1.52	1.12	1.80	7.90	4.63	52.38	1.11E+00	2.76E-03		1.21E+00	1.21E-03		-4.42E-01	3.14E-01		2.42E-01	5.92E-01		-7.73E-01	1.48E-07		2.73E+00	4.72E-291	Up	Unigene49490_All//gi|15233322|ref|NP_188864.1|//1.00E-135//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|9294091|dbj|BAB01943.1| UDP-glucose glucosyltransferase-like protein [Arabidopsis thaliana]	Unigene49490_All//5.00E-107//AT3G22250| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene49490_All//0.00E+00//CO078893		ko00940|Phenylpropanoid biosynthesis//ko00908|Zeatin biosynthesis//ko00460|Cyanoamino acid metabolism//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene49491_All	1217	23.17	56.83	16.98	37.00	55.32	43.38	15.53	31.63	42.16	1.29E+00	2.83E-75	Up	-4.49E-01	2.01E-05		5.80E-01	8.41E-23		2.30E-01	1.78E-03		1.03E+00	6.50E-36	Up	1.44E+00	1.91E-82	Up	Unigene49491_All//gi|87241311|gb|ABD33169.1|//8.00E-26//C2 [Medicago truncatula]	Unigene49491_All//4.00E-11//AT1G96070| SRC2 (SOYBEAN GENE REGULATED BY COLD-2); protein binding	Unigene49491_All//0.00E+00//TC171529				nr -
Unigene49494_All	864	2.18	0.53	3.88	2.08	3.11	2.25	1.22	2.37	3.04	-2.05E+00	1.17E-04	Down	8.33E-01	1.83E-02		5.83E-01	1.40E-01		1.15E-01	8.17E-01		9.54E-01	1.82E-02		1.31E+00	1.72E-04	Up			Unigene49494_All//1.00E-21//gi|78335624|gb|DY557898.1|DY557898				
Unigene49495_All	703	3.05	1.01	1.29	6.73	4.75	2.51	3.97	1.84	0.85	-1.60E+00	6.02E-04	Down	-1.24E+00	7.98E-03		-5.03E-01	6.33E-02		-1.43E+00	4.89E-07	Down	-1.11E+00	1.10E-03		-2.22E+00	5.64E-09	Down	Unigene49495_All//gi|115468596|ref|NP_001057897.1|//3.00E-23//Os06g0567000 [Oryza sativa Japonica Group] >gi|113595937|dbj|BAF19811.1|Os06g0567000 [Oryza sativa Japonica Group]	Unigene49495_All//2.00E-13//AT4G29735| unknown protein	Unigene49495_All//0.00E+00//gi|109880277|gb|DW509247.1|DW509247				nr +
Unigene49498_All	428	82.27	69.14	69.55	95.21	57.20	33.87	60.85	34.76	28.30	-2.51E-01	6.80E-03		-2.42E-01	1.27E-02		-7.35E-01	1.22E-21		-1.49E+00	4.31E-60	Down	-8.08E-01	1.04E-16		-1.10E+00	1.87E-28	Down			Unigene49498_All//2.00E-99//gi|48779196|gb|CO088562.1|CO088562				
Unigene4950_All	675	3.49	1.28	2.29	3.91	2.19	2.61	1.32	2.11	0.59	-1.45E+00	8.22E-04	Down	-6.09E-01	1.61E-01		-8.34E-01	2.34E-02		-5.84E-01	1.43E-01		6.79E-01	1.82E-01		-1.16E+00	7.15E-02		Unigene4950_All//gi|224121178|ref|XP_002318518.1|//9.00E-07//predicted protein [Populus trichocarpa] >gi|222859191|gb|EEE96738.1|predicted protein [Populus trichocarpa]		Unigene4950_All//0.00E+00//TC166157				nr -
Unigene49501_All	737	6.46	8.46	13.22	14.53	8.55	11.28	13.60	14.06	17.19	3.89E-01	1.10E-01		1.03E+00	9.76E-08	Up	-7.65E-01	1.79E-06		-3.66E-01	4.07E-02		4.88E-02	7.90E-01		3.38E-01	1.59E-02		Unigene49501_All//gi|255567262|ref|XP_002524612.1|//2.00E-32//hypothetical protein RCOM_1213740 [Ricinus communis] >gi|223536165|gb|EEF37820.1|hypothetical protein RCOM_1213740 [Ricinus communis]		Unigene49501_All//0.00E+00//TC151747				nr -
Unigene49502_All	797	1.44	7.69	7.95	7.25	10.80	17.45	7.11	7.55	5.90	2.41E+00	2.99E-16	Up	2.46E+00	1.39E-16	Up	5.75E-01	2.33E-03		1.27E+00	3.85E-16	Up	8.72E-02	7.26E-01		-2.69E-01	2.41E-01		Unigene49502_All//gi|224076964|ref|XP_002305070.1|//6.00E-59//f-box family protein [Populus trichocarpa] >gi|222848034|gb|EEE85581.1| f-box family protein [Populus trichocarpa]	Unigene49502_All//8.00E-38//AT2G34140| Dof-type zinc finger domain-containing protein	Unigene49502_All//0.00E+00//DT048472	C2C2-Dof			nr -
Unigene49503_All	998	1.78	1.68	2.24	6.19	7.38	5.70	3.05	0.46	0.64	-8.94E-02	8.47E-01		3.30E-01	4.62E-01		2.55E-01	2.91E-01		-1.18E-01	6.74E-01		-2.73E+00	1.19E-11	Down	-2.26E+00	7.06E-10	Down	Unigene49503_All//gi|29839287|sp|Q41709.2|FRI2_VIGUN//2.00E-50//RecName: Full=Ferritin-2, chloroplastic; Flags: Precursor >gi|2970654|gb|AAC06027.1|ferritin subunit cowpea2 precursor [Vigna unguiculata]	Unigene49503_All//8.00E-45//AT3G11050| ATFER2 (ferritin 2); binding / ferric iron binding / oxidoreductase/ transition metal ion binding	Unigene49503_All//0.00E+00//TC130145		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene49505_All	1047	18.74	15.87	15.21	14.46	16.77	17.51	28.43	22.95	11.95	-2.40E-01	6.65E-02		-3.01E-01	2.40E-02		2.14E-01	1.33E-01		2.76E-01	4.08E-02		-3.09E-01	5.52E-04		-1.25E+00	2.73E-39	Down	Unigene49505_All//gi|89001077|gb|ABD59128.1|//5.00E-39//At4g01897 [Arabidopsis thaliana]	Unigene49505_All//2.00E-40//AT4G01897| unknown protein	Unigene49505_All//0.00E+00//DW513961				nr +
Unigene49507_All	842	28.21	142.08	42.75	48.51	111.77	162.04	19.94	86.27	171.70	2.33E+00	2.70E-294	Up	6.00E-01	6.63E-11		1.20E+00	2.12E-108	Up	1.74E+00	3.26E-246	Up	2.11E+00	3.08E-194	Up	3.11E+00	0.00E+00	Up	Unigene49507_All//gi|14190517|gb|AK55739.1|AF380658_1//2.00E-43//At1g53031 [Arabidopsis thaliana] >gi|15899782|gb|AAL06819.1|At1g53031 [Arabidopsis thaliana]	Unigene49507_All//2.00E-36//AT3G15358| unknown protein	Unigene49507_All//0.00E+00//TC144069				nr -
Unigene49508_All	1008	3.37	2.92	1.48	2.22	2.39	2.73	0.34	0.54	2.29	-2.11E-01	5.56E-01		-1.19E+00	8.56E-04	Down	1.05E-01	8.24E-01		2.98E-01	4.78E-01		6.84E-01	4.49E-01		2.77E+00	2.46E-09	Up	Unigene49508_All//gi|15230214|ref|NP_189130.1|//4.00E-40//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	Unigene49508_All//3.00E-28//AT3G24860| hydroxyproline-rich glycoprotein family protein	Unigene49508_All//3.00E-44//EX164887	Trihelix			nr +
Unigene49509_All	643	3.25	1.89	3.89	10.77	6.32	6.74	5.06	2.21	4.09	-7.83E-01	7.79E-02		2.58E-01	5.55E-01		-7.69E-01	1.94E-04		-6.75E-01	2.06E-03		-1.20E+00	1.33E-04	Down	-3.08E-01	3.27E-01		Unigene49509_All//gi|255537349|ref|XP_002509741.1|//8.00E-10//conserved hypothetical protein [Ricinus communis] >gi|223549640|gb|EEF51128.1|conserved hypothetical protein [Ricinus communis]		Unigene49509_All//5.00E-76//gi|21094478|gb|BQ406803.1|BQ406803				nr -
Unigene4951_All	880	1.01	0.23	0.97	1.81	0.35	0.67	2.26	0.52	0.14	-2.13E+00	1.06E-02		-6.20E-02	9.45E-01		-2.36E+00	1.76E-05	Down	-1.44E+00	7.26E-03		-2.11E+00	5.15E-06	Down	-4.06E+00	3.04E-11	Down	Unigene4951_All//gi|8778702|gb|AAF79710.1|AC020889_18//1.00E-22//T1N15.20 [Arabidopsis thaliana]	Unigene4951_All//6.00E-26//AT1G48580| unknown protein	Unigene4951_All//0.00E+00//TC166157				nr +
Unigene49510_All	1452	10.23	4.64	6.45	4.43	3.32	3.89	1.31	0.40	0.27	-1.14E+00	6.55E-14	Down	-6.65E-01	9.33E-06		-4.15E-01	7.22E-02		-1.87E-01	4.82E-01		-1.70E+00	1.53E-04	Down	-2.26E+00	1.81E-06	Down	Unigene49510_All//gi|18407193|ref|NP_566089.1|//4.00E-61//NGA1 (NGATHA1); transcription factor [Arabidopsis thaliana] >gi|75100798|sp|Q82799.1|NGA1_ARATH RecName: Full=B3 domain-containing transcription factor NGA1; AltName: Full=Protein NGATHA 1	Unigene49510_All//1.00E-60//AT2G46870| NGA1 (NGATHA1); transcription factor	Unigene49510_All//0.00E+00//TC177638	ABI3VP1			nr -
Unigene49512_All	709	0.44	3.50	0.75	6.53	5.63	10.32	24.15	36.79	32.37	2.98E+00	1.46E-08	Up	7.62E-01	4.52E-01		-2.14E-01	5.03E-01		6.59E-01	2.05E-03		6.07E-01	1.88E-10		4.22E-01	2.23E-05		Unigene49512_All//gi|297798220|ref|XP_002866994.1|//3.00E-66//homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata] >gi|297312830|gb|EFH43253.1|homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata]	Unigene49512_All//8.00E-52//AT4G36740| ATHB40 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 40); DNA binding / transcription factor	Unigene49512_All//0.00E+00//TC139526	HB			nr +
Unigene49515_All	706	1.93	1.58	0.98	2.54	1.56	1.34	3.41	1.36	1.92	-2.87E-01	6.02E-01		-9.75E-01	1.09E-01		-7.03E-01	1.40E-01		-9.19E-01	6.19E-02		-1.33E+00	4.24E-04	Down	-8.31E-01	1.80E-02		Unigene49515_All//gi|242129048|gb|ACS83603.1|//7.00E-30//ATP synthase delta subunit 2 [Gossypium hirsutum]	Unigene49515_All//2.00E-25//AT5G47030| ATP synthase delta' chain, mitochondrial	Unigene49515_All//1.00E-30//gi|13247522|gb|BF270936.2|BF270936		ko00190|Oxidative phosphorylation		nr +
Unigene49516_All	1160	7.40	2.58	3.26	9.83	8.97	9.62	18.01	6.23	10.96	-1.52E+00	1.39E-12	Down	-1.18E+00	2.23E-08	Down	-1.34E-01	5.12E-01		-3.22E-02	8.80E-01		-1.53E+00	2.00E-36	Down	-7.17E-01	1.54E-11		Unigene49516_All//gi|297813577|ref|XP_002874672.1|//2.00E-69//mitochondrially targeted single-stranded DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297320509|gb|EFH50931.1|mitochondrially targeted single-stranded DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene49516_All//2.00E-66//AT4G11060| MTSSB (mitochondrially targeted single-stranded DNA binding protein); single-stranded DNA binding	Unigene49516_All//0.00E+00//TC138258		ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +
Unigene49517_All	548	91.94	14.89	30.41	57.45	61.58	36.76	90.27	31.04	36.20	-2.63E+00	1.04E-143	Down	-1.60E+00	5.95E-73	Down	1.00E-01	3.65E-01		-6.44E-01	4.92E-12		-1.54E+00	5.06E-86	Down	-1.32E+00	3.68E-70	Down	Unigene49517_All//gi|15241168|ref|NP_197478.1|//7.00E-70//TUA3; structural constituent of cytoskeleton [Arabidopsis thaliana] >gi|15241179|ref|NP_197479.1|TUA5; structural constituent of cytoskeleton [Arabidopsis thaliana] >gi|297808045|ref|XP_002871906.1|tubulin alpha-3 [Arabidopsis lyrata subsp. lyrata] >gi|297812159|ref|XP_002873963.1|tubulin alpha-3 [Arabidopsis lyrata subsp. lyrata] >gi|135406|sp|P20363.1|TBA3_ARATH RecName: Full=Tubulin alpha-3/alpha-5 chain >gi|13605805|gb|AAK32888.1|AF367301_1 AT5g19770/T29J13_190 [Arabidopsis thaliana] >gi|166912|gb|AAA32888.1| alpha-tubulin [Arabidopsis thaliana] >gi|166918|gb|AAA32891.1| alpha-5 tubulin [Arabidopsis thaliana] >gi|23505949|gb|AAN28834.1|At5g19770/T29J13_190 [Arabidopsis thaliana] >gi|297317743|gb|EFH48165.1|tubulin alpha-3 [Arabidopsis	Unigene49517_All//4.00E-71//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene49517_All//0.00E+00//gi|21092840|gb|BQ405153.1|BQ405153		ko04145|Phagosome		nr +
Unigene49518_All	595	29.37	78.43	44.84	721.43	698.43	595.17	116.96	164.23	77.87	1.42E+00	1.75E-58	Up	6.10E-01	1.68E-08		-4.67E-02	8.16E-02		-2.78E-01	2.03E-33		4.90E-01	2.86E-25		-5.87E-01	9.57E-26		Unigene49518_All//gi|32440933|dbj|BAC78827.1|//6.00E-51//caffeic acid O-methyltransferase [Rosa chinensis var. spontanea]	Unigene49518_All//2.00E-42//AT5G54160| ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase	Unigene49518_All//0.00E+00//gi|109866096|gb|DW495072.1|DW495072		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -

Unigene49519_All	782	23.35	11.86	6.81	40.96	22.85	17.96	10.76	8.28	7.23	-9.78E-01	2.53E-13		-1.78E+00	5.07E-31	Down	-8.42E-01	1.50E-21		-1.19E+00	1.58E-33	Down	-3.77E-01	3.92E-02		-5.73E-01	8.98E-04		Unigene49519_All//gi|124360158|gb|ABN08174.1|//2.00E-67//Histone H2A; Histone-fold [Medicago truncatula] >gi|124360160|gb|ABN08176.1| Histone H2A; Histone-fold [Medicago truncatula]	Unigene49519_All//5.00E-36//AT1G54690| GAMMA-H2AX (GAMMA HISTONE VARIANT H2AX); DNA binding	Unigene49519_All//0.00E+00//TC159998				nr +
Unigene4952_All	499	5.03	6.30	5.34	10.38	14.01	10.14	4.32	10.55	2.63	3.23E-01	3.70E-01		8.43E-02	8.30E-01		4.32E-01	5.22E-02		-3.45E-02	9.20E-01		1.29E+00	1.06E-07	Up	-7.14E-01	5.74E-02					Unigene4952_All//6.00E-124//TC147151				
Unigene49521_All	1387	6.00	7.12	12.86	1.40	2.56	1.89	0.00	0.00	0.00	2.48E-01	2.02E-01		1.10E+00	5.05E-15	Up	8.68E-01	6.39E-03		4.31E-01	3.11E-01		null	null		null	null		Unigene49521_All//gi|6671365|gb|AAF23176.1|AF216497_1//0.00E+00//P-glycoprotein [Gossypium hirsutum]	Unigene49521_All//0.00E+00//AT4G25960| PGP2 (P-GLYCOPROTEIN 2); ATPase, coupled to transmembrane movement of substances	Unigene49521_All//0.00E+00//TC141861		ko02010|ABC transporters		nr +
Unigene49522_All	779	16.93	34.47	21.81	13.11	14.99	9.39	7.65	10.19	10.02	1.03E+00	1.08E-20	Up	3.66E-01	1.02E-02		1.93E-01	3.11E-01		-4.81E-01	6.92E-03		4.14E-01	2.74E-02		3.89E-01	3.37E-02					Unigene49522_All//7.00E-91//TC167481				
Unigene49523_All	798	25.70	12.32	10.21	42.76	24.47	24.39	38.89	16.03	14.13	-1.06E+00	6.62E-17	Down	-1.33E+00	5.79E-23	Down	-8.05E-01	2.82E-21		-8.10E-01	4.24E-19		-1.28E+00	3.94E-41	Down	-1.46E+00	1.03E-51	Down	Unigene49523_All//gi|15220667|ref|NP_174303.1|//3.00E-74//ATNUDX25 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 25); bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) [Arabidopsis thaliana] >gi|75308841|sp|Q9C6Z2.1|NUD25_ARATH RecName: Full=Nudix hydrolase 25; Short=AtNUDT25; AltName: Full=Bis(5'-nucleosyl)-tetraphosphatase (asymmetrical) >gi|89860929|gb|ABF58948.1| At1g30110 [Arabidopsis thaliana]	Unigene49523_All//2.00E-75//AT1G30110| ATNUDX25 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 25); bis(5'-nucleosyl)-tetraphosphatase (asymmetrical)	Unigene49523_All//1.00E-135//DW496806		ko03018|RNA degradation		nr +
Unigene49526_All	925	28.96	17.53	27.63	20.57	20.03	14.11	10.92	7.73	5.04	-7.24E-01	8.16E-12		-6.77E-02	6.13E-01		-3.86E-02	8.27E-01		-5.44E-01	9.71E-06		-5.00E-01	1.88E-03		-1.12E+00	9.07E-12	Down	Unigene49526_All//gi|13937133|gb|AAK50060.1|AF372920_1//2.00E-61//AT3g27050/MOJ10_14 [Arabidopsis thaliana] >gi|21700871|gb|AAM70559.1| AT3g27050/MOJ10_14 [Arabidopsis thaliana]	Unigene49526_All//9.00E-63//AT3G27050| unknown protein	Unigene49526_All//0.00E+00//gi|164281816|gb|ES833402.1|ES833402				nr -
Unigene49527_All	1270	18.21	17.51	8.68	1.84	2.09	2.92	0.00	0.00	0.00	-5.61E-02	6.50E-01		-1.07E+00	2.14E-18	Down	1.80E-01	6.95E-01		6.62E-01	4.07E-02		null	null		null	null		Unigene49527_All//gi|41745624|gb|AAS10177.1|//4.00E-97//YABBY-like transcription factor GRAMINIFOLIA [Antirrhinum majus]	Unigene49527_All//1.00E-72//AT2G45190| AFO (ABNORMAL FLORAL ORGANS); protein binding / transcription factor/ transcription regulator	Unigene49527_All//0.00E+00//TC131979	C2C2-YABBY			nr -
Unigene49530_All	604	5.72	8.64	11.73	17.57	12.09	10.39	8.47	3.04	3.43	5.96E-01	2.33E-02		1.04E+00	7.67E-06	Up	-5.40E-01	9.83E-04		-7.57E-01	9.30E-06		-1.48E+00	4.66E-09	Down	-1.30E+00	6.34E-08	Down	Unigene49530_All//gi|212292507|gb|ACJ24185.1|//3.00E-16//CAPRICE [Gossypium hirsutum] >gi|212292511|gb|ACJ24187.1| CAPRICE [Gossypium hirsutum] >gi|212292515|gb|ACJ24189.1| CAPRICE [Gossypium hirsutum] >gi|212292519|gb|ACJ24191.1| CAPRICE [Gossypium hirsutum]	Unigene49530_All//3.00E-07//AT1G01380| ETC1 (ENHANCER OF TRY AND CPC 1); DNA binding / transcription factor	Unigene49530_All//2.00E-177//TC171752	MYB-related			nr -
Unigene49535_All	1389	0.72	0.91	0.77	2.22	0.77	0.68	6.39	2.98	2.90	3.50E-01	5.68E-01		9.93E-02	8.79E-01		-1.53E+00	7.19E-06	Down	-1.70E+00	4.79E-06	Down	-1.10E+00	6.58E-10	Down	-1.14E+00	8.41E-11	Down	Unigene49535_All//gi|84410195|ref|NP_565049.1|//6.00E-62//NF-YA3 (NUCLEAR FACTOR Y, SUBUNIT A3); transcription factor [Arabidopsis thaliana] >gi|81174954|sp|Q93ZH2.2|NFYA3_ARATH RecName: Full=Nuclear transcription factor Y subunit A-3; Short=AtNF-YA-3; AltName: Full=Transcriptional activator HAP2C >gi|5903072|gb|AAD55630.1|AC008017_3 Transcription Factor [Arabidopsis thaliana] >gi|317118816|gb|ADP88264.1| At1g72830 [Arabidopsis thaliana]	Unigene49535_All//3.00E-51//AT1G72830| NF-YA3 (NUCLEAR FACTOR Y, SUBUNIT A3); transcription factor	Unigene49535_All//0.00E+00//gi|78336573|gb|DT556847.1|DT556847	CCAAT			nr +
Unigene49538_All	890	1.88	8.37	4.31	5.15	4.57	4.26	2.28	3.62	2.24	2.15E+00	3.63E-17	Up	1.20E+00	3.24E-04	Up	-1.74E-01	5.83E-01		-2.73E-01	3.98E-01		6.65E-01	3.20E-02		-2.69E-02	9.63E-01		Unigene49538_All//gi|15220196|ref|NP_178180.1|//6.00E-29//RTL1 (RNase three-like protein 1); RNA binding / double-stranded RNA binding [Arabidopsis thaliana] >gi|28950719|gb|AAO63283.1| At1g80650 [Arabidopsis thaliana]	Unigene49538_All//2.00E-27//AT1G80650| RTL1 (RNase three-like protein 1); RNA binding / double-stranded RNA binding	Unigene49538_All//0.00E+00//TC136292				nr -
Unigene4954_All	1717	0.12	0.06	0.00	1.57	1.16	0.61	0.91	4.33	5.41	-1.05E+00	5.64E-01		-6.93E+00	1.45E-01		-4.30E-01	2.79E-01		-1.37E+00	4.31E-04	Down	2.25E+00	4.08E-22	Up	2.57E+00	1.37E-32	Up	Unigene4954_All//gi|224119946|ref|XP_002331099.1|//1.00E-155//cytochrome P450 [Populus trichocarpa] >gi|222872827|gb|EEF09958.1| cytochrome P450 [Populus trichocarpa]	Unigene4954_All//1.00E-142//AT4G37310| CYP81H1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene4954_All//0.00E+00//TC178809		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene49540_All	1168	7.97	24.99	16.32	3.07	3.36	1.16	0.00	0.07	0.00	1.65E+00	8.58E-46	Up	1.03E+00	1.63E-14	Up	1.30E-01	7.40E-01		-1.40E+00	2.19E-05	Down	6.16E+00	4.00E-01		null	null		Unigene49540_All//gi|115447703|ref|NP_001047631.1|//3.00E-16//Os02g0657700 [Oryza sativa Japonica Group] >gi|113537162|dbj|BAF09545.1| Os02g0657700 [Oryza sativa Japonica Group]	Unigene49540_All//1.00E-19//AT4G25170| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP012943 (InterPro:IPR016606); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61490.1); Has 87 Blast hits to 86 proteins in 16 species: Archae - 0; Bacteria - 4; Metazoa - 15; Fungi - 3; Plants - 63; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene49540_All//0.00E+00//TC167561				nr -
Unigene49543_All	1343	0.00	0.15	0.00	2.78	2.56	1.88	78.99	59.10	19.37	7.24E+00	1.36E-01		null	null		-1.18E-01	7.59E-01		-5.63E-01	8.12E-02		-4.19E-01	1.04E-20		-2.03E+00	2.37E-277	Down	Unigene49543_All//gi|79317331|ref|NP_001030998.1|//1.00E-151//bZIP family transcription factor [Arabidopsis thaliana] >gi|62321732|dbj|BAD95356.1| bZip protein AtbZip21 [Arabidopsis thaliana]	Unigene49543_All//1.00E-151//AT1G08320| bZIP family transcription factor	Unigene49543_All//1.00E-130//gi|48827973|gb|CO126363.1|CO126363	bZIP			nr +
Unigene49544_All	592	9.63	8.56	8.73	11.78	16.46	18.54	12.07	9.60	35.26	-1.71E-01	5.30E-01		-1.43E-01	6.31E-01		4.83E-01	6.76E-03		6.54E-01	1.05E-04		-3.30E-01	1.07E-01		1.55E+00	1.04E-37	Up	Unigene49544_All//gi|115475810|ref|NP_001061501.1|//2.00E-40//Os08g0305300 [Oryza sativa Japonica Group] >gi|113623470|dbj|BAF23415.1| Os08g0305300 [Oryza sativa Japonica Group]	Unigene49544_All//1.00E-40//AT5G19400| SMG7	Unigene49544_All//2.00E-139//TC138860				nr +
Unigene49545_All	1196	0.53	2.84	1.25	7.37	8.21	13.41	6.61	6.12	4.70	2.43E+00	2.23E-09	Up	1.25E+00	3.19E-02		1.55E-01	4.81E-01		8.63E-01	3.52E-10		-1.12E-01	6.31E-01		-4.93E-01	5.90E-03		Unigene49545_All//gi|164564739|dbj|BAF98220.1|//4.00E-12//CM02216.380.nc [Lotus japonicus]	Unigene49545_All//2.00E-40//AT5G66440| unknown protein	Unigene49545_All//0.00E+00//TC176387				nr +
Unigene49546_All	778	28.72	8.27	29.84	1.41	2.57	9.23	2.34	1.93	1.08	-1.80E+00	6.98E-40	Down	5.55E-02	6.65E-01		8.66E-01	5.93E-02		2.71E+00	8.38E-23	Up	-2.73E-01	5.70E-01		-1.12E+00	7.71E-03		Unigene49546_All//gi|297794051|ref|XP_002864910.1|//7.00E-44//C/VIF2 [Arabidopsis lyrata subsp. lyrata] >gi|297310745|gb|EFH41169.1| C/VIF2 [Arabidopsis lyrata subsp. lyrata]	Unigene49546_All//2.00E-37//AT5G64620| C/VIF2 (CELL WALL / VACUOLAR INHIBITOR OF FRUCTOSIDASE 2); enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor	Unigene49546_All//0.00E+00//gi|109889965|gb|DW518933.1|DW518933				nr -
Unigene49548_All	1901	0.44	0.53	0.56	3.77	4.96	3.59	4.72	1.19	2.87	2.76E-01	6.62E-01		3.47E-01	6.29E-01		3.95E-01	3.45E-02		-7.29E-02	7.62E-01		-1.99E+00	7.81E-23	Down	-7.16E-01	1.88E-05		Unigene49548_All//gi|297799994|ref|XP_002867881.1|//0.00E+00//subtilase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313717|gb|EFH44140.1| subtilase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49548_All//0.00E+00//AT4G20430| subtilase family protein	Unigene49548_All//0.00E+00//TC157351				nr +
Unigene4955_All	837	0.69	4.18	1.85	0.60	1.56	3.35	5.30	3.30	3.00	2.60E+00	2.46E-10	Up	1.42E+00	1.36E-02		1.39E+00	2.11E-02		2.49E+00	2.20E-08	Up	-6.87E-01	7.27E-03		-8.23E-01	9.20E-04					Unigene4955_All//1.00E-06//TC153989				
Unigene49551_All	859	1.22	3.78	1.86	2.49	1.52	2.10	1.87	1.51	3.39	1.63E+00	1.13E-05	Up	6.10E-01	2.61E-01		-7.11E-01	9.35E-02		-2.46E-01	6.38E-01		-3.10E-01	5.40E-01		8.56E-01	7.08E-03		Unigene49551_All//gi|2191168|gb|AAB61054.1|//8.00E-38//contains similarity to myosin heavy chain [Arabidopsis thaliana]	Unigene49551_All//9.00E-39//AT5G26760| unknown protein	Unigene49551_All//2.00E-146//AT731670				nr +
Unigene49553_All	920	81.04	89.33	115.82	34.76	37.95	31.27	50.64	21.94	26.46	1.41E-01	2.06E-02		5.15E-01	9.61E-24		1.27E-01	2.22E-01		-1.53E-01	1.51E-01		-1.21E+00	4.53E-56	Down	-9.37E-01	1.88E-38		Unigene49553_All//gi|224088838|ref|XP_002308562.1|//1.00E-162//precursor of carboxylase p-protein 1, glycine decarboxylase complex [Populus trichocarpa] >gi|222854538|gb|EEE92085.1| precursor of carboxylase p-protein 1, glycine decarboxylase complex [Populus trichocarpa]	Unigene49553_All//4.00E-154//AT4G33010| AtGLDP1 (Arabidopsis thaliana glycine decarboxylase P-protein 1); catalytic/ glycine dehydrogenase (decarboxylating)/ pyridoxal phosphate binding	Unigene49553_All//0.00E+00//gi|54116872|gb|CO492381.1|CO492381		ko00260|Glycine, serine and threonine metabolism		nr -
Unigene49554_All	823	8.20	19.76	15.33	27.72	39.67	23.54	2.36	19.15	4.74	1.27E+00	1.04E-17	Up	9.03E-01	5.50E-08		5.17E-01	3.02E-09		-2.36E-01	5.08E-02		3.02E+00	1.03E-63	Up	1.01E+00	2.16E-04	Up	Unigene49554_All//gi|9972391|gb|AAG10641.1|AC022521_19//5.00E-08//Hypothetical protein [Arabidopsis thaliana]		Unigene49554_All//3.00E-155//gi|109881790|gb|DW510760.1|DW510760				nr +
Unigene49555_All	834	3.01	6.26	3.70	17.38	29.27	32.76	28.14	57.33	70.84	1.06E+00	7.58E-05	Up	2.98E-01	4.22E-01		7.52E-01	3.33E-13		9.15E-01	1.27E-18		1.03E+00	1.86E-44	Up	1.33E+00	2.99E-84	Up	Unigene49555_All//gi|254047060|gb|ACT63839.1|//4.00E-86//cyclophilin [Gossypium hirsutum]	Unigene49555_All//3.00E-72//AT2G21130| peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase	Unigene49555_All//6.00E-119//gi|109827212|gb|DW225909.1|DW225909				nr +
Unigene49560_All	793	26.06	67.15	93.41	47.24	109.25	146.71	26.18	19.98	12.01	1.37E+00	4.80E-63	Up	1.84E+00	1.80E-131	Up	1.21E+00	1.64E-100	Up	1.63E+00	2.60E-192	Up	-3.90E-01	3.03E-04		-1.12E+00	1.66E-23	Down	Unigene49560_All//gi|15224863|ref|NP_181959.1|//2.00E-51//lipid transfer protein-related [Arabidopsis thaliana] >gi|30017223|gb|AAP12845.1| At2g44300 [Arabidopsis thaliana] >gi|84778478|dbj|BAE73206.1| xylogen like protein 10 [Arabidopsis thaliana]	Unigene49560_All//1.00E-39//AT2G44300| lipid transfer protein-related	Unigene49560_All//0.00E+00//gi|109879846|gb|DW508816.1|DW508816				nr -
Unigene49561_All	1119	5.00	0.27	0.57	5.65	2.12	6.74	3.14	3.96	0.82	-4.20E+00	8.07E-25	Down	-3.13E+00	9.94E-19	Down	-1.41E+00	3.45E-10	Down	2.54E-01	2.89E-01		3.36E-01	2.22E-01		-1.94E+00	1.99E-09	Down	Unigene49561_All//gi|224056411|ref|XP_002298843.1|//1.00E-172//S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Populus trichocarpa] >gi|222846101|gb|EEE83648.1| S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Populus trichocarpa]	Unigene49561_All//8.00E-159//AT5G55250| IAMT1 (IAA CARBOXYLMETHYLTRANSFERASE 1); S-adenosylmethionine-dependent methyltransferase/ indole acetic acid carboxyl methyltransferase	Unigene49561_All//0.00E+00//TC164400		ko00592|alpha-Linolenic acid metabolism		nr +

Unigene49562_All	779	10.61	12.36	5.81	8.38	16.53	27.36	48.25	73.56	84.02	2.20E-01	2.67E-01		-8.69E-01	3.58E-05		9.81E-01	5.93E-11		1.71E+00	9.11E-38	Up	6.08E-01	4.70E-22		8.00E-01	4.99E-41		Unigene49562_All//gi|224134094|ref|XP_002327754.1|//1.00E-50//calcium dependent protein kinase 18 [Populus trichocarpa] >gi|222836839|gb|EEE75232.1| calcium dependent protein kinase 18 [Populus trichocarpa]	Unigene49562_All//1.00E-48//AT5G66210| CPK28; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ protein kinase/ protein serine/threonine kinase	Unigene49562_All//0.00E+00//TC163977		ko04626|Plant-pathogen interaction		nr -
Unigene49563_All	688	17.80	36.01	27.55	16.94	20.32	15.56	13.27	9.60	11.70	1.02E+00	7.00E-19	Up	6.31E-01	1.41E-06		2.62E-01	9.44E-02		-1.23E-01	5.45E-01		-4.68E-01	6.21E-03		-1.83E-01	3.18E-01		Unigene49563_All//gi|107738160|gb|ABF83652.1|//1.00E-62//At4g33625 [Arabidopsis thaliana]	Unigene49563_All//3.00E-62//AT4G33625| unknown protein	Unigene49563_All//0.00E+00//gi|78351793|gb|DT572067.1|DT572067				nr +
Unigene49564_All	1075	0.68	1.18	1.83	5.70	4.84	3.95	20.29	7.97	18.53	7.90E-01	1.89E-01		1.43E+00	4.28E-03		-2.37E-01	3.64E-01		-5.29E-01	2.77E-02		-1.35E+00	1.45E-31	Down	-1.31E-01	2.49E-01		Unigene49564_All//gi|224053691|ref|XP_002297931.1|//1.00E-71//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222845189|gb|EEE82736.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene49564_All//4.00E-63//AT2G43000| anac042 (Arabidopsis NAC domain containing protein 42); transcription factor	Unigene49564_All//0.00E+00//CO124002	NAC			nr -
Unigene49565_All	1393	13.22	2.87	6.65	2.54	2.50	1.13	0.18	0.00	0.23	-2.20E+00	5.65E-43	Down	-9.91E-01	4.01E-13		-2.42E-02	9.49E-01		-1.16E+00	3.83E-04	Down	-7.51E+00	4.03E-02		3.29E-01	7.63E-01		Unigene49565_All//gi|168009664|ref|XP_001757525.1|//1.00E-151//ATP-binding cassette transporter, subfamily B, member 18, group MDR/PGP protein PpABCB18 [Physcomitrella patens subsp. patens] >gi|162691219|gb|EDQ77582.1| ATP-binding cassette transporter, subfamily B, member 18, group MDR/PGP protein PpABCB18 [Physcomitrella patens subsp. patens]	Unigene49565_All//2.00E-121//AT3G28860| ABCB19; ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter			ko02010|ABC transporters		nr -
Unigene49566_All	299	0.00	1.19	0.00	3.67	2.76	6.19	29.27	711.37	76.35	1.02E+01	2.46E-02		null	null		-4.07E-01	5.60E-01		7.57E-01	1.27E-01		4.60E+00	0.00E+00	Up	1.38E+00	5.60E-35	Up	Unigene49566_All//gi|283135850|gb|ADB11316.1|//5.00E-29//tau class glutathione transferase GSTU12 [Populus trichocarpa]	Unigene49566_All//5.00E-22//AT1G78340| ATGSTU22 (GLUTATHIONE S-TRANSFERASE TAU 22); glutathione transferase	Unigene49566_All//3.00E-149//BG445736		ko00480|Glutathione metabolism		nr +
Unigene49567_All	719	0.51	1.34	1.48	3.05	3.02	2.83	17.99	210.32	15.51	1.39E+00	5.77E-02		1.54E+00	3.53E-02		-1.48E-02	9.62E-01		-1.09E-01	8.04E-01		3.55E+00	0.00E+00	Up	-2.14E-01	1.40E-01		Unigene49567_All//gi|283135848|gb|ADB11315.1|//1.00E-54//tau class glutathione transferase GSTU11 [Populus trichocarpa]	Unigene49567_All//1.00E-35//AT1G78320| ATGSTU23 (GLUTATHIONE S-TRANSFERASE TAU 23); glutathione transferase	Unigene49567_All//0.00E+00//gi|13355388|gb|BG445736.1|BG445736		ko00480|Glutathione metabolism		nr +
Unigene49568_All	616	0.25	0.08	0.00	0.08	0.34	0.59	5.63	113.38	10.48	-1.63E+00	4.88E-01		-7.99E+00	2.44E-01		2.05E+00	3.94E-01		2.86E+00	9.44E-02		4.33E+00	0.00E+00	Up	8.97E-01	1.09E-05		Unigene49568_All//gi|283135850|gb|ADB11316.1|//1.00E-39//tau class glutathione transferase GSTU12 [Populus trichocarpa]	Unigene49568_All//4.00E-16//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	Unigene49568_All//2.00E-170//TC166439		ko00480|Glutathione metabolism		nr +
Unigene49569_All	863	5.21	4.46	7.59	5.31	11.29	5.50	1.86	2.81	6.69	-2.25E-01	4.49E-01		5.42E-01	2.49E-02		1.09E+00	7.49E-10	Up	4.93E-02	8.88E-01		5.93E-01	1.10E-01		1.85E+00	6.39E-14	Up	Unigene49569_All//gi|17978987|gb|AAL47454.1|//3.00E-09//At2g46730/F19D11.1 [Arabidopsis thaliana] >gi|20197318|gb|AAM15019.1| Expressed protein [Arabidopsis thaliana] >gi|21360425|gb|AAM47328.1| At2g46730/F19D11.1 [Arabidopsis thaliana]	Unigene49569_All//6.00E-05//AT2G46735| unknown protein					nr -
Unigene4957_All	1306	2.64	0.35	0.69	3.32	3.14	2.56	3.59	1.79	2.56	-2.92E+00	1.48E-11	Down	-1.93E+00	5.28E-07	Down	-8.08E-02	8.24E-01		-3.75E-01	2.30E-01		-1.00E+00	6.12E-05	Down	-4.88E-01	4.35E-02		Unigene4957_All//gi|15231815|ref|NP_190912.1|//1.00E-50//DNA binding [Arabidopsis thaliana] >gi|30693817|ref|NP_850691.1| DNA binding [Arabidopsis thaliana] >gi|29028920|gb|AAO64839.1| At3g53440 [Arabidopsis thaliana]	Unigene4957_All//3.00E-37//AT3G53440| DNA binding	Unigene4957_All//0.00E+00//TC140017				nr +
Unigene49570_All	628	1.25	3.95	1.19	4.76	3.24	3.02	5.05	2.46	3.30	1.66E+00	1.26E-04	Up	-7.41E-02	9.35E-01		-5.57E-01	1.16E-01		-6.56E-01	7.32E-02		-1.04E+00	9.55E-04	Down	-6.14E-01	4.07E-02		Unigene49570_All//gi|15242365|ref|NP_196487.1|//1.00E-33//KIWI; DNA binding / protein binding / transcription coactivator [Arabidopsis thaliana] >gi|37079587|sp|O65154.1|KIWI_ARATH RecName: Full=RNA polymerase II transcriptional coactivator KIWI >gi|28466805|gb|AAO44011.1| At5g09250 [Arabidopsis thaliana]	Unigene49570_All//2.00E-27//AT5G09250| KIWI; DNA binding / protein binding / transcription coactivator	Unigene49570_All//4.00E-178//TC156479				nr -
Unigene49571_All	706	0.30	0.00	1.06	1.41	1.90	3.07	3.89	2.31	1.19	-8.21E+00	1.22E-01		1.83E+00	5.05E-02		4.31E-01	5.15E-01		1.12E+00	1.14E-02		-7.54E-01	2.60E-02		-1.72E+00	1.54E-06	Down	Unigene49571_All//gi|15242365|ref|NP_196487.1|//4.00E-36//KIWI; DNA binding / protein binding / transcription coactivator [Arabidopsis thaliana] >gi|37079587|sp|O65154.1|KIWI_ARATH RecName: Full=RNA polymerase II transcriptional coactivator KIWI >gi|28466805|gb|AAO44011.1| At5g09250 [Arabidopsis thaliana]	Unigene49571_All//5.00E-30//AT5G09250| KIWI; DNA binding / protein binding / transcription coactivator	Unigene49571_All//0.00E+00//TC156479				nr -
Unigene49573_All	916	12.62	11.73	8.25	106.64	68.98	34.07	34.02	20.85	11.48	-1.06E-01	5.82E-01		-6.13E-01	3.95E-04		-6.29E-01	5.50E-39		-1.65E+00	5.25E-166	Down	-7.06E-01	7.16E-16		-1.57E+00	1.64E-57	Down	Unigene49573_All//gi|223029879|gb|ACM78621.1|//1.00E-32//non-specific lipid-transfer protein type 2 [Tamarix hispida]	Unigene49573_All//6.00E-27//AT3G18280| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene49573_All//0.00E+00//gi|164240817|gb|ES814138.1|ES814138				nr +
Unigene49577_All	700	39.46	16.29	18.64	37.57	36.16	30.26	50.31	37.68	27.83	-1.28E+00	5.50E-30	Down	-1.08E+00	2.66E-22	Down	-5.55E-02	6.77E-01		-3.12E-01	3.31E-03		-4.17E-01	2.14E-07		-8.54E-01	3.40E-25		Unigene49577_All//gi|34486086|gb|AAQ73425.1|//5.00E-44//TOC33 [Brassica napus]	Unigene49577_All//3.00E-45//AT1G02280| TOC33 (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 33); GTP binding / GTPase/ protein binding	Unigene49577_All//0.00E+00//TC138172				nr +
Unigene49579_All	652	1.12	0.54	0.49	2.29	1.58	1.25	27.62	17.31	63.79	-1.05E+00	2.14E-01		-1.20E+00	1.80E-01		-5.33E-01	3.21E-01		-8.78E-01	1.13E-01		-6.75E-01	7.50E-09		1.21E+00	3.14E-51	Up	Unigene49579_All//gi|17978970|gb|AAL47446.1|//4.00E-33//At2g36580/F10J11.21 [Arabidopsis thaliana]	Unigene49579_All//2.00E-34//AT2G36580| pyruvate kinase, putative	Unigene49579_All//1.00E-159//gi|73863724|gb|DT466463.1|DT466463		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene4958_All	1064	3.10	2.52	1.70	6.23	7.51	4.58	7.59	3.42	4.08	-2.96E-01	3.87E-01		-8.64E-01	1.55E-02		2.70E-01	2.24E-01		-4.42E-01	5.93E-02		-1.15E+00	1.09E-09	Down	-8.95E-01	6.28E-07		Unigene4958_All//gi|115475732|ref|NP_001061462.1|//1.00E-39//Os08g0290400 [Oryza sativa Japonica Group] >gi|113623431|dbj|BAF23376.1| Os08g0290400 [Oryza sativa Japonica Group]	Unigene4958_All//3.00E-61//AT4G39630| unknown protein	Unigene4958_All//0.00E+00//gi|109869006|gb|DW497982.1|DW497982				nr +
Unigene49582_All	639	1.39	3.57	4.08	1.17	3.07	2.19	2.12	2.16	2.49	1.36E+00	2.01E-03		1.55E+00	3.07E-04	Up	1.39E+00	2.83E-03		9.06E-01	1.23E-01		2.78E-02	9.89E-01		2.36E-01	6.16E-01				Unigene49582_All//1.00E-122//gi|3325905|gb|AI054791.1|AI054791				
Unigene49584_All	739	1.06	3.63	2.31	0.81	2.75	1.77	0.80	3.17	2.26	1.77E+00	2.49E-05	Up	1.12E+00	3.58E-02		1.77E+00	1.86E-04	Up	1.13E+00	6.33E-02		1.98E+00	1.85E-06	Up	1.50E+00	1.16E-03		Unigene49584_All//gi|3550519|emb|CAA07589.1|//8.00E-97//oxygenase [Nicotiana tabacum]	Unigene49584_All//5.00E-94//AT3G01420| DOX1; lipoxygenase	Unigene49584_All//0.00E+00//TC140323		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene49585_All	782	4.22	12.31	9.26	5.16	8.59	24.49	3.73	12.67	7.08	1.55E+00	2.86E-14	Up	1.14E+00	8.67E-07	Up	7.35E-01	6.82E-04		2.25E+00	1.47E-48	Up	1.76E+00	1.95E-21	Up	9.25E-01	3.20E-05		Unigene49585_All//gi|224053406|ref|XP_002297803.1|//3.00E-60//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222845061|gb|EEE82608.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene49585_All//5.00E-37//AT5G25190| ethylene-responsive element-binding protein, putative	Unigene49585_All//4.00E-18//TC146159	AP2-EREBP			nr +
Unigene49587_All	766	3.89	2.65	3.06	2.28	2.52	0.47	0.44	0.16	0.00	-5.57E-01	1.25E-01		-3.48E-01	3.85E-01		1.45E-01	8.16E-01		-2.27E+00	4.52E-05	Down	-1.43E+00	2.58E-01		-8.79E+00	8.14E-03		Unigene49587_All//gi|115473321|ref|NP_001060259.1|//1.00E-10//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]		Unigene49587_All//1.00E-70//TC146591				nr -
Unigene49589_All	767	6.75	3.17	2.15	8.51	9.02	6.54	7.94	2.29	3.06	-1.09E+00	4.67E-05	Down	-1.65E+00	2.42E-08	Down	8.50E-02	7.81E-01		-3.80E-01	1.17E-01		-1.79E+00	8.37E-14	Down	-1.37E+00	5.90E-10	Down	Unigene49589_All//gi|115488936|ref|NP_001066955.1|//1.00E-22//Os12g0541400 [Oryza sativa Japonica Group] >gi|113649462|dbj|BAF29974.1| Os12g0541400 [Oryza sativa Japonica Group]	Unigene49589_All//3.00E-35//AT4G15790| unknown protein	Unigene49589_All//3.00E-99//CA994014				nr -
Unigene4959_All	1070	3.52	1.42	2.49	5.17	4.28	3.55	3.67	2.30	2.35	-1.31E+00	6.30E-05	Down	-5.01E-01	1.40E-01		-2.72E-01	3.13E-01		-5.44E-01	3.32E-02		-6.73E-01	1.43E-02		-6.48E-01	1.45E-02		Unigene4959_All//gi|28300299|gb|AAO37645.1|//2.00E-29//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene4959_All//2.00E-06//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene4959_All//8.00E-150//TC179054				nr +
Unigene49591_All	793	21.51	15.97	15.18	29.08	23.23	38.61	48.04	21.45	25.57	-4.29E-01	1.45E-03		-5.03E-01	3.06E-04		-3.24E-01	3.00E-03		4.09E-01	1.79E-05		-1.16E+00	2.01E-43	Down	-9.10E-01	3.95E-30		Unigene49591_All//gi|209967445|gb|ACJ02351.1|//1.00E-59//60S ribosomal protein L31 [Vernicia fordii]	Unigene49591_All//9.00E-42//AT5G56710| 60S ribosomal protein L31 (RPL31C)	Unigene49591_All//0.00E+00//gi|109889936|gb|DW518904.1|DW518904		ko03010|Ribosome		nr -
Unigene49592_All	1106	0.09	6.28	2.26	1.94	1.84	8.58	72.67	38.92	20.35	6.05E+00	2.55E-36	Up	4.58E+00	2.25E-11	Up	-7.62E-02	8.57E-01		2.15E+00	6.07E-23	Up	-9.01E-01	7.29E-60		-1.84E+00	4.33E-184	Down	Unigene49592_All//gi|224139378|ref|XP_002323083.1|//3.00E-77//cytochrome P450 [Populus trichocarpa] >gi|222867713|gb|EEF04844.1| cytochrome P450 [Populus trichocarpa]	Unigene49592_All//2.00E-45//AT3G48310| CYP71A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene49592_All//0.00E+00//TC143510		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism		nr -
Unigene49594_All	933	2.58	10.37	11.02	11.27	6.83	28.22	1.63	3.32	1.92	2.01E+00	2.90E-20	Up	2.09E+00	6.18E-22	Up	-7.22E-01	8.29E-06		1.32E+00	3.50E-32	Up	1.02E+00	1.31E-03		2.36E-01	6.19E-01		Unigene49594_All//gi|16226275|gb|AAL16121.1|AF428289_1//8.00E-14//AT5g57340/MJB24_15 [Arabidopsis thaliana]	Unigene49594_All//4.00E-15//AT5G57340| unknown protein					nr +
Unigene49599_All	1162	135.85	287.71	175.79	149.49	333.12	817.10	123.49	132.15	100.93	1.08E+00	1.48E-272	Up	3.72E-01	6.72E-25		1.16E+00	0.00E+00	Up	2.45E+00	0.00E+00	Up	9.77E-02	1.36E-02		-2.91E-01	7.47E-15		Unigene49599_All//gi|15237656|ref|NP_201231.1|//1.00E-122//EXL2 (EXORDIUM LIKE 2) [Arabidopsis thaliana] >gi|14190477|gb|AAK55719.1|AF380638_1 AT5g64260/MSJ1_10 [Arabidopsis thaliana] >gi|9759402|dbj|BAB09857.1| phi-1-like protein [Arabidopsis thaliana] >gi|16323270|gb|AAL15369.1| AT5g64260/MSJ1_10 [Arabidopsis thaliana] >gi|21593241|gb|AAM65190.1| phi-1-like protein [Arabidopsis thaliana]	Unigene49599_All//6.00E-115//AT5G64260| EXL2 (EXORDIUM LIKE 2)	Unigene49599_All//0.00E+00//gi|78323973|gb|DT544247.1|DT544247				nr +

Unigene4960_All	884	3.79	3.96	6.08	33.98	31.71	12.93	6.79	1.80	2.03	6.23E-02	8.53E-01			6.84E-01	1.08E-02		-9.98E-02	3.95E-01		-1.39E+00	3.35E-40	Down	-1.92E+00	7.66E-15	Down	-1.74E+00	1.42E-13	Down	Unigene4960_All//gi|224077988|ref|XP_002305471.1|//3.00E-48//SAUR family protein [Populus trichocarpa] >gi|222848435|gb|EEE85982.1| SAUR family protein [Populus trichocarpa]	Unigene4960_All//1.00E-43//AT1G19840| auxin-responsive family protein	Unigene4960_All//8.00E-91//TC152621				nr +
Unigene4600_All	954	0.99	2.50	3.29	4.65	3.93	4.26	3.81	2.28	3.88	1.34E+00	1.76E-03			1.74E+00	1.09E-05	Up	-2.40E-01	4.52E-01		-1.25E-01	6.76E-01		-7.42E-01	9.75E-03		2.71E-02	9.48E-01			Unigene4600_All//0.00E+00//gi|78341304|gb|DT561578.1|DT561578				
Unigene4601_All	809	21.54	20.42	38.24	19.03	19.92	13.12	22.73	8.32	14.72	-7.69E-02	6.01E-01			8.28E-01	3.50E-16		6.62E-02	7.16E-01		-5.36E-01	1.12E-04		-1.45E+00	9.07E-30	Down	-6.27E-01	2.73E-08		Unigene4601_All//gi|224076798|ref|XP_002304998.1|//6.00E-16//predicted protein [Populus trichocarpa] >gi|222847962|gb|EEE85509.1| predicted protein [Populus trichocarpa]	Unigene4601_All//7.00E-05//AT4G27360| dynein light chain, putative	Unigene4601_All//0.00E+00//gi|48747870|gb|C0078389.1|C0078389				nr +
Unigene4602_All	1276	0.41	0.95	1.17	38.69	24.18	44.49	43.94	37.24	19.20	1.22E+00	5.24E-02			1.51E+00	1.11E-02		-6.78E-01	1.03E-22		2.02E-01	4.91E-03		-2.39E-01	1.83E-04		-1.19E+00	3.94E-68	Down	Unigene4602_All//gi|115345280|dbj|BAF33316.1|//1.00E-145//peroxidase [Populus alba]	Unigene4602_All//7.00E-144//AT5G06720| peroxidase, putative	Unigene4602_All//0.00E+00//TC165444		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene4603_All	2029	0.00	0.07	0.00	0.71	1.14	2.63	2.38	2.35	6.38	6.23E+00	2.35E-01			null	null		6.75E-01	1.14E-01		1.88E+00	3.85E-11	Up	-1.66E-02	9.80E-01		1.43E+00	4.08E-21	Up	Unigene4603_All//gi|224060245|ref|XP_002300103.1|//1.00E-180//cytochrome P450 [Populus trichocarpa] >gi|222847361|gb|EEE84908.1| cytochrome P450 [Populus trichocarpa]	Unigene4603_All//3.00E-138//AT3G48520| CYP94B3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene4603_All//7.00E-13//gi|78339905|gb|DT560179.1|DT560179		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene4605_All	2090	3.08	0.85	1.68	0.07	0.33	1.66	12.34	12.68	35.19	-1.86E+00	1.55E-12	Down	-8.73E-01	3.22E-04		2.20E+00	2.71E-02		4.54E+00	5.24E-17	Up	3.90E-02	7.34E-01		1.51E+00	1.80E-126	Up	Unigene4605_All//gi|18409382|ref|NP_564978.1|//0.00E+00//ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter [Arabidopsis thaliana]	Unigene4605_All//0.00E+00//AT1G69850| ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter	Unigene4605_All//0.00E+00//gi|164257850|gb|ES844381.1|ES844381				nr -
Unigene4606_All	1465	0.50	1.25	0.22	2.38	2.96	2.25	2.40	1.06	1.11	1.32E+00	8.22E-03			-1.20E+00	1.80E-01		3.15E-01	3.14E-01		-8.08E-02	8.20E-01		-1.18E+00	7.92E-05	Down	-1.10E+00	1.38E-04	Down	Unigene4606_All//gi|5882737|gb|AAD55290.1|AC008263_21//3.00E-21//P2S4.17 [Arabidopsis thaliana] >gi|98860977|gb|ABF58972.1| At1g74860 [Arabidopsis thaliana]	Unigene4606_All//2.00E-22//AT1G74860| unknown protein					nr -
Unigene4609_All	537	17.83	14.91	20.72	57.42	58.80	24.98	25.98	27.79	21.14	-2.58E-01	1.88E-01			2.17E-01	2.52E-01		3.43E-02	8.10E-01		-1.20E+00	8.61E-33	Down	9.68E-02	5.44E-01		-2.97E-01	2.62E-02		Unigene4609_All//gi|22597174|gb|AN03474.1|//3.00E-49//syntaxin [Glycine max]	Unigene4609_All//1.00E-43//AT5G46860| VAM3; SNAP receptor	Unigene4609_All//0.00E+00//TC130002		ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport		nr -
Unigene4961_All	1961	0.59	2214.08	95.31	0.00	0.56	2.28	0.19	1.36	2.01	1.19E+01	0.00E+00	Up	7.34E+00	0.00E+00	Up	9.13E+00	8.73E-07	Up	1.12E+01	5.47E-27	Up	2.81E+00	1.34E-10	Up	3.37E+00	1.70E-18	Up	Unigene4961_All//gi|79330664|ref|NP_001032061.1|//2.00E-75//LT165 (LOW-TEMPERATURE-INDUCED 65) [Arabidopsis thaliana]	Unigene4961_All//4.00E-62//AT5G52300| LT165 (LOW-TEMPERATURE-INDUCED 65)	Unigene4961_All//4.00E-122//gi|189092626|gb|FG548161.1|FG548161				nr +
Unigene4610_All	1749	0.93	0.75	0.09	0.57	0.22	1.47	1.98	1.22	1.80	-3.00E-01	5.73E-01			-3.34E+00	4.62E-06	Down	-1.39E+00	3.79E-02		1.37E+00	7.33E-04	Up	-7.02E-01	1.77E-02		-1.40E-01	6.36E-01		Unigene4610_All//gi|297794625|ref|XP_002865197.1|//1.00E-121//flagellin-sensitive 2 [Arabidopsis lyrata subsp. lyrata] >gi|297311032|gb|EFH41456.1| flagellin-sensitive 2 [Arabidopsis lyrata subsp. lyrata]	Unigene4610_All//5.00E-109//AT5G46330| FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / kinase/ protein binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr -
Unigene4612_All	528	26.26	14.20	9.18	25.94	21.39	10.09	1.92	2.61	2.41	-8.87E-01	7.13E-09			-1.52E+00	5.79E-19	Down	-2.78E-01	7.16E-02		-1.36E+00	5.59E-18	Down	4.43E-01	3.96E-01		3.29E-01	5.52E-01		Unigene4612_All//gi|224053681|ref|XP_002297926.1|//8.00E-48//AP2/EREBP domain-containing transcription factor [Populus trichocarpa] >gi|222845184|gb|EEE82731.1| AP2/EREBP domain-containing transcription factor [Populus trichocarpa]	Unigene4612_All//6.00E-26//AT5G47220| ERF2 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 2); DNA binding / transcription activator/ transcription factor	Unigene4612_All//0.00E+00//DW502086	AP2-EREBP			nr +
Unigene4613_All	1540	0.88	0.07	0.07	1.78	1.27	1.55	3.49	1.63	2.07	-3.75E+00	5.95E-06	Down	-3.67E+00	1.58E-05	Down	-4.81E-01	2.10E-01		-1.95E-01	6.39E-01		-1.10E+00	2.78E-06	Down	-7.53E-01	7.14E-04		Unigene4613_All//gi|115463371|ref|NP_001055285.1|//0.00E+00//0ud5g0354300 [Oryza sativa Japonica Group] >gi|113578836|dbj|BAF17199.1| 0s05g0354300 [Oryza sativa Japonica Group]	Unigene4613_All//0.00E+00//AT5G05560| EMB2771 (EMBRYO DEFECTIVE 2771); ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis		nr +
Unigene4618_All	850	1.11	1.79	3.45	1.82	2.11	1.65	3.43	2.36	2.72	6.91E-01	2.02E-01			1.64E+00	5.59E-05	Up	2.14E-01	7.11E-01		-1.42E-01	7.94E-01		-5.40E-01	1.05E-01		-3.36E-01	3.13E-01			Unigene4618_All//0.00E+00//CO101294				
Unigene4619_All	1135	0.32	0.49	0.89	2.24	1.15	2.15	21.38	2.61	33.06	6.06E-01	5.31E-01			1.47E+00	4.95E-02		-9.57E-01	1.06E-02		-5.89E-02	9.01E-01		-3.03E+00	1.35E-98	Down	6.29E-01	5.41E-16		Unigene4619_All//gi|15225770|ref|NP_180234.1|//3.00E-92//SPX2 (SPX DOMAIN GENE 2) [Arabidopsis thaliana]	Unigene4619_All//7.00E-89//AT2G26660| SPX2 (SPX DOMAIN GENE 2)	Unigene4619_All//0.00E+00//TC150090				nr -
Unigene4962_All	491	32.18	33.85	20.93	83.80	101.97	95.48	31.26	41.88	71.16	7.29E-02	6.14E-01			-6.21E-01	1.85E-05		2.83E-01	6.33E-05		1.88E-01	2.08E-02		4.22E-01	9.65E-05		1.19E+00	4.85E-42	Up	Unigene4962_All//gi|297817274|ref|XP_002876520.1|//8.00E-41//IQ-domain 13 [Arabidopsis lyrata subsp. lyrata] >gi|297322358|gb|EFH52779.1| IQ-domain 13 [Arabidopsis lyrata subsp. lyrata]	Unigene4962_All//2.00E-14//AT2G43680| IQD14; calmodulin binding	Unigene4962_All//0.00E+00//TC160688		ko03040|Spliceosome		nr +
Unigene4620_All	1505	0.97	0.57	0.50	3.71	4.85	2.58	1.43	21.02	0.48	-7.66E-01	1.59E-01		-9.75E-01	9.25E-02		3.88E-01	7.91E-02		-5.23E-01	4.01E-02		3.88E+00	6.89E-159	Up	-1.59E+00	7.54E-05	Down	Unigene4620_All//gi|224115540|ref|XP_002317059.1|//1.00E-156//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222860124|gb|EEE97671.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene4620_All//2.00E-82//AT2G46770| EMB2301 (EMBRYO DEFECTIVE 2301); transcription activator/ transcription factor	Unigene4620_All//0.00E+00//TC156365	NAC			nr +
Unigene4622_All	1413	8.85	1.86	6.41	7.61	4.26	2.17	0.87	0.06	0.00	-2.25E+00	4.24E-30	Down	-4.66E-01	5.25E-03		-8.36E-01	1.71E-07		-1.81E+00	2.86E-21	Down	-3.87E+00	1.15E-06	Down	-9.76E+00	4.03E-09	Down	Unigene4622_All//gi|46931222|gb|AAT06415.1|//5.00E-36//At2g42900 [Arabidopsis thaliana] >gi|48310431|gb|AAT41819.1| At2g42900 [Arabidopsis thaliana]	Unigene4622_All//2.00E-36//AT2G42900| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Plant Basic Secretory Protein (InterPro:IPR007541); Has 25 Blast hits to 25 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 0; Plants - 24; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene4622_All//0.00E+00//gi|78331211|gb|DT551485.1|DT551485				nr +
Unigene4623_All	803	15.44	19.31	15.52	24.26	25.00	31.16	7.48	9.26	2.48	3.22E-01	2.62E-02		7.00E-03	9.91E-01		4.37E-02	8.07E-01		3.61E-01	8.35E-04		3.09E-01	1.27E-01		-1.59E+00	5.00E-12	Down	Unigene4623_All//gi|255587090|ref|XP_002534131.1|//7.00E-45//Thioredoxin H-type [Ricinus communis] >gi|11135282|sp|Q43636.1|TRXH_RICC0 RecName: Full=Thioredoxin H-type; Short=Trx-H >gi|1255954|emb|CAA94534.1| thioredoxin [Ricinus communis] >gi|223525803|gb|EEF28248.1| Thioredoxin H-type [Ricinus communis]	Unigene4623_All//9.00E-25//AT1G45145| ATTRX5; oxidoreductase, acting on sulfur group of donors, disulfide as acceptor	Unigene4623_All//0.00E+00//TC160395				nr +
Unigene4624_All	844	10.97	7.98	8.27	19.83	16.08	17.93	18.44	7.03	6.42	-4.59E-01	1.58E-02		-4.09E-01	4.26E-02		-3.03E-01	2.41E-02		-1.46E-01	3.69E-01		-1.39E+00	8.66E-24	Down	-1.52E+00	5.78E-28	Down	Unigene4624_All//gi|297846718|ref|XP_002891240.1|//5.00E-63//At1g42480 [Arabidopsis lyrata subsp. lyrata] >gi|297337082|gb|EFH67499.1| At1g42480 [Arabidopsis lyrata subsp. lyrata]	Unigene4624_All//8.00E-47//AT1G42480| unknown protein	Unigene4624_All//0.00E+00//TC139923				nr -
Unigene4626_All	1235	2.63	6.85	6.64	0.44	0.98	7.24	6.64	4.81	30.48	1.38E+00	8.03E-11	Up	1.34E+00	1.26E-09	Up	1.14E+00	7.32E-02		4.03E+00	2.79E-40	Up	-4.67E-01	1.04E-02		2.20E+00	4.10E-108	Up	Unigene4626_All//gi|297829672|ref|XP_002882718.1|//1.00E-139//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328558|gb|EFH58977.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene4626_All//8.00E-140//AT3G11180| oxidoreductase, 20G-Fe(II) oxygenase family protein	Unigene4626_All//0.00E+00//TC170018		ko00941|Flavonoid biosynthesis		nr -
Unigene4628_All	1722	0.94	0.65	1.18	13.42	14.38	4.56	8.32	1.87	8.28	-5.41E-01	2.98E-01		3.19E-01	5.10E-01		9.92E-02	4.56E-01		-1.56E+00	1.64E-36	Down	-2.16E+00	6.55E-40	Down	-7.10E-03	9.68E-01		Unigene4628_All//gi|224137338|ref|XP_002327101.1|//0.00E+00//lysine/histidine transporter [Populus trichocarpa] >gi|222835416|gb|EEE73851.1| lysine/histidine transporter [Populus trichocarpa]	Unigene4628_All//0.00E+00//AT1G47670| amino acid transporter family protein	Unigene4628_All//0.00E+00//TC142375				nr +
Unigene4629_All	1122	2.47	0.90	0.33	3.60	2.79	2.94	7.08	3.05	2.17	-1.45E+00	2.37E-04	Down	-2.90E+00	7.82E-09	Down	-3.65E-01	2.46E-01		-2.91E-01	3.98E-01		-1.21E+00	2.57E-10	Down	-1.71E+00	3.08E-17	Down	Unigene4629_All//gi|297808779|ref|XP_002872273.1|//1.00E-103//protein translocase [Arabidopsis lyrata subsp. lyrata] >gi|297318110|gb|EFH48532.1| protein translocase [Arabidopsis lyrata subsp. lyrata]	Unigene4629_All//8.00E-99//AT5G27395| P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene4629_All//0.00E+00//TC161270				nr -
Unigene4963_All	901	19.28	17.26	16.19	23.66	28.55	27.32	3.94	8.12	8.71	-1.59E-01	2.75E-01		-2.52E-01	8.49E-02		2.71E-01	1.10E-02		2.07E-01	7.99E-02		1.04E+00	1.20E-07	Up	1.14E+00	1.35E-09	Up	Unigene4963_All//gi|297797583|ref|XP_002866676.1|//9.00E-55//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297312511|gb|EFH42935.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene4963_All//1.00E-46//AT5G65520| binding	Unigene4963_All//0.00E+00//TC171363				nr +
Unigene4630_All	631	1.16	9.64	1.77	2.05	6.17	34.07	0.40	2.45	3.22	3.05E+00	1.45E-20	Up	6.10E-01	3.75E-01		1.59E+00	4.51E-07	Up	4.05E+00	3.91E-97	Up	2.61E+00	5.83E-06	Up	3.00E+00	6.43E-09	Up	Unigene4630_All//gi|266690|sp|P29527.1|OLEO6_GOSHI//1.00E-71//RecName: Full=Oleosin 18.2 kDa >gi|167363|gb|AAA18524.1| 18.2 kDa oleosin [Gossypium hirsutum] >gi|167365|gb|AAA18525.1| 18.2 kDa oleosin [Gossypium hirsutum]	Unigene4630_All//6.00E-28//AT3G01570| glycine-rich protein / oleosin	Unigene4630_All//0.00E+00//TC163113				nr -
Unigene4631_All	754	24.15	19.96	24.51	61.44	45.40	18.33	9.03	4.05	3.59	-2.75E-01	4.04E-02		2.12E-02	8.91E-01		-4.37E-01	7.90E-10		-1.75E+00	1.08E-85	Down	-1.16E+00	2.31E-08	Down	-1.33E+00	1.55E-10	Down	Unigene4631_All//gi|14190467|gb|AAK55714.1|AF380632.1|//8.00E-15//At3g13171 [Arabidopsis thaliana] >gi|15809712|gb|AAL06784.1| At3g13171 [Arabidopsis thaliana]	Unigene4631_All//8.00E-10//AT3G13175| unknown protein	Unigene4631_All//5.00E-141//TC157109				nr -
Unigene4632_All	743	4.58	9.00	9.89	8.78	9.96	11.49	23.79	30.21	21.02	9.76E-01	2.34E-05		1.11E+00	1.14E-06	Up	1.82E-01	4.69E-01		3.87E-01	5.94E-02		3.45E-01	9.29E-04		-1.79E-01	1.49E-01		Unigene4632_All//gi|225464803|ref|XP_002268503.1|//9.00E-12//PREDICTED: similar to FHY3 (FAR-RED ELONGATED HYPOCOTYLS 3); transcription factor [Vitis vinifera]	Unigene4632_All//2.00E-08//AT3G22170| FHY3 (FAR-RED ELONGATED HYPOCOTYLS 3); transcription activator/ transcription factor	Unigene4632_All//0.00E+00//DW512082				nr +

Unigene49633_All	777	33.80	14.80	27.89	65.84	75.83	26.33	15.13	9.09	7.28	-1.19E+00	1.14E-25	Down	-2.77E-01	1.45E-02		2.04E-01	2.45E-03		-1.32E+00	7.88E-63	Down	-7.35E-01	6.62E-07		-1.06E+00	1.96E-12	Down							
Unigene49635_All	2223	54.96	40.96	43.93	15.48	16.02	10.97	0.46	0.34	0.04	-4.24E-01	6.48E-20		-3.23E-01	9.33E-12		4.88E-02	6.74E-01		-4.97E-01	1.92E-08		-4.32E-01	5.02E-01		-3.67E+00	1.15E-05	Down	Unigene49635_All//gi|224100153|ref|XP_002311765.1|//0.00E+00//low affinity inorganic phosphate transporter [Populus trichocarpa] >gi|222851585|gb|EEE89132.1| low affinity inorganic phosphate transporter [Populus trichocarpa]	Unigene49635_All//0.00E+00//AT3G26570| PHT2;1 (PHOSPHATE TRANSPORTER 2;1); low affinity phosphate transmembrane transporter	Unigene49635_All//0.00E+00//TC163112				nr -
Unigene49636_All	1128	5.75	6.56	13.60	4.59	8.24	9.69	31.19	20.68	7.77	1.89E-01	4.02E-01		1.24E+00	1.29E-15	Up	8.44E-01	2.24E-06		1.08E+00	5.01E-10	Up	-5.93E-01	2.75E-13		-2.00E+00	4.54E-91	Down	Unigene49636_All//gi|224097756|ref|XP_002334586.1|//4.00E-90//cytochrome P450 [Populus trichocarpa] >gi|222873361|gb|EEF10492.1| cytochrome P450 [Populus trichocarpa]	Unigene49636_All//0.00E+00//AT4G31500| CYP83B1 (CYTOCHROME P450 MONOOXYGENASE 83B1); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding	Unigene49636_All//0.00E+00//TC135538		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr -
Unigene49642_All	750	14.86	14.93	5.54	24.77	29.75	16.56	1.13	1.06	0.58	6.90E-03	9.86E-01		-1.42E+00	4.93E-14	Down	2.64E-01	2.37E-02		-5.81E-01	3.02E-06		-9.07E-02	9.00E-01		-9.48E-01	1.47E-01		Unigene49642_All//gi|3860333|emb|CAA10134.1|//1.00E-42//basic blue copper protein [Cicer arietinum]	Unigene49642_All//2.00E-33//AT2G02850| ARPN (PLANTACYANIN); copper ion binding / electron carrier	Unigene49642_All//0.00E+00//gi|109829832|gb|DW228392.1|DW228392				nr +
Unigene49645_All	748	5.67	3.39	6.76	13.65	11.74	9.36	18.26	10.84	8.42	-7.42E-01	1.17E-02		2.55E-01	4.02E-01		-2.18E-01	2.67E-01		-5.45E-01	2.00E-03		-7.52E-01	3.46E-08		-1.12E+00	1.29E-15	Down	Unigene49645_All//gi|297607562|ref|NP_001060171.2|//1.00E-19//Os07g0596300 [Oryza sativa Japonica Group] >gi|255677941|dbj|BAF22085.2| Os07g0596300 [Oryza sativa Japonica Group]	Unigene49645_All//6.00E-19//AT5G07780| formin homology 2 domain-containing protein / FH2 domain-containing protein	Unigene49645_All//2.00E-125//BE052160				nr +
Unigene49648_All	818	5.18	6.69	7.49	4.38	2.40	1.77	0.78	1.28	0.34	3.69E-01	1.58E-01		5.31E-01	3.46E-02		-8.70E-01	4.32E-03		-1.31E+00	6.40E-05	Down	7.20E-01	2.38E-01		-1.19E+00	1.33E-01		Unigene49648_All//gi|225454115|ref|XP_002269352.1|//1.00E-104//PREDICTED: similar to KEA1 (K EFFLUX ANTIPORTER 1); potassium:hydrogen antiporter [Vitis vinifera]	Unigene49648_All//5.00E-88//AT4G00630| KEA2; potassium ion transmembrane transporter/ potassium:hydrogen antiporter	Unigene49648_All//0.00E+00//TC158816				nr -
Unigene49649_All	1291	4.62	1.81	0.41	13.20	18.94	6.16	0.75	0.97	1.39	-1.36E+00	1.11E-07	Down	-3.49E+00	6.42E-22	Down	5.21E-01	3.72E-07		-1.10E+00	5.12E-16	Down	3.67E-01	5.29E-01		8.83E-01	3.63E-02		Unigene49649_All//gi|224085085|ref|XP_002307484.1|//9.00E-73//f-box family protein [Populus trichocarpa] >gi|222856933|gb|EEE94480.1| f-box family protein [Populus trichocarpa]	Unigene49649_All//2.00E-31//AT1G21340| Dof-type zinc finger domain-containing protein	Unigene49649_All//0.00E+00//TC156526	C2C2-Dof			nr +
Unigene49650_All	795	4.80	26.96	5.36	7.08	22.83	18.92	16.33	11.67	42.39	2.49E+00	2.69E-57	Up	1.58E-01	6.28E-01		1.69E+00	1.52E-34	Up	1.42E+00	1.48E-20	Up	-4.84E-01	5.17E-04		1.38E+00	7.13E-51	Up	Unigene49650_All//gi|11374278|gb|AB134703.1|//6.00E-14//DnaJ-like protein isoform [Solanum phureja]	Unigene49650_All//9.00E-15//AT4G13830| J20 (DNAJ-LIKE 20); heat shock protein binding	Unigene49650_All//0.00E+00//TC149561		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene49651_All	893	16.58	16.45	10.26	15.90	15.27	13.76	5.02	1.68	1.70	-1.10E-02	9.64E-01		-6.93E-01	4.09E-06		-5.81E-02	7.71E-01		-2.09E-01	2.09E-01		-1.57E+00	9.48E-09	Down	-1.57E+00	5.34E-09	Down	Unigene49651_All//gi|297614182|gb|AD148429.1|//1.00E-112//trichome birefringence [Arabidopsis thaliana]	Unigene49651_All//5.00E-114//AT5G06700| unknown protein	Unigene49651_All//0.00E+00//gi|78328344|gb|DT548618.1|DT548618				nr -
Unigene49654_All	757	1.87	3.61	3.10	3.75	2.64	4.30	6.81	6.63	2.21	9.54E-01	1.28E-02		7.30E-01	9.36E-02		-5.08E-01	1.68E-01		1.96E-01	6.43E-01		-4.05E-02	8.85E-01		-1.62E+00	9.76E-11	Down			Unigene49654_All//2.00E-122//BQ410736					
Unigene49655_All	564	12.71	17.88	15.48	16.34	11.97	24.42	7.27	6.30	3.25	4.92E-01	6.53E-03		2.85E-01	1.84E-01		-4.49E-01	1.36E-02		5.80E-01	9.27E-05		-2.07E-01	4.94E-01		-1.16E+00	1.36E-05	Down			Unigene49655_All//0.00E+00//BQ410736					
Unigene49657_All	491	5.01	10.53	11.39	2.03	4.35	4.14	3.36	4.77	21.26	1.07E+00	6.58E-05	Up	1.19E+00	9.84E-06	Up	1.10E+00	1.19E-02		1.03E+00	2.56E-02		5.05E-01	1.88E-01		2.66E+00	5.35E-38	Up								
Unigene49659_All	1102	1.33	0.60	0.19	0.50	1.16	1.15	0.38	1.33	1.23	-1.15E+00	3.81E-02		-2.78E+00	9.28E-05	Down	1.22E+00	4.61E-02		1.21E+00	5.27E-02		1.79E+00	7.25E-04	Up	1.68E+00	1.63E-03		Unigene49659_All//gi|18421967|ref|NP_568580.1|//5.00E-99//metal-dependent phosphohydrolase HD domain-containing protein [Arabidopsis thaliana] >gi|14488069|gb|AAK63855.1|AF38928 2_1 AT5g40270/MSN9_170 [Arabidopsis thaliana] >gi|20968076|gb|AAM26721.1| AT5g40270/MSN9_170 [Arabidopsis thaliana]	Unigene49659_All//2.00E-94//AT5G40270| metal-dependent phosphohydrolase HD domain-containing protein	Unigene49659_All//0.00E+00//gi|54122821|gb|CO498330.1|CO498330				nr -
Unigene49966_All	847	10.25	8.43	4.78	4.29	11.10	7.94	26.81	8.04	24.18	-2.82E-01	1.69E-01		-1.10E+00	1.22E-07	Down	1.37E+00	2.06E-13	Up	8.88E-01	7.41E-05		-1.74E+00	2.92E-47	Down	-1.49E-01	1.74E-01		Unigene49966_All//gi|87162589|gb|ABD28384.1|//3.00E-82//Tyrosine specific protein phosphatase and dual specificity protein phosphatase; Putative tyrosine phosphatase [Medicago truncatula]	Unigene49966_All//5.00E-78//AT3G02800| phosphatase/ phosphoprotein phosphatase/ protein tyrosine phosphatase	Unigene49966_All//0.00E+00//gi|164313479|gb|EX164477.1|EX164477				nr -
Unigene49660_All	952	133.22	1017.38	356.58	96.96	256.13	486.46	133.24	379.94	142.07	2.93E+00	0.00E+00	Up	1.42E+00	0.00E+00	Up	1.40E+00	0.00E+00	Up	2.33E+00	0.00E+00	Up	1.51E+00	0.00E+00	Up	9.26E-02	2.54E-02		Unigene49660_All//gi|15230680|ref|NP_187911.1|//4.00E-37//transporter-related [Arabidopsis thaliana] >gi|15809988|gb|AAL06921.1| AT3g13050/MGH6_16 [Arabidopsis thaliana] >gi|28416475|gb|AA042768.1| At3g13050/MGH6_16 [Arabidopsis thaliana]	Unigene49660_All//1.00E-33//AT3G13050| transporter-related	Unigene49660_All//0.00E+00//gi|188536299|gb|FG357314.1|FG357314				nr +
Unigene49661_All	551	43.58	26.48	19.14	102.79	62.31	93.03	77.96	65.16	49.67	-7.19E-01	1.53E-10		-1.19E+00	1.72E-22	Down	-7.22E-01	4.88E-29		-1.44E-01	5.82E-02		-2.59E-01	4.37E-04		-6.50E-01	2.53E-19		Unigene49661_All//gi|224087993|ref|XP_002308283.1|//5.00E-11//nucleosome/chromatin assembly factor group [Populus trichocarpa] >gi|222854259|gb|EEE91806.1| nucleosome/chromatin assembly factor group [Populus trichocarpa]		Unigene49661_All//0.00E+00//gi|21100273|gb|BQ412574.1|BQ412574				nr -
Unigene49664_All	823	15.26	12.56	18.05	24.09	20.50	9.99	13.15	1.93	0.97	-2.81E-01	9.02E-02		2.43E-01	1.34E-01		-2.33E-01	6.76E-02		-1.27E+00	3.43E-23	Down	-2.77E+00	2.16E-40	Down	-3.76E+00	1.84E-55	Down	Unigene49664_All//gi|117168149|gb|ABK32157.1|//2.00E-43//At1g61667 [Arabidopsis thaliana]	Unigene49664_All//3.00E-45//AT5G54530| unknown protein	Unigene49664_All//0.00E+00//ES813064				nr -
Unigene49666_All	607	17.58	99.67	49.13	51.13	145.40	88.24	60.74	175.03	194.99	2.50E+00	6.26E-162	Up	1.48E+00	5.12E-39	Up	1.51E+00	8.25E-143	Up	7.87E-01	5.02E-28		1.53E+00	2.21E-181	Up	1.68E+00	4.41E-237	Up	Unigene49666_All//gi|224073168|ref|XP_002304005.1|//3.00E-73//f-box family protein [Populus trichocarpa] >gi|222841437|gb|EEE78984.1| f-box family protein [Populus trichocarpa]	Unigene49666_All//2.00E-30//AT2G44130| kelch repeat-containing F-box family protein	Unigene49666_All//0.00E+00//gi|78339045|gb|DT559319.1|DT559319				nr -
Unigene49667_All	1343	0.51	0.60	0.63	2.11	1.21	0.74	16.56	16.81	13.50	2.53E-01	7.26E-01		3.25E-01	6.47E-01		-8.11E-01	2.14E-02		-1.51E+00	7.59E-05	Down	2.13E-02	8.70E-01		-2.95E-01	4.05E-03		Unigene49667_All//gi|30690333|ref|NP_195265.2|//2.00E-91//AGF1 (AT-hook protein of GA feedback 1); transcription factor [Arabidopsis thaliana] >gi|50198777|gb|AAT70422.1| At4g35390 [Arabidopsis thaliana] >gi|53828597|gb|AAU94408.1| At4g35390 [Arabidopsis thaliana] >gi|119657394|tpd|FAA00296.1| TPA: AT-hook motif nuclear localized protein 25 [Arabidopsis thaliana]	Unigene49667_All//1.00E-43//AT4G35390| AGF1 (AT-hook protein of GA feedback 1); transcription factor	Unigene49667_All//3.00E-85//gi|78324579|gb|DT544853.1|DT544853				nr -
Unigene49668_All	1256	1.62	4.88	3.56	0.71	0.47	1.44	1.85	2.03	2.47	1.59E+00	1.10E-09	Up	1.13E+00	1.85E-04	Up	-6.15E-01	4.02E-01		1.01E+00	4.14E-02		1.33E-01	7.24E-01		4.18E-01	1.84E-01		Unigene49668_All//gi|51557078|gb|AAU06309.1|//1.00E-100//MYB transcription factor [Hevea brasiliensis]	Unigene49668_All//4.00E-85//AT2G38090| myb family transcription factor	Unigene49668_All//0.00E+00//DW496561	MYB			nr -
Unigene49669_All	1507	3.26	0.87	1.20	6.12	6.03	2.79	4.52	1.14	1.03	-1.90E+00	5.10E-10	Down	-1.44E+00	1.18E-06	Down	-1.96E-02	9.30E-01		-1.13E+00	2.33E-09	Down	-1.99E+00	1.60E-17	Down	-2.13E+00	1.02E-19	Down	Unigene49669_All//gi|224119208|ref|XP_002318015.1|//1.00E-134//repressor, antagonist of e2f-dp complex [Populus trichocarpa] >gi|222858888|gb|EEE96235.1| repressor, antagonist of e2f-dp complex [Populus trichocarpa]	Unigene49669_All//9.00E-106//AT3G48160| DEL1 (DP-E2F-LIKE 1); DNA binding / transcription factor	Unigene49669_All//0.00E+00//TC171534	E2F-DP			nr -
Unigene49672_All	1261	21.08	4.50	12.12	18.41	17.78	21.63	0.87	0.27	0.54	-2.23E+00	1.18E-62	Down	-7.98E-01	3.78E-13		-5.03E-02	7.40E-01		2.33E-01	3.28E-02		-1.72E+00	5.68E-03		-6.99E-01	2.11E-01		Unigene49672_All//gi|297806207|ref|XP_002870987.1|//4.00E-76//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316824|gb|EFH47246.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49672_All//5.00E-57//AT5G02750| zinc finger (C3HC4-type RING finger) family protein	Unigene49672_All//0.00E+00//TC178405				nr +
Unigene49673_All	1497	2.03	0.71	0.57	3.96	3.73	1.84	5.68	1.54	4.82	-1.51E+00	6.39E-05	Down	-1.83E+00	7.38E-06	Down	-8.76E-02	7.79E-01		-1.11E+00	4.92E-06	Down	-1.89E+00	2.96E-20	Down	-2.37E-01	1.97E-01		Unigene49673_All//gi|224119208|ref|XP_002318015.1|//5.00E-96//repressor, antagonist of e2f-dp complex [Populus trichocarpa] >gi|222858888|gb|EEE96235.1| repressor, antagonist of e2f-dp complex [Populus trichocarpa]	Unigene49673_All//8.00E-85//AT3G01330| DEL3 (DP-E2F-LIKE PROTEIN 3); DNA binding / transcription factor	Unigene49673_All//0.00E+00//TC173382	E2F-DP			nr +
Unigene49674_All	693	1.06	2.19	3.30	1.15	1.04	0.78	9.76	12.85	9.31	1.05E+00	5.24E-02		1.64E+00	4.50E-04	Up	-1.40E-01	8.29E-01		-5.57E-01	4.98E-01		3.96E-01	2.43E-02		-6.79E-02	7.46E-01		Unigene49674_All//gi|224120650|ref|XP_002318383.1|//1.00E-77//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222859056|gb|EEE96603.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene49674_All//4.00E-75//AT5G61430| ANAC100 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 100); transcription factor	Unigene49674_All//0.00E+00//CO103080	NAC			nr -
Unigene49676_All	1142	0.64	0.75	0.56	1.00	2.02	1.70	4.18	3.44	13.57	2.34E-01	7.28E-01		-1.97E-01	7.99E-01		1.01E+00	1.53E-02		7.61E-01	1.14E-01		-2.82E-01	2.91E-01		1.70E+00	4.03E-32	Up	Unigene49676_All//gi|9958056|gb|AAG09545.1|AC011810_4//1.00E-62//Unknown protein [Arabidopsis thaliana]	Unigene49676_All//9.00E-54//AT1G13340| unknown protein	Unigene49676_All//0.00E+00//gi|78350406|gb|DT570680.1|DT570680				nr -
Unigene49677_All	701	53.74	16.84	15.12	72.84	65.04	93.48	82.39	26.00	37.17	-1.67E+00	1.33E-60	Down	-1.83E+00	3.66E-66	Down	-1.63E-01	3.13E-02		3.60E-01	9.11E-09		-1.66E+00	3.62E-112	Down	-1.15E+00	5.83E-66	Down	Unigene49677_All//gi|197312875|gb|ACH63218.1|//2.00E-49//ribosomal protein L36 [Rheum australe]	Unigene49677_All//3.00E-44//AT3G53740| 60S ribosomal protein L36 (RPL36B)	Unigene49677_All//0.00E+00//gi|164293654|gb|ES833495.1|ES833495		ko03010|Ribosome		nr +
Unigene49679_All	1194	6.49	5.39	4.24	2.84	6.55	5.86	1.91	0.63	0.57	-2.67E-01	2.26E-01		-6.14E-01	4.76E-03		1.21E+00	2.58E-09	Up	1.05E+00	2.20E-06	Up	-1.60E+00	6.24E-05	Down	-1.75E+00	1.02E-05	Down	Unigene49679_All//gi|159025731|emb|CAN88866.1|//1.00E-102//D6-type cyclin [Populus trichocarpa]	Unigene49679_All//8.00E-51//AT4G03270| CYCD6;1 (Cyclin D6;1); cyclin-dependent protein kinase	Unigene49679_All//0.00E+00//TC165416				nr -
Unigene4968_All	954	156.85	74.73	59.11	217.53	163.41	214.64	171.60	62.34	55.96	-1.07E+00	2.25E-120	Down	-1.41E+00	1.25E-179	Down	-4.13E-01	2.49E-38		-1.93E-02	6.92E-01		-1.46E+00	5.91E-262	Down	-1.62E+00	0.00E+00	Down			Unigene4968_All//2.00E-168//gi|164367269|gb|ES791195.1|ES791195					

Unigene49680_A11	1215	22.18	7.17	5.83	30.95	25.59	24.68	23.18	9.43	8.82	-1.63E+00	7.26E-42	Down	-1.93E+00	7.46E-51	Down	-2.74E-01	9.91E-04		-3.27E-01	1.41E-04		-1.30E+00	3.03E-38	Down	-1.39E+00	7.64E-44	Down	Unigene49680_A11//gi|15233637|ref|NP_193236.1|//4.00E-63//60S ribosomal protein L27 (RPL27C) [Arabidopsis thaliana] >gi|3123264|sp|P51419.2|RL273_ARATH RecName: Full=60S ribosomal protein L27-3 >gi|2244857|emb|CAB10279.1| ribosomal protein [Arabidopsis thaliana] >gi|7268246|emb|CAB78542.1| ribosomal protein [Arabidopsis thaliana] >gi|21553620|gb|AAM62713.1| ribosomal protein [Arabidopsis thaliana] >gi|10736737|dbj|BAF00331.1| ribosomal protein [Arabidopsis thaliana]	Unigene49680_A11//6.00E-57//AT4G15000| 60S ribosomal protein L27 (RPL27C)	Unigene49680_A11//0.00E+00//TC133807		ko03010|Ribosome		nr -
Unigene49681_A11	1195	48.77	48.80	51.56	18.30	18.76	19.46	15.78	9.65	6.33	9.00E-04	9.90E-01		8.00E-02	3.27E-01		3.58E-02	8.37E-01		8.90E-02	5.32E-01		-7.09E-01	5.35E-10		-1.32E+00	2.97E-27	Down	Unigene49681_A11//gi|18391311|ref|NP_563893.1|//1.00E-112//CLPP6; serine-type endopeptidase [Arabidopsis thaliana] >gi|75313132|sp|Q9SAA2.1|CLPP6_ARATH RecName: Full=ATP-dependent Clp protease proteolytic subunit 6, chloroplastic; AltName: Full=Endopeptidase ClpP6; Short=nClpP6; AltName: Full=nClpP1; Flags: Precursor >gi|4835782|gb|AAD30248.1|AC007296_9 Identical to gb|AF016621 ATP-dependent Clp protease proteolytic subunit from Arabidopsis thaliana and is a member of the PF|00574 CLP_protease family. ESTs gb|F13836 and gb|F13997 come from this gene >gi|21592854|gb|AAM64804.1| ATP-dependent Clp protease proteolytic subunit (ClpP6) [Arabidopsis thaliana]	Unigene49681_A11//8.00E-105//AT1G11750| CLPP6; serine-type endopeptidase	Unigene49681_A11//0.00E+00//TC163903				nr +
Unigene49686_A11	1410	0.33	2.08	1.96	0.81	0.32	1.63	3.54	1.04	2.09	2.64E+00	6.36E-09	Up	2.56E+00	7.60E-08	Up	-1.36E+00	2.74E-02		1.01E+00	1.82E-02		-1.77E+00	2.99E-11	Down	-7.59E-01	1.06E-03				Unigene49686_A11//0.00E+00//CO093213				
Unigene49687_A11	1183	1.28	0.60	0.27	1.26	1.11	0.53	4.43	3.25	3.10	-1.10E+00	4.35E-02		-2.25E+00	5.02E-04	Down	-1.92E-01	7.47E-01		-1.24E+00	2.45E-02		-4.47E-01	6.02E-02		-5.16E-01	2.24E-02		Unigene49687_A11//gi|296081092|emb|CBI18286.3|//7.00E-06//unnamed protein product [Vitis vinifera]		Unigene49687_A11//0.00E+00//TC133450				nr +
Unigene49688_A11	1124	0.37	0.09	0.28	0.80	0.21	1.41	3.27	1.19	1.13	-2.05E+00	1.20E-01		-3.89E-01	7.17E-01		-1.89E+00	1.06E-02		8.18E-01	1.31E-01		-1.46E+00	1.25E-06	Down	-1.53E+00	2.61E-07	Down	Unigene49688_A11//gi|2865437|gb|AAC02672.1|//3.00E-14//polyprotein [Arabidopsis arenosa]		Unigene49688_A11//0.00E+00//TC133450				nr +
Unigene49689_A11	1008	1.09	3.42	0.85	4.05	4.17	3.76	4.99	15.30	32.09	1.65E+00	4.66E-06	Up	-3.67E-01	6.01E-01		4.05E-02	9.13E-01		-1.07E-01	7.40E-01		1.62E+00	3.28E-29	Up	2.68E+00	2.37E-117	Up	Unigene49689_A11//gi|11074174|gb|AB084460.1|//6.00E-18//At5g08240 [Arabidopsis thaliana]	Unigene49689_A11//4.00E-16//AT5G08240| unknown protein	Unigene49689_A11//0.00E+00//ES795161				nr +
Unigene4969_A11	2359	12.35	13.64	11.72	18.69	19.44	17.25	19.23	8.52	13.04	1.43E-01	1.69E-01		-7.65E-02	5.33E-01		5.72E-02	5.73E-01		-1.16E-01	2.15E-01		-1.17E+00	2.48E-52	Down	-5.61E-01	7.96E-16		Unigene4969_A11//gi|297849172|ref|XP_002892467.1|//0.00E+00//glycosyl 1 transferase family 29 protein [Arabidopsis lyrata subsp. lyrata] >gi|297338309|gb|EFH68726.1| glycosyl transferase family 29 protein [Arabidopsis lyrata subsp. lyrata]	Unigene4969_A11//0.00E+00//AT1G08660| glycosyl transferase family 29 protein / sialyltransferase family protein	Unigene4969_A11//0.00E+00//TC162011				nr +
Unigene49690_A11	1217	0.17	0.12	0.61	4.34	5.89	2.60	2.47	0.58	1.37	-4.62E-01	7.58E-01		1.83E+00	5.05E-02		4.40E-01	4.40E-02		-7.40E-01	3.92E-03		-2.08E+00	1.45E-08	Down	-8.43E-01	6.55E-03		Unigene49690_A11//gi|42568402|ref|NP_199685.2|//1.00E-145//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] >gi|261664537|sp|C0LGV0.1|Y5487_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At5g48740; Flags: Precursor >gi|224589707|gb|ACN59385.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene49690_A11//5.00E-147//AT5G48740| leucine-rich repeat family protein / protein kinase family protein	Unigene49690_A11//0.00E+00//TC131935				nr +
Unigene49691_A11	310	15.36	7.36	6.18	20.09	23.22	21.71	50.60	25.62	22.75	-1.06E+00	1.49E-04	Down	-1.31E+00	1.05E-05	Down	2.09E-01	4.06E-01		1.12E-01	6.84E-01		-9.82E-01	3.94E-14		-1.15E+00	1.09E-18	Down	Unigene49691_A11//gi|3334320|sp|O22518.1|RSSA_SOYBN//6.00E-14//RecName: Full=40S ribosomal protein SA; AltName: Full=p40 >gi|2444420|gb|AAB82659.1| ribosome-associated protein p40 [Glycine max]	Unigene49691_A11//4.00E-13//AT3G04770| RPSAb (40S ribosomal protein SA B); structural constituent of ribosome	Unigene49691_A11//7.00E-129//gi|78354885|gb|DT575159.1|DT575159		ko03010|Ribosome		nr -
Unigene49693_A11	436	52.56	27.89	24.55	81.81	60.50	97.06	97.07	46.68	44.22	-9.14E-01	7.47E-15		-1.10E+00	5.01E-19	Down	-4.35E-01	1.18E-07		2.47E-01	2.94E-03		-1.06E+00	2.58E-41	Down	-1.13E+00	1.26E-47	Down	Unigene49693_A11//gi|21555157|gb|AAM63791.1|//1.00E-19//40S ribosomal protein S19-like [Arabidopsis thaliana]	Unigene49693_A11//1.00E-16//AT5G28060| 40S ribosomal protein S24 (RPS24B)	Unigene49693_A11//0.00E+00//TC147736		ko03010|Ribosome		nr +
Unigene49694_A11	685	3.21	4.81	2.10	10.33	7.39	4.88	4.26	4.21	2.38	5.84E-01	8.86E-02		-6.12E-01	1.79E-01		-4.83E-01	2.28E-02		-1.08E+00	7.55E-07	Down	-1.66E-02	9.95E-01		-8.37E-01	7.91E-03		Unigene49694_A11//gi|224111284|ref|XP_002332949.1|//9.00E-40//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834261|gb|EEE72738.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene49694_A11//5.00E-16//AT4G27220| disease resistance protein (NBS-LRR class), putative	Unigene49694_A11//0.00E+00//BG443054		ko04626|Plant-pathogen interaction		nr +
Unigene49696_A11	373	42.50	22.96	28.98	46.48	44.59	66.59	76.74	59.28	26.06	-8.89E-01	4.61E-10		-5.52E-01	1.37E-04		-5.97E-02	7.31E-01		5.19E-01	1.08E-06		-3.73E-01	3.77E-05		-1.56E+00	1.80E-52	Down	Unigene49696_A11//gi|115446617|ref|NP_001047088.1|//6.00E-24//Os02g0549600 [Oryza sativa Japonica Group] >gi|115458432|ref|NP_001052816.1|Os04g0430100 [Oryza sativa Japonica Group] >gi|109940154|sp|Q94YP4.2|RS10_ORYSJ RecName: Full=40S ribosomal protein S10 >gi|21740815|emb|CAD41005.1|OSJNBa0042L16.19 [Oryza sativa (japonica cultivar-group)] >gi|46390693|dbj|BAD16194.1| 40S ribosomal protein S10 [Oryza sativa Japonica Group] >gi|50725745|dbj|BAD33256.1| 40S ribosomal protein S10 [Oryza sativa Japonica Group] >gi|113536619|dbj|BAF09002.1|Os02g0549600 [Oryza sativa Japonica Group] >gi|113561387|dbj|BAF14730.1|Os04g0430100 [Oryza sativa Japonica Group] >gi|116309307|emb|CAH66395.1|B0222C05.3 [Oryza sativa (indica cultivar-group)]	Unigene49696_A11//2.00E-23//AT5G52650| 40S ribosomal protein S10 (RPS10C)	Unigene49696_A11//6.00E-142//TC135610		ko03010|Ribosome		nr +
Unigene49697_A11	269	8.95	4.52	7.52	8.70	9.22	8.73	57.53	29.06	21.33	-9.85E-01	1.66E-02		-2.50E-01	5.85E-01		8.27E-02	8.57E-01		4.50E-03	9.95E-01		-9.85E-01	5.00E-14		-1.43E+00	1.82E-25	Down			Unigene49697_A11//7.00E-73//gi|109825943|gb|DW224664.1|DW224664				
Unigene49699_A11	728	5.17	5.01	5.19	2.46	2.22	1.74	0.76	8.90	1.48	-4.63E-02	8.91E-01		5.20E-03	1.00E+00		-1.48E-01	7.95E-01		-5.04E-01	3.30E-01		3.56E+00	9.04E-31	Up	9.69E-01	9.17E-02		Unigene49699_A11//gi|18403810|ref|NP_566730.1|//5.00E-49//ALF5 (ABERRANT LATERAL ROOT FORMATION 5); antiporter/ drug transporter/ transporter [Arabidopsis thaliana] >gi|13384114|gb|AAK21273.1|AF337954_1 aberrant lateral root formation 5 [Arabidopsis thaliana] >gi|17064870|gb|AAL32389.1| Unknown protein [Arabidopsis thaliana]	Unigene49699_A11//2.00E-42//AT3G23560| ALF5 (ABERRANT LATERAL ROOT FORMATION 5); antiporter/ drug transporter/ transporter	Unigene49699_A11//3.00E-22//CO121800				nr +
Unigene49703_A11	224	22.89	22.17	12.60	62.05	33.97	50.41	133.45	38.62	39.13	-4.63E-02	8.67E-01		-8.61E-01	1.81E-03		-8.69E-01	4.00E-10		-3.00E-01	5.68E-02		-1.79E+00	1.47E-64	Down	-1.77E+00	1.47E-65	Down			Unigene49703_A11//2.00E-119//gi|21095882|gb|BQ408195.1|BQ408195		ko03010|Ribosome		kegg -
Unigene49706_A11	587	5.79	9.32	7.62	9.50	10.21	10.23	9.36	5.70	4.48	6.86E-01	7.12E-03		3.95E-01	2.01E-01		1.03E-01	7.44E-01		1.07E-01	6.86E-01		-7.17E-01	1.51E-03		-1.06E+00	2.32E-06	Down	Unigene49706_A11//gi|115461394|ref|NP_001051297.1|//5.00E-11//Os04g0682500 [Oryza sativa Japonica Group] >gi|113565868|dbj|BAF16211.1|Os04g0682500 [Oryza sativa Japonica Group]	Unigene49706_A11//3.00E-12//AT4G00590| asparaginase 2 family protein	Unigene49706_A11//0.00E+00//ES829117				nr +
Unigene49707_A11	627	7.84	5.82	2.89	6.12	5.22	8.50	28.73	7.20	7.50	-4.31E-01	1.20E-01		-1.44E+00	1.18E-06	Down	-2.30E-01	5.20E-01		4.75E-01	7.51E-02		-2.00E+00	2.40E-45	Down	-1.94E+00	5.56E-45	Down	Unigene49707_A11//gi|115460394|ref|NP_001053797.1|//3.00E-09//Os04g0605900 [Oryza sativa Japonica Group] >gi|113565368|dbj|BAF15711.1|Os04g0605900 [Oryza sativa Japonica Group]	Unigene49707_A11//5.00E-10//AT2G01250| 60S ribosomal protein L7 (RPL7B)	Unigene49707_A11//9.00E-136//gi|109838675|gb|DW237236.1|DW237236		ko03010|Ribosome		nr +
Unigene49711_A11	648	12.60	11.26	6.16	2.38	1.70	4.18	11.61	12.25	33.69	-1.62E-01	4.60E-01		-1.03E+00	1.48E-06	Down	-4.87E-01	3.67E-01		8.11E-01	3.65E-02		7.75E-02	7.18E-01		1.54E+00	5.01E-39	Up	Unigene49711_A11//gi|115479709|ref|NP_001063448.1|//8.00E-16//Os09g0472900 [Oryza sativa Japonica Group] >gi|113631681|dbj|BAF25362.1|Os09g0472900 [Oryza sativa Japonica Group]	Unigene49711_A11//2.00E-09//AT2G18660| EXLB3 (EXPANSIN-LIKE B3 PRECURSOR)	Unigene49711_A11//0.00E+00//gi|13248060|gb|BF273800.2|BF273800				nr -
Unigene49712_A11	577	51.14	120.57	93.58	70.62	88.45	115.53	122.44	136.83	105.85	1.24E+00	1.27E-70	Up	8.72E-01	2.69E-30		3.25E-01	2.60E-06		7.10E-01	3.94E-29		1.60E-01	3.29E-03		-2.10E-01	1.38E-04		Unigene49712_A11//gi|297848650|ref|XP_002892206.1|//7.00E-38//thioesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338048|gb|EFH68465.1| thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49712_A11//1.00E-37//AT1G04290| thioesterase family protein	Unigene49712_A11//0.00E+00//TC149678				nr +
Unigene49714_A11	689	1.22	2.06	4.17	102.95	113.05	66.86	1.04	2.12	0.40	7.61E-01	1.74E-01		1.78E+00	2.03E-05	Up	1.35E-01	2.77E-02		-6.23E-01	7.41E-25		1.03E+00	3.87E-02		-1.37E+00	6.51E-02		Unigene49714_A11//gi|15237330|ref|NP_197140.1|//1.00E-23//NC domain-containing protein [Arabidopsis thaliana]	Unigene49714_A11//2.00E-24//AT5G16360| NC domain-containing protein	Unigene49714_A11//0.00E+00//TC138730				nr -
Unigene49715_A11	409	7.16	12.26	15.10	12.67	16.92	13.80	24.71	35.87	24.06	7.76E-01	3.84E-03		1.08E+00	1.81E-05	Up	4.18E-01	6.39E-02		1.24E-01	6.80E-01		5.38E-01	3.52E-05		-3.83E-02	8.28E-01				Unigene49715_A11//0.00E+00//gi|21092915|gb|BQ405228.1|BQ405228				

Unigene49716_All	807	6.48	3.52	2.90	13.02	11.27	14.66	31.12	18.18	42.60	-8.83E-01	7.58E-04		-1.16E+00	3.09E-05	Down	-2.09E-01	2.82E-01		1.71E-01	3.84E-01		-7.76E-01	4.16E-15		4.53E-01	1.54E-08		Unigene49716_All//gi|226491243|ref|NP_001146854.1|//1.00E-47//RING zinc finger protein-like [Zea mays] >gi|195604260|gb|ACG23960.1|RING zinc finger protein-like [Zea mays]	Unigene49716_All//4.00E-40//AT5G20885| zinc finger (C3HC4-type RING finger) family protein	Unigene49716_All//2.00E-180//TC178117				nr -
Unigene49717_All	577	1.27	0.35	1.85	23.66	11.46	9.71	7.47	4.06	2.90	-1.85E+00	4.08E-02		5.40E-01	4.18E-01		-1.05E+00	1.99E-13	Down	-1.29E+00	2.00E-16	Down	-8.82E-01	7.19E-04		-1.37E+00	2.97E-07	Down	Unigene49717_All//gi|224078648|ref|XP_002305590.1|//4.00E-32//predicted protein [Populus trichocarpa] >gi|118482524|gb|ABK93184.1|unknown [Populus trichocarpa] >gi|222848854|gb|EEE86101.1|predicted protein [Populus trichocarpa]	Unigene49717_All//4.00E-20//AT4G21780| unknown protein	Unigene49717_All//0.00E+00//gi|109826582|gb|DW225292.1|DW225292				nr -
Unigene49718_All	570	0.83	0.89	0.09	14.59	7.19	2.06	0.74	0.95	0.49	1.06E-01	9.22E-01		-3.14E+00	4.00E-02		-1.02E+00	4.37E-08	Down	-2.82E+00	2.74E-28	Down	3.62E-01	6.73E-01		-6.01E-01	5.53E-01		Unigene49718_All//gi|224078648|ref|XP_002305590.1|//1.00E-32//predicted protein [Populus trichocarpa] >gi|118482524|gb|ABK93184.1|unknown [Populus trichocarpa] >gi|222848854|gb|EEE86101.1|predicted protein [Populus trichocarpa]	Unigene49718_All//4.00E-20//AT4G21780| unknown protein	Unigene49718_All//0.00E+00//gi|109826582|gb|DW225292.1|DW225292				nr -
Unigene49720_All	560	2.52	19.82	1.90	1.51	1.66	6.05	2.64	8.58	3.34	2.97E+00	3.76E-36	Up	-4.08E-01	4.86E-01		1.35E-01	8.71E-01		2.00E+00	7.91E-08	Up	1.70E+00	2.75E-10	Up	3.40E-01	4.26E-01		Unigene49720_All//gi|250841163|gb|AN72189.1|//2.00E-09//Unknown protein [Arabidopsis thaliana]	Unigene49720_All//2.00E-10//AT1G33055| unknown protein	Unigene49720_All//1.00E-171//gi|109844320|gb|DW242878.1|DW242878				nr +
Unigene49722_All	573	26.94	22.81	26.30	11.82	11.78	10.96	8.26	8.17	3.75	-2.40E-01	1.10E-01		-3.45E-02	8.31E-01		-5.40E-03	9.74E-01		-1.10E-01	6.85E-01		-1.66E-02	9.81E-01		-1.14E+00	3.81E-06	Down	Unigene49722_All//gi|15450922|gb|AB96732.1|//6.00E-22//Unknown protein [Arabidopsis thaliana]	Unigene49722_All//2.00E-16//AT4G40045| unknown protein	Unigene49722_All//0.00E+00//DW511884				nr +
Unigene49723_All	829	0.82	0.86	1.41	4.63	4.03	3.32	3.98	3.23	1.49	6.06E-02	9.57E-01		7.84E-01	2.38E-01		-2.00E-01	5.68E-01		-4.78E-01	1.40E-01		-3.02E-01	3.68E-01		-1.42E+00	5.00E-06	Down	Unigene49723_All//gi|5042407|gb|AAD38246.1|AC006193_2//2.00E-37//Hypothetical Protein [Arabidopsis thaliana] >gi|6633824|gb|AAF19683.1|AC009519_17 F1N19.27 [Arabidopsis thaliana] >gi|38454064|gb|AAR20726.1|At1g64700 [Arabidopsis thaliana] >gi|38604006|gb|AAR24746.1|At1g64700 [Arabidopsis thaliana]	Unigene49723_All//1.00E-38//AT1G64700| unknown protein	Unigene49723_All//0.00E+00//TC171689				nr -
Unigene49724_All	837	0.00	0.06	0.89	1.25	0.58	0.43	0.35	0.25	0.29	5.92E+00	6.16E-01		9.80E+00	3.27E-04	Up	-1.12E+00	8.44E-02		-1.53E+00	2.88E-02		-5.02E-01	6.77E-01		-3.08E-01	7.74E-01		Unigene49724_All//gi|5042407|gb|AAD38246.1|AC006193_2//2.00E-37//Hypothetical Protein [Arabidopsis thaliana] >gi|6633824|gb|AAF19683.1|AC009519_17 F1N19.27 [Arabidopsis thaliana] >gi|38454064|gb|AAR20726.1|At1g64700 [Arabidopsis thaliana] >gi|38604006|gb|AAR24746.1|At1g64700 [Arabidopsis thaliana]	Unigene49724_All//1.00E-38//AT1G64700| unknown protein	Unigene49724_All//0.00E+00//TC171689				nr +
Unigene49726_All	625	4.69	1.38	4.17	7.73	4.52	6.29	3.79	1.54	1.21	-1.77E+00	9.37E-06	Down	-1.67E-01	6.51E-01		-7.75E-01	2.44E-03		-2.98E-01	3.23E-01		-1.30E+00	6.01E-04	Down	-1.65E+00	1.81E-05	Down	Unigene49726_All//gi|15241346|ref|NP_199916.1|//3.00E-74//short-chain dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] >gi|9758250|dbj|BAB08749.1|carbonyl reductase-like protein [Arabidopsis thaliana] >gi|56121902|gb|AAV74232.1|At5g51030 [Arabidopsis thaliana] >gi|57222206|gb|AAW39010.1|At5g51030 [Arabidopsis thaliana]	Unigene49726_All//1.00E-69//AT5G51030| short-chain dehydrogenase/reductase (SDR) family protein	Unigene49726_All//0.00E+00//TC177651		ko04146|Peroxisome		nr -
Unigene49729_All	745	0.98	1.90	1.29	28.95	9.66	5.88	2.10	0.50	0.43	9.54E-01	9.02E-02		3.88E-01	6.08E-01		-1.58E+00	5.03E-40	Down	-2.30E+00	1.45E-57	Down	-2.06E+00	9.44E-05	Down	-2.30E+00	1.48E-05	Down								
Unigene49730_All	643	43.45	179.98	60.79	21.61	49.59	67.01	38.80	83.14	243.62	2.05E+00	2.73E-242	Up	4.84E-01	3.21E-08		1.20E+00	1.62E-36	Up	1.63E+00	3.08E-71	Up	1.10E+00	2.28E-55	Up	2.65E+00	0.00E+00	Up	Unigene49730_All//gi|206584339|gb|ACI15342.1|//6.00E-90//NAC domain protein NAC2 [Gossypium hirsutum] >gi|206584351|gb|ACI15348.1| NAC domain protein NAC2 [Gossypium hirsutum]	Unigene49730_All//1.00E-84//AT1G01720| ATAF1; transcription activator/ transcription factor	Unigene49730_All//0.00E+00//gi|109853666|gb|DW482645.1|DW482645	NAC			nr +
Unigene49733_All	587	12.21	42.30	15.88	9.25	11.44	17.62	5.91	10.11	11.47	1.79E+00	7.35E-44	Up	3.79E-01	5.97E-02		3.07E-01	2.09E-01		9.30E-01	1.29E-07		7.76E-01	3.45E-04		9.58E-01	1.77E-06			Unigene49733_All//3.00E-123//TC147513					
Unigene49734_All	1303	0.64	0.66	0.86	1.15	1.56	0.94	1.10	1.22	4.01	4.12E-02	9.74E-01		4.18E-01	5.32E-01		4.43E-01	3.67E-01		-2.94E-01	6.38E-01		1.44E-01	7.67E-01		1.86E+00	8.91E-13	Up	Unigene49734_All//gi|116310937|emb|CAH67874.1|//1.00E-138//OSIGBa0153E02-OSIGBa0093I20.3 [Oryza sativa (indica cultivar-group)]	Unigene49734_All//5.00E-95//AT4G23160| protein kinase family protein					nr -
Unigene49735_All	627	50.32	42.35	39.66	60.38	49.43	55.97	41.00	27.20	16.08	-2.49E-01	1.17E-02		-3.43E-01	6.14E-04		-2.89E-01	4.60E-04		-1.10E-01	2.89E-01		-5.92E-01	6.54E-10		-1.35E+00	2.88E-38	Down	Unigene49735_All//gi|33186651|gb|AAP97495.1|//2.00E-57//cellulose synthase [Solanum tuberosum]	Unigene49735_All//2.00E-48//AT5G05170| CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene49735_All//0.00E+00//gi|109874300|gb|DW503274.1|DW503274				nr -
Unigene49737_All	1408	3.23	1.19	1.63	0.88	1.05	1.32	1.62	0.59	0.74	-1.44E+00	1.40E-06	Down	-9.91E-01	8.59E-04		2.50E-01	6.91E-01		5.72E-01	2.58E-01		-1.45E+00	2.26E-04	Down	-1.14E+00	2.03E-03		Unigene49737_All//gi|30680811|ref|NP_849992.1|//3.00E-74//tRNA/rRNA methyltransferase (SpoU) family protein [Arabidopsis thaliana] >gi|17065308|gb|AAL32808.1|Unknown protein [Arabidopsis thaliana]	Unigene49737_All//2.00E-64//AT2G19870| tRNA/rRNA methyltransferase (SpoU) family protein	Unigene49737_All//0.00E+00//ES818825				nr +
Unigene49738_All	548	5.35	15.07	6.22	6.73	6.16	10.30	8.10	9.69	9.45	1.50E+00	8.68E-12	Up	2.18E-01	5.58E-01		-1.27E-01	7.35E-01		6.15E-01	1.43E-02		2.58E-01	3.12E-01		2.22E-01	3.69E-01									
Unigene49739_All	286	29.64	18.96	32.02	49.47	37.69	47.06	42.72	19.87	23.12	-6.45E-01	1.15E-03		1.12E-01	6.31E-01		-3.92E-01	6.01E-03		-7.20E-02	7.01E-01		-1.10E+00	2.22E-13	Down	-8.86E-01	7.30E-10		Unigene49739_All//gi|297807427|ref|XP_002871597.1|//5.00E-10//translocon-associated protein beta family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317434|gb|EFH47856.1|translocon-associated protein beta family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49739_All//3.00E-11//AT5G14030| translocon-associated protein beta (TRAPB) family protein	Unigene49739_All//8.00E-113//TC145111		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene4974_All	1512	1.76	3.05	1.37	3.72	3.87	2.78	7.38	15.42	9.67	7.89E-01	5.06E-03		-3.62E-01	3.99E-01		5.65E-02	8.42E-01		-4.22E-01	1.05E-01		1.06E+00	2.45E-23	Up	3.89E-01	2.37E-03		Unigene4974_All//gi|4587572|gb|AAD25803.1|AC006550_11//1.00E-128//Similar to gb|U70015 lysosomal trafficking regulator from Mus musculus and contains 2 PF|00400 WD40, G-beta repeats. ESTs gb|T43386 and gb|AA395236 come from this gene [Arabidopsis thaliana]	Unigene4974_All//7.00E-120//AT1G03060| WD-40 repeat family protein / beige-related	Unigene4974_All//4.00E-23//gi|109839610|gb|DW238171.1|DW238171				nr -
Unigene49740_All	842	1.24	0.96	0.89	4.08	3.48	3.59	3.21	2.28	0.80	-3.68E-01	5.90E-01		-4.89E-01	4.78E-01		-2.32E-01	5.42E-01		-1.84E-01	6.11E-01		-4.93E-01	1.59E-01		-2.00E+00	9.91E-08	Down	Unigene49740_All//gi|225441732|ref|XP_002283137.1|//6.00E-10//PREDICTED: hypothetical protein isoform 1 [Vitis vinifera] >gi|225441734|ref|XP_002283160.1|PREDICTED: hypothetical protein isoform 2 [Vitis vinifera]		Unigene49740_All//8.00E-100//DV848894				nr -
Unigene49741_All	1081	0.53	0.38	0.10	1.57	2.55	1.84	0.78	0.85	1.99	-5.06E-01	6.00E-01		-2.43E+00	4.40E-02		7.02E-01	6.46E-02		2.31E-01	6.48E-01		1.21E-01	8.54E-01		1.35E+00	6.13E-04	Up	Unigene49741_All//gi|48310446|gb|AAT41822.1|//3.00E-46//At2g13100 [Arabidopsis thaliana]	Unigene49741_All//2.00E-48//AT2G13100| glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative	Unigene49741_All//2.00E-45//DT463742				nr +
Unigene49742_All	563	0.28	0.00	0.85	1.15	1.28	1.28	12.62	32.29	76.00	-8.12E+00	2.15E-01		1.61E+00	1.82E-01		1.59E-01	8.68E-01		1.58E-01	8.59E-01		1.36E+00	1.31E-26	Up	2.59E+00	4.98E-149	Up	Unigene49742_All//gi|224139824|ref|XP_002323294.1|//2.00E-69//cytochrome P450 [Populus trichocarpa] >gi|222867924|gb|EEF05055.1|cytochrome P450 [Populus trichocarpa]	Unigene49742_All//1.00E-45//AT5G06900| CYP93D1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene49747_All	703	1.79	1.15	0.76	2.55	3.04	2.51	2.71	0.95	0.91	-6.31E-01	2.93E-01		-1.24E+00	5.53E-02		2.52E-01	5.99E-01		-2.59E-02	9.47E-01		-1.51E+00	5.93E-04	Down	-1.58E+00	2.42E-04	Down	Unigene49747_All//gi|116310096|emb|CAH67116.1|//3.00E-10//H0502G05.7 [Oryza sativa (indica cultivar-group)]		Unigene49747_All//1.00E-95//ES848194				nr -
Unigene49750_All	860	2.01	3.48	1.24	10.60	11.73	7.98	6.19	5.54	14.55	7.92E-01	2.83E-02		-6.97E-01	1.83E-01		1.46E-01	5.08E-01		-4.09E-01	3.55E-02		-1.61E-01	5.51E-01		1.23E+00	1.69E-16	Up	Unigene49750_All//gi|9972376|gb|AAG10626.1|AC022521_4//5.00E-53//Unknown protein [Arabidopsis thaliana]	Unigene49750_All//2.00E-46//AT4G02075| PITI (pitchoun 1); protein binding / zinc ion binding	Unigene49750_All//5.00E-89//DR453590				nr -
Unigene49755_All	1007	1.51	0.75	0.32	2.33	2.36	1.21	2.52	0.58	1.94	-9.97E-01	6.49E-02		-2.25E+00	5.02E-04	Down	2.13E-02	9.69E-01		-9.41E-01	2.39E-02		-2.12E+00	1.70E-07	Down	-3.78E-01	2.88E-01		Unigene49755_All//gi|15226168|ref|NP_178215.1|//1.00E-08//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene49755_All//4.00E-10//AT2G01050| nucleic acid binding / zinc ion binding	Unigene49755_All//0.00E+00//DR461078				nr +
Unigene49757_All	711	1.47	3.42	4.49	2.80	3.73	1.33	1.37	1.06	1.46	1.22E+00	3.60E-03		1.61E+00	2.92E-05	Up	4.12E-01	3.15E-01		-1.07E+00	2.00E-02		-3.70E-01	5.87E-01		9.11E-02	8.86E-01									
Unigene49758_All	665	2.36	8.23	3.20	3.30	2.54	2.11	3.69	3.77	3.65	1.80E+00	2.81E-10	Up	4.41E-01	3.57E-01		-3.77E-01	4.06E-01		-6.47E-01	1.44E-01		3.23E-02	9.55E-01		-1.30E-02	9.62E-01		Unigene49758_All//gi|223635742|sp|Q9LVD3.2|PP434_ARATH//2.00E-26//RecName: Full=Pentatricopeptide repeat-containing protein At5g57250, mitochondrial; Flags: Precursor	Unigene49758_All//1.00E-27//AT5G57250| EXPRESSED IN: 9 plant structures; EXPRESSED DURING: F mature embryo stage, 4 leaf senescence stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT1G62910.1); Has 30133 Blast hits to 8951 proteins in 186 species: Archae - 6; Bacteria - 22; Metazoa - 601; Fungi - 543; Plants - 27743; Viruses - 0; Other Eukaryotes - 1218 (source: NCBI BLink).						nr -
Unigene49759_All	642	0.00	0.00	0.00	15.75	6.11	7.39	14.88	15.89	16.26	null	null		null	null		-1.37E+00	3.34E-15	Down	-1.09E+00	1.18E-09	Down	9.39E-02	6.53E-01		1.27E-01	4.70E-01									
Unigene4976_All	1020	2.46	2.43	0.42	2.15	1.55	2.35	60.93	56.83	73.82	-1.66E-02	9.84E-01		-2.56E+00	3.86E-07	Down	-4.69E-01	2.94E-01		1.27E-01	7.70E-01		-1.01E-01	1.36E-01		2.77E-01	1.52E-07		Unigene4976_All//gi|259121381|gb|ACY92010.1|//5.00E-50//WRKY transcription factor 8 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene4976_All//2.00E-42//AT1G29280| WRKY65; transcription factor	Unigene4976_All//0.00E+00//TC148412	WRKY	ko04626|Plant-pathogen interaction		nr +

Unigene49760_All	782	2.41	3.76	0.34	5.35	5.86	5.95	22.87	56.33	154.51	6.42E-01	7.81E-02		-2.82E+00	5.01E-06	Down	1.30E-01	7.08E-01		1.53E-01	6.32E-01		1.30E+00	1.81E-59	Up	2.76E+00	0.00E+00	Up	Unigene49760_All//gi|115452105|ref|NP_001049653.1|//2.00E-44//0s03g0265900 [Oryza sativa Japonica Group] >gi|108707346|gb|ABF95141.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548124|dbj|BAF11567.1| Os03g0265900 [Oryza sativa Japonica Group]	Unigene49760_All//7.00E-23//AT4G37300| MEE59 (maternal effect embryo arrest 59)	Unigene49760_All//0.00E+00//gi|13246512|gb|BE053864.2|BE053864				nr +
Unigene49761_All	319	7.71	6.04	4.17	11.09	9.28	13.59	7.16	4.06	2.00	-3.53E-01	3.76E-01		-8.85E-01	3.75E-02		-2.56E-01	4.76E-01		2.94E-01	3.75E-01		-8.17E-01	3.07E-02		-1.84E+00	4.73E-06	Down				Unigene49761_All//6.00E-80//gi|78345153|gb|DT565427.1|DT565427				
Unigene49762_All	422	39.30	33.02	31.55	64.33	52.14	52.01	63.42	41.70	30.78	-2.51E-01	7.89E-02		-3.17E-01	3.01E-02		-3.03E-01	2.42E-03		-3.07E-01	3.36E-03		-6.05E-01	1.17E-10		-1.04E+00	1.08E-26	Down	Unigene49762_All//gi|110741159|dbj|BAE98672.1|//1.00E-60//Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]	Unigene49762_All//9.00E-62//AT4G34450| coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	Unigene49762_All//0.00E+00//TC136191				nr -
Unigene49763_All	987	1.48	0.51	1.35	3.18	2.86	3.16	2.40	0.68	0.89	-1.53E+00	7.80E-03		-1.38E-01	7.97E-01		-1.52E-01	6.98E-01		-1.02E-02	9.71E-01		-1.82E+00	6.14E-06	Down	-1.43E+00	1.25E-04	Down	Unigene49763_All//gi|30102682|gb|AAP21259.1|//2.00E-89//At4g27060 [Arabidopsis thaliana]	Unigene49763_All//4.00E-84//AT4G27060| TOR1 (TORTIFOLIA 1); microtubule binding	Unigene49763_All//3.00E-106//C0092484				nr -
Unigene49765_All	512	44.55	32.56	41.60	85.72	86.09	91.74	89.52	50.04	36.65	-4.53E-01	7.54E-05		-9.89E-02	4.62E-01		6.30E-03	9.51E-01		9.80E-02	2.92E-01		-8.39E-01	1.17E-30		-1.29E+00	7.83E-63	Down	Unigene49765_All//gi|225030812|gb|ACN78519.1|//9.00E-41//reduced leaflet 1 [Lotus japonicus]	Unigene49765_All//5.00E-17//AT5G22570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene49765_All//0.00E+00//gi|78325360|gb|DT545634.1|DT545634				nr -
Unigene49766_All	468	29.18	7.58	17.52	53.01	34.88	57.52	10.84	4.73	2.98	-1.94E+00	2.26E-27	Down	-7.36E-01	3.06E-06		-6.04E-01	1.50E-09		1.18E-01	3.50E-01		-1.20E+00	9.96E-07	Down	-1.86E+00	1.25E-12	Down				Unigene49766_All//4.00E-23//TC172854				
Unigene49767_All	567	2.86	1.70	1.88	7.03	2.31	4.86	9.47	6.63	3.58	-7.53E-01	1.41E-01		-6.07E-01	2.61E-01		-1.61E+00	6.53E-08	Down	-5.33E-01	8.82E-02		-5.14E-01	2.68E-02		-1.40E+00	3.86E-09	Down	Unigene49767_All//gi|15230697|ref|NP_187283.1|//5.00E-19//ribosomal protein L33 family protein [Arabidopsis thaliana] >gi|15239562|ref|NP_197380.1| ribosomal protein L33 family protein [Arabidopsis thaliana] >gi|297812063|ref|XP_002873915.1| ribosomal protein L33 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297829162|ref|XP_002882463.1| ribosomal protein L33 family protein [Arabidopsis lyrata subsp. lyrata] >gi|21536699|gb|AAM61031.1| ribosomal protein L33-like [Arabidopsis thaliana] >gi|38566500|gb|AAR24140.1| At5g18790 [Arabidopsis thaliana] >gi|40823687|gb|AAR92299.1| At5g18790 [Arabidopsis thaliana] >gi|109134211|gb|AB625103.1| At3g06320 [Arabidopsis thaliana] >gi|297319752|gb|EFH50174.1| ribosomal protein L33 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328303|gb|EFH58722.1| ribosomal protein L33 family	Unigene49767_All//3.00E-20//AT5G18790| ribosomal protein L33 family protein	Unigene49767_All//1.00E-128//TC177346		ko03010|Ribosome		nr +
Unigene49769_All	558	13.03	18.89	9.45	6.16	12.90	14.08	29.47	19.25	16.85	5.35E-01	2.35E-03		-4.64E-01	4.37E-02		1.07E+00	3.55E-07	Up	1.19E+00	1.40E-08	Up	-6.15E-01	4.89E-07		-8.07E-01	3.45E-11		Unigene49769_All//gi|56542451|gb|AAV82890.1|//3.00E-40//Avr9/Cf-9 rapidly elicited protein 20 [Nicotiana tabacum]	Unigene49769_All//3.00E-33//AT4G27280| calcium-binding EF hand family protein	Unigene49769_All//0.00E+00//gi|84155833|gb|DN817059.1|DN817059		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr +
Unigene4977_All	843	2.61	23.62	5.87	6.56	4.25	4.23	3.41	101.69	4.16	3.18E+00	7.84E-69	Up	1.17E+00	4.38E-05	Up	-6.27E-01	8.90E-03		-6.32E-01	1.20E-02		4.90E+00	0.00E+00	Up	2.86E-01	3.52E-01		Unigene4977_All//gi|159138941|gb|AB989170.1|//9.00E-65//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene4977_All//6.00E-50//AT3G46230| ATHSP17.4	Unigene4977_All//0.00E+00//gi|78339948|gb|DT560222.1|DT560222				nr -
Unigene49772_All	419	4.62	15.60	13.85	9.87	11.42	30.94	17.96	31.62	29.09	1.76E+00	9.80E-12	Up	1.58E+00	8.16E-09	Up	2.11E-01	5.21E-01		1.65E+00	4.84E-22	Up	8.16E-01	4.89E-09		6.96E-01	9.26E-07					Unigene49772_All//8.00E-09//ES797810				
Unigene49773_All	511	30.61	16.76	19.28	19.50	15.09	17.15	6.29	6.13	2.11	-8.69E-01	1.31E-09		-6.67E-01	4.73E-06		-3.69E-01	3.95E-02		-1.85E-01	3.85E-01		-3.57E-02	9.30E-01		-1.58E+00	9.20E-07	Down	Unigene49773_All//gi|115461126|ref|NP_001054163.1|//1.00E-57//Os04g0663300 [Oryza sativa Japonica Group] >gi|115463469|ref|NP_001055334.1| Os05g0367000 [Oryza sativa Japonica Group] >gi|225434558|ref|XP_002277443.1| PREDICTED: similar to translation initiation factor IF-2 [Vitis vinifera] >gi|255582964|ref|XP_002532111.1| Pre-mRNA-splicing factor ini1 [Ricinus communis] >gi|38346076|emb|CAE04844.2| OSJNBa0084K01.16 [Oryza sativa (japonica cultivar-group)] >gi|113565734|dbj|BAF16077.1| Os04g0663300 [Oryza sativa Japonica Group] >gi|113578885|dbj|BAF17248.1| Os05g0367000 [Oryza sativa Japonica Group] >gi|116309854|emb|CAH66889.1| OSIGBa0099E20.4 [Oryza sativa (indica cultivar-group)] >gi|223528214|gb|EEF30273.1| Pre-mRNA-splicing factor ini1 [Ricinus communis]	Unigene49773_All//4.00E-58//AT2G30000| LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: PHF5-like (InterPro:IPR005345); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G07170.2); Has 292 Blast hits to 292 proteins in 142 species: Archae - 0; Bacteria - 0; Metazoa - 110; Fungi - 75; Plants - 47; Viruses - 0; Other Eukaryotes - 60 (source: NCBI BLink).	Unigene49773_All//5.00E-106//gi|109868310|gb|DW497286.1|DW497286		ko03040|Spliceosome		nr -
Unigene49775_All	421	9.82	10.95	28.21	14.44	21.51	15.56	11.05	11.52	12.96	1.58E-01	6.22E-01		1.52E+00	1.83E-16	Up	5.76E-01	1.67E-03		1.08E-01	7.01E-01		6.00E-02	8.26E-01		2.31E-01	3.40E-01		Unigene49775_All//gi|87241162|gb|AB033020.1|//3.00E-09//Phosphatidate cytidylyltransferase [Medicago truncatula]	Unigene49775_All//8.00E-08//AT1G62430| ATCDS1; phosphatidate cytidylyltransferase			ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism		nr -
Unigene49777_All	746	0.35	1.83	0.57	1.40	1.66	3.81	8.05	59.05	32.63	2.39E+00	4.04E-04	Up	7.03E-01	5.54E-01		2.45E-01	7.39E-01		1.44E+00	1.75E-04	Up	2.88E+00	1.18E-168	Up	2.02E+00	4.86E-63	Up	Unigene49777_All//gi|2346974|dbj|BAA21921.1|//1.00E-33//ZPT2-12 [Petunia x hybrida]	Unigene49777_All//2.00E-24//AT2G28710| zinc finger (C2H2 type) family protein	Unigene49777_All//0.00E+00//TC155082	C2H2			nr +
Unigene49778_All	616	6.46	5.76	1.90	2.18	5.09	5.72	4.80	6.17	2.91	-1.65E-01	5.98E-01		-1.76E+00	4.00E-07	Down	1.22E+00	4.15E-04	Up	1.39E+00	3.91E-05	Up	3.62E-01	2.25E-01		-7.23E-01	2.04E-02		Unigene49778_All//gi|255573123|ref|XP_002527491.1|//5.00E-16//conserved hypothetical protein [Ricinus communis] >gi|223533131|gb|EEF34889.1| conserved hypothetical protein [Ricinus communis]	Unigene49778_All//2.00E-05//AT1G49700| unknown protein					nr +
Unigene49780_All	565	47.41	32.64	32.89	109.68	75.51	111.27	230.56	144.47	108.38	-5.39E-01	2.66E-07		-5.28E-01	1.03E-06		-5.39E-01	6.95E-19		2.08E-02	7.99E-01		-6.74E-01	7.93E-59		-1.09E+00	1.16E-135	Down	Unigene49780_All//gi|211906502|gb|ACJ11744.1|//2.00E-06//Isocitrate dehydrogenase [Gossypium hirsutum]		Unigene49780_All//0.00E+00//gi|5048631|gb|AI729779.1|AI729779				nr +
Unigene49785_All	1010	52.99	105.15	65.85	116.50	160.93	290.30	843.01	1655.40	1354.43	9.89E-01	5.27E-75		3.13E-01	2.18E-06		4.66E-01	7.21E-37		1.32E+00	0.00E+00	Up	9.74E-01	0.00E+00		6.84E-01	0.00E+00		Unigene49785_All//gi|148927394|gb|ABR18828.1|//1.00E-135//cysteine proteinase [Elaeis guineensis]	Unigene49785_All//9.00E-120//AT5G43060| cysteine proteinase, putative / thiol protease, putative	Unigene49785_All//0.00E+00//TC166225				nr +
Unigene49787_All	805	11.24	6.04	3.57	38.74	44.19	30.46	0.74	0.88	0.59	-8.96E-01	3.61E-06		-1.65E+00	3.49E-14	Down	1.90E-01	4.14E-02		-3.47E-01	2.70E-04		2.63E-01	7.21E-01		-3.08E-01	6.78E-01		Unigene49787_All//gi|8920587|gb|AAF81309.1|AC061957_5//1.00E-48//Contains a weak similarity to a farnesylated protein GMFP8 mRNA from Glycine max gb|U64916. ESTs gb|AI993148, gb|T44360 come from this gene [Arabidopsis thaliana]	Unigene49787_All//4.00E-12//AT1G01490| heavy-metal-associated domain-containing protein	Unigene49787_All//0.00E+00//gi|109878722|gb|DW507692.1|DW507692				nr +
Unigene49789_All	966	1.30	2.47	0.33	1.70	0.82	0.47	0.35	0.00	1.15	9.23E-01	2.56E-02		-1.97E+00	4.62E-03		-1.05E+00	3.11E-02		-1.86E+00	6.76E-04	Down	-8.45E+00	1.17E-02		1.72E+00	4.13E-03		Unigene49789_All//gi|18410769|ref|NP_565101.1|//2.00E-36//JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULATION RESPONSE 1); heat shock protein binding [Arabidopsis thaliana] >gi|15982795|gb|AAL09745.1| At1g75100/F9E10_5 [Arabidopsis thaliana] >gi|21655287|gb|AAM65355.1| At1g75100/F9E10_5 [Arabidopsis thaliana] >gi|74267412|dbj|BAE44203.1| auxilin-like J-domain protein [Arabidopsis thaliana]	Unigene49789_All//3.00E-38//AT1G75100| JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULATION RESPONSE 1); heat shock protein binding	Unigene49789_All//0.00E+00//TC176751				nr -
Unigene4979_All	1212	1.08	1.80	5.10	4.36	6.05	11.44	7.71	2.66	14.96	7.36E-01	9.04E-02		2.24E+00	1.64E-14	Up	4.74E-01	2.63E-02		1.39E+00	1.67E-18	Up	-1.54E+00	7.72E-17	Down	9.56E-01	6.54E-16		Unigene4979_All//gi|30686500|ref|NP_194166.2|//1.00E-108//phosphorylase family protein [Arabidopsis thaliana]	Unigene4979_All//5.00E-99//AT4G24350| phosphorylase family protein					nr -
Unigene49793_All	421	2.86	4.33	2.02	1.66	3.35	2.36	5.93	12.91	12.11	6.00E-01	2.15E-01		-4.98E-01	4.26E-01		1.02E+00	7.53E-02		5.11E-01	4.92E-01		1.12E+00	1.55E-06	Up	1.03E+00	1.14E-05	Up	Unigene49793_All//gi|30697711|ref|NP_177025.2|//1.00E-31//agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein [Arabidopsis thaliana] >gi|30725466|gb|AAF37755.1| At1g68580 [Arabidopsis thaliana]	Unigene49793_All//9.00E-33//AT1G68580| agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein	Unigene49793_All//5.00E-44//TC174998				nr +
Unigene49799_All	989	71.05	64.09	128.04	86.53	55.71	52.84	166.86	101.13	41.97	-1.49E-01	2.43E-02		8.50E-01	1.83E-67		-6.35E-01	7.32E-35		-7.12E-01	1.04E-37		-7.22E-01	9.09E-84		-1.99E+00	0.00E+00	Down				Unigene49799_All//0.00E+00//TC144864				
Unigene498_All	342	10.10	2.07	4.98	25.49	20.64	13.47	13.85	21.14	9.90	-2.28E+00	5.81E-09	Down	-1.02E+00	3.58E-03		-3.04E-01	1.31E-01		-9.20E-01	1.69E-06		6.11E-01	1.61E-03		-4.84E-01	4.41E-02					Unigene498_All//6.00E-74//TC175288				
Unigene4980_All	882	12.40	21.14	12.20	16.77	20.97	22.53	22.10	15.35	10.89	7.70E-01	2.69E-09		-2.37E-02	9.10E-01		3.22E-01	1.12E-02		4.26E-01	4.86E-04		-5.25E-01	2.24E-06		-1.02E+00	4.79E-19	Down	Unigene4980_All//gi|224080027|ref|XP_002365996.1|//2.00E-52//high mobility group family [Populus trichocarpa] >gi|222848960|gb|EEE86507.1| high mobility group family [Populus trichocarpa]	Unigene4980_All//9.00E-33//AT2G34450| high mobility group (HMG1/2) family protein	Unigene4980_All//0.00E+00//TC168531		ko03410|Base excision repair		nr +
Unigene49801_All	1086	3.47	0.51	1.47	2.71	2.41	3.58	1.17	0.96	0.26	-2.76E+00	7.35E-12	Down	-1.24E+00	2.50E-04	Down	-1.67E-01	6.73E-01		4.02E-01	2.29E-01		-2.80E-01	6.48E-01		-2.19E+00	1.97E-04	Down	Unigene49801_All//gi|116309014|emb|CAH66131.1|//6.00E-14//OSIGBa0133L04.5 [Oryza sativa (indica cultivar-group)]	Unigene49801_All//5.00E-10//AT3G09510| nucleic acid binding	Unigene49801_All//0.00E+00//gi|6461307|gb|AW186871.1|AW186871				nr -
Unigene49802_All	1061	0.39	1.15	0.70	1.69	3.83	4.43	0.76	2.84	1.20	1.54E+00	1.74E-02		8.33E-01	3.39E-01		1.18E+00	6.31E-05	Up	1.39E+00	1.25E-06	Up	1.91E+00	1.01E-07	Up	6.66E-01	2.01E-01		Unigene49802_All//gi|145337506|ref|NP_177527.3|//1.00E-111//ATP binding / microtubule motor [Arabidopsis thaliana] >gi|110739024|dbj|BAF01431.1| kinesin-related protein [Arabidopsis thaliana]	Unigene49802_All//7.00E-113//AT1G73860| ATP binding / microtubule motor	Unigene49802_All//0.00E+00//DR462361				nr +

Unigene49803_All	581	17.47	28.95	15.67	18.95	17.19	22.54	23.51	14.75	9.05	7.29E-01	8.97E-08		-1.57E-01	4.36E-01		-1.41E-01	4.89E-01		2.51E-01	1.37E-01		-6.73E-01	7.07E-07		-1.38E+00	2.48E-21	Down	Unigene49803_All//gi|98961003|gb|AB758985.1|/1.00E-28//At4g35980 [Arabidopsis thaliana]	Unigene49803_All//4.00E-22//AT4G35980| unknown protein	Unigene49803_All//0.00E+00//gi|109879769|gb|DW508739.1|DW508739				nr +
Unigene49807_All	421	54.43	33.94	30.36	84.01	51.94	57.93	25.81	12.91	12.68	-6.82E-01	2.88E-09		-8.43E-01	1.83E-12		-6.94E-01	4.75E-17		-5.36E-01	7.67E-10		-1.00E+00	2.56E-10		-1.03E+00	4.47E-11	Down	Unigene49807_All//gi|154269428|gb|ABS72341.1|//6.00E-33//rapid alkalinization factor precursor [Litchi chinensis]	Unigene49807_All//9.00E-33//AT4G15800| RALFL33 (ralf-like 33); signal transducer	Unigene49807_All//0.00E+00//TC161528				nr -
Unigene4981_All	860	2.62	1.24	0.62	3.53	1.36	2.21	1.67	0.92	1.07	-1.08E+00	1.21E-02		-2.08E+00	3.39E-05	Down	-1.38E+00	5.31E-05	Down	-6.80E-01	5.99E-02		-8.56E-01	8.67E-02		-6.50E-01	1.74E-01		Unigene4981_All//gi|42564975|ref|NP_188410.2|//1.00E-100//DNAJ heat shock family protein [Arabidopsis thaliana] >gi|115646890|gb|ABJ17154.1|At3g17830 [Arabidopsis thaliana]	Unigene4981_All//7.00E-82//AT3G17830| DNAJ heat shock family protein	Unigene4981_All//1.00E-160//TC164916				nr -
Unigene49810_All	556	137.48	89.22	95.49	231.69	180.29	191.46	91.94	50.14	40.41	-6.24E-01	5.90E-25		-5.26E-01	8.19E-18		-3.62E-01	8.86E-19		-2.75E-01	2.73E-10		-8.75E-01	1.51E-36		-1.19E+00	1.63E-61	Down	Unigene49810_All|gi|98961023|gb|AB758995.1|/5.00E-26//At1g22520 [Arabidopsis thaliana]	Unigene49810_All//2.00E-28//AT1G72170| unknown protein	Unigene49810_All//0.00E+00//gi|161249009|gb|ES800751.1|ES800751				nr -
Unigene49813_All	416	51.94	43.61	49.28	77.36	102.89	57.11	57.83	132.52	76.13	-2.52E-01	3.93E-02		-7.59E-02	6.10E-01		4.12E-01	4.56E-08		-4.38E-01	1.99E-06		1.20E+00	3.26E-65	Up	3.97E-01	2.09E-06		Unigene49813_All//gi|7768153|emb|CAB90634.1|/2.00E-64//protein phosphatase 2C (PP2C) [Fagus sylvatica]	Unigene49813_All//5.00E-63//AT3G51370| protein phosphatase 2C, putative / PP2C, putative	Unigene49813_All//0.00E+00//gi|164304049|gb|ES852344.1|ES852344				nr -
Unigene49814_All	417	43.79	36.33	36.14	74.66	58.88	73.21	114.78	58.53	42.70	-2.69E-01	4.40E-02		-2.77E-01	4.83E-02		-3.43E-01	1.56E-04		-2.82E-02	8.09E-01		-9.72E-01	1.01E-40		-1.43E+00	1.62E-76	Down	Unigene49814_All//gi|18423437|ref|NP_568778.1|/3.00E-33//NADH-ubiquinone oxidoreductase-related [Arabidopsis thaliana] >gi|25090853|sp|Q9FLX7.1|NDUA5_ARATH RecName: Full=Probable NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5, mitochondrial; Flags: Precursor >gi|15809966|gb|AAL06910.1|AT5g52840/MXC20_6 [Arabidopsis thaliana] >gi|18958052|gb|AAL79599.1|AT5g52840/MXC20_6 [Arabidopsis thaliana]	Unigene49814_All//2.00E-34//AT5G52840| NADH-ubiquinone oxidoreductase-related	Unigene49814_All//0.00E+00//TC145196		ko00190|Oxidative phosphorylation		nr -
Unigene49816_All	355	7.81	8.99	8.25	7.44	9.02	6.49	36.09	44.86	10.21	2.03E-01	5.93E-01		7.88E-02	8.31E-01		2.79E-01	4.84E-01		-1.97E-01	6.43E-01		3.14E-01	1.42E-02		-1.82E+00	1.07E-29	Down	Unigene49816_All|gi|224111880|ref|XP_002316010.1|/3.00E-41//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1|cytochrome P450 [Populus trichocarpa]	Unigene49816_All//4.00E-26//AT3G14690| CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene49816_All//4.00E-149//TC139220		ko04146|Peroxisome//ko00592|alpha-Linoleic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00906|Carotenoid biosynthesis		nr +
Unigene49817_All	819	90.84	118.48	131.14	54.62	62.48	39.92	53.79	113.29	21.84	3.83E-01	2.40E-13		5.30E-01	3.85E-25		1.94E-01	8.74E-03		-4.52E-01	3.71E-09		1.07E+00	4.58E-92	Up	-1.30E+00	2.67E-61	Down	Unigene49817_All//gi|224111880|ref|XP_002316010.1|/1.00E-80//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1|cytochrome P450 [Populus trichocarpa]	Unigene49817_All//2.00E-36//AT3G14680| CYP72A14; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene49817_All//0.00E+00//TC139220		ko04146|Peroxisome//ko00592|alpha-Linoleic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr -
Unigene49818_All	503	10.09	29.31	17.89	15.85	24.30	21.37	24.46	52.35	19.33	1.54E+00	2.55E-21	Up	8.26E-01	3.51E-05		6.17E-01	5.12E-05		4.32E-01	1.40E-02		1.10E+00	1.33E-27	Up	-3.40E-01	1.67E-02		Unigene49818_All//gi|24461857|gb|AN62344.1|AF506028_11//4.00E-08//CTV.15 [Citrus trifoliata]	Unigene49818_All//8.00E-06//AT5G25280| serine-rich protein-related	Unigene49818_All//0.00E+00//gi|164358386|gb|ES828868.1|ES828868				nr -
Unigene49819_All	594	32.24	70.72	36.49	35.22	34.26	41.13	60.00	131.30	89.67	1.13E+00	2.09E-37	Up	1.79E-01	1.81E-01		-3.99E-02	8.16E-01		2.24E-01	5.68E-02		1.13E+00	5.69E-84	Up	5.80E-01	2.06E-19		Unigene49819_All//gi|224100709|ref|XP_002311983.1|/3.00E-69//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222851803|gb|EEE89350.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene49819_All//2.00E-70//AT5G04410| NAC2; transcription factor	Unigene49819_All//5.00E-17//gi|54121286|gb|CO496795.1|CO496795	NAC			nr +
Unigene4982_All	936	3.19	2.17	2.90	10.32	9.34	9.94	4.47	1.74	1.75	-5.57E-01	1.25E-01		-1.35E-01	7.15E-01		-1.44E-01	5.17E-01		-5.48E-02	7.89E-01		-1.36E+00	8.99E-07	Down	-1.36E+00	5.23E-07	Down	Unigene4982_All//gi|145332657|ref|NP_001078194.1|/3.00E-41//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene4982_All//1.00E-34//AT3G20395| protein binding / zinc ion binding	Unigene4982_All//0.00E+00//TC148743				nr +
Unigene49821_All	730	28.67	12.56	12.25	9.35	12.93	4.58	0.70	0.00	0.22	-1.19E+00	1.40E-20	Down	-1.23E+00	1.17E-20	Down	4.67E-01	1.04E-02		-1.03E+00	3.56E-06	Down	-9.44E+00	8.89E-04	Down	-1.67E+00	7.78E-02		Unigene49821_All|gi|2495180|sp|Q43082.1|HEM3_PEA//4.00E-77//RecName: Full=Porphobilinogen deaminase, chloroplastic; Short=PBG; AltName: Full=Pre-uroporphyrinogen synthase; AltName: Full=Hydroxymethylbilane synthase; Short=HMBS; Flags: Precursor >gi|313724|emb|CAA51820.1|hydroxymethylbilane synthase [Pisum sativum]	Unigene49821_All//2.00E-70//AT5G08280| HEMC (HYDROXYMETHYLBILANE SYNTHASE); hydroxymethylbilane synthase	Unigene49821_All//0.00E+00//TC173026		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene49824_All	502	4.59	6.26	3.61	5.46	13.44	8.55	11.03	27.81	27.06	4.49E-01	2.14E-01		-3.47E-01	4.29E-01		1.30E+00	4.86E-09	Up	6.47E-01	2.87E-02		1.33E+00	4.05E-20	Up	1.29E+00	3.31E-19	Up	Unigene49824_All//gi|44021989|gb|AAS46633.1|/3.00E-06//At2g04495 [Arabidopsis thaliana] >gi|45773862|gb|AAS76735.1|At2g04495 [Arabidopsis thaliana]		Unigene49824_All//0.00E+00//DR456350				nr +
Unigene49826_All	657	2.71	5.71	1.78	3.03	1.89	2.20	4.63	2.67	8.97	1.08E+00	8.32E-04	Up	-6.03E-01	2.42E-01		-6.85E-01	1.25E-01		-4.63E-01	3.46E-01		-7.94E-01	1.26E-02		9.54E-01	9.46E-06				Unigene49826_All//4.00E-18//CO096150				
Unigene49828_All	525	22.82	20.27	21.40	42.70	27.42	44.30	85.61	56.13	25.42	-1.71E-01	3.47E-01		-9.27E-02	6.29E-01		-6.39E-01	1.48E-09		5.32E-02	6.86E-01		-6.09E-01	1.58E-17		-1.75E+00	9.19E-97	Down	Unigene49828_All|gi|15241504|ref|NP_196421.1|//4.00E-15//TOM5 (MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM5 HOMOLOG) [Arabidopsis thaliana] >gi|46577135|sp|Q9SD80.3|TOM5_ARATH RecName: Full=Mitochondrial import receptor subunit TOM5 homolog; AltName: Full=Translocase of outer membrane 5 kDa subunit homolog >gi|38566510|gb|AAR24145.1|At5g08040 [Arabidopsis thaliana] >gi|40823543|gb|AAR92288.1|At5g08040 [Arabidopsis thaliana]	Unigene49828_All//2.00E-16//AT5G08040| TOM5 (MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM5 HOMOLOG)	Unigene49828_All//0.00E+00//TC171859				nr +
Unigene4983_All	901	15.45	59.89	12.12	2.05	3.06	5.81	1.55	1.39	1.64	1.96E+00	2.19E-106	Up	-3.50E-01	2.89E-02		5.80E-01	1.37E-01		1.51E+00	3.50E-08	Up	-1.54E-01	7.65E-01		7.92E-02	8.80E-01		Unigene4983_All|gi|24461855|gb|AAN62342.1|AF506028_9//5.00E-31//Jp18 [Citrus trifoliata]	Unigene4983_All//4.00E-38//AT2G12462| unknown protein	Unigene4983_All//0.00E+00//gi|78326268|gb|DT546542.1|DT546542				nr +
Unigene49830_All	695	6.02	12.98	8.27	25.52	36.02	24.17	23.24	30.73	18.86	1.11E+00	2.40E-08	Up	4.58E-01	8.10E-02		4.97E-01	9.12E-07		-7.80E-02	6.21E-01		4.03E-01	1.46E-04		-3.01E-01	1.42E-02		Unigene49830_All|gi|18411140|ref|NP_565134.1|//1.00E-21//CP12-3 [Arabidopsis thaliana] >gi|28466821|gb|AAO44019.1|At1g76560 [Arabidopsis thaliana]	Unigene49830_All//6.00E-23//AT1G76560| CP12-3	Unigene49830_All//0.00E+00//gi|109831625|gb|DW230184.1|DW230184				nr -
Unigene49832_All	882	3.92	7.53	0.48	19.71	37.17	32.16	28.91	119.42	84.87	9.43E-01	4.47E-05		-3.02E+00	2.53E-11	Down	9.15E-01	2.17E-24		7.06E-01	1.33E-12		2.05E+00	5.37E-270	Up	1.55E+00	5.37E-134	Up	Unigene49832_All//gi|157313304|gb|ABV32545.1|//1.00E-158//beta-galactosidase protein 2 [Prunus persica]	Unigene49832_All//2.00E-159//AT3G13750| BGAL1 (Beta galactosidase 1); beta-galactosidase/ catalytic/ cation binding / heme binding / peroxidase/ sugar binding	Unigene49832_All//0.00E+00//AI725904		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series		nr +
Unigene49833_All	561	18.37	31.61	13.67	14.65	35.97	28.18	11.98	16.32	13.14	7.83E-01	4.05E-09		-4.27E-01	2.34E-02		1.30E+00	3.80E-26	Up	9.44E-01	1.42E-11		4.45E-01	9.42E-03		1.33E-01	5.43E-01		Unigene49833_All//gi|224083769|ref|XP_002307117.1|//5.00E-13//predicted protein [Populus trichocarpa] >gi|222856566|gb|EEE94113.1|predicted protein [Populus trichocarpa]		Unigene49833_All//5.00E-17//TC165474				nr -
Unigene49838_All	477	29.83	13.60	14.62	23.81	18.19	35.41	3.99	2.89	4.18	-1.13E+00	3.12E-13	Down	-1.03E+00	6.83E-11	Down	-3.88E-01	1.78E-02		5.73E-01	1.44E-05		-4.64E-01	2.90E-01		6.62E-02	8.84E-01		Unigene49838_All|gi|162280539|gb|ABX82930.1|//3.00E-34//transcription factor style2.1 [Solanum lycopersicum] >gi|162280541|gb|ABX82931.1|transcription factor style2.1 [Solanum pennellii] >gi|162280543|gb|ABX82932.1|transcription factor style2.1 [Solanum lycopersicum] >gi|162280545|gb|ABX82933.1|transcription factor style2.1 [Solanum pennellii]	Unigene49838_All//7.00E-31//AT1G26945| KDR (KIDAR1); transcription regulator	Unigene49838_All//0.00E+00//DT527245	bHLH			nr +
Unigene4984_All	802	3.00	2.84	4.71	5.96	6.74	7.10	11.02	4.27	4.72	-7.80E-02	8.44E-01		6.52E-01	4.83E-02		1.77E-01	5.59E-01		2.51E-01	3.83E-01		-1.37E+00	1.64E-13	Down	-1.22E+00	6.75E-12	Down	Unigene4984_All|gi|15228379|ref|NP_190414.1|//1.00E-29//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|62901491|sp|Q9STM4.1|C3H43_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 43; Short=AtC3H43; AltName: Full=Zinc finger CCCH domain-containing protein ZFN-like 6 >gi|194272236|gb|ACF37203.1|At3g48440 [Arabidopsis thaliana]	Unigene4984_All//6.00E-28//AT3G48440| zinc finger (CCCH-type) family protein			C3H	ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene49841_All	563	14.68	19.17	20.62	5.49	6.06	4.25	19.68	43.58	23.21	3.85E-01	2.91E-02		4.90E-01	4.78E-03		1.43E-01	7.34E-01		-3.68E-01	3.42E-01		1.15E+00	1.31E-27	Up	2.38E-01	9.55E-02		Unigene49841_All|gi|48310551|gb|AAT41837.1|//3.00E-25//At5g23850 [Arabidopsis thaliana]	Unigene49841_All//7.00E-26//AT5G23850| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Lipopolysaccharide-modifying protein (InterPro:IPR006598), Protein of unknown function DUF521, CAP10-like (InterPro:IPR008539); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G48980.1); Has 588 Blast hits to 567 proteins in 103 species: Archae - 2; Bacteria - 34; Metazoa - 301; Fungi - 69; Plants - 115; Viruses - 3; Other Eukaryotes - 64 (source: NCBI BLink).						nr +

Unigene49842_All	449	67.35	37.69	29.89	103.73	105.84	155.21	114.69	76.24	65.92	-8.38E-01	8.67E-17		-1.17E+00	1.25E-27	Down	2.90E-02	8.06E-01		5.81E-01	1.66E-21		-5.89E-01	7.37E-19		-7.99E-01	1.47E-32		Unigene49842_All//gi|257219572|gb|ACV50439.1|//1.00E-81//ribosomal protein L15 [Jatropha curcas]	Unigene49842_All//3.00E-67//AT4G16720| 60S ribosomal protein L15 (RPL15A)	Unigene49842_All//0.00E+00//ES817200		ko03010|Ribosome		nr +
Unigene49843_All	479	2.29	2.96	4.22	2.91	3.31	2.36	10.42	11.26	5.16	3.69E-01	5.15E-01		8.81E-01	6.42E-02		1.84E-01	7.85E-01		-3.05E-01	6.38E-01		1.12E-01	6.55E-01		-1.01E+00	1.76E-05	Down	Unigene49843_All//gi|34365745|gb|AAQ65184.1|//2.00E-25/At2g15560 [Arabidopsis thaliana]	Unigene49843_All//2.00E-26//AT2G15560| INVOLVED IN: response to oxidative stress; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF537 (InterPro:IPR007491); BEST Arabidopsis thaliana protein match is: EDA32 (embryo sac development arrest 32) (TAIR:AT3G22210.1); Has 184 Blast hits to 179 proteins in 38 species: Archae - 0; Bacteria - 4; Metazoa - 60; Fungi - 26; Plants - 90; Viruses - 0; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene49843_All//2.00E-13//TC133978				nr -
Unigene49846_All	1010	2.43	2.41	0.47	4.93	3.99	3.53	6.24	2.69	2.52	-1.58E-02	9.86E-01		-2.36E+00	1.94E-06	Down	-3.06E-01	2.88E-01		-4.82E-01	8.02E-02		-1.21E+00	2.44E-08	Down	-1.31E+00	1.45E-09	Down	Unigene49846_All//gi|42567943|ref|NP_197371.2|//4.00E-83//EMB3013 (embryo defective 3013); ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Unigene49846_All//2.00E-84//AT5G18700| EMB3013 (embryo defective 3013); ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene49846_All//2.00E-91//gi|73851221|gb|DT460241.1|DT460241				nr -
Unigene49849_All	969	1.84	0.52	1.32	3.39	2.52	2.75	3.10	0.82	1.52	-1.81E+00	6.58E-04	Down	-4.77E-01	3.67E-01		-4.27E-01	2.22E-01		-3.03E-01	4.20E-01		-1.92E+00	8.65E-08	Down	-1.03E+00	1.07E-03		Unigene49849_All//gi|46360445|gb|ASB0153.1|//1.00E-144//ACT11D09.9 [Cucumis melo]	Unigene49849_All//4.00E-144//AT2G01730| ATCPSF73-II (cleavage and polyadenylation specificity factor 73 kDa subunit-II); catalytic/ protein binding					nr -
Unigene4985_All	896	4.73	4.47	5.47	4.67	4.69	3.83	4.77	3.03	2.31	-8.23E-02	7.76E-01		2.09E-01	4.86E-01		5.70E-03	9.94E-01		-2.86E-01	3.98E-01		-6.53E-01	1.28E-02		-1.04E+00	5.27E-05	Down	Unigene4985_All//gi|15229447|ref|NP_188986.1|//4.00E-18//EDA6 (EMBRYO SAC DEVELOPMENT ARREST 6) [Arabidopsis thaliana]	Unigene4985_All//3.00E-20//AT5G44060| unknown protein	Unigene4985_All//0.00E+00//gi|48789425|gb|CO090739.1|CO090739				nr -
Unigene49855_All	487	21.59	37.56	35.21	33.55	38.75	51.47	72.58	218.08	66.51	7.99E-01	1.12E-09		7.05E-01	3.57E-07		2.08E-01	1.28E-01		6.17E-01	5.60E-09		1.59E+00	7.68E-192	Up	-1.26E-01	1.45E-01		Unigene49855_All//gi|86371808|gb|ABB89042.1|//6.00E-76//glutathione reductase [Vigna unguiculata]	Unigene49855_All//2.00E-71//AT3G24170| ATGR1 (glutathione-disulfide reductase); FAD binding / NADP or NADPH binding / glutathione-disulfide reductase/ oxidoreductase	Unigene49855_All//0.00E+00//gi|48818802|gb|CO120115.1|CO120115		ko00480|Glutathione metabolism		nr -
Unigene49857_All	483	27.95	74.59	42.78	31.04	42.06	36.47	42.46	90.86	91.39	1.42E+00	2.97E-45	Up	6.14E-01	8.33E-07		4.38E-01	1.44E-04		2.32E-01	1.04E-01		1.10E+00	1.79E-45	Up	1.11E+00	2.41E-47	Up	Unigene49857_All//gi|5702015|emb|CAB52141.1|//8.00E-14//GAL83 protein [Solanum tuberosum]	Unigene49857_All//2.00E-11//AT5G21170| 5'-AMP-activated protein kinase beta-2 subunit, putative	Unigene49857_All//8.00E-145//TC146790				nr -
Unigene49859_All	678	6.87	8.52	12.72	19.98	25.50	20.38	6.42	3.58	2.12	3.11E-01	2.29E-01		8.90E-01	1.45E-05		3.51E-01	7.13E-03		2.85E-02	8.88E-01		-8.45E-01	1.09E-03		-1.60E+00	4.89E-09	Down	Unigene49859_All//gi|115488582|ref|NP_001066778.1|//3.00E-53//Os12g0484700 [Oryza sativa Japonica Group] >gi|113649285|dbj|BAF29797.1|Os12g0484700 [Oryza sativa Japonica Group]	Unigene49859_All//2.00E-48//AT4G27745| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Yippee-like protein (InterPro:IPR004910); BEST Arabidopsis thaliana protein match is: yippee family protein (TAIR:AT5G53940.1); Has 697 Blast hits to 697 proteins in 149 species: Archae - 0; Bacteria - 0; Metazoa - 401; Fungi - 132; Plants - 110; Viruses - 0; Other Eukaryotes - 54 (source: NCBI BLink).	Unigene49859_All//0.00E+00//TC150857				nr -
Unigene4986_All	1086	3.95	1.07	3.38	3.99	3.65	3.12	2.30	1.35	0.88	-1.88E+00	1.02E-08	Down	-2.24E-01	4.89E-01		-1.30E-01	6.96E-01		-3.56E-01	2.56E-01		-7.70E-01	3.19E-02		-1.38E+00	1.26E-04	Down	Unigene4986_All//gi|229609815|gb|ACQ83523.1|//1.00E-143//CBL-interacting protein kinase 07 [Vitis vinifera]	Unigene4986_All//1.00E-121//AT5G58380| SIP1 (SOS3-INTERACTING PROTEIN 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene4986_All//0.00E+00//gi|5047351|gb|AI728499.1|AI728499		ko04140|Regulation of autophagy		nr +
Unigene49860_All	502	63.37	75.70	63.54	63.31	57.00	87.18	60.64	26.06	20.24	2.57E-01	3.84E-03		3.90E-03	9.95E-01		-1.51E-01	1.46E-01		4.62E-01	3.06E-09		-1.22E+00	1.81E-37	Down	-1.58E+00	4.72E-57	Down	Unigene49860_All//gi|2497538|sp|Q42806.1|KPYC_SOYBN//3.00E-20//RecName: Full=Pyruvate kinase, cytosolic isozyme; Short=PK >gi|466350|gb|AAA17000.1| pyruvate kinase [Glycine max]	Unigene49860_All//1.00E-19//AT5G08570| pyruvate kinase, putative	Unigene49860_All//0.00E+00//gi|164273528|gb|ES825931.1|ES825931		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene49861_All	642	4.07	0.95	2.32	5.97	5.26	2.60	3.82	2.21	1.12	-2.11E+00	2.26E-06	Down	-8.11E-01	4.75E-02		-1.85E-01	5.94E-01		-1.20E+00	1.27E-04	Down	-7.87E-01	2.99E-02		-1.77E+00	3.66E-06	Down	Unigene49861_All//gi|15238313|ref|NP_201300.1|//2.00E-07//mitochondrial transcription termination factor-related / mTERF-related [Arabidopsis thaliana]	Unigene49861_All//1.00E-08//AT5G64950| mitochondrial transcription termination factor-related / mTERF-related					nr +
Unigene49863_All	591	3.01	4.54	4.32	5.39	4.66	4.05	11.80	11.10	5.66	5.94E-01	1.24E-01		5.23E-01	2.16E-01		-2.11E-01	5.86E-01		-4.14E-01	2.65E-01		-8.83E-02	6.95E-01		-1.06E+00	8.60E-08	Down	Unigene49863_All//gi|12229923|sp|Q9M4T8.1|PSA5_SOYBN//9.00E-09//RecName: Full=Proteasome subunit alpha type-5; AltName: Full=20S proteasome alpha subunit E; AltName: Full=20S proteasome subunit alpha-5 >gi|7839485|gb|AAF70292.1|AF255338_1 20S proteasome subunit [Glycine max]	Unigene49863_All//3.00E-09//AT3G14290| PAE2; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene49863_All//3.00E-135//TC166116		ko03050|Proteasome		nr -
Unigene49867_All	311	37.68	57.02	16.95	59.26	51.38	11.62	21.75	13.98	8.97	5.98E-01	5.50E-06		-1.15E+00	8.69E-11	Down	-2.06E-01	1.32E-01		-2.35E+00	1.43E-50	Down	-6.38E-01	1.49E-03		-1.28E+00	6.47E-10	Down	Unigene49867_All//gi|124360549|gb|ABD33126.2|//4.00E-06//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene49867_All//2.00E-33//TC152025				nr +
Unigene49869_All	681	3.07	0.97	1.41	2.85	2.07	3.58	4.97	1.84	3.80	-1.67E+00	4.57E-04	Down	-1.13E+00	1.70E-02		-4.61E-01	3.22E-01		3.28E-01	4.76E-01		-1.43E+00	5.24E-06	Down	-3.85E-01	1.99E-01		Unigene49869_All//gi|15594035|emb|CAC69852.1|//4.00E-68//nucleic acid binding protein [Nicotiana tabacum]	Unigene49869_All//3.00E-42//AT1G47500| ATRBP47C (RNA-binding protein 47C"); RNA binding	Unigene49869_All//1.00E-119//gi|164314234|gb|ES837297.1|ES837297		ko03040|Spliceosome		nr -
Unigene4987_All	568	4.88	4.01	9.56	7.45	8.18	7.47	14.89	8.24	7.43	-2.82E-01	4.64E-01		9.70E-01	2.98E-04		1.35E-01	6.90E-01		3.80E-03	9.92E-01		-8.53E-01	1.76E-06		-1.00E+00	1.61E-08	Down	Unigene4987_All//gi|3355479|gb|AAC27841.1|//2.00E-13//expressed protein [Arabidopsis thaliana] >gi|14335016|gb|AAK59772.1|At2g39500/F12L6.16 [Arabidopsis thaliana]	Unigene4987_All//1.00E-16//AT2G39500| unknown protein	Unigene4987_All//0.00E+00//gi|21103257|gb|BQ415570.1|BQ415570				nr -
Unigene49876_All	614	9.29	3.22	3.99	5.52	2.75	2.35	3.24	1.02	0.84	-1.53E+00	1.12E-08	Down	-1.22E+00	4.76E-06	Down	-1.01E+00	1.38E-03		-1.23E+00	2.65E-04	Down	-1.66E+00	1.36E-04	Down	-1.94E+00	1.06E-05	Down			Unigene49876_All//4.00E-30//DW490632				
Unigene49878_All	555	20.65	8.13	10.55	18.40	19.36	11.72	70.39	36.00	57.50	-1.35E+00	6.81E-14	Down	-9.68E-01	4.08E-08		7.33E-02	7.55E-01		-6.51E-01	1.96E-04		-9.68E-01	3.61E-33		-2.92E-01	1.00E-04		Unigene49878_All//gi|15235668|ref|NP_193070.1|//3.00E-07//leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] >gi|75337952|sp|Q9T0K5.1|LRX3_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 3; Short=LRR/EXTENSIN3; Short=AtLRX3; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|4584539|emb|CAB40769.1|extensin-like protein [Arabidopsis thaliana] >gi|7268037|emb|CAB78376.1|extensin-like protein [Arabidopsis thaliana]		Unigene49878_All//2.00E-112//TC162845				nr +
Unigene4988_All	1140	0.87	3.20	1.21	1.01	1.33	2.50	2.00	2.27	3.18	1.88E+00	1.89E-07	Up	4.78E-01	4.06E-01		4.03E-01	5.14E-01		1.31E+00	5.61E-04	Up	1.83E-01	6.33E-01		6.67E-01	1.67E-02		Unigene4988_All//gi|15223566|ref|NP_173381.1|//1.00E-27//bZIP transcription factor family protein [Arabidopsis thaliana]	Unigene4988_All//5.00E-18//AT1G19490| bZIP transcription factor family protein		bZIP			nr +
Unigene49881_All	362	18.36	50.67	42.22	16.24	22.35	22.96	13.08	26.67	23.77	1.46E+00	1.49E-24	Up	1.20E+00	8.03E-15	Up	4.61E-01	2.18E-02		5.00E-01	1.35E-02		1.03E+00	1.23E-09	Up	8.62E-01	7.04E-07		Unigene49881_All//gi|30689144|ref|NP_194903.2|//6.00E-20//WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|75303285|sp|Q8RXY3.1|P2C59_ARATH RecName: Full=Probable protein phosphatase 2C 59; Short=AtPP2C59; AltName: Full=Protein phosphatase 2C WIN2; Short=PP2C WIN2; AltName: Full=HopW1-1-interacting protein 2	Unigene49881_All//2.00E-21//AT4G31750| WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase	Unigene49881_All//4.00E-47//TC143840				nr -
Unigene49882_All	628	3.42	4.52	5.51	9.12	7.35	5.90	5.12	2.20	0.89	4.04E-01	2.91E-01		6.90E-01	4.65E-02		-3.12E-01	2.29E-01		-6.29E-01	1.07E-02		-1.22E+00	1.13E-04	Down	-2.53E+00	9.47E-12	Down	Unigene49882_All//gi|124360022|gb|ABN08038.1|//4.00E-19//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene49882_All//4.00E-27//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene49882_All//2.00E-29//ES829634				nr -
Unigene49884_All	425	3.45	8.23	3.38	5.16	2.92	3.29	17.61	16.42	24.56	1.25E+00	2.28E-04	Up	-2.71E-02	9.82E-01		-8.22E-01	4.62E-02		-6.47E-01	1.44E-01		-1.01E-01	6.32E-01		4.80E-01	1.80E-03				Unigene49884_All//6.00E-25//TC138711				
Unigene49888_All	641	8.00	5.85	5.48	9.56	11.44	9.93	9.43	5.67	4.35	-4.52E-01	9.17E-02		-5.45E-01	4.98E-02		2.60E-01	2.79E-01		5.56E-02	8.42E-01		-7.34E-01	6.09E-04		-1.12E+00	2.14E-07	Down	Unigene49888_All//gi|169730526|gb|ACA64829.1|//1.00E-37//SKIP interacting protein 9 [Oryza sativa]	Unigene49888_All//2.00E-61//AT1G50710| unknown protein	Unigene49888_All//0.00E+00//gi|73864261|gb|DT467000.1|DT467000				nr +
Unigene49889_All	377	1.94	4.17	1.70	5.29	4.02	4.07	1.35	5.10	1.48	1.10E+00	3.95E-02		-1.97E-01	7.99E-01		-3.95E-01	4.08E-01		-3.76E-01	4.53E-01		1.92E+00	3.00E-05	Up	1.37E-01	8.76E-01		Unigene49889_All//gi|226531382|ref|NP_001149303.1|//6.00E-35//LOC100282926 [Zea mays] >gi|195626202|gb|ACG34931.1|PP1/PP2A phosphatases pleiotropic regulator PRL1 [Zea mays]	Unigene49889_All//2.00E-34//AT4G15900| PRL1 (PLEIOTROPIC REGULATORY LOCUS 1); basal transcription repressor/ nucleotide binding / protein binding	Unigene49889_All//1.00E-152//TC172989		ko03040|Spliceosome		nr -
Unigene49890_All	983	7.98	5.00	6.61	2.43	4.24	17.64	30.37	15.05	90.21	-6.75E-01	1.11E-03		-2.73E-01	2.33E-01		8.01E-01	5.54E-03		2.86E+00	1.04E-57	Up	-1.01E+00	1.81E-27	Down	1.57E+00	3.96E-161	Up	Unigene49890_All//gi|16416376|dbj|BAB21610.2|//4.00E-89//manngrin [Bruguiera sexangula]	Unigene49890_All//5.00E-64//AT1G13280| AOC4 (ALLENE OXIDE CYCLASE 4); allene-oxide cyclase	Unigene49890_All//0.00E+00//DW500651		ko00592|alpha-Linolenic acid metabolism		nr -

Unigene49893_All	466	25.82	90.03	33.94	23.30	58.30	55.34	52.08	125.21	222.36	1.80E+00	3.15E-74	Up	3.94E-01	7.43E-03		1.32E+00	3.00E-36	Up	1.25E+00	8.83E-29	Up	1.27E+00	2.75E-75	Up	2.09E+00	7.77E-279	Up	Unigene49893_All//gi|62286587|sp|O64894.1|ACOX2_CUCMA//9.00E-31//RecName: Full=Acyl-coenzyme A oxidase, peroxisomal; Short=AOX; AltName: Full=Long-chain acyl-CoA oxidase; Flags: Precursor >gi|7431668|pir|T07901 acyl CoA oxidase homolog - cucurbit >gi|3115374|gb|AAC15870.1| acyl CoA oxidase homolog [Cucurbita cv. Kurokawa Amakuri]	Unigene49893_All//2.00E-27//AT5G65110| ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase	Unigene49893_All//0.00E+00//TC141139		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene49897_All	572	5.49	1.77	2.89	3.57	3.97	4.26	3.33	1.32	2.72	-1.63E+00	1.49E-05	Down	-9.27E-01	1.19E-02		1.54E-01	7.80E-01		2.56E-01	5.92E-01		-1.34E+00	1.94E-03		-2.92E-01	4.94E-01		Unigene49897_All//gi|30697337|ref|NP_849849.1|//6.00E-16//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|122215314|sp|Q3ECH5.1|PP107_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g66345, mitochondrial; Flags: Precursor	Unigene49897_All//4.00E-10//AT1G66345| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene49898_All	798	1.18	8.38	4.67	0.75	1.29	1.81	6.36	11.16	7.99	2.83E+00	6.18E-21	Up	1.98E+00	8.59E-08	Up	7.89E-01	2.74E-01		1.27E+00	2.66E-02		8.11E-01	2.78E-06		3.29E-01	1.15E-01									
Unigene4990_All	1226	1.02	3.72	0.35	24.46	25.39	21.70	0.28	0.31	0.10	1.86E+00	4.88E-09	Up	-1.56E+00	1.90E-02		5.39E-02	6.59E-01		-1.73E-01	1.12E-01		1.53E-01	8.90E-01		-1.50E+00	2.10E-01		Unigene4990_All//gi|300669658|sp|A7QEU4.2|PER5_VITVI//5.00E-95//RecName: Full=Peroxidase 5; Flags: Precursor	Unigene4990_All//4.00E-71//AT4G11290| peroxidase, putative	Unigene4990_All//0.00E+00//C0073281		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene49901_All	611	1.11	2.49	1.05	1.71	3.38	2.22	1.73	13.75	12.84	1.16E+00	3.43E-02		-9.01E-02	9.22E-01		9.82E-01	2.82E-02		3.73E-01	5.63E-01		2.99E+00	6.08E-34	Up	2.89E+00	2.55E-31	Up								
Unigene49903_All	715	1.61	0.64	0.15	1.67	1.40	2.40	1.77	1.05	1.78	-1.34E+00	4.03E-02		-3.43E+00	1.54E-04	Down	-2.60E-01	6.78E-01		5.22E-01	3.34E-01		-7.54E-01	1.63E-01		7.30E-03	9.89E-01		Unigene49903_All//gi|15226737|ref|NP_181604.1|//4.00E-76//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75276036|sp|Q7XJN6.1|PP197_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g40720	Unigene49903_All//2.00E-77//AT2G40720| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene49904_All	747	1.89	7.53	4.70	5.47	6.50	5.68	2.43	2.69	2.77	1.99E+00	5.87E-12	Up	1.31E+00	1.99E-04	Up	2.49E-01	4.22E-01		5.56E-02	8.78E-01		1.42E-01	7.34E-01		1.88E-01	6.28E-01			Unigene49904_All//2.00E-14//PL577654					
Unigene49906_All	529	40.85	87.55	51.34	60.46	61.32	67.70	144.90	124.04	80.43	1.10E+00	2.91E-39	Up	3.30E-01	2.58E-03		2.05E-02	8.64E-01		1.63E-01	9.73E-02		-2.24E-01	3.04E-05		-8.49E-01	3.10E-53		Unigene49906_All//gi|211906448|gb|ACJ11717.1|//2.00E-32//alpha-soluble NSF attachment protein [Gossypium hirsutum]	Unigene49906_All//6.00E-20//AT3G56190| ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN 2); binding / soluble NSF attachment protein	Unigene49906_All//0.00E+00//gi|13354672|gb|BG445020.1|BG445020				nr -
Unigene49908_All	956	0.77	11.50	1.45	4.48	3.13	4.20	0.00	0.04	1.17	3.91E+00	1.98E-45	Up	9.19E-01	1.27E-01		-5.16E-01	7.23E-02		-9.20E-02	7.69E-01		5.45E+00	6.34E-01		1.02E+01	4.36E-08	Up	Unigene49908_All//gi|9802540|gb|AAF99712.1|AC004557_21//5.00E-68//F17L21.26 [Arabidopsis thaliana]	Unigene49908_All//3.00E-44//AT1G27461| unknown protein					nr +
Unigene4991_All	1267	0.33	0.64	1.09	14.55	23.18	30.01	105.78	60.10	79.71	9.54E-01	2.26E-01		1.73E+00	6.71E-03		6.72E-01	4.41E-13		1.04E+00	6.47E-32	Up	-8.16E-01	5.72E-84		-4.08E-01	1.59E-25		Unigene4991_All//gi|297823747|ref|XP_002839756.1|//1.00E-86//acid phosphatase class B family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325595|gb|EFH56015.1| acid phosphatase class B family protein [Arabidopsis lyrata subsp. lyrata]	Unigene4991_All//2.00E-87//AT2G38600| acid phosphatase class B family protein	Unigene4991_All//4.00E-81//gi|109828205|gb|DW226833.1|DW226833		ko03010|Ribosome		nr +
Unigene49910_All	635	4.37	3.11	1.51	4.00	4.72	5.12	3.20	4.15	2.26	-4.89E-01	2.02E-01		-1.53E+00	2.23E-04	Down	2.38E-01	5.71E-01		3.56E-01	3.49E-01		3.76E-01	3.10E-01		-5.01E-01	2.03E-01		Unigene49910_All//gi|224143705|ref|XP_002325046.1|//8.00E-21//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222866480|gb|EEF03611.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene49910_All//4.00E-05//AT5G57390| AIL5 (AINTEGUMENTA-LIKE 5); DNA binding / transcription factor	Unigene49910_All//0.00E+00//TC165722	AP2-EREBP			nr -
Unigene49913_All	656	29.67	8.50	11.93	29.16	30.50	38.07	71.67	30.52	30.06	-1.80E+00	4.74E-35	Down	-1.31E+00	2.22E-21	Down	6.48E-02	6.79E-01		3.85E-01	3.52E-04		-1.23E+00	2.07E-58	Down	-1.25E+00	9.23E-62	Down	Unigene49913_All//gi|15223001|ref|NP_172256.1|//2.00E-68//RPS15A (ribosomal protein s15a); structural constituent of ribosome [Arabidopsis thaliana] >gi|15238544|ref|NP_200793.1| 40S ribosomal protein S15A (RPS15aF) [Arabidopsis thaliana] >gi|42571385|ref|NP_973783.1| RPS15A (ribosomal protein s15a); structural constituent of ribosome [Arabidopsis thaliana] >gi|297796939|ref|XP_002866354.1| RPS15A [Arabidopsis lyrata subsp. lyrata] >gi|297815756|ref|XP_002875761.1| RPS15A [Arabidopsis lyrata subsp. lyrata] >gi|297849076|ref|XP_002892419.1| RPS15A [Arabidopsis lyrata subsp. lyrata] >gi|1173218|sp|P42798.2|R15A1_ARATH RecName: Full=40S ribosomal protein S15a-1 >gi|8439890|gb|AAF75076.1|AC007583_12 Strong similarity to 40S ribosomal protein S15A from Arabidopsis thaliana gb|L27461. EST gb|H30315 comes from this gene >gi|14423370|gb|AAK62367.1|AF38692	Unigene49913_All//1.00E-69//AT5G59850| 40S ribosomal protein S15A (RPS15aF)	Unigene49913_All//0.00E+00//TC170746		ko03010|Ribosome		nr +
Unigene49916_All	637	2.22	6.92	3.68	13.22	12.16	10.64	10.69	5.58	4.69	1.64E+00	1.71E-07	Up	7.30E-01	9.36E-02		-1.20E-01	6.12E-01		-3.14E-01	1.39E-01		-9.38E-01	3.63E-06		-1.19E+00	5.55E-09	Down	Unigene49916_All//gi|297827985|ref|XP_002881875.1|//3.00E-62//abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327714|gb|EFH58134.1| abscisic acid-responsive HVA22 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49916_All//2.00E-58//AT2G42820| HVA22F (HVA22-LIKE PROTEIN F)	Unigene49916_All//1.00E-147//DN759655				nr -
Unigene49918_All	382	39.04	17.11	20.21	58.81	52.91	63.25	59.10	29.21	30.04	-1.19E+00	7.12E-15	Down	-9.50E-01	4.73E-10		-1.52E-01	2.34E-01		1.05E-01	4.41E-01		-1.02E+00	4.13E-21	Down	-9.77E-01	2.06E-20		Unigene49918_All//gi|297609887|ref|NP_001063818.2|//1.00E-27//Os09g0542000 (Oryza sativa Japonica Group) >gi|255679102|dbj|BAF25732.2| Os09g0542000 (Oryza sativa Japonica Group)	Unigene49918_All//1.00E-26//AT1G76010| nucleic acid binding	Unigene49918_All//0.00E+00//TC174580				nr +
Unigene49920_All	410	2.94	0.49	2.08	1.22	1.01	0.22	1.86	1.02	1.55	-2.57E+00	5.35E-04	Down	-4.98E-01	4.26E-01		-2.70E-01	8.02E-01		-2.46E+00	4.82E-02		-8.65E-01	2.39E-01		-2.56E-01	6.97E-01		Unigene49920_All//gi|297797884|ref|XP_002866826.1|//2.00E-37//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312662|gb|EFH43085.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene49920_All//2.00E-26//AT4G38960| zinc finger (B-box type) family protein	Unigene49920_All//1.00E-75//DV848774	DBB	ko04712|Circadian rhythm - plant		nr +
Unigene49922_All	500	32.02	21.99	19.49	51.71	49.72	51.03	79.49	51.99	37.85	-5.42E-01	9.36E-05		-7.16E-01	6.71E-07		-5.64E-02	6.73E-01		-1.89E-02	9.00E-01		-6.12E-01	9.73E-16		-1.07E+00	7.39E-41	Down	Unigene49922_All//gi|297801354|ref|XP_002868561.1|//3.00E-82//AT5g42080/MJC20_19 [Arabidopsis lyrata subsp. lyrata] >gi|297314397|gb|EFH44820.1| AT5g42080/MJC20_19 [Arabidopsis lyrata subsp. lyrata]	Unigene49922_All//1.00E-82//AT5G42080| ADL1 (ARABIDOPSIS DYNAMIN-LIKE PROTEIN); GTP binding / GTPase/ protein binding	Unigene49922_All//0.00E+00//gi|5050451|gb|AI731599.1|AI731599		ko04144|Endocytosis		nr -
Unigene49924_All	1074	0.29	0.75	0.00	2.27	1.67	1.43	4.29	2.22	1.34	1.37E+00	9.21E-02		-8.19E+00	4.90E-02		-4.47E-01	2.87E-01		-6.69E-01	1.07E-01		-9.52E-01	1.59E-04		-1.68E+00	3.77E-10	Down	Unigene49924_All//gi|27764978|gb|AAO23610.1|//8.00E-08//At5g44005 [Arabidopsis thaliana]	Unigene49924_All//4.00E-09//AT5G44005| unknown protein	Unigene49924_All//0.00E+00//PL577746				nr -
Unigene49925_All	611	1.03	6.22	2.53	4.57	7.21	5.99	3.04	7.52	42.77	2.60E+00	3.73E-11	Up	1.30E+00	2.33E-02		6.60E-01	1.97E-02		3.91E-01	2.59E-01		1.31E+00	6.04E-07	Up	3.81E+00	8.19E-132	Up			Unigene49925_All//0.00E+00//gi|109887640|gb|DW516609.1|DW516609				
Unigene49927_All	421	5.84	21.30	7.84	40.70	14.40	16.52	96.31	23.33	59.52	1.87E+00	3.64E-17	Up	4.25E-01	2.44E-01		-1.50E+00	2.20E-29	Down	-1.30E+00	7.34E-21	Down	-2.05E+00	1.87E-104	Down	-6.94E-01	2.01E-20				Unigene49927_All//2.00E-145//gi|21093505|gb|BQ405818.1|BQ405818				
Unigene49928_All	888	2.59	5.25	2.88	3.59	3.06	3.81	78.28	118.56	50.34	1.02E+00	3.27E-04	Up	1.51E-01	7.03E-01		-2.29E-01	5.44E-01		8.74E-02	8.12E-01		5.99E-01	9.19E-39		-6.37E-01	1.27E-29		Unigene49928_All//gi|224078860|ref|XP_002305657.1|//1.00E-121//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222848621|gb|EEE86168.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene49928_All//3.00E-117//AT1G30410| ATMRP13; ATPase, coupled to transmembrane movement of substances	Unigene49928_All//3.00E-28//CO496671		ko02010|ABC transporters		nr -
Unigene49929_All	383	47.68	26.72	26.28	36.68	32.82	22.76	61.82	37.76	26.32	-8.35E-01	2.11E-10		-8.59E-01	2.18E-10		-1.61E-01	3.39E-01		-6.89E-01	2.27E-06		-7.11E-01	2.08E-12		-1.23E+00	1.00E-30	Down	Unigene49929_All//gi|4098246|gb|AAB00253.1|//4.00E-61//homeobox 2 protein [Solanum lycopersicum]	Unigene49929_All//6.00E-62//AT1G62990| KNAT7 (KNOTTED-LIKE HOMEOBOX OF ARABIDOPSIS THALIANA 7); DNA binding / transcription activator/ transcription factor	Unigene49929_All//0.00E+00//gi|54116833|gb|CO492342.1|CO492342	HB			nr +
Unigene4993_All	939	6.63	10.09	17.13	55.17	33.78	53.72	5.90	3.38	1.78	6.06E-01	1.17E-03		1.37E+00	6.31E-19	Up	-7.08E-01	1.11E-25		-3.84E-02	6.96E-01		-8.02E-01	3.72E-04		-1.73E+00	1.98E-12	Down	Unigene4993_All//gi|88900424|gb|ABD57524.1|//9.00E-28//At3g48550 [Arabidopsis thaliana]	Unigene4993_All//5.00E-29//AT3G48550| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 12 growth stages; BEST Arabidopsis thaliana protein match is: nucleic acid binding / transcription factor/ zinc ion binding (TAIR:AT2G01940.3); Has 40 Blast hits to 40 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene4993_All//2.00E-14//gi|109873257|gb|DW502232.1|DW502232				nr +
Unigene49931_All	837	1.44	1.70	0.25	4.29	3.79	2.86	11.01	4.74	7.09	2.38E-01	6.50E-01		-2.50E+00	1.15E-03		-1.79E-01	6.03E-01		-5.83E-01	7.68E-02		-1.22E+00	7.44E-12	Down	-6.35E-01	1.10E-04		Unigene49931_All//gi|166203228|gb|ABB84654.1|//3.00E-24//transcription factor [Glycine max]	Unigene49931_All//2.00E-22//AT4G31550| WRKY11; calmodulin binding / transcription factor	Unigene49931_All//0.00E+00//gi|78338953|gb|DT559227.1|DT559227	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene49932_All	1345	0.54	2.03	1.43	3.85	2.79	3.09	0.85	0.50	0.62	1.90E+00	7.24E-06	Up	1.39E+00	6.13E-03		-4.65E-01	7.27E-02		-3.18E-01	2.66E-01		-7.71E-01	1.81E-01		-4.48E-01	4.15E-01		Unigene49932_All//gi|53370641|gb|AB39136.1|//2.00E-14//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene49932_All//8.00E-10//AT3G09510| nucleic acid binding	Unigene49932_All//0.00E+00//TC157852				nr -

Unigene49933_All	571	5.50	12.60	8.11	5.67	4.22	3.80	14.88	11.93	12.14	1.20E+00	1.32E-07	Up	5.62E-01	5.67E-02		-4.26E-01	2.27E-01		-5.79E-01	1.01E-01		-3.19E-01	8.54E-02		-2.94E-01	1.00E-01		Unigene49933_All//gi|145334237|ref|NP_001078499.1|//3.00E-14//ATGB2 (GTP-BINDING 2); GTP binding [Arabidopsis thaliana]	Unigene49933_All//2.00E-15//AT4G35860| ATGB2 (GTP-BINDING 2); GTP binding	Unigene49933_All//0.00E+00//TC131641				nr +
Unigene49936_All	392	170.98	178.64	206.34	60.74	57.10	50.92	57.60	26.23	29.37	6.32E-02	3.87E-01		2.71E-01	5.79E-06		-8.92E-02	5.27E-01		-2.54E-01	2.87E-02		-1.13E+00	4.39E-25	Down	-9.72E-01	3.03E-20		Unigene49936_All//gi|56784144|dbj|BAD81529.1|//3.00E-68//P protein-like [Oryza sativa Japonica Group] >gi|56785304|dbj|BAD82264.1| P protein-like [Oryza sativa Japonica Group]	Unigene49936_All//3.00E-68//AT4G33010| AtGLDP1 (Arabidopsis thaliana glycine decarboxylase P-protein 1); catalytic/ glycine dehydrogenase (decarboxylating)/ pyridoxal phosphate binding	Unigene49936_All//0.00E+00//gi|164330233|gb|ES825034.1|ES825034	ko00260|Glycine, serine and threonine metabolism		nr -
Unigene49937_All	271	113.14	50.30	73.10	29.41	31.00	30.33	19.35	11.88	13.82	-1.17E+00	5.32E-29	Down	-6.30E-01	3.52E-10		7.61E-02	7.85E-01		4.45E-02	8.62E-01		-7.04E-01	2.43E-03		-4.85E-01	3.22E-02		Unigene49937_All//gi|297799522|ref|XP_002867645.1|//1.00E-35//RNA-binding protein cp31 [Arabidopsis lyrata subsp. lyrata] >gi|297313481|gb|EFH43904.1| RNA-binding protein cp31 [Arabidopsis lyrata subsp. lyrata]	Unigene49937_All//2.00E-36//AT4G24770| RBP31 (31-KDA RNA BINDING PROTEIN); RNA binding / poly(U) binding	Unigene49937_All//2.00E-138//TC151038	ko03040|Spliceosome		nr +
Unigene49938_All	1056	0.00	0.00	0.00	2.45	1.70	1.45	1.76	1.58	0.49	null	null		null	null		-5.33E-01	1.69E-01		-7.54E-01	5.64E-02		-1.54E-01	7.27E-01		-1.84E+00	4.29E-05	Down	Unigene49938_All//gi|148927336|gb|ABR19817.1|//5.00E-87//terminal ear1-like 1 protein [Populus tremula x Populus alba]	Unigene49938_All//4.00E-65//AT3G26120| TEL1 (TERMINAL EAR1-LIKE 1); RNA binding / nucleic acid binding / nucleotide binding	Unigene49938_All//2.00E-165//ES842215			nr -
Unigene49939_All	618	5.08	21.97	4.83	6.61	6.02	5.92	2.12	4.73	1.55	2.11E+00	4.88E-30	Up	-7.42E-02	8.38E-01		-1.35E-01	6.93E-01		-1.59E-01	6.37E-01		1.16E+00	4.82E-04	Up	-4.55E-01	3.76E-01		Unigene49939_All//gi|14625425|dbj|BAB61919.1|//6.00E-60//calmodulin NtCaM13 [Nicotiana tabacum]	Unigene49939_All//3.00E-53//AT3G22930| calmodulin, putative	Unigene49939_All//2.00E-99//gi|109835793|gb|DW234356.1|DW234356	ko04626|Plant-pathogen interaction		nr -
Unigene4994_All	1072	6.59	4.92	4.57	6.27	7.29	5.77	2.84	1.05	1.08	-4.23E-01	5.89E-02		-5.28E-01	2.27E-02		2.17E-01	3.54E-01		-1.20E-01	6.48E-01		-1.43E+00	1.75E-05	Down	-1.40E+00	1.56E-05	Down	Unigene4994_All//gi|46850513|gb|AAT02656.1|//1.00E-111//mitochondrial pyruvate dehydrogenase kinase isoform 2 [Glycine max]	Unigene4994_All//3.00E-106//AT3G06483| PDK (PYRUVATE DEHYDROGENASE KINASE); ATP binding / histidine phosphotransfer kinase/ pyruvate dehydrogenase (acetyl-transferring) kinase	Unigene4994_All//0.00E+00//ES848543			nr +
Unigene49942_All	577	6.35	16.60	9.14	2.59	6.21	7.83	29.60	31.15	25.89	1.39E+00	3.45E-12	Up	5.26E-01	5.52E-02		1.26E+00	8.07E-05	Up	1.60E+00	1.07E-07	Up	7.34E-02	6.32E-01		-1.93E-01	1.21E-01		Unigene49942_All//gi|30102798|gb|AAP21317.1|//7.00E-14//At5g49525 [Arabidopsis thaliana]	Unigene49942_All//4.00E-15//AT5G49525| unknown protein	Unigene49942_All//0.00E+00//DW501643			nr -
Unigene49943_All	500	57.55	61.11	41.96	61.87	55.65	47.96	58.94	32.68	20.72	8.65E-02	4.35E-01		-4.56E-01	1.17E-05		-1.53E-01	1.48E-01		-3.67E-01	1.13E-04		-8.51E-01	1.83E-20		-1.51E+00	1.61E-51	Down	Unigene49943_All//gi|115454931|ref|NP_001051066.1|//6.00E-21//Os03g0712700 [Oryza sativa Japonica Group] >gi|13324798|gb|AAK18846.1|AC08264 5_16 phosphoglucomutase [Oryza sativa Japonica Group] >gi|17981609|gb|AAL51086.1|AF45581 2_1 phosphoglucomutase [Oryza sativa] >gi|113549537|dbj|BAF12980.1| Os03g0712700 [Oryza sativa Japonica Group]	Unigene49943_All//6.00E-22//AT1G23190| phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative	Unigene49943_All//0.00E+00//CO118880	ko00500|Starch and sucrose metabolism//ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene49947_All	683	41.29	32.64	26.12	82.71	73.06	68.17	88.96	58.87	29.46	-3.39E-01	9.69E-04		-6.61E-01	3.50E-10		-1.79E-01	1.06E-02		-2.79E-01	5.24E-05		-5.96E-01	1.64E-22		-1.59E+00	3.28E-114	Down	Unigene49947_All//gi|224060319|ref|XP_002300140.1|//1.00E-74//f-box family protein [Populus trichocarpa] >gi|222847398|gb|EEE84945.1| f-box family protein [Populus trichocarpa]	Unigene49947_All//1.00E-61//AT1G12820| AFB3 (AUXIN SIGNALING F-BOX 3); auxin binding / ubiquitin-protein ligase	Unigene49947_All//0.00E+00//gi|164319949|gb|ES829371.1|ES829371	ko04626|Plant-pathogen interaction		nr -
Unigene49948_All	656	2.95	11.28	3.90	3.19	3.04	5.99	44.54	66.77	51.68	1.93E+00	6.16E-15	Up	4.01E-01	3.53E-01		-6.70E-02	8.77E-01		9.09E-01	3.14E-03		5.84E-01	6.39E-16		2.15E-01	9.78E-03		Unigene49948_All//gi|63334283|gb|AAY40471.1|//6.00E-50//LITAF-domain-containing protein [Pisum sativum]	Unigene49948_All//5.00E-56//AT5G13190| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: LPS-induced tumor necrosis factor alpha factor (InterPro:IPR006629); Has 21 Blast hits to 21 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene49948_All//0.00E+00//DW501890			nr -
Unigene4995_All	1065	3.29	4.23	4.95	4.40	2.17	2.93	1.23	0.78	0.56	3.63E-01	2.16E-01		5.89E-01	3.07E-02		-1.02E+00	8.31E-05	Down	-5.87E-01	3.63E-02		-6.49E-01	2.29E-01		-1.13E+00	2.59E-02		Unigene4995_All//gi|15223961|ref|NP_177270.1|//1.00E-110//MATE efflux family protein [Arabidopsis thaliana]	Unigene4995_All//1.00E-104//AT1G71140| MATE efflux family protein	Unigene4995_All//8.00E-08//CO087942			nr +
Unigene49950_All	561	137.75	16.89	17.56	41.91	25.23	14.65	16.96	3.73	12.14	-3.03E+00	4.52E-256	Down	-2.97E+00	7.65E-243	Down	-7.32E-01	1.35E-12		-1.52E+00	9.57E-36	Down	-2.19E+00	3.30E-27	Down	-4.82E-01	2.84E-03		Unigene49950_All//gi|25992536|gb|AAN77148.1|//2.00E-23//fiber protein Fb7 [Gossypium barbadense]	Unigene49950_All//2.00E-167//gi|11205879|gb|BF274809.1|BF274809				nr +
Unigene49951_All	434	8.68	21.72	17.42	16.07	31.10	25.39	17.44	12.90	13.59	1.32E+00	3.13E-11	Up	1.01E+00	6.42E-06	Up	9.53E-01	6.01E-11		6.60E-01	8.69E-05		-4.34E-01	2.35E-02		-3.60E-01	5.48E-02		Unigene49951_All//gi|115449841|ref|NP_001048565.1|//1.00E-26//Os02g0823000 [Oryza sativa Japonica Group] >gi|113538996|dbj|BAF10479.1| Os02g0823000 [Oryza sativa Japonica Group]	Unigene49951_All//3.00E-24//AT1G01650| aspartic-type endopeptidase/ peptidase	Unigene49951_All//4.00E-100//DW477504			nr +
Unigene49955_All	554	3.40	9.69	3.84	6.29	7.58	8.64	5.42	15.62	14.09	1.51E+00	4.78E-08	Up	1.77E-01	6.88E-01		2.69E-01	4.24E-01		4.57E-01	1.13E-01		1.53E+00	1.82E-15	Up	1.38E+00	1.77E-12	Up	Unigene49955_All//gi|115479571|ref|NP_001063379.1|//2.00E-06//Os09g0458900 [Oryza sativa Japonica Group] >gi|113631612|dbj|BAF25293.1| Os09g0458900 [Oryza sativa Japonica Group]		Unigene49955_All//0.00E+00//gi|109876223|gb|DW505197.1|DW505197			nr +
Unigene49957_All	540	41.86	16.70	26.82	32.84	9.82	13.13	14.56	3.41	8.41	-1.33E+00	4.34E-26	Down	-6.42E-01	6.39E-08		-1.74E+00	8.10E-38	Down	-1.32E+00	4.09E-22	Down	-2.10E+00	1.76E-21	Down	-7.92E-01	1.16E-05		Unigene49957_All//gi|109946527|gb|ABG48442.1|//2.00E-07//At5g05770 [Arabidopsis thaliana]	Unigene49957_All//1.00E-10//AT2G27315| unknown protein	Unigene49957_All//0.00E+00//TC153964			nr -
Unigene49958_All	359	48.53	18.63	19.58	86.59	71.17	56.49	49.46	16.42	30.52	-1.38E+00	1.48E-21	Down	-1.31E+00	4.26E-19	Down	-2.83E-01	2.37E-03		-6.16E-01	4.96E-11		-1.59E+00	7.27E-33	Down	-6.97E-01	1.65E-09		Unigene49958_All//gi|33341115|sp|O02342.1|ADT1_GOSHI//1.00E-28//RecName: Full=ADP,ATP carrier protein 1, mitochondrial; AltName: Full=ADP/ATP translocase 1; AltName: Full=Adenine nucleotide translocator 1; Short=ANT 1; Flags: Precursor >gi|2463664|gb|AAB72047.1| adenine nucleotide translocator 1 [Gossypium hirsutum]	Unigene49958_All//7.00E-23//AT5G13490| AAC2 (ADP/ATP carrier 2); ATP:ADP antiporter/ binding	Unigene49958_All//0.00E+00//EX171528			nr -
Unigene49959_All	410	35.09	31.14	30.00	39.24	40.06	45.27	27.53	16.51	13.31	-1.72E-01	2.86E-01		-2.26E-01	1.68E-01		2.98E-02	8.60E-01		2.06E-01	1.44E-01		-7.38E-01	1.05E-06		-1.05E+00	7.24E-12	Down			Unigene49959_All//2.00E-175//TC158558				
Unigene4996_All	1406	1.90	1.05	1.40	2.52	3.43	0.87	0.72	0.27	0.09	-8.61E-01	2.53E-02		-4.38E-01	2.89E-01		4.47E-01	1.11E-01		-1.54E+00	5.55E-06	Down	-1.43E+00	2.36E-02		-3.09E+00	5.36E-05	Down	Unigene4996_All//gi|38194913|gb|AAR15301.1|//3.00E-62//anthocyanin acyltransferase [Phaseolus vulgaris]	Unigene4996_All//4.00E-40//AT1G03495| transferase/ transferase, transferring acyl groups other than amino-acyl groups	Unigene4996_All//6.00E-37//ES792206	ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene49961_All	357	7.91	23.28	14.02	12.28	14.37	23.40	27.59	37.70	18.30	1.56E+00	1.58E-12	Up	8.25E-01	3.14E-03		2.27E-01	4.50E-01		9.31E-01	2.74E-06		4.50E-01	1.03E-03		-5.92E-01	1.77E-04			Unigene49961_All//3.00E-06//AT1G01650| aspartic-type endopeptidase/ peptidase	Unigene49961_All//3.00E-153//gi|164280151|gb|ES814890.1|ES814890.1				
Unigene49962_All	551	7.41	3.49	4.64	7.41	8.37	13.28	34.38	16.16	9.47	-1.08E+00	3.98E-04	Down	-6.75E-01	3.26E-02		1.76E-01	5.94E-01		8.41E-01	7.99E-05		-1.09E+00	7.10E-20	Down	-1.86E+00	9.50E-45	Down	Unigene49962_All//gi|257219570|gb|ACV50438.1|//5.00E-16//ribosomal protein L37 [Jatropha curcas]	Unigene49962_All//7.00E-14//AT3G16080| 60S ribosomal protein L37 (RPL37C)	Unigene49962_All//0.00E+00//TC166810	ko03010|Ribosome		nr -
Unigene49963_All	668	12.92	12.52	4.62	28.56	27.63	15.89	11.33	8.95	7.40	-4.63E-02	8.22E-01		-1.48E+00	1.19E-11	Down	-4.78E-02	7.83E-01		-8.46E-01	9.51E-12		-3.41E-01	8.39E-02		-6.15E-01	7.68E-04		Unigene49963_All//gi|15231209|ref|NP_190810.1|//2.00E-13//OEP7 (OUTER ENVELOPE MEMBRANE PROTEIN 7) [Arabidopsis thaliana] >gi|4886285|emb|CAB43440.1| outer envelope membrane protein-like protein [Arabidopsis thaliana] >gi|34365615|gb|AAQ65134.1| At3g52420 [Arabidopsis thaliana] >gi|51968692|dbj|BAD43038.1| outer envelope membrane protein-like protein [Arabidopsis thaliana] >gi|51969766|dbj|BAD43575.1| outer envelope membrane protein-like protein [Arabidopsis thaliana]	Unigene49963_All//2.00E-08//AT3G52420| OEP7 (OUTER ENVELOPE MEMBRANE PROTEIN 7)	Unigene49963_All//0.00E+00//gi|109887007|gb|DW515976.1|DW515976		GO:0009707	nr +
Unigene49964_All	683	5.21	3.64	5.07	1.90	3.63	3.17	3.16	3.92	19.48	-5.19E-01	1.16E-01		-3.97E-02	9.17E-01		9.37E-01	1.88E-02		7.43E-01	9.72E-02		3.11E-01	4.02E-01		2.63E+00	1.62E-47	Up			Unigene49964_All//9.00E-121//A1055009				
Unigene49966_All	530	38.60	388.05	86.00	61.00	120.26	88.71	78.18	122.47	300.07	3.33E+00	0.00E+00	Up	1.16E+00	1.40E-40	Up	9.79E-01	9.20E-53		5.40E-01	5.89E-13		6.48E-01	1.06E-27		1.94E+00	0.00E+00	Up	Unigene49966_All//gi|3851670|gb|AAC72399.1|//8.00E-11//J8 [Arabidopsis thaliana]	Unigene49966_All//1.00E-11//AT1G80920| J8; heat shock protein binding / unfolded protein binding	Unigene49966_All//0.00E+00//TC154765		GO:0005515//GO:0044267	nr -
Unigene49967_All	528	34.78	27.35	27.94	47.64	34.24	43.03	47.81	27.78	20.45	-3.47E-01	8.01E-03		-3.16E-01	2.21E-02		-4.77E-01	1.76E-06		-1.47E-01	2.33E-01		-7.83E-01	2.06E-15		-1.23E+00	2.03E-32	Down	Unigene49967_All//gi|110736575|dbj|BAF00253.1|//2.00E-50//arginyl-tRNA synthetase [Arabidopsis thaliana]	Unigene49967_All//1.00E-51//AT4G26300| emb1027 (embryo defective 1027); ATP binding / aminoacyl-tRNA ligase/ arginine-tRNA ligase/ nucleotide binding	Unigene49967_All//0.00E+00//TC154627	ko00970|Aminoacyl-tRNA biosynthesis	GO:0003006//GO:0004812//GO:0006418//GO:0009536//GO:0032559	nr +
Unigene49969_All	540	2.71	6.29	4.83	9.22	9.95	12.55	4.38	3.48	3.47	1.21E+00	4.37E-04	Up	8.33E-01	4.25E-02		1.09E-01	7.45E-01		4.44E-01	5.64E-02		-3.32E-01	4.00E-01		-3.39E-01	3.61E-01				Unigene49969_All//0.00E+00//DR454360				
Unigene49970_All	411	3.44	0.74	1.55	4.12	3.77	3.41	3.29	0.92	2.42	-2.22E+00	5.59E-04	Down	-1.14E+00	5.55E-02		-1.28E-01	8.22E-01		-2.75E-01	6.38E-01		-1.85E+00	9.22E-04	Down	-4.42E-01	3.81E-01				Unigene49970_All//9.00E-169//TC174025				
Unigene49979_All	1288	1.79	0.35	0.87	0.35	1.52	2.49	4.00	0.19	2.41	-2.34E+00	2.32E-06	Down	-1.04E+00	1.91E-02		2.13E+00	2.40E-05	Up	2.84E+00	6.90E-11	Up	-4.36E+00	1.25E-28	Down	-7.31E-01	1.29E-03		Unigene49979_All//gi|297813641|ref|XP_002874704.1|//1.00E-172//NADPH-dependent thioredoxin reductase B [Arabidopsis lyrata subsp. lyrata] >gi|297320541|gb|EFH50963.1| NADPH-dependent thioredoxin reductase B [Arabidopsis lyrata subsp. lyrata]	Unigene49979_All//4.00E-155//AT4G11610| C2 domain-containing protein	Unigene49979_All//0.00E+00//TC140472			nr -
Unigene49981_All	625	23.86	6.89	11.93	49.18	34.99	40.39	72.25	29.96	17.15	-1.79E+00	9.35E-27	Down	-1.00E+00	6.75E-11	Down	-4.91E-01	3.34E-08		-2.84E-01	3.82E-03		-1.27E+00	7.51E-59	Down	-2.08E+00	5.01E-122	Down	Unigene49981_All//gi|163930028|dbj|BAF85902.1|//5.00E-75//protein disulfide isomerase family [Glycine max] >gi|163930094|dbj|BAD42856.2| protein disulfide isomerse like protein [Glycine max]	Unigene49981_All//7.00E-62//AT1G04980| ATPDIL2-2 (PDI-LIKE 2-2); protein disulfide isomerase	Unigene49981_All//0.00E+00//gi|48819794|gb|CO121107.1|CO121107	ko04141|Protein processing in endoplasmic reticulum	GO:0016020//GO:0016862//GO:0019725//GO:0031410//GO:0033554//GO:0043231	nr +
Unigene49982_All	1177	0.13	1.25	0.54	3.60	3.04	1.80	24.10	98.68	4.70	3.23E+00	1.15E-05	Up	2.02E+00	5.58E-02		-2.42E-01	4.52E-01		-9.96E-01	6.48E-04		2.03E+00	3.01E-295	Up	-2.36E+00	3.99E-90	Down	Unigene49982_All//gi|297826949|ref|XP_002881357.1|//1.00E-145//EDA28/MEE23 [Arabidopsis lyrata subsp. lyrata] >gi|297327196|gb|EFH57616.1| EDA28/MEE23 [Arabidopsis lyrata subsp. lyrata]	Unigene49982_All//5.00E-132//AT2G34790| MEE23 (MATERNAL EFFECT EMBRYO ARREST 23); FAD binding / catalytic/ electron carrier/ oxidoreductase	Unigene49982_All//3.00E-32//ES841557			nr -

Unigene49985_All	661	8.71	13.80	16.92	36.78	27.45	28.77	75.22	31.81	44.60	6.64E-01	4.90E-04		9.58E-01	7.83E-08		-4.22E-01	3.97E-05		-3.55E-01	1.25E-03		-1.24E+00	1.60E-62	Down	-7.54E-01	1.46E-28		Unigene49985_All//gi|48675345|dbj|BAD22820.1|//2.00E-83//nitrate transporter [Prunus persica]	Unigene49985_All//2.00E-61//AT1G12110| NRT1.1: nitrate transmembrane transporter/ transporter	Unigene49985_All//0.00E+00//gi|48879654|gb|CO130676.1|CO130676			GO:0005488//GO:0006950//GO:0010035//GO:0015103//GO:0015698//GO:0015833//GO:0031224	nr -
Unigene49986_All	656	1.67	5.56	3.08	7.37	2.94	3.92	45.76	22.68	16.40	1.73E+00	9.26E-07	Up	8.81E-01	6.42E-02		-1.33E+00	3.25E-07	Down	-9.08E-01	7.56E-04		-1.01E+00	1.28E-27	Down	-1.48E+00	4.68E-51	Down	Unigene49986_All//gi|48675345|dbj|BAD22820.1|//3.00E-90//nitrate transporter [Prunus persica]	Unigene49986_All//1.00E-56//AT1G12110| NRT1.1: nitrate transmembrane transporter/ transporter	Unigene49986_All//0.00E+00//gi|48879654|gb|CO130676.1|CO130676			GO:0005488//GO:0006950//GO:0010035//GO:0015103//GO:0015698//GO:0015833//GO:0031224	nr +
Unigene49987_All	887	2.01	11.31	2.10	6.74	9.55	10.13	6.91	15.17	12.94	2.50E+00	3.35E-27	Up	6.73E-02	8.92E-01		5.03E-01	9.35E-03		5.88E-01	2.00E-03		1.13E+00	3.02E-15	Up	9.04E-01	1.49E-09		Unigene49987_All//gi|224079173|ref|XP_002305780.1|//4.00E-56//AP2/EBP domain-containing transcription factor [Populus trichocarpa] |gi|222848744|gb|EEE86291.1| AP2/EBP domain-containing transcription factor [Populus trichocarpa]	Unigene49987_All//2.00E-38//AT1G28360| EBP12 (EBP DOMAIN PROTEIN 12); DNA binding / transcription factor/ transcription repressor	Unigene49987_All//0.00E+00//gi|164271244|gb|ES825877.1|ES825877	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene49988_All	796	0.59	2.86	2.48	1.81	4.20	3.23	6.69	12.34	13.46	2.28E+00	4.37E-06	Up	2.06E+00	1.28E-04	Up	1.21E+00	2.73E-04	Up	8.34E-01	3.73E-02		8.83E-01	8.89E-08		1.01E+00	1.38E-10	Up			Unigene49988_All//9.00E-07//ES810769				
Unigene49992_All	763	31.61	19.86	13.12	35.65	34.71	46.47	66.72	30.13	29.92	-6.71E-01	1.81E-09		-1.27E+00	5.34E-25	Down	-3.86E-02	7.96E-01		3.82E-01	1.41E-05		-1.15E+00	1.69E-56	Down	-1.16E+00	6.17E-59	Down	Unigene49992_All//gi|15230011|ref|NP_187210.1|//4.00E-75//RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome [Arabidopsis thaliana] |gi|21431838|sp|P42791.2|RL182_ARATH RecName: Full=60S ribosomal protein L18-2 |gi|4335090|gb|AAK59824.1|AT3g05590/F18C1_14 [Arabidopsis thaliana] |gi|16974509|gb|AAL31164.1|AT3g05590/F18C1_14 [Arabidopsis thaliana]	Unigene49992_All//4.00E-69//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome	Unigene49992_All//0.00E+00//ES834081		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0016020	nr +
Unigene49993_All	1129	0.46	0.00	0.09	0.71	0.40	0.32	2.51	1.07	1.48	-8.86E+00	2.92E-03		-2.30E+00	6.76E-02		-8.32E-01	2.88E-01		-1.14E+00	1.63E-01		-1.22E+00	3.10E-04	Down	-7.60E-01	1.75E-02		Unigene49993_All//gi|224713823|gb|ACN62126.1|//1.00E-131//tryptophan decarboxylase [Capsicum annuum]	Unigene49993_All//5.00E-129//AT2G20340| tyrosine decarboxylase, putative	Unigene49993_All//0.00E+00//TC179318		ko00360|Phenylalanine metabolism//ko00380|Tryptophan metabolism//ko00350|Tyrosine metabolism//ko00340|Histidine metabolism//ko00950|Isoquinoline alkaloid biosynthesis//ko00901|Indole alkaloid biosynthesis//ko00965|Betalain biosynthesis	GO:0016831//GO:0044237//GO:0044281	nr -
Unigene49995_All	680	211.28	182.19	211.90	213.69	175.97	216.92	97.37	75.66	42.94	-2.14E-01	5.90E-07		4.20E-03	9.53E-01		-2.80E-01	3.60E-13		2.16E-02	6.73E-01		-3.64E-01	2.15E-10		-1.18E+00	6.54E-79	Down	Unigene49995_All//gi|12229936|sp|Q9SXU1.1|PSA7_CICAR//1.00E-105//RecName: Full=Proteasome subunit alpha type-7; AltName: Full=20S proteasome alpha subunit D; AltName: Full=20S proteasome subunit alpha-4 |gi|4586592|dbj|BAA76428.1| multicatalytic endopeptidase complex [Cicer arietinum]	Unigene49995_All//6.00E-104//AT5G66140| PAD2 (PROTEASOME ALPHA SUBUNIT D 2); endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene49995_All//0.00E+00//gi|13349919|gb|BG440268.1|BG440268		ko03050|Proteasome		nr -
Unigene49999_All	898	50.86	17.72	29.59	42.55	63.43	60.40	0.19	0.28	0.22	-1.52E+00	6.25E-64	Down	-7.82E-01	2.22E-21		5.76E-01	4.19E-19		5.06E-01	3.09E-13		5.69E-01	6.74E-01		2.36E-01	8.83E-01		Unigene49999_All//gi|133925931|gb|AB043717.1|//5.00E-74//profilin [Gossypium hirsutum] |gi|133925933|gb|AB043718.1| profilin [Gossypium hirsutum] |gi|133925935|gb|AB043719.1| profilin [Gossypium hirsutum] |gi|260871353|gb|ACX53268.1| profilin [Gossypium raimondii] |gi|260871355|gb|ACX53269.1| profilin [Gossypium arboreum]	Unigene49999_All//5.00E-63//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding	Unigene49999_All//0.00E+00//gi|13352142|gb|BG442394.1|BG442394			GO:0003779//GO:0005856//GO:0007010//GO:0043231//GO:0044444	nr +
Unigene5_All	888	0.35	1.94	2.64	2.02	1.71	1.47	5.09	7.34	3.99	2.46E+00	3.84E-05	Up	2.90E+00	1.35E-07	Up	-2.43E-01	6.16E-01		-4.53E-01	3.94E-01		5.27E-01	1.08E-02		-3.52E-01	1.67E-01		Unigene5_All//gi|124359633|gb|ABD32307.2|//1.00E-27//Nuclear factor related to kappa-B-binding protein , related [Medicago truncatula]	Unigene5_All//3.00E-15//AT3G45830| unknown protein	Unigene5_All//2.00E-150//BG446826				nr +
Unigene50_All	2266	2.68	1.86	2.49	6.55	7.60	6.64	8.84	1.81	18.32	-5.29E-01	2.79E-02		-1.05E-01	6.84E-01		2.14E-01	1.37E-01		1.88E-02	9.32E-01		-2.29E+00	7.60E-60	Down	1.05E+00	4.49E-41	Up	Unigene50_All//gi|224066625|ref|XP_002302169.1|//0.00E+00//cellulose synthase [Populus trichocarpa] |gi|222843895|gb|EEE81442.1| cellulose synthase [Populus trichocarpa]	Unigene50_All//0.00E+00//AT5G64740| CESA6 (CELLULOSE SYNTHASE 6); cellulose synthase/ transferase, transferring glycosyl groups	Unigene50_All//0.00E+00//DW485908				nr -
Unigene500_All	1330	11.29	6.36	3.40	41.87	31.46	29.24	12.02	23.98	25.76	-8.28E-01	1.42E-08		-1.73E+00	1.18E-24	Down	-4.13E-01	1.37E-10		-5.18E-01	2.91E-14		9.97E-01	1.61E-28		1.10E+00	1.24E-36	Up	Unigene500_All//gi|124360022|gb|AB098038.1|//2.00E-41//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene500_All//2.00E-27//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene500_All//0.00E+00//gi|13248568|gb|BF276201.2|BF276201				nr -
Unigene5000_All	1310	1.32	0.66	1.34	2.05	1.55	2.59	6.39	3.00	3.95	-1.00E+00	4.42E-02		2.54E-02	9.79E-01		-4.05E-01	3.13E-01		3.33E-01	3.80E-01		-1.09E+00	2.91E-09	Down	-6.93E-01	6.50E-05		Unigene5000_All//gi|240256429|ref|NP_199891.4|//2.00E-27//ATP binding [Arabidopsis thaliana]	Unigene5000_All//0.00E+00//AT5G23160| CYP86B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene5000_All//0.00E+00//BE055205				nr -
Unigene50000_All	1851	0.06	0.82	1.32	1.43	1.04	1.37	3.72	5.98	5.53	3.86E+00	1.23E-06	Up	4.55E+00	4.28E-11	Up	-4.53E-01	2.52E-01		-6.19E-02	8.91E-01		6.85E-01	7.01E-06		5.71E-01	2.32E-04		Unigene50000_All//gi|224094095|ref|XP_002310074.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] |gi|222825977|gb|EEE90524.1| cytochrome P450 [Populus trichocarpa]	Unigene50000_All//0.00E+00//AT5G23190| CYP86B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene50000_All//0.00E+00//TC165628		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0000038//GO:0005506//GO:0016712//GO:0043231	nr -
Unigene50002_All	3022	0.19	0.07	0.07	0.30	0.13	0.07	3.82	9.45	14.09	-1.50E+00	1.36E-01		-1.43E+00	1.75E-01		-1.24E+00	8.18E-02		-1.99E+00	1.36E-02		1.31E+00	4.48E-39	Up	1.88E+00	4.22E-100	Up	Unigene50002_All//gi|30686455|ref|NP_850249.1|//5.00E-21//BPC7 (BASIC PENTACYSTEINE 7); DNA binding / transcription factor [Arabidopsis thaliana] |gi|79524391|ref|NP_001031488.1| BPC7 (BASIC PENTACYSTEINE 7); DNA binding / transcription factor [Arabidopsis thaliana] |gi|145330368|ref|NP_001078009.1| BPC7 (BASIC PENTACYSTEINE 7); DNA binding / transcription factor [Arabidopsis thaliana] |gi|38639967|gb|AAR25826.1| basic pentacysteine 7 [Arabidopsis thaliana] |gi|111074168|gb|ABH04457.1| At2g35550 [Arabidopsis thaliana] |gi|156125014|gb|ABL50825.1| GAGA-binding transcriptional activator [Arabidopsis thaliana]	Unigene50002_All//2.00E-22//AT2G35550| BPC7 (BASIC PENTACYSTEINE 7); DNA binding / transcription factor	Unigene50002_All//0.00E+00//gi|21090428|gb|BQ402741.1|BQ402741	BBR/BPC	ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0001071//GO:0006351//GO:0016405//GO:0016703//GO:0043231	nr -
Unigene50003_All	1307	0.00	0.16	0.00	1.07	3.90	3.97	11.10	0.61	7.07	7.28E+00	1.36E-01		null	null		1.87E+00	2.62E-11	Up	1.90E+00	5.71E-11	Up	-4.19E+00	1.30E-77	Down	-6.50E-01	4.07E-07		Unigene50003_All//gi|27464177|gb|AA015998.1|AF516879_1//1.00E-120//expansin [Glycine max]	Unigene50003_All//6.00E-115//AT1G20190| ATEXPA11 (ARABIDOPSIS THALIANA EXPANSIN 11)	Unigene50003_All//0.00E+00//TC160817				nr +
Unigene50004_All	955	11.67	8.81	8.92	14.29	11.18	13.43	21.91	17.64	8.51	-4.06E-01	1.85E-02		-3.87E-01	3.26E-02		-3.55E-01	1.69E-02		-8.97E-02	6.18E-01		-3.13E-01	4.11E-03		-1.36E+00	8.43E-32	Down	Unigene50004_All//gi|17641414|gb|AA995391.1|//1.00E-108//ribosomal protein L2 [Gossypium arboreum]	Unigene50004_All//1.00E-59//AT2G44065| ribosomal protein L2 family protein	Unigene50004_All//0.00E+00//TC132405		ko03010|Ribosome	GO:0000315//GO:0003676//GO:0003824//GO:0005198//GO:0010467//GO:0043231	nr +
Unigene50008_All	876	2.75	2.89	5.59	3.07	3.30	3.45	0.53	0.52	0.73	7.41E-02	8.51E-01		1.03E+00	3.25E-04	Up	1.05E-01	8.37E-01		1.70E-01	6.84E-01		-1.67E-02	1.02E+00		4.55E-01	5.78E-01		Unigene50008_All//gi|6691123|gb|AAF24496.1|AF213695_1//7.00E-62//FH protein NFH1 [Nicotiana tabacum]	Unigene50008_All//4.00E-52//AT3G25500| AFH1 (FORMIN HOMOLOGY 1); actin binding / actin filament binding / protein binding	Unigene50008_All//6.00E-76//TC157132			GO:0003779//GO:0007010//GO:0016020	nr +
Unigene50009_All	651	1.45	20.08	4.91	12.09	9.79	28.44	12.02	37.56	141.85	3.80E+00	9.37E-53	Up	1.76E+00	7.12E-06	Up	-3.05E-01	1.55E-01		1.23E+00	1.80E-20	Up	1.64E+00	5.29E-47	Up	3.56E+00	0.00E+00	Up	Unigene50009_All//gi|297723973|ref|NP_001174350.1|//4.00E-08//Os05g0323400 [Oryza sativa Japonica Group] |gi|255676245|dbj|BAH93078.1| Os05g0323400 [Oryza sativa Japonica Group]		Unigene50009_All//0.00E+00//TC169936				nr -
Unigene5001_All	1148	13.99	3.44	14.66	8.50	9.96	3.46	1.40	0.55	0.69	-2.02E+00	9.20E-34	Down	6.71E-02	6.57E-01		2.28E-01	2.18E-01		-1.30E+00	4.51E-12	Down	-1.36E+00	4.47E-03		-1.01E+00	2.40E-02				Unigene5001_All//2.00E-58//gi|27883506|gb|CB074790.1|CB074790				
Unigene50010_All	1419	4.61	2.11	0.60	6.04	7.09	8.37	0.06	0.06	0.22	-1.13E+00	1.79E-06	Down	-2.94E+00	1.54E-20	Down	2.31E-01	2.45E-01		4.71E-01	4.06E-03		-1.70E-02	1.01E+00		1.91E+00	1.54E-01		Unigene50010_All//gi|5902370|gb|AAD55472.1|AC009322_12//2.00E-94//Similar to polygalacturonases [Arabidopsis thaliana]	Unigene50010_All//9.00E-87//AT1G80170| polygalacturonase, putative / pectinase, putative	Unigene50010_All//0.00E+00//gi|164296095|gb|ES829659.1|ES829659		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0005618//GO:0016798//GO:0031410	nr +
Unigene50011_All	847	1.61	0.48	0.88	8.00	5.20	1.39	5.84	2.42	1.13	-1.75E+00	4.61E-03		-8.68E-01	1.47E-01		-6.20E-01	3.42E-03		-2.53E+00	1.68E-20	Down	-1.27E+00	3.60E-07	Down	-2.37E+00	1.79E-16	Down	Unigene50011_All//gi|5042407|gb|AAD38246.1|AC006193_2//6.00E-31//Hypothetical Protein [Arabidopsis thaliana] |gi|6633824|gb|AAF19683.1|AC009519_17 F1N19.27 [Arabidopsis thaliana] |gi|38454064|gb|AAR20726.1| At1g64700 [Arabidopsis thaliana] |gi|38604006|gb|AAR24746.1| At1g64700 [Arabidopsis thaliana]	Unigene50011_All//3.00E-32//AT1G64700| unknown protein	Unigene50011_All//8.00E-29//gi|164311283|gb|ES835561.1|ES835561				nr -
Unigene50012_All	1239	6.21	4.01	5.76	2.53	0.89	0.95	0.65	1.08	0.51	-6.31E-01	2.58E-03		-1.08E-01	6.25E-01		-1.51E+00	7.77E-06	Down	-1.42E+00	7.40E-05	Down	7.35E-01	1.60E-01		-3.34E-01	6.19E-01		Unigene50012_All//gi|91208914|ref|YP_538947.1|//1.00E-79//envelope membrane protein [Gossypium hirsutum] |gi|122201400|sp|Q2L922.1|CEMA_GOSHI RecName: Full=Chloroplast envelope membrane protein |gi|85687428|gb|ABC73640.1| chloroplast envelope membrane protein [Gossypium hirsutum]	Unigene50012_All//2.00E-62//AT1G06530| hypothetical protein	Unigene50012_All//0.00E+00//TC145342			GO:0006818//GO:0009528//GO:0015077//GO:0031224	nr +
Unigene50015_All	1223	0.43	1.99	0.70	7.13	10.73	20.94	3.91	13.88	6.74	2.22E+00	2.89E-06	Up	7.03E-01	3.83E-01		5.90E-01	5.64E-05		1.55E+00	1.21E-39	Up	1.83E+00	5.36E-38	Up	7.88E-01	8.24E-06		Unigene50015_All//gi|87162727|gb|ABD28522.1|//2.00E-92//Cupin, RmlC-type [Medicago truncatula]	Unigene50015_All//1.00E-56//AT5G15120| unknown protein	Unigene50015_All//0.00E+00//gi|78353413|gb|DT573687.1|DT573687			GO:0016702//GO:0045333	nr +
Unigene50016_All	1170	37.74	156.60	89.80	19.29	15.39	23.01	4.55	4.47	1.02	2.05E+00	0.00E+00	Up	1.25E+00	2.16E-105	Up	-3.25E-01	3.25E-03		2.54E-01	1.89E-02		-2.81E-02	9.29E-01		-2.16E+00	7.96E-16	Down	Unigene50016_All//gi|224081248|ref|XP_002306351.1|//1.00E-65//stress enhanced protein 2 [Populus trichocarpa] |gi|222855800|gb|EEE93347.1| stress enhanced protein 2 [Populus trichocarpa]	Unigene50016_All//5.00E-47//AT2G21970| SEP2 (STRESS ENHANCED PROTEIN 2); chlorophyll binding	Unigene50016_All//0.00E+00//TC176948			GO:0001071//GO:0003006//GO:0003676//GO:0006091//GO:0009534//GO:0009791//GO:0046906	nr +
Unigene50017_All	1073	2.63	0.24	5.11	0.84	0.39	0.00	106.11	50.52	7.02	-3.48E+00	3.94E-11	Down	9.57E-01	3.26E-04		-1.12E+00	1.16E-01		-9.71E+00	1.21E-05	Down	-1.07E+00	2.64E-112	Down	-3.92E+00	0.00E+00	Down	Unigene50017_All//gi|257782114|gb|ACV65500.1|//1.00E-142//deoxyhemigossypol-6-O-methyltransferase [Gossypium hirsutum]	Unigene50017_All//4.00E-51//AT4G35160| O-methyltransferase family 2 protein	Unigene50017_All//0.00E+00//ES815595		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +

Unigene50018_All	1236	9.95	4.18	6.33	14.83	7.49	7.23	11.29	1.49	2.84	-1.25E+00	2.42E-13	Down	-6.52E-01	9.50E-05		-9.85E-01	3.25E-16		-1.04E+00	1.23E-15	Down	-2.92E+00	6.78E-55	Down	-1.99E+00	2.52E-36	Down	Unigene50018_All//gi|115465829|ref|NP_001056514.1|//4.00E-63//Os05g0595300 [Oryza sativa Japonica Group] >gi|113580065|dbj|BAF18428.1|Os05g0595300 [Oryza sativa Japonica Group]	Unigene50018_All//4.00E-66//AT4G27900| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: CCT domain (InterPro:IPR001022); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G53420.1); Has 876 Blast hits to 876 proteins in 63 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 853; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).	Unigene50018_All//0.00E+00//TC156797	C2C2-CO-like			nr -
Unigene50023_All	1203	0.87	3.75	0.09	0.46	0.37	0.79	2.78	1.88	3.74	2.11E+00	2.15E-10	Up	-3.30E+00	4.58E-04	Down	-2.92E-01	7.70E-01		7.92E-01	2.99E-01		-5.66E-01	6.45E-02		4.31E-01	8.67E-02		Unigene50023_All//gi|15222875|ref|NP_177708.1|//4.00E-93//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|6721098|gb|AAF26752.1|AC007396_1 T4012.3 [Arabidopsis thaliana] >gi|18377860|gb|AAL67116.1|At1g75800/T4012_2 [Arabidopsis thaliana] >gi|20334826|gb|AAM16169.1|At1g75800/T4012_2 [Arabidopsis thaliana]	Unigene50023_All//2.00E-94//AT1G75800| pathogenesis-related thaumatin family protein	Unigene50023_All//1.00E-93//CO131262			GO:0009607//GO:0031224	nr +
Unigene50024_All	205	0.77	0.00	1.04	126.84	91.55	83.94	12.37	3.47	2.33	-9.58E+00	2.15E-01		4.40E-01	7.75E-01		-4.71E-01	1.56E-06		-5.96E-01	8.05E-09		-1.84E+00	2.33E-06	Down	-2.41E+00	5.67E-09	Down	Unigene50024_All//gi|110277459|gb|ABG57264.1|//2.00E-13//microtubule-associated protein [Populus tremula x Populus tremuloides]	Unigene50024_All//6.00E-09//AT5G37478| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G15510.1); Has 39 Blast hits to 39 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene50024_All//1.00E-107//TC143923				nr -
Unigene50025_All	833	0.88	0.49	1.53	53.10	41.30	35.68	9.19	3.76	0.67	-8.54E-01	3.05E-01		8.03E-01	2.01E-01		-3.63E-01	8.14E-07		-5.74E-01	1.18E-13		-1.29E+00	7.54E-11	Down	-3.78E+00	1.64E-39	Down	Unigene50025_All//gi|110277459|gb|ABG57264.1|//2.00E-54//microtubule-associated protein [Populus tremula x Populus tremuloides]	Unigene50025_All//3.00E-38//AT5G37478| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G15510.1); Has 39 Blast hits to 39 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene50025_All//0.00E+00//gi|109826318|gb|DW225038.1|DW225038				nr -
Unigene50026_All	694	31.44	15.70	15.27	25.48	18.66	28.83	26.62	10.66	10.45	-1.00E+00	2.15E-16	Down	-1.04E+00	1.06E-16	Down	-4.50E-01	2.53E-04		1.78E-01	2.00E-01		-1.32E+00	4.99E-26	Down	-1.35E+00	1.03E-27	Down	Unigene50026_All//gi|115441259|ref|NP_001044909.1|//2.00E-44//Os01g0866700 [Oryza sativa Japonica Group] >gi|56785201|dbj|BAD81919.1| small nuclear ribonucleoprotein-like [Oryza sativa Japonica Group] >gi|113534440|dbj|BAF06823.1|Os01g0866700 [Oryza sativa Japonica Group]	Unigene50026_All//3.00E-45//AT1G21190| small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative	Unigene50026_All//0.00E+00//TC155375		ko03040|Spliceosome//ko03018|RNA degradation	GO:0030529//GO:0043231	nr -
Unigene50027_All	1298	7.62	8.08	5.42	13.78	11.12	8.98	6.78	5.67	2.76	8.50E-02	6.46E-01		-4.92E-01	9.85E-03		-3.10E-01	1.59E-02		-6.18E-01	1.17E-06		-2.58E-01	1.68E-01		-1.29E+00	7.43E-13	Down	Unigene50027_All//sp|P53214|MTL1_YEAST//5.00E-07//Protein MTL1 OS=Saccharomyces cerevisiae GN=MTL1 PE=2 SV=1		Unigene50027_All//0.00E+00//gi|164336467|gb|ES814102.1|ES814102				swissprot -
Unigene50028_All	379	8.01	10.16	6.04	11.30	9.09	5.72	17.29	10.37	2.10	3.44E-01	2.88E-01		-4.06E-01	2.91E-01		-3.15E-01	3.16E-01		-9.83E-01	7.02E-04		-7.38E-01	3.06E-04		-3.04E+00	4.54E-28	Down								
Unigene50029_All	1252	25.78	30.84	34.37	4.14	13.86	5.84	0.00	0.00	0.00	2.58E-01	3.28E-03		4.15E-01	6.52E-07		1.74E+00	1.54E-34	Up	4.98E-01	2.27E-02		null	null		null	null		Unigene50029_All//gi|47825031|gb|AAT38801.1|//5.00E-25//Putative phytochrome kinase substrate 1, identical [Solanum demissum]	Unigene50029_All//1.00E-11//AT1G14280| PKS2 (PHYTOCHROME KINASE SUBSTRATE 2)				GO:0009605//GO:0009639	nr +
Unigene5003_All	822	136.21	105.47	151.72	196.53	156.97	224.61	69.08	47.24	34.36	-3.69E-01	2.55E-14		1.56E-01	1.58E-03		-3.24E-01	3.93E-19		1.93E-01	1.33E-07		-5.48E-01	2.71E-18		-1.01E+00	1.45E-52	Down	Unigene5003_All//gi|118485459|gb|AB894148.1|//6.00E-10//unknown [Populus trichocarpa]		Unigene5003_All//0.00E+00//TC173288				nr -
Unigene50032_All	736	6.54	10.81	7.09	11.03	12.31	13.19	26.88	50.03	64.52	7.25E-01	4.35E-04		1.17E-01	6.72E-01		1.58E-01	4.96E-01		2.58E-01	2.04E-01		8.96E-01	1.36E-27		1.26E+00	1.42E-62	Up	Unigene50032_All//gi|223452416|gb|ACM89535.1|//1.00E-22//protein kinase [Glycine max]	Unigene50032_All//6.00E-18//AT1G07570| APK1A; kinase/ protein serine/threonine kinase	Unigene50032_All//0.00E+00//CO122519		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559//GO:0043231	nr +
Unigene50036_All	1035	6.12	421.95	5.40	2.21	12.34	10.08	1.18	5.29	25.87	6.11E+00	0.00E+00	Up	-1.79E-01	4.99E-01		2.48E+00	1.83E-39	Up	2.19E+00	8.93E-26	Up	2.16E+00	1.12E-15	Up	4.45E+00	1.65E-150	Up	Unigene50036_All//gi|89258594|gb|AB065473.1|//1.00E-120//DREB1-like transcription factor [Gossypium hirsutum]	Unigene50036_All//1.00E-48//AT5G51990| CBF4 (C- REPEAT-BINDING FACTOR 4); DNA binding / transcription activator/ transcription factor	Unigene50036_All//0.00E+00//TC129889	AP2-EREBP		GO:0006350//GO:0010468	nr +
Unigene50038_All	1293	1.90	1.06	1.03	1.16	1.28	1.29	2.09	3.65	0.52	-8.46E-01	3.66E-02		-8.85E-01	3.75E-02		1.45E-01	8.31E-01		1.61E-01	7.57E-01		8.04E-01	1.14E-03		-2.00E+00	9.91E-08	Down	Unigene50038_All//gi|22326944|ref|NP_680186.1|//3.00E-36//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|29294058|gb|AAO73895.1|proline-rich protein family [Arabidopsis thaliana] >gi|38454174|gb|AAR20781.1|At5g21280 [Arabidopsis thaliana] >gi|38604048|gb|AAR24767.1|At5g21280 [Arabidopsis thaliana]	Unigene50038_All//2.00E-12//AT5G21280| hydroxyproline-rich glycoprotein family protein				GO:0043231	nr +
Unigene50039_All	964	3.91	2.68	2.98	9.56	8.25	7.68	15.00	6.16	6.65	-5.44E-01	8.58E-02		-3.90E-01	2.47E-01		-2.12E-01	3.15E-01		-3.15E-01	1.19E-01		-1.28E+00	1.00E-19	Down	-1.17E+00	9.72E-18	Down	Unigene50039_All//gi|145324891|ref|NP_001077692.1|//1.00E-103//FU (FUSED); protein serine/threonine kinase [Arabidopsis thaliana] >gi|72004129|gb|AAZ66048.1| fused [Arabidopsis thaliana]	Unigene50039_All//2.00E-104//AT1G50240| FU (FUSED); protein serine/threonine kinase	Unigene50039_All//0.00E+00//TC156460			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene50040_All	980	54.72	65.66	53.79	324.61	318.49	205.40	288.84	165.18	134.68	2.63E-01	6.49E-05		-2.47E-02	7.74E-01		-2.74E-02	4.58E-01		-6.60E-01	1.02E-121		-8.06E-01	3.91E-173		-1.10E+00	4.29E-299	Down	Unigene50040_All//gi|255564345|ref|XP_002523169.1|//5.00E-97//sphingolipid fatty acid alpha hydroxylase [Ricinus communis] >gi|223537576|gb|EEF39200.1|sphingolipid fatty acid alpha hydroxylase [Ricinus communis]	Unigene50040_All//5.00E-89//AT2G34770| FAH1 (FATTY ACID HYDROXYLASE 1); catalytic/ fatty acid alpha-hydroxylase	Unigene50040_All//0.00E+00//DW224876			GO:0004497//GO:0005576//GO:0006631//GO:0009411//GO:0009699//GO:0012501//GO:0031224//GO:0043231//GO:0040914	nr +
Unigene50041_All	961	0.87	1.53	1.16	1.50	1.83	0.66	2.29	2.61	0.95	8.12E-01	1.36E-01		4.18E-01	5.32E-01		2.82E-01	5.96E-01		-1.19E+00	3.43E-02		1.90E-01	6.62E-01		-1.26E+00	9.51E-04	Down								
Unigene50042_All	678	17.05	10.09	12.88	18.52	19.86	13.92	4.12	1.60	1.82	-7.57E-01	5.99E-06		-4.05E-01	2.21E-02		1.01E-01	5.91E-01		-4.11E-01	1.02E-02		-1.36E+00	8.91E-05	Down	-1.18E+00	3.83E-04	Down	Unigene50042_All//gi|260505494|gb|ACX42226.1|//2.00E-55//heat shock protein 90 [Ipomoea nil]	Unigene50042_All//9.00E-45//AT2G04030| CR88; ATP binding	Unigene50042_All//2.00E-78//ES837739		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0003006//GO:0005515//GO:0006970//GO:0009416//GO:0009526//GO:0009532//GO:0010035//GO:0016020//GO:0032559//GO:0044267	nr -
Unigene50043_All	1075	4.38	1.41	2.38	10.75	5.25	4.54	26.82	25.04	26.35	-1.63E+00	6.16E-08	Down	-8.82E-01	2.38E-03		-1.03E+00	3.21E-11	Down	-1.24E+00	2.45E-13	Down	-9.93E-02	3.64E-01		-2.57E-02	8.03E-01		Unigene50043_All//gi|94549041|gb|AB539005.1|//3.00E-68//plant cell wall protein SlTFR88 [Solanum lycopersicum]	Unigene50043_All//5.00E-41//AT2G46150| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54200.1); Has 137 Blast hits to 136 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 133; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene50043_All//0.00E+00//TC171506			GO:0016020	nr -
Unigene50045_All	730	15.12	14.78	11.45	18.42	16.56	12.56	18.77	11.74	8.08	-3.27E-02	8.62E-01		-4.01E-01	2.72E-02		-1.54E-01	3.83E-01		-5.53E-01	2.25E-04		-6.77E-01	5.76E-07		-1.22E+00	8.44E-18	Down	Unigene50045_All//gi|18398731|ref|NP_565438.1|//3.00E-49//ribosomal protein L6 family protein [Arabidopsis thaliana]	Unigene50045_All//3.00E-45//AT2G18400| ribosomal protein L6 family protein	Unigene50045_All//4.00E-172//DN818061		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0033279//GO:0043231	nr +

Unigene50046_All	786	1.80	4.51	7.18	5.96	4.51	2.36	5.16	3.83	7.15	1.33E+00	9.56E-05	Up	2.00E+00	1.36E-11	Up	-4.01E-01	1.56E-01		-1.34E+00	2.15E-06	Down	-4.32E-01	1.23E-01		4.69E-01	3.24E-02		Unigene50046_All//gi|18418337|ref|NP_567945.1|//9.00E-85//OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase [Arabidopsis thaliana] >gi|75331830|sp|Q94096.1|SRK2E_ARATH RecName: Full=Serine/threonine-protein kinase SRK2E; AltName: Full=Serine/threonine-protein kinase OST1; AltName: Full=Protein OPEN STOMATA 1; AltName: Full=SNF1-related kinase 2.6; Short=SnRK2.6 >gi|15451088|gb|AAK96815.1| protein kinase - like protein [Arabidopsis thaliana] >gi|20148419|gb|AAM10100.1| protein kinase-like protein [Arabidopsis thaliana] >gi|22474449|emb|CAC87047.1| protein kinase [Arabidopsis thaliana]	Unigene50046_All//2.00E-79//AT4G33950|OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase	Unigene50046_All//1.00E-83//DW510390			GO:0004674//GO:0005984//GO:0006464//GO:0006633//GO:0006641//GO:0006800//GO:0006952//GO:0006970//GO:0009755//GO:0010118//GO:0032559//GO:0043231//GO:0044444//GO:0048827	nr -
Unigene50047_All	600	2.88	3.55	1.95	20.51	10.33	6.17	10.43	8.43	7.50	3.02E-01	5.04E-01		-5.60E-01	2.87E-01		-9.89E-01	4.08E-11		-1.73E+00	7.39E-23	Down	-3.07E-01	1.70E-01		-4.75E-01	2.05E-02		Unigene50047_All//gi|30841464|gb|AAP34368.1|//5.00E-42//fiber protein Fb21 [Gossypium barbadense]	Unigene50047_All//2.00E-38//AT3G43240| ARID/BRIGHT DNA-binding domain-containing protein	Unigene50047_All//0.00E+00//TC159549			GO:0003676//GO:0044464//GO:0046914	nr +
Unigene50048_All	800	64.16	132.63	84.87	59.59	88.15	93.32	173.35	155.64	1003.73	1.05E+00	2.19E-82	Up	4.04E-01	4.99E-10		5.65E-01	8.79E-23		6.47E-01	9.96E-28		-1.56E-01	9.17E-05		2.53E+00	0.00E+00	Up	Unigene50048_All//gi|147791048|emb|CAN65763.1|//2.00E-22//hypothetical protein [Vitis vinifera]		Unigene50048_All//0.00E+00//TC160613				nr -
Unigene5005_All	963	12.88	14.15	12.22	15.16	14.66	20.78	11.55	17.97	5.42	1.36E-01	4.09E-01		-7.54E-02	6.70E-01		-4.79E-02	8.16E-01		4.55E-01	1.69E-04		6.38E-01	8.41E-08		-1.09E+00	1.98E-12	Down	Unigene5005_All//gi|21536925|gb|AAM61257.1|//8.00E-08//calmodulin-like protein [Arabidopsis thaliana]	Unigene5005_All//3.00E-44//AT2G41410| calmodulin, putative	Unigene5005_All//0.00E+00//ES806106		ko04626|Plant-pathogen interaction		nr -
Unigene50050_All	1187	1.10	1.15	1.08	2.35	2.23	0.99	0.50	0.42	0.30	6.46E-02	9.17E-01		-3.35E-02	9.74E-01		-7.32E-02	8.41E-01		-1.25E+00	9.65E-04	Down	-2.39E-01	7.65E-01		-7.23E-01	3.71E-01		Unigene50050_All//gi|18401431|ref|NP_565651.1|//9.00E-98//sec23/sec24 transport family protein [Arabidopsis thaliana] >gi|4314388|gb|AAD15598.1| expressed protein [Arabidopsis thaliana] >gi|15450830|gb|AAK96686.1| Unknown protein [Arabidopsis thaliana] >gi|34098799|gb|AAQ56782.1| At2g27460 [Arabidopsis thaliana]	Unigene50050_All//2.00E-99//AT2G27460| sec23/sec24 transport family protein	Unigene50050_All//1.00E-148//TC169633			GO:0012507//GO:0015031//GO:0046914//GO:0048193	nr +
Unigene50051_All	746	5.12	12.70	3.64	2.67	2.40	3.39	5.44	29.41	103.12	1.31E+00	3.87E-11	Up	-4.92E-01	1.39E-01		-1.54E-01	7.69E-01		3.44E-01	4.37E-01		2.43E+00	3.61E-70	Up	4.24E+00	0.00E+00	Up	Unigene50051_All//gi|115442287|ref|NP_001045423.1|//5.00E-40//Os01g0952900 [Oryza sativa Japonica Group] >gi|113534954|dbj|BAF07337.1| Os01g0952900 [Oryza sativa Japonica Group]	Unigene50051_All//3.00E-48//AT5G12340| unknown protein	Unigene50051_All//9.00E-07//TC169293				nr +
Unigene50052_All	912	1.55	1.50	0.35	2.84	2.79	1.39	5.01	1.83	2.88	-4.63E-02	9.45E-01		-2.14E+00	1.24E-03		-2.37E-02	9.56E-01		-1.03E+00	8.31E-03		-1.45E+00	5.69E-08	Down	-7.96E-01	1.10E-03		Unigene50052_All//gi|240256033|ref|NP_193913.4|//7.00E-66//binding / calmodulin binding [Arabidopsis thaliana]	Unigene50052_All//8.00E-53//AT4G21820| binding / calmodulin binding					nr -
Unigene50053_All	909	47.26	25.70	15.99	12.17	6.67	5.52	11.12	16.28	26.34	-8.79E-01	1.82E-25		-1.56E+00	2.18E-60	Down	-8.68E-01	3.77E-08		-1.14E+00	3.18E-11	Down	5.50E-01	2.12E-05		1.24E+00	2.83E-31	Up	Unigene50053_All//gi|110749713|gb|ABG80382.1|//3.00E-51//lateral organ boundaries domain protein [Caragana korshinskii]	Unigene50053_All//5.00E-49//AT3G49940| LBD38 (LOB DOMAIN-CONTAINING PROTEIN 38)	Unigene50053_All//0.00E+00//gi|109868953|gb|DW497929.1|DW497929				nr -
Unigene50054_All	760	9.84	3.20	3.50	9.37	8.84	7.73	4.51	2.14	2.41	-1.62E+00	4.56E-12	Down	-1.49E+00	2.97E-10	Down	-8.52E-02	7.60E-01		-2.79E-01	2.42E-01		-1.07E+00	3.71E-04	Down	-9.02E-01	1.77E-03		Unigene50054_All//gi|31790111|gb|AAP58374.1|//3.00E-65//RPA 32kDa [Pisum sativum]	Unigene50054_All//2.00E-51//AT2G24490| RPA2 (REPLICON PROTEIN A2); protein binding	Unigene50054_All//0.00E+00//gi|78333446|gb|DT553720.1|DT553720		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair	GO:0005488//GO:0006259//GO:0043231	nr -
Unigene50056_All	693	14.34	7.82	6.84	18.19	16.30	28.74	5.06	4.34	7.01	-8.75E-01	1.84E-06		-1.07E+00	2.88E-08	Down	-1.58E-01	3.84E-01		6.60E-01	4.20E-08		-2.22E-01	5.03E-01		4.70E-01	4.89E-02		Unigene50056_All//gi|42570815|ref|NP_973481.1|//5.00E-53//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene50056_All//1.00E-49//AT2G17670| pentatricopeptide (PPR) repeat-containing protein	Unigene50056_All//0.00E+00//gi|21098335|gb|BQ410648.1|BQ410648				nr -
Unigene50059_All	625	0.84	5.92	1.96	2.55	1.98	2.96	0.61	0.94	0.32	2.82E+00	8.14E-12	Up	1.23E+00	6.00E-02		-3.63E-01	5.18E-01		2.16E-01	6.91E-01		6.21E-01	4.78E-01		-9.34E-01	3.79E-01		Unigene50059_All//gi|89001053|gb|AB359116.1|//6.00E-29//At3g58840 [Arabidopsis thaliana]	Unigene50059_All//7.00E-11//AT1G06530| myosin heavy chain-related	Unigene50059_All//2.00E-22//ES805742			GO:0016020//GO:0043231	nr +
Unigene50060_All	890	5.29	12.30	7.18	8.84	8.36	8.12	4.23	3.38	11.95	1.22E+00	1.94E-11	Up	4.40E-01	7.68E-02		-8.16E-02	7.58E-01		-1.23E-01	6.38E-01		-3.22E-01	2.87E-01		1.50E+00	8.64E-19	Up	Unigene50060_All//gi|4204289|gb|AAD10670.1|//3.00E-26//Unknown protein [Arabidopsis thaliana]	Unigene50060_All//3.00E-22//AT5G44060| unknown protein	Unigene50060_All//0.00E+00//gi|78323701|gb|DT543975.1|DT543975				nr -
Unigene50062_All	929	3.72	4.36	1.61	3.86	4.49	3.26	4.28	5.04	2.57	2.31E-01	4.66E-01		-1.21E+00	6.25E-04	Down	2.16E-01	5.49E-01		-2.45E-01	5.01E-01		2.36E-01	4.04E-01		-7.34E-01	5.34E-03		Unigene50062_All//gi|21553651|gb|AAM62744.1|//8.00E-80//thymidylate kinase-like protein [Arabidopsis thaliana]	Unigene50062_All//4.00E-81//AT5G39440| ZEU1 (ZEUS1); ATP binding / thymidylate kinase	Unigene50062_All//0.00E+00//gi|48775331|gb|CO084697.1|CO084697		ko00240|Pyrimidine metabolism	GO:0009197//GO:0009212//GO:0016776//GO:0031981//GO:0032559	nr -
Unigene50063_All	990	13.90	7.52	17.27	96.36	82.75	47.63	12.47	0.55	0.36	-8.86E-01	8.55E-09		3.13E-01	2.95E-02		-2.20E-01	9.65E-06		-1.02E+00	9.01E-77	Down	-4.51E+00	2.48E-69	Down	-5.11E+00	6.15E-77	Down	Unigene50063_All//gi|297817366|ref|XP_002876566.1|//8.00E-89//CYCP3_2 [Arabidopsis lyrata subsp. lyrata] >gi|297322404|gb|EFH52825.1| CYCP3_2 [Arabidopsis lyrata subsp. lyrata]	Unigene50063_All//7.00E-88//AT3G60550| CYCP3;2 (cyclin p3;2); cyclin-dependent protein kinase	Unigene50063_All//0.00E+00//TC159798			GO:0005488//GO:0007049	nr -
Unigene50064_All	828	1.96	3.12	4.12	38.50	18.13	64.53	4.65	8.78	1.78	6.72E-01	8.77E-02		1.07E+00	2.37E-03		-1.09E+00	8.37E-33	Down	7.45E-01	1.90E-25		9.19E-01	2.52E-06		-1.38E+00	1.11E-06	Down			Unigene50064_All//0.00E+00//gi|109865267|gb|DW494243.1|DW494243				ESTScan -
Unigene50065_All	1186	1.85	15.04	4.22	3.07	2.29	2.59	1.89	5.64	2.42	3.02E+00	1.02E-58	Up	1.19E+00	3.18E-05	Up	-4.19E-01	2.02E-01		-2.44E-01	5.00E-01		1.58E+00	1.11E-12	Up	3.56E-01	2.88E-01		Unigene50065_All//gi|27803890|gb|AAO22065.1|//1.00E-57//XrPRp27-like protein [Solanum tuberosum]	Unigene50065_All//1.00E-44//AT2G15220| secretory protein, putative	Unigene50065_All//0.00E+00//gi|78326892|gb|DT547166.1|DT547166				nr -
Unigene50067_All	688	14.68	29.53	34.52	20.20	21.02	22.45	47.32	34.57	18.01	1.01E+00	2.02E-15	Up	1.23E+00	1.17E-23	Up	5.75E-02	7.85E-01		1.52E-01	3.70E-01		-4.53E-01	6.77E-08		-1.39E+00	1.49E-50	Down	Unigene50067_All//gi|18416103|ref|NP_568217.1|//2.00E-32//BolA-like family protein [Arabidopsis thaliana] >gi|27808606|gb|AAO24583.1| At5g09830 [Arabidopsis thaliana]	Unigene50067_All//9.00E-34//AT5G09830| BolA-like family protein	Unigene50067_All//0.00E+00//gi|164358402|gb|ES832791.1|ES832791				nr -
Unigene50068_All	361	112.32	242.26	397.68	100.46	118.76	110.97	60.20	50.48	67.87	1.11E+00	1.57E-74	Up	1.82E+00	1.91E-251	Up	2.42E-01	2.34E-03		1.44E-01	1.29E-01		-2.54E-01	2.01E-02		1.73E-01	9.30E-02		Unigene50068_All//gi|21616031|emb|CAC86003.1|//3.00E-13//aspartic proteinase [Theobroma cacao]		Unigene50068_All//0.00E+00//gi|78336076|gb|DT556350.1|DT556350			GO:0004175//GO:0019538	nr +
Unigene5007_All	880	10.58	4.95	4.48	8.26	8.73	7.85	5.53	3.80	3.80	-1.10E+00	1.70E-08	Down	-1.24E+00	1.07E-09	Down	7.84E-02	7.85E-01		-7.38E-02	7.57E-01		-5.40E-01	2.76E-02		-5.39E-01	2.22E-02		Unigene5007_All//gi|124360022|gb|AB088038.1|//1.00E-12//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene5007_All//1.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene5007_All//7.00E-14//TC149648				nr +
Unigene50070_All	948	21.69	24.80	26.40	3.47	7.70	3.91	0.00	0.09	0.00	1.93E-01	1.09E-01		2.84E-01	1.48E-02		1.15E+00	3.82E-08	Up	1.72E-01	6.34E-01		6.46E+00	4.00E-01		null	null		Unigene50070_All//gi|224128003|ref|XP_002320217.1|//2.00E-52//predicted protein [Populus trichocarpa] >gi|222860990|gb|EEE98532.1| predicted protein [Populus trichocarpa]	Unigene50070_All//9.00E-23//AT2G46640| unknown protein	Unigene50070_All//4.00E-68//TC171986				nr -
Unigene50073_All	1078	9.17	9.35	12.79	11.41	5.27	5.20	11.53	5.74	6.06	2.81E-02	8.93E-01		4.80E-01	2.29E-03		-1.11E+00	1.91E-13	Down	-1.14E+00	2.54E-12	Down	-1.01E+00	8.17E-12	Down	-9.28E-01	9.20E-11		Unigene50073_All//gi|79564965|ref|NP_180387.2|//2.00E-60//nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana]	Unigene50073_All//2.00E-48//AT2G28200| nucleic acid binding / transcription factor/ zinc ion binding	Unigene50073_All//0.00E+00//TC152528	C2H2		GO:0005488	nr -
Unigene50074_All	684	2.60	43.63	2.18	16.39	59.31	48.53	62.37	139.38	183.76	4.07E+00	1.88E-126	Up	-2.55E-01	6.19E-01		1.86E+00	1.18E-87	Up	1.57E+00	8.00E-52	Up	1.16E+00	6.46E-107	Up	1.56E+00	1.39E-225	Up	Unigene50074_All//gi|37724583|gb|AAO12870.1|//3.00E-09//wound induced protein-like [Vitis vinifera]	Unigene50074_All//1.00E-06//AT4G05070| unknown protein	Unigene50074_All//5.00E-107//DW506534				nr -
Unigene50075_All	862	28.83	17.46	22.49	8.96	9.07	6.23	1.72	0.82	0.46	-7.24E-01	5.28E-11		-3.59E-01	1.73E-03		1.78E-02	9.60E-01		-5.23E-01	1.24E-02		-1.06E+00	3.15E-02		-1.89E+00	2.45E-04	Down	Unigene50075_All//gi|115487698|ref|NP_001066336.1|//3.00E-59//Os12g0189700 [Oryza sativa Japonica Group] >gi|77553230|gb|ABA96026.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113648843|dbj|BAF29355.1| Os12g0189700 [Oryza sativa Japonica Group]		Unigene50075_All//0.00E+00//TC143387			GO:0043231	nr -
Unigene50076_All	693	7.25	8.04	4.23	10.42	9.34	11.54	23.25	15.50	6.04	1.50E-01	5.99E-01		-7.78E-01	5.26E-03		-1.58E-01	5.45E-01		1.46E-01	5.60E-01		-5.85E-01	2.18E-06		-1.95E+00	1.62E-40	Down	Unigene50076_All//gi|3024501|sp|Q40193.1|RB11C_LOTJA//1.00E-86//RecName: Full=Ras-related protein Rab11C >gi|1370146|emb|CAA98179.1| RAB11C [Lotus japonicus]	Unigene50076_All//6.00E-79//AT3G46830| ATRABA2C (ARABIDOPSIS RAB GTPASE HOMOLOG A2C); GTP binding	Unigene50076_All//0.00E+00//TC139980			GO:0003824//GO:0015031//GO:0016020//GO:0032266//GO:0035556//GO:0043231//GO:0044444//GO:0051169	nr +
Unigene50077_All	849	5.85	6.27	5.39	9.39	8.27	9.31	9.81	6.84	4.83	9.81E-02	7.12E-01		-1.18E-01	6.77E-01		-1.82E-01	4.34E-01		-1.21E-02	9.50E-01		-5.20E-01	3.73E-03		-1.02E+00	1.20E-08	Down	Unigene50077_All//gi|115485903|ref|NP_001068095.1|//1.00E-35//Os11g0557900 [Oryza sativa Japonica Group] >gi|113645317|dbj|BAF28458.1| Os11g0557900 [Oryza sativa Japonica Group]	Unigene50077_All//5.00E-36//AT4G01710| CRK (CROOKED); actin binding	Unigene50077_All//0.00E+00//TC145769			GO:0000904//GO:0008064//GO:0008092//GO:0015629//GO:0016020//GO:0016049//GO:0016772	nr -
Unigene50078_All	767	5.73	3.24	4.93	25.78	16.70	6.12	3.64	1.74	0.57	-8.24E-01	4.29E-03		-2.17E-01	4.98E-01		-6.27E-01	3.24E-08		-2.07E+00	2.13E-46	Down	-1.06E+00	1.71E-03		-2.67E+00	6.57E-11	Down	Unigene50078_All//gi|297827555|ref|XP_002881660.1|//2.00E-47//nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327499|gb|EFH57919.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50078_All//8.00E-43//AT2G39510| nodulin MtN21 family protein	Unigene50078_All//0.00E+00//TC149246			GO:0044464	nr -
Unigene50081_All	537	18.41	33.97	38.97	26.34	24.94	36.84	23.86	22.65	15.51	8.83E-01	2.59E-11		1.08E+00	4.73E-17	Up	-7.88E-02	6.58E-01		4.84E-01	6.72E-05		-7.49E-02	6.39E-01		-6.22E-01	5.65E-06		Unigene50081_All//gi|226506332|ref|NP_001149812.1|//5.00E-28//ATP binding protein [Zea mays] >gi|195634813|gb|ACG36875.1| ATP binding protein [Zea mays]	Unigene50081_All//7.00E-20//AT1G75510| transcription initiation factor IIF beta subunit (TFIIF-beta) family protein	Unigene50081_All//0.00E+00//gi|21094902|gb|BQ407215.1|BQ407215		ko03022|Basal transcription factors	GO:0005667//GO:0006352//GO:0008135//GO:0030528//GO:0032559	nr -
Unigene50082_All	971	1.72	5.43	4.88	28.99	14.01	12.00	3.35	1.21	0.98	1.65E+00	6.74E-09	Up	1.50E+00	8.18E-07	Up	-1.05E+00	2.19E-27	Down	-1.27E+00	8.73E-33	Down	-1.48E+00	4.82E-06	Down	-1.77E+00	7.09E-08	Down	Unigene50082_All//gi|871487|emb|CAA58731.1|//4.00E-65//PAR-1b [Nicotiana tabacum]	Unigene50082_All//1.00E-56//AT5G52390| photoassimilate-responsive protein, putative	Unigene50082_All//0.00E+00//TC154160				nr +
Unigene50083_All	1026	2.70	2.22	1.04	2.23	1.98	1.72	4.24	5.38	4.27	-2.82E-01	4.64E-01		-1.38E+00	7.27E-04	Down	-1.74E-01	7.09E-01		-3.80E-01	4.02E-01		3.41E-01	1.51E-01		9.00E-03	9.69E-01		Unigene50083_All//gi|224109958|ref|XP_002315369.1|//1.00E-30//f-box family protein [Populus trichocarpa] >gi|222864409|gb|EEF01540.1| f-box family protein [Populus trichocarpa]	Unigene50083_All//4.00E-20//AT5G07610| F-box family protein	Unigene50083_All//0.00E+00//TC140435				nr +

Unigene50085_All	1923	0.22	0.00	0.00	0.52	1.09	0.28	35.86	8.26	3.13	-7.77E+00	1.05E-02		-7.77E+00	1.56E-02		1.08E+00	1.49E-02		-8.79E-01	2.20E-01		-2.12E+00	2.02E-185	Down	-3.52E+00	0.00E+00	Down	Unigene50085_All|gi|238481047|ref|XP_001154284.1|/0.00E+00//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene50085_All//0.00E+00//AT4G33330| transferase, transferring glycosyl groups	Unigene50085_All//0.00E+00//TC176106			GO:0035251	nr -
Unigene50086_All	1203	0.87	1.05	0.44	5.63	6.87	6.49	4.25	2.68	1.82	2.76E-01	6.17E-01		-9.75E-01	1.67E-01		2.87E-01	1.82E-01		2.06E-01	4.05E-01		-6.69E-01	4.55E-03		-1.22E+00	2.95E-07	Down	Unigene50086_All|gi|52139818|gb|AAU29199.1|/1.00E-165//cytosolic malate dehydrogenase [Solanum lycopersicum]	Unigene50086_All//4.00E-149//AT5G43330| malate dehydrogenase, cytosolic, putative	Unigene50086_All//0.00E+00//gi|164256939|gb|ES846400.1|ES846400		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene50087_All	647	11.56	29.76	32.51	37.80	34.22	26.11	2.61	2.33	2.71	1.36E+00	3.49E-23	Up	1.49E+00	6.61E-28	Up	-1.44E-01	2.45E-01		-5.34E-01	5.75E-07		-1.69E-01	7.23E-01		5.17E-02	9.25E-01		Unigene50087_All|gi|90093310|gb|ABD85168.1|/2.00E-20//At3g22970 [Arabidopsis thaliana]	Unigene50087_All//9.00E-20//AT4G14620| unknown protein	Unigene50087_All//0.00E+00//gi|21098340|gb|BQ410653.1|BQ410653				nr +
Unigene50088_All	1025	16.28	9.19	9.61	17.98	11.12	17.36	22.69	12.80	10.26	-8.25E-01	2.18E-09		-7.61E-01	7.07E-08		-6.93E-01	4.11E-09		-5.07E-02	7.34E-01		-8.25E-01	1.53E-15		-1.14E+00	5.88E-27	Down	Unigene50088_All|gi|104304209|gb|ABF72432.1|/3.00E-80//PIP1 [Capsicum annuum]	Unigene50088_All//1.00E-78//AT5G53160| unknown protein	Unigene50088_All//0.00E+00//gi|164339002|gb|ES814449.1|ES814449			GO:0004871//GO:0005488//GO:0009755//GO:0044424	nr -
Unigene50089_All	2013	0.91	0.38	1.14	1.14	0.29	0.85	32.51	82.82	43.90	-1.27E+00	1.00E-02		3.22E-01	4.69E-01		-1.97E+00	3.55E-06	Down	-4.17E-01	3.62E-01		1.35E+00	4.45E-236	Up	4.33E-01	5.95E-19		Unigene50089_All|gi|225457528|ref|XP_002270022.1|/1.00E-160//PREDICTED: similar to adenosine monophosphate binding protein 1 AMPBP1 [Vitis vinifera]	Unigene50089_All//5.00E-151//AT1G20560| AAE1 (ACYL ACTIVATING ENZYME 1): AMP binding			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene5009_All	1014	2.79	0.60	1.37	9.33	10.60	4.85	3.21	2.76	2.44	-2.22E+00	3.19E-07	Down	-1.03E+00	8.85E-03		1.83E-01	3.57E-01		-9.43E-01	2.90E-07		-2.17E-01	5.31E-01		-3.98E-01	1.93E-01		Unigene5009_All|gi|152153716|sp|Q9T068.1|EPF1_ARATH//2.00E-26//RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 2; Short=EPF-like protein 2; Flags: Precursor	Unigene5009_All//2.00E-16//AT4G37810| unknown protein	Unigene5009_All//0.00E+00//TC174876				nr +
Unigene50092_All	643	5.37	1.58	1.08	4.26	2.41	2.60	4.80	3.12	1.73	-1.77E+00	1.18E-06	Down	-2.32E+00	1.21E-08	Down	-8.22E-01	2.23E-02		-7.13E-01	6.30E-02		-6.22E-01	5.11E-02		-1.47E+00	5.86E-06	Down	Unigene50092_All|gi|15450511|gb|AA596548.1|/8.00E-16//At2g46420/F11C10.11 [Arabidopsis thaliana] >gi|20197824|gb|AAD23044.2| expressed protein [Arabidopsis thaliana] >gi|27363256|gb|AA011547.1| At2g46420/F11C10.11 [Arabidopsis thaliana]	Unigene50092_All//1.00E-19//AT2G46420| unknown protein	Unigene50092_All//0.00E+00//gi|164288009|gb|ES791428.1|ES791428				nr +
Unigene50096_All	819	0.96	0.80	0.46	3.47	1.39	1.49	2.32	2.09	1.22	-2.53E-01	7.26E-01		-1.07E+00	2.10E-01		-1.32E+00	1.81E-04	Down	-1.22E+00	1.10E-03		-1.51E-01	7.30E-01		-9.34E-01	2.11E-02		Unigene50096_All|gi|297829206|ref|XP_002882485.1|/8.00E-78//peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328325|gb|EFH58744.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50096_All//2.00E-70//AT3G66654| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	Unigene50096_All//0.00E+00//DW502565		ko03040|Spliceosome	GO:0016020//GO:0016859//GO:0043231//GO:0044267	nr -
Unigene50097_All	958	0.11	0.05	0.00	1.82	1.11	0.52	0.35	0.48	0.96	-1.05E+00	6.84E-01		-6.77E+00	3.92E-01		-7.08E-01	1.44E-01		-1.81E+00	5.79E-04	Down	4.43E-01	6.31E-01		1.44E+00	2.77E-02		Unigene50097_All|gi|297829206|ref|XP_002882485.1|/5.00E-67//peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328325|gb|EFH58744.1| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50097_All//1.00E-58//AT3G66654| peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein	Unigene50097_All//0.00E+00//gi|109870781|gb|DW499757.1|DW499757			GO:0016020//GO:0016853//GO:0043231	nr -
Unigene501_All	4882	11.77	2.07	3.26	27.79	18.98	14.27	13.95	15.60	16.26	-2.51E+00	1.41E-155	Down	-1.85E+00	2.18E-102	Down	-5.50E-01	1.48E-42		-9.62E-01	1.46E-99		1.61E-01	3.83E-03		2.21E-01	1.82E-05		Unigene501_All|gi|124360549|gb|AB033126.2|/1.00E-124//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene501_All//1.00E-31//AT4G28090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene501_All//0.00E+00//TC162673				nr -
Unigene5010_All	1349	1.55	0.15	0.24	26.77	13.15	3.25	7.37	1.24	0.68	-3.37E+00	3.53E-08	Down	-2.71E+00	2.17E-06	Down	-1.03E+00	8.52E-34	Down	-3.04E+00	1.55E-131	Down	-2.57E+00	2.78E-34	Down	-3.44E+00	2.76E-47	Down	Unigene5010_All|gi|225463464|ref|XP_002272948.1|/2.00E-69//PREDICTED: similar to cytochrome B561-related [Vitis vinifera]	Unigene5010_All//2.00E-63//AT4G18260| cytochrome B561-related	Unigene5010_All//2.00E-129//CD486453				nr +
Unigene50100_All	713	16.00	44.49	29.72	26.83	38.01	29.26	53.55	72.69	20.62	1.48E+00	2.06E-42	Up	8.94E-01	9.39E-13		5.03E-01	2.07E-07		1.25E-01	3.96E-01		4.41E-01	1.59E-11		-1.38E+00	4.60E-58	Down	Unigene50100_All|gi|7431428|pir||T10242//7.00E-59//(S)-2-hydroxy-acid oxidase (EC 1.1.3.15) - cucurbit >gi|217909|dbj|BAA03131.1| glycolate oxidase [Cucurbita cv. Kurokawa Amakuri]	Unigene50100_All//8.00E-58//AT3G14415| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene50100_All//0.00E+00//TC149991		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0000166//GO:0003973//GO:0005576//GO:0005840//GO:0008152//GO:0009532//GO:0042579	nr +
Unigene50101_All	996	4.47	1.93	2.73	3.35	6.02	3.08	3.61	0.34	0.88	-1.21E+00	4.26E-05	Down	-7.12E-01	1.76E-02		8.44E-01	2.58E-04		-1.20E-01	7.35E-01		-3.43E+00	7.57E-17	Down	-2.04E+00	3.18E-10	Down	Unigene50101_All|gi|28200788|emb|CAD45375.1|/9.00E-91//potyviral helper component protease-interacting protein 2 [Solanum tuberosum subsp. andigena]	Unigene50101_All//4.00E-79//AT4G27060| TOR1 (TORTIFOLIA 1); microtubule binding	Unigene50101_All//0.00E+00//gi|78347279|gb|DT567553.1|DT567553			GO:0000902//GO:0015631//GO:0050879//GO:0005028	nr +
Unigene50102_All	1726	0.67	1.67	0.96	7.56	8.16	8.90	3.53	0.80	2.61	1.33E+00	5.21E-04	Up	5.20E-01	3.42E-01		1.10E-01	5.46E-01		2.35E-01	1.32E-01		-2.14E+00	3.05E-17	Down	-4.36E-01	3.75E-02		Unigene50102_All|gi|397254113|emb|CAE09057.1|/4.00E-90//MYB transcription factor [Eucalyptus gunnii]	Unigene50102_All//2.00E-73//AT3G08500| MYB83 (myb domain protein 83); DNA binding / transcription factor	Unigene50102_All//1.00E-20//DW508945	MYB		GO:0006350	nr -
Unigene50105_All	733	15.70	102.38	41.26	21.14	22.46	45.35	20.13	24.92	45.00	2.70E+00	5.44E-219	Up	1.39E+00	4.13E-36	Up	8.74E-02	6.13E-01		1.10E+00	2.08E-30	Up	3.08E-01	9.35E-03		1.16E+00	2.19E-38	Up	Unigene50105_All|gi|283488487|gb|ADB24765.1|/6.00E-84//UDP-D-glucose dehydrogenase [Gossypium hirsutum]	Unigene50105_All//1.00E-78//AT3G29060| UDP-glucose 6-dehydrogenase, putative	Unigene50105_All//0.00E+00//DR454465		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions	GO:0000166//GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0016166//GO:0043231//GO:0044444	nr +
Unigene50106_All	734	17.54	208.27	29.09	65.02	207.03	149.70	111.92	298.09	477.90	3.57E+00	0.00E+00	Up	7.30E-01	2.85E-09		1.67E+00	8.50E-285	Up	1.20E+00	1.61E-114	Up	1.41E+00	0.00E+00	Up	2.09E+00	0.00E+00	Up	Unigene50106_All|gi|71725939|gb|AZ39087.1|/9.00E-73//nematode resistance protein [Beta procumbens]	Unigene50106_All//6.00E-61//AT2G40000| HSPRO2 (ARABIDOPSIS ORTHOLOG OF SUGAR BEET HS1 PRO-1 2)	Unigene50106_All//0.00E+00//gi|78326054|gb|DT546328.1|DT546328			GO:0010033//GO:0042742	nr -
Unigene50107_All	696	3.76	8.66	4.21	13.60	14.94	13.95	8.20	6.43	9.67	1.20E+00	1.45E-06	Up	1.63E-01	6.59E-01		1.36E-01	5.39E-01		3.69E-02	8.75E-01		-3.52E-01	1.33E-01		2.38E-01	2.57E-01		Unigene50107_All|gi|255565107|ref|XP_002523546.1|/3.00E-16//conserved hypothetical protein [Ricinus communis] >gi|223537253|gb|EEF38885.1| conserved hypothetical protein [Ricinus communis]	Unigene50107_All//8.00E-06//AT5G35110| unknown protein	Unigene50107_All//0.00E+00//gi|164318913|gb|ES828740.1|ES828740			GO:0016853	nr -
Unigene50109_All	492	4.04	47.06	6.39	6.99	6.72	4.04	8.77	13.25	9.64	3.54E+00	4.42E-88	Up	6.60E-01	7.35E-02		-5.62E-02	8.69E-01		-7.91E-01	1.71E-02		5.96E-01	3.71E-03		1.37E-01	6.06E-01		Unigene50109_All|gi|26451087|dbj|BAC42648.1|/3.00E-26//GPI-anchored protein [Arabidopsis thaliana] >gi|28416735|gb|AAO42898.1| At5g63500 [Arabidopsis thaliana]	Unigene50109_All//2.00E-19//AT3G48860| unknown protein	Unigene50109_All//0.00E+00//gi|13245072|gb|BE052724.2|BE052724			GO:0031224//GO:0031410	nr -
Unigene5011_All	1175	0.18	0.17	0.00	3.48	1.76	0.38	1.37	0.32	0.10	-4.61E-02	9.88E-01		-7.48E+00	1.45E-01		-9.83E-01	4.68E-04		-3.18E+00	8.52E-16	Down	-2.09E+00	5.87E-05	Down	-3.75E+00	9.85E-09	Down	Unigene5011_All|gi|225463464|ref|XP_002272948.1|/3.00E-74//PREDICTED: similar to cytochrome B561-related [Vitis vinifera]	Unigene5011_All//7.00E-68//AT4G18260| cytochrome B561-related	Unigene5011_All//2.00E-129//CD486453				nr -
Unigene50110_All	795	0.53	1.53	2.41	1.75	0.91	1.08	16.33	37.75	72.81	1.54E+00	1.74E-02		2.20E+00	8.21E-05	Up	-9.48E-01	8.16E-02		-7.01E-01	2.32E-01		1.21E+00	1.88E-36	Up	2.16E+00	5.76E-162	Up	Unigene50110_All|gi|92897781|gb|AB592893.1|/1.00E-30//Heavy metal transport/detoxification protein [Medicago truncatula]	Unigene50110_All//1.00E-12//AT1G01490| heavy-metal-associated domain-containing protein				GO:0006812//GO:0043169	nr -
Unigene50112_All	806	1.17	1.26	1.45	13.78	11.41	11.32	8.92	3.32	10.87	1.06E-01	8.72E-01		3.15E-01	6.23E-01		-2.73E-01	1.22E-01		-2.84E-01	1.20E-01		-1.43E+00	7.90E-12	Down	2.86E-01	1.06E-01		Unigene50112_All|gi|18405401|ref|NP_565933.1|/1.00E-77//LBD15 (LOB DOMAIN-CONTAINING PROTEIN 15) [Arabidopsis thaliana] >gi|29427824|sp|Q8L5T5.2|LBD15_ARATH RecName: Full=LOB domain-containing protein 15; AltName: Full=ASYMMETRIC LEAVES 2-like protein 11; Short=AS2-like protein 11 >gi|17227160|gb|AAL38034.1|AF447889_1 LOB DOMAIN 15 [Arabidopsis thaliana] >gi|2651309|gb|AAB87589.1| expressed protein [Arabidopsis thaliana] >gi|91806339|gb|ABE65897.1| LOB domain protein 15/lateral organ boundaries domain protein 15 [Arabidopsis thaliana] >gi|94442507|gb|ABF19041.1| At2g40470 [Arabidopsis thaliana] >gi|219807098|dbj|BAH10555.1| ASYMMETRIC LEAVES2-like 11 protein [Arabidopsis thaliana]	Unigene50112_All//8.00E-70//AT2G40470| LBD15 (LOB DOMAIN-CONTAINING PROTEIN 15)	Unigene50112_All//0.00E+00//gi|109890411|gb|DW519375.1|DW519375		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0005488//GO:0043231	nr -
Unigene50113_All	630	41.19	79.30	37.19	37.95	68.76	78.14	101.61	273.93	353.43	9.45E-01	4.04E-33		-1.47E-01	2.39E-01		8.57E-01	7.63E-29		1.04E+00	5.61E-41	Up	1.43E+00	3.55E-267	Up	1.80E+00	0.00E+00	Up	Unigene50113_All|gi|297797531|ref|XP_002866650.1|/1.00E-110//acyl-CoA oxidase [Arabidopsis lyrata subsp. lyrata] >gi|297312485|gb|EFH42909.1| acyl-CoA oxidase [Arabidopsis lyrata subsp. lyrata]	Unigene50113_All//2.00E-111//AT5G65110| ACX2 (ACYL-COA OXIDASE 2); acyl-CoA oxidase	Unigene50113_All//0.00E+00//gi|164263576|gb|ES850747.1|ES850747		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids	GO:0009062//GO:0016634//GO:0030554//GO:0042579	nr -
Unigene50117_All	3518	0.00	64.55	21.99	0.01	0.00	0.00	0.00	0.00	0.00	1.60E+01	0.00E+00	Up	1.44E+01	0.00E+00	Up	-3.83E+00	5.55E-01		-3.83E+00	6.34E-01		null	null		null	null									ESTscan -
Unigene50118_All	220	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.52	null	null		null	null		null	null		null	null		null	null		1.27E+01	2.48E-10	Up	Unigene50118_All|gi|52783264|sp|Q9FUL4.1|RL24_PRUAV//8.00E-17//RecName: Full=60S ribosomal protein L24 >gi|10180025|gb|AAG13986.1|AF298827_1 60S ribosomal protein L24 [Prunus avium]	Unigene50118_All//6.00E-16//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome	Unigene50118_All//1.00E-49//TC133972		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene50119_All	883	16.18	3.44	1.09	18.56	14.74	14.27	25.33	4.92	12.99	-2.23E+00	5.00E-34	Down	-3.90E+00	4.13E-57	Down	-3.32E-01	1.31E-02		-3.79E-01	5.86E-03		-2.36E+00	2.97E-69	Down	-9.63E-01	8.77E-20		Unigene50119_All|gi|192913038|gb|ACF06627.1|/9.00E-78//60S ribosomal protein L24 [Elaeis guineensis]	Unigene50119_All//8.00E-53//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome	Unigene50119_All//0.00E+00//TC133972		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr -

Unigene5012_All	1813	1.33	0.39	1.32	2.91	1.82	2.44	1.12	0.99	1.67	-1.76E+00	7.43E-05	Down	-6.30E-03	9.96E-01		-6.76E-01	5.71E-03		-2.55E-01	3.94E-01		-1.75E-01	6.76E-01		5.77E-01	6.35E-02		Unigene5012_All//gi|15239979|ref|NP_201453.1|//1.00E-62//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75171133|sp|Q9FJY7.1|PP449_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g66520 >gi|10177533|dbj|BAB10928.1| selenium-binding protein-like [Arabidopsis thaliana]	Unigene5012_All//6.00E-64//AT5G66520| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene50120_All	739	155.12	64.59	80.99	32.63	34.02	37.71	12.36	9.45	4.47	-1.26E+00	1.91E-120	Down	-9.38E-01	5.63E-72		6.02E-02	6.59E-01		2.09E-01	5.70E-02		-3.88E-01	2.54E-02		-1.47E+00	6.59E-16	Down	Unigene50120_All//gi|297836126|ref|XP_002885945.1|//7.00E-27//SWIB complex BAF60b domin-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331785|gb|EFH62204.1| SWIB complex BAF60b domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene50120_All//1.00E-30//AT2G14880| SWIB complex BAF60b domain-containing protein	Unigene50120_All//0.00E+00//TC149980			GO:0043231	nr -
Unigene50121_All	1263	1.49	4.81	5.23	5.92	8.59	13.16	0.00	0.07	0.09	1.69E+00	1.91E-10	Up	1.81E+00	7.27E-12	Up	5.38E-01	1.12E-03		1.15E+00	1.30E-16	Up	6.05E+00	4.00E-01		6.56E+00	2.43E-01		Unigene50121_All//gi|257782114|gb|ACV65500.1|//1.00E-145//deoxybemigossypol-6-O-methyltransferase [Gossypium hirsutum]	Unigene50121_All//1.00E-36//AT4G35150| O-methyltransferase family 2 protein	Unigene50121_All//1.00E-102//TC141688		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene50122_All	1174	2.05	0.78	0.45	4.92	3.02	5.58	4.21	0.93	2.10	-1.40E+00	1.02E-03		-2.18E+00	8.53E-06	Down	-7.04E-01	2.29E-03		1.81E-01	4.97E-01		-2.19E+00	1.72E-14	Down	-1.00E+00	2.37E-05	Down	Unigene50122_All//gi|297818174|ref|XP_002876970.1|//1.00E-142//methyltransferase/ nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297322808|gb|EFH53229.1| methyltransferase/ nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene50122_All//2.00E-143//AT3G26410| methyltransferase/ nucleic acid binding	Unigene50122_All//0.00E+00//TC142578				nr +
Unigene50129_All	1790	0.64	0.34	0.12	18.76	11.02	6.01	3.61	1.96	1.98	-9.21E-01	1.43E-01		-2.43E+00	1.85E-03		-7.67E-01	2.95E-19		-1.64E+00	3.97E-57	Down	-8.82E-01	2.13E-05		-8.68E-01	1.78E-05		Unigene50129_All//gi|20197184|gb|AC146076.2|//0.00E+00//expressed protein [Arabidopsis thaliana]	Unigene50129_All//0.00E+00//AT2G44260| unknown protein	Unigene50129_All//0.00E+00//gi|21096631|gb|BQ408944.1|BQ408944				nr -
Unigene50131_All	890	285.53	140.05	206.30	51.55	67.56	56.23	5.51	3.80	4.48	-1.03E+00	3.91E-191	Down	-4.69E-01	4.08E-47		3.90E-01	4.03E-10		1.25E-01	1.36E-01		-5.35E-01	2.85E-02		-3.00E-01	2.23E-01		Unigene50131_All//gi|20020|emb|CAA44226.1|//2.00E-61//ribosomal protein L12-1a [Nicotiana tabacum]	Unigene50131_All//2.00E-41//AT3G27850| RPL12-C (ribosomal protein L12-c); structural constituent of ribosome	Unigene50131_All//0.00E+00//TC142682		ko03010|Ribosome	GO:0000315//GO:0003676//GO:0005198//GO:0006952//GO:0009532//GO:0009534//GO:0010467	nr -
Unigene50132_All	824	4.89	1.72	4.20	9.13	4.26	4.17	2.00	0.96	1.06	-1.51E+00	3.10E-06	Down	-2.19E-01	5.14E-01		-1.10E+00	3.12E-08	Down	-1.13E+00	9.70E-08	Down	-1.05E+00	2.20E-02		-9.12E-01	3.80E-02		Unigene50132_All//gi|297802930|ref|XP_002860349.1|//3.00E-94//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297315185|gb|EFH45608.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene50132_All//5.00E-88//AT4G31010| RNA binding				GO:0003676//GO:0043231	nr -
Unigene50133_All	775	3.98	4.64	2.47	2.89	3.51	3.21	5.18	3.67	2.31	2.21E-01	5.23E-01		-6.87E-01	6.46E-02		2.79E-01	5.33E-01		1.48E-01	7.27E-01		-4.99E-01	7.18E-02		-1.16E+00	1.67E-05	Down	Unigene50133_All//gi|255548537|ref|XP_002515325.1|//9.00E-60//ATP binding protein, putative [Ricinus communis] >gi|223545805|gb|EEF47309.1| ATP binding protein, putative [Ricinus communis]	Unigene50133_All//2.00E-05//AT4G13030| unknown protein	Unigene50133_All//5.00E-33//CO105550				nr -
Unigene50136_All	735	8.68	4.07	5.87	13.35	11.95	11.18	12.77	5.12	5.69	-1.09E+00	4.55E-06	Down	-5.66E-01	2.09E-02		-1.60E-01	4.50E-01		-2.56E-01	2.03E-01		-1.32E+00	1.36E-13	Down	-1.17E+00	1.00E-11	Down	Unigene50136_All//gi|15240059|ref|NP_199210.1|//3.00E-27//TOM22-V (TRANSLOCASE OF OUTER MEMBRANE 22-V); P-P-bond-hydrolysis-driven protein transmembrane transporter [Arabidopsis thaliana] >gi|24212685|sp|Q9FN29.3|TO222_ARATH RecName: Full=Mitochondrial import receptor subunit TOM22 homolog 2; AltName: Full=Translocase of outer membrane 22 kDa subunit homolog 2; AltName: Full=Mitochondrial import receptor subunit TOM9-2; AltName: Full=Translocase of outer membrane 9 kDa subunit TOM9-2 >gi|15529292|gb|AAK97740.1| AT5g43970/MRH10_8 [Arabidopsis thaliana] >gi|16974415|gb|AAL31133.1| AT5g43970/MRH10_8 [Arabidopsis thaliana]	Unigene50136_All//2.00E-28//AT5G43970| TOM22-V (TRANSLOCASE OF OUTER MEMBRANE 22-V); P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene50136_All//0.00E+00//TC150667			GO:0006605//GO:0008320//GO:0031966	nr +
Unigene50137_All	1863	0.00	0.05	0.00	0.67	0.81	0.46	10.51	3.97	8.92	5.77E+00	3.86E-01		null	null		2.83E-01	6.27E-01		-5.37E-01	3.94E-01		-1.40E+00	3.75E-30	Down	-2.37E-01	3.54E-02		Unigene50137_All//gi|144905184|dbj|BAF56241.1|//0.00E+00//cytochrome P450 enzyme [Pisum sativum]	Unigene50137_All//4.00E-174//AT3G13730| CYP90D1; oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding	Unigene50137_All//4.00E-08//TC169211		ko00905|Brassinosteroid biosynthesis	GO:0005506//GO:0008152//GO:0016491	nr -
Unigene50138_All	1747	0.24	0.12	0.00	4.62	3.15	32.06	2.86	6.22	8.78	-1.05E+00	3.65E-01		-7.90E+00	1.56E-02		-5.51E-01	4.29E-03		2.79E+00	1.22E-181	Up	1.12E+00	2.78E-12	Up	1.62E+00	8.17E-30	Up	Unigene50138_All//gi|224053975|ref|XP_002298066.1|//3.00E-55//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222845324|gb|EEE82871.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene50138_All//3.00E-36//AT5G52020| AP2 domain-containing protein	Unigene50138_All//0.00E+00//TC136174	AP2-EREBP		GO:0001071//GO:0006351//GO:0006952//GO:0010468//GO:0030528//GO:0043231	nr -
Unigene50139_All	1411	0.85	6.28	0.98	3.32	2.56	8.93	5.96	5.75	7.28	2.88E+00	4.30E-28	Up	2.02E-01	7.12E-01		-3.73E-01	1.91E-01		1.43E+00	1.72E-17	Up	-5.34E-02	7.91E-01		2.89E-01	7.19E-02		Unigene50139_All//gi|27311725|gb|AA000828.1|//2.00E-29//Unknown protein [Arabidopsis thaliana] >gi|30725702|gb|AAP37873.1| At3g25590 [Arabidopsis thaliana]	Unigene50139_All//3.00E-22//AT3G25590| unknown protein	Unigene50139_All//0.00E+00//DW503739				nr -
Unigene5014_All	845	1.80	4.62	1.95	30.89	28.44	28.65	184.43	374.43	278.45	1.36E+00	2.61E-05	Up	1.22E-01	8.08E-01		-1.19E-01	3.27E-01		-1.09E-01	3.93E-01		1.02E+00	1.15E-287	Up	5.94E-01	2.04E-86		Unigene5014_All//gi|224087478|ref|XP_002308177.1|//1.00E-27//predicted protein [Populus trichocarpa] >gi|222854153|gb|EEE91700.1| predicted protein [Populus trichocarpa]	Unigene5014_All//1.00E-06//AT5G02090| unknown protein	Unigene5014_All//0.00E+00//TC152172				nr -
Unigene50141_All	1477	1.74	1.51	1.62	2.23	1.75	2.60	2.00	3.14	8.17	-2.02E-01	6.10E-01		-9.75E-02	8.08E-01		-3.48E-01	3.22E-01		2.24E-01	5.38E-01		6.49E-01	9.49E-03		2.03E+00	7.73E-32	Up	Unigene50141_All//gi|289707887|gb|ADD16954.1|//1.00E-125//SAC-like protein [Brassica rapa]	Unigene50141_All//2.00E-123//AT3G54160| RHD4 (ROOT HAIR DEFECTIVE4); phosphatidylinositol-4,5-bisphosphate 5-phosphatase/ phosphatidylinositol-4-phosphate phosphatase	Unigene50141_All//5.00E-161//gi|48881053|gb|CO132075.1|CO132075				nr -
Unigene50142_All	1778	0.94	1.45	0.69	3.11	1.18	0.84	4.07	4.44	4.53	6.26E-01	1.14E-01		-4.51E-01	3.99E-01		-1.40E+00	8.04E-09	Down	-1.89E+00	7.43E-12	Down	1.28E-01	5.67E-01		1.55E-01	4.36E-01		Unigene50142_All//gi|295311688|ref|YP_003387360.1|//2.00E-20//NADH dehydrogenase subunit 1 [Cucurbita pepo] >gi|259156816|gb|ACV96677.1| NADH dehydrogenase subunit 1 [Cucurbita pepo]	Unigene50142_All//1.00E-17//ATMG01275| Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C.	Unigene50142_All//0.00E+00//TC134059		ko00190|Oxidative phosphorylation	GO:0005746//GO:0022904//GO:0031224//GO:0031410//GO:0050136//GO:0051234	nr +
Unigene50143_All	616	10.79	9.54	10.81	7.68	6.76	5.79	5.77	1.90	3.04	-1.77E-01	4.70E-01		2.50E-03	9.90E-01		-1.84E-01	5.56E-01		-4.08E-01	1.62E-01		-1.60E+00	3.02E-07	Down	-9.24E-01	1.10E-03		Unigene50143_All//gi|15226866|ref|NP_178316.1|//5.00E-54//AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding >gi|41059987|emb|CAF18564.1| ID1-like zinc finger protein 2 [Arabidopsis thaliana]	Unigene50143_All//2.00E-45//AT2G02070| AtIDD5 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding	Unigene50143_All//0.00E+00//ES813407	C2H2		GO:0001071//GO:0009536//GO:0010468//GO:0046914	nr -
Unigene50144_All	1435	4.48	5.72	1.71	2.53	4.58	3.24	0.00	0.06	0.00	3.51E-01	9.16E-02		-1.39E+00	4.04E-08	Down	8.55E-01	9.18E-05		3.55E-01	2.37E-01		5.87E+00	4.00E-01		null	null		Unigene50144_All//gi|22328861|ref|NP_193906.2|//0.00E+00//ATML1 (MERISTEM LAYER 1); DNA binding / sequence-specific DNA binding / transcription factor [Arabidopsis thaliana] >gi|79325215|ref|NP_001031692.1| ATML1 (MERISTEM LAYER 1); DNA binding / sequence-specific DNA binding / transcription factor [Arabidopsis thaliana] >gi|75330714|sp|Q8RWU4.1|ATML1_ARATH RecName: Full=Homeobox-leucine zipper protein MERISTEM L1; AltName: Full=Homeodomain transcription factor ATML1; AltName: Full=HD-ZIP protein ATML1 >gi|110739777|dbj|BAF01795.1| L1 specific homeobox gene ATML1/ovule-specific homeobox protein A20 [Arabidopsis thaliana]	Unigene50144_All//0.00E+00//AT4G21750| ATML1 (MERISTEM LAYER 1); DNA binding / sequence-specific DNA binding / transcription factor	Unigene50144_All//0.00E+00//TC151822	HB		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0008544//GO:0009793//GO:0010468//GO:0043231//GO:0043234//GO:0044267	nr -
Unigene50145_All	1169	0.81	2.64	3.10	0.55	3.45	2.70	0.40	0.82	3.24	1.71E+00	8.87E-06	Up	1.94E+00	2.14E-07	Up	2.64E+00	2.05E-13	Up	2.29E+00	1.44E-08	Up	1.05E+00	1.03E-01		3.02E+00	3.89E-16	Up	Unigene50145_All//gi|297819764|ref|XP_002877765.1|//1.00E-107//UDP-glucosyl transferase 72E1 [Arabidopsis lyrata subsp. lyrata] >gi|297323603|gb|EFH54024.1| UDP-glucosyl transferase 72E1 [Arabidopsis lyrata subsp. lyrata]	Unigene50145_All//5.00E-109//AT3G50740| UGT72E1 (UDP-glucosyl transferase 72E1); UDP-glycosyltransferase/ coniferyl-alcohol glucosyltransferase/ transferase, transferring glycosyl groups	Unigene50145_All//0.00E+00//ES845892		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene50146_All	671	15.13	97.64	126.90	15.52	6.11	3.84	1.95	2.68	0.18	2.69E+00	3.97E-190	Up	3.07E+00	9.63E-278	Up	-1.35E+00	2.69E-15	Down	-2.02E+00	9.32E-24	Down	4.56E-01	3.20E-01		-3.46E+00	7.84E-07	Down	Unigene50146_All//gi|83853981|gb|AB574922.1|//2.00E-64//pathogenesis-related protein 1a [Malus x domestica]	Unigene50146_All//2.00E-59//AT2G14610| PR1 (PATHOGENESIS-RELATED GENE 1)	Unigene50146_All//0.00E+00//gi|109890249|gb|DW519213.1|DW519213		ko04626|Plant-pathogen interaction	GO:0009814//GO:0030312//GO:0033273	nr +
Unigene50149_All	1542	0.34	0.53	0.28	1.74	1.97	0.88	6.06	2.63	23.20	6.32E-01	4.02E-01		-2.96E-01	7.50E-01		1.72E-01	6.83E-01		-9.89E-01	9.79E-03		-1.20E+00	7.40E-12	Down	1.94E+00	2.17E-87	Up	Unigene50149_All//gi|224130624|ref|XP_002320887.1|//1.00E-178//cytochrome P450 [Populus trichocarpa] >gi|222861660|gb|EEE99202.1| cytochrome P450 [Populus trichocarpa]	Unigene50149_All//1.00E-163//AT3G61880| CYP78A9 (CYTOCHROME P450 78A9); monooxygenase/ oxygen binding	Unigene50149_All//0.00E+00//gi|164252486|gb|ES814546.1|ES814546		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +

Unigene50151_All	1139	1.65	3.03	1.31	1.44	2.66	3.09	5.38	6.90	36.34	8.71E-01	9.04E-03		-3.37E-01	5.04E-01		8.82E-01	1.20E-02		1.10E+00	8.72E-04	Up	3.58E-01	6.16E-02		2.76E+00	3.00E-154	Up	Unigene50151_All//gi|210111348|gb|ACJ07153.1|//5.00E-45//R2R3 MYB transcription factor [Gossypium hirsutum]	Unigene50151_All//7.00E-37//AT5G62470| MYB96 (myb domain protein 96); DNA binding / transcription factor	Unigene50151_All//2.00E-36//TC147251	MYB		GO:0003676//GO:0006970//GO:0009725//GO:0010468//GO:0043231	nr +
Unigene50154_All	441	3.32	2.64	4.83	10.28	5.93	1.64	6.62	2.09	4.16	-3.30E-01	5.56E-01		5.40E-01	2.45E-01		-7.93E-01	2.83E-03		-2.65E+00	1.38E-14	Down	-1.67E+00	2.16E-06	Down	-6.71E-01	3.29E-02		Unigene50154_All//gi|159895665|gb|ABX10443.1|//4.00E-36//phosphatidyl serine synthase [Gossypium hirsutum]	Unigene50154_All//3.00E-25//AT1G15110| phosphatidyl serine synthase family protein	Unigene50154_All//0.00E+00//gi|21093611|gb|BQ405924.1|BQ405924		ko00564|Glycerophospholipid metabolism	GO:0006658//GO:0044464	nr +
Unigene50155_All	1170	0.04	3.16	2.69	0.34	1.30	4.86	0.51	1.96	0.54	6.14E+00	1.65E-19	Up	5.91E+00	6.53E-16	Up	1.93E+00	8.33E-04	Up	3.84E+00	8.55E-25	Up	1.96E+00	2.90E-06	Up	1.07E-01	9.01E-01		Unigene50155_All//gi|297797657|ref|XP_002866713.1|//1.00E-37//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297312548|gb|EFH42972.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene50155_All//2.00E-73//AT4G24910| unknown protein	Unigene50155_All//0.00E+00//TC174674				nr +
Unigene50156_All	969	0.43	0.68	0.00	3.44	2.88	2.10	3.10	1.90	1.19	6.54E-01	4.48E-01		-8.75E+00	1.56E-02		-2.59E-01	4.89E-01		-7.16E-01	3.51E-02		-7.07E-01	2.81E-02		-1.38E+00	2.29E-05	Down	Unigene50156_All//gi|15222980|ref|NP_172845.1|//9.00E-27//remorin family protein [Arabidopsis thaliana] >gi|5080768|gb|AAD39278.1|AC007576_1 Hypothetical protein [Arabidopsis thaliana]	Unigene50156_All//1.00E-14//AT1G13920| remorin family protein	Unigene50156_All//2.00E-20//DW512129				nr +
Unigene50157_All	592	0.53	4.37	2.79	0.42	0.70	1.83	0.93	5.51	3.16	3.04E+00	4.88E-09	Up	2.39E+00	1.28E-04	Up	7.30E-01	5.86E-01		2.12E+00	4.32E-03		2.57E+00	1.19E-11	Up	1.77E+00	8.08E-05	Up	Unigene50157_All//gi|83356299|gb|ABC16634.1|//8.00E-74//protein phosphatase PP2C [Gossypium hirsutum]	Unigene50157_All//4.00E-42//AT3G11410| PP2CA (ARABIDOPSIS THALIANA PROTEIN PHOSPHATASE 2CA); protein binding / protein serine/threonine phosphatase	Unigene50157_All//0.00E+00//TC177550			GO:0004721//GO:0006464//GO:0043169//GO:0043234	nr +
Unigene50158_All	541	7.06	0.84	5.22	28.18	12.79	4.34	0.47	0.00	0.00	-3.07E+00	2.60E-13	Down	-4.37E-01	1.95E-01		-1.14E+00	3.97E-17	Down	-2.70E+00	4.58E-49	Down	-8.87E+00	4.03E-02		-8.87E+00	3.04E-02								
Unigene50159_All	629	21.71	15.87	22.35	69.38	67.01	71.73	48.60	32.56	23.75	-4.52E-01	3.04E-03		4.19E-02	8.02E-01		-5.01E-02	6.12E-01		4.82E-02	6.29E-01		-5.78E-01	3.63E-11		-1.03E+00	6.96E-30	Down	Unigene50159_All//gi|297850070|ref|XP_002892916.1|//7.00E-43//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297338758|gb|EFH69175.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	Unigene50159_All//4.00E-17//AT1G16610| SR45; RNA binding / protein binding	Unigene50159_All//0.00E+00//TC144391		ko03040|Spliceosome	GO:0000377//GO:0005488//GO:0009756//GO:0016604	nr -
Unigene50160_All	731	0.00	0.00	0.00	3.82	3.39	1.79	63.10	42.31	139.68	null	null		null	null		-1.70E-01	6.78E-01		-1.09E+00	3.65E-03		-5.77E-01	2.28E-16		1.15E+00	9.35E-115	Up	Unigene50160_All//gi|224111880|ref|XP_002316010.1|//7.00E-75//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene50160_All//8.00E-37//AT2G46960| CYP709B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene50160_All//1.00E-153//TC154355		ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0016491	nr +
Unigene50162_All	994	1.89	3.42	2.57	40.14	35.41	13.09	1.40	0.63	0.12	8.50E-01	1.15E-02		4.40E-01	2.98E-01		-1.81E-01	3.66E-02		-1.62E+00	2.80E-66	Down	-1.15E+00	2.40E-02		-3.55E+00	2.28E-07	Down	Unigene50162_All//gi|18405248|ref|NP_564679.1|//3.00E-52//PRA7 [Arabidopsis thaliana] >gi|75169467|sp|Q8C889.1|PRI1F2_ARATH RecName: Full=PRA1 family protein F2; Short=AtPRA1.F2	Unigene50162_All//2.00E-35//AT1G55190| PRA7	Unigene50162_All//2.00E-101//TC175940			GO:0005488//GO:0006810//GO:0043231	nr -
Unigene50163_All	921	1.48	0.99	0.58	3.73	1.20	1.28	3.67	4.13	2.12	-5.77E-01	3.19E-01		-1.35E+00	2.93E-02		-1.64E+00	4.27E-07	Down	-1.55E+00	6.75E-06	Down	1.69E-01	6.13E-01		-7.93E-01	6.10E-03		Unigene50163_All//gi|255591362|ref|XP_002535496.1|//2.00E-16//conserved hypothetical protein [Ricinus communis] >gi|255539632|ref|XP_002536626.1| conserved hypothetical protein [Ricinus communis] >gi|223519048|gb|EEF25756.1| conserved hypothetical protein [Ricinus communis] >gi|223522900|gb|EEF26887.1| conserved hypothetical protein [Ricinus communis]		Unigene50163_All//0.00E+00//TC178361				nr -
Unigene50169_All	898	0.29	1.52	2.13	1.33	1.23	0.65	48.82	30.77	26.13	2.39E+00	4.04E-04	Up	2.87E+00	2.94E-06	Up	-1.18E-01	8.27E-01		-1.03E+00	1.06E-01		-6.66E-01	6.08E-20		-9.02E-01	4.67E-34		Unigene50169_All//gi|2098713|gb|AAB57671.1|//1.00E-122//pectinesterase [Citrus sinensis]	Unigene50169_All//1.00E-112//AT2G45220| pectinesterase family protein	Unigene50169_All//0.00E+00//TC149971		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene50170_All	816	24.11	9.94	17.68	11.72	14.64	7.64	0.52	0.26	0.68	-1.28E+00	1.28E-21	Down	-4.47E-01	5.35E-04		3.21E-01	5.43E-02		-6.18E-01	6.83E-04		-1.02E+00	3.50E-01		4.00E-01	6.36E-01		Unigene50170_All//gi|13899099|gb|AAK48971.1|AF370544_1/6.00E-92//cyclin delta-3 [Arabidopsis thaliana] >gi|20148339|gb|AAM10060.1| cyclin delta-3 [Arabidopsis thaliana] >gi|110738184|dbj|BAF01023.1| cyclin delta-3 [Arabidopsis thaliana]	Unigene50170_All//3.00E-86//AT4G34090| unknown protein	Unigene50170_All//0.00E+00//TC148727			GO:0009532	nr +
Unigene50171_All	593	5.91	3.59	6.73	5.63	6.50	4.87	4.42	4.09	0.74	-7.20E-01	2.82E-02		1.88E-01	5.89E-01		2.09E-01	5.68E-01		-2.08E-01	6.08E-01		-1.13E-01	7.60E-01		-2.58E+00	6.10E-10	Down	Unigene50171_All//gi|224117064|ref|XP_002317467.1|//6.00E-15//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222860532|gb|EEE98079.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene50171_All//3.00E-15//AT1G53270| ABC transporter family protein	Unigene50171_All//0.00E+00//TC158367			GO:0000166//GO:0015405//GO:0017111	nr -
Unigene50172_All	660	3.41	3.69	0.32	3.85	5.27	3.90	1.15	3.42	0.36	1.12E-01	7.78E-01		-3.40E+00	2.44E-08	Down	4.53E-01	1.90E-01		1.91E-02	9.61E-01		1.57E+00	9.44E-05	Up	-1.67E+00	2.39E-02		Unigene50172_All//gi|15238973|ref|NP_196677.1|//2.00E-68//APT5 (Adenine phosphoribosyltransferase 5); adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|8953378|emb|CAB96651.1| adenine phosphoribosyltransferase-like protein [Arabidopsis thaliana]	Unigene50172_All//1.00E-69//AT5G11160| APT5 (Adenine phosphoribosyltransferase 5); adenine phosphoribosyltransferase	Unigene50172_All//0.00E+00//ES845532		ko00230|Purine metabolism	GO:0015103//GO:0016020//GO:0016763//GO:0043096//GO:0044444	nr -
Unigene50173_All	834	2.89	0.73	0.77	2.39	1.57	5.96	0.35	0.25	1.29	-1.98E+00	1.49E-05	Down	-1.91E+00	5.02E-05	Down	-6.07E-01	1.77E-01		1.32E+00	1.71E-06	Up	-5.02E-01	6.77E-01		1.86E+00	2.85E-03		Unigene50173_All//gi|224127045|ref|XP_002329370.1|//5.00E-77//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222870120|gb|EEF07551.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene50173_All//7.00E-32//AT2G20880| AP2 domain-containing transcription factor, putative	Unigene50173_All//4.00E-52//CO106720	AP2-EREBP		GO:0006350//GO:0009743//GO:0043231	nr +
Unigene50174_All	800	8.18	0.95	7.52	6.72	2.37	1.58	4.92	1.83	1.10	-3.11E+00	1.18E-22	Down	-1.20E-01	6.19E-01		-1.51E+00	1.40E-09	Down	-2.09E+00	4.36E-13	Down	-1.43E+00	7.98E-07	Down	-2.17E+00	5.96E-12	Down	Unigene50174_All//gi|115469808|ref|NP_001058503.1|//4.00E-42//Os06g0703900 [Oryza sativa Japonica Group] >gi|113596543|dbj|BAF20417.1| Os06g0703900 [Oryza sativa Japonica Group]	Unigene50174_All//1.00E-31//AT3G13040| myb family transcription factor	Unigene50174_All//0.00E+00//TC143314	G2-like		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene50176_All	522	23.75	11.45	21.22	4.87	6.46	3.46	0.00	0.00	0.00	-1.05E+00	2.14E-10	Down	-1.63E-01	3.91E-01		4.10E-01	2.56E-01		-4.92E-01	2.34E-01		null	null		null	null		Unigene50176_All//gi|48310646|gb|AAT41859.1|//1.00E-13//At1g73885 [Arabidopsis thaliana]	Unigene50176_All//4.00E-07//AT1G73885| unknown protein	Unigene50176_All//1.00E-128//TC149612			GO:0009507	nr -
Unigene50178_All	252	0.42	0.00	0.42	0.00	0.41	1.08	21.98	31.51	7.11	-8.70E+00	3.71E-01		2.55E-02	9.99E-01		8.68E+00	4.55E-01		1.01E+01	7.02E-02		5.20E-01	4.83E-03		-1.63E+00	1.70E-11	Down	Unigene50178_All//gi|124360168|gb|ABN08184.1|//8.00E-24//General substrate transporter [Medicago truncatula] >gi|124361038|gb|ABN09010.1| General substrate transporter [Medicago truncatula]	Unigene50178_All//1.00E-22//AT5G18840| sugar transporter, putative	Unigene50178_All//6.00E-138//TC162666			GO:0006810//GO:0008152//GO:0016628//GO:0022857//GO:0031224	nr +
Unigene5018_All	780	5.17	3.70	3.00	2.43	3.27	0.75	2.11	2.68	1.38	-4.80E-01	1.20E-01		-7.82E-01	1.37E-02		4.29E-01	3.10E-01		-1.69E+00	6.39E-04	Down	3.42E-01	4.15E-01		-6.16E-01	1.63E-01		Unigene5018_All//gi|115480279|ref|NP_001063733.1|//2.00E-19//Os09g0527900 [Oryza sativa Japonica Group] >gi|113631966|dbj|BAF25647.1| Os09g0527900 [Oryza sativa Japonica Group]	Unigene5018_All//6.00E-08//AT4G38960| zinc finger (B-box type) family protein	Unigene5018_All//2.00E-26//TC137101	Orphans			nr +
Unigene50182_All	640	0.16	0.00	0.83	0.00	0.22	0.42	15.99	2.48	6.41	-7.35E+00	3.71E-01		2.35E+00	5.87E-02		7.75E+00	3.18E-01		8.73E+00	7.02E-02		-2.69E+00	4.97E-37	Down	-1.32E+00	3.27E-15	Down	Unigene50182_All//gi|297814259|ref|XP_002875013.1|//1.00E-56//IQ-domain 17 [Arabidopsis lyrata subsp. lyrata] >gi|297320850|gb|EFH51272.1| IQ-domain 17 [Arabidopsis lyrata subsp. lyrata]	Unigene50182_All//3.00E-52//AT4G00820| iqd17 (IQ-domain 17); calmodulin binding	Unigene50182_All//0.00E+00//DR460766				nr -
Unigene50183_All	2034	0.05	0.10	0.16	0.22	0.41	0.22	12.35	2.24	4.97	9.54E-01	6.21E-01		1.61E+00	3.04E-01		8.82E-01	2.92E-01		1.04E-02	1.00E+00		-2.46E+00	1.55E-81	Down	-1.31E+00	8.84E-36	Down	Unigene50183_All//gi|297814259|ref|XP_002875013.1|//1.00E-156//IQ-domain 17 [Arabidopsis lyrata subsp. lyrata] >gi|297320850|gb|EFH51272.1| IQ-domain 17 [Arabidopsis lyrata subsp. lyrata]	Unigene50183_All//4.00E-134//AT4G00820| iqd17 (IQ-domain 17); calmodulin binding	Unigene50183_All//0.00E+00//gi|78350287|gb|DT570561.1|DT570561				nr +
Unigene50185_All	758	6.21	19.79	5.41	2.17	1.91	2.09	0.45	0.11	0.21	1.67E+00	2.52E-24	Up	-2.00E-01	5.20E-01		-1.85E-01	7.46E-01		-5.65E-02	9.28E-01		-2.02E+00	1.36E-01		-1.09E+00	3.55E-01		Unigene50185_All//gi|15220448|ref|NP_172015.1|//7.00E-89//HDG2 (HOMEODOMAIN GLABROUS 2); DNA binding / transcription factor [Arabidopsis thaliana] >gi|30679181|ref|NP_849596.1| HDG2 (HOMEODOMAIN GLABROUS 2); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75332091|sp|Q94C37.1|HDG2_ARATH RecName: Full=Homeobox-leucine zipper protein HDG2; AltName: Full=Homeodomain transcription factor HDG2; AltName: Full=HD-ZIP protein HDG2; AltName: Full=Protein HOMEODOMAIN GLABROUS 2; AltName: Full=Homeodomain GLABRA 2-like protein 2 >gi|14334996|gb|AAK59762.1| At1g05230/YUP8H12_16 [Arabidopsis thaliana] >gi|20147145|gb|AAM10289.1| At1g05230/YUP8H12_16 [Arabidopsis thaliana] >gi|222423025|dbj|BAH19495.1| AT1G05230 [Arabidopsis thaliana]	Unigene50185_All//2.00E-83//AT1G05230| HDG2 (HOMEODOMAIN GLABROUS 2); DNA binding / transcription factor	Unigene50185_All//0.00E+00//gi|13350562|gb|BG440910.1|BG440910	HB		GO:0000904//GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +

Unigene50187_All	823	212.27	94.44	172.69	23.79	27.11	15.75	0.10	0.05	0.53	-1.17E+00	6.76E-162	Down	-2.98E-01	2.92E-14		1.89E-01	1.32E-01		-5.95E-01	8.57E-07		-1.02E+00	7.24E-01		2.37E+00	4.04E-02		Unigene50187_All//gi|20453145|gb|AAM19814.1|/6.00E-81//AT3g10060/T22K18_11 [Arabidopsis thaliana] >gi|21689613|gb|AAW67428.1| AT3g10060/T22K18_11 [Arabidopsis thaliana]	Unigene50187_All//2.00E-82//AT3G10060| immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative	Unigene50187_All//2.00E-149//gi|54118735|gb|CO494244.1|CO494244			GO:0004672//GO:0005527//GO:0006464//GO:0009534//GO:0016859//GO:0032559	nr -
Unigene50189_All	1829	0.43	19.09	0.29	1.12	1.77	1.19	0.51	2.10	3.90	5.48E+00	1.53E-175	Up	-5.60E-01	4.96E-01		6.64E-01	5.33E-02		8.60E-02	8.62E-01		2.05E+00	1.51E-10	Up	2.94E+00	5.64E-29	Up	Unigene50189_All//gi|104294986|gb|ABF72002.1|/1.00E-78//U-box domain-containing protein [Musa acuminata]	Unigene50189_All//7.00E-21//AT1G20780| SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein ligase	Unigene50189_All//2.00E-161//CA994237		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene50192_All	1301	1455.57	617.38	1053.74	237.24	272.81	200.96	9.91	15.45	10.93	-1.24E+00	0.00E+00	Down	-4.66E-01	0.00E+00		2.02E-01	8.59E-17		-2.39E-01	2.23E-18		6.41E-01	5.39E-09		1.41E-01	3.38E-01		Unigene50192_All//gi|15233985|ref|NP_192703.1|//2.00E-75//ATPD (ATP SYNTHASE DELTA-SUBUNIT GENE); hydrogen ion transporting ATP synthase, rotational mechanism / proton-transporting ATPase, rotational mechanism [Arabidopsis thaliana] >gi|7267660|emb|CAB78088.1| H+-transporting ATP synthase-like protein [Arabidopsis thaliana] >gi|7321084|emb|CAB82132.1| H+-transporting ATP synthase-like protein [Arabidopsis thaliana] >gi|17473800|gb|AAL38334.1| H+-transporting ATP synthase-like protein [Arabidopsis thaliana] >gi|21386885|gb|AAM47896.1| H+-transporting ATP synthase-like protein [Arabidopsis thaliana] >gi|21593484|gb|AAM65451.1| H+-transporting ATP synthase-like protein [Arabidopsis thaliana]	Unigene50192_All//8.00E-73//AT4G09650| ATPD (ATP SYNTHASE DELTA-SUBUNIT GENE); hydrogen ion transporting ATP synthase, rotational mechanism / proton-transporting ATPase, rotational mechanism	Unigene50192_All//0.00E+00//TC138985		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis	GO:0006754//GO:0006818//GO:0006952//GO:0009526//GO:0009534//GO:0009570//GO:0009767//GO:0015078//GO:0019829//GO:0033178	nr +
Unigene50194_All	891	5.05	0.68	0.00	7.44	14.69	4.26	10.20	0.94	3.53	-2.89E+00	1.03E-14	Down	-1.23E+01	8.78E-25	Down	9.82E-01	3.86E-11		-8.04E-01	3.30E-04		-3.44E+00	6.28E-42	Down	-1.53E+00	7.97E-17	Down	Unigene50194_All//gi|89001041|gb|AB059110.1|/4.00E-54//At3g05980 [Arabidopsis thaliana]	Unigene50194_All//1.00E-42//AT3G05980| unknown protein					nr -
Unigene50196_All	695	0.00	0.36	0.31	3.73	3.37	2.99	8.15	6.49	2.75	8.51E+00	7.85E-02		8.26E+00	1.41E-01		-1.46E-01	7.47E-01		-3.18E-01	4.64E-01		-3.28E-01	1.63E-01		-1.57E+00	3.68E-11	Down	Unigene50196_All//gi|224111284|ref|XP_002332949.1|/2.00E-14//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834261|gb|EEE72738.1| cc-nbs-lrr resistance protein [Populus trichocarpa]						nr -
Unigene50197_All	444	37.00	68.02	90.67	50.49	80.74	97.55	64.09	73.71	81.47	8.78E-01	4.71E-18		1.29E+00	9.47E-43	Up	6.77E-01	4.48E-16		9.50E-01	4.26E-31		2.02E-01	2.25E-02		3.46E-01	8.88E-06		Unigene50197_All//gi|18422747|ref|NP_568675.1|/1.00E-75//LON2 (LON PROTEASE 2); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase [Arabidopsis thaliana] >gi|3914002|sp|O64948.1|LONP2_ARATH RecName: Full=Lon protease homolog 2, peroxisomal >gi|2935279|gb|AAC05085.1| Lon protease [Arabidopsis thaliana] >gi|9759446|dbj|BAB10243.1| mitochondrial Lon protease homolog 1 precursor [Arabidopsis thaliana]	Unigene50197_All//7.00E-77//AT5G47040| LON2 (LON PROTEASE 2); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase	Unigene50197_All//0.00E+00//TC163653			GO:0003676//GO:0004175//GO:0016558//GO:0019538//GO:0031980//GO:0032559//GO:0042623//GO:0044439//GO:0048528	nr +
Unigene50198_All	459	11.97	7.73	5.80	17.47	11.78	14.17	45.04	35.88	24.13	-6.31E-01	1.29E-02		-1.05E+00	9.68E-05	Down	-5.69E-01	3.17E-03		-3.02E-01	1.71E-01		-3.28E-01	2.73E-03		-9.01E-01	1.69E-16		Unigene50198_All//gi|297812799|ref|XP_002874283.1|/1.00E-77//TIF3B1 [Arabidopsis lyrata subsp. lyrata] >gi|297320120|gb|EFH50542.1| TIF3B1 [Arabidopsis lyrata subsp. lyrata]	Unigene50198_All//1.00E-78//AT5G27640| TIF3B1 (TRANSLATION INITIATION FACTOR 3B1); nucleic acid binding / translation initiation factor	Unigene50198_All//0.00E+00//ES826703			GO:0006412//GO:0008135//GO:0043231//GO:0043234//GO:0044444	nr -
Unigene50199_All	2209	0.14	0.18	0.12	0.25	0.69	0.80	5.00	12.20	138.02	3.69E-01	7.24E-01		-2.38E-01	8.50E-01		1.47E+00	7.97E-03		1.68E+00	1.32E-03		1.29E+00	3.47E-36	Up	4.79E+00	0.00E+00	Up	Unigene50199_All//gi|297843928|ref|XP_002889845.1|/1.00E-172//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335687|gb|EFH66104.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50199_All//8.00E-174//AT1G11050| protein kinase family protein	Unigene50199_All//0.00E+00//TC140751		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr -
Unigene5020_All	826	24.07	11.84	9.93	43.60	35.19	34.56	43.41	20.64	22.96	-1.02E+00	1.61E-15	Down	-1.28E+00	6.36E-21	Down	-3.09E-01	2.36E-04		-3.36E-01	1.33E-04		-1.07E+00	5.62E-36	Down	-9.19E-01	6.98E-29		Unigene5020_All//gi|15226590|ref|NP_179752.1|//2.00E-50//40S ribosomal protein S25 (RPS25B) [Arabidopsis thaliana] >gi|30580492|sp|Q8S182.1|RS252_ARATH RecName: Full=40S ribosomal protein S25-2 >gi|4567232|gb|AAD23647.1| 40S ribosomal protein S25 [Arabidopsis thaliana] >gi|15081638|gb|AAK82474.1| At2g21580/F2G1.15 [Arabidopsis thaliana] >gi|20147155|gb|AAM10294.1| At2g21580/F2G1.15 [Arabidopsis thaliana]	Unigene5020_All//8.00E-30//AT2G21580| 40S ribosomal protein S25 (RPS25B)	Unigene5020_All//0.00E+00//TC158556		ko03010|Ribosome		nr -
Unigene50200_All	938	2.01	0.97	0.68	3.45	0.88	0.43	1.35	5.08	0.51	-1.05E+00	2.79E-02		-1.56E+00	2.80E-03		-1.97E+00	1.61E-08	Down	-2.99E+00	6.33E-12	Down	1.91E+00	7.79E-12	Up	-1.41E+00	8.06E-03		Unigene50200_All//gi|223452526|gb|ACM89590.1|//2.00E-59//disease resistance protein [Glycine max]	Unigene50200_All//5.00E-47//AT1G58190| AtRLP9 (Receptor Like Protein 9); protein binding	Unigene50200_All//3.00E-38//DN828155		ko04626|Plant-pathogen interaction		nr +
Unigene50201_All	1184	0.80	0.81	1.17	1.98	1.31	4.12	1.36	1.77	1.11	3.18E-02	9.83E-01		5.56E-01	3.62E-01		-5.95E-01	1.48E-01		1.06E+00	1.00E-04	Up	3.79E-01	3.78E-01		-2.89E-01	5.47E-01		Unigene50201_All//gi|115473803|ref|NP_001060500.1|//1.00E-87//Os07g0655900 [Oryza sativa Japonica Group] >gi|23617115|dbj|BAC20797.1| integral membrane protein-like [Oryza sativa Japonica Group] >gi|113612036|dbj|BAF22414.1| Os07g0655900 [Oryza sativa Japonica Group]	Unigene50201_All//1.00E-74//AT1G03260| LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: SNARE associated Golgi protein (InterPro:IPR015414); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19070.1); Has 3432 Blast hits to 3432 proteins in 730 species: Archae - 8; Bacteria - 1831; Metazoa - 239; Fungi - 87; Plants - 162; Viruses - 0; Other Eukaryotes - 1105 (source: NCBI BLink).	Unigene50201_All//0.00E+00//DT460001			GO:0031410	nr +
Unigene50202_All	478	0.22	0.00	0.00	3.65	3.60	3.97	5.93	11.98	1.42	-7.77E+00	3.71E-01		-7.77E+00	3.92E-01		-1.81E-02	9.58E-01		1.22E-01	8.06E-01		1.02E+00	6.18E-06	Up	-2.06E+00	2.30E-08	Down	Unigene50202_All//gi|297735889|emb|CBI18658.3|//1.00E-11//unnamed protein product [Vitis vinifera]						nr -
Unigene50203_All	1253	0.08	0.04	0.00	8.11	5.61	4.47	4.93	2.84	2.23	-1.05E+00	6.84E-01		-6.38E+00	3.92E-01		-5.33E-01	1.54E-03		-8.60E-01	1.00E-06		-7.97E-01	1.69E-04		-1.15E+00	8.03E-08	Down	Unigene50203_All//gi|297597748|ref|NP_001044465.2|//5.00E-47//Os01g0784900 [Oryza sativa Japonica Group] >gi|53792455|dbj|BAD53363.1| bHLH transcription factor-like protein [Oryza sativa Japonica Group] >gi|255673738|dbj|BAF06379.2| Os01g0784900 [Oryza sativa Japonica Group]	Unigene50203_All//9.00E-46//AT1G61660| basic helix-loop-helix (bHLH) family protein	Unigene50203_All//5.00E-105//TC158064	bHLH		GO:0010468//GO:0043231	nr -
Unigene50204_All	1220	0.34	1.25	0.09	11.64	9.06	8.48	3.74	0.38	0.56	1.86E+00	1.61E-03		-1.97E+00	1.51E-01		-3.61E-01	1.24E-02		-4.57E-01	1.89E-03		-3.31E+00	1.21E-20	Down	-2.75E+00	6.27E-18	Down	Unigene50204_All//gi|156739648|gb|ABR93485.1|/1.00E-160//xyloglucan endotransglucosylase/hydrolase [Vigna angularis]	Unigene50204_All//4.00E-144//AT2G36870| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene50204_All//0.00E+00//gi|78325062|gb|DT545336.1|DT545336				nr -
Unigene50205_All	558	5.53	8.17	5.53	22.85	10.31	13.52	16.44	11.98	8.85	5.63E-01	4.72E-02		7.00E-04	9.97E-01		-1.15E+00	1.34E-14	Down	-7.58E-01	8.70E-07		-4.56E-01	7.54E-03		-8.93E-01	1.00E-07		Unigene50205_All//gi|149944379|gb|ABR46232.1|/3.00E-26//At5g42146 [Arabidopsis thaliana]	Unigene50205_All//1.00E-14//AT5G42146| unknown protein	Unigene50205_All//0.00E+00//DN501018				nr +
Unigene50206_All	378	9.14	6.17	12.12	12.26	10.66	14.10	59.62	30.63	17.18	-5.67E-01	8.82E-02		4.07E-01	1.78E-01		-2.02E-01	5.33E-01		2.02E-01	5.00E-01		-9.61E-01	2.88E-19		-1.80E+00	1.35E-50	Down	Unigene50206_All//gi|297819344|ref|XP_002877555.1|/6.00E-14//40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata] >gi|297323393|gb|EFH53814.1| 40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata]	Unigene50206_All//3.00E-15//AT5G62300| 40S ribosomal protein S20 (RPS20C)	Unigene50206_All//0.00E+00//gi|21099917|gb|BQ412230.1|BQ412230		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0031981	nr -
Unigene50208_All	523	4.80	10.08	3.67	2.57	3.42	3.45	20.21	36.44	21.10	1.07E+00	5.65E-05	Up	-3.90E-01	3.75E-01		4.13E-01	4.45E-01		4.26E-01	4.19E-01		8.51E-01	1.66E-13		6.21E-02	7.11E-01		Unigene50208_All//gi|15241076|ref|NP_200402.1|//4.00E-12//D6PK (D6 PROTEIN KINASE); kinase/ protein kinase [Arabidopsis thaliana] >gi|9758211|dbj|BAB08656.1| serine/threonine-specific protein kinase ATPK64 [Arabidopsis thaliana]	Unigene50208_All//2.00E-09//AT5G55910| D6PK (D6 PROTEIN KINASE); kinase/ protein kinase	Unigene50208_All//0.00E+00//gi|31072869|gb|CA993148.1|CA993148			GO:0004672//GO:0005488//GO:0006464//GO:0009926//GO:0016323//GO:0043234	nr +
Unigene50209_All	497	1.16	3.16	1.61	3.51	2.01	2.73	2.89	2.19	0.56	1.45E+00	8.58E-03		4.73E-01	5.65E-01		-8.04E-01	9.16E-02		-3.64E-01	4.94E-01		-4.04E-01	4.33E-01		-2.37E+00	2.52E-05	Down	Unigene50209_All//gi|188482311|gb|ACD50313.1|//8.00E-13//histone deacetylase RPD3/HDA1 class I isoform 1 [Hordeum vulgare]	Unigene50209_All//7.00E-13//AT3G44680| HDA9 (HISTONE DEACETYLASE 9); histone deacetylase	Unigene50209_All//0.00E+00//gi|3326190|gb|AI055076.1|AI055076			GO:0006476//GO:0016811	nr +
Unigene50210_All	424	2.34	1.67	1.00	10.69	5.60	7.88	4.49	0.49	2.07	-4.87E-01	4.72E-01		-1.22E+00	1.00E-01		-9.32E-01	4.19E-04		-4.40E-01	1.36E-01		-3.19E+00	1.16E-08	Down	-1.12E+00	6.32E-03					Unigene50210_All//4.00E-29//ES806892				
Unigene50212_All	698	0.45	3.41	0.92	2.71	0.99	6.73	1.21	9.40	25.28	2.92E+00	4.35E-08	Up	1.03E+00	2.81E-01		-1.46E+00	1.29E-03		1.31E+00	3.94E-06	Up	2.96E+00	2.41E-26	Up	4.38E+00	1.99E-98	Up	Unigene50212_All//gi|18401037|ref|NP_566538.1|//3.00E-19//thioesterase family protein [Arabidopsis thaliana] >gi|20166095|gb|AAM19969.1| At3g16179/At3g16179 [Arabidopsis thaliana]	Unigene50212_All//2.00E-20//AT3G16175| thioesterase family protein				GO:0003824	nr -
Unigene50214_All	584	26.52	22.91	37.57	22.09	22.76	12.91	23.82	20.68	11.46	-2.11E-01	1.61E-01		5.02E-01	3.15E-05		4.30E-02	8.23E-01		-7.75E-01	4.25E-07		-2.04E-01	1.66E-01		-1.06E+00	1.46E-14	Down	Unigene50214_All//gi|17065406|gb|AAL32857.1|/6.00E-06//Unknown protein [Arabidopsis thaliana]	Unigene50214_All//2.00E-32//AT1G42960| expressed protein localized to the inner membrane of the chloroplast.	Unigene50214_All//0.00E+00//gi|21100321|gb|BQ412634.1|BQ412634			GO:0003824//GO:0008152//GO:0009528//GO:0009534	nr +

Unigene50215_All	618	1.69	43.78	1.03	5.64	4.46	8.33	19.64	99.76	203.32	4.69E+00	8.57E-126	Up	-7.12E-01	3.15E-01		-3.40E-01	3.18E-01		5.62E-01	3.60E-02		2.35E+00	1.42E-187	Up	3.37E+00	0.00E+00	Up	Unigene50215_All//gi|224111734|ref|XP_002315958.1|//5.00E-06//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222864998|gb|EEF02129.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene50215_All//9.00E-06//AT3G25730| AP2 domain-containing transcription factor, putative	Unigene50215_All//0.00E+00//TC134879	AP2-EREBP			nr +
Unigene50216_All	538	64.57	139.29	66.81	156.85	121.10	193.41	118.82	127.72	89.90	1.11E+00	5.63E-64	Up	4.91E-02	6.27E-01		-3.73E-01	3.60E-13		3.02E-01	6.36E-10		1.04E-01	9.92E-02		-4.03E-01	2.40E-12		Unigene50216_All//gi|34581773|gb|AAQ76042.1|//1.00E-33//signal recognition particle receptor protein [Cucumis sativus]	Unigene50216_All//2.00E-34//AT4G30600| signal recognition particle receptor alpha subunit family protein	Unigene50216_All//0.00E+00//gi|164366624|gb|ES850630.1|ES850630		ko03060|Protein export	GO:0000270//GO:0003723//GO:0004871//GO:0006613//GO:0017111//GO:0030067//GO:0031224//GO:0032561//GO:0043021//GO:0048500	nr +
Unigene50217_All	691	25.97	113.14	17.18	38.71	27.81	42.09	212.87	121.21	188.12	2.12E+00	2.49E-171	Up	-5.96E-01	1.00E-05		-4.77E-01	7.18E-07		1.21E-01	3.10E-01		-8.12E-01	1.79E-91		-1.78E-01	1.73E-06		Unigene50217_All//gi|159465411|ref|XP_001690916.1|//3.00E-18//extracellular matrix protein [Chlamydomonas reinhardtii] >gi|158279602|gb|EDP05362.1| extracellular matrix protein [Chlamydomonas reinhardtii]		Unigene50217_All//9.00E-158//BE054108		ko04141|Protein processing in endoplasmic reticulum//ko00520|Amino sugar and nucleotide sugar metabolism//ko03420|Nucleotide excision repair	GO:0003824//GO:0008152	nr -
Unigene50218_All	431	3.64	1.65	2.97	3.47	3.04	3.14	21.39	10.57	7.39	-1.15E+00	3.18E-02		-2.97E-01	6.10E-01		-1.92E-01	7.47E-01		-1.41E-01	7.88E-01		-1.02E+00	4.24E-09	Down	-1.53E+00	4.46E-17	Down	Unigene50218_All//gi|79999275|gb|AB816984.1|//7.00E-23//thaliana 60S ribosomal protein L7 (At2g44120) [Solanum tuberosum]	Unigene50218_All//3.00E-17//AT2G01250| 60S ribosomal protein L7 (RPL7B)	Unigene50218_All//6.00E-127//gi|21100940|gb|BQ413253.1|BQ413253		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0030312	nr +
Unigene50219_All	673	6.53	14.91	6.80	10.36	6.86	8.52	12.00	11.55	11.60	1.19E+00	3.19E-10	Up	5.93E-02	8.42E-01		-5.96E-01	4.35E-03		-2.82E-01	2.43E-01		-5.49E-02	7.92E-01		-4.85E-02	8.04E-01		Unigene50219_All//gi|115456081|ref|NP_001051641.1|//1.00E-16//Os03g0807200 [Oryza sativa Japonica Group] >gi|108711656|gb|ABF99451.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550112|dbj|BAF13555.1| Os03g0807200 [Oryza sativa Japonica Group]	Unigene50219_All//7.00E-13//AT3G03880| unknown protein	Unigene50219_All//7.00E-103//gi|84167081|gb|DR455729.1|DR455729				nr +
Unigene50220_All	440	5.23	219.84	7.75	5.77	11.43	13.24	4.80	8.55	10.14	5.39E+00	0.00E+00	Up	5.66E-01	1.09E-01		9.85E-01	1.28E-04		1.20E+00	1.47E-06	Up	8.31E-01	3.20E-03		1.08E+00	2.23E-05	Up	Unigene50220_All//gi|15238685|ref|NP_200137.1|//5.00E-09//AGP22 (ARABINOGALACTAN PROTEIN 22) [Arabidopsis thaliana] >gi|751711157|sp|Q9FK16.1|AGP22_ARATH RecName: Full=Arabinogalactan peptide 22; Short=AG-peptide 22; Flags: Precursor >gi|38566508|gb|AAR24144.1| At5g53250 [Arabidopsis thaliana] >gi|40823626|gb|AAR92294.1| At5g53250 [Arabidopsis thaliana]		Unigene50220_All//5.00E-158//TC171243			GO:0031410	nr +
Unigene50223_All	702	116.19	88.06	187.21	15.54	14.42	15.18	1.08	0.36	0.06	-4.00E-01	3.01E-12		6.88E-01	1.13E-48		-1.08E-01	5.99E-01		-3.35E-02	8.77E-01		-1.60E+00	3.70E-02		-4.25E+00	8.65E-05	Down	Unigene50223_All//gi|14632512|gb|AK63984.1|//1.00E-41//At1g32080/F3C3_12 [Arabidopsis thaliana] >gi|20855884|gb|AAM26636.1| At1g32080/F3C3_12 [Arabidopsis thaliana]	Unigene50223_All//7.00E-43//AT1G32080| membrane protein, putative	Unigene50223_All//0.00E+00//gi|109847846|gb|DW476826.1|DW476826			GO:0009526	nr -
Unigene50224_All	618	10.75	15.66	10.51	15.23	21.17	24.12	13.41	3.65	2.97	5.43E-01	3.31E-03		-3.26E-02	9.03E-01		4.75E-01	1.43E-03		6.63E-01	2.86E-06		-1.88E+00	1.23E-19	Down	-2.18E+00	1.87E-24	Down	Unigene50224_All//gi|297842627|ref|XP_002889195.1|//2.00E-34//glycosyl hydrolase family protein 17 [Arabidopsis lyrata subsp. lyrata] >gi|297335036|gb|EFH65454.1| glycosyl hydrolase family protein 17 [Arabidopsis lyrata subsp. lyrata]	Unigene50224_All//8.00E-37//AT1G78520| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: X8 (InterPro:IPR012946); BEST Arabidopsis thaliana protein match is: glycosyl hydrolase family protein 17 (TAIR:AT2G43670.1); Has 747 Blast hits to 711 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 747; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene50224_All//0.00E+00//gi|109876378|gb|DW505352.1|DW505352			GO:0003824//GO:0031410	nr +
Unigene50225_All	651	1.53	0.39	0.98	7.88	2.49	2.29	22.73	17.27	12.55	-1.97E+00	9.93E-03		-6.38E-01	3.90E-01		-1.66E+00	1.55E-10	Down	-1.78E+00	3.11E-10	Down	-3.96E-01	2.45E-03		-8.58E-01	3.55E-11		Unigene50225_All//gi|184160103|gb|ACC68169.1|//3.00E-20//Zn/Cd P(IB)-type ATPase [Arabidopsis halleri subsp. halleri]	Unigene50225_All//2.00E-21//AT2G19110| HMA4; cadmium ion transmembrane transporter/ cadmium-transporting ATPase/ zinc ion transmembrane transporter				GO:0000041//GO:0005385//GO:0009206//GO:0015086//GO:0031224//GO:0032559//GO:0043169//GO:0043682	nr +
Unigene50227_All	604	53.79	11.66	13.84	2.31	1.94	2.92	0.42	2.56	0.26	-2.21E+00	1.53E-75	Down	-1.96E+00	1.49E-62	Down	-2.53E-01	6.57E-01		3.37E-01	5.42E-01		2.61E+00	5.83E-06	Up	-6.71E-01	6.05E-01										
Unigene50228_All	581	2.97	0.96	2.84	6.86	7.47	6.76	8.81	2.01	1.58	-1.63E+00	2.08E-03		-6.48E-02	9.03E-01		1.23E-01	7.42E-01		-2.04E-02	9.55E-01		-2.13E+00	1.73E-14	Down	-2.48E+00	6.80E-18	Down	Unigene50228_All//gi|11074242|gb|ABH04494.1|//3.00E-16//At3g15395 [Arabidopsis thaliana] >gi|222423962|dbj|BAH19943.1| AT3G15395 [Arabidopsis thaliana] >gi|222424311|dbj|BAH20112.1| AT3G15395 [Arabidopsis thaliana]	Unigene50228_All//1.00E-14//AT3G15395| unknown protein	Unigene50228_All//0.00E+00//gi|164256695|gb|ES830244.1|ES830244			GO:0043231	nr -
Unigene50229_All	1014	241.64	338.50	226.60	13.22	38.04	18.84	0.33	0.16	0.16	4.86E-01	6.19E-70		-9.27E-02	9.30E-03		1.53E+00	2.00E-63	Up	5.12E-01	3.41E-05		-1.02E+00	3.99E-01		-1.09E+00	3.55E-01		Unigene50229_All//gi|30841320|gb|AA96740.1|//3.00E-95//auxin binding protein [Gossypium hirsutum]	Unigene50229_All//8.00E-70//AT5G20630| GER3 (GERMIN 3); oxalate oxidase	Unigene50229_All//0.00E+00//TC136901			GO:0004871//GO:0005576//GO:0005618//GO:0006950//GO:0008152//GO:0009755//GO:0016209//GO:0016623//GO:0043231//GO:0046914	nr -
Unigene5023_All	435	3.73	1.86	1.71	5.15	3.25	4.46	6.90	4.04	2.84	-1.00E+00	5.37E-02		-1.12E+00	4.20E-02		-6.67E-01	1.08E-01		-2.07E-01	6.58E-01		-7.74E-01	1.60E-02		-1.28E+00	6.80E-05	Down	Unigene5023_All//gi|124360619|gb|AB033394.2|//4.00E-29//FAR1; Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene5023_All//2.00E-24//AT4G12850| far-red impaired responsive family protein / FAR1 family protein	Unigene5023_All//3.00E-159//gi|164257672|gb|ES831440.1|ES831440				nr +
Unigene50230_All	554	114.75	74.91	91.70	173.72	193.12	183.59	359.69	205.58	175.25	-6.15E-01	2.14E-20		-3.24E-01	1.81E-06		1.53E-01	1.91E-03		7.97E-02	1.88E-01		-8.07E-01	2.90E-122		-1.04E+00	2.47E-191	Down	Unigene50230_All//gi|283136136|gb|ADB11387.1|//3.00E-85//gamma class glutathione transferase EF1Bgamma2 [Populus trichocarpa]	Unigene50230_All//5.00E-63//AT1G57720| elongation factor 1B-gamma, putative / eEF-1B gamma, putative	Unigene50230_All//0.00E+00//TC135856			GO:0003824//GO:0006412//GO:0008135//GO:0043231//GO:0043234	nr +
Unigene50231_All	1433	0.22	1.13	0.00	0.35	0.36	1.95	19.80	36.14	209.56	2.37E+00	1.02E-04	Up	-7.78E+00	4.90E-02		5.26E-02	9.80E-01		2.49E+00	2.20E-08	Up	8.68E-01	1.63E-36		3.40E+00	0.00E+00	Up	Unigene50231_All//gi|227204287|dbj|BAH56995.1|//1.00E-169//AT4G18950 [Arabidopsis thaliana]	Unigene50231_All//8.00E-171//AT4G18950| ankyrin protein kinase, putative	Unigene50231_All//0.00E+00//TC157027		ko04140|Regulation of autophagy	GO:0004713//GO:0006464//GO:0007165//GO:0032559	nr -
Unigene50232_All	964	1.30	3.10	3.92	5.32	0.82	1.92	11.71	106.40	1.86	1.25E+00	7.72E-04	Up	1.59E+00	5.33E-06	Up	-2.70E+00	2.37E-19	Down	-1.47E+00	6.66E-08	Down	3.18E+00	0.00E+00	Up	-2.65E+00	1.43E-41	Down	Unigene50232_All//gi|284433794|gb|AD885103.1|//1.00E-101//glutathione S-transferase omega [Jatropha curcas]	Unigene50232_All//1.00E-87//AT5G02790| In2-1 protein, putative	Unigene50232_All//0.00E+00//TC170979		ko00480|Glutathione metabolism	GO:0016765//GO:0044424	nr -
Unigene50233_All	572	6.40	4.96	2.79	4.96	6.50	5.68	6.14	3.29	4.81	-3.68E-01	2.62E-01		-1.20E+00	4.68E-04	Down	3.89E-01	2.54E-01		1.96E-01	6.43E-01		-9.00E-01	2.19E-03		-3.52E-01	2.32E-01		Unigene50233_All//gi|195645272|gb|ACG42104.1|//3.00E-41//oral cancer overexpressed protein 1 [Zea mays]	Unigene50233_All//4.00E-31//AT2G20830| folic acid binding / transferase					nr -
Unigene50234_All	1313	0.24	0.39	0.00	1.10	0.55	0.14	8.44	2.48	2.00	6.91E-01	4.99E-01		-7.90E+00	4.90E-02		-9.98E-01	5.97E-02		-3.00E+00	1.34E-05	Down	-1.76E+00	5.92E-24	Down	-2.07E+00	1.55E-30	Down	Unigene50234_All//gi|124360057|gb|ABN08073.1|//1.00E-141//Lipolytic enzyme, G-D-S-L [Medicago truncatula]	Unigene50234_All//1.00E-139//AT5G37690| GDSL-motif lipase/hydrolase family protein	Unigene50234_All//0.00E+00//TC169045			GO:0016787//GO:0031410	nr +
Unigene50235_All	1070	1.42	1.89	2.09	10.24	13.55	157.10	309.95	1262.00	626.92	4.18E-01	3.77E-01		5.60E-01	2.20E-01		4.04E-01	4.67E-03		3.94E+00	0.00E+00	Up	2.03E+00	0.00E+00	Up	1.02E+00	0.00E+00	Up	Unigene50235_All//gi|34419961|gb|AAQ67366.1|//1.00E-180//PODP precursor [Gossypium hirsutum]	Unigene50235_All//2.00E-94//AT5G06720| peroxidase, putative	Unigene50235_All//0.00E+00//TC134559		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209	nr +
Unigene50236_All	545	27.94	32.63	20.62	25.59	19.14	24.53	31.19	21.24	10.09	2.24E-01	1.08E-01		-4.38E-01	3.42E-03		-4.19E-01	3.38E-03		-6.12E-02	7.21E-01		-5.54E-01	3.75E-06		-1.63E+00	1.55E-33	Down	Unigene50236_All//gi|88010872|gb|AB038866.1|//3.00E-29//At4g14615 [Arabidopsis thaliana]	Unigene50236_All//3.00E-17//AT4G14615| unknown protein	Unigene50236_All//0.00E+00//TC168966			GO:0005635//GO:0031410//GO:0051234	nr +
Unigene50238_All	495	1.59	0.61	0.75	2.21	1.95	1.82	4.19	1.35	0.64	-1.37E+00	9.59E-02		-1.07E+00	2.10E-01		-1.85E-01	8.01E-01		-2.79E-01	6.89E-01		-1.63E+00	1.21E-04	Down	-2.70E+00	2.21E-08	Down	Unigene50238_All//gi|27311577|gb|AA000754.1|//7.00E-12//Unknown protein [Arabidopsis thaliana]	Unigene50238_All//5.00E-13//AT1G38131| unknown protein	Unigene50238_All//2.00E-157//DT049764			GO:0009536	nr +
Unigene50239_All	1049	1.35	0.72	0.86	5.41	2.72	1.68	3.10	1.35	1.44	-8.94E-01	1.12E-01		-6.42E-01	2.75E-01		-9.91E-01	1.91E-05		-1.69E+00	1.76E-10	Down	-1.20E+00	1.33E-04	Down	-1.10E+00	2.51E-04	Down	Unigene50239_All//gi|27311577|gb|AA000754.1|//5.00E-79//Unknown protein [Arabidopsis thaliana]	Unigene50239_All//9.00E-81//AT1G38131| unknown protein	Unigene50239_All//0.00E+00//DT049764			GO:0009536	nr -
Unigene50240_All	637	1.64	15.27	1.67	2.97	3.30	1.99	1.26	0.59	0.63	3.22E+00	3.17E-34	Up	2.54E-02	9.89E-01		1.50E-01	8.01E-01		-5.82E-01	2.31E-01		-1.09E+00	1.29E-01		-1.01E+00	1.35E-01		Unigene50240_All//gi|15238001|ref|NP_199517.1|//2.00E-42//senescence-associated protein-related [Arabidopsis thaliana]	Unigene50240_All//6.00E-38//AT5G47060| senescence-associated protein-related	Unigene50240_All//0.00E+00//CO080640				nr +
Unigene50241_All	522	102.54	17.96	27.85	71.19	45.25	30.46	91.20	43.32	36.48	-2.51E+00	3.47E-145	Down	-1.88E+00	1.88E-97	Down	-6.54E-01	3.90E-16		-1.23E+00	1.16E-40	Down	-1.07E+00	1.19E-47	Down	-1.32E+00	7.42E-68	Down	Unigene50241_All//gi|224073154|ref|XP_002303998.1|//1.00E-29//tubulin alpha-2 chain [Populus trichocarpa] >gi|222841430|gb|EEE78977.1| tubulin alpha-2 chain [Populus trichocarpa]	Unigene50241_All//3.00E-20//AT1G64740| TUA1 (ALPHA-1 TUBULIN); structural constituent of cytoskeleton	Unigene50241_All//0.00E+00//TC163980		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene50245_All	806	1.62	1.89	0.79	2.10	2.01	2.13	0.94	1.40	3.51	2.17E-01	6.71E-01		-1.03E+00	9.64E-02		-6.55E-02	8.89E-01		1.91E-02	9.70E-01		5.68E-01	3.44E-01		1.89E+00	1.88E-07	Up	Unigene50245_All//gi|156138815|dbj|BAF75899.1|//3.00E-34//glucosyltransferase [Cyclamen persicum]	Unigene50245_All//1.00E-21//AT3G16520| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene50245_All//7.00E-14//TC149650			GO:0016740	nr -
Unigene50248_All	2461	0.45	0.47	0.48	0.40	0.77	1.36	1.08	5.86	11.44	8.47E-02	8.94E-01		9.23E-02	8.81E-01		9.27E-01	5.02E-02		1.75E+00	1.48E-06	Up	2.44E+00	2.21E-46	Up	3.40E+00	3.26E-129	Up	Unigene50248_All//gi|87162753|gb|ABD28548.1|//0.00E+00//Protein kinase; Type I EGF [Medicago truncatula]	Unigene50248_All//9.00E-162//AT1G21230| WAK5 (WALL ASSOCIATED KINASE 5); kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488	nr -
Unigene50249_All	924	15.68	10.20	10.49	24.58	24.04	22.00	9.84	6.79	4.57	-6.21E-01	2.35E-05		-5.81E-01	1.37E-04		-3.24E-02	8.16E-01		-1.61E-01	2.21E-01		-5.36E-01	1.65E-03		-1.11E+00	1.57E-10	Down	Unigene50249_All//gi|22329375|ref|NP_683280.1|//3.00E-11//TRFL7 (TRF-LIKE 7); DNA binding / transcription factor [Arabidopsis thaliana] >gi|41619018|gb|AAS10004.1| MYB transcription factor [Arabidopsis thaliana]	Unigene50249_All//1.00E-12//AT1G06910| TRFL7 (TRF-LIKE 7); DNA binding / transcription factor	Unigene50249_All//0.00E+00//TC134111	MYB-related		GO:0005488//GO:0010033	nr +
Unigene50250_All	995	3.58	4.18	5.83	1.80	2.53	4.09	7.90	5.04	3.72	2.24E-01	4.78E-01		7.06E-01	5.87E-03		4.87E-01	2.49E-01		1.18E+00	1.10E-04	Up	-6.49E-01	4.29E-04		-1.09E+00	5.52E-09	Down	Unigene50250_All//gi|116563481|gb|ABJ99761.1|//1.00E-116//PHD4 [Medicago truncatula]	Unigene50250_All//3.00E-94//AT5G05610| AL1 (ALFIN-LIKE 1); DNA binding / methylated histone residue binding	Unigene50250_All//2.00E-30//gi|48814886|gb|CO116199.1|CO116199	Alfin-like			nr +
Unigene50253_All	304	30.46	37.34	30.48	24.74	27.19	31.35	48.82	34.10	24.24	2.94E-01	9.41E-02		7.00E-04	9.96E-01		1.36E-01	5.83E-01		3.41E-01	8.02E-02		-5.18E-01	6.10E-05		-1.01E+00	1.88E-14	Down	Unigene50253_All//gi|222136863|gb|ACM45081.1|//6.00E-43//3-dehydroquinate synthase [Vitis vinifera]	Unigene50253_All//2.00E-35//AT5G66120| 3-dehydroquinate synthase, putative	Unigene50253_All//1.00E-161//gi|109876648|gb|DW505622.1|DW505622		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0008652//GO:0009536//GO:0016838	nr +
Unigene50254_All	744	2.46	2.04	1.43	1.41	1.71	1.88	1.31	2.92	3.27	-2.69E-01	5.97E-01		-7.82E-01	1.25E-01		2.85E-01	6.71E-01		4.21E-01	4.92E-01		1.16E+00	3.26E-03		1.32E+00	3.06E-04	Up	Unigene50254_All//gi|222423782|dbj|BAH19857.1|//8.00E-21//AT5G18310 [Arabidopsis thaliana]	Unigene50254_All//9.00E-22//AT5G18310| unknown protein	Unigene50254_All//1.00E-30//TC151614				nr -

Unigene50256_All	1810	0.03	0.17	0.12	0.11	0.46	1.40	31.02	7.04	2.38	2.54E+00	1.51E-01		2.03E+00	3.61E-01		2.05E+00	1.79E-02		3.67E+00	8.45E-11	Up	-2.14E+00	6.01E-153	Down	-3.71E+00	5.97E-282	Down	Unigene50256_All//gi|224131024|ref|XP_002328434.1//1.00E-173//cytochrome P450 [Populus trichocarpa] >gi|222838149|gb|EEE76514.1|cytochrome P450 [Populus trichocarpa]	Unigene50256_All//1.00E-136//AT1G75130| CYP721A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene50256_All//0.00E+00//TC131398		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +
Unigene50258_All	509	124.27	133.89	185.59	92.29	54.46	53.86	69.19	139.59	79.52	1.08E-01	1.24E-01		5.79E-01	6.32E-26		-7.61E-01	1.99E-26		-7.77E-01	2.57E-24		1.01E+00	3.46E-64	Up	2.01E-01	7.97E-03		Unigene50258_All//gi|71040671|gb|AAZ20284.1|//1.00E-14//calcium-binding pollen allergen [Arachis hypogaea]	Unigene50258_All//3.00E-15//AT1G24620| polcalcin, putative / calcium-binding pollen allergen, putative	Unigene50258_All//0.00E+00//gi|164298632|gb|ES809331.1|ES809331		ko04626|Plant-pathogen interaction	GO:0006950//GO:0016491//GO:0043231//GO:0046872	nr -
Unigene50260_All	628	0.33	0.48	1.70	22.37	17.00	9.42	3.50	2.53	1.59	5.39E-01	6.71E-01		2.35E+00	3.61E-03		-3.96E-01	5.69E-03		-1.25E+00	3.80E-16	Down	-4.69E-01	2.41E-01		-1.14E+00	2.48E-03		Unigene50260_All//gi|5668815|gb|AAD46041.1|AC007519_26//7.00E-35//ESTs gb|AA042581 and gb|H36253 come from this gene [Arabidopsis thaliana] >gi|48310110|gb|AAT41755.1|At1g47410 [Arabidopsis thaliana] >gi|52218788|gb|AAU29464.1|At1g47410 [Arabidopsis thaliana]	Unigene50260_All//8.00E-24//AT1G47410| unknown protein	Unigene50260_All//0.00E+00//TC156033				nr -
Unigene50264_All	619	13.19	9.66	7.74	18.51	14.91	10.21	24.86	13.37	10.62	-4.49E-01	2.82E-02		-7.68E-01	2.73E-04		-3.12E-01	6.50E-02		-8.58E-01	1.81E-07		-8.95E-01	5.25E-12		-1.23E+00	3.66E-20	Down			Unigene50264_All//4.00E-132//TC140292				
Unigene50265_All	811	3.55	2.31	0.59	1.66	0.55	1.00	1.04	0.72	4.08	-6.18E-01	9.41E-02		-2.59E+00	3.44E-08	Down	-1.59E+00	4.83E-03		-7.26E-01	2.23E-01		-5.31E-01	4.45E-01		1.97E+00	5.67E-09	Up	Unigene50265_All//gi|295913226|gb|ADG57871.1|//4.00E-56//transcription factor [Lycoris longituba]	Unigene50265_All//1.00E-52//AT3G19860| basic helix-loop-helix (bHLH) family protein	Unigene50265_All//0.00E+00//gi|73864622|gb|DT467361.1|DT467361	bHLH		GO:0001071//GO:0010468//GO:0043231	nr +
Unigene50267_All	716	0.37	2.41	0.60	1.95	1.68	1.89	3.84	6.54	5.62	2.72E+00	1.19E-05	Up	7.03E-01	5.54E-01		-2.11E-01	7.29E-01		-4.19E-02	9.52E-01		7.68E-01	1.96E-03		5.50E-01	3.72E-02				Unigene50267_All//6.00E-119//TC169932				
Unigene50268_All	680	45.78	35.10	80.97	1.90	3.24	1.79	2.80	0.25	0.41	-3.83E-01	7.27E-05		8.23E-01	4.97E-28		7.67E-01	7.80E-02		-8.69E-02	8.93E-01		-3.51E+00	2.32E-09	Down	-2.77E+00	6.03E-08	Down	Unigene50268_All//gi|18700129|gb|AAL77676.1|//1.00E-63//At2g36630/F1011.26 [Arabidopsis thaliana] >gi|22137236|gb|AAM91463.1|At2g36630/F1011.26 [Arabidopsis thaliana]	Unigene50268_All//6.00E-52//AT2G36630| unknown protein	Unigene50268_All//0.00E+00//gi|13245761|gb|BE052123.2|BE052123			GO:0031224//GO:0043231	nr -
Unigene5027_All	1051	3.53	12.34	6.33	1.61	1.21	1.98	1.09	2.11	3.83	1.80E+00	1.98E-23	Up	8.42E-01	3.89E-04		-4.11E-01	4.28E-01		2.95E-01	5.64E-01		9.56E-01	1.31E-02		1.82E+00	9.40E-10	Up	Unigene5027_All//gi|297820784|ref|XP_002878275.1|//6.00E-72//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324113|gb|EFH54534.1|leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5027_All//5.00E-71//AT3G59510| leucine-rich repeat family protein	Unigene5027_All//0.00E+00//gi|73863750|gb|DT466489.1|DT466489		ko04626|Plant-pathogen interaction		nr -
Unigene50271_All	1119	1.26	2.81	0.62	1.38	2.09	2.34	1.51	3.74	3.77	1.15E+00	1.29E-03		-1.03E+00	8.34E-02		6.01E-01	1.62E-01		7.62E-01	5.47E-02		1.31E+00	2.19E-06	Up	1.32E+00	9.76E-07	Up							
Unigene50272_All	632	6.95	21.09	12.13	7.25	10.24	12.51	23.48	24.87	21.62	1.60E+00	1.98E-20	Up	8.03E-01	2.39E-04		4.98E-01	2.98E-02		7.86E-01	1.13E-04		8.26E-02	6.12E-01		-1.19E-01	4.02E-01		Unigene50272_All//gi|23428796|gb|AAM23263.1|//5.00E-19//DnaJ-like protein [Glycine max]	Unigene50272_All//1.00E-17//AT1G56300| DNAJ heat shock N-terminal domain-containing protein	Unigene50272_All//0.00E+00//gi|164278550|gb|ES798278.1|ES798278			GO:0005515//GO:0044267//GO:0050896	nr +
Unigene50273_All	393	6.39	13.54	7.59	8.62	12.27	11.84	23.67	27.76	25.44	1.08E+00	4.24E-05	Up	2.48E-01	5.31E-01		5.09E-01	6.48E-02		4.58E-01	1.18E-01		2.30E-01	1.69E-01		1.04E-01	5.81E-01				Unigene50273_All//1.00E-87//TC148387				
Unigene50274_All	831	1.07	1.22	0.06	1.68	1.78	2.55	17.20	35.76	33.94	1.88E-01	7.64E-01		-4.06E+00	5.15E-04	Down	8.62E-02	8.96E-01		6.06E-01	1.94E-01		1.06E+00	3.27E-29	Up	9.81E-01	2.77E-25		Unigene50274_All//gi|145357850|ref|NP_196588.3|//4.00E-78//AtRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding [Arabidopsis thaliana] >gi|8953407|emb|CAB96682.1| GTP-binding protein [Arabidopsis thaliana]	Unigene50274_All//2.00E-79//AT5G10260| AtRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding	Unigene50274_All//0.00E+00//gi|109871281|gb|DW500257.1|DW500257			GO:0003924//GO:0006810//GO:0032561//GO:0035556	nr +
Unigene50275_All	896	5.90	5.77	12.36	8.45	9.57	6.35	1.04	1.26	1.11	-3.21E-02	9.16E-01		1.07E+00	3.86E-09	Up	1.79E-01	4.37E-01		-4.12E-01	5.85E-02		2.79E-01	6.41E-01		9.87E-02	8.78E-01		Unigene50275_All//gi|297813013|ref|XP_002874390.1|//1.00E-111//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297320227|gb|EFH50649.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene50275_All//2.00E-96//AT5G27270| EMB976 (EMBRYO DEFECTIVE 976)				GO:0043231	nr +
Unigene50276_All	746	4.14	1.77	2.00	4.54	4.02	3.09	3.51	3.14	3.47	-1.23E+00	7.17E-04	Down	-1.05E+00	4.96E-03		-1.77E-01	6.20E-01		-5.56E-01	1.07E-01		-1.64E-01	6.51E-01		-1.76E-02	9.73E-01		Unigene50276_All//gi|30698782|ref|NP_177277.2|//1.00E-42//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75151609|sp|Q8GZA6.1|PP113_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g71210 >gi|29029058|gb|AAO64908.1|At1g71210 [Arabidopsis thaliana]	Unigene50276_All//5.00E-44//AT1G71210| pentatricopeptide (PPR) repeat-containing protein	Unigene50276_All//0.00E+00//TC150133				nr -
Unigene50277_All	394	16.07	149.95	28.65	27.44	77.96	68.78	28.76	68.85	136.60	3.22E+00	4.70E-206	Up	8.35E-01	2.11E-06		1.51E+00	1.19E-49	Up	1.33E+00	3.80E-33	Up	1.26E+00	3.73E-35	Up	2.25E+00	1.45E-158	Up			Unigene50277_All//5.00E-50//TC162463				
Unigene50278_All	429	23.90	157.91	47.79	29.26	48.72	57.90	39.42	122.17	182.29	2.72E+00	2.99E-199	Up	9.99E-01	9.22E-15		7.36E-01	5.87E-11		9.85E-01	3.98E-19		1.63E+00	7.65E-99	Up	2.21E+00	2.99E-225	Up	Unigene50278_All//gi|117168087|gb|ABK32126.1|//3.00E-22//At1g52565 [Arabidopsis thaliana]	Unigene50278_All//4.00E-18//AT1G52565| unknown protein	Unigene50278_All//3.00E-147//TC159003				nr +
Unigene50279_All	316	25.83	64.14	45.67	68.57	91.54	84.04	85.63	80.28	85.22	1.31E+00	5.19E-23	Up	8.22E-01	8.31E-08		4.17E-01	9.57E-06		2.93E-01	6.05E-03		-9.30E-02	3.96E-01		-6.90E-03	9.66E-01		Unigene50279_All//gi|5425733|dbj|BAB64344.1|//7.00E-37//EIN3-like protein [Cucumis melo]	Unigene50279_All//3.00E-21//AT3G20770| EIN3 (ETHYLENE-INSENSITIVE3); transcription factor	Unigene50279_All//2.00E-178//TC140681	EIL		GO:0043231	nr +
Unigene50280_All	1006	0.83	1.16	1.96	2.43	2.53	1.71	0.97	0.62	2.61	4.77E-01	4.39E-01		1.23E+00	1.21E-02		6.21E-02	8.99E-01		-5.08E-01	2.28E-01		-6.33E-01	3.28E-01		1.44E+00	5.32E-05	Up	Unigene50280_All//gi|15218241|ref|NP_172439.1|//7.00E-48//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75097039|sp|O04491.1|PPR26_ARATH RecName: Full=Putative pentatricopeptide repeat-containing protein At1g09680 >gi|2160161|gb|AAB60724.1|F21M12.7 gene product [Arabidopsis thaliana]	Unigene50280_All//7.00E-61//AT1G12700| helicase domain-containing protein / pentatricopeptide (PPR) repeat-containing protein	Unigene50280_All//0.00E+00//ES801805				nr +
Unigene50281_All	1263	0.50	0.00	0.00	5.68	2.04	0.82	7.36	1.29	13.15	-8.96E+00	7.91E-04	Down	-8.96E+00	1.41E-03		-1.47E+00	3.20E-12	Down	-2.79E+00	4.13E-24	Down	-2.51E+00	2.54E-31	Down	8.37E-01	6.86E-12		Unigene50281_All//gi|42569681|ref|NP_181207.2|//1.00E-132//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana]	Unigene50281_All//2.00E-134//AT2G36690| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene50281_All//2.00E-178//DW498667		ko00941|Flavonoid biosynthesis		nr -
Unigene50282_All	588	15.39	12.67	8.60	18.30	16.28	14.98	45.08	16.99	27.03	-2.81E-01	1.58E-01		-8.39E-01	2.56E-05		-1.69E-01	3.93E-01		-2.89E-01	1.20E-01		-1.41E+00	9.74E-41	Down	-7.38E-01	4.18E-15				Unigene50282_All//5.00E-156//DW508803				
Unigene50283_All	380	16.80	4.13	12.33	51.65	35.52	9.15	7.57	5.06	2.52	-2.02E+00	7.94E-14	Down	-4.46E-01	7.31E-02		-5.40E-01	2.28E-06		-2.50E+00	8.63E-58	Down	-5.81E-01	8.20E-02		-1.59E+00	3.47E-06	Down							
Unigene50284_All	413	13.30	35.33	10.96	14.23	24.35	32.59	39.11	39.77	38.10	1.41E+00	1.28E-18	Up	-2.80E-01	3.24E-01		7.75E-01	5.34E-06		1.20E+00	2.60E-14	Up	2.43E-02	8.74E-01		-3.75E-02	7.85E-01		Unigene50284_All//gi|255590302|ref|XP_002535232.1|//4.00E-08//metal ion binding protein, putative [Ricinus communis] >gi|223523696|gb|EEF27151.1| metal ion binding protein, putative [Ricinus communis]		Unigene50284_All//4.00E-134//TC153121				nr +
Unigene50286_All	449	10.25	21.67	5.93	11.98	8.36	8.85	15.82	12.57	10.74	1.08E+00	1.31E-08	Up	-7.90E-01	7.16E-03		-5.19E-01	3.71E-02		-4.37E-01	1.02E-01		-3.32E-01	1.06E-01		-5.59E-01	3.19E-03				Unigene50286_All//2.00E-68//gi|109887352|gb|DW516321.1|DW516321				
Unigene50287_All	471	5.67	2.90	3.73	3.60	2.92	3.26	15.71	7.01	8.04	-9.64E-01	1.28E-02		-6.03E-01	1.38E-01		-2.98E-01	5.76E-01		-1.41E-01	7.81E-01		-1.16E+00	4.30E-09	Down	-9.67E-01	3.46E-07		Unigene50287_All//gi|126256295|gb|AB009801.1|//1.00E-43//F-box protein [Gossypium hirsutum]	Unigene50287_All//4.00E-16//AT4G24210| SLY1 (SLEEPY1)	Unigene50287_All//5.00E-106//TC132666			GO:0003006//GO:0005488//GO:0009740//GO:0031461//GO:0032501//GO:0043161//GO:0043231//GO:0043623	nr -
Unigene50288_All	402	10.02	91.26	15.23	3.47	46.00	37.64	1.05	6.24	17.05	3.19E+00	9.99E-127	Up	6.04E-01	1.54E-02		3.73E+00	1.85E-84	Up	3.44E+00	4.83E-60	Up	2.57E+00	4.08E-09	Up	4.02E+00	2.42E-36	Up	Unigene50288_All//gi|28416835|gb|AA042948.1|//1.00E-13//At1g73120 [Arabidopsis thaliana]	Unigene50288_All//6.00E-15//AT1G73120| unknown protein				GO:0006950	nr +
Unigene50289_All	417	16.19	8.51	7.15	22.10	19.24	21.01	91.35	36.58	21.78	-9.28E-01	4.67E-05		-1.18E+00	1.06E-06	Down	-2.00E-01	3.36E-01		-7.29E-02	7.33E-01		-1.32E+00	8.17E-53	Down	-2.07E+00	1.24E-102	Down			Unigene50289_All//9.00E-89//gi|13244678|gb|BE052041.2|BE052041				
Unigene50292_All	334	58.74	21.09	17.54	66.97	56.29	70.86	136.21	46.18	53.32	-1.48E+00	1.07E-26	Down	-1.74E+00	1.97E-32	Down	-2.51E-01	3.11E-02		8.14E-02	5.72E-01		-1.56E+00	1.04E-80	Down	-1.35E+00	3.17E-67	Down	Unigene50292_All//gi|257219572|gb|ACV50139.1|//2.00E-58//ribosomal protein L15 [Jatropha curcas]	Unigene50292_All//4.00E-42//AT4G16720| 60S ribosomal protein L15 (RPL15A)	Unigene50292_All//0.00E+00//TC139880		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene50293_All	311	50.47	20.69	36.47	85.37	56.69	109.64	53.56	33.46	33.43	-1.29E+00	1.49E-17	Down	-4.69E-01	1.37E-03		-5.91E-01	8.33E-10		3.61E-01	6.50E-05		-6.79E-01	2.50E-08		-6.80E-01	1.23E-08		Unigene50293_All//gi|25091502|sp|Q9LKA5.1|UMP1_ARATH//2.00E-31//RecName: Full=Uncharacterized protein At3g15000, mitochondrial >gi|16226543|gb|AAL16196.1|AF428427_1 AT3g15000/K15M2_14 [Arabidopsis thaliana] >gi|53828643|gb|AAU94431.1|At3g15000 [Arabidopsis thaliana]	Unigene50293_All//5.00E-07//AT3G15000| LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: plastid developmental protein DAG, putative (TAIR:AT3G06790.2); Has 50779 Blast hits to 24732 proteins in 941 species: Archae - 10; Bacteria - 4862; Metazoa - 25623; Fungi - 7071; Plants - 6957; Viruses - 900; Other Eukaryotes - 5356 (source: NCBI BLink).	Unigene50293_All//5.00E-173//gi|78329528|gb|DT549802.1|DT549802			GO:0031410//GO:0046914	nr +
Unigene50294_All	846	4.21	0.72	0.76	10.19	7.37	16.55	2.00	9.24	19.73	-2.55E+00	2.26E-10	Down	-2.48E+00	1.49E-09	Down	-4.67E-01	1.33E-02		7.00E-01	1.84E-06		2.21E+00	1.09E-22	Up	3.30E+00	8.43E-75	Up	Unigene50294_All//gi|297792823|ref|XP_002864296.1|//1.00E-33//ATHB52 (Arabidopsis lyrata subsp. lyrata) >gi|297310113|gb|EFH40555.1|ATHB52 [Arabidopsis lyrata subsp. lyrata]	Unigene50294_All//7.00E-32//AT5G33880| ATHB52 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 52); transcription factor		HB		GO:0001071//GO:0003677//GO:0006351//GO:0009970//GO:0009642//GO:0009725//GO:0010468//GO:0010557//GO:0030528//GO:0043231	nr +
Unigene50296_All	509	19.84	13.24	20.30	34.25	28.28	38.24	31.56	15.77	9.08	-5.83E-01	1.17E-03		3.29E-02	8.71E-01		-2.77E-01	3.81E-02		1.59E-01	2.72E-01		-1.00E+00	6.63E-15	Down	-1.80E+00	2.19E-36	Down	Unigene50296_All//gi|30691134|ref|NP_174292.2|//7.00E-43//PDF6 (PREFOLDIN 6); unfolded protein binding [Arabidopsis thaliana] >gi|88011191|gb|ABD38916.1|At1g29990 [Arabidopsis thaliana]	Unigene50296_All//4.00E-44//AT1G29990| PDF6 (PREFOLDIN 6); unfolded protein binding	Unigene50296_All//0.00E+00//TC159360			GO:0005515//GO:0031410//GO:0043234//GO:0044267	nr -
Unigene50297_All	346	19.96	18.31	16.31	32.39	31.95	36.81	36.05	13.89	13.59	-1.25E-01	5.95E-01		-2.91E-01	2.34E-01		-2.00E-02	9.20E-01		1.84E-01	3.11E-01		-1.38E+00	6.22E-19	Down	-1.41E+00	3.37E-20	Down	Unigene50297_All//gi|257219570|gb|ACV50138.1|//1.00E-20//ribosomal protein L37 [Jatropha curcas]	Unigene50297_All//2.00E-16//AT3G16080| 60S ribosomal protein L37 (RPL37C)	Unigene50297_All//0.00E+00//TC157997		ko03010|Ribosome	GO:0000785//GO:0003723//GO:0005198//GO:0010467//GO:0030529//GO:0003728//GO:0043169//GO:0043231	nr -
Unigene50303_All	257	53.34	27.21	26.52	70.94	66.32	76.97	262.07	123.92	108.35	-9.71E-01	4.28E-10		-1.01E+00	3.42E-10	Down	-9.71E-02	5.57E-01		1.18E-01	4.33E-01		-1.08E+00	9.98E-68	Down	-1.27E+00	2.22E-90	Down	Unigene50303_All//gi|3023858|sp|Q39836.1|GBLP_SOYBN//6.00E-38//RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein >gi|1256608|gb|AAB05941.1| G beta-like protein [Glycine max]	Unigene50303_All//1.00E-38//AT1G48630| RACK1B_AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding	Unigene50303_All//6.00E-141//TC151909		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis	GO:0004683//GO:0004871//GO:0005840//GO:0009536//GO:0010038//GO:0019897//GO:0031981//GO:0048513	nr +
Unigene50304_All	469	0.00	3.03	1.14	0.64	1.25	1.93	2.97	4.19	2.55	1.16E+01	4.06E-08	Up	1.01E+01	4.03E-03		9.70E-01	3.47E-01		1.60E+00	4.34E-02		4.94E-01	2.45E-01		-2.23E-01	6.37E-01				Unigene50304_All//2.00E-176//TC165547				
Unigene50306_All	377	4.30	6.05	5.37	1.98	2.92	1.68	3.14	2.55	0.53	4.91E-01	2.47E-01		3.19E-01	5.10E-01		5.60E-01	4.27E-01		-2.41E-01	7.56E-01		-3.00E-01	6.31E-01		-2.57E+00	6.97E-05	Down			Unigene50306_All//1.00E-170//FL576864				

Unigene50308_All	590	31.22	8.59	9.66	43.57	29.59	47.00	90.87	31.38	29.10	-1.86E+00	1.23E-34	Down	-1.69E+00	3.08E-29	Down	-5.58E-01	1.23E-08		1.10E-01	3.90E-01		-1.53E+00	1.27E-92	Down	-1.64E+00	2.85E-105	Down	Unigene50308_All//gi|209967443|gb|ACJ02350.1|//5.00E-66//60S ribosomal protein L13A (Vernicia fordii]	Unigene50308_All//2.00E-63//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene50308_All//0.00E+00//TC133357		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934	nr -
Unigene50309_All	281	62.56	45.98	26.15	39.18	52.57	72.17	140.98	64.26	108.32	-4.44E-01	7.87E-04		-1.26E+00	3.84E-18	Down	4.24E-01	2.47E-03		8.81E-01	3.68E-13		-1.13E+00	2.43E-43	Down	-3.80E-01	2.76E-07		Unigene50309_All//gi|110559491|gb|ABG76000.1|//9.00E-52//GRF-like protein 2 [Gossypium hirsutum]	Unigene50309_All//8.00E-51//AT3G08900| RGF3 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 3); transferase, transferring hexosyl groups	Unigene50309_All//3.00E-155//TC151227			GO:0005618//GO:0005911//GO:0009250//GO:0035251//GO:0043231//GO:0045229	nr +
Unigene5031_All	632	4.06	3.85	3.54	4.57	6.21	2.43	12.44	8.47	3.03	-7.60E-02	8.43E-01		-1.97E-01	6.16E-01		4.42E-01	1.65E-01		-9.12E-01	1.29E-02		-5.56E-01	2.64E-03		-2.04E+00	1.85E-21	Down	Unigene5031_All//gi|297822593|ref|XP_002879179.1|//5.00E-30//copper-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325018|gb|EFH55438.1| copper-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5031_All//5.00E-26//AT2G28860| copper-binding family protein	Unigene5031_All//0.00E+00//TC156654				nr -
Unigene50311_All	2683	0.00	0.00	0.00	0.00	0.06	0.03	9.88	1.81	4.35	null	null		null	null		6.00E+00	2.27E-01		5.07E+00	4.76E-01		-2.45E+00	1.49E-85	Down	-1.18E+00	3.16E-32	Down	Unigene50311_All//gi|115456994|ref|NP_001052097.1|//0.00E+00//Os04g0132500 [Oryza sativa Japonica Group] >gi|113563668|dbj|BAF14011.1| Os04g0132500 [Oryza sativa Japonica Group]	Unigene50311_All//2.00E-167//AT3G24240| leucine-rich repeat transmembrane protein kinase, putative	Unigene50311_All//0.00E+00//ES792979		ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488//GO:0044464	nr +
Unigene50314_All	214	11.49	14.44	9.70	12.10	10.94	26.17	22.72	30.66	28.67	3.30E-01	3.63E-01		-2.44E-01	5.92E-01		-1.46E-01	7.47E-01		1.11E+00	1.05E-05	Up	4.33E-01	3.87E-02		3.36E-01	1.16E-01		Unigene50314_All//gi|297811985|ref|XP_002873876.1|//3.00E-33//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319713|gb|EFH50135.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50314_All//1.00E-34//AT5G18190| protein kinase family protein	Unigene50314_All//2.00E-115//TC138605			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene50319_All	1626	3.28	2.74	1.21	1.81	3.07	1.81	0.49	0.18	0.05	-2.59E-01	3.50E-01		-1.44E+00	3.86E-07	Down	7.65E-01	3.15E-03		-1.70E-03	9.92E-01		-1.46E+00	4.65E-02		-3.33E+00	2.47E-04	Down	Unigene50319_All//gi|226529630|ref|NP_001152607.1|//7.00E-33//growth-regulating factor [Zea mays] >gi|195658087|gb|ACG48511.1| growth-regulating factor [Zea mays]	Unigene50319_All//3.00E-26//AT2G45480| AtGRF9 (GROWTH-REGULATING FACTOR 9); transcription activator	Unigene50319_All//0.00E+00//gi|78354490|gb|DT574764.1|DT574764	GRF		GO:0010468//GO:0016817//GO:0032559//GO:0043231	nr +
Unigene5032_All	873	4.49	1.39	3.48	7.48	6.07	5.48	6.73	6.46	2.14	-1.69E+00	4.76E-07	Down	-3.71E-01	2.63E-01		-2.99E-01	2.18E-01		-4.47E-01	5.83E-02		-5.87E-02	8.12E-01		-1.65E+00	2.26E-12	Down	Unigene5032_All//gi|297822593|ref|XP_002879179.1|//1.00E-36//copper-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325018|gb|EFH55438.1| copper-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5032_All//9.00E-33//AT2G28860| copper-binding family protein	Unigene5032_All//0.00E+00//TC156654				nr -
Unigene50320_All	3412	11.58	9.83	13.50	0.12	0.53	0.61	0.00	0.00	0.00	-2.36E-01	6.91E-03		2.22E-01	8.26E-03		2.20E+00	3.62E-05	Up	2.38E+00	4.55E-06	Up	null	null		null	null		Unigene50320_All//gi|77176831|gb|AB64521.1|//0.00E+00//sucrose-phosphate synthase isoform B [Nicotiana tabacum]	Unigene50320_All//0.00E+00//AT1G04920| ATSPS3F (sucrose phosphate synthase 3F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups	Unigene50320_All//0.00E+00//TC176340		ko00500|Starch and sucrose metabolism	GO:0005984//GO:0035251	nr -
Unigene50321_All	893	271.68	733.03	433.39	208.07	217.87	237.04	242.70	269.96	185.85	1.43E+00	0.00E+00	Up	6.74E-01	1.85E-137		6.64E-02	1.02E-01		1.88E-01	2.95E-08		1.54E-01	1.67E-07		-3.85E-01	1.42E-36		Unigene50321_All//gi|21616051|emb|CAC86003.1|//1.00E-102//aspartic proteinase [Theobroma cacao]	Unigene50321_All//8.00E-90//AT1G11910| aspartyl protease family protein	Unigene50321_All//0.00E+00//gi|164360703|gb|ESR04824.1|ESR04824			GO:0004175//GO:0019538//GO:0043231	nr +
Unigene50322_All	486	10.66	10.43	22.24	23.68	21.11	25.46	3.04	1.89	1.97	-3.18E-02	9.18E-01		1.06E+00	7.40E-09	Up	-1.65E-01	3.86E-01		1.05E-01	6.16E-01		-6.87E-01	1.64E-01		-6.30E-01	1.82E-01									
Unigene50323_All	1323	0.47	1.72	0.56	1.36	1.41	1.37	20.01	22.75	43.18	1.86E+00	6.77E-05	Up	2.48E-01	7.45E-01		5.23E-02	9.39E-01		1.06E-02	9.85E-01		1.85E-01	4.89E-02		1.11E+00	2.34E-61	Up	Unigene50323_All//gi|115460200|ref|NP_001053700.1|//2.00E-90//Os04g0589700 [Oryza sativa Japonica Group] >gi|38346713|emb|CAE04863.2| OSJNBa0086006.11 [Oryza sativa (japonica cultivar-group)] >gi|113565271|dbj|BAF15614.1| Os04g0589700 [Oryza sativa Japonica Group]	Unigene50323_All//8.00E-55//AT2G35930| PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase				nr -
Unigene50324_All	1418	11.66	7.33	7.74	8.71	8.04	4.62	1.61	0.47	3.09	-6.71E-01	9.62E-07		-5.92E-01	2.79E-05		-1.16E-01	5.67E-01		-9.16E-01	7.28E-09		-1.77E+00	1.47E-05	Down	9.41E-01	2.05E-04		Unigene50324_All//gi|297842251|ref|XP_002889007.1|//1.00E-21//J-domain protein required for chloroplast accumulation response 1 [Arabidopsis lyrata subsp. lyrata] >gi|297334848|gb|EFH65266.1| J-domain protein required for chloroplast accumulation response 1 [Arabidopsis lyrata subsp. lyrata]	Unigene50324_All//2.00E-17//AT1G75100| JAC1 (J-DOMAIN PROTEIN REQUIRED FOR CHLOROPLAST ACCUMULATION RESPONSE 1); heat shock protein binding	Unigene50324_All//0.00E+00//gi|73861676|gb|DT464415.1|DT464415				nr -
Unigene50325_All	1107	1.47	1.74	1.64	2.79	1.74	2.86	2.60	2.08	1.08	2.47E-01	6.22E-01		1.59E-01	7.37E-01		-6.80E-01	4.52E-02		3.37E-02	9.45E-01		-3.23E-01	3.72E-01		-1.27E+00	1.18E-04	Down	Unigene50325_All//gi|115454951|ref|NP_001051076.1|//8.00E-65//Os03g0715400 [Oryza sativa Japonica Group] >gi|113549547|dbj|BAF12990.1| Os03g0715400 [Oryza sativa Japonica Group]	Unigene50325_All//3.00E-71//AT1G67960| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Membrane protein,Tapt1/CMV receptor (InterPro:IPR008010); Has 243 Blast hits to 229 proteins in 123 species: Archae - 0; Bacteria - 0; Metazoa - 79; Fungi - 87; Plants - 18; Viruses - 0; Other Eukaryotes - 59 (source: NCBI BLink).	Unigene50325_All//0.00E+00//gi|78351068|gb|DT571342.1|DT571342			GO:0044464	nr -
Unigene50327_All	1485	1.16	0.55	0.39	0.94	0.65	0.18	9.31	14.21	12.88	-1.09E+00	2.99E-02		-1.56E+00	4.51E-03		-5.33E-01	3.44E-01		-2.36E+00	2.38E-04	Down	6.10E-01	1.08E-08		4.68E-01	2.09E-05		Unigene50327_All//gi|225457849|ref|XP_002279104.1|//0.00E+00//PREDICTED: similar to DNAJ heat shock N-terminal domain-containing protein [Vitis vinifera]	Unigene50327_All//4.00E-155//AT1G77020| DNAJ heat shock N-terminal domain-containing protein			ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene50329_All	340	15.54	32.34	24.59	7.33	13.57	11.16	7.96	21.64	32.69	1.06E+00	2.48E-09	Up	6.62E-01	1.43E-03		8.90E-01	1.00E-03		6.07E-01	5.89E-02		1.44E+00	2.91E-12	Up	2.04E+00	1.45E-29	Up			Unigene50329_All//9.00E-73//CO131581				
Unigene5033_All	2129	0.59	1.55	0.23	1.47	1.12	2.02	4.75	12.29	25.52	1.39E+00	9.96E-05	Up	-1.39E+00	3.39E-02		-4.02E-01	2.71E-01		4.51E-01	1.42E-01		1.37E+00	1.21E-38	Up	2.43E+00	1.70E-175	Up	Unigene5033_All//gi|15227189|ref|NP_182322.1|//0.00E+00//RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase [Arabidopsis thaliana] >gi|75319082|sp|P92050.1|RKF3_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase RKF3; AltName: Full=Receptor-like kinase in flowers 3; Flags: Precursor >gi|1785621|emb|CAB06335.1| AtPK2324 [Arabidopsis thaliana] >gi|2463927|gb|AAC50045.1| receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi|14335116|gb|AAK59837.1| At2g48010/T9J23.16 [Arabidopsis thaliana] >gi|23308235|gb|AAN18087.1| At2g48010/T9J23.16 [Arabidopsis thaliana]	Unigene5033_All//0.00E+00//AT2G48010| RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase	Unigene5033_All//0.00E+00//ES845519		ko04626|Plant-pathogen interaction		nr -
Unigene50330_All	311	18.00	26.88	38.52	18.42	17.83	39.65	30.45	60.74	26.13	5.79E-01	3.91E-03		1.10E+00	2.95E-10	Up	-4.72E-02	8.59E-01		1.11E+00	1.07E-11	Up	9.96E-01	3.25E-17		-2.21E-01	2.02E-01		Unigene50330_All//gi|224057577|ref|XP_002299276.1|//1.00E-20//glutathione reductase [Populus trichocarpa] >gi|222846534|gb|EEE84081.1| glutathione reductase [Populus trichocarpa]	Unigene50330_All//6.00E-19//AT3G24170| ATGR1 (glutathione-disulfide reductase); FAD binding / NADP or NADPH binding / glutathione-disulfide reductase/ oxidoreductase	Unigene50330_All//6.00E-49//TC132998		ko00480|Glutathione metabolism	GO:0000729//GO:0006790//GO:0009314//GO:0015038//GO:0019725//GO:0019953//GO:0030554//GO:0042579	nr +
Unigene50333_All	346	3.02	30.61	10.00	3.46	3.38	6.66	1.71	7.61	4.84	3.34E+00	1.72E-38	Up	1.73E+00	3.81E-06	Up	-3.02E-02	9.58E-01		9.46E-01	2.66E-02		2.15E+00	6.92E-08	Up	1.50E+00	1.16E-03				Unigene50333_All//4.00E-07//TC172112				
Unigene50335_All	549	46.41	48.45	73.52	8.44	15.56	6.75	9.09	20.40	12.19	6.21E-02	6.02E-01		6.64E-01	2.02E-14		8.82E-01	2.57E-06		-3.23E-01	2.93E-01		1.17E+00	2.23E-13	Up	4.24E-01	3.34E-02				Unigene50335_All//3.00E-117//TC160697				
Unigene50337_All	527	11.91	40.86	21.93	9.83	18.69	17.83	17.73	42.75	47.10	1.78E+00	1.02E-37	Up	8.80E-01	4.35E-07		9.27E-01	8.88E-08		8.59E-01	3.43E-06		1.27E+00	1.08E-29	Up	1.41E+00	5.02E-39	Up	Unigene50337_All//gi|21425669|emb|CAC95022.1|//1.00E-13//mitochondrial RNA polymerase [Nicotiana tabacum]	Unigene50337_All//6.00E-12//AT1G68990| DNA-directed RNA polymerase, mitochondrial (RPOMT)	Unigene50337_All//2.00E-77//DN816848			GO:0003676//GO:0010467//GO:0034062//GO:0043231//GO:0044444	nr +
Unigene50338_All	240	1.96	8.87	3.33	7.26	5.88	7.90	9.87	7.14	13.28	2.18E+00	1.82E-05	Up	7.62E-01	3.62E-01		-3.04E-01	5.58E-01		1.22E-01	8.06E-01		-4.66E-01	2.27E-01		4.29E-01	1.64E-01		Unigene50338_All//gi|115450285|ref|NP_001048743.1|//8.00E-38//Os03g0114300 [Oryza sativa Japonica Group] >gi|113547214|dbj|BAF10657.1| Os03g0114300 [Oryza sativa Japonica Group]	Unigene50338_All//7.00E-36//AT4G10730| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene50338_All//4.00E-83//TC141555		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004672//GO:0006464//GO:0032559	nr -
Unigene50339_All	568	3.22	1.43	3.47	8.07	4.85	3.98	1.19	1.25	0.63	-1.18E+00	1.60E-02		1.06E-01	8.15E-01		-7.34E-01	5.55E-03		-1.02E+00	2.53E-04	Down	7.08E-02	9.42E-01		-9.16E-01	2.21E-01		Unigene50339_All//gi|224098409|ref|XP_002311164.1|//6.00E-08//f-box family protein [Populus trichocarpa] >gi|222850984|gb|EEE88531.1| f-box family protein [Populus trichocarpa]	Unigene50339_All//0.00E+00//DW519582				nr -
Unigene50340_All	345	2.73	2.06	4.01	7.08	5.39	1.44	4.29	0.73	1.50	-4.09E-01	5.66E-01		5.56E-01	3.62E-01		-3.93E-01	3.47E-01		-2.30E+00	6.01E-07	Down	-2.56E+00	1.18E-05	Down	-1.51E+00	2.08E-03		Unigene50340_All//gi|297831228|ref|XP_002883496.1|//2.00E-07//glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata] >gi|297329336|gb|EFH59755.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata]	Unigene50340_All//5.00E-08//AT3G24040| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	Unigene50340_All//0.00E+00//BQ409128			GO:0035252//GO:0044464	nr -
Unigene50341_All	311	5.22	9.94	5.99	17.94	13.18	12.92	44.59	55.91	19.47	9.30E-01	9.03E-03		2.01E-01	6.69E-01		-4.45E-01	7.38E-02		-4.73E-01	6.73E-02		3.26E-01	7.07E-03		-1.20E+00	1.50E-17	Down		Unigene50341_All//8.00E-05//AT4G11260| SGT1B; protein binding	Unigene50341_All//4.00E-158//TC178408		ko04626|Plant-pathogen interaction		kegg +
Unigene50346_All	829	20.45	23.72	23.45	27.10	33.48	53.17	1044.31	657.14	2656.65	2.14E-01	1.06E-01		1.97E-01	1.57E-01		3.05E-01	2.23E-03		9.72E-01	7.44E-33		-6.68E-01	0.00E+00		1.35E+00	0.00E+00	Up	Unigene50346_All//gi|3287826|sp|O49853.1|DCS4_GOSAR//1.00E-152//RecName: Full=(+)-delta-cadinene synthase isozyme C2; Short=D-cadinene synthase C2 >gi|2879841|emb|CAA76223.1| (+)-delta-cadinene synthase [Gossypium arboreum]	Unigene50346_All//2.00E-63//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene50346_All//0.00E+00//TC129587		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0003824//GO:0046872	nr -
Unigene50348_All	553	63.96	75.23	67.02	42.97	54.61	36.02	114.07	261.43	55.18	2.34E-01	5.82E-03		6.75E-02	5.32E-01		3.46E-01	2.09E-04		-2.55E-01	2.88E-02		1.20E+00	6.44E-170	Up	-1.05E+00	4.06E-62	Down	Unigene50348_All//gi|145325447|ref|NP_001077728.1|//4.00E-12//dormancy/auxin associated family protein [Arabidopsis thaliana]	Unigene50348_All//2.00E-13//AT1G56220| dormancy/auxin associated family protein	Unigene50348_All//1.00E-119//DW237752				nr +

Unigene50349_All	411	0.00	0.00	0.00	0.85	0.25	0.22	4.53	3.97	1.45	null	null		null	null		-1.75E+00	1.90E-01		-1.95E+00	1.96E-01		-1.91E-01	6.62E-01		-1.64E+00	1.88E-04	Down	Unigene50349_All//gi|255563931|ref|XP_002522965.1|//2.00E-17//Disease resistance protein RPS2, putative [Ricinus communis] >gi|223537777|gb|EEF39395.1|Disease resistance protein RPS2, putative [Ricinus communis]		Unigene50349_All//4.00E-168//TC165695				nr +
Unigene50350_All	468	5.37	3.14	2.96	29.70	24.35	11.97	1.08	0.63	0.43	-7.73E-01	5.22E-02		-8.59E-01	4.12E-02		-2.86E-01	6.01E-02		-1.31E+00	3.15E-17	Down	-7.94E-01	4.02E-01		-1.35E+00	1.40E-01		Unigene50350_All//gi|255563909|ref|XP_002522954.1|//2.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223537766|gb|EEF39384.1|conserved hypothetical protein [Ricinus communis]		Unigene50350_All//0.00E+00//TC165695				nr +
Unigene50352_All	341	2.76	7.28	4.84	5.26	3.33	5.56	15.50	17.65	12.85	1.40E+00	8.73E-04	Up	8.10E-01	1.35E-01		-6.58E-01	1.66E-01		8.10E-02	8.85E-01		1.88E-01	4.38E-01		-2.70E-01	2.56E-01				Unigene50352_All//1.00E-87//TC171592				
Unigene50354_All	534	2.45	2.37	1.70	1.03	3.29	15.05	4.43	3.99	1.94	-4.63E-02	9.48E-01		-5.31E-01	3.86E-01		1.68E+00	1.03E-03		3.88E+00	3.25E-35	Up	-1.52E-01	7.01E-01		-1.19E+00	1.05E-03		Unigene50354_All//gi|27764978|gb|AA023610.1|//2.00E-07//At5g44005 [Arabidopsis thaliana]	Unigene50354_All//2.00E-65//AT5G44005| unknown protein	Unigene50354_All//1.00E-20//FL577746		GO:0016020	nr -
Unigene50356_All	1315	0.88	0.15	0.36	2.01	1.70	1.99	5.18	5.50	9.36	-2.51E+00	8.99E-04	Down	-1.26E+00	6.41E-02		-2.38E-01	5.74E-01		-1.13E-02	9.70E-01		8.71E-02	6.94E-01		8.55E-01	2.42E-09		Unigene50356_All//gi|15239894|ref|NP_199165.1|//1.00E-18//DC1 domain-containing protein [Arabidopsis thaliana]	Unigene50356_All//2.00E-19//AT5G43520| DC1 domain-containing protein	Unigene50356_All//0.00E+00//gi|78346353|gb|DT566627.1|DT566627			nr -
Unigene50358_All	433	4.59	5.27	6.39	10.01	10.34	13.56	41.69	20.46	20.79	1.98E-01	6.25E-01		4.78E-01	2.40E-01		4.67E-02	8.95E-01		4.38E-01	8.45E-02		-1.03E+00	2.60E-17	Down	-1.00E+00	3.15E-17	Down	Unigene50358_All//gi|209967441|gb|ACJ02349.1|//6.00E-08//60S ribosomal protein L35a [Vernicia fordii]	Unigene50358_All//1.00E-08//AT1G74270| 60S ribosomal protein L35a (RPL35aC)	Unigene50358_All//0.00E+00//TC163240		ko03010|Ribosome	nr +
Unigene50359_All	1100	4.23	1.06	3.63	2.94	2.16	2.38	21.72	14.59	22.78	-2.00E+00	3.99E-10	Down	-2.22E-01	4.70E-01		-4.47E-01	2.01E-01		-3.06E-01	4.19E-01		-5.74E-01	8.35E-09		6.90E-02	5.55E-01		Unigene50359_All//gi|297726841|ref|NP_001175784.1|//1.00E-23//Os09g0334900 [Oryza sativa Japonica Group] >gi|50252358|dbj|BAD28446.1|ankyrin repeat family protein-like [Oryza sativa Japonica Group] >gi|50252564|dbj|BAD28737.1|ankyrin repeat family protein-like [Oryza sativa Japonica Group] >gi|255678798|dbj|BAH94512.1|Os09g0334900 [Oryza sativa Japonica Group]	Unigene50359_All//5.00E-22//AT4G03450| ankyrin repeat family protein	Unigene50359_All//0.00E+00//TC175720			nr +
Unigene5036_All	580	27.78	15.20	14.87	16.40	15.56	22.50	31.93	10.45	12.91	-8.70E-01	6.93E-10		-9.02E-01	5.75E-10		-7.67E-02	7.49E-01		4.56E-01	3.34E-03		-1.61E+00	7.40E-35	Down	-1.31E+00	1.89E-26	Down	Unigene5036_All//gi|297795015|ref|XP_002863592.1|//1.00E-49//glutathione-dependent formaldehyde dehydrogenase [Arabidopsis lyrata subsp. lyrata] >gi|297311227|gb|EFH41651.1|glutathione-dependent formaldehyde dehydrogenase [Arabidopsis lyrata subsp. lyrata]	Unigene5036_All//8.00E-51//AT5G43940| HOT5 (sensitive to hot temperatures 5); S-(hydroxymethyl)glutathione dehydrogenase/ S-nitrosoglutathione reductase	Unigene5036_All//0.00E+00//gi|11205772|gb|BF274702.1|BF274702		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism	nr -
Unigene50361_All	771	0.20	0.53	0.35	0.78	2.59	0.12	2.58	3.74	2.48	1.37E+00	2.74E-01		7.62E-01	6.44E-01		1.74E+00	2.55E-04	Up	-2.73E+00	1.74E-02		5.37E-01	1.10E-01		-5.55E-02	9.02E-01		Unigene50361_All//gi|297808613|ref|XP_002872190.1|//1.00E-72//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318027|gb|EFH48449.1|leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50361_All//3.00E-73//AT5G25930| leucine-rich repeat family protein / protein kinase family protein	Unigene50361_All//2.00E-11//TC162436			GO:0004674//GO:0006464//GO:0016491//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene50363_All	676	1.78	0.15	0.79	1.77	2.39	1.74	4.07	1.11	1.83	-3.57E+00	3.63E-05	Down	-1.18E+00	7.58E-02		4.37E-01	4.45E-01		-2.59E-02	9.54E-01		-1.87E+00	5.66E-07	Down	-1.15E+00	5.37E-04	Down	Unigene50363_All//gi|115450299|ref|NP_001048750.1|//4.00E-85//Os03g0115200 [Oryza sativa Japonica Group] >gi|113547221|dbj|BAF10664.1|Os03g0115200 [Oryza sativa Japonica Group]	Unigene50363_All//3.00E-76//AT3G13230| RNA binding	Unigene50363_All//2.00E-133//ES804455			GO:0003676	nr +
Unigene50364_All	859	1.22	5.78	5.77	1.62	2.37	1.74	0.74	0.68	0.37	2.25E+00	2.97E-12	Up	2.24E+00	9.34E-12	Up	5.43E-01	2.58E-01		9.57E-02	8.79E-01		-1.16E-01	8.88E-01		-9.93E-01	2.02E-01		Unigene50364_All//gi|124359646|gb|ABD32321.2|//1.00E-13//Ribonuclease H [Medicago truncatula]	Unigene50364_All//3.00E-67//AT5G42905| nucleic acid binding / ribonuclease H	Unigene50364_All//0.00E+00//DN799902			GO:0005488	nr -
Unigene50366_All	350	21.23	9.55	30.12	33.16	27.06	33.29	15.22	6.69	13.32	-1.15E+00	1.89E-07	Down	5.05E-01	5.90E-03		-2.94E-01	8.36E-02		5.60E-03	9.75E-01		-1.19E+00	5.96E-07	Down	-1.93E-01	4.28E-01		Unigene50366_All//gi|211906820|gb|ACJ11753.1|//1.00E-29//UDP-D-apiose/UPD-D-xylose synthetase [Gossypium hirsutum]	Unigene50366_All//8.00E-29//AT1G08200| AXS2 (UDP-D-AP10SE/UDP-D-XYLOSE SYNTHASE 2); UDP-glucuronate decarboxylase	Unigene50366_All//3.00E-128//gi|5014708|gb|AI729856.1|AI729856		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0000166//GO:0005576//GO:0009225//GO:0016831//GO:0016836//GO:0044424//GO:0048037	nr +
Unigene50367_All	644	24.86	23.29	19.76	29.01	29.41	38.29	21.34	17.46	8.04	-9.42E-02	5.61E-01		-3.31E-01	2.59E-02		1.99E-02	9.05E-01		4.01E-01	2.11E-04		-2.90E-01	4.01E-02		-1.41E+00	3.63E-22	Down			Unigene50367_All//0.00E+00//TC162748				
Unigene50368_All	1365	24.80	8.83	9.17	31.46	30.80	17.24	1.27	0.21	1.31	-1.49E+00	4.50E-46	Down	-1.44E+00	4.48E-42	Down	-3.04E-02	8.01E-01		-8.68E-01	8.04E-27		-2.57E+00	1.60E-06	Down	4.85E-02	9.30E-01		Unigene50368_All//gi|259563723|gb|ACW83060.1|//1.00E-151//glycosyltransferase family GT8 protein [Populus deltoides]	Unigene50368_All//1.00E-140//AT1G19300| PARVUS (PARVUS); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene50368_All//0.00E+00//TC175620			nr -
Unigene50369_All	2003	0.60	0.48	1.12	7.56	8.46	8.52	2.87	1.17	1.27	-3.22E-01	6.18E-01		8.94E-01	4.60E-02		1.62E-01	3.00E-01		1.73E-01	2.61E-01		-1.30E+00	1.98E-08	Down	-1.17E+00	1.37E-07	Down	Unigene50369_All//gi|15983811|gb|AAL10502.1|//1.00E-159//AT5g60720/mup24_130 [Arabidopsis thaliana] >gi|27363288|gb|AA011563.1|At5g60720/mup24_130 [Arabidopsis thaliana]	Unigene50369_All//4.00E-155//AT5G60720| unknown protein	Unigene50369_All//0.00E+00//TC136835			nr -
Unigene50376_All	533	47.41	31.47	43.56	16.45	11.95	7.97	1.75	1.80	0.67	-5.92E-01	4.63E-08		-1.22E-01	3.45E-01		-4.61E-01	1.38E-02		-1.05E+00	6.34E-08	Down	4.76E-02	9.64E-01		-1.38E+00	3.03E-02		Unigene50376_All//gi|164605532|dbj|BAF98598.1|//3.00E-27//CM0545.330.nc [Lotus japonicus]	Unigene50376_All//2.00E-19//AT3G44020| thylakoid lumenal P17.1 protein	Unigene50376_All//2.00E-133//gi|109873739|gb|DW502714.1|DW502714			nr -
Unigene50378_All	338	6.81	6.75	8.03	8.99	7.64	10.96	10.63	5.19	6.48	-1.39E-02	9.87E-01		2.38E-01	5.75E-01		-2.35E-01	5.44E-01		2.85E-01	4.25E-01		-1.03E+00	3.98E-04	Down	-7.14E-01	1.05E-02		Unigene50378_All//gi|94807638|gb|ABF47116.1|//4.00E-12//At5g10745 [Arabidopsis thaliana]		Unigene50378_All//2.00E-116//ES845929		GO:0043231	nr -
Unigene50379_All	556	38.39	8.57	5.27	40.23	31.65	13.24	44.71	6.46	8.88	-2.16E+00	1.17E-48	Down	-2.87E+00	1.18E-64	Down	-3.46E-01	1.68E-03		-1.60E+00	6.87E-37	Down	-2.79E+00	9.99E-93	Down	-2.33E+00	4.96E-78	Down	Unigene50379_All//gi|195617694|gb|ACG30677.1|//2.00E-52//histone H4 [Zea mays]	Unigene50379_All//1.00E-40//AT5G59970| histone H4	Unigene50379_All//0.00E+00//TC170046			GO:0000785//GO:0003676//GO:0006950//GO:0009536//GO:0016020//GO:0031981//GO:0034728	nr -
Unigene5038_All	788	0.00	0.00	0.00	0.25	0.35	0.23	37.40	26.25	15.17	null	null		null	null		4.67E-01	8.16E-01		-1.41E-01	9.34E-01		-5.10E-01	8.68E-09		-1.30E+00	2.25E-41	Down	Unigene5038_All//gi|208972080|gb|ACI32639.1|//1.00E-26//STS1 [Humulus lupulus]	Unigene5038_All//6.00E-19//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene5038_All//1.00E-64//gi|48822193|gb|CO123506.1|CO123506		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis		nr +
Unigene50384_All	440	16.05	57.12	26.87	21.40	27.08	45.68	49.78	101.54	59.85	1.83E+00	1.07E-45	Up	7.43E-01	1.34E-05		3.40E-01	4.05E-02		1.09E+00	2.11E-18	Up	1.03E+00	1.05E-41	Up	2.66E-01	4.73E-03				Unigene50384_All//0.00E+00//TC142254				
Unigene50386_All	1040	1.21	5.26	0.61	0.67	0.76	1.00	10.73	21.34	16.40	2.12E+00	1.40E-12	Up	-9.75E-01	1.29E-01		1.83E-01	8.27E-01		5.75E-01	4.26E-01		9.92E-01	6.20E-20		6.11E-01	2.03E-07		Unigene50386_All//gi|124301012|gb|ABN04758.1|//2.00E-14//At3g51580 [Arabidopsis thaliana]	Unigene50386_All//2.00E-10//AT3G51580| unknown protein	Unigene50386_All//0.00E+00//TC169936			nr -
Unigene50387_All	881	2.49	6.67	4.78	0.90	1.60	0.77	0.72	0.09	0.23	1.42E+00	5.02E-08	Up	9.37E-01	2.50E-03		8.25E-01	1.57E-01		-2.35E-01	7.53E-01		-2.92E+00	4.19E-03		-1.67E+00	4.29E-02		Unigene50387_All//gi|297823649|ref|XP_002879707.1|//5.00E-75//aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325546|gb|EFH55966.1|aldo/keto reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50387_All//3.00E-75//AT2G37760| aldo/keto reductase family protein	Unigene50387_All//3.00E-152//C0092015		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism	GO:0004033//GO:0006970//GO:0008152//GO:0010038	nr +
Unigene50388_All	1116	3.47	5.90	9.50	2.54	4.10	3.40	0.49	0.00	0.11	7.67E-01	8.36E-04		1.45E+00	8.44E-14	Up	6.90E-01	1.22E-02		4.18E-01	2.17E-01		-8.94E+00	4.61E-04	Down	-2.20E+00	2.24E-02		Unigene50388_All//gi|3378650|emb|CAA66205.1|//1.00E-127//orf [Medicago sativa]	Unigene50388_All//2.00E-116//AT2G37760| aldo/keto reductase family protein	Unigene50388_All//0.00E+00//C0092015		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene50389_All	406	54.64	87.61	91.15	37.05	48.51	40.49	94.87	57.55	45.04	6.81E-01	6.82E-14		7.38E-01	7.00E-16		3.89E-01	1.08E-03		1.28E-01	4.41E-01		-7.21E-01	3.96E-20		-1.07E+00	7.10E-40	Down	Unigene50389_All//gi|10177953|dbj|BAB11312.1|//2.00E-27//aluminum-induced protein-like [Arabidopsis thaliana] >gi|21537246|gb|AAM61587.1|aluminum-induced protein-like [Arabidopsis thaliana]	Unigene50389_All//9.00E-29//AT5G43830| unknown protein	Unigene50389_All//3.00E-156//gi|5045658|gb|AI726806.1|AI726806			GO:0016020//GO:0043231//GO:0044444	nr +
Unigene50390_All	716	5.41	5.10	2.16	9.95	9.23	11.04	22.97	13.54	14.30	-8.58E-02	7.77E-01		-1.33E+00	7.74E-05	Down	-1.08E-01	6.72E-01		1.50E-01	5.49E-01		-7.62E-01	6.67E-10		-6.84E-01	1.29E-08		Unigene50390_All//gi|296881978|gb|ADH82414.1|//4.00E-06//actin [Jatropha curcas]	Unigene50390_All//1.00E-06//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene50390_All//5.00E-150//gi|48828174|gb|CO126564.1|CO126564		ko04145|Phagosome		nr +
Unigene50391_All	1144	0.14	5.18	1.49	4.66	6.23	14.21	0.81	1.83	1.36	5.24E+00	2.46E-29	Up	3.44E+00	1.59E-06	Up	4.19E-01	5.80E-02		1.61E+00	1.32E-26	Up	1.17E+00	3.80E-03		7.40E-01	1.07E-01		Unigene50391_All//gi|38112198|gb|AAR11193.1|//1.00E-135//9-cis-epoxycarotenoid dioxygenase 1 [Vitis vinifera]	Unigene50391_All//7.00E-135//AT3G14440| NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	Unigene50391_All//2.00E-113//TC175846		ko00906|Carotenoid biosynthesis		nr +
Unigene50392_All	833	1.44	1.64	1.66	10.35	8.72	8.13	3.96	2.16	1.39	1.85E-01	7.28E-01		2.02E-01	7.12E-01		-2.46E-01	2.43E-01		-3.47E-01	9.19E-02		-8.76E-01	3.99E-03		-1.51E+00	1.48E-06	Down	Unigene50392_All//gi|186494291|ref|NP_001117575.1|//2.00E-09//CLE26 (CLAVATA3/ESR-RELATED 26); protein binding / receptor binding [Arabidopsis thaliana]	Unigene50392_All//1.00E-10//AT1G69970| CLE26 (CLAVATA3/ESR-RELATED 26); protein binding / receptor binding	Unigene50392_All//0.00E+00//TC153231			nr +
Unigene50393_All	496	4.22	2.35	1.72	10.04	8.61	7.38	8.10	5.22	3.05	-8.45E-01	5.73E-02		-1.30E+00	6.74E-03		-2.22E-01	4.52E-01		-4.45E-01	1.11E-01		-6.32E-01	2.02E-02		-1.41E+00	4.31E-07	Down							
Unigene50394_All	1448	0.14	0.59	0.37	3.34	3.69	3.74	1.02	0.66	0.22	2.04E+00	1.59E-02		1.35E+00	2.25E-01		1.44E-01	6.26E-01		1.66E-01	6.01E-01		-6.22E-01	2.14E-01		-2.22E+00	4.14E-05	Down	Unigene50394_All//gi|224111420|ref|XP_002318849.1|//1.00E-106//rna-dependent RNA polymerase [Populus trichocarpa] >gi|222864889|gb|EEF02020.1| rna-dependent RNA polymerase [Populus trichocarpa]	Unigene50394_All//4.00E-88//AT1G14790| RDR1 (RNA-DEPENDENT RNA POLYMERASE 1); RNA-directed RNA polymerase/ nucleic acid binding				GO:0010033//GO:0010608//GO:0016779//GO:0048522//GO:0051707	nr +
Unigene50396_All	555	7.64	5.02	5.09	10.50	9.18	8.38	6.40	4.22	2.30	-6.05E-01	4.04E-02		-5.87E-01	5.86E-02		-1.94E-01	4.92E-01		-3.25E-01	2.22E-01		-6.02E-01	4.06E-02		-1.48E+00	8.72E-07	Down		Unigene50396_All//2.00E-06//AT3G58670| unknown protein	Unigene50396_All//0.00E+00//BE055778				
Unigene50397_All	810	0.26	0.19	0.00	2.34	2.17	2.45	5.38	3.87	10.87	-4.61E-01	7.58E-01		-8.01E+00	1.45E-01		-1.08E-01	8.17E-01		7.01E-02	9.04E-01		-4.74E-01	7.39E-02		1.02E+00	6.00E-09	Up			Unigene50397_All//4.00E-166//TC165778				
Unigene5040_All	1048	6.14	1.55	1.63	11.60	10.81	8.45	5.93	1.32	3.95	-1.99E+00	1.21E-13	Down	-1.92E+00	2.01E-12	Down	-1.02E-01	6.02E-01		-4.57E-01	4.58E-03		-2.17E+00	7.00E-18	Down	-5.85E-01	4.21E-03		Unigene5040_All//gi|51490665|emb|CAG26903.1|//5.00E-49//ALY protein [Nicotiana benthamiana]	Unigene5040_All//3.00E-35//AT5G02530| RNA and export factor-binding protein, putative	Unigene5040_All//0.00E+00//gi|78337283|gb|DT557557.1|DT557557		ko03040|Spliceosome		nr +
Unigene50400_All	859	668.11	145.22	292.78	110.12	126.08	138.86	0.00	0.00	0.00	-2.20E+00	0.00E+00	Down	-1.19E+00	0.00E+00	Down	1.95E-01	3.42E-05		3.34E-01	1.60E-13		null	null		null	null		Unigene50400_All//gi|297830242|ref|XP_002883003.1|//1.00E-121//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328843|gb|EFH59262.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50400_All//3.00E-110//AT3G16370| GDSL-motif lipase/hydrolase family protein	Unigene50400_All//0.00E+00//TC133076			GO:0016788	nr +
Unigene50401_All	470	10.46	27.17	18.58	13.46	14.51	36.23	85.01	450.95	361.34	1.38E+00	7.78E-16	Up	8.28E-01	4.57E-05		1.08E-01	6.99E-01		1.43E+00	1.85E-23	Up	2.41E+00	0.00E+00	Up	2.09E+00	0.00E+00	Up	Unigene50401_All//gi|22759723|dbj|BAC10910.1|//4.00E-21//protease inhibitor 2 [Zinnia elegans]	Unigene50401_All//6.00E-18//AT2G38870| protease inhibitor, putative				GO:0004866//GO:0006952//GO:0016787//GO:0030312	nr -
Unigene50402_All	1317	0.12	0.62	0.08	0.83	0.44	1.54	1.57	4.54	3.33	2.37E+00	1.01E-02		-5.59E-01	7.75E-01		-9.05E-01	1.55E-01		8.91E-01	5.35E-02		1.53E+00	6.13E-11	Up	1.08E+00	2.56E-05	Up			Unigene50402_All//0.00E+00//gi|21101613|gb|BQ413926.1|BQ413926				

Unigene50403_All	1029	46.27	3.45	14.33	10.51	10.07	3.34	0.74	0.81	0.35	-3.75E+00	1.98E-191	Down	-1.69E+00	7.46E-75	Down	-6.06E-02	7.98E-01		-1.66E+00	6.50E-19	Down	1.35E-01	8.42E-01		-1.09E+00	1.21E-01		Unigene50403_All//gi|297836564|ref|XP_002886164.1|//4.00E-30//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332004|gb|EFH62423.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50403_All//4.00E-30//AT2G18300| basic helix-loop-helix (bHLH) family protein	Unigene50403_All//0.00E+00//TC167832	bHLH	ko04712|Circadian rhythm - plant	GO:0009725	nr -
Unigene50407_All	459	5.02	9.05	3.48	3.47	13.50	4.92	26.44	56.64	80.81	8.52E-01	4.41E-03		-5.27E-01	2.36E-01		1.96E+00	1.57E-14	Up	5.03E-01	2.69E-01		1.10E+00	2.54E-27	Up	1.61E+00	2.20E-70	Up			Unigene50407_All//2.00E-151//gi|73860670|gb|DT463409.1|DT463409				
Unigene50408_All	810	1.55	6.07	5.00	6.46	11.86	10.26	0.52	0.93	1.23	1.97E+00	2.21E-10	Up	1.69E+00	7.02E-07	Up	8.77E-01	5.58E-07		6.68E-01	7.54E-04		8.31E-01	2.64E-01		1.24E+00	4.26E-02		Unigene50408_All//gi|3915023|sp|O22060.1|SPS1_CITUN//1.00E-124//RecName: Full=Sucrose-phosphate synthase 1; AltName: Full=UDP-glucose-fructose-phosphate glucosyltransferase 1 >gi|2588888|dbj|BAA23213.1| sucrose-phosphate synthase [Citrus unshiu]	Unigene50408_All//7.00E-114//AT5G20280| ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups	Unigene50408_All//0.00E+00//TC137668		ko00500|Starch and sucrose metabolism		nr -
Unigene50409_All	1268	0.45	0.08	0.08	18.74	5.95	1.42	4.00	0.33	0.94	-2.51E+00	2.93E-02		-2.43E+00	4.40E-02		-1.66E+00	4.88E-47	Down	-3.72E+00	6.76E-104	Down	-3.60E+00	1.52E-24	Down	-2.09E+00	1.61E-14	Down	Unigene50409_All//gi|16323145|gb|AAL15307.1|//1.00E-32//AT5g11000/T30N20_270 [Arabidopsis thaliana] >gi|21436003|gb|AAM51579.1| AT5g11000/T30N20_270 [Arabidopsis thaliana]	Unigene50409_All//9.00E-25//AT5G28150| unknown protein	Unigene50409_All//0.00E+00//gi|109879377|gb|DW508347.1|DW508347				nr -
Unigene5041_All	634	2.97	15.82	2.10	0.00	1.68	3.42	12.34	24.46	38.20	2.41E+00	3.47E-26	Up	-5.01E-01	3.23E-01		1.07E+01	1.43E-06	Up	1.17E+01	5.90E-13	Up	9.87E-01	4.47E-14		1.63E+00	5.09E-47	Up	Unigene5041_All//gi|56542449|gb|AAV92889.1|//2.00E-18//Avr9/Cf-9 rapidly elicited protein 19 [Nicotiana tabacum]	Unigene5041_All//1.00E-10//AT4G27280| calcium-binding EF hand family protein	Unigene5041_All//3.00E-163//TC156372				nr -
Unigene50410_All	924	0.00	0.71	0.00	0.11	1.08	0.88	16.24	15.38	51.39	9.48E+00	6.25E-04	Up	null	null		3.33E+00	2.50E-04	Up	3.03E+00	2.68E-03		-7.89E-02	6.40E-01		1.66E+00	7.34E-94	Up	Unigene50410_All//gi|297798220|ref|XP_002866994.1|//5.00E-59//homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata] >gi|297312830|gb|EFH43253.1| homeobox-leucine zipper protein ATHB-40 [Arabidopsis lyrata subsp. lyrata]	Unigene50410_All//5.00E-44//AT4G36740| ATHB40 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 40); DNA binding / transcription factor	Unigene50410_All//2.00E-57//TC139526	HB		GO:0001071//GO:0003677//GO:0006351//GO:0009725//GO:0010468//GO:0043231//GO:0048513	nr +
Unigene50411_All	419	16.61	13.18	11.06	13.79	15.12	8.84	35.62	23.34	16.83	-3.33E-01	1.44E-01		-5.87E-01	1.15E-02		1.33E-01	6.20E-01		-6.42E-01	8.76E-03		-6.10E-01	2.21E-06		-1.08E+00	3.69E-16	Down			Unigene50411_All//0.00E+00//gi|21100424|gb|BQ412737.1|BQ412737				
Unigene50412_All	542	0.97	4.49	2.75	2.85	1.52	1.25	2.03	3.24	1.32	2.22E+00	2.89E-06	Up	1.51E+00	1.11E-02		-9.02E-01	7.78E-02		-1.19E+00	2.78E-02		6.75E-01	1.33E-01		-6.16E-01	2.73E-01		Unigene50412_All//gi|223452408|gb|ACM89531.1|//2.00E-37//serine/threonine protein kinase [Glycine max]	Unigene50412_All//4.00E-34//AT3G59350| serine/threonine protein kinase, putative	Unigene50412_All//0.00E+00//gi|84171243|gb|DR459891.1|DR459891		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016020//GO:0032559	nr -
Unigene50413_All	1911	0.41	0.21	0.17	3.96	1.14	1.61	8.87	11.96	11.51	-9.53E-01	2.33E-01		-1.30E+00	1.38E-01		-1.80E+00	3.75E-17	Down	-1.30E+00	1.49E-09	Down	4.31E-01	2.34E-05		3.75E-01	2.42E-04		Unigene50413_All//gi|126363776|dbj|BAF47752.1|//0.00E+00//multi antimicrobial extrusion family protein [Nicotiana tabacum]	Unigene50413_All//0.00E+00//AT3G21690| MATE efflux family protein	Unigene50413_All//0.00E+00//TC139802			GO:0015291//GO:0015893//GO:0016020	nr -
Unigene50416_All	863	33.65	31.29	10.37	26.67	32.00	15.60	0.00	0.19	0.00	-1.05E-01	3.73E-01		-1.70E+00	4.38E-46	Down	2.63E-01	1.02E-02		-7.74E-01	3.89E-12		7.60E+00	1.39E-01		null	null		Unigene50416_All//gi|118562492|dbj|BAF37542.1|//7.00E-14//cell wall glycine-rich protein [Cucumis sativus]		Unigene50416_All//0.00E+00//gi|13244898|gb|BE054614.2|BE054614		ko03040|Spliceosome	GO:0009725	nr +
Unigene50417_All	708	82.18	132.97	111.54	161.97	154.28	167.45	228.06	235.72	62.80	6.94E-01	1.07E-36		4.41E-01	1.72E-13		-7.02E-02	2.08E-01		4.80E-02	4.24E-01		4.77E-02	2.64E-01		-1.86E+00	0.00E+00	Down	Unigene50417_All//gi|73761685|gb|AAZ83342.1|//2.00E-51//ACC oxidase 1 [Gossypium hirsutum]	Unigene50417_All//2.00E-38//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene50417_All//0.00E+00//TC129647		ko00270|Cysteine and methionine metabolism	GO:0003006//GO:0006555//GO:0016641//GO:0019842//GO:0043169//GO:0050896	nr -
Unigene50418_All	473	5.64	1.71	1.69	7.90	2.84	2.58	18.15	9.99	7.24	-1.72E+00	3.82E-05	Down	-1.74E+00	6.32E-05	Down	-1.48E+00	1.25E-06	Down	-1.62E+00	1.05E-06	Down	-8.62E-01	1.15E-06		-1.32E+00	5.38E-13	Down	Unigene50418_All//gi|25992536|gb|AAN77148.1|//1.00E-10//fiber protein Fb7 [Gossypium barbadense]		Unigene50418_All//0.00E+00//TC167563				nr -
Unigene50419_All	1098	0.76	0.23	0.39	3.86	1.69	1.93	2.16	3.39	2.25	-1.72E+00	3.63E-02		-9.75E-01	2.37E-01		-1.19E+00	1.84E-05	Down	-9.96E-01	6.48E-04		6.52E-01	2.19E-02		6.10E-02	8.78E-01		Unigene50419_All//gi|124360558|gb|ABN08564.1|//1.00E-16//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene50419_All//2.00E-05//AT1G43760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706), Endonuclease/exonuclease/phosphatase (InterPro:IPR005135); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40390.1); Has 2614 Blast hits to 2551 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 1517; Fungi - 2; Plants - 1086; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene50419_All//1.00E-25//TC163312			GO:0005488	nr -
Unigene5042_All	816	1.92	0.50	2.22	4.82	4.77	4.10	6.17	3.48	3.71	-1.95E+00	7.99E-04	Down	2.06E-01	6.64E-01		-1.63E-02	9.50E-01		-2.36E-01	4.96E-01		-8.24E-01	5.41E-04		-7.33E-01	1.48E-03		Unigene5042_All//gi|11994276|dbj|BAB01459.1|//1.00E-96//alpha 1,2-mannosidase-like protein [Arabidopsis thaliana]	Unigene5042_All//6.00E-101//AT1G51590| mannosyl-oligosaccharide 1,2-alpha-mannosidase, putative	Unigene5042_All//0.00E+00//gi|48802378|gb|CO103692.1|CO103692		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis		nr -
Unigene50420_All	451	12.65	28.65	14.05	17.67	9.85	14.82	33.47	25.76	20.67	1.18E+00	9.07E-13	Up	1.52E-01	5.80E-01		-8.43E-01	8.98E-06		-2.54E-01	2.66E-01		-3.78E-01	3.63E-03		-6.95E-01	3.45E-08		Unigene50420_All//gi|22022592|gb|AAM83252.1|//2.00E-17//AT3g13990/MDC16_11 [Arabidopsis thaliana] >gi|23308471|gb|AAN18205.1| At3g13990/MDC16_11 [Arabidopsis thaliana]	Unigene50420_All//1.00E-18//AT3G13990| unknown protein				GO:0043231//GO:0044444	nr +
Unigene50422_All	1046	1.50	1.36	0.81	4.86	3.23	2.76	1.98	0.56	0.50	-1.46E-01	7.63E-01		-8.82E-01	1.13E-01		-5.90E-01	2.01E-02		-8.14E-01	1.88E-03		-1.82E+00	2.74E-05	Down	-2.00E+00	4.09E-06	Down	Unigene50422_All//gi|224128414|ref|XP_002329156.1|//3.00E-10//nbs-lrr resistance protein [Populus trichocarpa] >gi|222860825|gb|EEF06956.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene50422_All//2.00E-10//AT1G12280| disease resistance protein (CC-NBS-LRR class), putative			ko04626|Plant-pathogen interaction		nr +
Unigene50425_All	450	18.02	12.72	28.40	10.29	5.66	4.82	4.13	0.28	1.42	-5.02E-01	1.38E-02		6.56E-01	5.77E-05		-8.62E-01	9.57E-04		-1.10E+00	8.31E-05	Down	-3.89E+00	7.06E-10	Down	-1.55E+00	3.64E-04	Down			Unigene50425_All//1.00E-07//FL577001				
Unigene50428_All	404	41.70	19.31	30.18	62.88	59.49	51.76	54.52	22.55	42.11	-1.11E+00	4.90E-15	Down	-4.66E-01	9.20E-04		-7.99E-02	5.44E-01		-2.81E-01	1.08E-02		-1.27E+00	3.08E-29	Down	-3.73E-01	2.54E-04		Unigene50428_All//gi|587562|emb|CAA56520.1|//1.00E-21//mitochondrial processing peptidase [Solanum tuberosum]	Unigene50428_All//2.00E-13//AT1G51980| mitochondrial processing peptidase alpha subunit, putative	Unigene50428_All//0.00E+00//TC142878			GO:0005746//GO:0006970//GO:0008152//GO:0009536//GO:0031980//GO:0032559//GO:0046872//GO:0070011	nr -
Unigene5043_All	1004	5.16	30.84	2.70	10.92	24.63	16.46	5.26	8.49	8.49	2.58E+00	5.81E-86	Up	-9.32E-01	7.12E-04		1.17E+00	1.77E-27	Up	5.93E-01	9.04E-06		6.90E-01	9.02E-05		6.90E-01	6.25E-05		Unigene5043_All//gi|27476089|gb|AAO17020.1|//4.00E-16//Hypothetical protein [Oryza sativa Japonica Group] >gi|108705833|gb|ABF93628.1| expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene5043_All//1.00E-46//AT4G24110| unknown protein	Unigene5043_All//0.00E+00//gi|78346980|gb|DT567254.1|DT567254				nr -
Unigene50430_All	588	1.42	1.81	1.36	1.52	1.00	5.84	3.67	3.55	2.85	3.46E-01	6.19E-01		-6.77E-02	9.40E-01		-6.15E-01	4.02E-01		1.94E+00	1.26E-07	Up	-4.52E-02	9.27E-01		-3.66E-01	3.56E-01				Unigene50430_All//2.00E-65//TC177393				
Unigene50431_All	1030	3.20	1.48	0.93	1.89	4.08	1.49	2.38	0.49	1.28	-1.12E+00	1.26E-03		-1.78E+00	4.29E-06	Down	1.11E+00	1.11E-04	Up	-3.39E-01	5.01E-01		-2.29E+00	6.20E-08	Down	-8.99E-01	9.92E-03		Unigene50431_All//gi|2190259|dbj|BAA20410.1|//1.00E-67//A-type cyclin [Catharanthus roseus]	Unigene50431_All//1.00E-55//AT1G47210| cyclin family protein	Unigene50431_All//0.00E+00//CO086677			GO:0007049//GO:0019887//GO:0043231	nr +
Unigene50433_All	1963	2.05	8.70	3.72	0.48	0.32	0.35	1.34	5.28	8.48	2.08E+00	5.82E-37	Up	8.57E-01	1.44E-04		-6.11E-01	3.90E-01		-4.83E-01	5.18E-01		1.98E+00	4.05E-26	Up	2.67E+00	2.58E-60	Up	Unigene50433_All//gi|15220529|ref|NP_176350.1|//0.00E+00//MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding [Arabidopsis thaliana] >gi|33112391|sp|Q94KB7.2|MLO6_ARATH RecName: Full=MLO-like protein 6; Short=AtMlo6 >gi|4585879|gb|AAD25552.1|AC005850_9 Highly Similar to Mlo proteins [Arabidopsis thaliana] >gi|241112257|gb|AAX53799.2|AF369567_1 membrane protein Mlo6 [Arabidopsis thaliana]	Unigene50433_All//7.00E-179//AT1G61560| MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding	Unigene50433_All//9.00E-77//ES793340			GO:0009987//GO:0010260//GO:0016020//GO:0050832	nr +
Unigene50435_All	1875	5.61	5.86	11.50	3.37	4.21	2.41	0.02	0.00	0.04	6.42E-02	7.22E-01		1.04E+00	2.09E-16	Up	3.18E-01	1.46E-01		-4.86E-01	4.08E-02		-4.49E+00	6.56E-01		9.18E-01	7.49E-01		Unigene50435_All//gi|206602441|gb|EDZ38922.1|//3.00E-07//transposase [Leptospirillum sp. Group II '5-way CG'] >gi|206603009|gb|EDZ39489.1| Transposase [Leptospirillum sp. Group II '5-way CG'] >gi|206603036|gb|EDZ39516.1| Transposase [Leptospirillum sp. Group II '5-way CG'] >gi|206603265|gb|EDZ39745.1| Putative transposase [Leptospirillum sp. Group II '5-way CG'] >gi|206603457|gb|EDZ39937.1| Transposase [Leptospirillum sp. Group II '5-way CG'] >gi|206603501|gb|EDZ39981.1| Transposase [Leptospirillum sp. Group II '5-way CG'] >gi|206603894|gb|EDZ40374.1| transposase [Leptospirillum sp. Group II '5-way CG']						nr +
Unigene50436_All	373	1.26	1.22	0.29	4.01	4.06	1.82	9.18	19.27	7.80	-4.62E-02	9.78E-01		-2.14E+00	1.03E-01		1.99E-02	9.85E-01		-1.14E+00	3.85E-02		1.07E+00	8.04E-08	Up	-2.36E-01	4.46E-01		Unigene50436_All//gi|115470545|ref|NP_001058871.1|//2.00E-15//Os07g0142500 [Oryza sativa Japonica Group] >gi|24059939|dbj|BAC21402.1| early nodulin 75 precursor-like protein [Oryza sativa Japonica Group] >gi|113610407|dbj|BAF20785.1| Os07g0142500 [Oryza sativa Japonica Group]		Unigene50436_All//4.00E-180//gi|13245569|gb|BE053369.2|BE053369				nr -

Unigene50437_All	655	0.96	10.21	7.24	10.72	9.78	8.69	23.95	38.80	15.57	3.41E+00	5.93E-25	Up	2.92E+00	5.90E-15	Up	-1.33E-01	6.05E-01		-3.04E-01	2.05E-01		6.96E-01	8.83E-13		-6.21E-01	4.20E-07		Unigene50437_All//gi|15242391|ref|NP_197082.1|//3.00E-17//pollen Ole e 1 allergen and extensin family protein [Arabidopsis thaliana] >gi|9755623|emb|CAC01777.1|proline-rich protein [Arabidopsis thaliana] >gi|27311645|gb|AA000788.1|proline-rich protein [Arabidopsis thaliana] >gi|53828649|gb|AAU94434.1|At5g15780 [Arabidopsis thaliana]		Unigene50437_All//0.00E+00//TC148715		ko03040|Spliceosome		nr -
Unigene50438_All	1438	2.47	2.04	2.15	14.90	10.94	8.20	4.18	1.95	1.47	-2.76E-01	4.04E-01		-2.04E-01	5.84E-01		-4.45E-01	5.25E-05		-8.62E-01	1.64E-13		-1.10E+00	6.03E-07	Down	-1.51E+00	3.55E-11	Down	Unigene50438_All//gi|115451595|ref|NP_001049398.1|//1.00E-122//Os03g0219100 (Oryza sativa Japonica Group) >gi|108706877|gb|ABF94672.1|CRAL/TRIO domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547869|dbj|BAF11312.1|Os03g0219100 [Oryza sativa Japonica Group]	Unigene50438_All//6.00E-128//AT4G22410| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Cellular retinaldehyde-binding/triple function, C-terminal (InterPro:IPR001251), Phosphatidylinositol transfer protein-like, N-terminal (InterPro:IPR011074); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G05370.1); Has 1032 Blast hits to 1032 proteins in 165 species: Archae - 0; Bacteria - 0; Metazoa - 245; Fungi - 243; Plants - 390; Viruses - 0; Other Eukaryotes - 154 (source: NCBI BLink).	Unigene50438_All//0.00E+00//gi|78326265|gb|DT546539.1|DT546539				nr -
Unigene50440_All	747	21.78	8.14	7.20	28.41	27.61	31.32	75.90	28.76	32.16	-1.42E+00	5.13E-21	Down	-1.60E+00	7.32E-24	Down	-4.10E-02	8.07E-01		1.41E-01	2.88E-01		-1.40E+00	1.61E-85	Down	-1.24E+00	5.81E-73	Down	Unigene50440_All//gi|15223001|ref|NP_172256.1|//9.00E-65//RPS15A (ribosomal protein s15a); structural constituent of ribosome [Arabidopsis thaliana] >gi|15238544|ref|NP_200793.1| 40S ribosomal protein S15A (RPS15aF) [Arabidopsis thaliana] >gi|42571385|ref|NP_973783.1|RPS15A (ribosomal protein s15a); structural constituent of ribosome [Arabidopsis thaliana] >gi|297796939|ref|XP_002866354.1|RPS15A [Arabidopsis lyrata subsp. lyrata] >gi|297815756|ref|XP_002875761.1|RPS15A [Arabidopsis lyrata subsp. lyrata] >gi|297849076|ref|XP_002892419.1|RPS15A [Arabidopsis lyrata subsp. lyrata] >gi|1172218|sp|P42798.2|R15A1_ARATH RecName: Full=40S ribosomal protein S15a-1 >gi|8439890|gb|AAF75076.1|AC007583_12 Strong similarity to 40S ribosomal protein S15A from Arabidopsis thaliana gb|L27461. EST gb|H30315 comes from this gene >gi|14423370|gb|AAK62367.1|AF38692	Unigene50440_All//5.00E-66//AT5G59850| 40S ribosomal protein S15A (RPS15aF)	Unigene50440_All//0.00E+00//TC145625		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0043231	nr +
Unigene50441_All	347	49.76	25.99	22.87	77.66	59.64	80.30	82.49	44.57	43.97	-9.37E-01	7.94E-12		-1.12E+00	5.81E-15	Down	-3.81E-01	9.41E-05		4.82E-02	6.89E-01		-8.88E-01	2.35E-21		-9.08E-01	8.80E-23		Unigene50441_All//gi|115465365|ref|NP_001056282.1|//2.00E-56//Os05g0556700 (Oryza sativa Japonica Group) >gi|113579833|dbj|BAF18196.1|Os05g0556700 [Oryza sativa Japonica Group]	Unigene50441_All//1.00E-57//AT5G20890| chaperonin, putative	Unigene50441_All//0.00E+00//TC153874			GO:0004672//GO:0005515//GO:0006464//GO:0030312//GO:0031225//GO:0032559//GO:0044424	nr +
Unigene50442_All	381	8.93	11.97	9.50	30.99	40.04	35.21	32.07	31.59	8.26	4.23E-01	1.40E-01		9.05E-02	7.83E-01		3.70E-01	8.27E-03		1.84E-01	3.01E-01		-2.16E-02	9.11E-01		-1.96E+00	3.55E-31	Down	Unigene50442_All//gi|124359958|gb|ABN07974.1|//2.00E-06//Universal stress protein (Usp) [Medicago truncatula]	Unigene50442_All//1.00E-06//AT3G17020| universal stress protein (USP) family protein	Unigene50442_All//7.00E-157//TC159141				nr +
Unigene50443_All	266	10.82	8.76	10.21	20.23	27.32	33.79	119.21	293.04	111.58	-3.04E-01	4.13E-01		-8.35E-02	8.25E-01		4.34E-01	4.55E-02		7.40E-01	8.99E-05		1.30E+00	2.72E-104	Up	-9.55E-02	3.25E-01		Unigene50443_All//gi|225380882|gb|ACN88682.1|//3.00E-37//monodehydroascorbate reductase [Malus x domestica]	Unigene50443_All//7.00E-36//AT3G52880| monodehydroascorbate reductase, putative	Unigene50443_All//1.00E-148//ES835477		ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009536//GO:0010038//GO:0016020//GO:0016655//GO:0019725//GO:0030554//GO:0042579//GO:0042743	nr -
Unigene50444_All	281	0.00	0.00	0.00	0.00	0.25	2.89	0.30	0.89	1.70	null	null		null	null		7.94E+00	6.08E-01		1.15E+01	6.95E-05	Up	1.57E+00	3.26E-01		2.50E+00	2.51E-02		Unigene50444_All//gi|58038194|emb|CAH05011.1|//3.00E-37//alpha-dioxygenase [Pisum sativum]	Unigene50444_All//2.00E-35//AT3G01420| DOX1; lipoxygenase			ko00592|alpha-Linolenic acid metabolism	GO:0005506//GO:0009607//GO:0010033//GO:0016209//GO:0050664	nr -
Unigene50445_All	1473	0.00	0.00	0.29	0.00	0.44	15.64	0.83	3.75	6.90	null	null		8.18E+00	1.38E-02		8.80E+00	4.92E-04	Up	1.39E+01	1.87E-141	Up	2.17E+00	6.87E-16	Up	3.05E+00	1.64E-42	Up	Unigene50445_All//gi|58038194|emb|CAH05011.1|//0.00E+00//alpha-dioxygenase [Pisum sativum]	Unigene50445_All//3.00E-169//AT3G01420| DOX1; lipoxygenase			ko00592|alpha-Linolenic acid metabolism	GO:0005506//GO:0009650//GO:0008152//GO:0016209//GO:0016701	nr -
Unigene50446_All	788	2.99	1.29	5.47	1.14	1.88	1.20	1.13	0.37	0.10	-1.22E+00	4.07E-03		8.73E-01	4.13E-03		7.24E-01	2.03E-01		8.10E-02	9.31E-01		-1.60E+00	2.18E-02		-3.48E+00	7.33E-05	Down	Unigene50446_All//gi|108706127|gb|ABF93922.1|//2.00E-27//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene50446_All//8.00E-33//AT2G26200| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Methyltransferase type 12 (InterPro:IPR013217); BEST Arabidopsis thaliana protein match is: methyltransferase (TAIR:AT1G54650.1); Has 1504 Blast hits to 1429 proteins in 277 species: Archae - 33; Bacteria - 213; Metazoa - 664; Fungi - 202; Plants - 139; Viruses - 0; Other Eukaryotes - 253 (source: NCBI BLink).	Unigene50446_All//0.00E+00//C00837000		ko00350|Tyrosine metabolism/ko00450|Selenoamino acid metabolism//ko00340|Histidine metabolism	GO:0031410	nr +
Unigene50448_All	628	5.25	14.52	9.16	13.80	13.60	14.67	12.59	15.71	16.18	1.47E+00	1.28E-12	Up	8.03E-01	1.83E-03		-2.14E-02	9.25E-01		8.81E-02	6.73E-01		3.19E-01	5.98E-02		3.62E-01	2.24E-02		Unigene50448_All//gi|224070092|ref|XP_002303113.1|//1.00E-144//predicted protein [Populus trichocarpa] >gi|222844839|gb|EEE82386.1|predicted protein [Populus trichocarpa]		Unigene50448_All//0.00E+00//TC139486				nr -
Unigene50449_All	530	2.86	2.49	6.63	12.50	13.38	9.12	0.40	0.95	1.05	-2.04E-01	6.81E-01		1.21E+00	5.40E-04	Up	9.86E-02	7.28E-01		-4.55E-01	5.04E-02		1.25E+00	2.04E-01		1.40E+00	1.12E-01		Unigene50449_All//gi|158828302|gb|ABW81177.1|//4.00E-12//gag non-LTR retrotransposase [Arabidopsis cebennensis]	Unigene50449_All//6.00E-13//AT2G01050| nucleic acid binding / zinc ion binding	Unigene50449_All//0.00E+00//ES796742			GO:0005488	nr +
Unigene50450_All	523	1.50	0.00	0.51	3.14	2.70	2.76	1.37	0.48	0.84	-1.06E+01	1.09E-04	Down	-1.56E+00	8.00E-02		-2.20E-01	6.81E-01		-1.86E-01	7.15E-01		-1.52E+00	5.42E-02		-7.14E-01	3.27E-01		Unigene50450_All//gi|87116463|dbj|BAE79384.1|//4.00E-06//unnamed protein product [Ipomoea batatas]		Unigene50450_All//0.00E+00//ES796742				nr -
Unigene50451_All	2758	0.15	0.04	0.15	0.23	0.27	0.82	4.00	5.64	22.59	-2.05E+00	1.20E-01		2.54E-02	1.00E+00		2.26E-01	8.32E-01		1.80E+00	8.39E-05	Up	4.95E-01	8.64E-05		2.50E+00	6.35E-208	Up	Unigene50451_All//gi|2181190|emb|CAA73134.1|//0.00E+00//serine/threonine kinase [Brassica oleracea]	Unigene50451_All//0.00E+00//AT1G61610| S-locus lectin protein kinase family protein	Unigene50451_All//2.00E-112//C0496758		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0009987//GO:0016020//GO:0030246	nr +
Unigene50452_All	848	4.20	11.11	10.86	11.34	29.97	19.28	0.00	0.00	0.00	1.41E+00	3.08E-12	Up	1.37E+00	3.87E-11	Up	1.40E+00	5.31E-37	Up	7.66E-01	1.40E-08		null	null		null	null		Unigene50452_All//gi|83853827|gb|ABC47859.1|//1.00E-126//membrane protein-like protein [Glycine max]	Unigene50452_All//1.00E-70//AT2G25737| unknown protein	Unigene50452_All//0.00E+00//gi|161247951|gb|ES800739.1|ES800739				nr -
Unigene50453_All	1085	2.85	2.29	0.69	6.98	12.38	9.07	7.13	2.04	21.08	-3.14E-01	3.89E-01		-2.05E+00	8.86E-07	Down	8.27E-01	1.06E-08		3.79E-01	4.41E-02		-1.80E+00	1.81E-17	Down	1.56E+00	7.29E-42	Up	Unigene50453_All//gi|15235484|ref|NP_195443.1|//5.00E-60//MYB73 (MYB DOMAIN PROTEIN 73); DNA binding / transcription factor [Arabidopsis thaliana] >gi|2464855|emb|CAB16756.1| myb-related protein [Arabidopsis thaliana] >gi|7270709|emb|CAB80392.1| myb-related protein [Arabidopsis thaliana] >gi|41619352|gb|AAS10083.1| MYB transcription factor [Arabidopsis thaliana]	Unigene50453_All//2.00E-55//AT4G37260| MYB73 (MYB DOMAIN PROTEIN 73); DNA binding / transcription factor	Unigene50453_All//0.00E+00//gi|164294493|gb|ES799407.1|ES799407	MYB		GO:0009725//GO:0009743//GO:0010038//GO:0010468	nr -
Unigene50454_All	419	31.22	20.80	22.88	58.14	45.12	43.76	52.98	34.31	17.11	-5.86E-01	1.62E-04		-4.49E-01	5.99E-03		-3.66E-01	4.36E-04		-4.10E-01	1.54E-04		-6.27E-01	1.67E-09		-1.63E+00	1.33E-43	Down	Unigene50454_All//gi|223453020|gb|ACM89774.1|//1.00E-33//beta-tubulin 14 [Gossypium hirsutum]	Unigene50454_All//7.00E-27//AT5G12250| TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton	Unigene50454_All//0.00E+00//gi|211000086|gb|BQ412399.1|BQ412399		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene50459_All	495	12.90	34.09	18.93	20.13	33.04	42.24	32.03	31.33	50.46	1.40E+00	2.94E-21	Up	5.54E-01	4.57E-03		7.15E-01	2.72E-08		1.07E+00	1.86E-18	Up	-3.21E-02	8.30E-01		6.56E-01	1.01E-11		Unigene50459_All//gi|1209756|gb|AAB53155.1|//3.00E-59//integral membrane protein [Beta vulgaris]	Unigene50459_All//4.00E-59//AT1G75220| integral membrane protein, putative	Unigene50459_All//0.00E+00//ES835903			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr -
Unigene50460_All	635	0.91	9.10	7.30	7.06	6.62	3.56	15.31	4.28	1.00	3.33E+00	3.77E-21	Up	3.01E+00	4.45E-15	Up	-9.38E-02	7.97E-01		-9.89E-01	4.57E-04		-1.84E+00	2.52E-22	Down	-3.93E+00	1.38E-51	Down	Unigene50460_All//gi|224081415|ref|XP_002306401.1|//1.00E-07//predicted protein [Populus trichocarpa] >gi|222855850|gb|EEE93397.1|predicted protein [Populus trichocarpa]		Unigene50460_All//0.00E+00//TC171251				nr +
Unigene50462_All	367	15.68	6.63	9.87	13.30	5.63	1.23	4.49	0.23	0.87	-1.24E+00	1.31E-06	Down	-6.69E-01	9.59E-03		-1.24E+00	1.28E-06	Down	-3.43E+00	3.67E-20	Down	-4.30E+00	2.19E-09	Down	-2.37E+00	5.20E-06	Down			Unigene50462_All//2.00E-71//TC170782				
Unigene50463_All	666	28.52	10.04	22.87	28.72	12.36	6.65	3.30	0.94	0.78	-1.51E+00	1.44E-26	Down	-3.19E-01	1.84E-02		-1.22E+00	9.33E-24	Down	-2.11E+00	6.12E-46	Down	-1.81E+00	1.62E-05	Down	-2.09E+00	9.49E-07	Down			Unigene50463_All//2.00E-103//gi|109879431|gb|DW508401.1|DW508401				
Unigene50464_All	822	2.36	1.17	2.53	2.00	1.47	0.93	4.63	4.17	1.79	-1.01E+00	3.12E-02		1.01E-01	8.18E-01		-4.48E-01	3.94E-01		-1.10E+00	3.43E-02		-1.51E-01	6.68E-01		-1.37E+00	1.63E-06	Down	Unigene50464_All//gi|2194136|gb|AAB61111.1|//2.00E-11//Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb|U12626) [Arabidopsis thaliana]		Unigene50464_All//7.00E-20//ES807842				nr +
Unigene50465_All	425	27.08	57.11	34.58	46.53	58.01	63.97	57.10	98.74	66.55	1.08E+00	3.16E-20	Up	3.53E-01	2.34E-02		3.18E-01	2.83E-03		4.59E-01	6.00E-06		7.90E-01	1.98E-25		2.21E-01	1.61E-02		Unigene50465_All//gi|6090833|gb|AAF03357.1|AF134486_1//1.00E-28//cytidine deaminase 1 [Arabidopsis thaliana]	Unigene50465_All//8.00E-26//AT2G19570| CDA1 (CYTIDINE DEAMINASE 1); cytidine deaminase	Unigene50465_All//0.00E+00//TC162261		ko00240|Pyrimidine metabolism		nr +

Unigene50466_All	513	22.34	34.17	27.40	45.93	18.06	36.62	16.15	17.03	10.64	6.14E-01	3.59E-06		2.95E-01	6.93E-02		-1.35E+00	3.24E-34	Down	-3.27E-01	3.81E-03		7.60E-02	7.07E-01		-6.03E-01	5.33E-04		Unigene50466_All//gi|297791835|ref|XP_002863802.1|//3.00E-06//ubiquitin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309637|gb|EFH40061.1| ubiquitin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50466_All//2.00E-07//AT5G42300| UBL5 (UBIQUITIN-LIKE PROTEIN 5)	Unigene50466_All//1.00E-116//TC173234				nr +
Unigene50468_All	1288	0.49	2.40	0.62	10.33	4.84	8.94	12.57	64.12	70.24	2.30E+00	4.34E-08	Up	3.47E-01	6.35E-01		-1.09E+00	4.61E-14	Down	-2.08E-01	2.30E-01		2.35E+00	7.26E-252	Up	2.48E+00	1.43E-299	Up	Unigene50468_All//gi|117582134|gb|ABK41486.1|//1.00E-98//WRKY transcription factor [Populus tremula x Populus alba]	Unigene50468_All//0.00E+00//gi|164273782|gb|EV496853.1|EV496853	Unigene50468_All//0.00E+00//gi|164273782|gb|EV496853.1|EV496853	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene5047_All	1140	6.61	26.85	14.15	11.49	22.23	28.96	2.11	1.10	1.12	2.02E+00	2.64E-63	Up	1.10E+00	1.30E-13	Up	9.52E-01	3.45E-20		1.33E+00	1.25E-40	Up	-9.43E-01	1.01E-02		-9.19E-01	9.16E-03		Unigene5047_All//gi|166203234|gb|AB184657.1|//1.00E-47//transcription factor [Glycine max]	Unigene5047_All//4.00E-35//AT1G80840| WRKY40; transcription factor	Unigene5047_All//0.00E+00//TC164618	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene50470_All	493	2.65	29.70	7.34	6.77	8.03	9.62	8.06	7.80	1.45	3.48E+00	4.43E-55	Up	1.47E+00	3.17E-05	Up	2.47E-01	4.89E-01		5.07E-01	7.46E-02		-4.76E-02	8.80E-01		-2.47E+00	5.24E-14	Down	Unigene50470_All//gi|145332933|ref|NP_001078332.1|//4.00E-08//RTFL14 (ROTUNDIFOLIA LIKE 14) [Arabidopsis thaliana] >gi|42822061|tpg|DAA02285.1| TPA_exp: DWL14 [Arabidopsis thaliana]	Unigene50470_All//3.00E-09//AT3G63088| RTFL14 (ROTUNDIFOLIA LIKE 14)	Unigene50470_All//7.00E-19//DW499853				nr +
Unigene50472_All	659	4.68	3.69	4.20	4.99	2.82	3.02	0.96	4.06	2.84	-3.44E-01	3.56E-01		-1.57E-01	6.64E-01		-8.22E-01	1.07E-02		-7.26E-01	3.38E-02		2.08E+00	1.12E-07	Up	1.56E+00	3.45E-04	Up	Unigene50472_All//gi|94807644|gb|ABF47119.1|//7.00E-10//At1g31335 [Arabidopsis thaliana]						nr -
Unigene50476_All	770	0.00	122.79	3.80	0.26	0.63	6.45	0.88	41.36	7.61	1.69E+01	0.00E+00	Up	1.19E+01	3.52E-16	Up	1.27E+00	2.92E-01		4.64E+00	1.53E-24	Up	5.56E+00	3.28E-198	Up	3.11E+00	2.81E-25	Up	Unigene50476_All//gi|224123482|ref|XP_002330325.1|//3.00E-28//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222871360|gb|EEF08491.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene50476_All//3.00E-19//AT5G61890| AP2 domain-containing transcription factor family protein	Unigene50476_All//0.00E+00//TC162689	AP2-EREBP			nr -
Unigene50477_All	761	6.67	16.05	25.47	14.27	40.50	43.20	7.33	34.55	38.43	1.27E+00	1.90E-13	Up	1.93E+00	5.87E-37	Up	1.50E+00	9.89E-50	Up	1.60E+00	7.80E-53	Up	2.24E+00	8.22E-76	Up	2.39E+00	5.05E-93	Up									ESTscan -
Unigene50479_All	581	27.20	17.79	23.83	28.55	23.41	27.13	46.36	28.85	20.71	-6.12E-01	1.22E-05		-1.91E-01	2.38E-01		-2.86E-01	3.60E-02		-7.37E-02	6.62E-01		-6.84E-01	3.89E-13		-1.16E+00	7.75E-32	Down	Unigene50479_All//gi|29028792|gb|AC64775.1|//5.00E-28//At5g53043 [Arabidopsis thaliana]	Unigene50479_All//3.00E-29//AT5G53045| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Transcription factor Pcc1 (InterPro:IPR015419); Has 78 Blast hits to 78 proteins in 41 species: Archae - 0; Bacteria - 0; Metazoa - 33; Fungi - 21; Plants - 19; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene50479_All//0.00E+00//gi|109889435|gb|DW518403.1|DW518403				nr -
Unigene50480_All	984	4.89	1.75	4.33	4.00	4.41	3.49	1.76	0.25	0.69	-1.48E+00	3.78E-07	Down	-1.76E-01	5.78E-01		1.41E-01	6.87E-01		-1.97E-01	5.88E-01		-2.79E+00	4.64E-07	Down	-1.36E+00	2.14E-03		Unigene50480_All//gi|297815990|ref|XP_002875878.1|//1.00E-113//aminoacyl-t-RNA synthetase [Arabidopsis lyrata subsp. lyrata] >gi|297321716|gb|EFH52137.1| aminoacyl-t-RNA synthetase [Arabidopsis lyrata subsp. lyrata]	Unigene50480_All//7.00E-109//AT3G48110| EDO1 (EMBRYO-DEFECTIVE-DEVELOPMENT 1); glycine-tRNA ligase			ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene50482_All	667	2.27	0.30	0.16	2.32	2.27	1.76	0.95	0.94	0.30	-2.90E+00	2.07E-05	Down	-3.83E+00	2.79E-06	Down	-2.74E-02	9.58E-01		-3.95E-01	4.84E-01		-1.66E-02	1.02E+00		-1.67E+00	4.29E-02		Unigene50482_All//gi|2129709|pir||S65812//5.00E-27//RNA-directed DNA polymerase (EC 2.7.7.49) (clone DM15) - Arabidopsis thaliana retrotransposon Ta11-1 >gi|976278|gb|AAA75254.1| reverse transcriptase [Arabidopsis thaliana]	Unigene50482_All//9.00E-09//ATMG01250| hypothetical protein	Unigene50482_All//1.00E-14//gi|3325985|gb|AI054871.1|AI054871				nr -
Unigene50483_All	570	7.34	2.58	4.39	8.91	10.27	12.44	11.27	8.43	12.09	-1.51E+00	1.80E-06	Down	-7.42E-01	1.68E-02		2.04E-01	4.75E-01		4.81E-01	3.16E-02		-4.19E-01	4.81E-02		1.01E-01	6.28E-01		Unigene50483_All//gi|255546127|ref|XP_002514123.1|//5.00E-13//DNA repair protein reca, putative [Ricinus communis] >gi|223546579|gb|EEF48077.1| DNA repair protein reca, putative [Ricinus communis]	Unigene50483_All//3.00E-05//AT2G19490| reca family protein	Unigene50483_All//0.00E+00//DW519865		ko03440|Homologous recombination		nr +
Unigene50484_All	646	65.04	28.39	79.38	44.19	69.30	34.61	1.11	0.52	0.31	-1.20E+00	7.17E-41	Down	2.88E-01	1.88E-04		6.49E-01	1.41E-18		-3.53E-01	4.24E-04		-1.10E+00	1.49E-01		-1.85E+00	1.78E-02		Unigene50484_All//gi|222422849|dbj|BAH19411.1|//7.00E-49//AT3G45780 [Arabidopsis thaliana]	Unigene50484_All//4.00E-42//AT3G45780| PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase	Unigene50484_All//0.00E+00//TC177868				nr +
Unigene50485_All	409	20.85	64.05	30.34	26.92	26.27	28.60	113.20	220.32	95.85	1.62E+00	3.74E-40	Up	5.41E-01	1.15E-03		-3.52E-02	8.56E-01		8.75E-02	6.69E-01		9.61E-01	1.68E-74		-2.40E-01	5.09E-04				Unigene50485_All//1.00E-143//gi|164239768|gb|ES817466.1|ES817466				
Unigene50486_All	928	0.85	0.44	0.11	1.23	2.08	2.19	1.55	0.18	1.29	-9.53E-01	2.33E-01		-2.88E+00	6.35E-03		7.51E-01	1.14E-01		8.27E-01	7.36E-02		-3.10E+00	1.52E-06	Down	-2.66E-01	6.10E-01		Unigene50486_All//gi|15224831|ref|NP_181947.1|//5.00E-09//EDE1 (ENDOSPERM DEFECTIVE 1); microtubule binding [Arabidopsis thaliana] >gi|63003818|gb|AAY25453.1| At2g44190 [Arabidopsis thaliana]		Unigene50486_All//0.00E+00//TC170349				nr +
Unigene50487_All	614	7.33	4.21	1.73	5.52	2.86	3.82	5.03	1.63	2.60	-8.00E-01	4.94E-03		-2.08E+00	8.97E-10	Down	-9.48E-01	2.59E-03		-5.28E-01	1.28E-01		-1.62E+00	1.70E-06	Down	-9.54E-01	1.90E-03		Unigene50487_All//gi|114733|sp|P13088.1|AUX22_SOYBN//2.00E-64//RecName: Full=Auxin-induced protein AUX22 >gi|169919|gb|AAA33944.1| auxin-regulated protein (Aux22) [Glycine max]	Unigene50487_All//3.00E-50//AT3G15540| IAA19 (INDOLE-3-ACETIC ACID INDUCIBLE 19); transcription factor	Unigene50487_All//1.00E-67//TC155437				nr +
Unigene50488_All	730	0.29	2.78	0.44	0.14	1.46	1.42	3.07	5.15	5.13	3.28E+00	1.11E-07	Up	6.10E-01	6.24E-01		3.42E+00	1.07E-04	Up	3.38E+00	2.04E-04	Up	7.47E-01	7.98E-03		7.41E-01	6.85E-03		Unigene50488_All//gi|209967439|gb|ACJ02348.1|//5.00E-07//60s ribosome protein L19 [Vernicia fordii]		Unigene50488_All//7.00E-26//DW499391		ko03010|Ribosome		nr -
Unigene50489_All	640	6.38	8.95	3.66	2.65	5.92	12.00	0.73	1.70	4.42	4.89E-01	5.11E-02		-8.01E-01	1.11E-02		1.16E+00	1.57E-04	Up	2.18E+00	5.14E-19	Up	1.22E+00	4.08E-02		2.60E+00	1.37E-10	Up	Unigene50489_All//gi|115452037|ref|NP_001049619.1|//4.00E-29//Os03g0260600 [Oryza sativa Japonica Group] >gi|108707285|gb|ABF95080.1| Helix-loop-helix DNA-binding domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548090|dbj|BAF11533.1| Os03g0260600 [Oryza sativa Japonica Group]	Unigene50489_All//3.00E-29//AT3G25710| BHLH32 (BASIC HELIX-LOOP-HELIX 32); DNA binding / transcription factor	Unigene50489_All//0.00E+00//gi|109884045|gb|DW513015.1|DW513015	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene50490_All	670	14.68	11.34	13.75	12.34	9.05	7.48	5.62	1.06	0.95	-3.72E-01	4.52E-02		-9.46E-02	6.29E-01		-4.48E-01	2.12E-02		-7.22E-01	2.48E-04		-2.40E+00	1.81E-12	Down	-2.56E+00	7.87E-14	Down	Unigene50490_All//gi|22330506|ref|NP_177040.2|//2.00E-28//zinc finger (DNL type) family protein [Arabidopsis thaliana] >gi|5734707|gb|AAD49972.1|AC008075_5 F24J5.3 [Arabidopsis thaliana]	Unigene50490_All//1.00E-29//AT1G68730| zinc finger (DNL type) family protein	Unigene50490_All//0.00E+00//TC151225				nr +
Unigene50491_All	757	0.07	11.18	1.55	0.79	2.14	1.97	2.79	1.66	1.00	7.34E+00	1.64E-46	Up	4.49E+00	1.90E-05	Up	1.44E+00	6.58E-03		1.32E+00	1.96E-02		-7.54E-01	5.72E-02		-1.48E+00	2.15E-04	Down	Unigene50491_All//gi|300172255|gb|AP12861.1|//1.00E-57//At2g40095 [Arabidopsis thaliana]	Unigene50491_All//7.00E-40//AT2G40095| unknown protein	Unigene50491_All//6.00E-82//DW224504				nr +
Unigene50493_All	694	0.98	2.63	2.00	2.08	5.61	5.01	1.64	2.53	3.04	1.42E+00	4.69E-03		1.03E+00	8.63E-02		1.43E+00	3.74E-06	Up	1.27E+00	1.67E-04	Up	6.21E-01	1.66E-01		8.87E-01	2.05E-02				Unigene50493_All//8.00E-07//DN803899				
Unigene50496_All	746	4.56	2.38	3.07	12.62	7.48	7.14	4.48	4.20	1.82	-9.39E-01	5.20E-03		-5.71E-01	1.07E-01		-7.55E-01	1.21E-05		-8.21E-01	7.34E-06		-9.16E-02	7.80E-01		-1.30E+00	1.83E-05	Down	Unigene50496_All//gi|297830204|ref|XP_002882984.1|//7.00E-28//thioesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328824|gb|EFH59243.1| thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50496_All//9.00E-28//AT3G16175| thioesterase family protein	Unigene50496_All//0.00E+00//TC142683				nr +
Unigene50497_All	855	2.20	14.10	5.67	6.76	12.12	6.18	2.47	6.94	17.75	2.68E+00	3.15E-35	Up	1.36E+00	4.08E-06	Up	8.43E-01	4.86E-07		-1.29E-01	6.51E-01		1.49E+00	1.73E-10	Up	2.84E+00	6.76E-59	Up	Unigene50497_All//gi|297810727|ref|XP_002873247.1|//4.00E-62//carboxy-lyase [Arabidopsis lyrata subsp. lyrata] >gi|297319084|gb|EFH49506.1| carboxy-lyase [Arabidopsis lyrata subsp. lyrata]	Unigene50497_All//2.00E-63//AT5G06300| carboxy-lyase	Unigene50497_All//0.00E+00//TC136273				nr -
Unigene50502_All	715	21.88	5.81	7.60	18.39	21.96	19.20	1.01	0.12	0.50	-1.91E+00	1.38E-30	Down	-1.53E+00	1.60E-21	Down	2.56E-01	8.16E-02		6.21E-02	7.22E-01		-3.10E+00	1.40E-03		-1.00E+00	1.66E-01		Unigene50502_All//gi|15234741|ref|NP_194770.1|//2.00E-30//transcription factor [Arabidopsis thaliana] >gi|42573087|ref|NP_974640.1| transcription factor [Arabidopsis thaliana] >gi|30102576|gb|AAP21206.1| At4g30410 [Arabidopsis thaliana] >gi|325630008|emb|CAE09173.1| bHLH transcription factor [Arabidopsis thaliana]	Unigene50502_All//1.00E-27//AT4G30410| transcription factor	Unigene50502_All//0.00E+00//TC152748				nr +
Unigene50503_All	1800	0.00	0.00	0.00	1.00	0.48	0.10	5.26	0.93	2.15	null	null		null	null		-1.06E+00	2.21E-02		-3.31E+00	1.98E-07	Down	-2.50E+00	9.98E-32	Down	-1.29E+00	9.28E-14	Down	Unigene50503_All//gi|15223264|ref|NP_172335.1|//0.00E+00//CLAVATA1 receptor kinase (CLV1) [Arabidopsis thaliana] >gi|9802553|gb|AAP99755.1|AC003981_5 F22O13.7 [Arabidopsis thaliana] >gi|224589384|gb|ACN59226.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene50503_All//0.00E+00//AT1G08590| CLAVATA1 receptor kinase (CLV1)	Unigene50503_All//0.00E+00//ES797986				nr +
Unigene50504_All	294	7.30	7.24	4.89	5.08	6.44	4.92	20.13	11.09	10.03	-1.15E-02	9.91E-01		-5.77E-01	2.17E-01		3.42E-01	5.30E-01		-4.83E-02	9.41E-01		-8.61E-01	7.69E-05		-1.01E+00	2.91E-06	Down	Unigene50504_All//gi|124360846|gb|ABN08818.1|//1.00E-18//Mov34-1 [Medicago truncatula]	Unigene50504_All//8.00E-19//AT1G10840| TIF3H1; translation initiation factor	Unigene50504_All//2.00E-98//gi|78342181|gb|DT562455.1|DT562455				nr +
Unigene50505_All	1692	0.25	0.00	0.13	0.09	0.04	0.72	7.22	3.26	2.12	-7.95E+00	1.05E-02		-9.75E-01	4.11E-01		-1.12E+00	5.83E-01		3.03E+00	1.10E-04	Up	-1.15E+00	3.56E-14	Down	-1.77E+00	2.82E-27	Down	Unigene50505_All//gi|115468816|ref|NP_001058007.1|//1.00E-101//Os06g0602500 [Oryza sativa Japonica Group] >gi|113596047|dbj|BAF19921.1| Os06g0602500 [Oryza sativa Japonica Group]	Unigene50505_All//1.00E-68//AT5G24080| protein kinase family protein	Unigene50505_All//0.00E+00//TC167600				nr -

Unigene50506_All	645	12.82	5.89	7.18	45.64	14.95	12.60	2.29	1.56	0.80	-1.12E+00	6.90E-08	Down	-8.35E-01	6.90E-05		-1.61E+00	6.42E-56	Down	-1.86E+00	1.84E-59	Down	-5.61E-01	2.61E-01		-1.51E+00	2.08E-03		Unigene50506_All//gi|224113471|ref|XP_002332583.1|//6.00E-51//f-box family protein [Populus trichocarpa] >gi|222832921|gb|EEE71398.1| f-box family protein [Populus trichocarpa]	Unigene50506_All//3.00E-36//AT5G02160| Dof-type zinc finger domain-containing protein	Unigene50506_All//1.00E-82//DW519582	C2C2-Dof			nr +
Unigene50507_All	561	194.64	405.17	423.82	34.90	74.58	95.32	10.48	82.85	72.65	1.06E+00	1.35E-178	Up	1.12E+00	9.55E-201	Up	1.10E+00	1.42E-41	Up	1.45E+00	2.58E-74	Up	2.98E+00	9.04E-185	Up	2.79E+00	3.81E-154	Up	Unigene50507_All//gi|169786772|gb|ACA79924.1|//6.00E-07//chloroplast N receptor-interacting protein 1 [Nicotiana benthamiana] >gi|169786774|gb|ACA79925.1| chloroplast N receptor-interacting protein 1 [Nicotiana benthamiana]	Unigene50507_All//5.00E-05//AT4G35770| SEN1 (SENESCENCE 1)	Unigene50507_All//6.00E-115//TC135068				nr -
Unigene50509_All	583	46.31	25.29	45.94	27.85	19.79	12.01	0.36	0.00	0.07	-8.73E-01	4.17E-16		-1.14E-02	9.40E-01		-4.93E-01	1.19E-04		-1.21E+00	8.06E-18	Down	-8.50E+00	7.43E-02		-2.41E+00	1.95E-01		Unigene50509_All//gi|15222901|ref|NP_177718.1|//2.00E-46//family II extracellular lipase 3 (EXL3) [Arabidopsis thaliana] >gi|75165254|sp|Q94CH6.1|EXL3_ARATH RecName: Full=GDSL esterase/lipase EXL3; AltName: Full=Family II extracellular lipase 3; Short=Family II lipase EXL3; Flags: Precursor >gi|15054386|gb|AAK30018.1| family II lipase EXL3 [Arabidopsis thaliana]	Unigene50509_All//1.00E-40//AT1G75900| family II extracellular lipase 3 (EXL3)	Unigene50509_All//0.00E+00//TC150885				nr +
Unigene50512_All	833	2.39	2.19	2.37	2.03	3.10	3.69	9.19	3.86	7.27	-1.24E-01	7.75E-01		-1.31E-02	1.00E+00		6.09E-01	1.31E-01		8.59E-01	1.64E-02		-1.25E+00	2.16E-10	Down	-3.38E-01	7.08E-02		Unigene50512_All//gi|297844776|ref|XP_002890269.1|//4.00E-66//At3g10110 [Arabidopsis lyrata subsp. lyrata] >gi|297336411|gb|EFH66528.1| At3g10110 [Arabidopsis lyrata subsp. lyrata]	Unigene50512_All//5.00E-52//AT3G10110| MEE67 (maternal effect embryo arrest 67); P-P-bond-hydrolysis-driven protein transmembrane transporter/ protein transporter	Unigene50512_All//0.00E+00//TC150537				nr -
Unigene50513_All	812	1.93	0.62	2.03	2.27	5.68	3.56	0.62	2.06	1.32	-1.63E+00	3.58E-03		7.27E-02	8.89E-01		1.32E+00	1.74E-06	Up	6.49E-01	8.53E-02		1.72E+00	4.01E-04	Up	1.08E+00	5.98E-02		Unigene50513_All//gi|18390920|ref|NP_563822.1|//2.00E-46//THA1 (Threonine Aldolase 1); aldehyde-lyase/ threonine aldolase [Arabidopsis thaliana] >gi|30680733|ref|NP_849614.1| THA1 (Threonine Aldolase 1); aldehyde-lyase/ threonine aldolase [Arabidopsis thaliana] >gi|30680739|ref|NP_849615.1| THA1 (Threonine Aldolase 1); aldehyde-lyase/ threonine aldolase [Arabidopsis thaliana] >gi|145322987|ref|NP_001031001.2| THA1 (Threonine Aldolase 1); aldehyde-lyase/ threonine aldolase [Arabidopsis thaliana]	Unigene50513_All//1.00E-47//AT1G08630| THA1 (Threonine Aldolase 1); aldehyde-lyase/ threonine aldolase	Unigene50513_All//6.00E-110//gi|48789432|gb|CO090746.1|CO090746		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene50514_All	632	0.41	1.28	2.53	2.52	11.33	7.07	4.55	8.07	9.96	1.63E+00	5.05E-02		2.61E+00	7.15E-05	Up	2.17E+00	5.59E-19	Up	1.49E+00	5.94E-07	Up	8.27E-01	4.77E-04		1.13E+00	9.74E-08	Up	Unigene50514_All//gi|224129682|ref|XP_002320645.1|//3.00E-45//glutaredoxin [Populus trichocarpa] >gi|222861418|gb|EEE98960.1| glutaredoxin [Populus trichocarpa]	Unigene50514_All//5.00E-42//AT3G62950| glutaredoxin family protein	Unigene50514_All//0.00E+00//gi|109825327|gb|DW224060.1|DW224060				nr +
Unigene50516_All	673	10.42	3.09	4.59	38.49	34.74	17.72	127.72	22.73	28.35	-1.75E+00	1.31E-12	Down	-1.18E+00	5.69E-07	Down	-1.48E-01	2.15E-01		-1.12E+00	9.65E-25	Down	-2.49E+00	1.98E-281	Down	-2.17E+00	1.53E-245	Down	Unigene50516_All//gi|147776618|emb|CAN63020.1|//3.00E-11//hypothetical protein [Vitis vinifera]		Unigene50516_All//0.00E+00//TC157001				nr +
Unigene50517_All	879	1.49	3.57	1.76	1.59	6.23	3.90	4.71	2.19	187.64	1.26E+00	4.83E-04	Up	2.40E-01	6.41E-01		1.97E+00	5.56E-13	Up	1.30E+00	1.33E-04	Up	-1.11E+00	4.34E-05	Down	5.31E+00	0.00E+00	Up	Unigene50517_All//gi|110931846|gb|ABH02922.1|//4.00E-55//MYB transcription factor MYB122 [Glycine max]	Unigene50517_All//1.00E-49//AT2G31180| MYB14 (MYB DOMAIN PROTEIN 14); DNA binding / transcription factor	Unigene50517_All//0.00E+00//TC147251	MYB			nr -
Unigene50518_All	476	14.51	31.83	12.75	12.56	23.29	13.66	39.70	50.40	27.54	1.13E+00	5.74E-14	Up	-1.86E-01	4.52E-01		8.91E-01	3.53E-08		1.22E-01	6.56E-01		3.44E-01	5.98E-04		-5.28E-01	1.77E-06				Unigene50518_All//3.00E-95//TC172414				
Unigene5052_All	795	10.20	13.51	16.81	88.41	75.50	69.42	15.90	11.15	6.61	4.06E-01	2.14E-02		7.21E-01	6.03E-06		-2.28E-01	1.14E-04		-3.49E-01	6.78E-09		-5.13E-01	2.86E-04		-1.27E+00	1.69E-17	Down	Unigene5052_All//gi|79584231|ref|NP_683496.2|//1.00E-07//oxidoreductase, acting on NADH or NADPH [Arabidopsis thaliana]	Unigene5052_All//6.00E-22//AT1G63310| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: oxidoreductase, acting on NADH or NADPH (TAIR:AT1G75260.1); Has 35 Blast hits to 35 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene5052_All//0.00E+00//gi|109867146|gb|DW496122.1|DW496122				nr -
Unigene50525_All	690	0.23	0.73	0.00	7.22	5.84	4.84	3.80	3.21	1.39	1.69E+00	1.34E-01		-7.83E+00	2.44E-01		-3.06E-01	2.88E-01		-5.76E-01	3.32E-02		-2.43E-01	5.32E-01		-1.46E+00	3.95E-05	Down	Unigene50525_All//gi|15231356|ref|NP_187356.1|//3.00E-28//DC1 domain-containing protein [Arabidopsis thaliana] >gi|133778846|gb|AB038763.1| At3g07000 [Arabidopsis thaliana]	Unigene50525_All//6.00E-30//AT1G58037| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular signaling cascade; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein kinase C, phorbol ester/diacylglycerol binding (InterPro:IPR002219), DC1 (InterPro:IPR004146), C1-like (InterPro:IPR011424); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT5G45730.1); Has 1201 Blast hits to 455 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 1193; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene50525_All//5.00E-82//DT047721		ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis		nr -
Unigene50526_All	746	0.00	0.00	0.00	12.89	16.29	18.16	14.91	3.53	1.82	null	null		null	null		3.38E-01	3.90E-02		4.95E-01	1.05E-03		-2.08E+00	9.50E-30	Down	-3.04E+00	4.30E-47	Down			Unigene50526_All//0.00E+00//ES809290				
Unigene50528_All	791	3.51	1.79	2.36	3.72	3.53	2.74	9.62	6.87	2.77	-9.67E-01	1.06E-02		-5.73E-01	1.46E-01		-7.55E-02	8.32E-01		-4.39E-01	2.54E-01		-4.86E-01	1.04E-02		-1.80E+00	1.16E-17	Down	Unigene50528_All//gi|7271117|emb|CAB81546.1|//2.00E-46//25.7 kDa protein [Cicer arietinum]	Unigene50528_All//2.00E-33//AT1G44835| YhaK/prolyl-tRNA synthetase family protein	Unigene50528_All//0.00E+00//gi|48815093|gb|CO116406.1|CO116406				nr +
Unigene50529_All	687	2.74	0.89	0.62	6.45	2.51	7.23	5.79	1.89	2.26	-1.63E+00	1.19E-03		-2.14E+00	1.32E-04	Down	-1.36E+00	5.98E-07	Down	1.64E-01	6.29E-01		-1.62E+00	4.04E-08	Down	-1.36E+00	1.11E-06	Down	Unigene50529_All//gi|115455781|ref|NP_001051491.1|//2.00E-29//Os03g0786700 [Oryza sativa Japonica Group] >gi|113549962|dbj|BAF13405.1| Os03g0786700 [Oryza sativa Japonica Group]	Unigene50529_All//4.00E-26//AT5G15810| N2,N2-dimethylguanosine tRNA methyltransferase family protein	Unigene50529_All//5.00E-73//gi|78346439|gb|DT566713.1|DT566713				nr +
Unigene50530_All	685	1.45	1.78	2.64	1.82	1.16	1.91	2.72	1.65	0.64	2.91E-01	6.04E-01		8.65E-01	8.81E-02		-6.53E-01	2.80E-01		7.27E-02	9.24E-01		-7.21E-01	9.25E-02		-2.09E+00	7.81E-06	Down			Unigene50530_All//8.00E-07//ES815123				
Unigene50531_All	341	138.70	354.54	188.17	57.85	49.89	31.12	134.65	213.88	63.91	1.35E+00	1.58E-140	Up	4.40E-01	4.72E-11		-2.14E-01	9.98E-02		-8.94E-01	2.89E-13		6.68E-01	1.07E-32		-1.08E+00	2.15E-47	Down	Unigene50531_All//gi|81176251|ref|YP_398330.1|//1.00E-42//photosystem I assembly protein Ycf3 [Lactuca sativa] >gi|297840977|ref|XP_002888370.1| photosystem I assembly protein Ycf3 [Arabidopsis lyrata subsp. lyrata] >gi|78675169|dbj|BAE47595.1| photosystem I assembly protein ycf3 [Lactuca sativa] >gi|297334211|gb|EFH64629.1| photosystem I assembly protein Ycf3 [Arabidopsis lyrata subsp. lyrata] >gi|225200|prf||1211235AE ORF 82	Unigene50531_All//1.00E-40//ATCG00360| Encodes a protein required for photosystem I assembly and stability. In Chlamydomonas reinhardtii, this protein seems to act as a PSI specific chaperone facilitating the assembly of the complex by interacting with PsaA and PsaD. A loss of function mutation in tobacco leads to a loss of photosystem I.	Unigene50531_All//5.00E-142//TC145203				nr -
Unigene50532_All	637	8.71	14.95	13.29	1.56	4.27	2.84	0.00	0.00	0.00	7.80E-01	2.94E-05		6.10E-01	3.13E-03		1.45E+00	1.55E-04	Up	8.59E-01	8.43E-02		null	null		null	null		Unigene50532_All//gi|8778574|gb|AAF79582.1|AC007945_2//3.00E-26//F28C11.6 [Arabidopsis thaliana] >gi|9295696|gb|AAF87002.1|AC005292_11 F26F24.29 [Arabidopsis thaliana]	Unigene50532_All//7.00E-25//AT1G23420| INO (INNER NO OUTER); protein binding / transcription factor		C2C2-YABBY			nr +
Unigene50533_All	632	2.40	0.32	1.60	2.36	1.53	1.79	1.61	1.12	0.95	-2.90E+00	2.07E-05	Down	-5.85E-01	3.05E-01		-6.32E-01	2.38E-01		-4.05E-01	4.80E-01		-5.14E-01	4.07E-01		-7.64E-01	1.95E-01				Unigene50533_All//0.00E+00//TC134821				
Unigene50534_All	723	0.94	1.96	0.29	2.00	0.62	1.37	24.50	27.81	57.86	1.06E+00	6.14E-02		-1.68E+00	8.70E-02		-1.69E+00	1.87E-03		-5.40E-01	3.59E-01		1.83E-01	1.31E-01		1.24E+00	1.18E-53	Up	Unigene50534_All//gi|255577687|ref|XP_002529720.1|//5.00E-23//conserved hypothetical protein [Ricinus communis] >gi|223530822|gb|EEF32686.1| conserved hypothetical protein [Ricinus communis]		Unigene50534_All//5.00E-42//DN800061				nr +
Unigene50536_All	225	0.23	1.58	0.00	0.00	0.31	0.20	0.75	2.41	4.43	2.76E+00	9.59E-02		-7.86E+00	6.22E-01		8.26E+00	6.08E-01		7.65E+00	6.95E-01		1.68E+00	7.91E-02		2.56E+00	3.91E-04	Up	Unigene50536_All//gi|15232509|ref|NP_191010.1|//2.00E-28//ATEP3; chitinase [Arabidopsis thaliana] >gi|7288020|emb|CAB81807.1| class IV chitinase (CHIV) [Arabidopsis thaliana] >gi|34146830|gb|AAQ62423.1| At3g54420 [Arabidopsis thaliana] >gi|51971118|dbj|BAD44251.1| class IV chitinase (CHIV) [Arabidopsis thaliana]	Unigene50536_All//1.00E-29//AT3G54420| ATEP3; chitinase	Unigene50536_All//3.00E-118//DT464466		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene50537_All	1142	0.78	1.69	0.56	0.96	0.21	1.98	1.00	3.07	8.48	1.11E+00	1.89E-02		-4.77E-01	5.33E-01		-2.18E+00	1.20E-03		1.04E+00	1.57E-02		1.62E+00	2.89E-07	Up	3.08E+00	5.72E-41	Up	Unigene50537_All//gi|15232509|ref|NP_191010.1|//6.00E-77//ATEP3; chitinase [Arabidopsis thaliana] >gi|7288020|emb|CAB81807.1| class IV chitinase (CHIV) [Arabidopsis thaliana] >gi|34146830|gb|AAQ62423.1| At3g54420 [Arabidopsis thaliana] >gi|51971118|dbj|BAD44251.1| class IV chitinase (CHIV) [Arabidopsis thaliana]	Unigene50537_All//5.00E-68//AT3G54420| ATEP3; chitinase	Unigene50537_All//0.00E+00//TC147047		ko00520|Amino sugar and nucleotide sugar metabolism		nr +

Unigene50538_All	499	0.31	0.00	0.00	1.00	0.35	0.09	2.54	0.42	2.32	-8.30E+00	2.15E-01		-8.30E+00	2.44E-01		-1.53E+00	1.45E-01		-3.46E+00	1.61E-02		-2.60E+00	5.14E-05	Down	-1.35E-01	7.87E-01		Unigene50538_All//gi|225348975|gb|ACN87400.1|//1.00E-30//NBS-containing resistance-like protein [Corylus avellana]	Unigene50538_All//6.00E-20//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene50538_All//1.00E-29//TC161728		ko04626|Plant-pathogen interaction		nr -
Unigene5054_All	1102	0.57	1.20	0.48	5.29	6.00	4.80	7.48	13.65	20.06	1.07E+00	7.10E-02		-2.38E-01	7.74E-01		1.82E-01	5.11E-01		-1.41E-01	6.47E-01		8.68E-01	3.46E-11		1.42E+00	2.31E-35	Up	Unigene5054_All//gi|9757821|dbj|BAB08339.1|//2.00E-30//rac GTPase activating protein [Arabidopsis thaliana] >gi|110738325|dbj|BAF01090.1| rac GTPase activating protein [Arabidopsis thaliana] >gi|111074188|gb|ABH04467.1| At5g22400 [Arabidopsis thaliana]	Unigene5054_All//8.00E-32//AT5G22400| rac GTPase activating protein, putative	Unigene5054_All//1.00E-93//TC142002				nr -
Unigene50541_All	669	0.00	0.30	0.00	15.64	9.52	5.06	77.55	52.60	105.52	8.24E+00	1.36E-01		null	null		-7.16E-01	1.07E-05		-1.63E+00	6.92E-18	Down	-5.60E-01	2.13E-17		4.44E-01	4.94E-16		Unigene50541_All//gi|18407840|ref|NP_566871.1|//3.00E-06//PSK1; growth factor [Arabidopsis thaliana] >gi|29428768|sp|Q8LA14.2|PSK6_ARATH RecName: Full=Putative phytosulfokines 6; Short=AtPSK6; Short=AtPSK3_2; Contains: RecName: Full=Phytosulfokine-alpha-like; Short=PSK-alpha-like; Short=Phytosulfokine-a-like; Contains: RecName: Full=Phytosulfokine-beta; Short=PSK-beta; Short=Phytosulfokine-b; Flags: Precursor >gi|27808144|dbj|BAB72177.2| phytosulfokine precursor 3_2 [Arabidopsis thaliana] >gi|88010851|gb|ABD38863.1| At3g44735 [Arabidopsis thaliana]	Unigene50541_All//9.00E-07//AT3G44735| PSK1; growth factor	Unigene50541_All//8.00E-44//DW505488				nr +
Unigene50542_All	1873	5907.42	3500.55	7814.61	674.77	631.51	449.32	11.02	2.79	5.47	-7.55E-01	0.00E+00		4.04E-01	0.00E+00		-9.56E-02	4.01E-14		-5.87E-01	0.00E+00		-1.98E+00	2.46E-51	Down	-1.01E+00	8.81E-20	Down	Unigene50542_All//gi|159895667|gb|ABX10444.1|//0.00E+00//phosphoethanolamine N-methyltransferase [Gossypium hirsutum]	Unigene50542_All//0.00E+00//TC129877			ko00564|Glycerophospholipid metabolism/ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00100|Steroid biosynthesis		nr +
Unigene50543_All	388	6.20	77.05	35.00	8.35	21.30	53.08	12.10	61.62	74.44	3.63E+00	4.16E-116	Up	2.50E+00	1.25E-35	Up	1.35E+00	1.33E-11	Up	2.67E+00	1.11E-63	Up	2.35E+00	3.11E-73	Up	2.62E+00	3.74E-102	Up	Unigene50543_All//gi|225458627|ref|XP_002284791.1|//8.00E-30//PREDICTED: ripening-related bZIP protein-like isoform 2 [Vitis vinifera] >gi|225458629|ref|XP_002284785.1| PREDICTED: ripening-related bZIP protein-like isoform 1 [Vitis vinifera]	Unigene50543_All//3.00E-17//AT4G34000| ABF3 (ABSCISIC ACID RESPONSIVE ELEMENTS-BINDING FACTOR 3); DNA binding / protein binding / transcription activator/ transcription factor	Unigene50543_All//6.00E-176//TC156582	bZIP			nr +
Unigene5055_All	1919	12.05	2.22	2.64	2.36	1.97	9.84	2.82	0.44	0.98	-2.44E+00	6.13E-61	Down	-2.19E+00	1.50E-51	Down	-2.59E-01	4.04E-01		2.06E+00	6.28E-43	Up	-2.69E+00	5.94E-20	Down	-1.53E+00	2.25E-10	Down	Unigene5055_All//gi|224088063|ref|XP_002308312.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222854288|gb|EEE91835.1| cytochrome P450 [Populus trichocarpa]	Unigene5055_All//0.00E+00//AT2G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene5055_All//0.00E+00//DR454918		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism/ko00071|Fatty acid metabolism/ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism/ko00906|Carotenoid biosynthesis		nr -
Unigene50550_All	1518	0.52	0.87	0.42	1.64	0.70	1.55	5.57	6.83	24.35	7.47E-01	2.05E-01		-2.97E-01	6.97E-01		-1.22E+00	1.28E-03		-8.48E-02	8.47E-01		2.94E-01	7.79E-02		2.13E+00	5.70E-102	Up	Unigene50550_All//gi|124360742|gb|ABN08719.1|//1.00E-114//Protein kinase [Medicago truncatula]	Unigene50550_All//4.00E-87//AT5G46080| protein kinase			ko04626|Plant-pathogen interaction		nr +
Unigene50551_All	395	32.05	18.99	12.67	21.94	25.54	16.81	72.04	39.89	15.03	-7.56E-01	2.05E-06		-1.34E+00	1.67E-14	Down	2.19E-01	2.79E-01		-3.85E-01	5.73E-02		-8.53E-01	7.24E-20		-2.26E+00	5.95E-86	Down	Unigene50551_All//gi|260766929|gb|ACX50406.1|//4.00E-17//histone H4 [Eriobotrya japonica]	Unigene50551_All//2.00E-18//AT5G59970| histone H4	Unigene50551_All//0.00E+00//TC138428				nr -
Unigene50553_All	491	1.17	21.05	1.30	0.41	3.16	1.29	4.39	7.07	11.93	4.17E+00	9.93E-45	Up	1.51E-01	8.55E-01		2.96E+00	6.10E-06	Up	1.67E+00	9.79E-02		6.86E-01	2.05E-02		1.44E+00	3.60E-10	Up							
Unigene50554_All	578	2.26	0.70	1.29	5.52	7.75	5.78	17.48	4.77	7.93	-1.69E+00	7.07E-03		-8.11E-01	1.90E-01		4.90E-01	9.12E-02		6.80E-02	8.64E-01		-1.87E+00	1.01E-23	Down	-1.14E+00	3.67E-12	Down	Unigene50554_All//gi|224120498|ref|XP_002331062.1|//2.00E-69//vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa] >gi|222872992|gb|EEF10123.1| vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa]	Unigene50554_All//2.00E-47//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene50554_All//0.00E+00//C0097639		ko00190|Oxidative phosphorylation		nr -
Unigene50555_All	391	0.40	3.11	2.59	3.57	4.84	8.43	5.95	27.90	23.13	2.95E+00	1.75E-04	Up	2.69E+00	2.08E-03		4.41E-01	3.93E-01		1.24E+00	3.44E-04	Up	2.23E+00	9.28E-32	Up	1.96E+00	4.95E-23	Up			Unigene50555_All//1.00E-72//gi|164362130|gb|ES804885.1|ES804885				
Unigene50556_All	1550	0.14	0.46	0.21	10.03	7.93	3.85	0.71	0.62	0.41	1.76E+00	5.60E-02		6.10E-01	6.24E-01		-3.38E-01	1.42E-02		-1.38E+00	8.86E-21	Down	-1.94E-01	7.34E-01		-7.86E-01	1.59E-01		Unigene50556_All//gi|115448793|ref|NP_001048176.1|//1.00E-136//0s02g0758100 [Oryza sativa Japonica Group] >gi|46805692|dbj|BAD17093.1| LMBR1 integral membrane protein-like [Oryza sativa Japonica Group] >gi|113537707|dbj|BAF10090.1| Os02g0758100 [Oryza sativa Japonica Group]	Unigene50556_All//2.00E-118//AT5G65290| LMBR1 integral membrane family protein	Unigene50556_All//2.00E-46//TC174234				nr -
Unigene50558_All	1050	0.40	12.69	3.25	1.38	1.18	2.15	0.08	0.12	0.08	4.99E+00	3.51E-64	Up	3.03E+00	2.89E-11	Up	-2.21E-01	7.04E-01		6.45E-01	1.44E-01		5.69E-01	7.81E-01		-8.49E-02	9.71E-01		Unigene50558_All//gi|289065767|gb|ADC80921.1|//1.00E-138//delta-8 sphingolipid desaturase [Vernicia fordii]	Unigene50558_All//3.00E-135//AT2G46210| delta-8 sphingolipid desaturase, putative	Unigene50558_All//0.00E+00//C0074841		ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene50561_All	940	4.12	1.83	2.32	0.74	0.33	0.48	1.57	4.58	0.30	-1.17E+00	2.34E-04	Down	-8.27E-01	1.10E-02		-1.17E+00	1.61E-01		-6.27E-01	4.76E-01		1.54E+00	3.54E-08	Up	-2.41E+00	1.48E-05	Down	Unigene50561_All//gi|224059584|ref|XP_002299919.1|//6.00E-54//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222847177|gb|EEE84724.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene50561_All//1.00E-15//AT3G14460| disease resistance protein (NBS-LRR class), putative					nr +
Unigene50562_All	1066	0.44	0.10	0.60	0.47	1.39	0.34	3.17	3.33	1.23	-2.22E+00	7.76E-02		4.41E-01	6.23E-01		1.57E+00	5.40E-03		-4.64E-01	6.59E-01		7.08E-02	8.24E-01		-1.36E+00	7.36E-06	Down			Unigene50562_All//2.00E-08//gi|78349867|gb|DT570141.1|DT570141				
Unigene50563_All	546	0.19	2.51	0.78	3.65	3.09	2.07	3.48	5.66	4.52	3.71E+00	7.17E-06	Up	2.03E+00	1.39E-01		-2.40E-01	6.05E-01		-8.20E-01	7.58E-02		7.01E-01	2.69E-02		3.77E-01	3.03E-01		Unigene50563_All//gi|28416873|gb|AA042967.1|//1.00E-35//At5g19875 [Arabidopsis thaliana]	Unigene50563_All//9.00E-23//AT5G19875| unknown protein	Unigene50563_All//0.00E+00//TC172611				nr +
Unigene50565_All	1504	1.15	2.36	0.96	2.25	1.67	1.32	5.12	1.64	6.07	1.04E+00	1.72E-03		-2.64E-01	6.37E-01		-4.30E-01	2.08E-01		-7.69E-01	2.15E-02		-1.64E+00	2.57E-15	Down	2.46E-01	1.62E-01		Unigene50565_All//gi|15229606|ref|NP_190544.1|//1.00E-108//AtRLP44 (Receptor Like Protein 44); protein binding [Arabidopsis thaliana] >gi|30102624|gb|AAP21230.1| At3g49750 [Arabidopsis thaliana]	Unigene50565_All//7.00E-98//AT3G49750| AtRLP44 (Receptor Like Protein 44); protein binding	Unigene50565_All//2.00E-120//DN779584		ko04626|Plant-pathogen interaction		nr -
Unigene50566_All	932	5.95	2.17	6.74	14.00	12.93	4.41	0.68	0.00	0.00	-1.45E+00	6.74E-08	Down	1.80E-01	4.97E-01		-1.15E-01	5.57E-01		-1.67E+00	5.85E-23	Down	-9.41E+00	1.23E-04	Down	-9.41E+00	7.10E-05	Down	Unigene50566_All//gi|224093533|ref|XP_002334831.1|//1.00E-109//amino acid permease [Populus trichocarpa] >gi|222875165|gb|EEF12296.1| amino acid permease [Populus trichocarpa]	Unigene50566_All//1.00E-95//AT1G77380| AAP3; amino acid transmembrane transporter	Unigene50566_All//0.00E+00//ES821203				nr +
Unigene50567_All	338	52.17	38.83	42.85	58.21	71.62	70.55	277.45	121.55	119.16	-4.26E-01	1.28E-03		-2.84E-01	4.68E-02		2.99E-01	5.96E-03		2.77E-01	1.60E-02		-1.19E+00	9.29E-110	Down	-1.22E+00	3.57E-117	Down	Unigene50567_All//gi|192910762|gb|ACF06489.1|//3.00E-55//ribosomal protein L10A [Elaeis guineensis]	Unigene50567_All//1.00E-42//AT1G08360| 60S ribosomal protein L10A (RPL10A)	Unigene50567_All//0.00E+00//gi|109828296|gb|DW226921.1|DW226921		ko03010|Ribosome		nr -
Unigene5057_All	1061	9.17	3.87	4.57	93.24	55.66	41.55	63.80	17.92	9.54	-1.25E+00	1.16E-10	Down	-1.01E+00	2.08E-07	Down	-7.44E-01	3.07E-53		-1.17E+00	1.84E-99	Down	-1.83E+00	3.61E-150	Down	-2.74E+00	1.07E-254	Down	Unigene5057_All//gi|115444275|ref|NP_001045917.1|//1.00E-53//0s02g0152400 [Oryza sativa Japonica Group] >gi|113535448|dbj|BAF07831.1| Os02g0152400 [Oryza sativa Japonica Group]	Unigene5057_All//2.00E-50//AT5G38410| ribulose bisphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B)	Unigene5057_All//0.00E+00//TC137624		ko00710|Carbon fixation in photosynthetic organisms//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene50570_All	764	144.98	12.53	21.47	8.48	3.61	7.63	0.00	0.11	0.00	-3.53E+00	0.00E+00	Down	-2.76E+00	0.00E+00	Down	-1.23E+00	1.60E-08	Down	-1.53E-01	5.88E-01		6.77E+00	4.00E-01		null	null		Unigene50570_All//gi|224080516|ref|XP_002306147.1|//1.00E-48//SAUR family protein [Populus trichocarpa] >gi|222849111|gb|EEE86658.1| SAUR family protein [Populus trichocarpa]	Unigene50570_All//4.00E-43//AT2G21220| auxin-responsive protein, putative	Unigene50570_All//3.00E-130//DW520620				nr +
Unigene50571_All	320	2.62	1.27	2.33	4.05	1.83	1.55	3.96	3.00	0.25	-1.05E+00	1.74E-01		-1.67E-01	8.16E-01		-1.15E+00	4.27E-02		-1.38E+00	2.30E-02		-4.00E-01	4.77E-01		-3.99E+00	2.56E-07	Down			Unigene50571_All//3.00E-162//gi|164287216|gb|ES840774.1|ES840774				
Unigene50572_All	1211	0.39	0.96	0.97	0.86	0.48	1.34	2.27	3.59	0.66	1.31E+00	4.44E-02		1.32E+00	5.10E-02		-8.38E-01	2.01E-01		6.36E-01	2.39E-01		6.61E-01	1.09E-02		-1.79E+00	7.27E-07	Down	Unigene50572_All//gi|296149181|gb|ADG96405.1|//1.00E-119//S-locus receptor kinase [Olea europaea]	Unigene50572_All//7.00E-119//AT4G27300| S-locus protein kinase, putative	Unigene50572_All//6.00E-15//gi|84150242|gb|DN781542.1|DN781542		ko04626|Plant-pathogen interaction		nr -
Unigene50577_All	575	19.38	3.26	4.54	5.98	6.65	9.03	1.47	0.44	0.28	-2.57E+00	1.92E-31	Down	-2.09E+00	1.18E-23	Down	1.53E-01	6.79E-01		5.96E-01	2.45E-02		-1.75E+00	1.64E-02		-2.41E+00	1.68E-03		Unigene50577_All//gi|224130286|ref|XP_002328572.1|//1.00E-49//glutaredoxin [Populus trichocarpa] >gi|222838554|gb|EEE76919.1| glutaredoxin [Populus trichocarpa]	Unigene50577_All//4.00E-43//AT3G21660| electron carrier/ protein disulfide oxidoreductase	Unigene50577_All//7.00E-10//TC167129				nr +
Unigene50578_All	296	15.55	45.88	27.34	61.93	95.86	144.19	33.85	38.27	31.49	1.56E+00	4.40E-20	Up	8.14E-01	1.24E-04		6.30E-01	2.45E-11		1.22E+00	1.19E-45	Up	1.77E-01	3.03E-01		-1.04E-01	5.79E-01		Unigene50578_All//gi|224144112|ref|XP_002325190.1|//4.00E-36//plant synaptotagmin [Populus trichocarpa] >gi|222866624|gb|EEF03755.1| plant synaptotagmin [Populus trichocarpa]	Unigene50578_All//8.00E-32//AT5G11100| SYTD	Unigene50578_All//1.00E-154//TC147565				nr -
Unigene50579_All	751	0.00	0.40	0.00	12.14	6.51	1.92	8.44	3.90	4.67	8.66E+00	4.42E-02		null	null		-8.99E-01	3.32E-07		-2.66E+00	5.34E-29	Down	-1.12E+00	1.92E-07	Down	-8.55E-01	2.80E-05		Unigene50579_All//gi|255585399|ref|XP_002533395.1|//1.00E-13//ankyrin repeat-containing protein, putative [Ricinus communis] >gi|223526769|gb|EEF28995.1| ankyrin repeat-containing protein, putative [Ricinus communis]		Unigene50579_All//1.00E-144//C0091281				nr +
Unigene5058_All	1535	3.54	4.16	4.89	3.28	3.72	7.30	0.19	0.14	0.23	2.31E-01	3.68E-01		4.65E-01	3.91E-02		1.84E-01	5.45E-01		1.15E+00	2.12E-11	Up	-5.02E-01	6.77E-01		2.77E-01	7.87E-01		Unigene5058_All//gi|224138238|ref|XP_002322764.1|//0.00E+00//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222867394|gb|EEF04525.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene5058_All//8.00E-153//AT5G06530| ABC transporter family protein	Unigene5058_All//0.00E+00//TC178626		ko03040|Spliceosome//ko02010|ABC transporters		nr -

Unigene50582_All	753	2.92	1.48	2.55	9.46	8.32	4.26	1.52	0.28	0.79	-9.79E-01	2.41E-02		-1.97E-01	6.46E-01		-1.85E-01	4.53E-01		-1.15E+00	1.49E-07	Down	-2.45E+00	2.46E-04	Down	-9.34E-01	8.80E-02		Unigene50582_All//gi|15234009|ref|NP_193611.1|//2.00E-53//AtRLP51 (Receptor Like Protein 51); protein binding [Arabidopsis thaliana]	Unigene50582_All//8.00E-45//AT4G18760| AtRLP51 (Receptor Like Protein 51); protein binding	Unigene50582_All//0.00E+00//gi|78339321|gb|DT559595.1|DT559595				nr -
Unigene50586_All	469	1.23	0.11	1.59	16.78	11.60	5.20	2.34	0.18	1.87	-3.51E+00	9.02E-03		3.73E-01	6.23E-01		-5.33E-01	6.67E-03		-1.69E+00	2.52E-14	Down	-3.72E+00	7.15E-06	Down	-3.27E-01	5.82E-01		Unigene50586_All//gi|38344244|emb|CAD41337.2|//1.00E-08//OJ991113_30.21 [Oryza sativa (japonica cultivar-group)]		Unigene50586_All//0.00E+00//gi|21092037|gb|BQ404350.1|BQ404350				nr -
Unigene50587_All	1115	1.97	0.82	0.62	4.29	3.86	7.62	8.80	14.47	13.18	-1.27E+00	4.15E-03		-1.67E+00	5.54E-04	Down	-1.52E-01	6.12E-01		8.28E-01	2.29E-05		7.18E-01	7.77E-09		5.84E-01	4.47E-06				Unigene50587_All//1.00E-09//TC149178				ESTscan +
Unigene50588_All	507	3.30	1.40	1.37	1.87	1.02	3.39	1.00	3.46	22.24	-1.24E+00	1.66E-02		-1.27E+00	1.95E-02		-8.74E-01	2.10E-01		8.59E-01	9.53E-02		1.79E+00	1.73E-04	Up	4.47E+00	7.56E-64	Up	Unigene50588_All//gi|94807648|gb|AB74712 1.1|//1.00E-16//At5g02220 [Arabidopsis thaliana]	Unigene50588_All//7.00E-18//AT5G02220| unknown protein	Unigene50588_All//3.00E-132//DW504069				nr -
Unigene50589_All	987	206.58	403.87	279.74	49.97	66.46	62.28	67.04	28.33	34.67	9.67E-01	5.53E-270		4.37E-01	4.34E-45		4.12E-01	4.24E-12		3.18E-01	1.12E-06		-1.24E+00	4.89E-83	Down	-9.51E-01	1.27E-55		Unigene50589_All//gi|112292669|gb|AB114813.1|//1.00E-88//chloroplast carbonic anhydrase [Pachysandra terminalis]	Unigene50589_All//3.00E-84//AT1G70410| carbonic anhydrase, putative / carbonate dehydratase, putative	Unigene50589_All//0.00E+00//gi|109834823|gb|DW233388.1|DW233388		ko00910|Nitrogen metabolism		nr -
Unigene5059_All	1374	0.38	1.92	0.47	6.67	5.24	4.96	2.98	1.83	2.90	2.33E+00	4.20E-07	Up	2.89E-01	7.25E-01		-3.49E-01	6.71E-02		-4.27E-01	2.69E-02		-7.10E-01	8.04E-03		-4.18E-02	8.91E-01		Unigene5059_All//gi|15232696|ref|NP_188201.1|//1.00E-137//glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Unigene5059_All//2.00E-123//AT3G15800| glycosyl hydrolase family 17 protein	Unigene5059_All//2.00E-18//TC161982		ko00500|Starch and sucrose metabolism		nr -
Unigene50590_All	700	1.64	0.36	1.07	2.85	1.67	2.00	3.14	1.55	1.20	-2.18E+00	2.45E-03		-6.27E-01	3.56E-01		-7.67E-01	8.22E-02		-5.09E-01	2.94E-01		-1.02E+00	8.74E-03		-1.39E+00	3.22E-04	Down	Unigene50590_All//gi|10176976|dbj|BAB10208.1|//8.00E-15//mitochondrial RNA helicase-like protein [Arabidopsis thaliana]	Unigene50590_All//4.00E-16//AT5G39840| ATP-dependent RNA helicase, mitochondrial, putative					nr -
Unigene50591_All	754	0.90	0.13	1.84	2.91	1.32	0.96	1.40	0.89	3.65	-2.75E+00	1.06E-02		1.03E+00	8.63E-02		-1.13E+00	5.60E-03		-1.60E+00	3.68E-04	Down	-6.61E-01	2.78E-01		1.38E+00	6.13E-05	Up	Unigene50591_All//gi|218193742|gb|EEC76169.1|//4.00E-06//hypothetical protein OsI_13484 [Oryza sativa Indica Group]		Unigene50591_All//0.00E+00//gi|78340479|gb|DT560753.1|DT560753				nr -
Unigene50595_All	546	44.56	48.63	32.18	63.59	54.43	65.68	83.40	68.89	34.80	1.26E-01	2.85E-01		-4.69E-01	3.97E-05		-2.25E-01	1.31E-02		4.66E-02	6.94E-01		-2.76E-01	1.01E-04		-1.26E+00	2.20E-60	Down	Unigene50595_All//gi|227937351|gb|ACF43316.1|//3.00E-26//20S proteasome beta subunit 5 [Citrus maxima]	Unigene50595_All//2.00E-22//AT1G13060| PBE1; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene50595_All//0.00E+00//gi|21103897|gb|BQ416210.1|BQ416210		ko03050|Proteasome		nr +
Unigene50598_All	376	4.31	2.70	4.67	5.70	4.03	5.89	34.41	34.79	14.52	-6.79E-01	1.89E-01		1.16E-01	8.09E-01		-5.00E-01	2.61E-01		4.71E-02	9.34E-01		1.60E-02	9.41E-01		-1.25E+00	1.83E-17	Down			Unigene50598_All//0.00E+00//gi|84168481|gb|DR457129.1|DR457129				
Unigene50599_All	428	5.01	8.41	7.34	8.73	5.15	5.07	20.35	21.09	9.12	7.46E-01	2.15E-02		5.51E-01	1.42E-01		-7.62E-01	1.09E-02		-7.85E-01	1.27E-02		5.18E-02	7.93E-01		-1.16E+00	7.91E-11	Down			Unigene50599_All//1.00E-168//TC171528				
Unigene50600_All	703	3.13	1.23	2.80	10.56	8.72	5.40	1.80	0.30	1.19	-1.35E+00	2.48E-03		-1.58E-01	7.17E-01		-2.76E-01	2.25E-01		-9.68E-01	4.47E-06		-2.60E+00	5.14E-05	Down	-6.00E-01	2.45E-01				Unigene50600_All//6.00E-131//TC139906				
Unigene50602_All	420	12.71	5.43	5.96	7.71	3.20	3.44	3.32	4.58	4.46	-1.23E+00	4.42E-06	Down	-1.09E+00	6.48E-05	Down	-1.27E+00	9.69E-05	Down	-1.16E+00	7.33E-04	Down	4.63E-01	2.89E-01		4.24E-01	3.19E-01		Unigene50602_All//gi|224053945|ref|XP_002298051.1|//9.00E-16//predicted protein [Populus trichocarpa] >gi|222845309|gb|EEE82856.1| predicted protein [Populus trichocarpa]						nr +
Unigene50603_All	1476	0.92	0.17	0.07	13.57	6.02	1.47	3.41	0.37	1.62	-2.43E+00	3.35E-04	Down	-3.67E+00	1.58E-05	Down	-1.17E+00	1.96E-23	Down	-3.21E+00	7.39E-77	Down	-3.21E+00	4.57E-22	Down	-1.07E+00	5.67E-06	Down	Unigene50603_All//gi|7715592|gb|AAF68110.1|AC010793_5//1.00E-47//F20B17.19 [Arabidopsis thaliana]	Unigene50603_All//2.00E-23//AT1G79760| DTA4 (DOWNSTREAM TARGET OF AGL15-4)			ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis		nr -
Unigene50604_All	1121	4.25	1.13	2.80	2.80	1.14	1.41	1.32	0.19	0.36	-1.91E+00	8.75E-10	Down	-6.00E-01	3.87E-02		-1.30E+00	9.11E-05	Down	-9.89E-01	4.57E-03		-2.82E+00	3.44E-06	Down	-1.89E+00	2.45E-04	Down			Unigene50604_All//9.00E-11//gi|11207985|gb|BF276915.1|BF276915				
Unigene50605_All	693	1.36	2.19	1.61	1.80	4.82	2.54	9.15	9.65	20.12	6.91E-01	2.02E-01		2.48E-01	6.90E-01		1.42E+00	2.56E-05	Up	5.00E-01	3.48E-01		7.65E-02	7.34E-01		1.14E+00	3.26E-16	Up	Unigene50605_All//gi|125991251|sp|A0Z278.1|YCF2_GOSBA//3.00E-80//RecName: Full=Protein ycf2 >gi|119224904|dbj|BAF41290.1| Hypothetical protein [Gossypium barbadense] >gi|119224922|dbj|BAF41308.1| Hypothetical protein [Gossypium barbadense]	Unigene50605_All//5.00E-77//ATCG01280| hypothetical protein	Unigene50605_All//0.00E+00//TC129552				nr -
Unigene50609_All	428	3.67	16.46	3.36	35.73	28.72	26.91	45.24	54.49	36.12	2.17E+00	2.23E-16	Up	-1.27E-01	8.07E-01		-3.15E-01	2.55E-02		-4.09E-01	4.04E-03		2.68E-01	1.01E-02		-3.25E-01	3.19E-03		Unigene50609_All//gi|115435412|ref|NP_001042464.1|//5.00E-19//Os01g0226400 [Oryza sativa Japonica Group] >gi|113531995|dbj|BAF04378.1| Os01g0226400 [Oryza sativa Japonica Group]	Unigene50609_All//3.00E-19//AT5G52882| ATP binding / nucleoside-triphosphatase/ nucleotide binding	Unigene50609_All//0.00E+00//TC156283				nr -
Unigene50611_All	266	46.22	152.20	60.26	95.32	135.67	124.96	84.08	105.59	83.57	1.72E+00	3.65E-67	Up	3.83E-01	9.03E-03		5.09E-01	6.51E-10		3.91E-01	1.85E-05		3.29E-01	3.54E-04		-8.80E-03	9.61E-01		Unigene50611_All//gi|163639437|gb|ABY28269.1|//4.00E-29//EIN3-like protein EIL1 [Actinidia deliciosa]	Unigene50611_All//1.00E-16//AT3G20770| EIN3 (ETHYLENE-INSENSITIVE3); transcription factor	Unigene50611_All//2.00E-141//gi|164282440|gb|ES815287.1|ES815287	EIL			nr -
Unigene50612_All	425	46.04	33.98	21.17	48.76	41.40	49.95	42.68	26.65	29.81	-4.38E-01	4.36E-04		-1.12E+00	7.49E-17	Down	-2.36E-01	5.58E-02		3.47E-02	8.08E-01		-6.79E-01	5.20E-09		-5.18E-01	4.54E-06		Unigene50612_All//gi|15230073|ref|NP_189058.1|//5.00E-07//PMP (PUTATIVE TYPE 1 MEMBRANE PROTEIN) [Arabidopsis thaliana] >gi|15450743|gb|AAK96643.1| AT3g24160/MUJ8_16 [Arabidopsis thaliana] >gi|22137144|gb|AAM91417.1| AT3g24160/MUJ8_16 [Arabidopsis thaliana]	Unigene50612_All//3.00E-08//AT3G24160| PMP (PUTATIVE TYPE 1 MEMBRANE PROTEIN)	Unigene50612_All//7.00E-111//gi|48743764|gb|CO074283.1|CO074283				nr -
Unigene50613_All	518	0.30	3.72	1.03	2.89	3.92	1.92	0.57	0.48	0.69	3.62E+00	6.74E-08	Up	1.76E+00	1.29E-01		4.43E-01	3.67E-01		-5.89E-01	3.04E-01		-2.39E-01	8.39E-01		2.77E-01	7.87E-01				Unigene50613_All//6.00E-07//EX164177				
Unigene50615_All	1248	0.17	0.24	0.00	16.17	15.64	12.05	28.97	8.98	7.05	5.39E-01	6.71E-01		-7.39E+00	1.45E-01		-4.72E-02	7.82E-01		-4.24E-01	4.35E-04		-1.69E+00	4.95E-72	Down	-2.04E+00	1.45E-95	Down	Unigene50615_All//gi|9280671|gb|AAF86540.1|AC002560_33//2.00E-93//F21B7.3 [Arabidopsis thaliana]	Unigene50615_All//9.00E-95//AT1G03410| 2A6; oxidoreductase	Unigene50615_All//0.00E+00//CO117592		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene50617_All	1230	0.17	0.08	0.09	2.15	3.19	4.30	0.96	3.43	4.89	-1.05E+00	5.64E-01		-9.74E-01	6.20E-01		5.72E-01	6.44E-02		1.00E+00	1.11E-04	Up	1.83E+00	4.71E-10	Up	2.35E+00	2.53E-19	Up	Unigene50617_All//gi|22328976|ref|NP_194480.2|//7.00E-95//PP11 (PROTON PUMP INTERACTOR 1); protein binding [Arabidopsis thaliana] >gi|13992437|emb|CAA05145.2| proton pump interactor [Arabidopsis thaliana] >gi|15215674|gb|AAX91382.1| AT4g27500/F27G19_100 [Arabidopsis thaliana] >gi|23569867|gb|AAN28853.1| At4g27500/F27G19_100 [Arabidopsis thaliana]	Unigene50617_All//2.00E-81//AT4G27500| PP11 (PROTON PUMP INTERACTOR 1); protein binding	Unigene50617_All//0.00E+00//TC151233				nr +
Unigene50618_All	910	2.76	2.90	4.45	21.46	15.59	22.58	6.32	3.17	1.36	6.92E-02	8.60E-01		6.88E-01	2.96E-02		-4.61E-01	6.84E-05		7.36E-02	6.17E-01		-9.96E-01	8.39E-06		-2.22E+00	1.31E-17	Down	Unigene50618_All//gi|8778581|gb|AAF79589.1|AC007945_9//3.00E-13//F28C11.16 [Arabidopsis thaliana] >gi|4056436|gb|AAC98009.1| EST gb|AA650912 comes from this gene [Arabidopsis thaliana] >gi|34365603|gb|AAQ65113.1| At1g23530 [Arabidopsis thaliana]	Unigene50618_All//6.00E-08//AT1G23530| unknown protein	Unigene50618_All//0.00E+00//DW503150				nr -
Unigene50619_All	429	10.49	8.98	11.92	10.68	9.23	9.58	48.00	18.90	5.85	-2.25E-01	4.49E-01		1.84E-01	5.37E-01		-2.11E-01	5.16E-01		-1.57E-01	6.16E-01		-1.34E+00	1.05E-29	Down	-3.04E+00	1.38E-86	Down			Unigene50619_All//0.00E+00//gi|13351303|gb|BG441651.1|BG441651				
Unigene50621_All	1245	6.30	4.68	2.61	2.68	2.85	1.23	0.00	0.03	0.00	-4.30E-01	4.08E-02		-1.27E+00	1.40E-08	Down	8.77E-02	8.20E-01		-1.12E+00	9.10E-04	Down	5.07E+00	6.34E-01		null	null		Unigene50621_All//gi|164562217|gb|AB161023.1|//2.00E-87//zinc finger homeodomain protein 1 [Saruma henryi]	Unigene50621_All//1.00E-58//AT4G24660| ATHB22 (HOMEOBOX PROTEIN 22); DNA binding / transcription factor	Unigene50621_All//0.00E+00//ES832284	zf-HD			nr -
Unigene50622_All	1363	25.53	7.21	23.95	4.93	3.99	2.65	0.37	0.00	0.00	-1.82E+00	4.44E-63	Down	-9.21E-02	3.98E-01		-3.06E-01	1.96E-01		-8.96E-01	5.59E-05		-8.54E+00	8.89E-04	Down	-8.54E+00	5.54E-04	Down	Unigene50622_All//gi|110931704|gb|ABR02851.1|//1.00E-118//MYB transcription factor MYB109 [Glycine max]	Unigene50622_All//1.00E-64//AT1G49010| myb family transcription factor	Unigene50622_All//0.00E+00//TC138095	MYB			nr +
Unigene50623_All	1132	2.40	5.73	4.70	7.00	10.98	11.93	0.19	0.00	0.74	1.25E+00	2.14E-07	Up	9.69E-01	3.50E-04		6.50E-01	1.58E-05		7.70E-01	2.97E-07		-7.54E+00	7.43E-02		1.99E+00	7.05E-03		Unigene50623_All//gi|297743543|emb|CBI36410.3|//1.00E-13//unnamed protein product [Vitis vinifera]						nr -
Unigene50624_All	667	1.80	0.91	0.40	10.75	10.79	5.69	3.93	1.13	1.08	-9.85E-01	1.13E-01		-2.18E+00	3.05E-03		4.80E-03	9.90E-01		-9.19E-01	1.84E-05		-1.80E+00	2.14E-06	Down	-1.87E+00	5.91E-07	Down	Unigene50624_All//gi|8408744|ref|NP_566913.1|//1.00E-54//copper-binding family protein [Arabidopsis thaliana]	Unigene50624_All//3.00E-43//AT3G48970| copper-binding family protein	Unigene50624_All//0.00E+00//TC153426				nr -
Unigene50625_All	678	0.00	2.69	0.00	3.01	2.29	0.93	3.55	6.47	9.11	1.14E+01	2.14E-10	Up	null	null		-3.98E-01	3.95E-01		-1.69E+00	3.48E-04	Down	8.65E-01	8.10E-04		1.36E+00	7.89E-10	Up			Unigene50625_All//0.00E+00//TC142103				
Unigene50626_All	475	2.09	1.49	1.35	7.34	4.06	4.75	5.43	2.64	1.59	-4.87E-01	4.72E-01		-6.38E-01	3.90E-01		-8.55E-01	5.83E-03		-6.27E-01	6.06E-02		-1.04E+00	3.25E-03		-1.77E+00	2.04E-06	Down	Unigene50626_All//gi|124359981|gb|ABN07997.1|//7.00E-15//contains similarity to reverse trancriptase, related [Medicago truncatula]	Unigene50626_All//3.00E-07//AT3G26855| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: reverse transcriptase-related (TAIR:AT2G02650.1); Has 97 Blast hits to 97 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 97; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene50626_All//0.00E+00//gi|18098710|gb|BM357964.1|BM357964				nr -
Unigene50627_All	266	15.54	19.05	14.61	15.17	17.09	22.58	42.60	24.83	19.92	2.94E-01	2.94E-01		-8.86E-02	7.76E-01		1.72E-01	6.10E-01		5.74E-01	1.83E-02		-7.79E-01	2.60E-07		-1.10E+00	9.63E-13	Down	Unigene50627_All//gi|168052699|ref|XP_001778777.1|//1.00E-44//26S proteasome regulatory complex, ATPase RPT6 [Physcomitrella patens subsp. patens] >gi|162669783|gb|EDQ56363.1| 26S proteasome regulatory complex, ATPase RPT6 [Physcomitrella patens subsp. patens]	Unigene50627_All//8.00E-46//AT5G20000| 26S proteasome AAA-ATPase subunit, putative	Unigene50627_All//7.00E-144//gi|78328196|gb|DT548470.1|DT548470		ko03050|Proteasome		nr -
Unigene50628_All	1195	0.09	0.42	0.00	0.25	0.46	0.60	115.45	17.14	40.87	2.28E+00	6.23E-02		-6.45E+00	3.92E-01		8.83E-01	4.21E-01		1.27E+00	1.56E-01		-2.75E+00	0.00E+00	Down	-1.50E+00	8.17E-236	Down	Unigene50628_All//gi|297810811|ref|XP_002873289.1|//2.00E-79//sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319126|gb|EFH49548.1| sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50628_All//8.00E-73//AT1G74100| SOT16 (SULFOTRANSFERASE 16); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene50628_All//1.00E-136//TC148002		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism		nr -
Unigene5063_All	1187	0.18	0.09	0.00	5.25	4.84	1.67	2.99	2.01	2.42	-1.05E+00	5.64E-01		-7.46E+00	1.45E-01		-1.15E-01	6.73E-01		-1.65E+00	4.61E-11	Down	-5.76E-01	5.03E-02		-3.08E-01	3.02E-01		Unigene5063_All//gi|289721336|gb|ADD17678.1|//1.00E-158//squalene epoxidase [Withania somnifera]	Unigene5063_All//1.00E-111//AT1G58440| XF1; squalene monooxygenase	Unigene5063_All//0.00E+00//ES815525		ko00100|Steroid biosynthesis		nr +
Unigene50630_All	815	0.39	0.75	1.31	3.42	2.96	2.38	6.90	3.33	4.30	9.54E-01	3.14E-01		1.76E+00	1.85E-02		-2.11E-01	6.08E-01		-5.23E-01	1.84E-01		-1.05E+00	3.92E-06	Down	-6.82E-01	1.62E-03		Unigene50630_All//gi|223452520|gb|ACM89587.1|//1.00E-107//LRR-like protein [Glycine max]	Unigene50630_All//5.00E-85//AT3G49750| AtRLP44 (Receptor Like Protein 44); protein binding	Unigene50630_All//1.00E-166//DN779584		ko04626|Plant-pathogen interaction		nr +
Unigene50631_All	578	1.63	0.00	0.83	3.62	1.31	2.50	4.83	3.76	1.59	-1.07E+01	1.46E-05	Down	-9.75E-01	2.00E-01		-1.47E+00	6.00E-04	Down	-5.34E-01	2.49E-01		-3.61E-01	3.15E-01		-1.61E+00	4.09E-06	Down							

Unigene50632_All	692	25.56	15.08	19.08	28.36	31.10	31.91	34.89	30.86	15.54	-7.61E-01	1.02E-08		-4.21E-01	2.20E-03		1.33E-01	3.27E-01		1.70E-01	1.96E-01		-1.77E-01	1.02E-01		-1.17E+00	8.93E-29	Down	Unigene50632_All//gi|224100795|ref|XP_002312018.1|//1.00E-115//chorismate synthase [Populus trichocarpa] >gi|222851838|gb|EEE89385.1| chorismate synthase [Populus trichocarpa]	Unigene50632_All//2.00E-112//AT1G48850| EMB1144 (embryo defective 1144); chorismate synthase	Unigene50632_All//0.00E+00//gi|164263591|gb|ES851107.1|ES851107		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene50634_All	398	4.21	4.20	1.87	3.00	1.73	2.16	2.02	0.11	1.00	-1.90E-03	9.94E-01		-1.17E+00	3.09E-02		-7.96E-01	1.87E-01		-4.79E-01	4.72E-01		-4.26E+00	8.47E-05	Down	-1.01E+00	1.35E-01						Unigene50634_All//3.00E-116//TC175419				
Unigene50636_All	1005	4.06	0.91	0.42	3.02	2.19	1.26	5.22	2.37	1.70	-2.16E+00	7.89E-10	Down	-3.26E+00	2.89E-14	Down	-4.63E-01	1.99E-01		-1.26E+00	4.42E-04	Down	-1.14E+00	1.83E-06	Down	-1.61E+00	8.32E-11	Down	Unigene50636_All//gi|15224316|ref|NP_181292.1|//1.00E-126//ORC2 (ORIGIN RECOGNITION COMPLEX SECOND LARGEST SUBUNIT 2); DNA replication origin binding / protein binding [Arabidopsis thaliana] >gi|2498706|sp|Q38899.1|ORC2_ARATH RecName: Full=Origin recognition complex subunit 2 >gi|1113103|gb|AAC49131.1| at0rc2p [Arabidopsis thaliana] >gi|3236239|gb|AAC23627.1| origin recognition complex protein [Arabidopsis thaliana] >gi|21593764|gb|AAM65731.1| origin recognition complex protein [Arabidopsis thaliana]	Unigene50636_All//9.00E-128//AT2G37560| ORC2 (ORIGIN RECOGNITION COMPLEX SECOND LARGEST SUBUNIT 2); DNA replication origin binding / protein binding	Unigene50636_All//0.00E+00//gi|164310901|gb|ES844638.1|ES844638				nr +
Unigene50638_All	788	2.46	0.51	1.69	5.31	7.56	3.90	14.59	21.38	35.19	-2.26E+00	2.83E-05	Down	-5.40E-01	2.70E-01		5.10E-01	3.43E-02		-4.46E-01	1.49E-01		5.51E-01	4.85E-06		1.27E+00	3.38E-37	Up	Unigene50638_All//gi|23197634|gb|AAN15344.1|//3.00E-12//Unknown protein [Arabidopsis thaliana]	Unigene50638_All//8.00E-16//AT2G23690| unknown protein	Unigene50638_All//0.00E+00//gi|109888673|gb|DW517642.1|DW517642				nr +
Unigene5064_All	1408	2.27	0.36	0.15	4.07	4.89	2.21	3.78	1.72	1.22	-2.65E+00	8.99E-10	Down	-3.91E+00	5.84E-13	Down	2.66E-01	2.86E-01		-8.78E-01	3.18E-04		-1.14E+00	1.54E-06	Down	-1.64E+00	3.56E-11	Down	Unigene5064_All//gi|15227652|ref|NP_181181.1|//6.00E-90//AtGRF3 (GROWTH-REGULATING FACTOR 3); transcription activator [Arabidopsis thaliana] >gi|21539884|gb|AAM52878.1| transcription activator [Arabidopsis thaliana] >gi|111074412|gb|ABH04579.1| At2g36400 [Arabidopsis thaliana]	Unigene5064_All//3.00E-68//AT2G36400| AtGRF3 (GROWTH-REGULATING FACTOR 3); transcription activator	Unigene5064_All//0.00E+00//gi|78353334|gb|DT573608.1|DT573608	GRF			nr -
Unigene50640_All	576	0.09	0.79	3.33	1.90	1.32	1.18	1.61	1.23	0.55	3.12E+00	3.58E-02		5.20E+00	2.58E-09	Up	-5.33E-01	4.20E-01		-6.94E-01	3.11E-01		-3.89E-01	5.75E-01		-1.55E+00	1.68E-02						Unigene50640_All//6.00E-35//AW187339				
Unigene50642_All	356	4.70	1.57	3.44	6.16	4.64	4.19	21.85	9.04	9.74	-1.59E+00	3.09E-03		-4.51E-01	3.99E-01		-4.07E-01	3.61E-01		-5.56E-01	2.19E-01		-1.27E+00	7.68E-11	Down	-1.17E+00	7.11E-10	Down					Unigene50642_All//5.00E-170//gi|21095909|gb|BQ408222.1|BQ408222				
Unigene50643_All	383	2.32	1.59	0.56	7.15	5.93	2.00	2.21	2.73	2.50	-5.49E-01	4.42E-01		-2.06E+00	1.78E-02		-2.70E-01	5.23E-01		-1.84E+00	5.93E-06	Down	3.05E-01	6.58E-01		1.77E-01	7.64E-01						Unigene50643_All//3.00E-97//FL577609				
Unigene50644_All	892	21.94	9.15	20.95	3.74	3.17	3.54	0.00	0.00	0.09	-1.26E+00	4.37E-21	Down	-6.62E-02	6.32E-01		-2.41E-01	5.30E-01		-7.82E-02	8.32E-01		null	null		6.48E+00	4.03E-01		Unigene50644_All//gi|15010676|gb|AAK73997.1|//1.00E-35//At1g64150/F22C12_10 [Arabidopsis thaliana] >gi|23505909|gb|AAN28814.1| At1g64150/F22C12_10 [Arabidopsis thaliana]	Unigene50644_All//9.00E-38//AT1G64150| unknown protein	Unigene50644_All//0.00E+00//TC164175				nr -
Unigene50646_All	264	19.03	163.72	19.97	42.08	68.22	52.86	32.67	59.69	129.63	3.11E+00	1.38E-145	Up	6.98E-02	7.99E-01		6.97E-01	1.05E-08		3.29E-01	3.43E-02		8.69E-01	1.04E-11		1.99E+00	1.50E-86	Up	Unigene50646_All//gi|292668927|gb|ADE41118.1|//3.00E-12//AP2 domain class transcription factor [Malus x domestica]		Unigene50646_All//4.00E-145//ES846516				nr -
Unigene50648_All	460	40.95	22.80	13.89	77.10	57.49	65.49	174.54	88.32	106.01	-8.45E-01	6.72E-11		-1.56E+00	1.25E-26	Down	-4.23E-01	2.92E-07		-2.36E-01	1.09E-02		-9.83E-01	4.43E-69		-7.19E-01	4.88E-42		Unigene50648_All//gi|87240702|gb|AB022560.1|//2.00E-11//Mitochondrial substrate carrier [Medicago truncatula]	Unigene50648_All//5.00E-05//AT5G14040| mitochondrial phosphate transporter	Unigene50648_All//0.00E+00//gi|164308375|gb|ES832709.1|ES832709				nr -
Unigene50649_All	317	69.49	29.09	28.22	65.37	58.01	87.90	103.37	41.40	42.23	-1.26E+00	1.81E-23	Down	-1.30E+00	9.75E-24	Down	-1.72E-01	1.90E-01		4.27E-01	2.06E-05		-1.32E+00	1.58E-45	Down	-1.29E+00	2.41E-45	Down	Unigene50649_All//gi|300257130|gb|EF141382.1|//2.00E-10//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene50649_All//1.00E-07//AT2G32060| 40S ribosomal protein S12 (RPS12C)	Unigene50649_All//3.00E-140//gi|13353155|gb|BG443503.1|BG443503		ko03010|Ribosome		nr +
Unigene50651_All	577	1.27	1.49	1.29	16.49	30.44	26.77	6.96	25.43	10.08	2.34E-01	7.28E-01		2.53E-02	9.95E-01		8.84E-01	1.60E-12		6.99E-01	4.85E-07		1.87E+00	6.39E-34	Up	5.34E-01	1.24E-02		Unigene50651_All//gi|127058161|dbj|BAF48663.1|//7.00E-09//leucine-rich repeat/extensin [Nicotiana plumbaginifolia] >gi|127058167|dbj|BAF48664.1| leucine-rich repeat/extensin [Nicotiana plumbaginifolia]	Unigene50651_All//7.00E-08//AT3G49845| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: XYPPX repeat (InterPro:IPR006031); Has 14038 Blast hits to 7746 proteins in 541 species: Archae - 8; Bacteria - 1083; Metazoa - 5225; Fungi - 1793; Plants - 3748; Viruses - 424; Other Eukaryotes - 1757 (source: NCBI BLink).	Unigene50651_All//0.00E+00//gi|109869580|gb|DW498556.1|DW498556				nr +
Unigene50652_All	514	0.71	0.49	1.14	2.91	1.21	2.20	3.54	2.03	1.16	-5.32E-01	6.27E-01		6.78E-01	4.82E-01		-1.27E+00	1.45E-02		-4.04E-01	4.80E-01		-7.99E-01	6.56E-02		-1.61E+00	2.86E-04	Down									
Unigene50653_All	480	43.60	22.06	18.42	53.86	37.30	64.36	83.50	39.53	35.11	-9.83E-01	2.78E-15		-1.24E+00	4.18E-21	Down	-5.30E-01	5.97E-08		2.57E-01	9.89E-03		-1.08E+00	1.59E-40	Down	-1.25E+00	1.46E-52	Down					Unigene50653_All//2.00E-114//TC151493				
Unigene50656_All	478	2.41	4.13	1.56	6.25	5.33	2.46	3.36	3.15	2.75	7.80E-01	9.03E-02		-6.27E-01	3.56E-01		-2.30E-01	5.60E-01		-1.35E+00	2.30E-04	Down	-9.46E-02	8.44E-01		-2.89E-01	5.47E-01		Unigene50656_All//gi|186478165|ref|NP_001117234.1|//3.00E-07//URH2 (URIDINE-RIBOHYDROLASE 2); hydrolase [Arabidopsis thaliana]	Unigene50656_All//6.00E-08//AT1G05620| URH2 (URIDINE-RIBOHYDROLASE 2); hydrolase	Unigene50656_All//0.00E+00//gi|13354273|gb|BG444621.1|BG444621				nr +
Unigene50658_All	581	26.57	17.97	30.98	0.94	1.60	2.18	0.51	1.01	3.22	-5.64E-01	6.76E-05		2.22E-01	1.29E-01		7.63E-01	3.19E-01		1.21E+00	5.27E-02		9.83E-01	2.59E-01		2.66E+00	2.08E-07	Up	Unigene50658_All//gi|67968357|dbj|BAE00072.1|//1.00E-41//PGR5 [Amaranthus hybridus]	Unigene50658_All//2.00E-38//AT2G05620| PGR5 (proton gradient regulation 5); electron carrier	Unigene50658_All//4.00E-116//ES831692				nr +
Unigene5066_All	905	3.70	5.37	4.65	34.57	49.12	22.31	7.57	5.87	2.86	5.39E-01	4.91E-02		3.29E-01	3.10E-01		5.07E-01	5.22E-12		-6.32E-01	1.41E-11		-3.68E-01	7.60E-02		-1.40E+00	1.96E-11	Down	Unigene5066_All//gi|283135872|gb|AB811327.1|//2.00E-69//tau class glutathione transferase GSTU45 [Populus trichocarpa]	Unigene5066_All//3.00E-66//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	Unigene5066_All//0.00E+00//TC149058		ko00480|Glutathione metabolism		nr +
Unigene50661_All	1169	0.09	0.39	0.46	1.28	0.91	3.17	0.87	13.77	3.71	2.12E+00	9.59E-02		2.35E+00	5.87E-02		-4.85E-01	3.82E-01		1.31E+00	5.81E-05	Up	3.99E+00	9.77E-83	Up	2.10E+00	1.88E-12	Up	Unigene50661_All//gi|259121423|gb|ACV92031.1|//3.00E-57//WRKY transcription factor 29 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene50661_All//1.00E-46//AT1G29860| WRKY71; transcription factor	Unigene50661_All//2.00E-24//TC179071	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene50663_All	416	9.94	4.63	5.89	17.24	11.84	8.47	27.95	9.14	9.96	-1.10E+00	2.93E-04	Down	-7.55E-01	1.57E-02		-5.43E-01	8.90E-03		-1.03E+00	2.04E-06	Down	-1.61E+00	3.49E-22	Down	-1.49E+00	1.83E-20	Down					Unigene50663_All//0.00E+00//TC132519				
Unigene50664_All	503	0.31	1.51	0.00	0.69	0.75	0.99	0.84	20.94	15.44	2.28E+00	1.60E-02		-8.29E+00	2.44E-01		1.20E-01	9.58E-01		5.11E-01	6.41E-01		4.64E+00	5.50E-60	Up	4.20E+00	2.13E-42	Up	Unigene50664_All//gi|15224473|ref|NP_181360.1|//3.00E-29//DNA-binding protein-related [Arabidopsis thaliana] >gi|17981040|gb|AAL50816.1|AF45358 2_1 GT-1 like transcription factor [Arabidopsis thaliana]	Unigene50664_All//7.00E-24//AT2G38250| DNA-binding protein-related		Trihelix			nr -
Unigene50665_All	740	3.61	5.34	7.56	7.14	4.14	4.39	5.26	3.67	2.80	5.67E-01	6.72E-02		1.07E+00	5.78E-05	Up	-7.85E-01	1.20E-03		-6.99E-01	6.51E-03		-5.18E-01	6.56E-02		-9.09E-01	7.17E-04		Unigene50665_All//gi|115472987|ref|NP_001060092.1|//1.00E-24//Os07g0577900 [Oryza sativa Japonica Group] >gi|113611628|dbj|BAF22006.1| Os07g0577900 [Oryza sativa Japonica Group]	Unigene50665_All//5.00E-15//AT4G14600| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Target SNARE coiled-coil region (InterPro:IPR000727); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G29060.1); Has 95 Blast hits to 95 proteins in 38 species: Archae - 0; Bacteria - 0; Metazoa - 27; Fungi - 19; Plants - 44; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene50665_All//0.00E+00//ES828502		ko04130|SNARE interactions in vesicular transport		nr +
Unigene50666_All	1486	1.20	0.58	0.32	1.24	1.44	0.97	2.62	1.15	1.45	-1.05E+00	3.38E-02		-1.89E+00	7.43E-04	Down	2.12E-01	6.75E-01		-3.51E-01	4.98E-01		-1.18E+00	2.89E-05	Down	-8.55E-01	1.42E-03		Unigene50666_All//gi|42565988|ref|NP_191276.2|//2.00E-74//N-acetylglucosaminyl transferase component family protein / Gpi1 family protein [Arabidopsis thaliana]	Unigene50666_All//5.00E-59//AT3G57170| N-acetylglucosaminyl transferase component family protein / Gpi1 family protein	Unigene50666_All//0.00E+00//D8462178				nr -
Unigene50669_All	303	8.81	5.85	4.75	12.00	8.41	10.28	92.65	32.14	26.82	-5.89E-01	1.27E-01		-8.92E-01	2.75E-02		-5.13E-01	1.06E-01		-2.23E-01	5.49E-01		-1.53E+00	1.45E-48	Down	-1.79E+00	1.67E-62	Down					Unigene50669_All//2.00E-122//gi|72275553|gb|DT050190.1|DT050190				
Unigene50671_All	768	2.04	0.26	0.00	3.89	1.66	1.23	4.57	0.87	1.04	-2.95E+00	1.18E-05	Down	-1.10E+01	1.42E-08	Down	-1.23E+00	3.05E-04	Down	-1.66E+00	1.14E-05	Down	-2.39E+00	1.32E-11	Down	-2.14E+00	1.34E-10	Down					Unigene50671_All//0.00E+00//D8458340				
Unigene50675_All	1101	1.05	1.61	0.29	2.71	5.69	4.92	20.97	1.97	8.97	6.24E-01	2.09E-01		-1.85E+00	1.07E-02		1.07E+00	2.48E-06	Up	8.59E-01	7.29E-04		-3.41E+00	9.63E-105	Down	-1.22E+00	1.08E-29	Down	Unigene50675_All//gi|18737954|gb|ACD03211.1|//1.00E-151//xyloglucan endotransglucosylase/hydrolase 1 [Actinidia eriantha]	Unigene50675_All//4.00E-143//AT1G11545| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene50675_All//0.00E+00//TC141338				nr +
Unigene50677_All	985	6.91	1.54	3.84	19.52	12.34	4.77	2.36	0.76	0.57	-2.16E+00	6.31E-16	Down	-8.47E-01	3.08E-04		-6.62E-01	9.08E-09		-2.03E+00	5.53E-44	Down	-1.63E+00	4.15E-05	Down	-2.06E+00	5.41E-07	Down	Unigene50677_All//gi|124359162|gb|ABN05685.1|//3.00E-15//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene50677_All//3.00E-10//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene50677_All//1.00E-129//TC153648				nr -
Unigene50678_All	564	26.07	174.65	17.47	29.76	74.30	71.83	113.35	333.62	576.95	2.74E+00	6.62E-292	Up	-5.78E-01	1.31E-04		1.32E+00	1.26E-55	Up	1.27E+00	3.11E-46	Up	1.56E+00	0.00E+00	Up	2.35E+00	0.00E+00	Up	Unigene50678_All//gi|225434421|ref|XP_002272040.1|//3.00E-91//PREDICTED: similar to DNA-binding protein [Vitis vinifera]	Unigene50678_All//1.00E-58//AT2G38470| WRKY33; transcription factor	Unigene50678_All//0.00E+00//gi|73865404|gb|DT468142.1|DT468142	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene50679_All	911	0.46	2.61	1.93	0.55	0.30	0.94	11.42	32.62	153.32	2.51E+00	5.46E-07	Up	2.07E+00	3.29E-04	Up	-8.55E-01	4.07E-01		7.85E-01	3.33E-01		1.51E+00	1.25E-50	Up	3.75E+00	0.00E+00	Up	Unigene50679_All//gi|255629990|gb|ACU15347.1|//6.00E-06//unknown [Glycine max]		Unigene50679_All//0.00E+00//TC169473				nr +
Unigene50681_All	263	26.86	33.52	30.17	47.92	28.28	15.11	34.08	41.80	32.72	3.20E-01	1.14E-01		1.68E-01	4.70E-01		-7.61E-01	1.89E-07		-1.67E+00	3.77E-22	Down	2.94E-01	6.72E-02		-5.88E-02	7.46E-01						Unigene50681_All//4.00E-62//gi|78332815|gb|DT553089.1|DT553089				
Unigene50684_All	730	3.15	2.92	3.36	1.98	3.30	2.72	1.56	0.80	0.33	-1.13E-01	7.78E-01		8.95E-02	8.26E-01		7.39E-01	7.29E-02		4.60E-01	3.58E-01		-9.64E-01	9.32E-02		-2.26E+00	3.40E-04	Down	Unigene50684_All//gi|27808522|gb|AAO24541.1|//9.00E-33//At4g33985 [Arabidopsis thaliana]	Unigene50684_All//3.00E-21//AT4G33985| unknown protein	Unigene50684_All//0.00E+00//TC147159				nr -
Unigene50685_All	1189	0.97	0.17	0.09	5.20	4.46	2.09	3.77	2.07	1.41	-2.51E+00	8.99E-04	Down	-3.43E+00	1.54E-04	Down	-2.20E-01	4.06E-01		-1.31E+00	5.12E-08	Down	-8.62E-01	7.18E-04		-1.42E+00	6.49E-08	Down					Unigene50685_All//4.00E-170//gi|13351648|gb|BG441996.1|BG441996				
Unigene50686_All	344	2.43	3.98	1.24	4.20	2.40	4.99	3.56	0.85	1.62	7.09E-01	2.15E-01		-9.75E-01	2.37E-01		-8.06E-01	1.35E-01		2.49E-01	6.49E-01		-2.07E+00	6.67E-04	Down	-1.14E+00	3.17E-02		Unigene50686_All//gi|225461311|ref|XP_002281726.1|//3.00E-22//PREDICTED: similar to MRE11 (MEIOTIC RECOMBINATION 11); protein serine/threonine phosphatase [Vitis vinifera]	Unigene50686_All//3.00E-22//AT5G54260| MRE11 (meiotic recombination 11); endonuclease/exonuclease/hydrolase/ manganese ion binding / protein serine/threonine phosphatase			ko03440|Homologous recombination//ko03450|Non-homologous end-joining		nr -

Unigene50687_All	505	46.93	13.34	13.08	50.60	45.41	72.98	118.72	45.11	44.10	-1.81E+00	7.18E-43	Down	-1.84E+00	3.52E-42	Down	-1.56E-01	1.86E-01		5.28E-01	6.67E-10		-1.40E+00	5.22E-90	Down	-1.43E+00	6.86E-96	Down	Unigene50687_All//gi|24473796|gb|AAL91663.1|/5.00E-46//60s acidic ribosomal protein [Prunus dulcis] >gi|111013714|gb|ABH03379.1| 60S acidic ribosomal protein [Prunus dulcis]	Unigene50687_All//8.00E-19//AT2G27710| 60S acidic ribosomal protein P2 (RPP2B)	Unigene50687_All//1.00E-152//gi|11204126|gb|BF273056.1|BF273056		ko03010|Ribosome		nr -
Unigene50688_All	228	45.67	71.56	35.73	60.08	38.36	92.31	15.21	47.66	29.18	6.48E-01	2.62E-06		-3.54E-01	6.25E-02		-6.47E-01	3.47E-06		6.20E-01	1.10E-07		1.65E+00	2.21E-21	Up	9.40E-01	3.01E-06		Unigene50688_All//gi|115463541|ref|NP_001055370.1|/2.00E-12//Os05g0373900 [Oryza sativa Japonica Group] >gi|113578921|dbj|BAF17284.1|Os05g0373900 [Oryza sativa Japonica Group]		Unigene50688_All//7.00E-122//gi|78350054|gb|DT570328.1|DT570328				nr +
Unigene5069_All	959	3.27	4.23	6.89	18.96	18.82	14.13	17.99	13.64	8.47	3.69E-01	2.32E-01		1.07E+00	9.05E-06	Up	-1.10E-02	9.51E-01		-4.24E-01	9.16E-04		-3.99E-01	8.66E-04		-1.09E+00	1.21E-18	Down	Unigene5069_All//gi|4206110|gb|AAD11424.1|/3.00E-62//cytochrome [Mesembryanthemum crystallinum]	Unigene5069_All//4.00E-63//AT1G14730| LOCATED IN: endomembrane system, integral to membrane; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Cytochrome b561, eukaryote (InterPro:IPR004877), Cytochrome b561/ferric reductase transmembrane (InterPro:IPR006593); BEST Arabidopsis thaliana protein match is: ACYB-1; carbon-monoxide oxygenase (TAIR:AT5G38630.1); Has 447 Blast hits to 446 proteins in 71 species: Archae - 0; Bacteria - 0; Metazoa - 321; Fungi - 5; Plants - 110; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink).	Unigene5069_All//0.00E+00//TC138253				nr -
Unigene50697_All	653	2.24	0.31	1.79	1.91	2.79	2.77	2.27	2.30	1.83	-2.85E+00	3.60E-05	Down	-3.23E-01	5.91E-01		5.51E-01	2.87E-01		5.37E-01	3.05E-01		2.40E-02	9.95E-01		-3.08E-01	5.38E-01		Unigene50697_All//gi|6633833|gb|AAF19692.1|AC009519_26//1.00E-52//F1N19.4 [Arabidopsis thaliana]	Unigene50697_All//2.00E-54//AT1G64460| phosphatidylinositol 3- and 4-kinase family protein	Unigene50697_All//0.00E+00//TC157041				nr +
Unigene50698_All	1213	3.28	1.71	3.64	20.99	14.39	8.38	4.91	1.96	0.85	-9.37E-01	2.30E-03		1.53E-01	6.34E-01		-5.44E-01	3.42E-08		-1.32E+00	1.36E-31	Down	-1.32E+00	5.80E-09	Down	-2.53E+00	3.93E-21	Down	Unigene50698_All//gi|115439887|ref|NP_001044223.1|/8.00E-30//Os01g0744200 [Oryza sativa Japonica Group] >gi|113533754|dbj|BAF06137.1|Os01g0744200 [Oryza sativa Japonica Group]	Unigene50698_All//2.00E-22//AT1G29760| DTA4 (DOWNSTREAM TARGET OF AGL15-4)		ko00270|Cysteine and methionine metabolism		nr +
Unigene507_All	975	5.10	32.74	19.06	12.21	9.85	9.08	3.21	1.67	2.66	2.68E+00	1.44E-92	Up	1.90E+00	1.04E-34	Up	-3.09E-01	6.10E-02		-4.28E-01	9.36E-03		-9.41E-01	2.78E-03		-2.73E-01	3.98E-01		Unigene507_All//gi|91694295|gb|ABE41799.1|//1.00E-150//tocopherol cyclase [Gossypium hirsutum]	Unigene507_All//7.00E-103//AT4G32770| VTE1 (VITAMIN E DEFICIENT 1); tocopherol cyclase	Unigene507_All//0.00E+00//gi|78325947|gb|DT546221.1|DT546221		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene5070_All	613	11.78	3.39	4.69	14.55	17.47	16.72	3.45	1.84	1.56	-1.80E+00	2.24E-13	Down	-1.33E+00	1.93E-08	Down	2.64E-01	1.55E-01		2.01E-01	3.27E-01		-9.06E-01	2.19E-02		-1.14E+00	3.04E-03		Unigene5070_All//gi|14423860|sp|Q9M7N0.1|PROF3_HEVBR//3.00E-63//RecName: Full=Profilin-3; AltName: Full=Pollen allergen Hev b 8.0201; AltName: Allergen=Hev b 8.0201 >gi|6979167|gb|AAF34341.1|AF119365_1 latex profilin Hev b 8 [Hevea brasiliensis]	Unigene5070_All//2.00E-47//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding	Unigene5070_All//0.00E+00//gi|13247380|gb|BF270231.2|BF270231				nr -
Unigene50701_All	860	5.48	2.83	5.20	5.39	6.57	2.15	0.39	0.10	0.00	-9.53E-01	6.46E-04		-7.41E-02	7.99E-01		2.86E-01	3.06E-01		-1.32E+00	3.11E-06	Down	-2.02E+00	1.36E-01		-8.62E+00	8.14E-03					Unigene50701_All//0.00E+00//ES810291				
Unigene50703_All	1143	0.64	1.42	0.09	1.74	0.93	1.30	3.51	1.61	1.12	1.15E+00	2.93E-02		-2.78E+00	1.04E-02		-9.01E-01	3.94E-02		-4.19E-01	3.88E-01		-1.13E+00	4.50E-05	Down	-1.66E+00	9.21E-09	Down	Unigene50703_All//gi|224133496|ref|XP_002321582.1|/1.00E-140//rna-dependent RNA polymerase [Populus trichocarpa] >gi|222868578|gb|EEF05709.1| rna-dependent RNA polymerase [Populus trichocarpa]	Unigene50703_All//2.00E-119//AT4G11130| RDR2 (RNA-DEPENDENT RNA POLYMERASE 2); RNA-directed RNA polymerase	Unigene50703_All//1.00E-114//gi|78342621|gb|DT562895.1|DT562895				nr -
Unigene50704_All	308	28.54	13.82	8.13	47.06	33.21	45.75	66.99	34.74	40.74	-1.05E+00	1.54E-07	Down	-1.81E+00	1.39E-15	Down	-5.03E-01	2.36E-04		-4.09E-02	8.12E-01		-9.47E-01	2.58E-17		-7.17E-01	2.00E-11		Unigene50704_All//gi|283049400|gb|ADB07168.1|/6.00E-51//DEAD-box RNA helicase-like protein [Prunus persica] >gi|283049402|gb|ADB07169.1| DEAD-box RNA helicase-like protein [Prunus persica]	Unigene50704_All//1.00E-50//AT1G54270| EIF4A-2; ATP-dependent helicase/ translation initiation factor	Unigene50704_All//1.00E-173//gi|13246968|gb|BE053417.2|BE053417				nr -
Unigene50705_All	490	25.20	37.95	65.20	36.80	30.50	42.12	214.51	27.81	41.55	5.91E-01	3.97E-06		1.37E+00	3.28E-37	Up	-2.71E-01	3.87E-02		1.95E-01	1.45E-01		-2.95E+00	0.00E+00	Down	-2.37E+00	0.00E+00	Down	Unigene50705_All//gi|258489604|gb|ACV72638.1|//9.00E-32//chalcone synthase 1 [Gossypium hirsutum]	Unigene50705_All//3.00E-29//AT5G13930| TT4 (TRANSPARENT TESTA 4); naringenin-chalcone synthase	Unigene50705_All//0.00E+00//gi|21100676|gb|BQ412989.1|BQ412989		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr +
Unigene50708_All	1542	0.14	19.32	2.14	0.36	1.03	7.82	1.10	0.54	3.82	7.15E+00	2.60E-163	Up	3.98E+00	1.16E-13	Up	1.53E+00	4.53E-03		4.46E+00	4.42E-58	Up	-1.02E+00	2.47E-02		1.80E+00	9.32E-14	Up	Unigene50708_All//gi|22330903|ref|NP_187381.2|/6.00E-35//nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	Unigene50708_All//1.00E-32//AT3G07250| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene50708_All//0.00E+00//DN780179				nr +
Unigene50709_All	866	0.36	2.16	0.55	0.23	0.32	0.42	13.18	9.56	173.48	2.58E+00	8.47E-06	Up	6.10E-01	5.86E-01		4.67E-01	8.16E-01		8.59E-01	5.42E-01		-4.64E-01	2.03E-03		3.72E+00	0.00E+00	Up	Unigene50709_All//gi|9759309|dbj|BAB09815.1|/7.00E-09//non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]		Unigene50709_All//7.00E-17//TC149671				nr -
Unigene50712_All	1372	0.00	0.00	0.00	0.76	0.15	0.20	1.39	1.01	1.31	null	null		null	null		-2.34E+00	9.24E-04	Down	-1.95E+00	7.52E-03		-4.64E-01	2.90E-01		-8.57E-02	8.36E-01		Unigene50712_All//gi|224134853|ref|XP_002321921.1|/1.00E-174//cytochrome P450 [Populus trichocarpa] >gi|222868917|gb|EEF06048.1| cytochrome P450 [Populus trichocarpa]	Unigene50712_All//8.00E-134//AT5G52400| CYP715A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene50712_All//0.00E+00//TC161990		ko00908|Zeatin biosynthesis		nr +
Unigene50713_All	559	0.37	6.89	1.14	17.02	9.18	22.38	8.77	4.64	12.61	4.20E+00	5.33E-17	Up	1.61E+00	1.11E-01		-8.91E-01	2.14E-07		3.95E-01	1.48E-02		-9.20E-01	1.50E-04		5.24E-01	6.24E-03		Unigene50713_All//gi|224124908|ref|XP_002319453.1|/2.00E-11//predicted protein [Populus trichocarpa] >gi|224150554|ref|XP_002336976.1|predicted protein [Populus trichocarpa] >gi|222837491|gb|EEE75870.1|predicted protein [Populus trichocarpa] >gi|222857829|gb|EEE95376.1|predicted protein [Populus trichocarpa]	Unigene50713_All//7.00E-09//AT3G05858| unknown protein	Unigene50713_All//0.00E+00//CO493827				nr +
Unigene50714_All	344	3.50	8.10	9.13	3.33	2.60	3.15	3.07	2.19	3.36	1.21E+00	1.70E-03		1.38E+00	2.65E-04	Up	-3.56E-01	5.88E-01		-8.00E-02	9.09E-01		-4.91E-01	4.22E-01		1.28E-01	8.11E-01					Unigene50714_All//1.00E-31//TC176148				
Unigene50716_All	897	56.58	79.37	256.87	10.38	10.06	4.43	0.00	0.05	0.00	4.88E-01	3.29E-15		2.18E+00	0.00E+00	Up	-4.61E-02	8.17E-01		-1.23E+00	1.16E-10	Down	5.54E+00	6.34E-01		null	null		Unigene50716_All//gi|27735182|sp|P47925.2|CWP3_ARATH//1.00E-12//RecName: Full=Putative cell wall protein; Flags: Precursor >gi|4454461|gb|AAD20908.1|expressed protein [Arabidopsis thaliana] >gi|149944375|gb|ABR46230.1|At2g20570 [Arabidopsis thaliana]	Unigene50716_All//9.00E-09//AT2G20870| cell wall protein precursor, putative	Unigene50716_All//0.00E+00//TC1318875				nr +
Unigene50717_All	1058	0.40	2.49	0.65	2.02	1.99	1.02	1.20	3.04	4.56	2.65E+00	4.19E-08	Up	7.26E-01	3.96E-01		-2.82E-02	9.51E-01		-9.83E-01	2.55E-02		1.34E+00	2.74E-05	Up	1.93E+00	2.18E-12	Up	Unigene50717_All//gi|149212746|gb|AAQ57648.2|/1.00E-100//WRKY 11 [Theobroma cacao]	Unigene50717_All//7.00E-54//AT5G56270| WRKY2; transcription factor	Unigene50717_All//0.00E+00//ES806405	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene50718_All	406	5.80	17.97	5.64	2.21	2.21	1.45	1.98	0.51	0.98	1.63E+00	8.09E-12	Up	-4.02E-02	9.38E-01		-2.20E-03	9.78E-01		-6.11E-01	4.26E-01		-1.94E+00	1.17E-02		-1.01E+00	1.35E-01		Unigene50718_All//gi|38566650|gb|AAR24215.1|/5.00E-07//At1g35180 [Arabidopsis thaliana] >gi|51536528|gb|AAU05502.1|At3g16870 [Arabidopsis thaliana]	Unigene50718_All//3.00E-08//AT1G35180| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: integral to membrane; CONTAINS InterPro DOMAIN/s: TRAM, LAG1 and CLN8 homology (InterPro:IPR006634); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G35170.1); Has 128 Blast hits to 128 proteins in 42 species: Archae - 0; Bacteria - 0; Metazoa - 49; Fungi - 4; Plants - 41; Viruses - 3; Other Eukaryotes - 31 (source: NCBI BLink).	Unigene50718_All//2.00E-65//TC177135				nr +
Unigene50719_All	252	13.91	19.30	7.61	23.13	15.58	25.45	80.20	46.94	33.20	4.73E-01	8.64E-02		-8.71E-01	1.16E-02		-5.70E-01	1.49E-02		1.38E-01	6.40E-01		-7.73E-01	3.00E-12		-1.27E+00	1.12E-27	Down				Unigene50719_All//4.00E-77//gi|164358758|gb|ES835314.1|ES835314				
Unigene50720_All	571	0.37	3.19	1.87	0.70	2.71	3.40	1.26	3.88	3.98	3.12E+00	1.05E-06	Up	2.35E+00	3.61E-03		1.96E+00	5.94E-04	Up	2.28E+00	1.81E-05	Up	1.62E+00	7.09E-05	Up	1.66E+00	2.88E-05	Up								
Unigene50723_All	1759	1.07	1.04	0.18	1.84	5.62	4.57	3.61	1.66	1.11	-4.63E-02	9.32E-01		-2.56E+00	1.68E-05	Down	1.61E+00	1.04E-17	Up	1.31E+00	4.66E-10	Up	-1.12E+00	1.92E-07	Down	-1.70E+00	8.07E-14	Down	Unigene50723_All//gi|224053725|ref|XP_002297948.1|/0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222845206|gb|EEE82753.1|cytochrome P450 [Populus trichocarpa]	Unigene50723_All//2.00E-177//AT3G61880| CYP78A9 (CYTOCHROME P450 78A9); monooxygenase/ oxygen binding	Unigene50723_All//2.00E-170//TC151338		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene50725_All	518	19.60	5.77	7.61	27.79	7.51	1.05	2.20	0.97	0.15	-1.76E+00	4.69E-18	Down	-1.37E+00	4.44E-12	Down	-1.89E+00	2.06E-34	Down	-4.73E+00	1.57E-74	Down	-1.19E+00	4.02E-02		-3.84E+00	1.74E-06	Down	Unigene50725_All//gi|22331053|ref|NP_683560.1|/6.00E-06//serine-rich protein-related [Arabidopsis thaliana] >gi|28416839|gb|AAO42950.1|At3g13227 [Arabidopsis thaliana]	Unigene50725_All//1.00E-05//AT3G13227| serine-rich protein-related	Unigene50725_All//0.00E+00//gi|109876874|gb|DW505848.1|DW505848				nr -
Unigene50726_All	2062	0.03	0.79	0.10	0.10	0.10	0.00	3.47	2.80	9.12	4.95E+00	4.63E-08	Up	2.02E+00	3.61E-01		5.28E-02	9.88E-01		-6.59E+00	1.33E-01		-3.09E-01	1.35E-01		1.40E+00	2.32E-29	Up	Unigene50726_All//gi|224137676|ref|XP_002327185.1|/1.00E-177//cytochrome P450 [Populus trichocarpa] >gi|222835500|gb|EEE73935.1|cytochrome P450 [Populus trichocarpa]	Unigene50726_All//2.00E-116//AT4G37320| CYP81D5; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene50727_All	622	0.67	0.16	1.03	1.52	3.16	3.19	2.24	2.22	4.87	-2.05E+00	1.20E-01		6.10E-01	5.09E-01		1.05E+00	2.24E-02		1.07E+00	2.21E-02		-1.66E-02	1.01E+00		1.12E+00	4.14E-04	Up	Unigene50727_All//gi|297733909|emb|CBI15156.3|//1.00E-34//unnamed protein product [Vitis vinifera]		Unigene50727_All//9.00E-56//TC148318				nr -
Unigene5073_All	828	3.85	2.57	1.67	4.99	3.66	7.20	16.75	6.51	4.38	-5.85E-01	9.30E-02		-1.20E+00	1.16E-03		-4.48E-01	1.36E-01		5.28E-01	3.21E-02		-1.36E+00	1.12E-20	Down	-1.94E+00	9.01E-35	Down	Unigene5073_All//gi|20197845|gb|AAM15277.1|//8.00E-65//expressed protein [Arabidopsis thaliana] >gi|20198066|gb|AAM15381.1|expressed protein [Arabidopsis thaliana]	Unigene5073_All//4.00E-66//AT2G31725| unknown protein	Unigene5073_All//0.00E+00//TC147364				nr +
Unigene50732_All	2041	0.05	0.52	0.76	0.27	0.05	1.55	5.82	14.85	36.72	3.35E+00	2.17E-04	Up	3.88E+00	1.75E-06	Up	-2.41E+00	2.44E-02		2.53E+00	1.50E-09	Up	1.35E+00	1.42E-43	Up	2.66E+00	4.68E-268	Up	Unigene50732_All//gi|11933414|dbj|BAB19760.1|//0.00E+00//nitrate transporter NRT1-5 [Glycine max]	Unigene50732_All//0.00E+00//AT5G62680| proton-dependent oligopeptide transport (POT) family protein	Unigene50732_All//0.00E+00//DN827906				nr +

Unigene50733_All	471	4.78	0.86	0.34	5.08	5.26	3.16	1.26	0.09	1.35	-2.47E+00	1.32E-06	Down	-3.82E+00	4.32E-09	Down	5.23E-02	9.19E-01		-6.82E-01	1.04E-01		-3.82E+00	1.78E-03		1.07E-01	9.01E-01		Unigene50733_All//gi|297816394|ref|XP_002876080.1|//3.00E-44//proline-rich family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321918|gb|EFH52339.1| proline-rich family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50733_All//2.00E-17//AT3G51290| proline-rich family protein	Unigene50733_All//0.00E+00//gi|78347142|gb|DT567416.1|DT567416		ko03040|Spliceosome		nr -
Unigene50735_All	392	24.29	52.48	25.27	45.11	45.33	38.83	114.65	108.43	70.63	1.11E+00	3.87E-18	Up	5.68E-02	7.75E-01		6.90E-03	9.65E-01		-2.17E-01	1.34E-01		-8.04E-02	3.53E-01		-6.99E-01	8.61E-23				Unigene50735_All//1.00E-158//TC159260				
Unigene50736_All	712	2.35	1.85	1.27	74.58	76.95	60.13	6.18	4.75	1.18	-3.46E-01	4.98E-01		-8.87E-01	9.62E-02		4.51E-02	6.11E-01		-3.11E-01	1.13E-05		-3.77E-01	1.61E-01		-2.39E+00	6.90E-15	Down	Unigene50736_All//gi|15226465|ref|NP_179707.1|//8.00E-49//disease resistance-responsive family protein [Arabidopsis thaliana] >gi|91806226|gb|ABE65841.1| disease resistance-responsive family protein [Arabidopsis thaliana]	Unigene50736_All//4.00E-50//AT2G21110| disease resistance-responsive family protein	Unigene50736_All//0.00E+00//TC141794				nr -
Unigene50739_All	1201	0.74	0.04	0.67	2.16	1.46	2.11	2.78	2.51	1.03	-4.13E+00	2.52E-04	Down	-1.55E-01	8.24E-01		-5.61E-01	1.50E-01		-3.45E-02	9.44E-01		-1.50E-01	6.34E-01		-1.44E+00	3.39E-06	Down	Unigene50739_All//gi|297810841|ref|XP_002873304.1|//1.00E-129//rhomboid family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319141|gb|EFH49563.1| rhomboid family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50739_All//4.00E-68//AT5G07250| ATRBL3 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 3)	Unigene50739_All//0.00E+00//TC155471				nr +
Unigene5074_All	631	16.75	21.44	20.34	7.66	16.64	21.76	1.47	3.51	4.48	3.56E-01	2.23E-02		2.80E-01	1.03E-01		1.12E+00	4.69E-11	Up	1.51E+00	1.55E-20	Up	1.25E+00	1.44E-03		1.60E+00	4.19E-06	Up	Unigene5074_All//gi|224091032|ref|XP_002309152.1|//2.00E-08//predicted protein [Populus trichocarpa] >gi|222855128|gb|EEE92675.1| predicted protein [Populus trichocarpa]		Unigene5074_All//0.00E+00//TC163667				nr -
Unigene50740_All	261	5.81	4.47	7.96	10.88	8.18	10.73	4.86	5.28	12.06	-3.81E-01	4.78E-01		4.53E-01	3.48E-01		-4.11E-01	2.88E-01		-2.01E-02	9.49E-01		1.21E-01	8.13E-01		1.31E+00	3.44E-05	Up			Unigene50740_All//1.00E-145//ES794311				
Unigene50741_All	509	78.64	191.93	46.76	55.59	108.18	82.61	164.97	163.98	289.28	1.29E+00	3.44E-105	Up	-7.50E-01	1.53E-17		9.61E-01	3.59E-44		5.72E-01	7.90E-13		-8.70E-03	9.04E-01		8.10E-01	3.86E-93		Unigene50741_All//gi|15231686|ref|NP_190848.1|//3.00E-24//zinc finger (AN1-like) family protein [Arabidopsis thaliana] >gi|122069797|sp|Q94IB40.2|SAP6_ARATH RecName: Full=Zinc finger A20 and AN1 domain-containing stress-associated protein 6; Short=AtSAP6 >gi|7669954|emb|CAB89241.1| zinc finger-like protein [Arabidopsis thaliana]	Unigene50741_All//2.00E-16//AT2G36320| zinc finger (AN1-like) family protein	Unigene50741_All//5.00E-168//TC139663				nr +
Unigene50742_All	715	3.29	0.99	0.89	3.83	3.42	3.35	2.31	0.76	0.72	-1.73E+00	1.14E-04	Down	-1.88E+00	7.74E-05	Down	-1.64E-01	6.94E-01		-1.95E-01	6.39E-01		-1.60E+00	8.96E-04	Down	-1.67E+00	3.93E-04	Down	Unigene50742_All//gi|15230593|ref|NP_187883.1|//1.00E-13//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene50742_All//1.00E-15//AT3G12770| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene50744_All	516	2.64	2.45	4.02	4.44	2.27	2.19	2.29	0.08	1.16	-1.03E-01	8.47E-01		6.10E-01	1.96E-01		-9.69E-01	1.52E-02		-1.02E+00	1.56E-02		-4.82E+00	2.83E-07	Down	-9.86E-01	6.53E-02				Unigene50744_All//0.00E+00//gi|78329285|gb|DT549559.1|DT549559				
Unigene50745_All	1001	0.42	0.76	0.74	5.08	4.40	2.26	1.90	0.33	1.43	8.61E-01	2.93E-01		8.33E-01	3.39E-01		-2.05E-01	4.99E-01		-1.17E+00	1.05E-05	Down	-2.51E+00	6.21E-07	Down	-4.08E-01	3.33E-01		Unigene50745_All//gi|30844109|gb|AAP36697.1|//1.00E-144//MAP kinase-like protein [Gossypium hirsutum]	Unigene50745_All//3.00E-95//AT3G48260| WNK3; kinase/ protein kinase	Unigene50745_All//0.00E+00//TC138635		ko04712|Circadian rhythm - plant		nr +
Unigene50747_All	599	0.00	0.00	0.00	2.74	1.44	3.47	111.10	77.10	223.73	null	null		null	null		-9.33E-01	5.72E-02		3.38E-01	4.92E-01		-5.27E-01	7.06E-20		1.01E+00	1.49E-122	Up	Unigene50747_All//gi|193876292|gb|ACF24768.1|//1.00E-22//sesquiterpene synthase [Santalum album]	Unigene50747_All//1.00E-10//AT3G29190| lyase/ magnesium ion binding	Unigene50747_All//0.00E+00//CO111119		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis		nr +
Unigene50748_All	661	151.66	314.67	241.36	135.80	139.10	156.88	51.43	80.68	70.09	1.05E+00	2.77E-162	Up	6.70E-01	2.38E-56		3.46E-02	6.13E-01		2.08E-01	3.36E-05		6.50E-01	4.88E-23		4.47E-01	6.24E-11		Unigene50748_All//gi|18402873|ref|NP_565737.1|//9.00E-58//lactoylglutathione lyase family protein / glyoxalase I family protein [Arabidopsis thaliana] >gi|16604547|gb|AAL24279.1| At2g32090/F22D22.16 [Arabidopsis thaliana] >gi|189958038|gb|AAL79592.1| At2g32090/F22D22.16 [Arabidopsis thaliana] >gi|20197625|gb|AAD15395.2| expressed protein [Arabidopsis thaliana]	Unigene50748_All//5.00E-59//AT2G32090| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene50748_All//0.00E+00//TC142101				nr -
Unigene50749_All	3176	0.00	0.00	0.00	0.00	0.00	0.00	1.28	4.68	11.43	null	null		null	null		null	null		null	null		1.87E+00	1.60E-34	Up	3.16E+00	1.88E-155	Up	Unigene50749_All//gi|297726959|ref|NP_001175843.1|//0.00E+00//Os09g0423000 [Oryza sativa Japonica Group] >gi|255678905|dbj|BAH94571.1| Os09g0423000 [Oryza sativa Japonica Group]	Unigene50749_All//0.00E+00//AT2G24130| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction		nr -
Unigene50750_All	481	83.65	109.77	83.47	55.72	66.72	59.25	36.30	76.29	56.73	3.92E-01	6.25E-08		-3.00E-03	9.99E-01		2.60E-01	5.42E-03		8.86E-02	4.76E-01		1.07E+00	1.03E-36	Up	6.44E-01	2.36E-12		Unigene50750_All//gi|78183416|dbj|BAE47038.1|//2.00E-79//sorbitol related enzyme [Solanum lycopersicum]	Unigene50750_All//4.00E-78//AT5G51970| sorbitol dehydrogenase, putative / L-iditol 2-dehydrogenase, putative	Unigene50750_All//0.00E+00//TC134234		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00051|Fructose and mannose metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism		nr +
Unigene50751_All	1683	0.22	0.09	0.22	1.89	0.29	1.05	10.35	9.21	6.20	-1.27E+00	3.36E-01		2.56E-02	1.00E+00		-2.73E+00	2.70E-12	Down	-8.56E-01	1.33E-02		-1.68E-01	2.09E-01		-7.39E-01	2.94E-10		Unigene50751_All//gi|224110992|ref|XP_002332999.1|//3.00E-41//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834484|gb|EEE72961.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene50751_All//4.00E-14//AT3G28270| nucleic acid binding	Unigene50751_All//0.00E+00//DW510783		ko04626|Plant-pathogen interaction		nr -
Unigene50752_All	872	0.00	11.33	1.89	0.97	5.29	3.73	0.15	0.10	0.23	1.35E+01	1.32E-56	Up	1.09E+01	4.30E-09	Up	2.45E+00	3.83E-14	Up	1.94E+00	2.84E-07	Up	-6.01E-01	7.66E-01		6.51E-01	6.65E-01		Unigene50752_All//gi|30683908|ref|NP_193436.2|//2.00E-85//ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1) [Arabidopsis thaliana] >gi|22095652|sp|Q23547.2|EXLB1_ARATH RecName: Full=Expansin-like B1; Short=AtEXLB1; Short=At-EXPR1; Short=AtEXPR1; AltName: Full=Ath-ExpBeta-3.1; Flags: Precursor >gi|29028846|gb|AAO64802.1| At4g17030 [Arabidopsis thaliana] >gi|110736418|dbj|BAF00176.1| Expansin-like protein [Arabidopsis thaliana]	Unigene50752_All//1.00E-86//AT4G17030| ATEXLB1 (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1)	Unigene50752_All//0.00E+00//gi|109874605|gb|DW503579.1|DW503579				nr -
Unigene50753_All	659	0.32	2.15	1.05	1.97	1.88	1.58	1.35	0.95	2.00	2.76E+00	7.71E-05	Up	1.73E+00	7.67E-02		-6.32E-02	9.04E-01		-3.18E-01	6.36E-01		-5.02E-01	4.60E-01		5.66E-01	2.69E-01		Unigene50753_All//gi|224116536|ref|XP_002331921.1|//3.00E-25//predicted protein [Populus trichocarpa] >gi|222874593|gb|EEF11724.1| predicted protein [Populus trichocarpa]						nr +
Unigene50755_All	546	0.58	3.99	1.76	6.11	4.98	8.11	7.90	8.80	8.97	2.79E+00	3.73E-07	Up	1.61E+00	4.07E-02		-2.95E-01	4.20E-01		4.07E-01	1.87E-01		1.56E-01	5.96E-01		1.84E-01	4.77E-01		Unigene50755_All//gi|66947623|emb|CAJ00007.1|//9.00E-29//serine rich protein [Medicago truncatula]		Unigene50755_All//0.00E+00//TC166292				nr -
Unigene50756_All	1026	0.00	1.83	0.67	0.97	0.84	1.89	14.01	26.56	31.57	1.08E+01	1.11E-10	Up	9.40E+00	6.15E-04	Up	-2.11E-01	7.79E-01		9.63E-01	4.20E-02		9.23E-01	1.23E-21		1.17E+00	2.79E-38	Up	Unigene50756_All//gi|18400725|ref|NP_566506.1|//7.00E-96//glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein [Arabidopsis thaliana] >gi|42572447|ref|NP_974319.1| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein [Arabidopsis thaliana] >gi|9294262|dbj|BAB02164.1| glycosylation enzyme-like protein [Arabidopsis thaliana] >gi|197155568|gb|AAL91610.1| AT3g15350/K7L4_15 [Arabidopsis thaliana] >gi|20856992|gb|AAM26694.1| AT3g15350/K7L4_15 [Arabidopsis thaliana]	Unigene50756_All//3.00E-89//AT3G15350| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	Unigene50756_All//0.00E+00//CO130940				nr -
Unigene50758_All	407	1.67	14.07	1.31	1.96	1.18	1.00	12.15	14.89	9.01	3.07E+00	1.61E-19	Up	-3.53E-01	6.64E-01		-7.25E-01	3.46E-01		-9.72E-01	2.30E-01		2.93E-01	2.05E-01		-4.33E-01	6.69E-02				Unigene50758_All//5.00E-07//gi|11201746|gb|BF270751.1|BF270751				
Unigene50759_All	916	0.11	0.00	0.06	3.15	0.79	0.74	2.26	2.69	3.31	-6.84E+00	3.71E-01		-9.75E-01	7.20E-01		-2.00E+00	8.52E-08	Down	-2.09E+00	2.67E-07	Down	2.51E-01	5.32E-01		5.47E-01	7.91E-02								
Unigene5076_All	1205	5.86	5.38	2.83	14.84	20.18	16.87	19.09	9.75	8.23	-1.23E-01	5.96E-01		-1.05E+00	6.22E-06	Down	4.43E-01	1.94E-05		1.85E-01	1.79E-01		-9.70E-01	6.17E-20		-1.21E+00	3.54E-29	Down	Unigene5076_All//gi|239056190|emb|CAQ58627.1|//1.00E-139//Kinase cdc2 homolog B [Vitis vinifera]	Unigene5076_All//6.00E-130//AT2G38620| CDKB1;2 (cyclin-dependent kinase B1;2); cyclin binding / kinase/ protein serine/threonine kinase	Unigene5076_All//0.00E+00//TC178522				nr -
Unigene50761_All	321	27.22	9.63	10.78	31.50	30.14	41.08	113.41	36.07	39.71	-1.50E+00	1.51E-12	Down	-1.34E+00	3.64E-10	Down	-6.36E-02	7.92E-01		3.83E-01	1.50E-02		-1.65E+00	2.88E-70	Down	-1.51E+00	9.24E-64	Down	Unigene50761_All//gi|75299406|sp|Q8GTZ3.1|RS3A_CICAR//2.00E-26//RecName: Full=40S ribosomal protein S3a >gi|28817254|emb|CAD56219.1| ribosomal protein S3a [Cicer arietinum]	Unigene50761_All//2.00E-25//AT4G34670| 40S ribosomal protein S3A (RPS3aB)	Unigene50761_All//5.00E-179//gi|21089745|gb|BQ402058.1|BQ402058		ko03010|Ribosome		nr -
Unigene50763_All	504	0.62	2.01	3.59	2.08	5.74	5.56	2.35	2.49	1.98	1.69E+00	2.14E-02		2.53E+00	2.82E-05	Up	1.47E+00	7.29E-05	Up	1.42E+00	2.46E-04	Up	8.29E-02	8.86E-01		-2.49E-01	6.27E-01		Unigene50763_All//gi|89001015|gb|ABD59097.1|//9.00E-17//At1g74055 [Arabidopsis thaliana]	Unigene50763_All//1.00E-15//AT1G74055| unknown protein					nr -
Unigene50764_All	679	2.00	1.64	1.18	2.35	1.88	1.33	2.30	0.18	2.70	-2.87E-01	6.02E-01		-7.68E-01	2.06E-01		-3.23E-01	5.52E-01		-8.20E-01	1.25E-01		-3.64E+00	5.20E-08	Down	2.28E-01	6.00E-01		Unigene50764_All//gi|75181359|sp|Q9LZX1.1|Y5I75_ARATH//1.00E-22//RecName: Full=UPF0706 protein At5g01750 >gi|13926237|gb|AAK49593.1|AF372877_1 AT5g01750/T20L15_20 [Arabidopsis thaliana] >gi|22655412|gb|AAM98298.1| At5g01750/T20L15_20 [Arabidopsis thaliana]	Unigene50764_All//3.00E-52//AT3G56180| unknown protein	Unigene50764_All//2.00E-22//ES829316				nr +

Unigene50765_All	997	0.58	1.88	0.75	11.94	9.67	7.07	1.87	0.63	0.80	1.70E+00	8.73E-04	Up	3.73E-01	6.23E-01		-3.04E-01	6.68E-02		-7.57E-01	2.26E-06		-1.57E+00	4.62E-04	Down	-1.22E+00	3.47E-03		Unigene50765_All//gi|115488670|ref|XP_001066822.1|//6.00E-48//0s12g0501400 [Oryza sativa Japonica Group] >gi|77555833|gb|ABA98629.1| universal stress protein family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113649329|dbj|BAF29841.1| Os12g0501400 [Oryza sativa Japonica Group]	Unigene50765_All//2.00E-33//AT2G03720| MOR6 (morphogenesis of root hair 6)	Unigene50765_All//0.00E+00//gi|164252344|gb|ES803662.1|ES803662				nr -
Unigene50767_All	386	8.27	6.69	2.76	49.04	30.69	46.92	1.86	2.17	1.14	-3.05E-01	3.81E-01		-1.58E+00	3.96E-05	Down	-6.76E-01	5.80E-09		-6.38E-02	6.95E-01		2.18E-01	7.44E-01		-7.14E-01	3.27E-01				Unigene50767_All//2.00E-138//BQ403027				
Unigene5077_All	1390	6.14	1.35	1.26	11.07	14.86	10.95	13.29	6.07	5.53	-2.19E+00	4.64E-20	Down	-2.28E+00	3.55E-20	Down	4.25E-01	2.08E-04		-1.63E-02	9.37E-01		-1.13E+00	1.54E-20	Down	-1.26E+00	3.75E-25	Down	Unigene5077_All//gi|239056190|emb|CAQ58627.1|//1.00E-164//Kinase cdc2 homolog B [Vitis vinifera]	Unigene5077_All//3.00E-153//AT2G38620| CDKB1;2 (cyclin-dependent kinase B1;2); cyclin binding / kinase/ protein serine/threonine kinase	Unigene5077_All//0.00E+00//TC136619				nr +
Unigene50771_All	818	1.73	0.74	1.04	6.15	3.28	4.36	2.74	0.26	0.78	-1.22E+00	3.33E-02		-7.30E-01	2.21E-01		-9.06E-01	2.67E-04		-4.96E-01	7.04E-02		-3.42E+00	1.03E-10	Down	-1.81E+00	7.47E-06	Down	Unigene50771_All//gi|297822877|ref|XP_002879321.1|//4.00E-94//EMB1381 [Arabidopsis lyrata subsp. lyrata] >gi|297325160|gb|EFH55580.1| EMB1381 [Arabidopsis lyrata subsp. lyrata]	Unigene50771_All//6.00E-89//AT2G31340| emb1381 (embryo defective 1381)					nr -
Unigene50774_All	600	1.83	6.25	4.62	3.90	2.81	0.60	1.34	0.28	1.20	1.77E+00	4.02E-07	Up	1.33E+00	1.03E-03		-4.73E-01	2.67E-01		-2.70E+00	6.56E-08	Down	-2.26E+00	4.82E-03		-1.64E-01	7.94E-01		Unigene50774_All//gi|89145872|gb|AB062086.1|//9.00E-34//polygalacturonase precursor [Glycine max]	Unigene50774_All//9.00E-32//AT1G10640| polygalacturonase	Unigene50774_All//0.00E+00//gi|109875900|gb|DW504874.1|DW504874		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene50775_All	830	1.39	0.12	0.13	1.68	0.79	1.25	0.97	0.81	1.92	-3.51E+00	6.57E-05	Down	-3.43E+00	1.54E-04	Down	-1.09E+00	4.31E-02		-4.25E-01	4.75E-01		-2.65E-01	7.04E-01		9.88E-01	2.95E-02		Unigene50775_All//gi|115478174|ref|NP_001062682.1|//1.00E-107//Os09g0251500 [Oryza sativa Japonica Group] >gi|47848472|dbj|BAD22327.1| pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa Japonica Group] >gi|47848643|dbj|BAD22491.1| pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa Japonica Group] >gi|113630915|dbj|BAF24596.1| Os09g0251500 [Oryza sativa Japonica Group]	Unigene50775_All//1.00E-69//AT4G02750| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene50776_All	1765	0.12	2.56	0.18	0.23	0.27	1.15	3.26	9.19	67.17	4.43E+00	1.69E-20	Up	6.10E-01	6.24E-01		2.74E-01	8.19E-01		2.35E+00	7.25E-06	Up	1.50E+00	1.75E-27	Up	4.37E+00	0.00E+00	Up	Unigene50776_All//gi|15220732|ref|NP_174326.1|//1.00E-155//lipase class 3 family protein [Arabidopsis thaliana]	Unigene50776_All//2.00E-156//AT1G30370| lipase class 3 family protein	Unigene50776_All//0.00E+00//C0118015				nr -
Unigene50779_All	1138	0.83	1.42	1.22	5.60	5.69	0.75	1.82	0.15	0.74	7.84E-01	1.31E-01		5.56E-01	3.62E-01		2.19E-02	9.53E-01		-2.89E+00	2.57E-22	Down	-3.63E+00	2.06E-10	Down	-1.31E+00	9.85E-04	Down	Unigene50779_All//gi|8886958|gb|AAF80644.1|AC069251_37//1.00E-32//F2D10.1 [Arabidopsis thaliana]	Unigene50779_All//2.00E-24//AT1G20530| unknown protein	Unigene50779_All//0.00E+00//gi|78323392|gb|DT543666.1|DT543666				nr +
Unigene5078_All	1050	24.86	11.97	22.42	6.97	5.90	3.91	1.21	1.71	1.14	-1.06E+00	4.07E-21	Down	-1.50E-01	2.28E-01		-2.41E-01	3.12E-01		-8.33E-01	8.10E-05		5.03E-01	2.62E-01		-8.59E-02	8.72E-01		Unigene5078_All//gi|115463777|ref|NP_001055488.1|//6.00E-72//Os05g0401300 [Oryza sativa Japonica Group] >gi|113579039|dbj|BAF17402.1| Os05g0401300 [Oryza sativa Japonica Group]	Unigene5078_All//4.00E-76//AT5G27390| LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Mog1/PsbP/DUF1795, alpha/beta/alpha sandwich (InterPro:IPR016124); Has 11 Blast hits to 11 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 11; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene5078_All//1.00E-133//C0101457				nr +
Unigene50782_All	690	0.00	0.29	0.00	3.03	0.70	3.01	20.96	70.08	50.81	8.20E+00	1.36E-01		null	null		-2.12E+00	3.34E-06	Down	-1.02E-02	9.75E-01		1.74E+00	5.07E-100	Up	1.28E+00	2.98E-47	Up	Unigene50782_All//gi|28372890|gb|AA039627.1|//3.00E-31//At3g10120 [Arabidopsis thaliana]	Unigene50782_All//2.00E-19//AT3G10120| unknown protein	Unigene50782_All//0.00E+00//TC159330				nr +
Unigene50783_All	1269	0.08	0.00	0.13	0.27	0.35	0.11	24.36	32.90	7.88	-6.37E+00	3.71E-01		6.10E-01	7.48E-01		3.61E-01	8.06E-01		-1.36E+00	3.37E-01		4.34E-01	3.37E-09		-1.63E+00	2.92E-60	Down	Unigene50783_All//gi|18378607|gb|AAL68641.1|AF458765_1//9.00E-40//polyprotein [Oryza sativa Japonica Group]		Unigene50783_All//3.00E-32//ES807842				nr -
Unigene50784_All	760	1.38	0.93	0.14	4.06	5.07	4.87	13.07	7.64	4.88	-5.61E-01	3.82E-01		-3.30E+00	4.58E-04	Down	3.21E-01	3.46E-01		2.62E-01	4.77E-01		-7.74E-01	1.88E-06		-1.42E+00	1.59E-16	Down	Unigene50784_All//gi|224116844|ref|XP_002317408.1|//2.00E-94//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222860473|gb|EEE98020.1| nucleobase ascorbate transporter [Populus trichocarpa]	Unigene50784_All//4.00E-91//AT2G34190| xanthine/uracil permease family protein	Unigene50784_All//0.00E+00//C0121052				nr -
Unigene50786_All	553	71.43	130.84	119.50	70.62	83.07	70.48	7.72	10.43	23.34	8.73E-01	8.34E-42		7.42E-01	3.66E-28		2.34E-01	2.19E-03		-2.90E-03	9.73E-01		4.34E-01	5.47E-02		1.60E+00	1.07E-24	Up	Unigene50786_All//gi|90962942|gb|ABE02395.1|//3.00E-11//At4g28290 [Arabidopsis thaliana]	Unigene50786_All//2.00E-07//AT4G28290| unknown protein	Unigene50786_All//0.00E+00//gi|109869431|gb|DW498407.1|DW498407				nr -
Unigene50787_All	1054	1.69	1.20	1.31	2.13	1.89	1.11	3.13	0.83	0.49	-4.90E-01	3.25E-01		-3.62E-01	4.82E-01		-1.67E-01	7.29E-01		-9.33E-01	2.93E-02		-1.91E+00	1.93E-08	Down	-2.67E+00	9.34E-13	Down	Unigene50787_All//gi|84002565|ref|NP_565593.1|//2.00E-25//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene50787_All//9.00E-27//AT2G46495| zinc finger (C3HC4-type RING finger) family protein					nr -
Unigene50789_All	598	0.00	0.68	0.00	5.41	1.04	3.78	3.54	0.84	1.53	9.40E+00	1.36E-02		null	null		-2.39E+00	9.51E-11	Down	-5.20E-01	1.44E-01		-2.08E+00	3.13E-06	Down	-1.21E+00	1.91E-03		Unigene50789_All//gi|224124694|ref|XP_002319398.1|//3.00E-92//GH3 family protein [Populus trichocarpa] >gi|222857774|gb|EEE95321.1| GH3 family protein [Populus trichocarpa]	Unigene50789_All//2.00E-92//AT4G27260| WES1; indole-3-acetic acid amido synthetase	Unigene50789_All//2.00E-16//DR461737				nr +
Unigene5079_All	1257	3.75	4.76	10.97	9.27	10.19	14.34	12.82	4.59	8.11	3.45E-01	1.69E-01		1.55E+00	1.58E-19	Up	1.36E-01	4.72E-01		6.29E-01	7.82E-07		-1.48E+00	5.46E-27	Down	-6.60E-01	5.50E-08		Unigene5079_All//gi|224612181|gb|ACN60162.1|//1.00E-132//peroxidase [Tamarix hispida]	Unigene5079_All//2.00E-116//AT5G51890| peroxidase			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene50790_All	1704	1.11	1.40	0.59	0.76	1.29	0.69	6.45	24.11	13.84	3.38E-01	4.13E-01		-8.97E-01	7.25E-02		7.67E-01	7.80E-02		-1.42E-01	8.06E-01		1.90E+00	6.10E-96	Up	1.10E+00	1.56E-25	Up	Unigene50790_All//gi|15232280|ref|NP_191581.1|//7.00E-85//ATL4; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|68565314|sp|Q9LY41.1|ATL3J_ARATH RecName: Full=RING-H2 finger protein ATL3J; AltName: Full=RING-H2 finger protein ATL4; AltName: Full=RING-H2 finger protein RHA1a >gi|7576198|emb|CAB87859.1| RING-H2 zinc finger protein ATL4 [Arabidopsis thaliana] >gi|66865934|gb|AAY57601.1| RING finger family protein [Arabidopsis thaliana] >gi|14050661|gb|AB149480.1| At3g60220 [Arabidopsis thaliana]	Unigene50790_All//1.00E-48//AT3G60220| ATL4; protein binding / zinc ion binding	Unigene50790_All//0.00E+00//gi|164257639|gb|ES830253.1|ES830253				nr +
Unigene50791_All	975	2.20	1.04	0.38	2.81	4.03	4.40	3.82	1.89	4.45	-1.08E+00	1.44E-02		-2.52E+00	4.25E-06	Down	5.19E-01	9.78E-02		6.47E-01	2.87E-02		-1.02E+00	3.76E-04	Down	2.23E-01	4.10E-01		Unigene50791_All//gi|115456383|ref|NP_001051792.1|//6.00E-21//Os03g0831200 [Oryza sativa Japonica Group] >gi|108711910|gb|ABF99705.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550263|dbj|BAF13706.1| Os03g0831200 [Oryza sativa Japonica Group]	Unigene50791_All//3.00E-12//AT3G06740| zinc finger (GATA type) family protein	Unigene50791_All//2.00E-45//TC160088	C2C2-GATA			nr +
Unigene50792_All	1773	2.60	0.51	0.90	1.43	2.82	1.73	6.96	1.08	3.84	-2.34E+00	5.05E-12	Down	-1.53E+00	9.09E-07	Down	9.75E-01	1.59E-04		2.74E-01	4.92E-01		-2.68E+00	1.84E-44	Down	-8.58E-01	1.78E-09		Unigene50792_All//gi|297813641|ref|XP_002874704.1|//0.00E+00//NADPH-dependent thioredoxin reductase B [Arabidopsis lyrata subsp. lyrata] >gi|297320541|gb|EFH59963.1| NADPH-dependent thioredoxin reductase B [Arabidopsis lyrata subsp. lyrata]	Unigene50792_All//0.00E+00//AT4G11610| C2 domain-containing protein	Unigene50792_All//0.00E+00//AI730262				nr +
Unigene50794_All	715	1.61	14.32	6.63	1.60	3.13	3.22	0.35	0.18	0.78	3.15E+00	2.58E-35	Up	2.04E+00	4.37E-10	Up	9.66E-01	2.28E-02		1.01E+00	1.82E-02		-1.02E+00	4.94E-01		1.14E+00	1.91E-01		Unigene50794_All//gi|259648119|dbj|BAI40367.1|//6.00E-25//actin [Larix gmelinii]	Unigene50794_All//6.00E-26//AT2G42090| ACT9 (ACTIN 9); ATP binding / protein binding / structural constituent of cytoskeleton			ko04145|Phagosome		nr +
Unigene50795_All	1066	0.83	2.00	1.40	0.79	3.36	4.32	6.03	24.27	17.75	1.26E+00	5.48E-03		7.45E-01	1.91E-01		2.08E+00	3.56E-09	Up	2.44E+00	3.30E-13	Up	2.01E+00	3.36E-65	Up	1.56E+00	1.28E-34	Up	Unigene50795_All//gi|224116296|ref|XP_002331947.1|//5.00E-44//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222874724|gb|EEF11855.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene50795_All//2.00E-22//AT5G47220| ERF2 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 2); DNA binding / transcription activator/ transcription factor	Unigene50795_All//0.00E+00//TC166993	AP2-EREBP			nr +
Unigene50797_All	833	0.06	1.34	0.58	0.48	0.33	0.38	2.28	2.91	2.10	4.41E+00	2.17E-05	Up	3.20E+00	3.48E-02		-5.33E-01	6.15E-01		-3.34E-01	7.56E-01		3.50E-01	3.79E-01		-1.18E-01	7.68E-01				Unigene50797_All//4.00E-09//TC177921				
Unigene50798_All	885	1.83	0.92	3.49	2.42	0.35	2.09	2.58	0.76	0.32	-1.00E+00	5.37E-02		9.29E-01	1.24E-02		-2.79E+00	1.34E-08	Down	-2.10E-01	6.61E-01		-1.77E+00	1.47E-05	Down	-3.03E+00	3.22E-10	Down	Unigene50798_All//gi|224125984|ref|XP_002319727.1|//1.00E-107//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222858103|gb|EEE95650.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene50798_All//3.00E-69//AT5G17850| cation exchanger, putative (CAX8)	Unigene50798_All//0.00E+00//gi|109871035|gb|DW500011.1|DW500011				nr -
Unigene508_All	2792	11.32	10.67	11.92	8.05	8.07	7.10	6.28	5.03	3.14	-8.50E-02	4.34E-01		7.47E-02	5.08E-01		3.50E-03	9.83E-01		-1.80E-01	1.60E-01		-3.21E-01	7.72E-03		-1.00E+00	1.04E-16	Down	Unigene508_All//gi|91694295|gb|ABE41799.1|//0.00E+00//tocopherol cyclase [Gossypium hirsutum]	Unigene508_All//0.00E+00//AT4G32770| VTE1 (VITAMIN E DEFICIENT 1); tocopherol cyclase	Unigene508_All//0.00E+00//TC129609		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0006778//GO:0006952//GO:0008643//GO:0009528//GO:0009570//GO:0009642//GO:0009975//GO:0016116//GO:0032787//GO:0042360	nr +
Unigene50800_All	703	0.67	0.72	2.88	0.92	1.76	0.96	0.90	1.43	1.81	1.06E-01	9.22E-01		2.10E+00	8.06E-05	Up	9.37E-01	1.36E-01		6.51E-02	9.49E-01		6.62E-01	2.96E-01		1.01E+00	5.22E-02									
Unigene50802_All	460	25.25	26.00	23.50	42.02	37.73	51.84	775.20	922.60	1765.80	4.20E-02	8.13E-01		-1.04E-01	6.13E-01		-1.55E-01	2.75E-01		3.03E-01	7.64E-03		2.51E-01	3.66E-31		1.19E+00	0.00E+00	Up	Unigene50802_All//gi|146760355|dbj|BAF62431.1|//2.00E-34//glyoxalase I [Cucurbita maxima]	Unigene50802_All//9.00E-35//AT1G08110| lactoylglutathione lyase, putative / glyoxalase I, putative	Unigene50802_All//0.00E+00//gi|109872146|gb|DW501122.1|DW501122		ko00620|Pyruvate metabolism		nr -
Unigene50804_All	560	1.87	17.19	6.18	0.71	1.29	0.81	0.98	2.99	8.11	3.20E+00	1.00E-33	Up	1.73E+00	3.81E-06	Up	8.60E-01	3.36E-01		1.81E-01	8.83E-01		1.60E+00	8.16E-04	Up	3.05E+00	2.34E-19	Up	Unigene50804_All//gi|297849514|ref|XP_002892638.1|//3.00E-35//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338480|gb|EFH68897.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50804_All//3.00E-34//AT1G11350| SD1-13 (S-DOMAIN-1 13); kinase/ protein kinase/ protein serine/threonine kinase	Unigene50804_All//1.00E-73//C0081718		ko04626|Plant-pathogen interaction		nr +

Unigene50805_All	580	0.45	0.00	0.09	5.50	3.56	1.32	4.88	2.81	2.75	-8.82E+00	6.69E-02			-2.30E+00	2.43E-01			-6.26E-01	6.27E-02			-2.05E+00	8.04E-08	Down	-7.97E-01	1.65E-02		-8.30E-01	9.53E-03		Unigene50805_All//gi|284026888|gb|AD866335.1|//1.00E-20//CC-NBS-LRR protein [Quercus suber]	Unigene50805_All//6.00E-07//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene50805_All//2.00E-78//gi|109870216|gb|DW499192.1|DW499192				nr -
Unigene50807_All	518	1.82	0.68	1.34	1.73	0.93	0.87	6.86	21.70	17.84	-1.41E+00	5.70E-02			-4.44E-01	5.54E-01			-8.95E-01	2.14E-01			-9.89E-01	1.96E-01		1.66E+00	2.32E-22	Up	1.38E+00	1.27E-14	Up				Unigene50807_All//4.00E-08//TC135212						nr -
Unigene50809_All	847	2.78	0.90	2.51	3.76	3.46	4.43	1.95	0.94	0.24	-1.63E+00	2.30E-04	Down	-1.45E-01	7.26E-01			-1.23E-01	7.71E-01			2.34E-01	5.18E-01		-1.05E+00	2.20E-02		-3.05E+00	1.31E-07	Down	Unigene50809_All//gi|18767374|gb|AAL79340.1|AC099402_4//7.00E-10//Putative 22 kDa kafirin cluster; Ty3-Gypsy type [Oryza sativa] >gi|21327374|gb|AAM48279.1|AC122148_32 Putative 22 kDa kafirin cluster; Ty3-Gypsy type [Oryza sativa Japonica Group]								nr -
Unigene5081_All	837	96.95	48.25	93.52	130.40	140.91	139.48	36.88	26.52	22.89	-1.01E+00	1.98E-59	Down	-5.20E-02	4.62E-01			1.12E-01	2.32E-02			9.72E-02	6.66E-02		-4.76E-01	3.67E-08		-6.88E-01	1.63E-15		Unigene5081_All//gi|15235763|ref|NP_194821.1|//4.00E-92//cytosol aminopeptidase family protein [Arabidopsis thaliana] >gi|857004652|sp|Q94497.2|AMPL3_ARATH RecName: Full=Leucine aminopeptidase 3, chloroplastic; AltName: Full=Leucyl aminopeptidase 3; Short=LAP 3; AltName: Full=Proline aminopeptidase 3; AltName: Full=Prolyl aminopeptidase 3; Flags: Precursor	Unigene5081_All//3.00E-80//AT4G30920| cytosol aminopeptidase family protein	Unigene5081_All//0.00E+00//gi|78341141|gb|DT561415.1|DT561415		ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene50810_All	860	1.70	2.24	0.56	5.33	5.93	15.75	7.52	7.63	3.57	3.94E-01	3.91E-01		-1.61E+00	8.14E-03			1.53E-01	6.11E-01			1.56E+00	2.23E-21	Up	2.06E-02	9.51E-01		-1.08E+00	1.87E-07	Down	Unigene50810_All//gi|110931710|gb|AB802854.1|//8.00E-63//MYB transcription factor MYB124 [Glycine max]	Unigene50810_All//5.00E-43//AT3G09230| AtMYB1 (myb domain protein 1); DNA binding / transcription factor	Unigene50810_All//1.00E-37//ES838677	MYB			nr -
Unigene50811_All	628	2.00	0.32	0.59	5.16	3.84	3.38	2.15	0.80	1.08	-2.63E+00	3.16E-04	Down	-1.75E+00	9.85E-03			-4.26E-01	2.27E-01			-6.09E-01	8.16E-02		-1.43E+00	7.15E-03		-9.98E-01	4.39E-02		Unigene50811_All//gi|145105398|gb|ABP35583.1|//2.00E-60//CBL-interacting protein kinase [Gossypium hirsutum]	Unigene50811_All//9.00E-30//AT5G10930| CIPK5 (CBL-INTERACTING PROTEIN KINASE 5); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene50811_All//6.00E-134//gi|54116825|gb|CO492334.1|CO492334				nr -
Unigene50812_All	872	230.22	25.04	124.51	7.77	9.68	3.21	0.00	0.00	0.18	-3.20E+00	0.00E+00	Down	-8.87E-01	1.39E-114			3.17E-01	1.31E-01			-1.27E+00	2.34E-08	Down	null	null		7.51E+00	1.40E-01		Unigene50812_All//gi|18399308|ref|NP_566396.1|//1.00E-71//NIL1 [Arabidopsis thaliana] >gi|9502172|gb|AAF88021.1|AF264697_1 NDR1/HIN1-Like protein 1 [Arabidopsis thaliana] >gi|21595601|gb|AAM66116.1| harpin-induced protein-like [Arabidopsis thaliana] >gi|56381911|gb|AAV85674.1| At3g11660 [Arabidopsis thaliana] >gi|58331799|gb|AAW70397.1| At3g11660 [Arabidopsis thaliana]	Unigene50812_All//8.00E-61//AT3G11660| NIL1	Unigene50812_All//7.00E-17//DR455543				nr +
Unigene50813_All	717	3.28	3.11	0.97	4.65	2.83	2.08	3.48	1.22	0.67	-7.87E-02	8.45E-01		-1.77E+00	1.68E-04	Down	-7.16E-01	2.64E-02			-1.16E+00	5.91E-04	Down	-1.51E+00	6.17E-05	Down	-2.38E+00	9.65E-09	Down	Unigene50813_All//gi|44917503|gb|AAS49076.1|//2.00E-34//At1g56260 [Arabidopsis thaliana]	Unigene50813_All//8.00E-31//AT1G56260| unknown protein					nr -
Unigene50816_All	518	1.31	3.81	5.35	4.23	2.79	3.05	5.63	3.55	2.85	1.54E+00	1.57E-03		2.03E+00	4.34E-06	Up	-6.00E-01	1.60E-01			-4.72E-01	3.08E-01		-6.66E-01	4.24E-02		-9.85E-01	1.94E-03		Unigene50816_All//gi|18408807|ref|NP_566916.1|//2.00E-18//DMS3 (DEFECTIVE IN MERISTEM SILENCING 3) [Arabidopsis thaliana] >gi|15146294|gb|AAK83630.1| AT3g49250/F2K15_110 [Arabidopsis thaliana] >gi|196990162|gb|AAL90947.1| AT3g49250/F2K15_110 [Arabidopsis thaliana]	Unigene50816_All//1.00E-19//AT3G49250| DMS3 (DEFECTIVE IN MERISTEM SILENCING 3)	Unigene50816_All//0.00E+00//gi|13352670|gb|BG443018.1|BG443018				nr -
Unigene50817_All	872	1.86	4.42	0.92	189.72	68.24	127.46	4335.71	2185.22	1301.97	1.25E+00	1.08E-04	Up	-1.02E+00	6.14E-02			-1.48E+00	2.99E-275	Down	-5.74E-01	1.71E-49		-9.89E-01	0.00E+00		-1.74E+00	0.00E+00	Down	Unigene50817_All//gi|74273314|gb|AB001325.1|//5.00E-75//VDR06 [Gossypium hirsutum] >gi|83356301|gb|ABC16635.1| bet vI [Gossypium hirsutum]	Unigene50817_All//2.00E-45//AT1G70830| MLP28 (MLP-LIKE PROTEIN 28)	Unigene50817_All//0.00E+00//gi|13354790|gb|BG445138.1|BG445138				nr -
Unigene50818_All	233	32.11	11.09	10.97	32.71	30.59	39.54	97.44	37.85	36.93	-1.53E+00	3.41E-11	Down	-1.55E+00	8.10E-11	Down	-9.66E-02	7.04E-01			2.74E-01	1.90E-01		-1.36E+00	2.13E-33	Down	-1.40E+00	9.55E-36	Down	Unigene50818_All//gi|297805734|ref|XP_002870751.1|//1.00E-31//40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata] >gi|297316987|gb|EFH47010.1| 40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata]	Unigene50818_All//1.00E-32//AT5G39850| 40S ribosomal protein S9 (RPS9C)	Unigene50818_All//3.00E-115//gi|11202123|gb|BF271128.1|BF271128		ko03010|Ribosome		nr -
Unigene50819_All	1634	0.38	0.06	1.69	0.98	0.80	0.77	1.81	6.19	4.85	-2.63E+00	1.78E-02		2.14E+00	1.76E-06	Up	-2.85E-01	6.01E-01			-3.34E-01	5.63E-01		1.77E+00	5.00E-22	Up	1.42E+00	3.31E-13	Up	Unigene50819_All//gi|15235633|ref|NP_195474.1|//9.00E-90//HLS1 (HOOKLESS 1); N-acetyltransferase [Arabidopsis thaliana] >gi|4468983|emb|CAB38297.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|7270740|emb|CAB80423.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|51969462|dbj|BAD43423.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|51970376|dbj|BAD43880.1| probable N-acetyltransferase hookless 1 [Arabidopsis thaliana] >gi|11074338|gb|AB004542.1| At4g37580 [Arabidopsis thaliana]	Unigene50819_All//6.00E-88//AT4G37580| HLS1 (HOOKLESS 1); N-acetyltransferase	Unigene50819_All//3.00E-178//ES827081				nr +
Unigene50821_All	233	39.52	23.05	28.57	65.21	74.04	85.29	269.11	116.60	120.03	-7.78E-01	4.22E-05		-4.68E-01	1.90E-02		1.83E-01	2.19E-01			3.87E-01	1.64E-03		-1.21E+00	3.46E-75	Down	-1.16E+00	3.69E-73	Down	Unigene50821_All//gi|19773452|dbj|BAB86847.1|//7.00E-39//elongation factor EF-2 [Pisum sativum]	Unigene50821_All//1.00E-39//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene50821_All//3.00E-127//gi|164260615|gb|ES838756.1|ES838756				nr -
Unigene50824_All	460	2.05	0.66	0.00	2.38	2.17	1.18	4.69	2.18	2.60	-1.63E+00	3.13E-02		-1.10E+01	3.34E-05	Down	-1.34E-01	8.25E-01			-1.02E+00	1.30E-01		-1.10E+00	5.07E-03		-8.51E-01	2.33E-02		Unigene50824_All//gi|26451087|dbj|BAC42648.1|//5.00E-25//GPI-anchored protein [Arabidopsis thaliana] >gi|28416735|gb|AAO42898.1| At5g63500 [Arabidopsis thaliana]	Unigene50824_All//3.00E-26//AT5G63500| unknown protein	Unigene50824_All//2.00E-31//DW507367				nr +
Unigene50825_All	438	10.39	3.70	9.85	54.82	45.60	46.30	6.08	3.91	1.55	-1.49E+00	7.63E-07	Down	-7.77E-02	7.94E-01		-2.66E-01	1.58E-02			-2.44E-01	3.68E-02		-6.36E-01	6.75E-02		-1.98E+00	1.60E-07	Down	Unigene50825_All//gi|225428877|ref|XP_002282482.1|//7.00E-13//PREDICTED: similar to leucine-rich repeat family protein [Vitis vinifera]		Unigene50825_All//9.00E-55//gi|78342633|gb|DT562907.1|DT562907				nr +
Unigene50826_All	257	36.85	99.56	58.43	56.02	81.60	73.81	53.80	89.93	61.85	1.43E+00	6.16E-33	Up	6.65E-01	8.03E-06		5.43E-01	1.21E-06			3.98E-01	1.61E-03		7.41E-01	5.74E-13		2.01E-01	1.20E-01		Unigene50826_All//gi|241740196|gb|ACS68205.1|//1.00E-41//ubiquitin 10.2 [Brassica napus]	Unigene50826_All//6.00E-43//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene50826_All//6.00E-141//BF277979				nr -
Unigene50827_All	485	195.47	142.29	182.48	141.02	137.88	200.58	254.38	149.43	115.00	-4.58E-01	6.60E-18		-9.93E-02	1.06E-01		-3.25E-02	7.01E-01			5.08E-01	1.69E-23		-7.68E-01	9.90E-70		-1.15E+00	2.27E-139	Down	Unigene50827_All//gi|4774163|dbj|BAA77508.1|//1.00E-29//F1-ATP synthase delta subunit [Ipomoea batatas]	Unigene50827_All//1.00E-21//AT5G13450| ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative	Unigene50827_All//0.00E+00//gi|11202445|gb|BF271450.1|BF271450		ko00190|Oxidative phosphorylation		nr -
Unigene50828_All	596	0.70	0.77	1.79	1.42	0.92	2.05	9.44	6.52	1.40	1.24E-01	9.11E-01		1.35E+00	6.01E-02		-6.20E-01	4.13E-01			5.26E-01	4.24E-01		-5.33E-01	1.80E-02		-2.75E+00	7.11E-22	Down	Unigene50828_All//gi|224057376|ref|XP_002299218.1|//6.00E-65//GRAS family transcription factor [Populus trichocarpa] >gi|222846476|gb|EEE84023.1| GRAS family transcription factor [Populus trichocarpa]	Unigene50828_All//2.00E-55//AT1G50420| SCL3; transcription factor	Unigene50828_All//2.00E-65//TC164451	GRAS			nr +
Unigene5083_All	1243	55.10	41.46	58.48	15.27	13.82	14.46	13.98	7.26	5.35	-4.10E-01	6.95E-11		8.58E-02	2.38E-01		-1.43E-01	3.18E-01			-7.84E-02	6.41E-01		-9.45E-01	1.20E-14		-1.39E+00	3.83E-27	Down	Unigene5083_All//gi|18406405|ref|NP_566003.1|//1.00E-125//OEP37; ion channel [Arabidopsis thaliana] >gi|20197072|gb|AAC23403.2| expressed protein [Arabidopsis thaliana]	Unigene5083_All//5.00E-109//AT2G43950| OEP37; ion channel	Unigene5083_All//0.00E+00//TC133482				nr -
Unigene50830_All	735	2.56	0.34	0.94	9.83	4.83	2.09	3.62	3.30	17.89	-2.89E+00	1.55E-06	Down	-1.44E+00	5.08E-03		-1.03E+00	3.83E-07	Down	-2.23E+00	6.84E-19	Down	-1.36E-01	7.17E-01		2.30E+00	1.89E-40	Up	Unigene50830_All//gi|297834874|ref|XP_002885319.1|//1.00E-13//beta-1,4-xylosidase [Arabidopsis lyrata subsp. lyrata] >gi|297331159|gb|EFH61578.1| beta-1,4-xylosidase [Arabidopsis lyrata subsp. lyrata]	Unigene50830_All//4.00E-12//AT3G19615| unknown protein	Unigene50830_All//4.00E-09//ES809679				nr -
Unigene50832_All	360	2.62	3.94	3.85	1.38	2.77	1.63	0.47	3.25	0.55	5.91E-01	2.94E-01		5.56E-01	3.62E-01		1.00E+00	1.65E-01		2.37E-01	7.98E-01		2.79E+00	5.82E-05	Up	2.36E-01	8.83E-01		Unigene50832_All//gi|206205617|gb|AC105957.1|//5.00E-45//kinase-like protein pac.Erf.9 [Platanus x acerifolia]	Unigene50832_All//7.00E-34//AT1G66910| protein kinase, putative	Unigene50832_All//6.00E-31//DT462618				nr +
Unigene50833_All	321	24.45	34.41	21.40	38.18	28.11	29.55	42.41	27.73	16.26	4.93E-01	4.06E-03		-1.92E-01	3.96E-01		-4.42E-01	4.00E-03		-3.70E-01	2.46E-02		-6.13E-01	6.12E-06		-1.38E+00	2.05E-21	Down			Unigene50833_All//2.00E-153//TC156101				
Unigene50834_All	1492	0.07	0.54	0.04	23.24	12.28	19.74	17.46	14.48	4.83	2.95E+00	3.28E-03		-9.74E-01	7.20E-01		-9.20E-01	4.43E-27		-2.36E-01	1.20E-02		-2.69E-01	5.79E-03		-1.85E+00	6.65E-61	Down	Unigene50834_All//gi|153805698|gb|ABS32574.1|//1.00E-165//nodulin family protein [Gossypium hirsutum]	Unigene50834_All//3.00E-129//AT4G08300| nodulin MtN21 family protein	Unigene50834_All//0.00E+00//TC160743				nr -
Unigene50835_All	797	1.84	0.13	0.27	0.94	0.39	1.42	2.02	1.73	1.05	-3.85E+00	1.75E-06	Down	-2.78E+00	9.28E-05	Down	-1.27E+00	1.12E-01		5.96E-01	3.98E-01		-2.20E-01	6.35E-01		-9.41E-01	3.51E-02		Unigene50835_All//gi|115456255|ref|NP_001051728.1|//8.00E-94//Os03g0821700 [Oryza sativa Japonica Group] >gi|108711802|gb|ABF99597.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550199|dbj|BAF13642.1| Os03g0821700 [Oryza sativa Japonica Group]	Unigene50835_All//2.00E-78//AT1G08070| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene50836_All	856	0.49	0.59	1.18	0.64	0.16	7.33	28.35	79.44	398.29	2.76E-01	7.64E-01		1.27E+00	8.36E-02		-1.99E+00	5.12E-02		3.52E+00	1.58E-25	Up	1.49E+00	8.49E-112	Up	3.81E+00	0.00E+00	Up	Unigene50836_All//gi|195973264|gb|AB869659.2|//1.00E-79//glutathione S-transferase [Gossypium hirsutum]	Unigene50836_All//4.00E-64//AT3G09270| ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	Unigene50836_All//0.00E+00//DN826606		ko00480|Glutathione metabolism		nr +
Unigene50837_All	929	3.38	0.44	0.69	2.31	1.48	0.68	3.55	0.85	0.04	-2.95E+00	1.13E-10	Down	-2.30E+00	7.91E-08	Down	-6.37E-01	1.39E-01		-1.76E+00	1.44E-04	Down	-2.05E+00	3.30E-09	Down	-6.37E+00	1.19E-22	Down	Unigene50837_All//gi|115440909|ref|NP_001044734.1|//6.00E-39//Os01g0836900 [Oryza sativa Japonica Group] >gi|113534265|dbj|BAF06648.1| Os01g0836900 [Oryza sativa Japonica Group]	Unigene50837_All//1.00E-11//AT2G39370| unknown protein	Unigene50837_All//5.00E-160//gi|164329437|gb|EX163928.1|EX163928				nr +
Unigene50840_All	347	9.95	27.31	20.56	4.88	2.68	2.34	4.26	3.01	0.92	1.46E+00	6.26E-13	Up	1.05E+00	5.78E-06	Up	-8.65E-01	7.39E-02		-1.06E+00	3.77E-02		-5.02E-01	3.26E-01		-2.22E+00	4.14E-05	Down							

Unigene50841_All	644	2.36	8.65	1.41	0.00	0.48	1.61	0.00	1.36	1.11	1.88E+00	5.23E-11	Up	-7.45E-01	1.88E-01		8.91E+00	4.54E-02		1.07E+01	3.33E-06	Up	1.04E+01	2.86E-06	Up	1.01E+01	2.63E-05	Up	Unigene50841_All//gi|7024449|dbj|BAA92155.1|//1.00E-28//glycine-rich protein [Citrus unshiu]	Unigene50841_All//3.00E-06//AT2G05540| glycine-rich protein	Unigene50841_All//0.00E+00//TC176475		ko03040|Spliceosome		nr +
Unigene50842_All	903	0.35	1.91	0.00	2.87	5.30	3.60	5.34	0.83	2.21	2.46E+00	3.84E-05	Up	-8.44E+00	4.90E-02		8.86E-01	8.12E-04		3.28E-01	4.04E-01		-2.68E+00	9.74E-18	Down	-1.27E+00	2.75E-07	Down	Unigene50842_All//gi|297834964|ref|XP_002885364.1|//9.00E-98//extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata] >gi|297331204|gb|EFH61623.1| extracellular ligand-gated ion channel [Arabidopsis lyrata subsp. lyrata]	Unigene50842_All//7.00E-92//AT3G20300| unknown protein	Unigene50842_All//0.00E+00//ES808030				nr +
Unigene50844_All	311	39.37	16.62	11.30	60.71	50.93	77.11	196.72	94.21	94.54	-1.24E+00	3.41E-13	Down	-1.80E+00	2.59E-21	Down	-2.53E-01	4.90E-02		3.45E-01	1.96E-03		-1.06E+00	6.37E-60	Down	-1.06E+00	3.67E-61	Down	Unigene50844_All//gi|6015065|sp|O23755.1|EF2_BETVU//7.00E-53//RecName: Full=Elongation factor 2; Short=EF-2 >gi|2369714|emb|CAB09900.1| elongation factor 2 [Beta vulgaris subsp. vulgaris]	Unigene50844_All//9.00E-52//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene50844_All//5.00E-173//TC150260				nr +
Unigene50845_All	668	1.25	3.11	1.99	2.61	0.46	0.54	2.47	4.44	4.41	1.31E+00	4.47E-03		6.69E-01	2.69E-01		-2.49E+00	2.66E-06	Down	-2.27E+00	4.52E-05	Down	8.48E-01	8.85E-03		8.38E-01	7.80E-03		Unigene50845_All//gi|5734724|gb|AAD49889.1|AC007259_2//7.00E-47//Very similar to receptor-like protein kinase [Arabidopsis thaliana]	Unigene50845_All//4.00E-48//AT1G11330| S-locus lectin protein kinase family protein	Unigene50845_All//4.00E-64//CO081719				nr +
Unigene50846_All	469	473.56	174.80	460.06	193.31	174.82	125.86	67.34	45.63	32.96	-1.44E+00	9.17E-284	Down	-4.17E-02	3.29E-01		-1.45E-01	7.94E-03		-6.19E-01	2.75E-31		-5.62E-01	5.65E-11		-1.03E+00	9.51E-31	Down	Unigene50846_All//gi|211906470|gb|ACJ11728.1|//8.00E-58//glyceraldehyde-3-phosphate dehydrogenase [Gossypium hirsutum]	Unigene50846_All//1.00E-54//AT1G13440| GAPC2 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene50846_All//0.00E+00//gi|84154275|gb|DN803630.1|DN803630		ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene50847_All	311	24.73	10.43	5.14	33.16	30.23	38.63	81.98	32.12	33.31	-1.25E+00	1.35E-08	Down	-2.27E+00	3.94E-18	Down	-1.33E-01	5.37E-01		2.20E-01	2.29E-01		-1.35E+00	6.82E-37	Down	-1.30E+00	8.30E-36	Down	Unigene50847_All//gi|76160947|gb|BAA04437.1|//7.00E-47//40S ribosomal protein S7-like protein [Solanum tuberosum] >gi|77999315|gb|ABB17004.1| ribosomal protein S7-like protein [Solanum tuberosum] >gi|82623373|gb|ABB87101.1| 40S ribosomal protein S7-like protein-like [Solanum tuberosum]	Unigene50847_All//4.00E-48//AT1G08830| 40S ribosomal protein S7 (RPS7A)	Unigene50847_All//7.00E-166//TC173896		ko03010|Ribosome		nr +
Unigene5085_All	1138	1.10	0.71	0.80	2.67	0.64	2.46	3.08	1.54	2.77	-6.31E-01	2.93E-01		-4.72E-01	4.42E-01		-2.07E+00	1.53E-08	Down	-1.18E-01	7.53E-01		-9.99E-01	7.10E-04		-1.57E-01	6.09E-01		Unigene5085_All//gi|186509871|ref|NP_187362.3|//6.00E-77//emb1974 (embryo defective 1974) [Arabidopsis thaliana]	Unigene5085_All//2.00E-78//AT3G07060| emb1974 (embryo defective 1974)	Unigene5085_All//0.00E+00//gi|164340649|gb|ES793230.1|ES793230				nr +
Unigene50851_All	493	10.61	15.42	10.26	18.69	15.30	17.41	70.58	47.48	29.09	5.39E-01	1.10E-02		-4.86E-02	8.65E-01		-2.89E-01	1.42E-01		-1.03E-01	6.47E-01		-5.72E-01	2.19E-12		-1.28E+00	2.28E-47	Down			Unigene50851_All//0.00E+00//TC151729				
Unigene50852_All	1033	1.98	4.41	3.09	0.72	1.50	0.92	0.12	0.69	0.31	1.16E+00	6.49E-05	Up	6.47E-01	7.69E-02		1.05E+00	5.02E-02		3.44E-01	6.49E-01		2.49E+00	5.53E-03		1.33E+00	2.93E-01		Unigene50852_All//gi|224104401|ref|XP_002313425.1|//9.00E-99//cytochrome P450 [Populus trichocarpa] >gi|222849833|gb|EEE87380.1| cytochrome P450 [Populus trichocarpa]	Unigene50852_All//5.00E-83//AT2G29090| CYP707A2; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	Unigene50852_All//0.00E+00//TC143465		ko00906|Carotenoid biosynthesis		nr -
Unigene50854_All	544	1.73	2.79	1.17	1.47	1.14	1.25	5.44	5.76	2.20	6.91E-01	2.02E-01		-5.60E-01	4.39E-01		-3.63E-01	6.23E-01		-2.35E-01	7.53E-01		8.29E-02	8.07E-01		-1.31E+00	5.75E-05	Down			Unigene50854_All//3.00E-80//TC147167				
Unigene50856_All	543	39.89	6.53	20.30	6.33	10.78	6.40	0.16	0.85	0.15	-2.61E+00	1.26E-61	Down	-9.75E-01	6.38E-15		7.68E-01	1.06E-03		1.69E-02	9.59E-01		2.44E+00	3.74E-02		-8.59E-02	9.71E-01		Unigene50856_All//gi|114050579|gb|ABI49439.1|//1.00E-36//At1g02070 [Arabidopsis thaliana]	Unigene50856_All//2.00E-35//AT1G02070| unknown protein	Unigene50856_All//0.00E+00//EX171215				nr +
Unigene50859_All	850	0.12	0.24	0.81	0.82	0.81	1.22	55.46	20.31	31.50	9.54E-01	6.21E-01		2.73E+00	1.40E-02		-1.82E-02	9.61E-01		5.75E-01	4.26E-01		-1.45E+00	5.15E-75	Down	-8.16E-01	5.59E-31		Unigene50859_All//gi|221272207|sp|A2A1A0.1|NCS1_COPJA//2.00E-72//RecName: Full=S-norcoclaurine synthase 1; Short=CjNCS1 >gi|123720767|dbj|BAF45337.1| norcoclaurine synthase [Coptis japonica var. dissecta] >gi|301072256|gb|ADK56103.1| 2OG/Fe(II)-dependent dioxygenase-like protein [synthetic construct]	Unigene50859_All//2.00E-59//AT4G25300| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene50859_All//2.00E-122//BE054468		ko00941|Flavonoid biosynthesis		nr +
Unigene50860_All	423	6.80	0.48	0.50	2.71	3.34	0.85	1.80	0.40	0.57	-3.83E+00	3.57E-12	Down	-3.76E+00	2.15E-11	Down	3.01E-01	6.16E-01		-1.66E+00	1.29E-02		-2.19E+00	7.77E-03		-1.67E+00	2.39E-02		Unigene50860_All//gi|297839865|ref|XP_002887814.1|//4.00E-07//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333655|gb|EFH64073.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50860_All//1.00E-07//AT1G80710| transducin family protein / WD-40 repeat family protein	Unigene50860_All//6.00E-28//DW502564				nr -
Unigene50861_All	422	3.47	2.64	2.90	5.55	4.24	1.93	2.40	0.99	1.51	-3.94E-01	4.70E-01		-2.58E-01	6.23E-01		-3.87E-01	3.73E-01		-1.53E+00	3.76E-04	Down	-1.28E+00	4.06E-02		-6.71E-01	2.53E-01		Unigene50861_All//gi|297839865|ref|XP_002887814.1|//6.00E-09//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333655|gb|EFH64073.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene50861_All//1.00E-09//AT1G80710| transducin family protein / WD-40 repeat family protein	Unigene50861_All//7.00E-34//DW502564				nr +
Unigene50862_All	902	2.44	1.80	0.47	7.90	4.73	4.71	8.25	3.20	7.20	-4.39E-01	3.23E-01		-2.37E+00	7.70E-06	Down	-7.38E-01	2.79E-04		-7.47E-01	5.10E-04		-1.37E+00	1.61E-11	Down	-1.97E-01	3.39E-01		Unigene50862_All//gi|124360233|gb|ABN08246.1|//1.00E-134//Solute carrier family 35 member B3, related [Medicago truncatula]	Unigene50862_All//7.00E-121//AT4G23010| UDP-galactose transporter-related	Unigene50862_All//4.00E-65//TC155300				nr -
Unigene50864_All	2180	0.05	0.33	0.73	0.41	0.39	0.58	16.00	16.39	35.38	2.76E+00	9.14E-03		3.93E+00	9.51E-07	Up	-5.87E-02	9.22E-01		4.96E-01	4.48E-01		3.49E-02	7.21E-01		1.14E+00	1.09E-86	Up	Unigene50864_All//gi|17865165|gb|AAL47166.1|AF449459_1//0.00E+00//diamine oxidase [Brassica juncea]	Unigene50864_All//0.00E+00//AT4G14940| ATAO1 (ARABIDOPSIS THALIANA AMINE OXIDASE 1); amine oxidase/ copper ion binding			ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr +
Unigene50865_All	1205	0.00	0.17	0.00	0.45	0.17	2.59	7.19	7.63	13.09	7.39E+00	1.36E-01		null	null		-1.41E+00	1.53E-01		2.51E+00	2.44E-09	Up	8.53E-02	6.54E-01		8.64E-01	6.37E-12		Unigene50865_All//gi|224104809|ref|XP_002313573.1|//8.00E-63//predicted protein [Populus trichocarpa] >gi|222849981|gb|EEE87528.1| predicted protein [Populus trichocarpa]		Unigene50865_All//0.00E+00//DW227494				nr +
Unigene50866_All	809	0.91	4.38	1.05	1.48	1.23	0.56	1.67	4.29	7.09	2.28E+00	4.48E-09	Up	2.18E-01	7.57E-01		-2.60E-01	6.78E-01		-1.40E+00	2.82E-02		1.36E+00	1.01E-05	Up	2.08E+00	4.48E-16	Up								
Unigene50870_All	263	15.32	15.80	20.65	18.56	24.22	20.44	104.33	32.90	34.84	4.45E-02	8.92E-01		4.31E-01	1.16E-01		3.84E-01	1.11E-01		1.39E-01	6.42E-01		-1.67E+00	1.03E-53	Down	-1.58E+00	1.80E-51	Down	Unigene50870_All//gi|2827080|gb|AAB99755.1|//2.00E-10//mmlate dehydrogenase precursor [Medicago sativa]	Unigene50870_All//1.00E-10//AT3G15020| mmlate dehydrogenase (NAD), mitochondrial, putative	Unigene50870_All//2.00E-119//TC158910		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene50871_All	561	5.32	11.92	5.98	7.99	4.42	3.70	2.41	0.89	0.78	1.17E+00	7.24E-07	Up	1.70E-01	6.17E-01		-8.55E-01	1.33E-03		-1.11E+00	9.34E-05	Down	-1.43E+00	7.15E-03		-1.63E+00	1.95E-03		Unigene50871_All//gi|195970469|gb|ACG60703.1|//1.00E-19//HcrVf1-like protein [Malus x domestica]	Unigene50871_All//2.00E-10//AT2G34930| disease resistance family protein	Unigene50871_All//4.00E-141//FL577455				nr -
Unigene50873_All	1249	3.85	2.72	0.34	0.64	0.47	0.40	3.55	12.31	6.48	-5.04E-01	6.78E-02		-3.50E+00	8.43E-18	Down	-4.45E-01	5.73E-01		-6.82E-01	4.05E-01		1.79E+00	1.32E-33	Up	8.65E-01	1.48E-06		Unigene50873_All//gi|115459964|ref|NP_001053582.1|//6.00E-31//Os04g0566600 [Oryza sativa Japonica Group] >gi|21741799|emb|CAD41286.1| OSJNBa0005N02.4 [Oryza sativa (japonica cultivar-group)] >gi|113565153|dbj|BAF15496.1| Os04g0566600 [Oryza sativa Japonica Group]	Unigene50873_All//2.00E-30//AT1G14600| DNA binding / transcription factor	Unigene50873_All//0.00E+00//TC143080	G2-like			nr +
Unigene50874_All	1814	0.72	1.26	0.76	0.41	0.34	0.42	19.00	29.93	58.55	8.02E-01	5.88E-02		8.19E-02	8.86E-01		-2.70E-01	7.48E-01		3.94E-02	9.59E-01		6.56E-01	8.05E-24		1.62E+00	2.61E-202	Up	Unigene50874_All//gi|269996964|gb|ACZ57767.1|//0.00E+00//phospholipase A1 [Nicotiana attenuata]	Unigene50874_All//3.00E-173//AT4G16820| lipase class 3 family protein	Unigene50874_All//0.00E+00//gi|78330595|gb|DT550869.1|DT550869				nr -
Unigene50875_All	757	6.84	1.74	5.14	4.80	4.23	2.21	0.45	0.50	0.00	-1.98E+00	5.02E-11	Down	-4.14E-01	1.41E-01		-1.83E-01	6.11E-01		-1.12E+00	4.76E-04	Down	1.53E-01	8.90E-01		-8.80E+00	8.14E-03		Unigene50875_All//gi|15222372|ref|NP_172210.1|//2.00E-14//josephin protein-related [Arabidopsis thaliana] >gi|38454076|gb|AAR20732.1| At1g07300 [Arabidopsis thaliana] >gi|38603992|gb|AAR24739.1| At1g07300 [Arabidopsis thaliana]	Unigene50875_All//1.00E-10//AT1G07300| Josephin protein-related	Unigene50875_All//0.00E+00//gi|109885542|gb|DW514512.1|DW514512				nr -
Unigene50877_All	1231	0.38	3.83	3.24	4.21	5.37	2.83	2.54	0.98	1.46	3.32E+00	2.47E-17	Up	3.08E+00	2.30E-13	Up	3.52E-01	1.43E-01		-5.75E-01	2.93E-02		-1.37E+00	2.69E-05	Down	-8.03E-01	7.88E-03		Unigene50877_All//gi|15218566|ref|NP_174686.1|//1.00E-28//phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] >gi|50916620|gb|AAD39608.1|AC002454_7 Contains similarity to gi|836774 FAB1 protein from Saccharomyces cerevisiae genome gb|D50617 [Arabidopsis thaliana]	Unigene50877_All//1.00E-22//AT1G34260| phosphatidylinositol-4-phosphate 5-kinase family protein	Unigene50877_All//3.00E-60//TC155630		ko04145|Phagosome//ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism		nr -
Unigene50879_All	358	6.72	11.46	13.39	6.54	6.06	5.05	22.91	54.87	39.06	7.70E-01	1.04E-02		9.94E-01	5.71E-04		-1.10E-01	8.22E-01		-3.74E-01	4.05E-01		1.26E+00	1.07E-25	Up	7.70E-01	6.51E-09				Unigene50879_All//5.00E-164//gi|109838027|gb|DW236588.1|DW236588				
Unigene5088_All	975	6.17	6.81	6.55	1.43	3.78	1.11	0.00	0.00	0.04	1.42E-01	5.82E-01		8.68E-02	7.24E-01		1.40E+00	1.07E-05	Up	-3.64E-01	5.56E-01		null	null		5.35E+00	6.44E-01		Unigene5088_All//gi|297801024|ref|XP_002868396.1|//1.00E-107//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314232|gb|EFH44655.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5088_All//3.00E-108//AT5G33370| GDSL-motif lipase/hydrolase family protein	Unigene5088_All//0.00E+00//TC135481				nr +
Unigene50880_All	618	4.23	4.02	6.38	13.06	9.86	14.69	5.40	2.50	2.13	-7.54E-02	8.43E-01		5.91E-01	6.77E-02		-4.05E-01	4.33E-02		1.70E-01	4.57E-01		-1.11E+00	2.84E-04	Down	-1.35E+00	1.07E-05	Down								
Unigene50881_All	548	0.76	0.55	1.17	40.18	47.95	32.14	8.95	6.41	27.55	-4.61E-01	6.50E-01		6.10E-01	5.09E-01		2.55E-01	1.64E-02		-3.22E-01	6.23E-03		-4.82E-01	4.99E-02		1.62E+00	2.06E-29	Up	Unigene50881_All//gi|18410665|ref|NP_565088.1|//7.00E-30//MIF1 (MINI ZINC FINGER 1); DNA binding / transcription factor [Arabidopsis thaliana] >gi|89111834|gb|ABD60689.1| At1g74660 [Arabidopsis thaliana]	Unigene50881_All//4.00E-31//AT1G74660| MIF1 (MINI ZINC FINGER 1); DNA binding / transcription factor		zf-HD			nr -
Unigene50882_All	1999	0.00	0.05	0.00	0.55	0.03	0.00	75.21	119.39	74.58	5.66E+00	3.86E-01		null	null		-3.99E+00	3.49E-06	Down	-9.10E+00	7.25E-07	Down	6.67E-01	6.87E-105		-1.23E-02	7.85E-01		Unigene50882_All//gi|224113975|ref|XP_002316632.1|//0.00E+00//polyphenol oxidase [Populus trichocarpa] >gi|222859697|gb|EEE97244.1| polyphenol oxidase [Populus trichocarpa]		Unigene50882_All//0.00E+00//CO085494		ko00350|Tyrosine metabolism//ko00950|Isoquinoline alkaloid biosynthesis		nr -

Unigene50883_All	434	1.81	4.44	1.35	3.90	3.89	2.50	2.63	0.19	1.84	1.29E+00	7.23E-03		-4.22E-01	6.21E-01		-5.40E-03	9.76E-01		-6.44E-01	2.19E-01		-3.77E+00	3.90E-06	Down	-5.19E-01	3.56E-01		Unigene50883_All//gi|15215582|gb|AK91336.1//5.00E-21//AT5g13880/MAC12_16 [Arabidopsis thaliana] >gi|20334870|gb|AAM16191.1| AT5g13880/MAC12_16 [Arabidopsis thaliana]	Unigene50883_All//6.00E-27//AT5G47920| unknown protein					nr -
Unigene50884_All	1057	0.94	0.05	0.91	0.80	0.81	0.98	2.72	3.48	1.70	-4.30E+00	7.30E-05	Down	-5.26E-02	9.54E-01		2.38E-02	9.92E-01		2.95E-01	6.93E-01		3.55E-01	2.40E-01		-6.81E-01	3.16E-02		Unigene50884_All//gi|255576695|ref|XP_002529236.1//1.00E-39//conserved hypothetical protein [Ricinus communis] >gi|223531309|gb|EEF33149.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene50885_All	757	3.87	1.07	4.15	10.46	8.69	7.99	1.51	1.49	0.26	-1.85E+00	4.31E-06	Down	1.01E-01	7.75E-01		-2.68E-01	2.22E-01		-3.88E-01	6.99E-02		-1.66E-02	1.01E+00		-2.52E+00	1.20E-04	Down	Unigene50885_All//gi|8778715|gb|AAF79723.1|AC005106_4//7.00E-33//T25N20.7 [Arabidopsis thaliana]	Unigene50885_All//9.00E-23//AT1G06420| OFP12 (OVATE FAMILY PROTEIN 12)	Unigene50885_All//0.00E+00//TC156577				nr -
Unigene50887_All	572	3.11	6.82	4.19	4.18	3.49	4.90	13.82	13.23	7.94	1.13E+00	3.39E-04	Up	4.30E-01	3.32E-01		-2.60E-01	5.56E-01		2.28E-01	6.17E-01		-6.37E-02	7.63E-01		-8.00E-01	9.01E-06									ESTScan -
Unigene50888_All	739	4.81	5.97	8.36	10.25	6.71	6.17	0.00	0.00	1.02	3.09E-01	3.09E-01		7.96E-01	1.28E-03		-6.11E-01	2.07E-03		-7.31E-01	4.22E-04		null	null		1.00E+01	1.39E-05	Up	Unigene50888_All//gi|297843570|ref|XP_002889666.1//1.00E-114//calcium-transporting ATPase 1, endoplasmic reticulum-type [Arabidopsis lyrata subsp. lyrata] >gi|297335508|gb|EFH65925.1| calcium-transporting ATPase 1, endoplasmic reticulum-type [Arabidopsis lyrata subsp. lyrata]	Unigene50888_All//3.00E-114//AT1G07670| calcium-transporting ATPase	Unigene50888_All//2.00E-115//gi|109888147|gb|DW517116.1|DW517116				nr +
Unigene50889_All	746	1.26	1.56	1.28	2.27	4.15	5.75	31.80	81.46	443.14	3.07E-01	6.13E-01		2.55E-02	9.91E-01		8.72E-01	1.19E-02		1.34E+00	7.87E-06	Up	1.36E+00	2.91E-87	Up	3.80E+00	0.00E+00	Up	Unigene50889_All//gi|224103111|ref|XP_002312929.1//1.00E-70//lysine/histidine transporter [Populus trichocarpa] >gi|222849337|gb|EEE86884.1| lysine/histidine transporter [Populus trichocarpa]	Unigene50889_All//8.00E-47//AT1G47670| amino acid transporter family protein	Unigene50889_All//1.00E-73//gi|73861718|gb|DT464457.1|DT464457				nr +
Unigene50890_All	766	140.16	157.50	277.09	166.61	201.62	219.45	29.20	73.28	32.09	1.68E-01	4.44E-04		9.83E-01	2.84E-144		2.75E-01	2.41E-13		3.97E-01	9.21E-26		1.33E+00	5.65E-78	Up	1.36E-01	1.98E-01		Unigene50890_All//gi|15724357|gb|AAL06571.1|AF412119_1//7.00E-28//At1g47960/T2J15_13 [Arabidopsis thaliana] >gi|15810209|gb|AAL07005.1| At1g47960/T2J15_13 [Arabidopsis thaliana] >gi|19699120|gb|AAL90926.1| At1g47960/T2J15_13 [Arabidopsis thaliana]	Unigene50890_All//2.00E-27//AT1G47960| C/VIF1 (CELL WALL / VACUOLAR INHIBITOR OF FRUCTOSIDASE 1); enzyme inhibitor/ pectinesterase/ pectinesterase inhibitor	Unigene50890_All//0.00E+00//gi|109879323|gb|DW508293.1|DW508293				nr +
Unigene50891_All	1267	3.18	1.04	2.02	2.83	2.64	2.71	12.91	11.25	4.91	-1.61E+00	8.40E-07	Down	-6.56E-01	3.97E-02		-1.03E-01	8.02E-01		-6.34E-02	8.62E-01		-1.99E-01	1.37E-01		-1.40E+00	6.36E-26	Down	Unigene50891_All//gi|18400820|ref|NP_565593.1|//1.00E-54//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene50891_All//7.00E-56//AT2G25410| protein binding / zinc ion binding					nr +
Unigene50892_All	717	0.58	1.27	1.49	16.81	9.56	12.66	10.44	3.32	0.44	1.12E+00	1.30E-01		1.35E+00	6.01E-02		-8.15E-01	5.48E-08		-4.09E-01	1.26E-02		-1.65E+00	4.92E-15	Down	-4.55E+00	5.81E-44	Down	Unigene50892_All//gi|18424977|ref|NP_569016.1|//3.00E-17//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|75180372|sp|Q9LS89.1|Y3566_ARATH RecName: Full=Uncharacterized protein At5g65660 >gi|30102568|gb|AAP21202.1| At5g65660 [Arabidopsis thaliana]	Unigene50892_All//2.00E-09//AT5G65660| hydroxyproline-rich glycoprotein family protein	Unigene50892_All//0.00E+00//TC156581				nr +
Unigene50895_All	966	6.17	57.07	6.73	4.02	4.92	5.28	0.53	31.15	0.87	3.21E+00	1.65E-191	Up	1.23E-01	6.09E-01		2.90E-01	3.36E-01		3.93E-01	1.63E-01		5.89E+00	1.08E-191	Up	7.22E-01	2.82E-01		Unigene50895_All//gi|159138943|gb|ABW89471.1|//1.00E-113//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene50895_All//2.00E-25//AT4G25200| ATHSP23.6-MITO (MITOCHONDRION-LOCALIZED SMALL HEAT SHOCK PROTEIN 23.6)	Unigene50895_All//0.00E+00//gi|109859199|gb|DW488178.1|DW488178				nr +
Unigene50896_All	1166	0.54	0.52	0.82	2.86	4.52	2.98	2.86	0.47	1.54	-4.63E-02	9.71E-01		6.10E-01	3.86E-01		6.59E-01	9.23E-03		5.93E-02	8.84E-01		-2.62E+00	3.28E-12	Down	-8.98E-01	2.15E-03		Unigene50896_All//gi|124359768|gb|ABN06095.1|//1.00E-141//Kinesin, motor region [Medicago truncatula]	Unigene50896_All//5.00E-135//AT3G44050| kinesin motor protein-related					nr +
Unigene50898_All	488	107.97	58.46	135.63	64.92	59.91	605.45	56.84	89.50	199.76	-8.85E-01	1.97E-31		3.29E-01	6.56E-07		-1.16E-01	3.00E-01		3.22E+00	0.00E+00	Up	6.55E-01	2.75E-19		1.81E+00	8.39E-217	Up	Unigene50898_All//gi|300793388|tpg|DAA33860.1|//2.00E-25//TPA: TPA_inf: aquaporin PIP1;6 [Gossypium hirsutum]	Unigene50898_All//1.00E-10//AT4G00430| PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel	Unigene50898_All//0.00E+00//gi|164320307|gb|EX170647.1|EX170647				nr -
Unigene509_All	1645	144.72	52.52	97.73	32.55	30.67	30.04	6.55	5.89	3.63	-1.46E+00	0.00E+00	Down	-5.66E-01	4.05E-62		-8.61E-02	3.05E-01		-1.16E-01	1.57E-01		-1.53E-01	4.04E-01		-8.51E-01	2.71E-08		Unigene509_All//gi|157169069|gb|ABV25894.1|//0.00E+00//starch synthase isoform II [Manihot esculenta]	Unigene509_All//0.00E+00//AT3G01180| AtSS2 (starch synthase 2); transferase, transferring glycosyl groups	Unigene509_All//0.00E+00//TC136757		ko00500|Starch and sucrose metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0046527	nr -
Unigene50904_All	578	1.63	0.96	1.01	2.41	1.91	1.09	3.80	1.23	1.03	-7.57E-01	2.86E-01		-6.85E-01	3.69E-01		-3.40E-01	5.62E-01		-1.14E+00	4.68E-02		-1.63E+00	7.07E-05	Down	-1.88E+00	5.33E-06	Down	Unigene50904_All//gi|75172985|sp|Q9FX64.1|HOP2_ARATH//7.00E-81//RecName: Full=Homologous-pairing protein 2 homolog; AltName: Full=Protein HOP2; Short=AtHOP2; AltName: Full=Protein ARABIDOPSIS HOMOLOG PAIRING 2; AltName: Full=Protein AHP2; Short=AtAHP2 >gi|9958066|gb|AAG09555.1|AC011810_14 Hypothetical Protein [Arabidopsis thaliana] >gi|29293664|gb|AAO67519.1| AHP2 [Arabidopsis thaliana] >gi|92856625|gb|ABE77410.1| At1g13330 [Arabidopsis thaliana] >gi|121490118|emb|CAF28783.1| Hop2 protein [Arabidopsis thaliana]	Unigene50904_All//4.00E-82//AT1G13330| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Tat binding protein 1-interacting (InterPro:IPR010776); Has 2425 Blast hits to 2142 proteins in 283 species: Archae - 50; Bacteria - 240; Metazoa - 929; Fungi - 179; Plants - 47; Viruses - 23; Other Eukaryotes - 957 (source: NCBI BLink).	Unigene50904_All//4.00E-153//ES815381				nr -
Unigene50905_All	893	2.75	3.97	3.76	5.24	4.16	2.58	1.94	0.80	0.58	5.28E-01	1.10E-01		4.48E-01	2.18E-01		-3.32E-01	2.56E-01		-1.02E+00	2.04E-04	Down	-1.29E+00	4.58E-03		-1.74E+00	1.65E-04	Down								
Unigene50907_All	533	22.87	8.84	3.50	9.07	10.01	4.91	46.56	12.47	10.46	-1.37E+00	3.79E-15	Down	-2.71E+00	6.67E-35	Down	1.44E-01	6.26E-01		-8.83E-01	1.05E-03		-1.90E+00	2.54E-58	Down	-2.15E+00	1.14E-70	Down	Unigene50907_All//gi|297724497|ref|NP_001174612.1|//8.00E-30//Os06g0159750 [Oryza sativa Japonica Group] >gi|255676736|dbj|BAH93340.1| Os06g0159750 [Oryza sativa Japonica Group]	Unigene50907_All//2.00E-20//AT5G10980| histone H3	Unigene50907_All//0.00E+00//TC143703				nr -
Unigene50908_All	432	34.03	38.35	23.17	38.74	29.33	43.07	184.98	188.18	57.82	1.73E-01	2.42E-01		-5.54E-01	2.45E-04		-4.01E-01	1.81E-03		1.53E-01	3.11E-01		2.48E-02	7.06E-01		-1.68E+00	2.49E-161	Down			Unigene50908_All//0.00E+00//TC153693				
Unigene5091_All	1420	6.37	5.57	2.93	9.33	8.25	9.13	8.13	13.10	19.72	-1.96E-01	3.55E-01		-1.12E+00	3.59E-08	Down	-1.79E-01	3.07E-01		-3.18E-02	8.70E-01		6.88E-01	2.10E-09		1.28E+00	5.66E-38	Up	Unigene5091_All//gi|15081757|gb|AAK82533.1|//3.00E-37//At1g68340/T22E19_3 [Arabidopsis thaliana] >gi|18252275|gb|AAL62018.1| At1g68340/T22E19_3 [Arabidopsis thaliana]	Unigene5091_All//8.00E-30//AT1G25370| unknown protein	Unigene5091_All//0.00E+00//TC130007				nr -
Unigene50911_All	566	2.59	0.18	0.94	6.07	4.93	6.14	1.05	0.30	1.48	-3.85E+00	1.75E-06	Down	-1.46E+00	1.49E-02		-3.01E-01	3.98E-01		1.68E-02	9.59E-01		-1.82E+00	4.71E-02		4.99E-01	4.61E-01		Unigene50911_All//gi|15231886|ref|NP_188076.1|//3.00E-30//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75274210|sp|Q9LU06.1|PP230_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At3g14580, mitochondrial; Flags: Precursor >gi|119935972|gb|ABM06049.1| At3g14580 [Arabidopsis thaliana]	Unigene50911_All//4.00E-30//AT3G14580| pentatricopeptide (PPR) repeat-containing protein	Unigene50911_All//0.00E+00//C0131134				nr -
Unigene50912_All	444	2.12	1.37	6.24	6.17	6.98	7.02	1.33	1.69	2.33	-6.31E-01	3.66E-01		1.56E+00	1.81E-04	Up	1.78E-01	6.62E-01		1.86E-01	6.39E-01		3.46E-01	6.20E-01		8.07E-01	1.68E-01				Unigene50912_All//2.00E-34//DT461884				
Unigene50913_All	357	6.60	3.12	6.26	4.19	3.28	14.04	1.54	1.52	7.37	-1.08E+00	1.01E-02		-7.41E-02	8.63E-01		-3.52E-01	5.49E-01		1.75E+00	1.53E-09	Up	-1.66E-02	1.02E+00		2.26E+00	1.61E-08	Up			Unigene50913_All//3.00E-137//BE653749				
Unigene50917_All	341	12.58	9.21	7.81	13.44	13.73	13.91	56.54	30.03	12.85	-4.50E-01	1.31E-01		-6.88E-01	2.49E-02		3.12E-02	9.37E-01		4.93E-02	8.88E-01		-9.13E-01	2.65E-15		-2.14E+00	1.50E-54	Down	Unigene50917_All//gi|297833934|ref|XP_002884849.1|//1.00E-10//40S ribosomal protein S14 [Arabidopsis lyrata subsp. lyrata] >gi|297330689|gb|EFH61108.1| 40S ribosomal protein S14 [Arabidopsis lyrata subsp. lyrata]	Unigene50917_All//2.00E-05//AT3G52580| 40S ribosomal protein S14 (RPS14C)	Unigene50917_All//2.00E-169//gi|84150191|gb|DN781491.1|DN781491		ko03010|Ribosome		nr -
Unigene50918_All	732	17.65	3.95	6.47	0.95	1.27	4.57	0.00	0.06	0.00	-2.16E+00	1.17E-29	Down	-1.45E+00	1.45E-16	Down	4.15E-01	6.06E-01		2.26E+00	6.56E-09	Up	5.84E+00	6.34E-01		null	null				Unigene50918_All//7.00E-63//TC169023				
Unigene5092_All	549	14.87	21.60	6.98	48.54	41.46	53.72	57.30	42.56	30.48	5.39E-01	1.07E-03		-1.09E+00	4.13E-07	Down	-2.28E-01	3.22E-02		1.46E-01	1.99E-01		-4.29E-01	5.27E-07		-9.11E-01	4.37E-25				Unigene5092_All//0.00E+00//TC144346				
Unigene50920_All	835	149.00	442.61	149.99	230.82	244.02	393.87	221.58	413.45	316.71	1.57E+00	0.00E+00	Up	9.50E-03	8.69E-01		8.02E-02	3.36E-02		7.71E-01	1.11E-163		9.00E-01	4.15E-254		5.15E-01	3.48E-75		Unigene50920_All//gi|194475604|gb|ACF74549.1|//4.00E-08//RAV [Nicotiana tabacum]	Unigene50920_All//5.00E-08//AT4G01500| NGA4 (NGATHA4); transcription factor	Unigene50920_All//0.00E+00//gi|73864248|gb|DT466987.1|DT466987	AB13VP1			nr +
Unigene50924_All	1216	0.22	18.13	1.01	0.25	1.70	2.86	1.56	0.41	1.05	6.40E+00	2.63E-117	Up	2.23E+00	2.23E-03		2.79E+00	2.07E-07	Up	3.54E+00	2.45E-14	Up	-1.92E+00	3.20E-05	Down	-5.78E-01	1.56E-01		Unigene50924_All//gi|9858781|gb|AAG01128.1|AF273333_13//9.00E-89//BAC19.13 [Solanum lycopersicum]	Unigene50924_All//1.00E-93//AT2G18540| cupin family protein					nr -
Unigene50926_All	980	0.75	0.00	0.00	6.30	3.06	1.43	2.16	0.68	0.41	-9.55E+00	2.11E-04	Down	-9.55E+00	4.13E-04	Down	-1.04E+00	2.36E-06	Down	-2.14E+00	2.05E-15	Down	-1.66E+00	7.98E-05	Down	-2.41E+00	1.32E-07	Down	Unigene50926_All//gi|224083805|ref|XP_002307129.1|//1.00E-105//cytochrome P450 [Populus trichocarpa] >gi|222856578|gb|EEE94125.1| cytochrome P450 [Populus trichocarpa]	Unigene50926_All//3.00E-90//AT5G09970| CYP78A7; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene50929_All	544	2.69	9.50	7.05	3.11	2.79	3.74	1.24	0.08	0.15	1.82E+00	7.33E-10	Up	1.39E+00	4.19E-05	Up	-1.61E-01	7.82E-01		2.63E-01	6.30E-01		-4.02E+00	5.36E-04	Down	-3.09E+00	1.45E-03		Unigene50929_All//gi|255572832|ref|XP_002527348.1|//3.00E-23//conserved hypothetical protein [Ricinus communis] >gi|223533267|gb|EEF35020.1| conserved hypothetical protein [Ricinus communis]		Unigene50929_All//0.00E+00//DW508517				nr -
Unigene50930_All	421	0.99	1.93	2.53	5.56	2.62	2.79	25.01	22.83	8.99	9.54E-01	2.26E-01		1.35E+00	6.01E-02		-1.09E+00	5.67E-03		-9.96E-01	1.69E-02		-1.31E-01	4.77E-01		-1.48E+00	2.19E-18	Down			Unigene50930_All//3.00E-116//gi|164317270|gb|ES807717.1|ES807717				
Unigene50931_All	245	86.49	19.23	32.38	28.06	21.08	15.30	37.62	45.38	41.46	-2.17E+00	1.94E-48	Down	-1.42E+00	5.25E-26	Down	-4.12E-01	6.22E-02		-8.75E-01	6.72E-05		2.71E-01	9.35E-02		1.40E-01	4.23E-01		Unigene50931_All//gi|255572650|ref|XP_002527258.1|//3.00E-09//transcription factor, putative [Ricinus communis] >gi|223533351|gb|EEF35102.1| transcription factor, putative [Ricinus communis]		Unigene50931_All//5.00E-129//TC149797				nr -
Unigene50932_All	421	1.49	26.84	1.26	4.97	10.63	3.43	7.33	5.76	12.87	4.17E+00	6.87E-49	Up	-2.38E-01	7.74E-01		1.10E+00	7.45E-05	Up	-5.34E-01	2.49E-01		-3.49E-01	3.05E-01		8.12E-01	2.73E-04									

Unigene50933_All	911	0.00	0.11	0.12	1.09	0.60	0.50	5.43	0.83	2.06	6.80E+00	3.86E-01		6.87E+00	3.97E-01		-8.55E-01	2.05E-01		-1.14E+00	1.09E-01		-2.72E+00	1.88E-18	Down	-1.40E+00	1.74E-08	Down	Unigene50933_All//gi|28466867|gb|AA044042.1|//4.00E-64//At4g01650 [Arabidopsis thaliana]	Unigene50933_All//2.00E-65//AT4G01650| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: L3 growth stages; CONTAINS InterPro DOMAIN/s: Streptomyces cyclase/dehydrase (InterPro:IPR005031); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G08720.1); Has 322 Blast hits to 309 proteins in 56 species: Archae - 0; Bacteria - 121; Metazoa - 0; Fungi - 0; Plants - 46; Viruses - 0; Other Eukaryotes - 155 (source: NCBI BLink).	Unigene50933_All//2.00E-63//CD486156				nr +
Unigene50935_All	1131	1.16	0.85	0.47	0.92	0.82	0.92	1.35	2.51	16.66	-4.42E-01	4.41E-01		-1.30E+00	4.12E-02		-1.70E-01	8.19E-01		-1.02E-02	9.79E-01		9.01E-01	6.73E-03		3.63E+00	1.57E-91	Up	Unigene50935_All//gi|15220485|ref|NP_176929.1|//1.00E-21//F-box family protein [Arabidopsis thaliana] >gi|75263152|sp|Q9FXC7.1|FB79_ARATH RecName: Full=Putative F-box protein At1g67623 >gi|11072021|gb|AAG28900.1|AC008113_16 F12A21.25 [Arabidopsis thaliana]	Unigene50935_All//7.00E-23//AT1G67623| F-box family protein	Unigene50935_All//0.00E+00//gi|164313035|gb|ES817823.1|ES817823				nr -
Unigene50936_All	390	10.33	6.24	7.24	36.15	22.96	20.15	58.76	18.86	14.81	-7.28E-01	1.62E-02		-5.14E-01	1.12E-01		-6.55E-01	1.80E-06		-8.43E-01	8.45E-09		-1.64E+00	5.28E-44	Down	-1.99E+00	5.99E-59	Down	Unigene50936_All//gi|297798126|ref|XP_002866947.1|//3.00E-09//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297312783|gb|EFH43206.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene50936_All//1.00E-173//TC145216				nr +
Unigene50938_All	528	0.10	0.00	0.00	73.40	12.52	8.55	6.41	13.38	1.89	-6.63E+00	6.10E-01		-6.63E+00	6.22E-01		-2.55E+00	3.93E-136	Down	-3.10E+00	8.28E-144	Down	1.06E+00	1.28E-07	Up	-1.76E+00	3.96E-08	Down	Unigene50938_All//gi|30102556|gb|AAP21196.1|//2.00E-07//At3g45160 [Arabidopsis thaliana]	Unigene50938_All//1.00E-08//AT3G45160| unknown protein	Unigene50938_All//2.00E-118//TC167470				nr +
Unigene5094_All	1099	0.81	0.28	0.87	3.54	1.60	2.88	2.35	1.56	1.78	-1.55E+00	4.56E-02		1.08E-01	8.75E-01		-1.15E+00	8.14E-05	Down	-2.98E-01	3.97E-01		-5.90E-01	9.75E-02		-4.02E-01	2.48E-01		Unigene5094_All//gi|297807667|ref|XP_002871717.1|//1.00E-158//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317554|gb|EFH47976.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene5094_All//2.00E-155//AT5G16420| pentatricopeptide (PPR) repeat-containing protein				nr +
Unigene50941_All	1002	0.31	0.56	0.74	1.34	1.75	2.88	0.97	0.50	4.13	8.28E-01	3.81E-01		1.25E+00	1.54E-01		3.85E-01	4.89E-01		1.10E+00	3.00E-03		-9.55E-01	1.35E-01		2.09E+00	7.09E-12	Up	Unigene50941_All//gi|300151491|gb|EFJ18137.1|//3.00E-52//ubiquitin-protein ligase, UPL1 [Selaginella moellendorffii]	Unigene50941_All//4.00E-40//AT1G70320| UPL2 (UBIQUITIN-PROTEIN LIGASE 2); ubiquitin-protein ligase	Unigene50941_All//0.00E+00//TC133607		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene50942_All	565	1.30	1.88	0.00	4.76	4.27	4.08	0.97	0.44	0.85	5.39E-01	4.03E-01		-1.03E+01	4.13E-04	Down	-1.58E-01	7.12E-01		-2.24E-01	6.26E-01		-1.13E+00	2.18E-01		-2.01E-01	7.93E-01					Unigene50942_All//2.00E-35//CO122884					
Unigene50943_All	957	0.87	0.64	0.61	2.08	0.83	1.32	2.92	0.92	1.50	-4.61E-01	5.43E-01		-5.15E-01	5.15E-01		-1.33E+00	2.30E-03		-6.56E-01	1.63E-01		-1.67E+00	3.67E-06	Down	-9.60E-01	3.15E-03		Unigene50943_All//gi|28300299|gb|AA037645.1|//1.00E-48//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene50943_All//2.00E-23//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene50943_All//2.00E-137//TC179054		ko04626|Plant-pathogen interaction		nr +
Unigene50944_All	510	15.80	3.48	2.51	20.32	6.08	7.97	16.66	3.28	3.98	-2.18E+00	5.66E-19	Down	-2.66E+00	1.06E-22	Down	-1.74E+00	3.19E-22	Down	-1.35E+00	1.48E-13	Down	-2.35E+00	1.65E-26	Down	-2.06E+00	1.80E-23	Down				Unigene50944_All//2.00E-81//ES833388					
Unigene50948_All	793	0.66	2.24	1.14	0.25	0.69	1.14	0.53	3.48	6.73	1.76E+00	9.42E-04	Up	7.91E-01	3.04E-01		1.47E+00	1.77E-01		2.18E+00	9.48E-03		2.71E+00	1.68E-10	Up	3.66E+00	1.61E-26	Up		Unigene50948_All//6.00E-06//AT2G28570| unknown protein					
Unigene50949_All	712	0.59	0.14	0.00	2.38	1.55	2.60	9.92	21.84	31.78	-2.05E+00	1.20E-01		-9.20E+00	1.56E-02		-6.20E-01	2.16E-01		1.29E-01	7.95E-01		1.14E+00	1.35E-17	Up	1.68E+00	7.38E-46	Up	Unigene50949_All//gi|224114680|ref|XP_002316826.1|//2.00E-64//f-box family protein [Populus trichocarpa] >gi|222859891|gb|EEE97438.1| f-box family protein [Populus trichocarpa]	Unigene50949_All//8.00E-52//AT1G29160| Dof-type zinc finger domain-containing protein	Unigene50949_All//5.00E-33//DT048472	C2C2-Dof			nr +
Unigene5095_All	936	9.17	49.75	9.16	6.44	8.61	6.85	1.76	2.55	0.38	2.44E+00	4.25E-121	Up	-1.20E-03	9.95E-01		4.19E-01	4.09E-02		8.95E-02	7.31E-01		5.31E-01	1.58E-01		-2.20E+00	1.44E-05	Down	Unigene5095_All//gi|15239849|ref|NP_196764.1|//1.00E-51//AT-HSP17.6A (ARABIDOPSIS THALIANA HEAT SHOCK PROTEIN 17.6A); unfolded protein binding [Arabidopsis thaliana] >gi|75279004|sp|Q81822.1|HS17_ARATH RecName: Full=17.7 kDa class II heat shock protein; AltName: Full=17.7 kDa heat shock protein; Short=AtHsp17.7 >gi|3256075|emb|CAA74399.1| Heat Shock Protein 17.6A [Arabidopsis thaliana] >gi|7573370|emb|CAB87676.1| heat shock protein 17.6A [Arabidopsis thaliana]	Unigene5095_All//1.00E-37//AT5G12020| HSP17.6II (17.6 KDA CLASS II HEAT SHOCK PROTEIN)	Unigene5095_All//0.00E+00//gi|11206923|gb|BF275805.1|BF275805				nr -
Unigene50951_All	379	19.05	40.38	38.50	14.85	15.36	9.65	51.76	96.60	54.77	1.08E+00	3.59E-13	Up	1.01E+00	6.04E-11	Up	4.80E-02	8.72E-01		-6.22E-01	1.26E-02		9.00E-01	1.19E-27		8.13E-02	5.22E-01					Unigene50951_All//3.00E-168//TC147700					
Unigene50952_All	423	46.26	22.64	54.13	6.01	4.15	6.51	0.60	0.00	0.38	-1.03E+00	1.87E-15	Down	2.27E-01	7.19E-02		-5.33E-01	1.75E-01		1.17E-01	7.73E-01		-9.23E+00	4.03E-02		-6.71E-01	6.05E-01					Unigene50952_All//0.00E+00//gi|13248234|gb|BF274872.2|BF274872					
Unigene50955_All	497	69.27	37.01	51.21	93.71	84.88	68.24	37.35	16.06	27.73	-9.04E-01	1.52E-21		-4.36E-01	3.77E-06		-1.43E-01	8.42E-02		-4.58E-01	1.05E-09		-1.22E+00	4.02E-23	Down	-4.29E-01	1.20E-04		Unigene50955_All//gi|16226450|gb|AAL16171.1|AF428403_1/1.00E-28//AT5g10780/T30N20_50 [Arabidopsis thaliana] >gi|14335060|gb|AAK59794.1| AT5g10780/T30N20_50 [Arabidopsis thaliana] >gi|16332254|gb|AAL15361.1| AT5g10780/T30N20_50 [Arabidopsis thaliana]	Unigene50955_All//8.00E-30//AT5G10780| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP017207, transmembrane protein 85 (InterPro:IPR016687), Protein of unknown function DUF1077 (InterPro:IPR009445); Has 281 Blast hits to 281 proteins in 136 species: Archae - 0; Bacteria - 0; Metazoa - 114; Fungi - 83; Plants - 23; Viruses - 0; Other Eukaryotes - 61 (source: NCBI BLink).	Unigene50955_All//5.00E-180//TC142368				nr -
Unigene50959_All	662	1.50	2.45	3.70	2.03	2.97	5.05	4.15	3.35	4.93	7.06E-01	1.73E-01		1.30E+00	2.78E-03		5.45E-01	2.68E-01		1.31E+00	1.46E-04	Up	-3.11E-01	4.08E-01		2.49E-01	4.31E-01					Unigene50959_All//1.00E-110//TC178455					
Unigene5096_All	516	54.65	93.68	63.47	87.17	57.06	59.96	10.82	10.37	4.94	7.77E-01	3.18E-23		2.16E-01	3.59E-02		-6.12E-01	2.68E-17		-5.40E-01	1.71E-12		-6.10E-02	8.10E-01		-1.13E+00	5.14E-07	Down	Unigene5096_All//gi|115449929|ref|NP_001048586.1|//2.00E-122//Os02g0826400 [Oryza sativa Japonica Group] >gi|113538117|dbj|BAF10500.1| Os02g0826400 [Oryza sativa Japonica Group]	Unigene5096_All//2.00E-14//AT4G10810| unknown protein	Unigene5096_All//0.00E+00//gi|109876218|gb|DW505192.1|DW505192				nr -
Unigene50961_All	671	0.31	0.15	0.00	2.23	2.05	1.88	84.75	3.86	33.49	-1.05E+00	5.64E-01		-8.28E+00	1.45E-01		-1.18E-01	8.23E-01		-2.41E-01	6.82E-01		-4.46E+00	0.00E+00	Down	-1.34E+00	1.50E-82	Down	Unigene50961_All//gi|255710053|gb|ACU30848.1|//1.00E-31//cold-regulated LTCOR12 [Jatropha curcas]	Unigene50961_All//4.00E-24//AT1G75750| GASA1 (GAST1 PROTEIN HOMOLOG 1)	Unigene50961_All//0.00E+00//DT052841				nr -
Unigene50962_All	871	0.24	7.85	2.51	0.57	0.71	0.93	0.58	2.83	5.67	5.03E+00	3.58E-33	Up	3.38E+00	4.02E-08	Up	3.15E-01	7.84E-01		7.07E-01	3.93E-01		2.28E+00	6.43E-08	Up	3.28E+00	1.78E-22	Up									ESTscan -
Unigene50964_All	1253	0.00	0.00	0.00	0.16	0.16	0.83	20.85	3.44	24.32	null	null		null	null		5.26E-02	9.88E-01		2.38E+00	2.54E-03		-2.60E+00	2.84E-90	Down	2.22E-01	1.17E-02		Unigene50964_All//gi|164605008|dbj|BAF98300.1|//4.00E-77//geranyl-diphosphate synthase [Hevea brasiliensis]	Unigene50964_All//2.00E-20//AT4G36810| GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltransfransferase	Unigene50964_All//0.00E+00//TC144366		ko00900|Terpenoid backbone biosynthesis	GO:0004659	nr +
Unigene50966_All	1279	0.00	0.16	0.00	18.85	21.38	9.50	0.20	0.88	1.43	7.31E+00	1.36E-01		null	null		1.82E-01	1.02E-01		-9.89E-01	6.31E-19		2.15E+00	8.74E-04	Up	2.85E+00	9.46E-08	Up	Unigene50966_All//gi|42561909|ref|NP_172575.2|//1.00E-137//scp131 (serine carboxypeptidase-like 31); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|133778908|gb|AB038794.1| At1g11080 [Arabidopsis thaliana]	Unigene50966_All//2.00E-138//AT1G11080| scp131 (serine carboxypeptidase-like 31); serine-type carboxypeptidase	Unigene50966_All//0.00E+00//TC160828				nr +
Unigene50967_All	232	45.56	27.52	22.49	68.71	56.85	78.65	227.99	129.35	76.41	-7.27E-01	3.41E-05		-1.02E+00	3.92E-08	Down	-2.73E-01	5.23E-02		1.95E-01	1.80E-01		-8.18E-01	9.04E-34		-1.58E+00	5.92E-98	Down	Unigene50967_All//gi|208964722|gb|ACI31551.1|//2.00E-35//heat shock protein 90-2 [Glycine max]	Unigene50967_All//1.00E-35//AT5G56010| HSP81-3; ATP binding / unfolded protein binding	Unigene50967_All//2.00E-128//TC165756		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr -
Unigene5097_All	1303	13.53	5.17	6.05	2.56	6.37	5.10	5.55	0.80	5.20	-1.39E+00	5.93E-22	Down	-1.16E+00	4.11E-16	Down	1.31E+00	3.51E-11	Up	9.92E-01	1.24E-05		-2.79E+00	2.04E-27	Down	-9.43E-02	6.43E-01		Unigene5097_All//gi|19698450|gb|AAL93153.1|AF485267_1//1.00E-178//class III peroxidase [Gossypium hirsutum]	Unigene5097_All//1.00E-119//AT4G25980| cationic peroxidase, putative	Unigene5097_All//0.00E+00//NP445708		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene50970_All	563	0.56	0.90	0.00	2.57	3.24	4.09	1.05	2.15	3.18	6.91E-01	4.99E-01		-9.12E+00	4.90E-02		3.37E-01	5.52E-01		6.73E-01	1.23E-01		1.03E+00	6.29E-02		1.60E+00	3.75E-04	Up	Unigene50970_All//gi|297840689|ref|XP_002888226.1|//1.00E-59//helicase domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297334067|gb|EFH64485.1| helicase domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene50970_All//2.00E-45//AT1G58060| helicase domain-containing protein				GO:0017111//GO:0032559//GO:0043231	nr +
Unigene50971_All	459	1.25	2.43	1.16	14.76	14.78	8.76	2.76	1.00	0.17	9.54E-01	1.40E-01		-1.12E-01	9.07E-01		1.90E-03	9.99E-01		-7.53E-01	6.65E-04		-1.46E+00	8.32E-03		-3.99E+00	2.56E-07	Down				Unigene50971_All//7.00E-105//TC171549					

Unigene50972_All	563	1.49	0.36	1.51	3.80	2.20	0.72	1.58	0.52	1.63	-2.05E+00	1.68E-02		2.54E-02	9.93E-01		-7.89E-01	6.06E-02		-2.40E+00	1.86E-06	Down	-1.60E+00	2.18E-02		4.54E-02	9.62E-01		Unigene50972_All//gi|729273|sp|P40781.1|CYP84_CYNCA/5.00E-64//RecName: Full=Protein CYP804 >gi|17959|emb|CAA49354.1| cypro4 [Cynara cardunculus]	Unigene50972_All//1.00E-64//AT3G19240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), Vacuolar import and degradation, Vid27-related (InterPro:IPR013863); BEST Arabidopsis thaliana protein match is: dem protein-related / defective embryo and meristems protein-related (TAIR:AT4G33400.1); Has 206 Blast hits to 202 proteins in 88 species: Archae - 0; Bacteria - 0; Metazoa - 11; Fungi - 117; Plants - 38; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink).	Unigene50972_All//0.00E+00//gi|73859965|gb|DT462704.1|DT462704			GO:0016020//GO:0043231//GO:0044444	nr +
Unigene50973_All	665	6.85	2.13	5.69	11.46	15.53	10.73	1.97	1.13	0.84	-1.68E+00	5.27E-08	Down	-2.68E-01	3.88E-01		4.39E-01	1.17E-02		-9.50E-02	6.77E-01		-8.01E-01	1.33E-01		-1.23E+00	1.61E-02		Unigene50973_All//gi|115467534|ref|NP_001057366.1|//1.00E-33//Os06g0272900 [Oryza sativa Japonica Group] >gi|55296963|dbj|BAD68439.1| leaf senescence protein-like [Oryza sativa Japonica Group] >gi|113595406|dbj|BAF19280.1| Os06g0272900 [Oryza sativa Japonica Group]	Unigene50973_All//3.00E-37//AT3G02440| unknown protein	Unigene50973_All//0.00E+00//TC131328				nr -
Unigene50974_All	330	52.96	46.83	43.08	82.42	80.98	78.97	64.19	24.32	38.51	-1.77E-01	2.18E-01		-2.98E-01	3.75E-02		-2.55E-02	8.33E-01		-6.17E-02	6.30E-01		-1.40E+00	1.92E-32	Down	-7.37E-01	3.14E-12		Unigene50974_All//gi|12580867|emb|CAC27142.1|//1.00E-36//60S ribosomal protein L13E [Picea abies]	Unigene50974_All//3.00E-28//AT3G49010| ATRBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome	Unigene50974_All//9.00E-153//gi|109825330|gb|DW224063.1|DW224063		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene50976_All	973	0.86	0.68	0.71	3.48	1.80	1.35	0.70	0.73	0.90	-3.46E-01	6.12E-01		-2.74E-01	7.05E-01		-9.48E-01	2.59E-03		-1.37E+00	5.78E-05	Down	7.07E-02	9.42E-01		3.74E-01	5.86E-01		Unigene50976_All//gi|53370641|gb|AU89136.1|//8.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]		Unigene50976_All//7.00E-36//TC173674				nr -
Unigene50977_All	741	0.64	0.34	0.22	1.88	1.02	0.98	1.31	0.17	0.48	-8.94E-01	3.89E-01		-1.56E+00	2.04E-01		-8.81E-01	1.06E-01		-9.49E-01	9.91E-02		-2.96E+00	1.89E-04	Down	-1.44E+00	2.09E-02		Unigene50977_All//gi|53370641|gb|AU89136.1|//5.00E-07//F-box domain containing protein [Oryza sativa Japonica Group]						nr -
Unigene50978_All	236	8.87	20.18	11.28	13.51	15.32	15.69	30.46	46.05	39.50	1.19E+00	3.00E-05	Up	3.47E-01	3.83E-01		1.82E-01	6.18E-01		2.16E-01	5.65E-01		5.96E-01	1.04E-04		3.75E-01	2.39E-02		Unigene50978_All//gi|186493263|ref|NP_564859.2|//3.00E-25//SMP1 (SWELLMAP 1); nucleic acid binding / single-stranded RNA binding [Arabidopsis thaliana] >gi|150417956|sp|Q9SHY8.2|SLU7A_ARATH RecName: Full=Pre-mRNA-splicing factor SLU7-A	Unigene50978_All//4.00E-09//AT4G37120| SMP2; single-stranded RNA binding	Unigene50978_All//2.00E-94//TC140745		ko03040|Spliceosome	GO:0003723//GO:0006396//GO:0008283//GO:0046914	nr -
Unigene50979_All	442	0.95	0.80	0.72	1.13	0.78	1.33	43.62	91.25	71.93	-2.39E-01	8.10E-01		-3.90E-01	7.17E-01		-5.33E-01	5.94E-01		2.37E-01	7.98E-01		1.06E+00	7.01E-40	Up	7.22E-01	3.43E-17		Unigene50979_All//gi|66475040|gb|AY47050.1|//7.00E-61//ascorbate oxidase [Solanum lycopersicum]	Unigene50979_All//7.00E-61//AT4G39830| L-ascorbate oxidase, putative	Unigene50979_All//9.00E-89//gi|73866197|gb|DT468935.1|DT468935		ko00053|Ascorbate and aldarate metabolism	GO:0008152//GO:0016682//GO:0031410//GO:0046914	nr +
Unigene5098_All	706	12.45	12.06	10.11	37.11	29.22	22.07	4.67	11.90	10.21	-4.63E-02	8.20E-01		-3.01E-01	1.54E-01		-3.45E-01	5.75E-04		-7.50E-01	4.96E-13		1.35E+00	1.25E-12	Up	1.13E+00	1.02E-08	Up	Unigene5098_All//gi|115149929|ref|NP_001048586.1|//1.00E-12//Os02g0826400 [Oryza sativa Japonica Group] >gi|113538117|dbj|BAF10500.1| Os02g0826400 [Oryza sativa Japonica Group]	Unigene5098_All//2.00E-11//AT4G10810| unknown protein	Unigene5098_All//0.00E+00//gi|21090687|gb|BQ403000.1|BQ403000				nr +
Unigene50980_All	646	0.16	6.59	3.54	0.31	0.00	0.42	3.67	11.58	4.26	5.35E+00	2.53E-21	Up	4.45E+00	2.89E-10	Up	-8.27E+00	8.41E-02		4.44E-01	7.63E-01		1.66E+00	4.22E-15	Up	2.15E-01	5.55E-01									
Unigene50984_All	503	0.31	2.52	2.22	0.69	1.51	0.99	1.85	2.24	3.25	3.01E+00	1.02E-04	Up	2.83E+00	7.34E-04	Up	1.12E+00	1.98E-01		5.11E-01	6.41E-01		2.79E-01	6.41E-01		8.12E-01	6.76E-02									
Unigene50988_All	747	0.91	262.23	15.18	2.67	0.92	1.15	0.11	0.62	0.91	8.17E+00	0.00E+00	Up	4.06E+00	4.87E-47	Up	-1.53E+00	5.23E-04	Down	-1.22E+00	8.56E-03		2.44E+00	3.74E-02		3.00E+00	2.00E-03		Unigene50988_All//gi|226507342|ref|NP_001151050.1|//6.00E-16//LOC100284683 [Zea mays] >gi|195643912|gb|ACG41424.1| USP family protein [Zea mays]	Unigene50988_All//3.00E-05//AT4G27320| universal stress protein (USP) family protein	Unigene50988_All//0.00E+00//gi|48751318|gb|CO081837.1|CO081837			GO:0043231//GO:0050896	nr -
Unigene50989_All	2023	0.00	0.00	0.11	0.42	0.20	0.87	10.49	9.55	2.82	null	null		6.72E+00	1.41E-01		-1.03E+00	1.62E-01		1.06E+00	3.64E-02		-1.36E-01	2.61E-01		-1.90E+00	2.10E-51	Down	Unigene50989_All//gi|28951043|gb|AA063445.1|//1.00E-151//At2g25737 [Arabidopsis thaliana]	Unigene50989_All//2.00E-111//AT2G25737| unknown protein	Unigene50989_All//2.00E-114//TC165856				nr +
Unigene5099_All	619	20.46	2.29	6.80	14.41	13.18	3.43	4.44	3.58	2.96	-3.16E+00	4.52E-44	Down	-1.59E+00	1.47E-18	Down	-1.28E-01	5.77E-01		-2.07E+00	3.99E-21	Down	-3.11E-01	4.08E-01		-5.85E-01	7.39E-02		Unigene5099_All//gi|297824677|ref|XP_002880221.1|//4.00E-44//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326060|gb|EFH56480.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5099_All//3.00E-34//AT2G46160| zinc finger (C3HC4-type RING finger) family protein	Unigene5099_All//0.00E+00//TC159779				nr -
Unigene50990_All	567	0.18	0.00	0.00	2.64	3.10	2.15	0.60	1.40	2.25	-7.53E+00	3.71E-01		-7.53E+00	3.92E-01		2.33E-01	6.80E-01		-2.93E-01	6.38E-01		1.23E+00	9.04E-02		1.91E+00	7.76E-04	Up	Unigene50990_All//gi|115473321|ref|NP_001060259.1|//2.00E-21//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]		Unigene50990_All//1.00E-08//ES807753			GO:0005488	nr -
Unigene50994_All	404	102.83	47.16	48.37	140.32	125.98	210.17	139.19	66.52	65.28	-1.12E+00	1.03E-36	Down	-1.09E+00	1.50E-33	Down	-1.56E-01	3.05E-02		5.83E-01	3.34E-26		-1.07E+00	2.18E-55	Down	-1.09E+00	2.53E-59	Down	Unigene50994_All//gi|192910756|gb|ACF06486.1|//7.00E-47//60S ribosomal protein L11 [Elaeis guineensis] >gi|192910758|gb|ACF06487.1| 60S ribosomal protein L11 [Elaeis guineensis]	Unigene50994_All//1.00E-47//AT5G45775| 60S ribosomal protein L11 (RPL11D)	Unigene50994_All//0.00E+00//TC137396		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene50995_All	1379	1.06	0.92	0.50	1.95	2.37	1.74	3.28	1.33	3.47	-2.10E-01	6.84E-01		-1.08E+00	6.36E-02		2.82E-01	4.67E-01		-1.68E-01	6.99E-01		-1.30E+00	8.20E-07	Down	7.96E-02	7.55E-01		Unigene50995_All//gi|9454546|gb|AAF87869.1|AC012561_2//1.00E-158//Unknown protein [Arabidopsis thaliana]	Unigene50995_All//6.00E-161//AT1G50660| unknown protein	Unigene50995_All//6.00E-148//DW496534			GO:0043231	nr +
Unigene50997_All	937	0.56	0.76	0.57	1.81	0.37	1.35	3.34	4.55	2.42	4.39E-01	6.16E-01		2.54E-02	9.99E-01		-2.30E+00	1.29E-05	Down	-4.22E-01	4.36E-01		4.46E-01	9.80E-02		-4.62E-01	1.33E-01		Unigene50997_All//gi|1920874|gb|AAB51377.1|//7.00E-82//MADS-box protein [Medicago sativa]	Unigene50997_All//7.00E-73//AT3G57230| AGL16 (AGAMOUS-LIKE 16); transcription factor	Unigene50997_All//0.00E+00//ES805118	MADS		GO:0001071//GO:0003677//GO:0006351//GO:0010374//GO:0010468//GO:0016128//GO:0043231	nr +
Unigene50998_All	576	2.73	2.29	0.18	4.76	4.07	3.45	1.17	0.29	1.38	-2.53E-01	6.23E-01		-3.88E+00	1.55E-06	Down	-2.27E-01	5.89E-01		-4.63E-01	2.45E-01		-2.02E+00	1.98E-02		2.36E-01	7.19E-01		Unigene50998_All//gi|297819256|ref|XP_002877511.1|//1.00E-22//translocon outer membrane complex 75-III [Arabidopsis lyrata subsp. lyrata] >gi|297323349|gb|EFH53770.1| translocon outer membrane complex 75-III [Arabidopsis lyrata subsp. lyrata]	Unigene50998_All//9.00E-07//AT3G46740| TOC75-III (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene50998_All//0.00E+00//gi|78347599|gb|DT567873.1|DT567873		ko03040|Spliceosome//ko04146|Peroxisome//ko03050|Proteasome	GO:0006605//GO:0009653//GO:0009707	nr -
Unigene51_All	3057	21.65	6.90	7.00	41.60	33.09	28.00	25.13	7.15	12.63	-1.65E+00	6.22E-104	Down	-1.63E+00	1.45E-98	Down	-3.30E-01	1.19E-15		-5.71E-01	6.89E-38		-1.81E+00	5.13E-168	Down	-9.93E-01	3.97E-69		Unigene51_All//gi|241740134|gb|ACS68195.1|//0.00E+00//cellulose synthase 5.1 catalytic subunit [Brassica napus]	Unigene51_All//0.00E+00//AT4G39350| CESA2 (CELLULOSE SYNTHASE A2); cellulose synthase/ transferase, transferring glycosyl groups	Unigene51_All//0.00E+00//TC137429				nr +
Unigene5100_All	1518	1.10	0.90	0.95	19.56	13.25	11.13	2.37	0.50	0.92	-2.91E-01	5.79E-01		-2.20E-01	6.59E-01		-5.62E-01	5.23E-10		-8.14E-01	7.99E-17		-2.26E+00	4.07E-11	Down	-1.37E+00	3.45E-06	Down	Unigene5100_All//gi|224136594|ref|XP_002326899.1|//1.00E-148//glycosyltransferase family GT8 [Populus trichocarpa] >gi|222835214|gb|EEE73649.1| glycosyltransferase family GT8 [Populus trichocarpa]	Unigene5100_All//2.00E-120//AT1G19300| PARVUS (PARVUS); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene5100_All//0.00E+00//TC138722				nr +
Unigene51000_All	300	2.79	5.91	1.07	9.13	6.89	6.02	2.82	8.08	1.99	1.08E+00	2.92E-02		-1.39E+00	9.66E-02		-4.07E-01	3.05E-01		-6.01E-01	1.24E-01		1.52E+00	7.42E-05	Up	-5.01E-01	4.47E-01				Unigene51000_All//2.00E-132//ES844619				
Unigene51003_All	307	2.05	13.53	2.08	0.97	2.92	1.62	13.08	13.48	103.30	2.73E+00	9.39E-13	Up	2.54E-02	9.97E-01		1.58E+00	4.38E-02		7.33E-01	5.16E-01		4.29E-02	8.93E-01		2.98E+00	2.36E-128	Up			Unigene51003_All//1.00E-102//TC139645				
Unigene51006_All	1024	1.69	0.89	0.00	1.95	1.68	1.06	10.16	10.00	88.16	-9.21E-01	6.50E-02		-1.07E+01	1.99E-09	Down	-2.11E-01	6.58E-01		-8.78E-01	5.70E-02		-2.25E-02	9.16E-01		3.12E+00	0.00E+00	Up	Unigene51006_All//gi|15223919|ref|NP_172939.1|//2.00E-68//atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase >gi|68565943|sp|Q9LQU5.1|NUD18_ARATH RecName: Full=Nudix hydrolase 18, mitochondrial; Short=AtNUDT18; Flags: Precursor >gi|8778216|gb|AAF79225.1|AC006917_10 F10B6.26 [Arabidopsis thaliana]	Unigene51006_All//9.00E-70//AT1G14860| atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase	Unigene51006_All//0.00E+00//gi|109889976|gb|DW518944.1|DW518944			GO:0016462	nr +
Unigene51007_All	760	1.79	5.00	4.34	1.05	1.09	3.51	0.45	0.66	1.99	1.48E+00	8.92E-06	Up	1.28E+00	4.59E-04	Up	5.23E-02	9.65E-01		1.74E+00	2.47E-05	Up	5.68E-01	5.63E-01		2.16E+00	5.30E-05	Up	Unigene51007_All//gi|224055423|ref|XP_002298503.1|//8.00E-06//predicted protein [Populus trichocarpa] >gi|222845761|gb|EEE83308.1| predicted protein [Populus trichocarpa]						nr -
Unigene5101_All	995	66.62	54.85	40.57	96.72	90.19	103.40	191.85	89.64	83.36	-2.81E-01	1.36E-05		-7.16E-01	1.69E-26		-1.01E-01	7.61E-02		9.63E-02	9.25E-02		-1.10E+00	1.24E-195	Down	-1.20E+00	1.23E-232	Down	Unigene5101_All//gi|52139816|gb|AAU29198.1|//1.00E-85//mitochondrial malate dehydrogenase [Solanum lycopersicum]	Unigene5101_All//8.00E-76//AT3G15020| malate dehydrogenase (NAD), mitochondrial, putative	Unigene5101_All//0.00E+00//TC153408		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene51014_All	793	1.72	0.00	0.27	7.48	5.25	3.13	5.12	1.37	0.50	-1.07E+01	6.50E-08	Down	-2.68E+00	2.60E-04	Down	-5.09E-01	3.05E-02		-1.25E+00	3.14E-07	Down	-1.90E+00	3.67E-10	Down	-3.35E+00	2.90E-19	Down	Unigene51014_All//gi|32815867|gb|AAP88333.1|//5.00E-42//At3g06890 [Arabidopsis thaliana]	Unigene51014_All//6.00E-19//AT3G06890| unknown protein	Unigene51014_All//0.00E+00//gi|164357729|gb|ES835262.1|ES835262			GO:0044464	nr +
Unigene51015_All	527	0.79	0.58	0.51	4.16	4.38	2.23	4.97	1.67	1.74	-4.61E-01	6.50E-01		-6.53E-01	5.94E-01		7.40E-02	8.81E-01		-9.00E-01	3.86E-02		-1.58E+00	1.89E-05	Down	-1.52E+00	2.13E-05	Down			Unigene51015_All//4.00E-11//TC172148				
Unigene51017_All	535	193.34	227.97	406.59	71.70	190.71	273.34	45.60	50.15	247.82	2.38E-01	3.39E-07		1.07E+00	1.54E-170	Up	1.41E+00	8.51E-150	Up	1.93E+00	3.82E-304	Up	1.37E-01	1.96E-01		2.44E+00	0.00E+00	Up	Unigene51017_All//gi|118132690|gb|ABK60196.1|//2.00E-43//PIP2 protein [Gossypium hirsutum]	Unigene51017_All//1.00E-33//AT3G53420| PIP2A (PLASMA MEMBRANE INTRINSIC PROTEIN 2A); water channel	Unigene51017_All//2.00E-164//gi|109865656|gb|DW494632.1|DW494632			GO:0006810//GO:0031224	nr -
Unigene51018_All	238	15.61	16.82	27.52	52.54	38.05	27.52	15.99	3.69	22.43	1.08E-01	7.22E-01		8.18E-01	6.21E-04		-4.65E-01	2.01E-03		-9.33E-01	3.14E-09		-2.12E+00	6.86E-11	Down	4.88E-01	3.03E-02				Unigene51018_All//1.00E-58//TC147310				
Unigene51019_All	600	0.17	0.25	1.86	1.33	0.80	0.53	1.48	2.09	2.59	5.38E-01	7.79E-01		3.42E+00	1.92E-04	Up	-7.25E-01	3.46E-01		-1.33E+00	1.06E-01		4.98E-01	3.82E-01		8.07E-01	7.83E-02								

Unigene5102_All	712	8.23	2.85	4.11	14.20	13.69	18.20	3.50	2.17	2.91	-1.53E+00	6.45E-09	Down	-1.00E+00	1.03E-04	Down	-5.33E-02	8.24E-01		3.58E-01	2.57E-02		-6.90E-01	5.52E-02		-2.68E-01	4.68E-01		Unigene5102_All//gi|18423847|ref|NP_568839.1|//3.00E-79//CSN6A [Arabidopsis thaliana] >gi|55976550|sp|Q8W206.2|CSN6A_ARATH RecName: Full=COP9 signalosome complex subunit 6a; Short=Signalosome subunit 6a; Short=AtCSN6a >gi|15809663|gb|AAL07275.1| COP9 complex subunit 6 [Arabidopsis thaliana] >gi|108385379|gb|ABF85779.1| At5g56280 [Arabidopsis thaliana]	Unigene5102_All//2.00E-72//AT5G56280| CSN6A	Unigene5102_All//0.00E+00//gi|78343031|gb|DT563305.1|DT563305				nr -
Unigene51022_All	432	53.77	71.90	44.99	84.29	66.08	63.56	157.96	89.98	75.71	4.19E-01	1.45E-05		-2.57E-01	3.67E-02		-3.51E-01	2.08E-05		-4.07E-01	2.30E-06		-8.12E-01	7.98E-43		-1.06E+00	1.63E-68	Down	Unigene51022_All//gi|225459611|ref|XP_002285872.1|//9.00E-20//PREDICTED: similar to PBC1 (20S proteasome beta subunit C1); peptidase isoform 2 [Vitis vinifera]	Unigene51022_All//2.00E-20//AT1G21720| PBC1 (PROTEASOME BETA SUBUNIT C1); peptidase/ threonine-type endopeptidase	Unigene51022_All//0.00E+00//gi|21100133|gb|BQ412446.1|BQ412446		ko03050|Proteasome	GO:0000502//GO:0004175//GO:0016020//GO:0019941//GO:0043231	nr -
Unigene51024_All	326	410.86	48.03	109.60	369.02	270.10	159.32	123.21	38.98	54.38	-3.10E+00	0.00E+00	Down	-1.91E+00	2.91E-248	Down	-4.50E-01	3.22E-26		-1.21E+00	1.83E-128	Down	-1.66E+00	5.69E-78	Down	-1.18E+00	3.79E-48	Down	Unigene51024_All//gi|295389386|dbj|BAJ06363.1|//7.00E-55//alpha-tubulin [Alopecurus aequalis]	Unigene51024_All//9.00E-37//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene51024_All//0.00E+00//ESS29513		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene51026_All	972	1.18	0.36	0.00	1.59	2.30	1.53	1.39	0.95	1.35	-1.70E+00	1.21E-02		-1.02E+01	2.60E-06	Down	5.36E-01	2.33E-01		-5.12E-02	9.34E-01		-5.57E-01	2.95E-01		-4.14E-02	9.50E-01		Unigene51026_All//gi|4678941|emb|CAB41332.1|//1.00E-41//gamma response I protein [Arabidopsis thaliana]	Unigene51026_All//3.00E-20//AT3G52115| ATGR1 (ARABIDOPSIS THALIANA GAMMA RESPONSE GENE 1)			ko03440|Homologous recombination//ko03450|Non-homologous end-joining	GO:0000729//GO:0009314//GO:0019953//GO:0042579	nr -
Unigene51028_All	242	63.78	28.48	26.63	55.58	58.77	65.88	146.93	82.04	43.62	-1.16E+00	7.43E-15	Down	-1.26E+00	4.88E-16	Down	8.05E-02	6.59E-01		2.45E-01	1.03E-01		-8.41E-01	4.70E-24		-1.75E+00	9.95E-77	Down	Unigene51028_All//gi|80973462|gb|AB853472.1|//4.00E-40//GDP-D-mannose-3',5'-epimerase [Malpighia glabra]	Unigene51028_All//6.00E-40//AT5G28840| GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-mannose 3,5-epimerase/ NAD or NADH binding / catalytic	Unigene51028_All//2.00E-134//gi|78346950|gb|DT567224.1|DT567224		ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00523|Polyketide sugar unit biosynthesis	GO:0008152//GO:0016857//GO:0048037	nr -
Unigene51029_All	1616	332.99	680.65	834.70	3.45	7.03	12.74	0.00	0.00	0.05	1.03E+00	0.00E+00	Up	1.33E+00	0.00E+00	Up	1.03E+00	2.00E-10	Up	1.88E+00	1.04E-41	Up	null	null		5.62E+00	4.03E-01		Unigene51029_All//gi|53850559|gb|AAU95456.1|//1.00E-166//At2g15020 [Arabidopsis thaliana]	Unigene51029_All//8.00E-154//AT2G15020| unknown protein	Unigene51029_All//0.00E+00//gi|109848749|gb|DW477729.1|DW477729				nr -
Unigene5103_All	1227	23.45	55.54	31.29	17.78	15.41	14.80	17.95	23.81	14.42	1.24E+00	9.16E-70	Up	4.16E-01	2.78E-06		-2.07E-01	9.11E-02		-2.65E-01	2.95E-02		4.07E-01	4.91E-06		-3.17E-01	2.06E-03		Unigene5103_All//gi|8671832|gb|AAF78395.1|AC009273.1|//1.00E-103//Strong similarity to polyphosphoinositide binding protein Ssh2 from soybean gb|AF024652. It contains a CRAL/TRIO domain PF|00650. EST gb|AI995792 comes from this gene [Arabidopsis thaliana]	Unigene5103_All//7.00E-103//AT1G01630| SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative	Unigene5103_All//0.00E+00//TC154005				nr +
Unigene51031_All	349	1.05	5.52	2.75	2.14	2.96	0.91	1.82	1.32	2.28	2.39E+00	1.59E-05	Up	1.39E+00	7.11E-02		4.67E-01	5.51E-01		-1.24E+00	1.45E-01		-4.64E-01	5.93E-01		3.29E-01	6.33E-01		Unigene51031_All//gi|89953403|gb|AB083295.1|//3.00E-06//Egenesh protein 81 [Beta vulgaris]	Unigene51031_All//9.00E-08//AT3G62940| OTU-like cysteine protease family protein	Unigene51031_All//4.00E-50//TC131497				nr -
Unigene51032_All	861	5.77	4.30	1.92	0.69	0.92	1.05	0.54	0.10	0.00	-4.26E-01	1.22E-01		-1.59E+00	1.18E-07	Down	4.06E-01	6.31E-01		5.96E-01	4.55E-01		-2.48E+00	3.38E-02		-9.08E+00	1.09E-03		Unigene51032_All//gi|18412676|ref|NP_568083.1|//8.00E-10//beta-galactosidase [Arabidopsis thaliana] >gi|56236102|gb|AAY84507.1| At5g01075 [Arabidopsis thaliana] >gi|111074276|gb|ABH04511.1| At5g01075 [Arabidopsis thaliana]		Unigene51032_All//0.00E+00//TC162773		GO:0016798//GO:0043234//GO:0044238//GO:0044464	nr -
Unigene51034_All	245	55.74	38.05	27.82	62.83	60.72	62.49	102.68	68.75	57.73	-5.51E-01	2.83E-04		-1.00E+00	4.53E-10	Down	-4.92E-02	8.07E-01		-7.70E-03	9.55E-01		-5.79E-01	2.32E-09		-8.31E-01	1.89E-17		Unigene51034_All//gi|115474241|ref|NP_001060719.1|//7.00E-39//Os07g0691800 [Oryza sativa Japonica Group] >gi|109940120|sp|P46466.2|PRS4_ORYSJ RecName: Full=26S protease regulatory subunit 4 homolog; AltName: Full=Tat-binding protein homolog 2 >gi|29837173|dbj|BAC75555.1| 26S proteasome regulatory subunit 4 homolog [Oryza sativa Japonica Group] >gi|113612255|dbj|BAF22633.1| Os07g0691800 [Oryza sativa Japonica Group]	Unigene51034_All//8.00E-40//AT2G20140| 26S protease regulatory complex subunit 4, putative	Unigene51034_All//4.00E-136//EX166507		ko03050|Proteasome	GO:0009057//GO:0032559//GO:0042623//GO:0043231//GO:0043234	nr +
Unigene51035_All	783	0.00	0.39	0.82	22.78	28.06	24.34	46.28	135.80	21.88	8.60E+00	4.42E-02		9.67E+00	1.16E-03		3.01E-01	9.12E-03		9.59E-02	5.48E-01		1.55E+00	4.26E-186	Up	-1.08E+00	6.71E-38	Down	Unigene51035_All//gi|119067548|gb|ABL60873.1|//3.00E-54//germin-like protein 4 [Vitis vinifera]	Unigene51035_All//8.00E-54//AT5G39110| germin-like protein, putative	Unigene51035_All//7.00E-125//gi|109825845|gb|DW224567.1|DW224567			GO:0004871//GO:0005576//GO:0008152//GO:0016209//GO:0016623//GO:0046914	nr +
Unigene51036_All	597	5.26	1.53	2.32	8.34	6.11	5.60	2.90	0.91	0.47	-1.78E+00	3.53E-06	Down	-1.18E+00	1.56E-03		-4.49E-01	9.18E-02		-5.76E-01	3.32E-02		-1.67E+00	3.96E-04	Down	-2.64E+00	5.69E-07	Down			Unigene51036_All//7.00E-78//TC150185				
Unigene51039_All	352	2.38	2.30	3.78	62.83	33.07	22.58	1.92	0.24	0.34	-4.62E-02	9.64E-01		6.69E-01	2.69E-01		-9.26E-01	1.33E-17		-1.48E+00	2.32E-32	Down	-3.02E+00	2.43E-03		-2.50E+00	4.78E-03		Unigene51039_All//gi|224131814|ref|XP_002321185.1|//4.00E-16//predicted protein [Populus trichocarpa] >gi|222861958|gb|EEE99500.1| predicted protein [Populus trichocarpa]		Unigene51039_All//4.00E-146//TC167447				nr -
Unigene5104_All	546	13.03	8.82	5.17	39.69	38.66	35.82	20.37	5.44	7.08	-5.64E-01	1.02E-02		-1.33E+00	2.22E-08	Down	-3.78E-02	8.16E-01		-1.48E-01	2.79E-01		-1.91E+00	1.26E-26	Down	-1.52E+00	2.75E-20	Down	Unigene5104_All//gi|166343833|gb|AB986659.1|//3.00E-73//beta-tubulin 13 [Gossypium hirsutum]	Unigene5104_All//2.00E-58//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene5104_All//0.00E+00//TC131067		ko04145|Phagosome		nr +
Unigene51040_All	348	25.86	132.64	51.57	45.23	69.76	72.42	6.56	21.14	20.61	2.36E+00	2.43E-115	Up	9.96E-01	6.34E-13		6.25E-01	1.23E-09		6.79E-01	1.47E-10		1.69E+00	3.37E-15	Up	1.65E+00	9.38E-15	Up			Unigene51040_All//6.00E-151//TC160055				
Unigene51046_All	412	0.00	0.00	0.78	5.68	4.26	2.41	1.64	2.23	5.03	null	null		9.60E+00	4.51E-02		-4.15E-01	3.25E-01		-1.24E+00	3.22E-03		4.43E-01	5.19E-01		1.61E+00	1.01E-04	Up	Unigene51046_All//gi|118137433|pdb|2CJJ|A//6.00E-19//Chain A, Crystal Structure Of The Myb Domain Of The Rad Transcripition Factor From Antirrhinum Majus >gi|61652985|gb|AAX48042.1| RADIALIS [Antirrhinum majus]	Unigene51046_All//6.00E-20//AT4G39250| ATRL1 (ARABIDOPSIS RAD-LIKE 1); DNA binding / transcription factor		MYB-related	GO:0003676//GO:0010468//GO:0043231	nr -
Unigene51048_All	923	0.40	0.49	0.69	1.57	1.01	0.78	5.27	3.71	18.43	3.16E-01	7.44E-01		8.03E-01	3.88E-01		-6.36E-01	2.46E-01		-9.99E-01	7.45E-02		-5.05E-01	4.03E-02		1.81E+00	2.75E-38	Up	Unigene51048_All//gi|115472321|ref|NP_001059759.1|//2.00E-16//Os07g0511000 [Oryza sativa Japonica Group] >gi|113611296|dbj|BAF21673.1| Os07g0511000 [Oryza sativa Japonica Group]	Unigene51048_All//4.00E-54//AT5G55060| unknown protein	Unigene51048_All//1.00E-61//gi|78346556|gb|DT566830.1|DT566830				nr -
Unigene5105_All	1444	3.55	4.18	4.65	4.93	3.67	5.19	6.82	3.42	1.88	2.34E-01	3.75E-01		3.88E-01	1.12E-01		-4.26E-01	4.75E-02		7.38E-02	7.57E-01		-9.98E-01	2.09E-09		-1.86E+00	1.01E-23	Down	Unigene5105_All//gi|22331732|ref|NP_190655.2|//5.00E-75//clathrin adaptor complex small chain family protein [Arabidopsis thaliana]	Unigene5105_All//2.00E-76//AT3G50860| clathrin adaptor complex small chain family protein	Unigene5105_All//0.00E+00//TC165101				nr -
Unigene51051_All	589	30.02	12.56	18.99	46.09	35.84	35.50	35.60	16.11	19.95	-1.26E+00	5.10E-19	Down	-6.61E-01	1.19E-06		-3.63E-01	1.99E-04		-3.77E-01	2.34E-04		-1.14E+00	1.17E-23	Down	-8.35E-01	7.95E-15		Unigene51051_All//gi|240846170|dbj|BAH79623.1|//1.00E-47//Rsdv1 resistance like protein [Glycine max]	Unigene51051_All//3.00E-47//AT3G20000| T0M40; P-P-bond-hydrolysis-driven protein transmembrane transporter/ voltage-gated anion channel	Unigene51051_All//0.00E+00//DW498780			GO:0004871//GO:0005244//GO:0005488//GO:0005741//GO:0006605//GO:0006811//GO:0008320//GO:0019866	nr -
Unigene51052_All	755	1.59	1.28	0.49	2.64	1.82	0.90	0.28	0.22	2.43	-3.22E-01	6.18E-01		-1.69E+00	1.44E-02		-5.33E-01	2.46E-01		-1.56E+00	1.01E-03		-3.39E-01	8.11E-01		3.12E+00	2.25E-08	Up	Unigene51052_All//gi|224127917|ref|XP_002329209.1|//2.00E-51//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870990|gb|EEF08121.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene51052_All//1.00E-32//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene51052_All//3.00E-34//TC147573		ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene51053_All	1297	0.20	0.08	0.16	1.65	1.30	0.70	10.33	6.22	2.98	-1.37E+00	3.83E-01		-2.97E-01	8.32E-01		-3.44E-01	4.52E-01		-1.25E+00	4.94E-03		-7.33E-01	1.01E-07		-1.79E+00	2.05E-30	Down	Unigene51053_All//gi|25453204|sp|Q96519.1|PER11_ARATH//1.00E-138//RecName: Full=Peroxidase 11; Short=Atperox P11; AltName: Full=ATP23a/ATP23b; Flags: Precursor >gi|12332216|gb|AAG51588.1|AC011665_9 peroxidase ATP23a [Arabidopsis thaliana] >gi|12324132|gb|AAG52033.1|AC011914_3 peroxidase ATP23a; 12312-13683 [Arabidopsis thaliana] >gi|1620371|emb|CAA70035.1| peroxidase ATP23a [Arabidopsis thaliana]	Unigene51053_All//3.00E-139//AT1G68850| peroxidase, putative	Unigene51053_All//0.00E+00//CO100547		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0046872	nr -
Unigene51057_All	301	2.09	4.38	3.18	7.28	9.84	8.40	6.32	19.16	11.51	1.07E+00	7.10E-02		6.10E-01	3.86E-01		4.34E-01	2.65E-01		2.07E-01	6.41E-01		1.60E+00	2.95E-11	Up	8.65E-01	2.62E-03									
Unigene51059_All	518	8.59	8.41	10.69	11.64	10.64	6.63	37.46	11.54	12.00	-2.94E-02	9.34E-01		3.16E-01	2.47E-01		-1.30E-01	6.24E-01		-8.12E-01	6.01E-04		-1.70E+00	2.68E-39	Down	-1.64E+00	1.20E-38	Down	Unigene51059_All//sp|P26360|ATPG3_IPOBA//7.00E-06//ATP synthase subunit gamma, mitochondrial OS=Ipomoea batatas GN=ATPC PE=1 SV=2	Unigene51059_All//4.00E-06//AT2G33040| ATP synthase gamma chain, mitochondrial (ATPC)	Unigene51059_All//4.00E-162//gi|18100723|gb|BM359977.1|BM359977		ko00190|Oxidative phosphorylation		swissprot -
Unigene51062_All	1025	0.82	0.30	0.52	1.94	2.22	2.03	1.57	3.75	3.93	-1.46E+00	6.69E-02		-6.53E-01	3.96E-01		1.90E-01	7.08E-01		6.02E-02	9.18E-01		1.26E+00	1.17E-05	Up	1.32E+00	1.74E-06	Up			Unigene51062_All//3.00E-16//CO123936				
Unigene51063_All	443	0.83	2.75	1.92	2.59	1.71	1.02	5.44	3.30	1.35	1.73E+00	8.94E-03		1.22E+00	1.38E-01		-5.97E-01	3.41E-01		-1.34E+00	4.01E-02		-7.20E-01	4.96E-02		-2.01E+00	5.00E-07	Down								
Unigene51065_All	732	4.50	0.28	0.36	3.47	3.29	1.42	2.89	0.63	1.52	-4.02E+00	2.27E-14	Down	-3.63E+00	1.14E-12	Down	-7.58E-02	8.43E-01		-1.29E+00	1.29E-03		-2.20E+00	1.20E-06	Down	-9.22E-01	1.54E-02		Unigene51065_All//gi|11993482|gb|AAG42759.1|AF302669_1/6.00E-23//ubiquitin-specific protease 21 [Arabidopsis thaliana]	Unigene51065_All//5.00E-22//AT5G46740| UBP21 (UBIQUITIN-SPECIFIC PROTEASE 21); ubiquitin thiolesterase/ ubiquitin-specific protease	Unigene51065_All//0.00E+00//gi|78338058|gb|DT558332.1|DT558332		ko04144|Endocytosis	GO:0008234	nr -
Unigene51068_All	1183	0.13	1.41	1.76	0.42	1.31	0.80	0.93	1.17	2.83	3.41E+00	1.20E-06	Up	3.73E+00	2.46E-08	Up	1.64E+00	3.03E-03		9.29E-01	2.19E-01		3.27E-01	5.53E-01		1.61E+00	4.45E-07	Up	Unigene51068_All//gi|297613455|ref|NP_001067177.2|//1.00E-32//Os12g0594200 [Oryza sativa Japonica Group] >gi|255670445|dbj|BAF30196.2| Os12g0594200 [Oryza sativa Japonica Group]	Unigene51068_All//1.00E-90//AT3G50380| INVOLVED IN: protein localization; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Vacuolar protein sorting-associated protein (InterPro:IPR009543); Has 239 Blast hits to 235 proteins in 73 species: Archae - 0; Bacteria - 0; Metazoa - 130; Fungi - 71; Plants - 23; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BLink).					nr -
Unigene51069_All	339	12.81	4.78	12.10	10.87	10.97	3.46	0.12	0.00	0.00	-1.42E+00	3.52E-06	Down	-8.29E-02	7.83E-01		1.28E-02	9.79E-01		-1.65E+00	8.22E-07	Down	-6.96E+00	6.56E-01		-6.96E+00	6.12E-01				Unigene51069_All//4.00E-07//EX167696				
Unigene5107_All	805	2.79	0.94	2.45	1.61	1.93	1.23	5.46	2.54	2.47	-1.57E+00	5.19E-04	Down	-1.91E-01	6.53E-01		2.59E-01	6.64E-01		-3.82E-01	5.50E-01		-1.10E+00	2.58E-05	Down	-1.14E+00	8.51E-06	Down			Unigene5107_All//1.00E-62//gi|48808713|gb|CO110027.1|CO110027				
Unigene51072_All	767	5.32	8.13	11.80	0.39	2.74	0.71	0.00	0.00	0.00	6.11E-01	9.93E-03		1.15E+00	1.82E-08	Up	2.81E+00	1.37E-07	Up	8.59E-01	4.23E-01		null	null		null	null				Unigene51072_All//4.00E-12//TC172737				
Unigene51073_All	837	0.38	0.36	1.15	1.19	2.10	0.65	6.06	12.38	15.71	-4.65E-02	9.84E-01		1.61E+00	4.07E-02		8.18E-01	1.03E-01		-8.78E-01	2.20E-01		1.03E+00	2.50E-10	Up	1.37E+00	2.63E-20	Up	Unigene51073_All//gi|28372862|gb|AA039913.1|//4.00E-13//At1g35210 [Arabidopsis thaliana]	Unigene51073_All//1.00E-07//AT1G22470| unknown protein	Unigene51073_All//0.00E+00//gi|73859933|gb|DT462672.1|DT462672				nr +

Unigene51074_All	679	4.08	1.27	1.73	4.26	3.04	1.86	1.81	0.25	0.70	-1.69E+00	3.37E-05	Down	-1.24E+00	2.08E-03		-4.84E-01	1.90E-01		-1.19E+00	1.24E-03		-2.87E+00	2.54E-05	Down	-1.36E+00	1.18E-02		Unigene51074_All//gi|186499332|ref|NP_178535.2|//8.00E-48//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene51074_All//2.00E-46//AT2G04560| transferase, transferring glycosyl groups				GO:0008194//GO:0008654//GO:0043231	nr +
Unigene51075_All	657	79.64	38.48	127.33	8.87	8.75	32.17	0.00	0.00	0.00	-1.05E+00	3.25E-41	Down	6.77E-01	2.69E-30		-1.93E-02	9.49E-01		1.86E+00	5.05E-42	Up	null	null		null	null		Unigene51075_All//gi|224077538|ref|XP_002365292.1|//4.00E-61//cytochrome P450 [Populus trichocarpa] >gi|222848256|gb|EEE85803.1| cytochrome P450 [Populus trichocarpa]	Unigene51075_All//2.00E-48//AT3G25180| CYP82G1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene51075_All//4.00E-129//gi|48827535|gb|CO125925.1|CO125925		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0008152//GO:0016709	nr +
Unigene51076_All	591	22.04	12.86	4.42	3.88	5.42	15.28	0.14	0.00	0.00	-7.77E-01	7.28E-07		-2.32E+00	2.93E-31	Down	4.83E-01	1.80E-01		1.98E+00	9.34E-20	Up	-7.16E+00	4.03E-01		-7.16E+00	3.58E-01		Unigene51076_All//gi|201490466|gb|AM12778.1|//6.00E-22//auxin-induced SAUR-like protein [Capsicum annuum]	Unigene51076_All//4.00E-22//AT4G38840| auxin-responsive protein, putative	Unigene51076_All//1.00E-150//DW512758			GO:0006950//GO:0009755//GO:0016020	nr +
Unigene51079_All	333	94.74	27.54	43.66	117.43	113.34	108.91	313.86	128.15	121.31	-1.78E+00	1.69E-55	Down	-1.12E+00	9.96E-27	Down	-5.12E-02	6.20E-01		-1.09E-01	2.84E-01		-1.29E+00	5.61E-139	Down	-1.37E+00	1.43E-156	Down	Unigene51079_All//gi|257219572|gb|ACN50439.1|//8.00E-59//ribosomal protein L15 [Jatropha curcas]	Unigene51079_All//8.00E-43//AT4G16720| 60S ribosomal protein L15 (RPL15A)	Unigene51079_All//0.00E+00//TC175481		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene51088_All	212	43.19	39.91	18.59	199.26	150.90	193.86	129.03	64.47	87.95	-1.14E-01	6.08E-01		-1.22E+00	2.85E-09	Down	-4.01E-01	8.97E-08		-3.96E-02	6.82E-01		-1.00E+00	8.70E-25	Down	-5.53E-01	1.11E-09		Unigene51088_All//gi|211906438|gb|ACJ11712.1|//3.00E-34//UDP-D-glucose dehydrogenase [Gossypium hirsutum]	Unigene51088_All//1.00E-31//AT3G29360| UDP-glucose 6-dehydrogenase, putative	Unigene51088_All//1.00E-116//EX167174		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions	GO:0000166//GO:0008152//GO:0016616//GO:0031410	nr +
Unigene51089_All	374	4.90	0.95	3.27	1.73	1.93	1.21	2.94	1.23	1.92	-2.37E+00	2.79E-05	Down	-5.80E-01	2.47E-01		1.59E-01	8.68E-01		-5.20E-01	5.88E-01		-1.26E+00	3.46E-02		-6.16E-01	2.73E-01		Unigene51089_All//gi|145359623|ref|NP_201203.2|//2.00E-20//SAL1; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase [Arabidopsis thaliana]	Unigene51089_All//1.00E-14//AT5G63980| SAL1; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase	Unigene51089_All//2.00E-157//CO072468		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism	GO:0008252//GO:0009536//GO:0044237	nr +
Unigene51090_All	345	4.40	9.69	5.25	10.40	7.79	6.15	4.41	6.91	5.66	1.14E+00	9.68E-04	Up	2.55E-01	6.40E-01		-4.17E-01	2.08E-01		-7.57E-01	1.94E-02		6.46E-01	8.21E-02		3.59E-01	3.89E-01					Unigene51090_All//3.00E-63//TC153496				
Unigene51091_All	595	0.00	0.00	0.00	6.70	6.13	5.69	3.48	0.84	0.67	null	null		null	null		-1.27E-01	7.23E-01		-2.35E-01	4.95E-01		-2.05E+00	5.01E-06	Down	-2.38E+00	2.25E-07	Down	Unigene51091_All//gi|75210732|sp|Q9SV72.1|EPF1_ARATH//1.00E-24//RecName: Full=EPIDERMAL PATTERNING FACTOR-like protein 9; Short=EPF-like protein 9; Flags: Precursor	Unigene51091_All//6.00E-26//AT4G12970| unknown protein	Unigene51091_All//1.00E-57//TC171862			GO:0031410	nr -
Unigene51092_All	319	2.13	5.88	4.34	4.68	11.55	5.10	1.72	1.70	0.75	1.46E+00	3.30E-03		1.03E+00	8.63E-02		1.30E+00	3.68E-05	Up	1.22E-01	8.26E-01		-1.66E-02	1.02E+00		-1.20E+00	1.64E-01					Unigene51092_All//4.00E-07//TC165049				
Unigene51093_All	522	6.01	4.08	8.77	2.29	0.99	1.47	0.24	0.32	1.91	-5.61E-01	1.13E-01		5.45E-01	6.70E-02		-1.21E-00	4.17E-02		-6.39E-01	3.24E-01		3.99E-01	8.14E-01		2.97E+00	1.11E-04	Up							
Unigene51094_All	263	0.00	3.85	0.00	0.00	1.05	1.03	0.00	0.64	0.30	1.19E+01	7.25E-06	Up	null	null		1.00E+01	7.01E-02		1.00E+01	7.02E-02		9.31E+00	1.39E-01		8.24E+00	4.03E-01		Unigene51094_All//gi|222822566|gb|ACM68432.1|//3.00E-25//xyloglucanase-specific endoglucanase inhibitor protein [Petunia x hybrida]	Unigene51094_All//7.00E-22//AT1G03220| extracellular dermal glycoprotein, putative / EDGP, putative	Unigene51094_All//4.00E-102//gi|73859191|gb|DT461930.1|DT461930			GO:0004175//GO:0005618//GO:0006970//GO:0016020//GO:0019538	nr +
Unigene51095_All	942	0.00	5.81	0.45	0.05	0.55	0.77	0.27	2.04	1.31	1.25E+01	3.24E-31	Up	8.82E+00	1.38E-02		3.37E+00	1.82E-02		3.86E+00	1.75E-03		2.92E+00	4.49E-08	Up	2.28E+00	1.88E-04	Up	Unigene51095_All//gi|62362434|gb|AA81888.1|//1.00E-98//nectarin IV [Nicotiana langsdorffii x Nicotiana sanderae]	Unigene51095_All//2.00E-86//AT1G03220| extracellular dermal glycoprotein, putative / EDGP, putative	Unigene51095_All//0.00E+00//TC130390			GO:0004175//GO:0005618//GO:0006970//GO:0016020//GO:0019538	nr -
Unigene51096_All	350	7.32	4.92	4.87	217.76	160.47	156.01	151.24	323.86	67.27	-5.74E-01	1.45E-01		-5.89E-01	1.54E-01		-4.40E-01	4.18E-16		-4.81E-01	6.42E-17		1.10E+00	2.27E-116	Up	-1.17E+00	3.09E-62	Down	Unigene51096_All//gi|224134158|ref|XP_002327770.1|//9.00E-29//cytochrome P450 5-hydroxylase for coniferaldehyde, coniferyl alcohol and ferulic acid [Populus trichocarpa] >gi|222836855|gb|EEE75248.1| cytochrome P450 5-hydroxylase for coniferaldehyde, coniferyl alcohol and ferulic acid [Populus trichocarpa]	Unigene51096_All//2.00E-29//AT4G36220| FAH1 (FERULIC ACID 5-HYDROXYLASE 1); ferulate 5-hydroxylase/ monooxygenase	Unigene51096_All//2.00E-135//DW225229		ko00940|Phenylpropanoid biosynthesis//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506//GO:0006631//GO:0009411//GO:0009699//GO:0012501//GO:0043231	nr +
Unigene51097_All	535	81.95	127.76	95.25	22.44	34.56	7.01	4.90	9.77	3.95	6.41E-01	2.19E-23		2.17E-01	6.26E-03		6.23E-01	1.99E-07		-1.68E+00	2.23E-21	Down	9.95E-01	2.47E-05		-3.12E-01	3.78E-01		Unigene51097_All//gi|257219564|gb|ACN50435.1|//1.00E-42//Al-induced protein [Jatropha curcas]	Unigene51097_All//4.00E-41//AT5G19140| AILP1	Unigene51097_All//0.00E+00//TC155850			GO:0009725//GO:0010038//GO:0016020	nr +
Unigene51098_All	368	7.39	2.20	8.68	4.47	5.43	3.19	0.80	0.68	0.87	-1.75E+00	2.50E-05	Down	2.32E-01	5.45E-01		2.81E-01	5.83E-01		-4.85E-01	3.82E-01		-2.39E-01	8.39E-01		1.07E-01	9.45E-01								
Unigene511_All	2496	23.75	10.45	24.90	6.39	6.15	4.00	2.39	1.57	1.25	-1.18E+00	1.70E-56	Down	6.81E-02	3.83E-01		-5.37E-02	7.79E-01		-6.75E-01	6.39E-07		-6.02E-01	5.43E-03		-9.40E-01	9.96E-06		Unigene511_All//gi|157169069|gb|ABV25894.1|//0.00E+00//starch synthase isoform II [Manihot esculenta]	Unigene511_All//0.00E+00//AT3G01180| AtSS2 (starch synthase 2); transferase, transferring glycosyl groups	Unigene511_All//0.00E+00//TC136757		ko00500|Starch and sucrose metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0046527	nr -
Unigene5110_All	1723	0.91	4.03	1.82	7.26	10.25	24.59	7.29	25.45	23.01	2.14E+00	5.77E-16	Up	1.00E+00	6.62E-03		4.99E-01	5.84E-05		1.76E+00	7.09E-78	Up	1.80E+00	3.00E-95	Up	1.66E+00	2.94E-78	Up	Unigene5110_All//gi|115488208|ref|NP_001066591.1|//2.00E-85//Os12g0288000 [Oryza sativa Japonica Group] >gi|77554969|gb|AB497765.1| Integral membrane protein DUF6 containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113649098|dbj|BAF29610.1| Os12g0288000 [Oryza sativa Japonica Group]	Unigene5110_All//5.00E-58//AT5G64700| nodulin MtN21 family protein	Unigene5110_All//0.00E+00//TC168758				nr +
Unigene51100_All	300	123.48	129.71	91.77	199.59	148.30	195.71	248.61	125.25	92.82	7.11E-02	4.76E-01		-4.28E-01	2.24E-06		-4.29E-01	3.86E-12		-2.83E-02	7.31E-01		-9.89E-01	6.77E-65		-1.42E+00	3.70E-118	Down	Unigene51100_All//gi|115476070|ref|NP_001061631.1|//4.00E-12//Os08g0359500 [Oryza sativa Japonica Group] >gi|75132349|sp|Q6YYB0.1|Y8359_ORYSJ RecName: Full=Uncharacterized protein Os08g0359500 >gi|113623600|dbj|BAF23545.1| Os08g0359500 [Oryza sativa Japonica Group]		Unigene51100_All//3.00E-103//gi|21090292|gb|BQ402605.1|BQ402605			GO:0016020	nr +
Unigene51101_All	778	1.75	0.46	0.68	1.09	1.86	0.75	2.61	1.45	0.67	-1.94E+00	2.18E-03		-1.35E+00	2.93E-02		7.72E-01	1.76E-01		-5.28E-01	5.02E-01		-8.47E-01	3.68E-02		-1.97E+00	6.60E-06	Down	Unigene51101_All//gi|15239462|ref|NP_200894.1|//1.00E-103//AtRABA1f (Arabidopsis Rab GTPase homolog A1f); GTP binding [Arabidopsis thaliana] >gi|10176913|dbj|BAB10106.1| GTP-binding protein, ras-like [Arabidopsis thaliana] >gi|28950757|gb|AAO63302.1| At5g60860 [Arabidopsis thaliana]	Unigene51101_All//3.00E-104//AT5G60860| AtRABA1f (Arabidopsis Rab GTPase homolog A1f); GTP binding	Unigene51101_All//0.00E+00//gi|48796583|gb|CO097897.1|CO097897			GO:0006810//GO:0032561//GO:0035556	nr +
Unigene51103_All	552	3.79	26.80	9.26	242.30	173.17	102.44	1905.75	1577.03	1748.71	2.82E+00	1.54E-45	Up	1.29E+00	6.11E-06	Up	-4.85E-01	2.66E-33		-1.24E+00	1.87E-148	Down	-2.73E-01	3.80E-89		-1.24E-01	1.41E-20		Unigene51103_All//gi|15232384|ref|NP_190966.1|//1.00E-64//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|30693968|ref|NP_850700.1| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|30102818|gb|AAF21327.1| At3g53980 [Arabidopsis thaliana]	Unigene51103_All//2.00E-39//AT3G53980| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene51103_All//0.00E+00//gi|48744779|gb|CO075298.1|CO075298			GO:0005488//GO:0006810//GO:0016787//GO:0044464	nr +
Unigene51104_All	284	0.74	1.78	3.38	1.93	1.33	3.50	0.60	2.80	4.35	1.28E+00	2.31E-01		2.20E+00	9.10E-03		-5.33E-01	5.85E-01		8.59E-01	2.35E-01		2.23E+00	5.75E-03		2.87E+00	1.78E-05	Up							
Unigene51109_All	384	94.70	197.00	153.79	85.36	81.43	91.15	159.54	191.78	81.23	1.06E+00	9.19E-60	Up	7.00E-01	8.71E-23		-6.81E-02	5.64E-01		9.47E-02	3.87E-01		2.66E-01	1.09E-06		-9.74E-01	1.38E-53		Unigene51109_All//gi|15241720|ref|NP_195843.1|//3.00E-29//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|30679562|ref|NP_850754.1| haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana] >gi|10773842 6|gb|ABF83695.1| At5g02230 [Arabidopsis thaliana]	Unigene51109_All//1.00E-30//AT5G02230| haloacid dehalogenase-like hydrolase family protein	Unigene51109_All//0.00E+00//gi|73861721|gb|DT464460.1|DT464460			GO:0003824	nr +
Unigene51112_All	503	2.81	0.91	0.42	5.35	2.74	3.59	1.93	3.32	8.95	-1.63E+00	6.15E-03		-2.73E+00	1.56E-04	Down	-9.66E-01	7.63E-03		-5.74E-01	1.45E-01		7.82E-01	8.76E-02		2.21E+00	1.06E-13	Up	Unigene51112_All//gi|301557932|gb|ADK78986.1|//4.00E-27//VAMP721 [Petunia integrifolia subsp. inflata]	Unigene51112_All//2.00E-27//AT1G04760| ATVAMP726	Unigene51112_All//0.00E+00//gi|109872072|gb|DW501048.1|DW501048		ko04130|SNARE interactions in vesicular transport	GO:0006810//GO:0031224	nr +
Unigene51113_All	1285	0.20	0.79	0.41	1.05	0.75	0.95	0.99	3.22	5.36	1.95E+00	1.01E-02		1.03E+00	3.42E-01		-4.80E-01	4.15E-01		-1.41E-01	8.01E-01		1.71E+00	5.27E-09	Up	2.44E+00	4.62E-23	Up	Unigene51113_All//gi|15226168|ref|NP_178215.1|//9.00E-07//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene51113_All//1.00E-07//AT2G01050| nucleic acid binding / zinc ion binding	Unigene51113_All//0.00E+00//TC139187				nr -
Unigene51117_All	445	0.82	0.00	1.44	3.81	1.55	1.12	3.71	0.85	1.88	-9.68E+00	1.96E-02		8.03E-01	3.88E-01		-1.30E+00	7.01E-03		-1.77E+00	9.00E-04	Down	-2.13E+00	3.64E-05	Down	-9.79E-01	2.63E-02		Unigene51117_All//gi|297837269|ref|XP_002886516.1|//9.00E-40//b binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297332357|gb|EFH62775.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene51117_All//4.00E-15//AT1G61690| phosphoinositide binding	Unigene51117_All//2.00E-09//gi|13353658|gb|BG444006.1|BG444006			GO:0005543//GO:0009314//GO:0046872//GO:0060089	nr +
Unigene51118_All	328	8.29	6.64	10.39	11.09	9.87	10.74	65.22	49.19	19.07	-3.21E-01	4.00E-01		3.25E-01	3.81E-01		-1.68E-01	6.22E-01		-4.58E-02	9.07E-01		-4.07E-01	1.22E-04		-1.77E+00	2.59E-47	Down				Unigene51118_All//6.00E-151//gi|5048984|gb|AI730132.1|AI730132				
Unigene51119_All	577	1.00	0.44	1.75	6.13	3.64	2.19	2.13	1.81	2.14	-1.18E+00	2.26E-01		8.14E-01	2.51E-01		-7.52E-01	1.53E-02		-1.48E+00	1.02E-05	Down	-2.31E-01	6.74E-01		1.04E-02	9.84E-01					Unigene51119_All//1.00E-63//CO104979				
Unigene5112_All	1225	1.45	2.07	1.61	4.80	6.44	4.28	1.55	1.06	5.66	5.10E-01	2.09E-01		1.47E-01	7.47E-01		4.24E-01	4.09E-02		-1.66E-01	5.67E-01		-5.54E-01	2.00E-01		1.87E+00	9.21E-17	Up	Unigene5112_All//gi|119657126|gb|AB486687.1|//1.00E-135//TLP1 [Gossypium barbadense]	Unigene5112_All//2.00E-88//AT1G75030| ATLP-3	Unigene5112_All//0.00E+00//TC149853				nr +
Unigene51121_All	365	10.32	4.58	5.54	5.32	4.72	4.70	1.62	0.34	0.33	-1.17E+00	2.82E-04	Down	-8.97E-01	6.74E-03		-1.74E-01	7.37E-01		-1.79E-01	7.02E-01		-2.24E+00	2.07E-02		-2.31E+00	1.36E-02					Unigene51121_All//2.00E-18//gi|13245058|gb|BE055658.2|BE055658				
Unigene51122_All	1047	0.85	1.45	1.58	1.67	1.15	1.38	3.88	5.23	8.30	7.73E-01	1.48E-01		8.92E-01	9.62E-02		-5.33E-01	2.92E-01		-2.71E-01	6.38E-01		4.32E-01	6.40E-02		1.10E+00	6.62E-10	Up	Unigene51122_All//gi|158828302|gb|ABW81177.1|//4.00E-07//gag non-LTR retrotransposase [Arabidopsis cebennensis]	Unigene51122_All//1.00E-07//AT2G01050| nucleic acid binding / zinc ion binding	Unigene51122_All//0.00E+00//BG441884				nr +
Unigene51126_All	395	117.62	38.23	36.94	148.06	122.66	182.94	190.10	108.35	101.87	-1.62E+00	2.71E-71	Down	-1.67E+00	7.36E-72	Down	-2.72E-01	2.46E-05		3.05E-01	3.26E-07		-8.11E-01	5.95E-47		-9.00E-01	1.74E-57		Unigene51126_All//gi|81074037|gb|AB855361.1|//4.00E-61//40S ribosomal protein S10-like [Solanum tuberosum] >gi|82400160|gb|ABB72819.1| 40S ribosomal protein S10-like protein [Solanum tuberosum]	Unigene51126_All//5.00E-25//AT5G41520| 40S ribosomal protein S10 (RPS10B)	Unigene51126_All//0.00E+00//gi|13353303|gb|BG443651.1|BG443651		ko03010|Ribosome	GO:0009536//GO:0010467//GO:0015935//GO:0030312	nr -
Unigene51129_All	506	27.19	63.59	51.99	51.00	93.98	107.02	40.61	12.97	319.02	1.23E+00	1.56E-32	Up	9.35E-01	7.35E-17		8.82E-01	3.60E-33		1.07E+00	5.79E-47	Up	-1.65E+00	8.62E-40	Down	2.97E+00	0.00E+00	Up	Unigene51129_All//gi|225451968|ref|XP_002279750.1|//2.00E-24//PREDICTED: similar to mangrin [Vitis vinifera]	Unigene51129_All//6.00E-09//AT3G25780| AOC3 (ALLENE OXIDE CYCLASE 3); allene-oxide cyclase	Unigene51129_All//0.00E+00//gi|78329940|gb|DT550214.1|DT550214		ko00592|alpha-Linolenic acid metabolism	GO:0003824//GO:0009536	nr +
Unigene51130_All	517	3.44	0.88	3.81	5.78	10.92	8.04	0.16	0.32	1.08	-1.96E+00	2.97E-04	Down	1.47E-01	7.47E-01		9.18E-01	1.27E-04		4.75E-01	1.29E-01		9.83E-01	6.33E-01		2.72E+00	9.38E-03								
Unigene51132_All	407	0.00	0.00	0.00	1.10	3.98	1.55	4.57	0.62	6.66	null	null		null	null		1.85E+00	7.37E-04	Up	4.96E-01	6.37E-01		-2.89E+00	8.75E-08	Down	5.42E-01	1.05E-01		Unigene51132_All//gi|164564727|dbj|BAF98210.1|//3.00E-19//CM0216.210.nc [Lotus japonicus]	Unigene51132_All//6.00E-12//AT2G17080| unknown protein					nr +

Unigene51133_All	1366	0.00	0.00	0.00	0.33	0.38	0.23	5.05	1.38	16.74	null	null		null	null		2.04E-01	8.59E-01			-5.04E-01	6.49E-01			-1.87E+00	2.02E-16	Down	1.73E+00	2.97E-48	Up	Unigene51133_All//gi|164564729|dbj|BAF98211.1|//1.00E-59//CM0216.240.nc [Lotus japonicus]	Unigene51133_All//6.00E-48//AT2G17080| unknown protein					nr -
Unigene51138_All	237	1.99	8.34	6.07	9.88	7.85	6.86	3.39	2.12	2.86	2.07E+00	7.23E-05	Up	1.61E+00	8.67E-03		-3.32E-01	4.57E-01			-5.26E-01	2.28E-01			-6.80E-01	3.53E-01		-2.46E-01	7.00E-01					Unigene51138_All//3.00E-22//TC167101					
Unigene5114_All	607	23.79	33.64	21.76	30.77	31.32	32.66	88.18	66.31	42.00	5.00E-01	3.92E-05		-1.29E-01	4.44E-01		2.51E-02	8.77E-01			8.59E-02	5.94E-01			-4.11E-01	1.51E-10		-1.07E+00	1.15E-54	Down	Unigene5114_All//gi|3219353|gb|AAC78469.1|//4.00E-89//manganese superoxide dismutase [Gossypium hirsutum]	Unigene5114_All//1.00E-42//AT3G10920| MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); metal ion binding / superoxide dismutase	Unigene5114_All//0.00E+00//gi|21097600|gb|BQ409913.1|BQ409913		ko04146|Peroxisome		nr -
Unigene51141_All	386	15.45	2.36	24.97	7.87	6.42	5.97	1.42	1.30	1.14	-2.71E+00	4.30E-18	Down	6.92E-01	3.01E-04		-2.94E-01	4.48E-01			-4.00E-01	3.02E-01			-1.32E-01	8.80E-01		-3.27E-01	6.72E-01					Unigene51141_All//0.00E+00//TC134799					
Unigene51142_All	318	79.14	66.28	47.72	115.29	92.59	138.61	176.43	87.67	54.37	-2.56E-01	2.26E-02		-7.30E-01	8.91E-11		-3.17E-01	1.39E-04			2.66E-01	9.17E-04			-1.01E+00	1.24E-50	Down	-1.70E+00	1.83E-115	Down	Unigene51142_All//gi|87240356|gb|ABD32214.1|//5.00E-53//Ribosomal protein L34e [Medicago truncatula] >gi|124360947|gb|ABN08919.1| Ribosomal protein L34e [Medicago truncatula]	Unigene51142_All//1.00E-53//AT1G26880| 60S ribosomal protein L34 (RPL34A)	Unigene51142_All//1.00E-179//TC149703		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0031981	nr -
Unigene51143_All	1373	0.11	0.30	0.16	1.60	0.70	1.18	3.14	6.45	1.97	1.37E+00	2.74E-01		4.40E-01	7.75E-01		-1.18E+00	3.86E-03			-4.31E-01	3.56E-01			1.04E+00	4.71E-09	Up	-6.71E-01	7.59E-03		Unigene51143_All//gi|124360145|gb|ABN08161.1|//1.00E-156//C2; von Willebrand factor, type A; Copine [Medicago truncatula]	Unigene51143_All//9.00E-146//AT4G08860| BON3 (BONZAI 3); calcium-dependent phospholipid binding	Unigene51143_All//0.00E+00//ES840226				nr +
Unigene51144_All	915	0.74	1.11	2.68	5.72	1.77	5.82	2.86	2.51	5.70	5.75E-01	3.83E-01		1.85E+00	6.30E-05	Up	-1.69E+00	5.55E-11	Down		2.70E-02	9.44E-01			-1.90E-01	6.51E-01		9.93E-01	1.73E-05		Unigene51144_All//gi|15221343|ref|NP_176996.1|//1.00E-119//ENDO 2 (endonuclease 2); T/G mismatch-specific endonuclease/ endonuclease/ nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease [Arabidopsis thaliana]	Unigene51144_All//2.00E-120//AT1G68290| ENDO 2 (endonuclease 2); T/G mismatch-specific endonuclease/ endonuclease/ nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease	Unigene51144_All//7.00E-150//C0106650			GO:0016788	nr +
Unigene51145_All	1548	13.08	3.83	5.26	0.32	0.60	0.00	0.00	0.00	0.00	-1.77E+00	1.46E-35	Down	-1.31E+00	3.33E-22	Down	9.00E-01	2.35E-01			-8.33E+00	2.97E-03			null	null		null	null		Unigene51145_All//gi|297817938|ref|XP_002876852.1|//2.00E-34//phytochrome kinase substrate 1 [Arabidopsis lyrata subsp. lyrata] >gi|297322690|gb|EFH53111.1| phytochrome kinase substrate 1 [Arabidopsis lyrata subsp. lyrata]	Unigene51145_All//3.00E-36//AT2G02950| PKS1 (PHYTOCHROME KINASE SUBSTRATE 1); protein binding	Unigene51145_All//2.00E-18//TC174616			GO:0009605//GO:0009639//GO:0032501	nr -
Unigene51147_All	536	3.51	2.84	3.38	7.25	6.36	3.54	5.76	5.46	6.54	-3.09E-01	5.23E-01		-5.71E-02	9.13E-01		-1.89E-01	5.83E-01			-1.03E+00	7.71E-04	Down	-7.72E-02	8.20E-01		1.84E-01	5.68E-01					Unigene51147_All//8.00E-96//ES842131					
Unigene51149_All	1496	0.24	0.07	0.64	11.22	13.10	5.07	0.25	0.03	0.35	-1.85E+00	1.87E-01		1.39E+00	7.11E-02		2.23E-01	8.79E-02			-1.15E+00	7.92E-17	Down	-3.19E+00	3.11E-02		4.45E-01	6.12E-01		Unigene51149_All//gi|61651585|dbj|BAD91162.1|//1.00E-158//gibberellin 3-beta hydroxylase [Prunus subhirtella]	Unigene51149_All//1.00E-116//AT1G80340| GA3OX2 (GIBBERELLIN 3-OXIDASE 2); gibberellin 3-beta-dioxygenase	Unigene51149_All//0.00E+00//DW235240		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene5115_All	684	1.22	35.56	2.18	5.61	8.36	16.77	0.37	6.23	1.92	4.86E+00	2.39E-115	Up	8.33E-01	1.43E-01		5.76E-01	1.82E-02			1.58E+00	1.89E-18	Up	4.07E+00	1.36E-22	Up	2.37E+00	7.20E-05	Up	Unigene5115_All//gi|27728729|gb|AA018638.1|//6.00E-30//cystatin [Malus x domestica]	Unigene5115_All//5.00E-18//AT2G31980| cysteine proteinase inhibitor-related	Unigene5115_All//0.00E+00//TC172594				nr -
Unigene51153_All	369	2.69	1.51	1.73	3.11	2.71	3.43	2.98	0.34	3.13	-8.35E-01	2.26E-01		-6.38E-01	3.90E-01		-1.98E-01	7.77E-01			1.42E-01	8.21E-01			-3.13E+00	3.47E-05	Down	7.17E-02	9.11E-01		Unigene51153_All//gi|37201986|gb|AAQ89668.1|//8.00E-68//At5g26910 [Arabidopsis thaliana]	Unigene51153_All//4.00E-10//AT3G58650| unknown protein	Unigene51153_All//3.00E-39//TC164831			GO:0016020//GO:0043231	nr +
Unigene51154_All	532	9.34	3.24	14.91	8.05	6.80	3.57	0.08	0.00	0.00	-1.53E+00	1.17E-07	Down	6.75E-01	1.61E-03		-2.45E-01	4.51E-01			-1.18E+00	5.99E-05	Down	-6.31E+00	6.56E-01		-6.31E+00	6.12E-01					Unigene51154_All//6.00E-07//EX167696					
Unigene51156_All	346	23.14	48.62	26.93	50.68	56.43	58.74	30.67	42.40	50.66	1.07E+00	3.73E-14	Up	2.19E-01	3.03E-01		1.55E-01	2.80E-01			2.13E-01	1.10E-01			4.67E-01	3.40E-04		7.24E-01	6.18E-10		Unigene51156_All//gi|50916616|gb|AAD39604.1|AC007454_3//5.00E-48//F23H19.3 [Arabidopsis thaliana]	Unigene51156_All//2.00E-49//AT1G34320| unknown protein	Unigene51156_All//3.00E-180//TC175353				nr -
Unigene51157_All	540	4.55	1.13	3.55	14.11	13.90	4.35	1.17	0.62	0.44	-2.02E+00	9.41E-06	Down	-3.59E-01	3.90E-01		-2.19E-02	9.29E-01			-1.70E+00	5.57E-14	Down	-9.23E-01	2.63E-01		-1.41E+00	7.94E-02		Unigene51157_All//gi|297835194|ref|XP_002885479.1|//6.00E-30//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297331319|gb|EFH61738.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	Unigene51157_All//7.00E-06//AT3G22070| proline-rich family protein			ko03040|Spliceosome	GO:0005488//GO:0044464	nr +
Unigene51159_All	403	24.02	61.36	30.92	35.35	37.26	41.24	56.76	96.35	116.95	1.35E+00	3.18E-29	Up	3.64E-01	3.27E-02		7.56E-02	6.76E-01			2.22E-01	1.35E-01			7.63E-01	2.76E-22		1.04E+00	5.67E-46	Up	Unigene51159_All//gi|297845328|ref|XP_002890545.1|//1.00E-44//T-complex protein 11 [Arabidopsis lyrata subsp. lyrata] >gi|297336387|gb|EFH66804.1| T-complex protein 11 [Arabidopsis lyrata subsp. lyrata]	Unigene51159_All//8.00E-46//AT1G22930| T-complex protein 11	Unigene51159_All//0.00E+00//DR463179			GO:0003676	nr +
Unigene5116_All	881	1.90	1.61	4.71	1.64	0.90	0.97	2.98	2.70	0.45	-2.39E-01	6.10E-01		1.31E+00	4.48E-05	Up	-8.67E-01	1.04E-01			-7.51E-01	1.90E-01			-1.38E-01	7.14E-01		-2.72E+00	1.79E-10	Down				Unigene5116_All//7.00E-79//ES799115					
Unigene51161_All	582	62.30	76.09	53.16	107.85	127.39	117.18	115.51	70.16	47.57	2.89E-01	3.44E-04		-2.29E-01	1.72E-02		2.40E-01	2.77E-05			1.20E-01	8.92E-02			-7.19E-01	2.39E-34		-1.28E+00	8.01E-91	Down	Unigene51161_All//gi|186478886|ref|NP_001117356.1|//4.00E-23//SP1L1 (SPIRALI-LIKE1) [Arabidopsis thaliana]	Unigene51161_All//2.00E-24//AT1G26355| SP1L1 (SPIRALI-LIKE1)	Unigene51161_All//0.00E+00//TC160381				nr -
Unigene51162_All	1188	0.00	0.00	0.00	1.30	0.38	0.19	7.79	2.99	1.37	null	null		null	null		-1.79E+00	6.85E-04	Down		-2.77E+00	1.51E-05	Down	-1.38E+00	2.37E-14	Down	-2.50E+00	4.44E-32	Down	Unigene51162_All//gi|79521554|ref|NP_197973.2|//8.00E-92//catalytic/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|226739226|sp|Q9XGZ9.2|PC72_ARATH RecName: Full=Probable protein phosphatase 2C 72; Short=AtPP2C72	Unigene51162_All//3.00E-90//AT5G26010| catalytic/ protein serine/threonine phosphatase	Unigene51162_All//0.00E+00//ES842729				nr +
Unigene51163_All	439	1.19	0.58	0.97	1.70	2.35	1.75	2.22	0.95	0.09	-1.05E+00	3.11E-01		-2.97E-01	7.50E-01		4.67E-01	5.51E-01			3.91E-02	9.59E-01			-1.22E+00	5.68E-02		-4.61E+00	3.32E-06	Down				Unigene51163_All//1.00E-07//ES807065					
Unigene51164_All	388	19.55	759.00	105.68	75.75	127.45	646.95	176.64	827.62	736.60	5.28E+00	0.00E+00	Up	2.43E+00	5.40E-104	Up	7.51E-01	2.84E-26			3.09E+00	0.00E+00	Up	2.23E+00	0.00E+00	Up	2.06E+00	0.00E+00	Up				Unigene51164_All//4.00E-143//TC173273					
Unigene51165_All	464	2.93	2.40	7.69	4.08	6.09	3.21	1.82	0.00	2.58	-2.87E-01	6.02E-01		1.39E+00	8.19E-05	Up	5.77E-01	1.32E-01			-3.45E-01	4.99E-01			-1.08E+01	4.39E-06	Down	4.99E-01	3.58E-01		Unigene51165_All//3.00E-57//AT1G01900| SBT11.1; serine-type endopeptidase [Arabidopsis thaliana]	Unigene51165_All//5.00E-12//AT1G01900| SBT11.1; serine-type endopeptidase	Unigene51165_All//2.00E-123//TC153075			GO:0008152//GO:0016787//GO:0030312//GO:0044421	nr +
Unigene51166_All	628	3.50	2.74	2.63	0.63	0.16	0.86	4.58	2.73	2.03	-3.51E-01	4.14E-01		-4.13E-01	3.82E-01		-1.95E+00	1.19E-01			4.44E-01	6.78E-01			-7.47E-01	2.35E-02		-1.17E+00	3.14E-04	Down	Unigene51166_All//gi|195636804|gb|AGG37870.1|//2.00E-59//choline/ethanolamine kinase [Zea mays]	Unigene51166_All//3.00E-57//AT2G26830| emb1187 (embryo defective 1187); kinase/ phosphotransferase, alcohol group as acceptor	Unigene51166_All//1.00E-91//TC154301		ko00564|Glycerophospholipid metabolism	GO:0003006//GO:0016301//GO:0016757	nr +
Unigene51167_All	480	391.97	185.47	361.55	76.59	93.76	50.62	0.88	0.35	0.66	-1.08E+00	1.69E-153	Down	-1.17E-01	3.83E-03		2.92E-01	1.02E-04			-5.97E-01	2.89E-12			-1.34E+00	2.24E-01		-4.08E-01	6.54E-01		Unigene51167_All//gi|251831338|gb|ACT21568.1|//7.00E-13//glyceraldehyde-3-phosphate dehydrogenase [Bruguiera gymnorhiza]	Unigene51167_All//1.00E-06//AT1G12900| GAPA-2 (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT 2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene51167_All//1.00E-106//TC160179		ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0005576//GO:0006007//GO:0008943//GO:0009526//GO:0009532	nr +
Unigene5117_All	921	1.87	0.99	1.50	4.33	3.40	5.44	2.80	3.36	5.75	-9.21E-01	6.50E-02		-3.19E-01	5.53E-01		-3.47E-01	2.82E-01			3.31E-01	2.57E-01			2.62E-01	4.46E-01		1.04E+00	6.49E-06	Up	Unigene5117_All//gi|297797589|ref|XP_002866679.1|//1.00E-114//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297312514|gb|EFH42938.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene5117_All//4.00E-114//AT5G65560| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene51171_All	1301	0.04	0.00	0.65	18.99	15.38	7.74	1.66	0.58	0.37	-5.33E+00	6.10E-01		4.03E+00	7.02E-04	Up	-3.05E-01	3.99E-03			-1.29E+00	1.26E-29	Down	-1.52E+00	2.06E-04	Down	-2.17E+00	6.08E-07	Down	Unigene51171_All//gi|15222565|ref|NP_176575.1|//4.00E-85//AtMYB103 (myb domain protein 103); DNA binding / transcription activator/ transcription factor [Arabidopsis thaliana] >gi|4161916|gb|AAS10034.1| MYB transcription factor [Arabidopsis thaliana]	Unigene51171_All//6.00E-77//AT1G63910| AtMYB103 (myb domain protein 103); DNA binding / transcription activator/ transcription factor	Unigene51171_All//0.00E+00//TC171049	MYB		GO:0003676//GO:0010468//GO:0030528//GO:0043231	nr -
Unigene51172_All	446	2.11	0.11	1.31	2.01	1.24	1.01	1.90	0.47	0.45	-4.22E+00	1.36E-04	Down	-6.85E-01	3.69E-01		-7.03E-01	3.25E-01			-9.89E-01	1.96E-01			-2.02E+00	7.45E-03		-2.09E+00	4.37E-03										
Unigene51173_All	281	7.26	1.62	3.41	3.72	3.92	5.14	1.35	0.30	0.00	-2.16E+00	2.79E-05	Down	-1.09E+00	2.30E-02		7.50E-02	9.33E-01			4.66E-01	4.40E-01			-2.19E+00	8.75E-02		-1.01E+01	4.19E-03					Unigene51173_All//3.00E-118//BF271302					
Unigene51174_All	1281	1.14	1.07	0.17	1.13	0.65	1.48	5.64	6.40	9.05	-9.87E-02	8.47E-01		-2.78E+00	9.28E-05	Down	-8.06E-01	1.35E-01			3.93E-01	4.53E-01			1.80E-01	3.91E-01		6.81E-01	2.87E-06		Unigene51174_All//gi|224106844|ref|XP_002333623.1|//2.00E-28//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837867|gb|EEE76232.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene51174_All//9.00E-14//AT1G09545| leucine-rich repeat family protein	Unigene51174_All//4.00E-164//TC171799				nr -
Unigene51175_All	3536	0.00	0.00	0.00	0.21	0.06	0.03	9.58	1.47	2.64	null	null		null	null		-1.86E+00	2.53E-02			-3.05E+00	3.33E-03			-2.71E+00	3.89E-122	Down	-1.86E+00	1.97E-79	Down	Unigene51175_All//gi|224141315|ref|XP_002324019.1|//0.00E+00//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222867021|gb|EEF04152.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene51175_All//0.00E+00//AT3G28380| PGP17 (P-GLYCOPROTEIN 17); ATP binding / ATPase/ ATPase, coupled to transmembrane movement of substances / nucleoside-triphosphatase/ nucleotide binding	Unigene51175_All//3.00E-16//TC154840		ko02010|ABC transporters	GO:0006810//GO:0015405//GO:0017111//GO:0031224//GO:0032559	nr -
Unigene51177_All	532	1.48	1.43	2.20	4.40	3.11	4.58	2.07	0.24	1.57	-4.63E-02	9.66E-01		5.78E-01	3.90E-01		-5.02E-01	2.29E-01			5.89E-02	9.09E-01			-3.13E+00	3.46E-05	Down	-3.94E-01	4.92E-01		Unigene51177_All//gi|3334147|sp|Q39799.1|CHI1_GOSHI//3.00E-22//RecName: Full=Endochitinase 1; Flags: Precursor >gi|14697887|gb|AAB67842.1| class I chitinase [Gossypium hirsutum] >gi|298106229|gb|ADI56257.1| class I chitinase [Gossypium hirsutum]	Unigene51177_All//2.00E-15//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene51177_All//0.00E+00//DT462531		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005975//GO:0009056//GO:0016787//GO:0043170	nr +
Unigene51178_All	687	0.30	0.30	1.09	3.99	4.21	3.02	3.75	3.04	0.75	-4.62E-02	9.88E-01		1.83E+00	5.05E-02		7.83E-02	8.53E-01			-3.99E-01	3.31E-01			-3.04E-01	4.18E-01		-2.32E+00	9.74E-09	Down	Unigene51178_All//gi|9369361|gb|AAF87110.1|AC006434_6//9.00E-32//F10A5.8 [Arabidopsis thaliana]	Unigene51178_All//7.00E-26//AT1G75720| unknown protein					nr +
Unigene5118_All	806	20.97	13.20	18.23	445.73	337.47	254.28	27.96	15.97	10.97	-6.67E-01	7.97E-07		-2.02E-01	1.85E-01		-4.01E-01	8.06E-63			-8.10E-01	2.68E-196			-8.08E-01	1.42E-14		-1.35E+00	1.32E-33	Down	Unigene5118_All//gi|435039|gb|AAA79360.1|//2.00E-68//proline-rich cell wall protein [Gossypium hirsutum]		Unigene5118_All//0.00E+00//TC131760		ko03040|Spliceosome		nr +
Unigene51180_All	335	85.90	34.79	52.14	161.49	166.93	96.26	22.34	11.10	9.04	-1.30E+00	3.19E-32	Down	-7.20E-01	5.71E-12		4.79E-02	6.00E-01			-7.46E-01	4.46E-26			-1.01E+00	1.89E-07	Down	-1.31E+00	3.32E-11	Down									
Unigene51182_All	560	17.94	15.47	10.94	16.28	20.23	17.98	10.12	3.96	6.76	-2.13E-01	2.70E-01		-7.14E-01	1.38E-04		3.14E-01	7.06E-02			1.44E-01	5.00E-01			-1.35E+00	7.69E-09	Down	-5.82E-01	6.91E-03					Unigene51182_All//5.00E-165//TC175793					
Unigene51183_All	465	3.15	1.63	3.32	4.71	5.33	6.12	0.45	1.17	2.83	-9.47E-01	8.40E-02		7.60E-02	8.89E-01		1.78E-01	7.14E-01			3.76E-01	3.60E-01			1.36E+00	1.44E-01		2.64E+00	2.27E-05	Up	Unigene51183_All//gi|3152595|gb|AAC17076.1|//1.00E-19//Similar to D. melanogaster sno gene gb|U95760. EST gb|N97148 and gb|Z26221 come from this gene [Arabidopsis thaliana]	Unigene51183_All//8.00E-18//AT1G79350| EMB1135 (embryo defective 1135); DNA binding / protein binding / zinc ion binding				GO:0005488	nr -
Unigene51190_All	432	6.54	8.21	7.40	10.26	10.92	15.79	30.93	20.61	12.73	3.28E-01	3.41E-01		1.77E-01	6.09E-01		8.96E-02	8.17E-01			6.21E-01	5.52E-03			-5.86E-01	1.87E-05		-1.28E+00	8.78E-19	Down	Unigene51190_All//gi|12229923|sp|Q9M4T8.1|PSA5_SOYBN//6.00E-08//RecName: Full=Proteasome subunit alpha type-5; AltName: Full=20S proteasome alpha subunit E; AltName: Full=20S proteasome subunit alpha-5 >gi|7839485|gb|AAF70292.1|AF255338_1 20S proteasome subunit [Glycine max]	Unigene51190_All//5.00E-08//AT3G14290| PAE2; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene51190_All//0.00E+00//TC131658		ko03050|Proteasome		nr -

Unigene51191_All	500	2.72	18.65	4.05	1.69	3.37	2.71	0.42	0.17	32.19	2.78E+00	2.05E-28	Up	5.73E-01	2.38E-01		9.95E-01	5.07E-02		6.78E-01	2.65E-01		-1.34E+00	4.29E-01		6.25E+00	3.03E-106	Up	Unigene51191_All//gi|225453136|ref|XP_002271724.1|//4.00E-22//PREDICTED: similar to Os01g0111700 [Vitis vinifera]	Unigene51191_All//9.00E-07//AT1G49000| unknown protein	Unigene51191_All//0.00E+00//DW507187			GO:0043231//GO:0044444	nr -
Unigene51192_All	316	3.48	0.32	4.04	5.52	3.38	1.57	1.61	0.93	0.50	-3.44E+00	1.19E-04	Down	2.18E-01	7.02E-01		-7.08E-01	1.44E-01		-1.81E+00	5.79E-04	Down	-7.94E-01	4.02E-01		-1.67E+00	7.78E-02				Unigene51192_All//4.00E-07//TC155487				
Unigene51193_All	395	0.40	0.26	0.40	2.52	0.44	0.00	0.00	0.00	0.00	-6.31E-01	7.27E-01		2.52E-02	1.00E+00		-2.53E+00	6.75E-04	Down	-1.13E+01	2.97E-06	Down	null	null		null	null		Unigene51193_All//gi|2827777|sp|P29136.2|MEP1_SOYBN//2.00E-21//RecName: Full=Metalloendoproteinase 1; AltName: Full=SMEP1; Flags: Precursor >gi|1679656|gb|AAB26959.1| metalloproteinase [Glycine max]	Unigene51193_All//1.00E-19//AT4G16640| matrix metalloproteinase, putative			GO:0008233	nr -
Unigene51195_All	609	1.12	0.83	0.79	29.77	29.18	32.56	2.43	0.55	1.50	-4.25E-01	5.97E-01		-5.05E-01	5.82E-01		-2.92E-02	8.45E-01		1.29E-01	3.95E-01		-2.15E+00	9.69E-05	Down	-6.92E-01	1.40E-01		Unigene51195_All//gi|226495069|ref|NP_001148030.1|//4.00E-14//zinc finger, C3HC4 type family protein [Zea mays] >gi|195615366|gb|ACG29513.1| zinc finger, C3HC4 type family protein [Zea mays]	Unigene51195_All//2.00E-13//AT3G51325| zinc finger (C3HC4-type RING finger) family protein	Unigene51195_All//2.00E-177//TC165745			GO:0046872	nr -
Unigene512_All	1524	2.57	3.49	3.07	4.45	3.34	3.76	3.86	1.43	3.90	4.39E-01	9.55E-02		2.56E-01	3.85E-01		-4.11E-01	6.63E-02		-2.40E-01	3.45E-01		-1.44E+00	6.71E-10	Down	1.44E-02	9.70E-01		Unigene512_All//gi|222422989|dbj|BAH19478.1|//1.00E-135//AT2G06000 [Arabidopsis thaliana]	Unigene512_All//6.00E-132//AT2G06000| pentatricopeptide (PPR) repeat-containing protein	Unigene512_All//0.00E+00//TC178852				nr +
Unigene51202_All	985	1.27	1.29	4.11	2.53	0.91	0.46	3.48	2.84	1.70	1.26E-02	9.80E-01		1.69E+00	7.02E-07	Up	-1.48E+00	1.28E-04	Down	-2.46E+00	1.24E-07	Down	-2.90E-01	3.79E-01		-1.03E+00	3.90E-04	Down	Unigene51202_All//gi|24285904|gb|AAL14199.1|//1.00E-104//cysteine proteinase precursor [Ipomoea batatas] >gi|56961686|gb|AAK15148.2| cysteine proteinase-like protein [Ipomoea batatas]	Unigene51202_All//1.00E-102//AT2G27420| cysteine proteinase, putative	Unigene51202_All//0.00E+00//TC133526				nr +
Unigene51204_All	416	1.51	5.72	0.26	4.19	5.05	5.54	0.81	2.81	2.78	1.92E+00	2.85E-05	Up	-2.56E+00	2.72E-02		2.69E-01	5.94E-01		4.02E-01	3.93E-01		1.79E+00	3.05E-03		1.77E+00	2.74E-03		Unigene51204_All//gi|297819734|ref|XP_002877750.1|//1.00E-11//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323388|gb|EFH54009.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51204_All//4.00E-12//AT3G50560| short-chain dehydrogenase/reductase (SDR) family protein	Unigene51204_All//2.00E-49//TC132892			GO:0003824//GO:0008152	nr -
Unigene51205_All	1090	1.68	1.44	1.27	3.29	2.72	1.41	1.36	0.65	0.95	-2.21E-01	6.22E-01		-4.03E-01	4.14E-01		-2.76E-01	4.30E-01		-1.22E+00	1.72E-04	Down	-1.06E+00	3.14E-02		-5.15E-01	2.80E-01		Unigene51205_All//gi|297602232|ref|NP_001052225.2|//2.00E-88//Os04g0201900 [Oryza sativa Japonica Group] >gi|255675212|dbj|BAF14139.2| Os04g0201900 [Oryza sativa Japonica Group]	Unigene51205_All//1.00E-84//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene51205_All//0.00E+00//ES819401		ko04626|Plant-pathogen interaction	GO:0004702//GO:0004713//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene51207_All	634	23.27	17.74	24.44	92.87	212.15	222.83	1.07	1.05	0.75	-3.91E-01	7.74E-03		7.07E-02	6.53E-01		1.19E+00	1.75E-152	Up	1.26E+00	1.16E-158	Up	-1.66E-02	1.02E+00		-5.01E-01	5.07E-01		Unigene51207_All//gi|21314549|gb|AAM47000.1|AF512542_1//3.00E-93//alpha-expansin precursor [Gossypium hirsutum]	Unigene51207_All//1.00E-91//AT2G28950| ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A6)	Unigene51207_All//2.00E-124//TC143912			GO:0000902//GO:0005618//GO:0009827	nr +
Unigene5121_All	636	2.96	7.41	5.27	7.05	4.87	5.47	4.06	5.32	4.20	1.32E+00	5.24E-06	Up	8.33E-01	1.83E-02		-5.33E-01	5.50E-02		-3.67E-01	2.33E-01		3.93E-01	2.16E-01		4.95E-02	9.03E-01				Unigene5121_All//9.00E-130//gi|13248403|gb|BF275680.2|BF275680				
Unigene51211_All	454	0.00	1.67	0.59	0.99	2.05	1.99	3.17	3.04	3.51	1.07E+01	1.76E-04	Up	9.20E+00	8.01E-02		1.05E+00	1.64E-01		1.01E+00	1.96E-01		-5.97E-02	9.19E-01		1.49E-01	7.46E-01		Unigene51211_All//gi|297809901|ref|XP_002872834.1|//7.00E-46//AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318671|gb|EFH49093.1| AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51211_All//4.00E-42//AT1G02890| AAA-type ATPase family protein	Unigene51211_All//1.00E-100//TC177835		ko04141|Protein processing in endoplasmic reticulum	GO:0003690//GO:0006260//GO:0006281//GO:0009108//GO:0016778//GO:0032559//GO:0034061//GO:0042623//GO:0042723//GO:0043231	nr +
Unigene51212_All	317	2.64	2.72	8.57	3.77	3.37	1.71	2.93	0.79	2.89	4.12E-02	9.74E-01		1.70E+00	7.10E-05	Up	-1.63E-01	8.15E-01		-1.14E+00	7.15E-02		-1.89E+00	6.92E-03		-2.17E-02	9.60E-01		Unigene51212_All//gi|15225722|ref|NP_180822.1|//4.00E-07//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75160493|sp|Q8S8F6.1|PP180_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g32630	Unigene51212_All//2.00E-08//AT2G32630| pentatricopeptide (PPR) repeat-containing protein				nr -
Unigene51215_All	678	35.27	12.78	18.14	6.69	5.43	6.26	0.56	0.99	0.00	-1.46E+00	5.96E-32	Down	-9.59E-01	5.48E-16		-2.99E-01	3.20E-01		-9.46E-02	7.57E-01		8.14E-01	3.15E-01		-9.13E+00	4.19E-03		Unigene51215_All//gi|20149046|gb|AAM12778.1|//4.00E-22//auxin-induced SAUR-like protein [Capsicum annuum]	Unigene51215_All//7.00E-23//AT4G38840| auxin-responsive protein, putative	Unigene51215_All//0.00E+00//gi|109876364|gb|DW505338.1|DW505338			GO:0006950//GO:0009755//GO:0016020	nr +
Unigene51217_All	381	21.01	12.24	7.27	24.97	15.82	26.91	60.92	23.70	28.96	-7.80E-01	1.45E-04		-1.53E+00	2.39E-11	Down	-6.59E-01	1.30E-04		1.08E-01	6.43E-01		-1.36E+00	4.69E-34	Down	-1.07E+00	2.58E-24	Down	Unigene51217_All//gi|255552912|ref|XP_002517499.1|//8.00E-06//60S ribosomal protein L30, putative [Ricinus communis] >gi|223545510|gb|EEF45041.1| 60S ribosomal protein L30, putative [Ricinus communis]	Unigene51217_All//5.00E-05//AT1G36240| 60S ribosomal protein L30 (RPL30A)	Unigene51217_All//2.00E-145//gi|21102778|gb|BQ415091.1|BQ415091		ko03010|Ribosome		nr +
Unigene5122_All	639	3.44	11.10	4.33	3.90	8.46	13.57	12.57	29.43	27.81	1.69E+00	4.59E-12	Up	3.34E-01	3.94E-01		1.12E+00	6.59E-06	Up	1.80E+00	8.84E-17	Up	1.23E+00	1.13E-23	Up	1.15E+00	1.17E-20	Up			Unigene5122_All//1.00E-76//gi|109871092|gb|DW500068.1|DW500068				
Unigene51221_All	463	62.15	27.25	36.69	221.31	193.15	134.12	140.63	77.27	89.40	-1.19E+00	5.46E-28	Down	-7.61E-01	4.30E-13		-1.96E-01	4.76E-05		-7.23E-01	3.10E-46		-8.64E-01	2.23E-45		-6.54E-01	4.59E-29				Unigene51221_All//0.00E+00//TC154257				
Unigene51223_All	241	27.79	47.31	48.61	200.91	237.19	125.37	178.42	518.72	253.08	7.68E-01	5.63E-06		8.07E-01	2.76E-06		2.40E-01	3.37E-04		-6.80E-01	5.73E-20		1.54E+00	6.16E-216	Up	5.04E-01	2.20E-17		Unigene51223_All//gi|161701632|gb|ABX73853.1|//4.00E-17//caffeoyl-CoA-O-methyltransferase [Acacia auriculiformis x Acacia mangium]	Unigene51223_All//2.00E-15//AT4G34050| caffeoyl-CoA 3-O-methyltransferase, putative	Unigene51223_All//3.00E-93//gi|84152904|gb|DN802259.1|DN802259		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0008171//GO:0009699//GO:0043169	nr +
Unigene51225_All	511	4.51	11.20	1.35	15.50	6.67	13.96	14.56	12.92	10.99	1.31E+00	4.59E-07	Up	-1.73E+00	2.51E-04	Down	-1.22E+00	4.33E-10	Down	-1.51E-01	5.42E-01		-1.72E-01	4.23E-01		-4.06E-01	3.05E-02				Unigene51225_All//5.00E-140//gi|18101178|gb|BM360432.1|BM360432				
Unigene51227_All	910	0.86	2.00	1.87	1.26	1.32	0.79	4.18	1.10	0.88	1.22E+00	1.36E-02		1.12E+00	3.58E-02		7.31E-02	9.30E-01		-6.65E-01	3.16E-01		-1.92E+00	1.04E-09	Down	-2.26E+00	3.77E-12	Down	Unigene51227_All//gi|18418353|ref|NP_568352.1|//1.00E-104//tatD-related deoxyribonuclease family protein [Arabidopsis thaliana] >gi|124301002|gb|ABN04753.1| At5g17570 [Arabidopsis thaliana]	Unigene51227_All//2.00E-105//AT5G17570| tatD-related deoxyribonuclease family protein	Unigene51227_All//0.00E+00//TC143856			GO:0004520	nr +
Unigene51228_All	290	149.93	54.51	74.73	170.06	153.18	229.40	289.40	143.98	166.91	-1.46E+00	2.81E-57	Down	-1.00E+00	7.38E-31	Down	-1.51E-01	5.61E-02		4.32E-01	3.28E-12		-1.01E+00	3.97E-75	Down	-7.94E-01	6.06E-52	Down	Unigene51228_All//gi|247421835|gb|ACS96445.1|//5.00E-47//S18.A ribosomal protein [Jatropha curcas]	Unigene51228_All//2.00E-48//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome	Unigene51228_All//6.00E-163//TC164555		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006412//GO:0015935//GO:0016020//GO:0003012//GO:0031981	nr +
Unigene51229_All	698	17.77	9.80	17.93	3.93	11.15	4.34	0.00	0.06	0.17	-8.58E-01	1.24E-07		1.32E-02	9.59E-01		1.51E+00	8.98E-13	Up	1.43E-01	7.09E-01		5.90E+00	6.34E-01		7.42E+00	2.43E-01		Unigene51229_All//gi|115462763|ref|NP_001054981.1|//4.00E-09//Os05g0232200 [Oryza sativa Japonica Group] >gi|113578832|dbj|BAF16895.1| Os05g0232200 [Oryza sativa Japonica Group]	Unigene51229_All//2.00E-19//AT5G56850| unknown protein	Unigene51229_All//2.00E-121//gi|84165525|gb|DR454173.1|DR454173				nr +
Unigene5123_All	972	151.10	113.90	176.24	32.13	33.02	20.49	11.48	5.63	4.39	-4.08E-01	3.72E-22		2.22E-01	2.72E-08		3.92E-02	7.76E-01		-6.49E-01	4.28E-12		-1.03E+00	5.00E-11	Down	-1.39E+00	8.16E-18	Down	Unigene5123_All//gi|297831548|ref|XP_002883656.1|//6.00E-63//Terredoxin thioredoxin reductase catalytic beta chain family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329496|gb|EFH59915.1| ferredoxin thioredoxin reductase catalytic beta chain family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5123_All//3.00E-64//AT2G04700| ferredoxin thioredoxin reductase catalytic beta chain family protein	Unigene5123_All//0.00E+00//TC156821				nr +
Unigene51231_All	555	1.41	3.38	2.69	2.51	6.27	4.48	1.37	0.83	1.08	1.26E+00	1.00E-02		9.26E-01	1.05E-01		1.32E+00	5.54E-05	Up	8.33E-01	4.12E-02		-7.27E-01	3.32E-01		-3.49E-01	6.12E-01				Unigene51231_All//0.00E+00//TC173359				
Unigene51232_All	634	8.67	4.56	6.38	4.95	3.42	1.99	0.80	0.13	0.19	-9.28E-01	2.87E-04		-4.41E-01	1.04E-01		-5.33E-01	1.24E-01		-1.31E+00	2.17E-04	Down	-2.60E+00	2.05E-02		-2.09E+00	3.64E-02		Unigene51232_All//gi|226491294|ref|NP_001147543.1|//5.00E-31//neurogenic locus notch protein precursor-like [Zea mays] >gi|195612086|gb|ACG27873.1| neurogenic locus notch protein precursor-like [Zea mays]	Unigene51232_All//8.00E-18//AT4G14746| INVOLVED IN: biological_process unknown; LOCATED IN: anchored to membrane; CONTAINS InterPro DOMAIN/s: EGF (InterPro:IPR006210); Has 201 Blast hits to 179 proteins in 41 species: Archae - 0; Bacteria - 0; Metazoa - 168; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).					nr -
Unigene51233_All	1162	1.44	16.35	6.00	4.42	5.16	7.58	5.39	12.52	7.17	3.50E+00	1.08E-71	Up	2.06E+00	9.77E-15	Up	2.24E-01	4.19E-01		7.79E-01	4.62E-05		1.22E+00	2.95E-18	Up	4.12E-01	1.92E-02		Unigene51233_All//gi|297849662|ref|XP_002892712.1|//1.00E-135//UDP-D-glucose/UDP-D-galactose 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297338554|gb|EFH68971.1| UDP-D-glucose/UDP-D-galactose 4-epimerase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene51233_All//2.00E-136//AT1G12780| UGE1 (UDP-D-glucose/UDP-D-galactose 4-epimerase 1); UDP-glucose 4-epimerase/ protein dimerization	Unigene51233_All//0.00E+00//TC162602		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism		nr -
Unigene51234_All	669	0.00	0.00	0.80	2.31	1.80	13.97	6.83	32.05	16.32	null	null		9.64E+00	4.03E-03		-3.58E-01	5.31E-01		2.60E+00	3.06E-28	Up	2.23E+00	8.48E-62	Up	1.26E+00	5.91E-15	Up	Unigene51234_All//gi|94966428|dbj|BAE94179.1|//8.00E-06//CLAVATA3/ESR-related 46 precursor [Arabidopsis thaliana] >gi|111074268|gb|ABR04507.1| At5g59305 [Arabidopsis thaliana]	Unigene51234_All//1.00E-05//AT5G59305| unknown protein	Unigene51234_All//2.00E-13//DW515284				nr -
Unigene51236_All	472	1.11	0.64	0.45	0.00	2.04	0.77	0.72	0.71	0.68	-7.83E-01	4.22E-01		-1.30E+00	2.42E-01		1.10E+01	6.32E-06	Up	9.58E+00	2.37E-02		-1.66E-02	1.02E+00		-8.59E-02	9.47E-01				Unigene51236_All//2.00E-15//TC135842				
Unigene51237_All	529	0.59	0.86	0.20	1.70	1.04	0.94	1.68	0.16	0.75	5.39E-01	6.02E-01		-1.56E+00	3.30E-01		-7.03E-01	3.24E-01		-8.52E-01	2.63E-01		-3.41E+00	1.40E-04	Down	-1.16E+00	7.15E-02				Unigene51237_All//3.00E-15//TC135842				
Unigene51238_All	385	1.63	0.26	0.14	1.16	2.24	2.82	36.90	32.68	99.34	-2.63E+00	1.78E-02		-3.56E+00	8.32E-03		9.41E-01	2.38E-01		1.27E+00	6.54E-02		-1.75E-01	2.38E-01		1.43E+00	6.86E-61	Up	Unigene51238_All//gi|125950374|gb|ABN58740.1|//3.00E-25//UGT protein [Gossypium hirsutum]	Unigene51238_All//5.00E-07//AT5G38040| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene51238_All//0.00E+00//TC132027			GO:0016757	nr +
Unigene51239_All	548	2.77	1.11	0.39	2.73	1.07	0.82	3.63	1.22	1.09	-1.32E+00	1.68E-02		-2.83E+00	5.52E-05	Down	-1.35E+00	9.45E-03		-1.73E+00	2.56E-03		-1.57E+00	2.71E-04	Down	-1.73E+00	5.14E-05	Down	Unigene51239_All//gi|223452506|gb|ACM89580.1|//7.00E-27//serine/threonine protein kinase-like protein [Glycine max]	Unigene51239_All//4.00E-13//AT5G15080| protein kinase, putative	Unigene51239_All//0.00E+00//TC161177			GO:0004672//GO:0016020	nr -

Unigene5124_All	1475	1.06	0.52	0.51	4.05	3.27	1.26	1.18	0.26	1.49	-1.05E+00	4.79E-02		-1.07E+00	5.45E-02		-3.10E-01	2.23E-01		-1.69E+00	5.10E-11	Down	-2.20E+00	1.38E-05	Down	3.38E-01	3.88E-01		Unigene5124_All//gi|115444287|ref|NP_001045923.1|//5.00E-38//Os02g0153000 [Oryza sativa Japonica Group] >gi|51535341|dbj|BAD38600.1|ternary complex factor MIP1-like [Oryza sativa Japonica Group] >gi|74272488|gb|ABA01090.1|ternary complex factor MIP1-like [Oryza rufipogon] >gi|76364057|gb|ABA41566.1|ternary complex factor MIP1-like [Oryza sativa Indica Group] >gi|113535454|dbj|BAF07837.1|Os02g0153000 [Oryza sativa Japonica Group]	Unigene5124_All//7.00E-43//AT1G16750| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF547 (InterPro:IPR006869); BEST Arabidopsis thaliana protein match is: transcription factor (TAIR:AT3G13000.2); Has 420 Blast hits to 403 proteins in 70 species: Archae - 0; Bacteria - 56; Metazoa - 34; Fungi - 2; Plants - 297; Viruses - 0; Other Eukaryotes - 31 (source: NCBI BLink).	Unigene5124_All//0.00E+00//ES812351				nr -
Unigene51245_All	349	28.33	14.23	20.75	16.70	16.77	14.23	58.76	30.90	27.74	-9.94E-01	9.10E-08		-4.49E-01	1.93E-02		6.40E-03	9.89E-01		-2.30E-01	4.06E-01		-9.27E-01	1.24E-16		-1.08E+00	6.64E-22	Down			Unigene51245_All//3.00E-69//TC152113				
Unigene51246_All	718	72.36	44.67	54.07	361.74	230.06	266.77	240.26	150.65	91.66	-6.96E-01	1.01E-20		-4.21E-01	2.15E-08		-6.53E-01	1.23E-110		-4.39E-01	1.01E-47		-6.73E-01	1.90E-77		-1.39E+00	2.22E-263	Down	Unigene51246_All//gi|211906466|gb|ACJ11726.1|//1.00E-62//serine hydroxymethyltransferase [Gossypium hirsutum]	Unigene51246_All//2.00E-54//AT4G13930| SHM4 (serine hydroxymethyltransferase 4); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene51246_All//0.00E+00//gi|109837514|gb|DW236075.1|DW236075		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate	GO:0009069//GO:0010038//GO:0016020//GO:0016742//GO:0044444//GO:0048037	nr +
Unigene51247_All	628	4.17	5.41	5.34	6.66	7.02	2.88	13.73	13.11	9.20	3.76E-01	2.76E-01		3.59E-01	3.31E-01		7.50E-02	8.25E-01		-1.21E+00	4.69E-05	Down	-6.70E-02	7.34E-01		-5.78E-01	6.71E-04				Unigene51247_All//1.00E-60//CO497386				
Unigene51248_All	591	2.12	0.17	0.09	4.64	2.80	1.83	1.86	0.78	0.47	-3.63E+00	1.99E-05	Down	-4.56E+00	8.14E-06	Down	-7.29E-01	4.46E-02		-1.34E+00	5.07E-04	Down	-1.26E+00	3.46E-02		-1.98E+00	1.39E-03				Unigene51248_All//2.00E-139//ES410620				
Unigene5125_All	686	19.22	230.45	11.02	15.61	14.16	19.29	35.44	39.48	34.67	3.58E+00	0.00E+00	Up	-8.02E-01	6.54E-07		-1.41E-01	4.95E-01		3.05E-01	6.06E-02		1.56E-01	1.33E-01		-3.16E-02	7.76E-01		Unigene5125_All//gi|21618074|gb|AAM67124.1|//4.00E-44//calmodulin-related protein [Arabidopsis thaliana]	Unigene5125_All//5.00E-45//AT4G66400| calmodulin-related protein, putative	Unigene5125_All//0.00E+00//DW225692		ko04626|Plant-pathogen interaction		nr +
Unigene51250_All	1171	0.09	0.00	0.14	2.51	2.44	0.46	2.53	0.46	2.52	-6.48E+00	3.71E-01		6.10E-01	7.48E-01		-4.03E-02	9.10E-01		-2.44E+00	8.12E-09	Down	-2.45E+00	3.91E-10	Down	-5.60E-03	9.81E-01		Unigene51250_All//gi|15228781|ref|NP_191154.1|//1.00E-140//CCR3 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 3); kinase [Arabidopsis thaliana] >gi|75335634|sp|Q9LY50.1|ACCR3_ARATH RecName: Full=Putative serine/threonine-protein kinase-like protein CCR3; AltName: Full=Protein CRINKLY 4 RELATED 3; Short=ACCR3; Flags: Precursor >gi|7573490|emb|CAB87849.1|receptor kinase-like protein [Arabidopsis thaliana]	Unigene51250_All//2.00E-132//AT3G55950| CCR3 (ARABIDOPSIS THALIANA CRINKLY4 RELATED 3); kinase	Unigene51250_All//8.00E-76//TC172298		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr -
Unigene51252_All	639	0.00	0.32	0.17	16.92	18.59	17.03	11.45	7.59	1.81	8.31E+00	1.36E-01		7.38E+00	3.97E-01		1.36E-01	4.99E-01		9.90E-03	9.55E-01		-5.93E-01	2.03E-03		-2.66E+00	2.74E-27	Down	Unigene51252_All//gi|15240620|ref|NP_199825.1|//8.00E-13//ankyrin repeat family protein [Arabidopsis thaliana] >gi|10177225|dbj|BAB10300.1|ankyrin-like protein [Arabidopsis thaliana]	Unigene51252_All//4.00E-14//AT5G50140| ankyrin repeat family protein	Unigene51252_All//0.00E+00//DV850040				nr +
Unigene51253_All	632	9.19	7.38	8.00	5.83	4.20	1.93	0.13	0.07	0.25	-3.17E-01	2.14E-01		-1.99E-01	4.65E-01		-4.75E-01	1.36E-01		-1.60E+00	1.60E-06	Down	-1.02E+00	7.24E-01		9.14E-01	6.24E-01		Unigene51253_All//gi|225459471|ref|XP_002284394.1|//1.00E-33//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene51253_All//8.00E-158//TC144104			GO:0044464//GO:0046914	nr +
Unigene51254_All	260	29.98	21.44	29.70	27.97	25.30	41.17	44.72	20.42	20.99	-4.84E-01	2.08E-02		-1.39E-02	9.72E-01		-1.45E-01	5.65E-01		5.58E-01	1.20E-03		-1.13E+00	3.01E-13	Down	-1.09E+00	5.94E-13	Down	Unigene51254_All//gi|196622026|gb|ACG32843.1|//1.00E-15//40S ribosomal protein S23 [Zea mays]	Unigene51254_All//1.00E-13//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene51254_All//2.00E-116//TC178652		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279//GO:0043231	nr +
Unigene51255_All	1205	2.08	0.34	0.49	1.61	2.11	3.15	1.02	0.59	1.88	-2.63E+00	9.22E-08	Down	-2.10E+00	8.65E-06	Down	3.91E-01	3.65E-01		9.66E-01	2.14E-03		-7.87E-01	1.52E-01		8.89E-01	1.55E-02		Unigene51255_All//gi|297601813|ref|NP_001051548.2|//7.00E-35//Os03g0795400 [Oryza sativa Japonica Group] >gi|255674962|dbj|BAF13462.2|Os03g0795400 [Oryza sativa Japonica Group]	Unigene51255_All//5.00E-20//AT5G46100| pentatricopeptide (PPR) repeat-containing protein	Unigene51255_All//2.00E-95//DT455947				nr +
Unigene51256_All	432	4.12	2.82	1.48	2.88	1.43	1.88	2.15	0.97	0.37	-5.49E-01	2.61E-01		-1.48E+00	5.78E-03		-1.01E+00	8.39E-02		-6.15E-01	3.33E-01		-1.15E+00	7.87E-02		-2.55E+00	5.79E-04	Down			Unigene51256_All//1.00E-29//TC140792				
Unigene51259_All	850	1.60	0.48	1.07	4.34	2.80	3.83	3.03	1.08	0.38	-1.75E+00	4.61E-03		-5.88E-01	3.36E-01		-6.34E-01	3.93E-02		-1.81E-01	6.41E-01		-1.49E+00	5.35E-05	Down	-3.02E+00	2.15E-11	Down	Unigene51259_All//gi|15220863|ref|NP_178203.1|//2.00E-18//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75200729|sp|Q9SAH2.1|PP137_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g80880, mitochondrial; Flags: Precursor >gi|91806121|gb|ABE65789.1|pentatricopeptide repeat-containing protein [Arabidopsis thaliana]	Unigene51259_All//4.00E-18//AT1G80880| pentatricopeptide (PPR) repeat-containing protein	Unigene51259_All//0.00E+00//DW503372			GO:0005840	nr -
Unigene51260_All	727	0.43	0.14	0.59	0.00	0.09	1.18	139.58	241.98	135.68	-1.63E+00	2.76E-01		4.41E-01	6.77E-01		6.57E+00	6.08E-01		1.02E+01	3.79E-05	Up	7.94E-01	6.68E-105		-4.08E-02	4.61E-01		Unigene51260_All//gi|124361158|gb|ABN09130.1|//1.00E-25//DC1; C1-like [Medicago truncatula]	Unigene51260_All//2.00E-20//AT2G16050| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: DC1 (InterPro:IPR004146); BEST Arabidopsis thaliana protein match is: DC1 domain-containing protein (TAIR:AT1G20990.1); Has 719 Blast hits to 448 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 717; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene51262_All	691	0.00	5.06	0.00	13.84	5.18	9.22	0.67	5.87	0.46	1.23E+01	6.73E-20	Up	null	null		-1.42E+00	3.11E-15	Down	-5.87E-01	1.29E-03		3.12E+00	2.15E-17	Up	-5.45E-01	5.65E-01		Unigene51262_All//gi|21322711|emb|CAD22154.1|//2.00E-63//pheropborin-dsl protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome	GO:0031410	nr -
Unigene51264_All	1936	0.00	0.65	0.28	0.69	0.69	2.12	0.22	0.63	8.50	9.35E+00	2.86E-07	Up	8.10E+00	4.03E-03		-2.10E-03	9.81E-01		1.61E+00	3.77E-07	Up	1.52E+00	8.16E-03		5.28E+00	9.87E-102	Up	Unigene51264_All//gi|225428013|ref|XP_002278408.1|//0.00E+00//PREDICTED: similar to KAK (KAKTUS) isoform 1 [Vitis vinifera]	Unigene51264_All//1.00E-167//AT4G38600| KAK (KAKTUS); ubiquitin-protein ligase	Unigene51264_All//0.00E+00//TC163055		ko04120|Ubiquitin mediated proteolysis	GO:0000904//GO:0006261//GO:0016020//GO:0016874	nr -
Unigene51266_All	786	2.80	1.03	0.07	2.73	1.14	0.75	6.24	1.28	2.74	-1.44E+00	1.41E-03		-5.37E+00	1.04E-10	Down	-1.26E+00	2.52E-03		-1.87E+00	6.85E-05	Down	-2.29E+00	3.63E-15	Down	-1.19E+00	1.01E-06	Down	Unigene51266_All//gi|71068360|gb|AZ23107.1|//1.00E-120//plastid ATP/ADP transport protein 2 [Manihot esculenta]	Unigene51266_All//1.00E-102//AT1G80300| NTT1 (NUCLEOTIDE TRANSPORTER 1); ATP:ADP antiporter	Unigene51266_All//0.00E+00//TC144800				nr -
Unigene51268_All	556	8.75	7.47	4.50	8.33	5.45	3.98	1.52	0.60	1.29	-2.28E-01	4.19E-01		-9.59E-01	7.86E-04		-6.12E-01	2.19E-02		-1.07E+00	1.26E-04	Down	-1.34E+00	5.68E-02		-2.38E-01	7.02E-01		Unigene51268_All//gi|190898232|gb|ACE97629.1|//6.00E-34//expressed protein [Populus tremula] >gi|190898234|gb|ACE97630.1|expressed protein [Populus tremula] >gi|190898236|gb|ACE97631.1|expressed protein [Populus tremula] >gi|190898240|gb|ACE97633.1|expressed protein [Populus tremula] >gi|190898242|gb|ACE97634.1|expressed protein [Populus tremula] >gi|190898246|gb|ACE97636.1|expressed protein [Populus tremula] >gi|190898248|gb|ACE97637.1|expressed protein [Populus tremula] >gi|190898250|gb|ACE97638.1|expressed protein [Populus tremula] >gi|190898254|gb|ACE97640.1|expressed protein [Populus tremula] >gi|190898256|gb|ACE97641.1|expressed protein [Populus tremula]	Unigene51268_All//7.00E-34//AT3G18800| unknown protein	Unigene51268_All//0.00E+00//TC146320			GO:0016020	nr -
Unigene51270_All	739	2.12	1.44	0.94	1.01	1.07	1.65	2.35	0.34	0.81	-5.61E-01	2.88E-01		-1.18E+00	3.61E-02		8.40E-02	9.44E-01		7.07E-01	2.77E-01		-2.79E+00	4.64E-07	Down	-1.54E+00	6.50E-04	Down	Unigene51270_All//gi|155242106|gb|ABT18095.1|//8.00E-42//FERONIA receptor-like kinase [Cardamine flexuosa]	Unigene51270_All//2.00E-41//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene51270_All//9.00E-10//gi|78333985|gb|DT554259.1|DT554259		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0031410//GO:0032559	nr +
Unigene51271_All	649	0.32	1.17	0.33	2.46	3.40	2.30	4.30	1.67	2.15	1.86E+00	3.73E-02		2.53E-02	1.00E+00		4.67E-01	3.07E-01		-9.71E-02	8.59E-01		-1.36E+00	8.91E-05	Down	-1.00E+00	2.14E-03				Unigene51271_All//0.00E+00//BQ409751				
Unigene51272_All	724	2.24	1.05	0.74	2.61	1.28	2.00	3.74	0.69	0.83	-1.09E+00	3.63E-02		-1.61E+00	5.02E-03		-1.03E+00	2.20E-02		-3.89E-01	4.48E-01		-2.43E+00	2.87E-09	Down	-2.18E+00	1.56E-08	Down	Unigene51272_All//gi|115433974|ref|NP_001041745.1|//1.00E-26//Os01g0101800 [Oryza sativa Japonica Group] >gi|113531276|dbj|BAF03659.1|Os01g0101800 [Oryza sativa Japonica Group]	Unigene51272_All//6.00E-29//AT3G23740| unknown protein	Unigene51272_All//0.00E+00//DW233123			GO:0043231	nr -
Unigene51273_All	227	29.27	12.05	13.61	43.23	43.23	52.92	68.54	33.69	31.77	-1.28E+00	8.02E-08	Down	-1.11E+00	4.91E-06	Down	1.00E-04	9.94E-01		2.92E-01	9.31E-02		-1.02E+00	5.60E-15	Down	-1.11E+00	1.78E-17	Down	Unigene51273_All//gi|40287508|gb|AB83868.1|//3.00E-35//60S ribosomal protein L12 [Capsicum annuum]	Unigene51273_All//2.00E-34//AT5G60670| 60S ribosomal protein L12 (RPL12C)	Unigene51273_All//2.00E-125//gi|21089610|gb|BQ401923.1|BQ401923		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr +
Unigene51275_All	692	132.31	99.36	89.88	302.12	250.85	197.95	465.69	191.04	154.00	-4.13E-01	1.89E-14		-5.58E-01	1.48E-23		-2.68E-01	2.64E-17		-6.10E-01	1.22E-69		-1.29E+00	0.00E+00	Down	-1.60E+00	0.00E+00	Down	Unigene51275_All//gi|195963827|gb|ACG59946.1|//1.00E-42//stearoyl-acyl-carrier protein desaturase [Ricinus communis] >gi|195963833|gb|ACG59949.1|stearoyl-acyl-carrier protein desaturase [Ricinus communis]	Unigene51275_All//2.00E-42//AT2G43710| SSI2; acyl-[acyl-carrier-protein] desaturase/ stearoyl-CoA 9-desaturase	Unigene51275_All//0.00E+00//gi|73862604|gb|DT465343.1|DT465343		ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0006631//GO:0009536//GO:0016717//GO:0046872	nr +

Unigene51276_All	1014	0.77	3.45	1.79	2.16	1.70	3.61	5.88	8.00	21.81	2.16E+00	1.99E-08	Up	1.21E+00	1.95E-02		-3.48E-01	4.48E-01		7.39E-01	2.23E-02		4.44E-01	1.60E-02		1.89E+00	1.26E-52	Up	Unigene51276_All//gi|224102125|ref|XP_002312557.1|//2.00E-58//autoinhibited calcium ATPase [Populus trichocarpa] >gi|222852377|gb|EEE89924.1| autoinhibited calcium ATPase [Populus trichocarpa]	Unigene51276_All//4.00E-45//AT3G63380| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12)	Unigene51276_All//0.00E+00//TC156972			GO:0000166//GO:0006811//GO:0008152//GO:0016020//GO:0042625	nr +
Unigene51278_All	370	0.42	0.82	0.86	6.46	2.33	1.95	0.91	1.69	2.15	9.54E-01	5.03E-01		1.03E+00	4.71E-01		-1.47E+00	1.89E-04	Down	-1.73E+00	6.61E-05	Down	8.90E-01	2.88E-01		1.24E+00	7.69E-02				Unigene51278_All//4.00E-07//EX166445				
Unigene51279_All	310	0.34	4.41	0.86	5.30	6.66	8.01	4.09	2.43	0.77	3.71E+00	7.17E-06	Up	1.35E+00	4.09E-01		3.30E-01	5.26E-01		5.96E-01	1.55E-01		-7.54E-01	1.63E-01		-2.41E+00	7.18E-05	Down	Unigene51279_All//gi|22327999|ref|NP_200933.2|//1.00E-20//AtGUS1 (Arabidopsis thaliana glucuronidase 1); beta-glucuronidase >gi|30697502|ref|NP_851238.1| AtGUS1 (Arabidopsis thaliana glucuronidase 1); beta-glucuronidase >gi|751539915|sp|Q8L608.1|HPSE2_ARATH RecName: Full=Heparanase-like protein 2; Flags: Precursor >gi|222424319|dbj|BAH20116.1| AT5G61250 [Arabidopsis thaliana]	Unigene51279_All//4.00E-22//AT5G61250| AtGUS1 (Arabidopsis thaliana glucuronidase 1); beta-glucuronidase	Unigene51279_All//7.00E-30//DW498596			GO:0005618//GO:0016787	nr +
Unigene51128_All	898	12.35	15.86	12.39	15.09	11.01	12.47	18.60	18.52	7.94	3.60E-01	1.71E-02		4.80E-03	1.00E+00		-4.55E-01	1.55E-03		-2.75E-01	9.03E-02		-5.70E-03	1.00E+00		-1.23E+00	8.11E-22	Down	Unigene5128_All//gi|18394379|ref|NP_564002.1|//1.00E-77//REV7; DNA binding [Arabidopsis thaliana] >gi|88190820|gb|ABD42969.1| Atlg16590 [Arabidopsis thaliana]	Unigene5128_All//5.00E-79//AT1G16590| REV7; DNA binding	Unigene5128_All//0.00E+00//DT527004				nr +
Unigene51280_All	502	17.09	7.57	19.20	7.14	3.64	3.78	2.02	0.08	0.16	-1.18E+00	9.94E-09	Down	1.68E-01	4.11E-01		-9.75E-01	1.33E-03		-9.19E-01	4.31E-03		-4.60E+00	3.67E-06	Down	-3.67E+00	1.15E-05	Down	Unigene51280_All//gi|115450671|ref|NP_001048936.1|//3.00E-25//Os03g0143000 [Oryza sativa Japonica Group] >gi|113547407|dbj|BAF10850.1| Os03g0143000 [Oryza sativa Japonica Group]	Unigene51280_All//3.00E-33//AT2G26200| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Methyltransferase type 12 (InterPro:IPR013217); BEST Arabidopsis thaliana protein match is: methyltransferase (TAIR:AT1G54650.1); Has 1504 Blast hits to 1429 proteins in 277 species: Archae - 33; Bacteria - 213; Metazoa - 664; Fungi - 202; Plants - 139; Viruses - 0; Other Eukaryotes - 253 (source: NCBI BLink).	Unigene51280_All//0.00E+00//CO083700		ko00350|Tyrosine metabolism//ko00450|Selenoamino acid metabolism//ko00340|Histidine metabolism	GO:0031410	nr +
Unigene51281_All	668	4.62	1.37	0.40	2.39	5.00	2.77	0.06	0.00	0.00	-1.76E+00	5.43E-06	Down	-3.54E+00	1.21E-11	Down	1.07E+00	1.23E-03		2.16E-01	6.91E-01		-5.98E+00	6.56E-01		-5.98E+00	6.12E-01		Unigene51281_All//gi|42562435|ref|NP_174416.2|//2.00E-37//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	Unigene51281_All//1.00E-10//AT2G35640| hydroxyproline-rich glycoprotein family protein	Unigene51281_All//0.00E+00//TC164245				nr +
Unigene51282_All	477	7.79	3.08	6.25	13.05	7.44	4.83	0.44	0.53	0.17	-1.34E+00	5.24E-05	Down	-3.17E-01	3.72E-01		-8.12E-01	2.14E-04		-1.43E+00	3.86E-09	Down	2.46E-01	8.53E-01		-1.41E+00	3.80E-01		Unigene51282_All//gi|159025701|emb|CAN88851.1|//2.00E-06//D1-type cyclin [Populus trichocarpa]		Unigene51282_All//0.00E+00//gi|73324373|gb|DT544647.1|DT544647				nr -
Unigene51283_All	858	0.85	3.54	0.99	1.57	2.29	2.26	0.89	2.73	3.02	2.05E+00	5.01E-07	Up	2.18E-01	7.57E-01		5.45E-01	2.68E-01		5.30E-01	2.89E-01		1.62E+00	4.26E-05	Up	1.77E+00	2.38E-06	Up	Unigene51283_All//gi|154678812|ref|NP_001057505.1|//1.00E-51//Os06g0318700 [Oryza sativa Japonica Group] >gi|75322005|sp|Q5Z A07.1|C3H41_ORYSJ RecName: Full=E3 ubiquitin-protein ligase makorin; AltName: Full=Zinc finger CCCH domain-containing protein 41; Short=OsC3H41 >gi|113395545|dbj|BAF19419.1| Os06g0318700 [Oryza sativa Japonica Group]	Unigene51283_All//2.00E-51//AT3G08505| zinc finger (CCCH-type/C3HC4-type RING finger) family protein	Unigene51283_All//0.00E+00//gi|109868994|gb|DW497970.1|DW497970	C3H		GO:0046914	nr -
Unigene51284_All	347	2.11	5.84	2.30	7.75	4.47	3.25	17.79	11.80	6.08	1.47E+00	2.05E-03		1.25E-01	8.66E-01		-7.96E-01	2.95E-02		-1.25E+00	1.20E-03		-5.92E-01	5.28E-03		-1.55E+00	6.97E-12	Down			Unigene51284_All//4.00E-87//TC159380				
Unigene51285_All	375	4.19	11.08	11.36	9.43	18.92	20.84	2.71	2.67	3.72	1.40E+00	7.96E-06	Up	1.44E+00	7.15E-06	Up	1.00E+00	1.79E-06	Up	1.14E+00	5.06E-08	Up	-1.66E-02	1.02E+00		4.59E-01	3.58E-01				Unigene51285_All//4.00E-07//BQ408443				
Unigene51286_All	1027	0.46	1.73	0.26	3.30	1.91	1.50	2.35	3.26	0.93	1.91E+00	4.26E-04	Up	-8.22E-01	4.57E-01		-7.87E-01	1.30E-02		-1.14E+00	6.61E-04	Down	4.72E-01	1.31E-01		-1.33E+00	2.65E-04	Down			Unigene51286_All//3.00E-41//FL577011				
Unigene51287_All	1147	0.78	0.35	0.93	4.39	3.90	2.44	3.47	1.28	2.08	-1.13E+00	1.30E-01		2.60E-01	6.82E-01		-1.69E-01	5.85E-01		-8.45E-01	1.32E-03		-1.44E+00	5.48E-07	Down	-7.34E-01	5.34E-03		Unigene51287_All//gi|38568043|emb|CAD40417.3|//5.00E-10//OSJNBa0065J03.13 [Oryza sativa (japonica cultivar-group)]							nr +
Unigene51288_All	466	54.45	71.98	75.30	103.37	86.01	111.94	135.82	120.45	67.88	4.03E-01	1.41E-05		4.68E-01	4.93E-07		-2.65E-01	2.43E-04		1.15E-01	1.72E-01		-1.73E-01	4.77E-03		-1.00E+00	7.50E-58	Down	Unigene51288_All//gi|14190445|gb|AK55703.1|AF378900_1//2.00E-48//At2g04520/T103.7 [Arabidopsis thaliana] >gi|15450561|gb|AAK96458.1| At2g04520/T103.7 [Arabidopsis thaliana]	Unigene51288_All//1.00E-38//AT2G04520| eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative	Unigene51288_All//6.00E-121//ES810424			GO:0006412//GO:0008135	nr +
Unigene51289_All	365	8.46	40.67	17.07	11.05	15.38	17.32	19.34	32.64	34.82	2.27E+00	1.02E-35	Up	1.01E+00	4.61E-05	Up	4.76E-01	5.91E-02		6.48E-01	5.55E-03		7.55E-01	2.85E-07		8.48E-01	1.70E-09		Unigene51289_All//gi|222423852|dbj|BAH19891.1|//2.00E-08//AT5G64170 [Arabidopsis thaliana]	Unigene51289_All//7.00E-10//AT5G64170| dentin sialophosphoprotein-related	Unigene51289_All//0.00E+00//TC176231				nr +
Unigene5129_All	534	17.05	55.89	22.94	17.82	23.73	30.79	49.64	56.82	31.71	1.71E+00	2.05E-49	Up	4.28E-01	1.19E-02		4.14E-01	7.48E-03		7.89E-01	4.88E-09		1.95E-01	3.61E-02		-6.47E-01	3.63E-12		Unigene5129_All//gi|39579116|gb|AAR28754.1|//3.00E-53//Bax inhibitor [Solanum lycopersicum]	Unigene5129_All//3.00E-53//AT5G47120| ATBI1 (BAX INHIBITOR 1)	Unigene5129_All//0.00E+00//TC153475				nr +
Unigene51290_All	1527	0.14	10.02	0.49	0.20	0.27	2.51	11.02	16.07	12.03	6.19E+00	1.31E-80	Up	1.83E+00	5.05E-02		4.68E-01	7.41E-01		3.68E+00	2.70E-16	Up	5.44E-01	2.92E-08		1.26E-01	3.26E-01		Unigene51290_All//gi|292677823|dbj|BAI99253.1|//2.00E-86//trehalose 6-phosphate phosphatase [Nicotiana tabacum]	Unigene51290_All//6.00E-89//AT1G35910| trehalose-6-phosphate phosphatase, putative	Unigene51290_All//5.00E-10//TC179008		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0019203	nr +
Unigene51291_All	680	10.16	2.24	8.77	12.75	11.24	9.03	7.34	2.77	2.93	-2.18E+00	2.33E-16	Down	-2.12E-01	3.97E-01		-1.81E-01	4.16E-01		-4.97E-01	1.12E-02		-1.41E+00	2.68E-08	Down	-1.32E+00	6.47E-08	Down	Unigene51291_All//gi|255546949|ref|XP_002514532.1|//4.00E-62//Diacylglycerol Cholinephosphotransferase [Ricinus communis] >gi|223546136|gb|EEF47638.1| Diacylglycerol Cholinephosphotransferase [Ricinus communis]	Unigene51291_All//3.00E-62//AT1G13560| AAPT1 (AMINOALCOHOLPHOSPHOTRANSFERASE 1); phosphatidyltransferase/ phosphotransferase, for other substituted phosphate groups	Unigene51291_All//0.00E+00//TC168382		ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism	GO:0006644//GO:0017169//GO:0043231	nr +
Unigene51292_All	439	13.23	17.20	17.59	28.03	18.12	18.93	17.82	8.19	5.35	3.79E-01	8.04E-02		4.11E-01	6.56E-02		-6.29E-01	2.28E-05		-5.66E-01	3.30E-04		-1.12E+00	4.60E-09	Down	-1.73E+00	2.62E-17	Down	Unigene51292_All//gi|225346677|gb|ACN86360.1|//3.00E-20//GID1-5 [Gossypium hirsutum]	Unigene51292_All//4.00E-17//AT5G27320| GID1C (GA INSENSITIVE DWARF1C); hydrolase	Unigene51292_All//3.00E-159//gi|78327948|gb|DT548222.1|DT548222			GO:0003006//GO:0004871//GO:0005488//GO:0009312//GO:0009740//GO:0016788	nr +
Unigene51293_All	1303	4.34	0.27	1.72	3.13	1.30	1.32	0.94	0.06	0.37	-3.99E+00	3.48E-24	Down	-1.34E+00	8.23E-07	Down	-1.28E+00	7.37E-06	Down	-1.25E+00	3.60E-05	Down	-3.87E+00	1.15E-06	Down	-1.36E+00	1.18E-02		Unigene51293_All//gi|92893902|gb|ABE91952.1|//4.00E-22//Zinc finger, CCHC-type [Medicago truncatula]	Unigene51293_All//4.00E-15//AT2G01050| nucleic acid binding / zinc ion binding	Unigene51293_All//5.00E-142//BQ408876				nr +
Unigene51294_All	254	57.06	47.68	51.15	54.52	59.52	53.70	120.18	72.57	55.05	-2.59E-01	9.19E-02		-1.58E-01	3.63E-01		1.27E-01	4.64E-01		-2.19E-02	9.17E-01		-7.28E-01	2.27E-16		-1.13E+00	3.15E-34	Down	Unigene51294_All//gi|2511576|emb|CAA73620.1|//8.00E-38//multicatalytic endopeptidase [Arabidopsis thaliana]	Unigene51294_All//3.00E-39//AT5G40580| PBR2; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene51294_All//2.00E-141//gi|18099171|gb|BM358425.1|BM358425		ko03050|Proteasome	GO:0000502//GO:0004175//GO:0019941//GO:0043231	nr +
Unigene51295_All	672	0.47	0.75	0.63	6.89	24.24	26.08	21.58	57.72	123.19	6.91E-01	4.99E-01		4.40E-01	6.77E-01		1.81E+00	3.48E-34	Up	1.92E+00	1.96E-36	Up	1.42E+00	7.71E-60	Up	2.51E+00	4.22E-278	Up	Unigene51295_All//gi|3426064|emb|CAA07575.1|//2.00E-57//monooxygenase [Arabidopsis thaliana] >gi|4467141|emb|CAB37510.1| monooxygenase 2 (MO2) [Arabidopsis thaliana] >gi|7270837|emb|CAB80518.1| monooxygenase 2 (MO2) [Arabidopsis thaliana]	Unigene51295_All//1.00E-58//AT4G38540| monooxygenase, putative (MO2)	Unigene51295_All//7.00E-32//gi|48787532|gb|CO090429.1|CO090429		ko00906|Carotenoid biosynthesis	GO:0008152//GO:0016491	nr +
Unigene51296_All	718	0.66	0.00	0.30	0.83	1.44	0.50	0.71	0.93	2.44	-9.36E+00	5.55E-03		-1.14E+00	3.32E-01		7.89E-01	2.74E-01		-7.26E-01	4.60E-01		3.99E-01	6.48E-01		1.79E+00	1.28E-04	Up	Unigene51296_All//gi|87116458|dbj|BAE79381.1|//4.00E-09//unnamed protein product [Ipomoea batatas]	Unigene51296_All//2.00E-05//AT2G01050| nucleic acid binding / zinc ion binding					nr -
Unigene51298_All	486	1.72	0.10	2.63	3.69	6.73	3.35	0.52	1.98	0.82	-4.05E+00	4.65E-04	Down	6.10E-01	3.33E-01		8.67E-01	9.59E-03		-1.41E-01	7.72E-01		1.92E+00	5.42E-03		6.51E-01	5.44E-01		Unigene51298_All//gi|124360549|gb|ABD33126.2|//1.00E-25//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene51298_All//8.00E-08//AT1G43760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706), Endonuclease/exonuclease/phosphatase (InterPro:IPR005135); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40390.1); Has 2614 Blast hits to 2551 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 1517; Fungi - 2; Plants - 1086; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene51298_All//4.00E-156//DW241491				nr +
Unigene5130_All	857	8.06	12.83	6.90	10.23	9.76	4.85	0.15	0.05	0.05	6.71E-01	9.32E-05		-2.25E-01	3.80E-01		-6.73E-02	7.98E-01		-1.08E+00	2.80E-08	Down	-1.60E+00	5.34E-01		-1.67E+00	4.77E-01		Unigene5130_All//gi|124359162|gb|ABN05685.1|//5.00E-20//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene5130_All//2.00E-15//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene5130_All//0.00E+00//TC135955				nr -
Unigene51300_All	834	864.05	90.16	134.34	5.38	6.94	1.14	0.15	0.20	0.19	-3.26E+00	0.00E+00	Down	-2.69E+00	0.00E+00	Down	3.68E-01	1.55E-01		-2.24E+00	5.87E-12	Down	3.99E-01	8.14E-01		3.29E-01	8.51E-01		Unigene51300_All//gi|17473703|gb|AL38307.1|//3.00E-74//germin-like protein [Arabidopsis thaliana] >gi|20148495|gb|AAM10138.1| germin-like protein [Arabidopsis thaliana]	Unigene51300_All//7.00E-69//AT1G72610| GER1 (GERMIN-LIKE PROTEIN 1); oxalate oxidase	Unigene51300_All//0.00E+00//TC140887			GO:0005618//GO:0006950//GO:0016209//GO:0016616//GO:0016623//GO:0019852//GO:0042353//GO:0043231//GO:0044421//GO:0046914	nr -
Unigene51301_All	541	8.41	20.70	9.35	3.41	7.26	1.84	0.00	0.00	0.00	1.30E+00	7.48E-13	Up	1.52E-01	6.29E-01		1.09E+00	2.71E-04	Up	-8.91E-01	6.61E-02		null	null		null	null				Unigene51301_All//6.00E-07//EX167301				
Unigene51302_All	274	25.21	8.32	11.27	46.72	35.82	42.20	7.56	6.25	8.58	-1.60E+00	5.45E-11	Down	-1.16E+00	1.07E-06	Down	-3.84E-01	1.19E-02		-1.47E-01	4.30E-01		-2.74E-01	5.35E-01		1.82E-01	6.38E-01				Unigene51302_All//5.00E-126//TC164500				
Unigene51304_All	918	0.34	1.66	0.75	3.15	1.35	1.28	0.41	1.00	0.09	2.28E+00	2.68E-04	Up	1.14E+00	2.18E-01		-1.22E+00	4.43E-04	Down	-1.30E+00	4.76E-04	Down	1.27E+00	5.59E-02		-2.26E+00	6.49E-02		Unigene51304_All//gi|15226168|ref|NP_178215.1|//6.00E-18//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene51304_All//4.00E-19//AT2G01050| nucleic acid binding / zinc ion binding					nr -

Unigene51307_All	525	116.60	280.47	133.78	347.18	232.06	425.65	113.31	83.75	43.56	1.27E+00	2.77E-154	Up	1.98E-01	2.91E-03		-5.81E-01	5.09E-63		2.94E-01	1.40E-19		-4.36E-01	7.23E-13		-1.38E+00	3.10E-90	Down	Unigene51307_All//gi|18399308|ref|NP_566396.1|//1.00E-37//NHL1 [Arabidopsis thaliana] >gi|9502172|gb|AAF88021.1|AF264697_1 NDR1/HIN1-Like protein 1 [Arabidopsis thaliana] >gi|21595601|gb|AAM66116.1| harpin-induced protein-like [Arabidopsis thaliana] >gi|56381911|gb|AAV85674.1| At3g11660 [Arabidopsis thaliana] >gi|58331799|gb|AAW70397.1| At3g11660 [Arabidopsis thaliana]	Unigene51307_All//6.00E-39//AT3G11660| NHL1	Unigene51307_All//0.00E+00//gi|84145585|gb|DN759827.1|DN759827			GO:0002252	nr -
Unigene51308_All	465	1.69	0.54	0.69	1.61	2.22	1.36	0.73	2.97	4.20	-1.63E+00	5.37E-02		-1.30E+00	1.38E-01		4.67E-01	5.51E-01		-2.41E-01	7.56E-01		2.03E+00	3.35E-04	Up	2.53E+00	2.55E-07	Up									
Unigene51309_All	454	0.58	0.67	0.59	0.44	0.99	1.09	0.19	1.57	3.16	2.17E-01	8.64E-01		2.56E-02	1.00E+00		1.17E+00	3.47E-01		1.32E+00	2.52E-01		3.07E+00	1.67E-03		4.08E+00	3.98E-08	Up									
Unigene5131_All	900	0.52	0.11	0.06	1.49	0.65	0.00	0.00	0.00	0.00	-2.22E+00	7.76E-02		-3.14E+00	4.00E-02		-1.20E+00	3.02E-02		-1.05E+01	2.08E-08	Down	null	null		null	null		Unigene5131_All//gi|124359162|gb|ABN05685.1|//5.00E-21//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene5131_All//2.00E-15//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene5131_All//0.00E+00//TC135955				nr -
Unigene51311_All	510	11.80	5.17	8.14	5.47	6.55	6.82	0.33	0.90	1.48	-1.19E+00	1.75E-06	Down	-5.35E-01	3.54E-02		2.60E-01	5.15E-01		3.18E-01	4.00E-01		1.44E+00	1.67E-01		2.16E+00	6.98E-03		Unigene51311_All//gi|15227067|ref|NP_178398.1|//2.00E-31//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|218546779|sp|Q8LK93.2|PP145_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g02980	Unigene51311_All//5.00E-29//AT2G02980| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene51312_All	417	1.51	0.00	1.02	2.75	3.47	3.68	1.72	1.50	0.57	-1.06E+01	7.91E-04	Down	-5.60E-01	5.53E-01		3.36E-01	5.83E-01		4.23E-01	4.76E-01		-1.97E-01	7.84E-01		-1.59E+00	3.62E-02		Unigene51312_All//gi|145359511|ref|NP_200919.2|//2.00E-10//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene51312_All//1.00E-11//AT5G41110| protein binding / zinc ion binding	Unigene51312_All//0.00E+00//TC142480			GO:0005488	nr +
Unigene51313_All	1175	2.63	2.11	5.39	0.00	0.00	0.00	0.29	0.07	0.00	-3.14E-01	3.89E-01		1.04E+00	2.59E-05	Up	null	null		null	null		-2.02E+00	1.36E-01		-8.17E+00	8.14E-03		Unigene51313_All//gi|57233444|gb|AAW48295.1|//8.00E-57//pore-forming toxin-like protein Hfr-2 [Triticum aestivum]		Unigene51313_All//2.00E-08//TC175906				nr +
Unigene51314_All	501	5.43	13.25	5.00	7.46	7.84	11.27	7.93	4.25	3.50	1.29E+00	7.85E-08	Up	-1.21E-01	7.54E-01		7.14E-02	8.38E-01		5.96E-01	1.80E-02		-8.99E-01	1.01E-03		-1.18E+00	1.45E-05	Down			Unigene51314_All//2.00E-108//gi|13245139|gb|BE054321.2|BE054321				
Unigene51318_All	543	11.27	8.21	5.30	10.46	5.14	7.07	0.16	0.15	0.29	-4.57E-01	5.87E-02		-1.09E+00	1.64E-05	Down	-1.03E+00	9.82E-06	Down	-5.65E-01	2.37E-02		-1.68E-02	1.01E+00		9.15E-01	6.24E-01		Unigene51318_All//gi|297851686|ref|XP_002893724.1|//1.00E-41//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339566|gb|EFH69983.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51318_All//2.00E-42//AT1G32450| NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	Unigene51318_All//3.00E-52//TC151543			GO:0004871//GO:0015833//GO:0044464	nr +
Unigene51320_All	433	1.21	2.93	0.25	1.38	2.07	2.19	0.78	2.51	6.72	1.28E+00	3.83E-02		-2.30E+00	6.76E-02		5.83E-01	4.72E-01		6.66E-01	3.93E-01		1.68E+00	6.95E-03		3.10E+00	7.46E-13	Up									
Unigene51321_All	630	2.24	6.68	1.94	1.50	3.39	2.87	0.54	1.59	9.74	1.57E+00	8.27E-07	Up	-2.06E-01	7.06E-01		1.17E+00	7.39E-03		9.33E-01	6.07E-02		1.57E+00	1.54E-02		4.18E+00	1.71E-33	Up									ESTscan +
Unigene51322_All	645	2.27	7.70	4.05	11.89	11.05	10.57	2444.91	4124.04	2480.74	1.76E+00	3.97E-09	Up	8.33E-01	4.25E-02		-1.06E-01	6.62E-01		-1.70E-01	4.85E-01		7.54E-01	0.00E+00		2.10E-02	8.99E-02		Unigene51322_All//gi|66276977|gb|AY144115.1|//2.00E-87//dirigent-like protein [Gossypium barbadense]	Unigene51322_All//1.00E-33//AT2G21110| disease resistance-responsive family protein	Unigene51322_All//0.00E+00//TC136177				nr +
Unigene51323_All	1869	0.00	0.00	0.23	0.67	0.29	0.00	29.00	4.09	0.58	null	null		7.83E+00	1.38E-02		-1.18E+00	4.23E-02		-9.38E+00	8.64E-08	Down	-2.83E+00	2.79E-204	Down	-5.66E+00	0.00E+00	Down	Unigene51323_All//gi|297851686|ref|XP_002893724.1|//0.00E+00//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339566|gb|EFH69983.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51323_All//0.00E+00//AT1G32450| NRT1.5 (NITRATE TRANSPORTER 1.5); nitrate transmembrane transporter/ transporter	Unigene51323_All//0.00E+00//TC160811			GO:0004871//GO:0015833//GO:0044464	nr -
Unigene51325_All	1353	0.70	0.19	0.31	28.98	26.49	16.12	3.09	0.56	0.47	-1.89E+00	1.53E-02		-1.14E+00	1.38E-01		-1.29E-01	1.67E-01		-8.46E-01	1.67E-23		-2.48E+00	3.07E-14	Down	-2.72E+00	2.90E-16	Down	Unigene51325_All//gi|30693682|ref|NP_175030.2|//1.00E-110//integral membrane family protein / nodulin MtN21-related [Arabidopsis thaliana] >gi|449517563|gb|AAS49106.1| Atlg43650 [Arabidopsis thaliana] >gi|51970578|dbj|BAD43981.1| nodulin-like protein [Arabidopsis thaliana]	Unigene51325_All//5.00E-94//AT1G43650| integral membrane family protein / nodulin MtN21-related	Unigene51325_All//0.00E+00//TC144095			GO:0044464	nr +
Unigene51326_All	534	1.37	0.95	2.99	0.56	2.26	2.54	2.85	2.58	3.13	-5.32E-01	5.13E-01		1.13E+00	4.27E-02		2.01E+00	2.81E-03		2.18E+00	8.25E-04	Up	-1.42E-01	7.70E-01		1.37E-01	7.54E-01		Unigene51326_All//gi|22327146|ref|NP_198205.2|//4.00E-41//FRS10 (FAR1-related sequence 10); zinc ion binding [Arabidopsis thaliana] >gi|257051024|sp|Q9LKR4.2|FRS10_ARATH RecName: Full=Putative protein FAR1-RELATED SEQUENCE 10	Unigene51326_All//2.00E-42//AT5G28530| FRS10 (FAR1-related sequence 10); zinc ion binding	Unigene51326_All//1.00E-128//ES806201			GO:0046914	nr +
Unigene51327_All	311	1.18	7.82	5.14	4.48	2.44	3.19	26.10	23.25	14.73	2.73E+00	9.67E-08	Up	2.13E+00	5.41E-04	Up	-8.81E-01	1.06E-01		-4.89E-01	4.09E-01		-1.67E-01	4.16E-01		-8.25E-01	3.54E-06				Unigene51327_All//2.00E-132//TC169574				
Unigene51328_All	727	4.68	1.81	4.91	11.17	14.45	29.07	0.00	0.23	0.00	-1.37E+00	8.83E-05	Down	6.91E-02	8.37E-01		3.71E-01	3.56E-02		1.38E+00	1.44E-27	Up	7.85E+00	1.39E-01		null	null		Unigene51328_All//gi|225456461|ref|XP_002284464.1|//2.00E-53//PREDICTED: similar to bHLH transcription factor Upa20 [Vitis vinifera]	Unigene51328_All//9.00E-22//AT3G07340| basic helix-loop-helix (bHLH) family protein	Unigene51328_All//2.00E-44//TC159484	bHLH	ko04712|Circadian rhythm - plant		nr -
Unigene51330_All	647	0.57	0.55	0.99	1.08	1.38	2.30	0.33	0.78	2.03	-4.64E-02	9.82E-01		8.03E-01	3.88E-01		3.60E-01	6.55E-01		1.10E+00	5.01E-02		1.25E+00	2.04E-01		2.64E+00	2.27E-05	Up	Unigene51330_All//gi|79334443|ref|NP_171714.2|//7.00E-07//VAD1 (VASCULAR ASSOCIATED DEATH1) [Arabidopsis thaliana]	Unigene51330_All//1.00E-07//AT1G02120| VAD1 (VASCULAR ASSOCIATED DEATH1)	Unigene51330_All//7.00E-72//CO109052				nr +
Unigene51333_All	379	3.87	0.40	3.51	4.99	3.27	0.72	16.73	2.10	1.79	-3.27E+00	8.97E-06	Down	-1.38E-01	7.97E-01		-6.11E-01	1.90E-01		-2.80E+00	9.56E-07	Down	-3.00E+00	6.40E-26	Down	-3.23E+00	9.36E-29	Down	Unigene51333_All//gi|297816776|ref|XP_002876271.1|//2.00E-06//PIP2_5/PIP2D [Arabidopsis lyrata subsp. lyrata] >gi|297322109|gb|EFH52530.1| PIP2_5/PIP2D [Arabidopsis lyrata subsp. lyrata]	Unigene51333_All//5.00E-07//AT3G53420| PIP2A (PLASMA MEMBRANE INTRINSIC PROTEIN 2A); water channel	Unigene51333_All//1.00E-31//TC166797			GO:0005372//GO:0006810//GO:0031224	nr +
Unigene51334_All	728	15.31	4.80	3.88	26.14	19.02	5.15	2.79	0.52	0.88	-1.67E+00	2.19E-18	Down	-1.98E+00	4.79E-22	Down	-4.59E-01	9.42E-05		-2.34E+00	5.18E-52	Down	-2.43E+00	4.04E-07	Down	-1.67E+00	6.85E-05	Down	Unigene51334_All//gi|2500715|sp|Q40374.1|PR1_MEDTR//7.00E-62//RecName: Full=Pathogenesis-related protein PR-1; Flags: Precursor >gi|505553|emb|CAA56174.1| PR-1 [Medicago truncatula]	Unigene51334_All//3.00E-59//AT4G36320| allergen V5/Tpx-1-related family protein	Unigene51334_All//0.00E+00//TC139677		ko04626|Plant-pathogen interaction	GO:0031410//GO:0050896	nr +
Unigene51336_All	232	59.31	36.04	27.54	76.22	61.89	87.80	112.44	38.01	52.55	-7.19E-01	2.15E-06		-1.11E+00	8.42E-12	Down	-3.00E-01	2.08E-02		2.04E-01	1.29E-01		-1.56E+00	8.92E-47	Down	-1.10E+00	3.27E-28	Down	Unigene51336_All//gi|192910792|gb|ACF06504.1|//7.00E-29//60S ribosomal protein L28 [Elaeis guineensis]	Unigene51336_All//2.00E-20//AT2G19730| 60S ribosomal protein L28 (RPL28A)	Unigene51336_All//2.00E-128//TC158764		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene51337_All	559	0.47	4.71	0.29	1.43	1.11	2.59	8.17	8.97	11.33	3.33E+00	5.96E-10	Up	-7.12E-01	6.22E-01		-3.63E-01	6.23E-01		8.59E-01	1.33E-01		1.35E-01	6.52E-01		4.72E-01	2.10E-02				Unigene51337_All//0.00E+00//TC144399				
Unigene51338_All	666	1.73	1.67	2.56	0.97	0.67	0.41	12.19	28.93	11.01	-4.62E-02	9.53E-01		5.66E-01	2.83E-01		-5.33E-01	5.38E-01		-1.26E+00	1.83E-01		1.25E+00	7.93E-25	Up	-1.47E-01	4.60E-01		Unigene51338_All//gi|224132940|ref|XP_002321447.1|//1.00E-42//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222868443|gb|EEF05574.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene51338_All//5.00E-29//AT5G61430| ANAC100 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 100); transcription factor	Unigene51338_All//0.00E+00//TC170082	NAC			nr -
Unigene5134_All	1811	0.69	0.56	0.12	0.30	0.51	0.67	1.91	3.83	5.81	-3.09E-01	6.21E-01		-2.56E+00	6.99E-04	Down	7.63E-01	3.19E-01		1.15E+00	7.02E-02		1.00E+00	7.05E-07	Up	1.60E+00	2.27E-20	Up	Unigene5134_All//gi|22087199|gb|AAM90876.1|AF487814_1//1.00E-131//RPS2 [Arabidopsis thaliana] >gi|22087201|gb|AAM90877.1|AF487815_1 RPS2 [Arabidopsis thaliana] >gi|22087203|gb|AAM90878.1|AF487816_1 RPS2 [Arabidopsis thaliana] >gi|156069022|gb|ABU44504.1| RPS2 [Arabidopsis thaliana]	Unigene5134_All//5.00E-128//AT4G26090| RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene51340_All	646	0.97	0.16	0.00	3.62	2.45	0.56	19.24	10.87	9.44	-2.63E+00	1.78E-02		-9.92E+00	1.41E-03		-5.64E-01	1.68E-01		-2.70E+00	6.56E-08	Down	-8.24E-01	1.14E-08		-1.03E+00	1.36E-12	Down	Unigene51340_All//gi|30017239|gb|AAP12853.1|//8.00E-37//At5g49350 [Arabidopsis thaliana]	Unigene51340_All//3.00E-33//AT5G49350| unknown protein	Unigene51340_All//0.00E+00//DW518446			GO:0044464	nr -
Unigene51343_All	1874	0.00	0.00	0.00	0.00	0.04	0.00	37.81	6.29	14.20	null	null		null	null		5.20E+00	6.08E-01		null	null		-2.59E+00	1.62E-242	Down	-1.41E+00	2.62E-111	Down	Unigene51343_All//gi|224111880|ref|XP_002316010.1|//1.00E-118//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene51343_All//4.00E-99//AT3G14620| CYP72A8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene51343_All//0.00E+00//TC133857		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0016491	nr +
Unigene51346_All	843	0.99	0.84	1.01	1.77	2.57	1.61	2.81	0.64	1.89	-2.39E-01	7.25E-01		2.55E-02	9.93E-01		5.38E-01	2.39E-01		-1.41E-01	7.88E-01		-2.12E+00	4.52E-07	Down	-5.71E-01	1.09E-01		Unigene51346_All//gi|79530257|ref|NP_199384.2|//2.00E-82//ATP-binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene51346_All//6.00E-68//AT5G45720| ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding	Unigene51346_All//6.00E-116//ES848555			GO:0000166//GO:0016779//GO:0043231	nr +
Unigene51347_All	1241	0.00	0.16	0.00	0.04	0.03	0.00	8.04	2.93	5.65	7.35E+00	1.36E-01		null	null		-5.34E-01	8.25E-01		-5.33E+00	6.34E-01		-1.46E+00	1.33E-16	Down	-5.09E-01	1.18E-03									
Unigene51349_All	674	8.93	2.86	3.40	6.65	3.68	2.21	0.75	0.43	0.24	-1.64E+00	4.94E-10	Down	-1.39E+00	1.23E-07	Down	-8.55E-01	1.33E-03		-1.59E+00	9.48E-08	Down	-7.94E-01	4.02E-01		-1.67E+00	7.78E-02		Unigene51349_All//gi|256002927|gb|ACU52707.1|//9.00E-51//bHLH transcription factor PTF1 [Glycine max]	Unigene51349_All//3.00E-34//AT3G57800| basic helix-loop-helix (bHLH) family protein	Unigene51349_All//0.00E+00//TC177000	bHLH		GO:0001071//GO:0003676//GO:0010468//GO:0043231	nr -
Unigene5135_All	1224	0.90	1.16	0.96	18.15	15.39	10.89	17.06	9.66	5.57	3.69E-01	5.15E-01		9.24E-02	8.81E-01		-2.38E-01	4.28E-02		-7.38E-01	7.55E-11		-8.20E-01	6.61E-14		-1.62E+00	1.38E-40	Down	Unigene5135_All//gi|53828519|gb|AAD94369.1|//8.00E-87//At1g78110 [Arabidopsis thaliana] >gi|55167926|gb|AAV43795.1| At1g78110 [Arabidopsis thaliana]	Unigene5135_All//3.00E-75//AT1G78110| unknown protein	Unigene5135_All//0.00E+00//TC171676				nr +
Unigene51350_All	213	215.92	125.84	180.75	83.73	91.34	96.48	60.34	23.35	23.38	-7.79E-01	2.88E-22		-2.57E-01	1.95E-03		1.26E-01	3.99E-01		2.05E-01	1.26E-01		-1.37E+00	2.31E-19	Down	-1.37E+00	6.13E-20	Down	Unigene51350_All//gi|224113289|ref|XP_002332617.1|//3.00E-31//precursor of carboxylase t-protein 2, glycine decarboxylase complex [Populus trichocarpa] >gi|222832818|gb|EEE71295.1| precursor of carboxylase t-protein 2, glycine decarboxylase complex [Populus trichocarpa]	Unigene51350_All//1.00E-31//AT1G11860| aminomethyltransferase, putative	Unigene51350_All//2.00E-115//BG445901		ko00910|Nitrogen metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate	GO:0005576//GO:0005840//GO:0006544//GO:0008168//GO:0009526//GO:0010038//GO:0016769//GO:0043234	nr -
Unigene51352_All	356	36.15	139.77	114.73	18.61	27.95	30.57	0.00	0.23	0.45	1.95E+00	7.49E-98	Up	1.67E+00	3.88E-63	Up	5.87E-01	6.75E-04		7.16E-01	2.33E-05		7.88E+00	4.00E-01		8.81E+00	1.40E-01				Unigene51352_All//4.00E-35//gi|109874872|gb|DW503846.1|DW503846				

Unigene51353_All	616	0.85	0.74	0.35	4.93	4.47	1.47	7.07	1.76	4.98	-1.98E-01	8.20E-01		-1.30E+00	2.42E-01		-1.42E-01	7.31E-01		-1.75E+00	3.65E-06	Down	-2.00E+00	1.44E-11	Down	-5.06E-01	4.46E-02		Unigene51353_All//gi|225458467|ref|XP_002282153.1|//3.00E-43//PREDICTED: similar to ATS/KAN4 (ABERRANT TESTA SHAPE); DNA binding / transcription factor [Vitis vinifera]	Unigene51353_All//8.00E-23//AT5G42630| ATS (ABERRANT TESTA SHAPE); DNA binding / transcription factor		G2-like		GO:0001071//GO:0003006//GO:0010468//GO:0030312	nr -
Unigene51354_All	651	0.00	1.71	0.00	9.26	8.99	9.44	1.62	1.61	1.96	1.07E+01	2.00E-06	Up	null	null		-4.22E-02	8.72E-01		2.72E-02	9.36E-01		-1.66E-02	1.01E+00		2.70E-01	6.10E-01		Unigene51354_All//gi|28628203|gb|AA027366.1|//3.00E-31//rapid alkalinization factor 1 precursor [Populus trichocarpa x Populus deltoides]	Unigene51354_All//3.00E-27//AT4G15800| RALFL33 (ralf-like 33); signal transducer	Unigene51354_All//3.00E-15//TC166256			GO:0005576//GO:0005618//GO:0060089	nr +
Unigene51355_All	760	4.34	1.53	0.21	4.19	1.36	1.07	0.50	0.66	0.31	-1.50E+00	3.18E-05	Down	-4.37E+00	2.15E-14	Down	-1.63E+00	1.54E-06	Down	-1.97E+00	1.90E-07	Down	3.98E-01	6.52E-01		-6.71E-01	5.30E-01		Unigene51355_All//gi|194136581|gb|ACF33513.1|//8.00E-99//salicylic acid methyl transferase-like protein [Glycine max]	Unigene51355_All//3.00E-91//AT4G36470| S-adenosyl-L-methionine:carboxyl methyltransferase family protein	Unigene51355_All//0.00E+00//ES847032		ko00592|alpha-Linolenic acid metabolism	GO:0008168	nr -
Unigene51358_All	523	2.50	1.65	6.62	1.52	2.90	1.64	1.46	0.96	1.75	-6.03E-01	3.07E-01		1.40E+00	9.49E-05	Up	9.27E-01	9.02E-02		1.06E-01	9.05E-01		-6.02E-01	4.12E-01		2.68E-01	6.61E-01		Unigene51358_All//gi|38345931|emb|CAE01923.2|//2.00E-32//OSJNBa0078D11.6 [Oryza sativa (japonica cultivar-group)]	Unigene51358_All//9.00E-35//AT4G38360| unknown protein	Unigene51358_All//9.00E-40//DT463109			GO:0031410//GO:0043231	nr +
Unigene51359_All	298	1.93	6.46	3.22	1.00	1.27	1.21	2.55	9.26	3.48	1.74E+00	5.85E-04	Up	7.36E-01	3.23E-01		3.42E-01	8.36E-01		2.74E-01	8.33E-01		1.86E+00	6.26E-07	Up	4.45E-01	4.58E-01					Unigene51359_All//2.00E-89//TC139073				
Unigene5136_All	1392	0.00	0.15	0.00	5.26	1.39	0.91	29.16	42.04	7.98	7.19E+00	1.36E-01		null	null		-1.93E+00	3.88E-18	Down	-2.53E+00	3.54E-22	Down	5.28E-01	1.32E-17		-1.87E+00	1.45E-95	Down	Unigene5136_All//gi|297837201|ref|XP_002886482.1|//1.00E-122//C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297323223|gb|EFH62741.1| C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5136_All//1.00E-101//AT1G62280| SLAH1 (SLAC1 HOMOLOGUE 1); transporter					nr +
Unigene51362_All	777	0.40	1.11	0.21	0.77	2.08	1.86	2.34	0.75	1.54	1.46E+00	6.59E-02		-9.75E-01	5.06E-01		1.44E+00	6.58E-03		1.27E+00	2.66E-02		-1.64E+00	3.51E-04	Down	-6.05E-01	1.46E-01		Unigene51362_All//gi|240256292|ref|NP_196927.4|//3.00E-86//protein binding [Arabidopsis thaliana]	Unigene51362_All//1.00E-87//AT5G14230| protein binding	Unigene51362_All//0.00E+00//gi|78327230|gb|DT547504.1|DT547504				nr +
Unigene51363_All	589	0.89	1.55	2.44	1.18	1.34	2.07	0.65	1.63	2.64	8.02E-01	2.71E-01		1.46E+00	1.58E-02		1.84E-01	8.27E-01		8.06E-01	2.11E-01		1.34E+00	4.02E-02		2.03E+00	8.65E-05	Up							
Unigene51365_All	357	1.91	1.99	1.49	4.19	2.99	0.51	2.72	0.94	1.12	6.06E-02	9.57E-01		-3.53E-01	6.64E-01		-4.85E-01	3.82E-01		-3.05E+00	7.42E-06	Down	-1.54E+00	1.90E-02		-1.29E+00	3.62E-02		Unigene51365_All//gi|116310214|emb|CAH67224.1|//2.00E-30//OSIGBa0145M07.6 [Oryza sativa (indica cultivar-group)]	Unigene51365_All//6.00E-31//AT5G18480| PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene51365_All//6.00E-71//A1727790			GO:0004527//GO:0005488//GO:0005975//GO:0031410//GO:0034641//GO:00352 51	nr -
Unigene51368_All	529	7.12	19.44	16.21	3.20	1.76	2.73	0.32	0.00	0.30	1.45E+00	7.07E-14	Up	1.19E+00	1.96E-08	Up	-8.65E-01	7.39E-02		-2.29E-01	6.77E-01		-8.32E+00	1.34E-01		-8.60E-02	9.65E-01		Unigene51368_All//gi|12002853|gb|AC43405.1|AF172901.1|//2.00E-59//homeobox 1 [Picea abies]	Unigene51368_All//2.00E-52//AT1G05230| HDG2 (HOMEODOMAIN GLABROUS 2); DNA binding / transcription factor	Unigene51368_All//0.00E+00//gi|78344128|gb|DT564402.1|DT564402	HB		GO:0000904//GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:00432 31	nr -
Unigene5137_All	2509	0.04	4.73	0.04	0.34	0.49	4.97	7.04	11.63	32.93	6.82E+00	3.42E-64	Up	2.40E-02	9.99E-01		5.50E-01	4.06E-01		3.88E+00	1.45E-54	Up	7.23E-01	1.70E-15		2.23E+00	4.51E-240	Up	Unigene5137_All//gi|297843872|ref|XP_002889817.1|//1.00E-175//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335659|gb|EFH66076.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5137_All//4.00E-173//AT1G10560| PUB18 (PLANT U-BOX 18); ubiquitin-protein ligase	Unigene5137_All//0.00E+00//TC172975		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene51371_All	439	15.26	4.16	8.61	42.10	37.10	25.00	7.22	15.42	16.15	-1.88E+00	3.62E-13	Down	-8.25E-01	4.89E-04		-1.82E-01	1.92E-01		-7.52E-01	2.04E-09		1.09E+00	1.16E-07	Up	1.16E+00	6.06E-09	Up				Unigene51371_All//9.00E-52//gi|78337086|gb|DT557360.1|DT557360				
Unigene51372_All	612	57.45	220.40	102.76	75.29	89.58	112.54	108.19	152.50	59.43	1.94E+00	1.80E-262	Up	8.39E-01	5.30E-33		2.51E-01	2.31E-04		5.80E-01	3.59E-21		4.95E-01	1.16E-24		-8.64E-01	1.80E-47					Unigene51372_All//5.00E-165//TC148036				
Unigene51375_All	1735	0.60	0.15	0.12	4.16	1.98	0.78	4.56	0.34	0.51	-2.05E+00	6.29E-03		-2.30E+00	4.70E-03		-1.07E+00	1.33E-07	Down	-2.41E+00	1.04E-20	Down	-3.76E+00	3.01E-39	Down	-3.17E+00	3.98E-35	Down	Unigene51375_All//gi|223452544|gb|ACM89599.1|//0.00E+00//receptor-kinase like protein [Glycine max]	Unigene51375_All//3.00E-64//AT4G08850| kinase	Unigene51375_All//3.00E-175//gi|31073637|gb|CA993916.1|CA993916		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016772	nr +
Unigene51376_All	1082	0.48	0.00	0.00	6.81	4.39	2.75	0.90	0.31	0.41	-8.92E+00	2.92E-03		-8.92E+00	4.75E-03		-6.34E-01	1.61E-03		-1.31E+00	2.30E-09	Down	-1.54E+00	1.90E-02		-1.15E+00	5.83E-02		Unigene51376_All//gi|506534|emb|CAA50374.1|//1.00E-154//protein kinase [Nicotiana tabacum]	Unigene51376_All//7.00E-150//AT2G20470| kinase	Unigene51376_All//3.00E-44//gi|84149431|gb|DN780731.1|DN780731				nr -
Unigene51383_All	1530	0.14	0.23	0.70	0.94	0.36	0.68	1.82	3.31	9.04	7.61E-01	5.57E-01		2.35E+00	3.61E-03		-1.39E+00	9.09E-03		-4.76E-01	4.15E-01		8.58E-01	3.14E-04		2.31E+00	1.30E-42	Up	Unigene51383_All//gi|22331831|ref|NP_191271.2|//1.00E-122//protein kinase family protein [Arabidopsis thaliana]	Unigene51383_All//6.00E-111//AT3G57120| protein kinase family protein	Unigene51383_All//9.00E-129//ES833011		ko04626|Plant-pathogen interaction		nr -
Unigene51384_All	621	61.93	74.33	76.57	118.08	122.66	106.04	107.37	76.66	46.13	2.63E-01	8.87E-04		3.06E-01	1.29E-04		5.49E-02	4.69E-01		-1.55E-01	1.53E-02		-4.86E-01	2.70E-17		-1.22E+00	1.65E-83	Down	Unigene51384_All//gi|211906514|gb|ACJ11750.1|//3.00E-42//lactoylglutathione lyase [Gossypium hirsutum]	Unigene51384_All//2.00E-35//AT1G11840| ATGLX1 (GLYOXALASE I HOMOLOG); lactoylglutathione lyase/ metal ion binding	Unigene51384_All//0.00E+00//gi|21101874|gb|BQ414187.1|BQ414187			GO:0016846//GO:0043169	nr -
Unigene51385_All	298	1.05	2.72	0.00	3.68	3.70	0.61	2.84	0.28	3.61	1.37E+00	9.21E-02		-1.00E+01	4.90E-02		7.90E-03	9.92E-01		-2.60E+00	7.13E-04	Down	-3.34E+00	2.51E-04	Down	3.47E-01	5.66E-01		Unigene51385_All//gi|6573744|gb|AAF17664.1|AC009398_13//6.00E-24//F20B24.20 [Arabidopsis thaliana]	Unigene51385_All//4.00E-25//AT1G10780| F-box family protein	Unigene51385_All//1.00E-160//ES851444				nr -
Unigene51387_All	664	32.54	38.31	29.19	521.70	541.63	523.39	265.52	221.25	100.92	2.35E-01	3.63E-02		-1.57E-01	2.42E-01		5.41E-02	6.23E-02		4.70E-03	9.11E-01		-2.63E-01	1.28E-14		-1.40E+00	8.43E-271	Down	Unigene51387_All//gi|258489588|gb|ACV72637.1|//3.00E-86//proline-rich protein 3 [Gossypium hirsutum]	Unigene51387_All//1.00E-33//AT2G33790| AGP30 (ARABINOGALACTAN PROTEIN30)	Unigene51387_All//0.00E+00//TC131312			GO:0009719	nr -
Unigene51388_All	361	159.43	189.62	196.04	120.60	103.69	115.47	96.04	155.72	247.64	2.50E-01	8.80E-05		2.98E-01	3.27E-06		-2.18E-01	5.88E-03		-6.27E-02	5.48E-01		6.97E-01	2.39E-27		1.37E+00	4.16E-132	Up	Unigene51388_All//gi|260513716|gb|ACX42570.1|//5.00E-18//CONSTANS-like zinc finger protein [Glycine max]	Unigene51388_All//6.00E-19//AT5G57660| zinc finger (B-box type) family protein	Unigene51388_All//0.00E+00//TC145664	C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0043231//GO:0046914	nr +
Unigene5139_All	602	29.72	9.51	8.23	36.82	26.14	36.91	55.55	14.44	18.53	-1.64E+00	2.12E-28	Down	-1.85E+00	3.65E-32	Down	-4.94E-01	3.85E-06		3.40E-03	9.78E-01		-1.94E+00	1.07E-80	Down	-1.58E+00	1.23E-62	Down	Unigene5139_All//gi|209967449|gb|ACJ02353.1|//1.00E-72//60S ribosomal protein L27A [Vernicia fordii]	Unigene5139_All//1.00E-66//AT1G23290| RPL27AB; structural constituent of ribosome	Unigene5139_All//0.00E+00//gi|21103573|gb|BQ415886.1|BQ415886		ko03010|Ribosome		nr -
Unigene51390_All	418	0.13	1.33	0.51	1.43	2.88	21.93	13.15	5.80	2.76	3.41E+00	1.24E-02		2.03E+00	3.61E-01		1.01E+00	1.11E-01		3.94E+00	1.25E-40	Up	-1.18E+00	4.24E-07	Down	-2.25E+00	3.79E-17	Down	Unigene51390_All//gi|297850348|ref|XP_002893055.1|//7.00E-07//low-molecular-weight cysteine-rich 78 [Arabidopsis lyrata subsp. lyrata] >gi|297338897|gb|EFH69314.1| low-molecular-weight cysteine-rich 78 [Arabidopsis lyrata subsp. lyrata]	Unigene51390_All//1.00E-05//AT5G44420| PDF1.2					nr -
Unigene51391_All	501	3.03	1.82	7.12	1.29	0.82	0.90	1.69	2.25	0.87	-7.34E-01	1.70E-01		1.23E+00	3.89E-04	Up	-6.48E-01	4.60E-01		-5.20E-01	5.88E-01		4.16E-01	4.92E-01		-9.48E-01	1.47E-01		Unigene51391_All//gi|91208869|ref|YP_538993.1|//5.00E-66//NADH dehydrogenase subunit 5 [Gossypium hirsutum] >gi|122201416|sp|Q2L960.1|NU5C_GOSHI RecName: Full=NAD(P)H-quinone oxidoreductase subunit 5, chloroplastic; AltName: Full=NAD(P)H dehydrogenase subunit 5; AltName: Full=NADH-plastoquinone oxidoreductase subunit 5 >gi|85687473|gb|ABC73685.1| NADH-plastoquinone oxidoreductase subunit 5 [Gossypium hirsutum]	Unigene51391_All//4.00E-42//ATCG01010| Chloroplast encoded NADH dehydrogenase unit.	Unigene51391_All//0.00E+00//gi|109857151|gb|DW486130.1|DW486130		ko00190|Oxidative phosphorylation	GO:0009534//GO:0022904//GO:0031224//GO:0048037//GO:0050136//GO:00512 34	nr -
Unigene51392_All	467	2.80	2.60	7.07	8.32	11.50	3.38	0.36	0.45	0.34	-1.05E-01	8.46E-01		1.34E+00	2.75E-04	Up	4.67E-01	7.29E-02		-1.30E+00	3.36E-05	Down	3.06E-01	8.36E-01		-8.58E-02	9.65E-01		Unigene51392_All//gi|4508075|gb|AAD21419.1|//1.00E-22//Unknown protein [Arabidopsis thaliana] >gi|11074464|gb|AB004605.1|Atig61740 [Arabidopsis thaliana]	Unigene51392_All//9.00E-11//AT4G21250| unknown protein				GO:0005488//GO:0031224//GO:0031410	nr +
Unigene51396_All	607	1.29	0.42	0.00	2.95	3.01	1.71	2.65	1.03	1.77	-1.63E+00	5.37E-02		-1.03E+01	2.21E-04	Down	2.53E-02	9.69E-01		-7.88E-01	1.13E-01		-1.36E+00	4.47E-03		-5.79E-01	2.00E-01		Unigene51396_All//gi|297839631|ref|XP_002887697.1|//2.00E-21//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333538|gb|EFH63956.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51396_All//7.00E-13//AT1G77720| protein kinase family protein	Unigene51396_All//0.00E+00//gi|78343509|gb|DT563783.1|DT563783			GO:0016740	nr -
Unigene51397_All	257	37.46	12.22	28.39	21.71	18.22	8.44	18.75	8.29	6.05	-1.62E+00	3.02E-15	Down	-4.00E-01	4.27E-02		-2.53E-01	3.52E-01		-1.36E+00	1.09E-07	Down	-1.18E+00	2.70E-06	Down	-1.63E+00	3.66E-10	Down	Unigene51397_All//gi|416652|sp|Q03666.1|GSTA4_TOBAC//2.00E-14//RecName: Full=Probable glutathione S-transferase; AltName: Full=Auxin-induced protein PCNT107 >gi|19793|emb|CAA39707.1| auxin-induced protein [Nicotiana tabacum]	Unigene51397_All//8.00E-06//AT1G78380| ATGSTU19 (GLUTATHIONE S-TRANSFERASE TAU 19); glutathione binding / glutathione transferase	Unigene51397_All//3.00E-115//TC146318		ko00480|Glutathione metabolism	GO:0009755//GO:0016209//GO:0016765//GO:0016846	nr +
Unigene51399_All	2262	0.00	0.36	0.00	0.00	0.00	0.06	1.50	4.16	7.57	8.49E+00	9.37E-05	Up	null	null		null	null		5.90E+00	3.11E-01		1.48E+00	5.97E-16	Up	2.34E+00	1.75E-53	Up	Unigene51399_All//gi|73624747|gb|AAZ79231.1|//1.00E-143//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene51399_All//6.00E-125//AT4G23990| ATCSLG3; cellulose synthase/ transferase/ transferase, transferring glycosyl groups	Unigene51399_All//0.00E+00//TC165164			GO:0009987//GO:0016020//GO:0016757	nr -
Unigene5140_All	514	11.20	11.24	11.40	40.03	40.67	33.13	22.62	24.07	11.24	5.30E-03	9.81E-01		2.54E-02	9.36E-01		2.29E-02	8.80E-01		-2.73E-01	2.98E-02		8.95E-02	6.31E-01		-1.01E+00	1.65E-11	Down	Unigene5140_All//gi|224085515|ref|XP_002307602.1|//7.00E-20//homocysteine s-methyltransferase [Populus trichocarpa] >gi|222857051|gb|EEE94598.1| homocysteine s-methyltransferase [Populus trichocarpa]	Unigene5140_All//4.00E-14//AT3G63250| HMT2 (HOMOCYSTEINE METHYLTRANSFERASE 2); homocysteine S-methyltransferase	Unigene5140_All//0.00E+00//TC154417		ko00270|Cysteine and methionine metabolism		nr +
Unigene51400_All	278	7.72	0.00	1.92	6.09	1.86	2.27	2.59	0.30	0.29	-1.29E+01	2.13E-12	Down	-2.01E+00	8.34E-05	Down	-1.71E+00	5.29E-04	Down	-1.42E+00	5.89E-03		-3.10E+00	1.40E-03		-3.17E+00	8.09E-04	Down				Unigene51400_All//8.00E-153//TC139588				
Unigene51402_All	504	342.37	451.60	640.16	66.22	87.66	57.44	10.57	6.80	4.98	4.00E-01	1.22E-32		9.03E-01	4.26E-190		4.05E-01	4.53E-08		-2.05E-01	3.69E-02		-6.36E-01	5.77E-03		-1.09E+00	2.27E-06	Down	Unigene51402_All//gi|2493694|sp|Q41387.1|PSBW_SPIOL//1.00E-38//RecName: Full=Photosystem II reaction center W protein, chloroplastic; AltName: Full=PSII 6.1 kDa protein; Flags: Precursor >gi|728716|emb|CAA59409.1| protein of photosystem II [Spinacia oleracea]	Unigene51402_All//3.00E-16//AT2G30570| PSBW (PHOTOSYSTEM II REACTION CENTER W)	Unigene51402_All//0.00E+00//TC163813		ko00195|Photosynthesis	GO:0009521//GO:0009534	nr +
Unigene51405_All	241	68.60	31.75	64.08	243.28	146.89	186.65	176.66	160.94	62.98	-1.11E+00	8.51E-15	Down	-9.85E-02	5.50E-01		-7.28E-01	1.83E-30		-3.82E-01	8.14E-09		-1.35E-01	9.45E-02		-1.49E+00	1.41E-72	Down	Unigene51405_All//gi|92885091|gb|ABE87611.1|//4.00E-37//Phosphoribosyltransferase; Orotidine 5-phosphate decarboxylase [Medicago truncatula]	Unigene51405_All//5.00E-38//AT3G54470| uridine 5'-monophosphate synthase / UMP synthase (PYRE-F) (UMPS)	Unigene51405_All//8.00E-134//EV494300		ko00240|Pyrimidine metabolism	GO:0006221//GO:0009267//GO:0010038//GO:0016763//GO:0016831//GO:00198 56	nr -
Unigene51408_All	2271	0.00	0.00	0.00	0.00	0.00	0.00	15.75	3.24	0.39	null	null		null	null		null	null		null	null		-2.28E+00	8.50E-106	Down	-5.35E+00	1.81E-227	Down	Unigene51408_All//gi|37548634|gb|AAN12272.1|//0.00E+00//subtilisin-like protease C1 [Glycine max] >gi|40556678|gb|AAO02075.4| subtilisin-like protease C1 [Glycine max]	Unigene51408_All//0.00E+00//AT5G59190| subtilase family protein	Unigene51408_All//2.00E-10//TC168091			GO:0004175//GO:0005515//GO:0019538//GO:0004092	nr -
Unigene5141_All	960	1.80	5.07	4.05	5.92	7.07	8.28	0.97	0.74	1.78	1.49E+00	2.99E-07	Up	1.17E+00	3.76E-04	Up	2.57E-01	3.12E-01		4.85E-01	2.00E-02		-3.89E-01	5.75E-01		8.81E-01	4.17E-02		Unigene5141_All//gi|27261731|gb|AAN86062.1|//2.00E-89//sugar transporter [Citrus unshiu]	Unigene5141_All//1.00E-84//AT1G67300| hexose transporter, putative	Unigene5141_All//0.00E+00//ES793275				nr +
Unigene51410_All	229	58.49	19.47	49.06	11.31	15.34	8.87	0.00	0.00	0.00	-1.59E+00	2.08E-20	Down	-2.54E-01	1.40E-01		4.39E-01	2.05E-01		-3.50E-01	4.08E-01		null	null		null	null					Unigene51410_All//1.00E-74//TC149389				

Unigene51412_All	432	1.82	2.35	5.42	3.11	0.88	0.94	0.20	0.00	0.00	3.69E-01	6.03E-01		1.58E+00	5.88E-04	Up	-1.83E+00	1.45E-03		-1.73E+00	4.68E-03		-7.61E+00	4.03E-01		-7.61E+00	3.58E-01		Unigene51412_All//gi|224084498|ref|XP_002307317.1|//6.00E-16//f-box family protein [Populus trichocarpa] >gi|222856766|gb|EEE94313.1| f-box family protein [Populus trichocarpa]	Unigene51412_All//3.00E-12//AT2G37590| Dof-type zinc finger domain-containing protein	Unigene51412_All//3.00E-11//TC178586	C2C2-Dof		GO:0003676//GO:0010468//GO:0046914	nr +
Unigene51413_All	360	3.92	0.42	7.10	2.21	2.58	1.76	0.00	0.00	0.11	-3.22E+00	1.60E-05	Down	8.56E-01	3.94E-02		2.22E-01	8.13E-01		-3.34E-01	6.86E-01		null	null		6.79E+00	6.44E-01										
Unigene51415_All	574	0.18	0.18	0.19	0.69	2.10	3.30	5.89	1.38	1.67	-4.66E-02	9.88E-01		2.51E-02	9.99E-01		1.60E+00	1.36E-02		2.25E+00	2.85E-05	Up	-2.09E+00	1.27E-09	Down	-1.82E+00	1.82E-08	Down	Unigene51415_All//gi|115468306|ref|NP_001057752.1|//2.00E-18//Os06g0523300 (Oryza sativa Japonica Group) >gi|113595792|dbj|BAF19666.1| Os06g0523300 (Oryza sativa Japonica Group)	Unigene51415_All//3.00E-18//AT3G09950| unknown protein	Unigene51415_All//0.00E+00//TC178337				nr -
Unigene51418_All	839	0.37	2.96	0.38	6.17	8.99	6.41	0.35	0.30	0.52	2.98E+00	1.46E-08	Up	2.52E-02	1.00E+00		5.42E-01	8.63E-03		5.30E-02	8.64E-01		-2.39E-01	8.39E-01		5.66E-01	5.78E-01		Unigene51418_All//gi|18406012|ref|NP_565978.1|//9.00E-72//LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|30689086|ref|NP_850374.1| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10) [Arabidopsis thaliana] >gi|6691165|gb|AAF24517.1|AF218765_1 177 protein [Arabidopsis thaliana] >gi|4559031|gb|AAD22993.1| expressed protein [Arabidopsis thaliana] >gi|28372972|gb|AAO39968.1| At2g42610 [Arabidopsis thaliana]	Unigene51418_All//1.00E-69//AT2G42610| LSH10 (LIGHT SENSITIVE HYPOCOTYLS 10)	Unigene51418_All//0.00E+00//DW504251				nr +
Unigene51419_All	617	2.20	8.79	7.34	17.28	12.33	54.02	38.10	106.22	122.55	1.99E+00	1.46E-11	Up	1.73E+00	6.90E-08	Up	-4.86E-01	3.22E-03		1.64E+00	8.84E-56	Up	1.48E+00	5.50E-107	Up	1.69E+00	4.86E-152	Up	Unigene51419_All//gi|224111880|ref|XP_002316010.1|//7.00E-46//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene51419_All//3.00E-24//AT2G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene51419_All//3.00E-114//gi|48796731|gb|CO098045.1|CO098045		ko00908|Zeatin biosynthesis//ko00591|Linoleic acid metabolism	GO:0005506//GO:0016491	nr -
Unigene51420_All	406	0.00	2.12	0.52	0.61	0.85	0.45	2.08	1.03	1.96	1.11E+01	4.94E-05	Up	9.04E+00	1.41E-01		4.67E-01	7.79E-01		-4.63E-01	7.44E-01		-1.02E+00	1.41E-01		-8.58E-02	9.02E-01					Unigene51420_All//9.00E-21//gi|164331102|gb|ES46279.1|ES46279				
Unigene51421_All	303	17.96	77.59	34.80	44.39	51.14	68.71	36.00	57.25	36.03	2.11E+00	1.61E-51	Up	9.54E-01	2.23E-07		2.04E-01	1.87E-01		6.30E-01	7.89E-08		6.69E-01	1.95E-08		1.00E-03	9.95E-01		Unigene51421_All//gi|222822685|gb|ACM68455.1|//8.00E-16//stress-associated protein 5 [Solanum pennellii]	Unigene51421_All//5.00E-14//AT1G51200| zinc finger (AN1-like) family protein	Unigene51421_All//1.00E-120//TC138898			GO:0003676//GO:0046914	nr +
Unigene51424_All	277	18.89	8.05	10.77	2.16	2.98	0.33	0.00	0.00	0.00	-1.23E+00	5.30E-06	Down	-8.11E-01	2.93E-03		4.67E-01	5.85E-01		-2.73E+00	1.74E-02		null	null		null	null		Unigene51424_All//gi|18447767|gb|AAL67994.1|//2.00E-08//acyltransferase-like protein [Gossypium hirsutum]		Unigene51424_All//1.00E-74//ES830616				nr -
Unigene51426_All	575	1.46	0.35	0.09	1.73	1.38	3.46	8.53	1.02	1.66	-2.05E+00	1.68E-02		-3.97E+00	9.08E-04	Down	-3.31E-01	6.19E-01		9.96E-01	3.32E-02		-3.07E+00	1.24E-20	Down	-2.36E+00	3.05E-16	Down	Unigene51426_All//gi|15221174|ref|NP_175273.1|//7.00E-09//F-box family protein [Arabidopsis thaliana] >gi|5733869|gb|AAD49757.1|AC007932_5 Contains F-box domain PF|00646 [Arabidopsis thaliana]				ko04120|Ubiquitin mediated proteolysis	GO:0003824	nr -
Unigene51428_All	404	0.52	5.39	0.26	1.60	2.13	1.57	1.57	2.69	0.99	3.38E+00	2.02E-08	Up	-9.75E-01	6.20E-01		4.11E-01	6.11E-01		-3.44E-02	9.53E-01		7.77E-01	1.94E-01		-6.71E-01	3.86E-01										
Unigene51429_All	288	7.27	17.95	19.60	3.11	2.99	0.63	0.00	0.00	0.00	1.30E+00	2.17E-06	Up	1.43E+00	1.71E-07	Up	-5.87E-02	9.22E-01		-2.31E+00	5.78E-03		null	null		null	null		Unigene51429_All//gi|18447767|gb|AAL67994.1|//2.00E-06//acyltransferase-like protein [Gossypium hirsutum]		Unigene51429_All//9.00E-128//TC136175				nr -
Unigene51431_All	712	0.00	1.14	0.07	6.02	6.00	2.66	4.69	0.76	1.57	1.02E+01	9.37E-05	Up	6.23E+00	6.35E-01		-4.70E-03	9.78E-01		-1.18E+00	5.99E-05	Down	-2.62E+00	3.28E-12	Down	-1.58E+00	5.14E-07	Down	Unigene51431_All//gi|54645913|gb|AAV36562.1|//2.00E-62//nhx1 antiporter [Vitis vinifera]	Unigene51431_All//4.00E-40//AT3G05030| NHX2 (SODIUM HYDROGEN EXCHANGER 2); sodium ion transmembrane transporter/ sodium:hydrogen antiporter	Unigene51431_All//3.00E-117//DW515056			GO:0005451//GO:0030001//GO:0031224//GO:0055067	nr +
Unigene51432_All	610	0.43	2.49	0.44	0.08	0.34	0.00	98.91	356.43	111.29	2.54E+00	9.21E-05	Up	2.53E-02	1.00E+00		2.05E+00	3.94E-01		-6.35E+00	6.34E-01		1.85E+00	0.00E+00	Up	1.70E-01	3.00E-03		Unigene51432_All//gi|124360970|gb|ABN08942.1|//1.00E-76//Quinonprotein alcohol dehydrogenase-like [Medicago truncatula]		Unigene51432_All//1.00E-23//CO071277			GO:0003676//GO:0005515//GO:0008152//GO:0016491//GO:0046914	nr +
Unigene51433_All	625	121.97	25.86	29.82	22.64	21.71	8.38	0.14	0.20	0.00	-2.24E+00	9.29E-180	Down	-2.03E+00	8.91E-154	Down	-6.04E-02	7.61E-01		-1.43E+00	5.35E-20	Down	5.68E-01	7.81E-01		-7.08E+00	3.58E-01		Unigene51433_All//gi|164519779|gb|ABV59947.1|//1.00E-33//nectar protein 1 [Jacaranda mimosifolia]	Unigene51433_All//1.00E-30//AT1G29670| GDSL-motif lipase/hydrolase family protein	Unigene51433_All//0.00E+00//gi|21103270|gb|BQ415583.1|BQ415583			GO:0016787//GO:0044238	nr -
Unigene51434_All	478	64.36	48.97	35.98	142.56	104.82	108.47	313.83	152.49	105.76	-3.94E-01	4.98E-05		-8.39E-01	2.11E-16		-4.44E-01	1.22E-14		-3.94E-01	1.05E-10		-1.04E+00	3.34E-141	Down	-1.57E+00	1.78E-274	Down	Unigene51434_All//gi|11131745|sp|P93308.1|CALR_RICCO//5.00E-21//RecName: Full=Calreticulin; Flags: Precursor >gi|1658197|gb|AAB71419.1| calreticulin [Ricinus communis] >gi|1763297|gb|AAB71420.1| calreticulin [Ricinus communis]		Unigene51434_All//0.00E+00//TC149432		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	GO:0005515//GO:0030246//GO:0033554//GO:0042742//GO:0042267//GO:0044132//GO:0046872	nr +
Unigene51436_All	478	0.00	0.53	0.00	2.40	1.15	0.76	0.80	0.96	2.92	9.05E+00	7.85E-02		null	null		-1.06E+00	8.44E-02		-1.66E+00	1.29E-02		2.73E-01	7.69E-01		1.87E+00	4.97E-04	Up	Unigene51436_All//gi|255550792|ref|XP_002516444.1|//7.00E-15//conserved hypothetical protein [Ricinus communis] >gi|223541264|gb|EEF45785.1| conserved hypothetical protein [Ricinus communis]		Unigene51436_All//0.00E+00//gi|78347581|gb|DT567855.1|DT567855				nr -
Unigene51437_All	525	1.89	1.45	0.10	1.14	1.38	1.72	3.14	0.64	1.21	-3.87E-01	5.79E-01		-4.22E+00	1.62E-04	Down	2.75E-01	8.00E-01		5.96E-01	4.55E-01		-2.30E+00	1.36E-05	Down	-1.37E+00	2.58E-03					Unigene51437_All//6.00E-07//TC147422				
Unigene51438_All	856	0.98	0.47	0.00	1.57	1.97	1.00	0.89	4.05	4.56	-1.05E+00	1.74E-01		-9.93E+00	1.19E-04	Down	3.27E-01	5.68E-01		-6.48E-01	2.83E-01		2.19E+00	2.33E-10	Up	2.36E+00	6.83E-13	Up	Unigene51438_All//gi|255539499|ref|XP_002510814.1|//5.00E-24//conserved hypothetical protein [Ricinus communis] >gi|223549929|gb|EEF51416.1| conserved hypothetical protein [Ricinus communis]		Unigene51438_All//9.00E-35//ES835715				nr +
Unigene51439_All	411	50.54	73.85	37.83	54.78	41.98	28.90	54.32	32.95	24.72	5.47E-01	2.33E-08		-4.18E-01	8.77E-04		-3.84E-01	3.90E-04		-9.23E-01	7.69E-16		-7.21E-01	5.16E-12		-1.14E+00	1.32E-25	Down	Unigene51439_All//gi|217426823|gb|ACK44531.1|//3.00E-11//AT5G09960-like protein [Arabidopsis arenosa]	Unigene51439_All//1.00E-11//AT5G09960| unknown protein	Unigene51439_All//0.00E+00//TC144801			GO:0016020	nr +
Unigene51444_All	725	3.54	15.93	4.92	7.35	14.96	14.51	7.58	2.48	3.96	2.17E+00	1.57E-26	Up	4.77E-01	1.66E-01		1.03E+00	5.92E-10	Up	9.81E-01	2.11E-08		-1.61E+00	6.71E-11	Down	-9.38E-01	2.46E-05					Unigene51444_All//2.00E-32//ES824206				
Unigene51442_All	532	15.15	37.72	16.52	38.11	25.63	43.64	31.15	25.22	15.80	1.32E+00	6.78E-23	Up	1.25E-01	5.90E-01		-5.72E-01	3.17E-07		1.95E-01	1.18E-01		-3.05E-01	1.50E-02		-9.79E-01	2.72E-15					Unigene51442_All//9.00E-111//DW234666				
Unigene51444_All	1243	0.00	0.00	0.00	0.00	0.00	0.07	117.96	8.71	28.11	null	null		null	null		null	null		6.18E+00	4.76E-01		-3.76E+00	0.00E+00	Down	-2.07E+00	0.00E+00	Down	Unigene51444_All//gi|575603|dbj|BAA07663.1|//1.00E-102//cationic peroxidase isozyme 38K precursor [Nicotiana tabacum]	Unigene51444_All//2.00E-86//AT4G11290| peroxidase, putative			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0046872	nr +
Unigene51447_All	544	0.10	0.00	0.00	3.85	1.52	0.08	4.12	2.69	1.25	-6.59E+00	6.10E-01		-6.59E+00	6.22E-01		-1.34E+00	1.57E-03		-5.53E+00	9.18E-12	Down	-6.15E-01	1.12E-01		-1.73E+00	1.59E-05	Down				Unigene51447_All//7.00E-10//TC144946				
Unigene51451_All	2045	0.00	0.00	0.00	1.49	0.98	0.57	0.10	0.02	0.08	null	null		null	null		-6.06E-01	8.18E-02		-1.37E+00	1.58E-04	Down	-2.34E+00	2.37E-01		-4.09E-01	7.55E-01		Unigene51451_All//gi|297803962|ref|XP_002869865.1|//0.00E+00//beta-glucosidase 47 [Arabidopsis lyrata subsp. lyrata] >gi|297315701|gb|EFH46124.1| beta-glucosidase 47 [Arabidopsis lyrata subsp. lyrata]	Unigene51451_All//5.00E-180//AT4G21760| BGLU47 (Beta-glucosidase 47); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene51451_All//0.00E+00//CO109602		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0015926//GO:0043167//GO:0044238	nr -
Unigene51452_All	323	29.81	34.83	14.84	44.42	61.62	36.77	60.61	412.52	27.63	2.25E-01	2.14E-01		-1.01E+00	2.43E-07	Down	4.72E-01	4.72E-05		-2.72E-01	8.18E-02		2.77E+00	0.00E+00	Up	-1.13E+00	1.74E-22	Down	Unigene51452_All//gi|124488472|gb|ABN12320.1|//3.00E-58//benzoquinone reductase [Gossypium hirsutum]	Unigene51452_All//8.00E-46//AT4G27270| quinone reductase family protein	Unigene51452_All//0.00E+00//DR452690			GO:0000166//GO:0006350//GO:0016020//GO:0016655//GO:0031410	nr +
Unigene51454_All	2965	0.00	110.81	45.74	0.07	0.12	0.03	0.00	0.00	0.00	1.68E+01	0.00E+00	Up	1.55E+01	0.00E+00	Up	7.89E-01	5.96E-01		-1.14E+00	5.68E-01		null	null		null	null		Unigene51454_All//sp|P13418|POLG_CRPV//1.00E-138//Genome polyprotein (Fragment) OS=Cricket paralysis virus PE=1 SV=2						swissprot -
Unigene51455_All	948	2.15	4.76	2.42	1.63	1.82	1.05	0.40	0.26	0.29	1.14E+00	8.89E-05	Up	1.66E-01	6.97E-01		1.57E-01	8.13E-01		-6.36E-01	2.47E-01		-6.02E-01	6.12E-01		-4.48E-01	6.41E-01		Unigene51455_All//gi|115465815|ref|NP_001056507.1|//1.00E-41//Os05g0594500 (Oryza sativa Japonica Group) >gi|113580058|dbj|BAF18421.1| Os05g0594500 (Oryza sativa Japonica Group)	Unigene51455_All//2.00E-18//AT3G48200| unknown protein					nr -
Unigene51457_All	862	1.09	0.35	0.00	2.31	1.04	2.25	5.59	0.87	1.99	-1.63E+00	3.13E-02		-1.01E+01	3.34E-05	Down	-1.15E+00	7.90E-03		-3.71E-02	9.48E-01		-2.68E+00	9.74E-18	Down	-1.49E+00	5.10E-09	Down	Unigene51457_All//gi|55859438|emb|CAG29372.1|//1.00E-59//protein kinase WEE1 [Solanum lycopersicum var. cerasiforme] >gi|84574987|emb|CAJ56085.1| protein kinase WEE1 [Solanum lycopersicum]	Unigene51457_All//2.00E-54//AT1G02970| WEE1 (ARABIDOPSIS WEE1 KINASE HOMOLOG); kinase/ protein kinase	Unigene51457_All//0.00E+00//ES797874			GO:0004672//GO:0006464//GO:0007165//GO:0022402//GO:0032559	nr +
Unigene5146_All	2173	4.14	1.35	2.38	12.40	8.80	9.17	2.96	1.92	4.79	-1.61E+00	2.75E-14	Down	-8.01E-01	6.10E-05		-4.96E-01	2.22E-07		-4.36E-01	1.82E-05		-6.21E-01	2.71E-03		6.94E-01	7.10E-06		Unigene5146_All//gi|297789582|ref|XP_002862740.1|//3.00E-37//prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297308444|gb|EFH38998.1| prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5146_All//7.00E-28//AT5G56230| PRA1.G2 (PRENYLATED RAB ACCEPTOR 1.G2)	Unigene5146_All//2.00E-161//DR454325				nr +
Unigene51460_All	340	3.23	7.90	8.46	3.96	2.23	3.45	0.75	0.61	0.12	1.29E+00	1.16E-03		1.39E+00	5.13E-04	Up	-8.28E-01	1.40E-01		-1.96E-01	7.30E-01		-2.80E-01	8.28E-01		-2.67E+00	1.15E-01										
Unigene51461_All	1094	0.00	0.28	0.00	0.18	0.06	0.00	128.77	103.31	43.66	8.12E+00	4.42E-02		null	null		-1.53E+00	4.15E-01		-7.51E+00	1.33E-01		-3.18E-01	1.31E-16		-1.56E+00	1.06E-255	Down	Unigene51461_All//gi|224063197|ref|XP_002301036.1|//1.00E-173//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222842762|gb|EEE80309.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene51461_All//3.00E-157//AT4G08620| SULTR1;1 (SULPHATE TRANSPORTER 1;1); sulfate transmembrane transporter	Unigene51461_All//5.00E-142//ES813014				nr -
Unigene51462_All	720	0.51	0.63	1.33	3.74	2.06	2.01	2.82	1.80	0.77	3.16E-01	7.44E-01		1.39E+00	7.11E-02		-8.61E-01	1.79E-02		-8.96E-01	1.94E-02		-6.47E-01	1.15E-01		-1.86E+00	1.51E-05	Down	Unigene51462_All//gi|56236070|gb|AAV84491.1|//7.00E-46//At5g12920 [Arabidopsis thaliana] >gi|56790198|gb|AAK30016.1| At5g12920 [Arabidopsis thaliana]	Unigene51462_All//4.00E-47//AT5G12920| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: CUL4 RING ubiquitin ligase complex; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), WD40/YVTN repeat-like (InterPro:IPR015943); Has 28 Blast hits to 28 proteins in 12 species: Archae - 0; Bacteria - 2; Metazoa - 6; Fungi - 2; Plants - 16; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene51462_All//2.00E-23//gi|21091825|gb|BQ404138.1|BQ404138			GO:0031461//GO:0043231	nr +

Unigene51464_All	1108	0.00	20.30	0.00	0.27	1.37	0.00	0.34	0.53	2.84	1.43E+01	1.62E-129	Up	null	null		2.34E+00	1.15E-04	Up	-8.08E+00	3.99E-02		6.21E-01	4.78E-01		3.05E+00	1.25E-13	Up	Unigene51464_All//gi|89258594|gb|AB065473.1|//6.00E-75//DREB1-like transcription factor [Gossypium hirsutum]	Unigene51464_All//5.00E-48//AT5G51990| CBF4 (C- REPEAT-BINDING FACTOR 4); DNA binding / transcription activator/ transcription factor	Unigene51464_All//0.00E+00//gi|78323093|gb|DT543367.1|DT543367	AP2-EREBP			nr +
Unigene51465_All	334	3.45	6.37	8.77	5.97	8.87	7.84	6.58	13.51	9.42	8.87E-01	4.43E-02		1.35E+00	6.17E-04	Up	5.72E-01	1.23E-01		3.95E-01	3.59E-01		1.04E+00	5.36E-05	Up	5.18E-01	9.14E-02					Unigene51465_All//4.00E-56//gi|48820950|gb|CO122263.1|CO122263				
Unigene51466_All	818	0.00	0.00	0.00	0.00	0.00	0.00	10.03	8.58	25.67	null	null		null	null		null	null		null	null		-2.24E-01	2.59E-01		1.36E+00	2.64E-31	Up	Unigene51466_All//gi|124360239|gb|ABN08252.1|//3.00E-50//Zinc finger, RING-type [Medicago truncatula] >gi|124360861|gb|ABN08833.1| Zinc finger, RING-type [Medicago truncatula]	Unigene51466_All//2.00E-17//AT4G10160| zinc finger (C3HC4-type RING finger) family protein	Unigene51466_All//2.00E-07//ES830919				nr -
Unigene51467_All	244	0.21	2.28	1.31	0.41	1.41	0.93	0.35	1.54	3.59	3.41E+00	1.24E-02		2.61E+00	1.46E-01		1.79E+00	2.57E-01		1.18E+00	5.49E-01		2.15E+00	9.44E-02		3.37E+00	1.32E-04	Up				Unigene51467_All//1.00E-135//ES837218				
Unigene51468_All	605	5.19	2.18	3.26	4.36	4.95	3.51	0.21	0.28	0.13	-1.25E+00	5.13E-04	Down	-6.72E-01	6.85E-02		1.82E-01	6.59E-01		-3.15E-01	4.65E-01		3.98E-01	8.14E-01		-6.71E-01	7.19E-01		Unigene51468_All//gi|224106153|ref|XP_002333717.1|//3.00E-28//cytochrome P450 [Populus trichocarpa] >gi|222838334|gb|EEE76699.1| cytochrome P450 [Populus trichocarpa]	Unigene51468_All//4.00E-20//AT3G26280| CYP71B4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene51468_All//2.00E-133//gi|48797654|gb|CO098968.1|CO098968		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene51471_All	318	31.43	72.50	49.06	19.27	15.70	12.92	7.45	7.89	9.40	1.21E+00	5.97E-23	Up	6.43E-01	1.04E-05		-2.95E-01	2.40E-01		-5.76E-01	1.56E-02		8.29E-02	8.29E-01		3.36E-01	3.11E-01		Unigene51471_All//gi|255536923|ref|XP_002509528.1|//3.00E-07//structural constituent of ribosome, putative [Ricinus communis] >gi|223549427|gb|EEF50915.1| structural constituent of ribosome, putative [Ricinus communis]		Unigene51471_All//3.00E-97//CO120094				nr +
Unigene51472_All	310	19.41	37.59	27.66	15.43	18.55	18.36	32.60	78.20	37.78	9.54E-01	1.93E-08		5.11E-01	1.37E-02		2.66E-01	3.26E-01		2.51E-01	3.83E-01		1.26E-00	1.28E-31	Up	2.13E-01	1.68E-01					Unigene51472_All//5.00E-142//TC132518				
Unigene51473_All	408	0.13	0.00	0.00	0.85	1.86	5.42	1.24	2.25	3.52	-7.00E+00	6.10E-01		-7.00E+00	6.22E-01		1.12E+00	1.98E-01		2.67E+00	3.32E-07	Up	8.58E-01	1.95E-01		1.50E+00	2.97E-03									
Unigene51474_All	382	1.37	8.49	3.62	1.17	3.43	1.89	1.00	0.77	1.46	2.63E+00	9.67E-10	Up	1.40E+00	2.28E-02		1.55E+00	1.14E-02		6.89E-01	4.48E-01		-3.79E-01	7.23E-01		5.52E-01	5.27E-01					Unigene51474_All//4.00E-07//EX164864				
Unigene51476_All	698	0.00	0.00	0.00	1.78	1.63	2.26	4.00	0.54	1.20	null	null		null	null		-1.32E-01	8.17E-01		3.44E-01	5.61E-01		-2.89E+00	2.30E-11	Down	-1.74E+00	9.92E-07	Down	Unigene51476_All//gi|270309004|dbj|BAI52955.1|//1.00E-62//calcium-binding EF-hand protein [Citrullus lanatus subsp. vulgaris]	Unigene51476_All//3.00E-57//AT1G05990| calcium-binding protein, putative	Unigene51476_All//5.00E-39//TC153671		ko04626|Plant-pathogen interaction		nr +
Unigene51477_All	1345	7.20	2.22	6.30	0.26	0.15	0.71	0.50	0.37	0.39	-1.70E+00	2.33E-16	Down	-1.93E-01	3.66E-01		-7.55E-01	5.67E-01		1.44E+00	5.71E-02		-4.32E-01	6.12E-01		-3.85E-01	5.98E-01		Unigene51477_All//gi|15233707|ref|NP_194145.1|//1.00E-151//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|19699292|gb|AAL91257.1| AT4g24140/T19F6_130 [Arabidopsis thaliana] >gi|25090311|gb|AAN72274.1| At4g24140/T19F6_130 [Arabidopsis thaliana]	Unigene51477_All//3.00E-148//AT4G24140| hydrolase, alpha/beta fold family protein	Unigene51477_All//3.00E-45//TC170405				nr +
Unigene51481_All	495	988.81	489.80	642.01	197.55	230.06	184.21	1.45	3.46	3.06	-1.01E+00	0.00E+00	Down	-6.23E-01	4.26E-151		2.20E-01	1.12E-06		-1.01E-01	8.35E-02		1.25E+00	6.05E-03		1.07E+00	2.22E-02		Unigene51481_All//gi|224072580|ref|XP_002303791.1|//6.00E-60//light-harvesting complex I protein Lhca2 [Populus trichocarpa] >gi|222841223|gb|EEE78770.1| light-harvesting complex I protein lhca2 [Populus trichocarpa]	Unigene51481_All//8.00E-59//AT3G61470| LHCA2; chlorophyll binding	Unigene51481_All//0.00E+00//TC157601		ko00196|Photosynthesis - antenna proteins		nr +
Unigene51482_All	349	29.08	186.13	118.86	25.55	72.82	157.10	13.08	39.40	28.42	2.68E+00	1.43E-187	Up	2.03E+00	5.18E-84	Up	1.51E+00	2.87E-41	Up	2.62E+00	7.97E-166	Up	1.59E+00	1.51E-25	Up	1.12E+00	1.60E-11	Up				Unigene51482_All//7.00E-86//TC143171				
Unigene51483_All	287	2.19	2.30	2.78	8.16	10.08	33.20	58.78	169.51	126.73	6.92E-02	9.50E-01		3.47E-01	6.35E-01		3.05E-01	4.60E-01		2.03E+00	1.94E-21	Up	1.53E+00	1.74E-83	Up	1.11E+00	2.68E-39	Up	Unigene51483_All//gi|224111880|ref|XP_002316010.1|//3.00E-32//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene51483_All//1.00E-24//AT3G14630| CYP72A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene51483_All//5.00E-80//TC154355		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00906|Carotenoid biosynthesis		nr +
Unigene51486_All	790	0.93	1.03	0.00	1.51	1.96	0.11	2.30	1.11	1.16	1.46E-01	8.39E-01		-9.86E+00	4.13E-04	Down	3.74E-01	5.45E-01		-3.73E+00	1.43E-05	Down	-1.05E+00	1.56E-02		-9.88E-01	1.76E-02		Unigene51486_All//gi|28558781|gb|AA045752.1|//3.00E-91//pol protein [Cucumis melo]		Unigene51486_All//2.00E-35//PL577614				nr +
Unigene51488_All	471	18.33	4.63	12.32	12.69	9.14	8.63	1.53	1.42	2.79	-1.99E+00	4.88E-18	Down	-5.73E-01	5.17E-03		-4.74E-01	4.44E-02		-5.56E-01	2.18E-02		-1.04E-01	8.93E-01		8.71E-01	8.59E-02					Unigene51488_All//4.00E-26//ES795903				ESTscan -
Unigene51489_All	519	0.50	0.29	0.00	1.82	1.66	2.44	2.44	0.56	1.15	-7.83E-01	6.20E-01		-8.98E+00	8.56E-02		-1.37E-01	8.18E-01		4.18E-01	5.23E-01		-2.12E+00	4.16E-04	Down	-1.09E+00	3.58E-02		Unigene51489_All//gi|14326582|gb|AAK60335.1|AF385745_1/3.00E-15//At1g67850/F12A21_2 [Arabidopsis thaliana] >gi|25090152|gb|AAN72241.1| At1g67850/F12A21_2 [Arabidopsis thaliana] >gi|222423797|dbj|BAH19864.1| AT1G67850 [Arabidopsis thaliana] >gi|222424761|dbj|BAH20333.1| AT1G67850 [Arabidopsis thaliana]	Unigene51489_All//8.00E-22//AT3G27470| unknown protein	Unigene51489_All//0.00E+00//gi|78333925|gb|DT554199.1|DT554199				nr -
Unigene5149_All	1279	19.27	17.95	24.48	21.15	19.63	12.29	4.00	1.37	1.00	-1.03E-01	3.98E-01		3.46E-01	5.92E-04		-1.08E-01	3.86E-01		-7.83E-01	1.93E-14		-1.54E+00	1.29E-09	Down	-2.00E+00	6.08E-14	Down	Unigene5149_All//gi|115473321|ref|NP_001060259.1|//2.00E-10//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]		Unigene5149_All//0.00E+00//BQ406432				nr +
Unigene51492_All	667	1.49	2.36	2.55	2.39	1.19	1.56	0.82	0.56	0.00	6.60E-01	2.16E-01		7.78E-01	1.39E-01		-1.01E+00	4.26E-02		-6.18E-01	2.53E-01		-5.47E-01	5.52E-01		-9.69E+00	2.80E-04	Down	Unigene51492_All//gi|7141243|gb|AAF37266.1|AF220405_1//2.00E-30//transcription factor [Vitis riparia]	Unigene51492_All//1.00E-18//AT1G30500| NF-YA7 (NUCLEAR FACTOR Y, SUBUNIT A7); specific transcriptional repressor/ transcription factor	Unigene51492_All//0.00E+00//TC164284	CCAAT			nr +
Unigene51494_All	405	2.33	1.50	4.08	7.26	5.78	1.12	0.00	0.10	0.20	-6.31E-01	3.66E-01		8.10E-01	1.35E-01		-3.28E-01	3.96E-01		-2.70E+00	8.04E-10	Down	6.69E+00	6.34E-01		7.62E+00	4.03E-01					Unigene51494_All//6.00E-22//TC133162				
Unigene51495_All	681	0.00	0.30	0.31	2.19	0.86	1.06	1.61	0.06	0.18	8.22E+00	1.36E-01		8.29E+00	1.41E-01		-1.35E+00	9.45E-03		-1.05E+00	5.67E-02		-4.72E+00	1.02E-06	Down	-3.20E+00	1.63E-05	Down	Unigene51495_All//gi|190897590|gb|ACE97308.1|//2.00E-47//pectinesterase inhibitor [Populus tremula]	Unigene51495_All//5.00E-47//AT2G01610| invertase/pectin methylesterase inhibitor family protein	Unigene51495_All//3.00E-71//TC144066		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene51496_All	447	0.00	0.11	0.00	1.23	0.31	0.20	3.50	2.15	0.80	6.83E+00	6.15E-01		null	null		-1.99E+00	5.12E-02		-2.60E+00	2.93E-02		-7.03E-01	1.40E-01		-2.13E+00	3.93E-05	Down								
Unigene51497_All	354	2.66	4.29	2.11	1.27	2.92	5.23	0.84	0.24	2.26	6.91E-01	2.02E-01		-3.37E-01	6.16E-01		1.20E+00	8.55E-02		2.05E+00	1.17E-04	Up	-1.82E+00	2.11E-01		1.50E+00	3.06E-02									
Unigene51498_All	334	3.29	9.56	5.74	5.52	5.67	7.30	1.65	0.50	1.31	1.54E+00	3.26E-05	Up	8.03E-01	1.02E-01		3.93E-02	9.62E-01		4.04E-01	3.70E-01		-1.72E+00	7.23E-02		-3.27E-01	6.72E-01					Unigene51498_All//1.00E-102//DW503763				
Unigene5150_All	706	12.52	11.27	10.03	9.53	8.44	10.56	16.83	8.52	7.56	-1.53E-01	4.70E-01		-3.20E-01	1.33E-01		-1.75E-01	5.11E-01		1.48E-01	5.68E-01		-9.81E-01	6.91E-11		-1.15E+00	2.20E-14	Down	Unigene5150_All//gi|115465821|ref|NP_001056510.1|//5.00E-44//Os05g0594900 [Oryza sativa Japonica Group] >gi|113380061|dbj|BAF18424.1| Os05g0594900 [Oryza sativa Japonica Group]	Unigene5150_All//7.00E-34//AT1G65700| small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative	Unigene5150_All//0.00E+00//ES816805		ko03040|Spliceosome//ko03018|RNA degradation		nr -
Unigene51500_All	606	0.35	4.35	0.53	1.07	1.82	1.94	1.05	2.21	2.04	3.65E+00	1.07E-10	Up	6.10E-01	6.24E-01		7.67E-01	2.69E-01		8.59E-01	1.95E-01		1.08E+00	4.02E-02		9.62E-01	6.77E-02					Unigene51500_All//9.00E-62//ES845776				
Unigene51503_All	1726	0.49	1.85	3.21	0.78	0.44	15.26	0.17	0.05	0.00	1.93E+00	7.70E-07	Up	2.73E+00	3.00E-16	Up	-8.28E-01	1.40E-01		4.29E+00	9.35E-124	Up	-1.83E+00	2.11E-01		-7.42E+00	1.58E-02		Unigene51503_All//gi|70779014|gb|AA208051.1|//1.00E-126//wax synthase [Petunia x hybrida]	Unigene51503_All//3.00E-115//AT3G49200| unknown protein	Unigene51503_All//1.00E-177//gi|48826842|gb|CO125232.1|CO125232				nr +
Unigene51505_All	564	0.46	0.09	0.00	0.71	0.55	0.48	1.20	2.08	4.10	-2.37E+00	2.14E-01		-8.86E+00	8.56E-02		-3.63E-01	7.54E-01		-5.56E-01	6.38E-01		7.91E-01	1.64E-01		1.77E+00	8.95E-06	Up	Unigene51505_All//gi|124359162|gb|ABN05685.1|//2.00E-42//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene51505_All//5.00E-16//AT4G01250| hypothetical protein					nr +
Unigene51507_All	480	0.00	3.48	0.78	0.42	0.86	0.56	1.85	1.39	4.90	1.18E+01	1.54E-09	Up	9.60E+00	2.50E-02		1.05E+00	4.26E-01		4.44E-01	7.63E-01		-4.09E-01	5.62E-01		1.40E+00	1.92E-04	Up				Unigene51507_All//6.00E-07//EX164900				
Unigene51511_All	685	0.15	0.67	0.78	1.02	0.40	0.92	16.85	48.93	14.83	2.12E+00	9.59E-02		2.35E+00	5.87E-02		-1.34E+00	1.09E-01		-1.42E-01	8.66E-01		1.54E+00	2.64E-58	Up	-1.84E-01	2.44E-01		Unigene51511_All//gi|38260640|gb|AAR15456.1|//5.00E-43//Cu2+ plastocyanin-like [Capsella rubella]	Unigene51511_All//5.00E-37//AT5G07475| plastocyanin-like domain-containing protein	Unigene51511_All//0.00E+00//TC154185				nr -
Unigene51512_All	1028	0.25	0.30	0.83	14.39	9.41	6.94	0.21	0.28	0.08	2.17E-01	8.64E-01		1.70E+00	4.53E-02		-6.13E-01	4.59E-06		-1.05E+00	4.75E-13	Down	4.69E-01	7.06E-01		-1.41E+00	3.80E-01		Unigene51512_All//gi|42570557|ref|NP_850951.2|//4.00E-66//KNAT6; DNA binding / transcription activator/ transcription factor [Arabidopsis thaliana] >gi|75146711|sp|Q84JS6.1|KNAT6_ARATH RecName: Full=Homeobox protein knotted-1-like 6; AltName: Full=Protein KNAT6	Unigene51512_All//4.00E-62//AT1G23380| KNAT6; DNA binding / transcription activator/ transcription factor	Unigene51512_All//0.00E+00//gi|109829217|gb|DW227805.1|DW227805	HB			nr -
Unigene51514_All	583	2.69	0.70	1.83	4.27	1.06	0.54	0.00	0.00	0.00	-1.95E+00	7.99E-04	Down	-5.60E-01	3.18E-01		-2.01E+00	7.97E-07	Down	-2.98E+00	3.13E-09	Down	null	null		null	null					Unigene51514_All//1.00E-08//PL576574				
Unigene51518_All	380	0.55	2.00	1.12	8.13	1.45	3.57	1.45	5.06	1.99	1.86E+00	3.73E-02		1.03E+00	3.96E-01		-2.49E+00	8.92E-11	Down	-1.19E+00	8.07E-04	Down	1.81E+00	6.77E-05	Up	4.62E-01	5.28E-01					Unigene51518_All//2.00E-89//AW187099				
Unigene51519_All	587	0.18	0.17	1.09	2.04	0.00	0.54	4.39	9.83	3.26	-4.69E-02	9.88E-01		2.61E+00	2.33E-02		-1.10E-01	7.57E-09	Down	-1.92E+00	4.13E-03		1.16E+00	3.19E-07	Up	-4.32E-01	2.12E-01					Unigene51519_All//0.00E+00//AW187099				
Unigene51522_All	923	1.13	0.00	0.52	7.50	4.40	3.38	1.05	0.63	0.26	-1.01E+01	3.80E-06	Down	-1.13E+00	1.17E-01		-7.69E-01	1.94E-04		-1.15E+00	2.32E-07	Down	-7.33E-01	2.48E-01		-2.02E+00	2.47E-03		Unigene51522_All//gi|297851290|ref|XP_002893526.1|//2.00E-69//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339368|gb|EFH69785.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51522_All//2.00E-66//AT1G28390| protein kinase family protein	Unigene51522_All//0.00E+00//gi|21102358|gb|BQ414671.1|BQ414671		ko04626|Plant-pathogen interaction		nr -
Unigene51523_All	475	1.10	1.60	2.58	6.19	6.02	6.66	4.01	1.23	1.34	5.39E-01	5.02E-01		1.23E+00	6.00E-02		-4.03E-02	9.10E-01		1.05E-01	7.83E-01		-1.70E+00	1.53E-04	Down	-1.58E+00	2.42E-04	Down				Unigene51523_All//6.00E-10//DN801677				
Unigene51524_All	431	25.37	100.16	66.10	25.89	38.35	38.14	73.08	86.79	63.96	1.98E+00	1.03E-86	Up	1.38E+00	1.38E-33	Up	5.67E-01	9.69E-06		5.59E-01	3.08E-05		2.48E-01	1.92E-03		-1.92E-01	2.81E-02					Unigene51524_All//5.00E-75//TC176740				
Unigene51525_All	630	0.00	0.16	1.35	0.00	0.66	0.00	14.36	5.51	7.97	7.33E+00	3.86E-01		1.04E+01	9.02E-05	Up	9.36E+00	1.25E-02		null	null		-1.38E+00	4.67E-14	Down	-8.50E-01	4.36E-07		Unigene51525_All//gi|7239501|gb|AAF43227.1|AC012654_11/2.00E-20//F14023.12 [Arabidopsis thaliana]	Unigene51525_All//1.00E-21//AT1G71740| unknown protein	Unigene51525_All//0.00E+00//gi|109887106|gb|DW516075.1|DW516075				nr +
Unigene51528_All	2073	0.05	0.05	0.21	0.00	0.03	0.04	1.84	4.78	4.00	-4.64E-02	9.88E-01		2.02E+00	1.39E-01		5.05E+00	6.08E-01		5.45E+00	4.75E-01		1.38E+00	3.05E-15	Up	1.12E+00	8.19E-10	Up	Unigene51528_All//gi|297795135|ref|XP_002865452.1|//1.00E-156//tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297311287|gb|EFH41711.1| tetratricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene51528_All//1.00E-151//AT5G43120| tetratricopeptide repeat (TPR)-containing protein	Unigene51528_All//1.00E-08//TC142146				nr +
Unigene5153_All	587	114.98	71.47	87.00	182.11	177.87	173.58	133.83	74.69	63.32	-6.86E-01	4.89E-26		-4.02E-01	6.49E-10		-3.41E-02	6.02E-01		-6.93E-02	2.44E-01		-8.41E-01	3.26E-52		-1.08E+00	5.50E-81	Down	Unigene5153_All//gi|225030812|gb|ACN79519.1|//4.00E-84//reduced leaflet 1 [Lotus japonicus]	Unigene5153_All//3.00E-77//AT5G23570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene5153_All//0.00E+00//TC176927				nr +
Unigene51530_All	309	5.25	36.40	11.20	2.10	1.00	6.28	0.00	0.14	0.26	2.79E+00	2.15E-34	Up	1.09E+00	1.78E-03		-1.06E+00	2.26E-01		1.58E+00	1.21E-03		7.08E+00	6.34E-01		8.01E+00	4.03E-01		Unigene51530_All//gi|110740671|dbj|BAE98438.1|//1.00E-50//very-long-chain fatty acid condensing enzyme CUT1 like protein [Arabidopsis thaliana]	Unigene51530_All//4.00E-52//AT1G19440| KCS4 (3-KETOACYL-COA SYNTHASE 4); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene51530_All//3.00E-174//gi|21093131|gb|BQ405444.1|BQ405444		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant		nr -

Unigene51531_All	559	0.28	0.73	0.57	3.65	1.79	0.48	8.24	5.08	7.06	1.37E+00	2.74E-01			1.03E+00	4.71E-01		-1.03E+00	1.58E-02		-2.91E+00	1.67E-07	Down	-6.97E-01	5.34E-03		-2.25E-01	3.92E-01		Unigene51531_All//gi|297828556|ref|XP_002882160.1|//1.00E-51//nodulin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328000|gb|EFH58419.1| nodulin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51531_All//8.00E-53//AT3G01930| nodulin family protein	Unigene51531_All//2.00E-109//DW231799				nr -
Unigene51532_All	304	0.86	0.17	1.23	10.81	3.06	2.08	0.28	0.41	0.52	-2.37E+00	2.14E-01			5.11E-01	6.54E-01		-1.82E+00	8.05E-08	Down	-2.38E+00	1.57E-09	Down	5.68E-01	7.81E-01		9.14E-01	6.24E-01					Unigene51532_All//1.00E-96//CO117764				
Unigene51533_All	2260	0.00	0.04	0.19	0.18	0.00	0.12	3.09	1.29	11.72	5.49E+00	3.86E-01			7.56E+00	1.38E-02		-7.46E+00	4.38E-03		-5.56E-01	6.38E-01		-1.25E+00	1.38E-09	Down	1.93E+00	2.14E-64	Up	Unigene51533_All//gi|19881587|gb|AAM00988.1|AC090482_17//1.00E-152//Putative receptor protein kinase [Oryza sativa Japonica Group] >gi|31431296|gb|AAP53098.1| Leucine Rich Repeat family protein [Oryza sativa (japonica cultivar-group)]	Unigene51533_All//7.00E-143//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction		nr +
Unigene51534_All	558	0.00	10.81	0.19	1.16	0.43	1.70	0.00	2.40	2.00	1.34E+01	2.02E-34	Up		7.58E+00	3.97E-01		-1.43E+00	1.05E-01		5.51E-01	4.82E-01		1.12E+01	1.88E-09	Up	1.10E+01	4.36E-08	Up	Unigene51534_All//gi|167383|gb|AAA33074.1|//1.00E-57//storage protein [Gossypium hirsutum]	Unigene51534_All//4.00E-10//AT3G17520| late embryogenesis abundant domain-containing protein / LEA domain-containing protein	Unigene51534_All//0.00E+00//TC168445				nr -
Unigene51535_All	241	8.68	1.89	6.85	2.27	1.57	1.87	4.56	0.52	1.98	-2.20E+00	1.71E-05	Down		-3.42E-01	4.64E-01		-5.33E-01	5.85E-01		-2.79E-01	7.57E-01		-3.13E+00	3.46E-05	Down	-1.20E+00	3.41E-02					Unigene51535_All//1.00E-126//CO496813				
Unigene51536_All	359	49.70	21.88	21.21	409.06	432.60	333.25	97.28	59.61	47.27	-1.18E+00	1.64E-17	Down		-1.23E+00	9.67E-18	Down	8.07E-02	7.09E-02		-2.96E-01	2.95E-13		-7.07E-01	1.03E-17		-1.04E+00	1.91E-34	Down	Unigene51536_All//gi|224103789|ref|XP_002313194.1|//1.00E-66//tubulin alpha-5 chain [Populus trichocarpa] >gi|222849602|gb|EEE87149.1| tubulin alpha-5 chain [Populus trichocarpa]	Unigene51536_All//1.00E-66//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene51536_All//0.00E+00//BF272426		ko04145|Phagosome		nr -
Unigene51539_All	353	5.04	7.75	2.26	39.37	25.66	19.45	164.21	652.51	183.17	6.21E-01	1.04E-01			-1.16E+00	2.66E-02		-6.18E-01	8.20E-06		-1.02E+00	1.13E-11	Down	1.99E+00	0.00E+00	Up	1.58E-01	7.94E-03		Unigene51539_All//gi|15242438|ref|NP_196515.1|//1.00E-34//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|7671436|emb|CAB89377.1| periaxin-like protein [Arabidopsis thaliana]		Unigene51539_All//2.00E-70//TC152654		ko03040|Spliceosome		nr +
Unigene51540_All	1606	0.42	0.38	0.40	10.17	4.67	3.99	0.74	0.08	0.10	-1.62E-01	8.32E-01			-9.00E-02	9.22E-01		-1.12E+00	6.81E-18	Down	-1.35E+00	4.87E-21	Down	-3.24E+00	1.10E-05	Down	-2.89E+00	2.03E-05	Down	Unigene51540_All//gi|240254117|ref|NP_173393.5|//1.00E-172//CYP722A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana]	Unigene51540_All//5.00E-160//AT1G19630| CYP722A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene51540_All//0.00E+00//TC176902		ko00906|Carotenoid biosynthesis		nr +
Unigene51541_All	431	16.15	16.69	15.57	26.93	18.30	14.88	15.70	5.92	11.46	4.82E-02	8.34E-01			-5.26E-02	8.27E-01		-5.58E-01	3.14E-04		-8.56E-01	1.55E-07		-1.41E+00	5.58E-11	Down	-4.54E-01	2.11E-02					Unigene51541_All//2.00E-77//TC154226				
Unigene51542_All	284	88.80	38.54	35.06	123.48	115.55	157.75	281.37	121.71	128.91	-1.20E+00	4.32E-25	Down		-1.34E+00	2.12E-28	Down	-9.58E-02	3.75E-01		3.53E-01	5.09E-06		-1.21E+00	6.34E-96	Down	-1.13E+00	3.94E-88	Down	Unigene51542_All//gi|209967441|gb|ACJ02349.1|//3.00E-49//60S ribosomal protein L35a [Vernicia fordii]	Unigene51542_All//3.00E-48//AT1G74270| 60S ribosomal protein L35a (RPL35aC)	Unigene51542_All//2.00E-159//TC160867		ko03010|Ribosome		nr +
Unigene51543_All	1050	2.49	14.33	2.28	0.57	1.18	3.10	0.08	0.32	0.11	2.52E+00	4.79E-41	Up		-1.27E-01	7.46E-01		1.05E+00	9.06E-02		2.44E+00	1.85E-09	Up	1.98E+00	1.44E-01		4.99E-01	8.07E-01		Unigene51543_All//gi|9972373|gb|AAG10623.1|AC022521_1//8.00E-53//Unknown protein [Arabidopsis thaliana]	Unigene51543_All//3.00E-42//AT1G02700| unknown protein	Unigene51543_All//7.00E-70//CK640639				nr -
Unigene51544_All	382	9.72	15.39	9.90	21.26	19.65	14.90	46.38	17.62	25.13	6.62E-01	6.83E-03			2.54E-02	9.55E-01		-1.13E-01	6.17E-01		-5.13E-01	1.16E-02		-1.40E+00	3.77E-27	Down	-8.84E-01	7.60E-14					Unigene51544_All//2.00E-86//gi|78348483|gb|DT568757.1|DT568757				
Unigene51545_All	250	17.37	24.12	32.16	79.11	119.15	194.56	0.34	0.33	0.48	4.74E-01	5.18E-02			8.89E-01	3.15E-05		5.91E-01	1.20E-10		1.30E+00	2.85E-57	Up	-1.63E-02	1.01E+00		4.99E-01	8.07E-01		Unigene51545_All//gi|159474026|ref|XP_001695130.1|//4.00E-06//cell wall protein pherophorin-C10 [Chlamydomonas reinhardtii] >gi|158276064|gb|EDP01838.1| cell wall protein pherophorin-C10 [Chlamydomonas reinhardtii]						nr +
Unigene51546_All	402	7.68	2.14	7.29	3.72	4.80	4.72	0.63	0.00	0.00	-1.84E+00	2.51E-06	Down		-7.59E-02	8.35E-01		3.68E-01	4.84E-01		3.44E-01	5.06E-01		-9.30E+00	4.03E-02		-9.30E+00	3.04E-02		Unigene51546_All//gi|255582439|ref|XP_002532007.1|//1.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223528338|gb|EEF30380.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene51547_All	664	1.42	1.83	0.00	1.50	0.88	1.36	2.10	3.34	2.40	3.69E-01	5.56E-01			-1.05E+01	3.34E-05	Down	-7.67E-01	2.60E-01		-1.41E-01	8.36E-01		6.67E-01	8.59E-02		1.92E-01	6.75E-01		Unigene51547_All//gi|224134645|ref|XP_002327455.1|//4.00E-23//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222836009|gb|EEE74430.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene51547_All//1.00E-14//AT1G69545| leucine-rich repeat family protein	Unigene51547_All//8.00E-41//TC138390				nr +
Unigene5155_All	814	5.21	1.00	3.01	13.46	6.26	15.59	16.73	4.67	7.00	-2.39E+00	2.18E-11	Down		-7.91E-01	1.03E-02		-1.10E+00	7.48E-12	Down	2.12E-01	2.30E-01		-1.84E+00	5.93E-31	Down	-1.26E+00	1.38E-18	Down	Unigene5155_All//gi|8778401|gb|AAF79409.1|AC068197_19//2.00E-33//F16A14.27 [Arabidopsis thaliana]	Unigene5155_All//9.00E-24//AT1G14060| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: GCK (InterPro:IPR012891); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G02210.1); Has 243 Blast hits to 215 proteins in 60 species: Archae - 0; Bacteria - 2; Metazoa - 93; Fungi - 27; Plants - 49; Viruses - 2; Other Eukaryotes - 70 (source: NCBI BLink).	Unigene5155_All//0.00E+00//TC159634				nr +
Unigene51550_All	727	1.94	1.05	1.46	1.30	2.89	1.99	1.80	0.63	0.22	-8.94E-01	1.12E-01			-4.08E-01	4.86E-01		1.15E+00	9.33E-03		6.11E-01	3.05E-01		-1.51E+00	5.71E-03		-3.04E+00	3.54E-06	Down	Unigene51550_All//gi|15229419|ref|NP_191896.1|//1.00E-59//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene51550_All//6.00E-61//AT3G63370| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene51551_All	300	312.01	46.78	96.92	35.70	32.71	55.70	0.56	0.56	0.00	-2.74E+00	4.29E-279	Down		-1.69E+00	1.79E-146	Down	-1.26E-01	5.61E-01		6.42E-01	1.33E-06		-1.65E-02	1.02E+00		-9.14E+00	1.08E-01		Unigene51551_All//gi|224140415|ref|XP_002323578.1|//4.00E-34//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222868208|gb|EEF05339.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene51551_All//2.00E-27//AT3G51860| CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	Unigene51551_All//4.00E-164//TC142837				nr -
Unigene51553_All	671	0.00	0.00	0.00	5.86	0.98	0.61	0.88	2.37	1.90	null	null			null	null		-2.59E+00	2.92E-14	Down	-3.28E+00	1.17E-15	Down	1.42E+00	3.29E-03		1.11E+00	3.37E-02		Unigene51553_All//gi|115459588|ref|NP_001053394.1|//1.00E-39//Os04g0531100 [Oryza sativa Japonica Group] >gi|122196004|sp|Q25AG5.1|ERG3_ORYSI RecName: Full=Elicitor-responsive protein 3; AltName: Full=16 kDa phloem protein; AltName: Full=RPP16 >gi|122234706|sp|Q0JBH9.1|ERG3_ORYSJ RecName: Full=Elicitor-responsive protein 3; AltName: Full=16 kDa phloem protein; AltName: Full=RPP16 >gi|3603473|gb|AAC35866.1| elicitor-responsive gene-3 [Oryza sativa Indica Group] >gi|21998839|dbj|BAC06444.1| RPP16 [Oryza sativa Japonica Group] >gi|38346762|emb|CAE03867.2| OSJNBa0081C01.13 [Oryza sativa (japonica cultivar-group)] >gi|90399378|emb|CAH68390.1| B1011H02.6 [Oryza sativa (indica cultivar-group)] >gi|113564965|dbj|BAF15308.1| Os04g0531100 [Oryza sativa Japonica Group] >gi|116312035|emb|CAJ86400.1| OS1G8a0125H19.3 [Oryza sativa	Unigene51553_All//4.00E-39//AT1G63220| C2 domain-containing protein	Unigene51553_All//2.00E-10//TC159531		ko04626|Plant-pathogen interaction//ko03040|Spliceosome		nr -
Unigene51554_All	527	2.28	3.17	1.11	9.74	7.38	8.06	7.86	3.65	5.75	4.75E-01	3.67E-01			-1.04E+00	1.14E-01		-3.99E-01	1.36E-01		-2.73E-01	3.57E-01		-1.11E+00	4.34E-05	Down	-4.53E-01	8.32E-02		Unigene51554_All//gi|113206404|gb|ABI34432.1|//2.00E-06//CRY [Pisum sativum]	Unigene51554_All//6.00E-06//AT1G66350| RGL1 (RGA-LIKE 1); transcription factor	Unigene51554_All//1.00E-69//TC169400	GRAS			nr -
Unigene51556_All	1212	0.60	0.42	0.09	7.19	9.92	4.25	1.67	0.48	0.56	-5.32E-01	5.13E-01			-2.78E+00	1.04E-02		4.63E-01	3.25E-03		-7.60E-01	7.01E-05		-1.79E+00	4.24E-05	Down	-1.58E+00	1.35E-04	Down	Unigene51556_All//gi|115474069|ref|NP_001060633.1|//1.00E-25//Os07g0677900 [Oryza sativa Japonica Group] >gi|33146126|dbj|BAC79534.1| myosin heavy chain-like [Oryza sativa Japonica Group] >gi|113612169|dbj|BAF22547.1| Os07g0677900 [Oryza sativa Japonica Group]	Unigene51556_All//3.00E-36//AT2G40480| unknown protein	Unigene51556_All//6.00E-83//gi|84146464|gb|DN760706.1|DN760706				nr -
Unigene51558_All	539	9.51	6.96	3.95	3.23	5.49	5.45	33.26	70.18	71.92	-4.52E-01	9.17E-02			-1.27E+00	8.24E-06	Down	7.64E-01	3.35E-02		7.52E-01	4.19E-02		1.08E+00	3.81E-38	Up	1.11E+00	4.54E-42	Up	Unigene51558_All//gi|44681326|gb|AAS47603.1|//9.00E-08//At3g20340 [Arabidopsis thaliana] >gi|45773836|gb|AAS76722.1| At3g20340 [Arabidopsis thaliana]	Unigene51558_All//3.00E-08//AT4G21920| unknown protein					nr +
Unigene51559_All	451	0.81	0.11	0.71	4.09	2.52	2.20	3.00	4.17	0.53	-2.85E+00	7.80E-02			-1.97E-01	8.66E-01		-6.98E-01	1.37E-01		-8.91E-01	6.61E-02		4.75E-01	2.81E-01		-2.50E+00	2.46E-05	Down				Unigene51559_All//6.00E-121//DW499339				
Unigene5156_All	1157	31.79	59.60	30.70	39.74	38.27	34.74	40.53	64.52	81.71	9.07E-01	1.85E-42			-5.04E-02	6.15E-01		-5.42E-02	5.85E-01		-1.94E-01	1.75E-02		6.71E-01	9.97E-34		1.01E+00	6.30E-87	Up	Unigene5156_All//gi|300510880|gb|ADK25058.1|//4.00E-56//AN1-like transcription factor [Glycine max]	Unigene5156_All//9.00E-50//AT3G12630| zinc finger (AN1-like) family protein	Unigene5156_All//0.00E+00//TC151503				nr -
Unigene51560_All	651	0.88	0.00	2.62	5.20	3.76	1.73	1.88	2.44	0.86	-9.79E+00	1.52E-03			1.57E+00	4.57E-03		-4.70E-01	1.62E-01		-1.59E+00	5.41E-06	Down	3.73E-01	4.48E-01		-1.14E+00	3.17E-02					Unigene51560_All//1.00E-107//DW499339				
Unigene51562_All	542	14.29	15.24	10.22	18.93	16.77	15.83	42.75	51.59	20.95	9.30E-02	6.58E-01			-4.84E-01	2.79E-02		-1.75E-01	3.88E-01		-2.58E-01	1.88E-01		2.71E-01	3.78E-03		-1.03E+00	9.82E-23	Down	Unigene51562_All//gi|2789660|gb|AAC83464.1|//7.00E-16//eIF3c [Arabidopsis thaliana]	Unigene51562_All//2.00E-08//AT3G56150| EIF3C (EUKARYOTIC TRANSLATION INITIATION FACTOR 3C); translation initiation factor	Unigene51562_All//0.00E+00//gi|48745063|gb|CO075582.1|CO075582				nr +

Unigene51564_All	731	1.50	1.11	1.17	4.09	3.25	1.24	2.66	1.09	0.49	-4.39E-01	4.95E-01		-3.67E-01	6.01E-01		-3.31E-01	3.87E-01		-1.73E+00	5.70E-06	Down	-1.29E+00	2.34E-03		-2.44E+00	3.73E-07	Down	Unigene51564_All//gi|297818068|ref|XP_002876917.1|//2.00E-61//nsp-interacting kinase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297322755|gb|EFH53176.1| nsp-interacting kinase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene51564_All//3.00E-60//AT3G25560| NIK2 (NSP-INTERACTING KINASE 2); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr -
Unigene51565_All	1142	0.96	0.67	0.37	6.24	0.27	0.75	5.96	1.54	1.53	-5.32E-01	3.95E-01		-1.37E+00	5.32E-02		-4.52E+00	1.89E-42	Down	-3.05E+00	2.92E-26	Down	-1.96E+00	3.87E-17	Down	-1.96E+00	9.71E-18	Down	Unigene51565_All//gi|38260688|gb|AAR15502.1|//7.00E-40//F-box protein [Arabidopsis arenosa]	Unigene51565_All//1.00E-36//AT5G07610| F-box family protein					nr -
Unigene51566_All	652	5.22	1.40	3.02	1.22	3.33	1.52	0.39	0.45	0.12	-1.90E+00	3.78E-07	Down	-7.88E-01	2.50E-02		1.44E+00	1.02E-03		3.18E-01	6.73E-01		2.06E-01	8.68E-01		-1.67E+00	2.56E-01				Unigene51566_All//1.00E-110//ES792370					
Unigene51569_All	506	10.13	6.41	6.21	7.97	5.51	2.86	2.76	1.40	1.26	-6.61E-01	1.23E-02		-7.07E-01	1.04E-02		-5.33E-01	7.26E-02		-1.48E+00	2.05E-06	Down	-9.74E-01	5.54E-02		-1.13E+00	2.13E-02		Unigene51569_All//gi|255561828|ref|XP_002521923.1|//4.00E-07//hypothetical protein RCOM_0641350 [Ricinus communis] >gi|223538848|gb|EEF40447.1| hypothetical protein RCOM_0641350 [Ricinus communis]						nr -
Unigene5157_All	438	0.60	6.02	2.07	3.18	2.04	1.96	2.22	1.15	4.73	3.33E+00	5.96E-10	Up	1.79E+00	3.07E-02		-6.40E-01	2.55E-01		-7.01E-01	2.32E-01		-9.55E-01	1.35E-01		1.09E+00	5.36E-03				Unigene5157_All//2.00E-12//DW504746					
Unigene51572_All	851	0.00	1.91	1.31	0.12	0.32	6.16	56.09	53.78	38.11	1.09E+01	2.96E-09	Up	1.04E+01	3.43E-06	Up	1.47E+00	4.20E-01		5.72E+00	1.59E-28	Up	-6.07E-02	4.78E-01		-5.58E-01	1.89E-16		Unigene51572_All//gi|118603318|gb|AAT06600.2|//2.00E-36//dehydrin [Lupinus albus]	Unigene51572_All//2.00E-10//AT1G20450| ERD10 (EARLY RESPONSIVE TO DEHYDRATION 10); actin binding			ko03040|Spliceosome		nr +
Unigene51577_All	876	0.00	0.17	0.00	0.00	0.00	0.00	87.17	5.39	20.51	7.44E+00	2.35E-01		null	null		null	null		null	null		-4.02E+00	0.00E+00	Down	-2.09E+00	1.79E-207	Down	Unigene51577_All//gi|224101327|ref|XP_002312234.1|//1.00E-114//metal tolerance protein [Populus trichocarpa] >gi|222852054|gb|EEE89601.1| metal tolerance protein [Populus trichocarpa]	Unigene51577_All//2.00E-100//AT1G16310| cation efflux family protein	Unigene51577_All//7.00E-08//CO115820				nr -
Unigene51578_All	396	0.66	0.90	1.61	4.40	5.30	2.28	2.46	0.32	1.41	4.39E-01	7.01E-01		1.29E+00	1.86E-01		2.69E-01	5.94E-01		-9.49E-01	5.79E-02		-2.96E+00	1.89E-04	Down	-8.02E-01	1.83E-01		Unigene51578_All//gi|145332817|ref|NP_001078274.1|//2.00E-19//DNA binding / hydrolase, acting on ester bonds / nuclease/ nucleic acid binding / recombinase [Arabidopsis thaliana]	Unigene51578_All//1.00E-20//AT3G52905| DNA binding / hydrolase, acting on ester bonds / nuclease/ nucleic acid binding / recombinase					nr -
Unigene5158_All	668	1.17	5.46	1.43	3.43	2.06	1.01	1.84	1.13	2.39	2.22E+00	4.79E-09	Up	2.88E-01	6.65E-01		-7.34E-01	7.05E-02		-1.76E+00	7.84E-05	Down	-7.05E-01	2.06E-01		3.78E-01	4.15E-01		Unigene5158_All//sp|P03554|POL_CAMVS//1.00E-06//Enzymatic polyprotein OS=Cauliflower mosaic virus (strain Strasbourg) GN=ORF VPE-3 SV=1		Unigene5158_All//5.00E-14//DW504746				swissprot +
Unigene51580_All	410	0.26	4.70	1.43	1.09	1.76	1.10	2.58	3.77	3.79	4.20E+00	1.02E-08	Up	2.49E+00	3.75E-02		6.90E-01	4.47E-01		1.05E-02	1.00E+00		5.49E-01	2.60E-01		5.56E-01	2.32E-01				Unigene51580_All//7.00E-34//TC146462					
Unigene51581_All	530	5.03	0.86	5.33	13.63	10.79	14.83	0.00	0.16	0.00	-2.55E+00	6.04E-08	Down	8.09E-02	8.32E-01		-3.38E-01	1.29E-01		1.22E-01	6.11E-01		7.30E+00	4.00E-01		null	null				Unigene51581_All//3.00E-12//ES826854					
Unigene51582_All	724	0.72	3.36	1.03	0.21	0.62	0.12	54.72	89.08	30.43	2.22E+00	2.89E-06	Up	5.11E-01	5.47E-01		1.58E+00	2.17E-01		-7.26E-01	7.15E-01		7.03E-01	1.08E-31		-8.47E-01	8.32E-28		Unigene51582_All//gi|169349|gb|AAA33765.1|//1.00E-78//hydroxyproline-rich glycoprotein [Phaseolus vulgaris]		Unigene51582_All//3.00E-19//DB455671		ko03040|Spliceosome//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr +
Unigene51585_All	336	2.34	2.41	2.22	3.71	2.25	1.21	2.52	1.99	0.36	4.68E-02	9.69E-01		-7.42E-02	9.35E-01		-7.17E-01	2.26E-01		-1.62E+00	1.08E-02		-3.39E-01	6.61E-01		-2.82E+00	5.38E-04	Down									
Unigene51586_All	313	5.85	9.55	5.78	5.25	6.71	6.78	17.02	6.81	8.66	7.07E-01	5.01E-02		-1.64E-02	9.96E-01		3.54E-01	4.78E-01		3.69E-01	4.54E-01		-1.32E+00	4.47E-08	Down	-9.76E-01	1.73E-05				Unigene51586_All//8.00E-144//TC162769					
Unigene51587_All	230	10.92	13.00	23.38	24.91	21.41	14.33	0.92	1.45	2.77	2.51E-01	5.05E-01		1.10E+00	5.35E-05	Up	-2.18E-01	4.26E-01		-7.97E-01	1.08E-03		6.62E-01	6.09E-01		1.59E+00	5.48E-02										
Unigene51589_All	341	2.92	1.78	6.56	3.65	2.63	9.54	0.25	0.25	0.35	-7.09E-01	3.05E-01		1.17E+00	1.00E-02		-4.76E-01	4.39E-01		1.38E+00	9.06E-05	Up	-1.70E-02	1.01E+00		4.99E-01	8.07E-01										
Unigene5159_All	1394	5.78	5.13	2.60	14.58	8.92	7.52	6.95	5.04	4.72	-1.74E-01	4.25E-01		-1.15E+00	1.23E-07	Down	-7.09E-01	2.23E-10		-9.56E-01	3.39E-15		-4.64E-01	5.07E-03		-5.59E-01	4.60E-04		Unigene5159_All//gi|102139855|gb|ABF70013.1|//1.00E-64//myb DNA-binding domain-containing protein [Musa acuminata]	Unigene5159_All//6.00E-38//AT2G03500| myb family transcription factor	Unigene5159_All//0.00E+00//ES841644	G2-like			nr +
Unigene51590_All	263	82.76	20.81	21.26	83.53	47.79	227.19	41.32	25.11	17.27	-1.99E+00	1.27E-44	Down	-1.96E+00	4.46E-42	Down	-8.06E-01	7.42E-14		1.44E+00	1.77E-82	Up	-7.19E-01	3.13E-06		-1.26E+00	4.82E-15	Down	Unigene51590_All//gi|3023847|sp|O24076.1|GBLP_MEDSA//2.00E-16//RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein >gi|2385376|emb|CAA69934.1| G protein beta subunit-like [Medicago sativa subsp. x varia]	Unigene51590_All//8.00E-16//AT1G48630| RACK1B_AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding	Unigene51590_All//4.00E-139//gi|78340597|gb|DT560871.1|DT560871				nr +
Unigene51592_All	467	13.56	6.62	7.75	17.17	13.94	16.73	58.21	23.18	20.13	-1.03E+00	1.43E-05	Down	-8.06E-01	9.65E-04		-3.01E-01	1.56E-01		-3.77E-02	8.83E-01		-1.33E+00	2.83E-38	Down	-1.53E+00	1.14E-48	Down	Unigene51592_All//gi|192910756|gb|ACF06486.1|//2.00E-47//60S ribosomal protein L11 [Elaeis guineensis] >gi|192910758|gb|ACF06487.1| 60S ribosomal protein L11 [Elaeis guineensis]	Unigene51592_All//7.00E-41//AT5G45775| 60S ribosomal protein L11 (RPL11D)	Unigene51592_All//0.00E+00//TC141832		ko03010|Ribosome		nr -
Unigene51594_All	660	1.82	0.15	0.89	2.11	1.10	1.30	1.09	0.19	0.78	-3.57E+00	3.63E-05	Down	-1.04E+00	1.14E-01		-9.48E-01	8.15E-02		-7.01E-01	2.32E-01		-2.52E+00	4.69E-03		-4.73E-01	5.20E-01		Unigene51594_All//gi|224102121|ref|XP_002312555.1|//2.00E-30//argonaute protein group [Populus trichocarpa] >gi|222852375|gb|EEE89922.1| argonaute protein group [Populus trichocarpa]	Unigene51594_All//1.00E-26//AT5G43810| ZLL (ZWILLE); translation initiation factor	Unigene51594_All//0.00E+00//TC134250				nr -
Unigene51595_All	1020	1.54	3.48	3.92	0.93	1.59	0.84	0.00	0.00	0.00	1.18E+00	4.49E-04	Up	1.35E+00	4.36E-05	Up	7.74E-01	1.47E-01		-1.41E-01	8.42E-01		null	null		null	null		Unigene51595_All//gi|289976573|gb|ADD21635.1|//2.00E-59//matrix metalloprotease 1 [Nicotiana benthamiana]	Unigene51595_All//2.00E-59//AT1G59970| matrixin family protein					nr -
Unigene51596_All	860	3.35	1.00	3.96	0.98	0.28	0.84	1.28	1.85	1.11	-1.74E+00	1.44E-05	Down	2.44E-01	5.06E-01		-1.81E+00	1.77E-02		-2.29E-01	7.51E-01		5.31E-01	2.71E-01		-2.01E-01	7.10E-01		Unigene51596_All//gi|212549818|gb|ACJ26769.1|//3.00E-94//AO2 [Arachis hypogaea]	Unigene51596_All//2.00E-85//AT5G20960| AAO1 (ARABIDOPSIS ALDEHYDE OXIDASE 1); aldehyde oxidase/ indole-3-acetaldehyde oxidase	Unigene51596_All//5.00E-52//DW233729		ko00230|Purine metabolism//ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00906|Carotenoid biosynthesis//ko00232|Caffeine metabolism		nr +
Unigene51598_All	462	0.00	2.19	1.04	2.16	0.97	1.37	3.94	0.63	1.47	1.11E+01	7.25E-06	Up	1.00E+01	7.47E-03		-1.15E+00	8.41E-02		-6.56E-01	3.71E-01		-2.64E+00	5.50E-07	Down	-1.42E+00	1.00E-03		Unigene51598_All//gi|240254403|ref|NP_178082.6|//1.00E-14//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase [Arabidopsis thaliana]	Unigene51598_All//1.00E-15//AT1G79640| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene51598_All//0.00E+00//gi|164362229|gb|ES833903.1|ES833903				nr +
Unigene51599_All	384	1.91	2.24	7.49	2.98	3.68	3.18	0.77	2.72	6.95	2.34E-01	7.28E-01		1.97E+00	4.12E-06	Up	3.01E-01	6.16E-01		8.99E-02	9.06E-01		1.82E+00	5.04E-03		3.17E+00	4.40E-12	Up			Unigene51599_All//4.00E-07//TC159973					
Unigene51601_All	516	1.12	0.79	1.86	0.97	2.20	4.29	1.31	3.56	1.85	-5.06E-01	6.00E-01		7.36E-01	3.23E-01		1.19E+00	7.15E-02		2.15E+00	9.17E-06	Up	1.44E+00	1.20E-03		4.99E-01	4.19E-01		Unigene51601_All//gi|218193365|gb|EEC75792.1|//7.00E-06//hypothetical protein Osl_12721 [Oryza sativa Indica Group]	Unigene51601_All//1.00E-05//AT3G04730| IAA16; transcription factor	Unigene51601_All//1.00E-32//gi|164338356|gb|ES814419.1|ES814419				nr -
Unigene51602_All	534	0.29	2.37	1.00	0.84	1.03	0.68	1.11	1.10	0.67	3.01E+00	1.02E-04	Up	1.76E+00	1.29E-01		2.97E-01	8.18E-01		-3.11E-01	7.57E-01		-1.66E-02	1.02E+00		-7.23E-01	3.71E-01										
Unigene51603_All	614	0.00	52.15	3.82	0.73	1.68	5.15	0.00	0.00	0.19	1.57E+01	1.10E-184	Up	1.19E+01	6.40E-13	Up	1.20E+00	8.55E-02		2.82E+00	1.16E-10	Up	null	null		7.61E+00	2.43E-01		Unigene51603_All//gi|15081694|gb|AK82502.1|//5.00E-25//AT5g66780/MUD21_2 [Arabidopsis thaliana] >gi|18252267|gb|AAL62014.1| AT5g66780/MUD21_2 [Arabidopsis thaliana]	Unigene51603_All//3.00E-26//AT5G66780| unknown protein					nr +
Unigene51605_All	359	3.94	9.88	3.11	2.78	4.70	5.16	8.13	11.99	28.41	1.33E+00	9.56E-05	Up	-3.37E-01	5.79E-01		7.60E-01	1.44E-01		8.94E-01	6.88E-02		5.61E-01	3.30E-02		1.81E+00	2.88E-23	Up			Unigene51605_All//3.00E-85//gi|84165350|gb|DR453998.1|DR453998					
Unigene51607_All	483	5.20	5.46	6.39	10.62	11.62	5.14	15.67	9.17	10.97	6.92E-02	8.60E-01		2.98E-01	4.22E-01		1.30E-01	6.63E-01		-1.05E+00	6.37E-05	Down	-7.73E-01	4.28E-05		-5.14E-01	5.01E-03				Unigene51607_All//2.00E-105//gi|21094225|gb|BQ406538.1|BQ406538					
Unigene51609_All	373	0.00	0.00	0.00	2.94	2.68	1.45	4.31	3.03	17.73	null	null		null	null		-1.34E-01	8.25E-01		-1.02E+00	1.30E-01		-5.10E-01	2.90E-01		2.04E+00	6.02E-18	Up	Unigene51609_All//gi|224139892|ref|XP_002323327.1|//4.00E-06//predicted protein [Populus trichocarpa] >gi|222867957|gb|EEF05088.1| predicted protein [Populus trichocarpa]		Unigene51609_All//1.00E-10//AI055471				nr -
Unigene5161_All	656	15.63	23.17	18.99	13.97	19.53	20.24	7.03	17.08	17.07	5.68E-01	7.22E-05		2.81E-01	1.09E-01		4.83E-01	1.35E-03		5.35E-01	4.37E-04		1.28E+00	2.28E-15	Up	1.28E+00	9.93E-16	Up	Unigene5161_All//gi|71041112|gb|AAZ20444.1|//3.00E-80//MYBR5 [Malus x domestica]	Unigene5161_All//1.00E-69//AT5G52660| myb family transcription factor	Unigene5161_All//0.00E+00//TC167152	MYB-related	ko04712|Circadian rhythm - plant		nr +
Unigene51610_All	335	0.62	6.66	6.84	0.00	3.70	23.59	0.00	2.12	0.48	3.41E+00	1.13E-08	Up	3.45E+00	1.24E-08	Up	1.19E+01	1.19E-07	Up	1.45E+01	4.64E-48	Up	1.11E+01	3.97E-05	Up	8.89E+00	1.40E-01										
Unigene51611_All	1774	0.53	0.97	0.18	4.63	4.91	3.79	2.15	0.87	0.70	8.71E-01	8.07E-02		-1.56E+00	4.90E-02		8.40E-02	7.48E-01		-2.89E-01	1.91E-01		-1.30E+00	7.40E-06	Down	-1.62E+00	3.88E-08	Down	Unigene51611_All//gi|124360202|gb|ABN08215.1|//1.00E-133//Zinc finger, CCCH-type [Medicago truncatula]	Unigene51611_All//2.00E-115//AT5G12850| zinc finger (CCCH-type) family protein	Unigene51611_All//3.00E-33//TC132093	C3H			nr -
Unigene51612_All	476	0.55	0.75	0.45	3.66	4.49	4.65	3.11	0.88	0.84	4.39E-01	7.01E-01		-2.97E-01	8.32E-01		2.92E-01	5.58E-01		3.44E-01	4.79E-01		-1.82E+00	5.43E-04	Down	-1.89E+00	2.45E-04	Down	Unigene51612_All//gi|195610468|gb|ACG27064.1|//2.00E-12//CHL-CPN10 [Zea mays] >gi|195653971|gb|ACG46453.1| CHL-CPN10 [Zea mays]	Unigene51612_All//1.00E-13//AT3G60210| chloroplast chaperonin 10, putative	Unigene51612_All//5.00E-137//gi|48792600|gb|CO093914.1|CO093914				nr +
Unigene51613_All	1436	0.29	1.20	2.48	0.52	2.04	9.44	0.27	0.12	4.49	2.04E+00	2.81E-04	Up	3.09E+00	5.19E-12	Up	1.97E+00	4.26E-07	Up	4.18E+00	1.44E-62	Up	-1.19E+00	3.09E-01		4.08E+00	1.19E-34	Up	Unigene51613_All//gi|28951055|gb|AA063451.1|//1.00E-171//At5g28237 [Arabidopsis thaliana]	Unigene51613_All//3.00E-166//AT5G28237| tryptophan synthase, beta subunit, putative	Unigene51613_All//4.00E-07//CO122972		ko00260|Glycine, serine and threonine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr +
Unigene51614_All	1839	0.31	0.30	0.69	5.91	0.09	0.15	7.27	0.09	0.32	-4.64E-02	9.74E-01		1.15E+00	6.95E-02		-5.98E+00	9.23E-75	Down	-5.32E+00	8.72E-60	Down	-6.32E+00	1.31E-87	Down	-4.48E+00	2.41E-77	Down	Unigene51614_All//gi|53749404|gb|AAL90262.1|//9.00E-12//integrase core domain containing protein [Oryza sativa Japonica Group]		Unigene51614_All//3.00E-42//FL577607				nr -
Unigene51615_All	1062	1.08	2.10	0.00	0.19	0.19	0.09	37.42	17.28	29.79	9.54E-01	2.68E-02		-1.01E+01	2.60E-06	Down	5.21E-02	9.88E-01		-1.14E+00	5.68E-01		-1.12E+00	2.34E-42	Down	-3.29E-01	8.62E-06		Unigene51615_All//gi|28950747|gb|AA063297.1|//1.00E-69//At2g45360 [Arabidopsis thaliana]	Unigene51615_All//5.00E-71//AT2G45360| unknown protein					nr -
Unigene51617_All	385	2.04	6.98	1.38	2.59	1.16	2.35	0.00	0.00	0.00	1.77E+00	2.49E-05	Up	-5.60E-01	4.96E-01		-1.15E+00	8.41E-02		-1.42E-01	8.36E-01		null	null		null	null				Unigene51617_All//3.00E-128//TC178874					
Unigene51618_All	281	11.54	10.46	3.79	13.12	13.23	17.84	46.34	35.55	22.26	-1.43E-01	6.74E-01		-1.61E+00	2.68E-05	Down	1.28E-02	9.79E-01		4.44E-01	1.15E-01		-3.83E-01	6.74E-03		-1.06E+00	9.70E-14	Down			Unigene51618_All//3.00E-112//ES849747					
Unigene5162_All	855	0.12	0.12	0.12	1.51	2.30	2.01	2.72	0.68	1.91	-4.67E-02	9.88E-01		2.57E-02	9.99E-01		6.00E-01	2.16E-01		4.06E-01	4.62E-01		-1.99E+00	1.81E-06	Down	-5.10E-01	1.62E-01		Unigene5162_All//gi|224056467|ref|XP_002298871.1|//7.00E-21//predicted protein [Populus trichocarpa] >gi|222846129|gb|EEE83676.1| predicted protein [Populus trichocarpa]						nr -
Unigene51620_All	663	3.16	4.05	4.66	0.90	0.99	0.34	1.79	0.82	0.30	3.60E-01	3.75E-01		5.62E-01	1.37E-01		1.30E-01	9.05E-01		-1.40E+00	1.58E-01		-1.12E+00	4.65E-02		-2.57E+00	6.97E-05	Down	Unigene51620_All//gi|297797429|ref|XP_002866599.1|//5.00E-34//methylase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312434|gb|EFH42858.1| methylase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51620_All//3.00E-35//AT5G64150| methylase family protein	Unigene51620_All//0.00E+00//TC176049				nr -
Unigene51621_All	388	200.79	52.37	206.41	130.06	70.02	63.21	141.01	96.63	33.27	-1.94E+00	1.02E-152	Down	3.99E-02	6.01E-01		-8.93E-01	2.47E-37		-1.04E+00	1.95E-42	Down	-5.45E-01	1.73E-17		-2.08E+00	1.76E-148	Down			Unigene51621_All//3.00E-144//gi|31406579|gb|CD485614.1|CD485614					
Unigene51624_All	403	1.56	10.81	4.36	0.87	0.94	1.23	0.00	0.00	0.00	2.80E+00	1.10E-13	Up	1.48E+00	5.78E-03		1.19E-01	9.58E-01		5.11E-01	6.41E-01		null	null		null	null				Unigene51624_All//1.00E-19//gi|164324625|gb|EV489221.1|EV489221					
Unigene51626_All	742	0.71	20.49	2.51	1.75	1.62	5.42	0.80	0.73	0.00	4.86E+00	3.73E-72	Up	1.83E+00	6.91E-04	Up	-1.04E-01	8.43E-01		1.63E+00	3.93E-07	Up	-1.23E-01	8.84E-01		-9.64E+00	1.41E-04	Down	Unigene51626_All//gi|19962|emb|CAA41437.1|//6.00E-56//pathogenesis-related protein 4A [Nicotiana tabacum]	Unigene51626_All//7.00E-36//AT3G04720| PR4 (PATHOGENESIS-RELATED 4); chitin binding	Unigene51626_All//2.00E-81//gi|84175243|gb|DR463891.1|DR463891				nr -
Unigene51627_All	679	0.23	0.00	0.24	2.13	1.01	1.00	3.55	10.77	18.89	-7.85E+00	2.15E-01		2.54E-02	1.00E+00		-1.07E+00	4.31E-02		-1.09E+00	5.14E-02		1.60E+00	4.38E-14	Up	2.41E+00	1.11E-41	Up									
Unigene51629_All	626	1.17	3.08	1.02	2.15	1.71	0.79	2.36	2.07	5.92	1.39E+00	4.12E-03		-1.97E-01	7.99E-01		-3.33E-01	5.81E-01		-1.44E+00	1.59E-02		-1.92E-01	7.03E-01		1.32E+00	4.87E-06	Up			Unigene51629_All//2.00E-07//TC146649					
Unigene5163_All	612	0.85	1.57	0.44	1.30	3.60	2.44	3.25	2.46	6.25	8.80E-01	2.13E-01		-9.75E-01	3.76E-01		1.47E+00	7.75E-04	Up	9.03E-01	1.09E-01		-4.01E-01	3.63E-01		9.45E-01	5.54E-04										

Unigene51630_All	482	61.98	119.21	49.27	90.43	106.16	86.67	99.38	189.47	317.72	9.44E-01	6.78E-38		-3.31E-01	1.40E-03		2.31E-01	1.25E-03		-6.12E-02	5.60E-01		9.31E-01	1.21E-71		1.68E+00	4.10E-305	Up	Unigene51630_All//gi|82469976|gb|AB877236.1|//2.00E-21//patellin 1 [Cucurbita pepo]	Unigene51630_All//5.00E-09//AT1G22530| PATL2 (PATELLIN 2); transporter	Unigene51630_All//0.00E+00//gi|48822916|gb|CO124229.1|CO124229				nr +
Unigene51631_All	968	0.00	0.00	0.00	0.00	0.00	0.00	15.59	5.57	5.97	null	null		null	null		null	null		null	null		-1.49E+00	2.01E-25	Down	-1.39E+00	1.04E-23	Down	Unigene51631_All//gi|124360970|gb|ABN08942.1|//1.00E-115//Quinonprotein alcohol dehydrogenase-like [Medicago truncatula]		Unigene51631_All//8.00E-17//CO071277				nr -
Unigene51632_All	780	0.13	0.00	0.00	3.70	1.85	2.20	1.90	0.21	0.66	-7.07E+00	3.71E-01		-7.07E+00	3.92E-01		-9.98E-01	3.93E-03		-7.51E-01	4.17E-02		-3.15E+00	8.54E-07	Down	-1.51E+00	2.08E-03		Unigene51632_All//gi|15238913|ref|NP_196658.1|//6.00E-32//zinc finger (C2H2 type) family protein [Arabidopsis thaliana] >gi|8979731|emb|CAB96852.1| zinc finger-like protein [Arabidopsis thaliana]	Unigene51632_All//4.00E-29//AT1G80730| ZFP1 (ZINC-FINGER PROTEIN 1); nucleic acid binding / transcription factor/ zinc ion binding	Unigene51632_All//3.00E-102//DW224855	C2H2			nr -
Unigene51634_All	375	2.09	0.54	3.98	9.30	3.03	0.60	2.25	1.34	1.91	-1.95E+00	2.62E-02		9.26E-01	1.05E-01		-1.62E+00	4.72E-07	Down	-3.95E+00	3.57E-16	Down	-7.54E-01	2.78E-01		-2.38E-01	7.02E-01		Unigene51634_All//gi|42565162|ref|NP_189089.3|//3.00E-20//TMS membrane family protein / tumour differentially expressed (TDE) family protein [Arabidopsis thaliana] >gi|17381270|gb|AAL36053.1| AT3g24470/MXP5_4 [Arabidopsis thaliana] >gi|37201996|gb|AAQ89613.1| At3g24470/MXP5_4 [Arabidopsis thaliana]	Unigene51634_All//2.00E-21//AT3G24460| TMS membrane family protein / tumour differentially expressed (TDE) family protein					nr -
Unigene51635_All	398	0.92	0.64	0.54	4.01	3.20	5.22	3.08	0.42	2.00	-5.32E-01	6.27E-01		-7.82E-01	5.53E-01		-3.23E-01	5.52E-01		3.82E-01	4.38E-01		-2.87E+00	2.54E-05	Down	-6.22E-01	2.39E-01		Unigene51635_All//gi|15238599|ref|NP_200813.1|//7.00E-42//PRL1-interacting factor-related [Arabidopsis thaliana]	Unigene51635_All//4.00E-43//AT5G60050| PRL1-interacting factor-related	Unigene51635_All//0.00E+00//ES799193				nr +
Unigene51637_All	330	55.97	125.29	95.20	24.15	33.18	25.46	55.35	39.90	18.47	1.16E+00	2.43E-38	Up	7.66E-01	1.92E-14		4.58E-01	6.01E-03		7.58E-02	7.38E-01		-4.72E-01	4.15E-05		-1.58E+00	1.41E-34	Down	Unigene51637_All//gi|166203457|gb|ABD94681.1|//4.00E-14//universal stress protein 1 [Gossypium arboreum] >gi|169248110|gb|ACA51838.1| universal stress protein 1 [Gossypium arboreum]	Unigene51637_All//1.00E-07//AT3G03270| universal stress protein (USP) family protein / early nodulin ENOD18 family protein	Unigene51637_All//0.00E+00//gi|120538827|gb|EE298190.1|EE298190				nr +
Unigene51642_All	526	2.88	3.76	2.02	5.49	4.06	1.97	7.56	4.05	3.48	3.81E-01	4.03E-01		-5.11E-01	3.80E-01		-4.37E-01	2.44E-01		-1.48E+00	9.26E-05	Down	-8.99E-01	1.01E-03		-1.12E+00	3.65E-05	Down	Unigene51642_All//gi|186511674|ref|NP_192917.2|//4.00E-43//hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana]	Unigene51642_All//2.00E-44//AT4G11800| hydrolase/ protein serine/threonine phosphatase	Unigene51642_All//4.00E-159//gi|84168201|gb|DR456849.1|DR456849				nr +
Unigene51643_All	1221	0.81	0.87	0.87	0.41	0.06	0.37	10.94	4.28	13.41	9.81E-02	8.80E-01		9.93E-02	8.79E-01		-2.85E+00	1.78E-02		-1.41E-01	8.92E-01		-1.35E+00	8.99E-20	Down	2.93E-01	1.65E-02		Unigene51643_All//gi|224126779|ref|XP_002329471.1|//1.00E-127//mtn21-like protein [Populus trichocarpa] >gi|222870151|gb|EEF07282.1| mtn21-like protein [Populus trichocarpa]	Unigene51643_All//3.00E-109//AT5G64700| nodulin MtN21 family protein	Unigene51643_All//1.00E-167//DW518494				nr +
Unigene51649_All	261	6.01	2.72	6.12	5.34	1.72	0.69	0.65	0.00	0.00	-1.15E+00	3.18E-02		2.54E-02	9.81E-01		-1.64E+00	3.03E-03		-2.95E+00	2.40E-05	Down	-9.34E+00	1.34E-01		-9.34E+00	1.08E-01				Unigene51649_All//1.00E-18//gi|78342767|gb|DT563041.1|DT563041				
Unigene51650_All	530	0.59	7.27	10.25	24.34	35.80	37.15	1.20	1.50	0.75	3.62E+00	2.80E-15	Up	4.11E+00	8.17E-23	Up	5.56E-01	2.58E-06		6.10E-01	4.69E-07		3.24E-01	6.33E-01		-6.71E-01	3.86E-01		Unigene51650_All//gi|211906484|gb|ACJ11735.1|//4.00E-23//granule bound starch synthase [Gossypium hirsutum]	Unigene51650_All//1.00E-19//AT1G32900| starch synthase, putative	Unigene51650_All//0.00E+00//gi|13349651|gb|BG440001.1|BG440001				nr +
Unigene51652_All	1346	0.00	0.00	0.00	0.00	0.00	0.00	41.34	12.95	20.24	null	null		null	null		null	null		null	null		-1.67E+00	4.69E-109	Down	-1.03E+00	2.10E-53	Down	Unigene51652_All//gi|297810811|ref|XP_002873289.1|//2.00E-79//sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319126|gb|EFH49548.1| sulfotransferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51652_All//7.00E-78//AT5G07010| ST2A (SULFOTRANSFERASE 2A); hydroxyjasmonate sulfotransferase/ sulfotransferase	Unigene51652_All//8.00E-172//TC148002		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism		nr -
Unigene51654_All	606	0.00	2.34	1.14	2.38	1.14	1.49	1.81	1.45	0.66	1.12E+01	4.06E-08	Up	1.02E+01	6.15E-04	Up	-1.07E+00	4.31E-02		-6.78E-01	2.32E-01		-3.25E-01	6.15E-01		-1.46E+00	1.18E-02		Unigene51654_All//gi|225432842|ref|XP_002279912.1|//1.00E-19//PREDICTED: similar to polyprotein [Vitis vinifera]						nr +
Unigene51655_All	433	7.49	5.50	12.67	18.06	22.11	42.14	5.86	3.19	5.80	-4.46E-01	2.05E-01		7.58E-01	4.17E-03		2.92E-01	1.37E-01		1.22E+00	7.04E-20	Up	-8.79E-01	1.32E-02		-1.54E-02	9.71E-01				Unigene51655_All//1.00E-146//gi|13353146|gb|BG443494.1|BG443494				
Unigene51658_All	409	1.28	0.74	2.21	9.50	6.74	4.75	4.24	1.43	1.27	-7.83E-01	4.22E-01		7.91E-01	3.04E-01		-4.96E-01	1.05E-01		-1.00E+00	1.13E-03		-1.57E+00	7.85E-04	Down	-1.74E+00	1.65E-04	Down	Unigene51658_All//gi|44681324|gb|AAS47602.1|//4.00E-26//At5g40980 [Arabidopsis thaliana] >gi|45773828|gb|AAS76718.1| At5g40980 [Arabidopsis thaliana]	Unigene51658_All//2.00E-27//AT5G40980| unknown protein	Unigene51658_All//4.00E-23//DW502398				nr -
Unigene5166_All	682	12.04	9.29	5.47	32.21	27.37	24.24	28.52	29.91	28.51	-3.75E-01	6.92E-02		-1.14E+00	1.24E-07	Down	-2.35E-01	4.77E-02		-4.10E-01	3.58E-04		6.86E-02	6.33E-01		-6.00E-04	9.95E-01		Unigene5166_All//gi|48958469|gb|AAT47787.1|//1.00E-29//At1g09645 [Arabidopsis thaliana] >gi|50897232|gb|AAT85755.1| At1g09645 [Arabidopsis thaliana]	Unigene5166_All//2.00E-13//AT1G09645| unknown protein	Unigene5166_All//0.00E+00//gi|109890412|gb|DW519376.1|DW519376				nr -
Unigene51664_All	594	5.99	1.02	3.32	8.39	4.87	0.84	0.14	0.00	0.27	-2.55E+00	2.26E-10	Down	-8.53E-01	1.27E-02		-7.84E-01	1.78E-03		-3.33E+00	5.36E-20	Down	-7.15E+00	4.03E-01		9.14E-01	6.24E-01		Unigene51664_All//gi|34015078|gb|AAQ56281.1|//4.00E-36//ethylene receptor [Litchi chinensis]	Unigene51664_All//5.00E-21//AT1G05420| OFP12 (OVATE FAMILY PROTEIN 12)	Unigene51664_All//0.00E+00//ES794718				nr +
Unigene51673_All	436	2.28	0.23	3.30	9.71	14.77	11.91	1.45	2.97	2.01	-3.29E+00	3.81E-04	Down	5.32E-01	3.71E-01		6.05E-01	7.18E-03		2.95E-01	3.12E-01		1.03E+00	5.33E-02		4.67E-01	4.76E-01				Unigene51673_All//5.00E-07//gi|78338262|gb|DT558536.1|DT558536				
Unigene51674_All	1792	0.00	0.54	0.18	5.06	0.27	0.20	8.09	23.74	567.83	9.07E+00	1.38E-05	Up	7.48E+00	4.51E-02		-4.23E+00	1.13E-51	Down	-4.65E+00	1.79E-46	Down	1.55E+00	7.74E-75	Up	6.13E+00	0.00E+00	Up	Unigene51674_All//gi|209954729|dbj|BAG80555.1|//1.00E-156//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene51674_All//5.00E-140//AT2G36790| UGT73C6 (UDP-glucosyl transferase 73C6); UDP-glucosyltransferase/ UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene51674_All//3.00E-58//DR463295		ko00908|Zeatin biosynthesis		nr +
Unigene51675_All	602	1.74	14.73	2.03	3.23	4.06	14.78	0.14	1.67	0.79	3.08E+00	5.10E-30	Up	2.27E-01	7.03E-01		3.32E-01	4.65E-01		2.20E+00	3.79E-22	Up	3.57E+00	3.07E-05	Up	2.50E+00	2.51E-02		Unigene51675_All//gi|75180217|sp|Q9LQ14.1|Y148T_ARATH//3.00E-49//RecName: Full=Uncharacterized protein At1g14870 >gi|87782226|gb|AAF79235.1|AC006917_20 F10B6.27 [Arabidopsis thaliana]	Unigene51675_All//1.00E-50//AT1G14870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: plasma membrane; EXPRESSED IN: callus; CONTAINS InterPro DOMAIN/s: EGF-type aspartate/asparagine hydroxylation conserved site (InterPro:IPR000152), Protein of unknown function Cys-rich (InterPro:IPR006461); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35525.1); Has 492 Blast hits to 491 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 93; Fungi - 76; Plants - 297; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink).	Unigene51675_All//0.00E+00//TC151395				nr +
Unigene51676_All	976	1.07	0.93	0.49	3.52	5.29	3.05	2.90	0.73	1.18	-1.98E-01	7.41E-01		-1.13E+00	1.17E-01		5.88E-01	2.32E-02		-2.06E-01	6.05E-01		-2.00E+00	9.64E-08	Down	-1.29E+00	1.00E-04	Down	Unigene51676_All//gi|27311577|gb|AA000754.1|//1.00E-119//Unknown protein [Arabidopsis thaliana]	Unigene51676_All//8.00E-121//AT1G38131| unknown protein	Unigene51676_All//0.00E+00//gi|78329137|gb|DT549411.1|DT549411				nr +
Unigene51677_All	419	4.25	10.16	4.19	6.90	6.57	6.36	4.34	2.00	3.33	1.26E+00	3.70E-05	Up	-1.77E-02	9.95E-01		-6.87E-02	8.51E-01		-1.17E-01	7.58E-01		-1.12E+00	1.02E-02		-3.83E-01	3.72E-01				Unigene51677_All//1.00E-66//TC166342				
Unigene5168_All	764	3.49	7.83	4.81	3.85	4.60	3.19	6.97	6.73	5.79	1.16E+00	3.25E-06	Up	4.62E-01	1.75E-01		2.57E-01	5.05E-01		-2.69E-01	5.02E-01		-5.14E-02	8.44E-01		-2.69E-01	2.56E-01				Unigene5168_All//0.00E+00//ES800699				ESTscan +
Unigene51680_All	1398	0.00	0.00	0.00	0.00	0.00	0.00	35.23	8.76	52.69	null	null		null	null		null	null		null	null		-2.01E+00	9.63E-124	Down	5.81E-01	1.40E-26		Unigene51680_All//gi|224071491|ref|XP_002303486.1|//1.00E-120//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222840918|gb|EEE78465.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene51680_All//1.00E-102//AT4G23340| oxidoreductase, 2OG-Fe(II) oxygenase family protein			ko00904|Diterpenoid biosynthesis		nr +
Unigene51681_All	335	7.97	4.99	8.27	4.31	1.13	0.27	0.38	0.00	0.00	-6.74E-01	7.88E-02		5.34E-02	8.95E-01		-1.93E+00	5.06E-04	Down	-4.00E+00	5.84E-07	Down	-8.56E+00	2.35E-01		-8.56E+00	1.99E-01									
Unigene51685_All	608	0.34	0.33	0.96	1.23	3.91	1.86	0.07	0.00	0.26	-4.60E-02	9.88E-01		1.48E+00	1.53E-01		1.67E+00	8.61E-05	Up	5.96E-01	3.98E-01		-6.12E+00	6.56E-01		1.92E+00	3.77E-01		Unigene51685_All//gi|2921336|gb|AAC04718.1|//1.00E-46//MYB-like DNA-binding domain protein [Gossypium hirsutum]	Unigene51685_All//3.00E-21//AT5G49330| AtMYB111 (myb domain protein 111); DNA binding / transcription factor	Unigene51685_All//9.00E-28//NP385922	MYB			nr -
Unigene51687_All	515	21.03	44.96	27.81	10.74	11.43	12.10	21.26	24.59	12.45	1.10E+00	6.76E-20	Up	4.03E-01	9.61E-03		9.08E-02	7.84E-01		1.73E-01	5.41E-01		2.10E-01	1.76E-01		-7.72E-01	3.04E-07		Unigene51687_All//gi|295913708|gb|ADG58095.1|//2.00E-16//transcription factor [Lycoris longituba]	Unigene51687_All//1.00E-10//AT1G20696| HMGB3 (HIGH MOBILITY GROUP B 3); DNA binding / chromatin binding / structural constituent of chromatin / transcription factor	Unigene51687_All//0.00E+00//ES830500		ko03410|Base excision repair		nr +
Unigene51689_All	753	9.59	1.75	7.71	5.82	4.80	8.52	9.66	23.98	7.99	-2.45E+00	1.50E-19	Down	-3.15E-01	1.85E-01		-2.78E-01	3.74E-01		5.49E-01	1.93E-02		1.31E+00	3.64E-25	Up	-2.74E-01	1.66E-01		Unigene51689_All//gi|78059502|gb|AB118115.1|//3.00E-34//RPN9 [Nicotiana benthamiana]	Unigene51689_All//9.00E-33//AT5G45620| 26S proteasome regulatory subunit, putative (RPN9)	Unigene51689_All//0.00E+00//gi|48800504|gb|CO101818.1|CO101818		ko03050|Proteasome		nr -
Unigene5169_All	749	24.03	22.80	25.81	42.90	35.03	36.96	22.02	17.30	9.47	-7.59E-02	5.99E-01		1.03E-01	4.87E-01		-2.92E-01	1.28E-03		-2.15E-01	3.12E-02		-3.48E-01	5.08E-03		-1.22E+00	2.80E-21	Down	Unigene5169_All//gi|115439979|ref|NP_001044269.1|//4.00E-60//Os01g0752800 [Oryza sativa Japonica Group] >gi|113533800|dbj|BAF06183.1| Os01g0752800 [Oryza sativa Japonica Group]	Unigene5169_All//4.00E-25//AT5G46020| unknown protein	Unigene5169_All//1.00E-113//EX168176		ko03022|Basal transcription factors		nr +
Unigene51690_All	1657	0.00	0.24	0.26	0.63	0.23	0.60	5.03	9.94	22.74	7.93E+00	1.36E-02		8.01E+00	1.38E-02		-1.47E+00	2.48E-02		-7.43E-02	9.22E-01		9.83E-01	8.32E-15		2.18E+00	5.72E-107	Up	Unigene51690_All//gi|224140467|ref|XP_002322604.1|//1.00E-125//GRAS family transcription factor [Populus trichocarpa] >gi|222868234|gb|EEF05365.1| GRAS family transcription factor [Populus trichocarpa]	Unigene51690_All//1.00E-16//AT5G66770| scarecrow transcription factor family protein		GRAS			nr -
Unigene51692_All	309	4.40	4.76	2.41	9.51	4.23	5.99	2.19	0.81	2.32	1.11E-01	8.31E-01		-8.68E-01	1.47E-01		-1.17E+00	6.71E-04	Down	-6.67E-01	7.10E-02		-1.43E+00	7.83E-02		8.41E-02	9.24E-01		Unigene51692_All//gi|226503071|ref|NP_001148359.1|//3.00E-26//AP-1 complex subunit sigma-2 [Zea mays] >gi|195618494|gb|ACG31077.1| AP-1 complex subunit sigma-2 [Zea mays]	Unigene51692_All//2.00E-27//AT4G35410| clathrin adaptor complex small chain family protein	Unigene51692_All//1.00E-120//gi|109866960|gb|DW495936.1|DW495936		ko04144|Endocytosis		nr -

Unigene51696_All	367	7.13	3.18	1.45	10.99	4.69	6.52	0.46	0.00	0.33	-1.17E+00	3.32E-03		-2.30E+00	1.28E-06	Down	-1.23E+00	1.71E-05	Down	-7.53E-01	1.24E-02		-8.85E+00	1.34E-01		-5.01E-01	7.46E-01		Unigene51696_All//gi|115452547|ref|NP_001049874.1|//8.00E-09//0s03g0303100 [Oryza sativa Japonica Group] >gi|108707708|gb|ABF95503.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548345|dbj|BAF11788.1| Os03g0303100 [Oryza sativa Japonica Group]		Unigene51696_All//2.00E-70//CO117875			nr +
Unigene51698_All	2873	0.00	0.00	0.11	0.35	0.00	0.00	7.73	12.87	21.53	null	null		6.80E+00	4.51E-02		-8.44E+00	2.21E-07	Down	-8.44E+00	2.97E-06	Down	7.37E-01	4.81E-20		1.48E+00	3.88E-103	Up	Unigene51698_All//gi|124302212|gb|ABN05291.1|//1.00E-177//ARK3 protein [Arabidopsis thaliana]	Unigene51698_All//6.00E-161//AT4G21380| ARK3 (A. THALIANA RECEPTOR KINASE 3); kinase/ transmembrane receptor protein serine/threonine kinase	Unigene51698_All//6.00E-91//gi|31073610|gb|CA993889.1|CA993889		ko04626|Plant-pathogen interaction		nr +
Unigene51699_All	386	16.54	33.34	19.45	21.94	29.97	25.27	45.79	88.90	39.43	1.01E+00	4.26E-10	Up	2.34E-01	3.30E-01		4.50E-01	5.33E-03		2.04E-01	3.35E-01		9.57E-01	1.08E-28		-2.16E-01	7.37E-02					Unigene51699_All//1.00E-87//TC134113				
Unigene51701_All	1740	0.09	0.23	0.18	0.09	0.32	0.10	0.95	6.80	4.79	1.37E+00	2.74E-01		1.03E+00	4.71E-01		1.88E+00	9.41E-02		2.73E-01	9.04E-01		2.84E+00	3.65E-45	Up	2.34E+00	2.47E-26	Up	Unigene51701_All//gi|297820040|ref|XP_002877903.1|//1.00E-175//UDP-glucosyl transferase 73D1 [Arabidopsis lyrata subsp. lyrata] >gi|297323741|gb|EFH54162.1| UDP-glucosyl transferase 73D1 [Arabidopsis lyrata subsp. lyrata]	Unigene51701_All//3.00E-170//AT3G53150| UGT73D1 (UDP-glucosyl transferase 73D1); UDP-glycosyltransferase/ transferase, transferring hexosyl groups	Unigene51701_All//2.00E-09//CO091033		ko00908|Zeatin biosynthesis		nr -
Unigene51703_All	396	0.53	6.14	0.67	2.26	1.39	1.82	2.24	1.16	1.51	3.54E+00	1.12E-09	Up	3.47E-01	7.97E-01		-7.03E-01	3.24E-01		-3.11E-01	6.88E-01		-9.50E-01	1.55E-01		-5.71E-01	3.71E-01					Unigene51703_All//5.00E-19//DR461672				
Unigene51704_All	331	4.58	5.82	3.38	1.81	5.62	3.27	5.62	2.78	5.18	3.44E-01	4.67E-01		-4.40E-01	4.23E-01		1.64E+00	8.82E-04	Up	8.59E-01	2.17E-01		-1.02E+00	1.76E-02		-1.19E-01	7.70E-01					Unigene51704_All//6.00E-43//BQ407450				
Unigene51706_All	674	1.01	0.45	1.26	0.52	2.61	1.27	6.77	1.36	4.43	-1.16E+00	1.89E-01		3.25E-01	6.46E-01		2.33E+00	2.58E-05	Up	1.30E+00	1.07E-01		-2.31E+00	2.50E-14	Down	-6.12E-01	1.20E-02		Unigene51706_All//gi|257831433|gb|ACV71017.1|//8.00E-25//TPA17 [Capsicum annuum]	Unigene51706_All//3.00E-19//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene51706_All//0.00E+00//gi|78349474|gb|DT569748.1|DT569748	GRF			nr +
Unigene51707_All	686	2.21	0.44	3.34	4.65	5.67	2.11	0.31	0.00	0.06	-2.32E+00	2.07E-04	Down	5.94E-01	1.81E-01		2.88E-01	4.12E-01		-1.14E+00	1.01E-03		-8.27E+00	7.43E-02		-2.41E+00	1.95E-01		Unigene51707_All//gi|124359339|gb|ABD28498.2|//1.00E-16//Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene51707_All//8.00E-06//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene51707_All//2.00E-10//TC174169				nr +
Unigene51708_All	924	0.00	0.00	0.00	0.00	0.00	0.00	4.03	1.31	1.42	null	null		null	null		null	null		null	null		-1.62E+00	1.18E-07	Down	-1.50E+00	3.29E-07	Down	Unigene51708_All//gi|108864366|gb|ABA93633.2|//4.00E-63//Protein kinase domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene51708_All//5.00E-27//AT1G70520| protein kinase family protein					nr +
Unigene51709_All	298	1.93	2.72	2.14	18.39	10.63	3.18	11.78	4.49	4.14	4.94E-01	5.26E-01		1.51E-01	8.55E-01		-7.91E-01	8.48E-04		-2.53E+00	1.11E-16	Down	-1.39E+00	5.60E-06	Down	-1.51E+00	6.97E-07	Down				Unigene51709_All//1.00E-117//TC166394				
Unigene5171_All	860	2.68	7.36	4.33	4.29	3.32	4.83	1.97	2.14	8.71	1.46E+00	6.33E-09	Up	6.95E-01	3.67E-02		-3.67E-01	2.74E-01		1.73E-01	6.41E-01		1.21E-01	7.84E-01		2.15E+00	1.65E-21	Up	Unigene5171_All//gi|15224138|ref|NP_179417.1|//2.00E-64//ATCOAD (4-phosphopantetheine adenylyltransferase); nucleotidyltransferase/ pantetheine-phosphate adenylyltransferase [Arabidopsis thaliana] >gi|75267775|sp|Q9ZPV8.1|COAD_ARATH RecName: Full=Phosphopantetheine adenylyltransferase; AltName: Full=Pantetheine-phosphate adenylyltransferase; AltName: Full=Dephospho-CoA pyrophosphorylase; Short=AtCoaD >gi|34365611|gb|AAQ65117.1| At2g18250 [Arabidopsis thaliana]	Unigene5171_All//1.00E-65//AT2G18250| ATCOAD (4-phosphopantetheine adenylyltransferase); nucleotidyltransferase/ pantetheine-phosphate adenylyltransferase	Unigene5171_All//0.00E+00//TC133452				nr +
Unigene51710_All	303	327.05	76.09	169.77	51.62	61.82	83.02	0.00	0.00	0.26	-2.10E+00	4.90E-216	Down	-9.46E-01	3.41E-63		2.60E-01	4.61E-02		6.86E-01	1.04E-10		null	null		8.04E+00	4.03E-01		Unigene51710_All//gi|297830242|ref|XP_002883003.1|//7.00E-26//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328843|gb|EFH59262.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51710_All//8.00E-27//AT3G16370| GDSL-motif lipase/hydrolase family protein	Unigene51710_All//3.00E-146//TC166759				nr -
Unigene51711_All	619	0.34	0.49	1.46	2.01	1.45	1.46	1.71	2.43	4.18	5.39E-01	6.71E-01		2.11E+00	1.42E-02		-4.76E-01	4.39E-01		-4.63E-01	4.78E-01		5.10E-01	3.12E-01		1.29E+00	2.41E-04	Up								
Unigene51712_All	1074	166.66	270.10	201.30	14.52	13.27	10.05	0.59	2.18	0.74	6.97E-01	2.70E-112		2.73E-01	6.82E-15		-1.29E-01	4.36E-01		-5.31E-01	1.19E-04		1.88E+00	4.35E-06	Up	3.29E-01	6.33E-01		Unigene51712_All//gi|218156192|dbj|BAH03328.1|//5.00E-39//chloroplast protein 12 [Fagus crenata]	Unigene51712_All//2.00E-34//AT3G62410| CP12-2; protein binding	Unigene51712_All//0.00E+00//gi|194346543|gb|FK817148.1|FK817148				nr +
Unigene51715_All	612	0.85	3.64	1.04	1.22	1.13	2.29	1.45	1.30	1.24	2.09E+00	1.86E-05	Up	2.88E-01	7.25E-01		-1.18E-01	8.62E-01		9.06E-01	1.23E-01		-1.61E-01	8.03E-01		-2.30E-01	7.05E-01									
Unigene51718_All	1831	0.00	0.00	0.00	0.00	0.00	0.05	30.87	34.67	12.90	null	null		null	null		null	null		5.62E+00	4.75E-01		1.68E-01	6.49E-03		-1.26E+00	1.46E-74	Down	Unigene51718_All//gi|2252851|gb|AAB62849.1|//1.00E-143//A_TM018A10.3 gene product [Arabidopsis thaliana] >gi|7267430|emb|CAB80900.1| AT4g00910 [Arabidopsis thaliana]	Unigene51718_All//6.00E-139//AT4G00910| unknown protein					nr +
Unigene51719_All	322	0.16	1.26	2.65	7.74	10.05	5.19	2.10	1.56	0.87	2.95E+00	5.91E-02		4.03E+00	7.02E-04	Up	3.78E-01	3.06E-01		-5.76E-01	1.65E-01		-4.32E-01	6.12E-01		-1.28E+00	9.48E-02									
Unigene5172_All	886	2.07	1.32	2.70	5.34	3.19	2.14	1.96	1.65	2.29	-6.52E-01	1.74E-01		3.88E-01	3.90E-01		-7.45E-01	4.11E-03		-1.32E+00	2.52E-06	Down	-2.45E-01	6.31E-01		2.29E-01	6.01E-01		Unigene5172_All//gi|227121298|gb|ACP19339.1|//1.00E-136//phosphate transporter [Glycine max]	Unigene5172_All//8.00E-117//AT3G54700| carbohydrate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter	Unigene5172_All//1.00E-37//gi|78339058|gb|DT559332.1|DT559332				nr +
Unigene51720_All	466	0.34	0.22	0.46	2.89	3.62	3.59	4.26	1.52	4.10	-6.31E-01	7.27E-01		4.41E-01	7.75E-01		3.27E-01	5.68E-01		3.13E-01	5.94E-01		-1.48E+00	5.15E-04	Down	-5.54E-02	9.02E-01		Unigene51720_All//gi|1335862|gb|AAC49294.1|//1.00E-22//clathrin heavy chain [Glycine max]	Unigene51720_All//2.00E-22//AT3G08530| clathrin heavy chain, putative	Unigene51720_All//7.00E-65//TC137329		ko04144|Endocytosis		nr +
Unigene51722_All	382	1.37	1.86	1.53	2.48	4.15	5.32	2.77	0.44	0.21	4.39E-01	6.16E-01		1.63E-01	8.50E-01		7.43E-01	1.67E-01		1.10E+00	1.69E-02		-2.66E+00	2.25E-04	Down	-3.73E+00	6.13E-06	Down	Unigene51722_All//gi|15236687|ref|NP_194942.1|//1.00E-21//ATVAMP711 (ARABIDOPSIS THALIANA VESICLE-ASSOCIATED MEMBRANE PROTEIN 711) [Arabidopsis thaliana] >gi|27805754|sp|Q49377.2|VA711_ARATH RecName: Full=Vesicle-associated membrane protein 711; Short=AtVAMP711; AltName: Full=v-SNARE synaptobrevin 7C; Short=AtVAMP7C >gi|16612292|gb|AAL27509.1|AF439840_1 AT4g32150/F10N7_40 [Arabidopsis thaliana] >gi|3858935|emb|CAA16574.1| synaptobrevin-like protein [Arabidopsis thaliana] >gi|4103357|gb|AAD01748.1| vesicle-associated membrane protein 7C [Arabidopsis thaliana] >gi|7270119|emb|CAB79933.1| synaptobrevin-like protein [Arabidopsis thaliana] >gi|21593706|gb|AAM65673.1| synaptobrevin-like protein [Arabidopsis thaliana] >gi|21928069|gb|AAM78063.1| AT4g32150/F10N7_40 [Arabidopsis thaliana] >gi|110740910|dbj|BAE98551.1|	Unigene51722_All//7.00E-23//AT4G32150| ATVAMP711 (ARABIDOPSIS THALIANA VESICLE-ASSOCIATED MEMBRANE PROTEIN 711)	Unigene51722_All//0.00E+00//gi|21092396|gb|BQ404709.1|BQ404709		ko04130|SNARE interactions in vesicular transport		nr -
Unigene51725_All	319	49.53	28.75	40.73	108.06	84.95	78.58	58.05	67.21	24.35	-7.85E-01	2.86E-08		-2.82E-01	6.40E-02		-3.47E-01	4.69E-05		-4.60E-01	2.06E-07		2.11E-01	6.11E-02		-1.25E+00	7.35E-25	Down	Unigene51725_All//gi|75099212|sp|Q64818.1|Y2309_ARATH//2.00E-15//RecName: Full=Uncharacterized protein At2g23090 >gi|3169182|gb|AAC17825.1| Expressed protein [Arabidopsis thaliana] >gi|15450484|gb|AAK96535.1| At2g23090/F21P24.15 [Arabidopsis thaliana] >gi|15912199|gb|AAL08233.1| At2g23090/F21P24.15 [Arabidopsis thaliana] >gi|23505759|gb|AAN28739.1| At2g23090/F21P24.15 [Arabidopsis thaliana]	Unigene51725_All//1.00E-16//AT2G23090| unknown protein	Unigene51725_All//4.00E-130//gi|13244719|gb|BE053605.2|BE053605				nr +
Unigene51726_All	264	4.16	3.07	0.81	7.74	10.57	5.99	12.49	2.06	1.96	-4.39E-01	4.95E-01		-2.37E+00	2.96E-03		4.50E-01	2.64E-01		-3.70E-01	4.55E-01		-2.60E+00	5.62E-12	Down	-2.67E+00	9.34E-13	Down								
Unigene51728_All	554	0.00	0.27	0.00	8.81	5.03	5.54	2.59	8.75	1.65	8.10E+00	2.35E-01		null	null		-8.08E-01	1.45E-03		-6.69E-01	1.34E-02		1.75E+00	8.43E-11	Up	-6.50E-01	1.74E-01		Unigene51728_All//gi|255567331|ref|XP_002524645.1|//2.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223536006|gb|EEF37664.1| conserved hypothetical protein [Ricinus communis]		Unigene51728_All//6.00E-180//gi|109838379|gb|DW236940.1|DW236940				nr -
Unigene51729_All	431	0.85	0.71	5.31	5.20	0.96	1.99	0.98	0.10	0.18	-2.69E-01	8.01E-01		2.64E+00	8.29E-07	Up	-2.44E+00	8.82E-08	Down	-1.39E+00	1.45E-03		-3.34E+00	1.80E-02		-2.41E+00	3.93E-02					Unigene51729_All//9.00E-166//TC150941				
Unigene51731_All	542	1.45	2.90	0.10	1.38	2.16	2.17	2.89	1.93	0.81	1.00E+00	5.98E-02		-3.88E+00	1.60E-03		6.48E-01	3.26E-01		6.52E-01	3.31E-01		-5.82E-01	2.33E-01		-1.84E+00	2.17E-04	Down				Unigene51731_All//6.00E-07//TC152941				
Unigene51732_All	400	1.70	0.38	2.26	4.98	6.54	4.97	7.82	3.13	4.68	-2.16E+00	2.84E-02		4.12E-01	5.94E-01		3.93E-01	3.51E-01		-3.90E-03	9.87E-01		-1.32E+00	4.68E-05	Down	-7.41E-01	1.41E-02		Unigene51732_All//gi|1335862|gb|AAC49294.1|//5.00E-35//clathrin heavy chain [Glycine max]	Unigene51732_All//3.00E-53//AT3G11130| clathrin heavy chain, putative	Unigene51732_All//5.00E-118//TC139935		ko04144|Endocytosis		nr -
Unigene51733_All	284	3.32	2.14	5.06	3.33	1.33	0.95	1.94	0.59	0.00	-6.31E-01	3.66E-01		6.10E-01	2.96E-01		-1.32E+00	5.61E-02		-1.80E+00	1.83E-02		-1.72E+00	7.23E-02		-1.09E+01	2.80E-04	Down				Unigene51733_All//3.00E-07//gi|48753795|gb|CO084314.1|CO084314				
Unigene51734_All	2038	0.21	0.05	0.00	0.17	0.20	0.35	9.21	4.16	5.88	-2.05E+00	1.20E-01		-7.68E+00	1.56E-02		2.45E-01	8.52E-01		1.05E+00	2.35E-01		-1.15E+00	2.63E-21	Down	-6.47E-01	7.10E-09		Unigene51734_All//gi|226504754|ref|NP_001147991.1|//1.00E-123//receptor kinase [Zea mays] >gi|195615010|gb|ACG29335.1| receptor kinase [Zea mays]	Unigene51734_All//1.00E-72//AT5G16590| LRR1; ATP binding / kinase/ protein serine/threonine kinase					nr +

Unigene51737_All	796	0.13	0.64	0.00	3.44	1.04	0.51	3.03	4.52	4.60	2.28E+00	6.23E-02			-7.04E+00	3.92E-01		-1.73E+00	3.57E-06	Down	-2.75E+00	2.31E-09	Down	5.77E-01	4.85E-02		6.05E-01	2.96E-02		Unigene51737_All//gi|18411317|ref|NP_565146.1|//3.00E-84//ACR3; amino acid binding [Arabidopsis thaliana] >gi|30699222|ref|NP_849896.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|30699224|ref|NP_849897.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|79321337|ref|NP_001031289.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|186985930|ref|NP_001117608.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|2829923|gb|AAC00631.1| Similar to uridylyl transferases [Arabidopsis thaliana] >gi|22138096|gb|AAM93428.1| ACR3 [Arabidopsis thaliana] >gi|2224241464|dbj|BAH20041.1| AT1G76990 [Arabidopsis thaliana]	Unigene51737_All//6.00E-86//AT1G76990| ACR3; amino acid binding	Unigene51737_All//0.00E+00//gi|78336965|gb|DT557239.1|DT557239				nr +
Unigene51738_All	210	5.48	3.14	6.09	16.84	12.46	16.13	78.32	24.88	23.52	-8.05E-01	2.05E-01			1.51E-01	7.90E-01		-4.35E-01	1.90E-01		-6.23E-02	8.66E-01		-1.65E+00	3.29E-32	Down	-1.74E+00	1.78E-35	Down			Unigene51738_All//1.00E-33//gi|48810924|gb|CO112237.1|CO112237				
Unigene5174_All	957	1.04	1.16	1.22	1.46	2.55	0.66	2.65	0.26	1.29	1.65E-01	7.79E-01			2.37E-01	6.97E-01		8.10E-01	4.51E-02		-1.14E+00	4.67E-02		-3.34E+00	8.28E-12	Down	-1.04E+00	2.62E-03		Unigene5174_All//gi|150416421|gb|AB868793.1|//3.00E-86//MYC2 [Citrus sinensis]	Unigene5174_All//2.00E-43//AT4G00480| myc-related transcription factor (MYC1)		bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene51740_All	681	0.23	1.12	1.33	3.07	5.82	10.61	2.17	7.12	7.20	2.28E+00	1.60E-02			2.53E+00	5.63E-03		9.21E-01	1.95E-03		1.79E+00	5.97E-14	Up	1.71E+00	1.81E-10	Up	1.73E+00	5.75E-11	Up	Unigene51740_All//gi|30685162|ref|NP_188532.2|//6.00E-06//leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] >gi|75335059|sp|Q9LJ64.1|PLRX1_ARATH RecName: Full=Pollen-specific leucine-rich repeat extensin-like protein 1; Short=Pollen-specific LRR/EXTENSIN1; Short=AtPEX1; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|9280319|dbj|BAB01698.1| extensin protein-like [Arabidopsis thaliana]						nr +
Unigene51741_All	707	0.52	0.14	0.15	0.63	0.68	1.15	1.55	0.06	1.86	-1.85E+00	1.87E-01			-1.78E+00	2.34E-01		1.05E-01	9.54E-01		8.59E-01	3.07E-01		-4.72E+00	1.02E-06	Down	2.58E-01	6.23E-01		Unigene51741_All//gi|30684540|ref|NP_193617.2|//4.00E-25//ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene51741_All//1.00E-24//AT4G18820| ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding	Unigene51741_All//9.00E-13//ES816108				nr +
Unigene51742_All	213	27.51	3.09	22.50	42.10	44.94	36.26	68.09	19.03	19.08	-3.15E+00	1.20E-20	Down	-2.90E-01	2.81E-01		9.44E-02	6.80E-01		-2.15E-01	3.24E-01		-1.84E+00	6.68E-33	Down	-1.84E+00	7.39E-34	Down			Unigene51742_All//2.00E-103//gi|18101568|gb|BM360822.1|BM360822				
Unigene51743_All	499	1.26	0.00	0.00	6.99	3.52	2.08	1.19	1.17	1.04	-1.03E+01	7.91E-04	Down	-1.03E+01	1.41E-03		-9.90E-01	1.35E-03		-1.75E+00	5.79E-07	Down	-1.66E-02	1.02E+00		-1.93E-01	7.94E-01				Unigene51743_All//2.00E-37//TC136748				
Unigene51747_All	389	1.61	0.78	0.27	6.15	4.87	2.21	2.17	0.11	0.92	-1.05E+00	2.50E-01			-2.56E+00	2.72E-02		-3.36E-01	4.41E-01		-1.48E+00	4.58E-04	Down	-4.34E+00	4.55E-05	Down	-1.24E+00	6.26E-02		Unigene51747_All//gi|224138558|ref|XP_002322844.1|//2.00E-14//predicted protein [Populus trichocarpa] >gi|222867474|gb|EEF04605.1| predicted protein [Populus trichocarpa]		Unigene51747_All//5.00E-19//DR457837				nr +
Unigene51748_All	452	0.00	0.00	0.00	1.76	0.69	1.00	4.58	1.39	2.73	null	null			null	null		-1.36E+00	7.74E-02		-8.19E-01	3.19E-01		-1.72E+00	5.88E-05	Down	-7.46E-01	5.19E-02		Unigene51748_All//gi|28300303|gb|AA037646.1|//2.00E-27//NBS-LRR resistance protein RGH2 [Manihot esculenta]	Unigene51748_All//1.00E-06//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene51748_All//3.00E-95//TC165835		ko04626|Plant-pathogen interaction		nr +
Unigene51753_All	739	22.44	23.52	33.72	1.69	5.64	11.80	0.00	0.23	0.00	6.75E-02	6.35E-01			5.87E-01	1.67E-07		1.74E+00	1.61E-08	Up	2.81E+00	1.29E-28	Up	7.82E+00	1.39E-01		null	null		Unigene51753_All//gi|224130436|ref|XP_002328608.1|//4.00E-43//glutaredoxin [Populus trichocarpa] >gi|222838590|gb|EEE76955.1| glutaredoxin [Populus trichocarpa]	Unigene51753_All//3.00E-42//AT5G18600| glutaredoxin family protein	Unigene51753_All//7.00E-63//gi|164294546|gb|EX167792.1|EX167792				nr -
Unigene51755_All	260	1.41	5.26	1.84	1.15	0.66	0.35	5.04	2.57	1.38	1.90E+00	2.58E-03			3.88E-01	6.97E-01		-7.96E-01	5.57E-01		-1.73E+00	2.89E-01		-9.71E-01	6.64E-02		-1.87E+00	6.93E-04	Down			Unigene51755_All//4.00E-108//DW511226				
Unigene51756_All	2358	0.00	0.00	0.09	0.04	0.00	0.04	0.95	3.99	6.17	null	null			6.50E+00	1.41E-01		-5.40E+00	3.12E-01		-1.43E-01	9.49E-01		2.07E+00	4.55E-25	Up	2.70E+00	2.06E-53	Up	Unigene51756_All//gi|87162753|gb|ABD28548.1|//0.00E+00//Protein kinase; Type I EGF [Medicago truncatula]	Unigene51756_All//6.00E-152//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase					nr +
Unigene51760_All	389	66.85	146.80	34.91	56.99	90.65	87.08	234.23	213.60	385.89	1.13E+00	1.00E-50	Up	-9.37E-01	1.03E-16		6.70E-01	1.63E-15		6.12E-01	1.00E-11		-1.33E-01	9.72E-03		7.20E-01	1.41E-77		Unigene51760_All//gi|14596167|gb|AK68811.1|//9.00E-26//zinc finger-like protein [Arabidopsis thaliana] >gi|18377546|gb|AAL66939.1| zinc finger-like protein [Arabidopsis thaliana]	Unigene51760_All//1.00E-25//AT2G36320| zinc finger (AN1-like) family protein	Unigene51760_All//2.00E-178//gi|31072455|gb|CA992734.1|CA992734				nr -
Unigene51761_All	593	2.03	1.97	0.00	2.35	2.44	2.59	1.57	3.24	1.28	-4.62E-02	9.51E-01			-1.10E+01	1.36E-06	Down	5.23E-02	9.53E-01		1.39E-01	8.01E-01		1.05E+00	1.28E-02		-2.97E-01	6.31E-01		Unigene51761_All//gi|224136620|ref|XP_002326905.1|//6.00E-06//predicted protein [Populus trichocarpa] >gi|222835220|gb|EEE73655.1| predicted protein [Populus trichocarpa]	Unigene51761_All//1.00E-06//AT1G47560| unknown protein	Unigene51761_All//1.00E-42//DW008686				nr +
Unigene51762_All	465	3.49	1.09	4.24	2.14	1.26	2.23	2.46	0.63	0.17	-1.68E+00	2.36E-03			2.81E-01	5.79E-01		-7.67E-01	2.60E-01		6.03E-02	9.47E-01		-1.96E+00	1.69E-03		-3.84E+00	1.74E-06	Down							
Unigene51766_All	846	4.14	5.87	0.82	7.95	7.65	7.53	2.95	1.28	1.37	5.02E-01	6.52E-02			-2.34E+00	7.41E-09	Down	-5.49E-02	8.27E-01		-7.87E-02	7.54E-01		-1.20E+00	1.00E-03		-1.11E+00	1.54E-03		Unigene51766_All//gi|195604664|gb|ACG24162.1|//2.00E-56//small nuclear ribonucleoprotein Sm D1 [Zea mays]	Unigene51766_All//2.00E-46//AT4G02840| small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative	Unigene51766_All//0.00E+00//TC141454		ko03040|Spliceosome		nr +
Unigene51767_All	362	4.48	0.00	0.59	3.03	1.90	1.25	4.09	0.12	0.99	-1.21E+01	2.11E-09	Down	-2.93E+00	1.92E-05	Down	-6.70E-01	3.06E-01		-1.28E+00	5.68E-02		-5.15E+00	2.98E-09	Down	-2.05E+00	1.05E-04	Down							
Unigene51769_All	265	2.96	1.53	2.81	6.96	0.65	3.41	2.55	0.63	0.75	-9.53E-01	2.33E-01			-7.42E-02	9.35E-01		-3.42E+00	5.08E-09	Down	-1.03E+00	3.31E-02		-2.02E+00	1.98E-02		-1.76E+00	2.80E-02								
Unigene51771_All	224	4.91	2.26	5.47	16.46	23.67	13.51	86.45	26.68	34.15	-1.12E+00	8.94E-02			1.57E-01	7.86E-01		5.25E-01	4.17E-02		-2.85E-01	4.20E-01		-1.70E+00	4.09E-39	Down	-1.34E+00	1.06E-28	Down	Unigene51771_All//gi|224146039|ref|XP_002325856.1|//8.00E-35//vitamin-b12 independent methionine synthase, 5-methyltetrahydropteroyltriglutamate-homocysteine [Populus trichocarpa] >gi|222862731|gb|EEF00238.1| vitamin-b12 independent methionine synthase, 5-methyltetrahydropteroyltriglutamate-homocysteine [Populus trichocarpa]	Unigene51771_All//2.00E-33//AT5G17920| ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase	Unigene51771_All//1.00E-123//TC140693		ko00270|Cysteine and methionine metabolism		nr -
Unigene51773_All	487	0.43	1.25	0.00	0.51	2.62	2.23	2.08	1.20	6.05	1.54E+00	1.22E-01			-8.75E+00	1.45E-01		2.35E+00	5.09E-04	Up	2.12E+00	4.32E-03		-7.94E-01	2.02E-01		1.54E+00	5.23E-06	Up			Unigene51773_All//8.00E-105//CO073349				
Unigene51775_All	643	2.69	0.47	1.24	2.25	2.89	1.33	0.13	0.13	0.00	-2.51E+00	2.66E-05	Down	-1.11E+00	3.58E-02		3.64E-01	5.05E-01		-7.52E-01	1.90E-01		-1.66E-02	1.01E+00		-7.04E+00	3.58E-01		Unigene51775_All//gi|12322008|gb|AAG51046.1|AC069473_8//6.00E-31//gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] >gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]						nr -
Unigene51776_All	545	1.34	2.70	3.62	2.56	4.11	2.40	3.34	1.07	1.39	1.00E+00	6.92E-02			1.43E+00	4.28E-03		6.82E-01	1.16E-01		-9.08E-02	8.82E-01		-1.64E+00	3.51E-04	Down	-1.26E+00	2.97E-03				Unigene51776_All//2.00E-65//ES801053				
Unigene51779_All	451	0.12	0.00	0.00	4.97	1.91	1.80	6.56	0.19	1.50	-6.86E+00	6.10E-01			-6.86E+00	6.22E-01		-1.38E+00	7.07E-04	Down	-1.46E+00	8.28E-04	Down	-5.15E+00	3.87E-18	Down	-2.13E+00	5.20E-09	Down	Unigene51779_All//gi|297843646|ref|XP_002889704.1|//1.00E-53//CLAVATA1 receptor kinase [Arabidopsis lyrata subsp. lyrata] >gi|297335546|gb|EFH65963.1| CLAVATA1 receptor kinase [Arabidopsis lyrata subsp. lyrata]	Unigene51779_All//2.00E-45//AT1G08590| CLAVATA1 receptor kinase (CLV1)					nr -
Unigene5178_All	564	6.22	4.13	8.88	15.63	22.53	11.69	6.22	3.48	2.12	-5.89E-01	7.44E-02			5.14E-01	6.98E-02		5.27E-01	4.50E-04		-4.19E-01	3.42E-02		-8.37E-01	4.30E-03		-1.55E+00	3.68E-07	Down	Unigene5178_All//gi|15229928|ref|NP_187811.1|//1.00E-47//DNA-3-methyladenine glycosylase (MAG) [Arabidopsis thaliana] >gi|2833373|sp|Q39147.1|3MG_ARATH RecName: Full=DNA-3-methyladenine glycosylase; AltName: Full=3-methyladenine DNA glycosidase >gi|12322001|gb|AAG51039.1|AC06947 3.1 DNA-3-methlyadenine glycosylase (MAG) 45351-46783 [Arabidopsis thaliana] >gi|429157|emb|CAA53763.1| 3-methyladenine glycosylase [Arabidopsis thaliana] >gi|10998145|dbj|BAB03116.1| DNA-3-methyladenine glycosylase (3-methyladenine DNA glycosidase) [Arabidopsis thaliana]	Unigene5178_All//2.00E-48//AT3G12040| DNA-3-methyladenine glycosylase (MAG)			ko03410|Base excision repair		nr -
Unigene51780_All	777	1.62	0.46	0.27	1.03	0.89	0.93	1.25	0.59	1.28	-1.82E+00	5.22E-03			-2.56E+00	6.99E-04	Down	-2.11E-01	8.06E-01		-1.41E-01	8.60E-01		-1.08E+00	8.88E-02		3.45E-02	9.70E-01		Unigene51780_All//gi|39930307|tpg|DAA00365.1|//1.00E-80//TPA: TPA_exp: SAB [Arabidopsis thaliana]	Unigene51780_All//5.00E-80//AT1G58250| SAB (SABRE)	Unigene51780_All//1.00E-178//CO105202				nr +
Unigene51781_All	527	1.39	3.08	0.91	2.46	7.71	3.86	0.88	5.00	1.13	1.15E+00	2.93E-02			-6.12E-01	4.70E-01		1.65E+00	9.46E-08	Up	6.50E-01	1.69E-01		2.50E+00	2.79E-09	Up	3.62E-01	6.37E-01				Unigene51781_All//9.00E-77//CK640462				
Unigene51782_All	730	0.00	0.69	1.02	2.32	2.64	1.42	2.49	1.37	3.11	9.44E+00	4.04E-03			1.00E+01	3.27E-04	Up	1.87E-01	7.48E-01		-7.05E-01	1.74E-01		-8.58E-01	4.74E-02		3.21E-01	3.98E-01		Unigene51782_All//gi|297811331|ref|XP_002873549.1|//1.00E-29//mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319386|gb|EFH49808.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene51782_All//2.00E-23//AT5G12080| MSL10 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 10); mechanically-gated ion channel					nr -
Unigene51784_All	530	0.10	0.76	2.31	1.50	0.78	0.09	1.68	0.87	0.45	2.95E+00	5.91E-02			4.55E+00	1.02E-05	Up	-9.48E-01	2.21E-01		-4.14E+00	4.13E-04	Down	-9.50E-01	1.55E-01		-1.89E+00	6.34E-03								
Unigene51785_All	554	0.00	0.18	0.00	1.89	1.55	1.22	1.14	1.66	4.53	7.51E+00	3.86E-01			null	null		-2.81E-01	6.74E-01		-6.27E-01	3.81E-01		5.36E-01	4.18E-01		1.98E+00	4.51E-07	Up	Unigene51785_All//gi|1732247|gb|AAB41101.1|//2.00E-64//transcription factor Nbb1 [Nicotiana tabacum] >gi|6552363|dbj|BAA88223.1| myb-related transcription factor LBM3 [Nicotiana tabacum]	Unigene51785_All//7.00E-60//AT3G22250| MYB15 (MYB DOMAIN PROTEIN 15); DNA binding / transcription factor	Unigene51785_All//5.00E-66//NP524477	MYB			nr +

Unigene51786_All	2316	0.00	0.00	0.00	0.00	0.00	0.00	4.03	2.49	61.63	null	null		null	null		null	null		null	null		-6.96E-01	3.20E-05		3.93E+00	0.00E+00	Up	Unigene51786_All//gi|240255784|ref|NP_192890.4|//1.00E-145//kinase [Arabidopsis thaliana]	Unigene51786_All//2.00E-102//AT4G11530| kinase	Unigene51786_All//8.00E-16//TC174638		ko04626|Plant-pathogen interaction		nr +
Unigene51788_All	504	16.92	13.37	16.38	274.37	231.07	190.96	236.82	72.89	60.07	-3.40E-01	9.56E-02		-4.72E-02	8.28E-01		-2.48E-01	4.95E-10		-5.23E-01	4.10E-35		-1.70E+00	2.74E-238	Down	-1.98E+00	4.01E-302	Down	Unigene51788_All//gi|124488476|gb|ABN12322.1|//4.00E-33//phenylcoumaran benzylic ether reductase-like protein [Gossypium hirsutum]	Unigene51788_All//4.00E-24//AT1G75280| isoflavone reductase, putative	Unigene51788_All//0.00E+00//gi|18100773|gb|BM360027.1|BM360027		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism		nr -
Unigene51791_All	762	0.27	0.13	0.35	2.35	1.76	1.07	4.49	0.99	1.36	-1.05E+00	5.64E-01		3.47E-01	7.97E-01		-4.17E-01	4.10E-01		-1.14E+00	2.04E-02		-2.19E+00	2.97E-10	Down	-1.73E+00	5.37E-08	Down	Unigene51791_All//gi|193788746|gb|ACF20472.1|//9.00E-52//At5g24620 [Arabidopsis thaliana]	Unigene51791_All//2.00E-49//AT5G24620| thaumatin-like protein, putative	Unigene51791_All//2.00E-10//TC179458				nr +
Unigene51792_All	237	7.06	4.70	3.37	21.86	17.44	14.67	9.10	5.11	3.70	-5.87E-01	2.42E-01		-1.07E+00	4.69E-02		-3.26E-01	2.32E-01		-5.75E-01	2.93E-02		-8.31E-01	3.36E-02		-1.30E+00	8.08E-04	Down	Unigene51792_All//gi|24461865|gb|AA62352.1|AF506028_19//1.00E-13//NBS-LRR type disease resistance protein [Citrus trifoliata]	Unigene51792_All//7.00E-09//AT5G63020| disease resistance protein (CC-NBS-LRR class), putative	Unigene51792_All//6.00E-76//ES832022		ko04626|Plant-pathogen interaction		nr -
Unigene51793_All	611	153.79	68.50	125.15	260.49	242.96	201.72	988.98	459.96	495.60	-1.17E+00	3.69E-87	Down	-2.97E-01	5.75E-08		-1.01E-01	1.59E-02		-3.69E-01	2.03E-21		-1.10E+00	0.00E+00	Down	-9.97E-01	0.00E+00		Unigene51793_All//gi|124488472|gb|ABN12320.1|//1.00E-76//benzoquinone reductase [Gossypium hirsutum]	Unigene51793_All//5.00E-68//AT5G54500| FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor	Unigene51793_All//0.00E+00//TC131108				nr -
Unigene51795_All	507	1.03	0.90	1.89	1.38	3.19	3.03	0.92	9.07	10.29	-1.98E-01	8.20E-01		8.73E-01	2.38E-01		1.21E+00	2.02E-02		1.14E+00	3.89E-02		3.31E+00	1.15E-20	Up	3.49E+00	5.80E-25	Up			Unigene51795_All//6.00E-07//gi|21089515|gb|BQ401828.1|BQ401828				
Unigene51798_All	272	3.08	5.22	6.85	0.55	4.30	8.97	0.31	0.00	0.00	7.61E-01	1.74E-01		1.15E+00	2.26E-02		2.97E+00	1.37E-04	Up	4.03E+00	3.84E-11	Up	-8.28E+00	4.03E-01		-8.28E+00	3.58E-01									
Unigene51799_All	1002	23.71	9.10	10.04	0.70	1.10	0.09	0.17	0.00	0.00	-1.38E+00	4.10E-29	Down	-1.24E+00	9.46E-24	Down	6.60E-01	3.38E-01		-2.95E+00	5.83E-03		-7.40E+00	1.34E-01		-7.40E+00	1.08E-01		Unigene51799_All//gi|1370154|emb|CAA98183.1|//3.00E-94//RAB11G [Lotus japonicus]	Unigene51799_All//2.00E-92//AT1G05810| RABA5E (RAB GTPASE HOMOLOG A5E); GTP binding	Unigene51799_All//0.00E+00//TC157278				nr -
Unigene5180_All	515	1.93	3.44	2.27	7.45	6.49	12.28	12.23	9.98	4.02	8.35E-01	8.91E-02		2.37E-01	6.97E-01		-2.00E-01	5.68E-01		7.21E-01	1.92E-03		-2.93E-01	1.93E-01		-1.60E+00	1.03E-12	Down			Unigene5180_All//8.00E-25//TC179148				
Unigene51801_All	1339	0.04	0.23	0.04	0.37	0.44	0.64	9.82	9.99	4.58	2.54E+00	1.51E-01		2.56E-02	9.94E-01		2.33E-01	8.26E-01		7.85E-01	3.33E-01		2.45E-02	8.88E-01		-1.10E+00	1.04E-14	Down	Unigene51801_All//gi|212717123|gb|ACJ37403.1|//6.00E-28//CC-NBS-LRR class disease resistance protein [Glycine max]	Unigene51801_All//1.00E-23//AT1G50180| disease resistance protein (CC-NBS-LRR class), putative	Unigene51801_All//0.00E+00//TC178870		ko04626|Plant-pathogen interaction		nr -
Unigene51807_All	569	0.00	0.80	0.00	0.53	1.88	0.00	0.45	2.28	4.62	9.65E+00	7.43E-03		null	null		1.84E+00	1.02E-02		-9.04E+00	3.99E-02		2.35E+00	1.25E-04	Up	3.37E+00	1.52E-12	Up							
Unigene51808_All	301	0.87	5.72	4.42	26.81	7.32	13.50	114.62	93.17	45.79	2.72E+00	1.19E-05	Up	2.35E+00	8.68E-04	Up	-1.87E+00	3.20E-19	Down	-9.89E-01	9.26E-07		-2.99E-01	2.86E-04		-1.32E+00	1.64E-49	Down	Unigene51808_All//gi|45644504|gb|AAS73002.1|//8.00E-08//proline-rich protein [Gossypium barbadense]		Unigene51808_All//1.00E-148//gi|11199744|gb|BF268761.1|BF268761				nr +
Unigene51809_All	1020	0.10	0.79	1.72	0.00	0.20	0.18	6.34	3.48	10.23	2.95E+00	3.28E-03		4.07E+00	1.51E-07	Up	7.66E+00	1.57E-01		7.47E+00	1.94E-01		-8.65E-01	3.01E-05		6.90E-01	7.62E-06		Unigene51809_All//gi|34538351|gb|AAQ74156.1|//1.00E-142//osmotin-like protein I [Gossypium hirsutum]	Unigene51809_All//2.00E-79//AT4G11650| AT0SM34 (osmotin 34)	Unigene51809_All//0.00E+00//TC129745				nr +
Unigene5181_All	320	1.80	1.11	5.16	8.41	7.32	4.38	5.81	5.36	1.62	-6.98E-01	4.49E-01		1.52E+00	6.71E-03		-2.00E-01	6.17E-01		-9.42E-01	1.39E-02		-1.19E-01	7.87E-01		-1.84E+00	4.29E-05	Down							
Unigene51811_All	1051	0.35	0.19	0.10	49.06	34.47	13.15	0.40	0.16	0.15	-8.54E-01	4.88E-01		-1.78E+00	2.34E-01		-5.09E-01	2.72E-14		-1.90E+00	3.73E-107	Down	-1.34E+00	2.24E-01		-1.41E+00	1.73E-01		Unigene51811_All//gi|219560134|gb|ACL27273.1|//1.00E-74//homeodomain leucine-zipper 1 [Capsicum annuum]	Unigene51811_All//3.00E-61//AT4G37790| HAT22; transcription factor	Unigene51811_All//0.00E+00//ES813228	HB			nr -
Unigene51812_All	568	2.03	3.03	1.88	41.13	26.98	24.57	10.50	2.87	1.61	5.82E-01	2.41E-01		-1.12E-01	8.56E-01		-6.09E-01	3.84E-09		-7.43E-01	1.61E-11		-1.87E+00	2.80E-14	Down	-2.70E+00	9.88E-23	Down	Unigene51812_All//gi|12039277|gb|AAG46067.1|AC079830_7//5.00E-07//expressed protein [Oryza sativa Japonica Group] >gi|108710365|gb|ABF98160.1| expressed protein [Oryza sativa (Japonica cultivar-group)]	Unigene51812_All//8.00E-08//AT4G10810| unknown protein	Unigene51812_All//0.00E+00//TC166067				nr -
Unigene51813_All	371	1.69	2.73	3.59	1.34	1.39	1.95	2.17	2.03	12.35	6.91E-01	3.18E-01		1.08E+00	7.96E-02		5.23E-02	9.80E-01		5.37E-01	5.60E-01		-9.47E-02	8.99E-01		2.51E+00	4.56E-16	Up	Unigene51813_All//gi|157782958|gb|ABV72393.1|//4.00E-33//coronatine-insensitive 1 [Hevea brasiliensis]	Unigene51813_All//7.00E-25//AT2G39940| COI1 (CORONATINE INSENSITIVE 1); protein binding / ubiquitin-protein ligase	Unigene51813_All//4.00E-38//TC175576		ko04626|Plant-pathogen interaction		nr +
Unigene51814_All	605	82.59	102.68	108.08	68.09	59.37	19.93	0.14	0.48	0.00	3.14E-01	2.40E-06		3.88E-01	4.70E-09		-1.98E-01	1.78E-02		-1.77E+00	6.47E-78	Down	1.79E+00	2.24E-01		-7.13E+00	3.58E-01					Unigene51814_All//0.00E+00//gi|13248259|gb|BF274970.2|BF274970				
Unigene51817_All	282	7.61	1.98	6.80	2.47	0.49	7.53	0.00	0.00	0.28	-1.94E+00	6.41E-05	Down	-1.62E-01	7.11E-01		-2.34E+00	1.01E-02		1.61E+00	5.57E-04	Up	null	null		8.14E+00	4.03E-01								
Unigene5182_All	1421	1.95	2.03	2.66	1.61	3.83	8.26	21.07	12.27	13.63	5.87E-02	8.79E-01		4.47E-01	1.83E-01		1.25E+00	5.94E-07	Up	2.36E+00	1.11E-31	Up	-7.80E-01	4.98E-18		-6.29E-01	5.45E-13		Unigene5182_All//gi|297832266|ref|XP_002884015.1|//2.00E-41//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329855|gb|EFH60274.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5182_All//9.00E-38//AT2G16750| protein kinase family protein	Unigene5182_All//2.00E-108//DR453396				nr -
Unigene51821_All	269	246.04	182.33	128.67	401.11	302.88	396.56	809.61	483.37	263.91	-4.32E-01	1.57E-11		-9.35E-01	1.51E-41		-4.05E-01	1.96E-19		-1.64E-02	7.88E-01		-7.44E-01	3.89E-116		-1.62E+00	0.00E+00	Down	Unigene51821_All//gi|38154482|gb|AAR12193.1|//3.00E-45//molecular chaperone Hsp90-1 [Nicotiana benthamiana]	Unigene51821_All//1.00E-44//AT5G56010| HSP81-3; ATP binding / unfolded protein binding	Unigene51821_All//2.00E-150//ES802514		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene51822_All	674	1.55	1.50	1.50	5.84	2.35	1.54	1.44	0.25	1.12	-4.63E-02	9.56E-01		-4.86E-02	9.57E-01		-1.31E+00	6.68E-06	Down	-1.92E+00	8.96E-09	Down	-2.54E+00	6.41E-04	Down	-3.62E-01	5.65E-01		Unigene51822_All//gi|15809986|gb|AAL06920.1|//1.00E-44//AT3g19540/T3J18_4 [Arabidopsis thaliana] >gi|22137022|gb|AAM91356.1| At3g19540/T3J18_4 [Arabidopsis thaliana]	Unigene51822_All//5.00E-38//AT3G19540| unknown protein	Unigene51822_All//0.00E+00//TC170086				nr -
Unigene51829_All	436	41.52	21.62	18.93	82.83	76.06	47.44	127.23	44.96	67.98	-9.42E-01	1.82E-12		-1.13E+00	6.65E-16	Down	-1.23E-01	2.23E-01		-8.04E-01	6.11E-20		-1.50E+00	8.50E-93	Down	-9.04E-01	4.98E-43				Unigene51829_All//0.00E+00//gi|21096066|gb|BQ408379.1|BQ408379				
Unigene5183_All	877	2.15	0.92	0.79	1.31	2.87	1.85	3.09	0.95	0.91	-1.22E+00	1.17E-02		-1.44E+00	5.08E-03		1.13E+00	4.08E-03		5.05E-01	3.72E-01		-1.69E+00	4.12E-06	Down	-1.76E+00	1.14E-06	Down	Unigene5183_All//gi|42565395|gb|AAS20972.1|//3.00E-16//cell wall hydrolase [Hyacinthus orientalis]		Unigene5183_All//0.00E+00//DW501480				nr -
Unigene51830_All	229	14.17	9.29	8.37	20.23	16.54	18.93	156.75	73.37	47.49	-6.08E-01	7.81E-02		-7.59E-01	3.56E-02		-2.91E-01	3.23E-01		-9.56E-02	7.51E-01		-1.10E+00	2.94E-37	Down	-1.72E+00	1.17E-75	Down			Unigene51830_All//3.00E-121//gi|21099726|gb|BQ412039.1|BQ412039				
Unigene51831_All	1371	0.46	0.11	0.04	0.18	0.20	0.56	10.95	7.87	4.68	-2.05E+00	4.46E-02		-3.56E+00	8.32E-03		1.45E-01	9.61E-01		1.62E+00	6.61E-02		-4.77E-01	2.07E-04		-1.23E+00	1.14E-19	Down	Unigene51831_All//gi|297805570|ref|XP_002870669.1|//8.00E-82//AT1G17GPT1 [Arabidopsis lyrata subsp. lyrata] >gi|297316505|gb|EFH46928.1| ATUK/UPRT1 [Arabidopsis lyrata subsp. lyrata]	Unigene51831_All//4.00E-13//AT5G40870| AtUK/UPRT1 (Uridine kinase/Uracil phosphoribosyltransferase 1); ATP binding / kinase/ uracil phosphoribosyltransferase/ uridine kinase	Unigene51831_All//1.00E-145//TC151599		ko00240|Pyrimidine metabolism		nr -
Unigene51832_All	334	2.51	2.88	2.23	6.41	2.47	1.62	1.27	1.13	0.24	2.02E-01	7.54E-01		-1.67E-01	8.16E-01		-1.37E+00	1.03E-03		-1.98E+00	3.06E-05	Down	-1.69E-01	8.65E-01		-2.41E+00	3.93E-02								
Unigene51834_All	797	0.00	0.00	0.00	1.25	1.08	0.40	13.95	2.05	6.15	null	null		null	null		-2.11E-01	7.79E-01		-1.66E+00	2.34E-02		-2.77E+00	1.67E-41	Down	-1.18E+00	5.18E-14	Down	Unigene51834_All//gi|107738065|gb|ABF83626.1|//6.00E-17//At4g33800 [Arabidopsis thaliana]		Unigene51834_All//3.00E-167//DW513924				nr +
Unigene51836_All	597	0.70	0.34	0.54	1.25	2.19	0.53	4.60	3.08	1.20	-1.05E+00	3.65E-01		-3.90E-01	7.17E-01		8.08E-01	1.84E-01		-1.24E+00	1.45E-01		-5.80E-01	9.09E-02		-1.94E+00	1.45E-07	Down	Unigene51836_All//gi|87240796|gb|ABD32654.1|//3.00E-50//Zinc finger, RING-type [Medicago truncatula]	Unigene51836_All//4.00E-34//AT4G03965| protein binding / zinc ion binding	Unigene51836_All//3.00E-24//TC154064		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene51837_All	766	0.00	0.00	0.07	0.20	0.27	1.71	5.02	0.93	8.95	null	null		6.12E+00	6.35E-01		4.67E-01	8.25E-01		3.13E+00	3.90E-05	Up	-2.44E+00	6.40E-13	Down	8.33E-01	2.19E-05		Unigene51837_All//gi|224130444|ref|XP_002328610.1|//6.00E-40//type-b response regulator [Populus trichocarpa] >gi|222838592|gb|EEE76957.1| type-b response regulator [Populus trichocarpa]	Unigene51837_All//3.00E-36//AT4G16110| ARR2 (ARABIDOPSIS RESPONSE REGULATOR 2); transcription factor/ two-component response regulator	Unigene51837_All//2.00E-174//TC158190	ARR-B	ko04712|Circadian rhythm - plant		nr -
Unigene51838_All	742	0.42	0.00	0.00	1.48	1.39	2.25	1.37	8.22	2.36	-8.72E+00	3.65E-02		-8.72E+00	4.90E-02		-8.52E-02	8.79E-01		6.09E-01	2.56E-01		2.59E+00	2.12E-21	Up	7.89E-01	6.43E-02		Unigene51838_All//gi|94549041|gb|ABF39005.1|//4.00E-14//plant cell wall protein S1TFR88 [Solanum lycopersicum]	Unigene51838_All//2.00E-17//AT1G64065| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G44000.1); Has 69 Blast hits to 69 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).					nr +
Unigene51839_All	573	0.00	2.21	1.21	0.70	0.42	0.87	5.61	9.99	4.80	1.11E+01	2.86E-07	Up	1.02E+01	6.15E-04	Up	-7.25E-01	5.46E-01		3.18E-01	7.57E-01		8.34E-01	1.70E-04		-2.25E-01	4.85E-01		Unigene51839_All//gi|18410530|ref|NP_567039.1|//1.00E-07//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|42572705|ref|NP_974448.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|79315364|ref|NP_001030874.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|66865932|gb|AAY57600.1| RING finger family protein [Arabidopsis thaliana]	Unigene51839_All//6.00E-09//AT3G56580| zinc finger (C3HC4-type RING finger) family protein	Unigene51839_All//0.00E+00//BQ406279				nr +
Unigene51840_All	715	0.22	2.62	1.04	1.32	0.34	0.38	1.54	1.87	0.50	3.58E+00	1.21E-07	Up	2.25E+00	2.35E-02		-1.97E+00	6.32E-03		-1.80E+00	1.83E-02		2.83E-01	6.33E-01		-1.62E+00	6.27E-03				Unigene51840_All//3.00E-34//TC164608				
Unigene51843_All	498	27.95	18.01	13.69	45.61	67.42	44.98	0.85	0.17	0.16	-6.34E-01	2.43E-05		-1.03E+00	1.10E-10	Down	5.64E-01	5.12E-11		-2.01E-02	9.00E-01		-2.34E+00	5.46E-02		-2.41E+00	3.93E-02		Unigene51843_All//gi|21615415|emb|CAD32927.1|//6.00E-31//nitrate transporter [Cicer arietinum]	Unigene51843_All//1.00E-12//AT3G26690| nitrate transporter (NTP2)	Unigene51843_All//0.00E+00//TC170041				nr -
Unigene51845_All	456	0.00	1.56	1.05	0.00	1.96	3.07	3.89	3.85	9.17	1.06E+01	3.32E-04	Up	1.00E+01	7.47E-03		1.09E+01	1.69E-05	Up	1.16E+01	2.43E-08	Up	-1.66E-02	1.01E+00		1.24E+00	4.03E-06	Up							
Unigene51847_All	462	0.23	0.66	0.46	0.54	1.57	1.76	0.92	2.35	6.12	1.54E+00	3.23E-01		1.03E+00	5.91E-01		1.54E+00	8.92E-02		1.71E+00	4.57E-02		1.36E+00	2.43E-02		2.74E+00	3.79E-11	Up	Unigene51847_All//gi|18407313|ref|NP_566098.1|//3.00E-11//transcription factor/ transcription regulator [Arabidopsis thaliana] >gi|75097628|sp|Q22901.1|BH151_ARATH RecName: Full=Transcription factor bHLH151; AltName: Full=Transcription factor EN 146; AltName: Full=bHLH transcription factor bHLH151; AltName: Full=Basic helix-loop-helix protein 151; Short=bHLH 151; Short=AtbHLH151 >gi|2275205|gb|AAB63827.1| expressed protein [Arabidopsis thaliana] >gi|89111836|gb|ABD60690.1| At2g47270 [Arabidopsis thaliana]	Unigene51847_All//6.00E-10//AT2G47270| transcription factor/ transcription regulator					nr -
Unigene51848_All	466	0.79	37.19	0.91	1.18	3.18	6.88	16.60	49.42	96.26	5.56E+00	9.76E-88	Up	2.18E-01	8.31E-01		1.43E+00	1.04E-02		2.55E+00	9.20E-10	Up	1.57E+00	1.22E-41	Up	2.54E+00	1.80E-152	Up	Unigene51848_All//gi|12903402|gb|AAG43558.1|AF211540_1//5.00E-15//Avr9/Cf-9 rapidly elicited protein 75 [Nicotiana tabacum]		Unigene51848_All//0.00E+00//TC145802				nr +

Unigene51849_All	591	0.18	2.23	1.62	0.00	0.00	0.23	1.79	2.33	6.61	3.65E+00	1.28E-05	Up	3.20E+00	1.02E-03		null	null		7.84E+00	3.11E-01		3.84E-01	4.75E-01		1.89E+00	6.36E-10	Up	Unigene51849_All//gi|224139090|ref|XP_002326765.1|//1.00E-12//predicted protein [Populus trichocarpa] >gi|222834087|gb|EEE72564.1| predicted protein [Populus trichocarpa]		Unigene51849_All//8.00E-59//gi|109885676|gb|DW514646.1|DW514646				nr +
Unigene5185_All	563	3.62	5.67	3.12	3.27	2.45	2.73	4.81	2.15	5.09	6.46E-01	6.43E-02		-2.16E-01	6.25E-01		-4.20E-01	3.95E-01		-2.63E-01	6.37E-01		-1.16E+00	8.31E-04	Down	8.41E-02	8.03E-01		Unigene5185_All//gi|212717155|gb|ACJ37419.1|//3.00E-50//NBS-LRR disease resistance protein [Glycine max]	Unigene5185_All//8.00E-22//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene5185_All//6.00E-72//gi|109864925|gb|DW493901.1|DW493901		ko04626|Plant-pathogen interaction		nr +
Unigene51851_All	859	4.02	1.95	1.12	0.46	1.44	2.00	0.00	0.00	0.00	-1.05E+00	1.82E-03		-1.85E+00	1.21E-06	Down	1.64E+00	1.01E-02		2.11E+00	1.69E-04	Up	null	null		null	null		Unigene51851_All//gi|224083948|ref|XP_002307182.1|//2.00E-78//cytochrome P450 [Populus trichocarpa] >gi|222856631|gb|EEE94178.1|cytochrome P450 [Populus trichocarpa]	Unigene51851_All//2.00E-66//AT2G23180| CYP96A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene51851_All//2.00E-08//CO115312		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr -
Unigene51853_All	1851	0.00	0.03	0.00	0.00	0.00	0.00	4.07	6.73	1.68	4.78E+00	6.15E-01		null	null		null	null		null	null		7.27E-01	3.85E-07		-1.28E+00	6.64E-11	Down	Unigene51853_All//gi|60327206|gb|AAX19026.1|//1.00E-96//Hcr2-p4.1 [Solanum pimpinellifolium]	Unigene51853_All//4.00E-36//AT5G40170| AtRLP54 (Receptor Like Protein 54); kinase/ protein binding	Unigene51853_All//4.00E-94//ES795055		ko04626|Plant-pathogen interaction		nr +
Unigene51854_All	414	2.15	0.61	0.00	2.17	1.91	1.75	1.63	1.31	1.35	-1.81E+00	2.38E-02		-1.11E+01	6.30E-05	Down	-1.79E-01	8.15E-01		-3.11E-01	6.88E-01		-3.16E-01	6.74E-01		-2.78E-01	6.89E-01		Unigene51854_All//gi|218546772|sp|Q6ZUT1.2|PP173_ARATH//1.00E-20//RecName: Full=Pentatricopeptide repeat-containing protein At2g27800, mitochondrial; Flags: Precursor	Unigene51854_All//7.00E-22//AT2G27800| CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G27300.1); Has 11283 Blast hits to 3897 proteins in 129 species: Archae - 1; Bacteria - 2; Metazoa - 118; Fungi - 74; Plants - 10832; Viruses - 0; Other Eukaryotes - 256 (source: NCBI BLink).					nr +
Unigene51857_All	584	333.01	202.07	291.14	473.32	546.31	335.63	96.07	99.12	39.36	-7.21E-01	2.59E-80		-1.94E-01	2.49E-07		2.07E-01	6.74E-16		-4.96E-01	2.62E-63		4.51E-02	5.83E-01		-1.29E+00	1.25E-76	Down	Unigene51857_All//gi|15148916|gb|AAK84885.1|AF402604.1//7.00E-28//homeodomain leucine zipper protein HDZ1 [Phaseolus vulgaris]		Unigene51857_All//0.00E+00//gi|78346099|gb|DT566373.1|DT566373				nr -
Unigene51859_All	700	3.96	0.94	3.04	3.34	4.23	6.58	0.00	0.24	0.46	-2.07E+00	1.34E-06	Down	-3.81E-01	3.60E-01		3.39E-01	4.01E-01		9.76E-01	4.97E-04		7.90E+00	1.39E-01		8.83E+00	1.34E-02		Unigene51859_All//gi|224092400|ref|XP_002306592.1|//2.00E-40//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222855568|gb|EEE93115.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene51859_All//7.00E-32//AT1G52800| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene51859_All//8.00E-149//gi|164286691|gb|ES834740.1|ES834740		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene51861_All	510	2.15	0.20	0.10	4.98	7.76	6.82	1.49	1.64	2.58	-3.44E+00	1.19E-04	Down	-4.37E+00	4.94E-05	Down	6.40E-01	3.50E-02		4.53E-01	1.97E-01		1.35E-01	8.42E-01		7.89E-01	1.19E-01			Unigene51861_All//2.00E-05//AT3G09510| nucleic acid binding	Unigene51861_All//9.00E-40//ES834205				
Unigene51864_All	319	4.26	4.45	3.51	2.50	3.45	2.55	7.16	3.28	2.87	6.07E-02	9.22E-01		-2.83E-01	6.05E-01		4.67E-01	5.30E-01		2.85E-02	9.71E-01		-1.13E+00	3.14E-03		-1.32E+00	4.63E-04	Down	Unigene51864_All//gi|297738293|emb|CBI27494.3|//9.00E-07//unnamed protein product [Vitis vinifera]		Unigene51864_All//3.00E-94//TC143969				nr -
Unigene51867_All	348	56.53	70.33	79.72	81.16	85.89	131.99	59.65	148.33	159.47	3.15E-01	4.91E-03		4.96E-01	2.82E-06		8.17E-02	5.20E-01		7.02E-01	7.92E-20		1.31E+00	1.17E-70	Up	1.42E+00	4.76E-87	Up	Unigene51867_All//gi|115459618|ref|NP_001053409.1|//9.00E-20//Os04g0533300 [Oryza sativa Japonica Group] >gi|32489830|emb|CAE04574.1|OSJNBa0039L24.13 [Oryza sativa (japonica cultivar-group)] >gi|113561980|dbj|BAF15323.1|Os04g0533300 [Oryza sativa Japonica Group]	Unigene51867_All//1.00E-11//AT2G45820| DNA-binding protein, putative	Unigene51867_All//4.00E-180//TC147908				nr -
Unigene51870_All	1014	0.31	0.00	1.05	0.39	0.27	0.27	41.99	48.72	15.91	-8.27E+00	3.65E-02		1.76E+00	1.85E-02		-5.33E-01	6.15E-01		-5.57E-01	6.38E-01		2.15E-01	1.92E-03		-1.40E+00	2.80E-66	Down	Unigene51870_All//gi|211906454|gb|ACJ11720.1|//1.00E-74//peroxiredoxin [Gossypium hirsutum]	Unigene51870_All//9.00E-69//AT1G65980| TPX1 (thioredoxin-dependent peroxidase 1); antioxidant/ oxidoreductase	Unigene51870_All//0.00E+00//gi|164268929|gb|ES794196.1|ES794196		ko04146|Peroxisome		nr +
Unigene51873_All	398	32.60	31.45	29.97	30.16	25.61	32.34	52.05	44.42	21.02	-5.21E-02	7.54E-01		-1.21E-01	5.09E-01		-2.36E-01	1.70E-01		1.01E-01	6.29E-01		-2.29E-01	4.43E-02		-1.31E+00	1.47E-29	Down			Unigene51873_All//1.00E-112//gi|109831134|gb|DW231409.1|DW231409				
Unigene51874_All	992	0.00	17.42	10.74	0.00	0.03	0.00	0.00	0.04	0.12	1.41E+01	2.51E-99	Up	1.34E+01	8.26E-60	Up	5.12E+00	8.29E-01		null	null		5.40E+00	6.34E-01		6.91E+00	2.43E-01		Unigene51874_All//gi|4501883|ref|NP_001604.1|//1.00E-64//actin, aortic smooth muscle [Homo sapiens] >gi|6671507|ref|NP_031418.1| actin, aortic smooth muscle [Mus musculus] >gi|78045238|ref|NP_001029674.1| actin, aortic smooth muscle [Bos taurus] >gi|110625958|ref|NP_112266.1| actin, aortic smooth muscle [Rattus norvegicus] >gi|156119362|ref|NP_001095152.1| actin, aortic smooth muscle [Oryctolagus cuniculus] >gi|197097944|ref|NP_001126814.1| actin, aortic smooth muscle [Pongo abelii] >gi|213688375|ref|NP_001135417.1| actin, aortic smooth muscle [Homo sapiens] >gi|257470979|ref|NP_001158122.1| actin, aortic smooth muscle [Sus scrofa] >gi|73996085|ref|XP_534781.2| PREDICTED: similar to Actin, aortic smooth muscle (Alpha-actin 2) [Canis familiaris] >gi|114631685|ref|XP_521550.2|	Unigene51874_All//3.00E-61//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene51874_All//9.00E-54//TC153744		ko04145|Phagosome		nr +
Unigene51876_All	634	2.15	4.64	1.34	7.23	6.95	4.20	3.13	0.99	0.38	1.11E+00	2.76E-03		-6.75E-01	2.58E-01		-5.62E-02	8.47E-01		-7.82E-01	5.00E-03		-1.66E+00	1.36E-04	Down	-3.06E+00	4.82E-09	Down	Unigene51876_All//gi|7769850|gb|AAF69528.1|AC008007.3//3.00E-19//F12M16.3 [Arabidopsis thaliana]	Unigene51876_All//5.00E-13//AT1G53163| unknown protein					nr +
Unigene51878_All	625	0.00	395.63	39.53	0.32	0.22	3.47	0.27	0.13	1.59	1.86E+01	0.00E+00	Up	1.53E+01	7.40E-140	Up	-5.33E-01	7.48E-01		3.44E+00	7.19E-09	Up	-1.02E+00	6.14E-01		2.56E+00	3.91E-04	Up	Unigene51878_All//gi|225450123|ref|XP_002275324.1|//6.00E-34//PREDICTED: similar to T6D22.8 [Vitis vinifera]	Unigene51878_All//3.00E-11//AT1G07985| Expressed protein	Unigene51878_All//7.00E-112//EY198055				nr +
Unigene5188_All	1454	5.07	5.09	2.64	15.52	17.12	27.05	18.73	7.70	19.89	4.00E-03	9.84E-01		-9.44E-01	2.75E-05		1.42E-01	2.56E-01		8.02E-01	2.30E-21		-1.28E+00	2.71E-36	Down	8.71E-02	3.97E-01		Unigene5188_All//gi|297823651|ref|XP_002879708.1|//1.00E-157//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297325547|gb|EFH55967.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene5188_All//1.00E-149//AT2G37770| aldo/keto reductase family protein	Unigene5188_All//0.00E+00//gi|164254727|gb|ES829026.1|ES829026		ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr -
Unigene51881_All	1000	1.15	0.51	0.53	1.00	2.82	2.48	0.08	0.00	0.00	-1.18E+00	6.62E-02		-1.11E+00	9.93E-02		1.50E+00	6.59E-05	Up	1.32E+00	1.40E-03		-6.40E+00	4.03E-01		-6.40E+00	3.58E-01				Unigene51881_All//0.00E+00//DN816875				ESTscan -
Unigene51883_All	558	0.00	0.00	0.00	0.00	0.25	0.00	2.88	2.92	52.12	null	null		null	null		7.95E+00	3.18E-01		null	null		2.08E-02	1.00E+00		4.18E+00	7.80E-157	Up	Unigene51883_All//gi|15234446|ref|NP_192951.1|//2.00E-10//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene51883_All//6.00E-09//AT4G12140| zinc finger (C3HC4-type RING finger) family protein	Unigene51883_All//0.00E+00//DW519947				nr +
Unigene51884_All	572	0.27	2.04	0.84	4.18	10.54	2.53	0.30	0.37	0.00	2.89E+00	2.98E-04	Up	1.61E+00	1.82E-01		1.33E+00	2.05E-08	Up	-7.26E-01	8.04E-02		3.05E-01	8.36E-01		-8.21E+00	1.08E-01				Unigene51884_All//5.00E-97//DW501308				
Unigene51885_All	485	1.51	0.00	0.11	3.80	1.35	3.72	2.53	0.60	0.99	-1.06E+01	2.11E-04	Down	-3.78E+00	2.79E-03		-1.49E+00	1.22E-03		-2.90E-02	9.56E-01		-2.07E+00	6.67E-04	Down	-1.36E+00	1.18E-02		Unigene51885_All//gi|297814019|ref|XP_002874893.1|//9.00E-48//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297320730|gb|EFH51152.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene51885_All//1.00E-48//AT4G02820| pentatricopeptide (PPR) repeat-containing protein	Unigene51885_All//2.00E-102//DR461863				nr -
Unigene51886_All	906	1.50	0.84	0.12	7.09	5.02	4.24	1.63	0.46	0.31	-8.40E-01	1.39E-01		-3.68E+00	1.58E-05	Down	-5.00E-01	2.59E-02		-7.43E-01	1.13E-03		-1.82E+00	5.43E-04	Down	-2.41E+00	1.48E-05	Down	Unigene51886_All//gi|60476420|gb|AAX21349.1|//8.00E-53//lateral organ boundaries-like 3 [Lotus japonicus]	Unigene51886_All//1.00E-50//AT3G27650| LBD25 (LOB DOMAIN-CONTAINING PROTEIN 25)	Unigene51886_All//1.00E-55//DW505234		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr +
Unigene5189_All	830	0.06	1.16	0.64	1.80	1.87	2.72	2.24	4.58	8.88	4.20E+00	1.29E-04	Up	3.35E+00	2.06E-02		5.23E-02	9.50E-01		5.96E-01	1.84E-01		1.03E+00	2.65E-04	Up	1.99E+00	3.05E-19	Up			Unigene5189_All//0.00E+00//TC162261				
Unigene51895_All	344	0.00	1.03	0.77	1.30	2.20	1.44	0.00	0.00	2.43	1.00E+01	2.46E-02		9.60E+00	8.01E-02		7.57E-01	3.95E-01		1.48E-01	9.05E-01		null	null		1.12E+01	3.88E-06	Up							
Unigene51898_All	317	11.72	8.95	5.21	15.87	13.04	20.80	2.40	4.48	0.50	-3.89E-01	2.34E-01		-1.17E+00	5.51E-04	Down	-2.84E-01	3.17E-01		3.90E-01	1.06E-01		9.01E-01	7.45E-02		-2.26E+00	4.68E-03			Unigene51898_All//2.00E-05//AT3G25270| nucleic acid binding	Unigene51898_All//2.00E-39//BQ408102				
Unigene5190_All	993	2.63	6.84	2.25	6.12	5.20	7.73	6.90	11.36	9.59	1.38E+00	9.06E-09	Up	-2.26E-01	6.09E-01		-2.35E-01	3.74E-01		3.37E-01	1.34E-01		7.20E-01	1.86E-06		4.75E-01	3.35E-03		Unigene5190_All//gi|15218489|ref|NP_172503.1|//1.00E-83//U2 snRNP auxiliary factor-related [Arabidopsis thaliana] >gi|229621703|sp|Q9SY74.2|C3H5_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 5; Short=AtC3H5	Unigene5190_All//2.00E-55//AT1G10320| U2 snRNP auxiliary factor-related	Unigene5190_All//0.00E+00//TC152585	C3H	ko03040|Spliceosome		nr +
Unigene51900_All	256	1.43	0.79	0.42	2.92	2.15	1.94	3.47	0.98	0.31	-8.54E-01	4.88E-01		-1.78E+00	2.34E-01		-4.40E-01	5.85E-01		-5.89E-01	4.87E-01		-1.82E+00	1.08E-02		-3.48E+00	7.33E-05	Down							
Unigene51902_All	676	1.16	3.15	0.24	1.92	1.48	1.14	2.44	0.31	2.42	1.44E+00	1.81E-03		-2.30E+00	1.79E-02		-3.75E-01	5.57E-01		-7.54E-01	2.18E-01		-2.98E+00	3.67E-07	Down	-1.37E-02	9.67E-01								
Unigene51903_All	1178	0.00	0.82	2.12	0.17	0.15	4.03	0.65	1.10	3.38	9.67E+00	1.38E-05	Up	1.11E+01	8.32E-14	Up	-2.10E-01	8.58E-01		4.57E+00	3.08E-23	Up	7.68E-01	1.50E-01		2.39E+00	2.56E-13	Up	Unigene51903_All//gi|115449221|ref|NP_001048390.1|//1.00E-109//Os02g0796600 [Oryza sativa Japonica Group] >gi|113537921|dbj|BAF10304.1|Os02g0796600 [Oryza sativa Japonica Group]	Unigene51903_All//1.00E-121//AT4G31020| unknown protein	Unigene51903_All//4.00E-124//CO104600				nr -
Unigene51907_All	1003	0.00	0.71	0.00	22.95	7.38	8.06	0.00	0.00	0.00	9.47E+00	3.32E-04	Up	null	null		-1.64E+00	8.68E-45	Down	-1.51E+00	9.17E-35	Down	null	null		null	null		Unigene51907_All//gi|183997780|ref|NP_566437.1|//7.00E-33//ASML2 (ACTIVATOR OF SPOMIN::LUC2); transcription activator [Arabidopsis thaliana] >gi|59894822|gb|AAX11222.1| activator of sporamin LUC 2 [Arabidopsis thaliana]	Unigene51907_All//3.00E-25//AT3G12890| ASML2 (ACTIVATOR OF SPOMIN::LUC2); transcription activator	Unigene51907_All//0.00E+00//TC140100	C2C2-CO-like	ko04712|Circadian rhythm - plant		nr +

Unigene51908_All	770	0.41	1.38	1.11	0.91	0.81	0.76	0.99	1.14	3.26	1.76E+00	1.43E-02		1.44E+00	8.22E-02		-1.70E-01	8.21E-01		-2.48E-01	7.56E-01		2.06E-01	7.54E-01		1.72E+00	5.41E-06	Up	Unigene51908_All//gi|15227701|ref|NP_180568.1|//7.00E-50//ATKT1 (POTASSIUM TRANSPORTER 1); potassium ion transmembrane transporter [Arabidopsis thaliana] >gi|38502834|sp|Q22397.2|POT1_ARATH RecName: Full=Potassium transporter 1; Short=AtPOT1; Short=AtKUP1; Short=AtKT1 >gi|2654088|gb|AAB87687.1| potassium transporter [Arabidopsis thaliana] >gi|2688979|gb|AAB88901.1| high-affinity potassium transporter [Arabidopsis thaliana] >gi|3150413|gb|AAC16965.1| high affinity K+ transporter (AtKUP1/AtKT1p) [Arabidopsis thaliana] >gi|20197230|gb|AAM14984.1| high affinity K+ transporter (AtKUP1 AtKT1p) [Arabidopsis thaliana] >gi|62320122|dbj|BAD94310.1| high affinity K+ transporter [Arabidopsis thaliana]	Unigene51908_All//2.00E-45//AT2G30070| ATKT1 (POTASSIUM TRANSPORTER 1); potassium ion transmembrane transporter	Unigene51908_All//3.00E-37//CA994015				nr +
Unigene51909_All	709	8.93	2.07	7.21	3.86	2.96	1.02	0.89	0.88	0.56	-2.11E+00	2.03E-14	Down	-3.09E-01	2.37E-01		-3.83E-01	3.22E-01		-1.92E+00	2.70E-06	Down	-1.65E-02	1.02E+00		-6.71E-01	3.86E-01		Unigene51909_All//gi|77557098|gb|ABA99894.1|//2.00E-64//Leucine Rich Repeat family protein [Oryza sativa (japonica cultivar-group)]	Unigene51909_All//7.00E-64//AT3G47090| leucine-rich repeat transmembrane protein kinase, putative	Unigene51909_All//4.00E-64//TC143249		ko04626|Plant-pathogen interaction		nr -
Unigene5191_All	590	5.41	28.68	17.78	10.98	19.38	31.77	32.68	35.85	76.23	2.41E+00	1.22E-43	Up	1.72E+00	2.96E-17	Up	8.20E-01	2.19E-07		1.53E+00	1.45E-28	Up	1.34E-01	2.76E-01		1.22E+00	2.22E-56	Up	Unigene5191_All//gi|270329002|dbj|BAI52954.1|//2.00E-08//sigma factor binding protein 1 [Citrullus lanatus subsp. vulgaris]	Unigene5191_All//8.00E-07//AT3G56710| SIB1 (SIGMA FACTOR BINDING PROTEIN 1); binding / protein binding	Unigene5191_All//0.00E+00//TC153562				nr +
Unigene51910_All	392	0.40	0.00	0.82	2.16	1.84	1.73	2.91	4.37	0.71	-8.65E+00	2.15E-01		1.03E+00	4.71E-01		-2.28E-01	7.78E-01		-3.22E-01	6.87E-01		5.86E-01	2.03E-01		-2.03E+00	8.63E-04	Down								
Unigene51917_All	604	0.52	6.21	1.06	0.66	0.80	1.27	1.12	10.52	129.01	3.58E+00	9.11E-15	Up	1.03E+00	2.81E-01		2.75E-01	8.19E-01		9.46E-01	2.73E-01		3.23E+00	9.16E-28	Up	6.85E+00	0.00E+00	Up	Unigene51917_All//gi|224146274|ref|XP_002325945.1|//1.00E-42//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|148372126|gb|ABQ62994.1| RAP2-like protein [Populus trichocarpa] >gi|222862820|gb|EEF00327.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene51917_All//5.00E-36//AT1G71520| AP2 domain-containing transcription factor, putative	Unigene51917_All//0.00E+00//TC167996	AP2-EREBP			nr +
Unigene51918_All	317	163.23	176.94	151.52	261.80	212.48	338.23	98.30	105.35	48.89	1.16E-01	1.34E-01		-1.07E-01	2.16E-01		-3.01E-01	8.24E-09		3.70E-01	1.33E-14		9.99E-02	3.11E-01		-1.01E+00	2.89E-29	Down			Unigene51918_All//2.00E-172//TC168990				
Unigene51920_All	510	0.21	2.09	2.19	1.17	0.20	0.09	4.39	3.85	2.81	3.35E+00	2.17E-04	Up	3.42E+00	1.92E-04	Up	-2.53E+00	1.36E-02		-3.73E+00	4.95E-03		-1.90E-01	6.25E-01		-6.44E-01	7.95E-02		Unigene51920_All//gi|15220348|ref|NP_172600.1|//2.00E-32//S-locus lectin protein kinase family protein [Arabidopsis thaliana]	Unigene51920_All//1.00E-29//AT1G11330| S-locus lectin protein kinase family protein	Unigene51920_All//4.00E-122//CO081719				nr +
Unigene51923_All	618	0.25	1.07	1.98	2.74	0.67	0.29	1.92	2.03	1.03	2.07E+00	3.93E-02		2.96E+00	2.55E-04	Up	-2.04E+00	6.77E-05	Down	-3.23E+00	6.72E-07	Down	8.29E-02	8.86E-01		-8.93E-01	9.53E-02			Unigene51923_All//5.00E-06//AT5G03520| ATRABSC; GTP binding	Unigene51923_All//5.00E-17//DR462206				kegg -
Unigene51927_All	1366	0.34	0.52	0.00	0.18	0.15	0.00	0.96	3.64	2.01	5.91E-01	4.78E-01		-8.43E+00	8.63E-03		-2.69E-01	8.23E-01		-7.51E+00	7.33E-02		1.92E+00	1.94E-12	Up	1.07E+00	1.32E-03		Unigene51927_All//gi|104294986|gb|ABF72002.1|//1.00E-78//U-box domain-containing protein [Musa acuminata]	Unigene51927_All//2.00E-22//AT1G20780| SAUL1 (SENESCENCE-ASSOCIATED E3 UBIQUITIN LIGASE 1); ubiquitin-protein ligase	Unigene51927_All//0.00E+00//TC144583				nr -
Unigene51928_All	464	2.71	0.22	3.21	0.43	1.34	0.39	2.28	2.34	1.72	-3.63E+00	1.99E-05	Down	2.48E-01	6.34E-01		1.64E+00	1.06E-01		-1.41E-01	9.34E-01		4.00E-02	9.73E-01		-4.08E-01	4.85E-01		Unigene51928_All//gi|47824985|gb|AAT38758.1|//4.00E-26//Putative gag-pol polyprotein, identical [Solanum demissum]						nr +
Unigene51929_All	829	0.38	0.61	0.26	0.18	0.12	0.11	3.52	17.19	33.64	6.91E-01	4.99E-01		-5.60E-01	6.63E-01		-5.33E-01	7.84E-01		-7.26E-01	7.15E-01		2.29E+00	1.36E-42	Up	3.26E+00	5.51E-123	Up			Unigene51929_All//3.00E-13//TC151488				
Unigene5193_All	866	1.81	2.05	2.58	2.24	3.54	2.56	3.08	2.17	0.78	1.76E-01	7.07E-01		5.11E-01	2.54E-01		6.58E-01	6.54E-02		1.88E-01	6.76E-01		-5.02E-01	1.54E-01		-1.98E+00	1.60E-07	Down	Unigene5193_All//gi|18379062|ref|NP_563677.1|//1.00E-92//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana]	Unigene5193_All//5.00E-94//AT1G03150| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene5193_All//0.00E+00//gi|109867426|gb|DW496402.1|DW496402				nr -
Unigene51930_All	422	2.48	0.00	0.00	5.90	7.10	4.82	0.40	0.50	0.19	-1.13E+01	3.80E-06	Down	-1.13E+01	9.32E-06	Down	2.66E-01	5.31E-01		-2.93E-01	5.03E-01		3.05E-01	8.36E-01		-1.09E+00	5.52E-01		Unigene51930_All//gi|224069338|ref|XP_002302959.1|//1.00E-23//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222844685|gb|EEE82232.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene51930_All//9.00E-09//AT3G44630| disease resistance protein RPP1-WsB-like (TIR-NBS-LRR class), putative	Unigene51930_All//6.00E-62//gi|48818621|gb|CO119934.1|CO119934				nr -
Unigene51931_All	1150	0.09	0.44	0.14	0.26	0.24	0.08	1.25	2.33	3.33	2.28E+00	6.23E-02		6.10E-01	7.48E-01		-1.18E-01	9.00E-01		-1.73E+00	2.89E-01		8.96E-01	9.32E-03		1.41E+00	9.50E-07	Up	Unigene51931_All//gi|224117250|ref|XP_002317519.1|//9.00E-43//nbs-lrr resistance protein [Populus trichocarpa] >gi|222860584|gb|EEE98131.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene51931_All//5.00E-37//AT1G61180| disease resistance protein (CC-NBS-LRR class), putative	Unigene51931_All//6.00E-120//DR463606		ko04626|Plant-pathogen interaction		nr +
Unigene51934_All	290	49.80	0.35	6.24	5.67	0.71	0.47	0.00	0.00	0.00	-7.16E+00	3.74E-80	Down	-3.00E+00	8.02E-46	Down	-2.99E+00	3.56E-07	Down	-3.60E+00	2.61E-07	Down	null	null		null	null				Unigene51934_All//9.00E-11//TC146782				
Unigene51937_All	219	113.00	207.77	125.71	348.70	522.35	1570.41	141.90	63.36	212.11	8.79E-01	7.95E-27		1.54E-01	1.96E-01		5.83E-01	7.16E-39		2.17E+00	0.00E+00	Up	-1.16E+00	1.42E-35	Down	5.80E-01	4.59E-17		Unigene51937_All//gi|164668308|gb|ABK60195.2|//2.00E-36//PIP2 protein [Gossypium hirsutum]	Unigene51937_All//1.00E-29//AT3G53420| PIP2A (PLASMA MEMBRANE INTRINSIC PROTEIN 2A); water channel	Unigene51937_All//1.00E-120//gi|13352184|gb|BG442532.1|BG442532				nr -
Unigene51938_All	889	5.65	12.43	6.17	0.34	0.12	0.71	0.00	0.00	0.13	1.14E+00	1.93E-10	Up	1.27E-01	6.30E-01		-1.53E+00	2.98E-01		1.08E+00	2.69E-01		null	null		7.07E+00	2.43E-01		Unigene51938_All//gi|297811939|ref|XP_002873853.1|//3.00E-60//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319690|gb|EFH50112.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene51938_All//5.00E-55//AT5G17780| hydrolase, alpha/beta fold family protein	Unigene51938_All//1.00E-27//CO069510				nr -
Unigene51939_All	1223	0.86	0.46	0.44	0.86	0.28	0.55	17.80	8.48	5.83	-9.09E-01	1.75E-01		-9.75E-01	1.67E-01		-1.60E+00	1.49E-02		-6.27E-01	3.81E-01		-1.07E+00	3.98E-22	Down	-1.61E+00	4.65E-42	Down	Unigene51939_All//gi|18409339|ref|NP_566951.1|//1.00E-110//YLS2; strictosidine synthase [Arabidopsis thaliana] >gi|18087629|gb|AAL58944.1|AF462858_1 AT3g51430/F26O13_70 [Arabidopsis thaliana] >gi|13122282|dbj|BAB32882.1| strictosidine synthase-like protein [Arabidopsis thaliana] >gi|18086443|gb|AAL57676.1| AT3g51430/F26O13_70 [Arabidopsis thaliana] >gi|21592926|gb|AAM64876.1| mucin-like protein [Arabidopsis thaliana] >gi|38564288|gb|AAR23723.1| At3g51430 [Arabidopsis thaliana]	Unigene51939_All//9.00E-112//AT3G51430| YLS2; strictosidine synthase	Unigene51939_All//2.00E-36//gi|164253905|gb|EV488177.1|EV488177		ko00901|Indole alkaloid biosynthesis		nr -
Unigene51940_All	1335	0.00	0.61	0.56	0.22	0.46	0.88	1.65	1.97	25.28	9.25E+00	9.37E-05	Up	9.13E+00	3.27E-04	Up	1.05E+00	2.99E-01		1.97E+00	4.50E-03		2.60E-01	4.98E-01		3.94E+00	2.12E-174	Up	Unigene51940_All//gi|297796379|ref|XP_002866074.1|//1.00E-101//MAPKKK15 [Arabidopsis lyrata subsp. lyrata] >gi|297311909|gb|EFH42333.1| MAPKKK15 [Arabidopsis lyrata subsp. lyrata]	Unigene51940_All//1.00E-102//AT5G55090| MAPKKK15; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr +
Unigene51947_All	585	1.25	1.73	2.28	0.00	1.24	0.15	0.72	1.43	0.61	4.68E-01	4.89E-01		8.62E-01	1.54E-01		1.03E+01	1.89E-04	Up	7.27E+00	4.75E-01		9.83E-01	1.58E-01		-2.38E-01	7.88E-01									
Unigene51948_All	477	2.63	13.92	22.55	4.80	21.44	13.26	0.09	0.00	0.17	2.40E+00	1.88E-17	Up	3.10E+00	1.57E-35	Up	2.16E+00	7.16E-27	Up	1.46E+00	2.25E-09	Up	-6.47E+00	6.56E-01		9.15E-01	7.49E-01		Unigene51948_All//gi|1483232|emb|CAA67969.1|//1.00E-40//AMDS3 protein [Betula pendula]	Unigene51948_All//3.00E-39//AT5G60910| AGL8 (agamous-like 8); transcription factor	Unigene51948_All//9.00E-46//TC143583	MADS			nr +
Unigene51949_All	416	0.38	1.95	0.00	3.11	0.99	0.54	0.71	1.11	0.67	2.37E+00	1.01E-02		-8.56E+00	2.44E-01		-1.65E+00	4.40E-03		-2.52E+00	2.43E-04	Down	6.36E-01	5.36E-01		-8.56E-02	9.52E-01									
Unigene5195_All	1599	2.03	2.38	1.67	4.70	4.65	4.58	8.04	2.56	4.56	2.28E-01	4.89E-01		-2.85E-01	4.36E-01		-1.62E-02	9.53E-01		-4.00E-02	8.79E-01		-1.65E+00	3.08E-25	Down	-8.18E-01	3.91E-09		Unigene5195_All//gi|297838617|ref|XP_002887190.1|//1.00E-151//proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333031|gb|EFH63449.1| proton-dependent oligopeptide transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5195_All//2.00E-144//AT1G68570| proton-dependent oligopeptide transport (POT) family protein					nr +
Unigene51952_All	1613	0.00	0.09	0.20	0.25	0.70	0.84	0.58	0.98	4.15	6.56E+00	2.35E-01		7.63E+00	4.51E-02		1.51E+00	2.36E-02		1.77E+00	4.50E-03		7.72E-01	1.02E-01		2.85E+00	2.15E-26	Up	Unigene51952_All//gi|18642681|gb|AAK02020.2|AC074283_1/2.00E-122//Putative gag-pol polyprotein [Oryza sativa]		Unigene51952_All//8.00E-46//TC147807				nr -
Unigene51953_All	304	9.98	5.83	6.66	19.17	13.48	18.42	84.42	49.49	40.36	-7.75E-01	2.99E-02		-5.85E-01	1.24E-01		-5.08E-01	3.24E-02		-5.76E-02	8.38E-01		-7.70E-01	3.01E-15		-1.06E+00	1.81E-26	Down			Unigene51953_All//2.00E-166//TC154941				
Unigene51955_All	390	5.23	7.15	16.79	2.55	5.03	3.94	21.03	20.04	11.85	4.50E-01	2.34E-01		1.68E+00	1.06E-10	Up	9.78E-01	3.42E-02		6.24E-01	2.70E-01		-6.96E-02	7.30E-01		-8.28E-01	2.93E-06				Unigene51955_All//5.00E-47//TC140057				
Unigene51956_All	669	2.19	3.56	0.96	10.42	7.67	4.86	0.82	1.81	0.30	7.01E-01	8.95E-02		-1.20E+00	4.21E-02		-4.43E-01	4.12E-02		-1.10E+00	6.17E-07	Down	1.14E+00	4.07E-02		-1.46E+00	9.76E-02									
Unigene51958_All	341	3.84	0.74	0.47	1.17	1.82	0.93	1.49	0.86	0.23	-2.37E+00	5.60E-04	Down	-3.03E+00	1.24E-04	Down	6.37E-01	5.49E-01		-3.34E-01	7.56E-01		-7.94E-01	4.02E-01		-2.67E+00	1.37E-02		Unigene51958_All//gi|297851420|ref|XP_002893591.1|//3.00E-24//At1g23470 [Arabidopsis lyrata subsp. lyrata] >gi|297339433|gb|EFH69850.1| At1g23470 [Arabidopsis lyrata subsp. lyrata]	Unigene51958_All//3.00E-25//AT1G23465| signal peptidase-related	Unigene51958_All//1.00E-59//BE054665		ko03060|Protein export		nr -
Unigene51963_All	624	0.42	0.49	0.43	1.20	0.72	1.01	1.96	8.51	1.09	2.17E-01	8.64E-01		2.56E-02	1.00E+00		-7.39E-01	3.57E-01		-2.41E-01	7.56E-01		2.11E+00	7.60E-15	Up	-8.56E-01	1.02E-01				Unigene51963_All//6.00E-66//ES813961				
Unigene51964_All	733	0.00	0.55	0.00	1.56	0.89	3.08	0.58	1.65	9.08	9.11E+00	1.36E-02		null	null		-8.08E-01	1.92E-01		9.79E-01	2.34E-02		1.52E+00	8.16E-03		3.98E+00	4.89E-35	Up								
Unigene51965_All	561	856.44	222.10	408.63	576.90	344.78	234.03	162.94	123.00	109.36	-1.95E+00	0.00E+00	Down	-1.07E+00	0.00E+00	Down	-7.43E-01	3.26E-173		-1.30E+00	0.00E+00	Down	-4.06E-01	5.35E-17		-5.75E-01	2.28E-32		Unigene51965_All//gi|75756039|gb|AB257072.1|//1.00E-22//T0109-12 [Taraxacum officinale]	Unigene51965_All//1.00E-13//AT1G69760| unknown protein	Unigene51965_All//0.00E+00//gi|21100738|gb|BQ413051.1|BQ413051				nr +
Unigene51968_All	384	11.04	188.03	156.01	6.62	8.97	11.76	0.11	0.44	0.10	4.09E+00	0.00E+00	Up	3.82E+00	1.64E-237	Up	4.39E-01	2.12E-01		8.30E-01	3.39E-03		1.98E+00	3.79E-01		-8.64E-02	9.71E-01		Unigene51968_All//gi|49615303|gb|AAT66913.1|//4.00E-11//dehydration-induced protein RD22-like protein 2 [Gossypium arboreum]		Unigene51968_All//1.00E-139//gi|78351384|gb|DT571658.1|DT571658				nr +
Unigene51969_All	1466	0.00	0.00	0.00	0.14	0.16	0.00	4.73	11.72	22.07	null	null		null	null		2.75E-01	8.95E-01		-7.09E+00	1.33E-01		1.31E+00	6.80E-24	Up	2.22E+00	3.17E-94	Up	Unigene51969_All//gi|13161397|dbj|BAB33033.1|//1.00E-158//CPRD2 [Vigna unguiculata]	Unigene51969_All//2.00E-130//AT1G30700| FAD-binding domain-containing protein	Unigene51969_All//0.00E+00//TC170571		ko00620|Pyruvate metabolism//ko00908|Zeatin biosynthesis		nr +
Unigene51971_All	1442	0.80	0.00	0.59	0.35	0.19	0.38	12.20	3.45	0.41	-9.64E+00	9.91E-07	Down	-4.34E-01	5.09E-01		-8.55E-01	4.07E-01		1.21E-01	9.21E-01		-1.82E+00	2.89E-39	Down	-4.88E+00	6.96E-107	Down	Unigene51971_All//gi|297800598|ref|XP_002868183.1|//4.00E-83//monooxygenase [Arabidopsis lyrata subsp. lyrata] >gi|297314019|gb|EFH44442.1| monooxygenase [Arabidopsis lyrata subsp. lyrata]	Unigene51971_All//3.00E-82//AT4G15760| MO1 (MONOOXYGENASE 1); electron carrier/ oxidoreductase	Unigene51971_All//0.00E+00//TC131992		ko00906|Carotenoid biosynthesis//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +

Unigene51972_All	896	0.00	0.11	0.12	14.84	0.38	0.30	1.93	0.75	9.74	6.82E+00	3.86E-01		6.89E+00	3.97E-01		-5.27E+00	1.03E-86	Down	-5.62E+00	5.45E-75	Down	-1.37E+00	2.67E-03		2.33E+00	1.71E-27	Up	Unigene51972_All//gi|38016023|gb|AB07518.1|/1.00E-52//At1g12030 [Arabidopsis thaliana]	Unigene51972_All//3.00E-48//AT1G12030| unknown protein	Unigene51972_All//0.00E+00//TC157088				nr +
Unigene51973_All	460	0.00	3.08	0.00	8.45	13.70	35.35	0.18	0.00	0.00	1.16E+01	4.06E-08	Up	null	null		6.98E-01	1.98E-03		2.07E+00	3.47E-37	Up	-7.52E+00	4.02E-01		-7.52E+00	3.58E-01		Unigene51973_All//gi|225470869|ref|XP_002269732.1|//3.00E-24//PREDICTED: (-)-a-terpineol synthase [Vitis vinifera]	Unigene51973_All//2.00E-17//AT4G16740| ATTPS03; (E)-beta-ocimene synthase/ myrcene synthase			ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0016829	nr -
Unigene51977_All	337	0.78	3.91	3.00	1.92	2.86	3.75	1.51	1.49	1.54	2.33E+00	6.54E-04	Up	1.95E+00	1.37E-02		5.74E-01	4.52E-01		9.66E-01	1.22E-01		-1.66E-02	1.02E+00		2.97E-02	9.70E-01				Unigene51977_All//1.00E-164//TC150446					
Unigene51978_All	343	24.10	75.49	32.76	34.57	28.21	45.03	37.35	65.07	37.63	1.65E+00	1.14E-40	Up	4.43E-01	1.31E-02		-2.93E-01	8.03E-02		3.82E-01	7.73E-03		8.01E-01	3.18E-14		1.09E-02	9.66E-01		Unigene51978_All//gi|297841113|ref|XP_002888438.1|/4.00E-17//Pre-mRNA-splicing factor SLU7-A [Arabidopsis lyrata subsp. lyrata] >gi|297334279|gb|EFH64697.1| Pre-mRNA-splicing factor SLU7-A [Arabidopsis lyrata subsp. lyrata]	Unigene51978_All//2.00E-18//AT1G65660| SMP1 (SWELLMAP 1); nucleic acid binding / single-stranded RNA binding			ko03040|Spliceosome	GO:0003723//GO:0006396//GO:0008283//GO:0046914	nr -
Unigene5198_All	883	0.06	1.49	1.93	6.54	3.82	0.10	0.24	0.00	1.71	4.65E+00	1.91E-06	Up	5.02E+00	3.41E-08	Up	-7.76E-01	7.28E-04		-6.00E+00	2.32E-33	Down	-7.90E+00	7.43E-02		2.84E+00	1.69E-06	Up	Unigene5198_All//gi|224081419|ref|XP_002306403.1|//2.00E-14//predicted protein [Populus trichocarpa] >gi|222855852|gb|EEE93399.1| predicted protein [Populus trichocarpa]		Unigene5198_All//0.00E+00//TC175417				nr +
Unigene51981_All	521	1.61	0.78	0.00	0.57	0.26	0.17	1.87	5.94	1.38	-1.05E+00	1.74E-01		-1.07E+01	1.19E-04	Down	-1.12E+00	4.24E-01		-1.73E+00	2.89E-01		1.67E+00	9.84E-07	Up	-4.39E-01	4.73E-01										
Unigene51982_All	918	0.00	0.00	0.00	0.00	0.00	0.00	2.07	6.15	1.61	null	null		null	null		null	null		null	null		1.57E+00	9.79E-11	Up	-3.68E-01	3.79E-01		Unigene51982_All//gi|110816488|sp|Q3BAT2.1|CY391_PHAAO//8.00E-08//RecName: Full=Uncharacterized protein 08F91		Unigene51982_All//2.00E-42//TC164844			GO:0009536	nr -
Unigene51983_All	1477	0.00	0.00	0.00	0.07	0.05	0.00	60.00	8.66	0.76	null	null		null	null		-5.35E-01	8.16E-01		-6.08E+00	3.99E-01		-2.79E+00	0.00E+00	Down	-6.31E+00	0.00E+00	Down	Unigene51983_All//gi|225425912|ref|XP_002267341.1|/1.00E-106//PREDICTED: similar to F21J9.9 [Vitis vinifera]	Unigene51983_All//1.00E-95//AT1G24430| transferase/ transferase, transferring acyl groups other than amino-acyl groups			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016740	nr +
Unigene51985_All	322	4.55	0.94	0.33	2.94	1.93	3.79	0.26	0.00	0.12	-2.27E+00	3.39E-04	Down	-3.78E+00	5.00E-06	Down	-6.11E-01	3.90E-01		3.66E-01	6.03E-01		-8.04E+00	4.02E-01		-1.09E+00	6.76E-01				Unigene51985_All//1.00E-111//TC139818					
Unigene51986_All	568	1.29	0.98	1.31	2.19	1.39	0.32	1.71	1.03	0.70	-3.94E-01	6.11E-01		2.54E-02	9.95E-01		-6.53E-01	2.80E-01		-2.79E+00	1.35E-04	Down	-7.33E-01	2.48E-01		-1.29E+00	3.62E-02		Unigene51986_All//gi|297795789|ref|XP_002865779.1|//8.00E-37//nucleotide binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297311614|gb|EFH42038.1| nucleotide binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene51986_All//2.00E-31//AT5G50230| nucleotide binding	Unigene51986_All//2.00E-65//TC164507			GO:0004683//GO:0019897//GO:0032501	nr +
Unigene5199_All	624	2.10	28.83	38.83	28.82	11.98	7.38	1.08	0.33	0.06	3.78E+00	2.96E-72	Up	4.21E+00	4.12E-103	Up	-1.27E+00	8.07E-24	Down	-1.96E+00	2.32E-39	Down	-1.69E+00	4.19E-02		-4.09E+00	3.10E-04	Down	Unigene5199_All//gi|224081419|ref|XP_002306403.1|//2.00E-23//predicted protein [Populus trichocarpa] >gi|222855852|gb|EEE93399.1| predicted protein [Populus trichocarpa]		Unigene5199_All//0.00E+00//DW503238				nr -
Unigene51993_All	385	2.58	2.50	1.38	3.88	2.15	0.59	3.07	0.43	0.72	-4.63E-02	9.58E-01		-9.01E-01	2.22E-01		-8.55E-01	1.02E-01		-2.73E+00	2.66E-05	Down	-2.82E+00	4.41E-05	Down	-2.09E+00	5.32E-04	Down			Unigene51993_All//3.00E-150//DR457573					
Unigene51995_All	473	2.21	4.28	0.11	0.74	0.95	2.01	0.36	0.88	3.03	9.54E-01	3.64E-02		-4.30E+00	9.00E-05	Down	3.60E-01	8.06E-01		1.44E+00	5.71E-02		1.31E+00	2.34E-01		3.08E+00	1.21E-06	Up	Unigene51995_All//gi|297794533|ref|XP_002865151.1|//3.00E-14//low-level beta-amylase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297310986|gb|EFH41410.1| low-level beta-amylase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene51995_All//8.00E-15//AT5G47010| LBA1 (LOW-LEVEL BETA-AMYLASE 1); ATP binding / DNA binding / RNA helicase/ hydrolase	Unigene51995_All//2.00E-80//gi|78336498|gb|DT556772.1|DT556772				nr +
Unigene51996_All	275	2.28	6.63	12.97	267.55	197.22	415.17	65.80	160.34	70.99	1.54E+00	2.55E-03		2.51E+00	9.53E-10	Up	-4.40E-01	1.56E-15		6.34E-01	1.22E-40		1.28E+00	1.97E-58	Up	1.09E-01	3.80E-01		Unigene51996_All//gi|153805698|gb|ABS52574.1|//6.00E-36//nodulin family protein [Gossypium hirsutum]	Unigene51996_All//8.00E-22//AT4G08300| nodulin MtN21 family protein	Unigene51996_All//7.00E-147//TC142141			GO:0044464	nr +
Unigene52_All	4334	13.29	8.71	7.18	29.45	27.52	22.39	22.69	6.29	28.87	-6.10E-01	2.84E-18		-8.89E-01	2.53E-33		-9.75E-02	4.22E-02		-3.95E-01	1.42E-19		-1.85E+00	3.61E-221	Down	3.48E-01	7.18E-18		Unigene52_All//0.00E+00//AT4G39350| CESA2 (CELLULOSE SYNTHASE A2); cellulose synthase/ transferase, transferring glycosyl groups	Unigene52_All//0.00E+00//ES833524				nr +
Unigene52002_All	463	0.79	0.33	1.04	0.65	2.75	1.07	3.29	0.45	3.10	-1.27E+00	3.36E-01		3.88E-01	6.97E-01		2.09E+00	1.41E-03		7.33E-01	5.16E-01		-2.86E+00	1.98E-06	Down	-8.58E-02	8.55E-01				Unigene52002_All//1.00E-91//gi|78348879|gb|DT569153.1|DT569153					
Unigene52003_All	543	0.77	2.89	3.92	1.28	0.38	0.17	4.75	12.93	13.87	1.91E+00	1.06E-03		2.35E+00	1.17E-05	Up	-1.76E+00	4.11E-02		-2.95E+00	5.83E-03		1.45E+00	9.12E-12	Up	1.55E+00	3.96E-14	Up	Unigene52003_All//gi|240255717|ref|NP_192059.4|//4.00E-06//NGA4 (NGATHA4); transcription factor [Arabidopsis thaliana]	Unigene52003_All//2.00E-07//AT4G01500| NGA4 (NGATHA4); transcription factor	Unigene52003_All//0.00E+00//DT463967	AB13VP1			nr +
Unigene52004_All	988	0.00	0.21	0.38	0.15	0.35	0.00	1.37	2.45	3.71	7.68E+00	1.36E-01		8.56E+00	2.50E-02		1.20E+00	4.26E-01		-7.24E+00	2.33E-01		8.41E-01	2.12E-02		1.44E+00	1.17E-06	Up	Unigene52004_All//gi|18414504|ref|NP_568136.1|/3.00E-07//OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|186520008|ref|NP_001119168.1| OTU-like cysteine protease family protein [Arabidopsis thaliana] >gi|90093272|gb|ABD85149.1| At5g04250 [Arabidopsis thaliana]	Unigene52004_All//1.00E-08//AT5G04250| OTU-like cysteine protease family protein	Unigene52004_All//2.00E-63//ES791705			GO:0070011	nr +
Unigene52006_All	520	1.31	0.00	0.00	7.38	11.46	2.26	0.08	0.00	0.15	-1.04E+01	4.10E-04	Down	-1.04E+01	7.63E-04	Down	6.35E-01	6.88E-03		-1.71E+00	2.22E-07	Down	-6.35E+00	6.56E-01		9.14E-01	7.49E-01				Unigene52006_All//6.00E-07//DW238152					
Unigene52007_All	406	69.85	155.75	103.09	11.04	15.35	17.24	0.00	0.00	0.10	1.16E+00	7.71E-58	Up	5.62E-01	3.03E-11		4.75E-01	4.38E-02		6.43E-01	3.45E-03		null	null		6.62E+00	6.44E-01		Unigene52007_All//gi|133902318|gb|AB041847.1|//2.00E-07//photosystem II protein [Gossypium hirsutum]		Unigene52007_All//3.00E-67//gi|109864987|gb|DW493963.1|DW493963				nr -
Unigene52009_All	385	0.41	1.32	0.00	1.16	1.79	1.29	0.44	1.85	2.79	1.69E+00	1.34E-01		-8.67E+00	2.44E-01		6.19E-01	5.30E-01		1.48E-01	9.05E-01		2.07E+00	1.45E-02		2.67E+00	1.42E-04	Up									ESTscan -
Unigene5201_All	529	12.76	16.38	16.41	15.44	16.47	34.06	14.39	24.10	13.48	3.60E-01	7.37E-02		3.63E-01	8.50E-02		9.28E-02	7.09E-01		1.14E+00	1.12E-17	Up	7.44E-01	1.46E-07		-9.39E-02	6.34E-01		Unigene5201_All//gi|6688816|emb|CAB65283.1|//5.00E-13//Enod93 protein [Medicago sativa subsp. x varia]		Unigene5201_All//2.00E-155//gi|13352333|gb|BG442681.1|BG442681				nr +
Unigene52010_All	527	9.93	6.44	3.84	8.32	8.89	7.46	10.27	6.50	5.75	-6.24E-01	1.68E-02		-1.37E+00	1.42E-06	Down	9.54E-02	8.07E-01		-1.58E-01	6.24E-01		-6.59E-01	3.86E-03		-8.38E-01	1.67E-04		Unigene52010_All//gi|297739057|emb|CBI28546.3|//3.00E-06//unnamed protein product [Vitis vinifera]		Unigene52010_All//3.00E-175//DT049188				nr +
Unigene52017_All	292	1.08	2.26	6.75	2.56	2.59	2.32	0.72	0.72	1.09	1.07E+00	2.36E-01		2.65E+00	5.97E-06	Up	1.99E-02	1.00E+00		-1.41E-01	8.60E-01		-1.66E-02	1.02E+00		5.92E-01	6.13E-01		Unigene52017_All//gi|226530349|ref|NP_001149923.1|//1.00E-27//developmentally-regulated GTP-binding protein 2 [Zea mays] >gi|195635479|gb|ACG37208.1| developmentally-regulated GTP-binding protein 2 [Zea mays]	Unigene52017_All//5.00E-29//AT1G72660| developmentally regulated GTP-binding protein, putative	Unigene52017_All//2.00E-107//C0105355			GO:0001883//GO:0017111//GO:0031410//GO:0032561	nr -
Unigene5202_All	851	0.43	2.20	1.06	3.98	1.50	0.85	28.67	47.54	23.41	2.36E+00	2.61E-05	Up	1.31E+00	9.77E-02		-1.41E+00	1.07E-05	Down	-2.23E+00	4.16E-09	Down	7.30E-01	1.68E-21		-2.93E-01	2.69E-03		Unigene5202_All//gi|297830982|ref|XP_002883373.1|//7.00E-48//protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329213|gb|EFH59632.1| protease inhibitor/seed storage/lipid transfer protein family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5202_All//5.00E-32//AT3G22620| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene5202_All//0.00E+00//gi|78345262|gb|DT565536.1|DT565536		ko03040|Spliceosome//ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene52020_All	423	68.52	77.74	71.25	23.08	29.47	26.27	121.04	69.46	28.35	1.82E-01	6.77E-02		5.63E-02	6.10E-01		3.53E-01	2.76E-02		1.86E-01	3.47E-01		-8.01E-01	1.27E-31		-2.09E+00	6.51E-140	Down			Unigene52020_All//4.00E-106//TC134561					
Unigene52021_All	226	106.26	76.68	61.97	75.38	72.53	84.93	42.65	37.17	21.15	-4.71E-01	2.25E-05		-7.78E-01	1.89E-11		-5.57E-02	7.57E-01		1.72E-01	2.32E-01		-1.99E-01	2.81E-01		-1.01E+00	9.88E-10	Down			Unigene52021_All//1.00E-98//TC160112					
Unigene52022_All	1257	0.17	1.29	0.08	1.70	4.25	7.37	0.20	0.17	0.19	2.95E+00	9.24E-06	Up	-9.75E-01	6.20E-01		1.32E+00	2.23E-07	Up	2.11E+00	5.81E-22	Up	-2.79E-01	8.28E-01		-8.54E-02	9.56E-01		Unigene52022_All//gi|115468542|ref|NP_001057870.1|//1.00E-95//Os06g0560700 [Oryza sativa Japonica Group] >gi|113595910|dbj|BAF19784.1| Os06g0560700 [Oryza sativa Japonica Group]	Unigene52022_All//1.00E-64//AT1G29670| GDSL-motif lipase/hydrolase family protein				GO:0005576//GO:0009536//GO:0030312	nr +
Unigene52023_All	586	0.00	0.00	0.36	3.49	3.47	0.85	0.94	0.93	0.34	null	null		8.51E+00	1.41E-01		-7.60E-03	9.72E-01		-2.04E+00	3.45E-05	Down	-1.67E-02	1.02E+00		-1.46E+00	9.76E-02		Unigene52023_All//gi|13605829|gb|AAK32900.1|AF367313_1/4.00E-28//AT5g04550/T32M21_140 [Arabidopsis thaliana]	Unigene52023_All//1.00E-32//AT5G51670| unknown protein				GO:0043231	nr -
Unigene52024_All	1063	0.30	0.52	0.10	0.00	0.06	0.76	44.83	101.17	199.68	8.28E-01	3.81E-01		-1.56E+00	3.30E-01		6.02E+00	6.08E-01		9.58E+00	6.95E-05	Up	1.17E+00	7.23E-123	Up	2.16E+00	0.00E+00	Up	Unigene52024_All//gi|300680026|gb|ADK27717.1|//1.00E-161//GH3 [Dimocarpus longan]	Unigene52024_All//6.00E-159//AT2G14960| GH3.1	Unigene52024_All//0.00E+00//TC141106				nr +
Unigene52028_All	533	0.00	0.29	0.00	0.75	0.45	0.34	1.27	2.27	4.04	8.16E+00	2.35E-01		null	null		-7.26E-01	5.46E-01		-1.14E+00	3.79E-01		8.41E-01	1.33E-01		1.67E+00	4.57E-05	Up									
Unigene5203_All	1035	17.95	86.70	145.24	3.51	12.18	8.81	0.00	0.00	0.08	2.27E+00	5.81E-214	Up	3.02E+00	0.00E+00	Up	1.79E+00	4.37E-26	Up	1.33E+00	1.59E-11	Up	null	null		6.27E+00	4.03E-01		Unigene5203_All//gi|22330531|ref|NP_177122.2|/3.00E-96//SBH1 (SPHINGOID BASE HYDROXYLASE 1); catalytic/ sphingosine hydroxylase [Arabidopsis thaliana] >gi|179795535|gb|AAL50102.1| At1g69640/F24J1.22 [Arabidopsis thaliana] >gi|23505995|gb|AAN28857.1| At1g69640/F24J1.22 [Arabidopsis thaliana]	Unigene5203_All//3.00E-95//AT1G14290| SBH2 (SPHINGOID BASE HYDROXYLASE 2); catalytic/ sphingosine hydroxylase	Unigene5203_All//0.00E+00//gi|109849264|gb|DW478243.1|DW478243		ko00100|Steroid biosynthesis		nr -
Unigene52030_All	445	0.00	0.91	1.08	4.14	3.17	1.73	4.09	0.56	3.49	9.83E+00	1.36E-02		1.01E+01	7.47E-03		-3.85E-01	4.43E-01		-1.26E+00	9.32E-03		-2.86E+00	1.53E-07	Down	-2.27E-01	5.99E-01		Unigene52030_All//gi|225348977|gb|ACN87401.1|//5.00E-37//NBS-containing resistance-like protein [Corylus avellana]	Unigene52030_All//3.00E-20//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene52030_All//2.00E-09//TC143926		ko04626|Plant-pathogen interaction		nr +
Unigene52032_All	1708	0.06	0.00	0.00	0.03	0.04	0.00	4.41	6.09	10.24	-5.94E+00	3.71E-01		-5.94E+00	3.92E-01		4.65E-01	9.57E-01		-4.87E+00	6.34E-01		4.68E-01	3.21E-03		1.22E+00	2.64E-22	Up	Unigene52032_All//gi|297835372|ref|XP_002885568.1|//1.00E-167//mate efflux family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331408|gb|EFH61827.1| mate efflux family protein [Arabidopsis lyrata subsp. lyrata]	Unigene52032_All//1.00E-152//AT3G23550| MATE efflux family protein	Unigene52032_All//5.00E-35//gi|48820486|gb|CO121799.1|CO121799			GO:0015291//GO:0015893//GO:0044464	nr -
Unigene52033_All	491	0.85	1.34	0.00	0.41	0.35	1.47	0.52	0.77	4.22	6.54E-01	4.48E-01		-9.74E+00	1.56E-02		-2.11E-01	8.58E-01		1.86E+00	4.71E-02		5.68E-01	6.37E-01		3.03E+00	3.73E-09	Up			Unigene52033_All//0.00E+00//DT464347					
Unigene52034_All	423	0.00	0.00	0.00	0.00	0.90	0.64	1.80	1.98	5.18	null	null		null	null		9.81E+00	1.96E-02		9.32E+00	7.02E-02		1.35E-01	8.42E-01		1.53E+00	1.25E-04	Up			Unigene52034_All//2.00E-172//DW495642					
Unigene52035_All	313	45.13	78.19	135.08	17.03	25.96	48.77	15.13	28.44	61.60	7.93E-01	1.56E-12		1.58E+00	1.19E-60	Up	6.09E-01	1.78E-03		1.52E+00	5.03E-23	Up	9.11E-01	1.82E-07		2.03E+00	2.65E-50	Up			Unigene52035_All//4.00E-133//gi|21100584|gb|BQ412897.1|BQ412897					
Unigene52039_All	466	0.00	0.00	0.00	0.75	0.30	4.56	0.54	7.35	5.64	null	null		null	null		-1.34E+00	3.08E-01		2.61E+00	8.89E-07	Up	3.76E+00	3.07E-17	Up	3.37E+00	1.52E-12	Up	Unigene52039_All//gi|6899646|gb|AAF31023.1|AC012189_5//2.00E-19//EST gb|AB015130 comes from this gene [Arabidopsis thaliana]	Unigene52039_All//5.00E-22//AT2G01300| unknown protein	Unigene52039_All//0.00E+00//gi|31406748|gb|CD485783.1|CD485783			GO:0006952	nr -
Unigene5204_All	1380	1.44	1.36	1.43	9.42	8.16	7.79	8.73	7.78	3.64	-8.48E-02	8.46E-01		-1.31E-02	1.00E+00		-2.07E-01	2.22E-01		-2.75E-01	9.92E-02		-1.66E-01	3.20E-01		-1.26E+00	1.11E-16	Down	Unigene5204_All//gi|15238770|ref|NP_197325.1|//1.00E-108//MYR1 (MYb-related protein 1); transcription factor [Arabidopsis thaliana] >gi|42573403|ref|NP_974798.1| MYR1 (MYb-related protein 1); transcription factor [Arabidopsis thaliana] >gi|9758906|dbj|BAB09482.1| transfactor-like protein [Arabidopsis thaliana]	Unigene5204_All//4.00E-109//AT5G18240| MYR1 (MYb-related protein 1); transcription factor	Unigene5204_All//0.00E+00//TC147592	G2-like			nr +
Unigene52041_All	278	10.73	8.57	15.52	26.16	24.03	11.53	3.65	1.05	0.86	-3.25E-01	3.80E-01		5.32E-01	8.42E-02		-1.23E-01	6.10E-01		-1.18E+00	5.43E-08	Down	-1.79E+00	6.30E-03		-2.09E+00	1.52E-03				Unigene52041_All//3.00E-124//gi|78343300|gb|DT563574.1|DT563574					
Unigene52042_All	244	16.73	31.36	24.44	14.90	17.50	10.18	20.62	10.28	13.39	9.07E-01	2.04E-05		5.47E-01	3.15E-02		2.32E-01	5.04E-01		-5.50E-01	9.53E-02		-1.00E+00	3.05E-05	Down	-6.23E-01	6.84E-03				Unigene52042_All//1.00E-67//TC174209					

Unigene52043_All	974	0.00	0.21	0.71	0.77	0.74	0.56	1.30	0.69	1.88	7.70E+00	1.36E-01		9.47E+00	6.15E-04	Up	-4.74E-02	9.43E-01		-4.64E-01	6.06E-01		-9.24E-01	8.68E-02		5.31E-01	2.07E-01		Unigene52043_All//gi|183604839|gb|ACC64519.1|//2.00E-63//neuroblastoma-amplified gene [Nicotiana benthamiana]	Unigene52043_All//2.00E-63//AT5G24350| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Secretory pathway Sec39 (InterPro:IPR013224); Has 170 Blast hits to 130 proteins in 45 species: Archae - 0; Bacteria - 5; Metazoa - 90; Fungi - 13; Plants - 54; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink).	Unigene52043_All//6.00E-21//TC146530				nr -
Unigene52044_All	539	0.00	0.00	0.10	146.30	65.48	33.77	1.96	0.85	0.37	null	null		6.63E+00	6.35E-01		-1.16E+00	7.31E-90	Down	-2.12E+00	8.41E-189	Down	-1.20E+00	4.78E-02		-2.41E+00	3.46E-04	Down	Unigene52044_All//gi|56236488|gb|AY88585.1|//3.00E-40//knotted-like homeobox protein [Populus tomentosa]	Unigene52044_All//7.00E-11//AT4G08150| KNAT1 (KNOTTED-LIKE FROM ARABIDOPSIS THALIANA); transcription factor	Unigene52044_All//0.00E+00//C0086238	HB		GO:0003677//GO:0006350//GO:0010468//GO:0043231	nr -
Unigene52045_All	607	2.67	0.33	0.53	4.10	3.12	1.71	0.28	0.41	0.20	-3.00E+00	6.72E-06	Down	-2.34E+00	1.96E-04	Down	-3.95E-01	3.36E-01		-1.26E+00	1.84E-03		5.68E-01	6.74E-01		-5.01E-01	7.46E-01		Unigene52045_All//gi|13447449|gb|AAK21965.1|//2.00E-06//receptor protein kinase PERK1 [Brassica napus]					GO:0004672//GO:0016020	nr +
Unigene52046_All	534	0.20	2.75	0.90	0.19	0.64	0.68	0.48	2.19	2.09	3.81E+00	2.22E-06	Up	2.20E+00	9.14E-02		1.79E+00	2.57E-01		1.86E+00	2.19E-01		2.21E+00	5.41E-04	Up	2.14E+00	7.62E-04	Up	Unigene52046_All//gi|255559276|ref|XP_002520658.1|//1.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223540043|gb|EEF41620.1| conserved hypothetical protein [Ricinus communis]		Unigene52046_All//1.00E-08//TC135387			GO:0005488	nr -
Unigene52047_All	993	0.05	0.00	0.11	0.10	0.14	0.00	5.54	2.23	1.64	-5.72E+00	6.10E-01		1.03E+00	7.02E-01		4.68E-01	8.76E-01		-6.65E+00	3.99E-01		-1.31E+00	3.23E-08	Down	-1.75E+00	1.46E-12	Down	Unigene52047_All//gi|30686351|ref|NP_850622.1|//3.00E-84//SGP2; GTP binding [Arabidopsis thaliana] >gi|22316556|emb|CAD44270.1| monomeric G-protein [Arabidopsis thaliana]	Unigene52047_All//1.00E-85//AT3G21700| SGP2; GTP binding	Unigene52047_All//0.00E+00//TC173658			GO:0032561//GO:0035556//GO:0044464	nr +
Unigene5205_All	925	1.13	1.59	0.46	1.51	2.31	2.05	1.42	3.21	2.58	4.90E-01	3.70E-01		-1.30E+00	7.46E-02		6.14E-01	1.75E-01		4.44E-01	3.98E-01		1.18E+00	3.51E-04	Up	8.67E-01	1.49E-02		Unigene5205_All//gi|6056391|gb|AAF02855.1|AC009324_4//1.00E-17//Similar to retrotransposon proteins [Arabidopsis thaliana]	Unigene5205_All//2.00E-08//AT1G34070| unknown protein	Unigene5205_All//5.00E-12//C0082743				nr +
Unigene52050_All	1574	0.00	13.52	5.11	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.77E-122	Up	1.23E+01	5.30E-45	Up	null	null		null	null		null	null		null	null		Unigene52050_All//gi|30683024|ref|NP_565617.2|//5.00E-29//CYP71A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|222423266|dbj|BAH19609.1| AT2G26170 [Arabidopsis thaliana]	Unigene52050_All//5.00E-23//AT2G26170| CYP71A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00591|Linoleic acid metabolism	GO:0008152//GO:0016491//GO:0044464	nr -
Unigene52054_All	345	23.66	6.46	14.05	1.59	1.30	1.18	2.33	1.94	1.50	-1.87E+00	7.53E-16	Down	-7.52E-01	3.60E-04		-2.92E-01	7.69E-01		-4.31E-01	6.67E-01		-2.65E-01	7.04E-01		-6.33E-01	3.56E-01		Unigene52054_All//gi|20386366|gb|AAM21638.1|AF492022_1//1.00E-24//geranylgeranyl pyrophosphate synthase [Cistus creticus]	Unigene52054_All//3.00E-22//AT4G36810| GGPS1 (GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1); farnesyltransftransferase	Unigene52054_All//2.00E-169//EX169110		ko00900|Terpenoid backbone biosynthesis	GO:0004659//GO:0009536//GO:0016109//GO:0016628//GO:0043169	nr +
Unigene52055_All	601	0.35	0.00	0.00	7.21	3.72	2.71	2.81	0.35	0.40	-8.44E+00	1.22E-01		-8.44E+00	1.45E-01		-9.53E-01	4.43E-04		-1.41E+00	1.98E-06	Down	-3.02E+00	2.08E-07	Down	-2.82E+00	2.86E-07	Down	Unigene52055_All//gi|48525331|gb|AAT49967.1|//4.00E-38//At5g10150 [Arabidopsis thaliana] >gi|50198938|gb|AAT70472.1| At5g10150 [Arabidopsis thaliana]	Unigene52055_All//1.00E-30//AT5G10150| unknown protein				nr +
Unigene52056_All	518	0.20	0.20	0.21	0.00	0.00	0.00	2.69	2.74	9.54	-4.64E-02	9.88E-01		2.55E-02	9.99E-01		null	null		null	null		2.64E-02	9.91E-01		1.82E+00	7.66E-12	Up	Unigene52056_All//gi|18409123|ref|NP_564943.1|//1.00E-12//CLE12 (CLAVATA3/ESR-RELATED 12); protein binding / receptor binding [Arabidopsis thaliana] >gi|89111846|gb|ABD60695.1| AtLg68795 [Arabidopsis thaliana]	Unigene52056_All//8.00E-12//AT1G68795| CLE12 (CLAVATA3/ESR-RELATED 12); protein binding / receptor binding	Unigene52056_All//0.00E+00//D8454415				nr +
Unigene52057_All	567	0.83	0.18	0.94	2.81	2.43	1.91	2.91	0.15	0.42	-2.22E+00	7.76E-02		1.78E-01	8.45E-01		-2.11E-01	7.04E-01		-5.56E-01	3.10E-01		-4.30E+00	2.19E-09	Down	-2.79E+00	5.06E-07	Down	Unigene52057_All//gi|18401114|gb|AAC49942.1|//6.00E-42//ADP-glucose pyrophosphorylase large subunit [Solanum lycopersicum]	Unigene52057_All//3.00E-42//AT1G27680| APL2 (ADPGLC-PPASE LARGE SUBUNIT); glucose-1-phosphate adenylyltransferase	Unigene52057_All//2.00E-72//ES801523		ko00500|Starch and sucrose metabolism/ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0070566	nr +
Unigene52059_All	373	0.56	0.82	0.29	1.07	1.38	2.06	0.57	2.24	3.10	5.39E-01	6.71E-01		-9.75E-01	6.20E-01		3.74E-01	7.71E-01		9.46E-01	2.73E-01		1.98E+00	8.87E-03		2.45E+00	1.69E-04	Up	Unigene52059_All//gi|115451341|ref|NP_001049271.1|//3.00E-06//Os03g0197300 [Oryza sativa Japonica Group] >gi|113547742|dbj|BAF111185.1| Os03g0197300 [Oryza sativa Japonica Group]				ko03040|Spliceosome	GO:0003824//GO:0005488//GO:0009058//GO:0044237	nr +
Unigene52060_All	1172	0.00	0.04	0.00	0.21	0.09	0.46	2.71	5.74	6.83	5.43E+00	6.15E-01		null	null		-1.27E+00	4.24E-01		1.12E+00	3.05E-01		1.09E+00	1.58E-07	Up	1.34E+00	3.21E-12	Up	Unigene52060_All//gi|22773264|gb|AAN06870.1|//2.00E-19//Putative gag-pol polyprotein [Oryza sativa Japonica Group]	Unigene52060_All//1.00E-09//AT5G48050| unknown protein	Unigene52060_All//1.00E-13//ES843702				nr -
Unigene52061_All	910	11.56	23.27	6.44	0.11	0.38	0.55	0.19	0.00	0.09	1.01E+00	4.48E-16	Up	-8.44E-01	4.14E-06		1.79E+00	2.57E-01		2.32E+00	6.88E-02		-7.54E+00	1.34E-01		-1.08E+00	5.52E-01		Unigene52061_All//gi|224116396|ref|XP_002317287.1|//9.00E-07//predicted protein [Populus trichocarpa] >gi|222860352|gb|EEE97899.1| predicted protein [Populus trichocarpa]		Unigene52061_All//8.00E-88//DW506888				nr -
Unigene52062_All	342	0.61	1.19	1.56	2.04	1.01	1.19	0.00	0.61	3.61	9.54E-01	4.14E-01		1.35E+00	2.25E-01		-1.02E+00	2.25E-01		-7.79E-01	3.93E-01		9.26E+00	7.85E-02		1.18E+01	6.29E-09	Up							
Unigene52063_All	329	130.72	53.90	82.06	93.57	105.92	108.31	67.47	23.50	25.31	-1.28E+00	2.29E-46	Down	-6.72E-01	1.28E-15		1.79E-01	6.09E-02		2.11E-01	2.50E-02		-1.52E+00	2.44E-38	Down	-1.41E+00	1.61E-35	Down	Unigene52063_All//gi|17621130|gb|AAB39827.1|//1.00E-24//chaperonin-60 beta subunit [Solanum tuberosum]	Unigene52063_All//4.00E-151//gi|13349887|gb|BG440236.1|BG440236		ko03018|RNA degradation	GO:0005515//GO:0005576//GO:0005840//GO:0009526//GO:0009532//GO:0009814//GO:0016020//GO:0031981//GO:0032559//GO:0051084	nr -
Unigene52064_All	757	0.00	0.00	0.00	0.00	0.00	0.24	5.42	2.48	4.00	null	null		null	null		null	null		7.90E+00	1.94E-01		-1.12E+00	3.78E-05	Down	-4.38E-01	9.75E-02		Unigene52064_All//gi|115476172|ref|NP_001061682.1|//6.00E-57//Os08g0377500 [Oryza sativa Japonica Group] >gi|113623651|dbj|BAF23596.1| Os08g0377500 [Oryza sativa Japonica Group]	Unigene52064_All//1.00E-42//AT5G46060| unknown protein				GO:0044464	nr -
Unigene52065_All	447	1.76	0.79	0.48	3.68	2.62	2.12	2.36	0.37	0.18	-1.15E+00	1.53E-01		-1.88E+00	4.13E-02		-4.90E-01	3.41E-01		-7.94E-01	1.31E-01		-2.66E+00	2.25E-04	Down	-3.73E+00	6.13E-06	Down							
Unigene52066_All	313	3.68	3.56	1.36	3.82	2.75	3.90	1.89	0.00	0.51	-4.63E-02	9.53E-01		-1.43E+00	3.87E-02		-4.74E-01	4.58E-01		2.85E-02	9.62E-01		-1.09E+01	2.39E-04	Down	-1.89E+00	3.22E-02				Unigene52066_All//2.00E-160//TC176367				
Unigene52067_All	319	16.40	232.06	33.39	21.71	36.16	45.87	169.52	330.44	180.21	3.82E+00	4.38E-299	Up	1.03E+00	2.69E-08	Up	7.36E-01	2.76E-06		1.08E+00	2.84E-13	Up	9.63E-01	2.44E-87		8.82E-02	1.98E-01				Unigene52067_All//5.00E-136//TC138383				
Unigene52070_All	568	0.37	0.00	0.19	0.35	0.97	0.64	6.77	14.64	8.00	-8.53E+00	1.22E-01		-9.75E-01	6.20E-01		1.47E+00	1.77E-01		8.59E-01	5.42E-01		1.11E+00	1.88E-09	Up	2.39E-01	3.66E-01		Unigene52070_All//gi|90399211|emb|CAH68282.1|//6.00E-34//B0306F12.4 [Oryza sativa (indica cultivar-group)]	Unigene52070_All//23//AT3G48590| NF-YC1 (NUCLEAR FACTOR Y, SUBUNIT C1); DNA binding / transcription activator/ transcription factor		CCAAT		GO:0003677//GO:0043231	nr +
Unigene52071_All	819	9.39	3.71	8.13	0.79	1.30	0.33	0.15	0.00	0.15	-1.34E+00	1.63E-09	Down	-2.09E-01	3.92E-01		7.21E-01	3.14E-01		-1.26E+00	1.83E-01		-7.28E+00	2.35E-01		-8.64E-02	9.69E-01		Unigene52071_All//gi|224074167|ref|XP_002304283.1|//1.00E-116//formyltetrahydrofolate deformylase [Populus trichocarpa] >gi|222841715|gb|EEE79262.1| formyltetrahydrofolate deformylase [Populus trichocarpa]	Unigene52071_All//3.00E-102//AT4G17360| formyltetrahydrofolate deformylase/ hydroxymethyl-, formyl- and related transferase/ methyltransferase	Unigene52071_All//2.00E-69//gi|164309517|gb|ES804544.1|ES804544		ko00630|Glyoxylate and dicarboxylate metabolism//ko00670|One carbon pool by folate	GO:0006188//GO:0016741//GO:0016811	nr +
Unigene52072_All	1147	0.09	0.04	0.28	1.69	0.81	0.32	8.81	0.44	5.87	-1.05E+00	6.84E-01		1.61E+00	3.04E-01		-1.06E+00	1.59E-02		-2.43E+00	5.50E-06	Down	-4.33E+00	2.00E-55	Down	-5.86E-01	1.70E-04		Unigene52072_All//gi|224082982|ref|XP_002306917.1|//5.00E-60//SAUR family protein [Populus trichocarpa] >gi|222856366|gb|EEE93913.1| SAUR family protein [Populus trichocarpa]	Unigene52072_All//5.00E-53//AT1G75590| auxin-responsive family protein	Unigene52072_All//0.00E+00//DT460588			GO:0009725	nr +
Unigene52074_All	493	0.21	11.00	46.77	0.00	0.00	4.76	0.00	0.00	0.00	5.69E+00	8.65E-28	Up	7.78E+00	4.42E-126	Up	null	null		1.22E+01	4.75E-14	Up	null	null		null	null		Unigene52074_All//gi|403160|gb|AAA33866.1|//4.00E-70//ribulose 1,5-bisphosphate carboxylase small subunit [Malus x domestica x Pyrus communis]	Unigene52074_All//1.00E-62//AT5G38420| ribulose bisphosphate carboxylase small chain 2B / RuBisCO small subunit 2B (RBCS-2B) (ATS2B)	Unigene52074_All//2.00E-16//gi|80999856|gb|BM359110.1|BM359110		ko00710|Carbon fixation in photosynthetic organisms//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005488//GO:0009536//GO:0015977//GO:0016491//GO:0016831//GO:0043494	nr +
Unigene52075_All	436	0.72	0.00	0.73	5.37	1.11	1.76	1.26	1.05	0.37	-9.49E+00	3.65E-02		2.54E-02	1.00E+00		-2.28E+00	1.67E-07	Down	-1.61E+00	2.00E-04	Down	-2.58E-01	7.60E-01		-1.79E+00	5.06E-02								
Unigene52077_All	369	58.99	61.65	38.82	53.19	52.91	70.50	351.19	382.73	137.44	6.39E-02	6.24E-01		-6.04E-01	6.28E-07		-7.50E-03	9.55E-01		4.07E-01	1.04E-04		1.24E-01	2.07E-03		-1.35E+00	4.31E-190	Down	Unigene52077_All//gi|293332291|ref|NP_001170482.1|//9.00E-36//ascorbate peroxidase [Zea mays] >gi|225542587|gb|ACN91229.1| cytosolic ascorbate peroxidase [Gossypium hirsutum] >gi|226897525|gb|ACO90192.1| ascorbate peroxidase [Zea mays]	Unigene52077_All//1.00E-24//AT3G09640| APX2 (ASCORBATE PEROXIDASE 2); L-ascorbate peroxidase	Unigene52077_All//0.00E+00//gi|73851890|gb|DT460910.1|DT460910		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0004601//GO:0005506//GO:0006950//GO:0008152	nr +
Unigene52078_All	983	0.00	0.00	0.00	4.31	1.40	0.00	0.34	3.06	3.89	null	null		null	null		-1.62E+00	1.82E-08	Down	-1.21E+01	9.92E-27	Down	3.15E+00	3.55E-13	Up	3.50E+00	1.66E-18	Up			Unigene52078_All//1.00E-12//TC153836				
Unigene52079_All	692	0.53	0.51	0.92	2.74	2.29	1.50	0.67	0.91	3.28	-4.63E-02	9.82E-01		8.03E-01	3.88E-01		-2.57E-01	6.08E-01		-8.66E-01	7.01E-02		4.31E-01	6.32E-01		2.29E+00	1.45E-07	Up	Unigene52079_All//gi|297822435|ref|XP_002879100.1|//1.00E-09//dsRNA-binding protein 2 [Arabidopsis lyrata subsp. lyrata] >gi|297324939|gb|EFH55359.1| dsRNA-binding protein 2 [Arabidopsis lyrata subsp. lyrata]	Unigene52079_All//7.00E-11//AT2G28380| DRB2 (DSRNA-BINDING PROTEIN 2); double-stranded RNA binding	Unigene52079_All//2.00E-63//TC141484			GO:0003723//GO:0044424	nr -
Unigene5208_All	1546	9.34	9.77	7.82	15.82	11.60	12.44	19.44	9.38	8.97	6.44E-02	6.80E-01		-2.57E-01	1.15E-01		-4.47E-01	1.12E-05		-3.46E-01	1.59E-03		-1.05E+00	2.24E-29	Down	-1.12E+00	2.92E-33	Down	Unigene5208_All//gi|18402055|ref|NP_566621.1|//1.00E-110//clast3-related [Arabidopsis thaliana] >gi|89000905|gb|ABD59042.1| At3g18940 [Arabidopsis thaliana]	Unigene5208_All//9.00E-112//AT3G18940| clast3-related	Unigene5208_All//0.00E+00//TC154806				nr -
Unigene52080_All	438	27.00	63.51	55.07	39.81	44.18	55.89	93.54	111.26	88.41	1.23E+00	1.56E-28	Up	1.03E+00	4.55E-18	Up	1.51E-01	3.03E-01		4.90E-01	5.18E-06		2.50E-01	2.69E-04		-8.14E-02	3.43E-01				Unigene52080_All//5.00E-152//gi|164241948|gb|ES822599.1|ES822599				
Unigene52081_All	458	0.00	1.00	1.63	0.65	0.23	1.08	2.12	1.83	0.70	9.96E+00	7.43E-03		1.07E+01	3.27E-04	Up	-1.53E+00	2.98E-01		7.33E-01	5.16E-01		-2.18E-01	7.24E-01		-1.61E+00	1.12E-02								
Unigene52090_All	312	2.35	0.00	0.00	2.39	0.99	0.43	1.90	1.34	0.77	-1.12E+01	2.11E-04	Down	-1.12E+01	4.13E-04	Down	-1.27E+00	1.12E-01		-2.46E+00	1.02E-02		-5.02E-01	5.74E-01		-1.31E+00	1.15E-01								
Unigene52092_All	414	0.25	2.69	1.03	0.60	1.41	3.71	70.06	117.51	97.38	3.41E+00	1.24E-04	Up	2.03E+00	1.39E-01		1.23E+00	2.33E-01		2.62E+00	4.41E-05	Up	7.46E-01	1.15E-26		4.75E-01	1.13E-10								
Unigene52093_All	863	12.00	40.45	15.61	0.17	0.40	0.21	0.20	0.05	0.18	1.75E+00	1.43E-59	Up	3.79E-01	1.96E-02		1.20E+00	4.26E-01		2.73E-01	9.04E-01		-2.02E+00	3.67E-01		-8.57E-02	9.65E-01		Unigene52093_All//gi|297803484|ref|XP_002869626.1|//2.00E-18//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315462|gb|EFH45885.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene52093_All//3.00E-08//AT5G56860| GNC (GATA, nitrate-inducible, carbon metabolism-involved); transcription factor	Unigene52093_All//0.00E+00//TC132897	C2C2-GATA		GO:0005488//GO:0010033	nr -
Unigene52096_All	267	0.78	5.50	3.79	0.75	1.68	2.88	0.16	2.04	0.60	2.81E+00	4.57E-05	Up	2.27E+00	5.76E-03		1.17E+00	3.47E-01		1.95E+00	3.23E-02		3.68E+00	3.69E-03		1.91E+00	3.77E-01				Unigene52096_All//3.00E-07//ES810135				
Unigene52097_All	426	3.19	0.00	1.13	3.74	1.94	2.54	2.88	3.14	1.96	-1.16E+01	6.50E-08	Down	-1.51E+00	1.69E-02		-9.48E-01	5.80E-02		-5.56E-01	3.10E-01		1.25E-01	8.14E-01		-5.51E-01	3.01E-01		Unigene52097_All//gi|9838482|ref|NP_064095.1|//4.00E-25//orf105b [Beta vulgaris subsp. vulgaris] >gi|9087344|dbj|BAA99488.1| orf105b [Beta vulgaris subsp. vulgaris]		Unigene52097_All//0.00E+00//AW187640				nr +

Unigene52098_All	680	0.00	0.07	0.00	0.88	0.00	0.40	1.24	9.04	4.28	6.22E+00	6.15E-01		null	null		-9.78E+00	1.78E-04	Down	-1.14E+00	2.42E-01		2.86E+00	6.43E-24	Up	1.78E+00	4.19E-07	Up	Unigene52098_All//gi|225440392|ref|XP_002267559.1|//3.00E-62//PREDICTED: ripening-related protein-like [Vitis vinifera]	Unigene52098_All//2.00E-49//AT5G02230| haloacid dehalogenase-like hydrolase family protein	Unigene52098_All//2.00E-47//TC169722			GO:0003824	nr -
Unigene52099_All	460	0.00	0.22	0.12	1.52	0.90	1.28	0.55	3.18	1.30	7.78E+00	3.86E-01		6.86E+00	6.35E-01		-7.55E-01	3.69E-01		-2.48E-01	7.56E-01		2.53E+00	1.65E-05	Up	1.24E+00	1.39E-01					Unigene52099_All//5.00E-07//TC172479				
Unigene5210_All	635	72.34	25.14	37.65	116.42	119.03	133.78	203.28	85.04	125.79	-1.53E+00	1.61E-64	Down	-9.42E-01	2.44E-29		3.21E-02	6.91E-01		2.01E-01	3.88E-04		-1.26E+00	2.59E-164	Down	-6.92E-01	1.00E-62		Unigene5210_All//gi|71370259|gb|AAZ30377.1|//1.00E-104//PHB2 [Nicotiana benthamiana]	Unigene5210_All//1.00E-100//AT4G28810| ATPHB1 (PROHIBITIN 1)	Unigene5210_All//0.00E+00//TC153736				nr -
Unigene52102_All	1629	0.00	0.00	0.00	0.00	0.00	0.00	9.71	2.90	0.39	null	null		null	null		null	null		null	null		-1.74E+00	2.57E-33	Down	-4.63E+00	2.54E-93	Down	Unigene52102_All//gi|224148020|ref|XP_002336576.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222836229|gb|EEE74650.1| cytochrome P450 [Populus trichocarpa]	Unigene52102_All//5.00E-131//AT5G42650| AOS (ALLENE OXIDE SYNTHASE); allene oxide synthase/ hydro-lyase/ oxygen binding	Unigene52102_All//1.00E-81//DW514686		ko00592|alpha-Linolenic acid metabolism	GO:0005506//GO:0016491	nr +
Unigene52104_All	415	0.00	0.98	0.00	0.36	0.75	2.72	3.57	25.48	28.32	9.93E+00	1.36E-02		null	null		1.05E+00	5.31E-01		2.92E+00	3.03E-04	Up	2.84E+00	2.31E-40	Up	2.99E+00	4.10E-48	Up	Unigene52104_All//gi|215398158|gb|AC165328.1|//2.00E-53//scarecrow-like protein [Capsicum annuum]	Unigene52104_All//3.00E-40//AT5G48150| PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor	Unigene52104_All//1.00E-167//TC173319	GRAS		GO:0010468	nr -
Unigene52106_All	807	2.53	0.94	6.93	0.93	2.60	1.01	0.10	0.26	0.25	-1.42E+00	2.41E-03		1.45E+00	1.36E-07	Up	1.49E+00	9.31E-04	Up	1.22E-01	8.93E-01		1.31E+00	4.47E-01		1.24E+00	4.68E-01					Unigene52106_All//4.00E-18//TC142769				
Unigene52108_All	821	0.00	3.76	0.91	2.18	1.93	5.17	0.05	0.46	0.10	1.19E+01	1.38E-17	Up	9.83E+00	3.27E-04	Up	-1.79E-01	7.42E-01		1.24E+00	3.23E-05	Up	3.15E+00	3.41E-02		9.13E-01	7.49E-01		Unigene52108_All//gi|85068670|gb|AB369415.1|//2.00E-78//CYP71AH2 [Nicotiana tabacum]	Unigene52108_All//4.00E-59//AT3G26210| CYP71B23; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene52108_All//0.00E+00//TC137189		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0016491	nr +
Unigene52111_All	893	0.12	0.00	0.00	6.19	1.47	1.06	0.76	0.00	0.04	-6.87E+00	3.71E-01		-6.87E+00	3.92E-01		-2.08E+00	2.99E-15	Down	-2.54E+00	6.34E-17	Down	-9.57E+00	6.34E-05	Down	-4.09E+00	3.10E-04	Down	Unigene52111_All//gi|224141937|ref|XP_002324317.1|//2.00E-38//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222865751|gb|EEF02882.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene52111_All//4.00E-25//AT5G25190| ethylene-responsive element-binding protein, putative	Unigene52111_All//0.00E+00//DW498682	AP2-EREBP		GO:0000160//GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043731	nr -
Unigene52112_All	409	16.12	151.88	17.45	40.80	157.95	94.52	100.58	170.45	167.63	3.24E+00	1.59E-217	Up	1.14E-01	6.21E-01		1.95E+00	2.18E-149	Up	1.21E+00	5.09E-41	Up	7.61E-01	3.81E-39		7.37E-01	2.40E-37					Unigene52112_All//6.00E-65//DW520332				
Unigene52115_All	1301	0.12	0.00	0.00	0.00	0.19	0.35	5.52	4.14	12.71	-6.91E+00	2.15E-01		-6.91E+00	2.44E-01		7.53E+00	1.04E-01		8.44E+00	7.75E-03		-4.15E-01	3.70E-02		1.20E+00	9.56E-21	Up	Unigene52115_All//gi|224083434|ref|XP_002307025.1|//5.00E-58//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222856474|gb|EEE94021.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene52115_All//5.00E-21//AT1G61190| disease resistance protein (CC-NBS-LRR class), putative	Unigene52115_All//0.00E+00//TC179258		ko04626|Plant-pathogen interaction		nr -
Unigene52116_All	616	0.51	0.16	0.17	2.59	2.52	0.59	3.29	0.34	0.84	-1.63E+00	2.76E-01		-1.56E+00	3.30E-01		-4.08E-02	9.33E-01		-2.14E+00	2.07E-04	Down	-3.28E+00	2.01E-09	Down	-1.97E+00	6.60E-06	Down	Unigene52116_All//gi|18413990|ref|NP_567403.1|//3.00E-99//MEE55 (maternal effect embryo arrest 55) [Arabidopsis thaliana]	Unigene52116_All//2.00E-100//AT4G13345| MEE55 (maternal effect embryo arrest 55)				GO:0003006//GO:0044464	nr -
Unigene52118_All	610	0.17	0.00	0.52	1.55	0.79	2.15	2.56	0.75	2.09	-7.42E+00	3.71E-01		1.61E+00	3.04E-01		-9.73E-01	1.60E-01		4.69E-01	4.67E-01		-1.77E+00	4.93E-04	Down	-2.95E-01	5.44E-01		Unigene52118_All//gi|297851454|ref|XP_002893608.1|//5.00E-41//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297339450|gb|EFH69867.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene52118_All//5.00E-42//AT1G30240| binding					nr +
Unigene52121_All	424	0.99	1.31	5.40	2.23	1.46	1.70	0.00	0.00	0.00	4.13E-01	6.36E-01		2.45E+00	2.61E-06	Up	-6.11E-01	3.90E-01		-3.89E-01	6.28E-01		null	null		null	null		Unigene52121_All//gi|224077858|ref|XP_002305439.1|//2.00E-26//predicted protein [Populus trichocarpa] >gi|222848403|gb|EEE85950.1| predicted protein [Populus trichocarpa]	Unigene52121_All//8.00E-10//AT5G53670| unknown protein				GO:0005488//GO:0008152//GO:0009987//GO:0016787//GO:0031410//GO:0043231	nr +
Unigene52122_All	293	0.18	3.63	1.27	4.76	2.00	4.32	16.59	10.13	6.12	4.35E+00	3.95E-05	Up	2.83E+00	9.30E-02		-1.25E+00	2.07E-02		-1.41E-01	7.96E-01		-7.12E-01	3.30E-03		-1.44E+00	1.17E-08	Down				Unigene52122_All//1.00E-105//gi|164245147|gb|ES823947.1|ES823947				
Unigene52123_All	1337	0.00	0.00	0.00	0.00	0.00	0.00	9.99	10.69	2.98	null	null		null	null		null	null		null	null		9.74E-02	5.49E-01		-1.75E+00	3.23E-29	Down	Unigene52123_All//gi|224129122|ref|XP_002320506.1|//4.00E-97//f-box family protein [Populus trichocarpa] >gi|222861279|gb|EEE98821.1| f-box family protein [Populus trichocarpa]	Unigene52123_All//1.00E-70//AT3G07870| F-box family protein					nr -
Unigene52124_All	259	0.40	3.13	5.55	14.62	3.59	1.74	402.23	303.38	349.32	2.95E+00	3.28E-03		3.78E+00	5.81E-06	Up	-2.03E+00	3.12E-10	Down	-3.07E+00	3.39E-14	Down	-4.07E-01	2.32E-19		-2.04E-01	5.18E-06					Unigene52124_All//7.00E-113//gi|164291341|gb|ES799315.1|ES799315				
Unigene52125_All	269	0.39	4.71	1.39	2.41	1.54	1.01	0.63	0.62	2.07	3.60E+00	2.27E-05	Up	1.83E+00	2.13E-01		-6.48E-01	4.60E-01		-1.26E+00	1.83E-01		-1.66E-02	1.02E+00		1.72E+00	5.91E-02					Unigene52125_All//3.00E-07//TC132071				
Unigene52128_All	714	0.44	0.43	0.60	0.28	0.39	0.51	1.30	1.76	4.46	-4.63E-02	9.84E-01		4.40E-01	6.77E-01		4.67E-01	8.16E-01		8.58E-01	5.42E-01		4.31E-01	4.41E-01		1.78E+00	1.12E-07	Up								
Unigene5213_All	630	33.88	17.37	14.71	43.96	36.84	32.47	116.37	36.49	35.85	-9.64E-01	4.21E-15		-1.20E+00	1.76E-20	Down	-2.55E-01	1.21E-02		-4.37E-01	1.30E-05		-1.67E+00	2.52E-143	Down	-1.70E+00	1.10E-150	Down	Unigene5213_All//gi|2780194|emb|CAA05979.1|//2.00E-43//adenine nucleotide translocator [Lupinus albus]	Unigene5213_All//7.00E-44//AT3G08580| AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/ binding	Unigene5213_All//0.00E+00//TC137759				nr -
Unigene52130_All	478	3.94	1.06	1.11	2.61	3.31	1.70	0.97	0.09	0.92	-1.89E+00	2.73E-04	Down	-1.82E+00	7.00E-04	Down	3.47E-01	5.55E-01		-6.15E-01	3.33E-01		-3.48E+00	1.03E-02		-8.58E-02	9.34E-01		Unigene52130_All//gi|76262498|gb|AB441399.1|//8.00E-30//pherophorin-C1 protein precursor [Chlamydomonas reinhardtii]		Unigene52130_All//3.00E-95//BG440954				nr -
Unigene52133_All	837	1.56	1.27	0.95	0.83	1.48	0.54	4.29	6.64	1.95	-2.98E-01	5.95E-01		-7.12E-01	2.42E-01		8.30E-01	1.88E-01		-6.27E-01	4.76E-01		6.29E-01	5.19E-03		-1.14E+00	7.20E-05	Down	Unigene52133_All//gi|111146892|gb|AB807384.1|//8.00E-65//CMR1 [Phaseolus vulgaris]	Unigene52133_All//4.00E-50//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene52133_All//1.00E-178//NP831321		ko04626|Plant-pathogen interaction	GO:0000166//GO:0006952//GO:0009987	nr -
Unigene52134_All	326	2.25	1.24	1.31	2.75	2.43	0.28	2.59	0.90	1.47	-8.54E-01	3.05E-01		-7.82E-01	3.80E-01		-1.79E-01	8.15E-01		-3.31E+00	5.79E-04	Down	-1.53E+00	3.21E-02		-8.23E-01	2.07E-01									
Unigene52135_All	291	0.00	0.00	0.00	5.99	3.67	2.33	1.89	0.86	0.00	null	null		null	null		-7.08E-01	1.44E-01		-1.36E+00	6.97E-03		-1.13E+00	2.18E-01		-1.09E+01	2.80E-04	Down	Unigene52135_All//gi|297827517|ref|XP_002881641.1|//7.00E-34//RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327480|gb|EFH57900.1| RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene52135_All//4.00E-35//AT2G39280| RAB GTPase activator	Unigene52135_All//9.00E-122//AT730222			GO:0005099//GO:0032318//GO:0044464	nr +
Unigene52137_All	241	105.29	36.37	42.64	371.85	430.37	184.40	198.07	60.53	113.07	-1.53E+00	3.23E-36	Down	-1.30E+00	2.11E-27	Down	2.11E-01	1.05E-05		-1.01E+00	1.35E-71	Down	-1.71E+00	1.76E-96	Down	-8.09E-01	7.10E-31		Unigene52137_All//gi|224103789|ref|XP_002313194.1|//5.00E-24//tubulin alpha-5 chain [Populus trichocarpa] >gi|222849602|gb|EEE87149.1| tubulin alpha-5 chain [Populus trichocarpa]	Unigene52137_All//2.00E-25//AT1G50010| TUA2; structural constituent of cytoskeleton	Unigene52137_All//1.00E-101//EV490622		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043423	nr -
Unigene52138_All	477	2.52	1.49	1.23	111.32	73.92	72.43	2.48	2.63	0.50	-7.62E-01	2.13E-01		-1.04E+00	1.14E-01		-5.91E-01	3.89E-19		-6.20E-01	1.30E-18		8.29E-02	8.86E-01		-2.31E+00	2.04E-04	Down	Unigene52138_All//gi|73761687|gb|AB283343.1|//1.00E-48//ACC oxidase 2 [Gossypium hirsutum]	Unigene52138_All//9.00E-33//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene52138_All//0.00E+00//TC129655		ko00270|Cysteine and methionine metabolism	GO:0003006//GO:0006555//GO:0016641//GO:0019842//GO:0043169//GO:0050896	nr -
Unigene52139_All	400	14.39	20.27	16.51	10.21	22.99	24.05	23.25	44.41	57.57	4.94E-01	1.58E-02		1.98E-01	4.28E-01		1.17E+00	2.13E-10	Up	1.24E+00	6.38E-11	Up	9.33E-01	1.19E-14		1.31E+00	1.88E-32	Up	Unigene52139_All//gi|82734828|gb|AB889735.1|//6.00E-06//ERD15 [Capsicum annuum]		Unigene52139_All//3.00E-51//gi|13247751|gb|BF272137.2|BF272137				nr +
Unigene52141_All	573	2.10	2.12	5.67	1.83	3.97	0.63	0.00	0.44	0.14	1.52E-02	9.86E-01		1.43E+00	1.29E-04	Up	1.12E+00	7.78E-03		-1.53E+00	2.88E-02		8.77E+00	4.31E-02		7.12E+00	4.03E-01		Unigene52141_All//gi|255560651|ref|XP_002521339.1|//1.00E-05//conserved hypothetical protein [Ricinus communis] >gi|223539417|gb|EEF41007.1| conserved hypothetical protein [Ricinus communis]		Unigene52141_All//1.00E-171//TC134349				nr +
Unigene52142_All	449	1.17	1.35	2.25	6.66	4.99	6.84	1.41	0.37	0.00	2.17E-01	7.92E-01		9.51E-01	1.87E-01		-4.17E-01	2.62E-01		3.92E-02	9.36E-01		-1.92E+00	3.09E-02		-1.05E+01	7.10E-05	Down	Unigene52142_All//gi|18401331|ref|NP_565638.1|//3.00E-10//heat shock family protein [Arabidopsis thaliana] >gi|4557057|gb|AAD22497.1| expressed protein [Arabidopsis thaliana] >gi|20197413|gb|AAM15067.1| expressed protein [Arabidopsis thaliana] >gi|89001043|gb|ABD59111.1| At2g27140 [Arabidopsis thaliana]	Unigene52142_All//2.00E-11//AT2G27140| heat shock family protein	Unigene52142_All//6.00E-161//DW509031				nr -
Unigene52145_All	975	0.38	13.10	0.16	0.20	0.71	0.65	0.48	1.41	17.94	5.12E+00	2.61E-62	Up	-1.20E+00	3.96E-01		1.79E+00	6.10E-02		1.67E+00	9.79E-02		1.57E+00	3.34E-03		5.23E+00	1.22E-107	Up	Unigene52145_All//gi|297813771|ref|XP_002874769.1|//2.00E-38//auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320606|gb|EFH51025.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene52145_All//5.00E-38//AT4G22620| auxin-responsive family protein	Unigene52145_All//0.00E+00//gi|109870016|gb|DW498992.1|DW498992				nr -
Unigene52146_All	473	0.00	0.11	0.00	11.69	5.68	1.53	1.16	1.06	1.09	6.74E+00	6.15E-01		null	null		-1.04E+00	9.94E-06	Down	-2.94E+00	1.09E-19	Down	-1.32E-01	8.80E-01		-8.58E-02	9.27E-01		Unigene52146_All//gi|226502604|ref|NP_001147572.1|//1.00E-08//flavonoid 3-monooxygenase [Zea mays] >gi|195612262|gb|ACG27961.1| flavonoid 3-monooxygenase [Zea mays]	Unigene52146_All//2.00E-05//AT4G37360| CYP81D2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene52146_All//1.00E-47//CO095211				nr +
Unigene52147_All	278	2.07	2.19	0.77	2.51	3.22	5.36	3.95	7.67	28.52	7.93E-02	9.41E-01		-1.43E+00	1.75E-01		3.60E-01	6.55E-01		1.10E+00	5.01E-02		9.55E-01	1.55E-02		2.85E+00	3.61E-31	Up	Unigene52147_All//gi|22331608|ref|NP_190090.2|//2.00E-06//phosphatidate cytidylyltransferase family protein [Arabidopsis thaliana]		Unigene52147_All//2.00E-24//gi|109850309|gb|DW479288.1|DW479288			GO:0016020//GO:0016772	nr -
Unigene52149_All	377	0.00	0.00	0.00	3.83	0.00	0.12	2.47	15.63	1.80	null	null		null	null		-1.19E+01	1.02E-10	Down	-5.00E+00	7.43E-08	Down	2.66E+00	2.47E-21	Up	-4.58E-01	4.67E-01		Unigene52149_All//gi|255647386|gb|AC124256.1|//4.00E-06//unknown [Glycine max]		Unigene52149_All//2.00E-30//gi|48805733|gb|CO107047.1|CO107047				nr -
Unigene52154_All	877	0.00	0.00	0.00	0.00	0.12	1.08	5.88	0.24	1.77	null	null		null	null		6.88E+00	4.55E-01		1.01E+01	1.13E-05	Up	-4.63E+00	1.18E-29	Down	-1.73E+00	1.13E-11	Down	Unigene52154_All//gi|74273631|gb|AB401483.1|//1.00E-143//gibberellin 3-hydroxylase 1 [Gossypium hirsutum] >gi|121755807|gb|ABM64801.1| anthocyanidin synthase [Gossypium hirsutum]	Unigene52154_All//2.00E-119//AT4G22880| LDOX (LEUCOANTHOCYANIDIN DIOXYGENASE); leucocyanidin oxygenase	Unigene52154_All//0.00E+00//TC135683		ko00941|Flavonoid biosynthesis		nr -
Unigene52156_All	756	1.80	9.38	2.75	0.99	3.01	0.96	0.22	0.00	0.37	2.38E+00	1.96E-18	Up	6.10E-01	1.96E-01		1.60E+00	2.15E-04	Up	-4.84E-02	9.50E-01		-7.81E+00	1.34E-01		7.22E-01	5.97E-01									
Unigene52157_All	990	0.37	92.74	78.53	0.10	0.28	0.32	0.00	0.00	0.20	7.97E+00	0.00E+00	Up	7.73E+00	0.00E+00	Up	1.47E+00	4.20E-01		1.67E+00	3.09E-01		null	null		7.65E+00	7.88E-02		Unigene52157_All//gi|10802935|gb|AAG23683.1|AF288091_28//1.00E-94//apocytochrome b [Thraustochytrium aureum]	Unigene52157_All//2.00E-67//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.			ko00190|Oxidative phosphorylation	GO:0003824//GO:0022900//GO:0043231//GO:0044425	nr +

Unigene52158_All	603	26.64	6.55	31.26	0.74	0.74	0.30	0.00	0.00	0.13	-2.02E+00	9.20E-34	Down	2.31E-01	1.00E-01		-2.10E-03	9.69E-01		-1.31E+00	2.73E-01		null	null		7.05E+00	4.03E-01		Unigene52158_All//gi|297809217|ref|XP_002872492.1|//6.00E-33//ATSPS4F [Arabidopsis lyrata subsp. lyrata] >gi|297318329|gb|EFH48751.1| ATSPS4F [Arabidopsis lyrata subsp. lyrata]	Unigene52158_All//2.00E-25//AT4G10120| ATSPS4F; sucrose-phosphate synthase/ transferase, transferring glycosyl groups			ko00500|Starch and sucrose metabolism	GO:0005984//GO:0016020//GO:0035251	nr +
Unigene5216_All	1633	0.99	0.43	1.21	1.34	1.01	0.89	6.81	7.73	2.24	-1.19E+00	2.32E-02		2.81E-01	5.79E-01		-4.07E-01	3.61E-01		-6.01E-01	1.81E-01		1.83E-01	2.46E-01		-1.60E+00	1.00E-21	Down	Unigene5216_All//gi|255550632|ref|XP_002516365.1|//1.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223544463|gb|EEF45982.1| conserved hypothetical protein [Ricinus communis]		Unigene5216_All//0.00E+00//TC156351				nr -
Unigene52164_All	503	1.14	1.81	2.43	3.17	2.46	1.17	2.52	1.25	0.16	6.64E-01	3.75E-01		1.09E+00	9.18E-02		-3.63E-01	5.18E-01		-1.44E+00	7.26E-03		-1.02E+00	5.93E-02		-3.99E+00	2.56E-07	Down	Unigene52164_All//gi|224065988|ref|XP_002301993.1|//6.00E-63//cytochrome P450 [Populus trichocarpa] >gi|222843719|gb|EEE81266.1| cytochrome P450 [Populus trichocarpa]	Unigene52164_All//8.00E-46//AT4G31500| CYP83B1 (CYTOCHROME P450 MONOOXYGENASE 83B1); oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen / oxygen binding	Unigene52164_All//2.00E-155//TC179123		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0004497//GO:0005506//GO:0008152	nr +
Unigene52165_All	302	0.35	4.36	1.41	2.64	3.42	3.14	0.00	0.28	0.00	3.65E+00	1.28E-05	Up	2.03E+00	1.39E-01		3.74E-01	6.04E-01		2.51E-01	7.24E-01		8.11E+00	4.00E-01		null	null								
Unigene52166_All	692	0.91	0.66	0.15	1.01	1.09	1.04	1.04	0.97	3.74	-4.61E-01	6.18E-01		-2.56E+00	2.72E-02		1.20E-01	9.05E-01		5.12E-02	9.48E-01		-1.04E-01	8.93E-01		1.85E+00	1.06E-06	Up			Unigene52166_All//3.00E-12//AI725893				
Unigene52167_All	579	2.44	0.35	2.58	2.75	2.91	1.09	0.95	0.00	0.69	-2.80E+00	6.22E-05	Down	7.79E-02	8.88E-01		8.20E-02	8.94E-01		-1.33E+00	1.23E-02		-9.89E+00	4.61E-04	Down	-4.64E-01	5.97E-01								
Unigene52168_All	306	2.56	0.00	0.35	4.72	2.25	2.21	7.05	1.37	4.69	-1.13E+01	1.09E-04	Down	-2.88E+00	6.34E-03		-1.07E+00	4.31E-02		-1.09E+00	5.14E-02		-2.37E+00	2.59E-07	Down	-5.88E-01	1.18E-01				Unigene52168_All//1.00E-65//DW507801				ESTscan +
Unigene5217_All	859	6.09	14.27	8.24	22.04	43.62	35.54	9.35	19.17	2.50	1.23E+00	6.56E-13	Up	4.37E-01	6.12E-02		9.85E-01	2.17E-31		6.90E-01	5.36E-13		1.04E+00	4.75E-16	Up	-1.90E+00	5.10E-20	Down	Unigene5217_All//gi|297834094|ref|XP_002884929.1|//1.00E-41//auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330769|gb|EFH61188.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5217_All//1.00E-42//AT3G12830| auxin-responsive family protein	Unigene5217_All//0.00E+00//TC141422				nr -
Unigene52175_All	272	0.38	6.71	4.11	1.65	2.66	0.17	1.87	1.54	1.17	4.12E+00	3.43E-08	Up	3.42E+00	1.92E-04	Up	6.90E-01	4.47E-01		-3.31E+00	2.84E-02		-2.80E-01	7.49E-01		-6.71E-01	4.48E-01								
Unigene52179_All	506	1.14	0.40	0.63	2.36	1.91	2.86	4.93	1.73	1.89	-1.51E+00	1.36E-01		-8.49E-01	3.97E-01		-3.10E-01	6.07E-01		2.74E-01	6.49E-01		-1.51E+00	6.17E-05	Down	-1.38E+00	1.26E-04	Down	Unigene52179_All//gi|225423792|ref|XP_002277492.1|//5.00E-34//PREDICTED: similar to protein transporter [Vitis vinifera]	Unigene52179_All//3.00E-33//AT1G26170| binding / protein transporter	Unigene52179_All//0.00E+00//TC135618			GO:0015031//GO:0022892	nr +
Unigene52181_All	488	4.40	16.82	14.62	10.00	20.82	19.99	0.17	0.00	0.41	1.94E+00	1.61E-16	Up	1.73E+00	4.46E-12	Up	1.06E+00	8.35E-10	Up	9.99E-01	4.78E-08		-7.44E+00	4.02E-01		1.24E+00	4.68E-01		Unigene52181_All//gi|15240044|ref|NP_196824.1|//1.00E-16//GRAM domain-containing protein / ABA-responsive protein-related [Arabidopsis thaliana] >gi|75181135|sp|Q9LV46.1|GEML5_ARATH RecName: Full=GEM-like protein 5 >gi|7529275|emb|CAB86627.1| ABA-responsive protein-like [Arabidopsis thaliana] >gi|38454154|gb|AAR20771.1| At5g13200 [Arabidopsis thaliana] >gi|46002484|gb|AAS92344.1| At5g13200 [Arabidopsis thaliana] >gi|110738428|dbj|BAF01140.1| ABA-responsive protein - like [Arabidopsis thaliana]	Unigene52181_All//1.00E-14//AT5G13200| GRAM domain-containing protein / ABA-responsive protein-related	Unigene52181_All//1.00E-85//gi|109872282|gb|DW501257.1|DW501257				nr +
Unigene52187_All	470	0.67	0.32	3.29	0.00	0.00	0.19	17.63	17.25	22.72	-1.05E+00	4.43E-01		2.30E+00	3.37E-04	Up	null	null		7.59E+00	4.75E-01		-3.14E-02	8.87E-01		3.66E-01	1.74E-02		Unigene52187_All//gi|37544101|gb|AAQ93035.1|//2.00E-26//gibberellin 2-oxidase [Populus alba x Populus tremuloides]	Unigene52187_All//9.00E-17//AT1G47990| ATGA2OX4 (ARABIDOPSIS THALIANA GIBBERELLIN 2-OXIDASE 4); gibberellin 2-beta-dioxygenase	Unigene52187_All//3.00E-30//gi|78324168|gb|DT544442.1|DT544442		ko00904|Diterpenoid biosynthesis	GO:0008152//GO:0016706//GO:0046914	nr +
Unigene52189_All	676	2.55	1.12	4.25	2.36	1.73	0.27	0.13	0.00	0.06	-1.18E+00	1.94E-02		7.36E-01	5.69E-02		-4.45E-01	4.08E-01		-3.14E+00	2.25E-06	Down	-6.97E+00	4.02E-01		-1.09E+00	6.76E-01		Unigene52189_All//gi|21928151|gb|AAC83103.1|//5.00E-36//AT3g53540/F4P12_240 [Arabidopsis thaliana] >gi|23308447|gb|AAN18193.1| At3g53540/F4P12_240 [Arabidopsis thaliana]	Unigene52189_All//1.00E-37//AT3G53540| unknown protein	Unigene52189_All//7.00E-35//TC161210				nr +
Unigene52190_All	388	4.18	0.65	4.67	8.60	5.50	4.19	1.20	0.97	0.00	-2.68E+00	2.43E-05	Down	1.59E-01	7.37E-01		-6.45E-01	4.74E-02		-1.04E+00	2.05E-03		-3.06E-01	7.36E-01		-1.02E+01	1.09E-03								
Unigene52192_All	366	1.43	0.69	0.73	2.45	0.56	0.25	1.85	4.80	1.31	-1.05E+00	3.11E-01		-9.75E-01	3.76E-01		-2.12E+00	5.22E-03		-3.31E+00	5.79E-04	Down	1.38E+00	2.50E-03		-5.01E-01	5.07E-01				Unigene52192_All//2.00E-30//gi|164263264|gb|ES808400.1|ES808400				
Unigene52193_All	245	0.00	1.24	3.91	3.46	3.94	2.95	2.07	1.88	0.33	1.03E+01	4.42E-02		1.19E+01	2.46E-05	Up	1.87E-01	8.11E-01		-2.29E-01	7.51E-01		-1.42E-01	8.76E-01		-2.67E+00	1.37E-02								
Unigene52195_All	653	0.08	0.00	0.00	0.15	0.00	0.00	46.10	41.48	9.09	-6.32E+00	6.10E-01		-6.32E+00	6.22E-01		-7.25E+00	3.12E-01		-7.25E+00	3.99E-01		-1.53E-01	1.17E-01		-2.34E+00	7.10E-95	Down			Unigene52195_All//1.00E-14//TC133518				
Unigene52199_All	415	0.00	0.49	1.80	2.28	2.07	1.74	1.32	0.91	0.00	8.93E+00	1.36E-01		1.08E+01	3.27E-04	Up	-1.37E-01	8.18E-01		-3.89E-01	6.28E-01		-5.47E-01	5.52E-01		-1.04E+01	2.80E-04	Down			Unigene52199_All//5.00E-07//gi|48790898|gb|CO092212.1|CO092212				
Unigene5220_All	783	3.54	3.49	4.15	22.46	23.53	20.88	19.98	7.53	6.56	-1.93E-02	9.78E-01		2.28E-01	5.49E-01		6.72E-02	6.81E-01		-1.05E-01	5.13E-01		-1.41E+00	2.28E-24	Down	-1.61E+00	2.43E-30	Down	Unigene5220_All//gi|3319353|gb|AAC26242.1|//2.00E-51//contains similarity to copper-binding proteins [Arabidopsis thaliana] >gi|45752728|gb|AAS76262.1| At5g26330 [Arabidopsis thaliana]	Unigene5220_All//2.00E-47//AT5G26330| plastocyanin-like domain-containing protein / mavicyanin, putative	Unigene5220_All//0.00E+00//TC141137				nr -
Unigene52203_All	506	49.43	46.76	41.25	17.52	18.78	21.33	72.11	51.54	23.07	-7.99E-02	5.32E-01		-2.61E-01	2.65E-02		1.00E-01	6.55E-01		2.84E-01	1.30E-01		-4.84E-01	8.67E-10		-1.64E+00	5.29E-72	Down			Unigene52203_All//8.00E-136//gi|13249025|gb|BF279643.2|BF279643				
Unigene52204_All	513	0.00	0.00	0.62	7.28	2.89	3.52	1.65	0.98	0.54	null	null		9.28E+00	4.51E-02		-1.34E+00	9.13E-06	Down	-1.05E+00	8.72E-04	Down	-7.54E-01	2.78E-01		-1.60E+00	2.02E-02		Unigene52204_All//gi|297792079|ref|XP_002863924.1|//3.00E-28//phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309759|gb|EFH40183.1| phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene52204_All//8.00E-28//AT5G48800| phototropic-responsive NPH3 family protein	Unigene52204_All//4.00E-42//TC136792			GO:0005488//GO:0009314//GO:0016020//GO:0043231//GO:0060089	nr -
Unigene52205_All	290	22.01	24.99	18.91	35.90	22.68	21.49	35.87	26.37	17.72	1.83E-01	4.28E-01		-2.19E-01	3.83E-01		-6.63E-01	4.99E-05		-7.40E-01	1.80E-05		-4.43E-01	5.33E-03		-1.02E+00	1.64E-10	Down			Unigene52205_All//7.00E-135//TC153297				
Unigene52206_All	355	0.00	0.43	0.00	2.67	0.97	1.40	2.62	0.24	0.11	8.74E+00	2.35E-01		null	null		-1.46E+00	3.60E-02		-9.30E-01	2.06E-01		-3.48E+00	7.79E-05	Down	-4.55E+00	6.41E-06	Down			Unigene52206_All//4.00E-07//ES835793				
Unigene52208_All	1153	0.00	0.00	0.00	0.00	0.06	1.18	26.37	6.42	12.54	null	null		null	null		5.90E+00	6.08E-01		1.02E+01	4.51E-08	Up	-2.04E+00	3.79E-78	Down	-1.07E+00	1.60E-31	Down	Unigene52208_All//gi|171854669|dbj|BAG16524.1|//1.00E-70//C2 domain-containing protein [Capsicum chinense]	Unigene52208_All//5.00E-53//AT4G34150| C2 domain-containing protein			ko04626|Plant-pathogen interaction//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr -
Unigene52209_All	720	0.58	1.76	1.55	1.04	1.43	0.50	4.93	2.90	1.49	1.60E+00	1.20E-02		1.42E+00	4.39E-02		4.67E-01	5.51E-01		-1.05E+00	2.21E-01		-7.65E-01	8.56E-03		-1.72E+00	3.00E-08	Down			Unigene52209_All//0.00E+00//C0117924				
Unigene52211_All	589	0.00	0.00	0.00	0.00	0.00	0.00	4.38	10.57	22.59	null	null		null	null		null	null		null	null		1.27E+00	8.36E-09	Up	2.37E+00	2.83E-42	Up								
Unigene52217_All	327	2.88	0.31	0.33	0.00	0.84	1.38	1.68	3.20	1.22	-3.22E+00	6.76E-04	Down	-3.14E+00	1.33E-03		9.72E+00	7.01E-02		1.04E+01	7.73E-03		9.27E-01	1.30E-01		-4.64E-01	5.97E-01								
Unigene5222_All	910	34.55	288.09	78.65	7.12	23.39	91.82	84.65	46.30	911.74	3.06E+00	0.00E+00	Up	1.19E+00	3.49E-66	Up	1.72E+00	2.16E-41	Up	3.69E+00	0.00E+00	Up	-8.71E-01	3.03E-54		3.43E+00	0.00E+00	Up			Unigene5222_All//0.00E+00//TC137672				ESTscan -
Unigene52222_All	1438	0.04	0.00	0.00	0.62	0.12	0.00	6.29	4.19	5.54	-5.19E+00	6.10E-01		-5.19E+00	6.22E-01		-2.38E+00	2.29E-03		-9.28E+00	1.21E-05	Down	-5.88E-01	5.52E-04		-1.83E-01	3.17E-01		Unigene52222_All//gi|71041104|gb|AAZ20440.1|//1.00E-77//MYB24 [Malus x domestica]	Unigene52222_All//2.00E-56//AT5G57620| MYB36 (myb domain protein 36); DNA binding / transcription factor	Unigene52222_All//2.00E-46//gi|109850159|gb|DW519123.1|DW519123	MYB			nr +
Unigene52224_All	277	2.64	0.00	0.38	0.00	0.12	0.00	8.70	8.75	4.89	-1.14E+01	2.11E-04	Down	-2.78E+00	1.04E-02		6.96E+00	8.29E-01		null	null		8.50E-03	1.02E+00		-8.31E-01	1.80E-02		Unigene52224_All//gi|30696622|ref|NP_850968.1|//5.00E-23//BGLU46 (BETA GLUCOSIDASE 46); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana] >gi|281312216|sp|Q80690.2|BGL46_ARATH RecName: Full=Beta-glucosidase 46; Short=AtBGLU46; Flags: Precursor	Unigene52224_All//2.00E-24//AT1G61820| BGLU46 (BETA GLUCOSIDASE 46); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene52224_All//5.00E-86//CO498724		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0008422//GO:0009699//GO:0031410//GO:0043167	nr -
Unigene52225_All	791	28.77	11.40	35.61	0.82	2.26	0.57	0.00	0.00	0.00	-1.34E+00	1.46E-26	Down	3.08E-01	4.30E-03		1.47E+00	3.16E-03		-5.20E-01	5.88E-01		null	null		null	null				Unigene52225_All//9.00E-07//EX169566				
Unigene52229_All	1895	0.00	0.37	0.42	0.00	0.15	0.10	2.21	2.01	11.46	8.55E+00	3.32E-04	Up	8.72E+00	1.72E-04	Up	7.18E+00	7.01E-02		6.57E+00	1.94E-01		-1.38E-01	6.22E-01		2.38E+00	9.24E-69	Up	Unigene52229_All//gi|13506810|gb|AAK28345.1|AF243040_1//1.00E-125//receptor-like protein kinase 3 [Solanum lycopersicum]	Unigene52229_All//2.00E-98//AT1G72460| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0000904//GO:0004672//GO:0044459	nr -
Unigene52230_All	1947	0.32	19.57	0.25	0.59	0.83	0.51	0.17	0.09	0.16	5.92E+00	9.49E-198	Up	-3.90E-01	6.46E-01		4.98E-01	3.75E-01		-2.06E-01	7.39E-01		-1.02E+00	3.99E-01		-8.55E-02	9.47E-01		Unigene52230_All//gi|75213086|sp|Q9SWB4.1|PARP3_SOYBN//0.00E+00//RecName: Full=Poly [ADP-ribose] polymerase 3; Short=PARP-3; AltName: Full=NAD(+) ADP-ribosyltransferase 3; Short=ADPRT-3; AltName: Full=Poly[ADP-ribose] synthase 3 >gi|5802246|gb|AAD51626.1|AF169023_1 seed maturation protein PM38 [Glycine max]	Unigene52230_All//0.00E+00//AT5G22470| NAD+ ADP-ribosyltransferase	Unigene52230_All//0.00E+00//TC166464		ko03410|Base excision repair	GO:0003676//GO:0006464//GO:0016628//GO:0016763//GO:0043231	nr +
Unigene52232_All	249	2.10	1.63	0.64	3.00	5.53	0.18	1.02	2.52	1.12	-3.68E-01	6.83E-01		-1.71E+00	1.40E-01		8.82E-01	1.33E-01		-4.05E+00	7.75E-04	Down	1.31E+00	1.26E-01		1.37E-01	9.29E-01								
Unigene52233_All	460	0.46	2.42	0.46	2.49	1.20	0.20	48.25	33.80	85.22	2.41E+00	1.59E-03		2.51E-02	1.00E+00		-1.06E+00	8.44E-02		-3.66E+00	2.69E-05	Down	-5.14E-01	6.83E-07		8.21E-01	5.47E-26		Unigene52233_All//gi|224083767|ref|XP_002307116.1|//1.00E-12//predicted protein [Populus trichocarpa] >gi|222856565|gb|EEE94112.1| predicted protein [Populus trichocarpa]		Unigene52233_All//4.00E-159//TC170753				nr +
Unigene52235_All	535	0.98	1.70	4.88	7.45	7.60	7.43	0.95	1.09	0.82	8.02E-01	2.71E-01		2.32E+00	1.06E-06	Up	2.80E-02	9.54E-01		-3.90E-03	9.86E-01		2.06E-01	8.00E-01		-2.11E-01	7.92E-01		Unigene52235_All//gi|115458264|ref|NP_001052232.1|//9.00E-11//Os04g0411200 [Oryza sativa Japonica Group] >gi|113564303|dbj|BAF14646.1| Os04g0411200 [Oryza sativa Japonica Group]					GO:0009798//GO:0009965//GO:0010051//GO:0010073//GO:0043231//GO:0043392	nr +
Unigene52236_All	961	0.44	0.53	0.33	4.15	5.30	3.62	1.28	0.17	0.79	2.76E-01	7.64E-01		-3.90E-01	7.17E-01		3.55E-01	2.10E-01		-1.97E-01	5.87E-01		-2.87E+00	2.54E-05	Down	-6.96E-01	1.86E-01		Unigene52236_All//gi|205326623|gb|ACI03401.1|//1.00E-110//peroxidase 1 [Litchi chinensis]	Unigene52236_All//7.00E-90//AT5G05340| peroxidase, putative	Unigene52236_All//0.00E+00//TC141039		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209	nr -
Unigene52240_All	312	7.71	2.11	3.07	1.28	2.76	1.74	0.14	0.54	0.64	-1.87E+00	3.44E-05	Down	-1.33E+00	2.62E-03		1.11E+00	1.63E-01		4.44E-01	6.78E-01		1.98E+00	3.79E-01		2.24E+00	2.49E-01								
Unigene52242_All	461	1.59	1.32	1.62	3.35	5.15	4.41	2.48	1.72	0.60	-2.69E-01	7.19E-01		2.54E-02	9.95E-01		6.22E-01	1.44E-01		3.96E-01	4.23E-01		-5.24E-01	3.82E-01		-2.03E+00	8.63E-04	Down			Unigene52242_All//5.00E-07//ES842684				
Unigene52244_All	498	1.79	1.73	5.13	1.60	4.70	3.99	0.17	0.08	0.16	-4.63E-02	9.62E-01		1.52E+00	4.46E-04	Up	1.55E+00	2.43E-04	Up	1.32E+00	5.29E-03		-1.02E+00	7.24E-01		-8.58E-02	9.71E-01				Unigene52244_All//6.00E-07//TC159753				
Unigene52246_All	549	0.00	0.00	0.00	1.36	2.70	3.21	4.24	1.75	5.81	null	null		null	null		9.87E-01	7.54E-02		1.24E+00	1.46E-02		-1.27E+00	8.52E-04	Down	4.53E-01	1.39E-01								
Unigene52247_All	908	0.00	0.00	0.00	0.00	0.00	0.00	1.40	3.08	1.76	null	null		null	null		null	null		null	null		1.14E+00	7.75E-04	Up	3.29E-01	4.87E-01		Unigene52247_All//gi|224087451|ref|XP_002308172.1|//2.00E-16//predicted protein [Populus trichocarpa] >gi|222854148|gb|EEE91695.1| predicted protein [Populus trichocarpa]						nr +
Unigene52250_All	582	0.00	1.65	0.00	2.05	2.25	1.47	0.73	1.72	0.89	1.07E+01	1.38E-05	Up	null	null		1.30E-01	8.39E-01		-4.78E-01	4.72E-01		1.25E+00	4.78E-02		2.93E-01	7.27E-01		Unigene52250_All//gi|2624386|emb|CAA70596.1|//2.00E-96//cinnamate 4-hydroxylase [Phaseolus vulgaris]	Unigene52250_All//9.00E-69//AT2G30490| C4H (CINNAMATE-4-HYDROXYLASE); trans-cinnamate 4-monooxygenase	Unigene52250_All//2.00E-16//gi|48801310|gb|CO102624.1|CO102624		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0005506//GO:0008152//GO:0016709//GO:0031410	nr +
Unigene52251_All	221	0.47	3.44	2.89	0.00	5.14	4.09	2.68	1.13	11.18	2.86E+00	5.51E-03		2.61E+00	2.33E-02		1.23E+01	5.31E-07	Up	1.20E+01	2.07E-05	Up	-1.24E+00	1.54E-01		2.06E+00	2.81E-07	Up			Unigene52251_All//2.00E-07//DW517923				

Unigene52252_All	1105	0.00	0.00	0.00	0.00	0.00	0.00	12.74	18.23	3.97	null	null		null	null		null	null		null	null		5.17E-01	2.17E-06		-1.68E+00	2.94E-29	Down	Unigene52252_All//gi|242070913|ref|XP_002450733.1|//2.00E-17//hypothetical protein SORBIDRAFT_05g016477 [Sorghum bicolor] >gi|241936576|gb|EES09721.1| hypothetical protein SORBIDRAFT_05g016477 [Sorghum bicolor]		Unigene52252_All//2.00E-51//gi|78348172|gb|DT568446.1|DT568446				nr -
Unigene52253_All	305	130.37	333.42	429.84	107.79	68.42	87.22	58.64	87.43	30.70	1.35E+00	2.19E-118	Up	1.72E+00	8.73E-212	Up	-6.56E-01	2.06E-14		-3.06E-01	1.07E-03		5.76E-01	8.57E-10		-9.34E-01	3.05E-15				Unigene52253_All//1.00E-74//gi|11208181|gb|BF277111.1|BF277111				
Unigene52255_All	521	0.00	0.00	0.00	1.72	1.85	0.35	7.87	1.12	1.22	null	null		null	null		1.05E-01	9.03E-01		-2.31E+00	5.78E-03		-2.81E+00	6.13E-16	Down	-2.69E+00	8.99E-16	Down	Unigene52255_All//gi|297802428|ref|XP_002869098.1|//2.00E-19//cyclase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314934|gb|EFH45357.1| cyclase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene52255_All//1.00E-20//AT4G35220| cyclase family protein	Unigene52255_All//3.00E-46//TC158981				nr -
Unigene52256_All	659	0.08	1.23	2.50	4.99	5.85	5.69	2.05	2.16	0.85	3.95E+00	7.52E-04	Up	4.98E+00	6.48E-08	Up	2.30E-01	5.36E-01		1.89E-01	6.30E-01		7.08E-02	8.99E-01		-1.28E+00	1.14E-02		Unigene52256_All//gi|224115986|ref|XP_002332020.1|//2.00E-15//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222875245|gb|EEF12376.1| BED finger-nbs-lrr resistance protein [Populus trichocarpa]		Unigene52256_All//2.00E-84//CO080430			GO:0005488	nr +
Unigene52261_All	370	1.98	1.37	0.58	3.77	0.56	0.98	0.11	0.00	0.32	-5.32E-01	5.13E-01		-1.78E+00	6.00E-02		-2.76E+00	1.09E-05	Down	-1.95E+00	1.43E-03		-6.84E+00	6.56E-01		1.50E+00	5.58E-01								
Unigene52262_All	979	0.00	0.52	0.00	0.10	0.04	1.29	0.73	1.79	13.02	9.02E+00	4.04E-03		null	null		-1.53E+00	5.86E-01		3.67E+00	1.38E-05	Up	1.29E+00	4.31E-03		4.15E+00	1.15E-68	Up			Unigene52262_All//1.00E-154//DT464105				
Unigene52264_All	576	0.64	0.53	0.28	0.26	1.20	0.39	0.51	2.25	1.38	-2.69E-01	8.01E-01		-1.20E+00	3.96E-01		2.20E+00	2.71E-02		5.96E-01	7.21E-01		2.13E+00	3.40E-04	Up	1.43E+00	4.39E-02				Unigene52264_All//0.00E+00//gi|163468373|gb|ES800670.1|ES800670				
Unigene52265_All	987	0.69	0.67	0.22	1.82	1.12	1.28	1.59	0.25	2.34	-4.62E-02	9.69E-01		-1.68E+00	8.70E-02		-7.03E-01	1.40E-01		-5.04E-01	3.30E-01		-2.64E+00	4.08E-06	Down	5.63E-01	1.23E-01		Unigene52265_All//gi|42561615|ref|NP_171710.3|//4.00E-65//transcriptional regulator-related [Arabidopsis thaliana]	Unigene52265_All//7.00E-66//AT1G02080| transcriptional regulator-related	Unigene52265_All//5.00E-117//TC142981		ko03018|RNA degradation		nr +
Unigene52267_All	304	0.34	0.33	0.00	7.05	2.72	4.31	2.50	0.41	7.08	-4.60E-02	9.88E-01		-8.43E+00	3.92E-01		-1.37E+00	1.03E-03		-7.10E-01	1.13E-01		-2.60E+00	2.81E-03		1.50E+00	1.81E-04	Up			Unigene52267_All//8.00E-33//gi|78343472|gb|DT563746.1|DT563746				
Unigene52271_All	757	0.00	0.00	0.00	0.00	0.00	0.00	2.51	9.88	2.74	null	null		null	null		null	null		null	null		1.98E+00	5.83E-19	Up	1.23E-01	7.55E-01		Unigene52271_All//gi|224069218|ref|XP_002302929.1|//2.00E-10//nbs-lrr resistance protein [Populus trichocarpa] >gi|222844655|gb|EEE82202.1| nbs-lrr resistance protein [Populus trichocarpa]		Unigene52271_All//4.00E-09//TC171440			GO:0005488	nr -
Unigene52272_All	579	0.72	1.05	0.64	3.87	2.02	0.70	2.48	3.10	1.10	5.39E-01	5.63E-01		-1.67E-01	8.79E-01		-9.37E-01	2.06E-02		-2.46E+00	6.31E-07	Down	3.22E-01	4.94E-01		-1.17E+00	1.53E-02				Unigene52272_All//1.00E-60//TC153940				
Unigene52273_All	727	1.15	4.11	0.37	2.33	4.50	2.11	1.11	1.15	1.21	1.84E+00	4.35E-06	Up	-1.65E+00	5.45E-02		9.50E-01	4.48E-03		-1.41E-01	7.81E-01		5.73E-02	9.54E-01		1.26E-01	8.48E-01		Unigene52273_All//gi|297795477|ref|XP_002865623.1|//2.00E-67//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314458|gb|EFH41882.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene52273_All//2.00E-61//AT3G07650| COL9 (CONSTANS-LIKE 9); transcription factor/ zinc ion binding	Unigene52273_All//0.00E+00//ES806566	C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0003676//GO:0010468//GO:0016020//GO:0043231//GO:0046914//GO:0048581	nr -
Unigene52276_All	332	1.26	0.00	1.28	4.80	3.22	1.22	1.02	0.00	0.00	-1.03E+01	1.05E-02		2.54E-02	1.00E+00		-5.79E-01	2.71E-01		-1.97E+00	4.88E-04	Down	-9.99E+00	1.17E-02		-9.99E+00	8.14E-03		Unigene52276_All//gi|154816299|gb|ABS87383.1|//1.00E-29//minichromosome maintenance factor [Lactuca sativa]	Unigene52276_All//1.00E-16//AT1G44900| ATP binding / DNA binding / DNA-dependent ATPase	Unigene52276_All//5.00E-68//TC151182		ko03030|DNA replication	GO:0003676//GO:0006259//GO:0032559//GO:0043231	nr -
Unigene52277_All	232	0.00	0.22	0.92	3.22	4.45	0.39	2.73	8.83	4.46	7.77E+00	6.15E-01		9.84E+00	1.41E-01		4.67E-01	5.51E-01		-3.05E+00	3.33E-03		1.69E+00	8.70E-05	Up	7.08E-01	2.28E-01				Unigene52277_All//3.00E-07//ES828702				
Unigene52280_All	249	368.98	207.77	210.43	351.70	232.89	267.90	172.35	99.37	76.32	-8.29E-01	1.38E-48		-8.10E-01	3.59E-45		-5.95E-01	1.06E-31		-3.93E-01	1.78E-13		-7.94E-01	2.92E-26		-1.18E+00	4.62E-51	Down	Unigene52280_All//gi|211906520|gb|AGJ11753.1|//7.00E-13//UDP-D-apiose/UPD-D-xylose synthetase [Gossypium hirsutum]	Unigene52280_All//3.00E-12//AT2G27860| AXS1 (UDP-D-apiose/UDP-D-xylose synthase 1); NAD or NADH binding / UDP-glucuronate decarboxylase	Unigene52280_All//2.00E-134//gi|13350130|gb|BG440479.1|BG440479		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0000166//GO:0005576//GO:0009225//GO:0016831//GO:0044424//GO:0048037	nr -
Unigene52284_All	416	3.02	1.34	2.05	0.60	0.17	4.02	14.43	9.95	4.69	-1.17E+00	5.48E-02		-5.60E-01	3.87E-01		-1.85E+00	2.75E-01		2.75E+00	1.01E-05	Up	-5.37E-01	1.31E-02		-1.62E+00	2.53E-12	Down	Unigene52284_All//gi|255582113|ref|XP_002531851.1|//2.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223528501|gb|EEF30529.1| conserved hypothetical protein [Ricinus communis]	Unigene52284_All//1.00E-97//gi|132465065|gb|BE053609.2|BE053609				nr +
Unigene52287_All	533	12.47	10.55	18.98	2.24	1.94	0.42	0.95	0.16	0.07	-2.41E-01	3.27E-01		6.07E-01	1.15E-03		-2.11E-01	7.52E-01		-2.40E+00	7.07E-04	Down	-2.60E+00	2.04E-02		-3.67E+00	3.75E-03				Unigene52287_All//2.00E-43//TC158923				
Unigene5229_All	745	6.39	10.61	3.65	7.69	13.91	6.55	4.14	5.27	26.31	7.31E-01	4.07E-04		-8.10E-01	4.87E-03		8.56E-01	3.34E-07		-2.32E-01	4.05E-01		3.48E-01	2.37E-01		2.67E+00	7.50E-71	Up	Unigene5229_All//gi|18401970|ref|NP_566616.1|//3.00E-34//MKS1 (MAP kinase substrate 1); protein binding [Arabidopsis thaliana] >gi|110279050|sp|Q8LGD5.2|MKS1_ARATH RecName: Full=Protein MKS1; AltName: Full=Protein MAP kinase 4 substrate 1 >gi|88196717|gb|ABD43001.1| At3g18690 [Arabidopsis thaliana]	Unigene5229_All//9.00E-17//AT3G18690| MKS1 (MAP kinase substrate 1); protein binding	Unigene5229_All//0.00E+00//TC144019				nr -
Unigene52290_All	825	0.00	0.12	0.00	0.00	0.21	0.38	1.85	1.42	60.94	6.94E+00	3.86E-01		null	null		7.71E+00	2.27E-01		8.58E+00	4.07E-02		-3.79E-01	4.49E-01		5.05E+00	1.43E-303	Up	Unigene52290_All//gi|224139376|ref|XP_002323082.1|//5.00E-78//cytochrome P450 [Populus trichocarpa] >gi|222867712|gb|EEF04843.1| cytochrome P450 [Populus trichocarpa]	Unigene52290_All//2.00E-47//AT3G48310| CYP71A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene52290_All//0.00E+00//gi|109855176|gb|DW484155.1|DW484155		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0005506//GO:0016020//GO:0016491	nr +
Unigene52291_All	614	0.17	6.11	0.26	0.32	0.45	0.37	20.52	13.27	100.38	5.16E+00	1.57E-18	Up	6.11E-01	7.48E-01		4.68E-01	8.16E-01		1.81E-01	9.35E-01		-6.29E-01	8.92E-06		2.29E+00	1.14E-185	Up			Unigene52291_All//6.00E-69//gi|73860914|gb|DT463653.1|DT463653				
Unigene52293_All	327	3.36	0.93	6.19	27.42	1.05	0.41	0.65	0.00	0.12	-1.85E+00	8.98E-03		8.81E-01	6.42E-02		-4.70E+00	8.60E-55	Down	-6.05E+00	5.84E-52	Down	-9.34E+00	7.43E-02		-2.41E+00	1.95E-01				Unigene52293_All//2.00E-09//DT463420				
Unigene52294_All	790	0.00	0.00	0.00	0.19	0.00	0.11	2.19	2.01	9.58	null	null		null	null		-7.56E+00	1.65E-01		-7.27E-01	7.15E-01		-1.26E-01	7.79E-01		2.13E+00	1.77E-21	Up	Unigene52294_All//gi|145357869|ref|NP_196633.2|//9.00E-08//AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase [Arabidopsis thaliana] >gi|74058448|gb|AAZ98829.1| cytokinin independent 2 [Arabidopsis thaliana]	Unigene52294_All//4.00E-09//AT5G10720| AHK5 (ARABIDOPSIS HISTIDINE KINASE 5); protein histidine kinase		Orphans		GO:0002237//GO:0004672//GO:0009738//GO:0009873//GO:0010119//GO:0016020//GO:0034614//GO:0043231//GO:0048513//GO:0071241	nr +
Unigene52295_All	1232	0.08	0.95	0.30	1.17	0.25	0.62	2.16	3.22	1.88	3.48E+00	7.08E-05	Up	1.83E+00	2.13E-01		-2.22E+00	1.08E-04	Down	-9.12E-01	1.06E-01		5.76E-01	3.68E-02		-2.05E-01	5.81E-01		Unigene52295_All//gi|224143380|ref|XP_002336033.1|//3.00E-06//predicted protein [Populus trichocarpa] >gi|222839399|gb|EEE77736.1| predicted protein [Populus trichocarpa]		Unigene52295_All//0.00E+00//DR462878				nr +
Unigene52296_All	477	0.44	3.08	2.46	2.40	1.37	0.66	3.37	3.86	1.75	2.81E+00	4.57E-05	Up	2.49E+00	1.35E-03		-8.08E-01	1.92E-01		-1.86E+00	6.47E-03		1.95E-01	6.56E-01		-9.41E-01	3.51E-02				Unigene52296_All//2.00E-108//TC174524				
Unigene52298_All	504	0.00	1.11	0.00	0.10	0.41	0.54	6.12	60.29	41.66	1.01E+01	2.18E-03		null	null		2.05E+00	3.94E-01		2.44E+00	2.22E-01		3.30E+00	3.00E-133	Up	2.77E+00	7.13E-79	Up	Unigene52298_All//gi|151301818|gb|ABN50365.2|//4.00E-34//ethylene responsive element binding protein 1 [Gossypium barbadense]	Unigene52298_All//8.00E-11//AT4G17500| AIERF-1 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene52298_All//2.00E-47//gi|109825974|gb|DW224695.1|DW224695	AP2-EREBP		GO:0000160//GO:0001071//GO:0002218//GO:0003676//GO:0006351//GO:0009743//GO:0010468//GO:0016557//GO:0030528//GO:0043231	nr +
Unigene5230_All	632	21.11	50.19	15.42	69.36	113.39	111.77	142.29	209.57	469.11	1.25E+00	4.74E-33	Up	-4.53E-01	4.89E-03		7.09E-01	2.04E-34		6.88E-01	3.21E-29		5.59E-01	6.50E-43		1.72E+00	0.00E+00	Up	Unigene5230_All//gi|206574946|gb|ACI14386.1|//3.00E-48//WRKY17-1 transcription factor [Brassica napus]	Unigene5230_All//2.00E-36//AT2G24570| WRKY17; calmodulin binding / transcription factor	Unigene5230_All//0.00E+00//gi|78351120|gb|DT571394.1|DT571394	WRKY			nr +
Unigene52300_All	389	2.69	1.04	2.19	1.54	2.74	0.00	0.98	0.00	0.00	-1.37E+00	4.74E-02		-2.97E-01	6.41E-01		8.37E-01	2.29E-01		-1.06E+01	7.70E-04	Down	-9.93E+00	6.17E-03		-9.93E+00	4.19E-03				Unigene52300_All//5.00E-07//FE896853				
Unigene52301_All	592	0.27	0.86	0.00	3.79	4.07	1.30	0.93	0.14	0.13	1.69E+00	1.34E-01		-8.05E+00	2.44E-01		1.05E-01	8.24E-01		-1.55E+00	4.57E-04	Down	-2.72E+00	1.22E-02		-2.79E+00	7.95E-03		Unigene52301_All//gi|15218859|ref|NP_171859.1|//2.00E-39//phagocytosis and cell motility protein ELMO1-related [Arabidopsis thaliana] >gi|124300970|gb|ABN04737.1| Atig03620 [Arabidopsis thaliana]	Unigene52301_All//1.00E-40//AT1G03620| phagocytosis and cell motility protein ELMO1-related				GO:0006897//GO:0043232	nr -
Unigene52307_All	1469	0.00	0.00	0.00	0.00	0.02	0.06	284.48	52.21	143.76	null	null		null	null		4.55E+00	8.29E-01		5.94E+00	4.75E-01		-2.45E+00	0.00E+00	Down	-9.85E-01	0.00E+00		Unigene52307_All//gi|224110984|ref|XP_002315705.1|//0.00E+00//high affinity inorganic phosphate transporter [Populus trichocarpa] >gi|222864745|gb|EEF01876.1| high affinity inorganic phosphate transporter [Populus trichocarpa]	Unigene52307_All//0.00E+00//AT2G38940| ATPT2 (ARABIDOPSIS THALIANA PHOSPHATE TRANSPORTER 2); carbohydrate transmembrane transporter/ inorganic phosphate transmembrane transporter/ phosphate transmembrane transporter/ sugar:hydrogen symporter	Unigene52307_All//1.00E-19//CO105486			GO:0015291//GO:0015698//GO:0031224	nr +
Unigene5231_All	970	11.06	16.19	9.28	17.56	26.23	36.97	38.23	56.66	77.99	5.50E-01	9.00E-05		-2.53E-01	1.90E-01		5.79E-01	7.37E-09		1.07E+00	1.82E-31	Up	5.68E-01	8.11E-19		1.03E+00	1.17E-71	Up	Unigene5231_All//gi|255671803|gb|ACU26534.1|//4.00E-85//dihydroxyacid dehydratase [Glycine max]	Unigene5231_All//8.00E-65//AT3G23940| dehydratase family	Unigene5231_All//0.00E+00//TC136783		ko00290|Valine, leucine and isoleucine biosynthesis//ko00770|Pantothenate and CoA biosynthesis		nr +
Unigene52310_All	1110	0.09	0.09	0.10	0.13	0.50	0.16	0.84	2.15	9.58	-4.66E-02	9.88E-01		2.43E-02	9.99E-01		1.88E+00	9.41E-02		2.74E-01	9.04E-01		1.36E+00	3.61E-04	Up	3.52E+00	1.46E-50	Up	Unigene52310_All//gi|297839373|ref|XP_002887568.1|//1.00E-105//GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333409|gb|EFH63827.1| GNS1/SUR4 membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene52310_All//8.00E-106//AT1G75000| GNS1/SUR4 membrane family protein	Unigene52310_All//6.00E-12//TC171527			GO:0044464	nr -
Unigene52311_All	452	0.93	3.81	2.24	0.88	1.90	1.70	2.15	1.85	2.82	2.04E+00	2.81E-04	Up	1.27E+00	8.36E-02		1.11E+00	1.63E-01		9.46E-01	2.73E-01		-2.18E-01	7.24E-01		3.91E-01	4.66E-01								
Unigene52315_All	1043	0.25	1.80	0.05	0.57	0.36	0.22	3.28	6.13	3.13	2.84E+00	2.43E-06	Up	-2.30E+00	2.43E-01		-6.58E-01	4.78E-01		-1.40E+00	1.58E-01		9.01E-01	1.67E-05		-6.81E-02	8.22E-01		Unigene52315_All//gi|113205290|gb|ABI34329.1|//4.00E-08//Integrase core domain containing protein [Solanum demissum]		Unigene52315_All//3.00E-72//ES823234			GO:0003676//GO:0006139//GO:0017111//GO:0019205//GO:0043170	nr -
Unigene52316_All	291	9.53	2.44	1.10	0.51	1.78	2.33	0.44	0.00	0.00	-1.97E+00	3.25E-06	Down	-3.12E+00	1.89E-09	Down	1.79E+00	1.26E-01		2.18E+00	3.14E-02		-8.77E+00	2.35E-01		-8.77E+00	1.99E-01		Unigene52316_All//gi|224094378|ref|XP_002310150.1|//1.00E-18//predicted protein [Populus trichocarpa] >gi|222853053|gb|EEE90600.1| predicted protein [Populus trichocarpa]		Unigene52316_All//8.00E-147//TC165985				nr +
Unigene52317_All	388	0.67	1.18	0.00	1.93	1.42	0.81	1.74	0.22	0.10	8.02E-01	4.60E-01		-9.40E+00	8.56E-02		-4.40E-01	5.85E-01		-1.24E+00	1.45E-01		-3.02E+00	2.43E-03		-4.09E+00	3.10E-04	Down			Unigene52317_All//5.00E-07//ES821082				
Unigene52318_All	1142	0.00	0.00	0.00	0.17	0.12	0.00	14.70	16.14	4.95	null	null		null	null		-5.33E-01	7.48E-01		-7.45E+00	1.33E-01		1.35E-01	3.12E-01		-1.57E+00	1.94E-31	Down	Unigene52318_All//gi|77378044|gb|AAZ79470.2|//1.00E-145//SUPERMAN-like zinc finger protein [Gossypium hirsutum]	Unigene52318_All//4.00E-21//AT5G06070| RBE (RABBIT EARS); nucleic acid binding / transcription factor/ zinc ion binding	Unigene52318_All//0.00E+00//TC130397	C2H2		GO:0005488	nr +
Unigene52319_All	445	2.23	0.46	5.86	1.79	1.24	2.13	0.48	0.38	0.90	-2.29E+00	4.05E-03		1.39E+00	9.94E-04	Up	-5.33E-01	5.10E-01		2.51E-01	7.24E-01		-3.39E-01	8.11E-01		9.14E-01	3.86E-01		Unigene52319_All//gi|302141901|emb|CBI19104.3|//7.00E-11//unnamed protein product [Vitis vinifera]						nr +
Unigene5232_All	902	1.51	3.48	1.95	2.04	2.37	0.90	6.42	7.14	3.75	1.21E+00	8.00E-04	Up	3.69E-01	4.72E-01		2.12E-01	6.75E-01		-1.18E+00	1.47E-02		1.52E-01	5.33E-01		-7.74E-01	2.85E-04								
Unigene52320_All	391	1.34	5.57	1.91	0.64	1.59	0.81	1.41	2.46	3.16	2.06E+00	2.92E-05	Up	5.11E-01	5.47E-01		1.32E+00	1.88E-01		3.44E-01	7.96E-01		8.07E-01	2.12E-01		1.17E+00	2.86E-02				Unigene52320_All//3.00E-14//ES817619				

Unigene52322_A11	582	0.18	1.65	0.18	0.94	1.36	1.63	5.59	4.60	3.83	3.20E+00	6.55E-04	Up	2.55E-02	9.99E-01		5.31E-01	5.39E-01		7.92E-01	2.99E-01		-2.83E-01	3.93E-01		-5.45E-01	6.63E-02		Unigene52322_A11//gi|297794445|ref|XP_002865107.1|//2.00E-47//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297310942|gb|EFH41366.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene52322_A11//9.00E-44//AT5G47690| binding	Unigene52322_A11//5.00E-97//TC138190			GO:0009536	nr -
Unigene52323_A11	499	0.63	6.60	0.11	3.09	1.38	1.36	3.73	3.43	17.96	3.39E+00	1.75E-12	Up	-2.56E+00	1.59E-01		-1.16E+00	2.17E-02		-1.19E+00	2.78E-02		-1.19E-01	7.87E-01		2.27E+00	2.46E-27	Up				Unigene52323_A11//5.00E-66//TC173621				
Unigene52324_A11	504	0.52	0.20	0.00	1.09	1.50	1.08	0.34	0.00	1.98	-1.37E+00	3.83E-01		-9.02E+00	8.56E-02		4.67E-01	6.07E-01		-1.59E-02	9.75E-01		-8.39E+00	1.34E-01		2.56E+00	3.91E-04	Up				Unigene52324_A11//6.00E-07//TC155881				
Unigene52326_A11	1455	0.00	0.21	0.00	0.00	0.00	0.19	0.12	1.78	16.18	7.71E+00	4.42E-02		null	null		null	null		7.54E+00	7.02E-02		3.94E+00	1.30E-13	Up	7.12E+00	6.45E-161	Up	Unigene52326_A11//gi|194466155|gb|ACF74308.1|//2.00E-22//heat shock protein 1 [Arachis hypogaea]	Unigene52326_A11//3.00E-19//AT5G59720| HSP18.2 (heat shock protein 18.2)	Unigene52326_A11//5.00E-58//TC152582				nr +
Unigene52329_A11	361	3.33	0.00	1.92	0.69	1.81	2.75	0.82	1.27	0.66	-1.17E+01	5.01E-07	Down	-7.98E-01	2.25E-01		1.39E+00	1.51E-01		2.00E+00	9.93E-03		6.36E-01	5.36E-01		-3.08E-01	7.74E-01					Unigene52329_A11//1.00E-96//gi|78335644|gb|DT555918.1|DT555918				
Unigene52330_A11	314	8.50	64.55	28.49	10.31	17.22	54.51	39.32	212.84	127.13	2.93E+00	1.50E-64	Up	1.75E+00	3.96E-15	Up	7.40E-01	2.74E-03		2.40E+00	4.77E-47	Up	2.44E+00	9.07E-213	Up	1.69E+00	4.01E-81	Up				Unigene52330_A11//2.00E-82//BQ404691				
Unigene52333_A11	386	0.27	5.25	0.00	8.00	9.37	22.70	1.20	9.10	0.52	4.28E+00	3.01E-09	Up	-8.08E+00	3.92E-01		2.27E-01	5.67E-01		1.50E+00	2.88E-13	Up	2.92E+00	3.37E-14	Up	-1.22E+00	2.00E-01					Unigene52333_A11//8.00E-12//TC170677				
Unigene52334_A11	449	1.51	1.02	1.78	0.78	4.22	2.51	2.92	0.56	3.28	-5.77E-01	4.94E-01		2.32E-01	7.49E-01		2.44E+00	5.59E-06	Up	1.70E+00	1.42E-02		-2.39E+00	9.40E-05	Down	1.69E-01	7.19E-01									
Unigene52335_A11	510	1.85	0.99	2.51	2.54	2.16	2.39	2.40	3.93	7.34	-8.94E-01	2.14E-01		4.41E-01	4.71E-01		-2.33E-01	7.04E-01		-8.69E-02	8.93E-01		7.10E-01	8.37E-02		1.61E+00	7.50E-08	Up				Unigene52335_A11//2.00E-37//TC176813				
Unigene52338_A11	311	1.18	2.61	10.62	2.56	10.19	3.34	0.14	0.00	6.40	1.15E+00	1.48E-01		3.17E+00	2.07E-11	Up	1.99E+00	9.49E-08	Up	3.82E-01	6.27E-01		-7.09E+00	6.56E-01		5.56E+00	6.69E-13	Up	Unigene52338_A11//gi|18409172|ref|NP_566938.1|//5.00E-13//UGT72E1 (UDP-glucosyl transferase 72E1); UDP-glycosyltransferase/ coniferyl-alcohol glucosyltransferase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|15146272|gb|AAK83619.1| AT3g50740/T3A5_120 [Arabidopsis thaliana] >gi|53749150|gb|AAU90060.1| At3g50740 [Arabidopsis thaliana]	Unigene52338_A11//2.00E-14//AT3G50740| UGT72E1 (UDP-glucosyl transferase 72E1); UDP-glycosyltransferase/ coniferyl-alcohol glucosyltransferase/ transferase, transferring glycosyl groups	Unigene52338_A11//4.00E-47//ES845892		ko00940|Phenylpropanoid biosynthesis	GO:0009698//GO:0035251	nr +
Unigene5234_A11	713	7.12	6.96	2.84	6.57	5.99	8.04	22.00	23.27	25.98	-3.15E-02	9.20E-01		-1.33E+00	4.01E-06	Down	-1.33E-01	6.71E-01		2.93E-01	2.89E-01		8.11E-02	6.09E-01		2.40E-01	3.91E-02					Unigene5234_A11//1.00E-169//TC139576				
Unigene52341_A11	1141	0.00	0.18	0.28	0.00	0.00	0.75	9.41	6.23	34.39	7.47E+00	1.36E-01		8.13E+00	4.51E-02		null	null		9.55E+00	3.79E-05	Up	-5.96E-01	1.16E-04		1.87E+00	2.24E-91	Up	Unigene52341_A11//gi|115469074|ref|NP_001058136.1|//1.00E-101//Os06g0634300 [Oryza sativa Japonica Group] >gi|51535777|dbj|BAD37816.1| MutT domain protein-like [Oryza sativa Japonica Group] >gi|51535894|dbj|BAD37977.1| MutT domain protein-like [Oryza sativa Japonica Group] >gi|113596176|dbj|BAF20050.1| Os06g0634300 [Oryza sativa Japonica Group]	Unigene52341_A11//7.00E-97//AT5G47650| ATNUDT2 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 2); ADP-ribose diphosphatase/ NAD or NADH binding / hydrolase	Unigene52341_A11//1.00E-179//TC163797			GO:0000166//GO:0006950//GO:0019144//GO:0044444	nr -
Unigene52342_A11	1046	0.05	0.53	0.20	0.29	0.63	0.22	4.81	10.03	16.15	3.41E+00	1.24E-02		2.03E+00	3.61E-01		1.13E+00	2.38E-01		-4.04E-01	7.51E-01		1.06E+00	6.74E-11	Up	1.75E+00	2.43E-36	Up	Unigene52342_A11//gi|158512960|sp|A1LAY2.1|ADH3_ARATH//7.00E-17//RecName: Full=Alcohol dehydrogenase-like 3 >gi|119935936|gb|ABM06039.1| At1g32780 [Arabidopsis thaliana]	Unigene52342_A11//3.00E-17//AT1G32780| alcohol dehydrogenase, putative	Unigene52342_A11//2.00E-48//DR457092		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism	GO:0003824//GO:0005488	nr +
Unigene52343_A11	388	4.32	0.91	5.76	2.31	2.40	1.40	1.42	0.97	0.92	-2.24E+00	1.26E-04	Down	4.18E-01	3.69E-01		5.23E-02	9.59E-01		-7.26E-01	3.45E-01		-5.47E-01	5.52E-01		-6.16E-01	4.68E-01					Unigene52343_A11//0.00E+00//TC178388				
Unigene52346_A11	479	722.33	340.72	712.82	81.95	80.16	40.45	0.18	0.00	0.17	-1.08E+00	9.03E-284	Down	-1.91E-02	6.01E-01		-3.19E-02	7.99E-01		-1.02E+00	5.62E-32	Down	-7.46E+00	4.02E-01		-8.59E-02	9.71E-01		Unigene52346_A11//gi|68999972|emb|CAB71293.1|//6.00E-19//chloroplast ferredoxin-NADP+ oxidoreductase precursor [Capsicum annuum]	Unigene52346_A11//3.00E-11//AT5G66190| FNR1 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron transp	Unigene52346_A11//2.00E-151//TC144844		ko00195|Photosynthesis	GO:0006091//GO:0008937//GO:0009532//GO:0009534//GO:0030554//GO:0034357//GO:0051234	nr -
Unigene52349_A11	372	0.00	0.00	0.00	3.48	3.05	2.91	3.52	1.35	0.86	null	null		null	null		-1.89E-01	7.73E-01		-2.57E-01	6.87E-01		-1.39E+00	1.04E-02		-2.04E+00	3.01E-04	Down	Unigene52349_A11//gi|559921|emb|CAA56570.1|//3.00E-07//axi 1 [Nicotiana tabacum]	Unigene52349_A11//2.00E-14//AT4G38390| unknown protein					nr -
Unigene5235_A11	702	18.26	16.53	19.57	22.78	29.87	52.24	6.99	3.10	1.87	-1.44E-01	3.95E-01		1.00E-01	5.91E-01		3.91E-01	6.29E-04		1.20E+00	3.27E-38	Up	-1.17E+00	2.28E-06	Down	-1.90E+00	1.56E-12	Down	Unigene5235_A11//gi|255568518|ref|XP_002525233.1|//3.00E-14//Pectinesterase inhibitor, putative [Ricinus communis] >gi|223535530|gb|EEF37199.1| Pectinesterase inhibitor, putative [Ricinus communis]		Unigene5235_A11//0.00E+00//gi|109874070|gb|DW503045.1|DW503045				nr -
Unigene52352_A11	240	2.18	8.02	2.22	2.49	2.44	2.26	0.35	0.35	0.33	1.88E+00	2.67E-04	Up	2.54E-02	9.99E-01		-3.01E-02	9.50E-01		-1.41E-01	8.79E-01		-1.65E-02	1.01E+00		-8.56E-02	9.71E-01					Unigene52352_A11//3.00E-07//ES821270				
Unigene52354_A11	302	0.69	1.34	2.47	3.30	0.46	2.39	1.54	1.66	0.53	9.54E-01	4.14E-01		1.83E+00	5.05E-02		-2.85E-00	2.37E-04	Down	-4.63E-01	5.26E-01		1.09E-01	9.14E-01		-1.55E+00	1.16E-01									
Unigene52355_A11	1043	0.00	0.00	0.00	0.00	0.00	0.09	39.04	7.37	5.39	null	null		null	null		null	null		6.44E+00	4.75E-01		-2.40E+00	3.58E-128	Down	-2.86E+00	2.44E-160	Down	Unigene52355_A11//gi|23394354|gb|AAN31467.1|//1.00E-103//ADP/ATP translocase [Phytophthora infestans]	Unigene52355_A11//1.00E-77//AT4G28390| AAC3 (ADP/ATP CARRIER 3); ATP:ADP antiporter/ binding	Unigene52355_A11//8.00E-08//TC159127			GO:0006862//GO:0009526//GO:0009987//GO:0015300//GO:0019866	nr -
Unigene52356_A11	332	55.63	25.33	55.82	372.56	348.50	482.38	242.22	749.68	343.79	-1.13E+00	5.72E-17	Down	4.80E-03	9.97E-01		-9.63E-02	5.00E-02		3.73E-01	7.29E-22		1.63E+00	0.00E+00	Up	5.05E-01	7.84E-32		Unigene52356_A11//gi|21322711|emb|CAD22154.1|//1.00E-21//pherophorin-dz1 protein [Volvox carteri f. nagariensis]		Unigene52356_A11//1.00E-13//TC138902				nr +
Unigene5236_A11	786	1.73	0.71	2.98	4.56	3.07	1.90	3.39	2.02	1.67	-1.29E+00	2.82E-02		7.84E-01	7.27E-02		-5.73E-01	7.03E-02		-1.27E+00	1.06E-04	Down	-7.46E-01	3.09E-02		-1.02E+00	2.37E-03					Unigene5236_A11//1.00E-67//ES834205				
Unigene52360_A11	289	4.89	2.45	1.84	4.83	0.48	1.56	0.73	0.87	1.65	-9.94E-01	7.78E-02		-1.41E+00	2.12E-02		-3.34E+00	8.78E-07	Down	-1.63E+00	5.90E-03		2.46E-01	8.53E-01		1.18E+00	2.18E-01		Unigene52360_A11//gi|109946589|gb|ABG48473.1|//6.00E-24//At3g19810 [Arabidopsis thaliana]	Unigene52360_A11//3.00E-22//AT3G19810| unknown protein	Unigene52360_A11//5.00E-117//gi|48748460|gb|CO078979.1|CO078979			GO:0009536	nr +
Unigene52361_A11	470	11.02	17.57	12.69	16.43	17.14	15.76	47.68	32.19	20.26	6.73E-01	8.37E-04		2.03E-01	4.43E-01		6.16E-02	8.34E-01		-6.00E-02	7.96E-01		-5.67E-01	3.84E-08		-1.23E+00	3.18E-29	Down				Unigene52361_A11//0.00E+00//TC159248				
Unigene52368_A11	331	0.63	0.00	3.86	1.35	3.43	2.05	0.26	1.01	1.20	-9.30E+00	1.22E-01		2.61E+00	5.00E-04	Up	1.34E+00	4.23E-02		5.96E-01	5.26E-01		1.98E+00	1.44E-01		2.24E+00	6.42E-02									
Unigene52369_A11	399	0.13	5.08	0.53	0.00	0.52	2.26	3.50	6.49	4.99	5.28E+00	2.99E-10	Up	2.03E+00	3.61E-01		9.02E+00	1.57E-01		1.11E+01	2.07E-05	Up	8.93E-01	1.10E-02		5.14E-01	2.00E-01		Unigene52369_A11//gi|20197329|gb|AAC63841.2|//2.00E-30//expressed protein [Arabidopsis thaliana] >gi|98960999|gb|ABF58983.1| At2g31090 [Arabidopsis thaliana]	Unigene52369_A11//1.00E-12//AT2G31090| unknown protein				GO:0031410	nr +
Unigene5237_A11	900	1.51	1.07	2.13	2.16	4.67	2.76	1.17	4.78	2.26	-4.99E-01	3.80E-01		4.95E-01	3.22E-01		1.11E+00	1.11E-04	Up	3.55E-01	4.23E-01		2.03E+00	1.42E-11	Up	9.43E-01	1.62E-02		Unigene5237_A11//gi|15218429|ref|NP_177982.1|//3.00E-25//MSL6 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 6) [Arabidopsis thaliana] >gi|75213461|sp|Q9SYM1.1|Y1861_ARATH RecName: Full=Uncharacterized mscS family protein At1g78610 >gi|4836872|gb|AAD30575.1|AC007260_6 Hypothetical protein [Arabidopsis thaliana]	Unigene5237_A11//2.00E-26//AT1G78610| MSL6 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 6)	Unigene5237_A11//3.00E-84//AI730054				nr +
Unigene52370_A11	708	0.52	0.64	0.23	0.42	0.58	0.26	5.49	17.59	3.49	3.16E-01	7.44E-01		-1.20E+00	3.96E-01		4.67E-01	7.41E-01		-7.26E-01	6.38E-01		1.68E+00	5.03E-25	Up	-6.55E-01	1.39E-02		Unigene52370_A11//gi|28372890|gb|AAO39927.1|//2.00E-16//At3g10120 [Arabidopsis thaliana]	Unigene52370_A11//7.00E-23//AT5G03890| unknown protein	Unigene52370_A11//0.00E+00//TC144126				nr -
Unigene52371_A11	315	0.66	0.00	0.00	6.80	2.73	0.57	0.54	1.72	0.38	-9.38E+00	1.22E-01		-9.38E+00	1.45E-01		-1.32E+00	1.63E-03		-3.57E+00	2.47E-09	Down	1.68E+00	7.91E-02		-5.01E-01	7.46E-01									
Unigene52372_A11	300	7.50	6.42	7.10	9.63	4.48	3.31	4.09	4.74	1.73	-2.25E-01	5.92E-01		-7.89E-02	8.56E-01		-1.11E+00	1.41E-03		-1.54E+00	5.05E-05	Down	2.13E-01	6.74E-01		-1.24E+00	1.98E-02					Unigene52372_A11//8.00E-73//gi|31073429|gb|CA993708.1|CA993708				
Unigene52373_A11	346	26.31	21.53	12.62	35.42	39.51	48.17	11.00	10.99	8.75	-2.90E-01	1.43E-01		-1.06E+00	1.55E-07	Down	1.58E-01	3.73E-01		4.44E-01	1.00E-03		-7.00E-04	9.97E-01		-3.30E-01	2.43E-01					Unigene52373_A11//2.00E-104//gi|109887671|gb|DW516640.1|DW516640				
Unigene52374_A11	523	4.70	2.52	4.28	5.14	3.16	1.64	0.65	0.16	0.00	-9.01E-01	2.59E-02		-1.37E-01	7.36E-01		-7.03E-01	5.69E-02		-1.65E+00	3.87E-05	Down	-2.02E+00	1.36E-01		-9.34E+00	8.14E-03					Unigene52374_A11//6.00E-07//EX164877				
Unigene52377_A11	740	0.00	2.40	0.65	0.00	0.00	0.37	2.17	9.66	111.87	1.12E+01	4.14E-10	Up	9.34E+00	7.47E-03		null	null		8.52E+00	7.02E-02		2.15E+00	3.45E-20	Up	5.69E+00	0.00E+00	Up				Unigene52377_A11//0.00E+00//TC159434				
Unigene52378_A11	368	0.57	3.99	0.29	0.00	1.22	0.49	0.57	1.02	2.27	2.81E+00	4.57E-05	Up	-9.75E-01	6.20E-01		1.02E+01	8.01E-03		8.94E+00	1.94E-01		8.31E-01	4.67E-01		1.98E+00	7.05E-03									
Unigene52381_A11	1651	0.19	0.06	0.52	0.24	0.42	0.19	5.92	5.95	20.20	-1.63E+00	2.76E-01		1.44E+00	8.22E-02		7.89E-01	4.04E-01		-3.34E-01	7.56E-01		8.10E-03	1.00E+00		1.77E+00	2.75E-72	Up	Unigene52381_A11//gi|121501706|gb|ABM55247.1|//1.00E-168//calmodulin-binding protein [Beta vulgaris]	Unigene52381_A11//4.00E-149//AT4G33050| EDA39 (embryo sac development arrest 39); calmodulin binding	Unigene52381_A11//7.00E-102//DN817850				nr -
Unigene52382_A11	1629	0.19	1.06	1.34	5.84	14.95	11.59	0.00	0.00	0.15	2.46E+00	3.84E-05	Up	2.80E+00	7.02E-07	Up	1.36E+00	1.04E-33	Up	9.89E-01	9.18E-15		null	null		7.20E+00	4.39E-02		Unigene52382_A11//gi|109628383|gb|ABG34547.1|//0.00E+00//cellulose synthase-like A1 [Pinus taeda]	Unigene52382_A11//0.00E+00//AT5G03760| ATCSLA09; mannan synthase/ transferase, transferring glycosyl groups	Unigene52382_A11//3.00E-45//TC136449			GO:0009292//GO:0016759//GO:0019187//GO:0044464//GO:0051707	nr +
Unigene52383_A11	356	2.79	7.97	9.12	5.88	3.19	5.07	1.43	0.12	0.45	1.51E+00	1.25E-04	Up	1.71E+00	9.75E-06	Up	-8.81E-01	3.80E-02		-2.12E-01	6.63E-01		-3.60E+00	5.77E-03		-1.67E+00	7.77E-02					Unigene52383_A11//9.00E-36//CO094199				
Unigene52384_A11	318	31.75	129.54	88.25	40.26	126.91	62.77	73.66	77.28	97.59	2.03E+00	2.36E-85	Up	1.47E+00	1.83E-36	Up	1.66E+00	1.20E-74	Up	6.41E-01	9.75E-08		6.93E-02	5.85E-01		4.06E-01	1.58E-06		Unigene52384_A11//gi|224134172|ref|XP_002321754.1|//2.00E-08//predicted protein [Populus trichocarpa] >gi|118488859|gb|ABK96239.1| unknown [Populus trichocarpa x Populus deltoides] >gi|222868750|gb|EEF05881.1| predicted protein [Populus trichocarpa]		Unigene52384_A11//1.00E-87//gi|109832491|gb|DW231050.1|DW231050				nr +
Unigene52387_A11	478	3.61	2.33	0.00	3.33	2.23	0.66	0.00	0.09	0.08	-6.31E-01	2.08E-01		-1.18E+01	1.99E-09	Down	-5.78E-01	2.71E-01		-2.33E+00	8.01E-05	Down	6.45E+00	6.34E-01		6.38E+00	6.44E-01					Unigene52387_A11//7.00E-96//gi|164306863|gb|ES841525.1|ES841525				
Unigene52388_A11	477	2.08	0.85	0.45	1.15	0.65	0.95	1.95	1.84	7.27	-1.29E+00	6.74E-02		-2.22E+00	7.48E-03		-8.22E-01	3.96E-01		-2.79E-01	7.57E-01		-8.37E-02	9.05E-01		1.90E+00	5.68E-09	Up								
Unigene52389_A11	943	0.00	0.00	0.00	0.00	0.00	0.53	3.77	5.54	46.89	null	null		null	null		null	null		9.04E+00	4.38E-03		5.57E-01	1.78E-02		3.64E+00	1.49E-214	Up	Unigene52389_A11//gi|62867641|gb|AAY17424.1|//1.00E-47//At2g01340 [Arabidopsis thaliana] >gi|94442481|gb|ABF19028.1| At2g01340 [Arabidopsis thaliana]	Unigene52389_A11//2.00E-49//AT2G01340| unknown protein	Unigene52389_A11//4.00E-34//FF403790			GO:0009416//GO:0009902//GO:0016020	nr +
Unigene5239_A11	811	5.55	0.94	3.15	3.81	2.63	1.78	0.83	0.21	1.42	-2.57E+00	4.89E-13	Down	-8.16E-01	6.12E-03		-5.33E-01	1.29E-01		-1.10E+00	1.92E-03		-2.02E+00	1.98E-02		7.72E-01	1.59E-01		Unigene5239_A11//gi|17065212|gb|AAL32760.1|//2.00E-87//Unknown protein [Arabidopsis thaliana]	Unigene5239_A11//3.00E-81//AT3G14850| unknown protein	Unigene5239_A11//0.00E+00//C0091936				nr -
Unigene52390_A11	414	2.91	12.61	5.66	3.13	3.74	14.40	61.07	138.71	117.01	2.12E+00	5.57E-12	Up	9.61E-01	2.79E-02		2.59E-01	6.64E-01		2.20E+00	4.80E-15	Up	1.18E+00	9.14E-67	Up	9.38E-01	8.70E-40					Unigene52390_A11//7.00E-111//EX169625				
Unigene52392_A11	2467	0.00	0.00	0.00	0.00	0.00	0.00	11.57	3.90	7.70	null	null		null	null		null	null		null	null		-1.57E+00	2.41E-51	Down	-5.87E-01	4.34E-11		Unigene52392_A11//gi|224098764|ref|XP_002311259.1|//0.00E+00//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222851079|gb|EEE88626.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene52392_A11//4.00E-125//AT5G17430| BBM (BABY BOOM); DNA binding / transcription factor	Unigene52392_A11//7.00E-38//TC140815	AP2-EREBP		GO:0006350//GO:0010468	nr +
Unigene52393_A11	431	6.07	1.06	3.21	2.31	2.72	1.47	0.39	0.00	0.18	-2.52E+00	1.03E-07	Down	-9.18E-01	2.49E-02		2.33E-01	7.69E-01		-6.56E-01	3.71E-01		-8.62E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene52393_A11//gi|15238110|ref|NP_196587.1|//5.00E-45//DOT3 (DEFECTIVELY ORGANIZED TRIBUTARIES 3); protein binding / signal transducer [Arabidopsis thaliana] >gi|8953406|emb|CAB96681.1| non-phototropic hypocotyl 3-like protein [Arabidopsis thaliana]	Unigene52393_A11//3.00E-46//AT5G10250| DOT3 (DEFECTIVELY ORGANIZED TRIBUTARIES 3); protein binding / signal transducer				GO:0005488//GO:0009314//GO:0009606//GO:0009888//GO:0010051//GO:0030522//GO:0048364//GO:0060089	nr +
Unigene52394_A11	570	1.01	1.07	0.37	2.18	1.57	2.93	1.56	4.03	8.46	7.92E-02	9.41E-01		-1.43E+00	1.75E-01		-4.76E-01	4.39E-01		4.24E-01	4.48E-01		1.37E+00	4.17E-04	Up	2.44E+00	2.39E-16	Up								

Unigene52396_All	766	329.36	160.74	159.33	391.17	392.27	388.07	307.94	154.63	162.11	-1.03E+00	5.79E-192	Down	-1.05E+00	5.61E-190	Down	4.10E-03	9.22E-01		-1.14E-02	7.57E-01		-9.94E-01	2.58E-205		-9.26E-01	2.11E-187		Unigene52396_All//gi|18413144|ref|NP_567338.1|//3.00E-27//SAM7 [Arabidopsis thaliana] >gi|4584110|emb|CAB10579.1| SAM7 protein [Arabidopsis thaliana] >gi|21553842|gb|AAM62935.1| allergen-like protein BRSn20 [Arabidopsis thaliana]	Unigene52396_All//1.00E-28//AT4G08685| SAM7	Unigene52396_All//0.00E+00//TC151040			GO:0044421	nr -
Unigene52397_All	322	1.46	2.52	0.50	5.72	1.60	0.42	3.81	0.78	0.99	7.84E-01	3.23E-01		-1.56E+00	2.04E-01		-1.84E+00	1.14E-04	Down	-3.77E+00	2.03E-08	Down	-2.29E+00	2.57E-04	Down	-1.94E+00	7.80E-04	Down				Unigene52397_All//4.00E-07//TC140654				
Unigene52398_All	224	56.29	7.92	11.17	20.24	6.30	3.43	0.76	0.00	0.00	-2.83E+00	2.33E-39	Down	-2.33E+00	1.79E-30	Down	-1.68E+00	1.65E-09	Down	-2.56E+00	4.55E-14	Down	-9.56E+00	1.34E-01		-9.56E+00	1.08E-01					Unigene52398_All//2.00E-11//CO998846				
Unigene52399_All	274	0.00	2.96	0.78	0.73	0.63	0.16	4.01	2.90	1.16	1.15E+01	9.37E-05	Up	9.60E+00	1.41E-01		-2.11E-01	8.58E-01		-2.14E+00	3.47E-01		-4.69E-01	4.31E-01		-1.79E+00	3.06E-03					Unigene52399_All//1.00E-71//TC179461				
Unigene5240_All	754	7.56	7.32	5.72	10.83	13.20	14.38	14.30	12.20	7.03	-4.63E-02	8.59E-01		-4.03E-01	1.35E-01		2.85E-01	1.39E-01		4.08E-01	2.06E-02		-2.30E-01	1.72E-01		-1.02E+00	5.46E-11	Down	Unigene5240_All//gi|4559355|gb|AAD23016.1|//3.00E-47//expressed protein [Arabidopsis thaliana] >gi|88900396|gb|ABD57510.1| At2g24970 [Arabidopsis thaliana]	Unigene5240_All//1.00E-43//AT2G24970| unknown protein	Unigene5240_All//0.00E+00//DN817122				nr -
Unigene52404_All	359	0.00	2.54	0.00	0.56	1.34	0.38	0.59	1.28	1.33	1.13E+01	2.62E-05	Up	null	null		1.27E+00	2.92E-01		-5.56E-01	7.32E-01		1.12E+00	2.74E-01		1.18E+00	2.18E-01										
Unigene52405_All	556	0.19	0.36	1.05	0.72	0.99	1.54	2.89	2.03	0.64	9.54E-01	6.21E-01		2.48E+00	3.75E-02		4.67E-01	6.68E-01		1.11E+00	1.67E-01		-5.10E-01	2.90E-01		-2.16E+00	2.38E-05	Down			Unigene52405_All//9.00E-31//CO128536				
Unigene52409_All	289	3.80	0.35	0.92	2.41	1.67	2.50	0.44	0.14	0.69	-3.44E+00	1.19E-04	Down	-2.05E+00	7.42E-03		-5.33E-01	5.45E-01		5.13E-02	9.48E-01		-1.60E+00	5.34E-01		6.51E-01	6.65E-01		Unigene52409_All//gi|240254313|ref|NP_176555.4|//4.00E-13//MURE; ATP binding / acid-amino acid ligase/ ligase [Arabidopsis thaliana]	Unigene52409_All//5.00E-65//AT1G63680| MURE; ATP binding / acid-amino acid ligase/ ligase	Unigene52409_All//2.00E-122//BQ404111				nr -
Unigene52412_All	773	0.00	66.14	26.73	0.00	0.00	0.00	0.00	0.00	0.00	1.60E+01	2.30E-295	Up	1.47E+01	8.56E-117	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene52413_All	816	0.13	0.00	0.13	0.12	0.08	0.00	20.47	54.45	407.37	-7.00E+00	3.70E-01		2.57E-02	9.99E-01		-5.33E-01	8.16E-01		-6.93E+00	3.99E-01		1.41E+00	7.01E-68	Up	4.32E+00	0.00E+00	Up	Unigene52413_All//gi|115442287|ref|NP_001045423.1|//1.00E-42//Os01g0952900 [Oryza sativa Japonica Group] >gi|113534954|dbj|BAF07337.1| Os01g0952900 [Oryza sativa Japonica Group]	Unigene52413_All//2.00E-46//AT5G12340| unknown protein					nr +
Unigene52414_All	1246	0.00	0.00	0.34	0.24	0.06	0.00	6.72	24.35	24.62	null	null		8.42E+00	1.38E-02		-2.12E+00	1.65E-01		-7.91E+00	3.99E-02		1.86E+00	7.86E-69	Up	1.87E+00	8.37E-72	Up	Unigene52414_All//gi|15227849|ref|NP_179935.1|//1.00E-167//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75099763|sp|Q80470.1|GDL38_ARATH RecName: Full=GDSL esterase/lipase At2g23540; AltName: Full=Extracellular lipase At2g23540; Flags: Precursor	Unigene52414_All//5.00E-169//AT2G23540| GDSL-motif lipase/hydrolase family protein	Unigene52414_All//0.00E+00//TC167644				nr -
Unigene52417_All	456	13.77	5.67	7.82	13.11	13.67	16.54	13.91	5.50	9.09	-1.28E+00	1.93E-07	Down	-8.15E-01	8.89E-04		6.03E-02	8.20E-01		3.35E-01	1.37E-01		-1.34E+00	1.23E-09	Down	-6.14E-01	2.35E-03				Unigene52417_All//3.00E-116//TC171254				
Unigene52418_All	563	1.21	0.00	2.18	1.15	2.14	2.97	0.60	0.97	0.78	-1.02E+01	4.10E-04	Down	8.49E-01	1.85E-01		8.96E-01	1.61E-01		1.37E+00	9.52E-03		6.84E-01	4.49E-01		3.74E-01	6.82E-01		Unigene52418_All//gi|29892204|gb|AF003013.1|//3.00E-53//seed calcium dependent protein kinase b [Glycine max]	Unigene52418_All//1.00E-52//AT1G35670| ATCDPK2 (CALCIUM-DEPENDENT PROTEIN KINASE 2); calmodulin-dependent protein kinase/ kinase	Unigene52418_All//4.00E-45//TC139849		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0009738//GO:0016020//GO:0032559//GO:0046872	nr +
Unigene52419_All	592	7.95	5.14	7.83	0.17	0.47	0.08	1.50	0.28	0.00	-6.31E-01	2.29E-02		-2.35E-02	9.54E-01		1.47E+00	4.20E-01		-1.14E+00	6.76E-01		-2.41E+00	1.79E-03		-1.06E+01	1.10E-06	Down	Unigene52419_All//gi|115445205|ref|NP_001046382.1|//2.00E-08//Os02g0234700 [Oryza sativa Japonica Group] >gi|113535913|dbj|BAF08296.1| Os02g0234700 [Oryza sativa Japonica Group]						nr -
Unigene52420_All	1025	0.36	0.00	0.73	0.29	0.27	0.18	4.08	1.55	3.73	-8.48E+00	1.96E-02		1.03E+00	2.37E-01		-1.18E-01	9.00E-01		-7.27E-01	6.38E-01		-1.40E+00	5.05E-07	Down	-1.30E-01	6.50E-01		Unigene52420_All//gi|224112635|ref|XP_002332743.1|//8.00E-79//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222833055|gb|EEE71532.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene52420_All//3.00E-31//AT4G27220| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction	GO:0005488//GO:0016787	nr +
Unigene52424_All	956	0.00	0.21	0.45	0.26	0.14	0.00	10.92	52.24	13.13	7.73E+00	1.36E-01		8.80E+00	1.38E-02		-8.54E-01	5.73E-01		-8.03E+00	7.33E-02		2.26E+00	3.17E-145	Up	2.65E-01	6.58E-02		Unigene52424_All//gi|2688828|gb|AAB88878.1|//7.00E-72//ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]	Unigene52424_All//9.00E-71//AT5G20400| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene52424_All//3.00E-112//C0125364		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis	GO:0009699//GO:0016701//GO:0016706	nr +
Unigene52426_All	457	1.72	1.11	2.68	5.01	4.37	1.78	0.19	0.00	0.00	-6.31E-01	4.08E-01		6.42E-01	3.19E-01		-1.98E-01	6.53E-01		-1.50E+00	5.62E-04	Down	-7.53E+00	4.02E-01		-7.53E+00	3.58E-01									
Unigene52427_All	416	3.65	1.83	8.45	5.15	1.90	3.37	1.22	0.30	0.38	-9.97E-01	6.49E-02		1.21E+00	5.40E-04	Up	-1.44E+00	6.37E-04	Down	-6.14E-01	1.77E-01		-2.02E+00	5.20E-02		-1.67E+00	7.77E-02		Unigene52427_All//gi|147799140|emb|CAN70392.1|//2.00E-14//hypothetical protein [Vitis vinifera]						nr -
Unigene52429_All	332	61.30	23.35	45.07	42.01	36.20	40.40	30.31	20.27	18.24	-1.39E+00	2.33E-25	Down	-4.44E-01	4.58E-04		-2.15E-01	1.80E-01		-5.64E-02	7.44E-01		-5.81E-01	2.95E-04		-7.33E-01	3.16E-06		Unigene52429_All//gi|5822270|pdb|1QGN|A//6.00E-51//Chain A, Cystathionine Gamma-Synthase From Nicotiana Tabacum >gi|5822271|pdb|1QGN|B Chain B, Cystathionine Gamma-Synthase From Nicotiana Tabacum >gi|5822272|pdb|1QGN|C Chain C, Cystathionine Gamma-Synthase From Nicotiana Tabacum >gi|5822273|pdb|1QGN|D Chain D, Cystathionine Gamma-Synthase From Nicotiana Tabacum >gi|5822274|pdb|1QGN|E Chain E, Cystathionine Gamma-Synthase From Nicotiana Tabacum >gi|5822275|pdb|1QGN|F Chain F, Cystathionine Gamma-Synthase From Nicotiana Tabacum >gi|5822276|pdb|1QGN|G Chain G, Cystathionine Gamma-Synthase From Nicotiana Tabacum >gi|5822277|pdb|1QGN|H Chain H, Cystathionine Gamma-Synthase From Nicotiana Tabacum >gi|15826471|pdb|1I41|A Chain A, Cystathionine Gamma-Synthase In Complex With The Inhibitor Appa >gi|15826472|pdb|1I41|B Chain B, Cystathionine Gamma-Synthase In	Unigene52429_All//7.00E-50//AT3G01120| MTO1 (METHIONINE OVERACCUMULATION 1); cystathionine gamma-synthase	Unigene52429_All//0.00E+00//TC133947		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0000097//GO:0009536//GO:0016765//GO:0048037	nr -
Unigene5243_All	824	8.45	183.25	7.30	10.22	64.15	39.30	35.61	95.82	72.04	4.44E+00	0.00E+00	Up	-2.10E-01	4.00E-01		2.65E+00	4.38E-176	Up	1.94E+00	4.06E-68	Up	1.43E+00	3.56E-122	Up	1.02E+00	2.49E-55	Up	Unigene5243_All//gi|88900428|gb|ABD57526.1|//7.00E-08//Atfg35090 [Arabidopsis thaliana]	Unigene5243_All//3.00E-07//AT5G11070| unknown protein	Unigene5243_All//0.00E+00//TC147695				nr +
Unigene52430_All	320	2.62	0.32	0.00	0.31	0.86	0.85	1.45	1.70	1.00	-3.05E+00	2.11E-03		-1.14E+01	1.19E-04	Down	1.47E+00	4.20E-01		1.44E+00	4.09E-01		2.24E-01	7.92E-01		-5.45E-01	5.65E-01		Unigene52430_All//gi|15236212|ref|NP_192199.1|//5.00E-34//early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana]	Unigene52430_All//1.00E-23//AT4G02900| early-responsive to dehydration protein-related / ERD protein-related	Unigene52430_All//4.00E-10//TC141805			GO:0016020	nr -
Unigene52433_All	258	2.23	0.20	0.83	4.63	6.67	2.98	53.92	50.71	23.32	-3.51E+00	9.02E-03		-1.43E+00	1.75E-01		5.26E-01	3.15E-01		-6.39E-01	3.24E-01		-8.85E-02	6.09E-01		-1.21E+00	6.58E-18	Down			Unigene52433_All//2.00E-128//TC156011				
Unigene52435_All	600	0.35	0.93	0.80	14.61	15.55	5.19	1.20	0.07	0.46	1.41E+00	1.69E-01		1.20E+00	3.02E-01		9.00E-02	7.06E-01		-1.49E+00	2.35E-13	Down	-4.10E+00	2.91E-04	Down	-1.37E+00	6.50E-02		Unigene52435_All//gi|156739648|gb|ABU93485.1|//5.00E-93//xyloglucan endotragluco sylase/hydrolase [Vigna angularis]	Unigene52435_All//1.00E-88//AT2G36870| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene52435_All//0.00E+00//gi|78331183|gb|DT551457.1|DT551457			GO:0005576//GO:0016758//GO:0016798//GO:0030312//GO:0044042	nr -
Unigene52436_All	762	0.00	0.00	0.00	0.00	0.00	0.00	45.17	28.63	21.96	null	null		null	null		null	null		null	null		-6.58E-01	1.74E-15		-1.04E+00	6.34E-34	Down	Unigene52436_All//gi|18390043|gb|AAL68830.1|AF463407_1|//2.00E-29//Enod8.3 [Medicago truncatula]	Unigene52436_All//2.00E-23//AT3G26430| GDSL-motif lipase/hydrolase family protein	Unigene52436_All//2.00E-159//DR457749			GO:0006950//GO:0016787//GO:0019865//GO:0044238	nr +
Unigene52438_All	647	0.16	0.16	0.00	1.31	0.85	0.07	2.81	3.36	1.29	-4.62E-02	9.88E-01		-7.34E+00	3.92E-01		-6.20E-01	4.13E-01		-4.23E+00	2.18E-04	Down	2.58E-01	5.51E-01		-1.12E+00	7.71E-03		Unigene52438_All//gi|227204351|dbj|BAH57027.1|//4.00E-27//AT3G26890 [Arabidopsis thaliana]	Unigene52438_All//2.00E-28//AT3G26890| unknown protein	Unigene52438_All//0.00E+00//ES827937				nr -
Unigene5244_All	1220	3.04	6.81	7.68	5.39	9.77	9.48	1.28	0.07	0.26	1.16E+00	2.66E-08	Up	1.34E+00	7.04E-11	Up	8.58E-01	3.10E-08		8.14E-01	7.06E-07		-4.23E+00	7.78E-09	Down	-2.30E+00	1.48E-05	Down	Unigene5244_All//gi|224121532|ref|XP_002318608.1|//2.00E-67//porin/voltage-dependent anion-selective channel protein [Populus trichocarpa] >gi|222859281|gb|EEE96828.1| porin/voltage-dependent anion-selective channel protein [Populus trichocarpa]	Unigene5244_All//3.00E-38//AT3G01280| VDAC1 (VOLTAGE DEPENDENT ANION CHANNEL 1); voltage-gated anion channel					nr -
Unigene52441_All	435	8.18	13.16	3.18	0.92	6.25	4.36	0.00	0.00	0.00	6.86E-01	5.69E-03		-1.36E+00	1.17E-04	Down	2.77E+00	1.33E-09	Up	2.25E+00	2.85E-05	Up	null	null		null	null		Unigene52441_All//gi|146742170|gb|ABQ42622.1|//4.00E-29//snakin-1 [Solanum chacoense]	Unigene52441_All//1.00E-24//AT5G59845| gibberellin-regulated family protein	Unigene52441_All//2.00E-160//gi|164297320|gb|ES811205.1|ES811205			GO:0006950//GO:0030312	nr -
Unigene52442_All	376	1.67	8.36	1.84	1.59	3.11	0.60	2.59	5.67	4.24	2.32E+00	2.66E-08	Up	1.41E-01	8.60E-01		9.70E-01	1.37E-01		-1.40E+00	1.58E-01		1.13E+00	4.44E-03		7.13E-01	1.15E-01		Unigene52442_All//gi|229609825|gb|ACQ83528.1|//9.00E-09//CBL-interacting protein kinase 12 [Vitis vinifera]	Unigene52442_All//4.00E-09//AT3G26890| CIPK3 (CBL-INTERACTING PROTEIN KINASE 3); kinase/ protein kinase/ protein serine/threonine kinase	Unigene52442_All//2.00E-132//gi|78354088|gb|DT574362.1|DT574362				nr +
Unigene52445_All	432	2.66	0.47	0.62	0.46	0.80	0.84	2.35	0.97	1.84	-2.51E+00	8.99E-04	Down	-2.11E+00	4.75E-03		7.89E-01	5.96E-01		8.59E-01	5.42E-01		-1.28E+00	4.06E-02		-3.49E-01	5.71E-01									
Unigene52446_All	1051	0.00	0.00	0.00	5.40	2.20	2.23	0.20	0.00	0.08	null	null		null	null		-1.30E+00	3.82E-08	Down	-1.27E+00	4.21E-07	Down	-7.65E+00	7.43E-02		-1.41E+00	3.80E-01		Unigene52446_All//gi|46402545|gb|AAS92346.1|//1.00E-115//MYB7 [Gossypium hirsutum]	Unigene52446_All//2.00E-39//AT3G13890| ATMYB26 (MYB DOMAIN PROTEIN 26); DNA binding / transcription factor	Unigene52446_All//0.00E+00//TC179183	MYB		GO:0003676//GO:0010468//GO:0043231	nr -
Unigene52449_All	658	0.00	59.22	21.61	0.00	0.52	0.00	0.00	0.00	0.00	1.59E+01	6.87E-225	Up	1.44E+01	4.21E-80	Up	9.03E+00	3.01E-02		null	null		null	null		null	null		Unigene52449_All//gi|239811670|gb|ACS27156.1|//1.00E-59//cytochrome c oxidase subunit II [Heterosigma akashiwo]	Unigene52449_All//2.00E-48//ATMG00160| cytochrome c oxidase subunit 2			ko00190|Oxidative phosphorylation	GO:0016020//GO:0046872//GO:0055114	nr +
Unigene5245_All	1103	7.02	6.48	7.72	9.71	8.52	8.52	6.55	3.07	1.66	-1.16E-01	6.01E-01		1.38E-01	5.51E-01		-1.88E-01	3.24E-01		-1.89E-01	3.46E-01		-1.09E+00	3.84E-08	Down	-1.98E+00	4.57E-19	Down	Unigene5245_All//gi|15231858|ref|NP_188063.1|//1.00E-109//CID9 (CTC-Interacting Domain 9); RNA binding / protein binding [Arabidopsis thaliana]	Unigene5245_All//3.00E-95//AT3G14450| CID9 (CTC-Interacting Domain 9); RNA binding / protein binding	Unigene5245_All//0.00E+00//TC144299				nr +
Unigene52452_All	588	0.80	0.17	0.18	2.63	1.00	0.46	2.95	0.36	0.61	-2.22E+00	7.76E-02		-2.14E+00	1.03E-01		-1.40E+00	6.23E-03		-2.51E+00	4.81E-05	Down	-3.05E+00	1.18E-07	Down	-2.27E+00	5.17E-06	Down	Unigene52452_All//gi|254789790|sp|B9SVG9.1|RBR_RICCO//4.00E-68//RecName: Full=Retinoblastoma-related protein	Unigene52452_All//1.00E-58//AT3G12280| RBR1 (RETINOBLASTOMA-RELATED 1); transcription factor binding	Unigene52452_All//0.00E+00//gi|3326125|gb|AI055011.1|AI055011			GO:0000904//GO:0005515//GO:0009566//GO:0010564//GO:0010049//GO:0033043//GO:0040029//GO:0043231//GO:0044444//GO:0045165//GO:0048229//GO:0048523//GO:0048827	nr -
Unigene52453_All	533	27.98	19.87	16.88	51.87	40.70	34.40	32.05	19.06	13.90	-4.94E-01	6.40E-04		-7.29E-01	1.20E-06		-3.50E-01	3.08E-04		-5.92E-01	2.99E-09		-7.50E-01	5.44E-10		-1.20E+00	1.14E-21	Down			Unigene52453_All//8.00E-28//DN511731				
Unigene52454_All	632	39.49	6.65	19.04	0.00	0.00	0.00	0.00	0.00	0.00	-2.57E+00	1.15E-69	Down	-1.05E+00	2.55E-19	Down	null	null		null	null		null	null		null	null		Unigene52454_All//gi|110931770|gb|ABH02884.1|//1.00E-25//MYB transcription factor WYB164 [Glycine max]	Unigene52454_All//6.00E-18//AT1G75250| ATRL6 (ARABIDOPSIS RAD-LIKE 6); transcription factor	Unigene52454_All//2.00E-38//TC159089	MYB-related		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene52456_All	489	1.39	0.21	1.74	0.00	0.14	1.94	0.09	4.27	0.08	-2.75E+00	1.06E-02		3.25E-01	6.46E-01		7.14E+00	6.08E-01		1.09E+01	1.13E-05	Up	5.63E+00	2.59E-13	Up	-8.59E-02	9.71E-01		Unigene52456_All//gi|78059502|gb|AB018115.1|//9.00E-08//RPN9 [Nicotiana benthamiana]	Unigene52456_All//6.00E-09//AT5G45620| 26S proteasome regulatory subunit, putative (RPN9)	Unigene52456_All//2.00E-37//TC139783		ko03050|Proteasome	GO:0005838//GO:0019941//GO:0043231	nr +
Unigene52457_All	488	0.64	0.93	2.07	2.65	1.34	0.37	3.38	2.06	2.04	5.39E-01	6.02E-01		1.69E+00	2.74E-02		-9.85E-01	8.32E-02		-2.84E+00	7.63E-05	Down	-7.17E-01	1.22E-01		-7.27E-01	9.84E-02		Unigene52457_All//gi|21425637|emb|CAC82574.2|//1.00E-11//phage-type RNA polymerase [Nicotiana tabacum]	Unigene52457_All//7.00E-12//AT1G68990| DNA-directed RNA polymerase, mitochondrial (RPOMT)	Unigene52457_All//1.00E-54//ES795849				nr +

Unigene52458_All	748	0.56	2.17	0.28	1.93	3.36	0.85	2.20	2.68	0.75	1.95E+00	6.79E-04	Up	-9.74E-01	4.11E-01		7.99E-01	4.42E-02		-1.19E+00	3.43E-02		2.83E-01	5.33E-01		-1.56E+00	7.74E-04	Down	Unigene52458_All//gi|212717155|gb|ACJ37419.1|//1.00E-26//NBS-LRR disease resistance protein [Glycine max]	Unigene52458_All//1.00E-10//AT3G04220| disease resistance protein (TIR-NBS-LRR class), putative	Unigene52458_All//2.00E-115//TC162835		ko04626|Plant-pathogen interaction		nr +
Unigene5246_All	1127	1.11	0.09	2.08	20.11	14.54	11.50	25.06	5.04	9.33	-3.63E+00	1.99E-05	Down	9.00E-01	3.97E-02		-4.68E-01	1.03E-05		-8.06E-01	8.59E-13		-2.31E+00	4.72E-85	Down	-1.43E+00	1.88E-45	Down	Unigene5246_All//gi|225322818|gb|ACN86251.1|//4.00E-27//At1g02570 [Arabidopsis lyrata subsp. petraea]	Unigene5246_All//5.00E-52//AT2G47360| unknown protein	Unigene5246_All//0.00E+00//TC136920				nr +
Unigene52462_All	641	0.65	1.26	0.42	2.25	1.02	2.04	0.99	3.72	1.74	9.54E-01	2.26E-01		-6.53E-01	5.94E-01		-1.14E+00	3.09E-02		-1.41E-01	7.93E-01		1.91E+00	2.78E-06	Up	8.15E-01	1.45E-01				Unigene52462_All//0.00E+00//gi|78347047|gb|DT567321.1|DT567321				
Unigene52463_All	324	1.29	2.97	0.66	3.08	3.51	3.48	0.78	3.74	1.60	1.20E+00	9.57E-02		-9.75E-01	4.11E-01		1.90E-01	8.14E-01		1.81E-01	7.84E-01		2.26E+00	3.35E-04	Up	1.03E+00	2.53E-01				Unigene52463_All//1.00E-121//ES811010				
Unigene52464_All	561	0.75	0.00	0.57	4.26	6.08	5.55	1.51	0.07	0.28	-9.54E+00	1.05E-02		-3.90E-01	7.17E-01		5.12E-01	1.38E-01		3.82E-01	3.23E-01		-4.34E+00	4.55E-05	Down	-2.41E+00	1.68E-03		Unigene52464_All//gi|224104873|ref|XP_002313601.1|//6.00E-15//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222850009|gb|EEE87556.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene52464_All//4.00E-07//AT5G22290| anac089 (Arabidopsis NAC domain containing protein 89); transcription factor	Unigene52464_All//0.00E+00//TC175276	NAC			nr +
Unigene52468_All	635	0.00	2.07	0.67	0.94	1.19	1.35	3.73	2.17	1.25	1.10E+01	1.50E-07	Up	9.39E+00	1.38E-02		3.42E-01	7.20E-01		5.22E-01	5.23E-01		-7.80E-01	3.51E-02		-1.57E+00	3.57E-05	Down	Unigene52468_All//gi|147856506|emb|CAN80763.1|//2.00E-06//hypothetical protein [Vitis vinifera]							nr -
Unigene52469_All	296	76.36	34.58	41.02	22.89	20.13	27.62	5.29	6.50	6.33	-1.14E+00	8.00E-21	Down	-8.97E-01	1.33E-13		-1.86E-01	4.68E-01		2.71E-01	2.26E-01		2.98E-01	5.17E-01		2.59E-01	5.61E-01		Unigene52469_All//gi|19032260|emb|CAD18921.1|//3.00E-45//RNA-binding protein precursor [Persea americana]	Unigene52469_All//9.00E-44//AT4G24770| RBP31 (31-KDA RNA BINDING PROTEIN); RNA binding / poly(U) binding	Unigene52469_All//4.00E-164//ES795659		ko03010|Ribosome		nr +
Unigene52475_All	438	1.08	0.46	1.46	1.14	4.56	1.75	0.00	0.19	0.18	-1.22E+00	2.72E-01		4.40E-01	6.23E-01		2.00E+00	4.50E-05	Up	6.24E-01	4.81E-01		7.58E+00	4.00E-01		7.51E+00	4.03E-01										
Unigene52476_All	350	2429.63	2573.28	3093.06	440.22	649.74	680.42	3.62	0.60	1.71	8.29E-02	7.26E-07		3.48E-01	4.92E-115		5.62E-01	4.12E-72		6.28E-01	6.38E-83		-2.60E+00	5.14E-05	Down	-1.09E+00	3.58E-02		Unigene52476_All//gi|295646225|gb|ADG23053.1|//9.00E-39//haloacid dehalogenase [Phaseolus vulgaris]	Unigene52476_All//3.00E-39//AT1G17710| phosphatase	Unigene52476_All//0.00E+00//TC177180				nr +
Unigene52477_All	444	2.95	22.03	4.08	2.24	3.41	3.56	8.28	19.58	21.00	2.90E+00	3.73E-31	Up	4.69E-01	3.69E-01		6.05E-01	2.97E-01		6.66E-01	2.29E-01		1.24E+00	1.47E-11	Up	1.34E+00	3.66E-14	Up			Unigene52477_All//7.00E-68//gi|164313297|gb|ES848807.1|ES848807				
Unigene52478_All	267	1.18	0.00	0.00	4.48	2.84	0.68	1.58	0.78	1.64	-1.02E+01	3.65E-02		-1.02E+01	4.90E-02		-6.58E-01	2.90E-01		-2.73E+00	2.36E-04	Down	-1.02E+00	3.50E-01		5.17E-02	9.74E-01				Unigene52478_All//6.00E-101//ES823717				
Unigene52479_All	371	0.99	0.00	1.58	4.57	3.53	1.22	0.23	0.00	0.00	-9.95E+00	1.96E-02		6.77E-01	4.82E-01		-3.72E-01	4.82E-01		-1.91E+00	4.25E-04	Down	-7.83E+00	4.02E-01		-7.83E+00	3.58E-01		Unigene52479_All//gi|297612697|ref|NP_001066197.2|//1.00E-07//Os12g0156200 [Oryza sativa Japonica Group] >gi|255670064|dbj|BAF29216.2| Os12g0156200 [Oryza sativa Japonica Group]							nr -
Unigene5248_All	711	8.39	5.70	7.26	13.52	11.87	10.16	27.89	12.99	10.20	-5.57E-01	2.17E-02		-2.08E-01	4.34E-01		-1.89E-01	3.61E-01		-4.12E-01	2.85E-02		-1.10E+00	3.76E-21	Down	-1.45E+00	4.78E-33	Down	Unigene5248_All//gi|225470816|ref|XP_002264634.1|//4.00E-16//PREDICTED: similar to Wound-induced basic protein [Vitis vinifera]	Unigene5248_All//1.00E-13//AT3G07230| wound-responsive protein-related	Unigene5248_All//0.00E+00//TC167621				nr -
Unigene52483_All	453	2.43	10.85	0.24	1.32	0.53	0.80	0.84	0.37	0.53	2.16E+00	1.33E-11	Up	-3.37E+00	2.67E-04	Down	-1.31E+00	1.56E-01		-7.26E-01	4.60E-01		-1.19E+00	3.09E-01		-6.71E-01	5.30E-01				Unigene52483_All//4.00E-122//ES796239				
Unigene52488_All	299	0.00	0.00	0.00	0.00	0.00	0.00	35.63	69.61	16.79	null	null		null	null		null	null		null	null		9.66E-01	5.46E-18		-1.09E+00	7.39E-12	Down			Unigene52488_All//4.00E-10//TC166107				
Unigene52489_All	476	0.00	0.75	0.11	0.21	0.07	0.66	21.67	45.57	143.79	9.54E+00	2.46E-02		6.81E+00	6.35E-01		-1.53E+00	5.86E-01		1.67E+00	3.09E-01		1.07E+00	4.66E-22	Up	2.73E+00	3.30E-252	Up	Unigene52489_All//gi|16648923|gb|AAL24313.1|//5.00E-10//Unknown protein [Arabidopsis thaliana]		Unigene52489_All//9.00E-09//TC170943		ko03040|Spliceosome		nr -
Unigene5249_All	1415	18.34	11.42	25.29	0.49	1.61	0.26	0.00	0.06	0.03	-6.83E-01	2.00E-10		4.64E-01	4.71E-07		1.70E+00	1.01E-04	Up	-9.49E-01	2.88E-01		5.89E+00	4.00E-01		4.82E+00	6.44E-01		Unigene5249_All//gi|115462763|ref|NP_001054981.1|//2.00E-12//Os05g0232200 [Oryza sativa Japonica Group] >gi|113578532|dbj|BAF16895.1| Os05g0232200 [Oryza sativa Japonica Group]	Unigene5249_All//1.00E-28//AT5G56850| unknown protein	Unigene5249_All//0.00E+00//TC160283				nr +
Unigene52490_All	932	6760.61	5029.00	7891.97	922.26	1134.96	1090.95	2.59	4.22	1.07	-4.27E-01	0.00E+00		2.23E-01	0.00E+00		2.99E-01	6.24E-105		2.42E-01	1.76E-60		7.05E-01	1.04E-02		-1.27E+00	4.48E-04	Down	Unigene52490_All//gi|300157857|gb|EF124481.1|//1.00E-108//light-harvesting complex [Selaginella moellendorffii]	Unigene52490_All//2.00E-100//AT2G40100| LHCB4.3 (light harvesting complex PSII); chlorophyll binding	Unigene52490_All//0.00E+00//TC130503		ko00196|Photosynthesis - antenna proteins		nr +
Unigene52492_All	375	0.00	0.27	0.28	1.33	4.32	1.32	0.56	3.01	1.38	8.08E+00	3.86E-01		8.15E+00	3.97E-01		1.70E+00	1.65E-03		-3.90E-03	9.87E-01		2.42E+00	3.17E-04	Up	1.29E+00	1.59E-01		Unigene52492_All//gi|30024598|dbj|BAC75671.1|//8.00E-06//transcription factor MYB101 [Lotus japonicus]							nr +
Unigene52495_All	490	0.00	0.31	0.00	0.41	0.56	1.57	2.33	6.14	29.92	8.28E+00	2.35E-01		null	null		4.68E-01	8.16E-01		1.95E+00	3.23E-02		1.40E+00	2.94E-05	Up	3.68E+00	3.59E-72	Up	Unigene52495_All//gi|112383512|gb|ABI17893.1|//2.00E-10//cell-wall invertase [Coffea canephora]	Unigene52495_All//2.00E-09//AT1G55120| ATFRUCT5 (BETA-FRUCTOFURANOSIDASE 5); hydrolase, hydrolyzing O-glycosyl compounds / levanase	Unigene52495_All//9.00E-46//TC147820		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr +
Unigene52496_All	546	0.00	0.00	0.00	0.00	0.00	0.00	2.87	2.22	0.00	null	null		null	null		null	null		null	null		-3.68E-01	4.58E-01		-1.15E+01	1.42E-11	Down	Unigene52496_All//gi|115485513|ref|NP_001067900.1|//1.00E-65//Os11g0482000 [Oryza sativa Japonica Group] >gi|113645122|dbj|BAF28263.1| Os11g0482000 [Oryza sativa Japonica Group]	Unigene52496_All//1.00E-65//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene52497_All	1023	0.66	0.50	0.00	1.27	1.65	0.44	1.61	0.61	0.51	-4.25E-01	5.97E-01		-9.38E+00	7.63E-04	Down	3.82E-01	5.10E-01		-1.52E+00	1.32E-02		-1.40E+00	3.12E-03		-1.67E+00	3.93E-04	Down	Unigene52497_All//gi|30688490|ref|NP_194720.2|//6.00E-97//ORC5 (ORIGIN RECOGNITION COMPLEX PROTEIN 5): protein binding [Arabidopsis thaliana] >gi|49659272|emb|CAE01429.1| origin recognition complex 5 subunit [Arabidopsis thaliana]	Unigene52497_All//5.00E-86//AT4G29910| ORC5 (ORIGIN RECOGNITION COMPLEX PROTEIN 5); protein binding					nr -
Unigene52499_All	727	1.37	0.07	0.73	2.06	2.37	4.47	0.17	0.23	0.27	-4.29E+00	7.30E-05	Down	-9.01E-01	2.22E-01		2.04E-01	7.38E-01		1.12E+00	1.22E-03		3.98E-01	8.14E-01		6.51E-01	6.65E-01				Unigene52499_All//1.00E-98//TC145186				
Unigene52500_All	1262	0.00	0.00	0.08	0.00	0.11	0.14	17.92	3.15	8.90	null	null		6.40E+00	3.97E-01		6.77E+00	3.18E-01		7.16E+00	1.94E-01		-2.51E+00	3.94E-75	Down	-1.01E+00	1.47E-21	Down	Unigene52500_All//gi|158706508|sp|Q56XQ0.2|U496I_ARATH//1.00E-35//RecName: Full=UPF0496 protein At2g18630	Unigene52500_All//4.00E-25//AT2G18630| unknown protein	Unigene52500_All//0.00E+00//TC164296				nr -
Unigene52502_All	378	65.61	25.87	50.71	39.93	30.06	13.74	0.34	0.00	0.11	-1.34E+00	4.11E-29	Down	-3.72E-01	1.15E-03		-4.10E-01	2.72E-03		-1.54E+00	1.25E-23	Down	-8.39E+00	2.35E-01		-1.67E+00	4.77E-01		Unigene52502_All//gi|82468803|gb|ABB76766.1|//6.00E-48//lupeol synthase [Ricinus communis]	Unigene52502_All//1.00E-44//AT1G78960| ATLUP2; beta-amyrin synthase/ lupeol synthase	Unigene52502_All//1.00E-143//C0082200		ko00100|Steroid biosynthesis		nr +
Unigene52506_All	305	5.32	1.50	1.05	0.65	1.81	0.15	0.97	0.00	0.13	-1.83E+00	1.15E-03		-2.34E+00	1.96E-04	Down	1.47E+00	1.77E-01		-2.14E+00	3.47E-01		-9.92E+00	2.17E-02		-2.89E+00	6.76E-02		Unigene52506_All//gi|254531189|sp|Q22959.1|PER19_ARATH//4.00E-13//RecName: Full=Peroxidase 19; Short=Atperox P19; AltName: Full=ATP51; Flags: Precursor	Unigene52506_All//8.00E-14//AT2G34060| peroxidase, putative			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene52508_All	1551	0.00	0.00	0.00	0.00	0.00	0.00	8.61	3.53	7.06	null	null		null	null		null	null		null	null		-1.29E+00	2.48E-18	Down	-2.86E-01	3.75E-02		Unigene52508_All//gi|297727031|ref|NP_001175879.1|//7.00E-70//Os09g0468700 [Oryza sativa Japonica Group] >gi|47497681|dbj|BAD19748.1| helix-loop-helix DNA-binding protein-like [Oryza sativa Japonica Group] >gi|47848400|dbj|BAD22258.1| helix-loop-helix DNA-binding protein-like [Oryza sativa Japonica Group] >gi|255678966|dbj|BAH94607.1| Os09g0468700 [Oryza sativa Japonica Group]	Unigene52508_All//4.00E-61//AT1G72210| basic helix-loop-helix (bHLH) family protein (bHLH096)	Unigene52508_All//2.00E-62//TC149787	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene52510_All	471	0.00	0.00	0.34	1.59	0.66	0.67	2.15	0.36	0.68	null	null		8.41E+00	2.38E-01		-1.27E+00	1.12E-01		-1.24E+00	1.45E-01		-2.60E+00	3.81E-04	Down	-1.67E+00	7.35E-03				Unigene52510_All//1.00E-143//ES841777				
Unigene52514_All	1263	0.29	0.04	0.08	0.12	0.22	0.25	2.21	0.66	12.62	-2.85E+00	7.80E-02		-1.78E+00	2.34E-01		8.83E-01	5.95E-01		1.08E+00	4.76E-01		-1.74E+00	1.76E-06	Down	2.51E+00	4.42E-54	Up	Unigene52514_All//gi|28300299|gb|AAO37645.1|//1.00E-75//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene52514_All//1.00E-44//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene52514_All//9.00E-39//TC177573		ko04626|Plant-pathogen interaction		nr +
Unigene52515_All	353	0.00	0.86	0.30	2.12	0.20	1.41	0.96	1.42	0.11	9.75E+00	4.42E-02		8.24E+00	3.97E-01		-3.44E+00	6.18E-04	Down	-5.89E-01	4.87E-01		5.68E-01	5.63E-01		-3.09E+00	3.91E-02										
Unigene52516_All	551	0.19	0.28	0.29	0.45	0.19	0.00	1.07	2.12	3.54	5.39E-01	7.79E-01		6.10E-01	7.48E-01		-1.27E+00	4.24E-01		-8.82E+00	7.33E-02		9.83E-01	8.30E-02		1.72E+00	7.69E-05	Up	Unigene52516_All//gi|28371844|gb|AAO38220.1|//3.00E-70//RCa9 [Manihot esculenta]	Unigene52516_All//5.00E-50//AT4G26090| RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding	Unigene52516_All//2.00E-13//TC155066		ko04626|Plant-pathogen interaction		nr -
Unigene52517_All	504	0.00	0.20	2.22	0.30	0.27	0.09	1.59	0.75	1.11	7.65E+00	3.86E-01		1.11E+01	3.43E-06	Up	-1.18E-01	9.10E-01		-1.73E+00	5.01E-01		-1.09E+00	1.29E-01		-5.26E-01	4.35E-01		Unigene52517_All//gi|91208893|ref|YP_538926.1|//6.00E-84//RNA polymerase beta' subunit [Gossypium hirsutum] >gi|122226160|sp|Q2LS24.1|RPOC1_GOSHI RecName: Full=DNA-directed RNA polymerase subunit beta'; AltName: Full=PEP; AltName: Full=Plastid-encoded RNA polymerase subunit beta'; Short=RNA polymerase subunit beta' >gi|85687407|gb|ABC73619.1| RNA polymerase beta [Gossypium hirsutum]	Unigene52517_All//8.00E-67//AT CG00180| RNA polymerase beta' subunit-1	Unigene52517_All//0.00E+00//TC153997		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene52518_All	802	0.00	17.63	7.64	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	3.56E-81	Up	1.29E+01	3.79E-34	Up	null	null		null	null		null	null		null	null		Unigene52518_All//gi|207083828|gb|ACI23255.1|//2.00E-82//ribosomal protein S5 [Auxenochlorella protothecoides]	Unigene52518_All//1.00E-80//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome	Unigene52518_All//2.00E-20//TC174458		ko03010|Ribosome		nr +
Unigene52519_All	786	0.00	0.00	0.00	0.00	0.00	0.00	7.10	2.77	0.20	null	null		null	null		null	null		null	null		-1.36E+00	9.00E-09	Down	-5.13E+00	4.29E-35	Down	Unigene52519_All//gi|18141289|gb|AAL60582.1|AF454960_1//6.00E-67//senescence-associated cysteine protease [Brassica oleracea]	Unigene52519_All//9.00E-68//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase					nr -
Unigene5252_All	1109	4.48	22.34	5.91	5.66	7.42	5.25	4.50	3.51	7.08	2.32E+00	7.35E-61	Up	3.98E-01	1.06E-01		3.91E-01	5.57E-02		-1.07E-01	6.77E-01		-3.60E-01	1.50E-01		6.54E-01	2.84E-04		Unigene5252_All//gi|224107941|ref|XP_002314662.1|//4.00E-84//autoinhibited calcium ATPase [Populus trichocarpa] >gi|222863702|gb|EEF00833.1| autoinhibited calcium ATPase [Populus trichocarpa]	Unigene5252_All//2.00E-56//AT3G63380| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12)	Unigene5252_All//0.00E+00//TC144636				nr -
Unigene52522_All	441	0.71	0.57	0.60	1.36	0.94	1.43	2.11	0.85	0.27	-3.09E-01	7.89E-01		-2.38E-01	8.50E-01		-5.33E-01	5.61E-01		8.10E-02	9.45E-01		-1.31E+00	4.81E-02		-2.96E+00	1.72E-04	Down			Unigene52522_All//0.00E+00//DR243854				
Unigene52529_All	546	0.00	53.64	17.26	0.00	0.00	0.00	0.00	0.00	0.00	1.57E+01	7.67E-169	Up	1.41E+01	7.42E-53	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene52530_All	362	0.43	0.56	0.00	1.10	1.62	1.00	0.58	0.92	4.95	3.69E-01	8.16E-01		-8.76E+00	2.44E-01		5.55E-01	5.99E-01		-1.41E-01	9.04E-01		6.62E-01	6.09E-01		3.08E+00	3.90E-08	Up	Unigene52530_All//gi|186511742|ref|NP_193111.2|//2.00E-25//ATP binding [Arabidopsis thaliana]	Unigene52530_All//2.00E-21//AT4G13750| ATP binding					nr +
Unigene52531_All	478	0.00	0.00	0.00	0.21	1.15	1.98	0.53	1.22	1.00	null	null		null	null		2.47E+00	4.04E-02		3.25E+00	5.84E-04	Up	1.21E+00	1.71E-01		9.14E-01	3.38E-01		Unigene52531_All//gi|56609044|gb|AAO03152.1|//4.00E-81//kinesin [Gossypium hirsutum]	Unigene52531_All//7.00E-35//AT2G47500| ATP binding / microtubule motor	Unigene52531_All//0.00E+00//TC129556				nr +
Unigene52532_All	284	1.84	3.03	6.38	0.70	4.85	2.70	0.60	0.59	0.84	7.19E-01	3.47E-01		1.79E+00	1.06E-03		2.79E+00	4.76E-05	Up	1.95E+00	3.23E-02		-1.66E-02	1.02E+00		4.99E-01	7.07E-01										
Unigene5254_All	1093	0.96	6.58	3.95	2.96	2.61	22.64	32.84	132.00	168.90	2.78E+00	4.24E-22	Up	2.04E+00	3.07E-09	Up	-1.80E-01	6.16E-01		2.93E+00	1.72E-84	Up	2.01E+00	0.00E+00	Up	2.36E+00	0.00E+00	Up	Unigene5254_All//gi|297805118|ref|XP_002870413.1|//1.00E-99//auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316279|gb|EFH46702.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5254_All//2.00E-89//AT5G35735| auxin-responsive family protein	Unigene5254_All//0.00E+00//TC146754				nr +

Unigene52544_All	215	3.89	5.89	6.69	8.57	8.01	6.09	15.93	24.11	7.41	5.98E-01	3.25E-01		7.80E-01	1.80E-01		-9.83E-02	8.22E-01		-4.93E-01	3.34E-01		5.98E-01	1.10E-02		-1.10E+00	1.68E-04	Down	Unigene52544_All//gi|225444708|ref|XP_002278146.1|//4.00E-09//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297738552|emb|CBI27797.3| unnamed protein product [Vitis vinifera]	Unigene52544_All//7.00E-07//AT5G20650| COPT5; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter	Unigene52544_All//1.00E-64//TC156099				nr -
Unigene52553_All	396	0.00	0.00	0.00	0.00	0.09	0.00	1.28	7.92	1.11	null	null		null	null		6.44E+00	8.29E-01		null	null		2.63E+00	1.70E-11	Up	-2.11E-01	7.92E-01		Unigene52553_All//gi|21700765|gb|AAG38144.1|//5.00E-19//phosphoglycerate mutase-like protein [Glycine max]	Unigene52553_All//4.00E-20//AT1G58280| LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64460.6); Has 337 Blast hits to 337 proteins in 68 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 175; Plants - 69; Viruses - 0; Other Eukaryotes - 89 (source: NCBI BLink).					nr +
Unigene52558_All	256	23.30	110.44	125.43	53.32	24.35	15.52	49.05	59.43	20.54	2.25E+00	9.52E-67	Up	2.43E+00	2.98E-81	Up	-1.13E+00	3.32E-15	Down	-1.78E+00	2.88E-26	Down	2.77E-01	3.81E-02		-1.26E+00	3.43E-17	Down			Unigene52558_All//6.00E-104//gi|109844456|gb|DW243014.1|DW243014				ESTscan +
Unigene52256_All	640	2.78	1.27	1.08	3.66	2.58	2.05	6.94	2.61	1.87	-1.13E+00	2.21E-02		-1.36E+00	1.01E-02		-5.02E-01	2.29E-01		-8.38E-01	4.48E-02		-1.41E+00	1.77E-07	Down	-1.89E+00	2.23E-11	Down	Unigene52256_All//gi|224096884|ref|XP_002310773.1|//2.00E-43//predicted protein [Populus trichocarpa] >gi|222853676|gb|EEE91223.1| predicted protein [Populus trichocarpa]	Unigene52256_All//2.00E-35//AT2G23755| unknown protein					nr -
Unigene52562_All	348	1.65	0.00	0.00	3.58	0.69	3.11	0.24	0.96	0.23	-1.07E+01	1.52E-03		-1.07E+01	2.60E-03		-2.37E+00	2.03E-04	Down	-2.00E-01	7.33E-01		1.98E+00	1.44E-01		-8.56E-02	9.71E-01									ESTscan -
Unigene52564_All	421	1.86	2.77	0.38	2.84	4.25	0.43	0.00	0.00	0.00	5.70E-01	3.77E-01		-2.30E+00	1.79E-02		5.83E-01	2.59E-01		-2.73E+00	2.36E-04	Down	null	null		null	null		Unigene52564_All//gi|30691739|ref|NP_198216.2|//2.00E-17//AN3 (ANGUSTIFOLIA 3); protein binding / transcription coactivator [Arabidopsis thaliana] >gi|21539890|gb|AAM52881.1| GRF1-interacting factor 1 [Arabidopsis thaliana]	Unigene52564_All//1.00E-18//AT5G28640| AN3 (ANGUSTIFOLIA 3); protein binding / transcription coactivator	Unigene52564_All//0.00E+00//ES804288				nr +
Unigene52567_All	385	1.90	6.58	0.97	1.04	1.52	1.06	0.77	0.11	0.93	1.79E+00	4.00E-05	Up	-9.75E-01	2.64E-01		5.55E-01	5.99E-01		2.86E-02	9.85E-01		-2.82E+00	8.84E-02		2.77E-01	7.87E-01				Unigene52567_All//1.00E-146//TC156081					
Unigene5257_All	448	1.64	1.24	2.14	6.78	4.46	2.82	3.96	1.03	1.96	-3.94E-01	6.11E-01		3.88E-01	6.08E-01		-6.05E-01	8.18E-02		-1.26E+00	4.42E-04	Down	-1.95E+00	5.36E-05	Down	-1.02E+00	1.59E-02		Unigene5257_All//gi|224096884|ref|XP_002310773.1|//8.00E-38//predicted protein [Populus trichocarpa] >gi|222853676|gb|EEE91223.1| predicted protein [Populus trichocarpa]	Unigene5257_All//3.00E-24//AT2G23755| unknown protein					nr +
Unigene52574_All	258	2.03	4.32	1.65	2.51	3.74	3.15	7.21	11.66	23.93	1.09E+00	9.57E-02		-2.97E-01	7.49E-01		5.74E-01	4.52E-01		3.28E-01	7.01E-01		6.94E-01	3.13E-02		1.73E+00	1.22E-13	Up			Unigene52574_All//3.00E-47//TC162004					
Unigene52577_All	443	0.00	1.83	0.96	1.46	0.31	0.51	4.10	3.96	1.53	1.08E+01	9.37E-05	Up	9.91E+00	1.38E-02		-2.23E+00	1.79E-02		-1.52E+00	1.12E-01		-5.05E-02	9.24E-01		-1.42E+00	1.00E-03		Unigene52577_All//gi|118488234|gb|ABK95936.1|//5.00E-06//unknown [Populus trichocarpa]	Unigene52577_All//2.00E-06//AT2G24260| basic helix-loop-helix (bHLH) family protein	Unigene52577_All//2.00E-95//TC135076	bHLH			nr -
Unigene5258_All	811	141.67	45.92	70.52	31.14	50.27	32.97	16.06	16.70	23.19	-1.63E+00	4.33E-176	Down	-1.01E+00	3.94E-81	Down	6.91E-01	7.28E-19		8.22E-02	5.37E-01		5.64E-02	7.24E-01		5.30E-01	1.83E-06		Unigene5258_All//gi|217794200|gb|ACX56123.1|//5.00E-40//ELF4-like protein [Solanum tuberosum]	Unigene5258_All//3.00E-34//AT2G06255| ELF4-L3 (ELF4-Like 3)	Unigene5258_All//4.00E-77//TC175686				nr +
Unigene52582_All	334	3.92	2.43	1.28	4.77	2.68	1.22	1.52	0.88	1.07	-6.90E-01	2.32E-01		-1.62E+00	1.33E-02		-8.32E-01	9.85E-02		-1.97E+00	4.88E-04	Down	-7.94E-01	4.02E-01		-5.01E-01	5.83E-01		Unigene52582_All//gi|297739353|emb|CBI29343.3|//2.00E-17//unnamed protein product [Vitis vinifera]	Unigene52582_All//2.00E-06//AT1G34150| tRNA pseudouridine synthase family protein					nr +
Unigene52584_All	265	442.06	136.14	351.85	91.92	82.64	54.37	0.16	0.00	0.00	-1.70E+00	2.82E-191	Down	-3.29E-01	1.08E-11		-1.54E-01	2.10E-01		-7.58E-01	2.29E-12		-7.32E+00	6.56E-01		-7.32E+00	6.12E-01				Unigene52584_All//1.00E-117//TC139902					
Unigene52586_All	372	0.98	1.09	1.72	0.67	2.04	1.21	1.59	0.00	1.18	1.47E-01	8.98E-01		8.03E-01	3.88E-01		1.60E+00	6.97E-02		8.59E-01	4.69E-01		-1.06E+01	2.39E-04	Down	-4.34E-01	6.08E-01									
Unigene52591_All	467	1.34	0.00	0.00	2.03	2.65	1.64	0.81	0.45	0.09	-1.04E+01	7.91E-04	Down	-1.04E+01	1.41E-03		3.89E-01	5.68E-01		-3.02E-01	6.89E-01		-8.65E-01	4.41E-01		-3.26E+00	2.22E-02				Unigene52591_All//0.00E+00//TC179483					
Unigene52594_All	358	0.58	0.00	0.60	1.67	2.89	0.63	0.59	0.47	3.89	-9.19E+00	1.22E-01		2.54E-02	1.00E+00		7.89E-01	2.74E-01		-1.40E+00	1.58E-01		-3.39E-01	8.11E-01		2.72E+00	8.11E-06	Up	Unigene52594_All//gi|3914467|sp|P93768.1|PSMD3_TOBAC//1.00E-17//RecName: Full=Probable 26S proteasome non-ATPase regulatory subunit 3; Short=26S proteasome subunit S3; AltName: Full=26S proteasome regulatory subunit RPN3; AltName: Full=Nuclear antigen 21D7 >gi|1864003|dbj|BAA19252.1| 21D7 [Nicotiana tabacum]	Unigene52594_All//5.00E-18//AT1G75990| 26S proteasome regulatory subunit S3, putative (RPN3)	Unigene52594_All//6.00E-31//TC172892		ko03050|Proteasome		nr -
Unigene52596_All	415	2.65	0.00	0.51	7.20	2.82	0.76	1.43	0.50	0.58	-1.14E+01	1.95E-06	Down	-2.37E+00	2.96E-03		-1.35E+00	8.14E-05	Down	-3.24E+00	7.13E-12	Down	-1.50E+00	9.13E-02		-1.31E+00	1.15E-01									
Unigene52607_All	381	0.55	0.80	0.00	0.78	1.90	0.71	3.88	1.65	1.15	5.39E-01	6.71E-01		-9.10E+00	1.45E-01		1.27E+00	1.56E-01		-1.42E-01	9.20E-01		-1.24E+00	1.26E-02		-1.76E+00	5.33E-04	Down	Unigene52607_All//gi|115436552|ref|NP_001043034.1|//7.00E-49//Os01g0363900 [Oryza sativa Japonica Group] >gi|113532565|dbj|BAF04948.1| Os01g0363900 [Oryza sativa Japonica Group]	Unigene52607_All//3.00E-31//AT3G05040| HST (HASTY); nucleocytoplasmic transporter	Unigene52607_All//5.00E-16//TC150444				nr -
Unigene52608_All	1150	0.14	0.48	0.00	0.00	0.00	0.00	1.29	1.24	9.15	1.83E+00	9.02E-02		-7.09E+00	2.44E-01		null	null		null	null		-5.85E-02	9.19E-01		2.83E+00	8.26E-41	Up	Unigene52608_All//gi|1770305|emb|CAA92278.1|//1.00E-155//1,3-beta-glucanase [Gossypium hirsutum]	Unigene52608_All//8.00E-101//AT3G57270| BG1 (BETA-1,3-GLUCANASE 1); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene52608_All//0.00E+00//TC142180		ko00500|Starch and sucrose metabolism		nr +
Unigene52609_All	561	2.89	0.63	5.51	0.00	0.00	0.32	0.00	0.00	0.43	-2.19E+00	2.05E-04	Down	9.29E-01	1.24E-02		null	null		8.33E+00	1.94E-01		null	null		8.74E+00	4.39E-02		Unigene52609_All//gi|9757821|dbj|BAB08339.1|//2.00E-46//rac GTPase activating protein [Arabidopsis thaliana] >gi|110738325|dbj|BAF01090.1| rac GTPase activating protein [Arabidopsis thaliana] >gi|111074188|gb|AB806467.1| At5g22400 [Arabidopsis thaliana]	Unigene52609_All//1.00E-42//AT5G22400| rac GTPase activating protein, putative	Unigene52609_All//3.00E-43//gi|109858743|gb|DW487722.1|DW487722				nr -
Unigene5261_All	978	8.19	0.31	0.65	2.65	2.46	1.94	2.16	1.71	2.32	-4.72E+00	5.91E-38	Down	-3.65E+00	1.88E-30	Down	-1.04E-01	8.24E-01		-4.50E-01	2.83E-01		-3.39E-01	4.16E-01		1.03E-01	7.85E-01		Unigene5261_All//gi|297812149|ref|XP_002873958.1|//4.00E-23//AT0FP8/OFP8 [Arabidopsis lyrata subsp. lyrata] >gi|297319795|gb|EFH50217.1| AT0FP8/OFP8 [Arabidopsis lyrata subsp. lyrata]	Unigene5261_All//2.00E-20//AT5G19650| OFP8 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 8)	Unigene5261_All//0.00E+00//ES821446				nr +
Unigene52610_All	249	2.52	0.00	0.00	2.20	1.66	0.73	0.00	0.00	0.00	-1.13E+01	7.91E-04	Down	-1.13E+01	1.41E-03		-4.07E-01	6.58E-01		-1.60E+00	1.32E-01		null	null		null	null										
Unigene52611_All	282	0.00	0.54	0.00	1.06	0.98	0.96	0.00	0.74	2.12	9.07E+00	2.35E-01		null	null		-1.18E-01	9.00E-01		-1.42E-01	9.20E-01		9.53E+00	7.84E-02		1.10E+01	1.75E-04	Up			Unigene52611_All//3.00E-146//DR452759					
Unigene52612_All	236	0.00	0.00	0.00	0.00	0.00	0.00	8.06	4.43	1.18	null	null		null	null		null	null		null	null		-8.65E-01	4.03E-02		-2.77E+00	6.03E-08	Down	Unigene52612_All//gi|1545805|dbj|BAA10929.1|//3.00E-08//cytochrome P450 like_TBP [Nicotiana tabacum]		Unigene52612_All//8.00E-17//gi|48821593|gb|CO122906.1|CO122906				nr -
Unigene52614_All	432	299.15	85.86	158.15	418.92	371.37	490.63	19.87	26.22	33.20	-1.80E+00	7.74E-229	Down	-9.20E-01	1.59E-78		-1.74E-01	8.35E-07		2.28E-01	1.12E-11		4.00E-01	8.77E-03		7.41E-01	1.37E-08		Unigene52614_All//gi|17367847|sp|Q9XFV7.1|RL4_PRUAR//6.00E-46//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32206.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene52614_All//5.00E-42//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)	Unigene52614_All//0.00E+00//TC153123		ko03010|Ribosome		nr +
Unigene52620_All	906	0.00	3.91	1.59	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	3.46E-20	Up	1.06E+01	6.30E-08	Up	null	null		null	null		null	null		null	null		Unigene52620_All//gi|38885083|gb|AB27546.1|//1.00E-113//heat shock protein 90 [Prorocentrum micans]	Unigene52620_All//1.00E-103//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene52622_All	298	4.92	0.68	2.68	4.01	2.54	0.30	0.00	0.00	0.00	-2.85E+00	3.60E-05	Down	-8.75E-01	1.34E-01		-6.58E-01	2.90E-01		-3.73E+00	1.43E-05	Down	null	null		null	null										
Unigene52623_All	807	0.91	0.25	0.00	0.49	0.38	1.06	1.21	2.49	1.33	-1.85E+00	4.08E-02		-9.83E+00	4.13E-04	Down	-3.63E-01	7.54E-01		1.11E+00	1.67E-01		1.04E+00	1.10E-02		1.46E-01	7.94E-01				Unigene52623_All//1.00E-15//FL577341					
Unigene52629_All	414	0.00	0.24	0.13	5.90	1.41	1.75	1.02	1.62	0.48	7.94E+00	3.86E-01		7.01E+00	6.35E-01		-2.06E+00	6.47E-07	Down	-1.76E+00	4.25E-05	Down	6.61E-01	4.02E-01		-1.09E+00	2.82E-01				Unigene52629_All//1.00E-29//TC133515					
Unigene5263_All	1655	0.89	0.61	0.48	5.00	5.35	3.17	1.53	0.68	0.63	-5.32E-01	3.39E-01		-8.75E-01	1.34E-01		9.79E-02	6.82E-01		-6.59E-01	8.57E-04		-1.17E+00	1.17E-03		-1.29E+00	2.58E-04	Down	Unigene5263_All//gi|79328626|ref|NP_001031936.1|//1.00E-178//catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds [Arabidopsis thaliana]	Unigene5263_All//9.00E-179//AT5G24318| catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds			ko00500|Starch and sucrose metabolism		nr +
Unigene52631_All	598	1.40	0.00	1.34	0.67	1.32	0.45	2.76	0.35	1.27	-1.05E+01	5.57E-05	Down	-6.77E-02	9.40E-01		9.91E-01	2.40E-01		-5.57E-01	6.38E-01		-2.98E+00	3.67E-07	Down	-1.12E+00	1.16E-02		Unigene52631_All//gi|297599291|ref|NP_001046939.2|//2.00E-80//Os02g0511900 [Oryza sativa Japonica Group] >gi|255670933|dbj|BAF08853.2| Os02g0511900 [Oryza sativa Japonica Group]	Unigene52631_All//2.00E-73//AT1G08260| TIL1 (TILTED 1); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding / zinc ion binding	Unigene52631_All//1.00E-137//gi|78332465|gb|DT552739.1|DT552739		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication		nr +
Unigene52632_All	634	1.40	0.96	2.10	1.18	0.54	1.00	2.00	5.08	1.26	-5.49E-01	4.42E-01		5.82E-01	3.47E-01		-1.12E+00	1.62E-01		-2.41E-01	7.55E-01		1.34E+00	2.74E-05	Up	-6.71E-01	1.95E-01				Unigene52632_All//0.00E+00//TC148263					
Unigene52634_All	254	91.46	40.50	50.52	79.43	63.04	107.22	139.82	119.96	43.60	-1.18E+00	2.53E-22	Down	-8.56E-01	5.85E-13		-3.33E-01	4.69E-03		4.33E-01	2.04E-05		-2.21E-01	7.97E-03		-1.68E+00	2.43E-72	Down	Unigene52634_All//gi|297795379|ref|XP_002865574.1|//3.00E-26//ribosomal protein S27 [Arabidopsis lyrata subsp. lyrata] >gi|297311409|gb|EFH41833.1| ribosomal protein S27 [Arabidopsis lyrata subsp. lyrata]	Unigene52634_All//7.00E-21//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome	Unigene52634_All//4.00E-133//TC163300		ko03010|Ribosome		nr -
Unigene52636_All	304	0.17	0.33	0.18	0.00	0.23	2.08	1.39	0.55	1.05	9.54E-01	7.25E-01		2.58E-02	9.94E-01		7.82E+00	6.08E-01		1.10E+01	7.60E-04	Up	-1.34E+00	2.24E-01		-4.08E-01	6.54E-01		Unigene52636_All//gi|15233401|ref|NP_193809.1|//2.00E-19//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene52636_All//7.00E-21//AT4G20770| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene52637_All	460	0.00	0.00	0.00	0.43	1.20	0.79	1.19	0.27	4.68	null	null		null	null		1.47E+00	1.77E-01		8.59E-01	5.42E-01		-2.13E+00	3.31E-02		1.97E+00	4.04E-06	Up	Unigene52637_All//gi|9279601|dbj|BAB01059.1|//8.00E-31//pyruvate kinase [Arabidopsis thaliana]	Unigene52637_All//5.00E-32//AT3G25960| pyruvate kinase, putative	Unigene52637_All//1.00E-17//TC140845		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene52638_All	716	0.00	0.07	0.00	0.00	0.10	0.00	15.71	1.46	13.19	6.15E+00	6.15E-01		null	null		6.59E+00	6.08E-01		null	null		-3.43E+00	1.52E-51	Down	-2.52E-01	1.02E-01		Unigene52638_All//gi|2961347|emb|CAA18105.1|//3.00E-61//glycine-rich protein [Arabidopsis thaliana] >gi|7269047|emb|CAB79157.1| glycine-rich protein [Arabidopsis thaliana]				ko03040|Spliceosome		nr -
Unigene52639_All	633	0.00	0.48	0.00	0.00	0.33	0.78	0.07	3.43	0.13	8.91E+00	4.42E-02		null	null		8.35E+00	1.57E-01		9.62E+00	4.38E-03		5.68E+00	6.99E-14	Up	9.14E-01	7.49E-01									
Unigene5264_All	1174	0.53	2.03	0.50	7.13	6.78	7.62	1.48	0.32	1.43	1.92E+00	2.85E-05	Up	-1.00E-01	9.15E-01		-7.32E-02	7.81E-01		9.56E-02	6.89E-01		-2.20E+00	1.38E-05	Down	-5.11E-02	9.21E-01		Unigene5264_All//gi|38454180|gb|AAR20784.1|//1.00E-36//At1g09610 [Arabidopsis thaliana] >gi|44681448|gb|AAS47664.1| At1g09610 [Arabidopsis thaliana]	Unigene5264_All//6.00E-56//AT4G24910| unknown protein	Unigene5264_All//0.00E+00//gi|78343237|gb|DT563511.1|DT563511				nr +
Unigene52640_All	235	111.54	53.69	57.10	120.19	112.54	140.87	210.32	120.94	110.87	-1.05E+00	3.38E-21	Down	-9.66E-01	1.13E-17		-9.49E-02	4.41E-01		2.29E-01	1.84E-02		-7.98E-01	2.29E-30		-9.24E-01	8.19E-40		Unigene52640_All//gi|1710587|sp|P50346.1|RLA0_SOYBN//3.00E-34//RecName: Full=60S acidic ribosomal protein P0 >gi|119689|gb|AAB63814.1| acidic ribosomal protein P0 [Glycine max]	Unigene52640_All//8.00E-35//AT3G09200| 60S acidic ribosomal protein P0 (RPP0B)	Unigene52640_All//3.00E-130//gi|13354385|gb|BG444733.1|BG444733		ko03010|Ribosome		nr -
Unigene52641_All	415	7.19	8.18	4.11	7.56	8.38	11.10	18.34	8.66	5.18	1.87E-01	6.18E-01		-8.08E-01	3.32E-02		1.48E-01	7.14E-01		5.54E-01	5.37E-02		-1.08E+00	2.18E-08	Down	-1.82E+00	5.30E-18	Down			Unigene52641_All//3.00E-107//gi|18100312|gb|BM359566.1|BM359566					

Unigene52642_All	395	15.23	2.05	8.49	11.10	12.20	5.49	0.32	0.11	0.10	-2.89E+00	1.69E-19	Down	-8.43E-01	8.08E-04		1.37E-01	6.74E-01		-1.02E+00	3.89E-04	Down	-1.60E+00	5.34E-01		-1.67E+00	4.77E-01		Unigene52642_All//gi|177666949|gb|ACB73191.1|//3.00E-22//desulfo-glucosinolate sulfotransferase [Arabidopsis thaliana]	Unigene52642_All//2.00E-12//AT1G74100| SOT16 (SULFOTRANSFERASE 16); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene52642_All//1.00E-149//gi|164357443|gb|ES850239.1|ES850239		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr +
Unigene52643_All	791	0.00	0.26	0.00	0.06	0.09	0.00	12.67	42.43	61.34	8.00E+00	1.36E-01		null	null		4.67E-01	9.57E-01		-5.98E+00	6.34E-01		1.74E+00	9.45E-70	Up	2.28E+00	3.49E-145	Up	Unigene52643_All//gi|115438082|ref|NP_001043453.1|//1.00E-16//Os01g0591000 [Oryza sativa Japonica Group] >gi|8574437|dbj|BAA96794.1| cytosolic aldehyde dehydrogenase [Oryza sativa Japonica Group] >gi|113532984|dbj|BAF05367.1| Os01g0591000 [Oryza sativa Japonica Group]	Unigene52643_All//1.00E-15//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene52643_All//8.00E-32//gi|164322141|gb|ES819657.1|ES819657		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr -
Unigene52644_All	465	0.56	0.44	1.95	1.82	1.63	0.49	3.18	1.17	0.69	-3.68E-01	7.78E-01		1.79E+00	3.07E-02		-1.61E-01	8.14E-01		-1.91E+00	2.14E-02		-1.45E+00	4.23E-03		-2.22E+00	4.14E-05	Down								
Unigene52645_All	588	0.00	0.00	0.00	0.00	0.00	0.00	18.98	8.53	0.07	null	null		null	null		null	null		null	null		-1.15E+00	3.86E-13	Down	-8.13E+00	4.09E-80	Down	Unigene52645_All//gi|298713887|emb|CBJ33763.1|//6.00E-19//conserved unknown protein [Ectocarpus siliculosus]		Unigene52645_All//7.00E-47//gi|109852906|gb|DW481885.1|DW481885				nr -
Unigene52648_All	364	28.46	26.03	23.99	35.44	32.64	26.43	39.84	18.60	19.70	-1.29E-01	5.16E-01		-2.46E-01	2.16E-01		-1.19E-01	5.38E-01		-4.24E-01	6.95E-03		-1.10E+00	1.30E-15	Down	-1.02E+00	2.79E-14	Down	Unigene52648_All//gi|282848224|gb|ADB02893.1|//2.00E-29//ubiquinol-cytochrome C reductase [Jatropha curcas]	Unigene52648_All//4.00E-29//AT3G52730| ubiquinol-cytochrome C reductase UQCRX/QCR9-like family protein	Unigene52648_All//2.00E-147//DW510130		ko00190|Oxidative phosphorylation		nr +
Unigene5265_All	669	9.46	11.66	10.75	12.43	11.22	10.53	4.80	3.75	1.79	3.02E-01	1.64E-01		1.83E-01	4.47E-01		-1.48E-01	5.40E-01		-2.40E-01	2.88E-01		-3.58E-01	2.75E-01		-1.43E+00	6.02E-06	Down	Unigene5265_All//gi|9797753|gb|AAF98571.1|AC013427|4//4.00E-53//ESTs gb|F13908, gb|F15460 come from this gene [Arabidopsis thaliana]	Unigene5265_All//2.00E-31//AT1G26470| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: regulation of transcription; LOCATED IN: nucleus, H4/H2A histone acetyltransferase complex; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: CT20 (InterPro:IPR012423); Has 39 Blast hits to 39 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 24; Fungi - 0; Plants - 15; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene5265_All//0.00E+00//TC154352				nr +
Unigene52651_All	290	12.27	8.39	15.06	8.59	9.14	3.27	0.00	0.00	0.14	-5.49E-01	9.40E-02		2.96E-01	3.61E-01		9.03E-02	8.34E-01		-1.39E+00	6.58E-04	Down	null	null		7.10E+00	6.44E-01				Unigene52651_All//1.00E-86//ES808843				
Unigene52652_All	300	8.55	3.38	2.13	3.15	4.13	3.61	1.41	2.09	0.93	-1.34E+00	1.04E-03		-2.00E+00	1.34E-05	Down	3.89E-01	5.68E-01		1.96E-01	7.67E-01		5.68E-01	5.01E-01		-6.00E-01	5.53E-01				Unigene52652_All//1.00E-43//TC146693				
Unigene52657_All	271	13.13	31.41	27.12	17.46	18.42	12.83	15.76	21.75	16.02	1.26E+00	1.61E-09	Up	1.05E+00	4.07E-06	Up	7.74E-02	8.40E-01		-4.45E-01	1.24E-01		4.65E-01	3.59E-02		2.42E-02	9.51E-01				Unigene52657_All//3.00E-69//DT463474				
Unigene52660_All	2018	0.10	0.15	0.00	0.00	0.03	0.00	21.73	9.86	16.82	5.39E-01	6.71E-01		-6.70E+00	1.45E-01		5.09E+00	6.08E-01		null	null		-1.14E+00	2.62E-48	Down	-3.69E-01	1.37E-07		Unigene52660_All//gi|297806735|ref|XP_002871251.1|//0.00E+00//laccase-13 precursor [Arabidopsis lyrata subsp. lyrata] >gi|297317088|gb|EFH47510.1| laccase-13 precursor [Arabidopsis lyrata subsp. lyrata]	Unigene52660_All//0.00E+00//AT5G07130| LAC13 (laccase 13); laccase	Unigene52660_All//2.00E-07//gi|164246155|gb|ES821488.1|ES821488		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene52666_All	265	0.59	0.19	0.40	8.46	3.25	1.87	2.87	5.05	11.28	-1.63E+00	4.88E-01		-5.60E-01	7.75E-01		-1.38E+00	7.07E-04	Down	-2.17E+00	4.72E-06	Down	8.13E-01	1.22E-01		1.97E+00	3.27E-08	Up			Unigene52666_All//4.00E-148//ES829137				
Unigene52668_All	642	0.08	1.58	0.00	0.31	0.48	0.14	0.79	0.91	2.42	4.28E+00	7.16E-05	Up	-6.35E+00	6.22E-01		6.37E-01	6.95E-01		-1.14E+00	5.68E-01		2.06E-01	8.00E-01		1.61E+00	9.55E-04	Up	Unigene52668_All//gi|297817502|ref|XP_002876634.1|//6.00E-48//nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297322472|gb|EFH52893.1| nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene52668_All//4.00E-45//AT3G61690| unknown protein	Unigene52668_All//1.00E-113//TC146298				nr +
Unigene52672_All	342	1.99	3.11	2.18	0.00	0.00	0.13	2.10	1.59	0.23	6.46E-01	3.37E-01		1.32E-01	8.64E-01		null	null		7.05E+00	6.95E-01		-4.04E-01	6.23E-01		-3.17E+00	8.09E-04	Down	Unigene52672_All//gi|22327064|ref|NP_197944.2|//4.00E-41//YUC6 (YUCCA6); FAD binding / NADP or NADPH binding / flavin-containing monooxygenase/ monooxygenase/ oxidoreductase [Arabidopsis thaliana]	Unigene52672_All//7.00E-36//AT5G25620| YUC6 (YUCCA6); FAD binding / NADP or NADPH binding / flavin-containing monooxygenase/ monooxygenase/ oxidoreductase			ko00380|Tryptophan metabolism		nr +
Unigene52673_All	292	0.18	1.56	3.46	0.85	0.71	2.78	1.45	1.57	1.64	3.12E+00	3.58E-02		4.27E+00	1.19E-04	Up	-2.70E-01	8.23E-01		1.71E+00	4.57E-02		1.21E-01	9.07E-01		1.77E-01	8.46E-01				Unigene52673_All//5.00E-111//ES833161				
Unigene52675_All	305	0.00	3.49	0.00	1.80	0.56	2.81	0.28	0.14	1.04	1.18E+01	3.81E-06	Up	null	null		-1.67E+00	9.26E-02		6.47E-01	4.23E-01		-1.02E+00	7.24E-01		1.91E+00	1.54E-01								
Unigene52677_All	412	0.76	1.48	2.33	2.06	1.00	0.77	0.21	0.91	1.84	9.54E-01	3.14E-01		1.61E+00	4.07E-02		-1.04E+00	1.62E-01		-1.42E+00	7.33E-02		2.15E+00	9.44E-02		3.16E+00	6.82E-04	Up								
Unigene52678_All	361	3.04	0.00	0.30	1.38	1.43	0.00	0.00	0.12	0.99	-1.16E+01	1.95E-06	Down	-3.37E+00	2.67E-04	Down	5.23E-02	9.80E-01		-1.04E+01	2.97E-03		6.86E+00	6.33E-01		9.96E+00	7.28E-03		Unigene52678_All//gi|54695180|dbj|BAD67155.1|//8.00E-16//PpPPR_98 [Physcomitrella patens]	Unigene52678_All//3.00E-14//AT3G26782| LOCATED IN: mitochondrion; EXPRESSED IN: seed; EXPRESSED DURING: E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT3G23330.1); Has 13812 Blast hits to 4961 proteins in 140 species: Archae - 0; Bacteria - 2; Metazoa - 58; Fungi - 30; Plants - 13522; Viruses - 0; Other Eukaryotes - 200 (source: NCBI BLink).					nr -
Unigene52681_All	324	2.91	0.00	1.31	1.85	0.85	0.00	0.00	0.00	0.00	-1.15E+01	1.46E-05	Down	-1.14E+00	1.38E-01		-1.12E+00	2.26E-01		-1.08E+01	7.70E-04	Down	null	null		null	null		Unigene52681_All//gi|224093160|ref|XP_002309814.1|//5.00E-19//calcium dependent protein kinase 24 [Populus trichocarpa] >gi|222852717|gb|EEE90264.1| calcium dependent protein kinase 24 [Populus trichocarpa]	Unigene52681_All//9.00E-18//AT2G31500| CPK24; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr +
Unigene52685_All	517	0.30	0.20	0.00	0.87	0.00	0.44	3.43	1.70	0.15	-6.31E-01	7.27E-01		-8.25E+00	2.44E-01		-9.76E+00	2.00E-03		-9.89E-01	3.94E-01		-1.02E+00	2.09E-02		-4.48E+00	1.00E-10	Down	Unigene52685_All//gi|21553703|gb|AAM62796.1|//1.00E-43//pR1B5 protein [Arabidopsis thaliana]	Unigene52685_All//5.00E-45//AT3G60450| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078), PR1B5 (InterPro:IPR012598); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G60440.1); Has 187 Blast hits to 185 proteins in 74 species: Archae - 0; Bacteria - 51; Metazoa - 14; Fungi - 36; Plants - 35; Viruses - 0; Other Eukaryotes - 51 (source: NCBI BLink).	Unigene52685_All//0.00E+00//TC149070				nr -
Unigene52687_All	348	33.08	155.94	82.78	11.02	9.60	30.76	0.00	0.84	0.69	2.24E+00	4.37E-127	Up	1.32E+00	7.80E-32	Up	-2.00E-01	5.68E-01		1.48E+00	9.93E-16	Up	9.72E+00	2.35E-02		9.42E+00	4.39E-02		Unigene52687_All//gi|145361948|ref|NP_850932.2|//9.00E-37//CER1 (ECERIFERUM 1); octadecanal decarbonylase [Arabidopsis thaliana] >gi|110742082|dbj|BAE98972.1| CER1 protein [Arabidopsis thaliana]	Unigene52687_All//8.00E-37//AT1G02205| CER1 (ECERIFERUM 1); octadecanal decarbonylase	Unigene52687_All//8.00E-138//gi|164243797|gb|ES799609.1|ES799609				nr +
Unigene52689_All	285	1.47	1.78	3.74	2.45	2.54	1.90	3.12	2.20	0.28	2.76E-01	7.64E-01		1.35E+00	6.01E-02		5.23E-02	9.65E-01		-3.64E-01	6.80E-01		-5.02E-01	4.60E-01		-3.48E+00	7.33E-05	Down			Unigene52689_All//1.00E-136//TC165688				
Unigene5269_All	719	4.15	1.48	4.07	6.72	7.62	6.66	2.35	1.86	1.61	-1.49E+00	9.41E-05	Down	-2.61E-02	9.63E-01		1.80E-01	5.44E-01		-1.34E-02	9.55E-01		-3.39E-01	4.82E-01		-5.50E-01	2.08E-01		Unigene5269_All//gi|224114395|ref|XP_002316747.1|//1.00E-06//predicted protein [Populus trichocarpa] >gi|222859812|gb|EEE97359.1| predicted protein [Populus trichocarpa]		Unigene5269_All//2.00E-69//DW513049				nr -
Unigene52690_All	353	0.00	0.72	0.75	0.00	0.00	0.00	59.53	150.25	36.57	9.49E+00	7.85E-02		9.56E+00	8.01E-02		null	null		null	null		1.34E+00	2.03E-74	Up	-7.03E-01	3.01E-11				Unigene52690_All//2.00E-67//CA992648				
Unigene52691_All	866	0.85	0.29	0.31	0.12	0.00	0.21	0.15	4.54	95.92	-1.53E+00	7.78E-02		-1.46E+00	1.12E-01		-6.85E+00	3.12E-01		8.59E-01	6.95E-01		4.95E+00	2.04E-23	Up	9.35E+00	0.00E+00	Up	Unigene52691_All//gi|222422893|dbj|BAH19433.1|//7.00E-11//AT4G27500 [Arabidopsis thaliana]	Unigene52691_All//2.00E-09//AT4G27500| PP11 (PROTON PUMP INTERACTOR 1); protein binding					nr -
Unigene52692_All	479	0.22	3.81	1.22	0.21	0.22	0.09	6.18	2.44	6.65	4.12E+00	3.43E-08	Up	2.48E+00	3.75E-02		5.24E-02	9.66E-01		-1.14E+00	6.76E-01		-1.34E+00	6.47E-05	Down	1.07E-01	7.39E-01				Unigene52692_All//3.00E-101//TC156591				
Unigene52693_All	286	0.00	2.48	2.23	5.05	3.01	0.79	0.59	1.17	0.84	1.13E+01	3.32E-04	Up	1.11E-01	1.16E-03		-7.47E-01	1.63E-01		-2.68E+00	4.68E-05	Down	9.83E-01	4.24E-01		4.99E-01	7.07E-01				Unigene52693_All//1.00E-37//TC143180				
Unigene52694_All	365	1.29	0.83	0.58	0.14	0.94	2.72	1.16	0.92	0.55	-6.31E-01	5.53E-01		-1.14E+00	3.32E-01		2.79E+00	1.14E-01		4.32E+00	6.32E-05	Up	-3.39E-01	7.30E-01		-1.09E+00	2.82E-01								
Unigene52698_All	324	0.97	2.82	2.63	0.92	6.16	4.18	0.26	0.00	0.49	1.54E+00	4.51E-02		1.44E+00	8.22E-02		2.74E+00	4.72E-07	Up	2.18E+00	8.25E-04	Up	-8.03E+00	4.02E-01		9.14E-01	6.24E-01		Unigene52698_All//gi|297826769|ref|XP_002881267.1|//2.00E-07//TMS membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327106|gb|EFH57526.1| TMS membrane family protein [Arabidopsis lyrata subsp. lyrata]		Unigene52698_All//8.00E-27//TC144118				nr +
Unigene5270_All	630	1.16	0.00	0.42	0.40	0.33	1.00	3.62	10.68	12.01	-1.02E+01	2.11E-04	Down	-1.46E+00	1.12E-01		-2.70E-01	8.23E-01		1.34E+00	1.73E-01		1.56E+00	1.48E-12	Up	1.73E+00	1.63E-16	Up	Unigene5270_All//gi|21592660|gb|AAM64609.1|//5.00E-30//phloem-specific lectin PP2-like protein [Arabidopsis thaliana]	Unigene5270_All//3.00E-31//AT1G09155| AtPP2-B15 (Phloem protein 2-B15); carbohydrate binding					nr -
Unigene52703_All	780	0.34	0.00	0.41	0.70	0.35	0.23	3.36	0.38	1.79	-8.39E+00	6.69E-02		2.88E-01	8.10E-01		-9.92E-01	3.13E-01		-1.60E+00	1.32E-01		-3.16E+00	1.24E-11	Down	-9.11E-01	6.75E-03		Unigene52703_All//gi|297609889|ref|NP_001063821.2|//1.00E-48//Os09g0542500 [Oryza sativa Japonica Group] >gi|255679103|dbj|BAF25735.2| Os09g0542500 [Oryza sativa Japonica Group]	Unigene52703_All//6.00E-17//AT3G51290| proline-rich family protein	Unigene52703_All//0.00E+00//DW515545				nr +
Unigene52704_All	289	0.00	0.18	0.92	0.52	1.67	0.16	0.15	0.29	2.34	7.45E+00	6.15E-01		9.85E+00	8.01E-02		1.69E+00	1.66E-01		-1.73E+00	5.01E-01		9.83E-01	7.31E-01		4.00E+00	4.29E-04	Up	Unigene52704_All//gi|145329971|ref|NP_001077971.1|//1.00E-21//SYD (SPLAYED); ATPase/ chromatin binding [Arabidopsis thaliana]	Unigene52704_All//4.00E-23//AT2G28290| SYD (SPLAYED); ATPase/ chromatin binding	Unigene52704_All//3.00E-134//TC135784				nr +

Unigene52705_All	315	10.46	8.69	8.96	7.91	7.98	8.46	4.16	0.80	2.78	-2.69E-01	4.41E-01		-2.24E-01	5.55E-01		1.33E-02	9.86E-01		9.74E-02	8.17E-01		-2.39E+00	9.40E-05	Down	-5.81E-01	2.51E-01		Unigene52705_All//gi|2654094|gb|AAC50014.1|//2.00E-15//aspartate aminotransferase glyoxysomal isozyme AAT1 precursor [Glycine max]	Unigene52705_All//9.00E-15//ATSG11520| ASP3 (ASPARTATE AMINOTRANSFERASE 3); L-aspartate:2-oxoglutarate aminotransferase	Unigene52705_All//7.00E-27//TC174220		ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism//ko00350|Tyrosine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene52706_All	284	10.87	8.03	2.25	1.23	1.70	0.80	0.60	0.15	0.14	-4.37E-01	2.25E-01		-2.27E+00	1.28E-07	Down	4.67E-01	7.04E-01		-6.27E-01	6.21E-01		-2.02E+00	3.67E-01		-2.09E+00	3.13E-01									
Unigene52709_All	537	0.00	26.89	0.40	0.37	0.38	1.51	1.02	0.23	2.15	1.47E+01	6.22E-83	Up	8.63E+00	1.41E-01		5.23E-02	9.88E-01		2.03E+00	2.17E-02		-2.13E+00	3.31E-02		1.07E+00	5.22E-02		Unigene52709_All//gi|15241122|ref|NP_200421.1|//6.00E-15//glycine-rich protein / oleosin [Arabidopsis thaliana] >gi|17064992|gb|AAL32650.1| Unknown protein [Arabidopsis thaliana]		Unigene52709_All//0.00E+00//gi|109884101|gb|DW513071.1|DW513071				nr -
Unigene5271_All	747	5.25	2.03	1.92	1.73	3.18	20.80	17.15	51.53	119.89	-1.37E+00	2.16E-05	Down	-1.45E+00	1.74E-05	Down	8.76E-01	3.29E-02		3.58E+00	7.48E-64	Up	1.59E+00	5.93E-70	Up	2.81E+00	0.00E+00	Up	Unigene5271_All//gi|21592660|gb|AAM64609.1|//5.00E-61//phloem-specific lectin PP2-like protein [Arabidopsis thaliana]	Unigene5271_All//4.00E-62//AT1G09155| AtPP2-B15 (Phloem protein 2-B15); carbohydrate binding	Unigene5271_All//2.00E-07//TC153333				nr +
Unigene52710_All	367	0.14	0.69	0.58	1.49	0.00	1.60	0.81	1.14	1.30	2.28E+00	2.34E-01		2.03E+00	3.61E-01		-1.05E+01	4.01E-04	Down	9.96E-02	9.36E-01		4.98E-01	6.33E-01		6.92E-01	4.63E-01		Unigene52710_All//gi|297839729|ref|XP_002887746.1|//5.00E-34//ATNADK-3/NADK3 kinase 3 [Arabidopsis lyrata subsp. lyrata] >gi|297333587|gb|EFH64005.1| ATNADK-3/NADK3 kinase 3 [Arabidopsis lyrata subsp. lyrata]	Unigene52710_All//3.00E-26//AT1G78590| NADK3 (NAD(H) KINASE 3); NAD+ kinase/ NADH kinase	Unigene52710_All//1.00E-176//gi|13247311|gb|BF269778.2|BF269778				nr +
Unigene52711_All	365	1.00	0.00	1.75	2.46	1.51	0.74	3.71	0.69	1.64	-9.97E+00	1.96E-02		8.03E-01	3.88E-01		-7.03E-01	3.24E-01		-1.73E+00	2.81E-02		-2.43E+00	5.63E-05	Down	-1.18E+00	1.86E-02		Unigene52711_All//gi|145338580|ref|NP_188247.2|//9.00E-34//TRZ4 (TRNASE Z 4); 3'-tRNA processing endoribonuclease/ catalytic [Arabidopsis thaliana]	Unigene52711_All//4.00E-35//AT3G16260| TRZ4 (TRNASE Z 4); 3'-tRNA processing endoribonuclease/ catalytic					nr -
Unigene52714_All	339	3.40	0.00	1.10	1.18	0.91	1.07	0.25	0.62	0.24	-1.17E+01	9.91E-07	Down	-1.63E+00	2.13E-02		-3.63E-01	7.54E-01		-1.42E-01	9.04E-01		1.31E-00	4.47E-01		-8.58E-02	9.71E-01									
Unigene52717_All	555	1.13	0.73	0.19	0.45	1.49	1.30	3.73	0.90	0.86	-6.31E-01	4.75E-01		-2.56E+00	2.72E-02		1.73E+00	3.97E-02		1.54E+00	9.17E-02		-2.05E+00	5.01E-06	Down	-2.12E+00	1.66E-06	Down								
Unigene5272_All	1629	9.41	7.68	4.77	18.53	13.55	4.63	0.34	0.15	0.10	-2.93E-01	4.63E-02		-9.80E-01	7.87E-11		-4.52E-01	5.45E-07		-2.00E+00	2.15E-67	Down	-1.13E+00	2.18E-01		-1.79E+00	5.06E-02		Unigene5272_All//gi|18410804|ref|NP_565106.1|//3.00E-72//AtHB33 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 33); DNA binding / transcription factor [Arabidopsis thaliana] >gi|114650583|gb|ABI49441.1| At1g75240 [Arabidopsis thaliana]	Unigene5272_All//3.00E-65//AT1G75240| AtHB33 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 33); DNA binding / transcription factor	Unigene5272_All//0.00E+00//TC148042	zf-HD			nr +
Unigene52721_All	280	0.00	2.90	0.00	0.00	0.25	0.32	1.06	2.84	4.13	1.15E+01	9.37E-05	Up	null	null		7.94E+00	6.08E-01		8.33E+00	4.75E-01		1.42E+00	5.34E-02		1.96E+00	1.21E-03									
Unigene52722_All	294	45.02	17.92	33.69	112.68	95.22	115.98	66.73	28.01	63.96	-1.33E+00	1.19E-15	Down	-4.18E-01	1.02E-02		-2.43E-01	8.20E-03		4.17E-02	7.06E-01		-1.25E+00	1.78E-25	Down	-6.12E-02	6.36E-01		Unigene52722_All//gi|11133775|sp|Q43116.1|PDI_RICCO//7.00E-20//RecName: Full=Protein disulfide-isomerase; Short=PDI; Flags: Precursor >gi|1134968|gb|AAB05641.1| protein disulphide isomerase PDI [Ricinus communis] >gi|1587210|prf||2206331A protein disulfide isomerase	Unigene52722_All//3.00E-19//AT1G21750| ATPDIL1-1 (PDI-LIKE 1-1); protein disulfide isomerase	Unigene52722_All//5.00E-148//gi|11200156|gb|BF269161.1|BF269161		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene52723_All	493	0.96	1.23	0.86	0.51	1.19	2.84	0.09	0.17	0.81	3.69E-01	6.60E-01		-1.45E-01	8.90E-01		1.23E+00	2.33E-01		2.49E+00	1.86E-04	Up	9.83E-01	7.31E-01		3.24E+00	2.14E-02		Unigene52723_All//gi|56550679|gb|AAY97793.1|//8.00E-52//At5g10750 [Arabidopsis thaliana] >gi|57222152|gb|AAW38983.1| At5g10750 [Arabidopsis thaliana]	Unigene52723_All//5.00E-53//AT5G10750| unknown protein	Unigene52723_All//0.00E+00//BQ404504				nr +
Unigene52725_All	349	0.45	2.18	0.46	0.43	0.49	1.04	0.12	0.36	5.82	2.28E+00	1.60E-02		2.54E-02	1.00E+00		2.04E-01	9.50E-01		1.27E+00	3.81E-01		1.57E+00	5.45E-01		5.59E+00	3.56E-13	Up								
Unigene52726_All	328	2.39	0.93	0.00	2.43	2.73	4.13	0.39	1.02	0.97	-1.37E+00	9.59E-02		-1.12E-01	2.21E-04	Down	1.68E-01	8.32E-01		7.66E-01	2.05E-01		1.40E+00	2.76E-01		1.33E+00	2.93E-01									
Unigene5273_All	550	13.51	28.47	22.85	31.07	46.58	40.73	38.44	51.14	39.33	1.08E+00	2.65E-13	Up	7.58E-01	4.36E-06		5.84E-01	4.66E-09		3.91E-01	6.51E-04		4.12E-01	6.00E-06		3.32E-02	7.81E-01		Unigene5273_All//gi|45476565|gb|AAS65948.1|//1.00E-17//At5g11600 [Arabidopsis thaliana] >gi|46339849|gb|AAS88788.1| At5g11600 [Arabidopsis thaliana]	Unigene5273_All//7.00E-15//AT5G11600| unknown protein	Unigene5273_All//2.00E-111//TC176086				nr +
Unigene52730_All	342	0.00	0.00	0.00	0.15	0.20	0.00	6.30	3.42	20.73	null	null		null	null		4.67E-01	9.57E-01		-7.19E+00	6.34E-01		-8.82E-01	2.39E-02		1.72E+00	2.20E-15	Up	Unigene52730_All//gi|224143389|ref|XP_002324940.1|//4.00E-42//histidine kinase cytokinin receptor [Populus trichocarpa] >gi|222866374|gb|EEF03505.1| histidine kinase cytokinin receptor [Populus trichocarpa]	Unigene52730_All//3.00E-22//AT5G10680| calmodulin-binding protein-related					nr -
Unigene52731_All	304	1.72	5.67	0.88	0.82	0.57	5.65	4.45	13.89	7.34	1.72E+00	1.41E-03		-9.75E-01	3.76E-01		-5.33E-01	7.12E-01		2.78E+00	6.14E-06	Up	1.64E+00	9.96E-09	Up	7.22E-01	5.14E-02		Unigene52731_All//gi|224133962|ref|XP_002327722.1|//5.00E-18//predicted protein [Populus trichocarpa] >gi|222836807|gb|EEE75200.1| predicted protein [Populus trichocarpa]		Unigene52731_All//9.00E-14//DR454610				nr -
Unigene52733_All	473	0.88	0.00	0.45	1.58	0.73	1.05	3.66	0.80	0.84	-9.79E+00	1.05E-02		-9.75E-01	4.11E-01		-1.12E+00	1.62E-01		-5.89E-01	4.87E-01		-2.20E+00	1.38E-05	Down	-2.12E+00	1.37E-05	Down	Unigene52733_All//gi|4538901|emb|CAB39638.1|//3.00E-10//RNA-directed DNA polymerase-like protein [Arabidopsis thaliana] >gi|7267666|emb|CAB28094.1| RNA-directed DNA polymerase-like protein [Arabidopsis thaliana]		Unigene52733_All//2.00E-49//TC158995				nr +
Unigene52734_All	434	0.00	0.00	0.00	5.39	3.17	1.04	0.58	0.67	0.00	null	null		null	null		-7.65E-01	5.52E-02		-2.37E+00	6.23E-07	Down	2.06E-01	8.68E-01		-9.19E+00	3.04E-02				Unigene52734_All//1.00E-149//gi|164249243|gb|ES810212.1|ES810212				
Unigene52736_All	1813	0.00	0.06	0.00	0.06	0.00	0.00	12.20	12.77	1.10	5.80E+00	3.86E-01		null	null		-5.78E+00	3.12E-01		-5.78E+00	3.99E-01		6.64E-02	6.20E-01		-3.47E+00	2.27E-105	Down	Unigene52736_All//gi|2252851|gb|AAB62849.1|//1.00E-108//A_TM018A10.3 gene product [Arabidopsis thaliana] >gi|7267430|emb|CAB80900.1| AT4g00910 [Arabidopsis thaliana]	Unigene52736_All//9.00E-134//AT4G00910| unknown protein					nr -
Unigene52737_All	1278	0.12	8.68	2.88	0.00	0.00	0.07	0.00	0.00	0.00	6.14E+00	2.62E-58	Up	4.55E+00	1.61E-16	Up	null	null		6.14E+00	4.75E-01		null	null		null	null		Unigene52737_All//gi|297819316|ref|XP_002877541.1|//2.00E-59//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297323379|gb|EFH53800.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene52737_All//6.00E-60//AT3G47080| binding					nr -
Unigene52739_All	959	0.00	0.00	0.00	0.00	0.00	0.00	4.14	1.57	0.25	null	null		null	null		null	null		null	null		-1.40E+00	9.96E-07	Down	-4.06E+00	6.56E-22	Down	Unigene52739_All//gi|94958151|gb|AB747216.1|//3.00E-77//cathepsin B [Nicotiana benthamiana]	Unigene52739_All//5.00E-60//AT1G02300| cathepsin B-like cysteine protease, putative					nr +
Unigene5274_All	784	7.01	2.97	4.69	13.79	7.38	4.67	4.42	3.31	1.32	-1.24E+00	2.64E-06	Down	-5.80E-01	2.94E-02		-9.02E-01	1.73E-08		-1.56E+00	1.87E-17	Down	-4.20E-01	1.72E-01		-1.74E+00	3.45E-08	Down	Unigene5274_All//gi|751277116|sp|Q6NPS8.1|U497B_ARATH//3.00E-71//RecName: Full=UPF0497 membrane protein At2g37200 >gi|38454082|gb|AAR20735.1| At2g37200 [Arabidopsis thaliana] >gi|38604002|gb|AAR24744.1| At2g37200 [Arabidopsis thaliana]	Unigene5274_All//5.00E-64//AT2G37200| integral membrane protein, putative	Unigene5274_All//0.00E+00//TC146841				nr +
Unigene52740_All	479	0.66	1.59	2.11	0.52	0.50	0.47	0.53	0.52	2.41	1.28E+00	1.28E-01		1.69E+00	2.74E-02		-4.74E-02	9.51E-01		-1.42E-01	9.29E-01		-1.67E-02	1.02E+00		2.19E+00	4.81E-04	Up			Unigene52740_All//6.00E-07//TC175090				
Unigene52743_All	693	1.28	1.02	0.46	0.43	0.05	0.33	0.00	0.06	4.83	-3.26E-01	6.21E-01		-1.48E+00	6.98E-02		-3.12E+00	7.56E-02		-4.04E-01	7.51E-01		5.91E+00	6.33E-01		1.22E+01	6.05E-24	Up	Unigene52743_All//gi|259121419|gb|ACV92029.1|//3.00E-54//WRKY transcription factor 27 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene52743_All//3.00E-42//AT4G23810| WRKY53; DNA binding / protein binding / transcription activator/ transcription factor	Unigene52743_All//2.00E-13//DT466729	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene52747_All	689	0.00	2.06	2.24	0.00	0.00	0.07	0.00	0.00	0.00	1.10E+01	4.06E-08	Up	1.11E+01	1.65E-08	Up	null	null		6.03E+00	6.95E-01		null	null		null	null		Unigene52747_All//gi|115477138|ref|NP_001062165.1|//5.00E-08//0s08g0501700 [Oryza sativa Japonica Group] >gi|113624134|dbj|BAF24079.1| Os08g0501700 [Oryza sativa Japonica Group]	Unigene52747_All//9.00E-08//AT1G21230| WAK5 (WALL ASSOCIATED KINASE 5); kinase/ protein serine/threonine kinase					nr +
Unigene52748_All	307	7.84	6.60	8.15	20.61	19.52	14.42	40.90	18.24	33.48	-2.48E-01	5.63E-01		5.64E-02	8.94E-01		-7.84E-02	8.00E-01		-5.15E-01	2.92E-02		-1.16E+00	6.92E-15	Down	-2.89E-01	4.26E-02				Unigene52748_All//1.00E-65//TC169170				
Unigene52749_All	570	0.00	0.00	0.00	0.00	0.00	0.00	7.94	5.35	0.28	null	null		null	null		null	null		null	null		-5.68E-01	2.58E-02		-4.83E+00	1.15E-27	Down	Unigene52749_All//gi|116222125|gb|AB180933.1|//3.00E-94//actin [Leucocryptos marina]	Unigene52749_All//1.00E-90//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene52749_All//6.00E-41//TC153744		ko04145|Phagosome		nr +
Unigene5275_All	741	24.22	24.96	14.37	52.44	66.04	33.40	27.22	9.31	23.92	4.34E-02	7.57E-01		-7.53E-01	2.80E-08		3.33E-01	2.47E-06		-6.51E-01	5.84E-15		-1.55E+00	8.67E-36	Down	-1.86E-01	1.03E-01		Unigene5275_All//gi|51988176|emb|CAE52516.1|//1.00E-115//beta tubulin [Setaria viridis]	Unigene5275_All//2.00E-105//AT5G12250| TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton	Unigene5275_All//0.00E+00//gi|13352760|gb|BG443108.1|BG443108		ko04145|Phagosome		nr +
Unigene52756_All	461	0.00	0.00	0.00	2.38	1.34	0.20	2.02	0.73	0.60	null	null		null	null		-8.22E-01	1.96E-01		-3.60E+00	5.02E-05	Down	-1.48E+00	2.77E-02		-1.74E+00	8.54E-03		Unigene52756_All//gi|224144987|ref|XP_002325485.1|//8.00E-48//cytochrome P450 [Populus trichocarpa] >gi|222862360|gb|EEE99866.1| cytochrome P450 [Populus trichocarpa]	Unigene52756_All//2.00E-20//AT5G36140| CYP716A2; electron carrier/ heme binding / iron ion binding / monooxygenase			ko00906|Carotenoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr -
Unigene52758_All	654	0.00	0.00	0.00	0.00	0.00	0.00	9.50	1.98	1.71	null	null		null	null		null	null		null	null		-2.26E+00	9.12E-19	Down	-2.48E+00	1.51E-21	Down	Unigene52758_All//gi|11466597|ref|NP_066487.1|//1.00E-79//cytochrome c oxidase subunit 3 [Rhodomonas salina] >gi|10441184|gb|AAG17758.1|AF28809_34 cytochrome c oxidase subunit 3 [Rhodomonas salina]	Unigene52758_All//7.00E-74//ATMG00730| Encodes cytochrome c oxidase subunit 3.			ko00190|Oxidative phosphorylation		nr +
Unigene52759_All	1270	0.99	0.04	0.25	0.24	0.14	0.32	4.43	4.18	3.95	-4.63E+00	3.10E-06	Down	-1.97E+00	4.62E-03		-7.95E-01	5.57E-01		4.44E-01	7.01E-01		-8.32E-02	7.34E-01		-1.64E-01	5.01E-01				Unigene52759_All//6.00E-12//TC164170				
Unigene5276_All	769	24.77	29.58	20.64	66.14	69.45	37.94	18.69	5.71	11.76	2.57E-01	3.10E-02		-2.63E-01	5.58E-02		7.05E-02	4.30E-01		-8.02E-01	1.02E-27		-1.71E+00	1.32E-29	Down	-6.69E-01	2.22E-07		Unigene5276_All//gi|51988176|emb|CAE52516.1|//1.00E-131//beta tubulin [Setaria viridis]	Unigene5276_All//8.00E-122//AT5G12250| TUB6 (BETA-6 TUBULIN); structural constituent of cytoskeleton	Unigene5276_All//0.00E+00//gi|78352163|gb|DT572437.1|DT572437		ko04145|Phagosome		nr -

Unigene52760_All	594	0.00	0.00	0.00	11.15	8.70	12.62	1.49	0.14	0.54	null	null		null	null		-3.59E-01	1.21E-01		1.78E-01	4.68E-01		-3.41E+00	1.40E-04	Down	-1.48E+00	2.51E-02		Unigene52760_All//gi|297729423|ref|NP_001177075.1|//2.00E-07//0s12g0633900 [Oryza sativa Japonica Group] >gi|77557155|gb|ABA99951.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|255670513|dbj|BAH95803.1| Os12g0633900 [Oryza sativa Japonica Group]		Unigene52760_All//0.00E+00//gi|109881716|gb|DW510686.1|DW510686					nr +
Unigene52765_All	336	0.47	1.21	1.58	4.74	1.02	0.81	1.13	0.50	0.59	1.37E+00	2.74E-01		1.76E+00	1.29E-01		-2.21E+00	4.28E-05	Down	-2.56E+00	2.78E-05	Down	-1.19E+00	3.09E-01		-9.34E-01	3.79E-01					Unigene52765_All//7.00E-21//TC164081					
Unigene52768_All	327	11.68	15.50	11.89	9.60	8.21	8.70	7.11	26.20	28.75	4.08E-01	1.35E-01		2.54E-02	9.54E-01		-2.25E-01	5.60E-01		-1.41E-01	6.99E-01		1.88E+00	2.68E-20	Up	2.02E+00	8.80E-25	Up	Unigene52768_All//gi|224053533|ref|XP_002297860.1|//3.00E-11//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222845118|gb|EEE82665.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene52768_All//1.00E-10//AT5G13180| ANAC083 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 83); transcription factor	Unigene52768_All//2.00E-83//DT465849	NAC			nr +
Unigene52769_All	344	3.95	0.00	2.63	2.75	2.40	2.49	0.00	0.36	0.46	-1.19E+01	6.50E-08	Down	-5.88E-01	3.36E-01		-1.96E-01	8.04E-01		-1.41E-01	8.42E-01		8.51E+00	2.40E-01		8.86E+00	1.40E-01		Unigene52769_All//gi|1272349|gb|AAA97903.1|//2.00E-14//secreted glycoprotein 3 [Ipomoea trifida]		Unigene52769_All//9.00E-15//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene52769_All//6.00E-83//CO096076				nr +
Unigene52771_All	496	0.21	0.00	0.00	7.33	2.01	0.46	1.28	0.00	0.16	-7.72E+00	3.70E-01		-7.72E+00	3.92E-01		-1.86E+00	7.44E-09	Down	-4.01E+00	4.88E-17	Down	-1.03E+01	1.23E-04	Down	-2.99E+00	2.58E-03		Unigene52771_All//gi|295799979|emb|CAX68207.1|//1.00E-07//Copia-like retrotransposon [Helianthus annuus]		Unigene52771_All//0.00E+00//CD486453					nr -
Unigene52772_All	281	523.21	223.05	299.03	619.58	442.39	817.12	145.80	108.28	87.90	-1.23E+00	7.14E-148	Down	-8.07E-01	1.39E-71		-4.86E-01	1.77E-43		3.99E-01	2.72E-35		-4.29E-01	7.04E-09		-7.30E-01	1.92E-22		Unigene52772_All//gi|226499354|ref|NP_001147027.1|//3.00E-28//polyubiquitin containing 7 ubiquitin monomers [Zea mays] >gi|195606596|gb|ACG25128.1| polyubiquitin containing 7 ubiquitin monomers [Zea mays]	Unigene52772_All//7.00E-29//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene52772_All//6.00E-132//TC141168		ko03010|Ribosome		nr +
Unigene52773_All	1132	0.69	0.09	0.00	0.13	0.55	0.56	1.20	3.84	2.39	-2.95E+00	3.66E-03		-9.44E+00	2.21E-04	Down	2.05E+00	5.13E-02		2.08E+00	4.69E-02		1.68E+00	2.90E-09	Up	1.00E+00	2.69E-03										
Unigene52774_All	374	0.00	0.95	0.00	0.27	0.64	1.81	216.83	106.28	104.39	9.89E+00	2.46E-02		null	null		1.27E+00	5.31E-01		2.77E+00	1.14E-02		-1.03E+00	3.66E-75	Down	-1.05E+00	1.84E-80	Down	Unigene52774_All//gi|292653531|gb|ADE34283.1|//1.00E-27//aquaporin TIP1;7 [Gossypium hirsutum]	Unigene52774_All//3.00E-24//AT4G01470| TIP1;3 (TONOPLAST INTRINSIC PROTEIN 1;3); urea transmembrane transporter/ water channel	Unigene52774_All//2.00E-58//TC152003				nr -
Unigene52775_All	271	0.77	1.50	0.39	6.99	2.54	1.83	2.34	0.77	0.88	9.54E-01	4.14E-01		-9.75E-01	6.20E-01		-1.46E+00	1.29E-03		-1.93E+00	1.45E-04	Down	-1.60E+00	6.27E-02		-1.41E+00	7.94E-02					Unigene52775_All//2.00E-85//TC173727					
Unigene52777_All	604	0.35	0.17	1.06	2.64	0.57	1.35	2.45	4.43	1.32	-1.05E+00	5.64E-01		1.61E+00	1.11E-01		-2.21E+00	4.28E-05	Down	-9.72E-01	6.67E-02		8.54E-01	1.30E-02		-8.93E-01	5.68E-02					Unigene52777_All//8.00E-05//AT4G04650| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cold; LOCATED IN: stromule; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43730.1); Has 608 Blast hits to 598 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 608; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					
Unigene5278_All	924	2.43	22.32	9.34	4.64	18.52	15.69	1.05	0.50	1.12	3.20E+00	1.29E-71	Up	1.94E+00	8.93E-17	Up	2.00E+00	9.31E-41	Up	1.76E+00	6.93E-27	Up	-1.08E+00	8.88E-02		9.11E-02	8.86E-01					Unigene5278_All//0.00E+00//ES824206					
Unigene52782_All	288	0.91	0.53	1.85	7.78	7.05	2.20	1.91	0.87	0.00	-7.83E-01	6.20E-01		1.03E+00	3.42E-01		-1.42E-01	7.78E-01		-1.83E+00	5.88E-05	Down	-1.13E+00	2.18E-01		-1.09E+01	2.80E-04	Down				Unigene52782_All//2.00E-11//PL577438					
Unigene52783_All	220	1.19	2.07	6.54	2.72	2.03	8.01	0.00	0.76	0.00	8.02E-01	4.60E-01		2.46E+00	3.26E-04	Up	-4.17E-01	6.27E-01		1.56E+00	2.64E-03		9.57E+00	1.39E-01		null	null		Unigene52783_All//gi|21554076|gb|AAM63157.1|//3.00E-15//similar to latex allergen from Hevea brasiliensis [Arabidopsis thaliana]	Unigene52783_All//3.00E-06//AT2G26560| PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	Unigene52783_All//3.00E-62//TC133986				nr +
Unigene52787_All	440	0.71	0.69	1.69	0.45	0.55	0.92	0.86	1.52	3.80	-4.64E-02	9.84E-01		1.25E+00	1.54E-01		2.75E-01	8.95E-01		1.03E+00	4.28E-01		8.13E-01	3.15E-01		2.14E+00	2.21E-05	Up	Unigene52787_All//gi|297836334|ref|XP_002886049.1|//2.00E-39//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331889|gb|EFH62308.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene52787_All//5.00E-38//AT2G19280| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene52789_All	393	0.67	0.13	0.00	2.79	1.66	0.46	1.40	0.64	0.30	-2.37E+00	2.14E-01		-9.38E+00	8.55E-02		-7.44E-01	2.45E-01		-2.60E+00	7.13E-04	Down	-1.13E+00	2.18E-01		-2.20E+00	2.24E-02		Unigene52789_All//gi|297812071|ref|XP_002873919.1|//2.00E-18//BUD2/SAMDC4 [Arabidopsis lyrata subsp. lyrata] >gi|297319756|gb|EFH50178.1| BUD2/SAMDC4 [Arabidopsis lyrata subsp. lyrata]	Unigene52789_All//2.00E-18//AT5G18930| BUD2 (BUSHY AND DWARF 2); adenosylmethionine decarboxylase	Unigene52789_All//0.00E+00//TC160079		ko00270|Cysteine and methionine metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene5279_All	1744	0.00	1.28	0.73	1.60	5.43	5.65	6.47	1.80	1.83	1.03E+01	1.09E-12	Up	9.52E+00	4.68E-07	Up	1.76E+00	3.19E-19	Up	1.82E+00	2.90E-19	Up	-1.85E+00	5.88E-26	Down	-1.82E+00	2.47E-26	Down	Unigene5279_All//gi|3913035|sp|O65015.1|AMYB_TRIRP//0.00E+00//RecName: Full=Beta-amylase; AltName: Full=1,4-alpha-D-glucan maltohydrolase >gi|2935474|gb|AAD04259.1| beta-amylase [Trifolium repens]	Unigene5279_All//0.00E+00//AT4G15210| BAM5 (BETA-AMYLASE 5); beta-amylase	Unigene5279_All//0.00E+00//TC170168		ko00500|Starch and sucrose metabolism		nr +
Unigene52790_All	231	9.97	17.99	11.06	14.23	16.10	18.77	55.46	52.11	25.01	8.52E-01	4.41E-03		1.51E-01	7.03E-01		1.78E-01	6.15E-01		3.99E-01	2.01E-01		-8.99E-02	6.18E-01		-1.15E+00	2.44E-15	Down				Unigene52790_All//9.00E-103//gi|164261476|gb|ES831497.1|ES831497					
Unigene52794_All	335	1.09	3.63	2.54	6.25	5.24	3.51	4.54	4.99	10.11	1.73E+00	8.94E-03		1.22E+00	1.38E-01		-2.53E-01	5.92E-01		-8.33E-01	6.36E-02		1.35E-01	7.71E-01		1.15E+00	1.11E-04	Up				Unigene52794_All//3.00E-146//CO118174					
Unigene52795_All	348	35.93	13.54	20.35	34.64	28.40	46.07	58.07	31.71	22.09	-1.41E+00	4.02E-16	Down	-8.20E-01	8.10E-07		-2.87E-01	8.32E-02		4.11E-01	3.05E-03		-8.73E-01	6.67E-15		-1.39E+00	9.90E-32	Down	Unigene52795_All//gi|1856971|dbj|BAA05057.1|//1.00E-28//cyc07 [Catharanthus roseus]	Unigene52795_All//4.00E-14//AT3G04840| 40S ribosomal protein S3A (RPS3AA)	Unigene52795_All//3.00E-162//gi|73944313|gb|DT527621.1|DT527621		ko03010|Ribosome		nr -
Unigene52797_All	821	0.00	34.31	15.24	0.06	0.00	0.00	0.00	0.00	0.00	1.51E+01	2.22E-162	Up	1.39E+01	2.09E-70	Up	-5.92E+00	5.55E-01		-5.92E+00	6.34E-01		null	null		null	null		Unigene52797_All//gi|17221648|dbj|BAB78478.1|//2.00E-14//preproMP73 [Cucurbita maxima]				ko03040|Spliceosome		nr +
Unigene52798_All	320	0.00	0.00	0.00	0.00	0.00	0.00	42.94	15.02	11.33	null	null		null	null		null	null		null	null		-1.52E+00	6.81E-24	Down	-1.92E+00	3.75E-34	Down				Unigene52798_All//1.00E-28//CO079579					
Unigene528_All	1666	0.82	1.22	2.14	2.78	1.98	3.12	2.46	2.86	5.79	5.75E-01	2.12E-01		1.39E+00	8.19E-05	Up	-4.87E-01	7.74E-02		1.65E-01	6.16E-01		2.16E-01	4.27E-01		1.23E+00	6.14E-13	Up	Unigene528_All//gi|42566063|ref|NP_191516.2|//8.00E-58//RabGAP/TBC domain-containing protein [Arabidopsis thaliana]	Unigene528_All//3.00E-59//AT3G59570| RabGAP/TBC domain-containing protein	Unigene528_All//0.00E+00//gi|73865683|gb|DT468421.1|DT468421				nr -
Unigene5280_All	975	597.96	583.14	663.14	211.16	287.28	230.40	4.25	10.33	5.97	-3.62E-02	1.25E-01		1.49E-01	5.44E-14		4.44E-01	5.03E-58		1.26E-01	2.26E-04		1.28E+00	6.63E-14	Up	4.89E-01	2.25E-02		Unigene5280_All//gi|218156192|dbj|BAH03328.1|//1.00E-38//chloroplast protein 12 [Fagus crenata]	Unigene5280_All//3.00E-31//AT2G47400| CP12-1	Unigene5280_All//0.00E+00//TC160239				nr +
Unigene52801_All	336	0.93	3.17	0.63	5.34	4.20	4.03	5.66	2.24	13.40	1.76E+00	1.43E-02		-5.60E-01	6.63E-01		-3.45E-01	5.12E-01		-4.04E-01	4.43E-01		-1.34E+00	1.94E-03		1.24E+00	1.44E-06	Up				Unigene52801_All//7.00E-86//ES847924					
Unigene52804_All	250	25.74	43.58	21.94	58.18	42.56	57.45	89.46	59.85	42.23	7.59E-01	1.17E-05		-2.31E-01	3.87E-01		-4.51E-01	1.08E-03		-1.83E-02	9.33E-01		-5.80E-01	1.93E-08		-1.08E+00	8.10E-24	Down				Unigene52804_All//9.00E-137//gi|13248728|gb|BF278212.2|BF278212					
Unigene52806_All	325	0.32	2.49	0.98	0.92	1.38	0.56	1.56	6.17	4.90	2.95E+00	3.28E-03		1.61E+00	3.04E-01		5.83E-01	6.26E-01		-7.26E-01	6.38E-01		1.98E+00	1.22E-05	Up	1.65E+00	6.43E-04	Up									
Unigene52811_All	277	4.34	1.10	0.77	73.19	44.50	30.16	872.01	105.92	693.08	-1.98E+00	3.71E-03		-2.50E+00	1.15E-03		-7.18E-01	1.45E-10		-1.28E+00	5.96E-24	Down	-3.04E+00	0.00E+00	Down	-3.31E-01	6.72E-31		Unigene52811_All//gi|224128918|ref|XP_002320453.1|//3.00E-09//predicted protein [Populus trichocarpa] >gi|222861226|gb|EEE98768.1| predicted protein [Populus trichocarpa]		Unigene52811_All//4.00E-127//AT729082				nr +
Unigene52817_All	355	0.00	0.00	0.60	0.70	0.97	2.54	2.50	0.82	0.34	null	null		9.23E+00	1.41E-01		4.67E-01	7.79E-01		1.86E+00	2.18E-02		-1.60E+00	2.18E-02		-2.89E+00	3.04E-04	Down	Unigene52817_All//gi|297819496|ref|XP_002877631.1|//2.00E-26//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297323469|gb|EFH53890.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene52817_All//1.00E-26//AT3G48770| ATP binding / DNA binding					nr -
Unigene52819_All	317	1.98	0.00	2.18	4.24	2.06	3.13	1.87	0.53	1.26	-1.10E+01	7.91E-04	Down	1.41E-01	8.60E-01		-1.04E+00	6.04E-02		-4.37E-01	4.70E-01		-1.82E+00	4.71E-02		-5.71E-01	4.78E-01		Unigene52819_All//gi|255558854|ref|XP_002520450.1|//4.00E-35//hypothetical protein RCOM_0731250 [Ricinus communis] >gi|223540292|gb|EEF41863.1| hypothetical protein RCOM_0731250 [Ricinus communis]		Unigene52819_All//5.00E-179//gi|109862456|gb|DW491433.1|DW491433				nr -
Unigene5282_All	573	18.63	65.44	23.79	11.30	21.09	25.46	27.23	70.61	27.32	1.81E+00	5.93E-67	Up	3.53E-01	2.95E-02		9.00E-01	5.17E-09		1.17E+00	5.26E-15	Up	1.37E+00	1.77E-59	Up	5.10E-03	9.66E-01		Unigene5282_All//gi|166203244|gb|AB184662.1|//3.00E-11//transcription factor [Glycine max]	Unigene5282_All//9.00E-08//AT3G56400| WRKY70; transcription factor/ transcription repressor	Unigene5282_All//0.00E+00//gi|109866046|gb|DW495022.1|DW495022	WRKY			nr -
Unigene52829_All	556	0.00	0.00	0.00	0.00	0.00	0.00	2.05	1.58	0.50	null	null		null	null		null	null		null	null		-3.79E-01	5.32E-01		-2.03E+00	8.63E-04	Down	Unigene52829_All//gi|159469668|ref|XP_001692985.1|//7.00E-70//ribosomal protein L8, component of cytosolic 80S ribosome and 60S large subunit [Chlamydomonas reinhardtii] >gi|158277787|gb|EDP03554.1| ribosomal protein L8 [Chlamydomonas reinhardtii]	Unigene52829_All//1.00E-68//AT2G18020| EMB2296 (embryo defective 2296); structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene52831_All	223	0.00	0.00	0.00	0.00	0.00	0.00	70.34	24.18	54.67	null	null		null	null		null	null		null	null		-1.54E+00	8.19E-28	Down	-3.64E-01	3.18E-03					Unigene52831_All//1.00E-15//gi|31072811|gb|CA993090.1|CA993090					
Unigene52839_All	367	0.29	3.04	0.58	5.29	7.79	7.14	1.84	0.34	0.33	3.41E+00	1.24E-04	Up	1.03E+00	5.91E-01		5.57E-01	1.45E-01		4.31E-01	3.11E-01		-2.43E+00	7.76E-03		-2.50E+00	4.78E-03		Unigene52839_All//gi|296082496|emb|CBI21501.3|//4.00E-09//unnamed protein product [Vitis vinifera]		Unigene52839_All//0.00E+00//DV850082				nr -
Unigene52840_All	290	2.17	5.77	7.71	3.26	4.27	1.87	0.44	1.01	0.69	1.41E+00	7.54E-03		1.83E+00	1.63E-04	Up	3.89E-01	5.68E-01		-8.04E-01	2.77E-01		1.21E+00	3.92E-01		6.51E-01	6.65E-01					Unigene52840_All//3.00E-07//DV513365					
Unigene52847_All	239	0.00	0.00	0.00	0.00	0.00	0.00	78.37	22.91	25.67	null	null		null	null		null	null		null	null		-1.71E+00	2.76E-40	Down	-1.61E+00	2.72E-36	Down									
Unigene52848_All	386	1.90	0.53	0.00	2.32	2.94	0.59	0.99	0.00	1.03	-1.85E+00	4.08E-02		-1.09E+01	4.13E-04	Down	3.42E-01	6.20E-01		-1.99E+00	1.36E-02		-9.95E+00	6.17E-03		6.62E-02	9.66E-01		Unigene52848_All//gi|225454234|ref|XP_002274163.1|//1.00E-27//PREDICTED: myc anthocyanin regulatory protein [Vitis vinifera]	Unigene52848_All//1.00E-24//AT5G41315| GL3 (GLABROUS 3); protein binding / transcription factor	Unigene52848_All//0.00E+00//ES824288	bHLH			nr -
Unigene52850_All	739	0.00	0.21	0.00	0.27	0.19	0.73	1.72	11.93	9.38	7.68E+00	2.35E-01		null	null		-5.32E-01	7.48E-01		1.44E+00	1.92E-01		2.80E+00	2.79E-33	Up	2.45E+00	2.80E-23	Up	Unigene52850_All//gi|195639720|gb|ACG39328.1|//6.00E-13//brain protein 44-like protein [Zea mays]	Unigene52850_All//1.00E-14//AT5G20090| unknown protein	Unigene52850_All//1.00E-15//DN827768				nr -
Unigene52858_All	325	122.83	55.50	125.83	91.05	101.82	53.22	1.43	0.77	2.57	-1.15E+00	2.25E-36	Down	3.48E-02	7.21E-01		1.61E-01	1.09E-01		-7.75E-01	1.89E-15		-8.91E-01	3.83E-01		8.47E-01	2.03E-01		Unigene52858_All//gi|58200403|gb|AAW66457.1|//5.00E-18//isochorismate synthase [Capsicum annuum]	Unigene52858_All//2.00E-18//AT1G18870| ICS2 (ISOCHORISMATE SYNTHASE 2); isochorismate synthase	Unigene52858_All//5.00E-133//gi|164358013|gb|ES820732.1|ES820732		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene5286_All	1366	3.06	3.60	1.09	6.89	6.38	7.84	15.60	29.04	47.68	2.32E-01	4.09E-01		-1.49E+00	5.14E-06	Down	-1.12E-01	5.94E-01		1.85E-01	3.66E-01		8.96E-01	1.12E-29		1.61E+00	4.99E-123	Up	Unigene5286_All//gi|82623379|gb|ABB87104.1|//2.00E-50//ChaC-like family protein-like [Solanum tuberosum]	Unigene5286_All//5.00E-49//AT4G31290| ChaC-like family protein	Unigene5286_All//0.00E+00//TC147173				nr +

Unigene52860_All	466	0.00	0.11	0.00	0.96	0.81	1.55	0.73	2.06	2.74	6.76E+00	6.15E-01		null	null		-2.43E-01	8.21E-01			6.89E-01	4.48E-01		1.51E+00	2.24E-02		1.91E+00	7.76E-04	Up	Unigene52860_All//gi|224055679|ref|XP_002298599.1|//3.00E-55//lysine/histidine transporter [Populus trichocarpa] >gi|222845857|gb|EEE83404.1| lysine/histidine transporter [Populus trichocarpa]	Unigene52860_All//3.00E-53//AT5G40780| LHT1; amino acid transmembrane transporter	Unigene52860_All//0.00E+00//TC162603				nr +
Unigene52863_All	358	1.46	5.52	0.74	2.92	1.35	0.25	1.06	0.23	0.67	1.92E+00	1.74E-04	Up	-9.75E-01	3.76E-01		-1.12E+00	8.44E-02			-3.53E+00	9.34E-05	Down	-2.19E+00	8.75E-02		-6.71E-01	5.30E-01		Unigene52863_All//gi|297852260|ref|XP_002894011.1|//8.00E-43//F27F5.25 [Arabidopsis lyrata subsp. lyrata] >gi|297339853|gb|EFH70270.1| F27F5.25 [Arabidopsis lyrata subsp. lyrata]	Unigene52863_All//1.00E-42//AT1G45170| unknown protein	Unigene52863_All//5.00E-59//TC150961				nr +
Unigene52867_All	926	0.00	0.00	0.00	0.05	0.00	0.00	2.74	2.71	0.00	null	null		null	null		-5.75E+00	5.55E-01			-5.75E+00	6.34E-01		-1.66E-02	9.98E-01		-1.14E+01	1.14E-18	Down	Unigene52867_All//gi|260516654|gb|ACX43954.1|//3.00E-67//cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516656|gb|ACX43955.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516658|gb|ACX43956.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516660|gb|ACX43957.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516662|gb|ACX43958.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516664|gb|ACX43959.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516666|gb|ACX43960.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516668|gb|ACX43961.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516670|gb|ACX43962.1| cysteine protease 2 [Brachiaria hybrid cultivar]	Unigene52867_All//3.00E-58//AT1G20850| XCP2 (xylem cysteine peptidase 2); cysteine-type peptidase/ peptidase					nr +
Unigene52869_All	941	0.00	0.00	0.00	0.00	0.00	0.00	45.52	5.91	9.02	null	null		null	null		null	null			null	null		-2.95E+00	1.11E-168	Down	-2.34E+00	3.26E-134	Down							
Unigene52872_All	487	0.00	0.00	0.00	0.00	0.00	0.00	67.20	15.02	50.31	null	null		null	null		null	null			null	null		-2.16E+00	1.40E-90	Down	-4.18E-01	3.54E-07		Unigene52872_All//gi|30725324|gb|AAP37684.1|//3.00E-14//At3g01680 [Arabidopsis thaliana]	Unigene52872_All//1.00E-14//AT3G01680| unknown protein	Unigene52872_All//3.00E-58//TC134810				nr +
Unigene52874_All	727	0.00	0.00	0.00	0.00	0.00	1.80	2.82	0.16	null	null		null	null		null	null			null	null		6.44E-01	1.15E-01		-3.46E+00	7.84E-07	Down	Unigene52874_All//gi|18378607|gb|AAL68641.1|AF455763.1|//3.00E-07//polyprotein [Oryza sativa Japonica Group]		Unigene52874_All//2.00E-35//ES807842				nr +
Unigene52877_All	867	0.24	0.06	0.00	0.11	0.04	0.05	5.95	2.60	14.11	-2.05E+00	3.33E-01		-7.92E+00	1.45E-01		-1.53E+00	5.86E-01			-1.14E+00	6.76E-01		-1.19E+00	8.39E-07	Down	1.25E+00	2.01E-16	Up	Unigene52877_All//gi|297602560|ref|NP_001052564.2|//3.00E-12//Os04g0370900 [Oryza sativa Japonica Group] >gi|253675378|dbj|BAF14478.2| Os04g0370900 [Oryza sativa Japonica Group]	Unigene52877_All//2.00E-11//AT1G16090| WAKL7 (wall associated kinase-like 7); protein serine/threonine kinase	Unigene52877_All//0.00E+00//TC134682				nr -
Unigene52879_All	414	0.00	0.00	0.00	16.60	10.73	6.55	1.12	0.20	0.67	null	null		null	null		-6.30E-01	2.66E-03			-1.34E+00	3.96E-09	Down	-2.48E+00	3.38E-02		-7.38E-01	4.26E-01		Unigene52879_All//gi|75096924|sp|Q40484.1|SCP31_ARATH//4.00E-25//RecName: Full=Serine carboxypeptidase-like 31; Flags: Precursor >gi|1931640|gb|AAB65475.1| Serine carboxypeptidase isolog; 30227-33069 [Arabidopsis thaliana]	Unigene52879_All//1.00E-19//AT1G11080| scpl31 (serine carboxypeptidase-like 31); serine-type carboxypeptidase	Unigene52879_All//1.00E-143//TC160828				nr +
Unigene5288_All	1095	13.38	7.36	6.61	15.42	13.15	15.67	53.05	75.88	51.08	-8.63E-01	6.07E-09		-1.02E+00	5.47E-11	Down	-2.30E-01	1.01E-01			2.33E-02	9.02E-01		5.16E-01	1.02E-23		-5.47E-02	4.54E-01		Unigene5288_All//gi|7106544|dbj|BAA92223.1|//1.00E-68//AT4WK9 [Arabidopsis thaliana]	Unigene5288_All//8.00E-61//AT3G18040| WPK9 (MAP KINASE 9); MAP kinase	Unigene5288_All//0.00E+00//TC145806				nr -
Unigene52884_All	447	22.01	23.92	17.87	35.10	24.34	35.87	36.04	35.16	15.95	1.20E-01	5.42E-01		-3.00E-01	1.36E-01		-5.28E-01	4.98E-05			3.11E-02	8.59E-01		-3.57E-02	8.10E-01		-1.18E+00	9.82E-20	Down	Unigene52884_All//gi|16223|emb|CAA78057.1|//9.00E-08//calmodulin [Arabidopsis thaliana]	Unigene52884_All//6.00E-09//AT5G37780| CAM1 (CALMODULIN 1); calcium ion binding	Unigene52884_All//4.00E-94//TC158005		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr +
Unigene52885_All	951	0.00	0.00	0.00	18.02	9.12	8.83	0.00	0.13	0.00	null	null		null	null		-9.82E-01	4.15E-15			-1.03E+00	1.70E-14	Down	7.04E+00	2.40E-01		null	null				Unigene52885_All//0.00E+00//TC151061				
Unigene52886_All	367	5.70	1.10	5.37	0.54	0.75	1.23	0.00	0.00	0.76	-2.37E+00	6.27E-06	Down	-8.71E-02	8.46E-01		4.67E-01	8.16E-01			1.18E+00	3.38E-01		null	null		9.57E+00	2.43E-02		Unigene52886_All//gi|15241035|ref|NP_198128.1|//2.00E-16//hypoxia-responsive family protein [Arabidopsis thaliana]	Unigene52886_All//9.00E-18//AT5G27760| hypoxia-responsive family protein	Unigene52886_All//1.00E-35//DR461620				nr +
Unigene52887_All	228	1.84	0.44	0.93	8.96	3.02	2.77	1.30	0.00	0.35	-2.05E+00	1.20E-01		-9.75E-01	4.11E-01		-1.57E+00	3.28E-04	Down	-1.69E+00	3.48E-04	Down	-1.03E+01	2.17E-02		-1.89E+00	1.68E-01									ESTscan -
Unigene5289_All	1414	2.07	1.08	1.21	3.45	3.56	3.71	6.43	4.23	2.73	-9.47E-01	9.80E-03		-7.82E-01	4.17E-02		4.25E-02	9.00E-01			1.02E-01	7.22E-01		-6.05E-01	3.67E-04		-1.23E+00	2.27E-12	Down	Unigene5289_All//gi|30696108|ref|NP_176031.2|//1.00E-101//pseudouridine synthase family protein [Arabidopsis thaliana] >gi|75140931|sp|Q7X465.1|PUS1_ARATH RecName: Full=RNA pseudourine synthase 1; AltName: Full=RNA-uridine isomerase 1; AltName: Full=RNA pseudouridylate synthase 1 >gi|33589806|gb|AAQ22669.1| At1g56345 [Arabidopsis thaliana]	Unigene5289_All//2.00E-88//AT1G56345| pseudouridine synthase family protein	Unigene5289_All//0.00E+00//AI732047				nr +
Unigene52893_All	356	3.38	8.54	7.03	9.66	7.64	6.85	55.23	52.71	53.94	1.34E+00	3.25E-04	Up	1.06E+00	1.24E-02		-3.37E-01	3.28E-01			-4.95E-01	1.51E-01		-6.71E-02	6.53E-01		-3.40E-02	7.85E-01				Unigene52893_All//4.00E-87//gi|11199756|gb|BF268773.1|BF268773				
Unigene52895_All	533	0.00	0.00	0.00	0.00	0.00	0.00	10.63	5.18	4.11	null	null		null	null		null	null			null	null		-1.04E+00	4.42E-06	Down	-1.37E+00	2.66E-09	Down							
Unigene52896_All	950	0.00	6.19	6.00	0.00	0.04	0.00	0.00	0.00	0.00	1.26E+01	1.51E-33	Up	1.26E+01	9.58E-32	Up	5.18E+00	8.29E-01			null	null		null	null		null	null		Unigene52896_All//gi|11467399|ref|NP_043256.1|//6.00E-23//RNA polymerase alpha subunit [Cyanophora paradoxa] >gi|1350840|sp|P48118.1|RPOA_CYAPA RecName: Full=DNA-directed RNA polymerase subunit alpha; Short=PEP; AltName: Full=Plastid-encoded RNA polymerase subunit alpha; Short=RNA polymerase subunit alpha >gi|1016200|gb|AAA81287.1| alpha subunit of RNA polymerase [Cyanophora paradoxa]	Unigene52896_All//2.00E-07//AT5G64650| ribosomal protein L17 family protein		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene52899_All	440	1.31	2.07	0.97	11.32	3.13	4.52	0.00	0.19	0.18	6.64E-01	3.75E-01		-4.34E-01	6.23E-01		-1.85E+00	7.27E-12	Down	-1.33E+00	1.14E-06	Down	7.57E+00	4.00E-01		7.50E+00	4.03E-01				Unigene52899_All//0.00E+00//TC158970				
Unigene529_All	3471	1.15	1.46	0.97	3.43	6.01	6.25	18.02	5.54	9.66	3.50E-01	2.08E-01		-2.45E-01	4.59E-01		8.10E-01	8.16E-13			8.65E-01	1.33E-13		-1.70E+00	2.86E-125	Down	-8.99E-01	6.89E-48		Unigene529_All//gi|186507757|ref|NP_001118516.1|//1.00E-158//RAB GTPase activator [Arabidopsis thaliana]	Unigene529_All//1.00E-152//AT2G43490| RAB GTPase activator	Unigene529_All//0.00E+00//C0121166		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene5290_All	999	23.73	6.39	13.59	25.88	19.03	16.41	13.54	5.36	2.63	-1.89E+00	2.28E-45	Down	-8.04E-01	6.42E-12		-4.44E-01	6.82E-06			-6.57E-01	2.49E-10		-1.34E+00	1.15E-19	Down	-2.36E+00	1.60E-43	Down	Unigene5290_All//gi|15239101|ref|NP_196157.1|//2.00E-78//PRA1.B3 (PRENYLATED RAB ACCEPTOR 1.B3) [Arabidopsis thaliana] >gi|75171434|sp|Q9FLB6.1|PRI83_ARATH RecName: Full=PRA1 family protein B3; Short=AtPRA1.B3; AltName: Full=Prenylated Rab acceptor 2 >gi|94142493|gb|ABF19034.1| At5g05380 [Arabidopsis thaliana]	Unigene5290_All//2.00E-40//AT5G05380| PRA1.B3 (PRENYLATED RAB ACCEPTOR 1.B3)	Unigene5290_All//0.00E+00//TC131926				nr -
Unigene52902_All	476	1.54	5.85	5.37	0.73	2.60	2.28	0.53	0.18	0.59	1.93E+00	4.69E-06	Up	1.80E+00	5.75E-05	Up	1.83E+00	4.77E-03			1.64E+00	2.06E-02		-1.60E+00	3.10E-01		1.37E-01	9.29E-01				Unigene52902_All//3.00E-30//gi|78335886|gb|DT556160.1|DT556160				
Unigene52905_All	846	0.00	0.00	0.00	0.12	0.00	0.00	53.08	182.55	396.79	null	null		null	null		-6.88E+00	3.12E-01			-6.88E+00	3.99E-01		1.78E+00	0.00E+00	Up	2.90E+00	0.00E+00	Up	Unigene52905_All//gi|145354603|ref|NP_195422.3|//3.00E-72//PLP4 (PATATIN-LIKE PROTEIN 4); nutrient reservoir [Arabidopsis thaliana] >gi|4006871|emb|CAB16789.1| patatin-like protein [Arabidopsis thaliana] >gi|7270654|emb|CAB80371.1| patatin-like protein [Arabidopsis thaliana]	Unigene52905_All//2.00E-73//AT4G37050| PLP4 (PATATIN-LIKE PROTEIN 4); nutrient reservoir					nr +
Unigene52907_All	481	0.00	0.00	0.00	0.21	0.14	0.38	2.46	3.65	9.69	null	null		null	null		-5.32E-01	8.16E-01			8.59E-01	6.95E-01		5.68E-01	2.11E-01		1.98E+00	2.14E-12	Up			Unigene52907_All//1.00E-131//C0080060				
Unigene5291_All	1443	0.33	2.11	0.41	3.07	4.49	4.57	1.76	0.75	0.30	2.69E+00	2.24E-09	Up	3.15E-01	7.19E-01		5.46E-01	1.59E-02			5.73E-01	1.27E-02		-1.22E+00	7.21E-04	Down	-2.53E+00	1.83E-09	Down	Unigene5291_All//gi|258618877|gb|ACN84256.1|//8.00E-39//LOX8 [Sorghum bicolor]	Unigene5291_All//1.00E-31//AT3G22400| LOX5; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Unigene5291_All//2.00E-92//DW513883		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr -
Unigene52911_All	221	19.18	22.01	13.73	25.92	19.01	23.91	85.52	49.17	38.22	1.99E-01	4.94E-01		-4.82E-01	1.28E-01		-4.47E-01	6.78E-02			-1.17E-01	6.96E-01		-7.98E-01	3.99E-12		-1.16E+00	1.36E-22	Down	Unigene52911_All//gi|115471133|ref|NP_001059165.1|//7.00E-33//Os07g0209000 [Oryza sativa Japonica Group] >gi|113610701|dbj|BAF21079.1| Os07g0209000 [Oryza sativa Japonica Group]	Unigene52911_All//3.00E-33//AT5G66680| DGL1; dolichyl-diphosphooligosaccharide-protein glycotransferase	Unigene52911_All//7.00E-122//gi|21103922|gb|BQ416235.1|BQ416235		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis		nr +
Unigene52915_All	244	2.57	0.83	0.44	7.15	1.69	5.74	0.00	0.00	0.00	-1.63E+00	9.23E-02		-2.56E+00	2.72E-02		-2.08E+00	3.84E-05	Down	-3.17E-01	5.66E-01		null	null		null	null		Unigene52915_All//gi|27735191|sp|P27483.2|GRP1_ARATH//4.00E-14//RecName: Full=Glycine-rich cell wall structural protein; Flags: Precursor				ko03040|Spliceosome		nr +
Unigene52920_All	220	3.57	1.61	0.00	1.36	1.41	0.82	0.38	2.28	1.45	-1.15E+00	1.53E-01		-1.18E+01	2.21E-04	Down	5.22E-02	9.98E-01			-7.26E-01	6.38E-01		2.57E+00	2.28E-02		1.91E+00	1.54E-01				Unigene52920_All//1.00E-06//ES804426				
Unigene52923_All	854	0.74	1.07	0.12	2.68	0.69	0.85	0.30	0.44	4.01	5.39E-01	4.49E-01		-2.56E+00	2.72E-02		-1.97E+00	3.55E-06	Down	-1.66E+00	1.58E-04	Down	5.68E-01	6.37E-01		3.76E+00	1.40E-17	Up	Unigene52923_All//gi|297851458|ref|XP_002893610.1|//2.00E-22//heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297339452|gb|EFH69869.1| heat shock protein binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene52923_All//3.00E-19//AT1G30280| heat shock protein binding	Unigene52923_All//0.00E+00//TC143397				nr -
Unigene52927_All	529	0.99	0.10	0.81	3.30	1.04	0.85	1.92	0.47	0.00	-3.37E+00	1.57E-02		-2.97E-01	7.49E-01		-1.66E+00	5.90E-04	Down	-1.95E+00	2.67E-04	Down	-2.02E+00	2.83E-03		-1.09E+01	1.35E-07	Down							

Unigene52928_All	412	0.25	1.48	2.59	2.78	4.26	2.30	0.41	0.00	0.19	2.54E+00	2.46E-02		3.35E+00	3.36E-04	Up	6.16E-01	2.33E-01		-2.73E-01	6.89E-01		-8.68E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene52928_All//gi|297723217|ref|NP_001173972.1|//4.00E-07//0s04g0465432 [Oryza sativa Japonica Group] >gi|21741223|emb|CAD40934.1|OSJNBb0048E02.10 [Oryza sativa (japonica cultivar-group)] >gi|255675536|dbj|BAH92700.1|Os04g0465432 [Oryza sativa Japonica Group]	Unigene52928_All//7.00E-13//AT3G28150| unknown protein	Unigene52928_All//0.00E+00//TC173964				nr -
Unigene52929_All	230	14.33	12.78	20.61	25.12	18.42	21.01	65.44	38.52	25.12	-1.66E-01	6.15E-01		5.24E-01	7.35E-02		-4.48E-01	6.56E-02		-2.58E-01	3.54E-01		-7.64E-01	3.57E-09		-1.38E+00	1.53E-23	Down	Unigene52929_All//gi|20161472|dbj|BAB90396.1|//1.00E-09//ADP-ribosylation factor [Oryza sativa Japonica Group]	Unigene52929_All//3.00E-10//AT1G70490| ARFA1D; GTP binding / phospholipase activator/ protein binding	Unigene52929_All//5.00E-98//gi|109858002|gb|DW486981.1|DW486981				nr -
Unigene5293_All	696	8.12	14.56	17.83	13.24	18.16	19.86	11.36	15.67	16.83	8.43E-01	3.38E-06		1.13E+00	3.82E-11	Up	4.56E-01	2.90E-03		5.85E-01	7.83E-05		4.64E-01	2.65E-03		5.67E-01	8.25E-05		Unigene5293_All//gi|297814848|ref|XP_002875307.1|//1.00E-26//regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321145|gb|EFH51566.1|regulator of chromosome condensation family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5293_All//8.00E-25//AT3G26100| regulator of chromosome condensation (RCC1) family protein	Unigene5293_All//0.00E+00//DW495270				nr +
Unigene52930_All	923	0.00	0.00	0.00	0.86	0.07	0.29	6.28	16.53	42.30	null	null		null	null		-3.53E+00	3.03E-04	Down	-1.56E+00	6.26E-02		1.40E+00	1.85E-23	Up	2.75E+00	2.21E-145	Up	Unigene52930_All//gi|94549041|gb|AB539005.1|//2.00E-43//plant cell wall protein S1TFR8B [Solanum lycopersicum]	Unigene52930_All//3.00E-25//AT2G46150| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54200.1); Has 137 Blast hits to 136 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 133; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene52930_All//3.00E-13//TC136055				nr -
Unigene52931_All	818	0.00	17.65	5.92	0.00	0.00	0.00	0.00	0.00	1.41E+01	6.21E-83	Up	1.25E+01	6.11E-27	Up	null	null		null	null		null	null		null	null		Unigene52931_All//gi|224005945|ref|XP_002291933.1|//1.00E-28//trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972452|gb|EED90784.1|trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]						nr +
Unigene52933_All	971	0.54	0.83	0.66	4.16	2.59	1.21	1.13	0.56	0.45	6.32E-01	4.02E-01		2.89E-01	7.25E-01		-6.83E-01	1.79E-02		-1.78E+00	3.70E-08	Down	-1.02E+00	8.43E-02		-1.33E+00	2.07E-02					Unigene52933_All//0.00E+00//gi|13353586|gb|BG443934.1|BG443934				
Unigene52934_All	453	1.39	0.00	0.71	0.99	1.67	2.39	0.84	0.74	0.70	-1.04E+01	7.91E-04	Down	-9.75E-01	3.16E-01		7.57E-01	3.95E-01		1.27E+00	6.54E-02		-1.87E-01	8.57E-01		-2.56E-01	7.85E-01		Unigene52934_All//gi|224084862|ref|XP_002307427.1|//2.00E-44//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222856876|gb|EEE94423.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene52934_All//3.00E-27//AT1G21910| AP2 domain-containing transcription factor family protein	Unigene52934_All//0.00E+00//DT466780	AP2-EREBP			nr -
Unigene52935_All	456	0.23	0.89	0.00	0.87	3.02	8.22	0.19	1.56	0.35	1.95E+00	1.44E-01		-7.84E+00	3.92E-01		1.79E+00	3.04E-03		3.23E+00	2.69E-14	Up	3.07E+00	1.67E-03		9.15E-01	6.24E-01		Unigene52935_All//gi|18402079|ref|NP_566623.1|//1.00E-59//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|9280317|dbj|BAB01696.1|oxylase-like protein [Arabidopsis thaliana]	Unigene52935_All//4.00E-52//AT3G19000| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene52935_All//0.00E+00//TC142693		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis		nr -
Unigene52938_All	673	0.16	0.08	1.11	0.00	0.10	0.13	10.24	31.36	160.89	-1.05E+00	6.84E-01		2.83E+00	8.52E-03		6.68E+00	6.08E-01		7.07E+00	4.75E-01		1.61E+00	1.18E-39	Up	3.97E+00	0.00E+00	Up	Unigene52938_All//gi|255551921|ref|XP_002517005.1|//1.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223543640|gb|EEF45168.1|conserved hypothetical protein [Ricinus communis]						nr -
Unigene52940_All	1054	0.00	1.92	0.40	0.28	0.46	0.51	1.16	2.93	3.21	1.09E+01	1.53E-11	Up	8.66E+00	1.38E-02		6.90E-01	5.66E-01		8.59E-01	4.23E-01		1.33E+00	4.50E-05	Up	1.47E+00	2.27E-06	Up	Unigene52940_All//gi|115474397|ref|NP_001060795.1|//1.00E-55//Os08g0107100 (Oryza sativa Japonica Group) >gi|113622764|dbj|BAF22709.1|Os08g0107100 (Oryza sativa Japonica Group)	Unigene52940_All//1.00E-18//AT1G31130| unknown protein	Unigene52940_All//1.00E-96//DW500649				nr -
Unigene52943_All	1055	3.77	0.91	1.41	0.71	1.73	1.54	0.08	0.12	0.26	-2.05E+00	5.31E-09	Down	-1.42E+00	2.20E-05	Down	1.29E+00	8.01E-03		1.12E+00	3.47E-02		5.68E-01	7.81E-01		1.72E+00	2.30E-01		Unigene52943_All//gi|15230734|ref|NP_187304.1|//3.00E-50//agenet domain-containing protein [Arabidopsis thaliana]	Unigene52943_All//1.00E-51//AT3G06520| agenet domain-containing protein	Unigene52943_All//0.00E+00//gi|164354001|gb|ES831662.1|ES831662				nr +
Unigene52945_All	741	0.00	0.00	0.00	4.97	4.32	2.26	0.00	0.11	0.00	null	null		null	null		-2.03E-01	5.70E-01		-1.14E+00	3.45E-04	Down	6.82E+00	4.00E-01		null	null					Unigene52945_All//5.00E-27//TC141466				
Unigene52946_All	573	2.01	0.00	0.37	0.52	1.08	1.50	1.62	0.58	0.83	-1.10E+01	9.91E-07	Down	-2.43E+00	1.85E-03		1.05E+00	2.99E-01		1.52E+00	6.17E-02		-1.48E+00	2.77E-02		-9.60E-01	1.20E-01		Unigene52946_All//gi|109676346|gb|ABG37655.1|//7.00E-07//integrase [Populus trichocarpa]		Unigene52946_All//6.00E-69//ES794043				nr +
Unigene52947_All	418	2.00	0.00	3.18	2.74	2.31	2.49	0.20	0.50	0.19	-1.10E+01	5.57E-05	Down	6.69E-01	2.69E-01		-2.49E-01	7.04E-01		-1.41E-01	8.21E-01		1.31E+00	4.47E-01		-8.59E-02	9.71E-01		Unigene52947_All//gi|297813827|ref|XP_002874797.1|//2.00E-24//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297320634|gb|EFH51056.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene52947_All//5.00E-16//AT4G04370| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene52950_All	498	5.25	4.99	4.28	11.80	9.96	5.17	7.90	3.94	1.92	-7.54E-02	8.43E-01		-2.97E-01	4.77E-01		-2.45E-01	3.54E-01		-1.19E+00	1.16E-06	Down	-1.00E+00	2.96E-04	Down	-2.04E+00	3.89E-11	Down	Unigene52950_All//gi|2920666|gb|AAC18566.1|//1.00E-67//2,4-D inducible glutathione S-transferase [Glycine max]	Unigene52950_All//3.00E-62//AT1G78380| ATGSTU19 (GLUTATHIONE S-TRANSFERASE TAU 19); glutathione binding / glutathione transferase	Unigene52950_All//0.00E+00//gi|31407476|gb|CD486511.1|CD486511		ko00480|Glutathione metabolism		nr +
Unigene52951_All	402	0.26	11.72	2.52	3.35	2.40	2.70	1.79	1.98	1.59	5.49E+00	7.62E-24	Up	3.27E+00	5.92E-04	Up	-4.80E-01	4.15E-01		-3.11E-01	6.37E-01		1.44E-01	8.36E-01		-1.73E-01	7.94E-01					Unigene52951_All//0.00E+00//gi|8379649|gb|BE052593.1|BE052593				
Unigene52955_All	317	6.93	9.59	13.61	13.67	20.53	18.38	386.39	288.88	148.42	4.68E-01	2.00E-01		9.73E-01	1.47E-03		5.87E-01	8.89E-03		4.27E-01	9.62E-02		-4.20E-01	6.82E-24		-1.38E+00	3.40E-185	Down				Unigene52955_All//2.00E-107//gi|109867616|gb|DW496592.1|DW496592				
Unigene52956_All	897	0.00	21.97	8.61	0.00	0.00	0.00	0.00	0.00	0.00	1.44E+01	2.16E-113	Up	1.31E+01	3.43E-43	Up	null	null		null	null		null	null		null	null		Unigene52956_All//sp|P54361|OAZ_DROME//2.00E-76//Ornithine decarboxylase antizyme OS=Drosophila melanogaster GN=Oda PE=1 SV=2						swissprot +
Unigene52958_All	668	26.79	16.99	12.04	39.75	27.63	42.93	49.43	25.03	22.30	-6.57E-01	5.32E-07		-1.15E+00	3.55E-16	Down	-5.25E-01	5.20E-08		1.11E-01	3.67E-01		-9.82E-01	7.67E-29		-1.15E+00	4.44E-38	Down	Unigene52958_All//gi|192913018|gb|ACF06617.1|//2.00E-49//40S ribosomal protein S8 [Elaeis guineensis]	Unigene52958_All//3.00E-38//AT5G59240| 40S ribosomal protein S8 (RPS8B)	Unigene52958_All//0.00E+00//gi|164248980|gb|ES797915.1|ES797915		ko03010|Ribosome		nr +
Unigene5296_All	1888	2.13	11.78	2.59	3.96	5.85	6.75	5.53	10.60	20.83	2.47E+00	8.44E-59	Up	2.82E-01	3.55E-01		5.65E-01	5.08E-04		7.69E-01	7.11E-07		9.39E-01	1.45E-16		1.91E+00	2.13E-94	Up	Unigene5296_All//gi|3643085|gb|AAC36698.1|//1.00E-141//protein phosphatase-2C [Mesembryanthemum crystallinum]	Unigene5296_All//3.00E-121//AT3G62260| protein phosphatase 2C, putative / PP2C, putative	Unigene5296_All//0.00E+00//gi|78346536|gb|DT566810.1|DT566810	DBP			nr -
Unigene52961_All	626	0.67	3.08	0.77	1.91	1.43	0.94	3.78	3.00	1.59	2.20E+00	4.47E-05	Up	1.95E-01	8.39E-01		-4.17E-01	5.22E-01		-1.03E+00	1.06E-01		-3.32E-01	4.00E-01		-1.25E+00	6.37E-04	Down				Unigene52961_All//8.00E-13//TC130256				
Unigene52963_All	601	0.52	0.67	0.18	0.41	1.49	0.38	2.25	0.63	2.25	3.69E-01	7.24E-01		-1.56E+00	3.30E-01		1.85E+00	2.15E-02		-1.41E-01	9.29E-01		-1.85E+00	9.22E-04	Down	1.70E-03	1.00E+00		Unigene52963_All//gi|224117086|ref|XP_002331783.1|//2.00E-13//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222832242|gb|EEE70719.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene52963_All//1.00E-06//AT4G26090| RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding	Unigene52963_All//3.00E-157//gi|48778816|gb|CO088182.1|CO088182		ko04626|Plant-pathogen interaction		nr +
Unigene52965_All	471	201.73	212.58	335.78	396.19	356.93	454.22	396.32	129.03	146.92	7.55E-02	2.01E-01		7.35E-01	1.26E-65		-1.51E-01	1.98E-05		1.97E-01	4.50E-09		-1.62E+00	0.00E+00	Down	-1.43E+00	6.36E-298	Down	Unigene52965_All//gi|211905341|gb|ACJ11250.1|//5.00E-85//S-adenosyl-L-homocystein hydrolase [Gossypium hirsutum]	Unigene52965_All//5.00E-73//AT4G13940| MES88 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding	Unigene52965_All//0.00E+00//ES809036		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -
Unigene52969_All	671	0.00	0.00	0.08	2.30	0.92	0.00	4.22	9.16	16.56	null	null		6.31E+00	6.35E-01		-1.32E+00	9.76E-03		-1.12E+01	1.19E-09	Down	1.12E+00	3.12E-07	Up	1.97E+00	2.35E-28	Up	Unigene52969_All//gi|224095706|ref|XP_002310444.1|//4.00E-42//glutathione peroxidase [Populus trichocarpa] >gi|222853347|gb|EEE90894.1|glutathione peroxidase [Populus trichocarpa]	Unigene52969_All//1.00E-34//AT4G31870| ATGPX7 (glutathione peroxidase 7); glutathione peroxidase	Unigene52969_All//1.00E-88//TC153836		ko00480|Glutathione metabolism//ko00590|Arachidonic acid metabolism		nr +
Unigene52971_All	245	0.21	2.48	0.87	2.03	0.00	0.37	2.93	2.39	2.60	3.54E+00	7.24E-03		2.03E+00	3.61E-01		-1.10E+01	8.98E-04	Down	-2.46E+00	4.82E-02		-2.97E-01	6.85E-01		-1.73E-01	7.94E-01					Unigene52971_All//2.00E-17//ES808539				
Unigene52972_All	676	0.62	9.67	3.47	0.00	0.20	1.20	0.00	0.00	0.00	3.96E+00	1.90E-27	Up	2.48E+00	1.56E-06	Up	7.67E+00	3.18E-01		1.02E+01	6.95E-05	Up	null	null		null	null		Unigene52972_All//gi|30692434|ref|NP_195677.2|//1.00E-68//glycolipid binding / glycolipid transporter [Arabidopsis thaliana] >gi|20022510|gb|AAM83214.1|AT4g39670/T19P19_60 [Arabidopsis thaliana] >gi|23308251|gb|AAN18095.1|At4g39670/T19P19_60 [Arabidopsis thaliana]	Unigene52972_All//6.00E-70//AT4G39670| glycolipid binding / glycolipid transporter	Unigene52972_All//0.00E+00//TC133871				nr -
Unigene52973_All	1304	0.00	0.04	0.04	0.00	0.08	0.00	1.33	1.15	2.69	5.28E+00	6.15E-01		5.35E+00	6.35E-01		6.31E+00	4.55E-01		null	null		-2.04E-01	6.48E-01		1.02E+00	4.35E-04	Up	Unigene52973_All//gi|34761728|gb|AAQ82037.1|//1.00E-124//gag/pol polyprotein [Pisum sativum]	Unigene52973_All//3.00E-13//AT3G01410| RNase H domain-containing protein	Unigene52973_All//2.00E-135//FL577502				nr -
Unigene52975_All	277	85.00	39.15	49.21	148.18	125.31	262.01	91.58	71.52	82.55	-1.12E+00	6.01E-21	Down	-7.88E-01	1.76E-11		-2.42E-01	2.70E-03		8.22E-01	1.14E-40		-3.57E-01	2.33E-04		-1.50E-01	1.44E-01		Unigene52975_All//gi|297827841|ref|XP_002881803.1|//1.00E-26//40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata] >gi|297327642|gb|EFH58062.1| 40S ribosomal protein S2 [Arabidopsis lyrata subsp. lyrata]	Unigene52975_All//5.00E-15//AT3G57490| 40S ribosomal protein S2 (RPS2D)	Unigene52975_All//3.00E-137//TC148145		ko03010|Ribosome		nr -
Unigene52976_All	1422	0.00	0.00	0.00	0.00	0.00	0.00	3.18	4.23	0.06	null	null		null	null		null	null		null	null		4.12E-01	6.27E-02		-5.83E+00	4.36E-30	Down	Unigene52976_All//gi|5733382|gb|AAD49555.1|AF095840_1/0.00E+00//b-tubulin [Entosiphon sulcatum]	Unigene52976_All//0.00E+00//AT5G62700| TUB3; GTP binding / GTPase/ structural molecule	Unigene52976_All//4.00E-44//gi|48790617|gb|CO091931.1|CO091931		ko04145|Phagosome		nr +
Unigene52977_All	1070	14.38	8.10	4.83	0.28	0.23	0.17	0.71	0.35	0.00	-8.28E-01	8.96E-09		-1.57E+00	3.95E-22	Down	-3.10E-01	8.20E-01		-7.27E-01	6.38E-01		-1.02E+00	1.69E-01		-9.47E+00	8.87E-06	Down	Unigene52977_All//gi|24461855|gb|AN62342.1|AF506028_9/1.00E-28//Jp18 [Citrus trifoliata]	Unigene52977_All//2.00E-31//AT2G12462| unknown protein	Unigene52977_All//0.00E+00//TC147305				nr -

Unigene52978_A11	466	0.00	0.00	0.57	0.32	0.00	0.19	111.42	81.80	35.31	null	null		9.16E+00	8.01E-02		-8.33E+00	1.65E-01		-7.27E-01	7.15E-01		-4.46E-01	8.96E-12		-1.66E+00	2.47E-103	Down	Unigene52978_A11|gi|108706319|gb|ABF94114.1|//8.00E-34//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene52978_A11//2.00E-36//AT4G14746| INVOLVED IN: biological_process unknown; LOCATED IN: anchored to membrane; CONTAINS InterPro DOMAIN/s: EGF (InterPro:IPR006210); Has 201 Blast hits to 179 proteins in 41 species: Archae - 0; Bacteria - 0; Metazoa - 168; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene52978_A11//0.00E+00//TC178815				nr +
Unigene5298_A11	843	1.92	3.19	2.27	2.30	2.86	1.77	1.35	0.25	1.23	7.28E-01	5.91E-02		2.41E-01	6.24E-01		3.11E-01	5.14E-01		-3.82E-01	4.51E-01		-2.45E+00	2.46E-04	Down	-1.40E-01	7.89E-01		Unigene5298_A11|gi|224103573|ref|XP_002313108.1|//2.00E-33//kip-related cyclin-dependent kinase inhibitor 7 [Populus trichocarpa] >gi|222849516|gb|EEE87063.1| kip-related cyclin-dependent kinase inhibitor 7 [Populus trichocarpa]	Unigene5298_A11//1.00E-17//AT1G49620| ICK5; cyclin binding / cyclin-dependent protein kinase inhibitor	Unigene5298_A11//0.00E+00//TC178764				nr -
Unigene52980_A11	519	81.25	47.06	58.79	159.90	153.93	129.40	155.84	96.07	62.33	-7.88E-01	6.95E-21		-4.67E-01	2.82E-08		-5.49E-02	4.44E-01		-3.05E-01	3.19E-08		-6.98E-01	4.41E-39		-1.32E+00	9.94E-115	Down	Unigene52980_A11|gi|189345252|gb|ACD92982.1|//2.00E-58//S-adenosylmethionine synthetase [Panax ginseng]	Unigene52980_A11//2.00E-57//AT4G01850| SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase	Unigene52980_A11//0.00E+00//TC132373		ko00270|Cysteine and methionine metabolism/ko00450|Selenoamino acid metabolism		nr +
Unigene52987_A11	1105	0.09	81.16	61.54	0.00	0.12	0.29	0.04	0.00	0.11	9.74E+00	0.00E+00	Up	9.34E+00	0.00E+00	Up	6.96E+00	3.18E-01		8.16E+00	4.07E-02		-5.26E+00	6.56E-01		1.50E+00	5.58E-01		Unigene52987_A11|gi|11466579|ref|NP_066169.1|//4.00E-29//NADH dehydrogenase subunit 5 [Rhodomonas salina] >gi|10441166|gb|AAG17740.1|AF28909_16 NADH dehydrogenase subunit 5 [Rhodomonas salina]	Unigene52987_A11//4.00E-23//ATMG00665| Mitochondrial NADH dehydrogenase subunit 5. The gene is trans-spliced from three different pre-cursors, NAD5a, NAD5b and NAD5c.		ko00190|Oxidative phosphorylation		nr -
Unigene52989_A11	492	1.49	0.00	0.76	4.66	0.63	1.38	0.77	0.51	0.24	-1.05E+01	2.11E-04	Down	-9.75E-01	2.64E-01		-2.89E+00	1.71E-09	Down	-1.76E+00	7.84E-05	Down	-6.02E-01	6.12E-01		-1.67E+00	1.40E-01		Unigene52989_A11|gi|115468066|ref|NP_001057632.1|//1.00E-42//Os06g0174500 [Oryza sativa Japonica Group] >gi|113595672|dbj|BAF19546.1| Os06g0174500 [Oryza sativa Japonica Group]	Unigene52989_A11//3.00E-43//AT1G10750| unknown protein	Unigene52989_A11//7.00E-28//CO103961				nr -
Unigene52992_A11	359	3.35	0.85	0.45	1.39	1.92	1.51	0.82	0.12	0.44	-1.98E+00	3.71E-03		-2.91E+00	3.56E-04	Down	4.67E-01	6.12E-01		1.22E-01	9.21E-01		-2.82E+00	8.84E-02		-8.93E-01	4.71E-01						Unigene52992_A11//4.00E-07//TC148859				
Unigene52994_A11	976	0.00	9.92	2.84	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	1.95E-55	Up	1.15E+01	2.74E-15	Up	null	null		null	null		null	null		null	null		Unigene52994_A11|gi|15235200|ref|NP_193716.1|//1.00E-16//glycosyl hydrolase family 18 protein [Arabidopsis thaliana] >gi|119360133|gb|ABL66795.1| At4g19810 [Arabidopsis thaliana]	Unigene52994_A11//2.00E-18//AT4G19810| glycosyl hydrolase family 18 protein					nr +
Unigene52998_A11	419	0.00	0.00	0.00	0.24	0.00	0.00	10.70	7.98	3.99	null	null		null	null		-7.89E+00	3.12E-01		-7.89E+00	3.99E-01		-4.23E-01	1.09E-01		-1.42E+00	6.49E-08	Down									
Unigene52999_A11	908	0.00	0.00	0.23	0.11	0.27	0.40	2.05	0.55	2.06	null	null		7.87E+00	1.41E-01		1.28E+00	5.31E-01		1.86E+00	2.19E-01		-1.89E+00	5.01E-05	Down	9.30E-03	9.81E-01		Unigene52999_A11|gi|21779966|gb|AAM77595.1|AF507018_1/1.00E-129//auxin transport protein [Arabidopsis thaliana]	Unigene52999_A11//2.00E-130//AT3G02260| BIG (BIG); binding / ubiquitin-protein ligase/ zinc ion binding	Unigene52999_A11//8.00E-97//TC141392				nr +
Unigene530_A11	2857	0.90	1.26	1.04	1.26	1.53	1.53	2.28	2.72	4.64	4.89E-01	1.37E-01		2.18E-01	5.91E-01		2.86E-01	3.79E-01		2.89E-01	3.82E-01		2.56E-01	2.08E-01		1.03E+00	2.95E-13	Up	Unigene530_A11|gi|186507757|ref|NP_001118516.1|//0.00E+00//RAB GTPase activator [Arabidopsis thaliana]	Unigene530_A11//0.00E+00//AT2G43490| RAB GTPase activator	Unigene530_A11//0.00E+00//gi|73865683|gb|DT468421.1|DT468421				nr -
Unigene5300_A11	985	17.48	63.63	17.46	13.45	13.81	11.78	5.28	61.40	1.70	1.86E+00	6.91E-116	Up	-1.20E-03	9.93E-01		3.78E-02	8.35E-01		-1.91E-01	2.78E-01		3.54E+00	5.95E-282	Up	-1.64E+00	6.38E-11	Down	Unigene5300_A11|gi|134103862|gb|AB066880.1|//5.00E-72//chloroplast small heat shock protein [Epilobium amurense]	Unigene5300_A11//2.00E-26//AT4G27670| HSP21 (HEAT SHOCK PROTEIN 21)	Unigene5300_A11//0.00E+00//TC153360				nr -
Unigene53002_A11	461	0.91	3.41	1.39	2.38	0.00	0.10	1.93	3.35	2.51	1.91E+00	1.06E-03		6.10E-01	5.09E-01		-1.12E+01	4.06E-08	Down	-4.60E+00	8.28E-06	Down	8.01E-01	9.44E-02		3.80E-01	5.04E-01		Unigene53002_A11|gi|255559989|ref|XP_002321013.1|//9.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223539850|gb|EEF41430.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene53003_A11	424	0.00	0.48	0.00	2.82	1.71	0.53	0.20	0.59	0.94	8.90E+00	1.36E-01		null	null		-7.25E-01	2.33E-01		-2.40E+00	7.07E-04	Down	1.57E+00	3.26E-01		2.24E+00	6.42E-02		Unigene53003_A11|gi|224089579|ref|XP_002308765.1|//1.00E-08//predicted protein [Populus trichocarpa] >gi|222854741|gb|EEE92288.1| predicted protein [Populus trichocarpa]		Unigene53003_A11//2.00E-31//TC158843				nr -
Unigene53004_A11	592	0.44	0.09	0.09	0.17	1.16	0.69	0.86	0.00	0.81	-2.37E+00	2.14E-01		-2.30E+00	2.43E-01		2.79E+00	9.45E-03		2.03E+00	1.49E-01		-9.74E+00	8.89E-04	Down	-8.58E-02	9.30E-01		Unigene53004_A11|gi|20197242|gb|AC28772.2|//4.00E-65//expressed protein [Arabidopsis thaliana]	Unigene53004_A11//6.00E-67//AT2G38320| unknown protein					nr -
Unigene5301_A11	1064	7.18	5.57	8.51	9.08	7.67	12.18	8.15	16.42	5.62	-3.66E-01	9.00E-02		2.45E-01	2.44E-01		-2.44E-01	2.18E-01		4.24E-01	7.08E-03		1.01E+00	2.32E-16	Up	-5.37E-01	1.57E-03		Unigene5301_A11|gi|116325920|gb|AB198561.1|//9.00E-34//At1g23850 [Arabidopsis thaliana]	Unigene5301_A11//2.00E-26//AT1G23850| unknown protein					nr +
Unigene53010_A11	2059	0.00	0.86	0.00	0.10	0.00	0.13	2.26	3.88	7.41	9.75E+00	4.14E-10	Up	null	null		-6.60E+00	8.41E-02		4.43E-01	7.63E-01		7.79E-01	2.16E-05		1.71E+00	4.67E-32	Up	Unigene53010_A11|gi|297796919|ref|XP_002866344.1|//1.00E-166//ATEXO70H7 [Arabidopsis lyrata subsp. lyrata] >gi|297312179|gb|EFH42603.1| ATEXO70H7 [Arabidopsis lyrata subsp. lyrata]	Unigene53010_A11//5.00E-148//AT5G59730| ATEXO70H7 (EXOCYST SUBUNIT EXO70 FAMILY PROTEIN H7); protein binding	Unigene53010_A11//0.00E+00//gi|78337474|gb|DT557748.1|DT557748				nr -
Unigene53011_A11	999	0.00	0.10	0.00	0.00	0.14	0.00	29.75	12.43	24.17	6.66E+00	3.86E-01		null	null		7.11E+00	3.18E-01		null	null		-1.26E+00	1.59E-38	Down	-3.00E-01	5.76E-04		Unigene53011_A11|gi|297835480|ref|XP_002885622.1|//1.00E-96//disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331462|gb|EFH61881.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene53011_A11//7.00E-87//AT3G24020| disease resistance-responsive family protein					nr +
Unigene53012_A11	341	152.51	55.28	123.21	2.63	5.15	1.72	0.00	0.00	0.00	-1.46E+00	1.04E-68	Down	-3.08E-01	5.16E-05		9.70E-01	5.07E-02		-6.11E-01	4.26E-01		null	null		null	null										
Unigene53013_A11	302	0.00	0.00	0.00	6.43	1.14	1.65	0.00	0.14	0.00	null	null		null	null		-2.50E+00	5.60E-07	Down	-1.97E+00	9.06E-05	Down	7.11E+00	6.33E-01		null	null		Unigene53013_A11|gi|15241759|ref|NP_201028.1|//1.00E-39//exostosin family protein [Arabidopsis thaliana]	Unigene53013_A11//3.00E-35//AT5G62220| exostosin family protein	Unigene53013_A11//6.00E-18//TC139149				nr +
Unigene53014_A11	430	0.49	3.06	1.36	0.93	0.88	0.32	6.29	7.10	5.84	2.65E+00	2.16E-04	Up	1.48E+00	1.53E-01		-7.33E-02	9.25E-01		-1.56E+00	2.31E-01		1.73E-01	6.57E-01		-1.09E-01	7.44E-01										
Unigene53015_A11	693	0.00	0.00	0.31	0.00	0.00	0.13	37.28	14.96	4.02	null	null		8.26E+00	1.41E-01		null	null		7.03E+00	4.75E-01		-1.32E+00	5.93E-36	Down	-3.21E+00	1.51E-114	Down	Unigene53015_A11|gi|37359170|gb|AAL05954.1|//2.00E-21//agglutinin [Amaranthus caudatus]		Unigene53015_A11//3.00E-68//TC159407				nr -
Unigene53018_A11	1213	0.47	0.00	0.09	1.07	0.20	0.37	15.06	2.03	5.19	-8.89E+00	1.52E-03		-2.43E+00	4.40E-02		-2.43E+00	1.10E-04	Down	-1.52E+00	1.32E-02		-2.89E+00	8.37E-71	Down	-1.54E+00	3.86E-33	Down	Unigene53018_A11|gi|15233437|ref|NP_195325.1|//1.00E-102//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|79326326|ref|NP_001031792.1| pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|3036805|emb|CAA18495.1| thaumatin-like protein [Arabidopsis thaliana] >gi|7270553|emb|CAB81510.1| thaumatin-like protein [Arabidopsis thaliana]	Unigene53018_A11//2.00E-101//AT4G36010| pathogenesis-related thaumatin family protein	Unigene53018_A11//0.00E+00//C0131262				nr -
Unigene53020_A11	782	0.13	0.39	0.75	1.08	0.26	0.00	1.35	0.64	1.27	1.54E+00	3.23E-01		2.48E+00	3.75E-02		-2.04E+00	9.04E-03		-1.01E+01	2.43E-05	Down	-1.08E+00	7.50E-02		-8.59E-02	8.85E-01						Unigene53020_A11//3.00E-56//CO083773				
Unigene53021_A11	229	0.46	0.00	0.00	2.61	0.45	0.00	0.74	0.00	0.35	-8.84E+00	3.70E-01		-8.84E+00	3.91E-01		-2.53E+00	1.36E-02		-1.14E+01	7.70E-04	Down	-9.53E+00	1.34E-01		-1.09E+00	5.52E-01						Unigene53021_A11//3.00E-78//BQ405840				
Unigene53022_A11	697	0.00	0.00	0.15	0.00	0.00	0.32	138.18	11.45	22.12	null	null		7.26E+00	3.97E-01		null	null		8.34E+00	1.19E-01		-3.59E+00	0.00E+00	Down	-2.64E+00	0.00E+00	Down	Unigene53022_A11|gi|224139376|ref|XP_002323082.1|//3.00E-62//cytochrome P450 [Populus trichocarpa] >gi|222867712|gb|EEF04843.1| cytochrome P450 [Populus trichocarpa]	Unigene53022_A11//2.00E-36//AT2G30770| CYP71A13 (cytochrome P450, family 71, subfamily A, polypeptide 13); indoleacetaldoxime dehydratase/ oxygen binding	Unigene53022_A11//7.00E-103//C0115886		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis/ko00903|Limonene and pinene degradation		nr +
Unigene53026_A11	1010	0.00	0.00	0.00	0.30	0.00	0.31	2.05	5.30	6.31	null	null		null	null		-8.21E+00	2.01E-02		8.11E-02	9.50E-01		1.37E+00	1.71E-08	Up	1.62E+00	6.83E-13	Up	Unigene53026_A11|gi|15242148|ref|NP_200558.1|//1.00E-140//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene53026_A11//2.00E-135//AT5G57500| transferase, transferring glycosyl groups					nr -
Unigene53027_A11	553	0.57	0.00	0.39	0.90	0.50	0.65	3.75	3.17	8.93	-9.15E+00	3.65E-02		-5.60E-01	6.63E-01		-8.55E-01	4.07E-01		-4.63E-01	6.59E-01		-2.39E-01	6.04E-01		1.25E+00	3.28E-07	Up	Unigene53027_A11|gi|2346972|dbj|BAA21920.1|//2.00E-40//ZPT2-11 [Petunia x hybrida]	Unigene53027_A11//4.00E-28//AT5G03510| zinc finger (C2H2 type) family protein	Unigene53027_A11//2.00E-13//EX169499	C2H2			nr -
Unigene53035_A11	450	24.65	21.84	23.55	0.44	2.83	1.20	0.00	0.00	0.09	-1.74E-01	3.61E-01		-6.59E-02	7.23E-01		2.68E+00	1.57E-04	Up	1.44E+00	1.92E-01		null	null		6.47E+00	6.44E-01						Unigene53035_A11//2.00E-167//ES830281				
Unigene53036_A11	352	0.00	0.00	0.00	0.00	0.00	0.00	158.55	51.29	94.96	null	null		null	null		null	null		null	null		-1.63E+00	4.50E-105	Down	-7.40E-01	6.50E-31		Unigene53036_A11|gi|255558488|ref|XP_002520269.1|//6.00E-08//Desacetoxyvindoline 4-hydroxylase, putative [Ricinus communis] >gi|223540488|gb|EEF42055.1| Desacetoxyvindoline 4-hydroxylase, putative [Ricinus communis]		Unigene53036_A11//1.00E-34//TC148687				nr +
Unigene53039_A11	464	0.00	0.00	0.00	0.00	0.00	0.00	54.03	47.83	15.03	null	null		null	null		null	null		null	null		-1.76E-01	9.56E-02		-1.85E+00	2.16E-58	Down	Unigene53039_A11|gi|89001065|gb|AB059122.1|//7.00E-07//At1g51355 [Arabidopsis thaliana]						nr +
Unigene5304_A11	680	13.46	27.79	24.12	64.32	107.56	120.15	7.90	18.44	94.50	1.05E+00	3.18E-15	Up	8.41E-01	4.27E-09		7.42E-01	5.87E-38		9.02E-01	2.35E-53		1.22E+00	5.63E-16	Up	3.58E+00	0.00E+00	Up					Unigene5304_A11//0.00E+00//TC154996				
Unigene53040_A11	475	0.00	0.00	0.00	0.42	0.00	0.00	37.74	11.09	18.20	null	null		null	null		-8.71E+00	8.41E-02		-8.71E+00	1.33E-01		-1.77E+00	2.22E-38	Down	-1.05E+00	2.03E-18	Down		Unigene53040_A11//9.00E-06//AT4G38700| disease resistance-responsive family protein	Unigene53040_A11//1.00E-23//EX172002				
Unigene53041_A11	805	1.36	10.76	7.67	0.37	0.09	0.73	0.05	0.00	0.00	2.98E+00	2.17E-28	Up	2.49E+00	2.13E-16	Up	-2.12E+00	1.65E-01		9.74E-01	3.46E-01		-5.71E+00	6.56E-01		-5.71E+00	6.12E-01		Unigene53041_A11|gi|224054274|ref|XP_002298178.1|//3.00E-88//light-harvesting complex II protein Lhcb6 [Populus trichocarpa] >gi|222845436|gb|EEE82983.1| light-harvesting complex II protein Lhcb6 [Populus trichocarpa]	Unigene53041_A11//6.00E-80//AT1G15820| LHCB6 (LIGHT HARVESTING COMPLEX PSII SUBUNIT 6); chlorophyll binding	Unigene53041_A11//0.00E+00//TC141239		ko00196|Photosynthesis - antenna proteins		nr +
Unigene53042_A11	503	2.50	1.11	0.42	0.69	1.10	1.80	0.92	0.58	0.24	-1.17E+00	5.48E-02		-2.56E+00	6.98E-04	Down	6.60E-01	5.44E-01		1.37E+00	7.76E-02		-6.69E-01	5.08E-01		-1.96E+00	5.82E-02		Unigene53042_A11|gi|297844988|ref|XP_002890375.1|//1.00E-46//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297336217|gb|EFH66634.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene53042_A11//2.00E-41//AT1G20230| pentatricopeptide (PPR) repeat-containing protein					nr +

Unigene53049_All	456	5.28	1.22	4.20	0.66	0.45	0.20	0.19	0.00	0.00	-2.11E+00	6.17E-06	Down	-3.28E-01	4.46E-01		-5.33E-01	6.78E-01		-1.73E+00	2.89E-01		-7.53E+00	4.02E-01		-7.53E+00	3.58E-01		Unigene53049_All//gi|224124584|ref|XP_002319368.1|//5.00E-44//GH3 family protein [Populus trichocarpa] >gi|222857744|gb|EEE95291.1| GH3 family protein [Populus trichocarpa]	Unigene53049_All//8.00E-30//AT4G03400| DFL2 (DWARF IN LIGHT 2)	Unigene53049_All//6.00E-161//gi|48752004|gb|CO082523.1|CO082523				nr +
Unigene53050_All	373	37.73	27.44	28.41	116.06	106.44	123.14	280.55	566.54	223.01	-4.60E-01	2.18E-03		-4.09E-01	9.23E-03		-1.25E-01	1.63E-01		8.55E-02	3.82E-01		1.01E+00	6.10E-190	Up	-3.31E-01	6.82E-14		Unigene53050_All|gi|17821|emb|CAA78762.1|//1.00E-13//glycine-rich protein_(as1-291) [Brassica napus]		Unigene53050_All//5.00E-158//TC172399		ko03040|Spliceosome		nr -
Unigene53056_All	937	15263.00	10622.74	14082.49	5479.99	5996.15	4651.78	22.11	12.00	2.98	-5.23E-01	0.00E+00		-1.16E-01	6.28E-183		1.30E-01	1.31E-111		-2.36E-01	1.31E-290		-8.82E-01	1.69E-15		-2.89E+00	5.91E-83	Down	Unigene53056_All|gi|226358409|gb|AC051067.1|//1.00E-154//chloroplast chlorophyll A-B binding protein [Gossypium hirsutum]	Unigene53056_All//2.00E-136//AT2G34430| LHB1B1; chlorophyll binding	Unigene53056_All//0.00E+00//gi|164309504|gb|EX168309.1|EX168309		ko00196|Photosynthesis - antenna proteins		nr +
Unigene53057_All	369	0.00	0.00	0.00	78.16	8.31	39.53	2.29	0.00	0.22	null	null		null	null		-3.23E+00	5.73E-131	Down	-9.83E-01	2.47E-22		-1.12E+01	4.39E-06	Down	-3.41E+00	1.35E-04	Down	Unigene53057_All|gi|296082442|emb|CBI21447.3|//3.00E-09//unnamed protein product [Vitis vinifera]	Unigene53057_All//2.00E-05//AT5G66815| unknown protein	Unigene53057_All//3.00E-51//DR460393				nr -
Unigene53059_All	1027	0.10	0.15	0.10	0.82	0.17	0.62	12.39	4.68	2.41	5.38E-01	7.79E-01		2.53E-02	9.99E-01		-2.30E+00	4.14E-03		-4.22E-01	6.18E-01		-1.40E+00	6.73E-20	Down	-2.37E+00	5.06E-41	Down	Unigene53059_All//gi|115488656|ref|NP_001066815.1|//1.00E-10//0s12g0498900 [Oryza sativa Japonica Group] >gi|77555810|gb|ABA98606.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113649322|dbj|BAF29834.1| Os12g0498900 [Oryza sativa Japonica Group]	Unigene53059_All//2.00E-13//AT2G04480| unknown protein	Unigene53059_All//0.00E+00//DW506053				nr -
Unigene53060_All	591	0.00	6.43	4.32	0.00	0.00	0.08	0.00	0.00	0.00	1.27E+01	1.23E-21	Up	1.21E+01	4.20E-14	Up	null	null		6.26E+00	6.95E-01		null	null		null	null		Unigene53060_All//gi|115434786|ref|NP_001042151.1|//6.00E-33//Os01g0172200 [Oryza sativa Japonica Group] >gi|113531682|dbj|BAF04065.1| Os01g0172200 [Oryza sativa Japonica Group]	Unigene53060_All//6.00E-30//AT1G55150| DEAD box RNA helicase, putative (RH20)			ko03040|Spliceosome		nr -
Unigene53061_All	1660	0.00	0.00	0.00	0.00	0.00	0.00	5.35	11.46	0.26	null	null		null	null		null	null		null	null		1.10E+00	3.41E-20	Up	-4.34E+00	1.59E-50	Down	Unigene53061_All|gi|298708845|emb|CBJ30803.1|//3.00E-45//endo alpha-1,4 polygalactosaminidase precusor [Ectocarpus siliculosus]						nr +
Unigene53062_All	1071	0.00	0.28	0.00	0.00	0.00	0.00	275.35	38.95	23.99	8.15E+00	4.42E-02		null	null		null	null		null	null		-2.82E+00	0.00E+00	Down	-3.52E+00	0.00E+00	Down	Unigene53062_All|gi|223588270|dbj|BAH22562.1|//4.00E-79//nicotianamine synthase [Lotus japonicus]	Unigene53062_All//9.00E-75//AT1G09240| NAS3 (NICOTIANAMINE SYNTHASE 3); nicotianamine synthase					nr -
Unigene53065_All	845	0.00	0.00	0.00	0.71	0.37	0.96	54.09	33.73	120.22	null	null		null	null		-9.48E-01	3.09E-01		4.44E-01	6.21E-01		-6.81E-01	1.54E-21		1.15E+00	4.04E-115	Up	Unigene53065_All|gi|284468415|gb|ADB90272.1|//3.00E-43//casbene synthase [Triadica sebifera]	Unigene53065_All//1.00E-37//AT5G23960| TPS21 (TERPENE SYNTHASE 21); (-)-E-beta-caryophyllene synthase/ alpha-humulene synthase	Unigene53065_All//2.00E-125//C0115197		ko00904|Diterpenoid biosynthesis		nr +
Unigene53066_All	802	0.00	40.81	14.61	0.00	0.00	0.00	0.00	0.00	0.00	1.53E+01	8.60E-189	Up	1.38E+01	7.34E-66	Up	null	null		null	null		null	null		null	null		Unigene53066_All//gi|301122631|ref|XP_002909042.1|//1.00E-78//40S ribosomal protein S6 [Phytophthora infestans T30-4] >gi|262099804|gb|EEY57856.1| 40S ribosomal protein S6 [Phytophthora infestans T30-4]	Unigene53066_All//2.00E-58//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene53069_All	322	2.11	0.00	0.00	0.46	0.53	0.84	1.84	1.69	0.74	-1.10E+01	4.10E-04	Down	-1.10E+01	7.63E-04	Down	2.04E-01	9.50E-01		8.59E-01	6.31E-01		-1.24E-01	8.84E-01		-1.31E+00	1.15E-01										
Unigene5307_All	624	57.27	21.92	7.68	38.64	33.77	20.48	62.61	9.18	11.68	-1.39E+00	1.18E-43	Down	-2.90E+00	1.95E-109	Down	-1.94E-01	9.62E-02		-9.16E-01	1.04E-16		-2.77E+00	2.54E-144	Down	-2.42E+00	6.61E-128	Down	Unigene5307_All//gi|15232146|ref|NP_189572.1|//9.00E-70//histone H3 [Arabidopsis thaliana] >gi|15238433|ref|NP_201339.1| histone H3 [Arabidopsis thaliana] >gi|18396992|ref|NP_563838.1| histone H3 [Arabidopsis thaliana] >gi|18416261|ref|NP_568227.1| histone H3 [Arabidopsis thaliana] >gi|18416264|ref|NP_568228.1| histone H3 [Arabidopsis thaliana] >gi|115441249|ref|NP_001044904.1| Os01g0866200 [Oryza sativa Japonica Group] >gi|115458352|ref|NP_001052776.1| Os04g0119600 [Oryza sativa Japonica Group] >gi|115464121|ref|NP_001055660.1| Os05g0438700 [Oryza sativa Japonica Group] >gi|115466556|ref|NP_001056877.1| Os06g0160100 [Oryza sativa Japonica Group] >gi|115484259|ref|NP_001065791.1| Os11g0155900 [Oryza sativa Japonica Group] >gi|212721652|ref|NP_001131276.1| histone H3.2 [Zea mays] >gi|297724495|ref|NP_001174611.1| Os06g0159501 [Oryza sativa	Unigene5307_All//2.00E-60//AT5G65360| histone H3	Unigene5307_All//0.00E+00//TC156474				nr +
Unigene53075_All	482	0.11	0.00	0.66	0.10	1.36	2.53	0.96	3.04	0.41	-6.76E+00	6.10E-01		2.61E+00	1.46E-01		3.72E+00	3.55E-03		4.61E+00	3.60E-06	Up	1.65E+00	1.52E-03		-1.22E+00	2.00E-01				Unigene53075_All//3.00E-95//gi|48747157|gb|CO077676.1|CO077676				
Unigene53078_All	393	16.51	10.19	10.43	26.87	23.22	13.56	51.53	24.57	25.04	-6.97E-01	2.52E-03		-6.62E-01	5.99E-03		-2.11E-01	2.76E-01		-9.87E-01	1.32E-08		-1.07E+00	1.42E-20	Down	-1.04E+00	2.33E-20	Down	Unigene53078_All|gi|99014568|emb|CAK22271.1|//2.00E-29//40S ribosomal protein S11 [Chenopodium rubrum]	Unigene53078_All//5.00E-30//AT5G23740| RPS11-BETA (RIBOSOMAL PROTEIN S11-BETA); structural constituent of ribosome	Unigene53078_All//1.00E-173//TC173100		ko03010|Ribosome		nr -
Unigene5308_All	1517	2.97	1.54	1.44	5.19	3.18	1.61	9.73	2.29	3.39	-9.49E-01	9.32E-04		-1.04E+00	5.16E-04	Down	-7.07E-01	2.29E-04		-1.69E+00	2.52E-14	Down	-2.09E+00	1.72E-39	Down	-1.52E+00	1.47E-26	Down	Unigene5308_All|gi|4586801|dbj|BAA76478.1|//1.00E-109//Ntcyc03-1 [Nicotiana tabacum]	Unigene5308_All//6.00E-90//AT4G34160| CYCD3;1 (CYCLIN D3;1); cyclin-dependent protein kinase regulator/ protein binding	Unigene5308_All//0.00E+00//ES795560				nr +
Unigene53083_All	962	0.00	0.11	0.44	0.10	0.21	0.94	2.37	3.00	14.08	6.72E+00	3.86E-01		8.79E+00	1.38E-02		1.05E+00	6.12E-01		3.18E+00	9.74E-04	Up	3.37E-01	3.47E-01		2.57E+00	3.29E-47	Up	Unigene53083_All|gi|294847482|gb|ADF43752.1|//8.00E-89//MYB [Camellia sinensis]	Unigene53083_All//7.00E-61//AT1G25340| MYB116 (myb domain protein 116); DNA binding / transcription factor	Unigene53083_All//0.00E+00//CA993655	MYB			nr +
Unigene53084_All	308	0.00	0.00	0.00	0.00	0.00	0.00	8.10	4.61	1.03	null	null		null	null		null	null		null	null		-8.12E-01	2.34E-02		-2.97E+00	6.99E-11	Down									
Unigene53088_All	388	0.27	24.03	6.59	0.00	3.73	7.57	0.00	0.22	0.21	6.48E+00	8.80E-50	Up	4.61E+00	1.19E-11	Up	1.19E+01	5.93E-09	Up	1.29E+01	1.29E-17	Up	7.75E+00	4.00E-01		7.68E+00	4.03E-01				Unigene53088_All//4.00E-171//TC168226				
Unigene53089_All	575	0.00	0.00	0.46	1.30	1.68	0.39	1.40	0.00	1.11	null	null		8.85E+00	8.01E-02		3.68E-01	6.24E-01		-1.73E+00	5.00E-02		-1.04E+01	8.57E-06	Down	-3.34E-01	6.19E-01		Unigene53089_All//gi|297825127|ref|XP_002880146.1|//2.00E-53//CYCD2_1 [Arabidopsis lyrata subsp. lyrata] >gi|297326285|gb|EFH56705.1| CYCD2_1 [Arabidopsis lyrata subsp. lyrata]	Unigene53089_All//2.00E-48//AT2G22490| CYCD2;1 (Cyclin D2;1); cyclin-dependent protein kinase regulator/ protein binding	Unigene53089_All//0.00E+00//gi|73848581|gb|DT457601.1|DT457601				nr +
Unigene5309_All	1258	1.00	13.61	2.62	0.40	0.47	0.36	6.52	26.01	27.23	3.77E+00	1.20E-68	Up	1.39E+00	1.59E-04	Up	2.33E-01	8.26E-01		-1.42E-01	8.92E-01		2.00E+00	1.33E-81	Up	2.06E+00	7.51E-91	Up		Unigene5309_All//3.00E-65//AT1G06570| PDS3 (PHYTOENE DESATURATION 1); 4-hydroxyphenylpyruvate dioxygenase	Unigene5309_All//3.00E-35//DW501556				
Unigene53093_All	555	1.32	0.82	0.19	0.09	0.12	0.73	3.43	0.53	2.94	-6.84E-01	3.86E-01		-2.78E+00	1.04E-02		4.67E-01	9.57E-01		3.03E+00	6.03E-02		-2.70E+00	1.87E-07	Down	-2.20E-01	6.01E-01				Unigene53093_All//0.00E+00//gi|109888881|gb|DW517850.1|DW517850				
Unigene53096_All	987	0.11	0.31	0.22	0.61	0.52	0.23	0.30	2.08	1.70	1.54E+00	3.23E-01		1.03E+00	5.91E-01		-2.11E-01	8.23E-01		-1.40E+00	1.58E-01		2.79E+00	3.35E-08	Up	2.50E+00	2.63E-06	Up	Unigene53096_All//gi|38567922|emb|CAE75905.1|//6.00E-33//OSJNBa0088I22.18 [Oryza sativa (japonica cultivar-group)]	Unigene53096_All//4.00E-18//AT4G23160| protein kinase family protein					nr -
Unigene53097_All	1066	0.00	0.29	0.00	0.00	0.00	0.00	1.27	4.67	3.40	8.16E+00	4.42E-02		null	null		null	null		null	null		1.88E+00	4.54E-12	Up	1.42E+00	1.68E-06	Up	Unigene53097_All//gi|30024604|dbj|BAC75674.1|//2.00E-71//transcription factor MYB101 [Glycine max]	Unigene53097_All//1.00E-64//AT3G02940| MYB107 (myb domain protein 107); DNA binding / transcription factor	Unigene53097_All//5.00E-09//TC141121	MYB			nr -
Unigene53098_All	312	0.67	4.22	0.00	1.12	2.21	1.16	0.27	0.27	0.13	2.65E+00	2.16E-04	Up	-9.39E+00	1.45E-01		9.82E-01	2.98E-01		5.12E-02	9.69E-01		-1.66E-02	1.01E+00		-1.09E+00	6.76E-01		Unigene53098_All//gi|2578033|emb|CAA65744.1|//6.00E-36//omega-6 desaturase [Gossypium hirsutum]	Unigene53098_All//2.00E-21//AT3G12120| FAD2 (FATTY ACID DESATURASE 2); delta12-fatty acid dehydrogenase/ omega-6 fatty acid desaturase	Unigene53098_All//2.00E-141//TC178159		ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene531_All	1044	2.46	9.32	5.05	8.73	9.76	17.95	21.95	47.84	90.06	1.92E+00	2.69E-19	Up	1.04E+00	1.47E-04	Up	1.61E-01	4.49E-01		1.04E+00	6.98E-16	Up	1.12E+00	1.27E-53	Up	2.04E+00	3.89E-244	Up	Unigene531_All//gi|15231963|ref|NP_187488.1|//5.00E-89//AT5G1K; ATP binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|194294570|gb|ACF40324.1| At3g08760 [Arabidopsis thaliana] >gi|222424853|dbj|BAH20378.1| AT3G08760 [Arabidopsis thaliana]	Unigene531_All//5.00E-68//AT3G08760| ATS1K; ATP binding / kinase/ protein kinase/ protein tyrosine kinase	Unigene531_All//0.00E+00//TC163373		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene5310_All	1304	0.60	0.16	0.25	0.42	0.77	0.14	6.23	0.64	3.12	-1.95E+00	2.62E-02		-1.30E+00	1.38E-01		8.66E-01	2.34E-01		-1.60E+00	1.32E-01		-3.28E+00	6.30E-36	Down	-9.98E-01	3.58E-08		Unigene5310_All|gi|15230441|ref|NP_190697.1|//1.00E-84//proline-rich family protein [Arabidopsis thaliana]	Unigene5310_All//2.00E-45//AT3G51290| proline-rich family protein	Unigene5310_All//0.00E+00//TC166071				nr -
Unigene53100_All	239	3.28	7.21	10.03	1.25	5.48	5.29	0.18	0.00	0.67	1.13E+00	2.51E-02		1.61E+00	3.96E-04	Up	2.13E+00	1.00E-03		2.08E+00	1.96E-03		-7.47E+00	6.56E-01		1.91E+00	3.77E-01										
Unigene53101_All	236	0.00	0.86	0.00	0.00	0.00	0.00	8.78	10.80	26.17	9.75E+00	1.36E-01		null	null		null	null		null	null		2.99E-01	4.30E-01		1.58E+00	4.79E-12	Up	Unigene53101_All|gi|62857020|dbj|BAD95895.1|//1.00E-09//Ser/Thr protein kinase [Lotus japonicus]	Unigene53101_All//2.00E-06//AT5G38260| serine/threonine protein kinase, putative					nr +
Unigene53102_All	539	0.00	0.00	0.00	0.00	0.00	0.00	103.31	68.78	40.87	null	null		null	null		null	null		null	null		-5.87E-01	3.47E-20		-1.34E+00	1.13E-80	Down	Unigene53102_All|gi|224084714|ref|XP_002307394.1|//2.00E-59//high affinity sulfate transporter SAT-1, Sulfate/bicarbonate/oxalate exchanger SLC26 family protein [Populus trichocarpa] >gi|222856843|gb|EEE94390.1| high affinity sulfate transporter SAT-1, Sulfate/bicarbonate/oxalate exchanger SLC26 family protein [Populus trichocarpa]	Unigene53102_All//4.00E-47//AT1G78000| SULTR1;2 (SULFATE TRANSPORTER 1;2); sulfate transmembrane transporter	Unigene53102_All//6.00E-07//DW489909				nr -
Unigene53106_All	589	0.00	0.09	0.00	0.00	0.06	0.15	6.82	14.69	9.60	6.43E+00	6.15E-01		null	null		5.87E+00	8.29E-01		7.26E+00	4.75E-01		1.11E+00	9.88E-10	Up	4.94E-01	2.33E-02		Unigene53106_All|gi|300078720|gb|ADJ67258.1|//5.00E-13//vacuolar H+-pyrophosphatase [Sorghum bicolor]	Unigene53106_All//3.00E-14//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene53106_All//5.00E-54//ES847568		ko00190|Oxidative phosphorylation		nr -
Unigene5311_All	1523	1.03	0.27	0.21	1.60	1.20	0.59	9.19	1.81	5.34	-1.95E+00	7.99E-04	Down	-2.30E+00	3.17E-04	Down	-4.20E-01	3.11E-01		-1.43E+00	5.53E-04	Down	-2.34E+00	3.83E-43	Down	-7.84E-01	3.10E-09		Unigene5311_All//gi|297816394|ref|XP_002876080.1|//1.00E-155//proline-rich family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321918|gb|EFH52339.1| proline-rich family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5311_All//4.00E-134//AT3G51290| proline-rich family protein	Unigene5311_All//0.00E+00//TC166071				nr -

Unigene53111_All	836	0.00	0.00	0.00	0.00	0.00	0.00	3.19	3.35	0.10	null	null		null	null		null	null		null	null		7.22E-02	8.42E-01		-5.06E+00	7.11E-17	Down	Unigene53111_All//gi|260516654|gb|ACX43954.1|//4.00E-71//cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516656|gb|ACX43955.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516658|gb|ACX43956.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516660|gb|ACX43957.1| cysteine protease 1 [Brachiaria hybrid cultivar] >gi|260516662|gb|ACX43958.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516664|gb|ACX43959.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516666|gb|ACX43960.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516668|gb|ACX43961.1| cysteine protease 2 [Brachiaria hybrid cultivar] >gi|260516670|gb|ACX43962.1| cysteine protease 2 [Brachiaria hybrid cultivar]	Unigene53111_All//2.00E-61//AT5G43060| cysteine proteinase, putative / thiol protease, putative					nr +
Unigene53114_All	425	1.48	0.24	0.00	2.58	3.48	3.72	4.87	1.08	1.03	-2.63E+00	1.78E-02		-1.05E+01	1.41E-03		4.34E-01	4.73E-01		5.28E-01	3.52E-01		-2.17E+00	1.96E-06	Down	-2.24E+00	6.30E-07	Down		Unigene53114_All//1.00E-07//TC157717					
Unigene53116_All	403	20.64	15.84	34.09	4.08	9.57	3.36	0.31	0.21	0.20	-3.82E-01	6.24E-02		7.24E-01	3.95E-06		1.23E+00	5.59E-05	Up	-2.79E-01	6.38E-01		-6.02E-01	7.66E-01		-6.71E-01	7.19E-01		Unigene53116_All//gi|158343304|gb|ABW35320.1|//1.00E-13//chloroplast photosystem II PsbR [Prosopis juliflora]	Unigene53116_All//2.00E-05//AT1G79040| PSBR (photosystem II subunit R)	Unigene53116_All//5.00E-41//gi|189092457|gb|FG547992.1|FG547992		ko00195|Photosynthesis		nr -
Unigene53120_All	833	2.14	5.23	4.22	25.30	34.77	15.99	37.15	34.52	20.37	1.29E+00	1.90E-05	Up	9.82E-01	4.36E-03		4.59E-01	9.33E-07		-6.61E-01	1.25E-08		-1.06E-01	2.99E-01		-8.67E-01	8.73E-23			Unigene53120_All//0.00E+00//TC171955					
Unigene53122_All	892	0.00	0.74	0.24	0.45	0.31	2.94	0.85	2.34	1.61	9.53E+00	6.25E-04	Up	7.90E+00	1.41E-01		-5.33E-01	6.15E-01		2.72E+00	1.34E-08	Up	1.46E+00	4.39E-04	Up	9.14E-01	5.82E-02		Unigene53122_All//gi|297836072|ref|XP_002885918.1|//1.00E-114//CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297331758|gb|EFH62177.1| CBS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene53122_All//3.00E-116//AT4G33700| CBS domain-containing protein	Unigene53122_All//0.00E+00//TC133787				nr -
Unigene53123_All	364	0.43	0.42	0.29	2.19	0.57	0.50	2.21	1.26	0.33	-4.62E-02	9.89E-01		-5.59E-01	7.75E-01		-1.95E+00	1.52E-02		-2.14E+00	1.54E-02		-8.05E-01	2.58E-01		-2.75E+00	9.42E-04	Down		Unigene53123_All//4.00E-07//DR458666					
Unigene53124_All	245	21.78	12.00	13.04	36.80	42.87	38.34	5.52	10.41	12.03	-8.61E-01	8.86E-04		-7.40E-01	6.01E-03		2.20E-01	2.62E-01		5.92E-02	7.87E-01		9.14E-01	9.97E-03		1.12E+00	4.75E-04	Up		Unigene53124_All//2.00E-23//ES795903					ESTscan -
Unigene5313_All	653	52.32	653.12	177.36	30.29	74.83	148.98	23.37	96.78	84.01	3.64E+00	0.00E+00	Up	1.76E+00	3.00E-193	Up	1.31E+00	9.89E-64	Up	2.30E+00	1.36E-252	Up	2.05E+00	1.64E-162	Up	1.85E+00	2.95E-125	Up	Unigene5313_All//gi|186513316|ref|NP_001119048.1|//1.00E-19//ATHVA22D [Arabidopsis thaliana]	Unigene5313_All//6.00E-21//AT4G24960| ATHVA22D	Unigene5313_All//0.00E+00//DW239565				nr +
Unigene53132_All	501	0.00	0.00	0.00	0.00	0.27	0.36	59.41	22.36	178.12	null	null		null	null		8.10E+00	3.18E-01		8.49E+00	1.94E-01		-1.41E+00	9.80E-46	Down	1.58E+00	4.19E-164	Up	Unigene53132_All//gi|297834358|ref|XP_002885061.1|//2.00E-61//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297330901|gb|EFH61320.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene53132_All//2.00E-61//AT3G13610| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene53132_All//3.00E-172//gi|3326271|gb|AI055157.1|AI055157		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene53135_All	432	0.24	6.69	0.99	0.12	0.00	0.42	0.98	2.42	8.30	4.79E+00	7.73E-14	Up	2.03E+00	1.39E-01		-6.85E+00	5.55E-01		1.86E+00	4.58E-01		1.31E+00	3.44E-02		3.08E+00	1.34E-15	Up		Unigene53135_All//5.00E-07//TC161737					
Unigene53136_All	847	0.00	14.66	7.04	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	3.19E-71	Up	1.28E+01	3.02E-33	Up	null	null		null	null		null	null		null	null		Unigene53136_All//gi|300120285|emb|CBK19839.2|//3.00E-14//Short-chain dehydrogenase/reductase [Blastocystis hominis]	Unigene53136_All//9.00E-14//AT1G49670| NQR; binding / catalytic/ oxidoreductase/ zinc ion binding			ko00564|Glycerophospholipid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis//ko00565|Ether lipid metabolism		nr +
Unigene5314_All	569	4.60	9.17	14.69	45.00	25.78	15.95	0.45	30.63	0.84	9.96E-01	1.74E-04		1.68E+00	1.99E-13	Up	-8.04E-01	5.24E-16		-1.50E+00	4.02E-38	Down	6.10E+00	1.97E-112	Up	9.14E-01	3.38E-01		Unigene5314_All//gi|255560812|ref|XP_002521419.1|//5.00E-09//diphosphonucleoside phosphohydrolase, putative [Ricinus communis] >gi|223539318|gb|EEF40909.1| diphosphonucleoside phosphohydrolase, putative [Ricinus communis]		Unigene5314_All//2.00E-65//gi|109837551|gb|DW236112.1|DW236112		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism		nr -
Unigene53142_All	471	0.33	0.32	2.60	0.00	0.88	0.48	0.00	0.00	0.00	-4.66E-02	9.89E-01		2.96E+00	2.55E-04	Up	9.78E+00	1.25E-02		8.91E+00	1.19E-01		null	null		null	null		Unigene53142_All//gi|226462731|gb|EEH60009.1|//4.00E-09//major facilitator superfamily [Micromonas pusilla CCMP1545]	Unigene53142_All//3.00E-07//AT2G35740| INT3 (NOSITOL TRANSPORTER 3); carbohydrate transmembrane transporter/ sugar:hydrogen symporter					nr -
Unigene53143_All	209	1.50	0.00	2.80	0.48	1.48	4.32	0.81	0.60	0.38	-1.06E+01	3.65E-02		9.00E-01	3.77E-01		1.64E+00	3.21E-01		3.18E+00	9.74E-04	Up	-4.32E-01	7.92E-01		-1.09E+00	5.52E-01			Unigene53143_All//5.00E-30//TC148807					
Unigene53144_All	339	1.39	1.35	5.34	1.03	1.12	1.60	1.00	0.86	0.12	-4.62E-02	9.78E-01		1.94E+00	4.89E-04	Up	1.20E-01	9.58E-01		6.36E-01	5.61E-01		-2.09E-01	8.50E-01		-3.09E+00	3.91E-02			Unigene53144_All//6.00E-157//ES797222					
Unigene53145_All	538	0.00	0.00	0.00	0.00	0.00	0.00	18.55	8.00	4.59	null	null		null	null		null	null		null	null		-1.21E+00	9.84E-13	Down	-2.01E+00	1.42E-26	Down							
Unigene53146_All	901	0.00	0.00	0.00	0.00	0.00	0.10	4.88	2.92	1.90	null	null		null	null		null	null		6.65E+00	4.75E-01		-7.40E-01	3.99E-03		-1.36E+00	2.46E-07	Down	Unigene53146_All//gi|297824773|ref|XP_002880269.1|//1.00E-69//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297326108|gb|EFH56528.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene53146_All//5.00E-70//AT2G46850| ATP binding / protein kinase/ protein tyrosine kinase			ko04626|Plant-pathogen interaction		nr +
Unigene53147_All	355	11.94	32.97	16.05	13.19	10.67	15.27	34.78	31.32	24.24	1.47E+00	6.06E-16	Up	4.27E-01	1.09E-01		-3.06E-01	3.07E-01		2.11E-01	4.69E-01		-1.51E-01	3.70E-01		-5.21E-01	1.88E-04			Unigene53147_All//2.00E-43//BM359338					
Unigene5315_All	1534	3.68	3.17	3.23	8.64	6.89	3.59	0.63	0.52	0.26	-2.16E-01	4.05E-01		-1.90E-01	4.98E-01		-3.26E-01	3.35E-02		-1.27E+00	1.32E-15	Down	-2.92E-01	6.31E-01		-1.29E+00	3.62E-02		Unigene5315_All//gi|138996985|dbj|BAF52855.1|//1.00E-172//repressor of silencing 1 [Nicotiana tabacum]	Unigene5315_All//6.00E-147//AT5G04560| DME (DEMETER); DNA N-glycosylase/ DNA-(apurinic or apyrimidinic site) lyase	Unigene5315_All//0.00E+00//gi|164246865|gb|ES797893.1|ES797893		ko03410|Base excision repair		nr +
Unigene53150_All	609	0.60	0.00	0.87	1.64	1.24	0.52	1.67	1.03	0.33	-9.23E+00	1.96E-02		5.40E-01	6.10E-01		-3.95E-01	5.73E-01		-1.66E+00	2.34E-02		-6.95E-01	2.63E-01		-2.35E+00	5.84E-04	Down							
Unigene53152_All	694	0.15	1.53	0.00	0.43	0.84	0.65	2.19	3.37	2.24	3.35E+00	2.17E-04	Up	-7.24E+00	3.91E-01		9.70E-01	3.47E-01		5.96E-01	6.40E-01		6.21E-01	9.95E-02		2.97E-02	9.69E-01			Unigene53152_All//0.00E+00//ES841748					
Unigene53153_All	690	0.00	0.00	0.00	0.00	0.00	0.00	1.23	6.54	52.19	null	null		null	null		null	null		null	null		2.42E+00	7.51E-15	Up	5.41E+00	6.70E-225	Up	Unigene53153_All//gi|63029720|gb|AY227751.1|//3.00E-91//allene oxide synthase [Hevea brasiliensis]	Unigene53153_All//4.00E-55//AT5G42650| AOS (ALLENE OXIDE SYNTHASE); allene oxide synthase/ hydro-lyase/ oxygen binding	Unigene53153_All//0.00E+00//TC132926		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene53159_All	401	10.70	1.90	6.37	2.11	2.23	1.13	1.27	1.46	0.30	-2.50E+00	4.19E-12	Down	-7.47E-01	1.45E-02		8.03E-02	9.41E-01		-9.07E-01	2.47E-01		2.06E-01	8.00E-01		-2.09E+00	3.64E-02		Unigene53159_All//gi|255084137|ref|XP_002508643.1|//4.00E-07//glyceraldehyde-3-phosphate dehydrogenase [Micromonas sp. RCC299] >gi|226523920|gb|ACO69901.1| glyceraldehyde-3-phosphate dehydrogenase [Micromonas sp. RCC299]	Unigene53159_All//1.00E-07//AT3G04120| GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene53159_All//6.00E-31//TC158306		ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene53160_All	528	0.20	0.19	0.91	0.28	0.33	0.17	2.00	5.15	1.43	-4.66E-02	9.88E-01		2.20E+00	9.14E-02		2.05E-01	9.50E-01		-7.26E-01	7.15E-01		1.36E+00	1.15E-04	Up	-4.82E-01	3.98E-01		Unigene53160_All//gi|124360549|gb|ABD33126.2|//5.00E-10//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]						nr +
Unigene53161_All	567	27.13	11.08	14.28	0.44	0.12	0.64	0.00	0.15	0.00	-1.29E+00	2.53E-17	Down	-9.26E-01	5.87E-10		-1.85E+00	2.75E-01		5.37E-01	6.94E-01		7.20E+00	4.00E-01		null	null		Unigene53161_All//gi|30686482|ref|NP_850251.1|//3.00E-16//aspartyl protease family protein [Arabidopsis thaliana]	Unigene53161_All//2.00E-17//AT2G35615| aspartyl protease family protein	Unigene53161_All//2.00E-176//gi|84156327|gb|DN817553.1|DN817553				nr +
Unigene53162_All	1073	0.20	0.33	0.00	0.84	0.51	0.00	21.79	5.41	10.54	7.62E-01	5.57E-01		-7.61E+00	1.45E-01		-7.03E-01	3.24E-01		-9.71E+00	1.21E-05	Down	-2.01E+00	4.03E-59	Down	-1.05E+00	1.42E-23	Down	Unigene53162_All//gi|6693036|gb|AAF24962.1|AC012375_25//5.00E-10//T22J5.12 [Arabidopsis thaliana] >gi|28950785|gb|AA063316.1| At1g27670 [Arabidopsis thaliana]	Unigene53162_All//4.00E-10//AT5G66440| unknown protein	Unigene53162_All//3.00E-10//TC139772				nr +
Unigene53163_All	464	0.45	0.22	0.46	2.36	0.74	0.00	0.82	0.63	0.52	-1.05E+00	5.64E-01		2.57E-02	1.00E+00		-1.67E+00	9.38E-03		-1.12E+01	7.25E-07	Down	-3.79E-01	7.23E-01		-6.71E-01	5.30E-01								ESTscan +
Unigene53167_All	679	0.00	0.00	0.00	0.00	0.00	0.00	7.29	4.86	0.00	null	null		null	null		null	null		null	null		-5.83E-01	1.58E-02		-1.28E+01	2.24E-36	Down							
Unigene53169_All	1502	0.07	0.00	0.00	0.13	0.00	0.00	3.21	0.83	2.68	-6.12E+00	3.70E-01		-6.12E+00	3.91E-01		-7.05E+00	8.41E-02		-7.05E+00	1.33E-01		-1.94E+00	2.97E-12	Down	-2.61E-01	3.07E-01		Unigene53169_All//gi|297802842|ref|XP_002869305.1|//1.00E-123//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315141|gb|EFH45564.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene53169_All//4.00E-110//AT4G31910| transferase family protein			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene53170_All	356	0.29	0.00	0.00	27.43	9.87	3.68	0.00	0.00	0.11	-8.20E+00	3.70E-01		-8.20E+00	3.91E-01		-1.48E+00	1.71E-16	Down	-2.90E+00	4.95E-34	Down	null	null		6.81E+00	6.44E-01		Unigene53170_All//gi|42572555|ref|NP_974373.1|//6.00E-29//MIF2 (MINI ZINC FINGER 2); DNA binding [Arabidopsis thaliana] >gi|88900352|gb|ABD57488.1| At3g28917 [Arabidopsis thaliana]	Unigene53170_All//3.00E-30//AT3G28917| MIF2 (MINI ZINC FINGER 2); DNA binding	Unigene53170_All//3.00E-174//TC164703	zf-HD			nr -
Unigene53172_All	429	0.00	0.00	0.00	0.00	0.00	0.00	9.26	3.80	0.93	null	null		null	null		null	null		null	null		-1.29E+00	5.32E-06	Down	-3.32E+00	9.95E-19	Down							
Unigene53174_All	291	0.36	0.00	0.55	7.70	0.83	0.31	4.36	0.57	3.97	-8.49E+00	3.70E-01		6.10E-01	7.48E-01		-3.22E+00	2.57E-10	Down	-4.63E+00	1.33E-11	Down	-2.92E+00	1.46E-05	Down	-1.35E-01	7.87E-01								
Unigene53179_All	1415	0.07	0.79	0.30	0.07	0.22	0.06	0.99	1.65	2.82	3.41E+00	1.24E-04	Up	2.02E+00	1.39E-01		1.64E+00	3.21E-01		-1.42E-01	9.49E-01		7.46E-01	4.55E-02		1.51E+00	1.17E-07	Up							ESTscan -
Unigene5318_All	970	1.35	0.57	0.16	20.59	18.96	10.52	1.39	0.56	0.25	-1.23E+00	3.96E-02		-3.03E+00	1.24E-04	Down	-1.19E-01	4.15E-01		-9.69E-01	2.87E-15		-1.32E+00	1.25E-02		-2.50E+00	2.46E-05	Down	Unigene5318_All//gi|226503978|ref|NP_001152323.1|//4.00E-66//rho GDP-dissociation inhibitor 1 [Zea mays] >gi|195655101|gb|ACG47018.1| rho GDP-dissociation inhibitor 1 [Zea mays]	Unigene5318_All//3.00E-57//AT3G07880| Rho GDP-dissociation inhibitor family protein	Unigene5318_All//1.00E-46//gi|48795943|gb|CO097257.1|CO097257				nr -
Unigene53180_All	470	0.45	1.08	0.68	0.85	0.59	0.19	2.16	3.11	5.42	1.28E+00	2.31E-01		6.10E-01	6.24E-01		-5.33E-01	6.15E-01		-2.14E+00	1.26E-01		5.28E-01	3.03E-01		1.33E+00	1.94E-04	Up		Unigene53180_All//6.00E-07//TC174058					
Unigene53181_All	602	0.00	0.00	0.27	0.41	0.51	1.28	94.88	322.77	9.46	null	null		8.05E+00	2.38E-01		3.15E-01	8.38E-01		1.62E+00	6.61E-02		1.77E+00	0.00E+00	Up	-3.33E+00	4.75E-261	Down	Unigene53181_All//gi|240254556|ref|NP_180668.4|//6.00E-36//triacylglycerol lipase [Arabidopsis thaliana]	Unigene53181_All//3.00E-37//AT2G31100| triacylglycerol lipase					nr -
Unigene53182_All	317	32.02	17.10	30.40	426.64	383.68	358.17	631.00	448.15	239.79	-9.05E-01	6.43E-07		-7.47E-02	7.03E-01		-1.53E-01	3.12E-04		-2.52E-01	3.14E-09		-4.94E-01	1.23E-51		-1.40E+00	0.00E+00	Down	Unigene53182_All//gi|258489633|gb|ACV72640.1|//2.00E-56//sucrose synthase 1 [Gossypium hirsutum]	Unigene53182_All//3.00E-51//AT5G20830| SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase	Unigene53182_All//5.00E-179//ES846339		ko00500|Starch and sucrose metabolism		nr -
Unigene53183_All	583	1.26	5.56	1.00	1.11	0.18	0.54	0.07	0.22	0.14	2.15E+00	7.84E-08	Up	-3.23E-01	6.81E-01		-2.65E+00	7.46E-03		-1.03E+00	2.68E-01		1.57E+00	5.45E-01		9.15E-01	7.49E-01		Unigene53183_All//gi|87116616|gb|ABD19672.1|//4.00E-25//At3g15110 [Arabidopsis thaliana]	Unigene53183_All//1.00E-21//AT3G15110| unknown protein	Unigene53183_All//0.00E+00//gi|48794993|gb|CO096307.1|CO096307				nr -
Unigene53185_All	328	3.83	0.46	3.08	0.46	0.63	0.28	2.06	0.76	0.24	-3.05E+00	9.00E-05	Down	-3.12E-01	6.41E-01		4.67E-01	8.25E-01		-7.26E-01	7.15E-01		-1.43E+00	7.83E-02		-3.09E+00	1.45E-03		Unigene53185_All//gi|240255805|ref|NP_193027.5|//3.00E-18//scp120 (serine carboxypeptidase-like 20); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|125987775|sp|Q8L7B2.2|SCP20_ARATH RecName: Full=Serine carboxypeptidase-like 20; Flags: Precursor	Unigene53185_All//1.00E-19//AT4G12910| scp120 (serine carboxypeptidase-like 20); serine-type carboxypeptidase	Unigene53185_All//2.00E-135//TC132342				nr +

Unigene53186_All	464	0.00	3.71	0.00	0.54	0.52	0.39	0.46	0.27	1.63	1.19E+01	7.99E-10	Up	null	null		-4.73E-02	9.51E-01		-4.64E-01	7.44E-01		-7.54E-01	6.31E-01		1.84E+00	1.64E-02		Unigene53186_All//gi|15224852|ref|NP_179571.1|//1.00E-09//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75220226|sp|082199.1|C3H20_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 20; Short=AtC3H20	Unigene53186_All//7.00E-11//AT2G19810| zinc finger (CCCH-type) family protein	Unigene53186_All//3.00E-45//TC155711	C3H			nr -
Unigene53188_All	274	159.44	41.05	96.20	297.07	280.13	188.40	225.60	72.76	105.12	-1.96E+00	5.88E-87	Down	-7.29E-01	3.30E-18		-8.47E-02	1.99E-01		-6.57E-01	3.15E-31		-1.63E+00	9.22E-117	Down	-1.10E+00	5.10E-66	Down	Unigene53188_All//gi|297795089|ref|XP_002865429.1|//5.00E-08//cytosolic malate dehydrogenase [Arabidopsis lyrata subsp. lyrata] >gi|297311264|gb|EFH11688.1| cytosolic malate dehydrogenase [Arabidopsis lyrata subsp. lyrata]	Unigene53188_All//2.00E-09//AT5G43330| malate dehydrogenase, cytosolic, putative	Unigene53188_All//4.00E-102//gi|164314863|gb|ES848837.1|ES848837		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene53319_All	1101	38.30	9.76	25.83	12.04	13.10	7.26	0.46	0.08	0.07	-1.97E+00	7.69E-85	Down	-5.69E-01	1.50E-11		1.23E-01	5.01E-01		-7.29E-01	1.30E-06		-2.60E+00	2.04E-02		-2.67E+00	1.37E-02		Unigene53319_All//gi|115448641|ref|NP_001048100.1|//1.00E-73//0s02g0744100 [Oryza sativa Japonica Group] >gi|46390636|dbj|BAD16119.1| UbiE/COQ5 methyltransferase-like [Oryza sativa Japonica Group] >gi|98991037|gb|ABF60543.1| As(III) methyltransferase [Oryza sativa Japonica Group] >gi|113537631|dbj|BAF10014.1| Os02g0744100 [Oryza sativa Japonica Group]	Unigene53319_All//2.00E-71//AT1G69523| UbiE/COQ5 methyltransferase family protein	Unigene53319_All//5.00E-114//AT1731954		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene53190_All	651	0.16	3.66	2.37	6.81	2.38	8.74	454.63	1662.20	1476.23	4.51E+00	4.03E-11	Up	3.88E+00	1.75E-06	Up	-1.52E+00	4.57E-08	Down	3.60E-01	1.80E-01		1.87E+00	0.00E+00	Up	1.70E+00	0.00E+00	Up	Unigene53190_All//gi|238055376|sp|B9H703.1|U4974_RICCO//3.00E-54//RecName: Full=UPF0497 membrane protein 4	Unigene53190_All//2.00E-25//AT4G15610| integral membrane family protein	Unigene53190_All//0.00E+00//gi|109862765|gb|DW491742.1|DW491742				nr -
Unigene53192_All	624	0.00	2.92	3.75	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.14E-10	Up	1.19E+01	6.40E-13	Up	null	null		null	null		null	null		null	null		Unigene53192_All//sp|P00736|C1R_HUMAN//6.00E-127//Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2						swissprot -
Unigene53193_All	566	0.46	1.61	3.10	14.35	0.85	0.48	75.00	120.81	89.04	1.80E+00	2.33E-02		2.75E+00	1.47E-05	Up	-4.07E+00	5.45E-45	Down	-4.91E+00	6.61E-43	Down	6.88E-01	2.55E-32		2.48E-01	1.70E-04		Unigene53193_All//gi|14582308|gb|AAK69445.1|//1.00E-62//proline-rich protein-1 [Gossypium hirsutum]		Unigene53193_All//9.00E-31//TC175607		ko03040|Spliceosome		nr -
Unigene53195_All	1014	0.00	0.60	0.00	0.00	0.00	0.00	13.34	4.66	14.85	9.23E+00	1.17E-03		null	null		null	null		null	null		-1.52E+00	1.33E-23	Down	1.55E-01	2.66E-01		Unigene53195_All//gi|297598701|ref|NP_001046103.2|//1.00E-92//0s02g0183000 [Oryza sativa Japonica Group] >gi|255670656|dbj|BAF08017.2| Os02g0183000 [Oryza sativa Japonica Group]	Unigene53195_All//2.00E-97//AT2G12646| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF597 (InterPro:IPR006734); BEST Arabidopsis thaliana protein match is: zinc-binding protein, putative (TAIR:AT3G60670.1); Has 191 Blast hits to 191 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 191; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene53195_All//5.00E-40//gi|3325907|gb|AI054793.1|AI054793	PLATZ			nr +
Unigene53196_All	499	0.31	1.12	2.35	0.50	0.41	0.36	1.86	0.59	0.56	1.83E+00	9.02E-02		2.90E+00	4.34E-04	Up	-2.69E-01	8.23E-01		-4.63E-01	7.44E-01		-1.67E+00	1.45E-02		-1.74E+00	8.54E-03				Unigene53196_All//2.00E-53//ES852319					
Unigene53197_All	707	0.30	0.00	0.08	0.00	0.05	0.57	1.79	13.24	7.16	-8.21E+00	1.22E-01		-1.97E+00	3.81E-01		5.61E+00	8.29E-01		9.17E+00	1.36E-02		2.88E+00	2.08E-36	Up	2.00E+00	1.53E-13	Up	Unigene53197_All//gi|198449163|gb|ACH88751.1|//3.00E-46//WRKY DNA binding protein [Fragaria x ananassa]	Unigene53197_All//6.00E-39//AT5G13080| WRKY75; transcription factor	Unigene53197_All//1.00E-73//TC143058	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene53199_All	529	3.96	1.72	0.40	2.92	4.23	2.48	0.16	0.32	0.38	-1.20E+00	8.12E-03		-3.30E+00	1.34E-07	Down	5.36E-01	2.33E-01		-2.38E-01	6.81E-01		9.84E-01	6.33E-01		1.24E+00	4.68E-01		Unigene53199_All//gi|6002055|emb|CAB56692.1|//9.00E-51//lipoxygenase [Arabidopsis thaliana]	Unigene53199_All//3.00E-52//AT1G17420| LOX3; electron carrier/ iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen			ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr +
Unigene532_All	2111	4.06	13.03	5.20	12.58	15.64	18.29	23.71	54.80	86.02	1.68E+00	2.00E-44	Up	3.54E-01	5.40E-02		3.15E-01	4.33E-04		5.40E-01	9.35E-11		1.21E+00	2.86E-138	Up	1.86E+00	0.00E+00	Up	Unigene532_All//gi|15231963|ref|NP_187488.1|//0.00E+00//ATSIK; ATP binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|194294570|gb|ACF40324.1| At3g08760 [Arabidopsis thaliana] >gi|222424853|dbj|BAH20378.1| AT3G08760 [Arabidopsis thaliana]	Unigene532_All//6.00E-165//AT3G08760| ATSIK; ATP binding / kinase/ protein kinase/ protein tyrosine kinase	Unigene532_All//0.00E+00//TC178915		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene53200_All	424	0.25	0.00	0.38	16.21	15.67	5.11	1.30	0.00	0.00	-7.95E+00	3.70E-01		6.11E-01	7.48E-01		-4.87E-02	8.38E-01		-1.67E+00	2.51E-12	Down	-1.03E+01	4.61E-04	Down	-1.03E+01	2.80E-04	Down	Unigene53200_All//gi|116781010|gb|ABK21924.1|//1.00E-06//unknown [Picea sitchensis] >gi|116785582|gb|ABK23780.1| unknown [Picea sitchensis] >gi|116792448|gb|ABK26369.1| unknown [Picea sitchensis] >gi|224285826|gb|ACN40627.1| unknown [Picea sitchensis]		Unigene53200_All//1.00E-87//DW233551				nr -
Unigene53201_All	406	0.00	0.00	0.00	0.61	0.17	0.22	49.15	100.89	46.41	null	null		null	null		-1.85E+00	2.75E-01		-1.46E+00	4.07E-01		1.04E+00	7.94E-39	Up	-8.28E-02	5.21E-01				Unigene53201_All//4.00E-69//TC148848				
Unigene53202_All	274	3.06	0.00	4.86	2.55	1.26	0.16	0.00	0.00	0.15	-1.16E+01	5.57E-05	Down	6.69E-01	2.68E-01		-1.02E+00	2.25E-01		-3.95E+00	1.46E-03		null	null		7.18E+00	6.44E-01				Unigene53202_All//8.00E-48//PL576750				
Unigene53204_All	682	0.00	12.04	5.47	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	5.84E-47	Up	1.24E+01	1.20E-20	Up	null	null		null	null		null	null		null	null		Unigene53204_All//gi|114326546|ref|NP_075907.2|//3.00E-76//phosphoglycerate mutase 1 [Mus musculus] >gi|20178035|sp|Q9DBJ1.3|PGAM1_MOUSE RecName: Full=Phosphoglycerate mutase 1; AltName: Full=Phosphoglycerate mutase isozyme B; Short=PGAM-B; AltName: Full=BPG-dependent PGAM 1 >gi|122065830|sp|P25113.4|PGAM1_RAT RecName: Full=Phosphoglycerate mutase 1; AltName: Full=Phosphoglycerate mutase isozyme B; Short=PGAM-B; AltName: Full=BPG-dependent PGAM 1 >gi|112128|pir||JC1132 phosphoglycerate mutase (EC 5.4.2.1) B chain - rat >gi|12805529|gb|AAH02241.1| Phosphoglycerate mutase 1 [Mus musculus] >gi|13542946|gb|AAH05661.1| Phosphoglycerate mutase 1 [Mus musculus] >gi|41350889|gb|AAH65582.1| Pgam1 protein [Rattus norvegicus] >gi|45219739|gb|AAH66844.1| Phosphoglycerate mutase 1 [Mus musculus]	Unigene53204_All//2.00E-26//AT1G22170| phosphoglycerate/bisphosphoglycerate mutase family protein			ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene53209_All	1847	0.00	6.80	2.42	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	4.23E-72	Up	1.12E+01	7.75E-25	Up	null	null		null	null		null	null		null	null		Unigene53209_All//gi|255080478|ref|XP_002503819.1|//0.00E+00//H+-or Na+-translocating f-type, v-type and A-type ATPase superfamily [Micromonas sp. RCC299] >gi|226519086|gb|ACO65077.1| H+-or Na+-translocating f-type, v-type and A-type ATPase superfamily [Micromonas sp. RCC299]	Unigene53209_All//0.00E+00//AT1G78900| VHA-A VACUOLAR ATP SYNTHASE SUBUNIT A1; ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism / hydrolase, acting on acid anhydrides, catalyzing transmembrane movement of substances / proton-transporting ATPase, rotational mechanism	Unigene53209_All//1.00E-10//TC179299		ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene5321_All	884	15.57	4.99	8.61	21.19	23.10	16.86	95.66	19.53	26.09	-1.64E+00	5.67E-22	Down	-8.54E-01	6.53E-08		1.25E-01	3.90E-01		-3.30E-01	1.08E-02		-2.29E+00	7.45E-251	Down	-1.87E+00	4.03E-199	Down	Unigene5321_All//gi|1762945|gb|AAC49975.1|//9.00E-57//ORF; able to induce HR-like lesions [Nicotiana tabacum]	Unigene5321_All//1.00E-42//AT4G14420| lesion inducing protein-related	Unigene5321_All//0.00E+00//TC141512				nr -
Unigene53210_All	900	0.41	0.00	0.12	0.61	0.31	0.55	30.21	38.08	11.02	-8.67E+00	1.96E-02		-1.78E+00	2.34E-01		-9.92E-01	3.13E-01		-1.41E-01	8.85E-01		3.34E-01	4.78E-05		-1.45E+00	4.02E-45	Down	Unigene53210_All//gi|124359568|gb|AB028696.2|//6.00E-48//NAD-dependent epimerase/dehydratase [Medicago truncatula]	Unigene53210_All//3.00E-17//AT4G27250| dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family			ko00941|Flavonoid biosynthesis		nr -
Unigene53212_All	476	0.11	0.21	1.34	0.10	2.03	0.76	3.20	2.99	1.67	9.54E-01	7.25E-01		3.61E+00	6.97E-03		4.27E+00	6.78E-05	Up	2.86E+00	9.44E-02		-9.91E-02	8.40E-01		-9.34E-01	4.27E-02									
Unigene53213_All	1007	0.00	0.00	0.00	0.00	0.00	0.00	2.86	8.30	0.00	null	null		null	null		null	null		null	null		1.54E+00	3.85E-15	Up	-1.15E+01	3.77E-21	Down	Unigene53213_All//gi|110225900|gb|AK586231.1|//1.00E-139//translation elongation factor-like protein [Karlodinium micrum]	Unigene53213_All//7.00E-61//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene53213_All//3.00E-10//gi|78327885|gb|DT548159.1|DT548159				nr +
Unigene5322_All	720	21.22	18.09	27.73	60.26	39.50	62.54	41.28	88.47	40.78	-2.31E-01	1.27E-01		3.86E-01	2.75E-03		-6.09E-01	1.37E-16		5.35E-02	6.25E-01		1.10E+00	7.92E-66	Up	-1.77E-02	8.72E-01		Unigene5322_All//gi|93280154|gb|AB106705.1|//8.00E-26//Joka8 [Nicotiana plumbaginifolia]	Unigene5322_All//1.00E-13//AT3G24260| basic helix-loop-helix (bHLH) family protein	Unigene5322_All//0.00E+00//gi|78341292|gb|DT561566.1|DT561566	bHLH			nr -
Unigene53222_All	1008	0.73	0.60	0.32	4.74	2.80	0.90	1.47	0.58	0.71	-2.69E-01	7.19E-01		-1.20E+00	1.80E-01		-7.60E-01	3.18E-03		-2.40E+00	8.38E-14	Down	-1.34E+00	7.48E-03		-1.05E+00	2.65E-02		Unigene53222_All//gi|162460667|ref|NP_001105909.1|//1.00E-150//12-oxo-phytodienoic acid reductase5 [Zea mays] >gi|630217227|gb|AAY26525.1| 12-oxo-phytodienoic acid reductase [Zea mays]	Unigene53222_All//7.00E-144//AT1G76680| OPR1; 12-oxophytodienoate reductase	Unigene53222_All//9.00E-17//AI725636		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene53225_All	793	0.13	0.00	0.00	0.00	0.69	0.00	75.12	18.39	56.17	-7.04E+00	3.70E-01		-7.04E+00	3.91E-01		9.44E+00	2.02E-03		null	null		-2.03E+00	1.09E-151	Down	-4.20E-01	2.02E-12		Unigene53225_All//gi|119067548|gb|ABL60873.1|//8.00E-88//germin-like protein 4 [Vitis vinifera]	Unigene53225_All//2.00E-81//AT5G38910| manganese ion binding / nutrient reservoir	Unigene53225_All//0.00E+00//gi|13350109|gb|BG440458.1|BG440458				nr +

Unigene53226_All	791	0.00	2.95	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.91E-13	Up	1.04E+01	6.62E-06	Up	null	null		null	null		null	null		null	null		Unigene53226_All//gi|15226618|ref|NP_182273.1|//2.00E-92//FUM1 (FUMARASE 1); catalytic/ fumarate hydratase [Arabidopsis thaliana] >gi|145331433|ref|NP_001078075.1| FUM1 (FUMARASE 1); catalytic/ fumarate hydratase [Arabidopsis thaliana] >gi|39931311|sp|P93033.2|FUM1_ARATH RecName: Full=Fumarate hydratase 1, mitochondrial; Short=Fumarase 1; Flags: Precursor >gi|2443751|gb|AAB71399.1| fumarase [Arabidopsis thaliana] >gi|15809968|gb|AAL06911.1| At2g47510/T30B22.19 [Arabidopsis thaliana]	Unigene53226_All//3.00E-86//AT2G47510| FUM1 (FUMARASE 1); catalytic/ fumarate hydratase			ko00020|Citrate cycle (TCA cycle)		nr +
Unigene53227_All	568	0.00	0.89	0.19	2.98	0.61	0.64	2.38	1.99	0.56	9.80E+00	4.04E-03		7.55E+00	3.97E-01		-2.30E+00	1.29E-05	Down	-2.23E+00	7.57E-05	Down	-2.62E-01	6.63E-01		-2.09E+00	1.85E-04	Down			Unigene53227_All//7.00E-07//TC139489				
Unigene53228_All	893	0.00	0.00	0.00	0.00	0.00	0.00	3.08	22.00	0.00	null	null		null	null		null	null		null	null		2.84E+00	1.84E-74	Up	-1.16E+01	3.21E-20	Down			Unigene53228_All//5.00E-15//gi|11207717|gb|BF276647.1|BF276647				
Unigene5323_All	1147	1.73	5.04	5.94	8.08	10.84	10.00	1.51	1.06	0.87	1.54E+00	8.42E-09	Up	1.78E+00	6.02E-12	Up	4.24E-01	6.51E-03		3.08E-01	8.16E-02		-5.16E-01	2.59E-01		-8.00E-01	6.02E-02		Unigene5323_All//gi|9954736|gb|AAG09089.1|AC026237_10//1.00E-122//Hypothetical protein [Arabidopsis thaliana]	Unigene5323_All//3.00E-110//AT1G16770| unknown protein				nr -
Unigene53233_All	237	4.64	8.12	13.26	1.89	1.74	1.91	0.89	0.88	0.17	8.09E-01	8.28E-02		1.52E+00	8.23E-05	Up	-1.18E-01	8.86E-01		1.06E-02	1.00E+00		-1.66E-02	1.02E+00		-2.41E+00	1.95E-01		Unigene53233_All//gi|147821135|emb|CAN62170.1|//9.00E-08//hypothetical protein [Vitis vinifera] >gi|296081293|emb|CBI17737.3| unnamed protein product [Vitis vinifera]	Unigene53233_All//2.00E-06//AT5G42510| disease resistance-responsive family protein	Unigene53233_All//7.00E-85//TC144221			nr +
Unigene53235_All	1796	0.00	0.00	0.00	0.00	0.00	0.00	21.68	1.28	0.64	null	null		null	null		null	null		null	null		-4.08E+00	4.97E-204	Down	-5.07E+00	2.83E-241	Down	Unigene53235_All//gi|15236615|ref|NP_194925.1|//0.00E+00//CYP82C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding [Arabidopsis thaliana] >gi|2827638|emb|CAA16592.1| Cytochrome P450-like protein [Arabidopsis thaliana] >gi|7270101|emb|CAB79915.1| Cytochrome P450-like protein [Arabidopsis thaliana]	Unigene53235_All//0.00E+00//AT4G31970| CYP82C2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene53235_All//0.00E+00//CD486273		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	nr +
Unigene53237_All	520	1.51	0.00	0.00	0.19	0.40	0.78	65.78	69.77	133.31	-1.06E+01	1.09E-04	Down	-1.06E+01	2.21E-04	Down	1.05E+00	6.12E-01		2.03E+00	1.49E-01		8.49E-02	3.84E-01		1.02E+00	9.92E-65	Up	Unigene53237_All//gi|224054176|ref|XP_002298129.1|//8.00E-30//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene53237_All//2.00E-23//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene53237_All//0.00E+00//TC173539		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis	nr -
Unigene53238_All	308	0.34	0.00	0.35	7.12	3.35	1.61	1.37	0.54	0.13	-8.41E+00	3.70E-01		2.57E-02	9.99E-01		-1.09E+00	8.04E-03		-2.14E+00	7.83E-06	Down	-1.34E+00	2.24E-01		-3.41E+00	1.24E-02				Unigene53238_All//7.00E-64//CO105172				
Unigene53239_All	246	12.34	16.48	12.12	26.53	19.18	24.05	19.42	17.16	7.45	4.18E-01	1.77E-01		-2.52E-02	9.65E-01		-4.68E-01	3.69E-02		-1.41E-01	6.27E-01		-1.79E-01	5.34E-01		-1.38E+00	4.51E-08	Down			Unigene53239_All//1.00E-80//DR463354				
Unigene5324_All	781	35.17	182.18	79.23	53.00	50.09	77.20	159.27	350.63	246.33	2.37E+00	0.00E+00	Up	1.17E+00	3.88E-56	Up	-8.16E-02	4.19E-01		5.43E-01	1.45E-16		1.14E+00	6.14E-297	Up	6.29E-01	2.70E-78		Unigene5324_All//gi|9958057|gb|AAG09546.1|AC011810_5//3.00E-42//Unknown Protein [Arabidopsis thaliana]	Unigene5324_All//6.00E-30//AT1G13360| unknown protein	Unigene5324_All//0.00E+00//TC150245			nr +
Unigene53241_All	366	0.00	0.83	0.00	3.81	2.63	0.49	1.50	0.00	0.54	9.70E+00	4.42E-02		null	null		-5.33E-01	3.44E-01		-2.95E+00	2.40E-05	Down	-1.06E+01	4.61E-04	Down	-1.46E+00	9.76E-02		Unigene53241_All//gi|225454428|ref|XP_002276498.1|//3.00E-10//PREDICTED: similar to Os11g0118600 [Vitis vinifera]	Unigene53241_All//1.00E-08//AT4G23720| unknown protein				nr -
Unigene53242_All	842	0.00	3.07	0.38	0.24	0.37	0.43	0.50	0.30	4.12	1.16E+01	1.06E-14	Up	8.57E+00	4.51E-02		6.38E-01	6.95E-01		8.59E-01	5.42E-01		-7.54E-01	4.77E-01		3.04E+00	6.99E-15	Up			Unigene53242_All//2.00E-11//PL576821				
Unigene53243_All	321	20.86	4.10	10.45	0.47	0.86	0.28	0.00	0.00	0.00	-2.35E+00	2.83E-17	Down	-9.97E-01	2.95E-05		8.82E-01	5.95E-01		-7.27E-01	7.15E-01		null	null		null	null				Unigene53243_All//2.00E-09//TC139496				
Unigene53247_All	370	0.99	0.82	0.00	0.67	0.74	0.37	0.34	0.34	2.37	-2.69E-01	8.00E-01		-9.95E+00	2.78E-02		1.45E-01	9.61E-01		-8.78E-01	6.16E-01		-1.65E-02	1.02E+00		2.79E+00	5.37E-04	Up			Unigene53247_All//3.00E-63//gi|3325917|gb|AI054803.1|AI054803				
Unigene53248_All	1521	0.07	0.43	0.00	0.13	0.16	0.30	8.31	4.09	5.06	2.65E+00	1.49E-02		-6.10E+00	3.91E-01		2.75E-01	8.95E-01		1.18E+00	3.38E-01		-1.02E+00	2.87E-12	Down	-7.17E-01	2.38E-07		Unigene53248_All//gi|27597229|dbj|BAC55155.1|//0.00E+00//purple acid phosphatase [Nicotiana tabacum]	Unigene53248_All//0.00E+00//AT2G16430| PAP10 (PURPLE ACID PHOSPHATASE 10); acid phosphatase/ protein serine/threonine phosphatase	Unigene53248_All//3.00E-168//gi|109878483|gb|DW507453.1|DW507453			nr +
Unigene53249_All	869	0.00	0.00	0.00	0.23	0.04	0.00	3.45	0.48	5.46	null	null		null	null		-2.53E+00	2.33E-01		-7.84E+00	1.33E-01		-2.84E+00	5.49E-12	Down	6.59E-01	5.85E-03		Unigene53249_All//gi|297602560|ref|NP_001062564.2|//2.00E-06//Os04g0370900 [Oryza sativa Japonica Group] >gi|255675378|dbj|BAF14478.2| Os04g0370900 [Oryza sativa Japonica Group]	Unigene53249_All//6.00E-05//AT1G16260| protein kinase family protein	Unigene53249_All//0.00E+00//TC148972			nr +
Unigene53250_All	445	0.47	1.71	3.35	2.46	3.40	2.13	3.71	1.60	4.83	1.86E+00	3.73E-02		2.83E+00	6.17E-05	Up	4.67E-01	4.26E-01		-2.09E-01	7.42E-01		-1.21E+00	9.00E-03		3.84E-01	3.35E-01		Unigene53250_All//gi|224065855|ref|XP_002301974.1|//7.00E-08//predicted protein [Populus trichocarpa] >gi|222843700|gb|EEE81247.1| predicted protein [Populus trichocarpa]		Unigene53250_All//8.00E-40//TC178060			nr +
Unigene53252_All	319	0.00	17.31	26.54	0.00	0.00	4.67	0.00	0.00	0.00	1.41E+01	1.66E-31	Up	1.47E+01	2.04E-47	Up	null	null		1.22E+01	7.03E-09	Up	null	null		null	null		Unigene53252_All//gi|2645999|gb|AAB87573.1|//4.00E-58//chlorophyll a/b binding protein of LHCII type I precursor [Panax ginseng]	Unigene53252_All//1.00E-57//AT1G29930| CAB1 (CHLOROPHYLL A/B BINDING PROTEIN 1); chlorophyll binding	Unigene53252_All//1.00E-65//TC135920		ko00196|Photosynthesis - antenna proteins	nr +
Unigene53253_All	759	3.03	4662.92	2708.24	1.51	0.91	21.18	3.96	3.74	3.36	1.06E+01	0.00E+00	Up	9.80E+00	0.00E+00	Up	-7.34E-01	2.38E-01		3.81E+00	2.11E-69	Up	-7.89E-02	8.18E-01		-2.36E-01	4.79E-01		Unigene53253_All//gi|301016726|dbj|BAJ11784.1|//3.00E-21//dehydration responsive protein [Corchorus olitorius]		Unigene53253_All//5.00E-70//TC152783			nr +
Unigene53255_All	364	62.24	40.09	35.84	72.26	68.40	82.01	250.66	106.10	112.51	-6.35E-01	3.53E-08		-7.96E-01	2.99E-11		-7.92E-02	5.39E-01		1.83E-01	9.01E-02		-1.24E+00	6.76E-114	Down	-1.16E+00	9.15E-105	Down	Unigene53255_All//gi|192910854|gb|ACF06535.1|//8.00E-24//60S ribosomal protein L27 [Elaeis guineensis]	Unigene53255_All//6.00E-15//AT4G15000| 60S ribosomal protein L27 (RPL27C)	Unigene53255_All//0.00E+00//gi|21089815|gb|BQ402128.1|BQ402128		ko03010|Ribosome	nr -
Unigene53258_All	409	0.77	2.97	1.56	2.31	0.51	1.33	4.55	10.22	22.89	1.95E+00	4.09E-03		1.03E+00	2.81E-01		-2.20E+00	2.99E-03		-8.04E-01	2.77E-01		1.17E+00	1.70E-05	Up	2.33E+00	1.92E-29	Up	Unigene53258_All//gi|227204135|dbj|BAH56919.1|//3.00E-28//AT3G21070 [Arabidopsis thaliana]	Unigene53258_All//1.00E-22//AT3G21070| NADK1 (NAD KINASE 1); NAD+ kinase/ NADH kinase/ calmodulin binding	Unigene53258_All//3.00E-119//TC149285		ko00760|Nicotinate and nicotinamide metabolism	nr -
Unigene53259_All	1733	0.00	0.00	0.00	0.00	0.00	0.05	1.24	1.50	4.51	null	null		null	null		null	null		5.70E+00	4.75E-01		2.65E-01	4.93E-01		1.86E+00	1.16E-18	Up	Unigene53259_All//gi|311698|emb|CAA80491.1|//8.00E-21//Lea protein [Glycine max]	Unigene53259_All//9.00E-12//AT3G53040| late embryogenesis abundant protein, putative / LEA protein, putative				nr -
Unigene5326_All	996	193.26	262.50	268.23	49.16	78.00	89.42	12.01	24.76	25.60	4.42E-01	6.67E-45		4.73E-01	2.50E-50		6.66E-01	1.96E-33		8.63E-01	5.02E-54		1.04E+00	6.56E-24	Up	1.09E+00	3.77E-27	Up	Unigene5326_All//gi|224085165|ref|XP_002307511.1|//5.00E-67//one helix protein 2 [Populus trichocarpa] >gi|222856960|gb|EEE94507.1| one helix protein 2 [Populus trichocarpa]	Unigene5326_All//4.00E-37//AT1G34000| OHP2 (ONE-HELIX PROTEIN 2)	Unigene5326_All//0.00E+00//gi|48791752|gb|CO093066.1|CO093066		ko04141|Protein processing in endoplasmic reticulum//ko03420|Nucleotide excision repair	nr +
Unigene53260_All	690	0.38	1.47	0.31	0.65	1.00	2.36	0.61	0.12	0.29	1.95E+00	1.01E-02		-2.96E-01	8.32E-01		6.19E-01	5.30E-01		1.86E+00	9.27E-04	Up	-2.34E+00	5.46E-02		-1.09E+00	2.82E-01		Unigene53260_All//gi|297610455|ref|NP_001064559.2|//7.00E-11//Os10g0405500 [Oryza sativa Japonica Group] >gi|255679389|dbj|BAF26473.2| Os10g0405500 [Oryza sativa Japonica Group]	Unigene53260_All//1.00E-07//AT2G46980| unknown protein	Unigene53260_All//2.00E-78//BF269929			nr -
Unigene53261_All	643	0.00	13.79	0.00	0.00	0.54	0.28	3.29	12.94	10.10	1.38E+01	9.33E-51	Up	null	null		9.06E+00	3.01E-02		8.13E+00	1.94E-01		1.98E+00	5.24E-21	Up	1.62E+00	4.30E-13	Up	Unigene53261_All//gi|50656897|gb|AAM95458.1|//3.00E-36//calmodulin-like protein [Datura metel]	Unigene53261_All//1.00E-31//AT1G76650| calcium-binding EF hand family protein	Unigene53261_All//0.00E+00//TC139274		ko04626|Plant-pathogen interaction	nr -
Unigene53262_All	230	6.82	0.44	2.78	8.23	4.94	2.55	0.55	0.00	0.17	-3.95E+00	5.06E-07	Down	-1.30E+00	2.26E-02		-7.36E-01	1.06E-01		-1.69E+00	6.39E-04	Down	-9.11E+00	2.35E-01		-1.67E+00	4.77E-01								
Unigene53267_All	922	0.00	3.52	4.56	0.00	0.15	0.00	0.05	0.00	0.00	1.18E+01	1.87E-18	Up	1.22E+01	2.43E-23	Up	7.22E+00	3.18E-01		null	null		-5.52E+00	6.56E-01		-5.52E+00	6.12E-01		Unigene53267_All//gi|297829676|ref|XP_002882720.1|//6.00E-80//60S acidic ribosomal protein P0 [Arabidopsis lyrata subsp. lyrata] >gi|297328560|gb|EFH58979.1| 60S acidic ribosomal protein P0 [Arabidopsis lyrata subsp. lyrata]	Unigene53267_All//1.00E-73//AT3G11250| 60S acidic ribosomal protein P0 (RPP0C)			ko03010|Ribosome	nr -
Unigene53268_All	532	0.39	2.57	0.60	0.19	0.97	0.08	0.32	0.00	0.15	2.71E+00	1.29E-04	Up	6.10E-01	6.24E-01		2.37E+00	5.64E-02		-1.14E+00	6.76E-01		-8.31E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene53268_All//gi|159895659|gb|ABX10440.1|//5.00E-81//3-ketoacyl-CoA synthase 10 [Gossypium hirsutum]	Unigene53268_All//1.00E-77//AT1G01120| KCS1 (3-KETOACYL-COA SYNTHASE 1); acyltransferase/ fatty acid elongase	Unigene53268_All//4.00E-125//TC135385			nr -
Unigene53272_All	1594	0.00	0.00	0.00	1.44	0.67	0.23	18.25	21.55	0.72	null	null		null	null		-1.10E+00	5.65E-03		-2.66E+00	1.16E-07	Down	2.40E-01	4.35E-03		-4.65E+00	7.89E-172	Down	Unigene53272_All//gi|74273619|gb|AB001477.1|//0.00E+00//cytochrome P450 DDWF1 [Gossypium hirsutum]	Unigene53272_All//6.00E-106//AT5G07990| TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	Unigene53272_All//0.00E+00//ES830064		ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	nr -
Unigene53273_All	281	0.00	0.36	0.00	1.42	0.74	1.13	0.45	0.30	13.89	8.49E+00	3.85E-01		null	null		-9.48E-01	4.21E-01		-3.34E-01	7.56E-01		-6.02E-01	7.66E-01		4.94E+00	1.12E-23	Up			Unigene53273_All//1.00E-12//BF276101				
Unigene53275_All	654	0.24	1.08	0.73	0.91	1.00	0.55	1.23	1.02	3.72	2.18E+00	2.50E-02		1.61E+00	1.82E-01		1.30E-01	9.05E-01		-7.26E-01	4.60E-01		-2.65E-01	7.04E-01		1.60E+00	2.49E-05	Up	Unigene53275_All//gi|145334203|ref|NP_001078482.1|//3.00E-97//DNA-directed DNA polymerase family protein [Arabidopsis thaliana] >gi|62241195|dbj|BAD93700.1| helicase and polymerase containing protein TEB1CH1 [Arabidopsis thaliana]	Unigene53275_All//6.00E-99//AT4G32700| DNA-directed DNA polymerase family protein				nr +
Unigene53278_All	303	57.16	95.82	51.14	82.86	67.28	83.47	156.28	137.66	69.42	7.45E-01	2.59E-13		-1.60E-01	2.99E-01		-3.01E-01	4.19E-03		1.06E-02	9.52E-01		-1.83E-01	1.13E-02		-1.17E+00	6.55E-56	Down			Unigene53278_All//4.00E-121//TC139562				
Unigene5328_All	1705	0.28	0.39	0.78	4.44	27.33	41.11	12.99	19.32	261.58	4.84E-01	5.90E-01		1.50E+00	1.84E-02		2.62E+00	2.54E-153	Up	3.21E+00	4.07E-261	Up	5.72E-01	9.33E-12		4.33E+00	0.00E+00	Up	Unigene5328_All//gi|63029720|gb|AAY27751.1|//0.00E+00//allene oxide synthase [Hevea brasiliensis]	Unigene5328_All//0.00E+00//AT5G42650| AOS (ALLENE OXIDE SYNTHASE); allene oxide synthase/ hydro-lyase/ oxygen binding	Unigene5328_All//0.00E+00//TC134042		ko00592|alpha-Linolenic acid metabolism	nr -
Unigene53285_All	915	0.00	0.00	0.00	0.00	0.00	0.00	13.72	65.32	8.27	null	null		null	null		null	null		null	null		2.25E+00	4.99E-173	Up	-7.30E-01	1.65E-07		Unigene53285_All//gi|111379984|gb|AAQ63185.2|//1.00E-96//germin-like protein 3 [Vitis vinifera]	Unigene53285_All//5.00E-82//AT5G39110| germin-like protein, putative	Unigene53285_All//5.00E-83//gi|109873402|gb|DW502377.1|DW502377			nr -
Unigene53286_All	650	2.09	8.34	4.59	0.23	0.90	1.46	0.39	0.13	0.00	1.99E+00	1.46E-11	Up	1.13E+00	3.09E-03		1.97E+00	7.03E-02		2.67E+00	2.14E-03		-1.60E+00	3.10E-01		-8.61E+00	3.04E-02		Unigene53286_All//gi|297803414|ref|XP_002869591.1|//7.00E-59//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315427|gb|EFH45850.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene53286_All//9.00E-60//AT4G26790| GDSL-motif lipase/hydrolase family protein	Unigene53286_All//0.00E+00//gi|48787524|gb|CO090421.1|CO090421			nr +
Unigene5329_All	1499	0.38	1.05	0.46	1.33	1.10	0.84	9.20	5.58	2.68	1.45E+00	8.58E-03		2.67E-01	7.36E-01		-2.70E-01	5.86E-01		-6.56E-01	1.63E-01		-7.22E-01	9.80E-08		-1.78E+00	7.82E-31	Down			Unigene5329_All//1.00E-118//ES834956				
Unigene53291_All	1872	0.17	0.00	0.00	0.00	0.00	0.00	8.15	0.74	6.04	-7.39E+00	3.65E-02		-7.39E+00	4.90E-02		null	null		null	null		-3.47E+00	1.79E-70	Down	-4.32E-01	5.14E-04		Unigene53291_All//gi|124361091|gb|ABN09063.1|//0.00E+00//Major facilitator superfamily [Medicago truncatula]	Unigene53291_All//0.00E+00//AT3G20660| At0CT4 (Arabidopsis thaliana ORGANIC CATION/CARNITINE TRANSPORTER4); carbohydrate transmembrane transporter/ sugar:hydrogen symporter				nr -

Unigene53293_A11	706	0.15	5.45	0.75	3.25	3.22	1.92	0.24	0.24	0.23	5.20E+00	4.34E-19	Up	2.35E+00	5.87E-02		-1.18E-02	9.62E-01		-7.58E-01	7.45E-02		-1.64E-02	1.02E+00		-8.56E-02	9.65E-01		Unigene53293_A11//gi|15223150|ref|NP_172295.1|//3.00E-38//histone H2B family protein [Arabidopsis thaliana] >gi|75337200|sp|Q9SGE3.1|H2B2_ARATH RecName: Full=Histone H2B.2; AltName: Full=HTB8 >gi|6579213|gb|AAF18256.1|AC011438_18 T23G18.3 [Arabidopsis thaliana] >gi|8778831|gb|AAF79830.1|AC026875_10 T6D22.26 [Arabidopsis thaliana] >gi|67633360|gb|AAY78605.1| histone H2B family protein [Arabidopsis thaliana]	Unigene53293_A11//1.00E-31//AT1G08170| histone H2B family protein					nr -
Unigene53294_A11	705	0.00	1.01	0.23	4.10	5.62	1.92	0.54	0.18	0.34	9.97E+00	3.32E-04	Up	7.82E+00	2.38E-01		4.55E-01	1.55E-01		-1.09E+00	2.96E-03		-1.60E+00	1.81E-01		-6.70E-01	5.30E-01		Unigene53294_A11//gi|9955728|emb|CAC05488.1|//1.00E-66//outward rectifying potassium channel [Populus tremula x Populus tremuloides]	Unigene53294_A11//4.00E-53//AT3G02850| SKOR; cyclic nucleotide binding / inward rectifier potassium channel/ outward rectifier potassium channel					nr +
Unigene53295_A11	933	0.00	0.33	0.00	0.11	0.26	0.10	16.99	2.46	27.54	8.35E+00	4.42E-02		null	null		1.27E+00	5.31E-01		-1.42E-01	9.49E-01		-2.79E+00	2.91E-59	Down	6.97E-01	2.79E-13									
Unigene53296_A11	449	10.95	3.16	3.20	0.44	1.00	0.40	0.09	0.00	0.35	-1.79E+00	2.55E-09	Down	-1.77E+00	9.83E-09	Down	1.17E+00	3.47E-01		-1.42E-01	9.34E-01		-6.56E+00	6.56E-01		1.91E+00	3.77E-01		Unigene53296_A11//gi|227204111|dbj|BAH56908.1|//2.00E-26//AT2G46300 [Arabidopsis thaliana]	Unigene53296_A11//1.00E-19//AT2G46300| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, sepal, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage, 4 anthesis; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G01453.1); Has 340 Blast hits to 339 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 2; Plants - 337; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr +
Unigene53297_A11	316	1.32	0.32	0.00	25.70	11.88	6.72	0.27	0.53	0.00	-2.05E+00	1.20E-01		-1.04E+01	1.56E-02		-1.11E+00	5.03E-09	Down	-1.94E+00	1.10E-17	Down	9.84E-01	6.33E-01		-8.06E+00	3.57E-01									
Unigene53298_A11	289	58.66	76.09	97.84	52.06	47.66	59.85	134.01	83.74	51.00	3.75E-01	1.42E-03		7.38E-01	2.81E-12		-1.27E-01	4.48E-01		2.01E-01	1.76E-01		-6.78E-01	2.95E-18		-1.39E+00	5.79E-60	Down		Unigene53298_A11//7.00E-144//gi|21098818|gb|BQ411131.1|BQ411131					
Unigene533_A11	2148	7.09	22.41	5.18	11.50	17.12	12.70	14.35	28.37	33.68	1.66E+00	5.97E-76	Up	-4.52E-01	2.47E-03		5.74E-01	2.12E-12		1.43E-01	2.28E-01		9.83E-01	1.34E-52		1.23E+00	3.43E-91	Up	Unigene533_A11//gi|15231963|ref|NP_187488.1|//0.00E+00//ATSIK; ATP binding / kinase/ protein kinase/ protein tyrosine kinase [Arabidopsis thaliana] >gi|194294570|gb|ACF40324.1| At3g08760 [Arabidopsis thaliana] >gi|222424853|dbj|BAH20378.1| AT3G08760 [Arabidopsis thaliana]	Unigene533_A11//2.00E-154//AT3G08760| ATSIK; ATP binding / kinase/ protein kinase/ protein tyrosine kinase	Unigene533_A11//0.00E+00//TC139503			GO:0004672//GO:0006464//GO:0032559	nr -
Unigene5330_A11	724	9.54	6.93	3.46	10.39	8.47	8.11	9.34	7.16	9.02	-4.61E-01	4.05E-02		-1.46E+00	2.78E-09	Down	-2.95E-01	1.82E-01		-3.57E-01	1.10E-01		-3.84E-01	6.44E-02		-5.02E-02	8.13E-01		Unigene5330_A11//gi|115451397|ref|NP_001049299.1|//2.00E-35//Os03g0201700 [Oryza sativa Japonica Group] >gi|108706711|gb|ABF94506.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547770|dbj|BAF11213.1| Os03g0201700 [Oryza sativa Japonica Group]	Unigene5330_A11//2.00E-29//AT2G18410| unknown protein	Unigene5330_A11//3.00E-136//TC148520				nr +
Unigene53304_A11	488	0.86	0.42	0.11	2.45	2.54	0.28	0.35	0.00	0.33	-1.05E+00	3.65E-01		-2.97E+00	6.45E-02		5.23E-02	9.61E-01		-3.14E+00	6.58E-05	Down	-8.44E+00	1.34E-01		-8.62E-02	9.65E-01		Unigene53304_A11//gi|2739377|gb|AAC14500.1|//9.00E-16//expressed protein [Arabidopsis thaliana]	Unigene53304_A11//2.00E-08//AT2G26520| unknown protein					nr -
Unigene53305_A11	367	0.00	0.00	0.00	0.00	0.19	1.23	36.06	87.58	35.17	null	null		null	null		7.55E+00	6.08E-01		1.03E+01	7.75E-03		1.28E+00	1.45E-42	Up	-3.60E-02	8.12E-01		Unigene53305_A11//gi|118572295|sp|Q8LB19.2|EDL16_ARATH//6.00E-06//RecName: Full=Sugar transporter ERD6-like 16 >gi|17381265|gb|AAL36051.1| AT5g18840/F17K4_90 [Arabidopsis thaliana] >gi|23309019|gb|AAN18269.1| At5g18840/F17K4_90 [Arabidopsis thaliana]	Unigene53305_A11//3.00E-07//AT5G18840| sugar transporter, putative	Unigene53305_A11//4.00E-38//TC168396				nr +
Unigene53306_A11	477	0.88	540.16	13.62	1.67	6.35	15.43	0.09	0.79	2.84	9.27E+00	0.00E+00	Up	3.96E+00	1.64E-26	Up	1.93E+00	3.85E-07	Up	3.21E+00	1.44E-27	Up	3.15E+00	3.41E-02		5.00E+00	1.51E-08	Up	Unigene53306_A11//gi|295393494|gb|ADG03603.1|//2.00E-33//galactinol synthase [Brassica napus]	Unigene53306_A11//2.00E-34//AT2G47180| AtGolS1 (Arabidopsis thaliana galactinol synthase 1); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene53306_A11//0.00E+00//TC138072				nr +
Unigene53309_A11	226	2.32	3.81	2.83	6.61	2.29	1.60	0.37	0.74	1.06	7.19E-01	3.47E-01		2.88E-01	7.25E-01		-1.53E+00	3.58E-03		-2.05E+00	5.54E-04	Down	9.83E-01	6.33E-01		1.50E+00	3.39E-01		Unigene53309_A11//gi|115456255|ref|NP_001051728.1|//2.00E-15//Os03g0821700 [Oryza sativa Japonica Group] >gi|108711802|gb|ABF99597.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550199|dbj|BAF13642.1| Os03g0821700 [Oryza sativa Japonica Group]	Unigene53309_A11//5.00E-16//AT2G46050| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene5331_A11	588	36.93	17.06	18.57	40.92	34.32	43.70	129.86	68.02	72.09	-1.11E+00	2.98E-19	Down	-9.92E-01	2.20E-15		-2.54E-01	2.19E-02		9.50E-02	4.83E-01		-9.33E-01	2.57E-60		-8.49E-01	5.14E-53		Unigene5331_A11//gi|247421835|gb|ACS96445.1|//5.00E-69//S18.A ribosomal protein [Jatropha curcas]	Unigene5331_A11//4.00E-61//AT4G08800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome	Unigene5331_A11//0.00E+00//TC152825		ko03010|Ribosome		nr +
Unigene53310_A11	469	0.33	1.51	0.91	0.42	0.29	1.44	2.43	0.80	0.42	2.18E+00	2.50E-02		1.44E+00	2.53E-01		-5.33E-01	7.48E-01		1.77E+00	6.95E-02		-1.60E+00	7.50E-03		-2.52E+00	1.20E-04	Down	Unigene53310_A11//gi|15227619|ref|NP_180537.1|//4.00E-58//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75100656|sp|O82380.1|PP175_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g29760, chloroplastic; Flags: Precursor	Unigene53310_A11//2.00E-59//AT2G29760| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene53312_A11	3329	0.00	0.00	0.00	0.09	0.01	0.00	24.27	28.24	7.12	null	null		null	null		-3.12E+00	7.56E-02		-6.49E+00	3.99E-02		2.18E-01	5.70E-06		-1.77E+00	8.77E-176	Down	Unigene53312_A11//gi|223452309|gb|ACM89482.1|//1.00E-166//receptor-like kinase [Glycine max]	Unigene53312_A11//9.00E-118//AT5G28680| protein kinase family protein					nr +
Unigene53314_A11	707	0.00	22.65	10.24	0.00	0.00	0.00	0.00	0.00	0.00	1.45E+01	5.27E-92	Up	1.33E+01	1.78E-40	Up	null	null		null	null		null	null		null	null		Unigene53314_A11//gi|196051521|gb|ACG68894.1|//3.00E-60//fructose-biphosphate aldolase [Sesuvium portulacastrum]	Unigene53314_A11//1.00E-61//AT4G26530| fructose-bisphosphate aldolase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene53315_A11	1186	0.18	0.04	0.18	0.25	0.12	0.38	2.32	0.67	7.63	-2.05E+00	3.33E-01		2.51E-02	1.00E+00		-1.12E+00	4.24E-01		5.96E-01	6.40E-01		-1.79E+00	1.26E-06	Down	1.72E+00	2.10E-19	Up	Unigene53315_A11//gi|224143990|ref|XP_002325148.1|//2.00E-65//type-b response regulator [Populus trichocarpa] >gi|222866582|gb|EEF03713.1| type-b response regulator [Populus trichocarpa]	Unigene53315_A11//4.00E-12//AT5G58080| ARR18 (ARABIDOPSIS RESPONSE REGULATOR 18); transcription factor/ two-component response regulator	Unigene53315_A11//1.00E-19//FG551524	ARR-B			nr -
Unigene53316_A11	360	3.49	0.56	0.89	1.52	0.86	0.88	0.94	3.02	3.54	-2.63E+00	3.16E-04	Down	-1.97E+00	4.62E-03		-8.22E-01	3.96E-01		-7.93E-01	4.44E-01		1.68E+00	6.95E-03		1.91E+00	7.76E-04	Up							
Unigene53317_A11	284	10.69	33.36	25.13	44.20	55.53	41.82	70.12	134.51	70.56	1.64E+00	2.87E-15	Up	1.23E+00	1.53E-07	Up	3.29E-01	1.85E-02		-7.98E-02	6.88E-01		9.40E-01	6.47E-31		9.00E-03	9.63E-01		Unigene53317_A11//gi|237682387|gb|ACR10243.1|//3.00E-45//phenylalanine ammonia-lyase [Comarium alpum]	Unigene53317_A11//4.00E-46//AT3G10340| PAL4 (Phenylalanine ammonia-lyase 4); ammonia ligase/ ammonia-lyase/ catalytic	Unigene53317_A11//3.00E-152//TC147618		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00910|Nitrogen metabolism		nr +
Unigene53318_A11	427	0.12	0.71	0.00	0.58	0.48	0.11	4.85	1.57	0.93	2.54E+00	1.51E-01		-6.94E+00	6.22E-01		-2.70E-01	8.23E-01		-2.46E+00	2.23E-01		-1.63E+00	1.21E-04	Down	-2.38E+00	2.25E-07	Down							
Unigene53320_A11	587	0.27	0.17	0.18	1.36	0.35	0.15	2.88	2.85	0.95	-6.32E-01	7.27E-01		-5.60E-01	7.75E-01		-1.95E+00	1.52E-02		-3.14E+00	1.88E-03		-1.66E-02	1.01E+00		-1.60E+00	5.13E-04	Down	Unigene53320_A11//gi|297794133|ref|XP_002864951.1|//2.00E-13//LMBR1 integral membrane family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310786|gb|EFH41210.1| LMBR1 integral membrane family protein [Arabidopsis lyrata subsp. lyrata]	Unigene53320_A11//4.00E-10//AT5G65290| LMBR1 integral membrane family protein	Unigene53320_A11//7.00E-115//BF268607				nr +
Unigene53321_A11	445	5.06	1.37	1.56	3.47	3.40	1.73	0.48	0.00	0.98	-1.89E+00	5.88E-05	Down	-1.70E+00	3.72E-04	Down	-2.74E-02	9.58E-01		-1.01E+00	6.16E-02		-8.89E+00	7.43E-02		1.05E+00	2.98E-01		Unigene53321_A11//gi|42573209|ref|NP_974701.1|//5.00E-11//GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein [Arabidopsis thaliana] >gi|209414522|gb|ACI46501.1| At4g37670 [Arabidopsis thaliana]	Unigene53321_A11//3.00E-12//AT4G37670| GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein	Unigene53321_A11//5.00E-07//CO094373		ko00330|Arginine and proline metabolism		nr +
Unigene53322_A11	694	0.00	0.00	0.15	0.00	0.00	0.00	15.47	29.87	3.90	null	null		7.26E+00	3.97E-01		null	null		null	null		9.49E-01	2.05E-17		-1.99E+00	4.79E-28	Down	Unigene53322_A11//gi|42567516|ref|NP_195882.2|//4.00E-32//disease resistance-responsive family protein [Arabidopsis thaliana]	Unigene53322_A11//4.00E-29//AT4G38700| disease resistance-responsive family protein	Unigene53322_A11//2.00E-32//EX172002				nr -
Unigene53323_A11	704	0.00	0.00	0.00	0.00	0.00	0.13	2.76	1.25	0.57	null	null		null	null		null	null		7.00E+00	4.75E-01		-1.15E+00	6.23E-03		-2.29E+00	1.08E-06	Down	Unigene53323_A11//gi|223452332|gb|ACM89593.1|//7.00E-99//leucine-rich repeat transmembrane protein kinase [Glycine max]	Unigene53323_A11//7.00E-72//AT1G34110| leucine-rich repeat transmembrane protein kinase, putative			ko03410|Base excision repair		nr -
Unigene53325_A11	609	0.00	14.73	6.82	0.00	0.00	0.15	0.00	0.00	0.00	1.38E+01	2.43E-51	Up	1.27E+01	4.83E-23	Up	null	null		7.21E+00	4.75E-01		null	null		null	null		Unigene53325_A11//gi|15824574|gb|AL09401.1|AF307336.1|//8.00E-60//ribosomal protein [Petunia x hybrida]	Unigene53325_A11//9.00E-59//AT1G67430| 60S ribosomal protein L17 (RPL17B)			ko03010|Ribosome		nr +
Unigene53327_A11	940	3.17	0.97	4.76	0.64	0.15	0.38	0.13	0.58	0.64	-1.71E+00	1.28E-05	Down	5.85E-01	5.08E-02		-2.12E+00	3.06E-02		-7.26E-01	4.60E-01		2.10E+00	3.71E-02		2.24E+00	1.67E-02		Unigene53327_A11//gi|124109191|gb|ABM91071.1|//3.00E-90//xyloglucan endotransglycosylase/hydrolase precursor XTH-14 [Populus tremula x Populus tremuloides]	Unigene53327_A11//2.00E-83//AT3G23730| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene53327_A11//6.00E-27//EX171950				nr +

Unigene53330_All	373	0.42	1.09	0.57	0.93	1.57	1.57	32.76	15.91	26.17	1.37E+00	2.73E-01		4.40E-01	7.75E-01		7.47E-01	4.81E-01		7.52E-01	4.67E-01		-1.04E+00	3.00E-12	Down	-3.24E-01	2.37E-02		Unigene53330_All//gi|224144535|ref|XP_002325324.1|//3.00E-21//cytochrome P450 [Populus trichocarpa]>gi|222862199|gb|EEE99705.1|cytochrome P450 [Populus trichocarpa]	Unigene53330_All//5.00E-15//AT3G14640| CYP72A10; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene53330_All//2.00E-145//C0090887		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr -
Unigene53334_All	252	10.59	6.64	3.38	2.77	2.60	2.87	0.17	0.00	0.00	-6.74E-01	7.88E-02		-1.65E+00	1.29E-04	Down	-9.21E-02	8.94E-01		5.12E-02	9.47E-01		-7.39E+00	6.56E-01		-7.39E+00	6.11E-01				Unigene53334_All//2.00E-42//TC162944					
Unigene53335_All	710	0.00	0.00	0.00	0.14	0.00	0.00	5.96	2.41	3.87	null	null		null	null		-7.13E+00	3.99E-01		-7.13E+00	3.99E-01		-1.30E+00	1.91E-06	Down	-6.21E-01	1.46E-02		Unigene53335_All//gi|15226465|ref|NP_179707.1|//5.00E-38//disease resistance-responsive family protein [Arabidopsis thaliana]>gi|91806226|gb|ABE65841.1|disease resistance-responsive family protein [Arabidopsis thaliana]	Unigene53335_All//3.00E-37//AT2G21110| disease resistance-responsive family protein	Unigene53335_All//6.00E-17//TC141794				nr +
Unigene53339_All	1142	0.00	0.49	0.23	0.22	0.03	0.16	0.70	1.28	4.08	8.93E+00	2.18E-03		7.86E+00	8.01E-02		-2.85E+00	1.37E-01		-4.63E-01	7.44E-01		8.65E-01	8.03E-02		2.54E+00	1.65E-16	Up	Unigene53339_All//gi|15231932|ref|NP_187467.1|//1.00E-129//KOB1 (KOBITO) [Arabidopsis thaliana]>gi|23452834|gb|AAN33186.1|elongation defective 1 [Arabidopsis thaliana]	Unigene53339_All//1.00E-112//AT3G08550| KOB1 (KOBITO)	Unigene53339_All//0.00E+00//TC176534				nr +
Unigene5334_All	872	12.12	14.58	16.61	22.34	15.80	14.66	14.35	5.90	6.62	2.67E-01	1.08E-01		4.55E-01	3.07E-03		-5.00E-01	1.45E-05		-6.08E-01	5.32E-07		-1.28E+00	3.73E-17	Down	-1.12E+00	2.41E-14	Down	Unigene5334_All//gi|297800772|ref|XP_002868270.1|//1.00E-64//RNA polymerase RpbP N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]>gi|297314106|gb|EFH44529.1| RNA polymerase RpbP N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene5334_All//2.00E-65//AT4G14660| NRPE7; DNA-directed RNA polymerase	Unigene5334_All//0.00E+00//BE052253		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene53340_All	855	0.00	14.10	10.71	0.12	0.24	0.11	0.00	0.00	0.00	1.38E+01	3.54E-69	Up	1.34E+01	2.42E-51	Up	1.05E+00	6.12E-01		-1.42E-01	9.49E-01		null	null		null	null		Unigene53340_All//gi|6978859|ref|NP_036980.1|//7.00E-54//ferritin heavy chain [Rattus norvegicus]>gi|309233|gb|AAA37612.1| ferritin heavy chain [Mus musculus]>gi|1433203|gb|AAB39890.1|ferritin-H subunit [Rattus norvegicus]>gi|127798856|gb|AAH81845.2|Ferritin, heavy polypeptide 1 [Rattus norvegicus]>gi|149062360|gb|EDM12783.1|rCG47136, isoform CRA_a [Rattus norvegicus]	Unigene53340_All//7.00E-27//AT2G40300| ATFER4 (ferritin 4); binding / ferric iron binding / oxidoreductase/ transition metal ion binding			ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene53348_All	968	0.76	0.00	0.22	2.01	0.46	0.56	0.57	0.82	3.09	-9.56E+00	2.11E-04	Down	-1.78E+00	6.00E-02		-2.12E+00	8.53E-06	Down	-1.84E+00	1.99E-04	Down	5.31E-01	4.67E-01		2.44E+00	2.00E-10	Up	Unigene53348_All//gi|2346972|dbj|BAA21920.1|//2.00E-45//ZPT2-11 [Petunia x hybrida]	Unigene53348_All//3.00E-25//AT5G03510| zinc finger (C2H2 type) family protein	Unigene53348_All//3.00E-13//EX169499	C2H2			nr +
Unigene53350_All	533	5.10	1.90	3.40	1.68	1.49	0.68	1.98	0.86	0.60	-1.42E+00	3.45E-04	Down	-5.88E-01	1.44E-01		-1.79E-01	8.15E-01		-1.31E+00	8.52E-02		-1.20E+00	4.78E-02		-1.73E+00	4.76E-03		Unigene53350_All//gi|15238878|ref|NP_200203.1|//4.00E-50//ribosomal protein L11 methyltransferase-related [Arabidopsis thaliana]>gi|10177254|dbj|BAB10722.1|ribosomal protein L11 methyltransferase-like protein [Arabidopsis thaliana]	Unigene53350_All//8.00E-46//AT5G53920| ribosomal protein L11 methyltransferase-related	Unigene53350_All//2.00E-31//gi|13349944|gb|BG440293.1|BG440293				nr +
Unigene53354_All	513	0.31	192.41	25.54	0.78	4.56	25.44	0.33	0.24	0.93	9.30E+00	0.00E+00	Up	6.38E+00	3.01E-68	Up	2.55E+00	1.16E-07	Up	5.03E+00	2.72E-67	Up	-4.32E-01	7.92E-01		1.50E+00	1.27E-01		Unigene53354_All//gi|42563995|ref|NP_187692.2|//8.00E-08//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]>gi|145651778|gb|ABP88114.1|At3g10810 [Arabidopsis thaliana]				ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene53356_All	581	122.56	81.54	175.51	26.32	36.21	19.90	0.15	1.29	1.44	-5.88E-01	4.95E-21		5.18E-01	5.60E-23		4.60E-01	4.34E-05		-4.04E-01	4.64E-03		3.15E+00	9.54E-04	Up	3.31E+00	2.30E-04	Up	Unigene53356_All//gi|75312318|sp|Q9MA79.1|F16P2_ARATH//3.00E-32//RecName: Full=Fructose-1,6-bisphosphatase, cytosolic; Short=FBPase; AltName: Full=D-fructose-1,6-bisphosphate 1-phosphohydrolase>gi|30984564|gb|AAP42745.1|At1g43670 [Arabidopsis thaliana]	Unigene53356_All//2.00E-33//AT1G43670| fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative	Unigene53356_All//7.00E-118//gi|109854519|gb|DW483498.1|DW483498		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene5336_All	1412	0.04	0.29	0.57	0.21	0.15	1.79	111.21	124.74	676.02	2.95E+00	5.91E-02		3.93E+00	1.25E-03		-5.33E-01	6.78E-01		3.08E+00	2.32E-09	Up	1.66E-01	1.79E-06		2.60E+00	0.00E+00	Up	Unigene5336_All//gi|224556525|ref|XP_002284739.1|//1.00E-150//PREDICTED: similar to MtN19-like protein [Vitis vinifera]	Unigene5336_All//1.00E-130//AT5G61820| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Stress up-regulated Nod 19 (InterPro:IPR011692); Has 27 Blast hits to 27 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene5336_All//0.00E+00//TC142983				nr -
Unigene53362_All	377	0.00	1.88	0.28	0.53	2.28	1.08	1.91	0.22	1.06	1.09E+01	3.32E-04	Up	8.14E+00	3.97E-01		2.11E+00	1.28E-02		1.03E+00	4.28E-01		-3.10E+00	1.40E-03		-8.51E-01	2.39E-01		Unigene53362_All//gi|9954728|gb|AAG09081.1|AC026237_2//4.00E-27//Similar to tRNA-splicing endonuclease positive effector SEN1 [Arabidopsis thaliana]	Unigene53362_All//2.00E-28//AT1G16800| tRNA-splicing endonuclease positive effector-related	Unigene53362_All//6.00E-105//TC138971				nr -
Unigene53364_All	892	0.41	0.57	0.84	1.73	2.97	0.66	2.46	0.33	1.74	4.68E-01	6.11E-01		1.03E+00	2.37E-01		7.80E-01	4.25E-02		-1.40E+00	1.06E-02		-2.91E+00	3.84E-09	Down	-5.01E-01	1.85E-01		Unigene53364_All//gi|15227758|ref|NP_179869.1|//3.00E-54//AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator [Arabidopsis thaliana]>gi|21539880|gb|AAM52876.1|transcription activator [Arabidopsis thaliana]	Unigene53364_All//1.00E-55//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene53364_All//7.00E-156//gi|78324863|gb|DT545137.1|DT545137	GRF			nr +
Unigene53367_All	525	36.08	25.19	5.68	40.71	31.55	22.88	71.59	24.36	16.69	-5.18E-01	4.19E-05		-2.67E+00	3.71E-53	Down	-3.68E-01	1.07E-03		-8.31E-01	1.04E-12		-1.56E+00	1.76E-66	Down	-2.10E+00	2.65E-103	Down	Unigene53367_All//gi|297724497|ref|NP_001174612.1|//1.00E-44//Os06g0159750 [Oryza sativa Japonica Group]>gi|255676736|dbj|BAH93340.1|Os06g0159750 [Oryza sativa Japonica Group]	Unigene53367_All//6.00E-35//AT5G65360| histone H3	Unigene53367_All//0.00E+00//TC157837				nr +
Unigene53368_All	546	1.34	0.37	0.98	5.93	4.23	2.48	1.78	2.37	2.55	-1.85E+00	4.08E-02		-4.60E-01	6.02E-01		-4.89E-01	1.55E-01		-1.26E+00	2.88E-04	Down	4.14E-01	4.51E-01		5.20E-01	2.99E-01		Unigene53368_All//gi|45826061|gb|AAS77675.1|//1.00E-24//resistance protein [Quercus suber]	Unigene53368_All//2.00E-13//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene53368_All//5.00E-91//ES793138				nr +
Unigene53369_All	723	0.00	0.00	0.00	0.07	0.05	0.62	9.24	3.82	1.38	null	null		null	null		-5.34E-01	8.25E-01		3.18E+00	3.78E-02		-1.28E+00	1.90E-09	Down	-2.75E+00	8.14E-26	Down	Unigene53369_All//gi|5262758|emb|CAB45906.1|//1.00E-49//pathogenesis-related protein homolog [Arabidopsis thaliana]>gi|7270050|emb|CAB79865.1|pathogenesis-related protein homolog [Arabidopsis thaliana]	Unigene53369_All//7.00E-51//AT4G31470| pathogenesis-related protein, putative	Unigene53369_All//8.00E-72//gi|164345926|gb|EX164581.1|EX164581		ko04626|Plant-pathogen interaction		nr +
Unigene5337_All	2076	0.23	0.56	0.21	0.74	1.09	0.70	1.71	4.43	7.56	1.31E+00	4.44E-02		-1.44E-01	8.90E-01		5.58E-01	2.09E-01		-9.56E-02	8.64E-01		1.37E+00	4.34E-14	Up	2.14E+00	3.92E-44	Up	Unigene5337_All//gi|42562225|ref|NP_173882.2|//4.00E-47//calcium-binding EF hand family protein [Arabidopsis thaliana]	Unigene5337_All//9.00E-44//AT1G21630| calcium-binding EF hand family protein	Unigene5337_All//0.00E+00//DT050876				nr -
Unigene53370_All	514	0.00	1.77	0.00	0.39	0.34	1.67	2.06	4.88	7.44	1.08E+01	2.62E-05	Up	null	null		-2.11E-01	8.58E-01		2.11E+00	1.44E-02		1.25E+00	6.46E-04	Up	1.86E+00	1.50E-09	Up	Unigene53370_All//gi|15231222|ref|NP_190813.1|//2.00E-33//PUB22 (PLANT U-BOX 22); ubiquitin-protein ligase [Arabidopsis thaliana]>gi|75211122|sp|Q9SVC6.1|PUB22_ARATH RecName: Full=U-box domain-containing protein 22; AltName: Full=Plant U-box protein 22>gi|53749136|gb|AAU90053.1|At3g52450 [Arabidopsis thaliana]>gi|55733745|gb|AAV59269.1|At3g52450 [Arabidopsis thaliana]	Unigene53370_All//1.00E-34//AT3G52450| PUB22 (PLANT U-BOX 22); ubiquitin-protein ligase	Unigene53370_All//7.00E-16//BE054387		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr -
Unigene53371_All	593	0.00	9.06	3.59	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	1.24E-30	Up	1.18E+01	9.77E-12	Up	null	null		null	null		null	null		null	null										
Unigene53372_All	565	0.00	0.63	0.00	0.26	0.06	0.00	41.76	79.89	150.12	9.29E+00	2.46E-02		null	null		-2.12E+00	3.86E-01		-8.05E+00	2.33E-01		9.36E-01	3.81E-36		1.85E+00	2.39E-193	Up	Unigene53372_All//gi|15234371|ref|NP_194533.1|//1.00E-89//nodulin MtN21 family protein [Arabidopsis thaliana]>gi|42573063|ref|NP_974628.1|nodulin MtN21 family protein [Arabidopsis thaliana]>gi|79325295|ref|NP_001031735.1|nodulin MtN21 family protein [Arabidopsis thaliana]>gi|79325300|ref|NP_001031736.1|nodulin MtN21 family protein [Arabidopsis thaliana]>gi|186514305|ref|NP_001119071.1|nodulin MtN21 family protein [Arabidopsis thaliana]>gi|138990061|gb|AAK49952.1|AF370525_1 Medicago nodulin N21-like protein [Arabidopsis thaliana]>gi|4455363|emb|CAB36773.1|Medicago nodulin N21-like protein [Arabidopsis thaliana]>gi|7269658|emb|CAB79606.1|Medicago nodulin N21-like protein [Arabidopsis thaliana]>gi|20148375|gb|AAM10078.1|Medicago nodulin N21-like protein [Arabidopsis thaliana]>gi|222424181|dbj|BAH20049.1|AT4G28040 [Arabidopsis thaliana]	Unigene53372_All//3.00E-36//AT4G28040| nodulin MtN21 family protein					nr +

Unigene53375_All	520	0.00	0.00	0.00	0.00	0.00	0.00	22.28	5.79	19.92	null	null		null	null		null	null		null	null		-1.94E+00	1.90E-28	Down	-1.62E-01	3.17E-01		Unigene53375_All//gi|73624747|gb|AAZ79231.1|//8.00E-24//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene53375_All//3.00E-20//AT4G23990| ATCSLG3: cellulose synthase/ transferase/ transferase, transferring glycosyl groups				nr -
Unigene53378_All	938	0.06	1.78	0.51	0.48	1.80	0.96	0.00	0.22	0.59	5.00E+00	2.47E-08	Up	3.19E+00	3.48E-02		1.91E+00	3.81E-04	Up	1.01E+00	1.96E-01		7.80E+00	7.84E-02		9.22E+00	3.28E-04	Up	Unigene53378_All//gi|297818370|ref|XP_002877068.1|//1.00E-120//rock-N-rollers [Arabidopsis lyrata subsp. lyrata] >gi|297322906|gb|EFH53327.1| rock-N-rollers [Arabidopsis lyrata subsp. lyrata]	Unigene53378_All//3.00E-120//AT3G27730| RCK (ROCK-N-ROLLERS): ATP binding / ATP-dependent helicase/ DNA helicase			ko03040|Spliceosome		nr -
Unigene53386_All	1163	0.00	0.00	0.00	0.00	0.00	24.14	69.97	2.64	null	null		null	null		null	null		null	null		1.54E+00	3.44E-140	Up	-3.19E+00	8.64E-124	Down	Unigene53386_All//gi|297838233|ref|XP_002886998.1|//7.00E-06//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332839|gb|EFH63257.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene53386_All//4.00E-25//ES844801				nr -
Unigene53387_All	795	0.00	0.00	0.00	0.00	0.00	14.68	6.73	13.68	null	null		null	null		null	null		null	null		-1.13E+00	3.47E-13	Down	-1.02E-01	5.54E-01		Unigene53387_All//gi|288559172|sp|B9HBX2.1|U4978_POPTR//2.00E-72//RecName: Full=UPF0497 membrane protein 8	Unigene53387_All//6.00E-49//AT5G06200| integral membrane family protein				nr -
Unigene53339_All	1230	1.66	1.11	1.00	4.62	5.18	2.20	4.88	3.30	3.89	-5.77E-01	2.05E-01		-7.37E-01	1.23E-01		1.66E-01	5.47E-01		-1.07E+00	1.58E-05	Down	-5.66E-01	8.71E-03		-3.29E-01	1.28E-01		Unigene53339_All//gi|145338625|ref|NP_188360.3|//1.00E-149//binding / protein transporter [Arabidopsis thaliana]	Unigene53339_All//1.00E-139//AT3G17340| binding / protein transporter	Unigene53339_All//0.00E+00//gi|78341547|gb|DT561821.1|DT561821				nr +
Unigene53393_All	236	0.44	5.15	4.96	3.38	5.40	2.30	0.72	1.77	1.35	3.54E+00	4.02E-05	Up	3.48E+00	1.09E-04	Up	6.77E-01	2.91E-01		-5.57E-01	4.98E-01		1.31E+00	2.34E-01		9.14E-01	4.52E-01						Unigene53393_All//1.00E-108//gi|164320836|gb|ES829760.1|ES829760				
Unigene53395_All	372	0.42	0.82	0.00	0.00	0.00	0.12	284.60	91.68	162.89	9.54E-01	5.03E-01		-8.72E+00	2.44E-01		null	null		6.92E+00	6.95E-01		-1.63E+00	7.21E-200	Down	-8.05E-01	7.71E-67		Unigene53395_All//gi|225470869|ref|XP_002269732.1|/8.00E-40//PREDICTED: (-)-a-terpineol synthase [Vitis vinifera]	Unigene53395_All//2.00E-33//AT3G25830| ATTPS-CIN (terpene synthase-like sequence-1,8-cineole); (E)-beta-ocimene synthase/ myrcene synthase	Unigene53395_All//0.00E+00//TC132273		ko00902|Monoterpenoid biosynthesis		nr -
Unigene53397_All	546	2.01	0.56	0.68	1.92	0.82	0.00	2.25	0.00	0.15	-1.85E+00	8.98E-03		-1.56E+00	3.05E-02		-1.22E+00	5.85E-02		-1.09E+01	1.47E-06	Down	-1.11E+01	9.98E-09	Down	-3.94E+00	4.86E-07	Down					Unigene53397_All//2.00E-148//ES846811				
Unigene53398_All	507	7.74	1.10	9.98	0.20	0.07	0.00	0.92	0.58	0.86	-2.82E+00	1.36E-12	Down	3.66E-01	2.06E-01		-1.53E+00	5.86E-01		-7.62E+00	3.99E-01		-6.69E-01	5.08E-01		-8.59E-02	9.34E-01		Unigene53398_All//gi|15391731|emb|CAA93316.2|//7.00E-59//nitrite transporter [Cucumis sativus]	Unigene53398_All//2.00E-39//AT1G68570| protoc-dependent oligopeptide transport (POT) family protein					nr -
Unigene53399_All	344	2.28	5.30	2.32	0.14	2.70	2.76	0.00	0.00	0.00	1.22E+00	1.36E-02		2.54E-02	9.94E-01		4.22E+00	1.07E-04	Up	4.25E+00	1.11E-04	Up	null	null		null	null						Unigene53399_All//5.00E-93//gi|78336123|gb|DT556397.1|DT556397				
Unigene53400_All	292	0.00	0.69	0.55	0.68	1.06	0.15	3.48	1.86	0.68	9.44E+00	1.36E-01		9.10E+00	2.38E-01		6.37E-01	6.95E-01		-2.14E+00	3.47E-01		-9.01E-01	1.44E-01		-2.35E+00	5.84E-04	Down					Unigene53400_All//4.00E-139//TC133230				
Unigene53402_All	707	0.00	30.89	12.05	0.00	0.00	0.00	0.00	0.00	0.00	1.49E+01	1.05E-125	Up	1.36E+01	1.03E-47	Up	null	null		null	null		null	null		null	null		Unigene53402_All//sp|Q54F11|HBX3_DICDI//1.00E-06//Homeobox protein 3 OS=Dictyostelium discoideum GN=hbx3 PE=2 SV=1						swissprot -
Unigene53407_All	1127	0.28	10.03	6.80	0.18	0.79	0.72	0.00	0.00	0.00	5.17E+00	2.12E-55	Up	4.61E+00	1.41E-34	Up	2.17E+00	9.20E-03		2.03E+00	2.17E-02		null	null		null	null		Unigene53407_All//gi|29467503|dbj|BAG87190.1|//1.00E-123//expansin [Pyrus communis]	Unigene53407_All//5.00E-111//AT2G40610| ATEXP38 (ARABIDOPSIS THALIANA EXPANSIN A8)	Unigene53407_All//8.00E-73//TC129679				nr +
Unigene53408_All	416	0.00	0.24	0.00	0.00	0.25	0.00	19.31	7.13	12.74	7.93E+00	3.85E-01		null	null		7.96E+00	4.55E-01		null	null		-1.44E+00	2.89E-13	Down	-6.00E-01	6.90E-04		Unigene53408_All//gi|30102554|gb|AAP21195.1|//1.00E-10//At2g16386 [Arabidopsis thaliana]	Unigene53408_All//7.00E-12//AT2G16385| unknown protein					nr +
Unigene53413_All	720	0.00	0.00	0.00	0.00	0.00	0.00	2.29	3.42	0.00	null	null		null	null		null	null		null	null		5.81E-01	1.15E-01		-1.12E+01	3.45E-12	Down	Unigene53413_All//gi|298715057|emb|CBJ27764.1|//3.00E-07//delta protein [Ectocarpus siliculosus]						nr -
Unigene53415_All	767	0.00	0.40	0.00	0.00	0.00	0.00	2.81	15.69	23.06	8.63E+00	4.42E-02		null	null		null	null		null	null		2.48E+00	1.22E-39	Up	3.04E+00	3.51E-73	Up									
Unigene53416_All	431	0.00	7.05	0.74	16.07	12.46	8.80	1.28	1.36	0.00	1.28E+01	2.67E-17	Up	9.53E+00	4.51E-02		-3.66E-01	1.03E-01		-8.68E-01	7.13E-05		9.02E-02	9.27E-01		-1.03E+01	2.80E-04	Down				Unigene53416_All//0.00E+00//gi|73851565|gb|DT460585.1|DT460585				ESTscan -
Unigene53418_All	563	0.19	0.00	0.57	0.71	0.18	0.40	3.08	0.37	1.34	-7.54E+00	3.70E-01		1.61E+00	3.04E-01		-1.95E+00	1.19E-01		-8.19E-01	5.06E-01		-3.05E+00	1.18E-07	Down	-1.20E+00	5.96E-03		Unigene53418_All//gi|212717139|gb|ACJ37411.1|//7.00E-59//receptor-like protein kinase [Glycine max]	Unigene53418_All//1.00E-55//AT4G36180| leucine-rich repeat family protein			ko04626|Plant-pathogen interaction		nr -
Unigene5342_All	1028	36.75	265.47	168.92	80.83	239.57	157.81	12.46	16.87	20.27	2.85E+00	0.00E+00	Up	2.20E+00	0.00E+00	Up	1.57E+00	0.00E+00	Up	9.65E-01	2.79E-118		4.37E-01	2.38E-04		7.02E-01	4.55E-11		Unigene5342_All//gi|115451437|ref|NP_001049319.1|//4.00E-13//Os03g0206100 [Oryza sativa Japonica Group] >gi|26006485|gb|AAN77294.1| Unknown protein [Oryza sativa Japonica Group] >gi|108706757|gb|ABF94552.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547790|dbj|BAF11233.1| Os03g0206100 [Oryza sativa Japonica Group]	Unigene5342_All//1.00E-12//AT5G43150| unknown protein	Unigene5342_All//0.00E+00//TC155753				nr -
Unigene53420_All	481	0.00	0.63	0.00	0.00	0.00	0.19	32.00	15.29	14.33	9.30E+00	4.42E-02		null	null		null	null		7.55E+00	4.75E-01		-1.07E+00	9.66E-16	Down	-1.16E+00	1.74E-18	Down				Unigene53420_All//1.00E-84//gi|62296160|gb|DN779405.1|DN779405				
Unigene53422_All	699	1.05	0.36	0.15	1.50	1.08	1.03	3.02	0.60	0.51	-1.53E+00	7.78E-02		-2.78E+00	1.04E-02		-4.66E-01	5.02E-01		-5.34E-01	4.55E-01		-2.34E+00	4.31E-07	Down	-2.56E+00	4.26E-08	Down	Unigene53422_All//gi|115462631|ref|NP_001054915.1|//2.00E-66//Os05g0210500 [Oryza sativa Japonica Group] >gi|113578466|dbj|BAF16829.1| Os05g0210500 [Oryza sativa Japonica Group]	Unigene53422_All//9.00E-64//AT5G32910| ATIM (TIMELESS)					nr -
Unigene53423_All	992	0.00	42.80	17.18	0.00	0.00	0.00	0.00	0.00	0.00	1.54E+01	3.80E-245	Up	1.41E+01	3.63E-96	Up	null	null		null	null		null	null		null	null		Unigene53423_All//gi|23394354|gb|AAN31467.1|//1.00E-114//ADP/ATP translocase [Phytophthora infestans]	Unigene53423_All//4.00E-70//AT3G08580| AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/ binding	Unigene53423_All//1.00E-09//EV483520				nr +
Unigene53429_All	236	0.00	0.00	0.00	0.00	0.00	0.00	2.15	1.95	0.00	null	null		null	null		null	null		null	null		-1.42E-01	8.76E-01		-1.11E+01	5.54E-04	Down	Unigene53429_All//gi|298714901|emb|CBJ27657.1|//6.00E-38//RAN, Ras superfamily GTPase [Ectocarpus siliculosus]	Unigene53429_All//1.00E-36//AT5G20010| RAN-1; GTP binding / GTPase/ protein binding	Unigene53429_All//4.00E-09//TC143784				nr +
Unigene5343_All	549	38.98	29.53	13.87	75.49	58.08	85.88	78.40	58.70	50.80	-4.00E-01	7.66E-04		-1.49E+00	2.78E-28	Down	-3.78E-01	6.71E-07		1.86E-01	2.19E-02		-4.18E-01	7.24E-09		-6.26E-01	3.73E-18		Unigene5343_All//gi|226528613|ref|NP_001148602.1|//7.00E-24//60S ribosomal protein L15 [Zea mays] >gi|195620698|gb|ACG32179.1| 60S ribosomal protein L15 [Zea mays] >gi|195637452|gb|ACG38194.1| 60S ribosomal protein L15 [Zea mays]	Unigene5343_All//3.00E-22//AT4G16720| 60S ribosomal protein L15 (RPL15A)	Unigene5343_All//0.00E+00//gi|21092926|gb|BQ405239.1|BQ405239		ko03010|Ribosome		nr +
Unigene53430_All	481	0.22	0.21	0.44	1.04	0.36	1.03	0.18	0.70	2.40	-4.65E-02	9.88E-01		1.03E+00	5.91E-01		-1.53E+00	1.45E-01		-3.90E-03	9.87E-01		1.98E+00	1.44E-01		3.77E+00	2.44E-06	Up	Unigene53430_All//gi|297800128|ref|XP_002867948.1|//2.00E-54//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297313784|gb|EFH44207.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene53430_All//2.00E-52//AT4G19220| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene53432_All	389	0.00	0.00	0.00	0.00	0.00	0.00	3.48	2.04	0.41	null	null		null	null		null	null		null	null		-7.69E-01	1.39E-01		-3.09E+00	1.96E-06	Down	Unigene53432_All//gi|159474294|ref|XP_001698264.1|//8.00E-54//heat shock protein 90A [Chlamydomonas reinhardtii] >gi|158276198|gb|EDP01972.1| heat shock protein 90A [Chlamydomonas reinhardtii]	Unigene53432_All//1.00E-53//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene53434_All	420	0.75	1.81	1.27	0.83	1.72	1.18	1.01	0.90	4.36	1.28E+00	1.28E-01		7.63E-01	4.52E-01		1.05E+00	2.40E-01		5.11E-01	6.41E-01		-1.69E-01	8.65E-01		2.12E+00	9.21E-06	Up	Unigene53434_All//gi|115453583|ref|NP_001050392.1|//1.00E-16//Os03g0423200 [Oryza sativa Japonica Group] >gi|113548863|dbj|BAF12306.1| Os03g0423200 [Oryza sativa Japonica Group]	Unigene53434_All//3.00E-16//AT4G18210| ATPUP10; purine transmembrane transporter	Unigene53434_All//1.00E-60//TC169626		ko00510|N-Glycan biosynthesis		nr +
Unigene53438_All	246	0.21	1.65	0.65	2.43	0.42	0.00	0.86	0.51	0.65	2.95E+00	5.91E-02		1.61E+00	5.11E-01		-2.53E+00	1.36E-02		-1.12E+01	7.70E-04	Down	-7.54E-01	6.31E-01		-4.08E-01	7.55E-01										
Unigene5344_All	1264	28.73	464.44	34.25	40.87	73.99	145.85	32.48	199.49	48.44	4.02E+00	0.00E+00	Up	2.54E-01	3.08E-03		8.56E-01	6.64E-62		1.84E+00	0.00E+00	Up	2.62E+00	0.00E+00	Up	5.77E-01	5.37E-22		Unigene5344_All//gi|15219201|ref|NP_178007.1|//1.00E-108//curculin-like (mannose-binding) lectin family protein [Arabidopsis thaliana] >gi|3834308|gb|AAC83024.1| Strong similarity to glycoprotein EP1 gb|L16983 Dauucus carota and a member of S locus glycoprotein family PF|00954. EST gb|AA720110 comes from this gene [Arabidopsis thaliana]	Unigene5344_All//2.00E-109//AT1G78860| curculin-like (mannose-binding) lectin family protein	Unigene5344_All//0.00E+00//TC139116				nr -
Unigene53448_All	243	4.74	4.80	2.85	0.82	1.70	7.06	0.00	0.52	0.00	1.79E-02	9.91E-01		-7.34E-01	2.67E-01		1.05E+00	4.26E-01		3.11E+00	1.54E-06	Up	9.01E+00	2.40E-01		null	null					Unigene53448_All//8.00E-51//gi|78340884|gb|DT561158.1|DT561158				
Unigene53450_All	285	0.00	0.00	0.00	0.35	0.36	0.16	2.37	1.91	40.26	null	null		null	null		5.23E-02	9.66E-01		-1.14E+00	6.76E-01		-3.16E-01	6.74E-01		4.08E+00	3.50E-61	Up				Unigene53450_All//4.00E-28//DR454610				nr -
Unigene53455_All	381	0.00	0.00	0.00	1.31	0.90	0.00	1.66	0.00	0.42	null	null		null	null		-5.33E-01	5.94E-01		-1.04E+01	2.97E-03		-1.07E+01	1.23E-04	Down	-1.99E+00	2.04E-02		Unigene53455_All//gi|147839950|emb|CAN70453.1|//2.00E-07//hypothetical protein [Vitis vinifera]						nr -
Unigene53457_All	309	1.52	0.16	0.52	2.74	0.67	0.15	0.55	0.00	0.00	-3.22E+00	2.73E-02		-1.56E+00	2.04E-01		-2.04E+00	9.04E-03		-4.23E+00	2.18E-04	Down	-9.10E+00	1.34E-01		-9.10E+00	1.08E-01		Unigene53457_All//gi|115455585|ref|NP_001051393.1|//3.00E-21//Os03g0769000 [Oryza sativa Japonica Group] >gi|113549864|dbj|BAF13307.1| Os03g0769000 [Oryza sativa Japonica Group]	Unigene53457_All//1.00E-24//AT5G66600| unknown protein	Unigene53457_All//2.00E-45//TC172096				nr -
Unigene5346_All	2832	0.41	0.93	0.64	0.11	0.15	0.35	4.37	11.25	37.05	1.20E+00	2.69E-03		6.54E-01	2.02E-01		4.68E-01	7.41E-01		1.73E+00	2.14E-02		1.36E+00	2.40E-46	Up	3.08E+00	0.00E+00	Up	Unigene5346_All//gi|15220348|ref|NP_172600.1|//0.00E+00//S-locus lectin protein kinase family protein [Arabidopsis thaliana]	Unigene5346_All//1.00E-120//AT1G11330| S-locus lectin protein kinase family protein	Unigene5346_All//0.00E+00//gi|73861336|gb|DT464075.1|DT464075		ko04626|Plant-pathogen interaction		nr -
Unigene53462_All	275	2.66	0.74	0.00	0.72	0.00	0.00	0.46	1.82	0.14	-1.85E+00	4.08E-02		-1.14E+01	4.13E-04	Down	-9.50E+00	8.41E-02		-9.50E+00	1.33E-01		1.98E+00	5.74E-02		-1.67E+00	4.77E-01										
Unigene53466_All	347	0.00	0.00	0.00	0.00	0.10	0.00	3.41	4.94	0.69	null	null		null	null		6.63E+00	8.29E-01		null	null		5.34E-01	2.44E-01		-2.31E+00	2.04E-04	Down	Unigene53466_All//gi|224144381|ref|XP_002336141.1|//2.00E-09//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222873976|gb|EEF11107.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]		Unigene53466_All//4.00E-50//TC150803		ko02010|ABC transporters	GO:0005773//GO:0006810//GO:0008152//GO:0016628//GO:0031090//GO:0031224//GO:0032559//GO:0042626	nr +

Unigene5347_All	606	7.08	19.15	15.11	1.23	1.31	2.09	2.44	2.97	1.58	1.44E+00	2.37E-15	Up	1.09E+00	5.86E-08	Up	8.40E-02	9.44E-01		7.59E-01	2.30E-01		2.80E-01	5.60E-01		-6.30E-01	1.82E-01		Unigene5347_All//gi|87162922|gb|AB D28717.1|//1.00E-58//Putative thiol-disulphide oxidoreductase DCC [Medicago truncatula]	Unigene5347_All//8.00E-36//AT1G52590| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plastoglobule; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Putative thiol-disulphide oxidoreductase DCC (InterPro:IPR007263); BEST Arabidopsis thaliana protein match is: RNase H domain-containing protein (TAIR:AT1G24090.1); Has 622 Blast hits to 622 proteins in 201 species: Archae - 0; Bacteria - 363; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 223 (source: NCBI BLink).	Unigene5347_All//0.00E+00//TC150772				nr -
Unigene53472_All	814	0.26	0.19	1.05	0.49	0.97	0.39	3.74	0.62	0.69	-4.62E-01	7.58E-01		2.03E+00	2.24E-02		9.91E-01	2.40E-01		-3.34E-01	7.56E-01		-2.60E+00	4.17E-11	Down	-2.45E+00	8.34E-11	Down	Unigene53472_All//gi|9989053|gb|AA G10816.1|AC011808.4//8.00E-72//Unknown protein [Arabidopsis thaliana]	Unigene53472_All//8.00E-74//AT1G16670| protein kinase family protein			ko04626|Plant-pathogen interaction	GO:0004713//GO:0006464//GO:0032559	nr +
Unigene5348_All	960	17.60	62.91	41.49	4.51	5.67	9.97	3.22	4.88	0.83	1.84E+00	1.64E-109	Up	1.24E+00	1.69E-39	Up	3.28E-01	2.31E-01		1.14E+00	1.08E-09	Up	6.01E-01	1.60E-02		-1.95E+00	1.79E-08	Down	Unigene5348_All//gi|87162922|gb|AB D28717.1|//6.00E-68//Putative thiol-disulphide oxidoreductase DCC [Medicago truncatula]	Unigene5348_All//2.00E-43//AT1G52590| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plastoglobule; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Putative thiol-disulphide oxidoreductase DCC (InterPro:IPR007263); BEST Arabidopsis thaliana protein match is: RNase H domain-containing protein (TAIR:AT1G24090.1); Has 622 Blast hits to 622 proteins in 201 species: Archae - 0; Bacteria - 363; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 223 (source: NCBI BLink).	Unigene5348_All//0.00E+00//TC150772				nr +
Unigene53488_All	242	0.00	2.72	1.10	0.21	0.57	1.31	0.00	0.00	0.00	1.14E+01	6.25E-04	Up	1.01E+01	8.00E-02		1.47E+00	6.18E-01		2.67E+00	1.44E-01		null	null		null	null									
Unigene5349_All	735	87.20	114.51	124.90	51.44	34.39	33.61	11.68	28.03	2.11	3.93E-01	3.29E-12		5.18E-01	9.19E-21		-5.81E-01	2.32E-13		-6.14E-01	3.36E-13		1.26E+00	4.99E-27	Up	-2.47E+00	2.73E-29	Down	Unigene5349_All//gi|224128011|ref|XP_002320219.1|//2.00E-47//SAUR family protein [Populus trichocarpa] >gi|222860992|gb|EEE98534.1| SAUR family protein [Populus trichocarpa]	Unigene5349_All//5.00E-33//AT2G46690| auxin-responsive family protein	Unigene5349_All//0.00E+00//TC174243				nr +
Unigene53495_All	289	0.00	0.00	0.00	0.34	0.00	0.31	74.17	51.05	166.38	null	null		null	null		-8.43E+00	3.12E-01		-1.42E-01	9.49E-01		-5.39E-01	3.23E-07		1.17E+00	6.32E-56	Up	Unigene53495_All//gi|40218371|gb|A AR83118.1|//3.00E-25//secretory laccase [Gossypium arboreum]	Unigene53495_All//2.00E-07//AT5G48100| TT10 (TRANSPARENT TESTA 10); copper ion binding / laccase	Unigene53495_All//8.00E-76//TC137114			GO:0005576//GO:0009808//GO:0016682 //GO:0046914	nr +
Unigene53497_All	514	0.00	0.00	0.00	0.00	0.00	0.00	46.23	15.69	9.69	null	null		null	null		null	null		null	null		-1.56E+00	1.95E-42	Down	-2.25E+00	1.22E-71	Down	Unigene53497_All//gi|30725286|gb|A AP37665.1|//1.00E-36//At2g21045 [Arabidopsis thaliana]	Unigene53497_All//6.00E-38//AT2G21045| INVOLVED IN: aging; EXPRESSED IN: hypocotyl, root; CONTAINS InterPro DOMAIN/s: Rhodanese-like (InterPro:IPR001763); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G66170.2); Has 1919 Blast hits to 1917 proteins in 542 species: Archae - 34; Bacteria - 1258; Metazoa - 17; Fungi - 21; Plants - 115; Viruses - 0; Other Eukaryotes - 474 (source: NCBI BLink).				GO:0009536//GO:0016783//GO:0032502	nr +
Unigene53499_All	268	0.39	0.38	0.40	6.69	4.50	1.85	0.79	0.78	1.64	-4.66E-02	9.88E-01		2.53E-02	9.99E-01		-5.73E-01	2.36E-01		-1.85E+00	3.68E-04	Down	-1.66E-02	1.02E+00		1.05E+00	2.98E-01		Unigene53499_All//gi|296279110|gb| ADH04387.1|//1.00E-34//cellulose synthase 6A [Salix miyabeana]	Unigene53499_All//7.00E-33//AT4G39350| CESA2 (CELLULOSE SYNTHASE A2); cellulose synthase/ transferase, transferring glycosyl groups	Unigene53499_All//1.00E-68//TC137289			GO:0003006//GO:0009250//GO:0009832 //GO:0016759//GO:0030865//GO:00312 24//GO:0040007//GO:0043231//GO:004 3234//GO:0045229//GO:0046914	nr -
Unigene53500_All	361	0.00	1.97	2.36	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	3.32E-04	Up	1.12E+01	9.02E-05	Up	null	null		null	null		null	null		null	null									
Unigene53501_All	717	0.00	1.41	8.69	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	7.25E-06	Up	1.31E+01	9.46E-35	Up	null	null		null	null		null	null		null	null		Unigene53501_All//gi|67973220|gb|A AY84147.1|//1.00E-83//glutathione S-transferase [Catharanthus roseus]	Unigene53501_All//3.00E-64//AT2G47730| ATGSTF8 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE PHI 8); glutathione binding / glutathione transferase			ko00480|Glutathione metabolism	GO:0005488//GO:0009755//GO:0016765	nr +
Unigene53502_All	301	0.00	5.22	1.06	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.70E-09	Up	1.01E+01	4.51E-02		null	null		null	null		null	null		null	null									
Unigene53503_All	258	0.00	21.01	7.84	0.00	0.00	0.00	0.00	0.00	0.00	1.44E+01	6.34E-31	Up	1.29E+01	3.79E-11	Up	null	null		null	null		null	null		null	null		Unigene53503_All//sp|Q9XY35|QCR9_D ROME//4.00E-19//Cytochrome b-c1 complex subunit 9 OS=Drosophila melanogaster GN=cx PE=1 SV=1						swissprot +
Unigene53505_All	622	0.00	0.00	0.00	0.80	0.55	0.58	0.41	0.07	2.88	null	null		null	null		-5.33E-01	5.94E-01		-4.63E-01	6.59E-01		-2.60E+00	1.44E-01		2.82E+00	1.60E-07	Up	Unigene53505_All//gi|22328738|ref| NP_680717.1|//3.00E-70//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene53505_All//8.00E-68//AT4G16835| pentatricopeptide (PPR) repeat-containing protein				GO:0043231	nr +
Unigene53508_All	263	0.00	0.00	0.00	0.00	0.00	0.00	3.54	2.54	0.00	null	null		null	null		null	null		null	null		-4.76E-01	4.76E-01		-1.18E+01	5.47E-07	Down	Unigene53508_All//gi|180867805|ref| NP_022529.2|//2.00E-06//40S ribosomal protein S2 [Mus musculus] >gi|78126159|ref|NP_114026.3| 40S ribosomal protein S2 [Rattus norvegicus] >gi|133914|sp|P27952.1|RS2_RAT RecName: Full=40S ribosomal protein S2 >gi|46397787|sp|P25444.3|RS2_MOUSE RecName: Full=40S ribosomal protein S2; AltName: Full=40S ribosomal protein S4; AltName: Full=Protein LLRep3 >gi|10179940|gb|AAG13953.1|AF28355 9_1 ribosomal protein S2 [Mus musculus] >gi|57718|emb|CAA40679.1| ribosomal protein S2 [Rattus rattus] >gi|12805427|gb|AAH02186.1| Ribosomal protein S2 [Mus musculus] >gi|86921737|gb|AAH87956.1| Ribosomal protein S2 [Mus musculus] >gi|61402217|gb|AAH91730.1| Ribosomal protein S2 [Mus musculus]						GO:0005198//GO:0005515//GO:0005634 //GO:0006413//GO:0015935	nr -
Unigene53509_All	262	0.00	9.86	3.46	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	1.06E-14	Up	1.18E+01	4.71E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene5351_All	765	3.69	4.04	1.60	3.06	3.78	3.19	6.25	2.84	4.53	1.30E-01	7.13E-01		-1.21E+00	2.43E-03		3.05E-01	4.60E-01		5.89E-02	9.09E-01		-1.14E+00	5.97E-06	Down	-4.63E-01	5.40E-02		Unigene5351_All//gi|124359981|gb|A BN07997.1|//5.00E-07//contains similarity to reverse trancriptase , related [Medicago truncatula]		Unigene5351_All//0.00E+00//TC177975				nr -
Unigene53516_All	496	0.00	0.00	0.00	0.00	0.00	0.00	2.30	2.78	0.00	null	null		null	null		null	null		null	null		2.73E-01	6.39E-01		-1.12E+01	1.64E-08	Down								ESTscan -
Unigene53519_All	342	0.76	0.30	2.02	3.93	10.67	6.47	0.25	0.24	0.47	-1.37E+00	3.83E-01		1.40E+00	1.39E-01		1.44E+00	7.36E-06	Up	7.18E-01	1.06E-01		-1.70E-02	1.01E+00		9.14E-01	6.24E-01		Unigene53519_All//gi|1621463|gb|AA B17192.1|//1.00E-11//laccase [Liriodendron tulipifera]	Unigene53519_All//1.00E-12//AT5G60020| LAC17 (laccase 17); laccase				GO:0005576//GO:0009808//GO:0016682 //GO:0046914	nr +
Unigene53523_All	210	0.00	14.96	8.62	0.24	0.00	0.00	0.00	0.00	0.00	1.39E+01	7.07E-18	Up	1.31E+01	5.69E-10	Up	-7.89E+00	5.55E-01		-7.89E+00	6.34E-01		null	null		null	null		Unigene53523_All//gi|300176061|emb| CBK23372.2|//3.00E-21//Ribosomal protein L37ae [Blastocystis hominis]	Unigene53523_All//5.00E-13//AT3G10950| 60S ribosomal protein L37a (RPL37aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene5353_All	723	21.64	21.38	16.50	21.91	22.53	20.18	55.85	31.62	24.30	-1.76E-02	9.22E-01		-3.91E-01	8.44E-03		4.01E-02	8.16E-01		-1.19E-01	4.76E-01		-8.21E-01	3.97E-26		-1.20E+00	1.01E-49	Down	Unigene5353_All//gi|115489068|ref| NP_001067021.1|//1.00E-25//Os12g0561000 [Oryza sativa Japonica Group] >gi|48428177|sp|Q9SXX7.3|COX5C_ORY SJ RecName: Full=Cytochrome c oxidase subunit 5C; AltName: Full=Cytochrome c oxidase polypeptide Vc >gi|4850330|dbj|BAA77682.1| cytochrome c oxidase subunit 5c [Oryza sativa Japonica Group] >gi|113649528|dbj|BAF30040.1| Os12g0561000 [Oryza sativa Japonica Group]	Unigene5353_All//2.00E-25//AT5G61310| cytochrome c oxidase subunit Vc, putative / COX5C, putative	Unigene5353_All//4.00E-172//gi|164248137|gb|EX171920.1|EX171920				nr -
Unigene53538_All	851	0.37	0.71	0.00	0.94	0.77	0.32	1.69	0.44	0.94	9.54E-01	3.14E-01		-8.53E+00	4.89E-02		-2.85E-01	7.21E-01		-1.56E+00	6.26E-02		-1.93E+00	3.78E-04	Down	-8.51E-01	7.34E-02		Unigene53538_All//gi|115472083|ref |NP_001059640.1|//5.00E-23//Os07g0481000 [Oryza sativa Japonica Group] >gi|113611176|dbj|BAF21554.1| Os07g0481000 [Oryza sativa Japonica Group]	Unigene53538_All//9.00E-16//AT1G70150| zinc ion binding	Unigene53538_All//0.00E+00//TC178723				nr -
Unigene53542_All	370	0.00	3.42	4.46	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.86E-07	Up	1.21E+01	4.30E-09	Up	null	null		null	null		null	null		null	null		Unigene53542_All//sp|Q54IX19|Y0124_ DICDI//4.00E-06//Probable inactive serine/threonine-protein kinase DDB_G0278909 OS=Dictyostelium discoideum GN=DDB_G0278909 PE=4 SV=1						swissprot +
Unigene53544_All	293	0.89	2.59	0.55	3.57	0.47	0.31	2.02	0.29	1.09	1.54E+00	7.40E-02		-7.12E-01	6.22E-01		-2.93E+00	1.21E-04	Down	-3.53E+00	9.34E-05	Down	-2.82E+00	7.17E-03		-8.93E-01	2.71E-01				Unigene53544_All//1.00E-77//DW488223				

Unigene53548_All	268	12.49	0.95	4.37	0.19	0.13	1.85	0.00	0.00	0.00	-3.72E+00	8.32E-14	Down	-1.52E+00	4.63E-05	Down	-5.33E-01	8.25E-01		3.32E+00	2.31E-02		null	null		null	null		Unigene53548_All//gi|225427826|ref|XP_002275947.1|/1.00E-08//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297744702|emb|CBI37964.3| unnamed protein product [Vitis vinifera]	Unigene53548_All//9.00E-07//AT4G38840| auxin-responsive protein, putative					nr +
Unigene53549_All	580	0.63	10.40	1.47	0.94	0.48	0.39	2.11	2.31	8.38	4.04E+00	1.07E-25	Up	1.22E+00	1.38E-01		-9.92E-01	3.13E-01		-1.28E+00	2.24E-01		1.25E-01	8.14E-01		1.99E+00	5.71E-13	Up	Unigene53549_All//gi|223452329|gb|ACM89492.1|/3.00E-70//protein kinase [Glycine max]	Unigene53549_All//2.00E-71//AT1G11330| S-locus lectin protein kinase family protein	Unigene53549_All//2.00E-34//C0081718		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene53552_All	228	1.15	8.89	8.17	8.52	27.64	65.96	2.78	9.53	39.14	2.95E+00	4.86E-07	Up	2.83E+00	5.06E-06	Up	1.70E+00	2.94E-12	Up	2.95E+00	9.44E-52	Up	1.78E+00	2.47E-05	Up	3.81E+00	2.18E-45	Up	Unigene53552_All//gi|225446289|ref|XP_002267226.1|/3.00E-10//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296090309|emb|CBI40128.3| unnamed protein product [Vitis vinifera]	Unigene53552_All//8.00E-06//AT2G16810| F-box family protein (FBX8)					nr +
Unigene53553_All	303	0.00	0.67	2.46	0.00	0.00	0.00	0.00	0.00	0.00	9.39E+00	1.36E-01		1.13E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene53553_All//sp|Q9VVT2|INDY1_DROME//2.00E-36//Protein I'm not dead yet OS=Drosophila melanogaster GN=Indy PE=1 SV=2							swissprot -
Unigene5356_All	1906	1.40	0.96	0.61	4.29	3.70	1.47	1.22	0.53	6.67	-5.49E-01	1.54E-01		-1.19E+00	3.88E-03		-2.11E-01	3.42E-01		-1.54E+00	4.16E-13	Down	-1.21E+00	1.42E-03		2.45E+00	4.76E-42	Up	Unigene5356_All//gi|110739125|dbj|BAF01479.1|/1.00E-116//protein kinase like protein [Arabidopsis thaliana]	Unigene5356_All//2.00E-108//AT3G46610| protein kinase family protein	Unigene5356_All//0.00E+00//gi|78324412|gb|DT544686.1|DT544686				nr +
Unigene53568_All	402	0.00	0.38	0.26	3.10	1.46	2.13	1.89	2.91	6.84	8.56E+00	2.35E-01		8.05E+00	3.97E-01		-1.09E+00	6.06E-02		-5.37E-01	3.94E-01		6.21E-01	2.81E-01		1.85E+00	4.44E-07	Up			Unigene53568_All//8.00E-15//TC171388					
Unigene5357_All	832	7.17	15.83	20.54	4.31	3.44	7.22	7.11	2.06	2.87	1.14E+00	2.09E-12	Up	1.52E+00	2.21E-23	Up	-3.28E-01	3.33E-01		7.44E-01	1.89E-03		-1.79E+00	2.20E-13	Down	-1.31E+00	4.51E-09	Down	Unigene5357_All//gi|51872289|gb|AAU12248.1|/3.00E-79//myb family transcription factor 2/fiber factor 1 [Gossypium arboreum] >gi|62869605|gb|AAY17953.1| myb family transcription factor 2 [Gossypium hirsutum]	Unigene5357_All//4.00E-27//AT4G01680| MYB55 (myb domain protein 55); DNA binding / transcription factor	Unigene5357_All//0.00E+00//TC154488	MYB			nr -
Unigene53571_All	478	0.00	0.00	0.00	0.00	0.00	2.74	2.10	0.33	null	null			null	null		null	null		null	null		-3.86E-01	4.87E-01		-3.04E+00	3.54E-06	Down	Unigene53571_All//gi|452596|dbj|BAA04844.1|/2.00E-06//ORF [Lilium longiflorum]						nr +
Unigene53572_All	311	0.00	0.00	0.00	0.32	0.00	0.15	18.22	45.02	124.90	null	null		null	null		-8.32E+00	3.12E-01		-1.14E+00	6.76E-01		1.31E+00	1.51E-19	Up	2.78E+00	5.09E-146	Up	Unigene53572_All//gi|297838233|ref|XP_002886998.1|/6.00E-09//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297323839|gb|EFH63257.1| expressed protein [Arabidopsis lyrata subsp. lyrata]				ko03040|Spliceosome	GO:0003824//GO:0005488//GO:0009058//GO:0043229//GO:0044237	nr +
Unigene53573_All	258	0.81	0.00	0.83	2.32	0.53	1.40	1.97	0.00	0.46	-9.66E+00	1.22E-01		2.54E-02	1.00E+00		-2.12E+00	3.06E-02		-7.26E-01	4.60E-01		-1.09E+01	8.89E-04	Down	-2.09E+00	3.64E-02		Unigene53573_All//gi|98961077|gb|ABF59022.1|/5.00E-07//At5g63150 [Arabidopsis thaliana]	Unigene53573_All//7.00E-05//AT5G63150| unknown protein	Unigene53573_All//9.00E-137//TC139588				nr +
Unigene53574_All	353	0.59	0.43	0.00	0.00	1.37	1.79	0.00	0.36	0.79	-4.61E-01	7.58E-01		-9.21E+00	1.45E-01		1.04E+01	5.07E-03		1.08E+01	7.60E-04	Up	8.47E+00	2.40E-01		9.63E+00	2.43E-02		Unigene53574_All//gi|297852428|ref|XP_002894095.1|/3.00E-69//C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297339937|gb|EFH70354.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene53574_All//4.00E-44//AT1G48090| phosphoinositide binding	Unigene53574_All//1.00E-37//TC135739			GO:0033036	nr +
Unigene53577_All	453	0.00	0.22	0.47	0.22	0.91	1.00	0.47	0.18	2.64	7.81E+00	3.85E-01		8.88E+00	1.40E-01		2.05E+00	1.47E-01		2.18E+00	1.03E-01		-1.34E+00	4.29E-01		2.50E+00	1.03E-04	Up			Unigene53577_All//5.00E-07//ES822680					
Unigene53583_All	222	0.47	0.68	0.72	1.35	1.24	1.22	0.19	0.38	3.77	5.39E-01	7.79E-01		6.10E-01	7.48E-01		-1.18E-01	9.00E-01		-1.41E-01	9.20E-01		9.83E-01	7.31E-01		4.31E+00	4.10E-05	Up								
Unigene53588_All	223	0.23	4.54	3.34	2.90	2.78	3.44	0.95	0.00	0.18	4.28E+00	7.16E-05	Up	3.83E+00	2.23E-03		-6.32E-02	9.25E-01		2.46E-01	7.57E-01		-9.89E+00	7.43E-02		-2.41E+00	1.95E-01				Unigene53588_All//6.00E-39//EV484468					
Unigene5359_All	635	9.39	20.43	15.01	12.39	37.85	20.77	1.13	2.57	1.25	1.12E+00	7.21E-12	Up	6.76E-01	4.49E-04		1.61E+00	9.10E-43	Up	7.45E-01	9.64E-07		1.18E+00	1.17E-02		1.49E-01	8.23E-01		Unigene5359_All//gi|8778830|gb|AAF79829.1|AC026875_9//1.00E-08//TG022.27 [Arabidopsis thaliana]	Unigene5359_All//3.00E-08//AT1G08180| unknown protein	Unigene5359_All//1.00E-135//BM511997				nr +
Unigene53590_All	285	2.75	0.36	1.87	6.47	2.05	2.22	5.64	2.93	2.10	-2.95E+00	3.66E-03		-5.60E-01	4.96E-01		-1.65E+00	4.01E-04	Down	-1.54E+00	1.84E-03		-9.43E-01	4.30E-02		-1.43E+00	2.13E-03				Unigene53590_All//1.00E-22//ES821095					
Unigene53591_All	244	0.21	3.53	1.09	0.41	0.42	0.00	0.35	0.69	0.82	4.01E+00	4.20E-04	Up	2.35E+00	2.39E-01		5.24E-02	9.66E-01		-8.67E+00	3.98E-01		9.83E-01	6.33E-01		1.24E+00	4.68E-01									
Unigene53593_All	311	19.18	0.65	13.18	7.05	1.77	1.74	0.00	0.27	0.00	-4.88E+00	7.17E-29	Down	-5.41E-01	3.42E-02		-1.98E+00	5.14E-06	Down	-2.02E+00	1.89E-05	Down	8.07E+00	4.00E-01		null	null				Unigene53593_All//4.00E-07//TC173304					
Unigene53594_All	330	3.49	2.15	0.48	1.36	1.77	2.60	1.54	1.27	0.36	-6.98E-01	2.66E-01		-2.85E+00	6.02E-04	Down	3.85E-01	7.32E-01		9.37E-01	2.38E-01		-2.80E-01	7.49E-01		-2.09E+00	3.64E-02									
Unigene53596_All	286	0.00	0.35	0.00	0.00	0.00	19.90	46.57	96.45	96.25	8.47E+00	3.85E-01		null	null		null	null		1.43E+01	1.83E-34	Up	1.05E+00	6.09E-27	Up	1.05E+00	2.06E-27	Up	Unigene53596_All//gi|3901018|emb|CAA10235.1|/3.00E-16//stress and pathogenesis-related protein [Fagus sylvatica]		Unigene53596_All//7.00E-101//CD486122			GO:0050896	nr -
Unigene53599_All	654	0.00	0.08	0.00	0.69	0.11	0.14	1.87	1.73	0.24	6.28E+00	6.15E-01		null	null		-2.70E+00	3.24E-02		-2.31E+00	7.80E-02		-1.20E-01	8.28E-01		-2.94E+00	1.14E-05	Down								
Unigene5360_All	1094	1.43	0.46	0.00	5.28	5.07	2.06	2.05	5.62	8.16	-1.63E+00	3.58E-03		-1.05E+01	1.42E-08	Down	-5.97E-02	8.25E-01		-1.36E+00	7.08E-08	Down	1.46E+00	1.72E-10	Up	1.99E+00	3.05E-23	Up	Unigene5360_All//gi|255555449|ref|XP_002518761.1|/1.00E-21//conserved hypothetical protein [Ricinus communis] >gi|223542142|gb|EEF43686.1| conserved hypothetical protein [Ricinus communis]	Unigene5360_All//4.00E-05//AT5G42900| unknown protein	Unigene5360_All//0.00E+00//gi|73852272|gb|DT461292.1|DT461292				nr -
Unigene53602_All	470	0.78	4.53	1.47	0.00	0.00	0.00	0.00	0.00	0.00	2.54E+00	2.15E-06	Up	9.19E-01	3.11E-01		null	null		null	null		null	null		null	null		Unigene53602_All//gi|255555833|ref|XP_002518952.1|/2.00E-08//transcription factor, putative [Ricinus communis] >gi|223541939|gb|EEF43485.1| transcription factor, putative [Ricinus communis]		Unigene53602_All//1.00E-29//TC173056				nr +
Unigene5361_All	1376	0.27	0.33	0.23	0.72	0.83	0.56	0.89	1.64	3.53	3.16E-01	7.44E-01		-1.97E-01	8.66E-01		1.90E-01	8.14E-01		-3.76E-01	6.31E-01		8.80E-01	2.08E-02		1.99E+00	5.71E-13	Up	Unigene5361_All//gi|88196729|gb|ABD43007.1|/3.00E-12//At4g33980 [Arabidopsis thaliana]	Unigene5361_All//3.00E-15//AT5G42900| unknown protein	Unigene5361_All//0.00E+00//gi|73852272|gb|DT461292.1|DT461292				nr +
Unigene53612_All	277	0.00	0.55	3.46	0.90	1.12	0.65	0.31	0.60	0.29	9.10E+00	2.35E-01		1.18E+01	2.46E-05	Up	3.15E-01	8.38E-01		-4.63E-01	7.44E-01		9.83E-01	6.33E-01		-8.62E-02	9.71E-01				Unigene53612_All//3.00E-07//TC145360					
Unigene53614_All	237	114.80	125.07	134.36	102.57	89.79	109.57	86.70	132.09	43.03	1.24E-01	2.63E-01		2.27E-01	2.84E-02		-1.92E-01	9.95E-02		9.53E-02	4.78E-01		6.07E-01	2.15E-12		-1.01E+00	1.07E-19	Down			Unigene53614_All//4.00E-102//TC142609					
Unigene53615_All	497	0.32	113.88	91.29	0.00	0.28	0.36	0.09	0.00	0.40	8.49E+00	0.00E+00	Up	8.18E+00	9.60E-251	Up	8.11E+00	3.18E-01		8.51E+00	1.94E-01		-6.41E+00	6.56E-01		2.24E+00	2.49E-01		Unigene53615_All//gi|166165082|gb|ABB33901.1|/4.00E-54//cytochrome oxidase subunit 1 [Globba sessiliflora]	Unigene53615_All//1.00E-48//ATMG01360| cytochrome c oxidase subunit I			ko00190|Oxidative phosphorylation	GO:0005506//GO:0015002//GO:0019866//GO:0031224//GO:0043231//GO:0045333//GO:0051234	nr +
Unigene53618_All	215	59.38	27.34	36.66	44.25	52.53	49.36	83.77	41.02	36.13	-1.12E+00	1.02E-11	Down	-6.96E-01	2.08E-05		2.48E-01	1.71E-01		1.58E-01	4.53E-01		-1.03E+00	2.30E-17	Down	-1.21E+00	4.86E-23	Down	Unigene53618_All//gi|225435480|ref|XP_002285503.1|/7.00E-34//PREDICTED: similar to ADP,ATP carrier protein, mitochondrial [Vitis vinifera]	Unigene53618_All//1.00E-33//AT3G08580| AAC1 (ADP/ATP CARRIER 1); ATP:ADP antiporter/ binding	Unigene53618_All//4.00E-111//TC139835			GO:0006810//GO:0019866//GO:0031224//GO:0043231	nr -
Unigene5362_All	1013	0.72	0.00	0.00	2.26	1.12	0.85	0.50	0.78	2.52	-9.50E+00	2.11E-04	Down	-9.50E+00	4.13E-04	Down	-1.01E+00	1.11E-02		-1.42E+00	9.93E-04	Down	6.46E-01	3.83E-01		2.33E+00	1.45E-08	Up	Unigene5362_All//gi|255555449|ref|XP_002518761.1|/8.00E-20//conserved hypothetical protein [Ricinus communis] >gi|223542142|gb|EEF43686.1| conserved hypothetical protein [Ricinus communis]	Unigene5362_All//7.00E-05//AT5G42900| unknown protein	Unigene5362_All//0.00E+00//gi|73852272|gb|DT461292.1|DT461292				nr -
Unigene53624_All	438	5.73	16.31	5.11	4.44	7.31	6.19	65.74	82.06	492.80	1.51E+00	2.02E-10	Up	-1.67E-01	6.79E-01		7.21E-01	3.60E-02		4.80E-01	2.34E-01		3.20E-01	6.59E-05		2.91E+00	0.00E+00	Up	Unigene53624_All//gi|11132838|sp|O64967.1|HMGR2_GOSHI//2.00E-75//RecName: Full=3-hydroxy-3-methylglutaryl-coenzyme A reductase 2; Short=HMG-CoA reductase 2 >gi|2935300|gb|AAC05089.1| 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 [Gossypium hirsutum]	Unigene53624_All//5.00E-71//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene53624_All//0.00E+00//TC177648		ko00900|Terpenoid backbone biosynthesis	GO:0000166//GO:0005740//GO:0006720//GO:0006732//GO:0009526//GO:0016616//GO:0031090//GO:0031224//GO:0048037	nr -
Unigene53625_All	347	0.75	2.77	0.31	3.73	0.79	1.04	0.61	0.48	1.03	1.88E+00	1.53E-02		-1.30E+00	4.36E-01		-2.23E+00	2.69E-04	Down	-1.84E+00	3.54E-03		-3.39E-01	8.11E-01		7.62E-01	4.99E-01		Unigene53625_All//gi|297830210|ref|XP_002882987.1|/2.00E-17//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297328827|gb|EFH59246.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene53625_All//4.00E-16//AT3G16230| RNA binding / catalytic	Unigene53625_All//8.00E-21//C0090169			GO:0043231//GO:0044260	nr -
Unigene53629_All	525	1.59	0.87	0.00	1.71	0.33	0.60	1.29	0.32	0.83	-8.76E-01	2.47E-01		-1.06E+01	1.19E-04	Down	-2.38E+00	2.29E-03		-1.50E+00	5.09E-02		-2.02E+00	1.98E-02		-6.26E-01	4.03E-01		Unigene53629_All//gi|104294990|gb|ABF72006.1|/7.00E-31//leucine-rich repeat-containing protein kinase family protein [Musa acuminata]	Unigene53629_All//2.00E-24//AT3G25790| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0016020//GO:0016772	nr -
Unigene53635_All	462	0.91	0.00	0.35	0.22	0.89	0.20	2.84	0.81	0.43	-9.82E+00	1.05E-02		-1.39E+00	2.80E-01		2.05E+00	1.47E-01		-1.41E-01	9.49E-01		-1.80E+00	1.43E-03		-2.72E+00	1.32E-05	Down								
Unigene53638_All	257	0.00	0.00	0.00	2.91	0.80	0.00	0.82	0.33	0.00	null	null		null	null		-1.85E+00	2.53E-02		-1.15E+01	9.80E-05	Down	-1.34E+00	4.29E-01		-9.68E+00	5.79E-02									
Unigene53640_All	242	78.27	98.41	104.74	150.68	177.44	159.94	100.28	145.94	48.07	3.30E-01	3.59E-03		4.20E-01	1.75E-04		2.36E-01	3.04E-03		8.60E-02	4.14E-01		5.41E-01	1.96E-11		-1.06E+00	6.07E-25	Down	Unigene53640_All//gi|33415266|gb|AAQ18141.1|/1.00E-19//poly(A)-binding protein C-terminal interacting protein 6 [Cucumis sativus]	Unigene53640_All//7.00E-10//AT2G41430| EBD15 (EARLY RESPONSIVE TO DEHYDRATION 15); protein binding	Unigene53640_All//1.00E-129//TC174898				nr -
Unigene53644_All	732	0.00	7.06	2.26	0.14	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.81E-29	Up	1.11E+01	4.30E-09	Up	-7.09E+00	3.12E-01		-7.09E+00	3.98E-01		null	null		null	null		Unigene53644_All//gi|301108920|ref|XP_002903541.1|/4.00E-15//conserved hypothetical protein [Phytophthora infestans T30-4] >gi|262097265|gb|EEY55317.1| conserved hypothetical protein [Phytophthora infestans T30-4]						nr -
Unigene53646_All	386	879.97	219.87	546.02	520.60	327.76	226.17	91.68	66.59	53.15	-2.00E+00	0.00E+00	Down	-6.89E-01	3.53E-125		-6.68E-01	4.66E-89		-1.20E+00	7.09E-212	Down	-4.61E-01	9.01E-09		-7.87E-01	4.43E-22		Unigene53646_All//gi|225425740|ref|XP_002276336.1|/4.00E-16//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene53646_All//1.00E-06//AT1G69760| unknown protein	Unigene53646_All//2.00E-169//TC150717				nr +
Unigene53647_All	407	0.00	0.00	0.00	0.00	0.00	0.00	3.22	1.23	0.20	null	null		null	null		null	null		null	null		-1.39E+00	1.04E-02		-4.04E+00	1.35E-07	Down	Unigene53647_All//gi|255078398|ref|XP_002502779.1|/4.00E-27//cysteine endopeptidase [Micromonas sp. RCC299] >gi|226518045|gb|ACO64037.1| cysteine endopeptidase [Micromonas sp. RCC299]	Unigene53647_All//5.00E-25//AT3G19390| cysteine proteinase, putative / thiol protease, putative				GO:0008152//GO:0070011	nr -
Unigene53651_All	286	0.00	0.00	0.00	8.19	2.77	0.32	0.30	0.15	0.42	null	null		null	null		-1.56E+00	1.03E-04	Down	-4.70E+00	3.40E-12	Down	-1.02E+00	7.24E-01		4.99E-01	8.07E-01									ESTscan -
Unigene53652_All	313	4.51	0.65	2.38	0.32	0.00	0.29	0.00	0.00	0.00	-2.80E+00	6.22E-05	Down	-9.22E-01	1.21E-01		-8.31E+00	3.12E-01		-1.41E-01	9.49E-01		null	null		null	null		Unigene53652_All//gi|82697971|gb|ABB89020.1|/2.00E-18//CXE carboxylesterase [Actinidia deliciosa]	Unigene53652_All//2.00E-18//AT5G23530| AtCXE18 (Arabidopsis thaliana carboxyesterase 18); carboxylesterase	Unigene53652_All//2.00E-169//TC154014			GO:0000904	nr +
Unigene53656_All	558	0.00	0.00	0.00	0.54	0.00	0.00	0.30	0.60	3.43	null	null		null	null		-9.07E+00	2.01E-02		-9.07E+00	3.99E-02		9.83E-01	4.23E-01		3.50E+00	1.45E-09	Up								
Unigene53664_All	500	0.00	4.56	2.34	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.63E-13	Up	1.12E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene53664_All//sp|Q6DBU8|LIPH_DANRE//7.00E-17//Lipase member H OS=Danio rerio GN=liph PE=2 SV=1						swissprot -
Unigene53667_All	394	14.34	36.65	29.19	27.69	25.43	45.74	47.65	38.72	28.31	1.35E+00	2.20E-17	Up	1.03E+00	6.63E-09	Up	-1.23E-01	5.44E-01		7.24E-01	1.41E-08		-2.99E-01	1.04E-02		-7.51E-01	2.84E-11		Unigene53667_All//gi|407938|gb|AAA81889.1|/1.00E-26//epoxide hydrolase [Solanum tuberosum]	Unigene53667_All//2.00E-25//AT3G26740| ATSEH (Arabidopsis thaliana soluble epoxide hydrolase); epoxide hydrolase	Unigene53667_All//8.00E-123//TC139490			GO:0006950//GO:0009725//GO:0016740//GO:0016803	nr -

Unigene5367_All	878	0.95	0.23	0.00	1.30	1.10	1.23	2.99	1.67	2.63	-2.05E+00	1.68E-02		-9.90E+00	1.19E-04	Down	-2.49E-01	7.04E-01		-8.00E-02	9.09E-01		-8.42E-01	1.56E-02		-1.82E-01	6.10E-01		Unigene5367_All//gi|297811331|ref|XP_002873549.1|//1.00E-92//mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319386|gb|EFH49808.1| mechanosensitive ion channel domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene5367_All//2.00E-67//AT5G12080| MSL10 (MECHANOSENSITIVE CHANNEL OF SMALL CONDUCTANCE-LIKE 10); mechanically-gated ion channel	Unigene5367_All//1.00E-111//gi|48881356|gb|CO132378.1|CO132378				nr -
Unigene53670_All	215	0.49	0.00	4.95	3.24	3.20	0.21	0.39	0.19	0.00	-8.93E+00	3.70E-01		3.35E+00	3.36E-04	Up	-1.81E-02	9.61E-01		-3.95E+00	1.46E-03		-1.02E+00	7.24E-01		-8.62E+00	3.57E-01					Unigene53670_All//2.00E-07//TC157418				
Unigene53671_All	815	0.00	0.00	0.00	0.00	0.00	0.44	0.88	0.92	19.06	null	null		null	null		null	null		8.79E+00	2.37E-02		6.59E-02	9.46E-01		4.43E+00	2.47E-87	Up	Unigene53671_All//gi|297721661|ref|NP_001173193.1|//2.00E-43//0s02g0806500 [Oryza sativa Japonica Group] >gi|154515723|gb|AAK98697.1|AC069158_9 Hypothetical protein [Oryza sativa Japonica Group] >gi|47497346|dbj|BAD19386.1| glycosyltransferase protein 2-like [Oryza sativa Japonica Group] >gi|255671332|dbj|BAH91922.1| Os02g0806500 [Oryza sativa Japonica Group]		Unigene53671_All//6.00E-36//DT462701			GO:0016740	nr +
Unigene53675_All	334	8.46	2.12	1.59	0.00	1.34	0.68	0.51	0.38	0.36	-1.99E+00	2.03E-06	Down	-2.41E+00	1.80E-07	Down	1.04E+01	8.00E-03		9.40E+00	1.19E-01		-4.32E-01	7.92E-01		-5.01E-01	7.46E-01		Unigene53675_All//gi|255569851|ref|XP_002525889.1|//2.00E-07//serine-threonine protein kinase, plant-type, putative [Ricinus communis] >gi|223534803|gb|EEF36493.1| serine-threonine protein kinase, plant-type, putative [Ricinus communis]	Unigene53675_All//1.00E-05//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative	Unigene53675_All//2.00E-52//DW516942			GO:0004672//GO:0006464//GO:0016020//GO:0016491//GO:0032559	nr +
Unigene53683_All	235	0.00	59.94	25.61	0.00	0.00	0.00	0.00	0.00	1.59E+01	6.98E-81	Up	1.46E+01	1.52E-33	Up	null	null		null	null		null	null		null	null		Unigene53683_All//gi|2497907|sp|Q40256.1|MT3_MUSAC//2.00E-17//RecName: Full=Metallothionein-like protein type 3; Short=MT-3; AltName: Full=MMT3 >gi|12006150|gb|AAG44759.1|AF268393_1 metallothionein-like protein [Musa acuminata] >gi|1213512|gb|AAB82615.1| metallothionein-like protein [Musa acuminata AAA Group]	Unigene53683_All//6.00E-06//AT3G15353| MT3 (METALLOTHIONEIN 3); copper ion binding	Unigene53683_All//1.00E-09//TC174105			GO:0043169	nr -
Unigene5369_All	1189	1.58	1.75	1.93	2.89	3.97	2.51	1.67	1.30	0.40	1.41E-01	7.39E-01		2.82E-01	5.35E-01		4.57E-01	1.07E-01		-2.06E-01	6.05E-01		-3.62E-01	3.96E-01		-2.06E+00	4.43E-06	Down	Unigene5369_All//gi|297829302|ref|XP_002882533.1|//2.00E-33//far-red impaired responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326373|gb|EFH58792.1| far-red impaired responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5369_All//1.00E-34//AT3G07500| far-red impaired responsive family protein / FAR1 family protein	Unigene5369_All//0.00E+00//gi|11202268|gb|BF271273.1|BF271273				nr -
Unigene53691_All	328	0.00	0.00	0.00	0.00	0.00	0.00	37.77	3.82	4.49	null	null		null	null		null	null		null	null		-3.30E+00	6.69E-55	Down	-3.07E+00	5.90E-53	Down			Unigene53691_All//2.00E-15//gi|109887275|gb|DW516244.1|DW516244				
Unigene53692_All	318	0.00	0.16	0.17	0.00	0.11	0.00	1.60	1.58	5.64	7.32E+00	6.15E-01		7.39E+00	6.35E-01		6.76E+00	8.29E-01		null	null		-1.66E-02	1.02E+00		1.82E+00	8.40E-05	Up	Unigene53692_All//gi|297819544|ref|XP_002877655.1|//1.00E-08//condensation domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297323493|gb|EFH53914.1| condensation domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene53692_All//6.00E-14//AT3G49210| unknown protein					nr -
Unigene53699_All	230	0.68	0.00	4.86	1.73	0.30	0.79	0.00	0.00	0.00	-9.41E+00	2.15E-01		2.83E+00	7.34E-04	Up	-2.53E+00	5.79E-02		-1.14E+00	3.79E-01		null	null		null	null									
Unigene53701_All	3356	0.22	0.50	0.38	0.31	0.62	0.44	1.66	0.57	9.33	1.19E+00	2.16E-02		8.03E-01	2.01E-01		9.82E-01	2.82E-02		5.11E-01	3.95E-01		-1.54E+00	2.28E-10	Down	2.49E+00	2.31E-104	Up	Unigene53701_All//gi|297833718|ref|XP_002884741.1|//1.00E-176//lipin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330581|gb|EFH61000.1| lipin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene53701_All//2.00E-158//AT3G09660| lipin family protein	Unigene53701_All//0.00E+00//TC139778				nr -
Unigene53702_All	474	15.56	22.77	13.37	27.11	23.83	26.96	86.08	47.70	24.04	5.49E-01	1.55E-03		-2.19E-01	3.76E-01		-1.86E-01	2.92E-01		-8.00E-03	9.57E-01		-8.52E-01	4.61E-28		-1.84E+00	4.32E-94	Down			Unigene53702_All//1.00E-152//gi|109848821|gb|DW477800.1|DW477800				
Unigene53709_All	364	0.14	0.28	0.00	2.46	2.27	1.61	2.67	0.00	0.33	9.54E-01	7.25E-01		-7.17E+00	6.22E-01		-1.18E-01	8.51E-01		-6.11E-01	4.26E-01		-1.14E+01	5.83E-07	Down	-3.02E+00	9.60E-05	Down	Unigene53709_All//gi|22448833|emb|CAB10255.1|//4.00E-23//centromere protein homolog [Arabidopsis thaliana] >gi|7268182|emb|CAB78518.1| centromere protein homolog [Arabidopsis thaliana]	Unigene53709_All//2.00E-24//AT4G14760| LOCATED IN: nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053), KIP1-like (InterPro:IPR011684); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT3G22790.1); Has 167525 Blast hits to 63593 proteins in 2151 species: Archae - 1921; Bacteria - 21978; Metazoa - 82150; Fungi - 11567; Plants - 6203; Viruses - 845; Other Eukaryotes - 42861 (source: NCBI BLink).	Unigene53709_All//2.00E-27//ES803076			GO:0016020	nr +
Unigene53710_All	434	0.00	0.00	0.00	0.00	0.00	0.00	1.17	5.39	0.00	null	null		null	null		null	null		null	null		2.21E+00	2.81E-07	Up	-1.02E+01	5.54E-04	Down	Unigene53710_All//gi|158513203|sp|A2WXX3.2|RL51_ORYSI//7.00E-13//RecName: Full=60S ribosomal protein L5-1	Unigene53710_All//6.00E-11//AT5G39740| 60S ribosomal protein L5 (RPL5B)			ko03010|Ribosome	GO:0005622	nr +
Unigene53714_All	257	0.20	0.20	0.00	1.36	1.61	2.11	1.81	2.60	8.68	-4.61E-02	9.85E-01		-7.67E+00	6.22E-01		2.45E-01	8.52E-01		6.36E-01	5.61E-01		5.24E-01	5.26E-01		2.26E+00	2.34E-07	Up	Unigene53714_All//gi|159031811|dbj|BAF91877.1|//3.00E-29//polyamine oxidase [Nicotiana benthamiana]	Unigene53714_All//5.00E-29//AT5G13700| ATPAO1 (ARABIDOPSIS THALIANA POLYAMINE OXIDASE 1); FAD binding / polyamine oxidase	Unigene53714_All//7.00E-79//gi|78327583|gb|DT547857.1|DT547857			GO:0008152//GO:0016647	nr +
Unigene53717_All	327	0.96	0.00	0.98	0.76	0.00	0.00	0.13	2.43	0.85	-9.91E+00	3.65E-02		2.55E-02	1.00E+00		-9.57E+00	4.18E-02		-9.57E+00	7.32E-02		4.23E+00	1.05E-04	Up	2.72E+00	9.93E-02									
Unigene53722_All	283	0.55	0.36	4.52	1.23	1.22	4.15	0.15	0.00	0.84	-6.31E-01	7.27E-01		3.03E+00	1.48E-04	Up	-1.81E-02	9.58E-01		1.75E+00	9.86E-03		-7.22E+00	6.56E-01		2.50E+00	1.59E-01		Unigene53722_All//gi|82697975|gb|AB088022.1|//3.00E-06//CXE carboxylesterase [Actinidia deliciosa]	Unigene53722_All//3.00E-07//AT3G27320| hydrolase	Unigene53722_All//6.00E-58//gi|78342283|gb|DT562557.1|DT562557				nr -
Unigene53726_All	319	4.59	8.89	12.52	9.84	14.57	12.46	9.15	6.03	4.62	9.54E-01	1.09E-02		1.45E+00	1.39E-05	Up	5.67E-01	4.15E-02		3.41E-01	3.11E-01		-6.02E-01	6.89E-02		-9.85E-01	1.94E-03		Unigene53726_All//gi|84468356|dbj|BAE71261.1|//2.00E-06//hypothetical protein [Trifolium pratense]		Unigene53726_All//2.00E-85//TC177443		ko03022|Basal transcription factors		nr +
Unigene53728_All	354	1.18	2.00	1.96	2.96	1.17	0.13	0.72	0.47	0.56	7.61E-01	3.62E-01		7.26E-01	3.96E-01		-1.34E+00	3.95E-02		-4.53E+00	1.60E-05	Down	-6.02E-01	6.47E-01		-3.49E-01	7.66E-01									
Unigene53729_All	456	0.00	0.00	0.00	0.00	0.00	0.00	3.52	7.33	0.26	null	null		null	null		null	null		null	null		1.06E+00	5.28E-04	Up	-3.75E+00	9.85E-09	Down	Unigene53729_All//gi|226495867|ref|NP_001151716.1|//9.00E-29//LOC100285352 [Zea mays] >gi|195649275|gb|ACG44105.1| actin-depolymerizing factor [Zea mays]	Unigene53729_All//2.00E-28//AT2G31200| ADF6 (ACTIN DEPOLYMERIZING FACTOR 6); actin binding				GO:0002218//GO:0044464//GO:0046872	nr -
Unigene5373_All	807	4.80	12.06	3.56	15.56	22.19	23.73	16.92	10.20	23.00	1.33E+00	1.20E-11	Up	-4.29E-01	2.00E-01		5.12E-01	3.05E-05		6.09E-01	7.23E-07		-7.30E-01	8.20E-08		4.43E-01	7.42E-05		Unigene5373_All//gi|530876|gb|AAB53953.1|//4.00E-18//amino acid feature: rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265 [Chlamydomonas reinhardtii]		Unigene5373_All//0.00E+00//gi|78345867|gb|DT566141.1|DT566141		ko00270|Cysteine and methionine metabolism//ko00620|Pyruvate metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis		nr +
Unigene53739_All	295	8.34	25.42	9.75	6.25	11.09	9.34	0.57	0.99	0.14	1.61E+00	6.79E-12	Up	2.26E-01	5.87E-01		8.28E-01	1.36E-02		5.80E-01	1.40E-01		7.91E-01	5.63E-01		-2.09E+00	3.13E-01									
Unigene5374_All	1327	1.10	1.60	1.04	4.13	2.67	1.43	5.35	6.46	5.10	5.39E-01	2.26E-01		-8.16E-02	8.85E-01		-6.28E-01	9.17E-03		-1.53E+00	7.17E-09	Down	2.71E-01	1.50E-01		-6.87E-02	7.45E-01		Unigene5374_All//gi|3775995|emb|CAA09200.1|//1.00E-18//RNA helicase [Arabidopsis thaliana]	Unigene5374_All//5.00E-20//AT3G22310| PMH1 (PUTATIVE MITOCHONDRIAL RNA HELICASE 1); ATP-dependent helicase/ DNA binding / RNA binding	Unigene5374_All//2.00E-49//gi|78354171|gb|DT574445.1|DT574445		ko03040|Spliceosome		nr -
Unigene53741_All	845	0.93	2.22	0.38	0.06	1.67	0.21	0.00	0.00	0.00	1.26E+00	1.00E-02		-1.30E+00	1.38E-01		4.82E+00	1.54E-07	Up	1.86E+00	4.58E-01		null	null		null	null		Unigene53741_All//gi|255547878|ref|XP_002514996.1|//4.00E-23//Ketoacyl-ACP Reductase (KAR) [Ricinus communis] >gi|223546047|gb|EEF47550.1| Ketoacyl-ACP Reductase (KAR) [Ricinus communis]	Unigene53741_All//3.00E-20//AT2G29260| tropinone reductase, putative / tropine dehydrogenase, putative			ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis	GO:0016491	nr +
Unigene53743_All	348	72.32	40.04	51.57	295.59	254.41	254.63	73.38	24.62	32.51	-8.53E-01	1.60E-14		-4.88E-01	1.30E-05		-2.17E-01	5.42E-06		-2.15E-01	1.78E-05		-1.58E+00	2.90E-46	Down	-1.17E+00	1.03E-30	Down	Unigene53743_All//gi|1087017|gb|AAB33284.1|//1.00E-13//arabinogalactan-protein [Nicotiana alata]		Unigene53743_All//2.00E-101//CO125711				nr +
Unigene53747_All	277	0.00	0.37	3.65	0.54	0.87	0.00	0.00	0.00	0.00	8.51E+00	3.85E-01		1.18E+01	1.27E-05	Up	6.90E-01	7.32E-01		-9.08E+00	2.33E-01		null	null		null	null		Unigene53747_All//gi|255604016|ref|XP_002538154.1|//1.00E-28//conserved hypothetical protein [Ricinus communis] >gi|223515562|gb|EEF24230.1| conserved hypothetical protein [Ricinus communis]					GO:0005506	nr +
Unigene53749_All	305	0.00	0.00	0.00	0.00	0.00	0.00	6.38	1.92	0.26	null	null		null	null		null	null		null	null		-1.73E+00	1.00E-04	Down	-4.61E+00	6.97E-12	Down			Unigene53749_All//4.00E-10//TC146107				
Unigene5375_All	1174	17.20	12.86	12.16	15.87	8.45	5.92	2.05	1.28	0.41	-4.20E-01	6.22E-04		-5.01E-01	7.62E-05		-9.10E-01	1.84E-14		-1.42E+00	7.44E-26	Down	-6.80E-01	6.49E-02		-2.33E+00	2.78E-08	Down	Unigene5375_All//gi|42566766|ref|NP_193135.2|//1.00E-132//exostosin family protein [Arabidopsis thaliana]	Unigene5375_All//2.00E-133//AT4G13990| exostosin family protein	Unigene5375_All//9.00E-116//ES813066				nr +
Unigene53754_All	287	1.46	0.35	1.11	209.84	177.46	89.70	2.80	2.04	0.56	-2.05E+00	1.20E-01		-3.90E-01	7.17E-01		-2.42E-01	1.62E-04		-1.23E+00	1.04E-65	Down	-4.57E-01	5.36E-01		-2.33E+00	2.82E-03									ESTscan -
Unigene53756_All	309	2.20	0.00	0.00	2.42	2.12	3.07	1.51	1.49	1.42	-1.11E+01	4.10E-04	Down	-1.11E+01	7.63E-04	Down	-1.92E-01	8.21E-01		3.44E-01	6.49E-01		-1.66E-02	1.02E+00		-8.58E-02	9.34E-01		Unigene53756_All//gi|22331920|ref|NP_191889.2|//2.00E-08//phosphoinositide binding [Arabidopsis thaliana]	Unigene53756_All//1.00E-07//AT3G63300| phosphoinositide binding	Unigene53756_All//7.00E-30//TC132277				nr -
Unigene53758_All	309	0.00	0.00	0.00	0.00	0.00	0.00	3.42	2.16	0.39	null	null		null	null		null	null		null	null		-6.61E-01	2.78E-01		-3.14E+00	2.96E-05	Down	Unigene53758_All//gi|226533381|ref|NP_001147395.1|//2.00E-42//40S ribosomal protein S15 [Zea mays] >gi|195605680|gb|ACG24670.1| 40S ribosomal protein S15 [Zea mays] >gi|195610984|gb|ACG27322.1| 40S ribosomal protein S15 [Zea mays] >gi|195617474|gb|ACG30567.1| 40S ribosomal protein S15 [Zea mays]	Unigene53758_All//4.00E-35//AT5G09510| 40S ribosomal protein S15 (RPS15D)	Unigene53758_All//4.00E-10//TC150923		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0032279	nr +

Unigene5376_All	1087	15.84	7.83	6.42	19.57	13.24	14.71	19.14	7.27	8.36	-1.02E+00	2.22E-13	Down	-1.30E+00	9.79E-19	Down	-5.63E-01	2.32E-07		-4.12E-01	4.34E-04		-1.40E+00	9.32E-32	Down	-1.20E+00	7.01E-26	Down	Unigene5376_All//gi|297807227|ref|XP_002871497.1|//2.00E-58//ribosomal protein L19 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317334|gb|EFH47756.1| ribosomal protein L19 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5376_All//5.00E-58//AT5G11750| ribosomal protein L19 family protein	Unigene5376_All//0.00E+00//TC131946				nr -
Unigene53760_All	329	0.00	0.00	0.00	0.00	0.00	0.00	2.83	7.62	0.12	null	null		null	null		null	null		null	null		1.43E+00	1.22E-04	Up	-4.55E+00	6.41E-06	Down								
Unigene53761_All	261	0.00	3.30	2.04	0.00	0.40	0.00	0.81	0.16	0.46	1.17E+01	4.94E-05	Up	1.10E+01	4.03E-03		8.63E+00	4.55E-01		null	null		-2.34E+00	2.37E-01		-8.23E-01	5.99E-01									
Unigene53765_All	338	0.31	4.20	2.52	0.00	0.00	0.00	0.00	0.00	0.00	3.76E+00	3.98E-06	Up	3.03E+00	3.01E-03		null	null		null	null		null	null		null	null		Unigene53765_All//sp|P00746|CFAD_HUMAN//1.00E-15//Complement factor D OS=Homo sapiens GN=CFD PE=1 SV=5							swissprot +
Unigene53769_All	487	0.00	0.00	0.00	2.15	0.71	0.00	0.35	0.00	0.00	null	null		null	null		-1.60E+00	1.49E-02		-1.11E+01	1.47E-06	Down	-8.44E+00	1.34E-01		-8.44E+00	1.08E-01		Unigene53769_All//gi|87116461|dbj|BAE79383.1|//6.00E-07//unnamed protein product [Ipomoea batatas]	Unigene53769_All//5.00E-05//AT2G01050| nucleic acid binding / zinc ion binding					nr -
Unigene53777_All	1721	0.91	0.74	0.50	7.67	6.16	7.24	11.37	7.24	3.98	-3.09E-01	5.66E-01		-8.81E-01	1.13E-01		-3.16E-01	4.10E-02		-8.27E-02	6.62E-01		-6.52E-01	4.77E-09		-1.51E+00	1.03E-34	Down	Unigene5377_All//gi|240256218|ref|NP_001078503.4|//1.00E-147//phospholipase C/ phosphoric diester hydrolase [Arabidopsis thaliana]	Unigene5377_All//2.00E-143//AT4G36945| phospholipase C/ phosphoric diester hydrolase	Unigene5377_All//0.00E+00//TC157376				nr +
Unigene53775_All	467	0.22	1.84	2.85	0.00	0.00	0.00	0.00	0.00	0.00	3.04E+00	1.94E-03		3.67E+00	1.90E-05	Up	null	null		null	null		null	null		null	null		Unigene53775_All//gi|15222901|ref|NP_177718.1|//2.00E-25//family II extracellular lipase 3 (EXL3) [Arabidopsis thaliana] >gi|75165254|sp|Q94CH6.1|EXL3_ARATH RecName: Full=GDSL esterase/lipase EXL3; AltName: Full=Family II extracellular lipase 3; Short=Family II lipase EXL3; Flags: Precursor >gi|15054386|gb|AAK30018.1| family II lipase EXL3 [Arabidopsis thaliana]	Unigene53775_All//2.00E-23//AT5G42170| carboxylesterase/ hydrolase, acting on ester bonds				GO:0000003//GO:0016747//GO:0016788	nr +
Unigene53776_All	293	0.00	3.29	2.36	0.34	0.00	0.46	1.73	0.86	1.63	1.17E+01	1.38E-05	Up	1.12E+01	6.15E-04	Up	-8.41E+00	3.12E-01		4.44E-01	8.61E-01		-1.02E+00	2.88E-01		-8.58E-02	9.30E-01					Unigene53776_All//6.00E-160//gi|78348029|gb|DT568303.1|DT568303					
Unigene53779_All	248	1.05	0.82	0.86	0.40	0.69	3.82	1.19	0.67	1.12	-3.68E-01	7.78E-01		-2.97E-01	8.32E-01		7.89E-01	7.70E-01		3.25E+00	5.84E-04	Up	-8.24E-01	5.40E-01		-8.58E-02	9.52E-01					Unigene53779_All//3.00E-07//TC157824					
Unigene53784_All	237	1.55	2.78	6.97	0.84	0.73	0.95	0.00	0.00	0.34	8.47E-01	3.48E-01		2.17E+00	3.37E-04	Up	-2.11E-01	8.58E-01		1.81E-01	9.35E-01		null	null		8.39E+00	4.03E-01					Unigene53784_All//6.00E-107//TC147128					
Unigene53786_All	508	0.00	8.98	5.24	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	5.54E-26	Up	1.24E+01	1.07E-14	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene53787_All	253	0.00	0.00	0.00	5.91	2.45	0.71	0.00	0.00	0.00	null	null		null	null		-1.27E+00	1.45E-02		-3.05E+00	7.42E-06	Down	null	null		null	null					Unigene53787_All//2.00E-100//gi|78351075|gb|DT571349.1|DT571349					ESTscan -
Unigene53793_All	290	18.04	47.35	34.70	44.32	46.31	90.79	41.84	76.39	55.50	1.39E+00	2.97E-17	Up	9.44E-01	5.88E-07		6.34E-02	7.68E-01		1.03E+00	6.46E-22	Up	8.68E-01	4.30E-16		4.08E-01	7.75E-04		Unigene53793_All//gi|226499354|ref|NP_001147027.1|//4.00E-10//polyubiquitin containing 7 ubiquitin monomers [Zea mays] >gi|195606596|gb|ACG25128.1| polyubiquitin containing 7 ubiquitin monomers [Zea mays]	Unigene53793_All//1.00E-10//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene53793_All//3.00E-69//gi|78334887|gb|DT555161.1|DT555161		ko03010|Ribosome	GO:0044424	nr +
Unigene53794_All	1013	0.00	9.80	3.26	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	6.75E-57	Up	1.17E+01	2.92E-18	Up	null	null		null	null		null	null		null	null		Unigene53794_All//gi|2941480|gb|AAC39370.1|//3.00E-23//trehalose-6-phosphate phosphatase [Arabidopsis thaliana]	Unigene53794_All//1.00E-24//AT1G78090| ATTPP6 (TREHALOSE-6-PHOSPHATE PHOSPHATASE); trehalose-phosphatase			ko00500|Starch and sucrose metabolism	GO:0008152	nr -
Unigene53796_All	356	1.03	1.42	0.60	1.40	0.29	1.27	1.78	0.00	0.11	4.68E-01	6.11E-01		-7.82E-01	5.53E-01		-2.27E+00	4.22E-02		-1.42E-01	8.92E-01		-1.08E+01	1.23E-04	Down	-3.99E+00	5.82E-04	Down				Unigene53796_All//6.00E-40//TC165396					
Unigene53797_All	253	190.26	364.70	280.14	278.80	344.49	258.66	252.85	331.89	123.45	9.39E-01	6.31E-60		5.58E-01	2.11E-18		3.05E-01	2.59E-09		-1.08E-01	1.26E-01		3.92E-01	8.70E-15		-1.03E+00	1.09E-61	Down	Unigene53797_All//gi|34541994|gb|AAQ74889.1|//1.00E-41//Al-induced protein [Gossypium hirsutum]	Unigene53797_All//1.00E-36//AT5G19140| AILP1	Unigene53797_All//6.00E-141//ES845588			GO:0009725//GO:0010038//GO:0016020	nr -
Unigene53798_All	401	0.00	1.01	0.66	0.37	3.26	0.68	0.00	0.63	1.69	9.98E+00	1.36E-02		9.38E+00	8.00E-02		3.13E+00	2.62E-05	Up	8.59E-01	6.31E-01		9.29E+00	4.31E-02		1.07E+01	4.96E-05	Up				Unigene53798_All//1.00E-32//TC136273					kegg +
Unigene5380_All	915	22.82	8.09	9.78	31.20	26.27	26.01	17.74	7.17	5.01	-1.50E+00	6.97E-29	Down	-1.22E+00	1.63E-20	Down	-2.48E-01	1.33E-02		-2.62E-01	1.14E-02		-1.31E+00	1.28E-22	Down	-1.83E+00	1.59E-37	Down	Unigene5380_All//gi|20856775|gb|AAM26684.1|//4.00E-29//At1g71970/F17M19_12 [Arabidopsis thaliana] >gi|235058005|gb|ANZ29762.1| At1g71970/F17M19_12 [Arabidopsis thaliana]	Unigene5380_All//4.00E-26//AT1G71970| unknown protein	Unigene5380_All//0.00E+00//TC163440				nr -
Unigene53801_All	438	0.00	1.16	0.00	0.00	0.79	3.30	0.00	1.05	0.00	1.02E+01	4.04E-03		null	null		9.62E+00	3.01E-02		1.17E+01	1.30E-08	Up	1.00E+01	1.94E-03		null	null									
Unigene53802_All	247	0.42	4.31	2.59	0.20	0.00	0.91	0.00	0.00	0.00	3.35E+00	2.17E-04	Up	2.61E+00	2.33E-02		-7.66E-00	5.54E-01		2.18E+00	3.23E-01		null	null		null	null										ESTscan -
Unigene53808_All	315	0.00	0.00	0.00	0.79	0.44	0.57	1.07	1.86	5.94	null	null		null	null		-8.55E-01	5.73E-01		-4.63E-01	7.44E-01		7.91E-01	3.74E-01		2.47E+00	6.92E-07	Up				Unigene53808_All//4.00E-07//TC137718					
Unigene53809_All	252	3.32	2.82	4.44	1.98	1.37	7.35	0.00	0.00	0.32	-2.39E-01	7.25E-01		4.18E-01	5.32E-01		-5.33E-01	5.94E-01		1.89E+00	2.78E-04	Up	null	null		8.30E+00	4.03E-01		Unigene53809_All//gi|75334121|sp|Q9FNE1.1|CRK42_ARATH//2.00E-10//RecName: Full=Cysteine-rich receptor-like protein kinase 42; Short=Cysteine-rich RLK42; Flags: Precursor >gi|10178148|dbj|BAB11593.1| receptor-like serine/threonine kinase [Arabidopsis thaliana]						nr +
Unigene5381_All	831	47.35	49.21	59.27	11.39	13.47	9.24	4.53	4.12	2.06	5.56E-02	5.87E-01		3.24E-01	3.34E-05		2.42E-01	1.89E-01		-3.02E-01	1.31E-01		-1.35E-01	6.53E-01		-1.14E+00	4.82E-05	Down	Unigene5381_All//gi|18417512|ref|NP_568306.1|//1.00E-36//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|45175226|gb|AAK62653.1| AT5g14910/F2G14_30 [Arabidopsis thaliana] >gi|15810113|gb|AAL06982.1| AT5g14910/F2G14_30 [Arabidopsis thaliana]	Unigene5381_All//6.00E-31//AT5G14910| heavy-metal-associated domain-containing protein	Unigene5381_All//0.00E+00//gi|109883571|gb|DW512541.1|DW512541				nr -
Unigene53811_All	534	0.88	1.42	2.99	2.61	2.00	0.42	7.60	10.72	3.43	6.91E-01	3.76E-01		1.76E+00	2.65E-03		-3.86E-01	5.20E-01		-2.63E+00	8.15E-05	Down	4.97E-01	2.67E-02		-1.15E+00	1.90E-05	Down	Unigene53811_All//gi|255556920|ref|XP_002519493.1|//7.00E-07//metal ion binding protein, putative [Ricinus communis] >gi|223541356|gb|EEF42907.1| metal ion binding protein, putative [Ricinus communis]	Unigene53811_All//2.00E-05//AT2G36950| heavy-metal-associated domain-containing protein	Unigene53811_All//2.00E-170//gi|78351932|gb|DT572206.1|DT572206				nr -
Unigene53813_All	263	0.40	4.62	2.63	2.08	3.80	2.58	2.89	0.64	1.21	3.54E+00	4.02E-05	Up	2.73E+00	1.40E-02		8.66E-01	2.34E-01		3.06E-01	7.22E-01		-2.19E+00	7.77E-03		-1.26E+00	7.70E-02		Unigene53813_All//gi|18419978|ref|NP_568017.1|//3.00E-34//SMP2; single-stranded RNA binding [Arabidopsis thaliana] >gi|148887129|sp|Q23174.3|SLU7B_ARATH RecName: Full=Pre-mRNA-splicing factor SLU7-B >gi|159122281|gb|AAL08274.1| AT4g37120/C7A10_240 [Arabidopsis thaliana]	Unigene53813_All//1.00E-35//AT4G37120| SMP2; single-stranded RNA binding	Unigene53813_All//8.00E-88//TC140745		ko03040|Spliceosome	GO:0003723//GO:0006396//GO:0008283//GO:0046914	nr -
Unigene53815_All	300	0.00	0.17	0.00	4.32	1.15	4.82	0.28	0.28	2.52	7.40E+00	6.13E-01		null	null		-1.91E+00	1.25E-03		1.58E-01	7.84E-01		-1.70E-02	1.01E+00		3.16E+00	6.82E-04	Up				Unigene53815_All//4.00E-164//ES833388					
Unigene53816_All	547	1.72	0.83	1.56	3.73	3.53	2.15	2.40	3.29	0.58	-1.05E+00	1.43E-01		-1.45E-01	8.31E-01		-8.29E-02	8.46E-01		-7.99E-01	7.94E-02		4.56E-01	3.20E-01		-2.04E+00	3.01E-04	Down				Unigene53816_All//2.00E-111//ES810067					
Unigene53818_All	513	0.20	0.59	2.49	0.58	1.61	0.35	0.00	0.00	0.00	1.54E+00	3.23E-01		3.61E+00	3.41E-05	Up	1.47E+00	7.56E-02		-7.26E-01	6.38E-01		null	null		null	null		Unigene53818_All//sp|Q6N5U3|OPGH_RHOPA//6.00E-11//Glucans biosynthesis glucosyltransferase H OS=Rhodopseudomonas palustris GN=opgH PE=3 SV=1						swissprot +
Unigene5382_All	560	146.31	887.17	223.17	126.49	148.38	264.69	49.91	93.07	44.61	2.60E+00	0.00E+00	Up	6.09E-01	2.22E-37		2.30E-01	1.93E-05		1.07E+00	4.66E-127	Up	8.99E-01	6.11E-39		-1.62E-01	9.16E-02		Unigene5382_All//gi|11596186|gb|AAG38521.1|AF283536_1//2.00E-26//cystatin-like protein [Citrus x paradisi]	Unigene5382_All//1.00E-24//AT5G47550| cysteine protease inhibitor, putative / cystatin, putative	Unigene5382_All//0.00E+00//gi|13245292|gb|BE052395.2|BE052395				nr -
Unigene53820_All	293	2.32	0.00	1.64	0.51	0.47	0.31	0.00	0.00	0.00	-1.12E+01	4.10E-04	Down	-5.05E-01	5.82E-01		-1.18E-01	9.10E-01		-7.26E-01	7.15E-01		null	null		null	null										
Unigene53827_All	475	0.00	0.00	0.00	3.25	1.96	0.19	0.00	0.18	0.08	null	null		null	null		-7.32E-01	1.59E-01		-4.10E+00	1.58E-07	Down	7.46E+00	4.00E-01		6.39E+00	6.44E-01		Unigene53827_All//gi|11994567|dbj|BAB02607.1|//9.00E-28//RNA-binding protein-like [Arabidopsis thaliana]	Unigene53827_All//2.00E-13//AT3G19090| RNA-binding protein, putative	Unigene53827_All//2.00E-151//CO123125			GO:0003676//GO:0003824//GO:0005506//GO:0006950//GO:0010467//GO:0016209//GO:0032991//GO:0043231	nr +
Unigene53828_All	262	0.00	0.00	0.00	0.00	0.13	0.34	0.48	1.75	26.00	null	null		null	null		7.04E+00	8.29E-01		8.43E+00	4.75E-01		1.86E+00	8.80E-02		5.75E+00	8.00E-44	Up				Unigene53828_All//2.00E-66//gi|48792264|gb|CO093578.1|CO093578					
Unigene5383_All	970	0.81	1.36	1.43	1.39	0.60	1.49	29.90	61.96	48.59	7.47E-01	2.05E-01		8.19E-01	1.67E-01		-1.20E+00	3.02E-02		1.04E-01	8.67E-01		1.05E+00	8.15E-58	Up	7.00E-01	8.01E-24		Unigene5383_All//gi|19911587|dbj|BAB86897.1|//5.00E-78//syringolide-induced protein B13-1-1 [Glycine max]	Unigene5383_All//2.00E-75//AT4G39830| L-ascorbate oxidase, putative	Unigene5383_All//7.00E-119//gi|73862288|gb|DT465027.1|DT465027		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene53830_All	234	1.34	8.44	2.50	1.92	3.83	4.05	0.36	2.50	0.51	2.65E+00	3.04E-06	Up	9.00E-01	3.77E-01		9.98E-01	1.99E-01		1.08E+00	1.48E-01		2.79E+00	8.26E-03		4.99E-01	8.07E-01									
Unigene53837_All	272	3.27	0.00	0.59	1.65	0.38	0.00	0.00	0.00	0.00	-1.17E+01	2.86E-05	Down	-2.48E+00	7.18E-03		-2.12E+00	7.27E-02		-1.07E+01	5.78E-03		null	null		null	null		Unigene53837_All//gi|224057042|ref|XP_002299116.1|//6.00E-30//neutral amino acid transport protein [Populus trichocarpa] >gi|222846374|gb|EEE83921.1| neutral amino acid transport protein [Populus trichocarpa]	Unigene53837_All//5.00E-23//AT3G13620| amino acid permease family protein	Unigene53837_All//3.00E-152//TC178019			GO:0015171//GO:0015837//GO:0031224	nr -
Unigene53838_All	340	1.85	0.30	2.35	1.17	0.81	1.86	2.49	1.11	0.23	-2.63E+00	1.78E-02		3.47E-01	6.35E-01		-5.33E-01	6.15E-01		6.66E-01	4.92E-01		-1.17E+00	9.29E-02		-3.41E+00	1.35E-04	Down				Unigene53838_All//2.00E-09//CO098114					
Unigene5384_All	1073	0.15	0.71	0.00	67.87	92.49	28.29	87.48	6.43	1.19	2.28E+00	1.59E-02		-7.19E+00	2.44E-01		4.47E-01	6.04E-21		-1.26E+00	4.04E-83	Down	-3.77E+00	0.00E+00	Down	-6.20E+00	0.00E+00	Down	Unigene5384_All//gi|108385345|gb|ABF85774.1|//1.00E-145//At2g21260 [Arabidopsis thaliana]	Unigene5384_All//4.00E-139//AT2G21250| mannose 6-phosphate reductase (NADPH-dependent), putative	Unigene5384_All//0.00E+00//ES810950		ko00010|Glycolysis / Gluconeogenesis//ko00561|Glycerolipid metabolism		nr +
Unigene53841_All	599	0.35	2.03	3.20	0.50	0.57	0.60	2.75	0.63	0.27	2.54E+00	5.98E-04	Up	3.20E+00	7.32E-07	Up	2.04E-01	9.01E-01		2.74E-01	8.33E-01		-2.13E+00	3.64E-05	Down	-3.37E+00	2.89E-08	Down	Unigene53841_All//gi|30699255|ref|NP_177866.2|//9.00E-61//BGAL16 (beta-galactosidase 16); beta-galactosidase/ catalytic/ cation binding / sugar binding [Arabidopsis thaliana] >gi|152013367|sp|Q8GX69.2|BGL16_ARATH RecName: Full=Beta-galactosidase 16; Short=Lactase 16; Flags: Precursor	Unigene53841_All//5.00E-62//AT1G77410| BGAL16 (beta-galactosidase 16); beta-galactosidase/ catalytic/ cation binding / sugar binding	Unigene53841_All//5.00E-08//EV485633		ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation	GO:0015925//GO:0030246//GO:0043167//GO:0044238	nr +
Unigene5385_All	781	44.82	7.92	8.32	31.00	29.06	51.18	122.35	53.52	42.03	-2.50E+00	1.43E-94	Down	-2.43E+00	3.28E-88	Down	-9.33E-02	4.96E-01		7.23E-01	3.00E-18		-1.19E+00	3.62E-112	Down	-1.54E+00	1.46E-170	Down	Unigene5385_All//gi|162461632|ref|NP_001065701.1|//2.00E-64//60S acidic ribosomal protein P1 [Zea mays] >gi|2431769|gb|AAB71079.1| acidic ribosomal protein P1a [Zea mays] >gi|195619428|gb|ACG31544.1| 60S acidic ribosomal protein P1 [Zea mays]	Unigene5385_All//1.00E-20//AT5G24510| 60s acidic ribosomal protein P1, putative	Unigene5385_All//3.00E-173//gi|164312758|gb|EV496692.1|EV496692		ko03010|Ribosome		nr +
Unigene53852_All	580	0.09	1.49	0.83	0.09	0.24	0.08	1.60	0.50	0.34	4.04E+00	4.20E-04	Up	3.20E+00	3.48E-02		1.47E+00	6.18E-01		-1.41E-01	9.52E-01		-1.67E+00	1.45E-02		-2.22E+00	1.63E-03		Unigene53852_All//gi|115470569|ref|NP_001058883.1|//2.00E-20//Os07g0145400 [Oryza sativa Japonica Group] >gi|113610419|dbj|BAF20797.1| Os07g0145400 [Oryza sativa Japonica Group]	Unigene53852_All//1.00E-21//AT2G27060| ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene53852_All//0.00E+00//CO070723			GO:0006464//GO:0016301//GO:0016787//GO:0031224//GO:0031410//GO:0032559	nr -

Unigene53858_All	321	0.16	0.00	0.00	0.62	0.11	0.14	2.37	0.26	0.99	-7.35E+00	6.10E-01		-7.35E+00	6.22E-01		-2.53E+00	2.33E-01		-2.14E+00	3.47E-01		-3.19E+00	7.92E-04	Down	-1.26E+00	7.70E-02		Unigene53858_All//gi|297824819|ref|XP_002880292.1|//8.00E-17//ribonuclease P [Arabidopsis lyrata subsp. lyrata] >gi|297326131|gb|EFH56551.1| ribonuclease P [Arabidopsis lyrata subsp. lyrata]	Unigene53858_All//3.00E-17//AT2G47300| ribonuclease P				GO:0004549//GO:0008033	nr -
Unigene53862_All	400	0.00	4.31	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.99E-10	Up	8.64E+00	2.38E-01		null	null		null	null		null	null		null	null		Unigene53862_All//gi|18421863|ref|NP_568564.1|//3.00E-16//binding / catalytic [Arabidopsis thaliana] >gi|90173749|sp|Q8LGI2.2|SCPDH_ARATH RecName: Full=Probable mitochondrial saccharopine dehydrogenase At5g39410; Short=SDH >gi|115646780|gb|ABJ17115.1| At5g39410 [Arabidopsis thaliana]	Unigene53862_All//1.00E-17//AT5G39410| binding / catalytic				GO:0009526//GO:0016020	nr +
Unigene53864_All	295	0.00	1.55	0.00	0.00	0.82	0.15	0.14	0.43	3.11	1.06E+01	7.43E-03		null	null		9.67E+00	1.04E-01		7.26E+00	6.95E-01		1.57E+00	5.45E-01		4.44E+00	1.24E-05	Up			Unigene53864_All//3.00E-07//TC163538				
Unigene5387_All	1755	6.89	1.99	2.88	9.54	4.32	4.45	7.18	5.93	9.65	-1.79E+00	8.74E-22	Down	-1.26E+00	1.24E-12	Down	-1.14E+00	6.92E-19	Down	-1.10E+00	9.89E-16	Down	-2.76E-01	6.48E-02		4.26E-01	2.93E-04		Unigene5387_All//gi|297827895|ref|XP_002881830.1|//3.00E-80//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327669|gb|EFH58889.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5387_All//1.00E-79//AT2G42280| basic helix-loop-helix (bHLH) family protein	Unigene5387_All//0.00E+00//gi|109852650|gb|DW481629.1|DW481629	bHLH	ko04712|Circadian rhythm - plant		nr +
Unigene53870_All	381	9.20	10.24	7.97	0.52	0.63	3.32	1.44	1.32	2.82	1.54E-01	6.11E-01		-2.08E-01	5.78E-01		2.75E-01	8.95E-01		2.67E+00	2.42E-04	Up	-1.32E-01	8.80E-01		9.69E-01	9.17E-02		Unigene53870_All//gi|149392583|gb|ABR26094.1|//9.00E-10//retrotransposon protein [Oryza sativa Indica Group]		Unigene53870_All//2.00E-46//gi|109853357|gb|DW482336.1|DW482336				nr -
Unigene53875_All	282	0.00	0.90	0.00	0.35	0.00	0.16	231.49	908.98	225.61	9.81E+00	7.85E-02		null	null		-8.46E+00	3.12E-01		-1.14E+00	6.76E-01		1.97E+00	0.00E+00	Up	-3.71E-02	6.21E-01		Unigene53875_All//gi|124360970|gb|AEN08942.1|//6.00E-30//Quinonprotein alcohol dehydrogenase-like [Medicago truncatula]		Unigene53875_All//1.00E-93//TC163308			GO:0008152//GO:0016491	nr +
Unigene53877_All	248	0.00	2.66	3.86	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.25E-04	Up	1.19E+01	2.46E-05	Up	null	null		null	null		null	null		null	null									
Unigene53879_All	259	0.20	0.00	3.29	2.89	1.46	1.22	0.00	0.32	0.00	-7.66E+00	6.10E-01		4.03E+00	7.02E-04	Up	-9.80E-01	2.23E-01		-1.24E+00	1.45E-01		8.33E+00	4.00E-01		null	null				Unigene53879_All//3.00E-19//TC176506				
Unigene53882_All	843	0.00	0.00	0.00	0.41	0.16	0.00	4.16	1.39	1.09	null	null		null	null		-1.34E+00	3.08E-01		-8.69E+00	2.12E-02		-1.58E+00	4.53E-07	Down	-1.94E+00	1.99E-09	Down	Unigene53882_All//gi|224064438|ref|XP_002301476.1|//1.00E-102//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222843202|gb|EEE80749.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene53882_All//1.00E-85//AT2G47800| ATMRP4 (ARABIDOPSIS THALIANA MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 4): ATPase, coupled to transmembrane movement of substances / folic acid transporter	Unigene53882_All//2.00E-82//ES834317		ko02010|ABC transporters	GO:0000166//GO:0005773//GO:0006950//GO:0009987//GO:0015405//GO:0015893//GO:0017111//GO:0031090//GO:0051183//GO:0051707	nr -
Unigene53883_All	235	0.00	6.68	2.95	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	5.70E-09	Up	1.15E+01	6.15E-04	Up	null	null		null	null		null	null		null	null									
Unigene53885_All	272	0.58	0.37	0.00	2.75	0.00	1.33	0.00	0.00	0.29	-6.31E-01	7.27E-01		-9.17E+00	2.44E-01		-1.14E+01	1.50E-05	Down	-1.05E+00	2.21E-01		null	null		8.19E+00	4.03E-01			Unigene53885_All//6.00E-06//AT4G22760| pentatricopeptide (PPR) repeat-containing protein					
Unigene53887_All	241	0.65	4.84	2.43	0.41	0.43	0.19	0.00	0.00	0.00	2.89E+00	2.98E-04	Up	1.90E+00	8.47E-02		5.24E-02	9.66E-01		-1.14E+00	6.76E-01		null	null		null	null									
Unigene53891_All	600	0.00	0.51	0.53	2.24	0.57	1.20	0.35	0.00	0.33	8.99E+00	4.42E-02		9.06E+00	4.51E-02		-1.97E+00	7.30E-04	Down	-8.96E-01	1.30E-01		-8.46E+00	7.43E-02		-8.56E-02	9.61E-01		Unigene53891_All//gi|15235900|ref|NP_192536.1|//1.00E-50//ATCSLC12 (CELLULOSE-SYNTHASE LIKE C12): cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|752162055|sp|Q9ZQB9.1|CSLCC_ARATH RecName: Full=Probable xyloglucan glycosyltransferase 12; AltName: Full=Cellulose synthase-like protein C12; Short=AtCslC12 >gi|31711706|gb|AAP68209.1| At4g07960 [Arabidopsis thaliana]	Unigene53891_All//2.00E-52//AT4G07960| ATCSLC12 (CELLULOSE-SYNTHASE LIKE C12): cellulose synthase/ transferase, transferring glycosyl groups	Unigene53891_All//0.00E+00//CO118717			GO:0016759//GO:0043231	nr +
Unigene53894_All	299	0.00	0.00	0.00	0.00	0.00	0.00	3.54	5.31	0.13	null	null		null	null		null	null		null	null		5.87E-01	2.24E-01		-4.73E+00	8.85E-07	Down	Unigene53894_All//gi|62751093|dbj|BAD95794.1|//4.00E-24//similar to 60S ribosomal protein L35 [Solanum lycopersicum]	Unigene53894_All//8.00E-16//AT5G02610| 60S ribosomal protein L35 (RPL35D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene53899_All	267	0.00	0.00	0.00	0.00	0.00	0.00	1.90	1.57	0.00	null	null		null	null		null	null		null	null		-2.80E-01	7.49E-01		-1.09E+01	5.54E-04	Down	Unigene53899_All//gi|14423905|sp|Q9XGL4.1|RL31_CYAPA//2.00E-17//RecName: Full=60S ribosomal protein L31 >gi|5123727|emb|CAB45375.1| ribosomal protein L31 [Cyanophora paradoxa]	Unigene53899_All//9.00E-13//AT5G56710| 60S ribosomal protein L31 (RPL31C)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0030312	nr -
Unigene53900_All	275	0.00	2.58	2.52	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.32E-04	Up	1.13E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene53900_All//sp|Q00963|SPTCB_DROME//2.00E-38//Spectrin beta chain OS=Drosophila melanogaster GN=beta-Spec PE=1 SV=2						swissprot +
Unigene53901_All	358	0.00	0.00	0.00	0.00	0.00	0.00	0.83	4.09	0.11	null	null		null	null		null	null		null	null		2.31E+00	4.93E-05	Up	-2.89E+00	6.76E-02		Unigene53901_All//gi|57471718|gb|AAW50990.1|//5.00E-29//ribosomal protein P1 [Triticum aestivum]	Unigene53901_All//6.00E-14//AT5G24510| 60s acidic ribosomal protein P1, putative			ko03010|Ribosome	GO:0006412//GO:0030529	nr -
Unigene53902_All	277	0.76	3.29	4.23	7.37	5.10	13.53	33.89	92.95	107.43	2.12E+00	1.04E-02		2.48E+00	1.35E-03		-5.33E-01	2.37E-01		8.76E-01	5.70E-03		1.46E+00	1.67E-41	Up	1.66E+00	2.85E-59	Up	Unigene53902_All//gi|224111880|ref|XP_002316010.1|//7.00E-26//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene53902_All//4.00E-07//AT2G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1): oxygen binding / steroid hydroxylase	Unigene53902_All//8.00E-79//TC137307		ko04146|Peroxisome//ko00592|alpha-Linoleic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0008152//GO:0016491	nr -
Unigene53909_All	256	0.00	0.00	2.91	2.53	0.40	0.35	0.66	0.82	0.31	null	null		1.15E+01	3.27E-04	Up	-2.65E+00	7.46E-03		-2.84E+00	1.02E-02		3.05E-01	8.36E-01		-1.09E+00	5.52E-01				Unigene53909_All//6.00E-67//TC177689				
Unigene5391_All	1223	12.88	12.47	11.49	15.64	17.63	15.66	26.10	13.81	11.86	-4.63E-02	7.58E-01		-1.64E-01	3.15E-01		1.72E-01	1.86E-01		1.50E-03	9.92E-01		-9.19E-01	4.64E-25		-1.14E+00	2.37E-36	Down	Unigene5391_All//gi|4836927|gb|AAD30629.1|AC006085_2//1.00E-87//unknown protein [Arabidopsis thaliana] >gi|28466907|gb|AAO44062.1| At1g51160 [Arabidopsis thaliana]	Unigene5391_All//6.00E-89//AT1G51160| synbindin, putative	Unigene5391_All//0.00E+00//TC133725				nr -
Unigene53913_All	312	0.84	2.76	1.02	1.28	0.22	0.72	2.71	0.27	0.26	1.72E+00	3.49E-02		2.88E-01	8.10E-01		-2.53E+00	5.79E-02		-8.19E-01	5.06E-01		-3.34E+00	2.51E-04	Down	-3.41E+00	1.35E-04	Down			Unigene53913_All//3.00E-134//C0118666				
Unigene53915_All	627	0.00	0.00	0.00	0.00	0.00	0.00	1.08	1.47	3.62	null	null		null	null		null	null		null	null		4.43E-01	5.19E-01		1.75E+00	1.36E-05	Up	Unigene53915_All//gi|224122948|ref|XP_002318956.1|//3.00E-42//vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa] >gi|222857332|gb|EEE94879.1| vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa]	Unigene53915_All//2.00E-25//AT1G15690| AVP1: ATPase/ hydrogen-translocating pyrophosphatase	Unigene53915_All//5.00E-79//TC161921		ko00190|Oxidative phosphorylation	GO:0006818//GO:0015405//GO:0016462//GO:0016491//GO:0031410	nr +
Unigene53916_All	498	3.99	4.88	4.06	7.00	2.97	2.27	0.51	0.34	0.96	2.91E-01	4.87E-01		2.54E-02	9.75E-01		-1.24E+00	7.17E-05	Down	-1.63E+00	2.33E-06	Down	-6.02E-01	6.47E-01		9.14E-01	3.38E-01		Unigene53916_All//gi|212717123|gb|ACJ37403.1|//5.00E-22//CC-NBS-LRR class disease resistance protein [Glycine max]	Unigene53916_All//2.00E-18//AT1G50180| disease resistance protein (CC-NBS-LRR class), putative				GO:0000166//GO:0016787	nr -
Unigene5392_All	1944	2.45	2.27	6.19	0.28	0.44	0.30	9.46	4.58	0.66	-1.11E-01	6.87E-01		1.34E+00	7.79E-14	Up	6.52E-01	4.25E-01		9.94E-02	9.36E-01		-1.05E+00	3.67E-18	Down	-3.85E+00	1.54E-95	Down	Unigene5392_All//gi|15218183|ref|NP_172630.1|//0.00E+00//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|751882219|sp|Q9M817.1|PTR2X_ARATH RecName: Full=Probable peptide transporter At1g52190	Unigene5392_All//1.00E-175//AT1G52190| proton-dependent oligopeptide transport (POT) family protein	Unigene5392_All//0.00E+00//C0081495				nr -
Unigene53920_All	533	0.20	0.00	0.80	1.12	0.00	0.00	0.00	0.00	0.00	-7.62E+00	3.70E-01		2.03E+00	1.39E-01		-1.01E+01	1.78E-04	Down	-1.01E+01	7.70E-04	Down	null	null		null	null		Unigene53920_All//gi|17402471|emb|CAD13178.1|//5.00E-96//alpha-tubulin [Nicotiana tabacum]	Unigene53920_All//4.00E-84//AT4G14960| TUA6: structural constituent of cytoskeleton	Unigene53920_All//6.00E-115//TC152174		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene53936_All	645	0.00	0.00	0.00	0.00	0.00	0.00	2.16	1.36	0.00	null	null		null	null		null	null		null	null		-6.69E-01	1.94E-01		-1.11E+01	2.40E-10	Down	Unigene53936_All//gi|119638443|gb|ABL85034.1|//5.00E-78//ribosomal subunit 8E protein [Brachypodium sylvaticum]	Unigene53936_All//2.00E-54//AT5G59240| 40S ribosomal protein S8 (RPS8B)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0030312//GO:0031981	nr +
Unigene53937_All	402	0.52	0.38	0.00	2.11	0.00	0.56	0.95	0.94	0.40	-4.61E-01	7.58E-01		-9.02E+00	1.45E-01		-1.10E+01	2.80E-06	Down	-1.91E+00	2.14E-02		-1.67E-02	1.02E+00		-1.26E+00	2.48E-01				Unigene53937_All//9.00E-135//TC141103				
Unigene5394_All	617	5.94	3.04	1.81	4.12	3.24	2.27	3.84	2.17	0.58	-9.66E-01	2.76E-03		-1.71E+00	2.26E-06	Down	-3.47E-01	4.10E-01		-8.60E-01	3.05E-02		-8.24E-01	2.57E-02		-2.72E+00	1.50E-09	Down	Unigene5394_All//gi|297601748|ref|NP_001051392.2|//8.00E-18//Os03g0768900 [Oryza sativa Japonica Group] >gi|255674928|dbj|BAF13306.2| Os03g0768900 [Oryza sativa Japonica Group]	Unigene5394_All//3.00E-32//AT2G23690| unknown protein	Unigene5394_All//0.00E+00//DW506594				nr -
Unigene53940_All	288	0.00	9.85	2.22	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	3.83E-16	Up	1.11E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene53940_All//gi|60543120|dbj|BAD98089.1|//8.00E-45//histone 3 [Conocephalum conicum]	Unigene53940_All//9.00E-45//AT5G65360| histone H3	Unigene53940_All//2.00E-18//gi|54123404|gb|CO198913.1|CO198913			GO:0000785//GO:0003676//GO:0009536//GO:0034728	nr +
Unigene53946_All	658	0.64	0.00	0.32	2.95	0.58	1.17	0.26	0.06	0.18	-9.31E+00	1.05E-02		-9.75E-01	4.11E-01		-2.36E+00	1.48E-06	Down	-1.34E+00	4.60E-03		-2.02E+00	3.67E-01		-5.01E-01	7.46E-01		Unigene53946_All//gi|255543100|ref|XP_002512613.1|//2.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223548574|gb|EEF50065.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene53949_All	235	0.00	4.53	3.63	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.81E-06	Up	1.18E+01	9.02E-05	Up	null	null		null	null		null	null		null	null									
Unigene5395_All	690	7.36	16.67	7.95	11.91	8.93	9.43	19.30	29.92	8.72	1.18E+00	1.85E-11	Up	1.12E-01	6.77E-01		-4.15E-01	3.60E-02		-3.38E-01	1.15E-01		6.33E-01	4.99E-09		-1.15E+00	7.36E-16	Down	Unigene5395_All//gi|224083799|ref|XP_002307127.1|//8.00E-25//predicted protein [Populus trichocarpa] >gi|222856576|gb|EEE94123.1| predicted protein [Populus trichocarpa]	Unigene5395_All//3.00E-05//AT5G64880| unknown protein	Unigene5395_All//0.00E+00//TC169879				nr -
Unigene53951_All	1244	0.00	0.00	0.00	0.76	0.72	0.65	3.50	27.11	0.86	null	null		null	null		-8.01E-02	8.94E-01		-2.19E-01	7.48E-01		2.95E+00	7.70E-133	Up	-2.02E+00	4.40E-12	Down	Unigene53951_All//gi|25453206|sp|Q9FX85.1|PER10_ARATH//1.00E-99//RecName: Full=Peroxidase 10; Short=Atperox P10; AltName: Full=ATP5a; Flags: Precursor >gi|10120418|gb|AAG13043.1|AC011807_2 peroxidase ATP5a [Arabidopsis thaliana] >gi|30017315|gb|AAP12891.1| At1g49570 [Arabidopsis thaliana]	Unigene53951_All//7.00E-101//AT1G49570| peroxidase, putative	Unigene53951_All//0.00E+00//TC139941		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0006950//GO:0008152//GO:0016209//GO:0043231//GO:0046872	nr +
Unigene53952_All	688	0.00	6.92	1.47	0.00	0.10	0.00	0.00	0.00	0.00	1.28E+01	3.82E-27	Up	1.05E+01	1.27E-05	Up	6.65E+00	6.08E-01		null	null		null	null		null	null		Unigene53952_All//gi|15822705|gb|AAL07519.1|//7.00E-29//RNA-binding protein precursor [Solanum tuberosum]	Unigene53952_All//3.00E-15//AT5G55550| RNA recognition motif (RRM)-containing protein			ko03040|Spliceosome	GO:0006355//GO:0043565//GO:0044424	nr -
Unigene53954_All	479	0.00	6.35	1.22	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.67E-17	Up	1.03E+01	2.17E-03		null	null		null	null		null	null		null	null									
Unigene53956_All	260	9.86	19.10	22.12	1.72	3.31	1.74	0.00	0.00	0.00	9.54E-01	4.54E-04		1.17E+00	9.62E-06	Up	9.41E-01	2.38E-01		1.07E-02	1.00E+00		null	null		null	null		Unigene53956_All//gi|225435828|ref|XP_002283771.1|//3.00E-16//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene53957_All	348	0.30	3.20	0.31	3.86	2.37	2.34	0.85	0.24	0.11	3.41E+00	1.24E-04	Up	2.52E-02	9.99E-01		-7.03E-01	2.18E-01		-7.26E-01	2.23E-01		-1.82E+00	2.11E-01		-2.89E+00	6.76E-02				Unigene53957_All//4.00E-07//EV482341				

Unigene53958_All	265	0.39	1.15	0.00	8.46	2.08	3.92	0.48	0.63	0.45	1.54E+00	3.23E-01			-8.63E+00	3.91E-01		-2.02E+00	2.91E-06	Down	-1.11E+00	9.63E-03		3.99E-01	8.14E-01		-8.57E-02	9.69E-01								
Unigene5396_All	1818	0.29	0.89	1.61	1.18	0.25	0.87	5.44	27.96	20.80	1.63E+00	3.13E-03			2.48E+00	5.01E-08	Up	-2.26E+00	7.84E-07	Down	-4.38E-01	3.53E-01		2.36E+00	5.50E-156	Up	1.93E+00	3.86E-92	Up	Unigene5396_All//gi|13161397|dbj|BAB33033.1|//1.00E-180//CP802 [Vigna unguiculata]	Unigene5396_All//2.00E-128//AT4G20820 FAD-binding domain-containing protein	Unigene5396_All//0.00E+00//DN817443		ko00620|Pyruvate metabolism		nr -
Unigene53961_All	375	0.00	0.00	0.00	25.11	16.62	3.13	0.00	0.00	0.00	null	null			null	null		-5.95E-01	6.43E-04		-3.00E+00	4.93E-34	Down	null	null		null	null		Unigene53961_All//gi|297725163|ref|XP_001174945.1|//2.00E-09//0x06g0666500 [Oryza sativa Japonica Group] >gi|52076527|dbj|BAD45404.1| RING zinc finger protein-like [Oryza sativa Japonica Group] >gi|255677304|dbj|BAH93673.1|0x06g0666500 [Oryza sativa Japonica Group]		Unigene53961_All//4.00E-140//TC145820			GO:0046914	nr +
Unigene53968_All	416	3.02	1.46	0.51	0.96	1.82	0.98	0.71	1.81	0.96	-1.05E+00	8.27E-02			-2.56E+00	6.98E-04	Down	9.27E-01	2.97E-01		2.85E-02	9.85E-01		1.35E+00	7.61E-02		4.29E-01	6.61E-01					Unigene53968_All//2.00E-170//ES837929				
Unigene5397_All	1137	7.32	2.18	2.29	9.99	7.27	13.39	16.62	7.46	10.16	-1.74E+00	1.03E-14	Down		-1.67E+00	2.79E-13	Down	-4.59E-01	4.14E-03		4.22E-01	3.12E-03		-1.16E+00	1.01E-21	Down	-7.10E-01	2.28E-10		Unigene5397_All//gi|186701238|gb|ACC91264.1|//1.00E-102//50S ribosomal protein [Capsella rubella]	Unigene5397_All//2.00E-91//AT4G23620| 50S ribosomal protein-related	Unigene5397_All//0.00E+00//TC166266		ko03010|Ribosome		nr +
Unigene53971_All	497	0.00	0.00	0.00	0.00	0.00	0.00	3.32	1.85	0.40	null	null			null	null		null	null		null	null		-8.43E-01	6.70E-02		-3.05E+00	1.31E-07	Down	Unigene53971_All//gi|300259453|gb|EFJ36580.1|//1.00E-32//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene53971_All//2.00E-27//AT4G25740| 40S ribosomal protein S10 (RPS10A)			ko03010|Ribosome		nr -
Unigene53973_All	233	0.67	1.09	1.14	0.00	0.89	0.19	9.44	9.51	3.76	6.91E-01	6.26E-01			7.62E-01	6.44E-01		9.79E+00	1.57E-01		7.60E+00	6.95E-01		1.09E-02	1.02E+00		-1.33E+00	5.61E-04	Down				Unigene53973_All//5.00E-58//CO079106				
Unigene53974_All	281	2.23	0.00	2.08	0.00	0.00	0.16	0.00	0.00	0.00	-1.11E-01	7.91E-01	Down		-1.00E-01	9.15E-01		null	null		7.33E+00	6.95E-01		null	null		null	null					Unigene53974_All//2.00E-17//BE368565				
Unigene53975_All	302	33.44	22.82	21.51	53.11	55.07	55.78	85.96	55.22	36.94	-5.51E-01	2.16E-03			-6.36E-01	6.52E-04		5.23E-02	7.87E-01		7.07E-02	6.80E-01		-6.39E-01	2.53E-11		-1.22E+00	4.86E-33	Down				Unigene53975_All//5.00E-148//gi|164255878|gb|ES843032.1|ES843032				
Unigene53979_All	341	0.00	1.93	3.75	0.15	0.81	0.93	0.00	0.00	0.00	1.09E+01	6.25E-04	Up		1.19E+01	4.68E-07	Up	2.47E+00	2.23E-01		2.67E+00	1.44E-01		null	null		null	null									
Unigene5398_All	544	24.53	40.33	27.70	34.16	24.62	33.96	72.20	51.94	34.35	7.18E-01	1.20E-09			1.76E-01	2.85E-01		-4.72E-01	7.21E-05		-8.50E-03	9.47E-01		-4.75E-01	3.84E-10		-1.07E+00	1.79E-40	Down	Unigene5398_All//gi|126508778|gb|AB015564.1|//8.00E-31//cysteine synthase [Glycine max]	Unigene5398_All//9.00E-22//AT3G59760| OASC (O-ACETYLSERINE (THIOL) LYASE ISOFORM C); ATP binding / cysteine synthase	Unigene5398_All//0.00E+00//TC139788		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr +
Unigene53980_All	252	28.44	10.05	23.03	24.12	21.18	34.77	9.06	8.46	9.01	-1.50E+00	1.94E-10	Down		-3.05E-01	2.07E-01		-1.87E-01	4.99E-01		5.28E-01	6.73E-03		-9.91E-02	8.02E-01		-7.80E-03	9.77E-01					Unigene53980_All//2.00E-113//TC161915				
Unigene53983_All	403	0.00	2.26	1.32	0.37	0.94	1.01	0.00	0.41	0.40	1.11E+01	2.62E-05	Up		1.04E+01	4.03E-03		1.34E+00	3.40E-01		1.44E+00	2.82E-01		8.70E+00	1.39E-01		8.63E+00	1.40E-01		Unigene53983_All//gi|160338267|gb|ABX26072.1|//7.00E-63//myb-like transcription factor 4 [Gossypium hirsutum] >gi|160338269|gb|ABX26073.1| myb-like transcription factor 4 [Gossypium hirsutum]		Unigene53983_All//9.00E-166//NP385922			GO:0003676//GO:0010468//GO:0043231	nr +
Unigene53987_All	260	19.92	66.65	27.44	0.19	0.66	0.17	0.16	0.16	0.15	1.74E+00	1.22E-29	Up		4.62E-01	4.57E-02		1.79E+00	5.20E-01		-1.42E-01	9.52E-01		-1.61E-02	1.00E+00		-8.59E-02	9.71E-01					Unigene53987_All//6.00E-67//DW506888				
Unigene53992_All	242	4.32	0.63	2.86	1.03	0.28	0.75	0.00	0.00	0.00	-2.78E+00	8.21E-04	Down		-5.96E-01	3.93E-01		-1.83E+00	2.75E-01		-4.63E-01	7.44E-01		null	null		null	null									
Unigene53996_All	411	0.00	2.96	1.81	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	5.47E-07	Up		1.08E+01	3.27E-04	Up	null	null		null	null		null	null		null	null									
Unigene53997_All	541	0.00	0.00	0.00	0.00	0.00	0.00	2.58	3.32	0.00	null	null			null	null		null	null		null	null		3.65E-01	4.23E-01		-1.13E+01	2.40E-10	Down	Unigene53997_All//gi|52788398|gb|AU87301.1|//9.00E-77//cyclophilin [Pinus halepensis]	Unigene53997_All//6.00E-66//AT2G21130| peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase	Unigene53997_All//1.00E-14//CD486136			GO:0016859//GO:0044267	nr -
Unigene53998_All	274	3.25	0.00	1.94	0.18	0.00	0.00	0.00	0.15	0.15	-1.17E+01	2.86E-05	Down		-7.40E-01	3.47E-01		-7.51E+00	5.54E-01		-7.51E+00	6.34E-01		7.25E+00	6.33E-01		7.18E+00	6.44E-01		Unigene53998_All//gi|297602164|ref|NP_001052155.2|//4.00E-16//0x04g0174800 [Oryza sativa Japonica Group] >gi|255675179|dbj|BAF14069.2|0x04g0174800 [Oryza sativa Japonica Group]	Unigene53998_All//7.00E-15//AT3G49170| EMB2261 (embryo defective 2261)				GO:0043231	nr -
Unigene54_All	355	4.57	6.99	5.70	0.98	3.01	4.45	0.24	0.12	1.35	6.14E-01	1.29E-01			3.19E-01	5.10E-01		1.61E+00	2.12E-02		2.18E+00	2.41E-04	Up	-1.02E+00	7.24E-01		2.50E+00	2.51E-02		Unigene54_All//gi|224121346|ref|XP_002330804.1|//1.00E-57//autoinhibited H+ ATPase [Populus trichocarpa] >gi|222872606|gb|EEF09737.1| autoinhibited H+ ATPase [Populus trichocarpa]	Unigene54_All//5.00E-43//AT4G30190| AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism	Unigene54_All//6.00E-142//gi|78352360|gb|DT572634.1|DT572634		ko00190|Oxidative phosphorylation		nr +
Unigene5400_All	834	103.39	85.06	142.38	93.12	94.14	94.93	33.71	17.99	14.57	-2.82E-01	4.66E-07			4.62E-01	1.05E-21		1.57E-02	8.29E-01		2.78E-02	6.99E-01		-9.06E-01	1.13E-21		-1.21E+00	2.44E-35	Down				Unigene5400_All//8.00E-171//gi|78323471|gb|DT543745.1|DT543745				
Unigene54001_All	256	0.41	0.00	0.00	1.17	0.00	0.18	2.48	1.31	9.34	-8.68E+00	3.70E-01			-8.68E+00	3.91E-01		-1.02E+01	2.01E-02		-2.73E+00	1.37E-01		-9.24E-01	2.63E-01		1.91E+00	1.68E-06	Up	Unigene54001_All//gi|297797645|ref|XP_002866707.1|//2.00E-10//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312542|gb|EFH42966.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene54001_All//2.00E-08//AT5G67340| armadillo/beta-catenin repeat family protein / U-box domain-containing protein	Unigene54001_All//2.00E-79//gi|164264941|gb|ES794132.1|ES794132			GO:0019787//GO:0032446//GO:0043234//GO:0044464	nr -
Unigene54002_All	212	30.60	21.27	24.11	63.91	65.13	42.18	91.54	59.93	31.76	-5.25E-01	2.38E-02			-3.44E-01	1.69E-01		2.73E-02	8.86E-01		-6.00E-01	5.61E-05		-6.11E-01	4.42E-08		-1.53E+00	7.67E-35	Down	Unigene54002_All//gi|223453020|gb|ACM89774.1|//3.00E-35//beta-tubulin 14 [Gossypium hirsutum]	Unigene54002_All//1.00E-35//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene54002_All//1.00E-116//gi|109824543|gb|DW009368.1|DW009368		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene54003_All	334	0.00	1.82	1.75	0.15	2.78	1.49	0.13	0.25	0.72	1.08E+01	1.17E-03			1.08E+01	2.17E-03		4.22E+00	1.07E-04	Up	3.32E+00	2.31E-02		9.83E-01	7.31E-01		2.50E+00	1.59E-01					Unigene54003_All//7.00E-15//CO115807				
Unigene54004_All	942	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.89	12.98	null	null			null	null		null	null		null	null		2.72E+00	1.18E-03		6.59E+00	4.90E-82	Up	Unigene54004_All//gi|75334084|sp|Q9FMS6.1|CAF1K_ARATH//2.00E-63//RecName: Full=Probable CCR4-associated factor 1 homolog 11 >gi|9757805|dbj|BAB08323.1| CCR4-associated factor-like protein [Arabidopsis thaliana]	Unigene54004_All//4.00E-62//AT5G22250| CCR4-NOT transcription complex protein, putative			ko03018|RNA degradation	GO:0004518	nr -
Unigene54005_All	729	0.00	0.00	0.00	0.00	0.00	0.00	20.18	1.15	0.38	null	null			null	null		null	null		null	null		-4.14E+00	4.83E-78	Down	-5.72E+00	1.92E-96	Down								
Unigene54012_All	333	0.00	0.61	0.00	0.45	0.31	0.00	1.52	4.39	4.67	9.25E+00	1.36E-01			null	null		-5.33E-01	7.84E-01		-8.81E+00	2.33E-01		1.53E+00	2.96E-03		1.61E+00	9.55E-04	Up	Unigene54012_All//gi|224058639|ref|XP_002299579.1|//1.00E-18//cytochrome P450 [Populus trichocarpa] >gi|222846837|gb|EEE84384.1| cytochrome P450 [Populus trichocarpa]	Unigene54012_All//4.00E-12//AT2G45550| CYP76C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene54012_All//5.00E-22//ES835059		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0005488	nr +
Unigene54018_All	629	0.00	3.30	2.20	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.94E-12	Up		1.11E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene54018_All//gi|3808062|dbj|BAA34056.1|//1.00E-08//PV100 [Cucurbita maxima]						GO:0005488//GO:0043231	nr -
Unigene54022_All	449	0.47	4.18	0.12	0.44	0.54	0.50	0.47	0.00	0.80	3.16E+00	5.97E-07	Up		-1.97E+00	3.81E-01		2.75E-01	8.95E-01		1.80E-01	9.35E-01		-8.88E+00	7.43E-02		7.62E-01	4.99E-01		Unigene54022_All//gi|229609803|gb|ACQ83517.1|//6.00E-56//CBL-interacting protein kinase 01 [Vitis vinifera]	Unigene54022_All//5.00E-42//AT4G18700| CIPK12 (CBL-INTERACTING PROTEIN KINASE 12); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene54022_All//3.00E-39//TC143203			GO:0004672//GO:0006464//GO:0023060//GO:0032559//GO:0043231	nr +
Unigene54028_All	417	0.00	0.85	0.00	0.00	0.58	0.22	0.30	4.21	1.53	9.73E+00	2.46E-02			null	null		9.18E+00	1.04E-01		7.76E+00	4.75E-01		3.79E+00	3.81E-09	Up	2.33E+00	1.05E-02					Unigene54028_All//0.00E+00//DT463200				
Unigene54029_All	266	0.00	4.57	2.80	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.47E-07	Up		1.15E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene54029_All//sp|Q24040|BGB_DROME//4.00E-11//Protein big brother OS=Drosophila melanogaster GN=Bgb PE=1 SV=3							swissprot +
Unigene5403_All	934	1.62	6.78	7.30	8.21	15.52	17.41	2.58	1.25	1.24	2.06E+00	6.07E-14	Up		2.17E+00	2.41E-15	Up	9.18E-01	4.67E-11		1.08E+00	9.01E-15	Up	-1.04E+00	4.61E-03		-1.06E+00	2.88E-03		Unigene5403_All//gi|87240376|gb|AB032234.1|//2.00E-30//Calcium-binding EF-hand [Medicago truncatula]	Unigene5403_All//5.00E-28//AT4G27280| calcium-binding EF hand family protein	Unigene5403_All//2.00E-26//TC152910				nr -
Unigene54032_All	289	0.00	0.00	0.00	0.00	0.00	0.00	2.93	2.17	0.00	null	null			null	null		null	null		null	null		-4.32E-01	5.47E-01		-1.15E+01	2.21E-06	Down	Unigene54032_All//gi|3915255|sp|Q43362.1|VATL_PLECA//4.00E-25//RecName: Full=V-type proton ATPase 16 kDa proteolipid subunit; Short=V-ATPase 16 kDa proteolipid subunit; AltName: Full=Vacuolar proton pump 16 kDa proteolipid subunit >gi|1208770|gb|AAB67833.1|V-type ATPase 16 kDa proteolipid subunit [Pleurochrysis carterae] >gi|2149129|gb|AAB58498.1|vacuolar-type H(+)-ATPase [Pleurochrysis carterae]	Unigene54032_All//3.00E-24//AT4G34720| AVA-P1; ATPase/ proton-transporting ATPase, rotational mechanism			ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0006754//GO:0006818//GO:0015078//GO:0031090//GO:0031224//GO:0031410//GO:0033176//GO:0033177//GO:0043231	nr +
Unigene54035_All	823	63.45	53.93	50.47	4.24	9.00	8.45	10.63	11.73	8.18	-2.34E-01	1.67E-03			-3.30E-01	1.24E-05		1.09E+00	1.41E-07	Up	9.96E-01	6.65E-06		1.42E-01	4.58E-01		-3.78E-01	2.73E-02		Unigene54035_All//gi|55168340|gb|AAV44205.1|//2.00E-42//unknow protein [Oryza sativa Japonica Group]		Unigene54035_All//1.00E-95//TC149394			GO:0009536	nr -
Unigene54036_All	418	0.00	4.12	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.98E-10	Up		1.06E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene54036_All//sp|P27878|VIT1_CERCA//4.00E-49//Vitellogenin-1 OS=Ceratitis capitata GN=VG1-GAMMA PE=2 SV=1							swissprot +
Unigene54037_All	282	0.19	6.83	1.51	0.88	3.17	0.80	2.40	1.63	5.65	5.20E+00	1.06E-09	Up		3.03E+00	5.73E-02		1.85E+00	2.15E-02		-1.41E-01	9.28E-01		-5.57E-01	4.89E-01		1.24E+00	7.44E-03									
Unigene5404_All	788	37.65	45.85	34.94	121.31	148.84	107.81	42.60	16.60	19.31	2.84E-01	1.68E-03			-1.08E-01	3.71E-01		2.95E-01	1.27E-11		-1.70E-01	1.56E-03		-1.36E+00	9.40E-49	Down	-1.14E+00	2.41E-38	Down	Unigene5404_All//gi|186531069|ref|NP_001119410.1|//1.00E-51//metal ion binding [Arabidopsis thaliana]	Unigene5404_All//7.00E-26//AT5G63530| ATPP3; metal ion binding / transition metal ion binding	Unigene5404_All//0.00E+00//TC167496				nr +
Unigene54040_All	1680	0.00	9.44	2.85	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	3.99E-91	Up		1.15E+01	1.22E-26	Up	null	null		null	null		null	null		null	null		Unigene54040_All//gi|298712549|emb|CBJ26817.1|//1.00E-170//Catalase is an enzyme, present in all aerobic cells, that decomposes hydrogen peroxide to molecular [Ectocarpus siliculosus]	Unigene54040_All//1.00E-98//AT1G20630| CAT1 (CATALASE 1); catalase			ko04146|Peroxisome//ko00380|Tryptophan metabolism	GO:0003824//GO:0046872	nr -
Unigene54042_All	346	0.30	3.51	0.00	0.00	0.00	0.26	0.98	0.85	0.81	3.54E+00	4.02E-05	Up		-8.24E+00	3.91E-01		null	null		8.03E+00	4.75E-01		-2.09E-01	8.50E-01		-2.79E-01	7.80E-01		Unigene54042_All//gi|229609807|gb|ACQ83519.1|//6.00E-49//CBL-interacting protein kinase 03 [Vitis vinifera]	Unigene54042_All//9.00E-50//AT4G30960| SIP3 (SOS3-INTERACTING PROTEIN 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene54042_All//3.00E-51//TC137020		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0006972//GO:0009926//GO:0023060//GO:0032401//GO:0032559	nr -
Unigene54044_All	260	0.00	4.87	1.43	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.86E-07	Up		1.05E+01	2.50E-02		null	null		null	null		null	null		null	null									
Unigene54048_All	354	0.00	1.43	0.00	0.00	0.00	0.38	0.00	0.47	2.36	1.05E+01	4.04E-03			null	null		null	null		8.58E+00	3.10E-01		8.88E+00	1.39E-01		1.12E+01	3.88E-06	Up	Unigene54048_All//gi|224087825|ref|XP_002308239.1|//3.00E-18//predicted protein [Populus trichocarpa] >gi|222854215|gb|EEE91762.1| predicted protein [Populus trichocarpa]		Unigene54048_All//0.00E+00//TC155759				nr -
Unigene54049_All	360	0.15	9.99	2.96	0.14	0.00	0.00	0.00	0.00	1.44	6.10E+00	6.06E-19	Up		4.35E+00	6.46E-05	Up	-7.11E+00	5.54E-01		-7.11E+00	6.34E-01		null	null		1.05E+01	6.13E-04	Up				Unigene54049_All//1.00E-34//FL577761				
Unigene5405_All	602	4.61	1.26	3.72	3.56	3.55	3.53	7.02	5.35	2.58	-1.87E+00	7.41E-06	Down		-3.10E-01	4.36E-01		-4.80E-03	9.78E-01		-1.31E-02	9.68E-01		-3.94E-01	1.50E-01		-1.44E+00	1.12E-07	Down	Unigene5405_All//gi|11762164|gb|AAG40360.1|AF325008_1//7.00E-45//AT4g22310 [Arabidopsis thaliana]	Unigene5405_All//4.00E-43//AT4G22310| unknown protein	Unigene5405_All//0.00E+00//gi|21099182|gb|BQ411495.1|BQ411495				nr -
Unigene54058_All	252	0.42	0.00	1.27	0.59	0.41	0.18	2.18	1.49	0.00	-8.70E+00	3.70E-01			1.61E+00	3.04E-01		-5.33E-01	7.84E-01		-1.73E+00	5.01E-01		-5.47E-01	5.52E-01		-1.11E+01	2.80E-04	Down								
Unigene5406_All	895	4.21	8.95	5.65	4.45	5.12	9.29	20.50	19.85	27.06	1.09E+00	2.65E-07	Up		4.25E-01	1.40E-01		2.01E-01	5.66E-01		1.06E+00	1.35E-07	Up	-4.69E-02	7.26E-01		4.01E-01	3.49E-05		Unigene5406_All//gi|22328997|ref|NP_194559.2|//1.00E-45//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana]	Unigene5406_All//2.00E-35//AT4G28300| hydroxyproline-rich glycoprotein family protein	Unigene5406_All//0.00E+00//gi|78344249|gb|DT564523.1|DT564523				nr -

Unigene54063_All	503	0.21	0.00	0.85	0.40	1.03	3.59	0.25	0.00	0.79	-7.70E+00	3.70E-01		2.03E+00	1.39E-01		1.37E+00	2.26E-01		3.18E+00	5.38E-07	Up	-7.98E+00	2.35E-01		1.65E+00	1.40E-01		Unigene54063_All//gi|255537982|ref|XP_002510056.1|//2.00E-15//conserved hypothetical protein [Ricinus communis] >gi|223550757|gb|EEF52243.1| conserved hypothetical protein [Ricinus communis]		Unigene54063_All//6.00E-44//ES817553				nr -
Unigene54065_All	252	0.00	1.01	0.00	0.40	0.00	1.97	7.72	3.81	0.32	9.97E+00	7.85E-02		null	null		-8.63E+00	3.12E-01		2.32E+00	6.88E-02		-1.02E+00	1.47E-02		-4.61E+00	6.97E-12	Down	Unigene54065_All//gi|297850466|ref|XP_002893114.1|//2.00E-09//opc-8:0 CoA ligase1 [Arabidopsis lyrata subsp. lyrata] >gi|297338956|gb|EFH69373.1| opc-8:0 CoA ligase1 [Arabidopsis lyrata subsp. lyrata]	Unigene54065_All//1.00E-100//AT1G20510 OPCL1 (OPC-8:0 COA LIGASE1); 4-coumarate-CoA ligase	Unigene54065_All//3.00E-50//DW499144		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0006950//GO:0009694//GO:0016405//GO:0016703//GO:0042579	nr +
Unigene54068_All	608	0.00	48.25	18.66	0.00	0.00	0.00	0.00	0.00	0.00	1.56E+01	3.90E-169	Up	1.42E+01	9.59E-64	Up	null	null		null	null		null	null		null	null		Unigene54068_All//gi|30690964|ref|NP_849729.1|//3.00E-48//60S ribosomal protein L18A (RPL18aA) [Arabidopsis thaliana]	Unigene54068_All//2.00E-49//AT1G29965| 60S ribosomal protein L18A (RPL18aA)			ko03010|Ribosome	GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr +
Unigene54070_All	648	10.58	36.20	16.60	19.53	18.60	13.24	10.50	8.84	6.39	1.78E+00	6.12E-41	Up	6.50E-01	3.04E-04		-7.01E-02	7.30E-01		-5.60E-01	3.07E-04		-2.50E-01	2.53E-01		-7.16E-01	2.33E-04				Unigene54070_All//0.00E+00//gi|73851845|gb|DT460865.1|DT460865				
Unigene54072_All	1780	0.00	0.06	0.12	0.90	0.15	0.15	11.26	19.94	7.09	5.83E+00	3.85E-01		6.90E+00	1.40E-01		-2.53E+00	6.66E-06	Down	-2.56E+00	2.78E-05	Down	8.24E-01	3.31E-23		-6.66E-01	7.08E-10		Unigene54072_All//gi|30687905|ref|NP_850317.1|//1.00E-35//F-box family protein [Arabidopsis thaliana] >gi|75251421|sp|Q5S4V7.1|FB129_ARATH RecName: Full=F-box protein At2g39490	Unigene54072_All//7.00E-37//AT2G39490| F-box family protein	Unigene54072_All//1.00E-17//TC177932				nr +
Unigene54074_All	414	0.00	21.66	9.52	0.00	0.00	0.22	0.00	0.00	0.00	1.44E+01	2.43E-51	Up	1.32E+01	7.61E-22	Up	null	null		7.77E+00	4.75E-01		null	null		null	null		Unigene54074_All//gi|301105230|ref|XP_002901699.1|//9.00E-47//40S ribosomal protein S11 [Phytophthora infestans T30-4] >gi|262100703|gb|EEY58755.1| 40S ribosomal protein S11 [Phytophthora infestans T30-4]	Unigene54074_All//2.00E-45//AT4G30800| 40S ribosomal protein S11 (RPS11B)	Unigene54074_All//3.00E-11//DR453672		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935	nr -
Unigene54075_All	485	0.00	0.00	0.11	0.21	0.21	0.19	1.31	1.55	3.70	null	null		6.78E+00	6.35E-01		5.24E-02	9.66E-01		-1.42E-01	9.49E-01		2.47E-01	7.31E-01		1.50E+00	7.33E-04	Up								
Unigene54076_All	665	0.00	0.00	0.00	0.00	0.00	0.00	0.70	5.78	0.96	null	null		null	null		null	null		null	null		3.05E+00	3.73E-16	Up	4.55E-01	5.78E-01		Unigene54076_All//gi|55168340|gb|AAV44205.1|//5.00E-15//unknown protein [Oryza sativa Japonica Group]		Unigene54076_All//2.00E-19//TC174737			GO:0009536	nr +
Unigene54079_All	556	0.00	8.29	4.98	0.00	0.00	0.00	0.00	0.00	0.14	1.30E+01	2.84E-26	Up	1.23E+01	2.74E-15	Up	null	null		null	null		null	null		7.16E+00	4.03E-01		Unigene54079_All//gi|226509811|ref|NP_001147421.1|//4.00E-32//60 ribosomal protein L14 [Zea mays] >gi|195611252|gb|ACG27456.1| 60 ribosomal protein L14 [Zea mays]	Unigene54079_All//2.00E-23//AT2G20450| 60S ribosomal protein L14 (RPL14A)			ko03010|Ribosome	GO:0009536//GO:0009987//GO:0015934//GO:0016020//GO:0031981//GO:0043170	nr +
Unigene5408_All	698	0.15	0.22	0.15	0.00	0.99	0.91	0.48	2.81	1.08	5.39E-01	7.79E-01		2.58E-02	9.99E-01		9.95E+00	3.05E-04	Up	9.82E+00	7.60E-04	Up	2.54E+00	3.39E-07	Up	1.16E+00	1.06E-01		Unigene5408_All//gi|224062625|ref|XP_002300863.1|//9.00E-45//NPR1/NIM1-like regulatory protein [Populus trichocarpa] >gi|222842589|gb|EEE80136.1| NPR1/NIM1-like regulatory protein [Populus trichocarpa]	Unigene5408_All//4.00E-26//AT5G45110| NPR3 (NPR1-LIKE PROTEIN 3); protein binding	Unigene5408_All//0.00E+00//CO107762				nr +
Unigene54081_All	537	0.00	0.00	0.00	0.00	0.00	0.17	0.47	3.50	2.52	null	null		null	null		null	null		7.39E+00	4.75E-01		2.89E+00	7.82E-08	Up	2.42E+00	4.42E-05	Up	Unigene54081_All//gi|225440392|ref|XP_002267559.1|//1.00E-30//PREDICTED: ripening-related protein-like [Vitis vinifera]	Unigene54081_All//3.00E-24//AT5G02230| haloacid dehalogenase-like hydrolase family protein	Unigene54081_All//1.00E-29//TC132555			GO:0003824	nr -
Unigene54082_All	489	0.96	0.10	1.52	0.10	0.21	0.46	1.12	2.99	47.99	-3.22E+00	2.73E-02		6.63E-01	4.19E-01		1.05E+00	8.07E-01		2.18E+00	3.23E-01		1.41E+00	5.47E-03		5.42E+00	1.26E-146	Up	Unigene54082_All//gi|14190445|gb|AAX55703.1|AF378900_1/3.00E-61//At2g04520/T103.7 [Arabidopsis thaliana] >gi|15450561|gb|AAK96458.1| At2g04520/T103.7 [Arabidopsis thaliana]	Unigene54082_All//2.00E-59//AT2G04520| eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative	Unigene54082_All//2.00E-90//gi|109828846|gb|DW227465.1|DW227465			GO:0006412//GO:0008135	nr -
Unigene54083_All	495	0.00	0.00	0.00	0.00	0.00	0.00	2.99	4.98	0.00	null	null		null	null		null	null		null	null		7.37E-01	4.17E-02		-1.15E+01	5.85E-11	Down	Unigene54083_All//gi|115457852|ref|NP_001052526.1|//4.00E-18//Os04g0349500 [Oryza sativa Japonica Group] >gi|32489919|emb|CAE05511.1| OSJNBa0038P21.4 [Oryza sativa (japonica cultivar-group)] >gi|113564097|dbj|BAF14440.1| Os04g0349500 [Oryza sativa Japonica Group]	Unigene54083_All//2.00E-14//AT5G20290| 40S ribosomal protein S8 (RPS8A)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0030312//GO:0031981	nr +
Unigene54086_All	718	2.62	0.00	1.56	4.16	1.77	0.63	1.94	0.64	0.61	-1.14E+01	6.73E-11	Down	-7.52E-01	1.34E-01		-1.23E+00	3.05E-04	Down	-2.73E+00	4.53E-10	Down	-1.60E+00	2.61E-03		-1.67E+00	1.27E-03		Unigene54086_All//gi|18399836|ref|NP_566442.1|//1.00E-12//myb family transcription factor [Arabidopsis thaliana] >gi|42572405|ref|NP_974298.1| myb family transcription factor [Arabidopsis thaliana]		Unigene54086_All//0.00E+00//TC134097				nr +
Unigene5409_All	1619	0.23	0.41	0.30	0.86	1.11	1.51	1.23	3.79	1.26	8.47E-01	3.48E-01		3.88E-01	6.97E-01		3.60E-01	5.21E-01		8.06E-01	5.10E-02		1.63E+00	3.17E-12	Up	3.21E-02	9.58E-01		Unigene5409_All//gi|224062625|ref|XP_002300863.1|//1.00E-173//NPR1/NIM1-like regulatory protein [Populus trichocarpa] >gi|222842589|gb|EEE80136.1| NPR1/NIM1-like regulatory protein [Populus trichocarpa]	Unigene5409_All//5.00E-114//AT5G45110| NPR3 (NPR1-LIKE PROTEIN 3); protein binding	Unigene5409_All//0.00E+00//CO107762				nr -
Unigene54091_All	534	0.00	0.00	0.00	0.00	0.00	0.00	1.35	1.96	8.65	null	null		null	null		null	null		null	null		5.40E-01	3.95E-01		2.68E+00	2.22E-17	Up								ESTscan +
Unigene54092_All	297	0.00	0.00	0.00	0.00	0.00	0.00	0.14	1.13	4.02	null	null		null	null		null	null		null	null		2.98E+00	5.73E-02		4.82E+00	1.77E-07	Up								
Unigene54093_All	408	0.00	0.00	0.00	0.00	0.00	0.00	9.12	0.41	3.91	null	null		null	null		null	null		null	null		-4.48E+00	4.22E-21	Down	-1.22E+00	1.63E-05	Down	Unigene54093_All//gi|224094394|ref|XP_002310153.1|//3.00E-08//predicted protein [Populus trichocarpa] >gi|224159501|ref|XP_002338090.1| predicted protein [Populus trichocarpa] >gi|222853056|gb|EEE90603.1| predicted protein [Populus trichocarpa] >gi|222870802|gb|EEF07933.1| predicted protein [Populus trichocarpa]						nr -
Unigene54095_All	557	0.00	3.64	1.24	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.53E-11	Up	1.03E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene54095_All//gi|225424204|ref|XP_002280594.1|//5.00E-06//PREDICTED: hypothetical protein [Vitis vinifera] >gi|147861928|emb|CAN80912.1| hypothetical protein [Vitis vinifera]						nr +
Unigene54096_All	606	0.00	6.52	5.36	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.66E-22	Up	1.24E+01	5.81E-18	Up	null	null		null	null		null	null		null	null		Unigene54096_All//gi|68565782|sp|Q7X9A0.1|RCA1_LARTR//1.00E-106//RecName: Full=Ribulose bisphosphate carboxylase/oxygenase activase 1, chloroplastic; Short=RuBisCO activase 1; Short=RA 1; AltName: Full=RuBisCO activase alpha form; Flags: Precursor >gi|32481065|gb|AAP83929.1| Rubisco activase alpha form precursor [Larrea tridentata]	Unigene54096_All//2.00E-106//AT2G39730| RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	Unigene54096_All//2.00E-133//gi|164361726|gb|EX168023.1|EX168023				nr -
Unigene5410_All	1153	1.04	0.44	0.74	1.77	1.49	2.00	4.99	1.96	2.14	-1.25E+00	4.69E-02		-4.98E-01	4.26E-01		-2.46E-01	6.10E-01		1.73E-01	6.91E-01		-1.35E+00	6.56E-09	Down	-1.22E+00	5.23E-08	Down	Unigene5410_All//gi|115481106|ref|NP_001064146.1|//1.00E-128//Os10g0141900 [Oryza sativa Japonica Group] >gi|16519465|gb|AAL25174.1|AC079852_7 Putative tRNA-guanine transglycosylase [Oryza sativa] >gi|19919982|gb|AAN08430.1|AC112513_16 Putative tRNA-guanine transglycosylase [Oryza sativa] >gi|31430120|gb|AAP52078.1| tRNA-guanine transglycosylases, various specificities family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|110288598|gb|ABG65910.1| tRNA-guanine transglycosylases, various specificities family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113638755|dbj|BAF26060.1| Os10g0141900 [Oryza sativa Japonica Group]		Unigene5410_All//0.00E+00//TC137426				nr +
Unigene54100_All	219	1.19	0.00	0.00	0.00	0.63	2.89	1.74	0.76	0.18	-1.02E+01	6.69E-02		-1.02E+01	8.55E-02		9.30E+00	3.18E-01		1.15E+01	7.59E-04	Up	-1.19E+00	3.09E-01		-3.26E+00	2.22E-02		Unigene54100_All//gi|124360447|gb|ABN08457.1|//5.00E-19//Tetratricopeptide-like helical [Medicago truncatula]	Unigene54100_All//3.00E-18//AT5G39350| pentatricopeptide (PPR) repeat-containing protein	Unigene54100_All//6.00E-116//ES809880			GO:0003006//GO:0043231	nr -
Unigene54102_All	1038	0.00	0.00	0.00	0.00	0.00	0.00	5.70	4.47	0.27	null	null		null	null		null	null		null	null		-3.52E-01	1.24E-01		-4.41E+00	3.42E-34	Down	Unigene54102_All//gi|125742947|gb|ABN54676.1|//1.00E-135//translation elongation factor 1 alpha [Aphanomyces cochlioides]	Unigene54102_All//3.00E-127//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene54102_All//2.00E-20//CD809343				nr +
Unigene54103_All	259	0.00	2.93	2.06	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	1.10E+01	4.03E-03		null	null		null	null		null	null		null	null									
Unigene54106_All	807	0.00	0.00	0.00	0.00	0.00	0.00	3.30	1.35	0.44	null	null		null	null		null	null		null	null		-1.29E+00	2.59E-04	Down	-2.89E+00	2.70E-11	Down	Unigene54106_All//gi|301122631|ref|XP_002909042.1|//6.00E-68//40S ribosomal protein S6 [Phytophthora infestans T30-4] >gi|262099804|gb|EEY57856.1| 40S ribosomal protein S6 [Phytophthora infestans T30-4]	Unigene54106_All//1.00E-36//AT4G31700| RPS6 (RIBOSOMAL PROTEIN S6); structural constituent of ribosome			ko03010|Ribosome	GO:0005622	nr +
Unigene54107_All	523	0.00	0.10	0.20	0.10	0.00	0.35	0.73	2.48	6.70	6.60E+00	6.15E-01		7.67E+00	3.97E-01		-6.57E+00	5.54E-01		1.86E+00	4.58E-01		1.77E+00	1.84E-03		3.20E+00	8.51E-16	Up	Unigene54107_All//gi|226503773|ref|NP_001150641.1|//2.00E-20//mitochondrial 2-oxoglutarate/malate carrier protein [Zea mays] >gi|195640804|gb|ACG39870.1| mitochondrial 2-oxoglutarate/malate carrier protein [Zea mays]	Unigene54107_All//2.00E-21//AT4G24570| mitochondrial substrate carrier family protein	Unigene54107_All//6.00E-41//TC141900			GO:0006810//GO:0009987//GO:0019866//GO:0031224//GO:0043231	nr +
Unigene54108_All	512	0.00	0.00	0.00	0.00	0.00	0.00	25.60	68.41	1.79	null	null		null	null		null	null		null	null		1.42E+00	4.86E-54	Up	-3.84E+00	4.52E-68	Down								
Unigene5411_All	677	2.01	1.27	2.44	3.02	1.68	0.67	2.81	2.53	1.71	-6.59E-01	2.44E-01		2.79E-01	6.20E-01		-8.46E-01	4.95E-02		-2.18E+00	1.41E-05	Down	-1.51E-01	7.30E-01		-7.20E-01	7.44E-02									

Unigene54110_All	710	0.15	1.64	0.38	0.84	1.16	2.99	0.00	0.00	0.00	3.48E+00	7.08E-05	Up	1.35E+00	4.09E-01		4.67E-01	5.85E-01		1.83E+00	1.26E-04	Up	null	null		null	null		Unigene54110_All//gi|297815580|ref|XP_002875673.1|//3.00E-57//oxidoreductase, acting on the CH-CH group of donors [Arabidopsis lyrata subsp. lyrata] >gi|297321511|gb|EFH51932.1| oxidoreductase, acting on the CH-CH group of donors [Arabidopsis lyrata subsp. lyrata]	Unigene54110_All//2.00E-50//AT3G44550| FAR5 (FATTY ACID REDUCTASE 5); binding / catalytic/ oxidoreductase, acting on the CH-CH group of donors			ko04146|Peroxisome	GO:0006633//GO:0006970//GO:0009555//GO:0016620//GO:0043231	nr -
Unigene54117_All	331	0.00	0.00	0.00	3.91	0.21	0.00	3.19	1.39	0.00	null	null		null	null		-4.23E+00	1.56E-07	Down	-1.19E+01	4.24E-08	Down	-1.20E+00	4.78E-02		-1.16E+01	6.71E-08	Down							
Unigene54118_All	1478	0.00	16.39	7.10	0.00	0.00	0.06	0.00	0.00	0.00	1.40E+01	1.72E-139	Up	1.28E+01	6.67E-59	Up	null	null		5.93E+00	4.75E-01		null	null		null	null		Unigene54118_All//gi|116055071|emb|CAL57467.1|//5.00E-09//unnamed protein product [Ostreococcus tauri]						nr -
Unigene5412_All	429	30.12	60.35	45.55	39.83	41.58	49.27	44.55	58.75	49.96	1.00E+00	2.97E-19	Up	5.97E-01	3.43E-06		6.21E-02	7.21E-01		3.07E-01	1.18E-02		3.99E-01	3.73E-05		1.66E-01	1.40E-01		Unigene5412_All//gi|192910812|gb|ACF06514.1|//9.00E-13//synaptobrevin 1 [Elaeis guineensis]		Unigene5412_All//0.00E+00//TC161149		ko04130|SNARE interactions in vesicular transport		nr +
Unigene54120_All	593	0.00	4.27	1.98	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.05E-14	Up	1.09E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene54120_All//gi|1620970|emb|CAA70100.1|//8.00E-40//L-lactate dehydrogenase [Solanum lycopersicum] >gi|1806117|emb|CAA71611.1| L-lactate dehydrogenase [Solanum lycopersicum]	Unigene54120_All//9.00E-32//AT4G17260| L-lactate dehydrogenase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00270|Cysteine and methionine metabolism//ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism	GO:0005975//GO:0016491//GO:0044237	nr +
Unigene54121_All	381	0.41	0.67	1.54	0.78	0.18	0.47	1.89	1.65	0.21	6.91E-01	6.26E-01		1.90E+00	8.47E-02		-2.12E+00	1.65E-01		-7.26E-01	6.38E-01		-1.97E-01	7.84E-01		-3.17E+00	8.09E-04	Down	Unigene54121_All//gi|296149177|gb|ADG96403.1|//8.00E-24//S-locus glycoprotein [Olea europaea]	Unigene54121_All//5.00E-18//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding				GO:0000166//GO:0004672//GO:0009987	nr -
Unigene54122_All	505	2.90	7.32	2.43	6.61	3.48	3.22	2.26	1.90	4.34	1.34E+00	5.94E-05	Up	-2.58E-01	6.23E-01		-9.26E-01	3.54E-03		-1.04E+00	2.05E-03		-2.48E-01	6.60E-01		9.41E-01	1.23E-02			Unigene54122_All//4.00E-150//TC167075					
Unigene54123_All	1044	0.40	0.58	0.51	0.10	0.07	0.17	0.93	1.36	2.86	5.39E-01	5.63E-01		3.48E-01	7.05E-01		-5.32E-01	8.15E-01		8.59E-01	6.95E-01		5.47E-01	2.90E-01		1.62E+00	1.79E-06	Up	Unigene54123_All//gi|16930479|gb|AAL31925.1|AF419593_1 At2g39210/T16B24.15 [Arabidopsis thaliana] >gi|3402684|gb|AAC28987.1| nodulin-like protein [Arabidopsis thaliana]	Unigene54123_All//3.00E-110//AT2G39210| nodulin family protein	Unigene54123_All//1.00E-09//gi|109857571|gb|DW486550.1|DW486550				nr -
Unigene54126_All	814	0.32	0.12	0.00	0.18	0.30	0.06	2.08	0.72	4.36	-1.37E+00	3.83E-01		-8.33E+00	8.55E-02		6.90E-01	7.32E-01		-1.73E+00	5.01E-01		-1.53E+00	1.16E-03		1.07E+00	2.13E-04	Up	Unigene54126_All//gi|224143990|ref|XP_002325148.1|//1.00E-107//type-b response regulator [Populus trichocarpa] >gi|222866582|gb|EEF03713.1| type-b response regulator [Populus trichocarpa]	Unigene54126_All//6.00E-86//AT2G25180| ARR12 (ARABIDOPSIS RESPONSE REGULATOR 12); transcription factor/ two-component response regulator	Unigene54126_All//4.00E-40//DR453553	ARR-B	ko04712|Circadian rhythm - plant	GO:0003676//GO:0004871//GO:0006351//GO:0010468//GO:0023060//GO:0043231	nr +
Unigene54128_All	380	0.00	5.07	1.40	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.73E-11	Up	1.05E+01	4.03E-03		null	null		null	null		null	null		null	null		Unigene54128_All//sp|Q9UKB1|FBW1B_HUMAN//8.00E-29//F-box/WD repeat-containing protein 11 OS=Homo sapiens GN=FBXW11 PE=1 SV=1						swissprot +
Unigene5413_All	967	11.09	20.85	12.00	20.86	23.40	17.89	20.46	15.43	9.06	9.11E-01	4.83E-13		1.14E-01	5.66E-01		1.65E-01	1.95E-01		-2.22E-01	9.21E-02		-4.07E-01	2.36E-04		-1.17E+00	5.18E-24	Down	Unigene5413_All//gi|224069292|ref|XP_002302948.1|//1.00E-73//high mobility group family [Populus trichocarpa] >gi|222844674|gb|EEE82221.1| high mobility group family [Populus trichocarpa]	Unigene5413_All//1.00E-32//AT1G14900| HMGA (HIGH MOBILITY GROUP A); DNA binding	Unigene5413_All//0.00E+00//TC131809				nr -
Unigene54132_All	316	0.00	3.85	1.69	0.00	0.22	0.00	0.00	0.00	0.00	1.19E+01	5.47E-07	Up	1.07E+01	4.03E-03		7.77E+00	6.08E-01		null	null		null	null		null	null		Unigene54132_All//sp|Q3SYZ8|PDLI3_BOVIN//2.00E-10//PDZ and LIM domain protein 3 OS=Bos taurus GN=PDLIM3 PE=2 SV=1						swissprot +
Unigene54135_All	904	0.00	51.01	19.20	0.00	0.00	0.00	0.00	0.00	0.00	1.56E+01	2.71E-266	Up	1.42E+01	5.47E-98	Up	null	null		null	null		null	null		null	null		Unigene54135_All//gi|159471131|ref|XP_001693710.1|//3.00E-88//ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|269969596|sp|A8HS48.1|RS3A_CHLRE RecName: Full=40S ribosomal protein S3a >gi|158283213|gb|EDP08964.1| ribosomal protein S3a [Chlamydomonas reinhardtii]	Unigene54135_All//3.00E-76//AT4G34670| 40S ribosomal protein S3A (RPS3aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene54138_All	860	0.00	0.00	0.00	0.00	0.00	0.00	6.15	9.04	0.00	null	null		null	null		null	null		null	null		5.57E-01	2.79E-03		-1.26E+01	7.25E-39	Down							ESTscan +
Unigene54139_All	529	0.00	0.57	0.00	0.57	0.20	0.00	0.72	1.74	5.65	9.17E+00	4.42E-02		null	null		-1.53E+00	2.98E-01		-9.14E+00	3.99E-02		1.27E+00	5.59E-02		2.97E+00	1.11E-12	Up	Unigene54139_All//gi|224138284|ref|XP_002326564.1|//4.00E-47//NBS resistance protein [Populus trichocarpa] >gi|222833886|gb|EEE72363.1| NBS resistance protein [Populus trichocarpa]	Unigene54139_All//6.00E-16//AT1G50180| disease resistance protein (CC-NBS-LRR class), putative			ko04626|Plant-pathogen interaction	GO:0000166//GO:0016787	nr -
Unigene5414_All	1356	5.86	12.29	10.45	11.90	13.89	8.83	0.62	0.65	0.53	1.07E+00	5.83E-14	Up	8.33E-01	7.86E-08		2.23E-01	9.72E-02		-4.31E-01	1.65E-03		5.38E-02	9.58E-01		-2.38E-01	7.02E-01		Unigene5414_All//gi|119360161|gb|AAL66809.1|//1.00E-121//At4g32290 [Arabidopsis thaliana]	Unigene5414_All//4.00E-106//AT4G32290| unknown protein	Unigene5414_All//0.00E+00//gi|78342817|gb|DT563091.1|DT563091				nr +
Unigene54140_All	999	0.00	0.00	0.00	0.00	0.00	0.00	3.05	6.19	0.12	null	null		null	null		null	null		null	null		1.02E+00	2.04E-06	Up	-4.67E+00	1.91E-18	Down							ESTscan +
Unigene54142_All	2140	0.00	0.00	0.00	0.00	0.00	0.00	5.06	10.47	0.20	null	null		null	null		null	null		null	null		1.05E+00	5.33E-22	Up	-4.63E+00	5.78E-64	Down	Unigene54142_All//gi|260446989|emb|CBG76271.1|//6.00E-80//00_Ba0005L10-00_Ba0081K17.22 [Oryza officinalis]	Unigene54142_All//4.00E-75//AT1G64390| AtGH9C2 (Arabidopsis thaliana glycosyl hydrolase 9C2); carbohydrate binding / catalytic/ hydrolase, hydrolyzing O-glycosyl compounds			ko00500|Starch and sucrose metabolism	GO:0016787	nr -
Unigene54145_All	503	0.00	5.14	2.75	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.06E-14	Up	1.14E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene54145_All//gi|288311314|gb|ADC45396.1|//3.00E-62//HSP90-2 [Glycine max]	Unigene54145_All//3.00E-55//AT5G56000| heat shock protein 81-4 (HSP81-4)			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr -
Unigene54146_All	591	0.00	4.20	0.00	0.00	0.00	0.00	0.07	0.21	0.88	1.20E+01	3.98E-14	Up	null	null		null	null		null	null		1.57E+00	5.45E-01		3.62E+00	4.19E-03		Unigene54146_All//gi|221410995|ref|XP_002323861.1|//7.00E-41//amino acid transporter [Populus trichocarpa] >gi|222866863|gb|EEF03994.1| amino acid transporter [Populus trichocarpa]	Unigene54146_All//8.00E-36//AT3G28960| amino acid transporter family protein	Unigene54146_All//0.00E+00//gi|48808989|gb|CO110303.1|CO110303			GO:0005275//GO:0016020	nr +
Unigene54147_All	1022	0.00	0.00	0.00	0.00	0.00	0.00	2.73	3.89	0.08	null	null		null	null		null	null		null	null		5.09E-01	6.78E-02		-5.13E+00	9.17E-18	Down	Unigene54147_All//gi|162460698|ref|NP_001105482.1|//9.00E-81//60S acidic ribosomal protein P0 [Zea mays] >gi|6094102|sp|O24573.3|RLA0_MAIZE RecName: Full=60S acidic ribosomal protein P0 >gi|1550814|emb|CAA69256.1| 60S acidic ribosomal protein P0 [Zea mays]	Unigene54147_All//6.00E-75//AT2G40010| 60S acidic ribosomal protein P0 (RPP0A)			ko03010|Ribosome	GO:0005198//GO:0006412//GO:0030529	nr -
Unigene54148_All	326	0.00	3.11	0.33	0.15	1.06	1.11	0.39	1.67	0.86	1.16E+01	7.25E-06	Up	8.35E+00	3.97E-01		2.79E+00	1.14E-01		2.86E+00	9.44E-02		2.10E+00	3.71E-02		1.14E+00	3.99E-01		Unigene54148_All//gi|115434676|ref|NP_001042096.1|//1.00E-12//Os01g0162300 (Oryza sativa Japonica Group) >gi|113531627|dbj|BAF04010.1| Os01g0162300 (Oryza sativa Japonica Group)	Unigene54148_All//9.00E-10//AT1G74190| AtRLP15 (Receptor Like Protein 15); protein binding				GO:0016491//GO:0031410	nr -
Unigene54149_All	988	0.00	0.00	0.00	0.30	0.07	0.00	9.89	0.17	9.31	null	null		null	null		-2.12E+00	1.65E-01		-8.24E+00	3.99E-02		-5.87E+00	1.71E-62	Down	-8.58E-02	6.43E-01		Unigene54149_All//gi|110931832|gb|AB802915.1|//3.00E-58//MYB transcription factor MYB94 [Glycine max]	Unigene54149_All//9.00E-53//AT4G25560| AtMYB18 (myb domain protein 18); DNA binding / transcription factor	Unigene54149_All//4.00E-65//TC175799	MYB		GO:0003676//GO:0006350//GO:0010033//GO:0010468//GO:0043231	nr +
Unigene54151_All	409	0.00	5.70	3.52	0.00	0.00	0.22	0.00	0.00	0.00	1.25E+01	2.91E-13	Up	1.18E+01	6.30E-08	Up	null	null		7.79E+00	4.75E-01		null	null		null	null		Unigene54151_All//gi|12229935|sp|Q9SM13.1|RS12_CYAPA//7.00E-41//RecName: Full=40S ribosomal protein S12 >gi|6012956|emb|CAB57311.1| 40s ribosomal protein S12 [Cyanophora paradoxa]	Unigene54151_All//4.00E-33//AT2G32060| 40S ribosomal protein S12 (RPS12C)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0033279	nr +
Unigene54153_All	561	0.00	6.95	3.13	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	3.25E-22	Up	1.16E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene54153_All//gi|115469274|ref|NP_001058236.1|//4.00E-11//Os06g0652600 (Oryza sativa Japonica Group) >gi|51535038|dbj|BAD37409.1| fibroin heavy chain precursor-like [Oryza sativa Japonica Group] >gi|113596276|dbj|BAF20150.1| Os06g0652600 (Oryza sativa Japonica Group)					ko03040|Spliceosome	GO:0005488//GO:0043231//GO:0044444	nr +
Unigene54155_All	354	1.92	0.00	0.00	1.13	1.07	0.64	1.43	2.01	0.79	-1.09E+01	4.09E-04	Down	-1.09E+01	7.63E-04	Down	-7.32E-02	9.25E-01		-8.19E-01	5.06E-01		4.86E-01	5.42E-01		-8.63E-01	3.39E-01		Unigene54155_All//gi|297811443|ref|XP_002873605.1|//4.00E-45//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319442|gb|EFH49864.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene54155_All//5.00E-46//AT5G13270| pentatricopeptide (PPR) repeat-containing protein				GO:0043231	nr -
Unigene54156_All	519	0.40	0.00	0.00	0.00	0.07	0.00	2.53	1.85	0.38	-8.66E+00	1.22E-01		-8.66E+00	1.45E-01		6.05E+00	8.29E-01		null	null		-4.47E-01	4.05E-01		-2.72E+00	1.32E-05	Down	Unigene54156_All//gi|259122791|gb|ACV92696.1|//3.00E-68//APX [Brassica rapa subsp. pekinensis]	Unigene54156_All//1.00E-59//AT1G07890| APX1 (ascorbate peroxidase 1); L-ascorbate peroxidase	Unigene54156_All//2.00E-96//DN802923		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0003006//GO:0004601//GO:0005506//GO:0006970//GO:0006979//GO:0009532//GO:0010038//GO:0016020//GO:0030312//GO:0042743	nr -
Unigene54157_All	679	0.00	0.00	0.00	0.00	0.00	0.00	2.68	2.95	0.06	null	null		null	null		null	null		null	null		1.42E-01	7.34E-01		-5.51E+00	4.49E-12	Down	Unigene54157_All//gi|116056034|emb|CAL58567.1|//2.00E-16//Nucleolar GTPase/ATPase p130 (ISS) [Ostreococcus tauri]						nr +
Unigene54158_All	231	0.00	0.00	0.46	0.65	0.00	0.00	4.03	0.72	0.52	null	null		8.85E+00	3.97E-01		-9.34E+00	1.65E-01		-9.34E+00	2.33E-01		-2.48E+00	1.07E-03		-2.96E+00	1.72E-04	Down			Unigene54158_All//5.00E-27//gi|78340040|gb|DT560314.1|DT560314					
Unigene54159_All	269	0.00	0.00	0.00	0.00	0.00	0.00	2.36	1.55	0.00	null	null		null	null		null	null		null	null		-6.02E-01	4.67E-01		-1.12E+01	7.10E-05	Down							ESTscan -
Unigene54163_All	737	0.00	5.84	1.81	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.56E-24	Up	1.08E+01	2.40E-07	Up	null	null		null	null		null	null		null	null		Unigene54163_All//gi|224155226|ref|XP_002337579.1|//5.00E-69//predicted protein [Populus trichocarpa] >gi|222839600|gb|EEE77937.1| predicted protein [Populus trichocarpa]						nr -

Unigene54165_All	332	0.00	1.83	2.41	0.00	0.21	0.00	0.25	0.00	0.00	1.08E+01	1.17E-03		1.12E+01	1.72E-04	Up	7.70E+00	6.08E-01		null	null		-7.99E+00	4.02E-01		-7.99E+00	3.57E-01		Unigene54165_All//sp|P08548|L1N1_NYCCO//2.00E-22//L1NE-1 reverse transcriptase homolog OS=Nycticebus coucang PE=1 SV=1						swissprot -
Unigene54167_All	247	0.00	3.90	3.02	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	1.16E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene54167_All//gi|115482462|ref|NP_001061824.1|//2.00E-10//Os10g0470900 [Oryza sativa Japonica Group] >gi|31432618|gb|AAP54226.1| RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639433|dbj|BAF26738.1| Os10g0470900 [Oryza sativa Japonica Group]	Unigene54167_All//5.00E-07//AT3G07810| heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative			ko03040|Spliceosome	GO:0006355//GO:0043565	nr -
Unigene54168_All	537	0.00	10.38	1.69	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	8.50E-32	Up	1.07E+01	4.71E-05	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene5417_All	1055	1.79	0.10	0.61	1.13	1.86	1.37	3.45	2.54	1.55	-4.22E+00	1.15E-08	Down	-1.56E+00	2.80E-03		7.15E-01	1.31E-01		2.74E-01	6.49E-01		-4.43E-01	1.36E-01		-1.15E+00	5.18E-05	Down	Unigene5417_All//gi|46360445|gb|AAS80153.1|//1.00E-115//ACT11D09.9 [Cucumis melo]	Unigene5417_All//5.00E-100//AT2G01730| ATCFSF73-II (cleavage and polyadenylation specificity factor 73 kDa subunit-II); catalytic/ protein binding					nr +
Unigene54172_All	277	4.34	0.73	2.11	1.44	1.49	0.65	0.76	0.60	0.58	-2.57E+00	5.35E-04	Down	-1.04E+00	1.14E-01		5.23E-02	9.89E-01		-1.14E+00	3.79E-01		-3.39E-01	8.11E-01		-4.08E-01	7.55E-01								
Unigene54173_All	542	0.58	2.99	0.79	4.96	3.56	2.17	0.94	0.93	2.06	2.37E+00	1.02E-04	Up	4.41E-01	6.77E-01		-4.80E-01	2.17E-01		-1.20E+00	1.91E-03		-1.66E-02	1.02E+00		1.14E+00	4.42E-02		Unigene54173_All//gi|4689474|gb|AA027910.1|//2.00E-74//expressed protein [Arabidopsis thaliana] >gi|51536602|gb|AAU05539.1| At2g04280 [Arabidopsis thaliana]	Unigene54173_All//1.00E-75//AT2G04280| unknown protein	Unigene54173_All//2.00E-112//gi|109872934|gb|DW501909.1|DW501909			GO:0016020//GO:0043231//GO:0046872	nr -
Unigene54179_All	384	0.00	0.26	0.00	1.30	0.90	0.00	1.76	0.11	0.73	8.04E+00	3.85E-01		null	null		-5.33E-01	5.94E-01		-1.03E+01	2.97E-03		-4.02E+00	5.36E-04	Down	-1.28E+00	9.48E-02		Unigene54179_All//gi|224105263|ref|XP_002313746.1|//4.00E-23//SAUR family protein [Populus trichocarpa] >gi|222850154|gb|EEE87701.1| SAUR family protein [Populus trichocarpa]	Unigene54179_All//7.00E-22//AT4G38825| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Auxin responsive SAUR protein (InterPro:IPR003676); BEST Arabidopsis thaliana protein match is: auxin-responsive protein, putative (TAIR:AT5G18030.1); Has 584 Blast hits to 581 proteins in 22 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 583; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene54179_All//3.00E-14//DW503615				nr +
Unigene54182_All	888	0.00	0.00	0.00	4.26	1.16	1.12	1.33	0.94	0.09	null	null		null	null		-1.87E+00	2.96E-09	Down	-1.93E+00	1.66E-08	Down	-5.02E-01	3.95E-01		-3.89E+00	9.21E-07	Down	Unigene54182_All//gi|42475462|dbj|BAD10885.1|//6.00E-80//zinc finger protein [Malus x domestica]	Unigene54182_All//2.00E-66//AT5G44160| NUC (nutcracker); nucleic acid binding / transcription factor/ zinc ion binding	Unigene54182_All//9.00E-103//ES815778	C2H2		GO:0044464//GO:0046914	nr -
Unigene54183_All	584	0.00	5.73	4.65	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	4.94E-19	Up	1.22E+01	5.42E-15	Up	null	null		null	null		null	null		null	null		Unigene54183_All//gi|224434366|dbj|BAH23802.1|//2.00E-16//cytochrome P450 monooxygenase [Oryza sativa Japonica Group]	Unigene54183_All//1.00E-17//AT3G26270| CYP71B25; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0002831//GO:0005488//GO:0006950//GO:0009700//GO:0009725//GO:0016831//GO:0042598//GO:0043231//GO:0051707	nr +
Unigene54184_All	293	0.00	3.11	0.73	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.62E-05	Up	9.51E+00	1.40E-01		null	null		null	null		null	null		null	null								ESTscan +
Unigene54188_All	618	0.00	1.07	0.00	0.08	0.39	0.07	0.48	1.89	2.58	1.01E+01	6.25E-04	Up	null	null		2.27E+00	3.05E-01		-1.41E-01	9.52E-01		1.98E+00	1.36E-03		2.43E+00	7.10E-06	Up	Unigene54188_All//gi|12322008|gb|AAG51046.1|AC069473.8/|3.00E-49//gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] >gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]					GO:0005488//GO:0009987	nr -
Unigene54189_All	499	0.00	0.00	0.00	0.00	0.00	0.00	3.81	3.60	0.00	null	null		null	null		null	null		null	null		-8.22E-02	8.54E-01		-1.19E+01	4.91E-14	Down	Unigene54189_All//gi|226460767|gb|EEH58061.1|//9.00E-25//profilin [Micromonas pusilla CCMP1545]	Unigene54189_All//2.00E-17//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding				GO:0044424	nr +
Unigene54190_All	383	0.55	0.40	0.70	0.65	0.27	0.35	2.21	1.75	0.21	-4.61E-01	7.58E-01		3.48E-01	7.97E-01		-1.27E+00	4.24E-01		-8.78E-01	6.16E-01		-3.39E-01	6.61E-01		-3.41E+00	1.35E-04	Down	Unigene54190_All//gi|110737098|dbj|BAF00501.1|//5.00E-44//zinc finger like protein [Arabidopsis thaliana]	Unigene54190_All//3.00E-45//AT3G57670| NTT (NO TRANSMITTING TRACT); nucleic acid binding / transcription factor/ zinc ion binding	Unigene54190_All//2.00E-34//TC163517	C2H2		GO:0000904//GO:0001071//GO:0010468//GO:0031410//GO:0043231//GO:0046914	nr -
Unigene54192_All	1330	0.08	0.00	0.00	0.22	0.05	0.00	9.41	0.25	3.41	-6.30E+00	3.70E-01		-6.30E+00	3.91E-01		-2.12E+00	1.65E-01		-7.81E+00	3.99E-02		-5.23E+00	3.37E-76	Down	-1.46E+00	2.08E-21	Down	Unigene54192_All//gi|89953439|gb|ABD83313.1|//3.00E-29//Fgenesh protein 60 [Beta vulgaris]	Unigene54192_All//4.00E-30//AT2G28580| unknown protein					nr -
Unigene54196_All	955	0.00	0.00	0.00	0.00	0.00	0.00	4.34	4.73	0.00	null	null		null	null		null	null		null	null		1.24E-01	6.52E-01		-1.21E+01	1.83E-30	Down							ESTscan -
Unigene54199_All	594	0.18	0.00	0.18	0.50	0.41	0.76	0.64	1.76	3.29	-7.46E+00	3.70E-01		2.52E-02	9.99E-01		-3.10E-01	8.20E-01		5.95E-01	6.40E-01		1.46E+00	1.98E-02		2.36E+00	7.98E-07	Up	Unigene54199_All//gi|297725141|ref|NP_001174934.1|//1.00E-45//Os06g0654500 [Oryza sativa Japonica Group] >gi|255677286|dbj|BAH93662.1| Os06g0654500 [Oryza sativa Japonica Group]	Unigene54199_All//4.00E-21//AT1G70460| protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0032559//GO:0043231	nr -
Unigene5420_All	1140	1.01	146.94	15.93	0.09	1.60	4.79	0.07	0.44	0.45	7.19E+00	0.00E+00	Up	3.98E+00	3.40E-74	Up	4.20E+00	5.00E-09	Up	5.78E+00	7.15E-30	Up	2.57E+00	2.28E-02		2.61E+00	1.55E-02		Unigene5420_All//gi|224082932|ref|XP_002306897.1|//9.00E-69//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222856346|gb|EEE93893.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene5420_All//1.00E-45//AT1G75490| DNA binding / transcription factor	Unigene5420_All//0.00E+00//TC178922	AP2-EREBP			nr -
Unigene54203_All	595	0.00	0.00	0.00	0.08	0.00	0.00	1.63	0.00	1.41	null	null		null	null		-6.39E+00	5.54E-01		-6.39E+00	6.34E-01		-1.07E+01	5.83E-07	Down	-2.17E-01	7.07E-01		Unigene54203_All//gi|14091840|gb|AAK53843.1|AC011806.20/|3.00E-21//Putative potassium transporter [Oryza sativa]	Unigene54203_All//4.00E-17//AT2G40540| KT2 (POTASSIUM TRANSPORTER 2); potassium ion transmembrane transporter				GO:0005488//GO:0044464	nr -
Unigene54204_All	408	16.54	291.10	27.80	19.78	71.40	141.58	692.96	1361.33	1305.89	4.14E+00	0.00E+00	Up	7.49E-01	1.83E-05		1.85E+00	8.87E-63	Up	2.84E+00	1.67E-190	Up	9.74E-01	0.00E+00		9.14E-01	0.00E+00		Unigene54204_All//gi|30385427|gb|AP23933.1|//1.00E-73//asparagine synthetase [Solanum lycopersicum]	Unigene54204_All//2.00E-70//AT5G10240| ASN3 (ASPARAGINE SYNTHETASE 3); asparagine synthase (glutamine-hydrolyzing)	Unigene54204_All//0.00E+00//TC132402		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0006528//GO:0009064//GO:0016884//GO:0032559	nr -
Unigene54205_All	544	0.00	0.00	0.00	0.00	0.00	0.17	2.25	5.15	0.81	null	null		null	null		null	null		7.38E+00	4.75E-01		1.19E+00	4.80E-04	Up	-1.48E+00	6.62E-03			Unigene54205_All//8.00E-167//CK640446					
Unigene54208_All	268	425.40	321.22	521.37	434.39	403.07	458.88	213.14	111.04	52.03	-4.05E-01	3.40E-17		2.94E-01	2.97E-11		-1.08E-01	3.01E-02		7.91E-02	1.37E-01		-9.41E-01	5.91E-46		-2.03E+00	2.89E-150	Down	Unigene54208_All//gi|79313339|ref|NP_001030749.1|//1.00E-27//dienelactone hydrolase family protein [Arabidopsis thaliana]	Unigene54208_All//4.00E-29//AT3G23600| dienelactone hydrolase family protein	Unigene54208_All//6.00E-141//gi|13353833|gb|BG444181.1|BG444181			GO:0003824//GO:0005576//GO:0006970//GO:0016020//GO:0043231	nr -
Unigene54209_All	349	0.00	11.61	3.81	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	4.39E-23	Up	1.19E+01	2.40E-07	Up	null	null		null	null		null	null		null	null		Unigene54209_All//gi|300268586|gb|EFJ52766.1|//1.00E-07//pathogenesis-related protein 1-like protein [Volvox carteri f. nagariensis]					GO:0005488//GO:0044464	nr -
Unigene5421_All	940	7.24	6.20	7.08	10.39	9.09	11.19	58.38	31.48	24.12	-2.23E-01	3.65E-01		-3.12E-02	9.07E-01		-1.93E-01	3.39E-01		1.08E-01	6.38E-01		-8.91E-01	2.10E-40		-1.28E+00	6.37E-74	Down	Unigene5421_All//gi|1170508|sp|P41381.1|IF4A8_TOBAC//1.00E-53//RecName: Full=Eukaryotic initiation factor 4A-8; Short=eIF-4A-8; AltName: Full=ATP-dependent RNA helicase eIF4A-8 >gi|475219|emb|CAA55639.1| translation initiation factor (eIF-4A) [Nicotiana tabacum] >gi|475221|emb|CAA55640.1| translation initiation factor (eIF-4A) [Nicotiana tabacum]	Unigene5421_All//1.00E-53//AT3G13920| EIF4A1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 4A1); ATP-dependent helicase/ translation initiation factor	Unigene5421_All//0.00E+00//TC156145				nr +
Unigene54213_All	541	0.00	2.72	1.38	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.11E-08	Up	1.04E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene54213_All//gi|7801679|emb|CAB91599.1|//2.00E-27//epsin-like protein [Arabidopsis thaliana]	Unigene54213_All//1.00E-20//AT3G58290| epsin N-terminal homology (ENTH) domain-containing protein				GO:0005515//GO:0044464	nr +
Unigene54218_All	721	0.00	0.00	0.00	0.00	0.00	0.06	0.29	1.33	3.04	null	null		null	null		null	null		5.97E+00	6.95E-01		2.19E+00	2.24E-03		3.37E+00	1.47E-10	Up	Unigene54218_All//gi|115484011|ref|NP_001065667.1|//8.00E-41//Os11g0133100 [Oryza sativa Japonica Group] >gi|77548585|gb|ABA91382.1| D-mannose binding lectin family protein [Oryza sativa (japonica cultivar-group)] >gi|113644371|dbj|BAF27512.1| Os11g0133100 [Oryza sativa Japonica Group]	Unigene54218_All//2.00E-38//AT1G34300| lectin protein kinase family protein			ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene54220_All	353	0.00	0.00	0.00	0.00	0.00	0.00	4.67	5.21	0.00	null	null		null	null		null	null		null	null		1.57E-01	7.24E-01		-1.22E+01	3.45E-12	Down	Unigene54220_All//gi|301117174|ref|XP_002906315.1|//9.00E-21//60S ribosomal protein L35a-4 [Phytophthora infestans T30-4] >gi|66270185|gb|AAY43422.1| ribosomal protein L35 [Phytophthora infestans] >gi|262107664|gb|EE065716.1| 60S ribosomal protein L35a-4 [Phytophthora infestans T30-4]	Unigene54220_All//6.00E-19//AT1G07070| 60S ribosomal protein L35a (RPL35aA)			ko03010|Ribosome	GO:0043231	nr +
Unigene54221_All	1126	0.00	0.05	0.00	0.13	0.21	0.00	1.80	4.01	12.60	5.49E+00	6.15E-01		null	null		6.90E-01	7.32E-01		-7.05E+00	2.33E-01		1.15E+00	9.00E-06	Up	2.80E+00	2.70E-54	Up	Unigene54221_All//gi|38943931|gb|AAC78596.1|//2.00E-46//Hcr2-5D [Solanum lycopersicum var. cerasiforme]	Unigene54221_All//6.00E-33//AT3G05660| ArRLP33 (Receptor Like Protein 33); kinase/ protein binding	Unigene54221_All//5.00E-105//EST95055				nr +
Unigene54222_All	305	1.89	0.33	0.70	1.80	6.32	14.07	0.83	1.23	0.26	-2.51E+00	2.93E-02		-1.43E+00	1.75E-01		1.82E+00	2.13E-04	Up	2.97E+00	4.45E-15	Up	5.68E-01	6.37E-01		-1.67E+00	2.56E-01		Unigene54222_All//gi|224103505|ref|XP_002313083.1|//2.00E-21//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222849491|gb|EEE87038.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene54222_All//7.00E-15//AT3G19010| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene54222_All//4.00E-118//gi|21093549|gb|BQ405862.1|BQ405862		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis	GO:0016491	nr -
Unigene54224_All	491	0.00	0.00	0.00	0.00	0.00	0.00	1.21	1.62	0.00	null	null		null	null		null	null		null	null		4.24E-01	5.77E-01		-1.02E+01	1.41E-04	Down							ESTscan -
Unigene54226_All	250	1.26	0.61	0.85	3.19	2.20	3.25	10.99	2.51	2.71	-1.05E+00	4.43E-01		-5.60E-01	6.63E-01		-5.33E-01	5.10E-01		2.85E-02	9.71E-01		-2.13E+00	3.92E-08	Down	-2.02E+00	6.12E-08	Down			Unigene54226_All//9.00E-60//gi|11200682|gb|BF269687.1|BF269687				
Unigene54227_All	799	0.46	0.25	0.13	0.75	1.85	0.79	2.38	0.94	0.90	-8.54E-01	4.88E-01		-1.78E+00	2.34E-01		1.31E+00	1.88E-02		8.10E-02	9.45E-01		-1.34E+00	1.94E-03		-1.41E+00	8.30E-04	Down	Unigene54227_All//gi|297849458|ref|XP_002892610.1|//1.00E-117//DNA helicase [Arabidopsis lyrata subsp. lyrata] >gi|297338452|gb|EFH68869.1| DNA helicase [Arabidopsis lyrata subsp. lyrata]	Unigene54227_All//8.00E-114//AT1G10930| RECQ4A; ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding	Unigene54227_All//0.00E+00//ES834572		ko03440|Homologous recombination	GO:0004003//GO:0006259//GO:0032559//GO:0044464	nr +

Unigene54229_All	754	0.00	0.40	0.00	0.40	0.00	0.00	320.91	1224.94	29.01	8.66E+00	4.42E-02		null	null		-8.63E+00	2.01E-02		-8.63E+00	3.99E-02		1.92E+00	0.00E+00	Up	-3.47E+00	0.00E+00	Down	Unigene54229_All//gi|293633437|gb|ADE60104.1|//8.00E-08//MIC-3 [Gossypium raimondii]		Unigene54229_All//0.00E+00//TC153556				nr -
Unigene54230_All	695	0.00	0.00	0.00	0.07	0.00	0.00	2.86	1.02	1.09	null	null		null	null		-6.16E+00	5.54E-01		-6.16E+00	6.34E-01		-1.48E+00	5.15E-04	Down	-1.39E+00	6.85E-04	Down	Unigene54230_All//gi|30692670|ref|NP_851093.1|//2.00E-55//AtGUS3 (Arabidopsis thaliana glucuronidase 3); beta-glucuronidase >gi|77416510|sp|Q9FZP1.2|HPSE3_ARATH RecName: Full=Heparanase-like protein 3; Flags: Precursor	Unigene54230_All//2.00E-54//AT5G24940| AtGUS3 (Arabidopsis thaliana glucuronidase 3); beta-glucuronidase	Unigene54230_All//4.00E-12//DR455799			GO:0005618//GO:0016787//GO:0031410//GO:0043167//GO:0044238	nr +
Unigene54231_All	648	0.73	0.16	1.15	6.30	1.65	6.48	0.26	0.32	0.00	-2.22E+00	7.76E-02		6.63E-01	4.19E-01		-1.94E+00	2.22E-10	Down	4.02E-02	9.21E-01		3.05E-01	8.35E-01		-8.03E+00	1.08E-01				Unigene54231_All//6.00E-20//DR499014				
Unigene54233_All	256	12.67	4.75	8.53	12.84	11.84	15.88	31.88	14.20	16.65	-1.42E+00	8.53E-05	Down	-5.71E-01	1.18E-01		-1.18E-01	7.78E-01		3.06E-01	3.71E-01		-1.17E+00	5.70E-10	Down	-9.37E-01	1.78E-07		Unigene54233_All//gi|115475908|ref|NP_001061550.1|//3.00E-13//Os08g0326400 [Oryza sativa Japonica Group] >gi|115480049|ref|NP_001063618.1|Os09g0507800 [Oryza sativa Japonica Group] >gi|548774|sp|P35685.1|RL7A_ORYSJ RecName: Full=60S ribosomal protein L7a >gi|303855|dbj|BAA02156.1| ribosomal protein L7A [Oryza sativa Japonica Group] >gi|38423963|dbj|BAD01672.1| 60S ribosomal protein L7A [Oryza sativa Japonica Group] >gi|38637005|dbj|BAD03264.1| 60S ribosomal protein L7A [Oryza sativa Japonica Group] >gi|113623519|dbj|BAF23464.1|Os08g0326400 [Oryza sativa Japonica Group] >gi|113631851|dbj|BAF25532.1|Os09g0507800 [Oryza sativa Japonica Group]	Unigene54233_All//2.00E-13//AT3G62870| 60S ribosomal protein L7A (RPL7aB)	Unigene54233_All//4.00E-62//TC165106		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0022613//GO:0030529//GO:0046872	nr +
Unigene54236_All	363	0.00	0.00	0.00	0.00	0.00	0.00	1.51	6.33	0.66	null	null		null	null		null	null		null	null		2.06E+00	1.18E-06	Up	-1.20E+00	1.64E-01		Unigene54236_All//gi|55168340|gb|AAV44205.1|//1.00E-16//unknow protein [Oryza sativa Japonica Group]		Unigene54236_All//3.00E-14//TC174737				nr -
Unigene54237_All	454	0.00	69.64	58.65	0.55	0.00	0.00	0.00	0.00	0.00	1.61E+01	2.44E-182	Up	1.58E+01	8.47E-151	Up	-9.10E+00	4.18E-02		-9.10E+00	7.32E-02		null	null		null	null		Unigene54237_All//gi|50261278|ref|YP_052885.1|//1.00E-06//NADH dehydrogenase subunit 4L [Saprolegnia ferax] >gi|48237591|gb|AAT40640.1| NADH dehydrogenase subunit 4L [Saprolegnia ferax]						nr +
Unigene54238_All	333	1.73	0.76	1.28	9.27	8.07	3.26	0.13	0.25	0.00	-1.18E+00	2.26E-01		-4.34E-01	6.23E-01		-2.02E-01	6.05E-01		-1.51E+00	3.39E-05	Down	9.83E-01	7.31E-01		-6.99E+00	6.11E-01			Unigene54238_All//3.00E-05//AT1G26960| AtHB23 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 23); DNA binding / transcription factor	Unigene54238_All//1.00E-31//TC177634				
Unigene54240_All	371	0.00	11.06	5.45	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.25E-23	Up	1.24E+01	3.79E-11	Up	null	null		null	null		null	null		null	null		Unigene54240_All//gi|81074037|gb|AB855361.1|//5.00E-26//40S ribosomal protein S10-like [Solanum tuberosum] >gi|82400160|gb|ABB72819.1| 40S ribosomal protein S10-like protein [Solanum tuberosum]	Unigene54240_All//1.00E-26//AT5G41520| 40S ribosomal protein S10 (RPS10B)			ko03010|Ribosome		nr -
Unigene54241_All	453	0.00	7.27	4.00	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	9.63E-19	Up	1.20E+01	5.69E-10	Up	null	null		null	null		null	null		null	null		Unigene54241_All//gi|226495473|ref|NP_001147336.1|//2.00E-58//glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Zea mays] >gi|30580446|sp|Q96UF2.1|G3P2_RHIRA RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase 2; Short=GAPDH 2 >gi|15722242|emb|CAC37404.1|glyceraldehyde-3-phosphate dehydrogenase [Mucor racemosus] >gi|195610190|gb|ACG26925.1|glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Zea mays]	Unigene54241_All//2.00E-54//AT1G16300| GAPCP-2; NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene54241_All//1.00E-07//ES839951		ko00010|Glycolysis / Gluconeogenesis	GO:0000166//GO:0006007//GO:0008943//GO:0009536//GO:0016861//GO:0048364	nr +
Unigene54243_All	230	2.96	0.00	0.46	0.43	2.40	0.20	0.00	0.00	0.00	-1.15E+01	4.09E-04	Down	-2.68E+00	1.69E-02		2.47E+00	4.04E-02		-1.14E+00	6.76E-01		null	null		null	null									
Unigene54244_All	606	0.43	0.50	0.88	8.06	6.14	2.01	0.56	0.34	0.13	2.17E-01	8.64E-01		1.03E+00	3.42E-01		-3.93E-01	1.55E-01		-2.00E+00	2.62E-11	Down	-6.95E-01	5.77E-01		-2.09E+00	1.07E-01									
Unigene54245_All	349	0.00	2.61	0.00	0.00	0.59	0.26	1.21	0.60	0.57	1.14E+01	2.62E-05	Up	null	null		9.21E+00	1.57E-01		8.02E+00	4.75E-01		-1.02E+00	3.50E-01		-1.09E+00	2.82E-01									
Unigene54249_All	214	2.20	0.47	1.49	1.40	7.24	5.28	0.00	0.39	0.93	-2.22E+00	7.76E-02		-5.60E-01	6.28E-01		2.37E+00	7.92E-05	Up	1.92E+00	6.72E-03		8.61E+00	4.00E-01		9.86E+00	7.88E-02									
Unigene54257_All	202	0.00	5.77	17.66	0.00	0.00	0.89	0.00	0.00	0.00	1.25E+01	1.05E-06	Up	1.41E+01	9.41E-20	Up	null	null		9.80E+00	1.94E-01		null	null		null	null		Unigene54257_All//gi|226431242|gb|ACO55633.1|//1.00E-18//chloroplast photosystem II type I chlorophyll a/b-binding protein [Arachis diogoi]	Unigene54257_All//1.00E-13//AT1G29930| CAB1 (CHLOROPHYLL A/B BINDING PROTEIN 1); chlorophyll binding	Unigene54257_All//4.00E-09//TC135920		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0006464//GO:0009521//GO:0009534//GO:0031224//GO:0043169//GO:0046906	nr +
Unigene54426_All	1056	5.30	8.78	5.09	10.94	7.96	11.29	18.50	29.37	63.53	7.28E-01	1.18E-04		-5.79E-02	8.31E-01		-4.60E-01	3.65E-03		4.50E-02	8.17E-01		6.67E-01	2.35E-14		1.78E+00	1.20E-145	Up	Unigene54426_All//gi|224053426|ref|XP_002297813.1|//6.00E-74//f-box family protein [Populus trichocarpa] >gi|222845071|gb|EEE82618.1| f-box family protein [Populus trichocarpa]	Unigene54426_All//3.00E-48//AT1G80110| ATPP2-B11 (ARABIDOPSIS THALIANA PHLOEM PROTEIN 2-B11); carbohydrate binding	Unigene54426_All//0.00E+00//TC157980				nr +
Unigene54261_All	374	0.00	2.30	0.85	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.94E-05	Up	9.74E+00	4.51E-02		null	null		null	null		null	null		null	null		Unigene54261_All//sp|P63219|GBG5_RAT//2.00E-31//Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 OS=Rattus norvegicus GN=Gng5 PE=2 SV=1						swissprot -
Unigene54262_All	484	0.00	2.51	2.64	0.00	0.00	0.00	0.00	0.00	0.08	1.13E+01	5.47E-07	Up	1.14E+01	4.68E-07	Up	null	null		null	null		null	null		6.36E+00	6.44E-01		Unigene54262_All//sp|Q07352|TISB_HUMAN//3.00E-42//Butyrate response factor 1 OS=Homo sapiens GN=ZFP36L1 PE=1 SV=1						swissprot +
Unigene54264_All	341	0.31	0.00	0.00	3.51	0.91	0.53	0.37	0.49	0.47	-8.26E+00	3.70E-01		-8.26E+00	3.91E-01		-1.95E+00	1.81E-03		-2.73E+00	2.36E-01	Down	3.98E-01	8.14E-01		3.29E-01	8.50E-01								ESTscan -
Unigene54266_All	225	0.00	4.05	3.31	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.62E-05	Up	1.17E+01	3.27E-04	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene54267_All	246	0.00	3.30	1.95	0.41	1.40	0.73	0.17	0.00	0.16	1.17E+01	9.37E-05	Up	1.09E+01	7.47E-03		1.79E+00	2.57E-01		8.59E-01	6.95E-01		-7.43E+00	6.56E-01		-8.65E-02	9.71E-01									
Unigene54268_All	346	0.00	53.89	26.93	0.00	0.10	0.00	0.00	0.00	0.00	1.57E+01	3.08E-107	Up	1.47E+01	2.99E-52	Up	6.64E+00	8.29E-01		null	null		null	null		null	null		Unigene54268_All//gi|15240463|ref|NP_198074.1|//4.00E-06//protein transport protein-related [Arabidopsis thaliana] >gi|2191186|gb|AAB61071.1|contains similarity to tropomyosin and kinesin [Arabidopsis thaliana]						nr +
Unigene54271_All	367	0.00	5.94	0.00	0.00	0.19	0.62	0.69	4.78	20.84	1.25E+01	2.11E-12	Up	null	null		7.55E+00	6.08E-01		9.27E+00	1.18E-01		2.79E+00	4.04E-07	Up	4.91E+00	7.74E-46	Up			Unigene54271_All//8.00E-18//TC170351				
Unigene54275_All	494	7.20	6.26	19.40	0.00	0.14	0.00	0.00	0.00	0.00	-2.03E-01	5.63E-01		1.43E+00	2.91E-12	Up	7.12E+00	6.08E-01		null	null		null	null		null	null		Unigene54275_All//gi|225429550|ref|XP_002279283.1|//1.00E-09//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296081660|emb|CBI20665.3|unnamed protein product [Vitis vinifera]						nr -
Unigene54276_All	445	0.00	0.00	0.00	0.00	0.00	0.00	2.19	2.16	0.00	null	null		null	null		null	null		null	null		-1.67E-02	1.02E+00		-1.11E+01	2.72E-07	Down	Unigene54276_All//gi|301121610|ref|XP_002908532.1|//9.00E-63//60S ribosomal protein L23 [Phytophthora infestans T30-4] >gi|66270163|gb|AAY43411.1|ribosomal protein L23 [Phytophthora infestans] >gi|262103563|gb|EEY61615.1| 60S ribosomal protein L23 [Phytophthora infestans T30-4]	Unigene54276_All//4.00E-62//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene54276_All//7.00E-34//gi|84150175|gb|DV781475.1|DV781475		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0010467//GO:0015934//GO:0031981	nr +
Unigene54277_All	796	0.00	0.00	0.00	0.00	0.00	0.00	9.88	9.98	4.60	null	null		null	null		null	null		null	null		1.41E-02	9.75E-01		-1.10E+00	3.57E-09	Down	Unigene54277_All//gi|224111284|ref|XP_002332949.1|//5.00E-13//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834261|gb|EEE72738.1| cc-nbs-lrr resistance protein [Populus trichocarpa]						nr -
Unigene54278_All	425	0.00	45.78	16.79	0.00	0.00	0.00	0.00	0.00	0.00	1.55E+01	6.28E-112	Up	1.40E+01	7.15E-40	Up	null	null		null	null		null	null		null	null		Unigene54278_All//gi|242070913|ref|XP_002450733.1|//5.00E-11//hypothetical protein SORBIDRAFT_05g016477 [Sorghum bicolor] >gi|241936576|gb|EES09721.1|hypothetical protein SORBIDRAFT_05g016477 [Sorghum bicolor]		Unigene54278_All//4.00E-26//TC166887				nr +
Unigene54281_All	1138	0.00	6.55	2.20	0.00	0.06	0.00	0.00	0.00	0.00	1.27E+01	1.39E-42	Up	1.11E+01	8.32E-14	Up	5.92E+00	6.08E-01		null	null		null	null		null	null		Unigene54281_All//gi|195605636|gb|ACG24648.1|//1.00E-65//triosephosphate isomerase, cytosolic [Zea mays] >gi|195658525|gb|ACG48730.1|triosephosphate isomerase, cytosolic [Zea mays]	Unigene54281_All//6.00E-62//AT3G55440| TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00562|Inositol phosphate metabolism//ko00051|Fructose and mannose metabolism	GO:0006007//GO:0006629//GO:0016853//GO:0032787	nr -
Unigene54283_All	921	0.40	0.99	0.00	1.73	1.12	0.78	3.40	4.18	0.48	1.32E+00	7.93E-02		-8.64E+00	2.78E-02		-6.26E-01	2.24E-01		-1.14E+00	3.09E-02		2.98E-01	3.28E-01		-2.84E+00	6.88E-13	Down			Unigene54283_All//1.00E-67//ES832413				
Unigene54284_All	821	0.00	0.00	0.00	0.00	0.00	0.00	1.08	1.27	28.87	null	null		null	null		null	null		null	null		2.35E-01	6.99E-01		4.74E+00	1.92E-138	Up	Unigene54284_All//gi|224137170|ref|XP_002327053.1|//2.00E-45//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|222835368|gb|EEE73803.1|AP2/EBF domain-containing transcription factor [Populus trichocarpa]	Unigene54284_All//7.00E-32//AT2G44840| ERF13 (ETHYLENE-RESPONSIVE ELEMENT BINDING FACTOR 13); DNA binding / transcription factor	Unigene54284_All//0.00E+00//DW511888	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231//GO:0050896	nr +

Unigene54285_All	227	37.11	17.86	22.52	44.11	45.51	50.14	137.83	55.05	71.08	-1.06E+00	2.39E-07	Down	-7.21E-01	5.02E-04		4.51E-02	8.26E-01		1.85E-01	3.45E-01		-1.32E+00	1.05E-43	Down	-9.55E-01	5.72E-27		Unigene54285_All//gi|21617886|gb|AM68936.1//6.00E-35//40S ribosomal protein S5 [Arabidopsis thaliana]	Unigene54285_All//2.00E-36//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN SB); structural constituent of ribosome	Unigene54285_All//2.00E-125//TC131397		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030312	nr +
Unigene54286_All	477	2.08	0.00	0.22	0.21	0.94	0.47	0.71	0.79	0.50	-1.10E+01	7.45E-06	Down	-3.22E+00	7.83E-04	Down	2.17E+00	1.06E-01		1.18E+00	5.49E-01		1.53E-01	8.90E-01		-5.01E-01	6.49E-01		Unigene54286_All//gi|15228829|ref|NP_188908.1|//2.00E-52//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene54286_All//1.00E-53//AT3G22690| pentatricopeptide (PPR) repeat-containing protein				GO:0009536//GO:0015995//GO:0016070//GO:0019684//GO:0043623	nr -
Unigene54288_All	399	0.00	0.00	0.13	0.00	0.00	0.00	2.86	1.05	7.89	null	null		7.06E+00	6.35E-01		null	null		null	null		-1.45E+00	1.40E-02		1.46E+00	5.75E-06	Up			Unigene54288_All//5.00E-07//TC129580				
Unigene54289_All	305	0.00	2.49	2.62	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.76E-04	Up	1.14E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene54289_All//sp|P55327|TPD52_HUMAN//5.00E-10//Tumor protein D52 OS=Homo sapiens GN=TPD52 PE=1 SV=2						swissprot +
Unigene5429_All	738	9.22	11.40	5.77	10.93	6.63	8.63	21.83	13.08	10.04	3.06E-01	1.37E-01		-6.75E-01	3.99E-03		-7.23E-01	1.31E-04		-3.42E-01	1.14E-01		-7.39E-01	3.06E-09		-1.12E+00	2.48E-18	Down	Unigene5429_All//gi|110739170|dbj|BAF01501.1|//2.00E-40//Sm-like protein [Arabidopsis thaliana]	Unigene5429_All//1.00E-41//AT5G48870| SAD1 (SUPERSENSITIVE TO ABA AND DROUGHT 1); RNA binding	Unigene5429_All//0.00E+00//TC132244		ko03040|Spliceosome//ko03018|RNA degradation		nr +
Unigene54290_All	322	3.41	0.00	0.17	1.55	0.21	0.28	0.00	0.00	0.00	-1.17E+01	1.95E-06	Down	-4.37E+00	4.94E-05	Down	-2.85E+00	1.78E-02		-2.46E+00	4.82E-02		null	null		null	null				Unigene54290_All//4.00E-07//TC147362				
Unigene54291_All	1083	0.00	0.00	0.00	0.78	0.38	0.08	5.97	1.12	0.74	null	null		null	null		-1.03E+00	1.62E-01		-3.23E+00	1.04E-03		-2.42E+00	4.80E-21	Down	-3.02E+00	1.49E-27	Down							
Unigene54293_All	595	0.00	2.73	0.98	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.96E-09	Up	9.94E+00	2.17E-03		null	null		null	null		null	null		null	null		Unigene54293_All//sp|P35502|ESTF_MYZPE//4.00E-17//Esterase FE4 OS=Myzus persicae PE=1 SV=1						swissprot +
Unigene54295_All	812	0.00	0.00	0.00	0.00	0.00	0.00	2.34	3.19	0.00	null	null		null	null		null	null		null	null		4.46E-01	2.25E-01		-1.12E+01	4.91E-14	Down	Unigene54295_All//gi|238617665|gb|ACR46954.1|//1.00E-135//alpha-tubulin [Rhodochaete parvula]	Unigene54295_All//2.00E-116//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene54295_All//1.00E-86//gi|78344103|gb|DT564377.1|DT564377		ko04145|Phagosome		nr +
Unigene54297_All	393	0.00	10.83	6.91	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	3.04E-24	Up	1.28E+01	5.42E-15	Up	null	null		null	null		null	null		null	null		Unigene54297_All//sp|097763|NPC2_PIG//2.00E-11//Epididymal secretory protein E1 OS=Sus scrofa GN=NPC2 PE=1 SV=1						swissprot -
Unigene54298_All	337	2.95	2.41	0.00	0.15	1.12	1.21	0.00	0.00	0.00	-2.94E-01	6.37E-01		-1.15E+01	1.77E-05	Down	2.93E+00	8.16E-02		3.03E+00	6.03E-02		null	null		null	null		Unigene54298_All//gi|229609833|gb|ACQ83532.1|//2.00E-35//CBL-interacting protein kinase 16 [Vitis vinifera]	Unigene54298_All//8.00E-30//AT5G45820| CIPK20 (CBL-INTERACTING PROTEIN KINASE 20); kinase/ protein serine/threonine kinase	Unigene54298_All//2.00E-157//C0096310			GO:0004674//GO:0006464//GO:0009725//GO:0023060//GO:0032559	nr -
Unigene5430_All	845	2.72	0.66	2.46	15.09	13.20	16.25	1.05	2.97	1.74	-2.05E+00	1.59E-05	Down	-1.49E-01	7.21E-01		-1.93E-01	2.72E-01		1.07E-01	5.77E-01		1.50E+00	6.53E-05	Up	7.31E-01	1.22E-01		Unigene5430_All//gi|255547766|ref|XP_002514940.1|//3.00E-19//conserved hypothetical protein [Ricinus communis] >gi|223545991|gb|EEF47494.1| conserved hypothetical protein [Ricinus communis]	Unigene5430_All//9.00E-05//AT3G27210| unknown protein	Unigene5430_All//1.00E-24//TC152551				nr +
Unigene54300_All	1668	0.19	0.00	0.00	0.48	0.08	0.19	0.33	9.15	1.70	-7.56E+00	3.65E-02		-7.56E+00	4.89E-02		-2.53E+00	3.08E-03		-1.33E+00	1.06E-01		4.79E+00	2.17E-88	Up	2.36E+00	1.44E-09	Up	Unigene54300_All//gi|15235905|ref|NP_194034.1|//1.00E-165//MATE efflux protein-related [Arabidopsis thaliana]	Unigene54300_All//4.00E-155//AT4G23030| MATE efflux protein-related	Unigene54300_All//1.00E-100//DN780885			GO:0015291//GO:0015893//GO:0044464	nr +
Unigene54301_All	441	0.00	4.14	2.54	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.14E-10	Up	1.13E+01	3.43E-06	Up	null	null		null	null		null	null		null	null								
Unigene54302_All	681	0.46	0.89	0.00	0.15	0.20	0.00	3.10	3.93	0.53	9.54E-01	3.14E-01		-8.85E+00	4.89E-02		4.68E-01	8.76E-01		-7.19E+00	3.98E-01		3.40E-01	3.69E-01		-2.56E+00	4.26E-08	Down							
Unigene54303_All	382	1.37	0.00	0.56	4.96	7.12	1.54	0.11	1.09	2.09	-1.04E+01	2.92E-03		-1.30E+00	2.42E-01		5.23E-01	1.87E-01		-1.69E+00	6.39E-04	Down	3.31E+00	2.00E-02		4.24E+00	7.42E-05	Up							
Unigene54304_All	548	0.00	4.99	3.40	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.44E-15	Up	1.17E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene54304_All//gi|224006323|ref|XP_002292122.1|//7.00E-16//trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972641|gb|EED90973.1| trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]					GO:0003824	nr -
Unigene54305_All	599	0.00	0.34	0.00	0.00	0.00	0.00	0.49	3.56	2.39	8.40E+00	1.36E-01		null	null		null	null		null	null		2.85E+00	1.12E-08	Up	2.28E+00	4.94E-05	Up							
Unigene54306_All	423	0.00	45.40	21.02	0.00	0.00	0.00	0.00	0.00	0.00	1.55E+01	1.84E-110	Up	1.44E+01	7.82E-50	Up	null	null		null	null		null	null		null	null		Unigene54306_All//gi|298706692|emb|CBJ34222.1|//1.00E-10//conserved unknown protein [Ectocarpus siliculosus] >gi|298713886|emb|CBJ33762.1| conserved unknown protein [Ectocarpus siliculosus]		Unigene54306_All//1.00E-23//TC148521				nr +
Unigene54309_All	1179	0.62	10.49	4.70	1.01	0.12	0.84	0.00	0.11	0.00	4.08E+00	1.24E-52	Up	2.92E+00	2.04E-17	Up	-3.12E+00	1.54E-05	Down	-2.67E-01	6.88E-01		6.73E+00	2.40E-01		null	null		Unigene54309_All//gi|213496554|emb|CAN88842.1|//1.00E-144//polyols transporter 1 [Hevea brasiliensis]	Unigene54309_All//1.00E-112//AT3G18830| ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann	Unigene54309_All//0.00E+00//ES816133				nr +
Unigene5431_All	1753	2.84	5.61	4.04	0.80	0.43	1.19	1.54	6.34	1.73	9.84E-01	1.40E-07		5.11E-01	2.70E-02		-8.81E-01	1.06E-01		5.75E-01	2.23E-01		2.04E+00	5.88E-29	Up	1.62E-01	6.30E-01		Unigene5431_All//gi|212717149|gb|AC137416.1|//1.00E-129//stress-induced receptor-like kinase [Glycine max]	Unigene5431_All//5.00E-88//AT1G66930| serine/threonine protein kinase family protein	Unigene5431_All//5.00E-115//C0081306		ko04626|Plant-pathogen interaction		nr -
Unigene54310_All	481	0.00	14.75	4.43	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	1.53E-40	Up	1.21E+01	9.77E-12	Up	null	null		null	null		null	null		null	null		Unigene54310_All//gi|115453349|ref|NP_001050275.1|//3.00E-20//Os03g0390400 [Oryza sativa Japonica Group] >gi|4586449|dbj|BAA76393.1| cytochrome c oxidase subunit 6b-1 [Oryza sativa Japonica Group] >gi|9967277|dbj|BAB12338.1| cytochrome c oxidase subunit 6b [Oryza sativa Japonica Group] >gi|37991922|gb|AAR06368.1| cytochrome c oxidase subunit 6b-1 [Oryza sativa Japonica Group] >gi|113548746|dbj|BAF12189.1| Os03g0390400 [Oryza sativa Japonica Group]	Unigene54310_All//8.00E-21//AT1G22450| COX6B (CYTOCHROME C OXIDASE 6B); cytochrome-c oxidase			ko00190|Oxidative phosphorylation	GO:0005746//GO:0022904	nr +
Unigene54314_All	342	0.00	3.56	1.09	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.47E-07	Up	1.01E+01	2.50E-02		null	null		null	null		null	null		null	null		Unigene54314_All//gi|219125385|ref|XP_002182963.1|//2.00E-08//spondin like protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|217405757|gb|EEC45699.1| spondin like protein [Phaeodactylum tricornutum CCAP 1055/1]						nr +
Unigene54316_All	446	0.00	24.88	4.78	0.00	0.00	0.00	0.00	0.00	0.00	1.46E+01	1.28E-63	Up	1.22E+01	9.77E-12	Up	null	null		null	null		null	null		null	null		Unigene54316_All//sp|P27779|CUP7_DROME//8.00E-25//Pupal cuticle protein Edg-78E OS=Drosophila melanogaster GN=Edg78E PE=1 SV=1						swissprot -
Unigene54318_All	384	0.00	0.00	0.00	0.13	0.00	0.00	21.36	16.11	1.97	null	null		null	null		-7.02E+00	5.54E-01		-7.02E+00	6.34E-01		-4.07E-01	2.70E-02		-3.44E+00	3.85E-39	Down	Unigene54318_All//gi|298713887|emb|CBJ33763.1|//9.00E-23//conserved unknown protein [Ectocarpus siliculosus]		Unigene54318_All//8.00E-49//TC146753				nr +
Unigene54319_All	491	0.00	0.00	0.00	0.00	0.00	0.00	1.55	2.98	0.00	null	null		null	null		null	null		null	null		9.43E-01	5.66E-02		-1.06E+01	8.87E-06	Down	Unigene54319_All//gi|50843988|gb|AAT84169.1|//2.00E-38//60S ribosomal protein L27 [Chara globularis]	Unigene54319_All//3.00E-35//AT4G15000| 60S ribosomal protein L27 (RPL27C)			ko03010|Ribosome	GO:0030529	nr -
Unigene5432_All	1008	1.35	3.42	1.69	3.95	3.25	4.53	5.79	2.65	4.07	1.34E+00	1.09E-04	Up	3.25E-01	5.44E-01		-2.85E-01	3.87E-01		1.95E-01	5.62E-01		-1.13E+00	5.44E-07	Down	-5.08E-01	1.69E-02		Unigene5432_All//gi|57899790|dbj|BAD87535.1|//1.00E-84//ALM beta-like [Oryza sativa Japonica Group]	Unigene5432_All//3.00E-84//AT4G32175| RNA binding	Unigene5432_All//0.00E+00//ES802880		ko03018|RNA degradation		nr +
Unigene54322_All	386	0.00	0.00	0.00	0.00	0.00	0.12	113.37	14.18	26.11	null	null		null	null		null	null		6.87E+00	6.95E-01		-3.00E+00	1.79E-175	Down	-2.12E+00	1.91E-121	Down	Unigene54322_All//gi|224139376|ref|XP_002323082.1|//3.00E-39//cytochrome P450 [Populus trichocarpa] >gi|222867712|gb|EEF04843.1| cytochrome P450 [Populus trichocarpa]	Unigene54322_All//3.00E-36//AT3G26230| CYP71B24; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene54322_All//2.00E-104//gi|109825823|gb|DW224545.1|DW224545		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506//GO:0008152	nr -
Unigene54329_All	340	0.00	0.00	0.94	0.00	0.20	0.27	0.00	0.49	2.23	null	null		9.88E+00	4.51E-02		7.66E+00	6.08E-01		8.05E+00	4.75E-01		8.94E+00	1.39E-01		1.11E+01	1.39E-05	Up	Unigene54329_All//gi|225453543|ref|XP_002276175.1|//3.00E-11//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene54329_All//3.00E-08//TC175019				nr +
Unigene5433_All	1160	0.81	1.57	0.64	1.80	1.16	1.75	4.34	1.69	1.72	9.54E-01	4.89E-02		-3.37E-01	6.16E-01		-6.40E-01	1.44E-01		-4.19E-02	9.39E-01		-1.36E+00	5.92E-08	Down	-1.34E+00	4.47E-08	Down	Unigene5433_All//gi|57899790|dbj|BAD87535.1|//2.00E-99//ALM beta-like [Oryza sativa Japonica Group]	Unigene5433_All//3.00E-99//AT4G32175| RNA binding	Unigene5433_All//0.00E+00//ES802880		ko03018|RNA degradation		nr +
Unigene54330_All	646	0.08	1.41	1.65	1.54	1.71	1.19	1.24	0.97	0.37	4.12E+00	2.34E-04	Up	4.35E+00	6.46E-05	Up	1.46E-01	8.37E-01		-3.76E-01	6.31E-01		-3.58E-01	6.48E-01		-1.75E+00	1.55E-02				Unigene54330_All//5.00E-39//gi|31072538|gb|CA992817.1|CA992817				
Unigene54331_All	420	0.00	30.52	11.92	0.00	0.00	0.00	0.00	0.00	0.00	1.49E+01	1.45E-73	Up	1.35E+01	7.65E-28	Up	null	null		null	null		null	null		null	null		Unigene54331_All//sp|Q9VAJ4|OB99A_DROME//2.00E-33//General odorant-binding protein 99a OS=Drosophila melanogaster GN=Obp99a PE=1 SV=2						swissprot +
Unigene54332_All	277	0.00	4.57	6.54	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.86E-07	Up	1.27E+01	5.69E-10	Up	null	null		null	null		null	null		null	null		Unigene54332_All//gi|297817582|ref|XP_002876674.1|//6.00E-11//CP12-2 [Arabidopsis lyrata subsp. lyrata] >gi|297322512|gb|EFH52933.1| CP12-2 [Arabidopsis lyrata subsp. lyrata]	Unigene54332_All//8.00E-11//AT3G62410| CP12-2; protein binding				GO:0005488//GO:0009314//GO:0009532//GO:0015977//GO:0018149//GO:0034285	nr +
Unigene54334_All	1299	0.00	0.00	0.00	0.00	0.00	0.00	12.40	9.94	0.00	null	null		null	null		null	null		null	null		-3.19E-01	1.20E-02		-1.36E+01	7.70E-119	Down	Unigene54334_All//gi|4139170|gb|AAD03711.1|//0.00E+00//elongation translation factor 1 alpha [Cyanophora paradoxa]	Unigene54334_All//5.00E-180//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene54334_All//8.00E-61//TC166357			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene5434_All	699	5.54	2.03	5.79	2.42	2.61	2.07	2.66	1.67	0.74	-1.45E+00	9.83E-06	Down	6.39E-02	8.40E-01		1.08E-01	8.39E-01		-2.29E-01	6.77E-01		-6.69E-01	1.22E-01		-1.84E+00	4.29E-05	Down	Unigene5434_All//gi|15237711|ref|NP_200668.1|//8.00E-82//PMR5 (POWDERY MILDEW RESISTANT 5) [Arabidopsis thaliana]	Unigene5434_All//1.00E-84//AT5G58600| PMR5 (POWDERY MILDEW RESISTANT 5)	Unigene5434_All//1.00E-122//gi|48827949|gb|CO126339.1|CO126339				nr +
Unigene54340_All	868	0.00	6.89	3.31	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	3.95E-34	Up	1.17E+01	6.96E-16	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene54341_All	361	1.88	12.63	7.52	0.14	0.76	0.38	0.00	0.00	0.44	2.75E+00	4.89E-14	Up	2.00E+00	6.82E-06	Up	2.47E+00	2.23E-01		1.44E+00	6.38E-01		null	null		8.79E+00	1.40E-01		Unigene54341_All//gi|37993655|gb|AAR06913.1|//4.00E-40//UDP-glycosyltransferase 85A8 [Stevia rebaudiana]	Unigene54341_All//3.00E-38//AT1G22380| AtUGT85A3 (UDP-glucosyl transferase 85A3); glucuronosyltransferase/ transcription factor/ transferase, transferring glycosyl groups	Unigene54341_All//2.00E-157//DT465722		ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0035251	nr -
Unigene54344_All	502	0.00	3.03	6.26	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.10E-08	Up	1.26E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene54344_All//sp|P01903|DRA_HUMAN//4.00E-10//HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1						swissprot -

Unigene54345_All	498	80.16	651.99	96.45	151.34	721.62	497.07	1037.99	2138.13	2118.09	3.02E+00	0.00E+00	Up	2.67E-01	9.02E-04		2.25E+00	0.00E+00	Up	1.72E+00	0.00E+00	Up	1.04E+00	0.00E+00	Up	1.03E+00	0.00E+00	Up	Unigene54345_All//gi|14030723|gb|AK53036.1|AF375452_1//3.00E-53//AT4g27450/F27G19_50 [Arabidopsis thaliana]	Unigene54345_All//8.00E-55//AT4G27450| unknown protein	Unigene54345_All//0.00E+00//EV485732		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0016020//GO:0043231//GO:0044444	nr +
Unigene54346_All	439	0.00	0.58	1.58	3.06	2.12	0.82	1.93	0.95	1.09	9.17E+00	7.85E-02		1.06E+01	6.15E-04	Up	-5.33E-01	3.57E-01		-1.90E+00	2.26E-03		-1.02E+00	1.41E-01		-8.23E-01	2.07E-01		Unigene54346_All//gi|225464047|ref|XP_002267841.1|//2.00E-25//PREDICTED: similar to cysteine proteinase inhibitor [Vitis vinifera]	Unigene54346_All//2.00E-22//AT3G12490| cysteine protease inhibitor, putative / cystatin, putative	Unigene54346_All//3.00E-27//ES826978			GO:0030414	nr -
Unigene54347_All	547	1.24	0.19	1.75	0.36	1.01	0.33	0.23	2.75	0.44	-2.75E+00	1.06E-02		4.95E-01	4.97E-01		1.47E+00	1.77E-01		-1.41E-01	9.34E-01		3.57E+00	1.40E-07	Up	9.14E-01	5.42E-01		Unigene54347_All//gi|75169169|sp|Q9C6S6.1|PPR67_ARATH//1.00E-40//RecName: Full=Putative pentatricopeptide repeat-containing protein At1g31840	Unigene54347_All//8.00E-42//AT1G31840| LOCATED IN: endomembrane system; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT3G22470.1); Has 23098 Blast hits to 5773 proteins in 180 species: Archae - 3; Bacteria - 16; Metazoa - 407; Fungi - 450; Plants - 21304; Viruses - 0; Other Eukaryotes - 918 (source: NCBI BLink).					nr -
Unigene54348_All	365	0.00	5.41	4.08	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.97E-11	Up	1.20E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene54348_All//gi|116000524|emb|CAL50204.1|//1.00E-26//ubiquitin family protein (ISS) [Ostreococcus tauri]	Unigene54348_All//1.00E-26//AT4G06599| ubiquitin family protein				GO:0016791//GO:0043231	nr -
Unigene5435_All	1220	0.69	0.12	1.40	1.10	0.62	0.44	2.43	1.10	0.42	-2.46E+00	6.70E-03		1.03E+00	5.24E-02		-8.28E-01	1.40E-01		-1.31E+00	2.66E-02		-1.15E+00	4.94E-04	Down	-2.51E+00	7.89E-11	Down	Unigene5435_All//gi|15237711|ref|NP_200668.1|//1.00E-139//PMR5 (POWDERY MILDEW RESISTANT 5) [Arabidopsis thaliana]	Unigene5435_All//1.00E-135//AT5G58600| PMR5 (POWDERY MILDEW RESISTANT 5)	Unigene5435_All//0.00E+00//TC162045				nr -
Unigene54350_All	409	0.00	0.74	0.00	0.00	0.00	1.33	0.10	2.45	1.36	9.54E+00	4.42E-02		null	null		null	null		1.04E+01	2.45E-03		4.57E+00	4.78E-06	Up	3.72E+00	2.38E-03		Unigene54350_All//gi|224082932|ref|XP_002306897.1|//3.00E-21//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222856346|gb|EEE93893.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene54350_All//7.00E-05//AT1G75490| DNA binding / transcription factor	Unigene54350_All//3.00E-17//TC178922	AP2-EREBP		GO:0006350	nr +
Unigene54351_All	221	0.00	7.57	1.20	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.54E-09	Up	1.02E+01	8.00E-02		null	null		null	null		null	null		null	null		Unigene54351_All//gi|112950081|gb|ABI26643.1|//2.00E-08//aspartic proteinase [Cucumis sativus]					GO:0016787	nr -
Unigene54352_All	243	0.00	4.38	0.00	0.00	0.00	1.86	0.00	0.34	0.00	1.21E+01	3.81E-06	Up	null	null		null	null		1.09E+01	7.75E-03		8.43E+00	4.00E-01		null	null		Unigene54352_All//gi|147794801|emb|CAN71427.1|//1.00E-08//hypothetical protein [Vitis vinifera]					GO:0005488	nr -
Unigene54353_All	507	0.10	0.40	0.32	5.70	2.58	1.51	0.92	3.13	0.08	1.95E+00	3.75E-01		1.61E+00	5.11E-01		-1.14E+00	9.74E-04	Down	-1.91E+00	1.47E-06	Down	1.77E+00	4.38E-04	Up	-3.54E+00	6.85E-03					Unigene54353_All//3.00E-18//DW512975				
Unigene54355_All	289	0.00	0.00	0.00	0.52	4.65	2.03	0.00	0.00	0.14	null	null		null	null		3.17E+00	1.71E-05	Up	1.97E+00	6.99E-02		null	null		7.11E+00	6.44E-01									ESTscan +
Unigene54357_All	1258	0.54	0.32	0.25	0.95	0.27	0.00	1.58	0.13	6.40	-7.47E-01	3.80E-01		-1.09E+00	2.39E-01		-1.80E+00	3.53E-03		-9.89E+00	1.76E-07	Down	-3.57E+00	6.95E-10	Down	2.02E+00	2.33E-21	Up	Unigene54357_All//gi|15239865|ref|NP_199155.1|//3.00E-84//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565310|sp|Q9LSW9.1|ATL5K_ARATH RecName: Full=RING-H2 finger protein ATL5K; AltName: Full=RING-H2 finger protein ATL16 >gi|30725342|gb|AAP37693.1| At5g43420 [Arabidopsis thaliana]	Unigene54357_All//9.00E-69//AT5G43420| zinc finger (C3HC4-type RING finger) family protein	Unigene54357_All//5.00E-28//CO091422		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis//ko03420|Nucleotide excision repair	GO:0005488	nr +
Unigene54358_All	989	0.11	0.41	0.00	0.71	0.66	0.55	8.21	21.68	3.83	1.95E+00	1.44E-01		-6.73E+00	3.91E-01		-9.23E-02	8.94E-01		-3.64E-01	6.80E-01		1.40E+00	8.44E-33	Up	-1.10E+00	1.96E-09	Down	Unigene54358_All//gi|283135902|gb|ADB11342.1|//2.00E-15//lambda class glutathione transferase GSTL2 [Populus trichocarpa]	Unigene54358_All//3.00E-12//AT5G02780| In2-1 protein, putative	Unigene54358_All//2.00E-48//TC166114		ko00480|Glutathione metabolism	GO:0016765//GO:0044424	nr -
Unigene5436_All	851	0.61	1.67	2.25	2.81	2.10	3.45	1.64	1.62	3.14	1.44E+00	1.37E-02		1.87E+00	4.53E-04	Up	-4.17E-01	3.15E-01		2.96E-01	4.78E-01		-1.65E-02	1.01E+00		9.36E-01	5.22E-03		Unigene5436_All//gi|30689748|ref|NP_190088.2|//3.00E-10//Ulp1 protease family protein [Arabidopsis thaliana]	Unigene5436_All//1.00E-11//AT4G33620| Ulp1 protease family protein					nr +
Unigene54361_All	672	0.93	0.00	0.00	4.37	3.54	5.78	2.27	0.50	0.18	-9.87E+00	7.91E-04	Down	-9.87E+00	1.41E-03		-3.07E-01	4.29E-01		4.02E-01	2.29E-01		-2.19E+00	5.96E-05	Down	-3.67E+00	3.49E-08	Down	Unigene54361_All//gi|30689711|ref|NP_849712.1|//1.00E-33//KDR (KIDARI): transcription regulator [Arabidopsis thaliana] >gi|28416803|gb|AAO42932.1| At1g26948 [Arabidopsis thaliana]	Unigene54361_All//1.00E-27//AT1G26945| KDR (KIDARI); transcription regulator	Unigene54361_All//0.00E+00//gi|109869247|gb|DW498223.1|DW498223		bHLH	GO:0009314//GO:0009536//GO:0010468	nr +
Unigene54362_All	481	0.11	0.42	0.22	3.94	1.65	1.13	0.18	0.09	0.17	1.95E+00	3.75E-01		1.03E+00	7.02E-01		-1.26E+00	5.12E-03		-1.80E+00	3.14E-04	Down	-1.02E+00	7.24E-01		-8.62E-02	9.71E-01									
Unigene54365_All	919	0.00	0.00	0.00	0.11	0.04	0.05	12.33	0.64	1.60	null	null		null	null		-1.53E+00	5.86E-01		-1.14E+00	6.76E-01		-4.28E+00	1.47E-61	Down	-2.94E+00	1.74E-46	Down	Unigene54365_All//gi|224125106|ref|XP_002329895.1|//4.00E-67//cytochrome P450 [Populus trichocarpa] >gi|222871132|gb|EEF08263.1| cytochrome P450 [Populus trichocarpa]	Unigene54365_All//1.00E-57//AT4G12300| CYP706A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene54365_All//0.00E+00//TC137030		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0016491//GO:0046872	nr +
Unigene54366_All	1074	0.00	11.23	3.07	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	3.54E-69	Up	1.16E+01	2.92E-18	Up	null	null		null	null		null	null		null	null		Unigene54366_All//gi|89212810|gb|AB063905.1|//2.00E-84//14-3-3-like protein [Gossypium hirsutum]	Unigene54366_All//8.00E-82//AT1G22300| GRF10 (GENERAL REGULATORY FACTOR 10); ATP binding / protein binding / protein phosphorylated amino acid binding	Unigene54366_All//2.00E-08//DV849765			GO:0009532//GO:0016020//GO:0032559//GO:0043401//GO:0051219	nr +
Unigene54367_All	613	0.00	1.32	0.17	0.33	0.28	0.29	1.93	1.70	3.25	1.04E+01	9.37E-05	Up	7.44E+00	3.97E-01		-2.11E-01	8.58E-01		-1.42E-01	9.34E-01		-1.80E-01	7.44E-01		7.51E-01	5.83E-02									
Unigene54370_All	416	0.50	0.61	0.00	0.96	1.99	0.98	2.64	1.41	0.57	2.76E-01	8.43E-01		-8.97E+00	1.45E-01		1.05E+00	1.99E-01		2.85E-02	9.85E-01		-9.10E-01	1.24E-01		-2.20E+00	5.65E-04	Down	Unigene54370_All//gi|42569411|ref|NP_180399.2|//6.00E-13//pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein [Arabidopsis thaliana]	Unigene54370_All//4.00E-14//AT2G28320| pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein	Unigene54370_All//1.00E-47//TC172466			GO:0005543	nr +
Unigene54371_All	866	0.00	0.00	0.00	0.00	0.00	0.00	1.66	3.67	0.00	null	null		null	null		null	null		null	null		1.14E+00	2.98E-04	Up	-1.07E+01	1.19E-10	Down	Unigene54371_All//gi|115452901|ref|NP_001050051.1|//3.00E-61//Os03g0337800 [Oryza sativa Japonica Group] >gi|113548522|dbj|BAF11965.1| Os03g0337800 [Oryza sativa Japonica Group]	Unigene54371_All//2.00E-52//AT1G02780| emb2386 (embryo defective 2386); structural constituent of ribosome			ko03010|Ribosome	GO:0009987//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene54372_All	772	0.00	0.00	0.00	0.00	0.00	0.00	4.16	5.68	0.00	null	null		null	null		null	null		null	null		4.50E-01	8.93E-02		-1.20E+01	1.24E-23	Down	Unigene54372_All//gi|3334320|sp|O02518.1|RSSA_SOYBN//2.00E-84//RecName: Full=40S ribosomal protein SA; AltName: Full=p40 >gi|2444420|gb|AAB82659.1| ribosome-associated protein p40 [Glycine max]	Unigene54372_All//9.00E-07//gi|164343954|gb|ES824631.1|ES824631	Unigene54372_All//9.00E-07//gi|164343954|gb|ES824631.1|ES824631		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene54375_All	546	0.00	9.84	10.83	0.00	0.06	0.17	0.00	0.00	0.00	1.33E+01	1.24E-30	Up	1.34E+01	6.03E-33	Up	5.98E+00	8.29E-01		7.37E+00	4.75E-01		null	null		null	null		Unigene54375_All//sp|P20065|TYB4_MOUSE//7.00E-19//Thymosin beta-4 OS=Mus musculus GN=Tmsb4x PE=1 SV=1						swissprot +
Unigene54379_All	767	0.00	19.55	5.14	0.00	0.00	0.00	0.00	0.00	0.00	1.43E+01	3.77E-86	Up	1.23E+01	7.61E-22	Up	null	null		null	null		null	null		null	null		Unigene54379_All//gi|301113692|ref|XP_002998616.1|//1.00E-76//calmodulin [Phytophthora infestans T30-4] >gi|115519|sp|P27165.2|CALM_PHYIN RecName: Full=Calmodulin; Short=CaM >gi|75326398|sp|Q71UH5.1|CALM_PYTSP RecName: Full=Calmodulin; Short=CaM >gi|9858458|gb|AAG01043.1|AF085344_1 calmodulin [Pythium splendens] >gi|169306|gb|AAA21424.1| calmodulin [Phytophthora infestans] >gi|169970351|gb|ACG60663.1| calmodulin [Phytophthora sojae] >gi|262111917|gb|EE169969.1| calmodulin [Phytophthora infestans T30-4]	Unigene54379_All//4.00E-74//AT3G43810| CAM7 (CALMODULIN 7); calcium ion binding	Unigene54379_All//1.00E-30//ES798602		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0046872	nr -
Unigene5438_All	280	44.29	20.45	18.45	35.23	29.02	37.26	54.66	25.82	26.18	-1.11E+00	2.44E-11	Down	-1.26E+00	4.73E-13	Down	-2.79E-01	1.41E-01		8.10E-02	6.82E-01		-1.08E+00	4.81E-16	Down	-1.06E+00	4.34E-16	Down	Unigene5438_All//gi|5706704|gb|AAD47346.1|AF112440_1//3.00E-22//ribosomal protein S26 [Pisum sativum]	Unigene5438_All//4.00E-11//AT3G56340| 40S ribosomal protein S26 (RPS26C)	Unigene5438_All//2.00E-138//TC146058		ko03010|Ribosome		nr -
Unigene54380_All	313	0.00	0.00	0.00	0.32	0.00	0.00	22.83	13.35	0.25	null	null		null	null		-8.31E+00	3.98E-01		-8.31E+00	3.98E-01		-7.74E-01	7.25E-05		-6.49E+00	5.21E-49	Down	Unigene54380_All//gi|14030611|gb|AAK52980.1|AF375396_1//1.00E-09//AT3g25190/MJL12_14 [Arabidopsis thaliana] >gi|17978889|gb|AAL47414.1| AT3g25190/MJL12_14 [Arabidopsis thaliana]	Unigene54380_All//5.00E-11//AT3G25190| nodulin, putative	Unigene54380_All//4.00E-50//DW514314				nr +
Unigene54381_All	738	0.00	4.81	3.97	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	3.46E-20	Up	1.20E+01	3.52E-16	Up	null	null		null	null		null	null		null	null		Unigene54381_All//sp|Q9UHZ2|MALAT_HUMAN//9.00E-27//Metastasis-associated lung adenocarcinoma transcript 1 OS=Homo sapiens GN=MALAT1 PE=2 SV=1						swissprot -
Unigene54383_All	676	0.00	7.12	2.76	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.96E-27	Up	1.14E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene54383_All//gi|255085034|ref|XP_002504948.1|//4.00E-76//ribosomal protein S8E [Micromonas sp. RCC299] >gi|226520217|gb|ACO66206.1| ribosomal protein S8E [Micromonas sp. RCC299]	Unigene54383_All//8.00E-67//AT5G06360| ribosomal protein S8e family protein				GO:0030529	nr -
Unigene54384_All	527	0.00	0.00	0.00	0.09	0.00	0.00	15.56	19.75	0.00	null	null		null	null		-6.56E+00	5.54E-01		-6.56E+00	6.34E-01		3.44E-01	3.49E-02		-1.39E+01	2.23E-60	Down	Unigene54384_All//gi|117606933|gb|ABK42021.1|//3.00E-06//vegetative cell wall protein [Chlamydomonas incerta]		Unigene54384_All//2.00E-07//TC142721		ko03030|DNA replication		nr +
Unigene54386_All	1024	0.00	0.00	0.00	0.00	0.00	0.00	4.87	3.35	0.16	null	null		null	null		null	null		null	null		-5.42E-01	2.47E-02		-4.97E+00	6.36E-31	Down								
Unigene54387_All	545	0.19	0.00	0.00	0.64	0.51	0.17	4.81	1.15	0.95	-7.59E+00	3.70E-01		-7.59E+00	3.91E-01		-3.40E-01	7.85E-01		-1.95E+00	1.96E-01		-2.06E+00	1.66E-07	Down	-2.34E+00	5.76E-09	Down	Unigene54387_All//gi|148270943|gb|ABQ53641.1|//2.00E-52//AWPM19-like protein [Cucumis melo]	Unigene54387_All//3.00E-47//AT1G29520| AWPM-19-like membrane family protein				GO:0031410	nr +
Unigene54389_All	415	0.00	0.00	0.00	0.84	0.17	0.00	0.71	6.75	2.50	null	null		null	null		-2.34E+00	1.01E-01		-9.71E+00	2.12E-02		3.24E+00	1.32E-12	Up	1.81E+00	4.32E-03									

Unigene54390_All	801	0.00	5.82	4.65	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.46E-26	Up	1.22E+01	1.20E-20	Up	null	null		null	null		null	null		Unigene54390_All//sp|Q9YJU5|POL1_BPMV//9.00E-22//RNA1 polyprotein OS=Bean-pod mottle virus (strain Kentucky G7) PE=3 SV=1						swissprot +
Unigene54394_All	452	45.49	14.57	27.45	82.99	66.59	58.95	71.75	9.89	31.64	-1.64E+00	1.73E-32	Down	-7.29E-01	6.58E-09		-3.18E-01	1.05E-04		-4.93E-01	5.04E-09		-2.86E+00	6.62E-124	Down	-1.18E+00	4.19E-39	Down			Unigene54394_All//2.00E-176//gi|199841181|gb|DW239744.1|DW239744				
Unigene54396_All	543	1.73	0.47	2.35	0.73	2.22	3.16	1.40	1.46	3.01	-1.89E+00	1.53E-02		4.40E-01	4.71E-01		1.60E+00	1.36E-02		2.11E+00	1.69E-04	Up	6.14E-02	9.50E-01		1.10E+00	1.44E-02				Unigene54396_All//2.00E-74//TC152618				
Unigene54398_All	305	2.92	0.50	1.05	7.51	3.73	2.37	1.39	0.41	1.57	-2.55E+00	4.05E-03		-1.48E+00	6.98E-02		-1.01E+00	1.11E-02		-1.67E+00	1.58E-04	Down	-1.75E+00	1.23E-01		1.77E-01	8.46E-01				Unigene54398_All//3.00E-100//DR457054				
Unigene54400_All	832	0.00	0.00	0.00	0.00	0.00	0.00	1.52	4.82	6.08	null	null		null	null		null	null		null	null		1.66E+00	1.83E-08	Up	2.00E+00	1.53E-13	Up	Unigene54400_All//gi|186528913|ref|NP_199170.2|//6.00E-12//serine-type endopeptidase inhibitor [Arabidopsis thaliana]	Unigene54400_All//3.00E-13//AT5G43570| serine-type endopeptidase inhibitor	Unigene54400_All//3.00E-44//TC175987				nr -
Unigene54406_All	286	0.00	3.01	3.35	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.94E-05	Up	1.17E+01	2.46E-05	Up	null	null		null	null		null	null		null	null		Unigene54406_All//gi|297845958|ref|XP_002890860.1|//2.00E-23//elongation factor 1-beta [Arabidopsis lyrata subsp. lyrata]|gi|297336702|gb|EFH67119.1| elongation factor 1-beta [Arabidopsis lyrata subsp. lyrata]	Unigene54406_All//1.00E-19//AT2G18110| elongation factor 1-beta, putative / EF-1-beta, putative				GO:0006412//GO:0008135//GO:0010038//GO:0016020//GO:0043234	nr +
Unigene54407_All	436	0.00	0.00	0.00	0.00	0.00	0.00	4.65	2.68	1.28	null	null		null	null		null	null		null	null		-7.94E-01	5.03E-02		-1.86E+00	1.51E-05	Down	Unigene54407_All//gi|145408590|ref|YP_001152214.1|//7.00E-13//O8F124 [Pinus koraiensis]|gi|145048839|gb|ABP35456.1| O8F124 [Pinus koraiensis]		Unigene54407_All//6.00E-19//gi|109850443|gb|DW479422.1|DW479422				nr -
Unigene54408_All	273	0.00	1.11	2.73	3.65	1.01	1.82	6.04	1.84	2.04	1.01E+01	4.42E-02		1.14E+01	3.27E-04	Up	-1.85E+00	7.41E-03		-1.00E+00	1.57E-01		-1.72E+00	4.44E-04	Down	-1.56E+00	7.74E-04	Down			Unigene54408_All//9.00E-125//gi|109886666|gb|DW515635.1|DW515635				
Unigene54409_All	275	3.42	1.84	5.03	153.43	94.79	89.34	714.61	188.76	625.10	-8.94E-01	2.14E-01		5.56E-01	3.62E-01		-6.95E-01	2.59E-20		-7.80E-01	4.73E-22		-1.92E+00	0.00E+00	Down	-1.93E-01	1.32E-09		Unigene54409_All//gi|169349|gb|AAA33765.1|//4.00E-50//hydroxyproline-rich glycoprotein [Phaseolus vulgaris]		Unigene54409_All//2.00E-70//DR455671		ko03040|Spliceosome//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism	GO:0005198//GO:0007047	nr +
Unigene5441_All	225	46.74	98.86	66.74	62.21	61.68	73.27	57.69	58.14	46.92	1.08E+00	1.01E-18	Up	5.14E-01	5.93E-04		-1.25E-02	9.51E-01		2.36E-01	1.13E-01		1.13E-02	9.73E-01		-2.98E-01	3.24E-02		Unigene5441_All//gi|15229253|ref|NP_187074.1|//1.00E-31//SEC (secret agent); transferase, transferring glycosyl groups [Arabidopsis thaliana]|gi|75336082|sp|Q9SEY0.1|SEC_ARATH RecName: Full=Probable UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase SEC; AltName: Full=Protein SECRET AGENT|gi|18139887|gb|AAL60196.1|AF441079_1 O-linked N-acetyl glucosamine transferase [Arabidopsis thaliana]|gi|110743062|dbj|BAE98963.1| O-linked GlcNAc transferase like protein [Arabidopsis thaliana]	Unigene5441_All//6.00E-33//AT3G04240| SEC (secret agent); transferase, transferring glycosyl groups	Unigene5441_All//7.00E-122//TC144694				nr +
Unigene54411_All	702	0.00	29.74	11.91	0.00	0.00	0.00	0.00	0.00	0.00	1.49E+01	3.94E-120	Up	1.35E+01	8.18E-47	Up	null	null		null	null		null	null		null	null		Unigene54411_All//gi|297822545|ref|XP_002879155.1|//7.00E-75//60S ribosomal protein L10A [Arabidopsis lyrata subsp. lyrata]|gi|297324994|gb|EFH55414.1| 60S ribosomal protein L10A [Arabidopsis lyrata subsp. lyrata]	Unigene54411_All//2.00E-66//AT2G27530| PGY1 (PIGGYBACK1); RNA binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003002//GO:0003676//GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0031981//GO:0048513	nr -
Unigene54413_All	232	0.00	0.00	0.00	0.00	0.00	0.00	51.76	183.94	65.60	null	null		null	null		null	null		null	null		1.83E+00	1.60E-94	Up	3.42E-01	6.79E-03		Unigene54413_All//gi|296082870|emb|CBI22171.3|//2.00E-06//unnamed protein product [Vitis vinifera]		Unigene54413_All//7.00E-11//TC163308				nr -
Unigene54414_All	577	0.18	0.00	0.37	0.26	0.00	0.00	28.50	1.38	7.32	-7.50E+00	3.70E-01		1.03E+00	5.91E-01		-8.02E+00	1.65E-01		-8.02E+00	2.33E-01		-4.37E+00	1.68E-90	Down	-1.96E+00	8.34E-42	Down	Unigene54414_All//gi|115455695|ref|NP_001051448.1|//1.00E-07//Os03g0780200 [Oryza sativa Japonica Group]|gi|113549919|dbj|BAF13362.1| Os03g0780200 [Oryza sativa Japonica Group]	Unigene54414_All//3.00E-05//AT1G31335| unknown protein					nr -
Unigene54415_All	1252	0.00	23.03	9.23	0.00	0.00	0.00	0.00	0.00	0.00	1.45E+01	3.37E-166	Up	1.32E+01	5.94E-65	Up	null	null		null	null		null	null		null	null		Unigene54415_All//gi|227937359|gb|ACF43319.1|//2.00E-50//translation elongation factor [Citrus maxima]	Unigene54415_All//5.00E-36//AT1G09640| elongation factor 1B-gamma, putative / eEF-1B gamma, putative				GO:0044464	nr +
Unigene54416_All	552	0.09	0.00	0.00	0.27	0.81	0.00	0.69	2.50	5.20	-6.57E+00	6.10E-01		-6.57E+00	6.22E-01		1.58E+00	2.17E-01		-8.08E+00	2.33E-01		1.86E+00	7.81E-04	Up	2.91E+00	5.63E-12	Up			Unigene54416_All//4.00E-48//DN801633				
Unigene54418_All	415	0.00	0.00	0.26	3.60	0.91	1.41	0.41	0.30	0.00	null	null		8.00E+00	3.97E-01		-1.98E+00	2.94E-04	Down	-1.35E+00	1.52E-02		-4.32E-01	7.92E-01		-8.67E+00	1.08E-01		Unigene54418_All//gi|297726841|ref|NP_001175784.1|//9.00E-15//Os09g0334900 [Oryza sativa Japonica Group]|gi|50252358|dbj|BAD28446.1| ankyrin repeat family protein-like [Oryza sativa Japonica Group]|gi|50252564|dbj|BAD28737.1| ankyrin repeat family protein-like [Oryza sativa Japonica Group]|gi|255678798|dbj|BAH94512.1| Os09g0334900 [Oryza sativa Japonica Group]	Unigene54418_All//2.00E-13//AT3G09550| protein binding	Unigene54418_All//2.00E-71//gi|48804414|gb|CO105728.1|CO105728				nr +
Unigene54419_All	854	0.00	0.00	0.00	0.00	0.00	0.00	2.97	5.43	0.00	null	null		null	null		null	null		null	null		8.71E-01	4.99E-04		-1.15E+01	1.14E-18	Down								ESTscan -
Unigene5442_All	874	28.61	13.68	5.06	14.53	17.30	15.24	21.29	10.04	10.58	-1.06E+00	1.51E-20	Down	-2.50E+00	3.24E-65	Down	2.51E-01	9.57E-02		6.88E-02	6.98E-01		-1.08E+00	2.22E-19	Down	-1.01E+00	7.10E-18	Down	Unigene5442_All//gi|224062285|ref|XP_002300810.1|//2.00E-66//histone 2 [Populus trichocarpa]|gi|222842536|gb|EEE80083.1| histone 2 [Populus trichocarpa]	Unigene5442_All//3.00E-53//AT3G54560| HTA11; DNA binding	Unigene5442_All//0.00E+00//gi|164309274|gb|ES848427.1|ES848427				nr -
Unigene54421_All	712	0.00	0.00	0.00	0.00	0.00	0.00	2.38	4.75	0.06	null	null		null	null		null	null		null	null		1.00E+00	9.04E-04	Up	-5.41E+00	3.52E-11	Down	Unigene54421_All//gi|114159830|gb|ABI53722.1|//1.00E-116//polyubiquitin [Porphyra yezoensis]	Unigene54421_All//5.00E-105//AT5G37640| UBQ9; protein binding	Unigene54421_All//5.00E-70//BM359461			GO:0044424	nr +
Unigene54423_All	561	0.00	0.00	0.00	0.00	0.00	0.00	2.94	2.68	0.00	null	null		null	null		null	null		null	null		-1.32E-01	7.79E-01		-1.15E+01	3.45E-12	Down	Unigene54423_All//gi|300265162|gb|EFJ49355.1|//3.00E-65//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene54423_All//5.00E-61//AT3G25520| ATL5 (A. THALIANA RIBOSOMAL PROTEIN L5); SS rRNA binding / structural constituent of ribosome			ko03010|Ribosome	GO:0003002//GO:0005198//GO:0009536//GO:0009887//GO:0010467//GO:0015934//GO:0016020//GO:0019843//GO:0022613//GO:0031981//GO:0046914//GO:0051169//GO:0065003	nr +
Unigene54424_All	232	0.00	0.00	0.00	3.65	0.15	1.75	0.00	0.00	0.00	null	null		null	null		-4.62E+00	2.79E-05	Down	-1.06E+00	1.81E-01		null	null		null	null										
Unigene54426_All	260	0.60	0.00	0.00	0.19	0.00	0.00	2.44	2.41	0.15	-9.24E+00	2.15E-01		-9.24E+00	2.44E-01		-7.58E+00	5.54E-01		-7.58E+00	6.34E-01		-1.66E-02	1.02E+00		-3.99E+00	5.82E-04	Down								
Unigene54428_All	1322	0.00	0.00	0.00	0.00	0.00	0.00	2.11	2.28	0.00	null	null		null	null		null	null		null	null		1.09E-01	7.51E-01		-1.10E+01	1.57E-20	Down	Unigene54428_All//gi|298711300|emb|CBJ26545.1|//6.00E-22//similar to ankyrin 2,3/unc44 [Ectocarpus siliculosus]	Unigene54428_All//2.00E-15//AT3G04710| ankyrin repeat family protein					nr -
Unigene5443_All	1486	2.01	1.30	1.97	2.08	2.48	2.61	6.94	5.20	1.15	-6.31E-01	7.96E-02		-2.61E-02	9.63E-01		2.55E-01	4.94E-01		3.31E-01	3.38E-01		-4.16E-01	9.63E-03		-2.59E+00	4.79E-37	Down	Unigene5443_All//gi|87162615|gb|AB028410.1|//1.00E-158//Exostosin-like [Medicago truncatula]|gi|116831751|gb|ABK28848.1| exostosin-like protein [Medicago truncatula]	Unigene5443_All//9.00E-72//AT4G38040| exostosin family protein	Unigene5443_All//0.00E+00//ES827236				nr -
Unigene54430_All	396	0.00	0.00	0.00	0.00	0.00	0.00	1.92	0.63	0.10	null	null		null	null		null	null		null	null		-1.60E+00	3.70E-02		-4.26E+00	8.65E-05	Down	Unigene54430_All//gi|255071139|ref|XP_002507651.1|//1.00E-28//60S ribosomal protein L19 [Micromonas sp. RCC299]|gi|226522926|gb|ACO68909.1| 60S ribosomal protein L19 [Micromonas sp. RCC299]	Unigene54430_All//3.00E-19//AT1G02780| emb2386 (embryo defective 2386); structural constituent of ribosome	Unigene54430_All//5.00E-13//DW499391		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene54434_All	883	0.00	9.12	5.43	0.00	0.00	0.10	0.00	0.00	0.00	1.32E+01	4.38E-46	Up	1.24E+01	1.22E-26	Up	null	null		6.68E+00	4.75E-01		null	null		null	null		Unigene54434_All//gi|255085060|ref|XP_002504961.1|//3.00E-10//COMPASS/Set1C complex protein [Micromonas sp. RCC299]|gi|226520230|gb|ACO66219.1| COMPASS/Set1C complex protein [Micromonas sp. RCC299]						nr -
Unigene54435_All	689	0.00	0.00	0.00	0.00	0.00	0.00	3.87	2.97	0.00	null	null		null	null		null	null		null	null		-3.79E-01	3.02E-01		-1.19E+01	1.34E-19	Down	Unigene54435_All//gi|68124015|emb|CAJ01915.1|//7.00E-08//DNA-directed RNA polymerase [Solanum tuberosum]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene54436_All	267	0.59	0.38	0.40	4.48	1.55	0.51	0.63	0.16	1.19	-6.32E-01	7.27E-01		-5.60E-01	7.75E-01		-1.53E+00	1.11E-02		-3.14E+00	6.58E-05	Down	-2.02E+00	3.67E-01		9.14E-01	4.52E-01		Unigene54436_All//gi|224139782|ref|XP_002323274.1|//3.00E-39//cytokinin oxidase [Populus trichocarpa]|gi|222867904|gb|EEF05035.1| cytokinin oxidase [Populus trichocarpa]	Unigene54436_All//3.00E-38//AT2G41510| CKX1 (CYTOKININ OXIDASE/DEHYDROGENASE 1); cytokinin dehydrogenase	Unigene54436_All//2.00E-08//ES837714		ko00908|Zeatin biosynthesis	GO:0009690//GO:0009888//GO:0016645//GO:0030554//GO:0043231	nr +
Unigene54437_All	1123	0.00	0.00	0.00	0.00	0.00	0.00	3.05	0.52	2.13	null	null		null	null		null	null		null	null		-2.55E+00	3.78E-12	Down	-5.19E-01	7.29E-02		Unigene54437_All//gi|75335017|sp|Q9LUP4.1|RCR2_ARATH//1.00E-106//RecName: Full=Receptor-like protein kinase 2; Flags: Precursor|gi|11994762|dbj|BAB03091.1| receptor protein kinase-like protein [Arabidopsis thaliana]	Unigene54437_All//5.00E-98//AT3G24240| leucine-rich repeat transmembrane protein kinase, putative				GO:0004672//GO:0005488	nr +
Unigene54438_All	479	0.00	4.55	0.11	0.21	0.00	0.00	0.18	0.17	2.74	1.22E+01	2.11E-12	Up	6.80E+00	6.35E-01		-7.70E+00	3.12E-01		-7.70E+00	3.98E-01		-1.64E-02	1.01E+00		3.96E+00	2.35E-07	Up	Unigene54438_All//gi|48596999|gb|AAT46040.1|//9.00E-18//At3g12960 [Arabidopsis thaliana]|gi|52627125|gb|AAU84689.1| At3g12960 [Arabidopsis thaliana]	Unigene54438_All//2.00E-18//AT3G12960| unknown protein					nr -
Unigene54439_All	333	0.00	3.35	0.80	0.00	0.21	0.54	1.65	0.63	1.20	1.17E+01	2.00E-06	Up	9.64E+00	8.00E-02		7.69E+00	6.08E-01		9.08E+00	1.94E-01		-1.40E+00	1.34E-01		-4.64E-01	5.97E-01									
Unigene54443_All	340	0.00	0.00	0.63	1.76	2.43	0.00	0.50	0.12	0.12	null	null		9.29E+00	1.40E-01		4.67E-01	5.85E-01		-1.08E+01	7.70E-04	Down	-2.02E+00	3.67E-01		-2.09E+00	3.13E-01									
Unigene5445_All	416	14.21	15.47	13.31	17.00	14.24	23.88	10.06	7.43	4.88	1.22E-01	6.22E-01		-9.43E-02	7.17E-01		-2.56E-01	2.84E-01		4.90E-01	7.02E-03		-4.37E-01	1.11E-01		-1.04E+00	6.46E-05	Down	Unigene5445_All//gi|15235369|ref|NP_193761.1|//2.00E-11//TAF11 (TBP-ASSOCIATED FACTOR 11); DNA binding / RNA polymerase II transcription factor/ transcription initiation factor [Arabidopsis thaliana]|gi|395450902|gb|AAR28014.1| TAF11 [Arabidopsis thaliana]	Unigene5445_All//3.00E-05//AT4G20280| TAF11 (TBP-ASSOCIATED FACTOR 11); DNA binding / RNA polymerase II transcription factor/ transcription initiation factor	Unigene5445_All//3.00E-113//DW512742		ko03022|Basal transcription factors		nr +
Unigene54450_All	808	0.00	4.95	2.31	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	8.55E-23	Up	1.12E+01	2.89E-10	Up	null	null		null	null		null	null		null	null										
Unigene54451_All	862	0.00	3.88	1.24	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.94E-19	Up	1.03E+01	6.62E-06	Up	null	null		null	null		null	null		null	null		Unigene54451_All//gi|255086926|ref|XP_002505386.1|//3.00E-06//predicted protein [Micromonas sp. RCC299]|gi|226520656|gb|ACO66644.1| predicted protein [Micromonas sp. RCC299]						nr +

Unigene54453_All	244	0.00	0.00	0.00	0.00	0.00	0.37	10.74	2.23	13.71	null	null		null	null		null	null		8.53E+00	4.75E-01		-2.27E+00	2.34E-08	Down	3.52E-01	2.48E-01		Unigene54453_All//gi|221272207|sp|A2A1A0.1|NCS1_COPJA//4.00E-10//RecName: Full=S-norcoclaurine synthase 1; Short=CjNCS1 >gi|123720767|dbj|BAF45337.1| norcoclaurine synthase [Coptis japonica var. dissecta] >gi|301072256|gb|ADK56103.1| 2OG/Fe(II)-dependent dioxygenase-like protein [synthetic construct]	Unigene54453_All//5.00E-06//AT4G25310| oxidoreductase, 2OG-Fe(II) oxygenase family protein				GO:0003824	nr +
Unigene54454_All	397	0.00	0.13	0.27	0.00	1.73	1.71	0.11	0.95	2.31	7.00E+00	6.15E-01		8.07E+00	3.97E-01		1.08E+01	3.05E-04	Up	1.07E+01	4.18E-04	Up	3.15E+00	3.41E-02		4.44E+00	1.24E-05	Up	Unigene54454_All//gi|224088834|ref|XP_002308560.1|//9.00E-07//predicted protein [Populus trichocarpa] >gi|222854536|gb|EEE92083.1| predicted protein [Populus trichocarpa]		Unigene54454_All//3.00E-144//gi|73847983|gb|DT457003.1|DT457003				nr +
Unigene54455_All	283	0.00	13.61	6.59	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	6.32E-22	Up	1.27E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene54455_All//gi|115469286|ref|NP_001058242.1|//6.00E-22//Os06g0653900 [Oryza sativa Japonica Group] >gi|113596282|dbj|BAF20156.1| Os06g0653900 [Oryza sativa Japonica Group]	Unigene54455_All//4.00E-15//AT5G50460| protein transport protein SEC61 gamma subunit, putative			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export	GO:0006886//GO:0008320//GO:0044464	nr -
Unigene54458_All	1505	0.14	7.74	5.94	0.00	0.00	0.06	0.00	0.00	0.00	5.80E+00	5.24E-60	Up	5.42E+00	8.10E-44	Up	null	null		5.91E+00	4.75E-01		null	null		null	null		Unigene54458_All//gi|194477040|ref|YP_002049219.1|/4.00E-76//preprotein translocase SecY [Paulinella chromatophora] >gi|171192047|gb|ACB43009.1| preprotein translocase SecY [Paulinella chromatophora]	Unigene54458_All//3.00E-52//AT2G18710| SCY1 (SecY Homolog 1); P-P-bond-hydrolysis-driven protein transmembrane transporter			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export	GO:0009536//GO:0016020	nr +
Unigene54459_All	258	0.41	0.00	0.83	9.27	7.34	2.80	3.61	0.65	2.32	-8.66E+00	3.70E-01		1.03E+00	5.91E-01		-3.36E-01	4.41E-01		-1.73E+00	6.61E-05	Down	-2.48E+00	1.07E-03		-6.38E-01	3.08E-01		Unigene54459_All//gi|224132268|ref|XP_002321297.1|//4.00E-41//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222862070|gb|EEE99612.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene54459_All//7.00E-41//AT1G04120| ATMRP5; ATPase, coupled to transmembrane movement of substances / sulfonylurea receptor	Unigene54459_All//4.00E-31//TC155668			GO:0004888//GO:0005773//GO:0006810//GO:0006875//GO:0006970//GO:0008152//GO:0015405//GO:0016628//GO:0017111//GO:0031090//GO:0031224//GO:0032559	nr +
Unigene54460_All	593	0.00	0.17	0.00	0.00	0.00	0.00	3.42	3.38	0.81	7.42E+00	3.85E-01		null	null		null	null		null	null		-1.66E-02	1.00E+00		-2.09E+00	2.72E-06	Down	Unigene54460_All//gi|212717161|gb|ACJ37422.1|//4.00E-40//receptor-like serine/threonine kinase [Glycine max]	Unigene54460_All//2.00E-38//AT1G53430| leucine-rich repeat family protein / protein kinase family protein			ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0032559	nr +
Unigene54461_All	623	1.93	9.27	4.96	0.40	0.66	0.22	0.00	0.40	0.00	2.26E+00	2.88E-14	Up	1.36E+00	3.75E-04	Up	7.30E-01	5.86E-01		-8.78E-01	6.16E-01		8.65E+00	4.31E-02		null	null		Unigene54461_All//gi|62956020|gb|AAY23355.1|/3.00E-96/3-ketoacyl-CoA reductase 2 [Gossypium hirsutum]	Unigene54461_All//2.00E-51//AT1G24470| short-chain dehydrogenase/reductase (SDR) family protein	Unigene54461_All//0.00E+00//TC136684	ko00903|Limonene and pinene degradation//ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis		GO:0008152//GO:0033764	nr +
Unigene54464_All	653	0.48	0.16	0.33	0.31	0.53	2.07	24.93	10.43	14.83	-1.63E+00	2.76E-01		-5.59E-01	6.63E-01		7.89E-01	5.96E-01		2.77E+00	9.12E-05	Up	-1.26E+00	2.22E-21	Down	-7.50E-01	7.20E-10									
Unigene54465_All	998	0.00	11.32	3.20	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	8.69E-65	Up	1.16E+01	1.15E-17	Up	null	null		null	null		null	null		null	null		Unigene54465_All//gi|32400971|gb|AAP80691.1|/2.00E-74/ubiquitin-conjugating enzyme [Griffithsia japonica]	Unigene54465_All//2.00E-69//AT5G56150| UBC30 (ubiquitin-conjugating enzyme 30); ubiquitin-protein ligase			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0006464//GO:0016881//GO:0060255	nr +
Unigene54466_All	544	0.67	0.56	0.78	0.55	0.82	0.33	0.23	2.07	0.88	-2.68E-01	8.00E-01		2.18E-01	8.31E-01		5.83E-01	6.26E-01		-7.26E-01	6.38E-01		3.15E+00	2.58E-05	Up	1.91E+00	6.30E-02									
Unigene54467_All	434	0.00	0.00	0.00	0.00	0.00	0.00	0.68	2.89	0.73	null	null		null	null		null	null		null	null		2.08E+00	5.41E-04	Up	1.07E-01	9.45E-01									ESTscan -
Unigene54473_All	706	0.00	145.55	56.95	0.00	0.00	0.00	0.00	0.00	0.00	1.72E+01	0.00E+00	Up	1.58E+01	2.40E-228	Up	null	null		null	null		null	null		null	null		Unigene54473_All//gi|192913004|gb|ACF06610.1|//9.00E-80//ribosomal protein L15 [Elaeis guineensis]	Unigene54473_All//3.00E-54//AT4G16720| 60S ribosomal protein L15 (RPL15A)	Unigene54473_All//2.00E-10//DV8419111	ko03010|Ribosome		GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene54475_All	289	0.00	11.05	4.97	0.00	0.24	0.00	0.00	0.00	0.00	1.34E+01	3.64E-18	Up	1.23E+01	6.30E-08	Up	7.90E+00	6.08E-01		null	null		null	null		null	null		Unigene54475_All//sp|P07737|PROF1_HUMAN//3.00E-26//Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2						swissprot +
Unigene54476_All	314	0.17	1.13	0.17	0.16	0.22	0.58	2.15	0.53	0.13	2.76E+00	9.59E-02		2.57E-02	9.94E-01		4.68E-01	9.57E-01		1.86E+00	4.58E-01		-2.02E+00	1.98E-02		-4.09E+00	3.10E-04	Down			Unigene54476_All//1.00E-09//TC170024				
Unigene54478_All	475	0.00	9.49	2.13	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.08E-25	Up	1.11E+01	1.27E-05	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene54479_All	284	0.00	2.32	2.44	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.25E-04	Up	1.13E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene54479_All//sp|P00736|C1R_HUMAN//4.00E-49//Complement C1r subcomponent OS=Homo sapiens GN=C1R PE=1 SV=2						swissprot -
Unigene5448_All	587	38.06	19.59	25.22	92.25	75.09	34.47	31.26	21.93	13.98	-9.58E-01	1.29E-15		-5.94E-01	6.59E-07		-2.97E-01	8.42E-06		-1.42E+00	3.97E-74	Down	-5.11E-01	8.44E-06		-1.16E+00	6.29E-22	Down	Unigene5448_All//gi|53370641|gb|AAU89136.1|//3.00E-06//F-box domain containing protein [Oryza sativa Japonica Group]	Unigene5448_All//6.00E-06//AT2G46460| nucleic acid binding	Unigene5448_All//0.00E+00//BQ401903				nr -
Unigene54480_All	621	0.67	0.00	0.17	0.16	0.28	0.15	11.44	10.10	0.45	-9.40E+00	1.05E-02		-1.97E+00	1.51E-01		7.90E-01	7.70E-01		-1.41E-01	9.49E-01		-1.80E-01	4.12E-01		-4.67E+00	2.21E-42	Down	Unigene54480_All//gi|224139824|ref|XP_002323294.1|//2.00E-32//cytochrome P450 [Populus trichocarpa] >gi|222867924|gb|EEF05055.1| cytochrome P450 [Populus trichocarpa]	Unigene54480_All//1.00E-24//AT5G06900| CYP93D1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene54480_All//6.00E-63//CO076520	ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0005506//GO:0016491	nr +
Unigene54482_All	457	0.23	0.00	0.82	0.44	0.23	0.10	1.48	6.68	4.53	-7.84E+00	3.70E-01		1.83E+00	2.13E-01		-9.47E-01	5.87E-01		-2.14E+00	3.47E-01		2.17E+00	4.01E-09	Up	1.61E+00	1.01E-04	Up			Unigene54482_All//3.00E-45//gi|78345047|gb|DT565321.1|DT565321				
Unigene54487_All	636	0.00	8.52	10.21	0.16	0.43	0.00	25.59	30.23	33.20	1.31E+01	6.34E-31	Up	1.33E+01	2.96E-36	Up	1.47E+00	4.19E-01		-7.29E+00	3.98E-01		2.40E-01	4.22E-02		3.75E-01	3.29E-04		Unigene54487_All//gi|253761396|ref|XP_002489102.1|//8.00E-15//hypothetical protein SORBIDRAFT_0070s002020 [Sorghum bicolor] >gi|241947393|gb|EES20538.1| hypothetical protein SORBIDRAFT_0070s002020 [Sorghum bicolor]		Unigene54487_All//7.00E-38//TC166887				nr -
Unigene5449_All	572	3.48	6.29	4.10	1.22	1.14	2.05	37.92	67.37	316.27	8.56E-01	8.54E-03		2.37E-01	6.13E-01		-9.21E-02	8.94E-01		7.52E-01	2.53E-01		8.29E-01	2.22E-25		3.06E+00	0.00E+00	Up	Unigene5449_All//gi|89111844|gb|ABD60694.1|//5.00E-17//At3g50900 [Arabidopsis thaliana]	Unigene5449_All//3.00E-16//AT3G50900| unknown protein	Unigene5449_All//0.00E+00//gi|109886265|gb|DW515235.1|DW515235				nr +
Unigene54495_All	333	0.00	0.00	0.00	0.00	0.00	0.00	1.90	2.26	0.00	null	null		null	null		null	null		null	null		2.46E-01	7.31E-01		-1.09E+01	7.10E-05	Down								
Unigene54496_All	734	1.78	0.14	0.00	0.27	0.00	0.00	16.01	3.13	0.22	-3.69E+00	1.09E-05	Down	-1.08E+01	3.71E-07	Down	-8.08E+00	8.41E-02		-8.08E+00	1.33E-01		-2.35E+00	1.49E-36	Down	-6.20E+00	2.20E-79	Down	Unigene54496_All//gi|254803073|gb|ACT82815.1|//5.00E-18//At1g29270 [Arabidopsis thaliana]	Unigene54496_All//1.00E-11//AT1G29270| unknown protein	Unigene54496_All//0.00E+00//gi|109881197|gb|DW510167.1|DW510167				nr +
Unigene54497_All	430	0.00	0.24	0.62	0.93	0.72	1.26	1.47	0.97	9.82	7.88E+00	3.85E-01		9.27E+00	8.00E-02		-3.63E-01	7.54E-01		4.44E-01	6.78E-01		-6.02E-01	4.67E-01		2.74E+00	2.99E-16	Up			Unigene54497_All//5.00E-07//ES803838				
Unigene54498_All	499	0.00	6.80	2.99	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.54E-19	Up	1.15E+01	3.22E-08	Up	null	null		null	null		null	null		null	null										
Unigene545_All	1437	32.81	24.93	23.90	32.59	28.80	40.23	39.84	19.14	18.52	-3.96E-01	2.64E-07		-4.57E-01	7.77E-09		-1.78E-01	2.37E-02		3.04E-01	7.18E-06		-1.06E+00	9.74E-56	Down	-1.11E+00	1.64E-61	Down	Unigene545_All//gi|297806557|ref|XP_002871162.1|//1.00E-159//protein synthesis initiation factor eIF2 alpha [Arabidopsis lyrata subsp. lyrata] >gi|297316999|gb|EFH47421.1| protein synthesis initiation factor eIF2 alpha [Arabidopsis lyrata subsp. lyrata]	Unigene545_All//5.00E-141//AT2G40290| eukaryotic translation initiation factor 2 subunit 1, putative / eIF-2A, putative / eIF-2-alpha, putative	Unigene545_All//0.00E+00//TC130001		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene54501_All	631	0.66	0.16	0.51	1.66	1.53	3.22	1.27	3.18	4.67	-2.05E+00	1.20E-01		-3.90E-01	7.17E-01		-1.18E-01	8.38E-01		9.58E-01	3.80E-02		1.32E+00	1.62E-03		1.88E+00	1.21E-07	Up	Unigene54501_All//gi|30680527|ref|NP_196066.2|//7.00E-70//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene54501_All//3.00E-65//AT5G04460| protein binding / zinc ion binding	Unigene54501_All//5.00E-128//DN758722			GO:0046914	nr +
Unigene54504_All	220	3.09	0.00	0.00	4.30	1.41	0.62	0.38	0.38	0.00	-1.16E+01	4.09E-04	Down	-1.16E+01	7.63E-04	Down	-1.61E+00	2.15E-02		-2.80E+00	1.18E-03		-1.66E-02	1.01E+00		-8.59E+00	3.57E-01		Unigene54504_All//gi|296087891|emb|CBI35174.3|//6.00E-06//unnamed protein product [Vitis vinifera]						nr -
Unigene54505_All	528	0.00	1.44	1.31	1.13	2.54	1.80	0.56	0.48	0.60	1.05E+01	1.76E-04	Up	1.04E+01	6.15E-04	Up	1.17E+00	4.76E-02		6.66E-01	3.93E-01		-2.39E-01	8.39E-01		1.07E-01	9.45E-01		Unigene54505_All//gi|297846082|ref|XP_002890922.1|//2.00E-07//F17F8.1 [Arabidopsis lyrata subsp. lyrata] >gi|297336764|gb|EFH67181.1| F17F8.1 [Arabidopsis lyrata subsp. lyrata]	Unigene54505_All//1.00E-08//AT1G31070| UDP-N-acetylglucosamine pyrophosphorylase-related	Unigene54505_All//2.00E-44//TC132203		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene54507_All	291	1.98	4.18	2.93	1.03	3.08	5.74	0.44	1.29	1.92	1.08E+00	8.15E-02		5.66E-01	4.61E-01		1.58E+00	4.38E-02		2.48E+00	3.36E-05	Up	1.57E+00	1.95E-01		2.14E+00	2.64E-02				Unigene54507_All//3.00E-44//DT462248				
Unigene54509_All	417	0.00	2.07	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	4.94E-05	Up	1.07E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene54509_All//gi|75282567|sp|Q43492.2|BSZ7_HORVU//4.00E-08//RecName: Full=Serpin-Z7; AltName: Full=HorvuZ7; AltName: Full=BSZ7 >gi|1197577|emb|CAA61599.1| serpin [Hordeum vulgare subsp. vulgare]	Unigene54509_All//2.00E-08//AT1G47710| serpin, putative / serine protease inhibitor, putative				GO:0004866//GO:0005576	nr +
Unigene5451_All	311	55.01	23.95	29.62	80.57	61.89	74.50	23.25	8.47	9.74	-1.20E+00	3.61E-17	Down	-8.93E-01	2.19E-10		-3.80E-01	1.86E-04		-1.13E-01	4.00E-01		-1.46E+00	2.94E-12	Down	-1.26E+00	2.85E-10	Down			Unigene5451_All//2.00E-141//TC179327				
Unigene54510_All	694	0.00	3.21	1.69	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.09E-12	Up	1.07E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene54510_All//gi|13434998|gb|AAK26104.1|AF132729_1//2.00E-59//SKP1-like protein ASK10 [Arabidopsis thaliana]	Unigene54510_All//4.00E-46//AT5G42190| ASK2 (ARABIDOPSIS SKP1-LIKE 2); protein binding / ubiquitin-protein ligase			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0003006//GO:0005488//GO:0019941//GO:0031461	nr -
Unigene54511_All	319	0.00	0.32	0.00	0.00	0.00	0.14	27.57	37.73	211.31	8.31E+00	3.85E-01		null	null		null	null		7.15E+00	6.95E-01		4.53E-01	1.95E-03		2.94E+00	2.54E-268	Up			Unigene54511_All//1.00E-22//gi|73860786|gb|DT463525.1|DT463525				
Unigene54512_All	525	0.00	0.00	0.00	0.57	0.39	0.34	5.07	0.32	3.26	null	null		null	null		-5.33E-01	6.78E-01		-7.26E-01	6.38E-01		-3.99E+00	3.57E-14	Down	-6.37E-01	5.56E-02		Unigene54512_All//gi|115470403|ref|NP_001058800.1|//2.00E-11//Os07g0123800 [Oryza sativa Japonica Group] >gi|113610336|dbj|BAF20714.1| Os07g0123800 [Oryza sativa Japonica Group]	Unigene54512_All//2.00E-12//AT1G58420| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031279 (InterPro:IPR016972); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10140.1); Has 28 Blast hits to 28 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 28; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene54512_All//3.00E-09//TC169661				nr -
Unigene54516_All	339	0.00	0.00	0.00	0.00	0.00	0.00	3.24	2.59	0.47	null	null		null	null		null	null		null	null		-3.25E-01	6.15E-01		-2.79E+00	6.37E-05	Down	Unigene54516_All//gi|152032511|sp|A2XF66.1|H2B1_ORYSI//2.00E-23//RecName: Full=Histone H2B.1 >gi|152032513|sp|A3AGM4.1|H2B1_ORYSJ RecName: Full=Histone H2B.1	Unigene54516_All//6.00E-19//AT5G02570| histone H2B, putative				GO:0043229	nr +
Unigene54522_All	667	0.00	16.71	5.27	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	6.54E-64	Up	1.24E+01	1.87E-19	Up	null	null		null	null		null	null		null	null		Unigene54522_All//sp|P27578|VIT1_CERCA//1.00E-93//Vitellogenin-1 OS=Ceratitis capitata GN=VG1-GAMMA PE=2 SV=1						swissprot +

Unigene54523_All	625	0.00	0.00	0.00	0.00	0.00	0.00	2.77	2.67	0.26	null	null		null	null		null	null		null	null		-5.23E-02	9.23E-01		-3.44E+00	8.41E-09	Down	Unigene54523_All//sp|P0A3U9|BP26_BRUSU//2.00E-12//26 kDa periplasmic immunogenic protein OS=Brucella suis GN=bp26 PE=3 SV=1						swissprot +
Unigene54527_All	485	0.00	0.21	0.22	3.80	4.54	2.61	4.27	0.52	1.48	7.71E+00	3.85E-01		7.78E+00	3.97E-01		2.58E-01	6.01E-01		-5.44E-01	2.82E-01		-3.05E+00	5.12E-09	Down	-1.53E+00	1.72E-04	Down	Unigene54527_All//gi|217426802|gb|ACK44510.1|//6.00E-23//AT5G10150-like protein [Arabidopsis arenosa]	Unigene54527_All//7.00E-22//AT5G10150| unknown protein	Unigene54527_All//0.00E+00//DT046641				nr -
Unigene54528_All	338	0.00	4.35	2.21	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.11E-08	Up	1.11E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene54528_All//gi|145340597|ref|XP_001415408.1|//2.00E-31//P-ATPase family transporter: sodium/potassium ion [Ostreococcus lucimarinus CCE9901] >gi|144576631|gb|ABO93700.1| P-ATPase family transporter: sodium/potassium ion [Ostreococcus lucimarinus CCE9901]	Unigene54528_All//4.00E-12//AT3G63380| calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12)				GO:0006812//GO:0009206//GO:0022890//GO:0031224//GO:0032559//GO:0042625	nr -
Unigene54529_All	617	0.00	0.16	0.00	0.00	0.00	0.07	6.44	2.57	4.00	7.36E+00	3.85E-01		null	null		null	null		6.19E+00	6.95E-01		-1.32E+00	3.10E-06	Down	-6.86E-01	9.10E-03		Unigene54529_All//gi|15234742|ref|NP_194771.1|//2.00E-81//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|7269943|emb|CAB79760.1| nodulin-like protein [Arabidopsis thaliana]	Unigene54529_All//7.00E-36//AT4G30420| nodulin MtN21 family protein				GO:0031410	nr +
Unigene54530_All	402	0.00	0.00	0.00	0.00	0.00	0.00	1.26	1.56	0.00	null	null		null	null		null	null		null	null		3.05E-01	7.04E-01		-1.03E+01	5.54E-04	Down	Unigene54530_All//gi|159477927|ref|XP_001697060.1|//4.00E-39//acidic ribosomal protein P0 [Chlamydomonas reinhardtii] >gi|158274972|gb|EDP00752.1| acidic ribosomal protein P0 [Chlamydomonas reinhardtii]	Unigene54530_All//2.00E-37//AT2G40010| 60S acidic ribosomal protein P0 (RPP0A)			ko03010|Ribosome	GO:0005198//GO:0006350//GO:0006412//GO:0010468//GO:0016829//GO:0030029//GO:0043229	nr +
Unigene54531_All	342	0.00	2.96	0.00	0.00	0.10	1.06	0.12	0.49	1.86	1.15E+01	7.25E-06	Up	null	null		6.65E+00	8.29E-01		1.00E+01	2.37E-02		1.98E+00	3.79E-01		3.91E+00	7.65E-04	Up			Unigene54531_All//4.00E-07//TC165904					
Unigene54532_All	603	0.00	0.84	0.00	0.33	0.23	0.00	0.28	2.36	1.85	9.71E+00	4.04E-03		null	null		-5.33E-01	7.48E-01		-8.37E+00	1.33E-01		3.07E+00	2.15E-06	Up	2.72E+00	8.54E-05	Up			Unigene54532_All//1.00E-45//DR510931					
Unigene54533_All	537	0.00	0.00	0.00	0.00	0.00	0.00	6.38	4.90	0.30	null	null		null	null		null	null		null	null		-3.79E-01	2.31E-01		-4.43E+00	4.70E-20	Down								
Unigene54535_All	352	0.30	2.45	3.63	0.00	0.00	0.64	0.00	0.00	0.45	3.04E+00	1.94E-03		3.61E+00	3.41E-05	Up	null	null		9.33E+00	1.18E-01		null	null		8.82E+00	1.40E-01									
Unigene54536_All	254	52.94	146.22	84.07	94.33	96.80	91.22	173.78	261.80	76.54	1.47E+00	4.57E-49	Up	6.67E-01	5.17E-08		3.72E-02	8.12E-01		-4.85E-02	7.14E-01		5.91E-01	3.15E-24		-1.18E+00	4.87E-53	Down	Unigene54536_All//gi|166865124|gb|ABZ01817.1|//2.00E-30//cinnamyl alcohol dehydrogenase [Gossypium hirsutum]	Unigene54536_All//2.00E-26//AT4G34230| ATCAD5 (CINNAMYL ALCOHOL DEHYDROGENASE 5); cinnamyl-alcohol dehydrogenase	Unigene54536_All//3.00E-127//gi|54118154|gb|CO493663.1|CO493663		ko00940|Phenylpropanoid biosynthesis	GO:0009699//GO:0016616//GO:0046914	nr -
Unigene54537_All	521	0.20	1.17	3.07	4.97	2.25	1.82	3.49	4.41	1.15	2.54E+00	2.46E-02		3.93E+00	9.51E-07	Up	-1.15E+00	1.97E-03		-1.45E+00	3.06E-04	Down	3.39E-01	4.00E-01		-1.61E+00	2.86E-04	Down			Unigene54537_All//6.00E-07//CD486134					
Unigene54538_All	497	0.00	0.00	0.00	0.20	0.07	0.00	6.13	5.13	0.80	null	null		null	null		-1.53E+00	5.86E-01		-7.65E+00	3.98E-01		-2.56E-01	4.63E-01		-2.93E+00	5.61E-13	Down	Unigene54538_All//gi|297836874|ref|XP_002886319.1|//2.00E-09//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332159|gb|EFH62578.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene54538_All//5.00E-29//DV849020				nr -
Unigene54539_All	600	0.17	0.00	0.18	0.42	0.11	0.15	4.23	1.46	1.59	-7.45E+00	3.70E-01		2.54E-02	9.99E-01		-1.85E+00	2.75E-01		-1.46E+00	4.07E-01		-1.53E+00	4.18E-05	Down	-1.41E+00	8.57E-05	Down			Unigene54539_All//5.00E-54//TC175252					
Unigene5454_All	256	33.31	17.81	19.55	29.38	35.38	35.46	69.20	32.49	41.08	-9.03E-01	6.27E-06		-7.69E-01	1.87E-04		2.68E-01	1.94E-01		2.71E-01	1.95E-01		-1.09E+00	1.11E-18	Down	-7.52E-01	1.02E-10		Unigene5454_All//gi|17367847|sp|Q9XF97.1|RL4_PRUAR//7.00E-39//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32296.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene5454_All//2.00E-30//AT5G02870| 60S ribosomal protein L4/L1 (RPL4D)	Unigene5454_All//1.00E-142//DN827755		ko03010|Ribosome		nr -
Unigene54541_All	494	0.00	3.18	2.05	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.70E-09	Up	1.10E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene54541_All//gi|299473361|emb|CBN77759.1|//5.00E-08//SBDS domain, zinc finger protein [Ectocarpus siliculosus]				ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03430|Mismatch repair	GO:0003824	nr +
Unigene54542_All	654	0.00	70.89	24.35	0.00	0.00	0.00	0.00	0.00	0.00	1.61E+01	9.20E-268	Up	1.46E+01	8.49E-90	Up	null	null		null	null		null	null		null	null		Unigene54542_All//gi|7594877|dbj|BAA94696.1|//3.00E-13//calmodulin [Chara corallina] >gi|7594879|dbj|BAA94697.1| calmodulin [Chara corallina] >gi|8388801|dbj|BAA96536.1| calmodulin [Chara corallina]	Unigene54542_All//2.00E-09//AT5G37780| CAM1 (CALMODULIN 1); calcium ion binding			ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0005488//GO:0044464//GO:0050896	nr -
Unigene54545_All	497	0.00	0.10	0.00	0.10	0.28	0.09	10.21	4.12	0.88	6.67E+00	6.15E-01		null	null		1.47E+00	6.18E-01		-1.41E-01	9.52E-01		-1.31E+00	1.26E-07	Down	-3.53E+00	4.96E-25	Down	Unigene54545_All//gi|297850466|ref|XP_002893114.1|//9.00E-11//opc-8:0 CoA ligase1 [Arabidopsis lyrata subsp. lyrata] >gi|297338956|gb|EFH69373.1| opc-8:0 CoA ligase1 [Arabidopsis lyrata subsp. lyrata]	Unigene54545_All//1.00E-11//AT1G20510| OPCL1 (OPC-8:0 COA LIGASE1); 4-coumarate-CoA ligase	Unigene54545_All//2.00E-157//gi|109870168|gb|DW499144.1|DW499144		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0006950//GO:0009694//GO:0016405//GO:0016703//GO:0042579	nr +
Unigene54550_All	392	1.87	0.00	1.22	3.81	0.53	1.04	1.83	1.07	0.61	-1.09E+01	2.11E-04	Down	-6.12E-01	4.70E-01		-2.85E+00	2.82E-06	Down	-1.88E+00	1.24E-03		-7.82E-01	3.10E-01		-1.59E+00	3.62E-02		Unigene54550_All//gi|297831650|ref|XP_002883707.1|//4.00E-54//xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329647|gb|EFH59966.1| xanthine/uracil permease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene54550_All//8.00E-48//AT2G05760| xanthine/uracil permease family protein	Unigene54550_All//0.00E+00//ES804248			GO:0005215//GO:0006810//GO:0031410	nr -
Unigene54552_All	502	0.00	61.07	21.85	0.00	0.27	0.00	0.00	0.00	0.00	1.59E+01	9.15E-177	Up	1.44E+01	1.26E-61	Up	8.10E+00	3.18E-01		null	null		null	null		null	null									ESTscan -
Unigene54557_All	460	1.02	0.55	0.58	0.11	0.15	0.00	2.57	0.18	0.17	-8.94E-01	3.88E-01		-8.23E-01	4.57E-01		4.67E-01	9.57E-01		-6.76E+00	6.34E-01		-3.82E+00	2.12E-06	Down	-3.89E+00	9.20E-07	Down								
Unigene5456_All	987	0.27	0.26	0.54	1.67	2.55	1.19	0.90	1.02	2.38	-4.59E-02	9.86E-01		1.03E+00	3.42E-01		6.13E-01	1.35E-01		-4.85E-01	3.82E-01		1.76E-01	7.73E-01		1.40E+00	1.92E-04	Up	Unigene5456_All//gi|92893902|gb|ABE91952.1|//1.00E-13//Zinc finger, CCHC-type [Medicago truncatula]	Unigene5456_All//8.00E-12//AT2G01050| nucleic acid binding / zinc ion binding	Unigene5456_All//1.00E-18//BG441884				nr +
Unigene54560_All	259	0.00	3.33	2.88	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.94E-05	Up	1.15E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene54560_All//gi|298708255|emb|CBJ48318.1|//1.00E-06//v-type h-atpase [Ectocarpus siliculosus]				ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0000325//GO:0009987//GO:0022857//GO:0031090//GO:0050896	nr +
Unigene54561_All	1337	0.00	13.68	6.33	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	3.46E-105	Up	1.26E+01	2.04E-47	Up	null	null		null	null		null	null		null	null		Unigene54561_All//sp|P27587|VIT2_CERCA//0.00E+00//Vitellogenin-2 OS=Ceratitis capitata GN=VG2-delta PE=2 SV=1						swissprot -
Unigene54562_All	431	0.00	0.00	2.22	0.92	0.32	0.52	0.00	0.00	0.00	null	null		1.11E+01	2.46E-05	Up	-1.53E+00	2.05E-01		-8.20E-01	5.06E-01		null	null		null	null		Unigene54562_All//gi|255595765|ref|XP_002536388.1|//2.00E-18//Ferric-pseudobactin 358 receptor precursor, putative [Ricinus communis] >gi|223519878|gb|EEF25995.1| Ferric-pseudobactin 358 receptor precursor, putative [Ricinus communis]						nr +
Unigene54565_All	748	0.00	0.00	0.00	0.53	0.00	0.00	7.29	7.99	2.02	null	null		null	null		-9.06E+00	4.38E-03		-9.06E+00	1.11E-02		1.32E-01	6.22E-01		-1.85E+00	2.21E-13	Down								
Unigene54566_All	256	0.41	0.20	4.99	3.31	1.21	0.71	1.98	1.80	0.62	-1.05E+00	6.84E-01		3.61E+00	3.41E-05	Up	-1.45E+00	5.13E-02		-2.23E+00	9.52E-03		-1.42E-01	8.76E-01		-1.67E+00	7.77E-02									
Unigene54567_All	440	9.28	5.76	3.99	5.55	9.39	5.95	15.76	48.35	72.98	-6.88E-01	2.23E-02		-1.22E+00	1.61E-04	Down	7.60E-01	9.16E-03		1.02E-01	8.07E-01		1.62E+00	4.73E-40	Up	2.21E+00	5.58E-93	Up	Unigene54567_All//gi|300137035|gb|EFJ04209.1|//2.00E-16//hypothetical protein SELMODRAFT_139061 [Selaginella moellendorffii]		Unigene54567_All//1.00E-47//TC148521				nr +
Unigene54569_All	529	0.00	0.00	0.00	0.00	0.00	0.00	0.80	3.87	33.06	null	null		null	null		null	null		null	null		2.28E+00	1.12E-06	Up	5.37E+00	6.20E-109	Up	Unigene54569_All//gi|224085109|ref|XP_002335302.1|//3.00E-15//predicted protein [Populus trichocarpa] >gi|222833249|gb|EEE71726.1| predicted protein [Populus trichocarpa]	Unigene54569_All//2.00E-05//AT1G06137| unknown protein					nr -
Unigene54576_All	376	0.00	1.21	0.00	0.00	0.00	0.12	0.00	0.44	4.98	1.02E+01	7.43E-03		null	null		null	null		6.91E+00	6.95E-01		8.80E+00	1.39E-01		1.23E+01	1.95E-13	Up			Unigene54576_All//4.00E-78//CO086896					
Unigene54582_All	377	0.00	53.76	15.96	0.00	0.00	0.00	0.00	0.00	0.00	1.57E+01	1.30E-116	Up	1.40E+01	1.52E-33	Up	null	null		null	null		null	null		null	null		Unigene54582_All//gi|300261322|gb|EFJ45536.1|//3.00E-23//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene54582_All//4.00E-22//AT5G02450| 60S ribosomal protein L36 (RPL36C)			ko03010|Ribosome	GO:0043229//GO:0044444	nr -
Unigene54584_All	334	0.00	0.00	0.00	0.30	0.00	0.00	27.72	28.66	0.24	null	null		null	null		-8.22E+00	3.12E-01		-8.22E+00	3.98E-01		4.78E-02	8.03E-01		-6.86E+00	2.18E-64	Down			Unigene54584_All//1.00E-10//ES794483					
Unigene54587_All	615	0.00	0.82	0.87	0.97	1.57	1.62	0.89	1.63	3.69	9.69E+00	4.04E-03		9.76E+00	4.03E-03		6.90E-01	3.61E-01		7.33E-01	3.21E-01		8.68E-01	1.64E-01		2.05E+00	1.06E-06	Up	Unigene54587_All//gi|42563023|ref|NP_176917.2|//6.00E-66//ATREV3 (ARABIDOPSIS THALIANA RECOVERY PROTEIN 3); DNA binding / DNA-directed DNA polymerase [Arabidopsis thaliana] >gi|34330129|dbj|BAC82450.1| catalytic subunit of polymerase zeta [Arabidopsis thaliana]	Unigene54587_All//3.00E-67//AT1G67500| ATREV3 (ARABIDOPSIS THALIANA RECOVERY PROTEIN 3); DNA binding / DNA-directed DNA polymerase				GO:0003676//GO:0006259//GO:0009411//GO:0034061//GO:0042575//GO:0016914	nr -
Unigene5459_All	692	0.98	2.86	4.31	2.38	3.68	8.62	2.57	1.33	1.84	1.54E+00	1.57E-03		2.13E+00	6.67E-07	Up	6.32E-01	1.16E-01		1.86E+00	3.42E-12	Up	-9.50E-01	3.09E-02		-4.78E-01	2.64E-01		Unigene5459_All//gi|28268678|dbj|BAC56864.1|//2.00E-62//respiratory burst oxidase homolog [Nicotiana benthamiana]	Unigene5459_All//4.00E-25//AT1G64060| ATRBOH F (ARABIDOPSIS THALIANA RESPIRATORY BURST OXIDASE PROTEIN F); NAD(P)H oxidase	Unigene5459_All//3.00E-99//DV848660		ko04626|Plant-pathogen interaction		nr +
Unigene54591_All	1001	0.00	5.52	2.39	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.66E-31	Up	1.12E+01	3.24E-13	Up	null	null		null	null		null	null		null	null		Unigene54591_All//gi|157093371|gb|ABV22340.1|//4.00E-16//calpenin domain-containing protein [Noctiluca scintillans]	Unigene54591_All//8.00E-07//AT2G47500| ATP binding / microtubule motor					nr +
Unigene54593_All	430	0.24	0.00	0.99	2.90	0.56	0.95	0.59	0.58	0.83	-7.93E+00	3.70E-01		2.03E+00	1.39E-01		-2.37E+00	2.03E-04	Down	-1.62E+00	1.08E-02		-1.67E-02	1.02E+00		4.99E-01	6.27E-01		Unigene54593_All//gi|225464505|ref|XP_002272128.1|//5.00E-07//PREDICTED: hypothetical protein [Vitis vinifera] >gi|302143836|emb|CBI22697.3| unnamed protein product [Vitis vinifera]		Unigene54593_All//4.00E-63//BG444853				nr +
Unigene54595_All	732	0.00	0.00	0.00	0.00	0.00	0.00	6.30	8.96	0.05	null	null		null	null		null	null		null	null		5.10E-01	1.35E-02		-6.85E+00	3.84E-32	Down	Unigene54595_All//gi|302128114|dbj|BAJ13478.1|//1.00E-117//actin 1 [Guillardia theta]	Unigene54595_All//3.00E-113//AT3G53750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene54595_All//3.00E-74//TC153744		ko04145|Phagosome		nr +
Unigene54597_All	1358	0.08	0.52	0.00	0.00	0.05	0.33	0.59	1.05	3.23	2.76E+00	9.14E-03		-6.27E+00	3.91E-01		5.66E+00	6.08E-01		8.38E+00	7.75E-03		8.23E-01	1.03E-01		2.45E+00	5.64E-15	Up	Unigene54597_All//gi|39577520|gb|AAR28377.1|//1.00E-40//EIX receptor 1 [Solanum lycopersicum]	Unigene54597_All//2.00E-25//AT2G34930| disease resistance family protein			ko04626|Plant-pathogen interaction		nr -
Unigene546_All	2529	8.40	5.65	5.56	24.92	21.21	20.18	18.16	8.45	11.56	-5.72E-01	1.48E-06		-5.96E-01	1.24E-06		-2.32E-01	2.18E-04		-3.04E-01	2.28E-06		-1.10E+00	4.61E-48	Down	-6.51E-01	1.25E-20		Unigene546_All//gi|13549160|gb|AAK29673.1|AF353096_1//1.00E-155//protein synthesis initiation factor eIF2 alpha [Arabidopsis thaliana]	Unigene546_All//5.00E-13//AT2G40290| eukaryotic translation initiation factor 2 subunit 1, putative / eIF-2A, putative / eIF-2-alpha, putative	Unigene546_All//0.00E+00//gi|78328027|gb|DT548301.1|DT548301		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene54600_All	243	0.00	6.26	1.97	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.10E-08	Up	1.09E+01	7.47E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene54603_All	655	0.00	0.15	0.00	0.00	0.00	0.00	0.19	7.85	12.16	7.27E+00	3.85E-01		null	null		null	null		null	null		5.34E+00	1.22E-31	Up	5.97E+00	6.39E-52	Up	Unigene54603_All//gi|145334337|ref|NP_001078550.1|//2.00E-13//SRT2 (SIRTUIN 2); DNA binding / NAD or NADH binding / NAD-dependent histone deacetylase/ zinc ion binding [Arabidopsis thaliana]	Unigene54603_All//1.00E-14//AT5G09230| SRT2 (SIRTUIN 2); DNA binding / NAD or NADH binding / NAD-dependent histone deacetylase/ zinc ion binding	Unigene54603_All//3.00E-74//gi|78334117|gb|DT554391.1|DT554391			GO:0003676//GO:0006351//GO:0006464//GO:0016458//GO:0016585//GO:0016811//GO:0046914//GO:0051287	nr -

Unigene54604_All	665	0.00	0.00	0.00	0.00	0.00	0.00	4.20	0.44	8.09	null	null		null	null		null	null		null	null		-3.25E+00	1.19E-12	Down	9.47E-01	2.89E-05		Unigene54604_All//gi|62732888|gb|AA95007.1|//4.00E-14//wall-associated protein kinase [Oryza sativa Japonica Group] >gi|77552657|gb|ABA95454.1| Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)]	Unigene54604_All//1.00E-13//AT1G16090| WAKL7 (wall associated kinase-like 7); protein serine/threonine kinase	Unigene54604_All//3.00E-151//TC134682			GO:0016301	nr +
Unigene54605_All	541	0.00	0.37	0.59	0.00	0.06	0.33	2.89	4.87	9.79	8.55E+00	1.36E-01		9.21E+00	4.51E-02		5.99E+00	8.29E-01		8.38E+00	1.94E-01		7.51E-01	3.10E-02		1.76E+00	4.44E-12	Up	Unigene54605_All//gi|8404612|ref|NP_566774.1|//5.00E-06//IDL1 (INFLORESCENCE DEFICIENT IN ABSCISSION (IDA)-LIKE 1) [Arabidopsis thaliana] >gi|12196655|sp|Q29PV4.1|IDL1_ARATH RecName: Full=Protein IDA-LIKE 1; Flags: Precursor >gi|89111826|gb|ABD60685.1| At3g25655 [Arabidopsis thaliana]					GO:0003006	nr -
Unigene54607_All	244	0.00	0.00	0.00	0.00	0.14	0.00	211.92	35.46	164.74	null	null		null	null		7.14E+00	8.29E-01		null	null		-2.58E+00	2.02E-176	Down	-3.63E-01	1.50E-08				Unigene54607_All//3.00E-121//TC158176				
Unigene54608_All	624	0.00	0.00	0.00	0.00	0.00	0.00	4.27	4.49	0.13	null	null		null	null		null	null		null	null		7.22E-02	8.42E-01		-5.06E+00	7.11E-17	Down	Unigene54608_All//gi|297811659|ref|XP_002873713.1|//2.00E-74//40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata] >gi|297319550|gb|EFH49972.1| 40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata]	Unigene54608_All//2.00E-58//AT5G15200| 40S ribosomal protein S9 (RPS9B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr +
Unigene54609_All	245	0.00	3.10	3.26	3.05	1.97	2.21	0.00	0.34	0.00	1.16E+01	1.76E-04	Up	1.17E+01	1.72E-04	Up	-6.32E-01	4.37E-01		-4.63E-01	6.06E-01		8.41E+00	4.00E-01		null	null								
Unigene5461_All	702	36.59	20.50	16.46	46.98	44.00	53.66	27.52	19.17	19.86	-8.36E-01	2.43E-14		-1.15E+00	6.22E-23	Down	-9.44E-02	4.01E-01		1.92E-01	3.87E-02		-5.22E-01	2.93E-06		-4.71E-01	1.60E-05		Unigene5461_All//gi|15230011|ref|NP_187210.1|//2.00E-87//RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome [Arabidopsis thaliana] >gi|21431838|sp|P42791.2|RL182_ARATH RecName: Full=60S ribosomal protein L18-2 >gi|14335090|gb|AAK59824.1| AT3g05590/F18C1_14 [Arabidopsis thaliana] >gi|16974509|gb|AAL31164.1| AT3g05590/F18C1_14 [Arabidopsis thaliana]	Unigene5461_All//1.00E-88//AT3G05590| RPL18 (RIBOSOMAL PROTEIN L18); structural constituent of ribosome	Unigene5461_All//0.00E+00//TC135351		ko03010|Ribosome		nr +
Unigene54611_All	287	2.37	3.88	0.74	0.69	0.48	1.42	1.92	11.07	6.66	7.13E-01	2.69E-01		-1.67E+00	8.70E-02		-5.33E-01	7.48E-01		1.03E+00	4.28E-01		2.53E+00	3.39E-11	Up	1.80E+00	5.34E-05	Up			Unigene54611_All//3.00E-112//TC154772				
Unigene54614_All	346	0.00	0.00	0.00	0.00	0.00	0.00	1.96	1.69	0.00	null	null		null	null		null	null		null	null		-2.09E-01	7.82E-01		-1.09E+01	3.56E-05	Down	Unigene54614_All//gi|12580867|emb|CAC27142.1|//7.00E-10//60S ribosomal protein L13E [Picea abies]				ko03010|Ribosome	GO:0005622	nr +
Unigene54615_All	530	0.00	0.19	0.00	0.66	0.52	0.26	2.79	1.26	0.15	7.58E+00	3.85E-01		null	null		-3.40E-01	7.85E-01		-1.36E+00	3.37E-01		-1.15E+00	2.04E-02		-4.22E+00	1.00E-08	Down	Unigene54615_All//gi|297810269|ref|XP_002873018.1|//6.00E-15//glycoside hydrolase starch-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297318855|gb|EFH49277.1| glycoside hydrolase starch-binding domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene54615_All//3.00E-13//AT5G01260| glycoside hydrolase starch-binding domain-containing protein	Unigene54615_All//0.00E+00//TC153798			GO:0005488//GO:0044238	nr -
Unigene54618_All	623	0.08	0.00	0.00	0.00	0.33	0.00	3.66	1.54	1.41	-6.39E+00	6.10E-01		-6.39E+00	6.22E-01		8.37E+00	1.57E-01		null	null		-1.25E+00	1.20E-03		-1.38E+00	2.67E-04	Down	Unigene54618_All//gi|224064438|ref|XP_002301476.1|//6.00E-87//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222843202|gb|EEES0749.1| multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene54618_All//6.00E-80//AT3G62700| ATMRP10; ATPase, coupled to transmembrane movement of substances			ko02010|ABC transporters	GO:0005773//GO:0006950//GO:0008152//GO:0009987//GO:0015405//GO:0015893//GO:0016628//GO:0017111//GO:0031090//GO:0031224//GO:0032559//GO:0051183//GO:0051707	nr -
Unigene54622_All	407	0.00	0.00	0.00	0.00	0.00	0.00	3.84	3.29	0.00	null	null		null	null		null	null		null	null		-2.26E-01	6.32E-01		-1.19E+01	1.42E-11	Down	Unigene54622_All//gi|2894306|emb|CAA11268.1|//5.00E-64//ubiquitin extension protein [Nicotiana tabacum] >gi|59800131|gb|AAX07419.1| ubiquitin/s27a 40S ribosomal protein [Nicotiana benthamiana]	Unigene54622_All//2.00E-41//AT2G47110| UBQ6; protein binding	Unigene54622_All//4.00E-29//gi|164316317|gb|ES828195.1|ES828195		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene54626_All	896	0.00	0.00	0.00	0.00	0.00	0.00	4.11	4.29	0.09	null	null		null	null		null	null		null	null		6.40E-02	8.37E-01		-5.53E+00	4.78E-24	Down	Unigene54626_All//gi|299473049|emb|CBN77442.1|//5.00E-18//Alkaline phytoceramidase [Ectocarpus siliculosus]	Unigene54626_All//2.00E-17//AT4G22330| ATCES1; catalytic/hydrolase, acting on carbon-nitrogen (but not peptide) bonds, in linear amides			ko00600|Sphingolipid metabolism	GO:0044464	nr +
Unigene54627_All	258	4.46	0.00	2.48	5.02	6.01	2.10	1.47	1.46	0.31	-1.21E+01	9.91E-07	Down	-8.49E-01	2.06E-01		2.59E-01	6.64E-01		-1.26E+00	3.78E-02		-1.66E-02	1.02E+00		-2.26E+00	6.49E-02				Unigene54627_All//2.00E-54//ES804897				
Unigene54628_All	511	2.66	0.20	2.71	1.27	0.47	0.80	0.17	0.00	0.00	-3.75E+00	5.95E-06	Down	2.54E-02	9.84E-01		-1.43E+00	1.05E-01		-6.72E-01	4.78E-01		-7.37E+00	4.02E-01		-7.37E+00	3.57E-01		Unigene54628_All//gi|3501190|gb|AAC34340.1|//6.00E-37//Hypothetical protein [Arabidopsis thaliana]	Unigene54628_All//6.00E-31//AT1G10090| unknown protein	Unigene54628_All//3.00E-12//CO106878			GO:0031410	nr +
Unigene54629_All	856	0.31	0.36	1.24	5.94	4.18	5.80	2.67	0.68	0.98	2.17E-01	8.64E-01		2.03E+00	8.68E-03		-5.05E-01	5.10E-02		-3.25E-02	9.28E-01		-1.96E+00	2.88E-06	Down	-1.45E+00	1.49E-04	Down	Unigene54629_All//gi|297852892|ref|XP_002894327.1|//7.00E-78//ATEX07OG2 [Arabidopsis lyrata subsp. lyrata] >gi|297340169|gb|EFH70586.1| ATEX07OG2 [Arabidopsis lyrata subsp. lyrata]	Unigene54629_All//5.00E-79//AT1G31640| ATEX07OG2 (exocyst subunit EXO70 family protein G2); protein binding				GO:0005488//GO:0043231//GO:0044444//GO:0048278	nr +
Unigene5463_All	1124	7.22	1.49	2.32	5.41	2.94	1.53	1.02	0.22	0.21	-2.28E+00	4.47E-20	Down	-1.64E+00	1.41E-12	Down	-8.78E-01	7.79E-05		-1.82E+00	2.22E-12	Down	-2.19E+00	6.83E-04	Down	-2.26E+00	3.40E-04	Down	Unigene5463_All//gi|115446615|ref|NP_001047087.1|//4.00E-90//Os02g0549200 [Oryza sativa Japonica Group] >gi|113536618|dbj|BAF09001.1| Os02g0549200 [Oryza sativa Japonica Group]	Unigene5463_All//1.00E-81//AT4G02630| protein kinase family protein	Unigene5463_All//3.00E-168//TC145261		ko04626|Plant-pathogen interaction		nr +
Unigene54630_All	488	0.00	0.62	2.95	0.10	0.99	0.09	0.00	0.00	0.00	9.28E+00	4.42E-02		1.15E+01	6.30E-08	Up	3.27E+00	2.68E-02		-1.43E-01	9.52E-01		null	null		null	null		Unigene54630_All//COG2307//9.00E-14//Uncharacterized protein conserved in bacteria						cog -
Unigene54632_All	877	0.00	0.00	0.00	0.00	0.00	0.00	0.43	2.00	4.41	null	null		null	null		null	null		null	null		2.21E+00	1.24E-05	Up	3.34E+00	5.31E-18	Up	Unigene54632_All//gi|297724457|ref|NP_001174592.1|//3.00E-56//Os06g0140000 [Oryza sativa Japonica Group] >gi|255676700|dbj|BAH93320.1| Os06g0140000 [Oryza sativa Japonica Group]	Unigene54632_All//2.00E-40//AT2G34930| disease resistance family protein			ko04626|Plant-pathogen interaction		nr -
Unigene54634_All	506	0.00	6.31	2.84	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	3.64E-18	Up	1.15E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene54634_All//sp|Q5EAE6|DAP1_BOVIN//3.00E-11//Death-associated protein 1 OS=Bos taurus GN=DAP PE=3 SV=3						swissprot -
Unigene54636_All	1055	0.00	0.00	0.00	0.00	0.00	0.00	8.10	1.55	1.66	null	null		null	null		null	null		null	null		-2.39E+00	3.26E-27	Down	-2.28E+00	1.11E-26	Down	Unigene54636_All//gi|255081576|ref|XP_002508010.1|//0.00E+00//alpha tubulin 2 [Micromonas sp. RCC299] >gi|255088289|ref|XP_002506067.1| alpha tubulin 1 [Micromonas sp. RCC299] >gi|226521338|gb|AC067325.1| alpha tubulin 1 [Micromonas sp. RCC299] >gi|226523286|gb|AC069268.1| alpha tubulin 2 [Micromonas sp. RCC299]	Unigene54636_All//4.00E-165//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene54636_All//1.00E-114//TC170591		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene54638_All	490	0.00	0.00	0.00	0.00	0.00	0.00	21.31	24.91	0.00	null	null		null	null		null	null		null	null		2.25E-01	1.50E-01		-1.44E+01	6.30E-77	Down							
Unigene5464_All	724	30.06	8.54	11.11	38.67	28.16	29.88	66.98	14.20	23.22	-1.82E+00	1.81E-39	Down	-1.44E+00	3.05E-27	Down	-4.58E-01	1.14E-06		-3.72E-01	2.20E-04		-2.24E+00	7.35E-140	Down	-1.53E+00	7.27E-86	Down	Unigene5464_All//gi|226491930|ref|NP_001151715.1|//3.00E-29//pale aleurone color1 [Zea mays] >gi|195649267|gb|ACG44101.1| mitochondrial import inner membrane translocase subunit Tim13 [Zea mays]	Unigene5464_All//1.00E-22//AT1G61570| TIM13 (TRANSLOCASE OF THE INNER MITOCHONDRIAL MEMBRANE 13); P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene5464_All//0.00E+00//TC162001				nr +
Unigene54641_All	714	0.00	24.20	10.07	0.00	0.00	0.00	0.00	0.00	0.00	1.46E+01	2.51E-99	Up	1.33E+01	3.57E-40	Up	null	null		null	null		null	null		null	null		Unigene54641_All//gi|224006319|ref|XP_002292120.1|//1.00E-30//probable trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972639|gb|EED90971.1| probable trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]					GO:0003824	nr -
Unigene54643_All	686	0.00	8.20	3.73	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	4.34E-32	Up	1.19E+01	4.20E-14	Up	null	null		null	null		null	null		null	null		Unigene54643_All//gi|71842332|ref|YP_277420.1|//1.00E-19//RNA polymerase alpha subunit [Emiliania huxleyi] >gi|90110842|sp|Q4G347.1|RPOA_EMIHU RecName: Full=DNA-directed RNA polymerase subunit alpha; Short=PEP; AltName: Full=Plastid-encoded RNA polymerase subunit alpha; Short=RNA polymerase subunit alpha >gi|60101575|gb|AAX13919.1| RNA polymerase alpha subunit [Emiliania huxleyi]	Unigene54643_All//1.00E-10//ATCG00740| RNA polymerase alpha subunit			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0016740//GO:0043231//GO:0044260//GO:0090304	nr +
Unigene54644_All	667	0.00	0.00	0.00	0.00	0.00	0.00	9.76	6.14	0.78	null	null		null	null		null	null		null	null		-6.69E-01	1.11E-03		-3.65E+00	8.13E-33	Down			Unigene54644_All//1.00E-67//TC175880				
Unigene54648_All	303	0.00	0.00	0.00	0.00	0.00	0.00	5.58	6.35	1.31	null	null		null	null		null	null		null	null		1.85E-01	6.68E-01		-2.09E+00	2.24E-05	Down							
Unigene54649_All	298	0.00	0.00	0.00	2.84	1.16	0.15	1.56	1.54	0.53	null	null		null	null		-1.30E+00	8.00E-02		-4.23E+00	2.18E-04	Down	-1.66E-02	1.02E+00		-1.55E+00	1.16E-01		Unigene54649_All//gi|297792079|ref|XP_002863924.1|//3.00E-36//phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309759|gb|EFH40183.1| phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene54649_All//9.00E-37//AT5G48800| phototropic-responsive NPH3 family protein	Unigene54649_All//2.00E-73//TC150737			GO:0000904//GO:0005488//GO:0009314//GO:0016020//GO:0060089	nr -
Unigene5465_All	543	0.77	4.11	1.86	0.83	1.65	1.25	1.71	2.39	2.13	2.41E+00	2.46E-06	Up	1.27E+00	8.36E-02		9.98E-01	1.99E-01		5.96E-01	5.26E-01		4.78E-01	3.95E-01		3.13E-01	5.99E-01				Unigene5465_All//2.00E-74//CO087728				
Unigene54654_All	354	0.30	1.72	0.30	0.14	0.78	0.51	0.36	0.83	2.48	2.54E+00	2.46E-02		2.52E-02	9.99E-01		2.47E+00	2.23E-01		1.86E+00	4.58E-01		1.21E+00	3.92E-01		2.79E+00	5.37E-04	Up			Unigene54654_All//1.00E-19//TC158540				
Unigene54655_All	424	0.00	0.12	0.25	1.41	1.87	1.28	3.19	0.59	1.97	6.90E+00	6.15E-01		7.97E+00	3.97E-01		4.06E-01	6.31E-01		-1.41E-01	8.79E-01		-2.43E+00	5.63E-05	Down	-6.94E-01	1.61E-01		Unigene54655_All//gi|116047943|gb|ABJ53197.1|//1.00E-70//myosin XI-2 [Nicotiana benthamiana]	Unigene54655_All//2.00E-61//AT1G04600| XIA (MYOSIN XI A); motor/ protein binding	Unigene54655_All//4.00E-109//TC176117			GO:0008092//GO:0015629//GO:0017111//GO:0032559	nr -
Unigene54657_All	281	0.00	3.07	0.57	0.00	0.49	4.02	3.01	1.04	1.42	1.16E+01	4.94E-05	Up	9.15E+00	2.38E-01		8.94E+00	3.18E-01		1.20E+01	9.83E-07	Up	-1.53E+00	3.21E-02		-1.09E+00	9.98E-02				Unigene54657_All//1.00E-126//TC153936				
Unigene54658_All	398	0.00	0.00	0.00	0.00	0.00	0.00	4.89	8.09	0.00	null	null		null	null		null	null		null	null		7.27E-01	1.88E-02		-1.23E+01	2.41E-14	Down			Unigene54658_All//7.00E-09//EV498805				

Unigene54659_All	284	0.00	0.00	0.00	0.00	0.00	0.00	1.79	5.89	0.00	null	null		null	null		null	null		null	null		1.72E+00	4.01E-04	Up	-1.08E+01	5.54E-04	Down	Unigene54659_All//gi|159486879|ref|XP_001701464.1|//7.00E-21//ribosomal protein S30, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158271646|gb|EDO97461.1| ribosomal protein S30 [Chlamydomonas reinhardtii] >gi|300255282|gb|EFJ39611.1| component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]				ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0031981	nr +
Unigene54666_All	423	30.43	35.22	27.57	8.36	11.15	14.31	12.79	26.28	27.50	2.11E-01	1.73E-01		-1.42E-01	4.21E-01		4.16E-01	1.52E-01		7.75E-01	1.14E-03		1.04E+00	3.76E-11	Up	1.10E+00	4.35E-13	Up	Unigene54666_All//gi|145325445|ref|NP_001077727.1|//9.00E-34//emb|3030| (embryo defective 1303) [Arabidopsis thaliana]		Unigene54666_All//0.00E+00//TC140488		ko04146|Peroxisome		nr +
Unigene54663_All	442	0.24	0.00	0.48	0.00	0.47	0.82	2.58	0.57	2.16	-7.89E+00	3.70E-01		1.03E+00	5.91E-01		8.87E+00	1.57E-01		9.67E+00	2.37E-02		-2.19E+00	6.83E-04	Down	-2.56E-01	6.49E-01									
Unigene54667_All	1745	0.00	0.00	0.03	2.03	1.01	0.13	0.00	0.00	0.07	null	null		4.93E+00	6.34E-01		-1.01E+00	9.76E-04	Down	-3.97E+00	1.85E-16	Down	null	null		6.10E+00	2.43E-01		Unigene54667_All//gi|15219860|ref|NP_176303.1|//6.00E-47//proline-rich family protein [Arabidopsis thaliana]	Unigene54667_All//8.00E-19//AT1G61080| proline-rich family protein			ko03040|Spliceosome		nr -
Unigene54669_All	1340	0.00	0.00	0.00	0.00	0.00	0.00	1.36	9.67	0.03	null	null		null	null		null	null		null	null		2.83E+00	3.03E-49	Up	-5.51E+00	4.49E-12	Down	Unigene54669_All//gi|2388584|gb|AA871465.1|//1.00E-11//EST gb|ATTS1136 comes from this gene [Arabidopsis thaliana]						nr +
Unigene54670_All	362	0.00	9.24	5.74	0.28	0.00	0.00	0.12	0.00	0.00	1.32E+01	4.94E-19	Up	1.25E+01	1.92E-11	Up	-8.10E+00	3.12E-01		-8.10E+00	3.98E-01		-6.87E+00	6.56E-01		-6.87E+00	6.11E-01		Unigene54670_All//gi|224482651|gb|ACN50182.1|//6.00E-08//annexin [Annona cherimola]	Unigene54670_All//7.00E-08//AT1G68090| ANN5; calcium ion binding / calcium-dependent phospholipid binding					nr -
Unigene54673_All	580	0.81	1.66	0.83	3.52	1.54	3.19	35.21	17.08	44.58	1.03E+00	1.45E-01		2.54E-02	1.00E+00		-1.19E+00	5.41E-03		-1.41E-01	7.57E-01		-1.04E+00	5.52E-20	Down	3.40E-01	2.84E-04		Unigene54673_All//gi|224072455|ref|XP_002303740.1|//4.00E-37//GH3 family protein [Populus trichocarpa] >gi|222841172|gb|EEE78719.1| GH3 family protein [Populus trichocarpa]	Unigene54673_All//6.00E-38//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene54673_All//0.00E+00//ES827343			GO:0009725//GO:0016881//GO:0043231//GO:0048878	nr -
Unigene54674_All	306	0.85	0.99	1.04	5.21	0.90	0.89	2.63	3.14	7.81	2.17E-01	8.64E-01		2.88E-01	8.10E-01		-2.53E+00	6.66E-06	Down	-2.56E+00	2.78E-05	Down	2.59E-01	6.78E-01		1.57E+00	3.67E-05	Up			Unigene54674_All//1.00E-108//TC154250				
Unigene54675_All	288	0.00	0.00	0.00	0.00	0.00	0.00	6.90	10.30	0.69	null	null		null	null		null	null		null	null		5.79E-01	7.82E-02		-3.32E+00	1.06E-09	Down								
Unigene54684_All	483	0.00	9.34	4.52	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.08E-25	Up	1.21E+01	4.94E-12	Up	null	null		null	null		null	null		null	null		Unigene54684_All//sp|Q5MY90|RTN1B_XENLA//2.00E-26//Reticulon-1-B OS=Xenopus laevis GN=rtn1-b PE=2 SV=1						swissprot +
Unigene54685_All	464	0.00	0.00	0.00	0.00	0.00	0.00	3.01	4.23	0.17	null	null		null	null		null	null		null	null		4.94E-01	2.45E-01		-4.13E+00	3.70E-08	Down	Unigene54685_All//gi|400404|sp|Q02254.1|NDK1_SPIOL//4.00E-46//RecName: Full=Nucleoside diphosphate kinase 1; AltName: Full=Nucleoside diphosphate kinase I; Short=NDP kinase 1; Short=NDPK 1; Short=NDK 1 >gi|218275|dbj|BAA01510.1| nucleoside diphosphate kinase I [Spinacia oleracea]	Unigene54685_All//4.00E-43//AT4G09320| NDPK1; ATP binding / nucleoside diphosphate kinase			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism	GO:0005576//GO:0006970//GO:0009206//GO:0009209//GO:0009536//GO:0010038//GO:0016020//GO:0016776//GO:0032559//GO:0042579//GO:0043169	nr -
Unigene54688_All	346	0.00	3.81	3.23	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.50E-07	Up	1.17E+01	3.43E-06	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene54469_All	710	14.74	5.64	8.40	12.35	7.57	7.44	11.37	3.71	5.61	-1.39E+00	2.58E-13	Down	-8.11E-01	9.92E-06		-7.07E-01	8.77E-05		-7.31E-01	1.26E-04		-1.62E+00	1.05E-15	Down	-1.02E+00	2.18E-08	Down	Unigene54469_All//gi|115451927|ref|NP_001049564.1|//1.00E-24//Os03g0249900 [Oryza sativa Japonica Group] >gi|113548035|dbj|BAF11478.1| Os03g0249900 [Oryza sativa Japonica Group]	Unigene54469_All//2.00E-12//AT1G19990| unknown protein	Unigene54469_All//0.00E+00//TC154596				nr +
Unigene54692_All	307	18.92	9.08	10.93	40.40	42.06	42.96	30.99	37.03	29.85	-1.06E+00	2.38E-05	Down	-7.92E-01	2.04E-03		5.81E-02	7.97E-01		8.84E-02	6.38E-01		2.57E-01	1.10E-01		-5.41E-02	7.61E-01		Unigene54692_All//gi|77416977|gb|AB881884.1|//1.00E-20//nuclear RNA binding protein-like [Solanum tuberosum]		Unigene54692_All//3.00E-168//TC160575				nr +
Unigene54695_All	2037	0.00	0.00	0.00	0.00	0.00	0.00	13.64	0.04	4.52	null	null		null	null		null	null		null	null		-8.38E+00	1.86E-193	Down	-1.59E+00	1.24E-52	Down	Unigene54695_All//gi|18400335|ref|NP_565554.1|//0.00E+00//sks16 (SKU5 Similar 16); copper ion binding / pectinesterase [Arabidopsis thaliana]	Unigene54695_All//0.00E+00//AT2G23630| sks16 (SKU5 Similar 16); copper ion binding / pectinesterase	Unigene54695_All//1.00E-11//TC151734		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0004091//GO:0005618//GO:0008152//GO:0016682//GO:0046914	nr +
Unigene54696_All	383	3.14	18.26	18.77	1.04	0.18	0.24	72.75	61.00	23.72	2.54E+00	1.64E-19	Up	2.58E+00	9.48E-20	Up	-2.53E+00	5.79E-02		-2.14E+00	1.26E-01		-2.54E-01	7.15E-03		-1.62E+00	6.85E-54	Down	Unigene54696_All//gi|224127388|ref|XP_002329265.1|//5.00E-06//predicted protein [Populus trichocarpa] >gi|222870719|gb|EEF07850.1| predicted protein [Populus trichocarpa]		Unigene54696_All//3.00E-20//FL576427				nr +
Unigene5470_All	720	4.94	1.83	2.81	4.64	2.92	3.26	4.17	3.66	1.83	-1.43E+00	2.88E-05	Down	-8.14E-01	1.70E-02		-6.68E-01	3.98E-02		-5.07E-01	1.47E-01		-1.89E-01	6.19E-01		-1.19E+00	1.84E-04	Down	Unigene5470_All//gi|1370182|emb|CAA98168.1|//7.00E-96//RAB7A [Lotus japonicus]	Unigene5470_All//2.00E-87//AT4G09720| Ras-related GTP-binding protein, putative	Unigene5470_All//0.00E+00//TC131512		ko04145|Phagosome//ko04144|Endocytosis		nr -
Unigene54700_All	429	6.71	13.35	9.19	12.66	12.76	28.32	22.67	40.04	55.35	9.93E-01	8.11E-05		4.54E-01	1.64E-01		1.20E-02	9.71E-01		1.16E+00	1.96E-12	Up	8.21E-01	1.38E-11		1.29E+00	1.13E-32	Up			Unigene54700_All//4.00E-97//TC157367				
Unigene54705_All	294	0.00	0.00	0.00	0.00	0.00	0.00	0.29	2.56	2.57	null	null		null	null		null	null		null	null		3.15E+00	9.54E-04	Up	3.16E+00	6.82E-04	Up								
Unigene54706_All	343	0.00	0.00	0.00	4.36	0.00	0.26	2.34	0.00	0.35	null	null		null	null		-1.21E+01	4.30E-11	Down	-4.05E+00	3.05E-07	Down	-1.12E+01	8.57E-06	Down	-2.75E+00	9.42E-04	Down	Unigene54706_All//gi|224084318|ref|XP_002307257.1|//1.00E-13//predicted protein [Populus trichocarpa] >gi|222856706|gb|EEE94253.1| predicted protein [Populus trichocarpa]	Unigene54706_All//5.00E-08//AT5G66816| unknown protein	Unigene54706_All//3.00E-29//DR460393				nr +
Unigene54709_All	322	6.34	12.75	6.78	1.24	3.42	2.24	0.00	0.00	0.25	1.01E+00	9.19E-04	Up	9.75E-02	8.21E-01		1.47E+00	3.09E-02		8.59E-01	3.42E-01		null	null		7.95E+00	4.03E-01				Unigene54709_All//4.00E-78//gi|31072680|gb|CA992959.1|CA992959				
Unigene5471_All	833	0.38	0.06	1.09	0.72	0.54	0.65	0.96	0.85	0.14	-2.63E+00	1.30E-01		1.53E+00	5.77E-02		-4.17E-01	6.27E-01		-1.41E-01	8.79E-01		-1.77E-01	7.93E-01		-2.75E+00	9.42E-04	Down	Unigene5471_All//gi|1370182|emb|CAA98168.1|//6.00E-90//RAB7A [Lotus japonicus]	Unigene5471_All//3.00E-82//AT4G09720| Ras-related GTP-binding protein, putative	Unigene5471_All//0.00E+00//TC131512		ko04145|Phagosome//ko04144|Endocytosis		nr +
Unigene54710_All	354	2.66	3.44	0.00	2.25	4.09	1.02	0.24	0.35	0.68	3.69E-01	5.56E-01		-1.14E+01	3.34E-05	Down	8.60E-01	1.31E-01		-1.14E+00	1.63E-01		5.68E-01	7.81E-01		1.50E+00	3.39E-01									
Unigene54712_All	571	0.00	0.00	0.00	0.00	0.00	0.00	1.26	1.83	3.70	null	null		null	null		null	null		null	null		5.40E-01	3.95E-01		1.55E+00	1.37E-04	Up			Unigene54712_All//1.00E-14//DN827152				
Unigene54717_All	800	0.00	0.00	0.27	0.25	0.00	0.00	4.12	0.00	1.15	null	null		8.06E+00	1.40E-01		-7.96E+00	8.41E-02		-7.96E+00	1.33E-01		-1.20E+01	2.53E-23	Down	-1.85E+00	2.06E-08	Down	Unigene54717_All//gi|224061202|ref|XP_002300368.1|//2.00E-74//cytochrome P450 [Populus trichocarpa] >gi|222847626|gb|EEE85173.1| cytochrome P450 [Populus trichocarpa]	Unigene54717_All//5.00E-33//AT3G48310| CYP71A22; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene54717_All//6.00E-159//ES824538		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506	nr -
Unigene54718_All	291	4.32	4.35	3.48	5.48	9.47	4.50	0.44	2.73	5.34	1.26E-02	9.80E-01		-3.12E-01	6.41E-01		7.89E-01	3.58E-02		-2.83E-01	6.38E-01		2.65E+00	1.99E-03		3.61E+00	4.47E-08	Up	Unigene54718_All//gi|221327743|gb|ACU17562.1|//4.00E-13//NBS-LRR disease resistance protein family-1 [Oryza brachyantha]	Unigene54718_All//3.00E-06//AT5G46910| disease resistance protein (CC-NBS-LRR class), putative	Unigene54718_All//7.00E-104//TC138390			GO:0005488//GO:0031410	nr -
Unigene5472_All	768	1.57	2.51	3.95	3.11	3.95	5.47	2.75	1.09	3.53	6.78E-01	1.45E-01		1.33E+00	5.32E-04	Up	3.42E-01	3.89E-01		8.13E-01	6.01E-03		-1.34E+00	9.81E-04	Down	3.58E-01	3.04E-01		Unigene5472_All//gi|42567348|ref|NP_195046.3|//2.00E-85//XI-1; motor/ protein binding [Arabidopsis thaliana] >gi|110737839|dbj|BAF00858.1| myosin - like protein [Arabidopsis thaliana]	Unigene5472_All//1.00E-86//AT4G33200| XI-I; motor/ protein binding					nr +
Unigene54720_All	382	0.55	0.27	0.42	0.26	2.61	0.35	0.77	0.66	1.56	-1.05E+00	5.64E-01		-3.90E-01	8.07E-01		3.33E+00	2.50E-04	Up	4.44E-01	8.61E-01		-2.39E-01	8.39E-01		1.01E+00	2.18E-01		Unigene54720_All//gi|116309786|emb|CAB66826.1|//6.00E-09//OSIGBa0148A10.3 [Oryza sativa (indica cultivar-group)]	Unigene54720_All//2.00E-25//AT1G72270| unknown protein					nr -
Unigene54721_All	487	0.00	0.52	0.33	0.20	1.13	1.30	0.87	1.03	3.84	9.02E+00	7.85E-02		8.36E+00	2.38E-01		2.47E+00	4.04E-02		2.67E+00	1.83E-02		2.46E-01	7.83E-01		2.15E+00	5.82E-06	Up	Unigene54721_All//gi|30679594|ref|NP_195851.2|//3.00E-50//PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase [Arabidopsis thaliana]	Unigene54721_All//2.00E-43//AT5G02310| PRT6 (PROTEOLYSIS 6); ubiquitin-protein ligase	Unigene54721_All//3.00E-172//TC171763			GO:0019787//GO:0046914	nr +
Unigene54723_All	277	0.76	0.18	0.00	2.52	0.12	0.98	1.07	1.66	1.29	-2.05E+00	3.33E-01		-9.56E+00	1.45E-01		-4.34E+00	2.80E-04	Down	-1.36E+00	1.31E-01		6.35E-01	5.36E-01		2.77E-01	7.87E-01		Unigene54723_All//gi|124360895|gb|ABN08867.1|//2.00E-21//Heavy metal transport/detoxification protein [Medicago truncatula]	Unigene54723_All//2.00E-10//AT4G05030| heavy-metal-associated domain-containing protein	Unigene54723_All//4.00E-31//gi|84153157|gb|DN802512.1|DN802512			GO:0006812//GO:0043169	nr -
Unigene54724_All	434	2.77	1.40	2.33	5.62	2.38	1.87	0.19	0.00	0.28	-9.85E-01	1.13E-01		-2.50E-01	6.75E-01		-1.24E+00	1.26E-03		-1.59E+00	1.66E-04	Down	-7.61E+00	4.02E-01		5.00E-01	8.07E-01		Unigene54724_All//gi|224116026|ref|XP_002317188.1|//4.00E-10//predicted protein [Populus trichocarpa] >gi|222860253|gb|EEE97800.1| predicted protein [Populus trichocarpa]						nr -
Unigene5473_All	570	13.59	41.16	7.57	8.22	20.78	23.85	7.71	16.35	7.76	1.60E+00	2.10E-35	Up	-8.44E-01	1.07E-04		1.34E+00	3.02E-16	Up	1.54E+00	6.12E-21	Up	1.08E+00	4.24E-10	Up	8.10E-03	9.72E-01				Unigene5473_All//2.00E-142//DW509842				
Unigene54732_All	258	0.00	3.73	1.86	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	1.09E+01	7.47E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene54735_All	690	0.00	0.15	1.23	1.59	8.98	1.31	0.00	0.00	0.00	7.20E+00	3.85E-01		1.03E+01	9.02E-05	Up	2.50E+00	2.18E-19	Up	-2.79E-01	6.89E-01		null	null		null	null		Unigene54735_All//gi|15227472|ref|NP_181725.1|//2.00E-11//ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|14517524|gb|AAK62652.1| At2g41940/T6D20.16 [Arabidopsis thaliana] >gi|15810111|gb|AAL06981.1| At2g41940/T6D20.16 [Arabidopsis thaliana]	Unigene54735_All//9.00E-13//AT2G41940| ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding		C2H2		GO:0001071//GO:0010468//GO:0035315//GO:0046914	nr -
Unigene54737_All	290	0.00	0.00	0.00	0.00	0.36	0.00	106.72	41.51	78.85	null	null		null	null		8.48E+00	4.55E-01		null	null		-1.36E+00	3.80E-45	Down	-4.37E-01	2.39E-07		Unigene54737_All//gi|225464057|ref|XP_002268269.1|//5.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene54737_All//2.00E-57//DT462481		ko00902|Monoterpenoid biosynthesis		nr +
Unigene54739_All	474	0.00	0.00	0.00	0.00	0.00	0.00	3.21	4.50	0.67	null	null		null	null		null	null		null	null		4.86E-01	2.37E-01		-2.26E+00	2.48E-05	Down			Unigene54739_All//1.00E-17//TC154054				
Unigene5474_All	738	21.55	30.69	38.31	1.15	3.31	1.35	0.06	0.00	0.11	5.10E-01	8.88E-06		8.30E-01	6.82E-15		1.53E+00	2.04E-04	Up	2.31E-01	7.41E-01		-5.84E+00	6.56E-01		9.14E-01	7.49E-01		Unigene5474_All//gi|1370182|emb|CAA98168.1|//5.00E-97//RAB7A [Lotus japonicus]	Unigene5474_All//8.00E-92//AT4G09720| Ras-related GTP-binding protein, putative	Unigene5474_All//0.00E+00//TC151003		ko04145|Phagosome//ko04144|Endocytosis		nr -
Unigene54740_All	635	0.33	2.63	1.01	2.20	2.82	0.92	0.13	0.33	0.38	3.00E+00	5.39E-06	Up	1.61E+00	1.11E-01		3.60E-01	5.21E-01		-1.25E+00	3.03E-02		1.30E+00	4.47E-01		1.50E+00	3.39E-01		Unigene54740_All//gi|16323095|gb|AAL15282.1|//3.00E-10//AT4g39900/T5J17_70 [Arabidopsis thaliana]	Unigene54740_All//2.00E-11//AT4G39900| unknown protein	Unigene54740_All//2.00E-143//TC173168				nr +
Unigene54742_All	608	0.00	10.08	2.19	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	5.26E-35	Up	1.11E+01	2.40E-07	Up	null	null		null	null		null	null		null	null		Unigene54742_All//sp|Q6LG06|LYS_CRAGI//2.00E-09//Lysozyme OS=Crassostrea gigas GN=lysoz PE=2 SV=1						swissprot +
Unigene54745_All	278	0.00	0.00	0.00	0.72	0.74	0.00	0.15	5.11	0.00	null	null		null	null		5.22E-02	9.88E-01		-9.49E+00	1.33E-01		5.07E+00	8.39E-09	Up	-7.25E+00	6.11E-01		Unigene54745_All//gi|229893769|gb|ACQ90242.1|//1.00E-22//cinnamyl alcohol dehydrogenase [Glycine max]	Unigene54745_All//2.00E-18//AT4G37980| ELI3-1 (ELICITOR-ACTIVATED GENE 3-1); binding / catalytic/ oxidoreductase/ zinc ion binding	Unigene54745_All//4.00E-16//TC179502		ko00940|Phenylpropanoid biosynthesis	GO:0008152//GO:0016616//GO:0046914	nr -

Unigene54746_All	487	0.00	0.00	0.00	2.05	0.42	0.19	3.91	0.17	0.00	null	null		null	null		-2.27E+00	1.67E-03		-3.46E+00	1.73E-04	Down	-4.51E+00	4.75E-11	Down	-1.19E+01	4.91E-14	Down	Unigene54746_All//gi|42571797|ref|NP_973989.1|//4.00E-07//Expressed protein [Arabidopsis thaliana] >gi|27808504|gb|AAO24532.1|Atlg48325 [Arabidopsis thaliana]	Unigene54746_All//7.00E-12//AT5G26620| unknown protein					nr -
Unigene54757_All	547	0.67	0.19	3.31	0.00	0.25	0.41	0.08	0.15	0.00	-1.85E+00	1.87E-01		2.31E+00	8.14E-05	Up	7.98E+00	3.18E-01		8.69E+00	1.18E-01		9.83E-01	7.31E-01		-6.27E+00	6.11E-01								ESTscan -
Unigene54758_All	505	0.00	1.00	0.00	0.59	3.55	1.97	0.00	0.00	0.00	9.97E+00	4.04E-03		null	null		2.58E+00	5.30E-06	Up	1.73E+00	2.14E-02		null	null		null	null		Unigene54758_All//gi|157273640|gb|ABV27474.1|//1.00E-51//fasciclin-like arabinogalactan protein 3 [Gossypium hirsutum]	Unigene54758_All//2.00E-33//AT2G04840| FLAT (FASCICLIN-LIKE ARABINOOGALACTAN 7)	Unigene54758_All//0.00E+00//TC174345			GO:0031225	nr +
Unigene54760_All	243	0.00	0.00	0.00	0.00	0.00	0.00	2.44	1.55	0.00	null	null		null	null		null	null		null	null		-6.54E-01	4.45E-01		-1.13E+01	1.41E-04	Down	Unigene54760_All//gi|159471131|ref|XP_001693710.1|//5.00E-11//ribosomal protein S3a, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|269969596|sp|A8HS48.1|RS3A_CHLRE RecName: Full=40S ribosomal protein S3a >gi|158283213|gb|EDP08964.1|ribosomal protein S3a [Chlamydomonas reinhardtii]	Unigene54760_All//1.00E-11//AT3G04840| 40S ribosomal protein S3A (RPS3aA)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030012//GO:0031981	nr -
Unigene54762_All	269	0.00	3.20	5.34	0.00	0.00	0.17	0.00	0.00	0.00	1.16E+01	4.94E-05	Up	1.24E+01	6.29E-08	Up	null	null		7.39E+00	6.95E-01		null	null		null	null		Unigene54762_All//sp|P31000|VIME_RAT//7.00E-44//Vimentin OS=Rattus norvegicus GN=Vim PE=1 SV=2						swissprot -
Unigene54769_All	624	0.00	0.00	0.00	0.00	0.00	0.00	3.18	5.22	0.00	null	null		null	null		null	null		null	null		7.14E-01	2.00E-02		-1.16E+01	1.18E-14	Down							ESTscan -
Unigene54770_All	305	2.92	0.00	0.35	2.78	1.81	1.18	2.50	0.00	0.13	-1.15E+01	2.86E-05	Down	-3.06E+00	2.25E-03		-6.20E-01	4.13E-01		-1.23E+00	1.20E-01		-1.13E+01	1.67E-05	Down	-4.26E+00	8.65E-05	Down	Unigene54770_All//gi|115468478|ref|NP_001057838.1|//5.00E-08//Os06g0551500 (Oryza sativa Japonica Group) >gi|113595878|dbj|BAF19752.1|Os06g0551500 (Oryza sativa Japonica Group)						GO:0043231	nr -
Unigene54774_All	931	0.00	1.52	0.11	0.32	0.18	0.34	0.23	0.40	3.12	1.06E+01	4.06E-08	Up	6.84E+00	3.97E-01		-7.96E-01	5.57E-01		8.13E-02	9.50E-01		8.31E-01	4.67E-01		3.78E+00	4.35E-15	Up	Unigene54774_All//gi|115477334|ref|NP_001062263.1|//3.00E-52//Os08g0519900 (Oryza sativa Japonica Group) >gi|113624232|dbj|BAF24177.1|Os08g0519900 (Oryza sativa Japonica Group)	Unigene54774_All//3.00E-35//AT4G31540| ATEXO70G1 (exocyst subunit EXO70 family protein G1); protein binding					GO:0044424	nr +
Unigene54775_All	371	0.00	0.00	0.00	0.00	0.00	0.00	2.39	0.00	2.36	null	null		null	null		null	null		null	null		-1.12E+01	2.24E-06	Down	-1.87E-02	9.66E-01		Unigene54775_All//gi|255583421|ref|XP_002532470.1|//5.00E-23//DNA binding protein, putative [Ricinus communis] >gi|223527828|gb|EEF29926.1| DNA binding protein, putative [Ricinus communis]	Unigene54775_All//1.00E-04//AT1G66470| basic helix-loop-helix (bHLH) family protein		bHLH			nr -
Unigene54777_All	366	14.72	202.12	447.97	0.68	0.47	2.59	2.66	0.46	9.91	3.78E+00	3.44E-296	Up	4.93E+00	0.00E+00	Up	-5.33E-01	7.12E-01		1.93E+00	1.48E-02		-2.54E+00	6.41E-04	Down	1.90E+00	2.37E-09	Up	Unigene54777_All//gi|416662|sp|P32765.1|ASP_THECC//1.00E-32//RecName: Full=21 kDa seed protein; Flags: Precursor >gi|99954|pir|S16252 trypsin inhibitor homolog - soybean >gi|21909|emb|CAA39860.1| 21 kDa seed protein [Theobroma cacao]	Unigene54777_All//1.00E-14//AT1G17860| trypsin and protease inhibitor family protein / Kunitz family protein	Unigene54777_All//0.00E+00//gi|164290031|gb|EV497238.1|EV497238			GO:0061135	nr -
Unigene54784_All	270	0.00	5.25	5.72	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.06E-08	Up	1.25E+01	1.65E-08	Up	null	null		null	null		null	null		null	null			Unigene54784_All//9.00E-05//AT5G56330| ACA8 (ALPHA CARBONIC ANHYDRASE 8); carbonate dehydratase/ zinc ion binding						ESTscan -
Unigene54786_All	379	0.14	1.20	2.25	0.00	0.27	0.00	0.00	0.00	0.00	3.12E+00	3.58E-02		4.03E+00	7.02E-04	Up	8.09E+00	4.55E-01		null	null		null	null		null	null		Unigene54786_All//sp|Q8BT18|SRRM2_MOUSE//9.00E-07//Serine/arginine repetitive matrix protein 2 OS=Mus musculus GN=Srrm2 PE=1 SV=2						swissprot -
Unigene54788_All	469	0.00	0.00	0.00	0.00	2.42	0.77	0.00	0.00	0.00	null	null		null	null		1.12E+01	5.31E-07	Up	9.59E+00	2.37E-02		null	null		null	null				Unigene54788_All//2.00E-12//gi|21103292|gb|BQ415605.1|BQ415605				
Unigene54791_All	542	0.00	0.00	0.00	0.00	0.00	0.00	2.42	2.54	0.00	null	null		null	null		null	null		null	null		7.36E-02	8.96E-01		-1.12E+01	9.85E-10	Down	Unigene54791_All//gi|301122321|ref|XP_002908887.1|//2.00E-28//40S ribosomal protein S10 [Phytophthora infestans T30-4] >gi|66270167|gb|AAY43413.1|ribosomal protein S10 [Phytophthora infestans] >gi|262099649|gb|EEY57701.1| 40S ribosomal protein S10 [Phytophthora infestans T30-4]	Unigene54791_All//7.00E-19//AT4G25740| 40S ribosomal protein S10 (RPS10A)			ko03010|Ribosome	GO:0015935//GO:0030312	nr +
Unigene54794_All	685	0.00	5.18	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.46E-20	Up	1.07E+01	3.43E-06	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene54798_All	367	0.00	1.79	0.15	0.27	0.19	0.74	0.23	0.00	2.28	1.08E+01	6.25E-04	Up	7.18E+00	6.34E-01		-5.33E-01	8.15E-01		1.44E+00	4.09E-01		-7.85E+00	4.02E-01		3.31E+00	2.30E-04	Up			Unigene54798_All//4.00E-07//EX168667				ESTscan -
Unigene548_All	1476	16.31	24.61	18.65	15.25	17.15	14.26	17.85	30.04	35.95	5.94E-01	2.75E-11		1.94E-01	9.14E-02		1.69E-01	1.57E-01		-9.74E-02	4.88E-01		7.52E-01	1.13E-24		1.01E+00	4.38E-49	Up	Unigene548_All//gi|6692098|gb|AAF24563.1|AC007764_5//1.00E-113//F22C12.10 [Arabidopsis thaliana]	Unigene548_All//2.00E-72//AT1G64140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: sperm cell, male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; BEST Arabidopsis thaliana protein match is: loricrin-related (TAIR:AT5G64550.1); Has 2298 Blast hits to 1429 proteins in 121 species: Archae - 0; Bacteria - 42; Metazoa - 1626; Fungi - 29; Plants - 243; Viruses - 9; Other Eukaryotes - 349 (source: NCBI BLink).	Unigene548_All//0.00E+00//gi|78354535|gb|DT574809.1|DT574809					nr +
Unigene54800_All	308	0.34	2.96	0.00	2.59	1.90	0.15	1.51	0.00	0.00	3.12E+00	1.14E-03		-8.41E+00	3.91E-01		-4.45E-01	5.73E-01		-4.14E+00	4.12E-04	Down	-1.06E+01	1.71E-03		-1.06E+01	1.09E-03								
Unigene54805_All	1098	0.24	20.95	0.97	0.54	0.66	0.62	0.81	0.46	0.00	6.46E+00	8.67E-123	Up	2.03E+00	8.68E-03		2.75E-01	8.00E-01		1.81E-01	8.44E-01		-8.24E-01	2.24E-01		-9.66E+00	1.10E-06	Down	Unigene54805_All//gi|126078|sp|P09444.1|LEA34_GOSHI//7.00E-70//RecName: Full=Late embryogenesis abundant protein D-34; Short=LEA D-34 >gi|18501|emb|CAA31594.1| D-34 Lea protein [Gossypium hirsutum] >gi|167385|gb|AAA33075.1| storage protein [Gossypium hirsutum] >gi|226556|prf||1601521F Lea D-34 gene	Unigene54805_All//1.00E-50//AT3G22490| late embryogenesis abundant protein, putative / LEA protein, putative					GO:0003006	nr -
Unigene54813_All	943	0.00	0.11	0.00	0.00	0.47	0.00	3.50	19.72	79.72	6.75E+00	3.85E-01		null	null		8.89E+00	8.00E-03		null	null		2.50E+00	2.67E-61	Up	4.51E+00	0.00E+00	Up	Unigene54813_All//gi|297801996|ref|XP_002868882.1|//1.00E-52//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314718|gb|EFH45141.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene54813_All//8.00E-52//AT4G38070| zinc finger (B-box type) family protein		DBB	ko04712|Circadian rhythm - plant	GO:0001071//GO:0009743//GO:0010468//GO:0044464//GO:0046914	nr -
Unigene54821_All	423	1.36	0.60	0.88	1.18	2.28	0.53	1.80	0.20	0.57	-1.18E+00	2.26E-01		-6.27E-01	5.27E-01		9.53E-01	1.98E-01		-1.14E+00	3.07E-01		-3.19E+00	7.92E-04	Down	-1.67E+00	2.39E-02		Unigene54821_All//gi|152271144|ref|NP_179798.1|//4.00E-12//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75206010|sp|Q9SHZ8.1|PP168_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g22070	Unigene54821_All//3.00E-13//AT2G22070| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene54824_All	392	0.13	0.00	0.00	0.25	0.00	0.12	1.19	2.77	5.89	-7.06E+00	6.10E-01		-7.06E+00	6.22E-01		-7.99E+00	3.12E-01		-1.14E+00	6.76E-01		1.22E+00	4.08E-02		2.31E+00	8.95E-08	Up							
Unigene54825_All	362	0.14	0.00	0.00	0.96	0.29	1.12	4.32	1.04	0.88	-7.17E+00	6.10E-01		-7.17E+00	6.22E-01		-1.76E+00	1.90E-01		2.21E-01	8.63E-01		-2.06E+00	9.44E-05	Down	-2.30E+00	1.48E-05	Down			Unigene54825_All//5.00E-13//DW238344				
Unigene54826_All	270	0.00	2.63	0.00	0.92	1.91	2.68	2.04	1.39	3.10	1.14E+01	3.32E-04	Up	null	null		1.05E+00	3.49E-01		1.54E+00	9.17E-02		-5.47E-01	5.52E-01		6.06E-01	3.65E-01		Unigene54826_All//gi|7444442|pir||T02087//2.00E-17//gag/pol polyprotein - maize retrotransposon Hopscotch >gi|531389|gb|AAA57005.1| copia-like retrotransposon Hopscotch polyprotein [Zea mays]		Unigene54826_All//5.00E-40//TC175019			GO:0005488	nr +
Unigene54827_All	273	0.77	7.98	1.37	0.55	1.39	3.81	4.34	3.06	4.09	3.38E+00	2.02E-08	Up	8.33E-01	5.16E-01		1.34E+00	3.40E-01		2.80E+00	8.12E-04	Up	-5.02E-01	3.95E-01		-8.58E-02	8.78E-01		Unigene54827_All//gi|224124668|ref|XP_002319389.1|//3.00E-07//predicted protein [Populus trichocarpa] >gi|222857765|gb|EEE95312.1|predicted protein [Populus trichocarpa]						nr -
Unigene54829_All	212	0.00	0.24	0.25	0.94	6.33	3.62	0.20	0.00	0.00	7.90E+00	6.15E-01		7.97E+00	6.34E-01		2.75E+00	7.11E-05	Up	1.95E+00	3.23E-02		-7.64E+00	6.56E-01		-7.64E+00	6.11E-01		Unigene54829_All//gi|115435338|ref|NP_001042427.1|//8.00E-16//Os01g0220500 (Oryza sativa Japonica Group) >gi|113531958|dbj|BAF04341.1|Os01g0220500 (Oryza sativa Japonica Group)	Unigene54829_All//4.00E-06//AT2G19170| SLP3; serine-type peptidase	Unigene54829_All//8.00E-72//TC164474			GO:0004175//GO:0005515//GO:0044092	nr -
Unigene5483_All	899	1.05	1.18	1.48	1.94	1.92	2.26	3.20	0.98	1.82	1.76E-01	7.74E-01		4.99E-01	3.93E-01		-1.81E-02	9.58E-01		2.21E-01	6.61E-01		-1.71E+00	1.59E-06	Down	-8.16E-01	1.02E-02				Unigene5483_All//2.00E-168//DW516418				
Unigene54834_All	355	0.00	0.29	0.00	0.70	0.00	0.00	0.24	2.59	4.94	8.16E+00	3.85E-01		null	null		-9.45E+00	4.18E-02		-9.45E+00	7.32E-02		3.44E+00	9.84E-05	Up	4.37E+00	3.23E-10	Up			Unigene54834_All//4.00E-07//TC174544				
Unigene54837_All	292	0.00	3.47	1.82	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.25E-06	Up	1.08E+01	4.03E-03		null	null		null	null		null	null		null	null								
Unigene54838_All	813	0.00	4.43	1.11	0.00	0.00	0.00	0.00	0.00	0.10	1.21E+01	1.77E-20	Up	1.01E+01	4.71E-05	Up	null	null		null	null		null	null		6.61E+00	4.03E-01		Unigene54838_All//gi|116311040|emb|CAH67971.1|//1.00E-09//OSIGBa0142I02-OSIGBa0101E20.14 [Oryza sativa (indica cultivar-group)]	Unigene54838_All//3.00E-05//AT2G32240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to cadmium ion; LOCATED IN: plasma membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Prefoldin (InterPro:IPR009053); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G05320.3); Has 221693 Blast hits to 95553 proteins in 2574 species: Archae - 2848; Bacteria - 44259; Metazoa - 97474; Fungi - 154490; Plants - 8386; Viruses - 1229; Other Eukaryotes - 52007 (source: NCBI BLink).					GO:0044464	nr +

Unigene54484_All	751	5.64	4.52	6.52	8.49	8.53	10.34	7.54	8.40	15.86	-3.20E-01	2.99E-01		2.09E-01	4.86E-01		6.50E-03	9.88E-01		2.85E-01	2.16E-01		1.56E-01	5.31E-01		1.07E+00	8.39E-13	Up	Unigene5484_All//gi|89000907|gb|AB D59043.1|//2.00E-42//At2g39650 [Arabidopsis thaliana]	Unigene5484_All//4.00E- 31//AT2G39650| unknown protein	Unigene5484_All//0.00E+00//TC167839				nr +
Unigene54843_All	369	0.00	1.65	0.14	0.00	0.19	0.00	2.52	0.00	0.22	1.07E+01	1.17E-03		7.17E+00	6.34E-01		7.54E+00	6.08E-01		null	null		-1.13E+01	1.14E-06	Down	-3.55E+00	3.97E-05	Down	Unigene54843_All//gi|290579513|gb| ADD51352.1|//1.00E-45//TT2 like MYB transcriptoin factor [Theobroma cacao]	Unigene54843_All//1.00E- 40//AT2G16720| MYB7 (MYB DOMAIN PROTEIN 7); DNA binding / transcription factor	Unigene54843_All//0.00E+00//TC169425	MYB		GO:0001071//GO:0003676//GO:0006351 //GO:0006970//GO:0010033//GO:00104 68//GO:0043231	nr +
Unigene54847_All	508	0.21	0.00	0.00	0.00	0.00	0.00	3.83	7.08	1.33	-7.69E+00	3.70E-01		-7.69E+00	3.91E-01		null	null		null	null		8.86E-01	2.24E-03		-1.52E+00	3.06E-04	Down	Unigene54847_All//gi|115479709|ref |NP_001063448.1|//4.00E- 18//Os09g0472900 [Oryza sativa Japonica Group] >gi|113631681|dbj|BAF25362.1| Os09g0472900 [Oryza sativa Japonica Group]	Unigene54847_All//3.00E- 11//AT2G18660| EXLB3 (EXPANSIN- LIKE B3 PRECURSOR)	Unigene54847_All//3.00E- 15//gi|109887102|gb|DW516071.1|DW516071				nr -
Unigene54848_All	376	0.00	0.00	0.00	0.00	0.00	1.35	2.89	0.00	null	null		null	null		null	null		null	null		1.10E+00	6.53E-02		-1.04E+01	5.54E-04	Down	Unigene54848_All//gi|224002825|ref |XP_002291084.1|//1.00E-44//dtdp- glucose 4,6-dehydratase [Thalassiosira pseudonanna CCMP1335] >gi|220972860|gb|EED91191.1| dtdp- glucose 4,6-dehydratase [Thalassiosira pseudonanna CCMP1335]	Unigene54848_All//1.00E- 44//AT3G14790| RHM3 (RHAMNOSE BIOSYNTHESIS 3); UDP-L-rhamnose synthase/ catalytic			ko00520|Amino sugar and nucleotide sugar metabolism//ko00523|Polyketide sugar unit biosynthesis	GO:0000267//GO:0003006//GO:0009226 //GO:0010191//GO:0016616//GO:0016168 36//GO:0016857//GO:0034637//GO:004 8037	nr -
Unigene5485_All	699	5.69	4.78	6.93	12.33	14.29	17.25	14.70	25.59	43.03	-2.50E-01	4.27E-01		2.85E-01	3.51E-01		2.13E-01	3.03E-01		4.85E-01	2.80E-03		8.00E-01	1.51E-11		1.55E+00	4.15E-54	Up	Unigene5485_All//gi|9858780|gb|AAG 01127.1|AF273333_12//1.00E- 24//BAC19.12 [Solanum lycopersicum]	Unigene5485_All//1.00E- 07//AT3G50700| AtIDD2 (Arabidopsis thaliana Indeterminate(ID)-Domain 2); nucleic acid binding / transcription factor/ zinc ion binding	Unigene5485_All//0.00E+00//TC167603	C2H2			nr -
Unigene54851_All	291	2.16	0.00	0.55	1.37	2.13	1.71	0.00	0.00	0.41	-1.11E+01	7.91E-04	Down	-1.97E+00	6.50E-02		6.37E-01	5.49E-01		3.18E-01	7.57E-01		null	null		8.68E+00	2.43E-01		Unigene54851_All//gi|224061845|ref |XP_002300627.1|//1.00E-47//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842353|gb|EEE79900.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene54851_All//2.00E- 37//AT1G76420| CUC3 (CUP SHAPED COTYLEDON3); transcription factor	Unigene54851_All//5.00E- 40//gi|78348936|gb|DT569210.1|DT569210	NAC		GO:0001071//GO:0003676//GO:0009933 //GO:0010160//GO:0010468	nr +
Unigene54858_All	490	3.31	0.72	0.87	0.71	0.70	1.66	1.12	0.26	0.24	-2.19E+00	2.05E-04	Down	-1.93E+00	1.19E-03		-1.80E-02	9.58E-01		1.22E+00	1.40E-01		-2.13E+00	3.31E-02		-2.20E+00	2.24E-02		Unigene54858_All//gi|209970603|gb| ACJ03064.1|//1.00E-40//AM19-5p [Malus floribunda]	Unigene54858_All//3.00E- 27//AT2G34930| disease resistance family protein				GO:0003824	nr +
Unigene5486_All	1801	0.00	0.00	0.00	1.08	0.67	0.80	1.22	1.14	6.28	null	null		null	null		-6.89E-01	1.29E-01		-4.27E-01	4.05E-01		-1.02E-01	7.99E-01		2.36E+00	5.41E-36	Up	Unigene5486_All//gi|59668642|emb|C AI53675.1|//1.00E-180//pyruvate kinase [Glycine max]	Unigene5486_All//1.00E- 173//AT4G26390| pyruvate kinase, putative	Unigene5486_All//1.00E-54//TC174139		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene54860_All	245	0.21	72.59	65.42	0.41	0.00	0.55	0.35	0.00	0.00	8.41E+00	5.04E-100	Up	8.26E+00	3.15E-88	Up	-8.67E+00	3.12E-01		4.44E-01	8.61E-01		-8.43E+00	4.02E-01		-8.43E+00	3.57E-01		Unigene54860_All//gi|11465624|ref| NP_049295.1|//2.00E- 13//apocytochrome b [Porphyra purpurea] >gi|4106931|gb|AAD03098.1| apocytochrome b [Porphyra purpurea]				ko00190|Oxidative phosphorylation	GO:0016020//GO:0055114	nr -
Unigene54865_All	474	2.43	0.21	2.25	1.26	1.24	1.91	0.00	0.00	0.17	-3.51E+00	6.57E-05	Down	-1.12E-01	8.56E-01		-3.02E-02	9.50E-01		5.96E-01	4.55E-01		null	null		7.39E+00	4.03E-01		Unigene54865_All//gi|15230734|ref| NP_187304.1|//5.00E-29//agenet domain-containing protein [Arabidopsis thaliana]	Unigene54865_All//3.00E- 30//AT3G06520| agenet domain- containing protein	Unigene54865_All//3.00E-70//DT048140				nr +
Unigene54866_All	254	0.00	6.58	1.05	0.00	0.81	0.00	0.00	0.00	0.00	1.27E+01	1.54E-09	Up	1.00E+01	8.00E-02		9.67E+00	1.57E-01		null	null		null	null		null	null					Unigene54866_All//7.00E-08//TC175494					
Unigene54869_All	327	0.96	0.16	2.61	1.83	0.84	0.00	2.97	0.26	0.24	-2.63E+00	1.30E-01		1.44E+00	8.22E-02		-1.12E+00	2.26E-01		-1.08E+01	7.70E-04	Down	-3.54E+00	4.32E-05	Down	-3.61E+00	2.14E-05	Down	Unigene54869_All//gi|18398942|ref| NP_566378.1|//2.00E-09//glycosyl transferase family 1 protein [Arabidopsis thaliana]	Unigene54869_All//8.00E- 11//AT3G10630| glycosyl transferase family 1 protein	Unigene54869_All//2.00E-156//ES809782				nr +
Unigene54870_All	531	6.50	0.38	1.81	0.09	0.13	0.00	0.00	0.16	0.00	-4.09E+00	3.35E-15	Down	-1.85E+00	1.21E-06	Down	4.68E-01	9.57E-01		-6.55E+00	6.34E-01		7.30E+00	4.00E-01		null	null		Unigene54870_All//gi|115473321|ref |NP_001060259.1|//7.00E- 08//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]					GO:0031410//GO:0043231	nr +
Unigene54878_All	269	1.17	1.51	1.78	8.52	5.38	5.54	15.25	3.42	3.11	3.69E-01	7.23E-01		6.10E-01	5.86E-01		-6.64E-01	1.05E-01		-6.21E-01	1.51E-01		-2.16E+00	6.00E-12	Down	-2.29E+00	2.79E-13	Down				Unigene54878_All//5.00E-49//TC163374					
Unigene5488_All	670	0.31	2.50	0.16	1.12	1.80	1.35	2.15	4.49	1.49	3.00E+00	5.39E-06	Up	-9.74E-01	6.20E-01		6.90E-01	2.98E-01		2.74E-01	7.10E-01		1.07E+00	1.01E-03		-5.30E-01	2.73E-01		Unigene5488_All//gi|145336732|ref| NP_564632.2|//5.00E-08//RSH3 (RELA/SPOT HOMOLOG 3); GTP diphosphokinase [Arabidopsis thaliana] >gi|4587556|gb|AAD25787.1|AC006577 _23 Similar to gi|1653162 (p)ppGpp 3-pyrophosphohydrolase from Synechocystis sp genome gb|D90911. EST gb|W43807 comes from this gene [Arabidopsis thaliana] >gi|110742595|dbj|BAE99211.1| RSH3 [Arabidopsis thaliana]	Unigene5488_All//3.00E- 09//AT3G14050| RSH2 (RELA-SPOT HOMOLOG 2); GTP diphosphokinase	Unigene5488_All//3.00E-25//TC151760				nr -
Unigene54882_All	282	0.00	5.57	5.48	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.70E-09	Up	1.24E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene54882_All//gi|170388|gb|AAA 34140.1|//9.00E-39//chlorophyll a/b-binding protein [Solanum lycopersicum] >gi|2328895|prf||1402358A photosystem I protein CAB	Unigene54882_All//3.00E- 39//AT3G54890| LHCA1; chlorophyll binding	Unigene54882_All//3.00E-47//TC161874		ko00196|Photosynthesis - antenna proteins	GO:0006464//GO:0009521//GO:0009526 //GO:0009534//GO:0009570//GO:00096 39//GO:0009765//GO:0031224//GO:004 3169//GO:0046906	nr -
Unigene54884_All	623	0.92	1.38	1.03	0.96	0.94	0.22	2.92	0.47	1.60	5.82E-01	4.27E-01		1.51E-01	8.55E-01		-3.02E-02	9.50E-01		-2.14E+00	4.39E-02		-2.64E+00	5.50E-07	Down	-8.68E-01	3.62E-02										
Unigene54890_All	358	0.00	0.14	0.30	0.83	0.38	1.14	0.71	0.82	6.90	7.14E+00	6.15E-01		8.22E+00	3.97E-01		-1.12E+00	4.24E-01		4.44E-01	7.01E-01		2.06E-01	8.68E-01		3.28E+00	1.46E-11	Up				Unigene54890_All//3.00E- 79//gi|109887102|gb|DW516071.1|DW516071				
Unigene54892_All	411	0.00	0.00	0.00	0.00	0.00	0.00	3.09	2.14	0.39	null	null		null	null		null	null		null	null		-5.31E-01	3.43E-01		-2.99E+00	6.36E-06	Down									ESTscan +
Unigene54893_All	354	0.00	0.43	0.00	0.99	1.65	0.77	0.48	0.24	2.70	8.75E+00	2.35E-01		null	null		7.48E-01	4.81E-01		-3.64E-01	7.55E-01		-1.02E+00	6.13E-01		2.50E+00	6.42E-04	Up	Unigene54893_All//gi|186501175|ref |NP_179383.2|//3.00E-46//binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor [Arabidopsis thaliana]	Unigene54893_All//8.00E- 43//AT2G17930| binding / inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor	Unigene54893_All//5.00E-28//TC142236			GO:0003676//GO:0006259//GO:0016772	nr +
Unigene54894_All	281	0.19	2.89	3.03	1.06	2.21	1.61	0.30	0.15	0.28	3.95E+00	7.52E-04	Up	4.03E+00	7.02E-04	Up	1.05E+00	2.99E-01		5.96E-01	6.40E-01		-1.02E+00	7.24E-01		-8.59E-02	9.71E-01										
Unigene54895_All	345	6.07	25.41	19.91	2.17	5.19	4.97	0.00	0.12	0.00	2.07E+00	4.29E-19	Up	1.71E+00	1.77E-11	Up	1.26E+00	1.02E-02		1.20E+00	1.97E-02		6.92E+00	6.33E-01		null	null		Unigene54895_All//gi|33578034|gb|A AQ22345.1|//2.00E-16//BURP domain- containing protein [Gossypium hirsutum]		Unigene54895_All//3.00E-63//TC153409				nr -
Unigene54897_All	386	0.00	0.00	0.00	0.00	0.00	0.00	0.33	3.03	6.50	null	null		null	null		null	null		null	null		3.21E+00	1.47E-05	Up	4.31E+00	2.84E-14	Up									
Unigene54898_All	412	0.76	0.00	0.52	6.05	2.09	0.22	0.10	0.00	0.00	-9.57E+00	3.63E-02		-5.60E-01	6.63E-01		-1.53E+00	7.55E-05	Down	-4.79E+00	4.33E-13	Down	-6.68E+00	6.56E-01		-6.68E+00	6.11E-01										
Unigene54900_All	307	0.00	4.13	2.78	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.86E-07	Up	1.14E+01	9.01E-05	Up	null	null		null	null		null	null		null	null		Unigene54900_All//gi|195618082|gb| ACG30871.1|//1.00E-27//40S ribosomal protein S26 [Zea mays] >gi|195622808|gb|ACG33234.1| 40S ribosomal protein S26 [Zea mays]	Unigene54900_All//7.00E- 23//AT3G56340| 40S ribosomal protein S26 (RPS26C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935 //GO:0022613	nr -
Unigene54901_All	507	136.94	226.86	475.05	110.44	189.50	352.76	0.17	0.25	0.31	7.28E-01	1.64E-48		1.79E+00	0.00E+00	Up	7.79E-01	3.81E-54		1.68E+00	0.00E+00	Up	5.68E-01	7.81E-01		9.14E-01	6.24E-01		Unigene54901_All//gi|71999169|gb|A AZ57444.1|//1.00E-65//lipoxygenase LOX1 [Populus deltoides]	Unigene54901_All//5.00E- 56//AT3G45140| LOX2 (LIPOXYGENASE 2); lipoxygenase	Unigene54901_All//0.00E+00//TC136874		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism	GO:0006633//GO:0016702//GO:0046914	nr -
Unigene54902_All	594	0.00	0.00	0.00	0.08	0.12	0.00	1.21	0.14	5.30	null	null		null	null		4.66E-01	9.57E-01		-6.39E+00	6.34E-01		-3.10E+00	1.40E-03		2.13E+00	2.07E-09	Up									ESTscan -
Unigene54903_All	249	0.00	0.00	0.21	1.60	0.00	0.00	3.23	0.00	0.16	null	null		7.74E+00	6.34E-01		-1.06E+01	4.38E-03		-1.06E+01	1.11E-02		-1.17E+01	8.57E-06	Down	-4.33E+00	4.54E-05	Down									
Unigene54904_All	260	0.00	5.65	2.05	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.11E-08	Up	1.10E+01	4.03E-03		null	null		null	null		null	null		null	null		Unigene54904_All//gi|224156524|ref |XP_002337726.1|//2.00E- 08//predicted protein [Populus trichocarpa] >gi|222860618|gb|EEF06749.1| predicted protein [Populus trichocarpa]						nr +
Unigene54906_All	335	8.28	8.92	10.97	15.02	10.48	7.15	17.67	8.61	7.97	1.09E-01	7.59E-01		4.06E-01	2.37E-01		-5.19E-01	4.53E-02		-1.07E+00	5.29E-05	Down	-1.04E+00	2.62E-06	Down	-1.15E+00	1.46E-07	Down	Unigene54906_All//gi|238478683|ref |NP_001154384.1|//1.00E- 20//double-stranded DNA-binding family protein [Arabidopsis thaliana]	Unigene54906_All//6.00E- 22//AT1G29850| double-stranded DNA-binding family protein	Unigene54906_All//6.00E- 74//gi|13352997|gb|BG443345.1|BG443345			GO:0043566	nr -
Unigene54907_All	274	0.00	5.92	1.75	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.96E-09	Up	1.08E+01	7.47E-03		null	null		null	null		null	null		null	null										
Unigene54909_All	209	0.25	5.09	0.00	0.24	1.65	2.16	0.00	0.00	0.00	4.35E+00	3.95E-05	Up	-7.97E+00	6.22E-01		2.79E+00	1.14E-01		3.18E+00	3.78E-02		null	null		null	null					Unigene54909_All//6.00E-82//DT527375					
Unigene5491_All	226	3.94	12.78	13.90	8.82	14.02	17.59	26.00	19.97	17.10	1.70E+00	2.16E-05	Up	1.82E+00	5.14E-06	Up	6.69E-01	5.49E-02		9.96E-01	1.14E-03		-3.81E-01	9.22E-02		-6.05E-01	4.14E-03					Unigene5491_All//4.00E- 120//gi|109850861|gb|DW479840.1|DW479840					
Unigene54910_All	794	3.43	0.51	1.41	0.69	0.65	0.23	0.69	3.68	0.65	-2.75E+00	1.03E-08	Down	-1.28E+00	1.73E-03		-8.53E-02	9.07E-01		-1.60E+00	1.32E-01		2.41E+00	7.54E-10	Up	-8.57E-02	9.27E-01		Unigene54910_All//gi|115487322|ref |NP_001066148.1|//1.00E- 75//Os12g0145700 [Oryza sativa Japonica Group] >gi|77553678|gb|ABA96474.1| pyruvate kinase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113648655|dbj|BAF29167.1| Os12g0145700 [Oryza sativa Japonica Group]	Unigene54910_All//1.00E- 74//AT3G52990| pyruvate kinase, putative	Unigene54910_All//9.00E-112//EV497296		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0006007//GO:0010038//GO:0016020 //GO:0016301//GO:0046872	nr -
Unigene54911_All	604	0.00	1.85	3.00	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	2.00E-06	Up	1.15E+01	5.69E-10	Up	null	null		null	null		null	null		null	null		Unigene54911_All//gi|5880464|gb|AA D54660.1|AF088901_1//2.00E- 21//actin bundling protein ABP135 [Lilium longiflorum]	Unigene54911_All//2.00E- 20//AT5G57320| villin, putative					nr -
Unigene54914_All	237	0.00	0.00	0.00	1.26	0.44	0.57	0.18	0.35	3.53	null	null		null	null		-1.53E+00	2.98E-01		-1.14E+00	4.57E-01		9.83E-01	7.31E-01		4.31E+00	4.10E-05	Up									
Unigene54915_All	239	121.06	98.37	131.01	2640.99	2455.42	3276.90	147.72	178.03	68.01	-2.99E-01	3.38E-03		1.14E-01	3.21E-01		-1.05E-01	1.05E-08		3.11E-01	6.77E-75		2.69E-01	2.63E-04		-1.12E+00	4.84E-39	Down	Unigene54915_All//gi|258489588|gb| ACV72637.1|//1.00E-32//proline- rich protein 3 [Gossypium hirsutum]		Unigene54915_All//9.00E-106//TC156457				nr -
Unigene54918_All	357	0.00	0.99	0.30	0.70	0.96	0.25	1.78	0.94	0.11	9.96E+00	2.46E-02		8.22E+00	3.97E-01		4.67E-01	7.79E-01		-1.46E+00	4.07E-01		-9.24E-01	2.63E-01		-3.99E+00	5.82E-04	Down				Unigene54918_All//4.00E-07//DW233076					
Unigene54919_All	267	0.78	2.47	0.40	0.00	2.45	0.00	0.32	0.78	0.30	1.65E+00	8.14E-02		-9.75E-01	6.20E-01		1.13E+01	4.92E-04	Up	null	null		1.31E+00	4.47E-01		-8.59E-02	9.71E-01		Unigene54919_All//gi|225468948|ref |XP_002271844.1|//8.00E- 16//PREDICTED: similar to Heavy metal transport/detoxification protein [Vitis vinifera]	Unigene54919_All//9.00E- 13//AT4G05030| heavy-metal- associated domain-containing protein	Unigene54919_All//5.00E- 114//gi|84153157|gb|DN802512.1|DN802512			GO:0006812//GO:0043169	nr +
Unigene54921_All	657	2717.42	1507.13	2083.72	329.90	374.60	296.41	1.22	3.24	0.79	-8.50E-01	0.00E+00		-3.83E-01	2.09E-226		1.83E-01	6.78E-10		-1.54E-01	5.50E-06		1.41E+00	5.52E-04	Up	-6.33E-01	3.56E-01		Unigene54921_All//gi|164470331|gb| ABY58016.1|//5.00E-90//plastidic aldolase [Solanum tuberosum]	Unigene54921_All//5.00E- 86//AT4G38970| fructose- bisphosphate aldolase, putative	Unigene54921_All//0.00E+00//gi|31072744|g b|CA993023.1|CA993023		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway	GO:0006007//GO:0016832//GO:0043231	nr +

Unigene54922_All	294	14.59	9.13	8.33	17.45	13.94	15.36	33.08	16.35	22.76	-6.76E-01	2.08E-02		-8.09E-01	8.21E-03		-3.24E-01	2.39E-01		-1.84E-01	5.53E-01		-1.02E+00	1.48E-09	Down	-5.39E-01	7.05E-04		Unigene54922_All//gi|195628036|gb|ACG33848.1|//2.00E-13//dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex [Zea mays]	Unigene54922_All//4.00E-14//AT5G55070| 2-oxoacid dehydrogenase family protein	Unigene54922_All//7.00E-107//BQ402139		ko00020|Citrate cycle (TCA cycle)//ko00310|Lysine degradation	GO:0005840//GO:0006950//GO:0009060//GO:0016751//GO:0043231//GO:0043434//GO:0046914	nr -
Unigene54923_All	344	0.00	1.62	2.17	0.00	0.00	0.13	0.00	0.00	0.00	1.07E+01	2.18E-03		1.11E+01	3.27E-04	Up	null	null		7.04E+00	6.95E-01		null	null		null	null		Unigene54923_All//gi|255074541|ref|XP_002500945.1|//2.00E-19//pyruvate kinase [Micromonas sp. RCC299] >gi|226516208|gb|AC062203.1|pyruvate kinase [Micromonas sp. RCC299]	Unigene54923_All//4.00E-18//AT5G08570| pyruvate kinase, putative				ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0016740	nr -
Unigene54925_All	326	0.00	0.00	0.00	0.00	0.00	0.00	5.32	2.18	0.00	null	null		null	null		null	null		null	null		-1.29E+00	4.58E-03		-1.24E+01	8.37E-13	Down								ESTscan +
Unigene54926_All	335	0.00	3.78	0.00	0.15	0.82	0.27	1.14	1.00	2.14	1.19E+01	2.86E-07	Up	null	null		2.47E+00	2.23E-01		8.58E-01	7.94E-01		-1.87E-01	8.57E-01		9.14E-01	2.12E-01		Unigene54926_All//gi|297839331|ref|XP_002887547.1|//1.00E-38//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333388|gb|EFH63806.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene54926_All//2.00E-38//AT1G74580| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene54928_All	264	0.00	6.91	4.03	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.14E-10	Up	1.20E+01	6.61E-06	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene54930_All	359	0.00	38.25	15.43	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	7.80E-79	Up	1.39E+01	7.61E-31	Up	null	null		null	null		null	null		null	null		Unigene54930_All//gi|192910792|gb|ACF06504.1|//5.00E-12//60S ribosomal protein L28 [Elaeis guineensis]	Unigene54930_All//1.00E-07//AT4G29410| 60S ribosomal protein L28 (RPL28C)				ko03010|Ribosome		nr +
Unigene54937_All	356	0.00	0.28	0.90	0.28	0.58	1.78	5.11	2.58	1.34	8.15E+00	3.85E-01		9.81E+00	4.50E-02		1.05E+00	6.12E-01		2.67E+00	1.83E-02		-9.84E-01	2.32E-02		-1.93E+00	3.03E-05	Down		Unigene54937_All//4.00E-07//TC165574					
Unigene54939_All	2236	0.00	0.00	0.00	0.00	0.00	0.00	4.18	11.63	24.07	null	null		null	null		null	null		null	null		1.48E+00	9.15E-43	Up	2.53E+00	4.63E-182	Up	Unigene54939_All//gi|226498624|ref|NP_001147903.1|//0.00E+00//protein kinase [Zea mays] >gi|195614480|gb|ACG29070.1|protein kinase [Zea mays]	Unigene54939_All//3.00E-149//AT5G10530| lectin protein kinase, putative				ko04626|Plant-pathogen interaction	GO:0003676//GO:0004713//GO:0006259//GO:0006464//GO:0030246//GO:0031410//GO:0032559//GO:0043231	nr +
Unigene54494_All	606	0.69	5.10	0.00	1.32	2.33	1.86	36.91	78.07	107.75	2.88E+00	3.48E-10	Up	-9.43E+00	1.55E-02		8.25E-01	1.57E-01		5.03E-01	4.76E-01		1.08E+00	8.98E-48	Up	1.55E+00	4.49E-116	Up	Unigene5494_All//gi|14625425|dbj|BAB61919.1|//4.00E-67//calmodulin NtCaM13 [Nicotiana tabacum]	Unigene5494_All//3.00E-65//AT3G22930| calmodulin, putative	Unigene5494_All//0.00E+00//DW502677		ko04626|Plant-pathogen interaction		nr -
Unigene54941_All	275	211.00	62.83	335.96	453.22	439.90	293.32	357.92	87.09	134.58	-1.75E+00	8.02E-99	Down	6.71E-01	6.89E-33		-4.30E-02	4.60E-01		-6.28E-01	7.12E-44		-2.04E+00	8.87E-252	Down	-1.41E+00	5.06E-154	Down	Unigene54941_All//gi|50313460|gb|AT74600.1|//4.00E-47//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene54941_All//9.00E-31//AT3G23510| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene54941_All//1.00E-151//TC129559			GO:0006629//GO:0008757//GO:0044464	nr +
Unigene54942_All	308	0.17	2.63	2.94	267.02	125.67	97.22	296.51	320.25	272.14	3.95E+00	7.52E-04	Up	4.11E+00	3.91E-04	Up	-1.09E+00	2.26E-84	Down	-1.46E+00	6.64E-117	Down	1.11E-01	2.75E-02		-1.24E-01	1.34E-02		Unigene54942_All//gi|4150446|gb|AK53065.1|//5.00E-38//subtilisin-type protease precursor [Glycine max]	Unigene54942_All//2.00E-36//AT1G20160| ATSBT5.2; identical protein binding / serine-type endopeptidase	Unigene54942_All//4.00E-158//gi|109842709|gb|DW241269.1|DW241269			GO:0004175//GO:0005515//GO:0005576//GO:0019538//GO:0031410//GO:0044092	nr +
Unigene54944_All	345	0.00	2.20	1.39	0.00	0.10	0.00	0.00	0.00	0.00	1.11E+01	1.76E-04	Up	1.04E+01	7.47E-03		6.64E+00	8.29E-01		null	null		null	null		null	null									
Unigene54945_All	474	0.22	0.00	0.00	4.83	3.20	1.24	0.00	0.00	0.00	-7.79E+00	3.70E-01		-7.79E+00	3.91E-01		-5.97E-01	1.53E-01		-1.96E+00	1.67E-05	Down	null	null		null	null		Unigene54945_All//gi|27476096|gb|AA017027.1|//1.00E-19//Putative transposable element [Oryza sativa Japonica Group]	Unigene54945_All//6.00E-19//AT1G48120| calcineurin-like phosphoesterase family protein					nr -
Unigene54948_All	486	0.00	5.73	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.43E-16	Up	1.06E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene54948_All//gi|2244977|emb|CAB10398.1|//4.00E-27//cysteine proteinase like protein [Arabidopsis thaliana] >gi|7268368|emb|CAB78661.1|cysteine proteinase like protein [Arabidopsis thaliana] >gi|14517442|gb|AAK62611.1|AT4g16190/d14135w [Arabidopsis thaliana] >gi|22136546|gb|AAM91059.1|AT4g16190/d14135w [Arabidopsis thaliana] >gi|22530956|gb|AAM96982.1|cysteine proteinase [Arabidopsis thaliana] >gi|110740834|dbj|BAE98514.1|cysteine proteinase like protein [Arabidopsis thaliana]	Unigene54948_All//2.00E-28//AT4G16190| cysteine proteinase, putative				GO:0008233//GO:0043231	nr -
Unigene5495_All	401	0.00	2.40	0.00	1.37	0.17	1.46	5.27	11.15	18.18	1.12E+01	1.38E-05	Up	null	null		-2.99E+00	9.38E-03		9.95E-02	9.36E-01		1.08E+00	3.06E-05	Up	1.79E+00	1.26E-16	Up	Unigene5495_All//gi|14625425|dbj|BAB61919.1|//5.00E-35//calmodulin NtCaM13 [Nicotiana tabacum]	Unigene5495_All//1.00E-33//AT3G22930| calmodulin, putative	Unigene5495_All//5.00E-152//DW502677		ko04626|Plant-pathogen interaction		nr -
Unigene54952_All	345	0.00	0.00	0.00	0.00	0.00	0.00	3.68	0.48	2.77	null	null		null	null		null	null		null	null		-2.92E+00	1.46E-05	Down	-4.08E-01	4.35E-01									
Unigene54956_All	356	0.00	0.00	0.00	2.24	0.68	0.51	2.26	0.47	0.11	null	null		null	null		-1.73E+00	2.86E-02		-2.14E+00	1.54E-02		-2.26E+00	4.82E-03		-4.33E+00	4.54E-05	Down	Unigene54956_All//gi|115482728|ref|NP_001061957.1|//8.00E-14//Os10g0497100 [Oryza sativa Japonica Group] >gi|113639566|dbj|BAF26871.1|Os10g0497100 [Oryza sativa Japonica Group]	Unigene54956_All//2.00E-10//AT4G30580| ATS2; 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase	Unigene54956_All//1.00E-13//DR455229		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0003006//GO:0009941//GO:0016020//GO:0016411//GO:0016471	nr -
Unigene54957_All	505	0.00	3.11	1.79	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.70E-09	Up	1.08E+01	4.71E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene54959_All	617	1.19	0.00	0.00	0.48	1.17	0.66	1.51	0.41	0.19	-1.02E+01	2.11E-04	Down	-1.02E+01	4.13E-04	Down	1.27E+00	1.56E-01		4.44E-01	7.01E-01		-1.89E+00	6.92E-03		-2.96E+00	1.72E-04	Down	Unigene54959_All//gi|145340316|ref|NP_193430.3|//5.00E-32//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|110738029|dbj|BAF00949.1|kinase like protein [Arabidopsis thaliana]	Unigene54959_All//9.00E-34//AT4G16970| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene54959_All//1.00E-137//ES803732			GO:0004672//GO:0006464//GO:0031410//GO:0032559	nr -
Unigene5496_All	306	4.10	4.80	3.31	3.91	1.80	2.36	19.48	15.16	8.85	2.27E-01	6.60E-01		-3.12E-01	6.41E-01		-1.12E+00	6.04E-02		-7.26E-01	2.56E-01		-3.62E-01	1.10E-01		-1.14E+00	1.66E-07	Down	Unigene5496_All//gi|297813423|ref|XP_002874595.1|//2.00E-06//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320432|gb|EFH50854.1|hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5496_All//8.00E-08//AT4G09900| MES12 (METHYL ESTERASE 12); hydrolase	Unigene5496_All//2.00E-141//gi|11201037|gb|BF270042.1|BF270042				nr +
Unigene54960_All	287	2018.09	963.43	1885.64	323.01	469.38	218.42	1.62	1.31	0.28	-1.07E+00	0.00E+00	Down	-9.79E-02	6.45E-06		5.39E-01	8.83E-40		-5.65E-01	3.60E-27		-3.06E-01	7.36E-01		-2.55E+00	2.35E-02		Unigene54960_All//gi|226358407|gb|AC051066.1|//2.00E-47//chloroplast chlorophyll A-B binding protein [Gossypium hirsutum]	Unigene54960_All//7.00E-31//AT4G10340| LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding	Unigene54960_All//3.00E-152//EX169624		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009503//GO:0009523//GO:0009570//GO:0009639//GO:0044906	nr -
Unigene54961_All	283	0.18	0.00	1.13	3.34	2.07	0.00	0.15	0.00	0.00	-7.53E+00	6.10E-01		2.61E+00	1.46E-01		-6.93E-01	3.15E-01		-1.17E+01	6.01E-06	Down	-7.22E+00	6.56E-01		-7.22E+00	6.11E-01			Unigene54961_All//1.00E-89//TC150426					
Unigene54964_All	287	212.93	101.69	122.83	294.20	321.56	179.71	275.93	145.92	175.87	-1.07E+00	2.77E-49	Down	-7.94E-01	3.52E-29		1.28E-01	2.12E-02		-7.11E-01	3.73E-37		-9.19E-01	5.27E-61		-6.50E-01	8.46E-35		Unigene54964_All//gi|292653543|gb|ADE34289.1|//3.00E-10//aquaporin TIP2;3 [Gossypium hirsutum]		Unigene54964_All//9.00E-88//gi|21102513|gb|BQ414826.1|BQ414826				nr +
Unigene5497_All	1012	2.79	0.75	2.05	37.80	25.86	20.35	0.54	0.62	0.43	-1.89E+00	4.74E-06	Down	-4.44E-01	2.62E-01		-5.48E-01	3.42E-12		-8.94E-01	3.81E-25		1.90E-01	8.11E-01		-3.27E-01	6.72E-01		Unigene5497_All//gi|127709419|gb|AB028750.1|//3.00E-62//knotted1-like homeobox transcription factor [Prunus persica]	Unigene5497_All//6.00E-42//AT1G23380| KNAT6; DNA binding / transcription activator/ transcription factor	Unigene5497_All//0.00E+00//TC153923	HB			nr -
Unigene54970_All	789	0.00	0.77	0.54	0.51	0.17	0.23	1.61	0.00	5.91	9.59E+00	1.17E-03		9.08E+00	1.38E-02		-1.53E+00	2.05E-01		-1.14E+00	3.79E-01		-1.07E+01	5.06E-09	Down	1.88E+00	1.24E-11	Up								
Unigene54971_All	1184	0.00	0.86	0.00	0.00	0.00	0.23	0.07	2.26	6.80	9.74E+00	7.25E-06	Up	null	null		null	null		7.84E+00	7.02E-02		4.98E+00	4.15E-16	Up	6.57E+00	5.40E-54	Up	Unigene54971_All//gi|126143480|dbj|BAF47279.1|//1.00E-139//lectin-receptor like protein kinase 3 [Nicotiana tabacum]	Unigene54971_All//4.00E-123//AT4G04960| lectin protein kinase, putative	Unigene54971_All//1.00E-121//DN780966		ko04626|Plant-pathogen interaction	GO:0005488//GO:0016020//GO:0016772	nr -
Unigene54973_All	504	0.00	5.93	31.27	0.00	0.00	0.09	0.00	0.00	0.00	1.25E+01	5.19E-17	Up	1.49E+01	6.92E-89	Up	null	null		6.49E+00	6.95E-01		null	null		null	null		Unigene54973_All//sp|P01834|IGKC_HUMAN//2.00E-54//Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=1						swissprot +
Unigene54978_All	593	0.00	1.88	0.00	0.00	0.06	0.00	0.14	0.07	2.96	1.09E+01	2.00E-06	Up	null	null		5.86E+00	8.29E-01		null	null		-1.02E+00	7.24E-01		4.37E+00	3.23E-10	Up	Unigene54978_All//gi|15233263|ref|NP_188224.1|//1.00E-35//CES101 (CALLUS EXPRESSION OF RBCS 101); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene54978_All//4.00E-37//AT3G16030| CES101 (CALLUS EXPRESSION OF RBCS 101); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene54978_All//4.00E-08//gi|78350521|gb|DT570795.1|DT570795			GO:0000166//GO:0004713//GO:0030246	nr +
Unigene5498_All	871	100.74	222.98	144.59	72.69	180.44	241.79	30.24	47.60	62.07	1.15E+00	8.23E-174	Up	5.21E-01	1.43E-28		1.31E+00	1.23E-206	Up	1.73E+00	0.00E+00	Up	6.55E-01	2.54E-18		1.04E+00	3.79E-52	Up	Unigene5498_All//gi|196196276|gb|ACG76109.1|//4.00E-75//pathogenesis-induced protein [Arachis hypogaea]	Unigene5498_All//6.00E-68//AT1G01360| unknown protein	Unigene5498_All//0.00E+00//TC145264				nr +
Unigene54985_All	335	0.00	0.00	0.00	0.00	0.00	0.00	5.05	2.74	0.36	null	null		null	null		null	null		null	null		-8.79E-01	5.21E-02		-3.82E+00	2.76E-09	Down	Unigene54985_All//gi|300256410|gb|EFJ40676.1|//1.00E-28//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene54985_All//8.00E-22//AT5G15200| 40S ribosomal protein S9 (RPS9B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0033279	nr -
Unigene54986_All	357	0.00	0.00	1.49	1.67	1.06	1.39	1.42	0.23	0.00	null	null		1.05E+01	4.03E-03		-6.58E-01	4.78E-01		-2.67E-01	7.57E-01		-2.60E+00	2.04E-02		-1.05E+01	5.54E-04	Down								
Unigene54988_All	412	0.00	0.00	0.00	0.00	0.00	0.00	4.21	0.51	26.59	null	null		null	null		null	null		null	null		-3.05E+00	1.18E-07	Down	2.66E+00	8.25E-40	Up	Unigene54988_All//gi|224121322|ref|XP_002330798.1|//5.00E-10//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222872600|gb|EEF09731.1|cc-nbs-lrr resistance protein [Populus trichocarpa]		Unigene54988_All//3.00E-125//gi|164293486|gb|EX167757.1|EX167757				nr +
Unigene5499_All	440	47.09	17.39	10.04	35.55	34.20	41.16	126.84	41.04	55.32	-1.44E+00	5.00E-27	Down	-2.23E+00	3.65E-47	Down	-5.58E-02	7.69E-01		2.11E-01	1.37E-01		-1.63E+00	4.49E-105	Down	-1.20E+00	4.40E-68	Down	Unigene5499_All//gi|1710587|sp|P50346.1|RLA0_SOYBN//5.00E-62//RecName: Full=60S acidic ribosomal protein P0 >gi|1190897|gb|AAB63814.1|acidic ribosomal protein P0 [Glycine max]	Unigene5499_All//5.00E-47//AT3G09200| 60S acidic ribosomal protein P0 (RPP0B)	Unigene5499_All//2.00E-176//gi|13245577|gb|BE053382.2|BE053382		ko03010|Ribosome		nr +
Unigene54991_All	492	0.00	0.00	0.00	0.00	0.00	0.00	1.55	1.95	0.08	null	null		null	null		null	null		null	null		3.37E-01	6.32E-01		-4.26E+00	8.65E-05	Down	Unigene54991_All//gi|195605604|gb|ACG24632.1|//2.00E-35//40S ribosomal protein S24 [Zea mays] >gi|195657831|gb|ACG48383.1|40S ribosomal protein S24 [Zea mays]	Unigene54991_All//5.00E-31//AT3G04920| 40S ribosomal protein S24 (RPS24A)			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0031981//GO:0034728	nr +
Unigene54994_All	389	1.61	0.52	0.82	1.15	2.66	2.32	2.72	0.21	1.02	-1.63E+00	9.23E-02		-9.75E-01	3.16E-01		1.20E+00	8.55E-02		1.01E+00	1.96E-01		-3.66E+00	1.31E-05	Down	-1.41E+00	1.72E-02				Unigene54994_All//3.00E-11//DW492985				ESTscan +
Unigene54998_All	370	0.00	2.74	0.86	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.23E-06	Up	9.75E+00	4.50E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene55000_All	380	0.00	0.40	0.00	0.26	0.18	0.95	6.79	3.41	0.52	8.64E+00	2.35E-01		null	null		-5.33E-01	8.15E-01		1.86E+00	2.19E-01		-9.93E-01	4.86E-03		-3.69E+00	1.70E-13	Down								
Unigene55001_All	351	0.00	0.00	0.00	0.00	0.00	0.00	2.05	2.74	0.00	null	null		null	null		null	null		null	null		4.20E-01	5.31E-01		-1.10E+01	1.78E-05	Down	Unigene55001_All//gi|298713087|emb|CBJ48862.1|//2.00E-38//n/a [Ectocarpus siliculosus]	Unigene55001_All//1.00E-28//AT5G38480| GRF3 (GENERAL REGULATORY FACTOR 3); ATP binding / protein binding / protein phosphorylated amino acid binding				GO:0009532//GO:0016020//GO:0032559//GO:0043401//GO:0051219	nr -
Unigene55006_All	357	3.81	0.85	1.64	4.19	1.16	3.29	0.47	0.00	0.11	-2.16E+00	9.05E-04	Down	-1.22E+00	4.79E-02		-1.85E+00	5.94E-04	Down	-3.48E-01	5.60E-01		-8.89E+00	1.34E-01		-2.09E+00	3.13E-01		Unigene55006_All//gi|116248669|gb|ABJ90469.1|//5.00E-48//beta-ketoacyl-ACP synthase II [Jatropha curcas]	Unigene55006_All//8.00E-46//AT1G74960| FAB1 (FATTY ACID BIOSYNTHESIS 1); 3-oxoacyl-[acyl-carrier-protein] synthase/ fatty-acid synthase	Unigene55006_All//2.00E-144//C0089213		ko00061|Fatty acid biosynthesis	GO:0004312//GO:0006631	nr +
Unigene5501_All	353	19.71	28.13	31.23	15.95	19.51	24.44	8.74	16.22	27.20	5.13E-01	4.85E-03		6.64E-01	1.83E-04		2.91E-01	2.27E-01		6.16E-01	1.55E-03		8.92E-01	6.09E-05		1.64E+00	3.00E-19	Up			Unigene5501_All//7.00E-46//C0083107				

Unigene55010_All	1441	0.07	0.14	0.07	0.14	0.33	0.41	0.32	0.29	7.22	9.55E-01	6.21E-01		2.56E-02	9.99E-01		1.27E+00	2.92E-01		1.56E+00	1.36E-01		-1.54E-01	8.70E-01		4.48E+00	5.40E-59	Up	Unigene55010_All//gi|297793133|ref|XP_002864451.1|//6.00E-66//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310286|gb|EFH40710.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene55010_All//4.00E-58//AT5G56340| zinc finger (C3HC4-type RING finger) family protein	Unigene55010_All//0.00E+00//TC174139			GO:0046872	nr +
Unigene55012_All	483	0.00	0.00	0.00	24.65	1.85	0.00	0.00	0.00	0.00	null	null		null	null		-3.73E+00	1.50E-61	Down	-1.46E+01	5.12E-76	Down	null	null		null	null		Unigene55012_All//gi|224137386|ref|XP_002327113.1|//1.00E-08//predicted protein [Populus trichocarpa] >gi|222835428|gb|EEE73863.1| predicted protein [Populus trichocarpa]	Unigene55012_All//4.00E-05//AT5G66816| unknown protein	Unigene55012_All//6.00E-07//TC158970				nr -
Unigene55013_All	383	0.00	0.00	0.00	0.00	0.00	0.00	2.98	2.84	0.21	null	null		null	null		null	null		null	null		-7.11E-02	9.12E-01		-3.84E+00	1.74E-06	Down	Unigene55013_All//sp|Q86XX4|FRAS1_HUMAN//8.00E-06//Extracellular matrix protein FRAS1 OS=Homo sapiens GN=FRAS1 PE=2 SV=1					swissprot -
Unigene55015_All	343	0.15	9.75	2.02	0.00	0.50	1.05	0.00	0.00	0.23	6.00E+00	1.58E-17	Up	3.73E+00	3.99E-03		8.97E+00	2.27E-01		1.00E+01	2.37E-02		null	null		7.86E+00	4.03E-01		Unigene55015_All//gi|225443419|ref|XP_002267647.1|//1.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]					GO:0003676//GO:0009987	nr -
Unigene55018_All	639	0.00	4.60	2.25	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.01E-16	Up	1.11E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene55018_All//gi|301095009|ref|XP_002896607.1|//6.00E-47//NADP-dependent malic enzyme [Phytophthora infestans T30-4] >gi|262108925|gb|EEY66977.1| NADP-dependent malic enzyme [Phytophthora infestans T30-4]	Unigene55018_All//3.00E-43//AT1G79750| ATNADP-ME4 (NADP-malic enzyme 4); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)// malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor			ko00620|Pyruvate metabolism/ko00710|Carbon fixation in photosynthetic organisms	GO:0005488//GO:0008152//GO:0016615	nr +
Unigene55019_All	615	0.68	0.91	0.87	1.05	3.53	1.54	0.76	1.16	2.01	4.13E-01	6.36E-01		3.47E-01	7.05E-01		1.74E+00	1.17E-04	Up	5.51E-01	4.82E-01		6.11E-01	4.27E-01		1.41E+00	9.74E-03								
Unigene55020_All	1532	0.00	0.00	0.00	0.00	0.00	0.00	4.94	5.07	0.10	null	null		null	null		null	null		null	null		3.87E-02	8.60E-01		-5.57E+00	3.18E-49	Down	Unigene55020_All//gi|41469358|gb|AAS07200.1|//1.00E-120//UDP-glucose dehydrogenase [Oryza sativa Japonica Group]	Unigene55020_All//4.00E-110//AT1G26570| UGD1 (UDP-GLUCOSE DEHYDROGENASE 1); NAD or NADH binding / UDP-glucose 6-dehydrogenase/ binding / catalytic/ coenzyme binding / oxidoreductase/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor			ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene55022_All	543	0.39	0.00	0.10	0.37	0.13	0.08	1.71	26.02	3.01	-8.59E+00	1.21E-01		-1.97E+00	3.81E-01		-1.53E+00	4.15E-01		-2.14E+00	3.47E-01		3.92E+00	7.58E-72	Up	8.12E-01	6.76E-02		Unigene55022_All//gi|18396059|ref|NP_564263.1|//2.00E-22//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|9295734|gb|AAF87040.1|AC006535_18 T24P13.19 [Arabidopsis thaliana] >gi|13605625|gb|AAK32806.1|AF36163 8_1 At1g26800/T24P13_21 [Arabidopsis thaliana] >gi|15450675|gb|AAO96609.1| At1g26800/T24P13_21 [Arabidopsis thaliana] >gi|15777873|gb|AAL05897.1| At1g26800/T24P13_21 [Arabidopsis thaliana]	Unigene55022_All//3.00E-19//AT1G26800| zinc finger (C3HC4-type RING finger) family protein	Unigene55022_All//2.00E-161//gi|78330649|gb|DT550923.1|DT550923			GO:0043231//GO:0046872	nr +
Unigene55023_All	330	21.40	9.21	6.29	7.85	3.13	5.88	15.63	20.52	19.92	-1.22E+00	1.09E-07	Down	-1.77E+00	3.27E-12	Down	-1.33E+00	3.73E-04	Down	-4.16E-01	3.24E-01		3.93E-01	5.81E-02		3.50E-01	8.80E-02		Unigene55023_All//gi|9294638|dbj|BAB02977.1|//3.00E-28//glycolate oxidase [Arabidopsis thaliana]	Unigene55023_All//1.00E-29//AT3G14130| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene55023_All//2.00E-135//TC172637		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0000166//GO:0003973//GO:0008152//GO:0042579	nr +
Unigene55031_All	356	8.52	5.69	8.53	5.60	4.84	7.61	47.98	103.32	129.03	-5.82E-01	1.05E-01		3.00E-04	9.98E-01		-2.11E-01	6.58E-01		4.44E-01	2.83E-01		1.11E+00	9.98E-39	Up	1.43E+00	7.69E-73	Up		Unigene55031_All//4.00E-109//TC146572					
Unigene55032_All	353	0.00	19.09	7.69	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	1.68E-38	Up	1.29E+01	5.42E-15	Up	null	null		null	null		null	null		null	null		Unigene55032_All//gi|115471095|ref|NP_001059146.1|//1.00E-07//Os07g0205000 [Oryza sativa Japonica Group] >gi|113610682|dbj|BAF21060.1| Os07g0205000 [Oryza sativa Japonica Group]	Unigene55032_All//4.00E-08//AT5G25450| ubiquinol-cytochrome C reductase complex 14 kDa protein, putative			ko00190|Oxidative phosphorylation	GO:0005746//GO:0022900	nr -
Unigene55033_All	439	0.60	0.35	0.00	0.00	0.00	0.00	3.08	1.52	0.18	-7.83E-01	6.20E-01		-9.22E+00	8.55E-02		null	null		null	null		-1.02E+00	4.99E-02		-4.09E+00	7.07E-08	Down							
Unigene55035_All	501	0.00	3.64	3.93	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.14E-10	Up	1.19E+01	7.45E-11	Up	null	null		null	null		null	null		null	null		Unigene55035_All//gi|38014843|gb|AAH60583.1|//4.00E-17//Cd81 protein [Rattus norvegicus] >gi|149061756|gb|EDM12179.1| rCG47614, isoform CRA_b [Rattus norvegicus]					GO:0008283//GO:0031224//GO:0044237//GO:0044238//GO:0044459//GO:0050794	nr -
Unigene55036_All	290	0.54	1.92	0.92	0.34	3.09	1.09	0.00	0.00	0.00	1.83E+00	9.02E-02		7.63E-01	6.44E-01		3.17E+00	8.78E-04	Up	1.67E+00	3.09E-01		null	null		null	null		Unigene55036_All//gi|224070935|ref|XP_002303298.1|//7.00E-10//predicted protein [Populus trichocarpa] >gi|222840730|gb|EEE78277.1| predicted protein [Populus trichocarpa]						nr -
Unigene55037_All	611	0.00	0.17	0.09	0.00	0.00	0.74	12.11	47.06	45.51	7.37E+00	3.85E-01		6.45E+00	6.34E-01		null	null		9.53E+00	7.75E-03		1.96E+00	5.26E-70	Up	1.91E+00	7.37E-67	Up	Unigene55037_All//gi|170076|gb|AAA34015.1|//2.00E-14//calmodulin [Glycine max] >gi|1583770|prf||2121384D calmodulin	Unigene55037_All//3.00E-13//AT3G51920| CAM9 (CALMODULIN 9); calcium ion binding	Unigene55037_All//6.00E-26//TC166294		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system	GO:0006970//GO:0008152//GO:0009593//GO:0009725//GO:0016628//GO:0019932//GO:0043229//GO:0046872	nr +
Unigene55038_All	338	0.00	0.00	0.00	0.00	0.00	0.00	3.38	5.69	0.12	null	null		null	null		null	null		null	null		7.52E-01	7.46E-02		-4.84E+00	2.34E-07	Down							
Unigene55039_All	331	0.47	1.84	4.02	3.16	2.81	2.18	0.51	1.52	0.96	1.95E+00	6.03E-02		3.08E+00	8.57E-05	Up	-1.70E-01	8.19E-01		-5.34E-01	4.55E-01		1.57E+00	1.18E-01		9.14E-01	4.52E-01			Unigene55039_All//6.00E-114//BQ408176					ESTscan +
Unigene5504_All	635	46.47	48.12	49.73	83.86	66.65	63.94	109.33	88.07	52.95	5.02E-02	6.39E-01		9.77E-02	3.92E-01		-3.31E-01	6.55E-07		-3.91E-01	2.14E-08		-3.12E-01	2.44E-08		-1.05E+00	4.27E-68	Down	Unigene5504_All//gi|115371812|gb|AB196209.1|//5.00E-45//ubiquitin-conjugating enzyme [Capsicum annuum]	Unigene5504_All//2.00E-44//AT4G36800| RCE1 (RUB1 CONJUGATING ENZYME 1); NEDD8 ligase/ small conjugating protein ligase	Unigene5504_All//0.00E+00//gi|48751290|gb|CO081809.1|CO081809		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene55044_All	548	0.00	3.24	1.75	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.14E-10	Up	1.08E+01	2.46E-05	Up	null	null		null	null		null	null		null	null		Unigene55044_All//gi|145350163|ref|XP_001419486.1|//5.00E-19//F-ATPase family transporter: protons (mitochondrial) [Ostreococcus lucimarinus CCE9901] >gi|14457918|gb|AB097779.1| F-ATPase family transporter: protons (mitochondrial) [Ostreococcus lucimarinus CCE9901]	Unigene55044_All//2.00E-09//AT5G47030| ATP synthase delta' chain, mitochondrial			ko00190|Oxidative phosphorylation	GO:0000275//GO:0006754//GO:0006970//GO:0015078//GO:0046914	nr -
Unigene55048_All	412	0.00	0.00	0.00	0.36	0.42	0.22	3.08	7.30	2.22	null	null		null	null		2.04E-01	9.49E-01		-7.27E-01	7.15E-01		1.25E+00	1.53E-04	Up	-4.69E-01	3.69E-01			Unigene55048_All//6.00E-19//gi|78343242|gb|DT563516.1|DT563516					
Unigene55051_All	407	0.00	6.22	3.27	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.05E-14	Up	1.17E+01	2.40E-07	Up	null	null		null	null		null	null		null	null		Unigene55051_All//gi|297828662|ref|XP_002882213.1|//3.00E-15//proteasome family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328053|gb|EFH58472.1| proteasome family protein [Arabidopsis lyrata subsp. lyrata]	Unigene55051_All//2.00E-16//AT3G02200| proteasome family protein			ko03050|Proteasome		nr -
Unigene55052_All	551	0.00	0.00	0.00	0.09	0.06	0.57	1.84	1.82	9.18	null	null		null	null		-5.33E-01	8.24E-01		2.67E+00	1.44E-01		-1.66E-02	1.02E+00		2.32E+00	3.70E-16	Up	Unigene55052_All//gi|224123518|ref|XP_002319099.1|//1.00E-49//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222857475|gb|EEE95022.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene55052_All//6.00E-32//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene55052_All//1.00E-51//CO091061	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene55053_All	351	0.00	5.77	5.16	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.53E-11	Up	1.23E+01	5.69E-10	Up	null	null		null	null		null	null		null	null								
Unigene55054_All	382	0.00	0.00	0.00	0.00	0.27	0.35	9.41	20.68	6.47	null	null		null	null		8.08E+00	4.55E-01		8.47E+00	3.10E-01		1.14E+00	2.65E-09	Up	-5.41E-01	5.43E-02		Unigene55054_All//gi|4741195|emb|CAB41861.1|//8.00E-16//ABC transporter-like protein [Arabidopsis thaliana]	Unigene55054_All//4.00E-17//AT3G47780| ATATH6; ATPase, coupled to transmembrane movement of substances / transporter	Unigene55054_All//2.00E-64//TC173968		ko02010|ABC transporters	GO:0017111//GO:0032559	nr +
Unigene55055_All	373	0.00	44.96	18.99	0.00	0.00	0.00	0.00	0.00	0.00	1.55E+01	2.14E-96	Up	1.42E+01	1.43E-39	Up	null	null		null	null		null	null		null	null		Unigene55055_All//gi|34394194|dbj|BAC84646.1|//3.00E-08//hypothetical protein [Oryza sativa Japonica Group] >gi|125601041|gb|EAZ40617.1| hypothetical protein Osj_25081 [Oryza sativa Japonica Group]					GO:0006464//GO:0032559	nr -
Unigene55057_All	494	0.00	0.00	0.00	0.00	0.00	0.00	1.80	3.38	0.00	null	null		null	null		null	null		null	null		9.13E-01	4.52E-02		-1.08E+01	1.10E-06	Down	Unigene55057_All//gi|2500354|sp|P93847.1|RL10_SOLME//3.00E-63//RecName: Full=60S ribosomal protein L10; AltName: Full=EQM >gi|1902894|dbj|BAA19462.1| QM family protein [Solanum melongena]	Unigene55057_All//5.00E-61//AT1G66580| 60S ribosomal protein L10 (RPL10C)	Unigene55057_All//7.00E-19//ES796971		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene55058_All	410	0.00	0.00	0.00	0.12	0.00	0.00	136.22	24.06	25.56	null	null		null	null		-6.92E+00	5.54E-01		-6.92E+00	6.34E-01		-2.50E+00	5.96E-184	Down	-2.41E+00	6.42E-182	Down		Unigene55058_All//1.00E-121//TC153220					
Unigene5506_All	467	6.61	15.30	7.64	6.61	6.93	4.74	16.39	17.63	11.09	1.21E+00	1.11E-07	Up	2.09E-01	5.69E-01		6.72E-02	8.68E-01		-4.81E-01	1.94E-01		1.06E-01	6.49E-01		-5.63E-01	1.96E-03			Unigene5506_All//6.00E-155//DT049074					
Unigene55060_All	410	2.17	1.85	1.43	0.49	2.77	1.43	0.93	1.12	0.97	-2.27E-01	7.27E-01		-6.03E-01	4.18E-01		2.51E+00	7.35E-04	Up	1.56E+00	1.36E-01		2.73E-01	7.69E-01		6.62E-02	9.66E-01			Unigene55060_All//3.00E-08//ES817289					
Unigene55063_All	671	0.31	0.91	0.95	0.00	0.10	0.27	1.95	1.62	0.30	1.54E+00	1.22E-01		1.61E+00	1.11E-01		6.68E+00	6.08E-01		8.07E+00	1.94E-01		-2.70E-01	6.56E-01		-2.72E+00	1.32E-05	Down	Unigene55063_All//gi|1743009|emb|CAA71142.1|//7.00E-87//SNF1-related protein kinase [Cucumis sativus]	Unigene55063_All//4.00E-83//AT3G01090| AKIN10 (Arabidopsis SNF1 kinase homolog 10); protein binding / protein kinase	Unigene55063_All//2.00E-87//TC167433		ko04140|Regulation of autophagy	GO:0000151//GO:0000172//GO:0006464//GO:0007568//GO:0007584//GO:0009755//GO:0009791//GO:0022414//GO:0032559//GO:0048364	nr +
Unigene55064_All	323	0.81	2.82	5.28	1.08	3.73	0.70	2.88	1.81	3.58	1.80E+00	2.33E-02		2.70E+00	2.50E-05	Up	1.79E+00	6.51E-03		-6.27E-01	6.20E-01		-6.69E-01	3.12E-01		3.13E-01	5.99E-01			Unigene55064_All//4.00E-07//EV498159					
Unigene55065_All	289	0.36	0.35	1.11	0.17	0.24	0.31	0.00	0.00	2.07	-4.62E-02	9.88E-01		1.61E+00	3.04E-01		4.67E-01	9.57E-01		8.58E-01	7.94E-01		null	null		1.10E+01	1.75E-04	Up	Unigene55065_All//gi|297826989|ref|XP_002881377.1|//2.00E-27//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297327216|gb|EFH57636.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene55065_All//7.00E-29//AT2G35130| pentatricopeptide (PPR) repeat-containing protein	Unigene55065_All//3.00E-121//CO096871			GO:0043231	nr +
Unigene55067_All	411	0.00	0.00	0.00	0.00	0.00	0.00	22.22	16.68	0.00	null	null		null	null		null	null		null	null		-4.14E-01	1.65E-02		-1.44E+01	3.03E-67	Down	Unigene55067_All//gi|13359451|dbj|BAB33421.1|//4.00E-15//putative senescence-associated protein [Pisum sativum]		Unigene55067_All//3.00E-42//DV849392				nr -

Unigene5507_All	1750	0.75	0.14	0.06	2.93	1.93	0.54	6.91	0.38	0.96	-2.37E+00	5.60E-04	Down	-3.62E+00	2.81E-05	Down	-6.04E-01	1.63E-02		-2.44E+00	5.42E-15	Down	-4.18E+00	1.24E-64	Down	-2.85E+00	5.03E-48	Down	Unigene5507_All//gi|224125358|ref|XP_002319566.1|//0.00E+00//cytochrome P450 probable flavone synthase [Populus trichocarpa] >gi|222857942|gb|EEE95489.1| cytochrome P450 probable flavone synthase [Populus trichocarpa]	Unigene5507_All//2.00E-90//AT5G26900 CYP93D1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene55070_All	759	0.21	0.20	0.00	0.26	0.23	0.36	4.01	0.22	2.05	-4.61E-02	9.89E-01		-7.69E+00	2.44E-01		-2.11E-01	8.58E-01		4.44E-01	7.63E-01		-4.19E+00	1.21E-16	Down	-9.70E-01	1.73E-03		Unigene55070_All//gi|184220078|ref|NP_568030.1|//2.00E-66//NPY5 (NAKED PINS IN YUC MUTANTS 5); protein binding / signal transducer [Arabidopsis thaliana]	Unigene55070_All//6.00E-68//AT4G37590 NPY5 (NAKED PINS IN YUC MUTANTS 5); protein binding / signal transducer	Unigene55070_All//3.00E-22//TC176157			GO:0005488//GO:0009314//GO:0009791//GO:0060089	nr +
Unigene55073_All	520	0.20	0.00	0.00	1.15	1.13	0.35	3.17	0.80	2.15	-7.65E+00	3.70E-01		-7.65E+00	3.91E-01		-3.02E-02	9.50E-01		-1.73E+00	9.03E-02		-1.98E+00	9.00E-05	Down	-5.64E-01	2.02E-01		Unigene55073_All//gi|33355392|gb|AAQ16126.1|//7.00E-92//homeodomain protein BNLGHI6313 [Gossypium hirsutum]	Unigene55073_All//4.00E-53//AT4G00730 ANL2 (ANTHOCYANINLESS 2); transcription factor/ transcription regulator	Unigene55073_All//0.00E+00//TC141134	HB		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231//GO:0043479//GO:0048513	nr -
Unigene55079_All	1182	0.00	8.36	1.08	0.00	0.06	0.00	0.00	0.00	0.00	1.30E+01	1.32E-56	Up	1.01E+01	4.68E-07	Up	5.87E+00	6.08E-01		null	null		null	null		null	null		Unigene55079_All//gi|116786145|gb|ABK23995.1|//6.00E-18//unknown [Picea sitchensis]						nr -
Unigene5508_All	502	2.71	10.09	5.09	7.14	8.44	6.66	7.16	9.99	11.35	1.90E+00	3.32E-10	Up	9.10E-01	2.79E-02		2.40E-01	4.83E-01		-1.02E-01	7.65E-01		4.81E-01	4.77E-02		6.65E-01	2.05E-03		Unigene5508_All//gi|2341042|gb|AAB70446.1|//1.00E-39//F19P19.26 [Arabidopsis thaliana]	Unigene5508_All//8.00E-41//AT1G04300 FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TRAF-like (InterPro:IPR008974), MATH (InterPro:IPR002083), TRAF-type (InterPro:IPR013322); BEST Arabidopsis thaliana protein match is: meprin and TRAF homology domain-containing protein / MATH domain-containing protein (TAIR:AT5G43560.2); Has 15585 Blast hits to 9972 proteins in 679 species: Archae - 16; Bacteria - 1260; Metazoa - 5683; Fungi - 2012; Plants - 671; Viruses - 109; Other Eukaryotes - 5834 (source: NCBI BLink).						nr -
Unigene55080_All	1095	0.00	0.00	0.00	0.00	0.00	0.00	23.79	1.15	0.00	null	null		null	null		null	null		null	null		-4.38E+00	3.16E-143	Down	-1.45E+01	1.91E-192	Down								ESTscan -
Unigene55082_All	595	0.00	3.41	0.98	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.53E-11	Up	9.94E+00	2.17E-03		null	null		null	null		null	null		null	null		Unigene55082_All//sp|Q9V496|APLP_DROME//2.00E-47//Apolipophorins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2						swissprot -
Unigene55084_All	447	0.12	0.00	0.12	0.89	0.39	0.20	7.85	19.54	2.76	-6.87E+00	6.10E-01		2.57E-02	9.94E-01		-1.21E+00	3.14E-01		-2.14E+00	1.26E-01		1.32E+00	1.23E-12	Up	-1.51E+00	6.97E-07	Down	Unigene55084_All//gi|37051105|dbj|BAC81649.1|//2.00E-21//glutathione S-transferase [Pisum sativum]	Unigene55084_All//4.00E-20//AT5G02790 Tn2-1 protein, putative	Unigene55084_All//2.00E-176//TC178497		ko00480|Glutathione metabolism		nr +
Unigene55086_All	532	0.00	10.95	3.60	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.96E-33	Up	1.18E+01	1.47E-10	Up	null	null		null	null		null	null		null	null		Unigene55086_All//gi|224006323|ref|XP_002292122.1|//2.00E-13//trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972641|gb|EED90973.1| trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]					GO:0016787	nr -
Unigene55089_All	581	0.00	5.06	2.75	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.01E-16	Up	1.14E+01	8.43E-09	Up	null	null		null	null		null	null		null	null		Unigene55089_All//gi|168259042|gb|ACA23209.1|//2.00E-09//serine protease [Phytophthora infestans]					GO:0003824	nr -
Unigene55090_All	280	0.93	1.45	0.38	2.31	0.00	1.45	0.00	0.00	0.00	6.32E-01	6.01E-01		-1.30E+00	4.36E-01		-1.12E+01	7.85E-05	Down	-6.72E-01	4.78E-01		null	null		null	null		Unigene55090_All//gi|297829692|ref|XP_002882728.1|//7.00E-29//initiation factor 3g [Arabidopsis lyrata subsp. lyrata] >gi|297328868|gb|EFH58987.1| initiation factor 3g [Arabidopsis lyrata subsp. lyrata]	Unigene55090_All//3.00E-30//AT3G11400 eukaryotic translation initiation factor 3G / eIF3g				GO:0006412//GO:0008135//GO:0016020//GO:0043234//GO:0046914	nr +
Unigene55095_All	477	0.00	4.04	1.56	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.73E-11	Up	1.06E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene55095_All//gi|195620650|gb|ACG32155.1|//7.00E-16//eukaryotic translation initiation factor 3 subunit 5 [Zea mays]	Unigene55095_All//2.00E-12//AT2G39990 EIF2; translation initiation factor					nr +
Unigene55097_All	462	0.00	110.66	50.71	0.00	0.15	0.00	0.00	0.00	0.00	1.68E+01	2.29E-295	Up	1.56E+01	1.40E-132	Up	7.22E+00	6.08E-01		null	null		null	null		null	null		Unigene55097_All//gi|301105188|ref|XP_002901678.1|//2.00E-48//60S ribosomal protein L32-1 [Phytophthora infestans T30-4] >gi|262100682|gb|EEY58734.1| 60S ribosomal protein L32-1 [Phytophthora infestans T30-4]	Unigene55097_All//1.00E-44//AT4G18100 60S ribosomal protein L32 (RPL32A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene551_All	4299	13.36	42.29	20.28	10.56	11.43	25.54	52.93	97.23	53.81	1.66E+00	9.45E-286	Up	6.02E-01	1.16E-25		1.15E-01	1.74E-01		1.27E+00	3.33E-125	Up	8.77E-01	1.13E-294		2.38E-02	5.28E-01		Unigene551_All//gi|223452311|gb|ACM89483.1|//0.00E+00//leucine-rich repeat family protein [Glycine max]	Unigene551_All//0.00E+00//AT5G48380| leucine-rich repeat family protein / protein kinase family protein	Unigene551_All//0.00E+00//TC166201		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0006464//GO:0016301//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene5510_All	419	3.00	6.53	3.56	9.87	19.72	23.50	2.12	3.29	3.04	1.12E+00	3.73E-03		2.48E-01	6.34E-01		9.99E-01	2.08E-07		1.25E+00	2.23E-11	Up	6.35E-01	2.25E-01		5.22E-01	3.24E-01			Unigene5510_All//5.00E-07//ESS51302					
Unigene55101_All	519	0.00	0.00	0.00	0.00	0.00	0.00	1.87	4.35	0.00	null	null		null	null		null	null		null	null		1.21E+00	1.71E-03		-1.09E+01	2.72E-07	Down	Unigene55101_All//gi|226509811|ref|NP_001147421.1|//3.00E-17//60 ribosomal protein L14 [Zea mays] >gi|195611252|gb|ACG27456.1| 60 ribosomal protein L14 [Zea mays]	Unigene55101_All//2.00E-11//AT4G27090 60S ribosomal protein L14 (RPL14B)			ko03010|Ribosome		nr -
Unigene55103_All	636	0.82	0.64	0.42	0.94	1.35	1.35	1.13	0.66	3.63	-3.68E-01	6.83E-01		-9.75E-01	3.76E-01		5.26E-01	5.45E-01		5.22E-01	5.23E-01		-7.82E-01	3.10E-01		1.68E+00	1.93E-05	Up	Unigene55103_All//gi|20177643|gb|AAM14698.1|AC097448.27//1.00E-07//Hypothetical protein [Oryza sativa Japonica Group]	Unigene55103_All//2.00E-66//AT4G38760| unknown protein					nr -
Unigene55109_All	352	0.00	0.00	0.00	0.00	0.00	0.00	0.12	2.73	2.38	null	null		null	null		null	null		null	null		4.51E+00	8.91E-06	Up	4.31E+00	4.10E-05	Up	Unigene55109_All//gi|38344471|emb|CAE85486.2|//2.00E-26//OSJNBa0022H21.6 [Oryza sativa (japonica cultivar-group)]	Unigene55109_All//4.00E-24//AT5G60900 RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene55109_All//5.00E-16//DT462365		ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene5511_All	491	48.80	34.57	8.57	31.86	30.16	22.35	36.51	21.79	20.61	-4.98E-01	7.56E-06		-2.51E+00	8.99E-63	Down	-7.91E-02	6.31E-01		-5.11E-01	2.09E-04		-7.45E-01	2.53E-10		-8.25E-01	1.49E-12		Unigene5511_All//gi|298712420|emb|CBJ33198.1|//1.00E-52//histone H4 [Ectocarpus siliculosus]	Unigene5511_All//1.00E-36//AT5G59970| histone H4	Unigene5511_All//0.00E+00//TC167201				nr -
Unigene55112_All	256	0.41	1.19	0.00	4.09	1.88	0.35	0.00	0.00	0.31	1.54E+00	3.23E-01		-8.68E+00	3.91E-01		-1.12E+00	8.44E-02		-3.53E+00	9.34E-05	Down	null	null		8.28E+00	4.03E-01									
Unigene55113_All	344	1.67	0.74	0.00	0.29	1.20	0.00	1.97	0.00	0.81	-1.18E+00	2.26E-01		-1.07E+01	2.60E-03		2.05E+00	1.47E-01		-8.18E+00	3.98E-01		-1.09E+01	6.34E-05	Down	-1.28E+00	9.48E-02		Unigene55113_All//gi|50234592|gb|AAT70497.1|//1.00E-36//S-locus-like receptor protein kinase [Prunus persica]	Unigene55113_All//2.00E-17//AT1G34300| lectin protein kinase family protein			ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0008037//GO:0030246//GO:0031410//GO:0032559	nr -
Unigene55114_All	364	0.29	3.62	0.59	0.82	0.00	0.99	0.23	0.00	0.00	3.65E+00	1.28E-05	Up	1.03E+00	5.91E-01		-9.68E+00	2.01E-02		2.74E-01	8.33E-01		-7.86E+00	4.02E-01		-7.86E+00	3.57E-01		Unigene55114_All//gi|168069792|ref|XP_001786580.1|//9.00E-13//predicted protein [Physcomitrella patens subsp. patens] >gi|162660956|gb|EDQ48608.1| predicted protein [Physcomitrella patens subsp. patens]						nr +
Unigene55116_All	1029	0.05	0.00	0.10	6.63	4.89	0.44	0.37	0.32	0.31	-5.67E+00	6.10E-01		1.03E+00	7.02E-01		-4.41E-01	4.46E-02		-3.92E+00	3.18E-31	Down	-1.87E-01	8.57E-01		-2.56E-01	7.85E-01		Unigene55116_All//gi|212717133|gb|ACJ37408.1|//1.00E-74//PK-LRR-TM resistance protein [Glycine max]	Unigene55116_All//3.00E-65//AT3G05660| ArRLP33 (Receptor Like Protein 33); kinase/ protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene55117_All	398	1.18	3.56	1.34	1.13	1.30	0.57	3.08	0.53	1.80	1.59E+00	7.37E-03		1.77E-01	8.45E-01		2.04E-01	8.59E-01		-9.89E-01	3.94E-01		-2.55E+00	8.70E-05	Down	-7.74E-01	1.40E-01				Unigene55117_All//4.00E-32//gi|109879658|gb|DW508628.1|DW508628				
Unigene55120_All	427	0.61	0.00	0.75	0.70	0.81	0.63	1.68	1.27	0.19	-9.26E+00	6.69E-02		2.88E-01	8.10E-01		2.04E-01	9.01E-01		-1.42E-01	9.20E-01		-4.04E-01	6.23E-01		-3.17E+00	8.09E-04	Down								
Unigene55121_All	444	0.24	3.54	0.96	0.11	0.85	1.32	1.52	0.66	1.62	3.91E+00	6.83E-07	Up	2.03E+00	1.39E-01		2.93E+00	8.16E-02		3.56E+00	8.48E-03		-1.21E+00	1.34E-01		8.41E-02	9.24E-01		Unigene55121_All//gi|124365538|gb|ABN09772.1|//1.00E-25//U box [Medicago truncatula]	Unigene55121_All//2.00E-08//AT3G06880| nucleotide binding				GO:0019787//GO:0032446//GO:0043231//GO:0043234	nr -
Unigene55122_All	367	3.56	0.00	4.79	0.81	0.28	0.49	0.12	0.00	0.00	-1.18E+01	1.28E-07	Down	4.26E-01	3.96E-01		-1.53E+00	2.98E-01		-7.27E-01	6.38E-01		-6.85E+00	6.55E-01		-6.85E+00	6.11E-01									
Unigene55124_All	600	0.00	0.00	0.00	0.00	0.00	0.00	2.82	4.32	0.00	null	null		null	null		null	null		null	null		6.16E-01	8.24E-02		-1.15E+01	1.70E-12	Down								
Unigene55125_All	318	0.00	3.66	3.01	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.05E-06	Up	1.16E+01	2.45E-05	Up	null	null		null	null		null	null		null	null										
Unigene55127_All	450	0.00	0.00	0.00	1.33	0.15	0.00	0.56	0.19	3.90	null	null		null	null		-3.12E+00	4.87E-03		-1.04E+01	7.70E-04	Down	-1.60E+00	3.10E-01		2.79E+00	2.72E-07	Up		Unigene55127_All//3.00E-06//AT3G50610| unknown protein					ESTscan -
Unigene55128_All	550	0.00	0.00	0.00	0.00	0.00	0.00	1.85	3.34	0.07	null	null		null	null		null	null		null	null		8.58E-01	4.63E-02		-4.67E+00	1.72E-06	Down	Unigene55128_All//gi|300266840|gb|EFJ51026.1|//6.00E-47//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene55128_All//7.00E-44//AT1G48830| 40S ribosomal protein S7 (RPS7A)			ko03010|Ribosome	GO:0003723//GO:0005840//GO:0009536	nr -
Unigene55129_All	445	0.00	0.00	0.84	0.00	0.08	0.00	0.76	3.85	1.25	null	null		9.71E+00	2.50E-02		6.27E+00	8.28E-01		null	null		2.34E+00	7.21E-06	Up	7.22E-01	3.99E-01		Unigene55129_All//gi|9759309|dbj|BAB09815.1|//2.00E-06//non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]	Unigene55129_All//3.00E-05//AT5G42905| nucleic acid binding / ribonuclease H					nr -
Unigene5513_All	452	29.86	57.51	41.70	26.78	24.07	27.18	104.39	77.21	34.55	9.45E-01	1.33E-17		4.82E-01	2.55E-04		-1.54E-01	4.16E-01		2.13E-02	9.30E-01		-4.35E-01	2.45E-10		-1.60E+00	6.25E-89	Down	Unigene5513_All//gi|20340249|gb|AAM19711.1|AF499724.1//1.00E-30//aluminum-induced protein-like protein [Thellungiella halophila]	Unigene5513_All//3.00E-32//AT3G22850| unknown protein	Unigene5513_All//0.00E+00//gi|72275883|gb|DT050356.1|DT050356				nr +
Unigene55137_All	457	0.00	0.00	0.00	0.33	0.00	0.00	2.87	10.97	0.96	null	null		null	null		-8.35E+00	1.65E-01		-8.35E+00	2.33E-01		1.94E+00	1.23E-12	Up	-1.58E+00	2.94E-03		Unigene55137_All//gi|115464331|ref|NP_001055765.1|//7.00E-22//Os03g0162000 [Oryza sativa Japonica Group] >gi|113579316|dbj|BAF17679.1| Os03g0162000 [Oryza sativa Japonica Group]	Unigene55137_All//3.00E-15//AT5G02580| unknown protein	Unigene55137_All//9.00E-52//TC157651				nr -
Unigene55139_All	228	0.00	4.89	2.10	0.00	0.91	0.40	0.00	0.73	0.35	1.23E+01	2.00E-06	Up	1.10E+01	7.47E-03		9.82E+00	1.57E-01		8.63E+00	4.75E-01		9.52E+00	1.39E-01		8.45E+00	4.03E-01									
Unigene55140_All	291	0.00	0.00	0.00	0.00	0.00	0.00	7.26	6.75	17.39	null	null		null	null		null	null		null	null		-1.06E-01	7.95E-01		1.26E+00	2.08E-07	Up			Unigene55140_All//3.00E-07//CD485591				
Unigene55141_All	497	0.53	0.61	0.86	1.00	2.01	0.91	1.19	0.76	0.00	2.17E-01	8.64E-01		7.03E-01	5.54E-01		1.00E+00	1.65E-01		-1.41E-01	8.92E-01		-6.54E-01	4.45E-01		-1.02E+01	1.41E-04	Down								
Unigene55142_All	459	1.94	0.00	0.46	0.87	0.08	0.49	0.28	0.09	2.08	-1.09E+01	2.86E-05	Down	-2.06E+00	1.78E-02		-3.53E+00	2.09E-02		-8.19E-01	5.06E-01		-1.60E+00	5.34E-01		2.91E+00	1.88E-04	Up	Unigene55142_All//gi|5080805|gb|AAD39314.1|AC007258.3//1.00E-51//Hypothetical protein [Arabidopsis thaliana]	Unigene55142_All//7.00E-53//AT1G59720| CRR28 (CHLORORESPIRATORY REDUCTION28); endonuclease				GO:0009451//GO:0009536	nr +
Unigene55143_All	512	0.00	5.94	3.02	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.67E-17	Up	1.16E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene55143_All//gi|75858825|gb|AB328989.1|//4.00E-27//Dna J-like protein 1 [Symbiodinium sp. C3]	Unigene55143_All//6.00E-20//AT4G28480| DNAJ heat shock family protein					nr +
Unigene55149_All	397	0.00	19.14	7.91	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	1.85E-43	Up	1.30E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene55149_All//gi|192910698|gb|ACF06457.1|//6.00E-33//60S ribosomal protein L35 [Elaeis guineensis]	Unigene55149_All//3.00E-27//AT5G02610| 60S ribosomal protein L35 (RPL35D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0003198 1	nr -

Unigene5515_All	429	73.54	30.47	32.89	127.15	87.01	147.49	111.56	58.36	44.30	-1.27E+00	6.54E-34	Down	-1.16E+00	2.32E-28	Down	-5.47E-01	3.69E-17		2.14E-01	1.31E-03		-9.35E-01	3.03E-38		-1.33E+00	4.68E-69	Down	Unigene5515_All//gi|1173209|sp|P46293.1|RS16_GOSHI//5.00E-54//RecName: Full=40S ribosomal protein S16 >gi|439654|emb|CAA53567.1| RS16 protein, 40S subunit [Gossypium hirsutum]	Unigene5515_All//2.00E-49//AT2G09990| 40S ribosomal protein S16 (RPS16A)	Unigene5515_All//0.00E+00//gi|109859435|gb|DW488414.1|DW488414		ko03010|Ribosome		nr +
Unigene55150_All	270	0.00	0.00	0.00	0.00	0.26	0.67	8.30	2.48	10.48	null	null		null	null		7.99E+00	6.08E-01		9.39E+00	1.94E-01		-1.74E+00	2.26E-05	Down	3.36E-01	3.25E-01									
Unigene55151_All	778	0.00	0.00	0.41	0.00	0.04	0.00	3.42	0.16	2.56	null	null		8.68E+00	4.50E-02		5.47E+00	8.28E-01		null	null		-4.41E+00	4.29E-15	Down	-4.19E-01	2.19E-01		Unigene55151_All//gi|224070883|ref|XP_002303279.1|//5.00E-84//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222840711|gb|EEE78258.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene55151_All//1.00E-77//AT3G15990| SULTR3;4 (SULFATE TRANSPORTER 3;4); sulfate transmembrane transporter	Unigene55151_All//3.00E-68//TC142582		GO:0006810//GO:0015103//GO:0016020	nr +
Unigene55152_All	287	0.18	3.35	0.56	0.87	0.60	0.47	0.00	0.00	0.56	4.20E+00	1.29E-04	Up	1.61E+00	5.11E-01		-5.33E-01	7.12E-01		-8.78E-01	6.16E-01		null	null		9.12E+00	1.40E-01				Unigene55152_All//3.00E-07//TC174739				
Unigene55157_All	505	0.00	0.00	0.00	1.78	0.75	1.25	3.35	1.24	1.18	null	null		null	null		-1.24E+00	8.17E-02		-5.04E-01	5.11E-01		-1.43E+00	2.16E-03		-1.50E+00	9.77E-04	Down	Unigene55157_All//gi|6692688|gb|AAF24822.1|AC007592_15/7.00E-76//F12K11.17 [Arabidopsis thaliana]	Unigene55157_All//4.00E-77//AT1G06490| ATGSL07 (glucan synthase-like 7); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups	Unigene55157_All//0.00E+00//C0118237			GO:0006074//GO:0031410//GO:0035251//GO:0043234	nr +
Unigene55158_All	395	0.00	0.00	0.00	0.13	0.00	0.00	0.43	4.02	1.71	null	null		null	null		-6.98E+00	5.54E-01		-6.98E+00	6.33E-01		3.23E+00	2.21E-07	Up	2.00E+00	1.69E-02				Unigene55158_All//5.00E-50//DW504452				
Unigene5516_All	519	2.62	2.44	2.26	13.15	23.42	18.36	13.44	5.48	6.29	-1.03E-01	8.47E-01		-2.16E-01	7.04E-01		8.33E-01	5.16E-08		4.82E-01	9.95E-03		-1.30E+00	4.79E-10	Down	-1.09E+00	3.65E-08	Down	Unigene5516_All//gi|255570611|ref|XP_002526262.1|//8.00E-13//conserved hypothetical protein [Ricinus communis] >gi|223534427|gb|EEF36131.1| conserved hypothetical protein [Ricinus communis]		Unigene5516_All//1.00E-11//TC143698				nr -
Unigene55160_All	910	0.00	11.08	4.04	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	8.98E-58	Up	1.20E+01	2.38E-20	Up	null	null		null	null		null	null		null	null		Unigene55160_All//gi|58613423|gb|AAW79298.1|//8.00E-43//chloroplast ATP synthase gamma subunit [Guillardia theta]	Unigene55160_All//1.00E-42//AT2G33040| ATP synthase gamma chain, mitochondrial (ATPC)			ko00190|Oxidative phosphorylation	GO:0006810//GO:0044464	nr +
Unigene55168_All	467	0.67	0.22	1.37	1.17	0.29	0.29	1.72	17.99	1.45	-1.63E+00	2.76E-01		1.03E+00	2.81E-01		-1.99E+00	5.12E-02		-2.02E+00	7.05E-02		3.39E+00	4.26E-38	Up	-2.46E-01	7.00E-01				Unigene55168_All//0.00E+00//TC164197				
Unigene55170_All	907	0.12	0.11	0.00	0.00	0.00	0.00	1.63	4.42	0.13	-4.70E-02	9.87E-01		-6.85E+00	3.91E-01		null	null		null	null		1.44E+00	5.16E-07	Up	-3.63E+00	6.55E-08	Down	Unigene55170_All//gi|7670832|gb|AAF56242.1|AF243180_1//2.00E-18//dicyanin [Solanum lycopersicum]	Unigene55170_All//4.00E-15//AT5G20230| ATBCB (ARABIDOPSIS BLUE-COPPER-BINDING PROTEIN); copper ion binding / electron carrier				nr +
Unigene55173_All	355	0.29	2.57	3.60	2.25	0.87	0.25	1.31	1.53	0.90	3.12E+00	1.14E-03		3.61E+00	3.41E-05	Up	-1.36E+00	7.74E-02		-3.14E+00	1.88E-03		2.24E-01	7.92E-01		-5.45E-01	5.65E-01				Unigene55173_All//8.00E-135//TC146220				
Unigene55174_All	449	0.12	0.00	0.95	4.77	1.53	0.91	0.38	0.19	0.09	-6.86E+00	6.10E-01		3.03E+00	5.72E-02		-1.64E+00	1.26E-04	Down	-2.40E+00	1.86E-06	Down	-1.02E+00	6.13E-01		-2.09E+00	3.13E-01									
Unigene55181_All	260	0.00	0.00	0.00	0.00	0.00	0.00	5.20	3.22	0.00	null	null		null	null		null	null		null	null		-6.95E-01	1.84E-01		-1.23E+01	4.86E-10	Down	Unigene55181_All//gi|298709870|emb|CBJ26210.1|//7.00E-33//Ribosomal protein S27 [Ectocarpus siliculosus]	Unigene55181_All//2.00E-32//AT5G47930| 40S ribosomal protein S27 (RPS27D)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0043169	nr +
Unigene55189_All	403	0.13	0.00	0.00	0.12	0.00	0.00	2.10	7.26	1.29	-7.02E+00	6.10E-01		-7.02E+00	6.22E-01		-6.95E+00	5.54E-01		-6.95E+00	6.33E-01		1.79E+00	5.49E-07	Up	-7.07E-01	2.81E-01				Unigene55189_All//5.00E-56//TC173362				
Unigene5519_All	683	6.51	9.05	15.83	31.73	37.91	48.60	28.60	115.17	38.09	4.75E-01	4.75E-02		1.28E+00	1.00E-11	Up	2.57E-01	1.64E-02		6.15E-01	1.28E-11		2.01E+00	5.10E-197	Up	4.13E-01	8.83E-06		Unigene5519_All//gi|294514718|gb|ADE95828.1|//1.00E-106//4-coumarate:CoA ligase 1 [Corchorus capsularis]	Unigene5519_All//2.00E-83//AT1G51680| 4CL1 (4-COUMARATE:COA LIGASE 1); 4-coumarate-CoA ligase	Unigene5519_All//0.00E+00//gi|109852530|gb|DW481509.1|DW481509		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene55190_All	316	0.00	1.28	0.00	0.00	1.20	0.00	2.94	1.98	0.38	1.03E+01	1.36E-02		null	null		1.02E+01	1.95E-02		null	null		-5.69E-01	4.02E-01		-2.96E+00	1.72E-04	Down								
Unigene55191_All	468	1.01	4.33	0.23	1.06	0.88	0.68	0.90	2.05	2.30	2.11E+00	4.59E-05	Up	-2.14E+00	1.03E-01		-2.70E-01	8.02E-01		-6.56E-01	5.50E-01		1.19E+00	6.64E-02		1.35E+00	2.20E-02				Unigene55191_All//7.00E-96//EX168731				
Unigene55194_All	335	0.00	0.00	0.00	0.00	0.00	0.00	7.19	1.87	4.88	null	null		null	null		null	null		null	null		-1.94E+00	1.72E-06	Down	-5.61E-01	1.12E-01		Unigene55194_All//gi|240255739|ref|NP_192257.4|//2.00E-07//protein binding [Arabidopsis thaliana]	Unigene55194_All//1.00E-08//AT4G03480| protein binding	Unigene55194_All//1.00E-40//CO091281			nr +
Unigene55195_All	492	0.00	0.21	0.00	0.20	0.91	0.28	1.89	0.00	0.24	7.69E+00	3.85E-01		null	null		2.17E+00	1.06E-01		4.44E-01	8.61E-01		-1.09E+01	1.14E-06	Down	-2.96E+00	1.72E-04	Down	Unigene55195_All//gi|32526675|dbj|BAC79198.1|//1.00E-52//Serine/threonine protein phosphatase 2A -like protein [Oryza sativa Japonica Group]	Unigene55195_All//5.00E-51//AT3G09880| ATB' BETA; protein phosphatase type 2A regulator	Unigene55195_All//2.00E-127//CA994251			GO:0006886//GO:0008287//GO:0008320//GO:0019888//GO:0023060//GO:0031224//GO:0043231	nr +
Unigene55196_All	1061	0.05	0.14	0.10	0.05	0.03	0.00	6.14	5.52	1.46	1.54E+00	5.31E-01		1.03E+00	7.02E-01		-5.32E-01	8.24E-01		-5.55E+00	6.33E-01		-1.54E-01	5.26E-01		-2.07E+00	3.35E-18	Down	Unigene55196_All//gi|11379068|gb|AB809321.1|//3.00E-17//leucine rich protein [Arachis hypogaea]		Unigene55196_All//4.00E-25//TC142190				nr +
Unigene55199_All	385	1.63	1.05	0.69	5.30	1.25	2.35	0.11	0.76	1.66	-6.31E-01	4.75E-01		-1.24E+00	2.13E-01		-2.08E+00	6.00E-06	Down	-1.18E+00	9.63E-03		2.79E+00	9.47E-02		3.91E+00	7.65E-04	Up	Unigene55199_All//gi|21554158|gb|AAM63237.1|//3.00E-08//amino acid permease-like protein [Arabidopsis thaliana]	Unigene55199_All//1.00E-09//AT5G41800| amino acid transporter family protein	Unigene55199_All//1.00E-16//DN802900			GO:0005275//GO:0016020	nr +
Unigene5520_All	1608	0.00	1.13	0.00	5.70	4.56	3.31	0.00	0.00	0.00	1.01E+01	2.14E-10	Up	null	null		-3.22E-01	9.55E-02		-7.82E-01	2.52E-05		null	null		null	null		Unigene5520_All//gi|75299757|sp|Q8HHB9.1|AMO_ARATH//0.00E+00//RecName: Full=Primary amine oxidase; AltName: Full=Amine oxidase [copper-containing]; Flags: Precursor >gi|23297202|gb|AAN12916.1| At1g62810/F23N19_18 [Arabidopsis thaliana]	Unigene5520_All//0.00E+00//AT1G62810| copper amine oxidase, putative	Unigene5520_All//3.00E-08//TC158386		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr +
Unigene55200_All	372	0.00	0.00	0.00	0.00	0.00	0.00	1.36	1.35	0.00	null	null		null	null		null	null		null	null		-1.67E-02	1.02E+00		-1.04E+01	5.54E-04	Down	Unigene55200_All//gi|300294856|gb|ADJ96635.1|//4.00E-41//S-adenosyl homocysteine hydrolase [Dunaliella salina]	Unigene55200_All//6.00E-37//AT4G13940| MEE58 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding			ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0003006//GO:0006342//GO:0010608//GO:0016020//GO:0016802//GO:0043231//GO:0046914	nr -
Unigene55208_All	451	5.22	0.90	0.83	1.22	1.68	1.10	4.97	0.74	3.36	-2.54E+00	4.62E-07	Down	-2.66E+00	5.47E-07	Down	4.67E-01	6.07E-01		-1.42E-01	8.85E-01		-2.74E+00	8.38E-09	Down	-5.66E-01	1.25E-01				Unigene55208_All//2.00E-92//gi|109888894|gb|DW517863.1|DW517863				
Unigene55210_All	292	0.72	1.74	0.00	3.58	4.95	2.17	0.29	1.29	2.87	1.28E+00	2.31E-01		-9.49E+00	1.45E-01		4.67E-01	4.44E-01		-7.26E-01	3.01E-01		2.15E+00	9.44E-02		3.31E+00	2.30E-04	Up								
Unigene55212_All	418	0.00	1.45	1.91	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	1.17E-03		1.09E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene55212_All//gi|5281040|emb|CAB45976.1|//1.00E-57//copper amine oxidase-like protein [Arabidopsis thaliana] >gi|7267930|emb|CAB78272.1| copper amine oxidase-like protein [Arabidopsis thaliana]	Unigene55212_All//5.00E-59//AT4G12290| amine oxidase/ copper ion binding / quinone binding	Unigene55212_All//6.00E-19//TC144348		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00350|Tyrosine metabolism//ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0006807//GO:0016641//GO:0031410//GO:0043231//GO:0046914//GO:0048037	nr -
Unigene55216_All	395	1.19	0.77	0.00	2.90	0.00	1.37	3.43	3.28	0.40	-6.31E-01	5.53E-01		-1.02E+01	8.63E-03		-1.15E+01	1.73E-08	Down	-1.08E+00	9.66E-02		-6.24E-02	9.17E-01		-3.09E+00	1.96E-06	Down			Unigene55216_All//9.00E-21//TC139470				
Unigene5522_All	1101	2.47	0.28	0.00	3.80	3.07	4.39	1.50	0.49	0.98	-3.16E+00	6.45E-10	Down	-1.13E+01	6.78E-15	Down	-3.10E-01	3.15E-01		2.08E-01	5.08E-01		-1.60E+00	8.96E-04	Down	-6.16E-01	1.63E-01		Unigene5522_All//gi|115476752|ref|NP_001061972.1|//2.00E-12//Os08g0459100 [Oryza sativa Japonica Group] >gi|113623941|dbj|BAF23886.1| Os08g0459100 [Oryza sativa Japonica Group]	Unigene5522_All//1.00E-23//AT2G06040| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: Leucine-rich repeat, cysteine-containing subtype (InterPro:IPR006553); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G21900.1); Has 3642 Blast hits to 1885 proteins in 175 species: Archae - 0; Bacteria - 109; Metazoa - 2066; Fungi - 492; Plants - 697; Viruses - 0; Other Eukaryotes - 278 (source: NCBI BLink).					nr +
Unigene55222_All	1570	0.00	0.00	0.00	0.00	0.00	0.00	0.67	7.53	18.02	null	null		null	null		null	null		null	null		3.48E+00	9.49E-55	Up	4.74E+00	3.28E-165	Up	Unigene55222_All//gi|269996964|gb|ACZ57767.1|//1.00E-177//phospholipase A1 [Nicotiana attenuata]	Unigene55222_All//1.00E-156//AT4G16820| lipase class 3 family protein	Unigene55222_All//0.00E+00//gi|78333850|gb|DT554124.1|DT554124			GO:0004091//GO:0044238	nr -
Unigene55225_All	494	0.00	3.38	2.48	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.54E-09	Up	1.13E+01	9.11E-07	Up	null	null		null	null		null	null		null	null		Unigene55225_All//gi|192910824|gb|ACF06520.1|//1.00E-52//60S ribosomal protein L7 [Elaeis guineensis]	Unigene55225_All//4.00E-47//AT2G44120| 60S ribosomal protein L7 (RPL7C)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr +
Unigene55227_All	1834	0.43	0.28	0.06	0.19	0.11	0.10	15.95	13.61	6.54	-6.31E-01	4.08E-01		-2.88E+00	6.34E-03		-7.54E-01	5.67E-01		-9.49E-01	4.81E-01		-2.30E-01	1.34E-02		-1.29E+00	2.34E-40	Down	Unigene55227_All//gi|297811191|ref|XP_002873479.1|//0.00E+00//integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319316|gb|EFH49738.1| integral membrane transporter family protein [Arabidopsis lyrata subsp. lyrata]	Unigene55227_All//3.00E-179//AT5G10820| integral membrane transporter family protein				GO:0044464//GO:0051234	nr +
Unigene55228_All	388	0.00	0.00	0.00	1.03	0.36	0.47	5.45	4.85	0.10	null	null		null	null		-1.53E+00	2.05E-01		-1.14E+00	3.79E-01		-1.69E-01	6.82E-01		-5.73E+00	3.61E-14	Down			Unigene55228_All//8.00E-15//TC137293				
Unigene5523_All	467	1.57	1.74	3.19	4.05	3.24	3.87	1.09	2.15	0.00	1.46E-01	8.39E-01		1.03E+00	7.47E-02		-3.21E-01	5.32E-01		-6.74E-02	9.03E-01		9.83E-01	1.16E-01		-1.01E+01	5.54E-04	Down								
Unigene55231_All	321	2.77	1.10	0.33	4.50	2.04	0.84	0.53	0.13	0.99	-1.33E+00	7.96E-02		-3.06E+00	2.25E-03		-1.14E+00	3.09E-02		-2.41E+00	1.41E-04	Down	-2.02E+00	3.67E-01		9.14E-01	4.52E-01									
Unigene55234_All	203	12.63	15.73	8.13	15.46	17.30	28.25	656.07	505.46	1376.30	3.16E-01	3.77E-01		-6.35E-01	1.30E-01		1.63E-01	6.74E-01		8.70E-01	4.01E-04		-3.76E-01	2.66E-21		1.07E+00	1.97E-279	Up	Unigene55234_All//gi|61354279|gb|AAX44033.1|//2.00E-32//(+)-delta-cadinene synthase [Gossypium hirsutum]	Unigene55234_All//3.00E-08//AT1G70080| terpene synthase/cyclase family protein	Unigene55234_All//2.00E-94//gi|48791700|gb|CO093014.1|CO093014		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0010334//GO:0046872	nr -
Unigene55236_All	272	8.66	9.13	20.75	20.51	22.91	26.40	0.00	0.15	0.00	7.66E-02	8.47E-01		1.26E+00	2.68E-06	Up	1.60E-01	5.73E-01		3.64E-01	1.16E-01		7.26E+00	6.33E-01		null	null		Unigene55236_All//gi|229893912|gb|ACQ90301.1|//7.00E-34//squalene epoxidase [Gynostemma pentaphyllum]	Unigene55236_All//1.00E-33//AT4G37760| SQE3 (squalene epoxidase 3); squalene monooxygenase	Unigene55236_All//2.00E-147//TC134279		ko00100|Steroid biosynthesis	GO:0004497//GO:0006694//GO:0006950//GO:0009719//GO:0030554//GO:0032124//GO:0031410//GO:0043231	nr +
Unigene55238_All	201	25.77	35.04	37.35	69.64	88.92	105.38	64.58	92.32	291.95	4.43E-01	4.69E-02		5.36E-01	1.61E-02		3.53E-01	5.81E-03		5.98E-01	2.72E-07		5.16E-01	6.27E-06		2.18E+00	4.53E-166	Up	Unigene55238_All//gi|224551852|gb|ACN54324.1|//1.00E-30//NADPH:cytochrome P450 reductase [Gossypium hirsutum]	Unigene55238_All//9.00E-21//AT4G30210| ATR2 (ARABIDOPSIS P450 REDUCTASE 2); NADPH-hemoprotein reductase	Unigene55238_All//5.00E-110//gi|13351588|gb|BG441936.1|BG441936			GO:0000166//GO:0006575//GO:0009536//GO:0016020//GO:0016653//GO:0046914	nr +
Unigene55239_All	201	40.09	34.03	39.47	41.39	40.09	54.38	55.95	28.28	25.77	-2.36E-01	2.76E-01		-2.22E-02	9.35E-01		-4.60E-02	8.30E-01		3.94E-01	2.52E-02		-9.84E-01	2.11E-10		-1.12E+00	4.86E-13	Down	Unigene55239_All//gi|297791703|ref|XP_002863736.1|//1.00E-29//20S proteasome subunit PAF1 [Arabidopsis lyrata subsp. lyrata] >gi|297309571|gb|EFH39995.1| 20S proteasome subunit PAF1 [Arabidopsis lyrata subsp. lyrata]	Unigene55239_All//5.00E-31//AT5G42790| PAF1; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene55239_All//5.00E-110//gi|21099443|gb|BQ411756.1|BQ411756		ko03050|Proteasome	GO:0004175//GO:0005839//GO:0010035//GO:0016020//GO:0019941//GO:0043234	nr +
Unigene55241_All	203	35.83	103.59	68.73	58.89	99.91	103.01	34.57	92.86	106.76	1.53E+00	6.56E-30	Up	9.40E-01	2.56E-09		7.63E-01	2.70E-11		8.07E-01	9.69E-12		1.43E+00	1.16E-29	Up	1.63E+00	5.20E-42	Up	Unigene55241_All//gi|297830310|ref|XP_002883037.1|//1.00E-30//ubiquitin-conjugating enzyme 31 [Arabidopsis lyrata subsp. lyrata] >gi|297328877|gb|EFH59296.1| ubiquitin-conjugating enzyme 31 [Arabidopsis lyrata subsp. lyrata]	Unigene55241_All//5.00E-32//AT3G17000| UBC32 (ubiquitin-conjugating enzyme 32); ubiquitin-protein ligase	Unigene55241_All//3.00E-111//gi|21092008|gb|BQ404321.1|BQ404321		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0006464//GO:0019787//GO:0019941//GO:0060255	nr +

Unigene55244_All	209	22.78	15.27	11.21	37.66	31.63	31.98	36.21	22.20	24.78	-5.77E-01	3.67E-02		-1.02E+00	4.28E-04	Down	-2.52E-01	2.60E-01		-2.36E-01	3.10E-01		-7.06E-01	1.78E-04		-5.47E-01	2.79E-03		Unigene55244_All//gi|115454963|ref|NP_001051082.1|//2.00E-16//0s03g0717600 [Oryza sativa Japonica Group] >gi|113549553|dbj|BAF12996.1|0s03g0717600 [Oryza sativa Japonica Group]	Unigene55244_All//2.00E-08//AT5G06160| ATO (ATROPOS); nucleic acid binding / zinc ion binding	Unigene55244_All//9.00E-115//TC136413		ko03040|Spliceosome	GO:0043231//GO:0044444//GO:0045595//GO:0046914	nr -
Unigene55247_All	212	13.08	13.38	9.54	15.27	39.31	21.52	16.95	12.22	19.17	3.32E-02	9.46E-01		-4.55E-01	2.54E-01		1.36E+00	7.58E-12	Up	4.94E-01	9.12E-02		-4.72E-01	1.13E-01		1.77E-01	5.53E-01		Unigene55247_All//gi|229609837|gb|ACQ83534.1|//7.00E-33//CBL-interacting protein kinase 18 [Vitis vinifera]	Unigene55247_All//8.00E-33//AT2G26980| CIPK3 (CBL-INTERACTING PROTEIN KINASE 3); kinase/ protein kinase/ protein serine/threonine kinase	Unigene55247_All//1.00E-116//TC133839		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0009755//GO:0023060//GO:0032559//GO:0043231	nr +
Unigene55248_All	215	31.88	64.34	43.84	34.06	38.92	41.80	102.85	64.93	38.36	1.01E+00	8.11E-11	Up	4.60E-01	1.97E-02		1.93E-01	4.08E-01		2.96E-01	1.54E-01		-6.64E-01	2.13E-10		-1.42E+00	1.07E-35	Down	Unigene55248_All//gi|192912956|gb|ACF06586.1|//7.00E-28//aluminum-induced protein [Elaeis guineensis]	Unigene55248_All//2.00E-26//AT5G43830| unknown protein	Unigene55248_All//2.00E-118//TC163020			GO:0031410//GO:0043231	nr +
Unigene55253_All	224	21.26	28.05	21.87	26.02	30.28	34.88	79.46	56.54	38.95	4.00E-01	9.58E-02		4.12E-02	8.92E-01		2.19E-01	3.95E-01		4.23E-01	4.81E-02		-4.91E-01	2.62E-05		-1.03E+00	1.16E-17	Down	Unigene55253_All//gi|3169287|gb|AAC17840.1|//1.00E-34//vacuolar H+-ATPase catalytic subunit [Gossypium hirsutum]	Unigene55253_All//5.00E-34//AT1G78900| VHA-A (VACUOLAR ATP SYNTHASE SUBUNIT A); ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism / hydrolase, acting on acid anhydrides, catalyzing transmembrane movement of substances / proton-transporting ATPase, rotational mechanism	Unigene55253_All//3.00E-121//gi|21096416|gb|BQ408729.1|BQ408729		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0015078//GO:0015986//GO:0019829//GO:0032559//GO:0033176	nr -
Unigene55254_All	228	31.90	739.82	120.28	75.81	128.98	300.30	65.65	204.21	237.28	4.54E+00	0.00E+00	Up	1.91E+00	1.77E-51	Up	7.67E-01	2.45E-16		1.99E+00	7.62E-148	Up	1.64E+00	2.65E-88	Up	1.85E+00	2.77E-124	Up			Unigene55254_All//4.00E-83//TC162170				
Unigene55255_All	229	76.54	64.61	30.00	119.86	126.91	125.63	23.26	71.00	53.23	-2.45E-01	7.85E-02		-1.35E+00	3.94E-20	Down	8.25E-02	5.23E-01		6.78E-02	6.19E-01		1.61E+00	1.39E-30	Up	1.19E+00	2.21E-15	Up			Unigene55255_All//3.00E-87//TC151939				
Unigene5526_All	507	7.22	4.60	12.18	10.81	11.21	6.41	6.25	2.47	7.78	-6.52E-01	4.21E-02		7.54E-01	2.26E-03		5.23E-02	8.59E-01		-7.53E-01	2.69E-03		-1.34E+00	3.28E-05	Down	3.15E-01	2.59E-01		Unigene5526_All//gi|224114089|ref|XP_002316664.1|//2.00E-60//f-box family protein [Populus trichocarpa] >gi|222859729|gb|EEE97276.1| f-box family protein [Populus trichocarpa]	Unigene5526_All//3.00E-39//AT3G62980| TIR1 (TRANSPORT INHIBITOR RESPONSE 1); auxin binding / protein binding / ubiquitin-protein ligase	Unigene5526_All//0.00E+00//TC140012		ko04626|Plant-pathogen interaction		nr -
Unigene55262_All	253	13.03	26.84	15.79	22.45	27.36	19.81	56.49	64.59	48.03	1.04E+00	5.93E-06	Up	2.77E-01	3.89E-01		2.86E-01	2.36E-01		-1.80E-01	5.39E-01		1.94E-01	1.49E-01		-2.34E-01	8.37E-02		Unigene55262_All//gi|22330577|ref|NP_177343.2|//2.00E-33//protease-associated zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene55262_All//8.00E-35//AT1G71980| protease-associated zinc finger (C3HC4-type RING finger) family protein	Unigene55262_All//2.00E-131//TC140581			GO:0016787//GO:0019538//GO:0031410//GO:0046914	nr -
Unigene55263_All	256	36.38	12.07	17.47	41.25	57.84	53.98	0.33	0.33	0.00	-1.59E+00	1.81E-14	Down	-1.06E+00	1.14E-07	Down	4.88E-01	4.08E-04		3.88E-01	1.11E-02		-1.67E-02	1.01E+00		-8.37E+00	3.57E-01		Unigene55263_All//gi|297825869|ref|XP_002880817.1|//4.00E-32//nitrate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326656|gb|EFH57076.1| nitrate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene55263_All//5.00E-26//AT2G26690| nitrate transporter (NTP2)	Unigene55263_All//1.00E-114//ES826513			GO:0005488//GO:0006950//GO:0009719//GO:0010035//GO:0015103//GO:0015698//GO:0015833//GO:0031224	nr +
Unigene55264_All	257	33.39	31.55	69.00	43.03	46.90	57.46	164.51	28.62	63.25	-8.19E-02	6.88E-01		1.05E+00	7.95E-14	Up	1.24E-01	5.48E-01		4.17E-01	4.18E-03		-2.52E+00	9.39E-141	Down	-1.38E+00	2.30E-64	Down	Unigene55264_All//gi|197259944|gb|ACH56521.1|//3.00E-43//chalcone synthase [Gossypium hirsutum]	Unigene55264_All//2.00E-37//AT5G13930| TT4 (TRANSPARENT TESTA 4); naringenin-chalcone synthase	Unigene55264_All//3.00E-143//BE052384		ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant	GO:0009699//GO:0016747	nr +
Unigene55266_All	269	42.98	56.13	35.24	25.74	38.66	45.50	46.84	82.66	117.29	3.85E-01	8.12E-03		-2.87E-01	1.17E-01		5.87E-01	4.84E-04		8.22E-01	2.40E-07		8.20E-01	1.04E-14		1.32E+00	5.41E-45	Up	Unigene55266_All//gi|18404463|ref|NP_565864.1|//2.00E-40//SLT1 (sodium- and lithium-tolerant 1) [Arabidopsis thaliana] >gi|3236240|gb|AAC23628.1| expressed protein [Arabidopsis thaliana] >gi|116111669|gb|AAG39003.1| SLT1 protein [Arabidopsis thaliana] >gi|15451174|gb|AAK96858.1| Unknown protein [Arabidopsis thaliana]	Unigene55266_All//9.00E-42//AT2G37570| SLT1 (sodium- and lithium-tolerant 1)	Unigene55266_All//4.00E-148//gi|78324913|gb|DT545187.1|DT545187			GO:0006972	nr -
Unigene55269_All	315	9.97	3.70	11.66	0.32	0.00	0.00	0.00	0.27	0.25	-1.43E+00	1.00E-04	Down	2.27E-01	5.19E-01		-8.31E+00	3.12E-01		-8.31E+00	3.98E-01		8.05E+00	4.00E-01		7.98E+00	4.03E-01				Unigene55269_All//5.00E-105//gi|164355198|gb|EX166982.1|EX166982				
Unigene5527_All	640	2.86	0.79	2.50	26.93	21.79	8.47	4.43	1.24	2.18	-1.85E+00	4.25E-04	Down	-1.97E-01	6.80E-01		-3.06E-01	2.02E-02		-1.67E+00	3.25E-30	Down	-1.83E+00	5.23E-07	Down	-1.02E+00	1.59E-03		Unigene5527_All//gi|156739648|gb|AB393485.1|//5.00E-50//xyloglucan endotraglucosylase/hydrolase [Vigna angularis]	Unigene5527_All//3.00E-46//AT2G36870| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene5527_All//0.00E+00//gi|109889534|gb|DW518502.1|DW518502				nr +
Unigene55271_All	236	0.67	4.51	0.00	1.06	1.02	0.38	0.54	0.89	0.84	2.76E+00	8.45E-04	Up	-9.38E+00	2.44E-01		-4.72E-02	9.51E-01		-1.46E+00	4.06E-01		7.20E-01	6.31E-01		6.51E-01	6.65E-01								
Unigene55274_All	203	0.00	20.97	6.30	0.00	0.17	0.00	0.00	0.00	0.00	1.44E+01	3.04E-24	Up	1.26E+01	4.68E-07	Up	7.41E+00	8.28E-01		null	null		null	null		null	null		Unigene55274_All//gi|224010946|ref|XP_002294430.1|//7.00E-09//rRNA intron-encoded homing endonuclease [Thalassiosira pseudonana CCMP1335] >gi|220969925|gb|EED88264.1| rRNA intron-encoded homing endonuclease [Thalassiosira pseudonana CCMP1335]		Unigene55274_All//2.00E-29//DV849020				nr -
Unigene55275_All	206	84.32	109.46	101.85	30.23	26.58	20.83	80.25	30.43	36.16	3.76E-01	1.17E-03		2.72E-01	3.57E-02		-1.86E-01	4.97E-01		-5.37E-01	2.37E-02		-1.40E+00	1.89E-25	Down	-1.15E+00	1.48E-19	Down	Unigene55275_All//gi|134142800|gb|AB061734.1|//9.00E-34//mitochondrial glycine decarboxylase complex P-protein [Populus tremuloides]	Unigene55275_All//4.00E-32//AT4G33010| AtGLDP1 (Arabidopsis thaliana glycine decarboxylase P-protein 1); catalytic/ glycine dehydrogenase (decarboxylating)/ pyridoxal phosphate binding	Unigene55275_All//8.00E-106//EX169140		ko00260|Glycine, serine and threonine metabolism	GO:0006546//GO:0016628//GO:0016642//GO:0048037	nr -
Unigene55277_All	206	42.67	37.14	10.86	51.02	54.16	47.58	101.60	42.61	41.00	-2.00E-01	3.49E-01		-1.97E+00	2.05E-17	Down	8.61E-02	6.86E-01		-1.01E-01	6.24E-01		-1.25E+00	3.67E-27	Down	-1.31E+00	6.93E-30	Down	Unigene55277_All//gi|15236497|ref|NP_193178.1|//3.00E-20//lesion inducing protein-related [Arabidopsis thaliana] >gi|2241798|emb|CAB10221.1| elicitor like protein [Arabidopsis thaliana] >gi|7268148|emb|CAB78484.1| elicitor like protein [Arabidopsis thaliana] >gi|15010600|gb|AAK73959.1| AT4g14420/d13250c [Arabidopsis thaliana] >gi|19699242|gb|AAL90987.1| AT4g14420/d13250c [Arabidopsis thaliana] >gi|21553825|gb|AAM62918.1| elicitor like protein [Arabidopsis thaliana]	Unigene55277_All//1.00E-13//AT4G14420| lesion inducing protein-related	Unigene55277_All//5.00E-113//BQ402658			GO:0031410	nr +
Unigene55279_All	212	56.02	54.02	51.74	152.03	125.40	114.40	339.44	364.14	164.05	-5.26E-02	7.62E-01		-1.15E-01	5.58E-01		-2.78E-01	2.34E-03		-4.10E-01	8.74E-06		1.01E-01	8.73E-02		-1.05E+00	6.95E-71	Down			Unigene55279_All//1.00E-116//gi|21091427|gb|BQ403740.1|BQ403740				
Unigene5528_All	375	20.37	31.35	29.39	28.69	34.44	36.49	55.58	44.14	21.46	6.22E-01	1.67E-04		5.29E-01	3.01E-03		2.63E-01	1.10E-01		3.47E-01	2.63E-02		-3.33E-01	2.24E-03		-1.37E+00	5.77E-32	Down	Unigene5528_All//gi|297828738|ref|XP_002882251.1|//4.00E-32//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328091|gb|EFH58510.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5528_All//1.00E-32//AT3G02790| zinc finger (C2H2 type) family protein	Unigene5528_All//3.00E-159//TC154220				nr +
Unigene55281_All	218	52.80	35.56	26.14	42.05	43.75	76.86	230.02	113.50	83.88	-5.70E-01	6.30E-04		-1.01E+00	9.50E-09	Down	5.75E-02	8.28E-01		8.70E-01	9.22E-11		-1.02E+00	4.50E-46	Down	-1.46E+00	1.43E-82	Down	Unigene55281_All//gi|209967449|gb|ACJ02353.1|//2.00E-28//60S ribosomal protein L27A [Vernicia fordii]	Unigene55281_All//1.00E-29//AT1G70600| structural constituent of ribosome	Unigene55281_All//4.00E-120//TC171217		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0031981	nr +
Unigene55284_All	226	0.46	7.62	1.41	0.88	2.29	1.20	0.19	1.29	0.35	4.04E+00	1.14E-07	Up	1.61E+00	3.04E-01		1.37E+00	2.26E-01		4.44E-01	7.63E-01		2.79E+00	9.47E-02		9.14E-01	7.49E-01				Unigene55284_All//3.00E-07//TC146077				
Unigene55286_All	227	105.56	49.33	45.51	126.84	119.23	135.29	206.37	89.67	97.40	-1.10E+00	1.10E-20	Down	-1.21E+00	3.24E-23	Down	-8.92E-02	4.67E-01		9.31E-02	4.40E-01		-1.20E+00	4.48E-56	Down	-1.08E+00	6.53E-49	Down	Unigene55286_All//gi|209967449|gb|ACJ02353.1|//4.00E-41//60S ribosomal protein L27A [Vernicia fordii]	Unigene55286_All//2.00E-42//AT1G70600| structural constituent of ribosome	Unigene55286_All//2.00E-125//gi|11204216|gb|BF273146.1|BF273146		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934	nr +
Unigene55287_All	230	11.15	9.25	18.98	7.36	12.88	17.87	11.40	8.72	7.62	-2.69E-01	5.10E-01		7.68E-01	1.11E-02		8.06E-01	2.44E-02		1.28E+00	2.87E-05	Up	-3.86E-01	2.96E-01		-5.81E-01	8.46E-02		Unigene55287_All//gi|18396344|ref|NP_564284.1|//3.00E-12//APT1 (ADENINE PHOSPHORIBOSYL TRANSFERASE 1); adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|38503396|sp|P31166.2|APT1_ARATH RecName: Full=Adenine phosphoribosyltransferase 1; Short=APRT 1 >gi|21536559|gb|AAM60891.1| adenine phosphoribosyltransferase 1, APRT [Arabidopsis thaliana]	Unigene55287_All//1.00E-13//AT1G27450| APT1 (ADENINE PHOSPHORIBOSYL TRANSFERASE 1); adenine phosphoribosyltransferase	Unigene55287_All//5.00E-95//TC173566		ko00230|Purine metabolism	GO:0005618//GO:0009536//GO:0010038//GO:0016020//GO:0016763//GO:0043096	nr +
Unigene55288_All	231	0.91	10.31	2.07	0.22	2.24	1.56	0.18	1.09	0.69	3.51E+00	2.01E-09	Up	1.20E+00	3.02E-01		3.37E+00	1.82E-02		2.86E+00	9.44E-02		2.57E+00	1.53E-01		1.91E+00	3.77E-01				Unigene55288_All//3.00E-07//TC143048				
Unigene55297_All	301	32.68	21.38	13.80	464.38	152.27	135.34	1052.23	554.59	551.39	-6.12E-01	7.80E-04		-1.24E+00	3.05E-10	Down	-1.61E+00	8.09E-265	Down	-1.78E+00	5.10E-265	Down	-9.24E-01	5.04E-244		-9.32E-01	1.96E-254				Unigene55297_All//1.00E-120//ES806863				
Unigene55299_All	224	15.65	12.67	9.03	53.15	32.13	46.37	208.38	158.41	48.91	-3.05E-01	3.66E-01		-7.93E-01	2.15E-02		-7.26E-01	1.48E-06		-1.97E-01	2.94E-01		-3.96E-01	1.04E-08		-2.09E+00	2.28E-127	Down	Unigene55299_All//gi|211906506|gb|ACJ11746.1|//1.00E-34//luminal binding protein [Gossypium hirsutum]	Unigene55299_All//9.00E-36//AT5G28540| BIP1; ATP binding	Unigene55299_All//3.00E-121//EV498779		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0000741//GO:0006950//GO:0009536//GO:0016020//GO:0016628//GO:0030012//GO:0032559//GO:0043161//GO:0044432	nr -
Unigene553_All	1090	2.06	0.79	0.88	7.31	7.74	5.93	2.33	0.92	0.99	-1.39E+00	1.73E-03		-1.23E+00	6.96E-03		8.20E-02	7.60E-01		-3.04E-01	1.71E-01		-1.34E+00	2.52E-04	Down	-1.24E+00	4.29E-04	Down	Unigene553_All//gi|297848308|ref|XP_002892035.1|//1.00E-102//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337877|gb|EFH68294.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene553_All//8.00E-103//AT1G01950| armadillo/beta-catenin repeat family protein / kinesin motor family protein	Unigene553_All//0.00E+00//ES815273			GO:0003774//GO:0004702//GO:0006468//GO:0007017//GO:0008104//GO:0015630//GO:0016020//GO:0032559//GO:0043231//GO:0044444//GO:0048513	nr +
Unigene55302_All	328	18.66	36.15	26.30	48.60	42.10	101.62	5.16	9.17	3.77	9.54E-01	1.43E-08		4.95E-01	1.64E-02		-2.07E-01	1.65E-01		1.06E+00	7.23E-29	Up	8.31E-01	9.66E-03		-4.54E-01	3.11E-01		Unigene55302_All//gi|240255895|ref|NP_193331.6|//5.00E-32//catalytic/ epoxide hydrolase [Arabidopsis thaliana]	Unigene55302_All//2.00E-33//AT4G15960| catalytic/ epoxide hydrolase	Unigene55302_All//6.00E-157//TC149045			GO:0006950//GO:0009725//GO:0016803	nr -
Unigene55306_All	203	60.83	50.42	43.54	79.75	55.98	53.40	55.61	26.15	24.92	-2.71E-01	1.08E-01		-4.82E-01	4.06E-03		-5.11E-01	6.74E-05		-5.79E-01	1.69E-05		-1.09E+00	3.66E-12	Down	-1.16E+00	8.91E-14	Down	Unigene55306_All//gi|47027061|gb|AT08745.1|//1.00E-28//HUELLENLOS-like protein [Hyacinthus orientalis]	Unigene55306_All//3.00E-18//AT5G46160| ribosomal protein L14 family protein / huellenlos paralog (HLP)	Unigene55306_All//3.00E-111//TC172867		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene55307_All	206	48.77	73.30	35.67	92.86	123.20	137.68	124.38	103.88	287.57	5.88E-01	4.26E-05		-4.51E-01	1.77E-02		4.08E-01	6.13E-05		5.68E-01	8.93E-09		-2.60E-01	8.64E-03		1.21E+00	9.08E-73	Up	Unigene55307_All//gi|110931706|gb|AB802852.1|//2.00E-06//MYB transcription factor MYB112 [Glycine max]	Unigene55307_All//7.00E-07//AT5G67300| MYBR1 (MYB DOMAIN PROTEIN R1); DNA binding / transcription factor	Unigene55307_All//3.00E-105//gi|73863986|gb|DT466725.1|DT466725	MYB			nr +

Unigene55312_All	215	29.20	26.16	17.09	36.38	45.81	40.54	34.81	21.00	14.64	-1.59E-01	5.38E-01		-7.73E-01	1.61E-03		3.33E-01	7.61E-02		1.56E-01	5.00E-01		-7.29E-01	1.21E-04		-1.25E+00	1.59E-10	Down	Unigene55312_All//gi|222136859|gb|ACM45079.1|//1.00E-31//chorismate synthase [Vitis vinifera]	Unigene55312_All//1.00E-30//AT1G48850| EMB1144 (embryo defective 1144); chorismate synthase	Unigene55312_All//1.00E-113//TC154512		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0003006//GO:0008652//GO:0009536//GO:0016838//GO:0031981	nr +
Unigene55313_All	218	118.80	71.12	57.16	153.78	123.84	184.59	216.64	110.62	110.93	-7.40E-01	7.40E-12		-1.06E+00	4.00E-20	Down	-3.12E-01	3.66E-04		2.63E-01	1.87E-03		-9.70E-01	4.54E-40		-9.66E-01	5.93E-41		Unigene55313_All//gi|247421866|gb|ACS96446.1|//1.00E-36//60S ribosomal protein L18a [Jatropha curcas]	Unigene55313_All//4.00E-37//AT3G14600| 60S ribosomal protein L18A (RPL18aC)	Unigene55313_All//4.00E-120//TC143573		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr -
Unigene55314_All	220	12.37	23.49	24.69	39.85	50.09	74.52	185.07	339.69	440.76	9.26E-01	4.87E-04		9.97E-01	2.03E-04		3.30E-01	5.91E-02		9.03E-01	3.53E-11		8.76E-01	3.88E-53		1.25E+00	3.36E-125	Up	Unigene55314_All//gi|58531952|gb|AW78691.1|//2.00E-29//peroxisomal acyl-CoA oxidase 1A [Solanum cheesmaniae]	Unigene55314_All//8.00E-30//AT4G16760| ACX1 (ACYL-COA OXIDASE 1); acyl-CoA oxidase	Unigene55314_All//9.00E-112//TC137718		ko01146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids	GO:0006952//GO:0009062//GO:0009694//GO:0010038//GO:0015002//GO:0016634//GO:0030554//GO:0042579//GO:0048229//GO:0051707	nr -
Unigene55317_All	232	0.00	6.77	5.74	0.00	0.15	0.00	0.00	0.00	0.00	1.27E+01	5.70E-09	Up	1.25E+01	2.39E-07	Up	7.21E+00	8.28E-01		null	null		null	null		null	null		Unigene55317_All//gi|258594255|dbj|BA139619.1|//7.00E-37//beta actin [Kandelia candel]	Unigene55317_All//8.00E-38//AT5G59370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene55317_All//2.00E-51//TC153744		ko04145|Phagosome	GO:0032559//GO:0043232	nr -
Unigene55319_All	236	0.00	3.65	1.81	2.53	0.88	1.53	0.18	0.35	0.34	1.18E+01	4.94E-05	Up	1.08E+01	1.38E-02		-1.53E+00	1.01E-01		-7.26E-01	4.60E-01		9.83E-01	7.31E-01		9.14E-01	7.49E-01				Unigene55319_All//7.00E-08//TC153096				
Unigene55320_All	239	20.80	48.97	27.18	25.43	24.35	32.50	90.93	187.82	76.84	1.24E+00	1.85E-12	Up	3.86E-01	1.21E-01		-6.25E-02	8.14E-01		3.54E-01	1.09E-01		1.05E+00	4.46E-43	Up	-2.43E-01	2.17E-02		Unigene55320_All//gi|167961942|dbj|BAG09369.1|//2.00E-37//peroxisomal acyl-CoA oxidase [Glycine max]	Unigene55320_All//2.00E-37//AT3G51840| ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase	Unigene55320_All//1.00E-132//TC137877		ko01146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation	GO:0003006//GO:0009062//GO:0016634//GO:0030554//GO:0042579	nr -
Unigene55321_All	242	0.00	46.27	14.96	0.00	0.57	0.00	0.00	0.00	0.00	1.55E+01	3.34E-64	Up	1.39E+01	4.74E-20	Up	9.15E+00	3.18E-01		null	null		null	null		null	null		Unigene55321_All//gi|157093615|gb|ABV22462.1|//2.00E-32//ribosomal protein S23e [Oxyrrhis marina]	Unigene55321_All//3.00E-24//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene55321_All//2.00E-26//DV850314		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene55324_All	249	0.00	27.67	8.77	0.00	0.00	0.00	0.00	0.00	0.00	1.48E+01	2.25E-39	Up	1.31E+01	4.94E-12	Up	null	null		null	null		null	null		null	null		Unigene55324_All//gi|159473469|ref|XP_001694856.1|//1.00E-12//acidic ribosomal protein P2 [Chlamydomonas reinhardtii] >gi|158276235|gb|EDP02008.1| acidic ribosomal protein P2 [Chlamydomonas reinhardtii]	Unigene55324_All//5.00E-11//AT2G27710| 60S acidic ribosomal protein P2 (RPP2B)			ko03010|Ribosome	GO:0043231	nr -
Unigene55325_All	254	0.00	6.58	4.61	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.54E-09	Up	1.22E+01	1.77E-06	Up	null	null		null	null		null	null		null	null										
Unigene55327_All	368	0.00	20.10	11.14	0.00	0.19	0.00	0.00	0.00	0.00	1.43E+01	2.72E-42	Up	1.34E+01	9.63E-23	Up	7.55E+00	6.08E-01		null	null		null	null		null	null		Unigene55327_All//gi|109389998|gb|ABG29728.1|//3.00E-65//chloroplast chlorophyll a/b binding protein [Brassica napus]	Unigene55327_All//2.00E-65//AT1G29930| CAB1 (CHLOROPHYLL A/B BINDING PROTEIN 1); chlorophyll binding	Unigene55327_All//1.00E-35//TC135920		ko00196|Photosynthesis - antenna proteins	GO:0005576//GO:0006091//GO:0006464//GO:0009521//GO:0009526//GO:0009534//GO:0009570//GO:0009639//GO:0031224//GO:0043169//GO:0046906	nr +
Unigene55328_All	632	0.08	69.51	24.69	0.00	0.16	0.00	0.20	0.40	0.00	9.71E+00	4.90E-251	Up	8.22E+00	8.14E-86	Up	7.35E+00	4.55E-01		null	null		9.83E-01	5.17E-01		-7.65E+00	1.99E-01		Unigene55328_All//gi|157011451|gb|ABV00887.1|//1.00E-116//actin [Rhodomonas sp. CCMP768]	Unigene55328_All//3.00E-113//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene55328_All//6.00E-103//TC153744		ko04145|Phagosome		nr +
Unigene5533_All	524	28.66	268.14	78.66	35.08	80.11	63.35	74.72	106.56	71.85	3.23E+00	0.00E+00	Up	1.46E+00	2.07E-52	Up	1.19E+00	1.36E-47	Up	8.53E-01	4.62E-20		5.12E-01	5.41E-16		-5.65E-02	5.43E-01		Unigene5533_All//gi|60317458|gb|AAX18706.1|//7.00E-47//cold-related protein Cor413 [Gossypium barbadense] >gi|115432869|gb|ABI97481.1| COR413-like protein [Gossypium barbadense]	Unigene5533_All//2.00E-34//AT3G50830| COR413-PM2 (COLD-REGULATED 413-PLASMA MEMBRANE 2)	Unigene5533_All//0.00E+00//gi|109875537|gb|DW504511.1|DW504511			nr +
Unigene55331_All	242	5.19	13.40	1.98	6.79	7.26	7.65	42.45	57.69	29.30	1.37E+00	1.42E-04	Up	-1.39E+00	3.39E-02		9.54E-02	8.67E-01		1.72E-01	7.30E-01		4.42E-01	1.00E-03		-5.35E-01	5.30E-04		Unigene55331_All//gi|145332907|ref|NP_001078319.1|//3.00E-25//EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G); translation initiation factor [Arabidopsis thaliana]	Unigene55331_All//1.00E-26//AT3G60240| EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G); translation initiation factor	Unigene55331_All//2.00E-122//TC155593			GO:0008135//GO:0044260//GO:0051707	nr -
Unigene55332_All	200	12.30	34.71	14.11	26.90	27.20	36.13	38.69	55.38	52.39	1.50E+00	4.80E-10	Up	1.99E-01	6.19E-01		1.62E-02	9.63E-01		4.26E-01	5.82E-02		5.18E-01	6.83E-04		4.37E-01	4.46E-03		Unigene55332_All//gi|1732363|gb|AAC06385.1|//4.00E-17//early fruit mRNA [Malus x domestica]		Unigene55332_All//3.00E-80//gi|21101733|gb|BQ414046.1|BQ414046			nr +
Unigene55338_All	209	76.60	37.09	49.17	124.89	111.54	146.29	178.22	137.99	105.41	-1.05E+00	4.44E-13	Down	-6.40E-01	8.72E-06		-1.63E-01	1.58E-01		2.28E-01	2.53E-02		-3.69E-01	2.34E-06		-7.58E-01	8.48E-22		Unigene55338_All//gi|40781605|gb|AAR88812.1|//5.00E-30//14-3-3 protein [Triticum aestivum]	Unigene55338_All//3.00E-30//AT3G02520| GRF7 (GENERAL REGULATORY FACTOR 7); protein binding / protein phosphorylated amino acid binding	Unigene55338_All//9.00E-115//gi|13247745|gb|BF272092.2|BF272092			GO:0004091//GO:0005515//GO:0006587//GO:0030291//GO:0031570//GO:0043231	nr -
Unigene55339_All	211	19.34	48.03	23.72	26.68	31.82	29.11	114.02	187.19	102.15	1.31E+00	7.07E-12	Up	2.95E-01	3.21E-01		2.55E-01	3.07E-01		1.26E-01	6.54E-01		7.15E-01	2.59E-20		-1.59E-01	1.31E-01		Unigene55339_All//gi|1370166|emb|CAA98160.1|//2.00E-33//RAB1C [Lotus japonicus]	Unigene55339_All//5.00E-32//AT4G17530| ATRABIC; GTP binding	Unigene55339_All//6.00E-116//C0132097			GO:0003824//GO:0006810//GO:0032561//GO:0035556	nr +
Unigene55345_All	221	27.70	19.26	18.07	32.46	31.94	46.19	145.97	66.57	45.07	-5.24E-01	2.86E-02		-6.16E-01	1.38E-02		-2.31E-02	9.26E-01		5.09E-01	4.33E-03		-1.13E+00	2.14E-35	Down	-1.70E+00	1.39E-66	Down	Unigene55345_All//gi|12054507|emb|CAC20221.1|//7.00E-36//ribosomal protein L2 [Glycine max]	Unigene55345_All//4.00E-37//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene55345_All//7.00E-122//TC164834		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0043231	nr +
Unigene55347_All	229	3.88	0.89	4.42	5.22	2.71	0.99	8.12	4.75	3.31	-2.13E+00	1.06E-02		1.86E-01	7.75E-01		-9.48E-01	1.12E-01		-2.40E+00	7.07E-04	Down	-7.76E-01	7.05E-02		-1.30E+00	2.09E-03				Unigene55347_All//3.00E-07//TC150664				
Unigene55348_All	230	275.71	674.34	398.68	48.95	54.20	82.47	0.00	0.00	0.17	1.29E+00	2.60E-167	Up	5.32E-01	1.01E-21		1.47E-01	4.40E-01		7.53E-01	1.42E-09		null	null		7.44E+00	6.44E-01		Unigene55348_All//gi|400890|sp|Q02060.1|PSBS_SPIOL//1.00E-13//RecName: Full=Photosystem II 22 kDa protein, chloroplastic; AltName: Full=CP22; Flags: Precursor >gi|213007|emb|CAA48557.1| 22kD-protein of PSII [Spinacia oleracea] >gi|260917|gb|AAB24338.1| photosystem II 22 kda polypeptide [Spinacia oleracea]	Unigene55348_All//1.00E-10//AT1G44575| NPQ4 (NONPHOTOCHEMICAL QUENCHING); chlorophyll binding / xanthophyll binding	Unigene55348_All//2.00E-122//TC163467		ko00195|Photosynthesis	GO:0009507//GO:0034357//GO:0044425	nr -
Unigene5535_All	731	273.34	77.63	213.07	223.18	225.93	126.28	2.95	6.92	3.38	-1.82E+00	0.00E+00	Down	-3.59E-01	7.14E-23		1.77E-02	7.68E-01		-8.22E-01	1.48E-91		1.23E+00	5.78E-07	Up	1.96E-01	5.97E-01		Unigene5535_All//gi|15230083|ref|NP_189624.1|//3.00E-08//RALFL27 (ralf-like 27); signal transducer [Arabidopsis thaliana]	Unigene5535_All//3.00E-08//AT3G29780| RALFL27 (ralf-like 27); signal transducer	Unigene5535_All//0.00E+00//gi|84155895|gb|DN817121.1|DN817121				nr -
Unigene55360_All	239	0.44	0.00	0.00	3.33	1.15	0.19	1.95	1.40	0.83	-8.77E+00	3.70E-01		-8.77E+00	3.91E-01		-1.53E+00	4.83E-02		-4.14E+00	4.12E-04	Down	-4.76E-01	6.59E-01		-1.22E+00	2.00E-01				Unigene55360_All//5.00E-52//TC165695				
Unigene55366_All	200	0.00	7.09	0.00	0.00	6.20	1.58	0.00	0.00	0.40	1.28E+01	4.06E-08	Up	null	null		1.26E+01	1.19E-07	Up	1.06E+01	4.07E-02		null	null		8.64E+00	4.03E-01									
Unigene5537_All	516	58.00	29.36	33.75	75.78	51.92	89.89	61.37	27.54	31.73	-9.82E-01	1.68E-21		-7.81E-01	3.28E-14		-5.46E-01	2.30E-12		2.46E-01	1.72E-03		-1.16E+00	6.87E-36	Down	-9.52E-01	4.12E-27		Unigene5537_All//gi|224092216|ref|XP_002309513.1|//9.00E-52//serine hydroxymethyltransferase 8 [Populus trichocarpa] >gi|222855489|gb|EEE93036.1| serine hydroxymethyltransferase 8 [Populus trichocarpa]	Unigene5537_All//9.00E-40//AT4G32520| SHM3 (SERINE HYDROXYMETHYLTRANSFERASE 3); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding	Unigene5537_All//0.00E+00//gi|84154313|gb|DN803668.1|DN803668		ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr +
Unigene55379_All	212	0.25	0.48	0.50	0.94	1.14	0.85	0.20	1.18	6.20	9.54E-01	7.25E-01		1.03E+00	7.02E-01		2.75E-01	8.95E-01		-1.42E-01	9.34E-01		2.57E+00	1.53E-01		4.96E+00	2.80E-08	Up			Unigene55379_All//2.00E-07//TC138233				
Unigene55383_All	216	14.78	5.16	3.70	18.45	19.29	25.30	56.96	38.89	21.39	-1.52E+00	3.72E-05	Down	-2.00E+00	8.75E-07	Down	6.43E-02	8.53E-01		4.56E-01	8.46E-02		-5.50E-01	1.23E-04		-1.41E+00	4.87E-20	Down	Unigene55383_All//gi|195620934|gb|ACG32297.1|//3.00E-35//60S ribosomal protein L23 [Zea mays]	Unigene55383_All//2.00E-36//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene55383_All//6.00E-119//gi|13246889|gb|BE052234.2|BE052234		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0010467//GO:0015934//GO:0031981	nr +
Unigene55385_All	224	0.00	0.00	0.00	10.90	2.61	0.40	0.94	0.00	0.18	null	null		null	null		-2.06E+00	6.47E-07	Down	-4.76E+00	8.61E-13	Down	-9.88E+00	7.43E-02		-2.41E+00	1.95E-01		Unigene55385_All//gi|224057862|ref|XP_002299361.1|//4.00E-07//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene55385_All//4.00E-05//AT5G54510| DFL1 (DWARF IN LIGHT 1); indole-3-acetic acid amido synthetase				nr +
Unigene55388_All	230	40.95	26.44	26.39	74.94	68.42	90.92	52.94	23.44	29.10	-6.31E-01	7.21E-04		-6.34E-01	1.12E-03		-1.31E-01	4.01E-01		2.79E-01	2.51E-02		-1.18E+00	1.18E-14	Down	-8.63E-01	1.87E-09		Unigene55388_All//gi|9294075|dbj|BAB02032.1|//1.00E-34//cytosolic chaperonin, delta-subunit [Arabidopsis thaliana]	Unigene55388_All//4.00E-36//AT3G18190| chaperonin, putative	Unigene55388_All//3.00E-127//gi|21093084|gb|BQ405397.1|BQ405397			GO:0005515//GO:0010038//GO:0032559//GO:0044267//GO:0044424	nr +
Unigene55390_All	246	45.30	39.13	34.20	80.39	78.11	66.83	74.76	58.28	23.48	-2.11E-01	2.43E-01		-4.06E-01	2.49E-02		-4.15E-02	8.14E-01		-2.67E-01	3.95E-02		-3.59E-01	1.99E-03		-1.67E+00	1.50E-37	Down	Unigene55390_All//gi|297814920|ref|XP_002875343.1|//5.00E-34//auxin signaling F-box 2 [Arabidopsis lyrata subsp. lyrata] >gi|297321181|gb|EFH51602.1| auxin signaling F-box 2 [Arabidopsis lyrata subsp. lyrata]	Unigene55390_All//2.00E-35//AT3G26810| AFB2 (AUXIN SIGNALING F-BOX 2); auxin binding / ubiquitin-protein ligase	Unigene55390_All//1.00E-129//TC172087		ko04626|Plant-pathogen interaction	GO:0009555//GO:0009607//GO:0009755//GO:0016020//GO:0042562//GO:0043178//GO:0048437	nr -
Unigene55394_All	253	0.00	0.00	0.42	156.92	106.44	74.62	0.33	0.66	0.00	null	null		8.72E+00	3.97E-01		-5.60E-01	3.89E-13		-1.07E+00	3.78E-35	Down	9.84E-01	6.33E-01		-8.38E+00	3.57E-01		Unigene55394_All//gi|55276120|gb|AAV48801.1|//2.00E-20//homeobox transcription factor KN2 [Populus trichocarpa x Populus deltoides]		Unigene55394_All//1.00E-74//TC141466			GO:0003677//GO:0006350//GO:0010468	nr -
Unigene55396_All	269	0.39	5.65	0.40	5.00	3.58	1.51	0.79	0.93	14.81	3.86E+00	1.23E-06	Up	2.54E-02	9.99E-01		-4.80E-01	4.15E-01		-1.73E+00	4.68E-03		2.46E-01	8.53E-01		4.24E+00	4.01E-22	Up			Unigene55396_All//1.00E-111//TC139022				
Unigene55398_All	323	27.70	40.63	36.76	67.09	68.44	81.94	195.82	111.15	497.18	5.53E-01	3.73E-04		4.08E-01	1.87E-02		2.89E-02	8.38E-01		2.89E-01	7.25E-03		-8.17E-01	3.60E-40		1.34E+00	6.89E-231	Up	Unigene55398_All//gi|15919089|emb|CAC86996.1|//2.00E-47//ATP citrate lyase b-subunit [Lupinus albus]	Unigene55398_All//2.00E-47//AT1G10670| ACLA-1; ATP citrate synthase	Unigene55398_All//0.00E+00//gi|13351200|gb|BG441548.1|BG441548		ko00020|Citrate cycle (TCA cycle)	GO:0004774//GO:0005982//GO:0006084//GO:0006633//GO:0006779//GO:0008361//GO:0009908//GO:0016109//GO:0032559//GO:0043234//GO:0043479//GO:0044444//GO:0048827//GO:2000026	nr +
Unigene554_All	1349	0.93	0.34	0.24	3.47	3.40	3.78	0.85	0.06	0.50	-1.46E+00	1.95E-02		-1.97E+00	4.62E-03		-3.20E-02	9.12E-01		1.24E-01	6.96E-01		-3.77E+00	3.90E-06	Down	-7.53E-01	1.68E-01		Unigene554_All//gi|297337877|ref|XP_002892035.1|//0.00E+00//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337877|gb|EFH68294.1| armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene554_All//0.00E+00//AT1G01950| armadillo/beta-catenin repeat family protein / kinesin motor family protein	Unigene554_All//0.00E+00//ES811588			GO:0003774//GO:0004702//GO:0006468//GO:0007017//GO:0008104//GO:0009536//GO:0015630//GO:0032559//GO:0048513	nr +
Unigene55405_All	200	34.01	13.17	22.10	92.90	65.08	68.42	344.37	252.86	76.69	-1.37E+00	9.21E-09	Down	-6.22E-01	8.04E-03		-5.14E-01	1.41E-05		-4.41E-01	4.61E-04		-4.46E-01	2.51E-15		-2.17E+00	2.39E-196	Down	Unigene55405_All//gi|211906506|gb|ACJ11746.1|//2.00E-30//luminal binding protein [Gossypium hirsutum]	Unigene55405_All//8.00E-32//AT5G42020| BIP2; ATP binding	Unigene55405_All//2.00E-109//TC139139		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0008152//GO:0016628//GO:0031410//GO:0032559//GO:0044432//GO:0050896	nr +
Unigene55409_All	204	0.26	1.74	0.26	0.73	0.51	2.66	0.41	1.84	4.10	2.76E+00	9.59E-02		2.51E-02	9.94E-01		-5.33E-01	7.84E-01		1.86E+00	1.02E-01		2.15E+00	9.44E-02		3.31E+00	2.30E-04	Up			Unigene55409_All//2.00E-07//DF463545				
Unigene5541_All	431	47.71	21.75	19.77	44.61	37.47	69.37	48.56	32.78	21.07	-1.13E+00	9.14E-19	Down	-1.27E+00	1.88E-21	Down	-2.52E-01	4.80E-02		6.37E-01	3.76E-11		-5.67E-01	1.15E-07		-1.20E+00	2.52E-26	Down	Unigene5541_All//gi|297794223|ref|XP_002864996.1|//9.00E-37//60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|297310831|gb|EFH41255.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene5541_All//9.00E-31//AT5G67510| 60S ribosomal protein L26 (RPL26B)	Unigene5541_All//7.00E-179//TC135089		ko03010|Ribosome		nr -
Unigene55413_All	210	20.43	108.82	47.42	11.15	17.87	29.25	33.22	69.26	54.45	2.41E+00	6.38E-59	Up	1.21E+00	4.93E-10	Up	6.81E-01	2.93E-02		1.39E+00	1.68E-08	Up	1.06E+00	8.58E-15	Up	7.13E-01	1.24E-06		Unigene55413_All//gi|222423852|dbj|BAH19891.1|//1.00E-15//AT5G64170 [Arabidopsis thaliana]	Unigene55413_All//6.00E-17//AT5G64170| dentin sialophosphoprotein-related	Unigene55413_All//2.00E-81//TC176231				nr +
Unigene55416_All	217	222.30	447.39	310.67	146.69	139.49	108.43	272.00	513.11	255.92	1.01E+00	5.92E-71	Up	4.83E-01	1.29E-13		-7.26E-02	5.63E-01		-4.36E-01	2.55E-06		9.16E-01	7.99E-85		-8.79E-02	1.96E-01		Unigene55416_All//gi|146216004|gb|ABQ10204.1|//9.00E-39//cysteine protease Cp6 [Actinidia deliciosa]	Unigene55416_All//4.00E-32//AT1G47128| RD21 (responsive to dehydration 21); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene55416_All//2.00E-119//TC148865			GO:0004175//GO:0005488//GO:0005576//GO:0006950//GO:0009536//GO:0016628//GO:0019538//GO:0031410	nr -
Unigene55425_All	233	10.10	14.14	32.00	1.92	2.36	6.59	0.36	0.36	0.68	4.84E-01	1.60E-01		1.66E+00	6.63E-12	Up	2.97E-01	8.18E-01		1.78E+00	2.04E-03		-1.64E-02	1.01E+00		9.14E-01	6.24E-01				Unigene55425_All//3.00E-07//TC166013				
Unigene55427_All	239	8.54	11.87	2.23	14.59	6.92	11.72	2.30	0.35	0.83	4.76E-01	2.13E-01		-1.94E+00	1.99E-04	Down	-1.08E+00	4.95E-04	Down	-3.17E-01	3.94E-01		-2.72E+00	1.22E-02		-1.46E+00	9.76E-02				Unigene55427_All//4.00E-28//DF458249				
Unigene55430_All	243	76.65	73.61	65.30	52.89	92.54	85.87	38.80	93.22	83.94	-5.85E-02	6.74E-01		-2.31E-01	1.03E-01		8.07E-01	1.05E-13		6.99E-01	2.77E-09		1.26E+00	1.12E-29	Up	1.11E+00	1.40E-22	Up	Unigene55430_All//gi|297827267|ref|XP_002881516.1|//6.00E-17//sodium-and lithium-tolerant 1 [Arabidopsis lyrata subsp. lyrata] >gi|297327355|gb|EFH57775.1| sodium-and lithium-tolerant 1 [Arabidopsis lyrata subsp. lyrata]	Unigene55430_All//2.00E-15//AT2G37570| SLT1 (sodium- and lithium-tolerant 1)	Unigene55430_All//5.00E-132//TC147359			GO:0006972	nr -

Unigene55433_All	256	0.41	0.40	2.91	0.78	5.52	2.65	0.50	0.00	0.47	-4.63E-02	9.87E-01		2.83E+00	8.52E-03		2.83E+00	3.18E-05	Up	1.77E+00	6.94E-02		-8.95E+00	2.35E-01		-8.58E-02	9.69E-01		Unigene55433_All//gi|15233503|ref|NP_193195.1|//1.00E-11//emb2739 (embryo defective 2739) [Arabidopsis thaliana]	Unigene55433_All//5.00E-13//AT4G14590| emb2739 (embryo defective 2739)				GO:0003006	nr +
Unigene55434_All	272	8.46	8.94	19.38	10.44	19.12	13.28	22.85	32.73	45.99	7.93E-02	8.44E-01		1.20E+00	1.64E-05	Up	8.73E-01	5.21E-04		3.48E-01	3.31E-01		5.18E-01	2.69E-03		1.01E+00	3.18E-12	Up	Unigene55434_All//gi|62319903|dbj|BAD93965.1|//8.00E-43//ARF1-binding protein [Arabidopsis thaliana]	Unigene55434_All//3.00E-44//AT5G62000| ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Unigene55434_All//2.00E-147//gi|164274883|gb|ES813828.1|ES813828	ARF		GO:0001071//GO:0003676//GO:0005515//GO:0006355//GO:0008283//GO:0009536//GO:0009755//GO:0009900//GO:0009908//GO:0010260	nr -
Unigene55435_All	290	35.18	33.55	24.61	75.24	71.96	88.30	174.81	130.00	85.86	-6.86E-02	7.19E-01		-5.16E-01	5.78E-03		-6.43E-02	6.51E-01		2.31E-01	4.15E-02		-4.27E-01	1.05E-10		-1.03E+00	2.05E-48	Down	Unigene55435_All//gi|49615095|dbj|BAD24714.2|//8.00E-46//protein disulfide isomerase-like protein [Glycine max]	Unigene55435_All//2.00E-42//AT2G47470| UNE5 (UNFERTILIZED EMBRYO SAC 5); protein disulfide isomerase	Unigene55435_All//6.00E-163//gi|109864926|gb|DW493902.1|DW493902		ko04141|Protein processing in endoplasmic reticulum	GO:0006091//GO:0016862//GO:0019725//GO:0031410//GO:0044432	nr +
Unigene55438_All	222	17.44	13.01	15.83	47.35	53.67	43.74	9.90	13.74	4.13	-4.23E-01	1.83E-01		-1.40E-01	6.63E-01		1.81E-01	3.27E-01		-1.14E-01	6.12E-01		4.73E-01	1.48E-01		-1.26E+00	9.51E-04	Down			Unigene55438_All//6.00E-113//TC171438				ESTscan -
Unigene55439_All	516	0.00	0.00	0.00	0.00	0.13	0.00	4.34	0.24	5.10	null	null		null	null		7.06E+00	6.08E-01		null	null		-4.16E+00	2.50E-12	Down	2.31E-01	5.35E-01		Unigene55439_All//gi|255545824|ref|XP_002513972.1|//1.00E-10//kinase, putative [Ricinus communis] >gi|223547058|gb|EEF48555.1| kinase, putative [Ricinus communis]		Unigene55439_All//2.00E-19//TC169886				nr +
Unigene55440_All	299	0.70	13.73	1.25	2.83	2.07	5.14	7.21	19.99	12.92	4.29E+00	2.44E-18	Up	8.33E-01	5.16E-01		-4.50E-01	5.52E-01		8.59E-01	1.21E-01		1.47E+00	2.23E-10	Up	8.42E-01	1.83E-03		Unigene55440_All//gi|19911211|dbj|BAB86932.1|//4.00E-41//glucosyltransferase-14 [Vigna angularis]	Unigene55440_All//2.00E-37//AT2G36760| UGT73C2 (UDP-glucosyl transferase 73C2); UDP-glycosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene55440_All//3.00E-149//TC137499		ko00908|Zeatin biosynthesis	GO:0035251	nr -
Unigene55441_All	531	0.00	0.00	0.00	0.00	0.00	0.00	8.36	13.07	0.38	null	null		null	null		null	null		null	null		6.44E-01	1.14E-03		-4.48E+00	5.00E-26	Down	Unigene55441_All//gi|115438909|ref|XP_001043334.1|//3.00E-16//Os01g0651800 [Oryza sativa Japonica Group] >gi|20146431|dbj|BAB89211.1| lipase-like [Oryza sativa Japonica Group] >gi|113533265|dbj|BAF05648.1| Os01g0651800 [Oryza sativa Japonica Group]	Unigene55441_All//2.00E-11//AT2G31100| triacylglycerol lipase					nr +
Unigene55443_All	200	20.93	46.36	19.97	58.28	42.18	45.84	93.23	94.67	87.84	1.15E+00	5.21E-09	Up	-6.77E-02	8.29E-01		-4.66E-01	3.00E-03		-3.46E-01	4.28E-02		2.21E-02	8.78E-01		-8.58E-02	5.20E-01		Unigene55443_All//gi|297798906|ref|XP_002867337.1|//3.00E-28//signal recognition particle receptor alpha subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313173|gb|EFH43596.1| signal recognition particle receptor alpha subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene55443_All//1.00E-29//AT4G30600| signal recognition particle receptor alpha subunit family protein	Unigene55443_All//2.00E-109//TC152131		ko03060|Protein export	GO:0000270//GO:0003723//GO:0004871//GO:0006613//GO:0017111//GO:0030867//GO:0031224//GO:0032561//GO:0043021//GO:0048500	nr -
Unigene55444_All	201	50.50	289.65	200.81	80.05	155.90	114.59	78.88	144.73	221.99	2.52E+00	4.59E-157	Up	1.99E+00	1.09E-79	Up	9.62E-01	2.68E-25		5.18E-01	3.12E-06		8.76E-01	3.67E-21		1.49E+00	1.26E-75	Up			Unigene55444_All//5.00E-110//TC133226				
Unigene55447_All	204	0.00	0.00	0.00	0.00	0.00	0.00	53.06	48.56	0.39	null	null		null	null		null	null		null	null		-1.28E-01	4.84E-01		-7.09E+00	8.23E-76	Down	Unigene55447_All//gi|126566050|gb|AB020854.1|//2.00E-07//hypothetical protein [Lilium longiflorum]		Unigene55447_All//2.00E-13//ES810795				nr +
Unigene55449_All	208	0.25	0.00	0.00	0.00	0.33	0.00	4.07	4.82	68.57	-7.97E+00	6.10E-01		-7.97E+00	6.22E-01		8.37E+00	6.08E-01		null	null		2.46E-01	6.89E-01		4.08E+00	8.04E-76	Up			Unigene55449_All//9.00E-75//DN800037				
Unigene55451_All	213	0.25	0.00	0.00	0.23	0.16	0.00	62.13	196.03	84.91	-7.94E+00	6.10E-01		-7.94E+00	6.22E-01		-5.33E-01	8.24E-01		-7.87E+00	6.33E-01		1.66E+00	1.16E-80	Up	4.51E-01	7.07E-05		Unigene55451_All//gi|124360970|gb|AB008942.1|//1.00E-26//quinoprotein alcohol dehydrogenase-like [Medicago truncatula]					GO:0003676//GO:0005515//GO:0008152//GO:0016491//GO:0046914	nr -
Unigene55455_All	221	78.13	31.18	70.36	144.03	101.59	109.33	44.58	35.74	25.60	-1.33E+00	4.24E-20	Down	-1.51E-01	3.35E-01		-5.04E-01	7.55E-09		-3.98E-01	1.93E-05		-3.19E-01	6.03E-02		-8.00E-01	5.62E-07		Unigene55455_All//gi|261351264|gb|ACX71299.1|//1.00E-24//RNA-binding protein RZ-1 [Capsicum annuum]	Unigene55455_All//6.00E-14//AT3G26420| ATRZ-1A; RNA binding / nucleotide binding	Unigene55455_All//7.00E-122//gi|84170357|gb|DR459005.1|DR459005			GO:0009409//GO:0046914	nr +
Unigene55458_All	229	46.15	37.17	21.86	68.74	61.05	12.42	30.65	20.26	17.05	-3.12E-01	8.44E-02		-1.08E+00	7.33E-09	Down	-1.71E-01	2.79E-01		-2.47E+00	8.42E-46	Down	-5.97E-01	2.42E-03		-8.46E-01	1.16E-05		Unigene55458_All//gi|108707503|gb|ABF95298.1|//6.00E-06//retrotransposon protein, putative, unclassified [Oryza sativa (japonica cultivar-group)]		Unigene55458_All//5.00E-30//TC165310				nr +
Unigene55463_All	236	0.00	0.00	0.00	0.00	0.00	0.00	27.41	28.69	3.04	null	null		null	null		null	null		null	null		6.58E-02	7.72E-01		-3.17E+00	7.27E-29	Down	Unigene55463_All//gi|224075052|ref|XP_002304537.1|//7.00E-31//cation proton exchanger [Populus trichocarpa] >gi|222841969|gb|EEE79516.1| cation proton exchanger [Populus trichocarpa]	Unigene55463_All//8.00E-22//AT4G23700| ATCHX17 (CATION/H+ EXCHANGER 17); monovalent cation:proton antiporter/ sodium:hydrogen antiporter				GO:0006811//GO:0015298//GO:0031224	nr -
Unigene55467_All	258	0.00	0.00	0.00	0.39	0.00	0.00	4.42	53.30	10.19	null	null		null	null		-8.59E+00	3.12E-01		-8.59E+00	3.98E-01		3.59E+00	3.39E-65	Up	1.20E+00	4.99E-04	Up							
Unigene55468_All	266	0.00	0.00	0.00	0.00	0.00	0.00	4.77	4.87	1.05	null	null		null	null		null	null		null	null		3.07E-02	9.85E-01		-2.19E+00	1.97E-04	Down	Unigene55468_All//gi|126566038|gb|AB020848.1|//4.00E-13//cytochrome P450-like TBP protein [Lilium longiflorum]		Unigene55468_All//2.00E-27//gi|45595417|gb|CK988266.1|CK988266				nr +
Unigene55469_All	279	1.50	3.09	0.00	1.07	0.37	0.00	4.55	9.89	11.71	1.04E+00	1.72E-01		-1.06E+01	1.55E-02		-1.53E+00	2.98E-01		-1.01E+01	3.99E-02		1.12E+00	1.06E-03		1.36E+00	1.22E-05	Up			Unigene55469_All//5.00E-80//TC163673				
Unigene5547_All	507	19.19	29.08	21.01	16.70	14.87	17.19	60.46	48.72	25.22	6.00E-01	3.83E-05		1.30E-01	5.22E-01		-1.67E-01	4.61E-01		4.17E-02	8.63E-01		-3.11E-01	3.92E-04		-1.26E+00	5.83E-41	Down	Unigene5547_All//gi|2511598|emb|CAA74030.1|//3.00E-16//multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana]	Unigene5547_All//2.00E-17//AT1G56450| PBG1; peptidase/ threonine-type endopeptidase	Unigene5547_All//0.00E+00//TC170013		ko03050|Proteasome		nr -
Unigene55470_All	285	0.00	0.00	0.00	0.00	0.00	0.00	3.86	5.13	0.00	null	null		null	null		null	null		null	null		4.12E-01	4.19E-01		-1.19E+01	3.33E-08	Down	Unigene55470_All//gi|27923850|sp|Q9SM12.1|RS21_CYAPA//8.00E-27//RecName: Full=40S ribosomal protein S21 >gi|6012958|emb|CAB57312.1| 40S ribosomal protein S21 [Cyanophora paradoxa]	Unigene55470_All//2.00E-26//AT5G27700| structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0031410	nr +
Unigene55474_All	345	7.43	11.46	5.56	12.71	11.48	11.78	7.72	15.63	15.94	6.24E-01	4.28E-02		-4.19E-01	3.27E-01		-1.47E-01	6.42E-01		-1.09E-01	7.24E-01		1.02E+00	1.19E-05	Up	1.05E+00	3.69E-06	Up	Unigene55474_All//gi|42569151|ref|NP_179539.2|//8.00E-11//recA family protein [Arabidopsis thaliana] >gi|209572665|sp|Q9ZUP2.2|RECA3_ARATH RecName: Full=DNA repair protein recA homolog 3, mitochondrial; AltName: Full=Recombinase A homolog 3; Flags: Precursor >gi|119935859|gb|ABM06015.1| At2g19490 [Arabidopsis thaliana]	Unigene55474_All//3.00E-12//AT2G19490| recA family protein	Unigene55474_All//8.00E-141//ES831821		ko03440|Homologous recombination	GO:0000166//GO:0003677//GO:0006259//GO:0033554//GO:0042623//GO:0043231	nr -
Unigene55475_All	230	0.00	0.00	0.46	0.00	0.00	0.00	4.96	6.18	1.04	null	null		8.85E+00	3.97E-01		null	null		null	null		3.16E-01	5.63E-01		-2.26E+00	3.40E-04	Down							
Unigene55476_All	284	17.13	9.63	6.56	22.98	16.01	20.20	47.94	25.02	27.92	-8.31E-01	2.31E-03		-1.38E+00	3.03E-06	Down	-5.22E-01	1.82E-02		-1.86E-01	4.80E-01		-9.38E-01	1.58E-11		-7.80E-01	6.16E-09		Unigene55476_All//gi|124360846|gb|ABN08818.1|//2.00E-46//Mov34-1 [Medicago truncatula]	Unigene55476_All//1.00E-45//AT1G10840| TIF3H1; translation initiation factor	Unigene55476_All//2.00E-159//TC170472			GO:0006412//GO:0008135//GO:0043234	nr -
Unigene55478_All	379	0.55	2.54	2.25	0.92	1.91	1.43	3.35	9.15	5.05	2.20E+00	6.58E-03		2.03E+00	2.24E-02		1.05E+00	2.40E-01		6.36E-01	5.61E-01		1.45E+00	3.08E-06	Up	5.92E-01	1.47E-01				Unigene55478_All//1.00E-16//TC161307				
Unigene5548_All	790	1.99	1.22	2.22	3.34	3.09	1.49	3.10	2.59	0.71	-7.05E-01	1.80E-01		1.63E-01	7.34E-01		-1.11E-01	8.17E-01		-1.17E+00	2.67E-03		-2.60E-01	5.18E-01		-2.14E+00	1.23E-07	Down	Unigene5548_All//gi|116309912|emb|CAH66946.1|//1.00E-06//B0809H07.1 [Oryza sativa (indica cultivar-group)]		Unigene5548_All//3.00E-56//ES807842				nr -
Unigene55480_All	200	0.00	1.27	0.00	0.00	0.00	0.00	0.21	3.34	4.78	1.03E+01	7.85E-02		null	null		null	null		null	null		3.98E+00	6.38E-04	Up	4.50E+00	6.81E-06	Up			Unigene55480_All//2.00E-07//TC135034				
Unigene55481_All	200	0.00	0.00	0.00	0.00	0.00	0.23	0.42	1.04	21.71	null	null		null	null		null	null		7.82E-00	6.95E-01		1.31E+00	4.47E-01		5.68E+00	6.23E-28	Up			Unigene55481_All//2.00E-47//DN800037				
Unigene55483_All	206	0.00	0.49	0.00	0.00	0.00	0.00	276.26	58.23	132.28	8.94E+00	3.85E-01		null	null		null	null		null	null		-2.25E+00	8.56E-165	Down	-1.06E+00	2.07E-57	Down	Unigene55483_All//gi|211906536|gb|ACJ11761.1|//3.00E-20//class III peroxidase [Gossypium hirsutum]	Unigene55483_All//4.00E-15//AT1G05260| RC13 (RARE COLD INDUCIBLE GENE 3); peroxidase	Unigene55483_All//3.00E-16//TC166713		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006972//GO:0008152//GO:0009414//GO:0016209//GO:0043231	nr +
Unigene55489_All	209	0.25	0.00	1.27	5.24	3.46	1.30	19.62	5.20	2.86	-7.97E+00	6.10E-01		2.35E+00	2.39E-01		-6.00E-01	3.53E-01		-2.02E+00	4.74E-03		-1.92E+00	2.33E-10	Down	-2.78E+00	2.48E-16	Down			Unigene55489_All//2.00E-109//TC168019				
Unigene5549_All	351	13.86	19.63	14.11	22.14	27.96	31.14	121.42	88.35	38.25	5.02E-01	2.54E-02		2.54E-02	9.44E-01		3.37E-01	7.28E-02		4.92E-01	4.16E-03		-4.59E-01	2.71E-10		-1.67E+00	1.39E-85	Down	Unigene5549_All//gi|145331431|ref|NP_001078074.1|//2.00E-28//UNE5 (UNFERTILIZED EMBRYO SAC 5); protein disulfide isomerase [Arabidopsis thaliana] >gi|222423259|dbj|BAH19606.1| AT2G47470 [Arabidopsis thaliana]	Unigene5549_All//8.00E-21//AT2G47470| UNE5 (UNFERTILIZED EMBRYO SAC 5); protein disulfide isomerase	Unigene5549_All//2.00E-141//gi|84171944|gb|DR460592.1|DR460592		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene55492_All	212	0.00	0.00	0.00	0.00	0.00	0.00	0.20	1.77	3.19	null	null		null	null		null	null		null	null		3.15E+00	3.41E-02		4.00E+00	4.29E-04	Up							
Unigene55494_All	215	226.80	114.30	98.33	396.43	408.10	282.95	320.35	98.56	123.96	-9.89E-01	6.13E-35		-1.21E+00	2.89E-46	Down	4.19E-02	5.64E-01		-4.87E-01	3.15E-19		-1.70E+00	8.28E-138	Down	-1.37E+00	3.00E-103	Down	Unigene55494_All//gi|214003725|gb|ACJ60905.1|//1.00E-32//alpha tubulin [Betula pendula]	Unigene55494_All//2.00E-33//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene55494_All//2.00E-118//EX172073		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene55495_All	215	0.00	0.00	0.25	0.23	0.32	0.63	1.57	2.14	17.79	null	null		7.95E+00	6.34E-01		4.67E-01	9.57E-01		1.44E+00	6.38E-01		4.43E-01	6.31E-01		3.50E+00	1.66E-18	Up							
Unigene55498_All	221	0.00	0.00	0.00	0.68	0.62	0.20	8.61	7.19	2.16	null	null		null	null		-1.18E-01	9.10E-01		-1.73E+00	5.00E-01		-2.61E-01	5.81E-01		-1.99E+00	1.17E-05	Down			Unigene55498_All//1.00E-76//DT463310				
Unigene55501_All	226	0.00	0.00	0.00	0.00	0.46	0.60	0.37	3.51	3.17	null	null		null	null		8.84E+00	4.55E-01		9.23E+00	3.10E-01		3.23E+00	5.44E-04	Up	3.08E+00	1.17E-03				Unigene55501_All//2.00E-08//EV488088				
Unigene55504_All	230	19.34	83.71	64.13	21.66	23.21	33.58	17.65	38.71	56.29	2.11E+00	2.26E-42	Up	1.73E+00	2.66E-24	Up	9.96E-02	7.74E-01		6.33E-01	2.30E-03		1.13E+00	2.43E-10	Up	1.67E+00	1.88E-26	Up			Unigene55504_All//1.00E-117//TC133995				
Unigene55506_All	231	38.73	39.92	28.12	50.03	52.32	41.45	88.22	54.46	42.25	4.37E-02	8.29E-01		-4.62E-01	2.33E-02		6.47E-02	7.76E-01		-2.72E-01	1.32E-01		-6.96E-01	2.03E-10		-1.06E+00	3.99E-21	Down	Unigene55506_All//gi|18410971|ref|NP_567066.1|//4.00E-39//PP2A-3 (PROTEIN PHOSPHATASE 2A-3); protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|297820682|ref|XP_002878224.1| protein phosphatase 2A-3 [Arabidopsis lyrata subsp. lyrata] >gi|1352664|sp|P48578.1|PP2A3_ARATH RecName: Full=Serine/threonine-protein phosphatase PP2A-3 catalytic subunit; AltName: Full=Protein phosphatase 2A isoform 3 >gi|473259|gb|AAA64941.1| Ser/Thr protein phosphatase [Arabidopsis thaliana] >gi|4204949|gb|AAD10855.1| serine/threonine protein phosphatase 2A-4 catalytic subunit [Arabidopsis thaliana] >gi|16209682|gb|AAL14399.1| AT3g58500/F14P22_90 [Arabidopsis thaliana] >gi|21360431|gb|AAM47331.1| AT3g58500/F14P22_90 [Arabidopsis thaliana] >gi|297324062|gb|EFH54483.1| protein phosphatase 2A-3 [Arabidopsis lyrata subsp. lyrata]	Unigene55506_All//2.00E-40//AT3G58500| PP2A-3 (PROTEIN PHOSPHATASE 2A-3); protein serine/threonine phosphatase	Unigene55506_All//7.00E-128//gi|164256000|gb|EV490000.1|EV490000			GO:0006464//GO:0008287//GO:0016020//GO:0016791//GO:0031981//GO:0043169	nr -
Unigene55507_All	232	6.09	29.70	18.13	1.93	2.82	11.49	0.73	8.47	7.73	2.29E+00	4.25E-17	Up	1.57E+00	1.63E-06	Up	5.45E-01	5.86E-01		2.57E+00	2.87E-08	Up	3.54E+00	1.14E-09	Up	3.41E+00	8.04E-09	Up			Unigene55507_All//7.00E-08//TC152303				
Unigene55508_All	233	31.89	52.63	32.68	70.55	90.60	105.25	74.40	102.61	302.98	7.23E-01	8.05E-06		3.55E-02	8.82E-01		3.61E-01	1.72E-03		5.77E-01	7.13E-08		4.64E-01	3.06E-06		2.03E+00	3.35E-182	Up	Unigene55508_All//gi|224551852|gb|ACN54324.1|//7.00E-39//NADPH:cytochrome P450 reductase [Gossypium hirsutum]	Unigene55508_All//1.00E-27//AT4G30210| ATR2 (ARABIDOPSIS P450 REDUCTASE 2); NADPH-hemoprotein reductase	Unigene55508_All//7.00E-122//TC157892			GO:0000166//GO:0006575//GO:0009536//GO:0016653//GO:0046914	nr +

Unigene5551_All	474	43.82	287.34	121.44	49.29	111.30	74.13	51.56	61.28	67.83	2.71E+00	0.00E+00	Up	1.47E+00	4.17E-74	Up	1.18E+00	1.63E-58	Up	5.89E-01	2.22E-11		2.49E-01	6.97E-03		3.96E-01	1.84E-06		Unigene5551_All//gi|60317458|gb|AAX18706.1|//8.00E-32//cold-related protein Cor413 [Gossypium barbadense] >gi|115432869|gb|ABI97481.1| COR413-like protein [Gossypium barbadense]	Unigene5551_All//3.00E-13//AT4G37220| stress-responsive protein, putative	Unigene5551_All//5.00E-177//gi|13349918|gb|BG440267.1|BG440267				nr -
Unigene55510_All	236	5.54	9.45	3.38	13.72	13.42	10.33	39.59	29.22	12.32	7.69E-01	7.33E-02		-7.12E-01	2.42E-01		-3.15E-02	9.30E-01		-4.09E-01	2.67E-01		-4.38E-01	9.76E-03		-1.68E+00	1.05E-19	Down	Unigene55510_All//gi|110740139|dbj|BAF01968.1|//5.00E-38//receptor protein kinase like protein [Arabidopsis thaliana]	Unigene55510_All//2.00E-39//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene55510_All//8.00E-131//TC146152			GO:0003006//GO:0004702//GO:0005982//GO:0006464//GO:0006950//GO:0007167//GO:0009536//GO:0009933//GO:0010073//GO:0016160//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene55511_All	239	27.80	20.78	29.86	42.31	38.47	29.10	42.81	32.88	21.00	-4.20E-01	6.95E-02		1.03E-01	6.60E-01		-1.37E-01	5.29E-01		-5.40E-01	2.34E-03		-3.81E-01	1.93E-02		-1.03E+00	1.64E-10	Down	Unigene55511_All//gi|115481880|ref|NP_001064533.1|//8.00E-30//Os10g0397200 [Oryza sativa Japonica Group] >gi|19881736|gb|AAM01137.1|AC108884_19 Putative Transcription initiation factor IIE, beta subunit [Oryza sativa Japonica Group] >gi|113639142|dbj|BAF26447.1| Os10g0397200 [Oryza sativa Japonica Group]	Unigene55511_All//4.00E-29//AT4G20330| transcription initiation factor-related	Unigene55511_All//1.00E-132//TC177443		ko03022|Basal transcription factors	GO:0005667//GO:0006352//GO:0008135//GO:0030528	nr +
Unigene55512_All	241	23.01	10.72	11.93	29.14	29.01	43.48	32.46	45.78	28.27	-1.10E+00	1.98E-05	Down	-9.48E-01	3.46E-04		-6.90E-03	9.68E-01		5.77E-01	9.13E-04		4.96E-01	1.17E-03		-1.99E-01	3.12E-01		Unigene55512_All//gi|53850802|gb|AAY56462.1|//2.00E-35//mitogen-activated protein kinase 9 [Brassica napus]	Unigene55512_All//1.00E-31//AT3G18040| MPK9 (MAP KINASE 9); MAP kinase	Unigene55512_All//2.00E-116//TC173934		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0009755//GO:0016020//GO:0023060//GO:0032559//GO:0043231//GO:0044444	nr +
Unigene55513_All	244	0.00	1.04	0.00	0.20	0.14	0.93	1.21	3.77	4.90	1.00E+01	7.85E-02		null	null		-5.33E-01	8.24E-01		2.18E+00	3.23E-01		1.64E+00	1.74E-02		2.01E+00	7.79E-04	Up			Unigene55513_All//3.00E-07//EX166670				
Unigene55514_All	244	0.43	0.42	1.53	0.00	0.56	1.11	28.94	60.64	35.43	-4.65E-02	9.87E-01		1.83E+00	2.13E-01		9.14E+00	3.18E-01		1.01E+01	7.02E-02		1.07E+00	3.42E-15	Up	2.92E-01	1.01E-01		Unigene55514_All//gi|42566473|ref|NP_192898.2|//1.00E-30//C2 domain-containing protein [Arabidopsis thaliana] >gi|110737276|dbj|BAF00585.1| phosphoribosylanthranilate transferase like protein [Arabidopsis thaliana]	Unigene55514_All//5.00E-32//AT4G11610| C2 domain-containing protein	Unigene55514_All//7.00E-76//TC145011			GO:0030312//GO:0043231	nr +
Unigene55515_All	245	0.00	0.62	0.00	0.00	0.14	0.37	0.17	3.24	3.74	9.28E+00	2.35E-01		null	null		7.14E+00	8.28E-01		8.53E+00	4.75E-01		4.23E+00	1.05E-04	Up	4.44E+00	1.24E-05	Up			Unigene55515_All//3.00E-07//DW499508				
Unigene55518_All	265	0.00	0.00	0.00	0.38	0.00	0.00	209.01	145.73	56.83	null	null		null	null		-8.55E+00	3.12E-01		-8.55E+00	3.98E-01		-5.20E-01	2.59E-16		-1.88E+00	4.14E-131	Down	Unigene55518_All//gi|297845226|ref|XP_002890494.1|//2.00E-34//F2E2.22 [Arabidopsis lyrata subsp. lyrata] >gi|297336336|gb|EFH66753.1| F2E2.22 [Arabidopsis lyrata subsp. lyrata]	Unigene55518_All//4.00E-35//AT1G22150| SULTR1;3; sulfate transmembrane transporter	Unigene55518_All//4.00E-68//ES813014			GO:0015103//GO:0015291//GO:0015698//GO:0031224	nr -
Unigene5552_All	476	32.54	275.28	61.19	13.40	22.28	25.14	24.96	46.54	37.58	3.08E+00	0.00E+00	Up	9.11E-01	7.57E-18		7.34E-01	8.59E-06		9.08E-01	2.09E-08		8.99E-01	5.20E-17		5.90E-01	2.51E-07		Unigene5552_All//gi|28268682|dbj|BAC56909.1|//2.00E-32//RelA homolog [Suneda japonica]	Unigene5552_All//6.00E-29//AT1G54130| RSH3 (RELA/SPOT HOMOLOG 3); GTP diphosphokinase	Unigene5552_All//0.00E+00//TC150225				nr -
Unigene55520_All	274	0.57	0.18	0.39	0.00	0.75	0.16	1.08	3.05	4.80	-1.63E+00	4.88E-01		-5.60E-01	7.75E-01		9.56E+00	1.57E-01		7.36E+00	6.95E-01		1.50E+00	3.73E-02		2.15E+00	2.01E-04	Up							
Unigene55521_All	276	0.00	0.92	0.00	0.00	0.12	0.00	295.04	87.38	163.40	9.84E+00	7.85E-02		null	null		6.96E+00	8.28E-01		null	null		-1.76E+00	2.90E-170	Down	-8.53E-01	7.33E-57		Unigene55521_All//gi|61161985|dbj|BAD91046.1|//1.00E-32//(E)-beta-ocimene synthase [Citrus unshiu]	Unigene55521_All//2.00E-26//AT3G25830| ATTPS-CIN (terpene synthase-like sequence-1,8-cineole); (E)-beta-ocimene synthase/ myrcene synthase	Unigene55521_All//8.00E-85//gi|109888657|gb|DW517626.1|DW517626		ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0010333//GO:0046872	nr +
Unigene55522_All	283	181.55	119.78	153.92	163.35	201.26	199.17	273.70	111.95	133.31	-6.00E-01	6.15E-16		-2.38E-01	2.31E-03		3.01E-01	3.95E-06		2.86E-01	3.41E-05		-1.29E+00	7.53E-103	Down	-1.04E+00	6.45E-75	Down	Unigene55522_All//gi|23507246|gb|AAN38066.1|//2.00E-34//oligomycin sensitivity conferring protein [Silene latifolia]	Unigene55522_All//4.00E-28//AT5G13450| ATP synthase delta chain, mitochondrial, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative	Unigene55522_All//9.00E-159//gi|11202445|gb|BF271450.1|BF271450		ko00190|Oxidative phosphorylation	GO:0000275//GO:0003824//GO:0006754//GO:0006818//GO:0015078	nr -
Unigene55523_All	290	63.15	33.90	26.99	90.87	76.95	85.65	139.38	83.30	67.31	-8.98E-01	1.10E-11		-1.23E+00	3.81E-18	Down	-2.40E-01	2.34E-02		-8.52E-02	5.16E-01		-7.43E-01	3.88E-22		-1.05E+00	2.84E-40	Down	Unigene55523_All//gi|195620934|gb|ACG32292.1|//7.00E-50//60S ribosomal protein L23 [Zea mays]	Unigene55523_All//2.00E-50//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene55523_All//2.00E-150//TC159257		ko03010|Ribosome	GO:0003006//GO:0005198//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene55524_All	297	8.63	3.92	7.53	14.09	14.72	14.75	31.89	16.04	13.82	-1.14E+00	4.51E-03		-1.97E-01	6.16E-01		6.37E-02	8.50E-01		6.62E-02	8.46E-01		-9.91E-01	5.60E-09		-1.21E+00	1.96E-12	Down			Unigene55524_All//2.00E-116//gi|21101812|gb|BQ414125.1|BQ414125				
Unigene55526_All	313	0.00	0.00	0.00	0.00	0.11	0.00	9.86	7.61	2.16	null	null		null	null		6.78E+00	8.28E-01		null	null		-3.74E-01	2.62E-01		-2.19E+00	1.15E-09	Down							
Unigene55527_All	374	0.00	0.00	0.00	0.00	0.00	0.00	1.47	4.25	4.37	null	null		null	null		null	null		null	null		1.53E+00	1.78E-03		1.57E+00	8.81E-04	Up							
Unigene5553_All	1054	0.15	0.38	0.20	9.64	9.12	4.97	75.21	73.88	8.20	1.37E+00	2.73E-01		4.41E-01	7.75E-01		-8.10E-02	7.16E-01		-9.56E-01	6.53E-08		-2.59E-02	6.95E-01		-3.20E+00	0.00E+00	Down	Unigene5553_All//gi|9294177|dbj|BAB02079.1|//1.00E-60//nodulin-like protein [Arabidopsis thaliana]	Unigene5553_All//1.00E-44//AT3G25190| nodulin, putative	Unigene5553_All//0.00E+00//gi|109868191|gb|DW497167.1|DW497167				nr -
Unigene55530_All	560	0.00	0.00	0.57	1.07	0.49	0.81	1.96	4.55	3.20	null	null		9.16E+00	4.50E-02		-1.12E+00	2.26E-01		-4.04E-01	6.73E-01		1.21E+00	7.71E-04	Up	7.06E-01	9.48E-02		Unigene55530_All//gi|18411317|ref|NP_565146.1|//2.00E-76//ACR3; amino acid binding [Arabidopsis thaliana] >gi|30699222|ref|NP_849896.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|30699224|ref|NP_849897.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|79321337|ref|NP_001031289.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|186495930|ref|NP_001117608.1| ACR3; amino acid binding [Arabidopsis thaliana] >gi|2829923|gb|AAC00631.1| Similar to uridylyl transferases [Arabidopsis thaliana] >gi|22138096|gb|AAM93428.1| ACR3 [Arabidopsis thaliana] >gi|222424164|dbj|BAH20041.1| AT1G76990 [Arabidopsis thaliana]	Unigene55530_All//1.00E-77//AT1G76990| ACR3; amino acid binding	Unigene55530_All//0.00E+00//gi|78340822|gb|DT561096.1|DT561096			GO:0031406//GO:0044444	nr -
Unigene55534_All	639	0.00	0.00	0.00	0.00	0.16	0.00	2.05	9.75	5.36	null	null		null	null		7.34E+00	4.55E-01		null	null		2.25E+00	1.29E-18	Up	1.39E+00	5.42E-06	Up	Unigene55534_All//gi|224109632|ref|XP_002315262.1|//1.00E-100//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222864302|gb|EEF01433.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene55534_All//5.00E-101//AT5G13580| ABC transporter family protein	Unigene55534_All//4.00E-144//CA994013		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015405//GO:0016020//GO:0017111//GO:0032559//GO:0051707	nr -
Unigene55537_All	203	0.00	0.00	0.00	0.25	0.00	0.67	257.01	30.68	44.94	null	null		null	null		-7.94E+00	5.54E-01		1.44E+00	6.38E-01		-3.07E+00	7.36E-214	Down	-2.52E+00	2.31E-178	Down	Unigene55537_All//gi|224139378|ref|XP_002323083.1|//1.00E-22//cytochrome P450 [Populus trichocarpa] >gi|222867713|gb|EEF04844.1| cytochrome P450 [Populus trichocarpa]	Unigene55537_All//3.00E-19//AT3G26330| CYP71B37; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene55537_All//5.00E-104//gi|109825823|gb|DW224545.1|DW224545		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0003006//GO:0004497//GO:0005506//GO:0008152//GO:0031090//GO:0031224//GO:0031410//GO:0042598//GO:0043231	nr -
Unigene55538_All	203	0.00	0.00	0.00	0.00	0.17	0.00	47.07	57.65	9.22	null	null		null	null		7.41E+00	8.28E-01		null	null		2.93E-01	5.88E-02		-2.35E+00	8.73E-31	Down	Unigene55538_All//gi|297801398|ref|XP_002868583.1|//5.00E-29//ATCHX18 [Arabidopsis lyrata subsp. lyrata] >gi|297314419|gb|EFH44842.1| ATCHX18 [Arabidopsis lyrata subsp. lyrata]	Unigene55538_All//2.00E-30//AT5G41610| ATCHX18; monovalent cation:proton antiporter/ sodium:hydrogen antiporter				GO:0006811//GO:0015298//GO:0031224	nr +
Unigene55539_All	203	0.00	0.00	0.00	0.00	0.00	0.00	110.39	23.88	81.44	null	null		null	null		null	null		null	null		-2.21E+00	6.44E-64	Down	-4.39E-01	1.30E-05		Unigene55539_All//gi|16648951|gb|AAL24327.1|//2.00E-07//Unknown protein [Arabidopsis thaliana] >gi|31711760|gb|AAP68236.1| At3g01670 [Arabidopsis thaliana]	Unigene55539_All//1.00E-08//AT3G01670| unknown protein	Unigene55539_All//1.00E-42//gi|164339641|gb|ES801569.1|ES801569				nr -
Unigene55540_All	203	0.00	0.00	0.00	0.00	0.17	0.00	194.11	157.09	59.46	null	null		null	null		7.41E+00	8.28E-01		null	null		-3.05E-01	6.40E-05		-1.71E+00	6.60E-82	Down	Unigene55540_All//gi|224084714|ref|XP_002307394.1|//3.00E-25//high affinity sulfate transporter SAT-1, Sulfate/bicarbonate/oxalate exchanger SLC26 family protein [Populus trichocarpa] >gi|222856843|gb|EEE94390.1| high affinity sulfate transporter SAT-1, Sulfate/bicarbonate/oxalate exchanger SLC26 family protein [Populus trichocarpa]	Unigene55540_All//6.00E-25//AT1G22150| SULTR1;3; sulfate transmembrane transporter	Unigene55540_All//6.00E-08//ES813014			GO:0015103//GO:0015291//GO:0015698//GO:0031224	nr -
Unigene55544_All	210	0.00	0.00	0.00	0.00	0.00	0.00	78.52	33.83	22.39	null	null		null	null		null	null		null	null		-1.21E+00	1.46E-20	Down	-1.81E+00	1.11E-37	Down	Unigene55544_All//gi|121490210|emb|CAK35186.1|//3.00E-18//pinene synthase [Quercus ilex]	Unigene55544_All//4.00E-69//AT3G25810| myrcene/ocimene synthase, putative	Unigene55544_All//4.00E-58//DW510560		ko00900|Terpenoid backbone biosynthesis//ko00902|Monoterpenoid biosynthesis	GO:0009536//GO:0010333//GO:0046872	nr +
Unigene55546_All	213	0.00	0.00	0.00	0.00	0.32	1.27	0.00	2.35	58.92	null	null		null	null		8.34E+00	6.08E-01		1.03E+01	7.02E-02		1.12E+01	1.02E-03		1.58E+01	4.60E-90	Up	Unigene55546_All//gi|83853828|gb|AB547860.1|//8.00E-16//N-hydroxycinnamoyl/benzoyltransferase 1 [Glycine max]	Unigene55546_All//5.00E-15//AT5G42830| transferase family protein				GO:0016740	nr +
Unigene55549_All	215	176.43	191.84	244.95	89.67	114.52	90.75	70.01	115.08	29.65	1.21E-01	1.91E-01		4.73E-01	2.03E-10		3.53E-01	7.90E-04		1.73E-02	9.28E-01		7.17E-01	4.33E-13		-1.24E+00	4.88E-20	Down	Unigene55549_All//gi|224111880|ref|XP_002316010.1|//1.00E-17//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene55549_All//1.00E-10//AT3G14640| CYP72A10; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene55549_All//1.00E-113//TC152138		ko00908|Zeatin biosynthesis//ko00591|Linoleic acid metabolism	GO:0005506//GO:0008152//GO:0016020//GO:0016491	nr +
Unigene5555_All	1184	0.00	0.17	0.00	1.30	1.28	1.75	4.86	1.41	1.82	7.42E+00	1.36E-01		null	null		-2.75E-02	9.58E-01		4.28E-01	3.90E-01		-1.78E+00	5.75E-13	Down	-1.42E+00	6.99E-10	Down	Unigene5555_All//gi|6094335|sp|O82147.1|SPDE_COFAR//1.00E-114//RecName: Full=Spermidine synthase; Short=SPDSY; AltName: Full=Putrescine aminopropyltransferase >gi|3242659|dbj|BAA29033.1| spermidine synthase [Coffea arabica]	Unigene5555_All//1.00E-103//AT1G23820| SPDS1 (spermidine synthase 1); spermidine synthase	Unigene5555_All//9.00E-11//TC142674		ko00270|Cysteine and methionine metabolism//ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism//ko00410|beta-Alanine metabolism		nr +
Unigene55551_All	218	69.84	29.29	27.36	101.00	119.26	123.68	99.88	64.42	67.62	-1.25E+00	2.07E-16	Down	-1.35E+00	1.42E-17	Down	2.40E-01	2.67E-02		2.92E-01	5.84E-03		-6.33E-01	1.72E-09		-5.63E-01	4.08E-08		Unigene55551_All//gi|192913036|gb|ACF06626.1|//1.00E-34//S6 ribosomal protein [Elaeis guineensis]	Unigene55551_All//8.00E-35//AT5G10360| EMB3010 (embryo defective 3010); structural constituent of ribosome	Unigene55551_All//2.00E-79//gi|109862643|gb|DW491620.1|DW491620		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene55555_All	221	76.94	62.59	66.26	86.78	72.14	95.44	65.24	33.85	20.73	-2.98E-01	3.15E-02		-2.16E-01	1.48E-01		-2.67E-01	3.50E-02		1.37E-01	3.34E-01		-9.46E-01	2.50E-12		-1.65E+00	3.31E-29	Down	Unigene55555_All//gi|222422853|dbj|BAH19413.1|//2.00E-34//AT5G62890 [Arabidopsis thaliana]	Unigene55555_All//9.00E-36//AT5G62890| permease, putative	Unigene55555_All//7.00E-122//ES791134			GO:0005215//GO:0006810//GO:0030312//GO:0043231	nr +
Unigene55556_All	221	20.83	48.38	31.56	44.40	72.77	77.66	32.71	80.00	68.32	1.22E+00	3.57E-11	Up	5.99E-01	9.52E-03		7.13E-01	4.11E-08		8.06E-01	9.63E-10		1.29E+00	4.83E-24	Up	1.06E+00	9.00E-16	Up	Unigene55556_All//gi|6090831|gb|AAF03356.1|AF134485_1//3.00E-17//cytidine deaminase 1 [Arabidopsis thaliana]	Unigene55556_All//1.00E-18//AT2G19570| CDA1 (CYTIDINE DEAMINASE 1); cytidine deaminase	Unigene55556_All//7.00E-122//gi|13352281|gb|BG442629.1|BG442629		ko00240|Pyrimidine metabolism	GO:0006216//GO:0016787//GO:0046872	nr +
Unigene55557_All	222	0.24	0.46	0.72	0.22	0.62	0.00	1.33	0.94	7.54	9.54E-01	7.25E-01		1.61E+00	5.11E-01		1.47E+00	6.18E-01		-7.81E+00	6.33E-01		-5.02E-01	6.77E-01		2.50E+00	2.63E-06	Up			Unigene55557_All//2.00E-07//TC138402				

Unigene55559_All	230	36.17	27.10	15.51	81.00	64.68	82.28	50.18	31.80	25.81	-4.17E-01	4.07E-02		-1.22E+00	1.56E-08	Down	-3.25E-01	9.04E-03		2.25E-02	9.00E-01		-6.58E-01	9.52E-06		-9.59E-01	1.39E-10		Unigene55559_All//gi|115469972|ref|NP_001058585.1|//2.00E-27//0s06g0715500 [Oryza sativa Japonica Group] >gi|113596625|dbj|BAF20499.1|Os06g0715500 [Oryza sativa Japonica Group]	Unigene55559_All//2.00E-24//AT2G21160| translocon-associated protein alpha (TRAP alpha) family protein	Unigene55559_All//7.00E-125//EV496941		ko04141|Protein processing in endoplasmic reticulum	GO:0031410	nr -
Unigene5556_All	301	2.26	7.58	4.95	2.81	2.40	12.30	424.49	627.49	1265.44	1.75E+00	1.48E-04	Up	1.13E+00	4.89E-02		-2.28E-01	7.78E-01		2.13E+00	3.69E-09	Up	5.64E-01	7.10E-62		1.58E+00	0.00E+00	Up	Unigene5556_All//gi|89258498|gb|ABD65462.1|//3.00E-37//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene5556_All//7.00E-12//AT1G52340| ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase	Unigene5556_All//3.00E-155//TC163778		ko00906|Carotenoid biosynthesis		nr -
Unigene55564_All	249	0.00	0.00	0.43	0.60	0.97	1.09	1.19	0.17	5.28	null	null		8.74E+00	3.97E-01		6.90E-01	7.32E-01		8.59E-01	6.31E-01		-2.82E+00	8.84E-02		2.15E+00	2.01E-04	Up								ESTscan +
Unigene55569_All	338	1.86	2.25	0.32	0.15	0.82	0.53	2.63	6.92	7.43	2.76E-01	7.10E-01		-2.56E+00	2.72E-02		2.47E+00	2.23E-01		1.86E+00	4.58E-01		1.40E+00	2.91E-04	Up	1.50E+00	4.49E-05	Up			Unigene55569_All//4.00E-07//TC149099					
Unigene5557_All	572	3.29	2.48	1.77	2.26	2.89	5.29	105.92	104.42	108.44	-4.09E-01	3.92E-01		-8.97E-01	7.25E-02		3.52E-01	5.61E-01		1.22E+00	7.75E-04	Up	-2.07E-02	7.82E-01		3.39E-02	6.42E-01		Unigene5557_All//gi|89258498|gb|ABD65462.1|//3.00E-39//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene5557_All//1.00E-11//AT4G03140| binding / catalytic/ oxidoreductase	Unigene5557_All//0.00E+00//TC146897		ko00906|Carotenoid biosynthesis		nr -
Unigene55570_All	435	0.24	0.00	0.00	0.00	0.00	0.31	270.11	149.31	132.25	-7.91E+00	3.70E-01		-7.91E+00	3.91E-01		null	null		8.28E+00	3.10E-01		-8.55E-01	7.12E-80		-1.03E+00	6.99E-112	Down	Unigene55570_All//gi|115476924|ref|NP_001062058.1|//1.00E-14//0s08g0480200 [Oryza sativa Japonica Group] >gi|113624027|dbj|BAF23972.1|Os08g0480200 [Oryza sativa Japonica Group]	Unigene55570_All//2.00E-13//AT2G44800| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene55570_All//3.00E-61//TC148687		ko00941|Flavonoid biosynthesis	GO:0008152//GO:0016706	nr -
Unigene55572_All	289	2.72	0.00	2.03	0.00	0.12	0.00	0.88	0.00	0.28	-1.14E+01	1.09E-04	Down	-4.22E-01	6.21E-01		6.90E+00	8.28E-01		null	null		-9.78E+00	4.03E-02		-1.67E+00	2.56E-01		Unigene55572_All//gi|2808682|emb|CAA05267.1|//1.00E-12//Hcr9-4C [Solanum habrochaites]	Unigene55572_All//2.00E-12//AT1G45616| AtRLP6 (Receptor Like Protein 6); protein binding	Unigene55572_All//1.00E-102//TC167958			GO:0023060//GO:0044464	nr -
Unigene55579_All	322	12.51	4.88	5.29	20.88	13.47	20.06	44.12	25.18	13.98	-1.36E+00	1.82E-05	Down	-1.24E+00	1.36E-04	Down	-6.32E-01	2.92E-03		-5.83E-02	8.19E-01		-8.09E-01	1.63E-09		-1.66E+00	6.90E-29	Down			Unigene55579_All//3.00E-125//gi|109839164|gb|DW237725.1|DW237725					
Unigene55582_All	275	12.94	25.98	11.81	23.91	19.66	18.89	87.64	107.76	60.99	1.01E+00	6.49E-06	Up	-1.31E-01	7.01E-01		-2.82E-01	2.45E-01		-3.40E-01	1.64E-01		2.98E-01	9.04E-04		-5.23E-01	6.85E-08		Unigene55582_All//gi|225348627|gb|ACN87275.1|//3.00E-19//short chain dehydrogenase/reductase [Nandina domestica]	Unigene55582_All//5.00E-19//AT1G01800| short-chain dehydrogenase/reductase (SDR) family protein	Unigene55582_All//3.00E-106//TC154214			GO:0008152//GO:0016491	nr -
Unigene5559_All	506	50.67	101.54	84.61	89.88	117.73	128.35	19.72	23.79	28.66	1.00E+00	1.67E-37	Up	7.40E-01	2.47E-18		3.89E-01	5.30E-10		5.14E-01	3.42E-16		2.71E-01	7.84E-02		5.39E-01	2.51E-05		Unigene5559_All//gi|18399975|ref|NP_566453.1|//3.00E-43//WD-40 repeat family protein [Arabidopsis thaliana] >gi|15081811|gb|AAK82560.1|AT3g13340/MDC11_13 [Arabidopsis thaliana] >gi|22655036|gb|AAM98109.1|At3g13340/MDC11_13 [Arabidopsis thaliana]	Unigene5559_All//2.00E-44//AT3G13340| WD-40 repeat family protein	Unigene5559_All//0.00E+00//gi|78353820|gb|DT574094.1|DT574094				nr -
Unigene55595_All	221	2.13	0.00	2.89	0.68	0.16	0.41	21.62	48.98	25.06	-1.11E+01	5.54E-03		4.40E-01	6.23E-01		-2.12E+00	3.86E-01		-7.26E-01	7.15E-01		1.18E+00	3.56E-13	Up	2.13E-01	3.74E-01		Unigene55595_All//gi|50363355|gb|AAT75354.1|//1.00E-12//laccase-like multicopper oxidase 130 [Ginkgo biloba]	Unigene55595_All//5.00E-11//AT2G40370| LAC5 (laccase 5); laccase	Unigene55595_All//2.00E-79//gi|78331794|gb|DT552068.1|DT552068			GO:0005576//GO:0009808//GO:0010038//GO:0016682//GO:0046914	nr +
Unigene5560_All	521	20.49	25.87	21.67	24.57	20.29	26.61	20.69	18.53	7.95	3.37E-01	3.19E-02		8.09E-02	6.63E-01		-2.76E-01	8.56E-02		1.15E-01	5.36E-01		-1.59E-01	3.78E-01		-1.38E+00	4.46E-17	Down	Unigene5560_All//gi|14596113|gb|AAK68784.1|//5.00E-28//Unknown protein [Arabidopsis thaliana]	Unigene5560_All//3.00E-28//AT1G20430| unknown protein	Unigene5560_All//0.00E+00//TC148310				nr -
Unigene55605_All	204	0.00	0.00	0.00	0.00	0.34	0.22	0.62	0.61	4.10	null	null		null	null		8.40E+00	6.08E-01		7.79E+00	6.95E-01		-1.68E-02	1.02E+00		2.72E+00	8.98E-04	Up								
Unigene5561_All	494	4.98	5.13	2.80	10.79	12.34	10.61	23.11	2.88	2.90	4.30E-02	9.27E-01		-8.29E-01	5.05E-02		1.94E-01	4.98E-01		-2.49E-02	9.42E-01		-3.01E+00	2.70E-46	Down	-2.99E+00	1.26E-47	Down	Unigene5561_All//gi|225435490|ref|XP_002285519.1|//9.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene55610_All	497	3.26	4.28	3.11	6.72	10.39	12.18	2.81	0.67	2.73	3.92E-01	3.80E-01		-7.09E-02	8.95E-01		6.30E-01	1.42E-02		8.59E-01	3.12E-04		-2.06E+00	2.51E-04	Down	-4.27E-02	9.47E-01		Unigene55610_All//gi|1335882|gb|AAC49294.1|//2.00E-40//clathrin heavy chain [Glycine max]	Unigene55610_All//4.00E-46//AT3G11130| clathrin heavy chain, putative	Unigene55610_All//1.00E-106//TC137329		ko04144|Endocytosis	GO:0005488//GO:0005905//GO:0009536//GO:0012510//GO:0015031	nr +
Unigene5562_All	914	3.03	1.77	5.83	6.10	7.72	5.83	3.98	8.69	2.22	-7.74E-01	3.96E-02		9.41E-01	5.06E-04		3.40E-01	1.43E-01		-6.61E-02	8.11E-01		1.13E+00	3.08E-09	Up	-8.40E-01	2.52E-03		Unigene5562_All//gi|239121397|gb|ACY92018.1|//5.00E-40//WRKY transcription factor 16 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene5562_All//1.00E-30//AT5G26170| WRKY50; transcription factor	Unigene5562_All//0.00E+00//DW496555	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene5566_All	899	0.64	0.06	0.24	4.54	3.33	2.26	0.89	1.02	2.61	-3.50E+00	9.02E-03		-1.43E+00	1.75E-01		-4.47E-01	1.39E-01		-1.01E+00	7.39E-04	Down	1.95E-01	7.62E-01		1.55E+00	5.38E-05	Up			Unigene5566_All//2.00E-70//C0083681					ESTscan -
Unigene5567_All	580	4.42	4.54	7.99	8.42	4.16	6.54	2.11	1.51	1.65	3.95E-02	9.34E-01		8.54E-01	3.51E-03		-1.02E+00	5.81E-05	Down	-3.64E-01	2.13E-01		-4.82E-01	4.08E-01		-3.59E-01	5.10E-01				Unigene5567_All//3.00E-111//gi|109835786|gb|DW234349.1|DW234349					
Unigene5568_All	843	0.00	0.24	0.63	7.21	0.57	37.98	24.43	99.66	87.29	7.91E+00	1.36E-01		9.30E+00	4.03E-03		-3.66E+00	6.87E-31	Down	2.40E+00	1.49E-87	Up	2.03E+00	5.62E-213	Up	1.84E+00	9.37E-167	Up	Unigene5568_All//gi|83853951|gb|ABC47922.1|//3.00E-59//pathogenesis-related protein 1a [Malus x domestica]	Unigene5568_All//2.00E-51//AT2G14610| PR1 (PATHOGENESIS-RELATED GENE 1)	Unigene5568_All//0.00E+00//gi|3326231|gb|AI055117.1|AI055117		ko04626|Plant-pathogen interaction		nr -
Unigene55692_All	209	4.51	0.24	3.06	0.00	0.00	0.00	0.00	0.00	0.76	-4.22E+00	1.36E-04	Down	-5.60E-01	4.39E-01		null	null		null	null		null	null		9.57E+00	1.40E-01		Unigene55692_All//gi|224131512|ref|XP_002328858.1|//3.00E-06//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222838273|gb|EEE76638.1| cc-nbs-lrr resistance protein [Populus trichocarpa]					GO:0006950//GO:0012501//GO:0016462//GO:0032559	nr +
Unigene5570_All	500	83.61	120.90	147.82	99.43	159.37	97.55	120.33	121.29	56.17	5.32E-01	4.16E-15		8.22E-01	2.09E-37		6.81E-01	1.28E-35		-2.75E-02	7.63E-01		1.15E-02	8.88E-01		-1.10E+00	4.93E-64	Down	Unigene5570_All//gi|186506150|ref|NP_001118462.1|//6.00E-08//CPuORF52 (Conserved peptide upstream open reading frame 52) [Arabidopsis thaliana] >gi|13926174|gb|AAK49569.1|AF370561_1 Unknown protein [Arabidopsis thaliana] >gi|4056498|gb|AAC98064.1| expressed protein [Arabidopsis thaliana]		Unigene5570_All//3.00E-129//TC171281				nr -
Unigene5573_All	451	14.62	18.76	17.24	6.30	10.77	10.72	13.97	7.51	5.04	3.60E-01	7.82E-02		2.38E-01	3.10E-01		7.74E-01	3.28E-03		7.67E-01	4.89E-03		-8.96E-01	2.12E-05		-1.47E+00	2.61E-11	Down	Unigene5573_All//gi|195626734|gb|ACG35197.1|//3.00E-21//Grave disease carrier protein [Zea mays]	Unigene5573_All//2.00E-12//AT4G01100| ADNT1 (ADENINE NUCLEOTIDE TRANSPORTER 1); ADP transmembrane transporter/ AMP transmembrane transporter/ ATP transmembrane transporter/ binding	Unigene5573_All//0.00E+00//gi|78333268|gb|DT553542.1|DT553542				nr +
Unigene5574_All	680	21.39	50.00	26.86	26.23	27.55	35.67	27.61	43.09	36.56	1.23E+00	2.55E-34	Up	3.29E-01	1.70E-02		7.10E-02	6.52E-01		4.44E-01	4.30E-05		6.42E-01	8.76E-13		4.05E-01	2.16E-05		Unigene5574_All//gi|15231750|ref|NP_190880.1|//2.00E-37//VPS37-1 [Arabidopsis thaliana] >gi|75202732|sp|Q9SCP9.1|VPS71_ARATH RecName: Full=Vacuolar protein-sorting-associated protein 37 homolog 1; Short=AtVPS37-1; AltName: Full=ESCRT-I complex subunit VPS37 homolog 1	Unigene5574_All//5.00E-35//AT3G53120| VPS37-1	Unigene5574_All//0.00E+00//TC151932		ko04144|Endocytosis		nr -
Unigene55745_All	204	3.33	0.00	1.57	0.00	0.84	0.66	0.00	0.41	0.00	-1.17E+01	4.09E-04	Down	-1.09E+00	2.39E-01		9.72E+00	2.27E-01		9.38E+00	3.10E-01		8.68E+00	4.00E-01		null	null									
Unigene55754_All	560	10.46	4.07	5.80	228.79	132.15	127.59	1117.56	341.23	798.69	-1.36E+00	1.31E-07	Down	-8.51E-01	8.65E-04		-7.92E-01	9.29E-77		-8.43E-01	3.66E-75		-1.71E+00	0.00E+00	Down	-4.85E-01	1.14E-158		Unigene55754_All//gi|1015937|emb|CAA62943.1|//4.00E-96//extensin class 1 protein [Vigna unguiculata]		Unigene55754_All//5.00E-29//TC163551		ko03040|Spliceosome		nr -
Unigene5576_All	1282	2.98	0.16	0.21	3.96	3.60	1.51	1.78	0.33	0.44	-4.24E+00	3.71E-17	Down	-3.84E+00	2.88E-15	Down	-1.39E-01	6.31E-01		-1.39E+00	3.12E-07	Down	-2.45E+00	5.49E-08	Down	-2.03E+00	8.82E-07	Down	Unigene5576_All//gi|9802540|gb|AAF99742.1|AC004557_21//1.00E-50//F17L21.26 [Arabidopsis thaliana]	Unigene5576_All//2.00E-49//AT1G27461| unknown protein	Unigene5576_All//6.00E-40//ES791879				nr +
Unigene55772_All	350	3.74	0.14	0.00	0.85	2.16	0.77	2.42	0.00	1.14	-4.69E+00	1.63E-06	Down	-1.19E+01	3.71E-07	Down	1.34E+00	1.23E-01		-1.42E-01	9.20E-01		-1.12E+01	4.39E-06	Down	-1.09E+00	9.98E-02		Unigene55772_All//gi|15220076|ref|NP_178136.1|//3.00E-40//PSF1 (PARTNER OF SLD FIVE 1) [Arabidopsis thaliana] >gi|5902373|gb|AAD55475.1|AC009322_15 Unknown protein [Arabidopsis thaliana] >gi|34365591|gb|AAQ65107.1|At1g80190 [Arabidopsis thaliana] >gi|51969246|dbj|BAD43315.1|At1g80190 [Arabidopsis thaliana]	Unigene55772_All//1.00E-41//AT1G80190| PSF1 (PARTNER OF SLD FIVE 1)	Unigene55772_All//8.00E-98//ES850894			GO:0006259//GO:0009536//GO:0043234	nr -
Unigene5578_All	530	1.78	3.25	0.70	0.47	2.01	4.77	3.51	2.68	3.31	8.71E-01	8.07E-02		-1.34E+00	8.48E-02		2.10E+00	4.32E-03		3.34E+00	4.82E-10	Up	-3.89E-01	3.99E-01		-8.58E-02	8.38E-01		Unigene5578_All//gi|30102914|gb|AAP21375.1|//5.00E-17//At3g61920 [Arabidopsis thaliana]	Unigene5578_All//3.00E-18//AT3G61920| unknown protein	Unigene5578_All//0.00E+00//DW499016				nr -
Unigene55788_All	202	1.04	0.25	0.00	0.00	0.00	0.00	0.42	4.55	0.00	-2.05E+00	3.33E-01		-1.00E+01	1.45E-01		null	null		null	null		3.44E+00	9.84E-05	Up	-8.71E+00	3.57E-01				Unigene55788_All//4.00E-15//BQ412901					
Unigene55797_All	236	6.21	3.22	4.96	2.32	0.58	3.64	1.61	6.38	3.55	-9.47E-01	8.40E-02		-3.23E-01	5.91E-01		-1.99E+00	5.12E-02		6.47E-01	4.23E-01		1.98E+00	2.06E-04	Up	1.14E+00	9.20E-02				Unigene55797_All//4.00E-34//DW242989					
Unigene558_All	430	1.70	0.47	0.87	4.52	3.52	1.47	0.59	0.29	0.37	-1.85E+00	4.08E-02		-9.75E-01	2.64E-01		-3.59E-01	4.59E-01		-1.62E+00	8.10E-04	Down	-1.02E+00	4.94E-01		-6.71E-01	6.05E-01		Unigene558_All//gi|124360022|gb|ABN08038.1|//1.00E-17//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene558_All//1.00E-09//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative				GO:0003676//GO:0016772//GO:0044238//GO:0044260//GO:0044464	nr -
Unigene5580_All	1568	0.00	0.00	0.14	0.60	0.42	0.26	23.41	19.89	98.02	null	null		7.09E+00	1.40E-01		-5.33E-01	4.51E-01		-1.22E+00	9.72E-02		-2.35E-01	3.78E-03		2.07E+00	0.00E+00	Up	Unigene5580_All//gi|15239586|ref|NP_197387.1|//0.00E+00//inosine-uridine preferring nucleoside hydrolase family protein [Arabidopsis thaliana] >gi|193104227|gb|ALS48950.1|AT5g18860/F17K4_110 [Arabidopsis thaliana] >gi|22137232|gb|AAM91461.1|AT5g18860/F17K4_110 [Arabidopsis thaliana]	Unigene5580_All//8.00E-180//AT5G18860| inosine-uridine preferring nucleoside hydrolase family protein	Unigene5580_All//5.00E-47//C0076142				nr +
Unigene5581_All	394	13.94	9.26	16.22	16.18	20.54	16.74	20.71	9.34	19.31	-5.91E-01	2.01E-02		2.18E-01	3.84E-01		3.44E-01	1.04E-01		4.84E-02	8.61E-01		-1.15E+00	9.14E-10	Down	-1.01E-01	6.13E-01		Unigene5581_All//gi|87241162|gb|ABD33020.1|//9.00E-10//Phosphatidate cytidylyltransferase [Medicago truncatula]	Unigene5581_All//2.00E-10//AT1G62430| ATCDS1; phosphatidate cytidylyltransferase	Unigene5581_All//3.00E-11//C0123529		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism		nr +
Unigene5582_All	1070	4.55	0.90	2.44	5.26	3.93	5.02	2.53	1.17	1.30	-2.34E+00	1.11E-12	Down	-8.99E-01	1.60E-03		-4.22E-01	8.98E-02		-6.68E-02	8.08E-01		-1.11E+00	1.31E-03		-9.57E-01	3.85E-03		Unigene5582_All//gi|297799948|ref|XP_002867858.1|//1.00E-103//bacterial transferase hexapeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297313694|gb|EFH44117.1| bacterial transferase hexapeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene5582_All//3.00E-103//AT4G21220| bacterial transferase hexapeptide repeat-containing protein					nr +
Unigene55838_All	431	0.36	1.41	0.25	0.12	0.24	0.21	2.06	0.10	0.65	1.95E+00	6.03E-02		-5.60E-01	7.75E-01		1.05E+00	8.07E-01		8.59E-01	7.94E-01		-4.41E+00	2.44E-05	Down	-1.67E+00	1.33E-02				Unigene55838_All//1.00E-161//C0493262					
Unigene55844_All	971	0.27	0.31	0.00	0.05	0.25	0.14	1.22	0.22	0.41	2.17E-01	8.64E-01		-8.07E+00	8.55E-02		2.27E+00	3.05E-01		1.44E+00	6.38E-01		-2.50E+00	1.47E-04	Down	-1.57E+00	5.26E-03		Unigene55844_All//gi|30680213|ref|NP_849971.1|//4.00E-13//PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein [Arabidopsis thaliana] >gi|13877655|gb|AAK43905.1|AF370586_1 Unknown protein [Arabidopsis thaliana]	Unigene55844_All//2.00E-14//AT2G18090| PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein	Unigene55844_All//0.00E+00//TC148899			GO:0005488//GO:0044238//GO:0044260	nr +

Unigene5586_All	462	47.22	20.18	18.90	31.59	34.81	44.28	92.06	73.73	89.42	-1.23E+00	1.98E-22	Down	-1.32E+00	4.31E-24	Down	1.40E-01	3.93E-01		4.87E-01	4.21E-05		-3.20E-01	1.15E-05		-4.20E-02	6.29E-01		Unigene5586_All//gi|56117813|gb|AAV73837.1|//6.00E-59//protein phosphatase 2c [Medicago sativa]	Unigene5586_All//1.00E-54//AT3G02750| protein phosphatase 2C family protein / PP2C family protein	Unigene5586_All//0.00E+00//TC164108				nr -
Unigene55874_All	362	3.18	2.66	2.79	3.58	1.33	0.00	0.12	0.00	0.22	-2.58E-01	6.57E-01		-1.86E-01	7.59E-01		-1.43E+00	1.25E-02		-1.18E+01	4.24E-08	Down	-6.87E+00	6.55E-01		9.14E-01	7.49E-01					Unigene55874_All//2.00E-39//DN802561				
Unigene55878_All	290	4.87	3.15	12.85	0.17	0.59	0.00	0.00	0.00	0.00	-6.31E-01	2.56E-01		1.40E+00	4.87E-05	Up	1.79E+00	5.20E-01		-7.42E+00	6.33E-01		null	null		null	null		Unigene55878_All//gi|224074167|ref|XP_002304283.1|//7.00E-26//formyltetrahydrofolate deformylase [Populus trichocarpa] >gi|222841715|gb|EEE79262.1| formyltetrahydrofolate deformylase [Populus trichocarpa]	Unigene55878_All//6.00E-25//AT4G17360| formyltetrahydrofolate deformylase/ hydroxymethyl-, formyl- and related transferase/ methyltransferase			ko00630|Glyoxylate and dicarboxylate metabolism//ko00670|One carbon pool by folate	GO:0006188//GO:0006760//GO:0016741//GO:0016811//GO:0043094//GO:0043231	nr -
Unigene5591_All	479	76.13	53.74	37.58	79.97	67.72	79.58	153.94	99.47	60.55	-5.03E-01	1.33E-08		-1.02E+00	1.45E-26	Down	-2.40E-01	4.36E-03		-7.10E-03	9.52E-01		-6.30E-01	6.36E-30		-1.35E+00	1.33E-107	Down	Unigene5591_All//gi|224131422|ref|XP_002328535.1|//1.00E-60//histone 2 [Populus trichocarpa] >gi|222838250|gb|EEE76615.1| histone 2 [Populus trichocarpa]	Unigene5591_All//2.00E-49//AT1G54690| GAMMA-H2AX (GAMMA HISTONE VARIANT H2AX); DNA binding	Unigene5591_All//0.00E+00//TC150168				nr -
Unigene5594_All	855	0.67	1.66	1.06	3.85	5.48	4.38	0.10	0.39	2.75	1.30E+00	2.42E-02		6.54E-01	3.86E-01		5.10E-01	6.96E-02		1.89E-01	6.30E-01		1.98E+00	1.44E-01		4.80E+00	3.23E-14	Up				Unigene5594_All//2.00E-38//CO083681				
Unigene55961_All	219	1.67	0.00	0.97	13.65	7.70	9.69	19.50	32.25	7.28	-1.07E+01	1.96E-02		-7.82E-01	5.53E-01		-8.25E-01	1.57E-02		-4.94E-01	1.95E-01		7.26E-01	2.14E-04		-1.42E+00	1.38E-07	Down	Unigene55961_All//gi|15217543|ref|NP_177315.1|//6.00E-14//ATCK1 (CHOLINE KINASE 1); choline kinase [Arabidopsis thaliana] >gi|30725296|gb|AAP37670.1| At1g71697 [Arabidopsis thaliana] >gi|110739418|dbj|BAF01619.1| choline kinase like protein [Arabidopsis thaliana] >gi|110741310|dbj|BAF02205.1| choline kinase like protein [Arabidopsis thaliana]	Unigene55961_All//2.00E-15//AT1G71697| ATCK1 (CHOLINE KINASE 1); choline kinase	Unigene55961_All//8.00E-100//gi|109844764|gb|DW243322.1|DW243322		ko00564|Glycerophospholipid metabolism	GO:0006950//GO:0016301	nr +
Unigene55963_All	229	3.20	3.54	1.86	6.74	3.16	1.58	4.43	3.65	7.31	1.46E-01	8.39E-01		-7.82E-01	3.80E-01		-1.09E+00	3.11E-02		-2.10E+00	3.41E-04	Down	-2.80E-01	6.37E-01		7.22E-01	1.01E-01									
Unigene5597_All	476	1.98	6.81	2.80	12.87	28.72	23.63	6.57	1.67	6.44	1.78E+00	2.56E-06	Up	4.99E-01	3.93E-01		1.16E+00	5.12E-15	Up	8.76E-01	1.66E-07		-1.98E+00	2.16E-08	Down	-2.85E-02	9.47E-01		Unigene5597_All//gi|297831530|ref|XP_002883647.1|//1.00E-34//indole-3-butyric acid response 5 [Arabidopsis lyrata subsp. lyrata] >gi|297329487|gb|EFH59906.1| indole-3-butyric acid response 5 [Arabidopsis lyrata subsp. lyrata]	Unigene5597_All//1.00E-35//AT2G04550| IBR5 (INDOLE-3-BUTYRIC ACID RESPONSE 5); MAP kinase phosphatase/ protein tyrosine/serine/threonine phosphatase	Unigene5597_All//0.00E+00//TC157072				nr +
Unigene55990_All	425	2.83	0.00	0.00	0.23	0.89	0.32	0.00	0.00	0.00	-1.15E+01	5.01E-07	Down	-1.15E+01	1.36E-06	Down	1.93E+00	1.94E-01		4.44E-01	8.61E-01		null	null		null	null		Unigene55990_All//gi|224136656|ref|XP_002326913.1|//6.00E-30//f-box family protein [Populus trichocarpa] >gi|222835228|gb|EEE73663.1| f-box family protein [Populus trichocarpa]	Unigene55990_All//8.00E-29//AT3G50410| OBP1 (OBF BINDING PROTEIN 1); DNA binding / protein binding / transcription factor	Unigene55990_All//3.00E-42//gi|109876744|gb|DW505718.1|DW505718	C2C2-Dof			nr +
Unigene56_All	2898	11.19	13.04	7.11	21.86	19.49	52.27	32.43	42.49	50.33	2.21E-01	1.43E-02		-6.55E-01	1.97E-11		-1.66E-01	1.22E-02		1.26E+00	5.06E-169	Up	3.90E-01	5.08E-21		6.34E-01	2.26E-60		Unigene56_All//gi|758250|emb|CAA59799.1|//0.00E+00//H(+)-transporting ATPase [Phaseolus vulgaris]	Unigene56_All//0.00E+00//AT2G24520| AHA5 (Arabidopsis H(+)-ATPase 5); ATPase	Unigene56_All//0.00E+00//gi|78324036|gb|DT544310.1|DT544310		ko00190|Oxidative phosphorylation		nr -
Unigene5600_All	480	0.76	2.53	8.32	2.08	5.17	10.35	5.64	14.11	14.03	1.73E+00	8.94E-03		3.45E+00	9.72E-15	Up	1.32E+00	1.05E-03		2.32E+00	2.18E-13	Up	1.32E+00	4.72E-10	Up	1.32E+00	3.53E-10	Up	Unigene5600_All//gi|297798562|ref|XP_002867165.1|//2.00E-21//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297313001|gb|EFH43424.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene5600_All//1.00E-07//TC177884				nr +
Unigene5601_All	569	2.30	9.71	17.78	13.57	17.07	26.19	5.72	13.74	19.18	2.08E+00	2.30E-12	Up	2.95E+00	7.10E-32	Up	3.31E-01	8.11E-02		9.49E-01	4.80E-11		1.26E+00	9.54E-11	Up	1.75E+00	9.57E-24	Up	Unigene5601_All//gi|226530419|ref|NP_001152533.1|//2.00E-26//adhesive/proline-rich protein [Zea mays] >gi|226958534|ref|NP_001152928.1| adhesive/proline-rich protein [Zea mays] >gi|195610792|gb|ACG27226.1| adhesive/proline-rich protein [Zea mays] >gi|195657199|gb|ACG48067.1| adhesive/proline-rich protein [Zea mays]		Unigene5601_All//2.00E-07//TC177884				nr +
Unigene56018_All	496	3.27	0.51	0.00	0.60	0.42	0.73	0.00	0.00	0.96	-2.68E+00	2.43E-05	Down	-1.17E+01	7.39E-09	Down	-5.33E-01	6.78E-01		2.74E-01	8.33E-01		null	null		9.91E+00	1.14E-03		Unigene56018_All//gi|224069236|ref|XP_002326308.1|//2.00E-37//SAUR family protein [Populus trichocarpa] >gi|222833501|gb|EEE71978.1| SAUR family protein [Populus trichocarpa]	Unigene56018_All//4.00E-21//AT5G20820| auxin-responsive protein-related	Unigene56018_All//5.00E-60//TC150243				nr +
Unigene5602_All	724	31.87	122.68	57.52	27.93	41.43	42.79	87.89	189.00	222.14	1.94E+00	1.36E-173	Up	8.52E-01	1.34E-22		5.69E-01	4.89E-10		6.15E-01	6.91E-11		1.10E+00	1.26E-141	Up	1.34E+00	1.61E-229	Up	Unigene5602_All//gi|301601262|dbj|BAJ113303.1|//2.00E-48//autophagy 8 [Ipomoea nil]	Unigene5602_All//3.00E-47//AT4G16520| ATG8F (autophagy 8F); microtubule binding	Unigene5602_All//0.00E+00//TC158642		ko04140|Regulation of autophagy		nr +
Unigene56020_All	293	3.57	0.00	0.00	0.00	1.18	0.00	0.00	0.00	0.00	-1.18E+01	3.80E-06	Down	-1.18E+01	9.32E-06	Down	1.02E+01	3.01E-02		null	null		null	null		null	null					Unigene56020_All//3.00E-06//AT2G01050| nucleic acid binding / zinc ion binding					ESTscan +
Unigene5603_All	569	6.07	25.74	17.03	10.77	17.13	21.03	8.77	6.32	8.75	2.08E+00	8.52E-32	Up	1.49E+00	4.00E-13	Up	6.70E-01	1.16E-04		9.66E-01	3.05E-09		-4.73E-01	5.26E-02		-2.70E-03	9.88E-01		Unigene5603_All//gi|224038408|gb|ACN38308.1|//8.00E-15//ARG05 [Brassica rapa subsp. pekinensis]		Unigene5603_All//1.00E-134//TC159512				nr +
Unigene56035_All	944	0.78	0.38	0.11	1.58	0.44	0.62	1.52	1.95	1.14	-1.05E+00	2.14E-01		-2.78E+00	1.04E-02		-1.85E+00	5.94E-04	Down	-1.35E+00	1.52E-02		3.55E-01	4.30E-01		-4.18E-01	3.91E-01		Unigene56035_All//gi|21553651|gb|AAM62744.1|//8.00E-74//thymidylate kinase-like protein [Arabidopsis thaliana]	Unigene56035_All//4.00E-75//AT5G59440| ZEU1 (ZEUS1); ATP binding / thymidylate kinase	Unigene56035_All//0.00E+00//gi|48775331|gb|CO084697.1|CO084697		ko00240|Pyrimidine metabolism		nr -
Unigene5604_All	899	9.43	27.39	9.48	17.62	18.42	20.80	16.27	33.80	19.23	1.54E+00	3.83E-35	Up	7.50E-03	9.95E-01		6.43E-02	7.22E-01		2.39E-01	7.99E-02		1.05E+00	8.90E-30	Up	2.41E-01	4.61E-02		Unigene5604_All//gi|18410249|ref|NP_565053.1|//1.00E-36//VPS46.2 [Arabidopsis thaliana] >gi|297839171|ref|XP_002887467.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata] >gi|5903092|gb|AAD55650.1|AC008017_23 Highly similar to developmental protein DG1118 [Arabidopsis thaliana] >gi|16648963|gb|AAL24333.1| Highly similar to developmental protein DG1118 [Arabidopsis thaliana] >gi|20148689|gb|AAM10235.1| similar to developmental protein DG1118 [Arabidopsis thaliana] >gi|297333308|gb|EFH63726.1| SNF7 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5604_All//7.00E-38//AT1G73030| VPS46.2	Unigene5604_All//0.00E+00//DW505499		ko04144|Endocytosis		nr +
Unigene5605_All	547	7.08	20.38	5.94	8.83	9.69	26.42	3.63	12.91	8.08	1.53E+00	4.20E-16	Up	-2.53E-01	4.49E-01		1.34E-01	6.60E-01		1.58E+00	4.08E-23	Up	1.83E+00	2.89E-16	Up	1.15E+00	7.46E-06	Up	Unigene5605_All//gi|147866710|emb|CAN78405.1|//8.00E-07//hypothetical protein [Vitis vinifera]		Unigene5605_All//1.00E-168//TC161623				nr -
Unigene5606_All	700	19.81	31.49	22.44	23.13	21.25	24.45	35.58	24.12	17.36	6.69E-01	1.17E-08		1.80E-01	2.56E-01		-1.22E-01	4.51E-01		8.04E-02	6.19E-01		-5.61E-01	8.42E-09		-1.04E+00	1.33E-24	Down	Unigene5606_All//gi|11385461|gb|AAG34813.1|AF243378_1//2.00E-16//glutathione S-transferase GST 23 [Glycine max]	Unigene5606_All//8.00E-17//AT5G41220| ATGSTT3 (GLUTATHIONE S-TRANSFERASE THETA 3); glutathione transferase	Unigene5606_All//0.00E+00//TC137316				nr -
Unigene5609_All	1315	34.18	9.21	24.66	0.15	0.42	0.17	1.29	0.60	2.39	-1.89E+00	1.82E-85	Down	-4.71E-01	6.72E-09		1.47E+00	1.77E-01		1.81E-01	9.35E-01		-1.09E+00	1.64E-02		8.96E-01	3.24E-03		Unigene5609_All//gi|226528780|ref|NP_001147559.1|//1.00E-108//NADP-dependent oxidoreductase P2 [Zea mays] >gi|195612186|gb|ACG27923.1| NADP-dependent oxidoreductase P2 [Zea mays]	Unigene5609_All//7.00E-90//AT5G16990| NADP-dependent oxidoreductase, putative	Unigene5609_All//7.00E-12//gi|54116317|gb|CO491826.1|CO491826				nr -
Unigene5612_All	670	4.37	2.34	2.46	7.29	2.72	2.70	1.33	1.62	31.99	-8.99E-01	1.37E-02		-8.28E-01	3.06E-02		-1.42E+00	4.88E-08	Down	-1.43E+00	2.69E-07	Down	2.92E-01	6.33E-01		4.59E+00	5.81E-123	Up	Unigene5612_All//gi|255578767|ref|XP_002530241.1|//1.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223530245|gb|EEF32147.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene56166_All	269	0.97	0.19	0.00	3.52	1.79	1.85	7.54	1.71	0.30	-2.37E+00	2.14E-01		-9.93E+00	8.55E-02		-9.73E-01	1.60E-01		-9.30E-01	2.06E-01		-2.14E+00	3.19E-06	Down	-4.67E+00	1.83E-12	Down	Unigene56166_All//gi|15237744|ref|NP_200683.1|//1.00E-11//wound-responsive protein-related [Arabidopsis thaliana] >gi|88435795|dbj|BAB97343.1| induced upon wounding stress-like protein [Arabidopsis thaliana] >gi|119360131|gb|ABL66794.1| At5g58750 [Arabidopsis thaliana]	Unigene56166_All//4.00E-13//AT5G58750| wound-responsive protein-related					nr +
Unigene56169_All	424	0.25	0.00	0.00	1.41	0.41	1.07	1.79	0.00	0.38	-7.95E+00	3.70E-01		-7.95E+00	3.91E-01		-1.80E+00	5.86E-02		-4.04E-01	6.73E-01		-1.08E+01	1.67E-05	Down	-2.26E+00	4.68E-03		Unigene56169_All//gi|87162884|gb|ABD28679.1|//5.00E-42//Tetratricopeptide-like helical [Medicago truncatula]	Unigene56169_All//7.00E-44//AT4G21705| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene56175_All	291	0.90	0.00	1.83	3.42	0.59	2.17	2.03	0.14	0.55	-9.81E+00	6.69E-02		1.03E+00	3.42E-01		-2.53E+00	6.75E-04	Down	-6.56E-01	3.71E-01		-3.82E+00	1.78E-03		-1.89E+00	3.22E-02		Unigene56175_All//gi|124360525|gb|ABN08535.1|//1.00E-12//Auxin Efflux Carrier [Medicago truncatula]	Unigene56175_All//3.00E-12//AT1G73590| PIN1 (PIN-FORMED 1); transporter	Unigene56175_All//2.00E-11//DW492561				nr -
Unigene5618_All	573	0.46	0.44	1.67	1.65	1.20	0.16	0.59	0.58	0.07	-4.66E-02	9.86E-01		1.87E+00	2.06E-02		-4.59E-01	5.36E-01		-3.39E+00	3.17E-04	Down	-1.67E-02	1.02E+00		-3.09E+00	3.91E-02		Unigene5618_All//gi|257831447|gb|ACV71024.1|//3.00E-25//UPA25 [Capsicum annuum]	Unigene5618_All//4.00E-19//AT4G37810| unknown protein	Unigene5618_All//0.00E+00//gi|21099702|gb|BQ412015.1|BQ412015				nr -
Unigene5620_All	1333	0.59	0.76	0.48	1.49	0.98	1.22	2.66	1.03	2.57	3.69E-01	6.03E-01		-2.97E-01	6.97E-01		-6.07E-01	1.77E-01		-2.93E-01	5.68E-01		-1.36E+00	6.91E-06	Down	-5.19E-02	8.69E-01		Unigene5620_All//gi|227463004|gb|ACP39954.1|//1.00E-155//pentatricopeptide repeat protein [Gossypium hirsutum] >gi|227463006|gb|ACP39955.1| pentatricopeptide repeat protein [Gossypium hirsutum]	Unigene5620_All//4.00E-125//AT1G71060| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene5621_All	882	0.53	1.03	0.42	1.92	1.21	0.97	3.93	0.66	2.08	9.54E-01	1.96E-01		-3.37E-01	7.34E-01		-6.66E-01	1.76E-01		-9.81E-01	5.37E-02		-2.57E+00	2.22E-12	Down	-9.20E-01	1.34E-03		Unigene5621_All//gi|297601300|ref|NP_001050610.2|//3.00E-57//Os03g0607600 [Oryza sativa Japonica Group] >gi|255674696|dbj|BAF12554.2| Os03g0607600 [Oryza sativa Japonica Group]	Unigene5621_All//5.00E-46//AT5G43080| CYCA3;1 (Cyclin A3;1); cyclin-dependent protein kinase regulator	Unigene5621_All//0.00E+00//DW505717				nr -

Unigene56220_All	359	0.73	0.28	1.34	1.39	1.73	1.13	3.30	0.23	1.00	-1.37E+00	3.83E-01		8.73E-01	4.17E-01		3.15E-01	7.84E-01		-2.94E-01	7.57E-01		-3.82E+00	2.12E-06	Down	-1.72E+00	2.66E-03		Unigene56220_All//gi|146286088|sp|Q94A40.2|COPA1_ARATH//5.00E-43//RecName: Full=Coatomer subunit alpha-1; AltName: Full=Alpha-coat protein 1; Short=Alpha-COP 1 >gi|3367534|gb|AAC28519.1| Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb|U24105 from Homo sapiens [Arabidopsis thaliana]	Unigene56220_All//2.00E-44//AT1G62020| coatomer protein complex, subunit alpha, putative	Unigene56220_All//1.00E-96//gi|54117698|gb|CO493207.1|CO493207				nr -
Unigene56221_All	441	0.71	0.69	1.09	0.68	2.03	1.43	2.30	0.38	1.81	-4.61E-02	9.84E-01		6.10E-01	5.86E-01		1.58E+00	4.38E-02		1.08E+00	2.69E-01		-2.60E+00	3.81E-04	Down	-3.49E-01	5.71E-01		Unigene56221_All//gi|109729860|gb|ABG46343.1|//2.00E-33//transport inhibitor response 1 [Gossypium hirsutum]	Unigene56221_All//2.00E-32//AT3G62980| TIR1 (TRANSPORT INHIBITOR RESPONSE 1); auxin binding / protein binding / ubiquitin-protein ligase	Unigene56221_All//6.00E-130//TC148414		ko04626|Plant-pathogen interaction		nr +
Unigene56227_All	405	1.68	0.00	0.53	0.25	0.43	0.11	0.00	0.21	0.00	-1.07E+01	4.09E-04	Down	-1.68E+00	8.70E-02		7.89E-01	7.70E-01		-1.14E+00	6.76E-01		7.69E+00	4.00E-01		null	null											ESTscan +
Unigene56232_All	235	11.80	8.19	17.45	7.84	11.72	10.19	38.86	26.68	17.97	-5.26E-01	1.64E-01		5.64E-01	7.57E-02		5.80E-01	1.37E-01		3.77E-01	4.01E-01		-5.43E-01	1.39E-03		-1.11E+00	1.14E-10	Down	Unigene56232_All//gi|225427566|ref|XP_002268140.1|//6.00E-16//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296085504|emb|CBI29236.3| unnamed protein product [Vitis vinifera]		Unigene56232_All//3.00E-127//BG446667				nr -
Unigene5625_All	547	2.39	4.72	3.89	4.19	5.10	5.86	8.19	22.85	13.91	9.82E-01	1.33E-02		7.04E-01	1.31E-01		2.84E-01	5.18E-01		4.85E-01	1.89E-01		1.48E+00	5.01E-21	Up	7.64E-01	3.41E-05				Unigene5625_All//6.00E-07//TC154522						
Unigene56266_All	205	0.00	1.24	0.26	0.00	0.17	0.44	0.21	1.63	3.30	1.03E+01	7.85E-02		8.02E+00	6.34E-01		7.39E+00	8.28E-01		8.78E+00	4.75E-01		2.98E+00	5.73E-02		4.00E+00	4.29E-04	Up			Unigene56266_All//8.00E-35//TC146612						
Unigene5627_All	549	4.77	60.64	21.44	7.71	19.32	24.51	35.20	28.85	32.15	3.67E+00	2.79E-130	Up	2.17E+00	3.52E-26	Up	1.32E+00	2.34E-14	Up	1.67E+00	2.99E-23	Up	-2.87E-01	1.29E-02		-1.31E-01	2.89E-01		Unigene5627_All//gi|297839669|ref|XP_002887716.1|//2.00E-15//Atlg78070/F28K19_28 [Arabidopsis lyrata subsp. lyrata] >gi|297333557|gb|EFH63975.1| Atlg78070/F28K19_28 [Arabidopsis lyrata subsp. lyrata]	Unigene5627_All//1.00E-05//AT1G78070| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: CUL4 RING ubiquitin ligase complex; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40 repeat-like (InterPro:IPR011046), WD40 repeat, region (InterPro:IPR017986), WD40/YVTN repeat-like (InterPro:IPR015943), WD40 repeat (InterPro:IPR001680); BEST Arabidopsis thaliana protein match is: WD-40 repeat family protein (TAIR:AT1G36070.1); Has 110 Blast hits to 110 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 28; Plants - 80; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene5627_All//3.00E-123//TC138397				nr -
Unigene5629_All	546	12.17	11.97	10.73	13.41	10.41	14.89	30.82	75.40	47.14	-2.37E-02	9.35E-01		-1.82E-01	4.76E-01		-3.66E-01	9.09E-02		1.51E-01	5.39E-01		1.29E+00	5.49E-55	Up	6.13E-01	8.64E-11		Unigene5629_All//gi|78096654|dbj|BAE46985.1|//1.00E-45//mitogen-activated protein kinase [Nicotiana tabacum]	Unigene5629_All//4.00E-44//AT4G01370| ATMPK4 (ARABIDOPSIS THALIANA MAP KINASE 4); MAP kinase/ kinase	Unigene5629_All//0.00E+00//TC174464		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene56293_All	341	4.91	0.89	0.78	0.15	0.81	3.84	0.12	0.00	0.35	-2.46E+00	4.49E-05	Down	-2.65E+00	4.00E-05	Down	2.47E+00	2.23E-01		4.72E+00	1.13E-06	Up	-6.95E+00	6.55E-01		1.50E+00	5.58E-01		Unigene56293_All//gi|159902535|gb|ABX10774.1|//1.00E-06//F-box GID2-like protein [Physcomitrella patens]	Unigene56293_All//4.00E-09//AT3G44326| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Cyclin-like F-box (InterPro:IPR001810); BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT2G27310.1); Has 56 Blast hits to 56 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene56299_All	209	3.76	0.00	2.55	0.00	0.66	0.00	0.00	0.00	0.00	-1.19E+01	1.09E-04	Down	-5.60E-01	4.96E-01		9.36E+00	3.18E-01		null	null		null	null		null	null		Unigene56299_All//gi|240254036|ref|NP_172263.4|//1.00E-07//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene56299_All//4.00E-09//AT1G07850| transferase, transferring glycosyl groups					nr -
Unigene5630_All	1367	10.76	1.96	8.92	1.75	0.91	0.63	0.00	0.00	0.00	-2.45E+00	3.81E-39	Down	-2.70E-01	9.07E-02		-9.48E-01	1.49E-02		-1.48E+00	4.58E-04	Down	null	null		null	null		Unigene5630_All//gi|47824984|gb|AAT38757.1|//9.00E-39//Putative phytochrome kinase substrate 1, identical [Solanum demissum]	Unigene5630_All//3.00E-27//AT2G02950| PKS1 (PHYTOCHROME KINASE SUBSTRATE 1); protein binding					nr +
Unigene56302_All	231	0.00	0.22	0.00	0.86	0.00	0.00	1515.86	7143.63	369.41	7.78E+00	6.15E-01		null	null		-9.75E+00	8.41E-02		-9.75E+00	1.33E-01		2.24E+00	0.00E+00	Up	-2.04E+00	0.00E+00	Down	Unigene56302_All//gi|293633663|gb|ADE60217.1|//1.00E-36//MIC-3 [Gossypium herbaceum] >gi|293633665|gb|ADE60218.1| MIC-3 [Gossypium herbaceum] >gi|293633667|gb|ADE60219.1| MIC-3 [Gossypium herbaceum]		Unigene56302_All//4.00E-83//NP12958110				nr -
Unigene5632_All	337	84.15	43.45	34.13	51.74	38.32	49.32	106.14	45.52	28.84	-9.54E-01	1.81E-19		-1.30E+00	1.73E-30	Down	-4.33E-01	5.00E-04		-6.91E-02	6.79E-01		-1.22E+00	4.67E-44	Down	-1.88E+00	5.61E-85	Down	Unigene5632_All//gi|298712420|emb|CBJ33198.1|//4.00E-48//histone H4 [Ectocarpus siliculosus]	Unigene5632_All//2.00E-36//AT5G59970| histone H4	Unigene5632_All//5.00E-173//TC173240				nr +
Unigene56330_All	259	6.06	9.00	13.98	8.27	10.90	7.50	8.98	8.07	8.00	5.70E-01	1.75E-01		1.21E+00	4.55E-04	Up	3.99E-01	3.14E-01		-1.41E-01	7.52E-01		-1.54E-01	6.98E-01		-1.67E-01	6.47E-01				Unigene56330_All//5.00E-117//TC177428						
Unigene5635_All	356	24.84	33.73	21.54	46.32	37.24	37.04	207.60	240.91	70.28	4.42E-01	7.32E-03		-2.06E-01	3.60E-01		-3.15E-01	1.96E-02		-3.22E-01	2.15E-02		2.15E-01	2.26E-05		-1.56E+00	9.32E-135	Down	Unigene5635_All//gi|110083391|dbj|BAE97400.1|//2.00E-61//heat shock protein 90 [Nicotiana tabacum]	Unigene5635_All//7.00E-61//AT5G56010| HSP81-3; ATP binding / unfolded protein binding	Unigene5635_All//0.00E+00//gi|78348022|gb|DT568296.1|DT568296		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene5636_All	392	8.01	18.10	6.93	8.77	6.50	10.83	25.24	33.91	23.17	1.18E+00	2.49E-07	Up	-2.09E-01	6.00E-01		-4.32E-01	2.02E-01		3.05E-01	3.58E-01		4.26E-01	2.12E-03		-1.23E-01	4.98E-01		Unigene5636_All//gi|62956018|gb|AAY23354.1|//1.00E-06//3-ketoacyl-CoA reductase 1 [Gossypium hirsutum]		Unigene5636_All//0.00E+00//TC173429				nr -
Unigene56365_All	224	2.80	0.00	0.00	0.44	0.31	0.00	0.00	0.00	0.00	-1.15E+01	7.91E-04	Down	-1.15E+01	1.41E-03		-5.33E-01	8.15E-01		-8.80E+00	3.98E-01		null	null		null	null											
Unigene56396_All	597	1.05	0.85	0.62	0.00	1.15	0.45	0.14	0.42	0.13	-3.09E-01	7.01E-01		-7.52E-01	4.11E-01		1.02E+01	3.05E-04	Up	8.83E+00	7.02E-02		1.57E+00	3.26E-01		-8.50E-02	9.71E-01										ESTscan +
Unigene56410_All	289	23.17	13.50	25.80	37.06	35.39	36.10	61.01	28.20	33.77	-7.80E-01	5.96E-04		1.55E-01	5.28E-01		-6.65E-02	7.73E-01		-3.78E-02	8.63E-01		-1.11E+00	3.43E-19	Down	-8.53E-01	4.93E-13		Unigene56410_All//gi|115475908|ref|NP_001061550.1|//3.00E-30//Os08g0326400 [Oryza sativa Japonica Group] >gi|115480049|ref|NP_001063618.1| Os09g0507800 [Oryza sativa Japonica Group] >gi|548774|sp|P35685.1|RL7A_ORYSJ RecName: Full=60S ribosomal protein L7a >gi|303855|dbj|BAA02156.1| ribosomal protein L7A [Oryza sativa Japonica Group] >gi|38423963|dbj|BAD01672.1| 60S ribosomal protein L7A [Oryza sativa Japonica Group] >gi|38637005|dbj|BAD03264.1| 60S ribosomal protein L7A [Oryza sativa Japonica Group] >gi|113623519|dbj|BAF23464.1| Os08g0326400 [Oryza sativa Japonica Group] >gi|113631851|dbj|BAF25532.1| Os09g0507800 [Oryza sativa Japonica Group]	Unigene56410_All//9.00E-18//AT3G62870| 60S ribosomal protein L7A (RPL7aB)	Unigene56410_All//3.00E-121//TC138582		ko03010|Ribosome		nr -
Unigene56418_All	1045	1.10	2.28	0.51	7.34	3.62	3.11	4.21	4.04	3.47	1.05E+00	1.20E-02		-1.11E+00	9.93E-02		-1.02E+00	1.83E-07	Down	-1.24E+00	5.44E-09	Down	-5.89E-02	8.37E-01		-2.79E-01	2.95E-01		Unigene56418_All//gi|145347396|ref|NP_194566.3|//1.00E-127//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|56236078|gb|AAV84495.1| At4g28370 [Arabidopsis thaliana]	Unigene56418_All//2.00E-117//AT4G28370| protein binding / zinc ion binding	Unigene56418_All//0.00E+00//TC141594				nr +
Unigene56423_All	421	0.00	0.00	0.00	0.00	0.00	1.71	0.00	0.47	null	null		null	null		null	null		null	null		-1.07E+01	3.26E-05	Down	-1.85E+00	1.78E-02		Unigene56423_All//gi|297844848|ref|XP_002890305.1|//1.00E-64//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297336147|gb|EFH66564.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene56423_All//1.00E-65//AT1G18900| pentatricopeptide (PPR) repeat-containing protein	Unigene56423_All//1.00E-112//gi|73860129|gb|DT462868.1|DT462868				nr +
Unigene5644_All	1008	2.80	2.31	1.06	3.90	5.57	5.78	29.70	19.11	39.36	-2.78E-01	4.68E-01		-1.41E+00	5.16E-04	Down	5.12E-01	4.06E-02		5.66E-01	2.25E-02		-6.36E-01	7.84E-13		4.07E-01	4.06E-08		Unigene5644_All//gi|30017255|gb|AAP12861.1|//7.00E-65//At2g40095 [Arabidopsis thaliana]	Unigene5644_All//3.00E-49//AT2G40095| unknown protein	Unigene5644_All//9.00E-23//DW224504			GO:0003824//GO:0009267	nr +
Unigene5648_All	557	3.85	3.64	0.76	3.40	3.34	5.68	17.16	12.23	9.23	-8.19E-02	8.46E-01		-2.33E+00	1.26E-05	Down	-2.57E-02	9.58E-01		7.40E-01	3.68E-02		-4.88E-01	3.30E-03		-8.95E-01	4.98E-08					Unigene5648_All//0.00E+00//gi|109866909|gb|DW495885.1|DW495885				
Unigene5649_All	465	4.84	4.03	8.70	22.82	12.14	9.71	3.18	3.33	1.11	-2.63E-01	5.55E-01		8.47E-01	7.45E-03		-9.10E-01	1.85E-08		-1.23E+00	4.11E-12	Down	6.35E-02	9.07E-01		-1.51E+00	2.08E-03				Unigene5649_All//7.00E-136//DW498863					
Unigene565_All	390	0.40	0.00	1.09	1.41	2.12	1.16	2.60	0.11	2.04	-8.65E+00	2.15E-01		1.44E+00	2.53E-01		5.93E-01	4.93E-01		-2.79E-01	7.57E-01		-4.60E+00	3.67E-06	Down	-3.49E-01	5.71E-01		Unigene565_All//gi|15219207|ref|NP_175722.1|//1.00E-61//dynamin family protein [Arabidopsis thaliana]	Unigene565_All//7.00E-63//AT1G53140| dynamin family protein	Unigene565_All//5.00E-87//TC164031		ko04144|Endocytosis	GO:0017111//GO:0032561//GO:0043231	nr +
Unigene56509_All	878	0.72	3.06	1.52	0.62	1.18	0.87	0.87	0.62	0.86	2.10E+00	1.94E-06	Up	1.08E+00	7.96E-02		9.15E-01	1.97E-01		4.87E-01	5.90E-01		-4.86E-01	5.25E-01		-7.80E-03	9.84E-01		Unigene56509_All//gi|124359697|gb|ABD32367.2|//2.00E-70//cig3, related [Medicago truncatula]	Unigene56509_All//6.00E-56//AT1G28260| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: SMG7 (TAIR:AT5G19400.1); Has 341 Blast hits to 340 proteins in 87 species: Archae - 0; Bacteria - 0; Metazoa - 225; Fungi - 71; Plants - 35; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink).				GO:0000212//GO:0000956	nr -

Unigene5651_All	625	77.27	80.10	57.25	208.26	201.54	200.38	62.57	17.05	13.13	5.19E-02	5.68E-01		-4.33E-01	3.10E-08		-4.73E-02	4.00E-01		-5.57E-02	3.18E-01		-1.88E+00	7.27E-90	Down	-2.25E+00	2.54E-117	Down	Unigene5651_All//gi|15237661|ref|NP_201236.1|//6.00E-15//AGP1 (ARABINOGALACTAN PROTEIN 1) [Arabidopsis thaliana] >gi|119361078|sp|Q8LCN5.2|AGP1_ARATH RecName: Full=Classical arabinogalactan protein 1; Flags: Precursor >gi|3883120|gb|AAC77823.1| arabinogalactan-protein [Arabidopsis thaliana] >gi|9759407|dbj|BAB09862.1| arabinogalactan-protein [Arabidopsis thaliana]		Unigene5651_All//0.00E+00//TC153450		ko04141|Protein processing in endoplasmic reticulum//ko00270|Cysteine and methionine metabolism//ko00620|Pyruvate metabolism//ko03420|Nucleotide excision repair//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis		nr +
Unigene5652_All	344	12.93	21.80	24.77	10.57	11.31	11.03	55.80	40.46	19.46	7.54E-01	4.08E-04		9.38E-01	6.07E-06		9.77E-02	8.10E-01		6.11E-02	8.72E-01		-4.64E-01	3.53E-05		-1.52E+00	3.09E-34	Down			Unigene5652_All//4.00E-84//TC150839				
Unigene56529_All	858	2.50	0.12	1.92	1.86	0.56	0.00	0.10	0.15	0.00	-4.40E+00	4.70E-10	Down	-3.78E-01	4.04E-01		-1.73E+00	7.76E-04	Down	-1.09E+01	5.79E-10	Down	5.67E-01	7.81E-01		-6.62E+00	3.57E-01		Unigene56529_All//gi|187765511|gb|ACD36581.1|//2.00E-07//stress-induced receptor-like kinase [Glycine max]	Unigene56529_All//3.00E-05//AT1G67000| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene56529_All//1.00E-126//TC150336			GO:0005488	nr -
Unigene5654_All	737	48.13	1403.55	199.20	55.15	141.48	365.84	69.19	337.37	384.06	4.87E+00	0.00E+00	Up	2.05E+00	1.41E-300	Up	1.36E+00	1.18E-144	Up	2.73E+00	0.00E+00	Up	2.29E+00	0.00E+00	Up	2.47E+00	0.00E+00	Up	Unigene5654_All//gi|1170745|sp|P46518.1|LEA14_GOSHI//2.00E-80//RecName: Full=Late embryogenesis abundant protein Lea14-A >gi|167326|gb|AAA18542.1| Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi|167328|gb|AAA18543.1| Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]	Unigene5654_All//6.00E-59//AT1G01470| LEA14 (LATE EMBRYOGENESIS ABUNDANT 14)	Unigene5654_All//0.00E+00//gi|109828193|gb|DW226822.1|DW226822			GO:0003006//GO:0006952//GO:0009414//GO:0009642	nr -
Unigene56565_All	227	3.69	12.72	7.98	5.05	19.42	15.92	1.30	0.55	0.88	1.79E+00	1.01E-05	Up	1.11E+00	3.00E-02		1.94E+00	2.55E-10	Up	1.66E+00	1.38E-06	Up	-1.24E+00	3.73E-01		-5.71E-01	6.28E-01			Unigene56565_All//7.00E-05//AT4G33950| OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase	Unigene56565_All//2.00E-23//TC172077				
Unigene5659_All	391	61.15	50.28	59.65	53.76	78.12	67.69	26.93	49.28	58.18	-2.82E-01	1.34E-02		-3.59E-02	7.76E-01		5.39E-01	2.51E-09		3.32E-01	1.64E-03		8.72E-01	3.37E-14		1.11E+00	5.11E-25	Up	Unigene5659_All//gi|62319903|dbj|BAD93968.1|//4.00E-36//ARF1-binding protein [Arabidopsis thaliana]	Unigene5659_All//2.00E-37//AT5G62000| ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Unigene5659_All//0.00E+00//gi|73863597|gb|DT466336.1|DT466336	ARF		GO:0003676//GO:0005515//GO:0006355//GO:0008283//GO:0009755//GO:0009900//GO:0009908//GO:0010260//GO:0043231	nr +
Unigene56607_All	540	4.65	0.00	1.58	0.18	0.51	0.33	0.00	0.15	0.00	-1.22E+01	1.66E-14	Down	-1.56E+00	4.06E-04	Down	1.47E+00	4.19E-01		8.58E-01	6.94E-01		7.27E+00	4.00E-01		null	null		Unigene56607_All//gi|83283979|gb|ABC01897.1|//9.00E-22//protein transport SEC13-like protein [Solanum tuberosum]	Unigene56607_All//4.00E-22//AT3G30050| transducin family protein / WD-40 repeat family protein	Unigene56607_All//2.00E-16//gi|5046512|gb|AI727660.1|AI727660			GO:0031981	nr +
Unigene5661_All	314	6.83	5.65	6.11	18.56	12.50	12.37	11.31	4.93	4.57	-2.75E-01	5.46E-01		-1.62E-01	7.11E-01		-5.70E-01	1.49E-02		-5.86E-01	1.70E-02		-1.20E+00	5.71E-05	Down	-1.31E+00	8.64E-06	Down			Unigene5661_All//1.00E-117//gi|164281270|gb|ES811942.1|ES811942				
Unigene5662_All	734	128.45	58.26	54.12	98.81	75.02	130.51	199.94	117.36	88.42	-1.14E+00	2.43E-84	Down	-1.25E+00	5.92E-94	Down	-3.98E-01	9.31E-13		4.01E-01	3.41E-15		-7.69E-01	5.25E-83		-1.18E+00	4.82E-173	Down	Unigene5662_All//gi|15229631|ref|NP_190560.1|//2.00E-69//60S ribosomal protein L26 (RPL26A) [Arabidopsis thaliana] >gi|297816242|ref|XP_002876004.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|27735242|sp|P51414.2|RL261_ARATH RecName: Full=60S ribosomal protein L26-1 >gi|6723436|emb|CAB66929.1| 60S RIBOSOMAL PROTEIN-like [Arabidopsis thaliana] >gi|297321842|gb|EFH52263.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene5662_All//8.00E-47//AT3G49910| 60S ribosomal protein L26 (RPL26A)	Unigene5662_All//0.00E+00//TC150014		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0006950//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene5663_All	880	0.24	1.32	0.54	1.59	2.11	1.33	1.78	0.38	1.22	2.48E+00	9.79E-04	Up	1.20E+00	3.02E-01		4.15E-01	4.27E-01		-2.48E-01	6.85E-01		-2.23E+00	3.66E-05	Down	-5.40E-01	2.40E-01		Unigene5663_All//gi|169240403|gb|AAL31655.1|AC079129.10//2.00E-31//Unknown protein [Oryza sativa] >gi|20042881|gb|AAM08709.1|AC116601_2 Unknown protein [Oryza sativa Japonica Group]						nr +
Unigene56631_All	319	0.82	0.32	0.33	0.47	0.76	0.42	2.39	0.39	0.00	-1.37E+00	3.83E-01		-1.30E+00	4.36E-01		6.90E-01	7.32E-01		-1.42E-01	9.43E-01		-2.60E+00	2.81E-03		-1.12E+01	8.87E-06	Down			Unigene56631_All//4.00E-84//gi|109872613|gb|DW501588.1|DW501588				
Unigene5664_All	561	49.52	21.32	29.52	53.45	58.07	42.99	34.44	34.79	29.61	-1.22E+00	5.49E-28	Down	-7.46E-01	2.81E-12		1.19E-01	2.78E-01		-3.14E-01	1.39E-03		1.46E-02	9.29E-01		-2.18E-01	5.74E-02		Unigene5664_All//gi|224097020|ref|XP_002310813.1|//3.00E-69//f-box family protein [Populus trichocarpa] >gi|222853716|gb|EEE91263.1| f-box family protein [Populus trichocarpa]	Unigene5664_All//5.00E-48//AT2G18280| ACTLP2 (TURBY LIKE PROTEIN 2); phosphoric diester hydrolase/ transcription factor	Unigene5664_All//0.00E+00//ES806120	TUB		GO:0003824	nr +
Unigene56657_All	232	9.47	7.64	9.18	12.67	10.39	11.29	12.39	8.47	5.84	-3.09E-01	4.83E-01		-4.50E-02	9.31E-01		-2.86E-01	4.66E-01		-1.66E-01	6.90E-01		-5.50E-01	1.01E-01		-1.09E+00	7.71E-04	Down			Unigene56657_All//2.00E-45//TC160511				
Unigene5667_All	451	30.63	12.25	10.39	31.48	24.28	34.45	62.90	20.57	24.29	-1.32E+00	3.50E-16	Down	-1.56E+00	1.17E-19	Down	-3.75E-01	9.10E-03		1.30E-01	4.50E-01		-1.61E+00	4.93E-53	Down	-1.37E+00	3.58E-43	Down	Unigene5667_All//gi|192910768|gb|ACF06492.1|//8.00E-20//ribosomal L9-like protein [Elaeis guineensis]	Unigene5667_All//3.00E-20//AT1G33140| PGY2 (PIGGYBACK2); structural constituent of ribosome	Unigene5667_All//0.00E+00//TC137377		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr -
Unigene56695_All	339	3.40	0.30	0.63	0.29	0.51	0.00	0.00	0.00	0.24	-3.51E+00	6.57E-05	Down	-2.43E+00	1.85E-03		7.89E-01	7.70E-01		-8.20E+00	3.98E-01		null	null		7.88E+00	4.03E-01		Unigene56695_All//gi|296084954|emb|CBI28363.3|//5.00E-23//unnamed protein product [Vitis vinifera]						nr -
Unigene567_All	1276	2.54	2.18	0.00	1.99	3.40	2.94	5.47	1.93	3.47	-2.19E-01	5.50E-01		-1.13E+01	8.65E-18	Down	7.72E-01	6.23E-03		5.61E-01	8.47E-02		-1.50E+00	2.41E-12	Down	-6.58E-01	5.95E-04		Unigene567_All//gi|297847698|ref|XP_002891720.1|//1.00E-159//dynamin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337572|gb|EFH67989.1| dynamin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene567_All//1.00E-146//AT1G53140| dynamin family protein	Unigene567_All//1.00E-84//DW231161				nr -
Unigene5670_All	552	1.33	0.64	0.10	0.36	0.87	0.57	11.57	2.42	2.81	-1.05E+00	2.14E-01		-3.78E+00	2.79E-03		1.27E+00	2.92E-01		6.66E-01	6.47E-01		-2.26E+00	3.46E-19	Down	-2.04E+00	1.46E-17	Down	Unigene5670_All//gi|75332302|sp|Q94KE0.1|ERDL3_ARATH//2.00E-24//RecName: Full=Sugar transporter ERD6-like 3; AltName: Full=Sugar transporter-like protein 2 >gi|14194109|gb|AAK56249.1|AF362760_1 At1g08920/F7G19_20 [Arabidopsis thaliana] >gi|22137064|gb|AAM91377.1| At1g08920/F7G19_20 [Arabidopsis thaliana] >gi|169403716|emb|CAQ16329.1| hexose transporter-like protein [Arabidopsis thaliana]	Unigene5670_All//4.00E-18//AT1G08920| sugar transporter, putative	Unigene5670_All//5.00E-140//TC147217			GO:0005215//GO:0006810//GO:0016020//GO:0016491	nr +
Unigene56709_All	219	0.48	0.46	0.97	0.68	0.16	1.03	14.09	4.96	2.73	-4.63E-02	9.87E-01		1.03E+00	5.91E-01		-2.12E+00	3.86E-01		5.96E-01	7.21E-01		-1.51E+00	6.42E-06	Down	-2.37E+00	1.47E-10	Down	Unigene56709_All//gi|225469932|ref|XP_002274290.1|//5.00E-07//PREDICTED: hypothetical protein isoform 1 [Vitis vinifera]		Unigene56709_All//3.00E-53//BQ411466				nr +
Unigene5672_All	914	0.97	2.16	1.11	1.04	0.98	1.48	2.64	5.62	14.04	1.15E+00	1.38E-02		1.86E-01	7.75E-01		-8.01E-02	8.94E-01		5.18E-01	4.01E-01		1.09E+00	5.36E-06	Up	2.41E+00	1.11E-41	Up	Unigene5672_All//gi|297596319|ref|NP_001042381.2|//2.00E-13//Os01g0213000 [Oryza sativa Japonica Group] >gi|255672993|dbj|BAF04295.2| Os01g0213000 [Oryza sativa Japonica Group]	Unigene5672_All//7.00E-10//AT3G18830| zinc finger (C3HC4-type RING finger) family protein	Unigene5672_All//0.00E+00//TC158284		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0046872	nr -
Unigene5674_All	725	1.88	1.26	4.26	4.33	2.71	1.56	0.58	0.63	0.22	-5.77E-01	3.19E-01		1.18E+00	1.67E-03		-6.77E-01	4.39E-02		-1.47E+00	4.15E-05	Down	1.21E-01	9.07E-01		-1.41E+00	1.73E-01		Unigene5674_All//gi|190898232|gb|ACE97629.1|//2.00E-29//expressed protein [Populus tremula] >gi|190898234|gb|ACE97630.1| expressed protein [Populus tremula] >gi|190898236|gb|ACE97631.1| expressed protein [Populus tremula] >gi|190898240|gb|ACE97633.1| expressed protein [Populus tremula] >gi|190898242|gb|ACE97634.1| expressed protein [Populus tremula] >gi|190898246|gb|ACE97636.1| expressed protein [Populus tremula] >gi|190898248|gb|ACE97637.1| expressed protein [Populus tremula] >gi|190898250|gb|ACE97638.1| expressed protein [Populus tremula] >gi|190898254|gb|ACE97640.1| expressed protein [Populus tremula] >gi|190898256|gb|ACE97641.1| expressed protein [Populus tremula]	Unigene5674_All//2.00E-29//AT3G18800| unknown protein	Unigene5674_All//2.00E-103//TC168850			GO:0016020	nr +
Unigene5675_All	864	2.06	1.47	0.37	3.40	2.19	2.72	5.68	2.66	2.07	-4.90E-01	3.25E-01		-2.48E+00	4.58E-05	Down	-6.34E-01	7.27E-02		-3.24E-01	4.16E-01		-1.09E+00	9.05E-06	Down	-1.45E+00	7.88E-09	Down	Unigene5675_All//gi|297823265|ref|XP_002879515.1|//2.00E-28//EMB1611/MEE22 [Arabidopsis lyrata subsp. lyrata] >gi|297325354|gb|EFH55774.1| EMB1611/MEE22 [Arabidopsis lyrata subsp. lyrata]	Unigene5675_All//8.00E-29//AT2G34780| MEE22 (MATERNAL EFFECT EMBRYO ARREST 22)	Unigene5675_All//0.00E+00//DR461479			GO:0048507//GO:0048523	nr -
Unigene56752_All	322	4.06	3.93	5.13	6.19	4.28	1.82	0.13	0.65	0.87	-4.63E-02	9.48E-01		3.36E-01	5.35E-01		-5.33E-01	2.46E-01		-1.76E+00	2.66E-04	Down	2.31E+00	2.40E-01		2.72E+00	9.93E-02		Unigene56752_All//gi|159121193|gb|ALO08230.1|//1.00E-23//AT4g22990/F7H19_170 [Arabidopsis thaliana]	Unigene56752_All//6.00E-25//AT4G22990| SPX (SYG1/Pho81/XPR1) domain-containing protein	Unigene56752_All//3.00E-88//TC138350			GO:0006810//GO:0031090	nr -

Unigene5677_All	592	2.65	10.96	3.24	11.02	14.31	16.71	5.86	3.11	11.98	2.05E+00	3.88E-14	Up	2.88E-01	5.72E-01		3.76E-01	6.21E-02		6.00E-01	8.39E-04		-9.15E-01	1.99E-03		1.03E+00	1.49E-07	Up	Unigene5677_All//gi|18423191|ref|NP_568744.1|//3.00E-46//ATHVA22E [Arabidopsis thaliana] >gi|57012614|sp|Q9FED2.1|HA22E_ARATH RecName: Full=HVA22-like protein e; Short=AtHVA22e >gi|9931544|gb|AAG02213.1|AF290892_1 AtHVA22e [Arabidopsis thaliana] >gi|11225589|gb|AAG33060.1|AF313484_1 AtHVA22e [Arabidopsis thaliana] >gi|21537153|gb|AAM61494.1| abscisic acid-induced-like protein [Arabidopsis thaliana] >gi|14050591|gb|ABI49445.1| At5g50720 [Arabidopsis thaliana] >gi|210062170|gb|ACJ06134.1| HVA22E [Arabidopsis thaliana] >gi|210062172|gb|ACJ06135.1| HVA22E [Arabidopsis thaliana] >gi|210062174|gb|ACJ06136.1| HVA22E [Arabidopsis thaliana] >gi|210062176|gb|ACJ06137.1| HVA22E [Arabidopsis thaliana] >gi|210062178|gb|ACJ06138.1| HVA22E [Arabidopsis thaliana] >gi|210062180|gb|ACJ06139.1| HVA22E [Arabidopsis thaliana] >gi|210062182|gb|ACJ06140.1| HVA22E [Arabidopsis thaliana]	Unigene5677_All//6.00E-47//AT5G50720| ATHVA22E	Unigene5677_All//1.00E-85//TC166347			GO:0044464	nr -
Unigene5678_All	498	2.42	10.89	5.35	5.00	1.38	34.55	37.19	132.69	152.47	2.17E+00	8.41E-13	Up	1.15E+00	5.09E-03		-1.85E+00	3.45E-06	Down	2.79E+00	8.49E-56	Up	1.84E+00	1.16E-146	Up	2.04E+00	3.63E-197	Up	Unigene5678_All//gi|18421491|ref|NP_568531.1|//2.00E-33//auxin-responsive family protein [Arabidopsis thaliana] >gi|13937202|gb|AAK50094.1|AF372955_1 At1g36580/F28J9_6 [Arabidopsis thaliana] >gi|25090111|gb|AAN72231.1| At1g36580/F28J9_6 [Arabidopsis thaliana]	Unigene5678_All//1.00E-34//AT3G35735| auxin-responsive family protein	Unigene5678_All//0.00E+00//gi|73863574|gb|DT466313.1|DT466313			GO:0016020	nr -
Unigene56786_All	414	0.00	0.00	0.00	0.00	0.00	0.11	0.00	1.72	0.29	null	null		null	null		null	null		6.77E+00	6.94E-01		1.07E+01	3.97E-05	Up	8.17E+00	2.43E-01		Unigene56786_All//gi|269538632|gb|ACZ48681.1|//1.00E-15//Bcl-2-associated athanogene-like protein [Vitis vinifera]		Unigene56786_All//2.00E-80//BQ408652				nr +
Unigene56796_All	242	0.00	0.00	0.00	0.21	0.00	0.19	11.36	4.84	5.60	null	null		null	null		-7.69E+00	5.54E-01		-1.41E-01	9.52E-01		-1.23E+00	3.68E-04	Down	-1.02E+00	1.95E-03		Unigene56796_All//gi|255557040|ref|XP_002519553.1|//1.00E-05//conserved hypothetical protein [Ricinus communis] >gi|223541416|gb|EEF42967.1| conserved hypothetical protein [Ricinus communis]		Unigene56796_All//2.00E-32//TC159407				nr -
Unigene568_All	2737	1.97	1.17	0.64	1.95	2.54	1.53	5.58	1.91	3.13	-7.56E-01	3.24E-03		-1.62E+00	1.99E-08	Down	3.84E-01	9.14E-02		-3.44E-01	2.19E-01		-1.55E+00	3.10E-27	Down	-8.34E-01	5.38E-11		Unigene568_All//gi|297847698|ref|XP_002891730.1|//0.00E+00//dynamin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337572|gb|EFH67989.1| dynamin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene568_All//0.00E+00//AT1G53140| dynamin family protein	Unigene568_All//0.00E+00//DW231161		ko04144|Endocytosis	GO:0017111//GO:0032561//GO:0043231	nr -
Unigene56816_All	335	4.37	0.00	0.00	0.15	0.21	0.00	0.00	0.00	0.00	-1.21E+01	1.63E-08	Down	-1.21E+01	5.25E-08	Down	4.67E-01	9.57E-01		-7.22E+00	6.33E-01		null	null		null	null					Unigene56816_All//5.00E-34//AI055663				
Unigene5682_All	574	4.47	10.77	3.90	2.43	1.44	4.80	18.93	43.03	228.83	1.27E+00	3.25E-07	Up	-1.97E-01	6.16E-01		-7.55E-01	1.67E-01		9.82E-01	1.02E-02		1.18E+00	3.25E-29	Up	3.60E+00	0.00E+00	Up				Unigene5682_All//0.00E+00//DW517774				
Unigene56820_All	220	4.76	12.21	11.38	13.59	12.52	15.40	6.73	11.40	6.34	1.36E+00	6.75E-04	Up	1.26E+00	3.30E-03		-1.18E-01	7.87E-01		1.81E-01	6.32E-01		7.61E-01	3.37E-02		-8.58E-02	8.58E-01		Unigene56820_All//gi|186512035|ref|NP_001119010.1|//3.00E-23//EDR2; lipid binding [Arabidopsis thaliana]	Unigene56820_All//1.00E-24//AT4G19040| EDR2; lipid binding	Unigene56820_All//1.00E-55//gi|72284091|gb|DT054315.1|DT054315			GO:0003676//GO:0000260//GO:0016020//GO:0034061	nr +
Unigene5683_All	557	1.32	0.82	1.82	30.50	18.11	19.05	13.89	8.85	1.07	-6.84E-01	3.86E-01		4.66E-01	5.11E-01		-7.52E-01	1.20E-09		-6.79E-01	2.20E-07		-6.50E-01	4.75E-04		-3.69E+00	3.05E-39	Down	Unigene5683_All//gi|15231684|ref|NP_190847.1|//2.00E-26//peptidoglycan-binding LysM domain-containing protein [Arabidopsis thaliana] >gi|27808562|gb|AAO24561.1| At3g52790 [Arabidopsis thaliana]	Unigene5683_All//9.00E-28//AT3G52790| peptidoglycan-binding LysM domain-containing protein	Unigene5683_All//0.00E+00//TC166421			GO:0009056	nr -
Unigene5684_All	624	3.52	18.76	10.33	3.59	7.51	17.59	15.58	12.59	7.66	2.41E+00	1.89E-30	Up	1.55E+00	1.89E-09	Up	1.06E+00	7.84E-05	Up	2.29E+00	1.16E-28	Up	-3.08E-01	7.43E-02		-1.02E+00	5.42E-10	Down	Unigene5684_All//gi|297610810|ref|NP_001065102.2|//1.00E-26//Os10g0523100 [Oryza sativa Japonica Group] >gi|255679572|dbj|BAF27016.2| Os10g0523100 [Oryza sativa Japonica Group]	Unigene5684_All//1.00E-26//AT4G16770| iron ion binding / oxidoreductase/ oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene5684_All//2.00E-177//gi|164300105|gb|ES834795.1|ES834795		ko00904|Diterpenoid biosynthesis	GO:0008152//GO:0016706//GO:0046914	nr +
Unigene5685_All	379	1.52	0.00	0.56	0.53	1.09	1.07	0.00	2.54	2.63	-1.06E+01	1.52E-03		-1.43E+00	1.75E-01		1.05E+00	4.25E-01		1.03E+00	4.28E-01		1.13E+01	7.61E-07	Up	1.14E+01	3.00E-07	Up	Unigene5685_All//gi|255570098|ref|XP_002526011.1|//1.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223534658|gb|EEF36351.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene5686_All	906	1.04	0.78	1.18	1.54	1.63	0.80	1.77	3.28	8.13	-4.09E-01	5.66E-01		1.77E-01	7.73E-01		8.62E-02	8.96E-01		-9.49E-01	9.91E-02		8.85E-01	6.28E-03		2.20E+00	8.83E-22	Up	Unigene5686_All//gi|255570098|ref|XP_002526011.1|//6.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223534658|gb|EEF36351.1| conserved hypothetical protein [Ricinus communis]		Unigene5686_All//3.00E-62//ES818197				nr +
Unigene56863_All	321	0.16	0.63	0.50	1.09	2.15	3.10	1.98	8.98	2.36	1.95E+00	3.75E-01		1.61E+00	5.11E-01		9.82E-01	2.98E-01		1.51E+00	4.09E-02		2.19E+00	1.03E-08	Up	2.55E-01	7.07E-01					Unigene56863_All//7.00E-98//gi|73863921|gb|DT466660.1|DT466660				
Unigene5687_All	1414	0.30	0.04	0.04	1.73	1.19	0.54	3.68	2.31	1.55	-3.05E+00	4.65E-02		-2.97E+00	6.45E-02		-5.33E-01	1.88E-01		-1.67E+00	8.56E-05	Down	-6.74E-01	3.89E-03		-1.25E+00	1.47E-07	Down	Unigene5687_All//gi|115447297|ref|NP_001047428.1|//5.00E-68//Os02g0614700 [Oryza sativa Japonica Group] >gi|113536959|dbj|BAF09342.1| Os02g0614700 [Oryza sativa Japonica Group]	Unigene5687_All//2.00E-47//AT4G06536| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: B302 (SPRY)-like (InterPro:IPR001870), SPla/RYanodine receptor SPRY (InterPro:IPR003877); Has 20 Blast hits to 20 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 7; Plants - 11; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene5687_All//0.00E+00//TC177253			GO:0043229//GO:0044444	nr +
Unigene5688_All	840	2.55	0.97	2.22	2.97	3.85	1.99	1.96	0.60	1.66	-1.40E+00	2.06E-03		-2.03E-01	6.39E-01		3.78E-01	3.06E-01		-5.76E-01	1.65E-01		-1.72E+00	4.44E-04	Down	-2.42E-01	5.92E-01		Unigene5688_All//gi|222820580|gb|ACM57640.1|//1.00E-110//BTB-POZ and MATH domain protein [Capsicum annuum]	Unigene5688_All//3.00E-109//AT3G03740| ATBPM4 (BTB-POZ and MATH domain 4); protein binding	Unigene5688_All//0.00E+00//TC179240				nr -
Unigene56881_All	321	15.32	20.84	21.23	14.43	8.26	6.75	0.66	0.65	0.62	4.44E-01	5.42E-02		4.71E-01	4.74E-02		-8.05E-01	2.10E-03		-1.10E+00	8.31E-05	Down	-1.67E-02	1.02E+00		-8.60E-02	9.60E-01		Unigene56881_All//gi|294829237|gb|ADF43023.1|//1.00E-09//nitrate transporter NRT1.1 [Medicago truncatula]	Unigene56881_All//6.00E-09//AT3G21670| nitrate transporter (NTP3)	Unigene56881_All//3.00E-66//gi|78337050|gb|DT557324.1|DT557324			GO:0015833//GO:0044464	nr -
Unigene5689_All	752	90.59	2.09	9.49	54.65	25.28	14.23	1.18	0.11	0.00	-5.44E+00	0.00E+00	Down	-3.26E+00	6.37E-234	Down	-1.11E+00	7.47E-44	Down	-1.94E+00	5.43E-88	Down	-3.41E+00	1.40E-04	Down	-1.02E+01	1.10E-06	Down	Unigene5689_All//gi|45379179|emb|CAC19183.2|//1.00E-75//alpha-expansin [Cicer arietinum]	Unigene5689_All//3.00E-62//AT3G29030| EXPA5 (EXPANSIN A5)	Unigene5689_All//0.00E+00//gi|109853286|gb|DW482265.1|DW482265			GO:0000902//GO:0009827//GO:0044464	nr +
Unigene56899_All	224	0.00	0.00	0.24	0.00	0.15	0.00	1.89	1.87	16.72	null	null		7.89E+00	6.34E-01		7.26E+00	8.27E-01		null	null		-1.66E-02	1.02E+00		3.15E+00	1.46E-16	Up	Unigene56899_All//gi|166787940|emb|CAM32756.1|//3.00E-12//heat shock factor A4d [Oryza sativa Indica Group]	Unigene56899_All//3.00E-08//AT4G13980| AT-HSFA5; DNA binding / transcription factor	Unigene56899_All//1.00E-43//gi|78328031|gb|DT548305.1|DT548305	HSF			nr +
Unigene569_All	808	8.74	2.01	6.99	20.28	21.35	16.60	10.94	13.55	8.73	-2.12E+00	3.72E-16	Down	-3.24E-01	1.77E-01		7.41E-02	6.52E-01		-2.89E-01	4.30E-02		3.09E-01	5.30E-02		-3.26E-01	5.93E-02		Unigene569_All//gi|126217792|gb|AB981349.1|//1.00E-138//auxin influx transport protein [Casuarina glauca] >gi|126217794|gb|ABN81350.1| auxin influx transport protein [Casuarina glauca]	Unigene569_All//4.00E-128//AT5G01240| amino acid permease, putative	Unigene569_All//0.00E+00//TC169259				nr -
Unigene5690_All	430	76.29	11.31	21.55	137.51	123.49	107.34	1.67	0.49	1.39	-2.75E+00	1.10E-98	Down	-1.82E+00	2.10E-57	Down	-1.55E-01	2.69E-02		-3.57E-01	6.57E-08		-1.78E+00	2.78E-02		-2.66E-01	6.93E-01		Unigene5690_All//gi|147776618|emb|CAN63020.1|//1.00E-13//hypothetical protein [Vitis vinifera]		Unigene5690_All//2.00E-80//DW509238				nr -
Unigene5691_All	645	0.08	0.31	0.99	2.32	4.22	3.71	8.91	8.29	2.84	1.95E+00	3.75E-01		3.61E+00	6.97E-03		8.64E-01	2.16E-02		6.80E-01	1.10E-01		-1.04E-01	6.71E-01		-1.65E+00	4.04E-12	Down	Unigene5691_All//gi|147776618|emb|CAN63020.1|//1.00E-10//hypothetical protein [Vitis vinifera]		Unigene5691_All//5.00E-85//DW509238				nr -
Unigene56916_All	390	3.76	0.78	0.82	0.00	0.18	0.00	0.00	0.00	0.00	-2.27E+00	3.39E-04	Down	-2.20E+00	7.90E-04	Down	7.46E+00	6.07E-01		null	null		null	null		null	null								
Unigene56932_All	349	3.00	0.15	1.83	0.57	0.00	0.26	0.00	0.24	0.34	-4.37E+00	3.91E-05	Down	-7.12E-01	3.15E-01		-9.16E+00	8.41E-02		-1.14E+00	5.68E-01		7.90E+00	4.00E-01		8.42E+00	2.43E-01								
Unigene5694_All	467	6.83	11.07	10.83	26.56	17.48	22.15	21.91	64.71	45.98	6.95E-01	8.24E-03		6.65E-01	1.68E-02		-6.04E-01	4.57E-05		-2.62E-01	1.30E-01		1.56E+00	7.69E-54	Up	1.07E+00	2.74E-22	Up	Unigene5694_All//gi|255581387|ref|XP_002531502.1|//4.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223528889|gb|EEF30889.1| conserved hypothetical protein [Ricinus communis]	Unigene5694_All//1.00E-06//AT5G04080| unknown protein	Unigene5694_All//6.00E-16//DW516228				nr -
Unigene56941_All	211	10.41	2.40	1.01	27.62	31.17	26.54	2.00	0.20	0.19	-2.12E+00	1.67E-05	Down	-3.37E+00	4.32E-08	Down	1.74E-01	5.32E-01		-5.76E-02	8.38E-01		-3.34E+00	1.80E-02		-3.41E+00	1.24E-02		Unigene56941_All//gi|134035508|gb|ABO47742.1|//2.00E-25//alpha-tubulin [Gossypium hirsutum]	Unigene56941_All//7.00E-26//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene56941_All//2.00E-38//ES817719		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene56958_All	266	7.87	1.14	0.20	0.00	1.04	0.00	0.00	0.00	0.00	-2.78E+00	6.12E-07	Down	-5.30E+00	3.75E-10	Down	1.00E+01	7.00E-02		null	null		null	null		null	null		Unigene56958_All//gi|297807861|ref|XP_002871814.1|//3.00E-13//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297317651|gb|EFH48073.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene56958_All//6.00E-14//AT5G18390| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene56977_All	262	6.79	0.97	8.54	2.09	2.50	2.76	0.97	0.16	0.76	-2.81E+00	4.70E-06	Down	3.30E-01	4.62E-01		2.56E-01	8.21E-01		3.99E-01	6.51E-01		-2.60E+00	1.44E-01		-3.49E-01	7.66E-01		Unigene56977_All//gi|211906442|gb|ACJ11714.1|//4.00E-07//Myo-inositol-1-phosphate synthase [Gossypium hirsutum]	Unigene56977_All//4.00E-08//AT2G22240| MIPS2 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 2); binding / catalytic/ inositol-3-phosphate synthase	Unigene56977_All//2.00E-51//TC140216		ko00562|Inositol phosphate metabolism		nr -

Unigene5698_All	405	19.38	10.63	15.78	49.20	34.01	37.80	24.74	70.79	33.05	-8.66E-01	3.35E-05		-2.97E-01	1.94E-01		-5.33E-01	2.60E-06		-3.80E-01	1.93E-03		1.52E+00	5.59E-49	Up	4.18E-01	1.87E-03		Unigene5698_All//gi|27808522|gb|AA024541.1|//3.00E-09//At4g33985 [Arabidopsis thaliana]	Unigene5698_All//2.00E-10//AT4G33985| unknown protein	Unigene5698_All//1.00E-161//gi|189092452|gb|FG548270.1|FG548270				nr +
Unigene5699_All	899	2.79	4.57	4.50	4.16	2.57	2.51	1.79	1.95	26.19	7.09E-01	1.85E-02		6.88E-01	2.96E-02		-6.95E-01	2.09E-02		-7.26E-01	2.17E-02		1.28E-01	7.81E-01		3.87E+00	2.95E-120	Up	Unigene5699_All//gi|297810453|ref|XP_002873110.1|//2.00E-31//AT-HSFA3 [Arabidopsis lyrata subsp. lyrata] >gi|297318947|gb|EFH49369.1| AT-HSFA3 [Arabidopsis lyrata subsp. lyrata]	Unigene5699_All//1.00E-32//AT5G03720| AT-HSFA3; DNA binding / transcription factor	Unigene5699_All//0.00E+00//gi|109859032|gb|DW488011.1|DW488011	HSF		GO:0001071//GO:0003677//GO:0006351//GO:0043231//GO:0050896	nr -
Unigene56992_All	500	2.30	0.00	0.21	0.00	0.07	0.18	0.00	0.00	0.00	-1.12E+01	9.91E-07	Down	-3.43E+00	1.54E-04	Down	6.11E+00	8.27E-01		7.50E+00	4.75E-01		null	null		null	null										
Unigene57004_All	444	0.71	1.26	0.84	2.36	3.02	6.92	1.05	1.32	0.54	8.28E-01	3.81E-01		2.48E-01	8.22E-01		3.60E-01	5.85E-01		1.55E+00	2.97E-05	Up	3.31E-01	6.88E-01		-9.60E-01	3.13E-01		Unigene57004_All//gi|15227277|ref|NP_179853.1|//8.00E-17//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|4314365|gb|AAD15576.1| copia-like retroelement pol polyprotein [Arabidopsis thaliana] >gi|70905061|gb|AAZ14056.1| At2g22680 [Arabidopsis thaliana]	Unigene57004_All//3.00E-18//AT2G22680| zinc finger (C3HC4-type RING finger) family protein	Unigene57004_All//2.00E-130//gi|84168831|gb|DR457479.1|DR457479			GO:0000741//GO:0016020//GO:0046872	nr +
Unigene5701_All	393	3.59	5.42	8.67	21.17	16.30	19.08	4.09	5.10	5.37	5.91E-01	1.83E-01		1.27E+00	3.90E-04	Up	-3.77E-01	5.83E-02		-1.50E-01	5.30E-01		3.20E-01	4.62E-01		3.94E-01	3.24E-01		Unigene5701_All//gi|145358912|ref|NP_199419.2|//2.00E-25//GTP binding / GTPase [Arabidopsis thaliana]	Unigene5701_All//7.00E-23//AT5G46070| GTP binding / GTPase	Unigene5701_All//0.00E+00//gi|109858186|gb|DW487165.1|DW487165			GO:0017111//GO:0032561	nr +
Unigene57027_All	663	0.08	1.53	1.12	0.30	0.52	0.00	0.32	0.13	0.06	4.28E+00	7.16E-05	Up	3.83E+00	2.23E-03		7.90E-01	5.95E-01		-8.23E+00	1.33E-01		-1.34E+00	4.29E-01		-2.41E+00	1.95E-01		Unigene57027_All//gi|15234839|ref|NP_194229.1|//6.00E-51//ATGP4 [Arabidopsis thaliana] >gi|75213044|sp|Q9SK27.1|MUB3_ARATH RecName: Full=Membrane-anchored ubiquitin-fold protein 3; Short=AtMUB3; AltName: Full=ATGP4; Flags: Precursor >gi|4455242|emb|CAB36741.1| geranylgeranylated protein ATGP4 [Arabidopsis thaliana] >gi|7269349|emb|CAB79408.1| geranylgeranylated protein ATGP4 [Arabidopsis thaliana] >gi|27765070|gb|AAO23656.1| At4g24990 [Arabidopsis thaliana] >gi|110742864|dbj|BAE99330.1| geranylgeranylated protein ATGP4 [Arabidopsis thaliana]	Unigene57027_All//3.00E-52//AT4G24990| ATGP4	Unigene57027_All//1.00E-169//C0085564			GO:0016020//GO:0043412	nr +
Unigene5703_All	471	1.22	5.16	1.92	1.59	3.58	2.59	3.32	2.66	2.37	2.08E+00	7.51E-06	Up	6.54E-01	3.86E-01		1.18E+00	2.09E-02		7.07E-01	2.77E-01		-3.19E-01	5.33E-01		-4.88E-01	2.93E-01		Unigene5703_All//gi|297833446|ref|XP_002884605.1|//4.00E-18//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297330445|gb|EFH60864.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene5703_All//7.00E-19//AT3G06670| binding	Unigene5703_All//1.00E-63//DW502252				nr -
Unigene57037_All	214	0.49	2.37	0.00	2.56	1.61	1.90	1.19	5.66	2.79	2.28E+00	6.22E-02		-8.93E+00	3.90E-01		-6.70E-01	4.96E-01		-4.31E-01	6.67E-01		2.26E+00	3.35E-04	Up	1.24E+00	1.39E-01					Unigene57037_All//1.00E-52//ES802888				
Unigene57040_All	614	1.36	0.50	0.00	1.62	1.74	0.96	2.07	0.61	0.78	-1.46E+00	6.69E-02		-1.04E+01	1.19E-04	Down	9.96E-02	9.02E-01		-7.63E-01	2.89E-01		-1.75E+00	2.19E-03		-1.41E+00	8.06E-03		Unigene57040_All//gi|2191167|gb|AAB61053.1|//5.00E-17//Hypothetical protein P2P16.18 [Arabidopsis thaliana]	Unigene57040_All//3.00E-18//AT5G26910| unknown protein	Unigene57040_All//6.00E-100//ES844286			GO:0043231	nr +
Unigene5705_All	660	6.50	19.42	6.29	16.76	15.34	21.35	40.23	35.53	31.39	1.58E+00	2.54E-19	Up	-4.68E-02	8.85E-01		-1.27E-01	5.45E-01		3.50E-01	2.25E-02		-1.79E-01	7.86E-02		-3.58E-01	1.01E-04		Unigene5705_All//gi|87241276|gb|ABD33134.1|//2.00E-09//Nucleic acid binding NABP [Medicago truncatula]	Unigene5705_All//4.00E-09//AT2G29140| APUM3 (Arabidopsis Pumilio 3); RNA binding / binding	Unigene5705_All//0.00E+00//gi|109890212|gb|DW519176.1|DW519176			GO:0003676//GO:0016020	nr +
Unigene5706_All	1178	0.80	0.43	0.45	0.25	0.38	0.46	4.09	1.95	1.49	-8.94E-01	2.14E-01		-8.23E-01	2.71E-01		5.83E-01	6.26E-01		8.59E-01	4.23E-01		-1.07E+00	1.67E-05	Down	-1.46E+00	9.43E-09	Down	Unigene5706_All//gi|34850945|dbj|BAC87845.1|//7.00E-93//leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	Unigene5706_All//2.00E-81//AT4G08850| kinase	Unigene5706_All//9.00E-08//gi|109874656|gb|DW503630.1|DW503630		ko03410|Base excision repair	GO:0000166//GO:0004672//GO:0016020	nr -
Unigene57060_All	1183	0.13	0.13	0.18	0.25	0.17	0.00	1.93	0.21	0.34	-4.64E-02	9.89E-01		4.41E-01	7.75E-01		-5.33E-01	6.78E-01		-7.98E+00	3.99E-02		-3.19E+00	2.85E-10	Down	-2.52E+00	1.53E-08	Down	Unigene57060_All//gi|186701236|gb|ACC91262.1|//1.00E-128//tiny root hair 1 protein [Capsella rubella]	Unigene57060_All//4.00E-118//AT4G23640| TRH1 (TINY ROOT HAIR 1); potassium ion transmembrane transporter	Unigene57060_All//0.00E+00//TC177567				nr +
Unigene57065_All	453	2.54	0.22	1.88	0.22	0.61	0.00	0.00	0.28	0.35	-3.51E+00	6.57E-05	Down	-4.34E-01	5.09E-01		1.47E+00	4.19E-01		-7.78E+00	3.98E-01		8.11E+00	2.40E-01		8.46E+00	1.40E-01		Unigene57065_All//gi|110931770|gb|ABH02884.1|//5.00E-28//MYB transcription factor MYB164 [Glycine max]	Unigene57065_All//1.00E-24//AT2G21650| MEE3 (MATERNAL EFFECT EMBRYO ARREST 3); DNA binding / transcription factor	Unigene57065_All//0.00E+00//TC159089	MYB-related		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene5707_All	368	94.12	36.07	40.52	116.28	96.94	150.71	95.93	37.03	39.41	-1.38E+00	2.93E-42	Down	-1.22E+00	2.01E-33	Down	-2.62E-01	7.28E-04		3.74E-01	4.93E-08		-1.37E+00	5.09E-52	Down	-1.28E+00	2.49E-48	Down	Unigene5707_All//gi|1173256|sp|P46299.1|RS4_GOSHI//2.00E-64//RecName: Full=40S ribosomal protein S4 >gi|488739|emb|CAA55882.1| ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene5707_All//3.00E-61//AT5G58420| 40S ribosomal protein S4 (RPS4D)	Unigene5707_All//0.00E+00//ES844282		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene5708_All	1386	0.19	0.77	0.85	26.17	18.46	14.57	3.48	1.54	0.23	2.02E+00	6.57E-03		2.16E+00	3.59E-03		-5.03E-01	5.43E-10		-8.45E-01	9.33E-22		-1.18E+00	2.70E-06	Down	-3.92E+00	8.29E-26	Down	Unigene5708_All//gi|42571455|ref|NP_973818.1|//1.00E-115//methyladenine glycosylase family protein [Arabidopsis thaliana]	Unigene5708_All//1.00E-101//AT1G13635| methyladenine glycosylase family protein	Unigene5708_All//3.00E-45//gi|109889913|gb|DW518881.1|DW518881		ko03410|Base excision repair	GO:0003905//GO:0006281	nr -
Unigene57085_All	408	0.13	0.00	0.00	0.37	0.00	0.89	37.72	11.47	23.04	-7.00E+00	6.09E-01		-7.00E+00	6.21E-01		-8.52E+00	1.65E-01		1.27E+00	3.81E-01		-1.72E+00	8.89E-32	Down	-7.11E-01	1.25E-08		Unigene57085_All//gi|295646769|gb|ADG23123.1|//5.00E-34//xyloglucan specific endoglucanase inhibitor [Solanum melongena]	Unigene57085_All//3.00E-28//AT1G03220| extracellular dermal glycoprotein, putative / EDGP, putative	Unigene57085_All//5.00E-81//TC139999			GO:0004175//GO:0005618//GO:0006970//GO:0016020//GO:0019538	nr -
Unigene5709_All	534	4.12	6.93	8.58	5.97	6.90	6.26	1.27	2.58	1.27	7.51E-01	1.87E-02		1.06E+00	3.64E-04	Up	2.09E-01	5.80E-01		6.81E-02	8.63E-01		1.03E+00	4.52E-02		1.70E-03	9.97E-01		Unigene5709_All//gi|297830028|ref|XP_002882896.1|//6.00E-36//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328736|gb|EFH59155.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5709_All//3.00E-32//AT1G53420| serine/threonine protein kinase-related	Unigene5709_All//5.00E-165//TC133547			GO:0004672//GO:0005488	nr +
Unigene57093_All	571	0.82	4.17	1.31	0.17	0.42	2.14	0.81	0.22	4.26	2.34E+00	1.67E-06	Up	6.63E-01	4.19E-01		1.27E+00	5.31E-01		3.61E+00	2.38E-05	Up	-1.89E+00	8.00E-02		2.39E+00	2.07E-08	Up	Unigene57093_All//gi|18411926|ref|NP_567231.1|//6.00E-18//SAG21 (SENESCENCE-ASSOCIATED GENE 21) [Arabidopsis thaliana] >gi|15294220|gb|AAK95287.1|AF410301_1 AT4g02380/T14P8_2 [Arabidopsis thaliana] >gi|14517508|gb|AAK62644.1| AT4g02380/T14P8_2 [Arabidopsis thaliana] >gi|15450609|gb|AAK96576.1| AT4g02380/T14P8_2 [Arabidopsis thaliana] >gi|15809760|gb|AAL06808.1| AT4g02380/T14P8_2 [Arabidopsis thaliana] >gi|21592389|gb|AAM64340.1| late embryogenis abundant protein [Arabidopsis thaliana] >gi|58395780|gb|AAW72736.1| late embryogenesis abundant-like protein [Arabidopsis thaliana]	Unigene57093_All//2.00E-09//AT4G02380| SAG21 (SENESCENCE-ASSOCIATED GENE 21)	Unigene57093_All//1.00E-63//DN799918			GO:0006979//GO:0007275//GO:0009414	nr -
Unigene571_All	2279	6.73	4.00	6.87	50.91	35.13	24.36	14.79	34.35	18.11	-7.49E-01	1.72E-07		3.03E-02	8.50E-01		-5.35E-01	1.21E-34		-1.06E+00	1.86E-100	Down	1.22E+00	1.08E-94	Up	2.93E-01	6.03E-05		Unigene571_All//gi|224090949|ref|XP_002309128.1|//0.00E+00//auxin influx carrier component [Populus trichocarpa] >gi|222855104|gb|EEE92651.1| auxin influx carrier component [Populus trichocarpa]	Unigene571_All//0.00E+00//AT5G01240| amino acid permease, putative	Unigene571_All//0.00E+00//TC172479			GO:0009755//GO:0015291//GO:0015837//GO:0031224	nr +
Unigene57108_All	213	1.23	0.00	0.75	1.87	0.97	1.27	5.76	2.35	0.37	-1.03E+01	6.68E-02		-7.12E-01	6.22E-01		-9.48E-01	4.20E-01		-5.57E-01	6.37E-01		-1.29E+00	2.09E-02		-3.94E+00	4.86E-07	Down	Unigene57108_All//gi|224110076|ref|XP_002315406.1|//2.00E-18//aminophospholipid ATPase [Populus trichocarpa] >gi|222864446|gb|EEF01577.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene57108_All//3.00E-12//AT5G04930| ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism				GO:0005548//GO:0006869//GO:0009206//GO:0031224//GO:0032559//GO:0042625//GO:0046872	nr -
Unigene5712_All	416	11.45	11.94	14.21	116.27	60.43	52.98	14.43	10.55	7.28	6.06E-02	8.26E-01		3.12E-01	2.41E-01		-9.44E-01	2.57E-39		-1.13E+00	1.04E-46	Down	-4.52E-01	3.95E-02		-9.88E-01	3.52E-06		Unigene5712_All//gi|298704978|emb|CBJ28468.1|//3.00E-06//similar to chromosome fragility associated gene 1 [Ectocarpus siliculosus]		Unigene5712_All//6.00E-102//DW500170				nr -
Unigene5713_All	536	32.99	14.37	18.28	41.82	41.05	37.75	59.56	30.26	35.38	-1.20E+00	1.04E-17	Down	-8.52E-01	6.10E-10		-2.68E-02	8.41E-01		-1.48E-01	2.69E-01		-9.77E-01	1.10E-27		-7.51E-01	1.51E-18		Unigene5713_All//gi|44681380|gb|AAS42630.1|//3.00E-87//At1g64650 [Arabidopsis thaliana] >gi|45773902|gb|AAS76755.1| At1g64650 [Arabidopsis thaliana]	Unigene5713_All//2.00E-76//AT1G64650| LOCATED IN: plasma membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27720.1); Has 565 Blast hits to 562 proteins in 197 species: Archae - 7; Bacteria - 312; Metazoa - 76; Fungi - 39; Plants - 85; Viruses - 0; Other Eukaryotes - 46 (source: NCBI BLink).	Unigene5713_All//0.00E+00//TC132167			GO:0031410	nr -
Unigene5714_All	564	13.64	8.18	5.29	18.02	21.55	15.13	1.72	1.48	3.53	-7.38E-01	4.28E-04		-1.37E+00	2.55E-09	Down	2.58E-01	1.35E-01		-2.52E-01	2.01E-01		-2.18E-01	7.24E-01		1.03E+00	9.53E-03		Unigene5714_All//gi|297827699|ref|XP_002881732.1|//2.00E-19//bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327571|gb|EFH57991.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5714_All//2.00E-15//AT2G40620| bZIP transcription factor family protein	Unigene5714_All//0.00E+00//gi|78330777|gb|DT551051.1|DT551051	bZIP			nr +
Unigene5716_All	592	0.09	2.65	2.61	9.26	16.05	16.78	3.00	0.99	1.95	4.91E+00	8.63E-08	Up	4.88E+00	2.34E-07	Up	7.95E-01	6.29E-06		8.59E-01	1.66E-06		-1.60E+00	5.26E-04	Down	-6.20E-01	1.41E-01		Unigene5716_All//gi|33323057|gb|AAQ07268.1|//4.00E-58//ripening induced protein [Ficus pumila var. awkeotsang]	Unigene5716_All//2.00E-11//AT1G24020| MLP423 (MLP-LIKE PROTEIN 423)	Unigene5716_All//0.00E+00//gi|84173742|gb|DR462390.1|DR462390			GO:0006950	nr -

Unigene5718_All	1011	3.73	1.80	2.21	7.24	6.40	5.36	6.06	7.11	2.92	-1.05E+00	1.05E-03		-7.52E-01	2.30E-02		-1.78E-01	4.70E-01		-4.34E-01	4.87E-02		2.30E-01	2.86E-01		-1.06E+00	6.36E-07	Down	Unigene5718_All//gi|75288399|sp|Q5YLB4.1|GYRB_NICBE//7.00E-09//RecName: Full=DNA gyrase subunit B, chloroplastic/mitochondrial; Flags: Precursor >gi|38017095|gb|AAR07943.1| DNA gyrase B subunit [Nicotiana benthamiana]	Unigene5718_All//6.00E-10//AT3G10270| ATP binding / DNA binding / DNA topoisomerase (ATP-hydrolyzing)	Unigene5718_All//4.00E-136//ES822006			GO:0003676//GO:0006259//GO:0046914	nr -
Unigene572_All	2294	62.88	15.33	40.67	83.75	90.92	65.97	17.84	15.94	14.01	-2.04E+00	2.62E-301	Down	-6.29E-01	1.72E-45		1.19E-01	5.74E-04		-3.44E-01	1.11E-22		-1.62E-01	4.21E-02		-3.48E-01	1.71E-06		Unigene572_All//gi|126217792|gb|ABN81349.1|//0.00E+00//auxin influx transport protein [Casuarina glauca] >gi|126217794|gb|ABN81350.1| auxin influx transport protein [Casuarina glauca]	Unigene572_All//0.00E+00//AT2G38120| AUX1 (AUXIN RESISTANT 1); amino acid transmembrane transporter/ auxin binding / auxin influx transmembrane transporter/ transporter	Unigene572_All//0.00E+00//TC169259			GO:0009755//GO:0015291//GO:0015837//GO:0031224	nr -
Unigene5720_All	535	57.02	100.20	71.86	98.23	120.49	121.39	31.61	65.78	31.65	8.14E-01	1.08E-27		3.34E-01	1.96E-04		2.95E-01	1.30E-06		3.05E-01	1.47E-06		1.06E+00	1.69E-34	Up	1.60E-03	9.89E-01		Unigene5720_All//gi|15238753|ref|NP_197910.1|//3.00E-28//serine-rich protein-related [Arabidopsis thaliana] >gi|30689801|ref|NP_851072.1| serine-rich protein-related [Arabidopsis thaliana] >gi|15146224|gb|AAK83595.1| AT5g25280/F18G18_20 [Arabidopsis thaliana] >gi|15529141|gb|AAX97665.1| AT5g25280/F18G18_20 [Arabidopsis thaliana] >gi|16974351|gb|AAL31101.1| AT5g25280/F18G18_20 [Arabidopsis thaliana]	Unigene5720_All//2.00E-19//AT5G25280| serine-rich protein-related	Unigene5720_All//0.00E+00//gi|109857822|gb|DW486801.1|DW486801				nr +
Unigene57206_All	455	1.49	2.67	3.28	0.66	0.45	4.86	1.49	1.01	1.49	8.38E-01	1.73E-01		1.13E+00	4.89E-02		-5.33E-01	6.78E-01		2.89E+00	8.90E-08	Up	-5.57E-01	4.89E-01		1.60E-03	9.97E-01		Unigene57206_All//gi|240256452|ref|NP_200624.5|//2.00E-56//actin binding [Arabidopsis thaliana]	Unigene57206_All//6.00E-58//AT5G58160| actin binding	Unigene57206_All//2.00E-19//TC133677			GO:0003916//GO:0006259//GO:0007010//GO:0008092//GO:0015629//GO:0016020//GO:0017111//GO:0032259	nr +
Unigene5721_All	396	8.32	30.71	14.66	6.04	9.13	7.76	26.37	51.40	21.63	1.88E+00	2.72E-23	Up	8.16E-01	1.44E-03		5.97E-01	6.62E-02		3.61E-01	3.60E-01		9.63E-01	1.63E-17		-2.86E-01	7.14E-02		Unigene5721_All//gi|119360109|gb|AL66783.1|//1.00E-23//At5g49710 [Arabidopsis thaliana]	Unigene5721_All//1.00E-21//AT5G49710| unknown protein	Unigene5721_All//0.00E+00//gi|164340014|gb|ES805602.1|ES805602			GO:0043231	nr +
Unigene5722_All	601	16.19	30.86	15.51	23.21	31.05	46.37	36.65	81.99	57.80	9.30E-01	1.84E-12		-6.26E-02	7.55E-01		4.20E-01	5.60E-04		9.98E-01	7.08E-22		1.16E+00	9.78E-56	Up	6.57E-01	5.22E-16		Unigene5722_All//gi|192910688|gb|ACF06452.1|//8.00E-36//ORMDL family protein-like [Elaeis guineensis]	Unigene5722_All//1.00E-35//AT1G01230| ORMDL family protein	Unigene5722_All//0.00E+00//TC151470			GO:0031224//GO:0043231//GO:0044267	nr +
Unigene5723_All	550	7.13	5.53	4.36	8.69	6.45	5.83	3.77	8.28	1.30	-3.68E-01	2.40E-01		-7.12E-01	2.74E-02		-4.31E-01	1.16E-01		-5.77E-01	3.78E-02		1.14E+00	1.05E-05	Up	-1.53E+00	1.72E-04	Down	Unigene5723_All//gi|15238180|ref|NP_196067.1|//1.00E-06//SIM (SIAMESE); cyclin-dependent protein kinase inhibitor [Arabidopsis thaliana] >gi|32815859|gb|AAP88332.1| At5g04470 [Arabidopsis thaliana]	Unigene5723_All//7.00E-07//AT5G04470| SIM (SIAMESE); cyclin-dependent protein kinase inhibitor	Unigene5723_All//0.00E+00//gi|109872823|gb|DW501798.1|DW501798			GO:0007049	nr +
Unigene5724_All	440	1.90	3.34	3.15	3.40	4.77	4.11	5.96	13.49	8.33	8.12E-01	1.36E-01		7.26E-01	2.28E-01		4.91E-01	3.07E-01		2.74E-01	6.40E-01		1.18E+00	1.43E-07	Up	4.84E-01	8.55E-02		Unigene5724_All//gi|27923880|sp|P59234|YIPL_SOLTU//2.00E-13//Protein yippee-like >gi|24745964|dbj|BAC23053.1| yippee-like protein [Solanum tuberosum] >gi|161579406|gb|ABX72226.1| yippee-like protein [Solanum tuberosum]	Unigene5724_All//4.00E-14//AT2G40110| yippee family protein	Unigene5724_All//0.00E+00//BG447138				nr +
Unigene57270_All	305	80.45	94.53	55.35	24.01	28.45	76.41	306.50	423.99	446.06	2.33E-01	2.62E-02		-5.40E-01	1.91E-06		2.45E-01	2.58E-01		1.67E+00	5.51E-40	Up	4.68E-01	1.30E-30		5.41E-01	1.06E-42		Unigene57270_All//gi|167859793|gb|AC404850.1|//4.00E-23//senescence-associated protein [Picea abies]		Unigene57270_All//4.00E-59//gi|84158163|gb|DN827210.1|DN827210				nr -
Unigene5728_All	385	14.68	7.24	8.30	18.76	14.85	17.13	86.10	33.00	27.01	-1.02E+00	5.74E-05	Down	-8.23E-01	1.60E-03		-3.38E-01	1.29E-01		-1.32E-01	6.37E-01		-1.38E+00	2.03E-49	Down	-1.67E+00	4.30E-67	Down	Unigene5728_All//gi|192910780|gb|ACF06496.1|//3.00E-20//ribosomal protein L18a [Elaeis guineensis]	Unigene5728_All//5.00E-21//AT2G34480| 60S ribosomal protein L18A (RPL18aB)	Unigene5728_All//0.00E+00//TC140689		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0010467//GO:0015934//GO:0016020//GO:0022613	nr +
Unigene5729_All	501	23.18	46.22	39.22	12.93	14.23	10.28	51.39	26.95	19.72	9.95E-01	4.16E-17		7.59E-01	4.02E-09		1.39E-01	5.98E-01		-3.31E-01	1.85E-01		-9.32E-01	7.83E-21		-1.38E+00	1.17E-39	Down	Unigene5729_All//gi|224088316|ref|XP_002308410.1|//1.00E-35//stress-induced hydrophobic peptide [Populus trichocarpa] >gi|222854386|gb|EEE91933.1| stress-induced hydrophobic peptide [Populus trichocarpa]	Unigene5729_All//4.00E-23//AT4G28088| hydrophobic protein, putative / low temperature and salt responsive protein, putative	Unigene5729_All//0.00E+00//TC170331			GO:0006952//GO:0006972//GO:0031224//GO:0031410	nr +
Unigene57301_All	364	1.01	11.28	3.95	15.74	15.80	16.25	5.46	2.87	0.11	3.49E+00	8.76E-16	Up	1.97E+00	2.09E-03		5.50E-03	9.90E-01		4.65E-02	8.79E-01		-9.27E-01	2.37E-02		-5.64E+00	2.87E-13	Down	Unigene57301_All//gi|18424977|ref|NP_569016.1|//1.00E-23//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|75180377|sp|Q9LSR9.1|Y5566_ARATH RecName: Full=Uncharacterized protein At5g65660 >gi|30102568|gb|AAP21202.1| At5g65660 [Arabidopsis thaliana]	Unigene57301_All//6.00E-25//AT5G65660| hydroxyproline-rich glycoprotein family protein	Unigene57301_All//2.00E-126//TC153114			GO:0016020	nr +
Unigene57319_All	606	4.14	2.76	9.23	3.12	2.10	2.24	0.00	0.07	0.00	-5.87E-01	1.40E-01		1.15E+00	1.56E-05	Up	-5.71E-01	2.26E-01		-4.83E-01	3.38E-01		6.11E+00	6.32E-01		null	null		Unigene57319_All//gi|224142619|ref|XP_002324652.1|//6.00E-60//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222860086|gb|EEF03217.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene57319_All//1.00E-41//AT1G15360| SHN1 (SHINE 1); DNA binding / sequence-specific DNA binding / transcription factor	Unigene57319_All//9.00E-176//ES805836	AP2-EREBP		GO:0000160//GO:0001071//GO:0003677//GO:0006351//GO:0006633//GO:0006950//GO:0010468//GO:0043231	nr +
Unigene5732_All	448	4.44	4.52	6.66	10.79	6.30	5.24	19.44	14.55	11.29	2.78E-02	9.71E-01		5.85E-01	1.28E-01		-7.75E-01	2.44E-03		-1.04E+00	1.22E-04	Down	-4.18E-01	1.85E-02		-7.84E-01	4.42E-06				Unigene5732_All//0.00E+00//gi|21100579|gb|BQ412892.1|BQ412892				
Unigene57326_All	442	2.84	1.60	0.48	0.56	0.31	1.12	0.10	0.66	0.27	-8.24E-01	1.69E-01		-2.56E+00	6.98E-04	Down	-8.55E-01	5.73E-01		9.96E-01	3.94E-01		2.79E+00	9.47E-02		1.50E+00	5.58E-01		Unigene57326_All//gi|219394463|gb|ACL14373.1|//8.00E-18//NO APICAL MERISTEM2 [Pisum sativum]		Unigene57326_All//5.00E-10//gi|78326446|gb|DT546720.1|DT546720			GO:0010016//GO:0048645//GO:0050789	nr +
Unigene5735_All	800	11.64	7.79	10.25	32.88	30.30	17.67	9.88	5.17	2.89	-5.80E-01	2.07E-03		-1.84E-01	3.90E-01		-1.18E-01	3.33E-01		-8.96E-01	1.54E-17		-9.34E-01	5.48E-07		-1.77E+00	5.04E-18	Down	Unigene5735_All//gi|256010124|gb|ACU55135.1|//8.00E-54//dirigent-like protein 1 [Gossypium hirsutum]	Unigene5735_All//3.00E-48//AT1G58170| disease resistance-responsive protein-related / dirigent protein-related	Unigene5735_All//0.00E+00//DW508982				nr +
Unigene5737_All	1262	4.02	1.65	1.98	4.78	5.38	2.00	0.84	0.23	0.88	-1.29E+00	3.22E-06	Down	-1.02E+00	2.71E-04	Down	1.71E-01	5.36E-01		-1.25E+00	2.53E-07	Down	-1.85E+00	4.09E-03		7.76E-02	9.04E-01		Unigene5737_All//gi|280967730|gb|ACZ98536.1|//1.00E-173//protein kinase [Malus x domestica]	Unigene5737_All//3.00E-153//AT2G26730| leucine-rich repeat transmembrane protein kinase, putative	Unigene5737_All//0.00E+00//gi|164285155|gb|ES832552.1|ES832552		ko04626|Plant-pathogen interaction		nr -
Unigene5738_All	754	57.11	27.22	41.53	233.74	178.89	148.25	74.19	56.76	59.92	-1.07E+00	4.28E-35	Down	-4.60E-01	3.21E-08		-3.86E-01	8.96E-29		-6.57E-01	5.18E-67		-3.86E-01	7.30E-10		-3.08E-01	5.68E-07		Unigene5738_All//gi|42572261|ref|NP_974226.1|//2.00E-23//heavy-metal-associated domain-containing protein [Arabidopsis thaliana]		Unigene5738_All//0.00E+00//TC158175				nr -
Unigene5739_All	689	1.75	0.96	0.31	1.95	3.15	4.52	2.09	1.76	2.54	-8.70E-01	1.56E-01		-2.50E+00	1.15E-03		6.90E-01	1.20E-01		1.21E+00	7.04E-04	Up	-2.46E-01	6.37E-01		2.86E-01	5.36E-01		Unigene5739_All//gi|115441193|ref|NP_001048876.1|//2.00E-19//Os01g0861000 [Oryza sativa Japonica Group] >gi|113534407|dbj|BAF06790.1| Os01g0861000 [Oryza sativa Japonica Group]	Unigene5739_All//3.00E-28//AT5G09270| unknown protein	Unigene5739_All//0.00E+00//TC153305				nr +
Unigene574_All	752	35.97	77.76	24.78	55.25	32.92	36.82	73.26	143.67	55.63	1.11E+00	2.80E-50	Up	-5.37E-01	5.55E-07		-7.47E-01	1.13E-22		-5.86E-01	2.57E-13		9.72E-01	7.47E-91		-3.97E-01	1.58E-10		Unigene574_All//gi|225465147|ref|XP_002277597.1|//8.00E-11//PREDICTED: similar to nad9 [Vitis vinifera]		Unigene574_All//0.00E+00//TC150231		ko00190|Oxidative phosphorylation		nr -
Unigene5740_All	993	1.79	1.48	1.39	5.12	4.33	6.64	7.71	17.34	94.24	-2.76E-01	5.91E-01		-3.62E-01	4.82E-01		-2.39E-01	4.13E-01		3.76E-01	1.21E-01		1.17E+00	3.21E-20	Up	3.61E+00	0.00E+00	Up	Unigene5740_All//gi|19911575|dbj|BAB88891.1|//5.00E-49//syringolide-induced protein 14-1-1 [Glycine max]	Unigene5740_All//1.00E-27//AT1G76070| unknown protein	Unigene5740_All//0.00E+00//DW502943			GO:0044464	nr +
Unigene57413_All	399	1.97	0.13	0.00	0.00	0.00	0.00	0.42	0.00	0.00	-3.95E+00	8.54E-04	Down	-1.09E+01	2.21E-04	Down	null	null		null	null		-8.73E+00	1.34E-01		-8.73E+00	1.08E-01		Unigene57413_All//gi|255571701|ref|XP_002526794.1|//3.00E-18//conserved hypothetical protein [Ricinus communis] >gi|223533870|gb|EEF35600.1| conserved hypothetical protein [Ricinus communis]	Unigene57413_All//1.00E-05//AT2G39370| unknown protein					nr -
Unigene5742_All	688	2.21	0.81	3.17	0.80	1.05	3.81	3.99	3.83	1.51	-1.44E+00	9.80E-03		5.25E-01	2.46E-01		4.00E-01	6.64E-01		2.26E+00	4.38E-07	Up	-6.17E-02	8.69E-01		-1.41E+00	4.02E-05	Down	Unigene5742_All//gi|225452688|ref|XP_002276846.1|//7.00E-16//PREDICTED: similar to Os01g0238200 [Vitis vinifera]		Unigene5742_All//0.00E+00//ES813362				nr +
Unigene57422_All	542	2.51	35.34	5.99	2.21	6.61	12.75	206.49	238.59	239.77	3.82E+00	1.86E-77	Up	1.26E+00	6.35E-04	Up	1.58E+00	1.61E-06	Up	2.53E+00	2.21E-20	Up	2.09E-01	2.67E-07		2.16E-01	5.20E-08		Unigene57422_All//gi|31326675|gb|AAC16325.1|//5.00E-93//asparagine synthetase [Elaeagnus umbellata]	Unigene57422_All//2.00E-84//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene57422_All//0.00E+00//gi|48823415|gb|CO124728.1|CO124728		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0006528//GO:0009267//GO:0009642//GO:0009746//GO:0016884//GO:0034285	nr -
Unigene57426_All	396	0.53	0.90	0.00	1.38	2.00	1.60	2.78	0.42	0.80	7.61E-01	5.57E-01		-9.05E+00	1.45E-01		5.32E-01	5.39E-01		2.07E-01	8.23E-01		-2.72E+00	1.31E-04	Down	-1.79E+00	3.08E-03		Unigene57426_All//gi|209865484|gb|ACI89426.1|//8.00E-11//cyclin B [Populus tomentosa]	Unigene57426_All//7.00E-10//AT1G76310| CYCB2;4 (CYCLIN B2;4); cyclin-dependent protein kinase regulator	Unigene57426_All//8.00E-126//DW501539			GO:0009987//GO:0043231	nr +
Unigene5743_All	1360	3.00	2.09	1.57	8.31	4.99	2.29	3.45	0.71	0.91	-5.24E-01	8.28E-02		-9.38E-01	3.00E-03		-7.37E-01	2.08E-06		-1.86E+00	3.61E-23	Down	-2.29E+00	1.58E-14	Down	-1.93E+00	3.07E-12	Down	Unigene5743_All//gi|15239123|ref|NP_201371.1|//0.00E+00//BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|2827715|emb|CAA16688.1| receptor protein kinase - like protein [Arabidopsis thaliana] >gi|10177328|dbj|BAB10677.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|20466696|gb|AAM20665.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|317117866|gb|AAP68249.1| At5g65700 [Arabidopsis thaliana] >gi|110741066|dbj|BAE98627.1| receptor protein kinase like protein [Arabidopsis thaliana] >gi|224589751|gb|ACN59407.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene5743_All//0.00E+00//AT5G65700| BAM1 (BARELY ANY MERISTEM 1); ATP binding / kinase/ protein serine/threonine kinase	Unigene5743_All//0.00E+00//TC141219			GO:0003006//GO:0004672//GO:0004871//GO:0005488//GO:0005982//GO:0006950//GO:0009536//GO:0009933//GO:0010073//GO:0016020//GO:0016160	nr +

Unigene5746_All	535	19.17	12.98	12.04	15.18	15.58	18.57	32.88	14.92	18.69	-5.63E-01	1.57E-03		-6.70E-01	2.93E-04		3.75E-02	8.78E-01		2.91E-01	1.35E-01		-1.14E+00	7.49E-20	Down	-8.15E-01	4.34E-12		Unigene5746_All//gi|1173256|sp|P46299.1|RS4_GOSHI//3.00E-21//RecName: Full=40S ribosomal protein S4 >gi|488739|emb|CAA55882.1| ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene5746_All//3.00E-21//AT5G07090| 40S ribosomal protein S4 (RPS4B)	Unigene5746_All//1.00E-153//gi|48804088|gb|CO105402.1|CO105402		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr -
Unigene57464_All	239	0.22	0.42	0.89	1.04	1.30	0.38	0.00	0.52	2.33	9.54E-01	7.25E-01		2.03E+00	3.61E-01		3.15E-01	8.38E-01		-1.46E+00	4.06E-01		9.04E+00	2.40E-01		1.12E+01	3.28E-04	Up	Unigene57464_All//gi|15233948|ref|NP_194205.1|//5.00E-08//AFC2 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 2); kinase/ protein kinase [Arabidopsis thaliana] >gi|1703200|sp|P51567.1|AFC2_ARATH RecName: Full=Serine/threonine-protein kinase AFC2 >gi|601789|gb|AAA57118.1| protein kinase [Arabidopsis thaliana] >gi|6421130|dbj|BAA08214.1| protein kinase [Arabidopsis thaliana] >gi|4220516|emb|CAA22989.1| protein kinase (AFC2) [Arabidopsis thaliana] >gi|7269325|emb|CAB79384.1| protein kinase (AFC2) [Arabidopsis thaliana] >gi|109134165|gb|ABG25080.1| At4g24740 [Arabidopsis thaliana] >gi|110742385|dbj|BAE99115.1| protein kinase [Arabidopsis thaliana]	Unigene57464_All//2.00E-09//AT4G24740| AFC2 (ARABIDOPSIS FUS3-COMPLEMENTING GENE 2); kinase/ protein kinase	Unigene57464_All//5.00E-52//gi|78344868|gb|DT565142.1|DT565142				nr +
Unigene5747_All	839	36.54	10.87	13.84	50.82	33.45	21.32	2.02	0.50	0.85	-1.75E+00	1.45E-52	Down	-1.40E+00	8.70E-37	Down	-6.04E-01	4.79E-16		-1.25E+00	2.75E-48	Down	-2.02E+00	5.66E-05	Down	-1.24E+00	5.14E-03		Unigene5747_All//gi|222139394|gb|AC045716.1|//1.00E-97//class IV chitinase [Pyrus pyrifolia]	Unigene5747_All//2.00E-95//AT3G54420| ATEP3; chitinase	Unigene5747_All//8.00E-97//TC131593		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0004553//GO:0006026//GO:0009793//GO:0030247//GO:0030312//GO:0033554	nr -
Unigene57471_All	230	0.00	0.00	0.00	0.00	0.30	0.00	2.57	0.00	0.52	null	null		null	null		8.23E+00	6.07E-01		null	null		-1.13E+01	2.39E-04	Down	-2.31E+00	1.36E-02		Unigene57471_All//gi|255564407|ref|XP_002523200.1|//3.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223537607|gb|EEF39231.1| conserved hypothetical protein [Ricinus communis]		Unigene57471_All//9.00E-66//ES807928				nr -
Unigene5748_All	1324	0.04	0.77	0.48	0.23	0.78	2.01	3.58	49.02	108.17	4.28E+00	7.16E-05	Up	3.61E+00	6.97E-03		1.79E+00	1.39E-02		3.16E+00	4.72E-10	Up	3.78E+00	0.00E+00	Up	4.92E+00	0.00E+00	Up	Unigene5748_All//gi|14249017|gb|AAK57699.1|AF377317_1//1.00E-170//myb-like transcription factor Myb 5 [Gossypium hirsutum]	Unigene5748_All//2.00E-63//AT5G49620| AtMYB78 (myb domain protein 78); DNA binding / transcription factor	Unigene5748_All//0.00E+00//TC131146	MYB			nr +
Unigene5749_All	1101	466.71	173.59	394.61	72.21	95.21	32.69	0.23	1.10	1.09	-1.43E+00	0.00E+00	Down	-2.42E-01	1.09E-27		3.99E-01	5.09E-18		-1.14E+00	1.74E-77	Down	2.26E+00	3.35E-04	Up	2.24E+00	3.02E-04	Up	Unigene5749_All//gi|45356861|gb|AAS58469.1|//3.00E-52//ultraviolet-B-repressible protein [Gossypium hirsutum]	Unigene5749_All//2.00E-19//AT2G06520| PSBX (photosystem II subunit X)	Unigene5749_All//0.00E+00//TC156050			GO:0009521//GO:0009534//GO:0044237	nr -
Unigene575_All	1663	5.07	8.53	4.48	6.44	3.85	3.91	15.20	21.11	6.88	7.52E-01	5.17E-07		-1.76E-01	4.24E-01		-7.42E-01	3.67E-06		-7.20E-01	2.25E-05		4.74E-01	4.29E-09		-1.14E+00	3.07E-29	Down	Unigene575_All//gi|225465147|ref|XP_002277597.1|//2.00E-10//PREDICTED: similar to nad9 [Vitis vinifera]		Unigene575_All//0.00E+00//gi|109852863|gb|DW481842.1|DW481842		ko00190|Oxidative phosphorylation		nr -
Unigene5750_All	1182	2.48	6.17	4.10	3.29	4.22	4.70	1.22	0.67	0.34	1.32E+00	8.33E-09	Up	7.26E-01	1.08E-02		3.62E-01	2.06E-01		5.16E-01	4.52E-02		-8.56E-01	8.67E-02		-1.85E+00	3.87E-04	Down	Unigene5750_All//gi|21700767|gb|AAG38145.1|//7.00E-51//phosphoglycerate mutase-like protein [Glycine max]	Unigene5750_All//6.00E-52//AT1G58280| LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Phosphoglycerate mutase (InterPro:IPR013078); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G64460.6); Has 337 Blast hits to 337 proteins in 68 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 175; Plants - 69; Viruses - 0; Other Eukaryotes - 89 (source: NCBI BLink).	Unigene5750_All//4.00E-07//gi|109827459|gb|DW226142.1|DW226142				nr +
Unigene5751_All	2173	2.53	1.14	1.32	6.14	4.03	7.38	9.07	4.60	4.69	-1.15E+00	1.11E-05	Down	-9.34E-01	4.51E-04		-6.10E-01	1.71E-05		2.64E-01	7.32E-02		-9.80E-01	1.75E-17		-9.50E-01	3.67E-17		Unigene5751_All//gi|79356046|ref|NP_564341.2|//0.00E+00//NRP2; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding [Arabidopsis thaliana]	Unigene5751_All//0.00E+00//AT1G29940| NRPA2; DNA binding / DNA-directed RNA polymerase/ ribonucleoside binding	Unigene5751_All//0.00E+00//TC130108		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0001882//GO:0003676//GO:0010467//GO:0034062//GO:0043231	nr +
Unigene5754_All	827	1.27	0.86	0.84	8.37	13.24	34.24	6.75	6.12	6.41	-5.61E-01	3.82E-01		-5.96E-01	3.93E-01		6.61E-01	4.56E-05		2.03E+00	3.65E-63	Up	-1.42E-01	6.06E-01		-7.49E-02	7.45E-01		Unigene5754_All//gi|192910810|gb|ACF06513.1|//1.00E-38//histidine-containing phosphotransfer protein Zmhp2 chain D [Elaeis guineensis]	Unigene5754_All//5.00E-33//AT3G21510| AHP1 (HISTIDINE-CONTAINING PHOSPHOTRANSMITTER 1); histidine phosphotransfer kinase	Unigene5754_All//0.00E+00//DW505530			GO:0004871//GO:0008152//GO:0009736//GO:0016628//GO:0019901//GO:0023060//GO:0031410//GO:0040007//GO:0043231//GO:0048229	nr +
Unigene57547_All	389	0.94	0.52	0.96	0.51	0.35	0.58	1.41	0.00	0.82	-8.54E-01	4.88E-01		2.54E-02	1.00E+00		-5.33E-01	7.48E-01		1.81E-01	9.35E-01		-1.05E+01	4.61E-04	Down	-7.86E-01	3.61E-01		Unigene57547_All//gi|15240072|ref|NP_201474.1|//3.00E-09//zinc finger (C2H2 type) family protein [Arabidopsis thaliana] >gi|8843731|dbj|BAA97279.1| zinc finger protein [Arabidopsis thaliana] >gi|20466786|gb|AAM20710.1| zinc finger protein [Arabidopsis thaliana] >gi|23198204|gb|AAN15629.1| zinc finger protein [Arabidopsis thaliana]		Unigene57547_All//5.00E-50//TC158963				nr +
Unigene5755_All	1395	0.38	1.31	0.23	3.14	2.12	1.30	4.58	53.54	1.91	1.80E+00	6.20E-04	Up	-7.12E-01	4.97E-01		-5.66E-01	4.23E-02		-1.28E+00	1.15E-05	Down	3.55E+00	0.00E+00	Up	-1.26E+00	3.38E-09	Down	Unigene5755_All//gi|224116296|ref|XP_002331947.1|//2.00E-48//AP2/EREBP domain-containing transcription factor [Populus trichocarpa] >gi|222874724|gb|EEF11855.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene5755_All//1.00E-29//AT3G23240| ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	Unigene5755_All//2.00E-43//TC166993	AP2-EREBP		GO:0010071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene57555_All	303	0.35	2.34	1.23	0.33	0.23	0.89	0.56	23.17	0.53	2.76E+00	9.13E-03		1.83E+00	2.12E-01		-5.33E-01	8.15E-01		1.44E+00	4.09E-01		5.38E+00	3.11E-43	Up	-8.60E-02	9.65E-01		Unigene57555_All//gi|159138941|gb|ABR89470.1|//8.00E-17//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene57555_All//4.00E-13//AT1G53540| 17.6 kDa class I small heat shock protein (HSP17.6C-CI) (AA 1-156)	Unigene57555_All//6.00E-89//gi|21093614|gb|BQ405927.1|BQ405927				nr +
Unigene5758_All	621	9.60	7.67	6.17	29.52	15.36	13.60	16.34	12.18	4.75	-3.25E-01	1.99E-01		-6.38E-01	1.19E-02		-9.43E-01	4.32E-15		-1.12E+00	1.22E-17	Down	-4.24E-01	8.90E-03		-1.78E+00	4.82E-23	Down	Unigene5758_All//gi|42570286|ref|NP_849997.2|//7.00E-32//CLASP (CLIP-ASSOCIATED PROTEIN); binding [Arabidopsis thaliana]	Unigene5758_All//4.00E-33//AT2G20190| CLASP (CLIP-ASSOCIATED PROTEIN); binding	Unigene5758_All//7.00E-72//TC179504			GO:0000087//GO:0005819//GO:0016020//GO:0031647//GO:0040007	nr +
Unigene576_All	3366	1.10	1.43	1.65	2.06	1.59	1.33	7.13	6.79	3.54	3.74E-01	1.87E-01		5.76E-01	2.97E-02		-3.76E-01	9.26E-02		-6.31E-01	4.12E-03		-7.10E-02	5.77E-01		-1.01E+00	6.69E-23	Down	Unigene576_All//gi|9280616|gb|AAF86496.1|AF279449_1//2.00E-99//NADH dehydrogenase subunit 9 [Lupinus angustifolius]	Unigene576_All//2.00E-97//ATMG00070| NADH dehydrogenase subunit 9	Unigene576_All//0.00E+00//gi|164310522|gb|ES848470.1|ES848470		ko00190|Oxidative phosphorylation	GO:0005746//GO:0015980//GO:0030964//GO:0046914//GO:0050136//GO:0051234	nr -
Unigene57606_All	212	2.96	0.00	0.50	1.41	2.92	0.43	0.60	0.59	0.94	-1.15E+01	7.91E-04	Down	-2.56E+00	2.72E-02		1.05E+00	2.99E-01		-1.73E+00	2.89E-01		-1.67E-02	1.02E+00		6.51E-01	6.65E-01		Unigene57606_All//gi|168988197|gb|ACA33268.1|//5.00E-18//DNA mismatch repair protein [Cucumis sativus]	Unigene57606_All//3.00E-12//AT3G24320| MSH1 (MUTL PROTEIN HOMOLOG 1); ATP binding / catalytic/ damaged DNA binding / mismatched DNA binding / nuclease					nr +
Unigene5761_All	630	14.87	12.55	11.83	11.78	13.77	13.33	18.93	19.24	7.84	-2.45E-01	2.18E-01		-3.29E-01	1.06E-01		2.25E-01	3.11E-01		1.79E-01	4.50E-01		2.37E-02	8.99E-01		-1.27E+00	1.15E-16	Down	Unigene5761_All//gi|88010908|gb|AB038871.1|//6.00E-22//At4g35905 [Arabidopsis thaliana]	Unigene5761_All//3.00E-24//AT4G35905| unknown protein	Unigene5761_All//0.00E+00//gi|164256475|gb|ES807115.1|ES807115			GO:0043231	nr +
Unigene57621_All	328	29.99	19.31	19.16	141.09	111.60	30.98	35.32	13.51	36.56	-6.35E-01	4.91E-04		-6.47E-01	6.43E-04		-3.38E-01	2.69E-06		-2.19E+00	1.03E-115	Down	-1.39E+00	7.57E-18	Down	4.98E-02	7.55E-01					Unigene57621_All//4.00E-44//TC165495				
Unigene5763_All	513	18.36	9.19	6.54	26.22	16.18	18.93	24.97	33.49	21.90	-9.99E-01	1.71E-07		-1.49E+00	9.82E-13	Down	-6.97E-01	7.46E-07		-4.70E-01	1.92E-03		4.23E-01	4.11E-04		-1.89E-01	2.00E-01					Unigene5763_All//0.00E+00//TC171198				
Unigene57631_All	1167	7.85	0.65	0.73	0.17	0.68	0.27	0.04	0.00	0.00	-3.59E+00	7.52E-36	Down	-3.43E+00	5.16E-33	Down	1.99E+00	2.46E-02		6.66E-01	6.47E-01		-5.18E+00	6.54E-01		-5.18E+00	6.10E-01		Unigene57631_All//gi|5020168|gb|AAD38033.1|AF149053_1//1.00E-24//phytochrome kinase substrate 1 [Arabidopsis thaliana]	Unigene57631_All//5.00E-20//AT2G02950| PKS1 (PHYTOCHROME KINASE SUBSTRATE 1); protein binding					nr -
Unigene5766_All	1137	0.69	0.45	0.28	5.52	4.27	2.94	2.42	4.67	8.06	-6.31E-01	4.08E-01		-1.30E+00	1.38E-01		-3.70E-01	1.19E-01		-9.09E-01	8.60E-05		9.50E-01	4.57E-05		1.74E+00	6.11E-20	Up				Unigene5766_All//0.00E+00//TC160234				
Unigene5767_All	1574	0.70	0.45	1.15	1.42	1.49	2.15	10.07	4.67	2.56	-6.31E-01	3.35E-01		7.21E-01	1.52E-01		6.29E-02	9.02E-01		5.96E-01	8.39E-02		-1.11E+00	3.26E-17	Down	-1.98E+00	8.84E-41	Down	Unigene5767_All//gi|50253510|gb|AAT71957.1|//1.00E-132//At5g46220 [Arabidopsis thaliana] >gi|56381965|gb|AAV85701.1| At5g46220 [Arabidopsis thaliana]	Unigene5767_All//1.00E-126//AT5G46220| unknown protein	Unigene5767_All//0.00E+00//CO124387			GO:0043231	nr +
Unigene57676_All	495	1.59	0.10	0.00	0.10	0.07	0.00	0.00	0.00	0.00	-3.95E+00	8.54E-04	Down	-1.06E+01	2.21E-04	Down	-5.32E-01	8.24E-01		-6.65E+00	6.32E-01		null	null		null	null		Unigene57676_All//gi|116061891|emb|CAL52609.1|//1.00E-06//Predicted fumarylacetoacetate hydralase (ISS) [Ostreococcus tauri]	Unigene57676_All//2.00E-06//AT1G12050| fumarylacetoacetase, putative			ko00350|Tyrosine metabolism		nr +
Unigene5768_All	900	8.37	2.59	4.26	4.54	1.22	3.91	1.64	1.58	0.66	-1.69E+00	7.20E-13	Down	-9.75E-01	1.24E-05		-1.89E+00	4.61E-10	Down	-2.14E-01	5.38E-01		-5.85E-02	9.19E-01		-1.31E+00	6.57E-03		Unigene5768_All//gi|240256121|ref|NP_194990.4|//4.00E-98//protein binding / zinc ion binding [Arabidopsis thaliana] >gi|240256123|ref|NP_001119101.4| protein binding / zinc ion binding [Arabidopsis thaliana] >gi|259016138|sp|Q9M081.2|SC24B_ARATH RecName: Full=Protein transport protein Sec24-like At4g32640	Unigene5768_All//7.00E-92//AT4G32640| protein binding / zinc ion binding	Unigene5768_All//7.00E-42//TC164995		ko03040|Spliceosome	GO:0006810//GO:0006950//GO:0043231//GO:0044444	nr -
Unigene5771_All	1239	7.31	5.64	7.26	13.55	10.51	14.95	23.17	8.33	9.23	-3.72E-01	5.68E-02		-8.40E-03	9.92E-01		-3.67E-01	4.75E-03		1.42E-01	3.55E-01		-1.48E+00	3.34E-47	Down	-1.33E+00	1.46E-41	Down	Unigene5771_All//gi|15222534|ref|NP_176564.1|//1.00E-134//IMP4 [Arabidopsis thaliana]	Unigene5771_All//3.00E-135//AT1G63780| IMP4	Unigene5771_All//0.00E+00//TC149828				nr -
Unigene57711_All	595	1.49	0.77	0.36	0.67	0.17	0.68	0.36	2.39	1.14	-9.64E-01	1.95E-01		-2.06E+00	1.78E-02		-1.95E+00	1.19E-01		2.84E-02	9.85E-01		2.75E+00	8.33E-06	Up	1.68E+00	3.70E-02									
Unigene5772_All	813	7.14	3.80	5.57	13.97	12.41	7.39	7.07	1.65	1.23	-9.10E-01	2.37E-04		-3.60E-01	1.77E-01		-1.71E-01	3.71E-01		-9.19E-01	3.01E-08		-2.10E+00	5.66E-16	Down	-2.53E+00	1.90E-20	Down	Unigene5772_All//gi|20856775|gb|AAM26684.1|//1.00E-34//At1g71970/F17M19_12 [Arabidopsis thaliana] >gi|23505805|gb|AAX29762.1| At1g71970/F17M19_12 [Arabidopsis thaliana]	Unigene5772_All//2.00E-25//AT1G71970| unknown protein	Unigene5772_All//0.00E+00//TC169910				nr +
Unigene5773_All	1295	1.01	3.29	2.84	1.46	2.34	1.33	5.81	5.16	12.06	1.70E+00	1.34E-07	Up	1.49E+00	2.18E-05	Up	6.79E-01	5.80E-02		-1.41E-01	7.64E-01		-1.70E-01	4.27E-01		1.05E+00	4.58E-16	Up	Unigene5773_All//gi|15239761|ref|NP_200295.1|//3.00E-97//SGP1: GTP binding [Arabidopsis thaliana] >gi|5824341|emb|CAB54517.1| SGP1 monomeric G-protein [Arabidopsis thaliana] >gi|9758264|dbj|BAB08763.1| SGP1 monomeric G-protein [Arabidopsis thaliana]	Unigene5773_All//2.00E-89//AT5G54840| SGP1; GTP binding	Unigene5773_All//0.00E+00//gi|78352953|gb|DT573227.1|DT573227			GO:0032561//GO:0035556//GO:0044464	nr -

Unigene57730_All	925	0.51	0.05	0.46	0.81	0.63	0.05	0.14	0.18	0.30	-3.22E+00	2.73E-02		-1.45E-01	8.89E-01		-3.52E-01	6.51E-01		-4.05E+00	7.75E-04	Down	3.98E-01	8.13E-01		1.14E+00	3.99E-01		Unigene57730_All//gi|15230653|ref|NP_187269.1|//8.00E-65//structural constituent of ribosome [Arabidopsis thaliana] >gi|62867643|gb|AAY17425.1| At3g06180 [Arabidopsis thaliana] >gi|90862960|gb|ABE02404.1| At3g06180 [Arabidopsis thaliana]	Unigene57730_All//3.00E-52//AT3G06180| structural constituent of ribosome	Unigene57730_All//2.00E-180//gi|78340478|gb|DT560752.1|DT560752		ko03040|Spliceosome		nr -
Unigene5774_All	1462	1.29	1.56	0.84	2.83	1.79	0.25	13.97	24.21	24.03	2.76E-01	5.29E-01		-6.21E-01	2.18E-01		-6.60E-01	2.04E-02		-3.52E+00	1.79E-17	Down	7.94E-01	9.44E-22		7.83E-01	1.20E-21		Unigene5774_All//gi|224064641|ref|XP_002301530.1|//1.00E-122//gibberellin 2-oxidase [Populus trichocarpa] >gi|222843256|gb|EEE80803.1| gibberellin 2-oxidase [Populus trichocarpa]	Unigene5774_All//4.00E-102//AT1G02400| GA2OX6 (GIBBERELLIN 2-OXIDASE 6); gibberellin 2-beta-dioxygenase	Unigene5774_All//1.00E-53//gi|164350585|gb|EX170755.1|EX170755		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr -
Unigene5775_All	802	11.81	7.46	5.18	31.43	18.46	14.75	6.75	2.97	2.58	-6.64E-01	3.65E-04		-1.19E+00	2.97E-09	Down	-7.68E-01	1.39E-14		-1.09E+00	3.95E-23	Down	-1.18E+00	5.03E-07	Down	-1.39E+00	4.68E-09	Down	Unigene5775_All//gi|74027078|gb|AAZ94630.1|//2.00E-83//zinc finger protein-like protein [Gossypium hirsutum]	Unigene5775_All//2.00E-58//AT3G15680| zinc finger (Ran-binding) family protein	Unigene5775_All//0.00E+00//TC144332			GO:0044464//GO:0046914	nr -
Unigene5777_All	800	20.08	12.03	15.24	29.45	21.35	25.57	47.88	37.93	20.77	-7.39E-01	1.23E-07		-3.98E-01	6.55E-03		-4.64E-01	7.65E-06		-2.04E-01	9.44E-02		-3.36E-01	1.35E-05		-1.21E+00	1.65E-47	Down	Unigene5777_All//gi|17977973|emb|AC80988.1|//1.00E-87//protein kinase 2 [Beta vulgaris]	Unigene5777_All//4.00E-86//AT5G67380| CKA1 (CASEIN KINASE ALPHA 1); kinase	Unigene5777_All//0.00E+00//gi|164254783|gb|ES832232.1|ES832232		ko04712|Circadian rhythm - plant	GO:0001071//GO:0004674//GO:0006464//GO:0009416//GO:0009791//GO:0016020//GO:0032559//GO:0043231	nr +
Unigene5778_All	1305	0.20	1.20	0.90	9.31	5.07	4.88	2.37	0.00	0.31	2.59E+00	5.51E-05	Up	2.16E+00	3.59E-03		-8.79E-01	4.41E-09		-9.33E-01	5.53E-09		-1.12E+01	7.94E-22	Down	-2.95E+00	3.12E-13	Down	Unigene5778_All//gi|15225398|ref|NP_182030.1|//2.00E-96//matrix metalloproteinase [Arabidopsis thaliana] >gi|31711730|gb|AAP68221.1| At2g45040 [Arabidopsis thaliana]	Unigene5778_All//5.00E-98//AT2G45040| matrix metalloproteinase				GO:0004175//GO:0019538//GO:0031224//GO:0046872	nr +
Unigene57782_All	574	2.28	9.62	2.50	2.08	1.68	2.68	0.81	2.99	7.29	2.08E+00	2.30E-12	Up	1.36E-01	7.98E-01		-3.10E-01	6.07E-01		3.61E-01	5.45E-01		1.88E+00	1.20E-04	Up	3.17E+00	1.54E-18	Up	Unigene57782_All//gi|115451009|ref|NP_001049105.1|//1.00E-10//Os03g0170100 [Oryza sativa Japonica Group] >gi|108706404|gb|ABF94199.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547576|dbj|BAF11019.1| Os03g0170100 [Oryza sativa Japonica Group]	Unigene57782_All//5.00E-06//AT2G35290| unknown protein	Unigene57782_All//1.00E-144//TC136603				nr +
Unigene5780_All	719	75.39	158.84	120.50	46.77	101.34	87.44	24.82	32.55	32.97	1.08E+00	1.98E-92	Up	6.77E-01	2.58E-31		1.12E+00	2.04E-74	Up	9.03E-01	2.88E-41		3.92E-01	1.05E-04		4.10E-01	2.82E-05		Unigene5780_All//gi|7768153|emb|CAB90634.1|//1.00E-117//protein phosphatase 2C (PP2C) [Fagus sylvatica]	Unigene5780_All//1.00E-112//AT3G51370| protein phosphatase 2C, putative / PP2C, putative	Unigene5780_All//0.00E+00//gi|78354020|gb|DT574294.1|DT574294				nr +
Unigene57807_All	563	0.19	0.45	0.00	0.62	0.80	1.04	4.06	6.90	43.80	1.28E+00	4.35E-01		-7.54E+00	3.90E-01		3.60E-01	8.06E-01		7.52E-01	4.67E-01		7.68E-01	5.49E-03		3.43E+00	4.31E-114	Up	Unigene57807_All//gi|40218371|gb|AA883118.1|//5.00E-85//secretory laccase [Gossypium arboreum]	Unigene57807_All//1.00E-45//AT5G48100| TT10 (TRANSPARENT TESTA 10); copper ion binding / laccase	Unigene57807_All//0.00E+00//TC156527		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene5783_All	1668	0.00	0.36	0.06	3.08	1.80	7.04	14.04	12.03	32.29	8.51E+00	1.17E-03		6.00E+00	3.97E-01		-7.76E-01	1.64E-03		1.19E+00	1.51E-12	Up	-2.24E-01	3.54E-02		1.20E+00	1.44E-65	Up	Unigene5783_All//gi|224066819|ref|XP_002302231.1|//0.00E+00//iaa-amino acid hydrolase 9 [Populus trichocarpa] >gi|222843957|gb|EEE81504.1| iaa-amino acid hydrolase 9 [Populus trichocarpa]	Unigene5783_All//3.00E-168//AT1G44350| ILL6; IAA-amino acid conjugate hydrolase/ metallopeptidase	Unigene5783_All//0.00E+00//gi|78334417|gb|DT554691.1|DT554691			GO:0005488//GO:0016811	nr +
Unigene57833_All	361	1.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-1.09E+01	4.09E-04	Down	-1.09E+01	7.63E-04	Down	null	null		null	null		null	null		null	null		Unigene57833_All//gi|297852976|ref|XP_002894369.1|//7.00E-11//dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340211|gb|EFH70628.1| dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene57833_All//3.00E-12//AT1G52240| ROPGEF11 (ROH GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor					nr +
Unigene57836_All	732	0.29	0.14	0.29	4.97	5.55	1.54	0.12	0.11	0.05	-1.05E+00	5.64E-01		2.55E-02	1.00E+00		1.60E-01	6.43E-01		-1.69E+00	6.38E-07	Down	-1.63E-02	1.01E+00		-1.09E+00	6.75E-01		Unigene57836_All//gi|115445589|ref|NP_001046574.1|//2.00E-37//Os02g0286200 [Oryza sativa Japonica Group] >gi|47847721|dbj|BAD21500.1| lipase class 3-like [Oryza sativa Japonica Group] >gi|113536105|dbj|BAF08488.1| Os02g0286200 [Oryza sativa Japonica Group]	Unigene57836_All//4.00E-36//AT2G05260| lipase class 3 family protein	Unigene57836_All//0.00E+00//TC161782				nr -
Unigene5784_All	564	3.43	1.53	6.14	7.24	6.84	7.29	1.65	2.30	4.24	-1.17E+00	1.36E-02		8.38E-01	1.55E-02		-8.29E-02	8.25E-01		8.80E-03	9.78E-01		4.78E-01	3.95E-01		1.36E+00	2.45E-04	Up	Unigene5784_All//gi|297797589|ref|XP_002866679.1|//4.00E-29//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297312514|gb|EFH42938.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene5784_All//6.00E-19//AT5G65560| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene57841_All	213	0.25	0.00	0.25	0.23	0.81	4.03	1.19	1.37	2.43	-7.94E+00	6.08E-01		2.56E-02	9.94E-01		1.79E+00	5.20E-01		4.11E+00	3.40E-04	Up	2.06E-01	8.68E-01		1.03E+00	2.53E-01					Unigene57841_All//2.00E-41//gi|78325275|gb|DT545549.1|DT545549				
Unigene5786_All	712	5.44	8.33	4.19	11.19	11.56	12.24	30.94	15.44	15.56	6.15E-01	1.17E-02		-3.77E-01	2.57E-01		4.63E-02	8.47E-01		1.29E-01	6.02E-01		-1.00E+00	3.54E-20	Down	-9.92E-01	1.94E-20					Unigene5786_All//3.00E-136//TC132099				
Unigene5788_All	1060	7.01	6.69	3.32	7.00	8.12	10.48	7.94	5.13	4.28	-6.67E-02	7.62E-01		-1.08E+00	1.90E-06	Down	2.14E-01	3.29E-01		5.82E-01	5.36E-04		-6.31E-01	3.75E-04		-8.90E-01	4.09E-07		Unigene5788_All//gi|18408807|ref|NP_566916.1|//1.00E-88//DMS3 (DEFECTIVE IN MERISTEM SILENCING 3) [Arabidopsis thaliana] >gi|15146294|gb|AAK83630.1| AT3g49250/F2K15_110 [Arabidopsis thaliana] >gi|19699162|gb|AAL90947.1| AT3g49250/F2K15_110 [Arabidopsis thaliana]	Unigene5788_All//7.00E-87//AT3G49250| DMS3 (DEFECTIVE IN MERISTEM SILENCING 3)	Unigene5788_All//0.00E+00//TC154616			GO:0005488//GO:0006305//GO:0016458	nr +
Unigene5789_All	1102	1.14	1.98	2.13	2.94	3.31	2.13	1.46	0.42	1.19	7.95E-01	6.74E-02		9.00E-01	3.97E-02		1.73E-01	6.33E-01		-4.63E-01	2.01E-01		-1.81E+00	3.20E-04	Down	-2.89E-01	5.47E-01		Unigene5789_All//gi|18408807|ref|NP_566916.1|//7.00E-84//DMS3 (DEFECTIVE IN MERISTEM SILENCING 3) [Arabidopsis thaliana] >gi|15146294|gb|AAK83630.1| AT3g49250/F2K15_110 [Arabidopsis thaliana] >gi|19699162|gb|AAL90947.1| AT3g49250/F2K15_110 [Arabidopsis thaliana]	Unigene5789_All//3.00E-85//AT3G49250| DMS3 (DEFECTIVE IN MERISTEM SILENCING 3)	Unigene5789_All//0.00E+00//TC154616			GO:0005488//GO:0006305//GO:0016458	nr +
Unigene57896_All	626	2.93	0.57	0.43	1.91	2.75	0.29	2.09	1.74	0.76	-2.37E+00	2.79E-05	Down	-2.78E+00	8.44E-06	Down	5.26E-01	3.15E-01		-2.73E+00	2.36E-04	Down	-2.70E-01	6.56E-01		-1.46E+00	5.49E-03					Unigene57896_All//6.00E-94//TC140827				ESTscan +
Unigene57899_All	207	0.00	0.00	0.00	11.55	5.82	3.05	0.00	0.00	0.00	null	null		null	null		-9.88E-01	1.09E-02		-1.92E+00	1.46E-05	Down	null	null		null	null					Unigene57899_All//2.00E-57//DW498546				
Unigene5791_All	1272	1.07	0.32	0.80	2.55	2.08	2.81	1.86	3.29	12.03	-1.75E+00	4.61E-03		-4.27E-01	4.72E-01		-2.88E-01	4.38E-01		1.40E-01	6.84E-01		8.20E-01	1.99E-03		2.69E+00	5.15E-56	Up	Unigene5791_All//gi|224064167|ref|XP_002301396.1|//7.00E-66//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222843122|gb|EEE80669.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene5791_All//2.00E-47//AT3G61630| CEF6 (CYTOKININ RESPONSE FACTOR 6); DNA binding / transcription factor	Unigene5791_All//0.00E+00//gi|78342833|gb|DT563107.1|DT563107	AP2-EREBP		GO:0006350//GO:0006606//GO:0009793//GO:0048827	nr +
Unigene57912_All	220	3.57	2.07	0.73	3.62	2.66	1.23	3.46	2.66	0.36	-7.83E-01	3.28E-01		-2.30E+00	1.79E-02		-4.45E-01	5.73E-01		-1.56E+00	6.26E-02		-3.79E-01	6.35E-01		-3.26E+00	4.48E-04	Down	Unigene57912_All//gi|13431449|sp|O48520.1|PODZ_ARATH//3.00E-25//RecName: Full=DNA polymerase delta small subunit	Unigene57912_All//1.00E-26//AT2G42120| POLD2 (DNA POLYMERASE DELTA SMALL SUBUNIT); DNA binding / DNA-directed DNA polymerase	Unigene57912_All//1.00E-92//CO075177		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair		nr +
Unigene57919_All	267	2.74	0.00	0.20	0.93	0.13	0.00	0.16	0.00	0.00	-1.14E+01	2.11E-04	Down	-3.78E+00	2.79E-03		-2.85E+00	1.37E-01		-9.87E+00	7.32E-02		-7.31E+00	6.54E-01		-7.31E+00	6.10E-01			Unigene57919_All//2.00E-05//AT5G54050| DC1 domain-containing protein	Unigene57919_All//2.00E-119//TC162929				ESTscan -
Unigene5792_All	1356	2.05	1.20	0.47	3.34	1.27	1.63	1.96	0.71	0.53	-7.74E-01	3.96E-02		-2.12E+00	2.21E-06	Down	-1.40E+00	2.47E-07	Down	-1.03E+00	2.32E-04	Down	-1.47E+00	4.62E-05	Down	-1.89E+00	3.72E-07	Down	Unigene5792_All//gi|4559351|gb|AAD23012.1|//7.00E-13//expressed protein [Arabidopsis thaliana] >gi|95147312|gb|ABF57291.1| Unigene5792_All//3.00E-14//AT2G25010| unknown protein [Arabidopsis thaliana]						nr -
Unigene57920_All	696	1.50	2.69	1.38	3.58	2.42	0.71	2.49	1.14	1.26	8.41E-01	7.75E-02		-1.27E-01	8.44E-01		-5.62E-01	1.58E-01		-2.33E+00	3.55E-07	Down	-1.13E+00	1.21E-02		-9.84E-01	2.16E-02		Unigene57920_All//gi|87240462|gb|AB032320.1|//5.00E-60//DNA-directed RNA polymerase, subunit C11/M/9 [Medicago truncatula]	Unigene57920_All//6.00E-60//AT3G16980| NRPB9A; DNA binding / DNA-directed RNA polymerase/ nucleic acid binding / transcription regulator/ zinc ion binding	Unigene57920_All//0.00E+00//TC162491		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene57925_All	260	3.22	0.19	1.84	6.13	4.77	2.26	1.30	0.16	0.46	-4.05E+00	4.65E-04	Down	-8.05E-01	3.22E-01		-3.63E-01	5.18E-01		-1.44E+00	7.26E-03		-3.02E+00	5.30E-02		-1.50E+00	2.10E-01					Unigene57925_All//4.00E-71//TC161946				
Unigene5793_All	720	0.58	1.20	2.66	2.84	3.59	1.88	3.93	2.32	1.94	1.04E+00	1.72E-01		2.20E+00	8.20E-05	Up	3.39E-01	4.42E-01		-5.92E-01	2.07E-01		-7.61E-01	2.21E-02		-1.02E+00	1.59E-03					Unigene5793_All//2.00E-180//gi|78333204|gb|DT553478.1|DT553478				
Unigene57944_All	246	0.85	0.00	0.87	2.03	0.84	0.92	2.75	0.00	0.00	-9.73E+00	1.21E-01		2.55E-02	1.00E+00		-1.27E+00	2.22E-01		-1.14E+00	3.07E-01		-1.14E+01	6.34E-05	Down	-1.14E+01	3.56E-05	Down	Unigene57944_All//gi|30679610|ref|NP_195857.2|//2.00E-19//kinesin motor protein-related [Arabidopsis thaliana] >gi|59958334|gb|AAX12877.1| At5g02370 [Arabidopsis thaliana]	Unigene57944_All//1.00E-20//AT5G02370| kinesin motor protein-related	Unigene57944_All//2.00E-91//TC139544				nr -
Unigene5795_All	1873	0.87	0.43	1.02	6.14	3.75	3.98	4.24	9.60	5.70	-1.00E+00	5.37E-02		2.41E-01	6.24E-01		-7.12E-01	3.69E-06		-6.27E-01	1.23E-04		1.18E+00	2.93E-21	Up	4.26E-01	5.22E-03		Unigene5795_All//gi|15238363|ref|NP_201321.1|//2.00E-26//VQ motif-containing protein [Arabidopsis thaliana] >gi|44917435|gb|AAS49042.1| At5g65170 [Arabidopsis thaliana] >gi|46931270|gb|AAT06439.1| At5g65170 [Arabidopsis thaliana]	Unigene5795_All//1.00E-25//AT5G65170| VQ motif-containing protein	Unigene5795_All//0.00E+00//TC175710				nr -
Unigene5796_All	1160	39.24	41.37	55.09	0.26	1.45	0.00	1.64	0.29	0.41	7.61E-02	3.91E-01		4.89E-01	3.04E-13		2.50E+00	1.72E-05	Up	-8.01E+00	3.98E-02		-2.51E+00	6.21E-07	Down	-1.99E+00	1.17E-05	Down	Unigene5796_All//gi|15230602|ref|NP_190093.1|//2.00E-67//sulfotransferase family protein [Arabidopsis thaliana] >gi|6911845|emb|CAB72145.1| sulfotransferase-like protein [Arabidopsis thaliana] >gi|44917543|gb|AAS49096.1| At3g45070 [Arabidopsis thaliana]	Unigene5796_All//1.00E-68//AT3G45070| sulfotransferase family protein	Unigene5796_All//0.00E+00//TC168630		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism	GO:0008146	nr +
Unigene57966_All	211	1.24	3.12	1.77	8.03	4.41	1.71	0.00	0.00	0.38	1.33E+00	1.45E-01		5.11E-01	6.54E-01		-8.65E-01	7.39E-02		-2.23E+00	7.57E-05	Down	null	null		8.56E+00	4.03E-01					Unigene57966_All//3.00E-50//AT728016				
Unigene5797_All	1527	0.65	0.33	1.08	1.76	1.96	2.16	1.33	1.81	4.62	-9.72E-01	1.58E-01		7.32E-01	1.71E-01		1.55E-01	7.28E-01		2.94E-01	4.47E-01		4.43E-01	2.10E-01		1.80E+00	3.10E-16	Up	Unigene5797_All//gi|42565171|ref|NP_189132.2|//7.00E-35//DNA binding [Arabidopsis thaliana]	Unigene5797_All//3.00E-36//AT3G24880| DNA binding					nr -
Unigene57985_All	213	0.74	0.00	0.00	0.23	0.00	0.00	2.78	0.00	0.00	-9.53E+00	2.15E-01		-9.53E+00	2.44E-01		-7.87E+00	5.53E-01		-7.87E+00	6.32E-01		-1.14E+01	2.39E-04	Down	-1.14E+01	1.41E-04	Down				Unigene57985_All//5.00E-33//gi|78329276|gb|DT549550.1|DT549550				

Unigene5799_All	666	23.65	10.58	32.86	17.43	19.29	19.60	3.75	2.82	2.09	-1.16E+00	4.29E-15	Down	4.75E-01	8.88E-05		1.46E-01	4.32E-01		1.69E-01	3.56E-01		-4.07E-01	2.79E-01		-8.39E-01	1.49E-02		Unigene5799_All//gi|15224262|ref|NP_179484.1|//8.00E-16//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75099137|sp|O64624.1|PP163_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g18940 >gi|15983785|gb|AAL10489.1| At2g18940/F19F24.14 [Arabidopsis thaliana] >gi|38564280|gb|AAR23719.1| At2g18940/F19F24.14 [Arabidopsis thaliana]		Unigene5799_All//4.00E-27//TC136777				nr -
Unigene5800_All	866	35.16	29.37	34.37	38.94	38.21	36.51	14.16	8.74	4.92	-2.60E-01	9.72E-03		-3.28E-02	7.74E-01		-2.73E-02	8.10E-01		-9.32E-02	4.06E-01		-6.97E-01	1.32E-06		-1.52E+00	2.86E-22	Down			Unigene5800_All//0.00E+00//TC153981				
Unigene5801_All	1314	1.51	3.62	2.59	2.58	2.07	2.68	1.42	2.83	1.03	1.26E+00	1.10E-05	Up	7.77E-01	2.60E-02		-3.16E-01	3.77E-01		5.65E-02	8.91E-01		1.00E+00	4.70E-04		-4.58E-01	2.74E-01		Unigene5801_All//gi|9795613|gb|AAF98431.1|AC021044_10//1.00E-144//Unknown protein [Arabidopsis thaliana]	Unigene5801_All//8.00E-140//AT1G28240| unknown protein	Unigene5801_All//1.00E-155//gi|48789460|gb|CO090774.1|CO090774				nr +
Unigene58015_All	838	0.06	0.00	0.13	0.54	0.29	0.05	0.86	0.00	0.14	-5.96E+00	6.08E-01		1.03E+00	7.02E-01		-8.96E-01	4.13E-01		-3.31E+00	2.84E-02		-9.74E+00	3.26E-05	Down	-2.59E+00	2.81E-03		Unigene58015_All//gi|306944417|ref|NP_199211.2|//2.00E-57//PDLP1 (PLASMODESMATA-LOCATED PROTEIN 1) [Arabidopsis thaliana] >gi|158563851|sp|Q8GXV7.2|CRR56_ARATH RecName: Full=Cysteine-rich repeat secretory protein 56; Flags: Precursor	Unigene58015_All//7.00E-50//AT5G43980| PDLP1 (PLASMODESMATA-LOCATED PROTEIN 1)			GO:0005911//GO:0010196	nr -
Unigene5802_All	673	21.69	3.99	10.68	13.32	4.25	4.36	8.17	5.96	4.62	-2.44E+00	1.11E-38	Down	-1.02E+00	4.83E-11	Down	-1.65E+00	7.43E-18	Down	-1.61E+00	3.37E-15	Down	-4.54E-01	4.94E-02		-8.23E-01	1.89E-04		Unigene5802_All//gi|15228437|ref|NP_187722.1|//1.00E-34//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565339|sp|Q8S3N0.1|ATL3D_ARATH RecName: Full=RING-H2 finger protein ATL3D >gi|12321864|gb|AAG50960.1|AC07339 5.2 RING zinc finger protein; 17145-17621 [Arabidopsis thaliana] >gi|182623796|gb|ACB88837.1| At3g11110 [Arabidopsis thaliana]	Unigene5802_All//4.00E-30//AT3G11110| zinc finger (C3HC4-type RING finger) family protein	Unigene5802_All//0.00E+00//DW519503			GO:0005488	nr -
Unigene58031_All	774	0.00	0.13	0.00	0.39	0.18	0.00	0.16	0.43	1.90	7.03E+00	3.85E-01		null	null		-1.12E+00	4.24E-01		-8.59E+00	3.98E-02		1.40E+00	2.76E-01		3.54E+00	1.41E-07	Up	Unigene58031_All//gi|224070615|ref|XP_002303179.1|//3.00E-23//chromatin remodeling complex subunit [Populus trichocarpa] >gi|222840611|gb|EEE78158.1| chromatin remodeling complex subunit [Populus trichocarpa]	Unigene58031_All//1.00E-14//AT3G12810| PIE1 (PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1); ATP binding / DNA binding / helicase/ nucleic acid binding	Unigene58031_All//2.00E-162//gi|78336933|gb|DT557207.1|DT557207			GO:0005488//GO:0043234//GO:0044464//GO:0048437//GO:0050896	nr +
Unigene58032_All	471	34.55	24.42	43.64	42.73	27.34	34.71	126.75	95.75	38.15	-5.01E-01	2.79E-04		3.37E-01	8.60E-03		-6.44E-01	9.55E-09		-3.00E-01	1.70E-02		-4.05E-01	2.40E-11		-1.73E+00	2.67E-126	Down	Unigene58032_All//gi|224065681|ref|XP_002301918.1|//8.00E-16//high mobility group family [Populus trichocarpa] >gi|222843644|gb|EEE81194.1| high mobility group family [Populus trichocarpa]	Unigene58032_All//5.00E-10//AT1G20696| HMGB3 (HIGH MOBILITY GROUP B 3); DNA binding / chromatin binding / structural constituent of chromatin / transcription factor	Unigene58032_All//0.00E+00//TC168621		ko03410|Base excision repair	GO:0003676//GO:0005198//GO:0006325//GO:0044427	nr -
Unigene58042_All	256	3.68	0.40	0.00	0.00	0.00	0.18	0.00	0.00	0.00	-3.22E+00	6.76E-04	Down	-1.18E+01	3.34E-05	Down	null	null		7.46E+00	6.93E-01		null	null		null	null		Unigene58042_All//gi|224127754|ref|XP_002329169.1|//1.00E-09//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870950|gb|EEF08081.1| tir-nbs-lrr resistance protein [Populus trichocarpa]					GO:0000166//GO:0006952//GO:0009987	nr +
Unigene58044_All	240	8.28	5.91	17.31	28.85	14.49	16.75	10.57	6.27	7.97	-4.87E-01	2.93E-01		1.06E+00	7.22E-04	Up	-9.93E-01	1.54E-06		-7.85E-01	3.27E-04		-7.54E-01	3.40E-02		-4.08E-01	2.47E-01		Unigene58044_All//gi|255573105|ref|XP_002527482.1|//8.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223533122|gb|EEF34880.1| conserved hypothetical protein [Ricinus communis]		Unigene58044_All//1.00E-77//gi|109871415|gb|DW500391.1|DW500391			GO:0000166	nr -
Unigene58046_All	549	0.38	3.60	3.59	2.18	2.51	2.22	0.54	0.99	0.07	3.24E+00	1.95E-07	Up	3.23E+00	4.12E-07	Up	2.04E-01	7.79E-01		2.85E-02	9.62E-01		8.76E-01	3.46E-01		-2.89E+00	6.76E-02				Unigene58046_All//3.00E-09//gi|73943606|gb|DT526914.1|DT526914				
Unigene5805_All	921	0.11	0.00	0.00	11.63	4.49	2.84	6.98	7.49	1.34	-6.83E+00	3.69E-01		-6.83E+00	3.90E-01		-1.37E+00	3.10E-16	Down	-2.03E+00	1.14E-24	Down	1.02E-01	6.43E-01		-2.38E+00	2.97E-21	Down							
Unigene5806_All	883	50.90	14.40	38.54	27.02	29.09	20.10	1.10	0.66	0.81	-1.82E+00	3.63E-81	Down	-4.01E-01	8.28E-07		1.07E-01	4.15E-01		-4.27E-01	9.34E-05		-7.33E-01	2.48E-01		-4.40E-01	4.73E-01		Unigene5806_All//gi|79579427|ref|NP_680473.2|//1.00E-119//protein binding / signal transducer [Arabidopsis thaliana]	Unigene5806_All//3.00E-120//AT5G67385| protein binding / signal transducer	Unigene5806_All//0.00E+00//TC143356			GO:0005488//GO:0009314//GO:0044464//GO:0060089	nr +
Unigene5807_All	1490	0.07	0.00	0.29	10.43	8.94	6.91	4.97	2.64	1.87	-6.13E+00	3.69E-01		2.03E+00	1.39E-01		-2.22E-01	1.38E-01		-5.94E-01	1.59E-05		-9.13E-01	2.24E-06		-1.41E+00	2.45E-12	Down	Unigene5807_All//5.00E-46//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68565207|sp|Q8LFY8.2|ATL10_ARATH RecName: Full=RING-H2 finger protein ATL10; AltName: Full=RING-H2 finger protein ATL11 >gi|15529216|gb|AAK97702.1| At1g72220/T9N14_22 [Arabidopsis thaliana] >gi|25141211|gb|AAN73300.1| At1g72220/T9N14_22 [Arabidopsis thaliana]	Unigene5807_All//5.00E-43//AT1G72220| zinc finger (C3HC4-type RING finger) family protein	Unigene5807_All//0.00E+00//TC162114			GO:0005488	nr +
Unigene5808_All	805	1.95	2.20	0.60	6.00	2.10	4.60	5.20	6.39	6.29	1.76E-01	7.07E-01		-1.71E+00	3.82E-03		-1.52E+00	9.38E-09	Down	-3.84E-01	1.90E-01		2.97E-01	2.39E-01		2.74E-01	2.64E-01		Unigene5808_All//gi|117168147|gb|AB832156.1|//2.00E-29//At5g05360 [Arabidopsis thaliana]	Unigene5808_All//4.00E-36//AT5G05360| unknown protein	Unigene5808_All//1.00E-30//DW520114				nr +
Unigene5809_All	821	0.64	18.82	4.09	7.83	11.03	11.28	1.03	7.28	7.86	4.88E+00	1.50E-73	Up	2.68E+00	7.30E-10	Up	4.95E-01	7.79E-03		5.27E-01	5.20E-03		2.82E+00	5.88E-23	Up	2.93E+00	3.11E-26	Up	Unigene5809_All//gi|34098921|gb|AAQ56843.1|//9.00E-30//At5g07330 [Arabidopsis thaliana]	Unigene5809_All//4.00E-31//AT5G07330| unknown protein	Unigene5809_All//0.00E+00//TC150067				nr -
Unigene5812_All	1036	2.53	2.64	0.21	3.51	4.42	9.85	3.22	5.81	5.46	6.48E-02	8.67E-01		-3.62E+00	4.17E-10	Down	3.33E-01	2.81E-01		1.49E+00	3.83E-15	Up	8.50E-01	8.18E-05		7.60E-01	4.62E-04		Unigene5812_All//gi|37730469|gb|AAO59439.1|//1.00E-178//ethylene-responsive element binding factor [Gossypium hirsutum]	Unigene5812_All//7.00E-35//AT5G07580| DNA binding / transcription factor	Unigene5812_All//0.00E+00//TC131478	AP2-EREBP		GO:0006350//GO:0006950//GO:0010468	nr -
Unigene5813_All	616	72.62	43.76	19.62	48.52	50.76	44.06	97.26	29.38	36.28	-7.31E-01	1.73E-19		-1.89E+00	6.45E-82	Down	6.51E-02	5.95E-01		-1.39E-01	2.22E-01		-1.73E+00	1.40E-122	Down	-1.42E+00	3.35E-95	Down	Unigene5813_All//gi|225435036|ref|XP_002284281.1|//1.00E-29//PREDICTED: similar to Histone H2B isoform 2 [Vitis vinifera]	Unigene5813_All//2.00E-30//AT5G59910| HTB4; DNA binding	Unigene5813_All//0.00E+00//TC171027			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr -
Unigene5814_All	1174	0.85	1.21	1.13	8.61	4.08	2.81	4.36	3.03	4.75	5.13E-01	3.73E-01		4.21E-01	4.84E-01		-1.08E+00	1.40E-10	Down	-1.62E+00	3.68E-17	Down	-5.26E-01	2.73E-02		1.25E-01	6.10E-01		Unigene5814_All//gi|146674816|gb|AB242347.1|//3.00E-62//Dof6 transcription factor [Glycine max]	Unigene5814_All//1.00E-26//AT1G28310| Dof-type zinc finger domain-containing protein	Unigene5814_All//0.00E+00//TC144934	C2C2-Dof		GO:0001071//GO:0003676//GO:0010468//GO:0046914	nr +
Unigene5815_All	1041	3.02	0.78	2.40	2.58	1.52	2.13	1.30	1.53	5.74	-1.95E+00	7.02E-07	Down	-3.27E-01	3.87E-01		-7.64E-01	3.72E-02		-2.82E-01	5.03E-01		2.31E-01	6.19E-01		2.14E+00	2.78E-17	Up	Unigene5815_All//gi|57281695|dbj|BAD86587.1|//3.00E-35//sphingosine kinase [Lotus japonicus]	Unigene5815_All//2.00E-35//AT5G23450| ATLCBK1 (A. THALIANA LONG-CHAIN BASE (LCB) KINASE 1); D-erythro-sphingosine kinase/ diacylglycerol kinase	Unigene5815_All//2.00E-91//DR463475			GO:0003676//GO:0006260//GO:0006665//GO:0007186//GO:0016020//GO:0001631//GO:0034061//GO:0043231	nr -
Unigene58163_All	267	14.11	17.08	12.56	8.40	6.71	18.61	0.00	0.00	0.00	2.76E-01	3.67E-01		-1.67E-01	6.31E-01		-3.24E-01	4.77E-01		1.15E+00	2.28E-05	Up	null	null		null	null				Unigene58163_All//7.00E-116//TC169023				
Unigene5820_All	1088	7.02	19.05	18.45	14.24	4.18	3.61	1.63	3.73	1.06	1.44E+00	5.79E-27	Up	1.39E+00	3.91E-24	Up	-1.77E+00	8.16E-34	Down	-1.98E+00	2.69E-34	Down	1.19E+00	1.69E-05	Up	-6.20E-01	1.41E-01		Unigene5820_All//gi|124294787|gb|AB003967.1|//1.00E-154//acidic chitinase [Gossypium hirsutum]	Unigene5820_All//1.00E-106//AT5G24090| acidic endochitinase (CHIB1)	Unigene5820_All//0.00E+00//TC145633		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene5821_All	1254	5.38	11.52	6.62	3.42	5.77	4.14	3.34	7.00	7.88	1.10E+00	1.03E-12	Up	3.00E-01	1.71E-01		7.55E-01	2.58E-04		2.78E-01	3.47E-01		1.07E+00	2.35E-09	Up	1.24E+00	2.49E-13	Up	Unigene5821_All//gi|45593281|gb|AAS68190.1|//2.00E-86//Myb transcription factor [Vitis vinifera]	Unigene5821_All//2.00E-65//AT3G13540| ATMYB5 (MYB DOMAIN PROTEIN 5); DNA binding / transcription factor	Unigene5821_All//0.00E+00//gi|78343006|gb|DT563280.1|DT563280	MYB		GO:0000904//GO:0003006//GO:0003676//GO:0007275//GO:0010192//GO:0010468	nr -
Unigene5822_All	1131	0.00	0.45	0.05	2.03	1.89	1.64	4.71	15.23	4.72	8.81E+00	4.03E-03		5.56E+00	6.34E-01		-1.02E-01	8.09E-01		-3.07E-01	5.02E-01		1.69E+00	1.07E-34	Up	3.00E-03	9.90E-01		Unigene5822_All//gi|21742317|emb|CAD40774.1|//5.00E-19//OSJNBa0039F02.5 [Oryza sativa (japonica cultivar-group)] >gi|38347155|emb|CAE05145.2| OSJNBa0039C07.1 [Oryza sativa (japonica cultivar-group)]	Unigene5822_All//3.00E-26//AT1G28080| unknown protein	Unigene5822_All//1.00E-16//gi|3326717|gb|AI055603.1|AI055603				nr -
Unigene5823_All	1634	0.32	1.24	0.00	0.73	1.24	0.72	31.54	39.06	94.16	1.95E+00	1.12E-04	Up	-8.32E+00	4.74E-03		7.65E-01	9.48E-02		-2.61E-02	9.54E-01		3.08E-01	1.41E-07		1.58E+00	7.06E-281	Up	Unigene5823_All//gi|119331584|gb|AB163118.1|//1.00E-112//AT-hook DNA-binding protein [Catharanthus roseus]	Unigene5823_All//1.00E-64//AT4G22810| DNA-binding protein-related	Unigene5823_All//3.00E-104//DN816904				nr -
Unigene58247_All	227	11.29	0.00	1.88	0.00	0.00	1.39	0.00	0.00	0.00	-1.35E+01	8.28E-15	Down	-2.59E+00	2.31E-07	Down	null	null		1.04E+01	4.07E-02		null	null		null	null		Unigene58247_All//gi|297813081|ref|XP_002874424.1|//4.00E-06//hypothetical protein ARALYDRAFT_489647 [Arabidopsis lyrata subsp. lyrata] >gi|297320261|gb|EFH50683.1| hypothetical protein ARALYDRAFT_489647 [Arabidopsis lyrata subsp. lyrata]						nr -
Unigene5825_All	1107	0.38	0.41	0.53	2.34	2.18	1.55	2.29	6.27	5.83	1.24E-01	9.11E-01		4.85E-01	6.30E-01		-1.04E-01	8.24E-01		-5.94E-01	1.39E-01		1.45E+00	1.04E-11	Up	1.35E+00	3.97E-10	Up			Unigene5825_All//5.00E-151//EX165353				
Unigene5826_All	578	3.71	7.36	7.65	5.69	10.19	12.97	3.73	2.82	5.58	9.89E-01	8.94E-04		1.04E+00	5.81E-04	Up	8.41E-01	3.15E-04		1.19E+00	3.55E-08	Up	-4.04E-01	3.31E-01		5.82E-01	5.25E-02		Unigene5826_All//gi|124360233|gb|AB008246.1|//1.00E-09//Solute carrier family 35 member B3, related [Medicago truncatula]	Unigene5826_All//1.00E-10//AT1G12600| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf whorl, petal, male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, 4 anthesis, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: UAA transporter (InterPro:IPR013657); BEST Arabidopsis thaliana protein match is: UDP-galactose transporter-related (TAIR:AT4G22010.1); Has 943 Blast hits to 943 proteins in 196 species: Archae - 2; Bacteria - 55; Metazoa - 506; Fungi - 148; Plants - 112; Viruses - 0; Other Eukaryotes - 120 (source: NCBI BLink).	Unigene5826_All//1.00E-39//BQ412149			GO:0006810//GO:0031224	nr -
Unigene58260_All	475	1.43	0.00	0.45	0.21	0.22	0.10	0.09	0.00	0.00	-1.05E+01	4.09E-04	Down	-1.68E+00	8.70E-02		5.27E-02	9.66E-01		-1.14E+00	6.76E-01		-6.48E+00	6.54E-01		-6.48E+00	6.10E-01				Unigene58260_All//1.00E-152//ES810291				

Unigene5827_All	1027	36.02	8.54	4.10	42.05	30.85	16.71	30.05	6.27	3.49	-2.08E+00	1.20E-79	Down	-3.14E+00	1.42E-122	Down	-4.47E-01	1.38E-09		-1.33E+00	1.12E-53	Down	-2.26E+00	2.16E-90	Down	-3.11E+00	2.11E-132	Down	Unigene5827_All//gi|1710401|sp|P49730.1|RIR2_TOBAC//1.00E-145//RecName: Full=Ribonucleoside-diphosphate reductase small chain; AltName: Full=Ribonucleotide reductase small subunit; AltName: Full=Ribonucleoside-diphosphate reductase R2 subunit >gi|1044912|emb|CAA63194.1| ribonucleotide reductase R2 [Nicotiana tabacum]	Unigene5827_All//3.00E-132//AT3G27060| TSO2 (TSO meaning 'ugly' in Chinese); oxidoreductase/ ribonucleoside-diphosphate reductase/ transition metal ion binding	Unigene5827_All//0.00E+00//gi|78336668|gb|DT556942.1|DT556942		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism		nr -
Unigene5828_All	847	14.76	2.09	1.38	4.35	2.44	8.80	1.80	4.59	2.92	-2.82E+00	7.27E-39	Down	-3.42E+00	6.64E-45	Down	-8.35E-01	5.37E-03		1.02E+00	1.86E-06	Up	1.35E+00	2.77E-06	Up	6.99E-01	4.50E-02		Unigene5828_All//gi|79565313|ref|NP_180417.2|//1.00E-61//LBD11 (LOB DOMAIN-CONTAINING PROTEIN 11) [Arabidopsis thaliana]	Unigene5828_All//5.00E-49//AT2G28500| LBD11 (LOB DOMAIN-CONTAINING PROTEIN 11)	Unigene5828_All//0.00E+00//DN802105		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0043231	nr +
Unigene5829_All	500	7.12	15.30	8.20	25.11	28.17	30.44	15.98	22.07	36.33	1.10E+00	3.56E-07	Up	2.05E-01	5.42E-01		1.66E-01	3.26E-01		2.78E-01	6.71E-02		4.66E-01	2.42E-03		1.18E+00	3.16E-22	Up	Unigene5829_All//gi|60459371|gb|AAX20031.1|//3.00E-14//RING-finger protein [Capsicum annuum]		Unigene5829_All//0.00E+00//BG447228			GO:0006725//GO:0016020//GO:0042445	nr +
Unigene5831_All	807	34.43	55.88	31.61	186.48	422.74	480.85	148.16	287.75	153.68	6.99E-01	3.60E-18		-1.23E-01	3.10E-01		1.18E+00	0.00E+00	Up	1.37E+00	0.00E+00	Up	9.58E-01	7.36E-190		5.27E-02	2.67E-01		Unigene5831_All//gi|15224852|ref|NP_179571.1|//3.00E-29//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75220226|sp|082199.1|C3H20_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 20; Short=AtC3H20	Unigene5831_All//3.00E-17//AT2G19810| zinc finger (CCCH-type) family protein	Unigene5831_All//0.00E+00//TC157582	C3H		GO:0005488	nr -
Unigene5832_All	963	47.92	36.99	32.40	42.21	36.55	47.56	63.66	42.06	30.16	-3.74E-01	1.64E-06		-5.65E-01	2.01E-12		-2.08E-01	1.25E-02		1.72E-01	4.00E-02		-5.98E-01	7.10E-23		-1.08E+00	3.15E-63	Down	Unigene5832_All//gi|4406372|gb|AAD19957.1|//4.00E-93//thiosulfate sulfurtransferase [Datisca glomerata]	Unigene5832_All//3.00E-90//AT1G79230| MST1 (MERCAPTOPYRUVATE SULFURTRANSFERASE 1); 3-mercaptopyruvate sulfurtransferase/ sulfurtransferase/ thiosulfate sulfurtransferase	Unigene5832_All//0.00E+00//TC138570			GO:0009536//GO:0015698//GO:0016783//GO:0032502	nr +
Unigene5834_All	999	0.89	8.47	2.13	3.74	4.86	28.53	1.65	11.76	12.44	3.25E+00	4.16E-30	Up	1.26E+00	7.49E-03		3.78E-01	1.89E-01		2.93E+00	3.63E-97	Up	2.83E+00	1.10E-44	Up	2.91E+00	1.43E-49	Up	Unigene5834_All//gi|15240090|ref|NP_196275.1|//1.00E-110//hydrolase [Arabidopsis thaliana] >gi|30681513|ref|NP_850782.1| hydrolase [Arabidopsis thaliana] >gi|30725374|gb|AAF37709.1| At5g06570 [Arabidopsis thaliana]	Unigene5834_All//1.00E-111//AT5G06570| hydrolase	Unigene5834_All//8.00E-11//gi|48796383|gb|CO097697.1|CO097697				nr -
Unigene5835_All	1244	30.53	19.59	33.26	0.76	2.91	0.80	0.14	0.00	0.00	-6.40E-01	2.31E-13		1.23E-01	2.03E-01		1.93E+00	1.76E-08	Up	7.01E-02	9.38E-01		-7.09E+00	1.34E-01		-7.09E+00	1.08E-01		Unigene5835_All//gi|534982|emb|CAA53507.1|//1.00E-154//phosphoglucomutase [Spinacia oleracea]	Unigene5835_All//1.00E-153//AT1G70820| phosphoglucomutase, putative / glucose phosphomutase, putative	Unigene5835_All//0.00E+00//TC157632		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism	GO:0009536//GO:0016866//GO:0044238	nr +
Unigene5837_All	3436	0.06	0.03	0.11	0.43	0.63	0.37	5.24	10.69	13.08	-1.05E+00	5.64E-01		8.33E-01	5.16E-01		5.38E-01	2.39E-01		-2.41E-01	6.82E-01		1.03E+00	2.01E-34	Up	1.32E+00	2.54E-63	Up	Unigene5837_All//gi|264664459|sp|C0LGJ1.1|Y1743_ARATH//0.00E+00//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g74360; Flags: Precursor >gi|224589485|gb|ACN59276.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene5837_All//0.00E+00//AT1G74360| leucine-rich repeat transmembrane protein kinase, putative	Unigene5837_All//0.00E+00//DT463861			GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016791//GO:0031224//GO:0031410//GO:0032559//GO:0043231	nr -
Unigene5838_All	842	309.14	321.47	407.28	151.45	265.63	293.35	3.36	21.39	26.40	5.64E-02	1.02E-01		3.98E-01	6.13E-47		8.11E-01	8.40E-135		9.54E-01	2.17E-176		2.67E+00	5.18E-64	Up	2.97E+00	6.80E-90	Up	Unigene5838_All//gi|20197599|gb|AAM15147.1|//3.00E-28//Expressed protein [Arabidopsis thaliana]	Unigene5838_All//3.00E-28//AT2G17972| unknown protein	Unigene5838_All//0.00E+00//gi|164295138|gb|ES810057.1|ES810057			GO:0009534	nr +
Unigene5839_All	496	25.74	20.23	10.63	35.85	22.84	38.88	49.78	27.47	23.29	-3.48E-01	3.10E-02		-1.28E+00	1.29E-13	Down	-6.51E-01	6.30E-08		1.17E-01	4.47E-01		-8.58E-01	1.63E-17		-1.10E+00	1.11E-26	Down	Unigene5839_All//gi|10176887|dbj|BAB10117.1|//2.00E-44//eukaryotic translation initiation factor 3 subunit 7 [Arabidopsis thaliana]	Unigene5839_All//1.00E-33//AT5G44320| eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative	Unigene5839_All//0.00E+00//gi|164295136|gb|ES810055.1|ES810055			GO:0006412//GO:0008135//GO:0009536	nr +
Unigene58394_All	314	1.00	0.00	0.51	1.43	2.41	2.59	8.75	2.40	2.54	-9.97E+00	3.64E-02		-9.75E-01	5.06E-01		7.57E-01	3.95E-01		8.59E-01	3.07E-01		-1.87E+00	5.66E-07	Down	-1.79E+00	7.27E-07	Down	Unigene58394_All//gi|239056193|emb|CAQ58630.1|//1.00E-21//Unknown gene [Vitis vinifera]	Unigene58394_All//3.00E-18//AT2G38640| unknown protein	Unigene58394_All//6.00E-86//TC155170				nr +
Unigene5840_All	711	7.06	4.85	5.62	14.36	14.77	11.69	79.51	41.50	29.81	-5.44E-01	4.30E-02		-3.31E-01	2.52E-01		4.05E-02	8.48E-01		-2.97E-01	1.19E-01		-9.38E-01	2.91E-45		-1.42E+00	3.49E-89	Down	Unigene5840_All//gi|224117452|ref|XP_002331716.1|//2.00E-97//Sec61 transport protein [Populus trichocarpa] >gi|222874322|gb|EEF11453.1| Sec61 transport protein [Populus trichocarpa]	Unigene5840_All//2.00E-96//AT1G29310| P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene5840_All//0.00E+00//TC157445		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export	GO:0006810//GO:0008320//GO:0016020//GO:0043231	nr +
Unigene58409_All	244	0.00	0.00	0.00	5.92	2.54	2.04	4.33	0.34	1.14	null	null		null	null		-1.22E+00	2.11E-02		-1.54E+00	7.34E-03		-3.66E+00	1.31E-05	Down	-1.92E+00	2.21E-03		Unigene58409_All//gi|42565930|ref|NP_567005.2|//3.00E-20//FBL17; ubiquitin-protein ligase [Arabidopsis thaliana] >gi|75331246|sp|Q8W104.1|FBL17_ARATH RecName: Full=F-box/LRR-repeat protein 17 >gi|18087570|gb|AAL58916.1|AF46282_1 AT3g54650/T5N23_10 [Arabidopsis thaliana] >gi|22655356|gb|AAM98270.1| At3g54650/T5N23_10 [Arabidopsis thaliana]	Unigene58409_All//1.00E-21//AT3G54650| FBL17; ubiquitin-protein ligase	Unigene58409_All//3.00E-99//TC136743			GO:0005488//GO:0007067//GO:0009536//GO:0009791//GO:0031461//GO:0043073//GO:0043161//GO:0048229	nr -
Unigene5841_All	795	3.55	7.78	5.36	5.33	7.49	6.14	1.97	1.73	1.95	1.13E+00	3.85E-06	Up	5.92E-01	5.48E-02		4.93E-01	4.19E-02		2.04E-01	5.16E-01		-1.82E-01	7.12E-01		-9.90E-03	9.76E-01		Unigene5841_All//gi|225443610|ref|XP_002279326.1|//6.00E-25//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297740424|emb|CBI30606.3| unnamed protein product [Vitis vinifera]		Unigene5841_All//0.00E+00//DW506308				nr -
Unigene58420_All	206	0.00	0.00	0.00	0.00	0.00	0.00	2.46	0.00	0.00	null	null		null	null		null	null		null	null		-1.13E+01	8.88E-04	Down	-1.13E+01	5.54E-04	Down			Unigene58420_All//1.00E-08//CA994022				ESTscan -
Unigene5843_All	802	10.76	5.37	7.37	34.47	24.52	25.00	54.46	34.60	20.02	-1.00E+00	5.57E-07	Down	-5.47E-01	7.75E-03		-4.92E-01	1.89E-07		-4.63E-01	3.66E-06		-6.54E-01	2.93E-19		-1.44E+00	3.53E-71	Down	Unigene5843_All//gi|1335862|gb|AAC49294.1|//9.00E-69//clathrin heavy chain [Glycine max]	Unigene5843_All//1.00E-37//AT3G08530| clathrin heavy chain, putative	Unigene5843_All//0.00E+00//TC147306		ko04144|Endocytosis	GO:0005488//GO:0005905//GO:0009536//GO:0012510//GO:0015031	nr -
Unigene5844_All	1332	1.77	3.96	2.92	6.10	5.38	6.27	4.29	3.73	3.20	1.16E+00	1.45E-05	Up	7.23E-01	2.53E-02		-1.81E-01	4.32E-01		4.12E-02	8.69E-01		-1.99E-01	4.22E-01		-4.21E-01	5.35E-02		Unigene5844_All//gi|192910684|gb|ACF06450.1|//1.00E-136//ribosomal protein L10 [Elaeis guineensis]	Unigene5844_All//7.00E-129//AT3G09200| 60S acidic ribosomal protein P0 (RPP0B)	Unigene5844_All//0.00E+00//TC149715		ko03010|Ribosome		nr +
Unigene58444_All	571	0.55	7.72	0.93	0.96	0.84	0.47	1.04	1.90	1.81	3.81E+00	3.93E-18	Up	7.62E-01	4.52E-01		-1.85E-01	8.25E-01		-1.02E+00	3.29E-01		8.77E-01	1.39E-01		8.07E-01	1.68E-01		Unigene58444_All//gi|111074300|gb|ABB04523.1|//3.00E-24//At3g27880 [Arabidopsis thaliana]	Unigene58444_All//1.00E-17//AT3G27880| unknown protein	Unigene58444_All//3.00E-148//TC146528				nr +
Unigene5845_All	1015	5.26	2.30	3.57	4.61	5.12	3.92	6.41	2.22	2.00	-1.20E+00	7.24E-06	Down	-5.60E-01	4.00E-02		1.51E-01	6.13E-01		-2.37E-01	4.56E-01		-1.53E+00	7.13E-12	Down	-1.68E+00	6.02E-14	Down	Unigene5845_All//gi|218744593|dbj|BAH03515.1|//4.00E-42//centromere specific histone H3 variant [Nicotiana tabacum] >gi|218744596|dbj|BAH03516.1| centromere specific histone H3 variant [Nicotiana sylvestris]	Unigene5845_All//7.00E-29//AT1G01370| HTR12; DNA binding	Unigene5845_All//0.00E+00//gi|78346398|gb|DT566672.1|DT566672			GO:0005488//GO:0009566//GO:0043231//GO:0044427	nr +
Unigene5848_All	974	3.55	1.09	3.88	19.38	17.57	11.31	12.94	4.03	0.53	-1.70E+00	2.46E-06	Down	1.31E-01	6.90E-01		-1.42E-01	3.21E-01		-7.77E-01	3.98E-10		-1.68E+00	2.09E-25	Down	-4.60E+00	3.57E-74	Down	Unigene5848_All//gi|42573015|ref|NP_974604.1|//2.00E-51//zinc finger (RING-H2 type) protein-related [Arabidopsis thaliana] >gi|51316423|sp|Q84TF5.1|RHA4A_ARATH RecName: Full=RING-H2 zinc finger protein RHA4a >gi|29028800|gb|AAO64779.1| At4g24010 [Arabidopsis thaliana]	Unigene5848_All//2.00E-37//AT4G24015| zinc finger (RING-H2 type) protein-related				GO:0046914	nr -
Unigene58481_All	356	1.62	9.25	3.59	7.98	5.03	7.87	1.19	1.64	1.01	2.52E+00	1.94E-09	Up	1.15E+00	6.95E-02		-6.65E-01	6.39E-02		-2.01E-02	9.49E-01		4.69E-01	6.13E-01		-2.38E-01	7.88E-01				Unigene58481_All//1.00E-99//TC169302				
Unigene58486_All	213	0.25	4.76	0.25	0.70	0.32	1.48	2.78	1.57	0.75	4.28E+00	7.16E-05	Up	2.56E-02	9.94E-01		-1.12E+00	5.83E-01		1.08E+00	4.76E-01		-8.24E-01	3.48E-01		-1.89E+00	3.22E-02				Unigene58486_All//8.00E-66//DW232659				
Unigene5849_All	777	2.15	0.07	0.27	68.21	49.06	38.48	2.72	2.53	0.10	-5.05E+00	1.72E-08	Down	-2.97E+00	1.13E-05	Down	-4.76E-01	5.35E-13		-8.26E-01	2.37E-30		-1.06E-01	7.95E-01		-4.73E+00	4.77E-13	Down	Unigene5849_All//gi|73761685|gb|AAZ83342.1|//1.00E-112//ACC oxidase 1 [Gossypium hirsutum]	Unigene5849_All//2.00E-92//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene5849_All//0.00E+00//ES851313		ko00270|Cysteine and methionine metabolism		nr +
Unigene58494_All	426	0.25	0.00	0.00	0.00	0.00	0.00	1.39	0.00	0.28	-7.94E+00	3.69E-01		-7.94E+00	3.90E-01		null	null		null	null		-1.04E+01	2.39E-04	Down	-2.31E+00	1.36E-02		Unigene58494_All//gi|30690286|ref|NP_849565.1|//1.00E-20//TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter [Arabidopsis thaliana] >gi|204531189|gb|AAM19835.1| AT4g35300/F23E12_140 [Arabidopsis thaliana]	Unigene58494_All//9.00E-17//AT4G35300| TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter	Unigene58494_All//8.00E-151//gi|78351597|gb|DT571871.1|DT571871			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr +
Unigene58495_All	370	3.54	0.14	1.01	0.81	0.56	0.37	0.00	0.00	0.00	-4.69E+00	1.63E-06	Down	-1.81E+00	6.66E-03		-5.33E-01	6.78E-01		-1.14E+00	4.57E-01		null	null		null	null		Unigene58495_All//gi|224077012|ref|XP_002305092.1|//6.00E-32//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222848056|gb|EEE85603.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]		Unigene58495_All//1.00E-16//gi|109849245|gb|DW478224.1|DW478224			GO:0004872//GO:0005216//GO:0005488//GO:0006810//GO:0016020	nr +
Unigene58508_All	557	2.07	0.36	1.15	1.97	1.61	0.81	0.15	0.30	0.57	-2.51E+00	8.99E-04	Down	-8.49E-01	2.06E-01		-2.92E-01	6.47E-01		-1.28E+00	5.68E-02		9.83E-01	6.33E-01		1.91E+00	1.54E-01				Unigene58508_All//4.00E-122//TC132227				
Unigene5851_All	987	46.75	31.78	28.16	59.91	37.23	67.40	43.39	28.84	13.72	-5.57E-01	1.07E-12		-7.31E-01	2.63E-19		-6.86E-01	1.02E-27		1.70E-01	1.11E-02		-5.90E-01	7.71E-16		-1.66E+00	1.37E-85	Down	Unigene5851_All//gi|115468596|ref|NP_001057897.1|//3.00E-25//Os06g0567000 [Oryza sativa Japonica Group] >gi|113595937|dbj|BAF19811.1| Os06g0567000 [Oryza sativa Japonica Group]	Unigene5851_All//2.00E-14//AT4G29735| unknown protein	Unigene5851_All//0.00E+00//TC169029			GO:0004672//GO:0006464//GO:0031410//GO:0032559	nr -
Unigene58521_All	252	1.25	1.01	1.69	4.35	4.24	2.51	10.07	4.31	3.64	-3.09E-01	7.89E-01		4.41E-01	6.77E-01		-3.79E-02	9.49E-01		-7.94E-01	2.34E-01		-1.22E+00	7.21E-04	Down	-1.47E+00	4.74E-05	Down		Unigene58521_All//6.00E-06//AT5G10360| EMB3010 (embryo defective 3010); structural constituent of ribosome	Unigene58521_All//3.00E-16//ES843317		ko03010|Ribosome		kegg -
Unigene58524_All	444	2.00	0.00	0.00	0.00	0.00	0.00	4.38	1.22	0.18	-1.10E+01	2.86E-05	Down	-1.10E+01	6.30E-05	Down	null	null		null	null		-1.84E+00	4.63E-05	Down	-4.61E+00	6.97E-12	Down	Unigene58524_All//gi|254803073|gb|ACT82815.1|//5.00E-08//At1g29270 [Arabidopsis thaliana]		Unigene58524_All//2.00E-154//TC156726				nr -
Unigene58526_All	539	2.62	0.19	0.89	0.00	0.45	0.00	0.63	0.31	0.37	-3.80E+00	3.23E-06	Down	-1.56E+00	1.19E-02		8.80E+00	1.04E-01		null	null		-1.02E+00	3.99E-01		-7.64E-01	5.01E-01		Unigene58526_All//gi|83776783|gb|ABC46707.1|//4.00E-20//chloroplast thioredoxin M-type [Arachis hypogaea]	Unigene58526_All//2.00E-14//AT4G03520| ATDM2; enzyme activator	Unigene58526_All//0.00E+00//ES813209			GO:0006091//GO:0009536//GO:0015036//GO:0016862//GO:0018904//GO:0019725//GO:0051234	nr -

Unigene5855_All	1516	4.21	1.14	0.28	8.71	9.65	5.54	13.64	1.57	8.09	-1.89E+00	1.07E-12	Down	-3.91E+00	1.22E-25	Down	1.49E-01	3.86E-01		-6.52E-01	1.53E-05		-3.12E+00	2.14E-86	Down	-7.53E-01	2.27E-12		Unigene5855_All//gi|124360612|gb|AB008611.1|//4.00E-87//CBS [Medicago truncatula]	Unigene5855_All//2.00E-92//AT5G53750| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to wounding; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage; CONTAINS InterPro DOMAIN/s: Cystathionine beta-synthase, core (InterPro:IPR000644); BEST Arabidopsis thaliana protein match is: CBS domain-containing protein (TAIR:AT4G27460.1); Has 79 Blast hits to 78 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 79; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene5855_All//0.00E+00//TC150702					nr +
Unigene5857_All	1769	0.53	1.00	0.51	1.15	1.97	0.69	3.49	4.70	10.63	9.13E-01	6.42E-02		-5.72E-02	9.49E-01		7.68E-01	1.80E-02		-7.44E-01	1.05E-01		4.30E-01	1.80E-02		1.61E+00	6.06E-36	Up	Unigene5857_All//gi|15241995|ref|NP_200506.1|//8.00E-73//basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] >gi|75311566|sp|Q9LT54.1|BHH41_ARATH RecName: Full=Putative transcription factor bHLH041; AltName: Full=Transcription factor EN 51; AltName: Full=bHLH transcription factor bHLH041; AltName: Full=Basic helix-loop-helix protein 41; Short=bHLH 41; Short=AtbHLH41	Unigene5857_All//2.00E-61//AT5G56960| basic helix-loop-helix (bHLH) family protein		bHLH	ko04626|Plant-pathogen interaction		nr +
Unigene58587_All	251	1.88	3.03	1.70	2.58	3.70	9.90	0.51	0.83	0.00	6.91E-01	3.76E-01		-1.45E-01	8.89E-01		5.22E-01	5.25E-01		1.94E+00	1.09E-05	Up	7.21E-01	6.31E-01		-8.98E+00	1.99E-01		Unigene58587_All//gi|407944|gb|AAA81892.1|//6.00E-12//epoxide hydrolase [Solanum tuberosum]	Unigene58587_All//7.00E-13//AT4G15960| catalytic/ epoxide hydrolase	Unigene58587_All//9.00E-66//TC149045			GO:0016740//GO:0016803	nr -
Unigene5859_All	699	3.59	18.48	8.99	4.92	10.49	6.66	3.69	3.41	11.57	2.36E+00	9.48E-33	Up	1.32E+00	2.05E-07	Up	1.09E+00	1.38E-07	Up	4.37E-01	1.37E-01		-1.15E-01	7.59E-01		1.65E+00	1.67E-16	Up			Unigene5859_All//4.00E-12//FL576574					
Unigene58595_All	219	4.06	0.00	1.22	1.14	0.16	0.00	1.16	0.00	0.18	-1.20E+01	2.88E-05	Down	-1.74E+00	3.79E-02		-2.88E+00	1.37E-01		-1.02E+01	7.32E-02		-1.02E+01	4.03E-02		-2.67E+00	1.15E-01										
Unigene586_All	666	3.54	2.43	0.64	2.39	3.83	3.73	0.32	0.00	0.00	-5.38E-01	1.99E-01		-2.47E+00	1.77E-06	Down	6.77E-01	9.04E-02		6.40E-01	1.26E-01		-8.31E+00	7.42E-02		-8.31E+00	5.79E-02		Unigene586_All//gi|115440297|ref|NP_001044428.1|//3.00E-53//Os01g0778700 [Oryza sativa Japonica Group] >gi|113533959|dbj|BAF06342.1|Os01g0778700 [Oryza sativa Japonica Group]	Unigene586_All//7.00E-45//AT4G14950| unknown protein	Unigene586_All//0.00E+00//TC178316			GO:0043231	nr -
Unigene5860_All	756	2.28	3.89	1.83	6.19	5.88	3.35	3.13	1.66	1.26	7.67E-01	3.59E-02		-3.19E-01	5.53E-01		-7.60E-02	8.31E-01		-8.89E-01	1.21E-03		-9.17E-01	1.31E-02		-1.31E+00	3.80E-04	Down			Unigene5860_All//0.00E+00//TC177802					ESTscan +
Unigene58604_All	246	2.55	0.00	0.00	0.81	0.14	0.18	0.17	0.00	0.16	-1.13E+01	7.91E-04	Down	-1.13E+01	1.41E-03		-2.53E+00	2.33E-01		-2.14E+00	3.47E-01		-7.43E+00	6.53E-01		-8.65E-02	9.70E-01										
Unigene5861_All	1792	0.32	0.17	0.09	1.89	0.86	2.72	7.08	2.45	3.94	-9.21E-01	3.43E-01		-1.85E+00	9.61E-02		-1.13E+00	3.40E-04	Down	5.26E-01	5.96E-02		-1.53E+00	1.92E-22	Down	-8.47E-01	1.59E-09		Unigene5861_All//gi|297834908|ref|XP_002885336.1|//1.00E-140//phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311176|gb|EFH61595.1|phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene5861_All//2.00E-130//AT3G19850| phototropic-responsive NPH3 family protein					nr -
Unigene58615_All	930	0.11	1.31	0.57	0.86	0.33	1.31	2.64	2.02	1.46	3.54E+00	4.02E-05	Up	2.35E+00	5.87E-02		-1.36E+00	7.74E-02		6.14E-01	3.52E-01		-3.83E-01	3.21E-01		-8.56E-01	1.39E-02		Unigene58615_All//gi|15240571|ref|NP_199799.1|//1.00E-101//mitotic checkpoint family protein [Arabidopsis thaliana] >gi|8777419|db|BAA97009.1|mitotic checkpoint protein-like [Arabidopsis thaliana]	Unigene58615_All//1.00E-103//AT5G49880| mitotic checkpoint family protein	Unigene58615_All//4.00E-99//CO077188			GO:0006461//GO:0016758//GO:0031224//GO:0043231	nr -
Unigene58626_All	456	2.07	0.00	0.23	0.22	0.00	0.00	0.00	0.00	0.00	-1.10E+01	1.46E-05	Down	-3.14E+00	1.33E-03		-7.77E+00	3.11E-01		-7.77E+00	3.98E-01		null	null		null	null		Unigene58626_All//gi|145338044|ref|NP_186956.2|//2.00E-20//ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene58626_All//1.00E-19//AT3G03060| ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene58626_All//2.00E-43//gi|164288615|gb|ES796506.1|ES796506			GO:0005618//GO:0032559//GO:0042623//GO:0043231//GO:0043234//GO:0046914	nr +
Unigene58634_All	405	0.26	0.50	0.00	1.72	1.19	0.22	18.27	7.64	26.36	9.54E-01	6.20E-01		-8.01E+00	3.90E-01		-5.33E-01	5.45E-01		-2.95E+00	5.83E-03		-1.26E+00	3.57E-10	Down	5.29E-01	4.82E-04		Unigene58634_All//gi|118430824|gb|ABK91948.1|//5.00E-42//proline dehydrogenase [Actinidia deliciosa]	Unigene58634_All//2.00E-39//AT3G30775| ERD5 (EARLY RESPONSIVE TO DEHYDRATION 5); proline dehydrogenase	Unigene58634_All//0.00E+00//gi|5049119|gb|AT30267.1|AT30267			GO:0005488//GO:0006536//GO:0006560//GO:0006950//GO:0016645//GO:0043231	nr +
Unigene58636_All	1043	0.20	1.07	0.26	0.86	0.69	0.13	0.04	0.76	0.53	2.41E+00	1.59E-03		3.47E-01	7.96E-01		-3.10E-01	6.65E-01		-2.73E+00	2.06E-03		4.23E+00	1.05E-04	Up	3.72E+00	2.38E-03		Unigene58636_All//gi|15229025|ref|NP_190449.1|//5.00E-37//sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	Unigene58636_All//1.00E-32//AT3G48800| sterile alpha motif (SAM) domain-containing protein	Unigene58636_All//0.00E+00//TC156752				nr -
Unigene58659_All	683	7.97	1.11	1.33	0.22	0.45	0.00	0.00	0.00	0.06	-2.84E+00	2.25E-17	Down	-2.59E+00	4.83E-15	Down	1.05E+00	5.31E-01		-7.77E+00	2.33E-01		null	null		5.87E+00	6.42E-01		Unigene58659_All//gi|836954|gb|AAC23542.1|//2.00E-14//receptor protein kinase [Ipomoea trifida]	Unigene58659_All//3.00E-13//AT4G27300| S-locus protein kinase, putative				GO:0004672//GO:0006464//GO:0032559	nr +
Unigene58672_All	422	0.50	0.00	0.00	0.24	0.16	0.21	2.40	0.00	0.19	-8.95E+00	1.21E-01		-8.95E+00	1.45E-01		-5.33E-01	8.15E-01		-1.42E-01	9.49E-01		-1.12E+01	2.97E-07	Down	-3.67E+00	1.15E-05	Down	Unigene58672_All//gi|225452807|ref|XP_002278154.1|//1.00E-43//PREDICTED: similar to ATSMC3 (ARABIDOPSIS THALIANA STRUCTURAL MAINTENANCE OF CHROMOSOME 3); ATP binding [Vitis vinifera]	Unigene58672_All//2.00E-39//AT5G48600| ATSMC3 (ARABIDOPSIS THALIANA STRUCTURAL MAINTENANCE OF CHROMOSOME 3); ATP binding / transporter				GO:0006996//GO:0032559//GO:0043231//GO:0043232	nr +
Unigene58679_All	308	9.85	18.92	60.17	57.09	16.77	17.74	400.43	409.14	190.14	9.41E-01	1.51E-04		2.61E+00	4.94E-51	Up	-1.77E+00	2.71E-38	Down	-1.69E+00	2.96E-31	Down	3.10E-02	5.74E-01		-1.07E+00	1.05E-125	Down	Unigene58679_All//gi|259190048|ref|NP_001159270.1|//3.00E-06//hypothetical protein LOC100304360 [Zea mays] >gi|223943115|gb|ACN25641.1|unknown [Zea mays]		Unigene58679_All//2.00E-166//gi|84158182|gb|DN827229.1|DN827229				nr -
Unigene5868_All	1420	26.71	27.23	33.49	3.79	8.00	10.72	0.00	0.29	0.22	2.74E-02	7.78E-01		3.26E-01	4.25E-05		1.08E+00	2.94E-11	Up	1.50E+00	1.42E-22	Up	8.20E+00	3.65E-03		7.81E+00	1.34E-02		Unigene5868_All//gi|15225053|ref|NP_181454.1|//1.00E-136//nodulin family protein [Arabidopsis thaliana] >gi|16930479|gb|AAL31925.1|AF419593_1 At2g39210/T16B24.15 [Arabidopsis thaliana] >gi|34026841|gb|AAC28987.1|nodulin-like protein [Arabidopsis thaliana]	Unigene5868_All//7.00E-138//AT2G39210| nodulin family protein	Unigene5868_All//0.00E+00//TC160183				nr +
Unigene587_All	1198	6.38	7.49	3.02	9.61	10.69	9.65	23.61	31.15	26.47	2.32E-01	2.57E-01		-1.08E+00	1.40E-06	Down	1.55E-01	4.05E-01		6.80E-03	9.69E-01		4.00E-01	2.94E-07		1.65E-01	6.37E-02		Unigene587_All//gi|53749170|gb|AAU90070.1|//1.00E-118//At4g14950 [Arabidopsis thaliana]	Unigene587_All//5.00E-112//AT4G14950| unknown protein	Unigene587_All//0.00E+00//ES813085				nr -
Unigene58706_All	837	0.31	0.48	0.32	0.36	0.12	0.32	3.23	0.85	0.62	6.32E-01	6.01E-01		2.56E-02	1.00E+00		-1.53E+00	2.98E-01		-1.41E-01	9.20E-01		-1.93E+00	3.86E-07	Down	-2.39E+00	2.00E-09	Down	Unigene58706_All//gi|15220639|ref|NP_176974.1|//6.00E-63//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|90093276|gb|ABDB5151.1|At1g68070 [Arabidopsis thaliana]	Unigene58706_All//6.00E-46//AT1G68070| zinc finger (C3HC4-type RING finger) family protein	Unigene58706_All//0.00E+00//gi|78329151|gb|DT549425.1|DT549425			GO:0007275//GO:0016020//GO:0046914	nr +
Unigene5871_All	1347	16.90	12.56	18.38	20.01	14.09	16.60	10.92	6.14	4.38	-4.27E-01	1.92E-04		1.22E-01	3.56E-01		-5.06E-01	1.20E-07		-2.70E-01	1.16E-02		-8.30E-01	3.13E-10		-1.32E+00	1.61E-21	Down	Unigene5871_All//gi|297851580|ref|XP_002893671.1|//3.00E-80//single-stranded DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297339513|gb|EFH69930.1|single-stranded DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene5871_All//2.00E-79//AT1G31010| OSB4 (organellar single-stranded DNA binding protein 4); single-stranded DNA binding	Unigene5871_All//0.00E+00//TC138949			GO:0000229//GO:0009536	nr +
Unigene58710_All	428	4.16	0.00	1.99	0.70	0.08	0.00	0.00	0.20	0.00	-1.20E+01	2.68E-10	Down	-1.06E+00	4.11E-02		-3.12E+00	7.55E-02		-9.45E+00	3.98E-02		7.61E+00	4.00E-01		null	null		Unigene58710_All//gi|119331584|gb|ABL63118.1|//3.00E-06//AT-hook DNA-binding protein [Catharanthus roseus]		Unigene58710_All//1.00E-78//TC131035				nr +
Unigene58717_All	955	0.88	0.21	0.11	0.63	1.23	0.76	1.59	0.57	0.50	-2.05E+00	1.68E-02		-2.97E+00	3.83E-03		9.70E-01	1.37E-01		2.74E-01	7.42E-01		-1.49E+00	2.91E-03		-1.67E+00	7.06E-04	Down	Unigene58717_All//gi|297795141|ref|XP_002865455.1|//3.00E-87//CYCA3_1 [Arabidopsis lyrata subsp. lyrata] >gi|297311290|gb|EFH41714.1|CYCA3_1 [Arabidopsis lyrata subsp. lyrata]	Unigene58717_All//2.00E-81//AT1G47230| cyclin, putative	Unigene58717_All//0.00E+00//TC155253			GO:0007049//GO:0016722//GO:0019887//GO:0043231	nr -
Unigene58719_All	305	2.74	0.00	0.17	0.49	0.23	0.00	0.00	0.00	0.13	-1.14E+01	5.57E-05	Down	-3.97E+00	9.08E-04	Down	-1.12E+00	5.83E-01		-8.94E+00	2.32E-01		null	null		7.03E+00	6.42E-01		Unigene58719_All//gi|224062353|ref|XP_002308821.1|//4.00E-07//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222842547|gb|EEE80094.1|sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene58719_All//3.00E-06//AT3G51895| SULTR3;1 (SULFATE TRANSPORTER 3;1); secondary active sulfate transmembrane transporter/ sulfate transmembrane transporter/ transporter	Unigene58719_All//2.00E-36//TC168996				nr -
Unigene58726_All	328	1.60	0.46	2.27	2.28	1.68	0.14	0.26	0.13	0.12	-1.78E+00	1.08E-01		5.11E-01	5.47E-01		-4.40E-01	5.85E-01		-4.05E+00	7.75E-04	Down	-1.02E+00	7.23E-01		-1.09E+00	6.75E-01				Unigene58726_All//4.00E-07//TC172937					
Unigene58729_All	798	4.33	0.38	0.27	0.25	0.26	0.00	0.85	0.63	0.40	-3.51E+00	1.44E-13	Down	-4.02E+00	2.81E-14	Down	5.22E-02	9.88E-01		-7.96E+00	1.33E-01		-4.32E-01	6.12E-01		-1.09E+00	1.50E-01		Unigene58729_All//gi|3047095|gb|AAC13607.1|//2.00E-45//similar to eukaryotic protein kinase domains (Pfam: pkinase,hmm, score: 72.39) [Arabidopsis thaliana] >gi|10178102|dbj|BAB11489.1|receptor-like protein kinase [Arabidopsis thaliana]	Unigene58729_All//8.00E-42//AT5G35390| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0003824//GO:0044459	nr +
Unigene5875_All	682	1.23	1.56	3.20	4.97	3.08	1.06	1.86	0.98	0.88	3.46E-01	6.19E-01		1.38E+00	3.18E-03		-6.89E-01	3.14E-02		-2.23E+00	4.16E-09	Down	-9.24E-01	8.68E-02		-1.09E+00	3.58E-02				Unigene5875_All//1.00E-122//gi|73861505|gb|DT461244.1|DT461244					ESTscan +
Unigene58750_All	546	34.31	11.23	18.73	14.69	12.36	7.78	0.46	0.23	0.51	-1.61E+00	7.19E-29	Down	-8.74E-01	6.47E-11		-2.49E-01	2.61E-01		-9.18E-01	5.19E-06		-1.02E+00	4.94E-01		1.37E-01	9.28E-01		Unigene58750_All//gi|18147596|dbj|BAB83088.1|//1.00E-47//beta-amyrin synthase [Betula platyphylla]	Unigene58750_All//1.00E-46//AT1G78955| CAMS1 (Camelliol C synthase 1); beta-amyrin synthase	Unigene58750_All//1.00E-146//gi|164302226|gb|ES807570.1|ES807570		ko00100|Steroid biosynthesis	GO:0031559	nr +
Unigene5876_All	565	18.24	16.77	13.29	27.77	26.94	22.46	13.02	6.29	8.81	-1.21E-01	5.46E-01		-4.57E-01	1.45E-02		-4.40E-02	8.18E-01		-3.06E-01	3.56E-02		-1.05E+00	8.76E-08	Down	-5.63E-01	2.46E-03				Unigene5876_All//0.00E+00//gi|21094435|gb|BQ406748.1|BQ406748					
Unigene58761_All	1788	1.79	1.62	1.73	0.00	0.04	0.00	1.42	1.78	0.49	-1.44E-01	6.73E-01		-4.74E-02	9.02E-01		5.27E+00	6.07E-01		null	null		3.24E-01	3.38E-01		-1.53E+00	2.53E-05	Down	Unigene58761_All//gi|115447847|ref|NP_001047703.1|//1.00E-107//Os02g0672100 [Oryza sativa Japonica Group] >gi|50251918|dbj|BAD27855.1|finger protein pcg1-like [Oryza sativa Japonica Group] >gi|113537234|dbj|BAF09617.1|Os02g0672100 [Oryza sativa Japonica Group]	Unigene58761_All//4.00E-84//AT2G02070| At1D05 (Arabidopsis thaliana Indeterminate(ID)-Domain 5); nucleic acid binding / transcription factor/ zinc ion binding	Unigene58761_All//0.00E+00//TC157511	C2H2	ko03018|RNA degradation	GO:0005488	nr -

Unigene5877_All	746	6.80	6.86	8.71	8.68	11.22	7.45	20.18	17.87	7.90	1.20E-02	9.85E-01		3.56E-01	1.50E-01		3.70E-01	7.00E-02		-2.21E-01	3.96E-01		-1.75E-01	2.27E-01		-1.35E+00	8.33E-23	Down	Unigene5877_All//gi|21555592|gb|AAW63893.1|//7.00E-62//3-hydroxyisobutyrate dehydrogenase-like protein [Arabidopsis thaliana]	Unigene5877_All//4.00E-63//AT4G20930| 3-hydroxyisobutyrate dehydrogenase, putative	Unigene5877_All//0.00E+00//TC138925		ko00280|Valine, leucine and isoleucine degradation	GO:0006007//GO:0006164//GO:0009081//GO:0016301//GO:0016616//GO:0031224//GO:0032559//GO:0043231//GO:0048037	nr +
Unigene5880_All	1011	1.04	3.31	2.48	4.14	3.47	4.65	1.21	1.16	0.83	1.68E+00	5.07E-06	Up	1.26E+00	3.30E-03		-2.53E-01	4.37E-01		1.67E-01	6.35E-01		-6.73E-02	9.14E-01		-5.52E-01	3.01E-01		Unigene5880_All//gi|115486399|ref|NP_001068343.1|//9.00E-49//Os11g0639300 [Oryza sativa Japonica Group] >gi|77552177|gb|ABA94974.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113645565|dbj|BAF28706.1| Os11g0639300 [Oryza sativa Japonica Group]	Unigene5880_All//2.00E-41//AT5G45470| unknown protein					nr +
Unigene58800_All	286	0.00	1.24	0.37	0.00	1.20	0.32	0.30	2.92	1.53	1.03E+01	2.46E-02		8.54E+00	3.96E-01		1.02E+01	3.01E-02		8.30E+00	4.74E-01		3.31E+00	3.10E-04	Up	2.37E+00	4.04E-02									
Unigene58801_All	1030	0.41	0.25	0.21	0.19	0.13	0.18	1.44	0.61	0.15	-7.24E-01	5.26E-01		-9.75E-01	4.11E-01		-5.33E-01	7.48E-01		-1.42E-01	9.34E-01		-1.24E+00	1.26E-02		-3.22E+00	3.28E-07	Down	Unigene58801_All//gi|115437880|ref|NP_001043403.1|//3.00E-78//Os01g0580000 [Oryza sativa Japonica Group] >gi|13161357|dbj|BAB32948.1| esterase/lipase/thioesterase family protein-like [Oryza sativa Japonica Group] >gi|18461257|dbj|BAB84453.1| esterase/lipase/thioesterase family protein-like [Oryza sativa Japonica Group] >gi|113532934|dbj|BAF05317.1| Os01g0580000 [Oryza sativa Japonica Group]	Unigene58801_All//4.00E-61//AT2G19550| esterase/lipase/thioesterase family protein	Unigene58801_All//0.00E+00//gi|48777664|gb|C0087030.1|C0087030			GO:0003824//GO:0043231	nr -
Unigene58808_All	284	1.29	3.39	0.75	1.05	0.61	0.16	1.04	3.38	4.21	1.39E+00	5.77E-02		-7.82E-01	5.53E-01		-7.96E-01	5.57E-01		-2.73E+00	1.37E-01		1.70E+00	1.17E-02		2.01E+00	7.79E-04	Up	Unigene58808_All//gi|34925359|sp|Q93394.1|RPOT1_NICSY//2.00E-07//RecName: Full=DNA-directed RNA polymerase 1, mitochondrial; AltName: Full=T7 bacteriophage-type single subunit RNA polymerase 1; AltName: Full=NsRpoT-A; Flags: Precursor >gi|15824083|dbj|BAB69431.1| T7 bacteriophage-type single subunit RNA polymerase [Nicotiana sylvestris]	Unigene58808_All//6.00E-08//AT1G68990| DNA-directed RNA polymerase, mitochondrial (RPOMT)	Unigene58808_All//5.00E-34//ES830875			GO:0003676//GO:0010467//GO:0034062//GO:0043231	nr -
Unigene58809_All	355	5.01	0.43	12.60	9.82	5.72	6.49	0.36	0.24	0.00	-3.55E+00	2.53E-07	Down	1.33E+00	1.61E-05	Up	-7.79E-01	1.24E-02		-5.98E-01	7.36E-02		-6.01E-01	7.65E-01		-8.48E+00	1.99E-01				Unigene58809_All//4.00E-47//DW232226				
Unigene5882_All	770	1.02	1.05	1.94	3.23	1.70	2.58	2.53	4.07	0.88	4.69E-02	9.69E-01		9.26E-01	1.05E-01		-9.29E-01	1.44E-02		-3.26E-01	4.63E-01		6.89E-01	2.86E-02		-1.52E+00	3.06E-04	Down	Unigene5882_All//gi|124360978|gb|ABN08850.1|//2.00E-53//KDPG and KHG aldolase [Medicago truncatula]		Unigene5882_All//0.00E+00//TC146344		ko00330|Arginine and proline metabolism//ko00040|Pentose and glucuronate interconversions//ko00030|Pentose phosphate pathway//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0016832//GO:0043231	nr -
Unigene58839_All	310	0.00	0.00	0.00	0.00	0.00	0.00	1.91	0.00	0.13	null	null		null	null		null	null		null	null		-1.09E+01	2.39E-04	Down	-3.89E+00	1.09E-03		Unigene58839_All//gi|186522588|ref|NP_196857.2|//2.00E-11//KEG (KEEP ON GOING); protein binding / protein kinase/ ubiquitin-protein ligase [Arabidopsis thaliana] >gi|218526495|sp|Q9FY48.2|KEG_ARATH RecName: Full=E3 ubiquitin-protein ligase KEG; AltName: Full=RING finger protein KEG; AltName: Full=Protein KEEP ON GOING >gi|83817349|gb|ABC46683.1| RING E3 ligase protein [Arabidopsis thaliana]	Unigene58839_All//6.00E-13//AT5G13530| KEG (KEEP ON GOING); protein binding / protein kinase/ ubiquitin-protein ligase	Unigene58839_All//5.00E-74//BQ409912			GO:0006950//GO:0009755//GO:0016301//GO:0019787//GO:0032446//GO:0032559//GO:0040007//GO:0043231//GO:0046914	nr -
Unigene5884_All	1469	12.89	12.69	15.77	16.82	14.60	13.28	31.46	18.64	15.68	-2.26E-02	8.78E-01		2.90E-01	1.67E-02		-2.04E-01	7.37E-02		-3.41E-01	1.81E-03		-7.55E-01	6.32E-26		-1.01E+00	8.86E-43	Down	Unigene5884_All//gi|224057471|ref|XP_002299235.1|//1.00E-138//ZIP transporter [Populus trichocarpa] >gi|222846493|gb|EEE84040.1| ZIP transporter [Populus trichocarpa]	Unigene5884_All//4.00E-103//AT3G20850| metal transporter family protein	Unigene5884_All//0.00E+00//TC153439			GO:0006810//GO:0031410	nr +
Unigene5885_All	1854	0.31	0.38	0.43	0.97	0.48	0.61	16.60	34.94	67.32	3.02E-01	6.93E-01		4.73E-01	5.65E-01		-1.00E+00	3.07E-02		-6.68E-01	1.86E-01		1.07E+00	2.04E-64	Up	2.02E+00	0.00E+00	Up	Unigene5885_All//gi|70609690|gb|AAZ05070.1|//0.00E-00//glutamate decarboxylase [Citrus sinensis]	Unigene5885_All//0.00E+00//AT2G02010| GAD4 (glutamate decarboxylase 4); calmodulin binding	Unigene5885_All//0.00E+00//gi|78342896|gb|DT563170.1|DT563170		ko00250|Alanine, aspartate and glutamate metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00430|Taurine and hypotaurine metabolism	GO:0005515//GO:0009064//GO:0016831//GO:0043231//GO:0044444//GO:0048037	nr -
Unigene58850_All	858	0.06	0.18	0.06	0.12	0.16	0.11	0.84	0.05	0.56	1.54E+00	5.31E-01		2.58E-02	9.94E-01		4.67E-01	8.76E-01		-1.41E-01	9.49E-01		-4.10E+00	2.91E-04	Down	-5.88E-01	4.09E-01		Unigene58850_All//gi|15229139|ref|NP_190511.1|//1.00E-63//Got1-like family protein [Arabidopsis thaliana] >gi|15240976|ref|NP_195763.1| Got1-like family protein [Arabidopsis thaliana] >gi|17065530|gb|AAL32919.1| Unknown protein [Arabidopsis thaliana] >gi|30102848|gb|AAP21342.1| At3g49420 [Arabidopsis thaliana]	Unigene58850_All//6.00E-55//AT5G01430| Got1-like family protein	Unigene58850_All//0.00E+00//DW512906			GO:0006810//GO:0031410	nr -
Unigene5886_All	689	22.33	15.59	11.44	42.58	38.18	49.82	70.02	29.48	30.07	-5.18E-01	2.64E-04		-9.65E-01	1.31E-10		-1.57E-01	1.47E-01		2.26E-01	1.75E-02		-1.25E+00	3.86E-61	Down	-1.22E+00	1.05E-60	Down	Unigene5886_All//gi|115462737|ref|NP_001054968.1|//5.00E-50//Os05g0227700 [Oryza sativa Japonica Group] >gi|113578519|dbj|BAF16882.1| Os05g0227700 [Oryza sativa Japonica Group]	Unigene5886_All//5.00E-61//AT5G25757| unknown protein	Unigene5886_All//0.00E+00//TC146190			GO:0008135//GO:0016020	nr +
Unigene5887_All	503	3.33	10.78	1.16	2.08	3.08	2.51	7.57	7.23	7.05	1.70E+00	2.00E-09	Up	-1.52E+00	6.55E-03		5.67E-01	3.13E-01		2.74E-01	6.79E-01		-6.55E-02	8.32E-01		-1.02E-01	7.19E-01		Unigene5887_All//gi|12003398|gb|AAG43556.1|AF211538_1//7.00E-09//Avr9/Cf-9 rapidly elicited protein 180 [Nicotiana tabacum]	Unigene5887_All//1.00E-10//AT5G46295| unknown protein	Unigene5887_All//0.00E+00//gi|109873062|gb|DW502037.1|DW502037				nr +
Unigene58876_All	291	11.69	14.97	9.70	53.07	44.61	46.72	39.37	130.13	42.30	3.58E-01	2.35E-01		-2.69E-01	4.53E-01		-2.50E-01	8.58E-02		-1.84E-01	2.51E-01		1.72E+00	2.11E-77	Up	1.04E-01	5.36E-01		Unigene58876_All//gi|124488474|gb|ABN12321.1|//3.00E-25//benzoquinone reductase [Gossypium hirsutum]	Unigene58876_All//2.00E-24//AT5G54500| FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor	Unigene58876_All//5.00E-108//gi|13243919|gb|BE055198.2|BE055198			GO:0000166//GO:0006350//GO:0016020//GO:0016655//GO:0043231	nr +
Unigene5889_All	924	7.59	2.74	2.31	14.61	8.24	4.15	12.31	0.41	3.84	-1.47E+00	6.26E-10	Down	-1.72E+00	1.07E-11	Down	-8.27E-01	4.34E-09		-1.81E+00	1.15E-26	Down	-4.92E+00	3.45E-67	Down	-1.68E+00	9.35E-24	Down	Unigene5889_All//gi|15224950|ref|NP_182002.1|//1.00E-71//CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase [Arabidopsis thaliana] >gi|75278850|sp|O80513.1|CCU41_ARATH RecName: Full=Cyclin-U4-1; Short=CycU4;1; AltName: Full=Cyclin-P4.1; Short=CycP4;1 >gi|62867623|gb|AAV17415.1| At2g44740 [Arabidopsis thaliana] >gi|66841350|gb|AAY57312.1| At2g44740 [Arabidopsis thaliana]	Unigene5889_All//8.00E-72//AT2G44740| CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	Unigene5889_All//0.00E+00//gi|164278670|gb|ES815215.1|ES815215			GO:0005488//GO:0007049//GO:0016772	nr -
Unigene58900_All	395	14.70	20.65	19.95	12.86	14.65	15.44	6.53	19.58	15.13	4.90E-01	1.63E-02		4.40E-01	4.41E-02		1.87E-01	5.32E-01		2.63E-01	3.31E-01		1.58E+00	1.27E-14	Up	1.21E+00	3.76E-08	Up	Unigene58900_All//gi|224993380|gb|ACN74469.1|//3.00E-15//CBL-interacting protein kinase 12 [Populus euphratica]	Unigene58900_All//1.00E-13//AT1G01140| CIPK9 (CBL-INTERACTING PROTEIN KINASE 9); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene58900_All//2.00E-101//TC144929			GO:0004674//GO:0006464//GO:0023060//GO:0032559//GO:0043231	nr -
Unigene5891_All	917	27.73	250.42	31.18	40.63	77.17	93.48	122.60	366.54	582.07	3.17E+00	0.00E+00	Up	1.69E-01	1.38E-01		9.25E-01	2.43E-53		1.20E+00	2.95E-89	Up	1.58E+00	0.00E+00	Up	2.25E+00	0.00E+00	Up	Unigene5891_All//gi|151934215|gb|AB518445.1|//2.00E-59//WRKY49 [Glycine max]	Unigene5891_All//4.00E-38//AT2G38470| WRKY33; transcription factor	Unigene5891_All//0.00E+00//TC141262	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0010467	nr +
Unigene58911_All	218	7.44	13.25	7.33	4.57	7.58	19.89	148.76	250.77	842.09	8.32E-01	2.43E-02		-2.19E-02	9.89E-01		7.30E-01	1.67E-01		2.12E+00	1.36E-10	Up	7.53E-01	2.34E-30		2.50E+00	0.00E+00	Up	Unigene58911_All//gi|224148856|ref|XP_002336723.1|//2.00E-21//cytochrome P450 [Populus trichocarpa] >gi|222836601|gb|EEE74994.1| cytochrome P450 [Populus trichocarpa]	Unigene58911_All//4.00E-18//AT4G31950| CYP82C3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene58911_All//2.00E-115//gi|84173960|gb|DR462608.1|DR462608		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0005506//GO:0008152//GO:0016709	nr +
Unigene5892_All	1354	9.16	2.96	5.39	16.15	10.66	9.97	5.34	1.11	2.94	-1.63E+00	1.09E-19	Down	-7.65E-01	4.33E-06		-6.00E-01	2.16E-08		-6.96E-01	1.06E-09		-2.26E+00	9.68E-22	Down	-8.60E-01	6.12E-06		Unigene5892_All//gi|15222229|ref|NP_177675.1|//1.00E-165//glycosyl transferase family 1 protein [Arabidopsis thaliana]	Unigene5892_All//2.00E-166//AT1G75420| glycosyl transferase family 1 protein	Unigene5892_All//0.00E+00//TC141216		ko00510|N-Glycan biosynthesis		nr -
Unigene58939_All	423	1.98	0.00	1.38	0.82	0.16	1.28	0.60	0.40	0.19	-1.10E+01	5.57E-05	Down	-5.15E-01	5.15E-01		-2.34E+00	1.01E-01		6.36E-01	5.61E-01		-6.02E-01	6.47E-01		-1.67E+00	2.56E-01		Unigene58939_All//gi|297827821|ref|XP_002881793.1|//9.00E-31//EMB2654 [Arabidopsis lyrata subsp. lyrata] >gi|297327632|gb|EFH58052.1| EMB2654 [Arabidopsis lyrata subsp. lyrata]	Unigene58939_All//1.00E-26//AT2G41720| EMB2654 (EMBRYO DEFECTIVE 2654)	Unigene58939_All//2.00E-157//ES807907				nr -
Unigene58944_All	320	4.74	0.48	3.00	0.62	0.43	0.00	0.53	0.00	0.00	-3.32E+00	5.00E-06	Down	-6.63E-01	2.41E-01		-5.33E-01	7.48E-01		-9.28E+00	1.33E-01		-9.05E+00	1.34E-01		-9.05E+00	1.08E-01		Unigene58944_All//gi|157863714|gb|ABV90878.1|//4.00E-26//inositol-1,4,5-triphosphate-5-phosphatase [Solanum lycopersicum]	Unigene58944_All//1.00E-08//AT2G32010| endonuclease/exonuclease/phosphatase family protein	Unigene58944_All//2.00E-166//C0071559			GO:0016787	nr +
Unigene58948_All	471	8.78	0.75	3.05	9.62	7.31	5.75	4.40	0.62	1.52	-3.54E+00	2.83E-16	Down	-1.52E+00	3.98E-06	Down	-3.97E-01	1.65E-01		-7.42E-01	8.27E-03		-2.82E+00	2.06E-08	Down	-1.53E+00	1.72E-04	Down			Unigene58948_All//4.00E-57//gi|78342857|gb|DT563131.1|DT563131				
Unigene5895_All	900	36.51	42.62	41.12	18.87	12.97	27.70	2.16	6.04	0.89	2.23E-01	1.24E-02		1.72E-01	8.08E-02		-5.41E-01	1.31E-05		5.54E-01	1.83E-07		1.48E+00	1.32E-09	Up	-1.29E+00	1.71E-03		Unigene5895_All//gi|17386128|gb|AAL38610.1|AF446877_1//1.00E-16//AT3g52740/F3C22_140 [Arabidopsis thaliana] >gi|15450655|gb|AAO96699.1| AT3g52740/F3C22_140 [Arabidopsis thaliana]	Unigene5895_All//6.00E-18//AT3G52740| unknown protein	Unigene5895_All//0.00E+00//TC144226			GO:0003676//GO:0005198//GO:0010467//GO:0030529//GO:0031224	nr -
Unigene58950_All	383	6.01	2.91	1.81	0.26	0.36	1.06	0.00	0.00	0.00	-1.05E+00	1.34E-02		-1.73E+00	2.51E-04	Down	4.67E-01	8.76E-01		2.03E+00	1.49E-01		null	null		null	null		Unigene58950_All//gi|110742278|dbj|BAE99064.1|//3.00E-17//Ca2+/H+-exchanging like protein [Arabidopsis thaliana]	Unigene58950_All//3.00E-18//AT3G51860| CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	Unigene58950_All//2.00E-67//EX169608			GO:0000325//GO:0005488//GO:0006875//GO:0006970//GO:0009409//GO:0010038//GO:0015368//GO:0015672//GO:0030005//GO:0031090//GO:0031224//GO:0044237//GO:0046873//GO:0051707//GO:0070838	nr +
Unigene58953_All	265	3.16	0.57	0.00	1.50	0.78	1.70	0.16	0.16	0.60	-2.46E+00	6.70E-03		-1.16E+01	1.19E-04	Down	-9.48E-01	4.20E-01		1.81E-01	8.83E-01		-1.64E-02	1.00E+00		1.91E+00	3.77E-01					Unigene58953_All//2.00E-85//TC178514				
Unigene58958_All	395	7.42	0.77	1.08	2.77	0.70	0.46	0.21	0.21	0.10	-3.27E+00	6.04E-11	Down	-2.78E+00	5.89E-09	Down	-1.99E+00	2.59E-03		-2.60E+00	7.13E-04	Down	-1.69E-02	1.01E+00		-1.09E+00	6.75E-01								

Unigene5896_All	790	27.29	55.93	23.25	59.59	49.56	27.04	4.92	9.63	0.91	1.04E+00	4.73E-34	Up	-2.31E-01	7.72E-02		-2.66E-01	2.84E-04		-1.14E+00	7.54E-46	Down	9.68E-01	4.21E-07		-2.44E+00	1.54E-13	Down	Unigene5896_All//gi|75099105|sp|Q6 4564.1|HS185_ARATH//1.00E-29//RecName: Full=18.5 kDa class IV heat shock protein; AltName: Full=18.5 kDa heat shock protein; Short=AtHsp18.5	Unigene5896_All//3.00E-24//AT2G19310| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress, response to high light intensity, response to hydrogen peroxide, response to heat; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: HSP20-like chaperone (InterPro:IPR008978); BEST Arabidopsis thaliana protein match is: HSP18.2 (heat shock protein 18.2) (TAIR:AT5G59720.1); Has 527 Blast hits to 527 proteins in 67 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 24; Plants - 479; Viruses - 0; Other Eukaryotes - 14 (source: NCBI BLink).	Unigene5896_All//0.00E+00//gi|164342563|gb|ES802994.1|ES802994			GO:0000302//GO:0009642	nr -
Unigene58967_All	343	0.46	0.44	1.40	2.61	4.22	3.42	4.19	2.68	10.57	-4.61E-02	9.89E-01		1.61E+00	1.82E-01		6.90E-01	2.34E-01		3.89E-01	5.80E-01		-6.45E-01	2.05E-01		1.33E+00	5.47E-06	Up	Unigene58967_All//gi|164605521|dbj|BAF98587.1|//2.00E-08//CM0216.530.nc [Lotus japonicus]	Unigene58967_All//5.00E-05//AT2G38800| calmodulin-binding protein-related	Unigene58967_All//1.00E-81//DT463724				nr +
Unigene5897_All	698	8.40	7.91	5.95	17.91	12.53	8.54	34.65	28.32	24.54	-8.54E-02	7.27E-01		-4.97E-01	5.50E-02		-5.16E-01	5.43E-04		-1.07E+00	2.15E-11	Down	-2.91E-01	4.03E-03		-4.98E-01	2.64E-07		Unigene5897_All//gi|75161694|sp|Q8 VZS8.1|PYL1_ARATH//3.00E-76//RecName: Full=Abscisic acid receptor PYL1; AltName: Full=PYR1-like protein 1; AltName: Full=ABI1-binding protein 6; AltName: Full=Regulatory components of ABA receptor 9	Unigene5897_All//1.00E-77//AT5G46790| unknown protein	Unigene5897_All//1.00E-172//TC165369			GO:0004871//GO:0009755//GO:0042802	nr +
Unigene58979_All	263	0.40	1.16	0.40	0.19	0.39	1.20	0.16	3.18	1.82	1.54E+00	3.23E-01		2.52E-02	9.99E-01		1.05E+00	8.07E-01		2.67E+00	1.44E-01		4.31E+00	5.67E-05	Up	3.50E+00	7.29E-03				Unigene58979_All//8.00E-85//CA994161				
Unigene58985_All	268	0.39	1.89	3.78	0.56	2.44	1.52	1.42	0.47	1.19	2.28E+00	6.22E-02		3.27E+00	5.92E-04	Up	2.13E+00	3.78E-02		1.44E+00	2.82E-01		-1.60E+00	1.81E-01		-2.56E-01	7.85E-01				Unigene58985_All//2.00E-24//TC152150				
Unigene5899_All	888	4.30	4.51	2.16	8.47	8.34	7.27	8.90	3.77	3.59	6.77E-02	8.26E-01		-9.95E-01	2.52E-03		-2.29E-02	9.25E-01		-2.20E-01	3.69E-01		-1.24E+00	1.31E-10	Down	-1.31E+00	7.39E-12	Down	Unigene5899_All//gi|48958483|gb|AA T47794.1|//2.00E-29//At5g42330 [Arabidopsis thaliana] >gi|51536556|gb|AAU05516.1| At5g42330 [Arabidopsis thaliana]	Unigene5899_All//3.00E-26//AT5G42330| unknown protein	Unigene5899_All//0.00E+00//TC139521				nr +
Unigene5900_All	726	3.89	1.40	1.32	3.09	2.75	1.62	1.46	0.52	1.59	-1.48E+00	1.63E-04	Down	-1.56E+00	1.54E-04	Down	-1.67E-01	7.29E-01		-9.33E-01	2.93E-02		-1.49E+00	1.64E-02		1.28E-01	8.11E-01		Unigene5900_All//gi|78099801|sp|Q9 SFU0.2|SC24A_ARATH//4.00E-19//RecName: Full=Protein transport protein Sec24-like At3g07100				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0005488//GO:0006810//GO:0044464	nr -
Unigene59008_All	243	8.18	6.26	2.19	3.89	5.38	9.48	0.70	0.00	0.66	-3.87E-01	3.88E-01		-1.90E+00	3.07E-04	Down	4.67E-01	4.71E-01		1.28E+00	2.91E-03		-9.44E+00	1.34E-01		-8.58E-02	9.65E-01		Unigene59008_All//gi|297826789|ref|XP_002881277.1|//2.00E-16//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327116|gb|EFH57536.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene59008_All//9.00E-18//AT2G33340| nucleotide binding / ubiquitin-protein ligase	Unigene59008_All//9.00E-69//TC138107		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0019787//GO:0032446//GO:0043234	nr +
Unigene59019_All	222	10.61	4.34	9.83	15.71	17.06	24.62	11.81	5.27	2.69	-1.29E+00	2.49E-03		-1.09E-01	7.94E-01		1.19E-01	7.74E-01		6.48E-01	1.11E-02		-1.16E+00	9.86E-04	Down	-2.13E+00	4.28E-08	Down			Unigene59019_All//2.00E-78//ES830437				
Unigene5902_All	511	61.33	71.69	21.47	210.56	152.77	112.95	108.56	39.10	29.86	2.25E-01	1.38E-02		-1.51E+00	3.56E-42	Down	-4.63E-01	1.03E-24		-8.99E-01	1.82E-70		-1.47E+00	2.65E-90	Down	-1.86E+00	1.01E-129	Down	Unigene5902_All//gi|806720|gb|AAA6 6362.1|//3.00E-16//arabinogalactan-protein precursor [Nicotiana alata]		Unigene5902_All//0.00E+00//TC164066		ko03040|Spliceosome//ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00620|Pyruvate metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko03020|RNA polymerase//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis		nr +
Unigene59031_All	421	7.71	2.05	2.66	0.71	1.96	0.75	0.00	0.00	0.38	-1.91E+00	6.49E-07	Down	-1.54E+00	5.17E-05	Down	1.47E+00	7.56E-02		8.10E-02	9.50E-01		null	null		8.56E+00	1.40E-01		Unigene59031_All//gi|88604930|gb|AB C55454.2|//3.00E-17//xyloglucan endotransglucosylase/hydrolase 2 [Rosa x borboniana]	Unigene59031_All//1.00E-14//AT5G65730| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene59031_All//5.00E-44//gi|48821533|gb|CO122846.1|CO122846			GO:0003824	nr +
Unigene5904_All	950	2.81	2.67	3.08	7.18	4.93	5.13	1.11	0.40	0.25	-7.48E-02	8.42E-01		1.34E-01	7.18E-01		-5.43E-01	1.10E-02		-4.85E-01	3.30E-02		-1.49E+00	1.64E-02		-2.14E+00	9.36E-04	Down	Unigene5904_All//gi|18700123|gb|AA L77673.1|//1.00E-39//At2g39560/F12L6.22 [Arabidopsis thaliana] >gi|21464575|gb|AAM52242.1| At2g39560/F12L6.22 [Arabidopsis thaliana]	Unigene5904_All//5.00E-16//AT2G39560| unknown protein	Unigene5904_All//0.00E+00//TC168438				nr +
Unigene59044_All	611	0.43	0.00	0.17	0.90	1.07	2.22	2.63	0.68	1.24	-8.74E+00	6.68E-02		-1.30E+00	4.36E-01		2.56E-01	8.21E-01		1.31E+00	2.93E-02		-1.94E+00	1.42E-04	Down	-1.09E+00	1.58E-02		Unigene59044_All//gi|18416534|ref|NP_567717.1|//9.00E-45//immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related [Arabidopsis thaliana] >gi|15982872|gb|AAL09783.1| AT4g25340/T30C3_20 [Arabidopsis thaliana] >gi|23506115|gb|AAN28917.1| At4g25340/T30C3_20 [Arabidopsis thaliana]	Unigene59044_All//3.00E-45//AT4G25340| immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related	Unigene59044_All//0.00E+00//DT457461			GO:0005488//GO:0016859//GO:0031410//GO:0043231//GO:0044267	nr -
Unigene59047_All	430	2.43	1.89	0.25	1.04	1.44	2.52	0.10	0.68	1.20	-3.68E-01	5.90E-01		-3.30E+00	4.58E-04	Down	4.67E-01	6.34E-01		1.27E+00	6.54E-02		2.79E+00	9.47E-02		3.62E+00	4.19E-03		Unigene59047_All//gi|285309967|emb|CBE71057.1|//8.00E-72//aconitate hydratase 3 [Citrus clementina]	Unigene59047_All//5.00E-66//AT4G35830| aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO)	Unigene59047_All//1.00E-155//TC156670		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0016836//GO:0043169//GO:0043231//GO:0044262//GO:0051536	nr -
Unigene59048_All	221	17.28	34.62	16.38	41.25	41.91	31.68	37.69	30.45	28.84	1.00E+00	3.03E-06	Up	-7.70E-02	8.12E-01		2.31E-02	9.29E-01		-3.81E-01	5.20E-02		-3.08E-01	1.03E-01		-3.86E-01	2.85E-02				Unigene59048_All//3.00E-105//DR459163				ESTscan +
Unigene59050_All	437	11.85	3.01	7.19	0.11	0.00	0.00	0.00	0.00	0.00	-1.98E+00	5.02E-11	Down	-7.21E-01	8.50E-03		-6.83E+00	5.53E-01		-6.83E+00	6.31E-01		null	null		null	null				Unigene59050_All//5.00E-07//ES843168				
Unigene59052_All	373	3.37	0.00	2.00	2.54	1.48	0.73	0.45	0.22	0.00	-1.17E+01	2.54E-07	Down	-7.52E-01	2.32E-01		-7.81E-01	2.68E-01		-1.80E+00	1.83E-02		-1.02E+00	6.13E-01		-8.82E+00	1.08E-01				Unigene59052_All//2.00E-73//gi|195983018|gb|FL577171.1|FL577171				
Unigene59053_All	277	2.08	0.91	0.58	1.80	2.24	1.47	0.31	0.60	3.45	-1.18E+00	2.26E-01		-1.85E+00	9.61E-02		3.15E-01	7.84E-01		-2.93E-01	7.57E-01		9.83E-01	6.33E-01		3.50E+00	4.29E-05	Up	Unigene59053_All//gi|25992001|gb|AAN77002.1|//2.00E-21//lecithine cholesterol acyltransferase-like protein [Medicago truncatula]	Unigene59053_All//2.00E-13//AT1G04010| phosphatidate-sterol O-acyltransferase/ phosphatidylcholine-sterol O-acyltransferase/ phosphatidylethanolamine-sterol O-acyltransferase				GO:0008374//GO:0031410//GO:0044238	nr +
Unigene59057_All	758	0.21	0.00	0.42	0.46	0.05	0.18	2.51	0.17	0.74	-7.69E+00	2.14E-01		1.03E+00	4.71E-01		-3.34E+00	4.06E-02		-1.36E+00	3.37E-01		-3.92E+00	3.80E-10	Down	-1.77E+00	5.92E-05	Down	Unigene59057_All//gi|15231803|ref|NP_188036.1|//4.00E-06//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana]		Unigene59057_All//9.00E-155//DW509717				nr -
Unigene5906_All	1369	0.00	0.22	0.00	0.44	1.21	1.62	3.64	2.99	15.22	7.80E+00	4.42E-02		null	null		1.47E+00	5.01E-03		1.89E+00	5.58E-05	Up	-2.85E-01	2.72E-01		2.06E+00	1.53E-55	Up	Unigene5906_All//gi|30315245|gb|AA P30841.1|//1.00E-132//nectarin 5 [Nicotiana langsdorffii x Nicotiana sanderae]	Unigene5906_All//3.00E-111//AT5G44390| FAD-binding domain-containing protein	Unigene5906_All//5.00E-53//gi|3326694|gb|AI055580.1|AI055580				nr -
Unigene59067_All	343	0.00	0.00	0.00	4.65	3.71	1.71	3.08	0.24	0.35	null	null		null	null		-3.23E-01	5.52E-01		-1.44E+00	7.26E-03		-3.66E+00	1.31E-05	Down	-3.14E+00	2.96E-05	Down	Unigene59067_All//gi|225446451|ref|XP_002275180.1|//3.00E-23//PREDICTED: similar to arabinogalactan-protein; AGP [Vitis vinifera]		Unigene59067_All//7.00E-89//gi|109829306|gb|DW227894.1|DW227894				nr -
Unigene59069_All	467	1.12	718.81	428.96	0.43	0.22	3.09	1.27	1.16	0.17	9.33E+00	0.00E+00	Up	8.58E+00	0.00E+00	Up	-9.48E-01	5.87E-01		2.86E+00	3.35E-05	Up	-1.24E-01	8.84E-01		-2.89E+00	4.53E-03				Unigene59069_All//1.00E-17//TC149074				
Unigene59084_All	1028	0.97	0.99	0.10	0.73	0.57	0.31	0.58	1.02	0.66	2.78E-02	9.86E-01		-3.22E+00	7.83E-04	Down	-3.52E-01	6.51E-01		-1.24E+00	1.45E-01		8.20E-01	1.79E-01		1.94E-01	7.87E-01		Unigene59084_All//gi|297807115|ref|XP_002871441.1|//8.00E-53//ubiquitin-specific protease 22 [Arabidopsis lyrata subsp. lyrata] >gi|297317278|gb|EFH47700.1| ubiquitin-specific protease 22 [Arabidopsis lyrata subsp. lyrata]	Unigene59084_All//7.00E-46//AT5G10790| UBP22 (UBIQUITIN-SPECIFIC PROTEASE 22); ubiquitin thiolesterase/ ubiquitin-specific protease/ zinc ion binding	Unigene59084_All//4.00E-133//DW239687			GO:0008233//GO:0043231	nr +
Unigene5909_All	517	10.42	5.00	11.02	6.94	5.86	5.77	3.84	3.40	1.54	-1.06E+00	4.92E-05	Down	8.04E-02	7.60E-01		-2.43E-01	5.05E-01		-2.67E-01	4.67E-01		-1.79E-01	6.74E-01		-1.32E+00	1.19E-03				Unigene5909_All//2.00E-22//gi|8785984|gb|CO097298.1|CO097298				
Unigene5910_All	280	26.16	70.76	66.37	25.62	23.12	40.32	5.89	11.64	12.81	1.44E+00	1.08E-25	Up	1.34E+00	3.53E-21	Up	-1.48E-01	5.57E-01		6.55E-01	7.96E-05		9.83E-01	1.41E-03		1.12E+00	1.01E-04	Up			Unigene5910_All//5.00E-114//gi|3325990|gb|AI054876.1|AI054876				
Unigene5912_All	359	3.64	0.85	1.93	11.38	5.08	3.52	22.26	9.66	7.44	-2.11E+00	1.46E-03		-9.18E-01	1.38E-01		-1.16E+00	3.92E-05	Down	-1.69E+00	1.01E-07	Down	-1.20E+00	3.03E-10	Down	-1.58E+00	1.36E-15	Down			Unigene5912_All//9.00E-33//DV849456				
Unigene59127_All	566	12.57	0.90	6.30	0.18	0.24	0.00	0.00	0.00	0.28	-3.81E+00	2.60E-29	Down	-9.96E-01	1.57E-05		4.68E-01	8.76E-01		-7.46E+00	3.97E-01		null	null		8.14E+00	1.39E-01		Unigene59127_All//gi|115458314|ref|NP_001052757.1|//6.00E-16//Os04g0415000 [Oryza sativa Japonica Group] >gi|32479729|emb|CAE01516.1| Q|991214_I2.5 [Oryza sativa (japonica cultivar-group)] >gi|113564328|dbj|BAF14671.1| Os04g0415000 [Oryza sativa Japonica Group] >gi|116309338|emb|CAH66422.1| H0622F05.5 [Oryza sativa (indica cultivar-group)]	Unigene59127_All//6.00E-19//AT5G06270| unknown protein	Unigene59127_All//3.00E-40//TC165228				nr -
Unigene5913_All	581	2.52	1.83	0.73	8.32	6.10	3.65	4.15	3.67	2.13	-4.61E-01	3.84E-01		-1.78E+00	4.08E-03		-4.46E-01	1.01E-01		-1.19E+00	1.44E-05	Down	-1.77E-01	6.37E-01		-9.65E-01	6.40E-03		Unigene5913_All//gi|297812129|ref|XP_002873948.1|//1.00E-54//calcium-dependent protein kinase 19 [Arabidopsis lyrata subsp. lyrata] >gi|297319785|gb|EFH50207.1| calcium-dependent protein kinase 19 [Arabidopsis lyrata subsp. lyrata]	Unigene5913_All//1.00E-55//AT5G19450| CDPK19 (CALCIUM-DEPENDENT PROTEIN KINASE 19); ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ protein kinase/ protein serine/threonine kinase	Unigene5913_All//0.00E+00//DT466661		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0016020//GO:0032559//GO:0046872	nr -
Unigene5914_All	804	9.18	7.31	6.23	12.64	12.68	13.87	12.57	28.70	13.68	-3.28E-01	1.37E-01		-5.60E-01	1.29E-02		4.40E-03	9.89E-01		1.35E-01	5.08E-01		1.19E+00	1.46E-27	Up	1.22E-01	4.75E-01				Unigene5914_All//4.00E-83//TC166107				
Unigene5916_All	641	3.84	2.45	2.74	0.78	0.75	2.18	5.61	0.13	0.44	-6.47E-01	1.11E-01		-4.85E-01	2.55E-01		-4.72E-02	9.49E-01		1.49E+00	1.20E-02		-5.43E+00	1.83E-22	Down	-3.69E+00	1.56E-18	Down	Unigene5916_All//gi|73761705|gb|AA Z83352.1|//9.00E-47//myb transcription factor MYB30 [Gossypium hirsutum]	Unigene5916_All//8.00E-21//AT3G28910| MYB30 (MYB DOMAIN PROTEIN 30); DNA binding / transcription factor	Unigene5916_All//0.00E+00//TC145072	MYB		GO:0009725//GO:0044237//GO:0044238	nr +
Unigene59164_All	281	0.19	0.00	0.57	3.37	1.59	1.13	3.46	0.15	2.41	-7.54E+00	6.08E-01		1.61E+00	5.11E-01		-1.08E+00	1.16E-01		-1.58E+00	3.51E-02		-4.54E+00	6.92E-06	Down	-5.22E-01	3.89E-01								ESTscan -
Unigene5917_All	531	4.43	4.20	5.82	5.07	4.93	3.23	13.62	2.60	2.10	-7.87E-02	8.45E-01		3.92E-01	3.05E-01		-3.96E-02	9.16E-01		-6.48E-01	9.71E-02		-2.39E+00	3.77E-23	Down	-2.70E+00	2.39E-27	Down	Unigene5917_All//gi|297725871|ref|NP_001175299.1|//3.00E-12//Os07g0620500 [Oryza sativa Japonica Group] >gi|255677975|dbj|BAH94027.1| Os07g0620500 [Oryza sativa Japonica Group]	Unigene5917_All//3.00E-11//AT5G02502| unknown protein	Unigene5917_All//1.00E-153//TC174259			GO:0031410	nr -
Unigene59173_All	552	5.78	3.21	4.44	2.08	6.24	3.93	2.68	2.80	1.23	-8.48E-01	1.45E-02		-3.82E-01	3.11E-01		1.59E+00	2.60E-06	Up	9.20E-01	3.83E-02		6.35E-02	9.07E-01		-1.13E+00	1.72E-02		Unigene59173_All//gi|108864209|gb|AB622437.1|//2.00E-22//RWP-RK domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene59173_All//5.00E-16//AT3G59580| RWP-RK domain-containing protein	Unigene59173_All//3.00E-52//TC151112	RWP-RK		GO:0046914	nr -

Unigene5918_All	1270	1.48	0.36	0.29	1.92	1.33	1.99	3.30	2.60	1.91	-2.05E+00	1.17E-04	Down	-2.34E+00	4.96E-05	Down	-5.33E-01	1.88E-01		5.12E-02	9.24E-01		-3.42E-01	2.28E-01		-7.85E-01	2.18E-03		Unigene5918_All//gi|297834384|ref|XP_002885074.1|//1.00E-125//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297330914|gb|EFH61333.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene5918_All//2.00E-124//AT3G15200| pentatricopeptide (PPR) repeat-containing protein	Unigene5918_All//6.00E-77//gi|164368455|gb|EX170125.1|EX170125			GO:0044464	nr +
Unigene59188_All	464	3.38	4.70	2.30	3.11	1.93	1.36	1.73	4.68	1.72	4.73E-01	2.83E-01		-5.60E-01	3.18E-01		-6.90E-01	2.06E-01		-1.19E+00	3.43E-02		1.44E+00	3.83E-04	Up	-1.18E-02	9.77E-01				Unigene59188_All//2.00E-90//TC1341145				
Unigene59189_All	419	3.50	0.36	0.76	0.36	0.33	0.32	0.20	0.00	0.00	-3.27E+00	8.97E-06	Down	-2.20E+00	7.90E-04	Down	-1.18E-01	9.10E-01		-1.41E-01	9.43E-01		-7.66E+00	4.01E-01		-7.66E+00	3.57E-01		Unigene59189_All//gi|298706171|emb|CBJ49099.1|//7.00E-113//Hypothetical leucine rich repeat protein [Ectocarpus siliculosus]	Unigene59189_All//3.00E-13//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0003824//GO:0005488	nr +
Unigene59192_All	259	0.00	0.00	1.23	1.73	1.33	0.35	5.88	23.88	11.38	null	null		1.03E+01	4.50E-02		-3.81E-01	7.21E-01		-2.31E+00	7.80E-02		2.02E+00	2.81E-16	Up	9.54E-01	2.62E-03		Unigene59192_All//gi|15451136|gb|AAK96839.1|//2.00E-31//periaxin-like protein [Arabidopsis thaliana]		Unigene59192_All//1.00E-37//TC152654			GO:0031410	nr +
Unigene592_All	1972	57.76	31.14	44.29	12.63	16.34	9.62	4.85	2.52	2.18	-8.91E-01	6.32E-68		-3.83E-01	6.34E-15		3.72E-01	3.04E-05		-3.93E-01	2.48E-04		-9.42E-01	2.20E-08		-1.15E+00	1.07E-11	Down	Unigene592_All//gi|16323119|gb|AAL15294.1|//0.00E+00//AT3g14930/K15M2.7 [Arabidopsis thaliana]	Unigene592_All//0.00E+00//AT3G14930| HEME1; uroporphyrinogen decarboxylase	Unigene592_All//0.00E+00//TC137282		ko00860|Porphyrin and chlorophyll metabolism	GO:0006778//GO:0009532//GO:0010038//GO:0016831	nr +
Unigene5920_All	549	0.67	2.40	3.49	1.45	2.76	1.32	0.77	1.07	1.52	1.85E+00	3.97E-03		2.39E+00	3.03E-05	Up	9.27E-01	9.02E-02		-1.42E-01	8.60E-01		4.69E-01	6.13E-01		9.85E-01	1.40E-01		Unigene5920_All//gi|30688039|ref|NP_850322.1|//2.00E-50//integral membrane Yip1 family protein [Arabidopsis thaliana]	Unigene5920_All//3.00E-51//AT2G39805| integral membrane Yip1 family protein	Unigene5920_All//0.00E+00//C0077864			GO:0044464	nr +
Unigene5921_All	962	0.98	3.16	1.33	6.94	5.37	3.47	0.62	0.52	0.66	1.69E+00	1.34E-05	Up	4.40E-01	4.71E-01		-3.70E-01	1.06E-01		-9.98E-01	8.78E-06		-2.39E-01	7.65E-01		1.07E-01	9.01E-01		Unigene5921_All//gi|296878|emb|CAA50609.1|//1.00E-87//ras-related GTP-binding protein [Nicotiana tabacum]	Unigene5921_All//1.00E-86//AT4G19640| ARA7; GTP binding	Unigene5921_All//0.00E+00//gi|21101448|gb|BQ413761.1|BQ413761		ko04145|Phagosome//ko04144|Endocytosis	GO:0001071//GO:0003006//GO:0006810//GO:0006950//GO:0009630//GO:0009725//GO:0016020//GO:0032561//GO:0035556//GO:0043231//GO:0048528	nr -
Unigene59225_All	474	1.44	0.53	0.00	0.11	0.65	0.00	0.18	0.18	0.50	-1.42E+00	1.16E-01		-1.05E+01	7.63E-04	Down	2.64E+00	1.61E-01		-6.72E+00	6.31E-01		-1.63E-02	1.01E+00		1.50E+00	3.39E-01		Unigene59225_All//gi|15221382|ref|NP_177616.1|//8.00E-36//nodulin family protein [Arabidopsis thaliana] >gi|5882744|gb|AAD5297.1|AC008263_28 Strong similarity to gb|AF031243 nodule-specific protein (Nlj70) from Lotus japonicus and is a member of the PF|00083 Sugar (and other) transporter family. EST gb|Z37715 comes from this gene [Arabidopsis thaliana]	Unigene59225_All//2.00E-37//AT1G74780| nodulin family protein	Unigene59225_All//1.00E-20//gi|78349229|gb|DT569503.1|DT569503			GO:0006810	nr +
Unigene59233_All	304	0.52	0.00	0.00	16.39	7.59	7.87	122.81	22.69	77.97	-9.01E+00	2.14E-01		-9.01E+00	2.43E-01		-1.11E+00	9.86E-06	Down	-1.06E+00	7.22E-05	Down	-2.44E+00	2.02E-119	Down	-6.55E-01	3.91E-17		Unigene59233_All//gi|791148|emb|CAA60021.1|//2.00E-13//extensin-like protein [Vigna unguiculata]		Unigene59233_All//1.00E-105//ES813279				nr -
Unigene59235_All	310	5.23	1.14	2.40	2.73	0.78	0.73	0.00	0.00	0.26	-2.19E+00	2.05E-04	Down	-1.12E+00	4.20E-02		-1.81E+00	1.77E-02		-1.91E+00	2.14E-02		null	null		8.01E+00	4.03E-01				Unigene59235_All//3.00E-32//ES833630				
Unigene59238_All	301	0.35	0.17	0.00	0.00	0.11	0.15	3.09	0.42	2.91	-1.05E+00	6.83E-01		-8.44E+00	3.89E-01		6.84E+00	8.26E-01		7.23E+00	6.93E-01		-2.89E+00	3.28E-04	Down	-8.58E-02	8.95E-01		Unigene59238_All//gi|297833864|ref|XP_002884814.1|//5.00E-06//hypothetical protein ARALYDRAFT_317879 [Arabidopsis lyrata subsp. lyrata] >gi|297330654|gb|EFH61073.1| hypothetical protein ARALYDRAFT_317879 [Arabidopsis lyrata subsp. lyrata]		Unigene59238_All//7.00E-30//gi|164323557|gb|ES829860.1|ES829860				nr -
Unigene59241_All	806	0.06	0.13	0.59	0.00	0.13	0.06	1.36	0.16	0.25	9.54E-01	7.25E-01		3.20E+00	3.48E-02		7.00E+00	4.55E-01		5.81E+00	6.93E-01		-3.13E+00	3.46E-05	Down	-2.46E+00	2.04E-04	Down	Unigene59241_All//gi|110289587|gb|ABG66263.1|//7.00E-35//ICE-like protease p20 domain containing protein, expressed {Oryza sativa (japonica cultivar-group)}	Unigene59241_All//2.00E-17//AT4G17080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WORN motif (InterPro:IPR003409); BEST Arabidopsis thaliana protein match is: WORN (Membrane Occupation and Recognition Nexus) repeat-containing protein /phosphatidylinositol-4-phosphate 5-kinase-related (TAIR:AT2G35170.1); Has 18005 Blast hits to 5199 proteins in 343 species: Archae - 0; Bacteria - 1726; Metazoa - 3046; Fungi - 93; Plants - 653; Viruses - 0; Other Eukaryotes - 12487 (source: NCBI BLink).	Unigene59241_All//0.00E+00//TC139046			GO:0016772//GO:0016787//GO:0043231	nr +
Unigene5925_All	587	1.16	4.06	2.54	0.85	2.93	1.69	1.58	0.78	0.68	1.81E+00	6.43E-05	Up	1.13E+00	4.89E-02		1.79E+00	6.43E-04	Up	9.96E-01	1.72E-01		-1.02E+00	1.21E-01		-1.22E+00	5.14E-02								
Unigene5927_All	668	18.95	25.26	28.78	10.81	4.12	9.26	57.34	254.59	92.38	4.14E-01	2.32E-03		6.02E-01	3.43E-06		-1.39E+00	2.70E-11	Down	-2.23E-01	3.73E-01		2.15E+00	0.00E+00	Up	6.88E-01	5.53E-30		Unigene5927_All//gi|192913048|gb|AC906632.1|//1.00E-36//glutathione transferase [Elaeis guineensis]	Unigene5927_All//4.00E-36//AT1G10370| ER09 (EARLY-RESPONSIVE TO DEHYDRATION 9); glutathione transferase	Unigene5927_All//0.00E+00//DR454850		ko00480|Glutathione metabolism	GO:0009404//GO:0009536//GO:0016765	nr +
Unigene59272_All	776	0.40	0.20	0.14	0.06	0.27	0.29	2.40	0.27	0.46	-1.05E+00	4.43E-01		-1.56E+00	3.30E-01		2.05E+00	3.94E-01		2.18E+00	3.23E-01		-3.15E+00	2.08E-08	Down	-2.38E+00	1.08E-06	Down	Unigene59272_All//gi|225460573|ref|XP_002278721.1|//3.00E-64//PREDICTED: similar to SPla/RYanodine receptor (SPRY) domain-containing protein [Vitis vinifera]	Unigene59272_All//1.00E-63//AT1G35470| SPla/RYanodine receptor (SPRY) domain-containing protein	Unigene59272_All//0.00E+00//gi|73850914|gb|DT459934.1|DT459934				nr +
Unigene59277_All	302	2.08	0.00	1.76	0.82	0.80	0.15	0.00	0.00	0.00	-1.10E+01	7.91E-04	Down	-2.38E-01	7.74E-01		-4.71E-02	9.51E-01		-2.46E+00	2.23E-01		null	null		null	null									ESTscan +
Unigene5929_All	1160	2.07	0.52	1.88	2.36	5.05	2.53	3.32	2.20	1.13	-1.98E+00	1.49E-05	Down	-1.41E-01	7.31E-01		1.10E+00	3.61E-06	Up	9.96E-02	7.98E-01		-5.94E-01	3.41E-02		-1.55E+00	9.74E-08	Down	Unigene5929_All//gi|22330953|ref|NP_187629.2|//8.00E-36//kinesin motor protein-related [Arabidopsis thaliana]	Unigene5929_All//4.00E-37//AT3G10180| kinesin motor protein-related	Unigene5929_All//0.00E+00//TC161853			GO:0005488	nr -
Unigene593_All	793	5.28	0.96	5.10	4.77	8.55	5.58	2.19	1.32	3.37	-2.46E+00	1.21E-11	Down	-4.86E-02	8.81E-01		8.42E-01	8.80E-05		2.25E-01	4.93E-01		-7.30E-01	1.03E-01		6.23E-01	6.23E-02		Unigene593_All//gi|115444363|ref|NP_001045961.1|//7.00E-41//Os02g0159200 [Oryza sativa Japonica Group] >gi|113535492|dbj|BAF07875.1| Os02g0159200 [Oryza sativa Japonica Group]	Unigene593_All//3.00E-53//AT4G32350| unknown protein	Unigene593_All//0.00E+00//TC146177				nr -
Unigene59308_All	919	0.68	0.00	0.29	0.60	0.97	0.34	0.09	0.27	0.09	-9.42E+00	7.90E-04	Down	-1.24E+00	2.13E-01		7.08E-01	3.74E-01		-7.94E-01	4.44E-01		1.57E+00	3.26E-01		-8.56E-02	9.71E-01		Unigene59308_All//gi|79516777|ref|NP_197441.3|//8.00E-33//SMG7 [Arabidopsis thaliana] >gi|159461469|gb|ABW96769.1| SMG7-like protein [Arabidopsis thaliana]	Unigene59308_All//4.00E-34//AT5G19400| SMG7	Unigene59308_All//0.00E+00//TC167505			GO:0000279//GO:0051321	nr -
Unigene5932_All	559	12.73	9.43	15.34	7.13	2.46	1.78	0.83	2.17	0.43	-4.33E-01	5.08E-02		2.69E-01	2.23E-01		-1.53E+00	2.05E-07	Down	-2.00E+00	2.39E-09	Down	1.38E+00	1.48E-02		-9.60E-01	3.13E-01		Unigene5932_All//gi|284519838|gb|ADB92669.1|//2.00E-47//cationic amino acid transporter 5 [Populus tremula x Populus alba]	Unigene5932_All//2.00E-44//AT2G34960| CAT5 (CATIONIC AMINO ACID TRANSPORTER 5); L-glutamate transmembrane transporter/ L-lysine transmembrane transporter/ arginine transmembrane transporter/ cationic amino acid transmembrane transporter	Unigene5932_All//5.00E-174//CO083056			GO:0015172//GO:0015174//GO:0015809//GO:0015813//GO:0031224//GO:0043227	nr -
Unigene59324_All	307	2.05	9.57	3.12	3.25	2.80	2.65	13.63	10.89	9.73	2.23E+00	1.85E-07	Up	6.10E-01	3.86E-01		-2.11E-01	7.79E-01		-2.93E-01	6.89E-01		-3.24E-01	2.50E-01		-4.86E-01	5.97E-02		Unigene59324_All//gi|224067156|ref|XP_002302383.1|//3.00E-08//amino acid transporter [Populus trichocarpa] >gi|222844109|gb|EEE81656.1| amino acid transporter [Populus trichocarpa]	Unigene59324_All//7.00E-05//AT3G56200| amino acid transporter family protein				GO:0031224	nr +
Unigene59333_All	493	1.70	0.00	0.65	1.01	0.70	0.09	0.69	0.25	0.00	-1.07E+01	5.57E-05	Down	-1.39E+00	9.66E-02		-5.33E-01	5.94E-01		-3.46E+00	1.61E-02		-1.43E+00	2.58E-01		-9.42E+00	8.13E-03									ESTscan +
Unigene5934_All	572	1.83	2.39	4.19	1.39	2.47	4.18	3.55	2.19	7.10	3.87E-01	5.01E-01		1.20E+00	6.24E-03		8.25E-01	1.57E-01		1.59E+00	2.41E-04	Up	-6.95E-01	8.83E-02		1.00E+00	1.63E-04	Up	Unigene5934_All//gi|297606541|ref|NP_001058631.2|//4.00E-54//Os06g0726600 [Oryza sativa Japonica Group] >gi|54291134|dbj|BAD61807.1| MAP kinase activating protein-like [Oryza sativa Japonica Group] >gi|255677415|dbj|BAF20545.2| Os06g0726600 [Oryza sativa Japonica Group]	Unigene5934_All//4.00E-63//AT4G38360| unknown protein	Unigene5934_All//9.00E-136//CO111280			GO:0031410//GO:0043231	nr -
Unigene59343_All	1101	0.76	0.14	0.68	0.45	0.38	1.03	1.31	0.61	0.33	-2.46E+00	6.70E-03		-1.67E-01	8.15E-01		-2.70E-01	8.02E-01		1.18E+00	7.75E-02		-1.10E+00	2.77E-02		-2.00E+00	1.70E-04	Down	Unigene59343_All//gi|18398046|ref|NP_566318.1|//1.00E-114//3' exoribonuclease family domain 1-containing protein [Arabidopsis thaliana] >gi|30680427|ref|NP_850537.1| 3' exoribonuclease family domain 1-containing protein [Arabidopsis thaliana] >gi|11762184|gb|AAG40370.1|AF325018_1 AT3g07750 [Arabidopsis thaliana] >gi|56744222|gb|AAW28551.1| At3g07750 [Arabidopsis thaliana]	Unigene59343_All//1.00E-103//AT3G07750| 3' exoribonuclease family domain 1-containing protein	Unigene59343_All//3.00E-146//DT467685		ko03018|RNA degradation	GO:0003676//GO:0008408//GO:0010467	nr -
Unigene59345_All	306	2.56	0.17	1.22	0.16	0.11	0.59	0.00	0.27	0.00	-3.95E+00	8.54E-04	Down	-1.07E+00	2.10E-01		-5.33E-01	8.24E-01		1.86E+00	4.58E-01		8.09E+00	4.00E-01		null	null									
Unigene5935_All	449	56.40	34.76	33.09	97.63	83.75	108.53	139.36	83.87	60.69	-6.98E-01	1.44E-10		-7.69E-01	8.10E-12		-2.21E-01	4.91E-03		1.53E-01	6.48E-02		-7.33E-01	4.72E-33		-1.20E+00	1.87E-76	Down	Unigene5935_All//gi|283049400|gb|ADB07168.1|//3.00E-78//DEAD-box RNA helicase-like protein [Prunus persica] >gi|283049402|gb|ADB07169.1| DEAD-box RNA helicase-like protein [Prunus persica]	Unigene5935_All//5.00E-77//AT1G54270| EIF4A-2; ATP-dependent helicase/ translation initiation factor	Unigene5935_All//0.00E+00//TC145006			GO:0008135//GO:0010467//GO:0032559//GO:0042623	nr -
Unigene59350_All	315	2.66	0.00	0.68	1.90	0.22	1.15	0.13	0.00	0.25	-1.14E+01	5.57E-05	Down	-1.97E+00	2.71E-02		-3.12E+00	4.87E-03		-7.26E-01	4.60E-01		-7.07E+00	6.53E-01		9.14E-01	7.49E-01		Unigene59350_All//gi|3894389|gb|AAC78594.1|//7.00E-12//Hcr2-2A [Solanum pimpinellifolium]	Unigene59350_All//5.00E-10//AT3G24982| protein binding				GO:0003824	nr +

Unigene5936_All	874	1.50	1.10	2.50	5.36	5.12	5.43	2.08	0.62	1.46	-4.42E-01	4.41E-01		7.39E-01	1.04E-01		-6.49E-02	8.29E-01		1.82E-02	9.47E-01		-1.74E+00	1.71E-04	Down	-5.12E-01	2.24E-01		Unigene5936_All//gi|297830448|ref|XP_002883106.1|//2.00E-96//beta-glucosidase [Arabidopsis lyrata subsp. lyrata] >gi|297328946|gb|EFH59365.1| beta-glucosidase [Arabidopsis lyrata subsp. lyrata]	Unigene5936_All//5.00E-96//AT3G18080| BGLU44 (B-S GLUCOSIDASE 44); (R)-amygdalin beta-glucosidase/ 4-methylumbelliferyl-beta-D-glucopyranoside beta-glucosidase/ beta-gentiobiose beta-glucosidase/ cellobiose glucosidase/ esculin beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene5936_All//0.00E+00//TC143835		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0005618//GO:0005840//GO:0008422//GO:0015923//GO:0031410//GO:0043167//GO:0044238	nr +
Unigene5937_All	891	38.58	15.18	16.49	2.12	2.59	2.43	0.00	0.00	0.00	-1.35E+00	3.26E-40	Down	-1.23E+00	1.37E-33	Down	2.86E-01	5.47E-01		1.96E-01	6.94E-01		null	null		null	null		Unigene5937_All//gi|15227472|ref|NP_181725.1|//1.00E-42//ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|14517524|gb|AAK62652.1| At2g41940/T6D20.16 [Arabidopsis thaliana] >gi|15810111|gb|AAL06981.1| At2g41940/T6D20.16 [Arabidopsis thaliana]	Unigene5937_All//3.00E-27//AT2G41940| ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding	Unigene5937_All//7.00E-82//gi|109839462|gb|DW238023.1|DW238023	C2H2		GO:0009725//GO:0035315	nr -
Unigene5938_All	488	3.86	13.50	5.46	3.88	2.89	10.55	32.92	71.69	32.74	1.81E+00	2.91E-12	Up	4.99E-01	2.29E-01		-4.23E-01	3.84E-01		1.44E+00	1.35E-07	Up	1.12E+00	1.01E-37	Up	-8.20E-03	9.67E-01		Unigene5938_All//gi|224058272|ref|XP_002299474.1|//9.00E-11//predicted protein [Populus trichocarpa] >gi|222846732|gb|EEE84279.1| predicted protein [Populus trichocarpa]		Unigene5938_All//6.00E-53//TC173088				nr -
Unigene59385_All	647	0.81	0.63	0.16	2.23	0.59	0.98	0.07	0.00	0.00	-3.68E-01	6.83E-01		-2.30E+00	6.76E-02		-1.93E+00	5.06E-04	Down	-1.19E+00	3.43E-02		-6.03E+00	6.53E-01		-6.03E+00	6.09E-01		Unigene59385_All//gi|15231703|ref|NP_191512.1|//1.00E-84//strictosidine synthase family protein [Arabidopsis thaliana] >gi|42572733|ref|NP_974462.1| strictosidine synthase family protein [Arabidopsis thaliana]	Unigene59385_All//7.00E-76//AT3G59530| strictosidine synthase family protein	Unigene59385_All//2.00E-143//gi|13352646|gb|BG442994.1|BG442994		ko00901|Indole alkaloid biosynthesis	GO:0008152//GO:0010208//GO:0016843//GO:0043231	nr +
Unigene594_All	2394	10.82	5.21	5.65	12.21	14.80	12.09	7.08	6.42	6.54	-1.06E+00	5.90E-21	Down	-9.37E-01	1.21E-16		2.77E-01	1.48E-03		-1.44E-02	9.22E-01		-1.41E-01	3.14E-01		-1.15E-01	3.92E-01		Unigene594_All//gi|115443363|ref|NP_001045961.1|//1.00E-59//Os02g0159200 [Oryza sativa Japonica Group] >gi|113535492|dbj|BAF07875.1| Os02g0159200 [Oryza sativa Japonica Group]	Unigene594_All//1.00E-52//AT4G32350| unknown protein	Unigene594_All//0.00E+00//gi|164359609|gb|EX165366.1|EX165366				nr -
Unigene59406_All	319	2.13	0.00	0.17	0.16	0.11	0.14	1.06	0.66	0.87	-1.11E+01	4.09E-04	Down	-3.68E+00	4.81E-03		-5.34E-01	8.24E-01		-1.42E-01	9.51E-01		-6.95E-01	5.77E-01		-2.78E-01	7.80E-01		Unigene59406_All//gi|255557871|ref|XP_002519965.1|//4.00E-11//Extensin-3 precursor, putative [Ricinus communis] >gi|223541011|gb|EEF42569.1| Extensin-3 precursor, putative [Ricinus communis]		Unigene59406_All//7.00E-132//ES829647				nr +
Unigene59408_All	380	2.89	0.00	0.00	0.92	0.54	0.83	0.00	0.00	0.00	-1.15E+01	1.95E-06	Down	-1.15E+01	4.93E-06	Down	-7.55E-01	5.67E-01		-1.41E-01	9.12E-01		null	null		null	null									
Unigene5941_All	1189	0.88	2.26	1.43	1.42	0.96	0.84	0.89	0.95	3.25	1.36E+00	6.75E-04	Up	7.03E-01	1.81E-01		-5.76E-01	2.53E-01		-7.69E-01	1.33E-01		9.44E-02	8.76E-01		1.87E+00	9.79E-10	Up	Unigene5941_All//gi|109676362|gb|AB637663.1|//1.00E-123//CCHC-type integrase [Populus trichocarpa]	Unigene5941_All//4.00E-73//AT5G60900| RLK1 (RECEPTOR-LIKE PROTEIN KINASE 1); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene5941_All//0.00E+00//DT462638			GO:0005488	nr -
Unigene59412_All	323	2.11	0.00	0.33	2.00	1.17	0.28	0.52	0.00	0.00	-1.10E+01	4.09E-04	Down	-2.68E+00	1.69E-02		-7.74E-01	3.81E-01		-2.84E+00	1.02E-02		-9.03E+00	1.34E-01		-9.03E+00	1.08E-01				Unigene59412_All//9.00E-08//gi|78332917|gb|DT553191.1|DT553191				
Unigene59419_All	932	0.95	0.87	0.17	0.80	0.33	0.63	4.31	0.90	1.37	-1.34E-01	8.41E-01		-2.48E+00	7.18E-03		-1.27E+00	1.12E-01		-3.48E-01	6.83E-01		-2.26E+00	2.15E-12	Down	-1.66E+00	9.21E-09	Down	Unigene59419_All//gi|225445342|ref|XP_002281542.1|//2.00E-87//PREDICTED: similar to GRV2 (KATAMARI2); binding / heat shock protein binding [Vitis vinifera]	Unigene59419_All//3.00E-66//AT2G26890| GRV2 (GRAVITROPISM DEFECTIVE 2); binding / heat shock protein binding	Unigene59419_All//0.00E+00//ES832580			GO:0003006//GO:0005515//GO:0005768//GO:0006605//GO:0006950//GO:0009630//GO:0009657//GO:0016192//GO:0031090//GO:0042598//GO:0044267//GO:0044431	nr -
Unigene5942_All	1277	0.57	0.48	0.17	4.60	2.18	1.38	2.02	0.92	1.22	-2.69E-01	7.19E-01		-1.78E+00	6.00E-02		-1.08E+00	2.37E-06	Down	-1.74E+00	2.95E-11	Down	-1.14E+00	1.36E-03		-7.31E-01	3.05E-02		Unigene5942_All//gi|22327464|ref|NP_198758.2|//2.00E-93//cdc2c4t (Arabidopsis thaliana cdc2c); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase >gi|209529775|gb|ACI49782.1| At5g39420 [Arabidopsis thaliana]	Unigene5942_All//4.00E-90//AT5G39420| cdc2c4t (Arabidopsis thaliana cdc2c); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene5942_All//2.00E-39//TC167382			GO:0004672//GO:0006464//GO:0032559//GO:0043231	nr -
Unigene59427_All	774	1.08	0.00	0.55	1.35	0.36	0.47	0.98	0.00	0.57	-1.01E+01	5.57E-05	Down	-9.75E-01	2.37E-01		-1.93E+00	4.39E-03		-1.53E+00	2.88E-02		-9.94E+00	1.67E-05	Down	-7.96E-01	2.52E-01		Unigene59427_All//gi|225440568|ref|XP_002273523.1|//1.00E-52//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene59427_All//3.00E-34//AT2G37960| unknown protein					nr -
Unigene5943_All	1288	1.06	2.36	0.41	0.62	1.93	9.85	0.59	3.21	7.49	1.16E+00	1.50E-03		-1.35E+00	2.93E-02		1.64E+00	7.32E-05	Up	3.99E+00	9.56E-57	Up	2.44E+00	7.78E-14	Up	3.66E+00	1.85E-47	Up	Unigene5943_All//gi|226499794|ref|NP_001148252.1|//1.00E-103//gibberellin 2-beta-dioxygenase 7 [Zea mays] >gi|195616962|gb|ACG30311.1| gibberellin 2-beta-dioxygenase 7 [Zea mays]	Unigene5943_All//2.00E-94//AT4G21200| GA2OX8 (GIBBERELLIN 2-OXIDASE 8); gibberellin 2-beta-dioxygenase	Unigene5943_All//0.00E+00//TC134243		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis	GO:0016706	nr -
Unigene59436_All	853	0.18	0.06	0.19	0.47	0.32	0.26	1.98	0.29	0.37	-1.63E+00	4.88E-01		2.56E-02	1.00E+00		-5.33E-01	6.15E-01		-8.20E-01	5.06E-01		-2.75E+00	8.02E-07	Down	-2.41E+00	3.07E-06	Down	Unigene59436_All//gi|115450491|ref|NP_001048846.1|//6.00E-97//Os03g0129200 [Oryza sativa Japonica Group] >gi|23306125|gb|AAN17392.1| Putative mitotic control protein dis3 [Oryza sativa Japonica Group] >gi|108705992|gb|ABF93787.1| ENB-like protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113547317|dbj|BAF10760.1| Os03g0129200 [Oryza sativa Japonica Group]	Unigene59436_All//6.00E-69//AT2G17510| EMB2763 (EMBRYO DEFECTIVE 2763); RNA binding / ribonuclease	Unigene59436_All//0.00E+00//TC147845		ko03018|RNA degradation	GO:0003676//GO:0008408	nr +
Unigene59444_All	595	0.18	0.00	0.45	0.50	0.17	0.15	2.77	0.35	0.67	-7.46E+00	3.69E-01		1.35E+00	4.09E-01		-1.53E+00	2.98E-01		-1.73E+00	2.89E-01		-2.98E+00	3.67E-07	Down	-2.05E+00	3.66E-05	Down	Unigene59444_All//gi|94549041|gb|AB539005.1|//5.00E-56//plant cell wall protein SlTPR8 [Solanum lycopersicum]	Unigene59444_All//1.00E-35//AT2G46150| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G54200.1); Has 137 Blast hits to 136 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 4; Plants - 133; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene59444_All//0.00E+00//gi|109828911|gb|DW227525.1|DW227525			GO:0016020	nr -
Unigene5945_All	658	49.54	105.19	60.70	67.61	71.85	86.62	110.20	205.36	208.76	1.09E+00	3.24E-57	Up	2.93E-01	9.42E-04		8.79E-02	3.35E-01		3.58E-01	1.27E-07		8.98E-01	1.69E-99		9.22E-01	5.26E-108		Unigene5945_All//gi|257815667|gb|ACV70146.1|//1.00E-25//phospholipase D [Gossypium arboreum]	Unigene5945_All//6.00E-25//AT1G52570| PLDALPHA2 (phospholipase d alpha 2); phospholipase D	Unigene5945_All//2.00E-87//TC160292		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism	GO:0004620//GO:0006650//GO:0009526//GO:0046872	nr -
Unigene5946_All	645	2.43	3.30	2.89	5.33	3.26	2.66	4.59	2.20	2.16	4.39E-01	3.33E-01		2.48E-01	6.18E-01		-7.11E-01	2.49E-02		-1.00E+00	2.43E-03		-1.06E+00	1.20E-03		-1.09E+00	6.29E-04	Down	Unigene5946_All//gi|297803426|ref|XP_002869597.1|//1.00E-33//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315433|gb|EFH45856.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene5946_All//2.00E-34//AT4G26680| pentatricopeptide (PPR) repeat-containing protein				GO:0042254	nr -
Unigene5947_All	727	1.08	1.12	1.32	7.40	4.64	3.23	2.50	0.06	0.77	4.68E-02	9.69E-01		2.88E-01	6.65E-01		-6.73E-01	5.39E-03		-1.20E+00	3.44E-06	Down	-5.44E+00	1.53E-11	Down	-1.70E+00	1.42E-04	Down	Unigene5947_All//gi|45752748|gb|AAS76272.1|//7.00E-38//At5g06790 [Arabidopsis thaliana]	Unigene5947_All//2.00E-35//AT5G06790| unknown protein				GO:0031410	nr -
Unigene5948_All	515	9.45	10.72	7.34	12.19	12.10	13.15	18.31	14.53	47.96	1.83E-01	5.03E-01		-3.64E-01	2.23E-01		-1.01E-02	9.63E-01		1.10E-01	6.89E-01		-3.34E-01	5.39E-02		1.39E+00	4.95E-38	Up	Unigene5948_All//gi|224551852|gb|ACN54324.1|//8.00E-40//NADPH:cytochrome P450 reductase [Gossypium hirsutum]	Unigene5948_All//2.00E-25//AT4G30210| ATR2 (ARABIDOPSIS P450 REDUCTASE 2); NADPH-hemoprotein reductase	Unigene5948_All//0.00E+00//C0097477			GO:0000166//GO:0006575//GO:0009536//GO:0016020//GO:0016653//GO:0046914	nr +
Unigene59481_All	645	3.97	16.89	6.60	56.38	76.34	232.33	17.24	24.11	86.60	2.09E+00	7.33E-24	Up	7.33E-01	1.69E-02		4.37E-01	3.12E-10		2.04E+00	0.00E+00	Up	4.84E-01	1.25E-04		2.33E+00	1.00E-171	Up	Unigene59481_All//gi|15225603|ref|NP_181527.1|//1.00E-78//transferase family protein [Arabidopsis thaliana] >gi|13937226|gb|AAK50105.1|AF37296 8_1 At2g39880/T28M21.14 [Arabidopsis thaliana] >gi|21700883|gb|AAM70565.1| At2g39880/T28M21.14 [Arabidopsis thaliana] >gi|91805487|gb|ABE65472.1| transferase family protein [Arabidopsis thaliana]	Unigene59481_All//2.00E-80//AT2G39880| transferase family protein	Unigene59481_All//0.00E+00//gi|18101590|gb|BM360844.1|BM360844		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016747	nr -
Unigene5949_All	950	0.22	0.91	0.56	7.03	8.30	8.94	18.07	8.14	7.97	2.04E+00	1.59E-02		1.35E+00	2.25E-01		2.40E-01	3.04E-01		3.47E-01	9.76E-02		-1.15E+00	1.11E-19	Down	-1.18E+00	3.99E-21	Down	Unigene5949_All//gi|3901018|emb|CAA10235.1|//3.00E-47//stress and pathogenesis-related protein [Fagus sylvatica]	Unigene5949_All//4.00E-10//AT1G24020| MLP423 (MLP-LIKE PROTEIN 423)				GO:0006950	nr -
Unigene59493_All	396	1.59	0.00	0.40	0.63	0.35	1.14	0.00	0.00	0.00	-1.06E+01	7.90E-04	Down	-1.97E+00	6.50E-02		-8.55E-01	5.73E-01		8.59E-01	4.69E-01		null	null		null	null				Unigene59493_All//2.00E-18//DW512511				
Unigene59497_All	387	2.84	0.00	0.28	0.26	1.07	0.23	0.00	0.00	0.00	-1.15E+01	1.95E-06	Down	-3.37E+00	2.67E-04	Down	2.05E+00	1.47E-01		-1.41E-01	9.49E-01		null	null		null	null									
Unigene595_All	2545	16.06	9.78	10.65	30.75	31.91	20.78	16.40	9.13	7.22	-7.16E-01	2.88E-17		-5.92E-01	5.13E-12		5.32E-02	4.69E-01		-5.65E-01	4.36E-23		-8.45E-01	2.68E-28		-1.18E+00	2.88E-50	Down	Unigene595_All//gi|115444363|ref|NP_001045961.1|//7.00E-25//Os02g0159200 [Oryza sativa Japonica Group] >gi|113535492|dbj|BAF07875.1| Os02g0159200 [Oryza sativa Japonica Group]	Unigene595_All//4.00E-36//AT4G32350| unknown protein	Unigene595_All//0.00E+00//TC139153				nr +
Unigene5950_All	601	2.96	0.67	1.15	0.91	2.12	1.95	1.69	2.50	0.93	-2.13E+00	1.23E-04	Down	-1.36E+00	1.01E-02		1.22E+00	4.61E-02		1.10E+00	9.17E-02		5.68E-01	2.50E-01		-8.64E-01	1.40E-01				Unigene5950_All//0.00E+00//ES791095				
Unigene5951_All	526	23.18	18.78	13.46	60.80	43.99	62.42	21.70	10.33	14.01	-3.03E-01	7.01E-02		-7.84E-01	3.24E-06		-4.67E-01	8.41E-08		3.80E-02	7.37E-01		-1.07E+00	5.43E-12	Down	-6.31E-01	1.51E-05				Unigene5951_All//1.00E-174//TC144728				
Unigene59513_All	429	1.95	1.18	0.00	0.00	0.00	0.00	0.49	2.53	0.56	-7.24E-01	3.48E-01		-1.09E+01	1.19E-04	Down	null	null		null	null		2.36E+00	5.23E-04	Up	1.77E-01	9.08E-01		Unigene59513_All//gi|283132367|dbj|BAI63589.1|//8.00E-39//UDP-glucose glucosyltransferase [Lotus japonicus]	Unigene59513_All//4.00E-29//AT4G34135| UGT73B2 (UDP-GLUCOSYLTRANSFERASE 73B2); UDP-glucosyltransferase/ UDP-glycosyltransferase/ flavonol 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase	Unigene59513_All//9.00E-92//TC169312		ko00908|Zeatin biosynthesis	GO:0035251	nr +

Unigene59518_All	638	0.82	0.95	1.17	2.19	3.56	1.27	2.19	0.46	2.56	2.17E-01	7.92E-01		5.11E-01	5.47E-01		7.04E-01	1.01E-01		-7.79E-01	1.82E-01		-2.25E+00	9.69E-05	Down	2.27E-01	6.25E-01		Unigene59518_All//gi|30983603|gb|AAP41107.1|//1.00E-104//kinesin-like calmodulin binding protein [Gossypium hirsutum]	Unigene59518_All//9.00E-92//AT5G65930| ZW1 (ZWICHEL); calmodulin binding / microtubule motor	Unigene59518_All//0.00E+00//TC129553			GO:0000904//GO:0003774//GO:0005515//GO:0007017//GO:0009856//GO:0016020//GO:0032559//GO:0043232	nr -
Unigene59952_All	362	27.61	15.96	21.77	47.20	45.09	55.52	123.57	71.93	52.16	-7.91E-01	1.35E-05		-3.43E-01	7.88E-02		-6.60E-02	6.95E-01		2.34E-01	7.39E-02		-7.81E-01	1.50E-26		-1.24E+00	3.93E-58	Down	Unigene5952_All//gi|3914394|sp|Q42908.1|PMG1_MESCR//3.00E-36//RecName: Full=2,3-bisphosphoglycerate-independent phosphoglycerate mutase; Short=BPG-independent PGAM; Short=Phosphoglyceromutase; AltName: Full=PGAM-I >gi|602426|gb|AAA86979.1| phosphoglyceromutase [Mesembryanthemum crystallinum]	Unigene5952_All//8.00E-35//AT3G08590| 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative	Unigene5952_All//0.00E+00//gi|21090541|gb|BQ402854.1|BQ402854		ko00010|Glycolysis / Gluconeogenesis	GO:0004619//GO:0005576//GO:0006007//GO:0010038//GO:0044444//GO:0046914	nr +
Unigene59521_All	401	0.13	2.27	1.59	0.12	0.09	0.00	0.11	0.21	0.30	4.12E+00	2.34E-04	Up	3.61E+00	6.97E-03		-5.32E-01	8.24E-01		-6.96E+00	6.31E-01		9.84E-01	7.30E-01		1.50E+00	5.57E-01					Unigene59521_All//1.00E-78//TC170579				
Unigene59524_All	400	2.09	0.13	0.00	0.25	0.52	0.23	1.37	0.84	0.20	-4.05E+00	4.65E-04	Down	-1.10E+01	1.19E-04	Down	1.05E+00	6.12E-01		-1.42E-01	9.49E-01		-7.17E-01	4.22E-01		-2.79E+00	7.95E-03		Unigene59524_All//gi|226494423|ref|XP_001152516.1|//1.00E-28//mTERF family protein [Zea mays] >gi|195657075|gb|ACG48005.1| mTERF family protein [Zea mays]	Unigene59524_All//9.00E-29//AT5G06810| mitochondrial transcription termination factor-related / mTERF-related				GO:0043231	nr +
Unigene59528_All	399	4.98	0.00	0.27	0.50	0.00	0.00	0.00	0.00	0.00	-1.23E+01	1.70E-11	Down	-4.22E+00	1.27E-08	Down	-8.96E+00	8.40E-02		-8.96E+00	1.33E-01		null	null		null	null		Unigene59528_All//gi|225445108|ref|XP_002283751.1|//2.00E-11//PREDICTED: malate dehydrogenase (NADP+) [Vitis vinifera]	Unigene59528_All//1.00E-65//AT1G79750| ATNADP-ME4 (NADP-malic enzyme 4); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor	Unigene59528_All//5.00E-07//gi|48744460|gb|C0074979.1|C0074979		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0005488//GO:0008152//GO:0016614	nr +
Unigene5953_All	788	0.66	16.01	0.34	3.86	3.80	9.23	4.72	4.72	5.16	4.59E+00	5.03E-58	Up	-9.75E-01	3.76E-01		-2.05E-02	9.61E-01		1.26E+00	1.25E-08	Up	-3.00E-04	9.98E-01		1.27E-01	6.45E-01		Unigene5953_All//gi|37202082|gb|AAQ89656.1|//9.00E-37//At5g38700 [Arabidopsis thaliana]	Unigene5953_All//2.00E-25//AT5G38700| unknown protein	Unigene5953_All//0.00E+00//gi|109828084|gb|DW226724.1|DW226724				nr +
Unigene59530_All	617	0.76	0.00	0.00	0.16	0.22	0.51	2.81	0.88	0.19	-9.58E+00	5.54E-03		-9.58E+00	8.63E-03		4.67E-01	8.76E-01		1.67E+00	3.09E-01		-1.67E+00	3.96E-04	Down	-3.86E+00	1.46E-09	Down	Unigene59530_All//gi|30690409|ref|NP_850456.1|//3.00E-31//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene59530_All//1.00E-32//AT2G46495| zinc finger (C3HC4-type RING finger) family protein					nr -
Unigene59534_All	420	1.99	0.00	1.52	0.71	0.00	0.00	0.00	0.00	0.00	-1.10E+01	5.57E-05	Down	-3.90E-01	6.41E-01		-9.47E+00	2.01E-02		-9.47E+00	3.98E-02		null	null		null	null										
Unigene5954_All	320	65.40	136.97	79.54	67.25	121.71	110.37	71.88	77.06	74.20	1.07E+00	2.04E-35	Up	2.82E-01	1.42E-02		8.56E-01	6.97E-26		7.15E-01	7.18E-16		1.01E-01	4.02E-01		4.59E-02	6.82E-01		Unigene5954_All//gi|241740196|gb|ACS68205.1|//4.00E-53//ubiquitin 10.2 [Brassica napus]	Unigene5954_All//2.00E-54//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene5954_All//0.00E+00//TC137628			GO:0044424	nr +
Unigene59548_All	429	0.98	1.54	5.21	0.00	0.00	0.00	0.00	0.00	0.00	6.54E-01	4.48E-01		2.42E+00	4.31E-06	Up	null	null		null	null		null	null		null	null										
Unigene5955_All	800	2.29	1.39	2.73	2.18	1.94	3.78	0.21	0.89	1.99	-7.16E-01	1.36E-01		2.54E-01	5.98E-01		-1.70E-01	7.62E-01		7.95E-01	2.81E-02		2.07E+00	1.45E-02		3.24E+00	1.34E-07	Up	Unigene5955_All//gi|224069146|ref|XP_002302911.1|//2.00E-17//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222844637|gb|EEE82184.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene5955_All//6.00E-12//AT3G14460| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction	GO:0003824	nr -
Unigene59551_All	724	0.72	3.92	0.74	0.83	1.05	0.81	0.47	1.27	0.28	2.44E+00	5.81E-08	Up	2.53E-02	9.99E-01		3.42E-01	7.20E-01		-2.59E-02	9.64E-01		1.44E+00	3.26E-02		-7.64E-01	5.01E-01		Unigene59551_All//gi|9651530|gb|AAF91178.1|AF203700_1//1.00E-108//ClpB [Phaseolus lunatus]	Unigene59551_All//1.00E-107//AT2G25140| CLPB4 (CASEIN LYTIC PROTEINASE B4); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding	Unigene59551_All//0.00E+00//ES799629			GO:0006950//GO:0009532//GO:0009657//GO:0017111//GO:0032559//GO:0043170	nr +
Unigene59562_All	758	0.55	0.27	0.00	0.39	0.73	0.77	1.28	0.72	0.00	-1.05E+00	3.65E-01		-9.11E+00	1.55E-02		8.83E-01	4.21E-01		9.74E-01	3.46E-01		-8.40E-01	1.87E-01		-1.03E+01	2.72E-07	Down	Unigene59562_All//gi|15230718|ref|NP_190139.1|//3.00E-29//DC1 domain-containing protein [Arabidopsis thaliana]	Unigene59562_All//6.00E-31//AT3G45530| DC1 domain-containing protein					nr +
Unigene59582_All	973	0.22	0.83	0.16	1.08	0.92	0.09	0.74	0.90	0.90	1.95E+00	2.43E-02		-3.90E-01	8.07E-01		-2.25E-01	7.53E-01		-3.53E+00	9.34E-05	Down	2.88E-01	6.58E-01		2.86E-01	6.45E-01		Unigene59582_All//gi|297844284|ref|XP_002890023.1|//1.00E-59//F16A14.4 [Arabidopsis lyrata subsp. lyrata] >gi|297335865|gb|EFH66282.1| F16A14.4 [Arabidopsis lyrata subsp. lyrata]	Unigene59582_All//2.00E-59//AT1G13810| DNA binding / nuclease	Unigene59582_All//0.00E+00//DW516231				nr +
Unigene59594_All	477	1.76	0.00	0.78	0.10	0.29	0.57	0.00	0.00	0.00	-1.08E+01	5.56E-05	Down	-1.17E+00	1.52E-01		1.47E+00	6.18E-01		2.44E+00	2.22E-01		null	null		null	null		Unigene59594_All//COG1620//3.00E-08//L-lactate permease							cog +
Unigene59595_All	639	4.75	1.27	1.42	1.33	1.83	0.71	1.79	1.11	1.68	-1.90E+00	1.76E-06	Down	-1.75E+00	1.59E-05	Down	4.67E-01	5.14E-01		-9.07E-01	2.47E-01		-6.84E-01	2.37E-01		-8.58E-02	8.81E-01		Unigene59595_All//gi|115480279|ref|NP_001063733.1|//2.00E-48//Os09g0527900 [Oryza sativa Japonica Group] >gi|113631966|dbj|BAF25647.1| Os09g0527900 [Oryza sativa Japonica Group]	Unigene59595_All//6.00E-37//AT4G38960| zinc finger (B-box type) family protein	Unigene59595_All//1.00E-91//TC137101	Orphans		GO:0010468//GO:0044464//GO:0046914	nr +
Unigene5960_All	1058	51.38	45.55	46.66	7.25	8.82	3.50	0.36	0.16	0.45	-1.74E-01	2.04E-02		-1.39E-01	8.55E-02		2.83E-01	1.58E-01		-1.05E+00	4.65E-07	Down	-1.19E+00	3.09E-01		3.29E-01	7.07E-01		Unigene5960_All//gi|224137478|ref|XP_002327136.1|//1.00E-121//light-harvesting complex I protein LhcA5 [Populus trichocarpa] >gi|222835451|gb|EEE73886.1| light-harvesting complex I protein LhcA5 [Populus trichocarpa]	Unigene5960_All//1.00E-84//AT1G45474| LHCA5; pigment binding	Unigene5960_All//0.00E+00//TC160120		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009536	nr -
Unigene59602_All	498	0.21	2.44	1.82	0.90	0.41	0.45	0.76	2.01	1.36	3.54E+00	4.02E-05	Up	3.11E+00	1.76E-03		-1.12E+00	3.15E-01		-9.90E-01	3.94E-01		1.40E+00	2.82E-02		8.32E-01	2.74E-01		Unigene59602_All//gi|67483357|gb|AY68034.1|//1.00E-66//3-hydroxy-methylglutaryl coenzyme A reductase [Tilia miqueliana]	Unigene59602_All//5.00E-43//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene59602_All//0.00E+00//gi|109855712|gb|DW484691.1|DW484691		ko00900|Terpenoid backbone biosynthesis	GO:0000166//GO:0005739//GO:0006720//GO:0006732//GO:0009536//GO:0016616//GO:0031090//GO:0031224//GO:0031967//GO:0048037	nr -
Unigene59603_All	494	13.03	0.00	0.65	0.50	0.14	0.00	0.00	0.00	0.00	-1.37E+01	2.69E-37	Down	-4.33E+00	9.07E-28	Down	-1.85E+00	2.75E-01		-8.98E+00	7.32E-02		null	null		null	null					Unigene59603_All//0.00E+00//DW481655				
Unigene59609_All	507	1.86	0.00	0.63	1.47	1.29	3.03	0.50	0.49	0.63	-1.09E+01	1.46E-05	Down	-1.56E+00	4.90E-02		-1.92E-01	8.21E-01		1.04E+00	5.90E-02		-1.68E-02	1.02E+00		3.29E-01	7.63E-01		Unigene59609_All//gi|297841913|ref|XP_002888838.1|//2.00E-31//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297334679|gb|EFH85097.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene59609_All//2.00E-30//AT1G71460| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene5961_All	502	10.63	6.76	9.97	22.72	30.18	17.18	14.91	12.16	5.40	-6.53E-01	1.14E-02		-9.24E-02	7.34E-01		4.10E-01	3.14E-03		-4.03E-01	1.77E-02		-2.94E-01	1.44E-01		-1.47E+00	3.40E-13	Down	Unigene5961_All//gi|18414122|ref|NP_567418.1|//3.00E-17//RALFL32 (ralf-like 32); signal transducer [Arabidopsis thaliana] >gi|89001071|gb|ABD59125.1| At4g14010 [Arabidopsis thaliana]	Unigene5961_All//9.00E-18//AT4G14010| RALFL32 (ralf-like 32); signal transducer	Unigene5961_All//0.00E+00//ES839970			GO:0019932	nr +
Unigene59611_All	508	1.85	1.60	6.92	0.10	1.22	0.36	0.00	0.08	0.55	-2.16E-01	7.32E-01		1.90E+00	5.26E-07	Up	3.64E+00	5.37E-03		1.86E+00	4.58E-01		6.36E+00	6.31E-01		9.10E+00	2.43E-02		Unigene59611_All//gi|3176659|gb|AAC18783.1|//3.00E-11//Strong similarity to receptor kinase gb|M80238 from A. thaliana [Arabidopsis thaliana]	Unigene59611_All//2.00E-12//AT1G67520| lectin protein kinase family protein				GO:0004672//GO:0005488//GO:0031410	nr +
Unigene59617_All	487	2.90	0.00	1.20	1.53	0.00	0.56	0.00	0.00	0.00	-1.15E+01	3.28E-08	Down	-1.27E+00	3.55E-02		-1.06E+01	1.50E-05	Down	-1.46E+00	9.03E-02		null	null		null	null					Unigene59617_All//6.00E-07//FL577491				
Unigene59629_All	562	2.70	2.07	1.33	7.09	6.74	3.54	1.58	1.41	1.56	-3.81E-01	4.78E-01		-1.03E+00	7.23E-02		-7.32E-02	8.23E-01		-1.00E+00	9.11E-04	Down	-1.61E-01	8.03E-01		-1.87E-02	9.66E-01		Unigene59629_All//gi|238481477|ref|NP_001154760.1|//5.00E-15//RING1A (RING 1A); protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene59629_All//3.00E-16//AT5G44280| RING1A (RING 1A); protein binding / zinc ion binding				GO:0006350//GO:0010074//GO:0010629//GO:0031519//GO:0045165//GO:0046872	nr +
Unigene5963_All	862	8.50	5.76	6.73	5.20	5.71	8.44	10.84	10.57	5.22	-5.61E-01	9.35E-03		-3.36E-01	1.48E-01		1.35E-01	6.75E-01		6.98E-01	1.12E-03		-3.63E-02	8.54E-01		-1.05E+00	4.77E-10	Down	Unigene5963_All//gi|115464671|ref|NP_001055935.1|//1.00E-16//Os05g0196000 [Oryza sativa Japonica Group] >gi|113579486|dbj|BAF17849.1| Os05g0196000 [Oryza sativa Japonica Group]	Unigene5963_All//1.00E-22//AT5G04000| unknown protein	Unigene5963_All//0.00E+00//gi|48791823|gb|C0093137.1|C0093137				nr +
Unigene59632_All	618	1.19	1.97	1.55	16.12	14.71	6.43	3.76	2.03	0.13	7.31E-01	2.35E-01		3.88E-01	6.08E-01		-1.32E-01	5.55E-01		-1.33E+00	1.02E-12	Down	-8.91E-01	1.72E-02		-4.87E+00	1.64E-14	Down	Unigene59632_All//gi|224127204|ref|XP_002320013.1|//1.00E-63//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222860786|gb|EEE98328.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene59632_All//4.00E-32//AT4G37750| ANT (AINTEGUMENTA); DNA binding / transcription factor	Unigene59632_All//0.00E+00//gi|48742368|gb|C0072887.1|C0072887	AP2-EREBP		GO:0005488//GO:0006350//GO:0010468	nr +
Unigene59639_All	661	2.85	0.15	1.37	0.60	0.68	0.14	0.96	0.06	0.72	-4.22E+00	1.15E-08	Down	-1.06E+00	3.50E-02		1.68E-01	9.04E-01		-2.14E+00	1.26E-01		-3.92E+00	9.80E-04	Down	-4.08E-01	6.19E-01		Unigene59639_All//gi|189046708|sp|A5YVF1.1|SGS3_SOLLC//6.00E-25//RecName: Full=Protein SUPPRESSOR OF GENE SILENCING 3; AltName: Full=SIGES3 >gi|148613844|gb|ABQ96272.1| SGS3-like protein [Solanum lycopersicum]	Unigene59639_All//8.00E-22//AT5G23570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene59639_All//4.00E-141//gi|78353936|gb|DT574210.1|DT574210			GO:0002252//GO:0009791//GO:0030422	nr +
Unigene5964_All	468	2.57	4.44	1.37	4.04	2.50	2.22	3.70	2.05	1.19	7.88E-01	7.72E-02		-9.13E-01	1.57E-01		-6.93E-01	1.33E-01		-8.66E-01	7.01E-02		-8.51E-01	5.62E-02		-1.64E+00	3.35E-04	Down	Unigene5964_All//gi|226508514|ref|NP_001149792.1|//1.00E-35//DCN1-like protein 4 [Zea mays] >gi|195634699|gb|ACG36818.1| DCN1-like protein 4 [Zea mays]	Unigene5964_All//2.00E-36//AT1G15860| INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Defective in cullin neddylation (InterPro:IPR014764), Protein of unknown function DUF298 (InterPro:IPR005176); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G12760.1); Has 576 Blast hits to 576 proteins in 121 species: Archae - 0; Bacteria - 0; Metazoa - 403; Fungi - 78; Plants - 51; Viruses - 0; Other Eukaryotes - 44 (source: NCBI BLink).	Unigene5964_All//5.00E-38//TC147999			GO:0046872	nr -
Unigene59642_All	790	8.34	1.73	2.22	0.50	0.52	0.11	0.00	0.00	0.00	-2.27E+00	2.29E-16	Down	-1.91E+00	1.25E-12	Down	5.25E-02	9.89E-01		-2.14E+00	1.26E-01		null	null		null	null		Unigene59642_All//gi|148270935|gb|ABQ53633.1|//1.00E-66//esterase [Cucumis melo]	Unigene59642_All//4.00E-65//AT5G23530| AtCXE18 (Arabidopsis thaliana carboxyesterase 18); carboxylesterase	Unigene59642_All//0.00E+00//TC142770			GO:0000904	nr -
Unigene5966_All	879	10.54	6.98	16.60	4.76	3.57	3.29	1.97	0.48	0.50	-5.95E-01	1.60E-03		6.56E-01	1.48E-05		-4.17E-01	1.66E-01		-5.34E-01	7.79E-02		-2.05E+00	3.55E-05	Down	-1.98E+00	3.36E-05	Down	Unigene5966_All//gi|167998414|ref|XP_001751913.1|//1.00E-07//Qc-SNARE, SYF5 family [Physcomitrella patens subsp. patens] >gi|162697011|gb|EDQ83348.1| Qc-SNARE, SYF5 family [Physcomitrella patens subsp. patens]	Unigene5966_All//2.00E-06//AT1G79590| SYP52 (SYNTAXIN OF PLANTS 52); SNAP receptor			ko04130|SNARE interactions in vesicular transport		nr -
Unigene59662_All	200	150.42	126.42	143.78	148.70	241.91	207.07	41.65	84.01	39.84	-2.51E-01	1.35E-02		-6.52E-02	6.02E-01		7.02E-01	6.07E-23		4.78E-01	2.60E-09		1.01E+00	8.61E-16	Up	-6.40E-02	7.43E-01		Unigene59662_All//gi|3242079|emb|CAA07370.1|//1.00E-25//proline-rich protein [Capsicum annuum]		Unigene59662_All//5.00E-107//TC134153			GO:0006812//GO:0043169	nr -

Unigene5968_All	858	0.85	1.42	1.74	2.38	0.84	2.11	16.71	57.09	15.83	7.31E-01	2.35E-01		1.03E+00	7.47E-02		-1.50E+00	5.63E-04	Down	-1.77E-01	6.97E-01		1.77E+00	7.66E-104	Up	-7.73E-02	6.05E-01		Unigene5968_All//gi|283136100|gb|ADB11369.1|//4.00E-80//tau class glutathione transferase GSTU43 [Populus trichocarpa]	Unigene5968_All//2.00E-51//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	Unigene5968_All//4.00E-157//DT464570		ko00480|Glutathione metabolism	GO:0016740//GO:0016829	nr -
Unigene5969_All	861	2.55	2.24	0.25	3.76	3.00	3.04	12.47	11.31	8.42	-1.91E-01	6.42E-01		-3.37E+00	4.31E-08	Down	-3.26E-01	3.72E-01		-3.06E-01	4.19E-01		-1.41E-01	4.30E-01		-5.67E-01	1.68E-04		Unigene5969_All//gi|2826811|emb|CAA05727.1|//3.00E-41//AtGBP2 [Arabidopsis thaliana]	Unigene5969_All//9.00E-33//ATG13850| GR-RBP2 (GLYCINE-RICH RNA-BINDING PROTEIN 2); ATP binding / RNA binding / double-stranded DNA binding / single-stranded DNA binding	Unigene5969_All//0.00E+00//gi|109882553|gb|DW511523.1|DW511523		ko03010|Ribosome//ko03040|Spliceosome	GO:0006950//GO:0032501//GO:0032559//GO:0043231//GO:0043566//GO:0046914	nr -
Unigene5970_All	903	1.80	0.95	0.71	4.96	2.56	2.45	3.46	6.20	4.76	-9.13E-01	7.77E-02		-1.34E+00	1.60E-02		-9.58E-01	3.12E-04		-1.02E+00	3.14E-04	Down	8.40E-01	1.83E-04		4.60E-01	7.30E-02		Unigene5970_All//gi|115475932|ref|NP_001061562.1|//4.00E-06//Os08g0330900 [Oryza sativa Japonica Group] >gi|113623531|dbj|BAF23476.1|Os08g0330900 [Oryza sativa Japonica Group]	Unigene5970_All//8.00E-06//AT3G09510| nucleic acid binding					nr +
Unigene59700_All	201	0.00	0.00	1.06	1.24	1.20	0.67	5.68	3.74	1.39	null	null		1.00E+01	1.40E-01		-4.73E-02	9.51E-01		-8.78E-01	6.16E-01		-6.02E-01	3.07E-01		-2.03E+00	8.63E-04	Down			Unigene59700_All//4.00E-24//TC145740				
Unigene59701_All	201	46.85	1125.57	396.06	159.11	370.74	523.09	0.00	0.21	0.00	4.59E+00	0.00E+00	Up	3.08E+00	1.40E-260	Up	1.22E+00	1.21E-87	Up	1.72E+00	2.70E-186	Up	7.70E+00	6.31E-01		null	null		Unigene59701_All//gi|157688320|gb|ABV64742.1|//1.00E-13//glycine-rich protein 1 [Boea hygrometrica]		Unigene59701_All//1.00E-107//DW508073		ko03040|Spliceosome	GO:0005488//GO:0031410	nr -
Unigene59714_All	201	55.97	15.38	25.96	168.03	127.46	107.40	515.57	436.46	362.31	-1.86E+00	1.90E-21	Down	-1.11E+00	8.78E-10	Down	-3.99E-01	2.90E-06		-6.46E-01	6.51E-13		-2.40E-01	1.21E-07		-5.09E-01	1.82E-29		Unigene59714_All//gi|211906474|gb|ACJ11730.1|//5.00E-15//glycine-rich RNA-binding protein [Gossypium hirsutum]	Unigene59714_All//3.00E-12//AT2G21660| CCR2 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	Unigene59714_All//8.00E-109//EX171122			GO:0005488	nr +
Unigene5972_All	763	221.76	81.22	153.12	34.15	25.63	28.65	1.22	0.71	0.73	-1.45E+00	7.44E-219	Down	-5.34E-01	6.84E-40		-4.14E-01	2.81E-05		-2.53E-01	2.15E-02		-7.76E-01	2.35E-01		-7.38E-01	2.33E-01		Unigene5972_All//gi|219842172|dbj|BAH10643.1|//2.00E-74//2-methyl-6-geranylgeranylbenzoquinone methyltranferase [Hevea brasiliensis]	Unigene5972_All//7.00E-63//AT3G63410| APG1 (ALBINO OR PALE GREEN MUTANT 1); 2-methyl-6-phytyl-1,4-benzoquinone methyltransferase/ S-adenosylmethionine-dependent methyltransferase/ methyltransferase	Unigene5972_All//0.00E+00//TC141722		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0008757//GO:0009528//GO:0042360//GO:0044423//GO:0045426	nr -
Unigene5973_All	862	7.83	11.05	6.61	15.20	15.78	19.54	11.04	24.20	14.84	4.97E-01	7.76E-03		-2.44E-01	3.40E-01		5.41E-02	8.02E-01		3.63E-01	8.01E-03		1.13E+00	4.00E-23	Up	4.27E-01	1.94E-03		Unigene5973_All//gi|30689268|ref|NP_173925.3|//9.00E-41//PFT1 (PHYTOCHROME AND FLOWERING TIME 1); transcription coactivator [Arabidopsis thaliana] >gi|32478899|gb|AAO39425.1| phytochrome and flowering time 1 protein [Arabidopsis thaliana]	Unigene5973_All//9.00E-17//AT1G25540| PFT1 (PHYTOCHROME AND FLOWERING TIME 1); transcription coactivator	Unigene5973_All//0.00E+00//TC134347		ko03022|Basal transcription factors	GO:0006952//GO:0007602//GO:0009639//GO:0009908//GO:0010557//GO:0030233//GO:0043231//GO:0043234	nr +
Unigene59762_All	203	72.42	39.44	26.49	58.40	62.25	110.57	225.56	106.65	62.01	-8.77E-01	3.35E-09		-1.45E+00	7.80E-19	Down	9.21E-02	6.23E-01		9.21E-01	1.42E-15		-1.08E+00	2.63E-46	Down	-1.86E+00	2.90E-107	Down	Unigene59762_All//gi|124359908|gb|ABD28456.2|//1.00E-26//Ribosomal protein S21e [Medicago truncatula]	Unigene59762_All//2.00E-27//AT5G27700| structural constituent of ribosome	Unigene59762_All//3.00E-111//TC156390		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene5977_All	479	6.99	9.20	15.01	6.97	8.63	4.24	3.62	1.40	1.58	3.97E-01	1.81E-01		1.10E+00	1.83E-06	Up	3.08E-01	3.47E-01		-7.16E-01	3.51E-02		-1.37E+00	2.67E-03		-1.20E+00	5.96E-03				Unigene5977_All//6.00E-07//TC171731				
Unigene59788_All	204	3.33	0.00	0.00	0.49	0.34	0.44	0.00	0.00	0.00	-1.17E+01	4.09E-04	Down	-1.17E+01	7.63E-04	Down	-5.33E-01	8.15E-01		-1.41E-01	9.49E-01		null	null		null	null									
Unigene598_All	779	3.90	4.10	4.03	9.72	9.46	8.41	25.40	17.60	9.00	7.30E-02	8.34E-01		5.01E-02	8.95E-01		-3.91E-02	8.67E-01		-2.09E-01	3.98E-01		-5.29E-01	1.54E-06		-1.50E+00	1.74E-34	Down	Unigene598_All//gi|3540195|gb|AAC34345.1|//1.00E-108//Unknown protein [Arabidopsis thaliana]	Unigene598_All//4.00E-109//AT1G77130| PGSIP2 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 2); transferase, transferring glycosyl groups	Unigene598_All//0.00E+00//gi|11206921|gb|BF275803.1|BF275803			GO:0016740	nr +
Unigene5981_All	689	1.90	2.28	2.01	7.45	4.95	4.85	2.82	1.76	0.40	2.64E-01	6.09E-01		8.20E-02	8.86E-01		-5.90E-01	1.96E-02		-6.19E-01	1.91E-02		-6.82E-01	1.03E-01		-2.80E+00	3.40E-08	Down	Unigene5981_All//gi|8894554|emb|CAB98832.1|//5.00E-85//NAD-dependent malic enzyme (malate oxidoreductase) [Cicer arietinum]	Unigene5981_All//4.00E-72//AT4G00570| malate oxidoreductase, putative	Unigene5981_All//3.00E-148//TC165997		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0004470//GO:0031980//GO:0043169//GO:0043648	nr -
Unigene59817_All	205	16.33	11.86	8.31	19.93	26.54	28.42	100.44	43.43	44.50	-4.61E-01	1.78E-01		-9.75E-01	6.09E-03		4.14E-01	1.16E-01		5.12E-01	4.08E-02		-1.21E+00	2.55E-25	Down	-1.17E+00	6.15E-25	Down	Unigene59817_All//gi|115440691|ref|NP_001044625.1|//7.00E-29//Os01g0817700 [Oryza sativa Japonica Group] >gi|113534156|dbj|BAF06539.1|Os01g0817700 [Oryza sativa Japonica Group]	Unigene59817_All//6.00E-28//AT3G08590| 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative	Unigene59817_All//2.00E-112//TC130230		ko00010|Glycolysis / Gluconeogenesis	GO:0004619//GO:0005576//GO:0006007//GO:0010038//GO:0044444//GO:0046914	nr +
Unigene59818_All	205	3.06	0.00	0.52	0.24	1.18	0.44	0.83	0.20	0.39	-1.16E+01	7.90E-04	Down	-2.56E+00	2.72E-02		2.27E+00	3.05E-01		8.59E-01	7.93E-01		-2.02E+00	3.67E-01		-1.09E+00	5.52E-01				Unigene59818_All//8.00E-72//TC175801				
Unigene5982_All	1145	0.69	0.44	1.26	1.17	0.63	0.91	33.75	10.77	4.31	-6.31E-01	4.08E-01		8.74E-01	1.38E-01		-8.95E-01	1.07E-01		-3.73E-01	5.53E-01		-1.65E+00	2.98E-74	Down	-2.97E+00	2.82E-158	Down	Unigene5982_All//gi|15230177|ref|NP_191256.1|//3.00E-35//BHLH038; DNA binding / transcription factor [Arabidopsis thaliana] >gi|75311784|sp|Q9MUK1.1|ORG2_ARATH RecName: Full=Transcription factor ORG2; AltName: Full=Transcription factor EN 8; AltName: Full=OBP3-responsive gene 2; AltName: Full=bHLH transcription factor bHLH038; AltName: Full=Basic helix-loop-helix protein 38; Short=bHLH 38; Short=AtbHLH38 >gi|11074306|gb|AH004526.1|At3g56970 [Arabidopsis thaliana]	Unigene5982_All//3.00E-34//AT3G56970| BHLH038; DNA binding / transcription factor	Unigene5982_All//9.00E-08//ES844541	bHLH		GO:0005488//GO:0006950//GO:0010468	nr +
Unigene59826_All	205	9.44	0.49	0.52	1.46	0.84	0.66	0.21	0.00	0.58	-4.26E+00	6.09E-09	Down	-4.18E+00	2.32E-08	Down	-7.96E-01	5.57E-01		-1.14E+00	4.57E-01		-7.69E+00	6.53E-01		1.50E+00	5.57E-01				Unigene59826_All//3.00E-16//DW501342				
Unigene59853_All	207	18.20	7.59	15.43	5.78	4.99	5.24	1.84	0.40	0.38	-1.26E+00	1.06E-04	Down	-2.38E-01	4.93E-01		-2.11E-01	7.52E-01		-1.41E-01	8.16E-01		-2.19E+00	8.75E-02		-2.26E+00	6.49E-02		Unigene59853_All//gi|295684201|gb|ADG27450.1|//1.00E-32//ADP glucose pyrophosphorylase small subunit 1-like protein [Malus x domestica]	Unigene59853_All//5.00E-34//AT5G48300| ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE 1); glucose-1-phosphate adenylyltransferase	Unigene59853_All//2.00E-106//TC163706		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0005977//GO:0005982//GO:0009536//GO:0032559//GO:0070566	nr +
Unigene59858_All	207	22.24	93.02	44.76	121.29	143.40	200.51	70.88	91.26	74.29	2.06E+00	4.13E-41	Up	1.01E+00	3.93E-07	Up	2.42E-01	1.51E-02		7.25E-01	5.17E-19		3.65E-01	1.44E-03		6.79E-02	6.47E-01		Unigene59858_All//gi|55419648|gb|AV51937.1|//3.00E-33//AP2/EREBP transcription factor ERF-2 [Gossypium hirsutum]	Unigene59858_All//2.00E-21//AT2G47520| AP2 domain-containing transcription factor, putative	Unigene59858_All//1.00E-113//EX164257	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene59860_All	207	6.82	0.73	0.26	16.85	7.82	1.96	72.92	5.05	7.70	-3.22E+00	1.60E-05	Down	-4.73E+00	1.31E-06	Down	-1.11E+00	3.44E-04	Down	-3.10E+00	3.05E-13	Down	-3.85E+00	5.86E-76	Down	-3.24E+00	8.13E-68	Down			Unigene59860_All//2.00E-88//gi|21094474|gb|BQ406799.1|BQ406799				
Unigene59867_All	207	96.30	115.05	176.99	368.19	512.37	975.27	203.64	193.43	268.67	2.57E-01	2.65E-02		8.78E-01	5.64E-21		4.77E-01	3.62E-25		1.41E+00	4.65E-267	Up	-7.42E-02	3.97E-01		4.00E-01	1.05E-10		Unigene59867_All//gi|164668308|gb|ABK60195.2|//5.00E-27//PIP2 protein [Gossypium hirsutum]	Unigene59867_All//3.00E-24//AT2G37170| PIP2B (PLASMA MEMBRANE INTRINSIC PROTEIN 2); water channel	Unigene59867_All//7.00E-97//gi|109826108|gb|DW224829.1|DW224829			GO:0006810//GO:0031224	nr -
Unigene5987_All	1159	1.35	3.50	2.25	2.02	2.38	2.30	3.87	4.18	2.06	1.37E+00	1.62E-05	Up	7.33E-01	7.42E-02		2.35E-01	5.86E-01		1.87E-01	6.73E-01		1.13E-01	6.72E-01		-9.07E-01	2.60E-04				Unigene5987_All//0.00E+00//gi|164323615|gb|ES846589.1|ES846589				
Unigene5988_All	858	6.65	19.78	18.18	6.10	13.00	9.11	0.99	1.66	2.46	1.57E+00	3.19E-25	Up	1.45E+00	4.90E-20	Up	1.09E+00	2.76E-11	Up	5.79E-01	5.21E-03		7.49E-01	1.39E-01		1.32E+00	8.64E-04	Up			Unigene5988_All//0.00E+00//CO094519				
Unigene5989_All	787	5.19	4.76	1.83	8.23	5.29	10.90	10.85	10.52	5.16	-1.22E-01	6.81E-01		-1.51E+00	5.79E-06	Down	-6.36E-01	3.40E-03		4.06E-01	4.55E-02		-4.55E-02	8.23E-01		-1.07E+00	1.70E-09	Down	Unigene5989_All//gi|297719947|ref|NP_00117235.1|//1.00E-18//Os01g0362000 [Oryza sativa Japonica Group] >gi|255673224|dbj|BAH91065.1|Os01g0362000 [Oryza sativa Japonica Group]	Unigene5989_All//5.00E-75//AT5G58920| unknown protein	Unigene5989_All//0.00E+00//DW517828			GO:0043231	nr +
Unigene59897_All	208	4.02	0.00	2.82	0.72	0.50	0.00	0.00	0.40	0.00	-1.20E+01	5.56E-05	Down	-5.15E-01	5.15E-01		-5.33E-01	7.84E-01		-9.49E+00	2.32E-01		8.65E+00	4.00E-01		null	null				Unigene59897_All//3.00E-102//TC159638				
Unigene599_All	1380	0.91	0.70	1.27	2.09	1.27	1.41	17.52	4.18	4.73	-3.83E-01	5.26E-01		4.85E-01	3.60E-01		-7.18E-01	4.16E-02		-5.73E-01	1.32E-01		-2.07E+00	1.86E-63	Down	-1.89E+00	4.54E-58	Down	Unigene599_All//gi|60657590|gb|AAX33316.1|//1.00E-179//secondary cell wall-related glycosyltransferase family 8 [Populus tremula x Populus tremuloides]	Unigene599_All//1.00E-144//AT1G77130| PGSIP2 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 2); transferase, transferring glycosyl groups	Unigene599_All//0.00E+00//gi|48821837|gb|CO123150.1|CO123150				nr +
Unigene5990_All	600	1.22	2.20	1.69	7.14	2.87	5.19	1.41	1.18	1.86	8.47E-01	1.46E-01		4.66E-01	5.11E-01		-1.32E+00	2.17E-06	Down	-4.59E-01	1.34E-01		-2.51E-01	7.13E-01		4.00E-01	4.88E-01									
Unigene5991_All	574	1.46	6.36	0.56	1.56	2.10	5.67	0.00	0.00	0.00	2.12E+00	1.28E-08	Up	-1.39E+00	9.66E-02		4.27E-01	5.52E-01		1.86E+00	6.66E-07	Up	null	null		null	null		Unigene5991_All//gi|144925078|gb|ABP03876.1|//2.00E-55//Hly-III related proteins [Medicago truncatula]	Unigene5991_All//1.00E-41//AT5G20270| HHP1 (HEPTAHELICAL TRANSMEMBRANE PROTEIN1); receptor	Unigene5991_All//2.00E-152//DW226877			GO:0004871//GO:0006970//GO:0009719//GO:0031224//GO:0034285	nr -
Unigene59928_All	209	22.03	58.91	11.97	25.50	52.23	61.80	58.06	44.60	61.00	1.42E+00	5.56E-16	Up	-8.79E-01	2.78E-03		1.03E+00	3.76E-10	Up	1.28E+00	3.38E-15	Up	-3.81E-01	9.75E-03		7.12E-02	6.42E-01				Unigene59928_All//3.00E-93//gi|109826680|gb|DW225390.1|DW225390				
Unigene5994_All	577	0.54	0.97	0.74	0.60	2.63	3.37	2.71	4.71	3.45	8.28E-01	3.81E-01		4.40E-01	6.77E-01		2.12E+00	3.26E-04	Up	2.48E+00	6.11E-06	Up	7.96E-01	1.97E-02		3.49E-01	4.00E-01		Unigene5994_All//gi|257219548|gb|ACV50427.1|//4.00E-63//profilin-like protein [Jatropha curcas]	Unigene5994_All//1.00E-43//AT2G19770| PRF5 (PROFILIN5); actin binding / actin monomer binding	Unigene5994_All//3.00E-43//gi|11201167|gb|BF270172.1|BF270172			GO:0005856//GO:0007010//GO:0008092	nr +
Unigene59953_All	210	9.22	9.65	7.86	3.56	4.59	3.23	4.43	14.73	2.09	6.62E-02	8.88E-01		-2.30E-01	6.13E-01		3.68E-01	6.24E-01		-1.41E-01	8.59E-01		1.73E+00	4.69E-07	Up	-1.09E+00	8.05E-02				Unigene59953_All//2.00E-35//EX171751				
Unigene59967_All	211	5.95	0.96	1.77	3.07	2.94	0.64	0.00	0.00	0.00	-2.63E+00	3.16E-04	Down	-1.75E+00	9.85E-03		-6.32E-02	9.25E-01		-2.26E+00	2.76E-02		null	null		null	null		Unigene59967_All//gi|6959488|gb|AAF53112.1|AF181883.1|//2.00E-09//RPT2 [Arabidopsis thaliana]	Unigene59967_All//6.00E-11//AT2G30520| RPT2 (ROOT PHOTOTROPISM 2); protein binding	Unigene59967_All//6.00E-51//EX167128				nr -
Unigene5997_All	1136	29.52	0.62	3.75	27.58	2.49	2.31	13.29	3.72	10.10	-5.56E+00	5.59E-172	Down	-2.98E+00	1.50E-105	Down	-3.47E+00	3.53E-152	Down	-3.58E+00	9.63E-133	Down	-1.84E+00	3.36E-34	Down	-3.96E-01	1.62E-03		Unigene5997_All//gi|15234627|ref|NP_193918.1|//3.00E-26//26.5 kDa class P-related heat shock protein (HSP26.5-P) [Arabidopsis thaliana] >gi|75278048|sp|Q49710.1|HS154_ARATH RecName: Full=15.4 kDa class V heat shock protein; AltName: Full=15.4 kDa heat shock protein; Short=AtHsp15.4 >gi|2894565|emb|CAA17154.1| heat shock protein - like [Arabidopsis thaliana] >gi|7269032|emb|CAB79142.1| heat shock protein-like [Arabidopsis thaliana] >gi|21592394|gb|AAM64345.1| heat shock protein-like [Arabidopsis thaliana] >gi|98961073|gb|ABF59020.1|At4g21870 [Arabidopsis thaliana]	Unigene5997_All//6.00E-27//AT4G21870| 26.5 kDa class P-related heat shock protein (HSP26.5-P)	Unigene5997_All//0.00E+00//ES815751			GO:0006950	nr +
Unigene59988_All	212	3.70	1.91	0.00	0.47	0.65	0.43	0.20	0.39	0.00	-9.53E-01	2.33E-01		-1.19E+01	2.21E-04	Down	4.67E-01	8.76E-01		-1.41E-01	9.49E-01		9.84E-01	7.30E-01		-7.64E+00	6.09E-01		Unigene59988_All//gi|115444975|ref|NP_001046267.1|//2.00E-11//Os02g0210700 [Oryza sativa Japonica Group] >gi|113535798|dbj|BAF08181.1|Os02g0210700 [Oryza sativa Japonica Group]	Unigene59988_All//3.00E-12//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction//ko00270|Cysteine and methionine metabolism		nr -
Unigene6_All	2087	8.12	3.06	7.45	11.60	13.48	7.88	5.00	0.90	2.65	-1.41E+00	1.31E-21	Down	-1.25E-01	4.16E-01		2.17E-01	3.94E-02		-5.58E-01	2.00E-07		-2.47E+00	1.85E-34	Down	-9.15E-01	5.38E-09		Unigene6_All//gi|15231259|ref|NP_190171.1|//0.00E+00//kinesin motor protein-related [Arabidopsis thaliana] >gi|7339486|emb|CAB82809.1| kinesin-related protein-like [Arabidopsis thaliana]	Unigene6_All//0.00E+00//AT3G45850| kinesin motor protein-related	Unigene6_All//0.00E+00//ES793376				nr +

Unigene6000_All	1144	1.23	2.88	1.16	2.79	5.63	2.49	0.07	0.07	0.35	1.22E+00	5.05E-04	Up	-8.56E-02	8.81E-01		1.01E+00	5.17E-06	Up	-1.64E-01	6.79E-01		-1.57E-02	1.01E+00		2.24E+00	6.42E-02		Unigene6000_All//gi|18411126|ref|NP_565133.1|//3.00E-86//auxin efflux carrier family protein [Arabidopsis thaliana] >gi|30699180|ref|NP_849892.1| auxin efflux carrier family protein [Arabidopsis thaliana]	Unigene6000_All//1.00E-87//AT1G76520| auxin efflux carrier family protein	Unigene6000_All//0.00E+00//ES841787			GO:0006810//GO:0016020//GO:0031410	nr -
Unigene6001_All	472	19.18	94.15	28.66	36.31	53.40	65.83	49.72	85.01	52.16	2.30E+00	1.75E-107	Up	5.80E-01	2.50E-04		5.57E-01	3.19E-08		8.59E-01	4.99E-19		7.74E-01	1.57E-23		6.93E-02	5.58E-01		Unigene6001_All//gi|254681442|gb|ACT78956.1|//2.00E-21//zinc finger protein [Gossypium arboreum]	Unigene6001_All//2.00E-19//AT1G51200| zinc finger (AN1-like) family protein	Unigene6001_All//0.00E+00//gi|21094763|gb|BQ407076.1|BQ407076			GO:0003676//GO:0043231//GO:0046914	nr +
Unigene6002_All	485	37.43	32.49	59.95	29.27	48.99	35.85	4.53	1.47	1.31	-2.04E-01	1.37E-01		6.79E-01	5.49E-11		7.43E-01	1.33E-12		2.93E-01	3.46E-02		-1.63E+00	7.07E-05	Down	-1.79E+00	1.17E-05	Down	Unigene6002_All//gi|87203076|gb|AB032234.1|//4.00E-34//Calcium-binding EF-hand [Medicago truncatula]	Unigene6002_All//4.00E-30//AT4G27280| calcium-binding EF hand family protein	Unigene6002_All//0.00E+00//TC152910			GO:0046872	nr +
Unigene6003_All	1108	0.80	1.01	1.15	7.82	6.84	2.89	1.95	0.57	0.50	3.26E-01	5.98E-01		5.23E-01	3.98E-01		-1.94E-01	3.79E-01		-1.43E+00	1.74E-12	Down	-1.78E+00	2.50E-05	Down	-1.95E+00	3.72E-06	Down	Unigene6003_All//gi|297816804|ref|XP_002876285.1|//1.00E-152//pectate lyase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297322123|gb|EFH52544.1| pectate lyase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6003_All//3.00E-146//AT3G55140| pectate lyase family protein	Unigene6003_All//0.00E+00//gi|78342616|gb|DT562890.1|DT562890		ko00040|Pentose and glucuronate interconversions		nr +
Unigene60030_All	215	0.73	0.00	0.00	3.24	0.16	0.42	0.39	0.19	0.74	-9.51E+00	2.14E-01		-9.51E+00	2.43E-01		-4.34E+00	2.79E-04	Down	-2.95E+00	5.83E-03		-1.02E+00	7.23E-01		9.14E-01	6.24E-01								
Unigene60035_All	215	71.06	42.89	51.27	107.51	100.90	118.48	110.72	41.60	43.36	-7.28E-01	3.78E-07		-4.71E-01	1.54E-03		-9.14E-02	5.22E-01		1.40E-01	2.63E-01		-1.41E+00	8.15E-37	Down	-1.35E+00	1.45E-35	Down	Unigene60035_All//gi|211947579|gb|ACJ13546.1|//4.00E-13//cytoplasmic ribosomal protein L2 [Bupleurum chinense]	Unigene60035_All//4.00E-14//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene60035_All//4.00E-77//gi|78331172|gb|DT551446.1|DT551446		ko03010|Ribosome		nr -
Unigene6004_All	1433	0.22	0.00	0.22	0.70	0.41	2.33	27.73	5.63	37.53	-7.78E+00	3.64E-02		2.55E-02	1.00E+00		-7.67E-01	2.60E-01		1.75E+00	1.48E-06	Up	-2.30E+00	1.12E-118	Down	4.36E-01	4.74E-12		Unigene6004_All//gi|297597194|ref|NP_001043519.2|//1.00E-45//Os01g0611000 [Oryza sativa Japonica Group] >gi|255673458|dbj|BAF05463.2| Os01g0611000 [Oryza sativa Japonica Group]	Unigene6004_All//1.00E-108//AT5G14150| unknown protein	Unigene6004_All//1.00E-87//CK640457				nr +
Unigene60045_All	215	5.11	0.24	0.25	0.00	0.00	0.00	0.00	0.00	0.00	-4.44E+00	2.09E-05	Down	-4.37E+00	4.94E-05	Down	null	null		null	null		null	null		null	null									
Unigene60051_All	215	0.73	0.94	0.50	44.25	29.47	28.78	368.72	84.76	291.47	3.69E-01	8.16E-01		-5.60E-01	7.75E-01		-5.87E-01	7.23E-04		-6.21E-01	6.67E-04		-2.12E+00	1.92E-213	Down	-3.39E-01	3.33E-11		Unigene60051_All//gi|791146|emb|CAA60020.1|//1.00E-29//extensin-like protein [Vigna unguiculata]		Unigene60051_All//7.00E-97//ES813279		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism/ko00565|Ether lipid metabolism		nr +
Unigene60056_All	216	21.80	4.46	26.63	10.84	4.62	0.84	0.39	0.00	0.00	-2.29E+00	5.21E-12	Down	2.88E-01	2.90E-01		-1.23E+00	1.83E-03		-3.70E+00	1.91E-10	Down	-8.61E+00	4.01E-01		-8.61E+00	3.57E-01				Unigene60056_All//5.00E-30//TC172737				
Unigene60059_All	216	43.12	59.82	61.14	114.39	90.07	103.29	22.51	46.83	26.01	4.72E-01	2.69E-03		5.04E-01	1.76E-03		-3.45E-01	8.99E-04		-1.47E-01	2.38E-01		1.06E+00	1.74E-10	Up	2.08E-01	3.79E-01				Unigene60059_All//1.00E-43//gi|84174084|gb|DR462732.1|DR462732				
Unigene6007_All	503	46.08	59.94	51.13	45.06	59.08	54.05	75.06	42.46	32.16	3.79E-01	1.18E-04		1.50E-01	2.30E-01		3.91E-01	2.71E-05		2.63E-01	1.43E-02		-8.22E-01	1.49E-24		-1.22E+00	6.50E-48	Down	Unigene6007_All//gi|226531203|ref|NP_001149476.1|//2.00E-52//vacuolar ATP synthase subunit F [Zea mays] >gi|195627436|gb|ACG35548.1| vacuolar ATP synthase subunit F [Zea mays]	Unigene6007_All//8.00E-51//AT4G02620| vacuolar ATPase subunit F family protein	Unigene6007_All//0.00E+00//TC173523		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0006754//GO:0015078//GO:0019829//GO:0033176//GO:0043231	nr -
Unigene6009_All	941	0.39	1.94	0.85	2.75	1.46	2.26	1.26	0.89	1.10	2.32E+00	4.22E-05	Up	1.12E+00	1.80E-01		-9.11E-01	1.40E-02		-2.87E-01	5.03E-01		-5.02E-01	3.95E-01		-1.93E-01	7.12E-01		Unigene6009_All//gi|223452528|gb|ACM89591.1|//4.00E-57//leucine-rich repeat family protein / protein kinase family protein [Glycine max]	Unigene6009_All//1.00E-42//AT5G46330| FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / kinase/ protein binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr +
Unigene60091_All	217	25.08	3.50	27.97	1.38	0.63	0.00	0.00	0.00	0.00	-2.84E+00	2.23E-17	Down	1.58E-01	5.71E-01		-1.12E+00	4.24E-01		-1.04E+01	3.98E-02		null	null		null	null				Unigene60091_All//3.00E-10//gi|109890889|gb|DW519852.1|DW519852				
Unigene601_All	471	0.11	1.94	0.23	2.01	2.71	7.38	1.97	15.88	8.80	4.12E+00	2.34E-04	Up	1.03E+00	7.02E-01		4.29E-01	5.32E-01		1.88E+00	1.97E-07	Up	3.01E+00	1.83E-30	Up	2.16E+00	2.65E-12	Up	Unigene601_All//gi|30697982|ref|NP_568988.2|//9.00E-14//2-nitropropane dioxygenase family / NPD family [Arabidopsis thaliana] >gi|9759401|dbj|BAB09856.1| 2-nitropropane dioxygenase-like protein [Arabidopsis thaliana]	Unigene601_All//8.00E-14//AT5G64250| 2-nitropropane dioxygenase family / NPD family	Unigene601_All//2.00E-120//gi|31406595|gb|CD485630.1|CD485630			GO:0008152//GO:0009608//GO:0010038//GO:0016703	nr +
Unigene6010_All	575	11.65	30.93	16.67	5.63	10.72	9.03	12.72	21.73	20.51	1.41E+00	1.59E-22	Up	5.17E-01	7.48E-03		9.29E-01	4.45E-05		6.82E-01	9.35E-03		7.73E-01	7.10E-08		6.89E-01	1.80E-06		Unigene6010_All//gi|229609825|gb|ACQ83528.1|//2.00E-28//CBL-interacting protein kinase 12 [Vitis vinifera]	Unigene6010_All//2.00E-27//AT1G01140| CIPK9 (CBL-INTERACTING PROTEIN KINASE 9); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene6010_All//0.00E+00//TC176460		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0006813//GO:0006970//GO:0009267//GO:0009743//GO:0009755//GO:0023060//GO:0032559//GO:0043231	nr -
Unigene6011_All	818	1.28	56.43	7.88	5.36	5.81	6.79	5.22	18.60	15.15	5.46E+00	7.01E-232	Up	2.62E+00	4.51E-18	Up	1.16E-01	7.44E-01		3.42E-01	2.14E-01		1.83E+00	2.97E-34	Up	1.54E+00	1.60E-22	Up	Unigene6011_All//gi|111074300|gb|AB804523.1|//4.00E-34//At3g27880 [Arabidopsis thaliana]	Unigene6011_All//1.00E-25//AT3G27880| unknown protein	Unigene6011_All//0.00E+00//TC146528				nr +
Unigene6012_All	1093	2.68	0.97	1.41	3.24	3.28	3.22	4.84	3.25	3.57	-1.46E+00	1.38E-04	Down	-9.24E-01	1.59E-02		1.80E-02	9.65E-01		-5.80E-03	9.82E-01		-5.73E-01	1.37E-02		-4.37E-01	5.48E-02		Unigene6012_All//gi|20197674|gb|AAM15195.1|//6.00E-19//Expressed protein [Arabidopsis thaliana]	Unigene6012_All//3.00E-20//AT2G27285| unknown protein	Unigene6012_All//7.00E-175//gi|21097108|gb|BQ409421.1|BQ409421				nr -
Unigene60120_All	219	2.87	0.00	0.49	0.68	0.00	0.00	0.00	0.00	0.00	-1.15E+01	7.90E-04	Down	-2.56E+00	2.72E-02		-9.41E+00	1.65E-01		-9.41E+00	2.32E-01		null	null		null	null									
Unigene60126_All	219	2.15	0.23	0.00	0.45	0.63	0.00	3.67	0.38	2.36	-3.22E+00	2.73E-02		-1.11E+01	8.62E-03		4.68E-01	8.76E-01		-8.83E+00	3.97E-01		-3.26E+00	4.48E-04	Down	-6.33E-01	3.56E-01				Unigene60126_All//5.00E-104//CO093589				
Unigene60127_All	219	16.25	5.09	10.70	2.50	2.20	6.19	0.00	0.38	0.00	-1.67E+00	2.16E-06	Down	-6.03E-01	7.90E-02		-1.85E-01	8.25E-01		1.31E+00	2.93E-02		8.58E+00	4.00E-01		null	null									
Unigene6013_All	2273	0.64	1.94	0.14	0.09	0.61	0.62	0.69	3.60	6.64	1.59E+00	3.43E-07	Up	-2.20E+00	7.90E-04	Down	2.79E+00	4.76E-05	Up	2.81E+00	5.55E-05	Up	2.39E+00	4.81E-26	Up	3.27E+00	4.05E-67	Up	Unigene6013_All//gi|297832096|ref|XP_002883930.1|//0.00E+00//phox domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297329770|gb|EFH60189.1| phox domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene6013_All//1.00E-161//AT2G15900| phox (PX) domain-containing protein	Unigene6013_All//0.00E+00//TC175189				nr -
Unigene60135_All	220	4.52	0.00	2.66	0.00	1.25	0.00	0.00	0.00	0.00	-1.21E+01	7.45E-06	Down	-7.63E-01	2.94E-01		1.03E+01	7.00E-02		null	null		null	null		null	null		Unigene60135_All//gi|60327214|gb|AAV19030.1|//7.00E-15//Hcr2-gT.1 [Solanum pimpinellifolium]	Unigene60135_All//4.00E-15//AT1G35710| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction		nr -
Unigene60141_All	220	5.23	6.45	3.39	9.51	6.73	6.77	4.23	8.17	14.31	3.02E-01	6.11E-01		-6.27E-01	3.56E-01		-4.99E-01	2.71E-01		-4.89E-01	3.03E-01		9.50E-01	2.97E-02		1.76E+00	1.69E-07	Up			Unigene60141_All//3.00E-71//ES841444				
Unigene6015_All	762	18.20	16.82	18.80	8.63	8.09	5.33	2.39	1.43	0.42	-1.13E-01	5.04E-01		4.70E-02	7.75E-01		-9.32E-02	7.44E-01		-6.94E-01	2.11E-03		-7.43E-01	8.75E-02		-2.51E+00	6.12E-07	Down	Unigene6015_All//gi|283970968|gb|ADB54810.1|//8.00E-43//universal stress protein 23267 [Hordeum vulgare subsp. vulgare]	Unigene6015_All//1.00E-36//AT1G68300| universal stress protein (USP) family protein	Unigene6015_All//0.00E+00//gi|109885500|gb|DW514470.1|DW514470			GO:0050896	nr -
Unigene60153_All	220	0.48	2.53	0.00	2.04	2.19	6.77	0.58	4.94	1.09	2.41E+00	3.93E-02		-8.89E+00	3.89E-01		1.05E-01	9.54E-01		1.73E+00	2.99E-03		3.10E+00	4.52E-05	Up	9.14E-01	5.41E-01		Unigene60153_All//gi|87162727|gb|ABD28522.1|//9.00E-13//Cupin, RmlC-type [Medicago truncatula]	Unigene60153_All//1.00E-12//AT5G38890| unknown protein	Unigene60153_All//7.00E-57//gi|109853606|gb|DW482585.1|DW482585				nr +
Unigene60158_All	221	4.97	0.69	2.65	0.45	0.00	0.00	0.00	0.00	0.00	-2.85E+00	4.76E-04	Down	-9.08E-01	1.87E-01		-8.82E+00	3.11E-01		-8.82E+00	3.97E-01		null	null		null	null				Unigene60158_All//9.00E-35//TC147907				
Unigene6016_All	824	2.35	0.80	0.71	2.12	2.17	1.10	3.44	2.54	2.32	-1.56E+00	1.54E-03		-1.72E+00	9.79E-04	Down	3.85E-02	9.50E-01		-9.49E-01	5.79E-02		-4.39E-01	2.07E-01		-5.67E-01	7.83E-02				Unigene6016_All//1.00E-101//DW518462				
Unigene60161_All	221	2.84	0.00	3.37	4.51	1.25	0.82	0.38	0.00	0.00	-1.15E+01	7.90E-04	Down	2.48E-01	7.45E-01		-1.85E+00	7.41E-03		-2.46E+00	2.07E-03		-8.58E+00	4.01E-01		-8.58E+00	3.57E-01		Unigene60161_All//gi|8409781|ref|NP_565014.1|//4.00E-11//6-phosphogluconate dehydrogenase NAD-binding domain-containing protein [Arabidopsis thaliana]	Unigene60161_All//1.00E-12//AT1G71180| 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein	Unigene60161_All//5.00E-67//gi|78333770|gb|DT554044.1|DT554044		ko00280|Valine, leucine and isoleucine degradation		nr +
Unigene6017_All	504	14.64	40.31	20.81	7.51	11.14	17.29	7.13	17.50	17.31	1.46E+00	4.93E-27	Up	5.08E-01	5.74E-03		5.68E-01	2.11E-02		1.20E+00	1.44E-09	Up	1.30E+00	1.83E-12	Up	1.28E+00	1.95E-12	Up	Unigene6017_All//gi|115462411|ref|NP_001054805.1|//7.00E-20//Os05g0179800 [Oryza sativa Japonica Group] >gi|57906680|gb|AAK57805.1| unknow protein [Oryza sativa Japonica Group] >gi|113578356|dbj|BAF16719.1| Os05g0179800 [Oryza sativa Japonica Group]		Unigene6017_All//0.00E+00//gi|109869816|gb|DW498792.1|DW498792				nr -
Unigene60170_All	221	4.73	1.83	0.48	0.45	0.62	0.00	0.38	0.38	0.00	-1.37E+00	4.74E-02		-3.30E+00	4.58E-04	Down	4.67E-01	8.76E-01		-8.82E+00	3.97E-01		-1.67E-02	1.01E+00		-8.58E+00	3.57E-01		Unigene60170_All//gi|38605925|emb|CAD40793.3|//5.00E-07//OSJNB0076422.4 [Oryza sativa (japonica cultivar-group)]	Unigene60170_All//2.00E-07//AT5G37450| leucine-rich repeat transmembrane protein kinase, putative					nr -
Unigene60176_All	222	4.01	0.46	3.12	3.37	2.64	4.07	8.19	2.82	1.97	-3.13E+00	1.19E-03		-3.62E-01	6.32E-01		-3.52E-01	6.51E-01		2.74E-01	7.10E-01		-1.54E+00	6.84E-04	Down	-2.05E+00	1.27E-05	Down			Unigene60176_All//7.00E-48//gi|109869139|gb|DW498115.1|DW498115				
Unigene6018_All	513	3.06	3.46	3.32	4.27	3.89	3.96	2.06	1.39	4.74	1.76E-01	7.07E-01		1.19E-01	8.07E-01		-1.34E-01	7.95E-01		-1.09E-01	8.04E-01		-5.73E-01	3.60E-01		1.20E+00	8.90E-04	Up	Unigene6018_All//gi|224101095|ref|XP_002312140.1|//1.00E-15//f-box family protein [Populus trichocarpa] >gi|222851960|gb|EEE89507.1| f-box family protein [Populus trichocarpa]	Unigene6018_All//8.00E-12//AT2G39940| COI1 (CORONATINE INSENSITIVE 1); protein binding / ubiquitin-protein ligase	Unigene6018_All//1.00E-88//TC154854		ko04626|Plant-pathogen interaction	GO:0005488//GO:0006952//GO:0009611//GO:0009639//GO:0009719//GO:0009908//GO:0019787//GO:0023033//GO:0031461//GO:0043161//GO:0051707	nr +
Unigene6019_All	311	13.80	3.91	11.81	19.54	15.61	24.25	17.54	8.20	6.92	-1.82E+00	2.27E-08	Down	-2.24E-01	4.89E-01		-3.24E-01	1.93E-01		3.12E-01	1.76E-01		-1.10E+00	2.34E-06	Down	-1.34E+00	9.90E-09	Down	Unigene6019_All//gi|115452749|ref|NP_001049975.1|//2.00E-10//Os03g0323800 [Oryza sativa Japonica Group] >gi|113548446|dbj|BAF11889.1| Os03g0323800 [Oryza sativa Japonica Group]	Unigene6019_All//2.00E-10//AT3G20000| TOM40; P-P-bond-hydrolysis-driven protein transmembrane transporter/ voltage-gated anion channel	Unigene6019_All//1.00E-167//BQ408856			GO:0005244//GO:0005488//GO:0005741//GO:0006605//GO:0008320//GO:0019866	nr +
Unigene602_All	2949	15.84	67.80	23.76	21.55	39.28	178.92	114.97	457.53	286.07	2.10E+00	0.00E+00	Up	5.85E-01	9.61E-20		8.66E-01	4.46E-78		3.05E+00	0.00E+00	Up	1.99E+00	0.00E+00	Up	1.32E+00	0.00E+00	Up	Unigene602_All//gi|296012006|gb|ADG65641.1|//1.00E-157//glycosyltransferase [Withania somnifera]	Unigene602_All//1.00E-146//AT5G64250| 2-nitropropane dioxygenase family / NPD family	Unigene602_All//0.00E+00//TC151235		ko00460|Cyanoamino acid metabolism/ko00061|Fatty acid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0035251	nr +
Unigene6020_All	802	3.65	3.29	9.43	7.52	4.94	3.49	6.70	3.28	0.55	-1.53E-01	6.68E-01		1.37E+00	3.29E-09	Up	-6.06E-01	7.86E-03		-1.11E+00	3.95E-06	Down	-1.03E+00	1.01E-05	Down	-3.62E+00	5.94E-27	Down			Unigene6020_All//2.00E-78//gi|13353374|gb|BG443722.1|BG443722				
Unigene6021_All	287	24.79	24.01	37.11	51.55	50.51	65.31	78.52	59.13	39.14	-4.63E-02	8.41E-01		5.82E-01	1.32E-03		-2.93E-02	8.61E-01		3.41E-01	8.31E-03		-4.09E-01	6.97E-05		-1.00E+00	2.67E-21	Down			Unigene6021_All//1.00E-123//gi|78339886|gb|DT560160.1|DT560160				ESTscan -
Unigene60210_All	224	15.18	14.70	12.60	9.56	4.30	2.42	0.00	0.00	0.36	-4.63E-02	8.98E-01		-2.69E-01	4.53E-01		-1.15E+00	5.55E-03		-1.98E+00	3.06E-05	Down	null	null		8.47E+00	4.03E-01				Unigene60210_All//4.00E-09//CO097901				
Unigene6022_All	364	13.94	16.84	20.04	26.41	23.84	24.69	30.90	24.80	14.78	2.73E-01	2.78E-01		5.24E-01	2.11E-02		-1.48E-01	5.01E-01		-9.72E-02	6.62E-01		-3.17E-01	4.32E-02		-1.06E+00	4.27E-12	Down	Unigene6022_All//gi|87240819|gb|ABD32677.1|//6.00E-17//Like-Sm ribonucleoprotein-related, core [Medicago truncatula]	Unigene6022_All//5.00E-18//AT3G11500| small nuclear ribonucleoprotein G, putative / snRNP-G, putative / Sm protein G, putative	Unigene6022_All//4.00E-112//TC141549		ko03040|Spliceosome	GO:0005488//GO:0030529//GO:0031981	nr +
Unigene6023_All	394	87.91	47.97	76.09	107.09	83.90	183.52	81.45	45.93	37.72	-8.74E-01	1.71E-20		-2.08E-01	3.73E-02		-3.52E-01	3.36E-06		7.77E-01	8.04E-37		-8.26E-01	3.53E-21		-1.11E+00	3.72E-35	Down	Unigene6023_All//gi|38564733|gb|AAR23806.1|//2.00E-19//initiation factor eIF4A-15 [Helianthus annuus]	Unigene6023_All//1.00E-15//AT3G13920| EIF4A1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 4A1); ATP-dependent helicase/ translation initiation factor	Unigene6023_All//0.00E+00//gi|13247579|gb|BF271156.2|BF271156			GO:0008135//GO:0010467//GO:0032559//GO:0042623	nr +
Unigene6024_All	407	1.41	31.25	5.50	0.98	2.62	5.55	9.14	27.21	51.00	4.47E+00	1.64E-57	Up	1.96E+00	7.33E-05	Up	1.42E+00	4.05E-02		2.50E+00	6.84E-07	Up	1.57E+00	1.98E-20	Up	2.48E+00	3.81E-69	Up			Unigene6024_All//3.00E-113//TC171569				
Unigene6025_All	441	52.56	13.10	23.30	84.27	69.73	64.21	51.39	36.11	30.71	-2.00E+00	7.13E-48	Down	-1.17E+00	2.53E-21	Down	-2.73E-01	1.14E-03		-3.92E-01	4.33E-06		-5.09E-01	6.42E-07		-7.43E-01	3.55E-13		Unigene6025_All//gi|224107417|ref|XP_002314474.1|//6.00E-25//dehydroquinate dehydratase/ shikimate dehydrogenase [Populus trichocarpa] >gi|222863514|gb|EEF00645.1| dehydroquinate dehydratase/ shikimate dehydrogenase [Populus trichocarpa]	Unigene6025_All//7.00E-24//AT3G06350| MEE32 (MATERNAL EFFECT EMBRYO ARREST 32); 3-dehydroquinate dehydratase/ NADP or NADPH binding / binding / catalytic/ shikimate 5-dehydrogenase	Unigene6025_All//0.00E+00//TC152499		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0000166//GO:0003006//GO:0008652//GO:0009532//GO:0016616//GO:0016836	nr -
Unigene60254_All	226	24.08	11.88	20.50	1.32	1.22	3.80	0.00	0.18	0.18	-1.02E+00	8.35E-05	Down	-2.32E-01	3.98E-01		-1.18E-01	9.00E-01		1.52E+00	6.17E-02		7.53E+00	6.31E-01		7.46E+00	6.42E-01				Unigene60254_All//4.00E-09//EX169608				
Unigene6026_All	357	36.64	18.31	27.30	87.91	86.72	88.30	62.30	21.07	41.07	-1.00E+00	4.03E-10	Down	-4.25E-01	9.48E-03		-1.97E-02	8.66E-01		6.50E-03	9.50E-01		-1.56E+00	5.91E-40	Down	-6.01E-01	3.39E-09		Unigene6026_All//gi|152963813|gb|ABS50234.1|//4.00E-26//Ran binding protein [Nicotiana benthamiana]	Unigene6026_All//1.00E-22//AT1G07140| SIRANBP; Ran GTPase binding	Unigene6026_All//2.00E-160//gi|50496642|gb|AI730790.1|AI730790			GO:0006606//GO:0017016	nr +
Unigene60262_All	227	3.23	1.12	0.00	0.22	0.76	0.40	0.37	0.37	0.53	-1.53E+00	7.78E-02		-1.17E+01	4.13E-04	Down	1.79E+00	5.20E-01		8.59E-01	7.93E-01		-1.68E-02	1.01E+00		4.99E-01	8.07E-01				Unigene60262_All//3.00E-102//CO120215				
Unigene60269_All	227	4.84	2.90	5.63	5.71	9.41	0.80	0.00	0.00	0.18	-7.38E-01	2.50E-01		2.18E-01	7.02E-01		7.21E-01	1.06E-01		-2.84E+00	7.63E-05	Down	null	null		7.46E+00	6.42E-01								

Unigene6028_All	302	6.58	4.19	7.05	4.78	7.53	6.88	36.12	17.02	12.53	-6.50E-01	1.53E-01			9.94E-02	8.20E-01		6.54E-01	1.33E-01		5.24E-01	2.72E-01		-1.09E+00	9.98E-12	Down	-1.53E+00	5.82E-20	Down			Unigene6028_All//1.00E-96//TC156388				
Unigene60283_All	228	3.21	2.22	0.00	1.53	0.60	0.40	0.56	0.55	0.87	-5.32E-01	5.12E-01			-1.16E+01	4.13E-04	Down	-1.34E+00	3.08E-01		-1.95E+00	1.96E-01		-1.67E-02	1.02E+00		6.51E-01	6.65E-01				Unigene60283_All//4.00E-15//CO085355				
Unigene6029_All	304	6.71	4.17	5.43	5.74	4.19	4.31	23.23	9.90	8.26	-6.88E-01	1.27E-01			-3.06E-01	5.29E-01		-4.53E-01	3.73E-01		-4.13E-01	4.39E-01		-1.23E+00	1.95E-09	Down	-1.49E+00	8.26E-13	Down			Unigene6029_All//1.00E-157//gi|21091262|gb|BQ403587.1|BQ403587				
Unigene60290_All	228	86.97	40.00	63.99	118.20	110.71	90.52	282.98	119.34	130.52	-1.12E+00	8.24E-18	Down	-4.43E-01	5.79E-04		-9.45E-02	4.50E-01		-3.85E-01	1.77E-04		-1.25E+00	2.76E-81	Down	-1.12E+00	2.41E-70	Down	Unigene60290_All//gi|211906490|gb|ACJ11738.1|//1.00E-35//malate dehydrogenase [Gossypium hirsutum]	Unigene60290_All//4.00E-36//AT1G04410| malate dehydrogenase, cytosolic, putative	Unigene60290_All//5.00E-126//gi|11199688|gb|BF268693.1|BF268693		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene6030_All	680	3.15	2.16	1.72	3.37	5.42	1.59	1.93	0.37	0.59	-5.46E-01	2.14E-01		-8.73E-01	5.80E-02		6.85E-01	2.99E-02		-1.08E+00	1.06E-02		-2.39E+00	9.40E-05	Down	-1.72E+00	1.48E-03									
Unigene60310_All	229	2.06	4.87	1.86	1.31	3.76	1.58	17.17	8.40	10.44	1.24E+00	6.10E-02		-1.45E-01	8.89E-01		1.53E+00	5.80E-02		2.74E-01	8.33E-01		-1.03E+00	1.98E-04	Down	-7.18E-01	6.74E-03		Unigene60310_All//gi|192910708|gb|ACF06462.1|//1.00E-13//24 kDa seed maturation protein [Elaeis guineensis]	Unigene60310_All//7.00E-13//AT4G23630| BTI1 (VIRB2-INTERACTING PROTEIN 1)	Unigene60310_All//1.00E-77//TC151737				nr -
Unigene60321_All	230	2.73	0.00	0.00	1.08	0.90	1.18	0.00	0.18	0.35	-1.14E+01	7.90E-04	Down	-1.14E+01	1.41E-03		-2.70E-01	8.22E-01		1.22E-01	9.44E-01		7.51E+00	6.31E-01		8.44E+00	4.02E-01		Unigene60321_All//gi|224103097|ref|XP_002312924.1|//4.00E-20//SAUR family protein [Populus trichocarpa] >gi|222849332|gb|EEE86879.1| SAUR family protein [Populus trichocarpa]	Unigene60321_All//7.00E-15//AT1G29490| auxin-responsive family protein	Unigene60321_All//1.00E-24//gi|11208036|gb|BF276966.1|BF276966				nr +
Unigene60323_All	230	1.82	0.66	2.32	9.96	16.77	13.75	7.72	3.82	0.52	-1.46E+00	2.34E-01		3.47E-01	7.05E-01		7.51E-01	1.36E-02		4.64E-01	2.14E-01		-1.02E+00	2.09E-02		-3.89E+00	7.68E-10	Down	Unigene60323_All//gi|212960297|gb|ACJ38663.1|//6.00E-14//myb-like transcription factor [Betula luminifera]	Unigene60323_All//1.00E-14//AT4G01680| MYB55 (myb domain protein 55); DNA binding / transcription factor	Unigene60323_All//6.00E-116//TC174804	MYB			nr +
Unigene60332_All	231	4.53	0.22	1.84	0.22	0.30	0.00	0.37	0.00	0.00	-4.37E+00	3.91E-05	Down	-1.30E+00	7.46E-02		4.67E-01	9.56E-01		-7.75E+00	6.30E-01		-8.52E+00	4.01E-01		-8.52E+00	3.57E-01		Unigene60332_All//gi|148726578|dbj|BAF63702.1|//3.00E-09//mixed amyrin synthase [Olea europaea]	Unigene60332_All//1.00E-09//AT1G78955| CAMS1 (Camelliol C synthase 1); beta-amyrin synthase	Unigene60332_All//2.00E-11//gi|164302226|gb|ES807570.1|ES807570		ko00100|Steroid biosynthesis		nr +
Unigene60337_All	231	3.85	0.22	0.00	0.86	0.30	0.98	0.00	0.00	0.00	-4.13E+00	2.52E-04	Down	-1.19E+01	6.30E-05	Down	-1.53E+00	4.15E-01		1.81E-01	9.35E-01		null	null		null	null		Unigene60337_All//gi|55419652|gb|AAV51939.1|//2.00E-11//SBP transcription factor [Gossypium hirsutum]		Unigene60337_All//2.00E-17//TC140334				nr +
Unigene60348_All	231	3.85	0.00	0.23	0.43	0.00	0.39	0.00	0.00	0.00	-1.19E+01	2.86E-05	Down	-4.06E+00	5.15E-04	Down	-8.75E+00	3.11E-01		-1.42E-01	9.49E-01		null	null		null	null		Unigene60348_All//gi|289540896|gb|ADD09572.1|//7.00E-23//salt tolerance-like protein [Trifolium repens]	Unigene60348_All//7.00E-20//AT4G39070| zinc finger (B-box type) family protein		DBB			nr +
Unigene6036_All	1325	5.61	3.02	1.13	12.67	8.84	4.50	12.35	3.28	6.19	-8.92E-01	3.48E-05		-2.32E+00	5.57E-18	Down	-5.20E-01	3.35E-05		-1.49E+00	4.16E-25	Down	-1.91E+00	5.22E-39	Down	-9.96E-01	1.69E-15		Unigene6036_All//gi|115447521|ref|NP_001047540.1|//1.00E-162//Os02g0639600 [Oryza sativa Japonica Group] >gi|113537071|dbj|BAF09454.1|Os02g0639600 [Oryza sativa Japonica Group]	Unigene6036_All//3.00E-159//AT4G04930| DES-1-LIKE; oxidoreductase/ sphingolipid delta-4 desaturase	Unigene6036_All//0.00E+00//TC165265		ko00600|Sphingolipid metabolism	GO:0008152	nr +
Unigene6037_All	419	2.75	20.32	5.08	3.21	4.03	8.52	3.43	7.88	10.36	2.89E+00	4.86E-27	Up	8.88E-01	5.42E-02		3.27E-01	5.68E-01		1.41E+00	2.78E-05	Up	1.20E+00	1.14E-04	Up	1.59E+00	7.39E-09	Up			Unigene6037_All//4.00E-146//gi|84153621|gb|DN802976.1|DN802976				
Unigene60383_All	234	66.18	499.33	160.21	255.24	614.24	599.09	265.43	527.63	285.17	2.92E+00	0.00E+00	Up	1.28E+00	5.26E-39	Up	1.27E+00	3.43E-179	Up	1.23E+00	2.57E-151	Up	9.91E-01	3.57E-107		1.04E-01	9.29E-02		Unigene60383_All//gi|270309006|dbj|BAI52956.1|//4.00E-24//auxin-repressed protein [Citrullus lanatus subsp. vulgaris]	Unigene60383_All//1.00E-15//AT1G28330| DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)	Unigene60383_All//3.00E-127//TC167022				nr +
Unigene6039_All	1404	0.37	1.48	1.67	0.99	0.86	0.68	0.18	0.18	0.06	1.99E+00	7.20E-05	Up	2.16E+00	1.20E-05	Up	-2.11E-01	7.29E-01		-5.56E-01	3.52E-01		-1.69E-02	1.02E+00		-1.67E+00	2.56E-01		Unigene6039_All//gi|297605228|ref|NP_001056895.2|//1.00E-101//Os06g0163300 [Oryza sativa Japonica Group] >gi|255676743|dbj|BAF18809.2|Os06g0163300 [Oryza sativa Japonica Group]	Unigene6039_All//8.00E-53//AT1G45688| unknown protein	Unigene6039_All//0.00E+00//TC139646				nr -
Unigene60396_All	235	2.67	0.00	0.00	1.06	0.15	0.19	0.18	0.18	0.85	-1.14E+01	7.90E-04	Down	-1.14E+01	1.41E-03		-2.86E+00	1.37E-01		-2.46E+00	2.23E-01		-1.61E-02	1.00E+00		2.24E+00	2.48E-01									
Unigene604_All	860	0.37	1.00	0.06	0.70	0.64	0.63	0.64	0.34	3.34	1.46E+00	6.59E-02		-2.56E+00	1.59E-01		-1.18E-01	8.75E-01		-1.41E-01	8.79E-01		-9.10E-01	3.19E-01		2.38E+00	8.81E-10	Up	Unigene604_All//gi|19423872|gb|AAL88715.1|AF488725_1//5.00E-63//dynamin-like protein E [Arabidopsis thaliana] >gi|7076772|emb|CAB75934.1|dynamin-like protein 4 (ADL4) [Arabidopsis thaliana]	Unigene604_All//2.00E-64//AT3G60190| ADL1E (ARABIDOPSIS DYNAMIN-LIKE 1E); GTP binding / GTPase	Unigene604_All//5.00E-126//TC165483			GO:0006810//GO:0006952//GO:0010038//GO:0016020//GO:0017111//GO:0032561//GO:0043231	nr -
Unigene6040_All	415	298.29	96.70	175.02	404.88	276.56	480.58	183.89	99.30	91.87	-1.63E+00	1.20E-189	Down	-7.69E-01	1.49E-55		-5.50E-01	1.41E-52		2.47E-01	8.71E-13		-8.89E-01	1.20E-55		-1.00E+00	1.24E-69	Down	Unigene6040_All//gi|156633990|gb|AB190994.1|//9.00E-47//ribosomal protein L9 [Sonneratia caseolaris] >gi|156633992|gb|ABE90995.1|ribosomal protein L9 [Sonneratia caseolaris] >gi|156633994|gb|ABE90996.1|ribosomal protein L9 [Sonneratia caseolaris] >gi|156633996|gb|ABE90997.1|ribosomal protein L9 [Sonneratia caseolaris] >gi|156633998|gb|ABE90998.1|ribosomal protein L9 [Sonneratia caseolaris] >gi|156634000|gb|ABE90999.1|ribosomal protein L9 [Sonneratia caseolaris] >gi|156634002|gb|ABE91000.1|ribosomal protein L9 [Sonneratia caseolaris] >gi|156634004|gb|ABE91001.1|ribosomal protein L9 [Sonneratia caseolaris] >gi|156634006|gb|ABE91002.1|ribosomal protein L9 [Sonneratia caseolaris] >gi|156634008|gb|ABE91003.1|ribosomal protein L9 [Sonneratia caseolaris]	Unigene6040_All//8.00E-44//AT1G33140| PG32 (PTGGYBACK2); structural constituent of ribosome	Unigene6040_All//0.00E+00//TC150849		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0030529	nr +
Unigene60408_All	236	2.66	0.00	0.90	0.00	0.00	0.00	0.00	0.00	0.00	-1.14E+01	7.90E-04	Down	-1.56E+00	1.29E-01		null	null		null	null		null	null		null	null		Unigene60408_All//sp|P54991|SNAA_STRPR//2.00E-09//Pristinamycin IIA synthase subunit A OS=Streptomyces pristinaespiralis GN=snaA PE=1 SV=3						swissprot -
Unigene6041_All	346	21.93	23.72	20.93	16.56	17.91	25.45	55.11	127.44	125.04	1.14E-01	5.99E-01		-6.71E-02	7.71E-01		1.14E-01	6.98E-01		6.20E-01	1.24E-03		1.21E+00	3.27E-53	Up	1.18E+00	1.59E-51	Up	Unigene6041_All//gi|195625072|gb|ACG43366.1|//2.00E-15//vesicle-associated membrane protein 725 [Zea mays]	Unigene6041_All//2.00E-15//AT1G04760| ATVAMP726	Unigene6041_All//2.00E-120//TC170076		ko04130|SNARE interactions in vesicular transport	GO:0006810//GO:0031224	nr -
Unigene6042_All	1387	1.66	0.80	0.50	8.01	7.30	4.07	1.92	0.18	1.26	-1.05E+00	1.34E-02		-1.73E+00	2.51E-04	Down	-1.34E-01	5.18E-01		-9.77E-01	7.11E-09		-3.41E+00	1.39E-12	Down	-6.04E-01	6.93E-02		Unigene6042_All//gi|297834520|ref|XP_002885142.1|//9.00E-81//IQ-domain 26 [Arabidopsis lyrata subsp. lyrata] >gi|297330982|gb|EFH61401.1| IQ-domain 26 [Arabidopsis lyrata subsp. lyrata]	Unigene6042_All//2.00E-65//AT3G16490| IQD26 (IQ-domain 26); calmodulin binding	Unigene6042_All//0.00E+00//TC132001				nr -
Unigene6045_All	604	1.13	2.35	1.94	0.99	2.00	2.02	3.57	2.84	8.77	1.06E+00	6.14E-02		7.84E-01	2.38E-01		1.01E+00	1.11E-01		1.03E+00	1.07E-01		-3.32E-01	4.22E-01		1.30E+00	4.87E-08	Up			Unigene6045_All//3.00E-157//gi|78340697|gb|DT560971.1|DT560971				
Unigene6046_All	1742	0.06	0.12	0.24	10.47	9.41	7.18	12.38	2.09	3.52	9.52E-01	6.20E-01		2.02E+00	1.39E-01		-1.54E-01	3.00E-01		-5.43E-01	1.60E-05		-2.57E+00	1.59E-73	Down	-1.81E+00	4.03E-49	Down	Unigene6046_All//gi|42562490|ref|NP_174610.2|//0.00E+00//proton-dependent oligopeptide transport (POT) family protein [Arabidopsis thaliana] >gi|62320582|dbj|BAD95216.1|nitrate transporter NTL1 [Arabidopsis thaliana]	Unigene6046_All//0.00E+00//AT1G33440| proton-dependent oligopeptide transport (POT) family protein	Unigene6046_All//0.00E+00//TC131764			GO:0015833//GO:0031224//GO:0051707	nr +
Unigene60460_All	239	1.09	0.00	1.56	2.50	0.14	0.00	0.35	0.00	0.00	-1.01E+01	6.66E-02		5.11E-01	6.54E-01		-4.12E+00	1.25E-03		-1.13E+01	7.69E-04	Down	-8.47E+00	4.01E-01		-8.47E+00	3.56E-01		Unigene60460_All//gi|224142097|ref|XP_002324395.1|//6.00E-08//predicted protein [Populus trichocarpa] >gi|222865829|gb|EEF02960.1|predicted protein [Populus trichocarpa]		Unigene60460_All//5.00E-12//CA993922				nr -
Unigene60466_All	239	2.63	0.00	1.34	0.21	0.29	0.00	0.71	0.00	0.67	-1.14E+01	7.90E-04	Down	-9.75E-01	3.16E-01		4.68E-01	9.56E-01		-7.70E+00	6.30E-01		-9.47E+00	1.34E-01		-8.57E-02	9.65E-01									
Unigene60473_All	240	1.09	4.64	3.11	9.96	16.36	8.66	61.13	29.95	25.07	2.09E+00	4.16E-03		1.51E+00	9.49E-02		7.15E-01	1.80E-02		-2.03E-01	6.52E-01		-1.03E+00	2.86E-14	Down	-1.29E+00	1.16E-20	Down			Unigene60473_All//2.00E-94//TC175269				
Unigene6048_All	391	2.68	14.25	6.95	1.53	3.17	3.00	3.24	6.95	6.11	2.41E+00	7.86E-15	Up	1.38E+00	8.47E-04	Up	1.05E+00	9.06E-02		9.74E-01	1.34E-01		1.10E+00	1.44E-03		9.14E-01	1.04E-02				Unigene6048_All//1.00E-28//EV489873				
Unigene6049_All	423	14.60	29.47	16.49	19.08	20.43	19.54	9.40	13.73	12.53	1.01E+00	7.88E-10	Up	1.76E-01	4.79E-01		9.90E-02	6.82E-01		3.44E-02	8.99E-01		5.48E-01	1.30E-02		4.15E-01	6.94E-02		Unigene6049_All//gi|30102910|gb|AAP21373.1|//1.00E-34//At2g38730 [Arabidopsis thaliana] >gi|45680872|gb|AAS75305.1| single domain cyclophilin type peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	Unigene6049_All//1.00E-33//AT2G38730| peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative	Unigene6049_All//1.00E-174//TC155653		ko03040|Spliceosome	GO:0016020//GO:0016859//GO:0043231//GO:0044267	nr +
Unigene60496_All	241	156.53	574.39	311.32	255.07	377.22	401.41	265.79	554.62	370.12	1.88E+00	1.77E-257	Up	9.92E-01	5.91E-52		5.65E-01	3.13E-29		6.54E-01	1.82E-36		1.06E+00	1.16E-129	Up	4.78E-01	9.90E-23		Unigene60496_All//gi|167963118|dbj|BAG09364.1|//1.00E-21//peroxisomal enoyl-CoA hydratase/isomerase family protein [Glycine max]	Unigene60496_All//1.00E-20//AT4G16210| ECHIA (ENOYL-COA HYDRATASE/ISOMERASE A); catalytic	Unigene60496_All//2.00E-116//gi|164299579|gb|ES813070.1|ES813070		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism	GO:0016829//GO:0042579	nr -
Unigene605_All	1950	5.02	7.93	3.00	6.31	9.06	8.22	1.82	1.31	4.96	6.60E-01	3.51E-06		-7.40E-01	9.96E-05		5.22E-01	2.48E-05		3.82E-01	6.37E-03		-4.78E-01	1.10E-01		1.45E+00	2.44E-16	Up	Unigene605_All//gi|19423872|gb|AAL88715.1|AF488725_1//1.00E-86//dynamin-like protein E [Arabidopsis thaliana] >gi|7076772|emb|CAB75934.1|dynamin-like protein 4 (ADL4) [Arabidopsis thaliana]	Unigene605_All//7.00E-88//AT3G60190| ADL1E (ARABIDOPSIS DYNAMIN-LIKE 1E); GTP binding / GTPase	Unigene605_All//0.00E+00//gi|48800555|gb|CO101869.1|CO101869		ko04144|Endocytosis	GO:0006810//GO:0006952//GO:0010038//GO:0016020//GO:0017111//GO:0032561//GO:0043231	nr -
Unigene6050_All	618	149.26	526.54	376.89	190.87	319.17	305.18	224.47	486.53	341.92	1.82E+00	0.00E+00	Up	1.34E+00	7.53E-259	Up	7.42E-01	4.46E-102		6.77E-01	5.15E-75		1.12E+00	0.00E+00	Up	6.07E-01	1.10E-80		Unigene6050_All//gi|167963118|dbj|BAG09364.1|//2.00E-69//peroxisomal enoyl-CoA hydratase/isomerase family protein [Glycine max]	Unigene6050_All//2.00E-61//AT4G16210| ECHIA (ENOYL-COA HYDRATASE/ISOMERASE A); catalytic	Unigene6050_All//0.00E+00//TC172499		ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism	GO:0016836//GO:0042579	nr -
Unigene6052_All	417	1.76	0.85	4.34	6.09	4.62	3.68	9.13	3.41	2.48	-1.05E+00	2.14E-01		1.31E+00	1.21E-02		-3.98E-01	3.25E-01		-7.26E-01	7.01E-02		-1.42E+00	1.35E-06	Down	-1.88E+00	9.08E-10	Down			Unigene6052_All//0.00E+00//DW503555				
Unigene60521_All	243	2.80	0.00	0.00	1.03	0.28	0.37	0.35	0.00	0.16	-1.15E+01	4.09E-04	Down	-1.15E+01	7.63E-04	Down	-1.85E+00	2.75E-01		-1.46E+00	4.06E-01		-8.44E+00	4.01E-01		-1.09E+00	6.75E-01				Unigene60521_All//2.00E-32//gi|48820869|gb|CO122182.1|CO122182				ESTscan +

Unigene60528_All	244	3.00	1.66	0.00	0.61	0.71	0.00	0.52	0.00	0.33	-8.54E-01	3.05E-01		-1.16E+01	4.13E-04	Down	2.04E-01	9.49E-01		-9.26E+00	2.32E-01		-9.02E+00	2.34E-01		-6.71E-01	7.19E-01		Unigene60528_All//gi|297797191|ref|XP_002866480.1|//2.00E-07//exostosin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312315|gb|EFH42739.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene60528_All//8.00E-09//AT5G62220| exostosin family protein					nr -
Unigene6053_All	1195	1.49	0.93	1.43	8.13	7.92	8.39	26.78	42.08	62.14	-6.74E-01	1.66E-01		-6.21E-02	9.06E-01		-3.67E-02	8.59E-01		4.57E-02	8.34E-01		6.52E-01	7.05E-22		1.21E+00	1.33E-91	Up	Unigene6053_All//gi|297843860|ref|XP_002889811.1|//1.00E-25//zinc finger protein 5, ZFP5 [Arabidopsis lyrata subsp. lyrata] >gi|297335653|gb|EFH66070.1| zinc finger protein 5, ZFP5 [Arabidopsis lyrata subsp. lyrata]	Unigene6053_All//2.00E-26//AT1G10480| ZFP5 (ZINC FINGER PROTEIN 5); nucleic acid binding / transcription factor/ zinc ion binding	Unigene6053_All//0.00E+00//TC164743	C2H2		GO:0043231	nr +
Unigene6055_All	524	8.49	8.12	4.37	11.41	12.68	15.86	34.53	30.63	76.79	-6.33E-02	8.26E-01		-9.58E-01	1.45E-03		1.53E-01	5.80E-01		4.75E-01	1.94E-02		-1.73E-01	1.80E-01		1.15E+00	3.81E-46	Up	Unigene6055_All//gi|297833916|ref|XP_002884840.1|//3.00E-18//organic anion transporter [Arabidopsis lyrata subsp. lyrata] >gi|297330680|gb|EFH61099.1| organic anion transporter [Arabidopsis lyrata subsp. lyrata]	Unigene6055_All//2.00E-19//AT3G11320| organic anion transmembrane transporter	Unigene6055_All//0.00E+00//TC155027			GO:0031224	nr +
Unigene6056_All	637	52.57	47.81	36.78	21.11	27.08	25.59	43.21	20.47	23.14	-1.37E-01	1.80E-01		-5.15E-01	6.66E-08		3.59E-01	5.82E-03		2.78E-01	5.58E-02		-1.08E+00	4.90E-28	Down	-9.01E-01	1.11E-21		Unigene6056_All//gi|211906518|gb|ACJ11752.1|//9.00E-57//glyceraldehyde-3-phosphate dehydrogenase C subunit [Gossypium hirsutum]	Unigene6056_All//3.00E-53//AT3G04120| GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene6056_All//0.00E+00//TC151197		ko00010|Glycolysis / Gluconeogenesis	GO:0000166//GO:0008943//GO:0019318	nr +
Unigene6057_All	1774	0.74	1.09	0.24	3.96	3.38	9.60	6.24	3.37	9.81	5.58E-01	2.31E-01		-1.62E+00	1.33E-02		-2.29E-01	3.38E-01		1.28E+00	7.13E-20	Up	-8.90E-01	8.53E-09		6.52E-01	2.27E-08		Unigene6057_All//gi|15221327|ref|NP_172704.1|//1.00E-149//ACR8; amino acid binding [Arabidopsis thaliana] >gi|8778647|gb|AAF79655.1|AC025416_29 F5O11.14 [Arabidopsis thaliana] >gi|22138106|gb|AAM93433.1| ACR8 [Arabidopsis thaliana] >gi|11074504|gb|ABH04625.1| At1g12420 [Arabidopsis thaliana]	Unigene6057_All//6.00E-146//AT1G12420| ACR8; amino acid binding	Unigene6057_All//0.00E+00//ES851188				nr +
Unigene6058_All	732	0.50	2.42	1.31	2.45	1.46	1.60	2.19	1.03	1.03	2.28E+00	6.80E-05	Up	1.39E+00	7.11E-02		-7.48E-01	1.12E-01		-6.11E-01	2.28E-01		-1.09E+00	1.97E-02		-1.09E+00	1.58E-02		Unigene6058_All//gi|297842759|ref|XP_002889261.1|//1.00E-31//kinase [Arabidopsis lyrata subsp. lyrata] >gi|297335102|gb|EFH65520.1| kinase [Arabidopsis lyrata subsp. lyrata]	Unigene6058_All//8.00E-29//AT1G79640| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene6058_All//0.00E+00//C0121502			GO:0016301	nr -
Unigene60585_All	248	3.38	0.00	1.50	1.21	0.28	0.18	0.17	0.17	0.64	-1.17E+01	5.56E-05	Down	-1.17E+00	1.52E-01		-2.12E+00	1.65E-01		-2.73E+00	1.37E-01		-1.70E-02	1.00E+00		1.91E+00	3.77E-01						Unigene60585_All//7.00E-08//DR460365					
Unigene6059_All	385	4.48	2.24	1.94	4.01	3.13	1.64	4.06	4.23	0.93	-1.00E+00	4.42E-02		-1.21E+00	2.32E-02		-3.58E-01	5.31E-01		-1.29E+00	1.75E-02		5.93E-02	9.13E-01		-2.13E+00	3.93E-05	Down					Unigene6059_All//3.00E-125//TC147753					
Unigene606_All	3516	4.87	16.82	5.44	5.51	6.77	13.05	10.50	17.58	30.20	1.79E+00	2.19E-103	Up	1.60E-01	2.67E-01		2.96E-01	7.15E-03		1.24E+00	1.39E-50	Up	7.44E-01	1.72E-33		1.52E+00	1.71E-184	Up	Unigene606_All//0.00E+00//AT3G60190| ADL1E (ARABIDOPSIS DYNAMIN-LIKE 1E); GTP binding / GTPase	Unigene606_All//0.00E+00//TC165483		ko04144|Endocytosis//ko00740|Riboflavin metabolism	GO:0006810//GO:0006952//GO:0010038//GO:0016020//GO:0017111//GO:0032561//GO:0043231	nr +
Unigene6060_All	371	1.97	1.91	0.00	2.69	2.60	1.46	1.37	2.37	1.29	-4.63E-02	9.68E-01		-1.09E+01	4.13E-04	Down	-4.72E-02	9.36E-01		-8.78E-01	2.20E-01		7.91E-01	2.41E-01		-8.58E-02	9.30E-01		Unigene6060_All//gi|229463809|gb|ACQ66330.1|//4.00E-39//N-acetylglutamate synthase [Populus maximowiczii x Populus nigra]	Unigene6060_All//1.00E-30//AT4G37670| GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein	Unigene6060_All//1.00E-56//ES822546		ko00330|Arginine and proline metabolism	GO:0006520//GO:0008080//GO:0043231	nr -
Unigene60606_All	249	5.46	0.00	0.43	0.60	0.00	0.36	0.00	0.00	0.00	-1.24E+01	6.50E-08	Down	-3.68E+00	1.58E-05	Down	-9.23E+00	1.65E-01		-7.26E-01	7.14E-01		null	null		null	null						Unigene60606_All//2.00E-103//DW493921					
Unigene6061_All	296	33.41	12.67	12.23	51.50	49.09	60.57	49.56	16.52	16.29	-1.40E+00	8.66E-13	Down	-1.45E+00	7.70E-13	Down	-6.90E-02	6.99E-01		2.34E-01	9.69E-02		-1.59E+00	3.91E-27	Down	-1.61E+00	1.68E-28	Down	Unigene6061_All//gi|297794223|ref|XP_002864996.1|//2.00E-36//60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata] >gi|297310831|gb|EFH41255.1| 60S ribosomal protein L26 [Arabidopsis lyrata subsp. lyrata]	Unigene6061_All//2.00E-30//AT5G67510| 60S ribosomal protein L26 (RPL26B)	Unigene6061_All//2.00E-159//DR455051		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0006950//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene6062_All	431	1.09	0.71	2.47	3.47	2.16	1.47	6.38	2.91	1.66	-6.31E-01	5.53E-01		1.18E+00	9.59E-02		-6.85E-01	1.99E-01		-1.24E+00	2.45E-02		-1.13E+00	9.60E-04	Down	-1.94E+00	1.45E-07	Down									
Unigene6063_All	581	2.34	6.80	5.77	2.40	2.37	2.18	1.82	1.94	0.89	1.54E+00	2.89E-06	Up	1.30E+00	3.27E-04	Up	-1.81E-02	9.59E-01		-1.41E-01	7.96E-01		9.44E-02	8.76E-01		-1.03E+00	7.30E-02						Unigene6063_All//7.00E-07//TC159624					
Unigene6064_All	1316	0.00	4.20	0.49	0.00	1.05	0.76	0.71	4.32	2.97	1.20E+01	1.66E-31	Up	8.92E+00	1.16E-03		1.00E+01	1.61E-08	Up	9.56E+00	6.14E-06	Up	2.61E+00	3.57E-20	Up	2.07E+00	4.23E-11	Up	Unigene6064_All//gi|260513724|gb|ACX42574.1|//3.00E-62//CONSTANS-like zinc finger protein [Glycine max]	Unigene6064_All//2.00E-31//AT3G21880| zinc finger (B-box type) family protein		C2C2-CO-like	ko04712|Circadian rhythm - plant	GO:0001071//GO:0010468//GO:0046914	nr -
Unigene60651_All	252	4.98	0.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-2.63E+00	3.16E-04	Down	-1.23E+01	7.11E-07	Down	null	null		null	null		null	null		null	null		Unigene60651_All//gi|13784983|gb|AAK38341.1|//1.00E-12//seven transmembrane protein Mlo5 [Zea mays]	Unigene60651_All//5.00E-07//AT4G02600| MLO1; calmodulin binding	Unigene60651_All//1.00E-108//C0104683			GO:0006950//GO:0009987//GO:0031224//GO:0031410	nr +
Unigene6067_All	358	1.75	5.38	3.12	20.73	10.00	10.09	3.90	3.74	0.78	1.62E+00	1.18E-03		8.33E-01	2.23E-01		-1.05E+00	1.32E-07	Down	-1.04E+00	9.76E-07	Down	-6.10E-02	9.18E-01		-2.32E+00	4.25E-05	Down	Unigene6067_All//gi|224071451|ref|XP_002303466.1|//3.00E-18//predicted protein [Populus trichocarpa] >gi|222840898|gb|EEE78445.1| predicted protein [Populus trichocarpa]						nr -
Unigene6068_All	317	3.30	4.64	8.90	15.87	15.10	11.83	20.94	59.46	19.86	4.90E-01	3.70E-01		1.43E+00	4.17E-04	Up	-7.19E-02	8.36E-01		-4.25E-01	1.29E-01		1.51E+00	3.98E-32	Up	-7.67E-02	7.20E-01		Unigene6068_All//gi|294514718|gb|ADE95828.1|//4.00E-32//4-coumarate:CoA ligase 1 [Corchorus capsularis]	Unigene6068_All//8.00E-24//AT3G21240| 4CL2 (4-COUMARATE:COA LIGASE 2); 4-coumarate-CoA ligase	Unigene6068_All//6.00E-163//TC148373		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0006575//GO:0016105//GO:0016703//GO:0032559	nr +
Unigene60682_All	254	85.28	227.21	154.30	265.15	326.86	349.04	43.61	109.92	234.33	1.41E+00	6.29E-72	Up	8.56E-01	1.86E-21		3.02E-01	1.00E-08		3.97E-01	8.27E-14		1.33E+00	1.90E-39	Up	2.43E+00	4.76E-192	Up					Unigene60682_All//2.00E-88//DW484687					
Unigene60685_All	254	2.68	0.00	1.05	0.20	0.14	0.18	0.00	0.00	0.00	-1.14E+01	4.09E-04	Down	-1.35E+00	1.50E-01		-5.32E-01	8.23E-01		-1.41E-01	9.51E-01		null	null		null	null		Unigene60685_All//gi|76880194|dbj|BAE45868.1|//8.00E-08//penicillin-binding protein [Physcomitrella patens] >gi|76880196|dbj|BAE45869.1| penicillin-binding protein [Physcomitrella patens]						GO:0003824//GO:0042546//GO:0044464	nr -
Unigene6069_All	1123	0.84	0.59	0.00	7.98	2.88	1.69	2.03	0.67	1.28	-5.16E-01	4.57E-01		-9.71E+00	3.34E-05	Down	-1.47E+00	4.18E-15	Down	-2.24E+00	1.98E-23	Down	-1.60E+00	6.24E-05	Down	-6.71E-01	6.45E-02		Unigene6069_All//gi|224126161|ref|XP_002319770.1|//1.00E-109//cytochrome P450 [Populus trichocarpa] >gi|222858146|gb|EEE95693.1| cytochrome P450 [Populus trichocarpa]	Unigene6069_All//1.00E-82//AT2G27690| CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene6069_All//0.00E+00//gi|164246221|gb|ES825866.1|ES825866		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0006091//GO:0016712//GO:0016713//GO:0031410//GO:0042598	nr -
Unigene607_All	529	2.87	1.25	2.01	4.43	4.95	5.21	7.03	4.66	3.31	-1.20E+00	2.75E-02		-5.11E-01	3.80E-01		1.61E-01	7.42E-01		2.35E-01	6.04E-01		-5.93E-01	3.78E-02		-1.09E+00	1.03E-04	Down	Unigene607_All//gi|297833482|ref|XP_002884623.1|//2.00E-82//GTP-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330463|gb|EFH60882.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene607_All//7.00E-83//AT3G07050| GTP-binding family protein	Unigene607_All//0.00E+00//gi|164324012|gb|ES829863.1|ES829863			GO:0031981//GO:0032561	nr -
Unigene6070_All	339	24.08	8.22	4.56	10.73	7.42	2.26	39.41	6.04	4.82	-1.55E+00	2.52E-12	Down	-2.40E+00	1.49E-20	Down	-5.33E-01	9.13E-02		-2.24E+00	8.21E-10	Down	-2.71E+00	1.67E-48	Down	-3.03E+00	2.41E-56	Down					Unigene6070_All//8.00E-64//DW225951					
Unigene6072_All	904	0.35	0.45	0.59	0.88	1.83	1.25	2.39	0.42	1.01	3.69E-01	7.23E-01		7.62E-01	4.52E-01		1.05E+00	4.14E-02		5.02E-01	4.76E-01		-2.52E+00	8.42E-08	Down	-1.23E+00	1.35E-03		Unigene6072_All//gi|264664473|sp|C0LGK4.1|Y2165_ARATH//5.00E-46//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At2g16250; Flags: Precursor >gi|224589511|gb|ACN59289.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene6072_All//5.00E-41//AT2G16250| leucine-rich repeat transmembrane protein kinase, putative	Unigene6072_All//2.00E-17//gi|78324286|gb|DT544560.1|DT544560			GO:0004672//GO:0005618//GO:0016020	nr +
Unigene60721_All	257	25.24	19.12	13.05	37.99	43.55	41.47	75.84	27.81	34.57	-4.01E-01	8.88E-02		-9.52E-01	8.67E-05		1.97E-01	3.12E-01		1.27E-01	5.58E-01		-1.45E+00	2.11E-31	Down	-1.13E+00	2.13E-22	Down	Unigene60721_All//gi|297803476|ref|XP_002869622.1|//3.00E-30//mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315458|gb|EFH45881.1| mitochondrial ATP synthase g subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene60721_All//2.00E-31//AT4G29480| mitochondrial ATP synthase g subunit family protein	Unigene60721_All//8.00E-128//ES849741		ko00190|Oxidative phosphorylation	GO:0005753//GO:0006754//GO:0006818//GO:0015077	nr -
Unigene60730_All	258	3.04	0.00	0.21	0.19	0.00	0.18	0.00	0.00	0.00	-1.16E+01	1.09E-04	Down	-3.88E+00	1.60E-03		-7.59E+00	5.52E-01		-1.41E-01	9.50E-01		null	null		null	null											ESTscan -
Unigene6074_All	344	41.22	14.73	12.54	33.31	27.23	43.46	115.29	43.25	32.08	-1.48E+00	1.28E-19	Down	-1.72E+00	4.60E-23	Down	-2.91E-01	8.86E-02		3.84E-01	8.57E-03		-1.41E+00	5.84E-61	Down	-1.85E+00	7.84E-92	Down	Unigene6074_All//gi|297819344|ref|XP_002877555.1|//3.00E-25//40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata] >gi|297323393|gb|EFH53814.1| 40S ribosomal protein S20 [Arabidopsis lyrata subsp. lyrata]	Unigene6074_All//1.00E-26//AT5G62300| 40S ribosomal protein S20 (RPS20C)	Unigene6074_All//0.00E+00//TC175099		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015935//GO:0030312//GO:0031981	nr +
Unigene60752_All	261	3.21	0.00	3.47	0.38	1.85	1.73	0.16	1.60	0.00	-1.16E+01	5.56E-05	Down	1.13E-01	8.72E-01		2.27E+00	7.83E-02		2.18E+00	1.03E-01		3.31E+00	2.00E-02		-7.34E+00	6.09E-01											
Unigene6076_All	591	13.46	14.06	10.18	32.03	21.56	11.16	9.16	4.31	3.24	6.34E-02	7.63E-01		-4.02E-01	6.77E-02		-5.71E-01	9.19E-07		-1.52E+00	5.15E-29	Down	-1.09E+00	3.18E-06	Down	-1.50E+00	4.25E-10	Down	Unigene6076_All//gi|125532038|gb|EAY78603.1|//3.00E-08//hypothetical protein Osi_33699 [Oryza sativa Indica Group]	Unigene6076_All//6.00E-06//AT2G02650| reverse transcriptase-related	Unigene6076_All//0.00E+00//TC163720				nr +
Unigene60766_All	263	4.58	0.00	2.23	0.19	1.05	1.37	0.16	0.00	0.30	-1.22E+01	5.01E-07	Down	-1.04E+00	1.14E-01		2.47E+00	2.23E-01		2.86E+00	9.44E-02		-7.33E+00	6.52E-01		9.14E-01	7.49E-01						Unigene60766_All//1.00E-77//TC141177					
Unigene6078_All	221	0.24	1.83	3.86	3.16	1.25	0.61	4.59	5.30	8.47	2.95E+00	5.90E-02		4.03E+00	7.02E-04	Up	-1.34E+00	1.09E-01		-2.36E+00	1.69E-02		2.06E-01	7.23E-01		8.84E-01	3.13E-02						Unigene6078_All//1.00E-89//gi|109876339|gb|DW505313.1|DW505313					
Unigene608_All	2024	7.03	5.18	5.84	13.12	9.43	16.45	11.74	5.47	5.67	-4.40E-01	3.17E-03		-2.68E-01	1.00E-01		-4.77E-01	8.15E-07		3.26E-01	4.18E-04		-1.10E+00	3.78E-25	Down	-1.05E+00	4.67E-24	Down	Unigene608_All//gi|297833482|ref|XP_002884623.1|//0.00E+00//GTP-binding family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330463|gb|EFH60882.1| GTP-binding family protein [Arabidopsis lyrata subsp. lyrata]	Unigene608_All//0.00E+00//AT3G07050| GTP-binding family protein	Unigene608_All//0.00E+00//gi|78347362|gb|DT567636.1|DT567636			GO:0031981//GO:0032561	nr -
Unigene6080_All	359	13.99	22.02	16.46	19.84	31.37	26.54	0.71	3.14	4.00	6.54E-01	1.54E-03		2.35E-01	4.03E-01		6.61E-01	3.46E-05		4.20E-01	2.70E-02		2.15E+00	8.74E-04	Up	2.50E+00	1.65E-05	Up					Unigene6080_All//3.00E-125//DW506918					
Unigene60809_All	268	4.49	0.76	0.00	0.56	0.90	0.00	0.16	0.31	0.30	-2.57E+00	5.35E-04	Down	-1.21E+01	1.36E-06	Down	6.90E-01	7.32E-01		-9.12E+00	2.32E-01		9.83E-01	7.30E-01		9.14E-01	7.49E-01						Unigene60809_All//3.00E-10//TC151951					
Unigene60810_All	268	2.93	0.00	0.79	1.49	0.26	0.17	0.00	0.00	0.00	-1.15E+01	1.09E-04	Down	-1.88E+00	4.13E-02		-2.53E+00	5.79E-02		-3.14E+00	4.87E-02		null	null		null	null		Unigene60810_All//gi|18401040|ref|NP_565616.1|//2.00E-26//ftsh4 (FtsH protease 4); ATP-dependent peptidase/ ATPase/ metallopeptidase [Arabidopsis thaliana] >gi|75100022|sp|Q80983.2|FTSH4_ARATH RecName: Full=Cell division protease ftsH homolog 4, mitochondrial; Short=AtFtsH4; Flags: Precursor	Unigene60810_All//9.00E-28//AT2G26140| ftsh4 (FtsH protease 4); ATP-dependent peptidase/ ATPase/ metallopeptidase				GO:0004175//GO:0009057//GO:0019538//GO:0032559//GO:0042623//GO:0043231	nr -
Unigene60812_All	268	4.88	0.19	0.99	2.42	1.03	0.17	1.10	1.40	0.45	-4.69E+00	1.63E-06	Down	-2.30E+00	1.21E-03		-1.23E+00	1.60E-01		-3.84E+00	2.70E-03		3.46E-01	7.38E-01		-1.31E+00	3.13E-01											

Unigene6082_All	312	20.12	24.69	15.70	23.63	28.25	29.39	34.15	26.52	15.58	2.95E-01	1.80E-01		-3.58E-01	1.57E-01		2.58E-01	2.25E-01		3.15E-01	1.22E-01		-3.65E-01	2.22E-02		-1.13E+00	1.26E-12	Down	Unigene6082_All//gi|9843653|emb|CAC03600.1|//3.00E-21//splicing factor SC35 [Arabidopsis thaliana]	Unigene6082_All//1.00E-22//AT5G64200| ATSC35; RNA binding / nucleic acid binding / nucleotide binding	Unigene6082_All//2.00E-141//gi|109856664|gb|DW485643.1|DW485643		ko03040|Spliceosome	GO:0005488	nr +
Unigene60820_All	269	13.81	3.39	3.76	9.81	5.63	7.22	1.41	49.10	2.22	-2.03E+00	2.32E-08	Down	-1.88E+00	3.14E-07	Down	-8.01E-01	3.00E-02		-4.43E-01	2.85E-01		5.12E+00	3.16E-79	Up	6.51E-01	4.23E-01				Unigene60820_All//9.00E-54//gi|13247208|gb|BF269264.2|BF269264				
Unigene60828_All	270	10.66	9.76	21.69	3.51	3.19	5.85	0.00	0.46	0.89	-1.27E-01	7.28E-01		1.03E+00	6.92E-05	Up	-1.37E-01	8.18E-01		7.40E-01	1.79E-01		8.86E+00	2.40E-01		9.79E+00	4.39E-02				Unigene60828_All//2.00E-67//TC163068				ESTscan -
Unigene6083_All	811	0.90	0.62	0.46	1.17	1.02	1.28	4.01	1.34	1.67	-5.32E-01	5.12E-01		-9.75E-01	2.64E-01		-1.96E-01	8.04E-01		1.34E-01	8.58E-01		-1.58E+00	1.32E-06	Down	-1.27E+00	3.76E-05	Down	Unigene6083_All//gi|15231994|ref|NP_187510.1|//2.00E-52//signal peptidase I family protein [Arabidopsis thaliana] >gi|92856564|gb|ABE77399.1|At3g08980 [Arabidopsis thaliana]	Unigene6083_All//2.00E-45//AT3G08980| signal peptidase I family protein	Unigene6083_All//0.00E+00//ES835382		ko03060|Protein export	GO:0016020//GO:0019538//GO:0043231//GO:0070011	nr +
Unigene60836_All	271	2.90	0.00	0.00	2.57	1.02	2.17	0.47	0.00	0.00	-1.15E+01	1.09E-04	Down	-1.15E+01	2.21E-04	Down	-1.34E+00	1.09E-01		-2.48E-01	7.56E-01		-8.87E+00	2.34E-01		-8.87E+00	1.99E-01		Unigene60836_All//gi|51705413|gb|AU09444.1|//2.00E-06//UDP-glucose glucosyltransferase [Fragaria x ananassa]	Unigene60836_All//7.00E-07//AT3G21760| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene60836_All//2.00E-14//TC175274			GO:0016757	nr -
Unigene6084_All	631	0.58	2.49	1.77	3.00	1.04	1.22	2.68	2.32	1.14	2.10E+00	4.40E-04	Up	1.61E+00	2.44E-02		-1.53E+00	7.71E-04	Down	-1.30E+00	6.55E-03		-2.09E-01	6.45E-01		-1.24E+00	5.14E-03				Unigene6084_All//7.00E-07//ES836839				
Unigene6085_All	300	83.36	98.30	102.06	104.78	95.84	141.51	131.63	54.89	45.15	2.38E-01	2.12E-02		2.92E-01	4.68E-03		-1.29E-01	2.33E-01		4.34E-01	4.42E-08		-1.26E+00	4.67E-51	Down	-1.54E+00	4.24E-71	Down	Unigene6085_All//gi|28192427|gb|AAL71857.1|//2.00E-30//dehydroascorbate reductase [Nicotiana tabacum]	Unigene6085_All//1.00E-29//AT1G19570| DHAR1 (dehydroascorbate reductase); copper ion binding / glutathione dehydrogenase (ascorbate)	Unigene6085_All//2.00E-150//TC155522		ko00480|Glutathione metabolism	GO:0005576//GO:0006164//GO:0009532//GO:0009608//GO:0009719//GO:0010038//GO:0015038//GO:0016020//GO:0042277//GO:0042579//GO:0043900//GO:0046914	nr +
Unigene6086_All	358	68.69	45.43	40.46	153.76	216.81	94.87	189.20	40.16	77.90	-5.96E-01	5.70E-08		-7.64E-01	2.33E-11		4.96E-01	7.45E-20		-6.97E-01	1.46E-23		-2.24E+00	6.03E-195	Down	-1.28E+00	1.47E-91	Down	Unigene6086_All//gi|134035504|gb|AB047740.1|//1.00E-26//alpha-tubulin [Gossypium hirsutum] >gi|223453026|gb|ACM89777.1|alpha-tubulin 10 [Gossypium hirsutum]	Unigene6086_All//6.00E-28//AT1G50010| TUA2; structural constituent of cytoskeleton	Unigene6086_All//9.00E-175//gi|78353740|gb|DT574014.1|DT574014		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene60862_All	274	2.48	0.00	0.19	0.00	0.13	0.16	0.15	0.00	0.00	-1.13E+01	4.09E-04	Down	-3.68E+00	4.81E-03		6.97E+00	8.25E-01		7.36E+00	6.92E-01		-7.27E+00	6.52E-01		-7.27E+00	6.09E-01		Unigene60862_All//gi|11597233|gb|AAG02246.2|//5.00E-14//NAD(P)H transhydrogenase [Acetabularia acetabulum]					GO:0008746	nr -
Unigene60869_All	275	2.28	0.00	0.00	0.36	0.00	0.00	0.00	0.00	0.00	-1.12E+01	7.90E-04	Down	-1.12E+01	1.40E-03		-8.50E+00	3.11E-01		-8.50E+00	3.97E-01		null	null		null	null		Unigene60869_All//gi|11467714|ref|NP_050766.1|//2.00E-14//acyl carrier protein [Guillardia theta] >gi|113196|sp|P29189.1|ACP_GLITH RecName: Full=Acyl carrier protein; Short=ACP >gi|3603039|gb|AAC35700.1| acyl carrier protein [Guillardia theta]	Unigene60869_All//2.00E-13//AT1G65290| mtACP2 (mitochondrial acyl carrier protein 2); acyl carrier/ metal ion binding			ko00190|Oxidative phosphorylation	GO:0006631//GO:0016597//GO:0022892//GO:0043231//GO:0044444	nr +
Unigene60874_All	275	8.37	1.11	1.55	0.00	0.50	0.16	2.15	4.71	0.72	-2.92E+00	6.54E-08	Down	-2.43E+00	2.90E-06	Down	8.97E+00	3.18E-01		7.36E+00	6.92E-01		1.13E+00	3.49E-02		-1.57E+00	6.49E-02				Unigene60874_All//3.00E-07//ES838507				
Unigene60889_All	278	12.05	4.37	10.73	17.20	28.74	11.37	0.15	0.15	0.00	-1.46E+00	4.00E-05	Down	-1.67E-01	6.24E-01		7.40E-01	1.45E-04		-5.97E-01	3.06E-02		-1.72E-02	1.00E+00		-7.25E+00	6.09E-01		Unigene60889_All//gi|166343775|gb|ABU86635.1|//5.00E-13//xyloglucan endotransglycosylase/hydrolase [Gossypium raimondii]	Unigene60889_All//8.00E-14//AT4G37800| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene60889_All//2.00E-116//TC169533			GO:0005576//GO:0016758//GO:0016798//GO:0030312//GO:0044042	nr +
Unigene60890_All	278	3.39	1.82	0.00	0.00	0.12	0.32	0.00	0.00	0.00	-8.94E-01	2.14E-01		-1.17E+01	3.34E-05	Down	6.95E+00	8.25E-01		8.34E+00	4.74E-01		null	null		null	null									
Unigene60893_All	279	12.75	1.82	1.91	0.71	0.86	1.13	0.00	0.00	0.00	-2.81E+00	1.83E-11	Down	-2.74E+00	1.31E-10	Down	2.75E-01	8.95E-01		6.66E-01	6.47E-01		null	null		null	null				Unigene60893_All//8.00E-08//DW505115				ESTscan +
Unigene60894_All	279	2.44	0.00	0.00	0.36	0.25	0.32	2.58	0.30	1.00	-1.13E+01	4.09E-04	Down	-1.13E+01	7.63E-04	Down	-5.33E-01	8.15E-01		-1.41E-01	9.48E-01		-3.10E+00	1.40E-03		-1.37E+00	6.50E-02				Unigene60894_All//5.00E-43//TC160212				ESTscan +
Unigene6090_All	406	5.67	1.87	6.82	2.45	3.82	4.34	0.73	0.93	1.86	-1.60E+00	3.45E-04	Down	2.66E-01	5.14E-01		6.37E-01	2.56E-01		8.22E-01	1.06E-01		3.46E-01	7.38E-01		1.35E+00	6.25E-02		Unigene6090_All//gi|297815228|ref|XP_002875497.1|//5.00E-24//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297321335|gb|EFH51756.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene6090_All//6.00E-25//AT3G29230| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene60905_All	280	4.30	0.00	0.76	0.53	0.49	0.48	1.06	0.45	1.28	-1.21E+01	5.01E-07	Down	-2.50E+00	1.15E-03		-1.18E-01	9.10E-01		-1.41E-01	9.43E-01		-1.24E+00	3.73E-01		2.77E-01	7.87E-01								ESTscan +
Unigene6091_All	280	25.79	29.86	11.03	40.03	30.38	38.23	58.89	79.56	50.79	2.12E-01	3.32E-01		-1.23E+00	1.57E-07	Down	-3.98E-01	1.55E-02		-6.64E-02	7.31E-01		4.34E-01	2.71E-05		-2.13E-01	9.05E-02		Unigene6091_All//gi|225453301|ref|XP_002269466.1|//2.00E-23//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene6091_All//2.00E-06//AT3G60240| EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G); translation initiation factor	Unigene6091_All//5.00E-145//gi|164258161|gb|ES791911.1|ES791911			GO:0005488	nr +
Unigene60911_All	282	2.41	0.00	0.00	0.53	0.12	0.00	0.45	0.15	0.00	-1.12E+01	4.09E-04	Down	-1.12E+01	7.63E-04	Down	-2.12E+00	3.86E-01		-9.05E+00	2.32E-01		-1.60E+00	5.33E-01		-8.81E+00	1.99E-01		Unigene60911_All//gi|30698967|ref|NP_177524.2|//6.00E-06//BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75299562|sp|Q8GWK7.1|BEE3_ARATH RecName: Full=Transcription factor BEE 3; AltName: Full=Protein Brassinosteroid enhanced expression 3; AltName: Full=Transcription factor EN 76; AltName: Full=bHLH transcription factor bHLH050; AltName: Full=Basic helix-loop-helix protein 50; Short=bHLH 50; Short=AtbHLH50	Unigene60911_All//2.00E-07//AT1G73830| BEE3 (BR ENHANCED EXPRESSION 3); DNA binding / transcription factor	Unigene60911_All//3.00E-103//DW510899	bHLH			nr -
Unigene6092_All	318	24.02	6.53	18.92	20.05	19.60	24.57	110.35	58.09	33.07	-1.88E+00	6.08E-15	Down	-3.44E-01	1.35E-01		-3.28E-02	8.99E-01		2.93E-01	1.96E-01		-9.26E-01	8.31E-28		-1.74E+00	6.35E-75	Down			Unigene6092_All//1.00E-164//gi|109826919|gb|DW225628.1|DW225628				
Unigene60927_All	285	59.11	75.56	100.89	54.71	87.36	69.88	203.09	177.01	571.58	3.54E-01	3.05E-03		7.71E-01	2.05E-13		6.75E-01	3.13E-11		3.53E-01	4.43E-03		-1.98E-01	1.83E-03		1.49E+00	3.43E-274	Up	Unigene60927_All//gi|67483357|gb|AAY68034.1|//5.00E-37//3-hydroxy-methylglutaryl coenzyme A reductase [Tilia mjeliana]	Unigene60927_All//2.00E-08//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene60927_All//6.00E-160//gi|13350705|gb|BG441053.1|BG441053		ko00900|Terpenoid backbone biosynthesis	GO:0000166//GO:0005740//GO:0006720//GO:0006732//GO:0009526//GO:0016616//GO:0031090//GO:0031224//GO:0048037	nr -
Unigene60929_All	285	30.47	168.72	115.84	17.48	9.30	30.90	0.00	0.29	0.42	2.47E+00	9.19E-127	Up	1.93E+00	2.04E-62	Up	-9.10E-01	2.71E-04		8.22E-01	1.77E-05		8.20E+00	3.99E-01		8.71E+00	2.42E-01		Unigene60929_All//gi|11547359|ref|NP_001047459.1|//2.00E-37//Os02g0621300 [Oryza sativa Japonica Group] >gi|113536990|dbj|BAF09373.1|Os02g0621300 [Oryza sativa Japonica Group]	Unigene60929_All//2.00E-36//AT1G02205| CER1 (ECERIFERUM 1); octadecanal decarbonylase	Unigene60929_All//2.00E-88//TC135810			GO:0003676//GO:0006260//GO:0006631//GO:0031224//GO:0034061//GO:0043231//GO:0046914	nr +
Unigene60935_All	287	2.19	0.00	0.19	0.52	0.00	0.16	0.59	0.00	0.14	-1.11E+01	7.90E-04	Down	-3.56E+00	8.32E-03		-9.02E+00	1.65E-01		-1.73E+00	5.00E-01		-9.20E+00	1.34E-01		-2.09E+00	3.13E-01		Unigene60935_All//gi|15232885|ref|NP_186882.1|//9.00E-28//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene60935_All//4.00E-29//AT3G02330| pentatricopeptide (PPR) repeat-containing protein	Unigene60935_All//1.00E-52//ES839159				nr -
Unigene60936_All	287	2.92	0.00	0.00	1.39	2.04	1.10	0.59	0.00	0.28	-1.15E+01	5.56E-05	Down	-1.15E+01	1.19E-04	Down	5.55E-01	5.99E-01		-3.34E-01	7.56E-01		-9.20E+00	1.34E-01		-1.09E+00	5.52E-01		Unigene60936_All//gi|15231707|ref|NP_191514.1|//1.00E-11//SYN3 [Arabidopsis thaliana] >gi|30913284|sp|Q9FQ19.2|SCC13_ARATH RecName: Full=Sister chromatid cohesion 1 protein 3; AltName: Full=SCC1 homolog 3; Short=AtRAD21-2 >gi|18157647|gb|AAL62059.1|AF400128_1 RAD21-2 [Arabidopsis thaliana]	Unigene60936_All//1.00E-08//AT3G59550| SYN3				GO:0000087//GO:0009553//GO:0031981	nr +
Unigene60938_All	288	3.63	0.00	1.11	1.04	0.36	0.31	0.00	0.00	0.42	-1.18E+01	3.80E-06	Down	-1.71E+00	2.35E-02		-1.53E+00	2.98E-01		-1.73E+00	2.89E-01		null	null		8.70E+00	2.42E-01		Unigene60938_All//gi|297610300|ref|NP_001064374.2|//2.00E-18//Os10g0337400 [Oryza sativa Japonica Group] >gi|255678310|dbj|BAF26288.2|Os10g0337400 [Oryza sativa Japonica Group]	Unigene60938_All//2.00E-14//AT3G47570| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672//GO:0005488//GO:0044464	nr +
Unigene60943_All	289	2.17	0.00	0.55	0.00	0.24	0.31	0.00	0.00	0.00	-1.11E+01	7.90E-04	Down	-1.97E+00	6.50E-02		7.90E+00	6.06E-01		8.29E+00	4.74E-01		null	null		null	null		Unigene60943_All//gi|301106653|ref|XP_002902409.1|//3.00E-09//medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262098283|gb|EEY56335.1|medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene60943_All//2.00E-07//AT3G45300| IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase			ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation	GO:0016491	nr +
Unigene60944_All	290	4.33	0.00	2.39	2.23	0.95	2.80	0.58	0.58	0.27	-1.21E+01	2.54E-07	Down	-8.59E-01	1.74E-01		-1.23E+00	1.60E-01		3.28E-01	7.01E-01		-1.67E-02	1.02E+00		-1.09E+00	5.52E-01		Unigene60944_All//gi|15225922|ref|NP_182129.1|//9.00E-18//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75100645|sp|Q82363.1|PP203_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At2g46050, mitochondrial; Flags: Precursor	Unigene60944_All//4.00E-19//AT2G46050| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene60947_All	290	2.17	0.00	0.00	0.34	0.24	0.00	0.00	0.00	0.00	-1.11E+01	7.90E-04	Down	-1.11E+01	1.40E-03		-5.32E-01	8.15E-01		-8.42E+00	3.97E-01		null	null		null	null									
Unigene60955_All	291	2.70	0.00	1.28	0.00	0.00	0.62	0.00	0.00	0.00	-1.14E+01	1.09E-04	Down	-1.07E+00	2.10E-01		null	null		9.28E+00	1.94E-01		null	null		null	null		Unigene60955_All//sp|P0A2T6|CRP_SALTY//4.00E-06//Catabolite gene activator OS=Salmonella typhimurium GN=crp PE=4 SV=1						swissprot -
Unigene6096_All	351	2.53	0.00	5.16	8.23	6.08	6.95	1.08	1.79	2.16	-1.13E+01	2.83E-05	Down	1.03E+00	4.43E-02		-4.36E-01	2.44E-01		-2.45E-01	5.61E-01		7.20E-01	4.02E-01		9.92E-01	1.63E-01		Unigene6096_All//gi|302143279|emb|CBI21840.3|//5.00E-08//unnamed protein product [Vitis vinifera]	Unigene6096_All//3.00E-05//AT2G20710| pentatricopeptide (PPR) repeat-containing protein	Unigene6096_All//2.00E-73//ES824314				nr +
Unigene60960_All	292	4.48	1.91	5.65	4.78	1.53	3.25	21.28	2.58	1.50	-1.23E+00	3.96E-02		3.36E-01	5.35E-01		-1.64E+00	3.03E-03		-5.56E-01	3.52E-01		-3.05E+00	8.18E-26	Down	-3.83E+00	1.62E-32	Down	Unigene60960_All//gi|37951219|dbj|BAD00018.1|//1.00E-10//histone 1 [Malus x domestica]		Unigene60960_All//1.00E-83//ES829812			GO:0043229	nr -
Unigene6097_All	538	7.10	17.42	7.42	25.37	25.60	29.47	44.72	19.89	8.15	1.30E+00	7.65E-11	Up	6.44E-02	8.39E-01		1.31E-02	9.59E-01		2.16E-01	1.62E-01		-1.17E+00	6.25E-28	Down	-2.46E+00	2.29E-80	Down	Unigene6097_All//gi|115459574|ref|NP_001053387.1|//6.00E-07//Os04g0530200 [Oryza sativa Japonica Group] >gi|113564958|dbj|BAF15301.1|Os04g0530200 [Oryza sativa Japonica Group]		Unigene6097_All//6.00E-118//DW238255			GO:0044464	nr -
Unigene60973_All	294	2.31	0.00	0.36	0.34	0.47	0.46	0.43	0.57	0.00	-1.12E+01	4.09E-04	Down	-2.68E+00	1.69E-02		4.67E-01	8.76E-01		4.44E-01	8.61E-01		3.98E-01	8.13E-01		-8.75E+00	1.99E-01				Unigene60973_All//8.00E-08//ES851271				
Unigene60976_All	295	2.84	0.17	1.08	0.00	0.12	0.00	0.43	0.43	0.54	-4.05E+00	4.65E-04	Down	-1.39E+00	9.66E-02		6.87E+00	8.25E-01		null	null		-1.69E-02	1.02E+00		3.29E-01	8.50E-01		Unigene60976_All//gi|15219665|ref|NP_171911.1|//4.00E-34//C2 domain-containing protein [Arabidopsis thaliana] >gi|3142295|gb|AAC16746.1| Strong similarity to phosphoribosylanthranilate transferase gb|D86180 from Pisum sativum [Arabidopsis thaliana]	Unigene60976_All//2.00E-35//AT1G04150| C2 domain-containing protein	Unigene60976_All//5.00E-145//TC161305			GO:0030312//GO:0043231	nr -

Unigene6098_All	630	61.54	29.68	13.27	197.28	196.55	137.64	243.35	96.26	103.58	-1.05E+00	7.36E-31	Down	-2.21E+00	2.83E-87	Down	-5.30E-03	9.37E-01		-5.19E-01	3.14E-31		-1.34E+00	9.09E-215	Down	-1.23E+00	2.73E-194	Down	Unigene6098_All//gi|134035502|gb|AB047739.1|/3.00E-54//alpha-tubulin [Gossypium hirsutum]	Unigene6098_All//1.00E-44//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene6098_All//0.00E+00//TC131805		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene60983_All	298	4.39	0.17	0.00	0.00	0.12	0.00	0.00	0.00	0.00	-4.69E+00	1.63E-06	Down	-1.21E+01	3.71E-07	Down	6.85E+00	8.25E-01		null	null		null	null		null	null		Unigene60983_All//gi|225458165|ref|XP_002281033.1|/3.00E-12//PREDICTED: hypothetical protein [Vitis vinifera] >gi|302142555|emb|CBI19758.3| unnamed protein product [Vitis vinifera]					GO:0003677//GO:0006350//GO:0010468	nr -
Unigene6099_All	479	8.74	23.17	9.34	13.10	12.29	12.63	13.95	14.57	10.48	1.41E+00	2.70E-14	Up	9.58E-02	7.45E-01		-9.21E-02	7.54E-01		-5.26E-02	8.50E-01		6.33E-02	7.79E-01		-4.12E-01	3.85E-02		Unigene6099_All//gi|149391353|gb|AB825694.1|/2.00E-11//syntaxin 51 [Oryza sativa Indica Group]		Unigene6099_All//5.00E-112//TC154909		ko04130|SNARE interactions in vesicular transport	GO:0005515//GO:0006810//GO:0031090//GO:0043231	nr -
Unigene60995_All	304	3.79	0.33	1.23	0.16	0.34	0.15	0.28	0.14	0.00	-3.51E+00	6.57E-05	Down	-1.63E+00	2.13E-02		1.05E+00	8.07E-01		-1.41E-01	9.50E-01		-1.02E+00	7.23E-01		-8.12E+00	3.56E-01				Unigene60995_All//6.00E-49//gi|109883863|gb|DW512833.1|DW512833				
Unigene60996_All	304	2.75	40.50	15.24	7.54	12.69	5.50	0.00	1.51	1.18	3.88E+00	1.53E-50	Up	2.47E+00	2.69E-12	Up	7.51E-01	1.36E-02		-4.56E-01	3.09E-01		1.06E+01	1.94E-03		1.02E+01	7.28E-03				Unigene60996_All//2.00E-101//gi|109834722|gb|DW233287.1|DW233287				
Unigene60999_All	304	2.41	0.00	0.00	0.16	0.45	0.00	0.00	0.00	0.00	-1.12E+01	2.11E-04	Down	-1.12E+01	4.12E-04	Down	1.47E+00	6.18E-01		-7.36E+00	6.29E-01		null	null		null	null		Unigene60999_All//COG0702//7.00E-19//Predicted nucleoside-diphosphate-sugar epimerases						cog -
Unigene610_All	1377	0.49	0.88	1.01	1.48	1.48	1.12	0.98	1.15	3.15	8.38E-01	1.73E-01		1.03E+00	8.63E-02		-7.60E-03	9.72E-01		-4.12E-01	3.91E-01		2.31E-01	6.19E-01		1.68E+00	1.73E-09	Up	Unigene610_All//gi|222424819|dbj|BAE82062.1|//2.00E-19//AT2G14850 [Arabidopsis thaliana]	Unigene610_All//2.00E-62//AT2G24530| unknown protein	Unigene610_All//8.00E-92//gi|78328282|gb|DT548556.1|DT548556				nr -
Unigene6100_All	349	24.74	26.57	11.75	79.50	70.75	94.08	125.27	73.77	62.67	1.03E-01	6.15E-01		-1.07E+00	2.53E-07	Down	-1.68E-01	1.27E-01		2.43E-01	1.20E-02		-7.64E-01	4.90E-25		-9.99E-01	3.86E-40		Unigene6100_All//gi|211906438|gb|AC111712.1|/9.00E-42//UDP-D-glucose dehydrogenase [Gossypium hirsutum]	Unigene6100_All//2.00E-40//AT5G39320| UDP-glucose 6-dehydrogenase, putative	Unigene6100_All//1.00E-167//gi|21092999|gb|BQ405312.1|BQ405312		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions	GO:0000166//GO:0008152//GO:0016616//GO:0030312//GO:0043231//GO:0044464//GO:0048037	nr +
Unigene61000_All	304	3.44	0.67	0.35	0.33	0.45	0.30	0.00	0.00	0.00	-2.37E+00	2.49E-03		-3.30E+00	4.58E-04	Down	4.68E-01	8.76E-01		-1.41E-01	9.48E-01		null	null		null	null											
Unigene61010_All	307	3.24	0.00	0.69	1.78	1.23	0.15	0.41	0.00	0.00	-1.17E+01	7.45E-06	Down	-2.22E+00	7.48E-03		-5.33E-01	5.85E-01		-3.60E+00	8.97E-03		-8.69E+00	2.34E-01		-8.69E+00	1.99E-01				Unigene61010_All//3.00E-54//TC161602					
Unigene61027_All	311	7.91	0.49	1.20	0.32	0.00	0.00	0.00	0.13	0.00	-4.02E+00	7.94E-11	Down	-2.72E+00	1.92E-07	Down	-8.32E+00	3.11E-01		-8.32E+00	3.97E-01		7.07E+00	6.31E-01		null	null		Unigene61027_All//gi|224137286|ref|XP_002327088.1|/2.00E-19//cytochrome P450 [Populus trichocarpa] >gi|222835403|gb|EEE73838.1| cytochrome P450 [Populus trichocarpa]	Unigene61027_All//1.00E-16//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene61027_All//6.00E-80//DR462245		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506	nr +
Unigene6104_All	722	4.13	1.33	2.29	2.35	1.57	1.31	0.00	0.00	0.00	-1.63E+00	2.60E-05	Down	-8.53E-01	2.46E-02		-5.76E-01	2.53E-01		-8.37E-01	1.03E-01		null	null		null	null		Unigene6104_All//gi|224092474|ref|XP_002309625.1|//5.00E-68//AP2/EREBP domain-containing transcription factor [Populus trichocarpa] >gi|222855601|gb|EEE93148.1| AP2/EREBP domain-containing transcription factor [Populus trichocarpa]	Unigene6104_All//3.00E-54//AT5G25390| SHN2 (shine2); DNA binding / transcription factor	Unigene6104_All//2.00E-57//TC131290	AP2-EREBP		GO:0000160//GO:0001071//GO:0003677//GO:0006351//GO:0006633//GO:0006950//GO:0010468//GO:0043231	nr +
Unigene61043_All	317	2.97	0.16	0.17	0.63	0.22	0.28	0.00	0.00	0.00	-4.22E+00	1.36E-04	Down	-4.14E+00	2.90E-04	Down	-1.53E+00	4.15E-01		-1.14E+00	5.68E-01		null	null		null	null		Unigene61043_All//gi|147790068|emb|CAN75990.1|/6.00E-08//hypothetical protein [Vitis vinifera]		Unigene61043_All//7.00E-172//TC146815				nr -
Unigene61046_All	319	6.56	0.00	2.17	0.00	0.00	0.00	0.00	0.00	0.00	-1.27E+01	4.25E-12	Down	-1.60E+00	1.18E-03		null	null		null	null		null	null		null	null											
Unigene6105_All	729	37.03	98.21	74.21	77.08	125.93	164.61	48.08	33.31	21.91	1.41E+00	1.92E-88	Up	1.00E+00	2.93E-38	Up	7.08E-01	6.29E-44		1.09E+00	1.50E-107	Up	-5.30E-01	5.98E-11		-1.13E+00	1.45E-39	Down	Unigene6105_All//gi|51457948|gb|AAU03263.1|/5.00E-89//wound/stress protein [Solanum lycopersicum]	Unigene6105_All//6.00E-55//AT4G29730| lipid-associated family protein	Unigene6105_All//0.00E+00//gi|109889740|gb|DW518708.1|DW518708			GO:0009534//GO:0016020	nr -
Unigene61054_All	322	2.44	0.00	0.17	0.62	0.32	0.00	0.00	0.00	0.00	-1.13E+01	1.09E-04	Down	-3.88E+00	1.59E-03		-9.48E-01	5.87E-01		-9.27E+00	1.33E-01		null	null		null	null		Unigene61054_All//gi|124696171|gb|ABN14311.1|/3.00E-07//secoisolariciresinol dehydrogenase [Sinopodophyllum hexandrum]					GO:0003824//GO:0008152	nr -
Unigene61056_All	322	2.76	0.94	0.00	0.93	0.86	0.00	0.00	0.00	0.00	-1.55E+00	4.56E-02		-1.14E+01	6.30E-05	Down	-1.18E-01	9.00E-01		-9.86E+00	3.98E-02		null	null		null	null		Unigene61056_All//gi|210110749|gb|AC107146.1|/2.00E-15//beta-ketoacyl-ACP reductase 1-3 [Arachis hypogaea]	Unigene61056_All//6.00E-16//AT1G24360| 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase			ko01040|Biosynthesis of unsaturated fatty acids//ko00061|Fatty acid biosynthesis	GO:0008152//GO:0016616//GO:0044464	nr +
Unigene6106_All	336	113.36	85.50	131.70	132.24	106.48	141.14	76.76	84.59	37.70	-4.07E-01	2.47E-06		2.16E-01	1.21E-02		-3.13E-01	2.62E-05		9.39E-02	3.11E-01		1.40E-01	1.69E-01		-1.03E+00	4.53E-25	Down	Unigene6106_All//gi|290490837|emb|CBJ34336.1|/8.00E-24//translation initiation factor eIF(iso)4E [Solanum tuberosum]	Unigene6106_All//5.00E-19//AT5G35620| LSP1 (LOSS OF SUSCEPTIBILITY TO POTYVIRUS 1); RNA 7-methylguanosine cap binding / RNA binding / translation initiation factor	Unigene6106_All//2.00E-154//gi|13349857|gb|BG440207.1|BG440207			GO:0000339//GO:0002698//GO:0006412//GO:0008135//GO:0043231//GO:0051707	nr -
Unigene61064_All	328	2.07	0.00	2.11	0.00	0.42	0.14	0.00	0.00	0.00	-1.10E+01	4.09E-04	Down	2.54E-02	9.96E-01		8.71E+00	3.18E-01		7.11E+00	6.92E-01		null	null		null	null											
Unigene61065_All	329	1.91	0.00	0.49	0.15	0.42	0.00	0.00	0.00	0.00	-1.09E+01	7.90E-04	Down	-1.97E+00	6.50E-02		1.47E+00	6.18E-01		-7.24E+00	6.29E-01		null	null		null	null		Unigene61065_All//COG0427//1.00E-15//Acetyl-CoA hydrolase						cog +
Unigene61068_All	332	2.68	0.00	0.16	0.60	0.83	0.82	0.64	0.25	0.36	-1.14E+01	2.85E-05	Down	-4.06E+00	5.15E-04	Down	4.67E-01	8.16E-01		4.44E-01	7.63E-01		-1.34E+00	4.29E-01		-8.23E-01	5.99E-01		Unigene61068_All//gi|33772185|gb|AAG45529.1|/2.00E-11//retroelement polyprotein-like [Malus x domestica]					GO:0003676	nr -
Unigene6107_All	512	27.80	23.95	12.58	75.21	49.97	44.72	159.46	84.49	55.01	-2.15E-01	1.75E-01		-1.14E+00	8.35E-13	Down	-5.90E-01	5.82E-14		-7.50E-01	7.16E-19		-9.16E-01	1.47E-62		-1.54E+00	5.36E-145	Down	Unigene6107_All//gi|224117452|ref|XP_002331716.1|/1.00E-38//Sec61 transport protein [Populus trichocarpa] >gi|222874322|gb|EEF11453.1| Sec61 transport protein [Populus trichocarpa]	Unigene6107_All//7.00E-40//AT2G34250| protein transport protein sec61, putative	Unigene6107_All//0.00E+00//gi|109884814|gb|DW513784.1|DW513784		ko04141|Protein processing in endoplasmic reticulum/ko04145|Phagosome//ko03060|Protein export	GO:0006810//GO:0008320//GO:0043231	nr +
Unigene61075_All	335	1.87	0.00	0.32	1.93	1.75	1.08	0.00	0.12	0.48	-1.09E+01	7.90E-04	Down	-2.56E+00	2.72E-02		-1.46E-01	8.39E-01		-8.42E-01	3.75E-01		6.96E+00	6.31E-01		8.89E+00	1.39E-01		Unigene61075_All//gi|18418552|ref|NP_567972.1|/9.00E-37//SLP2; serine-type peptidase [Arabidopsis thaliana] >gi|2924509|emb|CAA17763.1| subtilisin proteinase-like [Arabidopsis thaliana] >gi|7270449|emb|CAB80215.1| subtilisin proteinase-like [Arabidopsis thaliana]	Unigene61075_All//3.00E-38//AT4G34980| SLP2; serine-type peptidase				GO:0004175//GO:0005515//GO:0009664//GO:0019538//GO:0030312//GO:0044092	nr +
Unigene61077_All	337	2.33	0.00	0.16	0.15	0.00	0.00	0.00	0.00	0.00	-1.12E+01	1.09E-04	Down	-3.88E+00	1.59E-03		-7.21E+00	5.51E-01		-7.21E+00	6.29E-01		null	null		null	null		Unigene61077_All//gi|119416492|emb|CAI34837.1|/3.00E-30//ATP synthase beta chain, mitochondrial precursor [Polytomella sp. Pringsheim 198.80]	Unigene61077_All//1.00E-24//AT5G08690| ATP synthase beta chain 2, mitochondrial			ko00190|Oxidative phosphorylation	GO:0000275//GO:0015078//GO:0015662//GO:0015986//GO:0019829//GO:0032559	nr +
Unigene6108_All	557	11.18	22.65	7.55	13.95	14.84	13.70	20.57	22.89	13.52	1.02E+00	5.08E-10	Up	-5.66E-01	2.28E-02		8.88E-02	7.37E-01		-2.59E-02	9.28E-01		1.54E-01	3.50E-01		-6.06E-01	3.13E-05				Unigene6108_All//8.00E-99//BF274141					
Unigene61083_All	340	4.15	0.45	2.35	0.59	0.10	0.80	0.00	0.00	0.00	-3.22E+00	1.60E-05	Down	-8.23E-01	1.60E-01		-2.53E+00	2.33E-01		4.44E-01	7.63E-01		null	null		null	null		Unigene61083_All//gi|255634612|gb|ACU17668.1|/4.00E-23//unknown [Glycine max]		Unigene61083_All//1.00E-152//CO071225				nr +
Unigene61086_All	341	25.47	1330.93	140.23	111.46	183.59	639.04	559.69	2198.01	1750.91	5.71E+00	0.00E+00	Up	2.46E+00	8.13E-123	Up	7.20E-01	6.73E-31		2.52E+00	0.00E+00	Up	1.97E+00	0.00E+00	Up	1.65E+00	0.00E+00	Up	Unigene61086_All//gi|2865523|gb|AAC02689.1|/4.00E-11//cold regulated LTCOR18 [Lavatera thuringiaca]		Unigene61086_All//3.00E-137//TC160662			GO:0009628	nr -
Unigene611_All	2407	2.39	5.09	2.17	3.68	4.84	3.25	8.66	11.27	17.13	1.09E+00	8.02E-11	Up	-1.41E-01	6.34E-01		3.93E-01	1.69E-02		-1.83E-01	4.12E-01		3.80E-01	4.47E-05		9.84E-01	9.62E-37		Unigene611_All//gi|116310846|emb|CAH67788.1|/3.00E-63//OSIGBa0132E09-OSIGBa0108L24.2 [Oryza sativa (indica cultivar-group)]	Unigene611_All//3.00E-101//AT2G24530| unknown protein	Unigene611_All//4.00E-150//TC172870				nr -
Unigene6110_All	653	2.08	0.16	1.14	1.53	1.37	0.28	2.33	1.02	4.33	-3.75E+00	5.95E-06	Down	-8.68E-01	1.47E-01		-1.54E-01	8.40E-01		-2.46E+00	2.07E-03		-1.19E+00	1.47E-02		8.94E-01	5.71E-03		Unigene6110_All//gi|32527767|gb|AAP86285.1|/1.00E-43//CTR1-like kinase kinase kinase [Brassica juncea] >gi|32527769|gb|AAP86286.1| CTR1-like kinase kinase kinase [Brassica juncea]	Unigene6110_All//9.00E-34//AT1G18160| protein kinase family protein	Unigene6110_All//6.00E-54//DW518755			GO:0004674//GO:0006464//GO:0006970//GO:0032559	nr -
Unigene61102_All	351	2.09	0.14	0.00	0.43	0.39	0.26	0.00	0.00	0.00	-3.85E+00	1.56E-03		-1.10E+01	4.12E-04	Down	-1.18E-01	9.10E-01		-7.27E-01	7.14E-01		null	null		null	null		Unigene61102_All//gi|222423941|dbj|BAH19933.1|//1.00E-07//AT1G63940 [Arabidopsis thaliana]				ko00053|Ascorbate and aldarate metabolism		nr -
Unigene61103_All	351	3.88	0.29	1.97	0.85	0.69	0.26	0.36	0.00	0.11	-3.75E+00	5.95E-06	Down	-9.75E-01	1.09E-01		-3.10E-01	8.20E-01		-1.73E+00	2.89E-01		-8.50E+00	2.34E-01		-1.67E+00	4.76E-01										
Unigene61105_All	353	13.93	0.00	1.51	0.28	0.00	0.26	0.00	0.00	0.00	-1.38E+01	1.88E-28	Down	-3.21E+00	7.22E-17	Down	-8.14E+00	3.11E-01		-1.41E-01	9.48E-01		null	null		null	null											
Unigene61106_All	353	8.15	5.31	16.74	0.14	0.98	0.26	0.00	0.00	0.00	-6.18E-01	9.41E-02		1.01E+00	5.18E-05	Up	2.79E+00	1.14E-01		8.59E-01	7.93E-01		null	null		null	null				Unigene61106_All//7.00E-18//TC178284					
Unigene61107_All	356	3.09	0.00	0.00	0.00	0.77	0.25	0.00	0.00	0.00	-1.16E-01	1.95E-06	Down	-1.16E-01	4.93E-06	Down	9.60E+00	7.00E-02		7.99E+00	4.74E-01		null	null		null	null				Unigene61107_All//1.00E-07//DT462028					
Unigene61110_All	359	4.66	1.69	4.30	2.64	1.25	2.77	1.65	0.00	0.33	-1.46E+00	5.71E-03		-1.17E-01	8.14E-01		-1.08E+00	1.16E-01		7.01E-02	9.38E-01		-1.07E+01	2.39E-04	Down	-2.31E+00	1.36E-02		Unigene61110_All//gi|297719995|ref|NP_001172359.1|/9.00E-18//Os01g0388566 [Oryza sativa Japonica Group] >gi|255673262|dbj|BAH91089.1| Os01g0388566 [Oryza sativa Japonica Group]	Unigene61110_All//3.00E-28//AT2G48060| unknown protein				GO:0044464	nr +
Unigene61117_All	366	4.00	0.83	2.04	0.54	1.13	0.49	0.23	0.11	0.54	-2.27E+00	3.39E-04	Down	-9.75E-01	9.25E-02		1.05E+00	4.25E-01		-1.41E-01	9.34E-01		-1.02E+00	7.23E-01		1.24E+00	4.68E-01										
Unigene61118_All	366	3.86	0.00	0.58	0.14	0.00	0.12	0.00	0.00	0.00	-1.19E+01	3.28E-08	Down	-2.73E+00	1.56E-04	Down	-7.09E+00	5.51E-01		-1.41E-01	9.50E-01		null	null		null	null											
Unigene61120_All	367	2.42	0.28	0.00	1.09	0.84	0.49	0.00	0.11	0.00	-3.13E+00	1.19E-03		-1.12E+01	6.29E-05	Down	-3.63E-01	7.54E-01		-1.14E+00	3.79E-01		6.83E+00	6.31E-01		null	null		Unigene61120_All//gi|115435568|ref|NP_001042542.1|/5.00E-24//Os01g0239000 [Oryza sativa Japonica Group] >gi|113532073|dbj|BAF04156.1| Os01g0239000 [Oryza sativa Japonica Group]	Unigene61120_All//3.00E-22//AT2G20570| GPRI1 (GBF"S PRO-RICH REGION-INTERACTING FACTOR 1); transcription factor/ transcription regulator	Unigene61120_All//4.00E-180//TC150669	G2-like		GO:0001071//GO:0009657//GO:0009908//GO:0010557//GO:0015995//GO:0023060//GO:0032583//GO:0043565	nr -
Unigene61121_All	367	7.13	1.93	2.03	0.27	0.00	0.00	0.00	0.00	0.11	-1.88E+00	1.28E-05	Down	-1.81E+00	4.52E-05	Down	-8.08E+00	3.11E-01		-8.08E+00	3.97E-01		null	null		6.76E+00	6.42E-01		Unigene61121_All//gi|5814093|gb|AAD52097.1|AF088885_1/1.00E-33//receptor-like kinase CHRK1 [Nicotiana tabacum]	Unigene61121_All//1.00E-26//AT1G65800| ARK2 (A. THALIANA RECEPTOR KINASE 2); kinase/ protein kinase/ transmembrane receptor protein serine/threonine kinase	Unigene61121_All//4.00E-75//ES850423		ko04626|Plant-pathogen interaction	GO:0004553//GO:0004672//GO:0006026//GO:0006464//GO:0032559//GO:0043167	nr +
Unigene61125_All	369	1.99	0.00	1.15	0.00	0.84	0.00	0.23	0.00	0.00	-1.10E+01	2.11E-04	Down	-7.82E-01	3.80E-01		9.71E+00	4.54E-02		null	null		-7.84E+00	4.01E-01		-7.84E+00	3.56E-01		Unigene61125_All//gi|222839441|gb|EEE77778.1|//2.00E-10//predicted protein [Populus trichocarpa]						nr +
Unigene61128_All	373	3.79	1.09	0.57	0.27	1.02	0.24	0.00	0.00	0.00	-1.80E+00	3.03E-03		-2.73E+00	1.56E-04	Down	1.93E+00	1.94E-01		-1.41E-01	9.48E-01		null	null		null	null		Unigene61128_All//gi|1272349|gb|AAA97903.1|/4.00E-19//secreted glycoprotein 3 [Ipomoea trifida]	Unigene61128_All//2.00E-17//AT4G27290| ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding	Unigene61128_All//4.00E-32//TC142819			GO:0000166//GO:0004672//GO:0009987	nr -

Unigene61131_All	375	3.77	1.49	0.28	0.93	0.00	0.48	0.23	1.00	0.42	-1.34E+00	2.00E-02		-3.73E+00	8.89E-06	Down	-9.86E+00	9.44E-03		-9.49E-01	4.80E-01		2.15E+00	9.44E-02		9.14E-01	6.24E-01		Unigene61131_All//gi|18412763|ref|NP_567278.1|//2.00E-46//GSL1 (GLUCAN SYNTHASE-LIKE 1); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75199658|sp|Q8S8|0.1|CALSB_ARATH RecName: Full=Callose synthase 11; AltName: Full=1,3-beta-glucan synthase; AltName: Full=Protein GLUCAN SYNTHASE-LIKE 1 >gi|5732072|gb|AAD48971.1|AF162444_3 contains similarity to glucan synthases [Arabidopsis thaliana] >gi|7267256|emb|CAB81039.1|AT4g04970 [Arabidopsis thaliana]	Unigene61131_All//7.00E-48//AT4G04970| GSL1 (GLUCAN SYNTHASE-LIKE 1); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups	Unigene61131_All//1.00E-25//TC176933			GO:0002218//GO:0006074//GO:0009887//GO:0010260//GO:0016020//GO:0020333//GO:0031410//GO:0033251//GO:0043234//GO:0048229//GO:0051707//GO:0052482	nr -
Unigene61133_All	379	1.79	3.07	0.00	0.39	0.73	0.00	0.22	0.44	0.74	7.77E-01	2.17E-01		-1.08E+01	7.63E-04	Down	8.83E-01	5.95E-01		-8.62E+00	2.32E-01		9.83E-01	6.33E-01		1.72E+00	2.30E-01									ESTscan +
Unigene61136_All	382	2.33	0.00	3.62	0.39	0.36	0.12	0.00	0.00	0.42	-1.12E+01	2.85E-05	Down	6.38E-01	2.82E-01		-1.18E-01	9.10E-01		-1.73E+00	5.00E-01		null	null		8.70E+00	1.39E-01									
Unigene61138_All	383	1.78	0.00	0.14	0.39	0.45	0.00	0.00	0.00	0.00	-1.08E+01	4.09E-04	Down	-3.68E+00	4.81E-03		2.04E-01	9.49E-01		-8.61E+00	2.32E-01		null	null		null	null		Unigene61138_All//gi|160900595|ref|YP_001566177.1|//4.00E-19//ABC transporter related [Delftia acidovorans SPH-1] >gi|160366179|gb|ABX37792.1| ABC transporter related [Delftia acidovorans SPH-1]	Unigene61138_All//7.00E-07//AT1G65410| ATNAP11 (ARABIDOPSIS THALIANA NON-INTRINSIC ABC PROTEIN 11); transporter				GO:0006810//GO:0017111//GO:0022891//GO:0032559//GO:0043231//GO:0044444	nr -
Unigene61141_All	390	7.38	2.73	1.91	0.77	0.00	0.93	0.22	0.21	0.61	-1.44E+00	2.02E-04	Down	-1.95E+00	5.30E-06	Down	-9.58E+00	2.01E-02		2.74E-01	8.32E-01		-1.67E-02	1.01E+00		1.50E+00	3.39E-01		Unigene61141_All//gi|34550779|gb|AQ74955.1|//8.00E-27/Ghiaa-Re [Gossypium barbadense]	Unigene61141_All//5.00E-21//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene61141_All//5.00E-22//gi|164312964|gb|EX167835.1|EX167835			GO:0001071//GO:0003676//GO:0005515//GO:0006412//GO:0009755//GO:0010468//GO:0043231	nr +
Unigene61142_All	391	4.42	0.78	0.54	0.38	0.18	0.46	0.00	0.00	0.00	-2.51E+00	2.66E-05	Down	-3.02E+00	6.59E-06	Down	-1.12E+00	5.83E-01		2.74E-01	9.04E-01		null	null		null	null		Unigene61142_All//gi|73761705|gb|AA283352.1|//4.00E-54//myb transcription factor MYB30 [Gossypium hirsutum]	Unigene61142_All//2.00E-50//AT5G62470| MYB96 (myb domain protein 96); DNA binding / transcription factor	Unigene61142_All//5.00E-93//gi|11201104|gb|BF270109.1|BF270109	MYB		GO:0001071//GO:0003676//GO:0006970//GO:0009725//GO:0010468//GO:0043231	nr +
Unigene61143_All	393	3.86	0.00	0.14	0.38	0.35	0.34	0.00	0.00	0.00	-1.19E+01	8.33E-09	Down	-4.83E+00	3.80E-07	Down	-1.18E-01	9.10E-01		-1.41E-01	9.43E-01		null	null		null	null									
Unigene61144_All	393	3.59	0.64	1.22	0.51	0.00	0.46	0.43	0.43	0.91	-2.48E+00	2.00E-04	Down	-1.56E+00	1.19E-02		-8.99E+00	8.40E-02		-1.41E-01	9.34E-01		-1.65E-02	1.02E+00		1.08E+00	3.49E-01									
Unigene61145_All	400	2.75	0.25	0.00	0.25	1.12	0.23	0.21	0.00	0.40	-3.44E+00	1.19E-04	Down	-1.14E+01	4.93E-06	Down	2.17E+00	1.06E-01		-1.42E-01	9.48E-01		-7.72E+00	4.01E-01		9.14E-01	6.24E-01		Unigene61145_All//gi|6714305|gb|AAF26001.1|AC013354_20//4.00E-42//F15H18.4 [Arabidopsis thaliana]	Unigene61145_All//2.00E-43//AT1G18485| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene61156_All	413	3.29	0.74	1.68	0.00	0.83	1.20	0.20	0.00	0.39	-2.16E+00	9.05E-04	Down	-9.75E-01	1.09E-01		9.70E+00	3.01E-02		1.02E+01	4.38E-03		-7.68E+00	4.01E-01		9.14E-01	6.24E-01				Unigene61156_All//1.00E-07//gi|13351136|gb|BG441484.1|BG441484					
Unigene61158_All	421	0.50	0.24	1.01	0.00	0.08	0.00	2.01	0.50	0.28	-1.05E+00	5.64E-01		1.03E+00	3.96E-01		6.35E+00	8.24E-01		null	null		-2.02E+00	7.45E-03		-2.82E+00	5.38E-04	Down	Unigene61158_All//gi|297822505|ref|XP_002879135.1|//4.00E-47//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297324974|gb|EFH55394.1|nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene61158_All//1.00E-47//AT2G27790| nucleic acid binding / nucleotide binding	Unigene61158_All//0.00E+00//gi|164279280|gb|ES798292.1|ES798292			GO:0005488	nr -
Unigene61162_All	428	1.47	0.00	0.62	0.70	0.40	0.00	0.00	0.00	0.00	-1.05E+01	7.90E-04	Down	-1.24E+00	2.13E-01		-7.96E-01	5.56E-01		-9.45E+00	3.98E-02		null	null		null	null									ESTscan -
Unigene61163_All	428	1.59	0.00	0.37	0.00	0.64	0.53	0.00	0.00	0.00	-1.06E+01	4.09E-04	Down	-2.09E+00	4.38E-02		9.33E+00	7.00E-02		9.04E+00	1.18E-01		null	null		null	null		Unigene61163_All//gi|219125760|ref|XP_002183141.1|//2.00E-10//predicted protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|217405416|gb|EEC45359.1|predicted protein [Phaeodactylum tricornutum CCAP 1055/1]						nr -
Unigene61165_All	442	3.55	0.00	0.24	0.45	0.55	0.61	0.00	0.00	0.00	-1.18E+01	4.20E-09	Down	-3.88E+00	1.55E-06	Down	2.75E-01	8.95E-01		4.44E-01	7.63E-01		null	null		null	null		Unigene61165_All//gi|224097158|ref|XP_002310856.1|//6.00E-30//SAUR family protein [Populus trichocarpa] >gi|222853759|gb|EEE91306.1| SAUR family protein [Populus trichocarpa]	Unigene61165_All//3.00E-30//AT2G21220| auxin-responsive protein, putative	Unigene61165_All//3.00E-24//DW503189			GO:0009725	nr +
Unigene61166_All	442	1.18	4.36	3.25	0.56	0.31	0.10	0.00	0.00	0.09	1.88E+00	2.67E-04	Up	1.46E+00	1.58E-02		-8.55E-01	5.73E-01		-2.46E+00	2.23E-01		null	null		6.49E+00	6.42E-01		Unigene61166_All//gi|170111|gb|AAA34029.1|//5.00E-06//ferredoxin-NADP oxidoreductase [Spinacia oleracea]	Unigene61166_All//1.00E-06//AT5G66190| FNR1 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron transp	Unigene61166_All//8.00E-43//TC150641		ko00195|Photosynthesis		nr +
Unigene61171_All	461	2.04	3.85	3.00	1.40	2.02	2.74	3.58	1.09	1.21	9.13E-01	6.42E-02		5.56E-01	3.62E-01		5.22E-01	5.25E-01		9.66E-01	1.22E-01		-1.72E+00	4.44E-04	Down	-1.56E+00	7.74E-04	Down	Unigene61171_All//gi|115439877|ref|NP_001044218.1|//1.00E-23//Os01g0743400 [Oryza sativa Japonica Group] >gi|113533749|dbj|BAF06132.1|Os01g0743400 [Oryza sativa Japonica Group]	Unigene61171_All//2.00E-16//AT2G25840| ONA4 (ovule abortion 4); ATP binding / aminoacyl-tRNA ligase/ nucleotide binding / tryptophan-tRNA ligase	Unigene61171_All//0.00E+00//DW518946		ko00380|Tryptophan metabolism//ko00970|Aminoacyl-tRNA biosynthesis	GO:0003006//GO:0004812//GO:0006418//GO:0009536//GO:0032559	nr +
Unigene61174_All	554	2.36	0.91	0.19	0.09	0.81	1.06	1.14	0.00	0.07	-1.37E+00	2.40E-02		-3.62E+00	2.81E-05	Down	3.17E+00	3.95E-02		3.56E+00	8.47E-03		-1.02E+01	1.23E-04	Down	-3.99E+00	5.82E-04	Down	Unigene61174_All//gi|25453189|sp|O22959.1|PER19_ARATH//3.00E-71//RecName: Full=Peroxidase 19; Short=Atperox P19; AltName: Full=ATP51; Flags: Precursor	Unigene61174_All//2.00E-72//AT2G34060| peroxidase, putative			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209//GO:0031410	nr -
Unigene61175_All	575	5.64	2.56	0.37	0.00	0.60	0.16	0.00	0.00	0.00	-1.14E+00	1.12E-03		-3.93E+00	3.19E-13	Down	9.23E+00	3.01E-02		7.30E+00	4.74E-01		null	null		null	null		Unigene61175_All//gi|79536804|ref|NP_200133.2|//2.00E-65//SPCH (SPEECHLESS); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75294400|sp|Q700C7.1|SPCH_ARATH RecName: Full=Transcription factor SPEECHLESS; AltName: Full=Transcription factor EN 19; AltName: Full=bHLH transcription factor bHLH098; AltName: Full=Basic helix-loop-helix protein 98; Short=bHLH 98; Short=AtbHLH98 >gi|45935051|gb|AAS79560.1| basic helix-loop-helix family protein [Arabidopsis thaliana] >gi|112889216|gb|ABI26170.1|SPEECHLESS [Arabidopsis thaliana]	Unigene61175_All//3.00E-37//AT5G53210| SPCH (SPEECHLESS); DNA binding / transcription factor		bHLH		GO:0001071//GO:0009791//GO:0010468//GO:0043231	nr +
Unigene61176_All	593	3.09	0.34	0.99	0.67	0.23	0.61	0.14	0.00	0.00	-3.18E+00	6.73E-07	Down	-1.64E+00	2.15E-03		-1.53E+00	2.05E-01		-1.41E-01	9.04E-01		-7.16E+00	4.01E-01		-7.16E+00	3.56E-01		Unigene61176_All//gi|46931312|gb|AAT06460.1|//4.00E-12//At4g02810 [Arabidopsis thaliana]	Unigene61176_All//2.00E-09//AT4G02810| unknown protein	Unigene61176_All//0.00E+00//gi|78326786|gb|DT547060.1|DT547060				nr -
Unigene61177_All	596	3.16	0.77	1.34	1.00	0.46	0.15	0.78	0.63	0.27	-2.05E+00	1.17E-04	Down	-1.24E+00	1.45E-02		-1.12E+00	2.26E-01		-2.73E+00	1.74E-02		-3.06E-01	7.36E-01		-1.55E+00	1.16E-01		Unigene61177_All//gi|297848736|ref|XP_002892249.1|//2.00E-36//high mobility group family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338091|gb|EFH68508.1| high mobility group family protein [Arabidopsis lyrata subsp. lyrata]	Unigene61177_All//2.00E-37//AT1G04880| high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein	Unigene61177_All//0.00E+00//DT458816		ko03410|Base excision repair	GO:0001071//GO:0003676//GO:0010468//GO:0043231	nr -
Unigene61180_All	658	4.69	0.85	0.00	0.53	0.58	0.07	0.13	0.00	0.12	-2.47E+00	8.57E-09	Down	-1.22E+01	6.36E-17	Down	1.20E-01	9.58E-01		-2.95E+00	8.30E-02		-7.01E+00	4.01E-01		-8.56E-02	9.70E-01		Unigene61180_All//gi|152926166|gb|ABS32237.1|//2.00E-72//asymmetric leaves 2 [Carica papaya]	Unigene61180_All//2.00E-39//AT1G65620| AS2 (ASYMMETRIC LEAVES 2); protein binding	Unigene61180_All//0.00E+00//gi|78340302|gb|DT560576.1|DT560576		ko00240|Pyrimidine metabolism//ko03018|RNA degradation//ko00250|Alanine, aspartate and glutamate metabolism	GO:0005488//GO:0009943//GO:0031981//GO:0048437	nr -
Unigene61181_All	749	3.49	0.20	1.07	0.07	0.00	0.00	0.85	0.22	2.39	-4.11E+00	1.19E-11	Down	-1.71E+00	9.47E-05	Down	-6.06E+00	5.51E-01		-6.06E+00	6.29E-01		-1.92E+00	3.09E-02		1.50E+00	7.33E-04	Up	Unigene61181_All//gi|115472647|ref|NP_001059922.1|//5.00E-37//Os07g0546400 [Oryza sativa Japonica Group] >gi|113611458|dbj|BAF21836.1|Os07g0546400 [Oryza sativa Japonica Group]	Unigene61181_All//1.00E-30//AT3G22104| phototropic-responsive NPH3 protein-related	Unigene61181_All//7.00E-20//TC163220				nr -
Unigene61182_All	765	4.24	1.72	1.11	0.72	1.26	0.59	0.33	0.00	0.00	-1.30E+00	2.56E-04	Down	-1.93E+00	1.33E-06	Down	8.15E-01	2.80E-01		-2.79E-01	7.57E-01		-8.37E+00	4.03E-02		-8.37E+00	3.03E-02		Unigene61182_All//gi|27728716|gb|AA018665.1|//5.00E-51//wax synthase isoform 2 [Vitis vinifera]	Unigene61182_All//4.00E-45//AT5G55340| long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein	Unigene61182_All//0.00E+00//TC178778			GO:0005488//GO:0016740	nr -
Unigene61183_All	217	0.00	6.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.50E-07	Up	null	null		null	null		null	null		null	null		null	null									
Unigene61184_All	296	0.00	3.94	0.36	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.05E-06	Up	8.49E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene61184_All//sp|P33270|CP6A2_DROME//1.00E-17//Cytochrome P450 6a2 OS=Drosophila melanogaster GN=Cyp6a2 PE=2 SV=2						swissprot -
Unigene61187_All	344	4.87	5.01	3.41	3.04	3.00	4.07	3.81	4.01	1.04	4.12E-02	9.50E-01		-5.15E-01	3.44E-01		-1.81E-02	9.61E-01		4.21E-01	4.92E-01		7.36E-02	8.96E-01		-1.87E+00	6.93E-04	Down			Unigene61187_All//5.00E-59//ES843768					
Unigene61188_All	385	0.00	4.21	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.96E-09	Up	7.11E+00	6.34E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene61189_All	245	458.71	242.80	215.61	665.48	664.11	817.37	849.92	400.39	466.36	-9.18E-01	2.09E-70		-1.09E+00	2.90E-90	Down	-3.00E-03	9.51E-01		2.97E-01	6.82E-18		-1.09E+00	1.26E-209	Down	-8.66E-01	6.51E-148		Unigene61189_All//gi|66775524|gb|AAY56337.1|//4.00E-41//elongation factor-1 alpha [Musa acuminata]	Unigene61189_All//1.00E-40//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene61189_All//5.00E-129//BE054704			GO:0004779//GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene6119_All	490	8.01	6.10	3.80	20.43	18.48	18.16	20.28	11.69	14.47	-3.93E-01	2.13E-01		-1.07E+00	9.77E-04	Down	-1.45E-01	5.01E-01		-1.70E-01	4.17E-01		-7.95E-01	1.02E-06		-4.87E-01	2.01E-03				Unigene6119_All//6.00E-13//TC159992					
Unigene61191_All	648	1.29	0.63	1.23	1.69	0.21	0.07	0.00	0.00	0.18	-1.05E+00	1.74E-01		-6.78E-02	9.40E-01		-2.99E+00	6.16E-05	Down	-4.60E+00	8.28E-06	Down	null	null		7.53E+00	2.42E-01		Unigene61191_All//gi|62319841|dbj|BAD93873.1|//4.00E-19//dihydropyrimidinase like protein [Arabidopsis thaliana]	Unigene61191_All//2.00E-20//AT5G12200| dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2)	Unigene61191_All//2.00E-78//ES807046		ko00240|Pyrimidine metabolism//ko00410|beta-Alanine metabolism//ko00770|Pantothenate and CoA biosynthesis	GO:0016812//GO:0031410	nr -
Unigene61192_All	267	0.00	3.04	2.59	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.37E-05	Up	1.13E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene61192_All//sp|Q23997|CH47_DROME//7.00E-30//Chitinase-like protein DS47 OS=Drosophila melanogaster GN=Chit PE=1 SV=2						swissprot -

Unigene61193_All	360	0.00	9.43	2.96	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	2.54E-19	Up	1.15E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene61193_All//gi|51948476|ref|NP_001004250.1|//6.00E-36//cytochrome b-c1 complex subunit 1, mitochondrial precursor [Rattus norvegicus] >gi|81884378|sp|Q68FY0.1|QCR1_RAT RecName: Full=Cytochrome b-c1 complex subunit 1, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex core protein I; AltName: Full=Core protein I; AltName: Full=Complex III subunit 1; Flags: Precursor >gi|51259340|gb|AAH78923.1| Ubiquinol-cytochrome c reductase core protein I [Rattus norvegicus] >gi|149018490|gb|EDL77133.1| ubiquinol-cytochrome c reductase core protein 1, isoform CRA_a [Rattus norvegicus]	Unigene61193_All//8.00E-30//AT3G02090| mitochondrial processing peptidase beta subunit, putative				GO:0003824//GO:0005515//GO:0005746//GO:0009536//GO:0010033//GO:0019538//GO:0022904//GO:0030312//GO:0031980//GO:0031981//GO:0046914	nr -
Unigene61195_All	257	0.00	13.60	2.49	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	6.73E-20	Up	1.13E+01	1.16E-03		null	null		null	null		null	null		null	null								
Unigene61197_All	281	18.25	6.31	9.48	35.10	38.48	53.84	109.54	39.86	58.55	-1.53E+00	6.75E-08	Down	-9.46E-01	6.41E-04		1.33E-01	5.42E-01		6.17E-01	1.10E-05		-1.46E+00	1.10E-49	Down	-9.04E-01	2.97E-24		Unigene61197_All//gi|115439863|ref|NP_001044211.1|//3.00E-44//Os01g0742200 [Oryza sativa Japonica Group] >gi|113533742|dbj|BAF06125.1| Os01g0742200 [Oryza sativa Japonica Group]	Unigene61197_All//1.00E-43//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene61197_All//8.00E-153//gi|78339711|gb|DT559985.1|DT559985			GO:0008135//GO:0010467//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene61198_All	252	1.45	10.46	2.11	5.34	6.15	3.58	2.85	6.97	12.49	2.85E+00	1.15E-08	Up	5.40E-01	6.10E-01		2.04E-01	7.58E-01		-5.74E-01	3.45E-01		1.29E+00	4.31E-03		2.13E+00	2.07E-09	Up			Unigene61198_All//3.00E-87//ES841444				
Unigene61199_All	708	0.00	12.95	3.31	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.65E-52	Up	1.17E+01	6.40E-13	Up	null	null		null	null		null	null		null	null								GO:0003824	nr -
Unigene6120_All	327	13.92	3.41	5.21	25.59	23.90	37.57	68.79	26.84	44.59	-2.03E+00	4.20E-10	Down	-1.42E+00	4.49E-06	Down	-9.84E-02	6.76E-01		5.54E-01	4.91E-04		-1.36E+00	7.45E-33	Down	-6.25E-01	6.64E-10		Unigene6120_All//gi|196166896|gb|AGT0967.1|//4.00E-59//translation elongation factor 1 [Ziziphus jujuba]	Unigene6120_All//4.00E-60//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene6120_All//0.00E+00//gi|13354929|gb|BG445277.1|BG445277			GO:0006412//GO:0008135//GO:0016772//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene61200_All	332	0.00	4.88	0.96	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.96E-09	Up	9.91E+00	4.50E-02		null	null		null	null		null	null		null	null								ESTscan -
Unigene61202_All	327	0.00	12.24	2.12	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	8.54E-23	Up	1.10E+01	6.15E-04	Up	null	null		null	null		null	null		null	null								nr +
Unigene61203_All	483	0.00	2.62	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.86E-07	Up	9.78E+00	1.38E-02		null	null		null	null		null	null		null	null								
Unigene61204_All	478	0.00	7.95	0.89	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.23E-21	Up	9.80E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene61204_All//gi|301095248|ref|XP_002896725.1|//9.00E-53//enoyl-CoA hydratase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262108786|gb|EEY66838.1| enoyl-CoA hydratase, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene61204_All//3.00E-27//AT4G16810| enoyl-CoA hydratase, putative			ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism	GO:0016829	nr +
Unigene61208_All	235	0.00	9.27	2.04	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	2.11E-12	Up	1.10E+01	7.47E-03		null	null		null	null		null	null		null	null								
Unigene61209_All	577	0.00	2.28	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.49E-07	Up	9.85E+00	4.03E-03		null	null		null	null		null	null		null	null								ESTscan +
Unigene6122_All	423	29.07	19.64	18.00	36.74	29.23	29.25	92.46	39.42	40.22	-5.65E-01	4.39E-04		-6.91E-01	3.47E-05		-3.30E-01	1.73E-02		-3.29E-01	2.33E-02		-1.23E+00	1.34E-48	Down	-1.20E+00	3.21E-48	Down	Unigene6122_All//gi|297833728|ref|XP_002884746.1|//6.00E-27//40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata] >gi|297330586|gb|EFH61005.1| 40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata]	Unigene6122_All//4.00E-28//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene6122_All//0.00E+00//DW519268		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene61230_All	396	0.00	2.18	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	4.94E-05	Up	8.66E+00	2.38E-01		null	null		null	null		null	null		null	null		Unigene61230_All//gi|297814115|ref|XP_002874941.1|//1.00E-39//Os01g0254000 [Arabidopsis lyrata subsp. lyrata] >gi|297320778|gb|EFH51200.1| Os01g0254000 [Arabidopsis lyrata subsp. lyrata]	Unigene61230_All//8.00E-41//AT3G62560| GTP-binding protein, putative			ko04141|Protein processing in endoplasmic reticulum	GO:0000166//GO:0015031//GO:0043231	nr +
Unigene61233_All	202	0.78	1.00	0.00	1.48	0.51	1.34	8.58	25.45	56.60	3.69E-01	8.16E-01		-9.60E+00	2.43E-01		-1.53E+00	2.98E-01		-1.41E-01	9.20E-01		1.57E+00	7.54E-10	Up	2.72E+00	1.52E-42	Up	Unigene61233_All//gi|13111661|gb|AG45487.1|//2.00E-17//phospholipase PLDb1 [Solanum lycopersicum]	Unigene61233_All//1.00E-15//AT4G11850| PLDGAMMA1; phospholipase D	Unigene61233_All//4.00E-09//TC159458		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr -
Unigene61234_All	206	0.00	0.25	0.00	0.00	0.00	0.22	0.41	0.61	6.19	7.94E+00	6.14E-01		null	null		null	null		7.78E+00	6.92E-01		5.68E-01	7.81E-01		3.91E+00	4.24E-07	Up			Unigene61234_All//4.00E-43//DV850071				
Unigene6125_All	351	5.66	3.46	3.34	5.11	7.26	7.98	33.97	13.10	7.26	-7.09E-01	1.20E-01		-7.63E-01	1.14E-01		5.07E-01	2.25E-01		6.43E-01	9.59E-02		-1.37E+00	4.07E-18	Down	-2.23E+00	8.89E-36	Down	Unigene6125_All//gi|297833728|ref|XP_002884746.1|//4.00E-15//40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata] >gi|297330586|gb|EFH61005.1| 40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata]	Unigene6125_All//1.00E-12//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene6125_All//6.00E-151//gi|13349793|gb|BG440143.1|BG440143		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr +
Unigene6126_All	471	10.00	6.67	2.83	14.07	14.40	15.44	49.82	12.60	11.59	-5.84E-01	3.59E-02		-1.82E+00	1.12E-08	Down	3.41E-02	9.05E-01		1.34E-01	6.31E-01		-1.98E+00	2.38E-58	Down	-2.10E+00	6.41E-65	Down	Unigene6126_All//gi|297833728|ref|XP_002884746.1|//2.00E-16//40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata] >gi|297330586|gb|EFH61005.1| 40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata]	Unigene6126_All//1.00E-17//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene6126_All//4.00E-171//gi|13349793|gb|BG440143.1|BG440143		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene61266_All	450	0.00	3.60	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.96E-09	Up	1.07E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene61266_All//gi|6647578|sp|P70580.3|PGRC1_RAT//2.00E-26//RecName: Full=Membrane-associated progesterone receptor component 1; AltName: Full=Acidic 25 kDa protein; AltName: Full=25-DX; AltName: Full=Ventral midline antigen; Short=VEMA >gi|6572674|gb|AAF17359.1|AF163321_1 ventral midline antigen VEMA [Rattus norvegicus] >gi|38303845|gb|AAH62073.1| Pgrmc1 protein [Rattus norvegicus] >gi|149059999|gb|EDM10815.1| rCG53263 [Rattus norvegicus]	Unigene61266_All//4.00E-17//AT5G52240| MSBP1 (membrane steroid binding protein 1); steroid binding				GO:0005488//GO:0005634//GO:0006091//GO:0006935//GO:0016020//GO:0044446	nr -
Unigene6127_All	1829	0.00	0.80	0.06	0.05	0.30	2.05	23.28	14.35	79.35	9.65E+00	2.11E-08	Up	5.86E+00	3.96E-01		2.47E+00	4.04E-02		5.23E+00	1.08E-19	Up	-6.98E-01	5.78E-21		1.77E+00	0.00E+00	Up	Unigene6127_All//gi|15235965|ref|NP_194034.1|//0.00E+00//MATE efflux protein-related [Arabidopsis thaliana]	Unigene6127_All//2.00E-172//AT4G23030| MATE efflux protein-related	Unigene6127_All//0.00E+00//TC161363			GO:0015291//GO:0015893//GO:0044464	nr -
Unigene61284_All	680	0.00	3.28	0.47	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.09E-12	Up	8.88E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene61284_All//gi|224005945|ref|XP_002291933.1|//1.00E-13//trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972452|gb|EED90784.1| trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]					GO:0003824	nr +
Unigene6129_All	1419	1.92	0.64	0.68	7.76	3.47	5.54	1.61	0.44	0.67	-1.58E+00	1.00E-04	Down	-1.51E+00	3.26E-04	Down	-1.16E+00	7.21E-13	Down	-4.86E-01	4.26E-03		-1.86E+00	6.67E-06	Down	-1.26E+00	7.78E-04	Down	Unigene6129_All//gi|223452286|gb|ACM89471.1|//1.00E-122//FERONIA receptor-like kinase [Glycine max]	Unigene6129_All//7.00E-105//AT5G39000| protein kinase family protein	Unigene6129_All//2.00E-12//ES792591		ko04626|Plant-pathogen interaction		nr -
Unigene6130_All	1342	0.16	6.49	0.40	0.45	1.21	1.01	1.83	7.19	9.35	5.38E+00	1.49E-43	Up	1.35E+00	2.25E-01		1.44E+00	6.58E-03		1.18E+00	4.74E-02		1.98E+00	2.79E-24	Up	2.36E+00	1.11E-39	Up							
Unigene6131_All	1660	0.57	0.40	0.42	2.70	2.05	1.39	4.18	0.23	1.42	-5.16E-01	4.57E-01		-4.44E-01	5.54E-01		-3.95E-01	1.71E-01		-9.61E-01	6.60E-04		-4.20E+00	2.02E-37	Down	-1.56E+00	2.15E-13	Down	Unigene6131_All//gi|224115078|ref|XP_002316934.1|//2.00E-84//cyclic nucleotide-gated channel [Populus trichocarpa] >gi|222859999|gb|EEE97546.1| cyclic nucleotide-gated channel [Populus trichocarpa]						nr +
Unigene61310_All	1075	0.10	5.28	3.81	0.00	0.00	0.00	0.00	0.00	0.07	5.76E+00	3.32E-29	Up	5.29E+00	6.98E-20	Up	null	null		null	null		null	null		6.21E+00	4.02E-01		Unigene61310_All//gi|145353601|ref|XP_001421096.1|//1.00E-128//Receptor of activated protein kinase C 1A, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|145357301|ref|XP_001422858.1| Receptor of activated protein kinase C 1B, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|144581332|gb|AB099389.1| Receptor of activated protein kinase C 1A, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|144583102|gb|AB901217.1| Receptor of activated protein kinase C 1B, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901]	Unigene61310_All//5.00E-113//AT3G18130| RACK1C_AT (RECEPTOR FOR ACTIVATED C KINASE 1 C); nucleotide binding	Unigene61310_All//1.00E-15//TC154573		ko03040|Spliceosome//ko03022|Basal transcription factors		nr +
Unigene61314_All	457	0.00	3.22	1.17	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.11E-08	Up	1.02E+01	4.03E-03		null	null		null	null		null	null		null	null		Unigene61314_All//sp|P51911|CNN1_HUMAN//2.00E-37//Calponin-1 OS=Homo sapiens GN=CNN1 PE=1 SV=2						swissprot +
Unigene6132_All	788	3.45	7.33	7.10	12.52	9.75	14.21	5.31	4.72	3.54	1.09E+00	1.73E-05	Up	1.04E+00	8.76E-05	Up	-3.61E-01	4.53E-02		1.83E-01	3.56E-01		-1.70E-01	5.88E-01		-5.86E-01	2.22E-02				Unigene6132_All//7.00E-20//TC159803				
Unigene6133_All	1091	0.14	0.60	0.54	0.87	1.39	1.03	1.51	2.11	3.07	2.07E+00	3.92E-02		1.90E+00	8.47E-02		6.79E-01	2.26E-01		2.55E-01	6.91E-01		4.79E-01	2.23E-01		1.02E+00	5.76E-04	Up	Unigene6133_All//gi|297826853|ref|XP_002881309.1|//1.00E-07//Trigida-essential 1 [Arabidopsis lyrata subsp. lyrata] >gi|297327148|gb|EFH57568.1| trigida-essential 1 [Arabidopsis lyrata subsp. lyrata]	Unigene6133_All//5.00E-08//AT2G38835| FES1; nucleic acid binding / zinc ion binding	Unigene6133_All//0.00E+00//gi|164258324|gb|ES800887.1|ES800887	C3H			nr +

Unigene61339_All	356	0.00	3.99	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.06E-08	Up	1.04E+01	7.47E-03		null	null		null	null		null		null	null		Unigene61339_All//gi|15242041|ref|NP_197570.1|//1.00E-22//senescence-associated protein-related [Arabidopsis thaliana] >gi|30725354|gb|AAP37699.1|At5g20700 [Arabidopsis thaliana]	Unigene61339_All//1.00E-14//AT5G20700| senescence-associated protein-related					nr +
Unigene6135_All	1201	1.00	0.13	0.18	4.36	2.35	2.26	4.65	6.89	12.74	-2.98E+00	1.58E-04	Down	-2.50E+00	1.15E-03		-8.89E-01	2.49E-04		-9.49E-01	2.31E-04		5.68E-01	1.55E-03		1.45E+00	1.58E-25	Up	Unigene6135_All//gi|225322818|gb|ACN86251.1|//4.00E-22//At1g02570 [Arabidopsis lyrata subsp. petraea]	Unigene6135_All//3.00E-44//AT2G47360| unknown protein	Unigene6135_All//2.00E-24//TC136920				nr -
Unigene6136_All	673	0.00	0.00	0.16	4.29	1.18	1.34	18.41	9.13	5.39	null	null		7.31E+00	3.96E-01		-1.87E+00	3.73E-07	Down	-1.68E+00	1.37E-05	Down	-1.01E+00	7.29E-12	Down	-1.77E+00	1.01E-27	Down	Unigene6136_All//gi|255547379|ref|XP_002514747.1|//1.00E-16//conserved hypothetical protein [Ricinus communis] >gi|223546351|gb|EEF47853.1|conserved hypothetical protein [Ricinus communis]	Unigene6136_All//9.00E-07//AT3G47510| unknown protein					nr -
Unigene6138_All	1014	0.93	1.05	0.89	11.84	5.57	18.66	5.50	14.26	12.89	1.76E-01	7.74E-01		-5.70E-02	9.49E-01		-1.09E+00	1.23E-12	Down	6.57E-01	1.16E-07		1.37E+00	9.80E-22	Up	1.23E+00	4.15E-17	Up	Unigene6138_All//gi|15240535|ref|NP_199781.1|//3.00E-79//DNA-binding protein-related [Arabidopsis thaliana] >gi|119657378|tpd|FAA00288.1| TPA: AT-hook motif nuclear localized protein 17 [Arabidopsis thaliana]	Unigene6138_All//5.00E-43//AT5G49700| DNA-binding protein-related	Unigene6138_All//0.00E+00//gi|78352486|gb|DT572760.1|DT572760				nr -
Unigene6139_All	362	8.53	5.88	8.09	8.26	8.85	15.47	15.30	15.82	47.76	-5.37E-01	1.32E-01		-7.59E-02	8.35E-01		9.96E-02	8.35E-01		9.06E-01	2.82E-04		4.80E-02	8.50E-01		1.64E+00	3.86E-34	Up	Unigene6139_All//gi|223452480|gb|ACM89567.1|//6.00E-06//serine/threonine protein kinase [Glycine max]	Unigene6139_All//7.00E-05//AT3G62220| serine/threonine protein kinase, putative	Unigene6139_All//1.00E-173//TC139451				nr +
Unigene61414_All	595	0.00	6.81	3.85	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.39E-23	Up	1.19E+01	1.27E-12	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene6142_All	419	0.50	2.90	1.53	52.31	63.36	64.03	51.87	128.28	24.82	2.54E+00	5.98E-04	Up	1.61E+00	1.11E-01		2.77E-01	7.91E-03		2.92E-01	6.11E-03		1.31E+00	6.83E-73	Up	-1.06E+00	1.62E-22	Down	Unigene6142_All//gi|150415186|gb|AB868690.1|//4.00E-57//oxalate oxidase [Theobroma cacao]	Unigene6142_All//6.00E-47//AT5G39110| germin-like protein, putative	Unigene6142_All//1.00E-100//TC153262			GO:0004871//GO:0006005//GO:0016623//GO:0044421//GO:0044464//GO:0044914//GO:0048037	nr +
Unigene6143_All	551	1.99	2.94	4.64	5.97	5.12	5.00	5.06	5.92	2.10	5.61E-01	2.80E-01		1.22E+00	3.87E-03		-2.20E-01	5.59E-01		-2.55E-01	4.99E-01		2.24E-01	5.17E-01		-1.27E+00	1.43E-04	Down	Unigene6143_All//gi|195621524|gb|ACG32592.1|//6.00E-57//ubiquitin-conjugating enzyme E2 16 [Zea mays] >gi|195638874|gb|ACG38905.1|ubiquitin-conjugating enzyme E2 16 [Zea mays]	Unigene6143_All//3.00E-55//AT5G25760| PEX4 (PEROXIN4); protein binding / ubiquitin-protein ligase	Unigene6143_All//0.00E+00//gi|164284040|gb|ES805944.1|ES805944				nr +
Unigene61440_All	374	0.00	4.06	1.57	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.10E-08	Up	1.06E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene61440_All//sp|P02839|LCP1_DROME//7.00E-18//Larval cuticle protein 1 OS=Drosophila melanogaster GN=Lcp1 PE=1 SV=3						swissprot +
Unigene61452_All	316	0.00	2.73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.94E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene61452_All//sp|Q6DH69|FAH2A_DANRE//6.00E-06//Fatty-acid amide hydrolase 2-A OS=Danio rerio GN=Faah2a PE=2 SV=1						swissprot +
Unigene6146_All	464	3.04	7.32	8.03	3.86	13.36	6.81	1.00	2.34	3.86	1.26E+00	2.63E-04	Up	1.40E+00	4.87E-05	Up	1.79E+00	6.24E-13	Up	8.18E-01	2.03E-02		1.22E+00	4.08E-02		1.95E+00	3.62E-05	Up		Unigene6146_All//1.00E-54//gi|78323949|gb|DT544223.1|DT544223					nr +
Unigene6148_All	850	8.25	6.50	7.08	7.79	9.72	8.18	24.47	15.83	10.87	-3.44E-01	1.31E-01		-2.21E-01	3.87E-01		3.19E-01	1.32E-01		7.01E-02	7.82E-01		-6.28E-01	5.34E-09		-1.17E+00	4.74E-25	Down	Unigene6148_All//gi|20197854|gb|AAD21749.2|//7.00E-54//expressed protein [Arabidopsis thaliana]	Unigene6148_All//4.00E-55//AT2G20390| unknown protein	Unigene6148_All//0.00E+00//gi|164284177|gb|ES834663.1|ES834663				nr -
Unigene61484_All	432	0.00	5.98	0.86	0.00	0.00	0.00	0.00	0.00	0.09	1.25E+01	1.05E-14	Up	9.75E+00	2.50E-02		null	null		null	null		null	null		6.53E+00	6.42E-01		Unigene61484_All//gi|255084545|ref|XP_002508847.1|//4.00E-36//ribosomal protein L44 [Micromonas sp. RCC299] >gi|226524124|gb|ACO70105.1|ribosomal protein L44 [Micromonas sp. RCC299]	Unigene61484_All//5.00E-34//AT4G14320| 60S ribosomal protein L36a/L44 (RPL36aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0014071//GO:0030529	nr -
Unigene61486_All	449	0.00	2.03	0.12	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	2.62E-05	Up	6.89E+00	6.33E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene6149_All	394	2.66	6.82	1.62	3.67	4.81	5.50	0.97	2.86	2.73	1.36E+00	6.75E-04	Up	-7.12E-01	3.15E-01		3.91E-01	4.50E-01		5.86E-01	2.02E-01		1.57E+00	9.26E-03		1.50E+00	1.21E-02									
Unigene6151_All	793	1.98	1.34	0.87	8.29	5.43	2.22	3.52	1.11	0.70	-5.61E-01	2.88E-01		-1.18E+00	3.61E-02		-6.11E-01	4.64E-03		-1.90E+00	4.40E-14	Down	-1.67E+00	3.67E-06	Down	-2.32E+00	2.02E-09	Down		Unigene6151_All//2.00E-11//ES839980					
Unigene61514_All	268	0.20	0.38	0.00	1.86	1.28	1.18	8.68	2.96	5.95	9.54E-01	7.25E-01		-7.61E+00	6.19E-01		-5.33E-01	5.94E-01		-6.56E-01	5.50E-01		-1.55E+00	8.14E-05	Down	-5.45E-01	1.33E-01		Unigene61514_All//1.00E-11//AT2G44480| BGLU17 (BETA GLUCOSIDASE 17); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds	Unigene61514_All//4.00E-34//CA992613		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0016798	nr -
Unigene61516_All	256	0.00	3.17	1.46	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.37E-05	Up	1.05E+01	2.50E-02		null	null		null	null		null	null		null	null									
Unigene6152_All	216	69.28	43.63	55.47	102.63	93.90	100.36	80.25	47.79	40.02	-6.67E-01	3.89E-06		-3.21E-01	3.92E-02		-1.28E-01	3.33E-01		-3.22E-02	8.19E-01		-7.48E-01	4.45E-10		-1.00E+00	1.41E-16	Down	Unigene6152_All//gi|29826244|gb|AA091862.1|//2.00E-29//TGB12K interacting protein 3 [Nicotiana tabacum]	Unigene6152_All//3.00E-24//AT2G17390| AKR2B (ANKYRIN REPEAT-CONTAINING 2B); protein binding / transcription regulator	Unigene6152_All//6.00E-119//ES849681				nr +
Unigene61523_All	209	0.00	3.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene61524_All	323	0.00	2.35	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.76E-04	Up	7.37E+00	6.33E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene61544_All	417	0.00	2.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.81E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene61544_All//gi|159479620|ref|XP_001697888.1|//4.00E-33//26S proteasome regulatory subunit [Chlamydomonas reinhardtii] >gi|158273986|gb|EDO99771.1| 26S proteasome regulatory subunit [Chlamydomonas reinhardtii]	Unigene61544_All//1.00E-22//AT4G38630| RPN10 (REGULATORY PARTICLE NON-ATPASE 10); peptide receptor			ko03050|Proteasome	GO:0004872//GO:0005838//GO:0006511//GO:0006970//GO:0009725//GO:0009845//GO:0010260//GO:0033554//GO:0034285//GO:0043231//GO:0043248//GO:0044444//GO:0048229//GO:0048449//GO:0048588//GO:0048827	nr +
Unigene6155_All	1442	1.52	0.07	0.44	3.90	2.20	1.63	6.60	4.81	1.74	-4.44E+00	2.46E-10	Down	-1.78E+00	2.71E-04	Down	-8.29E-01	3.65E-04		-1.26E+00	6.01E-07	Down	-4.55E-01	6.47E-03		-1.92E+00	6.69E-24	Down	Unigene6155_All//gi|145335142|ref|NP_172040.2|//2.00E-82//chr31 (chromatin remodeling 31); ATP binding / DNA binding / helicase/ nucleic acid binding [Arabidopsis thaliana]	Unigene6155_All//8.00E-83//AT1G05490| chr31 (chromatin remodeling 31); ATP binding / DNA binding / helicase/ nucleic acid binding			ko03440|Homologous recombination		nr +
Unigene61558_All	207	0.51	4.65	0.00	0.48	0.17	0.44	0.00	0.00	0.00	3.20E+00	6.55E-04	Up	-8.98E+00	3.89E-01		-1.53E+00	5.85E-01		-1.41E-01	9.48E-01		null	null		null	null									
Unigene61559_All	207	1.26	0.73	0.00	1.68	0.50	0.22	2.66	0.20	0.00	-7.83E-01	6.20E-01		-1.03E+01	8.52E-02		-1.75E+00	1.90E-01		-2.95E+00	8.29E-02		-3.72E+00	3.23E-03		-1.14E+01	2.80E-04	Down	Unigene61559_All//gi|147834263|emb|CAN66027.1|//1.00E-08//hypothetical protein [Vitis vinifera]	Unigene61559_All//2.00E-05//AT3G14190| unknown protein	Unigene61559_All//1.00E-46//DR454620				nr -
Unigene61565_All	213	0.00	3.09	2.25	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.25E-04	Up	1.11E+01	7.47E-03		null	null		null	null		null	null		null	null		Unigene61565_All//sp|P43490|NAMPT_HUMAN//1.00E-30//Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1						swissprot -
Unigene6157_All	992	12.82	3.63	6.44	5.37	5.69	3.96	0.43	1.01	0.20	-1.82E+00	2.00E-23	Down	-9.93E-01	2.81E-09		8.34E-02	8.11E-01		-4.40E-01	1.01E-01		1.25E+00	4.78E-02		-1.09E+00	2.82E-01		Unigene6157_All//gi|124359162|gb|AB305685.1|//2.00E-09//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene6157_All//2.00E-131//gi|18099323|gb|BM358577.1|BM358577				nr -
Unigene61572_All	435	0.12	6.99	2.45	0.00	0.00	0.00	0.00	0.00	0.00	5.86E+00	7.77E-16	Up	4.35E+00	6.46E-05	Up	null	null		null	null		null	null		null	null			Unigene61572_All//1.00E-13//gi|164274109|gb|ES810363.1|ES810363					
Unigene61578_All	281	0.00	1.08	0.00	0.00	0.00	0.48	0.00	4.76	13.61	1.01E+01	4.42E-02		null	null		null	null		8.91E+00	3.10E-01		1.22E+01	1.88E-09	Up	1.37E+01	2.30E-27	Up	Unigene61578_All//gi|32401377|gb|AAP80858.1|//1.00E-12//ribosomal protein L19 [Triticum aestivum]	Unigene61578_All//8.00E-08//AT4G02230| 60S ribosomal protein L19 (RPL19C)	Unigene61578_All//8.00E-116//TC143184		ko03010|Ribosome		nr +
Unigene6158_All	588	3.65	2.24	3.26	1.44	2.87	1.92	7.12	2.70	1.22	-7.03E-01	1.09E-01		-1.62E-01	7.11E-01		9.95E-01	5.07E-02		4.15E-01	5.61E-01		-1.40E+00	5.05E-07	Down	-2.55E+00	3.40E-15	Down	Unigene6158_All//gi|284167479|gb|AAO42905.1|//4.00E-16//At5g53650 [Arabidopsis thaliana]	Unigene6158_All//4.00E-15//AT5G53650| unknown protein	Unigene6158_All//2.00E-56//gi|78330011|gb|DT550285.1|DT550285				nr +
Unigene61584_All	300	0.00	3.38	0.71	1.00	0.46	1.05	0.14	0.00	0.00	1.17E+01	7.25E-06	Up	9.47E+00	1.40E-01		-1.12E+00	4.24E-01		8.09E-02	9.50E-01		-7.14E+00	6.52E-01		-7.14E+00	6.08E-01		Unigene61584_All//gi|2578033|emb|CAA65744.1|//1.00E-49//omega-6 desaturase [Gossypium hirsutum]	Unigene61584_All//8.00E-29//AT3G12120| FAD2 (FATTY ACID DESATURASE 2); delta12-fatty acid dehydrogenase/ omega-6 fatty acid desaturase	Unigene61584_All//3.00E-137//TC178159		ko01040|Biosynthesis of unsaturated fatty acids	GO:0003824//GO:0044238	nr +
Unigene6159_All	424	8.02	168.62	14.69	27.49	121.42	72.86	30.81	61.51	155.69	4.39E+00	0.00E+00	Up	8.73E-01	3.98E-04		2.14E+00	5.84E-134	Up	1.41E+00	3.37E-41	Up	9.97E-01	1.70E-23		2.34E+00	9.62E-204	Up	Unigene6159_All//gi|255632262|gb|ACU16489.1|//6.00E-11//unknown [Glycine max]		Unigene6159_All//3.00E-147//DW507094				nr +
Unigene61592_All	204	0.00	3.48	1.57	1.22	0.68	1.99	0.00	0.00	0.00	1.18E+01	3.32E-04	Up	1.06E+01	4.50E-02		-8.55E-01	5.73E-01		7.07E-01	5.97E-01		null	null		null	null			Unigene61592_All//9.00E-10//DT467885					
Unigene61594_All	292	0.00	4.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.47E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene61594_All//gi|115463365|ref|NP_001055282.1|//7.00E-07//Os05g0353400 [Oryza sativa Japonica Group] >gi|3983663|dbj|BAA34861.1|importin-beta1 [Oryza sativa Japonica Group] >gi|55168010|gb|AAV43878.1|importin beta 1 [Oryza sativa Japonica Group] >gi|113578833|dbj|BAF17196.1|Os05g0353400 [Oryza sativa Japonica Group]	Unigene61594_All//7.00E-06//AT5G53480| importin beta-2, putative					nr +
Unigene6160_All	565	1.57	0.45	1.13	3.88	3.17	3.04	38.69	18.72	34.06	-1.81E+00	2.38E-02		-4.77E-01	5.33E-01		-2.92E-01	5.43E-01		-3.53E-01	4.57E-01		-1.05E+00	1.86E-21	Down	-1.84E-01	9.15E-02		Unigene6160_All//gi|4928460|gb|AAD33596.1|AF133127_1//4.00E-44//thioredoxin h [Hevea brasiliensis]	Unigene6160_All//2.00E-38//AT1G11530| ATCXS1 (C-terminal cysteine residue is changed to a serine 1); protein disulfide isomerase					nr -
Unigene61609_All	216	0.00	3.28	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	7.95E+00	6.33E-01		null	null		null	null		null	null		null	null									
Unigene6161_All	697	113.50	82.51	97.87	23.58	30.48	27.73	0.79	2.40	3.54	-4.60E-01	3.49E-15		-2.14E-01	5.40E-04		3.70E-01	1.20E-03		2.34E-01	8.21E-02		1.60E+00	8.16E-04	Up	2.17E+00	1.07E-07	Up	Unigene6161_All//gi|15224305|ref|NP_181884.1|//2.00E-53//immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein [Arabidopsis thaliana] >gi|20138146|sp|Q22870.2|FKBP2_ARATH RecName: Full=Probable FKBP-type peptidyl-prolyl cis-trans isomerase 2, chloroplastic; Short=PPIase; AltName: Full=Rotamase; Flags: Precursor >gi|20196864|gb|AAB64339.2| FKBP-type peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]	Unigene6161_All//1.00E-49//AT2G43560| immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	Unigene6161_All//0.00E+00//CO083296				nr -
Unigene61617_All	319	0.00	2.06	1.67	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.25E-04	Up	1.07E+01	4.03E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene61644_All	387	0.00	6.94	4.40	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.80E-15	Up	1.21E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene61644_All//gi|224013940|ref|XP_002296634.1|//3.00E-10//pyruvate formate-lyase [Thalassiosira pseudonana CCMP1335] >gi|220968986|gb|EED87330.1|pyruvate formate-lyase [Thalassiosira pseudonana CCMP1335]					GO:0016453//GO:0019318//GO:0044424	nr -
Unigene61653_All	489	0.00	2.80	0.76	0.00	0.00	0.09	0.00	0.00	0.00	1.15E+01	7.80E-08	Up	9.57E+00	2.50E-02		null	null		6.53E+00	6.91E-01		null	null		null	null		Unigene61653_All//gi|11561806|gb|AAC83688.2|//4.00E-09//101 kDa heat shock protein [Nicotiana tabacum]	Unigene61653_All//1.00E-07//AT1G74310| ATHSP101 (ARABIDOPSIS THALIANA HEAT SHOCK PROTEIN 101); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding					nr +

Unigene6166_All	943	0.83	1.07	2.15	2.27	1.28	1.63	2.56	1.24	1.06	3.69E-01	6.03E-01		1.37E+00	5.21E-03		-8.30E-01	4.74E-02		-4.80E-01	3.06E-01		-1.04E+00	4.61E-03		-1.27E+00	4.48E-04	Down	Unigene6166_All//gi|297831090|ref|XP_002883427.1|//6.00E-49//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297329267|gb|EFH59686.1|nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene6166_All//1.00E-42//AT3G23370| nucleic acid binding	Unigene6166_All//2.00E-76//DT455670				nr -
Unigene61672_All	530	0.00	1.91	1.41	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	7.25E-06	Up	1.05E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene61672_All//gi|167962017|dbj|BAG09366.1|//6.00E-22//peroxisomal short-chain dehydrogenase/reductase family protein [Glycine max]	Unigene61672_All//5.00E-14//AT4G05530| IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase			ko04146|Peroxisome	GO:0003824//GO:0009733//GO:0009850//GO:0042579//GO:0048588	nr +
Unigene61677_All	277	0.00	3.29	0.38	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.62E-05	Up	8.59E+00	3.96E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene6168_All	1061	0.30	0.10	0.25	5.73	4.25	1.96	0.48	0.16	0.15	-1.63E+00	2.76E-01		-2.38E-01	8.50E-01		-4.30E-01	7.00E-02		-1.55E+00	6.23E-10	Down	-1.60E+00	1.07E-01		-1.67E+00	7.77E-02		Unigene6168_All//gi|297724159|ref|NP_001174443.1|//1.00E-53//Os05g0434000 [Oryza sativa Japonica Group] >gi|255676397|dbj|BAH93171.1|Os05g0434000 [Oryza sativa Japonica Group]	Unigene6168_All//3.00E-08//AT4G20520| RNA binding / RNA-directed DNA polymerase	Unigene6168_All//1.00E-133//DW241491				nr -
Unigene6169_All	555	0.47	3.47	3.55	6.46	6.76	6.02	3.66	3.16	1.22	2.88E+00	1.43E-06	Up	2.91E+00	1.70E-06	Up	6.56E-02	8.58E-01		-1.02E-01	7.65E-01		-2.09E-01	6.68E-01		-1.58E+00	1.35E-04	Down	Unigene6169_All//gi|224111880|ref|XP_002316010.1|//3.00E-67//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1|cytochrome P450 [Populus trichocarpa]	Unigene6169_All//2.00E-48//AT3G14610| CYP72A7; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene6169_All//0.00E+00//ES837936		ko04146|Peroxisome//ko00592|alpha-Linoleic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00906|Carotenoid biosynthesis		nr +
Unigene6170_All	630	13.54	20.59	13.02	16.53	12.84	14.34	43.96	31.38	18.84	6.05E-01	1.09E-04		-5.65E-02	7.93E-01		-3.64E-01	3.76E-02		-2.05E-01	3.13E-01		-4.86E-01	1.13E-07		-1.22E+00	2.45E-35	Down	Unigene6170_All//gi|115450022|ref|NP_001048612.1|//4.00E-30//Os02g0830100 [Oryza sativa Japonica Group] >gi|48716335|dbj|BAD22947.1|oligopeptidase A-like [Oryza sativa Japonica Group] >gi|113538143|dbj|BAF10526.1|Os02g0830100 [Oryza sativa Japonica Group]	Unigene6170_All//4.00E-28//AT5G10540| peptidase M3 family protein / thimet oligopeptidase family protein	Unigene6170_All//0.00E+00//DR453010				nr -
Unigene6171_All	602	20.16	31.06	14.95	23.67	35.75	59.27	0.63	6.67	0.93	6.23E-01	1.09E-06		-4.32E-01	1.16E-02		5.95E-01	6.25E-08		1.32E+00	2.02E-43	Up	3.40E+00	1.51E-18	Up	5.52E-01	5.27E-01		Unigene6171_All//gi|3094012|gb|AAC15460.1|//1.00E-47//cold-regulated LTC0R12 [Lavatera thuringiaca]	Unigene6171_All//3.00E-30//AT1G75750| GASA1 (GAST1 PROTEIN HOMOLOG 1)	Unigene6171_All//0.00E+00//gi|109869716|gb|DW498692.1|DW498692				nr +
Unigene61714_All	695	15.13	2.41	10.27	9.53	9.02	7.99	1.03	0.48	0.23	-2.65E+00	9.77E-31	Down	-5.60E-01	2.22E-03		-8.02E-02	7.85E-01		-2.54E-01	3.20E-01		-1.10E+00	1.49E-01		-2.17E+00	7.75E-03		Unigene61714_All//gi|9502420|gb|AAF88119.1|AC021043_12//4.00E-35//Unknown protein [Arabidopsis thaliana] >gi|15529248|gb|AAK97718.1|At1g29190/F28N24_12 [Arabidopsis thaliana] >gi|16974401|gb|AAL31126.1|At1g29190/F28N24_12 [Arabidopsis thaliana]	Unigene61714_All//1.00E-33//AT1G29195| unknown protein	Unigene61714_All//0.00E+00//gi|48811319|gb|CO112632.1|CO112632			GO:0009536	nr +
Unigene61721_All	421	0.00	1.81	1.26	0.24	0.00	0.00	0.00	0.00	0.00	1.08E+01	1.76E-04	Up	1.03E+01	4.03E-03		-7.89E+00	3.11E-01		-7.89E+00	3.96E-01		null	null		null	null									
Unigene61726_All	795	0.00	10.26	3.22	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	1.14E-46	Up	1.17E+01	4.20E-14	Up	null	null		null	null		null	null		null	null		Unigene61726_All//gi|18087805|ref|NP_032529.2|//1.00E-113//40S ribosomal protein S2 [Mus musculus] >gi|78126159|ref|NP_114026.3| 40S ribosomal protein S2 [Rattus norvegicus] >gi|133914|sp|P27952.1|RS2_RAT RecName: Full=40S ribosomal protein S2 >gi|46397787|sp|P25444.3|RS2_MOUSE RecName: Full=40S ribosomal protein S2; AltName: Full=40S ribosomal protein S4; AltName: Full=Protein LLRep3 >gi|10179940|gb|AAG13953.1|AF283559_1 ribosomal protein S2 [Mus musculus] >gi|57718|emb|CAA40679.1|ribosomal protein S2 [Rattus rattus] >gi|12805427|gb|AAH02186.1|Ribosomal protein S2 [Mus musculus] >gi|56971737|gb|AAH87956.1|Ribosomal protein S2 [Mus musculus] >gi|61402217|gb|AAH91730.1|Ribosomal protein S2 [Mus musculus]	Unigene61726_All//5.00E-88//AT3G57490| 40S ribosomal protein S2 (RPS2D)	Unigene61726_All//7.00E-51//DW519163		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr +
Unigene6173_All	269	212.20	92.67	98.19	242.59	212.12	242.77	75.13	33.25	49.32	-1.20E+00	2.97E-55	Down	-1.11E+00	1.46E-47	Down	-1.94E-01	2.19E-03		1.10E-03	9.88E-01		-1.18E+00	8.18E-24	Down	-6.07E-01	1.41E-08		Unigene6173_All//gi|13899101|gb|AAK48972.1|AF370545_1//1.00E-08//alpha NAC-like protein [Arabidopsis thaliana] >gi|18377570|gb|AAL66951.1| alpha NAC-like protein [Arabidopsis thaliana]		Unigene6173_All//1.00E-136//DR044193				nr +
Unigene61745_All	205	0.00	3.21	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.25E-04	Up	9.61E+00	2.38E-01		null	null		null	null		null	null		null	null									
Unigene6175_All	594	2.20	1.19	1.52	3.61	4.99	2.05	3.20	1.76	0.74	-8.83E-01	1.32E-01		-5.31E-01	3.86E-01		4.67E-01	2.24E-01		-8.13E-01	6.70E-02		-8.65E-01	4.03E-02		-2.12E+00	4.75E-06	Down								
Unigene61750_All	334	0.00	3.34	0.96	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.00E-06	Up	9.90E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene61750_All//sp|Q9VH95|YC17_DROME//1.00E-19//Uncharacterized protein CG16817 OS=Drosophila melanogaster GN=CG16817 PE=1 SV=1						swissprot +
Unigene61753_All	351	0.00	1.88	0.91	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	6.24E-04	Up	9.83E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene61753_All//gi|117380755|gb|ABK31467.1|//4.00E-28//eukaryotic initiation factor 3e [Oryza sativa Japonica Group]	Unigene61753_All//7.00E-26//AT3G57290| EIF3E (EUKARYOTIC TRANSLATION INITIATION FACTOR 3E); translation initiation factor				GO:0008135//GO:0010467//GO:0044424	nr +
Unigene6176_All	390	1.88	7.80	4.23	5.62	11.04	5.67	5.42	6.97	7.35	2.05E+00	5.01E-07	Up	1.17E+00	3.12E-02		9.74E-01	5.61E-04		1.39E-02	9.75E-01		3.62E-01	3.23E-01		4.40E-01	1.80E-01		Unigene6176_All//gi|115447971|ref|NP_001017765.1|//1.00E-06//Os02g0685200 [Oryza sativa Japonica Group] >gi|113537296|dbj|BAF09679.1|Os02g0685200 [Oryza sativa Japonica Group]	Unigene6176_All//4.00E-07//AT1G18330| EPR1 (EARLY-PHYTOCHROME-RESPONSIVE1); DNA binding / transcription factor	Unigene6176_All//1.00E-167//TC148721	MYB-related			nr -
Unigene6177_All	985	0.74	2.67	0.27	1.42	0.52	0.73	1.50	4.16	2.35	1.85E+00	1.72E-05	Up	-1.46E+00	1.12E-01		-1.43E+00	8.64E-03		-9.49E-01	9.91E-02		1.47E+00	2.44E-07	Up	6.43E-01	7.71E-02				Unigene6177_All//2.00E-23//FL577567				
Unigene6178_All	414	48.02	18.24	25.47	56.79	51.07	54.55	91.30	53.00	58.03	-1.40E+00	6.62E-25	Down	-9.15E-01	1.95E-12		-1.53E-01	2.23E-01		-5.83E-02	6.87E-01		-7.85E-01	9.45E-23		-6.54E-01	2.84E-17		Unigene6178_All//gi|40823305|gb|AAR92274.1|//2.00E-26//At3g49310 [Arabidopsis thaliana] >gi|46518411|gb|AAS99687.1|At3g49310 [Arabidopsis thaliana]	Unigene6178_All//1.00E-27//AT3G49310| LOCATED IN: endomembrane system; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF791 (InterPro:IPR008509), Major facilitator superfamily, general substrate transporter (InterPro:IPR016196); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27720.1); Has 550 Blast hits to 545 proteins in 201 species: Archae - 5; Bacteria - 285; Metazoa - 85; Fungi - 33; Plants - 99; Viruses - 0; Other Eukaryotes - 43 (source: NCBI BLink).	Unigene6178_All//0.00E+00//TC154592				nr +
Unigene61782_All	217	0.24	2.57	1.96	0.46	0.95	4.16	2.92	3.08	1.29	3.41E+00	1.24E-02		3.03E+00	5.72E-02		1.05E+00	6.12E-01		3.18E+00	9.74E-04	Up	7.65E-02	9.37E-01		-1.19E+00	1.33E-01				Unigene61782_All//6.00E-11//CO116421				
Unigene618_All	1908	5.68	4.65	6.84	6.66	9.08	6.94	5.58	2.10	3.03	-2.89E-01	1.10E-01		2.69E-01	1.18E-01		4.47E-01	4.08E-04		5.90E-02	7.44E-01		-1.41E+00	7.39E-17	Down	-8.83E-01	1.12E-08		Unigene618_All//gi|294516726|gb|ADE96995.1|//1.00E-142//CIP73 protein [Lotus japonicus]	Unigene618_All//1.00E-82//AT5G25270| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: protein modification process; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin (InterPro:IPR000626); BEST Arabidopsis thaliana protein match is: ubiquitin family protein (TAIR:AT5G42220.1); Has 1533 Blast hits to 627 proteins in 167 species: Archae - 0; Bacteria - 307; Metazoa - 363; Fungi - 153; Plants - 33; Viruses - 41; Other Eukaryotes - 636 (source: NCBI BLink).	Unigene618_All//0.00E+00//TC132242		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene61804_All	262	0.00	3.09	1.22	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.37E-05	Up	1.03E+01	4.50E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene6182_All	384	79.98	95.67	61.85	48.91	45.64	103.62	35.89	32.76	20.33	2.58E-01	4.19E-03		-3.71E-01	2.49E-04		-9.96E-02	5.32E-01		1.08E+00	2.36E-35	Up	-1.32E-01	4.03E-01		-8.20E-01	9.19E-10		Unigene6182_All//gi|21593495|gb|AAM65462.1|//2.00E-40//glycine rich protein-like [Arabidopsis thaliana]	Unigene6182_All//1.00E-41//AT5G27720| emb1644 (embryo defective 1644)	Unigene6182_All//0.00E+00//TC151264		ko03040|Spliceosome//ko03018|RNA degradation		nr -
Unigene61827_All	401	0.00	0.00	0.66	3.35	2.06	0.23	1.69	0.63	0.20	null	null		9.38E+00	8.00E-02		-7.03E-01	2.18E-01		-3.90E+00	2.12E-06	Down	-1.43E+00	7.83E-02		-3.09E+00	1.45E-03		Unigene61827_All//gi|126217792|gb|ABN81349.1|//3.00E-34//auxin influx transport protein [Casuarina glauca] >gi|126217794|gb|ABN81350.1| auxin influx transport protein [Casuarina glauca]	Unigene61827_All//3.00E-22//AT2G38120| AUX1 (AUXIN RESISTANT 1); amino acid transmembrane transporter/ auxin binding / auxin influx transmembrane transporter/ transporter	Unigene61827_All//2.00E-142//gi|109865162|gb|DW494138.1|DW494138			GO:0001738//GO:0005275//GO:0009630//GO:0009755//GO:0010102//GO:0015291//GO:0015837//GO:0031224//GO:0042562//GO:0043231//GO:0048764//GO:0051707//GO:0060918//GO:0080161	nr -

Unigene6183_All	1750	0.09	0.17	0.00	3.42	0.96	1.03	6.23	6.40	18.46	9.53E-01	5.03E-01		-6.49E+00	2.43E-01		-1.82E+00	7.53E-14	Down	-1.73E+00	2.49E-11	Down	3.82E-02	8.31E-01		1.57E+00	5.76E-59	Up	Unigene6183_All//gi|15231960|ref|NP_187485.1|//1.00E-175//PK1 (PROTEIN-SERINE KINASE 1); kinase/ protein binding / protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|1170689|sp|P42818.1|KPK1_ARATH RecName: Full=Serine/threonine-protein kinase AtPK1/AtPK6 >gi|508308|gb|AAA21142.1| protein-serine kinase [Arabidopsis thaliana] >gi|867997|dbj|BAA07656.1| risosomal-protein S6 kinase homolog [Arabidopsis thaliana] >gi|914080|gb|AAB33197.1| ATPK6=ribosomal-protein S6 kinase homolog [Arabidopsis thaliana, Peptide, 465 aa]	Unigene6183_All//1.00E-161//AT3G08730| PK1 (PROTEIN-SERINE KINASE 1); kinase/ protein binding / protein kinase/ protein serine/threonine kinase	Unigene6183_All//0.00E+00//TC141956				nr -
Unigene61832_All	264	0.00	2.88	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	1.07E+01	1.38E-02		null	null		null	null		null	null		null	null								
Unigene6184_All	692	8.39	4.83	9.31	4.90	1.39	1.17	8.07	13.83	5.99	-7.96E-01	1.21E-03		1.50E-01	5.83E-01		-1.81E+00	5.48E-08	Down	-2.06E+00	2.68E-08	Down	7.78E-01	2.75E-06		-4.30E-01	5.13E-02								
Unigene61841_All	250	0.00	4.66	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.05E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene61841_All//gi|227206242|dbj|BAH57176.1|//9.00E-28//AT5G11200 [Arabidopsis thaliana]	Unigene61841_All//4.00E-29//AT5G11200| DEAD/DEAH box helicase, putative			ko03040|Spliceosome	GO:0010038//GO:0030312//GO:0031981//GO:0032259//GO:0042623	nr -
Unigene61847_All	204	0.00	4.47	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.62E-05	Up	8.03E+00	6.33E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene61862_All	217	1.45	0.47	0.98	5.97	3.97	1.04	2.53	2.89	2.02	-1.63E+00	2.76E-01		-5.60E-01	6.63E-01		-5.89E-01	3.13E-01		-2.52E+00	2.43E-04	Down	1.90E-01	8.10E-01		-3.27E-01	6.72E-01				Unigene61862_All//3.00E-50//gi|84172548|gb|DR461196.1|DR461196				ESTscan -
Unigene6188_All	394	1.59	2.31	6.76	2.78	2.36	2.29	1.93	0.42	0.81	5.39E-01	4.49E-01		2.08E+00	4.51E-06	Up	-2.37E-01	7.30E-01		-2.79E-01	6.89E-01		-2.19E+00	7.77E-03		-1.26E+00	7.70E-02				Unigene6188_All//0.00E+00//gi|78329814|gb|DT550088.1|DT550088				
Unigene61892_All	204	0.00	3.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null								
Unigene619_All	2788	4.41	3.60	3.95	4.81	5.69	5.44	5.99	5.59	2.92	-2.93E-01	7.78E-02		-1.58E-01	3.96E-01		2.45E-01	9.60E-02		1.79E-01	2.76E-01		-9.93E-02	5.02E-01		-1.04E+00	6.86E-17	Down	Unigene619_All//gi|294516726|gb|ADE96995.1|//1.00E-161//CIP73 protein [Lotus japonicus]	Unigene619_All//3.00E-94//AT5G25270| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: protein modification process; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Ubiquitin (InterPro:IPR000626); BEST Arabidopsis thaliana protein match is: ubiquitin family protein (TAIR:AT5G42220.1); Has 1533 Blast hits to 627 proteins in 167 species: Archae - 0; Bacteria - 307; Metazoa - 363; Fungi - 153; Plants - 33; Viruses - 41; Other Eukaryotes - 636 (source: NCBI BLink).	Unigene619_All//0.00E+00//TC133021		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene61900_All	205	0.77	2.47	1.04	3.16	0.00	0.22	2.06	1.02	0.19	1.69E+00	1.34E-01		4.40E-01	7.74E-01		-1.16E+01	7.85E-05	Down	-3.84E+00	2.70E-03		-1.02E+00	3.50E-01		-3.41E+00	1.24E-02		Unigene61900_All//gi|224114135|ref|XP_002332433.1|//8.00E-06//predicted protein [Populus trichocarpa] >gi|222832402|gb|EEE70879.1| predicted protein [Populus trichocarpa]		Unigene61900_All//8.00E-29//DT465312		GO:0005488	nr +
Unigene61902_All	402	0.00	2.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null								
Unigene61917_All	414	0.00	4.53	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.11E-10	Up	9.59E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene61917_All//gi|255072339|ref|XP_002499844.1|//3.00E-11//alpha-2 macroglobulin family-like protein [Micromonas sp. RCC299] >gi|226515106|gb|ACO61102.1| alpha-2 macroglobulin family-like protein [Micromonas sp. RCC299]					nr -
Unigene6192_All	309	53.34	173.82	148.89	74.64	107.21	100.12	117.67	99.96	81.87	1.70E+00	7.88E-88	Up	1.48E+00	6.36E-60	Up	5.22E-01	1.51E-09		4.24E-01	7.54E-06		-2.35E-01	3.93E-03		-5.23E-01	1.85E-11				Unigene6192_All//3.00E-115//TC168693				
Unigene6193_All	1563	0.77	0.84	0.27	1.72	1.45	0.43	2.65	3.42	4.41	1.31E-01	8.12E-01		-1.50E+00	2.71E-02		-2.43E-01	5.59E-01		-1.99E+00	1.90E-06	Down	3.69E-01	1.27E-01		7.34E-01	1.57E-04		Unigene6193_All//gi|240256061|ref|NP_194242.6|//7.00E-99//ATP binding / ATP-dependent DNA helicase/ DNA binding / hydrolase [Arabidopsis thaliana]	Unigene6193_All//3.00E-89//AT4G25120| ATP binding / ATP-dependent DNA helicase/ DNA binding / hydrolase	Unigene6193_All//0.00E+00//ES845060				nr +
Unigene61935_All	406	0.39	2.87	0.39	0.00	0.34	0.11	0.31	0.51	0.00	2.89E+00	2.98E-04	Up	2.55E-02	1.00E+00		8.41E+00	3.17E-01		6.80E+00	6.91E-01		7.20E-01	6.31E-01		-8.29E+00	1.99E-01		Unigene61935_All//gi|145408590|ref|YP_001152214.1|//5.00E-06//ORF124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1| ORF124 [Pinus koraiensis]		Unigene61935_All//1.00E-26//TC146107				nr +
Unigene6194_All	424	4.69	7.05	8.16	5.99	7.15	7.03	8.58	3.55	3.48	5.89E-01	1.06E-01		8.00E-01	2.11E-02		2.54E-01	5.56E-01		2.31E-01	5.91E-01		-1.27E+00	1.75E-05	Down	-1.30E+00	7.12E-06	Down	Unigene6194_All//gi|18395874|ref|NP_565315.1|//3.00E-21//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|20197980|gb|AAM15335.1| Expressed protein [Arabidopsis thaliana]	Unigene6194_All//6.00E-18//AT2G04845| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene6194_All//0.00E+00//gi|72271454|gb|DT048166.1|DT048166				nr +
Unigene61942_All	231	2.27	1.54	8.30	5.39	1.94	3.13	6.04	4.89	1.90	-5.61E-01	5.76E-01		1.87E+00	4.53E-04	Up	-1.48E+00	1.18E-02		-7.85E-01	2.08E-01		-3.06E-01	5.83E-01		-1.67E+00	1.27E-03		Unigene61942_All//gi|115455679|ref|NP_001051440.1|//7.00E-14//Os03g0777500 [Oryza sativa Japonica Group] >gi|108711352|gb|ABF99147.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549911|dbj|BAF13354.1| Os03g0777500 [Oryza sativa Japonica Group]	Unigene61942_All//2.00E-14//AT2G32580| unknown protein	Unigene61942_All//4.00E-80//TC155752				nr +
Unigene61953_All	431	0.00	3.76	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.96E-09	Up	9.95E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene61953_All//gi|298708959|emb|CBJ30912.1|//8.00E-06//SCAR-WAVE [Ectocarpus siliculosus]						nr +
Unigene6196_All	367	1.85	0.00	1.31	1.76	2.06	2.95	0.69	0.46	0.22	-1.09E+01	4.09E-04	Down	-5.05E-01	5.82E-01		2.26E-01	8.32E-01		7.43E-01	2.89E-01		-6.02E-01	6.47E-01		-1.67E+00	2.56E-01				Unigene6196_All//6.00E-68//TC173705				ESTscan -
Unigene61972_All	361	0.00	0.00	0.00	0.00	0.00	0.25	1.41	0.12	0.00	null	null		null	null		null	null		7.97E+00	4.73E-01		-3.60E+00	5.77E-03		-1.05E+01	5.54E-04	Down	Unigene61972_All//gi|115465163|ref|NP_001056181.1|//3.00E-41//Os05g0540300 [Oryza sativa Japonica Group] >gi|113579732|dbj|BAF18095.1| Os05g0540300 [Oryza sativa Japonica Group]	Unigene61972_All//8.00E-42//AT3G13860| HSP80-2A (HEAT SHOCK PROTEIN 60-3A); ATP binding / protein binding	Unigene61972_All//4.00E-121//CO100100		ko03018|RNA degradation	GO:0005515//GO:0005840//GO:0006457//GO:0006950//GO:0006996//GO:0010038//GO:0016020//GO:0031980//GO:0032559//GO:0046914	nr +
Unigene6198_All	376	22.82	15.36	9.77	28.88	30.59	25.58	39.47	27.01	20.98	-5.71E-01	3.79E-03		-1.22E+00	8.35E-09	Down	8.29E-02	6.96E-01		-1.75E-01	3.94E-01		-5.47E-01	2.25E-05		-9.12E-01	2.47E-12		Unigene6198_All//gi|297609887|ref|NP_001063818.2|//4.00E-37//Os09g0542000 [Oryza sativa Japonica Group] >gi|255679102|dbj|BAF25732.2| Os09g0542000 [Oryza sativa Japonica Group]	Unigene6198_All//2.00E-38//AT1G76010| nucleic acid binding	Unigene6198_All//0.00E+00//TC168018				nr -
Unigene61993_All	396	0.00	3.71	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.11E-08	Up	9.07E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene61993_All//gi|145352388|ref|XP_001420531.1|//8.00E-20//F-ATPase family transporter: protons (vacuolar) [Ostreococcus lucimarinus CCE9901] >gi|144580765|gb|ABO98824.1| F-ATPase family transporter: protons (vacuolar) [Ostreococcus lucimarinus CCE9901]	Unigene61993_All//2.00E-18//AT3G58730| vacuolar ATP synthase subunit D (VATD) / V-ATPase D subunit / vacuolar proton pump D subunit (VATPD)			ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0005773//GO:0006754//GO:0008324//GO:0031090//GO:0042626	nr +
Unigene6200_All	496	3.27	4.39	2.15	7.23	4.30	6.01	26.85	46.26	9.48	4.26E-01	3.43E-01		-6.07E-01	2.61E-01		-7.48E-01	1.49E-02		-2.67E-01	4.67E-01		7.85E-01	3.97E-14		-1.50E+00	1.27E-23	Down			Unigene6200_All//1.00E-94//gi|109832615|gb|DW231174.1|DW231174				
Unigene62002_All	452	0.00	3.25	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.11E-08	Up	7.88E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene62002_All//sp|Q04791|SASB_ANAPL//2.00E-06//Fatty acyl-CoA hydrolase precursor, medium chain OS=Anas platyrhynchos PE=1 SV=1						swissprot -
Unigene62003_All	334	0.00	4.85	1.43	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.96E-09	Up	1.05E+01	7.47E-03		null	null		null	null		null	null		null	null									
Unigene6201_All	395	64.51	28.22	35.86	99.88	97.20	91.01	109.71	72.38	60.51	-1.19E+00	5.72E-25	Down	-8.47E-01	6.56E-14		-3.92E-02	7.34E-01		-1.34E-01	1.63E-01		-6.00E-01	1.64E-16		-8.58E-01	4.91E-31		Unigene6201_All//gi|106879567|emb|CAJ38367.1|//2.00E-61//polyA-binding protein [Plantago major]	Unigene6201_All//2.00E-39//AT1G49760| PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor	Unigene6201_All//0.00E+00//gi|13350462|gb|BG440810.1|BG440810				nr +
Unigene62015_All	418	0.00	2.42	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	7.23E-06	Up	9.32E+00	8.00E-02		null	null		null	null		null	null		null	null		Unigene62015_All//gi|299469665|emb|CBN76519.1|//1.00E-09//carbonic anhydrase alpha type [Ectocarpus siliculosus]	Unigene62015_All//4.00E-09//AT5G04180| ACA3 (ALPHA CARBONIC ANHYDRASE 3); carbonate dehydratase/ zinc ion binding			ko00910|Nitrogen metabolism	GO:0043231//GO:0044444	nr +
Unigene6203_All	324	26.32	25.18	13.15	40.59	40.39	29.41	109.75	131.32	88.04	-6.41E-02	7.56E-01		-1.00E+00	1.56E-06	Down	-7.20E-03	9.64E-01		-4.65E-01	2.51E-03		2.59E-01	4.66E-04		-3.18E-01	5.40E-05		Unigene6203_All//gi|224110618|ref|XP_002315580.1|//8.00E-19//predicted protein [Populus trichocarpa] >gi|222864620|gb|EEF01751.1| predicted protein [Populus trichocarpa]		Unigene6203_All//2.00E-104//gi|54115259|gb|CO490768.1|CO490768		ko03040|Spliceosome		nr -
Unigene62035_All	201	0.00	1.51	4.24	0.00	1.54	0.00	0.42	0.42	1.19	1.06E+01	4.41E-02		1.20E+01	9.01E-05	Up	1.06E+01	4.54E-02		null	null		-1.66E-02	1.01E+00		1.50E+00	3.39E-01									
Unigene6204_All	1518	0.90	0.97	0.77	2.53	0.64	1.25	43.65	33.23	9.89	1.11E-01	8.31E-01		-2.16E-01	7.04E-01		-1.99E+00	3.84E-10	Down	-1.02E+00	1.04E-03		-3.93E-01	6.82E-12		-2.14E+00	4.60E-186	Down	Unigene6204_All//gi|224132940|ref|XP_002321447.1|//1.00E-148//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222868443|gb|EEF05574.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene6204_All//2.00E-122//AT5G61430| ANAC100 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 100); transcription factor	Unigene6204_All//0.00E+00//CO075517	NAC			nr -
Unigene62041_All	494	0.00	5.74	1.83	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	3.83E-16	Up	1.08E+01	4.71E-05	Up	null	null		null	null		null	null		null	null		Unigene62041_All//gi|106879575|emb|CAJ38371.1|//8.00E-14//HMG-protein [Plantago major]	Unigene62041_All//4.00E-06//AT5G23420| HMGB6; transcription factor			ko03410|Base excision repair	GO:0005488	nr -
Unigene62046_All	548	2.77	1.48	4.18	1.73	2.45	2.64	1.31	1.68	5.09	-9.04E-01	9.22E-02		5.94E-01	1.81E-01		5.05E-01	4.23E-01		6.11E-01	3.05E-01		3.55E-01	6.21E-01		1.96E+00	1.22E-07	Up	Unigene62046_All//gi|179743220|dbj|BAB78529.1|//2.00E-08//glycerol-3-phosphate acyltransferase [Citrus unshiu]	Unigene62046_All//2.00E-08//AT1G32200| ATS1; glycerol-3-phosphate O-acyltransferase	Unigene62046_All//4.00E-153//ES820979		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0003006//GO:0004497//GO:0006633//GO:0006950//GO:0006996//GO:0008374//GO:0009532//GO:0009725//GO:0016705//GO:0031224//GO:0046471//GO:0046872	nr -
Unigene62047_All	230	0.00	3.08	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.32E-04	Up	8.85E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene62047_All//gi|300160753|gb|EFJ27370.1|//7.00E-23//rab family GTPase [Selaginella moellendorffii] >gi|300166524|gb|EFJ33130.1| rab family GTPase [Selaginella moellendorffii]	Unigene62047_All//3.00E-24//AT4G17170| RABB1C (ARABIDOPSIS RAB GTPASE HOMOLOG B1C); GTP binding / GTPase				GO:0006810//GO:0032561//GO:0035556	nr +
Unigene62061_All	301	0.00	6.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.14E-10	Up	null	null		null	null		null	null		null	null		null	null		Unigene62061_All//sp|P23142|FBLN1_HUMAN//1.00E-25//Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4						swissprot -

Unigene6207_All	679	2.31	1.79	2.35	4.48	2.43	1.93	1.81	0.68	1.58	-3.68E-01	4.87E-01		2.54E-02	9.81E-01		-8.78E-01	9.15E-03		-1.21E+00	7.16E-04	Down	-1.42E+00	1.21E-02		-1.89E-01	7.12E-01		Unigene6207_All//gi|297830178|ref|XP_002882971.1|//9.00E-47//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328811|gb|EFH59230.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene6207_All//6.00E-47//AT3G16010| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene62070_All	501	0.00	4.65	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.91E-13	Up	8.73E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene62070_All//sp|O02350|CBPA1_ANOGA//3.00E-10//Zinc carboxypeptidase A 1 OS=Anopheles gambiae GN=AGAP009593 PE=2 SV=3						swissprot +
Unigene62072_All	203	0.00	2.25	0.00	0.25	0.00	2.89	0.21	3.50	1.77	1.11E+01	7.42E-03		null	null		-7.94E+00	5.51E-01		3.56E+00	8.47E-03		4.07E+00	3.51E-04	Up	3.08E+00	3.61E-02		Unigene62072_All//gi|264664531|sp|O0LGG8.1|Y5343_ARATH//2.00E-15//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g53430; Flags: Precursor >gi|224589438|gb|ACN59253.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene62072_All//9.00E-17//AT1G53430| leucine-rich repeat family protein / protein kinase family protein	Unigene62072_All//2.00E-48//TC163829		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006464//GO:0016020//GO:0016628//GO:0032559	nr +
Unigene6208_All	1429	1.21	1.35	0.89	1.22	2.48	0.92	2.40	0.73	1.14	1.57E-01	7.23E-01		-4.34E-01	3.93E-01		1.02E+00	1.27E-03		-4.13E-01	4.39E-01		-1.71E+00	1.23E-07	Down	-1.07E+00	2.59E-04	Down	Unigene6208_All//gi|115444033|ref|NP_001045796.1|//1.00E-35//Os02g0132200 [Oryza sativa Japonica Group] >gi|113535327|dbj|BAF07710.1| Os02g0132200 [Oryza sativa Japonica Group]	Unigene6208_All//4.00E-40//AT5G05240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP030365 (InterPro:IPR016953); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G40630.1); Has 24 Blast hits to 24 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 2; Plants - 22; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene6208_All//2.00E-80//TC170923				nr +
Unigene6209_All	1046	44.42	1705.90	214.17	39.72	40.59	306.04	11.88	92.14	51.84	5.26E+00	0.00E+00	Up	2.27E+00	0.00E+00	Up	3.14E-02	7.99E-01		2.95E+00	0.00E+00	Up	2.95E+00	0.00E+00	Up	2.13E+00	6.37E-149	Up	Unigene6209_All//gi|15232509|ref|NP_191010.1|//8.00E-88//ATEP3; chitinase [Arabidopsis thaliana] >gi|7288020|emb|CAB81807.1| class IV chitinase (CHIV) [Arabidopsis thaliana] >gi|34146830|gb|AAQ62423.1| At3g54420 [Arabidopsis thaliana] >gi|51971118|dbj|BAD44251.1| class IV chitinase (CHIV) [Arabidopsis thaliana]	Unigene6209_All//3.00E-82//AT3G54420| ATEP3; chitinase	Unigene6209_All//0.00E+00//TC149357		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene6210_All	829	23.86	43.33	28.97	20.91	21.06	18.69	12.85	12.30	6.01	8.61E-01	1.19E-20		2.80E-01	1.90E-02		1.02E-02	9.51E-01		-1.62E-01	2.93E-01		-6.32E-02	7.27E-01		-1.10E+00	4.78E-12	Down	Unigene6210_All//gi|15238881|ref|NP_200205.1|//3.00E-59//yippee family protein [Arabidopsis thaliana] >gi|27923898|sp|Q9FN32.1|YIPL7_ARATH RecName: Full=Protein yippee-like At5g53940 >gi|10177256|dbj|BAB10724.1| zinc-binding protein-like [Arabidopsis thaliana] >gi|21554253|gb|AAM63328.1| zinc-binding protein-like [Arabidopsis thaliana] >gi|51971218|dbj|BAD44301.1| zinc-binding protein-like [Arabidopsis thaliana] >gi|88011182|gb|ABD38914.1| At5g53940 [Arabidopsis thaliana]	Unigene6210_All//1.00E-60//AT5G53940| yippee family protein	Unigene6210_All//0.00E+00//TC139791				nr -
Unigene6211_All	1091	0.34	1.16	0.98	2.74	3.06	1.28	2.17	1.34	0.66	1.79E+00	5.96E-03		1.54E+00	3.52E-02		1.60E-01	6.91E-01		-1.09E+00	2.39E-03		-6.95E-01	6.14E-02		-1.72E+00	8.87E-06	Down	Unigene6211_All//gi|115471103|ref|NP_001059150.1|//1.00E-69//Os07g0205900 [Oryza sativa Japonica Group] >gi|34393302|dbj|BAC83231.1| cyclin-like protein [Oryza sativa Japonica Group] >gi|113610686|dbj|BAF21064.1| Os07g0205900 [Oryza sativa Japonica Group]	Unigene6211_All//2.00E-94//AT5G21080| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: cyclin-related (TAIR:AT2G41830.1); Has 203 Blast hits to 200 proteins in 66 species: Archae - 0; Bacteria - 4; Metazoa - 116; Fungi - 12; Plants - 64; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	Unigene6211_All//0.00E+00//TC170352				nr -
Unigene62110_All	528	0.00	4.13	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.11E-12	Up	9.24E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene62110_All//gi|115456147|ref|NP_001061674.1|//6.00E-30//Os03g0811700 [Oryza sativa Japonica Group] >gi|113550145|dbj|BAF13588.1| Os03g0811700 [Oryza sativa Japonica Group]	Unigene62110_All//5.00E-30//AT5G12190| RNA recognition motif (RRM)-containing protein			ko03040|Spliceosome	GO:0003676	nr -
Unigene6212_All	1040	2.06	0.68	1.08	12.60	5.89	4.69	10.41	7.52	2.11	-1.60E+00	6.02E-04	Down	-9.40E-01	4.24E-02		-1.10E+00	6.61E-14	Down	-1.43E+00	2.05E-18	Down	-4.70E-01	2.44E-03		-2.30E+00	6.00E-34	Down	Unigene6212_All//gi|13346194|gb|AAK19619.1|AF336286_1//3.00E-83//GHMYB9 [Gossypium hirsutum] >gi|207288825|gb|ACI23564.1| MYB-like protein 3 [Gossypium barbadense]	Unigene6212_All//6.00E-71//AT4G38620| MYB4; DNA binding / transcription factor	Unigene6212_All//5.00E-157//DW498579	MYB			nr -
Unigene62127_All	783	0.07	7.31	7.62	0.00	0.22	0.00	1.73	0.48	1.12	6.77E+00	6.23E-31	Up	6.83E+00	1.65E-31	Up	7.78E+00	2.26E-01		null	null		-1.85E+00	9.21E-04	Down	-6.26E-01	2.05E-01		Unigene62127_All//gi|253759874|ref|XP_002488851.1|//3.00E-17//hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor] >gi|241947058|gb|EES20203.1| hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor]		Unigene62127_All//1.00E-67//TC148521				nr +
Unigene6213_All	819	65.42	29.94	22.37	31.20	27.83	32.48	26.43	219.34	56.28	-1.13E+00	2.48E-47	Down	-1.55E+00	3.24E-74	Down	-1.65E-01	1.58E-01		5.79E-02	6.67E-01		3.05E+00	0.00E+00	Up	1.09E+00	2.74E-48	Up	Unigene6213_All//gi|18252504|gb|AAL66290.1|AF452450_1//2.00E-32//adenosine 5'-phosphosulfate reductase [Glycine max]	Unigene6213_All//2.00E-30//AT1G62180| APR2 (5'ADENYLYLPHOSPHOSULFATE REDUCTASE 2); adenylyl-sulfate reductase/ phosphoadenylyl-sulfate reductase (thioredoxin)	Unigene6213_All//0.00E+00//gi|73860885|gb|DT463624.1|DT463624				nr +
Unigene62131_All	208	0.00	3.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.37E-05	Up	null	null		null	null		null	null		null	null		null	null								
Unigene6214_All	212	25.67	36.09	17.83	39.24	32.65	43.03	180.09	299.67	60.13	4.92E-01	2.03E-02		-5.25E-01	5.07E-02		-2.65E-01	2.15E-01		1.33E-01	5.70E-01		7.35E-01	1.14E-33		-1.58E+00	2.79E-71	Down	Unigene6214_All//gi|297803438|ref|XP_002869603.1|//6.00E-33//early-responsive to dehydration 8 [Arabidopsis lyrata subsp. lyrata] >gi|297315439|gb|EFH45862.1| early-responsive to dehydration 8 [Arabidopsis lyrata subsp. lyrata]	Unigene6214_All//2.00E-33//AT5G56000| heat shock protein 81-4 (HSP81-4)	Unigene6214_All//6.00E-116//EV494709		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene62154_All	324	0.00	4.07	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.49E-07	Up	7.36E+00	6.33E-01		null	null		null	null		null	null		null	null		Unigene62154_All//gi|195644768|gb|ACG41852.1|//1.00E-06//pyruvate decarboxylase isozyme 1 [Zea mays]	Unigene62154_All//6.00E-06//AT5G54960| PDC2 (pyruvate decarboxylase-2); carboxy-lyase/ catalytic/ magnesium ion binding / pyruvate decarboxylase/ thiamin pyrophosphate binding			ko00010|Glycolysis / Gluconeogenesis//ko00380|Tryptophan metabolism		nr +
Unigene62156_All	209	0.00	3.64	0.51	0.00	0.00	0.00	0.00	0.00	0.19	1.18E+01	1.76E-04	Up	8.99E+00	3.96E-01		null	null		null	null		null	null		7.57E+00	6.41E-01		Unigene62156_All//sp|P06748|NPM_HUMAN//3.00E-33//Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2						swissprot +
Unigene6216_All	1001	0.52	2.48	0.21	5.08	5.99	5.96	7.94	3.97	4.26	2.25E+00	1.80E-06	Up	-1.30E+00	2.42E-01		2.38E-01	3.86E-01		2.31E-01	4.04E-01		-1.00E+00	8.84E-08	Down	-8.99E-01	7.07E-07		Unigene6216_All//gi|15228352|ref|NP_187679.1|//4.00E-12//heat shock protein-related [Arabidopsis thaliana]	Unigene6216_All//1.00E-11//AT3G10680| heat shock protein-related					nr -
Unigene62165_All	321	1.96	0.00	0.33	1.09	1.82	0.42	2.37	0.52	0.74	-1.09E+01	7.90E-04	Down	-2.56E+00	2.72E-02		7.47E-01	4.81E-01		-1.36E+00	3.37E-01		-2.19E+00	7.77E-03		-1.67E+00	2.39E-02		Unigene62165_All//gi|20147346|gb|AAM10386.1|//4.00E-16//AT5g38690/MEB18_24 [Arabidopsis thaliana] >gi|23463059|gb|AAN33199.1| At5g38690/MEB18_24 [Arabidopsis thaliana]	Unigene62165_All//2.00E-17//AT5G38690| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: DDT superfamily (InterPro:IPR018501), DDT subgroup (InterPro:IPR018500), Cell division cycle-associated protein (InterPro:IPR018866); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G67780.1); Has 492 Blast hits to 468 proteins in 97 species: Archae - 9; Bacteria - 41; Metazoa - 179; Fungi - 19; Plants - 99; Viruses - 2; Other Eukaryotes - 143 (source: NCBI BLink).	Unigene62165_All//8.00E-101//DT461206				nr +
Unigene62182_All	245	0.00	3.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.37E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene62182_All//gi|297828898|ref|XP_002882331.1|//7.00E-39//glyceraldehyde-3-phosphate dehydrogenase C subunit [Arabidopsis lyrata subsp. lyrata] >gi|297328171|gb|EFH58590.1| glyceraldehyde-3-phosphate dehydrogenase C subunit [Arabidopsis lyrata subsp. lyrata]	Unigene62182_All//1.00E-29//AT3G04120| GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene62182_All//1.00E-64//gi|54117119|gb|CO492628.1|CO492628		ko00010|Glycolysis / Gluconeogenesis	GO:0000166//GO:0000302//GO:0005576//GO:0006007//GO:0006952//GO:0006970//GO:0008943//GO:0009536//GO:0009791//GO:0010038//GO:0016020//GO:0030312//GO:0031967//GO:0031981//GO:0034285//GO:0046914//GO:0048608	nr +
Unigene6220_All	1207	0.56	2.22	0.40	1.44	2.05	4.75	2.87	4.54	7.62	1.98E+00	4.79E-06	Up	-5.05E-01	5.82E-01		5.08E-01	2.29E-01		1.72E+00	1.31E-10	Up	6.59E-01	3.65E-03		1.41E+00	5.39E-15	Up	Unigene6220_All//gi|32465891|gb|AAQ19327.1|//3.00E-09//bZIP-like protein [Oryza sativa Japonica Group]	Unigene6220_All//7.00E-05//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative					nr -

Unigene6221_All	1056	0.59	2.45	0.91	1.75	3.42	3.08	2.60	1.15	6.30	2.04E+00	4.81E-06	Up	6.10E-01	3.86E-01		9.72E-01	1.98E-03		8.19E-01	1.79E-02		-1.18E+00	6.00E-04	Down	1.28E+00	1.20E-09	Up	Unigene6221_All//gi|15237707|ref|NP_200666.1|//7.00E-36//ATL63 (ARABIDOPSIS TOኡXICOS EN LEVADURA); protein binding / zinc ion binding [Arabidopsis thaliana] >gi|68565312|sp|Q9LUZ9.1|ATL50_ARATH RecName: Full=RING-H2 finger protein ATL50 >gi|67633892|gb|AAY78870.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene6221_All//2.00E-22//AT5G58580| ATL63 (ARABIDOPSIS TOኡXICOS EN LEVADURA); protein binding / zinc ion binding	Unigene6221_All//0.00E+00//gi|13243656|gb|BE055048.2|BE055048				nr +
Unigene6225_All	772	4.74	0.59	0.83	6.13	3.79	6.08	13.47	4.44	7.53	-3.01E+00	1.48E-12	Down	-2.52E+00	5.37E-10	Down	-6.93E-01	7.93E-03		-1.08E-02	9.64E-01		-1.60E+00	9.54E-20	Down	-8.39E-01	7.53E-08		Unigene6225_All//gi|15240154|ref|NP_200925.1|//3.00E-67//40S ribosomal protein S19 (RPS19C) [Arabidopsis thaliana] >gi|297793669|ref|XP_002864719.1| 40S ribosomal protein S19 [Arabidopsis lyrata subsp. lyrata] >gi|27923837|sp|Q9FNP8.1|RS193_ARATH RecName: Full=40S ribosomal protein S19-3 >gi|9759463|dbj|BAB10379.1| 40S ribosomal protein S19 [Arabidopsis thaliana] >gi|34365671|gb|AAQ65147.1| At5g61170 [Arabidopsis thaliana] >gi|51970120|dbj|BAD43752.1| 40S ribosomal protein S19 - like [Arabidopsis thaliana] >gi|297310554|gb|EFH40978.1| 40S ribosomal protein S19 [Arabidopsis lyrata subsp. lyrata]	Unigene6225_All//1.00E-68//AT5G61170| 40S ribosomal protein S19 (RPS19C)	Unigene6225_All//0.00E+00//gi|164294101|gb|ES818241.1|ES818241		ko03010|Ribosome		nr +
Unigene6227_All	970	2.48	4.23	2.36	8.94	6.43	5.91	6.80	7.02	26.24	7.70E-01	1.04E-02		-7.19E-02	8.66E-01		-4.76E-01	1.12E-02		-5.96E-01	2.04E-03		4.67E-02	8.40E-01		1.95E+00	6.72E-63	Up	Unigene6227_All//gi|115479709|ref|NP_001063448.1|//5.00E-15//Os09g0472900 [Oryza sativa Japonica Group] >gi|113631681|dbj|BAF25362.1| Os09g0472900 [Oryza sativa Japonica Group]	Unigene6227_All//1.00E-08//AT2G18660| EXLB3 (EXPANSIN-LIKE B3 PRECURSOR)	Unigene6227_All//0.00E+00//gi|109887102|gb|DW516071.1|DW516071				nr +
Unigene62274_All	388	0.00	3.92	1.24	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.10E-08	Up	1.03E+01	7.47E-03		null	null		null	null		null	null		null	null		Unigene62274_All//gi|300120616|emb|CBK20170.2|//2.00E-12//unnamed protein product [Blastocystis hominis]						nr +
Unigene6229_All	399	59.53	30.99	29.23	158.81	97.70	87.61	299.99	238.83	70.39	-9.42E-01	4.02E-16		-1.03E+00	1.06E-17	Down	-7.01E-01	8.68E-31		-8.58E-01	1.37E-38		-3.29E-01	4.01E-15		-2.09E+00	0.00E+00	Down	Unigene6229_All//gi|1346172|sp|P49118.1|BIP_SOLLC//1.00E-63//RecName: Full=Luminal-binding protein; Short=BiP; AltName: Full=78 kDa glucose-regulated protein homolog; Short=GRP-78; Flags: Precursor >gi|170384|gb|AAA34139.1| glucose-regulated protein 78 [Solanum lycopersicum]	Unigene6229_All//5.00E-46//AT5G28540| BIP1; ATP binding	Unigene6229_All//0.00E+00//ES835095		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr +
Unigene62298_All	205	0.00	3.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene6230_All	810	3.49	4.38	3.88	4.49	4.04	4.29	2.51	1.44	0.74	3.28E-01	3.41E-01		1.53E-01	6.67E-01		-1.53E-01	6.66E-01		-6.44E-02	8.63E-01		-7.94E-01	5.02E-02		-1.76E+00	3.30E-05	Down	Unigene6230_All//gi|257781218|gb|ACV65036.1|//3.00E-81/3-hydroxy-3-methylglutaryl coenzyme A reductase [Panax quinquefolius]	Unigene6230_All//3.00E-68//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene6230_All//0.00E+00//TC169600		ko00900|Terpenoid backbone biosynthesis		nr +
Unigene6231_All	490	6.73	6.31	3.48	9.45	12.72	6.73	2.42	0.00	1.30	-9.28E-02	7.78E-01		-9.52E-01	7.85E-03		4.28E-01	7.50E-02		-4.91E-01	8.78E-02		-1.12E+01	1.97E-08	Down	-8.93E-01	9.53E-02		Unigene6231_All//gi|115441397|ref|NP_001014978.1|//1.00E-14//Os01g0878000 [Oryza sativa Japonica Group] >gi|113534509|dbj|BAF06892.1| Os01g0878000 [Oryza sativa Japonica Group]	Unigene6231_All//8.00E-27//AT1G11120| unknown protein	Unigene6231_All//3.00E-24//BG443522				nr -
Unigene6232_All	340	86.02	78.98	67.03	92.01	93.38	106.93	130.20	89.49	56.48	-1.23E-01	2.69E-01		-3.60E-01	5.62E-04		2.13E-02	8.59E-01		2.17E-01	1.93E-02		-5.41E-01	4.12E-14		-1.21E+00	9.66E-55	Down	Unigene6232_All//gi|124359794|gb|ABN06120.1|//3.00E-55//Peptidase T1A, proteasome beta-subunit [Medicago truncatula]	Unigene6232_All//4.00E-54//AT5G40580| PBB2; endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene6232_All//0.00E+00//gi|18099171|gb|BM358425.1|BM358425		ko03050|Proteasome		nr -
Unigene6233_All	1586	0.00	0.00	0.00	0.06	0.09	0.28	17.91	11.28	4.47	null	null		null	null		4.67E-01	8.76E-01		2.18E+00	1.03E-01		-6.68E-01	2.97E-13		-2.00E+00	1.39E-73	Down	Unigene6233_All//gi|1545805|dbj|BAA10929.1|//3.00E-07//cytochrome P450 like_TBP [Nicotiana tabacum]		Unigene6233_All//2.00E-49//gi|78348172|gb|DT568446.1|DT568446				nr -
Unigene62347_All	530	0.00	6.50	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.31E-19	Up	1.07E+01	9.01E-05	Up	null	null		null	null		null	null		null	null		Unigene62347_All//gi|58613403|gb|AAW79288.1|//7.00E-16//mitochondrial acyl carrier protein [Isochrysis galbana]	Unigene62347_All//4.00E-16//AT1G65290| mtACP2 (mitochondrial acyl carrier protein 2); acyl carrier/ metal ion binding			ko00190|Oxidative phosphorylation	GO:0006631//GO:0016597//GO:0022892//GO:0031980//GO:0046914	nr +
Unigene62350_All	208	0.00	3.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene62350_All//sp|Q9VZF4|FBXW7_DROME//9.00E-07//F-box/WD repeat-containing protein 7 OS=Drosophila melanogaster GN=ago PE=1 SV=1						swissprot -
Unigene62351_All	447	0.00	3.29	0.48	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.11E-08	Up	8.90E+00	1.40E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene62358_All	423	0.00	2.87	1.13	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	5.47E-07	Up	1.01E+01	7.47E-03		null	null		null	null		null	null		null	null		Unigene62358_All//gi|254973029|gb|ACT98425.1|//2.00E-07//low-molecular-weight glutenin subunit [Triticum aestivum]						nr +
Unigene6238_All	778	33.02	5.60	6.91	10.44	8.06	3.48	2.88	2.31	0.72	-2.56E+00	2.15E-71	Down	-2.26E+00	2.77E-59	Down	-3.74E-01	6.56E-02		-1.58E+00	1.74E-13	Down	-3.18E-01	4.31E-01		-2.01E+00	1.43E-06	Down	Unigene6238_All//gi|255581069|ref|XP_002531350.1|//1.00E-72//ER glycerol-phosphate acyltransferase [Ricinus communis] >gi|223529048|gb|EEF31034.1| ER glycerol-phosphate acyltransferase [Ricinus communis]	Unigene6238_All//3.00E-70//AT1G01610| GPAT4 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 4); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase	Unigene6238_All//0.00E+00//TC174193		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr +
Unigene62387_All	236	0.00	7.30	1.13	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	7.98E-10	Up	1.01E+01	8.00E-02		null	null		null	null		null	null		null	null									
Unigene6239_All	987	0.00	3.70	1.19	4.74	4.99	1.78	0.60	1.02	2.46	1.19E+01	9.10E-21	Up	1.02E+01	1.77E-06	Up	7.26E-02	8.22E-01		-1.41E+00	7.19E-07	Down	7.61E-01	2.28E-01		2.04E+00	4.42E-07	Up	Unigene6239_All//gi|15218397|ref|NP_177974.1|//1.00E-129//protein kinase family protein [Arabidopsis thaliana]	Unigene6239_All//4.00E-124//AT1G78530| protein kinase family protein	Unigene6239_All//0.00E+00//CO101985				nr -
Unigene6240_All	746	16.48	10.73	13.71	42.87	46.21	20.04	11.68	13.17	8.22	-6.19E-01	1.18E-04		-2.66E-01	1.38E-01		1.08E-01	3.10E-01		-1.10E+00	1.83E-29	Down	1.73E-01	3.60E-01		-5.06E-01	2.84E-03		Unigene6240_All//gi|297725701|ref|NP_001175214.1|//6.00E-14//Os07g0501200 [Oryza sativa Japonica Group] >gi|255677791|dbj|BAH93942.1| Os07g0501200 [Oryza sativa Japonica Group]	Unigene6240_All//7.00E-07//AT3G25270| nucleic acid binding	Unigene6240_All//0.00E+00//gi|21098994|gb|BQ411307.1|BQ411307				nr +
Unigene62418_All	456	0.00	2.89	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.49E-07	Up	9.45E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene62418_All//gi|5263319|gb|AA041421.1|AC007727_10//3.00E-67//ESTs gb|N96028, gb|F14286, gb|T20680, gb|F14443, gb|AA657300 and gb|N65244 come from this gene [Arabidopsis thaliana]	Unigene62418_All//4.00E-63//AT1G21680| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole, plant-type cell wall; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: WD40-like Beta Propeller (InterPro:IPR011659), Six-bladed beta-propeller, TolB-like (InterPro:IPR011042); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G21670.1); Has 6869 Blast hits to 3873 proteins in 790 species: Archae - 41; Bacteria - 3697; Metazoa - 41; Fungi - 39; Plants - 64; Viruses - 0; Other Eukaryotes - 2987 (source: NCBI BLink).	Unigene62418_All//5.00E-07//TC154204			GO:0005618//GO:0016020//GO:0031410//GO:0043231	nr +
Unigene6242_All	764	11.23	3.98	11.08	6.46	7.39	7.51	3.71	2.19	0.73	-1.50E+00	2.62E-12	Down	-1.93E-02	9.45E-01		1.96E-01	5.18E-01		2.18E-01	4.50E-01		-7.61E-01	2.21E-02		-2.34E+00	1.20E-09	Down	Unigene6242_All//gi|297812787|ref|XP_002874277.1|//1.00E-80//rhomboid family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320114|gb|EFH50536.1| rhomboid family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6242_All//4.00E-81//AT5G25752| RBL11 (RHOMBOID-LIKE PROTEIN 11)					nr +
Unigene6243_All	643	2.03	41.21	13.33	1.94	2.46	4.21	10.59	3.32	4.58	4.34E+00	2.08E-117	Up	2.71E+00	8.50E-25	Up	3.47E-01	5.55E-01		1.12E+00	3.76E-03		-1.68E+00	5.20E-14	Down	-1.21E+00	3.42E-09	Down	Unigene6243_All//gi|5306239|gb|AAD41972.1|//1.00E-06//expressed protein [Arabidopsis thaliana]	Unigene6243_All//6.00E-08//AT2G15960| unknown protein	Unigene6243_All//0.00E+00//TC164639				nr -
Unigene6244_All	878	2.86	6.64	6.13	1.70	3.10	3.60	0.48	0.38	0.00	1.21E+00	1.94E-06	Up	1.10E+00	5.35E-05	Up	8.64E-01	2.16E-02		1.08E+00	2.14E-03		-3.39E-01	7.30E-01		-8.91E+00	2.14E-03		Unigene6244_All//gi|229609831|gb|ACQ83531.1|//1.00E-110//CBL-interacting protein kinase 15 [Vitis vinifera]	Unigene6244_All//5.00E-91//AT5G10930| CIPK5 (CBL-INTERACTING PROTEIN KINASE 5); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene6244_All//0.00E+00//gi|78326208|gb|DT546482.1|DT546482				nr +
Unigene6245_All	712	0.29	0.85	0.30	3.57	2.85	2.98	3.98	1.59	1.45	1.54E+00	1.22E-01		2.58E-02	1.00E+00		-3.23E-01	4.48E-01		-2.59E-01	5.66E-01		-1.33E+00	1.09E-04	Down	-1.45E+00	1.85E-05	Down	Unigene6245_All//gi|44681466|gb|AAS47673.1|//3.00E-66//At2g32280 [Arabidopsis thaliana]	Unigene6245_All//1.00E-53//AT2G32280| unknown protein	Unigene6245_All//0.00E+00//TC142692				nr -
Unigene6246_All	708	2.29	3.22	2.93	5.14	4.09	2.49	4.18	78.10	3.66	4.91E-01	2.47E-01		3.57E-01	4.42E-01		-3.30E-01	3.22E-01		-1.05E+00	1.08E-03		4.22E+00	1.67E-295	Up	-1.93E-01	5.85E-01		Unigene6246_All//gi|269833632|gb|ACZ48681.1|//1.00E-16//Bcl-2-associated athanogene-like protein [Vitis vinifera]		Unigene6246_All//3.00E-173//gi|78335368|gb|DT555642.1|DT555642				nr -
Unigene6247_All	1017	4.73	2.79	1.62	5.44	6.03	5.02	1.54	0.16	0.90	-7.63E-01	5.34E-03		-1.54E+00	3.77E-07	Down	1.49E-01	6.03E-01		-1.16E-01	7.02E-01		-3.23E+00	2.68E-07	Down	-7.72E-01	8.85E-02		Unigene6247_All//gi|115438600|ref|NP_001043580.1|//7.00E-17//Os01g0616800 [Oryza sativa Japonica Group] >gi|113533111|dbj|BAF05494.1| Os01g0616800 [Oryza sativa Japonica Group]		Unigene6247_All//0.00E+00//gi|78329050|gb|DT549324.1|DT549324				nr +
Unigene62476_All	207	0.00	3.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene6248_All	866	1.39	0.88	1.78	2.47	2.43	4.54	176.98	234.75	460.17	-6.63E-01	2.79E-01		3.60E-01	5.20E-01		-2.82E-02	9.51E-01		8.75E-01	4.48E-03		4.08E-01	4.55E-37		1.38E+00	0.00E+00	Up	Unigene6248_All//gi|225442485|ref|XP_002278313.1|//7.00E-99//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene6248_All//4.00E-73//AT1G59870| PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	Unigene6248_All//0.00E+00//gi|73863885|gb|DT466624.1|DT466624		ko03040|Spliceosome//ko02010|ABC transporters		nr +

Unigene62489_All	681	0.00	3.79	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.05E-14	Up	7.29E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene62489_All//gi|224073580|ref|XP_002304115.1|//3.00E-06//predicted protein [Populus trichocarpa] >gi|222841547|gb|EEE79094.1| predicted protein [Populus trichocarpa]							nr +
Unigene6249_All	513	169.92	166.23	189.33	110.89	71.29	69.46	107.64	44.08	73.15	-3.16E-02	6.12E-01		1.56E-01	6.02E-03		-6.37E-01	1.99E-23		-6.75E-01	4.89E-23		-1.29E+00	2.23E-73	Down	-5.57E-01	7.51E-19		Unigene6249_All//gi|28466845|gb|AA044031.1|//6.00E-32//At5g50090 [Arabidopsis thaliana]	Unigene6249_All//4.00E-33//AT5G50090| unknown protein	Unigene6249_All//0.00E+00//TC147929				nr +
Unigene625_All	1870	10.74	8.75	7.52	19.05	14.44	18.16	22.93	16.05	10.03	-2.96E-01	1.88E-02		-5.15E-01	4.89E-05		-4.00E-01	1.32E-06		-6.86E-02	5.52E-01		-5.15E-01	1.39E-12		-1.19E+00	3.67E-52	Down	Unigene625_All//gi|297843902|ref|XP_002889832.1|//0.00E+00//clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335674|gb|EFH66091.1| clathrin adaptor complexes medium subunit family protein [Arabidopsis lyrata subsp. lyrata]	Unigene625_All//0.00E+00//AT1G60780| HAP13 (HAPLESS 13); protein binding	Unigene625_All//0.00E+00//gi|78336553|gb|DT556827.1|DT556827			GO:0005488//GO:0015031//GO:0030118//GO:0030119	nr -
Unigene6250_All	968	21.51	17.95	21.29	61.24	76.48	52.91	1.53	0.17	0.70	-2.61E-01	3.64E-02		-1.50E-02	9.26E-01		3.21E-01	1.01E-08		-2.11E-01	2.31E-03		-3.15E+00	8.54E-07	Down	-1.13E+00	1.72E-02		Unigene6250_All//gi|297825869|ref|XP_002880817.1|//1.00E-140//nitrate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326656|gb|EFH57076.1| nitrate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene6250_All//2.00E-134//AT2G26690| nitrate transporter (NTP2)	Unigene6250_All//0.00E+00//TC165066				nr +
Unigene6251_All	617	3.05	7.06	3.45	1.61	0.61	4.54	9.87	17.88	231.48	1.21E+00	5.32E-05	Up	1.77E-01	6.88E-01		-1.40E+00	3.79E-02		1.49E+00	1.33E-04	Up	8.58E-01	2.85E-08		4.55E+00	0.00E+00	Up	Unigene6251_All//gi|255545602|ref|XP_002513861.1|//2.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223546947|gb|EEF48444.1| conserved hypothetical protein [Ricinus communis]		Unigene6251_All//0.00E+00//gi|73860847|gb|DT463586.1|DT463586				nr -
Unigene62516_All	379	0.28	0.27	0.28	0.00	0.45	0.12	0.89	0.33	3.89	-4.62E-02	9.87E-01		2.54E-02	9.98E-01		8.83E+00	2.26E-01		6.90E+00	6.91E-01		-1.43E+00	2.58E-01		2.12E+00	8.39E-05	Up	Unigene62516_All//gi|224127272|ref|XP_002320031.1|//9.00E-36//f-box family protein [Populus trichocarpa] >gi|222860804|gb|EEE98346.1| f-box family protein [Populus trichocarpa]	Unigene62516_All//4.00E-22//AT5G43190| F-box family protein (FBX6)	Unigene62516_All//7.00E-09//TC160297				nr +
Unigene6252_All	595	17.50	9.88	6.35	24.03	18.11	29.22	13.43	6.53	8.24	-8.25E-01	3.61E-06		-1.46E+00	1.20E-13	Down	-4.08E-01	3.92E-03		2.82E-01	4.20E-02		-1.04E+00	2.89E-08	Down	-7.06E-01	7.40E-05		Unigene6252_All//gi|297823195|ref|XP_002879480.1|//3.00E-51//nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297325319|gb|EFH55739.1| nucleic acid binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene6252_All//4.00E-46//AT2G34160| nucleic acid binding	Unigene6252_All//0.00E+00//DW496504				nr -
Unigene62524_All	818	0.00	6.94	3.84	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.22E-32	Up	1.19E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene62524_All//gi|297601626|ref|NP_001051163.2|//5.00E-37//Os03g0730800 [Oryza sativa Japonica Group] >gi|255674865|dbj|BAF13077.2| Os03g0730800 [Oryza sativa Japonica Group]	Unigene62524_All//2.00E-34//AT1G10130| ECA3 (ENDOPLASMIC RETICULUM-TYPE CALCIUM-TRANSPORTING ATPASE 3); calcium-transporting ATPase/ calmodulin binding / manganese-transporting ATPase/ peroxidase					nr -
Unigene62537_All	346	0.00	3.08	1.08	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.81E-06	Up	1.01E+01	2.50E-02		null	null		null	null		null	null		null	null										
Unigene62549_All	384	0.00	4.22	1.39	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.96E-09	Up	1.04E+01	4.03E-03		null	null		null	null		null	null		null	null										
Unigene6256_All	859	0.06	3.19	1.49	2.44	2.24	3.73	3.35	4.72	2.04	5.71E+00	3.78E-14	Up	4.61E+00	5.50E-06	Up	-1.18E-01	8.19E-01		6.16E-01	8.29E-02		4.96E-01	7.25E-02		-7.14E-01	2.44E-02		Unigene6256_All//gi|115451217|ref|NP_001049209.1|//5.00E-10//Os03g0187400 [Oryza sativa Japonica Group] >gi|108706575|gb|ABF94370.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547680|dbj|BAF11123.1| Os03g0187400 [Oryza sativa Japonica Group]	Unigene6256_All//4.00E-05//AT1G02070| unknown protein	Unigene6256_All//8.00E-26//ES846443				nr +
Unigene62561_All	245	0.00	1.65	3.48	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	1.35E-02		1.18E+01	9.01E-05	Up	null	null		null	null		null	null		null	null										
Unigene62578_All	450	0.00	3.27	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.11E-08	Up	7.89E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene62578_All//sp|Q2FQH8|GDE_CANFA//4.00E-29//Glycogen debranching enzyme OS=Canis familiaris GN=AGL PE=2 SV=1							swissprot -
Unigene6258_All	700	0.60	5.21	1.83	3.56	3.44	2.58	7.43	31.41	0.85	3.12E+00	7.94E-13	Up	1.61E+00	1.45E-02		-4.73E-02	9.05E-01		-4.63E-01	2.77E-01		2.08E+00	5.07E-58	Up	-3.12E+00	5.46E-23	Down	Unigene6258_All//gi|159138937|gb|ABR89468.1|//2.00E-81//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene6258_All//8.00E-60//AT2G29500| 17.6 kDa class I small heat shock protein (HSP17.6B-CI)	Unigene6258_All//0.00E+00//gi|109836434|gb|DW234995.1|DW234995				nr -
Unigene62583_All	661	0.00	7.21	1.29	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	3.82E-27	Up	1.03E+01	9.01E-05	Up	null	null		null	null		null	null		null	null		Unigene62583_All//sp|Q1HRV8|ELVL1_AEDAE//8.00E-48//Elongation of very long chain fatty acids protein AAEL008004 OS=Aedes aegypti GN=AAEL008004 PE=2 SV=2							swissprot +
Unigene62586_All	861	0.12	0.35	0.00	0.00	0.04	0.16	0.74	0.00	0.37	1.54E+00	3.23E-01		-6.92E+00	3.89E-01		5.32E+00	8.24E-01		7.30E+00	3.10E-01		-9.52E+00	1.23E-04	Down	-9.93E-01	2.02E-01		Unigene62586_All//gi|297793499|ref|XP_002864634.1|//2.00E-26//ATTRP1 [Arabidopsis lyrata subsp. lyrata] >gi|297310469|gb|EFH40893.1| ATTRP1 [Arabidopsis lyrata subsp. lyrata]	Unigene62586_All//1.00E-27//AT5G59430| TRP1 (TELOMERIC REPEAT BINDING PROTEIN 1); DNA binding / double-stranded telomeric DNA binding	Unigene62586_All//2.00E-174//gi|48815813|gb|CO117126.1|CO117126	MYB-related			nr -
Unigene6259_All	748	0.98	1.35	0.57	2.00	8.15	12.86	4.01	14.81	25.03	4.68E-01	4.89E-01		-7.82E-01	3.80E-01		2.03E+00	6.37E-15	Up	2.69E+00	4.03E-30	Up	1.88E+00	4.69E-26	Up	2.64E+00	5.34E-67	Up	Unigene6259_All//gi|224060299|ref|XP_002300130.1|//2.00E-55//glutaredoxin [Populus trichocarpa] >gi|222847388|gb|EEE84935.1| glutaredoxin [Populus trichocarpa]	Unigene6259_All//6.00E-37//AT3G02000| ROXY1; disulfide oxidoreductase					nr -
Unigene62594_All	659	0.00	2.46	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	2.96E-09	Up	1.05E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene62594_All//sp|P01023|A2MG_HUMAN//5.00E-102//Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2							swissprot -
Unigene626_All	1263	13.42	9.55	11.22	87.87	72.52	72.30	18.65	11.28	6.78	-4.91E-01	2.63E-04		-2.59E-01	7.86E-02		-2.77E-01	5.71E-10		-2.81E-01	2.58E-09		-7.25E-01	1.00E-12		-1.46E+00	2.18E-39	Down	Unigene626_All//gi|2129602297|gb|ACJ38653.1|//9.00E-76//myb-like transcription factor [Betula luminifera]	Unigene626_All//5.00E-72//AT4G01680| MYB55 (myb domain protein 55); DNA binding / transcription factor	Unigene626_All//0.00E+00//gi|78335727|gb|DT556001.1|DT556001	MYB		GO:0001071//GO:0003676//GO:0010468//GO:0043231	nr +
Unigene6260_All	889	21.78	12.54	3.83	81.81	70.38	33.83	13.27	4.70	6.23	-7.96E-01	3.51E-10		-2.51E+00	1.15E-50	Down	-2.17E-01	1.93E-04		-1.27E+00	3.90E-84	Down	-1.50E+00	2.89E-20	Down	-1.09E+00	3.98E-13	Down	Unigene6260_All//gi|18423010|ref|NP_568708.1|//2.00E-39//hydroxyproline-rich glycoprotein family protein [Arabidopsis thaliana] >gi|21553492|gb|AAM62585.1| extensin like protein [Arabidopsis thaliana] >gi|194708810|gb|ACF88489.1| At5g19280 [Arabidopsis thaliana]		Unigene6260_All//6.00E-144//TC142331		ko03040|Spliceosome		nr -
Unigene62601_All	291	0.00	5.92	2.74	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.98E-10	Up	1.14E+01	1.72E-04	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene62629_All	703	0.00	4.11	1.06	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.97E-16	Up	1.01E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene62629_All//gi|115472739|ref|NP_001059968.1|//8.00E-07//Os07g0557500 [Oryza sativa Japonica Group] >gi|113611504|dbj|BAF21882.1| Os07g0557500 [Oryza sativa Japonica Group]							nr +
Unigene6263_All	4140	0.58	0.62	0.21	0.30	0.27	0.26	10.62	9.40	11.00	1.03E-01	7.88E-01		-1.50E+00	8.47E-04	Down	-1.76E-01	7.95E-01		-2.00E-01	7.33E-01		-1.76E-01	2.00E-02		5.04E-02	5.58E-01		Unigene6263_All//gi|225424965|ref|XP_002265191.1|//0.00E+00//PREDICTED: similar to Leucine Rich Repeat family protein [Vitis vinifera]	Unigene6263_All//0.00E+00//AT4G2014 0| GSO1 (GASSHO1); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase			ko04626|Plant-pathogen interaction		nr -
Unigene62634_All	485	0.00	9.09	2.53	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	4.10E-25	Up	1.13E+01	9.11E-07	Up	null	null		null	null		null	null		null	null		Unigene62634_All//gi|225446793|ref|XP_002283214.1|//3.00E-08//PREDICTED: glutathione S-transferase 3 [Vitis vinifera] >gi|134252326|gb|ABO64800.1| glutathione S-transferase [Vitis vinifera] >gi|158323770|gb|ABW34389.1| glutathione S-transferase 3 [Vitis vinifera]	Unigene62634_All//3.00E-07//AT2G02390| ATGSTZ1 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE ZETA 1); catalytic/ glutathione transferase			ko00350|Tyrosine metabolism		nr -
Unigene6264_All	642	1.06	22.89	2.65	1.24	1.61	2.60	16.73	10.16	10.49	4.43E+00	4.21E-66	Up	1.32E+00	1.40E-02		3.74E-01	6.04E-01		1.07E+00	4.03E-02		-7.20E-01	3.46E-06		-6.74E-01	8.35E-06		Unigene6264_All//gi|6899646|gb|AAF31023.1|AC012189_5//1.00E-18//EST gb|AB015130 comes from this gene [Arabidopsis thaliana]	Unigene6264_All//2.00E-18//AT2G01300| unknown protein	Unigene6264_All//0.00E+00//TC146747				nr +
Unigene6265_All	259	82.02	30.32	26.52	107.90	73.79	110.21	97.46	29.53	37.53	-1.44E+00	1.21E-27	Down	-1.63E+00	7.00E-32	Down	-5.48E-01	4.67E-09		3.05E-02	8.03E-01		-1.72E+00	7.29E-52	Down	-1.38E+00	1.13E-38	Down	Unigene6265_All//gi|62751093|dbj|BAD95794.1|//5.00E-23//similar to 60S ribosomal protein L35 [Solanum lycopersicum]	Unigene6265_All//3.00E-21//AT3G09500| 60S ribosomal protein L35 (RPL35A)	Unigene6265_All//1.00E-123//gi|13244847|gb|BE055017.2|BE055017		ko03010|Ribosome		nr +
Unigene62657_All	520	0.00	5.55	3.99	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.97E-16	Up	1.20E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene62657_All//gi|226458093|gb|EEH55391.1|//2.00E-42//type II secretory pathway family protein [Micromonas pusilla CCMP1545]	Unigene62657_All//2.00E-42//AT2G34250| protein transport protein sec61, putative			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export		nr -
Unigene6266_All	806	0.71	11.38	2.91	0.19	1.03	1.96	0.47	2.49	5.59	3.99E+00	1.45E-38	Up	2.03E+00	2.96E-05	Up	2.47E+00	6.72E-03		3.40E+00	1.62E-06	Up	2.40E+00	6.33E-07	Up	3.56E+00	5.31E-22	Up	Unigene6266_All//gi|224122288|ref|XP_002336586.1|//1.00E-43//amino acid permease [Populus trichocarpa] >gi|222872144|gb|EEF09275.1| amino acid permease [Populus trichocarpa]	Unigene6266_All//1.00E-37//AT5G23810| AAP7; amino acid transmembrane transporter					nr -

Unigene6267_All	1888	0.00	0.00	0.00	0.05	0.22	0.10	6.02	1.20	45.51	null	null		null	null		2.05E+00	1.47E-01		8.58E-01	6.94E-01		-2.33E+00	5.08E-35	Down	2.92E+00	0.00E+00	Up	Unigene6267_All//gi|5080804|gb|AAD39313.1|AC007258_2//2.00E-56//Hypothetical protein [Arabidopsis thaliana] >gi|15010642|gb|AAK73980.1| At1g59710/T30E16_31 [Arabidopsis thaliana] >gi|22137290|gb|AAM91490.1| At1g59710/T30E16_31 [Arabidopsis thaliana]	Unigene6267_All//1.00E-63//AT3G28630| FUNCTIONS IN: molecular function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: leaf whorl, male gametophyte, flower, pollen tube; EXPRESSED DURING: L mature pollen stage, W germinated pollen stage, 4 anthesis; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF569 (InterPro:IPR007679), Actin_cross-linking (InterPro:IPR008999); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G59710.1); Has 121 Blast hits to 110 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 4; Fungi - 0; Plants - 117; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene6267_All//1.00E-112//C0102597				nr +
Unigene6268_All	430	31.51	16.61	19.81	49.58	51.49	78.46	17.50	16.62	7.04	-9.24E-01	2.99E-09		-6.70E-01	2.27E-05		5.45E-02	7.30E-01		6.62E-01	2.37E-13		-7.45E-02	7.30E-01		-1.31E+00	2.30E-11	Down				Unigene6268_All//5.00E-13//ES836346				
Unigene627_All	1914	6.97	2.99	5.65	40.57	56.46	33.55	17.50	6.77	2.71	-1.22E+00	6.63E-14	Down	-3.04E-01	6.92E-02		4.77E-01	1.29E-25		-2.74E-01	1.98E-06		-1.37E+00	3.48E-49	Down	-2.69E+00	8.06E-124	Down	Unigene627_All//gi|212960297|gb|AC J38663.1|//1.00E-145//myb-like transcription factor [Betula luminifera]	Unigene627_All//9.00E-85//AT1G09540| MYB61 (MYB DOMAIN PROTEIN 61); DNA binding / transcription factor	Unigene627_All//0.00E+00//TC133967	MYB		GO:0003006//GO:0009725//GO:0010118 //GO:0050789	nr +
Unigene6270_All	1349	0.08	0.19	0.00	0.18	0.28	0.90	2.66	3.07	7.15	1.28E+00	4.35E-01		-6.28E+00	3.89E-01		6.05E-01	6.59E-01		2.29E+00	1.17E-03		2.03E-01	5.04E-01		1.42E+00	6.55E-16	Up	Unigene6270_All//gi|284449851|emb|CBJ19140.1|//1.00E-126//SLAC-homologous 1 protein [Citrus clementina]	Unigene6270_All//4.00E-83//AT1G62280| SLAH1 (SLAC1 HOMOLOGUE 1); transporter	Unigene6270_All//5.00E-25//ES795046				nr +
Unigene6271_All	859	15.11	17.34	9.11	130.02	79.85	55.05	69.20	183.68	42.85	1.99E-01	2.03E-01		-7.29E-01	6.87E-06		-7.03E-01	2.29E-54		-1.24E+00	1.10E-123	Down	1.41E+00	1.57E-238	Up	-6.91E-01	2.61E-29		Unigene6271_All//gi|4106378|gb|AAD02824.1|//9.00E-06//calcium-binding protein [Brassica napus]		Unigene6271_All//1.00E-74//C0092146				nr +
Unigene62713_All	208	0.00	3.41	0.51	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	9.00E+00	3.96E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene6272_All	1176	2.58	11.16	15.58	1.31	0.85	0.61	0.00	0.00	0.00	2.11E+00	4.81E-29	Up	2.59E+00	4.34E-50	Up	-6.29E-01	2.32E-01		-1.10E+00	4.18E-02		null	null		null	null		Unigene6272_All//gi|18398991|ref|NP_564430.1|//1.00E-150//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75153901|sp|Q8LSZ1.1|GDL17_ARATH RecName: Full=GDSL esterase/lipase At1g33811; AltName: Full=Extracellular lipase At1g33811; Flags: Precursor	Unigene6272_All//5.00E-140//AT1G33811| GDSL-motif lipase/hydrolase family protein	Unigene6272_All//9.00E-08//gi|21097005|gb|BQ409318.1|BQ409318				nr -
Unigene62734_All	294	0.00	2.93	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	4.94E-05	Up	null	null		null	null		null	null		null	null		null	null									
Unigene62736_All	211	0.00	4.56	1.77	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.38E-05	Up	1.08E+01	2.50E-02		null	null		null	null		null	null		null	null		Unigene62736_All//gi|301106653|ref|XP_002902409.1|//8.00E-22//medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262098283|gb|EEY56335.1| medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene62736_All//5.00E-11//AT3G45300| IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase			ko00280|Valine, leucine and isoleucine degradation		nr -
Unigene62738_All	327	0.00	7.59	2.44	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	3.98E-14	Up	1.13E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene62738_All//gi|168033635|ref|XP_001769320.1|//5.00E-06//predicted protein [Physcomitrella patens subsp. patens] >gi|162679426|gb|EDQ65874.1| predicted protein [Physcomitrella patens subsp. patens]				ko00190|Oxidative phosphorylation		nr +
Unigene62746_All	224	0.00	3.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene62760_All	235	0.00	0.43	0.00	0.00	0.00	0.38	0.00	0.00	2.54	8.75E+00	3.84E-01		null	null		null	null		8.59E-00	4.73E-01		null	null		1.13E+01	1.75E-04	Up								
Unigene62761_All	367	0.00	3.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.06E-08	Up	null	null		null	null		null	null		null	null		null	null									
Unigene62778_All	208	0.00	3.90	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.37E-05	Up	8.00E+00	6.33E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene6278_All	1534	0.24	0.30	0.42	2.57	1.73	1.41	4.60	1.72	0.65	3.16E-01	7.44E-01		8.03E-01	3.88E-01		-5.70E-01	5.64E-02		-8.60E-01	4.75E-03		-1.42E+00	1.34E-11	Down	-2.83E+00	4.58E-28	Down	Unigene6278_All//gi|256674141|gb|ACV04900.1|//1.00E-07//callose synthase 5 [Arabidopsis thaliana]	Unigene6278_All//5.00E-09//AT2G13680| CALS5 (CALLOSE SYNTHASE 5); 1,3-beta-glucan synthase					nr -
Unigene62781_All	523	0.00	2.52	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.49E-07	Up	7.67E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene62781_All//gi|18403249|ref|NP_566698.1|//8.00E-06//proline-rich family protein [Arabidopsis thaliana]						nr -
Unigene62793_All	258	0.00	2.55	0.62	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.24E-04	Up	9.27E+00	2.38E-01		null	null		null	null		null	null		null	null		Unigene62793_All//sp|O02387|CU17_BOMMU//9.00E-07//Larval cuticle protein LCP-17 OS=Bombyx mori GN=LCP17 PE=2 SV=1						swissprot -
Unigene62794_All	269	0.00	3.20	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.94E-05	Up	9.63E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene62794_All//gi|112253323|gb|ABI14249.1|//1.00E-21//phosphoglycerate mutase 1 [Pfiesteria piscicida]	Unigene62794_All//1.00E-13//AT1G78050| PGM (PHOSPHOGLYCERATE/BISPHOSPHOGLYCERATE MUTASE); catalytic/ intramolecular transferase, phosphotransferases			ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene62795_All	431	0.00	0.12	0.12	0.23	0.40	0.00	2.35	0.29	0.74	6.88E+00	6.14E-01		6.95E+00	6.33E-01		7.89E-01	7.70E-01		-7.85E+00	3.96E-01		-3.02E+00	1.08E-04	Down	-1.67E+00	7.35E-03									
Unigene628_All	1863	4.52	1.44	2.63	49.52	40.76	19.56	12.98	7.76	7.93	-1.65E+00	8.20E-14	Down	-7.82E-01	1.63E-04		-2.81E-01	1.35E-08		-1.34E+00	2.48E-115	Down	-7.42E-01	1.48E-13		-7.10E-01	5.01E-13		Unigene628_All//gi|212960297|gb|ACJ38663.1|//1.00E-135//myb-like transcription factor [Betula luminifera]	Unigene628_All//9.00E-88//AT1G09540| MYB61 (MYB DOMAIN PROTEIN 61); DNA binding / transcription factor	Unigene628_All//0.00E+00//TC166819	MYB		GO:0003006//GO:0009725//GO:0010118	nr +
Unigene6280_All	950	0.00	0.00	0.00	1.05	2.36	1.33	2.63	6.60	1.76	null	null		null	null		1.17E+00	5.98E-03		3.44E-01	6.24E-01		1.33E+00	1.98E-09	Up	-5.76E-01	9.73E-02		Unigene6280_All//gi|15223471|ref|NP_171680.1|//6.00E-63//ADF11 (ACTIN DEPOLYMERIZING FACTOR 11); actin binding [Arabidopsis thaliana] >gi|17366957|sp|Q9LQ81.1|ADF10_ARATH RecName: Full=Actin-depolymerizing factor 10; Short=ADF-10; Short=AtADF10 >gi|8671845|gb|AAF78408.1|AC009273_14 Contains similarity to actin depolymerizing factor 4 from Arabidopsis thaliana gb|AF102822. It contains cofilin/tropomyosin-type actin-binding proteins PF|00241. EST gb|AA720247 comes from this gene >gi|219303877|gb|AAM65844.1| Actin-depolymerizing factor like At1g01750 (ADF-like) [Arabidopsis thaliana]	Unigene6280_All//3.00E-64//AT1G01750| ADF11 (ACTIN DEPOLYMERIZING FACTOR 11); actin binding	Unigene6280_All//9.00E-26//EV484019				nr +
Unigene62802_All	654	0.08	1.24	0.49	0.91	0.58	0.35	1.75	1.02	0.30	3.95E+00	7.52E-04	Up	2.61E+00	1.46E-01		-6.58E-01	4.78E-01		-1.40E+00	1.58E-01		-7.72E-01	1.81E-01		-2.52E+00	1.20E-04	Down	Unigene62802_All//gi|255563196|ref|XP_002522601.1|//4.00E-10//conserved hypothetical protein [Ricinus communis] >gi|223538077|gb|EEF39688.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene62804_All	459	0.11	2.10	1.04	0.00	0.00	0.00	0.00	0.00	0.00	4.20E+00	1.29E-04	Up	3.20E+00	3.48E-02		null	null		null	null		null	null		null	null		Unigene62804_All//gi|11466311|ref|NP_051139.1|//3.00E-11//NADH dehydrogenase subunit 5 [Cafeteria roenbergensis] >gi|61880063|gb|AAF05790.1|AF193903_13 NADH dehydrogenase subunit 5 [Cafeteria roenbergensis]	Unigene62804_All//4.00E-07//ATMG00665| Mitochondrial NADH dehydrogenase subunit 5. The gene is trans-spliced from three different pre-cursors, NAD5a, NAD5b and NAD5c.			ko00190|Oxidative phosphorylation		nr +
Unigene62814_All	213	5.40	5.00	3.00	11.23	6.63	4.03	2.98	2.55	2.06	-1.13E-01	8.45E-01		-8.49E-01	2.06E-01		-7.60E-01	5.37E-02		-1.48E+00	4.57E-04	Down	-2.23E-01	7.73E-01		-5.33E-01	4.94E-01									
Unigene6282_All	1016	1.91	0.50	1.52	4.95	3.83	1.96	3.83	0.82	2.00	-1.93E+00	1.74E-04	Down	-3.26E-01	5.10E-01		-3.71E-01	1.72E-01		-1.34E+00	7.83E-07	Down	-2.22E+00	9.57E-12	Down	-9.37E-01	5.03E-04		Unigene6282_All//gi|15809986|gb|AAL06920.1|//1.00E-143//AT3g19540/T31J18_4 [Arabidopsis thaliana] >gi|22137022|gb|AAM91356.1| At3g19540/T31J18_4 [Arabidopsis thaliana]	Unigene6282_All//1.00E-144//AT3G19540| unknown protein	Unigene6282_All//0.00E+00//ES851680				nr +
Unigene62825_All	585	0.00	3.98	0.73	0.00	0.24	0.00	0.00	0.00	0.00	1.20E+01	2.91E-13	Up	9.51E+00	1.38E-02		7.88E+00	3.17E-01		null	null		null	null		null	null		Unigene62825_All//gi|56112311|gb|AAV71134.1|//4.00E-63//cytosolic class II fructose bisphosphate aldolase [Heterocapsa triquetra]					ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene6283_All	869	3.61	5.01	5.15	11.52	13.99	4.11	0.97	0.10	0.78	4.73E-01	1.09E-01		5.11E-01	9.08E-02		2.80E-01	9.89E-02		-1.49E+00	4.05E-15	Down	-3.34E+00	2.51E-04	Down	-3.20E-01	6.25E-01		Unigene6283_All//gi|124359565|gb|AB028693.2|//1.00E-119//Glycosyltransferase sugar-binding region containing DXD motif; Alpha 1,4-glycosyltransferase conserved region [Medicago truncatula]	Unigene6283_All//2.00E-95//AT1G61050| alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein	Unigene6283_All//8.00E-171//gi|54119987|gb|CO495496.1|CO495496				nr +
Unigene6284_All	445	1.41	1.71	1.44	27.54	26.08	25.98	63.75	62.36	147.27	2.76E-01	7.10E-01		2.54E-02	9.97E-01		-7.86E-02	6.91E-01		-8.39E-02	6.73E-01		-3.18E-02	7.73E-01		1.21E+00	2.82E-80	Up	Unigene6284_All//gi|115464269|ref|NP_001055734.1|//3.00E-07//0s05g0456900 [Oryza sativa Japonica Group] >gi|113579285|dbj|BAF17648.1| 0s05g0456900 [Oryza sativa Japonica Group]	Unigene6284_All//1.00E-06//AT5G02090| unknown protein	Unigene6284_All//0.00E+00//DW487884				nr +
Unigene62848_All	560	0.00	5.07	0.86	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.83E-16	Up	9.74E+00	7.46E-03		null	null		null	null		null	null		null	null		Unigene62848_All//gi|300151105|gb|EFJ17752.1|//8.00E-08//hypothetical protein SELMODRAFT_420061 [Selaginella moellendorffii]						nr -
Unigene6285_All	671	11.93	34.43	13.81	13.14	17.45	16.83	2.52	0.81	0.65	1.53E+00	1.01E-32	Up	2.11E-01	3.28E-01		4.09E-01	1.18E-02		3.57E-01	4.10E-02		-1.64E+00	5.96E-04	Down	-1.95E+00	5.40E-05	Down	Unigene6285_All//gi|224069236|ref|XP_002326308.1|//1.00E-42//SAUR family protein [Populus trichocarpa] >gi|222833501|gb|EEE71978.1| SAUR family protein [Populus trichocarpa]	Unigene6285_All//4.00E-22//AT5G20820| auxin-responsive protein-related	Unigene6285_All//0.00E+00//gi|109881996|gb|DW510966.1|DW510966				nr -
Unigene6286_All	585	2.24	0.61	1.91	2.64	2.94	3.40	6.00	1.71	3.20	-1.88E+00	3.39E-03		-2.26E-01	6.96E-01		1.57E-01	8.13E-01		3.64E-01	4.81E-01		-1.81E+00	2.40E-08	Down	-9.06E-01	1.45E-03					Unigene6286_All//1.00E-162//gi|78323967|gb|DT544241.1|DT544241				

Unigene62861_All	419	0.00	2.06	0.13	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	4.94E-05	Up	6.99E+00	6.33E-01		null	null		null	null		null	null		null	null		Unigene62861_All//sp|P15330|DORS_DROME//5.00E-31//Embryonic polarity protein dorsal OS=Drosophila melanogaster GN=dl PE=1 SV=2						swissprot -
Unigene62869_All	239	1.53	6.78	14.71	2.71	3.17	1.89	0.35	2.10	0.33	2.15E+00	2.79E-04	Up	3.26E+00	2.02E-12	Up	2.26E-01	8.32E-01		-5.20E-01	5.88E-01		2.57E+00	2.28E-02		-8.57E-02	9.70E-01				Unigene62869_All//5.00E-92//DV849413				
Unigene6287_All	739	3.19	8.91	5.55	2.49	1.54	0.37	12.07	11.03	2.16	1.48E+00	1.85E-09	Up	8.00E-01	1.07E-02		-6.98E-01	1.37E-01		-2.77E+00	1.70E-06	Down	-1.30E-01	5.29E-01		-2.49E+00	1.10E-30	Down	Unigene6287_All//gi|15218877|ref|NP_176723.1|//1.00E-63//TPX1 (thioredoxin-dependent peroxidase 1); antioxidant/ oxidoreductase [Arabidopsis thaliana] >gi|75338536|sp|Q9XEX2.1|PRX2B_ARATH RecName: Full=Peroxiredoxin-2B; AltName: Full=Peroxiredoxin IIB; AltName: Full=Thioredoxin reductase 2B; AltName: Full=Peroxiredoxin TPx1; AltName: Full=Thioredoxin-dependent peroxidase 1 >gi|4704730|gb|AAD28242.1|AF121355_1 peroxiredoxin TPx1 [Arabidopsis thaliana] >gi|6227022|gb|AAF06058.1|AC009513_14 Identical to gb|AF121355 peroxiredoxin TPx1 from Arabidopsis thaliana. ESTs gb|T43667, gb|T21559, gb|Z17702, gb|T46437, gb|T22793, gb|H36300, gb|AA712887, gb|N96902, gb|H76959, gb|T45886 and gb|Z17703 come from this gene >gi|18086474|gb|AAL57690.1|At1g65980/F12P19_14 [Arabidopsis thaliana]	Unigene6287_All//5.00E-63//AT1G65980| TPX1 (thioredoxin-dependent peroxidase 1); antioxidant/ oxidoreductase	Unigene6287_All//3.00E-19//TC147610		ko00940|Phenylpropanoid biosynthesis//ko04146|Peroxisome//ko00360|Phenylalanine metabolism		nr -
Unigene6288_All	704	4.31	1.58	1.13	1.20	1.08	1.15	0.00	0.00	0.00	-1.44E+00	1.18E-04	Down	-1.93E+00	3.31E-06	Down	-1.61E-01	8.13E-01		-5.90E-02	9.44E-01		null	null		null	null		Unigene6288_All//gi|255572832|ref|XP_002527348.1|//8.00E-20//conserved hypothetical protein [Ricinus communis] >gi|223533267|gb|EEF35020.1| conserved hypothetical protein [Ricinus communis]		Unigene6288_All//0.00E+00//gi|109886692|gb|DW515661.1|DW515661				nr -
Unigene62888_All	293	0.00	5.19	1.45	0.85	0.47	0.31	0.72	0.71	0.14	1.23E+01	1.10E-08	Up	1.05E+01	1.38E-02		-8.55E-01	5.73E-01		-1.46E+00	4.06E-01		-1.67E-02	1.02E+00		-2.41E+00	1.95E-01				Unigene62888_All//1.00E-53//FL577137				
Unigene62890_All	467	0.00	2.28	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.81E-06	Up	9.64E+00	2.50E-02		null	null		null	null		null	null		null	null									
Unigene62891_All	243	0.22	0.63	0.00	0.00	0.00	0.19	6.61	0.34	1.97	1.54E+00	5.31E-01		-7.75E+00	6.19E-01		null	null		7.54E+00	6.91E-01		-4.26E+00	4.13E-09	Down	-1.75E+00	2.96E-04	Down	Unigene62891_All//gi|15237656|ref|NP_201231.1|//5.00E-24//EXL2 (EXORDIUM LIKE 2) [Arabidopsis thaliana] >gi|14190477|gb|AAK55719.1|AF380638_1 AT5g64260/MSJ1_10 [Arabidopsis thaliana] >gi|9759402|dbj|BAB09857.1| phi-1-like protein [Arabidopsis thaliana] >gi|16323270|gb|AAL15369.1|AT5g64260/MSJ1_10 [Arabidopsis thaliana] >gi|21592241|gb|AAM65190.1| phi-1-like protein [Arabidopsis thaliana]	Unigene62891_All//1.00E-22//AT4G08950| EXO (EXORDIUM)	Unigene62891_All//1.00E-58//TC176216				nr +
Unigene62904_All	207	0.00	3.92	6.17	0.00	0.17	0.87	0.20	0.00	0.19	1.19E+01	9.37E-05	Up	1.26E+01	4.68E-07	Up	7.38E+00	8.24E-01		9.77E+00	1.94E-01		-7.67E+00	6.51E-01		-8.58E-02	9.69E-01				Unigene62904_All//1.00E-12//gi|78338048|gb|DT558322.1|DT558322				ESTscan -
Unigene6291_All	865	0.36	5.15	0.43	0.69	1.95	0.63	3.76	4.06	4.10	3.83E+00	2.16E-18	Up	2.48E-01	8.22E-01		1.50E+00	3.80E-03		-1.42E-01	8.79E-01		1.09E-01	7.26E-01		1.23E-01	6.76E-01									
Unigene62917_All	414	0.00	2.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	7.25E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene62917_All//gi|159483855|ref|XP_001699976.1|//2.00E-09//predicted protein [Chlamydomonas reinhardtii] >gi|158281918|gb|EDP07672.1| predicted protein [Chlamydomonas reinhardtii]						nr -
Unigene62918_All	390	0.00	3.12	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.47E-07	Up	7.09E+00	6.33E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene62919_All	731	0.00	3.47	0.36	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.05E-14	Up	8.51E+00	8.00E-02		null	null		null	null		null	null		null	null		Unigene62919_All//sp|Q3SZ27|APOOL_BOVIN//5.00E-07//Apolipoprotein O-like OS=Bos taurus GN=APOL PE=2 SV=1						swissprot +
Unigene6292_All	594	2.91	4.18	3.23	1.85	4.75	1.37	4.06	1.41	1.61	5.24E-01	2.00E-01		1.51E-01	7.44E-01		1.37E+00	2.42E-04	Up	-4.31E-01	5.37E-01		-1.53E+00	7.10E-05	Down	-1.33E+00	2.65E-04	Down	Unigene6292_All//gi|4432836|gb|AAD20685.1|//5.00E-19//expressed protein [Arabidopsis thaliana] >gi|26450173|dbj|BAC42205.1| GPI-anchored protein [Arabidopsis thaliana]	Unigene6292_All//2.00E-13//AT2G28410| unknown protein	Unigene6292_All//3.00E-21//DW505784				nr +
Unigene6293_All	587	1.16	1.64	3.08	4.50	8.33	34.62	8.72	17.52	13.78	5.01E-01	4.72E-01		1.41E+00	7.18E-03		8.89E-01	6.61E-04		2.94E+00	1.16E-69	Up	1.01E+00	6.72E-10	Up	6.61E-01	1.92E-04		Unigene6293_All//gi|18396344|ref|NP_564284.1|//2.00E-11//APT1 (ADENINE PHOSPHORIBOSYL TRANSFERASE 1); adenine phosphoribosyltransferase [Arabidopsis thaliana] >gi|38503396|sp|P31166.2|APT1_ARATH RecName: Full=Adenine phosphoribosyltransferase 1; Short=APRT 1 >gi|21536559|gb|AAM60891.1| adenine phosphoribosyltransferase 1, APRT [Arabidopsis thaliana]	Unigene6293_All//9.00E-13//AT1G27450| APT1 (ADENINE PHOSPHORIBOSYL TRANSFERASE 1); adenine phosphoribosyltransferase	Unigene6293_All//5.00E-122//TC154813		ko00230|Purine metabolism		nr -
Unigene62930_All	224	0.00	3.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene62937_All	406	0.00	3.37	0.66	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.80E-08	Up	9.36E+00	8.00E-02		null	null		null	null		null	null		null	null		Unigene62937_All//gi|159474294|ref|XP_001698264.1|//4.00E-58//heat shock protein 90A [Chlamydomonas reinhardtii] >gi|158276198|gb|EDP01972.1| heat shock protein 90A [Chlamydomonas reinhardtii]	Unigene62937_All//3.00E-54//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene62938_All	420	0.00	5.67	1.01	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.50E-13	Up	9.99E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene62938_All//sp|P34953|ISK2_MACFA//4.00E-07//Serine protease inhibitor Kazal-type 2 OS=Macaca fascicularis GN=SPINK2 PE=2 SV=1						swissprot +
Unigene62942_All	214	0.00	3.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene62948_All	237	0.00	3.85	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.62E-05	Up	9.81E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene62948_All//sp|P38936|CDN1A_HUMAN//9.00E-09//Cyclin-dependent kinase inhibitor 1 OS=Homo sapiens GN=CDKN1A PE=1 SV=3						swissprot -
Unigene6295_All	889	1.88	4.67	3.29	1.12	1.24	0.20	0.00	0.00	0.00	1.31E+00	2.50E-05	Up	8.07E-01	3.50E-02		1.45E-01	8.37E-01		-2.46E+00	2.07E-03		null	null		null	null		Unigene6295_All//gi|18395968|ref|NP_564251.1|//1.00E-15//CLE9 (CLAVATA3/ESR-RELATED 9); protein binding / receptor binding [Arabidopsis thaliana]	Unigene6295_All//2.00E-11//AT1G26600| CLE9 (CLAVATA3/ESR-RELATED 9); protein binding / receptor binding					nr -
Unigene62953_All	638	0.00	12.47	5.93	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	1.68E-45	Up	1.25E+01	6.02E-21	Up	null	null		null	null		null	null		null	null		Unigene62953_All//sp|Q94514|COX5A_DROME//3.00E-53//Cytochrome c oxidase subunit 5A, mitochondrial OS=Drosophila melanogaster GN=CoVa PE=1 SV=2						swissprot -
Unigene6296_All	841	1.37	2.59	2.28	4.86	4.05	1.29	0.65	2.63	1.09	9.21E-01	3.53E-02		7.36E-01	1.38E-01		-2.61E-01	4.25E-01		-1.91E+00	4.87E-09	Down	2.01E+00	2.99E-06	Up	7.37E-01	2.43E-01		Unigene6296_All//gi|297802270|ref|XP_002889019.1|//5.00E-60//transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297314855|gb|EFH45278.1| transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene6296_All//5.00E-64//AT5G42610| unknown protein	Unigene6296_All//1.00E-09//TC151488				nr +
Unigene6298_All	577	5.17	22.74	14.03	14.50	10.56	10.49	3.52	5.00	9.67	2.14E+00	1.80E-29	Up	1.44E+00	1.47E-10	Up	-4.57E-01	1.78E-02		-4.68E-01	2.04E-02		5.07E-01	1.33E-01		1.46E+00	6.99E-10	Up	Unigene6298_All//gi|255570809|ref|XP_002526357.1|//6.00E-16//conserved hypothetical protein [Ricinus communis] >gi|223534316|gb|EEF36028.1| conserved hypothetical protein [Ricinus communis]	Unigene6298_All//2.00E-06//AT5G60400| unknown protein	Unigene6298_All//6.00E-177//AW187827				nr +
Unigene6299_All	783	0.40	0.06	1.09	1.34	2.07	1.79	3.40	3.79	0.61	-2.63E+00	1.30E-01		1.44E+00	8.22E-02		6.30E-01	2.47E-01		4.21E-01	4.92E-01		1.56E-01	6.47E-01		-2.48E+00	1.13E-09	Down	Unigene6299_All//gi|224066817|ref|XP_002302230.1|//1.00E-55//type-a response regulator [Populus trichocarpa] >gi|222843956|gb|EEE81503.1| type-a response regulator [Populus trichocarpa]	Unigene6299_All//1.00E-37//AT3G57040| ARR9 (RESPONSE REGULATOR 9); transcription regulator/ two-component response regulator	Unigene6299_All//0.00E+00//TC157465	ARR-B	ko04712|Circadian rhythm - plant		nr -
Unigene62991_All	288	0.00	2.46	0.00	0.35	0.00	0.00	0.59	0.58	0.69	1.13E+01	3.32E-04	Up	null	null		-8.43E+00	3.11E-01		-8.43E+00	3.96E-01		-1.66E-02	1.02E+00		2.36E-01	8.83E-01		Unigene62991_All//gi|297790604|ref|XP_002863187.1|//4.00E-15//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309021|gb|EFH39446.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene62991_All//8.00E-16//AT4G13000| protein kinase family protein	Unigene62991_All//4.00E-139//TC142650				nr +
Unigene62992_All	207	0.00	11.02	1.03	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	5.63E-13	Up	1.00E+01	1.40E-01		null	null		null	null		null	null		null	null									
Unigene6300_All	520	55.64	45.89	33.79	80.47	76.29	100.40	104.07	47.50	53.48	-2.78E-01	6.87E-03		-7.19E-01	5.24E-12		-7.70E-02	4.49E-01		3.19E-01	8.01E-06		-1.13E+00	9.65E-59	Down	-9.61E-01	2.11E-46		Unigene6300_All//gi|247421835|gb|ACS96445.1|//3.00E-22//S18.A ribosomal protein [Jatropha curcas]	Unigene6300_All//2.00E-14//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome	Unigene6300_All//0.00E+00//TC153252		ko03010|Ribosome		nr +
Unigene6301_All	1852	6.55	0.11	3.05	0.05	0.09	0.00	13.61	3.36	1.10	-5.90E+00	9.53E-64	Down	-1.10E+00	1.85E-10	Down	7.90E-01	7.70E-01		-5.75E+00	3.96E-01		-2.02E+00	5.51E-64	Down	-3.63E+00	1.05E-124	Down	Unigene6301_All//gi|224139828|ref|XP_002323296.1|//1.00E-139//cytochrome P450 [Populus trichocarpa] >gi|222867926|gb|EEF05057.1| cytochrome P450 [Populus trichocarpa]	Unigene6301_All//3.00E-128//AT5G06905| CYP712A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00380|Tryptophan metabolism//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene63014_All	397	0.00	6.25	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	3.98E-14	Up	9.65E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene63014_All//sp|B4HI06|JUPIT_DROSE//3.00E-37//Microtubule-associated protein Jupiter OS=Drosophila sechellia GN=Jupiter PE=3 SV=1						swissprot -

Unigene63032_All	631	0.00	3.53	1.10	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.09E-12	Up	1.01E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene63032_All//gi|189095412|ref|YP_001936425.1|//2.00E-28//ribosomal protein L13 [Heterosigma akashiwo] >gi|157694755|gb|ABV66031.1| 50S ribosomal protein L13 [Heterosigma akashiwo] >gi|157777986|gb|ABV70172.1| 50S ribosomal protein L13 [Heterosigma akashiwo]	Unigene63032_All//6.00E-23//AT1G78630| emb1473 (embryo defective 1473); structural constituent of ribosome			ko03010|Ribosome		nr -
Unigene63042_All	281	0.56	0.18	0.38	0.89	1.72	0.32	3.31	0.30	1.42	-1.63E+00	4.88E-01		-5.60E-01	7.75E-01		9.53E-01	4.23E-01		-1.46E+00	4.06E-01		-3.48E+00	7.79E-05	Down	-1.22E+00	5.14E-02		Unigene63042_All//gi|223452349|gb|ACM89502.1|//5.00E-40//PERK1-like protein kinase [Glycine max]	Unigene63042_All//8.00E-40//AT4G34440| protein kinase family protein	Unigene63042_All//1.00E-80//gi|21098289|gb|BQ410602.1|BQ410602		ko04626|Plant-pathogen interaction		nr -
Unigene63055_All	256	0.00	5.34	6.45	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.79E-08	Up	1.27E+01	4.30E-09	Up	null	null		null	null		null	null		null	null		Unigene63055_All//COG0191//1.00E-11//Fructose/tagatose bisphosphate aldolase							cog +
Unigene6306_All	1287	2364.89	1160.75	2328.19	264.94	281.21	230.38	8.18	8.38	3.99	-1.03E+00	0.00E+00	Down	-2.26E-02	2.72E-02		8.60E-02	1.01E-03		-2.02E-01	1.03E-14		3.46E-02	8.52E-01		-1.03E+00	6.62E-11	Down	Unigene6306_All//gi|15236722|ref|NP_194953.1|//4.00E-73//ATP synthase family [Arabidopsis thaliana] >gi|2864617|emb|CAA16964.1| H+-transporting ATP synthase chain9 -like protein [Arabidopsis thaliana] >gi|5730141|emb|CAB52473.1| ATP synthase beta chain precursor (subunit II) [Arabidopsis thaliana] >gi|7270130|emb|CAB79944.1| H+-transporting ATP synthase chain 9-like protein [Arabidopsis thaliana] >gi|16604406|gb|AAL24209.1| AT4g32260/F10M6_100 [Arabidopsis thaliana] >gi|21554175|gb|AAM63254.1| H+-transporting ATP synthase chain 9-like protein [Arabidopsis thaliana]	Unigene6306_All//3.00E-52//AT4G32260| ATP synthase family	Unigene6306_All//0.00E+00//TC135773		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr -
Unigene63060_All	265	0.00	0.00	0.00	0.00	0.00	0.17	6.22	0.32	0.60	null	null		null	null		null	null		7.41E+00	6.91E-01		-4.30E+00	2.19E-09	Down	-3.37E+00	2.89E-08	Down			Unigene63060_All//1.00E-62//gi|11210271|gb|BF279201.1|BF279201				ESTscan -
Unigene63067_All	209	0.00	0.00	0.00	0.00	0.00	0.00	3.24	0.00	0.00	null	null		null	null		null	null		null	null		-1.17E+01	6.34E-05	Down	-1.17E+01	3.56E-05	Down	Unigene63067_All//gi|15234794|ref|NP_192719.1|//6.00E-08//transporter-related [Arabidopsis thaliana] >gi|38603966|gb|AAR24728.1| At4g09810 [Arabidopsis thaliana]	Unigene63067_All//3.00E-09//AT4G09810| transporter-related	Unigene63067_All//3.00E-53//TC176616				nr -
Unigene63070_All	323	0.00	2.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene63070_All//gi|156987446|gb|ABU89701.1|//2.00E-29//enolase [Phytophthora bisheria]	Unigene63070_All//1.00E-27//AT2G36530| LOS2; copper ion binding / phosphopyruvate hydratase			ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation		nr +
Unigene63083_All	480	0.00	2.64	2.88	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.86E-07	Up	1.15E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene63083_All//gi|301105535|ref|XP_002901851.1|//5.00E-24//villin-like protein [Phytophthora infestans T30-4] >gi|262099189|gb|EEY57241.1| villin-like protein [Phytophthora infestans T30-4]	Unigene63083_All//1.00E-14//AT3G57410| VLN3 (VILLIN 3); actin binding					nr -
Unigene63086_All	821	0.00	3.46	1.30	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.83E-16	Up	1.03E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene63086_All//gi|18734|emb|CAA36734.1|//2.00E-25//DNA-directed RNA polymerase [Glycine max]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene6309_All	389	3.77	1.95	2.05	12.29	8.68	4.88	8.91	2.69	7.89	-9.47E-01	8.40E-02		-8.75E-01	1.34E-01		-5.03E-01	6.13E-02		-1.33E+00	1.74E-06	Down	-1.73E+00	8.05E-08	Down	-1.77E-01	5.88E-01		Unigene6309_All//gi|224112227|ref|XP_002316125.1|//6.00E-06//predicted protein [Populus trichocarpa] >gi|222865165|gb|EEF02296.1| predicted protein [Populus trichocarpa]		Unigene6309_All//7.00E-37//gi|78340818|gb|DT561092.1|DT561092				nr +
Unigene631_All	1039	10.17	9.90	6.51	13.57	9.38	14.13	115.28	259.70	82.44	-3.91E-02	8.35E-01		-6.44E-01	3.99E-04		-5.33E-01	1.20E-04		5.82E-02	7.33E-01		1.17E+00	0.00E+00	Up	-4.84E-01	5.34E-31		Unigene631_All//gi|115476294|ref|NP_001061743.1|//8.00E-95//Os08g0398300 [Oryza sativa Japonica Group] >gi|113623712|dbj|BAF23657.1| Os08g0398300 [Oryza sativa Japonica Group]	Unigene631_All//7.00E-93//AT3G47780| ATATH6; ATPase, coupled to transmembrane movement of substances / transporter	Unigene631_All//0.00E+00//TC173968		ko02010|ABC transporters	GO:0032559//GO:0042626//GO:0043231	nr -
Unigene6310_All	829	18.05	2.75	8.93	13.22	7.48	4.30	0.41	0.55	0.29	-2.71E+00	1.35E-44	Down	-1.02E+00	3.40E-11	Down	-8.22E-01	2.04E-07		-1.62E+00	1.38E-18	Down	4.43E-01	6.31E-01		-5.01E-01	6.49E-01		Unigene6310_All//gi|13785469|dbj|BAB43908.1|//3.00E-78//phosphoenolpyruvate carboxykinase [Flaveria trinervia]	Unigene6310_All//7.00E-62//AT4G37870| PCK1 (PHOSPHOENOLPYRUVATE CARBOXYKINASE 1); ATP binding / phosphoenolpyruvate carboxykinase (ATP)/ phosphoenolpyruvate carboxykinase/ purine nucleotide binding	Unigene6310_All//0.00E+00//gi|78323926|gb|DT544200.1|DT544200		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)		nr -
Unigene63104_All	420	0.37	2.65	0.63	3.80	2.05	1.18	1.71	0.60	0.09	2.83E+00	5.03E-04	Up	7.62E-01	6.44E-01		-8.89E-01	7.64E-02		-1.68E+00	2.14E-03		-1.52E+00	5.41E-02		-4.17E+00	1.64E-04	Down			Unigene63104_All//1.00E-29//TC145334				
Unigene63106_All	301	0.00	3.54	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.81E-06	Up	7.47E+00	6.33E-01		null	null		null	null		null	null		null	null		Unigene63106_All//gi|13560783|gb|AAK30205.1|AF349964_1|/2.00E-11//poly(A)-binding protein [Daucus carota]	Unigene63106_All//4.00E-10//AT4G34110| PAB2 (POLY(A) BINDING 2); RNA binding / translation initiation factor			ko03040|Spliceosome		nr +
Unigene63109_All	224	0.00	7.69	1.90	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	7.98E-10	Up	1.09E+01	1.38E-02		null	null		null	null		null	null		null	null				Unigene63109_All//9.00E-05//AT2G17845| short-chain dehydrogenase/reductase (SDR) family protein					
Unigene63112_All	223	0.00	4.77	6.69	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	3.81E-06	Up	1.27E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene63112_All//sp|P81134|RENR_BOVIN//6.00E-11//Renin receptor OS=Bos taurus GN=ATP6AP2 PE=1 SV=2						swissprot -
Unigene63119_All	218	0.00	3.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null								ESTscan +
Unigene6312_All	304	7.23	122.84	7.88	0.33	0.00	1.34	5.98	3.71	13.10	4.09E+00	1.05E-158	Up	1.25E-01	7.61E-01		-8.36E+00	3.11E-01		2.03E+00	1.49E-01		-6.88E-01	1.16E-01		1.13E+00	3.20E-05	Up							
Unigene63126_All	305	0.00	3.99	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.47E-07	Up	7.45E+00	6.33E-01		null	null		null	null		null	null		null	null		Unigene63126_All//gi|115456667|ref|NP_001051934.1|//3.00E-06//Os03g0854000 [Oryza sativa Japonica Group] >gi|29126342|gb|AAO66534.1| expressed protein [Oryza sativa Japonica Group] >gi|108712162|gb|ABF99957.1| Uncharacterised protein family containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113550405|dbj|BAF13848.1| Os03g0854000 [Oryza sativa Japonica Group]	Unigene63126_All//8.00E-06//AT3G02910| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Butirosin biosynthesis, BtrG-like (InterPro:IPR013024), AIG2-like (InterPro:IPR009288); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G46720.1); Has 210 Blast hits to 210 proteins in 66 species: Archae - 2; Bacteria - 27; Metazoa - 122; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryotes - 18 (source: NCBI BLink).						nr +
Unigene6313_All	307	12.61	193.77	18.73	5.52	4.04	4.27	26.86	32.13	202.70	3.94E+00	4.55E-246	Up	5.71E-01	2.77E-02		-4.50E-01	3.87E-01		-3.71E-01	4.92E-01		2.59E-01	1.38E-01		2.92E+00	7.97E-246	Up			Unigene6313_All//2.00E-08//DT461826				
Unigene6314_All	212	53.31	23.90	30.90	89.29	86.25	93.52	151.77	38.25	32.51	-1.16E+00	5.36E-11	Down	-7.87E-01	7.38E-06		-5.00E-02	7.74E-01		6.68E-02	6.69E-01		-1.99E+00	5.04E-80	Down	-2.22E+00	4.44E-95	Down	Unigene6314_All//gi|261280336|gb|ACM67308.2|//4.00E-31//triosphosphate isomerase-like protein type I [Dimocarpus longan]	Unigene6314_All//8.00E-30//AT3G55440| TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase	Unigene6314_All//1.00E-116//TC164955		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00562|Inositol phosphate metabolism//ko00051|Fructose and mannose metabolism		nr +
Unigene63147_All	214	0.00	3.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.37E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene63147_All//gi|20138151|sp|Q2381A.1|GPX4_SPIOL//3.00E-11//RecName: Full=Probable phospholipid hydroperoxide glutathione peroxidase; Short=PHGPx >gi|2392021|dbj|BAA22194.1| phopholipid hydroperoxide glutathione peroxidase-like protein [Spinacia oleracea]	Unigene63147_All//5.00E-11//AT4G11600| ATGPX6 (GLUTATHIONE PEROXIDASE 6); glutathione peroxidase			ko00480|Glutathione metabolism//ko00590|Arachidonic acid metabolism		nr +
Unigene6315_All	349	6.15	15.53	10.53	23.69	19.93	16.18	34.65	38.08	35.84	1.34E+00	6.82E-07	Up	7.76E-01	2.04E-02		-2.50E-01	2.48E-01		-5.51E-01	5.82E-03		1.36E-01	3.94E-01		4.89E-02	7.54E-01		Unigene6315_All//gi|298155591|gb|ADI58769.1|//3.00E-13//RING-type ubiquitin E3 ligase [Gossypium hirsutum]		Unigene6315_All//0.00E+00//TC138348				nr +
Unigene63154_All	687	0.46	2.66	0.62	0.22	0.65	1.12	0.25	0.24	0.87	2.54E+00	1.40E-05	Up	4.40E-01	6.77E-01		1.58E+00	2.17E-01		2.36E+00	1.34E-02		-1.65E-02	1.02E+00		1.82E+00	3.94E-02				Unigene63154_All//3.00E-65//TC144724				
Unigene63157_All	212	0.00	3.59	0.00	0.47	0.32	0.00	0.00	0.20	0.38	1.18E+01	1.76E-04	Up	null	null		-5.32E-01	8.14E-01		-8.88E+00	3.96E-01		7.62E+00	6.30E-01		8.55E+00	4.02E-01		Unigene63157_All//gi|255575375|ref|XP_002528590.1|//7.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223531986|gb|EEF33798.1| conserved hypothetical protein [Ricinus communis]		Unigene63157_All//2.00E-60//TC177315				nr -
Unigene6316_All	1422	0.00	0.00	0.00	0.00	0.19	0.00	51.56	24.40	52.42	null	null		null	null		7.60E+00	7.00E-02		null	null		-1.08E+00	1.52E-73	Down	2.39E-02	7.08E-01		Unigene6316_All//gi|15225466|ref|NP_181475.1|//4.00E-95//disease resistance-responsive protein-related / dirigent protein-related [Arabidopsis thaliana] >gi|38454170|gb|AAR20779.1| At2g39430 [Arabidopsis thaliana] >gi|44022160|gb|AAS46642.1| At2g39430 [Arabidopsis thaliana]	Unigene6316_All//4.00E-83//AT2G39430| disease resistance-responsive protein-related / dirigent protein-related			ko04141|Protein processing in endoplasmic reticulum//ko03420|Nucleotide excision repair		nr +
Unigene63165_All	446	0.23	2.39	0.72	0.78	1.16	1.01	0.00	0.00	0.00	3.35E+00	2.17E-04	Up	1.61E+00	3.04E-01		5.67E-01	6.04E-01		3.73E-01	7.32E-01		null	null		null	null				Unigene63165_All//7.00E-145//TC168547				
Unigene63184_All	406	0.00	1.75	0.52	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	3.32E-04	Up	9.04E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene63184_All//gi|115445891|ref|NP_001046725.1|//7.00E-34//Os02g0332200 [Oryza sativa Japonica Group] >gi|113536256|dbj|BAF08639.1| Os02g0332200 [Oryza sativa Japonica Group]	Unigene63184_All//1.00E-33//AT3G18190| chaperonin, putative					nr +

Unigene63185_All	630	0.00	9.89	5.83	0.00	0.00	0.00	0.13	0.00	0.00	1.33E+01	1.38E-35	Up	1.25E+01	2.38E-20	Up	null	null		null	null		-7.07E+00	4.01E-01		-7.07E+00	3.56E-01		Unigene63185_All//gi|145345549|ref|XP_001417269.1|//9.00E-71//Ribosomal protein L10a, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CE9901] >gi|144577496|gb|ABO95562.1| Ribosomal protein L10a, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901]	Unigene63185_All//1.00E-58//AT2G27530| PGY1 (PIGGYBACK1); RNA binding / structural constituent of ribosome	Unigene63185_All//3.00E-09//gi|48753557|gb|CO084076.1|CO084076		ko03010|Ribosome		nr -
Unigene6319_All	797	1.12	3.88	1.80	6.50	10.67	17.00	0.85	15.99	0.80	1.80E+00	4.12E-06	Up	6.93E-01	2.40E-01		7.15E-01	1.41E-04		1.39E+00	5.54E-18	Up	4.24E+00	1.72E-68	Up	-8.58E-02	9.15E-01		Unigene6319_All//gi|159138935|gb|AB989467.1|//3.00E-75//low molecular weight heat shock protein [Gossypium hirsutum]	Unigene6319_All//6.00E-49//AT1G07400| 17.8 kDa class I heat shock protein (HSP17.8-CI)	Unigene6319_All//0.00E+00//gi|109889376|gb|DW518344.1|DW518344				nr +
Unigene63193_All	261	0.00	3.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.37E-05	Up	null	null		null	null		null	null		null	null		null	null											
Unigene632_All	2881	3.52	6.35	4.29	5.65	4.95	7.92	64.38	130.06	48.62	8.50E-01	1.13E-10		2.84E-01	1.07E-01		-1.92E-01	1.98E-01		4.86E-01	1.41E-05		1.01E+00	0.00E+00	Up	-4.05E-01	1.79E-34		Unigene632_All//gi|224121524|ref|XP_002318606.1|//0.00E+00//ABC transporter family, cholesterol/phospholipid flippase [Populus trichocarpa] >gi|222859279|gb|EEE96826.1| ABC transporter family, cholesterol/phospholipid flippase [Populus trichocarpa]	Unigene632_All//0.00E+00//AT3G47780| ATATH6; ATPase, coupled to transmembrane movement of substances / transporter	Unigene632_All//0.00E+00//TC173968		ko02010|ABC transporters	GO:0032559//GO:0042626//GO:0043231	nr +
Unigene6320_All	550	0.86	3.13	1.94	1.18	1.57	1.48	1.31	0.46	1.23	1.87E+00	6.55E-04	Up	1.18E+00	9.59E-02		4.11E-01	6.11E-01		3.28E-01	7.00E-01		-1.52E+00	5.41E-02		-8.57E-02	9.11E-01										
Unigene6321_All	613	3.41	4.88	1.04	5.12	3.76	3.68	5.31	4.64	6.50	5.14E-01	1.57E-01		-1.71E+00	6.07E-04	Down	-4.44E-01	2.14E-01		-4.75E-01	1.97E-01		-1.96E-01	5.82E-01		2.91E-01	3.03E-01					Unigene6321_All//2.00E-106//CO129561					
Unigene63220_All	417	0.00	0.00	0.00	0.12	0.00	0.11	40.86	6.01	20.16	null	null		null	null		-6.90E+00	5.51E-01		-1.42E-01	9.50E-01		-2.76E+00	4.07E-63	Down	-1.02E+00	1.05E-16	Down	Unigene63220_All//gi|13161397|dbj|BAB33033.1|//8.00E-32//CPN02 [Vigna unguiculata]	Unigene63220_All//1.00E-78//TC159819	Unigene63220_All//1.00E-78//TC159819				nr -
Unigene6324_All	1174	0.62	0.35	0.41	5.13	5.60	3.04	2.63	0.68	0.95	-8.54E-01	3.05E-01		-6.12E-01	4.70E-01		1.26E-01	6.37E-01		-7.57E-01	1.41E-03		-1.96E+00	3.44E-08	Down	-1.47E+00	5.86E-06	Down	Unigene6324_All//gi|3157936|gb|AAC17619.1|//1.00E-130//Contains similarity to NFATc3 gb|U28807 from Mus musculus [Arabidopsis thaliana]	Unigene6324_All//2.00E-119//AT1G11915| unknown protein	Unigene6324_All//0.00E+00//TC173693				nr -
Unigene63244_All	217	0.00	3.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene63244_All//sp|P07996|TSP1_HUMAN//2.00E-38//Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2									swissprot +
Unigene6325_All	518	26.97	21.42	11.10	32.60	29.85	39.93	115.66	49.46	39.92	-3.32E-01	3.05E-02		-1.28E+00	6.40E-15	Down	-1.27E-01	4.24E-01		2.93E-01	1.87E-02		-1.23E+00	1.22E-73	Down	-1.53E+00	1.49E-106	Down	Unigene6325_All//gi|192912994|gb|ACF06605.1|//1.00E-33//60S ribosomal protein L13E [Elaeis guineensis]	Unigene6325_All//7.00E-27//AT3G49010| ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome	Unigene6325_All//0.00E+00//TC171039		ko03010|Ribosome		nr +
Unigene63254_All	230	0.00	0.00	0.00	0.22	0.00	0.00	42.10	74.14	11.78	null	null		null	null		-7.76E+00	5.51E-01		-7.76E+00	6.28E-01		8.17E-01	2.07E-11		-1.84E+00	6.41E-23	Down	Unigene63254_All//gi|224054164|ref|XP_002298123.1|//6.00E-16//pleiotropic drug resistance, ABC transporter family protein [Populus trichocarpa] >gi|222845381|gb|EEE82928.1| pleiotropic drug resistance, ABC transporter family protein [Populus trichocarpa]	Unigene63254_All//1.00E-15//AT1G15520| PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	Unigene63254_All//2.00E-48//TC132787				nr +
Unigene6326_All	374	5.04	4.74	3.84	5.06	3.41	1.21	14.58	13.19	10.12	-8.69E-02	8.47E-01		-3.90E-01	4.24E-01		-5.71E-01	2.26E-01		-2.07E+00	6.29E-05	Down	-1.45E-01	6.00E-01		-5.27E-01	1.69E-02		Unigene6326_All//gi|1279590|emb|CAA96432.1|//8.00E-14//ras-related small GTP-binding protein [Nicotiana plumbaginifolia]	Unigene6326_All//8.00E-13//AT1G02130| ARA-5 (ARABIDOPSIS RAS 5); GTP binding	Unigene6326_All//8.00E-169//TC175856				nr +
Unigene6327_All	1029	0.10	0.64	0.62	3.29	4.48	3.82	7.11	4.35	1.70	2.65E+00	1.49E-02		2.61E+00	2.33E-02		4.46E-01	1.23E-01		2.14E-01	5.53E-01		-7.10E-01	2.20E-04		-2.06E+00	2.85E-20	Down	Unigene6327_All//gi|5777618|emb|CAB53479.1|//1.00E-100//CAA30376.1 protein [Oryza sativa]	Unigene6327_All//3.00E-98//AT1G77700| pathogenesis-related thaumatin family protein					nr +
Unigene63271_All	204	2.05	0.99	1.04	7.57	6.41	1.11	2.28	0.20	0.20	-1.05E+00	3.65E-01		-9.75E-01	4.11E-01		-2.39E-01	6.59E-01		-2.77E+00	1.51E-05	Down	-3.48E+00	1.03E-02		-3.55E+00	6.85E-03										
Unigene63272_All	204	0.00	3.23	0.00	0.00	0.17	0.00	0.00	0.61	0.00	1.17E+01	6.24E-04	Up	null	null		7.40E+00	8.23E-01		null	null		9.26E+00	2.40E-01		null	null											
Unigene63275_All	222	0.00	0.00	0.24	1.35	0.62	2.64	10.28	2.07	0.72	null	null		7.91E+00	6.33E-01		-1.12E+00	4.24E-01		9.74E-01	3.46E-01		-2.31E+00	1.64E-07	Down	-3.84E+00	2.31E-12	Down	Unigene63275_All//gi|153805698|gb|ABSS2574.1|//6.00E-19//nodulin family protein [Gossypium hirsutum]	Unigene63275_All//7.00E-07//AT4G08300| nodulin MtN21 family protein	Unigene63275_All//7.00E-51//TC142141				nr +
Unigene63277_All	213	0.00	3.81	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.37E-05	Up	1.10E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene63277_All//gi|302144136|emb|CBI23241.3|//1.00E-07//unnamed protein product [Vitis vinifera]					ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr -
Unigene6328_All	719	3.06	1.55	0.00	2.56	4.41	3.52	354.82	39.41	74.97	-9.79E-01	2.41E-02		-1.16E+01	5.20E-12	Down	7.81E-01	2.29E-02		4.57E-01	2.88E-01		-3.17E+00	0.00E+00	Down	-2.24E+00	0.00E+00	Down										ESTscan -
Unigene63286_All	317	0.00	2.08	1.01	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.24E-04	Up	9.98E+00	4.50E-02		null	null		null	null		null	null		null	null											
Unigene63298_All	213	0.00	4.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null											
Unigene6330_All	513	4.69	10.77	4.77	6.21	8.59	9.77	13.85	20.12	17.63	1.20E+00	4.89E-06	Up	2.54E-02	9.70E-01		4.67E-01	1.13E-01		6.53E-01	1.51E-02		5.39E-01	6.61E-04		3.48E-01	4.02E-02					Unigene6330_All//2.00E-09//TC164546					
Unigene6332_All	585	4.65	8.14	5.28	1.96	1.71	1.39	3.76	0.29	1.97	8.08E-01	3.49E-03		1.83E-01	6.35E-01		-1.98E-01	7.77E-01		-4.95E-01	4.65E-01		-3.72E+00	3.29E-11	Down	-9.28E-01	1.26E-02		Unigene6332_All//gi|225454428|ref|XP_002276498.1|//2.00E-19//PREDICTED: similar to Os11g0118600 [Vitis vinifera]	Unigene6332_All//3.00E-11//AT4G01140| unknown protein					nr -
Unigene63330_All	1397	0.00	5.44	2.06	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.85E-43	Up	1.10E+01	6.95E-16	Up	null	null		null	null		null	null		null	null		Unigene63330_All//gi|299471562|emb|CBN80048.1|//1.00E-08//beta strand repeat-containing protein [Ectocarpus siliculosus]								nr +
Unigene63339_All	1061	3.45	1.19	1.71	3.57	3.18	3.24	0.24	0.47	0.68	-1.53E+00	7.22E-06	Down	-1.02E+00	2.61E-03		-1.66E-01	6.18E-01		-1.41E-01	6.99E-01		9.83E-01	3.11E-01		1.50E+00	4.94E-02		Unigene63339_All//gi|297843864|ref|XP_002889813.1|//1.00E-142//EMB2004 [Arabidopsis lyrata subsp. lyrata] >gi|297335655|gb|EFH66072.1| EMB2004 [Arabidopsis lyrata subsp. lyrata]	Unigene63339_All//7.00E-128//AT1G10510| emb2004 (embryo defective 2004)	Unigene63339_All//0.00E+00//TC172054				nr +
Unigene63343_All	324	0.00	0.00	0.00	0.00	0.00	0.00	3.00	0.13	0.37	null	null		null	null		null	null		null	null		-4.54E+00	6.92E-06	Down	-3.02E+00	9.60E-05	Down	Unigene63343_All//gi|211906536|gb|ACJ11761.1|//2.00E-20//class III peroxidase [Gossypium hirsutum]	Unigene63343_All//2.00E-15//AT3G21770| peroxidase 30 (PER30) (P30) (PRX89)	Unigene63343_All//1.00E-43//TC143685		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene6335_All	477	3.51	2.97	1.90	4.49	3.25	4.07	30.49	10.25	10.86	-2.39E-01	6.10E-01		-8.87E-01	9.62E-02		-4.67E-01	3.03E-01		-1.41E-01	7.52E-01		-1.57E+00	1.32E-26	Down	-1.49E+00	2.08E-25	Down				Unigene6335_All//3.00E-79//gi|164341788|gb|ES823381.1|ES823381					
Unigene63351_All	316	0.00	2.08	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.24E-04	Up	8.40E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene63351_All//sp|Q32KY0|APOD_BOVIN//8.00E-08//Apolipoprotein D OS=Bos taurus GN=APOD PE=2 SV=1								swissprot -
Unigene6336_All	519	29.13	17.18	14.67	32.63	29.19	42.38	84.15	44.37	34.70	-7.62E-01	1.37E-07		-9.90E-01	7.32E-11		-1.61E-01	2.96E-01		3.77E-01	1.18E-03		-9.23E-01	2.88E-34		-1.28E+00	3.38E-59	Down	Unigene6336_All//gi|297805734|ref|XP_002870751.1|//7.00E-33//40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata] >gi|297316587|gb|EFH47010.1| 40S ribosomal protein S9 [Arabidopsis lyrata subsp. lyrata]	Unigene6336_All//1.00E-25//AT5G39850| 40S ribosomal protein S9 (RPS9C)	Unigene6336_All//0.00E+00//TC162317		ko03010|Ribosome		nr +
Unigene63372_All	215	0.00	0.00	0.00	0.23	0.00	1.26	24.58	0.19	0.37	null	null		null	null		-7.86E+00	5.51E-01		2.44E+00	2.22E-01		-6.98E+00	1.22E-35	Down	-6.05E+00	1.48E-35	Down	Unigene63372_All//gi|211906540|gb|ACJ11763.1|//3.00E-16//class III peroxidase [Gossypium hirsutum]	Unigene63372_All//6.00E-12//AT4G30170| peroxidase, putative	Unigene63372_All//7.00E-51//gi|109825772|gb|DW224495.1|DW224495		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene6338_All	669	94.94	31.36	102.36	22.04	16.88	4.86	21.80	8.06	3.04	-1.60E+00	3.01E-95	Down	1.09E-01	1.37E-01		-3.85E-01	5.90E-03		-2.18E+00	5.55E-37	Down	-1.44E+00	2.01E-23	Down	-2.84E+00	1.40E-57	Down				Unigene6338_All//0.00E+00//gi|82755910|gb|DV849472.1|DV849472					
Unigene63382_All	1123	0.75	0.50	0.62	0.40	0.34	0.28	1.84	3.05	0.64	-5.87E-01	4.26E-01		-2.74E-01	7.04E-01		-2.43E-01	8.21E-01		-5.04E-01	6.49E-01		7.26E-01	1.47E-02		-1.53E+00	1.72E-04	Down	Unigene63382_All//gi|9989053|gb|AAG10816.1|ACO11808.4|//1.00E-94//Unknown protein [Arabidopsis thaliana]	Unigene63382_All//6.00E-97//AT1G16670| protein kinase family protein	Unigene63382_All//0.00E+00//DW236306		ko04626|Plant-pathogen interaction		nr +
Unigene6339_All	390	2.82	10.26	5.73	1.66	5.56	5.67	2.06	4.93	2.15	1.87E+00	4.77E-08	Up	1.03E+00	2.31E-02		1.74E+00	1.17E-04	Up	1.77E+00	1.25E-04	Up	1.26E+00	3.19E-03		5.86E-02	9.50E-01					Unigene6339_All//5.00E-07//TC164157					
Unigene63390_All	224	3.74	0.23	0.24	0.44	1.84	1.81	0.00	0.93	1.07	-4.05E+00	4.65E-04	Down	-3.97E+00	9.08E-04	Down	2.05E+00	1.47E-01		2.03E+00	1.49E-01		9.87E+00	7.84E-02		1.01E+01	4.39E-02		Unigene63390_All//gi|297830600|ref|XP_002883182.1|//3.00E-14//pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329022|gb|EFH59441.1| pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene63390_All//2.00E-14//AT3G19410| pseudouridine synthase family protein	Unigene63390_All//2.00E-79//TC138007				nr -
Unigene63391_All	228	0.00	3.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.94E-05	Up	null	null		null	null		null	null		null	null		null	null											ESTscan +
Unigene6341_All	264	153.40	88.48	44.98	91.33	85.44	75.61	186.58	102.91	43.76	-7.94E-01	2.48E-20		-1.77E+00	6.36E-68	Down	-9.62E-02	4.77E-01		-2.72E-01	1.71E-02		-8.58E-01	3.62E-34		-2.09E+00	1.90E-134	Down	Unigene6341_All//gi|300681467|emb|CBH32561.1|//4.00E-27//histone H3, expressed [Triticum aestivum]	Unigene6341_All//1.00E-28//AT5G65360| histone H3	Unigene6341_All//6.00E-135//TC155239				nr -
Unigene6342_All	403	1.30	1.26	1.85	3.71	2.39	7.96	14.58	21.99	54.96	-4.63E-02	9.75E-01		5.11E-01	5.47E-01		-6.32E-01	2.38E-01		1.10E+00	1.62E-03		5.92E-01	5.91E-04		1.91E+00	1.42E-53	Up				Unigene6342_All//1.00E-167//gi|164345966|gb|EX169146.1|EX169146					
Unigene63425_All	214	0.24	7.10	1.99	1.16	1.77	0.00	0.59	0.78	1.30	4.86E+00	1.61E-07	Up	3.03E+00	5.72E-02		6.05E-01	6.59E-01		-1.02E+01	7.31E-02		3.98E-01	8.13E-01		1.14E+00	3.99E-01					Unigene63425_All//7.00E-23//BF278057					
Unigene6343_All	380	18.31	17.20	20.46	23.20	11.87	24.25	21.92	10.89	9.12	-9.03E-02	6.91E-01		1.60E-01	5.02E-01		-9.67E-01	7.76E-08		6.34E-02	7.69E-01		-1.01E+00	3.27E-08	Down	-1.26E+00	8.00E-12	Down	Unigene6343_All//gi|297725871|ref|NP_001175299.1|//7.00E-12//Os07g0620501 [Oryza sativa Japonica Group] >gi|255677975|dbj|BAH94027.1| Os07g0620501 [Oryza sativa Japonica Group]	Unigene6343_All//1.00E-12//AT3G12587| unknown protein	Unigene6343_All//1.00E-25//TC173593				nr +
Unigene63442_All	209	0.00	5.82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.47E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene63442_All//gi|3334346|sp|O48650.1|SUI1_SALBA//8.00E-16//RecName: Full=Protein translation factor SUI1 homolog >gi|2852445|dbj|BAA24697.1| SUI1 homolog [Salix bakko]	Unigene63442_All//9.00E-13//AT5G54760| eukaryotic translation initiation factor SUI1, putative					nr -
Unigene63443_All	575	0.00	4.14	0.93	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.50E-13	Up	9.86E+00	4.03E-03		null	null		null	null		null	null		null	null											ESTscan +
Unigene6345_All	547	5.83	2.22	3.41	4.19	2.27	2.56	0.93	0.76	0.87	-1.39E+00	1.23E-04	Down	-7.76E-01	3.32E-02		-8.86E-01	2.70E-02		-7.11E-01	9.71E-02		-2.80E-01	7.49E-01		-8.57E-02	9.30E-01		Unigene6345_All//gi|51536472|gb|AAU05474.1|//7.00E-27//At1g78010 [Arabidopsis thaliana] >gi|52421301|gb|AAU45220.1| At1g78010 [Arabidopsis thaliana]	Unigene6345_All//5.00E-13//AT1G78010| tRNA modification GTPase, putative	Unigene6345_All//0.00E+00//gi|78338468|gb|DT558742.1|DT558742				nr +
Unigene6346_All	610	4.29	6.56	2.71	6.12	2.82	3.18	7.07	6.99	2.09	6.14E-01	4.42E-02		-6.64E-01	1.06E-01		-1.12E+00	1.69E-04	Down	-9.44E-01	2.66E-03		-1.66E-02	9.84E-01		-1.76E+00	4.29E-10	Down				Unigene6346_All//9.00E-25//TC146744					
Unigene63461_All	209	0.75	0.73	0.00	2.62	0.00	2.59	0.61	0.80	0.57	-4.63E-02	9.88E-01		-9.55E+00	2.43E-01		-1.14E+01	4.01E-04	Down	-1.59E-02	9.75E-01		3.98E-01	8.13E-01		-8.59E-02	9.68E-01					Unigene63461_All//2.00E-35//CO086259					
Unigene63464_All	369	0.00	2.47	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	2.62E-05	Up	8.76E+00	2.38E-01		null	null		null	null		null	null		null	null											
Unigene6347_All	1248	0.00	0.97	0.43	2.16	1.57	2.24	1.73	26.26	6.16	9.93E+00	5.47E-07	Up	8.74E+00	4.03E-03		-4.55E-01	2.43E-01		5.79E-02	9.05E-01		3.93E+00	3.53E-166	Up	1.83E+00	4.17E-18	Up	Unigene6347_All//gi|15223463|ref|NP_176012.1|//2.00E-60//MYB72 (MYB DOMAIN PROTEIN 72); DNA binding / transcription factor [Arabidopsis thaliana] >gi|6056369|gb|AAF02833.1|AC009894_4 Putative transcription factor [Arabidopsis thaliana]	Unigene6347_All//1.00E-61//AT1G56160| MYB72 (MYB DOMAIN PROTEIN 72); DNA binding / transcription factor	Unigene6347_All//3.00E-72//NP524468	MYB			nr -
Unigene6348_All	244	42.46	27.62	32.74	55.12	71.13	68.49	226.48	129.16	111.03	-6.20E-01	4.55E-04		-3.75E-01	4.77E-02		3.68E-01	4.46E-03		3.13E-01	2.55E-02		-8.10E-01	1.04E-34		-1.03E+00	6.34E-53	Down	Unigene6348_All//gi|209967445|gb|ACJ02351.1|//4.00E-37//60S ribosomal protein L31 [Vernicia fordii]	Unigene6348_All//2.00E-25//AT5G56710| 60S ribosomal protein L31 (RPL31C)	Unigene6348_All//3.00E-133//ES796068		ko03010|Ribosome		nr +
Unigene63489_All	413	0.00	3.93	1.81	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.96E-09	Up	1.08E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene63489_All//gi|19070773|gb|AAL83989.1|//1.00E-16//NADH-ubiquinine oxido-reductase 24kD subunit [Oryza sativa]	Unigene63489_All//2.00E-12//AT4G02580| NADH-ubiquinone oxidoreductase 24 kDa subunit, putative			ko00190|Oxidative phosphorylation	GO:0043231	nr -

Unigene6350_All	655	10.54	4.25	3.74	16.50	14.62	15.93	19.95	10.34	14.11	-1.31E+00	2.33E-08	Down	-1.50E+00	1.49E-09	Down	-1.75E-01	3.71E-01		-5.12E-02	7.93E-01		-9.48E-01	2.79E-11		-4.99E-01	2.21E-04		Unigene6350_All//gi|115467892|ref|NP_001057545.1|//7.00E-12//0s06g0332500 [Oryza sativa Japonica Group] >gi|113595585|dbj|BAF19459.1|Os06g0332500 [Oryza sativa Japonica Group]	Unigene6350_All//2.00E-15//AT1G55205| unknown protein	Unigene6350_All//0.00E+00//gi|164337990|gb|EX171297.1|EX171297				nr +
Unigene6351_All	928	0.00	1.20	0.75	0.05	0.93	4.19	9.80	8.38	3.78	1.02E+01	2.00E-06	Up	9.54E+00	6.15E-04	Up	4.11E+00	2.60E-04	Up	6.28E+00	8.48E-22	Up	-2.26E-01	2.32E-01		-1.37E+00	1.86E-14	Down	Unigene6351_All//gi|9081845|gb|AAF82615.1|AF157011_1//2.00E-95//S-like ribonuclease [Prunus dulcis] >gi|11141363|gb|AG31920.1|AF202030_1 RNase PD2 [Prunus dulcis]	Unigene6351_All//2.00E-95//AT2G02990| RNS1 (RIBONUCLEASE 1); endoribonuclease/ ribonuclease	Unigene6351_All//0.00E+00//TC138665				nr -
Unigene6352_All	507	5.47	11.09	7.46	8.16	7.74	9.44	14.59	28.94	27.42	1.02E+00	6.28E-05	Up	4.47E-01	1.83E-01		-7.48E-02	8.15E-01		2.12E-01	5.01E-01		9.88E-01	2.29E-13		9.10E-01	1.68E-11					Unigene6352_All//2.00E-121//gi|21098970|gb|BQ411283.1|BQ411283				
Unigene6353_All	508	4.84	2.79	3.67	2.84	1.90	1.78	1.50	0.08	1.25	-7.94E-01	4.88E-02		-4.00E-01	3.65E-01		-5.83E-01	2.98E-01		-6.77E-01	2.32E-01		-4.19E+00	1.57E-04	Down	-2.56E-01	6.97E-01		Unigene6353_All//gi|15227306|ref|NP_181655.1|//2.00E-12//GLU2 (GLUTAMATE SYNTHASE 2); glutamate synthase (ferredoxin) [Arabidopsis thaliana] >gi|300669644|sp|Q9T0P4.2|GLTB2_ARATH RecName: Full=Ferredoxin-dependent glutamate synthase 2, chloroplastic; AltName: Full=Fd-GOGAT 2; Flags: Precursor >gi|3894200|gb|AAC78549.1|ferredoxin-dependent glutamate synthase (GLU2) [Arabidopsis thaliana]	Unigene6353_All//9.00E-14//AT2G41220| GLU2 (GLUTAMATE SYNTHASE 2); glutamate synthase (ferredoxin)	Unigene6353_All//4.00E-20//TC138643		ko00910|Nitrogen metabolism		nr +
Unigene63541_All	641	0.00	7.83	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.34E-28	Up	1.07E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene63541_All//gi|15233440|ref|NP_195326.1|//4.00E-30//CSDP1 (cold shock domain protein 1); RNA binding / double-stranded DNA binding / nucleic acid binding / single-stranded DNA binding [Arabidopsis thaliana] >gi|3036806|emb|CAA18496.1|glycine-rich protein [Arabidopsis thaliana] >gi|7270554|emb|CAB81511.1|glycine-rich protein [Arabidopsis thaliana] >gi|110741941|dbj|BAE98911.1|glycine-rich protein [Arabidopsis thaliana]	Unigene63541_All//1.00E-24//AT4G36020| CSDP1 (cold shock domain protein 1); RNA binding / double-stranded DNA binding / nucleic acid binding / single-stranded DNA binding		CSD		GO:0003677//GO:0009987//GO:0044424	nr +
Unigene6355_All	852	64.66	25.28	48.94	7.60	6.91	4.51	1.89	1.57	0.75	-1.36E+00	8.98E-65	Down	-4.02E-01	3.28E-08		-1.37E-01	6.10E-01		-7.54E-01	8.96E-04		-2.65E-01	6.15E-01		-1.33E+00	3.75E-03		Unigene6355_All//gi|15450643|gb|AAK96593.1|//1.00E-52//AT3g51510/F26013_150 [Arabidopsis thaliana]	Unigene6355_All//5.00E-54//AT3G51510| unknown protein	Unigene6355_All//0.00E+00//TC139766				nr +
Unigene6356_All	435	23.82	24.34	19.83	29.09	26.44	31.56	94.09	59.76	41.40	3.17E-02	8.71E-01		-2.64E-01	1.77E-01		-1.38E-01	4.54E-01		1.18E-01	5.25E-01		-6.55E-01	4.00E-18		-1.18E+00	2.43E-49	Down	Unigene6356_All//gi|297849408|ref|XP_002892585.1|//7.00E-20//ADP-ribosylation factor [Arabidopsis lyrata subsp. lyrata] >gi|297338427|gb|EFH68844.1| ADP-ribosylation factor [Arabidopsis lyrata subsp. lyrata]	Unigene6356_All//5.00E-21//AT3G62290| ATARFA1E (ADP-ribosylation factor A1E); GTP binding / phospholipase activator/ protein binding	Unigene6356_All//0.00E+00//TC157301				nr -
Unigene63569_All	715	0.00	2.98	0.37	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	4.10E-12	Up	8.54E+00	8.00E-02		null	null		null	null		null	null		null	null		Unigene63569_All//gi|30678625|ref|NP_567175.2|//1.00E-13//ANTR2; inorganic phosphate transmembrane transporter/ organic anion transmembrane transporter [Arabidopsis thaliana] >gi|75244391|sp|Q8GXT8.1|ANTR2_ARATH RecName: Full=Probable anion transporter 2, chloroplastic; AltName: Full=Phosphate transporter PHT4;4; Flags: Precursor >gi|32306495|gb|AAP78931.1|At4g00370 [Arabidopsis thaliana]	Unigene63569_All//6.00E-15//AT4G00370| ANTR2; inorganic phosphate transmembrane transporter/ organic anion transmembrane transporter				GO:0009528//GO:0015291	nr -
Unigene6357_All	492	14.57	34.29	19.59	44.04	38.91	37.82	53.28	146.62	165.99	1.24E+00	1.28E-17	Up	4.27E-01	2.86E-02		-1.79E-01	1.61E-01		-2.20E-01	8.16E-02		1.46E+00	1.69E-115	Up	1.64E+00	7.69E-158	Up	Unigene6357_All//gi|219560132|gb|ACL27274.1|//3.00E-23//homeodomain leucine-zipper 1 [Nicotiana benthamiana]	Unigene6357_All//1.00E-16//AT4G37790| HAT22; transcription factor	Unigene6357_All//0.00E+00//gi|109885227|gb|DW514197.1|DW514197	HB			nr -
Unigene63571_All	219	0.00	4.63	2.19	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.25E-06	Up	1.11E+01	7.46E-03		null	null		null	null		null	null		null	null		Unigene63571_All//gi|301095603|ref|XP_002896901.1|//1.00E-15//26S proteasome non-ATPase regulatory subunit 3 [Phytophthora infestans T30-4] >gi|262108548|gb|EEY66600.1| 26S proteasome non-ATPase regulatory subunit 3 [Phytophthora infestans T30-4]	Unigene63571_All//7.00E-07//AT1G26200| EMB2719 (EMBRYO DEFECTIVE 2719); enzyme regulator			ko03050|Proteasome	GO:0009894//GO:0043234	nr +
Unigene63572_All	210	0.50	0.00	0.51	0.00	0.00	0.22	4.23	0.40	0.00	-8.96E+00	3.68E-01		2.53E-02	9.98E-01		null	null		7.75E+00	6.91E-01		-3.41E+00	1.40E-04	Down	-1.20E+01	1.10E-06	Down			Unigene63572_All//7.00E-17//TC144809				
Unigene6358_All	412	2.79	0.25	1.81	2.30	1.59	1.53	1.44	2.03	1.45	-3.51E+00	6.57E-05	Down	-6.27E-01	3.56E-01		-5.33E-01	4.51E-01		-5.82E-01	4.37E-01		4.98E-01	4.86E-01		1.37E-02	9.87E-01				Unigene6358_All//5.00E-07//BQ407734				
Unigene63595_All	678	0.00	5.61	1.81	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.23E-21	Up	1.08E+01	9.11E-07	Up	null	null		null	null		null	null		null	null		Unigene63595_All//gi|301092712|ref|XP_002997209.1|//1.00E-44//ribosome biogenesis protein RLP24 [Phytophthora infestans T30-4] >gi|301126859|ref|XP_002909877.1|ribosome biogenesis protein RLP24 [Phytophthora infestans T30-4] >gi|262101245|gb|EEY59297.1|ribosome biogenesis protein RLP24 [Phytophthora infestans T30-4] >gi|262111519|gb|EEY69571.1|ribosome biogenesis protein RLP24 [Phytophthora infestans T30-4]	Unigene63595_All//8.00E-43//AT2G44860| 60S ribosomal protein L24, putative			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613//GO:0031981	nr -
Unigene6360_All	651	0.48	1.87	0.90	2.75	3.07	1.80	3.57	1.86	0.92	1.95E+00	4.09E-03		9.00E-01	3.77E-01		1.55E-01	7.98E-01		-6.11E-01	2.28E-01		-9.40E-01	1.20E-02		-1.96E+00	1.31E-06	Down							
Unigene63605_All	292	0.00	3.47	0.91	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.25E-06	Up	9.83E+00	8.00E-02		null	null		null	null		null	null		null	null		Unigene63605_All//gi|22328793|ref|NP_193656.2|//3.00E-36//ATRLI2; transporter [Arabidopsis thaliana] >gi|75330288|sp|Q8LPJ4.1|AB2E_ARATH RecName: Full=ABC transporter E family member 2; Short=ABC transporter ABCE.2; Short=AtABCE2; AltName: Full=RNase L inhibitor-like protein 2; Short=AthaRLI2; Short=AtRLI2 >gi|20466462|gb|AAM20548.1| RNase L inhibitor-like protein [Arabidopsis thaliana] >gi|23198180|gb|AAN15617.1| RNase L inhibitor-like protein [Arabidopsis thaliana] >gi|110742163|dbj|BAE99009.1|RNase L inhibitor-like protein [Arabidopsis thaliana]	Unigene63605_All//1.00E-37//AT4G19210| ATRLI2; transporter				GO:0019829//GO:0032559//GO:0051540	nr -
Unigene6361_All	635	1.65	0.48	0.84	4.31	2.71	1.85	2.93	0.66	0.94	-1.78E+00	1.36E-02		-9.75E-01	1.67E-01		-6.70E-01	6.81E-02		-1.22E+00	1.37E-03		-2.15E+00	8.47E-06	Down	-1.64E+00	1.88E-04	Down	Unigene6361_All//gi|18397057|ref|NP_565352.1|//6.00E-34//MGDC; 1,2-diacylglycerol 3-beta-galactosyltransferase [Arabidopsis thaliana] >gi|75206061|sp|Q9SI93.2|MGDG3_ARATH RecName: Full=Monogalactosyldiacylglycerol synthase 3, chloroplastic; Short=AtMGD3; AltName: Full=MGDG synthase type C; Flags: Precursor >gi|9927295|dbj|BAB12041.1| MGDG synthase type C [Arabidopsis thaliana] >gi|111074182|gb|ABH04464.1|At2g11810 [Arabidopsis thaliana]	Unigene6361_All//3.00E-33//AT5G20410| MGD2; 1,2-diacylglycerol 3-beta-galactosyltransferase/ UDP-galactosyltransferase/ transferase, transferring glycosyl groups	Unigene6361_All//0.00E+00//TC163689		ko00561|Glycerolipid metabolism		nr -
Unigene63619_All	208	0.00	3.65	0.00	0.24	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	null	null		-7.90E+00	5.51E-01		-7.90E+00	6.28E-01		null	null		null	null									
Unigene6362_All	478	3.06	6.78	7.02	2.61	3.67	3.21	0.27	0.17	0.00	1.15E+00	1.13E-03		1.20E+00	8.71E-04	Up	4.96E-01	3.46E-01		3.02E-01	6.35E-01		-6.02E-01	7.65E-01		-8.05E+00	1.99E-01									
Unigene6363_All	966	3.47	3.20	4.13	3.15	3.56	2.29	2.93	2.51	1.28	-1.16E-01	7.26E-01		2.54E-01	4.36E-01		1.80E-01	6.28E-01		-4.57E-01	2.26E-01		-2.25E-01	5.48E-01		-1.20E+00	2.74E-04	Down			Unigene6363_All//2.00E-11//TC133459				
Unigene6364_All	644	17.06	9.76	10.25	34.50	19.73	6.59	27.71	12.59	9.16	-8.06E-01	3.00E-06		-7.35E-01	3.70E-05		-8.06E-01	5.05E-14		-2.39E+00	4.94E-62	Down	-1.14E+00	4.47E-20	Down	-1.60E+00	3.17E-34	Down	Unigene6364_All//gi|115473321|ref|NP_001060259.1|//1.00E-12//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1|Os07g0613900 [Oryza sativa Japonica Group]	Unigene6364_All//6.00E-05//AT3G09510| nucleic acid binding	Unigene6364_All//0.00E+00//gi|109881747|gb|DW510717.1|DW510717				nr +
Unigene63646_All	255	0.00	2.58	2.30	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.24E-04	Up	1.12E+01	2.17E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene63648_All	434	3.13	2.10	1.35	4.59	6.59	2.81	10.33	4.33	3.49	-5.77E-01	3.19E-01		-1.22E+00	4.79E-02		5.20E-01	1.74E-01		-7.09E-01	1.31E-01		-1.25E+00	1.97E-06	Down	-1.57E+00	5.34E-09	Down			Unigene63648_All//1.00E-112//DW515131				

Unigene6365_All	647	211.63	89.12	43.95	127.65	148.55	71.06	124.81	33.46	24.45	-1.25E+00	7.25E-141	Down	-2.27E+00	0.00E+00	Down	2.19E-01	1.13E-05		-8.45E-01	7.23E-49		-1.90E+00	4.55E-188	Down	-2.35E+00	1.06E-254	Down	Unigene6365_All//gi|15232146|ref|NP_189372.1|//4.00E-68//histone H3 [Arabidopsis thaliana] >gi|15238433|ref|NP_201339.1| histone H3 [Arabidopsis thaliana] >gi|18390992|ref|NP_563838.1| histone H3 [Arabidopsis thaliana] >gi|18416261|ref|NP_568227.1| histone H3 [Arabidopsis thaliana] >gi|18416264|ref|NP_568228.1| histone H3 [Arabidopsis thaliana] >gi|115441249|ref|NP_001044904.1| Os01g0866200 [Oryza sativa Japonica Group] >gi|115458352|ref|NP_001052776.1| Os04g0419600 [Oryza sativa Japonica Group] >gi|115464121|ref|NP_001055660.1| Os05g0438700 [Oryza sativa Japonica Group] >gi|115466556|ref|NP_001056877.1| Os06g0160100 [Oryza sativa Japonica Group] >gi|115484259|ref|NP_001065791.1| Os11g0155900 [Oryza sativa Japonica Group] >gi|212721652|ref|NP_001131276.1| histone H3.2 [Zea mays] >gi|297724495|ref|NP_001174611.1| Os06g0159501 [Oryza sativa	Unigene6365_All//1.00E-58//AT5G65360| histone H3	Unigene6365_All//0.00E+00//gi|164276322|gb|ES804524.1|ES804524				nr -
Unigene63668_All	275	0.00	4.42	2.90	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.47E-07	Up	1.15E+01	1.72E-04	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene6367_All	551	7.79	5.89	2.80	9.13	7.56	8.93	8.59	4.32	2.53	-4.04E-01	1.77E-01		-1.47E+00	4.56E-06	Down	-2.72E-01	3.39E-01		-3.14E-02	9.31E-01		-9.91E-01	6.84E-05		-1.76E+00	4.79E-11	Down	Unigene6367_All//gi|255628915|gb|ACU14802.1|//5.00E-20//unknown [Glycine max]	Unigene6367_All//4.00E-16//AT1G01725| unknown protein	Unigene6367_All//0.00E+00//TC163988				nr +
Unigene6368_All	372	4.78	4.90	6.58	4.55	3.24	1.70	2.84	0.79	0.43	3.62E-02	9.58E-01		4.62E-01	2.84E-01		-4.91E-01	3.29E-01		-1.42E+00	5.89E-03		-1.85E+00	4.09E-03		-2.73E+00	1.12E-04	Down			Unigene6368_All//4.00E-10//TC145896				
Unigene63691_All	1512	1.76	1.64	1.69	1.22	1.39	1.08	1.26	1.55	0.32	-1.04E-01	7.77E-01		-6.21E-02	8.80E-01		1.89E-01	7.28E-01		-1.81E-01	7.08E-01		2.99E-01	4.54E-01		-1.99E+00	1.17E-05	Down	Unigene63691_All//gi|18410357|ref|NP_565064.1|//4.00E-52//calmodulin-related [Arabidopsis thaliana] >gi|11762206|gb|AAG40381.1|AF325029_1 At1g73440 [Arabidopsis thaliana]	Unigene63691_All//2.00E-33//AT1G73440| calmodulin-related	Unigene63691_All//0.00E+00//TC130075		ko04626|Plant-pathogen interaction//ko03410|Base excision repair	GO:0000741//GO:0005488	nr +
Unigene63695_All	266	0.20	3.43	0.00	1.31	0.26	2.04	0.64	0.63	0.30	4.12E+00	2.34E-04	Up	-7.62E+00	6.18E-01		-2.34E+00	1.01E-01		6.36E-01	5.61E-01		-1.67E-02	1.02E+00		-1.09E+00	5.52E-01									
Unigene637_All	2740	1.81	2.09	1.30	2.49	2.01	2.06	4.09	2.81	1.67	2.04E-01	4.34E-01		-4.78E-01	9.36E-02		-3.09E-01	1.86E-01		-2.74E-01	2.69E-01		-5.43E-01	3.27E-04		-1.29E+00	4.63E-16	Down	Unigene637_All//gi|186505512|ref|NP_181076.3|//0.00E+00//protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene637_All//0.00E+00//AT2G35330| protein binding / zinc ion binding	Unigene637_All//0.00E+00//TC130235			GO:0046914	nr -
Unigene6371_All	367	10.69	8.70	13.64	20.50	24.02	27.32	38.02	18.79	19.21	-2.98E-01	3.66E-01		3.51E-01	2.33E-01		2.29E-01	2.97E-01		4.15E-01	2.43E-02		-1.02E+00	2.34E-13	Down	-9.85E-01	4.04E-13		Unigene6371_All//gi|226503399|ref|NP_001151665.1|//8.00E-19//LOC100285098 [Zea mays] >gi|195646972|gb|ACG42954.1| elongation factor 2 [Zea mays]	Unigene6371_All//1.00E-19//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene6371_All//8.00E-126//TC132395				nr -
Unigene63710_All	211	0.00	3.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene63718_All	591	0.00	2.49	2.16	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	2.11E-08	Up	1.11E+01	4.68E-07	Up	null	null		null	null		null	null		null	null		Unigene63718_All//gi|531098|dbj|BAA06461.1|//6.00E-08//TED3 [Zinnia elegans]						nr +
Unigene6372_All	1249	5.49	9.53	15.22	2.47	2.04	0.87	0.95	0.60	1.18	7.97E-01	1.46E-06		1.47E+00	8.77E-25	Up	-2.77E-01	4.69E-01		-1.51E+00	3.39E-05	Down	-6.54E-01	2.47E-01		3.16E-01	5.32E-01		Unigene6372_All//gi|1770305|emb|CAA92278.1|//0.00E+00//1,3-beta-glucanase [Gossypium hirsutum]	Unigene6372_All//2.00E-99//AT3G57240| BG3 (BETA-1,3-GLUCANASE 3); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene6372_All//0.00E+00//TC142180		ko00500|Starch and sucrose metabolism		nr +
Unigene63720_All	222	0.00	0.68	0.00	0.00	0.00	0.00	2.48	28.81	37.33	9.42E+00	2.34E-01		null	null		null	null		null	null		3.54E+00	3.01E-30	Up	3.91E+00	5.23E-43	Up	Unigene63720_All//gi|45238345|emb|CAD70567.1|//8.00E-16//aldehyde dehydrogenase [Crocus sativus]	Unigene63720_All//2.00E-13//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene63720_All//1.00E-06//gi|164322141|gb|ES819657.1|ES819657		ko00940|Phenylpropanoid biosynthesis	GO:0008152//GO:0016620//GO:0043231	nr -
Unigene63728_All	213	0.00	4.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.94E-05	Up	null	null		null	null		null	null		null	null		null	null									
Unigene6374_All	1421	1.29	2.25	0.94	4.91	4.63	1.53	1.34	0.32	0.39	8.02E-01	2.12E-02		-4.60E-01	3.79E-01		-8.45E-02	7.68E-01		-1.69E+00	1.04E-12	Down	-2.05E+00	1.34E-05	Down	-1.77E+00	5.92E-05	Down	Unigene6374_All//gi|224143880|ref|XP_002325107.1|//1.00E-156//serine/threonine protein kinase [Populus trichocarpa] >gi|22286641|gb|EEF03672.1| serine/threonine protein kinase [Populus trichocarpa]	Unigene6374_All//3.00E-139//AT2G23950| leucine-rich repeat family protein / protein kinase family protein	Unigene6374_All//0.00E+00//DW513306		ko04626|Plant-pathogen interaction		nr +
Unigene63745_All	574	0.00	3.00	0.19	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.98E-10	Up	7.54E+00	3.96E-01		null	null		null	null		null	null		null	null									
Unigene6375_All	410	3.45	3.83	1.04	2.79	2.60	6.94	1.55	1.63	2.23	1.53E-01	7.58E-01		-1.73E+00	6.13E-03		-1.02E-01	8.56E-01		1.31E+00	5.61E-04	Up	7.66E-02	9.37E-01		5.31E-01	4.07E-01				Unigene6375_All//1.00E-103//DW476948				
Unigene6375Z_All	380	0.00	3.07	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.05E-06	Up	9.45E+00	7.99E-02		null	null		null	null		null	null		null	null									
Unigene6378_All	865	0.42	0.64	2.83	1.55	1.95	0.89	0.98	0.97	0.78	6.06E-01	5.30E-01		2.74E+00	1.65E-07	Up	3.27E-01	5.68E-01		-8.09E-01	1.73E-01		-1.66E-02	1.02E+00		-3.20E-01	6.25E-01									
Unigene63786_All	228	0.00	3.11	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.32E-04	Up	7.87E+00	6.32E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene6379_All	420	2.12	2.65	2.16	1.19	3.28	2.37	6.95	1.49	20.96	3.26E-01	5.98E-01		2.55E-02	9.92E-01		1.47E+00	1.25E-02		9.96E-01	1.72E-01		-2.22E+00	5.51E-09	Down	1.59E+00	4.42E-17	Up	Unigene6379_All//gi|125950374|gb|ABN58740.1|//6.00E-33//UGT protein [Gossypium hirsutum]	Unigene6379_All//3.00E-16//AT3G46690| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene6379_All//0.00E+00//TC134046		ko00908|Zeatin biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene638_All	536	0.59	2.65	1.69	3.53	4.75	4.30	4.10	3.74	3.86	2.18E+00	6.83E-04	Up	1.53E+00	5.77E-02		4.29E-01	3.10E-01		2.83E-01	5.56E-01		-1.32E-01	7.40E-01		-8.58E-02	8.20E-01		Unigene638_All//gi|115451679|ref|NP_001049440.1|//3.00E-70//Os03g0226600 [Oryza sativa Japonica Group] >gi|24421679|gb|AAN60986.1| Hypothetical protein [Oryza sativa Japonica Group] >gi|108706952|gb|ABF94747.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547911|dbj|BAF11354.1| Os03g0226600 [Oryza sativa Japonica Group]	Unigene638_All//2.00E-76//AT3G58050| unknown protein				GO:0043231	nr -
Unigene6380_All	577	6.62	3.78	4.43	9.32	10.62	14.25	47.19	57.51	163.77	-8.10E-01	9.66E-03		-5.80E-01	7.87E-02		1.88E-01	5.15E-01		6.12E-01	2.27E-03		2.86E-01	7.34E-04		1.80E+00	2.84E-207	Up	Unigene6380_All//gi|125950374|gb|ABN58740.1|//7.00E-62//UGT protein [Gossypium hirsutum]	Unigene6380_All//2.00E-36//AT3G46660| UGT76E12 (UDP-GLUCOSYL TRANSFERASE 76E12); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene6380_All//0.00E+00//TC166770		ko00908|Zeatin biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene63805_All	234	2.46	0.22	4.55	3.62	0.44	2.51	2.17	3.22	0.17	-3.51E+00	9.02E-03		8.88E-01	2.06E-01		-3.04E+00	5.54E-04	Down	-5.28E-01	5.02E-01		5.68E-01	4.47E-01		-3.67E+00	3.75E-03									
Unigene6381_All	229	42.95	13.28	12.79	69.39	50.37	81.25	135.52	37.23	31.31	-1.69E+00	1.34E-16	Down	-1.75E+00	1.49E-16	Down	-4.62E-01	4.03E-04		2.28E-01	1.01E-01		-1.86E+00	7.57E-71	Down	-2.11E+00	4.25E-86	Down	Unigene6381_All//gi|76573371|gb|ABA46790.1|//8.00E-32//60S ribosomal protein L13a-like protein [Solanum tuberosum]	Unigene6381_All//2.00E-32//AT5G48760| 60S ribosomal protein L13A (RPL13aD)	Unigene6381_All//1.00E-126//TC133357		ko03010|Ribosome		nr +
Unigene63813_All	291	0.00	2.79	0.55	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.37E-05	Up	9.10E+00	2.38E-01		null	null		null	null		null	null		null	null		Unigene63813_All//sp|P51884|LUM_HUMAN//3.00E-50//Lumican OS=Homo sapiens GN=LUM PE=1 SV=2	Unigene63813_All//1.00E-05//AT5G20690| ATP binding / kinase/ protein serine/threonine kinase					swissprot +
Unigene6382_All	922	0.23	0.44	0.00	4.27	1.34	5.63	4.59	1.59	1.81	9.54E-01	4.13E-01		-7.83E+00	1.45E-01		-1.67E+00	3.25E-08	Down	4.00E-01	1.49E-01		-1.53E+00	5.36E-08	Down	-1.34E+00	6.25E-07	Down	Unigene6382_All//gi|15220823|ref|NP_178188.1|//1.00E-35//ZFP1 (ZINC-FINGER PROTEIN 1); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|27923894|sp|Q42485.1|ZFP1_ARATH RecName: Full=Zinc finger protein 1 >gi|6503285|gb|AAF14661.1|AC011713_9 Identical to gi|S55881 zinc finger protein 1 from Arabidopsis thaliana >gi|790673|gb|AAA87297.1| zinc finger protein [Arabidopsis thaliana] >gi|1297186|gb|AAA98913.1| zinc finger protein 1 [Arabidopsis thaliana] >gi|110074280|gb|ABH04513.1| At1g80730 [Arabidopsis thaliana]	Unigene6382_All//2.00E-37//AT1G80730| ZFP1 (ZINC-FINGER PROTEIN 1); nucleic acid binding / transcription factor/ zinc ion binding	Unigene6382_All//5.00E-09//DW224855	C2H2			nr -
Unigene6384_All	971	0.75	0.63	1.32	2.21	1.70	1.35	3.44	2.24	1.68	-2.69E-01	7.19E-01		8.03E-01	2.01E-01		-3.74E-01	4.16E-01		-7.10E-01	1.13E-01		-6.20E-01	4.11E-02		-1.03E+00	4.78E-04	Down	Unigene6384_All//gi|34761718|gb|AAQ82031.1|//4.00E-40//pol [Pisum sativum]	Unigene6384_All//5.00E-05//ATMG00760| hypothetical protein					nr -
Unigene63843_All	396	0.00	8.19	1.08	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.87E-18	Up	1.01E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene63843_All//sp|Q9GR07|NONA_DROVI//2.00E-62//Protein no-on-transient A OS=Drosophila virilis GN=nonA PE=2 SV=1						swissprot -
Unigene63845_All	222	0.00	4.79	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	3.81E-06	Up	7.91E+00	6.32E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene6385_All	1136	0.18	0.00	0.00	4.17	2.97	0.87	24.45	10.56	12.80	-7.53E+00	1.21E-01		-7.53E+00	1.45E-01		-4.88E-01	7.28E-02		-2.25E+00	1.15E-12	Down	-1.21E+00	5.86E-34	Down	-9.34E-01	3.55E-23		Unigene6385_All//gi|15983819|emb|CAC30667.1|//2.00E-97//3-beta-hydroxysteroiddehydrogenase [Digitalis lanata] >gi|56900850|gb|AAW31720.1| 3-beta-hydroxysteroid dehydrogenase [Digitalis lanata] >gi|94962698|gb|ABF48560.1| 3 beta-hydroxysteroid dehydrogenase [Digitalis lanata]	Unigene6385_All//1.00E-92//AT2G47140| short-chain dehydrogenase/reductase (SDR) family protein	Unigene6385_All//0.00E+00//gi|109885570|gb|DW517539.1|DW517539		ko00906|Carotenoid biosynthesis		nr -
Unigene6387_All	1057	0.10	1.63	0.10	0.99	0.26	2.61	23.32	35.55	81.03	4.04E+00	1.14E-07	Up	2.60E-02	9.98E-01		-1.93E+00	4.39E-03		1.40E+00	3.46E-04	Up	6.08E-01	9.65E-15		1.80E+00	3.43E-188	Up	Unigene6387_All//gi|15230558|ref|NP_190736.1|//1.00E-118//short-chain dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] >gi|6580150|emb|CAB63154.1| short-chain alcohol dehydrogenase-like protein [Arabidopsis thaliana]	Unigene6387_All//6.00E-120//AT3G51680| short-chain dehydrogenase/reductase (SDR) family protein	Unigene6387_All//0.00E+00//TC145082		ko00906|Carotenoid biosynthesis		nr -
Unigene63879_All	300	0.00	3.21	1.24	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.38E-05	Up	1.03E+01	2.50E-02		null	null		null	null		null	null		null	null		Unigene63879_All//gi|115469620|ref|NP_001058409.1|//4.00E-29//Os06g0687700 [Oryza sativa Japonica Group] >gi|113596449|dbj|BAF20323.1| Os06g0687700 [Oryza sativa Japonica Group]	Unigene63879_All//1.00E-29//AT3G11830| chaperonin, putative	Unigene63879_All//2.00E-08//gi|109858075|gb|DW487054.1|DW487054			GO:0005515//GO:0010038//GO:0032559//GO:0044267//GO:0044424	nr -

Unigene63883_All	463	0.00	1.64	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	1.76E-04	Up	8.85E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene63883_All//gi|297813975|ref|XP_002874871.1|//5.00E-53//Rieskefes protein [Arabidopsis lyrata subsp. lyrata] >gi|297320708|gb|EFH51130.1| Rieske fes protein [Arabidopsis lyrata subsp. lyrata]	Unigene63883_All//7.00E-42//AT4G03280| PETC (PHOTOSYNTHETIC ELECTRON TRANSFER C); electron transporter, transferring electrons from cytochrome b6/f complex of photosystem II	Unigene63883_All//2.00E-18//TC174574		ko00195|Photosynthesis	GO:0006091//GO:0006952//GO:0009055//GO:0009416//GO:0009526//GO:0009534//GO:0015078//GO:0016679//GO:0031224//GO:0034357//GO:0043169//GO:0043234//GO:0051234//GO:0051536	nr -
Unigene6389_All	1345	0.58	0.00	0.48	3.04	1.13	0.71	5.12	1.58	0.18	-9.19E+00	1.09E-04	Down	-2.97E-01	6.97E-01		-1.43E+00	6.85E-07	Down	-2.11E+00	3.63E-10	Down	-1.69E+00	2.23E-14	Down	-4.85E+00	5.26E-42	Down	Unigene6389_All//gi|217037949|gb|ACJ76437.1|//1.00E-136//gibberellin 20-oxidase 1 [Glycine max]	Unigene6389_All//2.00E-85//AT5G51810| GA20OX2 (GIBBERELLIN 20 OXIDASE 2); gibberellin 20-oxidase	Unigene6389_All//0.00E+00//TC168612		ko00904|Diterpenoid biosynthesis		nr -
Unigene639_All	773	2.37	1.11	2.00	3.61	3.47	4.73	5.80	2.87	4.33	-1.09E+00	2.47E-02		-2.46E-01	6.28E-01		-5.46E-02	8.83E-01		3.91E-01	2.59E-01		-1.02E+00	7.74E-05	Down	-4.21E-01	9.37E-02		Unigene639_All//gi|115451679|ref|NP_001049440.1|//1.00E-102//0s03g0226600 [Oryza sativa Japonica Group] >gi|24421679|gb|AAN60986.1| Hypothetical protein [Oryza sativa Japonica Group] >gi|108706952|gb|ABF94747.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113547911|dbj|BAF11354.1| 0s03g0226600 [Oryza sativa Japonica Group]	Unigene639_All//6.00E-99//AT3G58050| unknown protein				GO:0043231	nr -
Unigene6390_All	407	21.08	49.80	28.65	23.62	30.54	16.53	39.58	46.83	73.02	1.24E+00	3.88E-21	Up	4.43E-01	1.12E-02		3.71E-01	1.98E-02		-5.15E-01	5.05E-03		2.43E-01	4.08E-02		8.84E-01	1.80E-22		Unigene6390_All//gi|11762168|gb|AAG40362.1|AF325010.1|//1.00E-122//AT5g16110 [Arabidopsis thaliana] >gi|15809652|gb|AAL06903.1| AT5g16110/T21H19_30 [Arabidopsis thaliana]	Unigene6390_All//2.00E-14//AT5G16110| unknown protein	Unigene6390_All//2.00E-145//TC131929				nr +
Unigene63909_All	348	0.00	4.22	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.11E-08	Up	1.10E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene63909_All//gi|21322711|emb|CAB22154.1|//6.00E-10//pherophorin-dz1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome		nr -
Unigene6391_All	833	76.82	32.36	53.25	34.68	38.53	28.79	0.25	0.45	0.53	-1.25E+00	4.08E-66	Down	-5.29E-01	3.76E-15		1.52E-01	1.48E-01		-2.69E-01	8.82E-03		8.31E-01	4.67E-01		1.05E+00	2.98E-01		Unigene6391_All//gi|2495180|sp|Q43082.1|HEM3_PEA//2.00E-76//RecName: Full=Porphobilinogen deaminase, chloroplastic; Short=PBG; AltName: Full=Pre-uroporphyrinogen synthase; AltName: Full=Hydroxymethylbilane synthase; Short=HMBS; Flags: Precursor >gi|313724|emb|CAA51820.1| hydroxymethylbilane synthase [Pisum sativum]	Unigene6391_All//7.00E-67//AT5G08280| HEMC (HYDROXYMETHYLBILANE SYNTHASE); hydroxymethylbilane synthase	Unigene6391_All//0.00E+00//gi|78335911|gb|DT556185.1|DT556185		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene6392_All	582	27.24	32.82	27.72	9.42	11.66	12.03	2.83	0.72	0.75	2.69E-01	3.99E-02		2.54E-02	8.76E-01		3.08E-01	2.03E-01		3.53E-01	1.32E-01		-1.98E+00	9.00E-05	Down	-1.91E+00	8.63E-05	Down	Unigene6392_All//gi|18412676|ref|NP_568083.1|//2.00E-14//beta-galactosidase [Arabidopsis thaliana] >gi|56236102|gb|AAY84507.1| At5g01075 [Arabidopsis thaliana] >gi|111074276|gb|ABH04511.1| At5g01075 [Arabidopsis thaliana]	Unigene6392_All//1.00E-06//AT5G01075| beta-galactosidase	Unigene6392_All//0.00E+00//gi|21092896|gb|BQ405209.1|BQ405209				nr +
Unigene6393_All	1297	5.77	11.37	6.28	9.03	8.89	11.04	3.72	3.90	7.83	9.79E-01	6.89E-11		1.23E-01	6.18E-01		-2.12E-02	9.10E-01		2.90E-01	6.31E-02		6.94E-02	7.94E-01		1.08E+00	4.20E-11	Up	Unigene6393_All//gi|15229025|ref|NP_190449.1|//4.00E-24//sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana]	Unigene6393_All//2.00E-25//AT3G48800| sterile alpha motif (SAM) domain-containing protein	Unigene6393_All//0.00E+00//TC156752				nr -
Unigene63937_All	316	0.33	3.85	0.84	0.32	2.18	0.71	1.87	1.32	1.64	3.54E+00	4.02E-05	Up	1.35E+00	4.09E-01		2.79E+00	9.45E-03		1.18E+00	5.49E-01		-5.02E-01	5.74E-01		-1.93E-01	7.94E-01					Unigene63937_All//6.00E-43//TC177531				
Unigene6394_All	364	4.17	2.92	3.07	3.42	3.50	4.84	8.60	14.93	17.62	-5.12E-01	3.50E-01		-4.40E-01	4.23E-01		3.29E-02	9.68E-01		5.00E-01	3.48E-01		7.96E-01	4.78E-04		1.04E+00	6.01E-07	Up	Unigene6394_All//gi|297827267|ref|XP_002881516.1|//2.00E-59//sodium- and lithium-tolerant 1 [Arabidopsis lyrata subsp. lyrata] >gi|297327355|gb|EFH57775.1| sodium-and lithium-tolerant 1 [Arabidopsis lyrata subsp. lyrata]	Unigene6394_All//9.00E-61//AT2G37570| SLT1 (sodium- and lithium-tolerant 1)	Unigene6394_All//7.00E-160//TC177960				nr -
Unigene63940_All	213	0.00	8.09	3.75	0.00	0.00	1.70	0.00	0.00	0.00	1.30E+01	7.98E-10	Up	1.19E+01	1.72E-04	Up	null	null		1.07E+01	2.37E-02		null	null		null	null		Unigene63940_All//sp|P0AFW2|RMF_ECOL1//4.00E-23//Ribosome modulation factor OS=Escherichia coli (strain K12) GN=rmf PE=1 SV=1						swissprot +
Unigene63942_All	314	0.00	2.74	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.94E-05	Up	9.99E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene63942_All//sp|Q24574|UBPE_DROME//4.00E-26//Ubiquitin carboxyl-terminal hydrolase 64E OS=Drosophila melanogaster GN=Ubp64E PE=1 SV=2						swissprot +
Unigene6395_All	533	54.48	38.12	36.37	20.19	8.59	38.64	0.32	1.96	2.69	-5.15E-01	2.65E-07		-5.83E-01	1.64E-08		-1.23E+00	8.19E-14	Down	9.37E-01	9.95E-15		2.63E+00	2.85E-04	Up	3.08E+00	1.21E-06	Up	Unigene6395_All//gi|21322711|emb|CAB22154.1|//5.00E-49//pherophorin-dz1 protein [Volvox carteri f. nagariensis]		Unigene6395_All//2.00E-43//gi|57901405|gb|CB066465.1|CB066465		ko03040|Spliceosome		nr +
Unigene6396_All	422	2.48	92.21	1.39	6.02	5.30	23.22	3.21	7.63	20.01	5.22E+00	2.30E-191	Up	-8.37E-01	2.34E-01		-1.83E-01	6.66E-01		1.95E+00	5.77E-21	Up	1.25E+00	8.04E-05	Up	2.64E+00	1.23E-30	Up	Unigene6396_All//gi|115478186|ref|NP_001062688.1|//1.00E-14//0s09g0253000 [Oryza sativa Japonica Group] >gi|2642217|gb|AAB86939.1| NOI protein [Oryza sativa] >gi|47848486|dbj|BAD22341.1| NOI protein [Oryza sativa Japonica Group] >gi|113630921|dbj|BAF24602.1| 0s09g0253000 [Oryza sativa Japonica Group]	Unigene6396_All//3.00E-13//AT5G55850| NOI	Unigene6396_All//0.00E+00//gi|109880397|gb|DW509367.1|DW509367		ko04626|Plant-pathogen interaction		nr +
Unigene63963_All	348	0.00	3.79	3.21	0.00	0.00	0.00	0.00	0.00	0.23	1.19E+01	1.49E-07	Up	1.16E+01	3.42E-06	Up	null	null		null	null		null	null		7.84E+00	4.02E-01		Unigene63963_All//gi|298707862|emb|CBJ30268.1|//1.00E-09//fructose-1,6-bisphosphate aldolase [Ectocarpus siliculosus]	Unigene63963_All//1.00E-08//AT3G52930| fructose-bisphosphate aldolase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene6397_All	290	64.77	33.37	32.87	99.11	90.48	105.28	148.86	70.04	59.21	-9.57E-01	3.16E-13		-9.79E-01	4.15E-13		-1.31E-01	2.49E-01		8.70E-02	4.83E-01		-1.09E+00	3.77E-44	Down	-1.33E+00	3.48E-62	Down	Unigene6397_All//gi|87241572|gb|AB033430.1|//3.00E-49//Translation protein SHS-like [Medicago truncatula]	Unigene6397_All//3.00E-50//AT4G36130| 60S ribosomal protein L8 (RPL8C)	Unigene6397_All//6.00E-163//TC163742		ko03010|Ribosome		nr +
Unigene63976_All	215	0.49	0.71	0.00	0.46	0.96	0.21	6.88	7.39	0.93	5.39E-01	7.78E-01		-8.93E+00	3.89E-01		1.05E+00	6.12E-01		-1.14E+00	6.75E-01		1.02E-01	8.34E-01		-2.89E+00	1.35E-06	Down				Unigene63976_All//6.00E-48//TC162706				
Unigene6398_All	1081	0.19	1.45	0.54	3.41	8.73	18.38	15.37	62.71	53.40	2.91E+00	1.58E-05	Up	1.48E+00	1.53E-01		1.36E+00	2.97E-13	Up	2.43E+00	2.58E-55	Up	2.03E+00	5.83E-172	Up	1.80E+00	5.04E-127	Up	Unigene6398_All//gi|194579021|gb|AF75514.1|//9.00E-31//At3g11690 [Arabidopsis thaliana]	Unigene6398_All//2.00E-10//AT3G11690| unknown protein	Unigene6398_All//2.00E-17//TC146993				nr +
Unigene6399_All	544	1.92	4.10	1.96	5.04	2.85	3.65	4.35	2.15	1.46	1.09E+00	1.21E-02		2.54E-02	9.89E-01		-8.22E-01	2.23E-02		-4.63E-01	2.45E-01		-1.02E+00	6.18E-03		-1.57E+00	3.57E-05	Down				Unigene6399_All//8.00E-28//AI055465				
Unigene64009_All	327	0.00	8.99	3.91	0.00	0.00	0.00	0.13	0.13	0.00	1.31E+01	1.01E-16	Up	1.19E+01	4.68E-07	Up	null	null		null	null		-1.68E-02	1.00E+00		-7.01E+00	6.07E-01		Unigene64009_All//gi|57864658|gb|AW56949.1|//8.00E-24//actin [Isochrysis galbana]	Unigene64009_All//2.00E-19//AT2G42100| actin, putative	Unigene64009_All//3.00E-14//gi|31406833|gb|CD485868.1|CD485868				nr +
Unigene6401_All	909	0.29	41.30	6.33	13.26	11.21	36.87	16.93	58.21	104.83	7.17E+00	6.01E-206	Up	4.46E+00	1.92E-25	Up	-2.42E-01	1.60E-01		1.48E+00	6.26E-48	Up	1.78E+00	7.12E-113	Up	2.63E+00	0.00E+00	Up	Unigene6401_All//gi|33324520|gb|AAQ08000.1|//9.00E-58//dehydration responsive element binding protein [Gossypium hirsutum] >gi|37727988|gb|AA043165.1| DRE binding protein 1 [Gossypium hirsutum]	Unigene6401_All//2.00E-35//AT1G46768| RAP2.1 (related to AP2 1); DNA binding / transcription factor	Unigene6401_All//0.00E+00//DW502467	AP2-EREBP			nr +
Unigene64013_All	300	0.00	5.07	1.78	0.00	0.11	0.00	0.00	0.00	0.00	1.23E+01	1.10E-08	Up	1.08E+01	4.03E-03		6.84E+00	8.23E-01		null	null		null	null		null	null		Unigene64013_All//gi|2935642|gb|AAC39372.1|//3.00E-24//Af12-amino acid [Avena fatua]	Unigene64013_All//3.00E-18//AT2G26300| GP ALPHA 1 (G PROTEIN ALPHA SUBUNIT 1); GTP binding / GTPase/ channel regulator/ signal transducer					nr -
Unigene6402_All	307	95.27	73.78	64.35	116.02	108.58	125.93	106.60	70.39	51.26	-3.69E-01	2.33E-04		-5.66E-01	3.68E-08		-9.56E-02	3.71E-01		1.18E-01	2.34E-01		-5.99E-01	1.26E-12		-1.06E+00	4.34E-33	Down				Unigene6402_All//4.00E-127//gi|21091503|gb|BQ403816.1|BQ403816				
Unigene64035_All	219	0.00	0.00	0.00	0.00	0.00	0.00	4.05	0.38	1.82	null	null		null	null		null	null		null	null		-3.41E+00	1.40E-04	Down	-1.16E+00	7.15E-02					Unigene64035_All//7.00E-54//gi|109839114|gb|DW237675.1|DW237675				
Unigene6404_All	747	1.82	0.27	1.43	7.27	3.92	4.47	1.19	0.28	0.37	-2.75E+00	1.08E-04	Down	-3.53E-01	5.65E-01		-8.92E-01	1.74E-04		-7.00E-01	5.65E-03		-2.09E+00	4.70E-03		-1.67E+00	1.33E-02		Unigene6404_All//gi|297831228|ref|XP_002883496.1|//4.00E-73//glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata] >gi|297329336|gb|EFH59755.1| glycosyltransferase family 14 protein [Arabidopsis lyrata subsp. lyrata]	Unigene6404_All//1.00E-68//AT3G24040| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	Unigene6404_All//8.00E-35//TC168843				nr +
Unigene6406_All	431	3.76	9.76	2.72	2.20	11.11	5.66	26.49	28.41	34.39	1.37E+00	1.01E-05	Up	-4.69E-01	3.87E-01		2.34E+00	6.11E-14	Up	1.37E+00	1.11E-03		1.01E-01	5.71E-01		3.77E-01	3.12E-03		Unigene6406_All//gi|297815202|ref|XP_002875484.1|//7.00E-33//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321322|gb|EFH51743.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6406_All//2.00E-33//AT5G39670| calcium-binding EF hand family protein	Unigene6406_All//0.00E+00//gi|109885980|gb|DW514950.1|DW514950		ko04626|Plant-pathogen interaction		nr -
Unigene64061_All	251	0.00	2.62	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.24E-04	Up	8.73E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene64061_All//gi|47600751|emb|CAF05588.1|//2.00E-12//dihydrolipoyl transacetylase [Euglena gracilis]	Unigene64061_All//2.00E-12//AT1G54220| dihydrolipoamide S-acetyltransferase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)		nr -
Unigene6407_All	720	4.00	21.68	3.92	3.94	11.57	6.96	32.18	43.94	43.55	2.44E+00	6.44E-41	Up	-2.80E-02	9.59E-01		1.55E+00	2.95E-14	Up	8.20E-01	2.06E-03		4.50E-01	1.36E-07		4.36E-01	2.11E-07		Unigene6407_All//gi|297805770|ref|XP_002870769.1|//8.00E-26//calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316605|gb|EFH47028.1| calcium-binding EF hand family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6407_All//2.00E-26//AT5G39670| calcium-binding EF hand family protein	Unigene6407_All//0.00E+00//gi|164348505|gb|EX165275.1|EX165275		ko04626|Plant-pathogen interaction		nr +
Unigene64076_All	380	0.00	7.60	2.10	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.97E-16	Up	1.10E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene64076_All//gi|195644804|gb|ACG41870.1|//2.00E-25//60S ribosomal protein L22-2 [Zea mays]	Unigene64076_All//3.00E-23//AT3G05560| 60S ribosomal protein L22-2 (RPL22B)			ko03010|Ribosome		nr -
Unigene6408_All	271	3.48	13.46	3.54	2.02	5.59	4.67	1.87	2.47	1.62	1.95E+00	8.05E-08	Up	2.54E-02	9.91E-01		1.47E+00	7.97E-03		1.21E+00	5.27E-02		3.98E-01	6.48E-01		-2.11E-01	7.92E-01									
Unigene64083_All	245	1.28	1.24	0.00	4.88	1.12	2.95	0.35	0.34	0.16	-4.62E-02	9.84E-01		-1.03E+01	4.88E-02		-2.12E+00	8.56E-04	Down	-7.26E-01	2.56E-01		-1.64E-02	1.01E+00		-1.09E+00	6.75E-01		Unigene64083_All//gi|115480191|ref|NP_001063689.1|//4.00E-11//0s09g0518700 [Oryza sativa Japonica Group] >gi|113631922|dbj|BAF25603.1| 0s09g0518700 [Oryza sativa Japonica Group]	Unigene64083_All//6.00E-11//AT2G43980| AtITPK4 (inositol 1,3,4-trisphosphate 5/6-kinase 4); ATP binding / catalytic/ inositol tetrakisphosphate 1-kinase/ inositol-1,3,4-trisphosphate 5/6-kinase/ magnesium ion binding	Unigene64083_All//7.00E-82//TC163090				nr +

Unigene6409_All	576	94.83	32.20	28.94	162.67	125.78	178.07	248.03	115.95	87.42	-1.56E+00	4.67E-79	Down	-1.71E+00	2.06E-87	Down	-3.71E-01	2.02E-14		1.30E-01	1.57E-02		-1.10E+00	2.19E-146	Down	-1.50E+00	1.03E-245	Down	Unigene6409_All//gi|3885884|gb|AAC78102.1|//6.00E-62//60S ribosomal protein L21 [Oryza sativa Japonica Group]	Unigene6409_All//4.00E-60//AT1G09690| 60S ribosomal protein L21 (RPL21C)	Unigene6409_All//0.00E+00//gi|13352548|gb|BG442896.1|BG442896		ko03010|Ribosome		nr +
Unigene64101_All	338	0.15	2.40	1.10	0.44	0.31	0.13	0.13	0.25	0.00	3.95E+00	7.52E-04	Up	2.83E+00	9.30E-02		-5.33E-01	7.84E-01		-1.73E+00	5.00E-01		9.83E-01	7.30E-01		-6.97E+00	6.07E-01								
Unigene64117_All	461	0.00	2.09	1.04	0.00	0.15	0.00	0.00	0.00	0.00	1.10E+01	1.38E-05	Up	1.00E+01	7.46E-03		7.22E+00	6.05E-01		null	null		null	null		null	null		Unigene64117_All//gi|297848236|ref|XP_002891999.1|//3.00E-12//emp24/gp25L/p24 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297337841|gb|EFH68258.1| emp24/gp25L/p24 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene64117_All//6.00E-13//AT1G37620| emp24/gp25L/p24 family protein				nr +
Unigene6412_All	1528	0.00	1.03	0.31	17.64	4.60	4.79	2.55	6.37	0.13	1.00E+01	5.70E-09	Up	8.29E+00	7.46E-03		-1.94E+00	1.11E-66	Down	-1.88E+00	1.93E-55	Down	1.32E+00	4.01E-14	Up	-4.29E+00	2.91E-22	Down	Unigene6412_All//gi|15219123|ref|NF_173607.1|//1.00E-119//nodulin MtN21 family protein [Arabidopsis thaliana]	Unigene6412_All//1.00E-114//AT1G21890| nodulin MtN21 family protein	Unigene6412_All//2.00E-24//TC150784				nr -
Unigene6413_All	628	48.32	115.54	64.95	20.94	19.69	18.27	29.89	44.32	23.98	1.26E+00	1.62E-75	Up	4.27E-01	6.48E-07		-8.92E-02	6.16E-01		-1.97E-01	2.60E-01		5.68E-01	5.89E-10		-3.18E-01	4.62E-03		Unigene6413_All//gi|297606535|ref|NP_001058612.2|//6.00E-14//Os06g0724400 [Oryza sativa Japonica Group] >gi|255677412|dbj|BAF20526.2| Os06g0724400 [Oryza sativa Japonica Group]	Unigene6413_All//1.00E-15//AT5G27280| zinc finger (DNL type) family protein	Unigene6413_All//0.00E+00//TC143435				nr +
Unigene6414_All	503	0.62	3.12	1.16	5.25	3.42	3.50	1.43	1.91	1.50	2.32E+00	1.67E-04	Up	9.00E-01	3.77E-01		-6.17E-01	1.03E-01		-5.84E-01	1.43E-01		4.19E-01	5.31E-01		7.46E-02	9.33E-01		Unigene6414_All//gi|255583115|ref|XP_002532324.1|//2.00E-06//oxysterol binding protein, putative [Ricinus communis] >gi|223527967|gb|EEF30051.1| oxysterol binding protein, putative [Ricinus communis]		Unigene6414_All//1.00E-41//TC173548				nr +
Unigene6416_All	1357	0.15	0.67	0.31	0.40	0.43	0.37	2.84	3.60	47.79	2.12E+00	1.04E-02		1.03E+00	3.96E-01		9.54E-02	9.50E-01		-1.41E-01	8.85E-01		3.46E-01	1.77E-01		4.08E+00	0.00E+00	Up	Unigene6416_All//gi|297609598|ref|NP_001063402.2|//3.00E-86//Os09g0462400 [Oryza sativa Japonica Group] >gi|255678957|dbj|BAF25316.2| Os09g0462400 [Oryza sativa Japonica Group]	Unigene6416_All//1.00E-66//AT2G26560| PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	Unigene6416_All//0.00E+00//TC144881				nr +
Unigene6417_All	1715	0.73	0.41	0.68	0.84	0.96	0.37	4.71	1.24	3.32	-8.24E-01	1.69E-01		-1.00E-01	8.66E-01		1.94E-01	7.64E-01		-1.19E+00	3.43E-02		-1.92E+00	9.43E-20	Down	-5.03E-01	4.40E-03		Unigene6417_All//gi|224071947|ref|XP_002303599.1|//0.00E+00//tir-nbs resistance protein [Populus trichocarpa] >gi|222841031|gb|EEE78578.1| tir-nbs resistance protein [Populus trichocarpa]	Unigene6417_All//0.00E+00//AT4G23440| nucleoside-triphosphatase/ nucleotide binding / transmembrane receptor	Unigene6417_All//4.00E-88//DR453777				nr -
Unigene64194_All	226	0.00	2.91	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene64194_All//gi|12644436|sp|Q43743.2|MDHG1_BRANA//2.00E-28//RecName: Full=Malate dehydrogenase 1, glyoxysomal; Flags: Precursor >gi|4995089|emb|CAB43994.1| malate dehydrogenase 1 [Brassica napus]	Unigene64194_All//3.00E-29//AT5G09660| PMDH2 (peroxisomal NAD-malate dehydrogenase 2); malate dehydrogenase	Unigene64194_All//4.00E-12//ES819715		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene642_All	919	2.22	1.65	1.16	3.36	2.70	3.54	5.61	2.36	3.77	-4.25E-01	3.64E-01		-9.38E-01	4.84E-02		-3.17E-01	4.02E-01		7.43E-02	8.55E-01		-1.25E+00	3.08E-07	Down	-5.74E-01	1.17E-02		Unigene642_All//gi|23326688|ref|NP_568213.2|//1.00E-134//KUP7: potassium ion transmembrane transporter [Arabidopsis thaliana] >gi|38503183|sp|Q9FT75.2|POT7_ARATH RecName: Full=Potassium transporter 7; Short=AtPOT7; Short=AtHAK7	Unigene642_All//9.00E-110//AT5G09400| KUP7; potassium ion transmembrane transporter	Unigene642_All//0.00E+00//gi|48821302|gb|CO122615.1|CO122615				nr -
Unigene6420_All	454	1.50	3.13	2.46	9.22	5.16	3.18	22.26	15.56	15.27	1.06E+00	6.14E-02		7.17E-01	2.87E-01		-8.38E-01	2.58E-03		-1.53E+00	6.07E-07	Down	-5.17E-01	1.29E-03		-5.44E-01	4.81E-04		Unigene6420_All//gi|156601584|gb|ABL86872.1|//3.00E-06//dehydrate responsive element-binding protein [Populus euphratica]		Unigene6420_All//6.00E-164//TC154256				nr -
Unigene64200_All	607	0.00	7.85	2.37	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	3.82E-27	Up	1.12E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene64200_All//sp|P15364|AMAL_DROME//2.00E-62//Protein amalgam OS=Drosophila melanogaster GN=Ama PE=1 SV=2						swissprot -
Unigene64208_All	462	0.00	1.65	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	1.76E-04	Up	9.85E+00	1.38E-02		null	null		null	null		null	null		null	null								
Unigene6421_All	234	47.85	14.51	26.63	69.40	60.04	60.02	105.70	33.04	42.39	-1.72E+00	3.27E-19	Down	-8.46E-01	1.79E-06		-2.09E-01	1.56E-01		-2.09E-01	1.70E-01		-1.68E+00	5.36E-49	Down	-1.32E+00	1.60E-35	Down	Unigene6421_All//gi|192913024|gb|ACF06620.1|//6.00E-20//ribosomal protein S14 [Elaeis guineensis]	Unigene6421_All//8.00E-19//AT3G52580| 40S ribosomal protein S14 (RPS14C)	Unigene6421_All//1.00E-126//gi|11201583|gb|BF270492.1|BF270492		ko03010|Ribosome		nr +
Unigene64217_All	215	3.16	3.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6.06E-02	9.57E-01		-1.16E+01	7.63E-04	Down	null	null		null	null		null	null		null	null								
Unigene6422_All	399	17.57	64.89	41.77	19.85	26.67	22.41	17.27	45.15	84.37	1.88E+00	6.43E-49	Up	1.25E+00	4.33E-17	Up	4.26E-01	1.30E-02		1.75E-01	4.42E-01		1.39E+00	3.03E-27	Up	2.29E+00	1.32E-101	Up	Unigene6422_All//gi|224059180|ref|XP_002299755.1|//8.00E-09//predicted protein [Populus trichocarpa] >gi|118487551|gb|ABK95602.1| unknown [Populus trichocarpa] >gi|222847013|gb|EEE84560.1| predicted protein [Populus trichocarpa]	Unigene6422_All//1.00E-65//AT1G52565| unknown protein	Unigene6422_All//5.00E-127//DN802534				nr +
Unigene64220_All	301	0.00	1.18	2.30	0.00	0.00	0.00	0.00	0.00	0.00	1.02E+01	2.45E-02		1.12E+01	6.15E-04	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene6423_All	1057	0.20	1.20	1.46	1.41	1.37	0.77	1.44	2.06	1.77	2.60E+00	3.59E-04	Up	2.88E+00	3.60E-05	Up	-4.72E-02	9.23E-01		-8.78E-01	1.13E-01		5.14E-01	2.02E-01		2.99E-01	4.92E-01		Unigene6423_All//gi|115480523|ref|NP_001063855.1|//2.00E-30//Os09g0548400 [Oryza sativa Japonica Group] >gi|50725113|dbj|BAD33730.1| flavin containing monooxygenase 3 -like [Oryza sativa Japonica Group] >gi|113632088|dbj|BAF25769.1| Os09g0548400 [Oryza sativa Japonica Group]	Unigene6423_All//1.00E-13//AT1G19250| FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase	Unigene6423_All//1.00E-37//TC138990				nr +
Unigene6424_All	694	0.83	0.44	1.53	13.28	8.29	4.16	15.78	5.84	66.93	-9.21E-01	3.43E-01		8.88E-01	2.06E-01		-6.80E-01	1.04E-04		-1.67E+00	1.93E-16	Down	-1.43E+00	9.67E-18	Down	2.08E+00	1.27E-124	Up	Unigene6424_All//gi|18202915|sp|Q9FS10.1|PSK_ASPOF//5.00E-09//RecName: Full=Phytosulfokines; Contains: RecName: Full=Phytosulfokine-alpha; Short=PSK-alpha; Short=Phytosulfokine-a; Contains: RecName: Full=Phytosulfokine-beta; Short=PSK-beta; Short=Phytosulfokine-b; Flags: Precursor >gi|12982023|dbj|BAB20706.1| preprophytosulfokine [Asparagus officinalis]	Unigene6424_All//3.00E-05//AT4G37720| ATPSK6 (PHYTOSULFOKINE 6 PRECURSOR); growth factor	Unigene6424_All//2.00E-13//TC168245				nr -
Unigene6425_All	792	17.84	7.36	12.64	7.93	28.96	33.30	0.00	0.00	0.00	-1.28E+00	1.03E-15	Down	-4.97E-01	1.36E-03		1.87E+00	4.72E-50	Up	2.07E+00	2.58E-60	Up	null	null		null	null		Unigene6425_All//gi|19715593|gb|AAL91620.1|//1.00E-47//AT5g01740/T20L15_10 [Arabidopsis thaliana] >gi|48310614|gb|AAT41853.1| At5g01740 [Arabidopsis thaliana]	Unigene6425_All//8.00E-49//AT5G01740| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 9 growth stages; CONTAINS InterPro DOMAIN/s: Wound-induced protein, Wun1 (InterPro:IPR009798); BEST Arabidopsis thaliana protein match is: SAG20 (SENESCENCE ASSOCIATED GENE 20) (TAIR:AT3G10985.1); Has 49 Blast hits to 49 proteins in 12 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene64250_All	819	0.00	3.84	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.07E-18	Up	1.00E+01	9.01E-05	Up	null	null		null	null		null	null		null	null		Unigene64250_All//gi|30682626|ref|NP_193123.2|//5.00E-15//WRNEXO (WERNER SYNDROME-LIKE EXONUCLEASE); 3'-5' exonuclease/ nucleic acid binding / protein binding [Arabidopsis thaliana] >gi|11121455|emb|CAC14871.1| exonuclease [Arabidopsis thaliana]	Unigene64250_All//2.00E-16//AT4G13870| WRNEXO (WERNER SYNDROME-LIKE EXONUCLEASE); 3'-5' exonuclease/ nucleic acid binding / protein binding					nr +
Unigene64254_All	628	0.17	0.08	0.34	0.24	0.93	0.50	1.75	0.13	0.00	-1.05E+00	6.83E-01		1.03E+00	5.90E-01		1.97E+00	7.03E-02		1.08E+00	4.76E-01		-3.72E+00	7.15E-06	Down	-1.08E+01	3.33E-08	Down	Unigene64254_All//gi|209976078|gb|ACJ04883.1|//8.00E-84//cyclopropyl isomerase [Solanum lycopersicum]	Unigene64254_All//0.00E+00//AT5G50375| CPI1 (CYCLOPROPYL ISOMERASE); cycloeucalenol cycloisomerase	Unigene64254_All//0.00E+00//gi|164360110|gb|ES833819.1|ES833819		ko00100|Steroid biosynthesis		nr +
Unigene64256_All	338	0.00	4.35	2.05	0.00	0.00	0.00	0.13	0.00	0.00	1.21E+01	2.11E-08	Up	1.10E+01	6.15E-04	Up	null	null		null	null		-6.97E+00	6.50E-01		-6.97E+00	6.07E-01		Unigene64256_All//gi|60543060|dbj|BAD90779.1|//2.00E-36//histone 3 [Conocephalum conicum]	Unigene64256_All//4.00E-24//AT5G10980| histone H3	Unigene64256_All//2.00E-08//BF279440				nr -
Unigene6427_All	320	8.18	5.38	4.16	5.14	4.52	7.90	34.75	20.90	4.98	-6.03E-01	1.22E-01		-9.75E-01	1.76E-02		-1.85E-01	7.46E-01		6.22E-01	1.34E-01		-7.34E-01	1.46E-06		-2.80E+00	2.08E-43	Down	Unigene6427_All//gi|73245585|sp|Q8LA47.1|PSB2B_ARATH//3.00E-06//RecName: Full=Proteasome subunit alpha type-2-B; AltName: Full=20S proteasome alpha subunit B-2 >gi|20453128|gb|AAM19806.1| At1g79210/YUP8H12R_1 [Arabidopsis thaliana] >gi|216898609|gb|AAW67426.1| At1g79210/YUP8H12R_1 [Arabidopsis thaliana]	Unigene6427_All//1.00E-07//AT1G79210| 20S proteasome alpha subunit B, putative	Unigene6427_All//7.00E-172//gi|164370314|gb|ES841482.1|ES841482		ko03050|Proteasome		nr +
Unigene6428_All	889	60.74	442.57	172.69	28.30	62.32	86.72	0.00	0.00	0.31	2.87E+00	0.00E+00	Up	1.51E+00	1.00E-204	Up	1.14E+00	1.62E-58	Up	1.62E+00	2.26E-125	Up	null	null		8.29E+00	2.43E-02		Unigene6428_All//gi|117957143|gb|ABR58040.1|//1.00E-54//R2R3 Myb30 transcription factor [Vitis vinifera]	Unigene6428_All//9.00E-33//AT1G74650| MYB31 (MYB DOMAIN PROTEIN 31); DNA binding / transcription factor	Unigene6428_All//5.00E-135//gi|164357473|gb|EV484170.1|EV484170	MYB			nr +
Unigene64281_All	511	2.97	0.99	0.31	3.12	2.63	1.94	0.17	0.16	0.23	-1.58E+00	5.32E-03		-3.25E+00	1.40E-05	Down	-2.47E-01	6.36E-01		-6.82E-01	2.07E-01		-1.67E-02	1.01E+00		4.99E-01	8.07E-01		Unigene64281_All//gi|18400719|ref|NP_565584.1|//6.00E-31//ribonuclease HII family protein [Arabidopsis thaliana] >gi|49086054|sp|Q8SE26.2|RNH2A_ARATH RecName: Full=Ribonuclease H2 subunit A; Short=RNase H2 subunit A; AltName: Full=Ribonuclease HI subunit A; AltName: Full=Ribonuclease HI large subunit; Short=RNase HI large subunit	Unigene64281_All//2.00E-32//AT2G25100| ribonuclease HII family protein	Unigene64281_All//3.00E-104//TC152575		ko03030|DNA replication		nr -

Unigene64300_All	441	0.24	0.46	0.00	0.23	0.16	0.20	2.30	0.09	0.27	9.54E-01	6.20E-01		-7.89E+00	3.89E-01		-5.32E-01	8.14E-01		-1.42E-01	9.48E-01		-4.60E+00	3.67E-06	Down	-3.09E+00	5.36E-05	Down	Unigene64300_All//gi|15146292|gb|AK83629.1|//3.00E-57//AT5g41970/MJC20_7 [Arabidopsis thaliana] >gi|19699166|gb|AAL90949.1|AT5g41970/MJC20_7 [Arabidopsis thaliana]	Unigene64300_All//1.00E-58//AT5G41970| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Metal-dependent protein hydrolase (InterPro:IPR003226); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G49320.1); Has 464 Blast hits to 461 proteins in 209 species: Archae - 0; Bacteria - 122; Metazoa - 131; Fungi - 87; Plants - 29; Viruses - 0; Other Eukaryotes - 95 (source: NCBI BLink).	Unigene64300_All//0.00E+00//gi|21090700|gb|BQ403013.1|BQ403013				nr -
Unigene64303_All	329	0.00	4.93	2.75	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.96E-09	Up	1.14E+01	4.71E-05	Up	null	null		null	null		null	null		null	null		Unigene64303_All//sp|P49716|CEBPD_HUMAN//6.00E-21//CCAAT/enhancer-binding protein delta OS=Homo sapiens GN=CEBPD PE=1 SV=2							swissprot +
Unigene64306_All	416	2.01	0.37	0.00	1.56	1.82	2.61	0.71	0.20	0.10	-2.46E+00	6.70E-03		-1.10E+01	1.19E-04	Down	2.26E-01	8.32E-01		7.43E-01	2.89E-01		-1.82E+00	2.10E-01		-2.89E+00	6.76E-02		Unigene64306_All//gi|7673355|gb|AAF66823.1|AF190655_1//5.00E-22//poly(A)-binding protein [Nicotiana tabacum]	Unigene64306_All//8.00E-19//AT4G34110| PAB2 (POLY(A) BINDING 2); RNA binding / translation initiation factor	Unigene64306_All//4.00E-128//TC151680				nr +
Unigene6431_All	559	6.65	4.08	7.72	21.48	21.07	18.42	7.41	2.84	5.49	-7.04E-01	2.64E-02		2.16E-01	5.06E-01		-2.77E-02	8.82E-01		-2.21E-01	2.23E-01		-1.38E+00	7.30E-07	Down	-4.34E-01	9.88E-02						Unigene6431_All//1.00E-23//TC174120				
Unigene6433_All	565	1.39	1.97	5.28	4.06	3.47	3.04	1.80	1.85	1.62	5.06E-01	4.22E-01		1.93E+00	3.87E-06	Up	-2.23E-01	6.06E-01		-4.17E-01	3.62E-01		4.23E-02	9.70E-01		-1.47E-01	7.92E-01										
Unigene64349_All	395	0.00	4.10	2.83	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.96E-09	Up	1.15E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene64349_All//sp|Q27415|NLP_DROME//1.00E-35//Nucleoplasmin-like protein OS=Drosophila melanogaster GN=Nlp PE=1 SV=1							swissprot +
Unigene6435_All	856	0.00	1.30	0.75	1.69	1.81	1.42	1.14	1.22	2.65	1.03E+01	2.00E-06	Up	9.54E+00	1.16E-03		1.01E-01	8.69E-01		-2.45E-01	6.84E-01		1.04E-01	8.68E-01		1.22E+00	1.15E-03		Unigene6435_All//gi|186511352|ref|NP_191849.2|//9.00E-28//zinc ion binding [Arabidopsis thaliana]	Unigene6435_All//6.00E-26//AT3G62900| zinc ion binding	Unigene6435_All//0.00E+00//ES798337				nr +
Unigene64360_All	215	0.00	3.30	0.74	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	9.54E+00	2.38E-01		null	null		null	null		null	null		null	null											
Unigene64361_All	378	0.00	3.22	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	5.47E-07	Up	9.46E+00	7.99E-02		null	null		null	null		null	null		null	null											ESTscan -
Unigene64372_All	485	0.00	3.66	2.31	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.14E-10	Up	1.12E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene64372_All//gi|299116090|emb|CBV74506.1|//4.00E-09//Glutathione S-transferase [Ectocarpus siliculosus]				ko00590|Arachidonic acid metabolism		nr +
Unigene6438_All	1482	0.07	51.76	0.79	0.00	0.81	3.50	0.00	0.76	1.29	9.52E+00	0.00E+00	Up	3.49E+00	1.09E-04	Up	9.67E+00	1.95E-07	Up	1.18E+01	2.04E-31	Up	9.57E+00	5.32E-08	Up	1.03E+01	1.02E-13	Up	Unigene6438_All//gi|119127|sp|P20075.1|LEAD8_DAUCA//8.00E-87//RecName: Full=Embryonic protein DC-8 >gi|9952464|emb|CAA34258.2|embryo-specific protein 66kDa [Daucus carota]	Unigene6438_All//9.00E-53//AT3G53040| late embryogenesis abundant protein, putative / LEA protein, putative					nr -
Unigene6439_All	436	12.24	1.98	2.56	19.42	13.27	10.46	3.98	2.20	0.46	-2.63E+00	9.17E-16	Down	-2.25E+00	1.19E-12	Down	-5.50E-01	3.32E-03		-8.93E-01	4.72E-06		-8.51E-01	5.62E-02		-3.12E+00	3.99E-08	Down	Unigene6439_All//gi|225447276|ref|XP_002272269.1|//2.00E-15//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene6439_All//9.00E-123//DW508119				nr +
Unigene64391_All	231	0.00	3.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null						Unigene64391_All//8.00E-20//TC152722				
Unigene64398_All	338	0.00	4.20	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.06E-08	Up	9.88E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene64398_All//gi|301116906|ref|XP_002906181.1|//2.00E-11//26S proteasome non-ATPase regulatory subunit 2 [Phytophthora infestans T30-4] >gi|262107530|gb|EEY65582.1| 26S proteasome non-ATPase regulatory subunit 2 [Phytophthora infestans T30-4]	Unigene64398_All//6.00E-09//AT2G20580| RPN1A (26S PROTEASOME REGULATORY SUBUNIT S2 1A); binding / enzyme regulator			ko03050|Proteasome		nr +
Unigene64400_All	833	0.00	4.01	2.11	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.94E-19	Up	1.10E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene64400_All//sp|P06996|OMPC_ECOLI//2.00E-123//Outer membrane protein C OS=Escherichia coli (strain K12) GN=ompC PE=1 SV=1						swissprot -
Unigene64401_All	440	0.00	1.84	1.69	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	9.37E-05	Up	1.07E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene64401_All//gi|115479005|ref|NP_001063096.1|//3.00E-12//Os09g0394900 [Oryza sativa Japonica Group] >gi|113631329|dbj|BAF25010.1|Os09g0394900 [Oryza sativa Japonica Group]	Unigene64401_All//4.00E-12//AT1G68090| ANN5; calcium ion binding / calcium-dependent phospholipid binding					nr +
Unigene64419_All	208	0.00	6.33	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.49E-07	Up	8.00E+00	6.32E-01		null	null		null	null		null	null		null	null		Unigene64419_All//sp|Q3B7N2|ACTN1_BOVIN//1.00E-19//Alpha-actinin-1 OS=Bos taurus GN=ACTN1 PE=2 SV=1						swissprot +
Unigene6442_All	274	56.71	33.29	35.95	81.08	72.01	97.58	70.52	24.10	32.42	-7.69E-01	6.89E-08		-6.58E-01	6.95E-06		-1.71E-01	1.73E-01		2.67E-01	1.33E-02		-1.55E+00	2.41E-34	Down	-1.12E+00	7.83E-22	Down	Unigene6442_All//gi|24817256|emb|CAD56220.1|//2.00E-23//ribosomal protein RL5 [Cicer arietinum]	Unigene6442_All//5.00E-24//AT5G45775| 60S ribosomal protein L11 (RPL11D)	Unigene6442_All//6.00E-132//TC139502		ko03010|Ribosome		nr +
Unigene6444_All	280	21.30	14.30	11.22	31.13	28.41	27.26	157.04	79.71	72.42	-5.75E-01	1.77E-02		-9.25E-01	2.70E-04		-1.32E-01	5.66E-01		-1.92E-01	3.89E-01		-9.78E-01	6.57E-38		-1.12E+00	3.04E-48	Down			Unigene6444_All//4.00E-139//gi|21090283|gb|BQ402596.1|BQ402596				
Unigene64441_All	400	0.00	5.70	1.60	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.63E-13	Up	1.06E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene64441_All//sp|Q9VCA8|ANKIM_DROME//3.00E-06//Ankyrin repeat and KH domain-containing protein mask OS=Drosophila melanogaster GN=mask PE=1 SV=2						swissprot +
Unigene64471_All	271	0.00	5.05	0.39	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.79E-08	Up	8.62E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene64471_All//sp|Q94901|LARK_DROME//4.00E-38//RNA-binding protein lark OS=Drosophila melanogaster GN=lark PE=1 SV=1	Unigene64471_All//2.00E-05//AT3G61860| RSF31; RNA binding / nucleic acid binding / nucleotide binding					swissprot -
Unigene64477_All	211	0.00	5.04	1.01	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.81E-06	Up	9.98E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene64477_All//gi|255593650|ref|XP_002535920.1|//8.00E-08//alpha-amylase, putative [Ricinus communis] >gi|223521525|gb|EEF26463.1|alpha-amylase, putative [Ricinus communis]				GO:0016787		nr -
Unigene6449_All	422	182.13	36.50	56.53	147.08	104.29	70.85	162.01	52.89	63.44	-2.32E+00	2.38E-189	Down	-1.69E+00	2.05E-120	Down	-4.96E-01	2.47E-16		-1.05E+00	3.95E-53	Down	-1.62E+00	4.24E-127	Down	-1.35E+00	1.50E-100	Down	Unigene6449_All//gi|134035494|gb|AB047735.1|//5.00E-79//alpha-tubulin [Gossypium hirsutum]	Unigene6449_All//1.00E-78//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene6449_All//0.00E+00//TC166585		ko04145|Phagosome		nr +
Unigene645_All	2152	0.07	0.28	0.17	0.30	0.08	0.10	0.67	0.19	0.13	1.95E+00	6.03E-02		1.25E+00	3.65E-01		-1.91E+00	3.63E-02		-1.52E+00	1.12E-01		-1.78E+00	8.40E-04	Down	-2.37E+00	2.52E-05	Down	Unigene645_All//gi|22326688|ref|NP_568213.2|//0.00E+00//KUP7; potassium ion transmembrane transporter [Arabidopsis thaliana] >gi|38503183|sp|Q9FY75.2|POT7_ARATH RecName: Full=Potassium transporter 7; Short=AtPOT7; Short=AtHAK7	Unigene645_All//0.00E+00//AT5G09400| KUP7; potassium ion transmembrane transporter	Unigene645_All//0.00E+00//TC143788			GO:0016020//GO:0030001//GO:0046873	nr +
Unigene64502_All	381	4.53	1.33	1.12	2.22	2.62	1.66	1.22	1.10	0.63	-1.77E+00	1.02E-03		-2.02E+00	5.05E-04	Down	2.38E-01	7.85E-01		-4.22E-01	6.18E-01		-1.54E-01	8.70E-01		-9.60E-01	3.13E-01		Unigene64502_All//gi|283488499|gb|ADB24771.1|//6.00E-25//UDP-D-glucuronic acid 4-epimerase [Gossypium hirsutum]	Unigene64502_All//3.00E-10//AT1G02000| GAE2 (UDP-D-GLUCURONATE 4-EPIMERASE 2); UDP-glucuronate 4-epimerase/ catalytic	Unigene64502_All//3.00E-165//C0128903		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0006139//GO:0016857//GO:0044464//GO:0048037	nr +
Unigene6451_All	380	14.73	11.47	9.67	17.44	12.96	27.45	58.30	21.12	17.93	-3.62E-01	1.60E-01		-6.08E-01	2.11E-02		-4.28E-01	5.70E-02		6.55E-01	1.61E-04		-1.47E+00	3.17E-36	Down	-1.70E+00	3.26E-46	Down	Unigene6451_All//gi|54039313|sp|P62302.1|RS13_SOYBN//7.00E-36//RecName: Full=40S ribosomal protein S13 >gi|44662862|gb|AAS47510.1|ribosomal protein S13 [Glycine max] >gi|161367348|gb|ABX71080.1|ribosomal protein S13 [Glycine max]	Unigene6451_All//3.00E-34//AT4G00100| ATRPS13A (ARABIDOPSIS THALIANA RIBOSOMAL PROTEIN S13A); structural constituent of ribosome	Unigene6451_All//2.00E-157//gi|21094638|gb|BQ406951.1|BQ406951		ko03010|Ribosome		nr +
Unigene64517_All	999	0.00	4.72	1.17	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.47E-27	Up	1.02E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene64517_All//gi|301105535|ref|XP_002901851.1|//1.00E-36//villin-like protein [Phytophthora infestans T30-4] >gi|262099189|gb|EEY57241.1|villin-like protein [Phytophthora infestans T30-4]	Unigene64517_All//4.00E-24//AT2G29880| VLN1 (VILLIN-LIKE 1); actin binding / actin filament binding				GO:0008154//GO:0071822	nr +
Unigene6452_All	564	1.39	1.44	0.57	4.33	1.53	2.88	1.65	1.04	2.19	4.68E-02	9.69E-01		-1.30E+00	1.38E-01		-1.50E+00	1.20E-04	Down	-5.86E-01	1.62E-01		-6.69E-01	3.12E-01		4.09E-01	4.50E-01		Unigene6452_All//gi|297720509|ref|NP_001172616.1|//6.00E-35//Os01g0812050 [Oryza sativa Japonica Group] >gi|255673803|dbj|BAH91346.1|Os01g0812050 [Oryza sativa Japonica Group]	Unigene6452_All//7.00E-50//AT5G17910| unknown protein					nr +
Unigene64522_All	757	0.00	3.15	0.70	0.20	0.23	0.36	0.34	0.00	0.00	1.16E+01	1.50E-13	Up	9.46E+00	4.03E-03		2.04E-01	9.49E-01		8.59E-01	6.30E-01		-8.39E+00	4.03E-02		-8.39E+00	3.03E-02		Unigene64522_All//gi|5031277|gb|AAD38144.1|AF139497_1//1.00E-24//homeobox leucine zipper protein [Prunus armeniaca]	Unigene64522_All//1.00E-20//AT2G46680| ATHB-7 (ARABIDOPSIS THALIANA HOMEOBOX 7); transcription activator/ transcription factor	Unigene64522_All//0.00E+00//ES813725	HB		GO:0001071//GO:0003677//GO:0006351//GO:0006970//GO:0009755//GO:0010468//GO:0010557//GO:0030528//GO:0043231	nr +
Unigene64528_All	902	0.58	0.34	0.53	0.44	0.46	0.15	0.94	0.14	0.53	-7.84E-01	4.22E-01		-1.27E-01	8.98E-01		5.23E-02	9.89E-01		-1.56E+00	2.31E-01		-2.75E+00	9.73E-04	Down	-8.23E-01	2.07E-01		Unigene64528_All//gi|19699077|gb|AAL90906.1|//1.00E-105//AT5g28150/T24G3_80 [Arabidopsis thaliana] >gi|23308357|gb|AAN18148.1|At5g28150/T24G3_80 [Arabidopsis thaliana]	Unigene64528_All//2.00E-102//AT5G28150| unknown protein	Unigene64528_All//0.00E+00//TC170095				nr -
Unigene6453_All	449	1.75	1.81	4.74	4.22	2.45	3.92	2.54	0.56	0.89	4.69E-02	9.69E-01		1.44E+00	2.59E-03		-7.81E-01	8.46E-02		-1.04E-01	8.32E-01		-2.19E+00	6.83E-04	Down	-1.52E+00	7.91E-03										
Unigene64534_All	237	0.00	2.99	0.45	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.32E-04	Up	8.81E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene64534_All//sp|Q9V9E3|PREP_DROME//8.00E-24//Presequence protease, mitochondrial OS=Drosophila melanogaster GN=CG3107 PE=1 SV=2						swissprot -
Unigene64535_All	221	0.00	0.69	0.72	0.00	0.00	0.41	0.19	0.00	4.15	9.43E+00	2.34E-01		9.50E+00	2.38E-01		null	null		8.67E+00	4.73E-01		-7.58E+00	6.50E-01		4.44E+00	1.24E-05	Up	Unigene64535_All//gi|224087825|ref|XP_002308239.1|//6.00E-06//predicted protein [Populus trichocarpa] >gi|222854215|gb|EEE91762.1|predicted protein [Populus trichocarpa]		Unigene64535_All//7.00E-57//DV850071				nr +

Unigene6454_All	610	6.60	2.24	2.88	8.82	4.97	6.81	5.96	3.84	2.68	-1.56E+00	1.64E-06	Down	-1.20E+00	2.20E-04	Down	-8.28E-01	5.32E-04		-3.73E-01	1.73E-01		-6.36E-01	2.76E-02		-1.15E+00	5.18E-05	Down	Unigene6454_All//gi|8778812|gb|AAF79817.1|AC007396_17//3.00E-25//T4012.27 [Arabidopsis thaliana]	Unigene6454_All//2.00E-26//AT1G76065| CONTAINS InterPro DOMAIN/s: Complex I LYR protein (InterPro:IPR008011); Has 53 Blast hits to 53 proteins in 27 species: Archae - 0; Bacteria - 0; Metazoa - 32; Fungi - 9; Plants - 12; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene6454_All//0.00E+00//TC161712				nr -
Unigene64549_All	681	0.00	2.38	1.09	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.96E-09	Up	1.01E+01	3.27E-04	Up	null	null		null	null		null	null		null	null		Unigene64549_All//gi|115455029|ref|NP_001051115.1|//2.00E-07//Os03g0723000 [Oryza sativa Japonica Group] >gi|108710814|gb|ABF98609.1| GRAS family transcription factor containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113549586|dbj|BAF13029.1| Os03g0723000 [Oryza sativa Japonica Group]						nr -
Unigene6456_All	236	28.16	17.82	16.70	33.14	25.83	27.37	27.77	30.64	62.46	-6.60E-01	3.73E-03		-7.54E-01	1.48E-03		-3.60E-01	8.35E-02		-2.76E-01	2.25E-01		1.42E-01	5.38E-01		1.17E+00	7.66E-18	Up	Unigene6456_All//gi|297834370|ref|XP_002885067.1|//7.00E-21//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330907|gb|EFH61326.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6456_All//1.00E-20//AT3G15070| zinc finger (C3HC4-type RING finger) family protein	Unigene6456_All//2.00E-116//CO094649				nr -
Unigene64561_All	614	0.00	4.46	1.39	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.44E-15	Up	1.04E+01	9.01E-05	Up	null	null		null	null		null	null		null	null		Unigene64561_All//gi|149063401|gb|EDM13724.1|//1.00E-51//rCG21519, isoform CRA_a [Rattus norvegicus] >gi|149063402|gb|EDM13725.1| rCG21519, isoform CRA_a [Rattus norvegicus] >gi|149063403|gb|EDM13726.1| rCG21519, isoform CRA_a [Rattus norvegicus]	Unigene64561_All//4.00E-44//AT1G23800| ALDH2B7; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)			ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0008152//GO:0016491	nr -
Unigene6457_All	444	53.50	71.67	46.53	48.69	49.25	80.97	119.32	85.76	50.88	4.22E-01	9.76E-06		-2.01E-01	1.08E-01		1.64E-02	9.16E-01		7.34E-01	7.22E-17		-4.77E-01	1.90E-13		-1.23E+00	1.88E-67	Down	Unigene6457_All//gi|282935440|gb|AQ803785.1|//2.00E-21//deleted in split hand/split foot protein 1 [Ipomoea batatas]		Unigene6457_All//0.00E+00//gi|133548864|gb|BG445212.1|BG445212		ko03050|Proteasome//ko03440|Homologous recombination		nr +
Unigene64571_All	225	0.00	3.60	1.89	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.36E-05	Up	1.09E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene64571_All//gi|297832954|ref|XP_002884359.1|//5.00E-06//NADH:ubiquinone oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330199|gb|EFH60618.1| NADH:ubiquinone oxidoreductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene64571_All//2.00E-07//AT3G03100| NADH:ubiquinone oxidoreductase family protein			ko00190|Oxidative phosphorylation	GO:0016020	nr -
Unigene64580_All	605	0.00	2.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.06E-08	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene64583_All	216	0.00	6.10	1.23	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.49E-07	Up	1.03E+01	7.99E-02		null	null		null	null		null	null		null	null		Unigene64583_All//gi|300268586|gb|EFJ52766.1|//1.00E-16//pathogenesis-related protein 1-like protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome	GO:0005488//GO:0006259//GO:0016874//GO:0033554	nr +
Unigene64591_All	477	0.11	2.23	0.11	0.00	0.07	0.00	0.00	0.00	0.00	4.35E+00	3.95E-05	Up	2.48E-02	9.93E-01		6.17E+00	8.23E-01		null	null		null	null		null	null		Unigene64591_All//sp|O05118|KPYK_METEA//9.00E-18//Pyruvate kinase OS=Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1) GN=pyk PE=3 SV=2						swissprot +
Unigene64593_All	238	0.00	3.19	1.12	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	1.01E+01	7.99E-02		null	null		null	null		null	null		null	null		Unigene64593_All//gi|124361137|gb|ABN09109.1|//1.00E-20//Helicase, C-terminal [Medicago truncatula]	Unigene64593_All//1.00E-21//AT1G54270| EIF4A-2; ATP-dependent helicase/ translation initiation factor				GO:0008135//GO:0010467//GO:0032559//GO:0042623	nr -
Unigene6460_All	1789	2.31	0.79	2.17	2.73	5.37	3.00	0.00	0.00	0.00	-1.54E+00	1.41E-06	Down	-8.85E-02	7.76E-01		9.77E-01	3.09E-08		1.39E-01	6.42E-01		null	null		null	null		Unigene6460_All//gi|297812269|ref|XP_002874018.1|//1.00E-126//pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319855|gb|EFH50277.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6460_All//2.00E-119//AT5G20860| pectinesterase family protein	Unigene6460_All//0.00E+00//DT048710		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene64604_All	395	0.00	2.05	0.27	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	9.36E-05	Up	8.07E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene64604_All//sp|Q3Z265|RL35_SHISS//3.00E-24//50S ribosomal protein L35 OS=Shigella sonnei (strain Ss046) GN=rpmI PE=3 SV=1						swissprot +
Unigene64609_All	222	0.00	3.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.36E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene64609_All//sp|Q99AD9|RWDD1_RAT//5.00E-08//RWD domain-containing protein 1 OS=Rattus norvegicus GN=Rwdd1 PE=2 SV=1						swissprot -
Unigene64618_All	494	0.00	2.67	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.49E-07	Up	9.56E+00	2.50E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene64627_All	330	0.00	4.45	0.48	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.11E-08	Up	8.92E+00	2.38E-01		null	null		null	null		null	null		null	null		Unigene64627_All//gi|159474294|ref|XP_001695264.1|//2.00E-10//heat shock protein 90A [Chlamydomonas reinhardtii] >gi|158276198|gb|EDP01972.1| heat shock protein 90A [Chlamydomonas reinhardtii]	Unigene64627_All//8.00E-08//AT5G56010| HSP81-2; ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0006970//GO:0009408//GO:0009791//GO:0009987//GO:0016020//GO:0030312//GO:0031647//GO:0031981//GO:0032559//GO:0044444//GO:0048827//GO:0051592	nr -
Unigene64639_All	252	0.00	3.02	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	7.72E+00	6.32E-01		null	null		null	null		null	null		null	null		Unigene64639_All//sp|P49963|SRP19_DROME//2.00E-10//Signal recognition particle 19 kDa protein OS=Drosophila melanogaster GN=Srp19 PE=2 SV=2						swissprot +
Unigene6464_All	797	5.78	3.31	2.47	4.13	5.66	7.48	15.81	7.50	10.25	-8.05E-01	4.12E-03		-1.22E+00	4.69E-05	Down	4.56E-01	1.18E-01		8.59E-01	3.53E-04		-1.08E+00	3.06E-13	Down	-6.26E-01	6.03E-06		Unigene6464_All//gi|50346893|gb|AAT75153.1|//2.00E-07//short-chain dehydrogenase/reductase [Solanum tuberosum]	Unigene6464_All//6.00E-08//AT1G52340| ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase	Unigene6464_All//0.00E+00//TC143278		ko00906|Carotenoid biosynthesis		nr +
Unigene64649_All	260	0.00	2.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene64649_All//sp|Q03427|LAMC_DROME//6.00E-16//Lamin-C OS=Drosophila melanogaster GN=LamC PE=1 SV=2						swissprot +
Unigene6466_All	622	3.45	1.55	6.76	6.17	3.38	1.45	3.40	1.81	1.86	-1.16E+00	9.39E-03		9.72E-01	1.75E-03		-8.69E-01	2.99E-03		-2.09E+00	1.81E-09	Down	-9.06E-01	2.19E-02		-8.72E-01	2.17E-02			Unigene6466_All//7.00E-07//TC147261					
Unigene64660_All	251	0.00	3.84	1.06	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	1.01E+01	7.99E-02		null	null		null	null		null	null		null	null		Unigene64660_All//sp|Q5RBH3|BAP31_PONAB//9.00E-09//B-cell receptor-associated protein 31 OS=Pongo abelii GN=BCAP31 PE=2 SV=3						swissprot -
Unigene6467_All	1278	0.25	0.28	0.33	0.78	0.59	0.99	1.82	4.22	5.42	1.76E-01	8.83E-01		4.41E-01	6.77E-01		-3.95E-01	5.73E-01		3.44E-01	6.24E-01		1.21E+00	3.10E-07	Up	1.58E+00	2.02E-13	Up	Unigene6467_All//gi|239056189|emb|CAQ58626.1|//1.00E-145//Serine-threonine phosphatase type 1 [Vitis vinifera]	Unigene6467_All//3.00E-129//AT4G11240| TOPP7; protein serine/threonine phosphatase	Unigene6467_All//9.00E-36//ES791190				nr -
Unigene64696_All	354	0.00	2.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	9.36E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene64696_All//sp|P54939|TLN1_CHICK//4.00E-09//Talin-1 OS=Gallus gallus GN=TLN1 PE=1 SV=2						swissprot +
Unigene64697_All	216	0.00	3.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene647_All	1127	47.21	41.99	62.27	53.00	40.52	19.20	8.70	4.97	8.87	-1.69E-01	2.62E-02		3.99E-01	3.67E-10		-3.87E-01	4.05E-10		-1.47E+00	1.21E-85	Down	-8.09E-01	8.20E-07		2.78E-02	8.88E-01		Unigene647_All//gi|19352051|dbj|BAB85919.1|//3.00E-09//auxin response factor 10 [Oryza sativa]	Unigene647_All//2.00E-54//AT4G30080| ARF16 (AUXIN RESPONSE FACTOR 16); miRNA binding / transcription factor	Unigene647_All//0.00E+00//TC145966	ARF		GO:0005488//GO:0006350//GO:0009725//GO:0010468	nr +
Unigene64700_All	208	0.00	7.80	5.63	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.96E-09	Up	1.25E+01	1.77E-06	Up	null	null		null	null		null	null		null	null									
Unigene64701_All	713	0.00	2.70	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	5.73E-11	Up	7.22E+00	3.96E-01		null	null		null	null		null	null		null	null		Unigene64701_All//gi|300120494|emb|CBK20048.2|//7.00E-08//unnamed protein product [Blastocystis hominis]						nr +
Unigene64713_All	668	2.58	0.61	1.43	1.94	1.65	0.74	1.14	0.25	0.42	-2.09E+00	1.98E-04	Down	-8.49E-01	1.05E-01		-2.33E-01	7.04E-01		-1.38E+00	2.29E-02		-2.19E+00	7.77E-03		-1.45E+00	4.46E-02		Unigene64713_All//gi|127519383|gb|AB028526.1|//1.00E-22//glutamate receptor [Malus hupehensis]	Unigene64713_All//4.00E-12//AT2G17260| GLR2 (GLUTAMATE RECEPTOR 2); intracellular ligand-gated ion channel	Unigene64713_All//1.00E-21//TC164303			GO:0005216//GO:0006810//GO:0006875//GO:0008066//GO:0009314//GO:0016020	nr +
Unigene6472_All	408	15.39	4.72	4.05	41.27	24.64	32.54	77.62	22.95	32.42	-1.71E+00	5.93E-11	Down	-1.93E+00	3.24E-12	Down	-7.44E-01	2.11E-09		-3.43E-01	1.25E-02		-1.76E+00	9.56E-67	Down	-1.26E+00	3.32E-42	Down	Unigene6472_All//gi|17367847|sp|Q9XF97.1|RL4_PRUAR//2.00E-13//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32206.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene6472_All//4.00E-14//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)	Unigene6472_All//0.00E+00//gi|21100184|gb|BQ412497.1|BQ412497		ko03010|Ribosome		nr +
Unigene64727_All	444	2.47	2.17	5.16	3.03	2.48	0.51	0.00	0.09	0.00	-1.91E-01	7.45E-01		1.06E+00	1.72E-02		-2.88E-01	6.12E-01		-2.57E+00	1.41E-04	Down	6.56E+00	6.30E-01		null	null		Unigene64727_All//gi|62751057|dbj|BAD95789.1|//4.00E-10//LSD-One-Like 1 [Brassica rapa]	Unigene64727_All//3.00E-11//AT1G32540| LOL1 (LSD ONE LIKE 1); DNA binding	Unigene64727_All//2.00E-151//TC145771			GO:0012502	nr +
Unigene64731_All	228	0.00	4.00	0.93	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.61E-05	Up	9.87E+00	1.40E-01		null	null		null	null		null	null		null	null									
Unigene6474_All	704	3.42	6.98	2.50	4.39	2.15	1.99	21.14	24.88	9.51	1.03E+00	1.81E-04	Up	-4.54E-01	3.02E-01		-1.03E+00	2.00E-03		-1.14E+00	1.26E-03		2.35E-01	6.13E-02		-1.15E+00	9.15E-18	Down	Unigene6474_All//gi|15228792|ref|NP_188895.1|//4.00E-46//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|119942288|dbj|BAB01471.1| alanine acetyl transferase-like protein [Arabidopsis thaliana] >gi|124301058|gb|ABN04781.1| At3g22560 [Arabidopsis thaliana]	Unigene6474_All//2.00E-36//AT3G22560| GCN5-related N-acetyltransferase (GNAT) family protein					nr +
Unigene6475_All	543	0.39	0.84	2.16	1.93	2.28	2.25	3.89	2.00	1.54	1.12E+00	3.28E-01		2.48E+00	1.35E-03		2.45E-01	7.39E-01		2.21E-01	7.22E-01		-9.60E-01	1.53E-02		-1.34E+00	6.80E-04	Down	Unigene6475_All//gi|297838857|ref|XP_002887310.1|//6.00E-10//hypothetical protein ARALYDRAFT_894871 [Arabidopsis lyrata subsp. lyrata] >gi|297333151|gb|EFH63569.1| hypothetical protein ARALYDRAFT_894871 [Arabidopsis lyrata subsp. lyrata]	Unigene6475_All//4.00E-11//AT1G70570| anthranilate phosphoribosyltransferase, putative	Unigene6475_All//5.00E-63//DR454687				nr -

Unigene64753_All	641	0.00	2.69	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	7.98E-10	Up	8.70E+00	7.99E-02		null	null		null	null		null	null		null	null		Unigene64753_All//gi|300265661|gb|EFJ49851.1|//1.00E-08//hypothetical protein VOLCADRAFT_58884 [Volvox carteri f. nagariensis]						nr -
Unigene64758_All	380	0.00	4.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.98E-10	Up	null	null		null	null		null	null		null	null		null	null									
Unigene6476_All	707	152.15	390.95	223.54	126.90	155.96	171.39	197.47	325.20	195.47	1.36E+00	0.00E+00	Up	5.55E-01	5.88E-40		2.98E-01	4.02E-11		4.34E-01	6.47E-22		7.20E-01	1.43E-115		-1.46E-02	7.50E-01		Unigene6476_All//gi|211906480|gb|ACJ11733.1|//4.00E-61//catalase [Gossypium hirsutum]	Unigene6476_All//3.00E-53//AT4G35090| CAT2 (CATALASE 2); catalase	Unigene6476_All//0.00E+00//gi|21102720|gb|BQ415033.1|BQ415033		ko04146|Peroxisome//ko00380|Tryptophan metabolism		nr +
Unigene6478_All	548	24.44	26.35	17.69	31.91	44.62	31.56	32.02	10.68	16.94	1.09E-01	5.17E-01		-4.67E-01	3.66E-03		4.84E-01	2.56E-06		-1.55E-02	9.35E-01		-1.58E+00	2.79E-32	Down	-9.19E-01	1.38E-14		Unigene6478_All//gi|194241584|gb|ACF35047.1|//8.00E-52//protein phosphatase 2C [Hevea brasiliensis]	Unigene6478_All//2.00E-48//AT5G53140| protein phosphatase 2C, putative / PP2C, putative	Unigene6478_All//0.00E+00//TC177849				nr -
Unigene64786_All	407	0.00	2.99	0.52	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	5.46E-07	Up	9.03E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene64786_All//sp|Q24574|UBPE_DROME//3.00E-08//Ubiquitin carboxyl-terminal hydrolase 64E OS=Drosophila melanogaster GN=Usp64E PE=1 SV=2						swissprot +
Unigene64789_All	378	0.00	2.14	0.28	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	9.36E-05	Up	8.14E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene64789_All//sp|Q5RCA9|ITB1_PONAB//7.00E-46//Integrin beta-1 OS=Pongo abelii GN=ITGB1 PE=2 SV=1						swissprot +
Unigene648_All	2171	6.87	5.02	4.56	8.56	6.20	3.54	5.61	1.73	5.82	-4.53E-01	1.80E-03		-5.90E-01	8.14E-05		-4.65E-01	9.54E-05		-1.28E+00	6.78E-22	Down	-1.69E+00	7.51E-25	Down	5.26E-02	7.41E-01		Unigene648_All//gi|19352051|dbj|BAB85919.1|//0.00E+00//auxin response factor 10 [Oryza sativa]	Unigene648_All//0.00E+00//AT4G30080| ARF16 (AUXIN RESPONSE FACTOR 16); miRNA binding / transcription factor	Unigene648_All//0.00E+00//ES832982	ARF		GO:0003723//GO:0005515//GO:0006351//GO:0007275//GO:0009755//GO:0010468//GO:0043231//GO:0048856	nr +
Unigene6482_All	448	1.87	6.45	2.02	1.11	2.69	4.44	3.40	3.17	2.76	1.79E+00	1.01E-05	Up	1.13E-01	8.72E-01		1.27E+00	4.45E-02		2.00E+00	7.99E-05	Up	-9.91E-02	8.40E-01		-3.02E-01	5.42E-01				Unigene6482_All//1.00E-69//BG446761				
Unigene64824_All	225	0.00	0.00	0.00	0.00	0.00	0.40	5.45	0.19	0.35	null	null		null	null		null	null		8.65E+00	4.73E-01		-4.87E+00	1.49E-07	Down	-3.94E+00	4.86E-07	Down	Unigene64824_All//gi|115454545|ref|NP_001050873.1|//2.00E-20//Os03g0672300 [Oryza sativa Japonica Group] >gi|113549344|dbj|BAF12787.1|Os03g0672300 [Oryza sativa Japonica Group]	Unigene64824_All//4.00E-13//AT3G22960| PKP-ALPHA; pyruvate kinase	Unigene64824_All//7.00E-85//TC158181			GO:0006007//GO:0016301//GO:0031420//GO:0043231	nr +
Unigene64831_All	608	0.00	4.08	1.14	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.98E-14	Up	1.02E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene64831_All//gi|301109146|ref|XP_002903654.1|//9.00E-56//phosphoglycerate kinase [Phytophthora infestans T30-4] >gi|262097378|gb|EEY55430.1|phosphoglycerate kinase [Phytophthora infestans T30-4]	Unigene64831_All//3.00E-33//AT1G56190| phosphoglycerate kinase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms	GO:0009532//GO:0010038//GO:0016740	nr +
Unigene6486_All	367	1.85	1.38	1.31	22.40	27.96	15.38	107.03	113.43	41.90	-4.25E-01	5.97E-01		-5.05E-01	5.82E-01		3.20E-01	8.19E-02		-5.42E-01	6.92E-03		8.38E-02	3.52E-01		-1.35E+00	3.83E-58	Down	Unigene6486_All//gi|224111870|ref|XP_002316008.1|//9.00E-31//cytochrome P450 [Populus trichocarpa] >gi|222865048|gb|EEF02179.1|cytochrome P450 [Populus trichocarpa]	Unigene6486_All//3.00E-21//AT3G14680| CYP72A14; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene6486_All//4.00E-140//gi|72271016|gb|DT047944.1|DT047944		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +
Unigene64874_All	283	0.00	3.04	1.69	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.94E-05	Up	1.07E+01	7.46E-03		null	null		null	null		null	null		null	null		Unigene64874_All//gi|301116101|ref|XP_002905779.1|//1.00E-17//glycerol-3-phosphate dehydrogenase [Phytophthora infestans T30-4] >gi|262109079|gb|EEY67131.1|glycerol-3-phosphate dehydrogenase [Phytophthora infestans T30-4]	Unigene64874_All//1.00E-14//AT5G40610| glycerol-3-phosphate dehydrogenase (NAD+) / GPDH			ko00564|Glycerophospholipid metabolism	GO:0000166//GO:0006072//GO:0016616//GO:0042802//GO:0043234//GO:0044464//GO:0048037	nr +
Unigene64878_All	315	0.00	2.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene6488_All	653	4.89	6.98	1.71	5.03	9.49	5.39	22.34	19.01	8.72	5.15E-01	7.12E-02		-1.51E+00	7.55E-05	Down	9.15E-01	5.43E-05		9.96E-02	7.83E-01		-2.33E-01	9.61E-02		-1.36E+00	3.12E-22	Down	Unigene6488_All//gi|224060459|ref|XP_002300210.1|//2.00E-44//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222847468|gb|EEE85015.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene6488_All//1.00E-36//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene6488_All//1.00E-125//ES794927				nr +
Unigene64881_All	284	0.00	5.35	2.06	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.10E-08	Up	1.10E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene64881_All//sp|Q9VGX3|FAU_DROME//4.00E-18//Protein anoxia up-regulated OS=Drosophila melanogaster GN=fau PE=1 SV=3						swissprot -
Unigene64895_All	385	0.00	3.55	3.32	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.79E-08	Up	1.17E+01	4.68E-07	Up	null	null		null	null		null	null		null	null		Unigene64895_All//gi|115469274|ref|NP_001058236.1|//2.00E-06//Os06g0652600 [Oryza sativa Japonica Group] >gi|51535038|dbj|BAD37409.1|fibroin heavy chain precursor-like [Oryza sativa Japonica Group] >gi|113596276|dbj|BAF20150.1|Os06g0652600 [Oryza sativa Japonica Group]						nr +
Unigene649_All	2479	10.09	4.44	9.49	6.83	4.72	5.32	2.15	1.25	2.78	-1.19E+00	2.68E-24	Down	-8.76E-02	5.06E-01		-5.33E-01	1.87E-05		-3.61E-01	7.86E-03		-7.85E-01	6.57E-04		3.72E-01	6.03E-02		Unigene649_All//gi|19352051|dbj|BAB85919.1|//0.00E+00//auxin response factor 10 [Oryza sativa]	Unigene649_All//0.00E+00//AT4G30080| ARF16 (AUXIN RESPONSE FACTOR 16); miRNA binding / transcription factor	Unigene649_All//0.00E+00//TC145966	ARF		GO:0003723//GO:0005515//GO:0006351//GO:0007275//GO:0009755//GO:0010468//GO:0043231//GO:0048856	nr +
Unigene6490_All	876	0.96	0.64	0.36	1.36	1.49	4.02	5.79	6.58	4.46	-5.87E-01	4.26E-01		-1.39E+00	9.66E-02		1.30E-01	8.39E-01		1.56E+00	5.86E-06	Up	1.85E-01	4.57E-01		-3.78E-01	1.07E-01		Unigene6490_All//gi|145567028|gb|AB981864.1|//5.00E-26//EARLY FLOWERING 3 [Pisum sativum]	Unigene6490_All//6.00E-23//AT2G25930| ELF3 (EARLY FLOWERING 3); protein C-terminus binding / transcription factor	Unigene6490_All//0.00E+00//CO082317		ko04712|Circadian rhythm - plant		nr +
Unigene64900_All	306	0.00	1.99	2.26	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.17E-03		1.11E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene64900_All//sp|Q1ZXL0|Y5795_DICDI//1.00E-05//PH domain-containing protein DDB_G0275795 OS=Dictyostelium discoideum GN=DDB_G0275795 PE=4 SV=1						swissprot -
Unigene6491_All	1234	1.61	0.49	0.35	4.04	5.27	5.27	0.86	1.25	1.03	-1.71E+00	5.22E-04	Down	-2.22E+00	5.21E-05	Down	3.86E-01	1.04E-01		3.85E-01	1.15E-01		5.49E-01	2.60E-01		2.70E-01	6.10E-01		Unigene6491_All//gi|18406260|ref|NP_564732.1|//1.00E-149//ZW18 [Arabidopsis thaliana] >gi|186491769|ref|NP_001117514.1|ZW18 [Arabidopsis thaliana] >gi|8979939|gb|AAF82253.1|AC008051_4 Identical to gene ZW18 from Arabidopsis thaliana gb|AB028199 >gi|6520167|dbj|BAA87940.1| ZW18 [Arabidopsis thaliana]	Unigene6491_All//7.00E-151//AT1G58350| ZW18	Unigene6491_All//0.00E+00//DR452744				nr +
Unigene6492_All	642	6.76	3.00	2.41	0.93	2.63	1.69	50.38	49.61	48.34	-1.17E+00	8.23E-05	Down	-1.49E+00	3.16E-06	Down	1.50E+00	3.80E-03		8.59E-01	2.17E-01		-2.23E-02	8.31E-01		-5.97E-02	5.59E-01		Unigene6492_All//gi|117168137|gb|AB832151.1|//7.00E-06//At3g01960 [Arabidopsis thaliana]	Unigene6492_All//4.00E-07//AT3G01960| unknown protein	Unigene6492_All//0.00E+00//gi|109832472|gb|DW231031.1|DW231031				nr +
Unigene6493_All	1405	3.80	1.98	3.34	0.78	0.25	0.23	1.66	0.33	1.84	-9.37E-01	3.15E-04		-1.88E-01	5.18E-01		-1.67E+00	9.38E-03		-1.79E+00	1.01E-02		-2.34E+00	9.85E-08	Down	1.55E-01	6.59E-01		Unigene6493_All//gi|144905179|dbj|BAF56240.1|//0.00E+00//cytochrome P450 enzyme [Pisum sativum]	Unigene6493_All//0.00E+00//AT3G26710| BAS1 (PHYB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene6493_All//7.00E-46//DR454918		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr -
Unigene64930_All	499	0.21	0.41	0.21	3.09	0.83	1.99	0.34	0.17	0.88	9.54E-01	6.20E-01		2.52E-02	9.98E-01		-1.90E+00	3.49E-04	Down	-6.36E-01	2.47E-01		-1.02E+00	6.13E-01		1.37E+00	1.82E-01				Unigene64930_All//9.00E-117//CO092314				ESTscan -
Unigene6494_All	927	1.19	1.20	1.55	0.91	2.34	1.90	1.51	0.54	3.57	2.08E-02	9.87E-01		3.88E-01	5.06E-01		1.36E+00	1.92E-03		1.06E+00	3.64E-02		-1.48E+00	4.92E-03		1.24E+00	4.62E-05	Up	Unigene6494_All//gi|33355392|gb|AAQ16126.1|//1.00E-73//homeodomain protein BNLGHi6313 [Gossypium hirsutum]	Unigene6494_All//1.00E-60//AT4G00730| ANL2 (ANTHOCYANINLESS 2); transcription factor/ transcription regulator	Unigene6494_All//7.00E-79//TC141134	HB			nr -
Unigene6495_All	561	167.22	169.17	132.79	199.52	189.67	224.05	379.99	300.54	165.25	1.67E-02	7.84E-01		-3.33E-01	1.15E-09		-7.31E-02	1.91E-01		1.67E-01	2.82E-04		-3.38E-01	1.11E-27		-1.20E+00	2.70E-259	Down	Unigene6495_All//gi|29419473|gb|AAO61853.1|//1.00E-65//glutathione S-transferase F1 [Malva pusilla]	Unigene6495_All//2.00E-47//AT1G02930| AT6STF6 (GLUTATHIONE S-TRANSFERASE6); copper ion binding / glutathione binding / glutathione transferase	Unigene6495_All//0.00E+00//gi|13247973|gb|BF273361.2|BF273361		ko00480|Glutathione metabolism		nr +
Unigene6496_All	601	8.44	18.80	12.05	5.06	5.16	5.49	8.51	9.67	4.84	1.15E+00	6.53E-11	Up	5.13E-01	2.47E-02		2.85E-02	9.48E-01		1.18E-01	7.49E-01		1.84E-01	4.60E-01		-8.15E-01	3.78E-04				Unigene6496_All//4.00E-138//TC174627				
Unigene64962_All	772	0.81	0.53	1.31	1.48	0.49	3.04	1.37	0.11	0.10	-6.31E-01	4.75E-01		6.88E-01	3.42E-01		-1.60E+00	1.02E-02		1.04E+00	1.40E-02		-3.66E+00	1.31E-05	Down	-3.73E+00	6.13E-06	Down	Unigene64962_All//gi|224103837|ref|XP_002313213.1|//1.00E-133//oligopeptide transporter OPT family [Populus trichocarpa] >gi|222849621|gb|EEE87168.1|oligopeptide transporter OPT family [Populus trichocarpa]	Unigene64962_All//2.00E-129//AT5G64110| OPT4 (OLIGOPEPTIDE TRANSPORTER 4); oligopeptide transporter	Unigene64962_All//2.00E-171//TC167359				nr +
Unigene64966_All	627	0.00	4.44	1.10	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.43E-16	Up	1.01E+01	6.15E-04	Up	null	null		null	null		null	null		null	null		Unigene64966_All//gi|75325222|sp|Q6YSF3.1|AN32I_ORYSJ//1.00E-20//RecName: Full=Acidic leucine-rich nuclear phosphoprotein 32-related protein 1; AltName: Full=AN32/acidic nuclear phosphoprotein-like protein 1 >gi|34395133|dbj|BAC84847.1|Amp32/Acidic nuclear phosphoprotein-like protein [Oryza sativa Japonica Group]	Unigene64966_All//7.00E-17//AT3G56090| leucine-rich repeat family protein			ko03040|Spliceosome		nr +
Unigene64973_All	515	0.00	3.64	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.11E-10	Up	7.69E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene64973_All//sp|O14607|UTY_HUMAN//4.00E-29//Histone demethylase UTY OS=Homo sapiens GN=UTY PE=1 SV=2						swissprot -
Unigene64975_All	223	0.00	3.64	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.36E-05	Up	7.90E+00	6.32E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene64982_All	477	0.22	0.21	0.00	0.10	0.22	0.19	2.13	0.35	1.17	-4.61E-02	9.87E-01		-7.78E+00	3.89E-01		1.05E+00	8.06E-01		8.59E-01	7.93E-01		-2.60E+00	3.81E-04	Down	-8.63E-01	1.40E-01		Unigene64982_All//gi|4557063|gb|AAD22502.1|//8.00E-09//expressed protein [Arabidopsis thaliana]		Unigene64982_All//3.00E-178//TC145931			GO:0009526	nr +
Unigene64985_All	449	0.00	2.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene64985_All//sp|Q6VHP0|DDX3_DROME//9.00E-22//ATP-dependent RNA helicase bel OS=Drosophila melanogaster GN=bel PE=1 SV=1						swissprot -
Unigene64986_All	387	0.00	5.11	1.79	0.00	0.18	0.00	0.00	0.00	0.00	1.23E+01	2.97E-11	Up	1.08E+01	6.14E-04	Up	7.48E+00	6.05E-01		null	null		null	null		null	null		Unigene64986_All//gi|1912312|gb|AAB50954.1|//3.00E-55//glycolytic glyceraldehyde-3-phosphate dehydrogenase [Pyrenomonas salina]	Unigene64986_All//1.00E-51//AT1G79530| GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene64986_All//2.00E-15//gi|78340424|gb|DT560698.1|DT560698		ko00010|Glycolysis / Gluconeogenesis	GO:0000166//GO:0006007//GO:0008943//GO:0043231	nr +
Unigene64987_All	224	6.31	3.85	13.79	14.01	7.84	1.81	6.04	0.75	2.13	-7.14E-01	2.05E-01		1.13E+00	2.60E-03		-8.38E-01	1.14E-02		-2.95E+00	2.10E-11	Down	-3.02E+00	4.74E-06	Down	-1.50E+00	3.72E-03									
Unigene64992_All	284	0.00	2.85	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.36E-05	Up	9.55E+00	1.40E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene64995_All	308	0.00	2.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null				Unigene64995_All//6.00E-12//ES796462				

Unigene64998_All	479	0.00	2.43	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.03E-06	Up	1.05E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene64998_All//sp|Q7JUY7|CED6_DROME//3.00E-54//PTB domain-containing adapter protein ced-6 OS=Drosophila melanogaster GN=ced-6 PE=1 SV=1						swissprot +
Unigene6500_All	442	48.41	90.56	48.67	146.63	142.88	135.29	65.05	51.82	29.20	9.04E-01	8.47E-25		7.60E-03	9.76E-01		-3.73E-02	6.51E-01		-1.16E-01	1.13E-01		-3.28E-01	3.02E-04		-1.16E+00	1.34E-33	Down	Unigene6500_All//gi|89212808|gb|AB063904.1|//5.00E-27//aquaporin 1 [Gossypium hirsutum]	Unigene6500_All//0.00E-27//ATIG01620| PIP1C (PLASMA MEMBRANE INTRINSIC PROTEIN 1C); water channel	Unigene6500_All//0.00E+00//TC139112				nr +
Unigene65006_All	369	0.71	1.10	0.58	1.89	2.80	3.67	0.92	3.06	8.21	6.32E-01	6.01E-01		-2.97E-01	8.31E-01		5.67E-01	4.45E-01		9.58E-01	1.09E-01		1.74E+00	4.63E-03		3.16E+00	1.42E-13	Up	Unigene65006_All//gi|225030812|gb|ACN79519.1|//6.00E-20//reduced leaflet 1 [Lotus japonicus]	Unigene65006_All//1.00E-15//AT5G23570| SGS3 (SUPPRESSOR OF GENE SILENCING 3)	Unigene65006_All//3.00E-174//gi|78352769|gb|DT573043.1|DT573043			GO:0002252//GO:0031047//GO:0044238//GO:0050896	nr +
Unigene65008_All	268	0.00	9.45	1.19	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	2.05E-14	Up	1.02E+01	4.50E-02		null	null		null	null		null	null		null	null		Unigene65008_All//gi|159464745|ref|XP_001690602.1|//4.00E-14//cysteine endopeptidase [Chlamydomonas reinhardtii] >gi|158280102|gb|EDF05861.1| cysteine endopeptidase [Chlamydomonas reinhardtii]	Unigene65008_All//3.00E-14//AT1G09850| XBCP3 (xylem bark cysteine peptidase 3); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene65008_All//5.00E-09//TC157327			GO:0043231//GO:0070011	nr +
Unigene6501_All	774	1.01	1.18	0.41	2.64	2.62	3.50	2.84	0.97	1.49	2.17E-01	7.42E-01		-1.30E+00	1.38E-01		-7.60E-03	9.72E-01		4.08E-01	3.29E-01		-1.55E+00	1.39E-04	Down	-9.28E-01	1.26E-02		Unigene6501_All//gi|15240727|ref|NP_196887.1|//1.00E-55//FtsJ-like methyltransferase family protein [Arabidopsis thaliana] >gi|5821280|dbj|BAA83750.1| FtsJ [Arabidopsis thaliana] >gi|10177649|dbj|BAB11111.1| FtsJ [Arabidopsis thaliana]	Unigene6501_All//6.00E-57//AT1G13830| FtsJ-like methyltransferase family protein	Unigene6501_All//0.00E+00//gi|164305530|gb|ES808622.1|ES808622				nr +
Unigene6502_All	789	0.13	0.58	0.00	1.14	2.31	4.81	2.57	12.45	4.65	2.12E+00	9.59E-02		-7.05E+00	3.89E-01		1.03E+00	3.41E-02		2.08E+00	4.00E-09	Up	2.27E+00	2.33E-29	Up	8.53E-01	2.18E-03					Unigene6502_All//4.00E-86//gi|164274494|gb|EV495066.1|EV495066				
Unigene65025_All	239	0.00	4.24	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.25E-06	Up	7.80E+00	6.32E-01		null	null		null	null		null	null		null	null		Unigene65025_All//sp|P0A910|OMPA_ECOL1//3.00E-19//Outer membrane protein A OS=Escherichia coli (strain K12) GN=ompA PE=1 SV=1		Unigene65025_All//1.00E-21//TC176494				swissprot -
Unigene6504_All	1221	0.00	0.50	0.09	0.73	0.79	1.18	2.87	1.64	64.51	8.96E+00	1.17E-03		6.45E+00	3.95E-01		1.05E-01	9.03E-01		6.89E-01	2.32E-01		-8.07E-01	5.92E-03		4.49E+00	0.00E+00	Up	Unigene6504_All//gi|115472809|ref|NP_001060003.1|//1.00E-138//Os07g0564500 [Oryza sativa Japonica Group] >gi|113611539|dbj|BAF21917.1| Os07g0564500 [Oryza sativa Japonica Group]	Unigene6504_All//5.00E-124//AT1G07180| NDA1 (ALTERNATIVE NAD(P)H DEHYDROGENASE 1); NADH dehydrogenase	Unigene6504_All//0.00E+00//TC173686		ko00190|Oxidative phosphorylation		nr +
Unigene65057_All	383	0.00	2.65	1.95	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	7.25E-06	Up	1.09E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene65057_All//gi|226528334|ref|NP_001149321.1|//2.00E-06//LOC100282944 [Zea mays] >gi|195626372|gb|ACG35016.1| nucleic acid binding protein [Zea mays]						nr -
Unigene6506_All	872	0.72	1.74	0.73	3.94	2.05	1.76	2.47	3.83	3.38	1.28E+00	2.09E-02		2.54E-02	9.97E-01		-9.41E-01	2.56E-03		-1.16E+00	4.75E-04	Down	6.33E-01	3.72E-02		4.51E-01	1.60E-01		Unigene6506_All//gi|225455084|ref|XP_002267679.1|//5.00E-09//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene6506_All//0.00E+00//ES821095				nr +
Unigene65060_All	374	0.00	3.66	3.56	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.79E-08	Up	1.18E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene65060_All//gi|15450751|gb|AAB96647.1|//5.00E-16//At2g21410/F3K23.17 [Arabidopsis thaliana] >gi|21700881|gb|AAM70564.1| At2g21410/F3K23.17 [Arabidopsis thaliana]	Unigene65060_All//2.00E-17//AT2G21410| VHA-A2 (VACUOLAR PROTON ATPASE A2); ATPase			ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0000325//GO:0009987//GO:0022857//GO:0031090//GO:0050896	nr +
Unigene6507_All	408	1.54	1.74	1.70	8.55	5.06	1.66	2.07	0.82	2.15	1.76E-01	8.17E-01		1.41E-01	8.60E-01		-7.55E-01	1.57E-02		-2.36E+00	5.24E-10	Down	-1.34E+00	5.68E-02		5.17E-02	9.56E-01		Unigene6507_All//gi|116041947|gb|ABJ53199.1|//7.00E-26//myosin XI-K [Nicotiana benthamiana]	Unigene6507_All//9.00E-27//AT1G08730| XIC; motor/ protein binding	Unigene6507_All//4.00E-109//TC163937				nr -
Unigene6509_All	844	3.04	1.92	1.58	5.08	6.41	1.66	0.30	0.35	0.33	-6.61E-01	9.37E-02		-9.46E-01	2.31E-02		3.36E-01	2.24E-01		-1.61E+00	1.38E-07	Down	2.05E-01	8.68E-01		1.36E-01	9.28E-01		Unigene6509_All//gi|280967730|gb|ACZ98536.1|//1.00E-80//protein kinase [Malus x domestica]	Unigene6509_All//5.00E-51//AT2G26730| leucine-rich repeat transmembrane protein kinase, putative	Unigene6509_All//0.00E+00//gi|78340425|gb|DT560699.1|DT560699		ko04626|Plant-pathogen interaction		nr +
Unigene65092_All	230	0.00	3.52	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.36E-05	Up	8.85E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene65092_All//gi|145348283|ref|XP_001418582.1|//8.00E-21//Ribosomal protein S5, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CE9901] >gi|144578812|gb|ABO96875.1| Ribosomal protein S5, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CE9901]	Unigene65092_All//7.00E-18//AT2G37270| ATRPS5B (RIBOSOMAL PROTEIN 5B); structural constituent of ribosome			ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene65096_All	430	0.00	5.30	0.74	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.63E-13	Up	9.54E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene65096_All//sp|Q75JZ0|GTAH_DICDI//1.00E-07//GATA zinc finger domain-containing protein 8 OS=Dictyostelium discoideum GN=gtaH PE=4 SV=1						swissprot -
Unigene65099_All	362	0.00	6.58	1.77	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.50E-13	Up	1.08E+01	1.16E-03		null	null		null	null		null	null		null	null										
Unigene651_All	1675	8.00	3.39	4.13	12.67	11.33	12.78	16.84	5.51	7.44	-1.24E+00	2.85E-14	Down	-9.52E-01	3.89E-09		-1.62E-01	2.23E-01		1.26E-02	9.44E-01		-1.61E+00	1.27E-52	Down	-1.18E+00	5.91E-34	Down	Unigene651_All//gi|217426816|gb|ACK44524.1|//1.00E-137//AT5G10010-like protein [Arabidopsis arenosa]	Unigene651_All//2.00E-122//AT5G10010| unknown protein	Unigene651_All//0.00E+00//TC179519				nr -
Unigene6510_All	922	9.42	16.93	4.33	6.54	11.91	3.18	1.79	0.77	0.91	8.46E-01	3.76E-09		-1.12E+00	7.76E-08	Down	8.66E-01	9.44E-08		-1.04E+00	1.35E-05	Down	-1.21E+00	9.00E-03		-9.79E-01	2.63E-02		Unigene6510_All//gi|109676362|gb|AB637663.1|//6.00E-60//CCHC-type integrase [Populus trichocarpa]	Unigene6510_All//3.00E-50//AT2G19130| S-locus lectin protein kinase family protein	Unigene6510_All//0.00E+00//TC170385		ko04626|Plant-pathogen interaction		nr +
Unigene6511_All	314	40.49	5.49	8.65	74.56	43.76	90.47	86.98	51.91	54.05	-2.88E+00	1.85E-40	Down	-2.23E+00	4.70E-29	Down	-7.69E-01	1.27E-13		2.79E-01	6.99E-03		-7.45E-01	2.68E-15		-6.87E-01	8.54E-14		Unigene6511_All//gi|74486736|gb|AB121221.1|//2.00E-54//translation elongation factor 1A-5 [Gossypium hirsutum]	Unigene6511_All//1.00E-52//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene6511_All//9.00E-153//TC152930				nr -
Unigene65113_All	233	0.00	3.91	2.06	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	1.10E+01	7.46E-03		null	null		null	null		null	null		null	null										
Unigene65116_All	207	3.79	2.45	3.34	8.90	3.33	2.84	1.23	1.01	0.77	-6.31E-01	4.08E-01		-1.81E-01	8.07E-01		-1.42E+00	2.01E-03		-1.65E+00	9.75E-04	Down	-2.80E-01	8.28E-01		-6.71E-01	6.05E-01				Unigene65116_All//4.00E-18//BF276543				
Unigene65118_All	320	0.00	3.33	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.81E-06	Up	9.70E+00	7.99E-02		null	null		null	null		null	null		null	null		Unigene65118_All//sp|Q16053|CDV3_DROYA//2.00E-15//Protein CDV3 homolog OS=Drosophila yakuba GN=GE14456 PE=2 SV=1						swissprot -
Unigene6512_All	450	3.02	17.34	12.66	28.23	33.06	16.36	6.11	5.85	7.53	2.52E+00	1.58E-21	Up	2.07E+00	3.43E-12	Up	2.28E-01	1.44E-01		-7.87E-01	3.55E-07		-6.17E-02	8.69E-01		3.01E-01	3.33E-01					Unigene6512_All//1.00E-121//TC169302				
Unigene6513_All	965	0.60	2.99	1.32	3.46	2.39	3.14	2.80	2.30	2.27	2.33E+00	1.06E-07	Up	1.15E+00	6.95E-02		-5.33E-01	1.09E-01		-1.41E-01	6.86E-01		-2.89E-01	4.29E-01		-3.05E-01	3.80E-01					Unigene6513_All//2.00E-20//gi|109850914|gb|DW479893.1|DW479893				
Unigene65146_All	352	0.00	3.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.46E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene65146_All//sp|P05552|ADF1_DROME//1.00E-37//Transcription factor Adf-1 OS=Drosophila melanogaster GN=Adf1 PE=1 SV=2						swissprot -
Unigene65150_All	216	0.00	1.64	0.49	1.38	0.80	1.25	2.54	1.55	12.54	1.07E+01	2.45E-02		8.95E+00	3.95E-01		-7.96E-01	5.56E-01		-1.41E-01	9.20E-01		-7.17E-01	4.22E-01		2.30E+00	6.17E-09	Up			Unigene65150_All//3.00E-53//DR461288				
Unigene6516_All	1054	0.79	2.16	1.21	4.73	8.59	7.80	1.20	2.50	4.23	1.45E+00	1.13E-03		6.10E-01	3.33E-01		8.62E-01	1.94E-06		7.23E-01	2.85E-04		1.05E+00	2.61E-03		1.81E+00	1.05E-10	Up	Unigene6516_All//gi|124339694|gb|ABD32361.2|//3.00E-28//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene6516_All//9.00E-27//AT4G20970| basic helix-loop-helix (bHLH) family protein	Unigene6516_All//0.00E+00//TC140947	bHLH			nr -
Unigene6517_All	563	0.37	1.35	2.08	1.95	4.71	8.02	6.91	40.09	33.89	1.86E+00	3.73E-02		2.48E+00	1.35E-03		1.27E+00	9.04E-04	Up	2.04E+00	1.58E-10	Up	2.54E+00	1.22E-75	Up	2.29E+00	4.21E-58	Up	Unigene6517_All//gi|164605529|dbj|BAF98595.1|//4.00E-22//CM0545.400.nc [Lotus japonicus]	Unigene6517_All//5.00E-21//AT3G28890| AtRLP43 (Receptor Like Protein 43); kinase/ protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene65178_All	367	0.00	3.18	1.74	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.05E-06	Up	1.08E+01	1.16E-03		null	null		null	null		null	null		null	null										
Unigene6518_All	1963	0.05	0.49	0.52	8.07	4.84	3.61	0.13	0.13	0.12	3.20E+00	6.55E-04	Up	3.27E+00	5.92E-04	Up	-7.37E-01	9.52E-09		-1.16E+00	3.26E-16	Down	-1.57E-02	1.02E+00		-8.51E-02	9.56E-01		Unigene6518_All//gi|255537021|ref|XP_002509577.1|//0.00E+00//Vacuolar-processing enzyme precursor [Ricinus communis] >gi|1351409|sp|P49042.1|VPE_RICCO RecName: Full=Vacuolar-processing enzyme; Short=VPE; Flags: Precursor >gi|471162|dbj|BAA04225.1| precursor of vacuolar processing enzyme [Ricinus communis] >gi|223549476|gb|EEF50964.1| Vacuolar-processing enzyme precursor [Ricinus communis]	Unigene6518_All//0.00E+00//AT1G62710| BETA-VPE (BETA VACUOLAR PROCESSING ENZYME); cysteine-type endopeptidase	Unigene6518_All//0.00E+00//TC159249				nr +
Unigene6519_All	965	0.11	76.19	13.08	0.46	2.64	8.00	0.22	0.22	0.83	9.46E+00	0.00E+00	Up	6.91E+00	3.63E-67	Up	2.51E+00	3.80E-08	Up	4.11E+00	2.81E-35	Up	-1.66E-02	1.02E+00		1.91E+00	1.08E-02		Unigene6519_All//gi|469313316|gb|AAT06462.1|//6.00E-31//At3g27250 [Arabidopsis thaliana]	Unigene6519_All//3.00E-31//AT3G27250| unknown protein	Unigene6519_All//8.00E-11//gi|84150005|gb|DN781305.1|DN781305				nr -
Unigene65193_All	537	0.00	5.76	3.67	0.19	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.38E-17	Up	1.18E+01	7.45E-11	Up	-7.54E+00	3.10E-01		-7.54E+00	3.96E-01		null	null		null	null		Unigene65193_All//gi|115469274|ref|NP_001058236.1|//3.00E-07//Os06g0652600 [Oryza sativa Japonica Group] >gi|51535038|dbj|BAD37409.1| fibroin heavy chain precursor-like [Oryza sativa Japonica Group] >gi|113596276|dbj|BAF20150.1| Os06g0652600 [Oryza sativa Japonica Group]						nr -
Unigene65202_All	285	0.18	3.38	2.24	0.87	2.66	1.90	5.19	2.49	3.77	4.20E+00	1.29E-04	Up	3.61E+00	6.97E-03		1.60E+00	6.97E-02		1.12E+00	3.05E-01		-1.06E+00	3.14E-02		-4.60E-01	3.42E-01					Unigene65202_All//1.00E-114//CO125265				
Unigene6521_All	574	5.01	14.74	4.08	6.16	5.40	4.88	1.33	0.44	0.90	1.56E+00	9.71E-13	Up	-2.97E-01	4.49E-01		-1.91E-01	5.98E-01		-3.37E-01	3.48E-01		-1.60E+00	3.70E-02		-5.55E-01	4.23E-01		Unigene6521_All//gi|11074252|gb|AB004499.1|//2.00E-11//At5g26790 [Arabidopsis thaliana]		Unigene6521_All//0.00E+00//gi|164251426|gb|ES819183.1|ES819183				nr +
Unigene65213_All	228	0.00	2.89	0.00	0.00	0.91	0.20	1.11	0.92	0.52	1.15E+01	6.24E-04	Up	null	null		9.82E+00	1.56E-01		7.63E+00	6.90E-01		-2.80E-01	8.28E-01		-1.09E+00	4.28E-01										
Unigene65227_All	480	0.98	0.74	0.67	0.42	0.79	0.66	1.50	0.00	0.50	-4.09E-01	6.68E-01		-5.60E-01	6.28E-01		9.27E-01	5.23E-01		6.66E-01	6.47E-01		-1.05E+01	3.26E-05	Down	-1.59E+00	3.62E-02		Unigene65227_All//gi|224126999|ref|XP_002329358.1|//8.00E-59//glycosyltransferase, CAZy family GT8 [Populus trichocarpa] >gi|222870408|gb|EEF07539.1| glycosyltransferase, CAZy family GT8 [Populus trichocarpa]	Unigene65227_All//1.00E-52//AT2G20810| GAUT10 (GALACTURONOSYLTRANSFERASE 10); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene65227_All//0.00E+00//CO073978			GO:0005975//GO:0008194//GO:0043231	nr -
Unigene6524_All	311	72.51	43.01	49.48	84.09	85.81	104.70	331.99	193.39	156.79	-7.53E-01	9.90E-11		-5.51E-01	3.46E-06		2.92E-02	8.26E-01		3.16E-01	7.60E-04		-7.80E-01	4.49E-60		-1.08E+00	1.32E-106	Down	Unigene6524_All//gi|225462164|ref|XP_002266780.1|//1.00E-52//PREDICTED: similar to elongation factor 2 [Vitis vinifera]	Unigene6524_All//9.00E-52//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene6524_All//2.00E-175//TC165810				nr +
Unigene65242_All	210	0.50	1.45	2.03	18.03	10.66	8.82	0.00	0.00	0.00	1.54E+00	3.23E-01		2.03E+00	1.39E-01		-7.58E-01	1.07E-02		-1.03E+00	9.53E-04	Down	null	null		null	null										
Unigene65249_All	405	0.00	3.50	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.06E-08	Up	9.85E+00	2.50E-02		null	null		null	null		null	null		null	null		Unigene65249_All//gi|219113287|ref|XP_002186227.1|//6.00E-09//predicted protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|209583077|gb|ACI65697.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1]						nr -

Unigene6525_All	1084	2.61	5.66	4.47	0.09	0.00	0.08	2.11	2.62	3.82	1.12E+00	5.24E-06	Up	7.78E-01	6.24E-03		-6.52E+00	3.10E-01		-1.42E-01	9.48E-01		3.16E-01	3.87E-01		8.60E-01	9.42E-04		Unigene6525_All//gi|224055327|ref|XP_002298482.1|//1.00E-113//20G-Fe(II) oxidoreductase [Populus trichocarpa] >gi|222845740|gb|EEE83287.1| 20G-Fe(II) oxidoreductase [Populus trichocarpa]	Unigene6525_All//5.00E-86//AT5G58660| oxidoreductase, 20G-Fe(II) oxygenase family protein	Unigene6525_All//0.00E+00//gi|48822095|gb|CO123408.1|CO123408		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis		nr -
Unigene65258_All	395	0.00	3.46	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.79E-08	Up	9.40E+00	7.99E-02		null	null		null	null		null	null		null	null		Unigene65258_All//gi|226459660|gb|EEH56955.1|//5.00E-06//predicted protein [Micromonas pusilla CCMP1545]						nr +
Unigene6527_All	1790	0.53	0.51	0.80	0.56	0.38	0.71	10.46	52.05	10.35	-4.63E-02	9.60E-01		6.10E-01	2.96E-01		-5.33E-01	4.45E-01		3.44E-01	6.24E-01		2.31E+00	8.60E-279	Up	-1.59E-02	9.19E-01		Unigene6527_All//gi|1685005|gb|AAB36653.1|//1.00E-149//immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]	Unigene6527_All//6.00E-125//AT4G34135| UGT73B2 (UDP-GLUCOSYLTRANSFERASE 73B2); UDP-glucosyltransferase/ UDP-glycosyltransferase/ flavonol 3-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase	Unigene6527_All//0.00E+00//gi|73864034|gb|DT466773.1|DT466773		ko00908|Zeatin biosynthesis		nr -
Unigene65270_All	511	0.00	3.17	0.83	0.10	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.96E-09	Up	9.70E+00	1.38E-02		-6.61E+00	5.50E-01		-6.61E+00	6.27E-01		null	null		null	null		Unigene65270_All//gi|21322711|emb|CAD22154.1|//2.00E-49//pherophorin-dz1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome	GO:0044464	nr +
Unigene65274_All	519	0.00	6.44	2.05	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	4.94E-19	Up	1.10E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene65274_All//sp|Q96MD7|C10B5_HUMAN//1.00E-06//Uncharacterized protein C9orf85 OS=Homo sapiens GN=C9orf85 PE=1 SV=1						swissprot -
Unigene6528_All	1741	1.95	0.58	0.55	3.29	3.11	3.45	4.30	2.23	3.55	-1.75E+00	1.82E-06	Down	-1.83E+00	1.84E-06	Down	-8.35E-02	7.95E-01		6.84E-02	7.99E-01		-9.45E-01	9.00E-07		-2.77E-01	1.52E-01		Unigene6528_All//gi|226490392|dbj|BAH56489.1|//0.00E+00//pectin methylesterase 1 [Prunus persica]	Unigene6528_All//0.00E+00//AT2G26440| pectinesterase family protein	Unigene6528_All//0.00E+00//CO106074		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene65280_All	829	0.00	3.30	2.57	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.44E-15	Up	1.13E+01	9.77E-12	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene65282_All	878	1.49	1.27	0.97	3.52	2.86	1.75	1.83	0.90	0.41	-2.31E-01	6.71E-01		-6.19E-01	3.20E-01		-2.97E-01	4.34E-01		-1.01E+00	4.23E-03		-1.02E+00	2.97E-02		-2.16E+00	2.38E-05	Down	Unigene65282_All//gi|30694398|ref|NP_191180.2|//4.00E-59//binding [Arabidopsis thaliana] >gi|145332873|ref|NP_001078302.1| binding [Arabidopsis thaliana] >gi|145332875|ref|NP_001078303.1| binding [Arabidopsis thaliana] >gi|38566594|gb|AAR24187.1| At3g56210 [Arabidopsis thaliana] >gi|40824082|gb|AAR92342.1| At3g56210 [Arabidopsis thaliana] >gi|222423263|dbj|BAH19608.1| AT3G56210 [Arabidopsis thaliana]	Unigene65282_All//2.00E-60//AT3G56210| binding	Unigene65282_All//0.00E+00//TC147381			GO:0043231	nr +
Unigene6529_All	595	0.26	12.86	6.26	0.33	1.39	2.66	0.14	0.28	0.40	5.61E+00	6.38E-39	Up	4.57E+00	8.43E-17	Up	2.05E+00	1.79E-02		2.99E+00	7.30E-06	Up	9.84E-01	6.33E-01		1.50E+00	3.39E-01		Unigene6529_All//gi|297836980|ref|XP_002886172.1|//3.00E-28//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297332012|gb|EFH62431.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene6529_All//2.00E-27//AT2G18465| DNAJ heat shock N-terminal domain-containing protein	Unigene6529_All//3.00E-55//TC149709				nr -
Unigene65292_All	416	0.00	1.95	0.13	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	9.36E-05	Up	7.00E+00	6.32E-01		null	null		null	null		null	null		null	null		Unigene65292_All//sp|P09758|TACD2_HUMAN//3.00E-34//Tumor-associated calcium signal transducer 2 OS=Homo sapiens GN=TACSTD2 PE=1 SV=3						swissprot -
Unigene65304_All	1042	0.00	4.28	1.43	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.10E-25	Up	1.05E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene65304_All//gi|224004478|ref|XP_002295890.1|//1.00E-07//predicted protein [Thalassiosira pseudonana CCMP1335] >gi|209585922|gb|ACI64607.1| predicted protein [Thalassiosira pseudonana CCMP1335]						nr +
Unigene65308_All	285	0.00	4.27	1.12	0.00	0.00	0.00	0.15	0.88	0.70	1.21E+01	5.46E-07	Up	1.01E+01	4.50E-02		null	null		null	null		2.57E+00	1.53E-01		2.24E+00	2.48E-01									
Unigene65316_All	321	0.00	3.00	1.16	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.38E-05	Up	1.02E+01	2.50E-02		null	null		null	null		null	null		null	null		Unigene65316_All//sp|A5A6L1|CYR61_PANTR//2.00E-23//Protein CYR61 OS=Pan troglodytes GN=CYR61 PE=2 SV=1						swissprot +
Unigene65334_All	264	0.00	2.69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene6534_All	402	7.16	2.52	5.03	10.04	4.45	5.95	15.04	2.60	5.95	-1.51E+00	1.10E-04	Down	-5.08E-01	1.97E-01		-1.17E+00	3.86E-05	Down	-7.53E-01	1.24E-02		-2.53E+00	8.89E-21	Down	-1.34E+00	1.50E-09	Down			Unigene6534_All//6.00E-99//TC130752				
Unigene65343_All	239	0.00	0.00	0.00	0.21	0.29	0.00	11.15	1.75	2.67	null	null		null	null		4.68E-01	9.56E-01		-7.70E+00	6.27E-01		-2.67E+00	4.54E-10	Down	-2.06E+00	6.61E-08	Down	Unigene65343_All//gi|22330270|ref|NP_175981.2|//2.00E-13//ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75161659|sp|Q8VZ89.1|CSLE1_ARATH RecName: Full=Cellulose synthase-like protein E1; Short=AtCslE1	Unigene65343_All//8.00E-15//AT1G55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups	Unigene65343_All//1.00E-30//TC178738			GO:0009250//GO:0016759//GO:0016798//GO:0019787//GO:0019941//GO:0031224//GO:0032446//GO:0032501//GO:0043231//GO:0045229//GO:0046914//GO:0051234	nr +
Unigene6535_All	469	12.94	38.46	20.55	44.61	95.45	75.59	72.66	151.68	98.96	1.57E+00	1.04E-26	Up	6.67E-01	4.94E-04		1.10E+00	1.40E-44	Up	7.61E-01	1.08E-17		1.06E+00	2.11E-69	Up	4.46E-01	6.66E-11		Unigene6535_All//gi|148645857|gb|ABR01221.1|//2.00E-38//MYB8 [Gossypium hirsutum]	Unigene6535_All//2.00E-38//AT4G09460| ATMYB6; DNA binding / transcription factor	Unigene6535_All//1.00E-168//gi|84153834|gb|DN803189.1|DN803189	MYB			nr -
Unigene65356_All	237	0.00	2.78	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.24E-04	Up	9.81E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene65356_All//gi|298708157|emb|CBJ30498.1|//2.00E-11//Trifunctional enzyme subunit alpha [Ectocarpus siliculosus]						nr -
Unigene65357_All	474	0.00	3.96	1.12	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.11E-10	Up	1.01E+01	4.03E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene6536_All	1168	1.12	0.74	0.27	2.09	2.21	0.93	2.93	1.04	1.60	-6.03E-01	3.07E-01		-2.03E+00	3.01E-03		8.15E-02	8.58E-01		-1.17E+00	4.10E-03		-1.50E+00	1.93E-06	Down	-8.71E-01	2.48E-03		Unigene6536_All//gi|108710823|gb|ABF98618.1|//4.00E-62//Leucine Rich Repeat family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene6536_All//5.00E-31//AT2G16250| leucine-rich repeat transmembrane protein kinase, putative	Unigene6536_All//0.00E+00//CA993146				nr -
Unigene65361_All	254	0.00	2.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene65374_All	387	0.14	2.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.01E+00	4.20E-04	Up	-7.08E+00	6.18E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene65377_All	694	0.00	1.97	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	7.79E-08	Up	7.83E+00	2.38E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene6538_All	315	9.63	5.31	8.45	6.17	6.23	10.47	15.84	9.02	7.46	-8.60E-01	1.61E-02		-1.89E-01	6.27E-01		1.48E-02	9.89E-01		7.63E-01	2.66E-02		-8.12E-01	6.90E-04		-1.09E+00	5.06E-06	Down	Unigene6538_All//gi|12697589|dbj|BAB21595.1|//4.00E-13//Tat binding protein like protein [Brassica rapa]	Unigene6538_All//4.00E-14//AT3G05530| RPT5A (REGULATORY PARTICLE TRIPLE-A ATPASE 5A); ATPase/ calmodulin binding	Unigene6538_All//9.00E-79//gi|3326764|gb|AI055650.1|AI055650		ko03050|Proteasome		nr +
Unigene65388_All	1072	0.00	6.57	3.18	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	3.00E-40	Up	1.16E+01	7.38E-19	Up	null	null		null	null		null	null		null	null		Unigene65388_All//gi|255563324|ref|XP_002522665.1|//5.00E-08//structural constituent of cell wall, putative [Ricinus communis] >gi|223538141|gb|EEF39752.1| structural constituent of cell wall, putative [Ricinus communis]						nr +
Unigene65394_All	372	0.00	2.86	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.81E-06	Up	8.75E+00	2.38E-01		null	null		null	null		null	null		null	null		Unigene65394_All//sp|Q16270|IBP7_HUMAN//5.00E-57//Insulin-like growth factor-binding protein 7 OS=Homo sapiens GN=IGFBP7 PE=1 SV=1						swissprot +
Unigene6540_All	1272	0.53	1.59	1.67	2.58	4.01	1.88	0.57	1.28	0.34	1.58E+00	1.08E-03		1.65E+00	7.52E-04	Up	6.32E-01	1.47E-02		-4.58E-01	2.03E-01		1.18E+00	1.17E-02		-7.14E-01	3.27E-01		Unigene6540_All//gi|38346596|emb|CAE04660.2|//3.00E-31//OSJNBa0061G20.16 [Oryza sativa (japonica cultivar-group)]	Unigene6540_All//3.00E-05//AT1G43760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: RNA-directed DNA polymerase (reverse transcriptase), related (InterPro:IPR015706), Endonuclease/exonuclease/phosphatase (InterPro:IPR005135); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G40390.1); Has 2614 Blast hits to 2551 proteins in 44 species: Archae - 0; Bacteria - 0; Metazoa - 1517; Fungi - 2; Plants - 1086; Viruses - 0; Other Eukaryotes - 9 (source: NCBI BLink).	Unigene6540_All//4.00E-10//TC137548				nr +
Unigene6541_All	844	2.23	2.28	1.32	24.73	0.29	0.11	56.46	0.69	3.87	3.17E-02	9.65E-01		-7.52E-01	1.34E-01		-6.44E+00	5.86E-148	Down	-7.85E+00	1.71E-129	Down	-6.35E+00	0.00E+00	Down	-3.87E+00	1.40E-247	Down	Unigene6541_All//gi|89243481|gb|ABD64879.1|//1.00E-78//nicotianamine synthase [Malus xiaojinensis]	Unigene6541_All//6.00E-68//AT1G09240| NAS3 (NICOTIANAMINE SYNTHASE 3); nicotianamine synthase	Unigene6541_All//0.00E+00//TC157313				nr +
Unigene65410_All	442	0.00	5.50	1.08	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.73E-14	Up	1.01E+01	7.46E-03		null	null		null	null		null	null		null	null		Unigene65410_All//gi|283135898|gb|ADB11340.1|//1.00E-06//zeta class glutathione transferase GSTZ2 [Populus trichocarpa]	Unigene65410_All//2.00E-06//AT5G41210| ATGSTT1 (GLUTATHIONE S-TRANSFERASE THETA 1); glutathione transferase			ko00480|Glutathione metabolism//ko00350|Tyrosine metabolism	GO:0044424	nr +
Unigene65411_All	533	0.00	8.18	3.20	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	8.00E-25	Up	1.16E+01	2.20E-09	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene65418_All	387	0.00	4.71	2.75	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.14E-10	Up	1.14E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene65418_All//gi|226509807|ref|NP_001149947.1|//5.00E-45//3-isopropylmalate dehydrogenase [Zea mays] >gi|195635671|gb|ACG37304.1| 3-isopropylmalate dehydrogenase [Zea mays]	Unigene65418_All//5.00E-45//AT5G03290| isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative			ko00020|Citrate cycle (TCA cycle)	GO:0000166//GO:0004448//GO:0006551//GO:0008652//GO:0009060//GO:0009536//GO:0046872	nr +
Unigene6542_All	602	2.09	2.02	1.15	4.47	1.66	2.48	2.04	1.18	0.53	-4.63E-02	9.50E-01		-8.59E-01	1.74E-01		-1.43E+00	9.85E-05	Down	-8.52E-01	2.65E-02		-7.87E-01	1.52E-01		-1.94E+00	7.80E-04	Down	Unigene6542_All//gi|227206454|dbj|BAH57282.1|//5.00E-70//AT5G50150| [Arabidopsis thaliana]	Unigene6542_All//3.00E-70//gi|11204407|gb|BF273337.1|BF273337					nr +
Unigene65429_All	601	0.17	4.97	0.71	0.00	0.00	0.00	0.56	0.00	0.07	4.84E+00	2.18E-14	Up	2.03E+00	1.39E-01		null	null		null	null		-9.14E+00	1.17E-02		-3.09E+00	3.91E-02				Unigene65429_All//9.00E-22//DT049498				
Unigene65436_All	220	0.00	3.92	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.94E-05	Up	7.92E+00	6.31E-01		null	null		null	null		null	null		null	null									
Unigene6544_All	236	37.25	22.54	14.44	32.51	27.14	36.93	42.82	35.77	21.10	-7.24E-01	1.94E-04		-1.37E+00	1.46E-10	Down	-2.60E-01	2.46E-01		1.84E-01	4.17E-01		-2.59E-01	1.34E-01		-1.02E+00	2.70E-10	Down	Unigene6544_All//gi|206573537|gb|ACI14380.1|//2.00E-08//60S acidic ribosomal protein P2-like protein [Forsythia suspensa]	Unigene6544_All//6.00E-08//AT2G27710| 60S acidic ribosomal protein P2 (RPP2B)	Unigene6544_All//2.00E-112//DW236539		ko03010|Ribosome		nr -
Unigene6545_All	526	3.38	10.79	3.75	4.64	8.25	8.84	11.90	25.51	17.19	1.67E+00	1.14E-09	Up	1.47E-01	7.47E-01		8.30E-01	3.19E-03		9.30E-01	8.31E-04		1.10E+00	1.63E-14	Up	5.31E-01	1.40E-03		Unigene6545_All//gi|22330656|ref|NP_177742.2|//4.00E-17//macC-like dehydratase domain-containing protein [Arabidopsis thaliana] >gi|17979531|gb|AAL50100.1| At1g76150/T23E18_38 [Arabidopsis thaliana] >gi|20147245|gb|AAM10336.1| At1g76150/T23E18_38 [Arabidopsis thaliana]	Unigene6545_All//3.00E-18//AT1G76150| macC-like dehydratase domain-containing protein	Unigene6545_All//6.00E-75//TC135341				nr +

Unigene65452_All	399	0.00	1.27	7.61	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	4.03E-03		1.29E+01	8.92E-17	Up	null	null		null	null		null	null		null	null		Unigene65452_All//sp|P01843|LAC1_MOUSE//4.00E-21//Ig lambda-1 chain C region OS=Mus musculus PE=1 SV=1						swissprot +
Unigene65454_All	401	0.00	12.38	2.39	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	2.63E-28	Up	1.12E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene65454_All//sp|Q9TTT7|CX6A1_RABIT//2.00E-23//Cytochrome c oxidase subunit 6A1, mitochondrial OS=Oryctolagus cuniculus GN=COX6A1 PE=3 SV=1						swissprot +
Unigene65459_All	334	0.00	2.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene65472_All	483	0.00	3.36	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.96E-09	Up	9.78E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene65472_All//gi|159464152|ref|XP_001690306.1|//2.00E-12//signal peptidase, 22 kDa subunit [Chlamydomonas reinhardtii] >gi|158284294|gb|EDP10014.1| signal peptidase, 22 kDa subunit [Chlamydomonas reinhardtii]	Unigene65472_All//2.00E-12//AT3G05230| signal peptidase subunit family protein			ko00310|Lysine degradation//ko00780|Biotin metabolism		nr -
Unigene65475_All	234	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.18	2.72	null	null		null	null		null	null		null	null		-1.69E-02	1.00E+00		3.91E+00	7.65E-04	Up	Unigene65475_All//gi|195973264|gb|ABW69659.2|//5.00E-20//glutathione S-transferase [Gossypium hirsutum]	Unigene65475_All//2.00E-17//AT3G09270| ATGSTU8 (GLUTATHIONE S-TRANSFERASE TAU 8); glutathione transferase	Unigene65475_All//1.00E-98//DN826606		ko00480|Glutathione metabolism		nr -
Unigene65479_All	234	0.00	4.98	5.01	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.05E-06	Up	1.23E+01	1.77E-06	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene65481_All	294	0.00	2.93	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	4.94E-05	Up	9.09E+00	2.38E-01		null	null		null	null		null	null													
Unigene6549_All	1425	1.25	0.64	0.52	2.59	0.65	1.27	5.93	5.95	2.35	-9.64E-01	4.89E-02		-1.25E+00	1.68E-02		-1.99E+00	9.79E-10	Down	-1.03E+00	1.18E-03		4.90E-03	1.02E+00		-1.34E+00	5.45E-13	Down	Unigene6549_All//gi|54606698|dbj|BAD66721.1|//6.00E-26//NADH dehydrogenase subunit 1 [Beta vulgaris subsp. vulgaris] >gi|54606742|dbj|BAD66765.1| NADH dehydrogenase subunit 1 [Beta vulgaris subsp. vulgaris]	Unigene6549_All//1.00E-17//ATMG01275| Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C.	Unigene6549_All//0.00E+00//ES839275		ko00190|Oxidative phosphorylation		nr +
Unigene65495_All	353	0.00	6.46	3.32	0.00	0.00	0.00	0.12	0.00	0.00	1.27E+01	5.63E-13	Up	1.17E+01	1.77E-06	Up	null	null		null	null		-6.90E+00	6.50E-01		-6.90E+00	6.06E-01		Unigene65495_All//gi|7799051|emb|CAB08826.1|//3.00E-43//ubiquitin [Cyanidium caldarium]	Unigene65495_All//2.00E-42//AT4G05320| UBQ10 (POLYUBIQUITIN 10); protein binding	Unigene65495_All//5.00E-62//BM559461				nr -
Unigene6551_All	409	3.58	3.72	5.60	12.06	6.65	8.83	4.34	2.15	1.17	5.33E-02	9.33E-01		6.44E-01	1.46E-01		-8.58E-01	6.45E-04		-4.49E-01	1.10E-01		-1.02E+00	2.09E-02		-1.89E+00	4.84E-05	Down			Unigene6551_All//1.00E-69//FL577043					
Unigene65513_All	358	0.88	2.69	2.08	2.09	1.25	6.06	2.83	0.47	0.22	1.62E+00	3.15E-02		1.25E+00	1.54E-01		-7.39E-01	3.57E-01		1.54E+00	7.57E-04	Up	-2.60E+00	3.81E-04	Down	-3.67E+00	1.15E-05	Down	Unigene65513_All//gi|13936812|gb|AAK49947.1|AF335551_1|//1.00E-31//TGF-beta receptor-interacting protein 1 [Phaseolus vulgaris]	Unigene65513_All//2.00E-31//AT2G46290| eukaryotic translation initiation factor 3 subunit 2, putative / eIF-3 beta, putative / eIF3i, putative	Unigene65513_All//5.00E-96//gi|164319789|gb|ES803921.1|ES803921				nr +
Unigene6553_All	812	1.22	0.25	0.00	0.92	1.53	0.78	3.91	0.67	2.65	-2.29E+00	4.05E-03		-1.03E+01	1.77E-05	Down	7.30E-01	2.54E-01		-2.41E-01	7.55E-01		-2.55E+00	2.80E-11	Down	-5.60E-01	6.32E-02		Unigene6553_All//gi|19310393|gb|AAL84936.1|//1.00E-10//At2g43990/F6E13.12 [Arabidopsis thaliana]	Unigene6553_All//2.00E-42//AT2G43990| unknown protein	Unigene6553_All//0.00E+00//ES803868				nr -
Unigene65537_All	326	0.00	4.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.49E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene65537_All//gi|297794187|ref|XP_002864978.1|//4.00E-37/E1 subunit of 2-oxoglutarate dehydrogenase [Arabidopsis lyrata subsp. lyrata] >gi|297310813|gb|EFH41237.1| E1 subunit of 2-oxoglutarate dehydrogenase [Arabidopsis lyrata subsp. lyrata]	Unigene65537_All//2.00E-38//AT3G55410| 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative			ko00380|Tryptophan metabolism//ko00020|Citrate cycle (TCA cycle)//ko00310|Lysine degradation		nr +
Unigene65549_All	585	0.00	2.86	0.00	0.26	0.00	0.08	0.07	0.00	0.14	1.15E+01	1.54E-09	Up	null	null		-8.00E+00	1.65E-01		-1.73E+00	5.00E-01		-6.18E+00	6.50E-01		9.14E-01	7.48E-01		Unigene65549_All//gi|297839211|ref|XP_002887487.1|//1.00E-29//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333328|gb|EFH63746.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene65549_All//9.00E-26//AT1G18360| hydrolase, alpha/beta fold family protein	Unigene65549_All//0.00E+00//TC154452				nr +
Unigene65557_All	310	6.58	6.37	3.78	12.21	14.44	13.69	19.37	7.95	6.55	-4.63E-02	9.28E-01		-8.01E-01	9.12E-02		2.42E-01	4.57E-01		1.65E-01	6.18E-01		-1.28E+00	1.21E-08	Down	-1.56E+00	9.74E-12	Down			Unigene65557_All//2.00E-79//gi|21101812|gb|BQ414125.1|BQ414125				
Unigene6556_All	621	3.79	1.22	1.89	7.62	7.99	8.80	1.50	0.67	1.80	-1.63E+00	2.30E-04	Down	-1.01E+00	2.16E-02		6.74E-02	8.22E-01		2.08E-01	4.76E-01		-1.15E+00	7.87E-02		2.62E-01	6.28E-01		Unigene6556_All//gi|115463661|ref|NP_001055430.1|//3.00E-33//Os05g0388600 [Oryza sativa Japonica Group] >gi|113578981|dbj|BAF17344.1| Os05g0388600 [Oryza sativa Japonica Group]	Unigene6556_All//3.00E-24//AT5G12470| unknown protein	Unigene6556_All//6.00E-168//ES843590				nr -
Unigene65562_All	382	0.00	2.65	1.25	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	7.25E-06	Up	1.03E+01	7.46E-03		null	null		null	null		null	null		null	null		Unigene65562_All//gi|112950081|gb|ABI26643.1|//7.00E-23//aspartic proteinase [Cucumis sativus]	Unigene65562_All//3.00E-13//AT1G11910| aspartyl protease family protein					nr +
Unigene6557_All	561	39.54	1192.31	373.13	24.86	105.33	179.45	36.63	73.09	79.96	4.91E+00	0.00E+00	Up	3.24E+00	0.00E+00	Up	2.08E+00	2.03E-148	Up	2.85E+00	0.00E+00	Up	9.97E-01	1.94E-36		1.13E+00	1.68E-49	Up	Unigene6557_All//gi|15228108|ref|NF_178507.1|//4.00E-39//XERICO; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|42570685|ref|NP_973416.1| XERICO; protein binding / zinc ion binding [Arabidopsis thaliana] >gi|11692878|gb|AAG40042.1|AF32469 1_1 T23O15.13 [Arabidopsis thaliana]	Unigene6557_All//2.00E-40//AT2G04240| XERICO; protein binding / zinc ion binding	Unigene6557_All//0.00E+00//gi|164341020|gb|ES801628.1|ES801628				nr -
Unigene6559_All	312	16.94	5.03	5.12	22.51	15.78	31.85	25.34	20.90	13.15	-1.75E+00	1.18E-09	Down	-1.73E+00	5.18E-09	Down	-5.12E-01	1.54E-02		5.00E-01	5.82E-03		-2.78E-01	1.57E-01		-9.46E-01	2.23E-07				Unigene6559_All//2.00E-135//gi|21103364|gb|BQ415677.1|BQ415677				
Unigene656_All	1654	6.42	4.07	3.09	9.43	11.01	10.87	7.52	4.04	4.09	-6.56E-01	1.71E-04		-1.06E+00	1.29E-08	Down	2.24E-01	1.02E-01		2.05E-01	1.55E-01		-8.94E-01	7.67E-10		-8.76E-01	7.51E-10		Unigene656_All//gi|297805444|ref|XP_002870606.1|//0.00E+00//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297316442|gb|EFH46865.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene656_All//2.00E-180//AT5G41950| binding	Unigene656_All//0.00E+00//TC158613			GO:0005488//GO:0005741//GO:0006612	nr +
Unigene6560_All	464	3.16	5.24	2.98	5.80	7.35	9.83	3.28	2.43	0.77	7.31E-01	7.31E-02		-8.15E-02	8.85E-01		3.42E-01	3.47E-01		7.62E-01	6.94E-03		-4.32E-01	4.02E-01		-2.09E+00	6.46E-05	Down	Unigene6560_All//gi|224091575|ref|XP_002309286.1|//4.00E-23//predicted protein [Populus trichocarpa] >gi|222855262|gb|EEE92809.1| predicted protein [Populus trichocarpa]						nr -
Unigene65606_All	362	0.00	3.64	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.49E-07	Up	9.79E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene65606_All//gi|300122475|emb|CBK23045.2|//5.00E-06//unnamed protein product [Blastocystis hominis]						nr +
Unigene65609_All	531	0.00	3.15	0.10	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.54E-09	Up	6.65E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene65609_All//sp|Q8R4U0|STAB2_MOUSE//1.00E-11//Stabilin-2 OS=Mus musculus GN=Stab2 PE=1 SV=1						swissprot +
Unigene6561_All	841	29.99	3.74	11.59	13.27	12.49	9.02	2.46	0.30	0.71	-3.01E+00	3.46E-83	Down	-1.37E+00	2.14E-29	Down	-8.74E-02	6.64E-01		-5.56E-01	8.66E-04		-3.05E+00	5.12E-09	Down	-1.79E+00	2.11E-05	Down	Unigene6561_All//gi|15234741|ref|NP_194770.1|//9.00E-33//transcription factor [Arabidopsis thaliana] >gi|42573087|ref|NP_974640.1| transcription factor [Arabidopsis thaliana] >gi|30102576|gb|AAP21206.1| At4g30410 [Arabidopsis thaliana] >gi|32563008|emb|CAE09173.1| bHLH transcription factor [Arabidopsis thaliana]	Unigene6561_All//4.00E-34//AT4G30410| transcription factor	Unigene6561_All//0.00E+00//TC161602				nr -
Unigene65612_All	702	0.15	0.14	0.30	0.28	0.10	0.06	4.58	0.65	0.91	-4.62E-02	9.87E-01		1.02E+00	5.90E-01		-1.53E+00	4.15E-01		-2.14E+00	3.46E-01		-2.81E+00	1.30E-12	Down	-2.33E+00	8.76E-11	Down			Unigene65612_All//8.00E-109//TC157001				
Unigene65619_All	284	0.37	8.21	0.38	0.00	0.00	0.00	0.30	0.29	0.00	4.48E+00	7.48E-11	Up	2.52E-02	9.98E-01		null	null		null	null		-1.66E-02	1.01E+00		-8.22E+00	3.56E-01									
Unigene6563_All	790	0.40	0.13	0.74	2.40	1.05	1.09	6.53	2.65	5.50	-1.63E+00	2.76E-01		9.00E-01	3.77E-01		-1.20E+00	7.69E-03		-1.14E+00	1.64E-02		-1.30E+00	1.07E-07	Down	-2.48E-01	3.13E-01		Unigene6563_All//gi|30686604|ref|NP_850254.1|//2.00E-54//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|68566250|sp|Q8RX29.1|ATL21_ARATH RecName: Full=RING-H2 finger protein ATL21	Unigene6563_All//1.00E-32//AT5G06490| zinc finger (C3HC4-type RING finger) family protein					nr -
Unigene65637_All	268	0.00	6.81	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.14E-10	Up	1.10E+01	4.03E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene6564_All	1168	0.13	0.30	0.09	5.50	1.30	2.24	1.34	0.54	0.89	1.18E+00	3.72E-01		-5.59E-01	7.75E-01		-2.08E+00	1.01E-17	Down	-1.29E+00	3.88E-08	Down	-1.32E+00	6.35E-03		-5.95E-01	1.95E-01		Unigene6564_All//gi|222875434|gb|ACM68923.1|//1.00E-63//gibberellin 20-oxidase [Gossypium hirsutum]	Unigene6564_All//6.00E-35//AT4G25420| GA20OX1; gibberellin 20-oxidase	Unigene6564_All//0.00E+00//TC168612		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene6565_All	805	17.29	7.36	8.40	21.72	17.28	23.62	34.19	15.16	16.18	-1.23E+00	1.16E-14	Down	-1.04E+00	7.24E-11	Down	-3.30E-01	1.05E-02		1.21E-01	4.29E-01		-1.17E+00	4.99E-32	Down	-1.08E+00	6.15E-29	Down	Unigene6565_All//gi|240846170|dbj|BAH79623.1|//3.00E-96//Rsdv1 resistance like protein [Glycine max]	Unigene6565_All//2.00E-88//AT3G20000| TOM40; P-P-bond-hydrolysis-driven protein transmembrane transporter/ voltage-gated anion channel	Unigene6565_All//0.00E+00//gi|78336057|gb|DT556331.1|DT556331				nr -
Unigene6566_All	320	31.39	110.21	55.91	38.92	68.12	62.81	125.52	255.74	177.66	1.81E+00	5.83E-63	Up	8.33E-01	1.04E-09		8.08E-01	2.60E-13		6.91E-01	8.69E-09		1.03E+00	1.66E-75	Up	5.01E-01	4.33E-16		Unigene6566_All//gi|77745436|gb|ABB02617.1|//1.00E-41//GALS3-like protein [Solanum tuberosum]	Unigene6566_All//2.00E-38//AT5G21170| 5'-AMP-activated protein kinase beta-2 subunit, putative	Unigene6566_All//0.00E+00//TC139764				nr +
Unigene65662_All	345	2.43	65.50	49.24	1.01	0.50	2.09	0.25	0.00	0.00	4.75E+00	6.99E-106	Up	4.34E+00	8.80E-74	Up	-1.02E+00	4.23E-01		1.05E+00	2.35E-01		-7.94E+00	4.00E-01		-7.94E+00	3.56E-01		Unigene65662_All//gi|49615303|gb|AAT66913.1|//3.00E-14//dehydration-induced protein RD22-like protein 2 [Gossypium arboreum]	Unigene65662_All//2.00E-65//AT5G25610| RD22; nutrient reservoir	Unigene65662_All//1.00E-53//EV482875				nr -
Unigene65664_All	590	0.00	2.23	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.49E-07	Up	7.50E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene65664_All//gi|299116884|emb|CBN74994.1|//4.00E-07//conserved unknown protein [Ectocarpus siliculosus]						nr -
Unigene65679_All	326	0.00	4.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.79E-08	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene6568_All	585	346.21	371.32	421.18	260.14	277.25	373.89	75.53	101.38	294.06	1.01E-01	5.33E-03		2.83E-01	4.51E-18		9.19E-02	2.96E-02		5.23E-01	5.45E-55		4.25E-01	2.98E-12		1.96E+00	0.00E+00	Up	Unigene6568_All//gi|13877691|gb|AAK43923.1|AF370604_1|//3.00E-33//Unknown protein [Arabidopsis thaliana] >gi|107738118|gb|ABF83640.1| At2g43340 [Arabidopsis thaliana]	Unigene6568_All//7.00E-29//AT2G31560| unknown protein	Unigene6568_All//0.00E+00//gi|78327379|gb|DT547653.1|DT547653				nr -
Unigene65685_All	458	0.00	3.65	2.44	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.54E-09	Up	1.13E+01	3.42E-06	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene65686_All	368	0.00	2.07	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.76E-04	Up	7.18E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene65686_All//sp|P06602|EVE_DROME//2.00E-08//Segmentation protein even-skipped OS=Drosophila melanogaster GN=eve PE=1 SV=3						swissprot -
Unigene65693_All	433	0.00	3.16	3.94	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.79E-08	Up	1.19E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene65693_All//sp|Q5RIY9|PGS2_PANTR//2.00E-42//Decorin OS=Pan troglodytes GN=DCN PE=2 SV=1						swissprot +
Unigene6570_All	658	61.94	57.75	105.85	70.48	119.53	534.69	386.75	455.69	321.37	-1.01E-01	2.86E-01		7.73E-01	8.87E-32		7.62E-01	1.01E-42		2.92E+00	0.00E+00	Up	2.37E-01	5.85E-20		-2.67E-01	6.44E-22		Unigene6570_All//gi|19569160|gb|AAL92037.1|AF488305_1|//2.00E-79//apoplastic anionic guiacol peroxidase [Gossypium hirsutum]	Unigene6570_All//3.00E-44//AT3G32980| peroxidase 32 (PER32) (P32) (PRXR3)	Unigene6570_All//0.00E+00//TC159680		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +

Unigene65703_All	612	0.00	1.66	0.09	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	7.25E-06	Up	6.44E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene65703_All//sp|P12276|FAS_CHICK//5.00E-46//Fatty acid synthase OS=Gallus gallus GN=FASN PE=1 SV=5						swissprot -
Unigene6572_All	525	5.38	2.61	5.58	6.45	2.95	5.59	0.40	1.03	0.23	-1.05E+00	5.46E-03		5.19E-02	8.95E-01		-1.13E+00	3.40E-04	Down	-2.07E-01	6.06E-01		1.36E+00	1.44E-01		-8.23E-01	5.98E-01			Unigene6572_All//8.00E-170//TC172327					
Unigene65733_All	224	0.00	6.11	3.57	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	7.79E-08	Up	1.18E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene65733_All//gi|301116101|ref|XP_002905779.1|//6.00E-10//glycerol-3-phosphate dehydrogenase [Phytophthora infestans T30-4] >gi|262109079|gb|EEY67131.1| glycerol-3-phosphate dehydrogenase [Phytophthora infestans T30-4]	Unigene65733_All//1.00E-07//AT5G40610| glycerol-3-phosphate dehydrogenase (NAD+) / GPDH			ko00564|Glycerophospholipid metabolism		nr +
Unigene65734_All	449	17.01	6.55	9.61	14.87	21.55	21.42	1.22	1.02	1.33	-1.38E+00	7.67E-10	Down	-8.25E-01	1.71E-04		5.36E-01	2.47E-03		5.27E-01	4.22E-03		-2.58E-01	7.60E-01		1.21E-01	8.88E-01		Unigene65734_All//gi|297797389|ref|XP_002866579.1|//5.00E-65//UVB-resistance 8 [Arabidopsis lyrata subsp. lyrata] >gi|297312414|gb|EFH42838.1| UVB-resistance 8 [Arabidopsis lyrata subsp. lyrata]	Unigene65734_All//2.00E-65//AT5G63860| UVR8 (UVB-RESISTANCE 8); chromatin binding / guanyl-nucleotide exchange factor	Unigene65734_All//4.00E-168//gi|164318915|gb|ES828742.1|ES828742		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene65741_All	402	0.00	2.65	1.72	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.81E-06	Up	1.07E+01	6.14E-04	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene65748_All	571	0.00	3.82	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.11E-12	Up	9.35E+00	2.50E-02		null	null		null	null		null	null		null	null		Unigene65748_All//sp|B4LY29|RAS1_DROVI//4.00E-17//Ras-like protein 1 OS=Drosophila virilis GN=Ras85D PE=3 SV=1						swissprot +
Unigene6575_All	718	57.20	23.78	63.56	18.87	43.26	14.09	1.41	0.17	0.89	-1.27E+00	1.11E-43	Down	1.52E-01	8.60E-02		1.20E+00	1.60E-35	Up	-4.22E-01	5.72E-03		-3.02E+00	1.08E-04	Down	-6.71E-01	2.53E-01		Unigene6575_All//gi|224098545|ref|XP_002311214.1|//3.00E-82//cytochrome P450 probable 6-deoxocathasterone to 6-deoxoteasterone or cathasterone to teasterone [Populus trichocarpa] >gi|222851034|gb|EEE88581.1| cytochrome P450 probable 6-deoxocathasterone to 6-deoxoteasterone or cathasterone to teasterone [Populus trichocarpa]	Unigene6575_All//4.00E-68//AT5G05690| CPD (CONSTITUTIVE PHOTOMORPHOGENIC DWARF); electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene6575_All//0.00E+00//gi|78347598|gb|DT567872.1|DT567872		ko00905|Brassinosteroid biosynthesis		nr +
Unigene65757_All	229	0.00	3.32	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.76E-04	Up	7.86E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene65757_All//gi|84180633|gb|ABC54740.1|//2.00E-12//glutamine synthetase [Helicosporidium sp. ex Simulium jonesi]	Unigene65757_All//3.00E-08//AT5G35630| GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase			ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene6577_All	1038	1.36	0.39	0.31	1.92	1.89	0.96	1.59	1.57	3.72	-1.80E+00	3.03E-03		-2.14E+00	1.24E-03		-2.17E-02	9.48E-01		-1.00E+00	2.91E-02		-1.66E-02	1.01E+00		1.23E+00	1.13E-05	Up	Unigene6577_All//gi|15220333|ref|NP_171976.1|//2.00E-55//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75192500|sp|Q9MAT2.1|PPR10_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g04840 >gi|7211995|gb|AAF40466.1|AC004809_24 F13M7.17 [Arabidopsis thaliana]	Unigene6577_All//1.00E-53//AT1G04840| pentatricopeptide (PPR) repeat-containing protein					nr -
Unigene65777_All	543	1.35	1.12	1.57	1.01	1.71	1.83	3.04	0.62	0.37	-2.69E-01	7.19E-01		2.18E-01	7.57E-01		7.63E-01	3.19E-01		8.59E-01	2.35E-01		-2.30E+00	1.36E-05	Down	-3.05E+00	1.31E-07	Down	Unigene65777_All//gi|118196907|gb|ABK78670.1|//1.00E-13//plastid phosphoenolpyruvate/phosphate translocator [Brassica napus] >gi|187940348|gb|ACD39395.1| plastid phosphoenolpyruvate/phosphate translocator [Brassica napus]		Unigene65777_All//2.00E-148//EV496608				nr +
Unigene6578_All	679	1.16	0.07	2.12	3.67	2.18	3.26	1.93	1.29	1.88	-3.95E+00	8.54E-04	Down	8.74E-01	1.38E-01		-7.50E-01	5.10E-02		-1.71E-01	6.71E-01		-5.78E-01	2.83E-01		-4.00E-02	9.54E-01		Unigene6578_All//gi|42563204|ref|NP_177488.2|//2.00E-50//protein kinase family protein [Arabidopsis thaliana]	Unigene6578_All//3.00E-38//AT1G73460| protein kinase family protein	Unigene6578_All//4.00E-104//TC172403				nr +
Unigene65789_All	225	0.00	5.63	2.60	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.86E-07	Up	1.13E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene65789_All//gi|294863157|sp|B9AIH3.1|TRXR1_EMIHU//5.00E-14//RecName: Full=Thioredoxin reductase SEP1; Short=EhSEP1 >gi|222425028|dbj|BAH20464.1| thioredoxin reductase [Emiliania huxleyi]	Unigene65789_All//7.00E-09//AT3G54660| GR (GLUTATHIONE REDUCTASE); ATP binding / glutathione-disulfide reductase			ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism		nr -
Unigene6579_All	849	94.17	202.44	155.48	84.31	120.75	109.96	147.21	195.44	171.55	1.10E+00	6.58E-145	Up	7.24E-01	2.39E-53		5.18E-01	2.96E-28		3.83E-01	1.22E-13		4.09E-01	1.38E-30		2.21E-01	3.03E-09		Unigene6579_All//gi|211906480|gb|ACJ11733.1|//1.00E-136//catalase [Gossypium hirsutum]	Unigene6579_All//2.00E-131//AT4G35090| CAT2 (CATALASE 2); catalase	Unigene6579_All//0.00E+00//gi|78352993|gb|DT573267.1|DT573267		ko04146|Peroxisome//ko00380|Tryptophan metabolism		nr -
Unigene65795_All	277	0.00	0.00	0.00	0.00	0.00	0.00	0.61	0.45	3.88	null	null		null	null		null	null		null	null		-4.31E-01	7.92E-01		2.67E+00	1.42E-04	Up	Unigene65795_All//gi|19911211|dbj|BAB86932.1|//2.00E-17//glucosyltransferase-14 [Vigna angularis]	Unigene65795_All//1.00E-16//AT2G36790| UGT73C6 (UDP-glucosyl transferase 73C6); UDP-glucosyltransferase/ UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene65795_All//3.00E-10//gi|3326620|gb|AI055506.1|AI055506		ko00908|Zeatin biosynthesis		nr -
Unigene65799_All	569	0.00	2.94	1.12	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.54E-09	Up	1.01E+01	1.16E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene6580_All	701	0.90	1.16	0.00	1.14	3.44	3.61	11.04	7.81	9.78	3.69E-01	6.22E-01		-9.81E+00	1.40E-03		1.60E+00	1.34E-04	Up	1.67E+00	7.87E-05	Up	-4.99E-01	7.78E-03		-1.75E-01	3.80E-01		Unigene6580_All//gi|89274163|gb|ABD65602.1|//8.00E-38//At1g06980 [Arabidopsis thaliana]	Unigene6580_All//3.00E-35//AT1G06980| unknown protein	Unigene6580_All//1.00E-14//DW509989				nr +
Unigene65801_All	533	0.00	2.95	1.20	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	5.70E-09	Up	1.02E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene65801_All//gi|144600706|gb|ABP01596.1|//7.00E-31//heat shock protein 60 [Ageratina adenophora]	Unigene65801_All//1.00E-29//AT3G23990| HSP60 (HEAT SHOCK PROTEIN 60); ATP binding			ko03018|RNA degradation		nr -
Unigene6583_All	746	0.14	0.54	0.57	5.48	6.69	3.03	6.01	2.86	2.03	1.95E+00	1.44E-01		2.03E+00	1.39E-01		2.90E-01	3.21E-01		-8.55E-01	4.11E-03		-1.07E+00	3.36E-05	Down	-1.57E+00	5.34E-09	Down	Unigene6583_All//gi|224113399|ref|XP_002316483.1|//3.00E-11//predicted protein [Populus trichocarpa] >gi|222865523|gb|EEF02654.1| predicted protein [Populus trichocarpa]		Unigene6583_All//0.00E+00//AW187725				nr +
Unigene65831_All	344	0.00	4.12	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.06E-08	Up	8.86E+00	2.38E-01		null	null		null	null		null	null		null	null		Unigene65831_All//gi|11320962|gb|AG33978.1|AF259964_1//3.00E-25//methionine aminopeptidase-like protein [Arabidopsis thaliana]	Unigene65831_All//1.00E-26//AT2G44180| MAP2A (METHIONINE AMINOPEPTIDASE 2A); aminopeptidase/ metalloexopeptidase					nr +
Unigene65836_All	381	0.55	7.85	2.24	0.13	0.00	1.42	0.00	0.00	0.10	3.84E+00	1.67E-12	Up	2.03E+00	2.24E-02		-7.03E+00	5.50E-01		3.44E+00	1.40E-02		null	null		6.71E+00	6.40E-01		Unigene65836_All//gi|239056193|emb|CAQ58630.1|//2.00E-13//Unknown gene [Vitis vinifera]	Unigene65836_All//3.00E-22//AT5G41590| unknown protein					nr -
Unigene65838_All	475	0.00	1.60	2.80	0.10	0.07	0.10	0.00	0.00	0.00	1.06E+01	1.76E-04	Up	1.15E+01	2.39E-07	Up	-5.33E-01	8.22E-01		-1.42E-01	9.50E-01		null	null		null	null									ESTscan -
Unigene65839_All	326	6.10	2.49	0.98	12.99	5.28	5.26	0.39	0.00	0.24	-1.29E+00	5.96E-03		-2.64E+00	6.10E-06	Down	-1.30E+00	3.31E-06	Down	-1.30E+00	1.23E-05	Down	-8.60E+00	2.34E-01		-6.71E-01	7.19E-01		Unigene65839_All//gi|297800188|ref|XP_002867978.1|//4.00E-10//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313814|gb|EFH44237.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]		Unigene65839_All//1.00E-16//AIT29616				nr -
Unigene6584_All	370	26.73	64.36	31.52	41.33	29.69	35.28	65.25	72.97	25.20	1.27E+00	1.48E-25	Up	2.38E-01	2.01E-01		-4.77E-01	3.38E-04		-2.29E-01	1.40E-01		1.61E-01	1.17E-01		-1.37E+00	7.12E-37	Down	Unigene6584_All//gi|49523567|emb|CAF18245.1|//2.00E-24//STYL05A protein [Antirrhinum majus]	Unigene6584_All//2.00E-25//AT4G32551| LUG (LEUNIG); protein binding / protein heterodimerization/ transcription repressor	Unigene6584_All//6.00E-77//TC176689				nr +
Unigene6585_All	779	1.01	0.91	0.75	5.56	4.24	2.32	2.12	0.43	1.43	-1.46E-01	8.37E-01		-4.22E-01	6.21E-01		-3.91E-01	1.88E-01		-1.26E+00	1.64E-05	Down	-2.30E+00	1.36E-05	Down	-5.64E-01	2.02E-01		Unigene6585_All//gi|124109199|gb|ABM91075.1|//1.00E-111//xyloglucan endotransglycosylase/hydrolase precursor XTH-21 [Populus tremula x Populus tremuloides]	Unigene6585_All//2.00E-104//AT3G23730| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene6585_All//0.00E+00//DR462601				nr -
Unigene6586_All	560	73.62	20.36	21.20	56.93	40.09	59.36	207.10	64.71	69.01	-1.85E+00	2.29E-76	Down	-1.80E+00	1.51E-70	Down	-5.06E-01	6.25E-09		6.02E-02	6.37E-01		-1.68E+00	2.22E-227	Down	-1.59E+00	1.41E-215	Down	Unigene6586_All//gi|284433792|gb|ADB85102.1|//6.00E-45//nucleoside diphosphate kinase B [Jatropha curcas]	Unigene6586_All//6.00E-45//AT4G09320| NDPK1; ATP binding / nucleoside diphosphate kinase	Unigene6586_All//0.00E+00//gi|21101510|gb|BQ413823.1|BQ413823		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism		nr +
Unigene65868_All	216	0.00	3.28	1.48	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	1.05E+01	4.50E-02		null	null		null	null		null	null		null	null									
Unigene65874_All	397	1.19	4.98	0.67	0.88	0.52	0.91	0.00	0.00	0.00	2.07E+00	7.23E-05	Up	-8.23E-01	4.57E-01		-7.55E-01	5.67E-01		5.13E-02	9.69E-01		null	null		null	null		Unigene65874_All//gi|87116616|gb|ABD19672.1|//1.00E-07//At3g15110 [Arabidopsis thaliana]	Unigene65874_All//1.00E-08//AT3G15110| unknown protein	Unigene65874_All//1.00E-127//TC139360				nr -
Unigene65877_All	322	0.00	3.15	0.50	0.00	0.00	0.00	0.13	0.00	0.00	1.16E+01	7.24E-06	Up	8.95E+00	2.38E-01		null	null		null	null		-7.04E+00	6.49E-01		-7.04E+00	6.06E-01									
Unigene6588_All	1172	3.39	1.56	4.23	0.55	1.18	0.77	0.07	0.36	0.17	-1.12E+00	3.10E-04	Down	3.17E-01	2.81E-01		1.09E+00	6.07E-02		4.80E-01	5.50E-01		2.30E+00	5.99E-02		1.24E+00	4.68E-01		Unigene6588_All//gi|52789958|gb|AAU87582.1|//1.00E-115//MADS9 protein [Gossypium hirsutum]	Unigene6588_All//4.00E-51//AT5G13790| AGL15 (AGAMOUS-LIKE 15); DNA binding / transcription factor	Unigene6588_All//0.00E+00//TC129654	MADS			nr -
Unigene65883_All	244	0.00	9.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	2.90E-13	Up	null	null		null	null		null	null		null	null		null	null									
Unigene6589_All	294	0.71	4.14	1.63	2.54	6.91	1.08	2.73	2.27	1.49	2.54E+00	5.98E-04	Up	1.20E+00	3.02E-01		1.44E+00	1.64E-03		-1.24E+00	1.45E-01		-2.65E-01	7.04E-01		-8.74E-01	1.96E-01				Unigene6589_All//1.00E-105//CO083574				
Unigene659_All	885	8.45	5.55	4.87	7.54	5.64	6.07	6.07	2.13	3.65	-6.06E-01	4.35E-03		-7.95E-01	3.39E-04		-4.19E-01	6.22E-02		-3.13E-01	2.04E-01		-1.51E+00	8.55E-10	Down	-7.35E-01	9.50E-04		Unigene659_All//gi|18397936|ref|NP_565381.1|//1.00E-109//SQN (SQUINT); peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi|75333353|sp|Q9C566.1|CYP40_ARATH RecName: Full=Peptidyl-prolyl cis-trans isomerase CYP40; Short=PPIase CYP40; AltName: Full=Cyclophilin of 40 kDa; Short=Cyclophilin-40; AltName: Full=Rotamase CYP40; AltName: Full=Protein SQUINT >gi|13442983|gb|AAK02067.1| cyclophilin-40 [Arabidopsis thaliana] >gi|20197802|gb|AAD41985.2| expressed protein [Arabidopsis thaliana] >gi|115311455|gb|ABI93908.1| At2g15790 [Arabidopsis thaliana]	Unigene659_All//4.00E-102//AT2G15790| SQN (SQUINT); peptidyl-prolyl cis-trans isomerase	Unigene659_All//0.00E+00//TC179340			GO:0016853	nr -
Unigene65907_All	228	0.00	5.78	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.49E-07	Up	7.87E+00	6.31E-01		null	null		null	null		null	null		null	null									ESTscan +

Unigene6591_All	933	1.46	2.28	1.48	2.83	5.35	5.95	1.59	0.94	2.48	6.46E-01	1.41E-01		2.54E-02	9.84E-01		9.19E-01	3.62E-04		1.07E+00	2.18E-05	Up	-7.54E-01	1.28E-01		6.43E-01	7.71E-02		Unigene6591_All//gi|224055525|ref|XP_002298522.1|//1.00E-67//aminophospholipid ATPase [Populus trichocarpa] >gi|222845780|gb|EEE83327.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene6591_All//3.00E-67//AT3G27870| haloacid dehalogenase-like hydrolase family protein					nr -
Unigene6592_All	597	4.47	1.27	1.43	1.92	2.19	0.91	1.98	0.56	0.87	-1.81E+00	1.81E-05	Down	-1.65E+00	1.29E-04	Down	1.92E-01	8.06E-01		-1.08E+00	9.66E-02		-1.82E+00	2.42E-03		-1.19E+00	2.80E-02		Unigene6592_All//gi|297851022|ref|XP_002893392.1|//1.00E-30//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297339234|gb|EFH69651.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6592_All//3.00E-30//AT1G26610| zinc finger (C2H2 type) family protein	Unigene6592_All//4.00E-144//DN803120	C2H2			nr -
Unigene65924_All	332	0.00	2.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	9.36E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene65924_All//sp|O70401|TSN6_MOUSE//1.00E-06//Tetraspanin-6 OS=Mus musculus GN=Tspan6 PE=1 SV=1						swissprot -
Unigene65928_All	586	0.18	5.45	0.00	0.34	0.29	0.31	0.36	1.28	0.34	4.93E+00	1.73E-15	Up	-7.48E+00	3.88E-01		-2.11E-01	8.58E-01		-1.41E-01	9.34E-01		1.83E+00	2.11E-02		-8.61E-02	9.60E-01									
Unigene6593_All	617	3.31	4.68	2.59	6.78	2.90	3.66	0.41	0.00	0.00	5.01E-01	1.80E-01		-3.53E-01	4.55E-01		-1.22E+00	1.20E-05	Down	-8.90E-01	2.44E-03		-8.68E+00	4.03E-02		-8.68E+00	3.03E-02									
Unigene65936_All	224	0.00	3.62	3.57	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.36E-05	Up	1.18E+01	1.72E-04	Up	null	null		null	null		null	null		null	null										
Unigene6594_All	434	5.55	10.62	4.66	11.82	7.70	12.18	16.95	31.78	42.13	9.38E-01	9.33E-04		-2.50E-01	5.85E-01		-6.19E-01	1.36E-02		4.25E-02	9.02E-01		9.07E-01	4.72E-11		1.31E+00	4.02E-26	Up	Unigene6594_All//gi|226529165|ref|NP_001151135.1|//3.00E-06//organic anion transporter [Zea mays] >gi|195644520|gb|ACG41728.1| organic anion transporter [Zea mays]	Unigene6594_All//5.00E-07//AT3G11320| organic anion transmembrane transporter	Unigene6594_All//1.00E-149//DW506958				nr +
Unigene65945_All	395	0.00	3.85	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.10E-08	Up	1.04E+01	4.03E-03		null	null		null	null		null	null		null	null		Unigene65945_All//gi|269101041|ref|YP_003289189.1|//6.00E-06//30S ribosomal protein S5 [Ectocarpus siliculosus] >gi|266631549|emb|CAV31220.1| Chloroplast 30S ribosomal protein S5 [Ectocarpus siliculosus] >gi|270118679|emb|CAT18742.1| Chloroplast 30S ribosomal protein S5 [Ectocarpus siliculosus]						nr -
Unigene65948_All	279	0.56	3.09	0.38	0.00	0.49	0.32	26.82	72.81	19.28	2.46E+00	6.26E-03		-5.60E-01	7.75E-01		8.95E+00	3.17E-01		8.34E+00	4.73E-01		1.44E+00	2.09E-32	Up	-4.77E-01	9.98E-03		Unigene65948_All//gi|1015937|emb|CAA62943.1|//3.00E-53//extensin class I protein [Vigna unguiculata]				ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr -
Unigene6595_All	789	0.00	12.27	2.02	1.52	1.44	3.09	0.11	30.57	0.00	1.36E+01	1.95E-55	Up	1.10E+01	8.43E-09	Up	-7.32E-02	8.95E-01		1.03E+00	1.25E-02		8.16E+00	1.78E-166	Up	-6.74E+00	3.56E-01		Unigene6595_All//gi|710434|gb|AAB03097.1|//9.00E-53//Hsp22.3 [Glycine max]	Unigene6595_All//2.00E-31//AT4G10250| ATHSP22.0	Unigene6595_All//0.00E+00//gi|109869841|gb|DW498817.1|DW498817				nr -
Unigene65968_All	248	0.00	3.47	3.01	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.94E-05	Up	1.16E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene65968_All//sp|Q9V3Y3|DFP_DROME//5.00E-07//Putative defense protein CG7532 OS=Drosophila melanogaster GN=CG7532 PE=2 SV=1						swissprot +
Unigene6597_All	772	0.14	0.00	0.14	2.84	2.68	1.58	16.27	33.67	10.94	-7.08E+00	3.68E-01		2.64E-02	9.98E-01		-8.52E-02	8.35E-01		-8.46E-01	5.17E-02		1.05E+00	2.06E-25	Up	-5.72E-01	3.47E-05		Unigene6597_All//gi|18407536|ref|NP_566127.1|//1.00E-46//EDA4 (embryo sac development arrest 4); lipid binding [Arabidopsis thaliana] >gi|15010684|gb|AAK74001.1| At2g48140/F11L15.4 [Arabidopsis thaliana] >gi|16974321|gb|AAL31145.1| At2g48140/F11L15.4 [Arabidopsis thaliana] >gi|84778470|dbj|BAE73262.1| xylogen like protein 6 [Arabidopsis thaliana]	Unigene6597_All//4.00E-29//AT2G48140| EDA4 (embryo sac development arrest 4); lipid binding	Unigene6597_All//0.00E+00//gi|109879771|gb|DW508741.1|DW508741				nr +
Unigene65972_All	977	0.00	3.99	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.25E-22	Up	1.06E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene65972_All//sp|Q86BB7|WMD4_DROME//4.00E-76//Modifier of mdg4 OS=Drosophila melanogaster GN=mod(mdg4) PE=1 SV=1						swissprot +
Unigene65987_All	302	0.00	1.17	2.47	1.48	2.51	4.19	0.28	0.00	0.66	1.02E+01	2.45E-02		1.13E+01	3.26E-04	Up	7.57E-01	3.95E-01		1.50E+00	1.82E-02		-8.13E+00	4.00E-01		1.24E+00	4.68E-01									
Unigene6599_All	369	1.99	4.26	4.33	2.97	3.83	4.16	1.49	2.83	5.40	1.10E+00	3.95E-02		1.12E+00	4.27E-02		3.65E-01	5.62E-01		4.87E-01	3.95E-01		9.27E-01	1.30E-01		1.86E+00	2.29E-05	Up	Unigene6599_All//gi|131054116|gb|AB032774.1|//1.00E-12//MYB transcription factor MYB35 [Medicago truncatula]	Unigene6599_All//2.00E-13//AT5G32660| myb family transcription factor	Unigene6599_All//0.00E+00//CO116917	MYB-related	ko04712|Circadian rhythm - plant		nr -
Unigene6600_All	1360	1.69	1.19	0.70	2.49	3.24	1.63	4.38	0.89	1.38	-5.06E-01	2.34E-01		-1.26E+00	5.02E-03		3.80E-01	2.17E-01		-6.14E-01	7.15E-02		-2.30E+00	2.30E-18	Down	-1.67E+00	9.54E-13	Down	Unigene6600_All//gi|15219117|ref|NP_173059.1|//1.00E-125//AtTLP8 (TUBBY LIKE PROTEIN 8); transcription factor [Arabidopsis thaliana] >gi|75199280|sp|Q9SN48.1|TLP8_ARATH RecName: Full=Tubby-like protein 8; Short=AtTLP8 >gi|6587813|gb|AAF18504.1|AC010924_17 Contains similarity to gi|1171967 phosphodiesterase from Mus musculus and is a member of the PF|01167 Tub family [Arabidopsis thaliana] >gi|333209869|gb|AAQ062242.1|AF487269_1 tubby-like protein TULP8 [Arabidopsis thaliana] >gi|98961117|gb|ABF59042.1| At1g16070 [Arabidopsis thaliana]	Unigene6600_All//1.00E-123//AT1G16070| AtTLP8 (TUBBY LIKE PROTEIN 8); transcription factor	Unigene6600_All//0.00E+00//gi|78352241|gb|DT572515.1|DT572515	TUB			nr +
Unigene66001_All	662	0.00	4.90	2.73	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.87E-18	Up	1.14E+01	5.69E-10	Up	null	null		null	null		null	null		null	null		Unigene66001_All//gi|300176285|emb|CBK23596.2|//1.00E-25//Acetate:succinate CoA Transferase (ASCT) [Blastocystis hominis]						nr -
Unigene66011_All	407	0.00	5.98	0.13	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.73E-14	Up	7.03E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene66011_All//sp|Q8K582|MCFD2_MOUSE//2.00E-17//Multiple coagulation factor deficiency protein 2 homolog OS=Mus musculus GN=Mcfd2 PE=2 SV=1						swissprot +
Unigene66017_All	434	0.00	1.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene66017_All//gi|299115354|emb|CBV74178.1|//1.00E-06//DEAD box helicase [Ectocarpus siliculosus]						nr -
Unigene6602_All	1077	0.10	0.56	0.00	1.34	0.77	0.34	1.49	2.48	0.85	2.54E+00	2.46E-02		-6.60E+00	3.88E-01		-8.06E-01	1.35E-01		-2.00E+00	8.90E-04	Down	7.35E-01	3.31E-02		-8.10E-01	6.84E-02									
Unigene6603_All	583	5.92	6.52	0.55	14.87	12.17	2.56	2.90	0.29	9.98	1.38E-01	6.59E-01		-3.43E+00	1.11E-12	Down	-2.89E-01	1.57E-01		-2.54E+00	3.02E-26	Down	-3.34E+00	4.60E-08	Down	1.78E+00	2.16E-13	Up	Unigene6603_All//gi|115441397|ref|NP_001014978.1|//2.00E-13//Os01g0878000 [Oryza sativa Japonica Group] >gi|113534509|dbj|BAF06892.1| Os01g0878000 [Oryza sativa Japonica Group]	Unigene6603_All//1.00E-33//AT1G111120| unknown protein					nr +
Unigene66042_All	388	0.00	2.48	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.38E-05	Up	7.10E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene66042_All//sp|P19096|FAS_MOUSE//4.00E-12//Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2						swissprot -
Unigene66048_All	453	0.00	3.47	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.70E-09	Up	7.88E+00	3.95E-01		null	null		null	null		null	null		null	null										
Unigene66053_All	302	0.00	2.68	0.53	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.36E-05	Up	9.05E+00	2.38E-01		null	null		null	null		null	null		null	null		Unigene66053_All//gi|70663909|emb|CAE01636.3|//4.00E-22//OSJNBa0029402.21 [Oryza sativa (japonica cultivar-group)]	Unigene66053_All//4.00E-16//AT2G39460| RPL23AA (RIBOSOMAL PROTEIN L23AA); RNA binding / nucleotide binding / structural constituent of ribosome	Unigene66053_All//1.00E-12//gi|82756363|gb|DV849925.1|DV849925		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0006950//GO:0009642//GO:0010467//GO:0015934//GO:0022613//GO:0030312//GO:0031981	nr -
Unigene66057_All	333	0.00	3.20	0.96	0.00	0.00	0.00	0.13	0.00	0.12	1.16E+01	3.81E-06	Up	9.91E+00	4.50E-02		null	null		null	null		-6.99E+00	6.49E-01		-8.66E-02	9.68E-01				Unigene66057_All//1.00E-10//CA993708					
Unigene66058_All	363	0.00	0.14	0.44	0.14	0.00	0.00	2.80	0.12	0.00	7.13E+00	6.13E-01		8.78E+00	2.38E-01		-7.10E+00	5.49E-01		-7.10E+00	6.27E-01		-4.60E+00	3.67E-06	Down	-1.14E+01	1.35E-07	Down	Unigene66058_All//gi|297841421|ref|XP_002888592.1|//5.00E-24//rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297334433|gb|EFH64851.1| rubber elongation factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene66058_All//4.00E-24//AT1G67360| rubber elongation factor (REF) family protein	Unigene66058_All//3.00E-165//gi|13354875|gb|BG445223.1|BG445223			GO:0043231	nr +
Unigene6606_All	392	1.87	6.08	2.99	1.91	3.34	0.81	1.40	1.07	12.81	1.70E+00	1.37E-04	Up	6.78E-01	3.04E-01		8.08E-01	1.84E-01		-1.24E+00	1.45E-01		-3.95E-01	6.34E-01		3.19E+00	2.96E-22	Up		Unigene6606_All//8.00E-06//AT4G14570| acylaminoacyl-peptidase-related	Unigene6606_All//2.00E-24//TC133642				kegg +
Unigene6607_All	335	1.87	3.78	1.59	0.59	0.72	1.89	0.25	0.87	10.11	1.01E+00	9.38E-02		-2.38E-01	7.74E-01		2.75E-01	8.95E-01		1.67E+00	9.79E-02		1.79E+00	2.24E-01		5.32E+00	2.66E-21	Up			Unigene6607_All//4.00E-10//TC133642					
Unigene66084_All	516	0.00	2.85	1.34	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.11E-08	Up	1.04E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene66084_All//gi|297592390|gb|AD147118.1|//7.00E-15//nicotinamide phosphoribosyltransferase [Chlamydomonas reinhardtii]						nr -
Unigene6609_All	372	10.55	1.91	4.87	4.02	3.05	1.82	1.02	0.22	0.75	-2.47E+00	5.48E-11	Down	-1.12E+00	6.32E-04	Down	-3.95E-01	4.86E-01		-1.14E+00	3.85E-02		-2.19E+00	8.74E-02		-4.48E-01	6.41E-01		Unigene6609_All//gi|296089856|emb|CBI39775.3|//1.00E-14//unnamed protein product [Vitis vinifera]	Unigene6609_All//5.00E-06//AT5G48910| pentatricopeptide (PPR) repeat-containing protein	Unigene6609_All//0.00E+00//TC147904				nr +
Unigene66099_All	226	1.85	0.90	0.71	2.65	2.74	2.60	4.86	4.62	19.21	-1.05E+00	3.65E-01		-1.39E+00	2.80E-01		5.23E-02	9.71E-01		-2.59E-02	9.64E-01		-7.32E-02	9.11E-01		1.98E+00	1.23E-11	Up			Unigene66099_All//2.00E-17//gi|164297531|gb|EV492478.1|EV492478					
Unigene6610_All	1491	1.05	1.05	0.64	12.83	10.21	3.21	3.01	0.64	0.64	1.10E-03	1.00E+00		-7.11E-01	2.02E-01		-3.30E-01	6.89E-03		-2.00E+00	8.81E-43	Down	-2.22E+00	1.93E-13	Down	-2.23E+00	5.69E-14	Down	Unigene6610_All//gi|223452498|gb|AC189576.1|//0.00E+00//protein kinase [Glycine max]	Unigene6610_All//7.00E-135//AT3G01300| protein kinase, putative	Unigene6610_All//0.00E+00//TC132193		ko04626|Plant-pathogen interaction		nr -
Unigene66104_All	320	2.13	1.74	0.00	1.40	0.75	0.99	0.40	0.39	0.12	-2.87E-01	7.10E-01		-1.11E+01	7.63E-04	Down	-8.95E-01	4.13E-01		-5.04E-01	6.49E-01		-1.68E-02	1.02E+00		-1.67E+00	4.76E-01		Unigene66104_All//gi|77551893|gb|AB494690.1|//4.00E-12//lipin, N-terminal conserved region family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene66104_All//7.00E-13//AT5G42870| lipin family protein	Unigene66104_All//2.00E-33//TC148394				nr +
Unigene66105_All	320	0.00	4.12	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.49E-07	Up	9.70E+00	7.99E-02		null	null		null	null		null	null		null	null		Unigene66105_All//sp|Q9CQJ8|NDUB9_MOUSE//1.00E-18//NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Mus musculus GN=Ndufb9 PE=1 SV=3						swissprot -
Unigene66109_All	221	0.00	3.44	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.76E-04	Up	7.91E+00	6.31E-01		null	null		null	null		null	null		null	null										
Unigene66111_All	457	0.00	5.32	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.73E-14	Up	9.45E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene66111_All//gi|168009419|ref|XP_001757403.1|//6.00E-47//NM-ALDH [Physcomitrella patens subsp. patens] >gi|162691526|gb|EDQ77888.1| NM-ALDH [Physcomitrella patens subsp. patens]	Unigene66111_All//9.00E-47//AT2G14170| ALDH6B2; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase			ko00562|Inositol phosphate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism	GO:0006950//GO:0009081//GO:0016620//GO:0043231//GO:0046914	nr +

Unigene66115_All	339	0.00	2.69	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.61E-05	Up	7.30E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene66115_All//gi|301107486|ref|XP_002902825.1|//4.00E-14//long-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4] >gi|262097943|gb|EEY55995.1| long-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4]					nr -
Unigene66117_All	687	1.98	2.07	2.48	3.12	2.41	3.68	5.05	2.13	5.51	6.06E-02	9.22E-01		3.25E-01	5.44E-01		-3.74E-01	4.16E-01		2.40E-01	6.16E-01		-1.24E+00	4.10E-05	Down	1.27E-01	6.61E-01		Unigene66117_All//gi|224124202|ref|XP_002330130.1|//2.00E-66//pseudo response regulator [Populus trichocarpa] >gi|222871264|gb|EEF08395.1| pseudo response regulator [Populus trichocarpa]	Unigene66117_All//3.00E-60//AT5G61380| TOC1 (TIMING OF CAB EXPRESSION 1); transcription regulator/ two-component response regulator	Unigene66117_All//6.00E-162//TC177016		ko04712|Circadian rhythm - plant	GO:0004871//GO:0006351//GO:0016772//GO:0023060//GO:0043231//GO:0043565//GO:0048511//GO:0050879	nr +
Unigene6612_All	410	38.54	14.46	13.64	47.02	31.83	49.46	190.36	67.69	39.26	-1.41E+00	2.63E-20	Down	-1.50E+00	3.57E-21	Down	-5.63E-01	1.04E-06		7.30E-02	6.23E-01		-1.49E+00	3.80E-129	Down	-2.28E+00	9.99E-237	Down	Unigene6612_All//gi|17367847|sp|Q9XF97.1|RL4_PRUAR//5.00E-11//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32206.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene6612_All//8.00E-12//AT5G02870| 60S ribosomal protein L4/L1 (RPL4D)	Unigene6612_All//0.00E+00//gi|11209660|gb|BF278590.1|BF278590		ko03010|Ribosome		nr -
Unigene66120_All	374	0.00	0.00	0.00	0.00	0.00	0.00	7.46	1.23	0.75	null	null		null	null		null	null		null	null		-2.60E+00	3.10E-10	Down	-3.32E+00	2.30E-13	Down	Unigene66120_All//gi|89258498|gb|AB065462.1|//3.00E-31//short chain alcohol dehydrogenase [Gossypium hirsutum]	Unigene66120_All//4.00E-10//AT4G03140| binding / catalytic/ oxidoreductase	Unigene66120_All//3.00E-119//EX169398		ko00906|Carotenoid biosynthesis	GO:0008152//GO:0016616	nr +
Unigene66125_All	257	0.00	3.35	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.94E-05	Up	7.69E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene66125_All//gi|226455756|gb|EEH53059.1|//2.00E-15//H+-or Na+-translocating f-type, v-type and A-type ATPase superfamily [Micromonas pusilla CCMP1545]	Unigene66125_All//6.00E-06//AT4G32530| vacuolar ATP synthase, putative / V-ATPase, putative			ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0006754//GO:0006818//GO:0015077//GO:0031224//GO:0033176	nr +
Unigene6613_All	996	0.84	0.61	0.43	1.00	0.90	1.22	37.36	7.89	1.76	-4.61E-01	5.43E-01		-9.75E-01	2.37E-01		-1.54E-01	8.40E-01		2.92E-01	6.61E-01		-2.24E+00	9.12E-108	Down	-4.41E+00	2.29E-212	Down	Unigene6613_All//gi|223452482|gb|ACM89553.1|//1.00E-107//Avr9/Cf-9 induced kinase [Glycine max]	Unigene6613_All//1.00E-91//AT2G26290| ARSK1 (root-specific kinase 1); kinase	Unigene6613_All//2.00E-101//TC154062		ko04626|Plant-pathogen interaction		nr -
Unigene66134_All	581	0.00	7.24	2.20	0.00	0.00	0.08	0.15	0.00	0.14	1.28E+01	5.92E-24	Up	1.11E+01	4.68E-07	Up	null	null		6.28E+00	6.90E-01		-7.18E+00	4.00E-01		-8.58E-02	9.70E-01		Unigene66134_All//gi|6094086|sp|O65353.1|RL5_HELAN//8.00E-48//RecName: Full=60S ribosomal protein L5 >gi|3153904|gb|AAC17448.1| RPL5A-related protein [Helianthus annuus]	Unigene66134_All//1.00E-27//AT5G39740| 60S ribosomal protein L5 (RPL5B)			ko03010|Ribosome	GO:0019843//GO:0030529//GO:0043229//GO:0044444	nr +
Unigene66141_All	276	0.00	7.34	4.63	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.53E-11	Up	1.22E+01	4.68E-07	Up	null	null		null	null		null	null		null	null									
Unigene66150_All	223	0.00	5.91	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.49E-07	Up	7.90E+00	6.31E-01		null	null		null	null		null	null		null	null									
Unigene66151_All	230	0.00	4.63	1.62	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	3.81E-06	Up	1.07E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene66151_All//sp|P42570|PLU_DROME//4.00E-07//DNA replication inhibitor plutonium OS=Drosophila melanogaster GN=plu PE=1 SV=1					swissprot -
Unigene6617_All	561	0.00	2.17	1.42	2.93	0.86	2.17	2.11	1.71	1.28	1.11E+01	5.46E-07	Up	1.05E+01	1.72E-04	Up	-1.77E+00	4.68E-04	Down	-4.31E-01	4.32E-01		-3.00E-01	6.31E-01		-7.23E-01	1.77E-01		Unigene6617_All//gi|15226168|ref|NP_178215.1|//1.00E-12//nucleic acid binding / zinc ion binding [Arabidopsis thaliana]	Unigene6617_All//1.00E-13//AT2G01050| nucleic acid binding / zinc ion binding	Unigene6617_All//2.00E-10//BF277456				nr -
Unigene6618_All	589	2.04	2.15	0.72	3.55	4.21	3.37	1.58	4.54	1.56	7.40E-02	9.06E-01		-1.50E+00	2.71E-02		2.45E-01	5.94E-01		-7.43E-02	8.82E-01		1.52E+00	2.68E-05	Up	-2.16E-02	9.60E-01				Unigene6618_All//0.00E+00//gi|109869636|gb|DW498612.1|DW498612				
Unigene66182_All	431	0.00	5.41	4.08	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.90E-13	Up	1.20E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene66182_All//gi|18406991|ref|NP_566065.1|//2.00E-07//reticulon family protein (RTNLB5) [Arabidopsis thaliana] >gi|75100637|sp|Q82352.1|RTNLE_ARATH RecName: Full=Reticulon-like protein B5; Short=AtRTNLB5 >gi|37022332|gb|AAC62889.1| expressed protein [Arabidopsis thaliana] >gi|15450759|gb|AAK96651.1| At2g46170/T3F17.18 [Arabidopsis thaliana] >gi|18491131|gb|AAL69534.1| At2g46170/T3F17.18 [Arabidopsis thaliana]	Unigene66182_All//1.00E-07//AT2G46170| reticulon family protein (RTNLB5)			GO:0016020//GO:0043231	nr -
Unigene6619_All	928	4.12	0.11	0.34	5.80	3.56	2.97	2.60	0.63	0.34	-5.24E+00	3.06E-19	Down	-3.58E+00	1.83E-14	Down	-7.03E-01	3.57E-03		-9.66E-01	1.41E-04		-2.04E+00	7.09E-07	Down	-2.92E+00	2.26E-10	Down	Unigene6619_All//gi|187372954|gb|ACD03211.1|//1.00E-153//xyloglucan endotransglucosylase/hydrolase 1 [Actinidia erianthа]	Unigene6619_All//2.00E-144//AT1G11545| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene6619_All//0.00E+00//AI728143				nr +
Unigene66193_All	360	0.00	1.97	9.76	0.00	0.00	0.13	0.35	0.35	0.11	1.09E+01	3.32E-04	Up	1.33E+01	1.87E-19	Up	null	null		6.97E+00	6.90E-01		-1.65E-02	1.02E+00		-1.67E+00	4.76E-01		Unigene66193_All//gi|57013942|ref|YP_173415.1|//4.00E-09//hypothetical protein NitaMp073 [Nicotiana tabacum] >gi|56806578|dbj|BAD83479.1| hypothetical protein [Nicotiana tabacum]		Unigene66193_All//2.00E-61//DW502679				nr -
Unigene66197_All	389	0.00	1.95	1.10	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	1.76E-04	Up	1.01E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene66197_All//gi|226499118|ref|NP_001149044.1|//4.00E-10//LOC100282664 [Zea mays] >gi|195621264|gb|ACG33962.1| ARP2/3 complex 34 kDa subunit [Zea mays] >gi|195653745|gb|ACG46340.1| ARP2/3 complex 34 kDa subunit [Zea mays]	Unigene66197_All//6.00E-08//AT1G30825| DIS2 (DISTORTED TRICHOMES 2); structural molecule					nr +
Unigene662_All	1405	13.26	30.58	12.05	21.31	21.00	21.73	39.66	52.80	59.23	1.21E+00	3.72E-42	Up	-1.38E-01	3.68E-01		-2.07E-02	8.61E-01		2.83E-02	8.14E-01		4.13E-01	2.22E-14		5.79E-01	9.79E-30		Unigene662_All//gi|159895671|gb|AB010446.1|//0.00E+00//ethanolamine-phosphate cytidylyltransferase 2 [Gossypium hirsutum]	Unigene662_All//3.00E-137//AT2G38670| PECT1 (PHOSPHORYLETHANOLAMINE CYTIDYLYLTRANSFERASE 1); ethanolamine-phosphate cytidylyltransferase	Unigene662_All//0.00E+00//TC146471		ko00564|Glycerophospholipid metabolism	GO:0008152//GO:0016772	nr +
Unigene6620_All	432	7.15	17.01	14.42	8.42	6.06	2.30	0.88	0.87	0.65	1.25E+00	2.99E-08	Up	1.01E+00	4.61E-05	Up	-4.75E-01	1.41E-01		-1.87E+00	6.85E-08	Down	-1.66E-02	1.02E+00		-4.48E-01	6.41E-01		Unigene6620_All//gi|124359981|gb|ABW07997.1|//1.00E-10//contains similarity to reverse trancriptase, related [Medicago truncatula]		Unigene6620_All//0.00E+00//ES842067				nr +
Unigene66209_All	217	0.00	3.04	0.98	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.24E-04	Up	9.94E+00	1.40E-01		null	null		null	null		null	null		null	null									
Unigene6621_All	665	3.23	1.22	3.12	7.34	3.47	2.24	3.56	2.89	4.13	-1.40E+00	2.06E-03		-4.68E-02	9.28E-01		-1.08E+00	2.05E-05	Down	-1.71E+00	2.96E-09	Down	-3.00E-01	4.48E-01		2.15E-01	5.55E-01		Unigene6621_All//gi|15219860|ref|NP_176303.1|//5.00E-06//proline-rich family protein [Arabidopsis thaliana]		Unigene6621_All//1.00E-147//gi|11209106|gb|BF278120.1|BF278120		ko03040|Spliceosome		nr +
Unigene6622_All	1164	0.09	0.00	0.27	1.41	3.28	1.36	141.26	22.26	21.05	-6.49E+00	3.68E-01		1.61E+00	3.04E-01		1.22E+00	7.20E-05	Up	-5.66E-02	9.28E-01		-2.67E+00	0.00E+00	Down	-2.75E+00	0.00E+00	Down	Unigene6622_All//gi|16118887|gb|AAL14644.1|AF417856_1//3.00E-96//AOP1.2 [Arabidopsis thaliana]	Unigene6622_All//1.00E-130//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene6622_All//0.00E+00//CD486481		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr -
Unigene66222_All	419	0.00	8.71	3.94	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	9.10E-21	Up	1.19E+01	4.30E-09	Up	null	null		null	null		null	null		null	null		Unigene66222_All//gi|23394396|gb|AN31487.1|//7.00E-26//thioredoxin peroxidase [Phytophthora infestans]	Unigene66222_All//3.00E-20//AT3G11630| 2-cys peroxiredoxin, chloroplast (BAS1)				GO:0005488//GO:0005576//GO:0006952//GO:0009526//GO:0009532//GO:0016209//GO:0016705//GO:0019725	nr +
Unigene66224_All	701	0.00	9.76	3.80	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	4.40E-39	Up	1.19E+01	1.07E-14	Up	null	null		null	null		null	null		null	null		Unigene66224_All//gi|301112332|ref|XP_002905245.1|//2.00E-08//conserved hypothetical protein [Phytophthora infestans T30-4] >gi|262095575|gb|EEY53627.1| conserved hypothetical protein [Phytophthora infestans T30-4]						nr -
Unigene66227_All	370	2.26	3.42	0.00	3.90	1.77	2.32	1.26	2.49	1.40	5.98E-01	3.25E-01		-1.11E+01	1.19E-04	Down	-1.14E+00	3.09E-02		-7.52E-01	1.90E-01		9.83E-01	1.36E-01		1.55E-01	8.60E-01				Unigene66227_All//5.00E-59//CF932161				
Unigene66228_All	396	0.00	0.00	0.00	0.13	0.09	0.23	1.60	0.00	0.00	null	null		null	null		-5.32E-01	8.22E-01		8.59E-01	7.93E-01		-1.06E+01	1.23E-04	Down	-1.06E+01	7.10E-05	Down	Unigene66228_All//gi|224831509|gb|ACN66754.1|//3.00E-52//GMP [Carica papaya]	Unigene66228_All//4.00E-112//gi|164287469|gb|ES791413.1|ES791413	Unigene66228_All//4.00E-112//gi|164287469|gb|ES791413.1|ES791413		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism	GO:0008152//GO:0008905	nr -
Unigene66237_All	604	0.00	3.10	0.97	0.16	0.00	0.52	0.63	0.14	0.00	1.16E+01	1.11E-10	Up	9.92E+00	2.17E-03		-7.37E+00	3.10E-01		1.67E+00	3.09E-01		-2.19E+00	8.74E-02		-9.30E+00	4.19E-03		Unigene66237_All//gi|193878348|gb|ACF25914.1|//2.00E-39//MLO-like protein 17 [Vitis vinifera]	Unigene66237_All//4.00E-37//AT1G61560| MLO6 (MILDEW RESISTANCE LOCUS O 6); calmodulin binding	Unigene66237_All//2.00E-62//CB066568			GO:0009987//GO:0010260//GO:0031224//GO:0050832	nr +
Unigene6624_All	309	1.02	6.89	5.17	1.45	5.01	12.42	2.46	9.33	10.96	2.76E+00	6.33E-07	Up	2.35E+00	2.09E-04	Up	1.79E+00	1.40E-03		3.10E+00	4.42E-14	Up	1.92E+00	1.65E-07	Up	2.15E+00	3.44E-10	Up			Unigene6624_All//2.00E-33//TC156582				
Unigene66253_All	467	0.00	3.36	1.48	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	5.70E-09	Up	1.05E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene66253_All//gi|159477885|ref|XP_001697039.1|//2.00E-07//COP-II coat subunit [Chlamydomonas reinhardtii] >gi|158274951|gb|EDP00731.1| COP-II coat subunit [Chlamydomonas reinhardtii]				ko03022|Basal transcription factors		nr -
Unigene66254_All	431	0.00	2.12	0.25	0.69	1.04	0.52	0.00	0.00	0.00	1.10E+01	2.61E-05	Up	7.95E+00	3.95E-01		5.83E-01	6.26E-01		-4.05E-01	7.51E-01		null	null		null	null		Unigene66254_All//gi|41351515|dbj|BAD08339.1|//2.00E-45//flowering locus T like protein [Populus nigra] >gi|50199496|dbj|BAD27481.1| flowering locus T like protein [Populus nigra]	Unigene66254_All//6.00E-38//AT5G62040| brother of FT and TFL1 protein (BFT)				GO:0005543	nr -
Unigene6627_All	680	3.00	0.15	0.78	1.61	2.28	2.46	2.36	1.78	1.35	-4.33E+00	1.70E-09	Down	-1.94E+00	1.99E-04	Down	5.00E-01	3.86E-01		6.09E-01	2.56E-01		-4.07E-01	3.95E-01		-8.10E-01	6.84E-02		Unigene6627_All//gi|297805312|ref|XP_002870540.1|//1.00E-59//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297316376|gb|EFH46799.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene6627_All//6.00E-60//AT5G37570| pentatricopeptide (PPR) repeat-containing protein	Unigene6627_All//0.00E+00//TC145761				nr -
Unigene66270_All	253	0.83	7.01	1.89	0.00	0.27	0.36	0.00	0.00	0.00	3.08E+00	1.81E-06	Up	1.20E+00	3.02E-01		8.09E+00	6.05E-01		8.48E+00	4.73E-01		null	null		null	null		Unigene66270_All//gi|7262670|gb|AAF43928.1|AC012188_5//1.00E-23//Contains similarity to acid phosphatase from Lupinus albus gb|AB023385 and contains a Sterol desaturase PF|01598 domain. EST gb|AI995340 comes from this gene [Arabidopsis thaliana]	Unigene66270_All//6.00E-25//AT1G14290| SBH2 (SPHINGOID BASE HYDROXYLASE 2); catalytic/ sphingosine hydroxylase	Unigene66270_All//5.00E-126//TC135070			GO:0006631//GO:0009639//GO:0016709//GO:0030148//GO:0031224//GO:0031410//GO:0043231//GO:0046914	nr -
Unigene66273_All	309	0.00	3.28	1.03	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.24E-06	Up	1.00E+01	4.50E-02		null	null		null	null		null	null		null	null		Unigene66273_All//gi|301103089|ref|XP_002900631.1|//1.00E-06//Fimbrin-like protein [Phytophthora infestans T30-4] >gi|262101894|gb|EEY59946.1| fimbrin-like protein [Phytophthora infestans T30-4]	Unigene66273_All//1.00E-05//AT5G48460| fimbrin-like protein, putative				GO:0005488	nr -
Unigene66274_All	222	0.00	3.42	0.00	0.00	0.00	0.00	1.14	0.19	1.26	1.17E+01	1.76E-04	Up	null	null		null	null		null	null		-2.60E+00	1.44E-01		1.37E-01	9.28E-01								

Unigene66278_All	222	0.00	2.97	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene6629_All//gi|62548111|gb|AAX86687.1|//1.00E-96//non-symbiotic hemoglobin protein [Gossypium hirsutum]	Unigene6629_All//4.00E-67//AT2G16060| AHB1 (ARABIDOPSIS HEMOGLOBIN 1); oxygen binding / oxygen transporter	Unigene6629_All//0.00E+00//TC135384				
Unigene6629_All	862	0.24	8.05	0.99	0.58	0.20	15.67	33.70	262.65	359.38	5.05E+00	9.92E-34	Up	2.03E+00	2.24E-02		-1.53E+00	1.45E-01		4.76E+00	1.36E-67	Up	2.96E+00	0.00E+00	Up	3.41E+00	0.00E+00	Up							nr +
Unigene66297_All	1321	0.44	0.23	0.20	0.53	0.70	0.44	2.18	1.11	0.75	-9.21E-01	3.43E-01		-1.11E+00	2.78E-01		4.15E-01	6.06E-01		-2.48E-01	7.56E-01		-9.75E-01	3.22E-03		-1.53E+00	6.68E-06	Down	Unigene66297_All//gi|32306491|gb|AP78929.1|//1.00E-168//At5g38880 [Arabidopsis thaliana]	Unigene66297_All//7.00E-170//AT5G38880| unknown protein	Unigene66297_All//0.00E+00//DW503392				nr +
Unigene6630_All	641	2.53	8.85	13.21	6.14	16.06	14.02	0.53	1.11	1.55	1.81E+00	1.14E-10	Up	2.38E+00	3.24E-21	Up	1.39E+00	6.34E-15	Up	1.19E+00	1.05E-09	Up	1.07E+00	1.67E-01		1.56E+00	1.33E-02				Unigene6630_All//4.00E-132//CO086021				
Unigene66303_All	616	0.00	7.32	1.64	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.08E-25	Up	1.07E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene66303_All//gi|29186315 7|sp|B9A1H5.1|TRXR1_EMIHU//1.00E-50//RecName: Full=Thioredoxin reductase SEP1; Short=EhSEP1 >gi|222425028|dbj|BAH20464.1| thioredoxin reductase [Emiliania huxleyi]	Unigene66303_All//3.00E-25//AT3G54660| GR (GLUTATHIONE REDUCTASE); ATP binding / glutathione-disulfide reductase			ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism	GO:0000166//GO:0008152//GO:0009987//GO:0016209//GO:0016651	nr -
Unigene66305_All	235	0.00	0.00	0.00	0.21	0.15	0.00	3.06	0.00	0.00	null	null		null	null		-5.33E-01	8.22E-01		-7.73E+00	6.27E-01		-1.16E+01	3.26E-05	Down	-1.16E+01	1.78E-05	Down	Unigene66305_All//gi|115481730|ref|NP_001064458.1|//1.00E-17//Os10g0370500 [Oryza sativa Japonica Group] >gi|19920182|gb|AAM08614.1|AC107314_5 Putative Glucan 1,3-beta-glucosidase precursor [Oryza sativa Japonica Group] >gi|20043013|gb|AAM08821.1|AC113335_1 Putative Glucan 1,3-beta-glucosidase precursor [Oryza sativa Japonica Group] >gi|31431628|gb|AAP53379.1| Cellulase containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113639067|dbj|BAF26372.1| Os10g0370500 [Oryza sativa Japonica Group]		Unigene66305_All//3.00E-96//BF272991		ko00500|Starch and sucrose metabolism	GO:0016798//GO:0043167//GO:0044238	nr -
Unigene6631_All	419	47.33	22.61	18.05	88.10	73.47	120.51	192.33	68.73	87.66	-1.07E+00	1.79E-16	Down	-1.39E+00	1.06E-23	Down	-2.62E-01	2.04E-03		4.52E-01	3.46E-10		-1.48E+00	2.23E-132	Down	-1.13E+00	8.19E-90	Down	Unigene6631_All//gi|6688812|emb|CAB65281.1|//2.00E-69//L3 Ribosomal protein [Medicago sativa subsp. x varia]	Unigene6631_All//2.00E-86//AT3G43170| ARP1 (ARABIDOPSIS RIBOSOMAL PROTEIN 1); structural constituent of ribosome	Unigene6631_All//0.00E+00//gi|13352160|gb|BG442412.1|BG442412		ko03010|Ribosome		nr +
Unigene66316_All	651	0.00	4.20	1.55	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.44E-15	Up	1.06E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene66316_All//gi|15986721|gb|AAL11721.1|AF406608_1//8.00E-11//glucanase inhibitor protein 2 [Phytophthora sojae]						nr -
Unigene66318_All	480	0.00	2.01	0.55	0.00	0.00	0.00	0.09	0.00	0.00	1.10E+01	1.38E-05	Up	9.12E+00	7.99E-02		null	null		null	null		-6.46E+00	6.49E-01		-6.46E+00	6.06E-01		Unigene66318_All//sp|P09651|ROA1_HUMAN//3.00E-22//Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5						swissprot +
Unigene66329_All	447	0.00	0.00	0.12	0.11	0.00	1.01	0.95	2.43	4.10	null	null		6.90E+00	6.31E-01		-6.80E+00	5.49E-01		3.18E+00	3.78E-02		1.36E+00	2.43E-02		2.12E+00	9.21E-06	Up			Unigene66329_All//2.00E-21//TC175063				ESTscan +
Unigene6633_All	878	1.61	0.87	1.03	8.79	7.88	2.37	9.01	0.90	2.50	-8.94E-01	1.12E-01		-6.42E-01	2.74E-01		-1.58E-01	5.27E-01		-1.89E+00	2.27E-16	Down	-3.32E+00	2.38E-35	Down	-1.85E+00	4.71E-19	Down	Unigene6633_All//gi|3334147|sp|Q39799.1|CHI1_GOSHI//2.00E-83//RecName: Full=Endochitinase 1; Flags: Precursor >gi|1469788|gb|AAB67842.1| class I chitinase [Gossypium hirsutum] >gi|298106229|gb|ADI56257.1| class I chitinase [Gossypium hirsutum]	Unigene6633_All//4.00E-67//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene6633_All//0.00E+00//gi|78333297|gb|DT553571.1|DT553571		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene66330_All	430	0.00	2.36	0.87	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	7.24E-06	Up	9.76E+00	2.49E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene66331_All	242	0.00	0.00	0.00	0.00	0.00	0.00	5.77	0.52	5.27	null	null		null	null		null	null		null	null		-3.48E+00	5.79E-07	Down	-1.30E-01	7.83E-01		Unigene66331_All//gi|15239359|ref|NP_200860.1|//9.00E-27//late embryogenesis abundant protein-related / LEA protein-related [Arabidopsis thaliana] >gi|40823110|gb|AAR92259.1| At5g60520 [Arabidopsis thaliana]	Unigene66331_All//4.00E-28//AT5G60520| late embryogenesis abundant protein-related / LEA protein-related	Unigene66331_All//3.00E-10//TC177555			GO:0044464	nr +
Unigene66337_All	312	3.19	0.16	2.39	1.28	0.66	0.29	0.00	0.00	0.00	-4.29E+00	7.30E-05	Down	-4.15E-01	5.72E-01		-9.48E-01	4.20E-01		-2.14E+00	1.26E-01		null	null		null	null									
Unigene66341_All	367	0.00	4.69	1.60	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.98E-10	Up	1.06E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene66341_All//gi|14253163|emb|CAC39319.1|//6.00E-17//YMP4 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome		nr -
Unigene66348_All	406	0.39	0.75	0.39	0.37	0.93	0.56	0.31	1.54	8.64	9.54E-01	5.03E-01		2.55E-02	1.00E+00		1.34E+00	3.40E-01		5.96E-01	7.21E-01		2.31E+00	1.46E-02		4.79E+00	5.77E-21	Up	Unigene66348_All//gi|115480473|ref|NP_001063830.1|//3.00E-08//Os09g0544300 [Oryza sativa Japonica Group] >gi|113632063|dbj|BAF25744.1| Os09g0544300 [Oryza sativa Japonica Group]	Unigene66348_All//3.00E-09//AT4G38470| protein kinase family protein	Unigene66348_All//7.00E-37//TC176323				nr +
Unigene6635_All	915	0.00	1.94	0.58	1.63	1.92	1.23	5.78	15.07	12.67	1.09E+01	4.14E-10	Up	9.18E+00	4.03E-03		2.33E-01	6.80E-01		-4.04E-01	4.80E-01		1.38E+00	5.37E-21	Up	1.13E+00	1.44E-13	Up	Unigene6635_All//gi|225442485|ref|XP_002278313.1|//1.00E-104//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene6635_All//1.00E-82//AT1G15210| PDR7 (PLEIOTROPIC DRUG RESISTANCE 7); ATPase, coupled to transmembrane movement of substances			ko03040|Spliceosome		nr +
Unigene66354_All	236	0.00	4.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene66354_All//sp|A1L1C7|PAN3_XENTR//3.00E-14//PAB-dependent poly(A)-specific ribonuclease subunit 3 OS=Xenopus tropicalis GN=pan3 PE=2 SV=1						swissprot +
Unigene66370_All	264	0.00	3.65	1.01	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.38E-05	Up	9.98E+00	7.99E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene6638_All	319	1.64	1.59	6.51	4.53	2.59	2.12	1.59	0.66	1.50	-4.63E-02	9.73E-01		1.99E+00	1.22E-04	Up	-8.06E-01	1.35E-01		-1.09E+00	5.14E-02		-1.28E+00	1.86E-01		-8.59E-02	9.30E-01				Unigene6638_All//3.00E-23//ES823829				
Unigene66386_All	1154	0.63	0.57	0.14	1.30	0.30	1.37	2.20	1.16	1.38	-1.53E-01	8.35E-01		-2.20E+00	2.77E-02		-2.12E+00	1.37E-04	Down	8.10E-02	9.00E-01		-9.24E-01	9.33E-03		-6.71E-01	4.94E-02		Unigene66386_All//gi|297816148|ref|XP_002875957.1|//4.00E-53//EMB1796 [Arabidopsis lyrata subsp. lyrata] >gi|297321795|gb|EFH52216.1| EMB1796 [Arabidopsis lyrata subsp. lyrata]	Unigene66386_All//4.00E-39//AT3G49240| emb1796 (embryo defective 1796); ATP binding	Unigene66386_All//0.00E+00//TC130580			GO:0003006//GO:0009536//GO:0032559	nr -
Unigene6639_All	465	156.17	150.48	165.13	184.47	168.84	166.18	92.47	59.77	44.64	-5.36E-02	4.56E-01		8.05E-02	2.53E-01		-1.28E-01	2.78E-02		-1.51E-01	1.01E-02		-6.30E-01	8.92E-18		-1.05E+00	7.79E-43	Down	Unigene6639_All//gi|295687227|gb|ADG27839.1|//5.00E-55//eukaryotic translation initiation factor 5A [Gossypium hirsutum]	Unigene6639_All//8.00E-52//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor	Unigene6639_All//0.00E+00//TC177240				nr -
Unigene66392_All	279	0.00	0.54	3.24	0.00	0.00	0.00	0.00	0.00	0.00	9.09E+00	2.33E-01		1.17E+01	4.71E-05	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene6640_All	212	29.86	103.01	61.79	52.63	100.87	142.73	67.41	88.13	69.53	1.79E+00	1.75E-38	Up	1.05E+00	2.08E-10	Up	9.38E-01	1.07E-16		1.44E+00	8.75E-42	Up	3.87E-01	7.53E-04		4.47E-02	7.56E-01		Unigene6640_All//gi|145567026|gb|ABP81863.1|//5.00E-30//LATE BLOOMER 1 [Pisum sativum]	Unigene6640_All//2.00E-31//AT1G22770| GI (GIGANTEA)	Unigene6640_All//1.00E-116//ES797024		ko04712|Circadian rhythm - plant		nr -
Unigene6641_All	1004	11.26	1.62	6.95	32.94	19.58	5.49	16.21	10.99	2.74	-2.80E+00	5.82E-35	Down	-6.96E-01	7.07E-05		-7.50E-01	2.78E-18		-2.59E+00	3.41E-101	Down	-5.61E-01	4.81E-06		-2.57E+00	2.11E-57	Down	Unigene6641_All//gi|145326696|ref|NP_001077795.1|//1.00E-12//RTFL15 (ROTUNDIFOLIA LIKE 15) [Arabidopsis thaliana] >gi|238479011|ref|NP_001154459.1| RTFL15 (ROTUNDIFOLIA LIKE 15) [Arabidopsis thaliana] >gi|37955430|gb|AAP13820.1| DVL5 [Arabidopsis thaliana]	Unigene6641_All//3.00E-11//AT1G13245| RTFL17 (ROTUNDIFOLIA LIKE 17)	Unigene6641_All//3.00E-44//TC170929				nr -
Unigene66412_All	371	0.00	5.33	1.44	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.97E-11	Up	1.05E+01	4.03E-03		null	null		null	null		null	null		null	null									
Unigene66418_All	210	4.24	4.34	4.82	4.98	2.62	7.31	0.81	6.37	0.38	3.62E-02	9.79E-01		1.86E-01	7.75E-01		-9.25E-01	1.55E-01		5.54E-01	3.36E-01		2.98E+00	6.56E-06	Up	-1.09E+00	5.52E-01				Unigene66418_All//8.00E-69//TC132668				
Unigene6642_All	984	0.90	0.51	0.54	3.24	4.13	1.29	0.90	1.10	2.87	-8.12E-01	2.68E-01		-7.40E-01	3.47E-01		3.50E-01	2.92E-01		-1.33E+00	1.50E-04	Down	2.92E-01	6.33E-01		1.67E+00	2.04E-06	Up	Unigene6642_All//gi|124359162|gb|AB058685.1|//6.00E-54//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene6642_All//2.00E-08//ATMG01250| hypothetical protein	Unigene6642_All//1.00E-142//TC171513				nr +
Unigene66425_All	234	0.00	2.82	0.00	0.00	0.00	0.00	0.00	0.00	0.51	1.15E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		9.00E+00	2.42E-01									
Unigene66426_All	228	0.00	2.89	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene6644_All	278	2.82	2.37	3.26	15.41	10.03	13.16	26.16	12.63	7.45	-2.53E-01	7.26E-01		2.06E-01	7.64E-01		-6.19E-01	2.73E-02		-2.28E-01	4.90E-01		-1.05E+00	1.04E-07	Down	-1.81E+00	4.20E-17	Down	Unigene6644_All//gi|296084004|emb|CB124392.3|//2.00E-06//unnamed protein product [Vitis vinifera]		Unigene6644_All//1.00E-37//TC140693				nr +
Unigene66449_All	233	0.00	3.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene66452_All	502	0.00	5.65	2.44	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	3.83E-16	Up	1.13E+01	9.11E-07	Up	null	null		null	null		null	null		null	null		Unigene66452_All//sp|Q94516|AT5F1_DROME//1.00E-67//ATP synthase subunit b, mitochondrial OS=Drosophila melanogaster GN=ATPsyn-b PE=1 SV=2						swissprot +
Unigene66453_All	234	0.00	3.03	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.32E-04	Up	8.83E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene66453_All//sp|P0A9T3|SERA_SHIFL//6.00E-27//D-3-phosphoglycerate dehydrogenase OS=Shigella flexneri GN=serA PE=3 SV=2						swissprot -
Unigene66454_All	246	0.00	2.68	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.24E-04	Up	8.76E+00	3.95E-01		null	null		null	null		null	null		null	null									
Unigene6646_All	752	1093.59	713.82	779.56	58.89	24.36	14.71	0.96	0.28	0.48	-6.15E-01	1.64E-255		-4.88E-01	2.06E-163		-1.27E+00	1.08E-58	Down	-2.00E+00	1.05E-98	Down	-1.78E+00	2.78E-02		-1.00E+00	1.66E-01		Unigene6646_All//gi|20502881|gb|AAM22683.1|AF482951_1//1.00E-73//carbonic anhydrase [Gossypium hirsutum]	Unigene6646_All//5.00E-21//AT3G01500| CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	Unigene6646_All//0.00E+00//TC147130		ko00910|Nitrogen metabolism		nr -
Unigene66472_All	320	0.49	1.74	3.66	2.80	2.26	4.66	3.17	2.09	0.87	1.83E+00	9.02E-02		2.90E+00	4.34E-04	Up	-3.10E-01	6.65E-01		7.33E-01	1.98E-01		-6.02E-01	3.45E-01		-1.86E+00	3.53E-03		Unigene66472_All//gi|33945873|emb|CAE45585.1|//3.00E-24//coatomer alpha subunit-like protein [Lotus japonicus]	Unigene66472_All//6.00E-25//AT2G21390| coatomer protein complex, subunit alpha, putative	Unigene66472_All//2.00E-52//TC163547			GO:0004683//GO:0005488//GO:0015031//GO:0030120	nr +
Unigene66475_All	315	0.00	3.38	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.81E-06	Up	7.40E+00	6.31E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene66478_All	575	0.00	0.18	0.00	0.61	1.68	0.86	0.88	0.00	0.28	7.46E+00	3.82E-01		null	null		1.47E+00	4.80E-02		5.11E-01	6.41E-01		-9.79E+00	8.88E-04	Down	-1.67E+00	7.77E-02		Unigene66478_All//gi|297819256|ref|XP_002877511.1|//9.00E-84//translocon outer membrane complex 75-III [Arabidopsis lyrata subsp. lyrata] >gi|297323349|gb|EFH53770.1| translocon outer membrane complex 75-III [Arabidopsis lyrata subsp. lyrata]	Unigene66478_All//5.00E-85//AT3G46740| TOC75-III (TRANSLOCON AT THE OUTER ENVELOPE MEMBRANE OF CHLOROPLASTS 75-III); P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene66478_All//5.00E-85//gi|84148743|gb|DN780043.1|DN780043			GO:0006605//GO:0008320//GO:0009653//GO:0009657//GO:0009707//GO:0031224	nr +
Unigene6648_All	996	4.26	6.10	8.88	0.30	1.52	1.81	0.00	0.13	0.04	5.21E-01	3.10E-02		1.06E+00	2.33E-07	Up	2.34E+00	1.15E-04	Up	2.60E+00	7.99E-06	Up	6.98E+00	2.40E-01		5.32E+00	6.40E-01		Unigene6648_All//gi|224131780|ref|XP_002328106.1|//6.00E-73//f-box family protein [Populus trichocarpa] >gi|222837621|gb|EEE75986.1| f-box family protein [Populus trichocarpa]	Unigene6648_All//2.00E-63//AT2G27310| F-box family protein	Unigene6648_All//0.00E+00//TC144688				nr +

Unigene66485_All	844	0.00	0.30	0.00	0.65	0.78	0.43	2.96	0.50	0.61	8.23E+00	7.81E-02		null	null		2.56E-01	8.21E-01		-6.01E-01	5.66E-01		-2.58E+00	3.91E-09	Down	-2.27E+00	2.76E-08	Down	Unigene66485_All//gi|15218086|ref|NP_173520.1|//3.00E-82//emb1507 (embryo defective 1507); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding / nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana] >gi|4836892|gb|AAD30595.1|AC007369_5 Putative RNA helicase [Arabidopsis thaliana]	Unigene66485_All//1.00E-54//AT1G20960| emb1507 (embryo defective 1507); ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding / nucleoside-triphosphatase/ nucleotide binding	Unigene66485_All//0.00E+00//TC153154		ko03040|Spliceosome	GO:0000166//GO:0003006//GO:0031981//GO:0042623	nr -
Unigene66495_All	281	0.00	2.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null										ESTscan -
Unigene66498_All	226	0.00	4.71	0.47	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	3.81E-06	Up	8.88E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene66498_All//sp|Q8VDJ3|VIGLN_MOUSE//2.00E-12//Viglin OS=Mus musculus GN=Hdlbp PE=1 SV=1							swissprot -
Unigene665_All	2726	24.16	18.75	24.03	35.14	36.57	36.95	20.91	43.39	13.77	-3.66E-01	1.27E-08		-8.20E-03	9.28E-01		5.75E-02	3.67E-01		7.23E-02	2.37E-01		1.05E+00	1.95E-113	Up	-6.03E-01	2.99E-22		Unigene665_All//gi|1708424|sp|P52581.1|FRH_LUPAL//1.00E-144//RecName: Full=Isoflavone reductase homolog >gi|1230614|gb|AAB67729.1| isoflavone reductase-like protein [Lupinus albus]	Unigene665_All//2.00E-128//AT3G18680| aspartate/glutamate/uridylate kinase family protein	Unigene665_All//0.00E+00//TC141188		ko00240|Pyrimidine metabolism//ko00640|Propanoate metabolism		nr -
Unigene6650_All	1555	0.81	1.56	0.86	2.88	3.48	1.80	3.86	0.13	0.69	9.54E-01	1.99E-02		8.43E-02	8.85E-01		2.70E-01	3.39E-01		-6.79E-01	1.69E-02		-4.84E+00	2.39E-35	Down	-2.48E+00	7.29E-21	Down	Unigene6650_All//gi|15228863|ref|NP_188920.1|//2.00E-64//phosphoinositide binding [Arabidopsis thaliana]	Unigene6650_All//8.00E-39//AT5G43870| phosphoinositide binding	Unigene6650_All//0.00E+00//gi|78325552|gb|DT545826.1|DT545826				nr +
Unigene6651_All	964	4.50	1.63	1.10	3.05	2.32	1.22	0.66	0.00	0.95	-1.47E+00	1.94E-06	Down	-2.03E+00	3.56E-09	Down	-3.93E-01	3.05E-01		-1.32E+00	3.33E-04	Down	-9.36E+00	1.23E-04	Down	5.31E-01	4.07E-01		Unigene6651_All//gi|257831433|gb|ACV71017.1|//9.00E-64//UPA17 [Capsicum annuum]	Unigene6651_All//5.00E-54//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene6651_All//0.00E+00//DW484430	GRF			nr +
Unigene66510_All	504	0.00	2.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	2.00E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene66510_All//gi|159478216|ref|XP_001697200.1|//4.00E-07//trf4 poly(A) polymerase [Chlamydomonas reinhardtii] >gi|158274674|gb|EDP00455.1| trf4 poly(A) polymerase [Chlamydomonas reinhardtii]				ko03018|RNA degradation		nr +
Unigene66514_All	566	0.00	0.90	0.56	0.26	1.03	0.64	1.94	0.37	0.99	9.81E+00	4.02E-03		9.14E+00	4.50E-02		1.97E+00	7.03E-02		1.27E+00	3.81E-01		-2.40E+00	4.11E-04	Down	-9.79E-01	8.01E-02		Unigene66514_All//gi|297847952|ref|XP_002891857.1|//8.00E-34//Poly(A)-specific ribonuclease [Arabidopsis lyrata subsp. lyrata] >gi|297337699|gb|EFH68116.1| Poly(A)-specific ribonuclease [Arabidopsis lyrata subsp. lyrata]	Unigene66514_All//1.00E-33//AT1G55870| AHG2 (ABA-HYPERSENSITIVE GERMINATION 2); nucleic acid binding / ribonuclease	Unigene66514_All//8.00E-164//DW243512		ko03018|RNA degradation	GO:0005488//GO:0009725//GO:0043231	nr -
Unigene66528_All	359	0.00	3.95	2.97	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.06E-08	Up	1.15E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene66528_All//gi|124361112|gb|ABN09084.1|//6.00E-07//Ribosomal protein S6 [Medicago truncatula]	Unigene66528_All//1.00E-07//AT3G17170| RFC3 (REGULATOR OF FATTY-ACID COMPOSITION 3); structural constituent of ribosome				GO:0003676//GO:0006952//GO:0044424	nr -
Unigene66535_All	466	0.00	2.94	1.14	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.79E-08	Up	1.02E+01	4.03E-03		null	null		null	null		null	null		null	null		Unigene66535_All//sp|Q6ID09|SARM1_DROME//5.00E-48//Sterile alpha and TIR motif-containing protein 1 OS=Drosophila melanogaster GN=Ect4 PE=2 SV=1							swissprot -
Unigene6654_All	282	7.05	18.33	10.95	3.18	7.20	5.12	25.34	38.54	29.67	1.38E+00	7.08E-07	Up	6.36E-01	8.68E-02		1.18E+00	9.07E-03		6.89E-01	2.32E-01		6.05E-01	8.25E-05		2.28E-01	2.23E-01				Unigene6654_All//2.00E-147//gi|78344997|gb|DT565271.1|DT565271				
Unigene66545_All	372	0.00	2.72	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	7.24E-06	Up	9.16E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene66545_All//gi|157093503|gb|ABV22406.1|//6.00E-09//unknown [Noctiluca scintillans]							nr +
Unigene66558_All	245	0.00	4.14	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.24E-06	Up	8.76E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene66558_All//gi|300121626|emb|CBK22144.2|//4.00E-08//unnamed protein product [Blastocystis hominis]							nr -
Unigene6656_All	871	0.00	0.35	0.12	3.20	0.95	1.19	5.00	2.45	1.56	8.45E+00	4.40E-02		6.93E+00	3.95E-01		-1.76E+00	2.13E-06	Down	-1.43E+00	2.02E-04	Down	-1.03E+00	8.20E-05	Down	-1.68E+00	1.21E-09	Down	Unigene6656_All//gi|224101833|ref|XP_002334238.1|//1.00E-73//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372981|gb|ABQ62972.1| TINY-like protein [Populus trichocarpa] >gi|222870106|gb|EEF07237.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene6656_All//9.00E-38//AT3G60490| AP2 domain-containing transcription factor TINY, putative	Unigene6656_All//0.00E+00//TC169975	AP2-EREBP			nr -
Unigene66564_All	623	1.18	0.24	0.26	0.08	0.00	0.00	1.63	0.00	0.13	-2.27E+00	1.78E-02		-2.20E+00	2.77E-02		-6.32E+00	5.49E-01		-6.32E+00	6.26E-01		-1.07E+01	2.97E-07	Down	-3.67E+00	1.15E-05	Down	Unigene66564_All//gi|224093250|ref|XP_002309852.1|//1.00E-13//GRAS family transcription factor [Populus trichocarpa] >gi|222852755|gb|EEE90302.1| GRAS family transcription factor [Populus trichocarpa]	Unigene66564_All//6.00E-08//AT3G49950| scarecrow transcription factor family protein		GRAS		GO:0010468	nr +
Unigene66567_All	241	0.65	0.42	0.44	0.41	0.57	0.75	6.32	1.04	1.49	-6.31E-01	7.26E-01		-5.60E-01	7.75E-01		4.67E-01	8.75E-01		8.59E-01	6.94E-01		-2.60E+00	6.96E-06	Down	-2.09E+00	6.46E-05	Down	Unigene66567_All//gi|15239502|ref|NP_197954.1|//2.00E-21//exostosin family protein [Arabidopsis thaliana]	Unigene66567_All//8.00E-23//AT5G25820| exostosin family protein	Unigene66567_All//5.00E-18//ES808098				nr -
Unigene6657_All	503	6.35	1.51	6.03	5.65	3.22	1.62	0.50	2.08	0.71	-2.07E+00	1.81E-07	Down	-7.25E-02	8.40E-01		-8.11E-01	2.14E-02		-1.80E+00	5.07E-06	Down	2.04E+00	2.21E-03		4.99E-01	6.27E-01									
Unigene66570_All	371	0.00	2.32	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.94E-05	Up	7.16E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene66570_All//gi|301097387|ref|XP_002897788.1|//5.00E-13//methylmalonate-semialdehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262106536|gb|EEV64588.1| methylmalonate-semialdehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene66570_All//5.00E-12//AT2G14170| ALH9E82; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase			ko00562|Inositol phosphate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism	GO:0006950//GO:0008152//GO:0016491//GO:0043231//GO:0046914	nr +
Unigene66578_All	620	0.00	4.90	1.37	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.67E-17	Up	1.04E+01	9.01E-05	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene6658_All	1147	442.93	144.06	334.91	464.27	449.22	223.02	40.07	13.30	4.83	-1.62E+00	0.00E+00	Down	-4.03E-01	4.49E-71		-4.75E-02	4.19E-02		-1.06E+00	0.00E+00	Down	-1.59E+00	7.85E-84	Down	-3.05E+00	1.38E-193	Down	Unigene6658_All//gi|197090689|gb|ACH41745.1|//1.00E-86//ST5a [Brassica rapa subsp. rapa] >gi|197090691|gb|ACH41746.1| ST5a [Brassica rapa subsp. pekinensis] >gi|197090697|gb|ACH41749.1| ST5a [Brassica rapa subsp. pekinensis] >gi|197090723|gb|ACH41762.1| ST5a [Brassica rapa subsp. rapa] >gi|197090725|gb|ACH41763.1| ST5a [Brassica rapa subsp. pekinensis]	Unigene6658_All//1.00E-86//AT1G74100| SOT16 (SULFOTRANSFERASE 16); desulfoglucosinolate sulfotransferase/ sulfotransferase	Unigene6658_All//0.00E+00//TC141297		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00920|Sulfur metabolism		nr -
Unigene66587_All	659	0.16	0.00	0.32	0.00	0.10	0.00	1.54	0.06	0.24	-7.31E+00	3.68E-01		1.03E+00	5.90E-01		6.71E+00	6.05E-01		null	null		-4.60E+00	3.67E-06	Down	-2.67E+00	1.94E-04	Down	Unigene66587_All//gi|157849724|gb|ABV89645.1|//1.00E-93//auxin resistant 1 [Brassica rapa]	Unigene66587_All//1.00E-94//AT1G05180| AXR1 (AUXIN RESISTANT 1); small protein activating enzyme	Unigene66587_All//0.00E+00//gi|164249322|gb|ES821183.1|ES821183			GO:0003824//GO:0005488//GO:0006259//GO:0006950//GO:0009755//GO:0009887//GO:0032446//GO:0042579//GO:0048878	nr -
Unigene6659_All	787	3.39	2.77	4.60	1.84	1.75	0.23	1.88	0.27	0.20	-2.92E-01	4.56E-01		4.40E-01	2.05E-01		-6.87E-02	8.93E-01		-3.00E+00	1.34E-05	Down	-2.82E+00	3.44E-06	Down	-3.22E+00	3.28E-07	Down	Unigene6659_All//gi|8886948|gb|AAF80634.1|AC069251_27//2.00E-24//F2D10.21 [Arabidopsis thaliana]	Unigene6659_All//1.00E-21//AT1G20720| ATP binding / ATP-dependent DNA helicase/ ATP-dependent helicase/ DNA binding / hydrolase, acting on acid anhydrides, in phosphorus-containing anhydrides / nucleic acid binding	Unigene6659_All//3.00E-87//CA993958				nr +
Unigene66594_All	203	5.67	7.24	0.52	8.34	4.92	5.56	25.41	13.59	9.62	3.52E-01	5.29E-01		-3.43E+00	1.53E-04	Down	-7.62E-01	1.18E-01		-5.85E-01	2.66E-01		-9.03E-01	1.28E-04		-1.40E+00	8.20E-09	Down	Unigene66594_All//gi|226529753|ref|NP_001151946.1|//3.00E-16//lariat debranching enzyme [Zea mays] >gi|195651279|gb|ACG45107.1| lariat debranching enzyme [Zea mays]	Unigene66594_All//7.00E-16//AT4G31770| calcineurin-like phosphoesterase family protein	Unigene66594_All//2.00E-103//BQ404308			GO:0005506//GO:0006396//GO:0006950//GO:0016209//GO:0016787//GO:0043234	nr +
Unigene66599_All	400	0.00	2.41	1.73	0.00	0.00	0.11	0.00	0.00	0.00	1.12E+01	1.38E-05	Up	1.08E+01	6.14E-04	Up	null	null		6.82E+00	6.90E-01		null	null		null	null										
Unigene666_All	1969	1.51	0.98	1.35	2.88	4.28	11.22	8.89	11.19	37.57	-6.31E-01	7.96E-02		-1.64E-01	6.56E-01		5.71E-01	2.85E-03		1.96E+00	4.55E-47	Up	3.32E-01	1.69E-03		2.08E+00	1.89E-197	Up	Unigene666_All//gi|30686404|ref|NP_850244.1|//0.00E+00//ribose-phosphate pyrophosphokinase 1 / phosphoribosyl diphosphate synthetase 1 (PRS1) [Arabidopsis thaliana] >gi|38503403|sp|Q42581.2|KPRS1_ARATH RecName: Full=Ribose-phosphate pyrophosphokinase 1; AltName: Full=Phosphoribosyl pyrophosphate synthase 1; AltName: Full=PRS 1 >gi|51968794|dbj|BAD43089.1| phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi|51969912|dbj|BAD43648.1| phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi|51969956|dbj|BAD43670.1| phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi|51971252|dbj|BAD44318.1| phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]	Unigene666_All//1.00E-173//AT2G35390| ribose-phosphate pyrophosphokinase 1 / phosphoribosyl diphosphate synthetase 1 (PRS1)	Unigene666_All//0.00E+00//DW498448		ko00230|Purine metabolism//ko00030|Pentose phosphate pathway	GO:0009124//GO:0009536//GO:0016778	nr -
Unigene6661_All	624	1.59	1.79	5.89	5.91	6.29	5.72	1.83	1.21	0.83	1.65E-01	7.78E-01		1.89E+00	3.13E-07	Up	9.08E-02	8.31E-01		-4.71E-02	9.03E-01		-6.02E-01	3.07E-01		-1.14E+00	3.90E-02				Unigene6661_All//8.00E-13//BF272487				
Unigene66614_All	367	9.55	4.69	4.50	13.71	14.73	15.75	17.74	4.56	8.03	-1.02E+00	2.04E-03		-1.09E+00	1.80E-03		1.04E-01	7.60E-01		2.00E-01	4.79E-01		-1.96E+00	1.72E-16	Down	-1.14E+00	3.61E-08	Down	Unigene66614_All//gi|242129044|gb|ACS83601.1|//1.00E-24//ATP synthase delta subunit 1 [Gossypium hirsutum]	Unigene66614_All//3.00E-20//AT5G47030| ATP synthase delta' chain, mitochondrial	Unigene66614_All//7.00E-89//ES838788		ko00190|Oxidative phosphorylation	GO:0000275//GO:0015078//GO:0015986//GO:0019829//GO:0032559	nr -
Unigene66616_All	1084	1.16	0.70	0.10	0.55	0.67	0.75	1.76	0.96	0.59	-7.24E-01	2.27E-01		-3.56E+00	4.96E-05	Down	2.75E-01	8.00E-01		4.44E-01	6.21E-01		-8.65E-01	4.03E-02		-1.58E+00	2.42E-04	Down	Unigene66616_All//gi|297824981|ref|XP_002880373.1|//1.00E-112//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326212|gb|EFH56632.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene66616_All//3.00E-113//AT2G21300| kinesin motor family protein	Unigene66616_All//0.00E+00//gi|54117664|gb|CO493173.1|CO493173				nr +

Unigene6662_All	608	0.52	30.92	6.13	1.07	5.15	7.43	0.70	4.06	8.52	5.90E+00	2.08E-97	Up	3.57E+00	3.52E-14	Up	2.27E+00	6.02E-09	Up	2.80E+00	5.65E-15	Up	2.54E+00	6.89E-09	Up	3.61E+00	1.67E-25	Up	Unigene6662_All//gi|224143001|ref|XP_002324813.1|//2.00E-36//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372136|gb|ABQ62999.1| RAP2-like protein [Populus trichocarpa] >gi|222866247|gb|EEF03378.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene6662_All//3.00E-23//AT1G19210| AP2 domain-containing transcription factor, putative	Unigene6662_All//2.00E-99//TC173514	AP2-EREBP			nr -
Unigene66622_All	244	0.00	3.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene66623_All	345	0.00	2.06	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	3.32E-04	Up	8.85E+00	2.38E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene66625_All	663	0.00	4.81	0.32	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	3.64E-18	Up	8.33E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene66625_All//sp|P36417|GBF_DICDI//7.00E-07//G-box-binding factor OS=Dictyostelium discoideum GN=gbfA PE=1 SV=2						swissprot +
Unigene66631_All	289	0.00	3.16	1.47	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.61E-05	Up	1.05E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene66631_All//gi|298707790|emb|CBJ30221.1|//6.00E-06//RNA polymerase II transcription elongation factor Elongin/SIII, subunit elongin C [Ectocarpus siliculosus]	Unigene66631_All//5.00E-06//AT5G59140| SKP1 family protein			ko04120|Ubiquitin mediated proteolysis		nr +
Unigene66646_All	702	0.00	4.33	1.44	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.67E-17	Up	1.05E+01	1.27E-05	Up	null	null		null	null		null	null		null	null									
Unigene66650_All	238	0.00	4.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.24E-06	Up	null	null		null	null		null	null		null	null		null	null									
Unigene66658_All	307	0.00	2.15	0.35	0.16	0.22	0.00	0.00	0.00	0.00	1.11E+01	6.24E-04	Up	8.44E+00	3.95E-01		4.67E-01	9.56E-01		-7.34E+00	6.26E-01		null	null		null	null		Unigene66658_All//gi|222874280|gb|EEF11411.1|//2.00E-06//predicted protein [Populus trichocarpa]						nr -
Unigene66660_All	254	0.00	3.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene66660_All//sp|Q2SY46|DCTN2_DROPS//5.00E-23//Probable dynactin subunit 2 OS=Drosophila pseudoobscura pseudoobscura GN=Dmn PE=3 SV=1						swissprot +
Unigene66662_All	403	0.00	2.14	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	4.94E-05	Up	9.63E+00	4.50E-02		null	null		null	null		null	null		null	null		Unigene66662_All//gi|3258569|gb|AAC24379.1|//7.00E-10//Similar to yeast general negative regulator of transcription subunit 1 [Arabidopsis thaliana]	Unigene66662_All//4.00E-11//AT1G02080| transcriptional regulator-related			ko03018|RNA degradation		nr -
Unigene66664_All	413	0.00	6.01	2.58	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	3.98E-14	Up	1.13E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene66664_All//sp|P31727|CYTA_SARPE//2.00E-17//Sarcocystatin-A OS=Sarcophaga peregrina PE=1 SV=1						swissprot +
Unigene66665_All	238	0.00	3.41	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.36E-05	Up	9.81E+00	1.40E-01		null	null		null	null		null	null		null	null									
Unigene66667_All	673	0.00	2.71	0.63	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.14E-10	Up	9.31E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene66667_All//sp|P07192|MAL3_DROME//6.00E-37//Probable maltase L OS=Drosophila melanogaster GN=LvpL PE=2 SV=2						swissprot +
Unigene66668_All	243	0.00	2.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene66668_All//gi|3893085|emb|CAA10192.1|//4.00E-07//glycine-rich protein 2 [Cicer arietinum]					GO:0005488	nr -
Unigene6669_All	485	234.85	114.71	124.07	321.99	244.53	484.51	117.08	63.94	78.03	-1.03E+00	8.15E-87	Down	-9.21E-01	2.24E-69		-3.97E-01	6.39E-27		5.90E-01	4.43E-73		-8.73E-01	2.40E-40		-5.85E-01	4.51E-21		Unigene6669_All//gi|145333113|ref|NP_001078392.1|//5.00E-32//60S ribosomal protein L27 (RPL27C) [Arabidopsis thaliana]	Unigene6669_All//3.00E-33//AT4G15000| 60S ribosomal protein L27 (RPL27C)	Unigene6669_All//2.00E-158//gi|13248957|gb|BF278113.2|BF278113		ko03010|Ribosome		nr +
Unigene667_All	1640	8.26	9.79	3.93	5.38	4.70	4.43	4.59	3.54	2.48	2.45E-01	9.28E-02		-1.07E+00	4.33E-11	Down	-1.93E-01	3.77E-01		-2.78E-01	1.91E-01		-3.73E-01	5.60E-02		-8.89E-01	1.88E-06		Unigene667_All//gi|30686404|ref|NP_850244.1|//0.00E+00//ribose-phosphate pyrophosphokinase 1 / phosphoribosyl diphosphate synthetase 1 (PRS1) [Arabidopsis thaliana] >gi|38503403|sp|Q42581.2|KPRS1_ARATH RecName: Full=Ribose-phosphate pyrophosphokinase 1; AltName: Full=Phosphoribosyl pyrophosphate synthase 1; AltName: Full=PRS 1 >gi|51968794|dbj|BAD43089.1| phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi|51969912|dbj|BAD43648.1| phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi|51969956|dbj|BAD43670.1| phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] >gi|51971252|dbj|BAD44318.1| phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]	Unigene667_All//3.00E-180//AT2G35390| ribose-phosphate pyrophosphokinase 1 / phosphoribosyl diphosphate synthetase 1 (PRS1)	Unigene667_All//0.00E+00//ES829350		ko00230|Purine metabolism//ko00030|Pentose phosphate pathway	GO:0009124//GO:0009536//GO:0016778	nr +
Unigene6670_All	461	2.50	4.62	2.19	1.08	0.30	1.67	26.41	64.37	29.21	8.87E-01	4.43E-02		-1.86E-01	7.59E-01		-1.85E+00	8.43E-02		6.24E-01	4.81E-01		1.29E+00	1.37E-39	Up	1.45E-01	3.39E-01		Unigene6670_All//gi|115446353|ref|NP_001046956.1|//3.00E-22//Os02g0515600 [Oryza sativa Japonica Group] >gi|113536487|dbj|BAF08870.1| Os02g0515600 [Oryza sativa Japonica Group]	Unigene6670_All//3.00E-21//AT5G13190| INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: LPS-induced tumor necrosis factor alpha factor (InterPro:IPR006629); Has 21 Blast hits to 21 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene6670_All//1.00E-152//DW501890				nr -
Unigene66701_All	386	0.00	4.73	0.28	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.14E-10	Up	8.11E+00	3.95E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene66704_All	614	0.00	4.37	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.80E-15	Up	1.00E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene66704_All//sp|Q9Y6H1|CHCH2_HUMAN//3.00E-09//Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial OS=Homo sapiens GN=CHCHD2 PE=1 SV=1						swissprot +
Unigene66706_All	240	0.00	2.74	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.24E-04	Up	7.79E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene66706_All//sp|P21333|FLNA_HUMAN//1.00E-32//Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4						swissprot -
Unigene6671_All	592	12.73	5.56	10.61	19.35	18.15	6.41	9.21	1.41	0.81	-1.19E+00	6.14E-08	Down	-2.62E-01	2.63E-01		-9.28E-02	6.29E-01		-1.59E+00	5.37E-19	Down	-2.71E+00	3.43E-20	Down	-3.51E+00	1.00E-26	Down	Unigene6671_All//gi|12039277|gb|AAG46067.1|ACO37830_7//2.00E-06//expressed protein [Oryza sativa Japonica Group] >gi|108710365|gb|ABF98160.1| expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene6671_All//2.00E-06//AT4G10810| unknown protein	Unigene6671_All//0.00E+00//gi|11209563|gb|BF278493.1|BF278493				nr -
Unigene66712_All	348	0.00	5.97	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.94E-12	Up	9.84E+00	4.50E-02		null	null		null	null		null	null		null	null									
Unigene6672_All	298	68.30	28.91	42.35	168.67	157.62	119.27	280.92	219.22	140.77	-1.24E+00	2.47E-21	Down	-6.90E-01	4.49E-08		-9.78E-02	2.58E-01		-5.00E-01	3.79E-12		-3.58E-01	1.51E-12		-9.97E-01	9.49E-76		Unigene6672_All//gi|223635289|sp|A7Q0V4.1|METK5_VITVI//3.00E-49//RecName: Full=S-adenosylmethionine synthase 5; Short=AdoMet synthase 5; AltName: Full=Methionine adenosyltransferase 5; Short=MAT 5	Unigene6672_All//1.00E-48//AT3G17390| MTO3 (METHIONINE OVER-ACCUMULATOR 3); methionine adenosyltransferase	Unigene6672_All//1.00E-167//gi|13349569|gb|BG439912.1|BG439912		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -
Unigene66721_All	615	0.00	1.81	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	2.00E-06	Up	8.76E+00	7.98E-02		null	null		null	null		null	null		null	null		Unigene66721_All//gi|159464817|ref|XP_001690638.1|//4.00E-08//secreted protease and protease inhibitor [Chlamydomonas reinhardtii] >gi|158280138|gb|EDP05897.1| secreted protease and protease inhibitor [Chlamydomonas reinhardtii]						nr +
Unigene6673_All	443	0.35	2.63	1.32	3.15	1.87	1.43	3.05	7.08	8.63	2.89E+00	2.98E-04	Up	1.90E+00	8.47E-02		-7.55E-01	1.67E-01		-1.14E+00	4.67E-02		1.21E+00	1.56E-04	Up	1.50E+00	2.69E-07	Up								
Unigene66735_All	356	0.00	0.14	0.15	0.14	0.00	0.13	1.43	0.12	0.00	7.15E+00	6.12E-01		7.23E+00	6.31E-01		-7.13E+00	5.49E-01		-1.41E-01	9.49E-01		-3.60E+00	5.77E-03		-1.05E+01	5.54E-04	Down	Unigene66735_All//gi|188509954|gb|ACD56638.1|//2.00E-34//trehalose synthase-like protein [Gossypioides kirkii]	Unigene66735_All//4.00E-23//AT1G06410| ATTPS7; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase	Unigene66735_All//5.00E-53//DR462877		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0019203//GO:0035251	nr -
Unigene66743_All	229	0.00	2.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene66744_All	234	0.00	2.60	0.23	0.00	1.47	4.05	33.43	23.40	37.97	1.13E+01	1.16E-03		7.83E+00	6.31E-01		1.05E+01	3.01E-02		1.20E+01	1.13E-05	Up	-5.15E-01	5.69E-03		1.84E-01	3.25E-01		Unigene66744_All//gi|296080964|emb|CBI18596.3|//4.00E-08//unnamed protein product [Vitis vinifera]		Unigene66744_All//4.00E-68//DW512725				nr -
Unigene66749_All	410	0.00	4.45	0.52	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.14E-10	Up	9.02E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene66749_All//gi|242080673|ref|XP_002445106.1|//3.00E-08//hypothetical protein SORBIDRAFT_07g004175 [Sorghum bicolor] >gi|241941456|gb|EES14601.1| hypothetical protein SORBIDRAFT_07g004175 [Sorghum bicolor]						nr +
Unigene6676_All	375	2.65	2.97	2.98	6.24	1.19	7.35	0.90	2.01	1.38	1.65E-01	7.78E-01		1.70E-01	7.78E-01		-2.39E+00	6.57E-08	Down	2.35E-01	6.04E-01		1.15E+00	1.26E-01		6.15E-01	4.93E-01				Unigene6676_All//1.00E-19//TC145384				
Unigene66766_All	423	0.37	0.72	0.25	0.12	0.00	0.32	1.70	0.69	6.40	9.54E-01	5.03E-01		-5.60E-01	7.75E-01		-6.88E+00	5.49E-01		1.44E+00	6.37E-01		-1.30E+00	9.44E-02		1.91E+00	2.92E-07	Up			Unigene66766_All//4.00E-17//TC149671				
Unigene6677_All	325	9.02	28.69	6.88	11.65	11.13	23.07	10.28	6.30	6.50	1.67E+00	2.25E-15	Up	-3.90E-01	3.27E-01		-6.64E-02	8.33E-01		9.86E-01	3.24E-06		-7.06E-01	1.97E-02		-6.62E-01	2.30E-02				Unigene6677_All//1.00E-25//TC152336				
Unigene66772_All	394	0.00	2.57	1.76	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	7.24E-06	Up	1.08E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene66772_All//sp|A5A6M0|K1C17_PANTR//6.00E-61//Keratin, type I cytoskeletal 17 OS=Pan troglodytes GN=KRT17 PE=2 SV=1						swissprot +
Unigene66783_All	250	0.00	3.24	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.36E-05	Up	7.73E+00	6.31E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene66791_All	404	0.00	4.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.11E-10	Up	null	null		null	null		null	null		null	null		null	null		Unigene66791_All//sp|Q9BDJ4|LIPH_RABIT//1.00E-18//Lipase member H OS=Oryctolagus cuniculus GN=LIPH PE=2 SV=1						swissprot +
Unigene66792_All	786	0.80	1.29	0.81	3.55	2.15	0.92	1.34	0.43	0.81	6.91E-01	3.18E-01		2.54E-02	9.97E-01		-7.25E-01	4.33E-02		-1.95E+00	1.68E-06	Down	-1.66E+00	8.54E-03		-7.30E-01	2.01E-01		Unigene66792_All//gi|75156737|sp|Q8LLE5.1|PPP_SOLLC//2.00E-28//RecName: Full=Filament-like plant protein; Short=LeFPP >gi|22652089|gb|AAN03605.1|AF40530 9_1 coiled-coil protein [Solanum lycopersicum]	Unigene66792_All//7.00E-19//AT1G77580| myosin heavy chain-related	Unigene66792_All//0.00E+00//CO092670				nr +
Unigene66796_All	396	0.00	3.84	0.27	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.10E-08	Up	8.07E+00	3.95E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene66798_All	259	0.00	3.33	1.85	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.94E-05	Up	1.09E+01	7.46E-03		null	null		null	null		null	null		null	null									ESTscan +

Unigene66799_All	352	0.00	2.30	0.30	0.00	0.00	0.13	0.00	0.95	1.25	1.12E+01	9.36E-05	Up	8.24E+00	3.95E-01		null	null		7.00E+00	6.90E-01		9.89E+00	1.27E-02		1.03E+01	2.13E-03		Unigene66799_All//gi|32483159|emb|CAE02147.1|//5.00E-06//OSJNBa0081G05.2 [Oryza sativa (japonica cultivar-group)] >gi|116309213|emb|CAH66305.1| OS1GBa0135K14.2 [Oryza sativa (indica cultivar-group)] >gi|116309230|emb|CAH66320.1| OS1GBa0150M16.3 [Oryza sativa (indica cultivar-group)]						nr -
Unigene668_All	424	1.11	0.36	0.63	0.82	1.54	1.81	3.69	1.08	0.56	-1.63E+00	1.58E-01		-8.23E-01	4.57E-01		9.08E-01	3.42E-01		1.14E+00	1.89E-01		-1.77E+00	4.93E-04	Down	-2.71E+00	1.57E-06	Down	Unigene668_All//gi|30681779|ref|NP_172528.2|//1.00E-30//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] >gi|133778818|gb|AB038749.1| Atlg10580 [Arabidopsis thaliana]	Unigene668_All//8.00E-32//AT1G10580| transducin family protein / WD-40 repeat family protein	Unigene668_All//0.00E+00//TC174180		ko03040|Spliceosome	GO:0008170//GO:0008649//GO:0031461//GO:0042254	nr -
Unigene6680_All	648	0.24	0.16	0.00	5.30	2.50	2.23	1.37	2.32	1.48	-6.31E-01	7.26E-01		-7.92E+00	2.43E-01		-1.09E+00	4.94E-04	Down	-1.25E+00	1.88E-04	Down	7.61E-01	1.21E-01		1.07E-01	8.67E-01		Unigene6680_All//gi|224085057|ref|XP_002307474.1|//1.00E-35//predicted protein [Populus trichocarpa] >gi|222856923|gb|EEE94470.1| predicted protein [Populus trichocarpa]		Unigene6680_All//0.00E+00//DW517304				nr +
Unigene66819_All	320	0.00	2.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene66819_All//gi|226460572|gb|EE057866.1|//3.00E-07//predicted protein [Micromonas pusilla CCMP1545]	Unigene66819_All//9.00E-07//AT5G53770| nucleotidyltransferase family protein			ko03018|RNA degradation		nr -
Unigene6682_All	771	82.04	40.48	47.17	295.01	239.80	253.52	287.57	146.10	131.30	-1.02E+00	2.13E-47	Down	-7.99E-01	1.72E-30		-2.99E-01	5.27E-23		-2.19E-01	1.32E-11		-9.77E-01	1.15E-187		-1.13E+00	6.41E-245	Down	Unigene6682_All//gi|211905341|gb|ACJ11250.1|//1.00E-145//S-adenosyl-L-homocystein hydrolase [Gossypium hirsutum]	Unigene6682_All//1.00E-130//AT4G13940| MEE58 (MATERNAL EFFECT EMBRYO ARREST 58); adenosylhomocysteinase/ copper ion binding	Unigene6682_All//0.00E+00//gi|78340432|gb|DT560706.1|DT560706		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -
Unigene66828_All	237	0.00	2.78	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.24E-04	Up	9.81E+00	1.40E-01		null	null		null	null		null	null		null	null									
Unigene66829_All	232	0.00	4.37	1.15	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.24E-06	Up	1.02E+01	7.98E-02		null	null		null	null		null	null		null	null		Unigene66829_All//sp|Q00963|SPTCB_DROME//7.00E-23//Spectrin beta chain OS=Drosophila melanogaster GN=beta-Spec PE=1 SV=2						swissprot +
Unigene66831_All	244	0.00	3.11	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	9.35E+00	2.38E-01		null	null		null	null		null	null		null	null									
Unigene66834_All	292	0.00	9.54	1.82	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	7.43E-16	Up	1.08E+01	4.03E-03		null	null		null	null		null	null		null	null		Unigene66834_All//gi|195654217|gb|ACG46576.1|//7.00E-13//acyl-CoA-binding protein [Zea mays]	Unigene66834_All//1.00E-12//AT1G31812| ACBP6 (acyl-CoA-binding protein 6); acyl-CoA binding / phosphatidylcholine binding				GO:0005488	nr -
Unigene66838_All	364	2.16	0.00	0.73	0.00	0.00	0.00	0.46	0.69	0.00	-1.11E+01	1.09E-04	Down	-1.56E+00	8.00E-02		null	null		null	null		5.68E-01	6.74E-01		-8.86E+00	1.08E-01		Unigene66838_All//gi|15219805|ref|NP_176274.1|//2.00E-07//oxidoreductase [Arabidopsis thaliana]	Unigene66838_All//1.00E-08//AT1G60750| oxidoreductase	Unigene66838_All//4.00E-07//TC148226			GO:0004033//GO:0008152	nr +
Unigene66847_All	376	0.42	4.04	0.85	0.00	0.00	0.00	0.00	0.11	0.11	3.28E+00	6.57E-06	Up	1.03E+00	4.71E-01		null	null		null	null		6.80E+00	6.29E-01		6.73E+00	6.40E-01									
Unigene66848_All	252	0.21	3.22	0.00	0.59	0.82	1.97	0.00	0.17	0.16	3.95E+00	7.52E-04	Up	-7.70E+00	6.17E-01		4.67E-01	8.25E-01		1.73E+00	1.45E-01		7.37E+00	6.29E-01		7.30E+00	6.40E-01									
Unigene6685_All	565	1.94	0.18	0.19	1.23	2.01	0.16	30.53	8.88	13.12	-3.44E+00	1.19E-04	Down	-3.37E+00	2.66E-04	Down	7.04E-01	3.06E-01		-2.95E+00	5.83E-03		-1.78E+00	2.20E-37	Down	-1.22E+00	2.88E-22	Down	Unigene6685_All//gi|147776618|emb|CAN63020.1|//1.00E-09//hypothetical protein [Vitis vinifera]		Unigene6685_All//6.00E-32//TC157001				nr -
Unigene6686_All	1478	0.50	0.00	0.61	4.99	3.40	3.97	1.32	0.00	1.02	-8.95E+00	2.11E-04	Down	3.06E-01	6.57E-01		-5.52E-01	6.65E-03		-3.29E-01	1.50E-01		-1.04E+01	9.14E-14	Down	-3.61E-01	3.81E-01		Unigene6686_All//gi|16648953|gb|AAL24328.1|//0.00E+00//Unknown protein [Arabidopsis thaliana]	Unigene6686_All//2.00E-169//AT5G42090| LOCATED IN: endomembrane system, integral to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Transmembrane receptor, eukaryota (InterPro:IPR009637); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G09570.1); Has 303 Blast hits to 300 proteins in 77 species: Archae - 0; Bacteria - 0; Metazoa - 180; Fungi - 10; Plants - 90; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).	Unigene6686_All//0.00E+00//EE593049				nr -
Unigene66866_All	249	0.00	3.87	2.35	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	1.12E+01	2.17E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene66879_All	421	0.00	5.30	0.89	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.09E-12	Up	9.79E+00	2.49E-02		null	null		null	null		null	null		null	null									
Unigene6688_All	1676	0.00	0.24	0.03	0.09	0.08	0.03	27.37	3.89	2.61	7.92E+00	1.35E-02		4.99E+00	6.31E-01		-1.18E-01	9.10E-01		-1.73E+00	5.00E-01		-2.81E+00	2.77E-172	Down	-3.39E+00	2.67E-213	Down	Unigene6688_All//gi|115471071|ref|NP_001059134.1|//2.00E-80//Os07g0202000 [Oryza sativa Japonica Group] >gi|136109670|dbj|BAF21048.1| Os07g0202000 [Oryza sativa Japonica Group]	Unigene6688_All//1.00E-67//AT5G65550| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene6688_All//0.00E+00//TC156230		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene66889_All	412	0.00	4.67	2.07	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.73E-11	Up	1.10E+01	9.01E-05	Up	null	null		null	null		null	null		null	null									
Unigene66890_All	332	0.00	2.75	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.61E-05	Up	9.33E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene66890_All//sp|Q80YR5|SAFB2_MOUSE//7.00E-14//Scaffold attachment factor B2 OS=Mus musculus GN=Safb2 PE=1 SV=2	Unigene66890_All//5.00E-06//AT1G07350| transformer serine/arginine-rich ribonucleoprotein, putative			ko03040|Spliceosome		swissprot -
Unigene66891_All	312	0.17	0.00	0.34	0.16	0.00	0.00	4.88	0.27	0.26	-7.39E+00	6.06E-01		1.03E+00	7.02E-01		-7.32E+00	5.49E-01		-7.32E+00	6.26E-01		-4.19E+00	1.46E-08	Down	-4.26E+00	5.22E-09	Down			Unigene66891_All//1.00E-62//gi|48743008|gb|C0073527.1|C0073527					ESTscan -
Unigene66892_All	569	0.37	0.27	1.03	0.70	1.27	0.87	2.01	0.29	0.63	-4.62E-01	7.57E-01		1.48E+00	1.53E-01		8.60E-01	3.36E-01		3.18E-01	7.57E-01		-2.77E+00	7.62E-05	Down	-1.67E+00	4.10E-03		Unigene66892_All//gi|15238238|ref|NP_199010.1|//7.00E-60//binding [Arabidopsis thaliana] >gi|133778836|gb|AB038758.1| At5g41950 [Arabidopsis thaliana]	Unigene66892_All//2.00E-61//AT5G41950| binding	Unigene66892_All//0.00E+00//ES810945			GO:0005488//GO:0005741//GO:0006612	nr +
Unigene66894_All	269	0.00	2.45	0.59	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.24E-04	Up	9.21E+00	2.38E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene66907_All	686	0.00	6.28	1.47	0.00	0.00	0.07	0.00	0.00	0.00	1.26E+01	1.56E-24	Up	1.05E+01	1.27E-05	Up	null	null		6.04E+00	6.90E-01		null	null		null	null		Unigene66907_All//gi|225685853|dbj|BAH30213.1|//7.00E-74//methionine S-adenosyl transferase [Cylindrotheca closterium]	Unigene66907_All//1.00E-57//AT3G17390| MTO3 (METHIONINE OVER-ACCUMULATOR 3); methionine adenosyltransferase			ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0000166//GO:0016740//GO:0046872	nr +
Unigene6691_All	878	0.77	1.21	0.36	0.11	0.47	0.26	2.94	6.28	2.54	6.46E-01	3.37E-01		-1.09E+00	2.39E-01		2.05E+00	1.47E-01		1.18E+00	5.49E-01		1.10E+00	2.07E-06	Up	-2.09E-01	5.79E-01		Unigene6691_All//gi|115465723|ref|NP_001056461.1|//2.00E-60//Os05g0586400 [Oryza sativa Japonica Group] >gi|113580012|dbj|BAF18375.1| Os05g0586400 [Oryza sativa Japonica Group]	Unigene6691_All//1.00E-63//AT3G61670| unknown protein	Unigene6691_All//1.00E-09//gi|21103723|gb|BQ416036.1|BQ416036				nr -
Unigene66911_All	538	0.00	3.39	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.14E-10	Up	9.63E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene66911_All//gi|270303614|gb|ACZ71033.1|//4.00E-67//eukaryotic release factor 1-3 [Brassica oleracea var. botrytis]	Unigene66911_All//7.00E-67//AT3G26618| ERF1-3 (eukaryotic release factor 1-3); translation release factor				GO:0003747//GO:0006412//GO:0016020//GO:0043234//GO:0044424	nr +
Unigene66918_All	462	0.00	2.30	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.81E-06	Up	8.85E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene66918_All//gi|124360402|gb|ABN08415.1|//4.00E-39//Helicase, C-terminal [Medicago truncatula]	Unigene66918_All//9.00E-40//AT1G55150| DEAD box RNA helicase, putative (RH20)	Unigene66918_All//6.00E-10//TC179191		ko03040|Spliceosome	GO:0000166//GO:0042623	nr -
Unigene6692_All	696	4.96	1.97	3.14	5.44	5.49	4.67	2.00	0.30	0.69	-1.34E+00	1.06E-04	Down	-6.61E-01	5.75E-02		1.38E-02	9.75E-01		-2.19E-01	5.45E-01		-2.74E+00	1.03E-05	Down	-1.55E+00	2.47E-03		Unigene6692_All//gi|15234795|ref|NP_194790.1|//5.00E-88//BRS1 (BRI1 SUPPRESSOR 1); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|57012021|sp|Q9M099.1|SCP24_ARATH RecName: Full=Serine carboxypeptidase 24; AltName: Full=Serine carboxypeptidase II; AltName: Full=Carboxypeptidase D; AltName: Full=Bril suppressor 1; Contains: RecName: Full=Serine carboxypeptidase 24 chain A; AltName: Full=Serine carboxypeptidase II chain A; Contains: RecName: Full=Serine carboxypeptidase 24 chain B; AltName: Full=Serine carboxypeptidase II chain B; Flags: Precursor >gi|72699962|emb|CAB79779.1| SERINE CARBOXYPEPTIDASE II-like protein [Arabidopsis thaliana]	Unigene6692_All//3.00E-89//AT4G30610| BRS1 (BRI1 SUPPRESSOR 1); serine-type carboxypeptidase	Unigene6692_All//0.00E+00//DR461746		ko00460|Cyanoamino acid metabolism		nr -
Unigene66921_All	281	2.05	7.93	3.03	2.84	2.45	1.29	0.30	0.30	0.00	1.95E+00	4.55E-05	Up	5.66E-01	4.61E-01		-2.11E-01	8.06E-01		-1.14E+00	1.63E-01		-1.64E-02	1.01E+00		-8.23E+00	3.56E-01				Unigene66921_All//3.00E-07//TC163597					
Unigene6693_All	452	13.77	8.41	9.19	45.52	40.00	28.48	13.75	3.79	16.04	-7.12E-01	2.56E-03		-5.84E-01	1.84E-02		-1.87E-01	1.54E-01		-6.77E-01	9.21E-09		-1.86E+00	9.86E-15	Down	2.22E-01	2.76E-01		Unigene6693_All//gi|61651608|dbj|BAD91177.1|//4.00E-11//plastidic phosphate translocator-like protein2 [Mesembryanthemum crystallinum]	Unigene6693_All//3.00E-10//AT5G05820| phosphate translocator-related	Unigene6693_All//0.00E+00//TC153396				nr +
Unigene66932_All	239	0.00	4.88	2.23	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.05E-06	Up	1.11E+01	4.03E-03		null	null		null	null		null	null		null	null		Unigene66932_All//gi|226531614|ref|NP_001151000.1|//3.00E-09//LOC100284633 [Zea mays] >gi|195643514|gb|ACG41225.1| prefoldin subunit 5 [Zea mays]	Unigene66932_All//1.00E-09//AT5G23290| PDF5 (PREFOLDIN 5); unfolded protein binding					nr +

Unigene66936_All	586	0.00	4.06	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.50E-13	Up	7.51E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene66936_All//gi|130751|sp|P08289.2|PPBT_RAT//4.00E-31//RecName: Full=Alkaline phosphatase, tissue-nonspecific isozyme; Short=AP-TNAP; Short=TNSALP; AltName: Full=Alkaline phosphatase liver/bone/kidney isozyme; Flags: Precursor >gi|3901092|emb|CAA34160.1| alkaline phosphatase [Rattus norvegicus] >gi|56789527|gb|AAH88399.1| Alkaline phosphatase, liver/bone/kidney [Rattus norvegicus] >gi|149024351|gb|EDL80848.1| alkaline phosphatase, tissue-nonspecific, isoform CRA_a [Rattus norvegicus] >gi|149024352|gb|EDL80849.1| alkaline phosphatase, tissue-nonspecific, isoform CRA_a [Rattus norvegicus] >gi|149024353|gb|EDL80850.1| alkaline phosphatase, tissue-nonspecific, isoform CRA_a [Rattus norvegicus]					GO:0002237//GO:0006796//GO:0016020//GO:0016791//GO:0031960//GO:0034505//GO:0044421	nr +
Unigene66953_All	442	0.00	5.50	0.96	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.73E-14	Up	9.91E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene66953_All//gi|226496693|ref|NP_001152403.1|//2.00E-47//NHP2-like protein 1 [Zea mays] >gi|195606330|gb|ACG24995.1| NHP2-like protein 1 [Zea mays] >gi|195637812|gb|ACG38374.1| NHP2-like protein 1 [Zea mays] >gi|195655917|gb|ACG47426.1| NHP2-like protein 1 [Zea mays]	Unigene66953_All//3.00E-33//AT4G22380| ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein	Unigene66953_All//1.00E-10//TC132217		ko03040|Spliceosome	GO:0022613//GO:0030529	nr +
Unigene66954_All	267	0.00	2.09	0.00	0.00	0.00	0.00	4.12	15.65	4.33	1.10E+01	2.18E-03		null	null		null	null		null	null		1.93E+00	1.37E-10	Up	7.17E-02	9.11E-01		Unigene66954_All//gi|225463472|ref|XP_002276613.1|//2.00E-20//PREDICTED: similar to sterol 22-desaturase [Vitis vinifera]	Unigene66954_All//2.00E-17//AT2G34500| CYP710A1 (cytochrome P450, family 710, subfamily A, polypeptide 1); C-22 sterol desaturase/ oxygen binding	Unigene66954_All//6.00E-67//gi|78334162|gb|DT554436.1|DT554436		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00100|Steroid biosynthesis	GO:0005506//GO:0006091//GO:0016717//GO:0031410	nr -
Unigene66959_All	411	0.00	2.22	0.52	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	2.61E-05	Up	9.02E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene66959_All//gi|8954388|ref|NP_059377.1|//1.00E-08//ATP synthase F0 subunit 9 [Cyanidioschyzon merolae] >gi|4115801|dbj|BAA36539.1| ATP synthase protein 9 [Cyanidioschyzon merolae strain 10D]				ko00190|Oxidative phosphorylation	GO:0006810//GO:0016020	nr +
Unigene6696_All	675	2.17	0.38	5.52	2.58	1.89	0.13	0.00	0.00	0.06	-2.53E+00	1.19E-04	Down	1.35E+00	8.53E-05	Up	-4.53E-01	3.73E-01		-4.27E+00	1.13E-08	Down	null	null		5.88E+00	6.40E-01		Unigene6696_All//gi|215272285|dbj|BAG84637.1|//2.00E-74//indole-3-acetamide hydrolase [Nicotiana tabacum]	Unigene6696_All//3.00E-58//AT1G08860| AMI1 (AMIDASE 1); amidase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds / indoleacetamide hydrolase	Unigene6696_All//0.00E+00//gi|109842605|gb|DW241165.1|DW241165		ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene66969_All	342	0.00	2.82	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.38E-05	Up	9.60E+00	7.98E-02		null	null		null	null		null	null		null	null		Unigene66969_All//gi|219109896|ref|XP_002176701.1|//3.00E-21//nucleoside diphosphate kinase 1 [Phaeodactylum tricornutum CCAP 1055/1] >gi|217411236|gb|EEC51164.1| nucleoside diphosphate kinase 1 [Phaeodactylum tricornutum CCAP 1055/1]	Unigene66969_All//2.00E-19//AT4G09320| NDPK1; ATP binding / nucleoside diphosphate kinase			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism	GO:0005576//GO:0006970//GO:0009206//GO:0009209//GO:0009536//GO:0010038//GO:0016020//GO:0016776//GO:0032559//GO:0042579//GO:0043169	nr +
Unigene66970_All	419	0.00	1.57	0.51	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	6.24E-04	Up	8.99E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene66970_All//gi|163676372|gb|ABV40381.1|//9.00E-13//low-molecular-weight glutenin subunit [Aegilops longissima]						nr -
Unigene66974_All	305	26.25	9.64	13.44	46.87	44.26	50.79	200.17	89.90	82.03	-1.45E+00	5.46E-11	Down	-9.65E-01	7.40E-06		-8.29E-02	6.30E-01		1.16E-01	4.97E-01		-1.15E+00	2.37E-68	Down	-1.29E+00	2.77E-83	Down	Unigene66974_All//gi|225462164|ref|XP_002266780.1|//2.00E-52//PREDICTED: similar to elongation factor 2 [Vitis vinifera]	Unigene66974_All//9.00E-52//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene66974_All//2.00E-169//gi|78346566|gb|DT566840.1|DT566840			GO:0006950//GO:0008135//GO:0009536//GO:0010467//GO:0016020//GO:0017111//GO:0031981//GO:0032561//GO:0046914	nr -
Unigene6698_All	533	41.23	7.03	44.96	6.36	3.17	1.86	0.00	0.00	0.00	-2.55E+00	6.45E-61	Down	1.25E-01	3.49E-01		-1.01E+00	1.38E-03		-1.77E+00	6.83E-07	Down	null	null		null	null		Unigene6698_All//gi|12620883|gb|AAG61121.1|AF329935_1|//9.00E-21//ribulose-1,5-bisphosphate carboxylase/oxygenase activase 2 [Gossypium hirsutum]	Unigene6698_All//2.00E-14//AT2G39730| RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	Unigene6698_All//2.00E-74//EX169525				nr +
Unigene66981_All	412	1.52	0.49	0.00	7.98	3.93	0.66	3.49	1.42	1.45	-1.63E+00	9.23E-02		-1.06E+01	1.40E-03		-1.02E+00	1.39E-03		-3.60E+00	3.10E-14	Down	-1.30E+00	1.07E-02		-1.27E+00	9.34E-03		Unigene66981_All//gi|75333913|sp|Q9FII5.1|Y5I48_ARATH//1.00E-30//RecName: Full=Probable leucine-rich repeat receptor-like protein kinase At5g61480; Flags: Precursor >gi|10177178|dbj|BAB10447.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|224589737|gb|ACN59400.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene66981_All//4.00E-32//AT5G61480| leucine-rich repeat transmembrane protein kinase, putative	Unigene66981_All//4.00E-137//DW520090			GO:0004672//GO:0004871//GO:0006464//GO:0016628//GO:0031224//GO:0031410//GO:0032559	nr -
Unigene66984_All	209	31.29	12.61	11.72	33.61	31.47	43.87	100.95	45.40	25.92	-1.31E+00	5.64E-08	Down	-1.42E+00	1.97E-08	Down	-9.48E-02	7.27E-01		3.84E-01	5.02E-02		-1.15E+00	4.46E-24	Down	-1.96E+00	2.21E-53	Down	Unigene66984_All//gi|17369182|sp|Q9ESN6.1|RL30_ELPES//8.00E-30//RecName: Full=60S ribosomal protein L30 >gi|6984132|gb|AAF34766.1|AF227621_1 60S ribosomal protein L30 [Euphorbia esula]	Unigene66984_All//1.00E-29//AT1G77940| 60S ribosomal protein L30 (RPL30B)	Unigene66984_All//9.00E-115//TC147407		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934	nr +
Unigene66988_All	520	0.00	5.36	1.33	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.43E-16	Up	1.04E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene66988_All//gi|15233853|ref|NP_194183.1|//6.00E-09//ATR1 (ARABIDOPSIS P450 REDUCTASE 1); NADPH-hemoprotein reductase [Arabidopsis thaliana] >gi|4220538|emb|CAA23011.1| NADPH-ferrihemoprotein reductase ATR1 [Arabidopsis thaliana] >gi|7269302|emb|CAB79362.1| NADPH-ferrihemoprotein reductase ATR1 [Arabidopsis thaliana] >gi|15451216|gb|AAK96879.1| NADPH-ferrihemoprotein reductase ATR1 [Arabidopsis thaliana] >gi|30725526|gb|AAP37785.1| At4g24520 [Arabidopsis thaliana]	Unigene66988_All//2.00E-10//AT4G24520| ATR1 (ARABIDOPSIS P450 REDUCTASE 1); NADPH-hemoprotein reductase			ko00330|Arginine and proline metabolism	GO:0006575//GO:0006950//GO:0009607//GO:0016653//GO:0043231	nr +
Unigene66991_All	406	0.00	3.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.86E-07	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene6700_All	1937	0.00	0.00	0.00	0.00	0.00	0.00	7.05	2.27	4.46	null	null		null	null		null	null		null	null		-1.64E+00	1.70E-26	Down	-6.60E-01	6.52E-07		Unigene6700_All//gi|224072801|ref|XP_002303888.1|//0.00E+00//AP2 domain-containing transcription factor [Populus trichocarpa] >gi|222841320|gb|EEE78867.1| AP2 domain-containing transcription factor [Populus trichocarpa]	Unigene6700_All//2.00E-169//AT1G51190| PLT2 (PLETHORA 2); transcription factor	Unigene6700_All//1.00E-51//gi|84171256|gb|DR459904.1|DR459904	AP2-EREBP			nr -
Unigene67000_All	328	0.00	4.63	1.30	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.10E-08	Up	1.03E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene67000_All//sp|Q9VQ66|NPLP4_DROME//2.00E-09//Neuropeptide-like 4 OS=Drosophila melanogaster GN=Nplp4 PE=1 SV=1						swissprot +
Unigene67002_All	606	0.00	2.09	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	2.86E-07	Up	9.46E+00	1.38E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene67006_All	366	0.00	2.08	1.16	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.76E-04	Up	1.02E+01	1.38E-02		null	null		null	null		null	null		null	null									
Unigene6701_All	780	13.15	7.54	7.58	7.47	15.58	5.85	0.00	0.00	0.00	-8.03E-01	7.44E-06		-7.95E-01	1.83E-05		1.06E+00	1.06E-11	Up	-3.54E-01	1.79E-01		null	null		null	null		Unigene6701_All//gi|60476418|gb|AAX21348.1|//6.00E-49//lateral organ boundaries-like 1 [Lotus japonicus]	Unigene6701_All//2.00E-48//AT3G11090| LBD21 (LOB DOMAIN-CONTAINING PROTEIN 21)	Unigene6701_All//0.00E+00//gi|164304328|gb|ES824510.1|ES824510		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene6702_All	468	1.68	5.52	3.41	3.83	3.75	4.15	0.81	3.48	2.55	1.72E+00	5.62E-05	Up	1.03E+00	6.23E-02		-3.02E-02	9.51E-01		1.15E-01	8.17E-01		2.10E+00	5.14E-05	Up	1.65E+00	3.87E-03				Unigene6702_All//3.00E-64//AI055130				
Unigene67021_All	241	0.00	3.78	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	7.79E+00	6.31E-01		null	null		null	null		null	null		null	null		Unigene67021_All//gi|301104697|ref|XP_002901433.1|//2.00E-07//UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase, putative [Phytophthora infestans T30-4] >gi|262100908|gb|EEY58960.1| UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase, putative [Phytophthora infestans T30-4]	Unigene67021_All//7.00E-05//AT1G25054| UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase					nr -
Unigene67029_All	644	0.00	2.99	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	5.73E-11	Up	9.69E+00	4.03E-03		null	null		null	null		null	null		null	null		Unigene67029_All//gi|300256056|gb|EFJ40332.1|//9.00E-12//hypothetical protein VOLCADRAFT_108214 [Volvox carteri f. nagariensis]						nr -
Unigene67032_All	334	0.00	3.03	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.24E-06	Up	9.32E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67032_All//sp|Q9NR09|BIRC6_HUMAN//2.00E-16//Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens GN=BIRC6 PE=1 SV=1						swissprot -
Unigene67036_All	241	0.43	1.05	0.00	0.21	0.43	0.00	1.93	0.87	24.47	1.28E+00	4.35E-01		-8.76E+00	3.88E-01		1.05E+00	8.06E-01		-7.69E+00	6.26E-01		-1.15E+00	2.53E-01		3.66E+00	2.90E-29	Up			Unigene67036_All//9.00E-66//DT463763				
Unigene6704_All	337	0.62	1.95	5.21	4.73	2.96	8.18	1.51	0.74	2.13	1.65E+00	8.13E-02		3.07E+00	3.99E-06	Up	-6.75E-01	1.88E-01		7.89E-01	3.96E-02		-1.02E+00	2.88E-01		4.99E-01	5.01E-01				Unigene6704_All//3.00E-137//gi|109861706|gb|DW490683.1|DW490683				ESTscan +
Unigene67042_All	241	0.00	2.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene67042_All//sp|P14785|CCNA_DROME//2.00E-15//G2/mitotic-specific cyclin-A OS=Drosophila melanogaster GN=CycA PE=2 SV=3						swissprot -
Unigene67046_All	344	0.91	1.03	0.31	6.37	1.90	1.18	0.86	0.49	0.12	1.76E-01	8.83E-01		-1.56E+00	3.29E-01		-1.74E+00	4.17E-05	Down	-2.43E+00	1.09E-06	Down	-8.24E-01	5.40E-01		-2.89E+00	6.76E-02		Unigene67046_All//gi|224096288|ref|XP_002308966.1|//7.00E-38//cation proton exchanger [Populus trichocarpa] >gi|222854942|gb|EEE92489.1| cation proton exchanger [Populus trichocarpa]	Unigene67046_All//7.00E-37//AT3G53720| ATCHX20 (CATION/H+ EXCHANGER 20); monovalent cation:proton antiporter/ sodium:hydrogen antiporter	Unigene67046_All//7.00E-160//gi|48830746|gb|CO129136.1|CO129136			GO:0006811//GO:0015298//GO:0031224//GO:0050896	nr -

Unigene67052_All	294	0.00	2.24	0.18	0.00	0.00	0.31	4.75	2.56	1.36	1.11E+01	6.24E-04	Up	7.50E+00	6.31E-01		null	null		8.26E+00	4.73E-01		-8.91E-01	7.94E-02		-1.81E+00	6.10E-04	Down	Unigene67052_All//gi|297849514|ref|XP_002892638.1|//2.00E-20//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338480|gb|EFH68897.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene67052_All//9.00E-21//AT1G11350| SD1-13 (S-DOMAIN-1 13); kinase/ protein kinase/ protein serine/threonine kinase	Unigene67052_All//5.00E-68//CO081718			GO:0000166//GO:0004672//GO:0009987	nr -
Unigene67063_All	220	3.33	1.61	5.57	62.72	37.25	24.22	10.57	1.71	0.91	-1.05E+00	2.14E-01		7.42E-01	2.46E-01		-7.52E-01	6.07E-08		-1.37E+00	2.59E-18	Down	-2.63E+00	9.93E-09	Down	-3.55E+00	7.48E-12	Down	Unigene67063_All//gi|41367038|emb|CAF22024.1|//2.00E-06//amino acid permease [Brassica napus]	Unigene67063_All//2.00E-07//AT5G09220| AAP2 (AMINO ACID PERMEASE 2); amino acid transmembrane transporter	Unigene67063_All//9.00E-75//gi|109850726|gb|DW479705.1|DW479705			GO:0016020	nr +
Unigene67065_All	269	0.00	0.19	0.00	0.00	0.00	0.00	2.51	0.00	0.44	7.56E+00	6.12E-01		null	null		null	null		null	null		-1.13E+01	6.34E-05	Down	-2.50E+00	4.78E-03		Unigene67065_All//gi|16604352|gb|AL24182.1|//4.00E-21//AT5g12010/F14F18_180 [Arabidopsis thaliana] >gi|251411199|gb|ANY32294.1| At5g12010/F14F18_180 [Arabidopsis thaliana]	Unigene67065_All//2.00E-19//AT5G12010| unknown protein	Unigene67065_All//8.00E-116//gi|78345767|gb|DT566041.1|DT566041			GO:0009536	nr -
Unigene67068_All	343	0.00	2.81	0.62	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.38E-05	Up	9.28E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67068_All//gi|224011237|ref|XP_002296393.1|//2.00E-07//aminopeptidase with a membrane alanine aminopeptidase domain [Thalassiosira pseudonana CCMP1335] >gi|209583424|gb|ACI64110.1| aminopeptidase with a membrane alanine aminopeptidase domain [Thalassiosira pseudonana CCMP1335]	Unigene67068_All//4.00E-08//AT4G33090| APM1 (AMINOPEPTIDASE M1); aminopeptidase				GO:0043231//GO:0070011	nr -
Unigene67069_All	298	0.00	2.89	1.07	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	4.94E-05	Up	1.01E+01	4.50E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene67072_All	425	0.00	4.17	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.14E-10	Up	1.07E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene67072_All//gi|951449|gb|AAB18280.1|//6.00E-22//aspartic protease precursor [Solanum lycopersicum]	Unigene67072_All//9.00E-22//AT4G04460| aspartyl protease family protein				GO:0004175//GO:0010038//GO:0019538//GO:0044464	nr +
Unigene67075_All	388	9.44	3.00	5.90	13.74	8.61	9.78	12.10	7.00	5.65	-1.65E+00	1.91E-06	Down	-6.78E-01	4.48E-02		-6.74E-01	5.55E-03		-4.91E-01	6.34E-02		-7.89E-01	1.45E-03		-1.10E+00	8.24E-06	Down	Unigene67075_All//gi|11066033|gb|AAG28426.1|AF194945.1|7.00E-56//cytosolic aconitase [Nicotiana tabacum]	Unigene67075_All//4.00E-56//AT2G05710| aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative	Unigene67075_All//2.00E-163//ES835565		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0016836//GO:0043169//GO:0043231//GO:0044262//GO:0051536	nr -
Unigene67082_All	294	0.00	3.96	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.05E-06	Up	9.09E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene67082_All//gi|298710746|emb|CBJ32167.1|//1.00E-07//acyl-CoA dehydrogenase [Ectocarpus siliculosus]				ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00410|beta-Alanine metabolism		nr +
Unigene67083_All	257	0.00	2.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene67083_All//gi|224007972|ref|XP_002292945.1|//9.00E-31//methionine aminopeptidase 2 [Thalassiosira pseudonana CCMP1335] >gi|220971071|gb|EED89406.1| methionine aminopeptidase 2 [Thalassiosira pseudonana CCMP1335]	Unigene67083_All//1.00E-30//AT3G59990| MAP2B (METHIONINE AMINOPEPTIDASE 2B); aminopeptidase/ metalloexopeptidase	Unigene67083_All//3.00E-10//TC166777			GO:0008237//GO:0008238//GO:0043169//GO:0044424//GO:0051604	nr +
Unigene67085_All	431	0.00	2.82	0.86	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	5.46E-07	Up	9.76E+00	2.49E-02		null	null		null	null		null	null		null	null		Unigene67085_All//gi|195658563|gb|ACG48749.1|//8.00E-08//histone H1 [Zea mays]						nr +
Unigene67087_All	209	0.00	5.33	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.00E-06	Up	1.03E+01	7.98E-02		null	null		null	null		null	null		null	null		Unigene67087_All//gi|219129966|ref|XP_002185147.1|//3.00E-06//isomerase glucose-6-phosphate isomerase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217403326|gb|EEC43279.1| isomerase glucose-6-phosphate isomerase [Phaeodactylum tricornutum CCAP 1055/1]					GO:0006007//GO:0016861//GO:0044424	nr +
Unigene6709_All	763	1.37	1.00	0.14	3.85	3.43	2.01	1.61	0.38	0.21	-4.61E-01	4.86E-01		-3.30E+00	4.58E-04	Down	-1.67E-01	6.73E-01		-9.37E-01	9.88E-03		-2.07E+00	6.67E-04	Down	-2.94E+00	1.14E-05	Down	Unigene6709_All//gi|296046565|gb|ADG86424.1|//1.00E-28//cyclin D1 [Passiflora morifolia]	Unigene6709_All//8.00E-28//AT1G70210| CYCD1;1 (CYCLIN D1;1); cyclin-dependent protein kinase regulator	Unigene6709_All//0.00E+00//gi|18099247|gb|BM358501.1|BM358501				nr -
Unigene67093_All	278	0.00	7.66	3.26	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	4.10E-12	Up	1.17E+01	4.71E-05	Up	null	null		null	null		null	null		null	null									
Unigene67097_All	268	0.39	4.73	0.00	0.00	0.64	1.01	0.00	0.00	0.59	3.60E+00	2.27E-05	Up	-8.61E+00	3.88E-01		9.33E+00	2.26E-01		9.98E+00	7.01E-02		null	null		9.22E+00	1.39E-01				Unigene67097_All//1.00E-58//CO073304					
Unigene671_All	503	3.85	7.35	4.23	5.74	3.15	2.33	3.95	3.91	3.01	9.34E-01	3.67E-03		1.38E-01	7.50E-01		-8.67E-01	1.26E-02		-1.30E+00	4.76E-04	Down	-1.66E-02	1.00E+00		-3.93E-01	3.41E-01		Unigene671_All//gi|31339162|dbj|BAC77065.1|//3.00E-61//NADP-specific isocitrate dehydrogenase [Lupinus albus]	Unigene671_All//1.00E-57//AT5G14590| isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	Unigene671_All//0.00E+00//TC170016		ko04146|Peroxisome//ko00480|Glutathione metabolism//ko00020|Citrate cycle (TCA cycle)	GO:0000166//GO:0004448//GO:0009060//GO:0009536//GO:0019752//GO:0046872	nr +
Unigene6710_All	436	3.36	8.72	11.24	1.71	1.82	1.45	0.19	0.00	0.00	1.38E+00	2.96E-05	Up	1.74E+00	1.58E-08	Up	8.40E-02	9.44E-01		-2.41E-01	7.55E-01		-7.60E+00	4.00E-01		-7.60E+00	3.56E-01				Unigene6710_All//5.00E-07//TC158902					
Unigene67119_All	251	0.00	3.84	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	1.05E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene67119_All//gi|16226772|gb|AAL16258.1|AF428328_1/2.00E-34//AT3g14420/MOA2_2 [Arabidopsis thaliana]	Unigene67119_All//2.00E-30//AT3G14420| (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative	Unigene67119_All//2.00E-30//ES804711		ko04146|Peroxisome//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0000166//GO:0003973//GO:0005576//GO:0005840//GO:0009532//GO:0009853//GO:0042579	nr +
Unigene67125_All	335	2.19	4.39	1.59	3.27	5.55	8.36	0.63	1.25	2.02	1.00E+00	6.92E-02		-4.60E-01	6.02E-01		7.63E-01	1.16E-01		1.35E+00	4.42E-04	Up	9.83E-01	3.73E-01		1.68E+00	3.70E-02				Unigene67125_All//7.00E-21//TC133282					
Unigene67128_All	303	0.17	3.68	1.76	0.00	0.00	0.00	1.26	0.69	1.58	4.41E+00	2.17E-05	Up	3.35E+00	2.06E-02		null	null		null	null		-8.65E-01	4.41E-01		3.29E-01	7.07E-01				Unigene67128_All//3.00E-07//TC178237					
Unigene67131_All	290	0.00	3.84	0.00	0.00	0.24	0.93	0.73	0.29	1.24	1.19E+01	2.00E-06	Up	null	null		7.89E+00	6.04E-01		9.87E+00	7.01E-02		-1.34E+00	4.29E-01		7.62E-01	4.99E-01				Unigene67131_All//2.00E-85//TC156766					
Unigene67132_All	420	0.00	0.24	0.13	0.36	0.16	0.22	1.71	0.00	0.09	7.91E+00	3.82E-01		6.99E+00	6.31E-01		-1.12E+00	5.82E-01		-7.26E-01	7.14E-01		-1.07E+01	3.26E-05	Down	-4.17E+00	1.64E-04	Down	Unigene67132_All//gi|297799222|ref|XP_002867495.1|//3.00E-18//band 7 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313331|gb|EFH43754.1| band 7 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene67132_All//3.00E-18//AT4G27585| band 7 family protein	Unigene67132_All//5.00E-149//gi|78323484|gb|DT543758.1|DT543758			GO:0043231//GO:0046914	nr +
Unigene67135_All	488	0.54	0.00	0.00	1.12	2.26	0.19	0.00	0.00	1.14	-9.07E+00	6.66E-02		-9.07E+00	8.51E-02		1.01E+00	1.37E-01		-2.60E+00	2.93E-02		null	null		1.02E+01	3.28E-04	Up	Unigene67135_All//gi|224118272|ref|XP_002317776.1|//3.00E-14//predicted protein [Populus trichocarpa] >gi|222858449|gb|EEE95996.1| predicted protein [Populus trichocarpa]	Unigene67135_All//5.00E-05//AT3G06240| F-box family protein	Unigene67135_All//3.00E-107//gi|11199253|gb|BF268222.1|BF268222				nr -
Unigene6714_All	404	1.94	1.00	1.32	3.58	5.11	2.46	2.93	0.31	1.68	-9.53E-01	2.33E-01		-5.60E-01	4.96E-01		5.16E-01	2.83E-01		-5.40E-01	3.59E-01		-3.24E+00	1.10E-05	Down	-8.06E-01	1.31E-01				Unigene6714_All//3.00E-147//TC175408					
Unigene67145_All	409	0.00	1.73	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	3.32E-04	Up	8.02E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene67145_All//sp|Q9I7U4|TITIN_DROME//1.00E-56//Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3						swissprot -
Unigene67148_All	800	0.00	4.50	1.07	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.77E-20	Up	1.01E+01	9.01E-05	Up	null	null		null	null		null	null		null	null		Unigene67148_All//sp|Q54KX0|GTAN_DICDI//6.00E-11//GATA zinc finger domain-containing protein 14 OS=Dictyostelium discoideum GN=gtaN PE=4 SV=1						swissprot +
Unigene67156_All	348	0.00	3.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.00E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene67156_All//sp|P11584|ITBX_DROME//1.00E-27//Integrin beta-PS OS=Drosophila melanogaster GN=mys PE=1 SV=3						swissprot -
Unigene6716_All	955	1.81	0.74	0.56	2.14	3.43	1.18	5.53	1.23	1.38	-1.28E+00	1.19E-02		-1.70E+00	2.33E-03		6.80E-01	4.55E-02		-8.55E-01	6.02E-02		-2.18E+00	2.45E-15	Down	-2.01E+00	2.13E-14	Down	Unigene6716_All//gi|297599291|ref|NP_001046939.2|//1.00E-114//Os02g0511900 [Oryza sativa Japonica Group] >gi|255670933|dbj|BAF08853.2| Os02g0511900 [Oryza sativa Japonica Group]	Unigene6716_All//1.00E-71//AT1G08260| TIL1 (TILTED 1); DNA binding / DNA-directed DNA polymerase/ nucleic acid binding / nucleotide binding / zinc ion binding	Unigene6716_All//0.00E+00//ES809684		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication		nr +
Unigene67161_All	761	0.00	10.85	2.45	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.97E-47	Up	1.13E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene67161_All//sp|B5DRY3|MAEL2_DROPS//2.00E-13//Protein maelstrom 2 OS=Drosophila pseudoobscura pseudoobscura GN=mael2 PE=3 SV=1						swissprot +
Unigene6717_All	829	2.84	0.37	0.64	3.73	2.53	0.33	1.89	0.35	0.72	-2.95E+00	3.71E-08	Down	-2.14E+00	1.35E-05	Down	-5.56E-01	1.09E-01		-3.51E+00	4.02E-13	Down	-2.42E+00	1.29E-05	Down	-1.39E+00	3.12E-03		Unigene6717_All//gi|115484951|ref|NP_001067619.1|//2.00E-07//Os11g0249300 [Oryza sativa Japonica Group] >gi|62733047|gb|AAX95164.1| expressed protein [Oryza sativa Japonica Group] >gi|77549574|gb|ABA92371.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113644841|dbj|BAF27982.1| Os11g0249300 [Oryza sativa Japonica Group]	Unigene6717_All//3.00E-19//AT4G16807| unknown protein	Unigene6717_All//0.00E+00//gi|78347391|gb|DT567665.1|DT567665				nr +
Unigene67170_All	376	0.00	11.72	8.07	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	4.10E-25	Up	1.30E+01	8.91E-17	Up	null	null		null	null		null	null		null	null		Unigene67170_All//gi|208293840|gb|ACI25444.1|//2.00E-07//DEP1 [Triticum aestivum]				ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)		nr +
Unigene67176_All	254	0.00	3.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.36E-05	Up	null	null		null	null		null	null		null	null		null	null									
Unigene67179_All	287	0.00	3.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene67179_All//sp|Q8CF90|MAFA_MOUSE//3.00E-06//Transcription factor MafA OS=Mus musculus GN=Mafa PE=1 SV=1						swissprot -
Unigene67182_All	602	0.61	0.76	0.44	0.08	2.06	0.00	0.42	0.00	0.93	3.16E-01	7.44E-01		-4.60E-01	6.97E-01		4.64E+00	1.66E-06	Up	-6.37E+00	6.26E-01		-8.72E+00	4.03E-02		1.14E+00	1.91E-01		Unigene67182_All//gi|146454480|gb|ABQ41906.1|//4.00E-45//protein kinase family protein [Sonneratia caseolaris]	Unigene67182_All//4.00E-39//AT2G45910| protein kinase family protein / U-box domain-containing protein	Unigene67182_All//5.00E-168//TC156957		ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0019787//GO:0032446//GO:0032559//GO:0043434//GO:0050896	nr -
Unigene67183_All	547	0.00	2.96	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.96E-09	Up	9.61E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene67183_All//gi|116058129|emb|CAL53318.1|//8.00E-40//TGF-beta receptor-interacting protein 1 (ISS) [Ostreococcus tauri]	Unigene67183_All//6.00E-32//AT2G46280| TRIP-1 (TGF-BETA RECEPTOR INTERACTING PROTEIN 1); nucleotide binding / protein binding					nr +
Unigene67193_All	489	0.00	3.73	2.29	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.14E-10	Up	1.12E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene67193_All//gi|299472262|emb|CBN77232.1|//9.00E-08//E1F3C (EUKARYOTIC TRANSLATION INITIATION FACTOR 3 subunit c) [Ectocarpus siliculosus]					GO:0006412//GO:0044424	nr +

Unigene6721_All	607	1.38	0.00	0.70	2.95	1.30	1.93	2.51	1.31	0.98	-1.04E+01	5.56E-05	Down	-9.75E-01	2.37E-01		-1.18E+00	1.09E-02		-6.11E-01	2.28E-01		-9.39E-01	5.17E-02		-1.35E+00	4.52E-03		Unigene6721_All//gi|15218705|ref|NP_171809.1|//2.00E-84//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75200246|sp|Q9SA60.1|PPR6_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g03100, mitochondrial; Flags: Precursor >gi|4587568|gb|AAD25799.1|AC006550_7 Contains PF|00637 Clathrin 7-fold repeat. EST gb|AA721862 comes from this gene [Arabidopsis thaliana] >gi|44917465|gb|AAS49057.1|At1g03100 [Arabidopsis thaliana]	Unigene6721_All//1.00E-85//AT1G03100| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene67216_All	1774	0.00	6.17	2.28	0.00	0.04	0.00	0.00	0.00	0.00	1.26E+01	9.67E-63	Up	1.12E+01	1.92E-22	Up	5.28E+00	6.04E-01		null	null		null	null		null	null		Unigene67216_All//gi|211906360|gb|ACJ11746.1|//0.00E+00//luminal binding protein [Gossypium hirsutum]	Unigene67216_All//0.00E+00//AT5G28540| BIP1; ATP binding	Unigene67216_All//4.00E-14//TC169169		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0008152//GO:0016628//GO:0031410//GO:0032559//GO:0044432//GO:0050896	nr -
Unigene6722_All	267	2.16	6.64	1.40	1.68	8.00	5.41	4.59	3.76	2.84	1.62E+00	1.94E-03		-6.27E-01	5.27E-01		2.25E+00	3.83E-06	Up	1.69E+00	4.38E-03		-2.90E-01	6.39E-01		-6.96E-01	1.86E-01								
Unigene67224_All	542	0.00	7.67	2.26	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.15E-23	Up	1.11E+01	9.11E-07	Up	null	null		null	null		null	null		null	null		Unigene67224_All//gi|99643827|emb|CAJ75753.1|//1.00E-55//heat shock protein 90 [Gymnodinium chlorophorum]	Unigene67224_All//7.00E-23//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr -
Unigene67225_All	386	0.00	0.26	0.28	0.26	0.09	0.00	1.64	0.43	0.10	8.04E+00	3.82E-01		8.11E+00	3.95E-01		-1.53E+00	5.85E-01		-8.01E+00	3.96E-01		-1.92E+00	3.09E-02		-3.99E+00	5.82E-04	Down	Unigene67225_All//gi|18398267|ref|NP_566335.1|//5.00E-41//RAPTOR1; nucleotide binding / protein binding [Arabidopsis thaliana] >gi|16648937|gb|AAL24320.1|Unknown protein [Arabidopsis thaliana] >gi|31711792|gb|AAP68252.1|At3g08850 [Arabidopsis thaliana] >gi|56266687|gb|AAY84960.1|raptorIB [Arabidopsis thaliana]	Unigene67225_All//2.00E-33//AT3G08850| RAPTOR1; nucleotide binding / protein binding	Unigene67225_All//2.00E-148//TC152853			GO:0003006//GO:0005488//GO:0031461//GO:0040007	nr -
Unigene67228_All	383	2.32	2.78	7.92	2.21	2.97	2.48	1.32	1.31	0.62	2.59E-01	6.75E-01		1.77E+00	1.21E-05	Up	4.24E-01	5.47E-01		1.63E-01	8.25E-01		-1.66E-02	1.02E+00		-1.09E+00	2.28E-01								
Unigene6723_All	317	10.23	2.56	9.74	15.87	9.12	2.56	4.13	6.07	1.38	-2.00E+00	2.77E-07	Down	-7.08E-02	8.43E-01		-7.99E-01	1.35E-03		-2.63E+00	5.16E-16	Down	5.53E-01	1.99E-01		-1.58E+00	2.94E-03			Unigene6723_All//3.00E-54//TC163720					
Unigene67236_All	324	0.16	0.00	0.00	0.46	0.53	0.14	1.96	0.00	0.98	-7.34E+00	6.06E-01		-7.34E+00	6.17E-01		2.04E-01	9.49E-01		-1.73E+00	5.00E-01		-1.09E+01	1.23E-04	Down	-9.93E-01	2.02E-01		Unigene67236_All//gi|82468805|gb|AB87677.1|//2.00E-45//cycloartenol synthase [Ricinus communis]	Unigene67236_All//7.00E-44//AT2G07050| CAS1 (cycloartenol synthase 1); cycloartenol synthase	Unigene67236_All//1.00E-74//CB350491		ko00100|Steroid biosynthesis	GO:0006350//GO:0009668//GO:0016104//GO:0031539//GO:0043231//GO:0048229	nr -
Unigene6724_All	1084	0.00	0.37	0.20	1.29	1.02	1.29	4.10	0.50	2.32	8.55E+00	1.35E-02		7.62E+00	1.40E-01		-3.40E-01	5.62E-01		5.50E-03	9.97E-01		-3.03E+00	1.59E-18	Down	-8.23E-01	9.20E-04		Unigene6724_All//gi|297815910|ref|XP_002873838.1|//1.00E-138//pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321676|gb|EFH52097.1|pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6724_All//2.00E-133//AT3G47400| pectinesterase family protein			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene67245_All	502	0.00	3.43	0.85	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.98E-10	Up	9.73E+00	1.38E-02		null	null		null	null		null	null		null	null								ESTscan +
Unigene6725_All	349	1.35	6.53	2.14	5.57	5.53	1.94	19.14	19.52	18.83	2.28E+00	4.37E-06	Up	6.63E-01	4.19E-01		-1.07E-02	9.65E-01		-1.52E+00	1.52E-03		2.83E-02	9.14E-01		-2.33E-02	9.32E-01			Unigene6725_All//3.00E-17//TC157767					
Unigene67269_All	233	1.80	0.87	1.37	1.71	1.03	3.68	4.54	8.61	0.51	-1.05E+00	3.65E-01		-3.90E-01	7.17E-01		-7.25E-01	5.46E-01		1.11E+00	1.67E-01		9.25E-01	2.36E-02		-3.14E+00	2.96E-05	Down		Unigene67269_All//8.00E-63//gi|48775848|gb|CO085214.1|CO085214					
Unigene67272_All	706	0.00	3.95	2.41	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.43E-16	Up	1.12E+01	2.20E-09	Up	null	null		null	null		null	null		null	null								
Unigene67276_All	246	0.43	2.68	0.87	1.42	1.40	2.57	20.45	20.90	49.39	2.65E+00	1.49E-02		1.03E+00	5.90E-01		-1.81E-02	9.57E-01		8.59E-01	3.90E-01		3.11E-02	9.20E-01		1.27E+00	7.79E-17	Up	Unigene67276_All//gi|38016531|gb|AA007601.1|//1.00E-32//fiber quinone-oxidoreductase [Gossypium barbadense]	Unigene67276_All//3.00E-30//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene67276_All//8.00E-91//gi|78326524|gb|DT546798.1|DT546798			GO:0008152//GO:0009534//GO:0016020//GO:0016655//GO:0046914	nr +
Unigene6728_All	436	174.96	193.15	164.88	238.90	188.21	244.05	282.00	195.75	127.56	1.43E-01	1.69E-02		-8.56E-02	2.34E-01		-3.44E-01	6.34E-14		3.07E-02	6.37E-01		-5.27E-01	5.68E-36		-1.14E+00	9.80E-139	Down	Unigene6728_All//gi|297797453|ref|XP_002866611.1|//2.00E-56//FK506-binding protein 12 kD [Arabidopsis lyrata subsp. lyrata] >gi|297312446|gb|EFH42870.1|FK506-binding protein 12 kD [Arabidopsis lyrata subsp. lyrata]	Unigene6728_All//9.00E-47//AT5G64350| FKBP12 (FK506-BINDING PROTEIN); FK506 binding / peptidyl-prolyl cis-trans isomerase	Unigene6728_All//0.00E+00//TC157581				nr -
Unigene6729_All	443	4.02	0.34	2.52	8.21	2.41	1.94	3.25	1.32	3.06	-3.55E+00	2.53E-07	Down	-6.70E-01	1.95E-01		-1.77E+00	2.94E-08	Down	-2.08E+00	5.43E-09	Down	-1.30E+00	1.07E-02		-8.58E-02	8.60E-01								
Unigene67290_All	400	0.00	3.93	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.70E-09	Up	9.64E+00	4.49E-02		null	null		null	null		null	null		null	null		Unigene67290_All//gi|149063401|gb|EDM13724.1|//2.00E-06//rCG21519, isoform CRA_a [Rattus norvegicus] >gi|149063402|gb|EDM13725.1|rCG21519, isoform CRA_a [Rattus norvegicus] >gi|149063403|gb|EDM13726.1|rCG21519, isoform CRA_a [Rattus norvegicus]	Unigene67290_All//5.00E-05//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase					nr -
Unigene673_All	1707	3.37	4.45	3.06	5.69	5.31	6.14	5.08	1.89	2.19	4.01E-01	6.28E-02		-1.41E-01	6.34E-01		-1.01E-01	6.28E-01		1.09E-01	6.39E-01		-1.43E+00	3.81E-14	Down	-1.21E+00	1.64E-11	Down	Unigene673_All//gi|31339162|dbj|BAC77065.1|//0.00E+00//NADP-specific isocitrate dehydrogenase [Lupinus albus]	Unigene673_All//0.00E+00//AT5G14590| isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	Unigene673_All//0.00E+00//TC160095		ko04146|Peroxisome//ko00480|Glutathione metabolism//ko00020|Citrate cycle (TCA cycle)	GO:0000166//GO:0004448//GO:0009060//GO:0009536//GO:0019752//GO:0046872	nr +
Unigene67301_All	212	4.44	1.67	0.00	6.11	4.55	1.49	18.15	13.60	10.52	-1.41E+00	5.69E-02		-1.21E+01	3.34E-05	Down	-4.26E-01	4.87E-01		-2.03E+00	1.62E-03		-4.16E-01	1.49E-01		-7.86E-01	3.43E-03			Unigene67301_All//4.00E-55//CD485516					
Unigene67312_All	561	0.19	2.53	0.38	0.18	0.00	0.00	0.23	0.30	0.85	3.76E+00	3.98E-06	Up	1.03E+00	5.90E-01		-7.47E+00	3.10E-01		-7.47E+00	3.96E-01		3.98E-01	8.13E-01		1.91E+00	6.30E-02		Unigene67312_All//gi|149688544|gb|ABR27717.1|//2.00E-32//dirigent-like protein [Picea sitchensis]	Unigene67312_All//2.00E-31//AT1G22900| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: defense response; LOCATED IN: endomembrane system; EXPRESSED IN: stamen; EXPRESSED DURING: 4 anthesis; CONTAINS InterPro DOMAIN/s: Plant disease resistance response protein (InterPro:IPR004265); BEST Arabidopsis thaliana protein match is: disease resistance-responsive family protein (TAIR:AT5G42500.1); Has 560 Blast hits to 559 proteins in 35 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 560; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene67301_All//4.00E-55//CD485516				nr -
Unigene67316_All	265	0.00	2.87	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	8.65E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene67316_All//sp|Q9Z1F9|SAE2_MOUSE//3.00E-18//SUMO-activating enzyme subunit 2 OS=Mus musculus GN=Uba2 PE=2 SV=1						swissprot -
Unigene67321_All	583	0.00	6.78	1.10	0.00	0.41	0.00	1.02	0.00	0.14	1.27E+01	1.66E-22	Up	1.01E+01	1.16E-03		8.69E+00	1.04E-01		null	null		-9.99E+00	2.39E-04	Down	-2.89E+00	4.53E-03		Unigene67321_All//gi|115485651|ref|NP_001067969.1|//2.00E-10//Os11g0514800 [Oryza sativa Japonica Group] >gi|77551091|gb|ABA93888.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113645191|dbj|BAF28332.1|Os11g0514800 [Oryza sativa Japonica Group]	Unigene67321_All//2.00E-07//AT5G14020| INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: vacuole; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: BR01 (InterPro:IPR003328); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73390.3); Has 53 Blast hits to 53 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 53; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene67321_All//9.00E-31//gi|164296825|gb|EX171041.1|EX171041				nr +
Unigene67326_All	582	0.00	3.31	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	5.72E-11	Up	7.52E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene67326_All//sp|B3MC75|EIF3M_DROAN//2.00E-95//Eukaryotic translation initiation factor 3 subunit M OS=Drosophila ananassae GN=Tango7 PE=3 SV=1						swissprot +
Unigene6733_All	1337	0.04	0.08	0.12	0.00	0.00	0.07	17.33	6.53	11.17	9.55E-01	7.25E-01		1.61E+00	5.10E-01		null	null		6.08E+00	4.73E-01		-1.41E+00	1.13E-35	Down	-6.33E-01	2.23E-10			Unigene6733_All//5.00E-28//TC154839					
Unigene67331_All	332	0.00	2.44	1.28	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	9.36E-05	Up	1.03E+01	1.38E-02		null	null		null	null		null	null		null	null								ESTscan -
Unigene67333_All	495	0.00	1.94	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	1.38E-05	Up	9.56E+00	2.49E-02		null	null		null	null		null	null		null	null		Unigene67333_All//gi|76262500|gb|AB441400.1|//5.00E-10//pherophorin-C2 protein precursor [Chlamydomonas reinhardtii]				ko03040|Spliceosome		nr +
Unigene67335_All	253	0.21	1.20	0.63	0.39	2.31	3.75	0.50	0.50	0.94	2.54E+00	1.51E-01		1.61E+00	5.10E-01		2.55E+00	2.84E-02		3.25E+00	5.84E-04	Up	-1.65E-02	1.02E+00		9.14E-01	5.41E-01			Unigene67335_All//3.00E-07//TC155472					
Unigene67339_All	220	0.00	17.27	11.13	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	1.23E-21	Up	1.34E+01	1.64E-13	Up	null	null		null	null		null	null		null	null		Unigene67339_All//gi|51849616|dbj|BAD42338.1|//5.00E-06//peptidyl-prolyl cis-trans isomerase [Nannochloris bacillaris]					GO:0016787	nr +
Unigene6734_All	705	0.00	0.00	0.00	28.69	2.30	7.82	303.16	259.73	155.79	null	null		null	null		-3.64E+00	1.80E-102	Down	-1.88E+00	1.46E-41	Down	-2.23E-01	5.15E-13		-9.60E-01	1.17E-180		Unigene6734_All//gi|115475509|ref|NP_001061351.1|//3.00E-42//Os08g0244500 [Oryza sativa Japonica Group] >gi|113623320|dbj|BAF23265.1|Os08g0244500 [Oryza sativa Japonica Group]	Unigene6734_All//1.00E-33//AT4G29360| glycosyl hydrolase family 17 protein	Unigene6734_All//0.00E+00//gi|109879585|gb|DW508555.1|DW508555				nr +
Unigene67349_All	298	0.00	3.91	1.43	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.05E-06	Up	1.05E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene67349_All//gi|301091276|ref|XP_002895826.1|//3.00E-38//ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4] >gi|262096576|gb|EEY54628.1| ATP-binding Cassette (ABC) Superfamily [Phytophthora infestans T30-4]	Unigene67349_All//2.00E-24//AT4G39850| PXA1 (PEROXISOMAL ABC TRANSPORTER 1); ATPase, coupled to transmembrane movement of substances			ko04146|Peroxisome//ko02010|ABC transporters	GO:0005778//GO:0009845//GO:0015405//GO:0015915//GO:0016887//GO:0032559	nr +
Unigene6735_All	882	26.64	0.40	15.27	2.03	1.72	2.51	0.10	0.00	0.09	-6.05E+00	2.00E-124	Down	-8.02E-01	8.75E-12		-2.43E-01	6.16E-01		3.03E-01	5.31E-01		-6.58E+00	4.00E-01		-8.68E-02	9.70E-01		Unigene6735_All//gi|9502420|gb|AAF88119.1|AC021043_12//1.00E-30//Unknown protein [Arabidopsis thaliana] >gi|15529248|gb|AAK97718.1|At1g29190/F28N24_12 [Arabidopsis thaliana] >gi|16974401|gb|AAL31126.1|At1g29190/F28N24_12 [Arabidopsis thaliana]	Unigene6735_All//1.00E-31//AT1G29195| unknown protein	Unigene6735_All//0.00E+00//DW508366				nr -
Unigene67352_All	575	0.00	2.82	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.96E-09	Up	9.34E+00	2.49E-02		null	null		null	null		null	null		null	null								ESTscan -
Unigene67356_All	411	0.89	2.96	2.33	1.58	1.68	0.88	2.26	0.31	0.87	1.73E+00	8.94E-03		1.39E+00	7.11E-02		8.89E-02	9.49E-01		-8.42E-01	3.75E-01		-2.89E+00	3.28E-04	Down	-1.38E+00	3.03E-02		Unigene67356_All//gi|225426979|ref|XP_002265557.1|//1.00E-26//PREDICTED: similar to oxysterol-binding family protein [Vitis vinifera]	Unigene67356_All//3.00E-14//AT4G12460| ORP2B (OSBP(OXYSTEROL BINDING PROTEIN)-RELATED PROTEIN 2B); oxysterol binding	Unigene67356_All//4.00E-35//TC150365				nr +
Unigene67363_All	272	0.00	2.42	0.59	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.24E-04	Up	9.20E+00	2.37E-01		null	null		null	null		null	null		null	null			Unigene67363_All//8.00E-14//DW511542					

Unigene67366_All	499	44.35	5.89	10.14	28.95	15.04	14.21	1.61	0.34	1.28	-2.91E+00	8.65E-71	Down	-2.13E+00	1.44E-47	Down	-9.44E-01	4.97E-12		-1.03E+00	2.79E-12	Down	-2.26E+00	4.82E-03		-3.34E-01	6.19E-01		Unigene67366_All//gi|3540181|gb|AAC34331.1|//1.00E-09//Unknown protein [Arabidopsis thaliana] >gi|40823449|gb|AAR92283.1|Atlg10020 [Arabidopsis thaliana] >gi|46518421|gb|AAS99692.1|Atlg10020 [Arabidopsis thaliana]	Unigene67366_All//3.00E-12//AT4G29310| unknown protein	Unigene67366_All//2.00E-170//TC144255			GO:0005618	nr -
Unigene67373_All	478	0.11	10.07	1.56	0.00	0.00	0.09	0.09	0.00	0.67	6.52E+00	8.98E-26	Up	3.83E+00	2.23E-03		null	null		6.56E+00	6.89E-01		-6.47E+00	6.49E-01		2.91E+00	5.99E-02		Unigene67373_All//gi|297810727|ref|XP_002873247.1|//2.00E-08//carboxy-lyase [Arabidopsis lyrata subsp. lyrata] >gi|297319084|gb|EFH49506.1|carboxy-lyase [Arabidopsis lyrata subsp. lyrata]		Unigene67373_All//4.00E-20//D9519735				nr -
Unigene67375_All	257	0.41	0.79	0.62	0.39	0.00	0.53	1.15	0.98	4.65	9.54E-01	6.20E-01		6.10E-01	7.47E-01		-8.60E+00	3.10E-01		4.43E-01	8.60E-01		-2.39E-01	8.39E-01		2.01E+00	7.79E-04	Up	Unigene67375_All//gi|36957198|gb|AAQ87021.1|//1.00E-23//VDAC1.3 [Lotus japonicus]	Unigene67375_All//3.00E-12//AT3G01280| VDAC1 (VOLTAGE DEPENDENT ANION CHANNEL 1); voltage-gated anion channel	Unigene67375_All//2.00E-82//BE054720			GO:0005244//GO:0005488//GO:0006811//GO:0009626//GO:0016021//GO:0022829//GO:0031966//GO:0051707	nr +
Unigene67378_All	338	2.79	1.95	1.89	1.77	1.12	0.00	2.13	0.25	0.83	-5.16E-01	4.57E-01		-5.60E-01	4.39E-01		-6.58E-01	4.78E-01		-1.08E+01	7.69E-04	Down	-3.10E+00	1.40E-03		-1.37E+00	6.50E-02		Unigene67378_All//gi|116311070|emb|CAH68000.1|//1.00E-16//OS1GGa0157K09-H0214G12.11 [Oryza sativa (indica cultivar-group)]	Unigene67378_All//6.00E-11//AT4G17940| binding				GO:0010467//GO:0044464	nr +
Unigene6738_All	1170	2.59	2.82	1.00	7.32	5.77	1.16	0.22	0.00	0.00	1.18E-01	7.24E-01		-1.37E+00	3.96E-04	Down	-3.44E-01	8.38E-02		-2.66E+00	2.54E-27	Down	-7.76E+00	4.03E-02		-7.76E+00	3.03E-02										
Unigene67381_All	357	0.00	3.12	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.00E-06	Up	1.00E+01	2.49E-02		null	null		null	null		null	null		null	null										
Unigene67384_All	394	0.00	1.93	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	1.76E-04	Up	7.08E+00	6.30E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene67387_All	206	0.00	6.40	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.49E-07	Up	8.01E+00	6.30E-01		null	null		null	null		null	null		null	null										
Unigene67392_All	338	0.00	1.95	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	6.24E-04	Up	7.30E+00	6.30E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene67394_All	295	0.00	15.63	4.69	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	2.84E-26	Up	1.22E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene67394_All//gi|288300146|gb|ADC45376.1|//1.00E-33//actin [Cleistogenes songorica]	Unigene67394_All//2.00E-31//AT5G59370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene67394_All//6.00E-49//TC153744		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0007015//GO:0008015//GO:0008092//GO:0012501//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0048747//GO:0051707//GO:0060115	nr +
Unigene67398_All	354	0.00	4.15	2.41	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.11E-08	Up	1.12E+01	9.01E-05	Up	null	null		null	null		null	null		null	null		Unigene67398_All//gi|300263934|gb|EFJ48132.1|//9.00E-26//eukaryotic translation initiation factor 3f [Volvox carteri f. nagariensis]	Unigene67398_All//9.00E-23//AT2G39990| EIF2; translation initiation factor				GO:0007275//GO:0009856//GO:0043231	nr +
Unigene67399_All	264	0.00	4.41	0.81	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	9.66E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67399_All//gi|159475511|ref|XP_001698582.1|//3.00E-11//glyoxal or galactose oxidase [Chlamydomonas reinhardtii] >gi|158275422|gb|EDP01199.1|glyoxal or galactose oxidase [Chlamydomonas reinhardtii]					GO:0031410	nr -
Unigene6741_All	1072	0.10	0.00	0.00	0.42	1.28	2.40	1.38	0.74	2.08	-6.61E+00	3.68E-01		-6.61E+00	3.88E-01		1.62E+00	6.44E-03		2.52E+00	7.59E-08	Up	-8.98E-01	6.74E-02		5.92E-01	1.11E-01		Unigene6741_All//gi|193734712|gb|ACF19982.1|//7.00E-82//MYC2 [Hevea brasiliensis]	Unigene6741_All//5.00E-47//AT5G46760| basic helix-loop-helix (bHLH) family protein	Unigene6741_All//0.00E+00//gi|11209440|gb|BF278370.1|BF278370	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene67415_All	471	0.00	2.47	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.05E-06	Up	8.41E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene67415_All//gi|150406473|ref|YP_001315124.1|//6.00E-59//NADH dehydrogenase subunit 7 [Chlorokybus atmophyticus] >gi|126507710|gb|AB015107.1| NADH dehydrogenase subunit 7 [Chlorokybus atmophyticus]	Unigene67415_All//7.00E-51//ATMG00510| NADH dehydrogenase subunit 7			ko00190|Oxidative phosphorylation	GO:0000166//GO:0006091//GO:0043231//GO:0044425//GO:0048037//GO:0050136//GO:0051234	nr +
Unigene67424_All	281	0.00	4.51	0.00	0.00	0.00	0.00	1.05	0.45	0.00	1.21E+01	2.86E-07	Up	null	null		null	null		null	null		-1.24E+00	3.72E-01		-1.00E+01	1.58E-02										
Unigene67429_All	382	0.00	2.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.00E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene67429_All//gi|226507822|ref|NP_001150087.1|//5.00E-34//LOC100283716 [Zea mays] >gi|195636596|gb|ACG37766.1| T-complex protein 1 subunit alpha [Zea mays]	Unigene67429_All//3.00E-35//AT3G20050| ATTCP-1; ATP binding / protein binding / unfolded protein binding				GO:0005515//GO:0032559//GO:0044267//GO:0044424	nr -
Unigene6743_All	847	0.31	0.42	0.50	1.82	0.69	0.32	1.40	4.79	1.36	4.39E-01	7.01E-01		7.03E-01	5.54E-01		-1.40E+00	6.23E-03		-2.51E+00	4.81E-05	Down	1.78E+00	2.67E-09	Up	-3.52E-02	9.63E-01		Unigene6743_All//gi|70663492|emb|CAJ15145.1|//5.00E-89//sialyltransferase-like protein [Gossypium raimondii]	Unigene6743_All//1.00E-76//AT1G08280| glycosyl transferase family 29 protein / sialyltransferase family protein	Unigene6743_All//2.00E-48//TC178826				nr +
Unigene6746_All	510	0.21	0.00	0.00	8.79	2.36	3.63	2.07	1.88	1.02	-7.68E+00	3.68E-01		-7.68E+00	3.88E-01		-1.90E+00	4.89E-11	Down	-1.28E+00	9.27E-06	Down	-1.37E-01	8.15E-01		-1.03E+00	7.30E-02		Unigene6746_All//gi|145839475|gb|ABD60294.2|//5.00E-60//R2R3-MYB transcription factor MYB3 [Picea glauca]	Unigene6746_All//5.00E-51//AT1G17950| MYB52 (MYB DOMAIN PROTEIN 52); DNA binding / transcription factor	Unigene6746_All//1.00E-72//TC178223	MYB			nr +
Unigene67464_All	485	0.00	3.66	0.33	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.14E-10	Up	8.36E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene67464_All//sp|Q9Y5X9|LIPE_HUMAN//1.00E-20//Endothelial lipase OS=Homo sapiens GN=LIPG PE=1 SV=1						swissprot -
Unigene67468_All	260	0.20	0.00	0.00	0.00	0.66	0.00	0.49	4.66	0.61	-7.65E+00	6.06E-01		-7.65E+00	6.17E-01		9.37E+00	2.26E-01		null	null		3.26E+00	8.29E-06	Up	3.29E-01	8.50E-01		Unigene67468_All//gi|223452375|gb|ACM89515.1|//2.00E-15//cysteine-rich receptor-like protein kinase [Glycine max]	Unigene67468_All//1.00E-10//AT4G23180| CRK10 (CYSTEINE-RICH RLK10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene67468_All//4.00E-25//TC164246			GO:0004674//GO:0006464//GO:0032559	nr +
Unigene67469_All	531	0.00	1.81	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	1.38E-05	Up	7.65E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene67469_All//gi|255596843|ref|XP_002536630.1|//7.00E-07//Hydroxypyruvate isomerase, putative [Ricinus communis] >gi|223519041|gb|EEF25752.1|Hydroxypyruvate isomerase, putative [Ricinus communis]						nr +
Unigene6748_All	785	1.40	0.26	1.29	1.97	3.55	2.59	3.50	0.53	1.12	-2.44E+00	1.50E-03		-1.19E-01	8.50E-01		8.53E-01	2.13E-02		3.96E-01	4.23E-01		-2.72E+00	1.53E-10	Down	-1.65E+00	3.14E-06	Down	Unigene6748_All//gi|186511249|ref|NP_191633.3|//1.00E-104//TTN1 (TITAN 1); tubulin binding [Arabidopsis thaliana] >gi|20514263|gb|AAM22960.1|AF486851_1 tubulin folding cofactor D [Arabidopsis thaliana]	Unigene6748_All//7.00E-97//AT3G60740| TTN1 (TITAN 1); tubulin binding	Unigene6748_All//3.00E-74//TC177706				nr +
Unigene67485_All	740	0.00	3.83	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	3.82E-16	Up	8.75E+00	4.49E-02		null	null		null	null		null	null		null	null		Unigene67485_All//gi|159464465|ref|XP_001690462.1|//1.00E-47//protein disulfide isomerase [Chlamydomonas reinhardtii] >gi|158279962|gb|EDP05721.1|protein disulfide isomerase [Chlamydomonas reinhardtii]	Unigene67485_All//9.00E-41//AT2G32920| ATPDIL2-3 (PDI-LIKE 2-3); protein disulfide isomerase			ko04141|Protein processing in endoplasmic reticulum	GO:0016020//GO:0031410//GO:0033554//GO:0043231	nr +
Unigene67489_All	418	0.00	1.58	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	6.24E-04	Up	9.32E+00	7.98E-02		null	null		null	null		null	null		null	null		Unigene67489_All//gi|15238732|ref|NP_200152.1|//3.00E-12//nuclear movement family protein [Arabidopsis thaliana] >gi|27765036|gb|AAO23639.1|At5g53400 [Arabidopsis thaliana]	Unigene67489_All//2.00E-11//AT5G53400| nuclear movement family protein					nr +
Unigene6749_All	535	3.42	0.00	2.69	1.86	2.12	0.93	0.24	0.39	0.22	-1.17E+01	1.34E-10	Down	-3.49E-01	4.94E-01		1.90E-01	8.14E-01		-1.00E+00	1.57E-01		7.20E-01	6.31E-01		-8.59E-02	9.68E-01		Unigene6749_All//gi|116059946|emb|CAL56005.1|//6.00E-06//Predicted membrane protein [patched superfamily] (ISS) [Ostreococcus tauri]		Unigene6749_All//0.00E+00//gi|78348488|gb|DT568762.1|DT568762				nr +
Unigene67490_All	326	0.00	2.33	0.82	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.76E-04	Up	9.67E+00	7.98E-02		null	null		null	null		null	null		null	null										ESTscan -
Unigene67499_All	308	0.00	2.30	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.32E-04	Up	8.43E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene67499_All//gi|47026859|gb|AAT08655.1|//3.00E-28//isocitrate dehydrogenases [Hyacinthus orientalis]	Unigene67499_All//8.00E-28//AT5G03290| isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative			ko00020|Citrate cycle (TCA cycle)	GO:0000166//GO:0004448//GO:0009060//GO:0043231//GO:0046872	nr +
Unigene675_All	3022	13.92	39.67	18.70	37.22	55.39	42.08	32.99	53.75	94.11	1.51E+00	2.86E-164	Up	4.26E-01	2.90E-09		5.74E-01	3.77E-55		1.77E-01	9.56E-05		7.04E-01	8.50E-79		1.51E+00	0.00E+00	Up	Unigene675_All//gi|297844792|ref|XP_002890277.1|//0.00E+00//lipase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336119|gb|EFH66536.1|lipase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene675_All//0.00E+00//AT1G73920| lipase family protein	Unigene675_All//0.00E+00//TC169921			GO:0004091//GO:0044238	nr -
Unigene6750_All	718	0.15	0.35	0.00	3.05	2.49	2.08	1.77	0.64	0.44	1.28E+00	4.35E-01		-7.19E+00	3.88E-01		-2.92E-01	5.43E-01		-5.56E-01	2.19E-01		-1.46E+00	8.32E-03		-1.99E+00	4.87E-04	Down	Unigene6750_All//gi|92870973|gb|ABE80134.1|//1.00E-104//WD40-like [Medicago truncatula]	Unigene6750_All//7.00E-102//AT3G18060| transducin family protein / WD-40 repeat family protein	Unigene6750_All//4.00E-15//TC154559		ko03040|Spliceosome		nr +
Unigene67511_All	441	0.00	4.48	0.48	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.97E-11	Up	8.92E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67511_All//gi|130750612|gb|ABO32293.1|//2.00E-07//75k gamma secalin [Secale sylvestre]						nr +
Unigene67517_All	393	0.00	7.48	5.01	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.01E-16	Up	1.23E+01	7.45E-11	Up	null	null		null	null		null	null		null	null										
Unigene6752_All	363	0.43	1.40	0.59	3.16	3.79	1.87	13.28	10.71	5.38	1.69E+00	1.34E-01		4.41E-01	7.74E-01		2.66E-01	6.81E-01		-7.58E-01	2.45E-01		-3.10E-01	2.34E-01		-1.00E+00	1.62E-07	Down		Unigene6752_All//4.00E-84//TC176997					
Unigene67526_All	260	0.00	2.73	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.32E-04	Up	1.00E+01	7.98E-02		null	null		null	null		null	null		null	null										
Unigene67529_All	574	0.00	9.27	2.13	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	2.43E-30	Up	1.11E+01	9.11E-07	Up	null	null		null	null		null	null		null	null		Unigene67529_All//gi|1346871|sp|P49108.1|PSBR_BRACM//1.00E-60//RecName: Full=Photosystem II 10 kDa polypeptide, chloroplastic; Flags: Precursor >gi|967968|gb|AAA74957.1|photosystem II 10kDa polypeptide [Brassica rapa subsp. campestris]	Unigene67529_All//1.00E-53//AT1G79040| PSBR (photosystem II subunit R)	Unigene67529_All//2.00E-16//EX168825		ko00195|Photosynthesis	GO:0009523//GO:0009534//GO:0010207	nr +
Unigene6753_All	526	1.99	0.00	1.32	3.69	3.60	2.15	2.97	1.27	1.82	-1.10E+01	3.80E-06	Down	-5.96E-01	3.93E-01		-3.67E-02	9.36E-01		-7.83E-01	9.68E-02		-1.23E+00	1.07E-02		-7.10E-01	1.16E-01									
Unigene6754_All	532	2.56	4.00	3.60	6.37	5.83	3.91	4.29	4.64	9.74	6.46E-01	1.41E-01		4.95E-01	3.22E-01		-1.28E-01	7.48E-01		-7.03E-01	3.63E-02		1.11E-01	7.70E-01		1.18E+00	6.23E-07	Up		Unigene6754_All//9.00E-40//FL577654					
Unigene67541_All	242	0.65	16.12	0.22	0.41	0.43	0.93	0.17	0.52	0.16	4.64E+00	2.95E-18	Up	-1.56E+00	5.32E-01		5.23E-02	9.65E-01		1.18E+00	5.49E-01		1.57E+00	5.44E-01		-8.59E-02	9.68E-01		Unigene67541_All//gi|15229544|ref|NP_189034.1|//3.00E-15//BAM1 (BETA-AMYLASE 1); beta-amylase [Arabidopsis thaliana] >gi|75335046|sp|Q9LIR6.1|BAM1_ARATH RecName: Full=Beta-amylase 1, chloroplastic; AltName: Full=1,4-alpha-D-glucan maltohydrolase; AltName: Full=Thioredoxin-regulated beta-amylase; Short=TR-BAMY; AltName: Full=Beta-amylase 7; Flags: Precursor >gi|14194173|gb|AAK56281.1|AF367293_1 AT3g23920/F14O13_11 [Arabidopsis thaliana] >gi|9294660|dbj|BAB03009.1| beta-amylase [Arabidopsis thaliana] >gi|18700274|gb|AAL77747.1|AT3g23920/F14O13_11 [Arabidopsis thaliana]	Unigene67541_All//2.00E-16//AT3G23920| BAM1 (BETA-AMYLASE 1); beta-amylase	Unigene67541_All//1.00E-52//EX164070		ko00500|Starch and sucrose metabolism	GO:0003006//GO:0005982//GO:0006464//GO:0006950//GO:0007167//GO:0009933//GO:0010073//GO:0016020//GO:0016160//GO:0016772//GO:0032559//GO:0043167//GO:0043231//GO:0044444	nr +
Unigene67542_All	252	0.00	0.80	1.06	0.79	0.14	0.36	3.36	0.50	2.53	9.65E+00	1.35E-01		1.00E+01	7.98E-02		-2.53E+00	2.33E-01		-1.14E+00	5.68E-01		-2.75E+00	9.73E-04	Down	-4.08E-01	5.49E-01			Unigene67542_All//3.00E-59//TC171445					
Unigene67545_All	318	0.00	4.94	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.70E-09	Up	8.97E+00	2.37E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene6755_All	426	3.93	0.95	1.25	7.48	6.06	1.80	0.89	0.00	1.03	-2.05E+00	3.19E-04	Down	-1.65E+00	3.47E-03		-3.04E-01	4.16E-01		-2.05E+00	8.04E-08	Down	-9.80E+00	6.17E-03		2.04E-01	8.26E-01		Unigene6755_All//gi|15232695|ref|NP_187562.1|//6.00E-06//nucleic acid binding [Arabidopsis thaliana]	Unigene6755_All//4.00E-07//AT3G09510| nucleic acid binding					nr -

Unigene67557_All	419	0.00	0.85	1.91	0.00	0.00	0.00	0.00	0.00	0.00	9.73E+00	2.45E-02		1.09E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene67557_All//sp|P18824|ARM_DROME//5.00E-56//Armadillo segment polarity protein OS=Drosophila melanogaster GN=arm PE=1 SV=1						swissprot +
Unigene67559_All	226	0.00	3.59	0.00	0.00	0.00	0.40	0.00	0.00	0.00	1.18E+01	9.36E-05	Up	null	null		null	null		8.64E+00	4.73E-01		null	null		null	null		Unigene67559_All//gi|256542214|dbj|BAH98060.1|//2.00E-11//galactinol synthase [Solanum lycopersicum]	Unigene67559_All//1.00E-12//AT1G09350| AtGolS3 (Arabidopsis thaliana galactinol synthase 3); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene67559_All//3.00E-47//TC156180				nr -
Unigene6756_All	298	4.92	6.29	10.19	6.69	10.17	10.00	1.99	6.17	2.01	3.56E-01	4.55E-01		1.05E+00	5.27E-03		6.05E-01	9.51E-02		5.81E-01	1.23E-01		1.64E+00	3.28E-04	Up	1.37E-02	9.87E-01				Unigene6756_All//6.00E-58//DT051298				
Unigene67560_All	590	0.35	3.61	2.17	1.35	0.93	1.00	1.93	2.41	1.22	3.35E+00	3.58E-08	Up	2.61E+00	5.00E-04	Up	-5.33E-01	5.10E-01		-4.41E-01	6.14E-01		3.16E-01	5.63E-01		-6.71E-01	2.20E-01		Unigene67560_All//gi|221082200|ref|XP_002366660.1|//4.00E-15//predicted protein [Populus trichocarpa] >gi|222856049|gb|EEE93596.1| predicted protein [Populus trichocarpa]	Unigene67560_All//2.00E-07//AT1G26380| unknown protein	Unigene67560_All//2.00E-139//BE054702			GO:0031410	nr -
Unigene67561_All	468	0.00	18.51	5.01	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	1.38E-49	Up	1.23E+01	6.40E-13	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene67567_All	320	0.65	10.77	0.50	0.78	1.61	0.42	0.40	0.26	1.49	4.04E+00	7.21E-15	Up	-3.90E-01	8.07E-01		1.05E+00	3.49E-01		-8.78E-01	6.16E-01		-6.02E-01	7.65E-01		1.91E+00	6.29E-02				Unigene67567_All//2.00E-156//DT463498				
Unigene6757_All	358	0.58	3.82	3.12	2.92	3.37	3.28	1.06	1.40	1.67	2.71E+00	1.29E-04	Up	2.42E+00	2.21E-03		2.04E-01	8.01E-01		1.67E-01	7.91E-01		3.99E-01	6.52E-01		6.51E-01	4.23E-01		Unigene6757_All//gi|18425121|ref|NP_569040.1|//8.00E-56//MAPKKK5; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Unigene6757_All//3.00E-57//AT5G66850| MAPKKK5; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene6757_All//1.00E-121//gi|73860712|gb|DT463451.1|DT463451		ko04626|Plant-pathogen interaction		nr +
Unigene67571_All	582	0.00	1.83	0.27	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	3.81E-06	Up	8.10E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene67571_All//gi|297845606|ref|XP_002890684.1|//2.00E-06//hypothetical protein ARALYDRAFT_472815 [Arabidopsis lyrata subsp. lyrata] >gi|297336526|gb|EFH66943.1| hypothetical protein ARALYDRAFT_472815 [Arabidopsis lyrata subsp. lyrata]						nr +
Unigene67575_All	524	0.00	6.77	2.24	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	3.46E-20	Up	1.11E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene67575_All//gi|65736671|dbj|BAD88525.1|//3.00E-22//chitinase A [Cycas revoluta]	Unigene67575_All//3.00E-21//AT4G19810| glycosyl hydrolase family 18 protein				GO:0016787	nr -
Unigene67582_All	566	0.00	2.78	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	5.70E-09	Up	8.56E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67582_All//gi|9294075|dbj|BAB02032.1|//1.00E-57//cytosolic chaperonin, delta-subunit [Arabidopsis thaliana]	Unigene67582_All//6.00E-59//AT3G18190| chaperonin, putative				GO:0000166//GO:0005515//GO:0010038//GO:0044267	nr +
Unigene67583_All	965	0.00	3.57	1.77	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.31E-19	Up	1.08E+01	2.20E-09	Up	null	null		null	null		null	null		null	null		Unigene67583_All//gi|34452231|gb|AAQ72567.1|//7.00E-73//mini-chromosome maintenance 7 [Pisum sativum]	Unigene67583_All//3.00E-68//AT4G02060| PRL (PROLIFERA); ATP binding / DNA binding / DNA-dependent ATPase/ nucleoside-triphosphatase/ nucleotide binding			ko03030|DNA replication	GO:0006261//GO:0009756//GO:0032559//GO:0042623//GO:0043231	nr +
Unigene67589_All	388	0.00	2.35	0.00	0.13	0.00	0.00	0.00	0.54	0.00	1.12E+01	2.61E-05	Up	null	null		-7.00E+00	5.49E-01		-7.00E+00	6.26E-01		9.07E+00	7.84E-02		null	null				Unigene67589_All//2.00E-64//TC134077				
Unigene6759_All	1008	1.09	0.00	0.00	17.54	9.94	10.75	14.14	2.65	5.26	-1.01E+01	1.95E-06	Down	-1.01E+01	4.93E-06	Down	-8.20E-01	1.44E-11		-7.06E-01	3.61E-08		-2.41E+00	1.83E-45	Down	-1.43E+00	2.06E-23	Down	Unigene6759_All//gi|21536939|gb|AAW61280.1|//4.00E-69//RNA binding protein-like [Arabidopsis thaliana]	Unigene6759_All//6.00E-52//AT3G54770| RNA recognition motif (RRM)-containing protein	Unigene6759_All//0.00E+00//TC152802		ko03040|Spliceosome		nr -
Unigene67590_All	697	1.65	0.29	1.91	2.50	3.75	1.88	0.36	0.48	0.23	-2.51E+00	8.99E-04	Down	2.10E-01	7.07E-01		5.86E-01	1.45E-01		-4.13E-01	4.39E-01		3.98E-01	7.24E-01		-6.71E-01	6.05E-01		Unigene67590_All//gi|15230526|ref|NP_190071.1|//3.00E-47//protein kinase-related [Arabidopsis thaliana]	Unigene67590_All//3.00E-49//AT3G44850| protein kinase-related	Unigene67590_All//0.00E+00//TC174816			GO:0004672//GO:0006464//GO:0032559	nr +
Unigene67594_All	433	0.00	3.16	2.09	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.79E-08	Up	1.10E+01	4.71E-05	Up	null	null		null	null		null	null		null	null									
Unigene67597_All	413	0.00	2.94	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	5.46E-07	Up	8.01E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene67597_All//sp|Q54LY8|Y6915_DICDI//5.00E-07//Uncharacterized protein DDB_G0286299 OS=Dictyostelium discoideum GN=DDB_G0286299 PE=4 SV=1						swissprot +
Unigene67599_All	329	0.00	2.16	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.32E-04	Up	9.34E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67599_All//gi|224005697|ref|XP_002291809.1|//8.00E-25//NADH dehydrogenase [Thalassiosira pseudonana CCMP1335] >gi|220972328|gb|EED90660.1| NADH dehydrogenase [Thalassiosira pseudonana CCMP1335]	Unigene67599_All//5.00E-21//AT4G02580| NADH-ubiquinone oxidoreductase 24 kDa subunit, putative			ko00190|Oxidative phosphorylation	GO:0003824//GO:0043231	nr -
Unigene6760_All	416	114.95	61.39	105.48	17.72	19.54	8.79	0.00	0.00	0.96	-9.05E-01	1.15E-29		-1.24E-01	1.57E-01		1.41E-01	5.69E-01		-1.01E+00	1.95E-06	Down	null	null		9.90E+00	3.96E-03		Unigene6760_All//gi|151368156|gb|ABS10813.1|//5.00E-31//rhodanese-like family protein-like protein [Gossypium barbadense]	Unigene6760_All//3.00E-29//AT3G08920| rhodanese-like domain-containing protein					nr +
Unigene67603_All	914	1.55	1.94	1.40	1.91	2.94	3.36	1.90	1.51	0.65	3.28E-01	5.12E-01		-1.45E-01	7.90E-01		6.24E-01	1.10E-01		8.17E-01	2.27E-02		-3.30E-01	4.90E-01		-1.54E+00	6.50E-04	Down	Unigene67603_All//gi|5902406|gb|AAD55508.1|ACO08148_18//3.00E-18//Hypothetical protein [Arabidopsis thaliana] >gi|46518435|gb|AAS99699.1| At1g70950 [Arabidopsis thaliana]	Unigene67603_All//2.00E-19//AT1G70950| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 6 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Targeting for Xklp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G23060.1); Has 875 Blast hits to 771 proteins in 143 species: Archae - 0; Bacteria - 102; Metazoa - 281; Fungi - 65; Plants - 205; Viruses - 3; Other Eukaryotes - 219 (source: NCBI BLink).	Unigene67603_All//1.00E-138//CO107797				nr -
Unigene67610_All	465	0.90	7.63	0.46	3.11	2.96	2.91	2.09	5.21	1.20	3.08E+00	2.43E-12	Up	-9.74E-01	4.11E-01		-6.87E-02	8.93E-01		-9.25E-02	8.76E-01		1.32E+00	4.44E-04	Up	-8.02E-01	1.83E-01		Unigene67610_All//gi|195610418|gb|ACG27039.1|//2.00E-13//membrane protein [Zea mays]	Unigene67610_All//1.00E-12//AT5G07250| ATRBL3 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 3)	Unigene67610_All//0.00E+00//TC143724			GO:0031224	nr +
Unigene67614_All	317	0.00	5.91	2.52	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.11E-10	Up	1.13E+01	1.72E-04	Up	null	null		null	null		null	null		null	null									
Unigene67615_All	239	0.00	4.03	0.00	0.00	0.00	0.00	0.53	0.00	0.50	1.20E+01	1.38E-05	Up	null	null		null	null		null	null		-9.05E+00	2.34E-01		-8.57E-02	9.68E-01		Unigene67615_All//gi|169659105|dbj|BAG12743.1|//2.00E-14//ABA 8-oxidase [Lactuca sativa]	Unigene67615_All//4.00E-15//AT4G19230| CYP707A1; (+)-abscisic acid 8'-hydroxylase/ oxygen binding	Unigene67615_All//3.00E-50//TC144424		ko00906|Carotenoid biosynthesis	GO:0003006//GO:0005506//GO:0006714//GO:0006952//GO:0009416//GO:0016709	nr -
Unigene6762_All	270	2.71	2.25	5.92	3.32	17.98	14.72	2.04	1.08	2.66	-2.69E-01	7.19E-01		1.13E+00	4.27E-02		2.44E+00	8.32E-15	Up	2.15E+00	6.75E-10	Up	-9.10E-01	3.19E-01		3.84E-01	5.96E-01				Unigene6762_All//1.00E-05//AT5G16600| MYB43 (myb domain protein 43); DNA binding / transcription factor	Unigene6762_All//3.00E-16//DT462062	MYB			kegg +
Unigene67622_All	490	0.00	6.00	2.39	0.00	0.00	0.00	0.00	0.00	0.08	1.26E+01	1.01E-16	Up	1.12E+01	1.77E-06	Up	null	null		null	null		null	null		6.35E+00	6.39E-01		Unigene67622_All//gi|161377377|gb|ABX71676.1|//1.00E-12//60S ribosomal protein L6-like protein [Panax quinquefolius]	Unigene67622_All//4.00E-05//AT1G74050| 60S ribosomal protein L6 (RPL6C)			ko03010|Ribosome	GO:0005488//GO:0009536//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene67628_All	321	0.00	7.58	3.32	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	7.72E-14	Up	1.17E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene67628_All//sp|P28678|OPS1_DROPS//1.00E-20//Opsin Rh1 OS=Drosophila pseudoobscura pseudoobscura GN=ninaE PE=1 SV=4						swissprot +
Unigene6763_All	352	21.55	52.83	31.31	115.48	127.57	129.84	206.96	722.76	189.80	1.29E+00	1.00E-20	Up	5.39E-01	2.48E-03		1.44E-01	9.20E-02		1.69E-01	4.41E-02		1.80E+00	0.00E+00	Up	-1.25E-01	2.83E-02		Unigene6763_All//gi|91771911|gb|ABE60812.1|//2.00E-59//caffeoyl coenzyme A 3-O-methyltransferase 2 [Leucaena leucocephala] >gi|105671456|gb|ABF74684.1| caffeoyl-CoA-O-methyltransferase [Leucaena leucocephala]	Unigene6763_All//1.00E-57//AT4G34050| caffeoyl-CoA 3-O-methyltransferase, putative	Unigene6763_All//0.00E+00//gi|164273422|gb|ES818100.1|ES818100		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene6764_All	1426	0.33	0.57	0.78	17.47	14.15	13.33	3.65	0.59	2.85	7.84E-01	3.23E-01		1.25E+00	7.15E-02		-3.04E-01	3.92E-03		-3.90E-01	2.84E-04		-2.64E+00	9.11E-19	Down	-3.56E-01	1.27E-01		Unigene6764_All//gi|4257173|ref|NP_973956.1|//3.00E-51//protein kinase family protein [Arabidopsis thaliana]	Unigene6764_All//1.00E-52//AT1G33260| protein kinase family protein	Unigene6764_All//0.00E+00//TC171796		ko04626|Plant-pathogen interaction		nr +
Unigene67640_All	826	0.00	6.38	2.13	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	4.74E-30	Up	1.11E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene67640_All//gi|195648550|gb|ACG43743.1|//3.00E-21//3-hydroxybutyryl-CoA dehydrogenase [Zea mays]	Unigene67640_All//9.00E-05//AT3G15290| 3-hydroxybutyryl-CoA dehydrogenase, putative			ko00650|Butanoate metabolism	GO:0003824//GO:0044464	nr +
Unigene67645_All	322	0.00	3.62	0.00	0.00	1.28	0.00	0.26	0.39	1.11	1.18E+01	1.05E-06	Up	null	null		1.03E+01	1.25E-02		null	null		5.68E-01	7.81E-01		2.08E+00	1.01E-01		Unigene67645_All//gi|226508646|ref|NP_001151502.1|//6.00E-20//calmodulin binding protein [Zea mays] >gi|195647270|gb|ACG43103.1| calmodulin binding protein [Zea mays]	Unigene67645_All//1.00E-20//AT3G24300| calmodulin-binding protein	Unigene67645_All//6.00E-15//ES817884		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene67647_All	333	0.00	4.72	1.12	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.70E-09	Up	1.01E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene67647_All//gi|219128797|ref|XP_002184591.1|//1.00E-06//predicted protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|217404041|gb|EEC43990.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1]						nr -
Unigene6765_All	380	0.96	1.87	1.54	1.05	1.00	1.43	2.89	0.55	1.36	9.54E-01	2.62E-01		6.77E-01	4.82E-01		-7.32E-02	9.25E-01		4.44E-01	6.78E-01		-2.40E+00	4.11E-04	Down	-1.09E+00	5.40E-02		Unigene6765_All//gi|195612002|gb|ACG27831.1|//7.00E-28//SEC1-family transport protein SLY1 [Zea mays]	Unigene6765_All//1.00E-27//AT2G17980| ATSLY1; protein transporter	Unigene6765_All//5.00E-96//TC141081				nr -
Unigene67650_All	265	0.00	0.57	3.01	0.00	0.00	0.00	0.00	0.00	0.00	9.16E+00	2.33E-01		1.16E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene67650_All//gi|301693384|ref|XP_002997539.1|//2.00E-12//T-complex protein 1 subunit beta [Phytophthora infestans T30-4] >gi|262110584|gb|EEY68636.1| T-complex protein 1 subunit beta [Phytophthora infestans T30-4]	Unigene67650_All//7.00E-13//AT5G20890| chaperonin, putative				GO:0005515//GO:0030312//GO:0031225//GO:0032559//GO:0044267//GO:0044424	nr -
Unigene67651_All	495	0.00	9.52	2.47	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	7.47E-27	Up	1.13E+01	9.11E-07	Up	null	null		null	null		null	null		null	null		Unigene67651_All//sp|Q8S361|OR56D_DROME//3.00E-21//General odorant-binding protein 56d OS=Drosophila melanogaster GN=Obp56d PE=1 SV=2						swissprot -

Unigene67652_All	261	0.00	4.08	1.43	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.81E-06	Up	1.05E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene67652_All//gi|20597|emb|CAA45022.1|//5.00E-19//aspartate aminotransferase [Panicum miliaceum]	Unigene67652_All//1.00E-17//AT3G30970| ASP1 (ASPARTATE AMINOTRANSFERASE 1); L-aspartate:2-oxoglutarate aminotransferase			ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism//ko00350|Tyrosine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis	GO:0006519//GO:0008483//GO:0043231	nr -
Unigene67655_All	253	0.00	3.00	0.84	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	9.72E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67655_All//gi|148612407|gb|ABQ96119.1|//7.00E-15//alpha-gliadin [Aegilops tauschii]				ko03022|Basal transcription factors		nr -
Unigene67656_All	611	0.00	5.22	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	3.64E-18	Up	9.45E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene67656_All//gi|15230232|ref|NP_191274.1|//2.00E-49//NAP57 (Arabidopsis thaliana homologue of NAP57); pseudouridine synthase >gi|67460428|sp|Q9LD90.1|DKC1_ARATH RecName: Full=H/ACA ribonucleoprotein complex subunit 4; AltName: Full=Nucleolar protein NAP57 homolog; AltName: Full=Nopp-140-associated protein of 57 kDa homolog; Short=AtNAP57	Unigene67656_All//8.00E-47//AT3G57150| NAP57 (Arabidopsis thaliana homologue of NAP57); pseudouridine synthase				GO:0003676//GO:0009451//GO:0010467//GO:0016866//GO:0031981//GO:0044444	nr -
Unigene6766_All	437	0.12	0.93	0.12	2.28	1.18	1.86	9.87	3.83	2.64	2.95E+00	5.90E-02		2.63E-02	9.93E-01		-9.48E-01	1.58E-01		-2.93E-01	6.89E-01		-1.37E+00	5.34E-07	Down	-1.90E+00	3.97E-11	Down				Unigene6766_All//0.00E+00//TC172700				
Unigene67663_All	442	0.00	4.47	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.97E-11	Up	7.91E+00	3.95E-01		null	null		null	null		null	null		null	null		Unigene67663_All//gi|226501820|ref|NP_001149334.1|//1.00E-21//heat-and acid-stable phosphoprotein [Zea mays] >gi|195609090|gb|ACG26375.1| heat-and acid-stable phosphoprotein [Zea mays] >gi|195626468|gb|ACG35064.1| heat-and acid-stable phosphoprotein [Zea mays]	Unigene67663_All//4.00E-14//AT5G46020| unknown protein				GO:0006350//GO:0010468	nr -
Unigene67666_All	216	0.00	7.98	0.74	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	7.98E-10	Up	9.53E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene67666_All//sp|P92201|LCP8_DROME//8.00E-08//Larval cuticle protein 8 OS=Drosophila melanogaster GN=Lcp65Ag1 PE=1 SV=1						swissprot +
Unigene6767_All	1029	0.36	0.59	0.05	1.36	0.67	0.92	1.40	2.11	4.72	7.31E-01	4.16E-01		-2.78E+00	1.03E-01		-1.02E+00	6.01E-02		-5.57E-01	3.52E-01		5.96E-01	1.34E-01		1.76E+00	3.97E-11	Up	Unigene6767_All//gi|42569431|ref|NP_180469.3|//2.00E-57//ATRBL1 (Arabidopsis thaliana Rhomboid-like 1)	Unigene6767_All//7.00E-48//AT3G29050| ATRBL1 (Arabidopsis thaliana Rhomboid-like 1)	Unigene6767_All//0.00E+00//gi|164349477|gb|ES790970.1|ES790970				nr +
Unigene67680_All	594	0.00	4.78	0.72	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	3.82E-16	Up	9.49E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene67680_All//gi|116292768|gb|ABJ97690.1|//8.00E-24//EBP1 [Solanum tuberosum]	Unigene67680_All//2.00E-21//AT3G51800| ATG2; aminopeptidase/ metalloexopeptidase				GO:0010260//GO:0016020//GO:0031981//GO:0070011	nr -
Unigene67690_All	217	0.24	3.97	2.21	2.98	2.70	1.25	0.78	0.77	1.29	4.04E+00	4.20E-04	Up	3.20E+00	3.48E-02		-1.46E-01	8.39E-01		-1.26E+00	1.83E-01		-1.68E-02	1.02E+00		7.21E-01	5.97E-01					Unigene67690_All//2.00E-07//TC142575				
Unigene67692_All	543	0.00	7.93	0.49	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.56E-24	Up	8.94E+00	7.98E-02		null	null		null	null		null	null		null	null										
Unigene67694_All	545	0.19	4.46	1.76	0.09	0.25	0.00	0.08	0.23	0.51	4.54E+00	2.17E-11	Up	3.20E+00	1.02E-03		1.47E+00	6.17E-01		-6.51E+00	6.26E-01		1.57E+00	5.44E-01		2.72E+00	9.93E-02		Unigene67694_All//gi|297836874|ref|XP_002886319.1|//6.00E-13//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297332159|gb|EFH62578.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene67694_All//2.00E-44//DV849020				nr -
Unigene67695_All	304	0.00	3.00	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.61E-05	Up	8.45E+00	3.94E-01		null	null		null	null		null	null		null	null										
Unigene6770_All	436	1.20	3.02	6.35	6.40	5.84	8.60	5.53	4.41	3.65	1.33E+00	2.73E-02		2.40E+00	2.34E-07	Up	-1.31E-01	7.69E-01		4.26E-01	2.08E-01		-3.26E-01	3.96E-01		-5.97E-01	9.17E-02					Unigene6770_All//2.00E-15//DW506121				
Unigene67702_All	415	0.00	2.69	0.13	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.00E-06	Up	7.00E+00	6.30E-01		null	null		null	null		null	null		null	null										
Unigene67703_All	415	0.00	2.44	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	7.24E-06	Up	8.59E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene67703_All//sp|Q5RD00|AAPK2_PONAB//2.00E-15//5'-AMP-activated protein kinase catalytic subunit alpha-2 OS=Pongo abelii GN=PRKAA2 PE=2 SV=1						swissprot +
Unigene67705_All	375	0.00	5.68	0.85	0.00	0.00	0.00	1.69	1.00	0.32	1.25E+01	4.10E-12	Up	9.73E+00	4.49E-02		null	null		null	null		-7.54E-01	3.73E-01		-2.41E+00	8.12E-03		Unigene67705_All//gi|229609807|gb|ACQ83519.1|//9.00E-21//CBL-interacting protein kinase 03 [Vitis vinifera]	Unigene67705_All//6.00E-20//AT4G30960| SIP3 (SOS3-INTERACTING PROTEIN 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene67705_All//6.00E-37//gi|78343813|gb|DT564087.1|DT564087		ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0006972//GO:0009926//GO:0023060//GO:0032501//GO:0032559	nr +
Unigene67714_All	431	0.73	0.94	0.49	1.27	2.56	0.42	1.96	1.26	9.89	3.69E-01	7.23E-01		-5.60E-01	6.63E-01		1.01E+00	1.37E-01		-1.60E+00	1.32E-01		-6.38E-01	3.70E-01		2.33E+00	7.73E-14	Up	Unigene67714_All//gi|18416834|ref|NP_568264.1|//2.00E-10//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|14586361|emb|CAC42892.1| RING finger-like protein [Arabidopsis thaliana] >gi|21436021|gb|AAM51588.1|AT5g19430/F7K24_180 [Arabidopsis thaliana]	Unigene67714_All//1.00E-11//AT5G12310| zinc finger (C3HC4-type RING finger) family protein	Unigene67714_All//3.00E-88//TC133680			GO:0046914	nr -
Unigene67723_All	253	0.00	3.20	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.36E-05	Up	8.72E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene67723_All//gi|282721186|gb|ADA83693.1|//3.00E-06//alpha-gliadin [Triticum turgidum subsp. durum]						nr -
Unigene6773_All	870	0.36	0.87	0.55	2.06	2.81	0.52	2.04	1.30	1.14	1.28E+00	1.28E-01		6.11E-01	5.86E-01		4.47E-01	3.12E-01		-1.99E+00	1.66E-04	Down	-6.54E-01	1.39E-01		-8.34E-01	4.69E-02		Unigene6773_All//gi|21555178|gb|AAM63797.1|//1.00E-44//transcription factor-like protein [Arabidopsis thaliana]	Unigene6773_All//8.00E-34//AT3G58870| MNP (MONOPOLE); transcription factor	Unigene6773_All//0.00E+00//gi|78325969|gb|DT546243.1|DT546243	C2C2-GATA			nr +
Unigene67732_All	504	0.21	0.00	0.53	0.20	0.61	0.00	1.01	0.00	0.24	-7.70E+00	3.68E-01		1.35E+00	4.09E-01		1.64E+00	3.21E-01		-7.63E+00	3.96E-01		-9.98E+00	8.88E-04	Down	-2.09E+00	3.64E-02		Unigene67732_All//gi|222423637|dbj|BAH19787.1|//5.00E-27//AT2G34560 [Arabidopsis thaliana] >gi|222423678|dbj|BAH19806.1|AT2G34560 [Arabidopsis thaliana]	Unigene67732_All//1.00E-28//AT2G34560| katanin, putative	Unigene67732_All//2.00E-154//AI730459			GO:0032559//GO:0042623//GO:0043170	nr -
Unigene67736_All	365	0.00	3.75	0.58	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.79E-08	Up	9.19E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67736_All//sp|Q5R563|RENR_PONAB//7.00E-07//Renin receptor OS=Pongo abelii GN=ATP6AP2 PE=2 SV=1						swissprot +
Unigene67738_All	443	0.00	2.29	0.12	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	7.24E-06	Up	6.91E+00	6.30E-01		null	null		null	null		null	null		null	null										
Unigene67739_All	437	0.00	1.51	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	6.24E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene67739_All//gi|77540212|gb|AAB86964.1|//3.00E-50//glyceraldehyde-3-phosphate dehydrogenase B subunit [Glycine max]	Unigene67739_All//8.00E-49//AT1G42970| GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase (NAD+)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene67739_All//5.00E-41//gi|164312007|gb|EX168406.1|EX168406		ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0005576//GO:0006950//GO:0008943//GO:0009314//GO:0009526//GO:0009532//GO:0009534//GO:0010038//GO:0015977//GO:0019318//GO:0034285	nr +
Unigene67740_All	253	0.00	3.40	0.00	0.79	1.09	0.36	0.67	1.82	0.00	1.17E+01	4.94E-05	Up	null	null		4.67E-01	8.16E-01		-1.14E+00	5.68E-01		1.44E+00	1.67E-01		-9.38E+00	1.08E-01										
Unigene67744_All	247	0.42	4.51	1.51	0.00	0.00	0.00	0.00	0.00	0.00	3.41E+00	1.24E-04	Up	1.83E+00	2.12E-01		null	null		null	null		null	null		null	null										
Unigene6775_All	579	0.54	0.18	0.09	1.89	1.37	11.08	78.72	37.18	42.80	-1.63E+00	2.76E-01		-2.56E+00	1.59E-01		-4.69E-01	4.82E-01		2.55E+00	4.31E-19	Up	-1.08E+00	3.26E-46	Down	-8.79E-01	6.55E-34		Unigene6775_All//gi|15485720|emb|CAC67501.1|//4.00E-83//selenium binding protein [Medicago sativa]	Unigene6775_All//6.00E-78//AT4G14030| SBP1 (selenium-binding protein 1); selenium binding	Unigene6775_All//0.00E+00//TC153864				nr +
Unigene67753_All	231	0.00	3.95	2.07	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	1.10E+01	7.46E-03		null	null		null	null		null	null		null	null										
Unigene67757_All	268	0.00	0.00	0.00	0.19	0.00	0.17	2.37	0.00	0.00	null	null		null	null		-7.54E+00	5.49E-01		-1.42E-01	9.49E-01		-1.12E+01	1.23E-04	Down	-1.12E+01	7.10E-05	Down	Unigene67757_All//gi|14275752|emb|CAC40032.1|//1.00E-31//P-type ATPase [Hordeum vulgare]	Unigene67757_All//8.00E-32//AT1G10130| ECA3 (ENDOPLASMIC RETICULUM-TYPE CALCIUM-TRANSPORTING ATPASE 3); calcium-transporting ATPase/ calmodulin binding / manganese-transporting ATPase/ peroxidase	Unigene67757_All//2.00E-85//AI727991			GO:0000041//GO:0005515//GO:0009206//GO:0019829//GO:0031224//GO:0032559//GO:0043231//GO:0048513//GO:0055066//GO:0070838	nr +
Unigene67760_All	433	0.00	6.09	1.84	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	5.45E-15	Up	1.08E+01	1.72E-04	Up	null	null		null	null		null	null		null	null										
Unigene67762_All	435	0.00	5.13	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.09E-12	Up	7.94E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene67762_All//sp|P98160|PGBM_HUMAN//7.00E-10//Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=3						swissprot +
Unigene67771_All	283	0.00	2.51	0.56	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.32E-04	Up	9.14E+00	2.37E-01		null	null		null	null		null	null		null	null										
Unigene67773_All	250	12.77	5.88	8.31	14.75	16.80	20.05	41.43	25.24	18.33	-1.12E+00	1.52E-03		-6.20E-01	8.98E-02		1.89E-01	5.81E-01		4.44E-01	1.15E-01		-7.15E-01	6.21E-06		-1.18E+00	5.00E-13	Down	Unigene67773_All//gi|297845688|ref|XP_002890725.1|//1.00E-10//60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata] >gi|297336567|gb|EFH66984.1| 60S ribosomal protein L17 [Arabidopsis lyrata subsp. lyrata]		Unigene67773_All//1.00E-71//TC146595		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020	nr +
Unigene67776_All	413	0.00	6.75	2.19	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	7.43E-16	Up	1.11E+01	4.71E-05	Up	null	null		null	null		null	null		null	null		Unigene67776_All//gi|297597448|ref|NP_001043989.2|//2.00E-18//Os01g0701500 [Oryza sativa Japonica Group] >gi|255673596|dbj|BAF05903.2|Os01g0701500 [Oryza sativa Japonica Group]	Unigene67776_All//8.00E-18//AT5G38450| CYP735A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00908|Zeatin biosynthesis//ko00100|Steroid biosynthesis//ko00590|Arachidonic acid metabolism	GO:0005488//GO:0043229//GO:0044444	nr +
Unigene67777_All	300	0.52	2.36	3.91	0.00	0.00	0.15	0.00	0.00	0.00	2.18E+00	2.50E-02		2.90E+00	4.34E-04	Up	null	null		7.23E+00	6.89E-01		null	null		null	null					Unigene67777_All//6.00E-12//gi|109847166|gb|DW476146.1|DW476146				
Unigene6778_All	425	0.00	0.72	0.63	1.99	1.22	0.53	1.89	0.20	1.31	9.48E+00	4.40E-02		9.29E+00	7.98E-02		-7.13E-01	3.36E-01		-1.91E+00	2.14E-02		-3.26E+00	4.48E-04	Down	-5.26E-01	4.34E-01		Unigene6778_All//gi|268053527|gb|ACY92425.1|//3.00E-08//exportin-1 [Solanum lycopersicum]	Unigene6778_All//5.00E-08//AT3G03110| XPO1B; binding / protein transporter					nr +
Unigene67781_All	443	0.00	8.01	4.45	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	3.45E-20	Up	1.21E+01	7.45E-11	Up	null	null		null	null		null	null		null	null		Unigene67781_All//gi|226457922|gb|EU655229.1|//2.00E-12//high mobility group family B protein [Micromonas pusilla CCMP1545]	Unigene67781_All//2.00E-09//AT5G23420| HMGB6; transcription factor			ko03410|Base excision repair		nr -
Unigene67789_All	258	0.00	2.75	0.21	0.00	0.80	0.88	0.00	0.00	0.00	1.14E+01	3.32E-04	Up	7.69E+00	6.30E-01		9.65E+00	1.56E-01		9.77E+00	1.18E-01		null	null		null	null										
Unigene6779_All	1881	0.39	0.05	0.82	0.61	0.75	0.67	1.60	1.22	7.71	-2.85E+00	6.26E-03		1.08E+00	5.58E-02		3.01E-01	6.16E-01		1.42E-01	8.21E-01		-3.85E-01	2.53E-01		2.27E+00	7.95E-44	Up	Unigene6779_All//gi|28300299|gb|AAO37645.1|//1.00E-86//NBS-LRR resistance protein RGH1 [Manihot esculenta]	Unigene6779_All//5.00E-32//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene6779_All//3.00E-39//TC179054		ko04626|Plant-pathogen interaction		nr -
Unigene67793_All	665	0.00	3.51	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.90E-13	Up	9.32E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene67793_All//gi|225430178|ref|XP_002284900.1|//1.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]						nr +
Unigene67795_All	683	0.00	2.67	0.55	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.14E-10	Up	9.09E+00	2.49E-02		null	null		null	null		null	null		null	null										ESTscan -

Unigene67797_All	235	0.00	2.80	2.04	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.24E-04	Up	1.10E+01	7.46E-03		null	null		null	null		null	null		null	null		Unigene67797_All//sp|Q29865|1C18_HUMAN//3.00E-10//HLA class I histocompatibility antigen, Cw-18 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=1						swissprot +
Unigene678_All	1879	2.00	1.62	2.49	6.50	5.86	6.25	3.33	1.51	2.42	-3.09E-01	3.56E-01		3.15E-01	3.03E-01		-1.47E-01	4.30E-01		-5.57E-02	7.63E-01		-1.14E+00	1.44E-07	Down	-4.62E-01	2.44E-02		Unigene678_All//gi|15226370|ref|NP_180393.1|//0.00E+00//ATCNG15; calmodulin binding / cation channel/ cyclic nucleotide binding [Arabidopsis thaliana] >gi|38503241|sp|Q8GL29.1|CNG15_ARATH RecName: Full=Putative cyclic nucleotide-gated ion channel 15; AltName: Full=Cyclic nucleotide- and calmodulin-regulated ion channel 15	Unigene678_All//0.00E+00//AT2G28260| ATCNG15; calmodulin binding / cation channel/ cyclic nucleotide binding	Unigene678_All//2.00E-161//TC179196		ko04626|Plant-pathogen interaction	GO:0005216//GO:0006811//GO:0031224	nr +
Unigene6780_All	1742	0.24	0.00	0.18	0.00	0.12	0.10	71.26	16.65	10.25	-7.91E+00	1.04E-02		-3.90E-01	7.17E-01		6.89E+00	1.56E-01		6.70E+00	1.94E-01		-2.10E+00	0.00E+00	Down	-2.80E+00	0.00E+00	Down	Unigene6780_All//gi|224111880|ref|XP_002316010.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene6780_All//1.00E-102//AT2G26710| BAS1 (PMDB ACTIVATION TAGGED SUPPRESSOR 1); oxygen binding / steroid hydroxylase	Unigene6780_All//3.00E-30//TC139537		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism		nr +
Unigene67800_All	351	0.00	3.90	1.21	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.79E-08	Up	1.02E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene67800_All//gi|226508688|ref|NP_001148076.1|//3.00E-06//receptor protein kinase PERK1 [Zea mays] >gi|195615664|gb|ACG29662.1| receptor protein kinase PERK1 [Zea mays]						nr -
Unigene67807_All	280	2.24	1.63	0.57	5.16	6.15	2.90	3.47	0.60	3.41	-4.61E-01	6.18E-01		-1.97E+00	6.50E-02		2.53E-01	6.46E-01		-8.29E-01	1.41E-01		-2.54E+00	6.41E-04	Down	-2.44E-02	9.71E-01		Unigene67807_All//gi|224057130|ref|XP_002299134.1|//1.00E-16//DNA methyltransferase [Populus trichocarpa] >gi|222846392|gb|EEE83939.1| DNA methyltransferase [Populus trichocarpa]	Unigene67807_All//3.00E-13//AT1G80740| CMT1 (CHROMOMETHYLASE 1); DNA binding / chromatin binding	Unigene67807_All//2.00E-88//DR463757		ko00270|Cysteine and methionine metabolism	GO:0003676//GO:0006305//GO:0006325//GO:0008757//GO:0009292//GO:0043231//GO:0044427	nr +
Unigene67808_All	468	0.00	3.14	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.11E-08	Up	9.15E+00	7.98E-02		null	null		null	null		null	null		null	null		Unigene67808_All//gi|297843714|ref|XP_002889738.1|//2.00E-26//20S proteasome beta subunit PBG1 [Arabidopsis lyrata subsp. lyrata] >gi|297335580|gb|EFH65997.1| 20S proteasome beta subunit PBG1 [Arabidopsis lyrata subsp. lyrata]	Unigene67808_All//3.00E-27//AT1G56450| PBG1; peptidase/ threonine-type endopeptidase			ko03050|Proteasome	GO:0000502//GO:0005840//GO:0006970//GO:0008233//GO:0010038//GO:0019941	nr +
Unigene6781_All	1645	1839.53	890.24	1523.37	402.93	533.57	377.42	18.69	13.52	13.83	-1.05E+00	0.00E+00	Down	-2.72E-01	3.38E-201		4.05E-01	2.40E-153		-9.44E-02	7.30E-07		-4.67E-01	6.89E-08		-4.34E-01	3.05E-07		Unigene6781_All//gi|19749359|gb|AAD28640.2|//0.00E+00//geranylgeranyl hydrogenase [Glycine max]	Unigene6781_All//0.00E+00//AT1G74470| geranylgeranyl reductase	Unigene6781_All//0.00E+00//TC148880		ko00900|Terpenoid backbone biosynthesis//ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene67826_All	688	0.00	1.10	0.39	0.00	0.00	0.00	0.00	0.00	0.06	1.01E+01	1.76E-04	Up	8.60E+00	7.98E-02		null	null		null	null		null	null		5.86E+00	6.39E-01		Unigene67826_All//gi|145344326|ref|XP_001416686.1|//3.00E-54//Ribosomal protein Sa, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901] >gi|225891597|sp|A4RUK2.1|RSSA_OSTLU RecName: Full=40S ribosomal protein SA >gi|144576912|gb|AB094979.1| Ribosomal protein Sa, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901]	Unigene67826_All//4.00E-41//AT3G04770| RPSAb (40S ribosomal protein SA B); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0006519//GO:0009536//GO:0010467//GO:0015935//GO:0016831//GO:0044106//GO:0044249	nr -
Unigene6783_All	530	1.38	4.40	3.72	1.50	1.17	2.56	0.88	0.63	0.45	1.67E+00	2.05E-04	Up	1.43E+00	4.28E-03		-3.63E-01	6.23E-01		7.66E-01	2.05E-01		-4.76E-01	6.59E-01		-9.60E-01	3.13E-01		Unigene6783_All//gi|225431605|ref|XP_002282776.1|//1.00E-07//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296088617|emb|CBI37608.3| unnamed protein product [Vitis vinifera]		Unigene6783_All//3.00E-24//TC138664				nr +
Unigene67833_All	581	0.00	1.57	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	2.61E-05	Up	8.84E+00	7.98E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene67834_All	431	0.00	2.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene67834_All//gi|90811673|gb|ABD98034.1|//8.00E-08//calmodulin [Striga asiatica]	Unigene67834_All//1.00E-08//AT4G14640| CAM8 (CALMODULIN 8); calcium ion binding			ko04626|Plant-pathogen interaction	GO:0004672//GO:0009612//GO:0009642//GO:0016020//GO:0019932//GO:0046872	nr -
Unigene67835_All	268	0.00	3.03	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.36E-05	Up	9.63E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67835_All//gi|52140006|gb|AAU29329.1|//8.00E-11//ASF/SF2-like pre-mRNA splicing factor SRP32' [Zea mays]	Unigene67835_All//1.00E-05//AT1G02840| SR1; RNA binding / nucleic acid binding / nucleotide binding			ko03040|Spliceosome	GO:0043231	nr +
Unigene6784_All	403	2.60	1.26	4.36	21.63	11.02	9.19	11.54	4.15	50.22	-1.05E+00	1.20E-01		7.48E-01	1.45E-01		-9.73E-01	7.94E-08		-1.24E+00	4.30E-10	Down	-1.48E+00	2.64E-08	Down	2.12E+00	6.19E-56	Up	Unigene6784_All//gi|115470939|ref|NP_001059068.1|//9.00E-15//Os07g0185900 [Oryza sativa Japonica Group] >gi|113610604|dbj|BAF20982.1| Os07g0185900 [Oryza sativa Japonica Group]	Unigene6784_All//7.00E-15//AT3G57450| unknown protein	Unigene6784_All//2.00E-15//TC166250				nr -
Unigene67841_All	450	0.00	9.80	4.14	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	4.10E-25	Up	1.20E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene67841_All//sp|P26352|TYB12_ONCMY//3.00E-06//Thymosin beta-12 OS=Oncorhynchus mykiss PE=1 SV=2						swissprot -
Unigene67845_All	525	0.00	3.86	1.83	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.53E-11	Up	1.08E+01	2.45E-05	Up	null	null		null	null		null	null		null	null									
Unigene67851_All	272	0.00	5.77	0.59	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.70E-09	Up	9.20E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene67851_All//gi|115449197|ref|NP_001048378.1|//9.00E-15//Os02g0794600 [Oryza sativa Japonica Group] >gi|113537909|dbj|BAF10292.1| Os02g0794600 [Oryza sativa Japonica Group]	Unigene67851_All//2.00E-15//AT3G15352| ATCOX17; copper chaperone			ko00190|Oxidative phosphorylation	GO:0000041//GO:0005507//GO:0005740//GO:0010038//GO:0051707	nr -
Unigene67855_All	436	0.00	3.37	0.73	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.11E-08	Up	9.52E+00	4.49E-02		null	null		null	null		null	null		null	null		Unigene67855_All//gi|20067064|gb|AAM09521.1|AF489954_1|//4.00E-16//BIP4 [Physcomitrella patens]						GO:0006810	nr -
Unigene67858_All	386	0.00	8.80	1.93	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.54E-19	Up	1.09E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene67858_All//gi|297849560|ref|XP_002892661.1|//2.00E-13//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338503|gb|EFH68920.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene67858_All//2.00E-14//AT1G11910| aspartyl protease family protein				GO:0005576//GO:0005773//GO:0008233//GO:0010038//GO:0044238	nr +
Unigene67859_All	488	0.00	4.78	2.51	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.90E-13	Up	1.13E+01	9.11E-07	Up	null	null		null	null		null	null		null	null		Unigene67859_All//sp|A5A6M0|KIC17_PANTR//9.00E-59//Keratin, type I cytoskeletal 17 OS=Pan troglodytes GN=KRT17 PE=2 SV=1						swissprot -
Unigene67863_All	268	0.00	3.59	0.60	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.38E-05	Up	9.22E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene67863_All//gi|13592093|ref|NP_112384.1|//8.00E-24//hsc70-interacting protein [Rattus norvegicus] >gi|1708200|sp|P50503.1|F10A1_RAT RecName: Full=Hsc70-interacting protein; Short=Hip; AltName: Full=Protein ST13 homolog; AltName: Full=Protein FAM10A1 >gi|4379408|emb|CAA57546.1| Hsc70-interacting protein [Rattus norvegicus] >gi|50927605|gb|AAH78804.1| Suppression of tumorigenicity 13 [Rattus norvegicus] >gi|149065853|gb|EDM15726.1| rCG60000 [Rattus norvegicus]	Unigene67863_All//8.00E-19//AT3G17880| ATTDX (TETRATICOPEPTIDE DOMAIN-CONTAINING THIOREDOXIN); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor / protein binding				GO:0009408//GO:0016667//GO:0031072//GO:0032269//GO:0032558//GO:0032991//GO:0042026//GO:0044444//GO:0051259	nr -
Unigene67866_All	283	0.00	4.12	1.32	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.05E-06	Up	1.04E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene67866_All//sp|Q25255|PE44_LUCCU//1.00E-13//Peritrophin-44 OS=Lucilia cuprina PE=1 SV=1						swissprot +
Unigene67875_All	291	0.00	0.70	0.18	0.00	0.00	0.00	1.74	0.29	0.00	9.44E+00	1.35E-01		7.52E+00	6.30E-01		null	null		null	null		-2.60E+00	2.04E-02		-1.08E+01	5.54E-04	Down	Unigene67875_All//gi|15238697|ref|NP_197299.1|//6.00E-25//C2 domain-containing protein [Arabidopsis thaliana] >gi|9757890|dbj|BAB08397.1| phosphoribosylanthranilate transferase-like protein [Arabidopsis thaliana]	Unigene67875_All//2.00E-26//AT5G17980| C2 domain-containing protein	Unigene67875_All//2.00E-94//ES848380			GO:0016020//GO:0016757	nr -
Unigene6788_All	344	5.02	5.01	8.98	13.76	9.31	6.70	26.79	19.44	29.88	-3.20E-03	9.92E-01		8.39E-01	2.37E-02		-5.63E-01	3.46E-02		-1.04E+00	1.51E-04	Down	-4.63E-01	6.52E-03		1.57E-01	3.62E-01				Unigene6788_All//3.00E-60//TC154011				
Unigene67881_All	492	0.00	2.37	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.05E-06	Up	7.76E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene67881_All//gi|2935529|gb|AAC05150.1|//3.00E-42//PHES7 gene product [Pinus radiata]	Unigene67881_All//2.00E-42//AT1G14520| MIOX1 (MYO-INISITOL OXYGENASE); inositol oxygenase/ oxidoreductase			ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0008152//GO:0009987//GO:0016701	nr +
Unigene67883_All	283	0.00	3.40	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.38E-05	Up	8.56E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene67883_All//sp|Q27245|YH24_CAEEL//4.00E-10//Putative aminopeptidase W07G4.4 OS=Caenorhabditis elegans GN=W07G4.4 PE=1 SV=1						swissprot +
Unigene67884_All	831	0.00	3.11	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.05E-14	Up	8.00E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene67884_All//sp|Q52K18|SRRM1_MOUSE//1.00E-06//Serine/arginine repetitive matrix protein 1 OS=Mus musculus GN=Srrm1 PE=1 SV=1						swissprot -
Unigene6789_All	313	0.33	6.48	4.93	0.80	3.74	3.75	3.78	1.74	6.24	4.28E+00	3.01E-09	Up	3.88E+00	1.75E-06	Up	2.23E+00	1.51E-03		2.24E+00	1.82E-03		-1.12E+00	4.65E-02		7.22E-01	7.13E-02				Unigene6789_All//9.00E-08//gi|78345719|gb|DT565993.1|DT565993				
Unigene67891_All	294	0.00	2.41	0.36	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.32E-04	Up	8.50E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene67891_All//sp|Q7KQM6|PERQ1_DROME//4.00E-25//PERQ amino acid-rich with GYF domain-containing protein CG11148 OS=Drosophila melanogaster GN=CG11148 PE=1 SV=1						swissprot -
Unigene67896_All	259	0.00	2.54	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.24E-04	Up	7.68E+00	6.30E-01		null	null		null	null		null	null		null	null		Unigene67896_All//gi|300261393|gb|EFJ45606.1|//7.00E-14//NADH:ubiquinone oxidoreductase 76 kDa subunit [Volvox carteri f. nagariensis]	Unigene67896_All//5.00E-13//AT5G37510| EMB1467 (embryo defective 1467); NADH dehydrogenase (ubiquinone)/ NADH dehydrogenase/ electron carrier/ iron-sulfur cluster binding / oxidoreductase/ oxidoreductase, acting on NADH or NADPH			ko00190|Oxidative phosphorylation	GO:0003954//GO:0016020//GO:0022900//GO:0051536	nr -

Unigene67898_All	361	0.00	2.39	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.94E-05	Up	7.20E+00	6.30E-01		null	null		null	null		null	null		null	null		Unigene67898_All//gi|299471555|emb|CBN80041.1|//5.00E-08//expressed unknown protein [Ectocarpus siliculosus]						nr -
Unigene6790_All	796	0.46	0.83	2.14	0.06	1.04	0.45	1.54	1.89	1.70	8.47E-01	3.48E-01		2.22E+00	2.12E-04	Up	4.05E+00	4.06E-04	Up	2.86E+00	9.44E-02		2.95E-01	5.82E-01		1.44E-01	7.70E-01				Unigene6790_All//5.00E-104//gi|78345719|gb|DT565993.1|DT565993				
Unigene67900_All	245	0.00	2.90	0.00	0.00	0.00	0.00	0.35	0.17	0.49	1.15E+01	3.32E-04	Up	null	null		null	null		null	null		-1.02E+00	7.22E-01		4.99E-01	8.06E-01									
Unigene67904_All	523	0.00	0.29	0.00	0.00	0.13	0.09	1.94	0.00	0.08	8.18E+00	2.33E-01		null	null		7.04E+00	6.04E-01		6.43E+00	6.89E-01		-1.09E+01	2.97E-07	Down	-4.67E+00	1.72E-06	Down	Unigene67904_All//gi|225457626|ref|XP_002274415.1|//3.00E-55//PREDICTED: hexose transporter-like [Vitis vinifera]	Unigene67904_All//1.00E-48//AT4G35300| TMT2 (TONOPLAST MONOSACCHARIDE TRANSPORTER2); carbohydrate transmembrane transporter/ nucleoside transmembrane transporter/ sugar:hydrogen symporter	Unigene67904_All//2.00E-155//EV485459			GO:0005402//GO:0006810//GO:0008152//GO:0016628//GO:0031224//GO:0043231	nr +
Unigene67908_All	272	0.00	3.54	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene6791_All	325	2.09	7.48	5.73	3.07	5.40	3.61	3.51	2.57	1.35	1.84E+00	4.23E-05	Up	1.45E+00	4.96E-03		8.18E-01	1.03E-01		2.37E-01	7.09E-01		-4.50E-01	4.44E-01		-1.38E+00	1.42E-02									
Unigene67912_All	260	0.00	0.19	0.00	0.00	0.00	0.00	10.41	0.32	1.07	7.61E+00	6.12E-01		null	null		null	null		null	null		-5.02E+00	2.03E-16	Down	-3.28E+00	7.82E-13	Down	Unigene67912_All//gi|211906536|gb|AC111761.1|//3.00E-21//class III peroxidase [Gossypium hirsutum]	Unigene67912_All//3.00E-14//AT3G21770| peroxidase 30 (PER30 (P30) (PRX3R9)	Unigene67912_All//1.00E-105//DN817536		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0005506//GO:0005618//GO:0006950//GO:0008152//GO:0016209//GO:0016640//GO:0031410//GO:0043231	nr +
Unigene6792_All	1556	5.58	0.29	1.20	0.00	0.02	0.12	7.53	0.67	3.99	-4.25E+00	1.35E-38	Down	-2.22E+00	6.57E-20	Down	4.47E+00	8.21E-01		6.86E+00	1.94E-01		-3.49E+00	1.90E-54	Down	-9.14E-01	5.82E-10		Unigene6792_All//gi|15228174|ref|NP_191129.1|//1.00E-145//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|7263558|emb|CAB81595.1| glucuronosyl transferase-like protein [Arabidopsis thaliana] >gi|11074514|gb|AB004630.1| At3g55700 [Arabidopsis thaliana]	Unigene6792_All//5.00E-146//AT3G55700| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene6792_All//0.00E+00//DR463546		ko00908|Zeatin biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene67922_All	355	0.00	4.28	1.50	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.10E-08	Up	1.06E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene67922_All//gi|300265646|gb|EFJ40809.1|//2.00E-16//superoxide dismutase [Mn] [Volvox carteri f. nagariensis]	Unigene67922_All//2.00E-13//AT3G10920| MSD1 (MANGANESE SUPEROXIDE DISMUTASE 1); metal ion binding / superoxide dismutase			ko04146|Peroxisome	GO:0004672//GO:0006800//GO:0016209//GO:0043169	nr -
Unigene67924_All	411	0.00	2.84	0.13	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.05E-06	Up	7.02E+00	6.30E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene67928_All	422	0.00	5.64	1.51	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.50E-13	Up	1.06E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene67928_All//gi|124365534|gb|ABN09768.1|//2.00E-10//Cyclin-like F-box; Calcium-binding EF-hand [Medicago truncatula]				ko00010|Glycolysis / Gluconeogenesis	GO:0005488	nr -
Unigene67932_All	784	0.00	3.81	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.18E-17	Up	9.99E+00	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene67932_All//gi|168259044|gb|ACA23210.1|//5.00E-14//glucanase inhibitor protein 2 [Phytophthora infestans]					GO:0003824	nr +
Unigene67934_All	471	0.00	3.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.54E-09	Up	null	null		null	null		null	null		null	null		null	null		Unigene67934_All//gi|15239928|ref|NP_196229.1|//3.00E-12//DNAJ heat shock N-terminal domain-containing protein / cell division protein-related [Arabidopsis thaliana] >gi|8978347|dbj|BAB98200.1| cell division related protein-like [Arabidopsis thaliana]						nr +
Unigene6794_All	529	2.77	6.80	4.13	3.67	2.34	3.33	2.16	1.66	0.08	1.30E+00	1.18E-04	Up	5.76E-01	2.13E-01		-6.48E-01	1.55E-01		-1.41E-01	7.62E-01		-3.79E-01	5.32E-01		-4.84E+00	2.34E-07	Down							
Unigene67942_All	256	0.00	3.96	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.24E-06	Up	8.70E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene67942_All//gi|300265661|gb|EFJ49851.1|//2.00E-06//hypothetical protein VOLCADRAFT_58884 [Volvox carteri f. nagariensis]						nr +
Unigene67949_All	498	0.00	2.14	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.81E-06	Up	9.55E+00	2.49E-02		null	null		null	null		null	null		null	null		Unigene67949_All//sp|043736|ITM2A_HUMAN//2.00E-09//Integral membrane protein 2A OS=Homo sapiens GN=ITM2A PE=1 SV=2						swissprot -
Unigene6795_All	572	2.93	0.00	1.12	2.44	1.32	1.74	2.66	0.88	1.67	-1.15E+01	1.06E-09	Down	-1.39E+00	1.16E-02		-8.81E-01	1.06E-01		-4.89E-01	4.09E-01		-1.60E+00	1.53E-03		-6.71E-01	1.45E-01		Unigene6795_All//gi|297819444|ref|XP_002877605.1|//8.00E-58//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297323443|gb|EFH53864.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene6795_All//5.00E-59//AT3G48250| pentatricopeptide (PPR) repeat-containing protein	Unigene6795_All//0.00E+00//gi|13243963|gb|BE055753.2|BE055753				nr -
Unigene67953_All	856	0.00	5.21	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.10E-25	Up	9.96E+00	9.01E-05	Up	null	null		null	null		null	null		null	null		Unigene67953_All//gi|18410234|ref|NP_565051.1|//8.00E-15//BGAL17 (beta-galactosidase 17); beta-galactosidase/ catalytic/ cation binding [Arabidopsis thaliana] >gi|75163694|sp|Q93224.1|BGL17_ARATH RecName: Full=Beta-galactosidase 17; Short=Lactase 17; Flags: Precursor >gi|16648842|gb|AAL25611.1| At1g72990/F3N23_19 [Arabidopsis thaliana] >gi|22655360|gb|AAM98272.1| At1g72990/F3N23_19 [Arabidopsis thaliana]	Unigene67953_All//4.00E-16//AT1G72990| BGAL17 (beta-galactosidase 17); beta-galactosidase/ catalytic/ cation binding			ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series	GO:0016798//GO:0043229//GO:0044444	nr +
Unigene67958_All	292	0.00	2.43	2.19	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.32E-04	Up	1.11E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene67958_All//gi|15230090|ref|NP_189072.1|//3.00E-26//AMT1;5 (AMMONIUM TRANSPORTER 1;5); ammonium transmembrane transporter [Arabidopsis thaliana] >gi|75273698|sp|Q9LK16.1|AMT15_ARATH RecName: Full=Putative ammonium transporter 1 member 5; Short=AtAMT1;5 >gi|11994690|dbj|BAB02928.1| ammonium transporter [Arabidopsis thaliana]	Unigene67958_All//1.00E-27//AT3G24290| AMT1;5 (AMMONIUM TRANSPORTER 1;5); ammonium transmembrane transporter	Unigene67958_All//2.00E-11//gi|78336379|gb|DT556653.1|DT556653			GO:0015101//GO:0015291//GO:0015695//GO:0031224//GO:0043231//GO:0043623	nr -
Unigene67959_All	264	0.00	3.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.35E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene67959_All//sp|Q9VD44|GLD2A_DROME//1.00E-17//Poly(A) RNA polymerase gld-2 homolog A OS=Drosophila melanogaster GN=Gld2 PE=1 SV=3						swissprot +
Unigene6796_All	500	2.93	5.57	2.77	4.38	9.92	4.88	1.10	0.84	0.40	9.28E-01	1.40E-02		-8.15E-02	8.85E-01		1.18E+00	7.01E-06	Up	1.54E-01	7.19E-01		-3.95E-01	6.34E-01		-1.46E+00	9.76E-02				Unigene6796_All//2.00E-99//ES804984				
Unigene67962_All	414	0.00	5.87	3.22	0.36	0.17	0.11	0.00	0.00	0.10	1.25E+01	7.72E-14	Up	1.17E+01	2.39E-07	Up	-1.12E+00	5.82E-01		-1.73E+00	5.00E-01		null	null		6.59E+00	6.39E-01		Unigene67962_All//gi|218189938|gb|EEC72365.1|//2.00E-31//hypothetical protein OsI_05623 [Oryza sativa Indica Group]		Unigene67962_All//3.00E-153//gi|109852087|gb|DW481066.1|DW481066				nr +
Unigene67969_All	461	0.00	4.51	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.94E-12	Up	9.85E+00	1.38E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene67970_All	546	0.00	2.97	1.27	0.00	0.00	0.08	0.00	0.00	0.00	1.15E+01	2.96E-09	Up	1.03E+01	6.14E-04	Up	null	null		6.37E+00	6.89E-01		null	null		null	null		Unigene67970_All//sp|P67809|YBOX1_HUMAN//2.00E-101//Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3						swissprot +
Unigene6798_All	574	458.58	680.51	672.77	243.52	287.54	493.49	224.29	213.42	189.27	5.69E-01	1.17E-105		5.53E-01	2.11E-96		2.40E-01	4.74E-11		1.02E+00	1.27E-225	Up	-7.17E-02	1.24E-01		-2.45E-01	6.47E-10		Unigene6798_All//gi|30693971|ref|NP_566991.2|//5.00E-44//universal stress protein (USP) family protein [Arabidopsis thaliana] >gi|11692860|gb|AAG40033.1|AF324682_1 AT3g53990 [Arabidopsis thaliana] >gi|11762224|gb|AAG40390.1|AF325038_1 AT3g53990 [Arabidopsis thaliana] >gi|13605748|gb|AAK32867.1|AF361855_1 AT3g53990/F5K20_290 [Arabidopsis thaliana] >gi|15450449|gb|AAO36518.1| AT3g53990/F5K20_290 [Arabidopsis thaliana] >gi|16974447|gb|AAL31227.1| AT3g53990/F5K20_290 [Arabidopsis thaliana] >gi|17979251|gb|AAL49942.1| AT3g53990/F5K20_290 [Arabidopsis thaliana] >gi|222423580|dbj|BAH19759.1| AT3G53990 [Arabidopsis thaliana]	Unigene6798_All//3.00E-45//AT3G53990| universal stress protein (USP) family protein	Unigene6798_All//0.00E+00//gi|73866075|gb|DT468813.1|DT468813				nr -
Unigene67984_All	891	0.59	0.57	0.06	0.84	0.77	0.41	0.81	0.05	0.22	-4.62E-02	9.75E-01		-3.30E+00	2.40E-02		-1.18E-01	8.62E-01		-1.05E+00	2.21E-01		-4.10E+00	2.91E-04	Down	-1.85E+00	1.78E-02		Unigene67984_All//gi|297839865|ref|XP_002887814.1|//3.00E-37//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333655|gb|EFH64073.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene67984_All//7.00E-33//AT1G80710| transducin family protein / WD-40 repeat family protein	Unigene67984_All//0.00E+00//TC149415				nr +
Unigene6799_All	504	0.73	0.90	0.00	0.79	0.14	0.90	78.94	174.40	227.49	3.16E-01	7.44E-01		-9.51E+00	2.77E-02		-2.53E+00	5.79E-02		1.81E-01	8.83E-01		1.14E+00	2.12E-96	Up	1.53E+00	1.05E-199	Up	Unigene6799_All//gi|224060661|ref|XP_002300248.1|//5.00E-63//GH3 family protein [Populus trichocarpa] >gi|222847506|gb|EEE85053.1| GH3 family protein [Populus trichocarpa]	Unigene6799_All//7.00E-61//AT2G23170| GH3.3; indole-3-acetic acid amido synthetase	Unigene6799_All//0.00E+00//TC137326				nr -
Unigene67994_All	259	0.61	4.50	0.62	4.23	2.79	4.36	6.86	3.23	3.54	2.89E+00	2.98E-04	Up	2.55E-02	1.00E+00		-6.00E-01	3.53E-01		4.30E-02	9.42E-01		-1.09E+00	1.38E-02		-9.55E-01	2.36E-02		Unigene67994_All//gi|224072260|ref|XP_002303678.1|//3.00E-30//f-box family protein [Populus trichocarpa] >gi|222841110|gb|EEE78657.1| f-box family protein [Populus trichocarpa]	Unigene67994_All//2.00E-21//AT4G24060| Dof-type zinc finger domain-containing protein	Unigene67994_All//2.00E-103//TC174670	C2C2-Dof		GO:0001071//GO:0003676//GO:0010468//GO:0046914	nr -
Unigene67995_All	469	0.00	5.83	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.44E-15	Up	9.15E+00	7.98E-02		null	null		null	null		null	null		null	null		Unigene67995_All//gi|21322711|emb|CAD22154.1|//6.00E-35//pherophorin-dz1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome		nr -

Unigene68003_All	511	0.00	3.27	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.54E-09	Up	1.04E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene68003_All//gi|15217918|ref|NP_173459.1|//7.00E-49//DRT112; copper ion binding / electron carrier [Arabidopsis thaliana] >gi|12644265|sp|P42699.2|PLAS2_ARATH RecName: Full=Plastocyanin major isoform, chloroplastic; AltName: Full=DNA-damage-repair/toleration protein DRT112; Flags: Precursor >gi|9558592|gb|AAF88155.1|AC026234_6 Contains similarity to a DNA-damage-repair/toleration protein DRT112 precursor from Arabidopsis thaliana gi|1169201 and is a member of the copper binding proteins family PF|00127. ESTs gb|BE039446, gb|T46296, gb|N54992, gb|T21043, gb|BE039361, gb|T41789, gb|AA728654, gb|T22293, gb|T42572, gb|R65100, gb|N65354, gb|N37323, gb|R90003, gb|BE039026, gb|BE038950, gb|AA713227 come from this gene >gi|11692900|gb|AAG40053.1|AF324702_1 At1g20340 [Arabidopsis thaliana] >gi|13605744|gb|AAK32865.1|AF361853_1 At1g20340/F14O10_4 [Arabidopsis thaliana]	Unigene68003_All//4.00E-40//AT1G20340| DRT112; copper ion binding / electron carrier	Unigene68003_All//3.00E-12//C0084424		ko00195|Photosynthesis	GO:0006091//GO:0006412//GO:0009416//GO:0009532//GO:0009534//GO:0010038//GO:0044436//GO:0046914//GO:0051234//GO:0055066	nr +
Unigene68005_All	262	0.00	2.51	1.83	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.24E-04	Up	1.08E+01	7.46E-03		null	null		null	null		null	null		null	null								
Unigene68006_All	257	0.00	3.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null								ESTscan +
Unigene6801_All	374	173.89	123.69	162.88	306.21	355.68	202.39	502.16	314.47	182.47	-4.91E-01	3.81E-14		-9.43E-02	2.25E-01		2.16E-01	1.77E-07		-5.97E-01	5.63E-37		-6.75E-01	1.18E-84		-1.46E+00	0.00E+00	Down	Unigene6801_All//gi|171190270|gb|ACB42441.1|//9.00E-28//aquaporin PIP2;4 [Gossypium hirsutum]	Unigene6801_All//1.00E-25//AT2G16850| PIP2;8 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;8); water channel	Unigene6801_All//8.00E-166//gi|109826664|gb|DW225374.1|DW225374				nr -
Unigene68014_All	653	0.00	3.41	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.09E-12	Up	8.67E+00	7.98E-02		null	null		null	null		null	null		null	null								
Unigene68017_All	497	0.00	2.14	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.81E-06	Up	9.07E+00	7.98E-02		null	null		null	null		null	null		null	null		Unigene68017_All//sp|P52034|K6PF_DROME//2.00E-45//6-phosphofructokinase OS=Drosophila melanogaster GN=Pfk PE=2 SV=2							swissprot +
Unigene6802_All	627	1.59	0.40	0.00	2.22	1.54	0.86	7.08	3.07	4.89	-1.97E+00	9.93E-03		-1.06E+01	1.77E-05	Down	-5.33E-01	3.44E-01		-1.36E+00	1.87E-02		-1.21E+00	4.57E-06	Down	-5.33E-01	3.18E-02		Unigene6802_All//gi|147840314|emb|CAN70691.1|//1.00E-06//hypothetical protein [Vitis vinifera]		Unigene6802_All//0.00E+00//TC153829				nr -
Unigene68021_All	362	0.14	4.06	0.44	0.00	0.10	0.00	0.00	0.00	0.00	4.81E+00	2.99E-07	Up	1.61E+00	5.10E-01		6.57E+00	8.21E-01		null	null		null	null		null	null			Unigene68021_All//4.00E-07//ES820852				
Unigene68022_All	468	0.00	11.04	2.50	0.00	0.00	0.10	0.00	0.00	0.00	1.34E+01	1.81E-29	Up	1.13E+01	1.77E-06	Up	null	null		6.59E+00	6.89E-01		null	null		null	null		Unigene68022_All//gi|5091552|gb|AAD39581.1|AC007067_21//1.00E-09//T10024.21 [Arabidopsis thaliana]	Unigene68022_All//1.00E-10//AT1G10580| transducin family protein / WD-40 repeat family protein			ko03040|Spliceosome		nr -
Unigene68026_All	1111	0.09	0.46	0.72	1.03	0.77	0.12	1.07	0.15	0.47	2.28E+00	6.22E-02		2.93E+00	5.05E-03		-4.12E-01	5.39E-01		-3.08E+00	1.19E-04	Down	-2.82E+00	4.41E-05	Down	-1.19E+00	2.80E-02		Unigene68026_All//gi|15226456|ref|NP_182212.1|//1.00E-127//oxidoreductase, acting on the CH-CH group of donors [Arabidopsis thaliana] >gi|56556695|gb|AAV97801.1|At2g16890 [Arabidopsis thaliana]	Unigene68026_All//5.00E-115//AT2G46890| oxidoreductase, acting on the CH-CH group of donors	Unigene68026_All//0.00E+00//TC134133			GO:0016020//GO:0031410//GO:0043231	nr +
Unigene68027_All	271	0.00	3.18	0.39	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.94E-05	Up	8.62E+00	3.94E-01		null	null		null	null		null	null		null	null								ESTscan +
Unigene68029_All	452	0.00	2.80	0.47	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.86E-07	Up	8.88E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene68029_All//gi|54290409|dbj|BAD61279.1|//2.00E-08//tetratricopeptide repeat protein 2-like [Oryza sativa Japonica Group]	Unigene68029_All//8.00E-09//AT4G12400| stress-inducible protein, putative			ko04626|Plant-pathogen interaction	GO:0000302//GO:0009642//GO:0043231	nr -
Unigene6803_All	559	1.50	0.00	0.76	1.96	0.68	2.10	0.68	0.00	3.99	-1.05E+01	5.56E-05	Down	-9.75E-01	2.37E-01		-1.53E+00	1.61E-02		9.96E-02	8.93E-01		-9.41E+00	6.17E-03		2.55E+00	2.46E-08	Up							
Unigene6804_All	353	5.04	5.89	3.02	4.80	5.37	1.28	1.44	0.95	1.02	2.24E-01	6.16E-01		-7.40E-01	1.46E-01		1.61E-01	7.95E-01		-1.91E+00	4.24E-04	Down	-6.02E-01	5.31E-01		-5.01E-01	5.83E-01								
Unigene68040_All	267	0.00	5.88	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.70E-09	Up	9.64E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene68040_All//sp|Q09666|AHNK_HUMAN//3.00E-43//Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2							swissprot +
Unigene6805_All	451	26.80	2.13	4.60	0.66	1.60	1.10	0.00	2.32	0.09	-3.65E+00	7.93E-48	Down	-2.54E+00	3.01E-32	Down	1.27E+00	1.56E-01		7.33E-01	5.16E-01		1.12E+01	2.02E-07	Up	6.46E+00	6.39E-01		Unigene6805_All//gi|297724175|ref|NP_001174451.1|//6.00E-14//Os05g0442000 [Oryza sativa Japonica Group] >gi|255676407|dbj|BAH93179.1|Os05g0442000 [Oryza sativa Japonica Group]	Unigene6805_All//1.00E-16//AT5G06270| unknown protein	Unigene6805_All//0.00E+00//TC158285				nr -
Unigene68050_All	278	0.00	2.92	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.35E-05	Up	9.17E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68050_All//sp|P09372|GRPE_ECOLI//1.00E-30//Protein grpE OS=Escherichia coli (strain K12) GN=grpE PE=1 SV=1							swissprot +
Unigene68052_All	320	0.00	2.69	1.16	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.94E-05	Up	1.02E+01	2.49E-02		null	null		null	null		null	null		null	null								ESTscan -
Unigene68055_All	257	0.00	2.56	0.62	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.23E-04	Up	9.28E+00	2.37E-01		null	null		null	null		null	null		null	null								ESTscan +
Unigene68058_All	285	0.00	3.73	0.93	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	3.81E-06	Up	9.87E+00	7.98E-02		null	null		null	null		null	null		null	null		Unigene68058_All//gi|300266756|gb|EFJ50942.1|//2.00E-09//eukaryotic translation initiation factor 4 [Volvox carteri f. nagariensis]	Unigene68058_All//3.00E-09//AT5G57870| eukaryotic translation initiation factor 4F, putative / eIF-4F, putative				GO:0008135//GO:0043234//GO:0046739//GO:0051707	nr -
Unigene6806_All	707	0.59	0.65	2.11	2.25	0.49	0.51	1.26	0.83	2.14	1.24E-01	9.11E-01		1.83E+00	2.94E-03		-2.21E+00	4.28E-05	Down	-2.14E+00	2.07E-04	Down	-6.02E-01	3.85E-01		7.70E-01	9.92E-02		Unigene6806_All//gi|170660047|gb|ACB28472.1|//2.00E-59//polyprotein [Ananas comosus]							nr -
Unigene68060_All	557	0.00	4.09	1.43	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.63E-13	Up	1.05E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene68060_All//gi|298710204|emb|CBJ26279.1|//2.00E-14//FKBP-type peptidyl-prolyl cis-trans isomerase 2 [Ectocarpus siliculosus]	Unigene68060_All//5.00E-14//AT5G48580| FKBP15-2; FK506 binding / peptidyl-prolyl cis-trans isomerase				GO:0016859//GO:0043231//GO:0044267	nr -
Unigene68062_All	393	0.00	4.90	1.36	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.72E-11	Up	1.04E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene68062_All//gi|21483549|gb|ABM54166.1|//3.00E-19//thioredoxin [Brassica juncea]	Unigene68062_All//3.00E-15//AT5G39950| ATTRX2 (THIOREDOXIN 2); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor				GO:0016020//GO:0016667//GO:0043231//GO:0044444	nr +
Unigene68065_All	293	2.14	1.21	4.54	11.39	5.52	1.08	0.29	0.00	0.00	-8.24E-01	3.75E-01		1.08E+00	7.96E-02		-1.04E+00	9.94E-04	Down	-3.40E+00	8.91E-14	Down	-8.17E+00	4.00E-01		-8.17E+00	3.55E-01		Unigene68065_All//gi|297596537|ref|NP_001042723.2|//1.00E-13//Os01g0275900 [Oryza sativa Japonica Group] >gi|255673109|dbj|BAF04637.2|Os01g0275900 [Oryza sativa Japonica Group]		Unigene68065_All//2.00E-79//TC147477				nr +
Unigene6807_All	671	3.27	0.30	0.95	10.02	14.16	10.84	2.65	0.25	0.36	-3.44E+00	1.06E-08	Down	-1.78E+00	2.71E-04	Down	4.99E-01	5.62E-03		1.13E-01	6.65E-01		-3.41E+00	1.40E-08	Down	-2.89E+00	9.05E-08	Down	Unigene6807_All//gi|94983836|gb|ABF50623.1|//2.00E-23//G93-GW [Glycine max]	Unigene6807_All//3.00E-17//AT5G19420| Ran GTPase binding / chromatin binding / zinc ion binding	Unigene6807_All//2.00E-171//DR463845				nr -
Unigene68071_All	522	0.00	5.14	1.02	0.10	0.13	0.00	0.00	0.00	0.00	1.23E+01	2.80E-15	Up	9.99E+00	4.02E-03		4.67E-01	9.55E-01		-6.58E+00	6.26E-01		null	null		null	null								ESTscan +
Unigene68075_All	286	0.00	3.72	0.37	0.00	0.12	0.00	0.00	0.00	0.28	1.19E+01	3.81E-06	Up	8.54E+00	3.94E-01		6.91E+00	8.21E-01		null	null		null	null		8.12E+00	4.02E-01				Unigene68075_All//2.00E-08//gi|78325606|gb|DT545880.1|DT545880				
Unigene68076_All	267	0.00	2.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null								ESTscan -
Unigene6808_All	744	0.56	0.54	0.86	2.01	0.93	0.36	4.15	1.91	0.86	-4.64E-02	9.80E-01		6.10E-01	5.09E-01		-1.12E+00	3.10E-02		-2.46E+00	8.25E-05	Down	-1.12E+00	4.79E-04	Down	-2.28E+00	4.20E-10	Down	Unigene6808_All//gi|121501699|gb|ABM55240.1|//1.00E-122//retrotransposon protein [Beta vulgaris]		Unigene6808_All//4.00E-15//FL577362				nr +
Unigene68080_All	400	0.00	2.28	0.53	0.00	0.09	0.00	0.00	0.00	0.10	1.12E+01	2.61E-05	Up	9.06E+00	1.40E-01		6.43E+00	8.21E-01		null	null		null	null		6.64E+00	6.39E-01		Unigene68080_All//gi|224072685|ref|XP_002303834.1|//2.00E-30//predicted protein [Populus trichocarpa] >gi|222841266|gb|EEE78813.1|predicted protein [Populus trichocarpa]						nr -
Unigene68086_All	266	0.00	4.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene68086_All//sp|Q17QR6|MOT13_BOVIN//9.00E-09//Monocarboxylate transporter 13 OS=Bos taurus GN=SLC16A13 PE=2 SV=1							swissprot +
Unigene6809_All	285	44.79	16.71	21.30	14.51	7.73	28.37	0.30	1.76	2.94	-1.42E+00	1.09E-16	Down	-1.07E+00	1.75E-10	Down	-9.08E-01	1.15E-03		9.67E-01	1.82E-06		2.57E+00	2.28E-02		3.31E+00	2.30E-04	Up	Unigene6809_All//gi|225428877|ref|XP_002282482.1|//1.00E-19//PREDICTED: similar to leucine-rich repeat family protein [Vitis vinifera]				ko03040|Spliceosome		nr -
Unigene68093_All	604	0.00	3.10	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.11E-10	Up	9.78E+00	4.02E-03		null	null		null	null		null	null		null	null								
Unigene68096_All	488	0.96	10.49	0.00	1.74	0.78	0.46	0.00	0.00	0.00	3.44E+00	2.39E-19	Up	-9.91E+00	8.62E-03		-1.16E+00	1.15E-01		-1.91E+00	2.14E-02		null	null		null	null								
Unigene6810_All	1623	0.00	0.00	0.00	0.00	0.11	0.00	111.57	175.89	17.94	null	null		null	null		6.73E+00	2.26E-01		null	null		6.57E-01	4.79E-122		-2.64E+00	0.00E+00	Down	Unigene6810_All//gi|224075052|ref|XP_002304537.1|//0.00E+00//cation proton exchanger [Populus trichocarpa] >gi|222841969|gb|EEE79516.1|cation proton exchanger [Populus trichocarpa]	Unigene6810_All//4.00E-163//AT5G41610| ATCHX18; monovalent cation:proton antiporter/ sodium:hydrogen antiporter					nr +
Unigene68103_All	641	0.00	2.45	0.66	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	5.70E-09	Up	9.38E+00	1.38E-02		null	null		null	null		null	null		null	null								ESTscan +
Unigene68105_All	310	0.00	2.45	0.52	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.76E-04	Up	9.01E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68105_All//gi|42565125|ref|NP_188924.3|//6.00E-09//emp24/gp25L/p24 protein-related [Arabidopsis thaliana] >gi|119947173|dbj|BAB03029.1|coated vesicle membrane protein-like [Arabidopsis thaliana] >gi|17979492|gb|AAL50082.1|AT3g22845/MWI23_22 [Arabidopsis thaliana] >gi|20147305|gb|AAM10366.1|AT3g22845/MWI23_22 [Arabidopsis thaliana]	Unigene68105_All//2.00E-10//AT3G22845| emp24/gp25L/p24 protein-related				GO:0043231	nr +
Unigene68108_All	311	0.00	2.93	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.61E-05	Up	8.42E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68108_All//sp|Q19Q77|CGL_PIG//1.00E-09//Cystathionine gamma-lyase OS=Sus scrofa GN=CTH PE=2 SV=1							swissprot +

Unigene6811_All	1849	0.00	0.00	0.00	0.00	0.04	0.39	6.79	17.81	63.78	null	null		null	null		5.22E+00	6.04E-01		8.61E+00	2.31E-04	Up	1.39E+00	1.99E-49	Up	3.23E+00	0.00E+00	Up	Unigene6811_All//gi|297850310|ref|XP_002893036.1|//0.00E+00//flavin-dependent monooxygenase 1 [Arabidopsis lyrata subsp. lyrata] >gi|297338878|gb|EFH69295.1| flavin-dependent monooxygenase 1 [Arabidopsis lyrata subsp. lyrata]	Unigene6811_All//0.00E+00//AT1G19250| FMO1 (FLAVIN-DEPENDENT MONOOXYGENASE 1); FAD binding / NADP or NADPH binding / electron carrier/ flavin-containing monooxygenase/ monooxygenase/ oxidoreductase			ko00380|Tryptophan metabolism		nr -
Unigene68115_All	547	0.00	6.30	2.63	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.31E-19	Up	1.14E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene68115_All//sp|Q7M4E9|CUD3_SCHGR//7.00E-16//Endocuticle structural glycoprotein SgAbd-3 OS=Schistocerca gregaria PE=1 SV=1						swissprot -
Unigene6812_All	632	0.00	1.20	0.67	1.50	1.58	2.07	13.71	77.90	96.32	1.02E+01	1.76E-04	Up	9.40E+00	1.38E-02		7.74E-02	9.37E-01		4.69E-01	4.67E-01		2.51E+00	4.41E-162	Up	2.81E+00	1.39E-231	Up	Unigene6812_All//gi|90811673|gb|AB098034.1|//4.00E-40//calmodulin [Striga asiatica]	Unigene6812_All//1.00E-38//AT5G37780| CAM1 (CALMODULIN 1); calcium ion binding	Unigene6812_All//0.00E+00//TC166294		ko04626|Plant-pathogen interaction		nr -
Unigene68123_All	839	0.00	4.17	1.59	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	6.73E-20	Up	1.06E+01	2.39E-07	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene68124_All	812	0.00	4.49	1.18	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	9.10E-21	Up	1.02E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene68124_All//gi|300257566|gb|EFJ41813.1|//1.00E-13//extracellular matrix glycoprotein pherophorin-V30 [Volvox carteri f. nagariensis]	Unigene68124_All//5.00E-06//AT4G18375| KH domain-containing protein					nr +
Unigene68129_All	286	0.00	3.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.94E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene68129_All//gi|226454229|gb|EEH51536.1|//2.00E-09//predicted protein [Micromonas pusilla CCMP1545]	Unigene68129_All//2.00E-06//AT1G16260| protein kinase family protein					nr -
Unigene68130_All	929	0.00	5.95	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.66E-31	Up	1.07E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene68130_All//sp|P98160|PGBM_HUMAN//5.00E-19//Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV=3						swissprot +
Unigene68132_All	294	0.00	3.79	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.00E-06	Up	1.07E+01	7.46E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene68133_All	317	0.00	4.32	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.79E-08	Up	8.98E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68133_All//sp|Q49ZU4|Y535_STAS1//2.00E-06//Uncharacterized lipoprotein SSP0535 OS=Staphylococcus saprophyticus subsp. saprophyticus (strain ATCC 15305 / DSM 20229) GN=SSP0535 PE=4 SV=1						swissprot +
Unigene68134_All	511	0.00	6.64	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.54E-19	Up	9.70E+00	1.38E-02		null	null		null	null		null	null		null	null		Unigene68134_All//gi|87241202|gb|ABD33060.1|//3.00E-11//Sec61beta [Medicago truncatula]	Unigene68134_All//6.00E-07//AT5G60160| sec61beta family protein			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export	GO:0016020	nr -
Unigene68136_All	295	0.00	4.81	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.06E-08	Up	7.50E+00	6.30E-01		null	null		null	null		null	null		null	null									
Unigene68137_All	398	0.00	2.93	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.05E-06	Up	9.06E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene68137_All//gi|22531014|gb|AAM57011.1|//2.00E-54//expressed protein [Arabidopsis thaliana] >gi|23197966|gb|AAN15510.1| expressed protein [Arabidopsis thaliana]	Unigene68137_All//1.00E-55//AT1G08380| PSAO (photosystem I subunit O)	Unigene68137_All//3.00E-14//TC147609			GO:0009521//GO:0009536//GO:0009765	nr -
Unigene68143_All	314	0.00	2.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene68143_All//gi|298710946|emb|CBJ32256.1|//5.00E-10//Imp2 homolog, Inner Membrane Peptidase complex subunit 2 [Ectocarpus siliculosus]	Unigene68143_All//7.00E-10//AT3G08980| signal peptidase I family protein			ko03060|Protein export	GO:0016787//GO:0044464	nr -
Unigene68146_All	497	0.00	5.00	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.98E-14	Up	9.55E+00	2.49E-02		null	null		null	null		null	null		null	null		Unigene68146_All//sp|Q9V7U0|RESIL_DROME//4.00E-06//Pro-resilin OS=Drosophila melanogaster GN=resilin PE=1 SV=1						swissprot +
Unigene68147_All	310	0.00	4.58	1.72	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.06E-08	Up	1.07E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene68147_All//sp|P13395|SPTCA_DROME//1.00E-45//Spectrin alpha chain OS=Drosophila melanogaster GN=alpha-Spec PE=1 SV=2						swissprot -
Unigene68149_All	299	0.00	2.54	2.49	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.76E-04	Up	1.13E+01	3.26E-04	Up	null	null		null	null		null	null		null	null									
Unigene68151_All	293	0.00	8.65	5.09	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.05E-14	Up	1.23E+01	3.22E-08	Up	null	null		null	null		null	null		null	null		Unigene68151_All//sp|Q00341|VIGLN_HUMAN//5.00E-16//Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2						swissprot +
Unigene68152_All	670	0.00	2.57	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	7.98E-10	Up	7.31E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68152_All//gi|1359894|emb|CAA81210.1|//5.00E-15//NADPH-ferrihemoprotein reductase [Helianthus tuberosus]	Unigene68152_All//2.00E-12//AT4G30210| ATR2 (ARABIDOPSIS P450 REDUCTASE 2); NADPH-hemoprotein reductase					nr +
Unigene68154_All	399	0.00	3.30	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.49E-07	Up	9.65E+00	4.49E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene68156_All	539	0.00	3.67	0.20	0.00	0.00	0.08	0.31	0.00	0.15	1.18E+01	2.97E-11	Up	7.63E+00	3.94E-01		null	null		6.39E+00	6.89E-01		-8.29E+00	1.34E-01		-1.09E+00	5.52E-01									
Unigene6816_All	439	0.36	7.85	0.49	1.82	1.02	1.34	10.50	10.76	5.72	4.46E+00	8.25E-16	Up	4.41E-01	7.74E-01		-8.32E-01	2.88E-01		-4.41E-01	6.14E-01		3.54E-02	9.10E-01		-8.77E-01	3.25E-04		Unigene6816_All//gi|110738762|dbj|BAF01305.1|//4.00E-28//cytochrome c1 precursor [Arabidopsis thaliana]	Unigene6816_All//4.00E-19//AT5G40810| cytochrome c1, putative	Unigene6816_All//2.00E-68//TC173185		ko00190|Oxidative phosphorylation		nr -
Unigene68163_All	571	0.00	4.53	0.93	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-14	Up	9.87E+00	4.02E-03		null	null		null	null		null	null		null	null		Unigene68163_All//gi|162459414|ref|NP_001105403.1|//7.00E-12//MEK homologl [Zea mays] >gi|2737973|gb|AAC83393.1| protein kinase ZmMEK1 [Zea mays]	Unigene68163_All//1.00E-10//AT1G73500| MKK9 (MAP KINASE KINASE 9); MAP kinase kinase/ kinase/ protein kinase activator			ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0000160//GO:0004712//GO:0005488//GO:0006468//GO:0006555//GO:0006970//GO:0009700//GO:0010557//GO:0019887	nr +
Unigene68164_All	502	0.00	3.03	0.11	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.10E-08	Up	6.73E+00	6.30E-01		null	null		null	null		null	null		null	null		Unigene68164_All//gi|255082742|ref|XP_002504357.1|//5.00E-06//resistance-nodulation-cell division superfamily [Micromonas sp. RCC299] >gi|226519625|gb|ACO65615.1| resistance-nodulation-cell division superfamily [Micromonas sp. RCC299]						nr +
Unigene68168_All	274	0.00	4.07	0.58	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.99E-06	Up	9.19E+00	2.37E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene6817_All	740	0.57	1.92	0.43	1.35	1.26	1.22	1.77	1.92	4.79	1.76E+00	3.72E-03		-3.89E-01	7.17E-01		-9.97E-02	8.68E-01		-1.41E-01	8.36E-01		1.17E-01	8.18E-01		1.44E+00	1.86E-06	Up			Unigene6817_All//5.00E-70//TC178103				
Unigene68174_All	302	0.00	2.85	2.82	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	4.93E-05	Up	1.15E+01	9.01E-05	Up	null	null		null	null		null	null		null	null									
Unigene68177_All	477	0.00	5.63	1.12	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.80E-15	Up	1.01E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene68177_All//sp|P18091|ACTN_DROME//8.00E-89//Alpha-actinin, sarcomeric OS=Drosophila melanogaster GN=Actn PE=2 SV=2						swissprot +
Unigene68178_All	326	1.44	1.40	0.00	4.43	2.01	0.97	3.50	1.03	1.34	-4.63E-02	9.78E-01		-1.05E+01	8.62E-03		-1.14E+00	3.09E-02		-2.19E+00	3.74E-04	Down	-1.77E+00	3.70E-03		-1.38E+00	1.42E-02		Unigene68178_All//gi|15237943|ref|NP_197229.1|//8.00E-16//tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana]	Unigene68178_All//3.00E-17//AT5G17270| tetratricopeptide repeat (TPR)-containing protein	Unigene68178_All//2.00E-156//TC145404			GO:0043231	nr -
Unigene68179_All	800	0.00	5.70	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.54E-26	Up	9.64E+00	1.16E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene68182_All	292	0.00	5.55	1.09	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.96E-09	Up	1.01E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene68182_All//gi|161727354|dbj|BAF94304.1|//2.00E-06//lactonase [Euglena gracilis]						nr +
Unigene68185_All	345	0.91	4.26	2.47	2.02	1.80	0.26	1.35	0.97	0.92	2.23E+00	4.29E-04	Up	1.44E+00	8.22E-02		-1.70E-01	8.21E-01		-2.95E+00	5.83E-03		-4.76E-01	6.59E-01		-5.45E-01	5.65E-01		Unigene68185_All//gi|3367536|gb|AAC28521.1|//2.00E-07//Contains similarity to symbiosis-related like protein F1N20.80 gi|29613343 from A. thaliana BAC gb|AL022140. EST gb|T04695 comes from this gene [Arabidopsis thaliana]	Unigene68185_All//2.00E-08//AT1G62040| ATG8C (autophagy 8c); microtubule binding	Unigene68185_All//3.00E-103//gi|21092153|gb|BQ404466.1|BQ404466		ko04140|Regulation of autophagy		nr +
Unigene68187_All	339	0.00	3.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.86E-07	Up	null	null		null	null		null	null		null	null		null	null									
Unigene68189_All	329	0.00	3.23	1.62	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.81E-06	Up	1.07E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene68189_All//gi|2511689|emb|CAB17074.1|//3.00E-09//cysteine proteinase precursor [Phaseolus vulgaris]	Unigene68189_All//2.00E-08//AT4G36880| CP1 (CYSTEINE PROTEINASE1); cysteine-type endopeptidase/ cysteine-type peptidase				GO:0008233//GO:0031410	nr +
Unigene68192_All	295	0.00	3.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.24E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene68192_All//gi|862342|dbj|BAA06731.1|//3.00E-06//NPK2 [Nicotiana tabacum]	Unigene68192_All//4.00E-07//AT5G40140| ATMKK3 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3); MAP kinase kinase			ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene68199_All	633	1.57	0.72	0.08	0.55	0.11	0.86	2.34	1.32	1.20	-1.12E+00	1.09E-01		-4.22E+00	1.62E-04	Down	-2.34E+00	1.01E-01		6.36E-01	5.61E-01		-8.24E-01	9.30E-02		-9.67E-01	3.93E-02		Unigene68199_All//gi|115488000|ref|NP_001066487.1|//3.00E-37//Os12g0244200 [Oryza sativa Japonica Group] >gi|77554416|gb|ABA97212.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113648994|dbj|BAF29506.1| Os12g0244200 [Oryza sativa Japonica Group]	Unigene68199_All//2.00E-38//AT3G01740| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Ribosomal protein L37, mitochondrial (InterPro:IPR013870); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G14290.1); Has 117 Blast hits to 117 proteins in 58 species: Archae - 0; Bacteria - 0; Metazoa - 56; Fungi - 22; Plants - 27; Viruses - 0; Other Eukaryotes - 12 (source: NCBI BLink).	Unigene68199_All//0.00E+00//gi|48778914|gb|CO088280.1|CO088280			GO:0043231	nr +
Unigene682_All	2577	1.99	1.47	2.48	1.80	2.79	3.89	6.74	5.42	34.57	-4.32E-01	1.09E-01		3.18E-01	2.16E-01		6.36E-01	2.37E-03		1.11E+00	9.95E-10	Up	-3.16E-01	9.33E-03		2.36E+00	1.08E-277	Up	Unigene682_All//gi|15226370|ref|NP_180393.1|//0.00E+00//ATCNG15; calmodulin binding / cation channel/ cyclic nucleotide binding [Arabidopsis thaliana] >gi|38502241|sp|Q8GL29.1|CNG15_ARATH RecName: Full=Putative cyclic nucleotide-gated ion channel 15; AltName: Full=Cyclic nucleotide- and calmodulin-regulated ion channel 15	Unigene682_All//0.00E+00//AT2G28260| ATCNGC15; calmodulin binding / cation channel/ cyclic nucleotide binding	Unigene682_All//0.00E+00//TC179196		ko04626|Plant-pathogen interaction	GO:0005267//GO:0030001//GO:0031224	nr -
Unigene6820_All	1280	0.04	0.32	0.00	0.00	0.16	0.14	132.22	21.62	77.87	2.95E+00	5.90E-02		-5.35E+00	6.17E-01		7.33E+00	1.56E-01		7.14E+00	1.94E-01		-2.61E+00	0.00E+00	Down	-7.64E-01	3.62E-97		Unigene6820_All//gi|15239359|ref|NP_200860.1|//1.00E-143//late embryogenesis abundant protein-related / LEA protein-related [Arabidopsis thaliana] >gi|40823110|gb|AAR92259.1| At5g60520 [Arabidopsis thaliana]	Unigene6820_All//1.00E-137//AT5G60520| late embryogenesis abundant protein-related / LEA protein-related	Unigene6820_All//0.00E+00//TC177555				nr -
Unigene68200_All	317	14.19	6.39	5.38	17.13	20.64	18.52	41.88	42.06	34.94	-1.15E+00	7.88E-05	Down	-1.40E+00	6.42E-06	Down	2.69E-01	2.96E-01		1.13E-01	6.77E-01		6.20E-03	1.01E+00		-2.62E-01	6.05E-02		Unigene68200_All//gi|6984134|gb|AAF34767.1|AF227622_1//1.00E-11//60S acidic ribosomal protein P0 [Euphorbia esula]		Unigene68200_All//1.00E-80//gi|13353912|gb|BG444260.1|BG444260		ko03010|Ribosome	GO:0005198//GO:0006412//GO:0016829//GO:0022613//GO:0030529	nr +

Unigene68204_All	573	0.00	5.66	1.12	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.87E-18	Up	1.01E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene68204_All//gi|115454751|ref|NP_001050976.1|//1.00E-31//Os03g0695600 [Oryza sativa Japonica Group] >gi|109940125|sp|Q9LST6.2|PSB2_ORYSJ RecName: Full=Proteasome subunit beta type-2; AltName: Full=20S proteasome alpha subunit D; AltName: Full=20S proteasome subunit beta-4 >gi|275525546|gb|AAO19369.1| 20S proteasome beta 4 subunit [Oryza sativa Japonica Group] >gi|113549447|dbj|BAF12890.1| Os03g0695600 [Oryza sativa Japonica Group] >gi|149390831|gb|ABR25433.1| 20S proteasome beta subunit d2 [Oryza sativa Indica Group]	Unigene68204_All//2.00E-31//AT3G22630| PBD1 (20S PROTEASOME BETA SUBUNIT D1); peptidase/ threonine-type endopeptidase			ko03050|Proteasome	GO:0000502//GO:0008233//GO:0019941	nr +
Unigene68205_All	309	0.00	3.44	0.52	0.64	0.22	0.00	0.41	0.54	0.00	1.17E+01	3.81E-06	Up	9.01E+00	2.37E-01		-1.53E+00	4.15E-01		-9.33E+00	1.33E-01		3.98E-01	8.13E-01		-8.68E+00	1.99E-01									
Unigene68207_All	718	0.36	1.83	0.15	0.14	0.82	0.19	0.88	0.58	0.17	2.33E+00	6.54E-04	Up	-1.30E+00	4.36E-01		2.55E+00	2.84E-02		4.43E-01	8.60E-01		-6.02E-01	4.67E-01		-2.41E+00	8.12E-03		Unigene68207_All//gi|1374772|dbj|BAA08856.1|//1.00E-17//diacylglycerol kinase [Arabidopsis thaliana]	Unigene68207_All//2.00E-19//AT5G07920| DGK1 (DIACYLGLYCEROL KINASE1); calcium ion binding / diacylglycerol kinase	Unigene68207_All//0.00E+00//TC162967		ko04070|Phosphatidylinositol signaling system//ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0007186//GO:0016301//GO:0046872	nr -
Unigene68208_All	310	0.00	2.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null									
Unigene6821_All	319	10.33	4.13	5.01	13.59	16.19	19.96	1.99	2.62	5.50	-1.32E+00	1.79E-04	Down	-1.05E+00	3.70E-03		2.53E-01	3.94E-01		5.55E-01	1.83E-02		3.98E-01	5.94E-01		1.47E+00	1.06E-03		Unigene6821_All//gi|255543897|ref|XP_002513011.1|//4.00E-10//tRNA-dihydrouridine synthase, putative [Ricinus communis] >gi|223548022|gb|EEF49514.1| tRNA-dihydrouridine synthase, putative [Ricinus communis]		Unigene6821_All//3.00E-168//gi|78323638|gb|DT543912.1|DT543912				nr +
Unigene68212_All	511	0.00	7.64	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	3.25E-22	Up	1.04E+01	6.14E-04	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene68214_All	318	0.00	2.07	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.23E-04	Up	8.97E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68214_All//gi|28395420|gb|AAO39008.1|/8.00E-43//plasma intrinsic protein 2,2 [Juglans regia]	Unigene68214_All//2.00E-43//AT2G37170| PIP2B (PLASMA MEMBRANE INTRINSIC PROTEIN 2); water channel	Unigene68214_All//2.00E-11//gi|48830204|gb|CO128594.1|CO128594			GO:0005372//GO:0006950//GO:0009536//GO:0031224//GO:0044244	nr +
Unigene68218_All	310	0.00	8.34	1.03	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.05E-14	Up	1.00E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene68218_All//gi|298712886|emb|CBJ33402.1|//3.00E-09//glucose-methanol-choline oxidoreductase [Ectocarpus siliculosus]						GO:0016491//GO:0030554//GO:0044281	nr +
Unigene6822_All	454	1.38	0.22	1.29	1.98	1.21	3.18	0.84	0.92	3.51	-2.63E+00	1.78E-02		-1.00E-01	9.15E-01		-7.03E-01	3.24E-01		6.89E-01	2.32E-01		1.35E-01	8.99E-01		2.07E+00	5.52E-05	Up			Unigene6822_All//2.00E-77//TC149897					
Unigene68224_All	273	0.00	14.11	3.12	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	6.32E-22	Up	1.16E+01	9.00E-05	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene68225_All	321	0.65	0.00	0.00	1.24	0.54	1.13	2.90	0.13	0.62	-9.35E+00	1.21E-01		-9.35E+00	1.44E-01		-1.21E+00	3.14E-01		-1.41E-01	9.04E-01		-4.48E+00	1.30E-05	Down	-2.22E+00	1.63E-03		Unigene68225_All//gi|225452336|ref|XP_002272790.1|//6.00E-16//PREDICTED: hypothetical protein [Vitis vinifera]	Unigene68225_All//9.00E-05//AT5G40480| EMB3012 (embryo defective 3012)	Unigene68225_All//4.00E-121//gi|164285966|gb|ES797025.1|ES797025				nr +
Unigene68229_All	688	0.00	4.35	0.39	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.18E-17	Up	8.60E+00	7.98E-02		null	null		null	null		null	null		null	null		Unigene68229_All//gi|56606102|ref|NP_001008526.1|//6.00E-10//BAG family molecular chaperone regulator 5 [Rattus norvegicus] >gi|68051940|sp|Q5QJC9.1|BAG5_RAT RecName: Full=BAG family molecular chaperone regulator 5; Short=BAG-5; AltName: Full=Bcl-2-associated athanogene 5 >gi|38176435|gb|AAR13081.1| BCL2-associated athanogene 5 [Rattus norvegicus] >gi|56788776|gb|AAH88418.1| BCL2-associated athanogene 5 [Rattus norvegicus] >gi|149044072|gb|EDL97454.1|rCG27645 [Rattus norvegicus]						GO:0008219//GO:0019899//GO:0031397//GO:0044087//GO:0044424	nr +
Unigene68237_All	498	0.32	0.61	0.86	0.50	0.35	0.91	1.87	1.18	0.24	9.54E-01	5.03E-01		1.44E+00	2.53E-01		-5.33E-01	7.12E-01		8.59E-01	4.69E-01		-6.69E-01	3.12E-01		-2.96E+00	1.72E-04	Down	Unigene68237_All//gi|30683798|ref|NP_849544.1|//5.00E-30//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|119360071|gb|ABL66764.1|At4g16765 [Arabidopsis thaliana]	Unigene68237_All//3.00E-31//AT4G16765| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene68237_All//4.00E-113//TC168658		ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016706//GO:0046914	nr +
Unigene6824_All	594	5.37	2.39	3.05	1.68	2.72	1.14	0.00	0.28	0.13	-1.17E+00	9.68E-04	Down	-8.18E-01	2.49E-02		7.00E-01	1.92E-01		-5.56E-01	4.47E-01		8.14E+00	1.38E-01		7.07E+00	4.02E-01		Unigene6824_All//gi|19920126|gb|AAM08538.1|AC092749_11/5.00E-13//Hypothetical protein [Oryza sativa Japonica Group]		Unigene6824_All//0.00E+00//gi|84154762|gb|DN804117.1|DN804117				nr +
Unigene68249_All	330	0.48	3.22	1.78	0.00	0.42	0.55	0.38	0.89	0.36	2.76E+00	8.45E-04	Up	1.90E+00	8.47E-02		8.71E+00	3.17E-01		9.10E+00	1.94E-01		1.21E+00	3.92E-01		-8.58E-02	9.68E-01				Unigene68249_All//4.00E-41//TC152112					
Unigene6825_All	818	7.61	8.98	9.50	4.14	7.07	3.31	4.50	12.26	12.95	2.39E-01	3.02E-01		3.20E-01	1.54E-01		7.72E-01	1.09E-03		-3.22E-01	3.93E-01		1.45E+00	1.65E-16	Up	1.53E+00	3.33E-19	Up	Unigene6825_All//gi|255555915|ref|XP_002518993.1|//2.00E-29//plastidial glycerol-phosphate acyltransferase [Ricinus communis] >gi|223541980|gb|EEF43526.1| plastidial glycerol-phosphate acyltransferase [Ricinus communis]	Unigene6825_All//8.00E-25//AT1G32200| ATS1; glycerol-3-phosphate O-acyltransferase	Unigene6825_All//0.00E+00//TC153178		ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr +
Unigene68252_All	323	0.16	1.10	0.66	1.54	0.53	1.82	0.39	2.85	0.49	2.76E+00	9.58E-02		2.03E+00	3.61E-01		-1.53E+00	1.45E-01		2.37E-01	7.98E-01		2.86E+00	4.09E-04	Up	3.29E-01	8.50E-01		Unigene68252_All//gi|297806717|ref|XP_002871242.1|//1.00E-26//bZIP transcription factor TGA2 [Arabidopsis lyrata subsp. lyrata] >gi|297317079|gb|EFH47501.1| bZIP transcription factor TGA2 [Arabidopsis lyrata subsp. lyrata]	Unigene68252_All//4.00E-28//AT5G06950| AHBP-1B; DNA binding / transcription activator/ transcription factor/ transcription repressor	Unigene68252_All//7.00E-89//TC136987	bZIP		GO:0001071//GO:0003677//GO:0005515//GO:0006351//GO:0009536//GO:0009627//GO:0030528//GO:0042221	nr +
Unigene68255_All	325	0.00	2.96	1.15	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.38E-05	Up	1.02E+01	2.49E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene68265_All	340	0.00	2.98	2.19	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.24E-06	Up	1.11E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene68265_All//sp|Q6NVR1|ENSA_XENTR//1.00E-10//Alpha-endosulfine OS=Xenopus tropicalis GN=ensa PE=2 SV=1						swissprot -
Unigene6827_All	300	4.19	5.07	6.39	17.93	9.07	6.62	4.93	3.62	7.04	2.76E-01	5.98E-01		6.10E-01	2.20E-01		-9.84E-01	3.87E-05		-1.44E+00	5.34E-08	Down	-4.46E-01	3.92E-01		5.13E-01	1.89E-01				Unigene6827_All//8.00E-76//ES842886					
Unigene68270_All	355	0.00	2.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.24E-06	Up	null	null		null	null		null	null		null	null		null	null									
Unigene68275_All	306	0.00	2.82	2.44	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	4.93E-05	Up	1.13E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene68275_All//gi|195605028|gb|ACG24344.1|//4.00E-34//photosystem I reaction center subunit XI [Zea mays]	Unigene68275_All//2.00E-25//AT4G12800| PSAL (photosystem I subunit L)	Unigene68275_All//1.00E-16//EX169380		ko00195|Photosynthesis	GO:0006091//GO:0009522//GO:0009526//GO:0009534//GO:0009570	nr +
Unigene68278_All	322	0.00	2.68	3.31	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.93E-05	Up	1.17E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene68278_All//sp|P14209|CD99_HUMAN//2.00E-49//CD99 antigen OS=Homo sapiens GN=CD99 PE=1 SV=1						swissprot -
Unigene6828_All	326	22.47	34.97	34.30	21.85	25.98	43.36	34.11	94.36	164.73	6.38E-01	1.46E-04		6.10E-01	5.30E-04		2.50E-01	2.53E-01		9.89E-01	3.31E-11		1.47E+00	4.76E-50	Up	2.27E+00	2.80E-160	Up	Unigene6828_All//gi|297843434|ref|XP_002889598.1|//6.00E-45//acyl-CoA oxidase 6 [Arabidopsis lyrata subsp. lyrata] >gi|297335440|gb|EFH65857.1| acyl-CoA oxidase 6 [Arabidopsis lyrata subsp. lyrata]	Unigene6828_All//6.00E-46//AT1G06310| ACX6 (ACYL-COA OXIDASE 6); FAD binding / acyl-CoA dehydrogenase/ acyl-CoA oxidase/ electron carrier/ oxidoreductase/ oxidoreductase, acting on the CH-CH group of donors	Unigene6828_All//7.00E-169//TC155839		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko01071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene68280_All	472	0.00	1.40	0.11	0.00	0.07	0.00	0.00	0.00	0.00	1.04E+01	6.23E-04	Up	6.82E+00	6.30E-01		6.19E+00	8.21E-01		null	null		null	null		null	null		Unigene68280_All//sp|Q9A2A3|Y3663_CAUCR//8.00E-24//Uncharacterized protein CC_3663 OS=Caulobacter crescentus GN=CC_3663 PE=3 SV=2						swissprot +
Unigene68282_All	345	0.00	2.94	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.24E-06	Up	9.59E+00	7.98E-02		null	null		null	null		null	null		null	null		Unigene68282_All//gi|5420276|emb|CAB46642.1|//2.00E-06//cyclin A2 [Solanum lycopersicum]						nr +
Unigene68288_All	339	0.00	2.39	1.10	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	9.35E-05	Up	1.01E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene68288_All//sp|Q9VAL0|SPCS1_DROME//5.00E-18//Signal peptidase complex subunit 1 OS=Drosophila melanogaster GN=Spase12 PE=1 SV=2						swissprot +
Unigene68292_All	414	0.00	3.43	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.06E-08	Up	null	null		null	null		null	null		null	null		null	null		Unigene68292_All//sp|Q29KT5|SPIR_DROPS//2.00E-27//Protein spire OS=Drosophila pseudoobscura pseudoobscura GN=spir PE=3 SV=2						swissprot -
Unigene68295_All	530	0.00	9.27	6.03	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	5.13E-28	Up	1.26E+01	1.15E-17	Up	null	null		null	null		null	null		null	null		Unigene68295_All//gi|50261283|ref|YP_052890.1|//8.00E-14//NADH dehydrogenase subunit 2 [Saprolegnia ferax] >gi|50261307|ref|YP_052916.1| NADH dehydrogenase subunit 2 [Saprolegnia ferax] >gi|48237596|gb|AAT40645.1| NADH dehydrogenase subunit 2 [Saprolegnia ferax] >gi|48237620|gb|AAT40669.1| NADH dehydrogenase subunit 2 [Saprolegnia ferax]				ko00190|Oxidative phosphorylation	GO:0043231	nr -
Unigene68299_All	336	0.00	4.83	3.33	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.96E-09	Up	1.17E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene68299_All//gi|301107564|ref|XP_002902864.1|//4.00E-08//conserved hypothetical protein [Phytophthora infestans T30-4] >gi|262097982|gb|EEY56034.1| conserved hypothetical protein [Phytophthora infestans T30-4]						nr +
Unigene683_All	2551	5.64	2.98	2.36	9.49	7.67	5.98	7.36	3.83	9.73	-9.21E-01	1.00E-09		-1.26E+00	6.05E-15	Down	-3.08E-01	3.99E-03		-6.65E-01	6.49E-10		-9.41E-01	1.19E-15		4.03E-01	2.44E-05		Unigene683_All//gi|297842769|ref|XP_002889266.1|//1.00E-154//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335107|gb|EFH65525.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene683_All//5.00E-133//AT1G79720| aspartyl protease family protein	Unigene683_All//0.00E+00//TC145755			GO:0043231	nr +
Unigene6830_All	472	77.71	179.49	58.89	85.80	52.02	75.30	73.54	276.81	228.48	1.21E+00	1.09E-82	Up	-4.00E-01	1.16E-05		-7.22E-01	7.38E-21		-1.88E-01	3.37E-02		1.91E+00	2.95E-306	Up	1.64E+00	1.75E-207	Up	Unigene6830_All//gi|224075517|ref|XP_002304662.1|//2.00E-40//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222842094|gb|EEE79641.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene6830_All//1.00E-35//AT5G13180| ANAC083 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 83); transcription factor	Unigene6830_All//0.00E+00//TC139632	NAC			nr +
Unigene68300_All	884	0.00	6.36	2.35	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	4.34E-32	Up	1.12E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene68300_All//gi|20067064|gb|AAM09521.1|AF489954_1/6.00E-13//BIP4 [Physcomitrella patens]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00270|Cysteine and methionine metabolism//ko03020|RNA polymerase		nr +
Unigene68301_All	343	0.00	2.07	0.00	0.00	0.10	0.13	0.12	0.12	0.00	1.10E+01	3.32E-04	Up	null	null		6.65E+00	8.21E-01		7.04E+00	6.89E-01		-1.65E-02	1.00E+00		-6.95E+00	6.05E-01									

Unigene68305_All	301	0.00	2.69	1.06	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.35E-05	Up	1.01E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene68305_All//gi|300123445|emb|CBK24718.2|//9.00E-23//unnamed protein product [Blastocystis hominis]						nr -
Unigene68306_All	350	0.00	2.90	1.98	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.24E-06	Up	1.09E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene68306_All//gi|51241757|dbj|BAD36766.1|//8.00E-20//6-phosphogluconate dehydrogenase [Cyanidioschyzon merolae]	Unigene68306_All//2.00E-12//AT5G41670| 6-phosphogluconate dehydrogenase family protein			ko00480|Glutathione metabolism//ko00030|Pentose phosphate pathway	GO:0000166//GO:0006007//GO:0016616//GO:0043231//GO:0048037	nr +
Unigene68307_All	345	0.00	3.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.81E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene68307_All//sp|Q86887|MMD4_DROME//1.00E-16//Modifier of mdg4 OS=Drosophila melanogaster GN=mod(mdg4) PE=1 SV=1						swissprot -
Unigene6831_All	609	3.18	5.16	2.54	7.77	7.46	8.01	3.75	6.38	1.37	6.99E-01	4.63E-02		-3.26E-01	5.10E-01		-5.81E-02	8.37E-01		4.36E-02	9.04E-01		7.68E-01	5.49E-03		-1.45E+00	1.49E-04	Down		Unigene6831_All//1.00E-91//gi|78333535|gb|DT553809.1|DT553809					
Unigene68319_All	306	0.00	10.27	2.26	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	7.07E-18	Up	1.11E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene68319_All//gi|157093295|gb|ABV22302.1|//3.00E-07//unknown [Karlodinium micrum]						nr +
Unigene68321_All	340	0.00	4.17	2.82	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.06E-08	Up	1.15E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene68321_All//gi|77553811|gb|AB496607.1|//3.00E-12//SWIRM domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]				ko03022|Basal transcription factors		nr -
Unigene68323_All	352	0.00	2.88	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.24E-06	Up	7.24E+00	6.30E-01		null	null		null	null		null	null		null	null		Unigene68323_All//gi|298715532|emb|CBJ28102.1|//2.00E-32//Acetyl-CoA acetyltransferase [Ectocarpus siliculosus]	Unigene68323_All//3.00E-29//AT5G48230| ACAT2 (ACETOACETYL-COA THIOLASE 2); acetyl-CoA C-acetyltransferase/ catalytic			ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00900|Terpenoid backbone biosynthesis//ko00072|Synthesis and degradation of ketone bodies	GO:0003006//GO:0016020//GO:0016453//GO:0042579	nr -
Unigene68324_All	321	0.00	4.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.79E-08	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene68325_All	534	0.00	2.09	1.10	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.99E-06	Up	1.01E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene68325_All//sp|Q9VNX8|EIF2A_DROME//3.00E-53//Eukaryotic translation initiation factor 2A OS=Drosophila melanogaster GN=CG7414 PE=1 SV=1						swissprot +
Unigene68329_All	630	0.00	3.06	0.85	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.72E-11	Up	9.72E+00	4.02E-03		null	null		null	null		null	null		null	null		Unigene68329_All//gi|11466364|ref|NP_038367.1|//1.00E-23//ribosomal protein L16 [Mesostigma viride] >gi|14548228|sp|Q9MLU3.1|RK16_MESVI RecName: Full=50S ribosomal protein L16, chloroplastic >gi|7259507|gb|AAF43808.1|AF166114_20 ribosomal protein L16 [Mesostigma viride]	Unigene68329_All//2.00E-23//ATCG00790| chloroplast gene encoding a ribosomal protein L16, which is a constituent of 50S large ribosomal subunit			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0033279	nr -
Unigene6833_All	859	21.81	5.90	9.79	7.36	9.30	5.42	0.25	0.00	0.28	-1.89E+00	7.83E-36	Down	-1.15E+00	6.41E-17	Down	3.37E-01	1.14E-01		-4.44E-01	6.59E-02		-7.94E+00	7.41E-02		1.77E-01	9.08E-01		Unigene6833_All//gi|5777616|emb|CAB53477.1|//3.00E-72//CAA30374.1 protein [Oryza sativa]	Unigene6833_All//7.00E-69//AT1G75710| zinc finger (C2H2 type) family protein	Unigene6833_All//0.00E+00//TC139011	C2H2			nr +
Unigene68332_All	335	0.00	4.54	1.59	0.00	0.00	0.13	0.00	0.00	0.00	1.21E+01	1.10E-08	Up	1.06E+01	4.02E-03		null	null		7.07E+00	6.89E-01		null	null		null	null									
Unigene68336_All	324	0.00	2.35	0.33	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.76E-04	Up	8.36E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68336_All//sp|Q5XHF3|PHR4B_XENLA//8.00E-27//Phosphatase and actin regulator 4-B OS=Xenopus laevis GN=phactr4-b PE=2 SV=1						swissprot -
Unigene68339_All	354	0.00	3.44	0.30	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	5.46E-07	Up	8.23E+00	3.94E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene68340_All	610	0.00	1.08	0.26	0.57	0.40	0.22	1.32	0.55	0.20	1.01E+01	6.23E-04	Up	8.03E+00	2.37E-01		-5.32E-01	6.45E-01		-1.36E+00	3.37E-01		-1.26E+00	7.97E-02		-2.75E+00	9.42E-04	Down	Unigene68340_All//gi|50657596|gb|AAT79582.1|//2.00E-53//endonuclease [Solanum tuberosum]	Unigene68340_All//4.00E-53//AT1G11190| BFN1 (BIFUNCTIONAL NUCLEASE 1); T/G mismatch-specific endonuclease/ endoribonuclease, producing 5'-phosphomonoesters / nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease	Unigene68340_All//3.00E-123//gi|21098255|gb|BQ410568.1|BQ410568			GO:0004520//GO:0004521//GO:0005488//GO:0006259//GO:0031410	nr -
Unigene68345_All	437	1.20	4.64	1.95	1.82	0.32	0.52	0.58	2.20	1.64	1.95E+00	1.12E-04	Up	7.04E-01	3.83E-01		-2.53E+00	3.08E-03		-1.82E+00	3.32E-02		1.92E+00	5.42E-03		1.50E+00	4.94E-02			Unigene68345_All//2.00E-34//TC136172					
Unigene68346_All	514	0.00	4.34	0.83	0.00	0.00	0.09	0.00	0.00	0.00	1.21E+01	1.09E-12	Up	9.69E+00	1.38E-02		null	null		6.46E+00	6.89E-01		null	null		null	null									
Unigene68348_All	829	0.00	2.63	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.11E-12	Up	9.59E+00	1.16E-03		null	null		null	null		null	null		null	null		Unigene68348_All//gi|4881868|gb|AAD31848.1|AF133532_1//2.00E-19//water channel protein MipA [Mesembryanthemum crystallinum]	Unigene68348_All//3.00E-19//AT4G01470| TIP1;3 (TONOPLAST INTRINSIC PROTEIN 1;3); urea transmembrane transporter/ water channel					nr +
Unigene6835_All	250	13.60	35.06	21.73	34.47	40.36	58.17	95.72	55.84	47.17	1.37E+00	5.50E-11	Up	6.76E-01	1.13E-02		2.28E-01	2.55E-01		7.55E-01	1.58E-07		-7.78E-01	1.71E-14		-1.02E+00	3.66E-23	Down	Unigene6835_All//gi|227204443|dbj|BAH57073.1|//2.00E-21//AT4G19160 [Arabidopsis thaliana]	Unigene6835_All//7.00E-23//AT4G19160| unknown protein	Unigene6835_All//5.00E-58//TC176726				nr -
Unigene68350_All	585	0.00	12.73	6.10	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	1.39E-42	Up	1.26E+01	9.41E-20	Up	null	null		null	null		null	null		null	null									
Unigene68352_All	575	0.00	5.99	1.57	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.31E-19	Up	1.06E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene68352_All//gi|223998414|ref|XP_002288880.1|//3.00E-49//ubiquitin conjugating enzyme [Thalassiosira pseudonana CCMP1335] >gi|220975988|gb|EED94316.1|ubiquitin conjugating enzyme [Thalassiosira pseudonana CCMP1335]	Unigene68352_All//1.00E-50//AT3G57870| SCE1 (SUMO CONJUGATION ENZYME 1); SUMO ligase			ko04120|Ubiquitin mediated proteolysis	GO:0003006//GO:0005488//GO:0009725//GO:0019787//GO:0032446//GO:0043231//GO:0060255//GO:0070646	nr +
Unigene68353_All	338	0.00	2.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene68353_All//gi|159978016|gb|AAV68608.1|//6.00E-22//cyclin-dependent kinases regulatory subunit [Ostreococcus tauri]	Unigene68353_All//5.00E-21//AT2G27960| CKS1 (CYCLIN-DEPENDENT KINASE-SUBUNIT 1); cyclin-dependent protein kinase/ protein binding				GO:0003676//GO:0006261//GO:0007049//GO:0016772//GO:0019887//GO:0043231	nr +
Unigene68354_All	357	0.00	4.68	1.19	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.54E-09	Up	1.02E+01	1.38E-02		null	null		null	null		null	null		null	null		Unigene68354_All//gi|226455509|gb|EEH52812.1|//2.00E-29//flagellar inner arm dynein light chain Tctex1 [Micromonas pusilla CCMP1545]					GO:0042995	nr -
Unigene68357_All	310	0.00	3.43	2.06	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.81E-06	Up	1.10E+01	1.16E-03		null	null		null	null		null	null		null	null									
Unigene6836_All	306	0.34	2.98	1.57	5.53	5.06	3.10	14.65	27.32	34.63	3.12E+00	1.14E-03		2.20E+00	9.14E-02		-1.28E-01	8.22E-01		-8.37E-01	1.03E-01		8.99E-01	6.26E-07		1.24E+00	2.82E-14	Up	Unigene6836_All//gi|15227173|ref|NP_179816.1|//2.00E-21//ATRABH1D (ARABIDOPSIS RAB GTPASE HOMOLOG H1D); GTP binding [Arabidopsis thaliana]	Unigene6836_All//9.00E-23//AT5G10260| ArRABH1e (Arabidopsis Rab GTPase homolog H1e); GTP binding	Unigene6836_All//4.00E-167//TC161276				nr +
Unigene68366_All	339	0.00	11.06	5.81	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.40E-21	Up	1.25E+01	7.45E-11	Up	null	null		null	null		null	null		null	null		Unigene68366_All//sp|Q17017|FABP_ANOGA//4.00E-26//Probable fatty acid-binding protein OS=Anopheles gambiae GN=ENSANG00000000821 PE=3 SV=2						swissprot -
Unigene68368_All	400	0.00	1.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene68368_All//gi|224014188|ref|XP_002296757.1|//1.00E-17//guanylate kinase-like protein [Thalassiosira pseudonana CCMP1335] >gi|220968612|gb|EED86958.1|guanylate kinase-like protein [Thalassiosira pseudonana CCMP1335]	Unigene68368_All//1.00E-16//AT2G41880| GK-1 (GUANYLATE KINASE 1); guanylate kinase			ko00230|Purine metabolism	GO:0009987//GO:0016772	nr +
Unigene6837_All	515	2.13	0.20	1.65	3.39	9.96	7.63	1.31	1.14	2.40	-3.44E+00	1.19E-04	Down	-3.67E-01	6.01E-01		1.56E+00	5.92E-09	Up	1.17E+00	1.65E-04	Up	-2.09E-01	7.82E-01		8.68E-01	9.95E-02		Unigene6837_All//gi|115458514|ref|NP_001052857.1|//4.00E-24//Os04g0437300 [Oryza sativa Japonica Group] >gi|38341067|emb|CAD40819.2|OSJNBa0006820.11 [Oryza sativa (japonica cultivar-group)] >gi|113564128|dbj|BAF14771.1|Os04g0437300 [Oryza sativa Japonica Group] >gi|116310783|emb|CAH67575.1|H0315A08.5 [Oryza sativa (indica cultivar-group)]	Unigene6837_All//4.00E-21//AT1G49790| PUB26 (PLANT U-BOX 26); binding / ubiquitin-protein ligase					nr +
Unigene68371_All	365	0.00	1.80	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	6.23E-04	Up	1.00E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene68371_All//gi|159483259|ref|XP_001699678.1|//5.00E-06//proline-glycine-tyrosine rich protein [Chlamydomonas reinhardtii] >gi|41529812|emb|CAC86432.1| PGYRP protein [Chlamydomonas reinhardtii] >gi|41529814|emb|CAD32174.1|proline-glycine-tyrosine rich protein [Chlamydomonas reinhardtii] >gi|158281620|gb|EDP07374.1|proline-glycine-tyrosine rich protein [Chlamydomonas reinhardtii]						nr -
Unigene68374_All	346	0.00	2.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene68374_All//gi|298200319|gb|ADI60057.1|//5.00E-07//fatty acyl-coenzyme A reductase [Euglena gracilis]	Unigene68374_All//3.00E-06//AT4G33790| CER4 (ECERIFERUM 4); fatty acyl-CoA reductase (alcohol-forming)/ oxidoreductase, acting on the CH-CH group of donors			ko04146|Peroxisome		nr +
Unigene68379_All	560	1.21	3.35	3.90	1.07	1.48	0.89	0.15	0.00	0.28	1.46E+00	3.30E-03		1.68E+00	5.07E-04	Up	4.67E-01	5.85E-01		-2.67E-01	7.57E-01		-7.24E+00	4.00E-01		9.14E-01	6.23E-01									
Unigene68381_All	337	0.00	3.16	1.74	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.81E-06	Up	1.08E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene68381_All//gi|112950081|gb|ABI26643.1|//4.00E-29//aspartic proteinase [Cucumis sativus]	Unigene68381_All//4.00E-21//AT1G62290| aspartyl protease family protein				GO:0004175//GO:0019538	nr +
Unigene6839_All	391	33.05	38.62	27.10	47.78	44.03	54.75	31.25	66.49	55.94	2.25E-01	1.39E-01		-2.86E-01	9.34E-02		-1.18E-01	4.37E-01		1.97E-01	1.34E-01		1.09E+00	6.23E-27	Up	8.40E-01	1.82E-15		Unigene6839_All//gi|297602829|ref|NP_001052948.2|//2.00E-17//Os04g0451900 [Oryza sativa Japonica Group] >gi|255675512|dbj|BAF14862.2|Os04g0451900 [Oryza sativa Japonica Group]	Unigene6839_All//1.00E-18//AT1G34750| protein phosphatase 2C, putative / PP2C, putative	Unigene6839_All//0.00E+00//gi|164248260|gb|ES821168.1|ES821168				nr +
Unigene68391_All	371	0.00	1.78	0.29	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	6.23E-04	Up	8.17E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68391_All//sp|Q08117|AES_HUMAN//7.00E-47//Amino-terminal enhancer of split OS=Homo sapiens GN=AES PE=1 SV=4						swissprot +

Unigene68393_All	357	0.00	2.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.24E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene68393_All//sp|Q5FWL7|ZDH15_XENLA//2.00E-08//Palmitoyltransferase ZDHHC15 OS=Xenopus laevis GN=zdhhc15 PE=2 SV=1						swissprot +
Unigene68394_All	732	3.72	2.35	2.69	5.04	3.20	2.65	5.08	1.94	2.88	-6.59E-01	8.26E-02		-4.66E-01	2.47E-01		-6.55E-01	3.23E-02		-9.25E-01	3.49E-03		-1.39E+00	2.84E-06	Down	-8.17E-01	2.86E-03		Unigene68394_All//gi|297802336|ref|XP_002860052.1|//1.00E-33//La domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297314888|gb|EFH45311.1| La domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene68394_All//2.00E-26//AT4G35890| La domain-containing protein	Unigene68394_All//0.00E+00//TC175238				nr +
Unigene68397_All	369	0.00	1.79	0.29	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	6.23E-04	Up	8.17E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68397_All//sp|Q96S65|CSRN1_HUMAN//4.00E-52//Cysteine/serine-rich nuclear protein 1 OS=Homo sapiens GN=CSRNP1 PE=2 SV=1						swissprot +
Unigene6810_All	347	0.45	0.00	0.46	3.16	1.29	1.04	16.33	4.46	2.53	-8.82E+00	2.14E-01		2.56E-02	1.00E+00		-1.29E+00	4.07E-02		-1.60E+00	1.95E-02		-1.87E+00	1.25E-13	Down	-2.69E+00	1.46E-21	Down			Unigene6840_All//4.00E-07//TC150292				
Unigene68401_All	364	0.00	3.76	1.17	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.79E-08	Up	1.02E+01	1.38E-02		null	null		null	null		null	null		null	null								
Unigene68409_All	540	0.00	3.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.14E-10	Up	null	null		null	null		null	null		null	null		null	null								
Unigene68411_All	371	0.00	2.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	9.35E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene68411_All//gi|226496980|ref|NP_001151324.1|//5.00E-16//mitochondrial RNA-splicing protein MRS3 [Zea mays] >gi|195645822|gb|ACG42379.1| mitochondrial RNA-splicing protein MRS3 [Zea mays]	Unigene68411_All//1.00E-10//AT1G07030| mitochondrial substrate carrier family protein				GO:0006810//GO:0016020	nr -
Unigene68415_All	338	0.00	2.40	0.47	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	9.35E-05	Up	8.88E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68415_All//gi|194476823|ref|YP_002049002.1|//1.00E-18//Phosphoglycerate kinase [Paulinella chromatophora] >gi|171191830|gb|ACB42792.1| Phosphoglycerate kinase [Paulinella chromatophora]	Unigene68415_All//3.00E-19//AT1G79550| PGK (PHOSPHOGLYCERATE KINASE); phosphoglycerate kinase			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0005576//GO:0006007//GO:0009536//GO:0016020//GO:0016301	nr +
Unigene6842_All	1292	2.39	1.18	0.33	4.20	4.82	4.54	18.69	5.31	12.30	-1.02E+00	4.17E-03		-2.86E+00	1.18E-09	Down	1.99E-01	4.70E-01		1.13E-01	6.77E-01		-1.82E+00	2.19E-53	Down	-6.03E-01	5.94E-10		Unigene6842_All//gi|15241528|ref|NP_196427.1|//1.00E-135//L-asparaginase / L-asparagine amidohydrolase [Arabidopsis thaliana] >gi|25108880|sp|P50287.2|ASPG1_ARATH RecName: Full=Isoaspartyl peptidase/L-asparaginase 1; AltName: Full=L-asparagine amidohydrolase 1; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase 1 subunit alpha; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase 1 subunit beta; Flags: Precursor >gi|8346547|emb|CAB93711.1| asparaginase [Arabidopsis thaliana] >gi|14517440|gb|AAK62610.1| AT5g08100/T22D6_40 [Arabidopsis thaliana] >gi|20147331|gb|AAM10379.1| AT5g08100/T22D6_40 [Arabidopsis thaliana]	Unigene6842_All//4.00E-129//AT5G08100| L-asparaginase / L-asparagine amidohydrolase	Unigene6842_All//0.00E+00//gi|78347096|gb|DT567370.1|DT567370				nr +
Unigene68425_All	338	0.00	3.90	0.63	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.49E-07	Up	9.30E+00	1.40E-01		null	null		null	null		null	null		null	null								ESTscan +
Unigene68428_All	841	1.00	2.17	1.33	1.66	0.78	1.24	2.92	2.14	1.18	1.12E+00	2.19E-02		4.18E-01	5.32E-01		-1.09E+00	4.31E-02		-4.25E-01	4.75E-01		-4.48E-01	2.32E-01		-1.30E+00	3.13E-04	Down	Unigene68428_All//gi|15228202|ref|NP_190343.1|//2.00E-84//esterase/lipase/thioesterase family protein [Arabidopsis thaliana] >gi|34146868|gb|AAQ62442.1| At3g47590 [Arabidopsis thaliana]	Unigene68428_All//8.00E-78//AT3G47590| esterase/lipase/thioesterase family protein	Unigene68428_All//0.00E+00//TC151785			GO:0003824	nr +
Unigene68430_All	385	0.00	2.37	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.61E-05	Up	7.11E+00	6.30E-01		null	null		null	null		null	null		null	null		Unigene68430_All//gi|298711533|emb|CBJ26621.1|//3.00E-10//acyltransferase [Ectocarpus siliculosus]	Unigene68430_All//9.00E-69//AT1G12640| membrane bound O-acyl transferase (MBOAT) family protein			ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism	GO:0044464	nr -
Unigene68432_All	334	0.00	1.52	2.23	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	4.02E-03		1.11E+01	3.26E-04	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene68436_All	337	0.00	4.21	0.63	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.05E-08	Up	9.30E+00	1.40E-01		null	null		null	null		null	null		null	null								ESTscan +
Unigene68437_All	381	0.00	3.59	0.28	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.79E-08	Up	8.13E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68437_All//gi|146220098|gb|ABQ11263.1|//3.00E-41//mago nashi-like protein 2 [Physalis pubescens] >gi|146220100|gb|ABQ11265.1| mago nashi-like protein 2 [Physalis pubescens]	Unigene68437_All//8.00E-39//AT1G02140| MAGO (MAGO NASHI); protein binding	Unigene68437_All//4.00E-07//gi|11201608|gb|BF270517.1|BF270517		ko03040|Spliceosome	GO:0003006//GO:0043231	nr +
Unigene68439_All	445	0.00	1.82	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	9.35E-05	Up	7.90E+00	3.94E-01		null	null		null	null		null	null		null	null								
Unigene6844_All	708	11.82	6.30	13.24	34.26	15.71	28.07	7.11	4.72	1.80	-9.09E-01	6.90E-06		1.63E-01	4.36E-01		-1.13E+00	1.71E-26	Down	-2.88E-01	1.08E-02		-5.90E-01	1.36E-02		-1.98E+00	1.60E-13	Down			Unigene6844_All//7.00E-97//TC143183				
Unigene68440_All	377	0.00	4.57	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.98E-10	Up	8.73E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68440_All//gi|116309516|emb|CAH66582.1|//2.00E-08//OSIGba0137004.8 [Oryza sativa (indica cultivar-group)]	Unigene68440_All//1.00E-08//AT2G31660| SAR2 (SUPER SENSITIVE TO ABA AND ROOT GHT2); binding / protein transporter					nr -
Unigene68441_All	359	0.00	3.11	0.30	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.99E-06	Up	8.21E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68441_All//gi|195625556|gb|ACG34608.1|//4.00E-22//dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDasubunit precursor [Zea mays]	Unigene68441_All//2.00E-23//AT5G66680| DGL1; dolichyl-diphosphooligosaccharide-protein glycotransferase			ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0000902//GO:0005618//GO:0005789//GO:0006487//GO:0007047//GO:0009250//GO:0016758//GO:0031410//GO:0031981	nr +
Unigene68448_All	647	0.00	4.54	3.05	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.01E-16	Up	1.16E+01	7.45E-11	Up	null	null		null	null		null	null		null	null		Unigene68448_All//gi|115457964|ref|NP_001052582.1|//3.00E-15//Os04g0376500 [Oryza sativa Japonica Group] >gi|383486118|emb|CAE04596.2| OSJNBb0006N15.13 [Oryza sativa (japonica cultivar-group)] >gi|113564153|dbj|BAF14496.1| Os04g0376500 [Oryza sativa Japonica Group]	Unigene68448_All//9.00E-17//AT1G10840| TIF3H1; translation initiation factor					nr -
Unigene68454_All	389	0.00	0.78	1.78	0.51	0.53	0.12	0.33	0.00	0.00	9.61E+00	4.39E-02		1.08E+01	6.14E-04	Up	5.23E-02	9.88E-01		-2.14E+00	3.46E-01		-8.35E+00	2.34E-01		-8.35E+00	1.99E-01				Unigene68454_All//7.00E-154//BQ407925				
Unigene68455_All	415	0.00	3.30	2.05	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.78E-08	Up	1.10E+01	9.00E-05	Up	null	null		null	null		null	null		null	null								
Unigene68456_All	390	0.00	2.99	0.55	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.05E-06	Up	9.09E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene68456_All//gi|255594188|ref|XP_002536043.1|//2.00E-06//Para-nitrobenzyl esterase, putative [Ricinus communis] >gi|223521112|gb|EEF26342.1| Para-nitrobenzyl esterase, putative [Ricinus communis]						nr -
Unigene6846_All	415	0.88	11.23	5.00	1.20	2.57	2.72	3.87	4.53	3.07	3.67E+00	1.32E-18	Up	2.50E+00	6.61E-06	Up	1.10E+00	1.09E-01		1.18E+00	7.75E-02		2.27E-01	6.48E-01		-3.34E-01	4.74E-01		Unigene6846_All//gi|231688|sp|P30567.1|CATA2_GOSHI//7.00E-18//RecName: Full=Catalase isozyme 2 >gi|18488|emb|CAA39998.1| subunit 2 of cotton catalase [Gossypium hirsutum]	Unigene6846_All//2.00E-18//AT4G35090| CAT2 (CATALASE 2); catalase	Unigene6846_All//7.00E-145//TC146350		ko04146|Peroxisome//ko00380|Tryptophan metabolism		nr +
Unigene68461_All	783	0.00	9.64	3.60	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	3.63E-43	Up	1.18E+01	1.38E-15	Up	null	null		null	null		null	null		null	null		Unigene68461_All//sp|Q5TGZ0|CA151_HUMAN//6.00E-08//UPF0327 protein C1orf151 OS=Homo sapiens GN=C1orf151 PE=1 SV=1						swissprot +
Unigene68465_All	389	0.00	2.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene68465_All//gi|297814864|ref|XP_002875315.1|//4.00E-51//glycosyl hydrolase family protein 27 [Arabidopsis lyrata subsp. lyrata] >gi|297321153|gb|EFH51574.1| glycosyl hydrolase family protein 27 [Arabidopsis lyrata subsp. lyrata]	Unigene68465_All//4.00E-52//AT3G26380| glycosyl hydrolase family protein 27 / alpha-galactosidase family protein / melibiase family protein	Unigene68465_All//4.00E-32//TC155727			GO:0015925//GO:0043167//GO:0043231//GO:0044238	nr -
Unigene68469_All	396	0.00	3.20	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.86E-07	Up	9.07E+00	1.40E-01		null	null		null	null		null	null		null	null								ESTscan -
Unigene68473_All	394	0.13	9.13	2.70	0.00	0.00	0.00	0.00	0.00	0.00	6.10E+00	6.06E-19	Up	4.35E+00	6.46E-05	Up	null	null		null	null		null	null		null	null								
Unigene68479_All	601	0.00	2.36	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.05E-08	Up	8.47E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene68479_All//gi|300121754|emb|CBK22329.2|//1.00E-13//Acetyl-CoA carboxylase [Blastocystis hominis]	Unigene68479_All//2.00E-06//AT1G36160| ACC1 (ACETYL-COENZYME A CARBOXYLASE 1); acetyl-CoA carboxylase			ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis		nr +
Unigene6848_All	1573	0.00	0.00	0.00	0.00	0.00	0.00	11.18	2.21	1.49	null	null		null	null		null	null		null	null		-2.34E+00	5.07E-54	Down	-2.90E+00	8.61E-71	Down	Unigene6848_All//gi|171259158|ref|YP_539000.2|//0.00E-00//cytochrome c oxidase subunit 1 [Physcomitrella patens] >gi|186942713|dbj|BAE93071.2| cytochrome c oxidase subunit 1 [Physcomitrella patens]	Unigene6848_All//3.00E-137//ATMG01360| cytochrome c oxidase subunit 1	Unigene6848_All//6.00E-19//TC149581		ko00190|Oxidative phosphorylation		nr -
Unigene68480_All	642	0.33	6.24	1.16	0.31	0.11	0.35	0.13	0.39	0.31	4.26E+00	8.39E-18	Up	1.83E+00	5.05E-02		-1.53E+00	4.15E-01		1.80E-01	9.34E-01		1.57E+00	3.26E-01		1.24E+00	4.68E-01		Unigene68480_All//gi|297812469|ref|XP_002874118.1|//2.00E-35//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319955|gb|EFH50377.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene68480_All//1.00E-35//AT5G23240| DNAJ heat shock N-terminal domain-containing protein	Unigene68480_All//0.00E+00//TC140457				nr -
Unigene68482_All	385	0.00	2.90	1.94	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.99E-06	Up	1.09E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene68482_All//gi|148886774|sp|A2XAZ3.1|ADHX_ORYSI//5.00E-37//RecName: Full=Alcohol dehydrogenase class-3; AltName: Full=Alcohol dehydrogenase class-III; AltName: Full=S-(hydroxymethyl)glutathione dehydrogenase; AltName: Full=Glutathione-dependent formaldehyde dehydrogenase; Short=GSH-FDH; Short=FALDH; Short=FDH	Unigene68482_All//1.00E-37//AT5G43940| HOT5 (sensitive to hot temperatures 5); S-(hydroxymethyl)glutathione dehydrogenase/ S-nitrosoglutathione reductase			ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism	GO:0006067//GO:0006081//GO:0009408//GO:0009791//GO:0016616//GO:0016657//GO:0042579//GO:0046914	nr +
Unigene68485_All	1026	0.00	0.30	0.26	0.29	0.20	0.22	0.08	0.45	0.74	8.21E+00	4.39E-02		8.02E+00	7.97E-02		-5.32E-01	6.78E-01		-4.04E-01	7.51E-01		2.44E+00	3.74E-02		3.16E+00	6.82E-04	Up	Unigene68485_All//gi|292668913|gb|ADE41111.1|//1.00E-56//AP2 domain class transcription factor [Malus x domestica]	Unigene68485_All//6.00E-15//AT5G44210| EKF9 (ERF DOMAIN PROTEIN 9); DNA binding / transcription factor/ transcription repressor	Unigene68485_All//1.00E-40//gi|78322782|gb|DT543056.1|DT543056	AP2-EREBP		GO:0006350	nr +

Unigene68487_All	862	0.00	14.93	6.49	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	7.41E-74	Up	1.27E+01	3.81E-31	Up	null	null		null	null		null	null		null	null		Unigene68487_All//gi|300120494|emb|CBK20048.2|//1.00E-06//unnamed protein product [Blastocystis hominis]						nr -
Unigene68488_All	363	0.00	2.93	0.59	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.81E-06	Up	9.20E+00	1.40E-01		null	null		null	null		null	null											ESTscan +
Unigene68489_All	370	0.00	10.54	3.74	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	3.25E-22	Up	1.19E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene68489_All//sp|Q9CQ69|QCR8_MOUSE//2.00E-14//Cytochrome b-c1 complex subunit 8 OS=Mus musculus GN=Uqcrq PE=1 SV=3						swissprot +
Unigene6849_All	1369	0.57	0.52	0.31	29.73	20.50	15.97	5.31	1.01	0.84	-1.46E-01	8.37E-01		-8.81E-01	2.95E-01		-5.36E-01	1.83E-12		-8.97E-01	7.10E-27		-2.40E+00	2.24E-23	Down	-2.65E+00	4.81E-27	Down	Unigene6849_All//gi|60657606|gb|AAX33324.1|//1.00E-123//secondary cell wall-related glycosyltransferase family 14 [Populus tremula x Populus tremuloides]	Unigene6849_All//1.00E-77//AT1G71070| glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein	Unigene6849_All//0.00E+00//TC145366				nr -
Unigene68496_All	903	2.78	2.41	2.59	1.99	2.40	1.55	2.43	0.51	0.62	-2.05E-01	6.07E-01		-1.00E-01	8.04E-01		2.75E-01	5.88E-01		-3.57E-01	4.96E-01		-2.26E+00	4.47E-07	Down	-1.98E+00	2.31E-06	Down	Unigene68496_All//gi|3482917|gb|AAC33202.1|//8.00E-85//Similar to Glucose-6-phosphate dehydrogenases, gi|2276344, gi|2829880, gi|2352919 and others [Arabidopsis thaliana]	Unigene68496_All//4.00E-86//AT1G09420| G6PD4 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 4); glucose-6-phosphate dehydrogenase	Unigene68496_All//0.00E+00//gi|109889218|gb|DW518186.1|DW518186		ko00480|Glutathione metabolism//ko00030|Pentose phosphate pathway	GO:0009536//GO:0016616//GO:0019318	nr -
Unigene68498_All	780	0.00	8.51	5.60	0.00	0.00	0.00	0.00	0.00	0.31	1.31E+01	6.43E-38	Up	1.25E+01	3.08E-24	Up	null	null		null	null		null	null		8.26E+00	4.39E-02		Unigene68498_All//gi|18087805|ref|NP_032529.2|//1.00E-126//40S ribosomal protein S2 [Mus musculus] >gi|78126159|ref|NP_114026.3| 40S ribosomal protein S2 [Rattus norvegicus] >gi|133914|sp|P27952.1|RS2_RAT RecName: Full=40S ribosomal protein S2 >gi|46397787|sp|P25444.3|RS2_MOUSE RecName: Full=40S ribosomal protein S2; AltName: Full=40S ribosomal protein S4; AltName: Full=Protein LLREp3 >gi|10179940|gb|AAG13953.1|AF283559_1 ribosomal protein S2 [Mus musculus] >gi|57718|emb|CAA40679.1| ribosomal protein S2 [Rattus rattus] >gi|12805427|gb|AAH02186.1| Ribosomal protein S2 [Mus musculus] >gi|56971737|gb|AAH87956.1| Ribosomal protein S2 [Mus musculus] >gi|61402217|gb|AAH91730.1| Ribosomal protein S2 [Mus musculus]	Unigene68498_All//5.00E-88//AT3G57490| 40S ribosomal protein S2 (RPS2D)	Unigene68498_All//1.00E-09//TC147684		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030312	nr +
Unigene685_All	1754	4.44	4.54	1.21	9.94	12.92	19.11	42.40	74.58	111.79	2.92E-02	9.04E-01		-1.87E+00	1.76E-14	Down	3.78E-01	5.65E-04		9.43E-01	7.23E-24		8.15E-01	9.41E-82		1.40E+00	2.58E-299	Up	Unigene685_All//gi|70609690|gb|AAZ05070.1|//0.00E+00//glutamate decarboxylase [Citrus sinensis]	Unigene685_All//0.00E+00//AT2G02010| GAD4 (glutamate decarboxylase 4); calmodulin binding	Unigene685_All//0.00E+00//TC147697		ko00250|Alanine, aspartate and glutamate metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00430|Taurine and hypotaurine metabolism	GO:0005515//GO:0009064//GO:0016831//GO:0043231//GO:0044444//GO:0048037	nr +
Unigene6850_All	719	8.30	1.83	3.63	3.46	5.32	4.02	0.00	0.06	0.06	-2.18E+00	3.51E-14	Down	-1.19E+00	4.18E-06	Down	6.18E-01	4.70E-02		2.15E-01	6.36E-01		5.86E+00	6.29E-01		5.79E+00	6.39E-01		Unigene6850_All//gi|224103099|ref|XP_002312925.1|//1.00E-44//SAUR family protein [Populus trichocarpa] >gi|222849333|gb|EEE86880.1| SAUR family protein [Populus trichocarpa]	Unigene6850_All//3.00E-28//AT1G29430| auxin-responsive family protein	Unigene6850_All//0.00E+00//gi|109883976|gb|DW512946.1|DW512946				nr -
Unigene68502_All	672	0.00	2.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.11E-10	Up	null	null		null	null		null	null		null	null		null	null		Unigene68502_All//gi|301114737|ref|XP_002999138.1|//3.00E-06//Non-selective Cation Channel-2 (NSCC2) Family [Phytophthora infestans T30-4] >gi|262111232|gb|EEY69284.1| Non-selective Cation Channel-2 (NSCC2) Family [Phytophthora infestans T30-4]				ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr -
Unigene68507_All	585	0.00	3.90	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.63E-13	Up	9.32E+00	2.49E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene68508_All	1228	0.17	0.74	0.74	0.16	0.70	0.40	1.27	0.10	0.68	2.12E+00	1.04E-02		2.11E+00	1.42E-02		2.11E+00	1.28E-02		1.32E+00	2.52E-01		-3.64E+00	5.20E-08	Down	-9.03E-01	4.62E-02		Unigene68508_All//gi|195658389|gb|ACG48662.1|//1.00E-89//HEAT-like [Zea mays]	Unigene68508_All//1.00E-91//AT3G58180| PBS lyase HEAT-like repeat-containing protein	Unigene68508_All//0.00E+00//TC148675			GO:0003824//GO:0030076	nr +
Unigene68509_All	383	0.00	4.10	1.95	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.69E-09	Up	1.09E+01	3.26E-04	Up	null	null		null	null		null	null		null	null									
Unigene68512_All	383	0.00	1.98	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.76E-04	Up	9.70E+00	4.49E-02		null	null		null	null		null	null		null	null		Unigene68512_All//sp|Q7JUY7|CED6_DROME//4.00E-24//PTB domain-containing adapter protein ced-6 OS=Drosophila melanogaster GN=ced-6 PE=1 SV=1						swissprot -
Unigene68517_All	367	0.00	6.63	3.34	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	7.72E-14	Up	1.17E+01	9.10E-07	Up	null	null		null	null		null	null		null	null		Unigene68517_All//gi|73912496|dbj|BAE20328.1|//2.00E-16//omega-5 gliadin [Triticum aestivum]				ko03022|Basal transcription factors	GO:0005622//GO:0006350//GO:0046983	nr -
Unigene68519_All	375	0.00	3.51	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.49E-07	Up	9.15E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene68519_All//gi|157093503|gb|ABV22406.1|//8.00E-08//unknown [Noctiluca scintillans]						nr -
Unigene6852_All	498	10.30	5.39	0.64	13.10	12.24	8.25	2.21	0.08	0.48	-9.33E-01	4.50E-04		-4.00E+00	5.14E-21	Down	-9.85E-02	7.26E-01		-6.67E-01	3.31E-03		-4.72E+00	1.02E-06	Down	-2.20E+00	5.65E-04	Down	Unigene6852_All//gi|25992536|gb|AAN77148.1|//2.00E-12//fiber protein Fb7 [Gossypium barbadense]		Unigene6852_All//0.00E+00//TC156102				nr -
Unigene68522_All	377	3.19	2.69	3.25	10.97	4.66	2.40	0.34	1.44	0.42	-2.48E-01	6.62E-01		2.54E-02	9.87E-01		-1.24E+00	1.17E-05	Down	-2.19E+00	8.46E-11	Down	2.10E+00	3.71E-02		3.30E-01	8.50E-01		Unigene68522_All//gi|42564151|ref|NP_566484.2|//2.00E-23//lipase class 3 family protein [Arabidopsis thaliana]	Unigene68522_All//1.00E-24//AT3G14360| lipase class 3 family protein	Unigene68522_All//6.00E-173//BG446666			GO:0004091//GO:0044238	nr +
Unigene68524_All	594	0.00	4.27	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.03E-14	Up	7.49E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68524_All//gi|30690937|ref|NP_849728.1|//8.00E-14//double-stranded DNA-binding family protein [Arabidopsis thaliana]	Unigene68524_All//2.00E-08//AT1G29850| double-stranded DNA-binding family protein				GO:0003677	nr +
Unigene68525_All	403	0.00	2.64	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.81E-06	Up	8.05E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68525_All//gi|281399029|gb|ADA68360.1|//1.00E-16//hsp organizing protein/stress-inducible protein [Dactylis glomerata]	Unigene68525_All//8.00E-14//AT1G12270| stress-inducible protein, putative				GO:0010038//GO:0016020//GO:0043231//GO:0044444	nr -
Unigene68528_All	399	0.00	9.27	2.67	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	4.67E-21	Up	1.14E+01	6.61E-06	Up	null	null		null	null		null	null												
Unigene6853_All	541	3.09	0.37	3.25	1.38	1.72	5.01	1.33	1.85	1.62	-3.05E+00	3.81E-06	Down	6.98E-02	8.91E-01		3.15E-01	7.04E-01		1.86E+00	7.49E-06	Up	4.81E-01	4.46E-01		2.86E-01	6.45E-01		Unigene6853_All//gi|22654989|gb|AAM98086.1|//4.00E-51//At1g73430/T9L24_16 [Arabidopsis thaliana]	Unigene6853_All//2.00E-52//AT1G73430| sec34-like family protein	Unigene6853_All//2.00E-68//gi|48800661|gb|CO101975.1|CO101975				nr +
Unigene68530_All	405	0.00	1.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene68530_All//gi|16226478|gb|AAL16178.1|AF428410_1//8.00E-09//AT5g63440/MLE2_7 [Arabidopsis thaliana] >gi|22137224|gb|AAM91457.1| AT5g63440/MLE2_7 [Arabidopsis thaliana]	Unigene68530_All//8.00E-07//AT5G63440| unknown protein					nr +
Unigene68531_All	652	0.00	5.28	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.31E-19	Up	8.67E+00	7.97E-02		null	null		null	null		null	null		null	null		Unigene68531_All//gi|297810843|ref|XP_002873305.1|//1.00E-20//tudor domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319142|gb|EFH49564.1| tudor domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene68531_All//1.00E-21//AT5G61780| tudor domain-containing protein / nuclease family protein					nr -
Unigene68532_All	723	0.29	4.63	0.96	0.00	0.00	0.00	0.00	0.00	0.00	4.00E+00	2.43E-14	Up	1.73E+00	7.67E-02		null	null		null	null		null	null		null	null		Unigene68532_All//gi|224086900|ref|XP_002308000.1|//3.00E-61//f-box family protein [Populus trichocarpa] >gi|222853976|gb|EEE91523.1| f-box family protein [Populus trichocarpa]	Unigene68532_All//2.00E-20//AT5G04010| unknown protein					nr -
Unigene68533_All	405	0.39	1.25	0.26	0.00	1.19	1.56	0.21	0.10	0.59	1.69E+00	1.34E-01		-5.60E-01	7.74E-01		1.02E+01	5.07E-03		1.06E+01	7.59E-04	Up	-1.02E+00	7.22E-01		1.50E+00	3.39E-01		Unigene68533_All//gi|225446426|ref|XP_002276115.1|//8.00E-27//PREDICTED: similar to haloacid dehalogenase-like hydrolase family protein [Vitis vinifera]	Unigene68533_All//2.00E-26//AT5G44240| haloacid dehalogenase-like hydrolase family protein	Unigene68533_All//2.00E-89//TC144036			GO:0005548//GO:0006869//GO:0009206//GO:0031224//GO:0031410//GO:0032559//GO:0042625//GO:0046872	nr +
Unigene68534_All	666	0.16	7.08	0.80	0.00	0.00	0.00	0.25	0.88	1.50	5.49E+00	7.62E-24	Up	2.35E+00	5.86E-02		null	null		null	null		1.79E+00	5.30E-02		2.56E+00	3.91E-04	Up	Unigene68534_All//gi|224140995|ref|XP_002323861.1|//2.00E-65//amino acid transporter [Populus trichocarpa] >gi|222866863|gb|EEF03994.1| amino acid transporter [Populus trichocarpa]	Unigene68534_All//9.00E-53//AT3G28960| amino acid transporter family protein	Unigene68534_All//0.00E+00//TC162866			GO:0031224	nr +
Unigene68538_All	422	1.36	7.44	3.41	0.94	1.47	3.21	116.72	140.44	241.01	2.45E+00	8.85E-09	Up	1.32E+00	2.70E-02		6.37E-01	5.49E-01		1.77E+00	4.50E-03		2.67E-01	1.36E-05		1.05E+00	1.10E-98	Up	Unigene68538_All//gi|117607067|gb|ABK42077.1|//2.00E-58//ubiquitin extension protein [Capsicum annuum]	Unigene68538_All//6.00E-39//AT3G62250| UBQ5 (ubiquitin 5); protein binding / structural constituent of ribosome	Unigene68538_All//5.00E-50//gi|164361414|gb|ES807417.1|ES807417		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene68539_All	419	0.00	2.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.05E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene68539_All//gi|16225442|gb|AAL15890.1|AF417302_1//4.00E-20//26S proteasome regulatory subunit S12 isoloq-like protein [Castanea sativa]	Unigene68539_All//8.00E-19//AT2G39990| EIF2; translation initiation factor				GO:0007275//GO:0009856//GO:0043231	nr +
Unigene6854_All	362	1.45	2.80	3.68	2.34	3.23	1.87	10.28	4.62	8.03	9.54E-01	1.65E-01		1.35E+00	3.17E-02		4.67E-01	5.14E-01		-3.22E-01	6.87E-01		-1.15E+00	6.53E-05	Down	-3.55E-01	2.11E-01				Unigene6854_All//2.00E-73//EX165632				
Unigene68543_All	400	0.52	0.51	1.46	0.50	1.03	2.26	0.21	3.03	1.99	-4.62E-02	9.87E-01		1.48E+00	1.53E-01		1.05E+00	4.25E-01		2.18E+00	9.48E-03		3.84E+00	1.57E-06	Up	3.24E+00	3.96E-04	Up	Unigene68543_All//gi|9665149|gb|AAF97333.1|ACO23628_14//6.00E-39//Hypothetical protein [Arabidopsis thaliana]	Unigene68543_All//1.00E-32//AT1G01220| GMMP kinase-related				GO:0006796//GO:0016301//GO:0032559//GO:0044424	nr -
Unigene68544_All	398	0.00	2.67	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.80E-06	Up	9.39E+00	7.97E-02		null	null		null	null		null	null		null	null		Unigene68544_All//sp|P07190|MAL2_DROME//1.00E-49//Probable maltase H OS=Drosophila melanogaster GN=LvpH PE=2 SV=2						swissprot +

Unigene68548_All	379	0.00	4.68	1.55	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.14E-10	Up	1.06E+01	2.17E-03		null	null		null	null		null	null		null	null		null	null		Unigene68548_All//gi|115465145|ref|NP_001056172.1|//2.00E-22//Os05g0539400 [Oryza sativa Japonica Group] >gi|122168850|sp|Q0DCD7.1|BGAL8_ORYSJ RecName: Full=Beta-galactosidase 8; Short=Lactase 8; Flags: Precursor >gi|113579723|dbj|BAF18086.1|Os05g0539400 [Oryza sativa Japonica Group]	Unigene68548_All//6.00E-23//AT1G72990| BGAL17 (beta-galactosidase 17); beta-galactosidase/ catalytic/ cation binding			ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series	GO:0016798//GO:0043229//GO:0044444	nr -
Unigene68549_All	387	0.00	3.27	0.55	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.86E-07	Up	9.10E+00	1.40E-01		null	null		null	null		null	null		null	null									
Unigene6855_All	786	1.46	2.13	2.17	0.82	1.58	1.21	0.70	3.83	0.51	5.39E-01	2.94E-01		5.66E-01	2.83E-01		9.37E-01	1.36E-01		5.51E-01	4.82E-01		2.45E+00	2.71E-10	Up	-4.64E-01	5.97E-01		Unigene6855_All//gi|297843666|ref|XP_002889714.1|//3.00E-35//prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335556|gb|EFH65973.1| prenylated rab acceptor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6855_All//2.00E-28//AT1G08770| PRA1.E (PRENYLATED RAB ACCEPTOR 1.E)	Unigene6855_All//0.00E+00//TC178057				nr +
Unigene68550_All	412	0.00	3.69	1.29	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.10E-08	Up	1.03E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene68550_All//gi|13626392|sp|Q9FUM1.1|EF1G_PRUAV//3.00E-12//RecName: Full=Elongation factor 1-gamma; Short=EF-1-gamma; AltName: Full=eEF-1B gamma >gi|10444415|gb|AAG17901.1|AF297712_1 translation elongation factor 1-gamma [Prunus avium]	Unigene68550_All//2.00E-10//AT1G57720| elongation factor 1B-gamma, putative / eEF-1B gamma, putative					nr +
Unigene68551_All	412	0.00	1.97	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	9.35E-05	Up	9.60E+00	4.49E-02		null	null		null	null		null	null		null	null									
Unigene68553_All	407	0.00	12.20	2.75	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	2.63E-28	Up	1.14E+01	3.42E-06	Up	null	null		null	null		null	null		null	null									
Unigene68554_All	744	0.00	8.58	1.50	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	1.84E-36	Up	1.06E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene68554_All//gi|1351858|sp|P49609.1|ACON_GRAVE//9.00E-86//RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor >gi|600171|gb|AAA80494.1| aconitase [Gracilaria gracilis]	Unigene68554_All//1.00E-06//AT4G35830| aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO)	Unigene68553_All//8.00E-09//gi|11208941|gb|BF277871.1|BF277871		ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0016491//GO:0016836//GO:0043169//GO:0044237//GO:0044424//GO:0051536	nr -
Unigene68555_All	423	0.49	2.76	2.90	2.94	1.71	2.67	0.00	1.88	1.88	2.48E+00	9.79E-04	Up	2.55E+00	8.25E-04	Up	-7.84E-01	1.82E-01		-1.41E-01	8.11E-01		1.09E+01	1.07E-05	Up	1.09E+01	7.36E-06	Up	Unigene68555_All//gi|224119014|ref|XP_002331304.1|//2.00E-35//bile acid:Na+ symporter family protein [Populus trichocarpa] >gi|222873887|gb|EEF11018.1| bile acid:Na+ symporter family protein [Populus trichocarpa]	Unigene68555_All//2.00E-34//AT1G78560| bile acid:sodium symporter family protein	Unigene68555_All//5.00E-152//C0115326			GO:0005343//GO:0009536//GO:0030001	nr +
Unigene68557_All	676	0.15	0.45	0.24	0.96	0.41	0.87	1.69	0.62	0.41	1.54E+00	3.23E-01		6.10E-01	7.47E-01		-1.23E+00	1.60E-01		-1.42E-01	8.73E-01		-1.45E+00	1.40E-02		-2.03E+00	8.63E-04	Down	Unigene68557_All//gi|297799510|ref|XP_002867639.1|//3.00E-25//AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313475|gb|EFH43888.1| AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene68557_All//3.00E-20//AT4G02480| AAA-type ATPase family protein	Unigene68557_All//2.00E-177//TC141927			GO:0000166//GO:0016887	nr -
Unigene68560_All	405	0.00	1.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene68560_All//sp|P45481|CBP_MOUSE//3.00E-06//CREB-binding protein OS=Mus musculus GN=Crebbp PE=1 SV=2						swissprot +
Unigene68563_All	837	0.00	0.97	0.19	0.00	0.00	0.00	0.00	0.00	0.00	9.92E+00	9.35E-05	Up	7.58E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68563_All//gi|74325193|ref|YP_316613.1|//2.00E-22//ATPase subunit 9 [Thalassiosira pseudonana] >gi|74100259|gb|AAZ99420.1| ATPase subunit 9 [Thalassiosira pseudonana]		Unigene68563_All//1.00E-18//TC166849		ko00190|Oxidative phosphorylation	GO:0003824//GO:0005740//GO:0006754//GO:0006818//GO:0015078//GO:0031224//GO:0032559//GO:0033177	nr -
Unigene68566_All	436	0.84	5.23	0.98	0.34	0.71	0.62	1.94	1.73	5.12	2.64E+00	4.65E-07	Up	2.18E-01	8.30E-01		1.05E+00	5.31E-01		8.58E-01	6.30E-01		-1.69E-01	7.99E-01		1.40E+00	3.05E-04	Up	Unigene68566_All//gi|15230680|ref|NP_187911.1|//3.00E-48//transporter-related [Arabidopsis thaliana] >gi|15809988|gb|AOL06921.1| AT3g13050/MGH6_16 [Arabidopsis thaliana] >gi|28416475|gb|AAO42768.1| At3g13050/MGH6_16 [Arabidopsis thaliana]	Unigene68566_All//2.00E-49//AT3G13050| transporter-related	Unigene68566_All//5.00E-121//TC170854			GO:0005402//GO:0006810//GO:0031224	nr -
Unigene68567_All	428	0.00	1.54	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	6.23E-04	Up	7.96E+00	3.94E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene68568_All	431	0.00	2.47	0.37	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.80E-06	Up	8.53E+00	2.37E-01		null	null		null	null		null	null		null	null									
Unigene6857_All	389	6.19	2.74	1.51	3.20	1.86	1.51	1.20	1.07	1.23	-1.18E+00	4.73E-03		-2.04E+00	2.15E-05	Down	-7.84E-01	1.82E-01		-1.08E+00	7.79E-02		-1.54E-01	8.70E-01		3.98E-02	9.76E-01		Unigene6857_All//gi|300120701|emb|CBK20255.2|//2.00E-06//RNA binding protein [Blastocystis hominis]		Unigene6857_All//1.00E-84//DW499680		ko03040|Spliceosome		nr -
Unigene68570_All	408	0.00	2.24	0.52	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	2.61E-05	Up	9.03E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene68570_All//sp|O43432|IF4G3_HUMAN//5.00E-08//Eukaryotic translation initiation factor 4 gamma 3 OS=Homo sapiens GN=EIF4G3 PE=1 SV=2						swissprot +
Unigene68573_All	419	0.00	3.75	0.13	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.69E-09	Up	6.99E+00	6.30E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene68575_All	398	0.00	14.13	4.28	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	4.34E-32	Up	1.21E+01	2.20E-09	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene68577_All	715	0.00	2.76	0.60	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.97E-11	Up	9.22E+00	1.37E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene68578_All	1560	0.00	5.10	1.19	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.68E-45	Up	1.02E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene68578_All//gi|226502706|ref|NP_001151475.1|//1.00E-149//endoplasmin [Zea mays] >gi|195647042|gb|ACG42989.1| endoplasmin precursor [Zea mays]	Unigene68578_All//3.00E-143//AT4G24190| SHD (SHEPHERD); ATP binding / unfolded protein binding	Unigene68578_All//8.00E-09//TC167157		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene68579_All	420	0.00	3.38	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.05E-08	Up	8.57E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68579_All//gi|115444877|ref|NP_001046218.1|//8.00E-55//Os02g0199900 [Oryza sativa Japonica Group] >gi|110941192|dbj|BAB17625.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa Japonica Group] >gi|46390379|dbj|BAD15843.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa Japonica Group] >gi|49388371|dbj|BAD25481.1| 26S proteasome regulatory particle triple-A ATPase subunit4 [Oryza sativa Japonica Group] >gi|113535749|dbj|BAF08132.1| Os02g0199900 [Oryza sativa Japonica Group]	Unigene68579_All//1.00E-55//AT5G43010| RPT4A; ATPase			ko03050|Proteasome	GO:0005838//GO:0016020//GO:0019941//GO:0030312//GO:0031981//GO:0032559//GO:0042623	nr +
Unigene6858_All	688	1.06	2.80	1.01	1.59	3.40	3.81	0.92	5.77	0.58	1.39E+00	4.12E-03		-8.15E-02	9.29E-01		1.10E+00	7.94E-03		1.26E+00	1.58E-03		2.65E+00	1.72E-14	Up	-6.71E-01	3.86E-01									
Unigene68580_All	436	0.00	3.25	0.12	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.05E-08	Up	6.93E+00	6.30E-01		null	null		null	null		null	null		null	null		Unigene68580_All//sp|Q8NF91|SYNE1_HUMAN//2.00E-07//Nesprin-1 OS=Homo sapiens GN=SYNE1 PE=1 SV=3						swissprot +
Unigene68584_All	434	0.00	3.97	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.98E-10	Up	null	null		null	null		null	null		null	null		null	null		Unigene68584_All//gi|149063401|gb|EDM13724.1|//1.00E-45//rCG21519, isoform CRA_a [Rattus norvegicus] >gi|149063402|gb|EDM13725.1| rCG21519, isoform CRA_a [Rattus norvegicus] >gi|149063403|gb|EDM13726.1| rCG21519, isoform CRA_a [Rattus norvegicus]	Unigene68584_All//3.00E-38//AT1G23800| ALDH2B7; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)			ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0004030//GO:0008152//GO:0043231	nr +
Unigene68585_All	434	0.00	2.69	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.05E-06	Up	7.94E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68585_All//gi|192910876|gb|ACF06546.1|//5.00E-15//ubiquitin-conjugating enzyme 1 [Elaeis guineensis]	Unigene68585_All//4.00E-16//AT1G78870| UBC35 (UBIQUITIN-CONJUGATING ENZYME 35); protein binding / ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis	GO:0005488//GO:0006281//GO:0009913//GO:0010038//GO:0016020//GO:0019787//GO:0019941//GO:0031371//GO:0070646	nr +
Unigene68586_All	434	0.00	4.79	1.84	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.94E-12	Up	1.08E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene68586_All//gi|224552413|gb|ACN54543.1|//1.00E-16//mother of FT and TFL1-like protein [Physcomitrella patens]	Unigene68586_All//8.00E-16//AT1G18100| E12A11; phosphatidylethanolamine binding				GO:0001071//GO:0005488//GO:0009648//GO:0009791//GO:0048506	nr +
Unigene68588_All	435	0.00	4.66	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.53E-11	Up	1.04E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene68588_All//gi|300259627|gb|EFJ43853.1|//4.00E-06//DP transcription factor [Volvox carteri f. nagariensis]						nr +
Unigene68590_All	440	0.00	3.45	1.82	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.10E-08	Up	1.08E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene68590_All//gi|301105781|ref|XP_002901974.1|//2.00E-16//DnaJ subfamily C protein [Phytophthora infestans T30-4] >gi|262099312|gb|EEY57364.1| DnaJ subfamily C protein [Phytophthora infestans T30-4]	Unigene68590_All//4.00E-12//AT5G65160| tetratricopeptide repeat (TPR)-containing protein			ko04141|Protein processing in endoplasmic reticulum	GO:0005488//GO:0009755	nr +
Unigene68592_All	411	0.00	4.44	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.14E-10	Up	1.07E+01	6.14E-04	Up	null	null		null	null		null	null		null	null									
Unigene68593_All	455	0.00	7.46	1.52	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.54E-19	Up	1.06E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene68593_All//gi|219122761|ref|XP_002181708.1|//3.00E-24//anti-viral guanylate-binding protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|217406984|gb|EEC46922.1| anti-viral guanylate-binding protein [Phaeodactylum tricornutum CCAP 1055/1]						nr +

Unigene68594_All	442	0.59	0.92	0.48	4.17	9.12	4.19	1.05	0.57	0.27	6.32E-01	6.01E-01		-2.97E-01	8.31E-01		1.13E+00	1.34E-04	Up	6.70E-03	9.92E-01		-8.91E-01	3.83E-01		-1.96E+00	5.81E-02		Unigene68594_All//gi|226491336|ref|NP_001151747.1|//8.00E-59//LOC100285382 [Zea mays] >gi|195649471|gb|ACG44203.1| boron transporter 1 [Zea mays]	Unigene68594_All//0.00E+00//gi|164330204|gb|ES813275.1|ES813275			GO:0006811//GO:0010035//GO:0015301//GO:0015562//GO:0031224//GO:0043231//GO:0043673//GO:0044459	nr +
Unigene68595_All	437	0.00	3.13	1.22	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.78E-08	Up	1.03E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene68595_All//gi|115447567|ref|NP_001047363.1|//2.00E-34//Os02g0644100 [Oryza sativa Japonica Group] >gi|113537094|dbj|BAF09477.1| Os02g0644100 [Oryza sativa Japonica Group]	Unigene68595_All//3.00E-28//AT1G62740| stress-inducible protein, putative				GO:0000302//GO:0009642//GO:0010038//GO:0016020//GO:0043231//GO:0044444	nr +
Unigene68597_All	697	0.00	2.54	2.37	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	4.14E-10	Up	1.12E+01	4.30E-09	Up	null	null		null	null		null	null		null	null		Unigene68597_All//gi|112950081|gb|AB126643.1|//1.00E-53//aspartic proteinase [Cucumis sativus]	Unigene68597_All//8.00E-52//AT1G62290| aspartyl protease family protein				GO:0016787//GO:0043231	nr +
Unigene68599_All	786	0.00	7.35	1.15	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	5.79E-33	Up	1.02E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene68599_All//gi|3915737|sp|O22478.2|IMA_SOLLC//1.00E-31//RecName: Full=Importin subunit alpha; AltName: Full=Karyopherin subunit alpha; Short=KAP alpha >gi|3228370|gb|AAC23722.1| importin alpha [Solanum lycopersicum]	Unigene68599_All//2.00E-32//AT4G16143| IMPA-2 (IMPORTIN ALPHA ISOFORM 2); binding / protein transporter				GO:0006886//GO:0031981//GO:0044444	nr +
Unigene686_All	1809	69.85	8.71	12.51	35.91	16.98	31.06	196.65	95.10	80.69	-3.00E+00	0.00E+00	Down	-2.48E+00	0.00E+00	Down	-1.08E+00	5.72E-66	Down	-2.09E-01	1.43E-03		-1.05E+00	0.00E+00	Down	-1.29E+00	0.00E+00	Down	Unigene686_All//gi|70609690|gb|AAZ05070.1|//0.00E+00//glutamate decarboxylase [Citrus sinensis]	Unigene686_All//0.00E+00//AT2G02010 GAD4 (glutamate decarboxylase 4); calmodulin binding	Unigene686_All//0.00E+00//gi|164324493|gb|ES818648.1|ES818648		ko00250|Alanine, aspartate and glutamate metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00430|Taurine and hypotaurine metabolism	GO:0005515//GO:0009064//GO:0016831//GO:0043231//GO:0044444//GO:0048037	nr +
Unigene6860_All	687	15.99	39.31	6.43	433.39	818.48	542.62	0.00	0.12	0.00	1.30E+00	6.57E-30	Up	-1.31E+00	2.55E-12	Down	9.17E-01	0.00E+00		3.24E-01	9.41E-39		6.93E+00	3.99E-01		null	null		Unigene6860_All//gi|300265098|gb|EFJ49291.1|//1.00E-29//extracellular matrix glycoprotein pherophorin-V32 [Volvox carteri f. nagariensis]				ko03040|Spliceosome		nr +
Unigene68604_All	458	0.00	3.21	0.70	0.00	0.08	0.00	0.00	0.00	0.00	1.16E+01	2.11E-08	Up	9.45E+00	4.49E-02		6.23E+00	8.21E-01		null	null		null	null		null	null		Unigene68604_All//gi|300262824|gb|EFJ47028.1|//8.00E-10//transcription factor jumonji domain-containing protein [Volvox carteri f. nagariensis]				ko03022|Basal transcription factors		nr +
Unigene68605_All	717	0.58	2.26	1.78	1.46	1.68	1.64	0.59	0.47	0.50	1.95E+00	6.79E-04	Up	1.61E+00	1.45E-02		2.04E-01	8.01E-01		1.67E-01	7.91E-01		-3.39E-01	7.30E-01		-2.38E-01	7.88E-01		Unigene68605_All//gi|225445838|ref|XP_002277707.1|//2.00E-07//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297743658|emb|CBI36541.3| unnamed protein product [Vitis vinifera]		Unigene68605_All//4.00E-18//DR459377				nr +
Unigene68607_All	727	0.00	2.58	0.15	0.07	0.09	0.19	0.00	0.00	0.00	1.13E+01	1.10E-10	Up	7.19E+00	3.94E-01		4.67E-01	9.55E-01		1.44E+00	6.37E-01		null	null		null	null		Unigene68607_All//gi|46931316|gb|AT06462.1|//2.00E-22//At3g27250 [Arabidopsis thaliana]	Unigene68607_All//2.00E-14//AT5G50360| unknown protein				nr +
Unigene68609_All	444	0.00	3.88	4.20	0.00	0.16	0.00	0.00	0.00	0.00	1.19E+01	7.97E-10	Up	1.20E+01	2.89E-10	Up	7.28E+00	6.04E-01		null	null		null	null		null	null		Unigene68609_All//gi|226509046|ref|NP_001151268.1|//2.00E-12//LOC100284901 [Zea mays] >gi|195609716|gb|ACG26688.1| 60S ribosomal protein L28 [Zea mays] >gi|195610086|gb|ACG26873.1| 60S ribosomal protein L28 [Zea mays] >gi|195645410|gb|ACG42173.1| 60S ribosomal protein L28 [Zea mays] >gi|195646860|gb|ACG42898.1| 60S ribosomal protein L28 [Zea mays]	Unigene68609_All//1.00E-10//AT2G19730| 60S ribosomal protein L28 (RPL28A)			ko03010|Ribosome		nr +
Unigene6861_All	964	4336.82	685.98	2590.08	4184.65	3688.18	4212.09	101.88	81.29	37.15	-2.66E+00	0.00E+00	Down	-7.44E-01	0.00E+00		-1.82E-01	6.47E-156		9.40E-03	3.46E-01		-3.26E-01	2.38E-12		-1.46E+00	5.39E-161	Down	Unigene6861_All//gi|254692064|emb|CBA10126.1|//1.00E-62//PME inhibitor [Nicotiana benthamiana]	Unigene6861_All//6.00E-60//AT5G62360| invertase/pectin methylesterase inhibitor family protein	Unigene6861_All//0.00E+00//TC132543		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene68612_All	480	0.00	2.32	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.99E-06	Up	7.79E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene68612_All//sp|P12109|CO6A1_HUMAN//1.00E-70//Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3						swissprot +
Unigene68613_All	442	1.42	0.46	0.72	1.69	2.03	2.45	3.35	0.76	0.54	-1.63E+00	9.23E-02		-9.75E-01	3.16E-01		2.61E-01	7.79E-01		5.37E-01	4.55E-01		-2.15E+00	9.69E-05	Down	-2.63E+00	4.77E-06	Down	Unigene68613_All//gi|30697452|ref|NP_851235.1|//3.00E-28//nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana]	Unigene68613_All//2.00E-29//AT5G60980| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein	Unigene68613_All//6.00E-124//BF275228			GO:0003676//GO:0051169	nr -
Unigene68614_All	771	0.00	3.29	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.05E-14	Up	8.43E+00	7.97E-02		null	null		null	null		null	null		null	null		Unigene68614_All//gi|3777559|gb|AAC64934.1|//2.00E-23//collagen-like [Griffithsia japonica]	Unigene68614_All//6.00E-08//AT1G64450| proline-rich family protein			ko03040|Spliceosome//ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene68615_All	460	2.27	1.54	0.00	12.35	8.91	7.07	0.46	0.55	0.35	-5.61E-01	3.82E-01		-1.12E+01	9.32E-06	Down	-4.71E-01	5.36E-02		-8.04E-01	1.03E-03		2.46E-01	8.53E-01		-4.08E-01	7.55E-01		Unigene68615_All//gi|30684004|ref|NP_193466.2|//2.00E-37//phosphoinositide binding [Arabidopsis thaliana] >gi|54606846|gb|AAV34771.1| At4g17350 [Arabidopsis thaliana] >gi|98960971|gb|ABF58969.1| At4g17350 [Arabidopsis thaliana]	Unigene68615_All//2.00E-17//AT4G17350| phosphoinositide binding	Unigene68615_All//0.00E+00//DR457190			GO:0005543//GO:0023060	nr +
Unigene68618_All	970	0.00	6.06	1.65	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.51E-33	Up	1.07E+01	8.43E-09	Up	null	null		null	null		null	null		null	null		Unigene68618_All//sp|P34714|SPRC_CAEEL//7.00E-45//SPARC OS=Caenorhabditis elegans GN=ost-1 PE=1 SV=1						swissprot +
Unigene68619_All	870	0.00	7.80	2.02	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	8.60E-39	Up	1.10E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene68619_All//gi|115441853|ref|NP_001045206.1|//1.00E-17//Os01g0918200 [Oryza sativa Japonica Group] >gi|113534737|dbj|BAF07120.1| Os01g0918200 [Oryza sativa Japonica Group]	Unigene68619_All//2.00E-18//AT5G55160| SUMO2 (SMALL UBIQUITIN-LIKE MODIFIER 2); protein binding / protein tag				GO:0005488//GO:0009408//GO:0016818//GO:0032446//GO:0043232//GO:0043492	nr -
Unigene6862_All	1475	1.45	0.27	0.87	0.81	0.05	0.09	1.55	5.36	5.73	-2.40E+00	3.76E-06	Down	-7.47E-01	1.05E-01		-4.12E+00	7.48E-07	Down	-3.14E+00	6.58E-05	Down	1.79E+00	1.34E-17	Up	1.89E+00	1.49E-20	Up	Unigene6862_All//gi|224145030|ref|XP_002325501.1|//7.00E-11//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222862376|gb|EEE99882.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene6862_All//3.00E-13//AT4G12010| disease resistance protein (TIR-NBS-LRR class), putative	Unigene6862_All//3.00E-23//ES795903				nr +
Unigene68621_All	476	0.33	2.45	0.90	0.21	0.22	0.00	0.00	0.00	0.00	2.89E+00	2.98E-04	Up	1.44E+00	2.53E-01		5.21E-02	9.65E-01		-7.71E+00	3.95E-01		null	null		null	null		Unigene68621_All//sp|P0A902|GST_ECOLI//3.00E-19//Glutathione S-transferase OS=Escherichia coli (strain K12) GN=gst PE=1 SV=1	Unigene68621_All//3.00E-06//AT2G02380| ATGSTZ2; catalytic/ glutathione transferase					swissprot +
Unigene68622_All	584	0.00	1.30	0.73	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	1.76E-04	Up	9.51E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene68622_All//sp|Q9V66X1|TPP2_DROME//1.00E-46//Tripeptidyl-peptidase 2 OS=Drosophila melanogaster GN=TppII PE=1 SV=2						swissprot +
Unigene68623_All	662	0.00	5.13	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.54E-19	Up	9.65E+00	4.02E-03		null	null		null	null		null	null		null	null		Unigene68623_All//gi|148612407|gb|AEQ96119.1|//5.00E-23//alpha-gliadin [Aegilops tauschii]	Unigene68623_All//5.00E-06//AT2G34450| high mobility group (HMG1/2) family protein			ko03022|Basal transcription factors		nr -
Unigene68624_All	474	0.00	1.82	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	4.93E-05	Up	9.40E+00	4.49E-02		null	null		null	null		null	null		null	null									
Unigene68625_All	459	0.00	2.65	1.88	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	5.46E-07	Up	1.09E+01	9.00E-05	Up	null	null		null	null		null	null		null	null									
Unigene68626_All	451	0.00	2.36	0.12	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.80E-06	Up	6.88E+00	6.30E-01		null	null		null	null		null	null		null	null		Unigene68626_All//gi|195647178|gb|ACG43057.1|//6.00E-41//succinate dehydrogenase flavoprotein subunit,mitochondrial precursor [Zea mays]	Unigene68626_All//8.00E-32//AT5G66760| SDH1-1; ATP binding / succinate dehydrogenase			ko00190|Oxidative phosphorylation//ko00020|Citrate cycle (TCA cycle)	GO:0000104//GO:0005746//GO:0009060//GO:0022904//GO:0030312//GO:0032559//GO:0046914	nr +
Unigene68628_All	498	5.67	3.66	1.39	0.00	0.00	0.00	0.00	0.00	0.00	-6.31E-01	9.03E-02		-2.03E+00	3.46E-06	Down	null	null		null	null		null	null		null	null		Unigene68628_All//gi|16648748|gb|AAL25566.1|//5.00E-09//AT5g02020/T7H20_70 [Arabidopsis thaliana] >gi|20334906|gb|AAM16209.1| AT5g02020/T7H20_70 [Arabidopsis thaliana]	Unigene68628_All//1.00E-17//AT3G55646| unknown protein	Unigene68628_All//8.00E-28//ES838392				nr -
Unigene68630_All	489	0.00	3.42	1.20	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.54E-09	Up	1.02E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene68630_All//gi|3415115|gb|AAC31606.1|//1.00E-11//villin 2 [Arabidopsis thaliana]	Unigene68630_All//8.00E-13//AT4G30160| VLN4 (ARABIDOPSIS THALIANA VILLIN 4); actin binding				GO:0005488	nr -
Unigene68633_All	470	0.00	3.34	2.04	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	5.69E-09	Up	1.10E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene68633_All//gi|310563|gb|AAA33948.1|//4.00E-14//calmodulin [Glycine max] >gi|1583771|prf|2121384E calmodulin	Unigene68633_All//3.00E-05//AT4G14640| CAM8 (CALMODULIN 8); calcium ion binding			ko04626|Plant-pathogen interaction		nr +
Unigene68635_All	489	0.00	3.32	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.96E-09	Up	9.35E+00	4.49E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene68636_All	500	0.63	3.55	3.41	1.00	1.38	2.53	4.40	2.26	3.35	2.50E+00	2.34E-05	Up	2.44E+00	7.80E-05	Up	4.67E-01	6.12E-01		1.34E+00	3.22E-02		-9.62E-01	1.28E-02		-3.94E-01	3.10E-01		Unigene68636_All//gi|227202562|dbj|BAH56754.1|//1.00E-23//AT5G22820 [Arabidopsis thaliana]	Unigene68636_All//3.00E-17//AT5G22820| binding					nr +
Unigene68638_All	487	0.00	3.75	1.09	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.14E-10	Up	1.01E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene68638_All//gi|195613498|gb|ACG28579.1|//4.00E-22//mitochondrial import inner membrane translocase subunit Tim17 [Zea mays]	Unigene68638_All//4.00E-26//AT2G37410| ATTIM17-2; P-P-bond-hydrolysis-driven protein transmembrane transporter/ protein transporter				GO:0005743//GO:0006810//GO:0008320//GO:0031224	nr +
Unigene68639_All	493	0.00	5.45	1.51	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.80E-15	Up	1.06E+01	3.26E-04	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene68641_All	474	0.00	3.85	1.24	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.14E-10	Up	1.03E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene68641_All//sp|Q9V4M2|WECH_DROME//4.00E-43//Protein wech OS=Drosophila melanogaster GN=wech PE=1 SV=2						swissprot -
Unigene68643_All	473	0.00	2.89	0.56	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.78E-08	Up	9.14E+00	7.97E-02		null	null		null	null		null	null		null	null		Unigene68643_All//gi|3777559|gb|AAC64934.1|//5.00E-30//collagen-like [Griffithsia japonica]				ko03040|Spliceosome		nr +
Unigene68647_All	493	0.00	6.89	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.54E-19	Up	9.34E+00	4.49E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene68648_All	481	10.88	10.53	6.97	15.43	15.18	13.52	8.09	2.87	4.39	-4.63E-02	8.65E-01		-6.41E-01	1.90E-02		-2.39E-02	9.21E-01		-1.91E-01	4.44E-01		-1.50E+00	3.41E-07	Down	-8.82E-01	1.02E-03		Unigene68648_All//gi|110737176|dbj|BAF00537.1|//8.00E-22//phosphoribosylaminoimidazole carboxylase like protein [Arabidopsis thaliana]	Unigene68648_All//2.00E-16//AT2G37690| phosphoribosylaminoimidazole carboxylase, putative / AIR carboxylase, putative	Unigene68648_All//0.00E+00//TC174381		ko00230|Purine metabolism	GO:0006188//GO:0009536//GO:0016831//GO:0032559//GO:0043234//GO:0048029	nr -
Unigene6865_All	1032	0.15	1.37	1.14	1.83	2.04	0.53	9.10	9.44	5.67	3.18E+00	1.99E-05	Up	2.90E+00	4.34E-04	Up	1.50E-01	8.01E-01		-1.80E+00	3.14E-04	Down	5.31E-02	7.81E-01		-6.81E-01	2.90E-05		Unigene6865_All//gi|44681324|gb|AAS47602.1|//1.00E-23//At5g40980 [Arabidopsis thaliana] >gi|45773828|gb|AAS76718.1| At5g40980 [Arabidopsis thaliana]	Unigene6865_All//5.00E-25//AT5G40980| unknown protein	Unigene6865_All//4.00E-22//DW502398				nr -
Unigene68650_All	500	0.00	2.63	0.96	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.49E-07	Up	9.90E+00	7.46E-03		null	null		null	null		null	null		null	null									
Unigene68652_All	512	0.00	7.92	3.02	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	4.39E-23	Up	1.16E+01	1.65E-08	Up	null	null		null	null		null	null		null	null									

Unigene68653_All	487	5.80	3.23	2.41	6.85	5.73	16.79	18.32	4.72	13.33	-8.47E-01	2.31E-02		-1.27E+00	1.49E-03		-2.59E-01	4.89E-01		1.29E+00	5.35E-10	Up	-1.96E+00	3.02E-22	Down	-4.58E-01	6.32E-03		Unigene68653_All//gi|3818416|gb|AAD03487.1|//9.00E-56//proline-rich cell wall protein [Medicago sativa]	Unigene68653_All//2.00E-27//AT3G22142| structural constituent of cell wall	Unigene68653_All//6.00E-50//gi|109838930|gb|DW237491.1|DW237491		ko03040|Spliceosome	GO:0006810	nr +
Unigene68655_All	519	0.30	0.39	0.21	0.48	0.07	0.00	1.14	0.00	0.15	3.69E-01	8.15E-01		-5.59E-01	7.74E-01		-2.86E+00	1.37E-01		-8.91E+00	7.31E-02		-1.02E+01	2.39E-04	Down	-2.89E+00	4.53E-03		Unigene68655_All|gi|297845610|ref|XP_002890686.1|/1.00E-59//aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata] >gi|297336528|gb|EFH66945.1| aspartyl protease family protein [Arabidopsis lyrata subsp. lyrata]	Unigene68655_All//1.00E-49//AT1G25510| aspartyl protease family protein	Unigene68655_All//0.00E+00//TC172187			GO:0004175//GO:0019538//GO:0044464	nr +
Unigene68656_All	476	0.00	7.45	5.15	0.00	0.00	0.19	0.00	0.00	0.00	1.29E+01	3.45E-20	Up	1.23E+01	1.64E-13	Up	null	null		7.57E+00	4.72E-01		null	null		null	null		Unigene68656_All|gi|585083|sp|P35450.2|EFGC_PEA//2.00E-31//RecName: Full=Elongation factor G, chloroplastic; Short=EF-G >gi|553080|gb|AAA33654.1| chloroplast EF-G [Pisum sativum]	Unigene68656_All//3.00E-32//AT1G62750| SCO1 (SNOWY COTYLEDON 1); ATP binding / translation elongation factor/ translation factor, nucleic acid binding				GO:0005576//GO:0006412//GO:0007275//GO:0008135//GO:0009526//GO:0009532//GO:0009657//GO:0017111//GO:0032559//GO:0032561	nr +
Unigene68657_All	513	0.20	8.40	2.08	0.39	0.54	0.79	0.00	0.24	0.23	5.36E+00	1.34E-21	Up	3.35E+00	3.36E-04	Up	4.67E-01	8.16E-01		1.03E+00	4.28E-01		7.93E+00	2.40E-01		7.86E+00	2.42E-01		Unigene68657_All//gi|82394632|gb|AB872405.1|//2.00E-19//seed maturation protein [Glycine canescens]	Unigene68657_All//2.00E-05//AT1G32560| late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein					nr +
Unigene68658_All	873	0.00	13.99	3.29	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	4.70E-70	Up	1.17E+01	6.95E-16	Up	null	null		null	null		null	null		null	null		Unigene68658_All|gi|159491160|ref|XP_001703541.1|/2.00E-08//flagellar associated protein [Chlamydomonas reinhardtii] >gi|158280465|gb|EDP06223.1| flagellar associated protein [Chlamydomonas reinhardtii]						nr +
Unigene68660_All	466	0.00	8.81	7.77	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.25E-23	Up	1.29E+01	4.73E-20	Up	null	null		null	null		null	null		null	null		Unigene68660_All|gi|226532924|ref|NP_001146968.1|/4.00E-42//ribosomal protein S24 [Zea mays] >gi|195605952|gb|ACG24806.1| 40S ribosomal protein S24 [Zea mays] >gi|195608026|gb|ACG25843.1| 40S ribosomal protein S24 [Zea mays]	Unigene68660_All//3.00E-32//AT3G04920| 40S ribosomal protein S24 (RPS24A)			ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0031981	nr +
Unigene68661_All	481	4.02	1.79	1.88	7.87	9.09	9.58	3.69	1.13	0.66	-1.17E+00	1.36E-02		-1.10E+00	2.63E-02		2.08E-01	5.58E-01		2.83E-01	3.79E-01		-1.71E+00	2.60E-04	Down	-2.48E+00	1.05E-06	Down	Unigene68661_All|gi|21553536|gb|AAM62629.1|//7.00E-36//receptor-like protein kinase [Arabidopsis thaliana]	Unigene68661_All//2.00E-36//AT5G51560| leucine-rich repeat transmembrane protein kinase, putative	Unigene68661_All//0.00E+00//gi|21093546|gb|BQ405859.1|BQ405859		ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016491//GO:0031224//GO:0031410//GO:0032559	nr +
Unigene68663_All	519	0.00	8.69	1.95	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	1.08E-25	Up	1.09E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene68663_All|gi|301102893|ref|XP_002900533.1|/9.00E-07//glutathione transferase, theta class [Phytophthora infestans T30-4] >gi|262101796|gb|EEY59848.1| glutathione transferase, theta class [Phytophthora infestans T30-4]	Unigene68663_All//3.00E-07//AT1G68860| ATGSTF14; glutathione transferase					nr +
Unigene68664_All	520	0.70	1.36	2.25	2.87	2.85	3.13	6.42	0.80	1.61	9.54E-01	2.62E-01		1.68E+00	1.64E-02		-1.33E-02	9.68E-01		1.22E-01	8.26E-01		-3.00E+00	5.97E-14	Down	-2.00E+00	2.40E-09	Down	Unigene68664_All|gi|145334281|ref|NP_001078522.1|/4.00E-24//CTV0RF47 (CONSERVED PEPTIDE UPSTREAM OPEN READING FRAME 47) [Arabidopsis thaliana]	Unigene68664_All//3.00E-30//AT3G34400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; BEST Arabidopsis thaliana protein match is: CTV0RF47 (CONSERVED PEPTIDE UPSTREAM OPEN READING FRAME 47) (TAIR:AT5G03190.1); Has 120 Blast hits to 120 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 115; Viruses - 0; Other Eukaryotes - 5 (source: NCBI BLink).	Unigene68664_All//0.00E+00//TC170795				nr +
Unigene68666_All	496	0.00	3.58	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.14E-10	Up	9.07E+00	7.97E-02		null	null		null	null		null	null		null	null		Unigene68666_All//sp|Q9JID1|PDCD4_RAT//1.00E-15//Programmed cell death protein 4 OS=Rattus norvegicus GN=Pdcd4 PE=1 SV=2						swissprot +
Unigene68667_All	526	0.00	6.17	6.48	0.09	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.87E-18	Up	1.27E+01	7.38E-19	Up	-6.57E+00	5.48E-01		-6.57E+00	6.26E-01		null	null		null	null		Unigene68667_All//gi|224000283|ref|XP_002289814.1|/6.00E-43//RL18a, ribosomal protein 18a 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335] >gi|220975022|gb|EED93351.1| RL18a, ribosomal protein 18a 60S large ribosomal subunit [Thalassiosira pseudonana CCMP1335]	Unigene68667_All//1.00E-40//AT1G29970| RPL18AA (60S RIBOSOMAL PROTEIN L18A-1)			ko03010|Ribosome	GO:0005622	nr -
Unigene68668_All	506	0.00	5.51	2.63	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.42E-16	Up	1.14E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene68668_All|gi|15232681|ref|NP_190278.1|/7.00E-39//deoxyuridine 5'-triphosphate nucleotidohydrolase family [Arabidopsis thaliana] >gi|5541665|emb|CAB51171.1| dUTP pyrophosphatase-like protein [Arabidopsis thaliana]	Unigene68668_All//9.00E-39//AT3G46940| deoxyuridine 5'-triphosphate nucleotidohydrolase family			ko00240|Pyrimidine metabolism	GO:0009211//GO:0047429	nr +
Unigene68669_All	524	0.00	5.61	0.81	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.01E-16	Up	9.67E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene68669_All|gi|1351858|sp|P49609.1|ACON_GRAVE//2.00E-64//RecName: Full=Aconitate hydratase, mitochondrial; Short=Aconitase; AltName: Full=Citrate hydro-lyase; Flags: Precursor >gi|600171|gb|AAA80494.1| aconitase [Gracilaria gracilis]	Unigene68669_All//2.00E-10//AT4G35830| aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO)			ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0000166//GO:0004448//GO:0009060//GO:0016836//GO:0043231//GO:0046872//GO:0051536	nr +
Unigene68670_All	525	0.00	7.14	3.96	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.40E-21	Up	1.19E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene68670_All//sp|P08493|MGP_HUMAN//3.00E-54//Matrix Gla protein OS=Homo sapiens GN=MGP PE=1 SV=2						swissprot +
Unigene68674_All	530	0.00	7.17	1.31	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.23E-21	Up	1.04E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene68674_All//gi|15235029|ref|NP_192772.1|//1.00E-88//LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding [Arabidopsis thaliana] >gi|28558077|sp|Q9XF89.1|CR26_ARATH RecName: Full=Chlorophyll a-b binding protein CP26, chloroplastic; AltName: Full=Light-harvesting complex II protein 5; AltName: Full=LHCB5; AltName: Full=LHCIIc; Flags: Precursor >gi|4741958|gb|AAD28776.1|AF134129_1 Lhcb5 protein [Arabidopsis thaliana] >gi|14190463|gb|AAK55712.1|AF380631_1 AT4g10340/F24G24_140 [Arabidopsis thaliana] >gi|15983446|gb|AAL11591.1|AF424597_1 AT4g10340/F24G24_140 [Arabidopsis thaliana] >gi|45389963|emb|CAB39287.1| chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi|7267731|emb|CAB78157.1| chlorophyll a/b-binding protein-like [Arabidopsis thaliana] >gi|15809718|gb|AAL06787.1| AT4g10340/F24G24_140 [Arabidopsis	Unigene68674_All//5.00E-81//AT4G10340| LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding	Unigene68674_All//2.00E-68//gi|31074011|gb|CA994290.1|CA994290		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009503//GO:0009523//GO:0009570//GO:0009639//GO:0046906	nr +
Unigene68676_All	551	0.47	3.13	0.39	0.27	0.56	0.25	0.38	0.23	0.36	2.72E+00	1.19E-05	Up	-2.97E-01	8.31E-01		1.05E+00	5.31E-01		-1.41E-01	9.42E-01		-7.54E-01	6.31E-01		-8.60E-02	9.60E-01		Unigene68676_All//gi|124359163|gb|ABN05686.1|//2.00E-17//Zinc finger, CCHC-type [Medicago truncatula]	Unigene68676_All//3.00E-08//AT3G31430| unknown protein				GO:0005488	nr +
Unigene68679_All	953	0.00	13.35	5.36	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	5.60E-73	Up	1.24E+01	1.92E-28	Up	null	null		null	null		null	null		null	null		Unigene68679_All|gi|159482727|ref|XP_001699419.1|/5.00E-40//transcription factor [Chlamydomonas reinhardtii] >gi|158272870|gb|EDO98665.1| transcription factor [Chlamydomonas reinhardtii]	Unigene68679_All//2.00E-28//AT1G17880| nascent polypeptide-associated complex (NAC) domain-containing protein / BTF3b-like transcription factor, putative					nr +
Unigene6888_All	489	0.21	0.31	0.00	0.31	0.49	0.18	9.25	3.85	8.15	5.39E-01	7.78E-01		-7.74E+00	3.88E-01		6.90E-01	7.32E-01		-7.27E-01	7.14E-01		-1.27E+00	1.40E-06	Down	-1.83E-01	5.00E-01				Unigene6888_All//5.00E-140//EX171785				
Unigene68680_All	572	0.00	4.43	1.30	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.05E-14	Up	1.03E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene68680_All//sp|P97801|SMN_MOUSE//4.00E-13//Survival motor neuron protein OS=Mus musculus GN=Smn1 PE=1 SV=1						swissprot +
Unigene68683_All	562	0.00	5.50	0.76	0.00	0.06	0.80	0.08	0.22	1.42	1.24E+01	1.38E-17	Up	9.57E+00	1.37E-02		5.94E+00	8.21E-01		9.65E+00	7.75E-03		1.57E+00	5.44E-01		4.24E+00	7.42E-05	Up							
Unigene68686_All	584	0.00	5.12	0.91	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.18E-17	Up	9.83E+00	4.02E-03		null	null		null	null		null	null		null	null		Unigene68686_All//sp|P11997|LSP1G_DROME//2.00E-35//Larval serum protein 1 gamma chain OS=Drosophila melanogaster GN=Lsp1gamma PE=2 SV=2						swissprot -
Unigene68687_All	567	0.00	2.59	2.07	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	2.11E-08	Up	1.10E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene68687_All//gi|297722781|ref|NP_001173754.1|/1.00E-08//Os04g0156200 [Oryza sativa Japonica Group] >gi|255675159|dbj|BAH92482.1| Os04g0156200 [Oryza sativa Japonica Group]				ko03018|RNA degradation		nr +
Unigene68688_All	581	0.00	5.41	1.65	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.07E-18	Up	1.07E+01	2.45E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene68689_All	614	0.00	3.05	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.10E-10	Up	8.02E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68689_All//gi|38325813|gb|AAR17079.1|//7.00E-82//heat shock protein 70-2 [Nicotiana tabacum]	Unigene68689_All//3.00E-78//AT5G02490| heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2)	Unigene68689_All//7.00E-07//TC166224		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0009941//GO:0016628//GO:0032559//GO:0050896	nr -
Unigene6869_All	468	3.91	2.38	4.44	9.37	9.42	10.62	8.13	3.57	8.60	-7.16E-01	1.36E-01		1.82E-01	6.84E-01		7.90E-03	9.89E-01		1.81E-01	5.76E-01		-1.19E+00	3.42E-05	Down	8.06E-02	7.73E-01				Unigene6869_All//1.00E-152//EX171785				

Unigene68690_All	613	0.00	8.18	0.69	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.34E-28	Up	9.44E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene68690_All//gi|192910924|gb|ACF06570.1|//3.00E-18//annexin P35 [Elaeis guineensis]	Unigene68690_All//6.00E-15//AT1G35720| ANNAT1 (ANNEXIN ARABIDOPSIS 1); ATP binding / calcium ion binding / calcium-dependent phospholipid binding / copper ion binding / peroxidase/ protein homodimerization					nr +
Unigene68691_All	624	0.00	3.33	0.68	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.94E-12	Up	9.42E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene68691_All//gi|15240002|ref|NP_196811.1|//6.00E-07//MSF1-like family protein [Arabidopsis thaliana] >gi|62867619|gb|AAY17413.1| At5g13070 [Arabidopsis thaliana] >gi|66841354|gb|AAU57314.1| At5g13070 [Arabidopsis thaliana]	Unigene68691_All//3.00E-08//AT5G13070| MSF1-like family protein					nr +
Unigene68692_All	635	0.00	14.52	5.70	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	8.41E-53	Up	1.25E+01	4.73E-20	Up	null	null		null	null		null	null		null	null		Unigene68692_All//gi|242043846|ref|XP_002459794.1|//8.00E-07//hypothetical protein SORBIDRAFT_02g010770 [Sorghum bicolor] >gi|241923171|gb|EER96315.1| hypothetical protein SORBIDRAFT_02g010770 [Sorghum bicolor]				ko00190|Oxidative phosphorylation		nr -
Unigene68693_All	617	0.00	4.93	1.81	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.67E-17	Up	1.08E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene68693_All//gi|1170370|sp|P41753.1|HSP70_ACHKL//7.00E-40//RecName: Full=Heat shock 70 kDa protein >gi|407302|gb|AAA17562.1| heat shock protein 70 [Achlya klebsiana]	Unigene68693_All//5.00E-27//AT1G16030| Hsp70b (heat shock protein 70B); ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0000166//GO:0016787	nr +
Unigene68694_All	628	0.00	6.21	0.68	0.00	0.00	0.14	0.00	0.00	0.00	1.26E+01	3.25E-22	Up	9.41E+00	1.37E-02		null	null		7.17E+00	4.72E-01		null	null		null	null		Unigene68694_All//gi|297806981|ref|XP_002871374.1|//2.00E-62//rab GDP-dissociation inhibitor [Arabidopsis lyrata subsp. lyrata] >gi|297317211|gb|EFH47633.1| rab GDP-dissociation inhibitor [Arabidopsis lyrata subsp. lyrata]	Unigene68694_All//3.00E-63//AT5G09550| RAB GDP-dissociation inhibitor				GO:0005092//GO:0006810//GO:0033124	nr +
Unigene68695_All	1646	0.00	7.88	3.33	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.92E-74	Up	1.17E+01	1.52E-30	Up	null	null		null	null		null	null		null	null		Unigene68695_All//gi|8928010|sp|O80433.1|CISY_DAUCA//1.00E-158//RecName: Full=Citrate synthase, mitochondrial; Flags: Precursor >gi|3493367|dbj|BAA32557.1| citrate synthase [Daucus carota]	Unigene68695_All//5.00E-145//AT2G44350| ATCS; ATP binding / ATP citrate synthase/ citrate (SI)-synthase			ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene68696_All	682	0.00	5.72	1.48	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	3.25E-22	Up	1.05E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene68696_All//gi|159474114|ref|XP_001695174.1|//7.00E-29//dihydrolipoamide acetyltransferase [Chlamydomonas reinhardtii] >gi|158276108|gb|EDP01882.1| dihydrolipoamide acetyltransferase [Chlamydomonas reinhardtii]	Unigene68696_All//4.00E-27//AT3G52200| LTA3; ATP binding / dihydrolipoyllysine-residue acetyltransferase			ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)	GO:0008415//GO:0009526//GO:0046914	nr -
Unigene68698_All	705	0.00	10.49	6.27	0.00	0.10	0.00	0.00	0.00	0.00	1.34E+01	2.72E-42	Up	1.26E+01	1.55E-24	Up	6.61E+00	6.04E-01		null	null		null	null		null	null		Unigene68698_All//gi|192913004|gb|ACF06610.1|//4.00E-72//ribosomal protein L15 [Elaeis guineensis]	Unigene68698_All//4.00E-56//AT4G16720| 60S ribosomal protein L15 (RPL15A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr -
Unigene68700_All	718	0.00	15.38	6.60	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	2.52E-63	Up	1.27E+01	2.43E-26	Up	null	null		null	null		null	null		null	null		Unigene68700_All//gi|300258158|gb|EFJ42397.1|//3.00E-090//hypothetical protein VOLCADRAFT_97458 [Volvox carteri f. nagariensis]						nr +
Unigene68701_All	725	0.00	13.14	9.25	0.00	0.10	0.00	0.06	0.00	0.11	1.37E+01	1.48E-54	Up	1.32E+01	1.84E-37	Up	6.57E+00	6.04E-01		null	null		-5.87E+00	6.48E-01		9.15E-01	7.48E-01		Unigene68701_All//gi|2500354|sp|P93847.1|RL10_SOLME//7.00E-77//RecName: Full=60S ribosomal protein L10; AltName: Full=EQM >gi|190289 4|dbj|BAA19462.1| QM family protein [Solanum melongena]	Unigene68701_All//2.00E-77//AT1G66580| 60S ribosomal protein L10 (RPL10C)	Unigene68701_All//2.00E-20//TC140923		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010224//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr -
Unigene68702_All	770	0.14	8.62	0.00	0.26	0.45	0.29	0.00	0.00	0.31	5.99E+00	1.31E-34	Up	-7.09E+00	3.88E-01		7.89E-01	5.95E-01		1.81E-01	9.34E-01		null	null		8.28E+00	4.39E-02		Unigene68702_All//gi|75213086|sp|Q9SWB4.1|PARP3_SOYBN//2.00E-69//RecName: Full=Poly (ADP-ribose) polymerase 3; Short=PARP-3; AltName: Full=NAD(+) ADP-ribosyltransferase 3; Short=ADPRT-3; AltName: Full=Poly[ADP-ribose] synthase 3 >gi|5802246|gb|AAD51626.1|AF169023_1 seed maturation protein PM38 [Glycine max]	Unigene68702_All//3.00E-54//AT5G22470| NAD+ ADP-ribosyltransferase			ko03410|Base excision repair	GO:0003676//GO:0005622//GO:0008152//GO:0016491//GO:0016757	nr -
Unigene68704_All	936	0.00	5.14	0.68	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.96E-27	Up	9.42E+00	1.16E-03		null	null		null	null		null	null		null	null		Unigene68704_All//gi|225459758|ref|XP_002285900.1|//1.00E-11//PREDICTED: similar to NRPB1 (RNA POLYMERASE II LARGE SUBUNIT); DNA binding / DNA-directed RNA polymerase [Vitis vinifera]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0043231//GO:0044444	nr +
Unigene68705_All	1031	0.00	6.24	3.41	0.10	0.00	0.00	0.00	0.00	0.00	1.26E+01	9.43E-37	Up	1.17E+01	1.87E-19	Up	-6.59E+00	3.10E-01		-6.59E+00	3.95E-01		null	null		null	null		Unigene68705_All//gi|157093371|gb|ABV22340.1|//1.00E-11//calponin domain-containing protein [Noctiluca scintillans]						nr -
Unigene68707_All	1272	0.00	7.65	5.86	0.00	0.00	0.14	0.00	0.00	0.00	1.29E+01	9.96E-56	Up	1.25E+01	1.11E-41	Up	null	null		7.15E+00	1.94E-01		null	null		null	null		Unigene68707_All//gi|301093682|ref|XP_002997686.1|//1.00E-146//60S ribosomal protein L3 [Phytophthora infestans T30-4] >gi|262109935|gb|EEY67987.1| 60S ribosomal protein L3 [Phytophthora infestans T30-4]	Unigene68707_All//6.00E-133//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene68707_All//1.00E-07//gi|13353022|gb|BG443370.1|BG443370		ko03010|Ribosome		nr -
Unigene6871_All	782	1.14	0.65	0.41	2.17	1.59	0.92	0.49	0.21	1.78	-8.12E-01	2.68E-01		-1.48E+00	6.98E-02		-4.50E-01	3.87E-01		-1.23E+00	1.61E-02		-1.19E+00	3.09E-01		1.87E+00	4.97E-04	Up	Unigene6871_All//gi|4191776|gb|AAD10145.1|//5.00E-18//expressed protein [Arabidopsis thaliana] >gi|20197011|gb|AAM14873.1| expressed protein [Arabidopsis thaliana] >gi|50253564|gb|AAT71984.1| At2g19160 [Arabidopsis thaliana]	Unigene6871_All//7.00E-18//AT5G11970| unknown protein	Unigene6871_All//0.00E+00//DW501795				nr -
Unigene68715_All	200	0.00	3.55	1.33	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.32E-04	Up	1.04E+01	7.97E-02		null	null		null	null		null	null		null	null									
Unigene68717_All	200	0.26	1.52	3.46	0.75	1.21	0.45	5.29	6.69	0.40	2.54E+00	1.51E-01		3.73E+00	3.99E-03		6.90E-01	7.32E-01		-7.26E-01	7.14E-01		3.40E-01	5.46E-01		-3.73E+00	6.13E-06	Down								
Unigene6872_All	680	85.94	22.35	228.97	27.76	15.14	7.37	0.37	0.92	0.00	-1.94E+00	5.46E-115	Down	1.41E+00	1.36E-188	Up	-8.75E-01	9.90E-14		-1.91E+00	7.30E-40	Down	1.31E+00	1.26E-01		-8.54E+00	3.03E-02									
Unigene68721_All	200	0.26	4.31	0.00	0.00	0.00	0.00	0.21	0.42	0.20	4.04E+00	4.20E-04	Up	-8.03E+00	6.17E-01		null	null		null	null		9.84E-01	7.29E-01		-8.58E-02	9.68E-01		Unigene68721_All//gi|3080388|emb|CAA18708.1|//6.00E-19//myb-related protein [Arabidopsis thaliana] >gi|3402763|emb|CAA20209.1| myb-related protein M4 [Arabidopsis thaliana] >gi|7268941|emb|CAB81251.1| myb-related protein M4 [Arabidopsis thaliana]	Unigene68721_All//3.00E-20//AT4G21440| ATMYB102 (ARABIDOPSIS MYB-LIKE 102); DNA binding / transcription factor	Unigene68721_All//2.00E-10//DR455595	MYB		GO:0001071//GO:0003676//GO:0006351//GO:0006970//GO:0009725//GO:0010468//GO:0043231	nr +
Unigene68727_All	200	10.73	7.60	10.12	10.96	11.02	9.71	106.76	40.54	45.02	-4.97E-01	2.58E-01		-8.42E-02	8.50E-01		7.90E-03	9.98E-01		-1.75E-01	6.88E-01		-1.40E+00	1.42E-32	Down	-1.25E+00	2.89E-28	Down	Unigene68727_All//gi|164521173|gb|ABV60448.1|//2.00E-16//ribosomal protein S25 [Adonis aestivalis var. palaestina]	Unigene68727_All//1.00E-17//AT4G39200| 40S ribosomal protein S25 (RPS25E)	Unigene68727_All//3.00E-65//ES824085		ko03010|Ribosome	GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0031981	nr -
Unigene68736_All	200	0.00	3.55	1.60	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.32E-04	Up	1.06E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene68736_All//gi|297840021|ref|XP_002887892.1|//8.00E-06//hypothetical protein ARALYDRAFT_474913 [Arabidopsis lyrata subsp. lyrata] >gi|297333733|gb|EFH64151.1| hypothetical protein ARALYDRAFT_474913 [Arabidopsis lyrata subsp. lyrata]						nr -
Unigene68739_All	200	0.00	3.55	0.53	0.50	0.52	0.68	1.90	1.04	0.20	1.18E+01	3.32E-04	Up	9.06E+00	3.94E-01		5.23E-02	9.65E-01		4.44E-01	8.60E-01		-8.65E-01	4.41E-01		-3.26E+00	2.22E-02									
Unigene68744_All	200	45.26	29.13	33.81	135.49	121.73	133.01	199.77	128.10	99.80	-6.35E-01	8.74E-04		-4.21E-01	3.88E-02		-1.55E-01	1.73E-01		-2.67E-02	8.38E-01		-6.41E-01	4.30E-17		-1.00E+00	6.85E-37	Down	Unigene68744_All//gi|151347486|gb|ABS01352.1|//3.00E-31//methionine synthase [Carica papaya]	Unigene68744_All//1.00E-31//AT3G03780| AtMS2; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase	Unigene68744_All//2.00E-109//TC141933		ko00270|Cysteine and methionine metabolism	GO:0000097//GO:0005576//GO:0006970//GO:0008172//GO:0009526//GO:0010038//GO:0016020//GO:0046914	nr +
Unigene6875_All	501	0.00	0.20	0.00	7.95	5.36	3.43	5.74	2.34	9.14	7.66E+00	3.82E-01		null	null		-5.69E-01	5.46E-02		-1.22E+00	7.24E-05	Down	-1.30E+00	1.31E-04	Down	6.72E-01	5.85E-03				Unigene6875_All//0.00E+00//DW512440				
Unigene6876_All	1796	0.44	1.35	1.04	42.71	34.47	17.73	0.57	0.09	0.00	1.63E+00	1.87E-04	Up	1.25E+00	1.41E-02		-3.09E-01	1.40E-08		-1.27E+00	3.63E-88	Down	-2.60E+00	3.81E-04	Down	-9.14E+00	1.35E-07	Down	Unigene6876_All//gi|297812427|ref|XP_002874097.1|//1.00E-166//serine carboxypeptidase S28 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319934|gb|EFH50356.1| serine carboxypeptidase S28 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene6876_All//1.00E-166//AT5G22860| serine carboxypeptidase S28 family protein	Unigene6876_All//0.00E+00//TC177677				nr -
Unigene68760_All	200	1.31	10.89	4.53	1.74	3.27	2.26	0.42	0.84	0.80	3.06E+00	9.39E-08	Up	1.79E+00	3.07E-02		9.08E-01	3.42E-01		3.73E-01	7.32E-01		9.83E-01	6.32E-01		9.14E-01	6.23E-01				Unigene68760_All//1.00E-08//DW239565				
Unigene6878_All	331	120.45	58.02	87.36	152.00	121.20	145.45	68.85	39.90	46.22	-1.05E+00	8.49E-32	Down	-4.63E-01	9.13E-08		-3.27E-01	2.12E-06		-6.36E-02	5.01E-01		-7.87E-01	4.09E-14		-5.75E-01	9.51E-09		Unigene6878_All//gi|145208313|gb|ABF38063.1|//3.00E-25//acyl carrier protein [Jatropha curcas] >gi|257187683|gb|ACV49879.1| acyl carrier protein [Jatropha curcas]	Unigene6878_All//2.00E-24//AT1G65290| mtACP2 (mitochondrial acyl carrier protein 2); acyl carrier/ metal ion binding	Unigene6878_All//2.00E-175//gi|109881668|gb|DW510638.1|DW510638		ko00190|Oxidative phosphorylation		nr +
Unigene68782_All	201	0.00	36.55	15.63	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	5.33E-42	Up	1.39E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene68782_All//sp|Q00571|CTRB1_LITVA//1.00E-05//Chymotrypsin BI OS=Litopenaeus vannamei PE=1 SV=1						swissprot -
Unigene68783_All	201	0.00	3.28	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	6.23E-04	Up	9.63E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene68783_All//sp|Q9EPL8|IPO7_MOUSE//4.00E-17//Importin-7 OS=Mus musculus GN=Ipo7 PE=1 SV=2						swissprot -
Unigene6879_All	414	0.38	3.92	1.41	0.48	3.83	1.96	11.13	25.24	22.52	3.37E+00	2.12E-06	Up	1.90E+00	8.47E-02		2.99E+00	4.00E-06	Up	2.03E+00	2.17E-02		1.18E+00	9.22E-13	Up	1.02E+00	1.96E-09	Up	Unigene6879_All//gi|15238685|ref|NP_200137.1|//7.00E-10//AGP22 (ARABINOGALACTAN PROTEIN 22) [Arabidopsis thaliana] >gi|75171157|sp|Q9FK16.1|AGP22_ARATH RecName: Full=Arabinogalactan peptide 22; Short=AG-peptide 22; Flags: Precursor >gi|38566508|gb|AAR24144.1| At5g53250 [Arabidopsis thaliana] >gi|40823626|gb|AAR92294.1| At5g53250 [Arabidopsis thaliana]		Unigene6879_All//1.00E-137//TC170225				nr +

Unigene6880_All	523	8.10	3.97	3.36	2.38	6.58	2.68	0.00	0.00	0.15	-1.03E+00	5.64E-04	Down	-1.27E+00	6.10E-05	Down	1.47E+00	1.08E-05	Up	1.69E-01	7.70E-01		null	null		7.25E+00	4.02E-01				Unigene6880_All//6.00E-07//ES818371			
Unigene68800_All	201	29.15	55.71	22.52	51.55	40.77	57.97	190.58	299.02	75.12	9.34E-01	6.87E-08		-3.73E-01	1.55E-01		-3.38E-01	5.64E-02		1.69E-01	3.95E-01		6.50E-01	7.24E-26		-1.34E+00	4.16E-56	Down	Unigene68800_All//gi|288311314|gb|ADC45396.1|//8.00E-33//HSP90-2 [Glycine max]	Unigene68800_All//2.00E-22//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene6880_All//2.00E-78//EY481961		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr +
Unigene68803_All	201	0.00	40.33	13.51	0.00	0.00	0.00	0.00	0.00	0.00	1.53E+01	2.24E-46	Up	1.37E+01	5.42E-15	Up	null	null		null	null		null	null		null	null		Unigene68803_All//sp|Q24388|LSP2_DROME//1.00E-20//Larval serum protein 2 OS=Drosophila melanogaster GN=Lsp2 PE=1 SV=2						swissprot -
Unigene6881_All	530	3.36	3.25	5.53	0.94	0.26	1.36	0.56	4.42	1.05	-4.63E-02	9.34E-01		7.19E-01	5.98E-02		-1.85E+00	8.43E-02		5.37E-01	5.60E-01		2.98E+00	7.00E-10	Up	9.14E-01	2.89E-01		Unigene6881_All//gi|212717129|gb|ACJ37406.1|//7.00E-10//stress-induced receptor-like kinase [Glycine max]	Unigene6881_All//7.00E-08//AT1G67025| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase (TAIR:AT1G18390.1); Has 101 Blast hits to 88 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 101; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene6881_All//2.00E-56//TC150336				nr -
Unigene68811_All	201	0.00	3.78	1.06	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.76E-04	Up	1.00E+01	1.40E-01		null	null		null	null		null	null		null	null		Unigene68811_All//gi|224056825|ref|XP_002299042.1|//7.00E-31//tubulin, beta chain [Populus trichocarpa]>gi|222846300|gb|EEE83847.1|tubulin, beta chain [Populus trichocarpa]	Unigene68811_All//2.00E-31//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene68811_All//4.00E-46//TC166231		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr -
Unigene68815_All	201	0.00	7.06	2.12	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	4.05E-08	Up	1.10E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene68815_All//gi|301100710|ref|XP_002899444.1|//3.00E-15//2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [Phytophthora infestans T30-4]>gi|262103752|gb|EEY61804.1| 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase [Phytophthora infestans T30-4]	Unigene68815_All//5.00E-07//AT1G22170| phosphoglycerate/bisphosphoglycerate mutase family protein			ko00010|Glycolysis / Gluconeogenesis	GO:0004619//GO:0006096//GO:0006098//GO:0019900//GO:0043231//GO:0004444	nr +
Unigene68817_All	201	0.00	4.29	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	4.93E-05	Up	8.05E+00	6.30E-01		null	null		null	null		null	null		null	null								
Unigene6882_All	622	2.27	7.01	7.45	1.04	2.44	17.72	0.07	0.34	0.06	1.63E+00	2.54E-07	Up	1.71E+00	6.21E-08	Up	1.23E+00	2.48E-02		4.09E+00	3.94E-50	Up	2.30E+00	2.40E-01		-8.75E-02	9.68E-01		Unigene6882_All//gi|44681328|gb|AAS47604.1|//2.00E-36//At4g15670 [Arabidopsis thaliana]>gi|45773840|gb|AAS76724.1|At4g15670 [Arabidopsis thaliana]	Unigene6882_All//4.00E-35//AT4G15670| glutaredoxin family protein	Unigene6882_All//8.00E-84//gi|109866735|gb|DW495711.1|DW495711				nr -
Unigene6883_All	676	0.08	0.15	0.08	1.69	1.88	1.27	4.32	0.99	2.65	9.54E-01	7.24E-01		2.59E-02	9.92E-01		1.53E-01	8.22E-01		-4.17E-01	5.42E-01		-2.13E+00	1.47E-08	Down	-7.03E-01	2.54E-02		Unigene6883_All//gi|42566850|ref|NP_193292.3|//2.00E-61//MAA3 (MAGATAMA 3) [Arabidopsis thaliana]>gi|209574484|gb|ACI63222.1| MAA3 [Arabidopsis thaliana]	Unigene6883_All//6.00E-63//AT4G15570| MAA3 (MAGATAMA 3)					nr -
Unigene68844_All	201	18.48	20.42	29.14	57.25	47.11	57.75	20.61	28.07	46.58	1.44E-01	6.27E-01		6.57E-01	1.01E-02		-2.81E-01	1.02E-01		1.25E-02	9.58E-01		4.46E-01	5.09E-02		1.18E+00	9.54E-12	Up			Unigene68844_All//7.00E-20//TC146585				
Unigene68868_All	200	0.00	6.59	0.27	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.49E-07	Up	8.06E+00	6.30E-01		null	null		null	null		null	null		null	null		Unigene68868_All//gi|301101527|ref|XP_002899852.1|//1.00E-07//glucanase inhibitor protein 3 [Phytophthora infestans T30-4]>gi|168259046|gb|ACA23211.1|glucanase inhibitor protein 3 [Phytophthora infestans]>gi|262102854|gb|EEY60906.1|glucanase inhibitor protein 3 [Phytophthora infestans T30-4]					GO:0008233	nr -
Unigene6887_All	488	1.93	0.62	0.00	2.55	1.76	0.93	4.07	1.97	1.22	-1.63E+00	3.13E-02		-1.09E+01	3.34E-05	Down	-5.33E-01	3.86E-01		-1.46E+00	1.95E-02		-1.05E+00	1.11E-02		-1.73E+00	5.14E-05	Down	Unigene6887_All//gi|229609827|gb|ACQ83529.1|//3.00E-46//CBL-interacting protein kinase 13 [Vitis vinifera]	Unigene6887_All//3.00E-30//AT5G58350| SIP1 (SOS3-INTERACTING PROTEIN 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene6887_All//2.00E-40//TC143167				nr -
Unigene68895_All	202	0.00	3.26	0.00	0.25	0.00	0.00	0.21	0.41	0.59	1.17E+01	6.23E-04	Up	null	null		-7.95E+00	5.48E-01		-7.95E+00	6.25E-01		9.83E-01	7.29E-01		1.50E+00	5.57E-01				Unigene68895_All//7.00E-103//gi|78343013|gb|DT563287.1|DT563287				
Unigene6890_All	903	2.03	1.01	4.01	2.21	1.94	6.25	0.47	0.09	0.04	-1.01E+00	3.73E-02		9.84E-01	3.72E-03		-1.82E-01	7.16E-01		1.50E+00	9.79E-09	Up	-2.34E+00	5.46E-02		-3.41E+00	1.24E-02		Unigene6890_All//gi|292668955|gb|ADE41132.1|//9.00E-74//AP2 domain class transcription factor [Malus x domestica]	Unigene6890_All//8.00E-51//AT5G11590| TINY2 (TINY2); DNA binding / transcription factor	Unigene6890_All//0.00E+00//gi|164364867|gb|EX167526.1|EX167526	AP2-EREBP			nr +
Unigene6891_All	1007	1.25	0.81	1.06	10.39	7.15	3.45	0.08	0.46	0.12	-6.31E-01	2.93E-01		-2.38E-01	6.85E-01		-5.40E-01	1.08E-03		-1.59E+00	2.65E-17	Down	2.44E+00	3.74E-02		4.99E-01	8.06E-01		Unigene6891_All//gi|163717541|gb|AB914073 1.1|//4.00E-89//FERONIA receptor-like kinase [Citrus trifoliata]	Unigene6891_All//2.00E-85//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene6891_All//0.00E+00//gi|73859174|gb|DT461913.1|DT461913		ko04626|Plant-pathogen interaction		nr -
Unigene68913_All	202	0.00	5.27	2.37	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	3.80E-06	Up	1.12E+01	7.46E-03		null	null		null	null		null	null		null	null								
Unigene68917_All	202	0.00	4.01	1.32	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	9.35E-05	Up	1.04E+01	7.97E-02		null	null		null	null		null	null		null	null								ESTscan -
Unigene68920_All	202	0.00	5.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.24E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene68920_All//sp|Q8C129|LCAP_MOUSE//4.00E-06//Leucyl-cystinyl aminopeptidase OS=Mus musculus GN=Lnpep PE=1 SV=1						swissprot -
Unigene68925_All	202	0.00	4.77	2.37	0.25	2.56	0.67	0.63	1.03	1.97	1.22E+01	1.38E-05	Up	1.12E+01	7.46E-03		3.37E+00	1.82E-02		1.44E+00	6.37E-01		7.20E-01	6.31E-01		1.65E+00	1.40E-01				Unigene68925_All//4.00E-24//CO120764				
Unigene6893_All	634	0.33	0.48	0.00	0.55	1.58	0.43	1.60	2.57	8.11	5.39E-01	6.71E-01		1.52E+00	3.74E-02		-3.64E-01	7.55E-01		-3.64E-01	7.55E-01		6.84E-01	1.42E-01		2.34E+00	1.39E-16	Up			Unigene6893_All//8.00E-07//ES815006				
Unigene68937_All	203	0.00	3.49	0.00	0.00	0.00	0.00	0.00	1.65	0.20	1.18E+01	3.32E-04	Up	null	null		null	null		null	null		1.07E+01	1.27E-02		7.62E+00	6.39E-01								
Unigene6894_All	515	5.28	13.77	5.38	7.54	5.01	4.91	16.01	76.04	43.40	1.38E+00	3.45E-09	Up	2.54E-02	9.66E-01		-5.89E-01	4.87E-02		-6.19E-01	4.72E-02		2.25E+00	2.25E-113	Up	1.44E+00	2.63E-36	Up			Unigene6894_All//3.00E-104//gi|164364535|gb|ES838257.1|ES838257				
Unigene6895_All	714	0.00	0.85	0.90	3.14	1.83	3.10	4.15	2.69	1.00	9.73E+00	1.16E-03		9.81E+00	1.16E-03		-7.77E-01	5.80E-02		-1.86E-02	9.56E-01		-6.22E-01	5.66E-02		-2.05E+00	1.31E-08	Down	Unigene6895_All//gi|224058056|ref|XP_002299441.1|//7.00E-46//f-box family protein [Populus trichocarpa]>gi|222846699|gb|EEE84246.1| f-box family protein [Populus trichocarpa]	Unigene6895_All//9.00E-32//AT3G61850| DAG1 (dof affecting germination 1); DNA binding / transcription factor	Unigene6895_All//0.00E+00//TC155656	C2C2-Dof			nr +
Unigene68958_All	203	0.00	2.00	3.67	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.35E-02		1.18E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene68958_All//gi|33326375|gb|AAQ08597.1|//4.00E-23//heat shock protein [Hevea brasiliensis]	Unigene68958_All//5.00E-23//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr +
Unigene6896_All	354	1.03	2.15	3.61	1.69	0.78	1.40	0.60	0.59	3.38	1.05E+00	2.05E-01		1.80E+00	7.48E-03		-1.12E+00	2.26E-01		-2.67E-01	7.57E-01		-1.68E-02	1.02E+00		2.50E+00	1.03E-04	Up			Unigene6896_All//3.00E-11//DW496806				
Unigene6897_All	358	1.75	3.82	1.93	3.34	2.12	1.89	5.67	2.92	0.33	1.12E+00	5.30E-02		1.41E-01	8.60E-01		-6.58E-01	2.90E-01		-8.20E-01	1.99E-01		-9.58E-01	1.83E-02		-4.09E+00	1.58E-11	Down			Unigene6897_All//4.00E-07//DW486618				
Unigene68970_All	203	6.96	7.74	9.44	35.09	33.93	17.13	52.69	33.97	28.06	1.53E-01	7.58E-01		4.40E-01	3.86E-01		-4.87E-02	8.34E-01		-1.03E+00	1.87E-06	Down	-6.33E-01	4.37E-05		-9.09E-01	4.26E-09				Unigene68970_All//1.00E-61//TC135390				
Unigene68975_All	203	2.58	4.74	0.00	0.25	1.87	1.33	2.08	8.03	5.30	8.80E-01	2.13E-01		-1.13E+01	4.73E-03		2.93E+00	8.16E-02		2.44E+00	2.22E-01		1.95E+00	1.26E-04	Up	1.35E+00	2.20E-02								
Unigene6898_All	475	4.41	6.83	14.01	1.68	3.12	2.28	1.16	0.44	0.84	6.32E-01	6.71E-02		1.67E+00	9.46E-11	Up	8.94E-01	1.08E-01		4.44E-01	5.39E-01		-1.29E+00	1.34E-01		-4.64E-01	5.91E-01				Unigene6898_All//2.00E-34//TC173468				
Unigene68988_All	204	0.00	19.13	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	3.24E-22	Up	8.03E+00	6.30E-01		null	null		null	null		null	null		null	null								
Unigene6899_All	585	25.94	73.02	21.39	286.96	273.30	248.59	239.23	298.57	153.16	1.49E+00	6.79E-58	Up	-2.78E-01	7.64E-02		-7.04E-02	1.07E-01		-2.07E-01	6.16E-08		3.20E-01	1.37E-20		-6.43E-01	9.49E-60		Unigene6899_All//gi|38016529|gb|AAR07600.1|//5.00E-63//fiber dTDP-glucose 4-6-dehydratase [Gossypium barbadense]	Unigene6899_All//3.00E-61//AT3G46440| UXS5; UDP-glucuronate decarboxylase/ catalytic	Unigene6899_All//0.00E+00//TC131082		ko00523|Polyketide sugar unit biosynthesis		nr +
Unigene68991_All	204	0.00	3.23	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	6.23E-04	Up	8.03E+00	6.30E-01		null	null		null	null		null	null		null	null		Unigene68991_All//sp|P48810|RB87F_DROME//2.00E-09//Heterogeneous nuclear ribonucleoprotein 87F OS=Drosophila melanogaster GN=Hrb87F PE=1 SV=2						swissprot -
Unigene68992_All	204	12.57	40.98	27.15	0.24	0.84	0.00	0.00	0.00	0.00	1.71E+00	2.97E-14	Up	1.11E+00	3.34E-05	Up	1.79E+00	5.20E-01		-7.93E+00	6.25E-01		null	null		null	null		Unigene68992_All//gi|297737189|emb|CBI26390.3|//2.00E-11//unnamed protein product [Vitis vinifera]		Unigene68992_All//1.00E-104//TC156979			GO:0009987//GO:0016020//GO:0016757	nr +
Unigene69010_All	204	0.00	4.72	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.38E-05	Up	9.61E+00	2.37E-01		null	null		null	null		null	null		null	null								
Unigene69022_All	204	0.00	3.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null								ESTscan +
Unigene69025_All	204	0.00	6.46	4.18	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.49E-07	Up	1.20E+01	9.00E-05	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene69034_All	204	0.00	4.47	0.52	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.61E-05	Up	9.03E+00	3.94E-01		null	null		null	null		null	null		null	null								ESTscan +
Unigene69037_All	204	0.00	4.47	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.61E-05	Up	9.61E+00	2.37E-01		null	null		null	null		null	null		null	null								
Unigene69043_All	204	0.00	4.72	3.65	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.38E-05	Up	1.18E+01	3.26E-04	Up	null	null		null	null		null	null		null	null								
Unigene69049_All	205	221.28	98.62	144.68	355.02	269.60	332.45	76.31	47.50	39.45	-1.17E+00	2.30E-42	Down	-6.13E-01	4.54E-14		-3.97E-01	8.98E-13		-9.48E-02	1.84E-01		-6.84E-01	5.77E-08		-9.52E-01	7.48E-14		Unigene69049_All//gi|102655942|gb|AAY33920.2|//3.00E-10//polyubiquitin [Euphorbia characias]	Unigene69049_All//1.00E-10//AT1G65350| UBQ13; protein binding	Unigene69049_All//2.00E-84//TC145848				nr +
Unigene6905_All	503	159.56	110.10	142.81	113.10	121.86	110.98	72.71	33.32	46.97	-5.35E-01	4.75E-20		-1.60E-01	1.15E-02		1.08E-01	1.54E-01		-2.73E-02	7.50E-01		-1.13E+00	1.24E-39	Down	-6.31E-01	9.53E-16		Unigene6905_All//gi|295687231|gb|ADG27841.1|//1.00E-31//triosephosphate isomerase [Gossypium hirsutum]	Unigene6905_All//1.00E-30//AT3G21170| TIM (TRIOSEPHOSPHATE ISOMERASE); catalytic/ triose-phosphate isomerase	Unigene6905_All//0.00E+00//TC161352		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00562|Inositol phosphate metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene69055_All	205	0.00	4.20	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.93E-05	Up	1.00E+01	1.40E-01		null	null		null	null		null	null		null	null		Unigene69055_All//sp|Q9VFP2|RDX_DROME//2.00E-31//Protein roadkill OS=Drosophila melanogaster GN=rdx PE=1 SV=2						swissprot +
Unigene6906_All	654	0.40	2.63	0.98	5.33	27.54	8.91	0.00	0.00	0.00	2.72E+00	1.19E-05	Up	1.29E+00	1.86E-01		2.37E+00	8.34E-53	Up	7.41E-01	2.40E-03		null	null		null	null				Unigene6906_All//3.00E-49//TC171748				
Unigene6907_All	1071	0.44	0.28	0.00	9.07	5.69	2.78	4.18	0.59	1.34	-6.31E-01	5.53E-01		-8.78E+00	8.61E-03		-6.72E-01	7.66E-05		-1.70E+00	9.36E-18	Down	-2.84E+00	1.55E-17	Down	-1.64E+00	1.37E-09	Down	Unigene6907_All//gi|89001065|gb|ABD59122.1|//7.00E-17//At1g51355 [Arabidopsis thaliana]	Unigene6907_All//6.00E-11//AT3G20898| unknown protein	Unigene6907_All//0.00E+00//TC176066				nr +
Unigene69072_All	205	0.00	3.21	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	1.00E+01	1.40E-01		null	null		null	null		null	null		null	null								
Unigene69082_All	205	0.00	5.44	1.82	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.99E-06	Up	1.08E+01	2.49E-02		null	null		null	null		null	null		null	null								ESTscan -
Unigene6909_All	413	0.76	0.49	3.74	3.98	6.25	4.05	0.92	1.72	1.33	-6.31E-01	6.21E-01		2.30E+00	3.37E-04	Up	6.52E-01	1.02E-01		2.37E-02	9.62E-01		9.01E-01	2.40E-01		5.52E-01	5.27E-01								ESTscan -
Unigene69095_All	205	0.00	4.70	1.30	2.43	0.50	1.54	1.44	0.82	0.58	1.22E+01	1.38E-05	Up	1.03E+01	7.97E-02		-2.27E+00	4.22E-02		-6.56E-01	5.50E-01		-8.24E-01	5.40E-01		-1.31E+00	3.13E-01				Unigene69095_All//7.00E-20//TC156319				
Unigene691_All	2485	14.63	16.43	13.80	26.32	19.69	18.65	24.33	17.63	9.81	1.68E-01	5.98E-02		-8.46E-02	4.15E-01		-4.19E-01	1.12E-12		-4.97E-01	1.77E-15		-4.65E-01	1.35E-14		-1.31E+00	8.78E-85	Down	Unigene691_All//gi|22324809|gb|AAM95646.1|//0.00E+00//WD-repeat protein GbTTG4 [Gossypium hirsutum]	Unigene691_All//0.00E+00//AT1G12910| ATAN11 (ANTHOCYANIN11); nucleotide binding	Unigene691_All//0.00E+00//TC162837			GO:0009648//GO:0009813	nr -
Unigene6910_All	706	1.85	1.08	1.66	0.64	1.17	0.90	8.02	1.78	1.98	-7.83E-01	1.81E-01		-1.59E-01	7.76E-01		8.82E-01	2.92E-01		4.96E-01	6.37E-01		-2.18E+00	2.13E-16	Down	-2.02E+00	1.60E-15	Down			Unigene6910_All//4.00E-15//TC166894				
Unigene69109_All	206	0.00	3.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.35E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene69109_All//sp|Q9VKM1|PIWI_DROME//3.00E-16//Protein piwi OS=Drosophila melanogaster GN=piwi PE=2 SV=1						swissprot -
Unigene6911_All	423	88.56	36.65	94.04	64.65	84.83	40.57	1.00	0.40	0.75	-1.27E+00	3.24E-40	Down	8.65E-02	3.94E-01		3.92E-01	2.66E-06		-6.72E-01	2.60E-11		-1.34E+00	2.24E-01		-4.08E-01	6.54E-01		Unigene6911_All//gi|60099456|dbj|BAD89967.1|//5.00E-70//phototropin [Phaseolus vulgaris]	Unigene6911_All//6.00E-67//AT3G45780| PHOT1 (PHOTOTROPIN 1); FMN binding / blue light photoreceptor/ kinase/ protein binding / protein serine/threonine kinase	Unigene6911_All//0.00E+00//gi|48797826|gb|CO099140.1|CO099140		ko04712|Circadian rhythm - plant		nr +
Unigene6912_All	449	2.33	2.60	1.19	0.89	0.92	1.61	2.07	1.86	5.06	1.55E-01	7.88E-01		-9.75E-01	1.67E-01		5.22E-02	9.89E-01		8.59E-01	3.42E-01		-1.54E-01	8.08E-01		1.29E+00	6.77E-04	Up							

Unigene69120_All	206	0.00	56.82	22.49	0.00	0.00	0.00	0.00	0.00	0.00	1.58E+01	3.96E-67	Up	1.45E+01	9.74E-26	Up	null	null		null	null		null	null		null	null		Unigene69120_All//gi|302128114|dbj|BAJ13478.1|//2.00E-22//actin 1 [Guillardia theta]	Unigene69120_All//3.00E-23//AT3G18780| ACT2 (ACTIN 2); structural constituent of cytoskeleton	Unigene69120_All//9.00E-10//gi|31406833|gb|CD485868.1|CD485868		ko04145|Phagosome	GO:0000267//GO:0000904//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0006970//GO:0007015//GO:0008015//GO:0008092//GO:0009536//GO:0009639//GO:0009642//GO:0009725//GO:0009913//GO:0012501//GO:0016020//GO:0017111//GO:0030017//GO:0030239//GO:0032432//GO:0032559//GO:0046914//GO:0048588//GO:0048747//GO:0051707//GO:0060415	nr +
Unigene69125_All	206	0.00	90.27	62.81	0.00	0.17	0.44	0.00	0.00	0.19	1.65E+01	6.06E-107	Up	1.59E+01	7.85E-73	Up	7.39E+00	8.21E-01		8.78E+00	4.72E-01		null	null		7.60E+00	6.39E-01		Unigene69125_All//gi|22550341|ref|NP_689390.1|//6.00E-11//NADH dehydrogenase subunit 3 [Chaetosphaeridium globosum] >gi|22417007|gb|AAM96606.1|AF49427 9_11 NADH dehydrogenase subunit 3 [Chaetosphaeridium globosum]	Unigene69125_All//2.00E-07//ATMG00990| NADH dehydrogenase subunit 3				ko00190|Oxidative phosphorylation	GO:0008152//GO:0016020	nr +
Unigene69138_All	206	0.00	7.38	1.03	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.10E-08	Up	1.00E+01	1.40E-01		null	null		null	null		null	null		null	null		Unigene69138_All//gi|299115210|emb|CBN74041.1|//5.00E-07//Importin-7 (Imp7) (Ran-binding protein 7) (RanBP7) [Ectocarpus siliculosus]	Unigene69138_All//3.00E-07//AT3G59020| binding / protein transporter					GO:0044424	nr +
Unigene6914_All	622	1.26	0.49	0.86	0.96	1.44	0.87	2.85	0.67	1.54	-1.37E+00	9.59E-02		-5.60E-01	4.96E-01		5.83E-01	4.72E-01		-1.41E-01	8.79E-01		-2.09E+00	2.21E-05	Down	-8.93E-01	3.36E-02		Unigene6914_All//gi|9615726|gb|AAT67045.1|//5.00E-86//DNA mismatch repair protein [Petunia x hybrida]	Unigene6914_All//2.00E-84//AT4G02070| MSH6 (MUTS HOMOLOG 6); damaged DNA binding				ko03430|Mismatch repair		nr -
Unigene69146_All	206	177.28	66.66	76.51	281.47	191.23	336.75	180.20	71.42	75.23	-1.41E+00	7.38E-46	Down	-1.21E+00	4.78E-35	Down	-5.58E-01	7.77E-19		2.59E-01	2.87E-05		-1.34E+00	2.24E-52	Down	-1.26E+00	2.32E-49	Down	Unigene69146_All//gi|192913018|gb|ACF06617.1|//2.00E-31//40S ribosomal protein S8 [Elaeis guineensis]	Unigene69146_All//4.00E-30//AT5G20290| 40S ribosomal protein S8 (RPS8A)	Unigene69146_All//5.00E-113//TC168894		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr -
Unigene69149_All	206	0.00	4.18	1.55	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.93E-05	Up	1.06E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene69149_All//gi|297816388|ref|XP_002876077.1|//3.00E-06//multicatalytic endopeptidase [Arabidopsis lyrata subsp. lyrata] >gi|297321915|gb|EFH52336.1| multicatalytic endopeptidase [Arabidopsis lyrata subsp. lyrata]	Unigene69149_All//2.00E-07//AT5G66140| PAD2 (PROTEASOME ALPHA SUBUNIT D 2); endopeptidase/ peptidase/ threonine-type endopeptidase				ko03050|Proteasome	GO:0004175//GO:0005488//GO:0005839//GO:0005840//GO:0009536//GO:0015630//GO:0016020//GO:0017111//GO:0019941//GO:0042435//GO:0042742	nr +
Unigene6916_All	531	5.03	2.00	1.91	3.28	3.24	4.76	36.23	44.08	40.44	-1.33E+00	8.72E-04	Down	-1.40E+00	8.28E-04	Down	-1.81E-02	9.58E-01		5.37E-01	2.02E-01		2.83E-01	6.18E-03		1.59E-01	1.59E-01		Unigene6916_All//gi|183239022|gb|AC60969.1|//1.00E-86//phytochrome A [Vitis riparia]	Unigene6916_All//6.00E-82//AT1G09570| PHYA (PHYTOCHROME A); G-protein coupled photoreceptor/ protein histidine kinase/ red or far-red light photoreceptor/ signal transducer	Unigene6916_All//1.00E-140//ES822585		ko04712|Circadian rhythm - plant		nr -
Unigene69161_All	207	0.00	4.41	1.03	0.24	0.17	0.22	0.20	0.00	0.00	1.21E+01	2.61E-05	Up	1.00E+01	1.40E-01		-5.32E-01	8.21E-01		-1.41E-01	9.49E-01		-7.67E+00	6.48E-01		-7.67E+00	6.05E-01		Unigene69161_All//gi|160897297|ref|YP_001562879.1|//3.00E-10//2Fe-2S iron-sulfur cluster binding domain-containing protein [Delftia acidovorans SPH-1] >gi|160362881|gb|ABX34494.1| (2Fe-2S)-binding domain protein [Delftia acidovorans SPH-1]					GO:0003824//GO:0008152//GO:0043169//GO:0051536	nr +
Unigene69165_All	207	0.00	3.43	0.77	1.44	0.50	0.87	0.61	0.40	0.19	1.17E+01	3.32E-04	Up	9.59E+00	2.37E-01		-1.53E+00	2.98E-01		-7.26E-01	6.38E-01		-6.02E-01	7.65E-01		-1.67E+00	4.76E-01				Unigene69165_All//2.00E-07//TC148917				
Unigene6917_All	832	1.07	3.84	2.11	0.78	3.10	2.23	0.51	0.55	0.38	1.84E+00	1.78E-06	Up	9.82E-01	5.82E-02		2.00E+00	2.09E-06	Up	1.52E+00	2.47E-03		1.21E-01	9.07E-01		-4.08E-01	6.54E-01								
Unigene69172_All	207	0.00	3.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null								ESTscan +
Unigene69174_All	207	0.00	5.14	1.29	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.80E-06	Up	1.03E+01	7.97E-02		null	null		null	null		null	null		null	null									
Unigene69183_All	207	73.55	37.94	36.01	121.29	102.97	64.36	322.11	136.49	165.32	-9.55E-01	7.66E-11		-1.03E+00	1.24E-11	Down	-2.36E-01	3.09E-02		-9.14E-01	2.49E-17		-1.24E+00	3.00E-83	Down	-9.62E-01	4.10E-57				Unigene69183_All//2.00E-78//TC141643				
Unigene69185_All	207	0.00	3.92	1.03	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.33E-05	Up	1.00E+01	1.40E-01		null	null		null	null		null	null		null	null									
Unigene69186_All	207	0.76	3.18	1.54	0.48	0.67	4.80	0.41	0.40	0.58	2.07E+00	3.92E-02		1.03E+00	4.71E-01		4.67E-01	8.75E-01		3.32E+00	3.47E-04	Up	-1.67E-02	1.01E+00		4.99E-01	8.06E-01				Unigene69186_All//6.00E-08//TC149795				ESTscan -
Unigene69188_All	207	0.00	3.67	2.32	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	1.12E+01	7.46E-03		null	null		null	null		null	null		null	null		Unigene69188_All//gi|145332797|ref|NP_001078264.1|//3.00E-09//SRp34a (Ser/Arg-rich protein 34a); RNA binding / nucleic acid binding / nucleotide binding [Arabidopsis thaliana]					ko03040|Spliceosome	GO:0003676//GO:0031981	nr +
Unigene6919_All	457	2.52	26.50	2.10	8.83	3.01	9.19	57.36	148.89	64.42	3.40E+00	1.33E-44	Up	-2.64E-01	6.64E-01		-1.55E+00	1.27E-07	Down	5.79E-02	8.72E-01		1.38E+00	1.12E-99	Up	1.68E-01	7.06E-02		Unigene6919_All//gi|62241063|dbj|BAD93688.1|//8.00E-18//glucosyltransferase [Nicotiana tabacum]	Unigene6919_All//3.00E-08//AT2G36750| UGT73C1 (UDP-GLUCOSYL TRANSFERASE 73C1); UDP-glucosyltransferase/ UDP-glycosyltransferase/ cis-zeatin O-beta-D-glucosyltransferase/ trans-zeatin O-beta-D-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene6919_All//5.00E-155//TC137499		ko00908|Zeatin biosynthesis		nr +
Unigene692_All	1444	0.91	0.84	1.03	1.14	0.91	0.72	2.49	1.74	0.69	-1.05E-01	8.46E-01		1.89E-01	7.21E-01		-3.29E-01	5.61E-01		-6.62E-01	2.13E-01		-5.19E-01	7.83E-02		-1.85E+00	4.08E-09	Down	Unigene692_All//gi|22324809|gb|AAM95646.1|//0.00E+00//WD-repeat protein GhTTG4 [Gossypium hirsutum]	Unigene692_All//0.00E+00//AT1G12910| ATAN11 (ANTHOCYANIN11); nucleotide binding	Unigene692_All//0.00E+00//TC162837			GO:0009648//GO:0009813	nr +
Unigene6920_All	530	1.09	6.88	0.60	2.07	4.22	3.41	3.19	4.10	3.61	2.66E+00	5.14E-11	Up	-8.49E-01	3.97E-01		1.03E+00	1.52E-02		7.21E-01	1.51E-01		3.62E-01	3.92E-01		1.77E-01	6.67E-01				Unigene6920_All//1.00E-35//AW186813				
Unigene69201_All	207	0.00	3.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene69201_All//gi|295149508|gb|ADF81075.1|//1.00E-13//PtsH [Corallina officinalis]	Unigene69201_All//1.00E-12//AT5G42270| VAR1 (VARIEGATED 1); ATP-dependent peptidase/ ATPase/ metallopeptidase				GO:0004175//GO:0016020//GO:0016462//GO:0019538//GO:0032559//GO:0043231	nr +
Unigene69204_All	207	0.00	4.90	1.54	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.24E-06	Up	1.06E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene69204_All//sp|Q9V3P6|PSMD1_DROME//8.00E-26//26S proteasome non-ATPase regulatory subunit 1 OS=Drosophila melanogaster GN=Rpn2 PE=1 SV=1							swissprot -
Unigene69229_All	208	0.00	3.65	1.28	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	1.03E+01	7.97E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene69231_All	208	5.28	1.71	0.00	2.87	2.65	2.82	0.20	0.40	0.00	-1.63E+00	1.81E-02		-1.24E+01	4.93E-06	Down	-1.18E-01	8.75E-01		-2.59E-02	9.64E-01		9.83E-01	7.29E-01		-7.67E+00	6.05E-01									ESTscan -
Unigene69233_All	208	0.00	5.12	0.51	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.80E-06	Up	9.00E+00	3.94E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene6924_All	1509	0.14	0.00	0.28	1.19	1.26	13.29	0.08	0.17	0.00	-7.12E+00	1.21E-01		1.03E+00	3.96E-01		7.88E-02	8.89E-01		3.48E+00	2.08E-80	Up	9.83E-01	5.17E-01		-6.39E+00	1.99E-01		Unigene6924_All//gi|30027167|gb|AAP06759.1|//1.00E-116//auxin response factor-like protein [Mangifera indica]	Unigene6924_All//3.00E-116//AT5G62000| ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Unigene6924_All//9.00E-21//ES830051	ARF			nr -
Unigene6925_All	576	93.29	78.03	80.80	119.09	145.63	112.59	46.10	48.76	16.12	-2.58E-01	4.02E-04		-2.07E-01	7.44E-03		2.90E-01	3.20E-08		-8.09E-02	2.89E-01		8.11E-02	4.66E-01		-1.52E+00	7.45E-47	Down			Unigene6925_All//3.00E-114//gi|48822920|gb|CO124233.1|CO124233				
Unigene69254_All	208	0.00	4.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene69254_All//gi|301090036|ref|XP_002895253.1|//5.00E-18//DNA-directed RNA polymerase II largest subunit [Phytophthora infestans T30-4] >gi|262101000|gb|EEY59052.1| DNA-directed RNA polymerase II largest subunit [Phytophthora infestans T30-4]	Unigene69254_All//2.00E-17//AT4G35800| NRP81 (RNA POLYMERASE II LARGE SUBUNIT); DNA binding / DNA-directed RNA polymerase			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0005488//GO:0006350//GO:0009536//GO:0016591//GO:0034062	nr -
Unigene69260_All	208	0.00	3.17	2.30	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	1.12E+01	7.46E-03		null	null		null	null		null	null		null	null									
Unigene69265_All	209	0.00	3.64	2.55	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	1.13E+01	4.02E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene6927_All	359	3.64	2.40	6.67	5.00	7.48	3.52	7.54	4.19	1.55	-6.03E-01	3.07E-01		8.73E-01	4.32E-02		5.83E-01	1.40E-01		-5.04E-01	3.30E-01		-8.47E-01	1.31E-02		-2.28E+00	5.73E-09	Down			Unigene6927_All//4.00E-07//TC169562				
Unigene69278_All	209	0.00	10.67	2.29	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.09E-12	Up	1.12E+01	7.46E-03		null	null		null	null		null	null		null	null									
Unigene6928_All	659	2.30	5.61	1.70	0.15	1.31	1.92	0.00	0.00	0.24	1.29E+00	1.03E-04	Up	-4.40E-01	4.23E-01		3.11E+00	1.31E-03		3.67E+00	1.38E-05	Up	null	null		7.92E+00	1.39E-01		Unigene6928_All//gi|15227323|ref|NP_181661.1|//2.00E-47//strictosidine synthase family protein [Arabidopsis thaliana] >gi|52627085|gb|AAU84669.1| At2g41290 [Arabidopsis thaliana] >gi|55167922|gb|AAY43793.1| At2g41290 [Arabidopsis thaliana]	Unigene6928_All//1.00E-48//AT2G41290| strictosidine synthase family protein	Unigene6928_All//0.00E+00//EX164109		ko00901|Indole alkaloid biosynthesis		nr +
Unigene69288_All	209	0.00	158.07	152.87	0.00	0.99	0.43	0.20	0.00	0.19	1.73E+01	1.50E-190	Up	1.72E+01	3.23E-181	Up	9.95E+00	1.56E-01		8.76E+00	4.72E-01		-7.66E+00	6.48E-01		-8.59E-02	9.68E-01		Unigene69288_All//gi|125971884|gb|ABN58963.1|//7.00E-20//cytochrome oxidase subunit III [Mesotaenium endlicherianum]	Unigene69288_All//2.00E-10//ATMG00730| Encodes cytochrome c oxidase subunit 3.			ko00190|Oxidative phosphorylation	GO:0016020//GO:0016491//GO:0022904	nr -
Unigene69289_All	209	0.00	3.64	0.25	0.95	0.00	1.08	1.01	0.40	0.19	1.18E+01	1.76E-04	Up	7.99E+00	6.29E-01		-9.90E+00	8.39E-02		1.81E-01	9.34E-01		-1.34E+00	4.29E-01		-2.41E+00	1.95E-01								
Unigene69292_All	209	0.25	0.24	0.51	0.00	0.00	0.00	0.61	1.40	13.72	-4.63E-02	9.83E-01		1.03E+00	7.01E-01		null	null		null	null		1.21E+00	3.92E-01		4.50E+00	1.16E-16	Up	Unigene69292_All//gi|2245023|emb|CAB10443.1|//5.00E-15//RNA helicase [Arabidopsis thaliana] >gi|7268418|emb|CAB78710.1| RNA helicase [Arabidopsis thaliana]	Unigene69292_All//2.00E-16//AT4G16680| RNA helicase, putative	Unigene69292_All//4.00E-49//TC148325		ko03040|Spliceosome	GO:0003006//GO:0003724//GO:0006396//GO:0016441//GO:0032559//GO:0042623//GO:0043231	nr +
Unigene69298_All	209	141.19	35.15	138.86	54.34	42.34	18.37	0.00	0.00	0.19	-2.01E+00	7.63E-61	Down	-2.40E-02	8.36E-01		-3.60E-01	3.00E-02		-1.56E+00	2.42E-18	Down	null	null		7.57E+00	6.39E-01				Unigene69298_All//1.00E-92//DW234427				
Unigene693_All	5256	1.59	3.79	3.11	5.83	4.37	3.27	9.47	1.85	2.80	1.25E+00	4.87E-21	Up	9.66E-01	2.84E-11		-4.16E-01	3.75E-06		-8.36E-01	3.85E-18		-2.35E+00	1.39E-152	Down	-1.76E+00	2.31E-107	Down	Unigene693_All//gi|22324809|gb|AAM95646.1|//0.00E+00//WD-repeat protein GhTTG4 [Gossypium hirsutum]	Unigene693_All//0.00E+00//AT1G12910| ATAN11 (ANTHOCYANIN11); nucleotide binding	Unigene693_All//0.00E+00//TC162837			GO:0009648//GO:0009813	nr -
Unigene69302_All	209	0.00	6.06	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.86E-07	Up	9.99E+00	1.40E-01		null	null		null	null		null	null		null	null									
Unigene69303_All	209	0.25	9.21	1.02	0.48	0.00	0.00	0.20	2.40	0.95	5.20E+00	1.06E-09	Up	2.03E+00	3.61E-01		-8.90E+00	3.10E-01		-8.90E+00	3.95E-01		3.57E+00	6.53E-03		2.24E+00	2.48E-01								
Unigene69304_All	209	0.00	3.39	0.00	0.00	0.16	0.65	1.21	0.40	0.76	1.17E+01	3.32E-04	Up	null	null		7.36E+00	8.21E-01		9.34E+00	3.09E-01		-1.60E+00	3.10E-01		-6.71E-01	6.05E-01				Unigene69304_All//2.00E-07//TC166847				
Unigene69316_All	209	0.00	7.52	0.76	0.24	0.00	0.00	0.00	0.00	0.00	1.29E+01	5.69E-09	Up	9.58E+00	2.37E-01		-7.90E+00	5.48E-01		-7.90E+00	6.25E-01		null	null		null	null		Unigene69316_All//gi|105829424|gb|ABF74693.1|//3.00E-16//At1g52655 [Arabidopsis thaliana]	Unigene69316_All//1.00E-17//AT1G52855| unknown protein	Unigene69316_All//2.00E-97//TC167882				nr -
Unigene6932_All	498	0.00	2.24	0.00	0.90	0.62	1.63	1.02	1.76	5.84	1.11E+01	1.99E-06	Up	null	null		-5.33E-01	5.96E-01		8.59E-01	3.07E-01		7.91E-01	2.41E-01		2.52E+00	1.68E-10	Up			Unigene6932_All//0.00E+00//BF274848				
Unigene6933_All	657	1.27	1.23	2.27	10.92	11.79	9.28	8.49	4.20	2.91	-4.62E-02	9.64E-01		8.33E-01	1.43E-01		1.11E-01	6.56E-01		-2.35E-01	3.45E-01		-1.02E+00	7.97E-06	Down	-1.55E+00	8.39E-11	Down	Unigene6933_All//gi|15227887|ref|NP_179363.1|//8.00E-50//DC1 domain-containing protein [Arabidopsis thaliana] >gi|34146812|gb|AAQ62414.1| At2g17740 [Arabidopsis thaliana]	Unigene6933_All//5.00E-51//AT2G44380| DC1 domain-containing protein					nr -
Unigene69336_All	210	0.00	3.62	0.25	4.98	1.48	1.08	15.91	19.70	21.82	1.18E+01	1.76E-04	Up	7.99E+00	6.29E-01		-1.76E+00	8.43E-03		-2.21E+00	3.25E-03		3.09E-01	2.83E-01		4.56E-01	6.50E-02				Unigene69336_All//2.00E-100//DW498142				
Unigene69340_All	210	0.00	3.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	null	null		null	null		null	null		null	null		null	null								ESTscan +
Unigene69344_All	210	0.00	3.38	0.76	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	9.57E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene69344_All//gi|193875680|gb|ACF24476.1|//3.00E-25//70 kDa heat shock protein [Goniomonas truncata]	Unigene69344_All//3.00E-23//AT1G16030| Hsp70b (heat shock protein 70B); ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0006950//GO:0009536//GO:0016020//GO:0016628//GO:0030312//GO:0032559//GO:0044267	nr +
Unigene6935_All	819	0.00	0.00	0.00	16.60	13.62	12.08	1.70	1.48	0.39	null	null		null	null		-2.86E-01	6.46E-02		-4.59E-01	2.33E-03		-2.03E-01	6.94E-01		-2.13E+00	1.13E-04	Down	Unigene6935_All//gi|270309068|dbj|BAU52974.1|//3.00E-56//G1-like protein [Selaginella moellendorffii]	Unigene6935_All//7.00E-38//AT5G28490| LSH1 (LIGHT-DEPENDENT SHORT HYPOCOTYLS 1)	Unigene6935_All//0.00E+00//DW224350				nr -
Unigene6936_All	888	0.00	0.11	0.00	2.86	2.06	0.71	12.52	15.06	6.55	6.83E+00	3.82E-01		null	null		-4.77E-01	2.34E-01		-2.01E+00	3.48E-06	Down	2.66E-01	6.61E-02		-9.35E-01	7.81E-10		Unigene6936_All//gi|8778315|gb|AAF79324.1|AC002304_17//2.00E-20//F14J16.29 [Arabidopsis thaliana]		Unigene6936_All//3.00E-07//TC148715		ko03040|Spliceosome		nr -
Unigene69365_All	210	0.00	3.62	2.54	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	1.13E+01	4.02E-03		null	null		null	null		null	null		null	null									
Unigene69367_All	210	0.25	4.10	2.79	0.24	0.98	1.08	0.00	0.00	0.00	4.04E+00	4.20E-04	Up	3.49E+00	1.21E-02		2.05E+00	3.94E-01		2.18E+00	3.22E-01		null	null		null	null				Unigene69367_All//2.00E-32//TC178594				

Unigene69369_All	210	0.00	4.58	1.78	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.38E-05	Up	1.08E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene69369_All//gi|301106653|ref|XP_002902409.1|//1.00E-20//medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262098283|gb|EEY56335.1| medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene69369_All//5.00E-11//AT3G45300| IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase			ko00280|Valine, leucine and isoleucine degradation	GO:0003995//GO:0008152//GO:0030554//GO:0043231	nr +
Unigene6937_All	616	0.85	51.82	0.17	1.62	3.13	1.47	2.13	11.53	159.94	5.93E+00	9.79E-166	Up	-2.30E+00	6.75E-02		9.53E-01	4.18E-02		-1.41E-01	8.36E-01		2.44E+00	3.20E-23	Up	6.23E+00	0.00E+00	Up	Unigene6937_All//gi|86155935|gb|ABC86705.1|//1.00E-22//R111 [Coffea arabica]	Unigene6937_All//2.00E-23//AT4G29780| unknown protein	Unigene6937_All//0.00E+00//TC140933				nr +
Unigene69374_All	211	0.00	3.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene69374_All//sp|Q5R9L3|G3BP2_PONAB//2.00E-09//Ras GTPase-activating protein-binding protein 2 OS=Pongo abelii GN=G3BP2 PE=2 SV=1						swissprot +
Unigene69376_All	211	0.00	5.52	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.05E-06	Up	8.98E+00	3.94E-01		null	null		null	null		null	null		null	null										
Unigene6938_All	306	148.58	58.45	77.96	245.49	214.38	246.63	312.13	144.51	122.51	-1.35E+00	5.18E-53	Down	-9.31E-01	1.86E-28		-1.96E-01	7.52E-04		6.70E-03	9.44E-01		-1.11E+00	4.16E-100	Down	-1.35E+00	1.27E-139	Down	Unigene6938_All//gi|195658081|gb|AC048508.1|//6.00E-25//60S ribosomal protein L21 [Zea mays]	Unigene6938_All//3.00E-25//AT1G57860| 60S ribosomal protein L21	Unigene6938_All//2.00E-125//gi|109873770|gb|DW502745.1|DW502745		ko03010|Ribosome		nr -
Unigene69380_All	211	0.00	14.89	3.79	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	7.07E-18	Up	1.19E+01	1.72E-04	Up	null	null		null	null		null	null		null	null										
Unigene69387_All	211	0.00	3.12	0.76	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	9.56E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene69387_All//gi|165874541|gb|ABV68154.1|//2.00E-11//NADH-dependent glutamate synthase [Oryza australiensis]	Unigene69387_All//4.00E-12//AT5G53460| GLT1; glutamate synthase (NADH)			ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0000166//GO:0006536//GO:0040007//GO:0043231//GO:0045181	nr +
Unigene69394_All	211	0.00	3.84	0.25	0.24	0.49	0.00	0.00	0.00	0.00	1.19E+01	9.35E-05	Up	7.98E+00	6.29E-01		1.05E+00	8.06E-01		-7.88E+00	6.25E-01		null	null		null	null										ESTscan +
Unigene69396_All	211	0.00	5.04	0.76	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.80E-06	Up	9.56E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene69396_All//sp|Q3YUZ7|RPOB_SHISS//2.00E-33//DNA-directed RNA polymerase subunit beta OS=Shigella sonnei (strain Ss046) GN=rpoB PE=3 SV=1						swissprot -
Unigene69400_All	211	0.00	3.84	2.52	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.35E-05	Up	1.13E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene69400_All//sp|Q7SX99|FUMH_DANRE//3.00E-06//Fumarate hydratase, mitochondrial OS=Danio rerio GN=fh PE=2 SV=1						swissprot -
Unigene6941_All	682	1.38	1.78	0.86	0.37	0.35	1.32	2.11	3.43	14.78	3.69E+01	5.56E-01		-6.85E-01	3.69E-01		-4.74E-02	9.51E-01		1.86E+00	2.18E-02		7.03E-01	6.01E-02		2.81E+00	7.33E-39	Up	Unigene6941_All//gi|259121419|gb|ACV92029.1|//4.00E-50//WRKY transcription factor 27 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene6941_All//2.00E-32//AT4G23810| WRKY53; DNA binding / protein binding / transcription activator/ transcription factor	Unigene6941_All//0.00E+00//gi|73864118|gb|DT466857.1|DT466857	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene69410_All	212	0.00	6.21	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.49E-07	Up	8.97E+00	3.94E-01		null	null		null	null		null	null		null	null										
Unigene69411_All	212	0.00	3.82	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.35E-05	Up	7.97E+00	6.29E-01		null	null		null	null		null	null		null	null										
Unigene69423_All	212	0.00	4.54	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.38E-05	Up	8.97E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene69423_All//gi|160895818|ref|YP_001561400.1|//2.00E-15//CsbD family protein [Delftia acidovorans SPH-1] >gi|160361402|gb|ABX33015.1| CsbD family protein [Delftia acidovorans SPH-1]						nr +
Unigene6943_All	413	2.79	41.35	55.83	4.10	0.67	0.87	2.76	1.72	0.00	3.89E+00	3.93E-70	Up	4.32E+00	6.80E-100	Up	-2.62E+00	1.81E-06	Down	-2.23E+00	7.57E-05	Down	-6.84E-01	2.37E-01		-1.14E+01	1.64E-08	Down	Unigene6943_All//gi|116311046|emb|CAH67977.1|//1.00E-26//OS1GRa0142102-OS1GRa0101B20.20 [Oryza sativa (indica cultivar-group)]		Unigene6943_All//0.00E+00//gi|109873144|gb|DW502119.1|DW502119				nr -
Unigene69439_All	212	0.00	6.45	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	7.78E-08	Up	9.56E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene69439_All//sp|P98166|VLDLR_RAT//2.00E-09//Very low-density lipoprotein receptor OS=Rattus norvegicus GN=Vldlr PE=2 SV=1						swissprot +
Unigene69445_All	212	0.00	4.78	1.51	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.24E-06	Up	1.06E+01	4.49E-02		null	null		null	null		null	null		null	null										ESTscan +
Unigene69453_All	213	0.00	3.57	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	1.10E+01	1.37E-02		null	null		null	null		null	null		null	null										ESTscan +
Unigene69456_All	213	0.00	3.81	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.35E-05	Up	1.10E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene69456_All//gi|109675118|gb|ABG37021.1|//3.00E-11//aspartic protease [Nicotiana tabacum]	Unigene69456_All//4.00E-09//AT1G62290| aspartyl protease family protein				GO:0004175//GO:0019538	nr +
Unigene69460_All	213	6.39	16.41	12.25	43.03	27.65	21.84	66.70	166.20	64.90	1.36E+00	7.74E-05	Up	9.40E-01	2.21E-02		-6.38E-01	2.94E-04		-9.79E-01	1.85E-07		1.32E+00	6.96E-49	Up	-3.93E-02	7.88E-01				Unigene69460_All//2.00E-72//TC145098					
Unigene69466_All	213	0.00	3.33	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	9.55E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene69466_All//sp|P42003|MAD_DROME//7.00E-38//Protein mothers against dpp OS=Drosophila melanogaster GN=Mad PE=1 SV=1						swissprot +
Unigene69471_All	213	0.00	3.09	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	8.97E+00	3.94E-01		null	null		null	null		null	null		null	null										
Unigene69478_All	213	0.00	3.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene69478_All//sp|P38054|CUSA_ECOLI//2.00E-19//Cation efflux system protein cusA OS=Escherichia coli (strain K12) GN=cusA PE=1 SV=2						swissprot +
Unigene6948_All	562	3.63	0.54	1.14	0.98	0.37	0.88	1.88	0.45	2.84	-2.75E+00	1.06E-06	Down	-1.68E+00	8.93E-04	Down	-1.41E+00	1.53E-01		-1.41E-01	8.85E-01		-2.08E+00	1.78E-03		5.92E-01	1.95E-01										
Unigene69485_All	213	0.00	3.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null										
Unigene69492_All	213	0.00	5.47	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.05E-06	Up	7.97E+00	6.29E-01		null	null		null	null		null	null		null	null		Unigene69492_All//sp|Q8NFU0|FMR1_DROME//5.00E-26//Fragile X mental retardation syndrome-related protein 1 OS=Drosophila melanogaster GN=Fmr1 PE=1 SV=1						swissprot +
Unigene69493_All	213	0.00	3.33	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.32E-04	Up	8.97E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene69493_All//sp|Q96GX5|MASTL_HUMAN//1.00E-07//Microtubule-associated serine/threonine-protein kinase-like OS=Homo sapiens GN=MASTL PE=1 SV=1						swissprot -
Unigene69494_All	213	0.00	3.81	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.35E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene69494_All//gi|114326516|ref|NP_075907.2|//9.00E-21//phosphoglycerate mutase 1 [Mus musculus] >gi|20178035|sp|Q9DBJ1.3|PGAM1_MOUSE RecName: Full=Phosphoglycerate mutase 1; AltName: Full=Phosphoglycerate mutase isozyme B; Short=PGAM-B; AltName: Full=BPG-dependent PGAM 1 >gi|122065830|sp|P25113.4|PGAM1_RAT RecName: Full=Phosphoglycerate mutase 1; AltName: Full=Phosphoglycerate mutase isozyme B; Short=PGAM-B; AltName: Full=BPG-dependent PGAM 1 >gi|112128|pir||JC1132 phosphoglycerate mutase (EC 5.4.2.1) B chain - rat >gi|12805529|gb|AAH02241.1| Phosphoglycerate mutase 1 [Mus musculus] >gi|13542946|gb|AAH05661.1| Phosphoglycerate mutase 1 [Mus musculus] >gi|41350889|gb|AAH65582.1| Pgam1 protein [Rattus norvegicus] >gi|45219759|gb|AAH66844.1| Phosphoglycerate mutase 1 [Mus musculus]	Unigene69494_All//3.00E-09//AT1G78050| PGM (PHOSPHOGLYCERATE/BISPHOSPHOGLYCERATE MUTASE); catalytic/ intramolecular transferase, phosphotransferases			ko00010|Glycolysis / Gluconeogenesis	GO:0004619//GO:0006096//GO:0006098//GO:0006796//GO:0019900//GO:0034016//GO:0043231//GO:0044444	nr -
Unigene69497_All	213	0.00	4.04	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.93E-05	Up	9.97E+00	1.40E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene6950_All	661	0.87	1.69	0.81	1.36	1.93	2.32	3.45	1.83	1.27	9.54E-01	1.40E-01		-1.12E-01	9.07E-01		5.07E-01	4.38E-01		7.76E-01	1.63E-01		-9.14E-01	1.56E-02		-1.45E+00	1.49E-04	Down	Unigene6950_All//gi|224100571|ref|XP_002311928.1|//5.00E-94//aminophospholipid ATPase [Populus trichocarpa] >gi|222851748|gb|EEE89295.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene6950_All//5.00E-83//AT5G04930| ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism					nr +
Unigene69506_All	214	386.54	198.65	157.26	774.91	602.62	838.06	1007.81	418.74	501.71	-9.60E-01	4.75E-56		-1.30E+00	1.04E-87	Down	-3.63E-01	3.56E-24		1.13E-01	4.31E-03		-1.27E+00	1.55E-277	Down	-1.01E+00	6.08E-197	Down	Unigene69506_All//gi|115451089|ref|NP_001049145.1|//6.00E-33//Os03g0177400 [Oryza sativa Japonica Group] >gi|115451091|ref|NP_001049146.1| Os03g0177500 [Oryza sativa Japonica Group] >gi|115451093|ref|NP_001049147.1| Os03g0177900 [Oryza sativa Japonica Group] >gi|115451095|ref|NP_001049148.1| Os03g0178000 [Oryza sativa Japonica Group] >gi|90110018|sp|Q64937.2|EF1A_ORYSJ RecName: Full=Elongation factor 1-alpha; Short=EF-1-alpha >gi|2662341|dbj|BAA23657.1| EF-1 alpha [Oryza sativa] >gi|2662345|dbj|BAA23659.1| EF-1 alpha [Oryza sativa] >gi|2662347|dbj|BAA23660.1| EF-1 alpha [Oryza sativa] >gi|113547616|dbj|BAF11059.1| Os03g0177400 [Oryza sativa Japonica Group] >gi|113547617|dbj|BAF11060.1| Os03g0177500 [Oryza sativa Japonica Group] >gi|113547618|dbj|BAF11061.1| Os03g0177900 [Oryza sativa	Unigene69506_All//2.00E-27//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene69506_All//6.00E-113//TC165550			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr -
Unigene69507_All	214	0.00	3.55	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	1.05E+01	4.49E-02		null	null		null	null		null	null		null	null										
Unigene69510_All	214	42.05	17.05	27.37	94.51	100.25	67.32	69.55	35.16	37.05	-1.30E+00	1.41E-10	Down	-6.20E-01	1.92E-03		8.51E-02	5.69E-01		-4.89E-01	4.05E-05		-9.84E-01	1.70E-13		-9.09E-01	2.68E-12				Unigene69510_All//1.00E-21//gi|54121873|gb|CO497382.1|CO497382					
Unigene69517_All	214	196.57	50.43	34.84	326.82	409.68	320.15	182.36	37.89	52.50	-1.96E+00	4.81E-84	Down	-2.50E+00	2.23E-109	Down	3.26E-01	1.55E-10		-2.97E-02	6.96E-01		-2.27E+00	1.86E-114	Down	-1.80E+00	4.20E-87	Down	Unigene69517_All//gi|134035508|gb|AB047742.1|//2.00E-36//alpha-tubulin [Gossypium hirsutum]	Unigene69517_All//3.00E-37//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene69517_All//2.00E-100//TC154292		ko04145|Phagosome	GO:0006970//GO:0007010//GO:0007017//GO:0009629//GO:0015630//GO:0016020//GO:0017111//GO:0030312//GO:0031981//GO:0032561//GO:0043234//GO:0043623//GO:0044444	nr +
Unigene69518_All	214	0.00	5.21	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.99E-06	Up	1.05E+01	4.49E-02		null	null		null	null		null	null		null	null										ESTscan -

Unigene6952_All	373	27.63	18.20	11.71	26.84	32.04	21.55	119.13	58.27	57.68	-6.02E-01	6.88E-04		-1.24E+00	1.21E-10	Down	2.55E-01	1.46E-01		-3.17E-01	9.69E-02		-1.03E+00	9.49E-42	Down	-1.05E+00	5.97E-44	Down	Unigene6952_All//gi|17367847|sp|Q9XF97.1|RL4_PRUAR//1.00E-18//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32206.1|AF134732_1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene6952_All//1.00E-17//AT5G02870| 60S ribosomal protein L4/L1 (RPL4D)	Unigene6952_All//5.00E-161//TC150974		ko03010|Ribosome		nr -
Unigene69529_All	214	0.00	3.31	1.74	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.31E-04	Up	1.08E+01	2.49E-02		null	null		null	null		null	null		null	null										ESTscan -
Unigene69530_All	214	0.00	4.03	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.93E-05	Up	8.96E+00	3.94E-01		null	null		null	null		null	null		null	null										
Unigene69535_All	215	0.00	0.94	3.47	0.00	0.00	0.00	0.00	0.00	0.00	9.88E+00	1.35E-01		1.18E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene69535_All//gi|300255672|gb|EF139963.1|//3.00E-21//26S proteasome regulatory complex [Volvox carteri f. nagariensis]	Unigene69535_All//6.00E-22//AT2G20580| RPN1A (26S PROTEASOME REGULATORY SUBUNIT S2 1A); binding / enzyme regulator			ko03050|Proteasome	GO:0005838//GO:0007049//GO:0009894//GO:0016020//GO:0019941//GO:0043231	nr +
Unigene69536_All	215	0.00	7.07	0.74	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.10E-08	Up	9.54E+00	2.37E-01		null	null		null	null		null	null		null	null										
Unigene69537_All	215	0.00	3.54	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene69537_All//sp|P30189|TOP1_DROME//3.00E-11//DNA topoisomerase 1 OS=Drosophila melanogaster GN=Top1 PE=1 SV=1							swissprot -
Unigene69545_All	215	0.00	6.60	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	4.05E-08	Up	8.95E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene69545_All//sp|O00151|PDLI1_HUMAN//2.00E-35//PDZ and LIM domain protein 1 OS=Homo sapiens GN=PDLIM1 PE=1 SV=4							swissprot -
Unigene69547_All	215	0.00	4.01	1.73	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.93E-05	Up	1.08E+01	2.49E-02		null	null		null	null		null	null		null	null										
Unigene69549_All	215	0.00	3.06	1.98	0.70	1.28	0.21	2.16	1.36	0.74	1.16E+01	6.23E-04	Up	1.10E+01	1.37E-02		8.82E-01	5.94E-01		-1.73E+00	5.00E-01		-6.69E-01	5.08E-01		-1.55E+00	1.16E-01				Unigene69549_All//4.00E-46//gi|164344830|gb|ES815150.1|ES815150					
Unigene6955_All	790	0.00	0.13	0.13	1.95	0.57	0.34	112.12	299.24	8.37	7.00E+00	3.82E-01		7.07E+00	3.94E-01		-1.79E+00	6.84E-04	Down	-2.51E+00	4.81E-05	Down	1.42E+00	0.00E+00	Up	-3.74E+00	0.00E+00	Down	Unigene6955_All//gi|226510224|ref|NP_001149813.1|//5.00E-33//triacylglycerol lipase [Zea mays] >gi|195634817|gb|ACG36877.1| triacylglycerol lipase [Zea mays]	Unigene6955_All//7.00E-29//AT2G31100| triacylglycerol lipase					nr +
Unigene69555_All	215	0.00	4.95	2.72	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.80E-06	Up	1.14E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene69555_All//gi|301120398|ref|XP_002907926.1|//1.00E-15//aldehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262102957|gb|EEY61009.1| aldehyde dehydrogenase, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene69555_All//1.00E-11//AT1G23800| ALDH2B7; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)			ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0003824//GO:0008152//GO:0043231	nr +
Unigene6956_All	1351	0.62	0.15	0.24	0.15	0.59	0.70	65.60	60.95	25.01	-2.05E+00	1.68E-02		-1.39E+00	9.66E-02		1.99E+00	2.46E-02		2.25E+00	6.12E-03		-1.06E-01	4.99E-02		-1.39E+00	8.29E-136	Down	Unigene6956_All//gi|211906456|gb|ACJ11721.1|//1.00E-125//quinone oxidoreductase [Gossypium hirsutum]	Unigene6956_All//2.00E-108//AT1G23740| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene6956_All//0.00E+00//ES792745		ko00062|Fatty acid elongation in mitochondria		nr +
Unigene69561_All	215	0.00	3.54	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	9.95E+00	1.40E-01		null	null		null	null		null	null		null	null										
Unigene69562_All	215	0.00	3.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null				Unigene69562_All//2.00E-07//ES810920					
Unigene69568_All	216	0.00	3.05	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	7.95E+00	6.29E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene6957_All	449	0.93	0.00	0.00	2.77	2.68	1.41	8.00	1.86	1.77	-9.86E+00	1.04E-02		-9.86E+00	1.55E-02		-4.72E-02	9.29E-01		-9.78E-01	1.14E-01		-2.10E+00	2.96E-10	Down	-2.17E+00	4.89E-11	Down	Unigene6957_All//gi|116309094|emb|CAH66201.1|//2.00E-11//OSIGBa0148D14.7 [Oryza sativa (indica cultivar-group)]	Unigene6957_All//3.00E-12//AT4G24970| ATP-binding region, ATPase-like domain-containing protein	Unigene6957_All//1.00E-155//DR461614				nr -
Unigene69570_All	216	0.48	5.86	1.97	0.46	0.16	0.00	0.00	0.00	0.00	3.60E+00	2.27E-05	Up	2.03E+00	1.39E-01		-1.53E+00	5.84E-01		-8.85E+00	3.95E-01		null	null		null	null				Unigene69570_All//8.00E-100//CO099377					
Unigene69571_All	216	0.00	3.05	0.49	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	8.95E+00	3.94E-01		null	null		null	null		null	null		null	null		Unigene69571_All//gi|8096269|db|BA95789.1|//6.00E-06//KED [Nicotiana tabacum]							nr -
Unigene69574_All	216	0.00	4.46	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.38E-05	Up	7.95E+00	6.29E-01		null	null		null	null		null	null		null	null		Unigene69574_All//gi|58613481|gb|AAW79327.1|//9.00E-23//phosphoglycerate kinase [Pavlova lutheri]	Unigene69574_All//5.00E-15//AT3G12780| PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms	GO:0005576//GO:0006007//GO:0006950//GO:0009526//GO:0009532//GO:0010038//GO:0016301//GO:0030312	nr +
Unigene69583_All	216	0.00	7.51	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.96E-09	Up	9.95E+00	1.40E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene69584_All	216	0.00	3.52	0.25	0.00	0.16	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	7.95E+00	6.29E-01		7.32E+00	8.20E-01		null	null		null	null		null	null		Unigene69584_All//gi|115489754|ref|NP_001067364.1|//1.00E-06//Os12g0636400 [Oryza sativa Japonica Group] >gi|77557178|gb|ABA99974.1| hydrolase, alpha/beta fold family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113649871|dbj|BAF30383.1| Os12g0636400 [Oryza sativa Japonica Group]							GO:0006950//GO:0009725//GO:0016803	nr -
Unigene69586_All	216	0.00	3.28	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.31E-04	Up	9.95E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene69586_All//sp|Q794C0|VA0E1_RAT//2.00E-08//V-type proton ATPase subunit e 1 OS=Rattus norvegicus GN=Atp6v0e1 PE=2 SV=3							swissprot +
Unigene6959_All	956	0.22	0.11	0.00	1.35	1.33	0.38	13.05	6.12	3.58	-1.05E+00	5.63E-01		-7.77E+00	1.44E-01		-2.37E-02	9.50E-01		-1.84E+00	3.54E-03		-1.09E+00	2.06E-13	Down	-1.86E+00	7.61E-30	Down	Unigene6959_All//gi|79344495|ref|NP_172900.2|//3.00E-47//protein binding [Arabidopsis thaliana]	Unigene6959_All//2.00E-46//AT5G54610| ANK (ankyrin); protein binding	Unigene6959_All//0.00E+00//TC175880				nr +
Unigene69591_All	216	0.00	3.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null										
Unigene69592_All	216	0.73	5.16	0.00	0.00	0.80	0.00	0.00	0.19	0.00	2.83E+00	5.03E-04	Up	-9.51E+00	2.43E-01		9.64E+00	2.26E-01		null	null		7.60E+00	6.28E-01		null	null				Unigene69592_All//6.00E-119//BG442305					
Unigene69598_All	216	0.00	3.99	0.00	0.23	0.00	0.21	0.00	0.00	0.00	1.20E+01	4.93E-05	Up	null	null		-7.85E+00	5.48E-01		-1.41E-01	9.49E-01		null	null		null	null		Unigene69598_All//COG0491//5.00E-20//Zn-dependent hydrolases, including glyoxylases							cog -
Unigene69602_All	217	0.00	3.50	0.98	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	9.94E+00	1.40E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene69608_All	217	0.00	3.04	0.74	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.23E-04	Up	9.52E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene69608_All//sp|Q5RCA9|ITB1_PONAB//2.00E-40//Integrin beta-1 OS=Pongo abelii GN=ITGB1 PE=2 SV=1							swissprot +
Unigene69612_All	217	0.00	6.77	1.23	0.00	0.95	0.42	0.39	0.96	0.37	1.27E+01	2.11E-08	Up	1.03E+01	7.97E-02		9.90E+00	1.56E-01		8.70E+00	4.72E-01		1.31E+00	4.47E-01		-8.58E-02	9.70E-01				Unigene69612_All//1.00E-12//DT048231					
Unigene69620_All	217	0.00	3.97	0.98	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.93E-05	Up	9.94E+00	1.40E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene69626_All	217	0.00	4.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null										
Unigene69629_All	218	0.00	9.06	2.93	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.97E-11	Up	1.15E+01	1.16E-03		null	null		null	null		null	null		null	null										
Unigene6963_All	710	0.59	1.43	1.50	2.18	1.99	3.05	1.97	0.41	1.12	1.28E+00	6.99E-02		1.35E+00	6.01E-02		-1.29E-01	8.32E-01		4.89E-01	2.99E-01		-2.25E+00	9.69E-05	Down	-8.08E-01	9.58E-02		Unigene6963_All//gi|226497650|ref|NP_001150774.1|//4.00E-68//cellulase containing protein [Zea mays] >gi|195641732|gb|ACG40334.1| cellulase containing protein [Zea mays]		Unigene6963_All//1.00E-150//TC148256		ko00500|Starch and sucrose metabolism		nr -
Unigene69637_All	218	0.00	2.32	3.42	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.01E-03		1.17E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene69637_All//gi|6562845|emb|CAB62553.1|//1.00E-21//heterogeneous nuclear ribonucleoprotein; type A/B hnRNP p40 [Rattus norvegicus] >gi|149052496|gb|EDM04313.1| rCG34663, isoform CRA_a [Rattus norvegicus]	Unigene69637_All//2.00E-06//AT5G47620| heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative			ko03040|Spliceosome	GO:0000904//GO:0001071//GO:0032583//GO:0032991//GO:0043231//GO:0043565	nr -
Unigene69638_All	218	0.00	3.49	0.49	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.76E-04	Up	8.93E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene69638_All//sp|Q00963|SPTCB_DROME//2.00E-30//Spectrin beta chain OS=Drosophila melanogaster GN=beta-Spec PE=1 SV=2							swissprot -
Unigene6964_All	2180	0.36	0.23	0.56	1.14	0.47	0.25	4.56	12.27	7.55	-6.31E-01	4.08E-01		6.42E-01	3.19E-01		-1.27E+00	8.49E-04	Down	-2.20E+00	9.51E-07	Down	1.43E+00	6.41E-42	Up	7.28E-01	1.87E-09		Unigene6964_All//gi|22330435|ref|NP_176722.2|//1.00E-173//zinc finger protein-related [Arabidopsis thaliana] >gi|75162418|sp|Q8W468.1|ARI8_ARATH RecName: Full=Probable E3 ubiquitin-protein ligase ARI8; AltName: Full=ARIADNE-like protein ARI8; AltName: Full=Protein ariadne homolog 8 >gi|17065464|gb|AAL32886.1| Unknown protein [Arabidopsis thaliana] >gi|29125030|emb|CAD52890.1| ARIADNE-like protein ARI8 [Arabidopsis thaliana] >gi|70905083|gb|AAZ14067.1| At1g65430 [Arabidopsis thaliana]	Unigene6964_All//5.00E-168//AT1G65430| zinc finger protein-related	Unigene6964_All//0.00E+00//TC165839				nr -
Unigene6965_All	617	1.61	1.23	1.81	1.86	2.68	1.32	3.02	0.27	1.03	-3.87E-01	5.79E-01		1.70E-01	7.78E-01		5.29E-01	3.27E-01		-4.95E-01	4.65E-01		-3.48E+00	4.23E-09	Down	-1.55E+00	3.64E-04	Down	Unigene6965_All//gi|42566730|ref|NP_193010.2|//2.00E-57//adenine-DNA glycosylase-related / MYH-related [Arabidopsis thaliana]	Unigene6965_All//5.00E-57//AT4G12740| adenine-DNA glycosylase-related / MYH-related			ko03410|Base excision repair		nr -
Unigene69660_All	218	0.00	4.18	1.22	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.61E-05	Up	1.03E+01	7.97E-02		null	null		null	null		null	null		null	null										
Unigene69665_All	219	0.00	5.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.99E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene69665_All//sp|Q9VEG6|PERC_DROME//3.00E-25//Chorion peroxidase OS=Drosophila melanogaster GN=pxt PE=2 SV=3							swissprot +
Unigene69666_All	219	0.00	3.93	0.97	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.93E-05	Up	9.93E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene69666_All//gi|255072551|ref|XP_002499950.1|//1.00E-10//alanine aminotransferase [Micromonas sp. RCC299] >gi|226515212|gb|ACO61208.1| alanine aminotransferase [Micromonas sp. RCC299]	Unigene69666_All//4.00E-08//AT1G17290| AlaAT1 (ALANINE AMINOTRANSFERAS); ATP binding / L-alanine:2-oxoglutarate aminotransferase			ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism	GO:0008152//GO:0016769//GO:0016846//GO:0043231//GO:0048037	nr +
Unigene6967_All	535	5.09	18.28	6.87	1.30	3.15	4.81	0.00	0.16	0.00	1.85E+00	2.22E-18	Up	4.34E-01	2.10E-01		1.27E+00	1.25E-02		1.88E+00	1.11E-05	Up	7.29E+00	3.99E-01		null	null										
Unigene69676_All	219	0.00	6.94	3.16	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.09E-08	Up	1.16E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene69676_All//gi|46810472|gb|AAT01617.1|//2.00E-08//omega gliadin [Triticum aestivum]				ko03022|Basal transcription factors	GO:0016787	nr +
Unigene69679_All	219	0.00	3.01	0.73	0.45	0.79	0.00	0.58	0.38	0.36	1.16E+01	6.23E-04	Up	9.51E+00	2.37E-01		7.89E-01	7.70E-01		-8.83E+00	3.95E-01		-6.02E-01	7.65E-01		-6.71E-01	7.18E-01				Unigene69679_All//2.00E-07//EX172539					
Unigene6968_All	1564	0.10	0.16	0.07	0.76	1.59	1.85	5.81	12.83	14.14	6.90E-01	6.26E-01		-5.60E-01	7.74E-01		1.05E+00	8.14E-03		1.27E+00	7.00E-04	Up	1.14E+00	1.44E-22	Up	1.28E+00	2.75E-30	Up	Unigene6968_All//gi|30691233|ref|NP_174300.2|//1.00E-155//glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Unigene6968_All//8.00E-149//AT1G30080| glycosyl hydrolase family 17 protein	Unigene6968_All//0.00E+00//CO117865		ko00500|Starch and sucrose metabolism		nr +
Unigene69684_All	219	0.00	3.70	1.46	0.45	0.31	0.62	0.58	0.00	0.18	1.19E+01	9.35E-05	Up	1.05E+01	4.49E-02		-5.33E-01	8.14E-01		4.44E-01	8.60E-01		-9.18E+00	2.34E-01		-1.67E+00	4.76E-01				Unigene69684_All//2.00E-78//TC145896					
Unigene69686_All	219	0.00	3.93	0.00	0.45	0.63	0.00	0.00	0.57	0.18	1.19E+01	4.93E-05	Up	null	null		4.68E-01	8.75E-01		-8.83E+00	3.95E-01		9.16E+00	2.40E-01		7.51E+00	6.39E-01				Unigene69686_All//3.00E-71//DR504121					
Unigene6969_All	1027	0.00	0.00	0.00	0.92	0.00	0.00	54.22	55.02	25.52	null	null		null	null		-9.85E+00	5.17E-07	Down	-9.85E+00	6.01E-06	Down	2.12E-02	7.85E-01		-1.09E+00	2.76E-58	Down			Unigene6969_All//7.00E-73//DR457635					
Unigene69691_All	219	3.82	11.34	4.13	19.56	15.72	45.37	44.40	65.46	82.04	1.57E+00	2.51E-04	Up	1.13E-01	8.72E-01		-3.15E-01	3.16E-01		1.21E+00	5.76E-11	Up	5.60E-01	2.11E-05		8.86E-01	5.46E-14				Unigene69691_All//6.00E-82//TC137593					
Unigene69692_All	219	0.00	3.24	0.73	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.31E-04	Up	9.51E+00	2.37E-01		null	null		null	null		null	null		null	null										

Unigene69694_All	220	0.00	7.83	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	7.97E-10	Up	1.05E+01	4.49E-02		null	null		null	null		null	null		null	null									nr +
Unigene6970_All	1461	3.29	1.21	0.58	17.80	7.09	17.84	765.64	455.83	1242.44	-1.44E+00	6.94E-07	Down	-2.50E+00	7.26E-13	Down	-1.33E+00	7.31E-37	Down	3.10E-03	9.79E-01		-7.48E-01	0.00E+00		6.98E-01	0.00E+00		Unigene6970_All//gi|222822564|gb|ACM68431.1|//1.00E-159//xyloglucan-specific endoglucanase inhibitor protein [Capsicum annuum]	Unigene6970_All//5.00E-133//AT1G03220| extracellular dermal glycoprotein, putative / EDGP, putative	Unigene6970_All//0.00E+00//TC139999				nr +
Unigene69704_All	220	0.00	4.15	0.48	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.61E-05	Up	8.92E+00	3.93E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene69705_All	220	0.00	7.14	1.21	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	5.69E-09	Up	1.02E+01	7.97E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene69707_All	220	0.00	3.92	3.15	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.93E-05	Up	1.16E+01	6.14E-04	Up	null	null		null	null		null	null		null	null									
Unigene6971_All	1439	0.51	0.35	0.00	9.45	4.36	5.93	88.62	79.87	228.76	-5.32E-01	5.12E-01		-8.99E+00	4.12E-04	Down	-1.12E+00	7.14E-15	Down	-6.72E-01	5.87E-06		-1.50E-01	3.39E-04		1.37E+00	0.00E+00	Up	Unigene6971_All//gi|222822564|gb|ACM68431.1|//1.00E-170//xyloglucan-specific endoglucanase inhibitor protein [Capsicum annuum]	Unigene6971_All//9.00E-143//AT1G03220| extracellular dermal glycoprotein, putative / EDGP, putative	Unigene6971_All//0.00E+00//TC139999				nr +
Unigene69712_All	220	299.42	203.60	173.06	3671.99	2350.36	1729.76	690.70	509.34	660.42	-5.56E-01	9.52E-18		-7.91E-01	3.22E-31		-6.44E-01	0.00E+00		-1.09E+00	0.00E+00	Down	-4.39E-01	5.38E-32		-6.47E-02	1.12E-01			Unigene69712_All//2.00E-116//TC169729					ESTscan +
Unigene69715_All	220	0.00	4.38	0.48	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.38E-05	Up	8.92E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene69715_All//gi|298706172|emb|CBJ49100.1|//8.00E-22//Sorbitol dehydrogenase [Ectocarpus siliculosus]	Unigene69715_All//8.00E-22//AT5G51970| sorbitol dehydrogenase, putative / L-iditol 2-dehydrogenase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00051|Fructose and mannose metabolism//ko00350|Tyrosine metabolism	GO:0008152//GO:0016491//GO:0046872	nr +
Unigene69717_All	220	0.00	3.69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.35E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene69719_All	220	0.00	3.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene69719_All//gi|224001624|ref|XP_002290484.1|//3.00E-30//ribonucleoside reductase [Thalassiosira pseudonana CCMP1335] >gi|220973906|gb|EED92236.1| ribonucleoside reductase [Thalassiosira pseudonana CCMP1335]	Unigene69719_All//1.00E-29//AT2G21790| RNR1 (RIBONUCLEOTIDE REDUCTASE 1); ATP binding / protein binding / ribonucleoside-diphosphate reductase			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism	GO:0006259//GO:0016728//GO:0032559//GO:0043234	nr -
Unigene69720_All	220	0.00	4.15	0.48	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.61E-05	Up	8.92E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene69720_All//sp|Q9VB31|C6A18_DROME//2.00E-08//Probable cytochrome P450 6a18 OS=Drosophila melanogaster GN=Cyp6a18 PE=2 SV=1							swissprot +
Unigene69727_All	221	0.00	2.98	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.23E-04	Up	7.91E+00	6.29E-01		null	null		null	null		null	null		null	null		Unigene69727_All//sp|Q24574|UBPE_DROME//2.00E-08//Ubiquitin carboxyl-terminal hydrolase 64E OS=Drosophila melanogaster GN=Usp64E PE=1 SV=2							swissprot +
Unigene6973_All	783	0.20	0.84	0.00	17.62	15.96	18.75	5.62	15.32	4.43	2.07E+00	3.92E-02		-7.65E+00	2.43E-01		-1.43E-01	4.18E-01		8.91E-02	6.47E-01		1.45E+00	1.34E-19	Up	-3.43E-01	1.86E-01		Unigene6973_All//gi|259121385|gb|ACY92012.1|//2.00E-76//WRKY transcription factor 10 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene6973_All//2.00E-41//AT4G39410| WRKY13; transcription factor	Unigene6973_All//0.00E+00//TC137709	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene69736_All	221	0.00	5.50	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.46E-07	Up	1.05E+01	4.49E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene69740_All	221	0.00	3.90	1.93	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.93E-05	Up	1.09E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene69740_All//gi|115442413|ref|NP_001045486.1|//9.00E-13//Os01g0963400 [Oryza sativa Japonica Group] >gi|113535017|dbj|BAF07400.1| Os01g0963400 [Oryza sativa Japonica Group]	Unigene69740_All//2.00E-13//AT1G43560| Aty2 (Arabidopsis thioredoxin y2); electron carrier/ protein disulfide oxidoreductase				GO:0008152//GO:0009314//GO:0009532//GO:0016667//GO:0030234//GO:0044093	nr +
Unigene69749_All	221	0.00	7.34	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.96E-09	Up	1.05E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene69749_All//gi|300120726|emb|CBK20280.2|//5.00E-06//unnamed protein product [Blastocystis hominis]							nr +
Unigene69755_All	221	0.00	5.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.05E-06	Up	null	null		null	null		null	null		null	null		null	null									
Unigene69761_All	221	0.00	3.21	0.00	0.23	0.00	0.00	0.38	0.38	1.08	1.16E+01	3.31E-04	Up	null	null		-7.82E+00	5.48E-01		-7.82E+00	6.25E-01		-1.67E-02	1.01E+00		1.50E+00	3.39E-01			Unigene69761_All//2.00E-57//DW508251					ESTscan +
Unigene69771_All	222	0.00	2.97	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.23E-04	Up	1.07E+01	2.49E-02		null	null		null	null		null	null		null	null									
Unigene6978_All	718	0.73	0.71	1.11	1.04	1.49	3.02	3.00	5.76	2.16	-4.63E-02	9.75E-01		6.10E-01	4.41E-01		5.15E-01	4.85E-01		1.54E+00	7.57E-04	Up	9.40E-01	4.51E-04		-4.73E-01	2.16E-01		Unigene6978_All//gi|224069342|ref|XP_002302960.1|//5.00E-39//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222846886|gb|EEE82233.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene6978_All//6.00E-18//AT1G69545| leucine-rich repeat family protein	Unigene6978_All//0.00E+00//TC172194				nr -
Unigene69781_All	222	0.00	2.97	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene6979_All	832	1.19	2.62	0.77	10.84	4.88	8.96	2.90	7.99	4.74	1.13E+00	1.05E-02		-6.38E-01	3.90E-01		-1.15E+00	1.80E-10	Down	-2.75E-01	1.91E-01		1.46E+00	2.25E-11	Up	7.11E-01	7.49E-03		Unigene6979_All//gi|15219349|ref|NP_177447.1|//4.00E-63//jacalin lectin family protein [Arabidopsis thaliana] >gi|5903093|gb|AAD55651.1|AC008017_24 Similar to jacalin [Arabidopsis thaliana] >gi|61656125|gb|AAV49365.1| At1g73040 [Arabidopsis thaliana] >gi|149944307|gb|ABR46196.1| At1g73040 [Arabidopsis thaliana]	Unigene6979_All//1.00E-61//AT1G73040| jacalin lectin family protein	Unigene6979_All//0.00E+00//gi|109852083|gb|DW481062.1|DW481062				nr -
Unigene698_All	1648	5.33	8.82	4.94	17.38	18.58	22.20	131.66	266.42	237.24	7.26E-01	8.56E-07		-1.10E-01	6.24E-01		9.59E-02	4.18E-01		3.53E-01	4.92E-05		1.02E+00	0.00E+00	Up	8.50E-01	1.04E-266		Unigene698_All//gi|224144104|ref|XP_002325187.1|//0.00E+00//vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa] >gi|222866621|gb|EEF03752.1| vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa]	Unigene698_All//0.00E+00//AT1G15690| AVP1; ATPase/ hydrogen-translocating pyrophosphatase	Unigene698_All//0.00E+00//TC170886		ko00190|Oxidative phosphorylation	GO:0006818//GO:0008152//GO:0015405//GO:0016462//GO:0016628//GO:0030190//GO:0031224//GO:0043231	nr +
Unigene6980_All	362	1.45	8.96	6.91	2.20	8.85	7.74	0.82	1.04	1.10	2.63E+00	9.67E-10	Up	2.26E+00	2.84E-06	Up	2.01E+00	6.68E-08	Up	1.81E+00	7.53E-06	Up	3.46E-01	7.38E-01		4.29E-01	6.61E-01			Unigene6980_All//4.00E-07//TC165103					
Unigene69800_All	223	0.00	5.00	2.87	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.99E-06	Up	1.15E+01	1.16E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene69805_All	223	0.00	2.95	0.96	0.00	0.00	0.41	0.00	0.00	0.00	1.15E+01	6.23E-04	Up	9.90E+00	1.40E-01		null	null		8.66E+00	4.72E-01		null	null		null	null		Unigene69805_All//COG4177//4.00E-16//ABC-type branched-chain amino acid transport system, permease component							cog -
Unigene69809_All	223	0.00	3.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene6981_All	922	0.74	0.55	0.23	2.59	2.24	2.25	2.61	18.50	6.35	-4.25E-01	5.97E-01		-1.68E+00	8.70E-02		-2.11E-01	6.15E-01		-2.03E-01	6.52E-01		2.82E+00	2.26E-64	Up	1.28E+00	1.21E-08	Up	Unigene6981_All//gi|297825169|ref|XP_002880467.1|//2.00E-10//VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297326306|gb|EFH56726.1| VQ motif-containing protein [Arabidopsis lyrata subsp. lyrata]		Unigene6981_All//1.00E-34//DW506377				nr +
Unigene69814_All	223	0.00	1.36	3.82	0.00	0.00	0.00	0.00	0.00	0.00	1.04E+01	4.38E-02		1.19E+01	9.00E-05	Up	null	null		null	null		null	null		null	null									
Unigene69818_All	223	0.00	4.54	0.72	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.23E-06	Up	9.48E+00	2.37E-01		null	null		null	null		null	null		null	null									
Unigene69820_All	224	42.74	17.87	28.76	113.19	111.45	129.44	164.59	59.52	86.26	-1.26E+00	1.17E-10	Down	-5.71E-01	3.07E-03		-2.24E-02	8.62E-01		1.94E-01	7.39E-02		-1.47E+00	6.55E-60	Down	-9.32E-01	2.25E-30			Unigene69820_All//6.00E-73//gi|78329680|gb|DT549954.1|DT549954					
Unigene69821_All	224	204.14	76.23	60.86	185.91	276.25	259.08	481.69	261.22	188.88	-1.42E+00	7.29E-58	Down	-1.75E+00	3.10E-75	Down	5.71E-01	1.96E-20		4.79E-01	7.63E-13		-8.83E-01	1.91E-77		-1.35E+00	6.85E-158	Down	Unigene69821_All//gi|119888004|gb|ABM05954.1|//1.00E-28//proline-rich protein [Gossypium hirsutum]		Unigene69821_All//1.00E-123//gi|13349730|gb|BG440080.1|BG440080				nr +
Unigene69822_All	224	0.00	7.92	0.00	0.00	0.15	0.40	0.19	0.00	0.71	1.30E+01	4.14E-10	Up	null	null		7.26E+00	8.20E-01		8.66E+00	4.72E-01		-7.56E+00	6.48E-01		1.91E+00	3.77E-01			Unigene69822_All//2.00E-119//gi|78339619|gb|DT559893.1|DT559893					
Unigene69825_All	224	0.00	4.30	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.38E-05	Up	7.89E+00	6.29E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene69826_All	224	0.00	2.94	0.24	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.23E-04	Up	7.89E+00	6.29E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene69830_All	224	0.00	3.17	1.19	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.31E-04	Up	1.02E+01	7.96E-02		null	null		null	null		null	null		null	null		Unigene69830_All//sp|P18091|ACTN_DROME//2.00E-24//Alpha-actinin, sarcomeric OS=Drosophila melanogaster GN=Actn PE=2 SV=2							swissprot -
Unigene69834_All	224	47.18	23.98	29.72	66.05	61.49	78.83	195.92	88.63	97.64	-9.77E-01	4.93E-08		-6.67E-01	2.46E-04		-1.03E-01	5.56E-01		2.55E-01	6.94E-02		-1.14E+00	1.19E-48	Down	-1.00E+00	1.18E-40	Down	Unigene69834_All//gi|15824574|gb|AL09401.1|AF307338.1|//2.00E-34//ribosomal protein [Petunia x hybrida]	Unigene69834_All//1.00E-34//AT1G27400| 60S ribosomal protein L17 (RPL17A)	Unigene69834_All//2.00E-109//TC146595		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0016787//GO:0019538//GO:0033279	nr +
Unigene6984_All	2404	0.00	0.00	0.00	0.00	0.20	0.00	53.36	16.22	21.06	null	null		null	null		7.65E+00	5.07E-03		null	null		-1.72E+00	6.78E-260	Down	-1.34E+00	1.52E-185	Down	Unigene6984_All//gi|224112579|ref|XP_002316233.1|//0.00E+00//laccase 3 [Populus trichocarpa] >gi|222865273|gb|EEF02404.1| laccase 3 [Populus trichocarpa]	Unigene6984_All//0.00E+00//AT2G38080| IRX12 (IRREGULAR XYLEM 12); laccase	Unigene6984_All//5.00E-79//gi|109863114|gb|DW492091.1|DW492091		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -
Unigene69847_All	225	0.00	6.53	1.18	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.11E-08	Up	1.02E+01	7.96E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene6985_All	497	0.84	0.00	0.21	34.58	16.35	12.63	12.68	13.71	5.05	-9.72E+00	1.04E-02		-1.97E+00	1.51E-01		-1.08E+00	1.07E-17	Down	-1.45E+00	1.13E-24	Down	1.13E-01	6.64E-01		-1.33E+00	8.44E-10	Down		Unigene6985_All//3.00E-15//gi|48796546|gb|CO097860.1|CO097860					
Unigene69851_All	225	0.00	3.60	3.31	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.34E-05	Up	1.17E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene69851_All//sp|Q13867|BLMH_HUMAN//3.00E-22//Bleomycin hydrolase OS=Homo sapiens GN=BLMH PE=1 SV=1							swissprot +
Unigene69852_All	225	0.00	7.88	2.13	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	4.14E-10	Up	1.11E+01	7.45E-03		null	null		null	null		null	null		null	null									
Unigene69859_All	225	0.00	5.63	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.85E-07	Up	9.89E+00	1.40E-01		null	null		null	null		null	null		null	null									
Unigene69862_All	225	0.00	5.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.85E-07	Up	null	null		null	null		null	null		null	null		null	null									
Unigene69863_All	225	0.00	3.60	0.24	0.22	0.15	0.00	0.00	0.00	0.00	1.18E+01	9.34E-05	Up	7.89E+00	6.29E-01		-5.33E-01	8.21E-01		-7.79E+00	6.25E-01		null	null		null	null									ESTscan -
Unigene69866_All	225	0.70	6.98	1.42	0.00	0.00	0.00	0.00	0.00	0.00	3.32E+00	3.75E-06	Up	1.03E+00	4.71E-01		null	null		null	null		null	null		null	null									
Unigene69868_All	225	0.00	3.83	0.00	0.00	0.15	0.00	0.00	0.00	0.00	1.19E+01	4.93E-05	Up	null	null		7.26E+00	8.20E-01		null	null		null	null		null	null			Unigene69868_All//3.00E-07//TC163606					
Unigene6987_All	301	22.08	44.44	33.26	23.33	33.41	34.96	39.47	65.82	62.87	1.01E+00	1.99E-10	Up	5.91E-01	1.63E-03		5.18E-01	2.85E-03		5.83E-01	7.73E-04		7.38E-01	3.83E-11		6.72E-01	1.89E-09		Unigene6987_All//gi|145329208|ref|NP_001077633.1|//4.00E-25//ubiquitin fusion degradation UFD1 family protein [Arabidopsis thaliana] >gi|222424176|dbj|BAH20047.1| AT2G21270 [Arabidopsis thaliana]	Unigene6987_All//2.00E-26//AT2G21270| ubiquitin fusion degradation UFD1 family protein	Unigene6987_All//2.00E-138//gi|78325987|gb|DT546261.1|DT546261				nr +
Unigene69876_All	226	0.00	5.38	0.71	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.46E-07	Up	9.47E+00	2.37E-01		null	null		null	null		null	null		null	null									
Unigene6988_All	447	1.76	5.67	1.07	1.89	3.39	3.13	0.85	1.78	1.43	1.69E+00	8.51E-05	Up	-7.12E-01	3.88E-01		8.39E-01	1.29E-01		7.25E-01	2.23E-01		1.06E+00	1.41E-01		7.44E-01	3.52E-01		Unigene6988_All//gi|269927077|gb|ACZ52907.1|//5.00E-24//proliferating cell nuclear antigen gene-controlling element binding factor [Pisum sativum]	Unigene6988_All//1.00E-20//AT5G23280| TCP family transcription factor, putative	Unigene6988_All//0.00E+00//gi|13248362|gb|BF275439.2|BF275439	TCP			nr +
Unigene69882_All	226	0.00	6.50	1.18	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.11E-08	Up	1.02E+01	7.96E-02		null	null		null	null		null	null		null	null		Unigene69882_All//gi|226453680|gb|EEH50988.1|//3.00E-06//predicted protein [Micromonas pusilla CCMP1545]				ko03030|DNA replication		nr +
Unigene69894_All	227	0.00	2.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene69894_All//sp|Q4R6W2|TM55B_MACFA//4.00E-29//Transmembrane protein 55B OS=Macaca fascicularis GN=TMEM55B PE=2 SV=1							swissprot -
Unigene69896_All	227	0.00	2.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene69896_All//sp|Q8WW11|LMO7_HUMAN//8.00E-37//LIM domain only protein 7 OS=Homo sapiens GN=LMO7 PE=1 SV=2							swissprot -

Unigene699_All	1807	2.90	3.53	1.59	13.48	13.32	12.62	32.22	8.53	15.63	2.87E-01	2.35E-01		-8.64E-01	1.55E-03		-1.72E-02	9.00E-01		-9.49E-02	4.80E-01		-1.92E+00	2.10E-137	Down	-1.04E+00	4.94E-57	Down	Unigene699_All//gi|224120498|ref|XP_002331062.1|//0.00E+00//vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa] >gi|222872992|gb|EEF10123.1|vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa]	Unigene699_All//0.00E+00//AT1G15690| AVP1: ATPase/ hydrogen-translocating pyrophosphatase	Unigene699_All//0.00E+00//TC168736		ko00190|Oxidative phosphorylation	GO:0000325//GO:0006818//GO:0006970//GO:0008152//GO:0009526//GO:0015405//GO:0016462//GO:0016628//GO:0031090//GO:0031224//GO:0048827//GO:0060918	nr -
Unigene6990_All	772	2.10	0.13	0.83	2.52	2.77	2.93	0.60	2.27	0.83	-4.00E+00	2.71E-07	Down	-1.34E+00	1.60E-02		1.36E-01	8.19E-01		2.17E-01	6.46E-01		1.92E+00	7.66E-05	Up	4.55E-01	5.78E-01											
Unigene69905_All	227	102.11	93.30	242.56	0.22	0.30	1.19	0.00	0.00	0.00	-1.30E-01	3.09E-01		1.25E+00	3.17E-55	Up	4.68E-01	9.55E-01		2.44E+00	2.22E-01		null	null		null	null		Unigene69905_All//gi|224101127|ref|XP_002312153.1|//2.00E-25//light-harvesting complex II protein Lhcb8 [Populus trichocarpa] >gi|222851973|gb|EEE89520.1|light-harvesting complex II protein Lhcb8 [Populus trichocarpa]	Unigene69905_All//1.00E-22//AT2G40100| LHCB4.3 (light harvesting complex PSII); chlorophyll binding	Unigene69905_All//4.00E-114//TC134181		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009534//GO:0009639//GO:0043234//GO:0046906	nr +
Unigene69907_All	227	70.53	205.36	168.43	143.30	190.84	228.01	195.20	227.02	276.76	1.54E+00	3.80E-66	Up	1.26E+00	7.75E-39	Up	4.13E-01	3.23E-08		6.70E-01	1.37E-20		2.18E-01	1.22E-03		5.04E-01	7.68E-18				Unigene69907_All//1.00E-89//gi|109849272|gb|DW478251.1|DW478251					
Unigene69913_All	227	0.00	5.36	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.46E-07	Up	9.46E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene69913_All//gi|298704874|emb|CBJ28391.1|//3.00E-06//membrane alanyl aminopeptidase [Ectocarpus siliculosus]						nr -
Unigene69916_All	227	0.00	4.46	1.17	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.23E-06	Up	1.02E+01	7.96E-02		null	null		null	null		null	null		null	null											
Unigene69917_All	227	0.69	6.92	1.41	1.98	1.21	4.58	0.37	0.55	0.70	3.32E+00	3.75E-06	Up	1.03E+00	4.70E-01		-7.03E-01	5.30E-01		1.21E+00	8.61E-02		5.69E-01	7.81E-01		9.14E-01	6.23E-01		Unigene69917_All//gi|115475836|ref|NP_001061514.1|//5.00E-09//Os08g0313200 [Oryza sativa Japonica Group] >gi|113623483|dbj|BAF23428.1|Os08g0313200 [Oryza sativa Japonica Group] >gi|258644543|dbj|BAI39797.1| CBS domain-containing protein -like [Oryza sativa Indica Group] >gi|258644675|dbj|BAI39922.1| CBS domain-containing protein -like [Oryza sativa Indica Group]	Unigene69917_All//2.00E-09//AT4G34120| LEJ1 (LOSS OF THE TIMING OF ET AND JA BIOSYNTHESIS 1)	Unigene69917_All//6.00E-45//TC164828				nr +
Unigene69920_All	227	0.00	2.90	1.41	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.23E-04	Up	1.05E+01	4.49E-02		null	null		null	null		null	null		null	null											
Unigene69921_All	227	0.00	6.03	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	7.78E-08	Up	9.46E+00	2.37E-01		null	null		null	null		null	null		null	null											
Unigene69926_All	227	0.00	4.46	0.00	0.00	0.30	0.00	0.00	0.00	0.00	1.21E+01	7.23E-06	Up	null	null		8.25E+00	6.04E-01		null	null		null	null		null	null		Unigene69926_All//gi|57867865|gb|AAW57312.1|//3.00E-25//alpha-tubulin [Ceratopteris richardii]	Unigene69926_All//5.00E-18//AT4G14960| TUA6; structural constituent of cytoskeleton			ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene69928_All	228	0.00	3.56	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.34E-05	Up	7.87E+00	6.29E-01		null	null		null	null		null	null		null	null		Unigene69928_All//gi|215368845|gb|AAM61177.1|//1.00E-15//Contains similarity to 21 KD subunit of the Arp2/3 protein complex (ARC21) [Arabidopsis thaliana]	Unigene69928_All//4.00E-17//AT1G60430| ARPC3 (actin-related protein C3); structural molecule				GO:0005488//GO:0007015//GO:0015629	nr +
Unigene6993_All	325	2.90	6.39	7.86	7.82	8.90	10.56	5.72	4.50	1.96	1.14E+00	1.21E-02		1.44E+00	8.04E-04	Up	1.87E-01	6.56E-01		4.34E-01	2.23E-01		-3.47E-01	4.40E-01		-1.55E+00	3.64E-04	Down			Unigene6993_All//1.00E-176//gi|78342249|gb|DT562523.1|DT562523					
Unigene69937_All	228	0.00	3.33	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.76E-04	Up	9.45E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene69937_All//gi|294610604|tpg|DAA12505.1|//5.00E-21//TPA: TPA_exp: cytosolic glutamine synthetase II [Emiliania huxleyi CCMP1516]	Unigene69937_All//3.00E-19//AT5G35630| GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase			ko00910|Nitrogen metabolism/ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0000166//GO:0006807//GO:0016874	nr -
Unigene6994_All	526	1.69	2.22	1.52	1.14	3.73	1.37	3.78	3.73	1.67	3.90E-01	5.39E-01		-1.55E-01	8.24E-01		1.72E+00	3.49E-04	Up	2.74E-01	7.42E-01		-1.66E-02	1.00E+00		-1.18E+00	3.26E-03				Unigene6994_All//2.00E-28//gi|72273807|gb|DT049340.1|DT049340					
Unigene69941_All	228	0.00	4.44	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.23E-06	Up	7.87E+00	6.29E-01		null	null		null	null		null	null		null	null		Unigene69941_All//gi|112253528|gb|ABI14351.1|//2.00E-21//acyl-CoA dehydrogenase protein 1 [Pfiesteria piscicida]	Unigene69941_All//6.00E-08//AT3G45300| IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase			ko00071|Fatty acid metabolism/ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00410|beta-Alanine metabolism	GO:0008152//GO:0016627	nr +
Unigene69947_All	228	0.00	3.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene69947_All//gi|298708157|emb|CBJ30498.1|//3.00E-19//Trifunctional enzyme subunit alpha [Ectocarpus siliculosus]				ko00592|alpha-Linolenic acid metabolism	GO:0003824//GO:0005488//GO:0008152	nr -
Unigene69952_All	229	0.00	3.32	1.16	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.76E-04	Up	1.02E+01	7.96E-02		null	null		null	null		null	null		null	null											
Unigene69956_All	229	0.00	3.54	1.86	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.34E-05	Up	1.09E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene69956_All//sp|Q9VV19|CHMP5_DROME//1.00E-31//Charged multivesicular body protein 5 OS=Drosophila melanogaster GN=CG6259 PE=1 SV=2				ko04144|Endocytosis		swissprot -
Unigene69961_All	229	0.00	3.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene69961_All//sp|Q09666|AHNK_HUMAN//4.00E-38//Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2						swissprot +
Unigene6997_All	517	1.21	1.18	0.41	15.61	4.80	10.74	33.53	50.45	20.03	-4.62E-02	9.71E-01		-1.56E+00	1.29E-01		-1.70E+00	7.53E-17	Down	-5.39E-01	7.96E-03		5.89E-01	5.90E-10		-7.43E-01	2.66E-10		Unigene6997_All//gi|15217543|ref|NP_177315.1|//2.00E-15//ATCK1 (CHOLINE KINASE 1); choline kinase [Arabidopsis thaliana] >gi|30725296|gb|AAP37670.1|At1g71697 [Arabidopsis thaliana] >gi|110739418|dbj|BAF01619.1|choline kinase like protein [Arabidopsis thaliana] >gi|110741310|dbj|BAF02205.1|choline kinase like protein [Arabidopsis thaliana]	Unigene6997_All//1.00E-16//AT1G71697| ATCK1 (CHOLINE KINASE 1); choline kinase	Unigene6997_All//0.00E+00//TC156508		ko00564|Glycerophospholipid metabolism		nr +
Unigene69975_All	229	0.00	5.31	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.46E-07	Up	7.86E+00	6.29E-01		null	null		null	null		null	null		null	null		Unigene69975_All//gi|300255389|gb|EFJ39700.1|//5.00E-10//26S proteasome regulatory complex [Volvox carteri f. nagariensis]	Unigene69975_All//3.00E-06//AT4G29040| RPT2a (regulatory particle AAA-ATPase 2a); ATPase			ko03050|Proteasome	GO:0009057//GO:0016020//GO:0017111//GO:0032559//GO:0043231//GO:0043234	nr -
Unigene69976_All	229	0.00	3.76	1.40	0.00	0.00	0.20	0.00	0.00	0.00	1.19E+01	4.93E-05	Up	1.04E+01	4.49E-02		null	null		7.62E+00	6.88E-01		null	null		null	null											
Unigene6998_All	529	3.86	15.61	9.66	1.13	1.11	1.45	2.16	1.03	1.28	2.02E+00	1.69E-17	Up	1.33E+00	3.59E-06	Up	-3.02E-02	9.50E-01		3.61E-01	6.80E-01		-1.07E+00	6.31E-02		-7.53E-01	1.68E-01				Unigene6998_All//6.00E-07//ES838914					
Unigene69981_All	230	0.00	3.52	2.32	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.34E-05	Up	1.12E+01	4.02E-03		null	null		null	null		null	null		null	null											
Unigene69982_All	230	0.00	4.19	0.93	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	9.86E+00	1.40E-01		null	null		null	null		null	null		null	null											ESTscan +
Unigene69983_All	230	0.00	5.95	1.62	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.78E-08	Up	1.07E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene69983_All//gi|15240795|ref|NP_196363.1|//4.00E-10//PMSR2 (PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 2); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor / peptide-methionine-(S)-S-oxide reductase [Arabidopsis thaliana] >gi|75264362|sp|Q9LY15.1|MSRA2_ARATH RecName: Full=Peptide methionine sulfoxide reductase A2; Short=A+MSRA2; AltName: Full=Protein-methionine-S-oxide reductase; AltName: Full=Peptide-methionine (S)-S-oxide reductase; Short=Peptide Met(O) reductase >gi|7576184|emb|CAB87935.1|peptide methionine sulfoxide reductase-like protein [Arabidopsis thaliana] >gi|38454142|gb|AAR20765.1|At5g07460 [Arabidopsis thaliana] >gi|46002480|gb|AAS82342.1|At5g07460 [Arabidopsis thaliana]	Unigene69983_All//2.00E-11//AT5G07460| PMSR2 (PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 2); oxidoreductase, acting on sulfur group of donors, disulfide as acceptor / peptide-methionine-(S)-S-oxide reductase				GO:0005488//GO:0006979//GO:0009532//GO:0009639//GO:0016671//GO:0043412	nr +
Unigene6999_All	507	43.34	13.69	29.83	22.11	16.98	11.31	0.00	0.16	0.00	-1.66E+00	2.81E-35	Down	-5.39E-01	7.70E-06		-3.81E-01	2.13E-02		-9.67E-01	8.28E-09		7.37E+00	3.99E-01		null	null		Unigene6999_All//gi|297839475|ref|XP_002887619.1|//7.00E-35//T4012.13 [Arabidopsis lyrata subsp. lyrata] >gi|297333460|gb|EFH63878.1|T4012.13 [Arabidopsis lyrata subsp. lyrata]	Unigene6999_All//4.00E-36//AT1G75900| family II extracellular lipase 3 (EXL3)	Unigene6999_All//0.00E+00//TC154333				nr +
Unigene69991_All	230	0.00	3.08	0.93	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.31E-04	Up	9.86E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene69991_All//sp|P27619|DYN_DROME//1.00E-28//Dynamin OS=Drosophila melanogaster GN=shi PE=1 SV=2						swissprot +
Unigene69993_All	230	0.00	7.71	3.01	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	4.14E-10	Up	1.16E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene69993_All//gi|14253163|emb|CAC39319.1|//4.00E-10//VMP4 protein [Volvox carteri f. nagariensis]						nr -
Unigene69995_All	230	0.00	4.19	1.39	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	1.04E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene69995_All//sp|Q9W4S7|MYC_DROME//2.00E-10//Myc protein OS=Drosophila melanogaster GN=dm PE=1 SV=2						swissprot -
Unigene700_All	1806	2.64	1.49	1.68	2.90	4.18	2.75	6.51	15.02	16.57	-8.26E-01	2.75E-03		-6.50E-01	2.47E-02		5.28E-01	1.07E-02		-7.43E-02	7.91E-01		1.21E+00	6.46E-33	Up	1.35E+00	7.43E-44	Up	Unigene700_All//gi|223452282|gb|ACN89469.1|//1.00E-111//serine/threonine protein kinase family protein [Glycine max]	Unigene700_All//6.00E-102//AT1G18390| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene700_All//0.00E+00//TC145672		ko04626|Plant-pathogen interaction		nr +
Unigene7000_All	755	0.83	1.95	0.28	4.42	5.84	3.59	2.18	0.44	0.47	1.23E+00	2.87E-02		-1.56E+00	1.29E-01		4.01E-01	1.85E-01		-3.01E-01	4.20E-01		-2.30E+00	1.36E-05	Down	-2.20E+00	1.44E-05	Down	Unigene7000_All//gi|115470595|ref|NP_001058896.1|//1.00E-37//Os07g0149900 [Oryza sativa Japonica Group] >gi|113610432|dbj|BAF20810.1|Os07g0149900 [Oryza sativa Japonica Group]	Unigene7000_All//1.00E-42//AT4G05430| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: X8 (InterPro:IPR012946); BEST Arabidopsis thaliana protein match is: glucan endo-1,3-beta-glucosidase-related (TAIR:AT1G59460.1); Has 776 Blast hits to 740 proteins in 35 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 3; Plants - 770; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink).	Unigene7000_All//0.00E+00//DW518050				nr -
Unigene70010_All	231	0.00	3.73	1.38	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.93E-05	Up	1.04E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene70010_All//sp|Q24040|BGB_DROME//2.00E-25//Protein big brother OS=Drosophila melanogaster GN=Bgb PE=1 SV=3						swissprot -

Unigene70011_All	231	0.00	0.66	0.00	0.43	0.45	0.59	0.18	0.00	3.10	9.36E+00	2.32E-01		null	null		5.22E-02	9.65E-01		4.43E-01	8.60E-01		-7.52E+00	6.48E-01		4.08E+00	2.41E-04	Up	Unigene70011_All//gi|1438881|gb|AAC19375.1|//1.00E-06//GmCK2p [Glycine max]	Unigene70011_All//1.00E-07//AT1G74320| choline kinase, putative	Unigene70011_All//2.00E-66//TC173621		ko00564|Glycerophospholipid metabolism		nr +
Unigene70016_All	231	0.00	4.39	0.69	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.23E-06	Up	9.43E+00	2.37E-01		null	null		null	null		null	null		null	null									
Unigene7002_All	965	0.76	0.32	0.33	2.84	3.35	1.64	4.82	2.04	3.43	-1.27E+00	1.36E-01		-1.20E+00	1.80E-01		2.41E-01	5.39E-01		-7.94E-01	3.75E-02		-1.24E+00	1.41E-06	Down	-4.92E-01	4.27E-02		Unigene7002_All//gi|30693719|ref|NP_566973.2|//3.00E-82//KIPK (KCBP-interacting protein kinase); kinase/ protein binding / protein kinase [Arabidopsis thaliana] >gi|30693721|ref|NP_850687.1| KIPK (KCBP-interacting protein kinase); kinase/ protein binding / protein kinase [Arabidopsis thaliana] >gi|7329713|emb|CAB88893.1| protein kinase-like [Arabidopsis thaliana] >gi|21703143|gb|AAW74511.1| AT3g52890/F8J2_60 [Arabidopsis thaliana] >gi|25090422|gb|AAN72297.1| At3g52890/F8J2_60 [Arabidopsis thaliana]	Unigene7002_All//1.00E-88//AT2G36350| protein kinase, putative	Unigene7002_All//0.00E+00//TC178180				nr -
Unigene70021_All	231	0.00	3.29	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70021_All//sp|Q96SZ4|ZSC10_HUMAN//2.00E-07//Zinc finger and SCAN domain-containing protein 10 OS=Homo sapiens GN=ZSCAN10 PE=2 SV=1						swissprot -
Unigene70027_All	231	0.00	3.73	1.84	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.93E-05	Up	1.08E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene70027_All//gi|116055804|emb|CAL57889.1|//8.00E-06//Protein required for actin cytoskeleton organization and cell cycle progression (ISS) [Ostreococcus tauri]						nr -
Unigene70028_All	231	0.00	13.82	4.84	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	3.64E-18	Up	1.22E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene70028_All//sp|P26686|SR455_DROME//2.00E-12//Serine-arginine protein 55 OS=Drosophila melanogaster GN=B52 PE=1 SV=4				ko03040|Spliceosome		swissprot +
Unigene70031_All	231	0.00	2.85	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.23E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70031_All//COG2351//7.00E-08//Transthyretin-like protein						cog -
Unigene7004_All	1383	0.26	0.04	0.69	7.02	7.69	6.20	1.59	0.42	0.78	-2.86E+00	7.79E-02		1.39E+00	7.11E-02		1.32E-01	5.53E-01		-1.79E-01	3.98E-01		-1.91E+00	7.17E-06	Down	-1.03E+00	5.87E-03		Unigene7004_All//gi|145326690|ref|NP_001077792.1|//5.00E-78//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|91806051|gb|ABE65754.1| zinc finger family protein [Arabidopsis thaliana]	Unigene7004_All//9.00E-68//AT1G68200| zinc finger (CCCH-type) family protein		C3H			nr +
Unigene7005_All	1119	0.14	1.00	0.57	0.27	0.52	0.48	61.74	42.28	15.38	2.83E+00	5.03E-04	Up	2.03E+00	5.58E-02		9.70E-01	3.47E-01		8.59E-01	4.23E-01		-5.46E-01	6.36E-22		-2.01E+00	3.44E-178	Down	Unigene7005_All//gi|158828210|gb|ABW81088.1|//1.00E-100//TRL10 [Cleome spinosa]	Unigene7005_All//1.00E-87//AT5G06060| tropinone reductase, putative / tropine dehydrogenase, putative	Unigene7005_All//0.00E+00//TC178949		ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis		nr -
Unigene70053_All	232	0.00	5.24	3.21	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.46E-07	Up	1.16E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene70053_All//gi|161898184|gb|ABX80188.1|//6.00E-06//lipopolysaccharide-induced TNF factor-like protein [Prorocentrum minimum]						nr +
Unigene70054_All	232	0.00	3.49	1.38	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.34E-05	Up	1.04E+01	4.49E-02		null	null		null	null		null	null		null	null		Unigene70054_All//gi|159489510|ref|XP_001702740.1|//2.00E-09//20S proteasome beta subunit B, type beta 2 [Chlamydomonas reinhardtii] >gi|158280762|gb|EDP06519.1| 20S proteasome beta subunit B, type beta 2 [Chlamydomonas reinhardtii]	Unigene70054_All//2.00E-08//AT5G40580| PBB2; endopeptidase/ peptidase/ threonine-type endopeptidase			ko03050|Proteasome	GO:0000502//GO:0008233//GO:0019941	nr -
Unigene7006_All	915	0.46	0.11	0.35	0.00	0.00	0.00	3.47	3.29	24.43	-2.05E+00	1.20E-01		-3.89E-01	7.17E-01		null	null		null	null		-7.55E-02	8.22E-01		2.82E+00	1.48E-85	Up			Unigene7006_All//0.00E+00//EX165818				
Unigene70061_All	232	0.90	6.12	0.00	0.00	0.00	0.00	0.00	1.62	1.37	2.76E+00	7.71E-05	Up	-9.82E+00	1.44E-01		null	null		null	null		1.07E+01	6.85E-03		1.04E+01	1.34E-02				Unigene70061_All//2.00E-113//DW514136				ESTscan +
Unigene70065_All	233	0.00	3.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.34E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70065_All//sp|Q24040|BGB_DROME//1.00E-37//Protein big brother OS=Drosophila melanogaster GN=Bgb PE=1 SV=3						swissprot -
Unigene70067_All	233	0.00	3.70	0.69	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.93E-05	Up	9.42E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene70067_All//gi|18379230|ref|NP_563700.1|//8.00E-11//PRP39; binding [Arabidopsis thaliana]	Unigene70067_All//3.00E-12//AT1G04080| PRP39; binding				GO:0048506	nr -
Unigene70068_All	233	0.00	2.83	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.22E-04	Up	7.84E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70068_All//sp|P13582|EAST_DROME//4.00E-11//Serine protease easter OS=Drosophila melanogaster GN=ea PE=1 SV=3						swissprot +
Unigene70069_All	233	0.00	10.00	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	2.90E-13	Up	8.84E+00	3.93E-01		null	null		null	null		null	null		null	null									
Unigene7007_All	609	0.17	65.40	48.44	4.17	18.49	56.73	0.14	0.00	0.13	8.57E+00	5.19E-225	Up	8.14E+00	1.23E-162	Up	2.15E+00	2.09E-29	Up	3.77E+00	1.07E-147	Up	-7.12E+00	3.99E-01		-8.67E-02	9.70E-01									
Unigene70071_All	233	0.00	3.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70071_All//gi|15667694|gb|AL05454.1|AF348913_1//2.00E-18//enolase [Nitella opaca]	Unigene70071_All//1.00E-13//AT2G36530| LOS2; copper ion binding / phosphopyruvate hydratase			ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation	GO:0006006//GO:0008943//GO:0016829//GO:0044424//GO:0046872	nr +
Unigene7008_All	465	10.24	3.49	3.32	5.14	3.41	1.07	16.64	3.87	4.37	-1.55E+00	1.57E-07	Down	-1.62E+00	1.44E-07	Down	-5.94E-01	1.44E-01		-2.27E+00	1.01E-06	Down	-2.11E+00	2.87E-21	Down	-1.93E+00	1.11E-19	Down	Unigene7008_All//gi|225435036|ref|XP_002284281.1|//2.00E-14//PREDICTED: similar to Histone H2B isoform 2 [Vitis vinifera]	Unigene7008_All//1.00E-15//AT5G59910| HTB4; DNA binding	Unigene7008_All//2.00E-130//gi|13245909|gb|BE054985.2|BE054985				nr -
Unigene70087_All	233	0.00	3.91	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	7.84E+00	6.28E-01		null	null		null	null		null	null		null	null									
Unigene70091_All	233	0.00	4.78	2.06	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.99E-06	Up	1.10E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene70091_All//gi|51535575|dbj|BAD37519.1|//3.00E-06//zinc finger (CCCH-type) protein-like [Oryza sativa Japonica Group]						nr +
Unigene70093_All	233	0.00	3.04	0.00	0.21	0.15	0.00	0.00	0.36	0.00	1.16E+01	3.31E-04	Up	null	null		-5.33E-01	8.21E-01		-7.74E+00	6.25E-01		8.49E+00	3.99E-01		null	null									
Unigene70094_All	233	0.00	3.70	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	4.93E-05	Up	8.84E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70094_All//sp|Q7KRW8|PRP39_DROME//3.00E-10//Pre-mRNA-processing factor 39 OS=Drosophila melanogaster GN=CG1646 PE=1 SV=1				ko03040|Spliceosome		swissprot -
Unigene70097_All	233	0.00	3.04	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.31E-04	Up	8.84E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70097_All//sp|P98163|VL_DROME//4.00E-18//Putative vitellogenin receptor OS=Drosophila melanogaster GN=yl PE=1 SV=2						swissprot -
Unigene70098_All	233	0.00	5.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.78E-08	Up	null	null		null	null		null	null		null	null		null	null			Unigene70098_All//1.00E-61//TC152747					
Unigene701_All	1580	5.07	3.21	5.46	1.86	2.16	1.43	1.26	3.94	3.50	-6.60E-01	1.26E-03		1.08E-01	6.35E-01		2.14E-01	5.87E-01		-3.80E-01	3.37E-01		1.65E+00	1.40E-12	Up	1.48E+00	5.32E-10	Up	Unigene701_All//gi|223452282|gb|ACM89469.1|//6.00E-21//serine/threonine protein kinase family protein [Glycine max]	Unigene701_All//2.00E-16//AT1G18390| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene701_All//0.00E+00//TC130541			GO:0016740	nr +
Unigene7010_All	588	1.69	0.52	0.54	1.44	1.23	2.46	1.51	0.21	0.54	-1.71E+00	2.08E-02		-1.64E+00	3.43E-02		-2.28E-01	7.78E-01		7.71E-01	1.85E-01		-2.82E+00	5.65E-04	Down	-1.48E+00	2.51E-02		Unigene7010_All//gi|2829881|gb|AAC00589.1|//2.00E-25//Hypothetical protein [Arabidopsis thaliana]	Unigene7010_All//2.00E-22//AT1G24270| unknown protein	Unigene7010_All//0.00E+00//TC137153				nr +
Unigene70103_All	234	0.00	5.63	1.82	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.49E-07	Up	1.08E+01	1.37E-02		null	null		null	null		null	null		null	null									
Unigene70104_All	234	0.00	6.06	2.05	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	4.05E-08	Up	1.10E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene70104_All//sp|P02516|HSP23_DROME//3.00E-28//Heat shock protein 23 OS=Drosophila melanogaster GN=Hsp23 PE=1 SV=2						swissprot -
Unigene70105_All	234	0.00	4.33	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.23E-06	Up	7.83E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70105_All//gi|2286200|gb|AAC50039.1|//4.00E-17//polymucleotide phosphorylase [Pisum sativum]	Unigene70105_All//3.00E-18//AT5G14580| polyribonucleotide nucleotidyltransferase, putative			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03018|RNA degradation	GO:0003676//GO:0006779//GO:0008408//GO:0009532//GO:0010322//GO:0010160//GO:0016117//GO:0016779	nr -
Unigene70107_All	234	0.00	3.90	0.91	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	9.83E+00	1.40E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene7011_All	973	2.37	0.62	2.08	3.43	2.58	3.34	1.26	0.95	0.61	-1.92E+00	3.76E-05	Down	-1.86E-01	6.58E-01		-4.09E-01	2.37E-01		-3.76E-02	9.33E-01		-4.15E-01	4.66E-01		-1.04E+00	4.87E-02		Unigene7011_All//gi|15239745|ref|NP_199702.1|//1.00E-119//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75170778|sp|Q9FI80.1|PP425_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g48910 >gi|10177180|dbj|BAB10314.1| selenium-binding protein-like [Arabidopsis thaliana]	Unigene7011_All//3.00E-121//AT5G48910| pentatricopeptide (PPR) repeat-containing protein	Unigene7011_All//0.00E+00//gi|78346295|gb|DT566569.1|DT566569				nr -
Unigene7012_All	297	31.18	18.94	27.07	21.64	19.36	6.69	0.57	0.28	0.54	-7.20E-01	1.38E-04		-2.04E-01	3.50E-01		-1.60E-01	5.44E-01		-1.69E+00	7.98E-12	Down	-1.02E+00	6.13E-01		-8.59E-02	9.65E-01		Unigene7012_All//gi|2706544|emb|CAA75859.1|//2.00E-07//Sig1 [Sinapis alba]	Unigene7012_All//4.00E-07//AT1G64860| SIG4 (SIGMA FACTOR A); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor	Unigene7012_All//5.00E-43//gi|164282378|gb|ES811130.1|ES811130	Sigma70-like			nr +
Unigene70123_All	234	0.00	3.03	0.91	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.31E-04	Up	9.83E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene70123_All//sp|Q24145|SHARK_DROME//9.00E-09//Tyrosine-protein kinase shark OS=Drosophila melanogaster GN=shark PE=2 SV=2						swissprot -
Unigene70126_All	234	0.00	3.90	1.14	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	1.02E+01	7.96E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene7013_All	402	0.39	3.78	0.79	1.86	2.48	1.46	3.79	2.18	3.07	3.28E+00	6.56E-06	Up	1.03E+00	4.70E-01		4.18E-01	5.85E-01		-3.48E-01	6.83E-01		-7.94E-01	1.00E-01		-3.02E-01	5.42E-01									
Unigene70135_All	234	0.00	2.60	2.96	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.16E-03		1.15E+01	6.14E-04	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene70137_All	235	0.00	3.67	0.91	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	9.82E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene70137_All//gi|556560|dbj|BAA04614.1|//2.00E-25//rice homologue of Tat binding protein [Oryza sativa Japonica Group]	Unigene70137_All//1.00E-25//AT3G05530| RPT5A (REGULATORY PARTICLE TRIPLE-A ATPASE 5A); ATPase/ calmodulin binding			ko03050|Proteasome	GO:0009057//GO:0032559//GO:0042623//GO:0043231//GO:0043234	nr -
Unigene70143_All	235	0.67	4.74	0.45	0.00	1.32	0.38	0.00	0.00	0.00	2.83E+00	5.03E-04	Up	-5.60E-01	7.74E-01		1.04E+01	4.54E-02		8.59E+00	4.72E-01		null	null		null	null									
Unigene70144_All	235	0.00	2.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	6.22E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70144_All//gi|301095228|ref|XP_002896715.1|//3.00E-07//5'-AMP-activated protein kinase subunit gamma, putative [Phytophthora infestans T30-4] >gi|262108776|gb|EE166828.1| 5'-AMP-activated protein kinase subunit gamma, putative [Phytophthora infestans T30-4]						nr +
Unigene70149_All	235	0.00	3.88	1.59	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	1.06E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene70149_All//sp|P02452|CO1A1_HUMAN//4.00E-41//Collagen alpha-1(I) chain OS=Homo sapiens GN=COL1A1 PE=1 SV=4						swissprot +
Unigene7015_All	632	54.72	90.76	71.70	73.62	71.92	72.96	74.46	149.99	211.36	7.30E-01	1.20E-24		3.90E-01	1.53E-06		-3.36E-02	7.58E-01		-1.29E-02	9.08E-01		1.01E+00	4.48E-85	Up	1.51E+00	1.05E-227	Up	Unigene7015_All//gi|12043533|emb|CAC19789.1|//4.00E-22//MYB-like DNA-binding protein [Catharanthus roseus]	Unigene7015_All//5.00E-18//AT3G46590| TRFL1 (TRF-LIKE 1); DNA bending/ DNA binding / telomeric DNA binding	Unigene7015_All//6.00E-131//gi|48822846|gb|CO124159.1|CO124159	MYB-related			nr +
Unigene70151_All	235	0.00	3.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70151_All//gi|22325475|ref|NP_178539.2|//4.00E-15//cation efflux family protein [Arabidopsis thaliana]					GO:0043231	nr +

Unigene70153_All	235	0.00	3.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70153_All//gi|300258296|gb|EFJ42534.1|//2.00E-32//serine/threonine kinase [Volvox carteri f. nagariensis]	Unigene70153_All//1.00E-31//AT1G72710| CKL2 (CASEIN KINASE I-LIKE PROTEIN 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase				GO:0000270//GO:0004672//GO:0006464//GO:0008375//GO:0019276//GO:0030258//GO:0032559	nr +
Unigene70155_All	235	0.00	3.88	1.59	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	1.06E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene70155_All//sp|Q5R6T1|PDIA6_PONAB//7.00E-07//Protein disulfide-isomerase A6 OS=Pongo abelii GN=PDIA6 PE=2 SV=1						swissprot -
Unigene7016_All	1879	1.53	9.68	1.93	0.64	0.27	0.79	1.01	11.72	2.42	2.66E+00	1.80E-52	Up	3.32E-01	3.55E-01		-1.21E+00	4.17E-02		3.18E-01	6.18E-01		3.53E+00	9.63E-103	Up	1.26E+00	1.04E-06	Up	Unigene7016_All//gi|1685005|gb|AAB36653.1|//1.00E-138//immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]	Unigene7016_All//1.00E-119//AT2G15480| UGT73B5 (UDP-glucosyl transferase 73B5); UDP-glucosyltransferase/ UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene7016_All//0.00E+00//TC169312		ko00908|Zeatin biosynthesis		nr +
Unigene70161_All	235	0.00	4.10	2.49	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	1.13E+01	2.17E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene7017_All	661	0.55	0.92	0.97	0.30	1.09	0.00	21.94	27.19	4.76	7.31E-01	4.16E-01		8.03E-01	3.88E-01		1.86E+00	4.52E-02		-8.24E+00	1.33E-01		3.10E-01	9.59E-03		-2.20E+00	7.76E-43	Down	Unigene7017_All//gi|115473159|ref|NP_001060178.1|//2.00E-42//Os07g0598000 [Oryza sativa Japonica Group] >gi|113611714|dbj|BAF22092.1|Os07g0598000 [Oryza sativa Japonica Group]	Unigene7017_All//3.00E-24//AT5G42800| DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase			ko00941|Flavonoid biosynthesis		nr -
Unigene70177_All	236	0.00	30.06	13.09	0.00	0.00	0.00	0.00	0.00	0.00	1.49E+01	1.53E-40	Up	1.37E+01	4.51E-17	Up	null	null		null	null		null	null		null	null		Unigene70177_All//gi|7799051|emb|CAB90826.1|//5.00E-29//ubiquitin [Cyanidium caldarium]	Unigene70177_All//4.00E-29//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene70177_All//1.00E-37//TC162949		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene70178_All	236	0.00	4.51	5.87	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.80E-06	Up	1.25E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene70178_All//gi|8778710|gb|AAF79718.1|AC020889.26//2.00E-08//T1N15.2 [Arabidopsis thaliana]	Unigene70178_All//9.00E-10//AT1G48410| AGO1 (ARGONAUTE 1); endoribonuclease/ miRNA binding / protein binding / siRNA binding				GO:0003006//GO:0003723//GO:0004519//GO:0007126//GO:0009553//GO:0009639//GO:0009725//GO:0009887//GO:0030574//GO:0035194//GO:0042445//GO:0044444//GO:0050267//GO:0048364//GO:0048468//GO:0070076	nr +
Unigene70179_All	236	0.00	2.79	0.23	0.21	0.00	0.38	1.43	1.06	0.17	1.14E+01	6.22E-04	Up	7.82E+00	6.28E-01		-7.72E+00	5.48E-01		8.58E-01	7.92E-01		-4.32E-01	7.03E-01		-3.09E+00	3.91E-02			Unigene70179_All//2.00E-06//AT4G05520| ATEHD2 (EPS15 HOMOLOGY DOMAIN 2); GTP binding / GTPase/ calcium ion binding	Unigene70179_All//7.00E-11//ES817856				
Unigene7018_All	574	3.83	2.12	3.90	3.64	2.94	2.12	1.25	1.38	3.33	-8.54E-01	4.74E-02		2.54E-02	9.72E-01		-3.10E-01	5.23E-01		-7.79E-01	8.29E-02		1.44E-01	8.36E-01		1.41E+00	8.61E-04	Up	Unigene7018_All//gi|30686506|ref|NP_173402.2|//9.00E-68//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75263158|sp|Q8FXH1.1|PPR52_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g19720; AltName: Full=Protein DYW7 >gi|10086495|gb|AAG12555.1|AC007797_15 Unknown Protein [Arabidopsis thaliana]	Unigene7018_All//5.00E-69//AT1G19720| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene70180_All	236	0.22	4.08	0.90	1.90	0.44	0.57	1.25	0.89	1.52	4.20E+00	1.29E-04	Up	2.03E+00	3.60E-01		-2.12E+00	7.27E-02		-1.73E+00	1.61E-01		-5.02E-01	6.77E-01		2.77E-01	7.87E-01								
Unigene70181_All	236	12.42	6.44	11.06	14.14	12.11	14.16	11.82	2.48	4.56	-9.47E-01	9.80E-03		-1.67E-01	6.51E-01		-2.24E-01	5.44E-01		2.00E-03	9.99E-01		-2.25E+00	8.87E-09	Down	-1.38E+00	4.88E-05	Down			Unigene70181_All//2.00E-97//gi|48799925|gb|CO101239.1|CO101239				
Unigene70183_All	236	0.00	2.79	0.00	0.00	0.00	0.00	1.07	0.71	1.01	1.14E+01	6.22E-04	Up	null	null		null	null		null	null		-6.02E-01	6.47E-01		-8.59E-02	9.56E-01		Unigene70183_All//gi|297849514|ref|XP_002892638.1|//2.00E-15//S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338480|gb|EFH68897.1| S-locus lectin protein kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene70183_All//3.00E-16//AT1G11350| SD1-13 (S-DOMAIN-113); kinase/ protein kinase/ protein serine/threonine kinase	Unigene70183_All//3.00E-25//TC149497			GO:0004672//GO:0005488//GO:0006468//GO:0016020	nr +
Unigene70189_All	236	0.22	70.64	37.00	0.00	0.29	0.00	0.00	0.00	0.00	8.32E+00	1.31E-93	Up	7.38E+00	5.09E-47	Up	8.19E+00	6.04E-01		null	null		null	null		null	null		Unigene70189_All//gi|8954370|ref|NP_059359.1|//3.00E-11//NADH dehydrogenase subunit 1 [Cyanidioschyzon merolae] >gi|4115783|dbj|BAA36521.1| NADH-ubiquinone oxidoreductase chain 1 [Cyanidioschyzon merolae strain 10D]	Unigene70189_All//3.00E-11//ATMG01275| Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C.			ko00190|Oxidative phosphorylation	GO:0005746//GO:0022904//GO:0031224//GO:0031410//GO:0050136//GO:0051234	nr +
Unigene70198_All	237	0.00	3.42	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	9.40E+00	2.37E-01		null	null		null	null		null	null		null	null									
Unigene702_All	2299	5.10	4.41	3.54	3.75	4.57	2.91	6.97	19.58	15.47	-2.10E-01	2.33E-01		-5.25E-01	2.33E-03		2.85E-01	1.23E-01		-3.67E-01	7.33E-02		1.49E+00	1.65E-74	Up	1.15E+00	8.88E-41	Up	Unigene702_All//gi|223452282|gb|ACM89469.1|//1.00E-183//serine/threonine protein kinase family protein [Glycine max]	Unigene702_All//7.00E-146//AT1G18390| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene702_All//0.00E+00//TC130541		ko04626|Plant-pathogen interaction		nr +
Unigene70200_All	237	0.00	4.06	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70200_All//sp|Q9JMB7|PIWL1_MOUSE//1.00E-13//Piwi-like protein 1 OS=Mus musculus GN=Piwil1 PE=1 SV=1						swissprot -
Unigene7021_All	829	0.13	0.00	0.00	8.65	2.70	3.98	5.36	0.61	0.96	-6.98E+00	3.68E-01		-6.98E+00	3.88E-01		-1.68E+00	9.58E-15	Down	-1.12E+00	2.60E-07	Down	-3.15E+00	3.50E-19	Down	-2.48E+00	1.31E-15	Down	Unigene7021_All//gi|13346192|gb|AAK19618.1|AF336285_1//1.00E-145//GHMYB38 [Gossypium hirsutum]	Unigene7021_All//7.00E-45//AT1G22640| MYB3 (MYB DOMAIN PROTEIN 3); DNA binding / transcription factor	Unigene7021_All//0.00E+00//TC150293	MYB			nr +
Unigene70210_All	237	0.00	3.21	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	9.81E+00	1.40E-01		null	null		null	null		null	null		null	null									
Unigene70211_All	237	0.00	2.78	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	9.81E+00	1.40E-01		null	null		null	null		null	null		null	null				Unigene70211_All//3.00E-19//ES848802					ESTscan -
Unigene70212_All	237	0.00	4.28	2.47	0.00	0.58	2.67	0.00	0.00	0.00	1.21E+01	7.23E-06	Up	1.13E+01	2.17E-03		9.18E+00	3.17E-01		1.14E+01	7.59E-04	Up	null	null		null	null		Unigene70212_All//gi|224096333|ref|XP_002310605.1|//8.00E-25//cytochrome P450 [Populus trichocarpa] >gi|222853508|gb|EEE91055.1|cytochrome P450 [Populus trichocarpa]	Unigene70212_All//6.00E-22//AT1G65340| CYP96A3; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene70212_All//1.00E-74//CO115312		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506//GO:0008152	nr -
Unigene70213_All	237	0.00	3.21	2.70	0.00	0.00	0.00	0.18	0.00	0.00	1.16E+01	1.76E-04	Up	1.14E+01	1.16E-03		null	null		null	null		-7.48E+00	6.48E-01		-7.48E+00	6.05E-01		Unigene70213_All//sp|Q15942|ZYX_HUMAN//6.00E-22//Zyxin OS=Homo sapiens GN=ZYX PE=1 SV=1						swissprot -
Unigene70216_All	237	0.00	2.99	0.45	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	8.81E+00	3.93E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70222_All	237	0.00	2.99	0.45	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	8.81E+00	3.93E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70227_All	238	0.00	4.05	1.57	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	1.06E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene70227_All//sp|P02461|CO3A1_HUMAN//2.00E-37//Collagen alpha-1(III) chain OS=Homo sapiens GN=COL3A1 PE=1 SV=4						swissprot -
Unigene7023_All	905	683.41	962.38	1227.52	478.33	444.88	597.65	89.47	70.06	29.23	4.94E-01	1.54E-181		8.45E-01	0.00E+00		-1.05E-01	4.33E-06		3.21E-01	4.77E-55		-3.53E-01	7.27E-12		-1.61E+00	1.25E-154	Down	Unigene7023_All//gi|116265932|gb|ABJ91214.1|//1.00E-90//CBL-interacting protein kinase 7 [Populus trichocarpa] >gi|116265934|gb|ABJ91215.1| CBL-interacting protein kinase 8 [Populus trichocarpa]	Unigene7023_All//6.00E-59//AT4G30960| SIP3 (SOS3-INTERACTING PROTEIN 3); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene7023_All//0.00E+00//gi|164288237|gb|ES826031.1|ES826031				nr -
Unigene70231_All	238	0.00	3.19	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	9.81E+00	1.40E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene70236_All	238	0.00	4.68	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.99E-06	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene70237_All	238	0.00	3.41	0.90	0.42	0.14	0.38	0.71	0.53	0.33	1.17E+01	9.34E-05	Up	9.81E+00	1.40E-01		-1.53E+00	5.84E-01		-1.42E-01	9.48E-01		-4.32E-01	7.92E-01		-1.09E+00	5.51E-01									
Unigene7024_All	615	0.34	2.39	0.61	0.32	1.46	2.28	0.28	2.51	2.53	2.81E+00	4.57E-05	Up	8.33E-01	5.16E-01		2.17E+00	9.20E-03		2.81E+00	5.55E-05	Up	3.19E+00	3.93E-07	Up	3.20E+00	2.33E-07	Up	Unigene7024_All//gi|222423500|dbj|BAH19720.1|//6.00E-22//AT1G10657| [Arabidopsis thaliana]	Unigene7024_All//4.00E-23//AT1G10657| unknown protein	Unigene7024_All//0.00E+00//gi|109855907|gb|DW484886.1|DW484886				nr -
Unigene70241_All	238	0.44	4.05	0.22	1.47	0.00	0.00	0.00	0.00	0.00	3.20E+00	6.55E-04	Up	-9.75E-01	7.19E-01		-1.05E+01	9.44E-03		-1.05E+01	2.12E-02		null	null		null	null									
Unigene70242_All	238	0.00	2.77	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	9.81E+00	1.40E-01		null	null		null	null		null	null		null	null		Unigene70242_All//sp|Q8VBX1|LIPE_RAT//1.00E-09//Endothelial lipase OS=Rattus norvegicus GN=Lipg PE=2 SV=2						swissprot +
Unigene70246_All	238	0.22	3.41	0.90	0.21	0.14	0.19	0.00	0.00	0.00	3.95E+00	7.52E-04	Up	2.03E+00	3.60E-01		-5.33E-01	8.21E-01		-1.41E-01	9.49E-01		null	null		null	null		Unigene70246_All//COG1238//5.00E-17//Predicted membrane protein						cog -
Unigene70249_All	238	0.00	2.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70249_All//gi|115481222|ref|NP_001064204.1|//9.00E-07//Os10g0160000 [Oryza sativa Japonica Group] >gi|78707833|gb|ABB46808.1|Ubiquitin carboxyl-terminal hydrolase family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113638813|dbj|BAF26118.1|Os10g0160000 [Oryza sativa Japonica Group]	Unigene70249_All//5.00E-08//AT4G10590| ubiquitin carboxyl-terminal hydrolase family protein				GO:0016787//GO:0044238//GO:0044260	nr +
Unigene7025_All	581	1.98	6.72	1.10	2.83	2.96	2.18	1.96	1.80	0.75	1.76E+00	2.49E-07	Up	-8.49E-01	2.06E-01		6.68E-02	9.14E-01		-3.79E-01	4.90E-01		-1.28E-01	8.22E-01		-1.38E+00	1.42E-02				Unigene7025_All//4.00E-101//CO120507				
Unigene70250_All	238	0.00	4.68	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.99E-06	Up	9.39E+00	2.37E-01		null	null		null	null		null	null		null	null									
Unigene70251_All	238	0.00	5.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.78E-08	Up	null	null		null	null		null	null		null	null		null	null									
Unigene70254_All	238	0.00	3.41	1.79	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	1.08E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene70254_All//gi|115468394|ref|NP_001057796.1|//2.00E-31//Os06g0538000 [Oryza sativa Japonica Group] >gi|113598836|dbj|BAF19710.1|Os06g0538000 [Oryza sativa Japonica Group]	Unigene70254_All//9.00E-31//AT5G26360| chaperonin, putative				GO:0005515//GO:0031410//GO:0032559//GO:0044267	nr +
Unigene70260_All	239	0.00	2.33	3.12	2.29	1.01	1.51	1.59	1.75	2.00	1.12E+01	2.17E-03		1.16E+01	3.26E-04	Up	-1.18E+00	2.25E-01		-6.01E-01	5.66E-01		1.35E-01	8.99E-01		3.29E-01	7.07E-01		Unigene70260_All//gi|51536572|gb|AAU05524.1|//1.00E-12//At3g26990 [Arabidopsis thaliana]	Unigene70260_All//6.00E-14//AT5G26990| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF618 (InterPro:IPR006903), Regulation of nuclear pre-mRNA protein (InterPro:IPR006569), ENTH/VHS (InterPro:IPR008942); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G10060.1); Has 815 Blast hits to 806 proteins in 138 species: Archae - 0; Bacteria - 10; Metazoa - 490; Fungi - 159; Plants - 81; Viruses - 1; Other Eukaryotes - 74 (source: NCBI BLink).	Unigene70260_All//3.00E-96//CO090902			GO:0031410	nr +
Unigene70267_All	239	0.00	3.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -

Unigene7027_All	524	3.59	2.22	0.91	5.51	3.81	9.05	18.64	18.98	36.34	-6.93E-01	1.39E-01		-1.97E+00	3.20E-04	Down	-5.33E-01	1.46E-01		7.15E-01	9.73E-03		2.64E-02	8.99E-01		9.63E-01	7.17E-17		Unigene7027_All//gi|33589722|gb|AAQ22627.1|//4.00E-10//At5g58375 [Arabidopsis thaliana]	Unigene7027_All//4.00E-21//AT5G18150| unknown protein	Unigene7027_All//0.00E+00//DW518067				nr -
Unigene70276_All	239	0.00	3.39	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	9.38E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene70276_All//sp|P12109|CO6A1_HUMAN//7.00E-31//Collagen alpha-1(VI) chain OS=Homo sapiens GN=COL6A1 PE=1 SV=3							swissprot +
Unigene70277_All	239	193.08	204.59	308.36	981.49	374.18	487.73	219.36	323.35	48.17	8.35E-02	3.47E-01		6.75E-01	1.23E-26		-1.39E+00	0.00E+00	Down	-1.01E+00	6.33E-186	Down	5.60E-01	1.77E-25		-2.19E+00	2.30E-151	Down			Unigene70277_All//1.00E-74//DW520360				
Unigene7028_All	1400	0.00	0.07	0.00	0.00	0.00	0.00	1.60	6.21	79.59	6.18E+00	3.81E-01		null	null		null	null		null	null		1.96E+00	1.23E-21	Up	5.64E+00	0.00E+00	Up	Unigene7028_All//gi|15234693|ref|NP_193934.1|//1.00E-112//F-box family protein [Arabidopsis thaliana]	Unigene7028_All//9.00E-89//AT4G04480| LOCATED IN: chloroplast; EXPRESSED IN: flower, pollen tube; EXPRESSED DURING: petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT4G22030.1); Has 51 Blast hits to 51 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene7028_All//4.00E-75//gi|78325351|gb|DT545625.1|DT545625				nr +
Unigene70281_All	239	0.00	4.24	0.45	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.23E-06	Up	8.80E+00	3.93E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene70283_All	239	0.00	3.60	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene70284_All	239	0.00	4.88	0.89	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.05E-06	Up	9.80E+00	1.39E-01		null	null		null	null		null	null		null	null									
Unigene70285_All	239	0.00	2.76	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	7.80E+00	6.28E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70293_All	239	0.00	4.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70293_All//gi|189026981|emb|CAQ65986.1|//3.00E-11//sterol C4 methyloxydase [Aphanomyces euteiches]	Unigene70293_All//6.00E-11//AT1G07420| SMO2-1 (STEROL 4-ALPHA-METHYL-OXIDASE 2-1); 4-alpha-methyl-delta7-sterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase		ko00100|Steroid biosynthesis	GO:0000254//GO:0009526	nr -
Unigene70294_All	239	0.00	2.97	1.11	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	1.01E+01	7.96E-02		null	null		null	null		null	null		null	null		Unigene70294_All//sp|P30044|PRDX5_HUMAN//2.00E-24//Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=3						swissprot +
Unigene70298_All	240	0.00	2.74	0.44	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	8.79E+00	3.93E-01		null	null		null	null		null	null		null	null									
Unigene703_All	995	1.31	1.02	1.23	4.96	3.67	2.13	2.29	0.71	1.44	-3.68E-01	5.31E-01		-9.49E-02	8.72E-01		-4.34E-01	1.06E-01		-1.22E+00	7.26E-06	Down	-1.68E+00	3.10E-05	Down	-6.71E-01	6.45E-02		Unigene703_All//gi|49523569|emb|CAF18246.1|//1.00E-116//STY-L protein [Antirrhinum majus]	Unigene703_All//7.00E-93//AT2G32700| WD-40 repeat family protein	Unigene703_All//0.00E+00//EE592846			GO:0005488//GO:0006350//GO:0009791//GO:0015031//GO:0031410//GO:0043234	nr +
Unigene70301_All	240	0.00	2.96	1.78	1.45	0.57	0.38	0.88	0.35	0.50	1.15E+01	3.31E-04	Up	1.08E+01	1.37E-02		-1.34E+00	3.08E-01		-1.95E+00	1.96E-01		-1.34E+00	4.29E-01		-8.23E-01	5.98E-01				Unigene70301_All//4.00E-117//CA993921				
Unigene70303_All	240	0.00	4.43	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.80E-06	Up	7.79E+00	6.28E-01		null	null		null	null		null	null		null	null									
Unigene7031_All	311	2.86	1.96	1.54	3.84	6.53	3.49	3.26	0.27	0.77	-5.49E-01	4.42E-01		-8.92E-01	2.46E-01		7.65E-01	9.48E-02		-1.41E-01	8.16E-01		-3.60E+00	2.38E-05	Down	-2.09E+00	1.52E-03				Unigene7031_All//1.00E-114//gi|109880331|gb|DW509301.1|DW509301				
Unigene7032_All	250	10.25	15.81	5.75	37.66	46.42	46.97	15.73	4.85	4.78	6.24E-01	4.28E-02		-8.34E-01	4.48E-02		3.02E-01	7.98E-02		3.19E-01	6.72E-02		-1.70E+00	1.46E-08	Down	-1.72E+00	5.21E-09	Down			Unigene7032_All//2.00E-110//gi|109880331|gb|DW509301.1|DW509301				
Unigene70321_All	240	0.22	5.07	0.67	1.66	1.43	0.56	1.06	0.52	0.50	4.54E+00	6.47E-06	Up	1.61E+00	5.10E-01		-2.11E-01	8.25E-01		-1.56E+00	2.31E-01		-1.02E+00	4.94E-01		-1.09E+00	4.28E-01				Unigene70321_All//3.00E-127//DW504883				
Unigene70322_All	240	0.00	4.01	0.89	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	9.79E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70322_All//gi|298707515|emb|CBJ30117.1|//6.00E-09//S-Adenosyl-Methionine synthetase [Ectocarpus siliculosus]	Unigene70322_All//2.00E-09//AT4G01850| SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr -
Unigene70323_All	240	0.00	3.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70323_All//sp|P25439|BRM_DROME//6.00E-16//ATP-dependent helicase brm OS=Drosophila melanogaster GN=brm PE=1 SV=2						swissprot -
Unigene70326_All	240	0.00	4.64	1.55	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.99E-06	Up	1.06E+01	2.49E-02		null	null		null	null		null	null		null	null									
Unigene70327_All	240	0.00	7.18	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	7.97E-10	Up	1.10E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene70327_All//gi|297833728|ref|XP_002884746.1|//2.00E-26//40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata] >gi|297330586|gb|EFH61005.1| 40S ribosomal protein S23 [Arabidopsis lyrata subsp. lyrata]	Unigene70327_All//7.00E-28//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene70327_All//2.00E-14//DV850314	ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene70334_All	240	0.00	2.96	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	9.38E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene70334_All//gi|301099111|ref|XP_002898647.1|//4.00E-09//conserved hypothetical protein [Phytophthora infestans T30-4] >gi|262104720|gb|EEY62772.1| conserved hypothetical protein [Phytophthora infestans T30-4]						nr +
Unigene70338_All	241	0.00	3.36	3.31	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	1.17E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene70338_All//gi|159485734|ref|XP_001700899.1|//2.00E-07//mitochondrial pyruvate dehydrogenase kinase [Chlamydomonas reinhardtii] >gi|158281398|gb|EDP07153.1| mitochondrial pyruvate dehydrogenase kinase [Chlamydomonas reinhardtii]	Unigene70338_All//2.00E-06//AT3G06483| PDK (PYRUVATE DEHYDROGENASE KINASE); ATP binding / histidine phosphotransfer kinase/ pyruvate dehydrogenase (acetyl-transferring) kinase			GO:0009987//GO:0016772	nr +
Unigene7034_All	963	0.54	1.05	1.38	1.19	1.22	0.61	3.86	3.78	1.78	9.54E-01	1.65E-01		1.35E+00	3.17E-02		3.13E-02	9.74E-01		-9.64E-01	1.37E-01		-3.31E-02	9.30E-01		-1.12E+00	6.69E-05	Down			Unigene7034_All//8.00E-88//TC144281				
Unigene70343_All	241	0.00	3.15	0.44	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	8.79E+00	3.93E-01		null	null		null	null		null	null		null	null									
Unigene70345_All	241	0.00	6.52	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	5.69E-09	Up	7.79E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70345_All//gi|284433772|gb|ADB85092.1|//6.00E-14//acyl-CoA-binding protein [Jatropha curcas]	Unigene70345_All//4.00E-14//AT1G31812| ACBP6 (acyl-CoA-binding protein 6); acyl-CoA binding / phosphatidylcholine binding			GO:0008289	nr +
Unigene70348_All	241	0.00	3.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene7035_All	329	2.86	4.16	2.27	5.00	3.45	1.92	26.86	16.52	7.51	5.39E-01	3.59E-01		-3.37E-01	6.16E-01		-5.33E-01	3.08E-01		-1.38E+00	8.58E-03		-7.02E-01	4.83E-05		-1.84E+00	5.17E-21	Down		Unigene7035_All//2.00E-06//AT2G24170| endomembrane protein 70, putative	Unigene7035_All//7.00E-169//gi|84167733|gb|DR456381.1|DR456381				
Unigene70352_All	241	0.00	5.47	4.20	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.49E-07	Up	1.20E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene70352_All//gi|297846544|ref|XP_002891153.1|//3.00E-11//At1g31330/T19E23_1 [Arabidopsis lyrata subsp. lyrata] >gi|297336995|gb|EFH67412.1| At1g31330/T19E23_1 [Arabidopsis lyrata subsp. lyrata]			ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)//ko00195|Photosynthesis	GO:0009522//GO:0009526//GO:0009534//GO:0009570//GO:0044237	nr -
Unigene70354_All	241	0.00	6.73	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.96E-09	Up	9.79E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene70355_All	241	0.00	2.73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70355_All//sp|Q1ZXF1|ECHM_DICDI//6.00E-06//Probable enoyl-CoA hydratase, mitochondrial OS=Dictyostelium discoideum GN=ech1 PE=3 SV=1	Unigene70355_All//2.00E-06//AT4G29010| AIM1 (ABNORMAL INFLORESCENCE MERISTEM); enoyl-CoA hydratase		ko00592|alpha-Linolenic acid metabolism		swissprot +
Unigene7036_All	1386	0.00	0.58	0.77	0.36	0.00	0.26	1.86	7.33	2.30	9.19E+00	9.34E-05	Up	9.59E+00	6.61E-06	Up	-8.49E+00	8.98E-04	Down	-4.63E-01	6.59E-01		1.98E+00	1.65E-25	Up	3.05E-01	3.43E-01		Unigene7036_All//gi|13161397|dbj|BAB33033.1|//1.00E-118//CPRD2 [Vigna unguiculata]	Unigene7036_All//6.00E-90//AT4G20820| FAD-binding domain-containing protein	Unigene7036_All//0.00E+00//TC170571				nr +
Unigene70361_All	241	0.00	2.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70361_All//sp|Q9NBL2|MSL3_DROVI//1.00E-17//Protein male-specific lethal-3 OS=Drosophila virilis GN=msl-3 PE=3 SV=1						swissprot +
Unigene70362_All	241	0.00	4.20	0.44	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.23E-06	Up	8.79E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70362_All//gi|297831216|ref|XP_002883490.1|//1.00E-21//transaminase [Arabidopsis lyrata subsp. lyrata] >gi|297329330|gb|EFH59749.1| transaminase [Arabidopsis lyrata subsp. lyrata]	Unigene70362_All//4.00E-23//AT3G24090| glutamine-fructose-6-phosphate transaminase (isomerizing)/ sugar binding / transaminase		ko00520|Amino sugar and nucleotide sugar metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0005975//GO:0008483//GO:0030246//GO:0043231	nr +
Unigene70370_All	242	0.00	7.96	1.98	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	5.72E-11	Up	1.10E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene70370_All//sp|Q5REJ1|RT05_PONAB//2.00E-06//28S ribosomal protein S5, mitochondrial OS=Pongo abelii GN=MRPS5 PE=2 SV=1						swissprot +
Unigene70375_All	242	0.00	2.72	0.44	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	8.78E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70375_All//gi|162458022|ref|NP_001165053.1|//2.00E-06//LOC541920 [Zea mays] >gi|16305113|gb|AAL16979.1| 50kD gamma zein [Zea mays]						nr +
Unigene70376_All	242	0.00	4.61	1.10	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.99E-06	Up	1.01E+01	7.96E-02		null	null		null	null		null	null		null	null		Unigene70376_All//sp|Q02645|HTS_DROME//7.00E-19//Protein hu-li tai shao OS=Drosophila melanogaster GN=hts PE=1 SV=2						swissprot +
Unigene7038_All	650	0.16	0.47	0.00	0.61	0.26	0.83	4.55	2.31	1.72	1.54E+00	3.23E-01		-7.33E+00	3.88E-01		-1.21E+00	3.14E-01		4.44E-01	6.78E-01		-9.76E-01	2.70E-03		-1.41E+00	1.89E-05	Down	Unigene7038_All//gi|6522540|emb|CAB61983.1|//2.00E-17//receptor-kinase like protein [Arabidopsis thaliana]	Unigene7038_All//1.00E-14//AT1G73080| PEPR1 (PEP1 receptor 1); ATP binding / kinase/ protein binding / protein serine/threonine kinase	Unigene7038_All//0.00E+00//TC179552	ko04626|Plant-pathogen interaction		nr -
Unigene70383_All	242	1.95	12.77	3.52	13.79	6.69	20.72	2.62	44.04	19.26	2.71E+00	1.32E-09	Up	8.56E-01	2.80E-01		-1.04E+00	9.94E-04	Down	5.87E-01	3.03E-02		4.07E+00	8.88E-56	Up	2.88E+00	8.61E-19	Up	Unigene70383_All//gi|21322711|emb|CAD22154.1|//1.00E-15//pherophorin-dn1 protein [Volvox carteri f. nagariensis]			ko03040|Spliceosome	GO:0016020	nr +
Unigene70385_All	242	0.00	4.40	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.80E-06	Up	9.78E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70385_All//gi|301120314|ref|XP_002907884.1|//2.00E-12//trifunctional enzyme subunit beta, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262102915|gb|EEY60967.1| trifunctional enzyme subunit beta, mitochondrial precursor [Phytophthora infestans T30-4]						nr -
Unigene7039_All	314	0.83	1.94	4.75	3.17	3.40	18.41	28.14	150.54	56.33	1.22E+00	2.07E-01		2.51E+00	1.98E-04	Up	9.96E-02	9.02E-01		2.54E+00	3.70E-17	Up	2.42E+00	2.16E-149	Up	1.00E+00	1.03E-16	Up	Unigene7039_All//gi|226506478|ref|NP_001148259.1|//5.00E-29//brain protein 44-like protein [Zea mays] >gi|195617004|gb|ACG30332.1| brain protein 44-like protein [Zea mays]	Unigene7039_All//4.00E-30//AT5G20090| unknown protein	Unigene7039_All//2.00E-21//gi|109872601|gb|DW501576.1|DW501576				nr -
Unigene70391_All	242	0.22	2.51	5.50	2.88	1.71	3.36	1.40	1.04	0.49	3.54E+00	7.24E-03		4.67E+00	2.95E-06	Up	-7.55E-01	3.69E-01		2.21E-01	7.78E-01		-4.32E-01	7.03E-01		-1.50E+00	2.10E-01				Unigene70391_All//1.00E-18//ES809349				
Unigene70392_All	242	0.00	3.35	2.86	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	1.15E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene70392_All//gi|269991320|emb|CAX12504.1|//3.00E-08//50S ribosomal protein L1 [Pucus vesiculosus]	Unigene70392_All//2.00E-07//AT3G63490| ribosomal protein L1 family protein				GO:0003723//GO:0005198//GO:0009532//GO:0009534//GO:0010467//GO:0033279	nr +
Unigene70395_All	242	0.00	3.98	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.38E-05	Up	9.78E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70395_All//sp|Q9DDA9|PACN2_XENLA//3.00E-16//Protein kinase C and casein kinase substrate in neurons protein 2 OS=Xenopus laevis GN=pacsin2 PE=2 SV=1						swissprot -
Unigene70398_All	242	0.00	3.56	1.32	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	1.04E+01	4.48E-02		null	null		null	null		null	null		null	null									
Unigene704_All	2653	9.15	4.77	9.59	5.58	7.05	3.29	1.12	0.44	0.38	-9.39E-01	2.33E-16		6.83E-02	6.18E-01		3.38E-01	6.95E-03		-7.63E-01	7.41E-08		-1.34E+00	6.47E-05	Down	-1.57E+00	2.94E-06	Down	Unigene704_All//gi|49523569|emb|CAF18246.1|//0.00E+00//STY-L protein [Antirrhinum majus]	Unigene704_All//0.00E+00//AT2G32700| WD-40 repeat family protein	Unigene704_All//0.00E+00//TC141910	ko03040|Spliceosome//ko03022|Basal transcription factors	GO:0005488//GO:0006350//GO:0006810//GO:0009791//GO:0016740//GO:0031410	nr -

Unigene7040_All	685	0.76	1.41	3.19	2.25	2.76	11.93	30.00	203.24	112.30	8.80E-01	2.13E-01		2.06E+00	4.88E-05	Up	2.95E-01	5.87E-01		2.40E+00	1.10E-22	Up	2.76E+00	0.00E+00	Up	1.90E+00	5.84E-183	Up	Unigene7040_All//gi|226506478|ref|NP_001148259.1|//7.00E-23//brain protein 44-like protein [Zea mays]>gi|195617004|gb|ACG30332.1| brain protein 44-like protein [Zea mays]	Unigene7040_All//2.00E-24//AT5G20090| unknown protein	Unigene7040_All//1.00E-24//DN827768				nr −
Unigene70400_All	243	0.00	2.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70400_All//gi|283476402|emb|CAY54134.1|//8.00E-06//alpha/beta gliadin precursor [Triticum aestivum]				ko03022|Basal transcription factors		nr +
Unigene70401_All	243	0.00	48.79	19.72	0.00	0.00	0.00	0.00	0.00	0.00	1.56E+01	5.23E-68	Up	1.43E+01	1.22E-26	Up	null	null		null	null		null	null		null	null									ESTscan −
Unigene70404_All	243	0.00	2.71	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	9.78E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan −
Unigene70405_All	243	0.00	2.92	1.75	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	1.08E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene70405_All//gi|116061052|emb|CAL56440.1|//6.00E-24//tousled-like kinase 2 (ISS) [Ostreococcus tauri]	Unigene70405_All//1.00E-18//AT5G20930| TSL (TOUSLED); kinase/ protein serine/threonine kinase				GO:0004672//GO:0005515//GO:0006464//GO:0009536//GO:0032559	nr +
Unigene7041_All	932	1.57	5.44	3.77	6.68	5.36	5.62	0.54	0.94	2.09	1.79E+00	1.71E-09	Up	1.26E+00	3.30E-04	Up	−3.19E-01	1.95E-01		−2.49E-01	3.51E-01		7.91E-01	2.41E-01		1.94E+00	1.51E-05	Up		Unigene7041_All//1.00E-09//DN801717					ESTscan −
Unigene70410_All	243	0.00	18.14	7.89	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	4.10E-25	Up	1.29E+01	1.47E-10	Up	null	null		null	null		null	null		null	null									ESTscan −
Unigene7042_All	516	0.41	0.59	0.10	5.02	4.67	1.05	9.50	3.24	6.33	5.39E-01	6.71E-01		−1.97E+00	3.80E-01		−1.04E-01	8.24E-01		−2.26E+00	3.39E-07	Down	−1.55E+00	2.51E-09	Down	−5.86E-01	1.22E-02		Unigene7042_All//gi|224122896|ref|XP_002318943.1|//1.00E-33//cc-nbs-lrr resistance protein [Populus trichocarpa]>gi|222857319|gb|EEE94866.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene7042_All//3.00E-25//AT1G62630| disease resistance protein (CC-NBS-LRR class), putative	Unigene7042_All//0.00E+00//ES852122		ko04626|Plant-pathogen interaction		nr +
Unigene70420_All	243	0.00	3.34	0.22	0.62	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	7.78E+00	6.28E-01		−9.26E+00	1.65E-01		−9.26E+00	2.32E-01		null	null		null	null									ESTscan −
Unigene70428_All	244	0.00	7.89	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	5.72E-11	Up	7.77E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70428_All//gi|301102815|ref|XP_002900494.1|//2.00E-25//P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]>gi|262101757|gb|EEY59809.1| P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]	Unigene70428_All//2.00E-19//AT4G37640| ACA2 (CALCIUM ATPASE 2); calcium ion transmembrane transporter/ calcium-transporting ATPase/ calmodulin binding				GO:0009206//GO:0019829//GO:0031224//GO:0032559//GO:0046873//GO:0070838	nr +
Unigene70429_All	244	0.00	3.74	1.31	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	1.04E+01	4.48E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene7043_All	820	0.13	0.12	0.32	0.61	1.22	0.99	9.75	6.78	3.55	−4.59E-02	9.87E-01		1.35E+00	4.09E-01		1.00E+00	1.65E-01		7.07E-01	3.93E-01		−5.24E-01	4.34E-03		−1.46E+00	6.30E-14	Down	Unigene7043_All//gi|260515145|gb|ACX43275.1|//5.00E-31//GTP binding protein gamma subunit [Brassica napus]	Unigene7043_All//5.00E-27//AT3G22942| AGG2 (G-PROTEIN GAMMA SUBUNIT 2)					nr −
Unigene70432_All	244	0.00	5.40	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.49E-07	Up	7.77E+00	6.28E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70436_All	244	0.00	3.11	2.18	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	1.11E+01	4.02E-03		null	null		null	null		null	null		null	null									
Unigene70437_All	244	0.00	17.65	8.29	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	1.56E-24	Up	1.30E+01	3.79E-11	Up	null	null		null	null		null	null		null	null		Unigene70437_All//gi|302128114|dbj|BAJ13478.1|//2.00E-16//actin 1 [Guillardia theta]	Unigene70437_All//3.00E-17//AT5G09810| ACT7 (ACTIN 7); structural constituent of cytoskeleton	Unigene70437_All//5.00E-12//DW226933		ko04145|Phagosome	GO:0000267//GO:0003015//GO:0005198//GO:0005884//GO:0006939//GO:0006950//GO:0007015//GO:0008015//GO:0008092//GO:0009314//GO:0009725//GO:0009913//GO:0012501//GO:0016020//GO:0017111//GO:0030017//GO:0030239//GO:0030312//GO:0031981//GO:0032432//GO:0032559//GO:0048588//GO:0048747//GO:0051707//GO:0060415	nr −
Unigene7044_All	385	0.68	0.53	1.11	3.88	2.50	10.56	8.79	12.70	4.14	−3.68E-01	7.78E-01		7.04E-01	5.54E-01		−6.32E-01	2.38E-01		1.44E+00	3.96E-06	Up	5.32E-01	2.99E-02		−1.09E+00	2.31E-04	Down	Unigene7044_All//gi|225441736|ref|XP_002283124.1|//1.00E-09//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene7044_All//8.00E-18//DW503349				nr +
Unigene70442_All	244	0.00	4.78	0.44	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.05E-06	Up	8.77E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70442_All//gi|297793741|ref|XP_002864755.1|//2.00E-11//tudor domain-containing protein [Arabidopsis lyrata subsp. lyrata]>gi|297310590|gb|EFH41014.1| tudor domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene70442_All//1.00E-12//AT5G61780| tudor domain-containing protein / nuclease family protein					nr +
Unigene70444_All	244	0.00	3.32	0.87	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	9.77E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan −
Unigene70445_All	244	0.00	3.11	0.44	0.00	0.00	0.00	0.00	0.00	0.33	1.16E+01	1.76E-04	Up	8.77E+00	3.93E-01		null	null		null	null		null	null		8.35E+00	4.01E-01		Unigene70445_All//gi|48431269|gb|AAT44124.1|//5.00E-18//F3H-like protein [Saussurea medusa]	Unigene70445_All//4.00E-19//AT4G10190| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene70445_All//1.00E-126//TC179429		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis	GO:0008152//GO:0016706//GO:0046914	nr +
Unigene70449_All	244	0.00	3.95	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	7.77E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70449_All//sp|Q292F9|GDAP2_DROPS//8.00E-21//Protein GDAP2 homolog OS=Drosophila pseudoobscura pseudoobscura GN=GA15091 PE=3 SV=1						swissprot +
Unigene7045_All	235	26.05	11.21	18.35	21.83	18.76	28.44	32.56	14.23	13.22	−1.22E+00	9.02E-07	Down	−5.05E-01	4.48E-02		−2.19E-01	4.51E-01		3.82E-01	1.12E-01		−1.19E+00	9.80E-10	Down	−1.30E+00	2.25E-11	Down	Unigene7045_All//gi|297597332|ref|NP_001043805.2|//1.00E-18//Os01g0666900 [Oryza sativa Japonica Group]>gi|255673532|dbj|BAF05719.2| Os01g0666900 [Oryza sativa Japonica Group]	Unigene7045_All//1.00E-17//AT2G34480| 60S ribosomal protein L18A (RPL18aB)	Unigene7045_All//6.00E-107//TC140689		ko03010|Ribosome		nr −
Unigene70451_All	245	0.00	2.90	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	8.76E+00	3.93E-01		null	null		null	null		null	null		null	null									
Unigene70453_All	245	0.00	4.76	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.05E-06	Up	7.76E+00	6.28E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70455_All	245	0.00	3.52	0.87	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	9.76E+00	1.39E-01		null	null		null	null		null	null		null	null									
Unigene70456_All	245	0.00	2.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene7046_All	531	0.89	1.05	1.30	1.13	2.27	1.70	1.35	0.63	4.13	2.43E-01	7.77E-01		5.56E-01	5.28E-01		1.01E+00	1.11E-01		5.96E-01	4.55E-01		−1.10E+00	1.49E-01		1.61E+00	6.34E-05	Up	Unigene7046_All//gi|224589671|gb|ACN59367.1|//2.00E-13//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene7046_All//2.00E-10//AT5G14210| leucine-rich repeat transmembrane protein kinase, putative					nr +
Unigene70461_All	245	0.00	4.14	1.30	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.23E-06	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene70462_All	245	0.00	2.90	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan −
Unigene7047_All	639	1.15	210.53	136.08	0.86	0.54	3.18	4.96	10.27	4.36	7.52E+00	0.00E+00	Up	6.89E+00	0.00E+00	Up	−6.70E-01	4.96E-01		1.89E+00	1.25E-04	Up	1.05E+00	5.22E-07	Up	−1.85E-01	5.87E-01		Unigene7047_All//gi|145408595|ref|YP_001152219.1|//8.00E-15//O8F58f [Pinus koraiensis]>gi|145048844|gb|ABP35460.1| O8F58f [Pinus koraiensis]		Unigene7047_All//2.00E-59//gi|109831956|gb|DW230515.1|DW230515				nr −
Unigene70470_All	245	0.00	9.72	3.69	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.50E-13	Up	1.19E+01	4.70E-05	Up	null	null		null	null		null	null		null	null									
Unigene70471_All	245	0.00	3.31	0.22	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	7.76E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70471_All//gi|223995573|ref|XP_002287460.1|//4.00E-17//alanine:glyoxylate aminotransferase [Thalassiosira pseudonana CCMP1335]>gi|220976576|gb|EED94903.1| alanine:glyoxylate aminotransferase [Thalassiosira pseudonana CCMP1335]	Unigene70471_All//3.00E-12//AT3G08860| alanine--glyoxylate aminotransferase, putative / beta-alanine:pyruvate aminotransferase, putative / AGT, putative			ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism	GO:0016740//GO:0043231	nr +
Unigene70473_All	245	0.00	5.38	0.00	0.20	0.42	0.00	0.00	0.00	0.16	1.24E+01	1.49E-07	Up	null	null		1.05E+00	8.06E-01		−7.67E+00	6.25E-01		null	null		7.35E+00	6.39E-01									
Unigene70475_All	245	0.00	3.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70475_All//sp|Q09225|NRF6_CAEEL//5.00E-08//Nose resistant to fluoxetine protein 6 OS=Caenorhabditis elegans GN=nrf-6 PE=1 SV=3						swissprot −
Unigene70479_All	246	0.00	2.68	1.30	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null									
Unigene7048_All	269	16.53	1.88	6.14	4.07	4.61	0.84	0.00	1.55	0.15	−3.13E+00	1.02E-15	Down	−1.43E+00	5.11E-06	Down	1.78E-01	8.19E-01		−2.28E+00	1.97E-03		1.06E+01	3.65E-03		7.21E+00	6.39E-01		Unigene7048_All//gi|255543699|ref|XP_002512912.1|//5.00E-20//conserved hypothetical protein [Ricinus communis]>gi|223547923|gb|EEF49415.1| conserved hypothetical protein [Ricinus communis]		Unigene7048_All//1.00E-129//TC167832				nr −
Unigene70481_All	246	0.21	5.36	1.52	0.00	0.70	0.55	0.34	0.85	0.32	4.65E+00	1.91E-06	Up	2.83E+00	9.30E-02		9.45E+00	2.26E-01		9.11E+00	3.09E-01		1.31E+00	4.47E-01		−8.56E-02	9.70E-01		Unigene70481_All//gi|266691|sp|P29528.1|OLEO7_GOSHI//7.00E-39//RecName: Full=Oleosin 16.4 kDa>gi|167361|gb|AAA18523.1| 16.4 kDa oleosin [Gossypium hirsutum]	Unigene70481_All//6.00E-17//AT3G27660| OLE04 (OLEOSIN 4)	Unigene70481_All//2.00E-134//TC148060			GO:0005811//GO:0009409//GO:0031224//GO:0048316	nr −
Unigene70485_All	246	0.00	2.88	0.87	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	9.76E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70486_All	246	0.00	3.09	1.08	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	1.01E+01	7.96E-02		null	null		null	null		null	null		null	null									
Unigene70488_All	246	0.00	10.71	9.31	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	5.44E-15	Up	1.32E+01	1.27E-12	Up	null	null		null	null		null	null		null	null									ESTscan −
Unigene70489_All	246	0.00	5.15	1.52	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.83E-07	Up	1.06E+01	2.49E-02		null	null		null	null		null	null		null	null									ESTscan −
Unigene7049_All	477	62.30	2.87	22.44	20.47	13.50	4.73	0.35	1.31	0.67	−4.44E+00	3.49E-135	Down	−1.47E+00	1.99E-38	Down	−6.01E-01	4.30E-04		−2.11E+00	1.13E-23	Down	1.89E+00	3.49E-02		9.14E-01	4.52E-01		Unigene7049_All//gi|22329164|ref|NP_195179.2|//7.00E-21//CIB1 (CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1); DNA binding / transcription factor [Arabidopsis thaliana]>gi|75299602|sp|Q8GY61.1|BH063_ARATH RecName: Full=Transcription factor bHLH63; AltName: Full=Transcription factor EN 84; AltName: Full=bHLH transcription factor bHLH063; AltName: Full=Basic helix-loop-helix protein 63; Short=bHLH 63; Short=AtbHLH63>gi|28950907|gb|AAO63377.1| At4g34530 [Arabidopsis thaliana]	Unigene7049_All//4.00E-22//AT4G34530| CIB1 (CRYPTOCHROME-INTERACTING BASIC-HELIX-LOOP-HELIX 1); DNA binding / transcription factor	Unigene7049_All//0.00E+00//TC167832	bHLH			nr +
Unigene70490_All	246	0.00	3.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	null	null		null	null		null	null		null	null		null	null									
Unigene70491_All	246	0.00	3.50	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	9.34E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene70491_All//sp|Q7K2G1|ADRM1_DROME//9.00E-25//Proteasomal ubiquitin receptor ADRM1 homolog OS=Drosophila melanogaster GN=CG13349 PE=1 SV=1						swissprot −
Unigene70497_All	246	1.70	0.62	0.87	4.25	0.56	1.29	1.55	2.04	1.62	−1.46E+00	2.34E-01		−9.75E-01	4.11E-01		−2.93E+00	1.21E-04	Down	−1.73E+00	1.55E-02		3.98E-01	6.52E-01		6.63E-02	9.66E-01			Unigene70497_All//6.00E-33//DT526950					
Unigene705_All	2668	3.45	2.41	3.89	16.77	12.75	8.99	4.28	1.94	2.39	−5.17E-01	6.48E-03		1.73E-01	3.90E-01		−3.95E-01	5.59E-08		−8.99E-01	1.24E-29		−1.14E+00	3.68E-13	Down	−8.41E-01	1.46E-08		Unigene705_All//gi|49523569|emb|CAF18246.1|//0.00E+00//STY-L protein [Antirrhinum majus]	Unigene705_All//0.00E+00//AT2G32700| WD-40 repeat family protein	Unigene705_All//0.00E+00//EE592846		ko03040|Spliceosome	GO:0005488//GO:0006350//GO:0006810//GO:0009791//GO:0016740//GO:0031410	nr −
Unigene7050_All	507	2.37	0.90	0.00	3.54	2.92	0.53	2.25	0.82	1.26	−1.40E+00	2.81E-02		−1.12E+01	1.36E-06	Down	−2.76E-01	5.85E-01		−2.73E+00	2.99E-06	Down	−1.45E+00	1.40E-02		−8.41E-01	1.23E-01		Unigene7050_All//gi|30693587|ref|NP_850683.1|//1.00E-36//ATGR1 (ARABIDOPSIS THALIANA GAMMA RESPONSE GENE 1) [Arabidopsis thaliana]>gi|259016242|sp|Q9ZRTL2|GR1_ARATH RecName: Full=Protein gamma response 1; AltName: Full=Protein gamma response 1>gi|115345801|gb|ABI95360.1| COM1/SAE2-like protein [Arabidopsis thaliana]	Unigene7050_All//6.00E-38//AT3G52115| ATGR1 (ARABIDOPSIS THALIANA GAMMA RESPONSE GENE 1)					nr −
Unigene70506_All	246	0.00	3.91	1.52	0.00	0.14	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	1.06E+01	2.49E-02		7.13E+00	8.20E-01		null	null		null	null		null	null		Unigene70506_All//gi|295913728|gb|ADG58103.1|//1.00E-13//transcription factor [Lycoris longituba]	Unigene70506_All//2.00E-05//AT1G10200| WLIM1; transcription factor/ zinc ion binding		LIM			nr +
Unigene70508_All	246	0.00	3.71	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	8.76E+00	3.93E-01		null	null		null	null		null	null		null	null									

Unigene7051_All	3500	0.22	0.19	0.23	0.38	0.16	0.32	5.35	11.28	11.72	-2.53E-01	7.26E-01		2.55E-02	9.94E-01		-1.29E+00	2.02E-02		-2.53E-01	6.86E-01		1.08E+00	9.55E-40	Up	1.13E+00	1.12E-45	Up	Unigene7051_All//gi|42563063|ref|NP_177060.3|//0.00E+00//armadillo/beta-catenin repeat protein-related / U-box domain-containing protein [Arabidopsis thaliana] >gi|75333632|sp|Q9CAA7.1|PUB42_ARATH RecName: Full=Putative U-box domain-containing protein 42; AltName: Full=Plant U-box protein 42	Unigene7051_All//0.00E+00//AT1G68940| armadillo/beta-catenin repeat protein-related / U-box domain-containing protein	Unigene7051_All//8.00E-134//CO498528				nr -
Unigene70511_All	246	0.00	3.30	0.65	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	9.34E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene70511_All//gi|171769901|sp|A2XQV4.1|ETFB_ORYSI//2.00E-19//RecName: Full=Electron transfer flavoprotein subunit beta, mitochondrial; Short=Beta-ETF; Flags: Precursor	Unigene70511_All//6.00E-16//AT5G43430| ETFBETA; electron carrier				GO:0006551//GO:0006787//GO:0043231	nr -
Unigene70513_All	246	0.00	2.88	1.08	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	1.01E+01	7.96E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene70515_All	246	0.00	3.71	1.30	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.61E-05	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene70515_All//sp|Q5ZJR8|ELOV6_CHICK//1.00E-06//Elongation of very long chain fatty acids protein 6 OS=Gallus gallus GN=ELOVL6 PE=2 SV=1							swissprot -
Unigene70519_All	247	0.00	9.23	5.39	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	5.63E-13	Up	1.24E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene70519_All//sp|P08123|CO1A2_HUMAN//5.00E-15//Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=6							swissprot +
Unigene7052_All	1020	20.21	14.56	27.62	4.30	5.17	4.21	0.83	0.08	0.31	-4.74E-01	8.90E-05		4.51E-01	1.87E-05		2.65E-01	3.60E-01		-3.10E-02	9.34E-01		-3.34E+00	2.51E-04	Down	-1.41E+00	3.70E-02		Unigene7052_All//gi|18414136|ref|NP_567420.1|//5.00E-54//transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75116576|sp|Q67X9.1|Y4141_ARATH RecName: Full=Uncharacterized protein At4g14100; Flags: Precursor >gi|88193798|gb|ABD42988.1| At4g14100 [Arabidopsis thaliana]	Unigene7052_All//2.00E-56//AT3G23760| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: transferase, transferring glycosyl groups (TAIR:AT4G14100.1); Has 63 Blast hits to 60 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 10; Fungi - 0; Plants - 51; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene7052_All//0.00E+00//gi|109881659|gb|DW510629.1|DW510629				nr -
Unigene70523_All	247	0.00	0.82	0.00	0.00	0.14	1.28	0.51	3.38	3.71	9.68E+00	1.35E-01		null	null		7.12E+00	8.20E-01		1.03E+01	4.07E-02		2.72E+00	1.18E-03		2.85E+00	3.18E-04	Up	Unigene70523_All//gi|6850900|emb|CAB71063.1|//4.00E-14//copia-type polyprotein [Arabidopsis thaliana]	Unigene70523_All//2.00E-09//AT1G48720| unknown protein	Unigene70523_All//1.00E-46//DT468735			GO:0005488	nr +
Unigene70524_All	247	0.00	3.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70524_All//gi|255589384|ref|XP_002534942.1|//5.00E-32//conserved hypothetical protein [Ricinus communis] >gi|223524320|gb|EEF27437.1| conserved hypothetical protein [Ricinus communis]							nr -
Unigene70536_All	247	0.00	3.28	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.34E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene70537_All	247	0.00	4.10	2.16	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.23E-06	Up	1.11E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene70537_All//gi|255084545|ref|XP_002508847.1|//1.00E-21//ribosomal protein L44 [Micromonas sp. RCC299] >gi|226524124|gb|ACO70105.1| ribosomal protein L44 [Micromonas sp. RCC299]	Unigene70537_All//7.00E-21//AT4G14320| 60S ribosomal protein L36a/L44 (RPL36aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene70539_All	248	0.00	5.31	1.07	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.49E-07	Up	1.01E+01	7.96E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene7054_All	741	0.00	0.62	0.22	0.40	1.72	1.46	4.45	13.82	7.85	9.27E+00	7.38E-03		7.75E+00	2.37E-01		2.09E+00	1.41E-03		1.86E+00	1.00E-02		1.63E+00	5.75E-20	Up	8.19E-01	1.36E-04			Unigene7054_All//9.00E-07//ES812029					
Unigene70540_All	248	0.00	12.46	3.65	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	1.38E-17	Up	1.18E+01	4.70E-05	Up	null	null		null	null		null	null		null	null									
Unigene70541_All	248	0.00	4.09	0.86	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.23E-06	Up	9.75E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70541_All//gi|301093942|ref|XP_002997370.1|//7.00E-28//ATP-citrate synthase [Phytophthora infestans T30-4] >gi|262110768|gb|EEY68820.1| ATP-citrate synthase [Phytophthora infestans T30-4]	Unigene70541_All//1.00E-23//AT1G09430| ACLA-3; ATP citrate synthase			ko00020|Citrate cycle (TCA cycle)	GO:0004774//GO:0005975//GO:0016747//GO:0032559//GO:0044424//GO:0016912	nr +
Unigene70544_All	248	0.00	2.66	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene70545_All	248	0.00	3.47	2.15	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	1.11E+01	4.02E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene70546_All	248	0.00	3.88	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	8.75E+00	3.93E-01		null	null		null	null		null	null		null	null									
Unigene70547_All	248	0.00	3.68	2.15	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	1.11E+01	4.02E-03		null	null		null	null		null	null		null	null									
Unigene7055_All	516	2.74	0.59	5.68	4.54	4.20	2.01	1.15	0.65	1.85	-2.22E+00	5.59E-04	Down	1.05E+00	6.29E-03		-1.10E-01	8.22E-01		-1.17E+00	5.07E-03		-8.24E-01	3.48E-01		6.92E-01	2.60E-01		Unigene7055_All//gi|75206301|sp|Q9SJN2.1|PP187_ARATH//2.00E-36//RecName: Full=Pentatricopeptide repeat-containing protein At2g36240	Unigene7055_All//2.00E-19//AT2G36240| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT1G09900.1); Has 18740 Blast hits to 5421 proteins in 159 species: Archae - 3; Bacteria - 12; Metazoa - 272; Fungi - 258; Plants - 17650; Viruses - 2; Other Eukaryotes - 543 (source: NCBI BLink).					nr -
Unigene70551_All	248	0.00	4.29	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.80E-06	Up	8.75E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70551_All//gi|301108545|ref|XP_002903354.1|//9.00E-07//mucin-like protein [Phytophthora infestans T30-4] >gi|262097726|gb|EEY55778.1| mucin-like protein [Phytophthora infestans T30-4]					GO:0009987	nr +
Unigene70555_All	248	0.00	3.06	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	9.33E+00	2.37E-01		null	null		null	null		null	null		null	null									
Unigene70559_All	248	0.00	3.47	1.72	0.00	0.28	0.36	0.00	0.17	0.96	1.18E+01	4.93E-05	Up	1.07E+01	1.37E-02		8.12E+00	6.04E-01		8.51E+00	4.72E-01		7.40E+00	6.28E-01		9.91E+00	4.39E-02									
Unigene70562_All	248	0.00	3.47	1.50	0.20	0.97	0.36	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	1.06E+01	2.49E-02		2.27E+00	3.05E-01		8.58E-01	7.92E-01		null	null		null	null									
Unigene70563_All	248	0.00	7.36	4.72	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.14E-10	Up	1.22E+01	1.77E-06	Up	null	null		null	null		null	null		null	null									
Unigene70564_All	248	0.00	2.86	3.01	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	1.16E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene70564_All//gi|301557932|gb|ADK78988.1|//4.00E-08//VAMP721 [Petunia integrifolia subsp. inflata]	Unigene70564_All//4.00E-05//AT1G04760| ATVAMP726			ko04130|SNARE interactions in vesicular transport	GO:0006810//GO:0016020//GO:0043231	nr -
Unigene70565_All	248	0.00	3.06	0.86	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	9.75E+00	1.39E-01		null	null		null	null		null	null		null	null									
Unigene70568_All	248	0.00	3.06	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	9.33E+00	2.37E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70576_All	248	0.00	4.90	1.29	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.46E-07	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene70576_All//gi|298706532|emb|CBQ29502.1|//4.00E-16//eukaryotic initiation factor 3b [Ectocarpus siliculosus]	Unigene70576_All//4.00E-11//AT5G27640| TIF3B1 (TRANSLATION INITIATION FACTOR 3B1); nucleic acid binding / translation initiation factor				GO:0003676	nr +
Unigene70578_All	248	127.43	30.24	33.07	120.52	57.62	61.01	94.45	730.08	43.37	-2.08E+00	4.82E-68	Down	-1.95E+00	2.40E-60	Down	-1.06E+00	9.11E-30	Down	-9.82E-01	4.48E-23		2.95E+00	0.00E+00	Up	-1.12E+00	2.43E-26	Down	Unigene70578_All//gi|93280156|gb|ABF06706.1|//1.00E-18//UP-9A [Nicotiana tabacum]	Unigene70578_All//4.00E-08//AT3G19570| LSU3 (RESPONSE TO LOW SULFUR 3)	Unigene70578_All//6.00E-138//BG445064				nr -
Unigene70579_All	248	0.00	2.66	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	7.75E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70579_All//gi|255073923|ref|XP_002500636.1|//1.00E-06//predicted protein [Micromonas sp. RCC299] >gi|226515899|gb|ACO61894.1| predicted protein [Micromonas sp. RCC299]				ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene7058_All	1028	0.10	9.86	1.66	0.00	0.13	0.09	4.24	3.94	16.04	6.60E+00	2.18E-54	Up	4.03E+00	2.79E-07	Up	7.07E+00	3.17E-01		6.46E+00	4.72E-01		-1.03E-01	7.24E-01		1.92E+00	2.73E-40	Up	Unigene7058_All//gi|297604030|ref|NP_001054880.2|//6.00E-59//Os05g0200100 [Oryza sativa Japonica Group] >gi|255676121|dbj|BAF16794.2| Os05g0200100 [Oryza sativa Japonica Group]	Unigene7058_All//8.00E-60//AT4G29670| thioredoxin family protein	Unigene7058_All//0.00E+00//TC159286				nr +
Unigene70581_All	249	0.00	2.85	0.00	0.00	0.00	0.18	0.51	0.50	1.28	1.15E+01	3.31E-04	Up	null	null		null	null		7.50E+00	6.88E-01		-1.65E-02	1.02E+00		1.33E+00	2.93E-01									
Unigene7059_All	640	26.49	3.56	19.30	15.72	7.26	3.95	0.40	0.00	0.31	-2.89E+00	5.55E-54	Down	-4.57E-01	1.15E-03		-1.11E+00	4.52E-11	Down	-1.99E+00	1.24E-22	Down	-8.63E+00	4.03E-02		-3.49E-01	7.66E-01		Unigene7059_All//gi|297720125|ref|NP_001172424.1|//8.00E-08//Os01g0564600 [Oryza sativa Japonica Group] >gi|255673372|dbj|BAH91154.1| Os01g0564600 [Oryza sativa Japonica Group]	Unigene7059_All//2.00E-06//AT3G47210| unknown protein	Unigene7059_All//5.00E-85//gi|11204961|gb|BF273903.1|BF273903				nr +
Unigene70591_All	249	0.00	2.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70591_All//gi|115471719|ref|NP_001059458.1|//2.00E-09//Os07g0414800 [Oryza sativa Japonica Group] >gi|113610994|dbj|BAF21372.1| Os07g0414800 [Oryza sativa Japonica Group]	Unigene70591_All//9.00E-10//AT3G05520| F-actin capping protein alpha subunit family protein				GO:0043231	nr -
Unigene70592_All	249	0.00	4.27	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.80E-06	Up	7.74E+00	6.28E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70594_All	249	0.00	3.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70594_All//gi|255074275|ref|XP_002500812.1|//1.00E-26//formaldehyde dehydrogenase/S-formylglutathione hydrolase [Micromonas sp. RCC299] >gi|226516075|gb|ACO62070.1| formaldehyde dehydrogenase/S-formylglutathione hydrolase [Micromonas sp. RCC299]	Unigene70594_All//4.00E-27//AT5G43940| HOT5 (sensitive to hot temperatures 5); S-(hydroxymethyl)glutathione dehydrogenase/ S-nitrosoglutathione reductase				ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism	GO:0006067//GO:0006081//GO:0009408//GO:0009791//GO:0016616//GO:0016557//GO:0016788//GO:0042579//GO:0046914	nr -
Unigene70595_All	249	0.00	3.05	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene70596_All	249	0.00	3.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.33E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene70597_All	249	0.42	4.68	1.07	0.00	0.00	0.00	0.00	0.00	0.00	3.48E+00	7.08E-05	Up	1.35E+00	4.09E-01		null	null		null	null		null	null		null	null		Unigene70597_All//gi|124360373|gb|ABN08386.1|//3.00E-32//Protein kinase [Medicago truncatula]	Unigene70597_All//1.00E-27//AT4G14480| protein kinase family protein			ko04626|Plant-pathogen interaction	GO:0004702//GO:0006464//GO:0016020//GO:0032559	nr -

Unigene70598_All	249	0.00	3.05	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	9.33E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene70598_All//gi|115447465|ref|NP_001047512.1|//1.00E-27//Os02g0634500 [Oryza sativa Japonica Group] >gi|113537043|dbj|BAF09426.1| Os02g0634500 [Oryza sativa Japonica Group]	Unigene70598_All//2.00E-24//AT5G23140| NCLPP7 (NUCLEAR-ENCODED CLP PROTEASE P7); serine-type endopeptidase				GO:0001071//GO:0000376//GO:0004175//GO:0004672//GO:0006351//GO:0006464//GO:0006810//GO:0032559//GO:0043231	nr -
Unigene70599_All	249	0.00	2.85	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	9.33E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene70599_All//sp|Q9UJM3|ERRF1_HUMAN//6.00E-43//ERBB receptor feedback inhibitor 1 OS=Homo sapiens GN=ERRFI1 PE=1 SV=1						swissprot -
Unigene70606_All	249	0.00	3.66	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	8.74E+00	3.93E-01		null	null		null	null		null	null		null	null									
Unigene70609_All	249	0.00	3.46	0.86	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	9.74E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70609_All//sp|Q9W261|RTF1_DROME//1.00E-25//RNA polymerase-associated protein Rtf1 OS=Drosophila melanogaster GN=Rtf1 PE=1 SV=1						swissprot +
Unigene70611_All	249	0.00	2.85	1.71	0.40	0.00	0.18	0.85	0.00	0.32	1.15E+01	3.31E-04	Up	1.02E+01	1.37E-02		-8.64E+00	3.10E-01		-1.14E+00	6.74E-01		-9.73E+00	7.41E-02		-1.41E+00	3.80E-01									
Unigene70612_All	249	0.00	3.66	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	8.74E+00	3.93E-01		null	null		null	null		null	null		null	null									
Unigene70613_All	249	0.00	2.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene70616_All	249	0.00	6.31	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	5.69E-09	Up	7.74E+00	6.28E-01		null	null		null	null		null	null		null	null									
Unigene70621_All	250	0.00	4.66	2.13	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.03E-06	Up	1.11E+01	4.02E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene70622_All	250	0.00	3.04	5.11	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	1.23E+01	4.68E-07	Up	null	null		null	null		null	null		null	null		Unigene70622_All//gi|115466902|ref|NP_001057050.1|//9.00E-07//Os06g0195900 [Oryza sativa Japonica Group] >gi|113595090|dbj|BAF18964.1| Os06g0195900 [Oryza sativa Japonica Group]	Unigene70622_All//8.00E-08//AT1G50920| GTP-binding protein-related				GO:0044464	nr -
Unigene70627_All	250	0.00	4.46	1.07	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.99E-06	Up	1.01E+01	7.96E-02		null	null		null	null		null	null		null	null		Unigene70627_All//gi|41203470|ref|NP_957730.1|//1.00E-11//NADH dehydrogenase subunit 3 [Emiliania huxleyi] >gi|33114156|gb|AAP94712.1| NADH dehydrogenase subunit 3 [Emiliania huxleyi]			ko00190|Oxidative phosphorylation	GO:0008152//GO:0016020	nr -
Unigene70629_All	250	0.00	4.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.80E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene70629_All//gi|300266442|gb|EFJ50629.1|//4.00E-08//hypothetical protein VOLCADRAFT_116802 [Volvox carteri f. nagariensis]						nr +
Unigene70633_All	250	0.00	4.26	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.80E-06	Up	1.05E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene70633_All//gi|226453736|gb|EEH51044.1|//2.00E-09//predicted protein [Micromonas pusilla CCMP1545]	Unigene70633_All//3.00E-05//AT1G30900| vacuolar sorting receptor, putative					nr -
Unigene70634_All	250	0.00	3.65	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	7.73E+00	6.28E-01		null	null		null	null		null	null		null	null									ESTScan +
Unigene70637_All	250	0.00	5.68	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	4.05E-08	Up	7.73E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70637_All//gi|75291596|sp|Q6QBA5.1|HXK2_TOBAC//2.00E-15//RecName: Full=Hexokinase-2, chloroplastic; AltName: Full=NtHxK2; Flags: Precursor >gi|45387405|gb|AAS60193.1| hexokinase 2 [Nicotiana tabacum]	Unigene70637_All//7.00E-13//AT1G47840| HXK3 (HEXOKINASE 3); ATP binding / fructokinase/ glucokinase/ hexokinase			ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism	GO:0016772//GO:0043231	nr -
Unigene70638_All	250	0.00	3.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene70639_All	250	0.00	3.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.93E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70639_All//gi|300262824|gb|EFJ47028.1|//1.00E-08//transcription factor jumonji domain-containing protein [Volvox carteri f. nagariensis]			ko04144|Endocytosis	GO:0005488	nr -
Unigene70646_All	250	0.00	2.63	2.56	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	1.13E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene70646_All//sp|P15260|INGR1_HUMAN//2.00E-42//Interferon gamma receptor 1 OS=Homo sapiens GN=IFNGR1 PE=1 SV=1						swissprot +
Unigene7065_All	323	3.08	1.57	10.22	7.87	6.18	5.73	4.19	3.75	4.44	-9.72E-01	1.58E-01		1.73E+00	6.46E-06	Up	-3.47E-01	4.10E-01		-4.56E-01	2.80E-01		-1.59E-01	7.61E-01		8.41E-02	8.72E-01				Unigene7065_All//5.00E-173//ES806165					
Unigene70650_All	251	0.42	4.04	0.85	0.60	0.41	0.00	0.00	0.17	1.75	3.28E+00	3.79E-04	Up	1.03E+00	5.90E-01		-5.33E-01	7.84E-01		-9.22E+00	2.32E-01		7.38E+00	6.28E-01		1.08E+01	2.13E-03		Unigene70650_All//gi|253741125|gb|ACT34899.1|//7.00E-08//GT4 [Medicago truncatula]	Unigene70650_All//3.00E-08//AT5G49690| UDP-glucoronosyl/UDP-glucosyl transferase family protein				GO:0016758	nr -
Unigene70651_All	251	0.00	4.64	1.06	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.03E-06	Up	1.01E+01	7.96E-02		null	null		null	null		null	null		null	null									
Unigene70652_All	251	0.00	5.65	0.85	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	4.05E-08	Up	9.73E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70652_All//sp|P08120|CO4A1_DROME//4.00E-30//Collagen alpha-1(IV) chain OS=Drosophila melanogaster GN=Cg25C PE=2 SV=3						swissprot +
Unigene70654_All	251	1.25	8.28	2.12	0.79	1.37	0.00	0.51	0.00	0.32	2.73E+00	1.07E-06	Up	7.62E-01	4.52E-01		7.89E-01	5.95E-01		-9.63E+00	1.33E-01		-8.98E+00	2.34E-01		-6.71E-01	7.18E-01									
Unigene70656_All	251	0.00	3.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene70657_All	251	0.21	3.43	0.21	0.00	0.00	0.00	0.00	0.00	0.00	4.04E+00	4.20E-04	Up	2.61E-02	9.92E-01		null	null		null	null		null	null		null	null									ESTScan +
Unigene7066_All	727	9.64	6.55	15.89	3.49	2.84	0.62	0.00	0.00	0.00	-5.58E-01	1.17E-02		7.21E-01	3.03E-05		-2.98E-01	4.89E-01		-2.49E+00	7.15E-08	Down	null	null		null	null				Unigene7066_All//0.00E+00//TC160926					
Unigene70660_All	251	0.00	9.08	2.76	0.40	0.27	1.08	0.17	1.50	0.00	1.31E+01	5.63E-13	Up	1.14E+01	6.14E-04	Up	-5.33E-01	8.14E-01		1.44E+00	4.09E-01		3.15E+00	3.41E-02		-7.40E+00	6.05E-01		Unigene70660_All//gi|21307619|gb|AAK56557.1|//2.00E-15//mannan endo-1,4-beta-mannosidase [Solanum lycopersicum]	Unigene70660_All//4.00E-10//AT1G02310| glycosyl hydrolase family protein 5 / cellulase family protein / (1-4)-beta-mannan endohydrolase, putative	Unigene70660_All//6.00E-135//BG445647			GO:0016798//GO:0043167//GO:0044238	nr +
Unigene70662_All	251	0.00	4.44	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.99E-06	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene70662_All//gi|297817282|ref|XP_002876524.1|//1.00E-06//predicted protein [Arabidopsis lyrata subsp. lyrata] >gi|297322362|gb|EFH52783.1| predicted protein [Arabidopsis lyrata subsp. lyrata]	Unigene70662_All//4.00E-07//AT3G59790| ATMPK10; MAP kinase/ kinase			ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene70667_All	251	0.00	4.04	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.23E-06	Up	8.73E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70667_All//sp|Q5R6J7|GPAT4_PONAB//3.00E-15//Glycerol-3-phosphate acyltransferase 4 OS=Pongo abelii GN=AGPAT6 PE=2 SV=2						swissprot -
Unigene70669_All	251	0.00	4.84	2.33	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.46E-07	Up	1.12E+01	2.17E-03		null	null		null	null		null	null		null	null									
Unigene70670_All	251	0.00	6.26	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	5.69E-09	Up	1.05E+01	2.49E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene70676_All	251	0.00	3.84	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	8.73E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70676_All//gi|301114519|ref|XP_002999029.1|//3.00E-28//argininosuccinate synthase [Phytophthora infestans T30-4] >gi|262111123|gb|EEY69175.1| argininosuccinate synthase [Phytophthora infestans T30-4]	Unigene70676_All//5.00E-22//AT4G24830| argininosuccinate synthase family			ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0006525//GO:0009532//GO:0016879//GO:0032559	nr +
Unigene70677_All	251	0.00	4.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.46E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene70677_All//gi|15227376|ref|NP_181684.1|//7.00E-15//SFGH (S-FORMYLGLUTATHIONE HYDROLASE); S-formylglutathione hydrolase/ hydrolase, acting on ester bonds [Arabidopsis thaliana] >gi|114152156|sp|Q8LAS8.2|SFGH_ARATH RecName: Full=S-formylglutathione hydrolase; Short=AtSFGH; AltName: Full=Esterase D >gi|14190395|gb|AAK55678.1|AF378875_1 At2g41530/T32G6.5 [Arabidopsis thaliana] >gi|17386096|gb|AAL38594.1|AF446861_1 At2g41530/T32G6.5 [Arabidopsis thaliana] >gi|19572942|emb|CAC87877.1| S-formylglutathione hydrolase [Arabidopsis thaliana]	Unigene70677_All//3.00E-16//AT2G41530| SFGH (S-FORMYLGLUTATHIONE HYDROLASE); S-formylglutathione hydrolase/ hydrolase, acting on ester bonds				GO:0005576//GO:0010038//GO:0016790//GO:0043231	nr +
Unigene70679_All	251	0.00	3.43	2.12	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.93E-05	Up	1.11E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene70679_All//gi|300793602|tpg|DAA33867.1|//2.00E-27//TPA: TPA_inf: aquaporin TIP1:4 [Gossypium hirsutum]	Unigene70679_All//3.00E-19//AT2G36830| GAMMA-TIP (GAMMA TONOPLAST INTRINSIC PROTEIN); water channel	Unigene70679_All//6.00E-30//EX168789			GO:0000322//GO:0000325//GO:0005372//GO:0009526//GO:0010476//GO:0031224//GO:0042044//GO:0042886//GO:0042887	nr +
Unigene70681_All	252	0.00	4.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.80E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene70681_All//sp|O95832|CLD1_HUMAN//9.00E-44//Claudin-1 OS=Homo sapiens GN=CLDN1 PE=1 SV=1						swissprot +
Unigene70683_All	252	0.00	3.82	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.38E-05	Up	8.72E+00	3.93E-01		null	null		null	null		null	null		null	null									
Unigene70689_All	252	0.21	3.62	1.06	0.20	0.41	0.54	0.00	0.50	0.63	4.12E+00	2.34E-04	Up	2.35E+00	2.39E-01		1.05E+00	8.06E-01		1.44E+00	6.37E-01		8.96E+00	2.40E-01		9.30E+00	1.39E-01				Unigene70689_All//1.00E-34//DN803832					
Unigene70690_All	252	0.00	3.42	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.93E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70690_All//gi|4325041|gb|AAD17230.1|//2.00E-38//FtsH-like protein Pftf precursor [Nicotiana tabacum]	Unigene70690_All//2.00E-39//AT2G30950| VAR2 (VARIEGATED 2); ATP-dependent peptidase/ ATPase/ metallopeptidase/ zinc ion binding	Unigene70690_All//1.00E-34//TC150567			GO:0004175//GO:0009526//GO:0009534//GO:0009668//GO:0009767//GO:0031224//GO:0032559//GO:0042623//GO:0044237//GO:0044436//GO:0016914	nr -
Unigene70695_All	252	0.00	2.61	0.00	0.59	0.41	1.08	0.50	0.00	0.32	1.14E+01	6.22E-04	Up	null	null		-5.33E-01	7.84E-01		8.59E-01	6.30E-01		-8.98E+00	2.34E-01		-6.71E-01	7.18E-01									ESTscan +
Unigene707_All	602	1.56	0.84	0.88	1.57	0.57	0.90	3.44	2.64	1.19	-8.94E-01	2.14E-01		-8.23E-01	2.71E-01		-1.46E+00	3.60E-02		-8.04E-01	2.77E-01		-3.83E-01	3.73E-01		-1.53E+00	1.72E-04	Down	Unigene707_All//gi|145308227|gb|ABP57378.1|//7.00E-42//GN0M-like 1 protein [Nicotiana tabacum]	Unigene707_All//7.00E-43//AT5G39500| pattern formation protein, putative	Unigene707_All//3.00E-34//TC143189			GO:0000578//GO:0000902//GO:0001738//GO:0003006//GO:0005083//GO:0009926//GO:0015300//GO:0032011//GO:0032386//GO:0033205//GO:0042802//GO:0044464//GO:0045229//GO:0048527//GO:0048764	nr +
Unigene70700_All	252	0.00	2.61	0.85	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.22E-04	Up	9.72E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70700_All//gi|62319194|dbj|BAD94376.1|//3.00E-06//spliceosome associated protein - like [Arabidopsis thaliana]	Unigene70700_All//2.00E-05//AT4G21660| proline-rich spliceosome-associated (PSP) family protein			ko03040|Spliceosome	GO:0043231	nr -
Unigene70705_All	252	0.00	3.22	2.54	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.33E-05	Up	1.13E+01	1.16E-03		null	null		null	null		null	null		null	null		Unigene70705_All//sp|Q09666|AHNK_HUMAN//1.00E-41//Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2						swissprot -
Unigene70711_All	253	0.00	3.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene70712_All	253	0.00	5.41	2.10	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.78E-08	Up	1.10E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene70712_All//sp|P22736|NR4A1_HUMAN//5.00E-46//Nuclear receptor subfamily 4 group A member 1 OS=Homo sapiens GN=NR4A1 PE=1 SV=1						swissprot +
Unigene70713_All	253	0.00	2.60	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	8.72E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70713_All//gi|115445085|ref|NP_001046322.1|//4.00E-12//Os02g0221500 [Oryza sativa Japonica Group] >gi|113535853|dbj|BAF08236.1| Os02g0221500 [Oryza sativa Japonica Group]	Unigene70713_All//3.00E-13//AT3G13224| RNA recognition motif (RRM)-containing protein			ko03040|Spliceosome	GO:0005488	nr +

Unigene70715_All	253	0.00	5.21	0.63	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.49E-07	Up	9.30E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene70715_All//gi|300264016|gb|EFJ48214.1|//1.00E-24//E1 subunit of 2-oxoglutarate dehydrogenase [Volvox carteri f. nagariensis]	Unigene70715_All//3.00E-25//AT5G65750| 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative			ko00380|Tryptophan metabolism//ko00020|Citrate cycle (TCA cycle)//ko00310|Lysine degradation	GO:0006607//GO:0010038//GO:0016624//GO:0016798//GO:0019842//GO:0043231//GO:0046914	nr +
Unigene70717_All	253	0.00	1.60	11.58	0.00	0.00	0.18	0.00	0.00	0.00	1.06E+01	1.34E-02		1.35E+01	3.52E-16	Up	null	null		7.48E+00	6.88E-01		null	null		null	null		Unigene70717_All//sp|P01876|IGHA1_HUMAN//3.00E-45//Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2						swissprot -
Unigene7072_All	265	1.38	1.53	0.40	2.82	2.99	5.97	1.28	6.15	4.21	1.46E-01	8.98E-01		-1.78E+00	2.33E-01		8.40E-02	9.44E-01		1.08E+00	4.49E-02		2.27E+00	1.94E-05	Up	1.72E+00	4.13E-03				Unigene7072_All//3.00E-07//TC133360				
Unigene70720_All	253	0.00	2.60	1.26	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene70720_All//sp|Q5T653|RM02_HUMAN//5.00E-13//39S ribosomal protein L2, mitochondrial OS=Homo sapiens GN=MRPL2 PE=1 SV=2						swissprot -
Unigene70724_All	253	0.00	2.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70724_All//sp|Q5R491|TMM66_PONAB//1.00E-44//Transmembrane protein 66 OS=Pongo abelii GN=TMEM66 PE=2 SV=2						swissprot -
Unigene70728_All	253	0.41	3.81	0.00	0.98	0.54	0.18	0.00	0.00	0.00	3.20E+00	6.55E-04	Up	-8.69E+00	3.88E-01		-8.55E-01	5.73E-01		-2.46E+00	2.23E-01		null	null		null	null		Unigene70728_All//gi|99646749|emb|CAE22425.1|//7.00E-15//WD-40 repeat family protein [Beta vulgaris]	Unigene70728_All//3.00E-13//AT3G18850| transducin family protein / WD-40 repeat family protein				GO:0004683	nr -
Unigene70729_All	253	0.00	4.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.23E-06	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene7073_All	363	1.73	1.54	1.32	7.82	7.49	3.11	1.98	0.92	0.55	-1.72E-01	8.29E-01		-3.90E-01	6.46E-01		-6.18E-02	8.68E-01		-1.33E+00	4.10E-04	Down	-1.10E+00	1.49E-01		-1.85E+00	1.78E-02				Unigene7073_All//1.00E-65//gi|78349324|gb|DT569598.1|DT569598				
Unigene70730_All	253	0.00	3.81	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.37E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70730_All//sp|Q9VUQ5|AGO2_DROME//6.00E-10//Protein argonaute-2 OS=Drosophila melanogaster GN=AGO2 PE=1 SV=3						swissprot +
Unigene70732_All	253	0.00	4.41	2.10	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.99E-06	Up	1.10E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene70732_All//gi|77176709|gb|AB461469.1|//1.00E-27//DNA-dependent RNA polymerase II largest subunit [Glaucocystis nostochinearum]	Unigene70732_All//4.00E-07//AT4G35800| NRPB1 (RNA POLYMERASE II LARGE SUBUNIT): DNA binding / DNA-directed RNA polymerase			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0005488//GO:0006350//GO:0009536//GO:0016591//GO:0034062	nr +
Unigene70734_All	253	0.00	4.01	1.26	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.23E-06	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene70734_All//sp|Q32NT4|LRC58_XENLA//6.00E-18//Leucine-rich repeat-containing protein 58 OS=Xenopus laevis GN=lrrc58 PE=2 SV=1						swissprot +
Unigene7074_All	313	5.18	0.97	2.72	13.69	11.55	8.66	1.62	0.80	0.89	-2.42E+00	7.51E-05	Down	-9.29E-01	8.76E-02		-2.45E-01	4.51E-01		-6.61E-01	2.40E-02		-1.02E+00	2.88E-01		-8.63E-01	3.39E-01		Unigene7074_All//gi|255545412|ref|XP_002513766.1|//5.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223546852|gb|EEF48349.1| conserved hypothetical protein [Ricinus communis]		Unigene7074_All//2.00E-138//AW187689				nr +
Unigene70740_All	253	0.00	2.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70740_All//gi|87241031|gb|AB032889.1|//2.00E-34//AAA ATPase; 26S proteasome subunit P45 [Medicago truncatula] >gi|124360940|gb|ABN08912.1| AAA ATPase; 26S proteasome subunit P45 [Medicago truncatula]	Unigene70740_All//5.00E-35//AT2G20140| 26S protease regulatory complex subunit 4, putative	Unigene70740_All//7.00E-08//ES836431		ko03050|Proteasome	GO:0009057//GO:0016020//GO:0032559//GO:0042623//GO:0043234//GO:0044424	nr +
Unigene70745_All	254	0.00	3.39	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	1.07E+01	1.37E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene70746_All	254	0.00	2.99	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	7.71E+00	6.28E-01		null	null		null	null		null	null		null	null									
Unigene7075_All	1008	0.00	0.15	0.00	0.10	1.13	0.99	54.02	29.48	50.11	7.24E+00	2.32E-01		null	null		3.51E+00	4.52E-05	Up	3.32E+00	3.47E-04	Up	-8.74E-01	8.06E-39		-1.08E-01	1.14E-01		Unigene7075_All//gi|42571383|ref|NP_973782.1|//1.00E-88//disease resistance-responsive family protein [Arabidopsis thaliana] >gi|84398894|gb|AAF75080.1|AC007583_16 Contains similarity to disease resistance response protein from Pisum sativum gb|M18250. EST gb|F13940 comes from this gene [Arabidopsis thaliana]	Unigene7075_All//8.00E-79//AT1G07730| disease resistance-responsive family protein					nr +
Unigene70751_All	254	0.00	3.19	0.84	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	9.71E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70751_All//gi|159477317|ref|XP_001696757.1|//6.00E-32//T-complex protein 1, beta subunit [Chlamydomonas reinhardtii] >gi|158275086|gb|EDP00865.1| T-complex protein 1, beta subunit [Chlamydomonas reinhardtii]	Unigene70751_All//1.00E-30//AT5G20890| chaperonin, putative				GO:0004672//GO:0005515//GO:0006464//GO:0032559//GO:0044424	nr +
Unigene70752_All	254	0.00	2.59	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	8.71E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70752_All//sp|B4QR46|SRRT_DROWI//4.00E-16//Serrate RNA effector molecule homolog OS=Drosophila willistoni GN=Ars2 PE=3 SV=1						swissprot +
Unigene70753_All	254	0.00	2.99	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	8.71E+00	3.93E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70757_All	254	0.00	2.59	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	8.71E+00	3.93E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene70758_All	254	0.00	4.19	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.80E-06	Up	1.07E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene70758_All//gi|115479005|ref|NP_001063096.1|//1.00E-13//Os09g0394900 [Oryza sativa Japonica Group] >gi|113631329|dbj|BAF25010.1| Os09g0394900 [Oryza sativa Japonica Group]	Unigene70758_All//3.00E-12//AT1G68090| ANN3; calcium ion binding / calcium-dependent phospholipid binding					nr -
Unigene7076_All	765	21.48	9.34	16.22	1.17	2.70	1.30	0.00	0.00	0.00	-1.20E+00	1.51E-16	Down	-4.05E-01	4.88E-03		1.20E+00	7.15E-03		1.48E-01	8.42E-01		null	null		null	null		Unigene7076_All//gi|38603902|gb|AAR24696.1|//3.00E-33//At4g32870 [Arabidopsis thaliana] >gi|38603986|gb|AAR24736.1| At4g32870 [Arabidopsis thaliana]	Unigene7076_All//2.00E-34//AT4G32870| unknown protein	Unigene7076_All//0.00E+00//TC148396				nr -
Unigene70761_All	254	0.00	3.19	1.05	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	1.00E+01	7.96E-02		null	null		null	null		null	null		null	null		Unigene70761_All//gi|301113300|ref|XP_002988420.1|//8.00E-32//H/ACA ribonucleoprotein complex subunit 4 [Phytophthora infestans T30-4] >gi|262111721|gb|EE169773.1| H/ACA ribonucleoprotein complex subunit 4 [Phytophthora infestans T30-4]	Unigene70761_All//8.00E-33//AT3G57150| NAP57 (Arabidopsis thaliana homologue of NAP57): pseudouridine synthase				GO:0003676//GO:0009451//GO:0010467//GO:0016866//GO:0031981//GO:0032991//GO:0044444	nr +
Unigene70765_All	254	0.00	3.19	0.84	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	9.71E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene70766_All	254	0.00	4.79	0.00	0.00	0.00	0.00	0.33	0.00	0.00	1.22E+01	5.46E-07	Up	null	null		null	null		null	null		-8.38E+00	3.99E-01		-8.38E+00	3.55E-01				Unigene70766_All//3.00E-13//FL577730				
Unigene70767_All	254	0.00	4.19	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.80E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene70767_All//sp|P08253|MMP2_HUMAN//2.00E-45//72 kDa type IV collagenase OS=Homo sapiens GN=MMP2 PE=1 SV=2						swissprot +
Unigene70769_All	254	0.00	2.99	0.21	0.59	0.27	0.18	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	7.71E+00	6.28E-01		-1.12E+00	5.82E-01		-1.73E+00	5.00E-01		null	null		null	null									
Unigene7077_All	1267	0.70	0.28	0.84	0.79	0.57	0.07	5.01	1.29	4.53	-1.33E+00	7.96E-02		2.60E-01	6.82E-01		-4.62E-01	5.18E-01		-3.46E+00	1.73E-04	Down	-1.96E+00	4.57E-16	Down	-1.45E-01	5.36E-01		Unigene7077_All//gi|297798392|ref|XP_002867080.1|//3.00E-72//RWP-RK domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297312916|gb|EFH43339.1| RWP-RK domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene7077_All//8.00E-73//AT4G35270| RWP-RK domain-containing protein		RWP-RK			nr -
Unigene70772_All	254	0.00	3.19	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	8.71E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70772_All//sp|Q8BUB4|WDFY2_MOUSE//4.00E-22//WD repeat and FYVE domain-containing protein 2 OS=Mus musculus GN=Wdfy2 PE=2 SV=1						swissprot -
Unigene7078_All	704	2.97	2.16	0.45	1.77	2.01	0.96	6.67	2.14	2.60	-4.61E-01	3.09E-01		-2.71E+00	2.17E-06	Down	1.81E-01	8.02E-01		-8.78E-01	1.55E-01		-1.64E+00	1.23E-09	Down	-1.36E+00	9.58E-08	Down	Unigene7078_All//gi|15239296|ref|NP_200842.1|//5.00E-51//musC-like dehydratase domain-containing protein [Arabidopsis thaliana]	Unigene7078_All//3.00E-50//AT5G60340| musC-like dehydratase domain-containing protein	Unigene7078_All//0.00E+00//gi|73850898|gb|DT459918.1|DT459918				nr -
Unigene70786_All	255	0.00	23.45	16.29	0.00	0.00	0.00	0.00	0.00	0.00	1.45E+01	3.95E-34	Up	1.40E+01	4.83E-23	Up	null	null		null	null		null	null		null	null		Unigene70786_All//gi|11466469|ref|NP_938172.1|//5.00E-18//NADH dehydrogenase subunit 5 [Chrysodidymus synuroideus] >gi|7110466|gb|AAF36938.1|AF222718_12 NADH dehydrogenase subunit 5 [Chrysodidymus synuroideus]	Unigene70786_All//3.00E-15//ATMG00665| Mitochondrial NADH dehydrogenase subunit 5. The gene is trans-spliced from three different pre-cursors, NAD5a, NAD5b and NAD5c.			ko00190|Oxidative phosphorylation	GO:0016491//GO:0022900//GO:0043231//GO:0044425	nr -
Unigene70788_All	255	21.13	120.81	41.76	31.26	26.60	48.88	42.45	73.59	63.27	2.52E+00	3.86E-83	Up	9.83E-01	8.79E-08		-2.33E-01	3.05E-01		6.45E-01	3.84E-05		7.94E-01	6.32E-12		5.76E-01	1.91E-06				Unigene70788_All//5.00E-86//TC147035				
Unigene70791_All	255	0.00	4.17	1.46	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.80E-06	Up	1.05E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene70791_All//sp|Q03567|YLD2_CAEEL//1.00E-07//Uncharacterized transporter C38C10.2 OS=Caenorhabditis elegans GN=C38C10.2 PE=1 SV=2						swissprot +
Unigene70794_All	255	0.00	3.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.37E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70794_All//sp|Q5RCY3|EMP1_PONAB//2.00E-41//Epithelial membrane protein 1 OS=Pongo abelii GN=EMP1 PE=2 SV=1						swissprot -
Unigene70797_All	255	0.00	5.76	2.92	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.11E-08	Up	1.15E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene70797_All//sp|P67937|TPM4_PIG//1.00E-20//Tropomyosin alpha-4 chain OS=Sus scrofa GN=TPM4 PE=1 SV=3						swissprot -
Unigene70799_All	255	0.00	3.58	0.63	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	9.29E+00	2.37E-01		null	null		null	null		null	null		null	null		Unigene70799_All//sp|P42280|TRYZ_DROME//2.00E-18//Trypsin zeta OS=Drosophila melanogaster GN=zetaTry PE=1 SV=2						swissprot -

Unigene708_All	4877	3.77	3.52	2.78	6.29	5.56	5.72	10.91	5.57	5.11	-9.65E-02	5.14E-01		-4.36E-01	1.19E-03		-1.77E-01	8.36E-02		-1.37E-01	2.24E-01		-9.69E-01	5.35E-45		-1.09E+00	3.43E-56	Down	Unigene708_All//gi|15220948|ref|NP_172851.1|//0.00E+00//GN (GNOM); GTP:GDP antiporter/ protein homodimerization [Arabidopsis thaliana] >gi|2498329|sp|Q42510.1|EMB30_ARATH RecName: Full=Pattern formation protein EMB30; AltName: Full=Protein EMBRYO DEFECTIVE 30 >gi|5080774|gb|AAD39284.1|AC007576_7 EMB30/GNOM gene product [Arabidopsis thaliana] >gi|8778395|gb|AAF79403.1|AC068197_13 F16A14.20 [Arabidopsis thaliana] >gi|1209633|gb|AAA91151.1| GNOM [Arabidopsis thaliana] >gi|1335997|gb|AAB01205.1| similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] >gi|1335999|gb|AAB01206.1| similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]	Unigene708_All//0.00E+00//AT1G13980; GN (GNOM); GTP:GDP antiporter/ protein homodimerization	Unigene708_All//0.00E+00//TC171636		ko04626|Plant-pathogen interaction	GO:0000578//GO:0000902//GO:0001738//GO:0003006//GO:0005083//GO:0009926//GO:0015300//GO:0032011//GO:0032386//GO:0033205//GO:0042802//GO:0044464//GO:0045229//GO:0048527//GO:0048764	nr +
Unigene7080_All	714	1.76	1.56	1.72	2.30	0.92	0.57	4.03	0.94	0.67	-1.72E-01	7.55E-01		-3.60E-02	9.71E-01		-1.33E+00	6.77E-03		-2.02E+00	3.04E-04	Down	-2.10E+00	2.39E-08	Down	-2.59E+00	7.30E-11	Down	Unigene7080_All//gi|297598391|ref|NP_001045505.2|//2.00E-53//Os01g0966900 [Oryza sativa Japonica Group] >gi|255674110|dbj|BAF07419.2| Os01g0966900 [Oryza sativa Japonica Group]	Unigene7080_All//7.00E-49//AT4G36670| mannitol transporter, putative	Unigene7080_All//0.00E+00//TC154069				nr +
Unigene70801_All	255	0.00	3.38	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	7.71E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70801_All//sp|P49908|SEPP1_HUMAN//7.00E-28//Selenoprotein P OS=Homo sapiens GN=SEPP1 PE=1 SV=3						swissprot +
Unigene70803_All	255	0.00	3.38	0.63	0.00	0.81	1.06	0.00	0.82	0.31	1.17E+01	4.92E-05	Up	9.29E+00	2.37E-01		9.66E+00	1.56E-01		1.01E+01	7.01E-02		9.68E+00	7.84E-02		8.29E+00	4.01E-01								
Unigene70805_All	255	0.00	3.58	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null								ESTscan +
Unigene70808_All	255	0.00	3.38	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70808_All//sp|P59722|EGLN1_RAT//4.00E-12//Egl nine homolog 1 OS=Rattus norvegicus GN=Egln1 PE=2 SV=1						swissprot -
Unigene7081_All	1316	0.48	1.54	0.20	0.45	0.89	0.34	1.16	6.38	7.02	1.69E+00	5.40E-04	Up	-1.24E+00	2.13E-01		9.70E-01	1.37E-01		-4.04E-01	6.73E-01		2.46E+00	1.17E-27	Up	2.60E+00	6.54E-33	Up			Unigene7081_All//0.00E+00//DR456458				
Unigene70810_All	255	0.00	2.78	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70810_All//gi|115485515|ref|NP_001067901.1|//7.00E-15//Os11g0482100 [Oryza sativa Japonica Group] >gi|113645123|dbj|BAF28264.1| Os11g0482100 [Oryza sativa Japonica Group]	Unigene70810_All//3.00E-16//AT3G44340| CEF (clone eighty-four); protein binding / transporter/ zinc ion binding				GO:0006810//GO:0006950//GO:0009987//GO:0043231//GO:0044444	nr +
Unigene70812_All	255	0.00	4.97	1.25	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.85E-07	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null								ESTscan +
Unigene70813_All	255	0.00	2.58	0.63	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	9.29E+00	2.37E-01		null	null		null	null		null	null		null	null								ESTscan +
Unigene70814_All	255	0.00	2.98	1.25	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene70814_All//gi|297796507|ref|XP_002866138.1|//1.00E-14//calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297311973|gb|EFH42397.1| calmodulin-binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene70814_All//4.00E-15//AT5G56360| calmodulin-binding protein			ko04141|Protein processing in endoplasmic reticulum	GO:0005515	nr +
Unigene70816_All	256	0.00	4.35	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.99E-06	Up	1.07E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene70816_All//sp|Q9JKL7|SFR12_RAT//3.00E-06//Splicing factor, arginine/serine-rich 12 OS=Rattus norvegicus GN=Sfrs12 PE=1 SV=1						swissprot -
Unigene70818_All	256	0.00	2.57	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	1.00E+01	7.96E-02		null	null		null	null		null	null		null	null								ESTscan -
Unigene7082_All	882	1.31	1.67	0.78	1.02	1.05	1.64	2.01	0.66	3.84	3.52E-01	5.29E-01		-7.34E-01	2.67E-01		5.23E-02	9.59E-01		6.89E-01	2.32E-01		-1.60E+00	5.26E-04	Down	9.31E-01	1.46E-03		Unigene7082_All//gi|115466608|ref|NP_001056903.1|//2.00E-19//Os06g0164500 [Oryza sativa Japonica Group] >gi|113594943|dbj|BAF18817.1| Os06g0164500 [Oryza sativa Japonica Group]	Unigene7082_All//1.00E-11//AT3G55350| unknown protein					nr +
Unigene70821_All	256	0.00	4.75	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.46E-07	Up	7.70E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70821_All//sp|Q6B855|TKT_BOVIN//6.00E-16//Transketolase OS=Bos taurus GN=TKT PE=2 SV=1						swissprot +
Unigene70822_All	256	0.00	3.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70822_All//gi|226528585|ref|NP_001149232.1|//3.00E-09//dehydrogenase/reductase SDR family member 2 [Zea mays] >gi|195625644|gb|ACG34652.1| dehydrogenase/reductase SDR family member 2 [Zea mays]	Unigene70822_All//1.00E-08//AT3G55310| binding / catalytic/ oxidoreductase			ko04146|Peroxisome	GO:0003824	nr -
Unigene70824_All	256	20.44	44.34	34.74	49.81	50.85	37.40	28.41	29.55	58.36	1.12E+00	1.97E-10	Up	7.65E-01	1.37E-04		2.96E-02	8.78E-01		-4.14E-01	9.06E-03		5.70E-02	7.92E-01		1.04E+00	4.40E-15	Up			Unigene70824_All//1.00E-55//TC164973				
Unigene70827_All	256	0.00	3.36	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	1.00E+01	7.96E-02		null	null		null	null		null	null		null	null		Unigene70827_All//gi|219121569|ref|XP_002181136.1|//2.00E-21//iron-sulphur assembly protein isc [Phaeodactylum tricornutum CCAP 1055/1] >gi|217407122|gb|EEC47059.1| iron-sulphur assembly protein isc [Phaeodactylum tricornutum CCAP 1055/1]	Unigene70827_All//5.00E-21//AT4G22220| ISU1; structural molecule				GO:0031163//GO:0043231//GO:0046914//GO:0051540	nr -
Unigene70828_All	256	0.00	2.97	2.08	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	1.10E+01	4.02E-03		null	null		null	null		null	null		null	null								
Unigene70830_All	256	0.00	2.97	0.62	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	9.29E+00	2.37E-01		null	null		null	null		null	null		null	null								
Unigene70831_All	256	0.00	3.76	1.46	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.37E-05	Up	1.05E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene70831_All//gi|3122234|sp|O24473.1|IF2B_WHEAT//3.00E-20//RecName: Full=Eukaryotic translation initiation factor 2 subunit beta; Short=eIF-2-beta; AltName: Full=P38 >gi|2306768|gb|AAB65774.1| eIF-2 beta subunit [Triticum aestivum]	Unigene70831_All//4.00E-19//AT5G20920| EIF2 BETA; translation initiation factor				GO:0005488//GO:0006412	nr -
Unigene70835_All	256	0.00	5.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.49E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene70835_All//gi|18266812|sp|P12347.2|PER_ACEAI//7.00E-15//RecName: Full=Period clock protein; AltName: Full=p230					GO:0005488//GO:0044444	nr -
Unigene70836_All	256	0.00	2.77	0.42	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	8.70E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70836_All//gi|301123875|ref|XP_002909664.1|//1.00E-24//selenide, water dikinase, putative [Phytophthora infestans T30-4] >gi|262100426|gb|EEY58478.1| selenide, water dikinase, putative [Phytophthora infestans T30-4]				ko00450|Selenoamino acid metabolism	GO:0016301	nr -
Unigene70837_All	256	117.31	55.82	54.08	146.91	165.18	185.06	183.65	121.47	152.66	-1.07E+00	8.81E-25	Down	-1.12E+00	1.94E-25	Down	1.69E-01	4.77E-02		3.33E-01	9.84E-06		-5.96E-01	1.18E-17		-2.67E-01	8.93E-05		Unigene70837_All//gi|15230312|ref|NP_191308.1|//4.00E-25//40S ribosomal protein S2 (RPS2D) [Arabidopsis thaliana] >gi|75313287|sp|Q9SCM3.1|RS24_ARATH RecName: Full=40S ribosomal protein S2-4 >gi|6706420|emb|CAB66106.1| 40S ribosomal protein S2 homolog [Arabidopsis thaliana] >gi|21536514|gb|AAM60846.1| 40S ribosomal protein S2 homolog [Arabidopsis thaliana] >gi|30017231|gb|AAP12849.1| At3g57490 [Arabidopsis thaliana] >gi|110736085|dbj|BAF00015.1| 40S ribosomal protein S2 homolog [Arabidopsis thaliana]	Unigene70837_All//2.00E-13//AT3G57490| 40S ribosomal protein S2 (RPS2D)	Unigene70837_All//8.00E-125//BE055613		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0031981	nr -
Unigene70839_All	256	0.00	5.74	2.91	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.11E-08	Up	1.15E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene70839_All//gi|19184|emb|CAA43590.1|//1.00E-20//Type I (26 kD) CP29 polypeptide [Solanum lycopersicum]	Unigene70839_All//3.00E-12//AT4G10340| LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding			ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009503//GO:0009523//GO:0009570//GO:0009639//GO:0046906	nr -
Unigene70840_All	256	0.00	8.12	3.54	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	7.94E-12	Up	1.18E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene70840_All//sp|Q3YV00|RL1_SHISS//7.00E-12//50S ribosomal protein L1 OS=Shigella sonnei (strain Ss046) GN=rplA PE=3 SV=1						swissprot -
Unigene70842_All	256	0.00	4.16	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.80E-06	Up	9.70E+00	1.39E-01		null	null		null	null		null	null		null	null								ESTscan -
Unigene70843_All	256	0.00	2.57	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	7.70E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70843_All//gi|255596218|ref|XP_002536489.1|//3.00E-06//2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase, putative [Ricinus communis] >gi|223519527|gb|EEF25895.1| 2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase, putative [Ricinus communis]					GO:0003824	nr +
Unigene70845_All	256	0.00	4.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.99E-06	Up	null	null		null	null		null	null		null	null		null	null								ESTscan +
Unigene70846_All	256	0.00	3.36	1.46	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	1.05E+01	2.49E-02		null	null		null	null		null	null		null	null								
Unigene70847_All	256	0.00	2.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70847_All//gi|192910692|gb|ACF86454.1|//7.00E-39//eukaryotic translation initiation factor 5A isoform IV [Elaeis guineensis]	Unigene70847_All//3.00E-36//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor	Unigene70847_All//1.00E-37//TC174576			GO:0006448//GO:0006449//GO:0008135//GO:0018205//GO:0043021	nr -
Unigene70849_All	257	0.00	2.96	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null								ESTscan -
Unigene70852_All	257	0.00	0.59	4.97	0.00	0.00	0.00	0.00	0.00	0.00	9.21E+00	2.32E-01		1.23E+01	4.68E-07	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene70854_All	257	0.00	3.94	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.23E-06	Up	1.05E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene70854_All//sp|Q08473|SQD_DROME//1.00E-06//RNA-binding protein squid OS=Drosophila melanogaster GN=sqd PE=1 SV=3						swissprot -
Unigene70855_All	257	0.00	2.56	1.24	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene70855_All//sp|P23654|NRT_DROME//2.00E-32//Neurotactin OS=Drosophila melanogaster GN=Nrt PE=1 SV=3						swissprot +

Unigene70856_All	257	0.00	2.76	2.07	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	1.10E+01	4.02E-03		null	null		null	null		null	null		null	null		Unigene70856_All//sp|Q9D5L7|SPSB1_MOUSE//7.00E-30//SPRY domain-containing SOCS box protein 1 OS=Mus musculus GN=Spsb1 PE=1 SV=1						swissprot +
Unigene70863_All	257	0.00	2.96	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	1.00E+01	7.96E-02		null	null		null	null		null	null		null	null		Unigene70863_All//sp|P27878|VIT1_CERCA//1.00E-33//Vitellogenin-1 OS=Ceratitis capitata GN=VG1-GAMMA PE=2 SV=1						swissprot -
Unigene70866_All	257	0.00	3.94	2.28	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.23E-06	Up	1.12E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene70866_All//gi|300121030|emb|CBK21412.2|//3.00E-07//unnamed protein product [Blastocystis hominis]						nr -
Unigene70868_All	257	0.00	5.52	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.05E-08	Up	9.69E+00	1.39E-01		null	null		null	null		null	null		null	null							
Unigene70875_All	257	0.00	12.42	6.01	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	3.64E-18	Up	1.26E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene70875_All//gi|300262824|gb|EFJ47028.1|//2.00E-07//transcription factor jumonji domain-containing protein [Volvox carteri f. nagariensis]						nr +
Unigene70876_All	257	0.00	2.56	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	null	null		null	null		null	null		null	null										
Unigene70879_All	257	0.00	3.55	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	7.69E+00	6.28E-01		null	null		null	null		null	null										ESTscan +
Unigene70880_All	257	0.00	3.15	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	9.69E+00	1.39E-01		null	null		null	null		null	null										ESTscan +
Unigene70881_All	258	0.00	4.91	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.85E-07	Up	null	null		null	null		null	null		null	null					Unigene70881_All//gi|226455089|gb|EEH52393.1|//5.00E-07//predicted protein [Micromonas pusilla CCMP1545]				ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene70888_All	258	0.20	3.14	0.00	0.00	0.00	0.00	0.00	0.32	0.46	3.95E+00	7.52E-04	Up	-7.66E+00	6.16E-01		null	null		null	null		8.34E+00	3.99E-01		8.86E+00	2.42E-01							
Unigene70892_All	258	110.52	70.31	60.89	295.41	237.31	358.51	809.22	393.50	372.14	-6.53E-01	1.48E-10		-8.60E-01	6.93E-16		-3.16E-01	7.35E-09		2.79E-01	9.55E-08		-1.04E+00	5.89E-196	Down	-1.12E+00	2.87E-227	Down	Unigene70892_All//gi|14484932|gb|AAK62818.1|//5.00E-40//fructose-1,6-bisphosphate aldolase [Solanum lycopersicum]	Unigene70892_All//1.00E-40//AT3G52930| fructose-bisphosphate aldolase, putative	Unigene70892_All//9.00E-137//gi|13243732|gb|BE052112.2|BE052112		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway	GO:0005576//GO:0006007//GO:0006970//GO:0009536//GO:0010038//GO:0016020//GO:0016832//GO:0030312//GO:0031967//GO:0031981//GO:0046914	nr +
Unigene70894_All	258	0.00	3.14	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	9.69E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70894_All//sp|Q3UHH1|K0913_MOUSE//1.00E-17//Zinc finger SWIM domain-containing protein KIAA0913 OS=Mus musculus GN=Kiaa0913 PE=1 SV=1						swissprot -
Unigene70896_All	258	0.00	5.11	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.49E-07	Up	9.69E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene70896_All//sp|Q5XIM5|CDV3_RAT//1.00E-36//Protein CDV3 homolog OS=Rattus norvegicus GN=Cdv3 PE=2 SV=1						swissprot +
Unigene709_All	1116	5.06	2.41	3.39	10.18	13.70	18.66	11.40	8.73	16.10	-1.07E+00	2.54E-05	Down	-5.80E-01	2.71E-02		4.29E-01	1.76E-03		8.74E-01	2.52E-13		-3.86E-01	6.93E-03		4.98E-01	1.22E-05		Unigene709_All//gi|297805526|ref|XP_002870647.1|//1.00E-106//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316483|gb|EFH46906.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene709_All//8.00E-107//AT5G41260| protein kinase family protein	Unigene709_All//0.00E+00//ES811845			GO:0004672//GO:0016020//GO:0032559//GO:0043401	nr +
Unigene7090_All	537	0.10	0.00	0.30	6.03	1.99	1.09	2.13	2.72	1.63	-6.61E+00	6.06E-01		1.61E+00	5.10E-01		-1.60E+00	1.70E-06	Down	-2.46E+00	9.17E-10	Down	3.58E-01	4.96E-01		-3.81E-01	4.99E-01							
Unigene70903_All	258	0.00	3.54	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70903_All//gi|242073342|ref|XP_002446607.1|//2.00E-06//hypothetical protein SORBIDRAFT_06g018810 [Sorghum bicolor] >gi|241937790|gb|EES10935.1| hypothetical protein SORBIDRAFT_06g018810 [Sorghum bicolor]				ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene70904_All	258	0.00	3.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null							
Unigene70905_All	258	0.00	3.93	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.23E-06	Up	7.69E+00	6.28E-01		null	null		null	null		null	null		null	null							ESTscan +
Unigene70906_All	258	0.00	3.34	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70906_All//sp|Q8R4E9|CDT1_MOUSE//6.00E-06//DNA replication factor Cdt1 OS=Mus musculus GN=Cdt1 PE=1 SV=1						swissprot +
Unigene70908_All	258	0.00	3.54	0.21	0.39	0.53	0.88	0.16	0.16	0.00	1.18E+01	2.61E-05	Up	7.69E+00	6.28E-01		4.67E-01	8.75E-01		1.18E+00	5.49E-01		-1.68E-02	9.99E-01		-7.36E+00	6.05E-01							
Unigene70909_All	258	0.00	2.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	null	null		null	null		null	null		null	null		null	null							ESTscan -
Unigene7091_All	1072	6.34	0.85	3.87	3.90	1.38	0.55	1.62	0.16	0.89	-2.90E+00	5.11E-22	Down	-7.12E-01	2.35E-03		-1.50E+00	1.61E-07	Down	-2.83E+00	1.79E-14	Down	-3.37E+00	2.54E-08	Down	-8.59E-01	4.40E-02		Unigene7091_All//gi|225451804|ref|XP_002281338.1|//1.00E-153//PREDICTED: brassinosteroid-6-oxidase [Vitis vinifera]	Unigene7091_All//1.00E-131//AT3G30180| BR6OX2 (BRASSINOSTEROID-6-OXIDASE 2); monooxygenase/ oxygen binding	Unigene7091_All//4.00E-31//TC166913		ko00906|Carotenoid biosynthesis//ko00905|Brassinosteroid biosynthesis		nr -
Unigene70912_All	258	0.00	5.50	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.05E-08	Up	8.69E+00	3.93E-01		null	null		null	null		null	null		null	null							
Unigene70913_All	258	0.00	3.73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.37E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70913_All//gi|115148078|ref|NP_001063986.1|//6.00E-12//Os09g0570400 [Oryza sativa Japonica Group] >gi|75253247|sp|Q652N5.1|PHT44_ORYSJ RecName: Full=Probable anion transporter 4, chloroplastic; AltName: Full=Phosphate transporter 4;4; Flags: Precursor >gi|113632219|dbj|BAF25900.1| Os09g0570400 [Oryza sativa Japonica Group]	Unigene70913_All//3.00E-09//AT4G00370| ANTR2; inorganic phosphate transmembrane transporter/ organic anion transmembrane transporter				GO:0009528//GO:0015291	nr +
Unigene70914_All	259	0.00	4.89	2.88	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.85E-07	Up	1.15E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene70914_All//gi|53801490|gb|AAL93947.1|//2.00E-22//thioredoxin H [Heliocsporidium sp. ex Simulium jonesi]	Unigene70914_All//5.00E-22//AT3G08710| ATH9 (thioredoxin H-type 9)				GO:0015036//GO:0018904//GO:0019725//GO:0043231//GO:0044444	nr -
Unigene70917_All	259	0.00	4.50	1.64	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	1.07E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene70917_All//sp|P0C6P7|FEM1B_RAT//2.00E-07//Protein fem-1 homolog B OS=Rattus norvegicus GN=Fem1b PE=1 SV=1						swissprot -
Unigene7092_All	656	1.99	0.00	1.14	1.14	1.31	6.33	0.97	1.66	0.79	-1.10E+01	1.28E-07	Down	-8.11E-01	1.90E-01		2.04E-01	8.40E-01		2.48E+00	3.98E-12	Up	7.77E-01	1.94E-01		-2.92E-01	6.84E-01		Unigene7092_All//gi|115444605|ref|NP_001046082.1|//7.00E-71//Os02g0179200 [Oryza sativa Japonica Group] >gi|113535613|dbj|BAF07996.1| Os02g0179200 [Oryza sativa Japonica Group]	Unigene7092_All//1.00E-68//AT4G30550| glutamine amidotransferase class-I domain-containing protein	Unigene7092_All//4.00E-138//gi|164365371|gb|EX167546.1|EX167546		ko00230|Purine metabolism		nr +
Unigene70925_All	259	0.00	2.74	3.08	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	1.16E+01	1.72E-04	Up	null	null		null	null		null	null		null	null							ESTscan +
Unigene70928_All	259	0.00	1.76	3.91	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	7.36E-03		1.19E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene70928_All//gi|298708975|emb|CBJ30928.1|//1.00E-13//Aldo/Keto Reductase [Ectocarpus siliculosus]	Unigene70928_All//2.00E-12//AT2G37770| aldo/keto reductase family protein			ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism	GO:0016491	nr +
Unigene7093_All	777	2.69	6.00	2.54	5.77	3.99	3.49	1.47	0.43	0.51	1.16E+00	5.58E-05	Up	-8.71E-02	8.46E-01		-5.33E-01	5.50E-02		-7.26E-01	1.03E-02		-1.77E+00	3.70E-03		-1.52E+00	7.91E-03		Unigene7093_All//gi|30684447|ref|NP_193591.2|//3.00E-92//proline-rich family protein [Arabidopsis thaliana] >gi|22135814|gb|AAM91093.1| AT4g18560/F28J12_220 [Arabidopsis thaliana] >gi|28416472|gb|AAO42769.1| At4g18560/F28J12_220 [Arabidopsis thaliana]	Unigene7093_All//2.00E-93//AT4G18570| proline-rich family protein	Unigene7093_All//0.00E+00//gi|164259478|gb|ES819790.1|ES819790				nr -
Unigene70931_All	259	0.00	5.28	3.50	0.38	2.39	2.79	0.00	0.81	0.00	1.24E+01	7.78E-08	Up	1.18E+01	4.70E-05	Up	2.64E+00	1.99E-02		2.86E+00	7.12E-03		9.66E+00	7.84E-02		null	null		Unigene70931_All//gi|46931316|gb|AAT06462.1|//2.00E-10//At3g27250 [Arabidopsis thaliana]	Unigene70931_All//7.00E-12//AT5G40800| unknown protein					nr -
Unigene70936_All	259	0.00	6.46	0.82	0.00	0.00	0.00	0.00	0.00	0.15	1.27E+01	1.54E-09	Up	9.68E+00	1.39E-01		null	null		null	null		null	null		7.26E+00	6.39E-01		Unigene70936_All//gi|2270990|gb|AAB71225.1|//3.00E-06//dehydrin [Glycine max]					GO:0050896	nr +
Unigene70937_All	259	0.00	2.54	1.64	0.19	0.13	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	1.07E+01	1.37E-02		-5.32E-01	8.21E-01		-7.59E+00	6.25E-01		null	null		null	null		Unigene70937_All//gi|194476967|ref|YP_002049146.1|//1.00E-08//enoyl-(acyl-carrier-protein) reductase (NADH) [Paulinella chromatophora] >gi|171191974|gb|ACB42936.1| enoyl-(acyl-carrier-protein) reductase (NADH) [Paulinella chromatophora]				ko00061|Fatty acid biosynthesis		nr -
Unigene70939_All	260	0.00	3.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70939_All//sp|Q5RFD3|PSME3_PONAB//9.00E-07//Proteasome activator complex subunit 3 OS=Pongo abelii GN=PSME3 PE=2 SV=1						swissprot +
Unigene7095_All	1303	0.08	0.39	0.61	0.54	0.77	1.28	2.21	2.25	14.58	2.28E+00	6.22E-02		2.93E+00	5.05E-03		5.18E-01	5.07E-01		1.26E+00	1.61E-02		2.52E-02	9.69E-01		2.72E+00	2.58E-70	Up	Unigene7095_All//gi|156105187|gb|AB149132.1|//1.00E-128//ser/thr protein kinase [Malus x domestica]	Unigene7095_All//9.00E-89//AT5G47070| protein kinase, putative	Unigene7095_All//0.00E+00//ES809886				nr -
Unigene70951_All	260	0.00	11.89	0.00	0.00	0.13	0.35	0.00	0.00	0.46	1.35E+01	1.38E-17	Up	null	null		7.05E+00	8.20E-01		8.44E+00	4.72E-01		null	null		8.84E+00	2.42E-01		Unigene70951_All//gi|95925785|gb|ABF57559.1|//3.00E-24//Ole1 [Camellia oleifera]	Unigene70951_All//1.00E-12//AT5G40420| OLEO2 (OLEOSIN 2)				GO:0005811//GO:0031224	nr -
Unigene70952_All	260	0.00	2.73	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	9.26E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene70952_All//gi|297600187|ref|NP_001048661.2|//1.00E-22//Os03g0102300 [Oryza sativa Japonica Group] >gi|255674138|dbj|BAF10575.2| Os03g0102300 [Oryza sativa Japonica Group]	Unigene70952_All//5.00E-21//AT1G02080| transcriptional regulator-related			ko03018|RNA degradation		nr +
Unigene70958_All	260	0.00	3.12	1.23	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	1.03E+01	4.48E-02		null	null		null	null		null	null		null	null							
Unigene7096_All	767	0.00	66.39	0.00	0.06	0.72	1.35	0.17	0.93	2.49	1.60E+01	3.41E-294	Up	null	null		3.47E+00	1.22E-02		4.38E+00	3.57E-05	Up	2.49E+00	5.53E-03		3.91E+00	2.32E-10	Up	Unigene7096_All//gi|111218108|gb|AB108746.1|//1.00E-66//CBF/DREB-like transcription factor 1 [Citrus trifoliata]	Unigene7096_All//2.00E-46//AT5G51990| CBF4 (C- REPEAT-BINDING FACTOR 4); DNA binding / transcription activator/ transcription factor	Unigene7096_All//0.00E+00//gi|109889194|gb|DW518162.1|DW518162	AP2-EREBP			nr -
Unigene70960_All	260	0.00	3.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.37E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene70960_All//sp|P16371|GROU_DROME//3.00E-45//Protein groucho OS=Drosophila melanogaster GN=gro PE=1 SV=3						swissprot +
Unigene70962_All	260	0.00	2.73	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null							
Unigene70963_All	260	0.00	5.07	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.49E-07	Up	7.68E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene70963_All//gi|300259488|gb|EFJ43715.1|//6.00E-22//polyubiquitin [Volvox carteri f. nagariensis]	Unigene70963_All//6.00E-22//AT2G35635| UBQ7; protein binding					nr -
Unigene70973_All	261	0.20	3.30	1.43	1.53	1.85	2.08	0.81	0.16	0.31	4.04E+00	4.20E-04	Up	2.83E+00	9.30E-02		2.75E-01	8.19E-01		4.44E-01	6.78E-01		-2.34E+00	2.36E-01		-1.41E+00	3.80E-01				Unigene70973_All//2.00E-76//gi|48790201|gb|CO091515.1|CO091515				

Unigene70974_All	261	0.00	3.30	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	8.67E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70974_All//gi|159479816|ref|XP_001697982.1|//1.00E-16//SR protein factor [Chlamydomonas reinhardtii] >gi|158273781|gb|EDO99567.1| SR protein factor [Chlamydomonas reinhardtii]				ko03040|Spliceosome		nr -
Unigene70975_All	261	0.00	3.88	0.41	0.00	0.26	0.00	0.00	0.00	0.00	1.19E+01	7.23E-06	Up	8.67E+00	3.93E-01		8.04E+00	6.04E-01		null	null		null	null		null	null									
Unigene70976_All	261	0.00	2.72	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	9.26E+00	2.36E-01		null	null		null	null		null	null		null	null									
Unigene70977_All	261	0.00	3.11	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	7.67E+00	6.28E-01		null	null		null	null		null	null		null	null									
Unigene70979_All	261	0.00	2.91	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	9.99E+00	7.96E-02		null	null		null	null		null	null		null	null									
Unigene70983_All	261	0.00	2.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene70983_All//sp|Q9SSP2|HRD1_DROME//1.00E-11//E3 ubiquitin-protein ligase HRD1 OS=Drosophila melanogaster GN=sip3 PE=1 SV=1						swissprot -
Unigene70984_All	261	0.00	5.05	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.49E-07	Up	8.67E+00	3.93E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene70985_All	261	0.00	2.52	2.45	0.00	0.13	0.35	0.16	0.96	0.46	1.13E+01	6.22E-04	Up	1.13E+01	1.16E-03		7.04E+00	8.20E-01		8.44E+00	4.72E-01		2.57E+00	1.53E-01		1.50E+00	5.57E-01									
Unigene70988_All	261	0.40	4.47	0.20	0.76	0.00	0.00	0.00	0.00	0.00	3.48E+00	7.08E-05	Up	-9.73E-01	7.19E-01		-9.58E+00	8.39E-02		-9.58E+00	1.33E-01		null	null		null	null									
Unigene70990_All	261	0.00	3.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene70992_All	261	0.00	3.30	0.61	0.38	0.40	0.00	0.32	0.00	0.00	1.17E+01	4.92E-05	Up	9.26E+00	2.36E-01		5.23E-02	9.65E-01		-8.58E+00	3.95E-01		-8.34E+00	3.99E-01		-8.34E+00	3.55E-01		Unigene70992_All//gi|124359163|gb|ABN05686.1|//7.00E-09//Zinc finger, CCHC-type [Medicago truncatula]		Unigene70992_All//6.00E-24//ES842067				nr +
Unigene70995_All	261	0.00	3.69	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.37E-05	Up	8.67E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene70995_All//sp|Q8INB9|AKT1_DROME//7.00E-06//RAC serine/threonine-protein kinase OS=Drosophila melanogaster GN=Akt1 PE=1 SV=3						swissprot +
Unigene70996_All	261	0.00	4.47	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	9.26E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene70996_All//sp|P38040|GBG1_DROME//2.00E-13//Guanine nucleotide-binding protein subunit gamma-1 OS=Drosophila melanogaster GN=Ggamma1 PE=2 SV=1						swissprot -
Unigene70998_All	261	0.00	6.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	5.69E-09	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene71000_All	261	0.00	2.52	0.82	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	9.67E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71000_All//gi|223995561|ref|XP_002287454.1|//2.00E-19//transaldolase [Thalassiosira pseudonana CCMP1335] >gi|220976570|gb|EED94897.1| transaldolase [Thalassiosira pseudonana CCMP1335]				ko00030|Pentose phosphate pathway		nr +
Unigene71001_All	261	0.00	14.95	4.08	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	3.24E-22	Up	1.20E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene71001_All//sp|Q66X93|SND1_RAT//5.00E-08//Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=2 SV=1						swissprot -
Unigene71010_All	262	0.00	5.03	0.81	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.49E-07	Up	9.67E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene71014_All	262	0.00	4.45	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	7.67E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene71014_All//gi|297839757|ref|XP_002887760.1|//3.00E-22//VHA-A [Arabidopsis lyrata subsp. lyrata] >gi|297333601|gb|EFH84019.1| VHA-A [Arabidopsis lyrata subsp. lyrata]	Unigene71014_All//1.00E-23//AT1G78900| VHA-A (VACUOLAR ATP SYNTHASE SUBUNIT A); ATP binding / hydrogen ion transporting ATP synthase, rotational mechanism / hydrolase, acting on acid anhydrides, catalyzing transmembrane movement of substances / proton-transporting ATPase, rotational mechanism			ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene71016_All	262	0.00	4.45	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	1.07E+01	1.37E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene71018_All	262	0.00	2.51	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.22E-04	Up	9.99E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71018_All//sp|Q499C7|CDO34_RAT//1.00E-10//Uncharacterized protein C4orf34 homolog OS=Rattus norvegicus PE=2 SV=1						swissprot +
Unigene71022_All	262	0.00	3.48	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	8.67E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene71022_All//sp|O00622|CYR61_HUMAN//1.00E-49//Protein CYR61 OS=Homo sapiens GN=CYR61 PE=1 SV=1						swissprot -
Unigene71023_All	262	0.00	2.90	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	8.67E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene71023_All//sp|Q7KKH3|SDA1_DROME//1.00E-37//Protein SDA1 homolog OS=Drosophila melanogaster GN=Mys45A PE=1 SV=1						swissprot +
Unigene71024_All	263	0.00	7.13	2.23	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.10E-10	Up	1.11E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene71024_All//gi|115465847|ref|NP_001056523.1|//3.00E-06//Os05g0597100 [Oryza sativa Japonica Group] >gi|113580074|dbj|BAF18437.1| Os05g0597100 [Oryza sativa Japonica Group]						nr +
Unigene71026_All	263	0.00	2.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.21E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71026_All//sp|O61491|FLOT1_DROME//6.00E-43//Flotillin-1 OS=Drosophila melanogaster GN=Flo PE=1 SV=1						swissprot +
Unigene71027_All	263	0.00	19.65	5.67	0.00	0.00	0.00	0.00	0.00	0.00	1.43E+01	1.80E-29	Up	1.25E+01	3.21E-08	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene71028_All	263	0.00	2.70	1.01	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	9.98E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71028_All//gi|11467743|ref|NP_050795.1|//6.00E-19//ribosomal protein S7 [Guillardia theta] >gi|133988|sp|P19458.1|RR7_GUITH RecName: Full=30S ribosomal protein S7, chloroplastic >gi|3603068|gb|AAC35729.1| ribosomal protein S7 [Guillardia theta]	Unigene71028_All//3.00E-16//ATCG00900| encodes a chloroplast ribosomal protein S7, a constituent of the small subunit of the ribosomal complex	Unigene71028_All//8.00E-51//TC168446		ko03010|Ribosome		nr -
Unigene71029_All	263	0.80	5.20	1.42	0.00	0.13	0.17	0.16	0.64	1.06	2.71E+00	1.29E-04	Up	8.33E-01	5.16E-01		7.03E+00	8.20E-01		7.42E+00	6.88E-01		1.98E+00	3.79E-01		2.72E+00	9.93E-02									
Unigene71034_All	263	0.00	3.08	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	7.66E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene71034_All//gi|110816007|gb|ABG91751.1|//8.00E-06//HyPRP1 [Gossypium hirsutum]						nr +
Unigene71035_All	263	0.00	3.47	2.02	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	1.10E+01	4.02E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene71044_All	263	0.00	3.47	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.61E-05	Up	7.66E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene71044_All//gi|42569129|ref|NP_179444.2|//3.00E-08//cupin family protein [Arabidopsis thaliana]				ko03040|Spliceosome		nr -
Unigene71047_All	264	0.00	2.69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene71048_All	264	0.00	2.69	1.01	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	9.98E+00	7.95E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene71049_All	264	0.00	2.88	1.01	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	9.98E+00	7.95E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene71058_All	264	0.00	2.50	0.81	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.21E-04	Up	9.66E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71058_All//gi|297726025|ref|NP_001175376.1|//7.00E-07//Os08g0143300 [Oryza sativa Japonica Group] >gi|75294087|sp|Q6YYZ2.1|4CLL3_ORYSJ RecName: Full=4-coumarate--CoA ligase-like 3 >gi|255678141|dbj|BAH94104.1| Os08g0143300 [Oryza sativa Japonica Group]	Unigene71058_All//7.00E-07//AT4G19010| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene7106_All	686	0.84	1.48	1.71	11.91	17.87	15.60	2.34	5.00	6.39	8.16E-01	2.35E-01		1.03E+00	1.24E-01		5.86E-01	1.23E-04		3.90E-01	2.90E-02		1.09E+00	2.90E-04	Up	1.45E+00	7.24E-08	Up	Unigene7106_All//2.00E-33//AT4G27590| copper-binding protein-related	Unigene7106_All//1.00E-172//gi|164259612|gb|ES836363.1|ES836363					nr -
Unigene71060_All	264	0.00	3.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71060_All//gi|9294523|dbj|BAB02785.1|//2.00E-23//protein transport protein Sec23 [Arabidopsis thaliana]	Unigene71060_All//1.00E-24//AT3G23660| transport protein, putative					nr -
Unigene71063_All	264	0.00	2.88	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	9.24E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71063_All//gi|195621288|gb|ACG32474.1|//1.00E-24//eukaryotic translation initiation factor 5A-1/2 [Zea mays]	Unigene71063_All//2.00E-25//AT1G13950| ELF5A-1 (EUKARYOTIC ELONGATION FACTOR 5A-1); translation initiation factor					nr -
Unigene7107_All	1116	2.44	1.45	1.05	1.70	1.97	0.61	4.51	1.46	4.64	-7.47E-01	4.92E-02		-1.22E+00	2.83E-03		2.19E-01	6.50E-01		-1.48E+00	2.25E-03		-1.63E+00	3.76E-10	Down	4.17E-02	8.78E-01		Unigene7107_All//gi|115461783|ref|NP_001054491.1|//2.00E-16//Os05g0120300 [Oryza sativa Japonica Group] >gi|113578042|dbj|BAF16405.1| Os05g0120300 [Oryza sativa Japonica Group]	Unigene7107_All//1.00E-13//AT5G02640| unknown protein	Unigene7107_All//1.00E-93//TC167395				nr +
Unigene71070_All	265	0.00	3.06	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	1.07E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71070_All//sp|Q33YV50|ZAPB_SHISS//4.00E-28//Cell division protein zapB OS=Shigella sonnei (strain Ss046) GN=zapB PE=3 SV=1						swissprot -
Unigene71071_All	265	0.00	7.46	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.97E-11	Up	9.97E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71071_All//gi|301114977|ref|XP_002999258.1|//5.00E-13//transaldolase [Phytophthora infestans T30-4] >gi|262111352|gb|EEY69404.1| transaldolase [Phytophthora infestans T30-4]						nr -
Unigene71073_All	265	0.00	3.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71073_All//sp|Q9NDJ2|DOM_DROME//6.00E-10//Helicase domino OS=Drosophila melanogaster GN=dom PE=1 SV=2						swissprot -
Unigene71076_All	265	0.00	3.06	0.80	0.00	0.26	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	9.65E+00	1.39E-01		8.02E+00	6.04E-01		null	null		null	null		null	null									ESTscan +
Unigene71078_All	265	13.62	4.21	4.42	26.13	34.57	17.72	0.00	0.00	0.00	-1.70E+00	1.43E-06	Down	-1.62E+00	6.79E-06	Down	4.04E-01	3.35E-02		-5.60E-01	1.16E-02		null	null		null	null		Unigene71078_All//gi|150022156|gb|ABR57406.1|//9.00E-31//alpha-expansin 3 [Gossypium arboreum] >gi|150022168|gb|ABR57412.1| alpha-expansin 3 [Gossypium raimondii]	Unigene71078_All//8.00E-27//AT5G02260| ATEXPA9 (ARABIDOPSIS THALIANA EXPANSIN A9)	Unigene71078_All//2.00E-94//ES819675				nr -
Unigene71079_All	265	0.00	5.35	3.62	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.05E-08	Up	1.18E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene71079_All//gi|226500540|ref|NP_001151739.1|//1.00E-27//heat shock 70 kDa protein [Zea mays] >gi|195649437|gb|ACG44186.1| heat shock 70 kDa protein [Zea mays]	Unigene71079_All//2.00E-27//AT4G37910| mtHsc70-1 (mitochondrial heat shock protein 70-1); ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03018|RNA degradation		nr +
Unigene7108_All	379	86.14	46.93	72.92	52.05	32.80	31.94	216.31	161.45	63.28	-8.76E-01	1.90E-19		-2.40E-01	1.79E-02		-6.66E-01	4.39E-09		-7.05E-01	5.27E-09		-4.22E-01	1.95E-16		-1.77E+00	6.33E-179	Down	Unigene7108_All//gi|7649161|gb|AAF65770.1|AF242312_1//3.00E-20//cyclophilin [Euphorbia esula]	Unigene7108_All//6.00E-19//AT4G38740| ROC1 (ROTAMASE CYP 1); peptidyl-prolyl cis-trans isomerase	Unigene7108_All//0.00E+00//gi|21103435|gb|BQ415748.1|BQ415748				nr -
Unigene71080_All	265	0.00	3.82	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.23E-06	Up	8.65E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene71080_All//gi|45775249|gb|AAS77222.1|//1.00E-19//ATP-binding cassette transporter [Pteris vittata]	Unigene71080_All//2.00E-19//AT5G60790| ATGCN1; transporter					nr +

Unigene71082_All	266	0.00	3.24	2.80	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	1.15E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene71082_All//gi|38524446|dbj|BAD02371.1|//5.00E-10//flowering locus T [Populus nigra] >gi|48474219|dbj|BAD08336.2| flowering locus T [Populus nigra] >gi|169990904|dbj|BAG12901.1| FLOWERING LOCUS T [Populus nigra] >gi|169990906|dbj|BAG12902.1| FLOWERING LOCUS T [Populus nigra] >gi|169990910|dbj|BAG12904.1| FLOWERING LOCUS T [Populus nigra]	Unigene71082_All//2.00E-09//AT1G65480| FT (FLOWERING LOCUS T); phosphatidylethanolamine binding / protein binding					nr -
Unigene71084_All	266	0.00	5.71	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.09E-08	Up	9.97E+00	7.95E-02		null	null		null	null		null	null		null	null									
Unigene71088_All	266	0.00	2.86	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.76E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71088_All//gi|62733756|gb|AAY85865.1|//3.00E-12//Serpin (serine protease inhibitor) [Oryza sativa Japonica Group] >gi|77549402|gb|ABA92199.1| Serpin family protein [Oryza sativa (japonica cultivar-group)]	Unigene71088_All//3.00E-09//AT3G45220| serpin, putative / serine protease inhibitor, putative					nr +
Unigene7109_All	970	0.16	1.41	0.22	1.64	0.89	0.98	16.35	172.87	13.31	3.12E+00	3.45E-05	Up	4.41E-01	7.74E-01		-8.89E-01	7.64E-02		-7.49E-01	1.61E-01		3.40E+00	0.00E+00	Up	-2.97E-01	1.69E-02		Unigene7109_All//gi|15220546|ref|NP_176947.1|//7.00E-50//SUFE2 (SULFUR E 2); enzyme activator [Arabidopsis thaliana] >gi|11072031|gb|AAG28910.1|AC008113_26 F12A21.6 [Arabidopsis thaliana] >gi|117958779|gb|ABK59690.1| At1g67810 [Arabidopsis thaliana]	Unigene7109_All//4.00E-51//AT1G67810| SUFE2 (SULFUR E 2); enzyme activator			ko00760|Nicotinate and nicotinamide metabolism		nr -
Unigene71090_All	266	0.00	4.38	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	8.65E+00	3.93E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene71092_All	266	0.00	6.10	2.60	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.96E-09	Up	1.13E+01	6.14E-04	Up	null	null		null	null		null	null		null	null		Unigene71092_All//gi|1877397|emb|CAA72330.1|//5.00E-24//shaggy-like kinase [Ricinus communis]	Unigene71092_All//3.00E-25//AT2G30980| ASKdZeta (Arabidopsis SHAGGY-related protein kinase dZeta); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase					nr -
Unigene71093_All	266	0.00	4.00	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.80E-06	Up	9.65E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71093_All//sp|P17671|E75BC_DROME//6.00E-13//Ecdysone-induced protein 75B, isoforms C/D OS=Drosophila melanogaster GN=EcpC75B PE=2 SV=2						swissprot +
Unigene71094_All	266	0.00	5.33	0.60	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.05E-08	Up	9.23E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71094_All//sp|P98163|YL_DROME//2.00E-16//Putative vitellogenin receptor OS=Drosophila melanogaster GN=yl PE=1 SV=2						swissprot +
Unigene71099_All	266	0.00	2.86	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.75E-04	Up	9.65E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71099_All//gi|224013446|ref|XP_002296387.1|//4.00E-27//dead box family RNA helicase [Thalassiosira pseudonana CCMP1335] >gi|220968739|gb|EED87083.1| dead box family RNA helicase [Thalassiosira pseudonana CCMP1335]	Unigene71099_All//5.00E-23//AT5G11200| DEAD/DEAH box helicase, putative	Unigene71099_All//5.00E-12//TC139943		ko03040|Spliceosome		nr +
Unigene711_All	617	1.53	5.58	0.78	2.42	3.01	3.81	7.40	9.89	12.40	1.87E+00	4.67E-07	Up	-9.75E-01	2.00E-01		3.15E-01	5.58E-01		6.52E-01	1.32E-01		4.18E-01	5.61E-02		7.44E-01	4.99E-05		Unigene711_All//gi|297844890|ref|XP_002890326.1|//2.00E-54//ubiquitin interaction motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297336168|gb|EFH66585.1| ubiquitin interaction motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene711_All//6.00E-50//AT1G19270| DA1 (DA 1); ubiquitin binding	Unigene711_All//0.00E+00//gi|73866371|gb|DT469109.1|DT469109	Orphans		GO:0003006//GO:0045926//GO:0046914	nr +
Unigene7110_All	1674	0.78	0.39	0.45	1.25	0.62	0.76	3.36	0.80	1.43	-9.90E-01	9.25E-02		-8.11E-01	1.90E-01		-1.02E+00	1.57E-02		-7.26E-01	1.09E-01		-2.07E+00	2.40E-15	Down	-1.23E+00	5.49E-08	Down	Unigene7110_All//gi|297611025|ref|NP_001065522.2|//5.00E-18//Os11g0103100 [Oryza sativa Japonica Group] >gi|255679684|dbj|BAF27367.2| Os11g0103100 [Oryza sativa Japonica Group]	Unigene7110_All//2.00E-28//AT5G60150| unknown protein					nr -
Unigene71102_All	266	0.00	2.48	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.21E-04	Up	9.65E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene71104_All	266	0.00	3.24	1.60	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	1.06E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71104_All//sp|P18848|ATF4_HUMAN//9.00E-47//Cyclic AMP-dependent transcription factor ATF-4 OS=Homo sapiens GN=ATF4 PE=1 SV=3						swissprot +
Unigene71105_All	266	0.00	2.48	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.21E-04	Up	7.65E+00	6.28E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene71106_All	267	0.00	2.47	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.21E-04	Up	9.64E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71106_All//gi|297611309|ref|NP_001065856.2|//1.00E-11//Os11g0170000 [Oryza sativa Japonica Group] >gi|255679826|dbj|BAF27701.2| Os11g0170000 [Oryza sativa Japonica Group]	Unigene71106_All//3.00E-10//AT1G08980| AM11 (AMIDASE 11); amidase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds / indoleacetamide hydrolase			ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene7111_All	894	109.50	15.59	37.29	13.15	15.45	17.38	0.71	0.42	0.31	-2.81E+00	1.68E-300	Down	-1.55E+00	3.81E-136	Down	2.32E-01	1.55E-01		4.02E-01	4.59E-03		-7.54E-01	3.73E-01		-1.19E+00	1.33E-01		Unigene7111_All//gi|222354619|gb|ACM48123.1|//1.00E-133//calcium antiporter 1 [Malus x domestica] >gi|223587975|gb|ACM48122.1| calcium antiporter 1 [Malus x domestica]	Unigene7111_All//3.00E-96//AT3G51860| CAX3 (CATION EXCHANGER 3); calcium:cation antiporter/ calcium:hydrogen antiporter/ cation:cation antiporter	Unigene7111_All//0.00E+00//TC166651				nr +
Unigene71110_All	267	0.00	3.04	0.00	0.00	0.13	0.34	0.00	0.31	0.00	1.16E+01	9.33E-05	Up	null	null		7.01E+00	8.20E-01		8.40E+00	4.72E-01		8.29E+00	3.99E-01		null	null									
Unigene71111_All	267	0.00	3.42	0.60	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	9.22E+00	2.36E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene71112_All	267	0.00	2.66	1.20	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.31E-04	Up	1.02E+01	4.48E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene71113_All	267	0.00	4.74	1.60	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.85E-07	Up	1.06E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71113_All//sp|Q6AZN4|RML5_XENLA//1.00E-17//39S ribosomal protein L15, mitochondrial OS=Xenopus laevis GN=mrpl15 PE=2 SV=1						swissprot +
Unigene71117_All	267	0.00	3.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71117_All//gi|298710057|emb|CBJ31774.1|//2.00E-18//26S proteasome subunit like protein [Ectocarpus siliculosus]	Unigene71117_All//6.00E-17//AT5G45620| 26S proteasome regulatory subunit, putative (RPN9)			ko03050|Proteasome		nr +
Unigene71122_All	267	0.00	6.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	7.97E-10	Up	null	null		null	null		null	null		null	null		null	null		Unigene71122_All//gi|42573009|ref|NP_974601.1|//4.00E-11//heavy-metal-associated domain-containing protein [Arabidopsis thaliana]	Unigene71122_All//1.00E-12//AT4G23882| heavy-metal-associated domain-containing protein					nr +
Unigene71125_All	268	0.00	4.54	2.98	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.46E-07	Up	1.15E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene71125_All//sp|P13084|NPM_RAT//3.00E-44//Nucleophosmin OS=Rattus norvegicus GN=Npm1 PE=1 SV=1						swissprot +
Unigene71127_All	268	0.00	8.70	1.39	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.90E-13	Up	1.04E+01	2.49E-02		null	null		null	null		null	null		null	null									
Unigene71128_All	268	0.00	4.35	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.03E-06	Up	1.10E+01	4.02E-03		null	null		null	null		null	null		null	null									
Unigene7113_All	800	0.00	2.91	0.53	0.50	0.73	1.98	149.25	74.08	26.79	1.15E+01	2.90E-13	Up	9.06E+00	1.37E-02		5.55E-01	5.99E-01		1.99E+00	6.07E-04	Up	-1.01E+00	3.82E-107	Down	-2.48E+00	0.00E+00	Down	Unigene7113_All//gi|224139376|ref|XP_002323082.1|//1.00E-74//cytochrome P450 [Populus trichocarpa] >gi|222867712|gb|EEF04843.1| cytochrome P450 [Populus trichocarpa]	Unigene7113_All//9.00E-63//AT3G26230| CYP71B24; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene7113_All//0.00E+00//gi|73851468|gb|DT460488.1|DT460488		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene71130_All	268	0.00	3.78	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.23E-06	Up	8.63E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene71130_All//gi|300266478|gb|EFJ50665.1|//3.00E-17//20S proteasome alpha subunit C [Volvox carteri f. nagariensis]	Unigene71130_All//7.00E-17//AT3G22110| PAC1; endopeptidase/ peptidase/ threonine-type endopeptidase			ko03050|Proteasome		nr -
Unigene71131_All	268	0.00	3.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene71132_All	268	0.00	4.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.49E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene71132_All//COG5137//6.00E-06//Histone chaperone involved in gene silencing						cog -
Unigene71136_All	268	0.00	3.78	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.23E-06	Up	1.10E+01	4.02E-03		null	null		null	null		null	null		null	null									
Unigene71138_All	268	0.00	3.40	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	8.63E+00	3.93E-01		null	null		null	null		null	null		null	null									
Unigene71139_All	268	0.00	2.84	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.75E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71139_All//sp|P47809|MP2K4_MOUSE//2.00E-09//Dual specificity mitogen-activated protein kinase kinase 4 OS=Mus musculus GN=Map2k4 PE=1 SV=2	Unigene71139_All//3.00E-06//AT5G40440| ATMKK3 (ARABIDOPSIS THALIANA MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3); MAP kinase kinase					swissprot +
Unigene7114_All	369	6.24	7.96	10.97	8.37	12.23	18.85	0.57	1.25	0.54	3.52E-01	3.60E-01		8.14E-01	1.00E-02		5.47E-01	5.49E-02		1.17E+00	1.83E-07	Up	1.12E+00	2.73E-01		-8.59E-02	9.60E-01			Unigene7114_All//3.00E-100//gi|109857622|gb|DW486601.1|DW486601					
Unigene71140_All	268	0.00	2.46	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.21E-04	Up	7.63E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene71140_All//gi|84468322|dbj|BAE71244.1|//2.00E-06//putative DNA binding protein [Trifolium pratense]	Unigene71140_All//1.00E-05//AT4G34110| PAR2 (POLY(A) BINDING 2); RNA binding / translation initiation factor					nr -
Unigene71142_All	268	0.00	13.61	2.19	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	9.10E-21	Up	1.11E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene71142_All//sp|Q00649|HSPB1_CHICK//1.00E-05//Heat shock protein beta-1 OS=Gallus gallus GN=HSPB1 PE=2 SV=1						swissprot +
Unigene71143_All	268	0.00	5.29	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.05E-08	Up	9.63E+00	1.39E-01		null	null		null	null		null	null		null	null									
Unigene71144_All	268	0.00	3.03	0.60	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	9.22E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71144_All//gi|224007978|ref|XP_002292948.1|//1.00E-15//eukaryotic protein kinase [Thalassiosira pseudonana CCMP1335] >gi|220971074|gb|EED89409.1| eukaryotic protein kinase [Thalassiosira pseudonana CCMP1335]	Unigene71144_All//2.00E-11//AT3G04530| PPCK2; kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr -
Unigene71146_All	268	0.00	13.23	3.78	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	3.45E-20	Up	1.19E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene71146_All//gi|115459838|ref|NP_001053519.1|//1.00E-09//Os04g0555700 [Oryza sativa Japonica Group] >gi|75233025|sp|Q7XSN9.2|ADF6_ORYSJ RecName: Full=Actin-depolymerizing factor 6; Short=ADF-6; Short=OsADF6 >gi|38345587|emb|CAE01864.2| OSJNBb0012E24.5 [Oryza sativa (japonica cultivar-group)] >gi|113565090|dbj|BAF15433.1| Os04g0555700 [Oryza sativa Japonica Group]	Unigene71146_All//2.00E-10//AT5G59890| ADF4 (ACTIN DEPOLYMERIZING FACTOR 4); actin binding					nr +

Unigene7115_All	661	0.63	1.00	0.08	0.90	1.72	1.57	12.60	31.68	35.32	6.54E-01	4.48E-01		-2.97E+00	6.45E-02		9.27E-01	1.63E-01		7.97E-01	2.63E-01		1.33E+00	1.17E-29	Up	1.49E+00	9.51E-40	Up	Unigene7115_All//gi|20197360|gb|AAM15041.1|//3.00E-10//Expressed protein [Arabidopsis thaliana] >gi|20197508|gb|AAM15101.1| Expressed protein [Arabidopsis thaliana]	Unigene7115_All//2.00E-11//AT2G25735| unknown protein					nr -
Unigene71150_All	268	0.00	1.70	3.18	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	7.35E-03		1.16E+01	9.00E-05	Up	null	null		null	null		null	null		null	null		Unigene71150_All//sp|P36975|SNP25_DROME//3.00E-24//Synaptosomal-associated protein 25 OS=Drosophila melanogaster GN=Snap25 PE=2 SV=1						swissprot -
Unigene71153_All	269	0.00	4.33	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	9.63E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71153_All//gi|226530890|ref|NP_001151865.1|//7.00E-28//serine hydroxymethyltransferase [Zea mays] >gi|195650403|gb|ACG44669.1| serine hydroxymethyltransferase [Zea mays]	Unigene71153_All//8.00E-19//AT5G26780| SHM2 (SERINE HYDROXYMETHYLTRANSFERASE 2); catalytic/ glycine hydroxymethyltransferase/ pyridoxal phosphate binding			ko00460|Cyanoamino acid metabolism//ko00260|Glycine, serine and threonine metabolism//ko00670|One carbon pool by folate		nr +
Unigene71154_All	269	0.19	5.84	0.00	0.56	0.00	0.50	0.00	1.24	0.15	4.91E+00	8.63E-08	Up	-7.60E+00	6.16E-01		-9.12E+00	1.65E-01		-1.41E-01	9.42E-01		1.03E+01	1.27E-02		7.21E+00	6.39E-01		Unigene71154_All//gi|15225457|ref|NP_182060.1|//3.00E-26//CRR4 (CHLORORESPIRATORY REDUCTION 4) [Arabidopsis thaliana]	Unigene71154_All//1.00E-27//AT2G45350| CRR4 (CHLORORESPIRATORY REDUCTION 4)	Unigene71154_All//4.00E-136//CO093316				nr -
Unigene71158_All	269	0.00	3.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.33E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71158_All//CO652927//8.00E-06//Cellobiohydrolase A (1,4-beta-cellobiosidase A)						cog +
Unigene7116_All	269	0.00	3.39	1.19	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	1.02E+01	4.48E-02		null	null		null	null		null	null		null	null									
Unigene7116_All	241	8.47	9.67	4.86	14.06	5.57	10.68	18.60	14.91	6.12	1.92E-01	6.30E-01		-8.01E-01	9.12E-02		-1.33E+00	2.79E-05	Down	-3.96E-01	2.71E-01		-3.18E-01	2.39E-01		-1.60E+00	2.73E-09	Down			Unigene7116_All//1.00E-46//gi|21103521|gb|BQ415834.1|BQ415834				
Unigene71162_All	269	0.00	3.77	1.39	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.22E-06	Up	1.04E+01	2.49E-02		null	null		null	null		null	null		null	null									
Unigene71165_All	269	0.00	3.20	1.98	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	1.10E+01	4.02E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene71167_All	269	0.00	4.14	2.38	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.99E-06	Up	1.12E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene71167_All//gi|116055402|emb|CAL58070.1|//3.00E-07//26S proteasome subunit RPN5b (ISS) [Ostreococcus tauri]	Unigene71167_All//3.00E-05//AT5G64760| RPN5B (REGULATORY PARTICLE NON-ATPASE SUBUNIT 5B)			ko03050|Proteasome		nr +
Unigene71168_All	269	0.00	3.39	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	8.63E+00	3.93E-01		null	null		null	null		null	null		null	null		Unigene71168_All//sp|Q9VVT2|NDY1_DROME//4.00E-39//Protein I'm not dead yet OS=Drosophila melanogaster GN=Indy PE=1 SV=2						swissprot +
Unigene7117_All	581	89.69	225.00	133.17	19.72	19.91	25.96	96.57	35.25	28.04	1.33E+00	2.68E-147	Up	5.70E-01	8.52E-21		1.42E-02	9.61E-01		3.97E-01	6.04E-03		-1.45E+00	1.50E-89	Down	-1.78E+00	1.10E-123	Down	Unigene7117_All//gi|56562175|emb|CAH60890.1|//2.00E-19//carbonic anhydrase [Solanum lycopersicum]	Unigene7117_All//7.00E-19//AT1G23730| BCA3 (BETA CARBONIC ANHYDRASE 4); carbonate dehydratase/ zinc ion binding	Unigene7117_All//0.00E+00//DT048348		ko00910|Nitrogen metabolism		nr -
Unigene71174_All	270	0.00	3.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.37E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71174_All//gi|297799218|ref|XP_002867493.1|//1.00E-24//pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313329|gb|EFH43752.1| pfkB-type carbohydrate kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene71174_All//5.00E-22//AT4G27600| pfkB-type carbohydrate kinase family protein	Unigene71174_All//5.00E-46//gi|164252485|gb|ES814545.1|ES814545				nr +
Unigene71179_All	270	0.00	3.19	0.20	0.74	0.26	0.33	0.00	0.15	0.00	1.16E+01	4.92E-05	Up	7.62E+00	6.28E-01		-1.53E+00	4.15E-01		-1.14E+00	5.68E-01		7.27E+00	6.28E-01		null	null									ESTscan -
Unigene7118_All	651	4.34	4.36	6.05	9.11	8.41	3.40	2.27	0.26	0.80	6.20E-03	9.85E-01		4.80E-01	1.41E-01		-1.15E-01	6.84E-01		-1.42E+00	1.28E-08	Down	-3.15E+00	8.54E-07	Down	-1.51E+00	2.08E-03		Unigene7118_All//gi|222424682|dbj|BAH20295.1|//2.00E-53//AT4G37250 [Arabidopsis thaliana]	Unigene7118_All//1.00E-51//AT4G37250| leucine-rich repeat family protein / protein kinase family protein	Unigene7118_All//0.00E+00//gi|48879433|gb|CO130455.1|CO130455		ko04626|Plant-pathogen interaction		nr -
Unigene71180_All	270	0.00	4.69	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.85E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene71180_All//sp|P16905|KAPR1_DROME//1.00E-07//cAMP-dependent protein kinase type I regulatory subunit OS=Drosophila melanogaster GN=Pka-R1 PE=1 SV=2						swissprot +
Unigene71182_All	270	0.00	4.69	1.18	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.85E-07	Up	1.02E+01	4.48E-02		null	null		null	null		null	null		null	null			Unigene71182_All//2.00E-05//AT5G48810| CB5-D (CYTOCHROME B5 ISOFORM D); heme binding					
Unigene71183_All	270	0.00	2.82	1.38	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.75E-04	Up	1.04E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene71183_All//gi|159480862|ref|XP_001698501.1|//3.00E-06//type I polyketide synthase [Chlamydomonas reinhardtii] >gi|158282241|gb|EDP07994.1| type I polyketide synthase [Chlamydomonas reinhardtii]	Unigene71183_All//1.00E-05//AT4G21580| oxidoreductase, zinc-binding dehydrogenase family protein					nr -
Unigene71185_All	270	0.00	2.82	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.75E-04	Up	9.95E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71185_All//gi|255070097|ref|XP_002507130.1|//8.00E-08//calmodulin [Micromonas sp. RCC299] >gi|226522405|gb|ACO68388.1| calmodulin [Micromonas sp. RCC299]	Unigene71185_All//1.00E-08//AT3G22930| calmodulin, putative			ko04626|Plant-pathogen interaction		nr +
Unigene71186_All	270	1.16	6.38	1.78	0.74	1.91	2.17	0.31	0.00	1.48	2.46E+00	3.84E-05	Up	6.10E-01	5.86E-01		1.37E+00	2.26E-01		1.56E+00	1.36E-01		-8.29E+00	3.99E-01		2.24E+00	6.42E-02				Unigene71186_All//1.00E-86//CO093399				
Unigene71188_All	271	0.00	4.11	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.99E-06	Up	7.62E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene71188_All//gi|116054753|emb|CAL56830.1|//3.00E-06//prohibitin 1-like protein (ISS) [Ostreococcus tauri]	Unigene71188_All//5.00E-07//AT4G28510| ATPHB1 (PROHIBITIN 1)					nr +
Unigene71189_All	271	0.00	4.86	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.49E-07	Up	9.62E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71189_All//sp|Q9V496|APLP_DROME//2.00E-24//Apolipoporins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2						swissprot -
Unigene7119_All	909	0.58	0.50	0.18	0.93	1.40	0.45	1.44	1.89	5.17	-1.98E-01	8.20E-01		-1.71E+00	1.40E-01		5.89E-01	3.55E-01		-1.06E+00	1.81E-01		3.87E-01	4.05E-01		1.84E+00	1.87E-11	Up	Unigene7119_All//gi|209484093|gb|AC147521.1|//3.00E-06//iron-sulfer cluster scaffold protein ISA1 [Eucalyptus grandis]	Unigene7119_All//1.00E-06//AT2G16710| hesB-like domain-containing protein	Unigene7119_All//4.00E-34//BQ401987				nr -
Unigene71191_All	271	0.00	5.80	0.98	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.69E-09	Up	9.94E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71191_All//gi|21554133|gb|AAM63213.1|//3.00E-20//endomembrane-associated protein [Arabidopsis thaliana]	Unigene71191_All//3.00E-09//AT4G20260| DREPP plasma membrane polypeptide family protein					nr +
Unigene71193_All	271	0.00	3.55	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.37E-05	Up	9.62E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71193_All//sp|Q1HPL8|NDUBA_BOMMO//3.00E-33//NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Bombyx mori PE=1 SV=1						swissprot +
Unigene71197_All	271	0.00	4.86	0.59	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.49E-07	Up	9.20E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71197_All//gi|116222135|gb|ABJ80939.1|//7.00E-39//Hsp90 [Cyanophora paradoxa]	Unigene71197_All//7.00E-39//AT5G52640| ATHSP90.1 (HEAT SHOCK PROTEIN 90.1); ATP binding / unfolded protein binding	Unigene71197_All//6.00E-18//EV488723		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene71198_All	271	0.00	4.30	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.05E-06	Up	7.62E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene71198_All//gi|115437984|ref|XP_001043429.1|//3.00E-29//Os01g0587000 [Oryza sativa Japonica Group] >gi|75158369|sp|Q8RU33.1|VA0D_ORYSJ RecName: Full=Probable V-type proton ATPase subunit d; Short=V-ATPase subunit d; AltName: Full=Vacuolar proton pump subunit d >gi|113532960|dbj|BAF05343.1| Os01g0587000 [Oryza sativa Japonica Group]	Unigene71198_All//2.00E-29//AT3G28710| H+-transporting two-sector ATPase, putative			ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene7120_All	653	0.24	0.23	0.00	12.13	4.01	4.50	2.33	3.52	2.93	-4.63E-02	9.88E-01		-7.91E+00	2.42E-01		-1.60E+00	4.10E-15	Down	-1.43E+00	1.98E-11	Down	5.95E-01	1.21E-01		3.29E-01	4.37E-01				Unigene7120_All//8.00E-07//DR459577				
Unigene71205_All	272	0.00	2.98	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.33E-05	Up	7.61E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene71205_All//gi|301106835|ref|XP_002902500.1|//2.00E-21//acyl-CoA dehydrogenase family member 9, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262098374|gb|EEY56426.1| acyl-CoA dehydrogenase family member 9, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene71205_All//3.00E-10//AT3G51840| ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase			ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation		nr -
Unigene71206_All	272	0.00	2.79	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	9.61E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71206_All//gi|68638022|emb|CAI99405.1|//5.00E-08//P-type ATPase [Porphyra yezoensis] >gi|115635846|dbj|BAF34369.1| Na+-ATPase [Porphyra yezoensis]	Unigene71206_All//7.00E-05//AT4G11730| ATPase, plasma membrane-type, putative / proton pump, putative					nr -
Unigene71208_All	272	3.27	15.09	3.92	0.37	0.76	1.00	0.00	0.15	0.88	2.21E+00	4.90E-10	Up	2.60E-01	6.82E-01		1.05E+00	6.11E-01		1.44E+00	4.09E-01		7.26E+00	6.28E-01		9.78E+00	4.39E-02				Unigene71208_All//3.00E-78//gi|164307656|gb|ES841560.1|ES841560				
Unigene71209_All	272	0.00	2.42	0.59	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.21E-04	Up	9.20E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71209_All//gi|226494945|ref|NP_001152185.1|//3.00E-29//pre-mRNA-splicing factor PRP17 [Zea mays] >gi|195653631|gb|ACG46283.1| pre-mRNA-splicing factor PRP17 [Zea mays]	Unigene71209_All//1.00E-28//AT1G10580| transducin family protein / WD-40 repeat family protein			ko03040|Spliceosome		nr +
Unigene7121_All	417	2.76	4.74	1.28	3.46	4.46	1.19	0.41	2.41	2.58	7.80E-01	9.03E-02		-1.11E+00	9.93E-02		3.64E-01	5.05E-01		-1.54E+00	7.34E-03		2.57E+00	4.79E-04	Up	2.67E+00	1.42E-04	Up								
Unigene71211_All	272	0.00	5.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.78E-08	Up	null	null		null	null		null	null		null	null		null	null									
Unigene71212_All	272	0.00	2.42	1.17	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.21E-04	Up	1.02E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene71212_All//gi|20146110|dbj|BAB88914.1|//3.00E-19//protein phosphatase 2C [Mesembryanthemum crystallinum]	Unigene71212_All//2.00E-20//AT5G24940| protein phosphatase 2C, putative / PP2C, putative					nr -
Unigene71216_All	273	0.00	3.53	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.37E-05	Up	9.61E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71216_All//sp|Q7ZV80|SPF30_DANRE//8.00E-18//Survival of motor neuron-related-splicing factor 30 OS=Danio rerio GN=smndc1 PE=2 SV=1				ko03040|Spliceosome		swissprot -
Unigene71219_All	273	0.00	6.68	0.98	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.14E-10	Up	9.93E+00	7.95E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene7122_All	1318	1.91	0.88	0.44	3.29	3.03	1.13	3.37	0.86	0.91	-1.11E+00	6.21E-03		-2.10E+00	8.65E-06	Down	-1.18E-01	7.34E-01		-1.54E+00	3.31E-07	Down	-1.98E+00	1.38E-11	Down	-1.89E+00	2.23E-11	Down	Unigene7122_All//gi|15221015|ref|NP_172361.1|//1.00E-144//emb2411 (embryo defective 2411); ATP binding / ATP-dependent DNA helicase/ DNA binding [Arabidopsis thaliana]	Unigene7122_All//1.00E-146//AT1G08840| emb2411 (embryo defective 2411); ATP binding / ATP-dependent DNA helicase/ DNA binding	Unigene7122_All//0.00E+00//CO082107		ko03030|DNA replication		nr +
Unigene71222_All	273	0.00	2.41	0.00	0.00	0.13	0.00	0.46	0.15	0.00	1.12E+01	6.21E-04	Up	null	null		6.98E+00	8.20E-01		null	null		-1.60E+00	5.33E-01		-8.86E+00	1.99E-01				Unigene71222_All//4.00E-56//DW497770				
Unigene71223_All	273	0.58	0.00	0.59	0.18	0.50	0.00	3.10	1.38	0.15	-9.17E+00	2.14E-01		2.54E-02	1.00E+00		1.47E+00	6.17E-01		-7.51E+00	6.25E-01		-1.17E+00	9.29E-02		-4.41E+00	2.37E-05	Down			Unigene71223_All//6.00E-95//TC154944				
Unigene71227_All	274	0.00	2.59	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene71228_All	274	0.00	4.44	0.39	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.46E-07	Up	8.60E+00	3.92E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene7123_All	697	1.35	1.53	0.38	1.57	2.57	0.97	4.61	2.22	2.92	1.76E-01	7.74E-01		-1.82E+00	2.53E-02		7.08E-01	1.59E-01		-6.94E-01	3.11E-01		-1.06E+00	7.09E-04	Down	-6.61E-01	2.62E-02		Unigene7123_All//gi|297853098|ref|XP_002894430.1|//2.00E-45//mitochondrial malate dehydrogenase [Arabidopsis lyrata subsp. lyrata] >gi|297340272|gb|EFH70689.1| mitochondrial malate dehydrogenase [Arabidopsis lyrata subsp. lyrata]	Unigene7123_All//2.00E-46//AT3G15020| malate dehydrogenase (NAD), mitochondrial, putative	Unigene7123_All//4.00E-141//TC130475		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene71230_All	274	0.00	3.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +

Unigene71232_All	274	0.00	5.18	0.19	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	4.05E-08	Up	7.60E+00	6.28E-01		null	null		null	null		null	null		null	null		Unigene71232_All//gi|192910660|gb|ACF06438.1|//3.00E-19//1-Cys peroxiredoxin [Elaeis guineensis]	Unigene71232_All//9.00E-18//AT1G48130| ATPER1: antioxidant/ thioredoxin peroxidase			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene71233_All	274	0.00	2.40	2.53	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.21E-04	Up	1.13E+01	6.13E-04	Up	null	null		null	null		null	null		null	null									
Unigene71235_All	274	0.00	3.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71235_All//sp|Q20930|MIG17_CAEEL//3.00E-06//ADAM family mig-17 OS=Caenorhabditis elegans GN=mig-17 PE=1 SV=3							swissprot +
Unigene71236_All	274	0.00	2.77	0.39	0.00	0.25	0.66	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	8.60E+00	3.92E-01		7.97E+00	6.03E-01		9.36E+00	1.93E-01		null	null		null	null									ESTscan +
Unigene71237_All	274	0.00	2.77	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene71238_All	275	0.00	3.69	0.19	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.22E-06	Up	7.60E+00	6.27E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene71239_All	275	0.00	3.32	3.49	0.00	0.00	0.33	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	1.18E+01	2.45E-05	Up	null	null		8.36E+00	4.72E-01		null	null		null	null			Unigene71239_All//1.00E-71//gi|109884878|gb|DW513848.1|DW513848					
Unigene71124_All	454	3.69	8.26	4.57	2.19	1.59	2.49	0.00	0.46	0.79	1.16E+00	3.35E-04	Up	3.11E-01	5.13E-01		-4.62E-01	5.18E-01		1.81E-01	7.84E-01		8.85E+00	7.84E-02		9.63E+00	7.28E-03			Unigene71124_All//5.00E-07//TC179249					
Unigene71240_All	275	0.57	6.26	0.77	1.09	0.50	0.82	0.77	0.30	0.72	3.46E+00	6.80E-07	Up	4.40E-01	7.74E-01		-1.12E+00	4.24E-01		-4.04E-01	7.51E-01		-1.34E+00	4.29E-01		-8.58E-02	9.60E-01		Unigene71240_All//gi|266691|sp|P29528.1|OLEO7_GOSHI//2.00E-32//RecName: Full=Oleosin 16.4 kDa >gi|167361|gb|AAA18523.1| 16.4 kDa oleosin [Gossypium hirsutum]		Unigene71240_All//2.00E-131//gi|109876479|gb|DW505453.1|DW505453				nr +
Unigene71242_All	275	0.00	3.69	1.94	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.22E-06	Up	1.09E+01	4.02E-03		null	null		null	null		null	null		null	null									
Unigene71244_All	275	0.00	3.13	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene71246_All	275	0.00	2.76	0.39	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	8.60E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71246_All//gi|152002673|emb|CAL90975.1|//8.00E-19//pescadillo-like protein [Zinnia elegans]	Unigene71246_All//1.00E-16//AT5G14520| pescadillo-related					nr +
Unigene71247_All	275	0.00	4.61	1.74	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.85E-07	Up	1.08E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene71247_All//gi|226500076|ref|NP_001150681.1|//2.00E-10//LOC100284314 [Zea mays] >gi|195641032|gb|ACG39984.1| zinc finger protein hangover [Zea mays]				ko04120|Ubiquitin mediated proteolysis		nr +
Unigene71248_All	275	0.19	3.13	0.00	0.00	0.00	0.16	0.00	0.15	0.29	4.04E+00	4.20E-04	Up	-7.57E+00	6.16E-01		null	null		7.36E+00	6.88E-01		7.25E+00	6.28E-01		8.18E+00	4.01E-01		Unigene71248_All//gi|291621327|dbj|BAI94501.1|//2.00E-22//sodium/calcium exchanger protein [Dianthus caryophyllus]	Unigene71248_All//6.00E-22//AT1G53210| sodium/calcium exchanger family protein / calcium-binding EF hand family protein	Unigene71248_All//1.00E-89//gi|73863410|gb|DT466149.1|DT466149				nr -
Unigene71125_All	1063	0.69	0.29	0.60	37.16	23.36	9.90	2.11	0.55	0.45	-1.27E+00	1.36E-01		-1.97E-01	7.99E-01		-6.70E-01	7.07E-18		-1.91E+00	1.08E-82	Down	-1.94E+00	4.55E-06	Down	-2.23E+00	2.21E-07	Down	Unigene71125_All//gi|77550719|gb|AB493516.1|//6.00E-19//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene71125_All//5.00E-41//AT3G25130| unknown protein	Unigene71125_All//0.00E+00//ES833961				nr -
Unigene71251_All	276	0.00	3.30	1.54	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	1.06E+01	1.37E-02		null	null		null	null		null	null		null	null									
Unigene71255_All	276	0.19	3.30	0.58	0.54	0.25	0.33	0.46	0.30	0.43	4.12E+00	2.33E-04	Up	1.61E+00	5.10E-01		-1.12E+00	5.82E-01		-7.26E-01	7.14E-01		-6.02E-01	7.65E-01		-8.60E-02	9.68E-01			Unigene71255_All//5.00E-46//FL577203					ESTscan -
Unigene71257_All	276	0.00	4.22	0.00	0.00	0.12	0.00	0.31	0.15	0.58	1.20E+01	1.05E-06	Up	null	null		6.96E+00	8.20E-01		null	null		-1.02E+00	7.22E-01		9.14E-01	6.23E-01		Unigene71257_All//gi|15229478|ref|NP_189001.1|//4.00E-17//RFR1 (REF4-related 1) [Arabidopsis thaliana]	Unigene71257_All//2.00E-18//AT3G23590| RFR1 (REF4-related 1)	Unigene71257_All//4.00E-19//ES813254				nr -
Unigene71258_All	276	0.00	3.49	0.39	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.37E-05	Up	8.59E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71258_All//gi|300121813|emb|CBK22387.2|//5.00E-07//unnamed protein product [Blastocystis hominis]							nr -
Unigene7126_All	488	2.79	8.00	10.04	2.14	1.48	1.85	3.99	5.48	8.41	1.52E+00	4.21E-06	Up	1.85E+00	3.36E-09	Up	-5.33E-01	4.27E-01		-2.12E-01	7.44E-01		4.60E-01	2.00E-01		1.08E+00	5.21E-05	Up		Unigene7126_All//4.00E-17//ES793411					
Unigene71260_All	276	0.00	3.12	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71260_All//sp|B4KJ11|INT3_DROMO//9.00E-41//Integrator complex subunit 3 homolog OS=Drosophila mojavensis GN=GI18256 PE=3 SV=1							swissprot +
Unigene71261_All	276	0.00	4.22	0.00	0.18	0.62	0.16	0.61	0.45	0.43	1.20E+01	1.05E-06	Up	null	null		1.79E+00	5.20E-01		-1.42E-01	9.49E-01		-4.32E-01	7.92E-01		-5.01E-01	7.46E-01			Unigene71261_All//2.00E-45//FL577491					
Unigene71263_All	276	0.00	4.59	0.58	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.85E-07	Up	9.18E+00	2.36E-01		null	null		null	null		null	null		null	null									
Unigene71265_All	276	0.00	2.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.33E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71265_All//sp|Q6BZ23|PANK2_HUMAN//1.00E-09//Pantothenate kinase 2, mitochondrial OS=Homo sapiens GN=PANK2 PE=1 SV=3							swissprot +
Unigene71267_All	276	0.00	3.30	0.58	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	9.18E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71267_All//sp|Q00341|VIGLN_HUMAN//4.00E-07//Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2							swissprot +
Unigene71268_All	276	0.00	2.75	0.77	0.00	0.00	1.15	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	9.59E+00	1.39E-01		null	null		1.02E+01	4.07E-02		null	null		null	null		Unigene71268_All//gi|192910800|gb|ACF06505.1|//4.00E-33//senescence-associated protein [Elaeis guineensis]	Unigene71268_All//2.00E-25//AT3G23810| TET8 (TETRASPANIN8)	Unigene71268_All//6.00E-21//gi|13351015|gb|BG441375.1|BG441375				nr +
Unigene71273_All	277	0.00	2.93	1.73	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.32E-05	Up	1.08E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene71273_All//gi|29409366|gb|AAM29179.1|//2.00E-40//prohibitin protein Wph [Triticum aestivum]	Unigene71273_All//8.00E-27//AT1G03860| ATPHB2 (PROHIBITIN 2)					nr -
Unigene71276_All	277	0.00	2.56	0.96	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	9.91E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71276_All//sp|077460|IPYR_DROME//1.00E-20//Inorganic pyrophosphatase OS=Drosophila melanogaster GN=Nurf-38 PE=1 SV=3							swissprot +
Unigene71279_All	277	0.00	2.38	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.21E-04	Up	8.59E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71279_All//gi|226347409|gb|ACO50115.1|//2.00E-33//elongation factor 1 alpha [Peranema trichophorum]	Unigene71279_All//2.00E-30//AT5G60390| elongation factor 1-alpha / EF-1-alpha					nr +
Unigene7128_All	893	195.22	125.34	179.85	30.85	26.95	14.62	0.00	0.00	0.09	-6.39E-01	1.92E-58		-1.18E-01	4.80E-03		-1.95E-01	7.01E-02		-1.08E+00	9.76E-25	Down	null	null		6.48E+00	4.01E-01		Unigene7128_All//gi|56744293|gb|AAW28572.1|//6.00E-64//Putative oxygen evolving enhancer protein 3, identical [Solanum demissum]	Unigene7128_All//9.00E-52//AT1G14150| oxygen evolving enhancer 3 (PsbQ) family protein	Unigene7128_All//0.00E+00//DW519134		ko00195|Photosynthesis		nr -
Unigene71281_All	277	0.00	2.56	0.38	0.00	0.12	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	8.59E+00	3.92E-01		6.96E+00	8.20E-01		null	null		null	null		null	null		Unigene71281_All//gi|P17535|JUND_HUMAN//4.00E-44//Transcription factor jun-D OS=Homo sapiens GN=JUND PE=1 SV=3	Unigene71281_All//4.00E-05//AT5G11260| HY5 (ELONGATED HYPOCOTYL 5); DNA binding / double-stranded DNA binding / transcription factor		bZIP			swissprot +
Unigene71282_All	277	0.00	3.66	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.22E-06	Up	9.59E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene71283_All	277	0.00	12.26	2.31	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	2.54E-19	Up	1.12E+01	1.15E-03		null	null		null	null		null	null		null	null									
Unigene71285_All	277	0.00	2.93	0.96	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.32E-05	Up	9.91E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71285_All//gi|190895764|gb|ACE96395.1|//1.00E-36//esterase/lipase/thioesterase [Populus tremula] >gi|190895766|gb|ACE96396.1| esterase/lipase/thioesterase [Populus tremula] >gi|190895768|gb|ACE96397.1| esterase/lipase/thioesterase [Populus tremula] >gi|190895770|gb|ACE96398.1| esterase/lipase/thioesterase [Populus tremula]	Unigene71285_All//1.00E-37//AT5G08530| CI51 (51 kDa subunit of complex I); 4 iron, 4 sulfur cluster binding / FMN binding / NAD or NADH binding / NADH dehydrogenase (ubiquinone)/ oxidoreductase, acting on NADH or NADPH			ko00190|Oxidative phosphorylation		nr +
Unigene71288_All	277	0.00	2.56	0.19	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	7.59E+00	6.27E-01		null	null		null	null		null	null		null	null									
Unigene71289_All	277	0.00	3.29	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	9.59E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71289_All//gi|225685853|dbj|BAH20213.1|//1.00E-30//methionine S-adenosyl transferase [Cylindrotheca closterium]	Unigene71289_All//1.00E-24//AT3G17390| MTO3 (METHIONINE OVER-ACCUMULATOR 3); methionine adenosyltransferase			ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr +
Unigene71291_All	278	0.00	2.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71291_All//sp|Q986X4|TM134_HUMAN//2.00E-08//Transmembrane protein 134 OS=Homo sapiens GN=TMEM134 PE=2 SV=1	Unigene71291_All//2.00E-05//AT2G19350| unknown protein					swissprot -
Unigene71292_All	278	0.00	3.10	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	9.58E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71292_All//sp|Q8C996|FA40B_MOUSE//5.00E-26//Protein FAM40B OS=Mus musculus GN=Fam40b PE=2 SV=1							swissprot -
Unigene71294_All	278	0.38	2.92	0.77	0.00	0.00	0.32	0.00	0.30	2.01	2.95E+00	3.28E-03		1.03E+00	5.90E-01		null	null		8.34E+00	4.72E-01		8.23E+00	3.99E-01		1.10E+01	3.28E-04	Up							
Unigene71295_All	278	0.00	9.84	0.38	0.18	0.37	0.32	0.00	0.30	0.00	1.33E+01	1.44E-15	Up	8.58E+00	3.92E-01		1.05E+00	8.06E-01		8.58E-01	7.92E-01		8.23E+00	3.99E-01		null	null		Unigene71295_All//gi|21592665|gb|AAM64614.1|//6.00E-33//lsp4-like protein [Arabidopsis thaliana]	Unigene71295_All//2.00E-34//AT5G64410| OPT4 (OLIGOPEPTIDE TRANSPORTER 4); oligopeptide transporter					nr -
Unigene71296_All	278	0.00	3.83	0.96	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	3.80E-06	Up	9.90E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71296_All//sp|A2ASS6|TITIN_MOUSE//3.00E-10//Titin OS=Mus musculus GN=Ttn PE=1 SV=1							swissprot +
Unigene71297_All	278	0.19	4.92	0.57	0.00	0.37	0.00	0.00	0.00	0.00	4.71E+00	1.03E-06	Up	1.61E+00	5.10E-01		8.54E+00	4.53E-01		null	null		null	null		null	null		Unigene71297_All//gi|226506956|ref|NP_001147516.1|//5.00E-32//transparent testa 12 protein [Zea mays] >gi|195611926|gb|ACG27793.1| transparent testa 12 protein [Zea mays]	Unigene71297_All//2.00E-32//AT3G23560| ALF5 (ABERRANT LATERAL ROOT FORMATION 5); antiporter/ drug transporter/ transporter	Unigene71297_All//3.00E-115//ES800251				nr +
Unigene713_All	2122	4.24	3.34	2.06	5.68	7.24	4.34	6.85	9.36	7.25	-3.43E-01	8.09E-02		-1.04E+00	2.76E-07	Down	3.49E-01	1.29E-02		-3.88E-01	1.89E-02		4.49E-01	4.61E-05		8.04E-02	6.01E-01		Unigene713_All//gi|115466772|ref|NP_001056985.1|//0.00E+00//Os06g0182500 [Oryza sativa (japonica cultivar-group)] >gi|55771369|dbj|BAD72536.1| LIM domain containing protein-like [Oryza sativa (japonica cultivar-group)] >gi|113595025|db|BAF18899.1|Os06g0182500 [Oryza sativa (japonica cultivar-group)]	Unigene713_All//0.00E+00//AT1G19270| DA1 (DA 1); ubiquitin binding	Unigene713_All//0.00E+00//TC176198	Orphans		GO:0003006//GO:0045926//GO:0046914	nr +
Unigene7130_All	725	0.00	1.47	0.29	5.91	2.75	1.81	19.94	6.40	28.52	1.05E+01	3.80E-06	Up	8.20E+00	1.39E-01		-1.10E+00	5.90E-05	Down	-1.71E+00	3.50E-08	Down	-1.64E+00	4.60E-28	Down	5.16E-01	1.00E-06			Unigene7130_All//0.00E+00//TC157207					
Unigene71301_All	278	0.00	2.55	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71301_All//gi|159469438|ref|XP_001692870.1|//4.00E-19//2-oxoglutarate dehydrogenase, E1 subunit [Chlamydomonas reinhardtii] >gi|158277672|gb|EDP03439.1| 2-oxoglutarate dehydrogenase, E1 subunit [Chlamydomonas reinhardtii]	Unigene71301_All//2.00E-16//AT3G55410| 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative			ko00380|Tryptophan metabolism//ko00020|Citrate cycle (TCA cycle)//ko00310|Lysine degradation		nr -
Unigene71303_All	278	0.00	2.73	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	1.06E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71303_All//gi|301121300|ref|XP_002908377.1|//7.00E-18//glycyl-tRNA synthetase [Phytophthora infestans T30-4] >gi|262103408|gb|EEY61460.1| glycyl-tRNA synthetase [Phytophthora infestans T30-4]	Unigene71303_All//1.00E-14//AT1G29880| glycyl-tRNA synthetase / glycine--tRNA ligase			ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene71304_All	278	0.00	4.37	3.45	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.46E-07	Up	1.18E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene71304_All//sp|Q5RBA4|MYL9_PONAB//5.00E-22//Myosin regulatory light polypeptide 9 OS=Pongo abelii GN=MYL9 PE=2 SV=3	Unigene71304_All//5.00E-07//AT3G51920| CAM9 (CALMODULIN 9); calcium ion binding			ko04626|Plant-pathogen interaction		swissprot -
Unigene71305_All	278	0.00	3.10	1.15	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	1.02E+01	4.48E-02		null	null		null	null		null	null		null	null									
Unigene71306_All	278	0.00	5.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	4.05E-08	Up	null	null		null	null		null	null		null	null		null	null		Unigene71306_All//gi|297802486|ref|XP_002869127.1|//5.00E-07//auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314963|gb|EFH45386.1| auxin-responsive family protein [Arabidopsis lyrata subsp. lyrata]						nr -

Unigene71309_All	279	0.00	4.00	0.19	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.99E-06	Up	7.58E+00	6.27E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene71310_All	279	0.00	4.72	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.49E-07	Up	9.16E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71310_All//sp|P82147|L2EFL_DROME//3.00E-25//Protein lethal(2)essential for life OS=Drosophila melanogaster GN=l(2)efl PE=1 SV=1							swissprot +
Unigene71312_All	279	0.00	3.63	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.22E-06	Up	8.58E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71312_All//gi|7385055|gb|AAF61673.1|//1.00E-12//beta-adaptin-like protein C [Arabidopsis thaliana]	Unigene71312_All//6.00E-14//AT4G23460| beta-adaptin, putative					nr -
Unigene71313_All	279	0.00	3.27	0.19	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	7.58E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71313_All//gi|162459683|ref|NP_001105241.1|//1.00E-24//DEAD box RNA helicase1 [Zea mays] >gi|396536663|gb|AAR29370.1| DEAD box RNA helicase [Zea mays]	Unigene71313_All//4.00E-24//AT1G55150| DEAD box RNA helicase, putative (RH20)			ko03040|Spliceosome		nr -
Unigene71314_All	279	0.00	4.36	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.46E-07	Up	9.16E+00	2.36E-01		null	null		null	null		null	null		null	null									
Unigene71315_All	279	0.00	4.18	3.05	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.05E-06	Up	1.16E+01	9.00E-05	Up	null	null		null	null		null	null		null	null		Unigene71315_All//gi|116309909|emb|CAH66944.1|//2.00E-10//OSIGBa0116M22.11 [Oryza sativa (indica cultivar-group)]	Unigene71315_All//8.00E-11//AT4G35650| isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative			ko00020|Citrate cycle (TCA cycle)		nr +
Unigene71316_All	279	0.00	3.27	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	1.06E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71316_All//gi|300268516|gb|EFJ52696.1|//4.00E-29//20S proteasome alpha subunit E [Volvox carteri f. nagariensis]	Unigene71316_All//4.00E-30//AT3G14290| PAE2; endopeptidase/ peptidase/ threonine-type endopeptidase			ko03050|Proteasome		nr +
Unigene71317_All	279	0.00	4.72	1.72	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.49E-07	Up	1.07E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene71317_All//sp|P16854|EST1_CULPI//4.00E-09//Esterase B1 OS=Culex pipiens GN=B1 PE=3 SV=1							swissprot +
Unigene71318_All	279	0.00	3.27	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	1.06E+01	1.37E-02		null	null		null	null		null	null		null	null									
Unigene71321_All	279	0.00	4.72	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.49E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene71321_All//gi|158828199|gb|ABW81077.1|//1.00E-06//Prp9 [Cleome spinosa]							nr -
Unigene71322_All	279	0.00	2.36	0.19	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.21E-04	Up	7.58E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71322_All//gi|301113592|ref|XP_002998566.1|//2.00E-07//pyruvate carboxylase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262111867|gb|EEY69919.1| pyruvate carboxylase, mitochondrial precursor [Phytophthora infestans T30-4]				ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)		nr +
Unigene71323_All	279	0.00	3.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null									
Unigene71324_All	280	0.00	4.89	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.78E-08	Up	8.57E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71324_All//gi|75180217|sp|Q9LQU4.1|Y1487_ARATH//2.00E-37//RecName: Full=Uncharacterized protein At1g14870 >gi|87782226|gb|AAF79235.1|AC006917_20 F10B6.27 [Arabidopsis thaliana]	Unigene71324_All//7.00E-39//AT1G14870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: plasma membrane; EXPRESSED IN: callus; CONTAINS InterPro DOMAIN/s: EGF-type aspartate/asparagine hydroxylation conserved site (InterPro:IPR000152), Protein of unknown function Cys-rich (InterPro:IPR006461); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G35525.1); Has 492 Blast hits to 491 proteins in 78 species: Archae - 0; Bacteria - 0; Metazoa - 93; Fungi - 76; Plants - 297; Viruses - 0; Other Eukaryotes - 26 (source: NCBI BLink).						nr +
Unigene71326_All	280	0.00	4.34	1.52	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.46E-07	Up	1.06E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71326_All//gi|255085931|ref|XP_002508932.1|//7.00E-20//also known as glycine decarboxylase l-protein [Micromonas sp. RCC299] >gi|226524210|gb|ACO70190.1| also known as glycine decarboxylase l-protein [Micromonas sp. RCC299]	Unigene71326_All//2.00E-19//AT1G48030| mtLPD1 (mitochondrial lipoamide dehydrogenase 1); ATP binding / dihydrolipoyl dehydrogenase			ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00020|Citrate cycle (TCA cycle)//ko00260|Glycine, serine and threonine metabolism		nr +
Unigene71327_All	280	0.00	2.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.21E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene71333_All	282	25.05	23.90	22.66	34.62	27.72	35.55	50.08	38.39	20.77	-6.78E-02	7.64E-01		-1.45E-01	5.78E-01		-3.21E-01	8.44E-02		3.83E-02	8.65E-01		-3.84E-01	4.41E-03		-1.27E+00	1.52E-19	Down	Unigene71333_All//gi|6599051|emb|CAB63651.1|//3.00E-06//26S proteasome subunit 8; Tat binding protein [Fagus sylvatica]	Unigene71333_All//3.00E-07//AT5G20000| 26S proteasome AAA-ATPase subunit, putative	Unigene71333_All//5.00E-145//gi|21103274|gb|BQ415587.1|BQ415587		ko03050|Proteasome		nr -
Unigene71330_All	280	0.00	5.43	1.52	0.36	1.48	0.97	0.00	0.00	0.00	1.24E+01	1.09E-08	Up	1.06E+01	1.37E-02		2.05E+00	1.47E-01		1.44E+00	4.09E-01		null	null		null	null									
Unigene71331_All	280	0.00	3.26	3.04	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.61E-05	Up	1.16E+01	9.00E-05	Up	null	null		null	null		null	null		null	null		Unigene71331_All//gi|227202816|dbj|BAH56881.1|//1.00E-24//AT2G21330 [Arabidopsis thaliana]	Unigene71331_All//5.00E-26//AT2G21330| fructose-bisphosphate aldolase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene71332_All	280	0.00	2.71	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	8.57E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71332_All//gi|115451341|ref|NP_001049271.1|//5.00E-06//Os03g0197300 [Oryza sativa Japonica Group] >gi|113547742|dbj|BAF111185.1| Os03g0197300 [Oryza sativa Japonica Group]							nr +
Unigene7134_All	490	0.00	0.00	0.00	27.86	15.46	2.58	0.17	0.17	0.00	null	null		null	null		-8.49E-01	1.36E-09		-3.43E+00	8.10E-56	Down	-1.68E-02	1.01E+00		-7.43E+00	3.55E-01				Unigene7134_All//3.00E-30//TC153771				
Unigene71341_All	280	0.19	4.89	0.38	0.53	0.37	0.97	0.00	0.00	0.14	4.71E+00	1.03E-06	Up	1.03E+00	7.01E-01		-5.33E-01	7.84E-01		8.59E-01	6.30E-01		null	null		7.15E+00	6.39E-01				Unigene71341_All//3.00E-07//EX167388				
Unigene71343_All	281	0.00	2.52	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	8.57E+00	3.92E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene71344_All	281	0.00	2.70	0.00	1.42	0.25	0.16	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	null	null		-2.53E+00	5.79E-02		-3.14E+00	4.87E-02		null	null		null	null		Unigene71344_All//sp|Q89J74|RPOB_BRAJA//2.00E-29//DNA-directed RNA polymerase submit beta OS=Bradyrhizobium japonicum GN=rpoB PE=3 SV=1							swissprot -
Unigene71346_All	281	0.00	2.34	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.21E-04	Up	8.57E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71346_All//gi|82623425|gb|AB887127.1|//3.00E-41//enolase-like [Solanum tuberosum]	Unigene71346_All//4.00E-42//AT2G36530| LOS2; copper ion binding / phosphopyruvate hydratase	Unigene71346_All//9.00E-14//ES806391		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation		nr -
Unigene71349_All	282	0.00	3.41	1.32	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.37E-05	Up	1.04E+01	2.49E-02		null	null		null	null		null	null		null	null									
Unigene71350_All	282	0.00	7.01	3.78	0.00	0.61	0.00	0.00	0.00	0.00	1.28E+01	2.96E-11	Up	1.19E+01	6.61E-06	Up	9.25E+00	2.26E-01		null	null		null	null		null	null									
Unigene71351_All	282	0.19	2.87	2.83	0.53	0.61	0.48	0.00	0.00	0.14	3.95E+00	7.52E-04	Up	3.93E+00	1.25E-03		2.05E-01	9.49E-01		-1.41E-01	9.42E-01		null	null		7.14E+00	6.39E-01									
Unigene71353_All	282	0.00	6.11	4.34	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	7.97E-10	Up	1.21E+01	9.10E-07	Up	null	null		null	null		null	null		null	null		Unigene71353_All//sp|P07602|SAP_HUMAN//2.00E-23//Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2							swissprot +
Unigene71354_All	282	0.00	2.70	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene71356_All	282	0.00	4.13	1.32	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.03E-06	Up	1.04E+01	2.49E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene71357_All	282	0.00	2.87	0.00	0.00	0.00	0.00	0.90	0.59	0.00	1.15E+01	9.32E-05	Up	null	null		null	null		null	null		-6.02E-01	6.47E-01		-9.81E+00	3.03E-02		Unigene71357_All//gi|133711974|gb|AB036677.1|//8.00E-22//vicilin [Pistacia vera]	Unigene71357_All//8.00E-09//AT3G22640| PAP85; nutrient reservoir					nr -
Unigene7136_All	1792	0.00	0.00	0.06	1.06	0.88	0.28	8.19	10.57	8.71	null	null		5.89E+00	3.92E-01		-2.57E-01	6.08E-01		-1.93E+00	1.45E-04	Down	3.68E-01	1.28E-03		9.01E-02	5.44E-01		Unigene7136_All//gi|115479653|ref|NP_001063420.1|//1.00E-105//Os09g0466800 [Oryza sativa Japonica Group] >gi|113631653|dbj|BAF25334.1| Os09g0466800 [Oryza sativa Japonica Group]	Unigene7136_All//1.00E-165//AT4G33600| unknown protein					nr -
Unigene71360_All	282	0.00	3.41	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.37E-05	Up	8.56E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71360_All//gi|298708179|emb|CBJ30519.1|//1.00E-08//NADH dehydrogenase (ubiquinone) [Ectocarpus siliculosus]	Unigene71360_All//1.00E-07//AT3G12260| complex I family protein / LVR family protein			ko00190|Oxidative phosphorylation		nr -
Unigene71361_All	282	0.00	2.34	1.89	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.21E-04	Up	1.09E+01	4.02E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene71363_All	283	0.00	6.98	1.88	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.96E-11	Up	1.09E+01	4.02E-03		null	null		null	null		null	null		null	null									
Unigene71365_All	283	0.00	5.55	2.45	0.00	0.00	0.00	0.45	0.00	0.56	1.24E+01	5.69E-09	Up	1.13E+01	6.13E-04	Up	null	null		null	null		-8.81E+00	2.34E-01		3.29E-01	8.50E-01		Unigene71365_All//gi|5902404|gb|AAD55506.1|AC008148_16//3.00E-35//unknown protein [Arabidopsis thaliana]	Unigene71365_All//3.00E-37//AT1G23110| unknown protein	Unigene71365_All//2.00E-153//gi|109869874|gb|DW498850.1|DW498850				nr -
Unigene71368_All	283	0.00	4.66	1.69	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.49E-07	Up	1.07E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene71368_All//gi|219128101|ref|XP_002184260.1|//2.00E-24//cystathionine gamma-lyase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217404491|gb|EEC44438.1| cystathionine gamma-lyase [Phaeodactylum tricornutum CCAP 1055/1]	Unigene71368_All//8.00E-16//AT3G57050| CBL (cystathionine beta-lyase); cystathionine beta-lyase			ko00270|Cysteine and methionine metabolism//ko00910|Nitrogen metabolism//ko00260|Glycine, serine and threonine metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism		nr -
Unigene71370_All	283	0.00	4.12	2.07	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.05E-06	Up	1.10E+01	2.17E-03		null	null		null	null		null	null		null	null									
Unigene71372_All	283	0.00	3.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene71373_All	283	0.00	6.62	1.13	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.10E-10	Up	1.01E+01	4.48E-02		null	null		null	null		null	null		null	null									
Unigene71375_All	283	0.00	2.51	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	8.56E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71375_All//sp|P09208|INSR_DROME//3.00E-12//Insulin-like receptor OS=Drosophila melanogaster GN=InR PE=1 SV=3							swissprot +
Unigene71376_All	283	0.00	5.37	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.09E-08	Up	null	null		null	null		null	null		null	null		null	null		Unigene71376_All//gi|301115380|ref|XP_002905419.1|//8.00E-48//serine/threonine-protein phosphatase PP1-gamma catalytic subunit [Phytophthora infestans T30-4] >gi|262110208|gb|EEY68260.1| serine/threonine-protein phosphatase PP1-gamma catalytic subunit [Phytophthora infestans T30-4]	Unigene71376_All//7.00E-44//AT5G43380| TOPP6; protein serine/threonine phosphatase					nr -
Unigene71378_All	283	0.92	7.70	0.94	0.88	0.49	0.96	0.45	0.30	0.56	3.06E+00	9.39E-08	Up	2.54E-02	1.00E+00		-8.55E-01	5.73E-01		1.22E-01	9.44E-01		-6.02E-01	7.65E-01		3.29E-01	8.50E-01									
Unigene7138_All	309	98.21	31.48	65.14	84.47	121.92	165.75	53.50	22.05	34.29	-1.64E+00	1.36E-47	Down	-5.92E-01	4.29E-09		5.29E-01	4.87E-11		9.72E-01	4.28E-38		-1.28E+00	2.78E-22	Down	-6.42E-01	7.95E-08		Unigene7138_All//gi|292653525|gb|ADE34280.1|//7.00E-13//aquaporin PIP1;11 [Gossypium hirsutum]	Unigene7138_All//5.00E-14//AT4G00430| PIP1;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;4); water channel	Unigene7138_All//1.00E-53//EX166998				nr +
Unigene71381_All	283	0.00	3.04	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +

Unigene71382_All	283	0.00	4.48	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.85E-07	Up	9.56E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71382_All//gi|159464080|ref|XP_001690270.1|//2.00E-10//cytochrome P450, CYP711 clan [Chlamydomonas reinhardtii] >gi|158284238|gb|EDP10008.1| cytochrome P450, CYP711 clan [Chlamydomonas reinhardtii]	Unigene71382_All//2.00E-10//AT3G14630| CYP72A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00591|Linoleic acid metabolism//ko00944|Flavone and flavonol biosynthesis		nr +
Unigene71384_All	284	0.00	4.46	0.94	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.85E-07	Up	9.87E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71384_All//gi|399014|sp|P31692.1|ADT_CHLKE//3.00E-26//RecName: Full=ADP,ATP carrier protein; AltName: Full=ADP/ATP translocase; AltName: Full=Adenine nucleotide translocator; Short=ANT >gi|516597|gb|AAA33027.1| ATP/ADP translocator [Parachlorella kessleri]	Unigene71384_All//4.00E-21//AT5G13490| AAC2 (ADP/ATP carrier 2); ATP:ADP antiporter/ binding					nr -
Unigene71386_All	284	0.00	3.03	1.69	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	1.07E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene71386_All//gi|195629766|gb|ACG36524.1|//8.00E-16//aldose reductase [Zea mays]	Unigene71386_All//6.00E-16//AT2G37770| aldo/keto reductase family protein			ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene7139_All	846	1.30	0.00	0.50	2.94	3.95	3.31	1.10	0.69	1.18	-1.03E+01	1.95E-06	Down	-1.37E+00	5.32E-02		4.23E-01	2.37E-01		1.69E-01	6.98E-01		-6.69E-01	3.12E-01		9.86E-02	8.78E-01		Unigene7139_All//gi|124359981|gb|ABW07997.1|//1.00E-20//contains similarity to reverse trancriptase, related [Medicago truncatula]	Unigene7139_All//2.00E-09//ATMG00310| hypothetical protein					nr +
Unigene71391_All	284	0.00	4.10	0.56	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.05E-06	Up	9.14E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71391_All//sp|B4LN42|EIF3J_DROVI//9.00E-20//Eukaryotic translation initiation factor 3 subunit J OS=Drosophila virilis GN=Adam PE=3 SV=1						swissprot +
Unigene71393_All	284	0.00	3.03	1.13	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	1.01E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene71393_All//gi|298713037|emb|CBJ48812.1|//7.00E-33//ubiquitin-activating enzyme E1 [Ectocarpus siliculosus]	Unigene71393_All//2.00E-23//AT5G06460| ATUBA2; ubiquitin activating enzyme/ ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis		nr +
Unigene71395_All	284	0.00	3.75	1.50	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	3.80E-06	Up	1.06E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71395_All//sp|Q8I9B4|MT4_DROME//1.00E-12//Metallothionein-4 OS=Drosophila melanogaster GN=MtnD PE=3 SV=1						swissprot +
Unigene71396_All	284	0.00	2.85	0.94	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.32E-05	Up	9.87E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71396_All//gi|15239274|ref|NP_201416.1|//2.00E-19//glycosyl hydrolase family 38 protein [Arabidopsis thaliana] >gi|10177130|dbj|BAB10420.1| alpha-mannosidase [Arabidopsis thaliana]	Unigene71396_All//9.00E-21//AT5G66150| glycosyl hydrolase family 38 protein			ko00511|Other glycan degradation		nr +
Unigene714_All	758	3.52	5.21	4.50	3.68	4.86	3.93	2.79	5.79	6.73	5.67E-01	6.72E-02		3.53E-01	3.35E-01		4.01E-01	2.37E-01		9.56E-02	8.06E-01		1.05E+00	5.54E-05	Up	1.27E+00	1.50E-07	Up	Unigene714_All//gi|224073682|ref|XP_002304130.1|//2.00E-94//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222841562|gb|EEE79109.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene714_All//6.00E-84//AT1G54115| CCX4 (CATION CALCIUM EXCHANGER 4); cation:cation antiporter	Unigene714_All//3.00E-167//C0091034			GO:0006811//GO:0006873//GO:0009651//GO:0012506//GO:0015082//GO:0015298//GO:0031224//GO:0043231//GO:0046873	nr +
Unigene7140_All	234	143.99	41.79	37.78	150.93	150.25	93.80	228.75	51.62	85.13	-1.78E+00	2.48E-59	Down	-1.93E+00	1.23E-63	Down	-6.50E-03	9.51E-01		-6.86E-01	6.10E-15		-2.15E+00	1.37E-146	Down	-1.43E+00	1.86E-85	Down	Unigene7140_All//gi|166343845|gb|AB986665.1|//4.00E-40//beta-tubulin 19 [Gossypium hirsutum]	Unigene7140_All//7.00E-41//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene7140_All//1.00E-129//TC142409		ko04145|Phagosome		nr -
Unigene71402_All	285	0.00	2.49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null									
Unigene71403_All	285	0.00	6.22	5.42	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	4.14E-10	Up	1.24E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene71403_All//gi|297819782|ref|XP_002877774.1|//3.00E-46//photosystem II subunit O-2 [Arabidopsis lyrata subsp. lyrata] >gi|297323612|gb|EFH54033.1| photosystem II subunit O-2 [Arabidopsis lyrata subsp. lyrata]	Unigene71403_All//3.00E-47//AT5G66570| PSB01 (PS II OXYGEN-EVOLVING COMPLEX 1); oxygen evolving/ poly(U) binding	Unigene71403_All//6.00E-15//EX169209		ko00195|Photosynthesis		nr +
Unigene71404_All	285	0.00	3.02	0.19	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	7.55E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71404_All//gi|148927394|gb|ABR19828.1|//8.00E-40//cysteine proteinase [Elaeis guineensis]	Unigene71404_All//1.00E-41//AT1G47128| RD21 (responsive to dehydration 21); cysteine-type endopeptidase/ cysteine-type peptidase	Unigene71404_All//5.00E-12//gi|78345798|gb|DT566072.1|DT566072				nr +
Unigene71405_All	285	0.00	3.02	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	9.55E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71405_All//gi|195656691|gb|ACG47813.1|//4.00E-07//heterogeneous nuclear ribonucleoprotein U-like protein 1 [Zea mays]						nr +
Unigene71407_All	285	0.00	3.02	0.93	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.92E-05	Up	9.87E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71407_All//gi|115465507|ref|NP_001056353.1|//9.00E-13//Os05g0567800 (Oryza sativa Japonica Group) >gi|113579904|dbj|BAF18267.1| Os05g0567800 (Oryza sativa Japonica Group)	Unigene71407_All//6.00E-09//AT3G05150| sugar transporter family protein					nr +
Unigene71408_All	285	0.37	1.78	0.75	1.92	0.00	0.00	0.00	0.00	0.00	2.28E+00	6.22E-02		1.03E+00	5.90E-01		-1.09E+01	4.00E-04	Down	-1.09E+01	1.52E-03		null	null		null	null		Unigene71408_All//gi|110289569|gb|ABB47982.2|//4.00E-08//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene71408_All//7.00E-07//AT5G47380| unknown protein					nr -
Unigene71409_All	285	0.00	5.33	1.87	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.09E-08	Up	1.09E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71409_All//gi|74229863|gb|AB|A00460.1|//5.00E-26//serine-glyoxylate aminotransferase [Spirodela polyrhiza]	Unigene71409_All//1.00E-26//AT2G13360| AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE); alanine-glyoxylate transaminase/ serine-glyoxylate transaminase/ serine-pyruvate transaminase	Unigene71409_All//4.00E-28//TC139658		ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism		nr +
Unigene71410_All	285	0.00	3.91	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.99E-06	Up	1.05E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71410_All//gi|298706463|emb|CBJ29450.1|//7.00E-10//protein tyrosine phosphatase [Ectocarpus siliculosus]						nr +
Unigene71411_All	286	0.00	2.48	0.37	0.17	0.72	0.16	0.44	0.58	0.00	1.13E+01	3.31E-04	Up	8.54E+00	3.92E-01		2.05E+00	3.94E-01		-1.42E-01	9.48E-01		3.99E-01	8.13E-01		-8.79E+00	1.99E-01				Unigene71411_All//3.00E-07//EX165054				
Unigene71412_All	286	0.00	4.07	0.56	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.05E-06	Up	9.13E+00	2.36E-01		null	null		null	null		null	null		null	null									
Unigene71414_All	286	0.00	3.72	0.56	0.00	0.12	0.00	0.00	0.00	0.00	1.19E+01	3.80E-06	Up	9.13E+00	2.36E-01		6.91E+00	8.20E-01		null	null		null	null		null	null									
Unigene71415_All	286	0.00	3.54	1.12	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.22E-06	Up	1.01E+01	4.48E-02		null	null		null	null		null	null		null	null									
Unigene71416_All	286	0.73	4.07	0.56	0.35	0.12	0.32	0.00	0.00	0.00	2.48E+00	9.79E-04	Up	-3.90E-01	8.06E-01		-1.53E+00	5.84E-01		-1.42E-01	9.48E-01		null	null		null	null									
Unigene71417_All	286	0.00	2.30	1.68	0.00	0.00	0.00	0.15	0.00	0.00	1.12E+01	6.21E-04	Up	1.07E+01	7.45E-03		null	null		null	null		-7.21E+00	6.48E-01		-7.21E+00	6.05E-01		Unigene71417_All//gi|224009890|ref|XP_002293903.1|//3.00E-18//heterotrimeric G protein alpha subunit 1 [Thalassiosira pseudonana CCMP1335] >gi|220970575|gb|EED88912.1| heterotrimeric G protein alpha subunit 1 [Thalassiosira pseudonana CCMP1335]	Unigene71417_All//9.00E-18//AT2G26300| GP ALPHA 1 (G PROTEIN ALPHA SUBUNIT 1); GTP binding / GTPase/ channel regulator/ signal transducer					nr -
Unigene71418_All	286	0.00	4.78	4.10	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.78E-08	Up	1.20E+01	1.77E-06	Up	null	null		null	null		null	null		null	null									
Unigene71421_All	286	0.37	3.54	0.37	1.05	0.00	0.32	0.89	0.29	0.42	3.28E+00	3.79E-04	Up	2.54E-02	9.98E-01		-1.00E+01	2.01E-02		-1.73E+00	2.89E-01		-1.60E+00	3.10E-01		-1.09E+00	4.28E-01		Unigene71421_All//gi|20269987|gb|AAM18135.1|AF498359_1/1.00E-21//small G-protein ROP9 [Medicago truncatula]	Unigene71421_All//5.00E-16//AT4G35020| ARAC3 (ARABIDOPSIS RAC-LIKE 3); GTP binding / GTPase	Unigene71421_All//2.00E-11//ES804445		ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity		nr +
Unigene71423_All	286	0.00	10.28	0.56	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	1.01E-16	Up	9.13E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71423_All//sp|P23226|MA205_DROME//6.00E-08//205 kDa microtubule-associated protein OS=Drosophila melanogaster GN=Map205 PE=1 SV=2						swissprot +
Unigene71424_All	287	0.00	6.36	0.56	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.14E-10	Up	9.12E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71424_All//sp|Q03751|CSP_DROME//1.00E-19//Cysteine string protein OS=Drosophila melanogaster GN=Csp PE=1 SV=1						swissprot -
Unigene71426_All	287	0.00	4.24	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.46E-07	Up	null	null		null	null		null	null		null	null		null	null									
Unigene71427_All	287	0.00	2.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	6.21E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene71429_All	287	0.00	5.12	1.11	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.11E-08	Up	1.01E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene71429_All//gi|223997572|ref|XP_002288459.1|//2.00E-39//precursor of hydrogenase [Thalassiosira pseudonana CCMP1335] >gi|220975567|gb|EED93895.1| precursor of hydrogenase [Thalassiosira pseudonana CCMP1335]	Unigene71429_All//3.00E-35//AT5G40650| SDH2-2; electron carrier/ succinate dehydrogenase			ko00190|Oxidative phosphorylation//ko00020|Citrate cycle (TCA cycle)		nr -
Unigene7143_All	834	0.38	0.97	0.77	2.75	2.48	1.46	2.79	0.80	1.24	1.37E+00	9.21E-02		1.03E+00	2.81E-01		-1.49E-01	7.60E-01		-9.10E-01	3.13E-02		-1.80E+00	9.52E-06	Down	-1.17E+00	1.46E-03		Unigene7143_All//gi|297813979|ref|XP_002874873.1|//6.00E-49//homeobox-leucine zipper family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320710|gb|EFH51132.1| homeobox-leucine zipper family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7143_All//1.00E-49//AT4G03250| homeobox-leucine zipper family protein	Unigene7143_All//7.00E-85//ES800363	HB			nr +
Unigene71431_All	288	0.00	4.05	0.55	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.05E-06	Up	9.12E+00	2.36E-01		null	null		null	null		null	null		null	null									
Unigene71432_All	288	0.00	3.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.22E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene71432_All//gi|18141289|gb|AAL60582.1|AF454960_1/2.00E-39//senescence-associated cysteine protease [Brassica oleracea]	Unigene71432_All//1.00E-40//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase	Unigene71432_All//2.00E-14//TC164623				nr +
Unigene71435_All	288	0.00	3.34	0.37	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.37E-05	Up	8.53E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71435_All//gi|195624410|gb|ACG34035.1|//7.00E-12//splicing factor, arginine/serine-rich 6 [Zea mays]	Unigene71435_All//7.00E-13//AT3G53500| zinc knuckle (CCHC-type) family protein			ko03040|Spliceosome		nr +
Unigene71436_All	288	0.36	3.87	0.92	0.69	0.48	0.00	0.00	0.00	0.00	3.41E+00	1.24E-04	Up	1.35E+00	4.09E-01		-5.33E-01	7.47E-01		-9.43E+00	1.33E-01		null	null		null	null									
Unigene71437_All	288	0.18	5.28	1.11	0.86	1.08	0.63	0.44	0.58	1.66	4.86E+00	1.61E-07	Up	2.61E+00	1.46E-01		3.15E-01	8.38E-01		-4.63E-01	7.44E-01		3.99E-01	8.13E-01		1.91E+00	6.29E-02				Unigene71437_All//2.00E-14//DT467565				
Unigene71439_All	288	0.00	2.46	0.00	0.00	0.00	0.47	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	null	null		null	null		8.88E+00	3.09E-01		null	null		null	null		Unigene71439_All//gi|160900596|ref|YP_001566178.1|//3.00E-13//ABC transporter related [Delftia acidovorans SPH-1] >gi|160366180|gb|ABX37793.1| ABC transporter related [Delftia acidovorans SPH-1]	Unigene71439_All//1.00E-07//AT5G14100| ATNAP14; transporter					nr +

Unigene7144_All	471	0.00	0.00	0.00	1.16	1.46	2.49	3.77	1.42	0.93	null	null		null	null		3.30E-01	7.52E-01		1.10E+00	9.17E-02		-1.41E+00	1.85E-03		-2.02E+00	2.07E-05	Down	Unigene7144_All//gi|18405136|ref|NP_565910.1|//5.00E-18//RTFL8 (ROTUNDIFOLIA LIKE 8) [Arabidopsis thaliana] >gi|20197045|gb|AAM14893.1| Expressed protein [Arabidopsis thaliana] >gi|42822055|tpg|DAA02282.1| TPA_exp: DVL11 [Arabidopsis thaliana]	Unigene7144_All//1.00E-12//AT2G39705| RTFL8 (ROTUNDIFOLIA LIKE 8)	Unigene7144_All//3.00E-147//ES845021				nr +
Unigene71440_All	288	0.00	3.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71440_All//sp|O01382|ICE_DROME//5.00E-45//Caspase OS=Drosophila melanogaster GN=Ice PE=1 SV=2						swissprot -
Unigene71441_All	288	0.00	2.82	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.32E-05	Up	null	null		null	null		null	null		null	null		null	null								ESTscan -
Unigene71442_All	288	0.00	5.98	0.37	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.97E-10	Up	8.53E+00	3.92E-01		null	null		null	null		null	null		null	null								ESTscan -
Unigene71443_All	289	0.00	3.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.61E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71443_All//gi|300176829|emb|CBK25398.2|//8.00E-11//putative polyketide synthase [Blastocystis hominis]						nr -
Unigene71444_All	289	0.00	4.73	1.29	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.78E-08	Up	1.03E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene71444_All//gi|159468796|ref|XP_001692560.1|//3.00E-08//predicted protein [Chlamydomonas reinhardtii] >gi|158278273|gb|EDP04038.1| predicted protein [Chlamydomonas reinhardtii]						nr +
Unigene71446_All	289	0.36	3.33	0.55	0.00	2.26	1.56	0.73	1.01	0.69	3.20E+00	6.55E-04	Up	6.10E-01	7.47E-01		1.11E+01	4.92E-04	Up	1.06E+01	7.75E-03		4.69E-01	7.06E-01		-8.59E-02	9.60E-01		Unigene71446_All//gi|226533064|ref|NP_001151695.1|//7.00E-25//gamma-interferon-inducible lysosomal thiol reductase [Zea mays] >gi|195649025|gb|ACG43980.1| gamma-interferon-inducible lysosomal thiol reductase precursor [Zea mays]	Unigene71446_All//4.00E-26//AT1G07080| gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein	Unigene71446_All//3.00E-121//TC158321				nr -
Unigene71449_All	289	0.00	3.68	0.37	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.80E-06	Up	8.53E+00	3.92E-01		null	null		null	null		null	null		null	null								
Unigene71450_All	289	0.00	3.16	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.61E-05	Up	7.53E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71450_All//sp|Q9VA73|CMC_DROME//1.00E-42//Calcium-binding mitochondrial carrier protein Aralar1 OS=Drosophila melanogaster GN=aralar1 PE=1 SV=1						swissprot -
Unigene71451_All	289	0.00	2.63	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	9.85E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71451_All//sp|Q867Z4|LOLA4_DROME//2.00E-20//Longitudinals lacking protein, isoforms F/I/K/T OS=Drosophila melanogaster GN=lola PE=1 SV=1						swissprot +
Unigene71452_All	289	0.00	8.42	2.40	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	7.72E-14	Up	1.12E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene71452_All//gi|149072010|ref|XP_001293581.1|//9.00E-20//50S ribosomal protein L4 [Rhodomonas salina] >gi|134302961|gb|AB070765.1| 50S ribosomal protein L4 [Rhodomonas salina]	Unigene71452_All//8.00E-16//AT2G20060| ribosomal protein L4 family protein			ko03010|Ribosome		nr +
Unigene71453_All	289	0.00	2.81	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	9.32E-05	Up	9.85E+00	7.95E-02		null	null		null	null		null	null		null	null								
Unigene71454_All	290	0.00	2.62	1.10	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	1.01E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene71454_All//sp|Q8MP30|Y7791_DICDI//1.00E-06//Uncharacterized histidine-rich protein DDB_G0274557 OS=Dictyostelium discoideum GN=DDB_G0274557 PE=4 SV=1						swissprot -
Unigene71455_All	290	0.54	6.81	1.10	1.20	0.95	0.93	0.15	0.00	0.14	3.65E+00	3.76E-08	Up	1.03E+00	4.70E-01		-3.40E-01	7.85E-01		-3.64E-01	7.55E-01		-7.19E+00	6.48E-01		-8.56E-02	9.68E-01		Unigene71455_All//gi|297740511|emb|CBI30693.3|//8.00E-06//unnamed protein product [Vitis vinifera]						nr +
Unigene71456_All	290	0.18	3.32	0.18	0.00	0.24	0.00	0.00	0.00	0.00	4.20E+00	1.29E-04	Up	2.54E-02	9.92E-01		7.89E+00	6.03E-01		null	null		null	null		null	null								
Unigene71460_All	290	0.00	2.97	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	4.92E-05	Up	null	null		null	null		null	null		null	null		null	null								
Unigene71461_All	290	0.00	3.15	1.29	0.00	0.24	0.00	0.00	0.00	0.00	1.16E+01	2.61E-05	Up	1.03E+01	2.49E-02		7.89E+00	6.03E-01		null	null		null	null		null	null								ESTscan -
Unigene71465_All	290	0.00	2.45	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.31E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71465_All//sp|Q9UTK4|NU189_SCHPO//7.00E-06//Nucleoporin nup189 OS=Schizosaccharomyces pombe GN=nup189 PE=1 SV=1						swissprot -
Unigene71466_All	290	0.00	4.37	0.55	0.17	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.85E-07	Up	9.11E+00	2.36E-01		-7.42E+00	5.48E-01		-7.42E+00	6.25E-01		null	null		null	null		Unigene71466_All//gi|25453062|sp|Q9FS88.1|IVD1_SOLTU//2.00E-07//RecName: Full=Isovaleryl-CoA dehydrogenase 1, mitochondrial; Short=IVD 1; Flags: Precursor >gi|10129808|emb|CAC08233.1| isovaleryl-CoA dehydrogenase [Solanum tuberosum]	Unigene71466_All//2.00E-07//AT3G45300| IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase			ko00280|Valine, leucine and isoleucine degradation		nr +
Unigene7147_All	630	0.00	0.32	0.00	0.40	0.00	0.93	25.84	36.95	136.78	8.33E+00	1.35E-01		null	null		-8.63E+00	4.17E-02		1.24E+00	2.31E-01		5.16E-01	3.07E-07		2.40E+00	6.26E-275	Up			Unigene7147_All//6.00E-20//gi|164305111|gb|ES808608.1|ES808608				
Unigene71470_All	291	0.00	5.05	0.37	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.11E-08	Up	8.52E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71470_All//gi|115458184|ref|NP_001052692.1|//2.00E-14//Os04g0402100 [Oryza sativa Japonica Group] >gi|21740628|emb|CAD40786.1| OSJNBb0012E08.10 [Oryza sativa (japonica cultivar-group)] >gi|113564263|dbj|BAF14606.1| Os04g0402100 [Oryza sativa Japonica Group] >gi|239737037|gb|ACS13098.1| calnexin [Oryza sativa Indica Group]	Unigene71470_All//3.00E-09//AT5G61790| calnexin 1 (CNX1)			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr +
Unigene71471_All	291	0.00	4.18	0.00	0.00	0.00	0.31	0.73	1.01	1.37	1.20E+01	5.46E-07	Up	null	null		null	null		8.28E+00	4.72E-01		4.69E-01	7.06E-01		9.14E-01	3.86E-01								
Unigene71475_All	291	0.00	2.61	0.37	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.75E-04	Up	8.52E+00	3.92E-01		null	null		null	null		null	null		null	null								ESTscan +
Unigene71476_All	291	0.00	4.20	0.37	0.17	0.24	0.47	0.15	0.29	0.82	1.22E+01	7.78E-08	Up	8.52E+00	3.92E-01		4.61E-01	9.55E-01		1.44E+00	6.37E-01		9.84E-01	7.29E-01		2.50E+00	1.59E-01								
Unigene71481_All	291	0.00	4.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	4.05E-08	Up	null	null		null	null		null	null		null	null		null	null		Unigene71481_All//gi|298713481|emb|CBJ27036.1|//1.00E-36//RME1, RME-1/EHD family ATPase with a C-terminal EH domain [Ectocarpus siliculosus]	Unigene71481_All//3.00E-36//AT4G05520| ATEHD2 (EPS15 HOMOLOGY DOMAIN 2); GTP binding / GTPase/ calcium ion binding					nr +
Unigene71482_All	292	0.00	2.08	2.55	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.16E-03		1.13E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene71482_All//gi|116000548|emb|CAL50228.1|//7.00E-09//RasGAP SH3 binding protein rasputin, contains NTF2 and RRM domains (ISS) [Ostreococcus tauri]	Unigene71482_All//6.00E-09//AT1G11570| nuclear transport factor 2 (NTF2), putative					nr +
Unigene71492_All	293	0.00	3.29	1.09	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.37E-05	Up	1.01E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene71492_All//gi|675491|gb|AAC37429.1|//9.00E-18//contains WCM2/3/5 family signature; PROSITE; PS00847; disruption leads to early lethal phenotype; similar to WCM2/3/5 family, most similar to YBR1441 [Arabidopsis thaliana]	Unigene71492_All//4.00E-19//AT4G02060| PRL (PROLIFERA); ATP binding / DNA binding / DNA-dependent ATPase/ nucleoside-triphosphatase/ nucleotide binding			ko03030|DNA replication		nr +
Unigene71494_All	293	0.00	2.42	0.73	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.31E-04	Up	9.51E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71494_All//sp|Q06393|SND1_RAT//5.00E-16//Staphylococcal nuclease domain-containing protein 1 OS=Rattus norvegicus GN=Snd1 PE=2 SV=1						swissprot +
Unigene71495_All	293	0.00	18.85	17.08	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	1.66E-31	Up	1.41E+01	7.65E-28	Up	null	null		null	null		null	null		null	null		Unigene71495_All//gi|115453811|ref|NP_001050506.1|//1.00E-18//Os03g0566800 [Oryza sativa Japonica Group] >gi|122246919|sp|Q10126.1|RH34_ORYSJ RecName: Full=DEAD-box ATP-dependent RNA helicase 34 >gi|113548977|dbj|BAF12420.1| Os03g0566800 [Oryza sativa Japonica Group]	Unigene71495_All//3.00E-17//AT1G54270| EIF4A-2; ATP-dependent helicase/ translation initiation factor			ko03040|Spliceosome		nr -
Unigene71496_All	293	0.00	2.77	1.64	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.32E-05	Up	1.07E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene71496_All//sp|Q9Y115|UN93L_DROME//4.00E-40//UNC93-like protein OS=Drosophila melanogaster GN=CG4928 PE=2 SV=1						swissprot -
Unigene71499_All	293	0.00	6.23	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.14E-10	Up	7.51E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71499_All//gi|297832104|ref|XP_002883934.1|//5.00E-16//zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329774|gb|EFH60193.1| zinc finger (CCCH-type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene71499_All//1.00E-12//AT2G20280| zinc finger (CCCH-type) family protein		C3H			nr -
Unigene715_All	2420	2.49	5.65	2.02	5.43	5.25	5.75	10.94	17.27	9.83	1.19E+00	1.45E-13	Up	-2.97E-01	2.59E-01		-4.96E-02	8.20E-01		8.10E-02	6.64E-01		6.59E-01	1.10E-18		-1.54E-01	1.21E-01		Unigene715_All//gi|18404796|ref|NP_564850.1|//0.00E+00//CCX4 (CATION CALCIUM EXCHANGER 4); cation:cation antiporter [Arabidopsis thaliana] >gi|75213438|sp|Q9SYG9.1|CCX4_ARATH RecName: Full=Cation/calcium exchanger 4; Short=AtCCX4; AltName: Full=Protein CATION CALCIUM EXCHANGER 4 >gi|4587554|gb|AAD25785.1|AC006577_21 Similar to gb|AJ005701 Na/Ca,K-exchanger from Caenorhabditis elegans. ESTs gb|T04173 and gb|AA585918 come from this gene [Arabidopsis thaliana]	Unigene715_All//0.00E+00//AT1G54115| CCX4 (CATION CALCIUM EXCHANGER 4); cation:cation antiporter	Unigene715_All//0.00E+00//C0091034			GO:0006811//GO:0015298//GO:0031224	nr -
Unigene71500_All	293	0.00	11.24	2.36	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	9.62E-19	Up	1.12E+01	6.13E-04	Up	null	null		null	null		null	null		null	null								
Unigene71501_All	294	0.00	5.34	2.54	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.69E-09	Up	1.13E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene71501_All//sp|P17210|KINH_DROME//7.00E-41//Kinesin heavy chain OS=Drosophila melanogaster GN=Khc PE=1 SV=2						swissprot +
Unigene71505_All	294	0.00	3.79	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.99E-06	Up	9.09E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71505_All//gi|75858825|gb|AB328989.1|//2.00E-15//Dna j-like protein 1 [Symbiodinium sp. C3]	Unigene71505_All//3.00E-11//AT5G25530| DNAJ heat shock protein, putative			ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene71506_All	294	0.00	2.76	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.32E-05	Up	1.07E+01	7.45E-03		null	null		null	null		null	null		null	null								

Unigene71508_All	294	0.00	4.14	0.91	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.45E-07	Up	9.82E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71508_All//gi|226457635|gb|EEH54934.1|//3.00E-10//JmjN/JmjC protein [Micromonas pusilla CCMP1545]	Unigene71508_All//3.00E-09//AT3G13350| high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein						nr -
Unigene71511_All	842	2.49	0.72	1.64	3.67	5.32	3.65	4.17	1.79	4.68	-1.78E+00	2.21E-04	Down	-5.96E-01	2.08E-01		5.36E-01	6.18E-02		-8.10E-03	9.76E-01		-1.22E+00	4.85E-05	Down	1.69E-01	5.82E-01				Unigene71511_All//0.00E+00//TC174380					
Unigene71510_All	294	0.00	3.45	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.22E-06	Up	9.09E+00	2.36E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene71511_All	294	0.00	2.76	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.32E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71511_All|gi|15223676|ref|NP_175505.1|//4.00E-17//GTP-binding protein-related [Arabidopsis thaliana] >gi|17368724|sp|Q9C618.1|NOG1_ARATH RecName: Full=Probable nucleolar GTP-binding protein 1	Unigene71511_All//8.00E-08//AT1G50920| GTP-binding protein-related						nr -
Unigene71513_All	294	0.00	6.55	1.09	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	5.72E-11	Up	1.01E+01	4.48E-02		null	null		null	null		null	null		null	null										
Unigene71516_All	295	0.00	31.26	0.18	0.00	0.00	0.31	0.00	0.00	0.00	1.49E+01	8.41E-53	Up	7.50E+00	6.27E-01		null	null		8.26E+00	4.72E-01		null	null		null	null		Unigene71516_All//gi|75161213|sp|Q8VRN6.1|RFS_PEA//2.00E-40//RecName: Full=Galactinol--sucrose galactosyltransferase; AltName: Full=Raffinose synthase >gi|18181865|emb|CAD20127.2| raffinose synthase [Pisum sativum]	Unigene71516_All//4.00E-36//AT5G40390| SIP1 (seed imbibition 1-like); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compounds				ko00052|Galactose metabolism		nr -
Unigene71152_All	794	0.00	0.13	0.00	0.00	0.00	0.91	57.24	86.49	91.82	7.00E+00	3.81E-01		null	null		null	null		9.83E+00	2.31E-04	Up	5.95E-01	2.67E-25		6.82E-01	1.03E-34		Unigene71152_All//gi|18403247|ref|NP_566697.1|//4.00E-70//receptor protein kinase-related [Arabidopsis thaliana] >gi|75273758|sp|Q9LRJ9.1|CRR38_ARATH RecName: Full=Cysteine-rich repeat secretory protein 38; Flags: Precursor >gi|90186230|gb|ABD91491.1| At3g22060 [Arabidopsis thaliana]	Unigene71152_All//2.00E-71//AT3G22060| receptor protein kinase-related	Unigene71152_All//0.00E+00//TC178206					nr +
Unigene71520_All	295	0.00	3.61	1.44	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.80E-06	Up	1.05E+01	1.37E-02		null	null		null	null		null	null		null	null										
Unigene71522_All	295	0.00	5.67	1.62	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.54E-09	Up	1.07E+01	7.45E-03		null	null		null	null		null	null		null	null										
Unigene71524_All	295	0.00	2.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	6.21E-04	Up	null	null		null	null		null	null		null	null		null	null										
Unigene71525_All	295	0.00	5.67	2.71	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.54E-09	Up	1.14E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene71525_All|gi|30691134|ref|NP_174292.2|//3.00E-16//FKBP6 (PREFOLDIN 6); unfolded protein binding [Arabidopsis thaliana] >gi|88011191|gb|ABD38916.1| At1g29990 [Arabidopsis thaliana]	Unigene71525_All//1.00E-17//AT1G29990| FKBP6 (PREFOLDIN 6); unfolded protein binding						nr -
Unigene71526_All	296	0.00	3.08	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.61E-05	Up	9.08E+00	2.36E-01		null	null		null	null		null	null		null	null										
Unigene71528_All	296	0.00	2.23	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	6.21E-04	Up	9.08E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71528_All//gi|4586021|gb|AAD25640.1|//3.00E-30//cytoplasmic aconitate hydratase [Arabidopsis thaliana]	Unigene71528_All//1.00E-31//AT2G05710| aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative				ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene71529_All	296	0.00	5.65	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.54E-09	Up	null	null		null	null		null	null		null	null		null	null		Unigene71529_All//sp|B3N3F7|SRRT_DROER/1.00E-19//Serrate RNA effector molecule homolog OS=Drosophila erecta GN=Ars2 PE=3 SV=1							swissprot +
Unigene71531_All	296	0.00	3.25	0.36	0.00	0.35	0.00	0.00	0.00	0.00	1.17E+01	1.37E-05	Up	8.49E+00	3.92E-01		8.45E+00	4.53E-01		null	null		null	null		null	null		Unigene71531_All//sp|P19920|DCMM_OLICO//4.00E-09//Carbon monoxide dehydrogenase medium chain OS=Oligotropha carboxidovorans (strain ATCC 49405 / DSM 1227 / OM5) GN=coxM PE=1 SV=2							swissprot -
Unigene71534_All	296	0.00	5.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	4.13E-10	Up	null	null		null	null		null	null		null	null		null	null		Unigene71534_All//gi|298710190|emb|CBJ26265.1|//9.00E-07//Glycosyltransferase, family GT8 [Ectocarpus siliculosus]							nr -
Unigene71535_All	296	0.00	3.94	0.36	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.04E-06	Up	8.49E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71535_All//gi|299116282|emb|CBN76090.1|//4.00E-08//eukaryotic initiation factor 4G [Ectocarpus siliculosus]	Unigene71535_All//9.00E-05//AT3G60240| EIF4G (EUKARYOTIC TRANSLATION INITIATION FACTOR 4G); translation initiation factor						nr -
Unigene71537_All	296	0.00	2.91	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	4.92E-05	Up	7.49E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71537_All//sp|Q9W1C9|PEB3_DROME//3.00E-26//Ejaculatory bulb-specific protein 3 OS=Drosophila melanogaster GN=PebIII PE=1 SV=2							swissprot -
Unigene71538_All	297	0.00	10.07	0.00	0.17	0.00	0.15	0.00	0.00	0.67	1.33E+01	5.18E-17	Up	null	null		-7.39E+00	5.48E-01		-1.41E-01	9.48E-01		null	null		9.39E+00	7.88E-02		Unigene71538_All|gi|78499709|gb|AB045861.1|//7.00E-18//DRE-binding protein 3b [Gossypium hirsutum]	Unigene71538_All//9.00E-07//AT1G12630| DNA binding / transcription activator/ transcription factor	Unigene71538_All//2.00E-162//DW235536	AP2-EREBP				nr -
Unigene71539_All	297	0.00	4.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.49E-07	Up	null	null		null	null		null	null		null	null		null	null										ESTscan +
Unigene71540_All	297	0.00	4.95	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.11E-08	Up	9.81E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71540_All|gi|159486535|ref|XP_001701294.1|//6.00E-14//zeta-cop, subunit of COP-I complex [Chlamydomonas reinhardtii] >gi|158271777|gb|EDO97589.1| zeta-cop, subunit of COP-I complex [Chlamydomonas reinhardtii]	Unigene71540_All//5.00E-14//AT1G60970| clathrin adaptor complex small chain family protein						nr -
Unigene71542_All	297	0.88	4.44	0.36	0.67	0.35	0.91	0.00	0.00	0.00	2.33E+00	6.54E-04	Up	-1.30E+00	4.36E-01		-9.48E-01	5.87E-01		4.44E-01	7.63E-01		null	null		null	null										
Unigene71543_All	297	0.00	7.68	0.72	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	5.63E-13	Up	9.49E+00	1.39E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene71544_All	297	0.00	2.22	2.87	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	6.21E-04	Up	1.15E+01	9.00E-05	Up	null	null		null	null		null	null		null	null										
Unigene71546_All	297	0.00	3.07	1.08	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.60E-05	Up	1.01E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene71546_All|gi|77549578|gb|ABA92375.1|//5.00E-15//RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene71546_All//3.00E-12//AT4G00830| RNA recognition motif (RRM)-containing protein						nr -
Unigene71549_All	298	0.00	3.06	0.36	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.60E-05	Up	8.48E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71549_All//gi|6562845|emb|CAB62553.1|//2.00E-17//heterogeneous nuclear ribonucleoprotein; type A/B hnRNP p40 [Rattus norvegicus] >gi|149052496|gb|EDM04313.1| rCG34663, isoform CRA_a [Rattus norvegicus]					ko03040|Spliceosome		nr -
Unigene7155_All	528	0.79	1.73	0.81	2.64	2.09	1.03	2.96	0.71	0.75	1.12E+00	1.30E-01		2.54E-02	1.00E+00		-3.40E-01	5.62E-01		-1.36E+00	1.87E-02		-2.06E+00	9.43E-05	Down	-1.97E+00	9.58E-05	Down			Unigene7155_All//0.00E+00//gi|109872717|gb|DW501692.1|DW501692					
Unigene71550_All	298	0.00	2.38	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.31E-04	Up	7.48E+00	6.27E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene71551_All	298	0.00	3.74	1.25	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.99E-06	Up	1.03E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene71551_All//sp|O14543|SOCS3_HUMAN//7.00E-55//Suppressor of cytokine signaling 3 OS=Homo sapiens GN=SOCS3 PE=1 SV=1							swissprot -
Unigene71553_All	298	0.00	2.38	2.32	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	1.12E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene71553_All//gi|99083509|gb|ABF66654.1|//7.00E-21//EBP1 [Ammopiptanthus mongolicus] >gi|146336945|gb|ABQ23586.1| EBP1 [Ammopiptanthus mongolicus]	Unigene71553_All//9.00E-20//AT3G51800| ATG2; aminopeptidase/ metalloexopeptidase						nr -
Unigene71554_All	298	0.00	5.78	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.97E-10	Up	1.07E+01	7.45E-03		null	null		null	null		null	null		null	null										ESTscan -
Unigene71555_All	298	0.00	3.23	0.36	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.37E-05	Up	8.48E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71555_All//sp|O95817|BAG3_HUMAN//1.00E-49//BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3							swissprot -
Unigene71556_All	298	0.00	2.89	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	4.92E-05	Up	9.07E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71556_All//gi|11253528|gb|AB114351.1|//1.00E-26//acyl-CoA dehydrogenase protein 1 [Pfiesteria piscicida]	Unigene71556_All//1.00E-15//AT3G51840| ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase				ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism		nr -
Unigene71558_All	298	0.00	3.06	0.00	0.00	0.12	0.00	0.00	0.00	0.00	1.16E+01	2.60E-05	Up	null	null		6.85E+00	8.20E-01		null	null		null	null		null	null				Unigene71558_All//3.00E-07//ES843958						
Unigene71559_All	298	1.40	29.42	4.47	1.84	0.69	2.88	0.57	0.00	0.40	4.39E+00	2.70E-39	Up	1.67E+00	9.89E-03		-1.41E+00	1.53E-01		6.47E-01	4.23E-01		-9.15E+00	1.34E-01		-5.01E-01	7.46E-01										
Unigene7156_All	760	0.62	11.60	1.26	0.79	1.86	6.06	0.28	0.71	0.94	4.23E+00	1.43E-38	Up	1.03E+00	1.68E-01		1.24E+00	3.03E-02		2.95E+00	4.83E-16	Up	1.36E+00	1.44E-01		1.76E+00	2.48E-02		Unigene7156_All|gi|75174963|sp|Q9LNG5.1|PPP7L_ARATH//1.00E-30//RecName: Full=Serine/threonine-protein phosphatase 7 long form homolog >gi|8778513|gb|AAF79521.1|AC023673_9 F21D18.16 [Arabidopsis thaliana]	Unigene7156_All//6.00E-32//AT1G48120| calcineurin-like phosphoesterase family protein	Unigene7156_All//9.00E-115//ES820963					nr +
Unigene71560_All	298	0.00	6.29	1.79	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.10E-10	Up	1.08E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71560_All//sp|Q9W420|SPT6H_DROME//9.00E-15//Transcription elongation factor SPT6 OS=Drosophila melanogaster GN=Spt6 PE=1 SV=1							swissprot -
Unigene71561_All	298	0.00	2.72	0.00	1.00	1.96	0.61	1.28	0.98	0.27	1.14E+01	9.32E-05	Up	null	null		9.70E-01	3.47E-01		-7.27E-01	6.38E-01		-3.79E-01	7.23E-01		-2.26E+00	6.49E-02										
Unigene71562_All	299	0.00	5.59	0.89	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.54E-09	Up	9.80E+00	7.95E-02		null	null		null	null		null	null		null	null										ESTscan +
Unigene71563_All	299	0.00	3.39	3.38	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.22E-06	Up	1.17E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene71563_All|gi|301508493|gb|ADK78215.1|//4.00E-24//methionine aminopeptiase [Hordeum vulgare]	Unigene71563_All//7.00E-23//AT3G51800| ATG2; aminopeptidase/ metalloexopeptidase						nr -
Unigene71564_All	299	0.00	4.24	1.96	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.85E-07	Up	1.09E+01	2.17E-03		null	null		null	null		null	null		null	null		Unigene71564_All//gi|124359510|gb|AB028627.2|//4.00E-12//RNA-directed DNA polymerase (Reverse transcriptase); Ribonuclease H [Medicago truncatula]							nr -
Unigene71566_All	299	0.00	2.71	0.71	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.32E-05	Up	9.48E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71566_All//sp|P07192|MAL3_DROME//8.00E-27//Probable maltase L OS=Drosophila melanogaster GN=LvpL PE=2 SV=2							swissprot -

Unigene71567_All	299	0.00	2.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	6.21E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71567_All//gi|114326546|ref|NP_075907.2|//4.00E-51//phosphoglycerate mutase 1 [Mus musculus] >gi|20178035|sp|Q9DBJ1.3|PGAM1_MOUSE RecName: Full=Phosphoglycerate mutase 1; AltName: Full=Phosphoglycerate mutase isozyme B; Short=PGAM-B; AltName: Full=BPG-dependent PGAM 1 >gi|22065830|sp|P25113.4|PGAM1_RAT RecName: Full=Phosphoglycerate mutase 1; AltName: Full=Phosphoglycerate mutase isozyme B; Short=PGAM-B; AltName: Full=BPG-dependent PGAM 1 >gi|112128|pir||JC1132 phosphoglycerate mutase (EC 5.4.2.1) B chain - rat >gi|12805529|gb|AAH02241.1| Phosphoglycerate mutase 1 [Mus musculus] >gi|13542946|gb|AAH05661.1| Phosphoglycerate mutase 1 [Mus musculus] >gi|41350889|gb|AAH65582.1| Pgam1 protein [Rattus norvegicus] >gi|45219739|gb|AAH66844.1| Phosphoglycerate mutase 1 [Mus musculus]	Unigene71567_All//1.00E-11//AT1G22170| phosphoglycerate/bisphosphoglycerate mutase family protein			ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene71568_All	299	0.00	4.75	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.05E-08	Up	7.48E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71568_All//gi|300268586|gb|EFJ52766.1|//3.00E-07//pathogenesis-related protein 1-like protein [Volvox carteri f. nagariensis]						nr -
Unigene71569_All	299	0.00	5.59	0.71	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.54E-09	Up	9.48E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71569_All//gi|224482651|gb|ACN50182.1|//2.00E-07//annexin [Annona cherimola]	Unigene71569_All//3.00E-07//AT1G68090| ANN3; calcium ion binding / calcium-dependent phospholipid binding					nr +
Unigene7157_All	588	0.53	0.00	0.72	0.93	1.17	0.61	9.56	7.39	185.78	-9.06E+00	3.63E-02		4.40E-01	6.77E-01		3.30E-01	7.52E-01		-6.01E-01	5.66E-01		-3.72E-01	1.12E-01		4.28E+00	0.00E+00	Up	Unigene7157_All//gi|6633839|gb|AAF19698.1|AC008047_5//1.00E-34//F2K11.21 [Arabidopsis thaliana]	Unigene7157_All//6.00E-36//AT1G63410| unknown protein	Unigene7157_All//0.00E+00//DW517934				nr +
Unigene71571_All	300	0.00	3.21	0.36	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	8.47E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71571_All//sp|Q9V813|MTAP_DROME//1.00E-07//Putative S-methyl-5'-thioadenosine phosphorylase OS=Drosophila melanogaster GN=CG4802 PE=1 SV=1						swissprot -
Unigene71575_All	300	0.00	6.25	3.91	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.10E-10	Up	1.19E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene71575_All//gi|194477017|ref|YP_002049196.1|//1.00E-31//elongation factor EF-2 [Paulinella chromatophora] >gi|171192024|gb|ACB42986.1| elongation factor EF-2 [Paulinella chromatophora]	Unigene71575_All//1.00E-27//AT1G62750| SCO1 (SNOWY COTYLEDON 1); ATP binding / translation elongation factor/ translation factor, nucleic acid binding					nr -
Unigene71576_All	300	0.00	3.72	0.36	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.99E-06	Up	8.47E+00	3.92E-01		null	null		null	null		null	null		null	null									
Unigene71579_All	301	0.00	2.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71579_All//gi|297849340|ref|XP_002892551.1|//8.00E-25//NF-X1 type zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338393|gb|EFH68810.1| NF-X1 type zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene71579_All//2.00E-18//AT1G10170| ATNFXL1 (ARABIDOPSIS THALIANA NF-X-LIKE 1); protein binding / transcription factor/ zinc ion binding					nr +
Unigene71580_All	301	0.00	2.19	0.53	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	6.21E-04	Up	9.05E+00	2.36E-01		null	null		null	null		null	null		null	null									
Unigene71583_All	301	0.00	4.88	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.11E-08	Up	null	null		null	null		null	null		null	null		null	null		Unigene71583_All//gi|145324014|ref|NP_001077596.1|//2.00E-08//PFT1 (PHYTOCHROME AND FLOWERING TIME 1); transcription coactivator [Arabidopsis thaliana]						nr -
Unigene71584_All	301	0.00	4.55	1.42	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.78E-08	Up	1.05E+01	1.37E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene71588_All	301	0.00	3.03	0.53	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.60E-05	Up	9.05E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71588_All//sp|Q8CHI8|ATS1_HUMAN//5.00E-56//A disintegrin and metalloproteinase with thrombospondin motifs 1 OS=Homo sapiens GN=ADAMTS1 PE=1 SV=4						swissprot +
Unigene7159_All	406	0.00	1.00	0.00	2.21	1.53	1.67	107.16	785.47	116.28	9.96E+00	1.34E-02		null	null		-5.33E-01	4.70E-01		-4.04E-01	6.23E-01		2.87E+00	0.00E+00	Up	1.18E-01	1.10E-01									
Unigene71591_All	302	0.00	3.02	1.41	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.60E-05	Up	1.05E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71591_All//gi|238617571|gb|ACR46918.1|//2.00E-48//beta-tubulin [Leucocryptos marina]	Unigene71591_All//1.00E-47//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene71591_All//6.00E-12//gi|54123250|gb|CO498759.1|CO498759		ko04145|Phagosome		nr +
Unigene71592_All	302	0.00	4.19	1.94	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.85E-07	Up	1.09E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene71592_All//gi|299473646|emb|CBN78040.1|//1.00E-10//conserved unknown protein [Ectocarpus siliculosus]						nr -
Unigene71593_All	302	0.00	2.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene71594_All	302	0.00	26.01	8.11	0.00	0.00	0.00	0.00	0.00	0.00	1.47E+01	6.45E-45	Up	1.30E+01	1.64E-13	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene71596_All	302	0.00	2.68	0.71	0.66	0.23	0.00	2.24	0.00	0.92	1.14E+01	9.32E-05	Up	9.46E+00	1.39E-01		-1.53E+00	4.15E-01		-9.37E+00	1.33E-01		-1.11E+01	6.33E-05	Down	-1.28E+00	9.48E-02		Unigene71596_All//gi|15450980|gb|AAK96761.1|//4.00E-16//Unknown protein [Arabidopsis thaliana] >gi|20197855|gb|AAD21765.2| expressed protein [Arabidopsis thaliana]	Unigene71596_All//2.00E-17//AT2G20230| LOCATED IN: plasma membrane, vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 16 growth stages; CONTAINS InterPro DOMAIN/s: Tetraspanin (InterPro:IPR018499); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G28770.1); Has 91 Blast hits to 91 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 90; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene71596_All//7.00E-132//gi|78327771|gb|DT548045.1|DT548045		ko03420|Nucleotide excision repair//ko03022|Basal transcription factors		nr +
Unigene71597_All	302	0.00	2.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	6.21E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71597_All//gi|299470215|emb|CBN79519.1|//1.00E-20//Vesicle coat complex COPII, subunit SEC23 [Ectocarpus siliculosus]	Unigene71597_All//3.00E-19//AT3G21630| transport protein, putative					nr -
Unigene71599_All	303	0.00	3.68	0.00	0.99	0.00	0.75	0.00	1.10	0.26	1.18E+01	1.99E-06	Up	null	null		-9.95E+00	2.01E-02		-4.04E-01	7.51E-01		1.01E+01	1.27E-02		8.04E+00	4.01E-01		Unigene71599_All//gi|167383|gb|AAA33074.1|//2.00E-37//storage protein [Gossypium hirsutum]		Unigene71599_All//2.00E-116//TC168445				nr +
Unigene71601_All	303	0.00	3.34	0.18	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.22E-06	Up	7.46E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71601_All//gi|115483755|ref|NP_001065539.1|//3.00E-10//Os11g0106400 [Oryza sativa Japonica Group] >gi|113644243|dbj|BAF27384.1| Os11g0106400 [Oryza sativa Japonica Group]	Unigene71601_All//1.00E-07//AT2G30110| ATUBA1; ubiquitin activating enzyme/ ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene71603_All	303	0.00	3.18	3.16	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	1.16E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene71603_All//gi|298713802|emb|CBJ27174.1|//2.00E-13//phosphatase PP1 [Ectocarpus siliculosus]	Unigene71603_All//3.00E-14//AT5G59160| TOPP2; protein serine/threonine phosphatase	Unigene71603_All//6.00E-09//TC174378				nr -
Unigene71604_All	303	0.00	3.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.60E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71604_All//sp|O18405|SURF4_DROME//3.00E-43//Surfeit locus protein 4 homolog OS=Drosophila melanogaster GN=Surf4 PE=2 SV=1						swissprot +
Unigene71608_All	303	0.00	2.17	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	6.21E-04	Up	8.46E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71608_All//sp|Q29BL9|LMBD2_DROPS//5.00E-21//LMBR1 domain-containing protein 2 homolog OS=Drosophila pseudoobscura pseudoobscura GN=GA20845 PE=3 SV=1						swissprot +
Unigene71609_All	303	0.00	7.53	4.22	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	5.63E-13	Up	1.20E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene71609_All//gi|2241977|emb|CAB10398.1|//2.00E-32//cysteine proteinase like protein [Arabidopsis thaliana] >gi|7268368|emb|CAB78661.1| cysteine proteinase like protein [Arabidopsis thaliana] >gi|14517442|gb|AAK62611.1| AT4g16190/d14135w [Arabidopsis thaliana] >gi|22136546|gb|AAM91059.1| AT4g16190/d14135w [Arabidopsis thaliana] >gi|22530956|gb|AAM96982.1| cysteine proteinase [Arabidopsis thaliana] >gi|110740834|dbj|BAE98514.1| cysteine proteinase like protein [Arabidopsis thaliana]	Unigene71609_All//1.00E-31//AT4G16190| cysteine proteinase, putative	Unigene71609_All//6.00E-09//CO129549				nr +
Unigene71613_All	304	0.00	2.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71613_All//sp|Q5BK13|TM199_RAT//1.00E-06//Transmembrane protein 199 OS=Rattus norvegicus GN=Tmem199 PE=2 SV=1						swissprot -
Unigene71614_All	304	0.00	2.17	1.23	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	6.21E-04	Up	1.03E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene71614_All//sp|095994|AGR2_HUMAN//2.00E-52//Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1						swissprot +
Unigene71617_All	304	0.00	4.17	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.85E-07	Up	9.45E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71617_All//gi|195623456|gb|ACG33558.1|//2.00E-29//T-complex protein 1 subunit beta [Zea mays]	Unigene71617_All//1.00E-18//AT5G20890| chaperonin, putative					nr -
Unigene7162_All	301	1.74	7.24	3.01	0.99	2.06	0.90	2.39	1.94	0.26	2.06E+00	2.92E-05	Up	7.91E-01	3.03E-01		1.05E+00	2.99E-01		-1.41E-01	9.20E-01		-2.97E-01	6.85E-01		-3.17E+00	8.09E-04	Down			Unigene7162_All//2.00E-39//TC138513				
Unigene71620_All	304	0.00	2.33	0.70	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	9.45E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71620_All//gi|301101008|ref|XP_002899593.1|//5.00E-11//conserved hypothetical protein [Phytophthora infestans T30-4] >gi|262103901|gb|EEY61953.1| conserved hypothetical protein [Phytophthora infestans T30-4]						nr -

Unigene71621_All	305	0.00	3.82	1.05	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.04E-06	Up	1.00E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene71621_All//sp|Q0MQH4|NDUS5_PANTR//2.00E-48//NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 OS=Pan troglodytes GN=NDUFS5 PE=3 SV=3						swissprot -
Unigene71623_All	305	0.00	3.82	0.52	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.04E-06	Up	9.03E+00	2.36E-01		null	null		null	null		null	null		null	null									
Unigene71624_All	305	0.00	2.49	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.75E-04	Up	8.45E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71624_All//gi|224111298|ref|XP_002315807.1|//4.00E-07//predicted protein [Populus trichocarpa] >gi|222864847|gb|EEF01978.1| predicted protein [Populus trichocarpa]				ko03040|Spliceosome		nr -
Unigene71625_All	305	0.00	4.65	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.05E-08	Up	8.45E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71625_All//sp|P29067|ARRB2_RAT//6.00E-29//Beta-arrestin-2 OS=Rattus norvegicus GN=Arrb2 PE=1 SV=1						swissprot +
Unigene71626_All	305	0.00	3.16	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	7.45E+00	6.27E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene71627_All	305	0.00	3.82	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.04E-06	Up	7.45E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71627_All//gi|116055828|emb|CAL57913.1|//7.00E-21//U-box domain-containing protein (ISS) [Ostreococcus tauri]	Unigene71627_All//4.00E-18//AT5G15400| U-box domain-containing protein			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis		nr +
Unigene7163_All	619	3.13	0.57	1.89	3.06	1.22	1.24	1.64	0.27	0.64	-2.45E+00	1.00E-05	Down	-7.25E-01	1.38E-01		-1.32E+00	3.34E-03		-1.30E+00	6.55E-03		-2.60E+00	3.81E-04	Down	-1.35E+00	2.51E-02		Unigene7163_All//gi|229609827|gb|ACQ83529.1|//2.00E-41//CBL-interacting protein kinase 13 [Vitis vinifera]	Unigene7163_All//9.00E-35//AT5G07070| CIPK2 (CBL-INTERACTING PROTEIN KINASE 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene7163_All//4.00E-39//TC143167		ko04140|Regulation of autophagy		nr -
Unigene71630_All	306	0.00	4.31	1.91	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.49E-07	Up	1.09E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene71630_All//gi|299115840|emb|CBN74403.1|//5.00E-14//Serine/threonine protein phosphatase [Ectocarpus siliculosus]	Unigene71630_All//1.00E-12//AT2G25070| protein phosphatase 2C, putative / PP2C, putative					nr +
Unigene71633_All	306	0.00	2.48	1.74	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.75E-04	Up	1.08E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71633_All//sp|P61980|HNRPK_RAT//2.00E-60//Heterogeneous nuclear ribonucleoprotein K OS=Rattus norvegicus GN=Hnrnpk PE=1 SV=1						swissprot -
Unigene71634_All	306	0.00	8.78	1.39	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.80E-15	Up	1.04E+01	1.37E-02		null	null		null	null		null	null		null	null									
Unigene71636_All	307	0.34	3.14	1.91	0.81	0.34	1.18	0.00	0.82	0.52	3.20E+00	6.55E-04	Up	2.48E+00	3.75E-02		-1.27E+00	4.23E-01		5.37E-01	6.94E-01		9.67E+00	4.30E-02		9.02E+00	1.39E-01									
Unigene7164_All	572	0.00	0.00	0.00	1.39	0.84	0.39	10.50	2.41	4.53	null	null		null	null		-7.25E-01	3.46E-01		-1.82E+00	3.32E-02		-2.12E+00	8.09E-17	Down	-1.21E+00	2.88E-08	Down	Unigene7164_All//gi|224057862|ref|XP_002296961.1|//8.00E-45//GH3 family protein [Populus trichocarpa] >gi|222846619|gb|EEE84166.1| GH3 family protein [Populus trichocarpa]	Unigene7164_All//8.00E-38//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene7164_All//2.00E-22//C0097810				nr -
Unigene71640_All	307	0.00	3.30	2.25	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.22E-06	Up	1.11E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene71640_All//sp|P17931|LEG3_HUMAN//5.00E-52//Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5						swissprot -
Unigene71641_All	307	0.00	5.12	3.12	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.69E-09	Up	1.16E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene71641_All//gi|30693010|ref|NP_174675.2|//6.00E-16//STT3B (staurosporin and temperature sensitive 3-like b); oligosaccharyl transferase [Arabidopsis thaliana] >gi|10086464|gb|AAG12524.1|AC01544 6_5 Putative integral membrane protein [Arabidopsis thaliana]	Unigene71641_All//4.00E-11//AT1G34130| STT3B (staurosporin and temperature sensitive 3-like b); oligosaccharyl transferase			ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis		nr +
Unigene71642_All	307	0.00	5.12	2.78	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.69E-09	Up	1.14E+01	9.00E-05	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene71643_All	307	0.00	3.96	0.00	0.00	1.35	0.44	0.00	0.00	0.00	1.20E+01	5.45E-07	Up	null	null		1.04E+01	1.25E-02		8.79E+00	3.09E-01		null	null		null	null									
Unigene71644_All	308	0.00	6.91	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	4.10E-12	Up	1.00E+01	4.48E-02		null	null		null	null		null	null		null	null									
Unigene71645_All	308	0.00	5.43	2.94	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.54E-09	Up	1.15E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene71645_All//gi|261746204|gb|ACJ94084.1|//1.00E-31//copper/zinc-superoxide dismutase [Bambusa oldhamii]	Unigene71645_All//5.00E-27//AT1G08830| CSD1 (COPPER/ZINC SUPEROXIDE DISMUTASE 1); superoxide dismutase	Unigene71645_All//6.00E-09//gi|164267428|gb|EV485457.1|EV485457		ko04146|Peroxisome		nr -
Unigene71646_All	308	0.00	3.78	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.04E-06	Up	8.43E+00	3.92E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene71647_All	308	0.00	2.80	0.86	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.92E-05	Up	9.76E+00	7.95E-02		null	null		null	null		null	null		null	null									
Unigene71648_All	308	0.00	2.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.32E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71648_All//sp|Q9VLJ6|ACER_DROME//4.00E-29//Angiotensin-converting enzyme-related protein OS=Drosophila melanogaster GN=Acer PE=1 SV=1						swissprot +
Unigene7165_All	579	0.36	6.91	0.37	0.00	1.72	2.89	0.29	1.08	4.33	4.26E+00	8.38E-18	Up	2.53E-02	1.00E+00		1.08E+01	3.85E-06	Up	1.15E+01	5.83E-10	Up	1.89E+00	3.49E-02		3.89E+00	2.29E-13	Up	Unigene7165_All//gi|102140004|gb|ABF70139.1|//3.00E-06//protein kinase family protein [Musa balbisiana]		Unigene7165_All//5.00E-26//CA993777				nr -
Unigene71651_All	308	0.85	6.58	0.00	0.00	0.00	1.17	0.27	0.81	1.42	2.95E+00	4.86E-07	Up	-9.73E+00	8.51E-02		null	null		1.02E+01	2.37E-02		1.57E+00	3.26E-01		2.37E+00	4.04E-02				Unigene71651_All//1.00E-99//ES796239				
Unigene71652_All	308	0.00	2.96	1.38	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.60E-05	Up	1.04E+01	1.37E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene71653_All	309	0.00	2.30	1.03	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	1.00E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene71653_All//gi|297609345|ref|NP_001062986.2|//2.00E-18//Os09g0362500 [Oryza sativa Japonica Group] >gi|255678835|dbj|BAF24900.2| Os09g0362500 [Oryza sativa Japonica Group]	Unigene71653_All//1.00E-13//AT4G33090| APM1 (AMINOPEPTIDASE M1); aminopeptidase					nr -
Unigene71654_All	309	0.00	5.74	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	4.13E-10	Up	8.43E+00	3.92E-01		null	null		null	null		null	null		null	null									
Unigene71655_All	309	0.00	3.77	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.04E-06	Up	7.43E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71655_All//gi|115487246|ref|NP_001066110.1|//1.00E-12//Os12g0137600 [Oryza sativa Japonica Group] >gi|113648617|dbj|BAF29129.1| Os12g0137600 [Oryza sativa Japonica Group]	Unigene71655_All//4.00E-11//AT2G03770| sulfotransferase family protein			ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr -
Unigene71656_All	309	0.00	7.38	3.62	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	5.63E-13	Up	1.18E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene71656_All//gi|223997030|ref|XP_002288188.1|//4.00E-42//rieske iron-sulfur protein 1 [Thalassiosira pseudonana CCMP1335] >gi|220975296|gb|EED93624.1| rieske iron-sulfur protein 1 [Thalassiosira pseudonana CCMP1335]	Unigene71656_All//3.00E-41//AT5G13430| ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative	Unigene71656_All//6.00E-09//TC168816		ko00190|Oxidative phosphorylation		nr -
Unigene71657_All	309	0.00	2.46	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.75E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71657_All//gi|224006279|ref|XP_002292100.1|//1.00E-28//precursor of hydrogenase glutaryl-coa dehydrogenase [Thalassiosira pseudonana CCMP1335] >gi|220972819|gb|EED90951.1| precursor of hydrogenase glutaryl-coa dehydrogenase [Thalassiosira pseudonana CCMP1335]	Unigene71657_All//1.00E-10//AT3G51840| ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase			ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation		nr +
Unigene71658_All	309	0.00	5.74	4.48	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	4.13E-10	Up	1.21E+01	1.23E-07	Up	null	null		null	null		null	null		null	null									
Unigene71659_All	309	0.00	2.62	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.32E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71659_All//gi|301122083|ref|XP_002908768.1|//9.00E-10//conserved hypothetical protein [Phytophthora infestans T30-4] >gi|262099530|gb|EEY57582.1| conserved hypothetical protein [Phytophthora infestans T30-4]						nr -
Unigene71661_All	309	0.00	5.25	1.03	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.96E-09	Up	1.00E+01	4.48E-02		null	null		null	null		null	null		null	null		Unigene71661_All//gi|162463923|ref|NP_001105011.1|//4.00E-13//homocysteine S-methyltransferase 1 [Zea mays] >gi|50400645|sp|Q9FUN0.1|HMT1_MAIZE RecName: Full=Homocysteine S-methyltransferase 1; AltName: Full=S-methylmethionine:homocysteine methyltransferase 1; Short=SMM:Hcy S-methyltransferase 1; AltName: Full=ZmHMT-1 >gi|10732785|gb|AAG22537.1|AF297044_1 homocysteine S-methyltransferase-1 [Zea mays] >gi|195647426|gb|ACG43181.1| homocysteine S-methyltransferase 1 [Zea mays]	Unigene71661_All//1.00E-11//AT3G25900| HMT-1; homocysteine S-methyltransferase			ko00270|Cysteine and methionine metabolism		nr +
Unigene71662_All	310	40.84	87.12	25.25	143.18	188.62	181.67	171.30	253.34	530.24	1.09E+00	5.74E-23	Up	-6.94E-01	2.41E-05		3.98E-01	3.40E-10		3.44E-01	4.83E-07		5.65E-01	2.92E-26		1.63E+00	0.00E+00	Up	Unigene71662_All//gi|151934217|gb|ABS18446.1|//7.00E-21//WRKY50 [Glycine max]	Unigene71662_All//8.00E-19//AT4G31550| WRKY11; calmodulin binding / transcription factor	Unigene71662_All//1.00E-157//gi|73864569|gb|DT467308.1|DT467308	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene71664_All	310	0.00	3.76	1.55	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.04E-06	Up	1.06E+01	7.45E-03		null	null		null	null		null	null		null	null		Unigene71664_All//gi|150406474|ref|YP_001315138.1|//8.00E-33//NADH dehydrogenase subunit 9 [Chlorokybus atmophyticus] >gi|126507711|gb|AB015108.1| NADH dehydrogenase subunit 9 [Chlorokybus atmophyticus]	Unigene71664_All//1.00E-25//ATMG00070| NADH dehydrogenase subunit 9			ko00190|Oxidative phosphorylation		nr +
Unigene71667_All	310	0.00	2.45	3.09	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.75E-04	Up	1.16E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene71667_All//gi|301105535|ref|XP_002901851.1|//5.00E-06//villin-like protein [Phytophthora infestans T30-4] >gi|262099189|gb|EEY57241.1| villin-like protein [Phytophthora infestans T30-4]	Unigene71667_All//6.00E-06//AT5G57320| villin, putative					nr -
Unigene71668_All	310	0.00	3.11	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71668_All//gi|300267151|gb|EFJ51336.1|//7.00E-07//hypothetical protein VOLCADRAFT_88061 [Volvox carteri f. nagariensis]						nr +
Unigene7167_All	1018	0.00	0.20	0.05	0.73	0.07	0.13	2.91	3.20	1.33	7.64E+00	1.35E-01		5.71E+00	6.27E-01		-3.44E+00	6.18E-04	Down	-2.46E+00	1.02E-02		1.40E-01	6.71E-01		-1.13E+00	4.06E-04	Down	Unigene7167_All//gi|224112233|ref|XP_002332812.1|//2.00E-59//leucine rich repeat family protein with ABC domain [Populus trichocarpa] >gi|222833206|gb|EEE71683.1| leucine rich repeat family protein with ABC domain [Populus trichocarpa]	Unigene7167_All//2.00E-31//AT1G58190| AtRLP9 (Receptor Like Protein 9); protein binding	Unigene7167_All//0.00E+00//DT466351		ko04626|Plant-pathogen interaction		nr -
Unigene71671_All	311	0.00	3.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.04E-06	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +

Unigene71672_All	311	0.00	3.10	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	8.42E+00	3.92E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene71673_All	311	0.00	8.31	1.54	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.05E-14	Up	1.06E+01	7.44E-03		null	null		null	null		null	null		null	null										ESTscan +
Unigene71676_All	312	0.00	5.03	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.69E-09	Up	7.42E+00	6.27E-01		null	null		null	null		null	null		null	null										
Unigene71677_All	312	0.00	3.41	1.88	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.80E-06	Up	1.09E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene71677_All//sp|O14493|CLD4_HUMAN//9.00E-52//Claudin-4 OS=Homo sapiens GN=CLDN4 PE=1 SV=1						swissprot -
Unigene71678_All	312	0.00	2.44	0.34	0.96	0.44	0.00	0.00	0.00	0.00	1.13E+01	1.75E-04	Up	8.41E+00	3.92E-01		-1.12E+00	4.24E-01		-9.90E+00	3.98E-02		null	null		null	null		Unigene71678_All//gi|222873073|gb|EEF10204.1|//1.00E-13//predicted protein [Populus trichocarpa]						nr +
Unigene71679_All	312	0.00	2.27	2.90	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	1.15E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene71679_All//sp|P78545|ELF3_HUMAN//7.00E-59//ETS-related transcription factor Elf-3 OS=Homo sapiens GN=ELF3 PE=1 SV=1						swissprot -
Unigene7168_All	1212	0.56	0.50	0.00	12.86	6.36	3.39	5.97	1.59	0.92	-1.62E-01	8.32E-01		-9.13E+00	7.63E-04	Down	-1.02E+00	1.46E-14	Down	-1.92E+00	3.06E-33	Down	-1.91E+00	1.24E-17	Down	-2.70E+00	2.39E-27	Down	Unigene7168_All//gi|16323147|gb|AAL15308.1|//6.00E-48//At1g10380/F14N23_32 [Arabidopsis thaliana] >gi|21436013|gb|AAM51584.1| At1g10380/F14N23_32 [Arabidopsis thaliana]	Unigene7168_All//3.00E-49//AT1G10380| unknown protein	Unigene7168_All//0.00E+00//TC157470				nr +
Unigene71680_All	312	0.00	2.76	0.00	0.32	0.22	0.87	0.00	0.13	0.00	1.14E+01	4.91E-05	Up	null	null		-5.33E-01	8.14E-01		1.44E+00	4.09E-01		7.07E+00	6.28E-01		null	null				Unigene71680_All//4.00E-07//DW239855					
Unigene71681_All	312	0.00	5.20	2.22	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.96E-09	Up	1.11E+01	6.13E-04	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene71682_All	312	0.00	3.09	0.51	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	9.00E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71682_All//gi|115469120|ref|NP_001058159.1|//2.00E-06//Os06g0639300 [Oryza sativa Japonica Group] >gi|113596199|dbj|BAF20073.1| Os06g0639300 [Oryza sativa Japonica Group]						nr -
Unigene71683_All	312	0.00	2.44	1.37	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.75E-04	Up	1.04E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71683_All//gi|157890948|dbj|BAF81515.1|//3.00E-19//oxygen-evolving enhancer protein 3-2 [Brassica rapa]	Unigene71683_All//1.00E-10//AT1G05180| PSBQ-2; calcium ion binding			ko00195|Photosynthesis		nr -
Unigene71684_All	312	0.00	5.52	3.58	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	7.97E-10	Up	1.18E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene71684_All//sp|Q94901|LARK_DROME//8.00E-48//RNA-binding protein lark OS=Drosophila melanogaster GN=lark PE=1 SV=1						swissprot +
Unigene71685_All	312	0.00	2.11	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.21E-04	Up	8.41E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71685_All//gi|25090250|gb|AAN72262.1|//5.00E-48//At1g44575/T18F15 [Arabidopsis thaliana]	Unigene71685_All//3.00E-37//AT1G44575| NPQ4 (NONPHOTOCHEMICAL QUENCHING); chlorophyll binding / xanthophyll binding	Unigene71685_All//1.00E-16//TC152485		ko00195|Photosynthesis		nr +
Unigene71686_All	312	0.00	7.80	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	7.72E-14	Up	8.41E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71686_All//gi|240254047|ref|NP_172382.4|//4.00E-17//BIP3; ATP binding [Arabidopsis thaliana] >gi|24496493|gb|AAN60163.1| BiP chaperone BIP-L [Arabidopsis thaliana]	Unigene71686_All//2.00E-18//AT1G09080| BIP3; ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis//ko03060|Protein export		nr -
Unigene71688_All	313	0.00	2.10	0.68	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.21E-04	Up	9.41E+00	1.39E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene71689_All	313	0.00	3.56	0.68	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.99E-06	Up	9.41E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71689_All//gi|148612407|gb|AEQ96119.1|//2.00E-14//alpha-gliadin [Aegilops tauschii]				ko03022|Basal transcription factors		nr +
Unigene7169_All	443	0.47	2.63	1.20	1.69	1.55	0.92	2.39	0.85	0.63	2.48E+00	9.79E-04	Up	1.35E+00	2.25E-01		-1.18E-01	8.62E-01		-8.78E-01	3.08E-01		-1.49E+00	1.64E-02		-1.92E+00	2.21E-03				Unigene7169_All//5.00E-07//BF277994					
Unigene71692_All	313	0.00	2.91	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.60E-05	Up	null	null		null	null		null	null		null	null		null	null										ESTscan +
Unigene71693_All	314	0.00	2.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.91E-05	Up	null	null		null	null		null	null		null	null		null	null										
Unigene71695_All	314	0.00	3.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.80E-06	Up	null	null		null	null		null	null		null	null		null	null										ESTscan -
Unigene71698_All	314	0.00	2.26	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.30E-04	Up	8.41E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71698_All//gi|20067064|gb|AAM09521.1|AF489954_1//2.00E-10//BIP4 [Physcomitrella patens]						nr +
Unigene71699_All	314	0.00	4.20	1.70	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.49E-07	Up	1.07E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71699_All//gi|15222757|ref|NP_175963.1|//7.00E-21//PSAG (PHOTOSYSTEM I SUBUNIT G) [Arabidopsis thaliana] >gi|20143884|sp|Q9STN7.1|PSAG_ARATH RecName: Full=Photosystem I reaction center subunit V, chloroplastic; AltName: Full=PSI-G; Flags: Precursor >gi|11692916|gb|AAG40061.1|AF324710_1 At1g55670 [Arabidopsis thaliana] >gi|14190363|gb|AAK55662.1|AF378859_1 At1g55670/F20N2_3 [Arabidopsis thaliana] >gi|8734520|emb|CAB52748.1| photosystem I subunit V precursor [Arabidopsis thaliana] >gi|152158663|gb|AAX91476.1| At1g55670/F20N2_3 [Arabidopsis thaliana]				ko03040|Spliceosome//ko00195|Photosynthesis		nr -
Unigene7170_All	2094	0.10	0.17	0.31	0.57	0.49	0.28	1.43	1.94	8.28	7.62E-01	5.57E-01		1.61E+00	1.11E-01		-2.11E-01	7.52E-01		-1.03E+00	1.06E-01		4.34E-01	1.22E-01		2.53E+00	3.67E-59	Up	Unigene7170_All//gi|30697422|ref|NP_172860.2|//1.00E-141//serine/threonine protein kinase family protein [Arabidopsis thaliana]	Unigene7170_All//1.00E-133//AT1G66880| serine/threonine protein kinase family protein	Unigene7170_All//0.00E+00//TC150848		ko04626|Plant-pathogen interaction		nr +
Unigene71700_All	315	0.00	4.34	0.68	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.78E-08	Up	9.40E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71700_All//sp|P17210|KINH_DROME//7.00E-35//Kinesin heavy chain OS=Drosophila melanogaster GN=Khc PE=1 SV=2						swissprot -
Unigene71702_All	315	0.00	2.41	0.51	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.75E-04	Up	8.99E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71702_All//gi|22330770|ref|NP_178157.2|//2.00E-18//EMB2753 (EMBRYO DEFECTIVE 2753); binding [Arabidopsis thaliana]	Unigene71702_All//7.00E-20//AT1G80410| EMB2753 (EMBRYO DEFECTIVE 2753); binding					nr -
Unigene71705_All	315	0.00	2.73	0.85	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.91E-05	Up	9.72E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71705_All//gi|231574|sp|P30362.1|ASPG_LUPAR//3.00E-12//RecName: Full=Isoaspartyl peptidase/L-asparaginase; AltName: Full=L-asparagine amidohydrolase; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase subunit alpha; Contains: RecName: Full=Isoaspartyl peptidase/L-asparaginase subunit beta; Flags: Precursor >gi|19137|emb|CAA36824.1| asparaginase [Lupinus arboreus]	Unigene71705_All//2.00E-12//AT3G16150| L-asparaginase, putative / L-asparagine amidohydrolase, putative					nr -
Unigene71706_All	315	0.00	2.57	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	9.32E-05	Up	1.04E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71706_All//sp|P91928|IMMT_DROME//2.00E-20//Putative mitochondrial inner membrane protein OS=Drosophila melanogaster GN=CG6155 PE=2 SV=4						swissprot -
Unigene71708_All	315	0.00	3.06	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	8.40E+00	3.92E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene7171_All	1171	0.27	0.43	0.09	5.91	4.21	2.35	0.00	0.00	0.20	6.91E-01	4.99E-01		-1.56E+00	3.29E-01		-4.92E-01	2.17E-02		-1.33E+00	4.65E-09	Down	null	null		7.67E+00	4.39E-02		Unigene7171_All//gi|210111348|gb|ACJ07153.1|//1.00E-117//R2R3 MYB transcription factor [Gossypium hirsutum]	Unigene7171_All//7.00E-87//AT3G01140| MYB106 (myb domain protein 106); DNA binding / transcription factor	Unigene7171_All//0.00E+00//TC152374	MYB			nr -
Unigene71710_All	316	0.00	2.89	0.84	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.60E-05	Up	9.72E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71710_All//gi|61229242|gb|AAX40985.1|//3.00E-18//S-adenosyl-L-homocysteine hydrolase [Pavlova lutheri]	Unigene71710_All//6.00E-16//AT3G23810| SAH2 (S-ADENOSYL-L-HOMOCYSTEINE (SAH) HYDROLASE 2); adenosylhomocysteinase/ binding / catalytic			ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr +
Unigene71712_All	316	0.00	2.89	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.60E-05	Up	7.40E+00	6.27E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene71714_All	316	0.00	3.05	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	1.04E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71714_All//gi|157093503|gb|ABV22406.1|//1.00E-08//unknown [Noctiluca scintillans]						nr -
Unigene71715_All	317	0.00	6.71	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	4.10E-12	Up	7.39E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71715_All//gi|298710366|emb|CBJ31983.1|//4.00E-23//aspartate aminotransferase [Ectocarpus siliculosus]	Unigene71715_All//3.00E-22//AT1G62800| ASP4 (ASPARTATE AMINOTRANSFERASE 4); catalytic/ pyridoxal phosphate binding / transaminase/ transferase, transferring nitrogenous groups			ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism//ko00350|Tyrosine metabolism//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene71717_All	317	0.17	2.72	0.50	0.16	1.41	0.85	0.13	0.40	0.00	4.04E+00	4.20E-04	Up	1.61E+00	5.10E-01		3.17E+00	3.95E-02		2.44E+00	2.22E-01		1.57E+00	5.44E-01		-7.06E+00	6.05E-01										
Unigene71718_All	317	0.00	4.64	1.18	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.11E-08	Up	1.02E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene71718_All//sp|Q7JUY7|CED6_DROME//2.00E-21//PTB domain-containing adapter protein ced-6 OS=Drosophila melanogaster GN=ced-6 PE=1 SV=1						swissprot +
Unigene71719_All	317	0.00	4.16	1.01	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.49E-07	Up	9.98E+00	4.48E-02		null	null		null	null		null	null		null	null		Unigene71719_All//gi|159471710|ref|XP_001693999.1|//1.00E-22//ser/thr kinase [Chlamydomonas reinhardtii] >gi|158277166|gb|EDP02935.1| ser/thr kinase [Chlamydomonas reinhardtii]	Unigene71719_All//2.00E-27//AT3G23340| ck110 (Casein Kinase I-like 10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase					nr +
Unigene71721_All	317	0.00	4.00	2.35	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.85E-07	Up	1.12E+01	3.26E-04	Up	null	null		null	null		null	null		null	null										
Unigene71723_All	317	0.00	3.68	0.84	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.04E-06	Up	9.71E+00	7.95E-02		null	null		null	null		null	null		null	null										ESTscan -
Unigene71725_All	318	0.00	3.35	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.80E-06	Up	null	null		null	null		null	null		null	null		null	null										ESTscan +
Unigene71726_All	318	0.00	2.39	0.33	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.75E-04	Up	8.39E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71726_All//gi|21537040|gb|AAM61381.1|//2.00E-16//contains similarity to peroxisomal membrane carrier protein [Arabidopsis thaliana]	Unigene71726_All//6.00E-17//AT5G66380| ATFOLT1 (ARABIDOPSIS THALIANA FOLATE TRANSPORTER 1); binding / folic acid transporter					nr -
Unigene71727_All	318	0.00	3.03	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	9.39E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71727_All//sp|P50535|MSL1_DROME//6.00E-06//Protein male-specific lethal-1 OS=Drosophila melanogaster GN=msl-1 PE=1 SV=2						swissprot -
Unigene71728_All	318	0.00	5.10	0.33	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.96E-09	Up	8.39E+00	3.92E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene71729_All	318	0.00	2.71	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.91E-05	Up	7.39E+00	6.27E-01		null	null		null	null		null	null		null	null										

Unigene71730_All	318	0.33	3.35	0.67	0.78	0.00	0.00	0.00	0.00	0.00	3.35E+00	2.17E-04	Up	1.03E+00	5.90E-01		-9.61E+00	4.17E-02		-9.61E+00	7.31E-02		null	null		null	null		Unigene71730_All//gi|242086625|ref|XP_002439145.1|//7.00E-07//hypothetical protein SORBIDRAFT_09g001307 [Sorghum bicolor] >gi|241944430|gb|EES17575.1| hypothetical protein SORBIDRAFT_09g001307 [Sorghum bicolor]							nr -
Unigene71731_All	318	0.00	3.66	3.18	0.00	0.00	0.57	0.00	0.00	0.00	1.18E+01	1.04E-06	Up	1.16E+01	1.27E-05	Up	null	null		9.15E+00	1.93E-01		null	null		null	null		Unigene71731_All//sp|P0AET1|HDEA_SHIFL//1.00E-46//Chaperone-like protein hdeA OS=Shigella flexneri GN=hdeA PE=2 SV=1							swissprot +
Unigene71732_All	318	0.00	2.55	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	9.32E-05	Up	8.97E+00	2.36E-01		null	null		null	null		null	null		null	null								
Unigene71734_All	319	0.00	2.06	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.21E-04	Up	8.97E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71734_All//gi|22947842|gb|AA07899.1|//1.00E-29//20S proteasome alpha 6 subunit [Nicotiana benthamiana]	Unigene71734_All//2.00E-23//AT5G42790| PAF1; endopeptidase/ peptidase/ threonine-type endopeptidase			ko03050|Proteasome		nr +
Unigene71735_All	319	0.00	6.04	3.51	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	5.72E-11	Up	1.18E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene71735_All//gi|75313847|sp|Q9ST57.1|SPZ2A_WHEAT//4.00E-12//RecName: Full=Serpin-Z2A; AltName: Full=TrianZ2a; AltName: Full=WSZ2a >gi|5734506|emb|CAB52710.1| serpin [Triticum aestivum]	Unigene71735_All//2.00E-08//AT1G47710| serpin, putative / serine protease inhibitor, putative					nr -
Unigene71736_All	319	1.15	5.88	1.17	0.00	0.22	0.00	0.00	0.66	0.12	2.36E+00	2.61E-05	Up	2.54E-02	1.00E+00		7.75E+00	6.03E-01		null	null		9.36E+00	7.84E-02		6.96E+00	6.39E-01		Unigene71736_All//gi|12322008|gb|AAG51046.1|AC069473.8/|2.00E-14//gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] >gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]						nr -
Unigene71737_All	319	0.00	4.45	2.34	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	4.05E-08	Up	1.12E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene71737_All//gi|94312269|ref|YP_585479.1|//2.00E-39//50S ribosomal protein L11 [Cupriavidus metallidurans CH34] >gi|113869448|ref|YP_727937.1| 50S ribosomal protein L11 [Ralstonia eutropha H16] >gi|194291039|ref|YP_002006946.1| 50S ribosomal protein L11 [Cupriavidus taiwanensis] >gi|118597280|sp|Q1L116.1|RL11_RALME RecName: Full=50S ribosomal protein L11 >gi|122946531|sp|Q0K602.1|RL11_RALEH RecName: Full=50S ribosomal protein L11 >gi|226702751|sp|B3R7U0.1|RL11_CUPTR RecName: Full=50S ribosomal protein L11 >gi|93356121|gb|ABF10210.1| 50S ribosomal subunit protein L11 [Cupriavidus metallidurans CH34] >gi|113528224|emb|CAJ94569.1| LSU ribosomal protein L11 [Ralstonia eutropha H16] >gi|193224874|emb|CAQ70885.1| 50S ribosomal subunit protein L11, N-terminal believed to regulate RelA [Cupriavidus taiwanensis]	Unigene71737_All//2.00E-23//AT1G32990| PRPL11 (PLASTID RIBOSOMAL PROTEIN L11); structural constituent of ribosome			ko03010|Ribosome		nr -
Unigene71739_All	320	0.00	3.48	3.66	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.99E-06	Up	1.18E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene71739_All//sp|P35441|TSP1_MOUSE//9.00E-60//Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1							swissprot -
Unigene71740_All	320	0.00	4.91	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.69E-09	Up	7.38E+00	6.27E-01		null	null		null	null		null	null		null	null								ESTscan -
Unigene71741_All	320	0.00	2.06	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.21E-04	Up	9.38E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71741_All//gi|195620064|gb|ACG31862.1|//7.00E-31//26S proteasome non-ATPase regulatory subunit 11 [Zea mays]	Unigene71741_All//5.00E-32//AT1G29150| ATS9 (ARABIDOPSIS NON-ATPASE SUBUNIT 9)			ko03050|Proteasome		nr +
Unigene71742_All	320	0.00	3.17	0.33	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.22E-06	Up	8.38E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71742_All//gi|226505274|ref|NP_001145712.1|//2.00E-06//hypothetical protein LOC100279216 [Zea mays] >gi|219884125|gb|ACL52437.1| unknown [Zea mays]	Unigene71742_All//4.00E-05//AT3G23900| RNA recognition motif (RRM)-containing protein					nr +
Unigene71743_All	320	0.00	4.75	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.09E-08	Up	null	null		null	null		null	null		null	null		null	null		Unigene71743_All//gi|6562845|emb|CAB62553.1|//3.00E-18//heterogeneous nuclear ribonucleoprotein; type A/B hnRNP p40 [Rattus norvegicus] >gi|149052496|gb|EDM04313.1| rCG34663, isoform CRA_a [Rattus norvegicus]	Unigene71743_All//3.00E-16//AT3G13224| RNA recognition motif (RRM)-containing protein			ko03040|Spliceosome		nr +
Unigene71744_All	320	0.00	4.75	0.33	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.09E-08	Up	8.38E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71744_All//gi|298710476|emb|CBJ25540.1|//3.00E-38//Glycogen synthase kinase-3 beta (GSK-3 beta) [Ectocarpus siliculosus]	Unigene71744_All//2.00E-32//AT1G06390| GSK1 (GSK3/SHAGGY-LIKE PROTEIN KINASE 1); glycogen synthase kinase 3/ kinase					nr +
Unigene71746_All	321	0.00	3.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.04E-06	Up	null	null		null	null		null	null		null	null		null	null								
Unigene71747_All	321	0.00	3.31	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.80E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene71747_All//gi|300259068|gb|EPJ43299.1|//3.00E-06//molecular chaperone [Volvox carteri f. nagariensis]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene71748_All	321	0.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.37E-05	Up	null	null		null	null		null	null		null	null		null	null								ESTscan +
Unigene7175_All	619	0.34	0.49	0.00	3.70	2.95	3.36	1.78	5.13	0.58	5.39E-01	6.71E-01		-8.40E+00	1.44E-01		-3.28E-01	4.60E-01		-1.41E-01	7.44E-01		1.53E+00	3.49E-06	Up	-1.62E+00	6.27E-03		Unigene7175_All//gi|53749430|gb|AAU90286.1|//1.00E-65//Putative pyridine nucleotide-disulphide oxidoreductase, identical [Solanum demissum]	Unigene7175_All//3.00E-61//AT3G44190| pyridine nucleotide-disulphide oxidoreductase family protein	Unigene7175_All//2.00E-44//TC162424				nr -
Unigene71750_All	321	0.00	1.89	2.16	0.31	0.21	0.00	0.00	0.00	0.00	1.09E+01	1.16E-03		1.11E+01	6.13E-04	Up	-5.33E-01	8.14E-01		-8.28E+00	3.95E-01		null	null		null	null		Unigene71750_All//gi|297837505|ref|XP_002886634.1|//1.00E-16//potassium transporter family protein [Arabidopsis lyrata subsp. lyrata] >gi|297332475|gb|EFH62893.1| potassium transporter family protein [Arabidopsis lyrata subsp. lyrata]	Unigene71750_All//9.00E-10//AT1G60160| potassium transporter family protein					nr -
Unigene71751_All	321	0.00	5.21	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.54E-09	Up	1.07E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71751_All//sp|P23438|SSRB_CANFA//2.00E-07//Translocon-associated protein subunit beta OS=Canis familiaris GN=SSR2 PE=1 SV=1							swissprot +
Unigene71753_All	321	0.00	4.58	2.16	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.11E-08	Up	1.11E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene71753_All//sp|Q02374|NDUB2_BOVIN//2.00E-12//NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 2, mitochondrial OS=Bos taurus GN=NDUFB2 PE=1 SV=1							swissprot -
Unigene71755_All	322	0.00	2.99	0.33	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.37E-05	Up	8.37E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71755_All//sp|Q9V447|KRH2_DROME//1.00E-22//Protein Kr-h2 OS=Drosophila melanogaster GN=Kr-h2 PE=1 SV=1							swissprot -
Unigene71756_All	322	14.79	4.41	15.71	0.62	0.43	0.00	0.00	0.00	0.00	-1.75E+00	9.48E-09	Down	8.75E-02	7.53E-01		-5.33E-01	7.47E-01		-9.27E+00	1.33E-01		null	null		null	null								ESTscan -
Unigene71757_All	322	0.00	4.88	1.32	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.69E-09	Up	1.04E+01	1.37E-02		null	null		null	null		null	null		null	null								ESTscan +
Unigene71758_All	322	0.00	3.78	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.45E-07	Up	9.95E+00	4.48E-02		null	null		null	null		null	null		null	null		Unigene71758_All//sp|Q9BYP8|KR171_HUMAN//1.00E-65//Keratin-associated protein 17-1 OS=Homo sapiens GN=KRTAP17-1 PE=2 SV=1							swissprot -
Unigene71759_All	323	0.00	2.67	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.91E-05	Up	9.95E+00	4.48E-02		null	null		null	null		null	null		null	null								ESTscan +
Unigene71760_All	323	0.00	5.65	3.46	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.14E-10	Up	1.18E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene71760_All//gi|301091913|ref|XP_002896131.1|//9.00E-18//bax inhibitor-like protein [Phytophthora infestans T30-4] >gi|262094965|gb|EEY53003.1| bax inhibitor-like protein [Phytophthora infestans T30-4]	Unigene71760_All//3.00E-12//AT5G47120| ATBI1 (BAX INHIBITOR 1)					nr +
Unigene71762_All	323	0.00	3.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.85E-07	Up	null	null		null	null		null	null		null	null		null	null						ko03018|RNA degradation		kegg +
Unigene71763_All	323	0.00	4.55	1.15	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.11E-08	Up	1.02E+01	2.49E-02		null	null		null	null		null	null		null	null								
Unigene71764_All	323	0.00	48.63	13.19	0.31	0.00	0.00	0.00	0.00	0.00	1.56E+01	3.01E-90	Up	1.37E+01	1.22E-23	Up	-8.27E+00	3.10E-01		-8.27E+00	3.95E-01		null	null		null	null		Unigene71764_All//gi|115464561|ref|NP_001055880.1|//3.00E-06//0s05g0486700 [Oryza sativa Japonica Group] >gi|113579431|dbj|BAF17794.1| Os05g0486700 [Oryza sativa Japonica Group]				ko03010|Ribosome		nr -
Unigene71765_All	323	0.00	2.20	0.33	0.00	0.00	0.00	0.92	0.52	4.69	1.11E+01	3.30E-04	Up	8.37E+00	3.92E-01		null	null		null	null		-8.24E-01	5.40E-01		2.35E+00	1.89E-05	Up			Unigene71765_All//7.00E-132//TC144424					
Unigene71766_All	323	0.16	2.98	1.32	0.15	0.21	0.84	1.18	0.39	0.25	4.20E+00	1.29E-04	Up	3.03E+00	5.72E-02		4.67E-01	9.55E-01		2.44E+00	2.21E-01		-1.60E+00	1.81E-01		-2.26E+00	6.49E-02								
Unigene71767_All	323	0.00	5.18	1.98	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.53E-09	Up	1.10E+01	1.15E-03		null	null		null	null		null	null		null	null								
Unigene71768_All	324	0.00	4.07	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.49E-07	Up	9.95E+00	4.47E-02		null	null		null	null		null	null		null	null								ESTscan +
Unigene71769_All	324	0.00	3.13	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.22E-06	Up	9.95E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene71769_All//gi|116059953|emb|CAL56012.1|//7.00E-07//Prolylcarboxypeptidase (angiotensinase C) (1SS) [Ostreococcus tauri]							nr -
Unigene71770_All	324	0.00	4.38	1.64	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	4.05E-08	Up	1.07E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71770_All//sp|Q9D1H9|MFAP4_MOUSE//3.00E-12//Microfibril-associated glycoprotein 4 OS=Mus musculus GN=Mfap4 PE=1 SV=1							swissprot +
Unigene71772_All	324	0.00	6.10	4.44	0.00	0.00	0.00	0.13	0.00	0.00	1.26E+01	2.96E-11	Up	1.21E+01	6.29E-08	Up	null	null		null	null		-7.03E+00	6.48E-01		-7.03E+00	6.05E-01		Unigene71772_All//sp|P08174|DAF_HUMAN//7.00E-60//Complement decay-accelerating factor OS=Homo sapiens GN=CD55 PE=1 SV=4							swissprot +
Unigene71776_All	324	0.00	2.35	0.33	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.75E-04	Up	8.36E+00	3.92E-01		null	null		null	null		null	null		null	null								ESTscan -
Unigene71777_All	325	0.00	2.81	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.60E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71777_All//sp|Q9V125|NCDN_DROME//3.00E-43//Neurochondrin homolog OS=Drosophila melanogaster GN=Neurochondrin PE=2 SV=1							swissprot +

Unigene71778_A11	325	0.00	2.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.30E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71778_A11|gi|255082394|ref|XP_002504183.1|/4.00E-09//lysosomal cystine transporter family [Micromonas sp. RCC299] >gi|226519451|gb|ACO65441.1| lysosomal cystine transporter family [Micromonas sp. RCC299]	Unigene71778_A11//2.00E-09//AT4G07390| PQ-loop repeat family protein / transmembrane family protein					nr -
Unigene7178_A11	1520	0.14	0.23	0.07	0.26	0.18	0.36	1.92	1.51	4.56	7.61E-01	5.57E-01		-9.74E-01	6.19E-01		-5.33E-01	6.15E-01		4.44E-01	6.78E-01		-3.44E-01	3.29E-01		1.25E+00	1.02E-09	Up	Unigene7178_A11|gi|290782380|gb|ADD62392.1|/0.00E+00//pectase lyase [Prunus persica]	Unigene7178_A11//0.00E+00//AT5G48900| pectate lyase family protein	Unigene7178_A11//0.00E+00//TC137036		ko00040|Pentose and glucuronate interconversions		nr -
Unigene71780_A11	325	0.00	2.65	0.33	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	4.91E-05	Up	8.36E+00	3.92E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene71781_A11	325	0.00	4.99	0.49	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.96E-09	Up	8.94E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71781_A11|gi|62286955|sp|Q9XG99.1|KPRS2_SPIOL//3.00E-18//RecName: Full=Ribose-phosphate pyrophosphokinase 2, chloroplastic; AltName: Full=Phosphoribosyl pyrophosphate synthase 2; Flags: Precursor >gi|4902851|emb|CAB43600.1| phosphoribosyl pyrophosphate synthase isozyme 2 [Spinacia oleracea]	Unigene71781_A11//1.00E-18//AT2G44530| ribose-phosphate pyrophosphokinase, putative / phosphoribosyl diphosphate synthetase, putative			ko00230|Purine metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene71782_A11	325	0.00	3.27	1.15	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.80E-06	Up	1.02E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene71782_A11//sp|Q9I7U4|TITIN_DROME//4.00E-07//Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3								swissprot -
Unigene71784_A11	326	0.00	2.02	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	6.21E-04	Up	9.35E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71784_A11|gi|41350273|gb|AAS00459.1|/6.00E-17//NADPH:cytochrome P450-reductase [Hypericum androsaemum]	Unigene71784_A11//1.00E-13//AT4G24520| ATR1 (ARABIDOPSIS P450 REDUCTASE 1); NADPH-hemoprotein reductase						nr +
Unigene71785_A11	327	0.00	2.94	0.81	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.37E-05	Up	9.67E+00	7.95E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene71788_A11	327	0.00	4.03	0.81	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.49E-07	Up	9.67E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71788_A11|gi|299116915|emb|CBN75025.1|/9.00E-01//conserved unknown protein [Ectocarpus siliculosus]						nr +
Unigene71789_A11	327	0.00	4.65	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.09E-08	Up	1.07E+01	4.01E-03		null	null		null	null		null	null		null	null									
Unigene71791_A11	327	0.00	18.75	11.72	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	5.26E-35	Up	1.35E+01	3.02E-21	Up	null	null		null	null		null	null		null	null		Unigene71791_A11|gi|115488784|ref|NP_001066879.1|/6.00E-09//Os12g0514100 [Oryza sativa Japonica Group] >gi|113649386|dbj|BAF29898.1| Os12g0514100 [Oryza sativa Japonica Group]	Unigene71791_A11//2.00E-08//AT1G27330| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: cellular_component unknown; EXPRESSED IN: male gametophyte, pollen tube; EXPRESSED DURING: L mature pollen stage, M germinated pollen stage; CONTAINS InterPro DOMAIN/s: Ribosome associated membrane RAMP4 (InterPro:IPR010580); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G27350.1); Has 267 Blast hits to 267 proteins in 83 species: Archae - 0; Bacteria - 0; Metazoa - 183; Fungi - 0; Plants - 55; Viruses - 0; Other Eukaryotes - 29 (source: NCBI BLink).						nr +
Unigene71792_A11	328	0.00	2.94	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.37E-05	Up	7.34E+00	6.27E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene71793_A11	328	0.00	2.16	1.14	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.30E-04	Up	1.02E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene71793_A11|sp|Q6DRG7|MYPT1_DANRE//3.00E-06//Protein phosphatase 1 regulatory subunit 12A OS=Danio rerio GN=ppp1r12a PE=2 SV=2						swissprot +
Unigene71794_A11	328	0.00	5.10	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.53E-09	Up	9.34E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene71796_A11	328	0.00	2.78	1.46	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.60E-05	Up	1.05E+01	7.44E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene71798_A11	328	0.48	3.55	0.16	0.30	0.00	0.00	0.00	0.00	0.00	2.89E+00	2.98E-04	Up	-1.56E+00	5.32E-01		-8.25E+00	3.10E-01		-8.25E+00	3.95E-01		null	null		null	null		Unigene71798_A11|gi|9759309|dbj|BAB08815.1|/2.00E-08//non-LTR retroelement reverse transcriptase-like [Arabidopsis thaliana]						nr +
Unigene71799_A11	328	0.00	3.40	0.49	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.99E-06	Up	8.93E+00	2.36E-01		null	null		null	null		null	null		null	null									
Unigene71800_A11	329	0.00	3.08	1.46	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.22E-06	Up	1.05E+01	7.44E-03		null	null		null	null		null	null		null	null									
Unigene71801_A11	329	0.00	5.39	1.62	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.13E-10	Up	1.07E+01	4.01E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene71802_A11	330	0.00	5.68	1.45	0.30	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.10E-10	Up	1.05E+01	7.44E-03		-8.24E+00	3.10E-01		-8.24E+00	3.95E-01		null	null		null	null		Unigene71802_A11|gi|226459456|gb|EEH56752.1|/1.00E-06//predicted protein [Micromonas pusilla CCMP1545]						nr -
Unigene71803_A11	330	0.00	3.07	0.32	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.22E-06	Up	8.33E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71803_A11|gi|255085060|ref|XP_002504961.1|/2.00E-18//COMPASS/Set1C complex protein [Micromonas sp. RCC299] >gi|226520230|gb|ACO66219.1| COMPASS/Set1C complex protein [Micromonas sp. RCC299]						nr -
Unigene71804_A11	330	0.00	2.00	0.65	0.00	0.00	0.14	0.00	0.00	0.00	1.10E+01	6.21E-04	Up	9.33E+00	1.39E-01		null	null		7.10E+00	6.88E-01		null	null		null	null				Unigene71804_A11//1.00E-07//PLS77219					ESTscan +
Unigene71805_A11	330	0.00	4.15	0.32	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.77E-08	Up	8.33E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71805_A11|gi|159482366|ref|XP_001699242.1|/2.00E-23//nucleolar protein, small subunit of H/ACA snoRNPs [Chlamydomonas reinhardtii] >gi|158273089|gb|EDO98882.1| nucleolar protein, small subunit of H/ACA snoRNPs [Chlamydomonas reinhardtii]	Unigene71805_A11//2.00E-22//AT5G08180| ribosomal protein L7Ae/L30e/S12e/Gad45 family protein					nr -
Unigene71807_A11	330	0.32	0.92	0.00	1.06	0.52	0.82	11.40	15.07	3.98	1.54E+00	3.23E-01		-8.31E+00	3.88E-01		-1.02E+00	4.23E-01		-3.64E-01	7.55E-01		4.03E-01	1.06E-01		-1.52E+00	2.20E-07	Down	Unigene71807_A11|gi|297845974|ref|XP_002890868.1|/2.00E-44//ATMRP13 [Arabidopsis lyrata subsp. lyrata] >gi|297336710|gb|EFH67127.1| ATMRP13 [Arabidopsis lyrata subsp. lyrata]	Unigene71807_A11//1.00E-45//AT1G30410| ATMRP13; ATPase, coupled to transmembrane movement of substances	Unigene71807_A11//6.00E-43//ES847972		ko02010|ABC transporters		nr +
Unigene71808_A11	331	0.00	8.88	2.25	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	1.01E-16	Up	1.11E+01	3.26E-04	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene71809_A11	331	0.00	3.67	0.32	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.45E-07	Up	8.33E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71809_A11|sp|O00472|ELL2_HUMAN//4.00E-06//RNA polymerase II elongation factor ELL2 OS=Homo sapiens GN=ELL2 PE=1 SV=2				ko03018|RNA degradation		swissprot -
Unigene71811_A11	331	0.00	2.45	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	9.32E-05	Up	1.05E+01	7.44E-03		null	null		null	null		null	null		null	null		Unigene71811_A11|gi|299471625|emb|CBN76847.1|/3.00E-14//RAC, RHO family GTPase [Ectocarpus siliculosus]	Unigene71811_A11//7.00E-15//AT2G44690| ARAC9; GTP binding			ko04145|Phagosome//ko04650|Natural killer cell mediated cytotoxicity		nr -
Unigene71812_A11	331	0.47	6.28	0.48	0.00	0.31	0.27	0.00	0.51	1.44	3.73E+00	1.15E-08	Up	2.53E-02	1.00E+00		8.29E+00	4.53E-01		8.09E+00	4.72E-01		8.98E+00	1.38E-01		1.05E+01	1.14E-03		Unigene71812_A11|gi|224123482|ref|XP_002330325.1|/2.00E-22//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222871360|gb|EEF08491.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene71812_A11//3.00E-12//AT5G61890| AP2 domain-containing transcription factor family protein	Unigene71812_A11//7.00E-18//gi|109887732|gb|DW516701.1|DW516701	AP2-EREBP			nr -
Unigene71813_A11	332	0.00	3.82	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.85E-07	Up	9.65E+00	7.95E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene71815_A11	332	0.00	2.29	0.48	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.75E-04	Up	8.91E+00	2.36E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene71816_A11	332	0.00	5.04	0.32	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.53E-09	Up	8.33E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71816_A11|gi|301113960|ref|XP_002998750.1|/4.00E-35//P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4] >gi|262112051|gb|EEY70103.1| P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]	Unigene71816_A11//3.00E-26//AT4G37640| ACA2 (CALCIUM ATPASE 2); calcium ion transmembrane transporter/ calcium-transporting ATPase/ calmodulin binding					nr -
Unigene71817_A11	333	0.00	3.20	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.80E-06	Up	9.32E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene71818_A11	333	0.00	5.33	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.13E-10	Up	null	null		null	null		null	null		null	null		null	null		Unigene71818_A11|sp|Q6ID09|SARM1_DROME//3.00E-12//Sterile alpha and TIR motif-containing protein 1 OS=Drosophila melanogaster GN=Ect4 PE=2 SV=1						swissprot -
Unigene71819_A11	333	0.00	3.35	2.08	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.99E-06	Up	1.10E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene71819_A11|sp|Q07152|IMDH_DROME//2.00E-12//Inosine-5'-monophosphate dehydrogenase OS=Drosophila melanogaster GN=ras PE=1 SV=1						swissprot +
Unigene7182_A11	1008	7.53	15.78	7.98	11.07	13.49	12.81	0.63	0.21	0.95	1.07E+00	2.26E-13	Up	8.39E-02	7.03E-01		2.86E-01	6.99E-02		2.11E-01	2.33E-01		-1.60E+00	6.27E-02		5.92E-01	3.45E-01		Unigene7182_A11|gi|164605008|dbj|BAF98300.1|/9.00E-81//geranyl-diphosphate synthase [Hevea brasiliensis]	Unigene7182_A11//1.00E-30//AT4G38460| GGR (geranylgeranyl reductase); farnesyltranstransferase	Unigene7182_A11//8.00E-11//TC144366		ko00900|Terpenoid backbone biosynthesis		nr +
Unigene71820_A11	333	0.16	3.80	0.48	0.00	0.21	0.00	0.00	0.13	0.00	4.60E+00	3.52E-06	Up	1.61E+00	5.10E-01		7.69E+00	6.03E-01		null	null		6.97E+00	6.28E-01		null	null									ESTscan +
Unigene71821_A11	333	0.00	2.74	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.60E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71821_A11|sp|O55098|STK10_MOUSE//3.00E-14//Serine/threonine-protein kinase 10 OS=Mus musculus GN=Stk10 PE=1 SV=1						swissprot +
Unigene71822_A11	334	0.00	2.12	0.32	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.30E-04	Up	8.32E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71822_A11|sp|Q9P2E9|RRBP1_HUMAN//6.00E-08//Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4						swissprot +
Unigene71824_A11	334	0.16	5.76	1.12	0.00	0.21	0.00	0.00	0.00	0.00	5.20E+00	1.06E-09	Up	2.83E+00	9.30E-02		7.69E+00	6.03E-01		null	null		null	null		null	null				Unigene71824_A11//4.00E-07//ES820852					
Unigene71825_A11	334	0.00	3.34	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.99E-06	Up	7.32E+00	6.27E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene71827_A11	334	0.00	3.19	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.80E-06	Up	9.32E+00	1.39E-01		null	null		null	null		null	null		null	null									
Unigene71828_A11	334	0.00	25.64	11.64	0.00	0.00	0.00	0.00	0.00	0.00	1.46E+01	5.27E-49	Up	1.35E+01	1.51E-21	Up	null	null		null	null		null	null		null	null									
Unigene71830_A11	335	0.00	5.45	1.91	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.14E-10	Up	1.09E+01	1.15E-03		null	null		null	null		null	null		null	null									
Unigene71832_A11	335	0.00	3.33	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.99E-06	Up	9.90E+00	4.47E-02		null	null		null	null		null	null		null	null									
Unigene71834_A11	335	0.00	4.99	2.07	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.53E-09	Up	1.10E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene71834_A11|gi|10177925|dbj|BAB11336.1|/2.00E-16//NADH dehydrogenase 10.5K chain-like protein [Arabidopsis thaliana] >gi|21593502|gb|AAM65469.1| NADH dehydrogenase 10.5K chain-like protein [Arabidopsis thaliana]	Unigene71834_A11//9.00E-18//AT5G47890| NADH-ubiquinone oxidoreductase B8 subunit, putative			ko00190|Oxidative phosphorylation		nr +
Unigene71835_A11	335	0.00	4.08	1.43	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.77E-08	Up	1.05E+01	7.44E-03		null	null		null	null		null	null		null	null		Unigene71835_A11|gi|8777580|dbj|BAA97098.1|/3.00E-06//unnamed protein product [Arabidopsis thaliana]						nr +

Unigene71836_All	335	0.00	4.99	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.53E-09	Up	9.90E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene71836_All//gi|297605712|ref|NP_001057499.2|//1.00E-07//Os06g0317400 [Oryza sativa Japonica Group] >gi|255676992|dbj|BAF19413.2| Os06g0317400 [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr +
Unigene71837_All	335	0.00	4.08	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.77E-08	Up	1.03E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71837_All//sp|Q0MQJ3|NDUBB_PONPY//8.00E-08//NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11, mitochondrial OS=Pongo pygmaeus GN=NDUFB11 PE=2 SV=1						swissprot +
Unigene71838_All	336	0.00	21.56	9.83	0.00	0.00	0.27	0.00	0.00	0.00	1.44E+01	2.04E-41	Up	1.33E+01	2.92E-18	Up	null	null		8.07E+00	4.72E-01		null	null		null	null		Unigene71838_All//gi|149072011|ref|YP_001293582.1|//2.00E-08//50S ribosomal protein L23 [Rhodomonas salina] >gi|134302962|gb|ABO70766.1| 50S ribosomal protein L23 [Rhodomonas salina]				ko03010|Ribosome		nr +
Unigene71839_All	336	0.00	3.32	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.99E-06	Up	9.89E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene71839_All//sp|P18489|SYB_DROME//7.00E-11//Synaptobrevin OS=Drosophila melanogaster GN=Syb PE=2 SV=3						swissprot +
Unigene7184_All	1568	0.00	0.00	0.00	0.00	0.00	0.00	11.59	10.26	2.85	null	null		null	null		null	null		null	null		-1.76E-01	1.69E-01		-2.03E+00	4.03E-48	Down	Unigene7184_All//gi|224146420|ref|XP_002326001.1|//1.00E-169//GRAS family transcription factor [Populus trichocarpa] >gi|222862876|gb|EEF00383.1| GRAS family transcription factor [Populus trichocarpa]	Unigene7184_All//9.00E-46//AT3G54220| SCR (SCARECROW); protein binding / protein homodimerization/ sequence-specific DNA binding / transcription factor		GRAS			nr +
Unigene71840_All	336	0.00	2.56	0.16	0.00	0.51	1.08	0.00	0.00	0.36	1.13E+01	4.91E-05	Up	7.31E+00	6.27E-01		9.00E+00	2.26E-01		1.01E+01	2.37E-02		null	null		8.47E+00	2.42E-01		Unigene71840_All//gi|15236212|ref|NP_192199.1|//8.00E-38//early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana]	Unigene71840_All//2.00E-35//AT4G02900| early-responsive to dehydration protein-related / ERD protein-related	Unigene71840_All//1.00E-96//gi|73943660|gb|DT526968.1|DT526968				nr +
Unigene71842_All	336	0.00	3.17	2.85	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.80E-06	Up	1.15E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene71842_All//gi|115446749|ref|NP_001047154.1|//6.00E-12//Os02g0562700 [Oryza sativa Japonica Group] >gi|250682258|gb|AAO72678.1| gamma hydroxybutyrate dehydrogenase-like protein [Oryza sativa Japonica Group] >gi|113536685|dbj|BAF09068.1| Os02g0562700 [Oryza sativa Japonica Group]	Unigene71842_All//1.00E-12//AT3G25530| GLYR1 (GLYOXYLATE REDUCTASE 1); 3-hydroxybutyrate dehydrogenase/ phosphogluconate dehydrogenase (decarboxylating)			ko00280|Valine, leucine and isoleucine degradation		nr -
Unigene71844_All	336	0.00	3.02	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.22E-06	Up	1.03E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71844_All//gi|299472976|emb|CBN77377.1|//5.00E-08//similar to bleomycin hydrolase [Ectocarpus siliculosus]						nr +
Unigene71845_All	336	0.00	6.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	5.63E-13	Up	null	null		null	null		null	null		null	null		null	null		Unigene71845_All//sp|Q5ZMM5|ZN706_CHICK//3.00E-22//Zinc finger protein 706 OS=Gallus gallus GN=ZNF706 PE=4 SV=1						swissprot +
Unigene71846_All	337	0.00	5.26	0.32	0.30	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.13E-10	Up	8.30E+00	3.92E-01		-8.21E+00	3.10E-01		-8.21E+00	3.95E-01		null	null		null	null										
Unigene71847_All	337	0.00	3.91	1.26	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.49E-07	Up	1.03E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71847_All//gi|300265098|gb|EFJ49291.1|//1.00E-07//extracellular matrix glycoprotein pherophorin-V32 [Volvox carteri f. nagariensis]				ko03040|Spliceosome		nr +
Unigene71849_All	337	0.00	12.33	9.48	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	1.15E-23	Up	1.32E+01	1.15E-17	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene7185_All	490	1.92	2.28	1.41	6.20	2.32	1.20	0.52	0.34	0.16	2.43E-01	6.82E-01		-4.44E-01	5.54E-01		-1.42E+00	3.26E-05	Down	-2.37E+00	8.02E-09	Down	-6.02E-01	6.47E-01		-1.67E+00	2.56E-01				Unigene7185_All//3.00E-30//ES813027					
Unigene71850_All	337	0.00	4.51	1.26	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.09E-08	Up	1.03E+01	1.37E-02		null	null		null	null		null	null		null	null										ESTscan -
Unigene71851_All	338	0.00	2.40	1.26	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	9.32E-05	Up	1.03E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71851_All//gi|3777559|gb|AAC64934.1|//2.00E-12//collagen-like [Griffithsia japonica]	Unigene71851_All//5.00E-05//AT1G76010| nucleic acid binding			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene71852_All	339	0.00	1.94	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	6.21E-04	Up	null	null		null	null		null	null		null	null		null	null										ESTscan -
Unigene71853_All	339	0.00	8.97	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	2.67E-17	Up	9.62E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71853_All//gi|300262824|gb|EFJ47028.1|//2.00E-14//transcription factor jumonji domain-containing protein [Volvox carteri f. nagariensis]				ko03022|Basal transcription factors		nr +
Unigene71854_All	339	0.00	3.29	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.99E-06	Up	7.30E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71854_All//gi|224003975|ref|XP_002291659.1|//5.00E-10//Rad23 like protein [Thalassiosira pseudonana CCMP1335] >gi|220973435|gb|EED91766.1| Rad23 like protein [Thalassiosira pseudonana CCMP1335]	Unigene71854_All//7.00E-09//AT1G16190| DNA repair protein RAD23, putative			ko04141|Protein processing in endoplasmic reticulum//ko03420|Nucleotide excision repair		nr +
Unigene71855_All	339	2.47	1.94	0.00	0.00	0.20	0.00	0.00	0.00	0.00	-3.46E-01	6.12E-01		-1.13E+01	1.19E-04	Down	7.67E+00	6.03E-01		null	null		null	null		null	null		Unigene71855_All//gi|124359343|gb|ABB28505.2|//4.00E-08//RNA-directed DNA polymerase (Reverse transcriptase): Polynucleotidyl transferase, Ribonuclease H fold [Medicago truncatula]	Unigene71855_All//5.00E-08//AT5G42905| nucleic acid binding / ribonuclease H					nr -
Unigene71859_All	340	0.00	3.43	2.04	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.04E-06	Up	1.10E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene71859_All//gi|225459609|ref|XP_002285871.1|//1.00E-32//PREDICTED: similar to PBC1 (20S proteasome beta subunit C1); peptidase isoform 1 [Vitis vinifera]	Unigene71859_All//1.00E-31//AT1G21720| PBC1 (PROTEASOME BETA SUBUNIT C1); peptidase/ threonine-type endopeptidase			ko03050|Proteasome		nr +
Unigene7186_All	520	108.36	92.96	96.46	183.93	147.48	151.12	107.65	66.79	38.23	-2.21E-01	2.07E-03		-1.68E-01	2.98E-02		-3.19E-01	3.74E-11		-2.83E-01	3.18E-08		-6.89E-01	1.10E-26		-1.49E+00	1.06E-95	Down	Unigene7186_All//gi|224135763|ref|XP_002322154.1|//8.00E-51//nucleobase ascorbate transporter [Populus trichocarpa] >gi|222869150|gb|EEF06281.1| nucleobase ascorbate transporter [Populus trichocarpa]	Unigene7186_All//4.00E-50//AT5G62890| permease, putative	Unigene7186_All//0.00E+00//TC145435				nr +
Unigene71861_All	340	0.00	5.66	0.63	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.72E-11	Up	9.29E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71861_All//gi|115435450|ref|NP_001042483.1|//2.00E-21//Os01g0229100 [Oryza sativa Japonica Group] >gi|113532014|dbj|BAF04397.1| Os01g0229100 [Oryza sativa Japonica Group]	Unigene71861_All//2.00E-16//AT5G25757| unknown protein					nr +
Unigene71862_All	341	0.00	3.42	0.94	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.04E-06	Up	9.87E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene71862_All//sp|Q8MZR6|HYEP1_CTEFE//4.00E-22//Juvenile hormone epoxide hydrolase 1 OS=Ctenocephalides felis GN=EH1 PE=1 SV=3						swissprot -
Unigene71863_All	341	0.00	3.27	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.99E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene71863_All//gi|1346180|sp|P49310.1|GRP1_SINAL//4.00E-14//RecName: Full=Glycine-rich RNA-binding protein GRP1A >gi|496233|gb|AAA59212.1| homology with RNA-binding proteins in meristematic tissue [Sinapis alba]				ko03040|Spliceosome		nr +
Unigene71864_All	341	0.00	2.08	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	3.30E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71864_All//sp|Q9VGX3|FAU_DROME//2.00E-46//Protein anoxia up-regulated OS=Drosophila melanogaster GN=fau PE=1 SV=3						swissprot +
Unigene71866_All	342	0.00	6.52	1.25	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.09E-12	Up	1.03E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71866_All//gi|159465002|ref|XP_001690724.1|//7.00E-37//histone H2B [Chlamydomonas reinhardtii] >gi|159466710|ref|XP_001691541.1| histone H2B [Chlamydomonas reinhardtii] >gi|1708105|sp|P54346.3|H2B3_CHLRE RecName: Full=Histone H2B.3; AltName: Full=H2B-III >gi|571477|gb|AAA98450.1| histone H2B [Chlamydomonas reinhardtii] >gi|158269141|gb|EDO95788.1| histone H2B [Chlamydomonas reinhardtii] >gi|158278887|gb|EDP04649.1| histone H2B [Chlamydomonas reinhardtii]	Unigene71866_All//4.00E-32//AT5G39910| HTB4; DNA binding					nr -
Unigene71867_All	342	0.00	5.04	2.02	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.97E-10	Up	1.10E+01	6.13E-04	Up	null	null		null	null		null	null		null	null										
Unigene71868_All	342	0.00	4.00	0.16	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.77E-08	Up	7.28E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71868_All//gi|15227225|ref|NP_179836.1|//2.00E-22//UCP5 (UNCOUPLING PROTEIN 5); binding [Arabidopsis thaliana] >gi|90567689|emb|CAJ86454.1| mitochondrial dicarboxylate carrier [Arabidopsis thaliana]	Unigene71868_All//6.00E-24//AT2G22500| UCP5 (UNCOUPLING PROTEIN 5); binding			ko04146|Peroxisome		nr +
Unigene71870_All	343	0.00	2.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.75E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71870_All//gi|300163388|gb|EFJ29999.1|//8.00E-08//ubiquitin-protein ligase, UPL3 [Selaginella moellendorffii]	Unigene71870_All//9.00E-07//AT4G38600| KAK (KAKTUS); ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene71871_All	343	0.00	5.91	1.55	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.53E-11	Up	1.06E+01	4.01E-03		null	null		null	null		null	null		null	null										
Unigene71873_All	343	0.00	6.80	2.17	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.90E-13	Up	1.11E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene71873_All//sp|P27779|CUP7_DROME//3.00E-11//Pupal cuticle protein Edg-78E OS=Drosophila melanogaster GN=Edg78E PE=1 SV=1						swissprot +
Unigene71874_All	344	0.00	3.24	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.99E-06	Up	8.86E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71874_All//gi|301120159|ref|XP_002907807.1|//5.00E-16//choline dehydrogenase, putative [Phytophthora infestans T30-4] >gi|262106319|gb|EEY64371.1| choline dehydrogenase, putative [Phytophthora infestans T30-4]						nr -

Unigene71876_All	344	0.00	3.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.80E-06	Up	null	null		null	null		null	null		null	null		null	null		Unigene71876_All//gi|298707301|emb|CBJ25928.1|//7.00E-39//Casein kinase (serine/threonine/tyrosine protein kinase) [Ectocarpus siliculosus]	Unigene71876_All//3.00E-34//AT3G23340| ck110 (Casein Kinase I-like 10); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase					nr +
Unigene71877_All	344	0.00	3.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.80E-06	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene71878_All	344	0.00	4.12	0.93	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.05E-08	Up	9.86E+00	4.47E-02		null	null		null	null		null	null													ESTscan +
Unigene7188_All	359	69.37	144.25	89.74	133.21	158.94	104.29	186.79	300.72	82.23	1.06E+00	4.50E-41	Up	3.71E-01	1.63E-04		2.55E-01	1.23E-04		-3.53E-01	2.13E-06		6.87E-01	1.88E-50		-1.18E+00	3.42E-80	Down	Unigene7188_All//gi|166865124|gb|BZ01817.1|/1.00E-68//cinnamyl alcohol dehydrogenase [Gossypium hirsutum]	Unigene7188_All//3.00E-45//AT3G19450| ATCAD4; cinnamyl-alcohol dehydrogenase	Unigene7188_All//0.00E+00//TC162490		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene71881_All	345	0.00	2.79	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.37E-05	Up	7.27E+00	6.27E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene71883_All	345	0.00	3.38	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.04E-06	Up	9.59E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71883_All//gi|37932204|gb|AF72958.1|/7.00E-58/26S proteasome subunit 7-like protein [Lactuca sativa]	Unigene71883_All//4.00E-48//AT1G53750| RPT1A (REGULATORY PARTICLE TRIPLE-A 1A); ATPase	Unigene71883_All//3.00E-08//CO076615		ko03050|Proteasome		nr +
Unigene71884_All	345	0.00	3.67	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.85E-07	Up	9.59E+00	7.95E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene71885_All	345	0.00	3.08	1.70	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.80E-06	Up	1.07E+01	2.16E-03		null	null		null	null		null	null													
Unigene71886_All	346	2.57	16.84	2.00	2.02	1.29	3.79	1.10	1.45	1.04	2.71E+00	1.51E-17	Up	-3.62E-01	6.32E-01		-6.40E-01	4.54E-01		9.09E-01	1.35E-01		3.98E-01	6.52E-01		-8.58E-02	9.43E-01			Unigene71886_All//1.00E-07//ES846114					
Unigene71887_All	346	0.00	6.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	7.94E-12	Up	null	null		null	null		null	null		null	null		null	null		Unigene71887_All//sp|Q9JLR9|HIG1A_MOUSE//1.00E-18//HIG1 domain family member 1A OS=Mus musculus GN=Higd1a PE=2 SV=1						swissprot +
Unigene71888_All	346	0.00	3.37	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.04E-06	Up	9.85E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene71888_All//gi|75282567|sp|Q43492.2|BSZ7_HORVU//1.00E-11//RecName: Full=Serpin-Z7; AltName: Full=HorvuZ7; AltName: Full=BSZ7 >gi|1197577|emb|CAA64599.1| serpin [Hordeum vulgare subsp. vulgare]	Unigene71888_All//6.00E-09//AT1G64030| serpin family protein / serine protease inhibitor family protein					nr +
Unigene71889_All	347	0.00	3.21	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.99E-06	Up	9.26E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71889_All//gi|300146120|gb|EFJ12792.1|/3.00E-40//RUB1-conjugating enzyme 2, E2 [Selaginella moellendorffii]	Unigene71889_All//1.00E-39//AT4G36800| RCE1 (RUB1 CONJUGATING ENZYME 1); NEDD8 ligase/ small conjugating protein ligase	Unigene71889_All//4.00E-07//TC174393		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene7189_All	1587	0.73	0.35	0.34	0.35	0.11	0.09	37.46	24.68	11.85	-1.05E+00	1.01E-01		-1.11E+00	9.93E-02		-1.67E+00	9.26E-02		-2.02E+00	7.04E-02		-6.02E-01	1.83E-22		-1.66E+00	1.83E-118	Down	Unigene7189_All//gi|119331584|gb|ABL63118.1|/5.00E-94//AT-hook DNA-binding protein [Catharanthus roseus]	Unigene7189_All//5.00E-55//AT2G45430| DNA-binding protein-related	Unigene7189_All//8.00E-12//gi|48789593|gb|CO090907.1|CO090907				nr -
Unigene71890_All	347	0.00	2.92	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.22E-06	Up	null	null		null	null		null	null		null	null		null	null									
Unigene71893_All	348	0.00	2.33	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	9.32E-05	Up	7.26E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71893_All//gi|300264245|gb|EFJ48442.1|//3.00E-46//eukaryotic translation initiation factor 2 gamma [Volvox carteri f. nagariensis]	Unigene71893_All//3.00E-43//AT2G18720| GTP binding / GTPase/ serine-type peptidase/ translation factor, nucleic acid binding					nr +
Unigene71895_All	348	0.00	7.43	3.52	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.05E-14	Up	1.18E+01	9.10E-07	Up	null	null		null	null		null	null		null	null		Unigene71895_All//gi|159470941|ref|XP_001693615.1|/4.00E-21//peptidyl-prolyl cis-trans isomerase, FKBP-type [Chlamydomonas reinhardtii] >gi|158283118|gb|EDF08869.1| peptidyl-prolyl cis-trans isomerase, FKBP-type [Chlamydomonas reinhardtii]	Unigene71895_All//7.00E-17//AT5G48570| peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative					nr -
Unigene71896_All	348	0.00	4.08	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.05E-08	Up	7.26E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71896_All//sp|Q9LL78|HECD1_HUMAN//7.00E-41//E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=2						swissprot +
Unigene71897_All	349	0.00	1.89	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	6.21E-04	Up	9.25E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71897_All//gi|148612407|gb|ABQ86119.1|//2.00E-20//alpha-gliadin [Aegilops tauschii]				ko03022|Basal transcription factors		nr +
Unigene71898_All	349	0.00	3.34	0.31	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.04E-06	Up	8.25E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71898_All//gi|195619838|gb|ACG31749.1|//7.00E-20//serine-threonine kinase receptor-associated protein [Zea mays]	Unigene71898_All//7.00E-20//AT1G62730| transducin family protein / WD-40 repeat family protein					nr +
Unigene71899_All	350	0.00	4.05	1.52	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.05E-08	Up	1.06E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71899_All//gi|254558248|gb|ACT67906.1|//2.00E-45//heat shock protein 70 [Ulva prolifera]	Unigene71899_All//8.00E-37//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene71899_All//1.00E-07//BG440611		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -
Unigene719_All	1324	2.53	1.65	1.53	4.63	3.23	3.96	7.98	3.60	4.42	-6.20E-01	6.63E-02		-7.27E-01	4.07E-02		-5.21E-01	2.32E-02		-2.26E-01	4.02E-01		-1.15E+00	2.06E-12	Down	-8.52E-01	3.71E-08		Unigene719_All//gi|297809525|ref|XP_002872646.1|//1.00E-145//esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318483|gb|EFH48905.1| esterase/lipase/thioesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene719_All//2.00E-143//AT4G12230| esterase/lipase/thioesterase family protein	Unigene719_All//0.00E+00//gi|78333598|gb|DT553872.1|DT553872				nr +
Unigene7190_All	1798	0.29	0.56	0.89	0.78	0.29	0.25	22.32	26.22	7.22	9.54E-01	1.65E-01		1.61E+00	5.21E-03		-1.43E+00	8.64E-03		-1.63E+00	5.90E-03		2.33E-01	9.60E-04		-1.63E+00	6.13E-78	Down	Unigene7190_All//gi|39573544|dbj|BAD04063.1|//0.00E+00//high-affinity nitrate transporter [Prunus persica] >gi|88675349|dbj|BAD22822.1| nitrate transporter [Prunus persica]	Unigene7190_All//0.00E+00//AT3G45060| ATNRT2.6; nitrate transmembrane transporter	Unigene7190_All//2.00E-12//CB074791				nr +
Unigene71900_All	350	0.00	4.49	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.69E-09	Up	9.25E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71900_All//sp|B0G163|EXOC5_DICDI//3.00E-06//Exocyst complex component 5 OS=Dictyostelium discoideum GN=exoc5 PE=3 SV=1						swissprot -
Unigene71902_All	351	0.00	5.20	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.14E-10	Up	9.25E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71902_All//gi|159484270|ref|XP_001700181.1|//2.00E-06//PP2A-twin subunit [Chlamydomonas reinhardtii] >gi|158272497|gb|EDO98296.1| PP2A-twin subunit [Chlamydomonas reinhardtii]	Unigene71902_All//2.00E-06//AT1G51690| ATB ALPHA; nucleotide binding / protein phosphatase type 2A regulator					nr -
Unigene71903_All	351	0.00	3.46	0.61	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.45E-07	Up	9.25E+00	1.39E-01		null	null		null	null		null	null		null	null									
Unigene71904_All	351	0.00	3.90	0.91	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.77E-08	Up	9.83E+00	4.47E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene71906_All	351	0.00	5.20	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.14E-10	Up	null	null		null	null		null	null		null	null		null	null									ESTscan -
Unigene71907_All	351	0.00	1.88	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	6.21E-04	Up	8.83E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71907_All//gi|301106871|ref|XP_002902518.1|//3.00E-06//protocadherin-like protein [Phytophthora infestans T30-4] >gi|262098392|gb|EEY56414.1| protocadherin-like protein [Phytophthora infestans T30-4]						nr +
Unigene71908_All	352	0.00	7.63	2.27	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.80E-15	Up	1.11E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene71908_All//gi|300259627|gb|EFJ43853.1|//5.00E-07//DP transcription factor [Volvox carteri f. nagariensis]						nr +
Unigene7191_All	370	22.34	39.03	31.23	34.33	37.69	39.91	86.05	49.48	41.99	8.05E-01	6.66E-08		4.83E-01	5.58E-03		1.35E-01	4.48E-01		2.17E-01	1.80E-01		-7.98E-01	7.38E-20		-1.04E+00	3.48E-31	Down	Unigene7191_All//gi|15241574|ref|NP_196446.1|//3.00E-48//YLS8; catalytic [Arabidopsis thaliana] >gi|11692866|gb|AAG40036.1|AF324685_1 AT5g08290 [Arabidopsis thaliana] >gi|14030633|gb|AAK52991.1|AF375407_1 AT5g08290/F8L15_20 [Arabidopsis thaliana] >gi|13122294|dbj|BAB32888.1| Diml homolog [Arabidopsis thaliana] >gi|17978897|gb|AAL47418.1| AT5g08290/F8L15_20 [Arabidopsis thaliana]	Unigene7191_All//1.00E-49//AT5G08290| YLS8; catalytic	Unigene7191_All//0.00E+00//gi|13246811|gb|BE055159.2|BE055159		ko03040|Spliceosome		nr -
Unigene71910_All	352	0.00	5.18	2.42	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.14E-10	Up	1.12E+01	9.00E-05	Up	null	null		null	null		null	null		null	null		Unigene71910_All//sp|Q865F1|MTP_PIG//4.00E-09//Microsomal triglyceride transfer protein large subunit OS=Sus scrofa GN=MTTP PE=2 SV=1						swissprot +
Unigene71911_All	352	0.00	7.63	1.06	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.80E-15	Up	1.00E+01	2.49E-02		null	null		null	null		null	null		null	null									
Unigene71913_All	353	2.08	8.33	3.32	2.68	6.15	5.76	0.60	3.32	4.85	2.00E+00	1.24E-06	Up	6.78E-01	3.04E-01		1.20E+00	5.78E-03		1.10E+00	1.69E-02		2.47E+00	1.92E-04	Up	3.02E+00	1.16E-07	Up	Unigene71913_All//gi|9295706|gb|AAF87012.1|AC005292_21//6.00E-19//F26F24.20 [Arabidopsis thaliana]	Unigene71913_All//2.00E-20//AT1G23330| unknown protein	Unigene71913_All//3.00E-63//TC161440				nr -
Unigene71914_All	354	0.00	2.29	0.30	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	9.32E-05	Up	8.23E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71914_All//gi|195620532|gb|ACG32096.1|//4.00E-34//UTP--glucose-1-phosphate uridylyltransferase [Zea mays]	Unigene71914_All//3.00E-34//AT5G17310| UTP--glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, putative			ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00040|Pentose and glucuronate interconversions//ko00052|Galactose metabolism		nr -
Unigene71915_All	354	0.00	3.58	0.45	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.85E-07	Up	8.82E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71915_All//gi|17064740|gb|AAL32524.1|//4.00E-30//ATP-dependent RNA helicase-like protein [Arabidopsis thaliana] >gi|21387105|gb|AAM47956.1| ATP-dependent RNA helicase-like protein [Arabidopsis thaliana]	Unigene71915_All//2.00E-31//AT3G58510| DEAD box RNA helicase, putative (RH11)					nr -
Unigene71916_All	354	0.00	2.15	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.75E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71916_All//gi|224006319|ref|XP_002292120.1|//3.00E-17//probable trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972639|gb|EED90971.1| probable trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]						nr +
Unigene71917_All	355	0.00	2.71	1.20	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.37E-05	Up	1.02E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71917_All//gi|224589270|gb|ACN59485.1|//1.00E-16//serpin 3 [Triticum aestivum]	Unigene71917_All//6.00E-08//AT2G26390| serpin, putative / serine protease inhibitor, putative					nr +
Unigene71918_All	355	0.00	5.42	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.72E-11	Up	null	null		null	null		null	null		null	null		null	null		Unigene71918_All//gi|14091836|gb|AAK53839.1|AC011806_16//9.00E-10//Putative cullin [Oryza sativa]	Unigene71918_All//2.00E-10//AT4G02570| ATCUL1 (ARABIDOPSIS THALIANA CULLIN 1); protein binding			ko04120|Ubiquitin mediated proteolysis		nr +
Unigene71919_All	356	0.00	2.28	0.45	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	9.32E-05	Up	8.81E+00	2.36E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene7192_All	295	2.31	2.40	0.36	6.75	2.45	2.60	148.20	220.74	177.05	6.07E-02	9.57E-01		-2.68E+00	1.69E-02		-1.46E+00	8.85E-04	Down	-1.38E+00	3.19E-03		5.75E-01	1.29E-22		2.57E-01	6.87E-05		Unigene7192_All//gi|188509943|gb|ACD56629.1|//2.00E-07//putative WRKY transcription factor [Gossypium raimondii]						nr +

Unigene71920_All	357	0.00	1.99	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	3.30E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene71920_All//gi|42567214|ref|NP_194570.2|//9.00E-34//aminotransferase-related [Arabidopsis thaliana]	Unigene71920_All//4.00E-35//AT4G28410| aminotransferase-related			ko00270|Cysteine and methionine metabolism//ko00360|Phenylalanine metabolism//ko00380|Tryptophan metabolism//ko00350|Tyrosine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis//ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis//ko00966|Glucosinolate biosynthesis//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis//ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene71921_All	357	1.17	11.64	0.90	0.28	0.10	1.52	0.00	0.00	0.00	3.31E+00	2.68E-15	Up	-3.90E-01	7.17E-01		-1.53E+00	5.84E-01		2.44E+00	4.41E-02		null	null		null	null					Unigene71921_All//5.00E-56//gi|109872227|gb|DW501202.1|DW501202					
Unigene71922_All	357	0.00	2.98	1.19	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.80E-06	Up	1.02E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71922_All//gi|115475493|ref|NP_001061343.1|//9.00E-12//Os08g0242800 [Oryza sativa Japonica Group] >gi|30698490|dbj|BAC76602.1| Sig6 [Oryza sativa Japonica Group] >gi|40253642|dbj|BAD05586.1| Sig6, plastid RNA polymerase sigma factor [Oryza sativa Japonica Group] >gi|40253689|dbj|BAD05631.1| Sig6, plastid RNA polymerase sigma factor [Oryza sativa Japonica Group] >gi|113623312|dbj|BAF23257.1| Os08g0242800 [Oryza sativa Japonica Group]	Unigene71922_All//2.00E-11//AT2G36990| SIGF (RNA POLYMERASE SIGMA-SUBUNIT F); DNA binding / DNA-directed RNA polymerase/ sigma factor/ transcription factor		Sigma70-like			nr +
Unigene71923_All	357	0.00	6.81	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	7.72E-14	Up	1.00E+01	2.49E-02		null	null		null	null		null	null		null	null		Unigene71923_All//gi|300156657|gb|EFJ23285.1|//1.00E-48//rab family GTPase [Selaginella moellendorffii]	Unigene71923_All//6.00E-46//AT4G17530| ATRAB1C; GTP binding					nr -
Unigene71925_All	358	0.00	2.26	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	9.31E-05	Up	7.22E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71925_All//gi|301100738|ref|XP_002899458.1|//4.00E-31//flavodoxin-like protein [Phytophthora infestans T30-4] >gi|262103766|gb|EEY61818.1| flavodoxin-like protein [Phytophthora infestans T30-4]	Unigene71925_All//1.00E-23//AT5G54500| FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor					nr -
Unigene71926_All	358	0.00	4.95	0.30	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	4.13E-10	Up	8.22E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71926_All//gi|111609767|gb|ABH11436.1|//7.00E-42//cytosolic glucose-6-phosphate isomerase [Pavlova lutheri]	Unigene71926_All//1.00E-23//AT5G42740| glucose-6-phosphate isomerase, cytosolic (PGIC)			ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene71927_All	358	0.00	8.35	3.27	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	5.18E-17	Up	1.17E+01	1.77E-06	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene71928_All	358	0.00	4.81	0.45	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.97E-10	Up	8.80E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71928_All//gi|115485231|ref|NP_001067759.1|//2.00E-29//Os11g0312400 [Oryza sativa Japonica Group] >gi|585338|sp|Q08480.1|KAD2_ORYSJ RecName: Full=Adenylate kinase B; Short=AK B; AltName: Full=ATP-AMP transphosphorylase B >gi|391879|dbj|BAA01181.1| adenylate kinase-b [Oryza sativa] >gi|62734015|gb|AAX96124.1| adenylate kinase b (ec 2.7.4.3) (atp-amp transphosphorylase) [Oryza sativa Japonica Group] >gi|113644981|dbj|BAF28122.1| Os11g0312400 [Oryza sativa Japonica Group]	Unigene71928_All//2.00E-30//AT5G63400| ADK1 (ADENYLATE KINASE 1); ATP binding / adenylate kinase/ nucleobase, nucleoside, nucleotide kinase/ nucleotide kinase/ phosphotransferase, phosphate group as acceptor			ko00230|Purine metabolism		nr +
Unigene71929_All	359	0.00	4.38	1.19	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.69E-09	Up	1.02E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene71929_All//gi|27311771|gb|AA000851.1|//8.00E-14//Unknown protein [Arabidopsis thaliana] >gi|30725542|gb|AAP37783.1| At5g61270 [Arabidopsis thaliana]						nr +
Unigene71930_All	359	0.00	3.11	0.30	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.99E-06	Up	8.21E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71930_All//gi|115435908|ref|NP_001042712.1|//2.00E-09//Os01g0273000 [Oryza sativa Japonica Group] >gi|113532243|dbj|BAF04626.1| Os01g0273000 [Oryza sativa Japonica Group]					ko03050|Proteasome//ko03440|Homologous recombination		nr +
Unigene71931_All	360	0.00	2.53	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	2.60E-05	Up	7.21E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71931_All//gi|1335862|gb|AAC49294.1|//4.00E-27//clathrin heavy chain [Glycine max]	Unigene71931_All//1.00E-31//AT3G08530| clathrin heavy chain, putative			ko04144|Endocytosis		nr -
Unigene71932_All	360	0.00	5.35	3.99	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.72E-11	Up	1.20E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene71932_All//gi|112950081|gb|ABI26643.1|//1.00E-16//aspartic proteinase [Cucumis sativus]	Unigene71932_All//1.00E-14//AT1G62290| aspartyl protease family protein					nr -
Unigene71933_All	361	0.00	6.04	0.59	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.11E-12	Up	9.20E+00	1.39E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene71935_All	361	0.00	4.35	0.30	0.55	0.00	0.50	0.00	0.12	0.00	1.21E+01	5.69E-09	Up	8.20E+00	3.92E-01		-9.11E+00	8.39E-02		-1.42E-01	9.34E-01		6.86E+00	6.28E-01		null	null					Unigene71935_All//5.00E-25//gi|21092896|gb|BQ405209.1|BQ405209					
Unigene71936_All	361	0.00	2.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.91E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71936_All//gi|110225684|ref|YP_665889.1|//2.00E-34//NADH dehydrogenase subunit 7 [Mesostigma viride] >gi|17222555|gb|AAL36728.1|AF353399_8 NADH dehydrogenase subunit 7 [Mesostigma viride]	Unigene71936_All//1.00E-30//ATMG00510| NADH dehydrogenase subunit 7			ko00190|Oxidative phosphorylation		nr +
Unigene71937_All	361	0.00	6.04	1.18	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.11E-12	Up	1.02E+01	1.37E-02		null	null		null	null		null	null		null	null										
Unigene71938_All	362	0.00	2.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	2.60E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71938_All//sp|088907|PIAS1_MOUSE|/5.00E-32//E3 SUMO-protein ligase PIAS1 OS=Mus musculus GN=Pias1 PE=1 SV=2						swissprot +
Unigene71939_All	362	0.00	3.50	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.83E-07	Up	7.20E+00	6.27E-01		null	null		null	null		null	null		null	null										
Unigene7194_All	871	0.24	0.12	1.35	7.72	5.61	2.85	0.49	0.00	0.18	-1.05E+00	5.63E-01		2.48E+00	1.35E-03		-4.60E-01	3.73E-02		-1.44E+00	7.66E-10	Down	-8.92E+00	3.25E-03		-1.41E+00	1.73E-01		Unigene7194_All//gi|30683971|ref|NP_193455.2|//1.00E-102//ATMAP70-5 (microtubule-associated proteins 70-5); microtubule binding [Arabidopsis thaliana] >gi|29028914|gb|AAO64836.1| At4g17220 [Arabidopsis thaliana] >gi|76058020|emb|CAJ31082.1| 70 kDa microtubule associated protein Type 5 [Arabidopsis thaliana]	Unigene7194_All//3.00E-95//AT4G17220| ATMAP70-5 (microtubule-associated proteins 70-5); microtubule binding	Unigene7194_All//2.00E-32//gi|84145930|gb|DN760172.1|DN760172				nr +
Unigene71940_All	362	0.00	3.08	0.44	0.00	0.00	0.00	0.00	0.00	0.22	1.16E+01	1.99E-06	Up	8.79E+00	2.36E-01		null	null		null	null		null	null		7.78E+00	4.01E-01		Unigene71940_All//sp|Q5R6D1|CATB_PONAB|/2.00E-11//Cathepsin B OS=Pongo abelii GN=CTSB PE=2 SV=1						swissprot -
Unigene71941_All	362	0.00	4.06	0.29	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.11E-08	Up	8.20E+00	3.92E-01		null	null		null	null		null	null		null	null										
Unigene71942_All	362	0.00	2.24	0.29	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	9.31E-05	Up	8.20E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71942_All//gi|15239024|ref|NP_196695.1|//2.00E-21//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|8953396|emb|CAB96669.1| separation anxiety protein-like [Arabidopsis thaliana] >gi|28416617|gb|AAO42839.1| At5g11340 [Arabidopsis thaliana] >gi|110743265|dbj|BAE99523.1| separation anxiety protein - like [Arabidopsis thaliana]	Unigene71942_All//6.00E-22//AT5G11340| GCN5-related N-acetyltransferase (GNAT) family protein					nr -
Unigene71943_All	363	0.00	9.07	0.73	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	9.62E-19	Up	9.52E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71943_All//gi|298712421|emb|CBJ33199.1|//3.00E-07//histone H1 [Ectocarpus siliculosus]						nr +
Unigene71944_All	363	0.00	7.26	0.44	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	5.44E-15	Up	8.78E+00	2.36E-01		null	null		null	null		null	null		null	null										
Unigene71945_All	363	0.00	1.81	0.44	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	6.21E-04	Up	8.78E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71945_All//gi|14091665|gb|AAK53813.1|AF370443_1//4.00E-17//Ran binding protein-1 [Solanum lycopersicum]	Unigene71945_All//4.00E-16//AT5G58590| RANBP1 (RAN BINDING PROTEIN 1); protein binding					nr -
Unigene71946_All	364	0.00	7.10	2.63	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.05E-14	Up	1.14E+01	2.45E-05	Up	null	null		null	null		null	null		null	null										
Unigene71947_All	364	0.00	3.34	1.46	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	5.45E-07	Up	1.05E+01	4.01E-03		null	null		null	null		null	null		null	null										
Unigene71948_All	365	0.00	9.58	2.19	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	6.73E-20	Up	1.11E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene71948_All//sp|B0BNA5|COTL1_RAT|/2.00E-12//Coactosin-like protein OS=Rattus norvegicus GN=Cotl1 PE=1 SV=1						swissprot +
Unigene7195_All	848	2.22	4.96	7.16	0.94	0.65	0.37	0.05	0.10	0.00	1.16E+00	1.37E-04	Up	1.69E+00	5.26E-10	Up	-5.33E-01	5.10E-01		-1.33E+00	1.06E-01		9.83E-01	7.29E-01		-5.64E+00	6.05E-01		Unigene7195_All//gi|15222901|ref|NP_177718.1|//6.00E-90//family II extracellular lipase 3 (EXL3) [Arabidopsis thaliana] >gi|75162254|sp|Q94CH6.1|EXL3_ARATH RecName: Full=GDSL esterase/lipase EXL3; AltName: Full=Family II extracellular lipase 3; Short=Family II lipase EXL3; Flags: Precursor >gi|15054386|gb|AAK30018.1| family II lipase EXL3 [Arabidopsis thaliana]	Unigene7195_All//9.00E-91//AT1G75900| family II extracellular lipase 3 (EXL3)	Unigene7195_All//0.00E+00//TC179294				nr +
Unigene71950_All	366	294.34	89.16	157.86	3378.66	3041.60	2615.90	422.80	386.33	666.05	-1.72E+00	1.90E-179	Down	-8.99E-01	4.70E-63		-1.52E-01	1.39E-33		-3.69E-01	3.15E-163		-1.30E-01	6.19E-04		6.56E-01	1.87E-106		Unigene71950_All//gi|21322711|emb|CAD22154.1|//8.00E-25//pherophorin-dcl protein [Volvox carteri f. nagariensis]		Unigene71950_All//8.00E-61//DW226698		ko03040|Spliceosome		nr +
Unigene71951_All	366	0.00	4.01	0.29	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.11E-08	Up	8.18E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71951_All//gi|124361010|gb|ABN08982.1|//4.00E-24//HEAT [Medicago truncatula]	Unigene71951_All//8.00E-25//AT5G19820| emb2734 (embryo defective 2734); binding / lyase					nr +
Unigene71952_All	366	0.00	6.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.09E-12	Up	null	null		null	null		null	null		null	null		null	null		Unigene71952_All//sp|Q9VAJ4|OB99A_DROME|/2.00E-06//General odorant-binding protein 99a OS=Drosophila melanogaster GN=Obp99a PE=1 SV=2						swissprot +

Unigene71953_All	367	0.00	2.35	0.15	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.91E-05	Up	7.18E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71953_All//sp|Q7YU24|MARF_DROME//2.00E-55//Transmembrane GTPase Marf OS=Drosophila melanogaster GN=Marf PE=1 SV=1						swissprot +
Unigene71954_All	367	0.00	2.90	1.31	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.80E-06	Up	1.04E+01	7.44E-03		null	null		null	null		null	null		null	null		Unigene71954_All//gi|27311839|gb|AAO0885.1|//4.00E-08//Unknown protein [Arabidopsis thaliana]						nr +
Unigene71955_All	367	0.00	2.49	2.03	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	2.60E-05	Up	1.10E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene71955_All//sp|Q14515|SPRL1_HUMAN//2.00E-51//SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2						swissprot -
Unigene71956_All	367	0.00	2.90	1.31	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.80E-06	Up	1.04E+01	7.44E-03		null	null		null	null		null	null		null	null		Unigene71956_All//gi|27544008|dbj|BAC54828.1|//8.00E-62//vacuolar processing enzyme-1b [Nicotiana tabacum]	Unigene71956_All//8.00E-63//AT4G32940| GAMMA-VPE (GAMMA VACUOLAR PROCESSING ENZYME); cysteine-type endopeptidase	Unigene71956_All//7.00E-43//TC175201				nr -
Unigene71957_All	367	0.00	7.59	2.18	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	7.42E-16	Up	1.11E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene71957_All//gi|3893085|emb|CAA10192.1|//2.00E-06//glycine-rich protein 2 [Cicer arietinum]				ko03040|Spliceosome		nr -
Unigene71959_All	368	0.00	8.81	3.76	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	1.87E-18	Up	1.19E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene71959_All//gi|11131946|sp|Q92ZN7.1|CALR_EUGGR//1.00E-20//RecName: Full=Calreticulin; Flags: Precursor >gi|3970687|emb|CAA70945.1| calreticulin precursor [Euglena gracilis]	Unigene71959_All//1.00E-19//AT1G56340| CRT1 (CALRETICULIN 1); calcium ion binding / unfolded protein binding			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr +
Unigene71962_All	369	0.00	3.57	1.44	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.49E-07	Up	1.05E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71962_All//sp|Q9V496|APLP_DROME//5.00E-44//Apolipophorins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2						swissprot -
Unigene71963_All	370	0.00	2.19	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	9.31E-05	Up	7.17E+00	6.27E-01		null	null		null	null		null	null										ESTscan -
Unigene71964_All	370	0.14	2.33	1.87	0.00	0.28	0.12	0.00	0.00	0.00	4.04E+00	4.20E-04	Up	3.73E+00	3.99E-03		8.13E+00	4.53E-01		6.93E+00	6.88E-01		null	null		null	null		Unigene71964_All//gi|226459082|gb|EEH56378.1|//1.00E-16//ubiquinol:cytochrome c oxidoreductase 14 kDa subunit-containing protein [Micromonas pusilla CCMP1545]						nr -
Unigene71965_All	371	0.00	6.42	0.29	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.50E-13	Up	8.17E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71965_All//gi|110617800|gb|ABG78615.1|//1.00E-17//J-domain protein [Triticum aestivum]	Unigene71965_All//7.00E-13//AT1G76700| DNAJ heat shock N-terminal domain-containing protein			ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene71966_All	371	0.00	15.43	7.18	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	1.13E-32	Up	1.28E+01	1.07E-14	Up	null	null		null	null		null	null		null	null		Unigene71966_All//gi|224006323|ref|XP_002292122.1|//2.00E-06//trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972641|gb|EED90973.1| trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]						nr -
Unigene71967_All	371	0.00	3.41	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.85E-07	Up	9.17E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71967_All//gi|55742813|ref|NP_446447.2|//2.00E-16//D-beta-hydroxybutyrate dehydrogenase, mitochondrial [Rattus norvegicus] >gi|55250770|gb|AAH85916.1| 3-hydroxybutyrate dehydrogenase, type 1 [Rattus norvegicus] >gi|149060752|gb|EDM11466.1| 3-hydroxybutyrate dehydrogenase, type 1, isoform CRA_a [Rattus norvegicus]	Unigene71967_All//1.00E-09//AT3G03330| short-chain dehydrogenase/reductase (SDR) family protein			ko00903|Limonene and pinene degradation//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr +
Unigene71968_All	371	0.00	4.78	2.30	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.13E-10	Up	1.12E+01	9.00E-05	Up	null	null		null	null		null	null		null	null								
Unigene71969_All	371	0.00	4.64	4.88	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.97E-10	Up	1.23E+01	5.68E-10	Up	null	null		null	null		null	null		null	null		Unigene71969_All//gi|159466194|ref|XP_001691294.1|//8.00E-11//plastid ribosomal protein L21 [Chlamydomonas reinhardtii] >gi|158279266|gb|EDP05027.1| plastid ribosomal protein L21 [Chlamydomonas reinhardtii]	Unigene71969_All//9.00E-09//AT4G30930| NFD1 (NUCLEAR FUSION DEFECTIVE 1); RNA binding / structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene7197_All	552	2.84	0.73	2.41	3.16	3.99	4.01	0.08	0.08	0.22	-1.95E+00	7.99E-04	Down	-2.38E-01	6.42E-01		3.38E-01	4.92E-01		3.44E-01	4.79E-01		-1.71E-02	9.99E-01		1.50E+00	5.57E-01		Unigene7197_All//gi|224112158|ref|XP_002332820.1|//6.00E-24//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834208|gb|EEE72685.1| cc-nbs-lrr resistance protein [Populus trichocarpa]						nr +
Unigene71970_All	371	0.00	5.19	2.30	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	5.72E-11	Up	1.12E+01	9.00E-05	Up	null	null		null	null		null	null		null	null		Unigene71970_All//sp|O44441|ATIF2_CAEEL//2.00E-20//ATPase inhibitor mai-2, mitochondrial OS=Caenorhabditis elegans GN=mai-2 PE=2 SV=1						swissprot +
Unigene71971_All	373	0.00	3.53	1.71	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.49E-07	Up	1.07E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene71971_All//sp|P69907|HBA_PANTR//1.00E-52//Hemoglobin subunit alpha OS=Pan troglodytes GN=HBA1 PE=1 SV=2						swissprot +
Unigene71972_All	373	0.00	1.49	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	2.16E-03		1.10E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene71972_All//gi|60543120|dbj|BAD90809.1|//6.00E-62//histone 3 [Conocephalum conicum]	Unigene71972_All//8.00E-61//AT4G40030| histone H3.2	Unigene71972_All//3.00E-23//CD485766				nr -
Unigene71973_All	374	0.00	2.30	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.91E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71973_All//sp|Q9VC57|ATLAS_DROME//2.00E-06//Atlastin OS=Drosophila melanogaster GN=atl PE=1 SV=1						swissprot +
Unigene71974_All	374	0.00	55.82	20.65	0.00	0.00	0.00	0.00	0.00	0.00	1.58E+01	3.93E-120	Up	1.43E+01	3.43E-43	Up	null	null		null	null		null	null		null	null		Unigene71974_All//sp|Q9VQ66|NPLP4_DROME//8.00E-13//Neuropeptide-like 4 OS=Drosophila melanogaster GN=Nplp4 PE=1 SV=1						swissprot -
Unigene71977_All	374	0.00	2.85	0.28	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.79E-06	Up	8.15E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene71977_All//sp|Q8IVP5|FUND1_HUMAN//9.00E-12//FUN14 domain-containing protein 1 OS=Homo sapiens GN=FUNDC1 PE=1 SV=1						swissprot +
Unigene71978_All	374	0.00	2.17	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	9.31E-05	Up	1.10E+01	3.26E-04	Up	null	null		null	null		null	null		null	null								ESTscan -
Unigene71979_All	374	0.00	3.25	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	5.45E-07	Up	1.10E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene71979_All//gi|297851050|ref|XP_002893406.1|//4.00E-21//B5 #6 [Arabidopsis lyrata subsp. lyrata] >gi|297339248|gb|EFH69665.1| B5 #6 [Arabidopsis lyrata subsp. lyrata]	Unigene71979_All//2.00E-21//AT1G26340| CBS-A (CYTOCHROME B5 ISOFORM A); heme binding			ko00910|Nitrogen metabolism		nr +
Unigene7198_All	593	5.12	2.65	0.36	2.35	4.94	2.21	0.00	0.00	0.00	-9.50E-01	8.13E-03		-3.83E+00	3.56E-12	Down	1.07E+00	2.85E-03		-9.08E-02	8.82E-01		null	null		null	null		Unigene7198_All//gi|115452977|ref|NP_001050089.1|//2.00E-22//Os03g0345300 [Oryza sativa Japonica Group] >gi|113548560|dbj|BAF12003.1| Os03g0345300 [Oryza sativa Japonica Group]	Unigene7198_All//6.00E-22//AT1G47980| unknown protein	Unigene7198_All//7.00E-78//TC156087				nr -
Unigene71980_All	374	0.00	1.90	0.43	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	3.30E-04	Up	8.74E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene71980_All//gi|300158422|gb|EFJ25045.1|//9.00E-13//ubiquitin-protein ligase, UPL3 [Selaginella moellendorffii]	Unigene71980_All//2.00E-07//AT4G38600| KAK (KAKTUS); ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene71981_All	375	0.00	5.00	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.10E-10	Up	9.15E+00	1.39E-01		null	null		null	null		null	null		null	null								ESTscan -
Unigene71982_All	375	0.28	7.16	2.13	0.27	0.37	0.24	0.00	0.00	0.00	4.68E+00	9.56E-13	Up	2.93E+00	5.05E-03		4.67E-01	8.75E-01		-1.41E-01	9.48E-01		null	null		null	null		Unigene71982_All//gi|30575840|gb|AAP32921.1|//6.00E-11//MYB1 [Paraboea crassifolia]						nr -
Unigene71983_All	375	0.00	3.51	1.42	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.49E-07	Up	1.05E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71983_All//gi|1703457|sp|P54209.1|ATC1_DUNBI//1.00E-38//RecName: Full=Cation-transporting ATPase CA1 >gi|11036646|emb|CAA63790.1| CA1; P-type ATPase [Dunaliella bioculata]	Unigene71983_All//3.00E-36//AT1G10130| ECA3 (ENDOPLASMIC RETICULUM-TYPE CALCIUM-TRANSPORTING ATPASE 3); calcium-transporting ATPase/ calmodulin binding / manganese-transporting ATPase/ peroxidase					nr +
Unigene71984_All	376	0.00	3.64	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.77E-08	Up	null	null		null	null		null	null		null	null		null	null								
Unigene71985_All	376	0.00	3.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.04E-06	Up	null	null		null	null		null	null		null	null		null	null								ESTscan +
Unigene71986_All	376	0.00	6.47	0.71	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.72E-14	Up	9.47E+00	7.95E-02		null	null		null	null		null	null		null	null		Unigene71986_All//gi|242091515|ref|XP_002441590.1|//6.00E-06//hypothetical protein SORBIDRAFT_09g029900 [Sorghum bicolor] >gi|241946875|gb|EES20020.1| hypothetical protein SORBIDRAFT_09g029900 [Sorghum bicolor]						nr -
Unigene71987_All	376	0.00	1.89	1.13	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	3.30E-04	Up	1.01E+01	1.37E-02		null	null		null	null		null	null		null	null								
Unigene71988_All	376	0.00	2.29	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.91E-05	Up	1.03E+01	7.44E-03		null	null		null	null		null	null		null	null								ESTscan +
Unigene71989_All	377	0.00	3.63	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.77E-08	Up	1.03E+01	7.44E-03		null	null		null	null		null	null		null	null		Unigene71989_All//gi|29839695|sp|Q92U25.1|MPPA1_ARATH//6.00E-06//RecName: Full=Probable mitochondrial-processing peptidase subunit alpha-1; AltName: Full=Alpha-MPP 1; Flags: Precursor >gi|4220446|gb|AAD12673.1| Strong similarity to gi|2062155 T02004.2 mitochondrial processing peptidase alpha subunit precusor isolog from Arabidopsis thaliana BAC gb|AC001645. ESTs gb|218504 and gb|AA395715 come from this gene	Unigene71989_All//3.00E-07//AT1G51980| mitochondrial processing peptidase alpha subunit, putative					nr -
Unigene7199_All	738	0.92	0.96	0.65	1.49	2.05	1.29	1.89	0.40	1.78	6.07E-02	9.57E-01		-5.05E-01	5.82E-01		4.67E-01	4.26E-01		-2.09E-01	7.42E-01		-2.25E+00	9.69E-05	Down	-8.58E-02	8.63E-01		Unigene7199_All//gi|18396347|ref|NP_564283.1|//3.00E-62//NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding [Arabidopsis thaliana] >gi|9802536|gb|AAF99738.1|AC004557_17 F17L21.25 [Arabidopsis thaliana] >gi|16226498|gb|AAL16183.1|AF428415_1 At1g27460/F17L21_26 [Arabidopsis thaliana] >gi|33589668|gb|AAQ22600.1| At1g27460/F17L21_26 [Arabidopsis thaliana]	Unigene7199_All//1.00E-56//AT1G27460| NPGR1 (NO POLLEN GERMINATION RELATED 1); calmodulin binding	Unigene7199_All//3.00E-145//TC162398				nr -
Unigene71990_All	377	0.00	4.97	4.10	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.10E-10	Up	1.20E+01	1.65E-08	Up	null	null		null	null		null	null		null	null								

Unigene71991_All	378	0.00	3.08	1.41	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.04E-06	Up	1.05E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene71991_All//gi|167113|gb|AAA21751.1|//2.00E-21//aldose reductase-related protein [Bromus inermis]	Unigene71991_All//2.00E-19//AT3G53880| aldo/keto reductase family protein			ko00010|Glycolysis / Gluconeogenesis//ko00051|Fructose and mannose metabolism//ko00561|Glycerolipid metabolism//ko00591|Linoleic acid metabolism//ko00650|Butanoate metabolism		nr +
Unigene71992_All	378	0.00	6.70	0.85	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	2.05E-14	Up	9.72E+00	4.47E-02		null	null		null	null		null	null		null	null									
Unigene71993_All	378	0.00	4.42	0.85	0.13	0.00	0.12	0.00	0.00	0.00	1.21E+01	1.53E-09	Up	9.72E+00	4.47E-02		-7.04E+00	5.48E-01		-1.41E-01	9.48E-01		null	null		null	null				Unigene71993_All//4.00E-146//DR462180				
Unigene71994_All	379	0.00	1.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	3.30E-04	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene71995_All	379	0.00	2.41	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.60E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene71995_All//gi|116047953|gb|ABJ53202.1|//5.00E-10//myosin VIII-B [Nicotiana benthamiana]	Unigene71995_All//1.00E-07//AT5G54280| ATM2 (ARABIDOPSIS THALIANA MYOSIN 2); motor					nr +
Unigene71996_All	380	0.00	2.80	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.79E-06	Up	7.13E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene71996_All//sp|Q54QQ1|PKG2_DICDI//6.00E-08//Serine/threonine-protein kinase phg2 OS=Dictyostelium discoideum GN=phg2 PE=1 SV=1						swissprot +
Unigene71998_All	380	0.00	6.13	2.80	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.90E-13	Up	1.15E+01	6.61E-06	Up	null	null		null	null		null	null		null	null		Unigene71998_All//gi|255085716|ref|XP_002505289.1|//5.00E-06//predicted protein [Micromonas sp. RCC299] >gi|226520558|gb|ACO66547.1| predicted protein [Micromonas sp. RCC299]	Unigene71998_All//2.00E-05//AT4G04780| MED21 (MEDIATOR 21)					nr +
Unigene71999_All	380	0.00	3.33	0.56	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.85E-07	Up	9.13E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene71999_All//gi|15228869|ref|NP_191183.1|//1.00E-34//CCH (COPPER CHAPERONE); copper chaperone [Arabidopsis thaliana] >gi|13605758|gb|AAK32872.1|AF36186 0_1 AT3g56240/F18021_200 [Arabidopsis thaliana] >gi|3168840|gb|AAC33510.1| copper homeostasis factor [Arabidopsis thaliana] >gi|7572922|emb|CAB87423.1| copper homeostasis factor [Arabidopsis thaliana] >gi|17978907|gb|AAL47423.1| AT3g56240/F18021_200 [Arabidopsis thaliana] >gi|21553785|gb|AAM62878.1| copper homeostasis factor [Arabidopsis thaliana]	Unigene71999_All//4.00E-33//AT3G56240| CCH (COPPER CHAPERONE); copper chaperone	Unigene71999_All//6.00E-25//TC169277				nr -
Unigene72_All	248	0.00	0.00	3.01	2.01	2.22	2.19	2.73	0.51	2.25	null	null		1.16E+01	3.26E-04	Up	1.45E-01	9.05E-01		1.22E-01	9.21E-01		-2.43E+00	7.76E-03		-2.79E-01	6.89E-01									
Unigene720_All	3177	1.93	2.36	2.08	3.15	2.82	2.43	2.99	2.05	1.24	2.93E-01	1.91E-01		1.09E-01	6.53E-01		-1.61E-01	4.38E-01		-3.75E-01	4.36E-02		-5.45E-01	1.01E-03		-1.27E+00	1.85E-13	Down	Unigene720_All//gi|15234483|ref|NP_192960.1|//1.00E-137//esterase/lipase/thioesterase family protein [Arabidopsis thaliana]	Unigene720_All//6.00E-136//AT4G12230| esterase/lipase/thioesterase family protein	Unigene720_All//0.00E+00//TC168517				nr +
Unigene7200_All	1147	2.83	0.44	1.30	7.99	6.36	2.80	0.00	0.18	0.00	-2.68E+00	5.20E-10	Down	-1.12E+00	2.13E-03		-3.28E-01	8.67E-02		-1.52E+00	3.05E-14	Down	7.51E+00	7.84E-02		null	null		Unigene7200_All//gi|223452288|gb|ACM89472.1|//6.60/FERONIA receptor-like kinase [Glycine max]	Unigene7200_All//5.00E-50//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene7200_All//5.00E-40//TC133874				nr -
Unigene72000_All	381	0.00	1.99	0.84	0.00	0.36	0.24	0.00	0.00	0.00	1.10E+01	1.75E-04	Up	9.71E+00	4.47E-02		8.50E+00	3.17E-01		7.89E+00	4.72E-01		null	null		null	null									ESTscan -
Unigene72001_All	381	0.00	2.66	1.82	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	7.22E-06	Up	1.08E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene72001_All//gi|1703227|sp|P52894.1|ALA2_HORVU//2.00E-30//RecName: Full=Alanine aminotransferase 2; Short=ALAAT-2; AltName: Full=Glutamic--pyruvic transaminase 2; AltName: Full=Glutamate pyruvate transaminase 2; Short=GPT; AltName: Full=Glutamic--alanine transaminase 2 >gi|469148|emb|CAA81231.1| alanine aminotransferase [Hordeum vulgare subsp. vulgare]	Unigene72001_All//1.00E-23//AT1G23310| GGT1 (GLUTAMATE:GLYOXYLATE AMINOTRANSFERASE); L-alanine:2-oxoglutarate aminotransferase/ glycine:2-oxoglutarate aminotransferase			ko00710|Carbon fixation in photosynthetic organisms//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene72003_All	381	0.00	15.16	2.94	0.00	0.00	0.00	0.00	0.00	0.00	1.39E+01	5.79E-33	Up	1.15E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene72003_All//sp|Q62425|NDUA4_MOUSE//8.00E-18//NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Mus musculus GN=Ndufa4 PE=1 SV=2						swissprot -
Unigene72004_All	381	0.00	17.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	4.83E-37	Up	null	null		null	null		null	null		null	null		null	null		Unigene72004_All//gi|187610414|gb|ACD13461.1|//2.00E-58//raffionse synthase 2 [Glycine max]	Unigene72004_All//8.00E-50//AT5G40390| SIP1 (seed imbibition 1-like); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene72004_All//2.00E-30//TC164748		ko00052|Galactose metabolism		nr -
Unigene72005_All	381	0.00	2.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.37E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene72005_All//sp|Q9V5M3|LOLA6_DROME//1.00E-15//Longitudinals lacking protein, isoforms N/0/W/X/Y OS=Drosophila melanogaster GN=lola PE=1 SV=3						swissprot +
Unigene72006_All	382	0.00	10.88	0.28	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.15E-23	Up	8.12E+00	3.92E-01		null	null		null	null		null	null		null	null									
Unigene72008_All	383	0.00	3.97	1.67	0.00	0.00	0.24	0.00	0.00	0.21	1.20E+01	1.09E-08	Up	1.07E+01	1.15E-03		null	null		7.88E+00	4.72E-01		null	null		7.70E+00	4.01E-01		Unigene72008_All//gi|145346330|ref|XP_001417642.1|//2.00E-32//Ribosomal protein L27, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901] >gi|144577870|gb|ABO95935.1| Ribosomal protein L27, component of cytosolic 80S ribosome and 60S large subunit [Ostreococcus lucimarinus CCE9901]	Unigene72008_All//8.00E-26//AT2G32220| 60S ribosomal protein L27 (RPL27A)			ko03010|Ribosome		nr -
Unigene72009_All	383	0.00	3.18	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.45E-07	Up	7.12E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene72009_All//sp|Q24524|SING_DROME//2.00E-47//Protein singed OS=Drosophila melanogaster GN=sn PE=2 SV=1						swissprot -
Unigene7201_All	1036	1.77	0.10	0.82	2.64	3.89	1.61	0.29	0.28	0.31	-4.18E+00	2.18E-08	Down	-1.10E+00	3.06E-02		5.56E-01	6.91E-02		-7.13E-01	6.30E-02		-1.68E-02	1.02E+00		1.07E-01	9.45E-01		Unigene7201_All//gi|15225286|ref|NP_180201.1|//1.00E-173//ER (ERECTA); transmembrane receptor protein kinase [Arabidopsis thaliana] >gi|75319658|sp|Q42371.1|ERECT_ARATH RecName: Full=LRR receptor-like serine/threonine-protein kinase ERECTA; AltName: Full=Protein QUANTITATIVE RESISTANCE TO PLECTOSPHAERELLA 1; AltName: Full=Protein QUANTITATIVE RESISTANCE TO RALSTONIA SOLANACEARUM 1; AltName: Full=Protein TRANSPIRATION EFFICIENCY 1; Flags: Precursor >gi|1345132|gb|AAC49302.1| ERECTA [Arabidopsis thaliana] >gi|1389566|dbj|BAA11869.1| receptor protein kinase [Arabidopsis thaliana] >gi|224589525|gb|ACN59296.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene7201_All//4.00E-156//AT2G26330| ER (ERECTA); transmembrane receptor protein kinase	Unigene7201_All//4.00E-130//CO092850		ko04626|Plant-pathogen interaction		nr -
Unigene72010_All	383	0.00	3.04	0.97	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.04E-06	Up	9.93E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72010_All//sp|P54674|PI3K2_DICDI//6.00E-08//Phosphatidylinositol 3-kinase 2 OS=Dictyostelium discoideum GN=pik8 PE=2 SV=2						swissprot -
Unigene72011_All	384	356.03	110.05	248.78	645.90	1004.00	510.56	0.99	0.54	0.21	-1.69E+00	3.70E-222	Down	-5.17E-01	1.72E-30		6.36E-01	1.12E-152		-3.39E-01	2.49E-28		-8.65E-01	4.41E-01		-2.26E+00	6.49E-02		Unigene72011_All//gi|155966601|gb|ABU41235.1|//3.00E-58//xyloglucan endotransglycosylase [Gossypium hirsutum] >gi|166343773|gb|ABY86634.1| xyloglucan endotransglycosylase/hydrolase [Gossypium arboreum]	Unigene72011_All//1.00E-39//AT4G37800| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene72011_All//0.00E+00//TC133020				nr -
Unigene72012_All	384	0.00	2.11	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	9.31E-05	Up	7.12E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene72012_All//gi|301119353|ref|XP_002907404.1|//3.00E-35//T-complex protein 1 subunit theta [Phytophthora infestans T30-4] >gi|262105916|gb|EE163968.1| T-complex protein 1 subunit theta [Phytophthora infestans T30-4]	Unigene72012_All//1.00E-26//AT3G03960| chaperonin, putative					nr +
Unigene72013_All	385	0.00	5.53	0.97	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.10E-12	Up	9.92E+00	2.48E-02		null	null		null	null		null	null		null	null									
Unigene72014_All	385	0.00	3.16	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.45E-07	Up	9.70E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene72014_All//sp|Q9QAE5|TSSP_MOUSE//7.00E-06//Thymus-specific serine protease OS=Mus musculus GN=Prss16 PE=2 SV=1						swissprot +
Unigene72015_All	386	0.00	3.41	1.52	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.49E-07	Up	1.06E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene72015_All//gi|192910876|gb|ACF06546.1|//1.00E-23//ubiquitin-conjugating enzyme 1 [Elaeis guineensis]	Unigene72015_All//2.00E-24//AT1G16890| ubiquitin-conjugating enzyme, putative			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene7202_All	328	6.70	8.03	6.98	1.97	2.20	0.00	0.00	0.00	0.00	2.62E-01	5.19E-01		5.93E-02	8.94E-01		1.59E-01	8.68E-01		-1.09E+01	3.90E-04	Down	null	null		null	null				Unigene7202_All//2.00E-21//TC151003				
Unigene72020_All	388	0.00	3.00	1.10	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.04E-06	Up	1.01E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene72020_All//gi|298706779|emb|CBJ29702.1|//4.00E-06//conserved unknown protein [Ectocarpus siliculosus]						nr -
Unigene72022_All	390	0.00	59.50	1.64	0.00	0.18	3.01	0.00	0.00	0.00	1.59E+01	1.27E-133	Up	1.07E+01	1.15E-03		7.46E+00	6.03E-01		1.16E+01	5.32E-07	Up	null	null		null	null		Unigene72022_All//gi|187610414|gb|ACD13461.1|//7.00E-29//raffionse synthase 2 [Glycine max]	Unigene72022_All//6.00E-20//AT5G40390| SIP1 (seed imbibition 1-like); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene72022_All//1.00E-10//DW481975		ko00052|Galactose metabolism		nr +
Unigene72023_All	390	0.00	7.15	3.41	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	7.42E-16	Up	1.17E+01	2.39E-07	Up	null	null		null	null		null	null		null	null									ESTscan -

Unigene72024_All	390	0.00	3.77	1.91	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.11E-08	Up	1.09E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene72024_All//gi|224014228|ref|XP_002296777.1|//4.00E-25//metalloprotease [Thalassiosira pseudonana CCMP1335] >gi|220968632|gb|EED86978.1| metalloprotease [Thalassiosira pseudonana CCMP1335]						nr -
Unigene72025_All	390	0.00	2.73	0.55	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.79E-06	Up	9.09E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72025_All//gi|299469797|emb|CBN76651.1|//5.00E-07//non ribosomal peptide synthase [Ectocarpus siliculosus]						nr -
Unigene72026_All	390	0.00	2.86	0.14	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.99E-06	Up	7.09E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene72026_All//gi|75313848|sp|Q9ST58.1|SPZ1C_WHEAT//3.00E-15//RecName: Full=Serpin-Z1C; AltName: Full=TriaoZ1c; AltName: Full=WSZ1c >gi|5734504|emb|CAB52709.1| serpin [Triticum aestivum]	Unigene72026_All//5.00E-13//AT1G47710| serpin, putative / serine protease inhibitor, putative					nr +
Unigene72027_All	390	0.00	8.96	3.82	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	6.73E-20	Up	1.19E+01	3.21E-08	Up	null	null		null	null		null	null		null	null		Unigene72027_All//sp|P06703|S10A6_HUMAN//8.00E-45//Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1						swissprot -
Unigene72028_All	391	0.00	8.29	1.36	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.87E-18	Up	1.04E+01	4.01E-03		null	null		null	null		null	null		null	null										ESTscan +
Unigene72029_All	391	0.00	3.50	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.77E-08	Up	8.67E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene72029_All//sp|Q9VCA8|ANKIM_DROME//7.00E-41//Ankyrin repeat and KH domain-containing protein mask OS=Drosophila melanogaster GN=mask PE=1 SV=2						swissprot -
Unigene7203_All	447	0.94	2.38	1.43	3.01	6.01	7.38	0.85	0.37	0.27	1.35E+00	5.00E-02		6.10E-01	5.09E-01		9.98E-01	8.33E-03		1.29E+00	2.02E-04	Up	-1.19E+00	3.09E-01		-1.67E+00	1.40E-01		Unigene7203_All//gi|22528850|gb|AAB62848.1|//1.00E-06//contains region of similarity to DNA binding protein [Arabidopsis thaliana]	Unigene7203_All//2.00E-10//AT2G46535| unknown protein					nr +
Unigene72030_All	391	0.00	8.55	4.63	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	4.94E-19	Up	1.22E+01	5.68E-10	Up	null	null		null	null		null	null		null	null		Unigene72030_All//sp|O46585|COX4I_PITP1//3.00E-28//Cytochrome c oxidase subunit 4 isoform 1, mitochondrial (Fragment) OS=Pithecia pithecia GN=COX4I1 PE=3 SV=1						swissprot -
Unigene72031_All	392	0.00	3.23	2.72	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.85E-07	Up	1.14E+01	6.60E-06	Up	null	null		null	null		null	null		null	null		Unigene72031_All//gi|3914431|sp|O24362.1|PSA3_SPIOL//3.00E-25//RecName: Full=Proteasome subunit alpha type-3; AltName: Full=20S proteasome alpha subunit G; AltName: Full=20S proteasome subunit alpha-7; AltName: Full=Proteasome component C8 >gi|2283802|dbj|BAA21651.1| 26S proteasome alpha subunit [Spinacia oleracea]	Unigene72031_All//5.00E-26//AT2G27020| PAG1; endopeptidase/ peptidase/ threonine-type endopeptidase			ko03050|Proteasome		nr +
Unigene72032_All	392	0.00	3.23	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.85E-07	Up	9.89E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72032_All//gi|42568925|ref|NP_178502.2|//2.00E-06//meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana] >gi|79321702|ref|NP_001031318.1| meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana]						nr +
Unigene72033_All	393	0.00	2.45	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.37E-05	Up	1.07E+01	1.15E-03		null	null		null	null		null	null		null	null										ESTscan +
Unigene72035_All	393	0.00	3.74	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.10E-08	Up	9.89E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72035_All//gi|260513739|gb|ACX42581.1|//2.00E-08//low molecular weight glutenin subunit [Aegilops umbellulata]						nr -
Unigene72036_All	394	0.00	3.22	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.85E-07	Up	9.08E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72036_All//sp|Q54UW4|Y0777_DICDI//1.00E-06//Bromodomain-containing protein DDB_G0280777 OS=Dictyostelium discoideum GN=DDB_G0280777 PE=4 SV=1						swissprot -
Unigene72037_All	394	0.27	5.14	0.00	0.00	0.17	0.00	1.29	1.38	0.40	4.28E+00	3.01E-09	Up	-8.05E+00	3.88E-01		7.45E+00	6.03E-01		null	null		9.88E-02	9.21E-01		-1.67E+00	7.77E-02		Unigene72037_All//gi|291360649|gb|ADD97801.1|//2.00E-15//pathogenesis-related protein 1 [Musa AAB Group]	Unigene72037_All//2.00E-12//AT2G14610| PR1 (PATHOGENESIS-RELATED GENE 1)			ko04626|Plant-pathogen interaction		nr +
Unigene72038_All	394	0.00	2.57	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	7.22E-06	Up	8.66E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene72038_All//sp|Q02818|NUCB1_HUMAN//3.00E-13//Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4						swissprot -
Unigene72039_All	394	0.00	3.34	0.41	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.49E-07	Up	8.66E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene72039_All//gi|301112192|ref|XP_002905175.1|//2.00E-33//cell division cycle protein 20 [Phytophthora infestans T30-4] >gi|262095505|gb|EEY53557.1| cell division cycle protein 20 [Phytophthora infestans T30-4]	Unigene72039_All//7.00E-32//AT4G22910| FZR2 (FIZZY-RELATED 2); signal transducer			ko04120|Ubiquitin mediated proteolysis		nr +
Unigene72040_All	395	0.00	2.69	0.13	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.79E-06	Up	7.07E+00	6.27E-01		null	null		null	null		null	null		null	null										
Unigene72041_All	396	0.00	3.58	0.13	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.05E-08	Up	7.07E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene72041_All//gi|15234749|ref|NP_194775.1|//5.00E-06//glycine-rich protein [Arabidopsis thaliana] >gi|7269947|emb|CAB79764.1| glycine-rich protein [Arabidopsis thaliana]						nr -
Unigene72042_All	397	0.00	5.11	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.53E-11	Up	9.39E+00	7.94E-02		null	null		null	null		null	null		null	null										ESTscan -
Unigene72043_All	397	0.00	3.96	2.41	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.68E-09	Up	1.12E+01	2.45E-05	Up	null	null		null	null		null	null		null	null										
Unigene72044_All	397	0.00	3.19	2.28	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	2.85E-07	Up	1.12E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene72044_All//gi|297800550|ref|XP_002868159.1|//6.00E-33//AT3g06720/F3E22_14 [Arabidopsis lyrata subsp. lyrata] >gi|297313965|gb|EFH44418.1| AT3g06720/F3E22_14 [Arabidopsis lyrata subsp. lyrata]	Unigene72044_All//3.00E-34//AT4G16143| IMPA-2 (IMPORTIN ALPHA ISOFORM 2); binding / protein transporter					nr +
Unigene72046_All	398	0.00	6.37	1.34	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.05E-14	Up	1.04E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene72046_All//sp|O43776|SYNC_HUMAN//3.00E-22//Asparagine|-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1						swissprot +
Unigene72047_All	399	0.00	4.06	0.27	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.96E-09	Up	8.06E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene72047_All//gi|28974492|gb|AAO61642.1|//1.00E-17//NAD-dependent isocitrate dehydrogenase alpha subunit [Brassica napus] >gi|28974494|gb|AAO61643.1| NAD-dependent isocitrate dehydrogenase alpha subunit [Brassica napus] >gi|28974496|gb|AAO61644.1| NAD-dependent isocitrate dehydrogenase alpha subunit [Brassica napus]	Unigene72047_All//1.00E-13//AT5G03290| isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative			ko00020|Citrate cycle (TCA cycle)		nr +
Unigene72048_All	400	0.00	4.31	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.97E-10	Up	8.64E+00	2.36E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene72050_All	400	0.00	2.66	0.53	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.79E-06	Up	9.06E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72050_All//sp|O70468|MYPC3_MOUSE//3.00E-08//Myosin-binding protein C, cardiac-type OS=Mus musculus GN=Mybpc3 PE=2 SV=1						swissprot +
Unigene72051_All	401	0.00	4.30	0.27	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.97E-10	Up	8.05E+00	3.92E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene72052_All	401	0.00	4.42	0.53	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	4.13E-10	Up	9.05E+00	1.39E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene72053_All	402	0.00	6.93	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	7.42E-16	Up	1.10E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene72053_All//gi|159462450|ref|XP_001689455.1|//1.00E-15//peroxiredoxin, type II [Chlamydomonas reinhardtii] >gi|158283443|gb|EDP09193.1| peroxiredoxin, type II [Chlamydomonas reinhardtii]	Unigene72053_All//5.00E-14//AT1G60740| peroxiredoxin type 2, putative			ko04146|Peroxisome		nr -
Unigene72054_All	402	0.00	4.29	1.32	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.97E-10	Up	1.04E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene72054_All//sp|Q95241|A4_SAISC//1.00E-36//Amyloid beta A4 protein OS=Saimiri sciureus GN=APP PE=2 SV=1						swissprot +
Unigene72055_All	403	0.00	5.03	2.51	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.53E-11	Up	1.13E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene72055_All//gi|298712066|emb|CBJ26646.1|//1.00E-27//beta chain succinyl-coa synthetase synthetase [Ectocarpus siliculosus]	Unigene72055_All//1.00E-24//AT2G20420| succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative			ko00020|Citrate cycle (TCA cycle)//ko00640|Propanoate metabolism		nr -
Unigene72056_All	404	2.72	3.26	3.56	7.64	3.49	5.37	5.86	2.59	1.68	2.62E-01	6.27E-01		3.88E-01	5.06E-01		-1.13E+00	6.90E-04	Down	-5.11E-01	1.66E-01		-1.18E+00	1.66E-03		-1.81E+00	4.17E-06	Down	Unigene72056_All//gi|15241121|ref|NP_200420.1|//4.00E-58//COX15 (cytochrome c oxidase 15) [Arabidopsis thaliana]	Unigene72056_All//2.00E-59//AT5G36090| COX15 (cytochrome c oxidase 15)	Unigene72056_All//0.00E+00//TC147653		ko00190|Oxidative phosphorylation//ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene72057_All	404	0.00	3.51	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.05E-08	Up	8.04E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene72057_All//gi|300266284|gb|EFJ50472.1|//4.00E-11//Bax inhibitor-1 [Volvox carteri f. nagariensis]						nr -
Unigene72058_All	404	0.00	2.01	0.66	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	9.31E-05	Up	9.36E+00	7.94E-02		null	null		null	null		null	null		null	null		Unigene72058_All//gi|133711722|gb|AB036543.1|//2.00E-39//plastid enolase [Helianthus annuus]	Unigene72058_All//2.00E-35//AT1G74030| enolase, putative	Unigene72058_All//1.00E-07//TC143279		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation		nr -
Unigene72059_All	405	0.00	2.50	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	7.22E-06	Up	9.62E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene72059_All//gi|298709041|emb|CBJ30991.1|//2.00E-06//conserved unknown protein [Ectocarpus siliculosus]						nr +
Unigene72060_All	405	0.00	2.88	2.76	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.04E-06	Up	1.14E+01	3.42E-06	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene72061_All	406	0.00	4.24	1.05	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.96E-10	Up	1.00E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene72061_All//sp|P82119|CU06_BLACR//7.00E-15//Cuticle protein 6 OS=Blaberus craniifer PE=1 SV=1						swissprot +
Unigene72062_All	406	0.00	6.86	1.18	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	7.42E-16	Up	1.02E+01	7.44E-03		null	null		null	null		null	null		null	null										
Unigene72063_All	407	0.00	5.98	2.36	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.72E-14	Up	1.12E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene72063_All//sp|Q9NHA8|BGBP3_DROME//3.00E-19//Gram-negative bacteria-binding protein 3 OS=Drosophila melanogaster GN=GNBP3 PE=1 SV=2						swissprot +
Unigene72064_All	407	0.00	5.73	3.27	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.90E-13	Up	1.17E+01	2.39E-07	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene72065_All	407	0.00	6.72	1.31	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.44E-15	Up	1.04E+01	4.01E-03		null	null		null	null		null	null		null	null										ESTscan +

Unigene72066_All	408	0.00	3.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.05E-08	Up	null	null		null	null		null	null		null	null		null	null		Unigene72066_All//sp|P32865|GPRK1_DROME//5.00E-15//G protein-coupled receptor kinase 1 OS=Drosophila melanogaster GN=Gprk1 PE=1 SV=2						swissprot -
Unigene72067_All	408	0.00	1.86	0.00	0.24	0.00	0.00	0.00	0.00	0.10	1.09E+01	1.75E-04	Up	null	null		-7.93E+00	3.10E-01		-7.93E+00	3.95E-01		null	null		6.61E+00	6.39E-01										
Unigene72068_All	408	0.00	3.35	1.04	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.77E-08	Up	1.00E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene72068_All//gi|12585296|sp|Q93M60.1|PGMC_PEA//3.00E-23//RecName: Full=Phosphoglucomutase, cytoplasmic; Short=PGM; AltName: Full=Glucose phosphomutase >gi|6272281|emb|CAB60127.1| cytosolic phosphoglucomutase [Pisum sativum]	Unigene72068_All//9.00E-24//AT1G23190| phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative			ko00500|Starch and sucrose metabolism//ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene72069_All	408	0.00	5.22	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	4.10E-12	Up	8.03E+00	3.92E-01		null	null		null	null		null	null		null	null										
Unigene7207_All	492	0.85	0.62	0.22	0.61	0.91	1.74	0.69	4.50	2.19	-4.61E-01	6.50E-01		-1.97E+00	1.51E-01		5.83E-01	6.26E-01		1.52E+00	6.17E-02		2.71E+00	1.41E-08	Up	1.67E+00	6.16E-03		Unigene7207_All//gi|124484383|dbj|BAF46302.1|//5.00E-60//cysteine proteinase precursor [Ipomoea nil]	Unigene7207_All//2.00E-50//AT4G16190| cysteine proteinase, putative	Unigene7207_All//0.00E+00//TC131323				nr +
Unigene72070_All	409	0.00	3.96	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.96E-09	Up	8.02E+00	3.92E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene72071_All	409	232.95	245.29	337.21	428.72	410.45	284.12	702.74	225.53	302.35	7.45E-02	2.09E-01		5.34E-01	1.46E-32		-6.28E-02	1.53E-01		-5.94E-01	1.08E-55		-1.64E+00	0.00E+00	Down	-1.22E+00	0.00E+00	Down	Unigene72071_All//gi|82659447|gb|AB888840.1|//2.00E-56//aquaporin [Stevia rebaudiana]	Unigene72071_All//4.00E-57//AT4G35100| PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel	Unigene72071_All//0.00E+00//gi|164273435|gb|ES819298.1|ES819298				nr -
Unigene72072_All	410	0.00	3.46	0.39	0.00	0.17	0.00	0.00	0.00	0.00	1.18E+01	4.05E-08	Up	8.61E+00	2.36E-01		7.39E+00	6.03E-01		null	null		null	null		null	null		Unigene72072_All//gi|226496988|ref|NP_001148851.1|//8.00E-62//fibrillarin-2 [Zea mays] >gi|195620340|gb|ACG32000.1| fibrillarin-2 [Zea mays]	Unigene72072_All//7.00E-61//AT4G25630| FIB2 (FIBRILLARIN 2); snoRNA binding					nr +
Unigene72073_All	410	0.00	2.35	2.08	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.37E-05	Up	1.10E+01	9.00E-05	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene72074_All	410	0.00	1.61	0.26	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	6.20E-04	Up	8.02E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene72074_All//gi|116059832|emb|CAL55539.1|//5.00E-26//Serine/threonine protein phosphatase (ISS) [Ostreococcus tauri]	Unigene72074_All//2.00E-22//AT4G31860| protein phosphatase 2C, putative / PP2C, putative					nr +
Unigene72075_All	410	0.00	2.72	1.43	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.99E-06	Up	1.05E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene72075_All//sp|Q99542|MMP19_HUMAN//6.00E-46//Matrix metalloproteinase-19 OS=Homo sapiens GN=MMP19 PE=1 SV=1						swissprot -
Unigene72076_All	411	0.13	1.97	0.65	2.42	0.84	0.88	0.21	0.10	0.29	3.95E+00	7.52E-04	Up	2.35E+00	2.39E-01		-1.53E+00	2.33E-02		-1.46E+00	4.18E-02		-1.02E+00	7.22E-01		5.00E-01	8.06E-01				Unigene72076_All//5.00E-07//gi|21092923|gb|BQ405236.1|BQ405236				
Unigene72078_All	412	0.00	4.55	2.46	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.10E-10	Up	1.13E+01	1.27E-05	Up	null	null		null	null		null	null		null	null										
Unigene72080_All	413	0.00	2.33	1.55	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.37E-05	Up	1.06E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene72080_All//gi|224003569|ref|XP_002291456.1|//1.00E-08//trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220973232|gb|EED91563.1| trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]						nr +
Unigene72081_All	413	0.00	4.17	1.16	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.96E-10	Up	1.02E+01	7.44E-03		null	null		null	null		null	null		null	null		Unigene72081_All//sp|P23142|FBLN1_HUMAN//2.00E-79//Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4						swissprot +
Unigene72082_All	414	0.00	4.77	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.96E-11	Up	9.81E+00	2.48E-02		null	null		null	null		null	null		null	null										ESTscan +
Unigene72083_All	414	0.00	5.14	1.03	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	4.10E-12	Up	1.00E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene72083_All//gi|3202042|gb|AAC19402.1|//1.00E-09//26S proteasome regulatory subunit S5A [Mesembryanthemum crystallinum]				ko03050|Proteasome		nr -
Unigene72084_All	414	0.00	1.96	0.39	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	9.31E-05	Up	8.59E+00	2.36E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene72085_All	414	0.00	2.82	1.54	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.04E-06	Up	1.06E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene72085_All//gi|14249144|ref|NP_116006.1|//4.00E-29//ras-related protein Rab-11B [Rattus norvegicus] >gi|78369332|ref|NP_001030468.1| ras-related protein Rab-11B [Bos taurus] >gi|190358517|ref|NP_004209.2| ras-related protein Rab-11B [Homo sapiens] >gi|109123235|ref|XP_001093925.1| PREDICTED: ras-related protein Rab-11B [Macaca mulatta] >gi|297703412|ref|XP_002828633.1| PREDICTED: ras-related protein Rab-11B-like [Pongo abelii] >gi|38258938|sp|Q15907.4|RB11B_HUMAN RecName: Full=Ras-related protein Rab-11B; AltName: Full=GTP-binding protein YPT3 >gi|50403673|sp|O35509.4|RB11B_RAT RecName: Full=Ras-related protein Rab-11B >gi|108860922|sp|Q3MHP2.3|RB11B_BOVIN RecName: Full=Ras-related protein Rab-11B >gi|9837357|gb|AAG00542.1|AF286534_1 GTP-binding protein RAB11B [Rattus norvegicus] >gi|20379070|gb|AAM21095.1|AF49894	Unigene72085_All//1.00E-26//AT1G16920| ATRAB41B (ARABIDOPSIS RAB GTPASE HOMOLOG A1B); GTP binding	Unigene72085_All//5.00E-07//BF273177		ko04144|Endocytosis		nr -
Unigene72086_All	415	0.00	6.59	1.92	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.44E-15	Up	1.09E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene72086_All//sp|P14199|REF2P_DROME//3.00E-09//Protein ref(2)P OS=Drosophila melanogaster GN=ref(2)P PE=1 SV=2						swissprot +
Unigene72087_All	415	0.00	3.30	1.28	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.77E-08	Up	1.03E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene72087_All//gi|226495473|ref|NP_001147336.1|//7.00E-55//glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Zea mays] >gi|30580446|sp|Q96UF2.1|G3P2_RHIRA RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase 2; Short=GAPDH 2 >gi|15722242|emb|CAC37404.1| glyceraldehyde-3-phosphate dehydrogenase [Mucor racemosus] >gi|195610190|gb|ACG26925.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Zea mays]	Unigene72087_All//7.00E-54//AT1G13440| GAPC2 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene72087_All//3.00E-11//TC151197		ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene72088_All	415	0.00	3.54	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.10E-08	Up	9.81E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72088_All//gi|301090047|ref|XP_002895257.1|//2.00E-20//14 kDa zinc-binding protein [Phytophthora infestans T30-4] >gi|262100991|gb|EEY59043.1| 14 kDa zinc-binding protein [Phytophthora infestans T30-4]	Unigene72088_All//3.00E-17//AT3G56490| zinc-binding protein, putative / protein kinase C inhibitor, putative					nr -
Unigene72090_All	415	0.00	3.42	2.31	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.05E-08	Up	1.12E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene72090_All//gi|118411132|ref|YP_874526.1|//5.00E-08//30S ribosomal protein S18 [Thalassiosira pseudonana] >gi|224015780|ref|XP_002297538.1| RR18, ribosomal protein 18 30S small ribosomal subunit, chloroplast, translation, protein biosynthesis [Thalassiosira pseudonana CCMP1335] >gi|125987698|sp|A0T0R4.1|RR18_THAPS RecName: Full=30S ribosomal protein S18, chloroplastic >gi|116739879|gb|ABK20749.1| 30S ribosomal protein S18 [Thalassiosira pseudonana] >gi|220967802|gb|EED86178.1| RR18, ribosomal protein 18 30S small ribosomal subunit, chloroplast, translation, protein biosynthesis [Thalassiosira pseudonana CCMP1335]	Unigene72090_All//8.00E-05//AT1G07210| 30S ribosomal protein S18 family					nr -
Unigene72092_All	417	0.00	2.55	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.79E-06	Up	9.58E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene72092_All//gi|301103438|ref|XP_002900805.1|//3.00E-21//diphthamide biosynthesis protein 1 [Phytophthora infestans T30-4] >gi|262101560|gb|EEY59612.1| diphthamide biosynthesis protein 1 [Phytophthora infestans T30-4]	Unigene72092_All//4.00E-17//AT5G62030| diphthamide synthesis DPH2 family protein					nr -
Unigene72093_All	418	0.00	4.97	1.40	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.94E-12	Up	1.05E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene72093_All//gi|1709617|sp|P80284.2|PDI_HORVU//7.00E-28//RecName: Full=Protein disulfide-isomerase; Short=PDI; AltName: Full=Endosperm protein E-1; Flags: Precursor >gi|493387|gb|AAA70344.1| disulfide isomerase [Hordeum vulgare subsp. vulgare] >gi|493589|gb|AAA70345.1| disulfide isomerase [Hordeum vulgare subsp. vulgare]	Unigene72093_All//5.00E-28//AT1G77510| ATPDIL1-2 (PDI-LIKE 1-2); protein disulfide isomerase			ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene72094_All	418	0.00	6.42	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.80E-15	Up	1.07E+01	6.13E-04	Up	null	null		null	null		null	null		null	null										
Unigene72095_All	419	0.00	7.01	2.80	0.00	0.58	0.00	0.00	0.00	0.00	1.28E+01	1.01E-16	Up	1.14E+01	1.77E-06	Up	9.17E+00	1.04E-01		null	null		null	null		null	null		Unigene72095_All//gi|299471562|emb|CBN80048.1|//3.00E-08//beta strand repeat-containing protein [Ectocarpus siliculosus]						nr -
Unigene72097_All	419	0.00	4.72	0.13	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.96E-11	Up	6.99E+00	6.27E-01		null	null		null	null		null	null		null	null		Unigene72097_All//gi|157093503|gb|ABV22406.1|//8.00E-06//unknown [Noctiluca scintillans]						nr +

Unigene72098_All	420	0.00	3.26	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.77E-08	Up	null	null		null	null		null	null		null	null		null	null		Unigene72098_All//gi|145324014|ref|NP_001077596.1|//2.00E-07//PFT1 (PHYTOCHROME AND FLOWERING TIME 1); transcription coactivator [Arabidopsis thaliana]						nr +
Unigene72099_All	420	0.00	7.96	2.41	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	4.94E-19	Up	1.12E+01	1.27E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene721_All	982	2.13	1.03	0.65	3.45	2.95	4.32	7.58	5.96	6.78	-1.05E+00	1.96E-02		-1.71E+00	6.07E-04	Down	-2.28E-01	5.57E-01		3.26E-01	3.18E-01		-3.47E-01	8.04E-02		-1.62E-01	4.31E-01		Unigene721_All//gi|297809901|ref|XP_002872834.1|//2.00E-38//AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318671|gb|EFH49093.1| AAA-type ATPase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene721_All//3.00E-39//AT4G02480| AAA-type ATPase family protein	Unigene721_All//0.00E+00//C0102571			GO:0009536//GO:0032559//GO:0042623	nr -
Unigene7210_All	723	3.76	6.24	8.76	16.60	28.86	32.73	5.67	10.93	9.09	7.29E-01	1.04E-02		1.22E+00	1.15E-06	Up	7.98E-01	1.67E-12		9.79E-01	4.36E-18		9.46E-01	4.23E-07		6.81E-01	6.23E-04		Unigene7210_All//gi|30725324|gb|AAP37684.1|//1.00E-38//At3g01680 [Arabidopsis thaliana]	Unigene7210_All//7.00E-40//AT3G01680| unknown protein	Unigene7210_All//0.00E+00//gi|109859889|gb|DW488868.1|DW488868				nr -
Unigene72100_All	421	0.00	3.13	0.89	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.49E-07	Up	9.79E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72100_All//gi|3777559|gb|AAC64934.1|//3.00E-18//collagen-like [Griffithsia japonica]	Unigene72100_All//2.00E-15//AT1G64450| proline-rich family protein			ko03040|Spliceosome//ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene72101_All	421	0.00	2.89	0.76	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	5.45E-07	Up	9.57E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene72101_All//sp|Q05AM4|FAH2B_DANRE//8.00E-15//Fatty-acid amide hydrolase 2-B OS=Danio rerio GN=faah2b PE=2 SV=1						swissprot +
Unigene72102_All	422	0.00	1.80	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	1.75E-04	Up	null	null		null	null		null	null		null	null		null	null		Unigene72102_All//sp|Q6DFM9|TOM20_XENTR//1.00E-28//Mitochondrial import receptor subunit TOM20 homolog OS=Xenopus tropicalis GN=tomm20 PE=2 SV=1						swissprot -
Unigene72103_All	423	0.00	8.03	3.02	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	2.54E-19	Up	1.16E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene72103_All//gi|297801152|ref|XP_002868460.1|//6.00E-08//eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297314296|gb|EFH44719.1| eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene72103_All//1.00E-06//AT5G36230| eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein					nr -
Unigene72104_All	424	0.00	1.55	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	6.20E-04	Up	8.97E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72104_All//gi|195619564|gb|ACG31612.1|//6.00E-19//zinc finger protein 511 [Zea mays]	Unigene72104_All//1.00E-18//AT5G14140| zinc finger (C2H2 type) family protein					nr -
Unigene72105_All	425	0.00	2.74	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.04E-06	Up	7.97E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene72105_All//gi|291196027|emb|CBE70787.1|//4.00E-22//NAP-related protein [Medicago sativa subsp. x varia]	Unigene72105_All//2.00E-15//AT1G74560| NRP1 (NAP1-RELATED PROTEIN 1); DNA binding / chromatin binding / histone binding					nr +
Unigene72106_All	425	0.00	2.74	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.04E-06	Up	9.97E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene72106_All//gi|298706859|emb|CBJ25823.1|//3.00E-41//Phosphoglycerate dehydrogenase / Phosphoserine aminotransferase [Ectocarpus siliculosus]	Unigene72106_All//6.00E-32//AT4G34200| EMB9 (embryo sac development arrest 9); ATP binding			ko00260|Glycine, serine and threonine metabolism		nr +
Unigene72107_All	425	0.00	3.22	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.77E-08	Up	9.55E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene72107_All//sp|Q89CJ0|TNR6C_HUMAN//4.00E-29//Trinucleotide repeat-containing gene 6C protein OS=Homo sapiens GN=TNRC6C PE=1 SV=3						swissprot -
Unigene72108_All	425	0.00	4.05	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.96E-10	Up	7.97E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene72108_All//gi|45238341|emb|CAD27343.1|//1.00E-32//protein kinase 2 beta chain [Nicotiana tabacum]	Unigene72108_All//1.00E-31//AT2G44680| CKB4 (CASEIN KINASE II BETA SUBUNIT 4); protein serine/threonine kinase			ko04712|Circadian rhythm - plant		nr +
Unigene72109_All	426	0.00	5.47	1.25	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.90E-13	Up	1.03E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene72109_All//gi|159463354|ref|XP_001690007.1|//9.00E-29//SR protein factor [Chlamydomonas reinhardtii] >gi|158283995|gb|EDP09745.1| SR protein factor [Chlamydomonas reinhardtii]	Unigene72109_All//4.00E-07//AT3G49430| SRp34a (Ser/Arg-rich protein 34a); RNA binding / nucleic acid binding / nucleotide binding			ko03040|Spliceosome		nr -
Unigene72110_All	427	0.00	3.56	1.25	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.09E-08	Up	1.03E+01	4.01E-03		null	null		null	null		null	null		null	null									
Unigene72111_All	427	0.00	1.54	0.37	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	6.20E-04	Up	8.55E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene72111_All//gi|115450022|ref|NP_001048612.1|//4.00E-16//Os02g0830100 [Oryza sativa Japonica Group] >gi|48716335|dbj|BAD22947.1| oligopeptidase A-like [Oryza sativa Japonica Group] >gi|113538143|dbj|BAF10526.1| Os02g0830100 [Oryza sativa Japonica Group]	Unigene72111_All//4.00E-17//AT5G10540| peptidase M3 family protein / thimet oligopeptidase family protein					nr +
Unigene72112_All	428	0.00	2.49	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	3.79E-06	Up	7.96E+00	3.92E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene72113_All	429	0.00	6.61	0.50	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	3.82E-16	Up	8.96E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72113_All//sp|Q6BUE3|PXR1_DEBHA//6.00E-06//Protein PXR1 OS=Debaryomyces hansenii GN=PXR1 PE=3 SV=1				ko03040|Spliceosome		swissprot +
Unigene72114_All	429	0.00	4.13	1.37	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.13E-10	Up	1.04E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene72114_All//gi|18644678|gb|AAL76325.1|AF394515_1//5.00E-46//6-phosphogluconate dehydrogenase [Porphyra yezoensis]	Unigene72114_All//3.00E-38//AT3G02360| 6-phosphogluconate dehydrogenase family protein			ko00480|Glutathione metabolism//ko00030|Pentose phosphate pathway		nr +
Unigene72115_All	430	0.00	1.77	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	1.75E-04	Up	1.07E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene72115_All//gi|255080110|ref|XP_002503635.1|//9.00E-29//proteasome regulatory complex component protein [Micromonas sp. RCC299] >gi|226518902|gb|ACO64893.1| proteasome regulatory complex component protein [Micromonas sp. RCC299]	Unigene72115_All//2.00E-22//AT1G04810| 26S proteasome regulatory subunit, putative			ko03050|Proteasome		nr -
Unigene72116_All	430	0.00	3.65	1.11	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.68E-09	Up	1.01E+01	7.44E-03		null	null		null	null		null	null		null	null		Unigene72116_All//gi|73912433|dbj|BAE20413.1|//5.00E-21//aspartic proteinase [Triticum aestivum]	Unigene72116_All//1.00E-18//AT1G11910| aspartyl protease family protein					nr -
Unigene72117_All	431	0.00	2.94	0.00	0.00	0.16	0.00	0.39	0.39	2.59	1.15E+01	2.85E-07	Up	null	null		7.32E+00	6.03E-01		null	null		-1.66E-02	1.02E+00		2.72E+00	8.54E-05	Up	Unigene72117_All//gi|297824921|ref|XP_002880343.1|//2.00E-49//structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata] >gi|297326182|gb|EFH56602.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	Unigene72117_All//4.00E-50//AT2G48110| REF4 (REDUCED EPIDERMAL FLUORESCENCE 4)	Unigene72117_All//5.00E-07//gi|78342988|gb|DT563262.1|DT563262				nr -
Unigene72118_All	433	0.00	4.56	0.74	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	2.96E-11	Up	9.53E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene72118_All//gi|115461653|ref|NP_001054426.1|//5.00E-23//Os05g0107700 [Oryza sativa Japonica Group] >gi|122169632|sp|Q0DLD3.1|T2AG_ORYSJ RecName: Full=Transcription initiation factor IIA subunit 2; AltName: Full=General transcription factor IIA subunit 2; AltName: Full=Transcription initiation factor IIA gamma chain; Short=TFIIA-gamma >gi|158513184|sp|A2XZI2.2|T2AG_ORYSI RecName: Full=Transcription initiation factor IIA subunit 2; AltName: Full=General transcription factor IIA subunit 2; AltName: Full=Transcription initiation factor IIA gamma chain; Short=TFIIA-gamma >gi|28195115|gb|AAO33769.1| transcription factor IIA small subunit [Oryza sativa Indica Group] >gi|55585041|gb|AAV53716.1| transcription factor IIA gamma subunit [Oryza sativa Indica Group] >gi|113577977|dbj|BAF16340.1| Os05g0107700 [Oryza sativa Japonica Group]	Unigene72118_All//2.00E-23//AT4G24440| transcription initiation factor IIA gamma chain / TFIIA-gamma (TFIIA-S)			ko03022|Basal transcription factors		nr -
Unigene72119_All	433	0.00	3.28	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.05E-08	Up	7.94E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene72119_All//sp|Q7YR42|IEX1_PANTR//2.00E-62//Radiation-inducible immediate-early gene IEX-1 OS=Pan troglodytes GN=IEX3 PE=3 SV=1						swissprot -
Unigene7212_All	2300	0.09	0.00	0.09	0.13	0.27	0.04	1.31	3.31	5.09	-6.51E+00	1.21E-01		2.51E-02	1.00E+00		1.05E+00	2.99E-01		-1.73E+00	2.89E-01		1.34E+00	2.03E-11	Up	1.96E+00	1.11E-29	Up	Unigene7212_All//gi|115469596|ref|NP_001058397.1|//0.00E+00//Os06g0685100 [Oryza sativa Japonica Group] >gi|52076665|dbj|BAD45565.1| COBRA-like protein [Oryza sativa Japonica Group] >gi|113596437|dbj|BAF20311.1| Os06g0685100 [Oryza sativa Japonica Group]	Unigene7212_All//1.00E-128//AT4G16120| COBL7 (COBRA-LIKE 7)	Unigene7212_All//5.00E-20//gi|78332169|gb|DT552443.1|DT552443				nr -
Unigene72120_All	433	0.24	2.81	1.97	0.00	0.16	0.00	0.00	0.00	0.00	3.54E+00	4.02E-05	Up	3.03E+00	3.00E-03		7.31E+00	6.03E-01		null	null		null	null		null	null									ESTscan -
Unigene72121_All	434	0.00	2.57	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.99E-06	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene72123_All	434	0.00	3.62	0.25	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.68E-09	Up	7.94E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene72123_All//gi|301120314|ref|XP_002907884.1|//5.00E-40//trifunctional enzyme subunit beta, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262102915|gb|EEY60967.1| trifunctional enzyme subunit beta, mitochondrial precursor [Phytophthora infestans T30-4]	Unigene72123_All//8.00E-16//AT2G33150| PKT3 (PEROXISOMAL 3-KETOACYL-COA THIOLASE 3); acetyl-CoA C-acyltransferase			ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids		nr +
Unigene72124_All	438	0.00	3.01	0.73	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.49E-07	Up	9.51E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene72124_All//gi|115446845|ref|NP_001047202.1|//5.00E-09//Os02g0573400 [Oryza sativa Japonica Group] >gi|113536733|dbj|BAF09116.1| Os02g0573400 [Oryza sativa Japonica Group]	Unigene72124_All//5.00E-08//AT4G39910| ATUBP3 (ARABIDOPSIS THALIANA UBIQUITIN-SPECIFIC PROTEASE 3); ubiquitin-specific protease					nr +

Unigene72125_All	438	0.60	11.22	0.00	0.34	0.79	1.24	0.68	0.76	0.73	4.23E+00	1.11E-21	Up	-9.22E+00	8.51E-02		1.20E+00	4.26E-01		1.86E+00	1.02E-01		1.76E-01	8.80E-01		1.07E-01	9.45E-01				Unigene72125_All//5.00E-07//TC143121				
Unigene72126_All	438	0.00	3.59	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.68E-09	Up	null	null		null	null		null	null		null	null		null	null			Unigene72126_All//gi|194477305|ref|YP_002049484.1|//3.00E-60//ATPase [Paulinella chromatophora] >gi|171192312|gb|ACB43274.1| ATPase [Paulinella chromatophora]	Unigene72126_All//7.00E-53//AT5G15450| CLPR3 (CASEIN LYTIC PROTEINASE B3); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding					nr -
Unigene72127_All	441	0.00	4.71	0.48	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.94E-12	Up	8.92E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan -
Unigene72128_All	442	0.00	5.04	0.48	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.09E-12	Up	8.91E+00	1.39E-01		null	null		null	null		null	null		null	null									ESTscan +
Unigene72129_All	443	0.00	6.52	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.97E-16	Up	null	null		null	null		null	null		null	null		null	null			Unigene72129_All//gi|300259627|gb|EFJ38853.1|//2.00E-09//DP transcription factor [Volvox carteri f. nagariensis]						nr +
Unigene7213_All	730	328.76	275.00	176.75	832.31	840.36	506.57	193.85	46.72	46.28	-2.58E-01	1.79E-15		-8.95E-01	3.54E-139		1.39E-02	6.17E-01		-7.16E-01	4.06E-268		-2.05E+00	0.00E+00	Down	-2.07E+00	0.00E+00	Down		Unigene7213_All//gi|171190270|gb|AB42441.1|//7.00E-96//aquaporin PIP2;4 [Gossypium hirsutum]	Unigene7213_All//2.00E-93//AT2G16850| PIP2;8 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;8); water channel	Unigene7213_All//0.00E+00//TC130099				nr -
Unigene72130_All	444	0.00	1.71	0.96	0.45	0.54	0.00	0.00	0.00	0.00	1.07E+01	1.75E-04	Up	9.91E+00	1.37E-02		2.75E-01	8.94E-01		-8.81E+00	1.33E-01		null	null		null	null			Unigene72130_All//gi|116058775|emb|CAL54482.1|//2.00E-16//enoyl CoA hydratase-like protein (ISS) [Ostreococcus tauri]	Unigene72130_All//1.00E-12//AT4G16800| enoyl-CoA hydratase, putative			ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism		nr -
Unigene72131_All	444	0.00	3.31	2.52	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.10E-08	Up	1.13E+01	3.42E-06	Up	null	null		null	null		null	null		null	null			Unigene72131_All//gi|255632826|gb|ACU16766.1|//2.00E-06//unknown [Glycine max]	Unigene72131_All//1.00E-05//AT3G22845| emp24/gp25L/p24 protein-related					nr +
Unigene72132_All	444	0.00	12.78	2.16	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	2.22E-32	Up	1.11E+01	2.45E-05	Up	null	null		null	null		null	null		null	null			Unigene72132_All//gi|27311795|gb|AA000863.1|//6.00E-59//Unknown protein [Arabidopsis thaliana]	Unigene72132_All//2.00E-44//AT1G51060| HTA10; DNA binding					nr +
Unigene72133_All	445	0.00	3.30	1.79	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.10E-08	Up	1.08E+01	1.72E-04	Up	null	null		null	null		null	null		null	null			Unigene72133_All//sp|P18102|TLL_DROME//8.00E-60//Protein tailless OS=Drosophila melanogaster GN=tll PE=1 SV=1						swissprot -
Unigene72134_All	446	0.00	2.05	0.96	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	2.60E-05	Up	9.90E+00	1.37E-02		null	null		null	null		null	null		null	null			Unigene72134_All//sp|P16989|DBPA_HUMAN//3.00E-65//DNA-binding protein A OS=Homo sapiens GN=CSDA PE=1 SV=4						swissprot -
Unigene72135_All	446	0.00	6.02	1.67	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.80E-15	Up	1.07E+01	3.26E-04	Up	null	null		null	null		null	null		null	null			Unigene72135_All//sp|P08729|K2C7_HUMAN//2.00E-75//Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=4						swissprot -
Unigene72136_All	446	0.00	6.13	1.91	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.44E-15	Up	1.09E+01	8.99E-05	Up	null	null		null	null		null	null		null	null			Unigene72136_All//sp|Q3UIT3|BRM1L_MOUSE//1.00E-25//Breast cancer metastasis-suppressor 1-like protein OS=Mus musculus GN=Brms1l PE=2 SV=1						swissprot +
Unigene72137_All	447	0.00	2.95	2.74	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.49E-07	Up	1.14E+01	9.10E-07	Up	null	null		null	null		null	null		null	null			Unigene72137_All//gi|6562845|emb|CAB62553.1|//6.00E-25//heterogeneous nuclear ribonucleoprotein; type A/B hnRNP p40 [Rattus norvegicus] >gi|49052496|gb|EDM04313.1| rCG34663, isoform CRA_a [Rattus norvegicus]	Unigene72137_All//6.00E-23//AT4G14300| heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative			ko03040|Spliceosome		nr -
Unigene72138_All	447	0.00	2.49	2.14	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.99E-06	Up	1.11E+01	2.45E-05	Up	null	null		null	null		null	null		null	null			Unigene72138_All//sp|P19967|CYB5R_DROME//2.00E-61//Cytochrome b5-related protein OS=Drosophila melanogaster GN=Cyt-b5-r PE=1 SV=2						swissprot -
Unigene7214_All	621	2.53	0.82	0.09	1.36	1.11	1.16	3.13	1.62	2.05	-1.63E+00	3.58E-03		-4.88E+00	2.04E-07	Down	-2.98E-01	6.93E-01		-2.29E-01	7.51E-01		-9.55E-01	2.18E-02		-6.09E-01	1.28E-01			Unigene7214_All//gi|15218140|ref|NP_173539.1|//1.00E-18//mitochondrial transcription termination factor family protein / mTERF family protein [Arabidopsis thaliana]	Unigene7214_All//1.00E-17//AT1G21150| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene7214_All//2.00E-174//TC164419				nr -
Unigene72141_All	449	0.00	9.48	2.13	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	3.04E-24	Up	1.11E+01	2.45E-05	Up	null	null		null	null		null	null		null	null			Unigene72141_All//gi|226456844|gb|EEH54144.1|//5.00E-52//histone H4 [Micromonas pusilla CCMP1545]	Unigene72141_All//2.00E-40//AT5G59970| histone H4	Unigene72141_All//3.00E-45//TC167353				nr -
Unigene72142_All	450	0.00	9.46	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	3.04E-24	Up	9.89E+00	1.37E-02		null	null		null	null		null	null		null	null			Unigene72142_All//gi|255083889|ref|XP_002508519.1|//2.00E-16//dihydrolipoamide s-acetyltransferase of the pyruvate dehydrogenase [Micromonas sp. RCC299] >gi|226523796|gb|ACO69777.1| dihydrolipoamide s-acetyltransferase of the pyruvate dehydrogenase [Micromonas sp. RCC299]	Unigene72142_All//6.00E-17//AT3G13930| dihydrolipoamide S-acetyltransferase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)		nr -
Unigene72143_All	451	0.00	4.49	1.77	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.53E-11	Up	1.08E+01	1.72E-04	Up	null	null		null	null		null	null		null	null			Unigene72143_All//sp|Q9VGX3|FAU_DROME//2.00E-51//Protein anoxia up-regulated OS=Drosophila melanogaster GN=fau PE=1 SV=3						swissprot +
Unigene72144_All	453	0.00	8.39	3.76	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.23E-21	Up	1.19E+01	2.19E-09	Up	null	null		null	null		null	null		null	null			Unigene72144_All//sp|Q9V4X2|PGSC2_DROME//2.00E-53//Peptidoglycan-recognition protein SC2 OS=Drosophila melanogaster GN=PGRP-SC2 PE=2 SV=1						swissprot +
Unigene72145_All	453	0.00	3.36	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.09E-08	Up	null	null		null	null		null	null		null	null		null	null			Unigene72145_All//gi|255070017|ref|XP_002507090.1|//7.00E-11//DNA topoisomerase I [Micromonas sp. RCC299] >gi|226522365|gb|ACO68348.1| DNA topoisomerase I [Micromonas sp. RCC299]	Unigene72145_All//2.00E-05//AT5G55310| TOP1BETA (DNA TOPOISOMERASE 1 BETA); DNA topoisomerase type I					nr +
Unigene72146_All	454	0.00	3.24	1.29	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.10E-08	Up	1.03E+01	2.16E-03		null	null		null	null		null	null		null	null									
Unigene72147_All	456	0.00	12.22	1.87	0.00	0.00	0.20	0.00	0.00	0.00	1.36E+01	8.49E-32	Up	1.09E+01	8.99E-05	Up	null	null		7.63E+00	4.72E-01		null	null		null	null			Unigene72147_All//gi|255602755|ref|XP_002537914.1|//1.00E-22//Outer membrane antigenic lipoprotein B precursor, putative [Ricinus communis] >gi|223514582|gb|EEF24470.1| Outer membrane antigenic lipoprotein B precursor, putative [Ricinus communis]						nr +
Unigene72148_All	457	0.00	11.53	0.00	0.00	0.00	0.00	0.19	0.00	0.00	1.35E+01	4.74E-30	Up	null	null		null	null		null	null		-7.53E+00	3.99E-01		-7.53E+00	3.55E-01			Unigene72148_All//gi|224055773|ref|XP_002298646.1|//1.00E-07//predicted protein [Populus trichocarpa] >gi|222845904|gb|EEE83451.1| predicted protein [Populus trichocarpa]						nr -
Unigene72149_All	458	0.00	2.21	0.12	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	7.22E-06	Up	6.86E+00	6.27E-01		null	null		null	null		null	null		null	null			Unigene72149_All//gi|6911862|emb|CAB72162.1|//6.00E-13//serine/threonine-protein kinase-like protein [Arabidopsis thaliana]	Unigene72149_All//3.00E-12//AT3G45240| GRIK1 (GEMINIVIRUS REP INTERACTING KINASE 1); kinase					nr -
Unigene7215_All	373	31.70	28.39	14.28	108.31	183.99	119.99	1.36	0.11	0.21	-1.59E-01	3.76E-01		-1.15E+00	7.44E-11	Down	7.65E-01	1.62E-37		1.48E-01	9.13E-02		-3.60E+00	5.77E-03		-2.67E+00	1.37E-02			Unigene7215_All//gi|38047399|gb|AAR06602.1|//1.00E-31//flavonoid 4"-O-methyltransferase [Mentha x piperita]	Unigene7215_All//2.00E-29//AT4G35160| O-methyltransferase family 2 protein	Unigene7215_All//1.00E-127//TC146009		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene72150_All	458	0.00	3.76	0.23	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.96E-10	Up	7.86E+00	3.92E-01		null	null		null	null		null	null		null	null			Unigene72150_All//gi|301098898|ref|XP_002898541.1|//1.00E-06//AMP-binding enzyme, putative [Phytophthora infestans T30-4] >gi|262104966|gb|EEY63018.1| AMP-binding enzyme, putative [Phytophthora infestans T30-4]						nr -
Unigene72151_All	458	0.00	6.42	2.21	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.01E-16	Up	1.11E+01	1.27E-05	Up	null	null		null	null		null	null		null	null			Unigene72151_All//gi|301094950|ref|XP_002896578.1|//5.00E-29//S-adenosylmethionine synthetase 2 [Phytophthora infestans T30-4] >gi|23394401|gb|AAN31489.1| S-adenosyl methionine synthetase [Phytophthora infestans] >gi|262108972|gb|EEY67024.1| S-adenosylmethionine synthetase 2 [Phytophthora infestans T30-4]	Unigene72151_All//4.00E-27//AT4G01850| SAM-2 (S-ADENOSYLMETHIONINE SYNTHETASE 2); copper ion binding / methionine adenosyltransferase			ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism		nr +
Unigene72153_All	460	0.00	4.19	2.55	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.72E-11	Up	1.13E+01	1.77E-06	Up	null	null		null	null		null	null		null	null			Unigene72153_All//sp|P30504|CD4_HUMAN//1.00E-61//HLA class I histocompatibility antigen, Cw-4 alpha chain OS=Homo sapiens GN=HLA-C PE=1 SV=1						swissprot +
Unigene72154_All	460	0.00	4.63	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.10E-12	Up	null	null		null	null		null	null		null	null		null	null			Unigene72154_All//sp|Q8WQA4|EXC4_CAEEL//2.00E-15//Chloride intracellular channel exc-4 OS=Caenorhabditis elegans GN=exc-4 PE=1 SV=2						swissprot +
Unigene72156_All	462	0.00	4.17	2.07	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.72E-11	Up	1.10E+01	2.45E-05	Up	null	null		null	null		null	null		null	null									
Unigene72157_All	463	0.00	4.60	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.10E-12	Up	1.03E+01	2.16E-03		null	null		null	null		null	null		null	null			Unigene72157_All//gi|255085060|ref|XP_002504961.1|//2.00E-07//COMPASS/Set1C complex protein [Micromonas sp. RCC299] >gi|226520230|gb|ACO66219.1| COMPASS/Set1C complex protein [Micromonas sp. RCC299]						nr -
Unigene72158_All	463	0.00	2.95	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.77E-08	Up	8.43E+00	2.36E-01		null	null		null	null		null	null		null	null			Unigene72158_All//sp|P15037|ETS2_MOUSE//1.00E-17//Protein C-ets-2 OS=Mus musculus GN=Ets2 PE=2 SV=1						swissprot +
Unigene72159_All	464	0.00	3.49	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.96E-09	Up	1.06E+01	3.26E-04	Up	null	null		null	null		null	null		null	null									
Unigene72160_All	464	0.00	2.40	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.99E-06	Up	null	null		null	null		null	null		null	null		null	null									ESTscan +
Unigene72161_All	465	0.00	13.95	9.05	0.00	0.15	0.19	0.00	0.00	0.34	1.38E+01	4.83E-37	Up	1.31E+01	2.43E-23	Up	7.21E+00	6.03E-01		7.60E+00	4.72E-01		null	null		8.42E+00	1.39E-01			Unigene72161_All//gi|298711489|emb|CBJ26577.1|//1.00E-45//40S ribosomal protein S17 [Ectocarpus siliculosus]	Unigene72161_All//1.00E-40//AT2G05220| 40S ribosomal protein S17 (RPS17B)			ko03010|Ribosome		nr +

Unigene72162_All	466	0.00	3.37	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	5.68E-09	Up	1.05E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene72162_All//gi|75858845|gb|AB428999.1|/4.00E-19//ubiquitin ligase 2 [Symbiodinium sp. C3]				ko04120|Ubiquitin mediated proteolysis		nr -
Unigene72163_All	469	0.00	3.89	0.68	0.00	0.00	0.00	0.00	0.00	0.08	1.19E+01	2.14E-10	Up	9.41E+00	4.47E-02		null	null		null	null		null	null		6.41E+00	6.39E-01										
Unigene72164_All	470	0.00	4.31	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.53E-11	Up	9.99E+00	7.44E-03		null	null		null	null		null	null		null	null		Unigene72164_All//gi|223996187|ref|XP_002287767.1|/2.00E-55//ran-type small G protein [Thalassiosira pseudonana CCMP1335] >gi|220976883|gb|EED95210.1| ran-type small G protein [Thalassiosira pseudonana CCMP1335]	Unigene72164_All//1.00E-49//AT5G20010| RAN-1; GTP binding / GTPase/ protein binding					nr -
Unigene72165_All	472	0.00	4.19	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.96E-11	Up	9.63E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72165_All//sp|Q02645|HTS_DROME//1.00E-80//Protein hu-li tai shao OS=Drosophila melanogaster GN=hts PE=1 SV=2						swissprot +
Unigene72166_All	475	0.00	6.19	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.01E-16	Up	1.07E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene72166_All//sp|Q7ZGQ2|RNKB_CERCA//5.00E-35//Ribonuclease kappa-B OS=Ceratitis capitata PE=3 SV=1						swissprot +
Unigene72167_All	476	0.00	9.15	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	8.00E-25	Up	1.07E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene72167_All//gi|2982297|gb|AAC32134.1|/2.00E-46//AIAA0107-like protein [Picea mariana]	Unigene72167_All//2.00E-47//AT4G24820| 26S proteasome regulatory subunit, putative (RPN7)			ko03050|Proteasome		nr +
Unigene72168_All	479	0.00	5.71	7.78	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.44E-15	Up	1.29E+01	1.20E-20	Up	null	null		null	null		null	null		null	null		Unigene72168_All//gi|27923849|sp|Q945U1.1|RS15_ELAOL//3.00E-60//RecName: Full=40S ribosomal protein S15 >gi|15425963|gb|AAK97632.1| 40S ribosomal protein S15 [Elaeis oleifera] >gi|192910788|gb|ACF06502.1| 40S ribosomal protein S15 [Elaeis guineensis]	Unigene72168_All//8.00E-37//AT5G09510| 40S ribosomal protein S15 (RPS15D)	Unigene72168_All//2.00E-12//EV483977		ko03010|Ribosome		nr +
Unigene72169_All	480	0.00	3.59	1.22	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.96E-10	Up	1.03E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene72169_All//sp|O02466|ILPR_BRALA//3.00E-16//Insulin-like peptide receptor OS=Branchiostoma lanceolatum PE=2 SV=1						swissprot +
Unigene72170_All	480	0.00	6.97	4.55	0.00	0.00	0.19	0.00	0.00	0.00	1.28E+01	4.94E-19	Up	1.22E+01	4.94E-12	Up	null	null		7.56E+00	4.72E-01		null	null													
Unigene72171_All	481	0.00	4.42	1.55	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	4.10E-12	Up	1.06E+01	3.26E-04	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene72172_All	482	0.00	4.52	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.11E-12	Up	1.10E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene72172_All//sp|P29279|CTGF_HUMAN//1.00E-95//Connective tissue growth factor OS=Homo sapiens GN=CTGF PE=1 SV=2						swissprot +
Unigene72173_All	482	0.00	4.73	0.99	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.63E-13	Up	9.96E+00	7.44E-03		null	null		null	null		null	null		null	null		Unigene72173_All//gi|124360279|gb|ABN08292.1|/3.00E-07//emp24/gp25L/p24 [Medicago truncatula]	Unigene72173_All//3.00E-06//AT1G09580| emp24/gp25L/p24 family protein					nr +
Unigene72174_All	485	0.00	7.42	2.42	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.77E-20	Up	1.12E+01	1.77E-06	Up	null	null		null	null		null	null													
Unigene72175_All	485	0.00	2.61	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.85E-07	Up	9.78E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene72175_All//gi|94309683|ref|YP_582893.1|/1.00E-53//electron transfer flavoprotein, subunit alpha [Cupriavidus metallidurans CH34] >gi|93353535|gb|ABF07624.1| Electron transfer flavoprotein subunit alpha (Alpha-ETF) (Electron transfer flavoprotein large subunit) (ETFLS) [Cupriavidus metallidurans CH34]	Unigene72175_All//3.00E-31//AT1G50940| ETFALPHA (electron transfer flavoprotein alpha); FAD binding / electron carrier	Unigene72175_All//2.00E-09//CO102919				nr -
Unigene72176_All	487	0.00	4.27	1.64	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.94E-12	Up	1.07E+01	1.72E-04	Up	null	null		null	null		null	null		null	null										
Unigene72177_All	488	0.00	1.87	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	2.60E-05	Up	null	null		null	null		null	null		null	null		null	null		Unigene72177_All//gi|301105535|ref|XP_002901851.1|/7.00E-37//villin-like protein [Phytophthora infestans T30-4] >gi|262099189|gb|EEY57241.1| villin-like protein [Phytophthora infestans T30-4]	Unigene72177_All//5.00E-34//AT2G41740| VLN2 (VILLIN 2); actin binding					nr -
Unigene72178_All	488	0.75	3.63	1.42	0.00	0.00	0.00	0.00	0.00	0.00	2.28E+00	6.80E-05	Up	9.18E-01	3.11E-01		null	null		null	null		null	null		null	null		Unigene72178_All//gi|229890093|sp|Q8LD23.2|GDL4_ARATH//3.00E-30//RecName: Full=GDSL esterase/lipase At1g20120; AltName: Full=Extracellular lipase At1g20120; Flags: Precursor	Unigene72178_All//2.00E-31//AT1G20120| family II extracellular lipase, putative					nr -
Unigene72179_All	490	0.00	6.41	0.54	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	7.07E-18	Up	9.09E+00	7.94E-02		null	null		null	null		null	null		null	null		Unigene72179_All//gi|299473413|emb|CBN77811.1|/3.00E-37//Sec11 homolog, catalytic subunit of the Signal Peptidase Complex [Ectocarpus siliculosus]	Unigene72179_All//1.00E-32//AT1G52600| signal peptidase, putative			ko03060|Protein export		nr -
Unigene7218_All	366	1.72	0.00	0.29	3.13	0.47	2.96	13.05	3.77	4.25	-1.07E+01	7.90E-04	Down	-2.56E+00	2.72E-02		-2.73E+00	9.92E-05	Down	-8.00E-02	9.09E-01		-1.79E+00	5.56E-11	Down	-1.62E+00	5.60E-10	Down	Unigene7218_All//gi|300681033|sp|A2VQ56.1|LONM_ORYSI//6.00E-20//RecName: Full=Lon protease homolog, mitochondrial; Flags: Precursor	Unigene7218_All//3.00E-20//AT5G26860| LON1 (LON PROTEASE 1); ATP binding / ATP-dependent peptidase/ serine-type peptidase	Unigene7218_All//0.00E+00//gi|21103340|gb|BQ415653.1|BQ415653				nr -
Unigene72180_All	490	0.00	4.03	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.96E-11	Up	1.07E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene72180_All//sp|Q9W2U4|PP4R2_DROME//2.00E-14//Serine/threonine-protein phosphatase 4 regulatory subunit 2 OS=Drosophila melanogaster GN=PPP4R2r PE=1 SV=2						swissprot +
Unigene72181_All	492	0.00	4.53	0.65	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.09E-12	Up	9.34E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene72181_All//gi|15221978|ref|NP_173356.1|/9.00E-06//ARF19 (AUXIN RESPONSE FACTOR 19); DNA binding / transcription factor [Arabidopsis thaliana] >gi|46576613|sp|Q8RYC8.2|ARFS_ARATH RecName: Full=Auxin response factor 19; AltName: Full=Auxin-responsive protein IAA22 >gi|375401554|gb|AAG35176.1| ARF11/IAA22 [Arabidopsis thaliana] >gi|49616363|gb|AAT67078.1| ARF19 [Arabidopsis thaliana] >gi|56961712|gb|AAB91321.2| early auxin-induced IAA22 [Arabidopsis thaliana]						nr -
Unigene72182_All	492	0.00	8.34	1.73	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	2.25E-23	Up	1.08E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene72182_All//gi|224014626|ref|XP_002296975.1|/9.00E-14//chitinase [Thalassiosira pseudonana CCMP1335] >gi|220968355|gb|EED86703.1| chitinase [Thalassiosira pseudonana CCMP1335]						nr -
Unigene72183_All	496	0.11	3.78	1.18	0.20	1.46	1.82	1.19	1.18	0.48	5.16E+00	2.00E-09	Up	3.48E+00	1.21E-02		2.86E+00	6.45E-03		3.18E+00	9.74E-04	Up	-1.67E-02	1.02E+00		-1.31E+00	1.15E-01		Unigene72183_All//gi|15222072|ref|NP_172738.1|/6.00E-76//UGE1 (UDP-D-glucose/UDP-D-galactose 4-epimerase 1); UDP-glucose 4-epimerase/ protein dimerization [Arabidopsis thaliana] >gi|12643760|sp|Q42605.2|GALE1_ARATH RecName: Full=UDP-glucose 4-epimerase 1; AltName: Full=UDP-galactose 4-epimerase 1; AltName: Full=Galactowaldenase 1 >gi|8698725|gb|AAF78483.1|AC012187_3 Strong similarity to UDPglucose 4-epimerase from Arabidopsis thaliana gi|2129759 and is a member of the NAD dependent Epimerase/Dehydratase PF|01370 family. ESTs gb|AI100184, gb|T22969, gb|T22968, gb|H76416, gb|AI998807 come from this gene >gi|15809880|gb|AAL06868.1| At1g12780/F13K23_21 [Arabidopsis thaliana] >gi|21539429|gb|AAM53267.1| uridine diphosphate glucose epimerase [Arabidopsis thaliana] >gi|23197648|gb|AAN15351.1| uridine diphosphate glucose epimerase [Arabidopsis thaliana]	Unigene72183_All//4.00E-77//AT1G12780| UGE1 (UDP-D-glucose/UDP-D-galactose 4-epimerase 1); UDP-glucose 4-epimerase/ protein dimerization	Unigene72183_All//0.00E+00//TC162602		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism		nr +
Unigene72185_All	498	0.00	4.88	0.86	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.72E-14	Up	9.74E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene72185_All//gi|115456697|ref|NP_001051949.1|/2.00E-12//0s03g0856400 [Oryza sativa Japonica Group] >gi|113550420|dbj|BAF13863.1| Os03g0856400 [Oryza sativa Japonica Group]	Unigene72185_All//2.00E-12//AT4G16360| AMP-activated protein kinase					nr +
Unigene72186_All	499	0.00	2.44	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	5.45E-07	Up	null	null		null	null		null	null		null	null		null	null		Unigene72186_All//sp|Q8R478|WBP2_RAT//9.00E-09//WW domain-binding protein 2 OS=Rattus norvegicus GN=Wbp2 PE=1 SV=1						swissprot +
Unigene72187_All	503	0.00	3.93	0.85	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.96E-11	Up	9.73E+00	1.37E-02		null	null		null	null		null	null		null	null										ESTscan -
Unigene72188_All	505	0.00	2.61	0.32	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.49E-07	Up	8.31E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene72188_All//gi|15237458|ref|NP_198877.1|/5.00E-39//glycerol-3-phosphate dehydrogenase (NAD+) / GPDH [Arabidopsis thaliana] >gi|75337065|sp|Q9SCX9.1|GPDA_ARATH RecName: Full=Glycerol-3-phosphate dehydrogenase [NAD+], chloroplastic; Flags: Precursor >gi|6688813|emb|CAB64726.1| dihydroxyacetone 3-phosphate reductase [Arabidopsis thaliana] >gi|9758088|dbj|BAB08532.1| dihydroxyacetone 3-phosphate reductase [Arabidopsis thaliana]	Unigene72188_All//3.00E-40//AT5G40610| glycerol-3-phosphate dehydrogenase (NAD+) / GPDH			ko00564|Glycerophospholipid metabolism		nr -
Unigene72189_All	506	0.00	3.81	0.84	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.72E-11	Up	9.72E+00	1.37E-02		null	null		null	null		null	null		null	null										ESTscan -

Unigene7219_All	2020	0.00	0.15	0.11	0.07	0.07	0.13	70.33	18.83	50.31	7.23E+00	4.37E-02		6.72E+00	1.39E-01		-1.18E-01	9.10E-01		8.58E-01	6.30E-01		-1.90E+00	0.00E+00	Down	-4.83E-01	1.63E-36		Unigene7219_All//gi|47078691|gb|AAT09980.1|//0.00E+00//cell wall apoplastic invertase [Vitis vinifera]	Unigene7219_All//0.00E+00//AT3G13790| ATBFRUCT1; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene7219_All//0.00E+00//CO130427		ko00500|Starch and sucrose metabolism//ko00052|Galactose metabolism		nr +
Unigene72190_All	506	0.00	8.41	0.74	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	3.03E-24	Up	9.52E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72190_All//gi|159482968|ref|XP_001699537.1|//1.00E-06//sar-type small GTPase [Chlamydomonas reinhardtii] >gi|158272804|gb|EDO98600.1| sar-type small GTPase [Chlamydomonas reinhardtii]	Unigene72190_All//1.00E-06//AT3G62560| GTP-binding protein, putative			ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene72191_All	510	0.00	3.28	0.31	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.53E-09	Up	8.29E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene72191_All//gi|300680982|sp|Q8LNW6.2|FLOT3_ORYSJ//4.00E-14//RecName: Full=Flotillin-like protein 3; AltName: Full=Nodulin-like protein 3	Unigene72191_All//4.00E-13//AT5G25260| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: cultured cell; CONTAINS InterPro DOMAIN/s: Band 7 protein (InterPro:IPR001107); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25250.1); Has 4214 Blast hits to 3442 proteins in 652 species: Archae - 14; Bacteria - 1365; Metazoa - 1204; Fungi - 198; Plants - 130; Viruses - 8; Other Eukaryotes - 1295 (source: NCBI BLink).					nr +
Unigene72192_All	510	0.92	27.82	5.01	0.20	0.41	1.42	0.66	0.33	0.78	4.91E+00	9.50E-68	Up	2.44E+00	6.04E-07	Up	1.05E+00	6.11E-01		2.86E+00	7.12E-03		-1.02E+00	3.99E-01		2.36E-01	8.04E-01									
Unigene72193_All	511	0.00	2.68	1.88	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	7.77E-08	Up	1.09E+01	2.45E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene72194_All	511	0.00	3.37	1.25	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.96E-10	Up	1.03E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene72194_All//gi|4501883|ref|NP_001604.1|//3.00E-93//actin, aortic smooth muscle [Homo sapiens] >gi|6671507|ref|NP_031418.1| actin, aortic smooth muscle [Mus musculus] >gi|78045238|ref|NP_001029674.1| actin, aortic smooth muscle [Bos taurus] >gi|110625958|ref|NP_112266.1| actin, aortic smooth muscle [Rattus norvegicus] >gi|156119362|ref|NP_001095152.1| actin, aortic smooth muscle [Oryctolagus cuniculus] >gi|197097944|ref|NP_001126814.1| actin, aortic smooth muscle [Pongo abelii] >gi|213688375|ref|NP_001135417.1| actin, aortic smooth muscle [Homo sapiens] >gi|257470979|ref|NP_001158122.1| actin, aortic smooth muscle [Sus scrofa] >gi|73996085|ref|XP_534781.2| PREDICTED: similar to Actin, aortic smooth muscle (Alpha-actin 2) [Canis familiaris] >gi|114631685|ref|XP_521550.2|	Unigene72194_All//1.00E-82//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene72194_All//1.00E-63//TC153744		ko04145|Phagosome		nr -
Unigene72195_All	512	0.00	1.58	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	9.31E-05	Up	1.04E+01	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene72195_All//sp|P51884|LUM_HUMAN//2.00E-53//Lumican OS=Homo sapiens GN=LUM PE=1 SV=2						swissprot -
Unigene72196_All	513	0.00	9.98	2.28	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	3.53E-29	Up	1.12E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene72196_All//sp|Q8NCE2|MTMR6_HUMAN//1.00E-21//Myotubularin-related protein 14 OS=Homo sapiens GN=MTMR14 PE=1 SV=2						swissprot +
Unigene72198_All	519	0.00	3.81	0.82	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.96E-11	Up	9.68E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene72198_All//gi|254680089|gb|ACT78691.1|//5.00E-07//DEP1 [Triticum urartu]						nr +
Unigene72199_All	520	0.00	3.61	1.84	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.10E-10	Up	1.08E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene72199_All//gi|416759|sp|Q04732.1|ARP_EUGGR//3.00E-14//RecName: Full=Calcium-binding acidic-repeat protein; Short=ARP; Flags: Precursor >gi|18408|emb|CAA48495.1| acidic repeat protein [Euglena gracilis]						nr +
Unigene72200_All	521	0.00	7.88	2.25	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.25E-23	Up	1.11E+01	1.77E-06	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene72201_All	521	0.00	5.15	0.61	0.19	0.00	0.00	0.00	0.00	0.08	1.23E+01	2.80E-15	Up	9.26E+00	4.47E-02		-7.58E+00	3.10E-01		-7.58E+00	3.95E-01		null	null		6.26E+00	6.39E-01				Unigene72201_All//2.00E-10//ES842151					
Unigene72202_All	522	0.00	4.27	2.45	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.09E-12	Up	1.13E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene72202_All//gi|12585492|sp|Q95NE7.1|VATE_CITLL//2.00E-36//RecName: Full=V-type proton ATPase subunit E; Short=V-ATPase subunit E; AltName: Full=Vacuolar proton pump subunit E; AltName: Full=CIVE-1 >gi|5733660|gb|AAD49706.1| vacuolar V-H+ATPase subunit E [Citrus limon]	Unigene72202_All//1.00E-20//AT4G11150| TUF (VACUOLAR ATP SYNTHASE SUBUNIT E1); proton-transporting ATPase, rotational mechanism			ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr +
Unigene72203_All	523	0.00	4.65	1.02	0.00	0.13	0.00	0.00	0.00	0.00	1.22E+01	7.72E-14	Up	9.99E+00	4.01E-03		7.04E+00	6.03E-01		null	null		null	null		null	null									ESTscan +
Unigene72204_All	526	0.00	4.24	0.40	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.09E-12	Up	8.66E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72204_All//gi|11994428|dbj|BAB02430.1|//2.00E-47//nucleolar protein [Arabidopsis thaliana]	Unigene72204_All//2.00E-36//AT3G12860| nucleolar protein Nop56, putative					nr -
Unigene72205_All	526	0.00	2.60	0.30	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	7.77E-08	Up	8.25E+00	2.36E-01		null	null		null	null		null	null		null	null		Unigene72205_All//gi|219563180|gb|ACL27948.1|//5.00E-06//keratin associated protein [Oryza sativa Indica Group]						nr +
Unigene72207_All	528	0.00	6.62	0.71	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	6.73E-20	Up	9.46E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72207_All//gi|3777559|gb|AAC64934.1|//7.00E-23//collagen-like [Griffithsia japonica]	Unigene72207_All//3.00E-06//AT1G76010| nucleic acid binding			ko03040|Spliceosome//ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr -
Unigene72208_All	532	0.00	2.48	1.20	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.49E-07	Up	1.02E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene72208_All//gi|168012021|ref|XP_001758701.1|//6.00E-54//SNF2 family DNA-dependent ATPase [Physcomitrella patens subsp. patens] >gi|162690311|gb|EDQ76679.1| SNF2 family DNA-dependent ATPase [Physcomitrella patens subsp. patens]	Unigene72208_All//2.00E-53//AT2G25170| PKL (PICKLE); ATPase/ DNA binding / DNA helicase					nr +
Unigene72209_All	533	0.00	1.90	1.20	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	7.22E-06	Up	1.02E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene72209_All//gi|17221648|dbj|BAB78478.1|//4.00E-11//preproMP73 [Cucurbita maxima]				ko03040|Spliceosome		nr +
Unigene7221_All	484	0.86	0.31	1.87	5.04	4.55	4.20	1.83	0.17	0.74	-1.46E+00	2.34E-01		1.11E+00	1.49E-01		-1.47E-01	7.54E-01		-2.64E-01	5.67E-01		-3.41E+00	1.40E-04	Down	-1.31E+00	4.40E-02				Unigene7221_All//2.00E-124//DR456034					
Unigene72210_All	534	0.00	67.56	22.04	0.00	0.00	0.00	0.00	0.00	0.00	1.60E+01	3.69E-208	Up	1.44E+01	3.65E-66	Up	null	null		null	null		null	null		null	null		Unigene72210_All//gi|159488703|ref|XP_001702342.1|//3.00E-47//ribosomal protein S7, component of cytosolic 80S ribosome and 40S small subunit [Chlamydomonas reinhardtii] >gi|158271136|gb|EDO96962.1| ribosomal protein S7 [Chlamydomonas reinhardtii]	Unigene72210_All//4.00E-40//AT1G48830| 40S ribosomal protein S7 (RPS7A)			ko03010|Ribosome		nr -
Unigene72211_All	536	0.00	3.78	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.53E-11	Up	9.63E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene72211_All//gi|115443623|ref|NP_001045591.1|//2.00E-18//Os02g0101700 [Oryza sativa Japonica Group] >gi|113535122|dbj|BAF07505.1| Os02g0101700 [Oryza sativa Japonica Group]	Unigene72211_All//3.00E-18//AT4G38600| KAK (KAKTUS); ubiquitin-protein ligase			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene72212_All	538	0.00	4.43	0.59	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.50E-13	Up	9.21E+00	4.47E-02		null	null		null	null		null	null		null	null		Unigene72212_All//gi|116056034|emb|CAL58567.1|//6.00E-07//Nucleolar GTPase/ATPase p130 (ISS) [Ostreococcus tauri]						nr -
Unigene72213_All	539	0.00	2.73	0.59	0.00	0.26	0.00	0.00	0.00	0.00	1.14E+01	2.10E-08	Up	9.21E+00	4.47E-02		8.00E+00	3.17E-01		null	null		null	null		null	null		Unigene72213_All//gi|300176285|emb|CBK23596.2|//9.00E-51//Acetate:succinate CoA Transferase (ASCT) [Blastocystis hominis]						nr -
Unigene72214_All	541	0.00	2.44	0.20	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.49E-07	Up	7.62E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene72214_All//sp|P11211|NCAP_CHAV//6.00E-27//Nucleoprotein OS=Chandipura virus (strain 1653514) GN=N PE=3 SV=1						swissprot -
Unigene72215_All	541	0.00	4.40	1.18	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.50E-13	Up	1.02E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene72215_All//sp|Q7ZYM8|C1O30_XENLA//6.00E-06//UPF0439 protein C9orf30 homolog OS=Xenopus laevis PE=2 SV=1						swissprot +
Unigene72216_All	544	0.00	3.45	2.74	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.10E-10	Up	1.14E+01	3.21E-08	Up	null	null		null	null		null	null		null	null									
Unigene72217_All	547	0.00	4.17	0.39	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.63E-13	Up	8.61E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72217_All//gi|186479005|ref|NP_001117376.1|//2.00E-07//WAVE2 [Arabidopsis thaliana]	Unigene72217_All//1.00E-08//AT1G29170| WAVE2					nr +
Unigene72218_All	549	0.00	8.21	2.62	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.08E-25	Up	1.14E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene72218_All//gi|157093371|gb|ABV22340.1|//2.00E-20//calponin domain-containing protein [Noctiluca scintillans]	Unigene72218_All//3.00E-07//AT2G47500| ATP binding / microtubule motor					nr -
Unigene72219_All	550	0.00	3.78	1.16	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.94E-12	Up	1.02E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene72219_All//gi|300264016|gb|EFJ48214.1|//5.00E-35//E1 subunit of 2-oxoglutarate dehydrogenase [Volvox carteri f. nagariensis]	Unigene72219_All//8.00E-34//AT5G65750| 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative			ko00380|Tryptophan metabolism//ko00020|Citrate cycle (TCA cycle)//ko00310|Lysine degradation		nr +

Unigene7222_All	528	4.46	23.70	12.51	5.66	8.22	22.58	12.73	10.29	5.58	2.41E+00	1.78E-32	Up	1.49E+00	3.98E-09	Up	5.38E-01	6.63E-02		2.00E+00	3.18E-26	Up	-3.07E-01	1.51E-01		-1.19E+00	6.77E-09	Down	Unigene7222_All//gi|2245030|emb|CAB10450.1|//6.00E-22//acyl-CoA oxidase like protein [Arabidopsis thaliana] >gi|7268426|emb|CAB78718.1| acyl-CoA oxidase like protein [Arabidopsis thaliana]	Unigene7222_All//1.00E-21//AT4G16765| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene7222_All//4.00E-51//TC168767				nr -
Unigene72220_All	550	0.00	5.71	1.45	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.07E-18	Up	1.05E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene72220_All//gi|159483795|ref|XP_001699946.1|//2.00E-08//gamete-specific transcription factor [Chlamydomonas reinhardtii] >gi|158281888|gb|EDP07642.1| gamete-specific transcription factor [Chlamydomonas reinhardtii]						nr -
Unigene72221_All	551	0.00	2.02	0.68	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.99E-06	Up	9.40E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72221_All//gi|42572531|ref|NP_974361.1|//1.00E-15//HMT-1; homocysteine S-methyltransferase [Arabidopsis thaliana]	Unigene72221_All//7.00E-17//AT3G25900| HMT-1; homocysteine S-methyltransferase			ko00270|Cysteine and methionine metabolism		nr +
Unigene72222_All	551	0.19	2.76	1.06	0.00	0.00	0.16	0.46	0.00	0.14	3.86E+00	1.23E-06	Up	2.49E+00	3.75E-02		null	null		7.36E+00	4.72E-01		-8.85E+00	4.03E-02		-1.67E+00	2.56E-01		Unigene72222_All//gi|15220428|ref|NP_176906.1|//2.00E-14//F-box family protein [Arabidopsis thaliana] >gi|75263210|sp|Q9FYF4.1|FB77_ARATH RecName: Full=Putative F-box protein At1g67390 >gi|8628620|gb|AAG00243.1|AC002130_8 F1N21.21 [Arabidopsis thaliana]	Unigene72222_All//1.00E-15//AT1G67390| F-box family protein					nr +
Unigene72223_All	553	0.00	4.76	1.54	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.44E-15	Up	1.06E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene72223_All//gi|121501708|gb|ABM55249.1|//5.00E-52//casein kinase [Beta vulgaris]	Unigene72223_All//7.00E-52//AT5G57015| ck1l2 (Casein Kinase I-like 12); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase					nr +
Unigene72224_All	554	0.00	8.41	2.21	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.46E-26	Up	1.11E+01	9.10E-07	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene72225_All	555	0.00	5.02	1.54	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.42E-16	Up	1.06E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene72225_All//gi|11141605|gb|AAG32022.1|AF277458_1//3.00E-10//LEUNIG [Arabidopsis thaliana]				ko03022|Basal transcription factors		nr +
Unigene72226_All	555	0.00	4.47	1.44	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.98E-14	Up	1.05E+01	1.72E-04	Up	null	null		null	null		null	null		null	null										
Unigene72227_All	556	0.00	6.01	0.96	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	4.94E-19	Up	9.90E+00	4.01E-03		null	null		null	null		null	null		null	null		Unigene72227_All//sp|Q9V496|APLP_DROME//2.00E-54//Apolipophorins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2						swissprot +
Unigene72228_All	557	0.00	4.00	1.15	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.09E-12	Up	1.02E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene72228_All//gi|255080116|ref|XP_002503638.1|//4.00E-08//predicted protein [Micromonas sp. RCC299] >gi|226518905|gb|ACO64896.1| predicted protein [Micromonas sp. RCC299]	Unigene72228_All//6.00E-05//AT3G24800| PRT1 (PROTEOLYSIS 1); ubiquitin-protein ligase					nr -
Unigene72229_All	558	0.00	2.63	0.76	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	2.10E-08	Up	9.58E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene72229_All//sp|Q9VLJ6|ACER_DROME//2.00E-89//Angiotensin-converting enzyme-related protein OS=Drosophila melanogaster GN=Acer PE=1 SV=1						swissprot -
Unigene7223_All	1024	0.36	1.19	0.68	4.28	2.93	1.98	0.08	0.12	0.00	1.73E+00	8.94E-03		9.18E-01	3.11E-01		-5.49E-01	4.99E-02		-1.11E+00	1.16E-04	Down	5.67E-01	7.80E-01		-6.37E+00	3.55E-01		Unigene7223_All//gi|85720770|gb|ABC75835.1|//5.00E-71//SOC1 [Glycine max]	Unigene7223_All//1.00E-55//AT2G45660| AGL20 (AGAMOUS-LIKE 20); transcription factor	Unigene7223_All//4.00E-22//ES835572	MADS			nr +
Unigene72230_All	559	0.00	4.53	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.05E-14	Up	8.57E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72230_All//gi|8118507|gb|AAF73006.1|AF262997_1//1.00E-60//NADP-dependent malic protein [Ricinus communis]	Unigene72230_All//1.00E-61//AT2G19900| ATNADP-ME1 (NADP-malic enzyme 1); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor			ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene72231_All	565	0.00	3.59	1.23	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.53E-11	Up	1.03E+01	6.13E-04	Up	null	null		null	null		null	null		null	null										
Unigene72232_All	565	0.00	4.22	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.50E-13	Up	null	null		null	null		null	null		null	null		null	null										ESTscan -
Unigene72233_All	567	0.09	5.27	2.16	0.18	0.24	0.00	0.00	0.00	0.28	5.84E+00	1.49E-15	Up	4.55E+00	1.02E-05	Up	4.67E-01	8.75E-01		-7.46E+00	3.95E-01		null	null		8.13E+00	1.39E-01		Unigene72233_All//gi|18379242|ref|NP_563701.1|//1.00E-67//SDD1 (STOMATAL DENSITY AND DISTRIBUTION); serine-type endopeptidase [Arabidopsis thaliana] >gi|3142298|gb|AAC16749.1| Strong similarity to protein SBT1 gb|X98929 from Lycopersicum esculentum [Arabidopsis thaliana]	Unigene72233_All//6.00E-69//AT1G04110| SDD1 (STOMATAL DENSITY AND DISTRIBUTION); serine-type endopeptidase					nr +
Unigene72234_All	567	0.00	4.02	3.29	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	5.63E-13	Up	1.17E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene72234_All//gi|18401141|ref|NP_566548.1|//1.00E-18//MPPalpha (mitochondrial processing peptidase alpha subunit); catalytic/ metal ion binding / metalloendopeptidase/ zinc ion binding [Arabidopsis thaliana] >gi|29839443|sp|O04308.1|MPPA2_ARATH RecName: Full=Probable mitochondrial-processing peptidase subunit alpha-2; AltName: Full=Alpha-MPP 2; Flags: Precursor >gi|2062185|gb|AAB63629.1| mitochondrial processing peptidase alpha subunit precusor isolog [Arabidopsis thaliana] >gi|9279647|dbj|BAB01147.1| mitochondrial processing peptidase alpha subunit [Arabidopsis thaliana]	Unigene72234_All//7.00E-20//AT3G16480| MPPalpha (mitochondrial processing peptidase alpha subunit); catalytic/ metal ion binding / metalloendopeptidase/ zinc ion binding			ko00190|Oxidative phosphorylation		nr -
Unigene72235_All	567	0.00	5.45	1.78	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.38E-17	Up	1.08E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene72235_All//sp|Q9V496|APLP_DROME//1.00E-35//Apolipophorins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2						swissprot -
Unigene72236_All	570	0.00	2.84	0.75	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.96E-09	Up	9.55E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene72236_All//sp|Q9I7U4|TITIN_DROME//2.00E-83//Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3						swissprot -
Unigene72237_All	573	0.00	9.02	2.51	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	1.80E-29	Up	1.13E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene72237_All//sp|Q9V427|INX2_DROME//7.00E-36//Innexin inx2 OS=Drosophila melanogaster GN=inx2 PE=1 SV=1						swissprot +
Unigene72238_All	573	0.00	7.60	1.77	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	8.00E-25	Up	1.08E+01	1.27E-05	Up	null	null		null	null		null	null		null	null										
Unigene72239_All	583	0.00	5.21	1.64	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.67E-17	Up	1.07E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene72239_All//gi|297604927|ref|NP_001056343.2|//4.00E-35//Os05g0566500 [Oryza sativa Japonica Group] >gi|255676582|dbj|BAF18257.2| Os05g0566500 [Oryza sativa Japonica Group]	Unigene72239_All//4.00E-35//AT4G20980| eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative					nr -
Unigene72240_All	583	0.00	4.17	0.64	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.72E-14	Up	9.32E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72240_All//gi|115470159|ref|NP_001058678.1|//2.00E-22//Os07g0101500 [Oryza sativa Japonica Group] >gi|113610214|dbj|BAF20592.1| Os07g0101500 [Oryza sativa Japonica Group]	Unigene72240_All//2.00E-22//AT1G07420| SMO2-1 (STEROL 4-ALPHA-METHYL-OXIDASE 2-1); 4-alpha-methyl-delta7-sterol-4alpha-methyl oxidase/ C-4 methylsterol oxidase			ko00100|Steroid biosynthesis		nr +
Unigene72241_All	585	0.00	6.67	0.46	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	3.24E-22	Up	8.83E+00	7.94E-02		null	null		null	null		null	null		null	null		Unigene72241_All//sp|Q24009|BICC_DROME//3.00E-35//Protein bicaudal C OS=Drosophila melanogaster GN=BicC PE=1 SV=2						swissprot +
Unigene72242_All	586	0.00	6.74	0.82	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.66E-22	Up	9.68E+00	7.44E-03		null	null		null	null		null	null		null	null		Unigene72242_All//gi|297840471|ref|XP_002888117.1|//2.00E-59//fed A [Arabidopsis lyrata subsp. lyrata] >gi|297333958|gb|EFH84376.1| fed A [Arabidopsis lyrata subsp. lyrata]	Unigene72242_All//2.00E-48//AT1G60950| FED A; 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding			ko00195|Photosynthesis		nr +
Unigene72243_All	587	0.00	4.14	0.45	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.71E-14	Up	8.83E+00	7.94E-02		null	null		null	null		null	null		null	null		Unigene72243_All//gi|8163730|gb|AAF73828.1|AF162665_1//8.00E-69//aldehyde dehydrogenase [Oryza sativa]	Unigene72243_All//1.00E-63//AT1G23800| ALDH2B7; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)			ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr +
Unigene72244_All	588	0.00	5.00	2.72	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.01E-16	Up	1.14E+01	8.43E-09	Up	null	null		null	null		null	null		null	null		Unigene72244_All//gi|226455037|gb|EEH52341.1|//1.00E-45//dead-box ATP-dependent RNA helicase [Micromonas pusilla CCMP1545]	Unigene72244_All//5.00E-36//AT1G55150| DEAD box RNA helicase, putative (RH20)					nr -
Unigene72245_All	588	0.00	5.26	0.91	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.38E-17	Up	9.82E+00	4.01E-03		null	null		null	null		null	null		null	null		Unigene72245_All//gi|149072021|ref|YP_001293592.1|//4.00E-26//ribosomal protein L5 [Rhodomonas salina] >gi|224493189|sp|A6WW13.1|RK5_RHDSA RecName: Full=50S ribosomal protein L5, chloroplastic >gi|134302972|gb|ABO70776.1| ribosomal protein L5 [Rhodomonas salina]	Unigene72245_All//6.00E-18//AT4G01310| ribosomal protein L5 family protein			ko03010|Ribosome		nr +
Unigene72246_All	591	0.00	5.74	1.08	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.54E-19	Up	1.01E+01	1.15E-03		null	null		null	null		null	null		null	null										ESTscan +
Unigene72247_All	591	0.00	7.80	2.16	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.84E-26	Up	1.11E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene72247_All//gi|37962884|gb|AAR05796.1|//7.00E-79//NADP+-isocitrate dehydrogenase [Pinus pinaster]	Unigene72247_All//1.00E-77//AT5G14590| isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative			ko04146|Peroxisome//ko00480|Glutathione metabolism//ko00020|Citrate cycle (TCA cycle)		nr -

Unigene72248_All	592	0.00	3.51	1.17	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.93E-12	Up	1.02E+01	6.13E-04	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene72249_All	598	0.00	3.47	0.80	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.93E-12	Up	9.65E+00	7.44E-03		null	null		null	null		null	null		null	null		Unigene72249_All//gi|115465145|ref|XP_001656172.1|//1.00E-33//Os05g0539400 [Oryza sativa Japonica Group] >gi|122168850|sp|Q0DGD7.1|BGAL8_ORYSJ RecName: Full=Beta-galactosidase 8; Short=Lactase 8; Flags: Precursor >gi|113579723|dbj|BAF18086.1|Os05g0539400 [Oryza sativa Japonica Group]	Unigene72249_All//2.00E-27//AT1G72990| BGAL17 (beta-galactosidase 17); beta-galactosidase/ catalytic/ cation binding			ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation//ko00531|Glycosaminoglycan degradation//ko00604|Glycosphingolipid biosynthesis - ganglio series		nr +
Unigene72250_All	598	0.00	5.59	1.42	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.94E-19	Up	1.05E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene72250_All//gi|301098633|ref|XP_002898409.1|//2.00E-08//lamin-like protein [Phytophthora infestans T30-4] >gi|262105180|gb|EEY63232.1| lamin-like protein [Phytophthora infestans T30-4]						nr -
Unigene72251_All	598	0.00	2.88	0.89	0.00	0.06	0.00	0.00	0.00	0.00	1.15E+01	7.96E-10	Up	9.80E+00	4.01E-03		5.85E+00	8.20E-01		null	null		null	null		null	null		Unigene72251_All//gi|34398263|gb|AAQ67226.1|//1.00E-104//protein phosphatase 2A catalytic subunit [Solanum lycopersicum]	Unigene72251_All//2.00E-16//ES838876	Unigene72251_All//2.00E-16//ES838876				nr -
Unigene72253_All	605	0.00	5.86	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	3.45E-20	Up	8.46E+00	1.39E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene72254_All	609	0.00	6.82	1.75	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.15E-23	Up	1.08E+01	6.60E-06	Up	null	null		null	null		null	null		null	null		Unigene72254_All//sp|Q6PA23|LIPHA_XENLA//1.00E-26//Lipase member H-A OS=Xenopus laevis GN=liph-a PE=2 SV=1						swissprot -
Unigene72255_All	610	0.00	2.49	0.17	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.09E-08	Up	7.45E+00	3.92E-01		null	null		null	null		null	null		null	null		Unigene72255_All//gi|159480530|ref|XP_001698335.1|//3.00E-07//hypothetical protein CHLREDRAFT_187642 [Chlamydomonas reinhardtii] >gi|158282075|gb|EDP07828.1| predicted protein [Chlamydomonas reinhardtii]						nr -
Unigene72256_All	611	0.00	3.81	1.48	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.90E-13	Up	1.05E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene72256_All//gi|224589272|gb|ACN39486.1|//3.00E-15//serpin 4 [Triticum aestivum]	Unigene72256_All//2.00E-16//AT2G26390| serpin, putative / serine protease inhibitor, putative					nr +
Unigene72257_All	612	0.00	2.98	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.14E-10	Up	null	null		null	null		null	null		null	null		null	null		Unigene72257_All//gi|12230437|sp|P93227.1|FNTA_SOLLC//4.00E-51//RecName: Full=Protein farnesyltransferase/geranylgeranyl transferase type-1 subunit alpha; AltName: Full=CAAX farnesyltransferase subunit alpha; AltName: Full=Ras proteins prenyltransferase subunit alpha; AltName: Full=FTase-alpha; AltName: Full=Type I protein geranyl-geranyltransferase subunit alpha; Short=GGTase-I-alpha >gi|1815666|gb|AAC49665.1| farnesyl protein transferase subunit A [Solanum lycopersicum]	Unigene72257_All//4.00E-43//AT3G59380| FTA (FARNESYLTRANSFERASE A); farnesyltransferase/ protein heterodimerization/ protein prenyltransferase					nr +
Unigene72258_All	616	0.00	3.37	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	7.93E-12	Up	8.43E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72258_All//sp|Q03141|MARK3_MOUSE//1.00E-10//MAP/microtubule affinity-regulating kinase 3 OS=Mus musculus GN=Mark3 PE=1 SV=2						swissprot -
Unigene72259_All	620	0.00	3.11	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.72E-11	Up	8.42E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72259_All//gi|1009234|gb|AAA79033.1|//8.00E-47//SUP2 [Nicotiana tabacum]	Unigene72259_All//7.00E-46//AT1G18070| EF-1-alpha-related GTP-binding protein, putative					nr +
Unigene72261_All	622	0.00	5.46	0.34	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	2.54E-19	Up	8.42E+00	1.39E-01		null	null		null	null		null	null		null	null										ESTscan -
Unigene72262_All	630	0.00	2.65	1.69	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.53E-09	Up	1.07E+01	6.60E-06	Up	null	null		null	null		null	null		null	null		Unigene72262_All//gi|225438483|ref|XP_002278249.1|//2.00E-43//PREDICTED: similar to 26S proteasome subunit RPN5b [Vitis vinifera]	Unigene72262_All//2.00E-43//AT5G09600| EMB2107 (EMBRYO DEFECTIVE 2107)			ko03050|Proteasome		nr +
Unigene72263_All	633	0.00	5.20	0.59	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	9.62E-19	Up	9.20E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72263_All//sp|Q99MY2|NUDT4_RAT//2.00E-16//Diphosphoinositol polyphosphate phosphohydrolase 2 OS=Rattus norvegicus GN=Nudt4 PE=2 SV=1						swissprot +
Unigene72264_All	634	0.00	3.60	1.26	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.62E-13	Up	1.03E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene72264_All//sp|P14199|REF2P_DROME//3.00E-19//Protein ref(2)P OS=Drosophila melanogaster GN=ref(2)P PE=1 SV=2						swissprot +
Unigene72265_All	639	0.66	16.26	4.00	0.00	0.00	0.57	0.00	0.07	0.00	4.63E+00	4.58E-48	Up	2.61E+00	1.93E-07	Up	null	null		9.14E+00	2.37E-02		6.03E+00	6.28E-01		null	null		Unigene72265_All//gi|148595724|emb|CAM12541.1|//2.00E-43//YA3 [Antirrhinum majus]	Unigene72265_All//3.00E-105//TC164284	CCAAT				nr -
Unigene72266_All	642	0.00	4.34	1.33	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.42E-16	Up	1.04E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene72266_All//gi|297812163|ref|XP_002873965.1|//5.00E-26//EMB2734 [Arabidopsis lyrata subsp. lyrata] >gi|297319802|gb|EFH50224.1| EMB2734 [Arabidopsis lyrata subsp. lyrata]	Unigene72266_All//8.00E-27//AT5G19820| emb2734 (embryo defective 2734); binding / lyase					nr +
Unigene72267_All	646	0.00	5.10	2.56	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	9.62E-19	Up	1.13E+01	4.30E-09	Up	null	null		null	null		null	null		null	null		Unigene72267_All//gi|159473597|ref|XP_001694920.1|//5.00E-37//rab GDP dissociation inhibitor protein [Chlamydomonas reinhardtii] >gi|158276299|gb|EDP02072.1| rab GDP dissociation inhibitor protein [Chlamydomonas reinhardtii]	Unigene72267_All//8.00E-37//AT2G44100| ATGDI1 (ARABIDOPSIS THALIANA GUANOSINE NUCLEOTIDE DIPHOSPHATE DISSOCIATION INHIBITOR 1); RAB GDP-dissociation inhibitor					nr +
Unigene72268_All	655	0.00	4.72	0.57	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.38E-17	Up	9.15E+00	2.48E-02		null	null		null	null		null	null		null	null		Unigene72268_All//gi|4587520|gb|AAD25751.1|AC007060 9//6.00E-35//Strong similarity to gb|X71057 protein kinase from Nicotiana tabacum and contains PF|00069 eukaryotic protein kinase domain [Arabidopsis thaliana]	Unigene72268_All//2.00E-34//AT1G30640| protein kinase, putative					nr -
Unigene72269_All	658	0.08	3.54	2.83	0.00	0.00	0.00	0.00	0.00	0.00	5.48E+00	6.51E-12	Up	5.15E+00	4.94E-09	Up	null	null		null	null		null	null		null	null		Unigene72269_All//gi|38014843|gb|AAB60583.1|//2.00E-27//CdS1 protein [Rattus norvegicus] >gi|149061756|gb|EDM12179.1| rCG47614, isoform CRA_b [Rattus norvegicus]						nr +
Unigene72270_All	669	0.00	4.70	1.83	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.07E-18	Up	1.08E+01	9.10E-07	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene72271_All	673	0.00	6.40	1.11	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.56E-24	Up	1.01E+01	3.26E-04	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene72272_All	674	0.00	4.21	0.32	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	3.82E-16	Up	8.30E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72272_All//gi|298713481|emb|CBJ27036.1|//8.00E-22//RME1, RME-1/EHD family ATPase with a C-terminal EH domain [Ectocarpus siliculosus]	Unigene72272_All//2.00E-18//AT3G20290| ATEHD1 (EPS15 HOMOLOGY DOMAIN 1); GTP binding / GTPase/ calcium ion binding					nr -
Unigene72273_All	678	0.00	6.50	1.57	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	4.10E-25	Up	1.06E+01	6.60E-06	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene72275_All	683	0.00	4.60	2.11	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.07E-18	Up	1.10E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene72275_All//gi|115445085|ref|NP_001046322.1|//4.00E-43//Os02g0221500 [Oryza sativa Japonica Group] >gi|113535853|dbj|BAF08236.1| Os02g0221500 [Oryza sativa Japonica Group]	Unigene72275_All//8.00E-44//AT3G07810| heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative			ko03040|Spliceosome		nr +
Unigene72276_All	686	0.00	29.03	12.42	0.00	0.00	0.00	0.00	0.00	0.00	1.48E+01	1.45E-114	Up	1.36E+01	1.02E-47	Up	null	null		null	null		null	null		null	null		Unigene72276_All//gi|40716077|gb|AAR88661.1|//8.00E-49//fructose-bisphosphate aldolase [Pandanus amaryllifolius]	Unigene72276_All//2.00E-45//AT4G26530| fructose-bisphosphate aldolase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene72277_All	705	0.00	6.11	1.81	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.56E-24	Up	1.08E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene72277_All//gi|1352831|sp|P48413.1|VATB_CYACA//2.00E-68//RecName: Full=V-type proton ATPase subunit B; Short=V-ATPase subunit B; AltName: Full=Vacuolar proton pump subunit B >gi|576661|gb|AAA85821.1| V-ATPase B subunit [Cyanidium caldarium]	Unigene72277_All//1.00E-62//AT4G38510| vacuolar ATP synthase subunit B, putative / V-ATPase B subunit, putative / vacuolar proton pump B subunit, putative / V-ATPase 57 kDa subunit, putative			ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene72278_All	709	0.00	5.50	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	3.24E-22	Up	9.82E+00	1.15E-03		null	null		null	null		null	null		null	null		Unigene72278_All//sp|Q9GRX4|NONA_DROLR//4.00E-47//Protein no-on-transient A OS=Drosophila litoralis GN=nonA PE=2 SV=1						swissprot -
Unigene72279_All	713	0.00	8.95	4.26	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	1.84E-36	Up	1.21E+01	8.91E-17	Up	null	null		null	null		null	null		null	null		Unigene72279_All//gi|208605348|emb|CAR82267.1|//3.00E-08//D-type LMW glutenin subunit [Triticum aestivum]						nr +
Unigene7228_All	255	3.49	27.02	6.06	8.40	6.75	8.86	64.17	59.83	455.41	2.95E+00	1.67E-22	Up	7.96E-01	1.50E-01		-3.15E-01	5.10E-01		7.62E-02	8.80E-01		-1.01E-01	4.97E-01		2.83E+00	0.00E+00	Up		Unigene7228_All//1.00E-89//TC149671					
Unigene72280_All	720	0.00	5.28	1.41	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.23E-21	Up	1.05E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene72280_All//sp|Q6UX71|PXDC2_HUMAN//7.00E-32//Plexin domain-containing protein 2 OS=Homo sapiens GN=PLXDC2 PE=1 SV=1						swissprot -
Unigene72281_All	727	0.00	4.39	0.95	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.64E-18	Up	9.90E+00	6.13E-04	Up	null	null		null	null		null	null		null	null		Unigene72281_All//gi|145340601|ref|XP_001415410.1|//3.00E-06//predicted protein [Ostreococcus lucimarinus CCE9901] >gi|144575633|gb|ABO93702.1| predicted protein [Ostreococcus lucimarinus CCE9901]						nr -
Unigene72282_All	729	0.00	24.12	7.45	0.00	0.00	0.00	0.00	0.00	0.00	1.46E+01	4.38E-101	Up	1.29E+01	3.03E-30	Up	null	null		null	null		null	null		null	null		Unigene72282_All//gi|42569129|ref|NP_179444.2|//6.00E-07//cupin family protein [Arabidopsis thaliana]	Unigene72282_All//2.00E-09//AT3G02930| unknown protein					nr +
Unigene72283_All	755	0.00	8.72	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	1.26E-37	Up	1.03E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene72283_All//gi|62857016|dbj|BAD95893.1|//7.00E-57//Ser/Thr protein kinase [Lotus japonicus]	Unigene72283_All//2.00E-56//AT1G03920| protein kinase, putative					nr -
Unigene72284_All	759	0.00	5.54	0.35	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	5.92E-24	Up	8.45E+00	7.94E-02		null	null		null	null		null	null		null	null		Unigene72284_All//gi|297735568|emb|CBI18062.3|//1.00E-07//unnamed protein product [Vitis vinifera]	Unigene72284_All//4.00E-05//AT3G51730| saposin B domain-containing protein					nr +

Unigene72285_All	786	0.00	11.47	3.73	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	1.24E-51	Up	1.19E+01	3.52E-16	Up	null	null		null	null		null	null		null	null		Unigene72285_All//sp|P08123|CO1A2_HUMAN//8.00E-155//Collagen alpha-2(I) chain OS=Homo sapiens GN=COL1A2 PE=1 SV=6					swissprot -
Unigene72286_All	836	0.00	5.27	0.76	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	4.10E-25	Up	9.58E+00	1.15E-03		null	null		null	null		null	null											ESTscan +
Unigene72287_All	841	0.00	9.88	2.53	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	1.52E-47	Up	1.13E+01	9.77E-12	Up	null	null		null	null		null	null		null	null		Unigene72287_All//gi|6491702|emb|CAB61875.1|//2.00E-30//myosin [Arabidopsis thaliana]	Unigene72287_All//9.00E-32//AT3G19960| ATM1 (ARABIDOPSIS THALIANA MYOSIN 1); motor				nr -
Unigene72289_All	844	0.00	4.44	0.76	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.40E-21	Up	9.56E+00	1.15E-03		null	null		null	null		null	null		null	null		Unigene72289_All//gi|115483552|ref|NP_001065446.1|//2.00E-40//Os10g0569200 [Oryza sativa Japonica Group] >gi|113639978|dbj|BAF27283.1| Os10g0569200 [Oryza sativa Japonica Group]	Unigene72289_All//9.00E-40//AT5G27640| TIF3B1 (TRANSLATION INITIATION FACTOR 3B1); nucleic acid binding / translation initiation factor				nr +
Unigene72290_All	848	0.00	34.72	0.13	0.00	0.00	0.53	0.10	0.00	0.00	1.51E+01	1.01E-169	Up	6.97E+00	3.92E-01		null	null		9.06E+00	7.74E-03		-6.64E+00	3.99E-01		-6.64E+00	3.55E-01		Unigene72290_All//gi|187610414|gb|ACD13461.1|//1.00E-141//raffionse synthase 2 [Glycine max]	Unigene72290_All//3.00E-126//AT5G40390| SIP1 (seed imbibition 1-like); galactinol-sucrose galactosyltransferase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene72290_All//4.00E-34//TC162566		ko00052|Galactose metabolism	nr +
Unigene72291_All	860	0.00	6.48	8.85	0.00	0.00	0.11	0.00	0.00	0.00	1.27E+01	8.49E-32	Up	1.31E+01	1.38E-42	Up	null	null		6.71E+00	4.72E-01		null	null		null	null		Unigene72291_All//sp|P04233|HG2A_HUMAN//9.00E-30//HLA class II histocompatibility antigen gamma chain OS=Homo sapiens GN=CD74 PE=1 SV=3					swissprot -
Unigene72292_All	871	0.00	19.02	9.48	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	3.18E-95	Up	1.32E+01	3.29E-46	Up	null	null		null	null		null	null		null	null		Unigene72292_All//gi|9858814|gb|AAG01147.1|AF283816_1/3.00E-95//calreticulin [Pinus taeda]	Unigene72292_All//5.00E-66//AT1G09210| calreticulin 2 (CRT2)			ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	nr +
Unigene72293_All	887	0.00	9.03	3.30	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	8.57E-46	Up	1.17E+01	3.52E-16	Up	null	null		null	null		null	null											ESTscan +
Unigene72294_All	908	0.00	5.86	1.06	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.43E-30	Up	1.00E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene72294_All//gi|20453062|gb|AAM19776.1|//8.00E-56//AT3g08530/T8G24_1 [Arabidopsis thaliana] >gi|21928019|gb|AAM78038.1| AT3g08530/T8G24_1 [Arabidopsis thaliana]	Unigene72294_All//6.00E-56//AT3G08530| clathrin heavy chain, putative			ko04144|Endocytosis	nr +
Unigene72295_All	965	0.00	4.83	1.21	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.46E-26	Up	1.02E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene72295_All//sp|Q05793|PGBM_MOUSE//4.00E-40//Basement membrane-specific heparan sulfate proteoglycan core protein OS=Mus musculus GN=Hspg2 PE=1 SV=1					swissprot +
Unigene72297_All	1129	0.00	7.76	5.52	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	3.58E-50	Up	1.24E+01	9.45E-35	Up	null	null		null	null		null	null		null	null		Unigene72297_All//gi|71000469|dbj|BAE07181.1|//1.00E-103//methionine synthase [Beta vulgaris]	Unigene72297_All//2.00E-102//AT5G20980| ATMS3 (methionine synthase 3); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase			ko00270|Cysteine and methionine metabolism	nr +
Unigene72298_All	1393	0.00	48.78	22.52	0.00	0.00	0.06	0.00	0.00	0.00	1.56E+01	0.00E+00	Up	1.45E+01	7.12E-178	Up	null	null		6.02E+00	4.72E-01		null	null		null	null		Unigene72298_All//gi|301101339|ref|XP_002899758.1|//3.00E-82//creatine kinase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262102760|gb|EEY60812.1| creatine kinase, mitochondrial precursor [Phytophthora infestans T30-4]				ko00330|Arginine and proline metabolism	nr -
Unigene72302_All	637	0.00	27.44	9.53	0.00	0.00	0.00	0.00	0.00	0.00	1.47E+01	1.69E-100	Up	1.32E+01	7.60E-34	Up	null	null		null	null		null	null		null	null		Unigene72302_All//gi|226501140|ref|NP_001152197.1|//1.00E-13//LOC100285835 [Zea mays] >gi|195653721|gb|ACG46328.1| keratin-associated protein 5-4 [Zea mays]				ko00520|Amino sugar and nucleotide sugar metabolism	nr -
Unigene72305_All	1132	0.00	21.89	6.02	0.00	0.00	0.00	0.00	0.00	0.00	1.44E+01	1.01E-142	Up	1.26E+01	4.59E-38	Up	null	null		null	null		null	null		null	null		Unigene72305_All//gi|40716077|gb|AAR88661.1|//1.00E-45//fructose-bisphosphate aldolase [Pandanus amaryllifolius]	Unigene72305_All//7.00E-42//AT4G26530| fructose-bisphosphate aldolase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway	nr +
Unigene72308_All	336	0.00	0.30	3.65	0.00	0.00	0.54	0.00	0.00	0.00	8.24E+00	3.81E-01		1.18E+01	9.10E-07	Up	null	null		9.07E+00	1.93E-01		null	null		null	null									ESTscan +
Unigene72309_All	215	179.84	131.27	144.39	171.45	161.61	160.07	111.31	72.12	53.18	-4.54E-01	1.13E-07		-3.17E-01	4.18E-04		-8.53E-02	4.23E-01		-9.91E-02	3.55E-01		-6.26E-01	3.62E-10		-1.07E+00	8.87E-25	Down	Unigene72309_All//gi|16973316|emb|CAC84110.1|//5.00E-35//F6 [Gossypium hirsutum]	Unigene72309_All//4.00E-31//AT2G33220| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: photorespiration; LOCATED IN: mitochondrion, mitochondrial membrane, plastid, respiratory chain complex I; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: GRIM-19 (InterPro:IPR009346); BEST Arabidopsis thaliana protein match is: MEE4 (maternal effect embryo arrest 4) (TAIR:AT1G04630.1); Has 226 Blast hits to 226 proteins in 98 species: Archae - 0; Bacteria - 0; Metazoa - 125; Fungi - 53; Plants - 38; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink).	Unigene72309_All//2.00E-118//TC155713		ko00190|Oxidative phosphorylation		nr -
Unigene72310_All	209	11.77	8.73	9.17	18.11	20.60	26.15	68.38	34.60	31.07	-4.31E-01	2.96E-01		-3.59E-01	3.90E-01		1.85E-01	5.85E-01		5.30E-01	4.11E-02		-9.83E-01	5.76E-13		-1.14E+00	9.30E-17	Down	Unigene72310_All//gi|224104989|ref|XP_002313645.1|//1.00E-13//histone deacetylase [Populus trichocarpa] >gi|222850053|gb|EEE87600.1| histone deacetylase [Populus trichocarpa]		Unigene72310_All//1.00E-70//TC145304			nr -
Unigene72312_All	375	0.00	6.08	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	5.62E-13	Up	1.10E+01	3.26E-04	Up	null	null		null	null		null	null		null	null		Unigene72312_All//gi|223996397|ref|XP_002287872.1|//1.00E-23//RS7, ribosomal protein 7 [Thalassiosira pseudonana CCMP1335] >gi|220976988|gb|EED95315.1| RS7, ribosomal protein 7 [Thalassiosira pseudonana CCMP1335]	Unigene72312_All//5.00E-15//AT3G02560| 40S ribosomal protein S7 (RPS7B)			ko03010|Ribosome	nr -
Unigene72313_All	368	0.43	0.55	0.87	0.00	0.28	0.74	8.50	65.19	8.34	3.69E-01	8.15E-01		1.03E+00	4.70E-01		8.13E+00	4.53E-01		9.52E+00	7.01E-02		2.94E+00	3.69E-94	Up	-2.85E-02	9.47E-01		Unigene72313_All//gi|283135850|gb|ADB11316.1|//2.00E-22//tau class glutathione transferase GSTU12 [Populus trichocarpa]	Unigene72313_All//2.00E-14//AT2G29420| ATGSTU7 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE TAU 7); glutathione transferase	Unigene72313_All//7.00E-83//gi|164314276|gb|ES842964.1|ES842964		ko00480|Glutathione metabolism	nr +
Unigene72314_All	240	0.00	3.80	0.89	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.60E-05	Up	9.79E+00	1.39E-01		null	null		null	null		null	null		null	null		Unigene72314_All//gi|51241757|dbj|BAD36766.1|//3.00E-19//6-phosphogluconate dehydrogenase [Cyanidioschyzon merolae]	Unigene72314_All//1.00E-19//AT3G02360| 6-phosphogluconate dehydrogenase family protein			ko00480|Glutathione metabolism//ko00030|Pentose phosphate pathway	nr +
Unigene7232_All	473	423.77	457.85	581.58	34.65	37.49	30.94	1.70	1.06	0.25	1.12E-01	1.89E-03		4.57E-01	1.26E-48		1.14E-01	4.80E-01		-1.64E-01	3.08E-01		-6.80E-01	3.53E-01		-2.75E+00	9.42E-04	Down	Unigene7232_All//gi|195655945|gb|ACG47440.1|//1.00E-07//CBF1 interacting corepressor [Zea mays]		Unigene7232_All//7.00E-99//gi|195983200|gb|FL576382.1|FL576382			nr +
Unigene72336_All	470	4.79	5.39	3.40	4.24	3.81	3.27	1.89	1.07	0.17	1.71E-01	6.57E-01		-4.94E-01	2.73E-01		-1.54E-01	7.69E-01		-3.76E-01	4.53E-01		-8.24E-01	2.24E-01		-3.48E+00	7.33E-05	Down	Unigene72336_All//gi|224074167|ref|XP_002304283.1|//3.00E-17//formyltetrahydrofolate deformylase [Populus trichocarpa] >gi|222841715|gb|EEE79262.1| formyltetrahydrofolate deformylase [Populus trichocarpa]	Unigene72336_All//1.00E-15//AT4G17360| formyltetrahydrofolate deformylase/ hydroxymethyl-, formyl- and related transferase/ methyltransferase	Unigene72336_All//3.00E-153//TC149291		ko00630|Glyoxylate and dicarboxylate metabolism//ko00670|One carbon pool by folate	nr -
Unigene7236_All	1580	0.00	0.00	0.00	0.06	0.04	0.00	18.01	2.41	3.35	null	null		null	null		-5.33E-01	8.14E-01		-5.98E+00	3.95E-01		-2.90E+00	1.47E-110	Down	-2.43E+00	1.71E-93	Down	Unigene7236_All//gi|115456205|ref|NP_001051703.1|//1.00E-134//Os03g0817900 [Oryza sativa Japonica Group] >gi|108711766|gb|ABF99561.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113550174|dbj|BAF13617.1| Os03g0817900 [Oryza sativa Japonica Group]	Unigene7236_All//1.00E-156//AT2G40320| unknown protein	Unigene7236_All//0.00E+00//gi|164368440|gb|EX169315.1|EX169315			nr -
Unigene7237_All	1034	0.00	0.10	0.00	1.16	0.27	0.70	5.40	5.58	2.70	6.61E+00	3.81E-01		null	null		-2.12E+00	8.56E-04	Down	-7.26E-01	2.56E-01		4.75E-02	8.52E-01		-1.00E+00	6.45E-06	Down	Unigene7237_All//gi|72255610|gb|AAZ66928.1|//1.00E-117//117M18_9 [Brassica rapa]	Unigene7237_All//6.00E-124//AT1G35910| trehalose-6-phosphate phosphatase, putative	Unigene7237_All//8.00E-11//TC143481		ko00500|Starch and sucrose metabolism	nr -
Unigene72374_All	512	3.88	6.14	2.81	0.58	0.87	3.09	0.17	0.00	0.00	6.60E-01	6.08E-02		-4.68E-01	3.45E-01		5.83E-01	6.26E-01		2.40E+00	8.62E-05	Up	-7.37E+00	3.99E-01		-7.37E+00	3.55E-01		Unigene72374_All//gi|146742170|gb|ABQ42622.1|//3.00E-24//snakin-1 [Solanum chacoense]	Unigene72374_All//1.00E-17//AT2G14900| gibberellin-regulated family protein	Unigene72374_All//5.00E-100//gi|164297320|gb|ES811205.1|ES811205			nr +
Unigene7239_All	593	0.00	0.51	0.72	0.25	0.58	0.61	29.95	104.88	45.08	9.00E+00	4.37E-02		9.49E+00	1.37E-02		1.20E+00	4.26E-01		1.27E+00	3.81E-01		1.81E+00	2.64E-135	Up	5.90E-01	1.69E-10		Unigene7239_All//gi|115489082|ref|NP_001067028.1|//5.00E-40//Os12g0562400 [Oryza sativa Japonica Group] >gi|113649535|dbj|BAF30047.1| Os12g0562400 [Oryza sativa Japonica Group]	Unigene7239_All//3.00E-40//AT3G08510| ATPLC2 (PHOSPHOLIPASE C 2); phospholipase C	Unigene7239_All//6.00E-103//CA994181		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	nr -
Unigene7241_All	423	0.74	0.96	0.50	0.94	1.38	0.64	4.10	4.55	0.85	3.69E-01	7.23E-01		-5.60E-01	6.63E-01		5.55E-01	5.99E-01		-5.57E-01	6.37E-01		1.49E-01	7.32E-01		-2.27E+00	5.17E-06	Down	Unigene7241_All//gi|115448991|ref|NP_001048275.1|//1.00E-30//Os02g0774500 [Oryza sativa Japonica Group] >gi|113537806|dbj|BAF10189.1| Os02g0774500 [Oryza sativa Japonica Group]	Unigene7241_All//3.00E-29//AT3G12040| DNA-3-methyladenine glycosylase (MAG)	Unigene7241_All//3.00E-144//TC174238		ko03410|Base excision repair	nr -
Unigene7242_All	429	3.41	1.42	4.97	6.39	5.38	1.26	1.48	0.00	0.37	-1.27E+00	2.39E-02		5.40E-01	2.45E-01		-2.48E-01	5.43E-01		-2.34E+00	6.98E-08	Down	-1.05E+01	1.23E-04	Down	-1.99E+00	2.04E-02								
Unigene7244_All	459	11.63	5.08	12.41	7.38	7.80	4.72	1.01	0.73	0.95	-1.20E+00	7.24E-06	Down	9.44E-02	7.21E-01		8.03E-02	8.22E-01		-6.44E-01	5.76E-02		-4.76E-01	6.59E-01		-8.59E-02	9.34E-01				Unigene7244_All//3.00E-101//TC153021				
Unigene7247_All	816	1.54	0.87	0.98	10.99	9.12	5.87	0.00	1.13	0.00	-8.24E-01	1.69E-01		-6.53E-01	3.04E-01		-2.70E-01	1.81E-01		-9.05E-01	1.67E-06		1.01E+01	1.48E-06	Up	null	null		Unigene7247_All//gi|224129686|ref|XP_002320646.1|//1.00E-41//glutaredoxin [Populus trichocarpa] >gi|222861419|gb|EEE98961.1| glutaredoxin [Populus trichocarpa]	Unigene7247_All//2.00E-40//AT2G30540| glutaredoxin family protein	Unigene7247_All//0.00E+00//DW501624			nr -
Unigene7248_All	413	260.21	41.22	64.73	71.04	64.70	26.79	0.00	0.20	0.00	-2.66E+00	0.00E+00	Down	-2.01E+00	2.47E-213	Down	-1.35E-01	2.26E-01		-1.41E+00	8.28E-40	Down	7.66E+00	3.99E-01		null	null		Unigene7248_All//gi|60459375|gb|AAX20033.1|//8.00E-61//GDSL-lipase protein [Capsicum annuum]	Unigene7248_All//5.00E-58//AT5G45670| GDSL-motif lipase/hydrolase family protein	Unigene7248_All//0.00E+00//TC140846			nr -
Unigene72480_All	225	0.23	3.60	1.89	0.00	0.00	0.00	0.00	0.19	0.00	3.95E+00	7.51E-04	Up	3.03E+00	5.72E-02		null	null		null	null		7.54E+00	6.28E-01		null	null								

Unigene7249_All	747	0.35	1.09	0.71	0.27	0.69	0.24	3.91	0.90	1.28	1.63E+00	5.05E-02		1.03E+00	3.42E-01		1.37E+00	2.26E-01		-1.41E-01	9.34E-01		-2.13E+00	1.47E-08	Down	-1.61E+00	2.28E-06	Down			Unigene7249_All//0.00E+00//gi|13248659|gb|BF276783.2|BF276783				
Unigene7252_All	840	0.12	2.11	0.89	1.84	1.02	1.02	3.42	2.14	3.37	4.08E+00	6.27E-08	Up	2.83E+00	8.51E-03		-8.43E-01	1.01E-01		-8.48E-01	1.18E-01		-6.78E-01	4.02E-02		-2.35E-02	9.61E-01									
Unigene7253_All	433	15.71	33.70	26.56	30.95	38.41	48.50	13.57	45.17	27.14	1.10E+00	6.57E-13	Up	7.58E-01	1.25E-05		3.12E-01	2.21E-02		6.48E-01	2.94E-08		1.73E+00	1.14E-40	Up	1.00E+00	2.24E-11				Unigene7253_All//3.00E-113//TC167487				
Unigene7254_All	284	1.84	2.68	0.19	2.81	2.06	1.91	16.23	15.89	133.26	5.39E-01	5.02E-01		-3.30E+00	2.40E-02		-4.45E-01	5.73E-01		-5.56E-01	4.98E-01		-2.99E-02	9.30E-01		3.04E+00	5.57E-156	Up			Unigene7254_All//3.00E-115//gi|109876675|gb|DW505649.1|DW505649					ESTscan -
Unigene72546_All	210	0.00	5.55	1.52	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	1.04E-06	Up	1.06E+01	4.47E-02		null	null		null	null		null	null		null	null		Unigene72546_All//gi|226454588|gb|EEH51894.1|//2.00E-08//flagellar outer dynein arm light chain 7 [Micromonas pusilla CCMP1545]					GO:0042995	nr -
Unigene72547_All	531	0.00	0.00	3.41	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	5.68E-10	Up	null	null		null	null		null	null		null	null		Unigene72547_All//gi|171452062|dbj|BAG15872.1|//1.00E-53//transcription factor [Bruguiera gymnorhiza]	Unigene72547_All//2.00E-09//AT2G40140| CZF1; transcription factor	Unigene72547_All//4.00E-11//ES827763	C3H		GO:0006952//GO:0009743//GO:0046914	nr +
Unigene72549_All	208	0.00	5.12	2.56	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.79E-06	Up	1.13E+01	4.01E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene7255_All	639	0.98	0.32	1.17	5.85	3.07	1.91	3.31	2.16	1.87	-1.63E+00	9.23E-02		2.48E-01	7.45E-01		-9.29E-01	1.74E-03		-1.62E+00	1.05E-06	Down	-6.16E-01	1.26E-01		-8.23E-01	3.02E-02				Unigene7255_All//8.00E-16//AI054967				
Unigene72564_All	201	0.00	0.25	0.26	0.25	0.00	0.00	3.16	0.42	0.20	7.98E+00	6.12E-01		8.05E+00	6.27E-01		-7.95E+00	5.48E-01		-7.95E+00	6.25E-01		-2.92E+00	4.19E-03		-3.99E+00	5.82E-04	Down								
Unigene7257_All	851	16.85	7.56	10.45	0.41	0.45	0.11	0.10	0.69	0.56	-1.16E+00	1.03E-13	Down	-6.89E-01	6.82E-06		1.19E-01	9.58E-01		-1.95E+00	1.96E-01		2.79E+00	8.26E-03		2.50E+00	2.51E-02		Unigene7257_All//gi|15236949|ref|NP_194433.1|//3.00E-86//small conjugating protein ligase [Arabidopsis thaliana]	Unigene7257_All//2.00E-85//AT4G27030| small conjugating protein ligase	Unigene7257_All//0.00E+00//C0105773				nr +
Unigene7258_All	522	1.90	0.29	1.22	5.53	3.56	1.99	2.51	0.24	1.14	-2.71E+00	1.41E-03		-6.38E-01	3.90E-01		-6.36E-01	7.51E-02		-1.48E+00	9.26E-05	Down	-3.39E+00	1.90E-06	Down	-1.13E+00	2.59E-02		Unigene7258_All//gi|42565719|ref|NP_190423.2|//9.00E-28//cytidine/deoxycytidylate deaminase family protein [Arabidopsis thaliana] >gi|91806546|gb|ABE66000.1| cytidine/deoxycytidylate deaminase family protein [Arabidopsis thaliana]	Unigene7258_All//3.00E-26//AT3G48540| cytidine/deoxycytidylate deaminase family protein	Unigene7258_All//8.00E-170//TC168869		ko00240|Pyrimidine metabolism		nr -
Unigene72587_All	568	0.18	0.36	0.09	0.79	0.61	0.48	2.23	0.29	1.89	9.54E-01	6.20E-01		-9.75E-01	7.19E-01		-3.81E-01	7.21E-01		-7.26E-01	5.32E-01		-2.92E+00	1.46E-05	Down	-2.38E-01	6.32E-01		Unigene72587_All//gi|225458914|ref|XP_002285475.1|//7.00E-06//PREDICTED: hypothetical protein [Vitis vinifera] >gi|302142156|emb|CBI19359.3| unnamed protein product [Vitis vinifera]						nr +
Unigene7259_All	243	35.74	92.16	65.74	77.69	108.12	122.11	94.65	114.21	75.41	1.37E+00	6.26E-27	Up	8.79E-01	1.61E-09		4.77E-01	1.37E-06		6.52E-01	1.59E-11		2.71E-01	3.97E-03		-3.28E-01	1.06E-03		Unigene7259_All//gi|110559491|gb|AB276000.1|//6.00E-17//GRP-like protein 2 [Gossypium hirsutum]	Unigene7259_All//1.00E-15//AT5G15650| RGP2 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 2); transferase, transferring hexosyl groups	Unigene7259_All//2.00E-82//gi|13246868|gb|BE052062.2|BE052062				nr +
Unigene726_All	565	2.32	0.72	0.38	1.85	1.16	0.80	2.25	1.55	3.31	-1.69E+00	7.07E-03		-2.62E+00	4.27E-04	Down	-6.77E-01	3.14E-01		-1.21E+00	7.81E-02		-5.31E-01	3.43E-01		5.62E-01	1.76E-01		Unigene726_All//gi|14517444|gb|AAK62612.1|//4.00E-75//AT5g35570/K2K18_1 [Arabidopsis thaliana] >gi|21360449|gb|AAM47340.1| AT5g35570/K2K18_1 [Arabidopsis thaliana]	Unigene726_All//7.00E-68//AT5G35570| unknown protein			GO:0009536	nr -
Unigene72607_All	310	0.00	0.33	3.95	0.00	0.44	0.00	0.00	0.00	0.00	8.35E+00	3.81E-01		1.19E+01	9.10E-07	Up	8.80E+00	3.17E-01		null	null		null	null		null	null									ESTscan +
Unigene7262_All	568	0.55	1.34	0.56	1.75	1.03	1.75	0.60	2.87	4.28	1.28E+00	1.28E-01		2.54E-02	1.00E+00		-7.67E-01	2.60E-01		-3.90E-03	9.88E-01		2.27E+00	1.94E-05	Up	2.84E+00	5.03E-10	Up	Unigene7262_All//gi|297843048|ref|XP_002889405.1|//6.00E-08//invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335247|gb|EFH65664.1| invertase/pectin methylesterase inhibitor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7262_All//3.00E-09//AT1G02550| invertase/pectin methylesterase inhibitor family protein	Unigene7262_All//0.00E+00//TC135512				nr +
Unigene72634_All	293	0.00	0.00	3.27	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene72634_All//gi|15219950|ref|NP_173692.1|//5.00E-31//PPL (POINTED FIRST LEAVES); RNA binding / nucleic acid binding / structural constituent of ribosome [Arabidopsis thaliana] >gi|15234790|ref|NP_192718.1| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome [Arabidopsis thaliana] >gi|18399100|ref|NP_564434.1| 40S ribosomal protein S18 (RPS18B) [Arabidopsis thaliana] >gi|464707|sp|P34731.1|RS18_ARATH RecName: Full=40S ribosomal protein S18 >gi|10086474|gb|AAG12534.1|AC01544 6_15 ribosomal protein S18 [Arabidopsis thaliana] >gi|10092450|gb|AAG12853.1|AC07928 6_10 40S ribosomal protein S18; 25853-24673 [Arabidopsis thaliana] >gi|14423408|gb|AAK62386.1|AF38694 1_1 S18.A ribosomal protein [Arabidopsis thaliana] >gi|15724158|gb|AAL06471.1|AF41178 1_1 At1g22780/T22J18_5 [Arabidopsis thaliana] >gi|405613|emb|CAA80684.1|	Unigene72634_All//3.00E-32//AT4G09800| RPS18C (S18 RIBOSOMAL PROTEIN); RNA binding / nucleic acid binding / structural constituent of ribosome	Unigene72634_All//6.00E-18//EV489048		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0006412//GO:0015935//GO:0016020//GO:0003012//GO:0031981	nr +
Unigene7265_All	338	50.46	35.23	21.11	174.35	187.15	190.54	47.78	32.52	41.49	-5.19E-01	1.10E-04		-1.26E+00	1.35E-17	Down	1.02E-01	1.66E-01		1.28E-01	7.44E-02		-5.55E-01	6.61E-06		-2.04E-01	1.11E-01		Unigene7265_All//gi|2058282|emb|CAA66045.1|//2.00E-29//atranbpla [Arabidopsis thaliana]	Unigene7265_All//1.00E-13//AT5G58590| RANBP1 (RAN BINDING PROTEIN 1); protein binding	Unigene7265_All//0.00E+00//gi|78343537|gb|DT563811.1|DT563811				nr -
Unigene7266_All	259	10.91	11.93	12.75	9.23	9.71	23.02	32.32	66.00	8.15	1.30E-01	7.13E-01		2.25E-01	5.53E-01		7.22E-02	8.76E-01		1.32E+00	1.15E-07	Up	1.03E+00	1.72E-16	Up	-1.99E+00	4.75E-22	Down	Unigene7266_All//gi|224092400|ref|XP_002309592.1|//7.00E-13//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222855568|gb|EEE93115.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene7266_All//3.00E-09//AT1G52810| 2-oxoglutarate-dependent dioxygenase-related	Unigene7266_All//6.00E-70//EX168369				nr -
Unigene72665_All	230	0.00	0.00	0.93	16.89	14.37	0.79	0.37	0.00	1.39	null	null		9.86E+00	1.39E-01		-2.33E-01	5.06E-01		-4.43E+00	2.01E-19	Down	-8.52E+00	3.99E-01		1.91E+00	1.53E-01		Unigene72665_All//gi|15224291|ref|NP_181282.1|//5.00E-19//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|4056506|gb|AAC98072.1| nodulin-like protein [Arabidopsis thaliana] >gi|14994253|gb|AAK73261.1| nodulin-like protein [Arabidopsis thaliana]	Unigene72665_All//2.00E-20//AT2G37460| nodulin MtN21 family protein	Unigene72665_All//5.00E-15//ES836178			GO:0044464	nr -
Unigene72666_All	320	0.00	0.00	2.33	0.00	0.32	0.00	0.00	0.00	0.00	null	null		1.12E+01	3.26E-04	Up	8.33E+00	4.53E-01		null	null		null	null		null	null									ESTscan +
Unigene7267_All	594	0.00	0.51	0.81	3.77	2.55	1.37	1.28	0.56	0.34	9.00E+00	4.37E-02		9.66E+00	7.44E-03		-5.65E-01	1.81E-01		-1.46E+00	8.28E-04	Down	-1.19E+00	1.12E-01		-1.93E+00	1.14E-02		Unigene7267_All//gi|297852976|ref|XP_002843369.1|//3.00E-40//dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297340211|gb|EFH70628.1| dynein light chain type 1 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7267_All//1.00E-40//AT1G52240| ROPGEF11 (RHO GUANYL-NUCLEOTIDE EXCHANGE FACTOR 11); Rho guanyl-nucleotide exchange factor	Unigene7267_All//0.00E+00//DW514359				nr +
Unigene7268_All	492	30.73	66.94	20.46	10.12	7.14	5.42	0.00	0.00	0.00	1.12E+00	4.58E-29	Up	-5.87E-01	7.77E-05		-5.04E-01	5.43E-02		-9.03E-01	6.56E-04		null	null		null	null									
Unigene72683_All	432	0.24	3.05	0.12	0.12	0.00	0.63	0.20	0.10	0.00	3.65E+00	1.28E-05	Up	-9.74E-01	7.19E-01		-6.85E+00	5.48E-01		2.44E+00	2.21E-01		-1.02E+00	7.22E-01		-7.61E+00	3.55E-01		Unigene72683_All//gi|297725715|ref|NP_001175221.1|//9.00E-07//Os07g0513300 [Oryza sativa Japonica Group] >gi|255677803|dbj|BAH93949.1| Os07g0513300 [Oryza sativa Japonica Group]	Unigene72683_All//8.00E-08//AT1G17930| unknown protein	Unigene72683_All//1.00E-53//CO105636				nr +
Unigene72684_All	210	0.00	0.00	6.59	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.27E+01	1.23E-07	Up	null	null		null	null		null	null		null	null									
Unigene7270_All	570	1.01	0.80	1.03	5.33	5.98	2.06	1.11	0.22	0.28	-3.36E-01	6.90E-01		2.54E-02	9.98E-01		1.66E-01	6.71E-01		-1.37E+00	1.58E-04	Down	-2.34E+00	1.27E-02		-1.99E+00	2.04E-02		Unigene7270_All//gi|18412253|ref|NP_567126.1|//8.00E-58//glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein [Arabidopsis thaliana] >gi|11762132|gb|AAG40344.1|AF32499 2_1 AT3g62110 [Arabidopsis thaliana]	Unigene7270_All//5.00E-59//AT3G62110| glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein	Unigene7270_All//8.00E-133//TC158871				nr -
Unigene7272_All	324	47.31	21.27	25.80	76.57	52.93	63.56	186.35	71.59	91.97	-1.15E+00	1.43E-14	Down	-8.75E-01	4.48E-09		-5.33E-01	1.01E-07		-2.69E-01	1.70E-02		-1.38E+00	4.57E-89	Down	-1.02E+00	7.47E-57	Down	Unigene7272_All//gi|297806181|ref|XP_002870974.1|//7.00E-07//60S ribosomal protein L36 [Arabidopsis lyrata subsp. lyrata] >gi|297316811|gb|EFH47233.1| 60S ribosomal protein L36 [Arabidopsis lyrata subsp. lyrata]	Unigene7272_All//4.00E-08//AT3G53740| 60S ribosomal protein L36 (RPL36B)	Unigene7272_All//8.00E-178//gi|21100602|gb|BQ412915.1|BQ412915		ko03010|Ribosome		nr -
Unigene72729_All	223	0.00	2.50	4.06	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	2.16E-03		1.20E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene72729_All//gi|110738301|dbj|BAF01079.1|//1.00E-13//5-methyltetrahydropteroyltriglutamate- homocysteine S-methyltransferase - like protein [Arabidopsis thaliana]	Unigene72729_All//5.00E-15//AT5G20980| ATMS3 (methionine synthase 3); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase			ko00270|Cysteine and methionine metabolism	GO:0008172//GO:0008652//GO:0009536	nr -
Unigene72730_All	228	0.00	6.89	3.97	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	5.68E-09	Up	1.20E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene72730_All//sp|O01479|TM0D_CAEEL//2.00E-08//Tropomodulin OS=Caenorhabditis elegans GN=unc-94 PE=1 SV=2						swissprot -
Unigene7274_All	377	0.56	4.30	4.66	1.06	2.47	1.44	0.67	2.22	1.59	2.95E+00	9.24E-06	Up	3.07E+00	3.99E-06	Up	1.22E+00	1.05E-01		4.44E-01	6.78E-01		1.72E+00	1.93E-02		1.24E+00	1.39E-01									
Unigene7275_All	514	0.41	0.00	0.21	7.95	8.17	4.66	3.45	6.51	10.31	-8.67E+00	1.21E-01		-9.75E-01	6.19E-01		4.05E-02	9.13E-01		-7.71E-01	9.89E-03		9.13E-01	2.55E-03		1.58E+00	1.81E-10	Up	Unigene7275_All//gi|296087208|emb|CBI33582.3|//6.00E-29//unnamed protein product [Vitis vinifera]						nr +
Unigene72769_All	264	0.00	0.00	3.43	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene72769_All//gi|257222608|gb|ACV52582.1|//4.00E-14//thiazole biosynthetic enzyme [Nicotiana benthamiana]						nr +
Unigene7277_All	1796	0.00	0.00	0.00	0.28	0.12	0.00	43.74	7.75	46.80	null	null		null	null		-1.27E+00	2.22E-01		-8.12E+00	2.97E-03		-2.50E+00	5.21E-258	Down	9.77E-02	7.13E-02		Unigene7277_All//gi|131613971|dbj|BAB33033.1|//1.00E-163//CPRD2 [Vigna unguiculata]	Unigene7277_All//9.00E-127//AT4G20820| FAD-binding domain-containing protein	Unigene7277_All//0.00E+00//TC160215		ko00620|Pyruvate metabolism//ko00908|Zeatin biosynthesis		nr +

Unigene72795_All	332	0.00	0.00	2.41	0.00	0.10	0.00	0.00	0.00	0.00	null	null		1.12E+01	1.72E-04	Up	6.70E+00	8.19E-01		null	null		null	null		null	null		Unigene72795_All//gi|297809607|ref|XP_002872687.1|//1.00E-17//malonyl-CoA decarboxylase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318524|gb|EFH48946.1| malonyl-CoA decarboxylase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene72795_All//3.00E-15//AT4G04320| malonyl-CoA decarboxylase family protein			ko04146|Peroxisome//ko00640|Propanoate metabolism//ko00410|beta-Alanine metabolism	GO:0016740//GO:0016829//GO:0042579//GO:0044255	nr +
Unigene728_All	2450	8.33	2.63	3.30	9.43	7.83	10.27	6.90	3.51	7.17	-1.66E+00	7.16E-33	Down	-1.33E+00	6.67E-23	Down	-2.69E-01	1.67E-02		1.22E-01	3.48E-01		-9.74E-01	5.61E-15		5.50E-02	6.71E-01		Unigene728_All//gi|14517444|gb|AAK62612.1|//0.00E+00//AT5g35570/K2K18_1 [Arabidopsis thaliana] >gi|21360449|gb|AAM47340.1| AT5g35570/K2K18_1 [Arabidopsis thaliana]	Unigene728_All//0.00E+00//AT5G35570| unknown protein	Unigene728_All//0.00E+00//TC150265			GO:0009536	nr -
Unigene7280_All	727	7.84	5.09	3.30	1.92	0.76	0.62	0.00	0.00	0.00	-6.25E-01	1.19E-02		-1.25E+00	2.89E-06	Down	-1.34E+00	1.36E-02		-1.63E+00	5.90E-03		null	null		null	null		Unigene7280_All//gi|32189293|gb|AAP75801.1|//2.00E-31//At3g16660 [Arabidopsis thaliana]	Unigene7280_All//4.00E-26//AT3G16660| unknown protein					nr +
Unigene72818_All	409	0.13	3.22	1.82	0.24	0.25	0.44	0.52	0.20	0.78	4.65E+00	1.91E-06	Up	3.83E+00	2.23E-03		5.23E-02	9.65E-01		8.59E-01	6.94E-01		-1.34E+00	4.29E-01		5.92E-01	6.13E-01					Unigene72818_All//9.00E-61//TC175180				
Unigene7282_All	2060	0.00	0.00	0.00	6.26	0.70	0.18	10.69	2.41	0.10	null	null		null	null		-3.16E+00	3.57E-57	Down	-5.16E+00	5.71E-70	Down	-2.15E+00	1.13E-60	Down	-6.79E+00	1.27E-152	Down	Unigene7282_All//gi|297812551|ref|XP_002874159.1|//0.00E+00//C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata] >gi|297319996|gb|EFH50418.1| C4-dicarboxylate transporter/malic acid transport family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7282_All//8.00E-159//AT5G24030| SLAH3 (SLAC1 HOMOLOGUE 3); transporter	Unigene7282_All//1.00E-106//gi|11206590|gb|BF275520.1|BF275520				nr -
Unigene7284_All	347	33.47	17.08	17.65	34.45	28.98	42.82	64.70	28.67	19.75	-9.70E-01	1.15E-08		-9.24E-01	1.20E-07		-2.50E-01	1.48E-01		3.14E-01	3.77E-02		-1.17E+00	2.62E-26	Down	-1.71E+00	3.13E-47	Down	Unigene7284_All//gi|40287472|gb|AAR83850.1|//2.00E-15//hypom protein [Capsicum annuum]	Unigene7284_All//1.00E-16//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome	Unigene7284_All//3.00E-162//gi|13245312|gb|BE053779.2|BE053779		ko03010|Ribosome		nr +
Unigene72840_All	204	0.00	0.25	1.31	2.44	0.00	0.00	0.21	0.20	0.00	7.96E+00	6.12E-01		1.03E+01	7.94E-02		-1.13E+01	8.97E-04	Down	-1.13E+01	2.97E-03		-1.68E-02	9.99E-01		-7.70E+00	6.04E-01					Unigene72840_All//3.00E-31//DN508833				
Unigene7288_All	462	3.17	3.73	1.96	26.96	28.32	11.83	2.10	0.54	2.33	2.34E-01	6.17E-01		-6.95E-01	2.36E-01		7.14E-02	7.30E-01		-1.19E+00	2.33E-13	Down	-1.96E+00	4.44E-03		1.46E-01	7.94E-01		Unigene7288_All//gi|115464887|ref|NP_001056043.1|//1.00E-07//Os05g0516100 [Oryza sativa Japonica Group] >gi|113579594|dbj|BAF17957.1| Os05g0516100 [Oryza sativa Japonica Group]			Unigene7288_All//0.00E+00//gi|109887367|gb|DW516336.1|DW516336				nr -
Unigene72904_All	206	0.25	15.50	1.81	1.45	0.50	2.41	5.54	32.67	38.87	5.93E+00	1.11E-16	Up	2.83E+00	9.30E-02		-1.53E+00	2.98E-01		7.33E-01	5.16E-01		2.56E+00	3.04E-23	Up	2.81E+00	5.02E-31	Up				Unigene72904_All//5.00E-39//gi|21092608|gb|BQ404921.1|BQ404921				
Unigene72914_All	207	1.52	0.49	4.37	1.68	1.00	7.64	0.20	0.40	0.19	-1.63E+00	2.76E-01		1.53E+00	5.77E-02		-7.55E-01	5.67E-01		2.18E+00	2.41E-04	Up	9.83E-01	7.29E-01		-8.58E-02	9.67E-01					Unigene72914_All//1.00E-49//TC146120				
Unigene7292_All	319	2.79	0.00	4.34	1.87	0.86	0.42	2.39	6.16	0.75	-1.14E+01	2.85E-05	Down	6.38E-01	2.82E-01		-1.12E+00	2.26E-01		-2.14E+00	4.39E-02		1.37E+00	1.31E-03		-1.67E+00	2.39E-02					Unigene7292_All//5.00E-28//gi|48825326|gb|CO125026.1|CO125026				
Unigene7293_All	556	5.18	3.37	6.61	3.67	2.79	0.89	0.30	0.15	0.79	-6.18E-01	9.41E-02		3.53E-01	3.12E-01		-3.98E-01	3.95E-01		-2.04E+00	3.45E-05	Down	-1.02E+00	6.13E-01		1.37E+00	1.82E-01					Unigene7293_All//4.00E-08//TC178241				
Unigene7294_All	1268	0.00	0.08	0.08	0.24	0.00	0.00	15.64	17.14	47.69	6.32E+00	3.81E-01		6.39E+00	3.91E-01		-7.88E+00	2.01E-02		-7.88E+00	3.98E-02		1.32E-01	2.73E-01		1.61E+00	6.05E-114	Up	Unigene7294_All//gi|145348229|ref|NP_194623.2|//1.00E-125//catalytic [Arabidopsis thaliana]	Unigene7294_All//4.00E-116//AT4G28940| catalytic					nr +
Unigene72945_All	456	0.11	0.22	2.45	0.11	0.15	0.20	0.00	0.00	0.00	9.54E-01	7.24E-01		4.42E+00	3.51E-05	Up	4.68E-01	9.55E-01		8.59E-01	7.92E-01		null	null		null	null		Unigene72945_All//sp|O25827|AK_HELPY//4.00E-13//Aspartokinase OS=Helicobacter pylori GN=lysC PE=3 SV=1						swissprot +
Unigene7296_All	711	3.24	1.14	0.90	14.99	27.46	9.91	1.19	1.59	1.12	-1.51E+00	6.57E-04	Down	-1.85E+00	1.18E-04	Down	8.73E-01	1.36E-13		-5.98E-01	4.75E-04		4.16E-01	4.92E-01		-8.58E-02	9.02E-01		Unigene7296_All//gi|224069236|ref|XP_002326308.1|//7.00E-40//SAUR family protein [Populus trichocarpa] >gi|222833501|gb|EEE71978.1| SAUR family protein [Populus trichocarpa]	Unigene7296_All//2.00E-21//AT5G20820| auxin-responsive protein-related	Unigene7296_All//0.00E+00//gi|109867016|gb|DW495992.1|DW495992				nr -
Unigene7298_All	372	18.28	27.11	26.63	29.06	23.88	26.35	100.36	65.05	47.66	5.68E-01	1.62E-03		5.42E-01	4.19E-03		-2.83E-01	1.12E-01		-1.41E-01	4.89E-01		-6.26E-01	2.26E-15		-1.07E+00	1.17E-38	Down	Unigene7298_All//gi|192910876|gb|ACF06546.1|//2.00E-07//ubiquitin-conjugating enzyme 1 [Elaeis guineensis]	Unigene7298_All//3.00E-08//AT1G16890| ubiquitin-conjugating enzyme, putative	Unigene7298_All//0.00E+00//TC137822		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene72992_All	337	0.00	0.00	2.53	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene72992_All//gi|15235152|ref|NP_195118.1|//5.00E-16//protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] >gi|75279001|sp|Q81760.1|P2C63_ARATH RecName: Full=Probable protein phosphatase 2C 63; Short=AtPP2C63 >gi|13937198|gb|AAK50092.1|AF372953_1 AT4g33920/F17I5_110 [Arabidopsis thaliana] >gi|19568015|gb|AAL87371.1| AT4g33920/F17I5_110 [Arabidopsis thaliana]	Unigene72992_All//7.00E-13//AT4G33920| protein phosphatase 2C family protein / PP2C family protein					nr +
Unigene7300_All	407	325.11	97.60	107.81	345.15	311.44	192.42	387.79	86.26	143.50	-1.74E+00	1.33E-222	Down	-1.59E+00	1.18E-190	Down	-1.48E-01	3.83E-04		-8.43E-01	1.91E-82		-2.17E+00	0.00E+00	Down	-1.43E+00	1.06E-252	Down	Unigene7300_All//gi|297819272|ref|XP_002877519.1|//4.00E-74//tubulin beta-2 [Arabidopsis lyrata subsp. lyrata] >gi|297323357|gb|EFH53778.1| tubulin beta-2 [Arabidopsis lyrata subsp. lyrata]	Unigene7300_All//5.00E-69//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene7300_All//0.00E+00//TC172866		ko04145|Phagosome		nr +
Unigene7302_All	740	0.42	11.91	7.77	0.00	0.09	0.85	1.43	5.03	3.55	4.81E+00	1.03E-41	Up	4.20E+00	1.81E-24	Up	6.54E+00	6.03E-01		9.74E+00	7.59E-04	Up	1.82E+00	7.83E-09	Up	1.31E+00	1.72E-04	Up	Unigene7302_All//gi|61658206|gb|AAX49393.1|//2.00E-46//OLE-5 [Coffea canephora]	Unigene7302_All//8.00E-31//AT3G18570| glycine-rich protein / oleosin	Unigene7302_All//2.00E-07//AI729425				nr -
Unigene73024_All	505	0.00	0.70	1.69	0.39	0.27	0.00	0.00	0.08	0.00	9.46E+00	2.43E-02		1.07E+01	8.99E-05	Up	-5.33E-01	7.47E-01		-8.62E+00	1.33E-01		6.37E+00	6.28E-01		null	null		Unigene73024_All//COG0477//5.00E-62//Permeases of the major facilitator superfamily						cog +
Unigene7304_All	393	1.33	6.06	5.96	2.66	1.49	2.64	0.75	0.96	0.51	2.19E+00	4.62E-06	Up	2.16E+00	1.20E-05	Up	-8.38E-01	2.01E-01		-1.02E-02	9.79E-01		3.46E-01	7.37E-01		-5.71E-01	6.28E-01					Unigene7304_All//2.00E-108//gi|48752890|gb|CO083409.1|CO083409				
Unigene7305_All	646	1.05	1.49	0.91	0.54	1.07	0.49	28.27	27.04	78.81	5.01E-01	4.72E-01		-2.16E-01	7.88E-01		9.82E-01	2.98E-01		-1.41E-01	9.12E-01		-6.42E-02	6.30E-01		1.48E+00	5.10E-85	Up				Unigene7305_All//5.00E-88//gi|72268761|gb|DT046884.1|DT046884				
Unigene7307_All	257	47.23	26.42	21.13	103.12	85.08	69.06	56.59	41.15	45.88	-8.38E-01	3.15E-07		-1.16E+00	2.93E-11	Down	-2.77E-01	7.01E-03		-5.78E-01	1.51E-08		-4.60E-01	4.50E-04		-3.03E-01	2.03E-02		Unigene7307_All//gi|227204507|dbj|BAH57105.1|//2.00E-40//AT4G18710 [Arabidopsis thaliana]	Unigene7307_All//9.00E-42//AT4G18710| BIN2 (BRASSINOSTEROID-INSENSITIVE 2); glycogen synthase kinase 3/ kinase/ protein kinase	Unigene7307_All//3.00E-143//TC177307				nr -
Unigene73077_All	257	2.04	1.77	4.14	2.33	1.88	1.41	9.21	6.67	3.88	-1.98E-01	8.20E-01		1.03E+00	1.43E-01		-3.10E-01	7.41E-01		-7.26E-01	4.60E-01		-4.66E-01	2.27E-01		-1.25E+00	6.37E-04	Down	Unigene73077_All//gi|3281851|emb|CAA19746.1|//8.00E-22//RNA lariat debranching enzyme - like protein [Arabidopsis thaliana] >gi|7270080|emb|CAB79895.1| RNA lariat debranching enzyme-like protein [Arabidopsis thaliana]	Unigene73077_All//3.00E-23//AT4G31770| calcineurin-like phosphoesterase family protein	Unigene73077_All//2.00E-128//TC179490				nr -
Unigene7308_All	589	0.36	3.70	0.27	5.33	3.16	3.14	5.74	24.06	15.42	3.38E+00	2.02E-08	Up	-3.90E-01	8.06E-01		-7.55E-01	2.34E-02		-7.61E-01	3.01E-02		2.07E+00	2.40E-37	Up	1.43E+00	4.62E-15	Up	Unigene7308_All//gi|18400628|ref|NP_565577.1|//5.00E-15//AtGDU4 (Arabidopsis thaliana GLUTAMINE DUMPER 4) >gi|20198236|gb|AAM15477.1| Expressed protein [Arabidopsis thaliana] >gi|88900418|gb|ABD57521.1| At2g24762 [Arabidopsis thaliana]	Unigene7308_All//1.00E-05//AT5G38770| AtGDU7 (Arabidopsis thaliana GLUTAMINE DUMPER 7)	Unigene7308_All//0.00E+00//gi|164250776|gb|ES847152.1|ES847152				nr -
Unigene73088_All	680	2.62	2.24	1.72	7.11	11.50	4.65	0.99	0.80	3.34	-2.27E-01	6.18E-01		-6.03E-01	2.42E-01		6.94E-01	4.52E-04		-6.12E-01	2.54E-02		-3.16E-01	6.74E-01		1.75E+00	1.36E-05	Up	Unigene73088_All//gi|224113543|ref|XP_002332559.1|//7.00E-34//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222835043|gb|EEE73492.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene73088_All//3.00E-23//AT5G47230| ERF5 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 5); DNA binding / transcription activator/ transcription factor	Unigene73088_All//0.00E+00//gi|78332655|gb|DT552929.1|DT552929	AP2-EREBP			nr +
Unigene7309_All	945	0.06	0.32	0.11	0.69	0.44	0.29	1.25	1.95	4.34	2.54E+00	1.51E-01		1.02E+00	7.01E-01		-6.48E-01	4.60E-01		-1.28E+00	1.83E-01		6.36E-01	1.44E-01		1.79E+00	9.13E-10	Up								
Unigene7311_All	651	0.00	1.01	0.65	0.54	1.53	1.04	2.27	3.47	3.61	9.98E+00	6.20E-04	Up	9.35E+00	1.37E-02		1.52E+00	3.74E-02		9.58E-01	3.09E-01		6.09E-01	1.16E-01		6.68E-01	6.31E-02					Unigene7311_All//0.00E+00//BF270949				
Unigene73116_All	222	2.36	7.53	8.40	6.96	4.34	6.51	3.05	1.88	1.79	1.68E+00	2.13E-03		1.83E+00	6.91E-04	Up	-6.80E-01	1.93E-01		-9.56E-02	8.64E-01		-6.95E-01	3.94E-01		-7.64E-01	3.12E-01					Unigene73116_All//2.00E-41//TC161792				
Unigene7313_All	926	1.30	1.09	1.04	5.92	6.17	3.46	3.15	1.67	0.77	-2.48E-01	6.62E-01		-3.28E-01	6.27E-01		6.10E-02	8.29E-01		-7.73E-01	2.04E-03		-9.16E-01	5.13E-03		-2.02E+00	2.13E-08	Down	Unigene7313_All//gi|38605536|sp|Q9ZVK1.1|XTH10_ARATH//1.00E-130//RecName: Full=Probable xyloglucan endotransglucosylase/hydrolase protein 10; Short=At-XTH10; Short=XTH-10; Flags: Precursor	Unigene7313_All//9.00E-132//AT2G14620| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative					nr -
Unigene7314_All	313	6.35	7.77	1.36	7.64	5.28	3.32	1.62	0.93	2.04	2.91E-01	4.87E-01		-2.22E+00	5.21E-05	Down	-5.33E-01	1.94E-01		-1.20E+00	3.63E-03		-7.94E-01	4.02E-01		3.29E-01	6.60E-01					Unigene7314_All//1.00E-09//ES829721				ESTscan +
Unigene73143_All	368	0.00	1.79	1.30	0.00	0.00	0.00	0.00	0.00	0.11	1.08E+01	6.20E-04	Up	1.03E+01	7.44E-03		null	null		null	null		null	null		6.76E+00	6.38E-01		Unigene73143_All//gi|225431477|ref|XP_002280908.1|//2.00E-11//PREDICTED: similar to Os12g0187800 [Vitis vinifera]						nr -
Unigene73148_All	206	0.00	4.92	0.78	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.22E-06	Up	9.60E+00	2.36E-01		null	null		null	null		null	null		null	null									
Unigene73151_All	642	0.00	1.42	1.49	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	2.60E-05	Up	1.05E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene73151_All//gi|298705150|emb|CBJ28593.1|//3.00E-19//glycin-rich protein [Ectocarpus siliculosus]				ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene7316_All	288	14.72	314.05	76.36	8.99	4.54	4.70	1.03	4.21	0.97	4.42E+00	0.00E+00	Up	2.38E+00	2.78E-54	Up	-9.85E-01	7.79E-03		-9.35E-01	1.70E-02		2.03E+00	8.61E-04	Up	-8.58E-02	9.51E-01					Unigene7316_All//2.00E-64//gi|48780200|gb|CO089566.1|CO089566				
Unigene7317_All	1126	0.37	0.00	0.00	7.21	12.94	22.10	0.49	0.26	0.96	-8.54E+00	1.04E-02		-8.54E+00	1.55E-02		8.43E-01	1.08E-09		1.62E+00	1.01E-40	Up	-9.10E-01	3.19E-01		9.69E-01	9.17E-02		Unigene7317_All//gi|163889364|gb|ABY48134.1|//7.00E-82//bHLH transcription factor [Medicago truncatula]	Unigene7317_All//5.00E-52//AT5G65640| bHLH093 (beta HLH protein 93); DNA binding / transcription factor	Unigene7317_All//0.00E+00//ES792399	bHLH	ko04626|Plant-pathogen interaction		nr -
Unigene73186_All	470	0.11	3.45	0.57	0.11	0.51	1.06	1.08	2.67	1.10	4.95E+00	4.63E-08	Up	2.35E+00	2.39E-01		2.27E+00	3.05E-01		3.32E+00	2.31E-02		1.31E+00	1.82E-02		2.96E-02	9.70E-01		Unigene73186_All//gi|15220023|ref|NP_178108.1|//3.00E-40//BAC2; L-ornithine transmembrane transporter/ binding / carnitine:acyl carnitine antiporter [Arabidopsis thaliana]	Unigene73186_All//1.00E-41//AT1G29600| BAC2; L-ornithine transmembrane transporter/ binding / carnitine:acyl carnitine antiporter	Unigene73186_All//6.00E-161//TC164412				nr +
Unigene7319_All	904	0.06	0.17	0.35	1.54	2.25	1.30	1.54	0.97	5.24	1.54E+00	5.30E-01		2.61E+00	1.45E-01		5.43E-01	2.58E-01		-2.48E-01	6.85E-01		-6.69E-01	1.94E-01		1.76E+00	6.26E-11	Up	Unigene7319_All//gi|7767672|gb|AAF69169.1|AC007915_21//5.00E-49//F27F5.21 [Arabidopsis thaliana]	Unigene7319_All//4.00E-09//ATMG01250| hypothetical protein	Unigene7319_All//3.00E-167//gi|73847811|gb|DT456831.1|DT456831				nr +
Unigene732_All	2038	14.86	6.39	8.36	30.65	19.46	17.02	12.45	5.21	5.16	-1.22E+00	1.59E-30	Down	-8.30E-01	6.95E-16		-6.55E-01	5.95E-27		-8.49E-01	2.34E-37		-1.26E+00	7.02E-33	Down	-1.27E+00	2.01E-34	Down	Unigene732_All//gi|124359155|gb|ABD28356.2|//0.00E+00//Protein phosphatase 2C-like [Medicago truncatula]	Unigene732_All//0.00E+00//AT1G09160| protein phosphatase 2C-related / PP2C-related	Unigene732_All//0.00E+00//TC161534			GO:0004721//GO:0016020	nr -
Unigene7320_All	426	39.30	38.78	44.50	1.40	2.10	0.00	0.30	0.00	0.00	-1.95E-02	9.06E-01		1.79E-01	2.18E-01		5.83E-01	4.72E-01		-1.05E+01	7.69E-04	Down	-8.22E+00	2.34E-01		-8.22E+00	1.99E-01									
Unigene73202_All	393	0.13	0.00	3.12	0.13	0.00	0.00	0.00	0.00	0.00	-7.06E+00	6.03E-01		4.53E+00	1.02E-05	Up	-6.99E+00	5.47E-01		-6.99E+00	6.24E-01		null	null		null	null										ESTscan +
Unigene73209_All	202	0.52	0.50	3.16	2.71	0.00	0.45	0.00	0.00	0.00	-4.61E-02	9.87E-01		2.61E+00	2.33E-02		-1.14E+01	4.00E-04	Down	-2.60E+00	2.93E-02		null	null		null	null										
Unigene7323_All	300	10.81	3.88	6.57	4.98	9.76	4.22	30.72	6.13	6.91	-1.48E+00	4.69E-05	Down	-7.19E-01	4.60E-02		9.70E-01	6.79E-03		-2.41E-01	6.82E-01		-2.33E+00	2.13E-28	Down	-2.15E+00	9.43E-27	Down				Unigene7323_All//2.00E-119//TC167659				

Unigene7324_All	743	2.46	0.82	3.58	2.68	3.06	4.98	0.00	0.00	1.02	-1.59E+00	1.79E-03		5.40E-01	1.86E-01		1.90E-01	7.08E-01		8.94E-01	5.07E-03		null	null		9.99E+00	1.39E-05	Up	Unigene7324_All//gi|269819290|gb|AC44835.1|/1.00E-74//glycosyltransferase [Malus x domestica]	Unigene7324_All//1.00E-70//AT2G29730| UGT71D1 (UDP-GLUCOSYL TRANSFERASE 71D1); UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene7324_All//6.00E-11//TC172462		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene73252_All	563	0.00	0.63	1.89	0.00	0.00	0.00	0.00	0.00	0.00	9.30E+00	2.43E-02		1.09E+01	6.60E-06	Up	null	null		null	null		null	null		null	null		Unigene73252_All//gi|194477041|ref|YP_002049220.1|//9.00E-09//50S ribosomal protein L15 [Paulinella chromatophora] >gi|171192048|gb|ACB43010.1| 50S ribosomal protein L15 [Paulinella chromatophora]			ko03010|Ribosome		nr +
Unigene73255_All	739	1.49	1.65	1.51	2.36	1.07	2.44	1.89	0.45	1.02	1.46E-01	7.97E-01		2.54E-02	9.88E-01		-1.14E+00	1.57E-02		5.12E-02	9.37E-01		-2.06E+00	2.51E-04	Down	-8.82E-01	6.81E-02		Unigene73255_All//gi|18420385|ref|NP_568408.1|/1.00E-56//FBX2 (F-BOX PROTEIN 2) [Arabidopsis thaliana] >gi|75332042|sp|Q94AD8.1|FBW3_ARATH RecName: Full=F-box/WD-40 repeat-containing protein At5g21040 >gi|15081723|gb|AAK82516.1|T10F18_70/T10F18_70 [Arabidopsis thaliana] >gi|27363380|gb|AAO11609.1|At5g21040/T10F18_70 [Arabidopsis thaliana]	Unigene73255_All//1.00E-58//AT5G21040| FBX2 (F-BOX PROTEIN 2)	Unigene73255_All//5.00E-101//DW483691				nr +
Unigene7326_All	325	3.70	1.09	4.75	14.10	3.71	5.28	1.82	0.00	0.49	-1.76E+00	7.96E-03		3.60E-01	5.20E-01		-1.93E+00	1.62E-11	Down	-1.42E+00	8.87E-07	Down	-1.08E+01	2.39E-04	Down	-1.89E+00	3.22E-02		Unigene7326_All//gi|15220455|ref|NP_176918.1|//2.00E-07//leucine-rich repeat family protein [Arabidopsis thaliana] >gi|3176660|gb|AAC18784.1| Similar to ERECTA receptor protein kinase gb|U47029 from A. thaliana [Arabidopsis thaliana] >gi|224589465|gb|ACN59266.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]					nr -
Unigene73268_All	244	0.00	0.00	5.89	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.25E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene73268_All//gi|4827251|dbj|BAA77604.1|/1.00E-37//plastidic aldolase NPALDP1 [Nicotiana paniculata]	Unigene73268_All//4.00E-38//AT4G38970| fructose-bisphosphate aldolase, putative	Unigene73268_All//2.00E-42//DN780073		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway		nr -
Unigene73276_All	620	0.51	4.66	5.33	0.48	0.83	0.51	46.17	32.16	36.88	3.20E+00	1.70E-10	Up	3.39E+00	4.27E-12	Up	7.89E-01	4.98E-01		8.09E-02	9.50E-01		-5.22E-01	7.06E-09		-3.24E-01	2.59E-04		Unigene73276_All//gi|253759874|ref|XP_002488951.1|//2.00E-17//hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor] >gi|241947058|gb|EES20203.1| hypothetical protein SORBIDRAFT_1292s002010 [Sorghum bicolor]		Unigene73276_All//4.00E-61//TC148521			nr +
Unigene7328_All	886	0.00	0.00	0.00	0.11	0.00	0.00	1.62	1.89	4.81	null	null		null	null		-6.81E+00	3.10E-01		-6.81E+00	3.95E-01		2.18E-01	6.32E-01		1.57E+00	1.60E-08	Up	Unigene7328_All//gi|18390661|ref|NP_563768.1|//1.00E-109//GPAT1 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 1); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase [Arabidopsis thaliana] >gi|83288231|sp|Q9SHJ5.1|GPAT1_ARATH RecName: Full=Glycerol-3-phosphate acyltransferase 1; Short=AtGPAT1 >gi|6692682|gb|AAF24816.1|AC007592_9 F12K11.15 [Arabidopsis thaliana] >gi|190082237|gb|ACF09412.1|At1g06520 [Arabidopsis thaliana]	Unigene7328_All//3.00E-110//AT1G06520| GPAT1 (GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE 1); 1-acylglycerol-3-phosphate O-acyltransferase/ acyltransferase			ko00564|Glycerophospholipid metabolism//ko00561|Glycerolipid metabolism		nr +
Unigene7329_All	589	0.18	2.32	1.45	2.37	1.34	1.92	2.73	4.47	3.86	3.71E+00	7.17E-06	Up	3.03E+00	3.00E-03		-8.16E-01	1.37E-01		-3.05E-01	6.38E-01		7.13E-01	4.06E-02		4.99E-01	1.82E-01				Unigene7329_All//2.00E-109//ES842492				
Unigene733_All	1991	3.57	1.53	1.74	4.35	3.63	2.16	6.16	2.86	2.42	-1.23E+00	7.76E-08	Down	-1.04E+00	7.03E-06	Down	-2.61E-01	2.10E-01		-1.01E+00	1.74E-07	Down	-1.11E+00	1.63E-13	Down	-1.35E+00	1.24E-18	Down	Unigene733_All//gi|124359155|gb|AB028356.2|/0.00E+00//Protein phosphatase 2C-like [Medicago truncatula]	Unigene733_All//1.00E-179//AT1G09160| protein phosphatase 2C-related / PP2C-related	Unigene733_All//0.00E+00//TC161534			GO:0016791	nr -
Unigene73308_All	362	0.00	3.08	4.41	0.00	0.00	0.00	0.00	0.00	0.11	1.16E+01	1.99E-06	Up	1.21E+01	8.43E-09	Up	null	null		null	null		null	null		6.78E+00	6.38E-01		Unigene73308_All//gi|300269034|gb|EFJ53214.1|//9.00E-10//ribosomal protein S27A component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene73308_All//7.00E-08//AT3G52590| UBQ1 (UBIQUITIN EXTENSION PROTEIN 1); protein binding / structural constituent of ribosome			ko03010|Ribosome		nr +
Unigene7331_All	743	0.00	0.00	0.00	0.00	0.00	0.00	3.47	2.42	0.54	null	null		null	null		null	null		null	null		-5.21E-01	1.46E-01		-2.69E+00	3.14E-10	Down	Unigene7331_All//gi|156144851|gb|ABL52986.1|/4.00E-50//beta-tubulin [Karenia brevis]	Unigene7331_All//9.00E-44//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene7331_All//1.00E-12//CO104631		ko04145|Phagosome		nr -
Unigene73310_All	320	0.16	1.43	2.83	0.00	0.43	0.00	0.00	0.00	0.00	3.12E+00	3.58E-02		4.11E+00	3.91E-04	Up	8.75E+00	3.17E-01		null	null		null	null		null	null		Unigene73310_All//sp|Q98N33|RPOA_RHILO/2.00E-39//DNA-directed RNA polymerase subunit alpha OS=Rhizobium loti GN=rpoA PE=3 SV=1					swissprot +
Unigene73321_All	214	0.00	3.79	1.24	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.31E-05	Up	1.03E+01	7.94E-02		null	null		null	null		null	null		null	null										
Unigene73331_All	345	0.00	3.38	3.40	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.04E-06	Up	1.17E+01	1.77E-06	Up	null	null		null	null		null	null		null	null										
Unigene73336_All	206	0.00	0.00	3.62	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	3.26E-04	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene7334_All	468	183.57	430.26	212.89	305.06	309.26	323.48	377.09	608.90	144.29	1.23E+00	3.79E-201	Up	2.14E-01	8.02E-05		1.97E-02	7.51E-01		8.46E-02	6.90E-02		6.91E-01	2.35E-133		-1.39E+00	3.41E-268	Down	Unigene7334_All//gi|166865124|gb|AB201817.1|/1.00E-79//cinnamyl alcohol dehydrogenase [Gossypium hirsutum]	Unigene7334_All//1.00E-55//AT3G19450| ATCAD4; cinnamyl-alcohol dehydrogenase	Unigene7334_All//0.00E+00//gi|54124143|gb|CO499652.1|CO499652		ko00940|Phenylpropanoid biosynthesis		nr -
Unigene7335_All	759	2.07	5.67	0.84	8.01	11.30	3.69	0.00	0.00	0.00	1.46E+00	2.70E-06	Up	-1.30E+00	2.26E-02		4.97E-01	9.76E-03		-1.12E+00	2.86E-06	Down	null	null		null	null		Unigene7335_All//gi|15236282|ref|NP_195242.1|//3.00E-47//O-methyltransferase family 2 protein [Arabidopsis thaliana] >gi|4455342|emb|CAB36723.1| O-methyltransferase-like protein [Arabidopsis thaliana] >gi|7270467|emb|CAB80233.1| O-methyltransferase-like protein [Arabidopsis thaliana] >gi|20466674|gb|AAK20654.1| O-methyltransferase-like protein [Arabidopsis thaliana] >gi|23198188|gb|AAN15621.1| O-methyltransferase-like protein [Arabidopsis thaliana]	Unigene7335_All//3.00E-49//AT4G35160| O-methyltransferase family 2 protein	Unigene7335_All//0.00E+00//TC146009		ko00940|Phenylpropanoid biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr +
Unigene73363_All	216	0.00	0.00	0.00	0.23	0.00	0.00	3.91	0.00	0.00	null	null		null	null		-7.85E+00	5.47E-01		-7.85E+00	6.24E-01		-1.19E+01	4.39E-06	Down	-1.19E+01	2.21E-06	Down	Unigene73363_All//gi|33772236|gb|AAQ54553.1|/2.00E-08/thaumatin-like pathogenesis-related protein [Malus x domestica]	Unigene73363_All//6.00E-09//AT4G36000| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to other organism; LOCATED IN: cellular_component unknown; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Thaumatin, pathogenesis-related (InterPro:IPR001938); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G24180.1); Has 1043 Blast hits to 945 proteins in 126 species: Archae - 0; Bacteria - 6; Metazoa - 42; Fungi - 41; Plants - 948; Viruses - 2; Other Eukaryotes - 4 (source: NCBI BLink).	Unigene73363_All//6.00E-48//TC179458				nr +
Unigene7337_All	681	9.07	1.41	2.27	1.68	2.78	0.40	0.12	0.00	0.06	-2.68E+00	1.68E-18	Down	-2.00E+00	1.38E-12	Down	7.25E-01	1.35E-01		-2.08E+00	2.95E-03		-6.96E+00	3.99E-01		-1.09E+00	6.74E-01		Unigene7337_All//gi|224065781|ref|XP_002301961.1|//3.00E-79//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222843687|gb|EEE81234.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene7337_All//3.00E-71//AT1G27940| PGP13 (P-GLYCOPROTEIN 13); ATPase, coupled to transmembrane movement of substances			ko02010|ABC transporters		nr +
Unigene7338_All	641	3.43	6.48	4.82	14.69	13.05	16.28	23.15	38.14	61.65	9.19E-01	2.21E-03		4.91E-01	1.93E-01		-1.70E-01	4.24E-01		1.48E-01	4.76E-01		7.20E-01	4.84E-13		1.41E+00	7.21E-62	Up	Unigene7338_All//gi|58531952|gb|AAW78691.1|//3.00E-11//peroxisomal acyl-CoA oxidase 1A [Solanum cheesmaniae]	Unigene7338_All//7.00E-12//AT4G16760| ACX1 (ACYL-COA OXIDASE 1); acyl-CoA oxidase	Unigene7338_All//1.00E-57//TC137718		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene73387_All	337	0.00	1.80	2.05	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	1.16E-03		1.10E+01	6.13E-04	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene7339_All	486	2.48	0.31	0.99	1.85	3.90	4.83	0.35	0.43	0.82	-2.98E+00	1.58E-04	Down	-1.33E+00	4.65E-02		1.08E+00	2.22E-02		1.39E+00	1.21E-03		3.05E-01	8.35E-01		1.24E+00	2.51E-01		Unigene7339_All//gi|115441741|ref|NP_001045150.1|//1.00E-27//Os01g0909400 [Oryza sativa Japonica Group] >gi|113534681|dbj|BAF07064.1|Os01g0909400 [Oryza sativa Japonica Group]	Unigene7339_All//2.00E-23//AT4G12690| unknown protein	Unigene7339_All//2.00E-96//TC161823				nr -
Unigene734_All	1961	24.76	11.94	11.57	38.18	27.06	19.12	15.89	10.21	7.11	-1.05E+00	1.71E-38	Down	-1.10E+00	1.04E-39	Down	-4.97E-01	1.17E-19		-9.98E-01	1.52E-58		-6.38E-01	2.04E-13		-1.16E+00	1.42E-36	Down	Unigene734_All//gi|124359155|gb|AB028356.2|/0.00E+00//Protein phosphatase 2C-like [Medicago truncatula]	Unigene734_All//0.00E+00//AT1G09160| protein phosphatase 2C-related / PP2C-related	Unigene734_All//0.00E+00//TC149472			GO:0004721//GO:0016020	nr -
Unigene7341_All	713	56.58	9.88	87.60	0.00	0.00	0.13	0.00	0.00	0.00	-2.52E+00	9.55E-110	Down	6.31E-01	3.89E-20		null	null		6.99E+00	4.72E-01		null	null		null	null		Unigene7341_All//gi|225457285|ref|XP_002284441.1|//2.00E-38//PREDICTED: hypothetical protein [Vitis vinifera]					nr +
Unigene7342_All	386	4.20	11.68	4.69	5.68	8.12	6.67	24.65	18.08	22.40	1.48E+00	1.15E-06	Up	1.59E-01	7.37E-01		5.16E-01	1.56E-01		2.32E-01	6.29E-01		-4.47E-01	7.64E-03		-1.38E-01	4.50E-01				Unigene7342_All//8.00E-166//TC145639				
Unigene73426_All	219	0.00	0.00	3.16	0.00	0.00	0.21	0.00	0.00	0.00	null	null		1.16E+01	6.13E-04	Up	null	null		7.69E+00	6.88E-01		null	null		null	null										ESTscan +
Unigene7345_All	384	0.00	0.79	1.11	1.43	1.26	1.53	1.43	4.35	1.45	9.63E+00	4.37E-02		1.01E+01	1.37E-02		-1.83E-01	8.25E-01		9.96E-02	9.36E-01		1.60E+00	8.16E-04	Up	2.11E-02	9.79E-01										
Unigene7452_All	204	0.00	0.00	3.92	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.19E+01	1.72E-04	Up	null	null		null	null		null	null		null	null										
Unigene7348_All	599	0.17	1.78	0.53	0.00	1.55	0.38	1.41	1.33	6.38	3.35E+00	2.17E-04	Up	1.61E+00	3.04E-01		1.06E+01	1.03E-05	Up	8.56E+00	1.18E-01		-9.07E-02	9.00E-01		2.18E+00	1.49E-11	Up									

Unigene7349_All	531	2.27	1.53	0.40	1.69	1.49	1.79	2.47	0.87	0.53	-5.70E-01	3.65E-01			-2.50E+00	1.15E-03		-1.79E-01	8.15E-01		8.10E-02	9.31E-01		-1.51E+00	5.71E-03		-2.23E+00	1.19E-04	Down	Unigene7349_All//gi|297600629|ref|XP_001049519.2|//6.00E-46//0s03g0241800 [Oryza sativa Japonica Group] >gi|255674356|dbj|BAF11433.2|0s03g0241800 [Oryza sativa Japonica Group]	Unigene7349_All//9.00E-46//AT4G33990| EMB2758 (embryo defective 2758)	Unigene7349_All//1.00E-11//ES795077				nr -
Unigene73499_All	223	0.00	3.64	1.91	0.89	0.00	0.20	0.00	0.56	0.00	1.18E+01	9.31E-05	Up	1.09E+01	1.37E-02		-9.80E+00	8.39E-02		-2.14E+00	3.46E-01		9.14E+00	2.40E-01		null	null				Unigene73499_All//2.00E-66//TC169202				
Unigene735_All	476	4.84	1.70	2.57	4.50	4.56	2.47	1.87	1.76	2.34	-1.51E+00	6.57E-04	Down	-9.11E-01	3.99E-02		1.83E-02	9.79E-01		-8.67E-01	4.89E-02		-8.70E-02	9.03E-01		3.29E-01	5.83E-01		Unigene735_All//gi|115455745|ref|NP_001051473.1|//9.00E-66//0s03g0784000 [Oryza sativa Japonica Group] >gi|113549944|dbj|BAF13387.1|0s03g0784000 [Oryza sativa Japonica Group]	Unigene735_All//1.00E-70//AT3G22290| unknown protein	Unigene735_All//0.00E+00//TC171682				nr -
Unigene7350_All	378	5.95	0.40	5.35	3.95	2.92	2.51	0.56	0.77	0.32	-3.89E+00	9.87E-10	Down	-1.53E-01	7.22E-01		-4.40E-01	4.27E-01		-6.56E-01	2.40E-01		4.69E-01	7.06E-01		-8.23E-01	5.98E-01				Unigene7350_All//5.00E-50//TC139702				
Unigene73536_All	264	0.00	0.00	3.03	0.00	0.00	0.00	2.88	0.16	0.60	null	null		1.16E+01	1.72E-04	Up	null	null		null	null		-4.19E+00	1.57E-04	Down	-2.26E+00	4.68E-03									
Unigene73538_All	209	0.00	7.03	5.10	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.10E-08	Up	1.23E+01	6.60E-06	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene7354_All	420	2.24	8.81	6.09	16.01	41.81	27.31	0.20	0.20	0.19	1.97E+00	5.16E-08	Up	1.44E+00	8.04E-04	Up	1.38E+00	3.59E-25	Up	7.71E-01	2.84E-06		-1.66E-02	1.01E+00		-8.56E-02	9.69E-01		Unigene7354_All//gi|76262500|gb|AB441400.1|//2.00E-10//pherophorin-C2 protein precursor [Chlamydomonas reinhardtii]				ko03040|Spliceosome		nr -
Unigene73550_All	562	3.44	5.77	8.43	11.97	11.46	8.68	13.84	5.65	5.67	7.44E-01	3.09E-02		1.29E+00	1.40E-05	Up	-6.26E-02	8.36E-01		-4.63E-01	4.40E-02		-1.29E+00	4.50E-11	Down	-1.29E+00	2.19E-11	Down	Unigene73550_All//gi|297844510|ref|XP_002890136.1|//2.00E-34//XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335978|gb|EFH66395.1| XH/XS domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene73550_All//5.00E-32//AT1G15910| XH/XS domain-containing protein / XS zinc finger domain-containing protein	Unigene73550_All//0.00E+00//gi|18098776|gb|BM358042.1|BM358042				nr -
Unigene7356_All	263	2.59	13.29	11.34	2.08	3.27	1.37	54.50	47.99	15.45	2.36E+00	2.51E-09	Up	2.13E+00	6.67E-07	Up	6.52E-01	4.25E-01		-6.01E-01	5.66E-01		-1.83E-01	2.15E-01		-1.82E+00	4.65E-33	Down	Unigene7356_All//gi|224139090|ref|XP_002326765.1|//2.00E-12//predicted protein [Populus trichocarpa] >gi|222834087|gb|EEE72564.1|predicted protein [Populus trichocarpa]		Unigene7356_All//7.00E-147//DW243014				nr +
Unigene73566_All	209	0.00	4.61	2.29	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.37E-05	Up	1.12E+01	7.44E-03		null	null		null	null		null	null		null	null									
Unigene7357_All	2387	0.00	0.00	0.00	0.04	0.00	0.00	29.90	84.45	24.17	null	null		null	null		-5.38E+00	3.10E-01		-5.38E+00	3.95E-01		1.50E+00	0.00E+00	Up	-3.07E-01	1.37E-08		Unigene7357_All//gi|37548634|gb|AAN12272.1|//0.00E+00//subtilisin-like protease C1 [Glycine max] >gi|405566678|gb|ADO02075.4|subtilisin-like protease C1 [Glycine max]	Unigene7357_All//5.00E-175//AT5G59100| subtilase family protein	Unigene7357_All//9.00E-62//TC175719				nr -
Unigene7358_All	510	0.41	0.79	0.84	3.61	1.28	0.62	2.49	1.88	0.31	9.54E-01	4.13E-01		1.03E+00	3.96E-01		-1.49E+00	1.22E-03		-2.54E+00	5.49E-06	Down	-4.00E-01	4.77E-01		-2.99E+00	6.36E-06	Down			Unigene7358_All//6.00E-155//DW515231				
Unigene7360_All	529	3.17	0.86	0.50	3.20	2.08	1.20	2.24	2.53	2.56	-1.88E+00	7.32E-04	Down	-2.65E+00	4.00E-05	Down	-6.20E-01	2.16E-01		-1.42E+00	5.89E-03		1.76E-01	7.33E-01		1.94E-01	6.93E-01		Unigene7360_All//gi|225444547|ref|XP_002269568.1|//1.00E-86//PREDICTED: similar to intron maturase, type II family protein [Vitis vinifera]	Unigene7360_All//2.00E-85//AT1G30010| intron maturase, type II family protein					nr +
Unigene73602_All	219	0.00	0.00	0.73	0.00	0.00	0.21	2.32	0.00	0.73	null	null		9.51E+00	2.36E-01		null	null		7.69E+00	6.87E-01		-1.12E+01	8.88E-04	Down	-1.67E+00	7.77E-02									
Unigene73605_All	241	0.00	0.63	3.31	0.41	1.00	1.69	0.35	0.17	0.50	9.30E+00	2.32E-01		1.17E+01	1.72E-04	Up	1.27E+00	5.31E-01		2.03E+00	1.49E-01		-1.02E+00	7.22E-01		4.99E-01	8.06E-01		Unigene73605_All//gi|224074901|ref|XP_002304482.1|//7.00E-10//predicted protein [Populus trichocarpa] >gi|222841914|gb|EEE79461.1|predicted protein [Populus trichocarpa]	Unigene73605_All//3.00E-06//AT1G12800| S1 RNA-binding domain-containing protein	Unigene73605_All//6.00E-27//ES850534				nr +
Unigene73607_All	878	0.30	0.58	0.85	0.68	0.24	0.41	2.65	0.57	0.86	9.54E-01	3.73E-01		1.51E+00	9.49E-02		-1.53E+00	1.01E-01		-7.26E-01	4.60E-01		-2.21E+00	2.77E-07	Down	-1.62E+00	2.77E-05	Down	Unigene73607_All//gi|225445069|ref|XP_002280317.1|//1.00E-125//PREDICTED: similar to protein kinase family protein / WD-40 repeat family protein [Vitis vinifera]	Unigene73607_All//1.00E-97//AT4G29080| protein kinase family protein / WD-40 repeat family protein	Unigene73607_All//0.00E+00//TC143569		ko04140|Regulation of autophagy	GO:0004672//GO:0005488//GO:0009987	nr +
Unigene7361_All	910	1.78	2.28	1.29	4.22	3.78	0.84	0.46	0.09	0.48	3.57E-01	4.24E-01		-4.69E-01	3.87E-01		-1.56E-01	6.45E-01		-2.32E+00	9.92E-11	Down	-2.34E+00	5.46E-02		5.18E-02	9.74E-01		Unigene7361_All//gi|122162768|sp|Q01JD1.1|SPL7_ORYSI//3.00E-22//RecName: Full=Squamosa promoter-binding-like protein 7 >gi|116310136|emb|CAH67152.1|OS1GBa0122F23.9 [Oryza sativa (indica cultivar-group)]	Unigene7361_All//5.00E-09//AT2G33810| SPL3 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 3); DNA binding / transcription factor	Unigene7361_All//5.00E-55//gi|78338631|gb|DT558905.1|DT558905	SBP			nr +
Unigene7362_All	781	5.09	1.10	1.98	4.08	2.25	1.62	1.46	2.14	0.71	-2.21E+00	7.97E-10	Down	-1.36E+00	3.89E-05	Down	-8.60E-01	8.63E-03		-1.33E+00	1.50E-04	Down	5.50E-01	2.37E-01		-1.03E+00	5.95E-02		Unigene7362_All//gi|582010024|gb|AAW66657.1|//5.00E-94//thiamine biosynthetic enzyme [Picrorhiza kurroa]	Unigene7362_All//6.00E-89//AT5G54770| THI1; protein homodimerization	Unigene7362_All//0.00E+00//gi|164322593|gb|ES819671.1|ES819671				nr -
Unigene73620_All	435	1.08	4.43	2.94	1.72	1.19	2.08	0.29	0.19	2.01	2.03E+00	1.13E-04	Up	1.44E+00	2.61E-02		-5.33E-01	5.26E-01		2.74E-01	7.10E-01		-6.01E-01	7.65E-01		2.79E+00	5.37E-04	Up							
Unigene73621_All	221	0.00	0.00	4.82	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	6.60E-06	Up	null	null		null	null		null	null		null	null		Unigene73621_All//gi|40287520|gb|AA883874.1|//9.00E-15//induced stolon tip protein [Capsicum annuum]						nr +
Unigene7363_All	285	2.20	1.24	1.12	6.12	12.69	8.56	2.08	1.61	1.96	-8.24E-01	3.75E-01		-9.75E-01	3.16E-01		1.05E+00	8.19E-04	Up	4.84E-01	2.66E-01		-3.65E-01	6.48E-01		-8.58E-02	9.23E-01		Unigene7363_All//gi|224139814|ref|XP_002323289.1|//8.00E-24//predicted protein [Populus trichocarpa] >gi|222867919|gb|EEF05050.1|predicted protein [Populus trichocarpa]	Unigene7363_All//7.00E-07//AT3G57950| unknown protein					nr +
Unigene73631_All	980	0.05	0.00	2.72	0.00	0.00	0.00	0.00	0.00	0.00	-5.74E+00	6.05E-01		5.67E+00	2.61E-13	Up	null	null		null	null		null	null		null	null		Unigene73631_All//gi|475169|emb|CAA83649.1|//1.00E-141//beta-glucuronidase [synthetic construct] >gi|14594803|emb|CAC43287.1| beta-glucuronidase [Arabidopsis thaliana] >gi|14594807|emb|CAC43289.1| beta-glucuronidase [Arabidopsis thaliana] >gi|16903091|gb|AAL30401.1| beta-glucuronidase [Cloning vector pWS31] >gi|16903094|gb|AAL30403.1| beta-glucuronidase [Cloning vector pWS32] >gi|29150589|gb|AA063175.1| beta-glucuronidase [Cloning Vector pHRGFPGUS] >gi|30025557|gb|AAP04590.1| beta-glucuronidase [Cloning vector pHR50] >gi|30523396|gb|AAP31913.1| beta-glucuronidase [Cloning vector pHREi-km] >gi|55724884|emb|CAH64894.1| beta-glucuronidase [Cloning vector pRU1064] >gi|55724887|emb|CAH64918.1| beta-glucuronidase [Cloning vector pRU1075] >gi|55724890|emb|CAH64920.1| beta-glucuronidase [Cloning vector	Unigene73631_All//3.00E-07//AT3G54440| glycoside hydrolase family 2 protein			ko00052|Galactose metabolism//ko00600|Sphingolipid metabolism//ko00511|Other glycan degradation	GO:0016772	nr -
Unigene7364_All	733	0.57	0.55	0.29	4.01	7.70	4.56	2.36	0.63	1.14	-4.62E-02	9.80E-01		-9.75E-01	4.11E-01		9.42E-01	8.44E-05		1.85E-01	6.22E-01		-1.91E+00	8.45E-05	Down	-1.05E+00	1.45E-02		Unigene7364_All//gi|115444855|ref|NP_001046207.1|//6.00E-15//Os02g0198400 [Oryza sativa Japonica Group] >gi|113535738|dbj|BAF08121.1|Os02g0198400 [Oryza sativa Japonica Group]	Unigene7364_All//2.00E-11//AT5G48310| unknown protein					nr -
Unigene73644_All	219	0.00	4.40	1.95	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.37E-05	Up	1.09E+01	1.37E-02		null	null		null	null		null	null		null	null		Unigene73644_All//gi|192913004|gb|ACF06610.1|//2.00E-17//ribosomal protein L15 [Elseis guineensis]	Unigene73644_All//7.00E-18//AT4G16720| 60S ribosomal protein L15 (RPL15A)			ko03010|Ribosome		nr +
Unigene73645_All	431	1.21	13.28	0.49	0.00	0.88	1.36	0.78	1.94	1.57	3.45E+00	1.22E-21	Up	-1.30E+00	2.42E-01		9.78E+00	1.95E-02		1.04E+01	1.37E-03		1.31E+00	6.56E-02		1.00E+00	1.91E-01		Unigene73645_All//gi|34550779|gb|AAQ74955.1|//2.00E-12//Gbiaa-Re [Gossypium barbadense]	Unigene73645_All//6.00E-13//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene73645_All//1.00E-93//gi|73863704|gb|DT466443.1|DT466443				nr +
Unigene73651_All	403	1.30	3.27	4.76	5.81	7.09	5.04	0.52	0.41	0.30	1.33E+00	2.73E-02		1.87E+00	4.53E-04	Up	2.88E-01	5.04E-01		-2.04E-01	6.53E-01		-3.39E-01	8.11E-01		-8.23E-01	5.98E-01				Unigene73651_All//7.00E-117//gi|164241899|gb|ES821080.1|ES821080				
Unigene7366_All	295	0.35	0.86	0.18	1.18	2.10	0.92	5.02	9.07	11.07	1.28E+00	4.35E-01		-9.75E-01	7.19E-01		8.30E-01	4.15E-01		-3.64E-01	7.55E-01		8.54E-01	1.30E-02		1.14E+00	1.73E-04	Up			Unigene7366_All//3.00E-07//ES795981				
Unigene7367_All	286	0.18	5.49	5.96	3.83	4.33	3.32	1.92	0.29	0.70	4.91E+00	8.63E-08	Up	5.03E+00	3.41E-08	Up	1.78E-01	8.19E-01		-2.09E-01	7.42E-01		-2.72E+00	1.22E-02		-1.46E+00	9.76E-02								
Unigene73690_All	202	0.00	10.28	3.16	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	7.93E-12	Up	1.16E+01	1.15E-03		null	null		null	null		null	null		null	null									
Unigene73691_All	221	0.00	2.52	1.69	0.68	0.93	5.31	2.49	5.30	2.34	1.13E+01	2.16E-03		1.07E+01	2.48E-02		4.67E-01	8.24E-01		2.97E+00	1.83E-04	Up	1.09E+00	5.52E-02		-8.59E-02	9.27E-01		Unigene73691_All//gi|42569078|ref|NP_179266.2|//2.00E-07//protein kinase family protein [Arabidopsis thaliana] >gi|209414532|gb|ACI46506.1|At2g16750 [Arabidopsis thaliana]	Unigene73691_All//1.00E-08//AT2G16750| protein kinase family protein				GO:0004672	nr -
Unigene73692_All	316	0.00	0.00	4.55	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	6.29E-08	Up	null	null		null	null		null	null		null	null		Unigene73692_All//gi|115452901|ref|NP_001050051.1|//1.00E-40//Os03g0337800 [Oryza sativa Japonica Group] >gi|113548522|dbj|BAF11965.1|Os03g0337800 [Oryza sativa Japonica Group]	Unigene73692_All//5.00E-35//AT4G02230| 60S ribosomal protein L19 (RPL19C)	Unigene73692_All//6.00E-49//gi|109827128|gb|DW225829.1|DW225829		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene7370_All	368	62.98	24.92	31.11	99.49	86.09	91.43	131.78	61.33	80.54	-1.34E+00	4.19E-27	Down	-1.02E+00	4.68E-17	Down	-2.09E-01	1.88E-02		-1.22E-01	2.31E-01		-1.10E+00	1.18E-50	Down	-7.10E-01	3.34E-25		Unigene7370_All//gi|15241291|ref|NP_196908.1|//5.00E-42//mitochondrial phosphate transporter [Arabidopsis thaliana] >gi|9757785|dbj|BAB08283.1|mitochondrial phosphate translocator [Arabidopsis thaliana] >gi|16604460|gb|AAL24236.1|AT5g14040/MUA22_4 [Arabidopsis thaliana] >gi|23505897|gb|AAN28808.1|At5g14040/MUA22_4 [Arabidopsis thaliana]	Unigene7370_All//1.00E-40//AT5G14040| mitochondrial phosphate transporter	Unigene7370_All//0.00E+00//gi|78327576|gb|DT547850.1|DT547850				nr +
Unigene73700_All	363	0.00	2.79	3.52	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	7.21E-06	Up	1.18E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene73700_All//sp|Q4R7H5|EF1G_MACFA//3.00E-42//Elongation factor 1-gamma OS=Macaca fascicularis GN=EEF1G PE=2 SV=1						swissprot -
Unigene73702_All	534	0.00	1.52	2.09	0.00	0.32	0.08	0.32	0.23	0.15	1.06E+01	9.31E-05	Up	1.10E+01	3.42E-06	Up	8.33E+00	2.26E-01		6.40E+00	6.87E-01		-4.32E-01	7.92E-01		-1.09E+00	5.51E-01									

Unigene7372_All	558	1.59	0.73	0.95	0.71	1.11	2.35	1.97	0.30	1.43	-1.13E+00	1.30E-01			-7.40E-01	3.47E-01		6.37E-01	5.49E-01		1.72E+00	6.55E-03		-2.72E+00	1.31E-04	Down	-4.64E-01	4.07E-01		Unigene7372_All//gi|255562731|ref|XP_002522371.1|//2.00E-22//mRNA, complete cds, clone: raf124-09-C04, putative [Ricinus communis] >gi|223538449|gb|EEF40055.1| mRNA, complete cds, clone: raf124-09-C04, putative [Ricinus communis]	Unigene7372_All//3.00E-11//AT2G23470| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: stem, stamen; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF647 (InterPro:IPR006968); BEST Arabidopsis thaliana protein match is: emb1879 (embryo defective 1879) (TAIR:AT5G49820.1); Has 259 Blast hits to 258 proteins in 85 species: Archae - 0; Bacteria - 0; Metazoa - 92; Fungi - 35; Plants - 93; Viruses - 0; Other Eukaryotes - 39 (source: NCBI BLink).	Unigene7372_All//0.00E+00//BF272982				nr -
Unigene7373_All	396	0.79	1.28	3.90	3.02	0.87	0.23	0.43	0.63	1.81	6.91E-01	4.99E-01			2.30E+00	3.37E-04	Up	-1.80E+00	3.53E-03		-3.73E+00	1.43E-05	Down	5.68E-01	6.73E-01		2.08E+00	1.09E-02					Unigene7373_All//1.00E-93//C0093267				
Unigene7374_All	1391	0.49	0.22	0.08	1.83	0.62	0.52	3.16	4.84	30.70	-1.16E+00	1.89E-01			-2.67E+00	1.69E-02		-1.56E+00	4.72E-05	Down	-1.81E+00	1.72E-05	Down	6.14E-01	2.34E-03		3.28E+00	2.71E-189	Up	Unigene7374_All//gi|206574958|gb|ACI14392.1|//3.00E-57//WRKY127-1 transcription factor [Brassica napus]	Unigene7374_All//1.00E-49//AT5G52830| WRKY27; transcription factor	Unigene7374_All//3.00E-08//TC136977	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene7375_All	803	0.00	0.38	0.00	4.84	3.95	1.46	64.76	20.30	12.25	8.56E+00	4.37E-02		null	null		-2.95E-01	3.77E-01		-1.73E+00	1.43E-07	Down	-1.67E+00	6.86E-102	Down	-2.40E+00	2.17E-168	Down	Unigene7375_All//gi|297840071|ref|XP_002887917.1|//8.00E-65//disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333758|gb|EFH64176.1| disease resistance-responsive family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7375_All//4.00E-61//AT1G64160| disease resistance-responsive family protein / dirigent family protein	Unigene7375_All//0.00E+00//TC151751				nr +
Unigene73766_All	665	0.39	0.08	2.00	0.15	0.36	0.00	0.00	0.00	0.00	-2.37E+00	2.14E-01			2.35E+00	8.68E-04	Up	1.27E+00	5.31E-01		-7.23E+00	3.95E-01		null	null		null	null		Unigene73766_All//gi|255598529|ref|XP_002537029.1|//2.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223517756|gb|EEF25354.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene73779_All	279	0.00	0.00	3.82	0.00	0.00	0.00	0.00	0.00	0.00	null	null			1.19E+01	6.60E-06	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene73782_All	210	0.00	0.72	4.31	0.00	0.00	0.00	0.00	0.00	0.00	9.50E+00	2.32E-01			1.21E+01	4.70E-05	Up	null	null		null	null		null	null		null	null									
Unigene73789_All	355	1.47	1.14	6.90	0.14	0.39	0.00	0.60	0.24	0.22	-3.68E-01	6.83E-01			2.23E+00	4.62E-06	Up	1.47E+00	6.17E-01		-7.13E+00	6.24E-01		-1.34E+00	4.29E-01		-1.41E+00	3.79E-01		Unigene73789_All//gi|297842595|ref|XP_002889179.1|//2.00E-06//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335020|gb|EFH65438.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene73789_All//4.00E-07//AT1G78210| hydrolase, alpha/beta fold family protein	Unigene73789_All//8.00E-21//TC139638		GO:0003824		nr -
Unigene7379_All	904	0.29	0.50	1.77	2.81	4.57	3.20	1.82	1.57	0.93	8.02E-01	4.60E-01			2.61E+00	7.15E-05	Up	7.02E-01	1.67E-02		1.86E-01	6.55E-01		-2.15E-01	6.40E-01		-9.79E-01	2.63E-02		Unigene7379_All//gi|38603874|gb|AAR24682.1|//8.00E-71//At5g49320 [Arabidopsis thaliana] >gi|45732654|gb|AAS76225.1| At5g49320 [Arabidopsis thaliana]	Unigene7379_All//3.00E-70//AT5G49320| unknown protein					nr -
Unigene73798_All	354	1.18	0.00	0.60	3.38	2.04	1.66	1.31	5.31	0.11	-1.02E+01	1.04E-02			-9.75E-01	4.11E-01		-7.25E-01	2.33E-01		-1.03E+00	1.06E-01		2.02E+00	1.98E-05	Up	-3.55E+00	6.85E-03		Unigene73798_All//gi|224138076|ref|XP_002326512.1|//9.00E-18//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222833834|gb|EEE72311.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene73798_All//6.00E-11//AT4G17980| anac071 (Arabidopsis NAC domain containing protein 71); transcription factor		NAC	GO:0001071//GO:0005488//GO:0032501	nr +
Unigene7380_All	515	0.00	0.00	0.00	0.19	0.00	0.18	6.24	30.51	8.12	null	null		null	null		-7.60E+00	3.10E-01		-1.42E-01	9.48E-01		2.29E+00	6.22E-47	Up	3.81E-01	1.51E-01		Unigene7380_All//gi|15241383|ref|NP_197555.1|//4.00E-39//oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] >gi|21537316|gb|AAM61657.1| ethylene-forming-enzyme-like dioxygenase-like [Arabidopsis thaliana] >gi|133778810|gb|AB038745.1| At5g20550 [Arabidopsis thaliana]	Unigene7380_All//2.00E-40//AT5G20550| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene7380_All//2.00E-124//CO125365		ko00941|Flavonoid biosynthesis		nr +
Unigene7381_All	880	1.13	0.52	0.79	1.36	2.39	0.41	0.19	0.71	1.49	-1.12E+00	1.09E-01			-5.22E-01	4.60E-01		8.13E-01	6.93E-02		-1.73E+00	8.52E-03		1.89E+00	3.49E-02		2.96E+00	6.13E-06	Up	Unigene7381_All//gi|15240937|ref|NP_198698.1|//7.00E-39//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|122214236|sp|Q3E911.1|PP400_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g27460	Unigene7381_All//8.00E-39//AT5G27460| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene73811_All	224	0.23	0.23	0.00	0.89	0.00	0.20	35.49	8.96	18.67	-4.64E-02	9.83E-01			-7.87E+00	6.16E-01		-9.80E+00	8.39E-02		-2.14E+00	3.46E-01		-1.99E+00	2.73E-20	Down	-9.26E-01	3.49E-07		Unigene73811_All//gi|224054176|ref|XP_002298129.1|//2.00E-15//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene73811_All//1.00E-13//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene73811_All//1.00E-49//DW504431		GO:0016491//GO:0044464		nr -
Unigene7385_All	1170	0.00	0.00	0.00	0.00	0.00	0.00	47.56	15.18	15.56	null	null		null	null		null	null		null	null		-1.65E+00	1.58E-106	Down	-1.61E+00	2.72E-106	Down	Unigene7385_All//gi|124360970|gb|ABN08942.1|//1.00E-139//Quinoprotein alcohol dehydrogenase-like [Medicago truncatula]		Unigene7385_All//1.00E-37//C0071277				nr +
Unigene7387_All	791	0.99	693.49	10.50	1.20	5.70	13.02	0.21	2.11	5.74	9.45E+00	0.00E+00	Up	3.40E+00	5.54E-30	Up	2.25E+00	1.33E-12	Up	3.44E+00	5.67E-41	Up	3.31E+00	6.97E-08	Up	4.75E+00	6.71E-27	Up	Unigene7387_All//gi|167858183|gb|ACA04032.1|//1.00E-106//galactinol synthase 3 [Populus trichocarpa]	Unigene7387_All//6.00E-104//AT1G56600| AtGolS2 (Arabidopsis thaliana galactinol synthase 2); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	Unigene7387_All//0.00E+00//TC156180				nr +
Unigene73879_All	211	0.00	1.44	4.54	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	4.37E-02			1.21E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene73879_All//gi|33520419|gb|AAQ21121.1|//1.00E-15//photosystem I psaH protein [Trifolium pratense]	Unigene73879_All//1.00E-15//AT1G52230| PSAM2 (PHOTOSYSTEM I SUBUNIT H2)	Unigene73879_All//4.00E-18//EX166886		ko00195|Photosynthesis	GO:0005740//GO:0009522//GO:0009534//GO:0009570//GO:0015078//GO:0022904//GO:0031224	nr -
Unigene7388_All	1892	0.28	0.00	0.11	1.03	0.89	0.57	14.39	4.99	1.07	-8.11E+00	2.92E-03			-1.30E+00	2.42E-01		-2.03E-01	6.79E-01		-8.42E-01	7.33E-02		-1.53E+00	4.04E-47	Down	-3.74E+00	4.27E-138	Down	Unigene7388_All//gi|2739004|gb|AAB94590.1|//0.00E+00//CYP82C1p [Glycine max]	Unigene7388_All//2.00E-153//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene7388_All//1.00E-07//EV494861		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene73881_All	231	0.00	3.29	4.15	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.75E-04	Up	1.20E+01	2.45E-05	Up	null	null		null	null		null	null		null	null									
Unigene7389_All	255	38.78	33.38	23.81	44.93	42.27	56.14	56.21	27.70	30.78	-2.16E-01	2.67E-01			-7.04E-01	1.95E-04		-8.81E-02	6.55E-01		3.21E-01	3.66E-02		-1.02E+00	8.69E-14	Down	-8.69E-01	4.45E-11		Unigene7389_All//gi|226531828|ref|NP_001148017.1|//2.00E-12//40S ribosomal protein S25-1 [Zea mays] >gi|195615172|gb|ACG29416.1| 40S ribosomal protein S25-1 [Zea mays] >gi|195658723|gb|ACG48829.1| 40S ribosomal protein S25-1 [Zea mays]		Unigene7389_All//2.00E-94//gi|109875007|gb|DW503981.1|DW503981		ko03010|Ribosome		nr +
Unigene7390_All	652	0.32	0.47	1.63	0.31	0.26	0.83	32.81	17.12	100.88	5.39E-01	6.71E-01			2.35E+00	3.61E-03		-2.11E-01	8.58E-01		1.44E+00	1.92E-01		-9.39E-01	1.14E-17		1.62E+00	3.81E-125	Up	Unigene7390_All//gi|65993863|gb|AAS73001.2|//1.00E-52//dirigent-like protein [Gossypium barbadense]	Unigene7390_All//5.00E-35//AT2G21110| disease resistance-responsive family protein	Unigene7390_All//7.00E-35//ES791694				nr +
Unigene73909_All	215	0.00	4.24	2.72	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.60E-05	Up	1.14E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene73909_All//sp|B3MF94|EIF3H_DROAN//7.00E-26//Eukaryotic translation initiation factor 3 subunit H OS=Drosophila ananassae GN=eIF-3p40 PE=3 SV=1						swissprot +
Unigene7393_All	677	0.70	1.20	0.47	0.96	0.46	1.33	1.87	0.37	1.59	7.84E-01	3.23E-01			-5.60E-01	6.28E-01		-1.06E+00	2.26E-01		4.80E-01	5.50E-01		-2.34E+00	1.56E-04	Down	-2.38E-01	6.32E-01								
Unigene73932_All	206	0.00	3.20	1.55	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.20E-04	Up	1.06E+01	4.47E-02		null	null		null	null		null	null		null	null		Unigene73932_All//gi|300150325|gb|EFJ16976.1|//2.00E-15//Sar1, ras family GTPase [Selaginella moellendorffii]	Unigene73932_All//4.00E-16//AT4G02080| ATSAR2 (ARABIDOPSIS THALIANA SECRETION-ASSOCIATED RAS SUPER FAMILY 2); GTP binding			ko04141|Protein processing in endoplasmic reticulum	GO:0005622//GO:0006810	nr +
Unigene7394_All	584	1.79	2.08	1.00	1.88	2.36	1.47	4.71	9.52	2.93	2.17E-01	7.05E-01			-8.37E-01	2.34E-01		3.30E-01	6.09E-01		-3.53E-01	6.35E-01		1.02E+00	8.56E-06	Up	-6.82E-01	3.63E-02		Unigene7394_All//gi|224130338|ref|XP_002328584.1|//2.00E-21//nbs-lrr resistance protein [Populus trichocarpa] >gi|222838566|gb|EEE76931.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene7394_All//2.00E-13//AT1G69545| leucine-rich repeat family protein	Unigene7394_All//2.00E-149//ES850520		ko04626|Plant-pathogen interaction		nr -
Unigene73945_All	326	0.16	0.00	0.16	1.99	0.63	0.28	6.87	2.95	0.24	-7.33E+00	6.05E-01			2.50E-02	9.92E-01		-1.65E+00	6.52E-02		-2.84E+00	1.02E-02		-1.22E+00	1.68E-03		-4.81E+00	6.33E-14	Down			Unigene73945_All//3.00E-32//CO120954				
Unigene7395_All	436	76.56	31.03	45.31	17.94	21.96	21.75	225.95	467.42	192.25	-1.30E+00	3.19E-37	Down	-7.57E-01	5.81E-15		2.92E-01	1.37E-01		2.78E-01	1.72E-01		1.05E+00	1.32E-193	Up	-2.33E-01	3.58E-07		Unigene7395_All//gi|297816226|ref|XP_002875996.1|//2.00E-11//ATPSK4 [Arabidopsis lyrata subsp. lyrata] >gi|297321834|gb|EFH52255.1| ATPSK4 [Arabidopsis lyrata subsp. lyrata]	Unigene7395_All//7.00E-12//AT3G49780| ATPSK4 (PHYTOSULFOKINE 4 PRECURSOR); growth factor	Unigene7395_All//2.00E-25//TC156906				nr +
Unigene7396_All	831	50.12	15.91	30.89	14.03	14.75	14.57	9.36	19.62	10.36	-1.66E+00	7.33E-66	Down	-6.98E-01	3.57E-16		7.27E-02	7.35E-01		5.43E-02	7.74E-01		1.07E+00	1.18E-16	Up	1.46E-01	4.52E-01		Unigene7396_All//gi|18202915|sp|Q9FS10.1|PSK_ASPOF//8.00E-09//RecName: Full=Phytosulfokines; Contains: RecName: Full=Phytosulfokine-alpha; Short=PSK-alpha; Short=Phytosulfokine-a; Contains: RecName: Full=Phytosulfokine-beta; Short=PSK-beta; Short=Phytosulfokine-b; Flags: Precursor >gi|12082023|dbj|BAB20706.1| preprophytosulfokine [Asparagus officinalis]	Unigene7396_All//7.00E-09//AT3G49780| ATPSK4 (PHYTOSULFOKINE 4 PRECURSOR); growth factor	Unigene7396_All//3.00E-25//TC156906				nr -

Unigene73967_All	796	0.00	2.16	1.94	0.00	0.00	0.00	0.00	0.00	1.11E+01	7.96E-10	Up	1.09E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene73967_All//gi|159485390|ref|XP_001700727.1|//3.00E-30//calcium-transporting ATPase, endoplasmic reticulum-type [Chlamydomonas reinhardtii] >gi|158281226|gb|EDF06981.1| calcium-transporting ATPase, endoplasmic reticulum-type [Chlamydomonas reinhardtii]	Unigene73967_All//2.00E-21//AT1G10130| ECA3 (ENDOPLASMIC RETICULUM-TYPE CALCIUM-TRANSPORTING ATPASE 3); calcium-transporting ATPase/ calmodulin binding / manganese-transporting ATPase/ peroxidase					nr -
Unigene7397_All	383	0.41	0.79	1.53	2.47	1.98	3.30	3.42	4.26	12.69	9.54E-01	5.03E-01		1.90E+00	8.47E-02		-3.21E-01	6.38E-01		4.18E-01	5.23E-01		3.15E-01	5.36E-01		1.89E+00	3.36E-12	Up			Unigene7397_All//6.00E-28//BG443852				
Unigene73974_All	397	0.26	0.13	2.82	0.25	0.26	0.11	0.00	0.00	0.00	-1.05E+00	6.83E-01		3.42E+00	1.92E-04	Up	5.19E-02	9.65E-01		-1.14E+00	6.74E-01		null	null		null	null		Unigene73974_All//gi|116059755|emb|CAL55462.1|//1.00E-08//DNA helicase RecG (ISS) [Ostreococcus tauri]				ko03440|Homologous recombination		nr -
Unigene74_All	891	0.65	1.71	2.21	3.13	5.26	3.60	4.84	3.33	3.22	1.40E+00	1.22E-02		1.78E+00	6.26E-04	Up	7.47E-01	5.56E-03		2.01E-01	6.36E-01		-5.39E-01	4.02E-02		-5.88E-01	1.94E-02		Unigene74_All//gi|297815528|ref|XP_002875647.1|//2.00E-33//kinase [Arabidopsis lyrata subsp. lyrata] >gi|297321485|gb|EFH51906.1| kinase [Arabidopsis lyrata subsp. lyrata]	Unigene74_All//5.00E-25//AT3G44200| NEK6 ("NIMA (NEVER IN MITOSIS, GENE A)-RELATED 6"); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene74_All//0.00E+00//gi|21103128|gb|BQ415441.1|BQ415441				nr -
Unigene7400_All	233	161.90	45.89	42.05	349.98	438.20	273.50	166.40	69.60	104.47	-1.82E+00	4.13E-68	Down	-1.94E+00	6.35E-72	Down	3.24E-01	4.46E-12		-3.56E-01	1.43E-10		-1.26E+00	7.09E-50	Down	-6.72E-01	1.67E-18		Unigene7400_All//gi|214003725|gb|ACJ60065.1|//1.00E-32//alpha tubulin [Betula pendula]	Unigene7400_All//1.00E-33//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene7400_All//2.00E-116//ES832636		ko04145|Phagosome		nr -
Unigene7401_All	463	2.15	6.13	4.60	2.90	3.64	4.00	10.96	12.01	13.85	1.51E+00	1.25E-04	Up	1.10E+00	1.82E-02		3.27E-01	5.68E-01		4.61E-01	3.81E-01		1.32E-01	6.38E-01		3.38E-01	1.06E-01		Unigene7401_All//gi|297804456|ref|XP_002870112.1|//2.00E-11//Mo25 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315948|gb|EFH46371.1| Mo25 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7401_All//1.00E-10//AT5G47540| binding	Unigene7401_All//9.00E-80//TC164898				nr +
Unigene74030_All	507	0.21	0.00	2.00	0.00	0.14	0.00	0.00	0.00	0.00	-7.69E+00	3.68E-01		3.27E+00	5.92E-04	Up	7.09E+00	6.03E-01		null	null		null	null		null	null										ESTscan -
Unigene74033_All	208	10.31	1.95	2.82	679.68	318.53	811.86	420.77	38.78	94.04	-2.40E+00	3.76E-06	Down	-1.87E+00	1.90E-04	Down	-1.09E+00	2.44E-146	Down	2.56E-01	1.18E-11		-3.44E+00	0.00E+00	Down	-2.16E+00	1.37E-248	Down	Unigene74033_All//gi|110816009|gb|AB691752.1|//4.00E-11//HyPRP2 [Gossypium hirsutum]		Unigene74033_All//3.00E-16//TC168341				nr -
Unigene7404_All	251	1.46	5.85	8.70	18.46	8.51	9.54	4.21	0.83	1.90	2.00E+00	1.09E-03		2.58E+00	2.37E-06	Up	-1.12E+00	2.01E-05	Down	-9.53E-01	5.76E-04		-2.34E+00	6.78E-04	Down	-1.14E+00	4.77E-02		Unigene7404_All//gi|297834874|ref|XP_002885319.1|//1.00E-12//beta-1,4-xylosidase [Arabidopsis lyrata subsp. lyrata] >gi|297331159|gb|EFH61578.1| beta-1,4-xylosidase [Arabidopsis lyrata subsp. lyrata]	Unigene7404_All//6.00E-12//AT3G19620| glycosyl hydrolase family 3 protein			ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanosamino acid metabolism		nr -
Unigene7406_All	437	8.38	17.97	14.26	13.57	13.95	12.40	9.09	11.86	7.48	1.10E+00	2.65E-07	Up	7.67E-01	1.83E-03		4.01E-02	8.94E-01		-1.29E-01	6.45E-01		3.83E-01	1.18E-01		-2.83E-01	3.15E-01		Unigene7406_All//gi|113367148|gb|AB134631.1|//1.00E-20//bZIP transcription factor bZIP86 [Glycine max]	Unigene7406_All//7.00E-16//AT1G32150| bZIP transcription factor family protein	Unigene7406_All//2.00E-74//DW489946	bZIP			nr +
Unigene74063_All	578	0.09	0.88	2.76	0.26	0.00	0.16	0.00	0.00	0.00	3.28E+00	2.10E-02		4.93E+00	1.23E-07	Up	-8.01E+00	1.65E-01		-7.26E-01	7.14E-01		null	null		null	null		Unigene74063_All//gi|222834344|gb|EEE72821.1|//5.00E-07//predicted protein [Populus trichocarpa]						nr +
Unigene7408_All	509	1.03	0.70	1.05	3.43	4.60	4.61	1.08	1.15	4.15	-5.61E-01	5.76E-01		2.55E-02	9.99E-01		4.26E-01	3.40E-01		4.30E-01	3.46E-01		9.04E-02	9.27E-01		1.94E+00	6.27E-06	Up	Unigene7408_All//gi|28951031|gb|AA063439.1|//5.00E-41//At5g60990 [Arabidopsis thaliana]	Unigene7408_All//3.00E-42//AT5G60990| DEAD/DEAH box helicase, putative (RH10)	Unigene7408_All//1.00E-115//TC131780				nr -
Unigene74080_All	240	0.00	0.00	0.00	0.00	0.00	0.00	8.81	3.31	3.65	null	null		null	null		null	null		null	null		-1.41E+00	5.54E-04	Down	-1.27E+00	1.15E-03		Unigene74080_All//gi|115461410|ref|NP_001054305.1|//8.00E-27//Os04g0683800 [Oryza sativa Japonica Group] >gi|32488702|emb|CAE03445.1| OSJNBa0088H09.3 [Oryza sativa (japonica cultivar-group)] >gi|113568876|dbj|BAF16219.1| Os04g0683800 [Oryza sativa Japonica Group]	Unigene74080_All//4.00E-26//AT4G11610| C2 domain-containing protein	Unigene74080_All//5.00E-52//TC168486				nr -
Unigene7409_All	639	0.08	1.11	0.67	0.78	1.02	1.13	0.40	0.13	3.30	3.76E+00	2.36E-03		3.03E+00	5.72E-02		3.93E-01	6.98E-01		5.37E-01	5.60E-01		-1.60E+00	3.10E-01		3.06E+00	2.16E-09	Up	Unigene7409_All//gi|60656553|gb|AAX33299.1|//9.00E-83//pyruvate decarboxylase 2 [Petunia x hybrida]	Unigene7409_All//3.00E-77//AT4G33070| pyruvate decarboxylase, putative	Unigene7409_All//0.00E+00//C0110104		ko00010|Glycolysis / Gluconeogenesis//ko00380|Tryptophan metabolism		nr +
Unigene7411_All	670	0.39	1.13	0.64	1.12	0.93	0.88	0.82	2.37	2.50	1.54E+00	7.40E-02		7.03E-01	5.54E-01		-2.70E-01	7.48E-01		-3.48E-01	6.83E-01		1.53E+00	1.78E-03		1.61E+00	5.97E-04	Up								
Unigene74113_All	465	2.25	1.20	4.81	4.93	2.52	1.17	1.45	0.09	0.60	-9.09E-01	1.75E-01		1.10E+00	1.53E-02		-9.69E-01	1.52E-02		-2.08E+00	7.11E-06	Down	-4.02E+00	5.36E-04	Down	-1.28E+00	9.48E-02				Unigene74113_All//3.00E-98//ES839516				
Unigene7412_All	429	1.10	0.94	1.99	0.46	2.01	2.84	1.77	1.07	1.86	-2.16E-01	8.17E-01		8.56E-01	2.80E-01		2.11E+00	1.28E-02		2.61E+00	3.93E-04	Up	-7.27E-01	3.32E-01		6.62E-02	9.42E-01		Unigene7412_All//gi|224115686|ref|XP_002332117.1|//4.00E-45//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222874937|gb|EEF12068.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene7412_All//6.00E-21//AT3G14460| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction		nr +
Unigene74149_All	358	0.00	0.00	0.00	1.39	0.00	1.01	0.35	0.12	0.11	null	null		null	null		-1.04E+01	8.97E-04	Down	-4.63E-01	6.59E-01		-1.60E+00	5.32E-01		-1.67E+00	4.76E-01		Unigene74149_All//gi|224098515|ref|XP_002311202.1|//3.00E-27//laccase [Populus trichocarpa] >gi|222851022|gb|EEE88569.1| laccase [Populus trichocarpa]	Unigene74149_All//1.00E-19//AT5G58910| LAC16 (laccase 16); laccase	Unigene74149_All//8.00E-101//TC166199				nr -
Unigene7416_All	1004	0.00	0.96	0.11	1.14	2.88	4.72	0.38	1.96	0.44	9.91E+00	1.37E-05	Up	6.73E+00	3.91E-01		1.34E+00	2.59E-04	Up	2.05E+00	4.54E-11	Up	2.37E+00	1.05E-06	Up	2.04E-01	8.26E-01		Unigene7416_All//gi|15218707|ref|NP_171811.1|//2.00E-28//ATRAR28 [Arabidopsis thaliana] >gi|4587565|gb|AAD25796.1|AC006550_4 Similar to rab28 protein gb|X59138 from Zea mays. EST gb|AA042774 comes from this gene [Arabidopsis thaliana]	Unigene7416_All//3.00E-25//AT1G03120| ATRAR28					nr +
Unigene74169_All	505	0.00	0.40	1.69	0.59	0.55	0.00	0.00	0.00	0.00	8.65E+00	1.35E-01		1.07E+01	8.99E-05	Up	-1.18E-01	9.00E-01		-9.21E+00	3.98E-02		null	null		null	null		Unigene74169_All//sp|Q89EK2|SSUD_BRAJA/|1.00E-51//Alkanesulfonate monooxygenase OS=Bradyrhizobium japonicum GN=ssuD PE=3 SV=1						swissprot +
Unigene7417_All	320	8.67	8.39	10.32	7.78	2.91	10.73	18.76	44.02	32.74	-4.63E-02	9.11E-01		2.52E-01	4.98E-01		-1.42E+00	2.12E-04	Down	4.63E-01	1.94E-01		1.23E+00	5.37E-18	Up	8.03E-01	2.32E-07									
Unigene7418_All	511	0.20	1.49	0.42	1.46	0.74	2.21	2.48	0.65	0.86	2.86E+00	5.51E-03		1.03E+00	5.90E-01		-9.80E-01	2.23E-01		5.96E-01	3.98E-01		-1.92E+00	9.98E-04	Down	-1.53E+00	4.40E-03		Unigene7418_All//gi|297811525|ref|XP_002873646.1|//2.00E-13//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319483|gb|EFH49905.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene7418_All//2.00E-13//AT5G14080| pentatricopeptide (PPR) repeat-containing protein	Unigene7418_All//0.00E+00//ES836030				nr +
Unigene7419_All	535	0.88	1.99	0.60	1.58	2.00	3.55	1.66	4.37	6.93	1.18E+00	8.18E-02		-5.60E-01	6.28E-01		3.34E-01	6.42E-01		1.16E+00	1.59E-02		1.40E+00	2.91E-04	Up	2.06E+00	1.60E-10	Up	Unigene7419_All//gi|158828301|gb|AB981176.1|//3.00E-07//non-LTR reverse transcriptase [Arabidopsis cebennensis]						nr +
Unigene742_All	1296	13.65	35.62	16.64	19.80	22.93	22.97	27.93	38.70	27.45	1.38E+00	7.35E-56	Up	2.86E-01	2.41E-02		2.12E-01	3.76E-02		2.14E-01	4.09E-02		4.71E-01	1.67E-12		-2.48E-02	7.87E-01		Unigene742_All//gi|157043074|gb|ABV02070.1|//2.00E-88//transcription factor 1R-MYB1 [Chimonanthus praecox]	Unigene742_All//3.00E-58//AT5G52660| myb family transcription factor	Unigene742_All//0.00E+00//gi|109840887|gb|DW239447.1|DW239447	MYB-related	ko04712|Circadian rhythm - plant	GO:0003676//GO:0010468//GO:0043231	nr +
Unigene74209_All	639	0.00	0.16	1.08	0.08	0.00	0.00	0.00	0.00	0.00	7.31E+00	3.81E-01		1.01E+01	6.13E-04	Up	-6.29E+00	5.47E-01		-6.29E+00	6.24E-01		null	null		null	null				Unigene74209_All//2.00E-62//TC159814				
Unigene7422_All	236	37.02	87.17	54.83	27.86	32.54	47.84	91.55	136.01	49.12	1.24E+00	2.54E-21	Up	5.67E-01	4.82E-04		2.24E-01	3.40E-01		7.80E-01	2.65E-06		5.71E-01	1.89E-11		-8.98E-01	3.99E-17		Unigene7422_All//gi|14719274|gb|AAK73101.1|AF390555_1//2.00E-33//Bax inhibitor 1 [Brassica napus] >gi|17981374|gb|AAL50979.1|AF453320_1 bax inhibitor-like protein [Brassica oleracea]	Unigene7422_All//1.00E-34//AT5G47120| ATBI1 (BAX INHIBITOR 1)	Unigene7422_All//8.00E-131//gi|13244986|gb|BE055654.2|BE055654				nr -
Unigene74222_All	343	1.37	2.66	2.33	9.29	7.83	3.16	12.33	10.97	13.82	9.54E-01	1.96E-01		7.62E-01	3.62E-01		-2.47E-01	5.29E-01		-1.56E+00	1.50E-05	Down	-1.69E-01	5.90E-01		1.65E-01	5.48E-01									
Unigene74230_All	219	0.00	1.85	3.65	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	1.34E-02		1.18E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene74230_All//sp|Q7KQN6|PERQ1_DROME//4.00E-13//PERQ amino acid-rich with GYF domain-containing protein CG11148 OS=Drosophila melanogaster GN=CG11148 PE=1 SV=1						swissprot -
Unigene74233_All	390	0.00	0.39	1.78	0.26	0.18	0.23	0.00	0.00	0.00	8.61E+00	2.32E-01		1.08E+01	6.12E-04	Up	-5.33E-01	8.13E-01		-1.42E-01	9.48E-01		null	null		null	null		Unigene74233_All//COG3672//5.00E-06//Predicted periplasmic protein						cog -
Unigene74234_All	502	0.00	1.62	0.21	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	9.31E-05	Up	7.73E+00	3.91E-01		null	null		null	null		null	null		null	null		Unigene74234_All//gi|226495039|ref|NP_001141249.1|//7.00E-06//hypothetical protein LOC100273336 [Zea mays] >gi|194703524|gb|ACF58846.1| unknown [Zea mays]						nr +
Unigene74249_All	604	0.78	0.17	0.18	1.81	0.51	0.37	0.98	0.00	0.07	-2.22E+00	7.75E-02		-2.14E+00	1.03E-01		-1.82E+00	5.10E-03		-2.28E+00	1.97E-03		-9.94E+00	2.39E-04	Down	-3.89E+00	1.09E-03		Unigene74249_All//gi|2500715|sp|Q40374.1|PR1_MEDTR//1.00E-52//RecName: Full=Pathogenesis-related protein PR-1; Flags: Precursor >gi|505553|emb|CAA56174.1| PR-1 [Medicago truncatula]	Unigene74249_All//2.00E-49//AT4G30320| allergen V5/Tpx-1-related family protein	Unigene74249_All//0.00E+00//TC139677		ko04626|Plant-pathogen interaction		nr -
Unigene7425_All	336	1.09	1.06	1.58	5.49	1.13	2.29	1.26	2.24	2.73	-4.63E-02	9.82E-01		5.40E-01	6.10E-01		-2.28E+00	5.07E-06	Down	-1.26E+00	9.32E-03		8.31E-01	2.64E-01		1.12E+00	7.92E-02									
Unigene7426_All	505	10.98	18.06	23.09	13.81	8.73	10.82	47.22	24.33	10.89	7.18E-01	1.69E-04		1.07E+00	1.19E-09	Up	-6.62E-01	1.38E-03		-3.52E-01	1.32E-01		-9.57E-01	3.42E-20		-2.12E+00	1.82E-66	Down	Unigene7426_All//gi|3334113|sp|Q39779.1|ACBP_GOSHL//9.00E-12//RecName: Full=Acyl-CoA-binding protein; Short=ACBP >gi|1006831|gb|AAB67736.1| acyl-CoA-binding protein [Gossypium hirsutum]	Unigene7426_All//2.00E-11//AT1G31812| ACBP6 (acyl-CoA-binding protein 6); acyl-CoA binding / phosphatidylcholine binding	Unigene7426_All//0.00E+00//gi|109831881|gb|DW230440.1|DW230440				nr -
Unigene74262_All	225	0.93	2.48	0.95	0.00	0.15	3.41	0.00	0.00	0.00	1.41E+00	1.69E-01		2.55E-02	1.00E+00		7.26E+00	8.19E-01		1.17E+01	1.27E-04	Up	null	null		null	null				Unigene74262_All//1.00E-49//TC157891				
Unigene7427_All	761	0.14	168.05	9.38	0.39	0.27	2.97	0.94	1.70	1.57	1.03E+01	0.00E+00	Up	6.09E+00	1.57E-36	Up	-5.33E-01	6.78E-01		2.92E+00	5.32E-08	Up	8.50E-01	1.12E-01		7.34E-01	1.73E-01		Unigene7427_All//gi|117168087|gb|AB632126.1|//1.00E-23//At1g52565 [Arabidopsis thaliana]	Unigene7427_All//5.00E-20//AT1G52565| unknown protein	Unigene7427_All//0.00E+00//DW509775				nr -
Unigene7429_All	956	0.49	0.85	0.89	5.68	7.06	11.43	0.80	0.74	0.08	7.84E-01	3.23E-01		8.55E-01	2.80E-01		3.14E-01	1.93E-01		1.01E+00	4.39E-09	Up	-9.92E-02	8.96E-01		-3.26E+00	4.48E-04	Down	Unigene7429_All//gi|152955979|emb|CAM56862.1|//4.00E-80//a-type carbonic anhydrase [Lotus japonicus]	Unigene7429_All//2.00E-81//AT4G20990| ACA4 (ALPHA CARBONIC ANHYDRASE 4); carbonate dehydratase/ zinc ion binding			ko00910|Nitrogen metabolism		nr +
Unigene74292_All	284	0.00	0.71	8.25	0.00	0.00	0.00	0.00	0.00	0.00	9.48E+00	1.35E-01		1.30E+01	6.40E-13	Up	null	null		null	null		null	null		null	null		Unigene74292_All//gi|157497145|gb|ABV58319.1|//6.00E-25//metallothionein class I type 3 [Avicennia marina] >gi|157497147|gb|ABV58320.1| metallothionein class I type 3 [Avicennia marina]	Unigene74292_All//2.00E-18//AT3G15353| MT3 (METALLOTHIONEIN 3); copper ion binding	Unigene74292_All//2.00E-20//TC174105				nr +
Unigene74299_All	822	0.19	0.00	0.06	0.30	0.59	0.38	0.77	0.20	0.05	-7.58E+00	2.14E-01		-1.56E+00	5.32E-01		9.53E-01	4.23E-01		3.44E-01	7.96E-01		-1.92E+00	3.09E-02		-3.99E+00	5.82E-04	Down	Unigene74299_All//gi|223452272|gb|ACM89464.1|//9.00E-67//receptor protein kinase [Glycine max]	Unigene74299_All//4.00E-49//AT1G56720| protein kinase family protein	Unigene74299_All//0.00E+00//gi|54121212|gb|CO496721.1|CO496721		ko04626|Plant-pathogen interaction		nr +

Unigene743_All	2561	2.84	2.75	2.04	5.78	5.20	5.57	5.00	7.82	13.55	-4.63E-02	8.39E-01			-4.79E-01	3.66E-02		-1.51E-01	3.64E-01			-5.19E-02	7.56E-01		6.44E-01	4.87E-09		1.44E+00	7.93E-56	Up	Unigene743_All//gi|297606463|ref|NP_001058508.2|//6.00E-50//0s06g0704100 [Oryza sativa Japonica Group] >gi|255677375|dbj|BAF20422.2| Os06g0704100 [Oryza sativa Japonica Group]	Unigene743_All//7.00E-09//AT4G01280| myb family transcription factor	Unigene743_All//3.00E-86//DW239447	MYB-related			nr -
Unigene7433_All	330	1277.58	315.84	268.35	170.27	97.36	49.54	88.40	19.25	85.59	-2.02E+00	0.00E+00	Down	-2.25E+00	0.00E+00	Down	-8.07E-01	6.95E-35		-1.78E+00	6.98E-107	Down	-2.20E+00	1.42E-82	Down	-4.66E-02	6.42E-01		Unigene7433_All//gi|3094012|gb|AAC15460.1|//1.00E-20//cold-regulated LTCOR12 [Lavatera thuringiaca]	Unigene7433_All//1.00E-07//AT1G75750| GASA1 (GAST1 PROTEIN HOMOLOG 1)	Unigene7433_All//5.00E-145//TC162017				nr -
Unigene7434_All	374	1.82	1.08	0.71	8.39	8.29	4.59	3.39	0.00	1.60	-7.47E-01	3.80E-01		-1.35E+00	1.50E-01		-1.81E-02	9.49E-01		-8.71E-01	1.26E-02		-1.17E+01	5.06E-09	Down	-1.09E+00	3.58E-02		Unigene7434_All//gi|115469660|ref|NP_001058429.1|//2.00E-16//0s06g0692800 [Oryza sativa Japonica Group] >gi|53792826|dbj|BAD53859.1| ternary complex factor MIP1-like [Oryza sativa Japonica Group] >gi|53793306|dbj|BAD54528.1| ternary complex factor MIP1-like [Oryza sativa Japonica Group] >gi|113596469|dbj|BAF20343.1| Os06g0692800 [Oryza sativa Japonica Group]	Unigene7434_All//1.00E-16//AT3G13000| transcription factor	Unigene7434_All//3.00E-119//C0099117				nr +
Unigene7438_All	783	0.00	0.19	0.54	0.19	0.44	0.81	0.70	2.51	1.88	7.60E+00	2.32E-01		9.09E+00	1.37E-02		1.20E+00	4.26E-01		2.08E+00	4.69E-02		1.84E+00	4.40E-05	Up	1.42E+00	3.87E-03		Unigene7438_All//gi|15231451|ref|NP_190238.1|//7.00E-15//epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related [Arabidopsis thaliana]	Unigene7438_All//7.00E-17//AT3G46540| epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related	Unigene7438_All//3.00E-25//TC135529				nr -
Unigene7439_All	351	6.56	2.02	5.01	10.36	6.57	9.65	1.33	1.19	0.45	-1.70E+00	1.75E-04	Down	-3.90E-01	4.02E-01		-6.56E-01	3.33E-02		-1.02E-01	7.63E-01		-1.54E-01	8.70E-01		-1.55E+00	1.16E-01					Unigene7439_All//3.00E-125//gi|164343789|gb|ES790503.1|ES790503				
Unigene744_All	4548	0.33	0.88	0.76	3.60	3.87	3.72	3.58	3.59	4.37	1.40E+00	1.30E-05	Up	1.19E+00	7.36E-04	Up	1.03E-01	5.45E-01		4.74E-02	7.63E-01		5.70E-03	1.01E+00		2.88E-01	8.55E-03		Unigene744_All//gi|224074429|ref|XP_002304369.1|//1.00E-123//nbs-lrr resistance protein [Populus trichocarpa] >gi|222841801|gb|EEE79348.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene744_All//9.00E-72//AT4G19050| ATP binding / protein binding	Unigene744_All//0.00E+00//TC131656				nr +
Unigene7440_All	333	119.57	54.47	198.13	137.48	76.94	104.03	7.75	3.39	4.19	-1.13E+00	1.09E-35	Down	7.29E-01	3.11E-27		-8.37E-01	2.23E-30		-4.02E-01	1.16E-07		-1.19E+00	8.48E-04	Down	-8.87E-01	8.76E-03					Unigene7440_All//4.00E-10//TC161037				
Unigene74405_All	223	0.00	0.91	4.78	0.00	0.00	1.82	0.00	0.00	0.00	9.83E+00	1.35E-01		1.22E+01	6.60E-06	Up	null	null		1.08E+01	1.36E-02		null	null		null	null		Unigene74405_All//gi|290490134|gb|AD031474.1|//1.00E-25//ATP synthase CF1 epsilon subunit protein [Plumbago auriculata]	Unigene74405_All//2.00E-24//ATCG00470| ATPase epsilon subunit	Unigene74405_All//1.00E-64//TC176987		ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr -
Unigene7442_All	294	242.74	108.06	175.33	78.62	60.91	65.44	69.46	45.92	27.51	-1.17E+00	2.03E-66	Down	-4.69E-01	1.15E-13		-3.68E-01	5.89E-04		-2.65E-01	2.44E-02		-5.97E-01	3.75E-08		-1.34E+00	4.28E-30	Down	Unigene7442_All//gi|211906470|gb|AGJ11728.1|//1.00E-51//glyceraldehyde-3-phosphate dehydrogenase [Gossypium hirsutum]	Unigene7442_All//5.00E-37//AT3G04120| GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene7442_All//6.00E-163//TC158306		ko00010|Glycolysis / Gluconeogenesis		nr +
Unigene74420_All	220	3.57	0.23	0.24	3.17	1.72	3.90	5.19	1.33	1.99	-3.95E+00	8.54E-04	Down	-3.88E+00	1.59E-03		-8.81E-01	2.99E-01		2.99E-01	6.86E-01		-1.96E+00	1.69E-03		-1.38E+00	1.42E-02					Unigene74420_All//7.00E-57//DW506684				
Unigene74453_All	520	0.00	0.58	2.25	0.00	0.00	0.00	0.00	0.00	0.00	9.19E+00	4.37E-02		1.11E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene74453_All//gi|298708610|emb|CBJ26097.1|//2.00E-17//Actin-related protein 2/3 complex subunit ARPC2 or p34-Arc (Arp2/3 complex 34 kDa subunit) [Ectocarpus siliculosus]	Unigene74453_All//7.00E-14//AT1G30825| DIS2 (DISTORTED TRICHOMES 2); structural molecule					nr -
Unigene7446_All	958	5.68	5.45	7.56	1.04	0.61	0.00	0.04	0.09	0.04	-6.02E-02	8.16E-01		4.12E-01	7.60E-02		-7.67E-01	2.60E-01		-1.00E-01	2.97E-06	Down	9.85E-01	7.29E-01		-8.42E-02	9.67E-01					Unigene7446_All//2.00E-11//C0088137				
Unigene74469_All	413	4.05	3.93	3.61	1.45	3.84	7.98	0.72	0.30	0.39	-4.63E-02	9.37E-01		-1.67E-01	7.36E-01		1.41E+00	8.63E-03		2.46E+00	1.14E-09	Up	-1.24E+00	3.72E-01		-8.93E-01	4.71E-01									
Unigene74470_All	207	0.00	1.47	4.37	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	4.37E-02		1.21E+01	4.70E-05	Up	null	null		null	null		null	null		null	null										
Unigene7448_All	497	2.95	7.03	4.39	0.30	0.49	0.36	1.62	2.86	4.09	1.25E+00	2.28E-04	Up	5.76E-01	2.13E-01		6.90E-01	7.32E-01		2.74E-01	9.04E-01		8.23E-01	1.03E-01		1.34E+00	9.75E-04	Up				Unigene7448_All//4.00E-156//C0123445				
Unigene7449_All	320	3.43	0.32	3.16	1.40	2.26	1.27	0.40	0.00	0.12	-3.44E+00	1.19E-04	Down	-1.19E-01	8.50E-01		6.90E-01	4.47E-01		-1.41E-01	9.00E-01		-8.63E+00	2.34E-01		-1.67E+00	4.76E-01		Unigene7449_All//gi|118487801|gb|ABK95724.1|//3.00E-14//unknown [Populus trichocarpa]		Unigene7449_All//7.00E-132//C0127170				nr -
Unigene74495_All	229	0.00	0.00	0.00	0.00	0.00	0.00	9.05	0.37	1.22	null	null		null	null		null	null		null	null		-4.63E+00	3.60E-12	Down	-2.89E+00	6.04E-09	Down	Unigene74495_All//gi|255583202|ref|XP_002532366.1|//3.00E-10//1-aminocyclopropane-1-carboxylate oxidase, putative [Ricinus communis] >gi|223527922|gb|EEF30009.1| 1-aminocyclopropane-1-carboxylate oxidase, putative [Ricinus communis]	Unigene74495_All//3.00E-05//AT1G55290| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene74495_All//3.00E-53//C0128240				nr +
Unigene74511_All	1021	0.15	0.05	0.21	0.20	0.07	0.35	0.95	0.16	0.23	-1.63E+00	4.88E-01		4.41E-01	7.74E-01		-1.53E+00	4.15E-01		8.58E-01	5.41E-01		-2.54E+00	6.41E-04	Down	-2.02E+00	2.47E-03		Unigene74511_All//gi|32489310|emb|CAE03706.1|//1.00E-59//OSJNBa0060820.14 [Oryza sativa (japonica cultivar-group)]		Unigene74511_All//0.00E+00//TC160360		ko03040|Spliceosome		nr -
Unigene74513_All	254	4.33	1.60	0.84	6.28	0.95	2.31	2.83	0.33	0.16	-1.44E+00	3.36E-02		-2.37E+00	2.96E-03		-2.73E+00	2.30E-06	Down	-1.44E+00	7.25E-03		-3.10E+00	1.39E-03		-4.17E+00	1.64E-04	Down	Unigene74513_All//gi|218533691|gb|ACK87021.1|//6.00E-11//cysteine protease inhibitor [Gossypium hirsutum]		Unigene74513_All//5.00E-52//TC166388				nr +
Unigene7452_All	345	7.89	1.91	6.02	15.02	13.37	15.97	31.62	11.27	12.47	-2.05E+00	2.16E-06	Down	-3.90E-01	3.51E-01		-1.67E-01	5.81E-01		8.89E-02	7.53E-01		-1.49E+00	1.18E-18	Down	-1.34E+00	1.37E-16	Down	Unigene7452_All//gi|226503399|ref|NP_001151465.1|//8.00E-19//LOC100285098 [Zea mays] >gi|195646972|gb|ACG42954.1| elongation factor 2 [Zea mays]	Unigene7452_All//1.00E-19//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene7452_All//1.00E-127//gi|78346296|gb|DT566570.1|DT566570				nr -
Unigene74523_All	215	0.73	5.18	0.00	0.46	0.96	2.10	0.59	0.00	0.19	2.83E+00	5.03E-04	Up	-9.51E+00	2.42E-01		1.05E+00	6.11E-01		2.18E+00	1.02E-01		-9.20E+00	2.34E-01		-1.67E+00	4.76E-01		Unigene74523_All//gi|224152016|ref|XP_002337181.1|//2.00E-09//predicted protein [Populus trichocarpa] >gi|222838419|gb|EEE76784.1| predicted protein [Populus trichocarpa]	Unigene74523_All//7.00E-05//AT4G08950| EXO (EXORDIUM)	Unigene74523_All//7.00E-51//EX165687				nr +
Unigene74524_All	210	0.00	1.69	2.28	1.19	0.66	0.86	350.52	629.32	155.56	1.07E+01	2.43E-02		1.12E+01	7.43E-03		-8.55E-01	5.73E-01		-4.63E-01	7.44E-01		8.44E-01	1.01E-87		-1.17E+00	1.39E-86	Down	Unigene74524_All//gi|225431838|ref|XP_002273952.1|//8.00E-06//PREDICTED: hypothetical protein [Vitis vinifera] >gi|296083304|emb|CBI22940.3| unnamed protein product [Vitis vinifera]		Unigene74524_All//6.00E-48//TC148379				nr -
Unigene74538_All	219	2.87	0.00	0.73	3.18	3.77	1.86	0.00	0.00	0.00	-1.15E+01	7.90E-04	Down	-1.97E+00	6.50E-02		2.45E-01	8.03E-01		-7.79E-01	3.93E-01		null	null		null	null					Unigene74538_All//7.00E-51//ES827797				
Unigene74545_All	207	0.00	3.18	0.77	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.20E-04	Up	9.59E+00	2.35E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene7455_All	759	0.07	0.67	1.82	1.58	2.45	2.56	0.22	0.11	0.00	3.28E+00	2.10E-02		4.73E+00	1.57E-06	Up	6.37E-01	1.99E-01		7.00E-01	1.45E-01		-1.02E+00	6.13E-01		-7.80E+00	1.08E-01		Unigene7455_All//gi|226502598|ref|NP_001151627.1|//1.00E-17//type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 [Zea mays] >gi|195648200|gb|ACG43568.1| type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2 [Zea mays]	Unigene7455_All//4.00E-17//AT2G32010| endonuclease/exonuclease/phosphatase family protein	Unigene7455_All//0.00E+00//gi|21103238|gb|BQ415551.1|BQ415551				nr +
Unigene74559_All	204	0.00	2.48	3.65	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	4.00E-03		1.18E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene74559_All//gi|115470729|ref|NP_001058963.1|//8.00E-06//0s07g0164800 [Oryza sativa Japonica Group] >gi|22202765|dbj|BAC07421.1| Neurofilament triplet M protein-like protein [Oryza sativa Japonica Group] >gi|113610499|dbj|BAF20877.1| Os07g0164800 [Oryza sativa Japonica Group]						nr -
Unigene7457_All	290	44.74	3.49	10.83	7.56	7.60	0.31	1.17	0.86	2.20	-3.68E+00	1.21E-51	Down	-2.05E+00	1.13E-26	Down	7.90E-03	9.98E-01		-4.60E+00	2.64E-11	Down	-4.32E-01	7.03E-01		9.14E-01	2.47E-01		Unigene7457_All//gi|224080516|ref|XP_002306147.1|//1.00E-41//SAUR family protein [Populus trichocarpa] >gi|222849111|gb|EEE86658.1| SAUR family protein [Populus trichocarpa]	Unigene7457_All//3.00E-35//AT4G34760| auxin-responsive family protein	Unigene7457_All//1.00E-148//DW503189				nr +
Unigene7458_All	825	2.66	1.04	2.78	3.68	2.92	0.71	2.72	0.30	1.45	-1.35E+00	2.48E-03		5.94E-02	8.94E-01		-3.34E-01	3.79E-01		-2.37E+00	8.02E-09	Down	-3.16E+00	5.10E-10	Down	-9.07E-01	1.36E-02		Unigene7458_All//gi|29374148|gb|AAO72990.1|//4.00E-54//cyclin D [Populus alba]	Unigene7458_All//1.00E-34//AT3G50070| CYCD3;3 (CYCLIN D3;3); cyclin-dependent protein kinase	Unigene7458_All//0.00E+00//C0070031				nr -
Unigene7459_All	358	4.53	0.28	3.27	1.53	1.73	1.89	0.00	0.00	0.00	-4.00E+00	2.71E-07	Down	-4.69E-01	3.87E-01		1.78E-01	8.64E-01		3.06E-01	7.22E-01		null	null		null	null										
Unigene746_All	1685	2.58	2.83	2.62	7.95	7.62	5.44	5.02	2.11	1.47	1.33E-01	6.27E-01		2.54E-02	9.49E-01		-6.11E-02	7.68E-01		-5.48E-01	2.69E-04		-1.25E+00	2.03E-11	Down	-1.78E+00	3.14E-19	Down	Unigene746_All//gi|15238511|ref|NP_200782.1|//1.00E-160//UDP-galactose/UDP-glucose transporter-related [Arabidopsis thaliana] >gi|449175651|gb|AAS49107.1| At5g59740 [Arabidopsis thaliana]	Unigene746_All//3.00E-161//AT5G59740| UDP-galactose/UDP-glucose transporter-related	Unigene746_All//0.00E+00//TC175257				nr +
Unigene74603_All	236	0.00	3.86	2.71	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.60E-05	Up	1.14E+01	1.15E-03		null	null		null	null		null	null		null	null										ESTscan +
Unigene74614_All	356	0.00	0.00	1.94	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.09E+01	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene74614_All//sp|Q30154|DRB5_HUMAN//1.00E-53//HLA class II histocompatibility antigen, DR beta 5 chain OS=Homo sapiens GN=HLA-DRB5 PE=1 SV=1						swissprot +

Unigene7463_All	317	1.82	2.72	6.38	4.09	3.26	3.70	5.74	3.69	2.51	5.82E-01	4.27E-01		1.81E+00	4.14E-04	Up	-3.26E-01	5.86E-01		-1.41E-01	8.06E-01		-6.36E-01	1.45E-01		-1.19E+00	4.84E-03		Unigene7463_All//gi|15219265|ref|NP_178022.1|//4.00E-15//NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial (TYKY) [Arabidopsis thaliana] >gi|297842689|ref|XP_002889226.1| NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial [Arabidopsis lyrata subsp. lyrata] >gi|3929364|sp|Q42599.1|NDUS8_ARATH RecName: Full=NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial; AltName: Full=NADH-ubiquinone oxidoreductase 23 kDa subunit; AltName: Full=Complex I-23kD; Short=CI-23kD; AltName: Full=Complex I-28.5kD; Short=CI-28.5kD; Flags: Precursor >gi|666977|emb|CAA59061.1| NADH dehydrogenase; NADH:ubiquinone oxidoreductase (complex I) [Arabidopsis thaliana] >gi|3152573|gb|AAC17054.1| Match to NADH:ubiquinone oxidoreductase gb|X84318 from A.thaliana. ESTs gb|Z27005, gb|T04711, gb|T45078 and gb|Z28689 come from this gene [Arabidopsis thaliana] >gi|15081697|gb|AAK82503.1|	Unigene7463_All//7.00E-16//AT1G29010| NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial (TYKY)	Unigene7463_All//3.00E-66//TC173887		ko00190|Oxidative phosphorylation		nr +
Unigene74638_All	394	0.00	0.13	2.57	0.00	0.00	0.23	0.00	0.00	0.00	7.01E+00	6.11E-01		1.13E+01	1.27E-05	Up	null	null		7.84E+00	4.71E-01		null	null		null	null		Unigene74638_All//COG1346//6.00E-17//Putative effector of murein hydrolase						cog +
Unigene7464_All	520	5.94	6.82	5.43	7.95	8.61	7.99	8.54	3.94	6.82	2.00E-01	5.71E-01		-1.29E-01	7.23E-01		1.15E-01	7.59E-01		7.10E-03	9.83E-01		-1.12E+00	1.89E-05	Down	-3.24E-01	2.09E-01		Unigene7464_All//gi|297844602|ref|XP_002890182.1|//5.00E-55//ATML014 [Arabidopsis lyrata subsp. lyrata] >gi|9989050|gb|AAG10813.1|AC011808_1 Putative NADH-ubiquinone oxidoreductase [Arabidopsis thaliana] >gi|16649105|gb|AAL24404.1| Putative NADH-ubiquinone oxidoreductase [Arabidopsis thaliana] >gi|297336024|gb|EFH66441.1| ATML014 [Arabidopsis lyrata subsp. lyrata]	Unigene7464_All//6.00E-55//AT1G16700| NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial, putative	Unigene7464_All//9.00E-114//gi|48822172|gb|CO123485.1|CO123485		ko00190|Oxidative phosphorylation		nr +
Unigene7467_All	278	3.39	0.36	2.68	1.61	3.10	1.95	1.37	0.60	0.57	-3.22E+00	6.76E-04	Down	-3.37E-01	6.16E-01		9.41E-01	2.38E-01		2.74E-01	7.82E-01		-1.19E+00	3.09E-01		-1.26E+00	2.48E-01								
Unigene7468_All	537	3.31	0.85	7.64	9.93	9.94	9.42	1.26	1.79	0.67	-1.96E+00	2.97E-04	Down	1.20E+00	1.70E-04	Up	2.00E-03	9.99E-01		-7.55E-02	7.94E-01		5.07E-01	4.32E-01		-9.16E-01	2.21E-01		Unigene7468_All//gi|15222460|ref|NP_174459.1|//9.00E-19//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75169166|sp|Q9C689.1|PPR66_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At1g31790 >gi|11074348|gb|AB804547.1| At1g31790 [Arabidopsis thaliana]	Unigene7468_All//6.00E-16//AT1G31790| pentatricopeptide (PPR) repeat-containing protein	Unigene7468_All//5.00E-140//gi|21096772|gb|BQ409085.1|BQ409085				nr +
Unigene74690_All	234	0.67	0.22	1.37	2.55	3.68	0.00	26.92	8.75	20.77	-1.63E+00	4.88E-01		1.03E+00	4.70E-01		5.26E-01	5.45E-01		-1.13E+01	7.69E-04	Down	-1.62E+00	1.82E-12	Down	-3.74E-01	7.13E-02		Unigene74690_All//gi|115482738|ref|NP_001064962.1|//1.00E-08//Os10g0497800 [Oryza sativa Japonica Group] >gi|113639571|dbj|BAF26876.1| Os10g0497800 [Oryza sativa Japonica Group]	Unigene74690_All//1.00E-09//AT1G20270| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene74690_All//3.00E-53//TC163350				nr -
Unigene74693_All	223	0.70	0.23	0.96	6.03	2.78	0.41	0.00	0.00	1.25	-1.63E+00	4.88E-01		4.40E-01	7.74E-01		-1.12E+00	4.30E-02		-3.90E+00	2.12E-06	Down	null	null		1.03E+01	2.43E-02			Unigene74693_All//5.00E-18//TC158808					
Unigene7470_All	437	40.95	21.22	15.35	462.35	401.64	346.11	142.90	68.48	44.12	-9.48E-01	1.82E-12		-1.42E+00	5.44E-22	Down	-2.03E-01	5.45E-10		-4.18E-01	5.85E-34		-1.06E+00	4.64E-61	Down	-1.70E+00	3.94E-128	Down	Unigene7470_All//gi|134035504|gb|AB047740.1|//2.00E-50//alpha-tubulin [Gossypium hirsutum] >gi|223453026|gb|ACM89777.1| alpha-tubulin 10 [Gossypium hirsutum]	Unigene7470_All//1.00E-40//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene7470_All//0.00E+00//gi|13350719|gb|BG441067.1|BG441067		ko04145|Phagosome		nr -
Unigene74704_All	265	0.00	0.00	3.01	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene74704_All//gi|47971184|dbj|BAD22534.1|//2.00E-17//harpin inducing protein 1-like 18 [Nicotiana tabacum]	Unigene74704_All//1.00E-10//AT2G35460| harpin-induced family protein / HIN1 family protein / harpin-responsive family protein		ko04145|Phagosome//ko04130|SNARE interactions in vesicular transport		nr +
Unigene74710_All	866	0.00	0.23	4.67	0.00	0.00	0.00	0.00	0.00	0.00	7.87E+00	1.35E-01		1.22E+01	1.92E-22	Up	null	null		null	null		null	null		null	null		Unigene74710_All//gi|3759184|dbj|BAA33810.1|//3.00E-90//phi-1 [Nicotiana tabacum]	Unigene74710_All//6.00E-91//AT4G08950| EXO (EXODIUM)	Unigene74710_All//1.00E-24//gi|48744378|gb|CO074897.1|CO074897				nr -
Unigene7472_All	886	0.12	0.80	1.20	9.67	7.31	7.75	4.29	5.61	0.99	2.76E+00	9.13E-03		3.35E+00	3.36E-04	Up	-4.04E-01	3.69E-02		-3.20E-01	1.29E-01		3.86E-01	1.24E-01		-2.12E+00	2.69E-11	Down		Unigene7472_All//0.00E+00//DR454214					
Unigene7473_All	411	9.93	10.23	5.18	10.30	10.31	10.55	20.88	16.47	6.30	4.34E-02	8.95E-01		-9.38E-01	3.00E-03		4.00E-04	9.91E-01		3.42E-02	9.34E-01		-3.42E-01	6.10E-02		-1.73E+00	7.99E-19	Down		Unigene7473_All//1.00E-109//TC162513					
Unigene7474_All	374	2.24	0.00	0.14	2.00	1.20	0.97	0.23	1.12	0.85	-1.11E+01	5.56E-05	Down	-3.97E+00	9.08E-04	Down	-7.39E-01	3.57E-01		-1.05E+00	2.21E-01		2.31E+00	5.99E-02		1.91E+00	1.53E-01		Unigene7474_All//gi|297848728|ref|XP_002892245.1|//5.00E-08//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297338087|gb|EFH68504.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]		Unigene7474_All//0.00E+00//TC151039				nr +
Unigene7475_All	371	2.26	0.82	1.72	3.63	1.11	3.17	0.46	0.56	2.79	-1.46E+00	6.68E-02		-3.90E-01	6.41E-01		-1.70E+00	2.73E-03		-1.96E-01	7.30E-01		3.05E-01	8.35E-01		2.61E+00	2.37E-04	Up							
Unigene74769_All	334	0.00	0.30	3.03	0.00	0.31	0.27	0.00	0.00	0.00	8.25E+00	3.81E-01		1.16E+01	1.27E-05	Up	8.27E+00	4.53E-01		8.08E+00	4.71E-01		null	null		null	null								ESTscan -
Unigene74770_All	560	0.00	4.43	3.61	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	3.98E-14	Up	1.18E+01	3.79E-11	Up	null	null		null	null		null	null		null	null		Unigene74770_All//gi|159488530|ref|XP_001702260.1|//9.00E-17//DEAH-box RNA helicase [Chlamydomonas reinhardtii] >gi|158271237|gb|EDO97061.1| DEAH-box RNA helicase [Chlamydomonas reinhardtii]				ko03040|Spliceosome		nr +
Unigene74772_All	408	0.00	0.37	1.70	0.00	0.08	0.00	0.00	0.00	0.00	8.54E+00	2.32E-01		1.07E+01	6.12E-04	Up	6.40E+00	8.18E-01		null	null		null	null		null	null		Unigene74772_All//gi|255608035|ref|XP_002538833.1|//3.00E-65//Transcriptional activator protein ahyR/assaR, putative [Ricinus communis] >gi|223510221|gb|EEF23550.1| Transcriptional activator protein ahyR/assaR, putative [Ricinus communis]						nr -
Unigene7478_All	877	29.53	16.76	23.44	6.30	6.20	3.14	0.58	0.19	0.32	-8.18E-01	6.15E-14		-3.33E-01	3.02E-03		-2.33E-02	9.36E-01		-1.01E+00	5.86E-05	Down	-1.60E+00	1.07E-01		-8.63E-01	3.39E-01		Unigene7478_All//gi|222066068|emb|CAA28542.1|//5.00E-71//NBS-LLR resistance protein [Gossypium arboreum]	Unigene7478_All//5.00E-55//AT5G17680| disease resistance protein (TIR-NBS-LRR class), putative	Unigene7478_All//0.00E+00//TC164037		ko04626|Plant-pathogen interaction		nr -
Unigene7479_All	671	0.94	1.81	0.63	1.26	0.36	2.69	0.50	2.30	1.78	9.54E-01	1.22E-01		-5.60E-01	5.53E-01		-1.81E+00	1.77E-02		1.09E+00	2.78E-02		2.19E+00	5.11E-05	Up	1.82E+00	1.82E-03		Unigene7479_All//gi|122312296|gb|AAG49032.1|AF204785_1//5.00E-90//ripening regulated protein DDTFR18 [Solanum lycopersicum]	Unigene7479_All//8.00E-83//AT5G65380| ripening-responsive protein, putative	Unigene7479_All//0.00E+00//TC137464				nr -
Unigene748_All	3208	8.97	6.59	9.76	23.70	26.17	23.85	18.89	7.44	14.73	-4.46E-01	9.41E-06		1.22E-01	2.80E-01		1.43E-01	1.31E-02		9.30E-03	9.20E-01		-1.34E+00	7.28E-86	Down	-3.59E-01	1.19E-09		Unigene748_All//gi|225435610|ref|XP_002283298.1|//0.00E+00//PREDICTED: similar to Callose synthase 3 [Vitis vinifera]	Unigene748_All//0.00E+00//AT5G13000| ATGSL12 (glucan synthase-like 12); 1,3-beta-glucan synthase/transferase, transferring glycosyl groups	Unigene748_All//1.00E-06//TC163464		GO:0006074//GO:0016020//GO:0035251//GO:0043234		nr -
Unigene7480_All	918	0.34	1.21	0.12	0.00	0.00	0.59	16.72	46.03	216.47	1.83E+00	9.60E-03		-1.56E+00	3.29E-01		null	null		9.21E+00	2.45E-03		1.46E+00	5.41E-68	Up	3.69E+00	0.00E+00	Up	Unigene7480_All//gi|15221409|ref|NP_177012.1|//3.00E-17//VQ motif-containing protein [Arabidopsis thaliana] >gi|28372822|gb|AAO39893.1| At1g68450 [Arabidopsis thaliana]	Unigene7480_All//9.00E-18//AT1G68450| VQ motif-containing protein					nr +
Unigene7481_All	1097	0.14	0.46	0.44	0.82	1.57	1.11	0.73	1.49	6.39	1.69E+00	1.34E-01		1.61E+00	1.82E-01		9.41E-01	6.16E-02		4.44E-01	5.00E-01		1.02E+00	2.79E-02		3.13E+00	3.08E-30	Up	Unigene7481_All//gi|224122042|ref|XP_002330716.1|//8.00E-06//predicted protein [Populus trichocarpa] >gi|222872320|gb|EEF09451.1| predicted protein [Populus trichocarpa]	Unigene7481_All//3.00E-06//AT1G28510| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Optic atrophy 3-like (InterPro:IPR010754); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G58150.1); Has 279 Blast hits to 279 proteins in 116 species: Archae - 0; Bacteria - 0; Metazoa - 133; Fungi - 74; Plants - 40; Viruses - 0; Other Eukaryotes - 32 (source: NCBI BLink).	Unigene7481_All//0.00E+00//gi|73863146|gb|DT465885.1|DT465885				nr +
Unigene74810_All	234	2.46	7.36	8.42	0.00	0.15	0.19	0.00	0.18	0.00	1.58E+00	2.84E-03		1.78E+00	6.26E-04	Up	7.20E+00	8.18E-01		7.59E+00	6.87E-01		7.48E+00	6.27E-01		null	null			Unigene74810_All//3.00E-96//gi|48744950|gb|CO075469.1|CO075469					
Unigene74826_All	628	0.42	0.24	0.59	0.95	0.82	0.00	0.94	0.00	0.25	-7.83E-01	6.19E-01		5.11E-01	6.54E-01		-2.11E-01	8.22E-01		-9.89E+00	7.69E-04	Down	-9.88E+00	2.39E-04	Down	-1.89E+00	3.22E-02		Unigene74826_All//gi|18411885|ref|NP_565175.1|//8.00E-34//RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] >gi|21537200|gb|AAM61541.1| RNA recognition motif-containing protein SEB-4 [Arabidopsis thaliana] >gi|124300976|gb|ABN04740.1| At1g78260 [Arabidopsis thaliana]	Unigene74826_All//1.00E-31//AT1G78260| RNA recognition motif (RRM)-containing protein	Unigene74826_All//1.00E-162//gi|78328852|gb|DT549126.1|DT549126				nr +
Unigene7483_All	625	1.76	4.78	1.28	1.83	2.09	0.87	6.22	9.43	6.95	1.44E+00	1.44E-04	Up	-4.60E-01	4.97E-01		1.92E-01	8.06E-01		-1.08E+00	9.65E-02		5.99E-01	5.97E-03		1.59E-01	5.87E-01		Unigene7483_All//gi|297811289|ref|XP_002873528.1|//1.00E-48//glycine-rich protein [Arabidopsis lyrata subsp. lyrata] >gi|297319365|gb|EFH49787.1| glycine-rich protein [Arabidopsis lyrata subsp. lyrata]	Unigene7483_All//3.00E-44//AT5G11700| glycine-rich protein	Unigene7483_All//1.00E-64//gi|84165215|gb|DR453863.1|DR453863				nr +

Unigene74832_A11	374	0.00	0.00	0.00	0.00	0.09	0.24	1.36	0.00	0.21	null	null		null	null		6.53E+00	8.18E-01		7.92E+00	4.71E-01		-1.04E+01	8.88E-04	Down	-2.67E+00	1.37E-02		Unigene74832_A11//gi|226496399|ref|XP_00114812 5.1|//5.00E-54//protein binding protein [Zea mays] >gi|195615984|gb|ACG29822.1| protein binding protein [Zea mays]	Unigene74832_A11//7.00E-59//AT3G04470| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Ankyrin (InterPro:IPR002110); BEST Arabidopsis thaliana protein match is: ankyrin repeat family protein (TAIR:AT1G04780.1); Has 842 Blast hits to 642 proteins in 95 species: Archae - 0; Bacteria - 6; Metazoa - 523; Fungi - 26; Plants - 165; Viruses - 4; Other Eukaryotes - 118 (source: NCBI BLink).	Unigene74832_A11//2.00E-179//gi|78343319|gb|DT563593.1|DT563593				nr -
Unigene74834_A11	208	0.00	4.38	5.63	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.60E-05	Up	1.25E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene74834_A11//sp|P10909|CLUS_HUMAN//5.00E-20//Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1						swissprot +
Unigene74841_A11	1477	0.00	0.17	0.61	0.30	0.28	0.15	0.43	0.11	0.19	7.42E+00	7.77E-02		9.26E+00	4.70E-05	Up	-1.17E-01	8.86E-01		-9.89E-01	3.94E-01		-1.92E+00	3.09E-02		-1.19E+00	1.33E-01		Unigene74841_A11//gi|224112050|ref|XP_002316067.1|//1.00E-110//DNA methyltransferase [Populus trichocarpa] >gi|222865107|gb|EEF02238.1| DNA methyltransferase [Populus trichocarpa]	Unigene74841_A11//4.00E-81//AT3G17310| methyltransferase family protein	Unigene74841_A11//0.00E+00//TC147043				nr +
Unigene7488_A11	364	69.71	31.04	33.50	75.41	60.92	84.25	102.68	63.04	63.26	-1.17E+00	4.69E-24	Down	-1.06E+00	8.83E-20	Down	-3.08E-01	1.90E-03		1.60E-01	1.40E-01		-7.04E-01	8.97E-19		-6.99E-01	4.22E-19		Unigene7488_A11//gi|223469631|gb|ACM90156.1|//8.00E-46//40S ribosomal protein S15-like protein [Jatropha curcas]	Unigene7488_A11//0.00E+00//gi|109828644|gb|DW227265.1|DW227265		ko03010|Ribosome		nr +
Unigene74880_A11	465	0.00	2.18	0.92	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	7.21E-06	Up	9.84E+00	1.37E-02		null	null		null	null		null	null		null	null		Unigene74880_A11//gi|121309841|dbj|BAF44222.1|//1.00E-41//malate dehydrogenase like-protein [Iris x hollandica]	Unigene74880_A11//1.00E-34//AT1G04410| malate dehydrogenase, cytosolic, putative			ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene7489_A11	208	46.79	19.24	24.58	58.68	56.12	116.82	91.88	52.65	50.18	-1.28E+00	4.12E-11	Down	-9.29E-01	1.42E-06		-6.42E-02	7.67E-01		9.93E-01	5.44E-19		-8.03E-01	2.25E-12		-8.73E-01	1.44E-14		Unigene7489_A11//gi|806279|gb|AAA66161.1|//1.00E-11//ribosomal protein [Arabidopsis thaliana]	Unigene7489_A11//6.00E-12//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene7489_A11//8.00E-106//gi|78352309|gb|DT572583.1|DT572583		ko03010|Ribosome		nr +
Unigene74899_A11	559	0.75	0.82	0.48	1.96	1.36	1.62	4.61	2.69	1.71	1.24E-01	9.11E-01		-6.53E-01	5.94E-01		-5.33E-01	4.20E-01		-2.79E-01	6.89E-01		-7.77E-01	2.70E-02		-1.43E+00	5.84E-05	Down	Unigene74899_A11//gi|10177699|dbj|BAB11025.1|//2.00E-50//pattern formation protein [Arabidopsis thaliana]	Unigene74899_A11//6.00E-45//AT1G13980| GN (GNOM); GTP:GDP antiporter/ protein homodimerization	Unigene74899_A11//2.00E-176//gi|48807326|gb|CO108640.1|CO108640				nr -
Unigene7490_A11	514	6.11	50.87	15.95	0.39	0.87	4.22	0.49	0.65	1.16	3.06E+00	6.56E-87	Up	1.39E+00	4.08E-10	Up	1.17E+00	3.47E-01		3.44E+00	7.19E-09	Up	3.99E-01	7.24E-01		1.24E+00	1.39E-01		Unigene7490_A11//gi|61658206|gb|AAX49393.1|//7.00E-35//OLE-5 [Coffea canephora]	Unigene7490_A11//2.00E-21//AT1G48990| glycine-rich protein / oleosin	Unigene7490_A11//3.00E-24//gi|78330133|gb|DT550407.1|DT550407				nr +
Unigene7491_A11	341	2.45	2.97	3.90	4.24	2.52	0.26	0.00	0.00	0.00	2.76E-01	6.62E-01		6.69E-01	2.68E-01		-7.47E-01	1.63E-01		-4.00E+00	5.84E-07	Down	null	null		null	null									
Unigene7494_A11	429	0.00	2.95	1.61	0.46	0.72	0.00	2.66	1.36	2.04	1.15E+01	2.85E-07	Up	1.07E+01	6.12E-04	Up	6.37E-01	6.94E-01		-8.86E+00	1.33E-01		-9.64E-01	9.32E-02		-3.81E-01	4.99E-01									
Unigene7497_A11	463	0.57	0.33	0.00	2.15	1.71	0.98	2.74	2.80	0.43	-7.83E-01	6.19E-01		-9.14E+00	8.51E-02		-3.31E-01	6.19E-01		-1.14E+00	1.09E-01		3.07E-02	9.85E-01		-2.67E+00	2.31E-05	Down	Unigene7497_A11//gi|124359162|gb|AB005685.1|//7.00E-20//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene7497_A11//1.00E-11//ATMG01250| hypothetical protein	Unigene7497_A11//5.00E-07//TC176949				nr +
Unigene7498_A11	432	1.09	135.59	11.22	0.00	0.80	2.72	1.47	0.19	1.66	6.96E+00	0.00E+00	Up	3.36E+00	1.96E-17	Up	9.64E+00	3.00E-02		1.14E+01	5.32E-07	Up	-2.92E+00	4.19E-03		1.77E-01	7.99E-01					Unigene7498_A11//0.00E+00//CA993545				
Unigene74986_A11	303	0.52	0.67	0.35	5.75	2.95	0.60	0.56	0.00	0.13	3.69E-01	8.15E-01		-5.59E-01	7.74E-01		-9.62E-01	4.14E-02		-3.27E+00	3.65E-07	Down	-9.12E+00	1.34E-01		-2.09E+00	3.13E-01		Unigene74986_A11//gi|297825631|ref|XP_002880698.1|//2.00E-30//sulfate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326537|gb|EFH56957.1| sulfate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene74986_A11//5.00E-28//AT2G25680| MOT1 (molybdate transporter 1); molybdate ion transmembrane transporter/ sulfate transmembrane transporter	Unigene74986_A11//8.00E-70//TC170155			GO:0015103//GO:0015698//GO:0031224//GO:0043231	nr -
Unigene7500_A11	392	1.47	5.82	4.21	2.54	0.88	1.96	1.62	6.08	0.81	1.99E+00	2.91E-05	Up	1.52E+00	6.71E-03		-1.53E+00	2.33E-02		-3.76E-01	6.31E-01		1.91E+00	2.78E-06	Up	-9.93E-01	2.02E-01					Unigene7500_A11//3.00E-17//TC164963				
Unigene7502_A11	429	0.49	2.95	1.74	1.51	1.77	0.42	2.66	4.19	1.86	2.60E+00	3.59E-04	Up	1.83E+00	5.05E-02		2.26E-01	8.32E-01		-1.84E+00	6.00E-02		6.53E-01	1.38E-01		-5.19E-01	3.56E-01									
Unigene7503_A11	432	1.09	5.04	1.85	2.19	1.36	2.40	0.69	0.58	0.46	2.21E+00	1.14E-05	Up	7.62E-01	3.62E-01		-6.93E-01	3.15E-01		1.34E-01	8.58E-01		-2.39E-01	8.39E-01		-5.71E-01	6.28E-01					Unigene7503_A11//2.00E-22//TC172937				
Unigene7507_A11	1206	0.09	34.91	12.50	0.50	2.00	5.21	0.32	0.69	0.66	8.65E+00	3.58E-238	Up	7.17E+00	5.90E-81	Up	2.01E+00	4.60E-06	Up	3.39E+00	9.35E-25	Up	1.14E+00	1.06E-01		1.07E+00	1.22E-01		Unigene7507_A11//gi|296278600|gb|AD404264.1|//5.00E-38//HB1 [Nicotiana benthamiana]	Unigene7507_A11//1.00E-36//AT3G61890| ATHB-12 (ARABIDOPSIS THALIANA HOMEOBOX 12); transcription activator/ transcription factor	Unigene7507_A11//0.00E+00//TC175955	HB			nr +
Unigene7511_A11	490	1.71	0.10	0.00	1.32	1.34	0.46	2.07	0.94	1.30	-4.05E+00	4.65E-04	Down	-1.07E+01	1.19E-04	Down	1.48E-02	9.91E-01		-1.52E+00	1.12E-01		-1.14E+00	6.62E-02		-6.71E-01	2.53E-01		Unigene7511_A11//gi|18397766|ref|NP_565370.1|//4.00E-06//TINC-50 family protein [Arabidopsis thaliana] >gi|14190389|gb|AAK55675.1|AF378872_1 At2g15240/F15A23.2 [Arabidopsis thaliana] >gi|15450545|gb|AAK96450.1| At2g15240/F15A23.2 [Arabidopsis thaliana] >gi|20197743|gb|AAD25568.2| expressed protein [Arabidopsis thaliana]		Unigene7511_A11//7.00E-28//ES845797				nr -
Unigene7514_A11	343	17.24	57.76	38.19	12.78	9.24	6.72	106.75	151.95	52.38	1.74E+00	7.37E-34	Up	1.15E+00	6.19E-12	Up	-4.69E-01	1.02E-01		-9.28E-01	1.15E-03		5.09E-01	7.67E-15		-1.03E+00	2.71E-35	Down				Unigene7514_A11//1.00E-142//TC166042				
Unigene75145_A11	322	1.95	7.40	4.13	0.15	1.82	1.12	0.26	0.91	0.37	1.92E+00	2.85E-05	Up	1.08E+00	7.96E-02		3.55E+00	8.14E-03		2.86E+00	9.44E-02		1.79E+00	2.24E-01		4.99E-01	8.06E-01					Unigene75145_A11//4.00E-50//gi|164243049|gb|ES825819.1|ES825819				
Unigene75150_A11	264	0.00	0.19	4.64	0.00	0.00	0.00	0.00	0.00	0.00	7.58E+00	6.11E-01		1.22E+01	9.10E-07	Up	null	null		null	null		null	null		null	null			Unigene75150_A11//7.00E-05//AT3G16360| AHP4 (HPT PHOSPHOTRANSMITTER 4); histidine phosphotransfer kinase/ transferase, transferring phosphorus-containing groups	Unigene75150_A11//4.00E-34//TC164475				
Unigene7516_A11	588	151.09	141.24	145.71	184.94	166.73	171.67	93.84	69.59	44.65	-9.73E-02	1.11E-01		-5.23E-02	4.33E-01		-1.50E-01	2.09E-03		-1.07E-01	4.63E-02		-4.31E-01	9.06E-12		-1.07E+00	1.86E-56	Down	Unigene7516_A11//gi|194466097|gb|AF742279.1|//4.00E-44//double-stranded DNA-binding protein [Arachis hypogaea]	Unigene7516_A11//4.00E-34//AT1G29850| double-stranded DNA-binding family protein	Unigene7516_A11//0.00E+00//TC168239				nr +
Unigene75165_A11	220	2.85	0.00	1.21	0.91	0.63	0.00	0.19	0.95	0.72	-1.15E+01	7.90E-04	Down	-1.24E+00	2.13E-01		-5.33E-01	7.47E-01		-9.82E+00	1.33E-01		2.31E+00	2.39E-01		1.91E+00	3.77E-01		Unigene75165_A11//gi|15238599|ref|NP_200813.1|//5.00E-07//PRLI-interacting factor-related [Arabidopsis thaliana]	Unigene75165_A11//2.00E-08//AT5G60050| PRLI-interacting factor-related	Unigene75165_A11//3.00E-50//ES836438				nr +
Unigene7517_A11	619	0.51	4.17	0.43	1.05	0.89	0.80	0.68	1.49	0.90	3.04E+00	4.87E-09	Up	-2.38E-01	8.50E-01		-2.33E-01	8.06E-01		-3.82E-01	6.78E-01		1.12E+00	8.95E-02		4.00E-01	6.36E-01		Unigene7517_A11//gi|224125626|ref|XP_002329678.1|//2.00E-14//predicted protein [Populus trichocarpa] >gi|222870586|gb|EEF07717.1| predicted protein [Populus trichocarpa]						nr -
Unigene7518_A11	605	0.95	0.75	0.35	3.62	1.65	1.94	6.71	2.69	0.26	-3.36E-01	6.90E-01		-1.43E+00	1.75E-01		-1.13E+00	5.60E-03		-9.00E-01	3.86E-02		-1.32E+00	2.64E-06	Down	-4.67E+00	1.98E-24	Down	Unigene7518_A11//gi|115485585|ref|NP_001067936.1|//3.00E-23//Os11g0496500 [Oryza sativa Japonica Group] >gi|113645158|dbj|BAF28299.1| Os11g0496500 [Oryza sativa Japonica Group]	Unigene7518_A11//3.00E-14//AT3G27030| unknown protein	Unigene7518_A11//2.00E-99//DW242882				nr -
Unigene7519_A11	617	1.87	1.81	0.00	3.47	2.46	1.17	2.33	2.57	1.49	-4.63E-02	9.53E-01		-1.09E+01	2.60E-06	Down	-5.00E-01	2.61E-01		-1.57E+00	5.56E-04	Down	1.44E-01	7.67E-01		-6.50E-01	1.74E-01					Unigene7519_A11//6.00E-106//TC172808				
Unigene75199_A11	276	0.00	0.55	2.89	0.36	0.50	1.47	0.31	1.06	0.29	9.11E+00	2.32E-01		1.15E+01	1.72E-04	Up	4.67E-01	8.75E-01		2.03E+00	1.49E-01		1.79E+00	2.24E-01		-8.58E-02	9.69E-01					Unigene75199_A11//6.00E-21//DT463765				
Unigene75204_A11	322	0.16	2.05	1.16	0.77	0.75	1.96	3.28	0.65	2.23	3.65E+00	4.10E-03		2.83E+00	9.29E-02		-4.72E-02	9.51E-01		1.34E+00	1.73E-01		-2.34E+00	6.78E-04	Down	-5.60E-01	3.39E-01		Unigene75204_A11//gi|115478034|ref|NP_001062612.1|//1.00E-36//Os09g0127800 [Oryza sativa Japonica Group] >gi|122234492|sp|Q0J3D9.1|COPA3_ORYSJ RecName: Full=Coatomer subunit alpha-3; AltName: Full=Alpha-coat protein 3; Short=Alpha-COP 3 >gi|113630845|dbj|BAF24526.1| Os09g0127800 [Oryza sativa Japonica Group]	Unigene75204_A11//1.00E-35//AT1G62020| coatomer protein complex, subunit alpha, putative	Unigene75204_A11//4.00E-90//gi|48826529|gb|CO125065.1|CO125065			GO:0004683//GO:0005488//GO:0015031//GO:0030120//GO:0031461//GO:0048193	nr -
Unigene75205_A11	214	0.00	0.00	4.98	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.23E+01	6.60E-06	Up	null	null		null	null		null	null		null	null		Unigene75205_A11//gi|151347473|gb|ABS01349.1|//7.00E-13//hypersensitive-induced response protein [Carica papaya]	Unigene75205_A11//1.00E-13//AT5G62740| band 7 family protein				GO:0019901	nr +
Unigene7522_A11	326	42.21	56.89	74.81	37.74	61.90	40.87	97.53	95.64	733.96	4.31E-01	8.23E-04		8.26E-01	8.03E-13		7.14E-01	4.45E-10		1.15E-01	5.50E-01		-2.82E-02	7.86E-01		2.91E+00	0.00E+00	Up	Unigene7522_A11//gi|67483357|gb|AAY68034.1|//1.00E-24//3-hydroxy-methylglutaryl coenzyme A reductase [Tilia miqueliana]	Unigene7522_A11//9.00E-18//AT2G17370| HMG2 (3-HYDROXY-3-METHYLGLUTARYL-COA REDUCTASE 2); hydroxymethylglutaryl-CoA reductase	Unigene7522_A11//1.00E-173//TC164133		ko00900|Terpenoid backbone biosynthesis		nr -
Unigene7523_A11	517	8.80	5.78	3.50	2.41	1.27	0.79	0.08	0.16	0.23	-6.07E-01	3.22E-02		-1.33E+00	1.38E-05	Down	-9.29E-01	1.11E-01		-1.62E+00	1.08E-02		9.83E-01	7.29E-01		1.50E+00	5.57E-01		Unigene7523_A11//gi|224144996|ref|XP_002325489.1|//4.00E-60//type-a response regulator [Populus trichocarpa] >gi|222862364|gb|EEE99870.1| type-a response regulator [Populus trichocarpa]	Unigene7523_A11//1.00E-53//AT3G56380| ARR17 (ARABIDOPSIS RESPONSE REGULATOR 17); transcription regulator/ two-component response regulator	Unigene7523_A11//1.00E-66//TC163836	ARR-B	ko04712|Circadian rhythm - plant		nr +
Unigene75241_A11	226	0.00	3.59	0.71	0.00	0.00	0.00	0.00	0.00	0.18	1.18E+01	9.31E-05	Up	9.47E+00	2.35E-01		null	null		null	null		null	null		7.46E+00	6.38E-01		Unigene75241_A11//gi|255084545|ref|XP_002508847.1|//5.00E-18//ribosomal protein L44 [Micromonas sp. RCC299] >gi|226524124|gb|ACO70105.1| ribosomal protein L44 [Micromonas sp. RCC299]	Unigene75241_A11//4.00E-19//AT4G14320| 60S ribosomal protein L36a/L44 (RPL36aB)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0042221	nr -
Unigene7525_A11	841	0.37	0.42	0.00	0.59	1.31	2.20	2.11	1.69	4.22	1.76E-01	8.83E-01		-8.54E+00	4.88E-02		1.15E+00	8.79E-02		1.89E+00	2.78E-04	Up	-3.22E-01	4.96E-01		9.98E-01	5.00E-04		Unigene7525_A11//gi|108711620|gb|AB799415.1|//1.00E-85//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene7525_A11//2.00E-85//AT4G13750| ATP binding					nr -
Unigene75252_A11	921	0.34	1.98	0.52	1.08	0.75	0.78	9.09	5.76	7.14	2.54E+00	1.40E-05	Up	6.10E-01	5.86E-01		-5.33E-01	4.45E-01		-4.63E-01	5.26E-01		-6.57E-01	2.20E-04		-3.49E-01	4.89E-02		Unigene75252_A11//gi|297821154|ref|XP_002878460.1|//9.00E-34//ATBZIP53 [Arabidopsis lyrata subsp. lyrata] >gi|297324298|gb|EFH54719.1| ATBZIP53 [Arabidopsis lyrata subsp. lyrata]	Unigene75252_A11//3.00E-34//AT3G62420| ATBZIP53 (BASIC REGION/LEUCINE ZIPPER MOTIF 53); DNA binding / protein heterodimerization/ sequence-specific DNA binding / transcription factor	Unigene75252_A11//0.00E+00//TC133102	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0003677//GO:0006351//GO:0043231//GO:0046983	nr +
Unigene7526_A11	615	0.51	0.99	0.95	3.48	2.58	0.73	0.96	1.70	1.36	9.54E-01	3.14E-01		9.00E-01	3.77E-01		-4.35E-01	3.25E-01		-2.25E+00	5.08E-06	Down	8.20E-01	1.79E-01		4.99E-01	4.61E-01									
Unigene75282_A11	503	0.00	0.60	2.54	0.20	0.00	0.81	0.00	0.00	0.00	9.24E+00	4.37E-02		1.13E+01	4.67E-07	Up	-7.63E+00	3.09E-01		2.03E+00	1.49E-01		null	null		null	null		Unigene75282_A11//gi|30575840|gb|AF329921.1|//4.00E-16//MYB1 [Paraboea crassifolia]	Unigene75282_A11//2.00E-07//AT4G05100| AtMYB74 (myb domain protein 74); DNA binding / transcription factor		MYB		GO:0009719//GO:0010033	nr -

Unigene75289_All	314	0.00	0.00	2.37	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.12E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene75289_All//gi|806720|gb|AAA66362.1|//8.00E-14//arabinogalactan-protein precursor [Nicotiana alata]				ko00500|Starch and sucrose metabolism//ko00270|Cysteine and methionine metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene7529_All	1123	6.43	2.93	2.89	11.05	10.00	10.70	15.02	5.92	7.95	-1.13E+00	4.32E-07	Down	-1.15E+00	6.75E-07	Down	-1.44E-01	4.42E-01		-4.61E-02	8.01E-01		-1.34E+00	1.82E-24	Down	-9.19E-01	4.62E-14		Unigene7529_All//gi|87162669|gb|AB028464.1|//2.00E-29//Ribosomal protein L30 [Medicago truncatula]	Unigene7529_All//5.00E-23//AT3G13580| 60S ribosomal protein L7 (RPL7D)	Unigene7529_All//0.00E+00//gi|193217977|gb|EY197169.1|EY197169		ko03010|Ribosome		nr +
Unigene7531_All	273	1.53	25.43	6.05	2.55	1.77	5.46	20.91	88.64	39.55	4.05E+00	1.41E-29	Up	1.98E+00	8.05E-04	Up	-5.33E-01	5.45E-01		1.10E+00	5.01E-02		2.08E+00	5.81E-64	Up	9.20E-01	2.84E-09		Unigene7531_All//gi|255633890|gb|ACU17306.1|//3.00E-16//unknown [Glycine max]		Unigene7531_All//5.00E-43//TC175178				nr -
Unigene75317_All	243	1.29	4.80	4.16	2.46	3.68	8.74	1.91	1.38	2.62	1.89E+00	6.32E-03		1.69E+00	2.74E-02		5.83E-01	4.72E-01		1.83E+00	1.26E-04	Up	-4.76E-01	6.59E-01		4.55E-01	5.78E-01					Unigene75317_All//5.00E-58//ES794311				
Unigene7532_All	1642	0.00	0.00	0.00	0.00	0.00	0.00	7.18	1.20	2.21	null	null		null	null		null	null		null	null		-2.59E+00	7.73E-41	Down	-1.70E+00	5.07E-25	Down								ESTscan +
Unigene75332_All	327	0.00	10.07	5.21	0.00	0.11	0.00	0.00	0.00	0.00	1.33E+01	9.62E-19	Up	1.23E+01	2.19E-09	Up	6.72E+00	8.18E-01		null	null		null	null		null	null										
Unigene7534_All	359	24.63	57.44	23.88	42.04	34.34	62.65	40.04	42.15	27.52	1.22E+00	5.12E-21	Up	-4.46E-02	8.34E-01		-2.92E-01	4.23E-02		5.75E-01	3.05E-07		7.38E-02	6.33E-01		-5.41E-01	2.46E-05		Unigene7534_All//gi|115434880|ref|NP_001042198.1|//3.00E-09//Os01g0179300 [Oryza sativa Japonica Group] >gi|113531729|dbj|BAF04112.1|Os01g0179300 [Oryza sativa Japonica Group]		Unigene7534_All//2.00E-126//gi|164319467|gb|ES836148.1|ES836148				nr +
Unigene7535_All	574	363.78	106.99	83.03	239.26	262.76	139.35	107.32	35.68	38.10	-1.77E+00	0.00E+00	Down	-2.13E+00	0.00E+00	Down	1.35E-01	9.37E-04		-7.80E-01	1.46E-70		-1.59E+00	6.58E-112	Down	-1.49E+00	2.86E-105	Down	Unigene7535_All//gi|224099519|ref|XP_002311516.1|//5.00E-61//high mobility group family [Populus trichocarpa] >gi|222851336|gb|EEE88883.1| high mobility group family [Populus trichocarpa]	Unigene7535_All//2.00E-23//AT1G14900| HMGA (HIGH MOBILITY GROUP A); DNA binding	Unigene7535_All//0.00E+00//gi|164279953|gb|ES795576.1|ES795576				nr +
Unigene7536_All	410	1.66	2.47	3.38	1.70	2.18	4.19	0.72	2.85	3.69	5.75E-01	3.83E-01		1.03E+00	8.63E-02		3.60E-01	6.55E-01		1.30E+00	1.19E-02		1.98E+00	1.36E-03		2.35E+00	1.89E-05	Up				Unigene7536_All//5.00E-155//EY495339				
Unigene7538_All	269	0.39	8.10	3.56	1.85	0.77	4.70	0.47	0.62	1.33	4.38E+00	4.79E-10	Up	3.20E+00	1.02E-03		-1.27E+00	2.22E-01		1.34E+00	3.21E-02		3.99E-01	8.13E-01		1.50E+00	2.03E-01					Unigene7538_All//3.00E-07//TC145350				
Unigene75388_All	219	0.00	0.00	3.40	0.91	0.00	0.00	0.77	0.00	0.00	null	null		1.17E+01	3.25E-04	Up	-9.83E+00	8.39E-02		-9.83E+00	1.33E-01		-9.59E+00	1.34E-01		-9.59E+00	1.08E-01										
Unigene7539_All	632	0.58	1.28	0.93	0.79	0.87	1.64	2.27	4.43	5.36	1.15E+00	1.48E-01		6.77E-01	4.82E-01		1.45E-01	9.05E-01		1.06E+00	1.32E-01		9.62E-01	4.20E-03		1.24E+00	4.07E-05	Up	Unigene7539_All//gi|292630778|sp|Q9FFN2.2|GLYT3_ARATH//1.00E-63//RecName: Full=Probable glycosyltransferase At5g03795	Unigene7539_All//5.00E-65//AT5G03795| LOCATED IN: membrane; EXPRESSED IN: embryo, sepal, flower; EXPRESSED DURING: C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Exostosin-like (InterPro:IPR004263); BEST Arabidopsis thaliana protein match is: exostosin family protein (TAIR:AT3G07620.1); Has 866 Blast hits to 860 proteins in 87 species: Archae - 0; Bacteria - 9; Metazoa - 265; Fungi - 4; Plants - 504; Viruses - 0; Other Eukaryotes - 84 (source: NCBI BLink).	Unigene7539_All//8.00E-13//TC143482				nr -
Unigene754_All	2078	5.92	9.70	6.25	13.64	6.53	6.17	57.19	80.33	45.26	7.14E-01	7.36E-09		7.96E-02	6.41E-01		-1.06E+00	3.57E-28	Down	-1.14E+00	5.75E-28	Down	4.90E-01	1.19E-42		-3.38E-01	3.41E-16		Unigene754_All//gi|295311663|ref|YP_003587235.1|//1.00E-160//ribosomal protein S4 [Citrullus lanatus] >gi|259156791|gb|ACY96653.1| ribosomal protein S4 [Citrullus lanatus]	Unigene754_All//2.00E-117//ATMG00290| encodes a mitochondrial ribosomal protein S4, a constituent of the small subunit of the ribosomal complex	Unigene754_All//0.00E+00//ES851673		ko03010|Ribosome		nr +
Unigene7541_All	535	2.05	0.38	1.09	5.87	3.73	4.47	3.87	0.31	0.74	-2.44E+00	1.50E-03		-9.07E-01	1.87E-01		-6.52E-01	5.36E-02		-3.91E-01	3.05E-01		-3.63E+00	2.06E-10	Down	-2.38E+00	2.25E-07	Down	Unigene7541_All//gi|18201934|gb|AAK92458.3|AF398149_1//5.00E-82//kinesin-like protein heavy chain [Arabidopsis thaliana]	Unigene7541_All//3.00E-83//AT3G44730| kinesin motor protein-related	Unigene7541_All//7.00E-84//CO086398				nr +
Unigene7542_All	738	0.43	1.24	0.07	2.36	0.89	1.53	3.90	1.08	2.16	1.54E+00	4.51E-02		-2.56E+00	1.59E-01		-1.41E+00	2.95E-03		-6.27E-01	2.22E-01		-1.86E+00	3.35E-07	Down	-8.51E-01	7.38E-03		Unigene7542_All//gi|17428897|emb|CAD13472.1|//8.00E-47//helicase [Arabidopsis thaliana]	Unigene7542_All//4.00E-48//AT1G27880| ATP-dependent DNA helicase, putative					nr +
Unigene75444_All	228	0.00	3.11	0.93	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.30E-04	Up	9.87E+00	1.39E-01		null	null		null	null		null	null		null	null										ESTscan +
Unigene75446_All	211	2.73	3.60	4.04	2.60	1.80	3.21	8.02	5.74	1.32	4.01E-01	6.01E-01		5.66E-01	4.61E-01		-5.33E-01	5.85E-01		3.06E-01	7.22E-01		-4.81E-01	3.09E-01		-2.60E+00	9.91E-07	Down				Unigene75446_All//3.00E-37//DR453052				
Unigene7545_All	289	71.69	26.12	31.88	85.15	82.45	94.70	84.41	40.06	37.22	-1.46E+00	1.48E-27	Down	-1.17E+00	5.10E-19	Down	-4.64E-02	7.57E-01		1.53E-01	1.92E-01		-1.08E+00	7.49E-25	Down	-1.18E+00	1.19E-29	Down	Unigene7545_All//gi|146454510|gb|ABQ41921.1|//1.00E-45//60S ribosomal protein large subunit 9 [Sonneratia caseolaris] >gi|156633898|gb|ABU90948.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633900|gb|ABU90949.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633902|gb|ABU90950.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633904|gb|ABU90951.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633906|gb|ABU90952.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633908|gb|ABU90953.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633910|gb|ABU90954.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633912|gb|ABU90955.1| ribosomal protein L9 [Sonneratia caseolaris] >gi|156633914|gb|ABU90956.1| ribosomal protein L9 [Sonneratia	Unigene7545_All//3.00E-41//AT1G33140| PGY2 (PIGGYBACK2); structural constituent of ribosome	Unigene7545_All//2.00E-162//BF273343		ko03010|Ribosome		nr -
Unigene7549_All	782	0.07	0.13	0.41	4.65	2.03	7.05	27.25	54.84	62.31	9.54E-01	7.24E-01		2.61E+00	1.45E-01		-1.20E+00	7.62E-05	Down	6.00E-01	1.89E-02		1.01E+00	7.84E-39	Up	1.19E+00	9.17E-59	Up	Unigene7549_All//gi|116325970|gb|AB198586.1|//7.00E-07//Atig64405 [Arabidopsis thaliana]		Unigene7549_All//0.00E+00//gi|164258122|gb|ES791660.1|ES791660				nr +
Unigene75496_All	233	0.22	0.00	1.14	3.42	8.57	2.52	13.79	3.59	1.03	-7.81E+00	6.04E-01		2.35E+00	2.39E-01		1.33E+00	3.95E-03		-4.41E-01	6.14E-01		-1.94E+00	2.05E-08	Down	-3.75E+00	7.58E-17	Down	Unigene75496_All//gi|225437298|ref|XP_002267051.1|//5.00E-07//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297743854|emb|CBI36824.3| unnamed protein product [Vitis vinifera]						nr +
Unigene755_All	1917	0.74	0.40	0.31	0.68	0.54	0.52	3.79	2.51	1.23	-8.94E-01	1.12E-01		-1.27E+00	3.55E-02		-3.26E-01	5.86E-01		-3.82E-01	5.50E-01		-5.97E-01	1.95E-03		-1.63E+00	7.49E-15	Down	Unigene755_All//gi|295311663|ref|YP_003587235.1|//1.00E-160//ribosomal protein S4 [Citrullus lanatus] >gi|259156791|gb|ACY96653.1| ribosomal protein S4 [Citrullus lanatus]	Unigene755_All//2.00E-117//ATMG00290| encodes a mitochondrial ribosomal protein S4, a constituent of the small subunit of the ribosomal complex	Unigene755_All//0.00E+00//ES851673		ko03010|Ribosome		nr -
Unigene75510_All	278	26.73	17.86	11.49	49.46	47.94	37.04	65.40	53.22	60.19	-5.81E-01	6.58E-03		-1.22E+00	1.17E-07	Down	-4.50E-02	8.30E-01		-4.17E-01	5.84E-03		-2.97E-01	1.26E-02		-1.20E-01	3.59E-01		Unigene75510_All//gi|15237500|ref|NP_199487.1|//1.00E-31//AGD9 (ARF-GAP DOMAIN 9); ARF GTPase activator/ DNA binding / zinc ion binding [Arabidopsis thaliana] >gi|75262520|sp|Q9FIQ0.1|AGD9_ARATH RecName: Full=Probable ADP-ribosylation factor GTPase-activating protein AGD9; Short=ARF GAP AGD9; AltName: Full=Protein ARF-GAP DOMAIN 9; Short=AtAGD9 >gi|9758511|dbj|BAB08919.1| zinc finger protein Glo3-like [Arabidopsis thaliana] >gi|20466454|gb|AAM20544.1| zinc finger protein Glo3-like [Arabidopsis thaliana] >gi|22136388|gb|AAM91272.1| zinc finger protein Glo3-like [Arabidopsis thaliana]	Unigene75510_All//3.00E-28//AT5G46750| AGD9 (ARF-GAP DOMAIN 9); ARF GTPase activator/ DNA binding / zinc ion binding	Unigene75510_All//2.00E-153//EX164332		ko04144|Endocytosis	GO:0003006//GO:0005083//GO:0032012//GO:0043231//GO:0046914//GO:0048229	nr +
Unigene7552_All	723	0.94	7.22	1.62	0.00	1.10	0.50	0.06	1.39	0.06	2.94E+00	4.18E-17	Up	7.84E-01	2.38E-01		1.01E+01	7.26E-05	Up	8.96E+00	2.37E-02		4.57E+00	4.78E-06	Up	-8.64E-02	9.67E-01		Unigene7552_All//gi|115490848|gb|AB197958.1|//2.00E-80//alpha-crystalline heat shock protein [Gossypium arboreum] >gi|115490850|gb|AB197959.1| alpha-crystalline heat shock protein [Gossypium arboreum]	Unigene7552_All//3.00E-55//AT4G27670| HSP21 (HEAT SHOCK PROTEIN 21)	Unigene7552_All//0.00E+00//TC148146				nr +
Unigene75521_All	209	0.00	0.00	0.76	0.00	0.00	0.00	256.92	635.54	324.81	null	null		9.58E+00	2.35E-01		null	null		null	null		1.31E+00	3.43E-179	Up	3.38E-01	1.17E-09					Unigene75521_All//1.00E-49//TC162503				
Unigene75537_All	279	0.00	1.45	0.00	0.00	0.00	0.00	0.61	13.03	27.13	1.05E+01	1.34E-02		null	null		null	null		null	null		4.43E+00	2.09E-20	Up	5.48E+00	9.28E-48	Up	Unigene75537_All//gi|71979887|dbj|BAE17114.1|//1.00E-08//Cys2-His2 type zinc finger protein [Nicotiana tabacum]		Unigene75537_All//6.00E-61//TC165666			GO:0006950//GO:0009628//GO:0042221	nr +
Unigene7554_All	239	69.18	22.68	27.85	75.66	61.09	84.28	99.24	30.78	47.01	-1.61E+00	1.66E-25	Down	-1.31E+00	3.26E-18	Down	-3.09E-01	1.57E-02		1.56E-01	2.73E-01		-1.69E+00	1.80E-47	Down	-1.08E+00	5.04E-25	Down	Unigene7554_All//gi|1173256|sp|P46299.1|RS4_GOSHI//1.00E-38//RecName: Full=40S ribosomal protein S4 >gi|488739|emb|CAA55882.1| ribosomal protein, small subunit 4e (RS4e) [Gossypium hirsutum]	Unigene7554_All//3.00E-36//AT5G07090| 40S ribosomal protein S4 (RPS4B)	Unigene7554_All//1.00E-132//ES842223		ko03010|Ribosome		nr -
Unigene75557_All	443	0.00	5.72	4.09	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.03E-14	Up	1.20E+01	5.68E-10	Up	null	null		null	null		null	null		null	null		Unigene75557_All//gi|15217294|gb|AAX92638.1|AC079633_18//7.00E-40//Putative 40S Ribosomal protein [Oryza sativa Japonica Group] >gi|213959144|gb|ACJ54906.1| 40S ribosomal protein [Oryza sativa Japonica Group]	Unigene75557_All//1.00E-37//AT1G72370| P40; structural constituent of ribosome			ko03010|Ribosome	GO:0005840//GO:0006519//GO:0016831//GO:0044106//GO:0044249	nr -
Unigene7556_All	386	2.17	0.13	1.38	0.65	2.94	2.22	0.66	0.00	2.06	-4.05E+00	4.65E-04	Down	-6.53E-01	3.96E-01		2.19E+00	2.15E-03		1.78E+00	3.19E-02		-9.36E+00	4.03E-02		1.65E+00	2.32E-02										
Unigene75562_All	739	0.00	7.54	2.59	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	8.49E-32	Up	1.13E+01	1.47E-10	Up	null	null		null	null		null	null		null	null										
Unigene75564_All	867	1.51	1.11	2.09	1.61	1.51	0.52	1.56	1.64	0.46	-4.42E-01	4.41E-01		4.69E-01	3.69E-01		-9.21E-02	8.58E-01		-1.63E+00	5.90E-03		7.08E-02	8.99E-01		-1.76E+00	9.57E-04	Down	Unigene75564_All//gi|20197504|gb|AM15099.1|//6.00E-70//Expressed protein [Arabidopsis thaliana]	Unigene75564_All//5.00E-72//AT2G06005| unknown protein	Unigene75564_All//0.00E+00//gi|73861670|gb|DT464409.1|DT464409			GO:0044464	nr -
Unigene7557_All	409	356.14	223.24	403.09	153.22	148.35	143.99	137.18	194.26	64.29	-6.74E-01	1.14E-53		1.79E-01	1.64E-05		-4.66E-02	5.82E-01		-8.96E-02	2.53E-01		5.02E-01	1.27E-21		-1.09E+00	2.75E-59	Down	Unigene7557_All//gi|2677828|gb|AAB97142.1|//4.00E-48//cysteine protease [Prunus armeniaca]	Unigene7557_All//6.00E-45//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase	Unigene7557_All//0.00E+00//TC165261				nr +

Unigene7558_All	1104	1.47	2.39	0.63	2.93	3.15	2.86	4.94	0.76	1.73	7.00E-01	7.23E-02		-1.23E+00	2.64E-02		1.03E-01	8.12E-01		-3.45E-02	9.38E-01		-2.71E+00	3.43E-20	Down	-1.51E+00	2.84E-10	Down	Unigene7558_All//gi|22796151|emb|CAD42234.1|//1.00E-137//kinesin-like protein [Arabidopsis thaliana]	Unigene7558_All//7.00E-131//AT3G43210| TES (TETRASPORE); microtubule motor	Unigene7558_All//0.00E+00//TC161420				nr +
Unigene756_All	1853	3.70	2.73	3.45	6.05	3.49	4.70	13.48	9.09	2.99	-4.36E-01	5.48E-02		-1.01E-01	6.74E-01		-7.92E-01	3.95E-07		-3.63E-01	3.78E-02		-5.69E-01	4.77E-09		-2.17E+00	5.59E-72	Down	Unigene756_All//gi|255589962|ref|XP_002535139.1|//2.00E-36//conserved hypothetical protein [Ricinus communis] >gi|223523944|gb|EEF27245.1| conserved hypothetical protein [Ricinus communis]		Unigene756_All//0.00E+00//TC140964				nr +
Unigene7560_All	415	8.70	13.67	8.21	5.64	5.97	3.81	9.17	9.27	20.83	6.53E-01	8.96E-03		-8.31E-02	8.04E-01		8.27E-02	8.57E-01		-5.67E-01	1.93E-01		1.51E-02	9.94E-01		1.18E+00	5.08E-11	Up			Unigene7560_All//7.00E-71//DW491315				
Unigene7561_All	753	0.76	0.74	0.07	1.06	2.24	1.50	5.39	1.89	1.22	-4.62E-02	9.74E-01		-3.43E+00	1.41E-02		1.08E+00	3.35E-02		5.02E-01	4.76E-01		-1.51E+00	1.36E-07	Down	-2.15E+00	3.45E-12	Down	Unigene7561_All//gi|124360422|gb|AB008432.1|//3.00E-84//Peptidase C50, separase [Medicago truncatula]	Unigene7561_All//3.00E-80//AT4G22970| AESP (ARABIDOPSIS HOMOLOG OF SEPARASE); peptidase	Unigene7561_All//0.00E+00//TC175803				nr +
Unigene75610_All	218	2.88	0.00	1.95	1.37	1.11	0.83	0.19	0.00	1.46	-1.15E+01	7.90E-04	Down	-5.60E-01	5.53E-01		-3.10E-01	8.20E-01		-7.26E-01	6.38E-01		-7.60E+00	6.46E-01		2.91E+00	5.98E-02								
Unigene7562_All	453	0.69	3.36	0.35	1.21	2.28	1.40	2.24	6.18	9.85	2.28E+00	2.68E-04	Up	-9.75E-01	5.05E-01		9.15E-01	1.97E-01		2.07E-01	8.23E-01		1.46E+00	3.05E-05	Up	2.14E+00	4.69E-13	Up			Unigene7562_All//0.00E+00//TC130432				
Unigene7563_All	562	1.58	1.62	0.85	3.46	4.90	3.46	7.97	11.16	19.00	3.62E-02	9.79E-01		-8.92E-01	2.46E-01		5.04E-01	2.04E-01		-5.00E-04	9.95E-01		4.84E-01	2.28E-02		1.25E+00	1.46E-14	Up			Unigene7563_All//0.00E+00//gi|78339734|gb|DT560008.1|DT560008				
Unigene7564_All	645	0.00	1.41	1.16	0.15	0.48	0.35	1.97	1.68	1.05	1.05E+01	2.60E-05	Up	1.02E+01	3.25E-04	Up	1.64E+00	3.21E-01		1.18E+00	5.48E-01		-2.23E-01	6.77E-01		-9.05E-01	7.78E-02								
Unigene7565_All	293	6.25	2.77	1.45	13.77	5.64	3.85	0.43	0.57	0.54	-1.18E+00	1.60E-02		-2.10E+00	2.07E-04	Down	-1.29E+00	7.14E-06	Down	-1.84E+00	1.73E-08	Down	3.98E-01	8.13E-01		3.29E-01	8.50E-01		Unigene7565_All//gi|159025703|emb|CAN88852.1|//2.00E-21//D1-type cyclin [Populus trichocarpa]		Unigene7565_All//3.00E-137//TC140799				nr +
Unigene75665_All	599	0.70	0.51	3.20	0.42	0.12	0.15	0.00	0.00	0.00	-4.62E-01	6.50E-01		2.20E+00	8.20E-05	Up	-1.85E+00	2.75E-01		-1.46E+00	4.06E-01		null	null		null	null		Unigene75665_All//gi|255598719|ref|XP_002537066.1|//3.00E-15//Basal-body rod modification protein flgD, putative [Ricinus communis] >gi|223517601|gb|EEF25315.1| Basal-body rod modification protein flgD, putative [Ricinus communis]						nr -
Unigene75667_All	215	0.00	3.54	2.48	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.75E-04	Up	1.13E+01	4.01E-03		null	null		null	null		null	null		null	null		Unigene75667_All//sp|P09211|GSTP1_HUMAN//8.00E-23//Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2						swissprot -
Unigene7568_All	946	0.22	0.21	0.00	2.53	0.95	0.48	32.85	57.04	2.82	-4.64E-02	9.87E-01		-7.79E+00	1.44E-01		-1.42E+00	3.12E-04	Down	-2.40E+00	3.65E-07	Down	7.96E-01	6.94E-33		-3.54E+00	2.16E-150	Down	Unigene7568_All//gi|9294177|dbj|BAB02079.1|//2.00E-66//nodulin-like protein [Arabidopsis thaliana]	Unigene7568_All//2.00E-45//AT3G25190| nodulin, putative	Unigene7568_All//0.00E+00//gi|109885344|gb|DW514314.1|DW514314				nr -
Unigene75682_All	454	0.00	2.12	1.88	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.37E-05	Up	1.09E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene75682_All//gi|300257426|gb|EFJ41674.1|//4.00E-06//hypothetical protein VOLCADRAFT_119608 [Volvox carteri f. nagariensis]				ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene75692_All	241	0.00	0.63	0.00	0.00	0.00	0.00	6.32	1.91	2.64	9.30E+00	2.32E-01		null	null		null	null		null	null		-1.73E+00	7.56E-04	Down	-1.26E+00	7.68E-03		Unigene75692_All//gi|113734309|dbj|BAF30480.1|//3.00E-22//cytochrome c oxidase subunit Vb [Pisum sativum]	Unigene75692_All//1.00E-16//AT3G15640| cytochrome c oxidase family protein	Unigene75692_All//3.00E-93//gi|21094646|gb|BQ406959.1|BQ406959		ko00190|Oxidative phosphorylation	GO:0009534//GO:0015002//GO:0031967//GO:0046914	nr -
Unigene75699_All	224	0.00	0.00	3.33	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene75699_All//gi|226507767|ref|NP_001147360.1|//1.00E-20//40S ribosomal protein S4 [Zea mays] >gi|195610502|gb|ACG27081.1| 40S ribosomal protein S4 [Zea mays]	Unigene75699_All//8.00E-18//AT5G07090| 40S ribosomal protein S4 (RPS4B)			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0031981	nr -
Unigene75702_All	244	0.00	2.28	12.00	0.00	0.00	0.00	1.56	1.20	0.33	1.12E+01	2.16E-03		1.36E+01	3.52E-16	Up	null	null		null	null		-3.79E-01	7.23E-01		-2.26E+00	6.49E-02		Unigene75702_All//gi|145408581|ref|YP_001152205.1|//1.00E-09//ORF58e [Pinus koraiensis] >gi|145048830|gb|ABP35448.1| ORF58e [Pinus koraiensis]		Unigene75702_All//6.00E-64//gi|109859341|gb|DW488320.1|DW488320			GO:0009536	nr -
Unigene7571_All	322	2.92	1.73	0.50	0.31	1.39	1.12	5.91	1.43	2.23	-7.57E-01	2.86E-01		-2.56E+00	4.40E-03		2.17E+00	1.06E-01		1.86E+00	2.19E-01		-2.05E+00	1.34E-05	Down	-1.41E+00	8.30E-04	Down			Unigene7571_All//2.00E-107//TC162471				
Unigene7572_All	305	136.89	301.69	203.22	158.43	203.90	177.69	116.17	167.18	136.37	1.14E+00	6.29E-82	Up	5.70E-01	8.98E-17		3.64E-01	2.97E-09		1.66E-01	2.96E-02		5.25E-01	2.53E-15		2.31E-01	1.67E-03			Unigene7572_All//2.00E-05//AT1G54290| eukaryotic translation initiation factor SUI1, putative	Unigene7572_All//3.00E-140//TC152001				
Unigene75727_All	229	0.00	3.98	3.95	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.60E-05	Up	1.19E+01	4.70E-05	Up	null	null		null	null		null	null		null	null									
Unigene7573_All	527	0.00	1.06	2.02	1238.08	1519.27	1277.00	39.39	52.34	37.42	1.00E+01	2.16E-03		1.10E+01	6.60E-06	Up	2.95E-01	2.17E-77		4.47E-02	3.61E-02		4.10E-01	8.33E-06		-7.41E-02	5.63E-01		Unigene7573_All//gi|223469635|gb|ACM80158.1|//7.00E-31//trypsin-alpha amylase inhibitor [Jatropha curcas]	Unigene7573_All//2.00E-08//AT5G48485| DIR1 (DEFECTIVE IN INDUCED RESISTANCE 1); lipid binding / lipid transporter	Unigene7573_All//0.00E+00//TC170488				nr -
Unigene75756_All	1002	0.00	0.66	0.69	0.00	0.00	0.00	0.00	0.00	0.00	9.36E+00	6.20E-04	Up	9.43E+00	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene75756_All//gi|224009464|ref|XP_002293690.1|//1.00E-118//eukaryotic translation initiation factor 4A [Thalassiosira pseudonana CCMP1335] >gi|220970362|gb|EED88699.1| eukaryotic translation initiation factor 4A [Thalassiosira pseudonana CCMP1335]	Unigene75756_All//1.00E-106//AT3G13920| EIF4A1 (EUKARYOTIC TRANSLATION INITIATION FACTOR 4A1); ATP-dependent helicase/ translation initiation factor	Unigene75756_All//2.00E-14//DT048646		ko03040|Spliceosome		nr +
Unigene7576_All	549	1.43	1.48	1.26	1.45	2.01	3.04	3.70	0.84	1.16	4.69E-02	9.69E-01		-1.81E-01	8.07E-01		4.67E-01	5.30E-01		1.07E+00	4.03E-02		-2.14E+00	3.19E-06	Down	-1.67E+00	6.85E-05	Down	Unigene7576_All//gi|8778307|gb|AAF79316.1|AC002304_9//1.00E-25//F14J16.15 [Arabidopsis thaliana]	Unigene7576_All//2.00E-16//AT1G55900| TIM50	Unigene7576_All//0.00E+00//gi|78327271|gb|DT547545.1|DT547545				nr -
Unigene7578_All	984	1.12	1.75	0.38	0.35	0.63	0.92	6.57	17.75	7.41	6.49E-01	1.97E-01		-1.56E+00	3.05E-02		8.30E-01	4.15E-01		1.37E+00	7.76E-02		1.43E+00	8.93E-28	Up	1.73E-01	4.01E-01		Unigene7578_All//gi|224053426|ref|XP_002297813.1|//2.00E-55//f-box family protein [Populus trichocarpa] >gi|222845071|gb|EEE82618.1| f-box family protein [Populus trichocarpa]	Unigene7578_All//6.00E-43//AT5G24560| AtPP2-B12 (Phloem protein 2-B12); carbohydrate binding	Unigene7578_All//0.00E+00//TC148176				nr +
Unigene7579_All	590	1.33	1.29	3.07	7.85	6.95	8.80	2.51	3.61	5.20	-4.63E-02	9.66E-01		1.21E+00	1.95E-02		-1.77E-01	5.81E-01		1.65E-01	6.16E-01		5.27E-01	1.94E-01		1.05E+00	7.60E-04	Up	Unigene7579_All//gi|87162908|gb|AB028703.1|//5.00E-35//TIR [Medicago truncatula]	Unigene7579_All//2.00E-30//AT5G36930| disease resistance protein (TIR-NBS-LRR class), putative	Unigene7579_All//3.00E-114//gi|109858933|gb|DW487912.1|DW487912				nr -
Unigene7581_All	257	1.02	0.00	3.94	1.74	4.56	2.11	0.00	0.16	5.43	-9.99E+00	6.66E-02		1.95E+00	1.37E-02		1.38E+00	3.33E-02		2.74E-01	7.82E-01		7.35E+00	6.27E-01		1.24E+01	4.73E-10	Up			Unigene7581_All//6.00E-70//TC151757				
Unigene7582_All	417	0.25	1.09	2.55	3.11	2.97	3.14	0.41	0.50	0.96	2.12E+00	9.58E-02		3.35E+00	3.36E-04	Up	-6.32E-02	9.04E-01		1.62E-02	9.80E-01		3.05E-01	8.35E-01		1.24E+00	2.51E-01		Unigene7582_All//gi|56269839|gb|AAV85474.1|//2.00E-41//myb family transcription factor-related protein [Populus tomentosa]	Unigene7582_All//1.00E-41//AT1G79430| APL (ALTERED PHLOEM DEVELOPMENT); transcription factor/ transcription regulator	Unigene7582_All//1.00E-140//TC132408	G2-like			nr -
Unigene7584_All	799	0.20	0.00	0.67	2.93	1.42	1.30	1.69	0.47	1.50	-7.62E+00	2.14E-01		1.76E+00	1.29E-01		-1.04E+00	8.02E-03		-1.17E+00	5.07E-03		-1.85E+00	9.21E-04	Down	-1.79E-01	7.13E-01		Unigene7584_All//gi|238481123|ref|NP_001154289.1|//8.00E-57//RCE1 (RUB1 CONJUGATING ENZYME 1); NEDD8 ligase/ small conjugating protein ligase [Arabidopsis thaliana] >gi|240256206|ref|NP_568008.4| RCE1 (RUB1 CONJUGATING ENZYME 1); NEDD8 ligase/ small conjugating protein ligase [Arabidopsis thaliana] >gi|297798212|ref|XP_002866990.1| NEDD8-conjugating enzyme Ubc12 [Arabidopsis lyrata subsp. lyrata] >gi|75313330|sp|Q9SDY5.1|RCE1_ARATH RecName: Full=NEDD8-conjugating enzyme Ubc12; AltName: Full=RUB1-conjugating enzyme 1; AltName: Full=RUB1-protein ligase 1; AltName: Full=RUB1 carrier protein 1 >gi|6635457|gb|AAF19827.1|AF202771_1 RUB1 conjugating enzyme [Arabidopsis thaliana] >gi|15081636|gb|AAK82473.1| AT4g36800/CTA10_560 [Arabidopsis thaliana] >gi|20453317|gb|AAM19897.1| AT4g36800/CTA10_560 [Arabidopsis thaliana] >gi|297312826|gb|EFH43249.1|	Unigene7584_All//9.00E-59//AT4G36800| RCE1 (RUB1 CONJUGATING ENZYME 1); NEDD8 ligase/ small conjugating protein ligase	Unigene7584_All//3.00E-71//TC144970		ko04120|Ubiquitin mediated proteolysis		nr -
Unigene7585_All	612	52.75	98.52	106.94	17.50	27.96	21.47	0.35	0.14	0.33	9.01E-01	7.62E-37		1.02E+00	1.89E-47	Up	6.76E-01	6.71E-08		2.95E-01	7.22E-02		-1.34E+00	4.29E-01		-8.56E-02	9.60E-01		Unigene7585_All//gi|60099458|dbj|BAD89968.1|//5.00E-33//phototropin [Phaseolus vulgaris]	Unigene7585_All//7.00E-30//AT5G58140| PHOT2 (PHOTOTROPIN 2); FMN binding / blue light photoreceptor/ kinase/ protein serine/threonine kinase	Unigene7585_All//0.00E+00//TC139009				nr +
Unigene7586_All	648	5.57	5.32	6.82	0.46	2.87	1.74	0.00	0.00	0.00	-6.73E-02	8.35E-01		2.92E-01	3.65E-01		2.64E+00	2.39E-06	Up	1.92E+00	6.72E-03		null	null		null	null		Unigene7586_All//gi|60099458|dbj|BAD89968.1|//2.00E-27//phototropin [Phaseolus vulgaris]	Unigene7586_All//6.00E-24//AT5G58140| PHOT2 (PHOTOTROPIN 2); FMN binding / blue light photoreceptor/ kinase/ protein serine/threonine kinase	Unigene7586_All//0.00E+00//TC139009				nr +
Unigene7588_All	1281	0.49	1.23	0.21	0.04	0.05	0.35	7.86	15.07	28.24	1.32E+00	1.50E-02		-1.24E+00	2.13E-01		4.68E-01	9.54E-01		3.18E+00	3.78E-02		9.40E-01	4.82E-16		1.85E+00	7.29E-83	Up	Unigene7588_All//gi|297829432|ref|XP_002882598.1|//1.00E-114//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328438|gb|EFH58857.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7588_All//6.00E-109//AT3G09010| protein kinase family protein	Unigene7588_All//0.00E+00//DT464039		ko04626|Plant-pathogen interaction		nr +
Unigene7592_All	609	4.47	4.83	11.98	1.80	9.73	3.41	0.21	0.89	0.26	1.11E-01	7.56E-01		1.42E+00	2.05E-09	Up	2.43E+00	5.42E-18	Up	9.23E-01	4.23E-02		2.10E+00	3.71E-02		3.29E-01	8.50E-01		Unigene7592_All//gi|125550682|gb|EAY96391.1|//1.00E-06//hypothetical protein OsI_18290 [Oryza sativa Indica Group]		Unigene7592_All//6.00E-23//FL577736				nr +
Unigene7593_All	1423	0.07	0.00	0.00	0.21	0.07	0.22	6.54	1.88	3.86	-6.20E+00	3.67E-01		-6.20E+00	3.87E-01		-1.53E+00	2.98E-01		8.15E-02	9.49E-01		-1.80E+00	9.52E-21	Down	-7.59E-01	3.94E-06		Unigene7593_All//gi|224053889|ref|XP_002298030.1|//1.00E-26//predicted protein [Populus trichocarpa] >gi|222845288|gb|EEE82835.1| predicted protein [Populus trichocarpa]	Unigene7593_All//6.00E-17//AT1G63670| unknown protein					nr -
Unigene7594_All	539	56.98	49.17	104.03	10.54	9.20	4.69	0.00	0.08	0.22	-2.13E-01	3.65E-02		8.69E-01	3.02E-31		-1.96E-01	4.93E-01		-1.17E+00	2.83E-06	Down	6.28E+00	6.27E-01		7.79E+00	2.42E-01		Unigene7594_All//gi|110348215|gb|ABG72805.1|//2.00E-31//phytoene synthase protein [Carica papaya]	Unigene7594_All//1.00E-28//AT5G17230| phytoene synthase (PSY) / geranylgeranyl-diphosphate geranylgeranyl transferase	Unigene7594_All//3.00E-154//gi|164515863|gb|ES841106.1|ES841106		ko00906|Carotenoid biosynthesis		nr +
Unigene75941_All	349	0.15	11.03	2.29	1.14	7.30	5.95	0.00	0.48	3.08	6.20E+00	2.32E-20	Up	3.93E+00	1.25E-03		2.68E+00	1.04E-08	Up	2.38E+00	4.55E-06	Up	8.90E+00	1.38E-01		1.16E+01	8.30E-08	Up	Unigene75941_All//gi|224146425|ref|XP_002326003.1|//8.00E-24//sucrose proton symporter [Populus trichocarpa] >gi|222862878|gb|EEF00385.1| sucrose proton symporter [Populus trichocarpa]	Unigene75941_All//1.00E-22//AT1G22710| SUC2 (SUCROSE-PROTON SYMPORTER 2); carbohydrate transmembrane transporter/ sucrose transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen symporter	Unigene75941_All//2.00E-92//gi|78323853|gb|DT544127.1|DT544127			GO:0005351//GO:0015154//GO:0015766//GO:0016021	nr +

Unigene75945_All	309	1.35	2.79	2.07	0.81	0.56	0.58	1.64	5.55	0.13	1.04E+00	1.72E-01		6.10E-01	5.09E-01		-5.33E-01	7.12E-01		-4.64E-01	7.44E-01		1.76E+00	2.63E-04	Up	-3.67E+00	3.75E-03				Unigene75945_All//4.00E-99//gi|109832615|gb|DW231174.1|DW231174					
Unigene7595_All	563	0.19	1.08	0.00	1.68	1.35	0.96	3.98	1.34	15.64	2.54E+00	2.46E-02		-7.54E+00	3.87E-01		-3.21E-01	6.38E-01		-8.04E-01	2.77E-01		-1.57E+00	9.33E-05	Down	1.97E+00	1.17E-22	Up	Unigene7595_All//gi|224130624|ref|XP_002320887.1|//5.00E-68//cytochrome P450 [Populus trichocarpa] >gi|222861660|gb|EEE99202.1|cytochrome P450 [Populus trichocarpa]	Unigene7595_All//2.00E-49//AT2G46660| CYP78A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene7595_All//0.00E+00//gi|78339202|gb|DT559476.1|DT559476		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis		nr +
Unigene7596_All	512	1.43	0.40	4.68	3.50	4.30	1.94	1.24	0.98	0.78	-1.85E+00	4.08E-02		1.71E+00	2.01E-04	Up	2.97E-01	5.67E-01		-8.52E-01	8.34E-02		-3.39E-01	6.63E-01		-6.71E-01	3.86E-01										
Unigene7597_All	730	3.08	0.14	2.70	2.52	2.22	1.48	1.22	0.52	0.55	-4.47E+00	1.29E-10	Down	-1.91E-01	6.53E-01		-1.88E-01	7.20E-01		-7.66E-01	1.18E-01		-1.24E+00	6.79E-02		-1.16E+00	7.15E-02										
Unigene7598_All	658	0.64	0.23	0.32	0.76	0.84	0.55	1.86	4.26	0.36	-1.46E+00	2.34E-01		-9.75E-01	4.11E-01		1.45E-01	9.05E-01		-4.63E-01	6.59E-01		1.19E+00	4.80E-04	Up	-2.36E+00	1.22E-04	Down	Unigene7598_All//gi|34850945|dbj|BAC87845.1|//3.00E-57//leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	Unigene7598_All//4.00E-47//AT1G35710| leucine-rich repeat transmembrane protein kinase, putative	Unigene7598_All//0.00E+00//TC170852		ko03410|Base excision repair		nr +
Unigene75986_All	327	0.00	0.00	2.44	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene75986_All//gi|21665866|emb|CAD37200.1|//1.00E-40//GDA2 protein [Pisum sativum]	Unigene75986_All//2.00E-39//AT3G27090| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Development and cell death domain (InterPro:IPR013989), Kelch related (InterPro:IPR013089); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G42050.1); Has 642 Blast hits to 564 proteins in 35 species: Archae - 0; Bacteria - 2; Metazoa - 12; Fungi - 0; Plants - 155; Viruses - 0; Other Eukaryotes - 473 (source: NCBI BLink).	Unigene75986_All//2.00E-30//gi|48791097|gb|CO092411.1|CO092411				nr +
Unigene7599_All	724	2.17	6.30	4.93	2.82	3.38	2.12	5.55	2.94	1.32	1.54E+00	4.14E-07	Up	1.18E+00	6.20E-04	Up	2.60E-01	5.83E-01		-4.12E-01	3.91E-01		-9.14E-01	7.76E-04		-2.07E+00	1.45E-11	Down			Unigene7599_All//8.00E-143//TC178975					
Unigene76_All	2709	1.80	1.10	1.55	6.69	4.74	2.50	2.98	0.77	1.32	-7.03E-01	9.76E-03		-2.10E-01	4.87E-01		-4.97E-01	3.48E-05		-1.42E+00	3.81E-25	Down	-1.95E+00	3.96E-20	Down	-1.17E+00	2.79E-10	Down	Unigene76_All//gi|162958329|dbj|BAF95588.1|//1.00E-102//AtNEK6 [Arabidopsis thaliana]	Unigene76_All//1.00E-94//AT3G44200| NEK6 ("NIMA (NEVER IN MITOSIS, GENE A)-RELATED 6"); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene76_All//0.00E+00//TC160369				nr +
Unigene7601_All	1173	0.22	0.39	0.09	0.13	0.41	0.27	1.59	3.56	4.14	8.02E-01	4.60E-01		-1.30E+00	4.36E-01		1.69E+00	1.66E-01		1.08E+00	4.75E-01		1.17E+00	1.70E-05	Up	1.39E+00	3.86E-08	Up	Unigene7601_All//gi|16648773|gb|AAL25577.1|//1.00E-32//At1g68440/T2E12_1 [Arabidopsis thaliana] >gi|21700823|gb|AAM70535.1|At1g68440/T2E12_1 [Arabidopsis thaliana]	Unigene7601_All//9.00E-26//AT1G68440| unknown protein	Unigene7601_All//3.00E-17//gi|164252644|gb|ES830191.1|ES830191				nr -
Unigene76012_All	223	0.23	5.45	0.72	1.34	1.08	1.82	0.00	0.75	1.07	4.54E+00	6.47E-06	Up	1.61E+00	5.10E-01		-3.10E-01	8.20E-01		4.44E-01	7.01E-01		9.55E+00	1.38E-01		1.01E+01	4.39E-02										
Unigene76017_All	270	0.00	3.75	1.38	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.21E-06	Up	1.04E+01	2.48E-02		null	null		null	null		null	null		null	null		Unigene76017_All//sp|P47179|DAN4_YEAST//2.00E-10//Cell wall protein DAN4 OS=Saccharomyces cerevisiae GN=DAN4 PE=2 SV=1						swissprot -
Unigene7603_All	590	31.13	16.15	26.81	1.94	1.11	0.15	0.14	0.00	0.88	-9.47E-01	9.61E-13		-2.16E-01	1.38E-01		-8.08E-01	1.92E-01		-3.66E+00	2.69E-05	Down	-7.16E+00	3.99E-01		2.61E+00	1.55E-02		Unigene7603_All//gi|297826393|ref|XP_002881079.1|//1.00E-92//NDA2 H dehydrogenase 2 [Arabidopsis lyrata subsp. lyrata] >gi|297326918|gb|EFH57338.1| NDA2 H dehydrogenase 2 [Arabidopsis lyrata subsp. lyrata]	Unigene7603_All//1.00E-93//AT2G29990| NDA2 (ALTERNATIVE NADPH DEHYDROGENASE 2); FAD binding / NADH dehydrogenase/ oxidoreductase	Unigene7603_All//2.00E-152//CO099390		ko00190|Oxidative phosphorylation		nr -
Unigene76041_All	439	0.00	0.35	2.06	0.11	0.16	0.51	0.00	0.00	0.00	8.44E+00	2.32E-01		1.10E+01	4.70E-05	Up	4.67E-01	9.54E-01		2.18E+00	3.22E-01		null	null		null	null		Unigene76041_All//sp|P44442|RND_HAEIN//4.00E-06//Ribonuclease D OS=Haemophilus influenzae GN=rnd PE=3 SV=1						swissprot +
Unigene76045_All	329	1.43	0.00	0.65	2.42	0.73	0.00	0.90	0.13	0.00	-1.05E+01	5.53E-03		-1.14E+00	3.32E-01		-1.73E+00	2.86E-02		-1.12E+01	4.90E-05	Down	-2.82E+00	8.84E-02		-9.81E+00	1.58E-02		Unigene76045_All//gi|15223991|ref|NP_172953.1|//4.00E-22//scp150 (serine carboxypeptidase-like 50); serine-type carboxypeptidase [Arabidopsis thaliana] >gi|75336113|sp|Q9M9Q6.1|SCP50_ARATH RecName: Full=Serine carboxypeptidase-like 50; Flags: Precursor >gi|6899645|gb|AAF31022.1|AC012189_4 Contains similarity to serine-type carboxypeptidase like protein from Arabidopsis thaliana gi|4678929 and contains two Serine carboxypeptidase domains PF|00450 >gi|19715607|gb|AAL91626.1|At1g15000/T15D22_7 [Arabidopsis thaliana] >gi|27363234|gb|AAO11536.1|At1g15000/T15D22_7 [Arabidopsis thaliana]	Unigene76045_All//2.00E-23//AT1G15000| scp150 (serine carboxypeptidase-like 50); serine-type carboxypeptidase			ko00940|Phenylpropanoid biosynthesis	GO:0004180//GO:0019538//GO:0031410//GO:0043231	nr +
Unigene76053_All	542	0.00	0.00	0.10	0.00	0.06	0.00	1.01	0.08	0.00	null	null		6.62E+00	6.25E-01		5.99E+00	8.17E-01		null	null		-3.72E+00	3.23E-03		-9.99E+00	2.80E-04	Down	Unigene76053_All//gi|297848900|ref|XP_002892331.1|//2.00E-52//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297338173|gb|EFH68590.1|pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene76053_All//4.00E-44//AT1G06270| pentatricopeptide (PPR) repeat-containing protein	Unigene76053_All//0.00E+00//DR457371				nr +
Unigene76054_All	248	0.00	0.00	0.43	2.61	2.22	1.27	17.39	16.35	3.05	null	null		8.75E+00	3.90E-01		-2.33E-01	8.06E-01		-1.03E+00	2.68E-01		-8.91E-02	7.55E-01		-2.51E+00	2.12E-15	Down	Unigene76054_All//gi|14030611|gb|AAS32980.1|AF375396.1|//6.00E-16//AT3g25190/MJL12_14 [Arabidopsis thaliana] >gi|17978889|gb|AAL47414.1|AT3g25190/MJL12_14 [Arabidopsis thaliana]		Unigene76054_All//2.00E-57//gi|109868191|gb|DW497167.1|DW497167			GO:0044464	nr +
Unigene76057_All	447	5.03	0.57	0.60	4.90	5.55	4.34	0.19	0.75	0.18	-3.15E+00	2.80E-08	Down	-3.08E+00	1.13E-07	Down	1.78E-01	7.14E-01		-1.75E-01	6.88E-01		1.98E+00	1.44E-01		-8.64E-02	9.69E-01										ESTscan +
Unigene7606_All	332	47.91	25.79	48.92	61.52	64.51	51.97	67.24	35.50	33.36	-8.93E-01	3.54E-10		3.01E-02	8.49E-01		6.86E-02	6.35E-01		-2.44E-01	5.87E-02		-9.22E-01	7.38E-18		-1.01E+00	2.42E-21	Down	Unigene7606_All//gi|211906520|gb|AC111753.1|//1.00E-31//UDP-D-apiose/UPD-D-xylose synthetase [Gossypium hirsutum]	Unigene7606_All//2.00E-28//AT1G08200| AXS2 (UDP-D-APIOSE/UDP-D-XYLOSE SYNTHASE 2); UDP-glucuronate decarboxylase	Unigene7606_All//5.00E-145//gi|78327354|gb|DT547628.1|DT547628		ko00520|Amino sugar and nucleotide sugar metabolism		nr -
Unigene7608_All	1100	0.05	0.00	0.00	3.53	2.22	1.60	4.50	0.46	1.38	-5.57E+00	6.04E-01		-5.57E+00	6.15E-01		-6.68E-01	2.36E-02		-1.14E+00	2.23E-04	Down	-3.30E+00	2.97E-22	Down	-1.71E+00	4.91E-11	Down	Unigene7608_All//gi|15226456|ref|NP_182212.1|//1.00E-147//oxidoreductase, acting on the CH-CH group of donors [Arabidopsis thaliana] >gi|66550695|gb|AAV97801.1|At2g46890 [Arabidopsis thaliana]	Unigene7608_All//4.00E-139//AT2G46890| oxidoreductase, acting on the CH-CH group of donors	Unigene7608_All//0.00E+00//DR459624				nr -
Unigene7609_All	719	0.95	1.06	0.00	1.52	2.16	1.19	0.71	1.05	2.22	1.60E-01	8.28E-01		-9.89E+00	7.63E-04	Down	5.00E-01	3.86E-01		-3.53E-01	6.35E-01		5.68E-01	4.47E-01		1.65E+00	6.43E-04	Up	Unigene7609_All//gi|18379277|ref|NP_565274.1|//1.00E-93//ankyrin repeat family protein [Arabidopsis thaliana] >gi|75315914|sp|Q9ZU96.1|Y2168_ARATH RecName: Full=Ankyrin repeat-containing protein At2g01680 >gi|4220480|gb|AAD12703.1|expressed protein [Arabidopsis thaliana]	Unigene7609_All//6.00E-95//AT2G01680| ankyrin repeat family protein	Unigene7609_All//1.00E-73//TC171065				nr -
Unigene7610_All	572	1.74	0.18	0.56	1.65	2.71	1.11	1.85	0.80	2.02	-3.29E+00	3.81E-04	Down	-1.64E+00	3.43E-02		7.11E-01	1.98E-01		-5.82E-01	4.37E-01		-1.20E+00	4.78E-02		1.28E-01	8.11E-01		Unigene7610_All//gi|18407090|ref|NP_566076.1|//1.00E-45//phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana] >gi|42571253|ref|NP_973700.1|phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein [Arabidopsis thaliana] >gi|16930425|gb|AAL31898.1|AF419566_1 At2g46500/F11C10.19 [Arabidopsis thaliana] >gi|4415831|gb|AAD20161.1|expressed protein [Arabidopsis thaliana] >gi|20197828|gb|AAM15268.1|expressed protein [Arabidopsis thaliana] >gi|27363382|gb|AAO11610.1|At2g46500/F11C10.19 [Arabidopsis thaliana]	Unigene7610_All//2.00E-47//AT2G46500| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	Unigene7610_All//0.00E+00//gi|54116329|gb|CO491838.1|CO491838				nr +
Unigene76102_All	222	0.00	4.11	2.16	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.60E-05	Up	1.11E+01	7.43E-03		null	null		null	null		null	null		null	null										
Unigene7611_All	899	0.35	0.00	0.24	14.46	10.38	10.20	4.47	0.23	0.71	-8.45E+00	3.63E-02		-5.60E-01	6.63E-01		-4.78E-01	1.11E-03		-5.04E-01	1.04E-03		-4.26E+00	4.50E-22	Down	-2.66E+00	2.78E-15	Down	Unigene7611_All//gi|297844266|ref|XP_002890014.1|//3.00E-97//methyladenine glycosylase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338856|gb|EFH66273.1|methyladenine glycosylase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7611_All//6.00E-85//AT1G13635| methyladenine glycosylase family protein	Unigene7611_All//4.00E-120//TC175754		ko03410|Base excision repair		nr -
Unigene76116_All	489	0.00	0.93	5.01	0.00	0.00	0.00	0.00	0.00	0.00	9.87E+00	7.35E-03		1.23E+01	1.64E-13	Up	null	null		null	null		null	null		null	null		Unigene76116_All//sp|P01857|IGHG1_HUMAN//1.00E-63//Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1 SV=1						swissprot -

Unigene7612_All	1227	0.00	0.00	0.00	3.86	1.74	1.36	2.17	0.10	0.03	null	null		null	null		-1.15E+00	9.48E-06	Down	-1.50E+00	1.49E-07	Down	-4.41E+00	4.29E-15	Down	-6.06E+00	4.32E-18	Down	Unigene7612_All//gi|297844266|ref|XP_002890014.1|//1.00E-106//methyladenine glycosylase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297335856|gb|EFH66273.1| methyladenine glycosylase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7612_All//2.00E-95//AT1G13635| methyladenine glycosylase family protein	Unigene7612_All//0.00E+00//TC175754		ko03410|Base excision repair		nr +
Unigene7614_All	2557	0.00	0.04	0.00	0.10	0.13	0.32	4.66	14.19	8.41	5.31E+00	3.81E-01		null	null		4.68E-01	7.79E-01		1.71E+00	4.57E-02		1.61E+00	4.72E-67	Up	8.51E-01	1.46E-15		Unigene7614_All//gi|42741727|gb|AAS45124.1|//0.00E+00//WAK-like kinase [Solanum lycopersicum]	Unigene7614_All//9.00E-176//AT2G23450| protein kinase family protein	Unigene7614_All//0.00E+00//TC179459		ko04626|Plant-pathogen interaction		nr +
Unigene76146_All	213	0.00	3.09	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.20E-04	Up	9.97E+00	1.38E-01		null	null		null	null		null	null		null	null		Unigene76146_All//sp|Q33UJ8|CH10_SHISS/3.00E-14//10 kDa chaperonin OS=Shigella sonnei (strain Ss046) GN=groS PE=3 SV=1						swissprot +
Unigene7615_All	608	192.50	25.33	45.81	41.38	37.49	20.28	0.00	0.00	0.00	-2.93E+00	0.00E+00	Down	-2.07E+00	4.80E-242	Down	-1.42E-01	2.42E-01		-1.03E+00	5.07E-21	Down	null	null		null	null		Unigene7615_All//gi|15220512|ref|NP_174259.1|//8.00E-70//GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] >gi|75169353|sp|Q9CTN5.1|GDL14_ARATH RecName: Full=GDSL esterase/lipase At1g29660; AltName: Full=Extracellular lipase At1g29660; Flags: Precursor >gi|15215768|gb|AAK91429.1| At1g29660/F15D2_21 [Arabidopsis thaliana] >gi|221370090|gb|AAM91390.1| At1g29660/F15D2_21 [Arabidopsis thaliana]	Unigene7615_All//2.00E-68//AT1G29660| GDSL-motif lipase/hydrolase family protein	Unigene7615_All//0.00E+00//gi|5048388|gb|AI729536.1|AI729536				nr -
Unigene7616_All	512	1.53	1.19	0.10	3.21	2.35	0.35	1.40	2.12	0.54	-3.68E-01	6.23E-01		-3.88E+00	1.59E-03		-4.48E-01	3.94E-01		-3.19E+00	1.23E-06	Down	5.96E-01	3.28E-01		-1.37E+00	6.50E-02					Unigene7616_All//6.00E-07//FL577052				
Unigene76165_All	220	0.00	0.00	4.60	1.81	1.88	1.03	0.58	0.19	0.91	null	null		1.22E+01	1.27E-05	Up	5.23E-02	9.89E-01		-8.20E-01	5.06E-01		-1.60E+00	5.32E-01		6.51E-01	6.65E-01									
Unigene7617_All	458	2.40	1.11	1.63	4.46	1.58	1.68	2.49	2.28	3.31	-1.12E+00	8.94E-02		-5.60E-01	3.93E-01		-1.50E+00	5.63E-04	Down	-1.41E+00	2.19E-03		-1.28E-01	8.22E-01		4.07E-01	3.97E-01		Unigene7617_All//gi|115436784|ref|NP_001043135.1|//1.00E-10//Os01g0502400 [Oryza sativa Japonica Group] >gi|56201538|dbj|BAD73185.1| oxidoreductase, 2OG-Fe(II) oxygenase-like protein [Oryza sativa Japonica Group] >gi|56201807|dbj|BAD73257.1| oxidoreductase, 2OG-Fe(II) oxygenase-like protein [Oryza sativa Japonica Group] >gi|113532666|dbj|BAF05049.1| Os01g0502400 [Oryza sativa Japonica Group]	Unigene7617_All//6.00E-69//AT1G22950| iron ion binding / oxidoreductase/ oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene7617_All//1.00E-69//TC144901				nr +
Unigene76170_All	397	0.00	3.70	2.55	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.10E-08	Up	1.13E+01	1.27E-05	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene7618_All	565	0.83	1.26	0.94	4.14	2.74	1.44	2.54	1.11	2.47	5.91E-01	4.78E-01		1.78E-01	8.45E-01		-5.95E-01	1.48E-01		-1.53E+00	3.76E-04	Down	-1.20E+00	1.76E-02		-4.40E-02	9.44E-01					Unigene7618_All//2.00E-84//ES844237				
Unigene76182_All	454	0.23	0.33	2.46	0.22	0.15	0.10	0.00	0.00	0.00	5.39E-01	7.78E-01		3.42E+00	1.92E-04	Up	-5.32E-01	8.13E-01		-1.14E+00	6.74E-01		null	null		null	null		Unigene76182_All//sp|P0A8R4|YBAK_SHIFL/3.00E-13//Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase ybaK OS=Shigella flexneri GN=ybaK PE=3 SV=1						swissprot -
Unigene76192_All	325	0.00	7.02	3.44	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	5.62E-13	Up	1.17E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene76192_All//sp|P31727|CYTA_SARPE/3.00E-07//Sarcocystatin-A OS=Sarcophaga peregrina PE=1 SV=1						swissprot +
Unigene76195_All	247	15.04	18.67	7.76	18.76	19.38	30.72	103.56	67.69	31.29	3.12E-01	2.89E-01		-9.54E-01	4.25E-03		4.71E-02	8.90E-01		7.12E-01	6.52E-04		-6.14E-01	1.85E-10		-1.73E+00	2.50E-54	Down		Unigene76195_All//1.00E-06//AT1G27400| 60S ribosomal protein L17 (RPL17A)	Unigene76195_All//4.00E-136//TC149006		ko03010|Ribosome		kegg -
Unigene7620_All	344	56.73	32.40	30.49	104.99	95.10	89.15	109.39	54.92	51.42	-8.08E-01	1.70E-10		-8.96E-01	8.32E-12		-1.43E-01	1.43E-01		-2.36E-01	9.93E-03		-9.94E-01	2.06E-33		-1.09E+00	8.36E-40	Down	Unigene7620_All//gi|4206124|gb|AAD11431.1|//2.00E-54//T-complex protein 1 epsilon subunit [Mesembryanthemum crystallinum]	Unigene7620_All//2.00E-55//AT1G24510| T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative	Unigene7620_All//0.00E+00//gi|5044527|gb|AI725675.1|AI725675				nr -
Unigene7621_All	1350	0.00	0.00	0.00	0.00	0.00	0.00	2.44	1.61	7.11	null	null		null	null		null	null		null	null		-6.02E-01	4.98E-02		1.54E+00	1.01E-17	Up	Unigene7621_All//gi|9794868|gb|AAF98368.1|AF158027_1//1.00E-100//patatin-like protein 1 [Nicotiana tabacum]	Unigene7621_All//7.00E-98//AT4G37070| patatin, putative	Unigene7621_All//4.00E-32//TC129599				nr -
Unigene76213_All	321	2.93	15.31	10.29	0.00	0.00	0.00	0.00	0.00	0.00	2.38E+00	5.63E-13	Up	1.81E+00	3.06E-06	Up	null	null		null	null		null	null		null	null		Unigene76213_All//gi|115447359|ref|NP_001047459.1|//3.00E-15//Os02g0621300 [Oryza sativa Japonica Group] >gi|113536990|dbj|BAF09373.1| Os02g0621300 [Oryza sativa Japonica Group]	Unigene76213_All//8.00E-14//AT1G02205| CER1 (ECERIFERUM 1); octadecanal decarbonylase	Unigene76213_All//6.00E-120//ES833625			GO:0003676//GO:0044237//GO:0044238//GO:0044464	nr -
Unigene7623_All	275	79.53	125.11	101.27	14.67	15.40	12.15	15.53	20.97	7.24	6.54E-01	1.42E-12		3.49E-01	1.16E-03		7.00E-02	8.34E-01		-2.72E-01	4.20E-01		4.34E-01	5.47E-02		-1.10E+00	2.25E-05	Down			Unigene7623_All//1.00E-136//TC137840				
Unigene76249_All	244	0.00	0.00	2.84	0.00	0.00	0.74	0.00	0.00	0.00	null	null		1.15E+01	6.12E-04	Up	null	null		9.53E+00	1.93E-01		null	null		null	null		Unigene76249_All//COG0183//5.00E-08//Acetyl-CoA acetyltransferase						cog -
Unigene7625_All	264	0.59	6.91	0.40	2.08	7.96	1.88	3.20	1.58	2.26	3.54E+00	2.15E-07	Up	-5.60E-01	7.74E-01		1.94E+00	4.07E-05	Up	-1.41E-01	8.85E-01		-1.02E+00	1.41E-01		-5.01E-01	4.47E-01									
Unigene76266_All	399	0.00	1.02	2.54	0.00	0.35	0.34	0.00	0.00	0.00	9.99E+00	1.34E-02		1.13E+01	1.27E-05	Up	8.43E+00	3.17E-01		8.41E+00	3.09E-01		null	null		null	null		Unigene76266_All//sp|O79438|NU6M_RABIT//8.00E-37//NADH-ubiquinone oxidoreductase chain 6 OS=Oryctolagus cuniculus GN=MT-ND6 PE=3 SV=1						swissprot +
Unigene7627_All	1396	0.00	13.47	6.87	0.07	0.00	0.00	0.00	0.00	0.00	1.37E+01	4.07E-108	Up	1.27E+01	9.27E-54	Up	-6.16E+00	3.09E-01		-6.16E+00	3.94E-01		null	null		null	null		Unigene7627_All//sp|Q9V496|APLP_DROME//5.00E-103//Apolipophorins OS=Drosophila melanogaster GN=RFabg PE=1 SV=2						swissprot +
Unigene76273_All	452	0.00	4.60	4.59	0.00	0.30	0.00	0.00	0.00	0.00	1.22E+01	7.93E-12	Up	1.22E+01	1.92E-11	Up	8.25E+00	3.17E-01		null	null		null	null		null	null		Unigene76273_All//gi|226509046|ref|NP_001151268.1|//4.00E-13//LOC100284901 [Zea mays] >gi|195609716|gb|ACG26688.1| 60S ribosomal protein L28 [Zea mays] >gi|195610086|gb|ACG26873.1| 60S ribosomal protein L28 [Zea mays] >gi|195645410|gb|ACG42173.1| 60S ribosomal protein L28 [Zea mays] >gi|195646860|gb|ACG42898.1| 60S ribosomal protein L28 [Zea mays]	Unigene76273_All//4.00E-11//AT2G19730| 60S ribosomal protein L28 (RPL28A)			ko03010|Ribosome		nr -
Unigene7628_All	460	0.23	1.32	1.16	1.41	0.75	1.47	0.92	6.09	1.65	2.54E+00	2.46E-02		2.35E+00	5.86E-02		-9.11E-01	3.04E-01		6.50E-02	9.49E-01		2.73E+00	9.78E-11	Up	8.40E-01	2.38E-01				Unigene7628_All//0.00E+00//gi|78325999|gb|DT546273.1|DT546273				
Unigene7629_All	229	99.62	36.07	42.32	134.43	147.21	168.23	242.97	95.64	122.65	-1.47E+00	1.49E-30	Down	-1.24E+00	1.01E-22	Down	1.31E-01	2.12E-01		3.24E-01	1.41E-04		-1.35E+00	5.23E-79	Down	-9.86E-01	8.90E-50		Unigene7629_All//gi|226502084|ref|NP_001147139.1|//6.00E-33//60S ribosomal protein L7a [Zea mays] >gi|195607614|gb|ACG25637.1| 60S ribosomal protein L7a [Zea mays]	Unigene7629_All//3.00E-29//AT2G47610| 60S ribosomal protein L7A (RPL7aA)	Unigene7629_All//4.00E-123//TC130022		ko03010|Ribosome		nr +
Unigene76299_All	215	0.00	3.06	3.22	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.20E-04	Up	1.17E+01	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene76299_All//sp|Q6P97B|TBB2C_RAT//1.00E-07//Tubulin beta-2C chain OS=Rattus norvegicus GN=Tubb2c PE=1 SV=1				ko04145|Phagosome		swissprot +
Unigene763_All	2647	4.94	3.64	2.33	10.63	11.67	7.11	11.02	1.63	4.68	-4.42E-01	4.69E-03		-1.08E+00	7.06E-11	Down	1.34E-01	2.24E-01		-5.80E-01	4.54E-09		-2.76E+00	1.72E-107	Down	-1.24E+00	8.19E-38	Down	Unigene763_All//gi|15242132|ref|NP_199973.1|//0.00E+00//PLE (PLEIADE); microtubule binding [Arabidopsis thaliana] >gi|75262488|sp|Q9FGM4.1|MA653_ARATH RecName: Full=65-kDa microtubule-associated protein 3; Short=AtMAP65-3; AltName: Full=Protein PLEIADE	Unigene763_All//0.00E+00//AT5G51600| PLE (PLEIADE); microtubule binding	Unigene763_All//0.00E+00//TC150077			GO:0005881//GO:0015631//GO:0031109//GO:0048285//GO:0051707//GO:0052093	nr +
Unigene7631_All	275	6.28	3.69	2.32	13.59	8.51	4.76	7.99	5.17	3.48	-7.69E-01	1.21E-01		-1.43E+00	8.20E-03		-6.74E-01	2.59E-02		-1.51E+00	3.73E-06	Down	-6.30E-01	1.07E-01		-1.20E+00	1.56E-03				Unigene7631_All//2.00E-23//BQ405261				
Unigene76314_All	495	1.90	0.00	1.18	1.91	0.35	0.00	0.00	0.00	0.00	-1.09E+01	1.46E-05	Down	-6.85E-01	3.69E-01		-2.46E+00	1.25E-03		-1.09E+01	6.01E-06	Down	null	null		null	null								
Unigene76317_All	655	0.08	0.08	0.33	1.06	0.37	0.62	1.10	0.06	0.36	-4.59E-02	9.83E-01		2.03E+00	3.60E-01		-1.53E+00	7.01E-02		-7.79E-01	3.93E-01		-4.10E+00	2.91E-04	Down	-1.59E+00	3.62E-02		Unigene76317_All//gi|224115548|ref|XP_002317062.1|//2.00E-99//microtubule organization protein [Populus trichocarpa] >gi|222860127|gb|EEE97674.1| microtubule organization protein [Populus trichocarpa]	Unigene76317_All//2.00E-92//AT2G35630| MOR1 (MICROTUBULE ORGANIZATION 1); microtubule binding	Unigene76317_All//0.00E+00//TC160119			GO:0000919//GO:0015031//GO:0015630//GO:0015631//GO:0044444	nr +
Unigene7632_All	637	4.11	2.07	4.01	1.02	0.81	0.92	1.26	0.00	2.38	-9.90E-01	1.16E-02		-3.35E-02	9.49E-01		-3.26E-01	7.10E-01		-1.41E-01	8.73E-01		-1.03E+01	8.57E-06	Down	9.14E-01	5.00E-02		Unigene7632_All//gi|264664531|sp|Q8LGG8.1|Y5343_ARATH//5.00E-51//RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g53430; Flags: Precursor >gi|224589438|gb|ACN59253.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene7632_All//2.00E-42//AT1G53430| leucine-rich repeat family protein / protein kinase family protein	Unigene7632_All//6.00E-97//TC144376		ko04626|Plant-pathogen interaction		nr +
Unigene7633_All	247	0.00	0.82	1.72	33.08	10.60	6.03	5.65	1.35	0.81	9.68E+00	1.35E-01		1.08E+01	1.37E-02		-1.64E+00	3.34E-16	Down	-2.45E+00	8.14E-24	Down	-2.06E+00	2.51E-04	Down	-2.81E+00	4.25E-06	Down			Unigene7633_All//3.00E-07//TC143852				
Unigene7634_All	394	1.46	3.09	4.19	12.01	6.90	6.19	0.97	1.80	3.94	1.08E+00	8.15E-02		1.52E+00	6.71E-03		-7.99E-01	2.01E-03		-9.56E-01	4.65E-04		9.01E-01	2.40E-01		2.03E+00	8.65E-05	Up			Unigene7634_All//2.00E-67//TC144002				
Unigene76349_All	345	0.00	0.00	3.55	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	9.10E-02	Up	null	null		null	null		null	null		null	null									
Unigene7636_All	430	0.73	2.12	1.11	1.74	1.28	1.47	2.26	0.00	1.76	1.54E+00	4.51E-02		6.10E-01	5.86E-01		-4.40E-01	5.85E-01		-2.41E-01	7.55E-01		-1.11E+01	5.83E-07	Down	-3.62E-01	5.65E-01		Unigene7636_All//gi|297811705|ref|XP_002873736.1|//2.00E-34//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297319573|gb|EFH49995.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene7636_All//1.00E-35//AT5G15680| binding	Unigene7636_All//0.00E+00//TC150390				nr +
Unigene76363_All	237	0.00	4.28	1.80	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	7.21E-06	Up	1.08E+01	1.37E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene7638_All	341	0.31	1.19	1.72	1.61	3.64	7.15	0.50	0.12	0.12	1.95E+00	1.44E-01		2.48E+00	3.75E-02		1.18E+00	5.84E-02		2.15E+00	2.65E-06	Up	-2.02E+00	3.66E-01		-2.09E+00	3.13E-01				Unigene7638_All//4.00E-07//TC154565				
Unigene76383_All	393	0.00	2.84	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.99E-06	Up	1.07E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene76383_All//sp|A1L595|K1C17_BOVIN//2.00E-52//Keratin, type I cytoskeletal 17 OS=Bos taurus GN=KRT17 PE=2 SV=1						swissprot -
Unigene76392_All	374	0.98	0.68	1.14	2.26	1.66	1.33	1.81	0.22	0.00	-5.32E-01	6.27E-01		2.18E-01	8.30E-01		-4.50E-01	5.52E-01		-7.70E-01	3.34E-01		-3.02E+00	2.43E-03		-1.08E+01	3.56E-05	Down	Unigene76392_All//gi|225465333|ref|XP_002271674.1|//3.00E-41//PREDICTED: similar to DNA gyrase subunit A, chloroplastic/mitochondrial [Vitis vinifera]	Unigene76392_All//1.00E-33//AT3G10690| DNA gyrase subunit A family protein	Unigene76392_All//1.00E-127//TC176289			GO:0001071//GO:0003916//GO:0006259//GO:0006351//GO:0009536//GO:0032559//GO:0043232	nr +

Unigene764_All	2396	4.15	4.82	1.84	7.19	8.03	7.94	5.70	3.35	2.26	2.17E-01	2.26E-01		-1.17E+00	1.91E-09	Down	1.59E-01	2.67E-01		1.42E-01	3.45E-01		-7.67E-01	1.92E-08		-1.33E+00	2.33E-20	Down	Unigene764_All//gi|15242132|ref|NP_199973.1|//0.00E+00//PLE (PLEIADE); microtubule binding [Arabidopsis thaliana] >gi|75262488|sp|Q9FHM4.1|MA653_ARATH RecName: Full=65-kDa microtubule-associated protein 3; Short=AtMAP65-3; AltName: Full=Protein PLEIADE	Unigene764_All//0.00E+00//AT5G51600| PLE (PLEIADE); microtubule binding	Unigene764_All//0.00E+00//TC178796			GO:0005881//GO:0015631//GO:0031109//GO:0048285//GO:0051707//GO:0052093	nr +
Unigene7640_All	675	0.85	137.97	11.68	1.40	0.31	0.74	0.00	0.37	0.12	7.34E+00	0.00E+00	Up	3.78E+00	5.30E-31	Up	-2.20E+00	2.99E-03		-9.30E-01	2.06E-01		8.54E+00	4.30E-02		6.88E+00	4.01E-01		Unigene7640_All//gi|115440349|ref|NP_001044454.1|//1.00E-39//Os01g0783500 [Oryza sativa Japonica Group] >gi|53791695|dbj|BAD53290.1| universal stress protein-like [Oryza sativa Japonica Group] >gi|113533985|dbj|BAF06368.1| Os01g0783500 [Oryza sativa Japonica Group]	Unigene7640_All//1.00E-39//AT1G11360| universal stress protein (USP) family protein	Unigene7640_All//0.00E+00//gi|48795858|gb|CO097172.1|CO097172				nr -
Unigene76414_All	503	0.00	0.10	3.39	0.00	0.00	0.00	0.00	0.00	0.00	6.65E+00	6.10E-01		1.17E+01	2.19E-09	Up	null	null		null	null		null	null		null	null		Unigene76414_All//gi|66271031|gb|AY43793.1|//2.00E-13//E6-4 [Gossypium hirsutum]						nr +
Unigene7642_All	377	77.58	13.04	21.19	23.39	13.79	16.89	0.56	0.55	0.00	-2.57E+00	1.07E-81	Down	-1.87E+00	4.56E-53	Down	-7.62E-01	2.14E-05		-4.70E-01	1.61E-02		-1.66E-02	1.02E+00		-9.13E+00	5.78E-02		Unigene7642_All//gi|21322711|emb|CAD22154.1|//9.00E-39//pherophorin-dz1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome		nr +
Unigene76426_All	207	0.00	2.94	4.12	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.16E-03		1.20E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene76426_All//sp|P25815|S100P_HUMAN//4.00E-29//Protein S100-P OS=Homo sapiens GN=S100P PE=1 SV=2						swissprot +
Unigene7643_All	350	0.45	1.59	0.46	1.28	1.67	2.06	0.00	0.48	2.16	1.83E+00	9.02E-02		2.52E-02	1.00E+00		3.85E-01	7.32E-01		6.89E-01	4.48E-01		8.90E+00	1.38E-01		1.11E+01	1.39E-05	Up								
Unigene7644_All	1225	0.00	0.00	0.00	0.00	0.00	0.00	0.97	4.54	2.99	null	null		null	null		null	null		null	null		2.23E+00	1.53E-16	Up	1.63E+00	8.05E-08	Up								
Unigene76445_All	228	0.00	3.11	1.87	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	3.30E-04	Up	1.09E+01	1.37E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene7645_All	358	0.00	0.00	0.30	1.95	0.29	1.39	1.54	1.63	0.00	null	null		8.22E+00	3.89E-01		-2.75E+00	3.99E-03		-4.89E-01	5.98E-01		9.03E-02	9.27E-01		-1.06E+01	2.80E-04	Down			Unigene7645_All//3.00E-165//DW499811					
Unigene76451_All	426	0.00	0.12	2.38	0.00	0.00	0.00	0.00	0.00	0.00	6.89E+00	6.10E-01		1.12E+01	1.27E-05	Up	null	null		null	null		null	null		null	null										
Unigene76457_All	444	2.00	5.02	3.48	3.14	7.29	4.78	0.19	0.00	0.90	1.33E+00	2.82E-03		7.96E-01	1.50E-01		1.21E+00	3.37E-04	Up	6.06E-01	1.94E-01		-7.57E+00	3.99E-01		2.24E+00	6.42E-02		Unigene76457_All//gi|255540053|ref|XP_002511091.1|//2.00E-06//RNA-binding protein, putative [Ricinus communis] >gi|223550206|gb|EEF51693.1| RNA-binding protein, putative [Ricinus communis]						nr -
Unigene7646_All	575	2.37	8.81	1.57	4.85	3.59	4.87	0.81	0.73	0.42	1.90E+00	3.32E-10	Up	-5.88E-01	3.36E-01		-4.33E-01	2.62E-01		5.40E-03	9.91E-01		-1.54E-01	8.70E-01		-9.60E-01	3.13E-01				Unigene7646_All//2.00E-38//TC139389					
Unigene76460_All	580	0.54	0.26	0.18	0.34	0.71	1.56	1.09	3.82	2.75	-1.05E+00	4.43E-01		-1.56E+00	3.29E-01		1.05E+00	4.25E-01		2.18E+00	9.48E-03		1.80E+00	1.61E-05	Up	1.33E+00	4.32E-03		Unigene76460_All//gi|115480840|ref|XP_001064013.1|//1.00E-57//Os10g0101000 [Oryza sativa Japonica Group] >gi|18481964|gb|AAL73562.1|AC07963_2_6 Putative receptor-like protein kinase [Oryza sativa Japonica Group] >gi|19920204|gb|AAM08636.1|AC10888_3_9 Putative receptor-like protein kinase [Oryza sativa Japonica Group] >gi|31429736|gb|AAP51745.1| Protein kinase domain containing protein, expressed [Oryza sativa {japonica cultivar-group}] >gi|113638622|dbj|BAF25927.1| Os10g0101000 [Oryza sativa Japonica Group]	Unigene76460_All//7.00E-38//AT1G34300| lectin protein kinase family protein	Unigene76460_All//2.00E-152//DW233905		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006464//GO:0008037//GO:0016020//GO:0030246//GO:0032559	nr +
Unigene76477_All	255	7.18	1.59	4.39	4.30	3.38	2.30	0.50	0.00	0.62	-2.18E+00	7.58E-05	Down	-7.12E-01	1.56E-01		-3.48E-01	5.96E-01		-9.00E-01	1.81E-01		-8.96E+00	2.34E-01		3.29E-01	8.50E-01				Unigene76477_All//6.00E-70//TC173067					
Unigene7648_All	512	22.89	14.15	11.23	85.03	68.27	60.95	84.48	93.47	36.80	-6.94E-01	2.75E-05		-1.03E+00	4.60E-09	Down	-3.17E-01	2.47E-05		-4.80E-01	6.64E-10		1.46E-01	4.88E-02		-1.20E+00	4.49E-53	Down	Unigene7648_All//gi|193290377|gb|AB165001.1|//1.00E-35//14-3-3b protein [Gossypium hirsutum]	Unigene7648_All//2.00E-36//AT4G09000| 14-3-3-like protein GF14 chi / general regulatory factor 1 (GRF1)	Unigene7648_All//8.00E-65//gi|78331479|gb|DT551753.1|DT551753			GO:0005576//GO:0009536//GO:0010038//GO:0016020//GO:0043401//GO:0051219	nr +
Unigene76489_All	220	0.00	0.00	0.00	0.00	0.00	0.00	1.35	0.57	6.88	null	null		null	null		null	null		null	null		-1.24E+00	3.72E-01		2.35E+00	1.88E-05	Up								
Unigene7649_All	533	0.29	2.38	0.20	0.65	0.52	0.42	0.71	3.37	1.27	3.01E+00	1.02E-04	Up	-5.60E-01	7.74E-01		-3.40E-01	7.85E-01		-6.27E-01	6.20E-01		2.24E+00	7.60E-06	Up	8.32E-01	2.74E-01								ESTscan -
Unigene76494_All	850	0.00	1.07	0.88	0.00	0.00	0.00	0.00	0.00	0.00	1.01E+01	2.60E-05	Up	9.78E+00	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene76494_All//sp|P27587|VIT2_CERCA//2.00E-83//Vitellogenin-2 OS=Ceratitis capitata GN=VG2-delta PE=2 SV=1						swissprot -
Unigene76496_All	217	0.00	3.97	2.21	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.91E-05	Up	1.11E+01	7.43E-03		null	null		null	null		null	null		null	null		Unigene76496_All//sp|A6TGC1|HSLU_KLEPT//8.00E-10//ATP-dependent hsl protease ATP-binding subunit hslU OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=hslU PE=3 SV=1						swissprot +
Unigene76499_All	290	0.00	1.22	3.86	0.00	0.24	0.00	0.00	0.00	0.00	1.03E+01	2.43E-02		1.19E+01	3.42E-06	Up	7.89E+00	6.02E-01		null	null		null	null		null	null		Unigene76499_All//sp|P21333|FLNA_HUMAN//2.00E-52//Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4						swissprot +
Unigene765_All	2459	2.40	2.51	0.80	5.83	4.50	4.46	7.15	4.32	3.21	6.43E-02	7.92E-01		-1.59E+00	6.02E-09	Down	-3.76E-01	8.34E-03		-3.87E-01	9.41E-03		-7.28E-01	8.56E-10		-1.16E+00	6.04E-21	Down	Unigene765_All//gi|113205145|gb|AAT40494.2|//0.00E+00//Putative microtubule-associated protein, identical [Solanum demissum]	Unigene765_All//0.00E+00//AT5G51600| PLE (PLEIADE); microtubule binding	Unigene765_All//0.00E+00//TC178796			GO:0005881//GO:0015631//GO:0031109//GO:0048285//GO:0051707//GO:0052093	nr -
Unigene7650_All	828	0.00	0.06	0.00	0.12	0.00	0.00	2.25	1.77	31.13	5.94E+00	6.10E-01		null	null		-6.91E+00	3.09E-01		-6.91E+00	3.94E-01		-3.47E-01	4.40E-01		3.79E+00	1.77E-129	Up	Unigene7650_All//gi|297793643|ref|XP_002864706.1|//2.00E-27//bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310541|gb|EFH40965.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7650_All//1.00E-20//AT5G60830| AtbZIP70 (Arabidopsis thaliana basic leucine-zipper 70); DNA binding / transcription factor	Unigene7650_All//0.00E+00//gi|84164538|gb|DR453186.1|DR453186	bZIP	ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0001071//GO:0003677//GO:0006351//GO:0042802//GO:0043231//GO:0046983	nr +
Unigene76511_All	1043	0.00	2.28	1.02	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.50E-13	Up	1.00E+01	6.60E-06	Up	null	null		null	null		null	null		null	null		Unigene76511_All//gi|255563324|ref|XP_002522665.1|//8.00E-10//structural constituent of cell wall, putative [Ricinus communis] >gi|223538141|gb|EEF39752.1| structural constituent of cell wall, putative [Ricinus communis]						nr +
Unigene76525_All	709	0.00	1.14	0.38	0.00	0.00	0.00	0.00	0.00	0.00	1.02E+01	9.31E-05	Up	8.55E+00	7.92E-02		null	null		null	null		null	null		null	null									ESTscan -
Unigene7653_All	730	0.29	0.56	0.36	1.64	0.09	0.74	2.32	1.20	1.42	9.54E-01	4.13E-01		3.47E-01	7.96E-01		-4.12E+00	7.48E-07	Down	-1.14E+00	7.15E-02		-9.46E-01	3.66E-02		-7.07E-01	1.03E-01		Unigene7653_All//gi|224075299|ref|XP_002304889.1|//1.00E-17//nbs-lrr resistance protein [Populus trichocarpa] >gi|222842021|gb|EEE79568.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene7653_All//7.00E-12//AT1G50180| disease resistance protein (CC-NBS-LRR class), putative	Unigene7653_All//0.00E+00//gi|73862708|gb|DT465447.1|DT465447		ko04626|Plant-pathogen interaction	GO:0000166//GO:0016020	nr +
Unigene7654_All	699	0.00	0.00	0.00	0.29	0.20	2.00	1.57	0.12	1.42	null	null		null	null		-5.33E-01	7.47E-01		2.81E+00	5.55E-05	Up	-3.72E+00	7.15E-06	Down	-1.43E-01	7.90E-01		Unigene7654_All//gi|297738827|emb|CBI28072.3|//8.00E-25//unnamed protein product [Vitis vinifera]		Unigene7654_All//1.00E-175//gi|78323488|gb|DT543762.1|DT543762				nr -
Unigene7655_All	339	0.00	1.94	2.20	1.03	0.91	1.47	2.12	0.62	0.94	1.09E+01	6.20E-04	Up	1.11E+01	3.25E-04	Up	-1.70E-01	8.57E-01		5.11E-01	6.41E-01		-1.78E+00	2.78E-02		-1.17E+00	1.09E-01									
Unigene76551_All	352	0.00	0.00	3.18	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene76551_All//gi|225456577|ref|XP_002266021.1|//2.00E-18//PREDICTED: similar to hydrolase, alpha/beta fold family protein [Vitis vinifera]	Unigene76551_All//9.00E-19//AT1G26355| SP1L1 (SPIRAL1-LIKE1)	Unigene76551_All//4.00E-07//EX164877				nr -
Unigene76555_All	318	0.00	12.75	5.69	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	4.38E-23	Up	1.25E+01	5.68E-10	Up	null	null		null	null		null	null		null	null										
Unigene76598_All	597	0.00	1.02	1.69	0.00	0.29	0.45	0.00	0.00	0.00	9.99E+00	1.16E-03		1.07E+01	1.27E-05	Up	8.17E+00	2.26E-01		8.83E+00	7.01E-02		null	null		null	null		Unigene76598_All//gi|222874761|gb|EEF11892.1|//1.00E-40//predicted protein [Populus trichocarpa]						nr -
Unigene766_All	892	0.00	0.34	0.00	0.28	0.15	0.81	1.19	1.03	2.72	8.41E+00	4.37E-02		null	null		-8.55E-01	5.73E-01		1.54E+00	9.17E-02		-2.01E-01	7.28E-01		1.20E+00	8.89E-04	Up	Unigene766_All//gi|9758979|dbj|BAB09489.1|//2.00E-11//disease resistance protein-like [Arabidopsis thaliana]	Unigene766_All//3.00E-13//AT4G19510| disease resistance protein (TIR-NBS-LRR class), putative					nr -
Unigene76605_All	521	0.00	1.56	1.12	0.00	0.00	0.09	0.73	0.08	0.08	1.06E+01	9.31E-05	Up	1.01E+01	2.16E-03		null	null		6.44E+00	6.86E-01		-3.19E+00	3.11E-02		-3.26E+00	2.22E-02		Unigene76605_All//gi|224104361|ref|XP_002313411.1|//2.00E-22//copper transporter [Populus trichocarpa] >gi|222849819|gb|EEE87366.1| copper transporter [Populus trichocarpa]	Unigene76605_All//1.00E-15//AT3G46900| COPT2; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter	Unigene76605_All//2.00E-10//BQ404364			GO:0005375//GO:0006825//GO:0007275//GO:0009987//GO:0031224	nr +
Unigene7661_All	598	17.06	3.39	4.81	7.83	5.18	0.91	0.21	0.00	0.00	-2.33E+00	8.70E-26	Down	-1.83E+00	3.40E-18	Down	-5.95E-01	2.55E-02		-3.11E+00	1.06E-17	Down	-7.73E+00	2.34E-01		-7.73E+00	1.99E-01		Unigene7661_All//gi|18415376|ref|NP_568172.1|//5.00E-42//ST2A (SULFOTRANSFERASE 2A); hydroxyjasmonate sulfotransferase/ sulfotransferase [Arabidopsis thaliana] >gi|20466686|gb|AAM20660.1| steroid sulfotransferase-like protein [Arabidopsis thaliana] >gi|21537216|gb|AAM61557.1| steroid sulfotransferase-like protein [Arabidopsis thaliana] >gi|31711860|gb|AAP68286.1| At5g07010 [Arabidopsis thaliana]	Unigene7661_All//3.00E-43//AT5G07010| ST2A (SULFOTRANSFERASE 2A); hydroxyjasmonate sulfotransferase/ sulfotransferase	Unigene7661_All//2.00E-87//TC178273		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0008146//GO:0009719//GO:0031407	nr +
Unigene7663_All	396	1.98	0.26	1.34	3.52	0.87	2.17	0.64	0.84	0.60	-2.95E+00	3.66E-03		-5.60E-01	4.96E-01		-2.02E+00	4.21E-04	Down	-7.01E-01	2.32E-01		3.99E-01	7.24E-01		-8.58E-02	9.56E-01		Unigene7663_All//gi|15237721|ref|NP_200670.1|//6.00E-40//zinc finger (CCCH-type) family protein [Arabidopsis thaliana] >gi|75311611|sp|Q9LUZ4.1|C3H66_ARATH RecName: Full=Zinc finger CCCH domain-containing protein 66; Short=AtC3H66 >gi|8843784|dbj|BAA97332.1| zinc finger transcription factor-like protein [Arabidopsis thaliana] >gi|15809818|gb|AAL06837.1| AT5g58620/mzn1_70 [Arabidopsis thaliana] >gi|17064830|gb|AAL32569.1| zinc finger transcription factor-like protein [Arabidopsis thaliana] >gi|21653307|gb|AAM65365.1| AT5g58620/mzn1_70 [Arabidopsis thaliana] >gi|25083596|gb|AAN72094.1| zinc finger transcription factor-like protein [Arabidopsis thaliana]	Unigene7663_All//3.00E-41//AT5G58620| zinc finger (CCCH-type) family protein	Unigene7663_All//2.00E-58//TC171216	C3H		GO:0001071//GO:0010468//GO:0046914	nr -

Unigene76633_All	538	0.00	4.24	3.07	0.00	0.06	0.00	13.36	15.07	31.10	1.20E+01	5.62E-13	Up	1.16E+01	4.30E-09	Up	6.00E+00	8.17E-01		null	null		1.74E-01	4.01E-01		1.22E+00	1.92E-21	Up	Unigene76633_All//gi|157503121|gb|ABV58643.1|//3.00E-48//ubiquitin [Catharanthus roseus]	Unigene76633_All//4.00E-26//AT5G37640| UBQ9; protein binding	Unigene76633_All//2.00E-37//gi|164361414|gb|ES807417.1|ES807417		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene76635_All	658	0.72	0.00	0.08	0.30	0.00	0.00	1.03	0.25	0.06	-9.48E+00	5.53E-03		-3.14E+00	3.99E-02		-8.24E+00	8.38E-02		-8.24E+00	1.33E-01		-2.02E+00	1.98E-02		-4.09E+00	3.10E-04	Down	Unigene76635_All//gi|281372499|gb|ADM63835.1|//4.00E-16//serine-threonine protein kinase [Triticum aestivum]	Unigene76635_All//6.00E-12//AT1G12680| PEPKR2 (Phosphoenolpyruvate carboxylase-related kinase 2); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene76635_All//0.00E+00//ES798924			GO:0004672//GO:0005488	nr -
Unigene7665_All	589	0.71	2.15	1.63	0.68	1.52	0.61	10.91	19.16	37.81	1.60E+00	1.20E-02		1.20E+00	1.15E-01		1.17E+00	1.33E-01		-1.42E-01	9.04E-01		8.12E-01	9.24E-08		1.79E+00	2.37E-49	Up	Unigene7665_All//gi|30102564|gb|AAP21200.1|//4.00E-16//At3g19660 [Arabidopsis thaliana]	Unigene7665_All//2.00E-09//AT3G19660| unknown protein	Unigene7665_All//4.00E-150//DW504286				nr -
Unigene76656_All	238	1.10	1.06	0.90	0.84	1.74	1.14	0.00	1.23	3.18	-4.63E-02	9.86E-01		-2.97E-01	8.31E-01		1.05E+00	4.25E-01		4.44E-01	7.63E-01		1.03E+01	2.35E-02		1.16E+01	1.39E-05	Up	Unigene76656_All//gi|79510650|ref|NP_200702.2|//2.00E-24//CRCK1 (CALMODULIN-BINDING RECEPTOR-LIKE CYTOPLASMIC KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|50253524|gb|AAT71964.1| At5g58940 [Arabidopsis thaliana] >gi|53850531|gb|AAU95442.1| At5g58940 [Arabidopsis thaliana]	Unigene76656_All//9.00E-26//AT5G58940| CRCK1 (CALMODULIN-BINDING RECEPTOR-LIKE CYTOPLASMIC KINASE 1); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene76656_All//2.00E-100//ES801361		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006464//GO:0032559//GO:0043231	nr +
Unigene7666_All	289	1.81	1.58	0.37	1.03	2.03	5.00	0.73	2.75	0.69	-1.98E-01	8.20E-01		-2.30E+00	6.75E-02		9.70E-01	3.47E-01		2.27E+00	3.41E-04	Up	1.91E+00	1.37E-02		-8.59E-02	9.60E-01								ESTscan +
Unigene76660_All	223	0.00	0.00	3.82	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.19E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene76660_All//gi|6960455|gb|AAD42963.2|AF141384|//3.00E-29//serine carboxypeptidase precursor [Matricaria chamomilla]	Unigene76660_All//4.00E-29//AT3G45010| scp148 (serine carboxypeptidase-like 48); serine-type carboxypeptidase	Unigene76660_All//7.00E-14//TC140177		ko00940|Phenylpropanoid biosynthesis	GO:0004180//GO:0019538//GO:0043231	nr +
Unigene7667_All	310	19.92	18.96	24.56	23.14	14.33	19.52	29.46	16.99	12.72	-7.09E-02	7.71E-01		3.03E-01	1.91E-01		-6.91E-01	6.60E-04		-2.45E-01	3.16E-01		-7.94E-01	3.13E-06		-1.21E+00	4.32E-12	Down	Unigene7667_All//gi|297843714|ref|XP_002889738.1|//2.00E-08//20S proteasome beta subunit PBG1 [Arabidopsis lyrata subsp. lyrata] >gi|297335580|gb|EFH65997.1| 20S proteasome beta subunit PBG1 [Arabidopsis lyrata subsp. lyrata]	Unigene7667_All//1.00E-07//AT1G56450| PBG1; peptidase/ threonine-type endopeptidase	Unigene7667_All//5.00E-77//TC154335		ko03050|Proteasome	GO:0000502//GO:0004175//GO:0006508//GO:0043231	nr -
Unigene7668_All	501	0.00	2.23	0.64	0.30	0.55	1.35	0.51	0.25	2.39	1.11E+01	1.99E-06	Up	9.32E+00	4.46E-02		8.82E-01	5.94E-01		2.18E+00	3.14E-02		-1.02E+00	4.94E-01		2.24E+00	3.02E-04	Up	Unigene7668_All//gi|124365538|gb|ABN09772.1|//8.00E-23//U box [Medicago truncatula]					GO:0044424	nr -
Unigene767_All	2309	0.43	0.42	1.36	0.39	0.36	0.47	6.15	7.98	9.89	-4.63E-02	9.58E-01		1.66E+00	2.22E-05	Up	-1.18E-01	8.51E-01		2.74E-01	6.70E-01		3.76E-01	1.18E-03		6.84E-01	1.47E-11		Unigene767_All//gi|224145021|ref|XP_002323498.1|//1.00E-94//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222862373|gb|EEE99879.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene767_All//1.00E-69//AT1G27170| ATP binding / protein binding / transmembrane receptor	Unigene767_All//6.00E-69//TC140957		ko04626|Plant-pathogen interaction		nr -
Unigene76702_All	449	0.00	3.39	1.42	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.09E-08	Up	1.05E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene76702_All//gi|51948476|ref|NP_001004250.1|//4.00E-37//cytochrome b-c1 complex subunit 1, mitochondrial precursor [Rattus norvegicus] >gi|81884378|sp|Q68FY0.1|QCR1_RAT RecName: Full=Cytochrome b-c1 complex subunit 1, mitochondrial; AltName: Full=Ubiquinol-cytochrome-c reductase complex core protein 1; AltName: Full=Core protein I; AltName: Full=Complex III subunit 1; Flags: Precursor >gi|51259340|gb|AAH78923.1| Ubiquinol-cytochrome c reductase core protein I [Rattus norvegicus] >gi|149018490|gb|EDL77131.1| ubiquinol-cytochrome c reductase core protein 1, isoform CRA_a [Rattus norvegicus]	Unigene76702_All//1.00E-26//AT3G02090| mitochondrial processing peptidase beta subunit, putative				GO:0005515//GO:0005746//GO:0009536//GO:0010033//GO:0022900//GO:0030312//GO:0031980//GO:0031981//GO:0046914	nr +
Unigene7671_All	353	1.78	0.86	0.30	0.00	1.95	0.38	2.52	1.54	0.45	-1.05E+00	2.50E-01		-2.56E+00	2.72E-02		1.09E+01	3.05E-04	Up	8.58E+00	3.09E-01		-7.09E-01	2.97E-01		-2.48E+00	9.93E-04	Down			Unigene7671_All//4.00E-07//C0098007				
Unigene76728_All	425	0.12	0.00	2.88	0.23	0.49	0.00	0.00	0.00	0.00	-6.94E+00	6.04E-01		4.55E+00	1.02E-05	Up	1.05E+00	6.11E-01		-7.87E+00	3.94E-01		null	null		null	null		Unigene76728_All//COG1651//1.00E-27//Protein-disulfide isomerase						cog +
Unigene7673_All	302	2.08	0.00	0.00	1.98	2.17	1.35	0.42	0.28	0.13	-1.10E+01	7.90E-04	Down	-1.10E+01	1.40E-03		1.30E-01	9.05E-01		-5.57E-01	5.75E-01		-6.02E-01	7.65E-01		-1.67E+00	4.76E-01								
Unigene7674_All	568	0.74	0.54	0.38	1.67	1.94	5.88	2.16	3.38	4.14	-4.61E-01	6.50E-01		-9.75E-01	4.11E-01		2.19E-01	7.93E-01		1.82E+00	6.71E-07	Up	6.49E-01	1.28E-01		9.39E-01	9.21E-03				Unigene7674_All//5.00E-23//TC148303				
Unigene76742_All	349	0.60	0.00	3.51	1.57	0.10	0.26	0.00	0.00	0.11	-9.23E+00	1.21E-01		2.55E+00	8.25E-04	Up	-3.99E+00	2.60E-03		-2.60E+00	2.93E-02		null	null		6.84E+00	6.37E-01								
Unigene7675_All	618	5.67	3.44	9.56	0.32	0.61	1.02	43.31	20.22	10.44	-7.20E-01	2.82E-02		7.54E-01	2.95E-03		9.27E-01	5.23E-01		1.67E+00	9.79E-02		-1.10E+00	4.02E-28	Down	-2.05E+00	1.36E-71	Down			Unigene7675_All//4.00E-39//gi|109826782|gb|DW225491.1|DW225491				
Unigene76765_All	474	0.00	1.39	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.04E+01	6.20E-04	Up	1.04E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene76765_All//gi|171769899|sp|A3AB67.1|FH16_ORYSJ//6.00E-08//RecName: Full=Formin-like protein 16; AltName: Full=OsFH16; Flags: Precursor						nr +
Unigene7677_All	974	2.36	1.09	0.22	6.19	0.81	0.88	0.35	0.30	0.16	-1.11E+00	8.93E-03		-3.43E+00	1.38E-08	Down	-2.93E+00	8.32E-25	Down	-2.81E+00	1.64E-20	Down	-2.09E-01	8.50E-01		-1.09E+00	3.55E-01				Unigene7677_All//2.00E-153//TC157942				
Unigene76774_All	330	0.79	0.15	0.97	0.00	0.10	0.27	3.20	0.25	0.72	-2.37E+00	2.13E-01		2.89E-01	8.09E-01		6.70E+00	8.17E-01		8.10E+00	4.71E-01		-3.66E+00	1.31E-05	Down	-2.14E+00	9.36E-04	Down	Unigene76774_All//gi|15809822|gb|AL06839.1|//5.00E-27//AT5g25460/F18G18_200 [Arabidopsis thaliana]	Unigene76774_All//4.00E-29//AT5G11420| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cell wall, plant-type cell wall; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25460.1); Has 185 Blast hits to 157 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 185; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene76774_All//1.00E-68//TC138865			GO:0005618	nr -
Unigene7678_All	748	0.14	0.07	0.00	0.73	0.83	0.30	1.81	0.17	2.82	-1.05E+00	6.83E-01		-7.13E+00	3.87E-01		1.78E-01	8.64E-01		-1.28E+00	2.23E-01		-3.43E+00	1.05E-06	Down	6.42E-01	9.48E-02		Unigene7678_All//gi|112280265|gb|AB114669.1|//1.00E-45//ubiquitin-protein ligase [Aegiceras corniculatum]	Unigene7678_All//1.00E-34//AT1G55860| UPL1 (UBIQUITIN-PROTEIN LIGASE 1); ubiquitin-protein ligase	Unigene7678_All//1.00E-116//DW487940		ko04120|Ubiquitin mediated proteolysis	GO:0016879//GO:0043412//GO:0044464	nr -
Unigene7679_All	567	1.02	1.25	0.38	3.60	2.37	0.64	3.28	1.03	1.69	3.02E-01	6.93E-01		-1.43E+00	1.75E-01		-6.05E-01	1.71E-01		-2.50E+00	1.87E-06	Down	-1.67E+00	2.33E-04	Down	-9.60E-01	1.93E-02		Unigene7679_All//gi|115455513|ref|NP_001051357.1|//1.00E-06//Os03g0762100 [Oryza sativa Japonica Group] >gi|108711220|gb|ABF99015.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113549828|dbj|BAF13271.1| Os03g0762100 [Oryza sativa Japonica Group]	Unigene7679_All//2.00E-07//AT1G26620| unknown protein	Unigene7679_All//0.00E+00//DR463168				nr -
Unigene768_All	3715	21.59	8.28	17.99	5.62	5.25	4.84	0.22	0.30	0.73	-1.38E+00	6.16E-97	Down	-2.63E-01	1.24E-05		-9.88E-02	5.08E-01		-2.16E-01	9.69E-02		4.91E-01	4.01E-01		1.75E+00	1.51E-06	Up	Unigene768_All//gi|224127754|ref|XP_002329169.1|//1.00E-103//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222870950|gb|EEF08081.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene768_All//6.00E-92//AT4G12010| disease resistance protein (TIR-NBS-LRR class), putative	Unigene768_All//5.00E-92//ES818783		ko04626|Plant-pathogen interaction		nr -
Unigene7680_All	527	0.00	5.38	1.21	0.47	1.05	2.23	0.56	1.43	0.15	1.24E+01	3.82E-16	Up	1.02E+01	1.15E-03		1.15E+00	2.97E-01		2.24E+00	1.82E-03		1.35E+00	7.61E-02		-1.89E+00	1.68E-01		Unigene7680_All//gi|124359588|gb|ABD28718.2|//1.00E-31//Protein secE/sec61-gamma protein; Rhomboid-like protein [Medicago truncatula]	Unigene7680_All//1.00E-21//AT1G52580| ATRBL5 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 5)	Unigene7680_All//4.00E-54//CO116418			GO:0044464	nr +
Unigene7683_All	658	0.16	0.00	0.24	0.00	0.00	0.00	6.81	2.67	7.63	-7.31E+00	3.67E-01		6.11E-01	7.47E-01		null	null		null	null		-1.35E+00	3.89E-07	Down	1.64E-01	5.39E-01		Unigene7683_All//gi|115469422|ref|NP_001058310.1|//4.00E-09//Os06g0666800 [Oryza sativa Japonica Group] >gi|113596350|dbj|BAF20224.1| Os06g0666800 [Oryza sativa Japonica Group]	Unigene7683_All//4.00E-11//AT4G19980| unknown protein				GO:0043231	nr -
Unigene76877_All	421	0.00	1.56	1.14	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	6.20E-04	Up	1.02E+01	7.43E-03		null	null		null	null		null	null		null	null								
Unigene7688_All	434	0.24	0.70	0.12	0.46	1.82	2.50	1.27	0.00	1.65	1.54E+00	3.22E-01		-9.75E-01	7.19E-01		1.99E+00	2.46E-02		2.44E+00	1.61E-03		-1.03E+01	4.61E-04	Down	3.84E-01	5.96E-01		Unigene7688_All//gi|10176937|dbj|BAB10136.1|//8.00E-21//serine/threonine-specific kinase like protein [Arabidopsis thaliana]	Unigene7688_All//3.00E-12//AT5G58830| lectin protein kinase, putative	Unigene7688_All//0.00E+00//DW516505			GO:0004672//GO:0006464//GO:0016020//GO:0030246//GO:0032559	nr -
Unigene76899_All	237	0.00	6.63	0.00	0.42	0.58	4.19	9.46	76.01	54.63	1.27E+01	5.68E-09	Up	null	null		4.67E-01	8.75E-01		3.32E+00	3.47E-04	Up	3.01E+00	1.74E-72	Up	2.53E+00	2.05E-44	Up	Unigene76899_All//gi|8099159|dbj|BAA96251.1|//7.00E-27//asparagine synthetase [Astragalus sinicus]	Unigene76899_All//2.00E-27//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene76899_All//3.00E-53//EX164853		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0006528//GO:0009064//GO:0009267//GO:0009642//GO:0009746//GO:0016884//GO:0032559//GO:0034285	nr +
Unigene769_All	1613	9.67	4.71	6.57	15.35	12.92	18.23	16.23	7.13	9.36	-1.04E+00	1.41E-12	Down	-5.57E-01	1.39E-04		-2.49E-01	2.26E-02		2.48E-01	1.61E-02		-1.19E+00	4.74E-31	Down	-7.94E-01	8.27E-17		Unigene769_All//gi|15242217|ref|NP_197625.1|//0.00E+00//RIN1 (RESISTANCE TO PSEUDOMONAS SYRINGAE PV MACULICOLA INTERACTOR 1); protein binding [Arabidopsis thaliana] >gi|9757813|dbj|BAB08331.1| Ruv DNA-helicase-like protein [Arabidopsis thaliana] >gi|21536838|gb|AAM61170.1| Ruv DNA-helicase-like protein [Arabidopsis thaliana]	Unigene769_All//0.00E+00//AT5G22330| RIN1 (RESISTANCE TO PSEUDOMONAS SYRINGAE PV MACULICOLA INTERACTOR 1); protein binding	Unigene769_All//0.00E+00//gi|78354017|gb|DT574291.1|DT574291			GO:0004175//GO:0004386//GO:0009536//GO:0009888//GO:0019538//GO:0031981//GO:0032559//GO:0042623	nr +
Unigene7690_All	1064	0.10	0.71	0.00	0.19	0.06	0.17	7.31	17.48	82.04	2.86E+00	5.51E-03		-6.62E+00	3.87E-01		-1.53E+00	4.15E-01		-1.42E-01	9.34E-01		1.26E+00	2.68E-24	Up	3.49E+00	0.00E+00	Up	Unigene7690_All//gi|18406390|ref|NP_564747.1|//3.00E-26//ZCF37 [Arabidopsis thaliana] >gi|8778744|gb|AAF79752.1|AC009317_11 T30E16.15 [Arabidopsis thaliana] >gi|6520221|dbj|BAA87954.1| ZCF37 [Arabidopsis thaliana] >gi|89111900|gb|ABD60722.1| AtLg59590 [Arabidopsis thaliana]	Unigene7690_All//7.00E-19//AT1G59590| ZCF37	Unigene7690_All//0.00E+00//TC178620				nr -
Unigene76907_All	436	0.00	1.63	12.21	0.23	0.00	0.31	0.00	0.00	0.00	1.07E+01	3.30E-04	Up	1.36E+01	1.21E-29	Up	-7.84E+00	3.09E-01		4.44E-01	8.60E-01		null	null		null	null		Unigene76907_All//sp|P01876|IGHA1_HUMAN//1.00E-65//Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 SV=2						swissprot +

Unigene76916_All	218	0.24	0.46	1.47	4.34	1.58	3.73	6.98	1.34	0.55	9.54E-01	7.24E-01		2.61E+00	1.45E-01		-1.46E+00	3.60E-02		-2.19E-01	7.48E-01		-2.38E+00	2.15E-05	Down	-3.67E+00	3.49E-08	Down			Unigene76916_All//3.00E-28//TC139126				
Unigene7694_All	683	0.08	0.52	0.47	0.66	2.22	0.13	1.42	3.12	4.61	2.76E+00	9.58E-02		2.61E+00	1.45E-01		1.76E+00	1.93E-03		-2.31E+00	7.80E-02		1.13E+00	4.44E-03		1.69E+00	3.63E-07	Up			Unigene7694_All//8.00E-07//TC167085				
Unigene76953_All	442	0.00	17.77	6.26	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	6.44E-45	Up	1.26E+01	2.74E-15	Up	null	null		null	null		null	null		null	null		Unigene76953_All//gi|300262824|gb|EFJ47028.1|//3.00E-13//transcription factor jumonji domain-containing protein [Volvox carteri f. nagariensis]				ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00020|Citrate cycle (TCA cycle)		nr -
Unigene7699_All	756	0.14	0.87	0.00	0.92	2.78	1.31	3.86	4.64	7.01	2.65E+00	1.49E-02		-7.11E+00	3.87E-01		1.59E+00	4.65E-04	Up	5.11E-01	4.92E-01		2.67E-01	3.96E-01		8.61E-01	1.45E-04				Unigene7699_All//2.00E-07//TC176376				
Unigene77_All	3751	1.77	1.15	1.41	4.66	4.64	3.73	4.60	2.20	2.71	-6.26E-01	5.99E-03		-3.34E-01	1.78E-01		-7.90E-03	9.56E-01		-3.21E-01	1.79E-02		-1.07E+00	1.34E-17	Down	-7.64E-01	1.02E-10		Unigene77_All//gi|297815528|ref|XP_002857647.1|//1.00E-114//kinase [Arabidopsis lyrata subsp. lyrata] >gi|297321485|gb|EFH51906.1| kinase [Arabidopsis lyrata subsp. lyrata]	Unigene77_All//1.00E-102//AT3G44200| NEK6 (^NIMA (NEVER IN MITOSIS, GENE A)-RELATED 6^); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene77_All//0.00E+00//gi|164321644|gb|ES794968.1|ES794968			nr -
Unigene770_All	1670	14.00	8.19	9.69	20.76	23.09	20.17	13.19	5.46	7.18	-7.74E-01	1.40E-11		-5.31E-01	5.15E-06		1.54E-01	9.68E-02		-4.13E-02	7.04E-01		-1.27E+00	3.08E-29	Down	-8.77E-01	8.44E-17		Unigene770_All//gi|15242217|ref|NP_197625.1|//0.00E+00//RIN1 (RESISTANCE TO PSEUDOMONAS SYRINGAE PV MACULICOLA INTERACTOR 1); protein binding [Arabidopsis thaliana] >gi|9757813|dbj|BAB08331.1| Ruv DNA-helicase-like protein [Arabidopsis thaliana] >gi|21536838|gb|AAM61170.1| Ruv DNA-helicase-like protein [Arabidopsis thaliana]	Unigene770_All//0.00E+00//AT5G22330| RIN1 (RESISTANCE TO PSEUDOMONAS SYRINGAE PV MACULICOLA INTERACTOR 1); protein binding	Unigene770_All//0.00E+00//TC153568			GO:0004175//GO:0004386//GO:0009536//GO:0009888//GO:0019538//GO:0031981//GO:0032559//GO:0042623	nr -
Unigene77008_All	264	0.99	2.69	5.24	2.64	5.48	1.20	3.04	2.53	1.66	1.44E+00	1.06E-01		2.40E+00	5.37E-04	Up	1.05E+00	6.14E-02		-1.14E+00	2.01E-01		-2.65E-01	7.04E-01		-8.74E-01	1.96E-01				Unigene77008_All//5.00E-49//AW187143				
Unigene77021_All	420	0.00	1.57	1.39	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	6.20E-04	Up	1.04E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene77021_All//gi|238480901|ref|NP_001154263.1|//3.00E-06//unknown protein [Arabidopsis thaliana]						nr +
Unigene77025_All	282	0.00	0.36	0.00	0.18	0.00	0.16	3.15	0.00	0.00	8.49E+00	3.81E-01		null	null		-7.46E+00	5.45E-01		-1.41E-01	9.48E-01		-1.16E+01	2.24E-06	Down	-1.16E+01	1.10E-06	Down	Unigene77025_All//gi|297844236|ref|XP_002889999.1|//2.00E-09//myb family transcription factor [Arabidopsis lyrata subsp. lyrata] >gi|297335841|gb|EFH86258.1| myb family transcription factor [Arabidopsis lyrata subsp. lyrata]	Unigene77025_All//2.00E-07//AT1G13300| myb family transcription factor	Unigene77025_All//6.00E-126//gi|109873268|gb|DW502243.1|DW502243	G2-like			nr +
Unigene77028_All	376	0.00	0.27	2.12	0.13	0.00	0.12	0.00	0.00	0.00	8.07E+00	3.81E-01		1.11E+01	1.72E-04	Up	-7.05E+00	5.45E-01		-1.42E-01	9.48E-01		null	null		null	null		Unigene77028_All//sp|P55425|Y4EB_RHISN//5.00E-12//Uncharacterized protein y4eB OS=Rhizobium sp. (strain NGR234) GN=NGR_a03910 PE=4 SV=1						swissprot +
Unigene7703_All	294	130.09	48.08	74.98	229.42	221.96	278.05	54.36	34.55	30.76	-1.44E+00	3.00E-49	Down	-7.95E-01	1.65E-18		-4.77E-02	5.60E-01		2.77E-01	7.62E-07		-6.54E-01	1.44E-07		-8.22E-01	3.26E-11				Unigene7703_All//8.00E-73//ES809586				
Unigene7705_All	863	0.00	0.23	0.49	4.21	5.43	5.60	2.74	0.58	2.86	7.88E+00	1.35E-01		8.95E+00	1.37E-02		3.65E-01	2.21E-01		4.10E-01	1.57E-01		-2.24E+00	1.69E-07	Down	6.10E-02	8.78E-01		Unigene7705_All//gi|297798488|ref|XP_002867128.1|//3.00E-68//hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297312964|gb|EFH43387.1| hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene7705_All//1.00E-79//AT3G53010| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF303, acetylesterase putative (InterPro:IPR0051811); BEST Arabidopsis thaliana protein match is: hydrolase (TAIR:AT4G34215.2); Has 199 Blast hits to 199 proteins in 58 species: Archae - 0; Bacteria - 119; Metazoa - 0; Fungi - 1; Plants - 56; Viruses - 0; Other Eukaryotes - 23 (source: NCBI BLink).	Unigene7705_All//1.00E-107//gi|78343875|gb|DT564149.1|DT564149			GO:0003824//GO:0043231	nr +
Unigene7706_All	386	2.17	0.00	0.00	1.29	2.77	2.57	1.20	1.84	0.72	-1.11E+01	5.56E-05	Down	-1.11E+01	1.19E-04	Down	1.10E+00	1.09E-01		9.96E-01	1.72E-01		6.11E-01	4.27E-01		-7.38E-01	4.26E-01		Unigene7706_All//gi|15239173|ref|NP_196176.1|//7.00E-31//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene7706_All//4.00E-32//AT5G05570| transducin family protein / WD-40 repeat family protein			GO:0006810//GO:0031224	nr -
Unigene7707_All	511	9.83	13.39	13.13	8.58	4.58	2.92	0.17	0.00	0.00	4.46E-01	4.96E-02		4.18E-01	8.43E-02		-9.05E-01	7.92E-04		-1.56E+00	2.19E-07	Down	-7.37E+00	3.98E-01		-7.37E+00	3.54E-01				Unigene7707_All//0.00E+00//DW520122				
Unigene77097_All	500	0.21	0.30	2.02	0.20	0.14	0.18	0.00	0.08	0.00	5.39E-01	7.78E-01		3.27E+00	5.92E-04	Up	-5.33E-01	8.13E-01		-1.41E-01	9.47E-01		6.39E+00	6.27E-01		null	null		Unigene77097_All//COG5569//4.00E-08//Uncharacterized conserved protein						cog +
Unigene771_All	1184	3.40	7.02	3.28	8.08	8.23	7.25	10.36	10.55	10.77	1.04E+00	4.01E-07	Up	-5.16E-02	8.76E-01		2.70E-02	9.10E-01		-1.57E-01	4.84E-01		2.75E-02	8.77E-01		5.62E-02	7.21E-01		Unigene771_All//gi|297826489|ref|XP_002881127.1|//1.00E-149//RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297326966|gb|EFH57386.1| RabGAP/TBC domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene771_All//2.00E-144//AT2G30710| RabGAP/TBC domain-containing protein	Unigene771_All//0.00E+00//ES839747			GO:0005099//GO:0032318//GO:0044464	nr -
Unigene7710_All	317	0.66	6.87	0.34	0.31	0.98	2.42	2.27	4.22	2.01	3.38E+00	2.02E-08	Up	-9.74E-01	6.19E-01		1.64E+00	3.21E-01		2.95E+00	4.39E-03		8.96E-01	8.68E-02		-1.73E-01	7.94E-01				Unigene7710_All//5.00E-148//CO087728				
Unigene77125_All	398	0.13	0.13	0.00	0.13	0.69	0.11	1.49	0.95	19.72	-4.68E-02	9.83E-01		-7.04E+00	6.15E-01		2.47E+00	2.23E-01		-1.42E-01	9.48E-01		-6.54E-01	4.45E-01		3.73E+00	2.71E-39	Up	Unigene77125_All//gi|15225174|ref|NP_180763.1|//3.00E-25//GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] >gi|89111890|gb|ABD60717.1| At2g32030 [Arabidopsis thaliana]	Unigene77125_All//2.00E-26//AT2G32030| GCN5-related N-acetyltransferase (GNAT) family protein	Unigene77125_All//2.00E-132//TC144122			nr +
Unigene77135_All	441	0.00	1.26	4.95	0.00	0.00	0.61	0.00	0.00	0.00	1.03E+01	2.16E-03		1.23E+01	4.94E-12	Up	null	null		9.26E+00	7.01E-02		null	null		null	null		Unigene77135_All//gi|266856|sp|P29795.1|PSBP_SOLLC//5.00E-55//RecName: Full=Oxygen-evolving enhancer protein 2, chloroplastic; Short=OEE2; AltName: Full=23 kDa subunit of oxygen evolving system of photosystem II; AltName: Full=OEC 23 kDa subunit; AltName: Full=23 kDa thylakoid membrane protein; Flags: Precursor >gi|19317|emb|CAA44736.1| photosystem II 23 kDa protein [Solanum lycopersicum]	Unigene77135_All//2.00E-55//AT2G30790| PSBP-2 (photosystem II subunit P-2); calcium ion binding	Unigene77135_All//3.00E-08//TC135055		ko00195|Photosynthesis		nr +
Unigene77140_All	293	0.18	0.00	0.36	2.21	2.00	3.70	5.19	14.41	35.49	-7.48E+00	6.03E-01		1.03E+00	7.01E-01		-1.46E-01	8.39E-01		7.43E-01	2.89E-01		1.47E+00	1.46E-07	Up	2.77E+00	1.64E-39	Up	Unigene77140_All//gi|1170745|sp|P46518.1|LEA14_GOSHI//1.00E-06//RecName: Full=Late embryogenesis abundant protein Lea14-A >gi|167326|gb|AAA18542.1| Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi|167328|gb|AAA18543.1| Group 4 late embryogenesis-abundant protein [Gossypium hirsutum]		Unigene77140_All//4.00E-59//BF272993				nr +
Unigene7716_All	610	0.17	1.66	0.52	0.90	0.96	0.22	1.52	0.82	1.50	3.28E+00	3.79E-04	Up	1.61E+00	3.04E-01		9.54E-02	9.50E-01		-2.02E+00	7.04E-02		-8.91E-01	1.72E-01		-2.17E-02	9.60E-01				Unigene7716_All//0.00E+00//DT462826				
Unigene77165_All	292	0.00	2.43	1.09	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	1.01E+01	4.46E-02		null	null		null	null		null	null		null	null		Unigene77165_All//sp|Q00341|VIGLN_HUMAN//2.00E-16//Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2						swissprot +
Unigene77184_All	240	0.44	0.00	0.44	0.62	2.01	4.52	7.40	12.54	15.60	-8.77E+00	3.67E-01		2.53E-02	9.97E-01		1.69E+00	1.66E-01		2.86E+00	4.97E-04	Up	7.61E-01	1.80E-02		1.08E+00	1.21E-04	Up	Unigene77184_All//gi|297834070|ref|XP_002884917.1|//3.00E-27//EMB2742 [Arabidopsis lyrata subsp. lyrata] >gi|297330757|gb|EFH61176.1| EMB2742 [Arabidopsis lyrata subsp. lyrata]	Unigene77184_All//1.00E-28//AT3G12670| emb2742 (embryo defective 2742); CTP synthase/ catalytic	Unigene77184_All//2.00E-91//TC176389		ko00240|Pyrimidine metabolism		nr +
Unigene7719_All	336	2.18	13.42	2.69	5.49	6.76	6.86	9.56	12.56	6.05	2.62E+00	3.00E-13	Up	3.06E-01	6.57E-01		3.02E-01	5.45E-01		3.22E-01	4.88E-01		3.94E-01	1.51E-01		-6.61E-01	2.62E-02				Unigene7719_All//5.00E-136//gi|164276435|gb|ES817792.1|ES817792				
Unigene77208_All	227	2.30	0.00	1.17	23.48	13.20	4.18	0.19	0.00	0.00	-1.12E+01	2.92E-03		-9.75E-01	3.76E-01		-8.31E-01	5.44E-04		-2.49E+00	5.92E-16	Down	-7.54E+00	6.45E-01		-7.54E+00	6.02E-01		Unigene77208_All//gi|124359815|gb|ABO33072.2|//2.00E-09//Nitrate/chlorate transporter, related [Medicago truncatula]	Unigene77208_All//3.00E-09//AT3G45660| proton-dependent oligopeptide transport (POT) family protein					nr +
Unigene7721_All	515	3.05	0.39	1.34	4.06	0.40	1.32	0.90	0.41	0.15	-2.95E+00	1.18E-05	Down	-1.18E+00	3.61E-02		-3.34E+00	5.54E-10	Down	-1.63E+00	4.42E-04	Down	-1.15E+00	2.53E-01		-2.55E+00	2.35E-02		Unigene7721_All//gi|30688201|ref|NP_850863.1|//6.00E-62//CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase [Arabidopsis thaliana] >gi|66773939|sp|Q9FUJ1.1|CKX7_ARATH RecName: Full=Cytokinin dehydrogenase 7; AltName: Full=Cytokinin oxidase 7; Short=CK07; Short=AtCKX7; Short=AtCKX5 >gi|11120514|gb|AAG30908.1|AF303981_1 cytokinin oxidase [Arabidopsis thaliana] >gi|29294045|gb|AAO73882.1| FAD-linked oxidoreductase family [Arabidopsis thaliana]	Unigene7721_All//5.00E-63//AT5G21482| CKX7 (CYTOKININ OXIDASE 7); cytokinin dehydrogenase/ oxidoreductase	Unigene7721_All//5.00E-177//ES790738		ko00908|Zeatin biosynthesis	GO:0006091//GO:0009690//GO:0016645//GO:0030554//GO:0031410	nr -
Unigene7722_All	584	0.00	0.00	0.00	0.00	0.00	0.31	153.12	72.57	154.78	null	null		null	null		null	null		8.27E+00	1.93E-01		-1.08E+00	3.12E-89	Down	1.56E-02	7.88E-01		Unigene7722_All//gi|79606086|ref|NP_973975.2|//7.00E-31//TLL1 (TRIACYLGLYCEROL LIPASE-LIKE 1); triacylglycerol lipase [Arabidopsis thaliana]	Unigene7722_All//2.00E-25//AT1G45201| TLL1 (TRIACYLGLYCEROL LIPASE-LIKE 1); triacylglycerol lipase	Unigene7722_All//2.00E-10//TC151789			GO:0043231	nr +
Unigene7723_All	325	28.82	16.68	19.83	62.23	46.94	46.69	33.17	19.03	12.50	-7.89E-01	2.79E-05		-5.40E-01	5.91E-03		-4.07E-01	3.90E-04		-4.14E-01	5.86E-04		-8.02E-01	2.62E-07		-1.41E+00	1.41E-17	Down			Unigene7723_All//2.00E-132//TC175034				
Unigene77234_All	599	0.00	1.61	2.04	0.08	0.00	0.00	0.14	0.00	0.00	1.07E+01	1.37E-05	Up	1.10E+01	9.09E-07	Up	-6.38E+00	5.45E-01		-6.38E+00	6.22E-01		-7.14E+00	3.98E-01		-7.14E+00	3.54E-01		Unigene77234_All//gi|192910906|gb|ACF06561.1|//3.00E-41//ribosomal protein L18a [Elaeis guineensis]	Unigene77234_All//1.00E-41//AT1G29970| RPL18AA (60S RIBOSOMAL PROTEIN L18A-1)			ko03010|Ribosome		nr +
Unigene7724_All	458	1.03	0.44	0.81	0.11	1.13	1.38	4.43	2.56	1.30	-1.22E+00	2.72E-01		-3.37E-01	7.34E-01		3.37E+00	1.82E-02		3.67E+00	5.05E-03		-7.94E-01	5.02E-02		-1.76E+00	3.30E-05	Down								
Unigene7725_All	1258	0.83	0.60	0.34	13.62	17.52	7.93	1.68	0.17	0.54	-4.61E-01	4.86E-01		-1.30E+00	7.46E-02		3.63E-01	1.20E-03		-7.80E-01	2.61E-09		-3.34E+00	6.18E-10	Down	-1.64E+00	5.85E-05	Down	Unigene7725_All//gi|87162706|gb|ABD28501.1|//2.00E-24//Zinc finger, C2H2-type [Medicago truncatula]	Unigene7725_All//3.00E-05//AT1G55110| AtIDD7 (Arabidopsis thaliana Indeterminate(ID)-Domain 7); nucleic acid binding / transcription factor/ zinc ion binding	Unigene7725_All//2.00E-24//TC140948	C2H2			nr +

Unigene7726_All	401	1.17	1.26	0.53	4.72	6.70	3.49	0.00	1.56	1.29	1.06E-01	9.22E-01		-1.14E+00	3.32E-01		5.05E-01	2.12E-01		-4.35E-01	4.01E-01		1.06E+01	1.47E-04	Up	1.03E+01	6.13E-04	Up	Unigene7726_All//gi|115467528|ref|NP_001057363.1|//2.00E-58//0s06g0272000 [Oryza sativa Japonica Group] >gi|113595403|dbj|BAF19277.1|Os06g0272000 [Oryza sativa Japonica Group]	Unigene7726_All//6.00E-12//AT3G47110| leucine-rich repeat transmembrane protein kinase, putative	Unigene7726_All//1.00E-72//TC179552		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152//GO:0016020	nr -
Unigene77280_All	373	0.00	3.40	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.85E-07	Up	1.10E+01	3.25E-04	Up	null	null		null	null		null	null		null	null									
Unigene77288_All	289	0.18	0.35	3.13	0.00	0.24	0.00	0.00	0.00	0.00	9.54E-01	7.24E-01		4.11E+00	3.91E-04	Up	7.90E+00	6.02E-01		null	null		null	null		null	null									ESTscan -
Unigene7729_All	330	0.00	2.92	0.00	0.60	1.98	2.33	0.00	1.27	0.97	1.15E+01	1.37E-05	Up	null	null		1.72E+00	8.16E-02		1.95E+00	3.23E-02		1.03E+01	3.65E-03		9.92E+00	1.34E-02		Unigene7729_All//gi|18405611|ref|NP_566829.1|//2.00E-35//nodulin MtN3 family protein [Arabidopsis thaliana] >gi|25090096|gb|AAN72227.1|At3g28008/At3g28008 [Arabidopsis thaliana]	Unigene7729_All//7.00E-37//AT3G28007| nodulin MtN3 family protein				GO:0016020	nr -
Unigene773_All	3823	3.13	3.67	2.67	36.89	34.74	21.90	24.14	9.02	10.73	2.28E-01	1.49E-01		-2.29E-01	2.15E-01		-8.65E-02	6.25E-02		-7.52E-01	4.97E-68		-1.42E+00	7.42E-142	Down	-1.17E+00	5.48E-108	Down	Unigene773_All//gi|127519339|gb|AB028522.1|//0.00E+00//kinesin-related protein [Gossypium hirsutum]	Unigene773_All//0.00E+00//AT2G47500| ATP binding / microtubule motor	Unigene773_All//0.00E+00//TC167954			GO:0003774//GO:0006950//GO:0007017//GO:0015630//GO:0032559	nr +
Unigene7730_All	623	0.50	0.16	1.79	1.68	1.66	1.16	8.69	3.62	1.22	-1.63E+00	2.76E-01		1.83E+00	1.24E-02		-1.81E-02	9.61E-01		-5.34E-01	4.55E-01		-1.26E+00	1.11E-07	Down	-2.84E+00	8.85E-22	Down	Unigene7730_All//gi|15223919|ref|NP_172939.1|//3.00E-14//atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase >gi|68565943|sp|Q9LQ5.1|NUD18_ARATH RecName: Full=Nudix hydrolase 18, mitochondrial; Short=AtNUDT18; Flags: Precursor >gi|8778216|gb|AAF79225.1|AC006917_10 F10B6.26 [Arabidopsis thaliana]	Unigene7730_All//2.00E-15//AT1G14860| atnudt18 (Arabidopsis thaliana Nudix hydrolase homolog 18); hydrolase	Unigene7730_All//6.00E-63//TC142601			GO:0016462	nr +
Unigene77303_All	281	0.00	1.08	3.41	0.00	0.25	0.00	0.15	0.30	0.00	1.01E+01	4.37E-02		1.17E+01	2.45E-05	Up	7.94E+00	6.02E-01		null	null		9.83E-01	7.29E-01		-7.23E+00	6.02E-01									
Unigene77308_All	266	0.98	1.90	0.20	3.56	5.57	1.36	2.86	0.31	0.45	9.54E-01	3.73E-01		-2.30E+00	2.42E-01		6.46E-01	2.65E-01		-1.39E+00	6.08E-02		-3.19E+00	7.92E-04	Down	-2.67E+00	1.64E-03									
Unigene7731_All	458	0.00	0.11	0.00	10.01	5.56	6.51	12.37	4.02	2.00	6.79E+00	6.10E-01		null	null		-8.47E-01	1.27E-03		-6.21E-01	2.81E-02		-1.62E+00	2.61E-11	Down	-2.63E+00	5.13E-21	Down	Unigene7731_All//gi|224131814|ref|XP_002321185.1|//3.00E-11//predicted protein [Populus trichocarpa] >gi|222861958|gb|EEE99500.1|predicted protein [Populus trichocarpa]						nr +
Unigene77318_All	352	0.00	0.00	2.12	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.10E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene77318_All//gi|10945615|gb|AAG24616.1|AF298594_1/2.00E-17//arabinogalactan protein [Nicotiana alata]						nr -
Unigene77329_All	260	0.00	0.19	0.82	0.00	0.00	0.00	0.81	0.96	5.67	7.61E+00	6.10E-01		9.68E+00	1.38E-01		null	null		null	null		2.46E-01	8.53E-01		2.80E+00	2.86E-06	Up	Unigene77329_All//gi|18404212|ref|NP_566749.1|//1.00E-26//ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase [Arabidopsis thaliana] >gi|118398574|sp|Q56V10.2|AL2C4_ARATH RecName: Full=Aldehyde dehydrogenase family 2 member C4; AltName: Full=ALDH1a; AltName: Full=Protein REDUCED EPIDERMAL FLUORESCENCE 1 >gi|9294041|dbj|BAB01998.1|aldehyde dehydrogenase [Arabidopsis thaliana] >gi|15912241|gb|AAL08254.1|aldehyde dehydrogenase [Arabidopsis thaliana] >gi|20530143|gb|AAM27004.1|aldehyde dehydrogenase ALDH1a [Arabidopsis thaliana]	Unigene77329_All//1.00E-25//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene77329_All//1.00E-111//TC157786		ko00940|Phenylpropanoid biosynthesis		nr +
Unigene77336_All	758	2.76	3.07	2.18	4.99	5.22	1.73	0.95	1.05	0.16	1.55E-01	7.01E-01		-3.42E-01	4.64E-01		6.49E-02	8.57E-01		-1.53E+00	2.49E-06	Down	1.44E-01	8.36E-01		-2.59E+00	2.81E-03		Unigene77336_All//gi|297724159|ref|NP_001174443.1|//6.00E-20//Os05g0434000 [Oryza sativa Japonica Group] >gi|255676397|dbj|BAH93171.1|Os05g0434000 [Oryza sativa Japonica Group]						nr -
Unigene77339_All	252	1.66	1.41	0.42	3.95	0.41	0.36	2.68	2.49	1.11	-2.39E-01	8.09E-01		-1.97E+00	1.51E-01		-3.27E+00	6.96E-05	Down	-3.46E+00	1.73E-04	Down	-1.10E-01	8.90E-01		-1.28E+00	9.48E-02		Unigene77339_All//gi|15231343|ref|NP_190199.1|//6.00E-12//MYB111 (MYB DOMAIN PROTEIN 111); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75335604|sp|Q9LX82.1|MYB48_ARATH RecName: Full=Transcription factor MYB48; AltName: Full=Myb-related protein 48; Short=AtMYB48 >gi|7799001|emb|CAB90940.1| Myb DNA binding protein-like [Arabidopsis thaliana] >gi|41619274|gb|AAS10064.1| MYB transcription factor [Arabidopsis thaliana]	Unigene77339_All//2.00E-13//AT3G46130| MYB111 (MYB DOMAIN PROTEIN 111); DNA binding / transcription factor	Unigene77339_All//8.00E-11//gi|78348549|gb|DT568823.1|DT568823	MYB			nr +
Unigene7734_All	659	0.00	0.00	0.00	0.00	0.00	0.00	1.54	1.78	11.91	null	null		null	null		null	null		null	null		2.06E-01	7.23E-01		2.95E+00	5.92E-32	Up	Unigene7734_All//gi|72255633|gb|AAZ66951.1|//3.00E-63//117M18_32 [Brassica rapa]	Unigene7734_All//5.00E-63//AT5G10530| lectin protein kinase, putative	Unigene7734_All//4.00E-27//ES839443		ko04626|Plant-pathogen interaction	GO:0003676//GO:0004702//GO:0004713//GO:0006260//GO:0006325//GO:0006464//GO:0030246//GO:0032559//GO:0034061//GO:0043231//GO:0044427	nr -
Unigene77340_All	400	0.13	0.00	2.40	0.00	0.17	0.00	0.00	0.00	0.00	-7.03E+00	6.03E-01		4.20E+00	2.16E-04	Up	7.43E+00	6.02E-01		null	null		null	null		null	null									ESTscan -
Unigene7735_All	2195	0.00	0.00	0.00	0.00	0.00	0.00	1.12	1.22	9.33	null	null		null	null		null	null		null	null		1.25E-01	7.34E-01		3.06E+00	2.57E-85	Up	Unigene7735_All//gi|7671450|emb|CAB89390.1|//0.00E+00//lectin-like protein kinase-like [Arabidopsis thaliana] >gi|91806848|gb|ABE66151.1| lectin protein kinase [Arabidopsis thaliana]	Unigene7735_All//0.00E+00//AT5G10530| lectin protein kinase, putative	Unigene7735_All//4.00E-79//CA994027		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004674//GO:0004713//GO:0004871	nr -
Unigene77365_All	271	0.00	1.12	2.55	0.00	0.13	0.00	0.00	0.00	0.00	1.01E+01	4.37E-02		1.13E+01	6.12E-04	Up	6.99E+00	8.16E-01		null	null		null	null		null	null		Unigene77365_All//gi|224140965|ref|XP_002323847.1|//8.00E-11//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222866849|gb|EEF03980.1|multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene77365_All//7.00E-12//AT3G28860| ABCB19; ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter			ko02010|ABC transporters		nr -
Unigene77368_All	418	0.50	0.24	2.93	0.48	0.16	0.00	0.00	0.00	0.00	-1.05E+00	5.63E-01		2.55E+00	8.25E-04	Up	-1.53E+00	4.15E-01		-8.90E+00	1.33E-01		null	null		null	null		Unigene77368_All//gi|116058760|emb|CAL54467.1|//1.00E-23//COG0013: Alanyl-tRNA synthetase (ISS) [Ostreococcus tauri]	Unigene77368_All//7.00E-22//AT1G50200| ALATS (ALANYL-TRNA SYNTHETASE); ATP binding / alanine-tRNA ligase/ ligase, forming aminoacyl-tRNA and related compounds / nucleic acid binding / nucleotide binding			ko00970|Aminoacyl-tRNA biosynthesis		nr -
Unigene7738_All	656	4.79	1.78	5.93	7.06	4.51	1.10	0.19	0.57	0.36	-1.43E+00	1.00E-04	Down	3.08E-01	3.73E-01		-6.46E-01	1.52E-02		-2.68E+00	4.38E-15	Down	1.57E+00	1.95E-01		9.14E-01	5.41E-01				Unigene7738_All//4.00E-21//TC139318				
Unigene77399_All	230	0.00	0.00	5.79	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.25E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene77399_All//gi|288563554|gb|ADC53692.1|//7.00E-36//heat shock protein 90-1 [Cryptocoryne ciliata]	Unigene77399_All//1.00E-15//AT5G56010| HSP81-3; ATP binding / unfolded protein binding	Unigene77399_All//4.00E-43//EV496890		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene774_All	1037	6.36	1.81	1.28	10.57	5.11	3.05	8.24	3.22	5.57	-1.81E+00	2.00E-12	Down	-2.31E+00	6.12E-16	Down	-1.05E+00	6.71E-11	Down	-1.79E+00	2.09E-21	Down	-1.35E+00	6.67E-13	Down	-5.64E-01	9.74E-04		Unigene774_All//gi|3695063|gb|AAC62626.1|//1.00E-83//rac GTPase activating protein 3 [Lotus japonicus]	Unigene774_All//3.00E-81//AT4G03100| rac GTPase activating protein, putative	Unigene774_All//0.00E+00//TC160759			GO:0023060//GO:0044464	nr +
Unigene7741_All	261	4.41	4.66	11.22	0.95	2.51	0.35	0.97	1.12	0.46	7.93E-02	9.00E-01		1.35E+00	6.17E-04	Up	1.39E+00	1.51E-01		-1.46E+00	4.06E-01		2.06E-01	8.68E-01		-1.09E+00	4.28E-01				Unigene7741_All//9.00E-20//DR463788				
Unigene7742_All	755	3.47	4.76	4.94	4.95	5.38	5.26	3.14	1.00	2.80	4.60E-01	1.62E-01		5.11E-01	1.32E-01		1.21E-01	7.58E-01		8.92E-02	7.96E-01		-1.65E+00	2.75E-05	Down	-1.65E-01	6.47E-01				Unigene7742_All//8.00E-75//ES839952				
Unigene77425_All	424	2.47	0.24	1.26	3.05	3.74	2.66	4.59	2.46	1.50	-3.37E+00	2.13E-04	Down	-9.75E-01	1.67E-01		2.91E-01	6.10E-01		-1.98E-01	7.33E-01		-8.96E-01	3.11E-02		-1.61E+00	1.60E-04	Down	Unigene77425_All//gi|115453553|ref|NP_001050377.1|//6.00E-16//Os03g0418800 [Oryza sativa Japonica Group] >gi|108708852|gb|ABF96647.1|Nuclear transport factor 2 domain containing protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548848|dbj|BAF12291.1|Os03g0418800 [Oryza sativa Japonica Group]	Unigene77425_All//7.00E-14//AT5G60980| nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein					nr +
Unigene7743_All	2027	0.15	0.45	0.00	0.05	0.14	1.38	0.71	1.01	9.69	1.54E+00	4.51E-02		-7.28E+00	4.88E-02		1.47E+00	4.19E-01		4.81E+00	3.67E-14	Up	5.11E-01	2.23E-01		3.77E+00	2.29E-98	Up	Unigene7743_All//gi|15235905|ref|NP_194034.1|//0.00E+00//MATE efflux protein-related [Arabidopsis thaliana]	Unigene7743_All//3.00E-174//AT4G23030| MATE efflux protein-related	Unigene7743_All//2.00E-78//gi|161434434|gb|EX167260.1|EX167260			GO:0015291//GO:0015893//GO:0044464	nr -
Unigene77466_All	210	0.00	3.86	0.76	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.31E-05	Up	9.57E+00	2.35E-01		null	null		null	null		null	null		null	null		Unigene77466_All//sp|P17207|SER3_DROME//4.00E-07//Serine protease 3 OS=Drosophila melanogaster GN=Jon99Ci PE=2 SV=2						swissprot +
Unigene7748_All	355	6.19	25.26	10.35	10.52	10.38	10.05	26.56	35.56	17.28	2.03E+00	4.41E-19	Up	7.42E-01	2.66E-02		-2.00E-02	9.58E-01		-6.64E-02	8.55E-01		4.21E-01	3.23E-03		-6.20E-01	1.30E-04		Unigene7748_All//5.00E-18//AT4G21980| APG8A (AUTOPHAGY 8A); APG8 activating enzyme/ APG8-specific protease/ Atg8 ligase	Unigene7748_All//0.00E+00//gi|164289745|gb|ES798808.1|ES798808			ko04140|Regulation of autophagy	GO:0004871//GO:0005488//GO:0008641//GO:0016879//GO:0019783//GO:0044248//GO:0044437	nr +

Unigene77480_All	259	0.00	0.00	3.08	0.77	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	1.72E-04	Up	-9.59E+00	8.38E-02		-9.59E+00	1.33E-01		null	null		null	null		Unigene77480_All//gi|132104|sp|P07180.1|RBS3A_SOLLC//7.00E-49//RecName: Full=Ribulose bisphosphate carboxylase small chain 3A/3C, chloroplastic; Short=RuBisCO small subunit 3A/3C; Flags: Precursor >gi|19334|emb|CAA29402.1| ribulose 1,5-bisphosphate carboxylase/oxygenase [Solanum lycopersicum] >gi|19338|emb|CAA29404.1| ribulose 1,5-bisphosphate carboxylase/oxygenase [Solanum lycopersicum] >gi|170500|gb|AAA34190.1| ribulose-1,5-bisphophate carboxylase/ oxygenase small subunit [Solanum lycopersicum]	Unigene77480_All//6.00E-40//AT1G67090| RBCS1A (RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A); copper ion binding / ribulose-bisphosphate carboxylase	Unigene77480_All//2.00E-11//EX167659		ko00710|Carbon fixation in photosynthetic organisms//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005488//GO:0009536//GO:0015977//GO:0016491//GO:0016831//GO:0043094	nr +
Unigene77482_All	237	0.66	0.00	0.00	0.42	0.15	0.19	16.23	29.80	2.86	-9.37E+00	2.14E-01		-9.37E+00	2.42E-01		-1.53E+00	5.84E-01		-1.14E+00	6.74E-01		8.77E-01	9.22E-06		-2.51E+00	8.49E-14	Down			Unigene77482_All//1.00E-46//TC154834				
Unigene77490_All	381	0.00	2.79	2.66	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.79E-06	Up	1.14E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene77490_All//sp|Q27415|NLP_DROME//1.00E-46//Nucleoplasmin-like protein OS=Drosophila melanogaster GN=Nlp PE=1 SV=1					swissprot +
Unigene775_All	601	0.96	0.00	0.53	0.91	0.86	0.60	3.24	0.56	1.99	-9.90E+00	1.52E-03		-8.49E-01	3.97E-01		-8.52E-02	9.07E-01		-6.01E-01	5.66E-01		-2.54E+00	3.67E-07	Down	-7.03E-01	7.80E-02		Unigene775_All//gi|3695063|gb|AAC62626.1|//7.00E-68//rac GTPase activating protein 3 [Lotus japonicus]	Unigene775_All//3.00E-65//AT4G03100| rac GTPase activating protein, putative	Unigene775_All//0.00E+00//TC176649			GO:0023060//GO:0044464	nr -
Unigene77502_All	563	0.19	0.36	2.65	0.09	0.06	0.00	0.00	0.00	0.00	9.54E-01	6.20E-01		3.83E+00	3.20E-06	Up	-5.32E-01	8.20E-01		-6.47E+00	6.21E-01		null	null		null	null		Unigene77502_All//COG4986//4.00E-44//ABC-type anion transport system, duplicated permease component						cog -
Unigene77532_All	297	4.40	3.92	2.51	6.54	9.39	8.52	15.66	3.24	8.45	-1.67E-01	7.57E-01		-8.11E-01	1.90E-01		5.22E-01	1.80E-01		3.81E-01	3.95E-01		-2.27E+00	2.61E-14	Down	-8.90E-01	2.49E-04		Unigene77532_All//gi|115479367|ref|NP_001063277.1|//4.00E-30//Os09g0439700 [Oryza sativa Japonica Group] >gi|51091402|dbj|BAD36145.1| membrane protein PTM1-like [Oryza sativa Japonica Group] >gi|113631510|dbj|BAF25191.1| Os09g0439700 [Oryza sativa Japonica Group]	Unigene77532_All//6.00E-38//AT1G72480| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: Golgi apparatus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Transmembrane receptor, eukaryota (InterPro:IPR009637); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G01070.1); Has 422 Blast hits to 420 proteins in 121 species: Archae - 0; Bacteria - 0; Metazoa - 208; Fungi - 101; Plants - 83; Viruses - 0; Other Eukaryotes - 30 (source: NCBI BLink).	Unigene77532_All//7.00E-141//DW516840			GO:0031224//GO:0031410//GO:0043231	nr -
Unigene77537_All	314	0.00	2.58	0.68	0.00	0.00	0.00	0.00	0.00	1.13E+01	9.31E-05	Up	9.41E+00	1.38E-01		null	null		null	null		null	null		null	null		Unigene77537_All//sp|Q7JUY7|CED6_DROME//3.00E-12//PTB domain-containing adapter protein ced-6 OS=Drosophila melanogaster GN=ced-6 PE=1 SV=1					swissprot -
Unigene77554_All	508	0.00	0.00	6.08	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.26E+01	4.50E-17	Up	null	null		null	null		null	null		null	null		Unigene77554_All//gi|75181359|sp|Q9LZX1.1|Y5175_ARATH//7.00E-47//RecName: Full=UPF0706 protein At5g01750 >gi|13926237|gb|AAK49593.1|AF372877_1 AT5g01750/T20L15_20 [Arabidopsis thaliana] >gi|22655412|gb|AAM98298.1| At5g01750/T20L15_20 [Arabidopsis thaliana]	Unigene77554_All//2.00E-48//AT5G01750| unknown protein				GO:0009536	nr +
Unigene7756_All	474	0.00	0.00	0.45	0.84	2.54	1.24	2.50	0.53	2.27	null	null		8.81E+00	1.38E-01		1.60E+00	1.36E-02		5.59E-01	6.01E-01		-2.24E+00	4.21E-04	Down	-1.38E-01	7.88E-01		Unigene7756_All//gi|15221507|ref|NP_172136.1|//3.00E-65//ATGSL07 (glucan synthase-like 7); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|189081841|sp|Q9SHJ3.2|CALS7_ARATH RecName: Full=Callose synthase 7; AltName: Full=1,3-beta-glucan synthase; AltName: Full=Protein GLUCAN SYNTHASE-LIKE 7	Unigene7756_All//4.00E-66//AT1G06490| ATGSL07 (glucan synthase-like 7); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups				GO:0006074//GO:0016020//GO:0035251//GO:0043234	nr -
Unigene7757_All	1425	0.00	28.30	10.99	0.00	0.05	0.00	0.00	0.00	0.00	1.48E+01	8.16E-233	Up	1.34E+01	2.81E-88	Up	5.59E+00	6.02E-01		null	null		null	null		null	null		Unigene7757_All//sp|P11996|LSP1B_DROME//8.00E-135//Larval serum protein 1 beta chain OS=Drosophila melanogaster GN=Lsp1beta PE=2 SV=3					swissprot +
Unigene7758_All	644	0.00	0.00	0.00	0.00	0.00	0.00	14.64	2.99	2.04	null	null		null	null		null	null		null	null		-2.29E+00	1.43E-28	Down	-2.84E+00	1.85E-37	Down	Unigene7758_All//gi|215536418|gb|AAM62711.1|//2.00E-06//ankyrin-like protein [Arabidopsis thaliana]		Unigene7758_All//2.00E-72//TC175720				nr +
Unigene77582_All	277	1.32	2.20	3.46	3.96	6.84	4.57	3.97	2.26	10.36	7.31E-01	4.16E-01		1.39E+00	7.11E-02		7.89E-01	9.95E-02		2.07E-01	7.34E-01		-8.10E-01	1.69E-01		1.38E+00	3.85E-05	Up	Unigene77582_All//gi|145359475|ref|NP_200825.2|//2.00E-06//RNA binding / nucleic acid binding / nucleotide binding / protein binding / zinc ion binding [Arabidopsis thaliana]	Unigene77582_All//6.00E-08//AT5G60170| RNA binding / nucleic acid binding / nucleotide binding / protein binding / zinc ion binding	Unigene77582_All//2.00E-24//gi|109861541|gb|DW490518.1|DW490518		ko03018|RNA degradation		nr +
Unigene7759_All	366	9.58	7.89	8.29	18.92	14.87	18.26	24.49	17.93	10.23	-2.80E-01	4.01E-01		-2.08E-01	5.78E-01		-3.48E-01	1.25E-01		-5.09E-02	8.46E-01		-4.50E-01	9.45E-03		-1.26E+00	1.43E-12	Down			Unigene7759_All//2.00E-111//gi|21098840|gb|BQ411153.1|BQ411153				
Unigene77593_All	269	0.00	0.00	2.77	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.14E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene77593_All//gi|224131780|ref|XP_002328106.1|//6.00E-17//f-box family protein [Populus trichocarpa] >gi|222837621|gb|EEE75986.1| f-box family protein [Populus trichocarpa]	Unigene77593_All//2.00E-18//AT3G44326| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: Cyclin-like F-box (InterPro:IPR001810); BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT2G27310.1); Has 56 Blast hits to 56 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).				GO:0009536	nr -
Unigene776_All	2152	1.60	0.38	0.32	1.11	0.40	0.55	1.69	3.32	9.94	-2.09E+00	4.11E-08	Down	-2.32E+00	1.21E-08	Down	-1.47E+00	1.89E-04	Down	-1.03E+00	1.26E-02		9.75E-01	8.51E-07		2.56E+00	9.46E-74	Up	Unigene776_All//gi|3695063|gb|AAC62626.1|//7.00E-73//rac GTPase activating protein 3 [Lotus japonicus]	Unigene776_All//2.00E-75//AT4G03100| rac GTPase activating protein, putative	Unigene776_All//0.00E+00//TC160759			GO:0023060//GO:0044464	nr -
Unigene77609_All	214	0.00	1.66	3.23	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	2.43E-02		1.17E+01	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene77609_All//sp|Q6IFU8|K1C17_RAT//1.00E-10//Keratin, type I cytoskeletal 17 OS=Rattus norvegicus GN=Krt17 PE=2 SV=1					swissprot +
Unigene77617_All	409	0.00	0.37	2.99	0.00	0.00	0.00	0.00	0.00	0.00	8.54E+00	2.32E-01		1.15E+01	9.09E-07	Up	null	null		null	null		null	null		null	null		Unigene77617_All//gi|8131701|dbj|BAA96367.1|//2.00E-50//ribosomal protein L27 [Panax ginseng]	Unigene77617_All//1.00E-48//AT4G15000| 60S ribosomal protein L27 (RPL27C)	Unigene77617_All//2.00E-28//gi|78337699|gb|DT557973.1|DT557973		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr -
Unigene7763_All	400	2.75	0.13	1.46	2.12	0.77	0.68	1.16	1.78	1.79	-4.44E+00	2.09E-05	Down	-9.07E-01	1.87E-01		-1.45E+00	5.13E-02		-1.64E+00	4.17E-02		6.11E-01	4.27E-01		6.25E-01	3.96E-01				Unigene7763_All//8.00E-89//gi|109863405|gb|DW492382.1|DW492382				
Unigene77646_All	219	0.48	5.78	0.00	0.00	0.16	0.00	0.00	0.00	0.00	3.60E+00	2.27E-05	Up	-8.90E+00	3.87E-01		7.30E+00	8.16E-01		null	null		null	null		null	null				Unigene77646_All//2.00E-54//DW504421				ESTscan +
Unigene77648_All	354	0.00	0.29	1.96	0.42	0.29	0.00	0.00	0.00	0.00	8.16E+00	3.81E-01		1.09E+01	6.12E-04	Up	-5.33E-01	7.83E-01		-8.72E+00	2.31E-01		null	null		null	null		Unigene77648_All//gi|219116887|ref|XP_002179238.1|//3.00E-08//dolichyl-phosphate mannosyltransferase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217409129|gb|EEC49061.1| dolichyl-phosphate mannosyltransferase [Phaeodactylum tricornutum CCAP 1055/1]	Unigene77648_All//2.00E-07//AT1G20575| dolichyl-phosphate beta-D-mannosyltransferase, putative / dolichol-phosphate mannosyltransferase, putative / mannose-P-dolichol synthase, putative			ko00510|N-Glycan biosynthesis		nr +
Unigene7766_All	1672	1.16	0.85	1.72	2.41	1.89	0.59	4.48	0.72	0.48	-4.48E-01	3.48E-01		5.71E-01	1.42E-01		-3.49E-01	2.75E-01		-2.02E+00	1.46E-09	Down	-2.63E+00	1.36E-26	Down	-3.23E+00	7.53E-34	Down	Unigene7766_All//gi|224114037|ref|XP_002332458.1|//1.00E-149//cytochrome P450 [Populus trichocarpa] >gi|222832529|gb|EEE71006.1| cytochrome P450 [Populus trichocarpa]	Unigene7766_All//1.00E-91//AT5G25130| CYP71B12; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene7766_All//0.00E+00//TC167076		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		nr +
Unigene7767_All	695	0.60	1.60	2.15	1.94	2.68	0.45	5.54	8.00	2.01	1.41E+00	3.61E-02		1.83E+00	2.94E-03		4.67E-01	3.64E-01		-2.09E+00	1.00E-03		5.31E-01	1.94E-02		-1.46E+00	3.43E-07	Down	Unigene7767_All//gi|297720735|ref|NP_001172729.1|//5.00E-43//Os01g0935200 [Oryza sativa Japonica Group] >gi|148921414|dbj|BAF64446.1| HAP3 subunit of HAP complex [Oryza sativa Japonica Group] >gi|255674039|dbj|BAH91459.1| Os01g0935200 [Oryza sativa Japonica Group]	Unigene7767_All//2.00E-42//AT2G47810| NF-YB5 (NUCLEAR FACTOR Y, SUBUNIT B5); transcription factor	Unigene7767_All//5.00E-11//ES838097	CCAAT	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03420|Nucleotide excision repair//ko03410|Base excision repair//ko03030|DNA replication	GO:0001071//GO:0003677//GO:0006351//GO:0043231	nr +
Unigene77676_All	392	0.00	0.13	0.14	0.13	0.18	0.00	2.48	0.64	0.10	7.01E+00	6.10E-01		7.09E+00	6.25E-01		4.67E-01	9.54E-01		-6.99E+00	6.21E-01		-1.96E+00	4.44E-03		-4.61E+00	3.32E-06	Down	Unigene77676_All//gi|18414447|ref|NP_567465.1|//3.00E-49//PRLI-interacting factor K [Arabidopsis thaliana] >gi|17933289|gb|AAL48228.1|AF446353_1 AT4g15420/d13755w [Arabidopsis thaliana] >gi|21554166|gb|AAM63245.1| UFD1 like protein [Arabidopsis thaliana] >gi|23506013|gb|AAN28866.1| At4g15420/d13755w [Arabidopsis thaliana] >gi|111609946|gb|ABH11523.1| UFD1d [Arabidopsis thaliana]	Unigene77676_All//1.00E-50//AT4G15420| PRLI-interacting factor K	Unigene77676_All//9.00E-175//TC164093			GO:0016787//GO:0019941//GO:0044464//GO:0046914	nr -

Unigene7768_All	1145	0.00	9.74	3.12	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	6.54E-64	Up	1.16E+01	9.41E-20	Up	null	null		null	null		null	null		null	null		Unigene7768_All//gi|224001520|ref|XP_002290432.1|//1.00E-06//hypothetical protein THAPSDRAFT_262644 [Thalassiosira pseudonana CCMP1335] >gi|220973854|gb|EED92184.1| hypothetical protein THAPSDRAFT_262644 [Thalassiosira pseudonana CCMP1335]						nr -
Unigene7769_All	452	1.16	0.22	0.00	4.19	4.80	6.20	2.15	0.55	0.18	-2.37E+00	4.75E-02		-1.02E+01	4.73E-03		1.97E-01	7.04E-01		5.65E-01	1.48E-01		-1.96E+00	4.44E-03		-3.61E+00	2.14E-05	Down							
Unigene777_All	2139	4.62	1.78	1.62	5.99	4.80	3.12	1.74	0.49	0.76	-1.38E+00	1.54E-12	Down	-1.51E+00	1.16E-13	Down	-3.19E-01	4.17E-02		-9.38E-01	1.66E-09		-1.83E+00	5.85E-09	Down	-1.19E+00	2.65E-05	Down	Unigene777_All//gi|3695063|gb|AAC62626.1|//1.00E-143//rac GTPase activating protein 3 [Lotus japonicus]	Unigene777_All//5.00E-141//AT4G03100| rac GTPase activating protein, putative	Unigene777_All//0.00E+00//gi|164263392|gb|ES822208.1|ES822208				nr +
Unigene77712_All	766	0.20	0.13	0.35	0.59	0.54	0.53	1.55	0.22	0.16	-6.31E-01	7.26E-01		7.63E-01	6.43E-01		-1.18E-01	8.86E-01		-1.42E-01	9.00E-01		-2.82E+00	4.41E-05	Down	-3.31E+00	4.89E-06	Down	Unigene77712_All//gi|226502036|ref|NP_001148766.1|//1.00E-29//nucleic acid binding protein [Zea mays] >gi|195621990|gb|ACG32825.1| nucleic acid binding protein [Zea mays]	Unigene77712_All//5.00E-20//AT4G26000| PEP (PEPPER); RNA binding / nucleic acid binding	Unigene77712_All//0.00E+00//DW502134			GO:0003676//GO:0016787//GO:0048438//GO:0048513	nr -
Unigene77719_All	353	1.19	1.87	1.36	11.57	2.73	3.07	0.36	0.36	0.23	6.54E-01	4.48E-01		1.95E-01	8.39E-01		-2.08E+00	2.13E-11	Down	-1.91E+00	4.87E-09	Down	-1.66E-02	1.02E+00		-6.71E-01	7.18E-01		Unigene77719_All//gi|255587500|ref|XP_002534293.1|//4.00E-21//nucleic acid binding protein, putative [Ricinus communis] >gi|223525559|gb|EEF28090.1| nucleic acid binding protein, putative [Ricinus communis]		Unigene77719_All//2.00E-110//TC176541				nr +
Unigene7772_All	665	4.48	1.14	2.08	4.57	5.13	3.33	2.42	0.31	0.84	-1.97E+00	1.20E-06	Down	-1.11E+00	3.86E-03		1.66E-01	6.71E-01		-4.57E-01	2.26E-01		-2.94E+00	6.45E-07	Down	-1.53E+00	1.16E-03				Unigene7772_All//3.00E-12//BG446899				
Unigene77728_All	718	0.00	0.00	0.07	2.29	1.15	0.88	4.42	0.17	0.50	null	null		6.21E+00	6.25E-01		-9.92E-01	4.23E-02		-1.38E+00	8.58E-03		-4.66E+00	1.82E-18	Down	-3.14E+00	2.20E-14	Down	Unigene77728_All//gi|115444275|ref|NP_001045917.1|//5.00E-44//Os02g0152400 [Oryza sativa Japonica Group] >gi|113535448|dbj|BAF07831.1| Os02g0152400 [Oryza sativa Japonica Group]	Unigene77728_All//5.00E-42//AT5G38410| ribulose bisphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B)	Unigene77728_All//0.00E+00//TC137624	ko00710|Carbon fixation in photosynthetic organisms//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0009536//GO:0015977//GO:0016491//GO:0016831//GO:0043094	nr +
Unigene7773_All	1873	0.00	0.00	0.06	0.00	0.00	0.00	15.01	1.36	1.00	null	null		5.83E+00	3.89E-01		null	null		null	null		-3.46E+00	2.91E-129	Down	-3.91E+00	1.81E-147	Down	Unigene7773_All//gi|224139824|ref|XP_002332394.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222867924|gb|EEF05055.1| cytochrome P450 [Populus trichocarpa]	Unigene7773_All//1.00E-148//AT5G06900| CYP93D1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene7773_All//0.00E+00//CO076520	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0004497//GO:0005506//GO:0008152	nr -
Unigene77735_All	316	2.81	1.92	0.84	1.26	1.63	4.14	2.41	1.59	0.13	-5.49E-01	4.42E-01		-1.74E+00	3.79E-02		3.74E-01	7.71E-01		1.72E+00	6.54E-03		-6.02E-01	4.12E-01		-4.26E+00	8.65E-05	Down	Unigene77735_All//gi|17065276|gb|AAL32792.1|//3.00E-18//Unknown protein [Arabidopsis thaliana]	Unigene77735_All//1.00E-19//AT5G06210| RNA-binding protein, putative	Unigene77735_All//3.00E-134//TC144450		ko03010|Ribosome//ko03040|Spliceosome	GO:0003676//GO:0043231	nr +
Unigene7774_All	436	14.04	5.69	5.37	26.39	11.29	15.54	4.07	2.11	2.92	-1.30E+00	1.93E-07	Down	-1.39E+00	1.08E-07	Down	-1.22E+00	1.35E-14	Down	-7.64E-01	2.82E-06		-9.50E-01	3.09E-02		-4.78E-01	2.64E-01				Unigene7774_All//1.00E-26//TC130951				
Unigene77748_All	385	0.14	0.13	3.18	0.13	0.36	0.47	0.00	0.00	0.00	-4.64E-02	9.82E-01		4.55E+00	1.02E-05	Up	1.47E+00	6.17E-01		1.86E+00	4.57E-01		null	null		null	null		Unigene77748_All//COG1108//2.00E-25//ABC-type Mn2+/Zn2+ transport systems, permease components						cog +
Unigene7775_All	496	0.21	0.31	2.15	0.00	0.28	0.18	32.31	5.22	6.43	5.39E-01	7.78E-01		3.35E+00	3.36E-04	Up	8.12E+00	3.17E-01		7.51E+00	4.71E-01		-2.63E+00	3.06E-56	Down	-2.33E+00	1.54E-50	Down							
Unigene77764_All	207	0.00	1.96	0.51	0.00	0.50	0.00	0.61	1.41	4.04	1.09E+01	1.34E-02		9.01E+00	3.89E-01		8.96E+00	4.53E-01		null	null		1.21E+00	3.92E-01		2.72E+00	8.98E-04	Up			Unigene77764_All//2.00E-26//ES802395				ESTscan -
Unigene77777_All	389	1.48	9.64	4.11	21.90	11.77	8.82	1.63	4.41	2.15	2.70E+00	1.79E-11	Up	1.47E+00	9.57E-03		-8.95E-01	9.95E-07		-1.31E+00	8.75E-11	Down	1.43E+00	1.99E-03		4.00E-01	5.65E-01		Unigene77777_All//gi|30682547|ref|NP_849375.1|//7.00E-11//four F5 protein-related / 4F5 protein-related [Arabidopsis thaliana] >gi|28416731|gb|AAO42896.1| At4g13612 [Arabidopsis thaliana]		Unigene77777_All//8.00E-123//gi|13247283|gb|BF269631.2|BF269631				nr -
Unigene7778_All	1562	0.70	0.84	1.23	0.67	0.04	1.42	7.71	22.13	11.09	2.62E-01	6.27E-01		8.03E-01	1.02E-01		-3.92E+00	7.51E-06	Down	1.08E+00	1.35E-02		1.52E+00	4.30E-59	Up	5.24E-01	6.31E-06		Unigene7778_All//gi|297806791|ref|XP_002871279.1|//3.00E-52//F box protein family [Arabidopsis lyrata subsp. lyrata] >gi|34013883|gb|AAQ56109.1| F box protein family [Arabidopsis lyrata subsp. lyrata] >gi|297317116|gb|EFH47538.1| F box protein family [Arabidopsis lyrata subsp. lyrata]	Unigene7778_All//7.00E-45//AT5G07610| F-box family protein	Unigene7778_All//0.00E+00//DT462251				nr +
Unigene7779_All	510	245.29	246.79	348.00	252.29	247.87	268.15	84.73	182.59	124.52	8.80E-03	8.77E-01		5.05E-01	9.14E-38		-2.55E-02	6.68E-01		8.79E-02	7.29E-02		1.11E+00	5.05E-97	Up	5.55E-01	2.41E-21		Unigene7779_All//gi|225460694|ref|XP_002270196.1|//2.00E-19//PREDICTED: hypothetical protein [Vitis vinifera] >gi|147859485|emb|CAN81435.1| hypothetical protein [Vitis vinifera]		Unigene7779_All//0.00E+00//TC133113			GO:0005488	nr +
Unigene778_All	1728	6.72	4.87	2.96	5.45	6.32	6.12	5.65	1.14	2.24	-4.66E-01	5.31E-03		-1.18E+00	3.90E-11	Down	2.13E-01	2.70E-01		1.67E-01	4.17E-01		-2.31E+00	7.12E-30	Down	-1.34E+00	7.15E-15	Down	Unigene778_All//gi|3695063|gb|AAC62626.1|//1.00E-146//rac GTPase activating protein 3 [Lotus japonicus]	Unigene778_All//2.00E-127//AT4G03100| rac GTPase activating protein, putative	Unigene778_All//0.00E+00//ES812040				nr +
Unigene7780_All	1441	0.00	0.28	0.44	0.24	0.29	0.13	2.73	4.73	6.50	8.14E+00	1.34E-02		8.79E+00	1.15E-03		2.45E-01	8.52E-01		-9.49E-01	4.80E-01		7.93E-01	7.71E-05		1.25E+00	7.30E-13	Up	Unigene7780_All//gi|35187439|gb|AAQ84311.1|//3.00E-42//fiber protein Fb17 [Gossypium barbadense]	Unigene7780_All//9.00E-05//AT2G16900| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Phospholipase-like, arabidopsis (InterPro:IPR007942); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G35110.4); Has 353 Blast hits to 254 proteins in 60 species: Archae - 2; Bacteria - 4; Metazoa - 73; Fungi - 16; Plants - 115; Viruses - 51; Other Eukaryotes - 92 (source: NCBI BLink).	Unigene7780_All//0.00E+00//TC149710				nr -
Unigene77803_All	219	0.00	0.23	4.62	0.00	0.00	0.21	0.00	0.00	0.00	7.85E+00	6.10E-01		1.22E+01	1.27E-05	Up	null	null		7.69E+00	6.85E-01		null	null		null	null		Unigene77803_All//gi|8954295|gb|AAD27880.2|AF139468_1//1.00E-16//photosystem I reaction center subunit III [Vigna radiata]	Unigene77803_All//1.00E-14//AT1G31330| PSAF (photosystem I subunit F)			ko00195|Photosynthesis	GO:0009522//GO:0009526//GO:0009534//GO:0009570//GO:0044237	nr +
Unigene7781_All	390	2.55	0.26	1.91	4.60	6.36	3.47	0.54	0.75	0.41	-3.29E+00	3.81E-04	Down	-4.15E-01	5.72E-01		4.67E-01	2.80E-01		-4.04E-01	4.43E-01		4.69E-01	7.06E-01		-4.08E-01	7.55E-01								
Unigene7783_All	476	1.10	1.06	0.34	1.99	1.09	1.14	3.29	0.61	0.17	-4.63E-02	9.73E-01		-1.71E+00	1.40E-01		-8.74E-01	2.10E-01		-8.04E-01	2.77E-01		-2.42E+00	1.29E-05	Down	-4.30E+00	2.71E-09	Down	Unigene7783_All//gi|115474919|ref|NP_001061056.1|//9.00E-23//Os08g0162200 [Oryza sativa Japonica Group] >gi|113623025|dbj|BAF22970.1| Os08g0162200 [Oryza sativa Japonica Group]	Unigene7783_All//9.00E-22//AT3G24000| INVOLVED IN: biological_process unknown; EXPRESSED IN: shoot apex, carpel; EXPRESSED DURING: petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT3G23330.1); Has 15874 Blast hits to 5333 proteins in 187 species: Archae - 1; Bacteria - 6; Metazoa - 100; Fungi - 81; Plants - 15349; Viruses - 0; Other Eukaryotes - 337 (source: NCBI BLink).						nr +
Unigene7784_All	468	2.46	0.22	1.71	7.24	3.24	2.61	1.17	0.00	0.60	-3.51E+00	6.57E-05	Down	-5.27E-01	4.10E-01		-1.16E+00	2.33E-04	Down	-1.47E+00	1.86E-05	Down	-1.02E+01	4.61E-04	Down	-9.79E-01	2.50E-01		Unigene7784_All//gi|147846709|emb|CAN80639.1|//2.00E-27//hypothetical protein [Vitis vinifera]		Unigene7784_All//0.00E+00//TC151507			GO:0006351//GO:0030528	nr +
Unigene77844_All	365	0.29	0.69	2.77	2.05	1.60	1.86	2.32	1.26	2.40	1.28E+00	4.35E-01		3.27E+00	5.92E-04	Up	-3.52E-01	6.51E-01		-1.42E-01	8.59E-01		-8.79E-01	2.07E-01		5.17E-02	9.56E-01		Unigene77844_All//gi|115485835|ref|NP_001068061.1|//6.00E-08//Os11g0545800 [Oryza sativa Japonica Group] >gi|113645283|dbj|BAF28424.1| Os11g0545800 [Oryza sativa Japonica Group]	Unigene77844_All//5.00E-08//AT5G08710| regulator of chromosome condensation (RCC1) family protein / UVB-resistance protein-related	Unigene77844_All//7.00E-43//TC159378				nr +
Unigene77846_All	257	2.85	12.03	8.29	0.39	0.00	0.53	0.00	0.65	0.00	2.08E+00	3.16E-07	Up	1.54E+00	1.42E-03		-8.60E+00	3.09E-01		4.43E-01	8.60E-01		9.35E+00	1.38E-01		null	null		Unigene77846_All//gi|159481769|ref|XP_001698950.1|//1.00E-07//hypothetical protein CHLREDRAFT_155068 [Chlamydomonas reinhardtii] >gi|158269841|gb|EDO95983.1| predicted protein [Chlamydomonas reinhardtii]		Unigene77846_All//3.00E-32//CD486359				nr -
Unigene77848_All	515	0.20	0.00	3.31	0.19	0.27	0.35	0.00	0.00	0.00	-7.67E+00	3.67E-01		4.03E+00	2.79E-07	Up	4.67E-01	8.75E-01		8.58E-01	6.94E-01		null	null		null	null								ESTscan +
Unigene77855_All	209	7.26	7.27	4.59	12.87	28.50	20.10	10.32	31.60	40.79	2.60E-03	9.97E-01		-6.63E-01	2.41E-01		1.15E+00	1.06E-06	Up	6.43E-01	3.21E-02		1.61E+00	6.19E-13	Up	1.98E+00	4.28E-22	Up			Unigene77855_All//3.00E-90//TC136687				
Unigene7787_All	415	1.26	0.00	0.00	4.80	1.49	0.65	83.03	245.74	35.61	-1.03E+01	2.92E-03		-1.03E+01	4.73E-03		-1.68E+00	1.67E-04	Down	-2.88E+00	3.00E-07	Down	1.57E+00	1.42E-180	Up	-1.22E+00	1.04E-43	Down	Unigene7787_All//gi|225452634|ref|XP_002276408.1|//1.00E-30//PREDICTED: similar to ABC transporter family protein [Vitis vinifera]	Unigene7787_All//1.00E-29//AT3G28345| ABC transporter family protein			ko02010|ABC transporters	GO:0000166//GO:0006810//GO:0015405//GO:0016020//GO:0016887	nr -
Unigene77878_All	458	0.00	0.22	0.23	0.87	1.43	1.18	1.38	4.93	0.26	7.79E+00	3.80E-01		7.86E+00	3.89E-01		7.15E-01	4.64E-01		4.44E-01	6.78E-01		1.83E+00	1.05E-05	Up	-2.41E+00	8.12E-03		Unigene77878_All//gi|224115096|ref|XP_002332236.1|//8.00E-40//cytochrome P450 [Populus trichocarpa] >gi|222831849|gb|EEE70326.1| cytochrome P450 [Populus trichocarpa]	Unigene77878_All//3.00E-30//AT4G37330| CYP81D1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0016491//GO:0043231//GO:0046872	nr +
Unigene77889_All	315	0.00	0.32	2.37	0.00	0.22	0.14	0.00	0.00	0.00	8.33E+00	3.80E-01		1.12E+01	3.25E-04	Up	7.77E+00	6.02E-01		7.16E+00	6.85E-01		null	null		null	null								ESTscan -
Unigene77917_All	523	0.20	0.97	1.93	0.00	0.20	0.17	0.00	0.00	0.00	2.28E+00	6.22E-02		3.27E+00	5.92E-04	Up	7.63E+00	4.53E-01		7.43E+00	4.71E-01		null	null		null	null								ESTscan +
Unigene77921_All	402	0.13	0.25	2.91	0.62	0.34	0.00	0.11	0.00	0.00	9.53E-01	7.24E-01		4.48E+00	1.90E-05	Up	-8.55E-01	5.73E-01		-9.28E+00	7.30E-02		-6.72E+00	6.44E-01		-6.72E+00	6.02E-01		Unigene77921_All//gi|300164082|gb|EFJ30692.1|//2.00E-06//hypothetical protein SELMODRAFT_89801 [Selaginella moellendorffii]						nr -
Unigene77934_All	570	0.00	0.00	3.36	0.00	0.00	0.16	0.00	0.00	0.00	null	null		1.17E+01	1.47E-10	Up	null	null		7.31E+00	4.71E-01		null	null		null	null		Unigene77934_All//gi|18072797|emb|CAC80373.1|//1.00E-84//glyceraldehyde-3-phosphate dehydrogenase [Capsicum annuum]	Unigene77934_All//5.00E-73//AT3G26650| GAPA (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase/ protein binding	Unigene77934_All//5.00E-63//TC159838		ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0005576//GO:0006950//GO:0008943//GO:0009314//GO:0009526//GO:0009532//GO:0009534//GO:0015977//GO:0019318//GO:0034285	nr +

Unigene7794_All	538	2.82	10.55	2.57	7.69	13.25	8.48	0.63	0.31	0.00	1.90E+00	2.17E-11	Up	-1.32E-01	8.01E-01		7.86E-01	1.62E-04		1.42E-01	6.70E-01		-1.02E+00	3.99E-01		-9.30E+00	8.13E-03		Unigene7794_All//gi|8778830|gb|AAF79829.1|AC026875_9//3.00E-08//T6D22.27 [Arabidopsis thaliana]	Unigene7794_All//5.00E-97//DN800038			GO:0005488	nr -
Unigene77951_All	200	0.52	0.00	0.00	0.00	2.75	3.16	0.00	0.63	3.19	-9.03E+00	3.67E-01		-9.03E+00	3.87E-01		1.14E+01	2.02E-03		1.16E+01	7.59E-04	Up	9.29E+00	2.39E-01		1.16E+01	9.33E-05	Up	Unigene77951_All//gi|242199346|gb|ACS87994.1|//7.00E-08//UDP-glucosyltransferase family 1 protein [Citrus sinensis]	Unigene77951_All//5.00E-67//TC160427			GO:0016740	nr -
Unigene77954_All	247	0.00	0.00	3.23	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	1.72E-04	Up	null	null		null	null		null	null		null	null		Unigene77954_All//gi|115469602|ref|NP_001058400.1|//4.00E-09//Os06g0686400 [Oryza sativa Japonica Group] >gi|113596440|dbj|BAF20314.1|Os06g0686400 [Oryza sativa Japonica Group]	Unigene77954_All//1.00E-65//AT1G62790| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein				GO:0006810//GO:0031410	nr +
Unigene77956_All	408	0.51	0.25	3.92	0.24	0.17	0.00	0.00	0.00	0.00	-1.05E+00	5.63E-01		2.93E+00	2.09E-05	Up	-5.33E-01	8.13E-01		-7.93E+00	3.94E-01		null	null		null	null		Unigene77956_All//gi|194476549|ref|XP_002048728.1|//2.00E-24//polyribonucleotide nucleotidyltransferase [Paulinella chromatophora] >gi|171191556|gb|ACB42518.1|polyribonucleotide nucleotidyltransferase [Paulinella chromatophora]	Unigene77956_All//2.00E-14//AT3G03710| RIF10 (resistant to inhibition with FSM 10); 3'-5'-exoribonuclease/ RNA binding / nucleic acid binding / polyribonucleotide nucleotidyltransferase			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03018|RNA degradation	GO:0003676//GO:0003824//GO:0006779//GO:0009532//GO:0010322//GO:0016117	nr +
Unigene7796_All	441	0.00	2.41	3.14	0.00	0.16	0.00	6.62	2.27	1.08	1.12E+01	3.79E-06	Up	1.16E+01	1.23E-07	Up	7.29E+00	6.02E-01		null	null		-1.54E+00	8.48E-06	Down	-2.61E+00	4.19E-11	Down	Unigene7796_All//gi|167859793|gb|ACA04850.1|//8.00E-27//senescence-associated protein [Picea abies]	Unigene7796_All//8.00E-40//gi|84159051|gb|DN828115.1|DN828115				nr +
Unigene77964_All	376	0.00	2.56	1.13	0.27	1.01	0.72	0.00	0.00	0.00	1.13E+01	1.37E-05	Up	1.01E+01	1.36E-02		1.93E+00	1.94E-01		1.44E+00	4.09E-01		null	null		null	null		Unigene77964_All//gi|224115096|ref|XP_002332236.1|//1.00E-11//cytochrome P450 [Populus trichocarpa] >gi|222831849|gb|EEE70326.1|cytochrome P450 [Populus trichocarpa]	Unigene77964_All//2.00E-06//AT4G37330| CYP81D8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005488	nr +
Unigene7797_All	1012	0.16	0.40	0.53	0.89	0.82	1.47	1.84	0.50	2.32	1.37E+00	2.73E-01		1.76E+00	1.29E-01		-1.18E-01	8.51E-01		7.33E-01	1.98E-01		-1.89E+00	5.01E-05	Down	3.37E-01	3.70E-01		Unigene7797_All//gi|30690436|ref|NP_182179.2|//1.00E-39//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene7797_All//2.00E-34//AT2G46560| transducin family protein / WD-40 repeat family protein				nr +
Unigene77978_All	254	0.00	2.59	1.47	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.20E-04	Up	1.05E+01	2.48E-02		null	null		null	null		null	null		null	null							ESTscan +
Unigene78_All	3748	5.79	1.57	2.70	18.42	18.72	9.41	12.00	3.18	5.78	-1.89E+00	2.08E-41	Down	-1.10E+00	3.82E-18	Down	2.28E-02	8.10E-01		-9.69E-01	1.89E-51		-1.92E+00	2.37E-106	Down	-1.05E+00	5.74E-45	Down	Unigene78_All//gi|162958329|dbj|BAF95588.1|//0.00E+00//AtNEK6 [Arabidopsis thaliana]	Unigene78_All//0.00E+00//AT3G44200| NEK6 ("NIMA (NEVER IN MITOSIS, GENE A)-RELATED 6"); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene78_All//0.00E+00//TC179546			nr -
Unigene78001_All	245	0.00	41.16	21.30	0.00	0.00	0.00	0.00	0.00	0.00	1.53E+01	8.98E-58	Up	1.44E+01	4.81E-29	Up	null	null		null	null		null	null		null	null		Unigene78001_All//sp|P83972|LYSD_DROME//2.00E-29//Lysozyme D OS=Drosophila melanogaster GN=LysD PE=2 SV=1					swissprot +
Unigene7801_All	355	3.10	2.14	3.75	2.53	2.52	2.67	4.76	1.18	2.58	-5.32E-01	3.95E-01		2.77E-01	6.16E-01		-2.20E-03	9.78E-01		8.10E-02	9.31E-01		-2.02E+00	5.66E-05	Down	-8.84E-01	4.08E-02		Unigene7801_All//gi|117650693|gb|ABK54296.1|//4.00E-20//glycine-rich protein [Gossypium hirsutum]		Unigene7801_All//4.00E-72//BG441355	ko03040|Spliceosome		nr -
Unigene78010_All	511	0.00	0.00	4.59	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	6.40E-13	Up	null	null		null	null		null	null		null	null		Unigene78010_All//gi|5802244|gb|AAD51625.1|AF169022_1//4.00E-69//seed maturation protein PM37 [Glycine max]	Unigene78010_All//1.00E-56//AT5G22060| ATJ2; protein binding	Unigene78010_All//7.00E-22//TC147555	ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0006950//GO:0032559//GO:0043169//GO:0044267//GO:0044424	nr +
Unigene78015_All	266	0.00	0.00	3.60	0.37	0.39	0.00	0.00	0.00	0.00	null	null		1.18E+01	2.45E-05	Up	5.26E-02	9.65E-01		-8.55E+00	3.94E-01		null	null		null	null							ESTscan -
Unigene78021_All	331	0.00	0.31	0.00	0.15	0.00	0.00	1.92	0.00	0.24	8.26E+00	3.80E-01		null	null		-7.23E+00	5.45E-01		-7.23E+00	6.21E-01		-1.09E+01	1.23E-04	Down	-2.99E+00	2.58E-03		Unigene78021_All//gi|18391101|ref|NP_563858.1|//3.00E-33//ERG28 (Arabidopsis homolog of yeast ergosterol28) [Arabidopsis thaliana] >gi|152112226|sp|Q80594.2|ERG28_ARATH RecName: Full=Ergosterol biosynthetic protein 28 >gi|317117112|gb|AAP68212.1|At1g10030 [Arabidopsis thaliana]	Unigene78021_All//4.00E-26//AT1G10030| ERG28 (Arabidopsis homolog of yeast ergosterol28)	Unigene78021_All//7.00E-89//TC165589			GO:0031224//GO:0043231	nr -
Unigene78026_All	886	0.00	1.89	1.80	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	1.53E-09	Up	1.08E+01	8.43E-09	Up	null	null		null	null		null	null		null	null							ESTscan -
Unigene7803_All	347	7.09	9.20	10.90	18.66	17.17	16.92	19.74	11.56	6.89	3.76E-01	2.94E-01		6.21E-01	6.01E-02		-1.20E-01	6.42E-01		-1.41E-01	6.30E-01		-7.72E-01	1.12E-04		-1.52E+00	9.31E-13	Down		Unigene7803_All//4.00E-07//TC177610				
Unigene7804_All	510	3.28	3.58	1.46	0.00	0.20	2.13	0.00	0.00	0.00	1.24E-01	7.86E-01		-1.17E+00	3.09E-02		7.66E+00	4.53E-01		1.11E+01	1.82E-06	Up	null	null		null	null		Unigene7804_All//gi|147776306|emb|CAN76472.1|//1.00E-10//hypothetical protein [Vitis vinifera]					nr -
Unigene7806_All	389	0.54	0.65	0.55	2.95	3.10	2.55	2.28	2.36	11.37	2.76E-01	8.43E-01		2.55E-02	1.00E+00		7.31E-02	9.30E-01		-2.06E-01	7.39E-01		5.05E-02	9.61E-01		2.32E+00	3.31E-14	Up	Unigene7806_All//gi|209970622|gb|ACJ03072.1|//6.00E-16//HB06p [Malus floribunda]	Unigene7806_All//2.00E-09//AT2G34930| disease resistance family protein	Unigene7806_All//5.00E-161//TC136096			GO:0003824	nr +
Unigene7807_All	451	0.46	0.45	0.00	1.10	1.22	0.70	1.78	3.89	8.48	-4.61E-02	9.87E-01		-8.86E+00	1.44E-01		1.46E-01	9.05E-01		-6.56E-01	5.50E-01		1.13E+00	1.16E-02		2.25E+00	5.31E-12	Up	Unigene7807_All//gi|297825203|ref|XP_002880484.1|//2.00E-07//armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326323|gb|EFH56743.1|armadillo/beta-catenin repeat family protein [Arabidopsis lyrata subsp. lyrata]		Unigene7807_All//4.00E-54//TC132832			GO:0019787//GO:0032446//GO:0043234//GO:0044464	nr -
Unigene7808_All	583	3.59	0.70	1.00	0.94	1.65	0.62	1.02	0.65	0.07	-2.37E+00	6.27E-06	Down	-1.84E+00	2.90E-04	Down	8.15E-01	2.80E-01		-6.01E-01	5.66E-01		-6.54E-01	4.45E-01		-3.89E+00	1.09E-03		Unigene7808_All//gi|227206174|dbj|BAH57142.1|//7.00E-60//AT1G72880 [Arabidopsis thaliana]	Unigene7808_All//6.00E-51//AT1G72880| acid phosphatase survival protein SurE, putative	Unigene7808_All//0.00E+00//gi|78340752|gb|DT561026.1|DT561026		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00760|Nicotinate and nicotinamide metabolism	GO:0008252//GO:0043169//GO:0043231	nr -
Unigene78094_All	236	0.00	0.00	3.16	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene78094_All//gi|224006742|ref|XP_002292331.1|//1.00E-07//RS1, ribosomal protein 1 [Thalassiosira pseudonana CCMP1335] >gi|220971973|gb|EED90306.1| RS1, ribosomal protein 1 [Thalassiosira pseudonana CCMP1335]	Unigene78094_All//1.00E-07//AT5G30510| RPS1 (RIBOSOMAL PROTEIN S1); RNA binding / structural constituent of ribosome			ko03010|Ribosome	GO:0009532	nr -
Unigene781_All	1306	4.45	2.95	2.12	3.93	3.96	2.70	1.20	0.22	2.10	-5.93E-01	1.59E-02		-1.07E+00	4.02E-05	Down	9.60E-03	9.80E-01		-5.43E-01	4.19E-02		-2.42E+00	1.29E-05	Down	8.13E-01	1.31E-02		Unigene781_All//gi|15242914|ref|NP_200605.1|//1.00E-101//methyladenine glycosylase family protein [Arabidopsis thaliana] >gi|79331243|ref|NP_001032091.1|methyladenine glycosylase family protein [Arabidopsis thaliana] >gi|27765038|gb|AAO23640.1|At5g57970 [Arabidopsis thaliana]	Unigene781_All//4.00E-78//AT5G57970| methyladenine glycosylase family protein	Unigene781_All//0.00E+00//TC165920		ko03410|Base excision repair	GO:0003824//GO:0006281//GO:0043231	nr -
Unigene78102_All	247	0.00	0.00	0.00	0.20	0.70	0.55	5.48	3.55	0.16	null	null		null	null		1.79E+00	5.19E-01		1.44E+00	6.37E-01		-6.24E-01	2.33E-01		-5.09E+00	8.12E-09	Down	Unigene78102_All//gi|6714534|dbj|BAA89481.1|//5.00E-19//beta-1,3-glucanase [Salix gilgiana]	Unigene78102_All//3.00E-17//AT3G07320| glycosyl hydrolase family 17 protein	Unigene78102_All//2.00E-100//ES8168855			GO:0005618//GO:0008422//GO:0031410//GO:0043167//GO:0044238	nr +
Unigene7811_All	1346	0.47	0.34	0.44	1.22	0.54	0.34	15.27	40.46	13.38	-4.61E-01	6.18E-01		-1.00E-01	9.15E-01		-1.18E+00	1.54E-02		-1.86E+00	6.76E-04	Down	1.41E+00	1.46E-82	Up	-1.90E-01	9.03E-02		Unigene7811_All//gi|110931814|gb|ABH02906.1|//4.00E-79//MYB transcription factor MYB161 [Glycine max]	Unigene7811_All//2.00E-62//AT3G49690| MYB84 (MYB DOMAIN PROTEIN 84); DNA binding / transcription factor	Unigene7811_All//3.00E-60//TC144511	MYB		GO:0003676//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene78113_All	211	0.00	0.00	0.00	0.00	0.33	0.21	2.40	0.00	0.57	null	null		null	null		8.35E+00	6.02E-01		7.74E+00	6.85E-01		-1.12E+01	8.88E-04	Down	-2.09E+00	3.64E-02		Unigene78113_All//gi|2702270|gb|AAB91973.1|//2.00E-28//expressed protein [Arabidopsis thaliana]	Unigene78113_All//1.00E-29//AT2G32970| unknown protein	Unigene78113_All//2.00E-72//TC135430				nr -
Unigene78119_All	238	0.00	0.00	0.00	0.00	0.00	0.19	6.22	0.18	0.17	null	null		null	null		null	null		7.57E+00	6.85E-01		-5.15E+00	2.98E-09	Down	-5.22E+00	1.06E-09	Down	Unigene78119_All//gi|260408332|gb|ACX37459.1|//1.00E-07//calcium dependent protein kinase 1 [Gossypium hirsutum]		Unigene78119_All//1.00E-64//TC148481				nr +
Unigene78138_All	288	0.00	1.41	3.88	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	1.34E-02		1.19E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene78138_All//gi|81237625|gb|AAX77224.2|//1.00E-32//14-3-3 protein [Dunaliella salina] >gi|157062258|gb|ABV03825.1| 14-3-3 protein [Dunaliella salina]	Unigene78138_All//1.00E-29//AT4G09000| 14-3-3-like protein GF14 chi / general regulatory factor 1 (GRF1)				GO:0005515//GO:0010468//GO:0016817//GO:0043231	nr -
Unigene7816_All	530	10.37	20.65	12.26	7.90	10.85	31.87	22.18	30.91	37.73	9.94E-01	1.75E-08		2.42E-01	3.58E-01		4.59E-01	6.69E-02		2.01E+00	2.21E-37	Up	4.79E-01	9.12E-05		7.67E-01	2.73E-12		Unigene7816_All//gi|241740196|gb|ACS68205.1|//2.00E-14//ubiquitin 10.2 [Brassica napus]	Unigene7816_All//1.00E-15//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene7816_All//4.00E-122//TC168663		ko03010|Ribosome	GO:0044424	nr -
Unigene78163_All	462	0.00	7.02	3.34	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.87E-18	Up	1.17E+01	1.65E-08	Up	null	null		null	null		null	null		null	null								
Unigene78166_All	239	0.00	0.42	2.90	0.00	0.14	0.00	0.35	0.00	0.00	8.73E+00	3.80E-01		1.15E+01	6.12E-04	Up	7.17E+00	8.16E-01		null	null		-8.47E+00	3.98E-01		-8.47E+00	3.54E-01								
Unigene78177_All	339	0.00	0.00	3.61	0.00	0.20	0.13	0.00	0.00	0.00	null	null		1.18E+01	9.09E-07	Up	7.67E+00	6.02E-01		7.06E+00	6.85E-01		null	null		null	null							ESTscan -
Unigene78184_All	212	0.49	1.20	5.78	0.47	0.00	0.21	0.80	0.00	0.00	1.28E+00	4.34E-01		3.55E+00	6.10E-05	Up	-8.88E+00	3.09E-01		-1.14E+00	6.74E-01		-9.64E+00	1.34E-01		-9.64E+00	1.08E-01			Unigene78184_All//5.00E-33//DN510012				
Unigene782_All	2034	5.61	6.25	8.17	10.58	14.36	11.08	15.03	7.05	5.64	1.57E-01	3.62E-01		5.43E-01	1.19E-04		4.40E-01	2.35E-06		6.66E-02	6.42E-01		-1.09E+00	1.02E-31	Down	-1.41E+00	1.54E-48	Down	Unigene782_All//gi|15242914|ref|NP_200605.1|//1.00E-107//methyladenine glycosylase family protein [Arabidopsis thaliana] >gi|79331243|ref|NP_001032091.1|methyladenine glycosylase family protein [Arabidopsis thaliana] >gi|27765038|gb|AAO23640.1|At5g57970 [Arabidopsis thaliana]	Unigene782_All//2.00E-98//AT5G57970| methyladenine glycosylase family protein	Unigene782_All//0.00E+00//TC174155		ko03410|Base excision repair	GO:0043231	nr -
Unigene7820_All	601	0.00	0.00	0.00	0.00	0.00	0.00	60.99	1.60	1.46	null	null		null	null		null	null		null	null		-5.25E+00	2.03E-223	Down	-5.39E+00	8.01E-234	Down							
Unigene78206_All	454	0.35	1.00	3.17	0.00	0.23	0.30	0.00	0.00	0.00	1.54E+00	1.96E-01		3.20E+00	2.79E-05	Up	7.83E+00	4.53E-01		8.22E+00	3.09E-01		null	null		null	null		Unigene78206_All//gi|222839444|gb|EEE77781.1|//1.00E-10//predicted protein [Populus trichocarpa]					GO:0030313	nr -
Unigene78212_All	528	0.10	0.10	1.71	0.00	0.39	0.00	0.00	0.00	0.00	-4.59E-02	9.82E-01		4.11E+00	3.91E-04	Up	8.61E+00	1.56E-01		null	null		null	null		null	null		Unigene78212_All//gi|222871727|gb|EEF08858.1|//3.00E-28//predicted protein [Populus trichocarpa]						nr +
Unigene78233_All	246	0.21	0.62	1.30	1.01	0.28	0.37	2.92	9.34	1.94	1.54E+00	5.30E-01		2.61E+00	1.45E-01		-1.85E+00	2.75E-01		-1.46E+00	4.06E-01		1.68E+00	3.15E-05	Up	-5.88E-01	4.09E-01		Unigene78233_All//gi|224078860|ref|XP_002305657.1|//2.00E-19//multidrug resistance protein ABC transporter family [Populus trichocarpa] >gi|222848621|gb|EEE86168.1|multidrug resistance protein ABC transporter family [Populus trichocarpa]	Unigene78233_All//3.00E-19//AT1G30410| ATMRP13; ATPase, coupled to transmembrane movement of substances				GO:0006810//GO:0015405//GO:0016491//GO:0017111//GO:0031224//GO:0032559	nr +
Unigene7825_All	856	0.67	0.36	0.37	1.57	1.25	0.26	2.27	2.25	1.35	-9.21E-01	3.43E-01		-8.49E-01	3.97E-01		-3.33E-01	5.81E-01		-2.57E+00	1.41E-04	Down	-1.67E-02	1.00E+00		-7.51E-01	5.89E-02							
Unigene78252_All	273	0.00	0.00	7.22	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.28E+01	7.45E-11	Up	null	null		null	null		null	null		null	null		Unigene78252_All//gi|70780051|gb|AAZ08349.1|//4.00E-25//xyloglucan endotransglycosylase/hydrolase 16 protein [Solanum lycopersicum]	Unigene78252_All//1.00E-22//AT4G30210| XTH9 (XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 9); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase				GO:0005576//GO:0016758//GO:0016798//GO:0030312//GO:0044042	nr +

Unigene78255_A11	245	0.64	0.21	0.00	0.20	0.28	0.18	58.16	135.79	205.05	-1.63E+00	4.88E-01		-9.32E+00	2.42E-01		4.68E-01	9.54E-01		-1.42E-01	9.47E-01		1.22E+00	4.56E-41	Up	1.82E+00	1.97E-112	Up	Unigene78255_A11//gi|18404212|ref|NP_566749.1|//3.00E-20//ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase [Arabidopsis thaliana] >gi|118595574|sp|Q56YU0.2|AL2C4_ARATH RecName: Full=Aldehyde dehydrogenase family 2 member C4; AltName: Full=ALDH1a; AltName: Full=Protein REDUCED EPIDERMAL FLUORESCENCE 1 >gi|9294041|dbj|BAB01998.1| aldehyde dehydrogenase [Arabidopsis thaliana] >gi|15912241|gb|AAL08254.1| aldehyde dehydrogenase [Arabidopsis thaliana] >gi|20530143|gb|AAM27004.1| aldehyde dehydrogenase ALDH1a [Arabidopsis thaliana]	Unigene78255_A11//1.00E-21//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene78255_A11//2.00E-17//TC157786		ko00940|Phenylpropanoid biosynthesis	GO:0004030//GO:0009698	nr +
Unigene78259_A11	398	0.00	0.00	2.68	0.13	0.61	0.23	0.00	0.00	0.00	null	null		1.14E+01	6.60E-06	Up	2.27E+00	3.05E-01		8.59E-01	7.91E-01		null	null		null	null		Unigene78259_A11//sp|P54908|TRBC_RHIRD//3.00E-07//Conjugal transfer protein trbC OS=Rhizobium radiobacter GN=trbC PE=3 SV=1						swissprot -
Unigene78264_A11	271	0.00	0.00	2.75	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.14E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene78264_A11//gi|115470305|ref|NP_001058751.1|//1.00E-27//Os07g0114300 [Oryza sativa Japonica Group] >gi|113610287|dbj|BAF20665.1| Os07g0114300 [Oryza sativa Japonica Group]	Unigene78264_A11//5.00E-29//AT2G23090| unknown protein	Unigene78264_A11//2.00E-42//TC173781				nr +
Unigene78271_A11	304	0.00	0.00	2.63	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.14E+01	1.72E-04	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene78276_A11	223	0.00	0.91	0.48	0.00	1.08	2.63	10.62	12.74	30.73	9.83E+00	1.35E-01		8.90E+00	3.89E-01		1.01E+01	1.04E-01		1.14E+01	1.37E-03		2.64E-01	4.67E-01		1.53E+00	8.61E-13	Up							
Unigene7829_A11	441	5.93	4.71	4.11	9.26	4.69	5.43	43.05	21.89	15.09	-3.33E-01	3.90E-01		-5.31E-01	2.02E-01		-9.83E-01	4.68E-04		-7.71E-01	9.89E-03		-9.75E-01	9.42E-17		-1.51E+00	1.24E-33	Down	Unigene7829_A11//gi|73761683|gb|AAZ83341.1|//5.00E-23//ubiquitin extension protein [Gossypium hirsutum]	Unigene7829_A11//4.00E-21//AT2G47110| UBQ6; protein binding	Unigene7829_A11//0.00E+00//DW232728		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene7830_A11	773	0.34	0.52	0.14	0.52	1.43	1.40	2.63	0.49	1.19	6.32E-01	6.01E-01		-1.30E+00	4.36E-01		1.47E+00	3.09E-02		1.44E+00	3.84E-02		-2.43E+00	4.04E-07	Down	-1.15E+00	3.74E-03		Unigene7830_A11//gi|115464839|ref|NP_001056019.1|//7.00E-18//Os05g0512000 [Oryza sativa Japonica Group] >gi|113578570|dbj|BAF17933.1| Os05g0512000 [Oryza sativa Japonica Group]	Unigene7830_A11//8.00E-16//AT4G21070| ATBRCA1; ubiquitin-protein ligase				GO:0046872	nr -
Unigene78302_A11	328	0.00	0.00	2.76	1.37	0.63	0.41	0.77	0.64	0.24	null	null		1.14E+01	4.70E-05	Up	-1.12E+00	3.15E-01		-1.73E+00	1.61E-01		-2.80E-01	8.28E-01		-1.67E+00	2.56E-01								ESTscan +
Unigene78305_A11	585	6.26	5.63	0.73	6.47	8.24	7.10	2.02	0.64	1.09	-1.53E-01	6.25E-01		-3.10E+00	2.70E-12	Down	3.49E-01	2.33E-01		1.34E-01	6.79E-01		-1.65E+00	5.03E-03		-8.93E-01	9.53E-02		Unigene78305_A11//gi|224068426|ref|XP_002302742.1|//2.00E-32//histone H1 [Populus trichocarpa] >gi|222844468|gb|EEE82015.1| histone H1 [Populus trichocarpa]	Unigene78305_A11//7.00E-05//AT1G06760| histone H1, putative	Unigene78305_A11//0.00E+00//TC145886			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr -
Unigene78306_A11	250	0.00	0.00	4.05	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.20E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene78306_A11//gi|193237571|dbj|BAG50062.1|//6.00E-12//transcription factor C2H2 [Lotus japonicus]	Unigene78306_A11//3.00E-09//AT3G28210| PMZ; zinc ion binding		C2H2		GO:0046914	nr -
Unigene78311_A11	270	0.00	0.38	3.94	0.00	0.26	0.00	0.00	0.31	0.00	8.55E+00	3.80E-01		1.19E+01	6.60E-06	Up	7.99E+00	6.02E-01		null	null		8.27E+00	3.98E-01		null	null		Unigene78311_A11//gi|160901078|ref|YP_001566660.1|//3.00E-07//short-chain dehydrogenase/reductase SDR [Delftia acidovorans SPH-1] >gi|160366662|gb|ABX38275.1| short-chain dehydrogenase/reductase SDR [Delftia acidovorans SPH-1]						nr -
Unigene7832_A11	497	52.95	26.41	27.32	105.14	72.06	104.41	31.31	16.31	13.47	-1.00E+00	1.13E-19	Down	-9.55E-01	2.07E-17		-5.45E-01	2.43E-16		-1.00E-02	9.29E-01		-9.40E-01	4.19E-13		-1.22E+00	4.05E-20	Down		Unigene7832_A11//0.00E+00//TC167160					
Unigene78332_A11	248	0.00	0.61	3.22	0.20	0.28	0.36	0.17	0.00	0.16	9.26E+00	2.32E-01		1.17E+01	1.72E-04	Up	4.67E-01	9.54E-01		8.58E-01	7.91E-01		-7.41E+00	6.44E-01		-8.63E-02	9.66E-01		Unigene78332_A11//gi|297834714|ref|XP_002885239.1|//6.00E-25//EMB1270 [Arabidopsis lyrata subsp. lyrata] >gi|297231029|gb|EFH61498.1| EMB1270 [Arabidopsis lyrata subsp. lyrata]	Unigene78332_A11//5.00E-26//AT3G18110| EMB1270 (embryo defective 1270)				GO:0003006//GO:0016798//GO:0043231//GO:0044238	nr -
Unigene78335_A11	739	0.07	0.07	0.07	0.00	0.05	0.06	0.80	0.00	0.05	-4.55E-02	9.82E-01		2.62E-02	9.91E-01		5.54E+00	8.16E-01		5.93E+00	6.85E-01		-9.65E+00	2.39E-04	Down	-3.89E+00	1.09E-03		Unigene78335_A11//gi|205271112|emb|CAP06392.1|//1.00E-101//sterol C-14 reductase [Triticum aestivum] >gi|205271118|emb|CAP06395.1| sterol C-14 reductase [Aegilops tauschii]	Unigene78335_A11//1.00E-51//AT3G52940| FK (FACKEL); deltal4-sterol reductase	Unigene78335_A11//0.00E+00//TC162663		ko00100|Steroid biosynthesis	GO:0008152//GO:0016628//GO:0031410	nr +
Unigene78338_A11	403	0.00	3.02	2.11	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.45E-07	Up	1.10E+01	8.99E-05	Up	null	null		null	null		null	null		null	null		Unigene78338_A11//gi|189095412|ref|YP_001936425.1|//3.00E-19//ribosomal protein L13 [Heterosigma akashiwo] >gi|157694755|gb|ABV66003.1| 50S ribosomal protein L13 [Heterosigma akashiwo] >gi|157777986|gb|ABV70172.1| 50S ribosomal protein L13 [Heterosigma akashiwo]	Unigene78338_A11//1.00E-14//AT1G78630| emb1473 (embryo defective 1473); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0030529	nr -
Unigene7834_A11	532	58.32	8.38	38.64	2.81	1.68	2.04	0.00	0.00	0.00	-2.80E+00	5.39E-95	Down	-5.94E-01	2.49E-09		-7.39E-01	1.63E-01		-4.63E-01	4.20E-01		null	null		null	null		Unigene7834_A11//gi|21595357|gb|AAM66094.1|//7.00E-32//cytochrom P450-like protein [Arabidopsis thaliana]	Unigene7834_A11//5.00E-33//AT5G04660| CYP77A4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene7834_A11//1.00E-14//gi|48809204|gb|CO110518.1|CO110518		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0003006//GO:0005506//GO:0006633//GO:0009566//GO:0009791//GO:0016709//GO:0043231	nr +
Unigene7835_A11	486	5.38	0.31	1.21	4.30	1.84	1.67	0.26	0.00	0.00	-4.11E+00	1.19E-11	Down	-2.16E+00	3.44E-06	Down	-1.22E+00	3.72E-03		-1.36E+00	2.60E-03		-8.03E+00	2.34E-01		-8.03E+00	1.98E-01		Unigene7835_A11//gi|50512303|gb|AAT77550.1|//1.00E-36//90C3 [Solanum pimpinellifolium]	Unigene7835_A11//2.00E-16//AT2G33050| AtRLP26 (Receptor Like Protein 26); kinase/ protein binding	Unigene7835_A11//9.00E-09//gi|78354692|gb|DT574966.1|DT574966			GO:0003824	nr -
Unigene78351_A11	540	0.78	0.19	4.34	0.37	0.57	0.17	0.00	0.00	0.00	-2.05E+00	1.20E-01		2.48E+00	1.56E-06	Up	6.37E-01	6.94E-01		-1.14E+00	5.68E-01		null	null		null	null		Unigene78351_A11//COG1804//7.00E-48//Predicted acyl-CoA transferases/carnitine dehydratase						cog +
Unigene78359_A11	464	0.00	0.44	3.33	0.00	0.00	0.00	0.00	0.00	0.00	8.77E+00	1.35E-01		1.17E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene78359_A11//gi|259072339|ref|XP_002499844.1|//4.00E-25//alpha-2 macroglobulin family-like protein [Micromonas sp. RCC299] >gi|226515106|gb|ACO81102.1| alpha-2 macroglobulin family-like protein [Micromonas sp. RCC299]						nr -
Unigene78366_A11	412	5.08	0.00	1.55	8.46	4.01	12.17	6.05	1.62	3.00	-1.23E+01	4.25E-12	Down	-1.71E+00	6.07E-04	Down	-1.08E+00	4.95E-04	Down	5.24E-01	5.63E-02		-1.90E+00	1.61E-06	Down	-1.01E+00	3.56E-03		Unigene78366_A11//gi|90654201|gb|ABD95975.1|//8.00E-28//mitochondrial import receptor-like protein [Nicotiana tabacum]	Unigene78366_A11//2.00E-18//AT3G20000| TOM40; P-P-bond-hydrolysis-driven protein transmembrane transporter/ voltage-gated anion channel	Unigene78366_A11//8.00E-117//ES812199			GO:0004871//GO:0005244//GO:0005488//GO:0005741//GO:0006605//GO:0006811//GO:0008320//GO:0019866	nr +
Unigene7837_A11	627	0.25	0.00	1.95	0.56	1.37	1.01	2.23	1.60	0.95	-7.97E+00	2.14E-01		2.96E+00	2.55E-04	Up	1.30E+00	1.02E-01		8.59E-01	3.89E-01		-4.76E-01	3.74E-01		-1.22E+00	1.33E-02		Unigene7837_A11//gi|224074695|ref|XP_002304428.1|//1.00E-71//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222841860|gb|EEE79407.1| NAC domain protein, IPR003441 [Populus trichocarpa]	Unigene7837_A11//4.00E-33//AT1G12260| ANAC007 (ARABIDOPSIS NAC 007); transcription factor	Unigene7837_A11//1.00E-11//TC152071	NAC		GO:0003676//GO:0010468	nr +
Unigene7839_A11	340	0.46	2.83	1.10	2.49	0.51	0.66	62.43	39.58	23.55	2.62E+00	2.34E-03		1.25E+00	3.65E-01		-2.30E+00	4.14E-03		-1.91E+00	2.14E-02		-6.57E-01	7.36E-10		-1.41E+00	1.04E-33	Down	Unigene7839_A11//gi|28416777|gb|AAA042919.1|//5.00E-11//At3g29034 [Arabidopsis thaliana]	Unigene7839_A11//3.00E-05//AT3G29034| unknown protein					nr -
Unigene784_A11	1746	6.95	5.66	5.31	5.11	6.47	5.30	4.82	11.37	3.26	-2.97E-01	7.80E-02		-3.90E-01	2.39E-02		3.41E-01	4.56E-02		5.43E-02	8.02E-01		1.24E+00	2.71E-25	Up	-5.63E-01	1.10E-03		Unigene784_A11//gi|54606850|gb|AAV34773.1|//0.00E+00//At1g73390 [Arabidopsis thaliana]	Unigene784_A11//3.00E-160//AT1G73390| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: BR01 (InterPro:IPR004328); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17940.1); Has 95 Blast hits to 95 proteins in 25 species: Archae - 0; Bacteria - 0; Metazoa - 19; Fungi - 23; Plants - 53; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene784_A11//0.00E+00//AW187232				nr +
Unigene7840_A11	390	0.13	0.00	0.55	3.32	1.32	1.04	4.88	2.36	1.84	-7.07E+00	6.03E-01		2.03E+00	3.60E-01		-1.33E+00	1.98E-02		-1.67E+00	7.13E-03		-1.05E+00	1.31E-02		-1.41E+00	8.30E-04	Down	Unigene7840_A11//gi|115485585|ref|NP_001067936.1|//7.00E-26//Os11g0496500 [Oryza sativa Japonica Group] >gi|113645158|dbj|BAF28299.1| Os11g0496500 [Oryza sativa Japonica Group]	Unigene7840_A11//1.00E-26//AT5G08391| unknown protein	Unigene7840_A11//2.00E-27//DW242882			GO:0031410	nr +
Unigene7841_A11	485	135.71	118.99	61.05	144.20	297.42	215.02	313.57	277.40	135.94	-1.90E-01	4.41E-03		-1.15E+00	5.03E-58	Down	1.04E+00	1.61E-132	Up	5.76E-01	1.99E-31		-1.77E-01	2.30E-06		-1.21E+00	2.97E-186	Down	Unigene7841_A11//gi|74229677|gb|AB400453.1|//2.00E-84//cytoplasmic Cu/ZnSOD [Gossypium hirsutum]	Unigene7841_A11//8.00E-74//AT1G08830| CSD1 (COPPER/ZINC SUPEROXIDE DISMUTASE 1); superoxide dismutase	Unigene7841_A11//0.00E+00//gi|13246905|gb|BE052260.2|BE052260		ko04146|Peroxisome	GO:0003824//GO:0006800//GO:0016209//GO:0043169//GO:0044424	nr +
Unigene78411_A11	247	2.54	0.00	0.00	2.42	2.09	5.12	0.68	0.34	0.00	-1.13E+01	7.90E-04	Down	-1.13E+01	1.40E-03		-2.11E-01	8.22E-01		1.08E+00	8.18E-02		-1.02E+00	6.13E-01		-9.42E+00	1.08E-01		Unigene78411_A11//gi|7939621|gb|AAF70823.1|AF154422_1|//8.00E-20//beta-galactosidase [Solanum lycopersicum]	Unigene78411_A11//2.00E-15//AT5G63810| BGAL10 (beta-galactosidase 10); beta-galactosidase/ catalytic/ cation binding	Unigene78411_A11//6.00E-70//TC162243			GO:0005618//GO:0015925//GO:0030246//GO:0031410//GO:0043167//GO:0044238	nr -
Unigene78413_A11	214	12.96	0.00	2.24	1.40	0.80	0.42	0.00	0.00	0.00	-1.37E+01	5.13E-16	Down	-2.53E+00	9.64E-08	Down	-7.96E-01	5.56E-01		-1.73E+00	2.89E-01		null	null		null	null			Unigene78413_A11//4.00E-12//TC146782					
Unigene78423_A11	607	0.52	3.59	1.75	0.57	2.84	3.13	0.84	0.90	1.44	2.79E+00	3.73E-07	Up	1.76E+00	1.85E-02		2.30E+00	3.73E-05	Up	2.44E+00	9.81E-06	Up	9.87E-02	9.21E-01		7.89E-01	2.24E-01		Unigene78423_A11//gi|225454460|ref|XP_002276685.1|//1.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene78424_A11	270	0.78	0.56	1.78	2.21	0.38	0.50	3.29	0.00	0.30	-4.61E-01	7.57E-01		1.20E+00	3.02E-01		-2.53E+00	1.36E-02		-2.14E+00	4.39E-02		-1.17E+01	2.24E-06	Down	-3.48E+00	7.33E-05	Down			Unigene78424_A11//1.00E-111//BG444301				
Unigene7843_A11	508	34.30	67.13	89.41	50.70	74.23	82.15	35.62	36.61	48.70	9.69E-01	8.95E-24		1.38E+00	2.32E-53	Up	5.50E-01	8.37E-12		6.96E-01	7.70E-18		3.96E-02	7.72E-01		4.51E-01	2.35E-06				Unigene7843_A11//2.00E-145//gi|73864027|gb|DT466766.1|DT466766				
Unigene78434_A11	740	0.35	1.10	0.86	0.47	1.21	0.31	3.31	1.58	1.45	1.63E+00	5.05E-02		1.29E+00	1.86E-01		1.36E+00	8.05E-02		-6.27E-01	6.20E-01		-1.07E+00	3.41E-03		-1.19E+00	8.55E-04	Down	Unigene78434_A11//gi|255641849|gb|ACU21193.1|//4.00E-43//unknown [Glycine max]		Unigene78434_A11//0.00E+00//gi|164320036|gb|ES848281.1|ES848281				nr +

Unigene7844_All	274	21.20	19.97	11.66	35.45	17.59	10.05	11.42	7.78	10.18	-8.58E-02	7.27E-01		-8.62E-01	7.92E-04		-1.01E+00	3.41E-09	Down	-1.82E+00	2.21E-19	Down	-5.54E-01	8.20E-02		-1.66E-01	6.11E-01				Unigene7844_All//2.00E-24//TC156887				
Unigene78442_All	453	3.12	0.11	2.35	2.97	2.20	3.29	0.47	0.18	0.18	-4.80E+00	4.49E-07	Down	-4.08E-01	4.86E-01		-4.30E-01	4.68E-01		1.48E-01	7.88E-01		-1.34E+00	4.29E-01		-1.41E+00	3.79E-01		Unigene78442_All//gi|223452516|gb|ACM89585.1//2.00E-15//receptor-like protein kinase [Glycine max]	Unigene78442_All//5.00E-14//AT5G48940| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0016628//GO:0031224//GO:0032559	nr +
Unigene78458_All	249	0.00	0.81	3.42	0.00	0.00	0.00	0.00	0.00	0.00	9.67E+00	1.35E-01		1.17E+01	8.98E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene78468_All	238	0.00	2.98	1.57	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.30E-04	Up	1.06E+01	2.48E-02		null	null		null	null		null	null		null	null									
Unigene78475_All	291	0.18	0.35	4.39	2.23	1.66	1.24	2.91	0.29	1.10	9.54E-01	7.24E-01		4.61E+00	5.50E-06	Up	-4.26E-01	6.08E-01		-8.42E-01	3.75E-01		-3.34E+00	2.51E-04	Down	-1.41E+00	3.70E-02									
Unigene78483_All	237	3.97	0.43	2.92	0.00	1.16	0.00	1.61	0.53	0.00	-3.22E+00	6.76E-04	Down	-4.44E-01	5.54E-01		1.02E+01	7.00E-02		null	null		-1.60E+00	1.81E-01		-1.06E+01	4.19E-03		Unigene78483_All//gi|4894211|gb|AD32302.1|//8.00E-29//ribonucleotide reductase small subunit [Glycine max]	Unigene78483_All//1.00E-29//AT3G23580| RNR2A (RIBONUCLEOTIDE REDUCTASE 2A); ribonucleoside-diphosphate reductase	Unigene78483_All//4.00E-114//TC130406		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko00480|Glutathione metabolism	GO:0006259//GO:0007049//GO:0009132//GO:0016728//GO:0016757//GO:0031224//GO:0032501//GO:0043234//GO:0046572	nr +
Unigene7849_All	729	0.00	4.66	0.00	0.82	7.42	11.83	0.00	0.00	0.11	1.22E+01	2.54E-19	Up	null	null		3.18E+00	1.57E-21	Up	3.85E+00	1.34E-37	Up	null	null		6.77E+00	4.01E-01		Unigene7849_All//gi|157101710|gb|AB223568.1|//8.00E-71//MADS-box protein [Populus deltoides]	Unigene7849_All//2.00E-37//AT2G42830| SHP2 (SHATTERPROOF 2); protein binding / transcription factor	Unigene7849_All//0.00E+00//ES811311	MADS		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene78491_All	281	0.00	0.90	3.41	0.00	0.12	0.32	0.00	0.00	0.00	9.82E+00	7.76E-02		1.17E+01	2.45E-05	Up	6.94E+00	8.15E-01		8.33E+00	4.71E-01		null	null		null	null		Unigene78491_All//sp|P0AEP9|GLCD_ECOLI//7.00E-14//Glycolate oxidase subunit glcD OS=Escherichia coli (strain K12) GN=glcD PE=3 SV=1							swissprot -
Unigene78498_All	380	0.00	0.00	2.52	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene78498_All//gi|225426282|ref|XP_002266388.1|//1.00E-08//PREDICTED: similar to R2 protein [Vitis vinifera]							nr +
Unigene7850_All	409	0.00	0.00	2.34	1.71	0.84	0.00	2.48	1.12	2.44	null	null		1.12E+01	2.45E-05	Up	-1.02E+00	2.25E-01		-1.07E+01	1.96E-04	Down	-1.14E+00	6.62E-02		-2.69E-02	9.74E-01									
Unigene78507_All	432	0.00	0.35	1.73	0.00	0.00	0.00	0.00	0.00	0.00	8.46E+00	2.32E-01		1.08E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene78507_All//sp|Q04695|K1C17_HUMAN//5.00E-62//Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2							swissprot -
Unigene78509_All	317	0.17	0.00	3.86	0.00	0.11	0.00	0.00	0.00	0.00	-7.37E+00	6.03E-01		4.55E+00	1.02E-05	Up	6.76E+00	8.15E-01		null	null		null	null		null	null		Unigene78509_All//sp|Q8RIA5|HLDD_FUSNN//9.00E-17//ADP-L-glycero-D-manno-heptose-6-epimerase OS=Fusobacterium nucleatum subsp. nucleatum GN=hldD PE=3 SV=1							swissprot -
Unigene7851_All	529	1.58	0.67	2.01	0.66	1.76	2.73	2.16	0.63	2.71	-1.24E+00	1.15E-01		3.47E-01	6.29E-01		1.41E+00	6.25E-02		2.05E+00	8.82E-04	Up	-1.77E+00	3.70E-03		3.29E-01	5.18E-01		Unigene7851_All//gi|28200788|emb|CAD45375.1|//2.00E-53//potyviral helper component protease-interacting protein 2 [Solanum tuberosum subsp. andigena]	Unigene7851_All//4.00E-47//AT4G27060| TOR1 (TORTIFOLIA 1); microtubule binding	Unigene7851_All//4.00E-45//gi|78347279|gb|DT567553.1|DT567553			GO:0000902//GO:0015631//GO:0016787//GO:0030879//GO:0055028	nr +
Unigene7852_All	1496	0.00	0.00	0.00	0.00	0.00	0.00	6.47	1.73	4.90	null	null		null	null		null	null		null	null		-1.90E+00	3.26E-23	Down	-4.02E-01	1.28E-02		Unigene7852_All//gi|297529824|ref|XP_002882794.1|//1.00E-122//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297328634|gb|EFH59053.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene7852_All//8.00E-118//AT3G12900| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene7852_All//0.00E+00//TC134433		ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0009699//GO:0012501//GO:0016491	nr -
Unigene78539_All	377	0.00	8.33	4.24	0.13	0.00	0.00	3.59	2.55	0.00	1.30E+01	7.06E-18	Up	1.20E+01	8.43E-09	Up	-7.05E+00	5.45E-01		-7.05E+00	6.21E-01		-4.93E-01	3.67E-01		-1.18E+01	4.86E-10	Down	Unigene78539_All//gi|298713887|emb|CBJ33763.1|//2.00E-18//conserved unknown protein [Ectocarpus siliculosus]		Unigene78539_All//4.00E-63//TC146753				nr -
Unigene78543_All	510	0.92	0.10	1.04	1.86	1.35	2.21	4.64	0.82	3.36	-3.22E+00	2.73E-02		1.77E-01	8.45E-01		-4.59E-01	5.36E-01		2.55E-01	6.91E-01		-2.50E+00	1.92E-08	Down	-4.67E-01	2.00E-01		Unigene78543_All//gi|30408013|gb|AAP30051.1|//3.00E-25//RCa6.1 NBS type resistance protein [Manihot esculenta]	Unigene78543_All//3.00E-14//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene78543_All//2.00E-25//TC143926		ko04626|Plant-pathogen interaction	GO:0006950//GO:0012501//GO:0032559	nr -
Unigene78556_All	537	0.00	7.64	3.47	0.00	0.00	0.08	0.00	0.00	0.00	1.29E+01	2.25E-23	Up	1.18E+01	2.89E-10	Up	null	null		6.39E+00	6.85E-01		null	null		null	null		Unigene78556_All//gi|242043846|ref|XP_002459794.1|//2.00E-06//hypothetical protein SORBIDRAFT_02g010770 [Sorghum bicolor] >gi|241923171|gb|EER96315.1| hypothetical protein SORBIDRAFT_02g010770 [Sorghum bicolor]				ko00190|Oxidative phosphorylation		nr -
Unigene78575_All	536	0.49	0.76	3.18	0.46	0.84	0.17	0.00	0.00	0.00	6.32E-01	6.01E-01		2.70E+00	2.50E-05	Up	8.46E-01	5.13E-01		-1.46E+00	4.06E-01		null	null		null	null		Unigene78575_All//gi|223994057|ref|XP_002286712.1|//2.00E-29//hypothetical protein THAPSDRAFT_260875 [Thalassiosira pseudonana CCMP1335] >gi|220978027|gb|EED96353.1| hypothetical protein THAPSDRAFT_260875 [Thalassiosira pseudonana CCMP1335]						nr -
Unigene7858_All	597	0.88	0.93	0.00	1.00	2.65	1.06	4.04	0.70	2.20	9.12E-02	9.32E-01		-9.78E+00	4.73E-03		1.41E+00	8.63E-03		8.10E-02	9.45E-01		-2.53E+00	1.13E-08	Down	-8.74E-01	1.30E-02		Unigene7858_All//gi|297724275|ref|NP_001174501.1|//8.00E-14//Os05g0532500 [Oryza sativa Japonica Group] >gi|255676518|dbj|BAH93229.1| Os05g0532500 [Oryza sativa Japonica Group]	Unigene7858_All//2.00E-08//AT4G12540| unknown protein	Unigene7858_All//0.00E+00//gi|109850500|gb|DW479479.1|DW479479				nr +
Unigene7860_All	348	15.94	37.71	31.06	6.01	15.93	15.31	0.49	0.00	0.57	1.24E+00	5.40E-14	Up	9.63E-01	1.20E-07		1.41E+00	2.24E-08	Up	1.35E+00	3.82E-07	Up	-8.92E+00	1.34E-01		2.36E-01	8.83E-01		Unigene7860_All//gi|28416781|gb|AA042921.1|//5.00E-18//At4g16146 [Arabidopsis thaliana]	Unigene7860_All//2.00E-18//AT4G16146| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Lg106-like (InterPro:IPR012482); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G69510.3); Has 94 Blast hits to 94 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 94; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene7860_All//4.00E-44//DW498176				nr -
Unigene7861_All	307	5.45	11.55	5.03	4.06	6.39	6.62	32.78	91.49	33.74	1.08E+00	1.13E-03		-1.17E-01	8.14E-01		6.56E-01	1.66E-01		7.07E-01	1.33E-01		1.48E+00	2.36E-46	Up	4.17E-02	8.08E-01				Unigene7861_All//2.00E-116//gi|13247785|gb|BF272334.2|BF272334		ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation		kegg +
Unigene78610_All	541	4.35	1.22	4.72	2.58	1.97	0.92	0.00	0.08	0.00	-1.84E+00	5.34E-05	Down	1.19E-01	7.66E-01		-3.86E-01	5.20E-01		-1.49E+00	1.09E-02		6.27E+00	6.26E-01		null	null		Unigene78610_All//gi|60203059|gb|AAX14716.1|//1.00E-25//beta-amyrin synthase [Aster sedifolius]	Unigene78610_All//7.00E-25//AT1G78955| CAMS1 (Camelliol C synthase 1); beta-amyrin synthase	Unigene78610_All//2.00E-74//gi|164302226|gb|ES807570.1|ES807570		ko00100|Steroid biosynthesis	GO:0016853	nr +
Unigene78616_All	388	0.00	0.00	4.25	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.21E+01	4.29E-09	Up	null	null		null	null		null	null		null	null		Unigene78616_All//gi|224131780|ref|XP_002328106.1|//2.00E-37//f-box family protein [Populus trichocarpa] >gi|222837621|gb|EEE75986.1| f-box family protein [Populus trichocarpa]	Unigene78616_All//5.00E-27//AT2G27310| F-box family protein					nr +
Unigene7862_All	450	82.90	1.01	5.68	40.85	17.14	16.46	1.03	0.00	0.00	-6.35E+00	6.65E-201	Down	-3.87E+00	2.64E-148	Down	-1.25E+00	6.49E-24	Down	-1.31E+00	1.31E-22	Down	-1.00E+01	1.71E-03		-1.00E+01	1.09E-03		Unigene7862_All//gi|150022156|gb|AB857406.1|//4.00E-44//alpha-expansin 3 [Gossypium arboreum] >gi|150022168|gb|ABR57412.1| alpha-expansin 3 [Gossypium raimondii]	Unigene7862_All//2.00E-29//AT1G69530| ATEXPA1 (ARABIDOPSIS THALIANA EXPANSIN A1)	Unigene7862_All//0.00E+00//ES811949			GO:0000902//GO:0009827//GO:0044464	nr -
Unigene78627_All	430	0.00	0.00	0.25	0.23	0.08	0.11	0.49	1.26	2.96	null	null		7.95E+00	3.89E-01		-1.53E+00	5.83E-01		-1.14E+00	6.74E-01		1.36E+00	1.44E-01		2.59E+00	3.78E-05	Up	Unigene78627_All//gi|224132554|ref|XP_002321349.1|//6.00E-35//pseudo response regulator [Populus trichocarpa] >gi|222868345|gb|EEF05476.1| pseudo response regulator [Populus trichocarpa]	Unigene78627_All//3.00E-22//AT5G24470| APRR5 (ARABIDOPSIS PSEUDO-RESPONSE REGULATOR 5); transcription regulator/ two-component response regulator	Unigene78627_All//2.00E-114//TC175726		ko04712|Circadian rhythm - plant	GO:0004871//GO:0006351//GO:0023060	nr +
Unigene78628_All	317	0.00	0.96	2.69	0.00	0.22	0.28	0.00	0.00	0.00	9.91E+00	4.37E-02		1.14E+01	8.98E-05	Up	7.76E+00	6.02E-01		8.15E+00	4.71E-01		null	null		null	null		Unigene78628_All//gi|15220005|ref|NP_178105.1|//3.00E-13//oxidoreductase family protein [Arabidopsis thaliana] >gi|17978983|gb|AAL47452.1| At1g79870/F19K16_17 [Arabidopsis thaliana] >gi|21360429|gb|AAM47330.1| At1g79870/F19K16_17 [Arabidopsis thaliana]	Unigene78628_All//1.00E-14//AT1G78570| oxidoreductase family protein			ko00620|Pyruvate metabolism//ko00260|Glycine, serine and threonine metabolism//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005488//GO:0016616	nr +
Unigene78631_All	357	0.00	0.00	2.39	0.14	0.10	0.13	0.00	0.00	0.00	null	null		1.12E+01	8.98E-05	Up	-5.32E-01	8.20E-01		-1.41E-01	9.47E-01		null	null		null	null		Unigene78631_All//COG0683//6.00E-06//ABC-type branched-chain amino acid transport systems, periplasmic component						cog +
Unigene78652_All	211	1.98	54.03	7.32	0.00	0.00	0.00	0.00	0.00	0.00	4.77E+00	1.34E-53	Up	1.88E+00	1.93E-03		null	null		null	null		null	null		null	null				Unigene78652_All//2.00E-11//gi|164274109|gb|ES810363.1|ES810363				
Unigene78661_All	1311	0.12	0.19	0.37	0.04	0.03	0.07	0.42	0.00	0.03	6.91E-01	6.26E-01		1.61E+00	1.81E-01		-5.31E-01	8.20E-01		8.59E-01	7.91E-01		-8.71E+00	4.61E-04	Down	-3.79E+00	2.03E-03		Unigene78661_All//gi|2970447|gb|AAC05981.1|//0.00E+00//aspartokinase-homoserine dehydrogenase [Glycine max]	Unigene78661_All//0.00E+00//AT4G19710| bifunctional aspartate kinase/homoserine dehydrogenase, putative / AK-HSDH, putative	Unigene78661_All//0.00E+00//gi|78336278|gb|DT556552.1|DT556552		ko00270|Cysteine and methionine metabolism//ko00260|Glycine, serine and threonine metabolism//ko00300|Lysine biosynthesis	GO:0000097//GO:0009536//GO:0016616//GO:0016774//GO:0031406//GO:0032559	nr -
Unigene78662_All	269	0.00	17.71	9.30	0.00	0.00	0.00	0.00	0.00	0.00	1.41E+01	3.82E-27	Up	1.32E+01	8.32E-14	Up	null	null		null	null		null	null		null	null									
Unigene7868_All	558	0.47	0.00	0.38	4.46	3.58	1.30	0.08	0.07	0.00	-8.87E+00	6.65E-02		-2.97E-01	8.31E-01		-3.19E-01	4.51E-01		-1.79E+00	2.71E-05	Down	-1.72E-02	9.98E-01		-6.24E+00	6.01E-01		Unigene7868_All//gi|11066213|gb|AAG28503.1|AF196966_1//2.00E-58//hexokinase [Citrus sinensis]	Unigene7868_All//8.00E-52//AT2G19860| HXK2 (HEXOKINASE 2); ATP binding / fructokinase/ glucokinase/ hexokinase	Unigene7868_All//2.00E-22//AI730201		ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism//ko00052|Galactose metabolism	GO:0004396//GO:0006007//GO:0009527//GO:0031224//GO:0032559	nr +
Unigene78681_All	427	0.00	0.00	3.12	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene78681_All//gi|291621301|dbj|BAI94488.1|//3.00E-49//GRAS family transcription factor [Dianthus caryophyllus]	Unigene78681_All//5.00E-36//AT5G48150| PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor	Unigene78681_All//4.00E-35//TC162586	GRAS		GO:0009639//GO:0010468//GO:0044424//GO:0060089	nr +
Unigene78690_All	250	0.00	16.21	4.26	0.00	0.00	0.00	0.00	0.00	0.00	1.40E+01	4.38E-23	Up	1.21E+01	6.60E-06	Up	null	null		null	null		null	null		null	null									

Unigene787_All	2436	2.34	1.68	0.66	9.65	8.98	11.79	9.46	10.48	14.49	-4.75E-01	5.91E-02			-1.84E+00	1.76E-10	Down	-1.05E-01	4.37E-01			2.89E-01	4.75E-03			1.48E-01	1.68E-01		6.15E-01	1.49E-14		Unigene787_All//gi|22327670|ref|NP_680410.1|//0.00E+00//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|8978263|dbj|BAA98154.1| retroelement pol polyprotein-like [Arabidopsis thaliana] >gi|23306382|gb|AAN17418.1| Unknown protein [Arabidopsis thaliana] >gi|34098795|gb|AAQ56780.1| At5g49665 [Arabidopsis thaliana]	Unigene787_All//0.00E+00//AT5G49665| zinc finger (C3HC4-type RING finger) family protein	Unigene787_All//0.00E+00//gi|78333022|gb|DT553296.1|DT553296			GO:0016020//GO:0046914	nr -
Unigene7870_All	554	1.51	0.18	0.10	2.61	1.86	2.28	1.14	1.13	1.80	-3.05E+00	2.11E-03			-3.97E+00	9.08E-04	Down	-4.84E-01	3.91E-01			-1.92E-01	7.24E-01			-1.66E-02	1.02E+00		6.51E-01	2.81E-01		Unigene7870_All//gi|75273297|sp|Q9LHN3.1|PP242_ARATH//2.00E-54//RecName: Full=Putative pentatricopeptide repeat-containing protein At3g18840	Unigene7870_All//1.00E-39//AT2G22070| pentatricopeptide (PPR) repeat-containing protein	Unigene7870_All//3.00E-15//gi|21103699|gb|BQ416012.1|BQ416012			GO:0043231	nr -
Unigene78702_All	594	0.00	3.50	1.17	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.93E-12	Up		1.02E+01	6.12E-04	Up	null	null			null	null			null	null		null	null		Unigene78702_All//gi|6094086|sp|O65353.1|RL5_HELAN//3.00E-44//RecName: Full=60S ribosomal protein L5 >gi|3153904|gb|AAC17448.1| RPL5A-related protein [Helianthus annuus]	Unigene78702_All//4.00E-25//AT5G39740| 60S ribosomal protein L5 (RPL5B)			ko03010|Ribosome	GO:0019843//GO:0030529//GO:0043229//GO:0044444	nr +
Unigene7871_All	239	6.79	3.82	4.01	4.79	3.60	4.72	26.89	13.12	8.83	-8.31E-01	1.08E-01			-7.59E-01	1.59E-01		-4.12E-01	5.39E-01			-2.11E-02	9.62E-01			-1.04E+00	9.15E-07	Down	-1.61E+00	5.74E-13	Down				Unigene7871_All//7.00E-116//TC143952				
Unigene78712_All	402	0.13	0.38	2.78	0.37	1.20	0.90	0.11	0.42	0.30	1.54E+00	5.30E-01			4.42E+00	3.51E-05	Up	1.69E+00	1.66E-01			1.27E+00	3.81E-01			1.98E+00	3.78E-01		1.50E+00	5.57E-01					Unigene78712_All//3.00E-08//TC178353				
Unigene78713_All	632	1.82	3.53	3.88	2.92	1.31	4.50	3.14	2.65	0.95	9.54E-01	2.68E-02			1.09E+00	1.10E-02		-1.16E+00	1.11E-02			6.26E-01	1.03E-01			-2.49E-01	5.93E-01		-1.73E+00	5.14E-05	Down	Unigene78713_All//gi|75146626|sp|Q84JC0.1|RRP8_ARATH//6.00E-42//RecName: Full=Ribosomal RNA-processing protein 8	Unigene78713_All//3.00E-48//AT5G40530| EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Methyltransferase-related (InterPro:IPR007823); Has 293 Blast hits to 293 proteins in 141 species: Archae - 0; Bacteria - 0; Metazoa - 93; Fungi - 88; Plants - 22; Viruses - 0; Other Eukaryotes - 90 (source: NCBI BLink).	Unigene78713_All//0.00E+00//gi|21099879|gb|BQ412192.1|BQ412192			GO:0043231	nr +
Unigene78717_All	900	0.00	0.00	0.83	0.44	0.88	1.30	19.64	82.85	53.91	null	null			9.69E+00	3.25E-04	Up	9.91E-01	2.40E-01			1.56E+00	1.95E-02			2.08E+00	6.09E-195	Up	1.46E+00	2.63E-79	Up	Unigene78717_All//gi|40218371|gb|AR83118.1|//3.00E-72//secretory laccase [Gossypium arboreum]	Unigene78717_All//2.00E-50//AT5G09360| LAC14 (laccase 14); laccase	Unigene78717_All//0.00E+00//TC174717		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0016491	nr -
Unigene78722_All	673	0.16	0.90	2.22	0.07	0.20	0.07	0.00	0.00	0.00	2.54E+00	2.46E-02			3.83E+00	3.20E-06	Up	1.47E+00	6.17E-01			-1.41E-01	9.47E-01			null	null		null	null									ESTscan +
Unigene78729_All	243	0.00	0.00	3.29	0.00	0.14	0.00	0.00	0.00	0.00	null	null			1.17E+01	1.71E-04	Up	7.15E+00	8.15E-01			null	null			null	null		null	null									
Unigene78732_All	229	23.30	11.51	13.49	373.06	216.09	157.78	1468.54	428.36	930.55	-1.02E+00	9.98E-05	Down		-7.89E-01	3.42E-03		-7.88E-01	8.70E-51			-1.24E+00	6.98E-95	Down		-1.78E+00	0.00E+00	Down	-6.58E-01	3.10E-148		Unigene78732_All//gi|791150|emb|CAA60022.1|//1.00E-37//extensin-like protein [Vigna unguiculata]		Unigene78732_All//3.00E-25//BG443889		ko03040|Spliceosome	GO:0005198//GO:0007047	nr -
Unigene7874_All	407	0.00	4.23	0.92	0.00	0.00	0.78	9.35	22.59	13.12	1.20E+01	7.96E-10	Up		9.84E+00	2.47E-02		null	null			9.60E+00	4.07E-02			1.27E+00	1.22E-12	Up	4.88E-01	3.03E-02		Unigene7874_All//gi|30102798|gb|AAF21317.1|//9.00E-12//At5g49525 [Arabidopsis thaliana]	Unigene7874_All//1.00E-05//AT5G49525| unknown protein				nr +
Unigene78767_All	453	0.12	1.57	2.59	0.00	0.68	0.00	0.00	0.00	0.00	3.76E+00	2.36E-03			4.48E+00	1.90E-05	Up	9.42E+00	4.54E-02			null	null			null	null		null	null		Unigene78767_All//COG3920//2.00E-08//Signal transduction histidine kinase						cog +
Unigene7878_All	530	2.86	7.84	6.43	2.54	2.08	1.87	1.91	0.00	0.30	1.45E+00	4.36E-06	Up		1.17E+00	1.01E-03		-2.88E-01	6.12E-01			-4.37E-01	4.70E-01			-1.09E+01	2.97E-07	Down	-2.67E+00	1.94E-04	Down	Unigene7878_All//gi|8886948|gb|AAF80634.1|AC069251_27//3.00E-25//F2D10.21 [Arabidopsis thaliana]	Unigene7878_All//5.00E-25//AT1G20750| helicase-related	Unigene7878_All//6.00E-149//gi|31073679|gb|CAI993958.1|CAI993958			GO:0005488//GO:0016818	nr -
Unigene78790_All	259	7.27	4.70	1.03	113.67	42.81	29.99	136.80	56.96	82.45	-6.31E-01	1.83E-01			-2.82E+00	5.01E-06	Down	-1.41E+00	9.81E-46	Down	-1.92E+00	2.55E-62	Down	-1.26E+00	5.23E-46	Down	-7.31E-01	1.49E-19				Unigene78790_All//9.00E-60//DW496587				
Unigene78796_All	274	0.00	0.92	4.66	0.00	0.00	0.66	0.00	0.00	0.00	9.85E+00	7.76E-02			1.22E+01	4.67E-07	Up	null	null			9.36E+00	1.93E-01			null	null		null	null		Unigene78796_All//gi|12620883|gb|AAG61121.1|AF329935_1/3.00E-46//ribulose-1,5-bisphosphate carboxylase/oxygenase activase 2 [Gossypium hirsutum]	Unigene78796_All//5.00E-47//AT2G39730| RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	Unigene78796_All//5.00E-40//TC154510			GO:0001071//GO:0032559//GO:0043231	nr -
Unigene7880_All	748	0.00	24.12	0.21	0.00	0.46	2.23	0.11	0.61	1.97	1.46E+01	1.01E-103	Up		7.74E+00	2.34E-01		8.85E+00	3.00E-02			1.11E+01	5.83E-10	Up		2.44E+00	3.74E-02		4.12E+00	2.19E-08	Up	Unigene7880_All//gi|4539485|emb|CAA79329.1|//2.00E-36//BP8 [Betula pendula]	Unigene7880_All//3.00E-26//AT2G36640| ATECP63 (EMBRYONIC CELL PROTEIN 63)					nr -
Unigene78806_All	346	0.00	0.29	5.69	0.00	0.00	0.00	1.96	0.97	0.23	8.19E+00	3.80E-01			1.25E+01	7.45E-11	Up	null	null			null	null			-1.02E+00	2.04E-01		-3.09E+00	1.45E-03		Unigene78806_All//gi|24371055|dbj|BAC22125.1|//2.00E-58//eukaryotic elongation factor 1A [Bruguiera sexangula]	Unigene78806_All//3.00E-50//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene78806_All//3.00E-103//TC140283			GO:0004779//GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene7882_All	973	6.08	0.62	2.46	0.31	0.35	0.05	8.17	0.26	2.29	-3.28E+00	1.35E-21	Down		-1.30E+00	7.59E-07	Down	2.04E-01	9.01E-01			-2.73E+00	1.36E-01			-4.99E+00	2.13E-47	Down	-1.83E+00	6.65E-19	Down	Unigene7882_All//gi|297795877|ref|XP_002865823.1|//2.00E-86//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311658|gb|EFH42082.1| nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene7882_All//2.00E-80//AT5G50790| nodulin MtN3 family protein	Unigene7882_All//0.00E+00//gi|78344325|gb|DT564599.1|DT564599			GO:0031224//GO:0031410	nr +
Unigene7884_All	311	3.87	1.79	0.68	1.92	1.55	1.31	10.20	5.24	29.46	-1.11E+00	7.50E-02			-2.50E+00	1.15E-03		-3.10E-01	7.41E-01			-5.56E-01	5.75E-01			-9.60E-01	2.11E-03		1.53E+00	8.72E-17	Up			Unigene7884_All//6.00E-117//TC141447				
Unigene78841_All	378	4.98	0.27	2.54	2.11	1.09	0.72	0.22	0.00	0.32	-4.22E+00	1.15E-08	Down		-9.75E-01	5.03E-02		-9.48E-01	2.21E-01			-1.56E+00	6.26E-02			-7.81E+00	3.98E-01		4.99E-01	8.06E-01		Unigene78841_All//gi|225451804|ref|XP_002281338.1|//2.00E-59//PREDICTED: brassinosteroid-6-oxidase [Vitis vinifera]	Unigene78841_All//3.00E-53//AT5G38970| BR6OX1 (BRASSINOSTEROID-6-OXIDASE 1); monooxygenase/ oxygen binding	Unigene78841_All//8.00E-92//TC166913		ko00905|Brassinosteroid biosynthesis	GO:0005506//GO:0016129//GO:0016491//GO:0031224//GO:0048878	nr +
Unigene7886_All	412	0.64	2.34	1.03	0.48	0.50	0.44	2.77	0.51	1.64	1.88E+00	1.53E-02			7.03E-01	5.53E-01		5.24E-02	9.88E-01			-1.41E-01	9.34E-01			-2.45E+00	2.46E-04	Down	-7.53E-01	1.68E-01				Unigene7886_All//1.00E-38//TC156402				
Unigene7887_All	633	4.46	0.24	3.36	0.16	1.41	0.43	0.33	0.00	0.13	-4.22E+00	9.18E-13	Down		-4.08E-01	3.12E-01		3.17E+00	8.78E-04	Up		1.44E+00	4.09E-01			-8.38E+00	7.41E-02		-1.41E+00	3.79E-01		Unigene7887_All//gi|7444442|pir||T02087//5.00E-09//gag/pol polyprotein - maize retrotransposon Hopscotch >gi|531389|gb|AAA57005.1| copia-like retrotransposon Hopscotch polyprotein [Zea mays]	Unigene7887_All//2.00E-22//TC175742				nr -
Unigene78881_All	575	0.00	1.50	1.85	0.35	0.24	1.57	8.24	0.73	1.04	1.05E+01	4.91E-05	Up		1.09E+01	6.60E-06	Up	-5.33E-01	7.47E-01			2.18E+00	9.48E-03			-3.50E+00	2.00E-22	Down	-2.99E+00	3.93E-20	Down	Unigene78881_All//gi|260401276|gb|ACX37118.1|//1.00E-41//MATE transporter [Medicago truncatula]	Unigene78881_All//6.00E-36//AT3G59030| TT12 (TRANSPARENT TESTA 12); antiporter/ solute:hydrogen antiporter/ transmembrane transporter/ transporter	Unigene78881_All//2.00E-170//TC160666			GO:0000325//GO:0003006//GO:0009813//GO:0015298//GO:0015893	nr +
Unigene7889_All	304	3.27	4.33	9.81	4.42	4.98	2.97	0.14	0.00	0.26	4.06E-01	4.87E-01			1.58E+00	7.34E-05	Up	1.72E-01	8.06E-01			-5.74E-01	3.45E-01			-7.12E+00	6.44E-01		9.14E-01	7.47E-01				Unigene7889_All//3.00E-20//TC136126				
Unigene78899_All	937	4.91	1.35	5.91	0.85	0.29	0.05	0.00	0.00	0.00	-1.86E+00	3.43E-09	Down		2.66E-01	3.50E-01		-1.53E+00	4.83E-02			-4.14E+00	4.12E-04	Down		null	null		null	null		Unigene78899_All//gi|242085688|ref|XP_002443269.1|//2.00E-06//hypothetical protein SORBIDRAFT_08g016660 [Sorghum bicolor] >gi|241943962|gb|EES17107.1| hypothetical protein SORBIDRAFT_08g016660 [Sorghum bicolor]						nr +
Unigene78900_All	212	0.00	0.00	5.78	0.00	0.00	0.00	0.00	0.00	0.00	null	null			1.25E+01	9.09E-07	Up	null	null			null	null			null	null		null	null		Unigene78900_All//gi|195635283|gb|ACG37110.1|//8.00E-38//ubiquitin-conjugating enzyme E2-17 kDa [Zea mays]	Unigene78900_All//3.00E-38//AT2G02760| ATUBC2 (UBIQUITING-CONJUGATING ENZYME 2); ubiquitin-protein ligase	Unigene78900_All//2.00E-38//ES836735		ko04120|Ubiquitin mediated proteolysis	GO:0006464//GO:0019787//GO:0032559//GO:0060255	nr +
Unigene78903_All	267	0.00	0.00	2.59	0.00	0.00	0.00	0.00	0.00	0.00	null	null			1.13E+01	6.12E-04	Up	null	null			null	null			null	null		null	null		Unigene78903_All//gi|39579116|gb|AAR28754.1|//6.00E-24//Bax inhibitor [Solanum lycopersicum]	Unigene78903_All//9.00E-12//AT5G47120| ATB11 (BAX INHIBITOR 1)				GO:0005488//GO:0006631//GO:0006950//GO:0006984//GO:0012505//GO:0031224//GO:0043066//GO:0043231	nr +
Unigene7891_All	289	17.92	5.08	12.53	11.03	7.51	0.16	0.00	0.58	0.14	-1.82E+00	6.08E-10	Down		-5.17E-01	6.29E-02		-5.55E-01	1.04E-01			-6.14E+00	1.55E-18	Down		9.18E+00	1.38E-01		7.11E+00	6.36E-01				Unigene7891_All//2.00E-08//TC133986				
Unigene78913_All	319	0.33	0.64	0.33	0.00	0.11	0.00	0.80	0.52	3.62	9.54E-01	6.20E-01			2.57E-02	9.97E-01		6.75E+00	8.15E-01			null	null			-6.02E-01	6.47E-01		2.19E+00	4.81E-04	Up	Unigene78913_All//gi|297827389|ref|XP_002881577.1|//2.00E-19//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297327416|gb|EFH57836.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene78913_All//7.00E-21//AT2G38300| DNA binding / transcription factor		G2-like		GO:0001071//GO:0003676//GO:0010468//GO:0043231	nr -
Unigene7892_All	1341	0.00	0.00	0.00	0.00	0.00	0.00	4.04	3.71	0.18	null	null			null	null		null	null			null	null			-1.22E-01	6.20E-01		-4.50E+00	1.04E-31	Down								ESTscan +
Unigene7893_All	804	0.00	11.28	6.36	0.00	0.00	0.00	0.00	0.00	0.00	1.35E+01	6.32E-52	Up		1.26E+01	1.92E-28	Up	null	null			null	null			null	null		null	null		Unigene7893_All//gi|124360119|gb|ABN08135.1|//2.00E-25//Zinc finger, AN1-type; Zinc finger, A20-type [Medicago truncatula]	Unigene7893_All//1.00E-15//AT1G51200| zinc finger (AN1-like) family protein					nr -
Unigene78930_All	253	0.00	2.60	10.10	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	6.20E-04	Up		1.33E+01	4.20E-14	Up	null	null			null	null			null	null		null	null									
Unigene78947_All	405	2.45	2.38	1.18	3.20	3.06	2.23	6.47	2.68	3.64	-4.63E-02	9.58E-01			-1.05E+00	1.48E-01		-6.32E-02	9.04E-01			-5.20E-01	4.01E-01			-1.27E+00	3.66E-04	Down	-8.31E-01	1.32E-02		Unigene78947_All//gi|3914467|sp|P93768.1|PSMD3_TOBAC//2.00E-56//RecName: Full=Probable 26S proteasome non-ATPase regulatory subunit 3; Short=26S proteasome subunit S3; AltName: Full=26S proteasome regulatory subunit RPN3; AltName: Full=Nuclear antigen 21D7 >gi|1864003|dbj|BAA19252.1| 21D7 [Nicotiana tabacum]	Unigene78947_All//3.00E-57//AT1G20200| EMB2719 (EMBRYO DEFECTIVE 2719); enzyme regulator	Unigene78947_All//0.00E+00//gi|13351505|gb|BG441853.1|BG441853		ko03050|Proteasome	GO:0003006//GO:0005488//GO:0009894//GO:0016020//GO:0019941//GO:0043231//GO:0043234	nr +
Unigene78957_All	360	0.00	0.56	1.92	0.00	0.00	0.00	0.00	0.12	0.22	9.14E+00	1.35E-01			1.09E+01	6.12E-04	Up	null	null			null	null			6.86E+00	6.26E-01		7.79E+00	4.01E-01		Unigene78957_All//gi|148524123|gb|ABQ81924.1|//1.00E-37//aminotransferase 2 [Cucumis sativus]	Unigene78957_All//2.00E-28//AT2G13360| AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE); alanine-glyoxylate transaminase/ serine-glyoxylate transaminase/ serine-pyruvate transaminase	Unigene78957_All//2.00E-46//DR455432		ko00250|Alanine, aspartate and glutamate metabolism//ko00260|Glycine, serine and threonine metabolism	GO:0005576//GO:0008483//GO:0009532//GO:0016020//GO:0042579//GO:0043094//GO:0048037	nr -
Unigene78958_All	249	0.00	3.66	1.28	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.60E-05	Up		1.03E+01	4.45E-02		null	null			null	null			null	null		null	null									
Unigene78965_All	701	0.00	2.17	1.22	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.09E-08	Up		1.02E+01	8.98E-05	Up	null	null			null	null			null	null		null	null		Unigene78965_All//sp|Q05204|LAMP1_BOVIN//7.00E-07//Lysosome-associated membrane glycoprotein 1 OS=Bos taurus GN=LAMP1 PE=1 SV=2						swissprot -
Unigene7897_All	276	9.48	2.94	4.63	9.57	6.24	2.62	1.53	0.00	0.00	-1.69E+00	5.80E-05	Down		-1.03E+00	1.22E-02		-6.17E-01	1.03E-01			-1.87E+00	6.88E-06	Down		-1.06E+01	3.25E-03		-1.06E+01	2.14E-03		Unigene7897_All//gi|224138386|ref|XP_002322801.1|//1.00E-10//predicted protein [Populus trichocarpa] >gi|222867431|gb|EEF04562.1| predicted protein [Populus trichocarpa]		Unigene7897_All//2.00E-153//TC160904				nr +
Unigene78970_All	465	0.00	0.22	4.81	0.00	0.00	0.00	0.00	0.00	0.00	7.77E+00	3.80E-01			1.22E+01	2.50E-12	Up	null	null			null	null			null	null		null	null		Unigene78970_All//gi|9663769|emb|CAC01238.1|//3.00E-25//RNA Binding Protein 47 [Nicotiana plumbaginifolia]				ko03022|Basal transcription factors	GO:0005488//GO:0009639//GO:0009987//GO:0050789	nr +

Unigene78978_All	212	6.66	0.24	4.77	0.24	0.97	0.21	0.00	0.20	0.00	-4.80E+00	4.49E-07	Down	-4.82E-01	3.97E-01		2.05E+00	3.94E-01		-1.42E-01	9.47E-01		7.62E+00	6.26E-01		null	null		Unigene78978_All//gi|115459796|ref|NP_001053498.1|//4.00E-09//Os04g0551600 [Oryza sativa Japonica Group] >gi|38345466|emb|CAE01684.2|OSJNBa0010H02.4 [Oryza sativa (japonica cultivar-group)] >gi|113565069|dbj|BAF15412.1|Os04g0551600 [Oryza sativa Japonica Group] >gi|166310137|emb|CAH67153.1|OSIGBa0122F23.10 [Oryza sativa (indica cultivar-group)]	Unigene78978_All//3.00E-10//AT1G02070| unknown protein	Unigene78978_All//4.00E-46//EX171215				nr +
Unigene7898_All	861	0.43	2.24	0.25	0.23	0.12	0.31	1.08	2.33	32.20	2.39E+00	1.59E-05	Up	-7.82E-01	5.53E-01		-9.47E-01	5.87E-01		4.44E-01	7.63E-01		1.11E+00	7.07E-03		4.90E+00	7.00E-165	Up	Unigene7898_All//gi|62867613|gb|AAY17410.1|//1.00E-12//At1g29290 [Arabidopsis thaliana]	Unigene7898_All//8.00E-12//AT1G29290| unknown protein	Unigene7898_All//0.00E+00//gi|73861048|gb|DT463787.1|DT463787				nr -
Unigene78980_All	263	0.00	0.00	0.00	0.38	0.00	0.00	30.22	36.71	12.27	null	null		null	null		-8.57E+00	3.09E-01		-8.57E+00	3.93E-01		2.81E-01	1.09E-01		-1.30E+00	8.76E-12	Down	Unigene78980_All//gi|74273314|gb|AB001325.1|//9.00E-15//VDR6G [Gossypium hirsutum] >gi|83356301|gb|ABC16635.1| bet vI [Gossypium hirsutum]	Unigene78980_All//1.00E-12//AT1G70850| MLP34 (MLP-LIKE PROTEIN 34)	Unigene78980_All//1.00E-83//TC140594				nr -
Unigene78985_All	484	0.00	0.00	2.42	0.00	57.27	0.00	0.00	0.00	0.00	null	null		1.12E+01	1.77E-06	Up	1.58E+01	1.14E-181	Up	null	null		null	null		null	null		Unigene78985_All//gi|297850648|ref|XP_002893205.1|//1.00E-06//predicted protein [Arabidopsis lyrata subsp. lyrata] >gi|297339047|gb|EFH69464.1| predicted protein [Arabidopsis lyrata subsp. lyrata]						nr +
Unigene7899_All	795	0.13	0.45	0.00	0.13	0.39	0.80	19.89	85.85	92.66	1.76E+00	2.18E-01		-7.04E+00	3.87E-01		1.64E+00	3.21E-01		2.67E+00	1.82E-02		2.11E+00	4.08E-182	Up	2.22E+00	1.83E-213	Up	Unigene7899_All//gi|194466169|gb|ACF74315.1|//1.00E-59//lactoylglutathione lyase [Arachis hypogaea]	Unigene7899_All//1.00E-56//AT1G80160| lactoylglutathione lyase family protein / glyoxalase I family protein	Unigene7899_All//0.00E+00//TC177400		GO:0003824//GO:0044238		nr +
Unigene79_All	960	3.87	4.75	4.27	4.72	4.77	4.89	4.58	6.44	10.00	2.96E-01	3.24E-01		1.42E-01	6.44E-01		1.48E-02	9.67E-01		5.12E-02	8.83E-01		4.92E-01	2.16E-02		1.13E+00	2.74E-11	Up	Unigene79_All//gi|79516777|ref|NP_197441.3|//2.00E-31//SMG7 [Arabidopsis thaliana] >gi|159461469|gb|ABW96769.1| SMG7-like protein [Arabidopsis thaliana]	Unigene79_All//8.00E-31//AT5G19400| SMG7	Unigene79_All//0.00E+00//TC167505				nr -
Unigene79005_All	561	0.19	0.18	2.37	0.36	0.12	0.00	0.00	0.00	0.00	-4.64E-02	9.86E-01		3.67E+00	1.90E-05	Up	-1.53E+00	4.14E-01		-8.47E+00	1.33E-01		null	null		null	null		Unigene79005_All//COG0726//6.00E-15//Predicted xylanase/chitin deacetylase						cog +
Unigene79008_All	500	0.00	0.81	1.92	0.00	0.00	0.00	0.00	0.00	9.66E+00	1.34E-02			1.09E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene79008_All//sp|P09382|LEG1_HUMAN//4.00E-55//Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2						swissprot +
Unigene7901_All	438	0.60	1.27	0.36	0.34	0.08	0.41	19.60	50.57	81.68	1.09E+00	2.74E-01		-7.12E-01	6.21E-01		-2.12E+00	3.85E-01		2.74E-01	9.04E-01		1.37E+00	1.13E-32	Up	2.06E+00	1.18E-94	Up	Unigene7901_All//gi|297824541|ref|XP_002880153.1|//1.00E-27//matrix metalloproteinase [Arabidopsis lyrata subsp. lyrata] >gi|297325992|gb|EFH56412.1| matrix metalloproteinase [Arabidopsis lyrata subsp. lyrata]	Unigene7901_All//7.00E-29//AT2G45010| matrix metalloproteinase			GO:0004175//GO:0019538//GO:0031224//GO:0031410//GO:0044421//GO:0046914	nr +
Unigene7902_All	1555	0.00	0.00	0.00	0.00	0.00	0.00	24.58	18.55	0.10	null	null		null	null		null	null		null	null		-4.06E-01	1.30E-07		-7.91E+00	1.83E-273	Down	Unigene7902_All//gi|55168349|gb|AAY44205.1|//5.00E-10//unknow protein [Oryza sativa Japonica Group]		Unigene7902_All//5.00E-13//TC152267				nr -
Unigene79025_All	485	0.11	0.63	0.55	0.10	0.28	0.19	0.26	0.78	2.63	2.54E+00	1.51E-01		2.35E+00	2.39E-01		1.47E+00	6.17E-01		8.58E-01	7.91E-01		1.57E+00	1.95E-01		3.33E+00	2.39E-06	Up	Unigene79025_All//gi|115521215|gb|ABJ09073.1|//6.00E-15//heat shock transcription factor 1 [Medicago sativa] >gi|115521222|gb|ABJ09076.1| heat shock transcription factor 1 [Medicago sativa]	Unigene79025_All//8.00E-16//AT5G16820| HSF3 (HEAT SHOCK FACTOR 3); DNA binding / transcription factor	Unigene79025_All//4.00E-116//gi|21091966|gb|BQ404279.1|BQ404279	HSF	GO:0001071//GO:0003677//GO:0006351//GO:0006950//GO:0043231		nr -
Unigene79033_All	533	0.20	0.57	3.30	0.00	0.00	0.17	0.00	0.00	0.00	1.54E+00	3.22E-01		4.07E+00	1.51E-07	Up	null	null		7.41E+00	4.70E-01		null	null		null	null		Unigene79033_All//COG2908//4.00E-38//Uncharacterized protein conserved in bacteria						cog +
Unigene7904_All	365	43.72	102.59	101.54	84.48	60.00	28.83	190.09	170.96	412.90	1.23E+00	5.43E-38	Up	1.22E+00	8.32E-36	Up	-4.94E-01	2.69E-08		-1.55E+00	2.66E-48	Down	-1.53E-01	9.70E-03		1.12E+00	1.19E-162	Up			Unigene7904_All//2.00E-73//TC175228				
Unigene79040_All	264	0.40	0.00	0.40	0.57	0.91	0.86	1.92	0.00	0.75	-8.63E+00	3.67E-01		2.53E-02	9.97E-01		6.90E-01	7.32E-01		5.96E-01	7.21E-01		-1.09E+01	8.88E-04	Down	-1.35E+00	1.40E-01		Unigene79040_All//gi|255539677|ref|XP_002510903.1|//3.00E-14//conserved hypothetical protein [Ricinus communis] >gi|223550018|gb|EEF51505.1| conserved hypothetical protein [Ricinus communis]	Unigene79040_All//2.00E-08//AT5G51670| unknown protein	Unigene79040_All//3.00E-13//TC178814		GO:0009536		nr -
Unigene7905_All	704	0.74	7.13	1.82	1.98	3.23	2.12	0.54	3.38	3.17	3.26E+00	4.06E-18	Up	1.29E+00	4.48E-02		7.04E-01	1.01E-01		9.56E-02	8.79E-01		2.65E+00	5.85E-09	Up	2.55E+00	2.46E-08	Up	Unigene7905_All//gi|34393414|dbj|BAC82948.1|//1.00E-07//immunophilin/FKBP-type peptidyl-prolyl cis-trans isomerase-like protein [Oryza sativa Japonica Group] >gi|50509301|dbj|BAD30608.1| immunophilin/FKBP-type peptidyl-prolyl cis-trans isomerase-like protein [Oryza sativa Japonica Group]	Unigene7905_All//7.00E-09//AT5G13410| immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	Unigene7905_All//1.00E-36//TC137831				nr -
Unigene79058_All	412	0.00	1.97	3.49	0.00	0.25	0.22	0.00	0.00	0.00	1.09E+01	9.31E-05	Up	1.18E+01	6.29E-08	Up	7.97E+00	4.52E-01		7.78E+00	4.70E-01		null	null		null	null		Unigene79058_All//gi|7025493|gb|AAF35901.1|AF230332_1//8.00E-27//expansin 2 [Zinnia violacea]	Unigene79058_All//4.00E-18//AT1G26770| ATEXPA10 (ARABIDOPSIS THALIANA EXPANSIN A 10); structural constituent of cell wall	Unigene79058_All//1.00E-32//TC164848		GO:0007047//GO:0044464		nr +
Unigene79069_All	527	0.40	0.29	2.63	0.19	0.20	0.00	0.00	0.00	0.00	-4.61E-01	7.57E-01		2.73E+00	1.78E-04	Up	5.25E-02	9.65E-01		-7.56E+00	3.93E-01		null	null		null	null		Unigene79069_All//sp|P71512|HPPK_METEA//9.00E-10//2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase OS=Methylobacterium extorquens (strain ATCC 14718 / DSM 1338 / AM1) GN=folK PE=3 SV=2						swissprot -
Unigene79083_All	468	0.67	0.65	3.41	0.11	0.22	0.39	0.00	0.00	0.00	-4.63E-02	9.84E-01		2.35E+00	2.09E-04	Up	1.05E+00	8.05E-01		1.86E+00	4.57E-01		null	null		null	null		Unigene79083_All//gi|158517778|sp|P0C300.1|RDYB_ORYSI//3.00E-21//RecName: Full=1-Cys peroxiredoxin B; Short=1-Cys Prx B; AltName: Full=Thioredoxin peroxidase B	Unigene79083_All//2.00E-22//AT1G48130| ATPER1; antioxidant/ thioredoxin peroxidase			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0016491	nr +
Unigene79087_All	498	0.11	0.20	2.03	0.00	0.14	0.00	0.00	0.00	0.00	9.53E-01	7.24E-01		4.27E+00	1.19E-04	Up	7.11E+00	6.01E-01		null	null		null	null		null	null									ESTscan +
Unigene7909_All	588	1.07	1.72	0.18	1.19	2.52	4.45	6.69	9.31	15.11	6.91E-01	3.18E-01		-2.56E+00	2.72E-02		1.09E+00	4.96E-02		1.91E+00	7.37E-06	Up	4.78E-01	3.86E-02		1.18E+00	3.44E-11	Up			Unigene7909_All//1.00E-76//ES802684				
Unigene79090_All	268	0.00	4.16	2.98	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.99E-06	Up	1.15E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene79090_All//gi|255073219|ref|XP_002500284.1|//5.00E-07//cold-shock DNA binding protein [Micromonas sp. RCC299] >gi|226515546|gb|ACO61542.1| cold-shock DNA binding protein [Micromonas sp. RCC299]	Unigene79090_All//3.00E-06//AT4G36020| CSDP1 (cold shock domain protein 1); RNA binding / double-stranded DNA binding / nucleic acid binding / single-stranded DNA binding		CSD			nr -
Unigene7912_All	354	5.91	13.74	8.27	28.85	30.06	120.18	10.03	59.51	43.21	1.22E+00	1.58E-05	Up	4.85E-01	2.16E-01		5.93E-02	8.14E-01		2.06E+00	2.33E-96	Up	2.57E+00	1.23E-71	Up	2.11E+00	4.14E-42	Up	Unigene7912_All//gi|224151719|ref|XP_002337145.1|//1.00E-18//cytochrome P450 [Populus trichocarpa] >gi|222838355|gb|EEE76720.1| cytochrome P450 [Populus trichocarpa]	Unigene7912_All//4.00E-11//AT2G25160| CYP82F1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene7912_All//6.00E-117//TC131128		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506//GO:0008152	nr -
Unigene79124_All	549	0.19	0.65	2.04	0.27	0.25	0.25	0.00	0.00	0.15	1.76E+00	2.18E-01		3.42E+00	1.92E-04	Up	-1.18E-01	9.09E-01		-1.41E-01	9.42E-01		null	null		7.18E+00	4.01E-01									
Unigene7913_All	934	5.77	0.76	1.82	1.33	1.33	0.68	0.00	0.09	0.21	-2.93E+00	9.97E-18	Down	-1.66E+00	9.88E-09	Down	-6.60E-03	9.73E-01		-9.78E-01	1.14E-01		6.48E+00	3.98E-01		7.74E+00	7.88E-02		Unigene7913_All//gi|6692128|gb|AAF24593.1|AC007654_9//7.00E-84//T19E23.14 [Arabidopsis thaliana]	Unigene7913_All//3.00E-78//AT1G31350| F-box family protein					nr -
Unigene7914_All	276	1.14	20.93	5.79	3.97	15.35	5.07	11.03	15.75	9.67	4.20E+00	2.72E-25	Up	2.35E+00	2.09E-04	Up	1.95E+00	5.65E-10	Up	3.53E-01	5.79E-01		5.14E-01	5.10E-02		-1.90E-01	5.86E-01		Unigene7914_All//gi|213053826|gb|ACJ39218.1|//1.00E-09//cold-regulated protein [Glycine max]	Unigene7914_All//6.00E-09//AT2G19970| COR413-PM1	Unigene7914_All//8.00E-42//TC140066				nr -
Unigene7915_All	398	0.39	0.00	1.20	5.88	2.51	1.93	0.96	0.11	0.40	-8.62E+00	2.14E-01		1.61E+00	1.81E-01		-1.23E+00	1.83E-03		-1.61E+00	2.00E-04	Down	-3.19E+00	3.11E-02		-1.26E+00	2.48E-01		Unigene7915_All//gi|15223416|ref|NP_171656.1|//8.00E-09//heavy-metal-associated domain-containing protein [Arabidopsis thaliana] >gi|79316252|ref|NP_001030928.1| heavy-metal-associated domain-containing protein [Arabidopsis thaliana]		Unigene7915_All//1.00E-81//gi|78325870|gb|DT546144.1|DT546144			GO:0006812//GO:0043169	nr -
Unigene79151_All	811	0.00	0.00	5.32	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.24E+01	6.13E-24	Up	null	null		null	null		null	null		null	null		Unigene79151_All//gi|11967906|dbj|BAB19779.1|//1.00E-147//alpha tubulin [Nicotiana tabacum]	Unigene79151_All//8.00E-135//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene79151_All//1.00E-107//TC172217		ko04145|Phagosome		nr -
Unigene79163_All	485	0.00	0.84	3.07	0.00	0.00	0.00	0.00	0.00	0.00	9.71E+00	1.34E-02		1.16E+01	3.21E-08	Up	null	null		null	null		null	null		null	null		Unigene79163_All//sp|P02751|FINC_HUMAN//2.00E-82//Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=3						swissprot +
Unigene79176_All	388	0.00	2.48	1.51	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.37E-05	Up	1.06E+01	2.16E-03		null	null		null	null		null	null		null	null									
Unigene79178_All	258	2.23	3.34	2.27	5.99	6.54	2.98	8.85	1.94	3.71	5.82E-01	4.27E-01		2.54E-02	9.98E-01		1.28E-01	8.26E-01		-1.01E+00	6.16E-02		-2.19E+00	4.53E-07	Down	-1.26E+00	7.78E-04	Down			Unigene79178_All//3.00E-90//gi|164357012|gb|ES828810.1|ES828810				
Unigene7919_All	419	26.97	6.29	3.94	34.48	15.86	41.50	11.91	1.20	0.48	-2.10E+00	4.12E-25	Down	-2.78E+00	3.25E-33	Down	-1.12E+00	7.91E-16	Down	2.67E-01	5.69E-02		-3.31E+00	1.64E-22	Down	-4.65E+00	7.97E-30	Down	Unigene7919_All//gi|118483458|gb|ABK93628.1|//3.00E-11//unknown [Populus trichocarpa]		Unigene7919_All//6.00E-90//gi|13356837|gb|BG447185.1|BG447185				nr +
Unigene79193_All	429	0.00	2.01	4.59	0.12	0.00	0.00	0.00	0.00	0.00	1.10E+01	4.91E-05	Up	1.22E+01	7.44E-11	Up	-6.86E+00	5.44E-01		-6.86E+00	6.20E-01		null	null		null	null		Unigene79193_All//sp|Q5R7C4|SERF2_PONAB//5.00E-26//Small EDRK-rich factor 2 OS=Pongo abelii GN=SERF2 PE=3 SV=1						swissprot +
Unigene792_All	2357	2.80	1.25	2.76	2.37	2.06	13.95	2.76	11.35	11.32	-1.17E+00	8.18E-07	Down	-2.11E-02	9.49E-01		-2.01E-01	4.83E-01		2.56E+00	6.65E-97	Up	2.04E+00	1.17E-68	Up	2.04E+00	9.39E-70	Up	Unigene792_All//gi|282161430|gb|ADA79674.1|//0.00E+00//shaker-like potassium channel 1 [Populus euphratica]	Unigene792_All//0.00E+00//AT2G26650| AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel	Unigene792_All//0.00E+00//TC177956		ko04626|Plant-pathogen interaction	GO:0000166//GO:0005249//GO:0006970//GO:0030001//GO:0031224//GO:0048588	nr -
Unigene7920_All	936	0.34	0.97	0.28	1.06	0.81	0.29	2.12	2.86	0.77	1.54E+00	4.51E-02		-2.38E-01	8.50E-01		-3.95E-01	5.73E-01		-1.88E+00	1.18E-02		4.29E-01	2.37E-01		-1.47E+00	3.81E-04	Down								
Unigene79205_All	359	0.00	2.12	1.04	0.14	0.00	0.38	0.12	0.00	0.00	1.10E+01	1.75E-04	Up	1.00E+01	2.47E-02		-7.12E+00	5.44E-01		1.44E+00	6.37E-01		-6.88E+00	6.44E-01		-6.88E+00	6.01E-01		Unigene79205_All//gi|239056193|emb|CAQ58630.1|//2.00E-20//Unknown gene [Vitis vinifera]	Unigene79205_All//3.00E-26//AT5G41590| unknown protein					nr +
Unigene79210_All	425	0.00	2.38	1.75	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	7.21E-06	Up	1.08E+01	3.25E-04	Up	null	null		null	null		null	null		null	null									
Unigene79216_All	249	1.05	2.24	1.71	0.60	2.21	1.81	11.04	7.89	154.07	1.09E+00	2.74E-01		7.04E-01	5.53E-01		1.88E+00	9.41E-02		1.60E+00	2.05E-01		-4.84E-01	1.64E-01		3.80E+00	6.09E-193	Up	Unigene79216_All//gi|67483357|gb|AAV68034.1|//3.00E-14//3-hydroxy-methylglutaryl coenzyme A reductase [Tilia miqueliana]		Unigene79216_All//1.00E-74//TC164133		ko00900|Terpenoid backbone biosynthesis	GO:0000166//GO:0005740//GO:0006720//GO:0006732//GO:0008610//GO:0009026//GO:0016616//GO:0031090//GO:0031224//GO:0048037	nr -
Unigene79223_All	295	0.00	1.03	2.53	0.00	0.00	0.00	0.00	0.00	0.00	1.00E+01	4.37E-02		1.13E+01	3.25E-04	Up	null	null		null	null		null	null		null	null									
Unigene79229_All	279	0.00	3.27	1.15	0.00	0.25	0.00	0.00	0.00	0.00	1.17E+01	2.60E-05	Up	1.02E+01	4.45E-02		7.95E+00	6.01E-01		null	null		null	null		null	null									
Unigene7924_All	605	0.00	0.00	0.00	0.00	0.00	0.00	8.25	1.31	2.24	null	null		null	null		null	null		null	null		-2.65E+00	3.91E-18	Down	-1.88E+00	1.40E-12	Down								

Unigene79250_All	276	0.00	1.84	2.70	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	3.99E-03		1.14E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene79250_All//sp|Q24537|HMG2_DROME//1.00E-19//High mobility group protein DSP1 OS=Drosophila melanogaster GN=Dsp1 PE=2 SV=1						swissprot +
Unigene79251_All	499	0.00	3.86	5.12	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.72E-11	Up	1.23E+01	4.20E-14	Up	null	null		null	null		null	null		null	null		Unigene79251_All//sp|Q8T697|TYB_APLCA//5.00E-06//Thymosin beta OS=Aplysia californica PE=1 SV=1						swissprot -
Unigene79257_All	263	4.97	0.77	0.81	3.98	4.06	1.20	1.45	0.00	0.00	-2.69E+00	1.84E-04	Down	-2.62E+00	4.27E-04	Down	2.92E-02	9.80E-01		-1.73E+00	1.55E-02		-1.05E+01	6.17E-03		-1.05E+01	4.19E-03		Unigene79257_All//gi|15241489|ref|NP_196419.1|//2.00E-26//RPA70B (RPA70-KDA SUBUNIT B); DNA binding / nucleic acid binding [Arabidopsis thaliana] >gi|6562316|emb|CAB62614.1| replication factor A-like protein [Arabidopsis thaliana]	Unigene79257_All//7.00E-28//AT5G08020| RPA70B (RPA70-KDA SUBUNIT B); DNA binding / nucleic acid binding	Unigene79257_All//2.00E-94//TC130012		ko03420|Nucleotide excision repair//ko03030|DNA replication//ko03440|Homologous recombination//ko03430|Mismatch repair	GO:0003676//GO:0006259//GO:0009411//GO:0043231	nr +
Unigene79259_All	930	1.18	0.87	0.97	2.14	2.89	1.55	1.64	0.40	0.17	-4.39E-01	4.95E-01		-2.79E-01	6.54E-01		4.31E-01	3.04E-01		-4.63E-01	3.46E-01		-2.02E+00	1.50E-04	Down	-3.26E+00	1.79E-07	Down	Unigene79259_All//gi|15237011|ref|NP_195272.1|//1.00E-48//leucine-rich repeat family protein [Arabidopsis thaliana] >gi|57868150|gb|AAW57413.1| plant intracellular Ras-group-related LRR protein 4 [Arabidopsis thaliana]	Unigene79259_All//1.00E-46//AT4G35470| leucine-rich repeat family protein	Unigene79259_All//2.00E-178//DW477599				nr +
Unigene79262_All	260	0.00	5.65	3.07	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.10E-08	Up	1.16E+01	1.71E-04	Up	null	null		null	null		null	null		null	null								
Unigene7927_All	754	1.04	0.27	0.28	1.65	1.55	2.88	3.03	0.11	0.63	-1.95E+00	2.62E-02		-1.88E+00	4.13E-02		-8.91E-02	8.70E-01		8.00E-01	7.32E-02		-4.77E+00	1.41E-13	Down	-2.26E+00	1.32E-07	Down	Unigene7927_All//gi|87162592|gb|AB028387.1|//1.00E-66//Asp/Glu racemase [Medicago truncatula]	Unigene7927_All//3.00E-61//AT1G15410| aspartate-glutamate racemase family	Unigene7927_All//0.00E+00//TC133035			GO:0006519//GO:0009536//GO:0016854	nr -
Unigene79271_All	384	0.00	0.26	2.91	0.26	0.54	0.24	0.00	0.00	0.00	8.04E+00	3.80E-01		1.15E+01	3.42E-06	Up	1.05E+00	6.11E-01		-1.41E-01	9.47E-01		null	null		null	null								ESTscan -
Unigene79277_All	884	0.12	0.11	0.06	0.11	0.04	0.10	0.77	0.09	0.05	-4.71E-02	9.86E-01		-9.76E-01	7.19E-01		-1.53E+00	5.83E-01		-1.41E-01	9.47E-01		-3.02E+00	2.43E-03		-4.08E+00	3.10E-04	Down	Unigene79277_All//gi|297816108|ref|XP_002875937.1|//2.00E-49//RNA polymerase III subunit RPC82 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321775|gb|EFH52196.1| RNA polymerase III subunit RPC82 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene79277_All//2.00E-45//AT3G49000| RNA polymerase III subunit RPC82 family protein	Unigene79277_All//0.00E+00//TC168509		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase		nr +
Unigene79278_All	508	1.13	0.50	3.56	0.59	0.95	0.53	1.58	5.59	4.86	-1.18E+00	2.26E-01		1.65E+00	2.13E-03		6.90E-01	5.66E-01		-1.42E-01	9.20E-01		1.82E+00	5.89E-07	Up	1.62E+00	1.69E-05	Up	Unigene79278_All//gi|222820383|gb|ACM67554.1|//5.00E-93//ADP-ribosylation factor-like protein [Musa acuminata AAA Group]	Unigene79278_All//6.00E-94//AT2G47170| ARF1A1C; GTP binding / phospholipase activator/ protein binding	Unigene79278_All//2.00E-139//gi|164251198|gb|ES801851.1|ES801851			GO:0003824//GO:0015031//GO:0016020//GO:0032561//GO:0035556//GO:0043231//GO:0046914//GO:0060229	nr +
Unigene79282_All	492	0.00	4.43	2.49	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.11E-12	Up	1.13E+01	9.09E-07	Up	null	null		null	null		null	null		null	null		Unigene79282_All//gi|297608798|ref|NP_001062164.2|//5.00E-08//Os08g0501500 [Oryza sativa Japonica Group] >gi|255678555|dbj|BAF24078.2| Os08g0501500 [Oryza sativa Japonica Group]	Unigene79282_All//2.00E-05//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase				GO:0005488//GO:0005622	nr +
Unigene79288_All	402	0.26	1.89	2.12	5.58	4.80	1.91	2.52	1.56	1.09	2.86E+00	5.51E-03		3.03E+00	3.00E-03		-2.17E-01	6.15E-01		-1.55E+00	4.57E-04	Down	-6.95E-01	2.63E-01		-1.21E+00	4.17E-02				Unigene79288_All//2.00E-09//TC168210					ESTscan +
Unigene79295_All	552	0.76	1.01	0.77	0.72	1.00	1.23	0.46	1.59	3.32	4.13E-01	6.36E-01		2.53E-02	1.00E+00		4.67E-01	6.68E-01		7.66E-01	4.10E-01		1.79E+00	1.27E-02		2.85E+00	9.46E-08	Up	Unigene79295_All//gi|15227189|ref|NP_182322.1|//1.00E-27//RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase [Arabidopsis thaliana] >gi|75319082|sp|P93050.1|RKF3_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase RKF3; AltName: Full=Receptor-like kinase in flowers 3; Flags: Precursor >gi|1785621|emb|CAB06335.1| AtPK2324 [Arabidopsis thaliana] >gi|2465927|gb|AAC50045.1| receptor-like serine/threonine kinase [Arabidopsis thaliana] >gi|14335116|gb|AAK59837.1| At2g48010/T9J23.16 [Arabidopsis thaliana] >gi|23308235|gb|AAN18087.1| At2g48010/T9J23.16 [Arabidopsis thaliana]	Unigene79295_All//5.00E-25//AT2G48010| RKF3 (RECEPTOR-LIKE KINASE IN IN FLOWERS 3); kinase/ receptor signaling protein serine/threonine kinase	Unigene79295_All//8.00E-93//CO127342			GO:0004674//GO:0006464//GO:0016020//GO:0032559	nr +
Unigene793_All	3234	0.36	0.97	1.02	1.48	2.26	2.23	28.84	12.26	29.22	1.45E+00	8.95E-05	Up	1.52E+00	4.86E-05	Up	6.10E-01	3.34E-03		5.96E-01	5.96E-03		-1.23E+00	2.01E-115	Down	1.89E-02	7.44E-01		Unigene793_All//gi|282161430|gb|ADA79674.1|//0.00E+00//shaker-like potassium channel 1 [Populus euphratica]	Unigene793_All//0.00E+00//AT2G26650| AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel	Unigene793_All//0.00E+00//TC177956		ko04626|Plant-pathogen interaction	GO:0000166//GO:0005249//GO:0006970//GO:0030001//GO:0031224//GO:0048588	nr -
Unigene79300_All	291	0.18	2.96	0.37	1.20	0.00	0.00	0.15	0.00	0.00	4.04E+00	4.20E-04	Up	1.03E+00	7.00E-01		-1.02E+01	9.43E-03		-1.02E+01	2.12E-02		-7.18E+00	6.43E-01		-7.18E+00	6.01E-01								
Unigene79309_All	540	1.65	3.00	6.41	0.28	0.51	0.00	0.47	0.15	0.07	8.66E-01	9.50E-02		1.96E+00	3.58E-07	Up	8.83E-01	5.94E-01		-8.11E+00	2.31E-01		-1.60E+00	3.10E-01		-2.67E+00	1.15E-01		Unigene79309_All//gi|71068415|gb|AA23128.1|//3.00E-55//mitogen-activated protein kinase 1 [Arachis hypogaea]	Unigene79309_All//3.00E-50//AT2G43790| ATMPK6 (ARABIDOPSIS THALIANA MAP KINASE 6); MAP kinase/ kinase	Unigene79309_All//7.00E-87//TC130313		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0000166//GO:0004674//GO:0007049	nr -
Unigene79312_All	263	0.20	1.54	3.44	0.38	0.26	0.86	0.16	1.27	0.15	2.95E+00	5.90E-02		4.11E+00	3.91E-04	Up	-5.32E-01	8.13E-01		1.18E+00	5.48E-01		2.98E+00	5.73E-02		-8.59E-02	9.66E-01		Unigene79312_All//gi|224085910|ref|XP_002307735.1|//2.00E-07//plant synaptotagmin [Populus trichocarpa] >gi|222857184|gb|EEE94731.1| plant synaptotagmin [Populus trichocarpa]					GO:0031410	nr +
Unigene79331_All	381	10.16	0.93	3.77	12.42	3.34	1.42	1.22	0.00	0.10	-3.45E+00	6.04E-15	Down	-1.43E+00	2.49E-05	Down	-1.89E+00	1.32E-11	Down	-3.13E+00	5.73E-18	Down	-1.03E+01	1.71E-03		-3.54E+00	6.85E-03		Unigene79331_All//gi|224080516|ref|XP_002306147.1|//5.00E-36//SAUR family protein [Populus trichocarpa] >gi|222849111|gb|EEE86658.1| SAUR family protein [Populus trichocarpa]	Unigene79331_All//1.00E-35//AT4G34760| auxin-responsive family protein	Unigene79331_All//2.00E-24//DW503189			GO:0009725	nr -
Unigene79341_All	322	0.00	0.16	2.15	0.15	0.11	0.56	0.00	0.00	0.00	7.30E+00	6.09E-01		1.11E+01	6.12E-04	Up	-5.33E-01	8.19E-01		1.86E+00	4.57E-01		null	null		null	null		Unigene79341_All//COG0277//7.00E-16//FAD/FMN-containing dehydrogenases						cog +
Unigene7935_All	908	0.00	0.00	0.00	0.00	0.00	0.00	9.22	9.25	3.16	null	null		null	null		null	null		null	null		5.10E-03	1.02E+00		-1.55E+00	8.93E-16	Down	Unigene7935_All//gi|224075052|ref|XP_002304537.1|//1.00E-135//cation proton exchanger [Populus trichocarpa] >gi|222841969|gb|EEE79516.1| cation proton exchanger [Populus trichocarpa]	Unigene7935_All//1.00E-95//AT5G11610| ATCHX18; monovalent cation:proton antiporter/ sodium:hydrogen antiporter	Unigene7935_All//7.00E-48//BG446460				nr -
Unigene79386_All	515	0.20	0.20	2.69	0.29	0.27	0.09	0.00	0.00	0.00	-4.62E-02	9.86E-01		3.73E+00	1.05E-05	Up	-1.18E-01	9.09E-01		-1.73E+00	4.99E-01		null	null		null	null		Unigene79386_All//COG3387//7.00E-22//Glucoamylase and related glycosyl hydrolases						cog +
Unigene7939_All	565	0.19	0.00	0.00	0.18	0.00	1.12	17.06	1.78	33.07	-7.53E+00	3.66E-01		-7.53E+00	3.87E-01		-7.46E+00	3.09E-01		2.67E+00	1.82E-02		-3.26E+00	2.23E-42	Down	9.55E-01	2.44E-16		Unigene7939_All//gi|255536905|ref|XP_002509519.1|//3.00E-19//conserved hypothetical protein [Ricinus communis] >gi|223549418|gb|EEF50906.1| conserved hypothetical protein [Ricinus communis]	Unigene7939_All//3.00E-05//AT5G14150| unknown protein				GO:0031224	nr +
Unigene79396_All	737	0.43	0.83	0.72	1.35	0.65	1.04	2.07	0.57	1.03	9.54E-01	3.14E-01		7.63E-01	4.52E-01		-1.05E+00	1.16E-01		-3.76E-01	6.31E-01		-1.86E+00	3.50E-04	Down	-1.01E+00	2.94E-02		Unigene79396_All//gi|297838807|ref|XP_002887285.1|//7.00E-33//sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333126|gb|EFH63544.1| sterile alpha motif domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene79396_All//4.00E-28//AT1G70180| sterile alpha motif (SAM) domain-containing protein	Unigene79396_All//0.00E+00//gi|78342445|gb|DT562719.1|DT562719				nr +
Unigene79397_All	276	0.00	0.00	3.09	0.00	0.12	0.49	0.00	0.00	0.00	null	null		1.16E+01	8.98E-05	Up	6.96E+00	8.15E-01		8.94E+00	3.09E-01		null	null		null	null		Unigene79397_All//gi|224004038|ref|XP_002295670.1|//7.00E-10//copper transporter [Thalassiosira pseudonana CCMP1335] >gi|209585702|gb|ACI64387.1| copper transporter [Thalassiosira pseudonana CCMP1335]	Unigene79397_All//2.00E-10//AT1G63440| HMA5 (HEAVY METAL ATPASE 5); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism				GO:0005488//GO:0009636//GO:0010038//GO:0015075//GO:0016818//GO:0016820//GO:0044464	nr -
Unigene794_All	2892	1.23	0.53	0.55	0.28	0.55	3.92	1.24	3.05	3.36	-1.23E+00	2.50E-04	Down	-1.16E+00	8.62E-04	Down	9.91E-01	6.19E-02		3.83E+00	3.73E-49	Up	1.30E+00	1.83E-12	Up	1.44E+00	3.18E-16	Up	Unigene794_All//gi|282161430|gb|ADA79674.1|//0.00E+00//shaker-like potassium channel 1 [Populus euphratica]	Unigene794_All//0.00E+00//AT2G26650| AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel	Unigene794_All//0.00E+00//TC177956		ko04626|Plant-pathogen interaction	GO:0000166//GO:0005249//GO:0006970//GO:0030001//GO:0031224//GO:0048588	nr +
Unigene7940_All	392	0.27	0.00	0.00	0.89	0.79	0.35	4.85	6.40	1.63	-8.06E+00	3.66E-01		-8.06E+00	3.87E-01		-1.70E-01	8.57E-01		-1.36E+00	3.37E-01		3.98E-01	2.92E-01		-1.58E+00	2.42E-04	Down			Unigene7940_All//5.00E-07//TC169016					
Unigene79411_All	522	0.40	0.49	3.16	0.19	0.07	0.00	0.08	0.00	0.00	2.76E-01	8.43E-01		2.98E+00	1.21E-05	Up	-1.53E+00	5.83E-01		-7.58E+00	3.93E-01		-6.34E+00	6.43E-01		-6.34E+00	6.01E-01								ESTscan -
Unigene79418_All	265	0.79	3.63	2.01	0.75	1.30	1.53	6.54	3.94	1.05	2.20E+00	6.58E-03		1.35E+00	2.25E-01		7.89E-01	5.95E-01		1.03E+00	4.28E-01		-7.30E-01	1.03E-01		-2.64E+00	5.69E-07	Down	Unigene79418_All//1.00E-05//AT3G05230| signal peptidase subunit family protein	Unigene79418_All//2.00E-107//gi|21092419|gb|BQ404732.1|BQ404732		ko00310|Lysine degradation//ko00780|Biotin metabolism		kegg +
Unigene79419_All	465	0.00	2.51	1.26	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.04E-06	Up	1.03E+01	2.16E-03		null	null		null	null		null	null		null	null								ESTscan +
Unigene7942_All	665	0.31	0.00	0.00	6.22	6.37	2.78	0.38	0.00	0.12	-8.30E+00	1.21E-01		-8.30E+00	1.44E-01		3.48E-02	9.31E-01		-1.16E+00	1.04E-04	Down	-8.58E+00	4.03E-02		-1.67E+00	2.56E-01		Unigene7942_All//gi|22022592|gb|AAM83252.1|//1.00E-18//AT3g13990/MDC16_11 [Arabidopsis thaliana] >gi|23308471|gb|AAN18205.1| At3g13990/MDC16_11 [Arabidopsis thaliana]	Unigene7942_All//2.00E-21//AT3G13990| unknown protein	Unigene7942_All//3.00E-49//TC143903			GO:0043231//GO:0044444	nr +
Unigene79425_All	301	0.35	1.18	3.36	1.32	1.26	0.45	0.00	0.14	0.00	1.76E+00	2.18E-01		3.27E+00	5.92E-04	Up	-7.33E-02	9.25E-01		-1.56E+00	2.31E-01		7.12E+00	6.26E-01		null	null								
Unigene7943_All	382	3.29	0.27	2.79	1.70	0.99	0.95	0.00	0.44	0.00	-3.63E+00	1.99E-05	Down	-2.38E-01	6.85E-01		-7.74E-01	3.81E-01		-8.42E-01	3.75E-01		8.77E+00	1.38E-01		null	null								
Unigene7944_All	1677	0.19	0.12	0.00	0.18	0.37	0.46	2.17	0.45	34.64	-6.31E-01	6.21E-01		-7.55E+00	4.88E-02		1.05E+00	2.99E-01		1.36E+00	1.18E-01		-2.27E+00	2.46E-11	Down	4.00E+00	2.04E-303	Up	Unigene7944_All//gi|224062173|ref|XP_002300789.1|//1.00E-109//cytochrome P450 [Populus trichocarpa] >gi|222842515|gb|EEE80062.1| cytochrome P450 [Populus trichocarpa]	Unigene7944_All//6.00E-163//AT2G27690| CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene7944_All//0.00E+00//ES837393		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0031410	nr -
Unigene7945_All	527	0.99	4.62	0.00	1.13	0.33	0.17	1.04	0.95	0.76	2.22E+00	2.89E-06	Up	-9.96E+00	4.73E-03		-1.80E+00	5.86E-02		-2.73E+00	1.74E-02		-1.32E-01	8.80E-01		-4.64E-01	5.97E-01		Unigene7945_All//gi|288559178|sp|B9RW00.1|U4979_RICCO//8.00E-51//RecName: Full=UPF0197 membrane protein 9	Unigene7945_All//8.00E-44//AT4G03540| integral membrane family protein				GO:0000902//GO:0009725//GO:0031224//GO:0031410	nr -

Unigene79463_All	390	0.27	0.00	3.41	0.51	0.00	0.35	0.00	0.00	0.00	-8.07E+00	3.66E-01		3.67E+00	1.90E-05	Up	-9.00E+00	8.38E-02		-5.56E-01	7.32E-01		null	null		null	null		Unigene79463_All//gi|15242330|ref|NP_199329.1|//2.00E-32//root hair defective 3 GTP-binding (RHD3) family protein [Arabidopsis thaliana] >gi|9759601|dbj|BAB11389.1| GTP-binding protein-like; root hair defective 3 protein-like [Arabidopsis thaliana]	Unigene79463_All//7.00E-34//AT5G45160| root hair defective 3 GTP-binding (RHD3) family protein	Unigene79463_All//0.00E+00//TC179128			GO:0003924//GO:0031224//GO:0032561//GO:0043231	nr +
Unigene79467_All	775	0.07	0.13	0.00	0.06	0.13	0.06	1.80	0.38	1.13	9.54E-01	7.24E-01		-6.08E+00	6.15E-01		1.05E+00	8.05E-01		-1.41E-01	9.47E-01		-2.25E+00	9.69E-05	Down	-6.71E-01	1.68E-01		Unigene79467_All//gi|1022801|gb|AAA79704.1|//2.00E-55//OBP33pep [Arabidopsis thaliana]	Unigene79467_All//6.00E-51//AT4G15520| tRNA/rRNA methyltransferase (SpoU) family protein	Unigene79467_All//0.00E+00//gi|78336839|gb|DT557113.1|DT557113			GO:0003676//GO:0008168//GO:0010467//GO:0043231	nr -
Unigene79471_All	474	3.20	5.13	4.72	7.25	4.50	5.15	9.90	6.26	4.37	6.81E-01	9.55E-02		5.60E-01	2.20E-01		-6.87E-01	3.06E-02		-4.95E-01	1.51E-01		-6.61E-01	7.62E-03		-1.18E+00	2.10E-06	Down	Unigene79471_All//gi|297828377|ref|XP_002882071.1|//9.00E-40//phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327910|gb|EFH58330.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene79471_All//1.00E-40//AT2G46500| phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein	Unigene79471_All//2.00E-127//gi|82755803|gb|DV849365.1|DV849365			GO:0016772	nr +
Unigene7948_All	258	0.00	0.00	0.00	26.26	9.74	9.98	6.23	0.65	0.46	null	null		null	null		-1.43E+00	4.50E-11	Down	-1.40E+00	1.63E-09	Down	-3.26E+00	1.49E-07	Down	-3.75E+00	9.85E-09	Down	Unigene7948_All//gi|296086251|emb|CBI31692.3|//3.00E-09//unnamed protein product [Vitis vinifera]		Unigene7948_All//1.00E-52//ES797004				nr -
Unigene79480_All	313	0.00	0.65	2.55	0.00	0.00	0.00	0.00	0.00	0.00	9.34E+00	1.35E-01		1.13E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene79480_All//gi|115461767|ref|NP_001054483.1|//3.00E-21//Os05g0119300 [Oryza sativa Japonica Group] >gi|33668156|gb|AAQ24632.1| GPRP [Oryza sativa Indica Group] >gi|113578034|dbj|BAF16397.1| Os05g0119300 [Oryza sativa Japonica Group]					GO:0043231	nr -
Unigene79488_All	284	1.66	0.89	0.00	3.68	3.15	0.48	0.89	0.00	0.00	-8.94E-01	3.88E-01		-1.07E+01	8.61E-03		-2.25E-01	7.53E-01		-2.95E+00	3.82E-04	Down	-9.80E+00	4.03E-02		-9.80E+00	3.03E-02		Unigene79488_All//gi|297736396|emb|CBI25119.3|//4.00E-09//unnamed protein product [Vitis vinifera]		Unigene79488_All//6.00E-15//TC145425				nr -
Unigene7949_All	1196	0.00	0.42	0.18	0.08	0.00	0.15	1.03	2.66	7.59	8.73E+00	3.99E-03		7.48E+00	1.38E-01		-6.38E+00	3.09E-01		8.58E-01	6.94E-01		1.37E+00	2.21E-05	Up	2.89E+00	4.25E-36	Up	Unigene7949_All//gi|71067056|dbj|BAE16280.1|//3.00E-83//NbPCL1 [Nicotiana benthamiana]	Unigene7949_All//3.00E-66//AT3G46640| PCL1 (PHYTOCLOCK 1); DNA binding / transcription factor	Unigene7949_All//0.00E+00//C0128665	G2-like		GO:0048511	nr -
Unigene79497_All	311	0.00	0.33	2.40	0.00	0.11	0.00	0.00	0.00	0.00	8.35E+00	3.80E-01		1.12E+01	3.25E-04	Up	6.79E+00	8.15E-01		null	null		null	null		null	null									ESTscan -
Unigene79498_All	354	0.44	1.00	2.11	2.81	3.02	1.91	8.48	9.21	4.05	1.18E+00	3.72E-01		2.25E+00	2.34E-02		9.96E-02	9.02E-01		-5.57E-01	4.47E-01		1.19E-01	7.17E-01		-1.07E+00	7.05E-04	Down	Unigene79498_All//gi|62956022|gb|AY23356.1|//8.00E-30//3-ketoacyl-CoA reductase 3 [Gossypium hirsutum]	Unigene79498_All//1.00E-14//AT4G23430| short-chain dehydrogenase/reductase (SDR) family protein	Unigene79498_All//6.00E-114//gi|13356481|gb|BG446829.1|BG446829			GO:0008152//GO:0009528//GO:0016628	nr +
Unigene7950_All	371	0.00	0.00	0.00	7.25	8.35	6.82	67.35	46.53	29.32	null	null		null	null		2.04E-01	6.02E-01		-8.89E-02	8.28E-01		-5.34E-01	3.80E-08		-1.20E+00	4.31E-31	Down	Unigene7950_All//gi|224111880|ref|XP_002316010.1|//7.00E-37//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene7950_All//1.00E-20//AT2G46960| CYP709B1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene7950_All//4.00E-118//TC154355		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00906|Carotenoid biosynthesis	GO:0005506//GO:0016491	nr -
Unigene7951_All	289	4.71	3.68	3.69	1.03	2.50	2.03	4.68	3.90	0.96	-3.54E-01	5.40E-01		-3.53E-01	5.65E-01		1.27E+00	1.56E-01		9.74E-01	3.46E-01		-2.62E-01	6.63E-01		-2.28E+00	7.13E-05	Down			Unigene7951_All//3.00E-103//C0129388				
Unigene79511_All	284	0.00	0.00	3.00	0.00	0.00	0.16	0.00	0.00	0.00	null	null		1.16E+01	8.98E-05	Up	null	null		7.31E+00	6.84E-01		null	null		null	null									
Unigene79518_All	443	0.00	0.34	3.85	0.00	0.00	0.41	0.00	0.00	0.00	8.42E+00	2.32E-01		1.19E+01	2.19E-09	Up	null	null		8.67E+00	1.93E-01		null	null		null	null		Unigene79518_All//gi|270342124|gb|ACZ74707.1|//2.00E-60//carbonic anhydrase [Phaseolus vulgaris]	Unigene79518_All//1.00E-23//AT3G01500| CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	Unigene79518_All//3.00E-11//gi|48745870|gb|C0076389.1|C0076389		ko00910|Nitrogen metabolism	GO:0005576//GO:0009526//GO:0009532//GO:0009534//GO:0010035//GO:0010118//GO:0016836//GO:0046914//GO:0050832	nr +
Unigene7952_All	360	144.32	109.22	127.36	187.36	171.89	176.26	241.58	103.91	77.02	-4.02E-01	3.64E-08		-1.80E-01	2.48E-02		-1.24E-01	6.69E-02		-8.81E-02	2.40E-01		-1.22E+00	1.93E-105	Down	-1.65E+00	2.71E-171	Down	Unigene7952_All//gi|211906490|gb|ACJ11738.1|//1.00E-58//malate dehydrogenase [Gossypium hirsutum]	Unigene7952_All//2.00E-47//AT5G43330| mdate dehydrogenase, cytosolic, putative	Unigene7952_All//0.00E+00//gi|164339135|gb|ES845644.1|ES845644		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0006007//GO:0009060//GO:0016615//GO:0016747//GO:0043848//GO:0044424	nr -
Unigene79520_All	320	0.00	0.16	2.50	0.00	0.32	0.00	0.00	0.00	0.00	7.31E+00	6.09E-01		1.13E+01	1.71E-04	Up	8.33E+00	4.52E-01		null	null		null	null		null	null		Unigene79520_All//COG1295//4.00E-14//Predicted membrane protein							cog -
Unigene79523_All	386	0.27	0.39	0.28	0.52	0.27	0.23	0.22	1.30	5.57	5.39E-01	7.78E-01		2.53E-02	9.97E-01		-9.48E-01	5.87E-01		-1.14E+00	5.67E-01		2.57E+00	2.28E-02		4.67E+00	7.12E-13	Up			Unigene79523_All//2.00E-70//D#517774				
Unigene79524_All	299	0.00	0.00	0.00	0.00	0.00	0.15	2.83	0.28	0.00	null	null		null	null		null	null		7.24E+00	6.84E-01		-3.34E+00	2.51E-04	Down	-1.15E+01	2.21E-06	Down	Unigene79524_All//gi|34452231|gb|AGZ2567.1|//1.00E-39//mini-chromosome maintenance 7 [Pisum sativum]	Unigene79524_All//1.00E-34//AT4G02060| PRL (PROLIFERA); ATP binding / DNA binding / DNA-dependent ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene79524_All//8.00E-116//TC153692		ko03030|DNA replication	GO:0003676//GO:0006261//GO:0009756//GO:0032559//GO:0042623//GO:0043231	nr +
Unigene79525_All	320	0.00	0.00	0.00	0.00	0.11	0.00	0.13	0.91	2.61	null	null		null	null		6.75E+00	8.15E-01		null	null		2.79E+00	9.47E-02		4.31E+00	4.10E-05	Up	Unigene79525_All//gi|297814588|ref|XP_002875177.1|//2.00E-24//kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321015|gb|EFH51436.1| kelch repeat-containing F-box family protein [Arabidopsis lyrata subsp. lyrata]	Unigene79525_All//3.00E-25//AT2G02870| kelch repeat-containing F-box family protein	Unigene79525_All//2.00E-104//TC140708			GO:0042579	nr +
Unigene7953_All	281	2.61	0.00	2.08	12.76	7.48	8.52	0.15	0.60	0.00	-1.13E+01	2.11E-04	Down	-3.23E-01	6.81E-01		-7.72E-01	1.18E-02		-5.83E-01	7.68E-02		1.98E+00	3.78E-01		-7.23E+00	6.01E-01		Unigene7953_All//gi|18401317|ref|NP_565634.1|//5.00E-06//harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana] >gi|42570933|ref|NP_973540.1| harpin-induced protein-related / HIN1-related / harpin-responsive protein-related [Arabidopsis thaliana] >gi|13877665|gb|AAK43910.1|AF37059_1_1 Unknown protein [Arabidopsis thaliana] >gi|3883338|gb|AAC77866.1| expressed protein [Arabidopsis thaliana] >gi|15450381|gb|AAK96484.1| At2g27080/T20F8.13 [Arabidopsis thaliana] >gi|16974489|gb|AAL31248.1| At2g27080/T20F8.13 [Arabidopsis thaliana]		Unigene7953_All//3.00E-115//gi|164242793|gb|EX164859.1|EX164859				nr -
Unigene79546_All	344	0.00	1.91	4.02	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	6.20E-04	Up	1.20E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene79546_All//gi|7799051|emb|CAB90826.1|//9.00E-34//ubiquitin [Cyanidium caldarium]	Unigene79546_All//7.00E-34//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene79546_All//2.00E-49//BF277514			GO:0043231	nr -
Unigene79547_All	323	0.65	2.20	0.16	2.93	4.58	3.22	6.81	8.67	20.84	1.76E+00	5.60E-02		-1.97E+00	3.80E-01		6.46E-01	2.65E-01		1.34E-01	8.58E-01		3.49E-01	3.34E-01		1.61E+00	1.71E-13	Up		Unigene79547_All//2.00E-06//AT2G34250| protein transport protein sec61, putative	Unigene79547_All//6.00E-83//TC135106		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export		kegg -
Unigene79551_All	692	0.00	0.00	7.31	0.14	0.00	0.00	0.00	0.00	0.00	null	null		1.28E+01	3.83E-28	Up	-7.17E+00	3.09E-01		-7.17E+00	3.93E-01		null	null		null	null		Unigene79551_All//gi|38679405|gb|AAR26524.1|//2.00E-45//abscisic stress ripening-like protein [Glycine max]						nr -
Unigene79558_All	332	3.31	6.56	1.60	5.85	1.97	2.86	4.84	2.01	0.12	9.88E-01	2.43E-02		-1.05E+00	1.35E-01		-1.57E+00	4.84E-04	Down	-1.03E+00	2.69E-02		-1.26E+00	7.60E-03		-5.33E+00	1.38E-10	Down	Unigene79558_All//gi|15229349|ref|NP_187130.1|//1.00E-32//ribose 5-phosphate isomerase-related [Arabidopsis thaliana]	Unigene79558_All//5.00E-34//AT3G04790| ribose 5-phosphate isomerase-related	Unigene79558_All//2.00E-123//gi|78324514|gb|DT544788.1|DT544788		ko00710|Carbon fixation in photosynthetic organisms//ko00030|Pentose phosphate pathway	GO:0006098//GO:0006952//GO:0009526//GO:0009532//GO:0009534//GO:0015977//GO:0016861	nr +
Unigene7956_All	1043	1.20	0.00	0.26	0.05	0.07	0.26	5.92	3.25	2.10	-1.02E+01	2.54E-07	Down	-2.24E+00	1.94E-03		4.66E-01	9.54E-01		2.44E+00	2.21E-01		-8.67E-01	4.60E-05		-1.49E+00	2.50E-11	Down							
Unigene79563_All	292	0.00	0.00	2.74	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.14E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene79563_All//sp|O05494|YDHC_BACSU//4.00E-07//Uncharacterized HTH-type transcriptional regulator ydhC OS=Bacillus subtilis GN=ydhC PE=4 SV=1						swissprot -
Unigene79572_All	300	0.00	0.17	2.31	0.50	0.00	0.00	0.00	0.00	0.00	7.40E+00	6.09E-01		1.12E+01	6.12E-04	Up	-8.96E+00	1.64E-01		-8.96E+00	2.31E-01		null	null		null	null		Unigene79572_All//gi|94313700|ref|YP_586909.1|//5.00E-14//high-affinity branched-chain amino acid transport protein of the ABC transporter ATP binding [Cupriavidus metallidurans CH34] >gi|93357552|gb|ABF11640.1| high-affinity branched-chain amino acid transport protein of the ABC transporter, ATP binding [Cupriavidus metallidurans CH34] >gi|222834352|gb|EEE72829.1| ABC transporter family protein [Populus trichocarpa]	Unigene79572_All//6.00E-06//AT1G67940| ATNAP3; transporter				GO:0003676//GO:0005215//GO:0017111//GO:0032559//GO:0043231//GO:0043232//GO:0051276	nr -
Unigene79574_All	586	0.00	1.64	0.55	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	1.37E-05	Up	9.09E+00	4.45E-02		null	null		null	null		null	null		null	null		Unigene79574_All//gi|145339693|ref|NP_191569.2|//5.00E-74//CSY5 (citrate synthase 5); citrate (SI)-synthase/ transferase, transferring acyl groups, acyl groups converted into alkyl on transfer [Arabidopsis thaliana]	Unigene79574_All//8.00E-76//AT3G60100| CSY5 (citrate synthase 5); citrate (SI)-synthase/ transferase, transferring acyl groups, acyl groups converted into alkyl on transfer			ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005975//GO:0009060//GO:0009536//GO:0010038//GO:0030312//GO:0031980//GO:0032559//GO:0046912//GO:0046914	nr +
Unigene79577_All	678	0.00	0.00	3.53	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	3.24E-13	Up	null	null		null	null		null	null		null	null		Unigene79577_All//gi|6850916|emb|CAB71126.1|//3.00E-57//calmodulin-binding protein [Cicer arietinum]	Unigene79577_All//8.00E-22//AT2G18750| calmodulin-binding protein	Unigene79577_All//9.00E-13//TC148452		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene79578_All	305	0.00	5.65	5.06	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.96E-10	Up	1.23E+01	1.65E-08	Up	null	null		null	null		null	null		null	null									
Unigene7958_All	373	41.24	51.89	43.69	51.82	56.22	50.73	19.84	19.95	9.51	3.32E-01	9.37E-03		8.31E-02	6.32E-01		1.18E-01	4.14E-01		-3.05E-02	8.46E-01		7.90E-03	1.01E+00		-1.06E+00	3.16E-08	Down	Unigene7958_All//gi|195625106|gb|ACG43383.1|//4.00E-15//mannose-1-phosphate guanyltransferase [Zea mays]	Unigene7958_All//3.00E-09//AT1G74910| ADP-glucose pyrophosphorylase family protein	Unigene7958_All//0.00E+00//TC166316			GO:0008152//GO:0008905//GO:0010038//GO:0042579	nr +
Unigene79585_All	441	0.00	0.00	3.62	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	8.43E-09	Up	null	null		null	null		null	null		null	null		Unigene79585_All//gi|225434984|ref|XP_002284008.1|//8.00E-71//PREDICTED: similar to HSC70-1 (heat shock cognate 70 kDa protein 1); ATP binding isoform 1 [Vitis vinifera]	Unigene79585_All//2.00E-69//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene79585_All//3.00E-64//EV485612		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr -
Unigene79587_All	335	0.00	0.00	2.38	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.12E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene79587_All//gi|224061216|ref|XP_002300374.1|//1.00E-45//ZIP transporter [Populus trichocarpa] >gi|222847632|gb|EEE85175.1| ZIP transporter [Populus trichocarpa]	Unigene79587_All//3.00E-46//AT1G55910| ZIP11 (ZINC TRANSPORTER 11 PRECURSOR); cation transmembrane transporter/ metal ion transmembrane transporter	Unigene79587_All//4.00E-10//TC176195			GO:0000041//GO:0008152//GO:0015082//GO:0016628//GO:0031224	nr -

Unigene7959_All	760	0.00	0.13	0.00	0.00	0.00	0.00	7.68	1.81	5.61	7.06E+00	3.80E-01		null	null		null	null		null	null		-2.08E+00	5.59E-16	Down	-4.53E-01	3.43E-02		Unigene7959_All//gi|224113231|ref|XP_002316430.1|//2.00E-52//SAUR family protein [Populus trichocarpa] >gi|222865470|gb|EEF02601.1| SAUR family protein [Populus trichocarpa]	Unigene7959_All//1.00E-33//AT2G24400| auxin-responsive protein, putative / small auxin up RNA (SAUR_D)				GO:0005515//GO:0009725	nr +
Unigene79594_All	343	0.00	0.89	2.02	0.00	0.00	0.00	0.00	0.00	0.00	9.79E+00	4.37E-02		1.10E+01	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene79594_All//gi|109649528|gb|ABG36709.1|//5.00E-06//cytochrome P450 CYP85A1 [Nicotiana tabacum]	Unigene79594_All//1.00E-05//AT3G30180| BR6OX2 (BRASSINOSTEROID-6-OXIDASE 2); monooxygenase/ oxygen binding					nr +
Unigene7960_All	216	98.59	104.39	123.02	92.25	70.15	137.58	49.13	56.89	24.16	8.25E-02	5.40E-01		3.19E-01	4.01E-03		-3.95E-01	6.65E-04		5.77E-01	2.17E-09		2.12E-01	1.80E-01		-1.02E+00	8.14E-11	Down	Unigene7960_All//gi|24473796|gb|AAL91663.1|//4.00E-08//60s acidic ribosomal protein [Prunus dulcis] >gi|11013714|gb|AB003379.1| 60S acidic ribosomal protein [Prunus dulcis]	Unigene7960_All//3.00E-08//AT3G44590| 60S acidic ribosomal protein P2 (RPP2D)	Unigene7960_All//5.00E-104//TC160286		ko03010|Ribosome	GO:0005198//GO:0006412//GO:0030529//GO:0043231	nr -
Unigene79602_All	343	0.00	5.02	1.24	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.96E-10	Up	1.03E+01	1.36E-02		null	null		null	null		null	null		null	null								
Unigene79603_All	560	0.00	5.70	1.90	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	3.64E-18	Up	1.09E+01	6.59E-06	Up	null	null		null	null		null	null		null	null		Unigene79603_All//gi|1174749|sp|P46226.3|TPIS_SECCE//3.00E-54//RecName: Full=Triosephosphate isomerase, cytosolic; Short=TIM; Short=Triose-phosphate isomerase >gi|407525|emb|CAA81487.1| triosephosphate isomerase [Secale cereale] >gi|1095493|prf|2109226A triosephosphate isomerase	Unigene79603_All//8.00E-51//AT3G55440| TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase			ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00562|Inositol phosphate metabolism//ko00051|Fructose and mannose metabolism	GO:0006007//GO:0006631//GO:0016861//GO:0044424	nr -
Unigene7961_All	565	1.39	1.52	2.07	2.73	0.61	0.88	0.52	0.15	0.42	1.34E-01	8.47E-01		5.78E-01	3.90E-01		-2.16E+00	7.69E-05	Down	-1.64E+00	3.26E-03		-1.82E+00	2.10E-01		-3.08E-01	7.74E-01		Unigene7961_All//gi|224132258|ref|XP_002328224.1|//3.00E-33//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837739|gb|EEE76104.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene7961_All//5.00E-19//AT3G14460| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction	GO:0005488	nr -
Unigene79611_All	369	0.28	0.14	4.33	1.62	0.37	2.08	0.80	1.13	0.43	-1.05E+00	6.82E-01		3.93E+00	9.51E-07	Up	-2.12E+00	3.06E-02		3.61E-01	6.79E-01		4.98E-01	6.32E-01		-8.93E-01	4.71E-01		Unigene79611_All//gi|226495995|ref|NP_001150110.1|//7.00E-15//LOC100283739 [Zea mays] >gi|195627538|gb|ACG35599.1| coiled-coil domain-containing protein 25 [Zea mays] >gi|195636814|gb|ACG37875.1| coiled-coil domain-containing protein 25 [Zea mays]	Unigene79611_All//5.00E-15//AT5G11500| unknown protein	Unigene79611_All//6.00E-37//TC170861			nr +
Unigene79613_All	324	0.00	0.31	6.90	0.00	0.00	0.00	0.00	0.00	0.00	8.29E+00	3.80E-01		1.28E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene79613_All//gi|3759184|dbj|BAA33810.1|//1.00E-16//phi-1 [Nicotiana tabacum]	Unigene79613_All//3.00E-15//AT4G08950| EXO (EXORDIUM)	Unigene79613_All//2.00E-08//ES834057			GO:0005618//GO:0009725	nr -
Unigene79614_All	305	0.00	0.83	3.49	0.33	0.23	0.59	0.00	0.00	0.00	9.70E+00	7.76E-02		1.18E+01	6.59E-06	Up	-5.33E-01	8.13E-01		8.58E-01	6.94E-01		null	null		null	null		Unigene79614_All//gi|255599488|ref|XP_002537241.1|//4.00E-08//acyl-CoA dehydrogenase, putative [Ricinus communis] >gi|223517007|gb|EEF25140.1| acyl-CoA dehydrogenase, putative [Ricinus communis]					GO:0016491	nr +
Unigene79616_All	352	0.00	0.00	2.87	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene79616_All//gi|228480908|gb|ACQ42220.1|//1.00E-24//R2R3 transcription factor WVB108-like protein 1 [Vitis vinifera]						nr -
Unigene79619_All	301	0.00	0.00	2.48	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene79619_All//gi|77553656|gb|AB96452.1|//1.00E-34//GRF zinc finger family protein [Oryza sativa (japonica cultivar-group)]	Unigene79619_All//2.00E-35//AT5G42300| UBL5 (UBIQUITIN-LIKE PROTEIN 5)	Unigene79619_All//2.00E-45//TC164960			GO:0043412	nr -
Unigene79623_All	344	0.00	0.00	6.35	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.26E+01	4.94E-12	Up	null	null		null	null		null	null		null	null		Unigene79623_All//gi|283837110|emb|CB196235.1|//1.00E-34//major intrinsic protein 1 [Solanum tuberosum]	Unigene79623_All//2.00E-31//AT2G45960| PIP1B (NAMED PLASMA MEMBRANE INTRINSIC PROTEIN 1B); water channel	Unigene79623_All//3.00E-29//TC152372			GO:0006810//GO:0031224//GO:0050896	nr -
Unigene79629_All	471	0.00	2.80	0.79	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.49E-07	Up	9.63E+00	2.47E-02		null	null		null	null		null	null		null	null		Unigene79629_All//sp|Q94516|AT5F1_DROME//1.00E-62//ATP synthase subunit b, mitochondrial OS=Drosophila melanogaster GN=ATPsyn-b PE=1 SV=2						swissprot -
Unigene79963_All	229	3.20	1.33	1.16	1.74	7.07	2.56	1.11	1.28	0.70	-1.27E+00	1.36E-01		-1.46E+00	1.12E-01		2.02E+00	3.01E-04	Up	5.59E-01	6.01E-01		2.06E-01	8.68E-01		-6.71E-01	6.05E-01				Unigene79963_All//3.00E-07//DR453012				
Unigene79634_All	486	0.00	0.00	4.05	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.20E+01	7.44E-11	Up	null	null		null	null		null	null		null	null		Unigene79634_All//gi|209978913|gb|ACJ04728.1|//9.00E-31//WRKY transcription factor-30 [Capsicum annuum]	Unigene79634_All//2.00E-15//AT4G11070| WRKY41; transcription factor	Unigene79634_All//6.00E-07//gi|78331396|gb|DT551670.1|DT551670	WRKY	ko04626|Plant-pathogen interaction	GO:0003677//GO:0010167	nr -
Unigene79635_All	346	0.00	1.17	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.02E+01	1.34E-02		1.10E+01	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene79635_All//sp|P0A910|OMPA_ECOLI//1.00E-44//Outer membrane protein A OS=Escherichia coli (strain K12) GN=ompA PE=1 SV=1		Unigene79635_All//1.00E-10//AJ514182				swissprot -
Unigene7964_All	240	0.22	3.59	1.33	0.83	1.29	1.32	0.53	0.70	0.66	4.04E+00	4.20E-04	Up	2.61E+00	1.45E-01		6.37E-01	6.94E-01		6.66E-01	6.47E-01		3.98E-01	8.13E-01		3.29E-01	8.50E-01				Unigene7964_All//4.00E-09//ES825258				
Unigene79644_All	348	0.00	2.91	1.68	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.21E-06	Up	1.07E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene79644_All//gi|186493960|ref|NP_177041.3|//3.00E-09//AGP19 (ARABINOGALACTAN-PROTEIN 19) [Arabidopsis thaliana]				ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko03420|Nucleotide excision repair		nr +
Unigene79646_All	345	0.00	1.91	2.16	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	6.20E-04	Up	1.11E+01	3.25E-04	Up	null	null		null	null		null	null		null	null								
Unigene79649_All	344	3.50	0.00	0.77	0.00	0.00	0.00	0.00	0.00	0.00	-1.18E+01	5.01E-07	Down	-2.18E+00	3.04E-03		null	null		null	null		null	null		null	null								
Unigene7965_All	761	0.55	0.53	0.14	0.72	0.50	0.59	21.61	80.79	44.24	-4.61E-02	9.80E-01		-1.98E+00	1.51E-01		-5.32E-01	5.85E-01		-2.79E-01	7.57E-01		1.90E+00	2.70E-143	Up	1.03E+00	1.31E-32	Up	Unigene7965_All//gi|84043333|gb|ABC50164.1|//7.00E-66//phospholipase C [Petunia integrifolia subsp. inflata]	Unigene7965_All//3.00E-59//AT5G58670| PLC1 (PHOSPHOLIPASE C 1); phospholipase C	Unigene7965_All//7.00E-94//TC146670		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism	GO:0004629	nr +
Unigene79653_All	351	0.00	0.00	2.88	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene79653_All//gi|110293351|gb|ABG66307.1|//7.00E-49//CCR4 associated factor 1-related protein [Capsicum annuum]	Unigene79653_All//1.00E-45//AT5G22250| CCR4-NOT transcription complex protein, putative	Unigene79653_All//5.00E-22//TC148665		ko03018|RNA degradation	GO:0000175//GO:0005488//GO:0006950//GO:0016070//GO:0043231	nr -
Unigene79656_All	1368	2.26	2.96	1.87	2.62	2.54	3.80	3.46	2.87	1.25	3.93E-01	2.10E-01		-2.72E-01	4.75E-01		-4.44E-02	8.94E-01		5.34E-01	4.58E-02		-2.69E-01	3.21E-01		-1.47E+00	1.13E-08	Down	Unigene79656_All//gi|22328173|ref|NP_567165.2|//1.00E-133//mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein [Arabidopsis thaliana]	Unigene79656_All//6.00E-136//AT4G00290| mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein	Unigene79656_All//0.00E+00//AI728050			GO:0043231	nr +
Unigene79657_All	342	0.15	0.00	3.11	0.29	0.00	0.40	0.00	0.00	0.00	-7.26E+00	6.02E-01		4.35E+00	6.45E-05	Up	-8.19E+00	3.09E-01		4.44E-01	8.60E-01		null	null		null	null		Unigene79657_All//gi|226497440|ref|NP_001143758.1|//2.00E-06//hypothetical protein LOC100276520 [Zea mays] >gi|195626450|gb|ACG35055.1| hypothetical protein [Zea mays]						nr +
Unigene7966_All	386	2.30	14.31	2.21	7.74	12.13	4.10	2.30	4.44	1.75	2.63E+00	3.62E-16	Up	-6.20E-02	9.45E-01		6.48E-01	1.77E-02		-9.19E-01	1.05E-02		9.49E-01	3.49E-02		-3.91E-01	5.53E-01		Unigene7966_All//gi|115457130|ref|NP_001052165.1|//1.00E-10//Os04g0176400 [Oryza sativa Japonica Group] >gi|38344210|emb|CAE01973.2| OSJNBb0051N19.2 [Oryza sativa (japonica cultivar-group)] >gi|113563736|dbj|BAF14079.1| Os04g0176400 [Oryza sativa Japonica Group]	Unigene7966_All//6.00E-09//AT2G22960| serine carboxypeptidase S10 family protein	Unigene7966_All//7.00E-09//TC162267		ko00940|Phenylpropanoid biosynthesis	GO:0004180//GO:0019538//GO:0031410//GO:0043231	nr -
Unigene79663_All	471	1.11	0.22	4.07	0.21	0.58	0.00	0.00	0.00	0.00	-2.37E+00	4.75E-02		1.87E+00	4.53E-04	Up	1.47E+00	4.19E-01		-7.72E+00	3.93E-01		null	null		null	null		Unigene79663_All//gi|222874712|gb|EEF11843.1|//6.00E-08//predicted protein [Populus trichocarpa]						nr +
Unigene79665_All	346	0.00	8.35	1.85	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.97E-16	Up	1.09E+01	1.15E-03		null	null		null	null		null	null		null	null								
Unigene79685_All	356	0.00	2.85	1.94	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.21E-06	Up	1.09E+01	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene79685_All//gi|195644804|gb|ACG41870.1|//7.00E-26//60S ribosomal protein L22-2 [Zea mays]	Unigene79685_All//5.00E-13//AT3G05560| 60S ribosomal protein L22-2 (RPL22B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene79688_All	370	0.28	0.00	0.29	0.40	0.28	0.49	5.71	0.23	12.38	-8.14E+00	3.66E-01		2.53E-02	9.97E-01		-5.33E-01	7.83E-01		2.74E-01	9.04E-01		-4.66E+00	1.89E-12	Down	1.12E+00	9.14E-06	Up	Unigene79688_All//gi|79330866|ref|NP_001032078.1|//6.00E-14//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana]	Unigene79688_All//3.00E-15//AT5G55410| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene79688_All//2.00E-163//DW512993			nr -
Unigene7969_All	450	59.41	45.60	94.90	95.64	103.99	78.28	210.46	67.52	89.33	-3.82E-01	2.87E-04		6.76E-01	1.08E-15		1.21E-01	1.63E-01		-2.89E-01	3.23E-04		-1.64E+00	8.89E-180	Down	-1.24E+00	6.08E-121	Down	Unigene7969_All//gi|300793598|tpg|DAA33865.1|//3.00E-61//TPA: TPA_inf: aquaporin PIP2;10 [Gossypium hirsutum]	Unigene7969_All//2.00E-49//AT5G60660| PIP2;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;4); water channel	Unigene7969_All//2.00E-114//TC166797			GO:0006810//GO:0016020	nr -
Unigene79695_All	418	0.00	0.00	1.78	0.12	0.16	0.43	0.00	0.00	0.00	null	null		1.08E+01	3.25E-04	Up	4.67E-01	9.54E-01		1.86E+00	4.57E-01		null	null		null	null		Unigene79695_All//gi|301119701|ref|XP_002907578.1|//4.00E-27//ATP-dependent protease hslV [Phytophthora infestans T30-4] >gi|262106090|gb|EEY64142.1| ATP-dependent protease hslV [Phytophthora infestans T30-4]					GO:0000502//GO:0004175//GO:0006000//GO:0006508//GO:0009057	nr +
Unigene79697_All	360	0.29	0.56	1.78	2.21	0.19	1.76	0.59	0.00	0.44	9.54E-01	6.20E-01		2.61E+00	2.33E-02		-3.53E+00	3.03E-04	Down	-3.34E-01	6.86E-01		-9.20E+00	7.41E-02		-4.08E-01	7.55E-01								
Unigene79702_All	371	0.28	0.41	2.87	0.13	0.28	0.24	0.00	0.00	0.00	5.38E-01	7.78E-01		3.35E+00	3.36E-04	Up	1.05E+00	8.05E-01		8.59E-01	7.91E-01		null	null		null	null								ESTscan +
Unigene7971_All	790	2.05	0.58	1.42	5.86	6.15	5.03	2.41	0.53	0.91	-1.83E+00	1.15E-03		-5.37E-01	3.31E-01		6.77E-02	8.24E-01		-2.21E-01	4.82E-01		-2.19E+00	5.20E-06	Down	-1.41E+00	8.29E-04	Down	Unigene7971_All//gi|145338056|ref|NP_566199.4|//3.00E-91//DCL2 (DICER-LIKE 2); ATP binding / ATP-dependent helicase/ RNA binding / double-stranded RNA binding / helicase/ nucleic acid binding / ribonuclease III [Arabidopsis thaliana]	Unigene7971_All//1.00E-92//AT3G03300| DCL2 (DICER-LIKE 2); ATP binding / ATP-dependent helicase/ RNA binding / double-stranded RNA binding / helicase/ nucleic acid binding / ribonuclease III	Unigene7971_All//7.00E-165//TC138289			GO:0002252//GO:0003723//GO:0006259//GO:0016891//GO:0030422//GO:0035195//GO:0042623//GO:0043231	nr +
Unigene79723_All	837	0.38	0.48	2.29	0.00	0.33	0.05	0.00	0.00	0.00	3.69E-01	7.23E-01		2.61E+00	1.00E-05	Up	8.36E+00	7.00E-02		5.75E+00	6.84E-01		null	null		null	null		Unigene79723_All//gi|255593863|ref|XP_002535966.1|//5.00E-09//Protein srpB, putative [Ricinus communis] >gi|223521358|gb|EEF26417.1| Protein srpB, putative [Ricinus communis]						nr +
Unigene79732_All	364	0.00	1.25	3.51	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	7.34E-03		1.18E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene79732_All//sp|Q01469|FABP5_HUMAN//6.00E-46//Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3						swissprot +
Unigene79737_All	360	0.00	1.69	4.29	0.00	0.00	0.00	0.12	0.12	0.00	1.07E+01	1.16E-03		1.21E+01	1.65E-08	Up	null	null		null	null		-1.61E-02	9.98E-01		-6.88E+00	6.01E-01								

Unigene7974_All	1631	0.00	11.12	4.51	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	2.61E-104	Up	1.21E+01	4.44E-41	Up	null	null		null	null		null	null		null	null		Unigene7974_All//gi|115468188|ref|NP_001057693.1|//1.00E-11//Os06g0496000 [Oryza sativa Japonica Group] >gi|52077401|dbj|BAD46512.1|alphaSNRP(R)-like [Oryza sativa Japonica Group] >gi|113595733|dbj|BAF19607.1|Os06g0496000 [Oryza sativa Japonica Group]				ko03040|Spliceosome//ko03018|RNA degradation		nr -
Unigene79740_All	373	0.00	0.00	2.00	0.40	0.09	0.36	0.00	0.00	0.00	null	null		1.10E+01	3.25E-04	Up	-2.12E+00	3.85E-01		-1.42E-01	9.42E-01		null	null		null	null									ESTscan +
Unigene79759_All	373	0.14	0.82	0.71	1.74	2.12	1.09	2.04	0.00	1.17	2.54E+00	1.51E-01		2.35E+00	2.39E-01		2.90E-01	7.70E-01		-6.72E-01	4.78E-01		-1.10E+01	1.67E-05	Down	-7.96E-01	2.52E-01		Unigene79759_All//gi|82568706|dbj|BAE48666.1|//2.00E-13//Serine carboxypeptidase [Prunus mume]	Unigene79759_All//3.00E-10//AT3G45010| scpl48 (serine carboxypeptidase-like 48); serine-type carboxypeptidase	Unigene79759_All//3.00E-08//TC139716		ko00940|Phenylpropanoid biosynthesis	GO:0016787//GO:0043231	nr -
Unigene79761_All	451	0.81	0.45	1.42	5.19	4.20	1.90	2.06	1.20	1.50	-8.54E-01	4.88E-01		8.03E-01	3.88E-01		-3.06E-01	4.99E-01		-1.45E+00	6.78E-04	Down	-7.76E-01	2.35E-01		-4.58E-01	4.67E-01		Unigene79761_All//gi|42563167|ref|NP_177385.2|//2.00E-08//COP1-interacting protein-related [Arabidopsis thaliana]	Unigene79761_All//1.00E-09//AT1G72410| COP1-interacting protein-related	Unigene79761_All//3.00E-141//TC178937				nr +
Unigene79764_All	653	0.00	7.99	4.73	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	9.24E-30	Up	1.22E+01	4.50E-17	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene79765_All	369	0.00	3.43	1.59	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.85E-07	Up	1.06E+01	2.16E-03		null	null		null	null		null	null		null	null		Unigene79765_All//sp|Q9CQ69|QCR8_MOUSE//2.00E-14//Cytochrome b-c1 complex subunit 8 OS=Mus musculus GN=Uqcrq PE=1 SV=3						swissprot +
Unigene79767_All	379	0.00	1.34	2.11	1.31	2.63	1.91	1.34	0.33	0.63	1.04E+01	3.99E-03		1.10E+01	1.71E-04	Up	1.00E+00	1.65E-01		5.37E-01	5.60E-01		-2.02E+00	5.20E-02		-1.09E+00	2.28E-01		Unigene79767_All//gi|147765651|emb|CAN64742.1|//4.00E-20//hypothetical protein [Vitis vinifera]	Unigene79767_All//2.00E-10//AT2G34530| unknown protein	Unigene79767_All//1.00E-136//TC151654				nr +
Unigene79769_All	392	0.13	1.42	2.17	0.00	0.35	0.00	0.00	0.00	0.00	3.41E+00	1.24E-02		4.03E+00	7.02E-04	Up	8.46E+00	3.17E-01		null	null		null	null		null	null		Unigene79769_All//gi|255588936|ref|XP_002534770.1|//4.00E-11//Aliphatic amidase expression-regulating protein, putative [Ricinus communis] >gi|223524603|gb|EEF27616.1|Aliphatic amidase expression-regulating protein, putative [Ricinus communis]						nr -
Unigene7977_All	305	119.22	51.17	97.77	2.78	10.05	0.30	0.00	0.00	0.00	-1.22E+00	1.31E-36	Down	-2.86E-01	2.25E-03		1.86E+00	6.80E-07	Up	-3.23E+00	1.04E-03		null	null		null	null		Unigene7977_All//gi|144925053|gb|ABP03851.1|//1.00E-16//Plant lipid transfer/seed storage/trypsin-alpha amylase inhibitor [Medicago truncatula]		Unigene7977_All//5.00E-151//gi|78346878|gb|DT567152.1|DT567152			GO:0005576//GO:0009534	nr +
Unigene79772_All	381	0.00	0.27	1.96	0.26	0.00	0.36	0.00	0.00	0.00	8.06E+00	3.80E-01		1.09E+01	3.25E-04	Up	-8.03E+00	3.09E-01		4.43E-01	8.60E-01		null	null		null	null									ESTscan -
Unigene79774_All	365	0.00	4.03	2.48	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.10E-08	Up	1.13E+01	4.70E-05	Up	null	null		null	null		null	null		null	null									
Unigene79778_All	385	0.14	0.53	3.18	0.26	0.81	0.00	0.00	0.00	0.00	1.95E+00	3.74E-01		4.55E+00	1.02E-05	Up	1.64E+00	3.21E-01		-8.02E+00	3.93E-01		null	null		null	null									
Unigene79783_All	363	0.00	0.00	2.93	0.14	0.09	0.00	0.00	0.00	0.00	null	null		1.15E+01	6.59E-06	Up	-5.32E-01	8.19E-01		-7.10E+00	6.20E-01		null	null		null	null		Unigene79783_All//gi|222834325|gb|EEE72802.1|//5.00E-15//predicted protein [Populus trichocarpa]						nr +
Unigene79785_All	415	0.00	0.49	2.05	1.32	1.83	1.74	1.53	0.20	0.19	8.93E+00	1.35E-01		1.10E+01	8.98E-05	Up	4.67E-01	6.07E-01		3.99E-01	6.51E-01		-2.92E+00	4.19E-03		-2.99E+00	2.58E-03		Unigene79785_All//gi|225452080|ref|XP_002284052.1|//8.00E-31//PREDICTED: plastid hexose transporter [Vitis vinifera] >gi|51574116|gb|AAU07980.1|plastid hexose transporter [Vitis vinifera]	Unigene79785_All//2.00E-28//AT5G16150| PGLCT (PLASTIDIC GLC TRANSLOCATOR); carbohydrate transmembrane transporter/ sugar:hydrogen symporter	Unigene79785_All//2.00E-43//TC143191			GO:0006810//GO:0009526//GO:0022891//GO:0031224	nr +
Unigene79789_All	349	0.30	0.00	3.05	0.00	0.30	1.29	0.00	0.00	0.00	-8.23E+00	3.66E-01		3.35E+00	3.36E-04	Up	8.21E+00	4.52E-01		1.03E+01	7.74E-03		null	null		null	null		Unigene79789_All//gi|269994009|dbj|BAI50641.1|//1.00E-35//NADP-dependent isocitrate dehydrogenase [Eucalyptus grandis x Eucalyptus urophylla]	Unigene79789_All//2.00E-36//AT5G14590| isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative		ko04146|Peroxisome//ko00480|Glutathione metabolism//ko00020|Citrate cycle (TCA cycle)	GO:0000166//GO:0004448//GO:0009060//GO:0019752//GO:0044262//GO:0044424//GO:0046872	nr +
Unigene79791_All	355	0.44	0.14	3.75	0.28	0.29	0.38	0.00	0.00	0.00	-1.63E+00	4.87E-01		3.08E+00	8.57E-05	Up	5.25E-02	9.65E-01		4.44E-01	8.60E-01		null	null		null	null									ESTscan +
Unigene79792_All	503	0.00	0.00	0.00	0.10	0.00	0.00	1.51	0.00	0.00	null	null		null	null		-6.63E+00	5.44E-01		-6.63E+00	6.20E-01		-1.06E+01	1.67E-05	Down	-1.06E+01	8.87E-06	Down	Unigene79792_All//gi|16226063|gb|AAL16065.1|AF422239_1//2.00E-35//S-adenosyl-L-methionine decarboxylase [Dendrobium crumenatum]	Unigene79792_All//1.00E-32//AT3G02470| SAMDC (S-ADENOSYLMETHIONINE DECARBOXYLASE); adenosylmethionine decarboxylase	Unigene79792_All//2.00E-121//TC178051		ko00270|Cysteine and methionine metabolism//ko00330|Arginine and proline metabolism	GO:0006596//GO:0016831	nr +
Unigene79795_All	951	0.00	0.96	1.74	0.00	0.00	0.00	0.00	0.00	0.00	9.91E+00	2.60E-05	Up	1.08E+01	4.29E-09	Up	null	null		null	null		null	null		null	null		Unigene79795_All//gi|145335601|ref|XP_001421096.1|//1.00E-114//Receptor of activated protein kinase C 1A, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|145357301|ref|XP_001422858.1|Receptor of activated protein kinase C 1B, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|144581332|gb|ABD99389.1|Receptor of activated protein kinase C 1A, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901] >gi|144583102|gb|ABF01217.1|Receptor of activated protein kinase C 1B, component of 40S small ribosomal subunit [Ostreococcus lucimarinus CCE9901]	Unigene79795_All//2.00E-98//AT3G18130| RACK1C_AT (RECEPTOR FOR ACTIVATED C KINASE 1 C); nucleotide binding	Unigene79795_All//2.00E-08//gi|13356321|gb|BG446669.1|BG446669		ko03040|Spliceosome//ko03022|Basal transcription factors		nr +
Unigene798_All	1127	2.23	2.92	1.80	5.66	3.85	3.81	2.59	3.45	1.06	3.91E-01	2.63E-01		-3.12E-01	4.62E-01		-5.55E-01	1.25E-02		-5.72E-01	1.40E-02		4.14E-01	1.49E-01		-1.29E+00	8.24E-05	Down	Unigene798_All//gi|115463395|ref|NP_001055297.1|//1.00E-146//Os05g0357600 [Oryza sativa Japonica Group] >gi|113578848|dbj|BAF17211.1|Os05g0357600 [Oryza sativa Japonica Group]	Unigene798_All//1.00E-124//AT1G72660| developmentally regulated GTP-binding protein, putative	Unigene798_All//0.00E+00//TC141020				nr -
Unigene7980_All	586	0.00	0.00	0.00	2.04	0.71	0.85	0.43	3.78	3.06	null	null		null	null		-1.53E+00	1.11E-02		-1.27E+00	4.58E-02		3.13E+00	8.76E-10	Up	2.82E+00	1.60E-07	Up								ESTscan +
Unigene79809_All	380	0.00	0.00	8.55	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.31E+01	5.81E-18	Up	null	null		null	null		null	null		null	null		Unigene79809_All//gi|15217879|ref|NP_174150.1|//2.00E-24//AGP31 (arabinogalactan-protein 31) [Arabidopsis thaliana] >gi|9795608|gb|AAF98426.1|AC021044_5 Unknown protein [Arabidopsis thaliana] >gi|119360033|gb|ABL66745.1|At1g28290 [Arabidopsis thaliana]				ko00500|Starch and sucrose metabolism//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00040|Pentose and glucuronate interconversions//ko00565|Ether lipid metabolism	GO:0009719//GO:0016787	nr +
Unigene79812_All	395	0.13	0.13	3.10	0.00	0.00	0.11	0.00	0.00	0.00	-4.65E-02	9.82E-01		4.55E+00	1.02E-05	Up	null	null		6.84E+00	6.84E-01		null	null		null	null		Unigene79812_All//gi|159488628|ref|XP_001702307.1|//8.00E-25//allophanate hydrolase [Chlamydomonas reinhardtii] >gi|158271212|gb|EDO97037.1|allophanate hydrolase [Chlamydomonas reinhardtii]	Unigene79812_All//3.00E-10//AT1G08980| AMI1 (AMIDASE 1); amidase/ hydrolase, acting on carbon-nitrogen (but not peptide) bonds / indoleacetamide hydrolase			ko00970|Aminoacyl-tRNA biosynthesis	GO:0009683//GO:0016811//GO:0044424	nr +
Unigene79819_All	675	1.63	0.53	0.00	1.77	1.38	1.47	15.41	9.35	6.20	-1.63E+00	1.81E-02		-1.07E+01	4.93E-06	Down	-3.63E-01	5.70E-01		-2.67E-01	6.88E-01		-7.21E-01	4.99E-06		-1.31E+00	2.23E-15	Down	Unigene79819_All//gi|224117452|ref|XP_002331716.1|//7.00E-93//Sec61 transport protein [Populus trichocarpa] >gi|222874322|gb|EEF11453.1| Sec61 transport protein [Populus trichocarpa]	Unigene79819_All//6.00E-92//AT1G29310| P-P-bond-hydrolysis-driven protein transmembrane transporter	Unigene79819_All//0.00E+00//TC157445		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome//ko03060|Protein export	GO:0006810//GO:0008320//GO:0016020//GO:0043231	nr +
Unigene7982_All	485	0.97	1.25	2.53	13.35	13.49	13.41	13.51	6.46	3.20	3.69E-01	6.60E-01		1.38E+00	3.74E-02		1.48E-02	9.62E-01		6.10E-03	9.80E-01		-1.06E+00	3.74E-07	Down	-2.08E+00	2.04E-18	Down			Unigene7982_All//5.00E-32//TC175613				
Unigene79828_All	400	1.05	4.18	2.93	2.99	4.48	4.40	0.32	1.88	2.29	2.00E+00	4.38E-04	Up	1.48E+00	3.03E-02		5.83E-01	2.59E-01		5.59E-01	2.88E-01		2.57E+00	3.32E-03		2.85E+00	3.18E-04	Up			Unigene79828_All//1.00E-161//TC173915				ESTscan +
Unigene7983_All	1622	0.00	0.00	0.00	0.80	0.32	0.00	33.47	18.84	2.60	null	null		null	null		-1.33E+00	1.98E-02		-9.64E+00	4.24E-08	Down	-8.29E-01	1.80E-35		-3.68E+00	2.57E-271	Down	Unigene7983_All//gi|186514561|ref|NP_194618.3|//2.00E-96//protein binding / ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana] >gi|68565150|sp|Q5XF85.2|ATL4J_ARATH RecName: Full=RING-H2 finger protein ATL4J; Flags: Precursor >gi|66869954|gb|AAY57611.1| RING finger family protein [Arabidopsis thaliana]	Unigene7983_All//8.00E-79//AT4G28890| protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene7983_All//0.00E+00//gi|109876623|gb|DW505597.1|DW505597			GO:0019787//GO:0032446//GO:0046914	nr +
Unigene79831_All	394	0.00	0.00	1.76	0.00	0.70	0.00	0.00	0.00	0.00	null	null		1.08E+01	6.12E-04	Up	9.45E+00	7.00E-02		null	null		null	null		null	null		Unigene79831_All//gi|18405433|ref|NP_565936.1|//6.00E-12//KT2 (POTASSIUM TRANSPORTER 2); potassium ion transmembrane transporter [Arabidopsis thaliana] >gi|145330713|ref|NP_001078032.1|KT2 (POTASSIUM TRANSPORTER 2); potassium ion transmembrane transporter [Arabidopsis thaliana] >gi|38502835|sp|Q22881.2|POT2_ARATH RecName: Full=Potassium transporter 2; Short=AtPOT2; Short=AtKUP2; Short=AtKT2	Unigene79831_All//2.00E-08//AT2G40540| KT2 (POTASSIUM TRANSPORTER 2); potassium ion transmembrane transporter				GO:0016020	nr +
Unigene79832_All	393	0.00	1.55	1.76	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	1.16E-03		1.08E+01	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene79832_All//sp|Q5ISS9|RTN1_PANTR//2.00E-10//Reticulon-1 OS=Pan troglodytes GN=RTN1 PE=2 SV=1						swissprot -
Unigene79834_All	408	0.00	0.12	1.96	0.00	0.25	0.22	0.00	0.00	0.00	6.96E+00	6.09E-01		1.09E+01	1.71E-04	Up	7.98E+00	4.52E-01		7.79E+00	4.70E-01		null	null		null	null									ESTscan +
Unigene79836_All	406	0.90	1.62	0.66	4.42	2.88	1.33	0.31	0.00	0.00	8.47E-01	3.48E-01		-4.60E-01	6.97E-01		-6.15E-01	2.02E-01		-1.73E+00	7.60E-04	Down	-8.29E+00	2.34E-01		-8.29E+00	1.98E-01				Unigene79836_All//5.00E-16//TC160880				
Unigene79837_All	628	1.50	3.07	1.36	2.93	2.30	1.94	4.78	2.00	1.52	1.03E+00	2.87E-02		-1.45E-01	8.31E-01		-3.50E-01	4.93E-01		-5.96E-01	2.34E-01		-1.26E+00	1.33E-04	Down	-1.65E+00	9.80E-07	Down	Unigene79837_All//gi|224107859|ref|XP_002314629.1|//8.00E-63//SIN3 component, histone deacetylase complex [Populus trichocarpa] >gi|222863669|gb|EEF00800.1| SIN3 component, histone deacetylase complex [Populus trichocarpa]	Unigene79837_All//1.00E-53//AT1G70060| SNL4 (SIN3-LIKE 4)	Unigene79837_All//6.00E-168//TC163104			GO:0006351//GO:0043231	nr +
Unigene79843_All	406	0.00	1.50	1.71	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	1.16E-03		1.07E+01	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene79843_All//sp|P06703|S10A6_HUMAN//3.00E-33//Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1						swissprot -

Unigene7985_All	800	0.46	0.06	0.00	3.42	0.34	1.13	5.55	2.04	5.28	-2.85E+00	7.79E-02		-8.84E+00	2.77E-02		-3.31E+00	6.96E-13	Down	-1.60E+00	4.92E-05	Down	-1.45E+00	9.68E-08	Down	-7.22E-02	7.84E-01		Unigene7985_All//gi|75249799|sp|Q94AW5.1|ERF03_ARATH//2.00E-67//RecName: Full=Ethylene-responsive transcription factor ERF003 >gi|15010716|gb|AAK74017.1|AT5g25190/F21J6_103 [Arabidopsis thaliana] >gi|16974345|gb|AAL31157.1|AT5g25190/F21J6_103 [Arabidopsis thaliana]	Unigene7985_All//2.00E-47//AT5G25190| ethylene-responsive element-binding protein, putative	Unigene7985_All//1.00E-98//TC146159	AP2-EREBP		GO:0000160//GO:0001071//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene79851_All	413	0.00	6.63	5.42	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	1.44E-15	Up	1.24E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene79851_All//gi|6094086|sp|O65353.1|RL5_HELAN//2.00E-45//RecName: Full=60S ribosomal protein L5 >gi|3153904|gb|AAC17448.1| RPL5A-related protein [Helianthus annnuus]	Unigene79851_All//2.00E-35//AT5G39740| 60S ribosomal protein L5 (RPL5B)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0019843//GO:0030529	nr -
Unigene79852_All	632	0.75	0.88	0.17	2.44	1.14	0.64	1.34	0.46	0.38	2.43E-01	7.77E-01		-2.14E+00	1.03E-01		-1.09E+00	3.11E-02		-1.93E+00	7.77E-04	Down	-1.53E+00	3.21E-02		-1.82E+00	9.93E-03		Unigene79852_All//gi|297727881|ref|NP_001176304.1|//1.00E-16//Os11g0107450 [Oryza sativa Japonica Group] >gi|255679696|dbj|BAH95032.1|Os11g0107450 [Oryza sativa Japonica Group]	Unigene79852_All//6.00E-11//AT3G62450| unknown protein	Unigene79852_All//2.00E-167//TC148347			GO:0031410	nr -
Unigene79855_All	418	0.00	0.00	3.18	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene79855_All//gi|171452362|dbj|BAG15872.1|//3.00E-57//transcription factor [Bruguiera gymnorhiza]	Unigene79855_All//3.00E-51//AT2G41900| zinc finger (CCCH-type) family protein	Unigene79855_All//7.00E-31//TC137552	C3H		GO:0046914	nr +
Unigene7986_All	1665	0.35	0.43	0.16	0.51	0.56	0.92	5.33	14.38	17.11	3.01E-01	6.93E-01		-1.11E+00	2.78E-01		1.35E-01	8.71E-01		8.59E-01	1.21E-01		1.43E+00	1.02E-37	Up	1.68E+00	1.40E-57	Up	Unigene7986_All//gi|224074401|ref|XP_002304364.1|//1.00E-158//4-coumarate-coa ligase [Populus trichocarpa] >gi|222841796|gb|EEE79343.1| 4-coumarate-coa ligase [Populus trichocarpa]	Unigene7986_All//9.00E-126//AT4G19010| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene7986_All//0.00E+00//BQ402740		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene79861_All	411	0.00	12.94	7.13	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	2.43E-30	Up	1.28E+01	3.51E-16	Up	null	null		null	null		null	null		null	null									
Unigene7987_All	740	0.00	0.00	0.00	0.13	0.00	0.12	0.63	2.71	1.99	null	null		null	null		-7.07E+00	3.09E-01		-1.41E-01	9.47E-01		2.11E+00	4.88E-06	Up	1.66E+00	1.03E-03		Unigene7987_All//gi|224074401|ref|XP_002304364.1|//1.00E-106//4-coumarate-coa ligase [Populus trichocarpa] >gi|222841796|gb|EEE79343.1| 4-coumarate-coa ligase [Populus trichocarpa]	Unigene7987_All//2.00E-90//AT4G19010| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein	Unigene7987_All//0.00E+00//BQ402740		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0008152//GO:0016491//GO:0031410	nr -
Unigene79874_All	762	0.00	1.86	1.61	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	4.05E-08	Up	1.07E+01	9.09E-07	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene79875_All	746	0.00	1.22	3.14	0.00	0.05	0.06	0.00	0.00	0.00	1.03E+01	2.60E-05	Up	1.16E+01	6.40E-13	Up	5.53E+00	8.15E-01		5.92E+00	6.84E-01		null	null		null	null		Unigene79875_All//sp|P67809|YBOX1_HUMAN//3.00E-108//Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3							swissprot -
Unigene79876_All	426	0.00	0.00	2.38	0.00	0.24	0.00	0.00	0.00	0.00	null	null		1.12E+01	1.27E-05	Up	7.92E+00	4.52E-01		null	null		null	null		null	null									ESTscan +
Unigene79877_All	665	0.00	3.12	2.08	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	7.93E-12	Up	1.10E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene79877_All//gi|226457635|gb|EEH54934.1|//3.00E-10//JmJN/JmJC protein [Micromonas pusilla CCMP1545]					GO:0005488	nr +
Unigene79880_All	419	1.87	1.93	3.30	2.97	3.86	3.45	2.62	1.20	6.56	4.68E-02	9.69E-01		8.19E-01	1.67E-01		3.78E-01	5.26E-01		2.15E-01	7.04E-01		-1.13E+00	5.52E-02		1.32E+00	1.09E-04	Up	Unigene79880_All//gi|297852502|ref|XP_002894132.1|//3.00E-33//delta-adaptin [Arabidopsis lyrata subsp. lyrata] >gi|297339974|gb|EFH70391.1|delta-adaptin [Arabidopsis lyrata subsp. lyrata]	Unigene79880_All//8.00E-34//AT1G48760| delta-ADR (delta-adaptin); binding / clathrin binding / protein binding / protein transporter				GO:0005515//GO:0015031//GO:0022892//GO:0043231//GO:0043234	nr -
Unigene79884_All	433	0.00	0.00	4.43	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.21E+01	1.47E-10	Up	null	null		null	null		null	null		null	null		Unigene79884_All//gi|547733|sp|Q03199.1|PI1B_TOBAC//4.00E-31//RecName: Full=Proteinase inhibitor I-B; Short=PI-IB; AltName: Full=Inhibitor of microbial serine proteinases major isoform; Flags: Precursor >gi|19913|emb|CAA78269.1| pre-pro-proteinase inhibitor I [Nicotiana tabacum] >gi|398177|emb|CAA47461.1|inhibitor of microbial serine proteinases (major isoform) [Nicotiana tabacum]	Unigene79884_All//3.00E-13//AT2G38870| protease inhibitor, putative				GO:0004866//GO:0006950//GO:0043231	nr -
Unigene79888_All	440	0.12	0.23	3.51	0.11	0.08	0.21	0.00	0.00	0.00	9.54E-01	7.24E-01		4.88E+00	2.34E-07	Up	-5.32E-01	8.19E-01		8.59E-01	7.91E-01		null	null		null	null		Unigene79888_All//gi|226532142|ref|NP_001147240.1|//2.00E-17//dihydroneopterin aldolase [Zea mays] >gi|195607706|gb|ACG25683.1|dihydroneopterin aldolase [Zea mays] >gi|195608960|gb|ACG26310.1|dihydroneopterin aldolase [Zea mays]	Unigene79888_All//3.00E-13//AT5G62980| dihydroneopterin aldolase, putative			ko00790|Folate biosynthesis	GO:0043231	nr -
Unigene79890_All	395	0.13	0.77	3.37	0.13	0.00	0.23	0.00	0.00	0.00	2.54E+00	1.51E-01		4.67E+00	2.95E-06	Up	-6.98E+00	5.44E-01		8.59E-01	7.91E-01		null	null		null	null									ESTscan +
Unigene79896_All	418	0.00	3.76	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	5.68E-09	Up	1.06E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene79896_All//gi|157093371|gb|ABV22340.1|//4.00E-09//calponin domain-containing protein [Noctiluca scintillans]						nr -
Unigene79897_All	402	0.26	0.50	3.97	0.00	0.09	0.34	0.00	0.00	0.00	9.54E-01	6.20E-01		3.93E+00	9.51E-07	Up	6.42E+00	8.15E-01		8.40E+00	3.09E-01		null	null		null	null		Unigene79897_All//sp|P55635|Y4RB_RHISN//3.00E-08//Putative integrase/recombinase y4rB OS=Rhizobium sp. (strain NGR234) GN=NGR_a01850 PE=3 SV=1						swissprot -
Unigene79898_All	499	0.00	12.90	6.30	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	9.43E-37	Up	1.26E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene79898_All//gi|112950081|gb|AB126643.1|//8.00E-41//aspartic proteinase [Cucumis sativus]	Unigene79898_All//2.00E-30//AT1G11910| aspartyl protease family protein				GO:0008233//GO:0044238	nr +
Unigene79902_All	1012	0.00	0.15	0.79	0.00	0.00	0.00	0.00	0.00	0.00	7.23E+00	2.32E-01		9.62E+00	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene79902_All//gi|71000469|dbj|BAE07181.1|//2.00E-78//methionine synthase [Beta vulgaris]	Unigene79902_All//6.00E-78//AT5G20980| ATMS3 (methionine synthase 3); 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase			ko00270|Cysteine and methionine metabolism	GO:0008172//GO:0008652//GO:0009536	nr -
Unigene79904_All	446	0.00	0.00	1.67	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.07E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene79904_All//gi|226497208|ref|NP_001150045.1|//1.00E-61//calmodulin binding protein [Zea mays] >gi|195636296|gb|ACG37616.1|calmodulin binding protein [Zea mays]	Unigene79904_All//1.00E-47//AT2G18750| calmodulin-binding protein	Unigene79904_All//3.00E-27//gi|78349859|gb|DT570133.1|DT570133		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr +
Unigene79907_All	453	0.23	0.00	2.70	0.00	0.53	0.30	0.00	0.00	0.00	-7.85E+00	3.66E-01		3.55E+00	6.10E-05	Up	9.06E+00	1.04E-01		8.22E+00	3.09E-01		null	null		null	null		Unigene79907_All//COG5458//3.00E-18//Uncharacterized conserved protein						cog +
Unigene79908_All	440	7.37	4.15	5.93	9.40	5.87	9.24	4.80	3.42	0.81	-8.31E-01	1.57E-02		-3.14E-01	4.00E-01		-6.79E-01	1.69E-02		-2.46E-02	9.53E-01		-4.91E-01	2.34E-01		-2.56E+00	4.26E-08	Down	Unigene79908_All//gi|225459685|ref|XP_002285888.1|//8.00E-52//PREDICTED: similar to BTB/POZ domain-containing protein [Vitis vinifera]	Unigene79908_All//5.00E-48//AT4G08455| BTB/POZ domain-containing protein	Unigene79908_All//0.00E+00//gi|109826126|gb|DW224847.1|DW224847			GO:0005488	nr +
Unigene7991_All	316	2.98	7.86	1.52	4.57	3.38	2.57	1.07	0.13	0.00	1.40E+00	8.73E-04	Up	-9.75E-01	2.00E-01		-4.37E-01	4.44E-01		-8.30E-01	1.41E-01		-3.02E+00	5.30E-02		-1.01E+01	8.13E-03		Unigene7991_All//gi|224551850|gb|ACN54323.1|//8.00E-51//NADPH:cytochrome P450 reductase [Gossypium hirsutum]	Unigene7991_All//2.00E-45//AT4G24520| ATR1 (ARABIDOPSIS P450 REDUCTASE 1); NADPH-hemoprotein reductase	Unigene7991_All//2.00E-178//gi|164243789|gb|ES799151.1|ES799151			GO:0000166//GO:0008152//GO:0016653//GO:0031090//GO:0043231//GO:0046914	nr +
Unigene79913_All	945	0.00	0.11	11.10	0.00	0.00	0.00	0.00	0.00	0.00	6.74E+00	3.80E-01		1.34E+01	6.67E-59	Up	null	null		null	null		null	null		null	null		Unigene79913_All//gi|115481540|ref|NP_001064363.1|//2.00E-10//Os10g0330000 [Oryza sativa Japonica Group] >gi|22655738|gb|AAN04155.1|Unknown protein [Oryza sativa Japonica Group] >gi|31431205|gb|AAP53020.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113638972|dbj|BAF26277.1|Os10g0330000 [Oryza sativa Japonica Group]	Unigene79913_All//3.00E-05//AT1G13930| Involved in response to salt stress. Knockout mutants are hypersensitive to salt stress.				GO:0006970//GO:0009526//GO:0009532//GO:0010038//GO:0016020	nr +
Unigene79914_All	449	0.12	0.45	2.73	0.00	0.00	0.10	0.00	0.00	0.00	1.95E+00	3.74E-01		4.55E+00	1.02E-05	Up	null	null		6.65E+00	6.84E-01		null	null		null	null									ESTscan +
Unigene7992_All	400	0.00	0.25	0.00	0.87	0.09	14.34	7.19	8.57	31.67	7.98E+00	3.80E-01		null	null		-3.34E+00	4.06E-02		4.04E+00	6.04E-26	Up	2.54E-01	4.33E-01		2.14E+00	1.10E-35	Up							
Unigene79920_All	534	0.00	0.47	1.40	0.00	0.00	0.00	0.00	0.00	0.00	8.89E+00	7.76E-02		1.04E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene79920_All//sp|P22736|NR4A1_HUMAN//3.00E-76//Nuclear receptor subfamily 4 group A member 1 OS=Homo sapiens GN=NR4A1 PE=1 SV=1						swissprot +
Unigene79922_All	461	0.00	1.32	3.58	0.00	0.00	0.00	0.00	0.00	0.00	1.04E+01	1.16E-03		1.18E+01	4.29E-09	Up	null	null		null	null		null	null		null	null		Unigene79922_All//gi|282848236|gb|ADR02899.1|//2.00E-27//gamma-thionin PPT precursor defensin 1-like protein [Jatropha curcas]	Unigene79922_All//1.00E-24//AT2G02100| LCR69 (LOW-MOLECULAR-WEIGHT CYSTEINE-RICH 69); peptidase inhibitor				GO:0001906//GO:0006952//GO:0016787	nr +
Unigene79925_All	466	2.25	0.65	0.80	6.52	4.14	3.30	3.54	2.24	1.20	-1.78E+00	1.36E-02		-1.49E+00	4.42E-02		-6.56E-01	5.68E-02		-9.85E-01	5.66E-03		-6.58E-01	1.54E-01		-1.56E+00	7.74E-04	Down	Unigene79925_All//gi|15238981|ref|NP_196656.1|//7.00E-52//sks3 (SKU5 Similar 3); copper ion binding / oxidoreductase [Arabidopsis thaliana]	Unigene79925_All//4.00E-53//AT5G48450| sks3 (SKU5 Similar 3); copper ion binding / oxidoreductase	Unigene79925_All//0.00E+00//gi|164290968|gb|ES826109.1|ES826109		ko00053|Ascorbate and aldarate metabolism	GO:0008152//GO:0016020//GO:0016682//GO:0043231//GO:0046914	nr +
Unigene79927_All	444	0.00	0.46	1.80	0.22	0.31	0.61	0.00	0.00	0.18	8.83E+00	1.35E-01		1.08E+01	1.71E-04	Up	4.67E-01	8.75E-01		1.44E+00	4.09E-01		null	null		7.49E+00	4.01E-01		Unigene79927_All//gi|17064459|gb|AAL34531.1|AF439861_1//3.00E-39//sucrose-phosphate synthase [Ipomoea batatas]	Unigene79927_All//4.00E-34//AT5G11110| ATSPS2F (SUCROSE PHOSPHATE SYNTHASE 2F); sucrose-phosphate synthase	Unigene79927_All//3.00E-110//TC141369		ko00500|Starch and sucrose metabolism	GO:0005984//GO:0035251	nr +
Unigene7993_All	394	8.10	2.83	7.97	6.70	6.90	7.22	0.75	0.42	0.81	-1.52E+00	3.72E-05	Down	-2.27E-02	9.70E-01		4.32E-02	9.35E-01		1.08E-01	7.91E-01		-8.24E-01	5.40E-01		1.07E-01	9.45E-01		Unigene7993_All//gi|8778702|gb|AAF79710.1|AC020889_18//2.00E-14//T1N15.20 [Arabidopsis thaliana]						nr +
Unigene79931_All	469	0.00	0.43	3.29	0.42	0.66	0.00	0.00	0.00	0.00	8.76E+00	1.35E-01		1.17E+01	1.65E-08	Up	6.37E-01	6.94E-01		-8.73E+00	1.32E-01		null	null		null	null		Unigene79931_All//sp|P71539|ACDC_MYCTU//2.00E-21//Acyl-CoA dehydrogenase fadE12 OS=Mycobacterium tuberculosis GN=fadE12 PE=1 SV=2						swissprot +
Unigene79955_All	448	0.00	25.90	8.08	0.00	0.08	0.00	0.00	0.00	0.00	1.47E+01	1.52E-66	Up	1.30E+01	4.73E-20	Up	6.26E+00	8.15E-01		null	null		null	null		null	null									ESTscan +
Unigene79959_All	481	0.00	0.21	5.76	0.00	0.00	0.00	0.00	0.00	0.00	7.72E+00	3.80E-01		1.25E+01	2.74E-15	Up	null	null		null	null		null	null		null	null		Unigene79959_All//gi|241740196|gb|ACS68205.1|//4.00E-69//ubiquitin 10.2 [Brassica napus]	Unigene79959_All//2.00E-70//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene79959_All//2.00E-46//TC136513			GO:0044424	nr +

Unigene7996_All	636	0.00	0.00	0.00	0.47	0.54	1.14	30.51	18.20	258.89	null	null		null	null		2.04E-01	9.01E-01		1.27E+00	1.56E-01		-7.45E-01	4.00E-11		3.08E+00	0.00E+00	Up		Unigene7996_All//4.00E-05//AT4G27500| PP11 (PROTON PUMP INTERACTOR 1); protein binding	Unigene7996_All//0.00E+00//gi|73861604|gb|DT464343.1|DT464343				ESTscan -
Unigene79967_All	528	0.10	0.10	0.00	0.28	0.20	0.17	2.48	0.48	0.38	-4.59E-02	9.82E-01		-6.63E+00	6.15E-01		-5.32E-01	7.83E-01		-7.26E-01	7.13E-01		-2.39E+00	9.39E-05	Down	-2.72E+00	1.32E-05	Down	Unigene79967_All//gi|18400020|ref|NP_565539.1|//5.00E-43//NIC1 (NICOTINAMIDASE 1); catalytic/ nicotinamidase [Arabidopsis thaliana] >gi|20197887|gb|AAM15300.1| expressed protein [Arabidopsis thaliana]	Unigene79967_All//3.00E-44//AT3G22570| NIC1 (NICOTINAMIDASE 1); catalytic/ nicotinamidase	Unigene79967_All//0.00E+00//TC155746			GO:0009725//GO:0016811//GO:0019363	nr -
Unigene7997_All	309	1.52	1.15	2.76	0.00	3.90	0.58	1.23	1.76	2.06	-4.09E-01	6.68E-01		8.56E-01	2.80E-01		1.19E+01	1.95E-07	Up	9.19E+00	1.93E-01		5.14E-01	5.89E-01		7.44E-01	3.52E-01			Unigene7997_All//4.00E-05//AT5G17240| SDG40 (SET DOMAIN GROUP 40)	Unigene7997_All//4.00E-16//DW504270				
Unigene79970_All	575	0.00	4.05	0.83	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.90E-13	Up	9.70E+00	7.42E-03		null	null		null	null		null	null		null	null		Unigene79970_All//gi|115460488|ref|NP_001053844.1|//4.00E-06//Os04g0612300 [Oryza sativa Japonica Group] >gi|38568018|emb|CAE05203.3| OSJNBa0070C17.10 [Oryza sativa (japonica cultivar-group)] >gi|113565415|dbj|BAF15758.1| Os04g0612300 [Oryza sativa Japonica Group]						nr +
Unigene79971_All	554	0.94	0.55	4.23	0.18	0.25	0.16	0.00	0.00	0.00	-7.83E-01	4.22E-01		2.16E+00	1.20E-05	Up	4.67E-01	8.75E-01		-1.42E-01	9.47E-01		null	null		null	null										ESTscan -
Unigene79977_All	580	0.00	3.67	1.74	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	4.10E-12	Up	1.08E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene79977_All//gi|195648550|gb|ACG43743.1|//4.00E-12//3-hydroxybutyryl-CoA dehydrogenase [Zea mays]				ko00650|Butanoate metabolism	GO:0003824//GO:0044464	nr -
Unigene79978_All	588	0.18	0.52	1.27	1.02	0.47	0.38	3.16	0.64	0.81	1.54E+00	3.22E-01		2.83E+00	8.51E-03		-1.12E+00	2.26E-01		-1.40E+00	1.58E-01		-2.31E+00	3.11E-06	Down	-1.96E+00	1.89E-05	Down	Unigene79978_All//gi|115456721|ref|NP_001051961.1|//5.00E-71//Os03g0858400 [Oryza sativa Japonica Group] >gi|113550432|dbj|BAF13875.1| Os03g0858400 [Oryza sativa Japonica Group]	Unigene79978_All//5.00E-79//AT4G00090| transducin family protein / WD-40 repeat family protein	Unigene79978_All//0.00E+00//TC134733		ko03040|Spliceosome//ko04120|Ubiquitin mediated proteolysis	GO:0031410	nr -
Unigene7998_All	438	2.27	0.93	0.61	0.00	0.00	0.00	21.04	2.39	11.92	-1.29E+00	6.74E-02		-1.90E+00	1.69E-02		null	null		null	null		-3.14E+00	4.06E-39	Down	-8.21E-01	7.78E-07				Unigene7998_All//1.00E-121//DW513197				
Unigene79982_All	591	0.00	0.00	0.09	0.00	0.06	0.08	1.79	0.07	0.20	null	null		6.49E+00	6.24E-01		5.87E+00	8.15E-01		6.26E+00	6.84E-01		-4.66E+00	1.94E-06	Down	-3.14E+00	2.96E-05	Down	Unigene79982_All//gi|14091473|gb|AK53760.1|AF367866_1//3.00E-59//potassium transporter HAK3p [Mesembryanthemum crystallinum]	Unigene79982_All//2.00E-47//AT1G70300| KUP6; potassium ion transmembrane transporter	Unigene79982_All//1.00E-63//TC171906			GO:0016020//GO:0030001//GO:0046873	nr +
Unigene79984_All	585	0.00	2.43	2.09	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	4.04E-08	Up	1.10E+01	9.09E-07	Up	null	null		null	null		null	null		null	null		Unigene79984_All//gi|1170370|sp|P41753.1|HSP70_ACHKL//3.00E-34//RecName: Full=Heat shock 70 kDa protein >gi|407302|gb|AAA17562.1| heat shock protein 70 [Achlya klebsiana]	Unigene79984_All//2.00E-20//AT1G16030| Hsp70b (heat shock protein 70B); ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0000166//GO:0016787	nr +
Unigene79985_All	635	5.85	4.87	6.29	8.08	11.93	10.60	4.39	1.25	1.88	-2.65E-01	4.14E-01		1.05E-01	7.40E-01		5.62E-01	6.03E-03		3.91E-01	9.98E-02		-1.81E+00	8.12E-07	Down	-1.22E+00	2.37E-04	Down	Unigene79985_All//gi|20138107|sp|Q9M5Q1.1|FUT1_PEA//3.00E-48//RecName: Full=Galactoside 2-alpha-L-fucosyltransferase; AltName: Full=Xyloglucan alpha-(1,2)-fucosyltransferase; AltName: Full=PsFT1 >gi|7453579|gb|AAF62896.1|AF223643_1 xyloglucan fucosyltransferase [Pisum sativum]	Unigene79985_All//2.00E-38//AT2G03220| FT1 (FUCOSYLTRANSFERASE 1); fucosyltransferase/ transferase, transferring glycosyl groups	Unigene79985_All//0.00E+00//TC138301			GO:0000139//GO:0031127//GO:0031224//GO:0045229//GO:0070882	nr +
Unigene79988_All	610	0.00	0.58	1.31	0.00	0.00	0.00	0.00	0.00	0.00	9.18E+00	2.43E-02		1.04E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene79988_All//sp|Q1HPU0|TPM1_BOMMO//3.00E-49//Tropomyosin-1 OS=Bombyx mori PE=1 SV=1						swissprot -
Unigene79990_All	1136	0.00	0.09	7.55	0.00	0.00	0.00	0.00	0.00	0.00	6.48E+00	3.80E-01		1.29E+01	5.10E-48	Up	null	null		null	null		null	null		null	null		Unigene79990_All//gi|8096269|dbj|BAB95789.1|//1.00E-60//XED [Nicotiana tabacum]				ko03040|Spliceosome		nr +
Unigene79992_All	626	0.17	0.49	0.17	0.16	0.28	0.00	0.41	0.40	3.44	1.54E+00	3.22E-01		2.48E-02	9.97E-01		7.89E-01	7.69E-01		-7.31E+00	3.93E-01		-1.65E-02	1.02E+00		3.08E+00	1.25E-09	Up	Unigene79992_All//gi|259121427|gb|ACV92033.1|//1.00E-24//WRKY transcription factor 31 [(Populus tomentosa x P. bolleana) x P. tomentosa]		Unigene79992_All//0.00E+00//TC140811			GO:0003677//GO:0010468	nr -
Unigene79995_All	1154	0.00	0.97	11.95	0.00	0.00	0.00	0.00	0.00	0.00	9.92E+00	1.99E-06	Up	1.35E+01	1.12E-77	Up	null	null		null	null		null	null		null	null		Unigene79995_All//gi|75333650|sp|Q9CA13.1|CAD01_ARATH//1.00E-148//RecName: Full=Probable cinnamyl alcohol dehydrogenase 1; Short=AtCAD1 >gi|27311669|gb|AA000800.1| Unknown protein [Arabidopsis thaliana] >gi|317118416|gb|AAP68279.1| At1g72680 [Arabidopsis thaliana]	Unigene79995_All//2.00E-132//AT1G72680| cinnamyl-alcohol dehydrogenase, putative			ko00940|Phenylpropanoid biosynthesis		nr -
Unigene8_All	2295	12.47	2.67	6.10	6.71	6.81	4.62	6.67	0.98	2.24	-2.22E+00	3.03E-67	Down	-1.03E+00	2.28E-21	Down	2.24E-02	9.03E-01		-5.36E-01	1.12E-04		-2.76E+00	1.07E-56	Down	-1.57E+00	6.97E-29	Down	Unigene8_All//gi|15186760|gb|AAK91129.1|//0.00E+00//KRP120-2 [Daucus carota]	Unigene8_All//0.00E+00//AT3G45850| kinesin motor protein-related	Unigene8_All//0.00E+00//TC156194				nr -
Unigene8000_All	684	1.45	0.15	0.31	2.99	1.71	3.50	3.34	0.43	1.46	-3.29E+00	3.81E-04	Down	-2.22E+00	7.48E-03		-8.03E-01	6.37E-02		2.29E-01	6.46E-01		-2.96E+00	1.24E-09	Down	-1.20E+00	1.27E-03		Unigene8000_All//gi|30685792|ref|NP_180922.2|//3.00E-36//zinc finger (DHHC type) family protein [Arabidopsis thaliana] >gi|75254668|sp|Q0WD03.1|ZDHC3_ARATH RecName: Full=Probable S-acyltransferase At2g33640; AltName: Full=Probable palmitoyltransferase At2g33640; AltName: Full=Zinc finger DHHC domain-containing protein At2g33640	Unigene8000_All//2.00E-37//AT2G33640| zinc finger (DHHC type) family protein	Unigene8000_All//0.00E+00//gi|164240077|gb|ES852407.1|ES852407			GO:0016020//GO:0031410//GO:0046914	nr -
Unigene80001_All	1810	0.00	3.22	2.44	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.96E-33	Up	1.13E+01	1.55E-24	Up	null	null		null	null		null	null		null	null		Unigene80001_All//gi|301101339|ref|XP_002899758.1|//4.00E-82//creatine kinase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262102760|gb|EEY60812.1| creatine kinase, mitochondrial precursor [Phytophthora infestans T30-4]				ko00330|Arginine and proline metabolism	GO:0005488//GO:0005737//GO:0006599//GO:0007417//GO:0016020//GO:0016301//GO:0030320	nr -
Unigene80002_All	786	0.67	0.00	0.54	1.27	0.18	0.34	0.27	0.58	0.10	-9.38E+00	2.91E-03		-2.97E-01	7.49E-01		-2.85E+00	2.37E-04	Down	-1.88E+00	1.18E-02		1.12E+00	2.73E-01		-1.41E+00	3.79E-01		Unigene80002_All//gi|223452468|gb|ACM89561.1|//1.00E-107//receptor-like protein kinase precusor-like protein [Glycine max] >gi|223452268|gb|ACM89611.1| receptor-like protein kinase [Glycine max]	Unigene80002_All//1.00E-100//AT4G00340| RLK4 (RECEPTOR-LIKE PROTEIN KINASE 4); protein kinase/ sugar binding	Unigene80002_All//2.00E-162//TC169836		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0008037//GO:0030246//GO:0032559//GO:0043231	nr -
Unigene80003_All	804	0.00	0.63	7.42	0.00	0.00	0.11	0.00	0.00	0.00	9.30E+00	3.99E-03		1.29E+01	3.02E-33	Up	null	null		6.81E+00	4.70E-01		null	null		null	null		Unigene80003_All//gi|3759184|dbj|BAA33810.1|//1.00E-120//phi-1 [Nicotiana tabacum]	Unigene80003_All//7.00E-104//AT4G08950| EXO (EXORDIUM)	Unigene80003_All//2.00E-17//gi|109853442|gb|DW482421.1|DW482421				nr -
Unigene80005_All	836	0.00	6.49	2.93	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	6.34E-31	Up	1.15E+01	1.64E-13	Up	null	null		null	null		null	null		null	null		Unigene80005_All//gi|18087805|ref|NP_032529.2|//1.00E-115//40S ribosomal protein S2 [Mus musculus] >gi|78126159|ref|NP_114026.3| 40S ribosomal protein S2 [Rattus norvegicus] >gi|133914|sp|P27952.1|RS2_RAT RecName: Full=40S ribosomal protein S2 >gi|46397787|sp|P25444.3|RS2_MOUSE RecName: Full=40S ribosomal protein S2; AltName: Full=40S ribosomal protein S4; AltName: Full=Protein LIRes3 >gi|10179940|gb|AAG13953.1|AF283559_1 ribosomal protein S2 [Mus musculus] >gi|57718|emb|CAA40679.1| ribosomal protein S2 [Rattus rattus] >gi|12805427|gb|AAH02186.1| Ribosomal protein S2 [Mus musculus] >gi|56971737|gb|AAH87956.1| Ribosomal protein S2 [Mus musculus] >gi|61402217|gb|AAH91730.1| Ribosomal protein S2 [Mus musculus]	Unigene80005_All//5.00E-88//AT3G57490| 40S ribosomal protein S2 (RPS2D)	Unigene80005_All//3.00E-53//DW519163		ko03010|Ribosome		nr -
Unigene80006_All	964	0.00	0.21	3.81	0.00	0.00	0.00	0.00	0.00	0.00	7.72E+00	1.35E-01		1.19E+01	2.38E-20	Up	null	null		null	null		null	null		null	null		Unigene80006_All//gi|226531952|ref|NP_001149536.1|//2.00E-54//src2-like protein [Zea mays] >gi|195627870|gb|ACG35765.1| src2-like protein [Zea mays]	Unigene80006_All//1.00E-35//AT1G09070| SRC2 (SOYBEAN GENE REGULATED BY COLD-2); protein binding			ko04626|Plant-pathogen interaction//ko03040|Spliceosome		nr +
Unigene80008_All	959	3.93	1.53	2.61	2.03	1.72	3.30	0.26	0.17	0.29	-1.36E+00	3.67E-05	Down	-5.90E-01	7.72E-02		-2.33E-01	6.16E-01		7.03E-01	4.76E-02		-6.02E-01	6.47E-01		1.37E-01	9.28E-01		Unigene80008_All//gi|297830494|ref|XP_002883129.1|//2.00E-97//EMB1865 [Arabidopsis lyrata subsp. lyrata] >gi|297328969|gb|EFH59388.1| EMB1865 [Arabidopsis lyrata subsp. lyrata]	Unigene80008_All//2.00E-68//AT3G18390| EMB1865 (embryo defective 1865); RNA binding	Unigene80008_All//0.00E+00//CO096538			GO:0003006//GO:0005506//GO:0009536	nr +
Unigene80009_All	1002	0.00	0.51	8.18	0.00	0.00	0.00	0.00	0.00	0.00	8.98E+00	3.99E-03		1.30E+01	6.60E-46	Up	null	null		null	null		null	null		null	null		Unigene80009_All//gi|3759184|dbj|BAA33810.1|//1.00E-108//phi-1 [Nicotiana tabacum]	Unigene80009_All//4.00E-105//AT4G08950| EXO (EXORDIUM)	Unigene80009_All//9.00E-57//gi|48775173|gb|CO084539.1|CO084539				nr -
Unigene8001_All	1015	0.46	0.25	0.42	3.04	1.97	1.16	1.96	1.03	1.22	-8.94E-01	3.88E-01		-1.45E-01	8.89E-01		-6.29E-01	6.69E-02		-1.40E+00	1.08E-04	Down	-9.27E-01	2.37E-02		-6.86E-01	8.11E-02		Unigene8001_All//gi|297793389|ref|XP_002864579.1|//3.00E-44//glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297310414|gb|EFH40838.1| glutaredoxin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8001_All//1.00E-37//AT5G58530| glutaredoxin family protein	Unigene8001_All//8.00E-153//gi|78330522|gb|DT550796.1|DT550796			GO:0043231	nr +

Unigene80013_All	200	0.00	0.51	3.73	0.00	0.00	0.00	0.00	0.00	0.00	8.99E+00	3.80E-01		1.19E+01	3.25E-04	Up	null	null		null	null		null		null	null		Unigene80013_All//gi|219113303|ref|XP_002186235.1|//5.00E-10//short chain acyl-coenzyme A dehydrogenase [Phaeodactylum tricornutum CCAP 1055/1] >gi|209983085|gb|ACI65705.1| short chain acyl-coenzyme A dehydrogenase [Phaeodactylum tricornutum CCAP 1055/1]	Unigene80013_All//9.00E-05//AT3G45300| IVD (ISOVALERYL-COA-DEHYDROGENASE); ATP binding / isovaleryl-CoA dehydrogenase				GO:0016627	nr -
Unigene8002_All	523	0.10	2.03	0.31	2.29	2.17	1.38	0.32	0.16	0.23	4.35E+00	3.95E-05	Up	1.61E+00	5.09E-01		-7.32E-02	8.95E-01		-7.26E-01	2.56E-01		-1.02E+00	6.13E-01		-5.01E-01	7.45E-01		Unigene8002_All//gi|195624422|gb|ACG34041.1|//2.00E-37//RCL-2 binding anthanogene-1 [Zea mays]	Unigene8002_All//1.00E-28//AT5G14360| ubiquitin family protein	Unigene8002_All//9.00E-114//TC173054			GO:0005488//GO:0012501	nr -
Unigene8005_All	511	0.00	2.38	0.42	0.20	0.54	1.50	2.40	1.96	24.40	1.12E+01	5.45E-07	Up	8.70E+00	1.38E-01		1.47E+00	4.19E-01		2.95E+00	4.39E-03		-2.90E-01	6.39E-01		3.35E+00	1.09E-56	Up	Unigene8005_All//gi|115436162|ref|NP_001042839.1|//6.00E-08//Os01g0304400 [Oryza sativa Japonica Group] >gi|113532370|dbj|BAF04753.1|Os01g0304400 [Oryza sativa Japonica Group]		Unigene8005_All//0.00E+00//DV850071				nr +
Unigene8006_All	524	22.47	29.59	22.05	20.25	22.47	15.77	48.01	33.18	16.80	3.97E-01	5.50E-03		-2.68E-02	8.91E-01		1.51E-01	4.44E-01		-3.60E-01	4.54E-02		-5.33E-01	3.53E-08		-1.51E+00	2.27E-44	Down	Unigene8006_All//gi|18087587|gb|AAL58924.1|AF462836_1//3.00E-21//AT5g47570/MXJ7_16 [Arabidopsis thaliana] >gi|20453263|gb|AAM19870.1|AT5g47570/MXJ7_16 [Arabidopsis thaliana]	Unigene8006_All//2.00E-22//AT5G47570| unknown protein	Unigene8006_All//0.00E+00//TC147969			GO:0005515//GO:0005746//GO:0016462//GO:0030964//GO:0032559//GO:0044267	nr +
Unigene8008_All	709	1.77	0.00	0.00	0.28	0.49	1.72	2.98	0.71	1.91	-1.08E+01	2.54E-07	Down	-1.08E+01	7.11E-07	Down	7.90E-01	5.95E-01		2.61E+00	3.93E-04	Up	-2.08E+00	3.13E-06	Down	-6.42E-01	9.20E-02		Unigene8008_All//gi|158536490|gb|AAW72739.1|//4.00E-68//flagellin-sensing 2-like protein [Eruca vesicaria]	Unigene8008_All//4.00E-60//AT5G46330| FLS2 (FLAGELLIN-SENSITIVE 2); ATP binding / kinase/ protein binding / protein serine/threonine kinase/ transmembrane receptor protein serine/threonine kinase			ko04626|Plant-pathogen interaction	GO:0005488//GO:0006952//GO:0009987//GO:0016020//GO:0016301//GO:0051179	nr +
Unigene8009_All	1174	0.09	0.47	0.73	0.13	0.12	0.46	47.03	28.66	293.97	2.41E+00	3.93E-02		3.03E+00	3.00E-03		-1.18E-01	9.09E-01		1.86E+00	1.02E-01		-7.15E-01	4.66E-28		2.64E+00	0.00E+00	Up	Unigene8009_All//gi|67483357|gb|AAY68034.1|//1.00E-173//3-hydroxy-methylglutaryl coenzyme A reductase [Tilia miqueliana]	Unigene8009_All//5.00E-122//AT1G76490| HMG1 (HYDROXY METHYLGLUTARYL COA REDUCTASE 1); hydroxymethylglutaryl-CoA reductase	Unigene8009_All//0.00E+00//gi|78329466|gb|DT549740.1|DT549740	ko00900|Terpenoid backbone biosynthesis			nr -
Unigene80099_All	201	121.30	93.27	76.03	106.07	123.69	122.68	103.70	82.14	44.20	-3.79E-01	6.24E-04		-6.74E-01	3.48E-09		2.22E-01	4.93E-02		2.10E-01	7.49E-02		-3.36E-01	1.99E-03		-1.23E+00	4.25E-27	Down	Unigene80099_All//gi|300793584|tpg|DAA33859.1|//2.00E-27//TPA: TPA_inf: aquaporin PIP1;5 [Gossypium hirsutum]	Unigene80099_All//3.00E-24//AT4G23400| PIP1;5 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;5); water channel	Unigene80099_All//3.00E-90//TC152372			GO:0006810//GO:0031224	nr +
Unigene80111_All	201	0.00	2.02	4.24	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.34E-02		1.20E+01	8.98E-05	Up	null	null		null	null		null	null		null	null										
Unigene80119_All	201	0.00	0.25	3.97	0.00	0.00	0.22	0.00	0.00	0.00	7.98E+00	6.09E-01		1.20E+01	1.71E-04	Up	null	null		7.81E+00	6.84E-01		null	null		null	null		Unigene80119_All//gi|493723|emb|CAA45523.1|//5.00E-30//photosystem I light-harvesting chlorophyll a/b-binding protein [Nicotiana tabacum]	Unigene80119_All//9.00E-31//AT3G54890| LHCA1; chlorophyll binding	Unigene80119_All//2.00E-35//gi|48782336|gb|CO089894.1|CO089894	ko00196|Photosynthesis - antenna proteins		GO:0006464//GO:0009521//GO:0009526//GO:0009534//GO:0009570//GO:0009639//GO:0009765//GO:0031224//GO:0043169//GO:0046906	nr -
Unigene80123_All	201	0.00	0.00	4.50	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.21E+01	4.70E-05	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene8013_All	1511	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.86	1.98	null	null		null	null		null	null		null	null		-1.25E+00	1.13E-04	Down	-4.69E-02	8.95E-01		Unigene8013_All//gi|110006646|gb|ABG37650.2|//1.00E-13//CCHC-type integrase [Populus trichocarpa]		Unigene8013_All//7.00E-151//DT466328			GO:0005488	nr -
Unigene80143_All	202	0.00	0.25	4.22	0.00	0.00	0.67	0.00	0.83	0.20	7.97E+00	6.09E-01		1.20E+01	8.98E-05	Up	null	null		9.39E+00	3.09E-01		9.69E+00	1.38E-01		7.62E+00	6.36E-01									
Unigene8015_All	632	0.91	0.16	0.42	1.50	0.71	0.36	2.41	0.66	1.39	-2.51E+00	2.93E-02		-1.11E+00	2.78E-01		-1.08E+00	1.16E-01		-2.07E+00	8.57E-03		-1.86E+00	3.50E-04	Down	-7.96E-01	8.34E-02		Unigene8015_All//gi|297606758|ref|NP_001058915.2|//1.00E-46//Os07g0154400 [Oryza sativa Japonica Group] >gi|255677527|dbj|BAF20829.2|Os07g0154400 [Oryza sativa Japonica Group]	Unigene8015_All//4.00E-26//AT4G14970| unknown protein					nr +
Unigene80163_All	202	0.00	1.51	3.43	0.49	0.34	1.79	13.61	7.86	1.18	1.06E+01	4.36E-02		1.17E+01	6.12E-04	Up	-5.33E-01	8.13E-01		1.86E+00	2.19E-01		-7.91E-01	1.95E-02		-3.52E+00	8.04E-14	Down	Unigene80163_All//gi|90658394|gb|ABD97102.1|//3.00E-06//cytochrome P450 monooxygenase CYP83G2 [Medicago truncatula]	Unigene80163_All//6.00E-06//AT3G26300| CYP71B34; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene80163_All//3.00E-71//ES805212	ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation		GO:0004497//GO:0005506//GO:0008152//GO:0016705	nr -
Unigene80172_All	202	0.00	3.26	1.32	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	6.20E-04	Up	1.04E+01	7.89E-02		null	null		null	null		null	null		null	null		Unigene80172_All//sp|Q7KRI2|LOLAL_DROME//2.00E-34//Longitudinals lacking protein-like OS=Drosophila melanogaster GN=lolal PE=1 SV=1						swissprot -
Unigene80173_All	202	15.80	14.05	14.76	18.25	18.24	24.59	35.58	17.17	23.07	-1.70E-01	6.12E-01		-9.80E-02	7.81E-01		-7.00E-04	9.87E-01		4.31E-01	1.30E-01		-1.05E+00	1.24E-07	Down	-6.25E-01	9.09E-04		Unigene80173_All//gi|124360846|gb|ABN08818.1|//2.00E-30//Mtx34-1 [Medicago truncatula]	Unigene80173_All//1.00E-29//AT1G10840| TIF2H1; translation initiation factor	Unigene80173_All//8.00E-106//TC152925			GO:0006412//GO:0008135//GO:0043234	nr -
Unigene80185_All	202	0.00	4.01	1.85	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	9.31E-05	Up	1.08E+01	2.47E-02		null	null		null	null		null	null		null	null		Unigene80185_All//sp|Q5R8W2|ATP5I_PONAB//1.00E-06//ATP synthase subunit e, mitochondrial OS=Pongo abelii GN=ATP5I PE=3 SV=3						swissprot +
Unigene80196_All	202	0.00	5.02	2.11	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	7.21E-06	Up	1.10E+01	1.36E-02		null	null		null	null		null	null		null	null										
Unigene8020_All	1248	0.00	135.04	60.03	0.00	0.06	0.00	0.00	0.00	0.00	1.70E+01	0.00E+00	Up	1.59E+01	0.00E+00	Up	5.79E+00	6.01E-01		null	null		null	null		null	null		Unigene8020_All//gi|74231225|gb|AB A00716.1|//0.00E+00//translation elongation factor 1 alpha [Phytophthora parasitica]	Unigene8020_All//2.00E-174//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene8020_All//0.00E+00//TC166357			GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0044424	nr +
Unigene8021_All	498	0.00	0.20	0.96	1.30	1.18	2.27	1.95	0.17	2.64	7.67E+00	3.80E-01		9.91E+00	7.41E-03		-1.46E-01	8.39E-01		8.02E-01	2.30E-01		-3.54E+00	4.32E-05	Down	4.35E-01	4.04E-01		Unigene8021_All//gi|112280265|gb|AB114669.1|//4.00E-59//ubiquitin-protein ligase [Aegiceras corniculatum]	Unigene8021_All//1.00E-15//AT1G55860| UPL1 (UBIQUITIN-PROTEIN LIGASE 1); ubiquitin-protein ligase	Unigene8021_All//5.00E-137//TC133607	ko04120|Ubiquitin mediated proteolysis		GO:0019787//GO:0043231//GO:0043412//GO:0044267//GO:0044444	nr -
Unigene8022_All	396	0.40	1.02	1.34	2.89	1.13	0.91	2.14	2.53	5.53	1.37E+00	2.73E-01		1.76E+00	1.29E-01		-1.36E+00	2.74E-02		-1.66E+00	1.29E-02		2.46E-01	6.89E-01		1.37E+00	4.33E-04	Up								
Unigene80237_All	203	0.00	3.49	2.62	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.30E-04	Up	1.14E+01	4.00E-03		null	null		null	null		null	null		null	null										
Unigene80239_All	203	37.11	82.37	47.48	46.38	47.33	41.16	182.45	313.16	173.29	1.15E+00	1.10E-15	Up	3.55E-01	7.44E-02		2.92E-02	9.02E-01		-1.72E-01	4.29E-01		7.79E-01	3.03E-37		-7.43E-02	4.06E-01		Unigene80239_All//gi|297836048|ref|XP_002885906.1|//2.00E-27//ALDH6B2 [Arabidopsis lyrata subsp. lyrata] >gi|297331746|gb|EFH62165.1|ALDH6B2 [Arabidopsis lyrata subsp. lyrata]	Unigene80239_All//9.00E-29//AT2G14170| ALDH6B2; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase	Unigene80239_All//8.00E-109//gi|72268304|gb|DT046697.1|DT046697	ko00562|Inositol phosphate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism		GO:0006950//GO:0009081//GO:0016620//GO:0043231//GO:0046914	nr -
Unigene8024_All	590	2.48	0.94	0.36	3.55	2.04	1.61	1.00	0.00	0.34	-1.39E+00	1.39E-02		-2.78E+00	9.28E-05	Down	-7.96E-01	6.21E-02		-1.14E+00	1.08E-02		-9.97E+00	2.39E-04	Down	-1.57E+00	6.49E-02		Unigene8024_All//gi|107738065|gb|ABF83626.1|//5.00E-15//At4g33800 [Arabidopsis thaliana]	Unigene8024_All//3.00E-16//AT4G33800| unknown protein					nr -
Unigene80251_All	203	0.00	3.99	2.36	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	9.31E-05	Up	1.12E+01	7.41E-03		null	null		null	null		null	null		null	null										
Unigene8026_All	1838	0.00	0.00	0.03	0.08	0.00	0.02	4.97	2.23	5.22	null	null		4.86E+00	6.24E-01		-6.35E+00	1.64E-01		-1.72E+00	4.99E-01		-1.16E+00	6.20E-11	Down	7.22E-02	6.84E-01		Unigene8026_All//gi|224127456|ref|XP_002329282.1|//0.00E+00//cytochrome P450 [Populus trichocarpa] >gi|222870736|gb|EEF07867.1|cytochrome P450 [Populus trichocarpa]	Unigene8026_All//0.00E+00//AT5G38450| CYP735A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding		ko00908|Zeatin biosynthesis		GO:0005506//GO:0008152//GO:0016634//GO:0044464	nr +
Unigene80281_All	204	0.00	0.50	3.65	0.00	0.00	0.00	0.00	0.00	0.00	8.96E+00	3.80E-01		1.18E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene80281_All//sp|Q5RA66|SEPT2_PONAB//9.00E-33//Septin-2 OS=Pongo abelii GN=SEPT2 PE=2 SV=1						swissprot +
Unigene80286_All	204	0.00	6.71	8.35	0.00	0.00	12.18	30.47	38.93	225.75	1.27E+01	7.77E-08	Up	1.30E+01	2.19E-09	Up	null	null		1.36E+01	7.19E-15	Up	3.54E-01	6.38E-02		2.89E+00	2.38E-180	Up		Unigene80286_All//2.00E-29//TC138648					
Unigene80292_All	204	0.00	0.50	3.39	0.00	0.00	0.00	0.00	0.00	0.00	8.96E+00	3.80E-01		1.17E+01	6.12E-04	Up	null	null		null	null		null	null		null	null		Unigene80292_All//sp|P16975|SPRC_RAT//3.00E-36//SPARC OS=Rattus norvegicus GN=Sparc PE=1 SV=4						swissprot +
Unigene80297_All	204	0.00	3.48	2.35	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.30E-04	Up	1.12E+01	7.41E-03		null	null		null	null		null	null		null	null										ESTscan -
Unigene803_All	1535	20.35	8.78	22.93	36.64	24.81	29.54	41.78	79.45	39.27	-1.21E+00	3.12E-31	Down	1.72E-01	8.80E-02		-5.62E-01	1.48E-18		-3.11E-01	5.77E-06		9.27E-01	8.64E-95		-8.96E-02	1.64E-01		Unigene803_All//gi|147886439|gb|ABQ52428.1|//0.00E+00//boron transporter [Citrus macrophylla]	Unigene803_All//2.00E-147//AT3G62270| anion exchange family protein	Unigene803_All//0.00E+00//TC166022			GO:0006811//GO:0015301//GO:0031224	nr +
Unigene80323_All	205	0.00	5.19	3.38	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	3.79E-06	Up	1.17E+01	6.12E-04	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene80330_All	205	0.26	4.45	2.60	0.24	0.50	0.44	0.21	0.00	0.00	4.12E+00	2.33E-04	Up	3.35E+00	2.06E-02		1.05E+00	8.05E-01		8.59E-01	7.91E-01		-7.69E+00	6.43E-01		-7.69E+00	6.01E-01		Unigene80330_All//gi|33339152|gb|AAQ14258.1|AF247005_1//7.00E-29//auxin efflux carrier [Momordica charantia]	Unigene80330_All//1.00E-29//AT2G01420| PIN4 (PIN-FORMED 4); auxin:hydrogen symporter/ transporter	Unigene80330_All//1.00E-45//TC149217			GO:0000578//GO:0000904//GO:0009606//GO:0010015//GO:0012505//GO:0015294//GO:0015562//GO:0031224//GO:0044459//GO:0048588//GO:0060918	nr +
Unigene8034_All	1015	0.05	0.10	0.26	0.98	1.66	0.89	2.04	0.99	0.39	9.55E-01	7.24E-01		2.35E+00	2.39E-01		7.60E-01	1.44E-01		-1.42E-01	8.36E-01		-1.05E+00	9.27E-03		-2.38E+00	2.25E-07	Down	Unigene8034_All//gi|46395620|sp|O65039.1|CYSEP_RICCO//4.00E-61//RecName: Full=Vignain; AltName: Full=Cysteine endopeptidase; Flags: Precursor >gi|2944446|gb|AAC62396.1|cysteine endopeptidase precursor [Ricinus communis]	Unigene8034_All//2.00E-50//AT3G48340| cysteine-type endopeptidase/ cysteine-type peptidase	Unigene8034_All//4.00E-96//gi|54121019|gb|CO496528.1|CO496528			GO:0016787//GO:0043231//GO:0044444	nr +
Unigene8036_All	339	1.08	1.05	1.57	5.14	2.34	2.80	1.87	0.12	0.35	-4.63E-02	9.82E-01		5.40E-01	6.10E-01		-1.14E+00	1.57E-02		-8.78E-01	7.89E-02		-3.92E+00	9.80E-04	Down	-2.41E+00	8.12E-03				Unigene8036_All//4.00E-07//TC144771				
Unigene80366_All	206	0.00	0.98	4.39	0.00	0.00	0.00	0.00	0.00	0.00	9.94E+00	1.34E-01		1.21E+01	4.70E-05	Up	null	null		null	null		null	null		null	null										
Unigene8037_All	704	0.00	0.50	0.76	2.12	0.78	0.90	5.04	2.91	0.79	8.98E+00	2.43E-02		9.56E+00	4.00E-03		-1.44E+00	5.91E-03		-1.24E+00	2.45E-02		-7.94E-01	6.33E-03		-2.67E+00	1.11E-13	Down	Unigene8037_All//gi|28372892|gb|AAO39928.1|//1.00E-11//At1g71910 [Arabidopsis thaliana]	Unigene8037_All//6.00E-09//AT1G71910| unknown protein	Unigene8037_All//0.00E+00//TC158394				nr -
Unigene80371_All	206	4.83	9.59	2.07	8.95	16.05	33.32	23.60	106.32	112.17	9.91E-01	3.27E-02		-1.22E+00	1.00E-01		8.43E-01	1.14E-02		1.90E+00	2.46E-14	Up	2.17E+00	5.08E-61	Up	2.25E+00	1.68E-68	Up		Unigene80371_All//2.00E-60//DW508855					
Unigene80373_All	206	0.00	6.15	4.14	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.85E-07	Up	1.20E+01	8.98E-05	Up	null	null		null	null		null	null		null	null										
Unigene80376_All	206	0.00	0.00	3.88	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.19E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene80376_All//gi|300265473|gb|EFJ49664.1|//6.00E-09//component of cytosolic 80S ribosome and 40S small subunit [Volvox carteri f. nagariensis]	Unigene80376_All//1.00E-09//AT5G18380| 40S ribosomal protein S16 (RPS16C)		ko03010|Ribosome			nr -
Unigene8039_All	418	19.28	23.76	18.22	28.60	13.43	14.15	75.05	36.10	20.68	3.02E-01	1.12E-01		-8.15E-02	7.13E-01		-1.09E+00	1.23E-12	Down	-1.01E+00	4.37E-10	Down	-1.06E+00	7.87E-31	Down	-1.86E+00	1.48E-73	Down		Unigene8039_All//7.00E-151//gi|164243205|gb|EV486231.1|EV486231					
Unigene80395_All	206	0.00	0.00	4.65	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	2.45E-05	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene804_All	2427	6.66	2.32	9.37	11.47	7.21	8.54	17.53	24.47	20.72	-1.52E+00	4.17E-23	Down	4.92E-01	3.24E-05		-6.71E-01	9.28E-13		-4.26E-01	2.08E-05		4.82E-01	3.04E-15		2.41E-01	2.59E-04		Unigene804_All//gi|224133550|ref|XP_002321602.1|//0.00E+00//anion exchanger family protein [Populus trichocarpa] >gi|222868598|gb|EEF05729.1| anion exchanger family protein [Populus trichocarpa]	Unigene804_All//0.00E+00//AT2G47160| BOR1 (BEQUIRES HIGH BORON 1); anion exchanger/ boron transporter	Unigene804_All//0.00E+00//gi|48827675|gb|CO126065.1|CO126065			GO:0006811//GO:0010035//GO:0015301//GO:0031224	nr +
Unigene8040_All	257	4.28	11.04	5.18	3.88	3.62	4.39	9.21	7.97	5.12	1.37E+00	4.19E-04	Up	2.77E-01	6.16E-01		-9.97E-02	8.68E-01		1.81E-01	7.84E-01		-2.09E-01	6.32E-01		-8.49E-01	1.68E-02				Unigene8040_All//3.00E-127//gi|164341492|gb|ES840201.1|ES840201				
Unigene80422_All	207	0.51	251.14	134.03	0.24	0.17	0.65	0.41	0.40	0.38	8.96E+00	2.93E-295	Up	8.05E+00	1.19E-152	Up	-5.32E-01	8.19E-01		1.44E+00	6.36E-01		-1.67E-02	1.01E+00		-8.59E-02	9.69E-01				Unigene80422_All//1.00E-18//gi|109856609|gb|DW485588.1|DW485588				
Unigene80432_All	207	75.57	24.72	37.30	15.88	22.13	21.82	1.63	0.81	1.35	-1.61E+00	3.02E-24	Down	-1.02E+00	9.90E-12	Down	4.78E-01	9.58E-02		4.58E-01	1.26E-01		-1.02E+00	3.99E-01		-2.78E-01	7.80E-01				Unigene80432_All//2.00E-69//TC138556				
Unigene80433_All	207	0.00	3.43	4.63	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.30E-04	Up	1.22E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene80433_All//gi|301108545|ref|XP_002903354.1|//9.00E-10//mucin-like protein [Phytophthora infestans T30-4] >gi|262097726|gb|EEY55778.1|mucin-like protein [Phytophthora infestans T30-4]						GO:0005515//GO:0006810//GO:0044267//GO:0044464	nr +
Unigene80434_All	207	48.78	40.88	34.21	52.46	44.75	113.89	60.46	71.07	88.72	-2.55E-01	1.80E-01		-5.12E-01	6.54E-03		-2.29E-01	2.19E-01		1.12E+00	3.03E-22	Up	2.33E-01	9.39E-02		5.53E-01	8.95E-07		Unigene80434_All//gi|18416906|ref|NP_567764.1|//6.00E-25//ATRBP45C; RNA binding [Arabidopsis thaliana]	Unigene80434_All//6.00E-16//AT4G27000| ATRBP45C; RNA binding	Unigene80434_All//3.00E-111//TC137988			GO:0005488	nr +

Unigene8045_All	349	1.05	0.00	0.15	1.00	0.89	1.29	1.82	0.84	0.11	-1.00E+01	1.95E-02		-2.78E+00	1.03E-01		-1.70E-01	8.57E-01		3.73E-01	7.32E-01		-1.12E+00	1.80E-01		-3.99E+00	5.82E-04	Down	Unigene8045_All//gi|223635616|sp|P0C842.1|PP323_ARATH//5.00E-42//RecName: Full=Pentatricopeptide repeat-containing protein At4g19191, mitochondrial; Flags: Precursor	Unigene8045_All//2.00E-43//AT4G19191| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 10 growth stages; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: CRR22 (CHLORORESPIRATORY REDUCTION22); endonuclease (TAIR:AT1G11290.1); Has 16668 Blast hits to 5144 proteins in 160 species: Archae - 1; Bacteria - 6; Metazoa - 71; Fungi - 62; Plants - 16190; Viruses - 0; Other Eukaryotes - 338 (source: NCBI BLink).				GO:0043231	nr +
Unigene80453_All	208	0.00	136.17	49.41	0.00	0.17	0.00	0.00	0.00	0.00	1.71E+01	2.92E-163	Up	1.56E+01	1.08E-57	Up	7.37E+00	8.14E-01		null	null		null	null		null	null				Unigene80453_All//4.00E-12//ES817455					
Unigene8046_All	749	0.21	0.07	0.36	0.13	0.18	0.48	1.07	1.34	2.77	-1.63E+00	4.87E-01		7.62E-01	6.43E-01		4.68E-01	8.75E-01		1.86E+00	2.19E-01		3.20E-01	6.45E-01		1.37E+00	6.87E-04	Up	Unigene8046_All//gi|170660047|gb|ACB28472.1|/4.00E-57//polyprotein [Ananas comosus]					GO:0003676//GO:0003824//GO:0006259//GO:0043229	nr +
Unigene80461_All	208	0.00	1.22	5.89	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	7.76E-02		1.25E+01	9.09E-07	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene80489_All	209	0.00	0.00	6.11	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.26E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene80489_All//gi|195620934|gb|ACG32297.1|//3.00E-33//60S ribosomal protein L23 [Zea mays]	Unigene80489_All//2.00E-34//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene80489_All//7.00E-23//DW231030		ko03010|Ribosome		nr -
Unigene8049_All	1154	0.00	0.18	0.00	0.26	0.24	0.08	4.76	12.50	4.28	7.46E+00	1.34E-01		null	null		-1.18E-01	9.00E-01		-1.73E+00	2.89E-01		1.39E+00	4.34E-22	Up	-1.54E-01	5.41E-01		Unigene8049_All//gi|34850945|dbj|BAC87845.1|//2.00E-88//leucine-rich repeat receptor-like protein kinase 1 [Populus nigra]	Unigene8049_All//3.00E-87//AT4G08850| kinase			ko03410|Base excision repair	GO:0000166//GO:0004672//GO:0004871//GO:0008152//GO:0016020//GO:0016491	nr -
Unigene80495_All	209	0.00	6.06	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	2.85E-07	Up	1.06E+01	4.44E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene80497_All	209	0.00	50.43	19.11	0.00	0.00	0.00	0.00	0.00	0.00	1.56E+01	2.10E-60	Up	1.42E+01	3.82E-22	Up	null	null		null	null		null	null		null	null		Unigene80497_All//sp|P17205|SER1_DROME//4.00E-19//Serine proteases 1/2 OS=Drosophila melanogaster GN=Jon99Cii PE=1 SV=2								swissprot -
Unigene80504_All	209	0.00	0.00	5.86	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.25E+01	9.09E-07	Up	null	null		null	null		null	null		null	null		Unigene80504_All//gi|226507284|ref|NP_001151623.1|/1.00E-21//60S ribosomal protein L27a-3 [Zea mays] >gi|195627178|gb|ACG33419.1| 60S ribosomal protein L27a-3 [Zea mays] >gi|195648174|gb|ACG43555.1| 60S ribosomal protein L27a-3 [Zea mays]	Unigene80504_All//5.00E-23//AT1G70600| structural constituent of ribosome	Unigene80504_All//8.00E-29//TC169611		ko03010|Ribosome		nr +
Unigene8051_All	267	11.17	18.03	23.53	15.11	19.86	28.92	31.83	36.32	23.72	6.91E-01	1.18E-02		1.08E+00	1.52E-05	Up	3.94E-01	1.46E-01		9.37E-01	6.40E-06		1.90E-01	3.07E-01		-4.24E-01	1.43E-02		Unigene8051_All//gi|3913996|sp|O04979.1|LONM_SPIOL//2.00E-33//RecName: Full=Lon protease homolog, mitochondrial; Flags: Precursor >gi|2208927|dbj|BAA20482.1| ATP-dependent protease Lon [Spinacia oleracea]	Unigene8051_All//5.00E-21//AT5G47040| LON2 (LON PROTEASE 2); ATP binding / ATP-dependent peptidase/ nucleoside-triphosphatase/ nucleotide binding / serine-type endopeptidase/ serine-type peptidase	Unigene8051_All//7.00E-147//gi|84154720|gb|DN804075.1|DN804075			GO:0003676//GO:0004175//GO:0016558//GO:0019538//GO:0031980//GO:0032559//GO:0042623//GO:0044439//GO:0048528	nr +
Unigene80510_All	209	3.50	0.00	1.02	0.48	0.49	0.00	0.00	0.20	0.00	-1.18E+01	2.11E-04	Down	-1.78E+00	6.00E-02		5.23E-02	9.65E-01		-8.90E+00	3.93E-01		7.64E+00	6.26E-01		null	null		Unigene80510_All//gi|83283979|gb|ABC01897.1|/4.00E-08//protein transport SEC13-like protein [Solanum tuberosum]	Unigene80510_All//3.00E-07//AT3G01340| protein transport protein SEC13 family protein / WD-40 repeat family protein	Unigene80510_All//1.00E-09//AI730908				nr +
Unigene80513_All	209	0.00	3.15	2.29	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.20E-04	Up	1.12E+01	7.41E-03		null	null		null	null		null	null		null	null		Unigene80513_All//sp|Q94522|SUCA_DROME//1.00E-10//Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial OS=Drosophila melanogaster GN=Scsalpha PE=2 SV=3				ko00020|Citrate cycle (TCA cycle)//ko00640|Propanoate metabolism		swissprot +
Unigene8052_All	231	35.79	57.03	32.96	37.52	34.73	54.16	95.91	116.88	47.08	6.72E-01	1.49E-05		-1.19E-01	6.29E-01		-1.11E-01	6.15E-01		5.29E-01	7.78E-04		2.85E-01	2.71E-03		-1.03E+00	1.08E-21	Down	Unigene8052_All//gi|18404032|ref|NP_565834.1|//8.00E-35//ubiquitin-conjugating enzyme family protein [Arabidopsis thaliana] >gi|75313485|sp|Q9SJ44.1|UEV1C_ARATH RecName: Full=Ubiquitin-conjugating enzyme E2 variant 1C; Short=Ubc enzyme variant 1C; AltName: Full=Protein MMS ZWEI HOMOLOG 3	Unigene8052_All//3.00E-36//AT2G36060| ubiquitin-conjugating enzyme family protein	Unigene8052_All//2.00E-125//gi|21089369|gb|BQ401682.1|BQ401682			GO:0005488//GO:0006281//GO:0006464//GO:0016881//GO:0031371//GO:0060255	nr +
Unigene80532_All	210	0.00	74.56	27.89	0.00	0.00	0.00	0.00	0.00	0.00	1.62E+01	5.92E-90	Up	1.48E+01	1.20E-32	Up	null	null		null	null		null	null		null	null		Unigene80532_All//sp|P92192|LCP5_DROME//2.00E-14//Larval cuticle protein 5 OS=Drosophila melanogaster GN=Lcp65Abl PE=1 SV=1								swissprot -
Unigene80535_All	210	0.00	0.48	12.43	0.00	0.00	0.00	0.00	0.00	0.00	8.91E+00	3.80E-01		1.36E+01	2.12E-14	Up	null	null		null	null		null	null		null	null									
Unigene8054_All	514	1.02	1.87	0.52	3.10	2.14	0.70	1.32	0.33	0.39	8.80E-01	2.13E-01		-9.75E-01	3.76E-01		-5.33E-01	3.18E-01		-2.14E+00	2.07E-04	Down	-2.02E+00	1.98E-02		-1.76E+00	2.80E-02		Unigene8054_All//gi|147805050|emb|CAN71439.1|//2.00E-18//hypothetical protein [Vitis vinifera]		Unigene8054_All//5.00E-35//TC169015			GO:0005488	nr +
Unigene80541_All	210	0.00	3.14	2.28	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	6.20E-04	Up	1.12E+01	7.41E-03		null	null		null	null		null	null		null	null		Unigene80541_All//sp|P00921|CAH2_BOVIN//3.00E-11//Carbonic anhydrase 2 OS=Bos taurus GN=CA2 PE=1 SV=3								swissprot +
Unigene80546_All	210	0.00	4.58	2.54	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.37E-05	Up	1.13E+01	4.00E-03		null	null		null	null		null	null		null	null									
Unigene80549_All	210	0.00	3.86	1.52	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.30E-05	Up	1.06E+01	4.44E-02		null	null		null	null		null	null		null	null									
Unigene8055_All	989	1.32	1.13	0.16	0.50	1.67	0.91	4.02	1.01	1.37	-2.31E-01	6.71E-01		-3.03E+00	1.24E-04	Down	1.73E+00	1.21E-03		8.59E-01	2.69E-01		-1.99E+00	1.63E-10	Down	-1.55E+00	5.46E-08	Down	Unigene8055_All//gi|297812057|ref|XP_002873912.1|//2.00E-90//EMB3013 [Arabidopsis lyrata subsp. lyrata] >gi|297319749|gb|EFH50171.1| EMB3013 [Arabidopsis lyrata subsp. lyrata]	Unigene8055_All//3.00E-92//AT5G18700| EMB3013 (embryo defective 3013); ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene8055_All//2.00E-23//CO197002			GO:0000166//GO:0004672//GO:0044238//GO:0044260	nr -
Unigene80558_All	210	0.00	1.93	3.30	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	1.34E-02		1.17E+01	6.11E-04	Up	null	null		null	null		null	null		null	null									
Unigene8058_All	322	2.60	6.77	8.43	5.88	5.77	16.13	5.91	6.88	1.86	1.38E+00	2.27E-03		1.70E+00	7.10E-05	Up	-2.57E-02	9.58E-01		1.46E+00	9.52E-08	Up	2.19E-01	6.26E-01		-1.67E+00	1.23E-04	Down							
Unigene806_All	1681	9.40	17.93	10.04	6.73	8.34	9.56	9.68	13.25	20.59	9.32E-01	7.75E-20		9.53E-02	5.60E-01		3.10E-01	4.17E-02		5.08E-01	1.98E-04		4.53E-01	1.19E-05		1.09E+00	2.12E-36	Up	Unigene806_All//gi|223452418|gb|ACM89536.1|//1.00E-158//protein kinase [Glycine max]	Unigene806_All//3.00E-160//AT2G17220| protein kinase, putative	Unigene806_All//0.00E+00//TC166050		ko04626|Plant-pathogen interaction		nr -
Unigene8060_All	502	58.37	61.17	134.61	112.43	39.31	16.19	1.09	0.92	0.40	6.76E-02	5.62E-01		1.21E+00	4.16E-64	Up	-1.52E+00	6.89E-98	Down	-2.80E+00	3.94E-188	Down	-2.58E-01	7.60E-01		-1.46E+00	9.76E-02		Unigene8060_All//gi|28565534|gb|AAO43000.1|//8.00E-18//early tobacco anther 1 [Nicotiana tabacum]	Unigene8060_All//1.00E-16//AT5G48480| unknown protein	Unigene8060_All//0.00E+00//TC151304				nr +
Unigene80602_All	211	0.00	4.08	2.52	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.91E-05	Up	1.13E+01	4.00E-03		null	null		null	null		null	null		null	null									
Unigene80606_All	212	5.43	2.63	3.27	5.87	2.76	5.97	9.97	4.73	3.01	-1.05E+00	1.01E-01		-7.34E-01	2.67E-01		-1.09E+00	6.06E-02		2.21E-02	9.71E-01		-1.08E+00	6.86E-03		-1.73E+00	2.86E-05	Down			Unigene80606_All//4.00E-40//TC169687				
Unigene80611_All	212	0.00	4.06	6.28	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	4.91E-05	Up	1.26E+01	2.39E-07	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene80612_All	212	12.34	10.04	4.77	11.98	12.02	11.72	53.65	21.88	24.81	-2.98E-01	4.51E-01		-1.37E+00	1.16E-03		4.40E-03	9.98E-01		-3.25E-02	9.49E-01		-1.29E+00	7.64E-16	Down	-1.11E+00	4.50E-13	Down	Unigene80612_All//gi|116310298|emb|CAH67316.1|//4.00E-37//OSIGBa0106G07.12 [Oryza sativa (indica cultivar-group)]	Unigene80612_All//3.00E-38//AT2G42490| copper amine oxidase, putative	Unigene80612_All//1.00E-116//TC161926		ko00360|Phenylalanine metabolism//ko00260|Glycine, serine and threonine metabolism/ko00350|Tyrosine metabolism/ko00410|beta-Alanine metabolism//ko00960|Tropane, piperidine and pyridine alkaloid biosynthesis/ko00950|Isoquinoline alkaloid biosynthesis		nr -
Unigene8062_All	245	5.77	1.24	1.96	9.15	6.47	4.98	21.57	4.95	7.64	-2.22E+00	5.59E-04	Down	-1.56E+00	1.19E-02		-5.01E-01	2.44E-01		-8.78E-01	4.04E-02		-2.12E+00	6.53E-15	Down	-1.50E+00	7.58E-10	Down	Unigene8062_All//gi|18414198|ref|NP_567427.1|//2.00E-41//dehydration-responsive protein-related [Arabidopsis thaliana] >gi|79325109|ref|NP_001031639.1| dehydration-responsive protein-related [Arabidopsis thaliana] >gi|75249435|sp|Q93YV7.1|PMT3_ARATH RecName: Full=Probable methyltransferase PMT3	Unigene8062_All//8.00E-43//AT4G14360| dehydration-responsive protein-related	Unigene8062_All//4.00E-136//TC139117			GO:0016020//GO:0016741//GO:0043231//GO:0046914	nr -
Unigene80636_All	212	0.74	3.82	5.53	0.00	0.49	1.07	0.80	0.39	0.56	2.37E+00	1.01E-02		2.90E+00	4.34E-04	Up	8.93E+00	4.52E-01		1.01E+01	1.18E-01		-1.02E+00	6.13E-01		-5.01E-01	7.45E-01									
Unigene8064_All	348	0.30	0.29	3.06	2.15	2.37	1.82	0.97	1.68	1.72	-4.63E-02	9.86E-01		3.35E+00	3.36E-04	Up	1.45E-01	8.70E-01		-2.41E-01	7.55E-01		7.91E-01	3.74E-01		8.21E-01	3.20E-01		Unigene8064_All//gi|124360392|gb|ABN08405.1|//8.00E-06//Peptidase aspartic, active site [Medicago truncatula]					GO:0003676//GO:0003824//GO:0006259//GO:0043229	nr -
Unigene80640_All	212	0.25	121.65	89.17	0.00	0.00	0.21	0.20	0.00	0.00	8.95E+00	3.40E-146	Up	8.50E+00	1.53E-104	Up	null	null		7.73E+00	6.84E-01		-7.64E+00	6.43E-01		-7.64E+00	6.01E-01		Unigene80640_All//sp|P03928|ATP8_HUMAN//2.00E-29//ATP synthase protein 8 OS=Homo sapiens GN=MT-ATP8 PE=1 SV=1								swissprot -
Unigene80649_All	213	0.00	0.00	4.25	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.21E+01	4.70E-05	Up	null	null		null	null		null	null		null	null		Unigene80649_All//gi|194466103|gb|ACF74282.1|//2.00E-16//embryo-abundant protein EMB [Arachis hypogaea]	Unigene80649_All//2.00E-16//AT2G41380| embryo-abundant protein-related					nr +
Unigene80657_All	213	9.83	2.62	8.00	5.61	7.11	3.18	0.40	0.20	0.56	-1.91E+00	1.01E-04	Down	-2.97E-01	5.35E-01		3.42E-01	5.76E-01		-8.20E-01	1.99E-01		-1.02E+00	7.21E-01		4.99E-01	8.06E-01		Unigene80657_All//gi|15240499|ref|NP_200348.1|//1.00E-12//long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein [Arabidopsis thaliana] >gi|75170973|sp|Q9FJ73.1|WAXS2_ARATH RecName: Full=Probable long-chain-alcohol O-fatty-acyltransferase 2; AltName: Full=Wax synthase 2 >gi|9758169|dbj|BAB08554.1| wax synthase-like protein [Arabidopsis thaliana]	Unigene80657_All//5.00E-14//AT5G55370| long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein	Unigene80657_All//1.00E-110//BE052379				nr -
Unigene8066_All	895	1.11	0.34	1.19	0.17	0.19	0.00	1.94	4.62	6.59	-1.71E+00	2.08E-02		9.94E-02	8.79E-01		2.04E-01	9.49E-01		-7.38E+00	2.31E-01		1.26E+00	5.27E-06	Up	1.77E+00	2.08E-13	Up	Unigene8066_All//gi|19911575|dbj|BAB88891.1|//5.00E-45//syringolide-induced protein 14-1-1 [Glycine max]	Unigene8066_All//3.00E-29//AT1G76070| unknown protein	Unigene8066_All//0.00E+00//DW497873				nr -
Unigene80666_All	214	0.00	1.89	5.23	0.00	0.00	0.21	0.00	0.00	0.00	1.09E+01	1.34E-02		1.24E+01	3.42E-06	Up	null	null		7.72E+00	6.83E-01		null	null		null	null		Unigene80666_All//sp|P15814|IGLL1_HUMAN//2.00E-24//Immunoglobulin lambda-like polypeptide 1 OS=Homo sapiens GN=IGLL1 PE=1 SV=1								swissprot -
Unigene80667_All	214	0.00	0.24	3.23	0.70	0.64	0.21	0.40	0.00	0.19	7.89E+00	6.08E-01		1.17E+01	6.11E-04	Up	-1.18E-01	9.09E-01		-1.73E+00	4.99E-01		-8.63E+00	3.98E-01		-1.09E+00	6.73E-01				Unigene80667_All//2.00E-115//TC134425				

Unigene8067_All	328	10.53	3.55	10.88	7.44	4.93	5.65	4.38	2.68	4.98	-1.57E+00	9.76E-06	Down	4.71E-02	8.94E-01		-5.93E-01	1.39E-01		-3.99E-01	3.70E-01		-7.12E-01	1.55E-01		1.84E-01	6.76E-01		Unigene8067_All//gi|15233571|ref|NP_194672.1|//1.00E-23//rps15ae (ribosomal protein S15A E); structural constituent of ribosome [Arabidopsis thaliana] >gi|297803094|ref|XP_002869431.1| RPS15AE [Arabidopsis lyrata subsp. lyrata] >gi|75311751|sp|Q9M0E0.1|R15A5_ARATH RecName: Full=40S ribosomal protein S15a-5 >gi|7269842|emb|CAB79701.1| ribosomal protein S15a homolog [Arabidopsis thaliana] >gi|21553914|gb|AAM62997.1| ribosomal protein S15a homolog [Arabidopsis thaliana] >gi|110737866|dbj|BAF00871.1| ribosomal protein S15a homolog [Arabidopsis thaliana] >gi|111074474|gb|ABH04610.1| At4g29430 [Arabidopsis thaliana] >gi|297315267|gb|EFH45690.1| RPS15AE [Arabidopsis lyrata subsp. lyrata]	Unigene8067_All//6.00E-25//AT4G29430| rps15ae (ribosomal protein S15A E); structural constituent of ribosome	Unigene8067_All//4.00E-93//gi|78351665|gb|DT571939.1|DT571939		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0043231	nr -
Unigene80675_All	214	0.00	3.79	1.99	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	9.30E-05	Up	1.10E+01	1.36E-02		null	null		null	null		null	null		null	null		Unigene80675_All//sp|Q29718|1B82_HUMAN//1.00E-31//HLA class I histocompatibility antigen, B-82 alpha chain OS=Homo sapiens GN=HLA-B PE=2 SV=1						swissprot -
Unigene80689_All	214	0.49	147.27	118.44	0.23	0.16	1.06	0.40	0.00	0.19	8.23E+00	4.34E-177	Up	7.92E+00	4.70E-139	Up	-5.33E-01	8.19E-01		2.18E+00	3.22E-01		-8.63E+00	3.98E-01		-1.09E+00	6.73E-01		Unigene80689_All//gi|260766526|gb|ACX50285.1|//1.00E-11//cytochrome oxidase subunit 1 [Guillardia theta]	Unigene80689_All//2.00E-09//ATMG01360| cytochrome c oxidase subunit 1			ko00190|Oxidative phosphorylation		nr -
Unigene8069_All	501	191.01	459.87	297.92	228.69	241.60	298.48	19.58	39.21	22.74	1.27E+00	1.63E-241	Up	6.41E-01	8.47E-49		7.92E-02	1.33E-01		3.84E-01	1.29E-21		1.00E+00	4.97E-18	Up	2.16E-01	1.68E-01		Unigene8069_All//gi|15233068|ref|NP_191685.1|//1.00E-22//DNA-binding family protein / remorin family protein [Arabidopsis thaliana] >gi|75182856|sp|Q9ZD8.1|Y3126_ARATH RecName: Full=Uncharacterized protein At3g61260	Unigene8069_All//1.00E-13//AT3G61260| DNA-binding family protein / remorin family protein	Unigene8069_All//0.00E+00//TC174872			GO:0016020//GO:0043168//GO:0043231	nr -
Unigene80693_All	214	0.73	2.13	1.49	0.70	0.00	1.27	0.20	0.78	3.16	1.54E+00	1.96E-01		1.03E+00	4.70E-01		-9.45E+00	1.64E-01		8.59E-01	6.30E-01		1.98E+00	3.78E-01		4.00E+00	4.29E-04	Up			Unigene80693_All//2.00E-07//CO126194				
Unigene80698_All	214	0.00	0.00	3.48	0.47	0.16	0.21	0.00	0.00	0.00	null	null		1.18E+01	3.25E-04	Up	-1.53E+00	5.83E-01		-1.14E+00	6.73E-01		null	null		null	null									ESTscan +
Unigene807_All	1631	5.20	9.97	3.89	4.86	5.66	6.65	10.55	17.48	27.72	9.40E-01	3.28E-11		-4.20E-01	4.67E-02		2.21E-01	3.04E-01		4.53E-01	9.27E-03		7.28E-01	2.47E-15		1.39E+00	3.13E-69	Up	Unigene807_All//gi|15146244|gb|AAK83605.1|//1.00E-161//At2g17220/T23A1.8 [Arabidopsis thaliana] >gi|23506217|gb|AAX31120.1| At2g17220/T23A1.8 [Arabidopsis thaliana]	Unigene807_All//7.00E-155//AT2G17220| protein kinase, putative	Unigene807_All//0.00E+00//TC166050		ko04626|Plant-pathogen interaction		nr +
Unigene8070_All	1387	0.04	0.00	0.00	0.00	0.05	0.13	2.47	12.66	2.04	-5.24E+00	6.01E-01		-5.24E+00	6.15E-01		5.64E+00	6.01E-01		7.02E+00	1.93E-01		2.36E+00	3.41E-54	Up	-2.76E-01	3.66E-01		Unigene8070_All//gi|115485947|ref|NP_001068117.1|//2.00E-37//Os11g0569500 [Oryza sativa Japonica Group] >gi|113645339|dbj|BAF28480.1| Os11g0569500 [Oryza sativa Japonica Group]	Unigene8070_All//2.00E-31//AT3G47090| leucine-rich repeat transmembrane protein kinase, putative	Unigene8070_All//4.00E-10//CO121590		ko04626|Plant-pathogen interaction	GO:0016740	nr -
Unigene80705_All	215	1.46	0.24	1.98	0.70	1.60	1.68	16.32	30.52	37.43	-2.63E+00	1.30E-01		4.41E-01	6.76E-01		1.20E+00	4.26E-01		1.27E+00	3.81E-01		9.03E-01	1.20E-05		1.20E+00	1.73E-10	Up	Unigene80705_All//gi|297834070|ref|XP_002884917.1|//3.00E-17//EMB2742 [Arabidopsis lyrata subsp. lyrata] >gi|297330757|gb|EFH61176.1| EMB2742 [Arabidopsis lyrata subsp. lyrata]	Unigene80705_All//1.00E-18//AT3G12670| emb2742 (embryo defective 2742); CTP synthase/catalytic	Unigene80705_All//4.00E-74//ES818469		ko00240|Pyrimidine metabolism		nr -
Unigene80707_All	215	8.03	7.31	4.95	12.51	11.53	9.87	39.72	26.05	15.56	-1.37E-01	7.70E-01		-6.97E-01	1.83E-01		-1.18E-01	8.04E-01		-3.42E-01	4.11E-01		-6.09E-01	5.37E-04		-1.35E+00	2.60E-13	Down	Unigene80707_All//gi|42565520|gb|AAS21023.1|//3.00E-27//coatomer protein gamma subunit [Hyacinthus orientalis]	Unigene80707_All//4.00E-28//AT4G34450| coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative	Unigene80707_All//6.00E-116//gi|82755772|gb|DV849334.1|DV849334				nr -
Unigene80708_All	215	0.00	13.43	6.44	0.23	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.97E-16	Up	1.27E+01	1.23E-07	Up	-7.86E+00	5.44E-01		-7.86E+00	6.19E-01		null	null		null	null									
Unigene8071_All	267	2.16	1.90	0.80	5.78	3.87	5.41	2.38	0.78	0.15	-1.84E-01	8.25E-01		-1.43E+00	1.75E-01		-5.80E-01	2.80E-01		-9.56E-02	8.64E-01		-1.60E+00	6.26E-02		-3.99E+00	5.82E-04	Down								
Unigene80711_All	215	3.65	0.24	5.45	0.93	1.44	1.26	0.20	0.00	0.19	-3.95E+00	8.54E-04	Down	5.78E-01	3.90E-01		6.37E-01	6.94E-01		4.44E-01	7.63E-01		-7.62E+00	6.43E-01		-8.61E-02	9.66E-01				Unigene80711_All//2.00E-23//TC142285				
Unigene80714_All	215	0.00	4.71	2.23	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	7.21E-06	Up	1.11E+01	7.41E-03		null	null		null	null		null	null		null	null		Unigene80714_All//sp|Q9VUQ5|AGO2_DROME//2.00E-12//Protein argonaute-2 OS=Drosophila melanogaster GN=AGO2 PE=1 SV=3						swissprot +
Unigene80718_All	215	0.00	0.24	3.22	0.00	0.00	0.00	0.00	0.00	0.00	7.88E+00	6.08E-01		1.17E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene80718_All//gi|159478092|ref|XP_001697138.1|//1.00E-07//hypothetical protein CHLREDRAFT_192466 [Chlamydomonas reinhardtii] >gi|158274612|gb|EDP00393.1| predicted protein [Chlamydomonas reinhardtii]						nr -
Unigene80726_All	216	0.24	154.35	79.38	0.00	0.00	0.00	0.00	0.00	0.00	9.32E+00	8.34E-190	Up	8.36E+00	1.44E-94	Up	null	null		null	null		null	null		null	null		Unigene80726_All//gi|57864672|gb|AW56956.1|//1.00E-29//actin [Rhodomonas salina]	Unigene80726_All//4.00E-29//AT3G18780| ACT2 (ACTIN 2); structural constituent of cytoskeleton	Unigene80726_All//7.00E-20//gi|31406833|gb|CD485868.1|CD485868				nr -
Unigene80728_All	216	0.00	1.64	3.20	0.00	0.00	0.42	0.00	0.00	0.00	1.07E+01	2.43E-02		1.16E+01	6.11E-04	Up	null	null		8.71E+00	4.70E-01		null	null		null	null									
Unigene80732_All	216	0.00	7.04	2.22	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	1.09E-08	Up	1.11E+01	7.41E-03		null	null		null	null		null	null		null	null									
Unigene8074_All	638	0.00	1.19	0.83	6.01	8.20	3.33	0.20	0.66	0.19	1.02E+01	1.75E-04	Up	9.70E+00	4.00E-03		4.49E-01	9.17E-02		-8.54E-01	5.79E-03		1.72E+00	1.35E-01		-8.60E-02	9.68E-01									
Unigene80743_All	216	0.00	5.86	2.47	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.85E-07	Up	1.13E+01	4.00E-03		null	null		null	null		null	null		null	null		Unigene80743_All//gi|219118523|ref|XP_002180032.1|//2.00E-25//atp-citrate synthase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217408289|gb|EEC48223.1| atp-citrate synthase [Phaeodactylum tricornutum CCAP 1055/1]	Unigene80743_All//2.00E-18//AT5G49460| ACLB-2 (ATP CITRATE LYASE SUBUNIT B 2); ATP citrate synthase			ko00020|Citrate cycle (TCA cycle)		nr +
Unigene80748_All	217	0.00	0.70	6.38	0.00	0.00	0.00	0.00	0.00	0.00	9.45E+00	2.32E-01		1.26E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene80748_All//gi|161788876|dbj|BAF95072.1|//2.00E-19//voltage-dependent anion channel [Nicotiana tabacum]	Unigene80748_All//3.00E-18//AT3G01280| VDAC1 (VOLTAGE DEPENDENT ANION CHANNEL 1); voltage-gated anion channel	Unigene80748_All//3.00E-19//TC173544				nr +
Unigene8075_All	501	1.04	58.15	7.65	0.40	11.68	21.45	0.00	0.00	0.32	5.80E+00	5.52E-150	Up	2.87E+00	5.20E-12	Up	4.88E+00	1.37E-31	Up	5.75E+00	9.21E-59	Up	null	null		8.31E+00	1.39E-01		Unigene8075_All//gi|240254706|gb|ACS49840.1|//5.00E-13//seed biotinylated protein 68 kDa isoform [Glycine max]	Unigene8075_All//2.00E-11//AT2G42560| late embryogenesis abundant domain-containing protein / LEA domain-containing protein					nr +
Unigene80751_All	217	0.72	0.93	5.64	0.23	0.32	1.04	0.97	0.58	0.73	3.69E-01	8.15E-01		2.96E+00	2.55E-04	Up	4.67E-01	9.53E-01		2.18E+00	3.22E-01		-7.54E-01	6.31E-01		-4.08E-01	7.55E-01		Unigene80751_All//gi|87241294|gb|ABD33152.1|//2.00E-33//Helicase, C-terminal; Haem peroxidase, plant/fungal/bacterial [Medicago truncatula]	Unigene80751_All//5.00E-34//AT3G02060| DEAD/DEAH box helicase, putative	Unigene80751_All//3.00E-62//gi|78348240|gb|DT568514.1|DT568514		ko03440|Homologous recombination		nr -
Unigene80757_All	217	1.93	1.17	8.59	0.00	1.27	0.42	0.00	0.00	0.00	-7.24E-01	5.25E-01		2.15E+00	1.31E-04	Up	1.03E+01	7.00E-02		8.70E+00	4.70E-01		null	null		null	null									
Unigene8076_All	621	0.00	0.00	0.00	0.00	0.11	0.87	2.66	6.46	15.27	null	null		null	null		6.79E+00	6.01E-01		9.77E+00	2.45E-03		1.28E+00	5.08E-06	Up	2.52E+00	1.26E-32	Up	Unigene8076_All//gi|297803576|ref|XP_002869672.1|//5.00E-09//basix helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315508|gb|EFH45931.1| basix helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8076_All//2.00E-09//AT4G25410| DNA binding / transcription factor	Unigene8076_All//2.00E-19//ES805839	bHLH		GO:0001071//GO:0010468	nr +
Unigene8077_All	486	0.22	0.10	0.66	1.44	0.64	0.00	4.09	4.39	0.82	-1.05E+00	6.82E-01		1.61E+00	3.04E-01		-1.17E+00	1.61E-01		-1.05E+01	1.96E-04	Down	1.01E-01	8.07E-01		-2.32E+00	6.40E-07	Down	Unigene8077_All//gi|30023714|gb|AAP13390.1|//3.00E-07//At5g44170 [Arabidopsis thaliana]	Unigene8077_All//3.00E-07//AT5G44170| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: Expressed protein (TAIR:AT1G08125.1); Has 565 Blast hits to 565 proteins in 102 species: Archae - 0; Bacteria - 6; Metazoa - 261; Fungi - 146; Plants - 99; Viruses - 0; Other Eukaryotes - 53 (source: NCBI BLink).					nr +
Unigene80785_All	218	0.00	100.41	39.08	0.00	0.00	0.00	0.00	0.00	0.00	1.66E+01	5.35E-126	Up	1.53E+01	1.02E-47	Up	null	null		null	null		null	null		null	null		Unigene80785_All//sp|P92192|LCP5_DROME//2.00E-08//Larval cuticle protein 5 OS=Drosophila melanogaster GN=Lcp65Abl PE=1 SV=1						swissprot +
Unigene80793_All	218	0.00	3.25	1.47	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	3.30E-04	Up	1.05E+01	4.44E-02		null	null		null	null		null	null		null	null		Unigene80793_All//gi|255593650|ref|XP_002535920.1|//2.00E-10//alpha-amylase, putative [Ricinus communis] >gi|223521525|gb|EEF26463.1| alpha-amylase, putative [Ricinus communis]						nr -
Unigene80798_All	218	44.64	34.17	53.01	20.34	20.53	16.99	43.44	18.79	16.08	-3.86E-01	3.91E-02		2.48E-01	1.80E-01		1.40E-02	9.70E-01		-2.60E-01	4.18E-01		-1.21E+00	4.48E-12	Down	-1.43E+00	5.86E-16	Down			Unigene80798_All//5.00E-104//gi|78345154|gb|DT565428.1|DT565428				
Unigene808_All	1586	3.23	5.59	2.38	2.92	3.84	4.10	5.94	9.07	13.21	7.90E-01	4.86E-05		-4.40E-01	1.22E-01		3.96E-01	1.08E-01		4.89E-01	3.80E-02		6.09E-01	3.71E-06		1.15E+00	1.96E-24	Up	Unigene808_All//gi|223452418|gb|ACM89536.1|//1.00E-162//protein kinase [Glycine max]	Unigene808_All//3.00E-150//AT2G17220| protein kinase, putative	Unigene808_All//0.00E+00//TC166050		ko04626|Plant-pathogen interaction		nr -
Unigene80800_All	218	9.84	5.58	3.18	3.20	3.95	1.86	0.00	0.58	0.18	-8.19E-01	6.15E-02		-1.63E+00	8.10E-04	Down	3.04E-01	7.36E-01		-7.79E-01	3.93E-01		9.17E+00	2.39E-01		7.51E+00	6.36E-01									
Unigene80801_All	218	0.00	0.70	3.91	0.00	0.16	0.00	0.00	0.00	0.00	9.45E+00	2.32E-01		1.19E+01	8.98E-05	Up	7.30E+00	8.14E-01		null	null		null	null		null	null		Unigene80801_All//gi|210110834|gb|ACJ07147.1|//3.00E-25//beta-hydroxyacyl-ACP dehydrase 1 [Arachis hypogaea]	Unigene80801_All//1.00E-25//AT2G22230| beta-hydroxyacyl-ACP dehydratase, putative	Unigene80801_All//1.00E-33//gi|54121792|gb|CO497301.1|CO497301		ko00061|Fatty acid biosynthesis		nr -

Unigene80806_A11	218	0.00	0.46	4.89	0.23	0.00	0.00	0.00	0.00	0.00	8.86E+00	3.80E-01		1.23E+01	6.59E-06	Up	-7.84E+00	5.44E-01		-7.84E+00	6.19E-01		null	null		null	null		Unigene80806_A11//gi|15230639|ref|NP_187263.1|//4.00E-07//MUTE (MUTE); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75312289|sp|Q96886.1|MUTE_ARATH RecName: Full=Transcription factor MUTE; AltName: Full=Transcription factor EN 20; AltName: Full=bHLH transcription factor bHLH045; AltName: Full=Basic helix-loop-helix protein 45; Short=bHLH 45; Short=AtbHLH45 >gi|91806385|gb|ABE65920.1| basic helix-loop-helix family protein [Arabidopsis thaliana] >gi|113206517|gb|ABI34465.1| basic helix-loop-helix protein [Arabidopsis thaliana] >gi|114446160|gb|ABI74926.1| helix-loop-helix protein [Arabidopsis thaliana]	Unigene80806_A11//2.00E-06//AT3G06120| MUTE (MUTE); DNA binding / transcription factor	Unigene80806_A11//2.00E-115//TC169232	bHLH			nr -
Unigene8081_A11	401	2.09	0.13	2.12	1.86	0.34	1.80	1.05	1.56	1.59	-4.05E+00	4.65E-04	Down	2.54E-02	9.93E-01		-2.44E+00	5.60E-03		-4.83E-02	9.50E-01		5.68E-01	5.03E-01		5.92E-01	4.53E-01				Unigene8081_A11//5.00E-07//gi|21090134|gb|BQ402459.1|BQ402459				
Unigene80811_A11	219	3.34	3.24	6.57	4.09	0.31	8.46	0.00	0.38	0.36	-4.63E-02	9.68E-01		9.73E-01	9.57E-02		-3.70E+00	7.11E-05	Down	1.05E+00	3.23E-02		8.58E+00	3.98E-01		8.51E+00	4.01E-01								ESTscan -
Unigene8082_A11	472	1.66	0.00	1.69	2.64	2.12	0.96	2.42	0.27	0.51	-1.07E+01	1.09E-04	Down	2.55E-02	9.94E-01		-3.19E-01	6.08E-01		-1.46E+00	1.95E-02		-3.19E+00	1.96E-05	Down	-2.26E+00	3.40E-04	Down	Unigene8082_A11//gi|296084808|emb|CB127690.3|//5.00E-28//unnamed protein product [Vitis vinifera]						nr -
Unigene80827_A11	219	0.00	0.23	4.62	0.00	0.47	0.00	0.00	0.00	0.00	7.85E+00	6.08E-01		1.22E+01	1.27E-05	Up	8.88E+00	4.52E-01		null	null		null	null		null	null		Unigene80827_A11//gi|4501883|ref|NP_001604.1|//4.00E-35//actin, aortic smooth muscle [Homo sapiens] >gi|6671507|ref|NP_031418.1| actin, aortic smooth muscle [Mus musculus] >gi|78045238|ref|NP_001029674.1| actin, aortic smooth muscle [Bos taurus] >gi|110625958|ref|NP_112266.1| actin, aortic smooth muscle [Rattus norvegicus] >gi|156119362|ref|NP_001095152.1| actin, aortic smooth muscle [Oryctolagus cuniculus] >gi|197097944|ref|NP_001126814.1| actin, aortic smooth muscle [Pongo abelii] >gi|213688375|ref|NP_001135417.1| actin, aortic smooth muscle [Homo sapiens] >gi|257470979|ref|NP_001158122.1| actin, aortic smooth muscle [Sus scrofa] >gi|73996085|ref|XP_534781.2| PREDICTED: similar to Actin, aortic smooth muscle (Alpha-actin 2) [Canis familiaris] >gi|114631685|ref|XP_521550.2|	Unigene80827_A11//4.00E-34//AT3G12110| ACT11 (actin-11); structural constituent of cytoskeleton	Unigene80827_A11//4.00E-15//TC153744		ko04145|Phagosome		nr +
Unigene80832_A11	219	0.24	18.97	3.40	53.00	73.43	249.12	29.54	67.94	124.25	6.31E+00	4.57E-22	Up	3.83E+00	2.23E-03		4.70E-01	3.54E-04		2.23E+00	8.86E-137	Up	1.20E+00	2.62E-18	Up	2.07E+00	9.38E-73	Up	Unigene80832_A11//gi|297810275|ref|XP_002873021.1|//4.00E-34//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297318858|gb|EFH49280.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene80832_A11//2.00E-35//AT5G01210| transferase family protein	Unigene80832_A11//2.00E-106//DR461983				nr -
Unigene80833_A11	219	0.00	0.69	3.16	0.00	0.00	0.00	0.00	0.00	0.00	9.44E+00	2.32E-01		1.16E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene80833_A11//sp|Q16690|DUS5_HUMAN//4.00E-37//Dual specificity protein phosphatase 5 OS=Homo sapiens GN=DUSP5 PE=1 SV=2						swissprot -
Unigene80834_A11	219	0.00	25.22	14.10	0.00	0.00	0.00	0.00	0.00	0.00	1.46E+01	1.66E-31	Up	1.38E+01	4.50E-17	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene80837_A11	219	0.00	0.00	4.13	0.00	0.16	0.00	0.00	0.00	0.00	null	null		1.20E+01	4.70E-05	Up	7.30E+00	8.14E-01		null	null		null	null		null	null								ESTscan +
Unigene8084_A11	929	0.00	0.00	0.46	4.29	4.04	7.44	1.82	0.27	0.56	null	null		8.84E+00	1.36E-02		-8.64E-02	8.17E-01		7.94E-01	3.12E-04		-2.75E+00	8.02E-07	Down	-1.71E+00	2.56E-04	Down	Unigene8084_A11//gi|15223333|ref|NP_174567.1|//1.00E-105//transferase family protein [Arabidopsis thaliana] >gi|6910569|gb|AAF31274.1|AC006424_3 Highly similar to YUP8H12R.39 [Arabidopsis thaliana]	Unigene8084_A11//3.00E-102//AT1G32910| transferase family protein	Unigene8084_A11//0.00E+00//DW488553		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0003824	nr -
Unigene80841_A11	220	0.00	0.00	3.39	0.00	0.00	0.00	0.38	0.57	0.00	null	null		1.17E+01	3.25E-04	Up	null	null		null	null		5.68E-01	7.80E-01		-8.59E+00	3.54E-01		Unigene80841_A11//gi|225437539|ref|XP_002275815.1|//5.00E-24//PREDICTED: similar to 60S ribosomal protein L29 [Vitis vinifera]	Unigene80841_A11//2.00E-23//AT3G06680| 60S ribosomal protein L29 (RPL29B)	Unigene80841_A11//4.00E-37//gi|164340872|gb|EV497834.1|EV497834		ko03010|Ribosome		nr -
Unigene80849_A11	220	0.00	0.69	5.81	0.00	0.00	0.00	0.00	0.00	0.00	9.43E+00	2.32E-01		1.25E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene80849_A11//gi|225456238|ref|XP_002283171.1|//1.00E-33//PREDICTED: similar to Glutamine synthetase cytosolic isozyme 1 [Vitis vinifera] >gi|1707955|sp|P51118.1|GLNA1_VITVI RecName: Full=Glutamine synthetase cytosolic isozyme 1; AltName: Full=Glutamate--ammonia ligase >gi|1134896|emb|CAA63981.1| glutamine synthetase [Vitis vinifera]	Unigene80849_A11//3.00E-33//AT5G37600| ATGSR1; copper ion binding / glutamate-ammonia ligase	Unigene80849_A11//9.00E-41//TC129771		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene8085_A11	843	0.19	0.42	0.00	3.43	2.57	1.07	2.16	0.69	0.33	1.18E+00	3.72E-01		-7.54E+00	2.42E-01		-4.13E-01	2.79E-01		-1.68E+00	1.37E-05	Down	-1.64E+00	3.51E-04	Down	-2.70E+00	1.86E-07	Down	Unigene8085_A11//gi|10176937|dbj|BAB10136.1|//1.00E-124//serine/threonine-specific kinase like protein [Arabidopsis thaliana]	Unigene8085_A11//1.00E-125//AT5G55830| lectin protein kinase, putative	Unigene8085_A11//0.00E+00//gi|72279592|gb|DT052110.1|DT052110		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0016020//GO:0030246	nr -
Unigene80850_A11	220	0.00	0.00	3.39	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene80850_A11//gi|113473614|gb|ABI35986.1|//8.00E-37//methionine synthase [Phelipanche ramosa]	Unigene80850_A11//4.00E-36//AT3G03780| AtMS2; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase	Unigene80850_A11//7.00E-51//TC141539		ko00270|Cysteine and methionine metabolism		nr +
Unigene80858_A11	221	0.00	1.83	14.22	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	1.34E-02		1.38E+01	2.28E-17	Up	null	null		null	null		null	null		null	null		Unigene80858_A11//gi|124359683|gb|ABD32351.2|//1.00E-18//Ubiquitin [Medicago truncatula]	Unigene80858_A11//7.00E-20//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene80858_A11//6.00E-36//TC164984		ko03010|Ribosome		nr +
Unigene8086_A11	534	0.10	0.00	0.20	0.75	1.55	1.86	0.16	3.21	1.27	-6.61E+00	6.01E-01		1.02E+00	7.00E-01		1.05E+00	1.99E-01		1.32E+00	7.15E-02		4.34E+00	9.66E-10	Up	3.00E+00	2.00E-03				Unigene8086_A11//0.00E+00//TC159444				
Unigene80860_A11	221	11.13	2.98	5.06	18.71	19.01	12.47	133.92	52.76	47.41	-1.90E+00	2.20E-05	Down	-1.14E+00	8.12E-03		2.30E-02	9.50E-01		-5.86E-01	5.25E-02		-1.34E+00	2.55E-42	Down	-1.50E+00	3.21E-51	Down			Unigene80860_A11//3.00E-102//gi|21098690|gb|BQ411003.1|BQ411003				
Unigene80866_A11	221	5.21	5.27	5.30	6.31	6.70	6.74	36.16	27.61	16.76	1.79E-02	9.91E-01		2.54E-02	9.87E-01		8.62E-02	8.96E-01		9.56E-02	8.79E-01		-3.89E-01	3.84E-02		-1.11E+00	2.12E-09	Down	Unigene80866_A11//gi|226493054|ref|NP_001151067.1|//2.00E-30//LOC100284700 [Zea mays] >gi|195644058|gb|ACG41497.1| 26S proteasome non-ATPase regulatory subunit 11 [Zea mays]	Unigene80866_A11//3.00E-29//AT1G29150| ATS9 (ARABIDOPSIS NON-ATPASE SUBUNIT 9)	Unigene80866_A11//7.00E-122//ES819212		ko03050|Proteasome		nr +
Unigene8087_A11	552	1.80	0.46	0.10	0.72	0.81	3.44	0.08	0.08	2.67	-1.97E+00	9.93E-03		-4.22E+00	1.62E-04	Down	1.68E-01	9.04E-01		2.25E+00	2.85E-05	Up	-1.71E-02	9.98E-01		5.12E+00	2.34E-09	Up	Unigene8087_A11//gi|224080516|ref|XP_002306147.1|//3.00E-42//SAUR family protein [Populus trichocarpa] >gi|222849111|gb|EEE86658.1| SAUR family protein [Populus trichocarpa]	Unigene8087_A11//1.00E-36//AT4G34760| auxin-responsive family protein	Unigene8087_A11//0.00E+00//DW506611			GO:0009725	nr -
Unigene80877_A11	221	0.00	0.00	3.13	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene80877_A11//gi|115449257|ref|NP_001048408.1|//1.00E-21//Os02g0799300 [Oryza sativa Japonica Group] >gi|113537939|dbj|BAF10322.1| Os02g0799300 [Oryza sativa Japonica Group]	Unigene80877_A11//5.00E-13//AT2G12400| unknown protein					nr +
Unigene8088_A11	743	0.00	0.00	0.00	3.35	1.25	1.58	2.56	0.23	0.70	null	null		null	null		-1.42E+00	2.12E-04	Down	-1.08E+00	6.93E-03		-3.51E+00	2.32E-09	Down	-1.88E+00	2.70E-05	Down	Unigene8088_A11//gi|297600888|ref|NP_001050070.2|//8.00E-13//Os03g0341200 [Oryza sativa Japonica Group] >gi|255674489|dbj|BAF11984.2| Os03g0341200 [Oryza sativa Japonica Group]	Unigene8088_A11//5.00E-12//AT5G49110| unknown protein					nr +
Unigene80890_A11	222	0.00	4.79	6.96	0.00	0.00	0.41	0.00	0.00	0.00	1.22E+01	3.79E-06	Up	1.28E+01	1.65E-08	Up	null	null		8.67E+00	4.70E-01		null	null		null	null								ESTscan +
Unigene80894_A11	222	0.00	7.53	4.80	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	1.53E-09	Up	1.22E+01	6.59E-06	Up	null	null		null	null		null	null		null	null		Unigene80894_A11//gi|2949588|emb|CAA75514.1|//1.00E-13//Importin alpha-like protein [Arabidopsis thaliana]	Unigene80894_A11//4.00E-15//AT4G02150| MOS6 (MODIFIER OF SNC1, 6); binding / protein transporter					nr +
Unigene809_A11	1735	1.72	4.50	2.64	0.95	1.31	1.07	4.22	3.76	6.34	1.39E+00	4.42E-10	Up	6.19E-01	3.65E-02		4.67E-01	3.10E-01		1.72E-01	7.30E-01		-1.66E-01	4.48E-01		5.88E-01	8.08E-05		Unigene809_A11//gi|15146244|gb|AAK83605.1|//1.00E-155//At2g17220/T23A1.8 [Arabidopsis thaliana] >gi|23506217|gb|AAN31120.1| At2g17220/T23A1.8 [Arabidopsis thaliana]	Unigene809_A11//1.00E-152//AT2G17220| protein kinase, putative	Unigene809_A11//0.00E+00//gi|109889688|gb|DW518656.1|DW518656		ko04626|Plant-pathogen interaction		nr -
Unigene80900_A11	222	20.98	23.51	27.82	32.54	30.71	26.04	37.52	52.90	12.56	1.65E-01	5.69E-01		4.08E-01	1.10E-01		-8.32E-02	7.67E-01		-3.21E-01	1.68E-01		4.96E-01	7.84E-04		-1.58E+00	3.60E-16	Down	Unigene80900_A11//gi|3452091|emb|CAA06199.1|//5.00E-10//rudimentary enhancer [Glycine max]	Unigene80900_A11//2.00E-07//AT5G10810| ATER	Unigene80900_A11//6.00E-82//TC160037				nr -

Unigene80903_All	222	0.00	37.66	10.79	0.00	0.00	0.00	0.00	0.00	0.00	1.52E+01	7.77E-48	Up	1.34E+01	3.24E-13	Up	null	null		null	null		null	null		null	null		Unigene80903_All//gi|15229438|ref|NP_188981.1|//1.00E-26//60S ribosomal protein L36a/L44 (RPL36aA) [Arabidopsis thaliana] >gi|15236469|ref|NP_193168.1| 60S ribosomal protein L36a/L44 (RPL36aB) [Arabidopsis thaliana] >gi|297800816|ref|XP_002868292.1| 60S ribosomal protein L36a/L44 [Arabidopsis lyrata subsp. lyrata] >gi|297831094|ref|XP_002883429.1| 60S ribosomal protein L36a/L44 [Arabidopsis lyrata subsp. lyrata] >gi|3122753|sp|O23290.3|RL36A_ARATH RecName: Full=60S ribosomal protein L36a >gi|2244789|emb|CAB10211.1| ribosomal protein [Arabidopsis thaliana] >gi|7268137|emb|CAB78474.1| ribosomal protein [Arabidopsis thaliana] >gi|11994324|dbj|BAB02283.1| 60S ribosomal protein L44-like [Arabidopsis thaliana] >gi|170655558|gb|AAL32933.1| 60S ribosomal protein L44-like [Arabidopsis thaliana] >gi|17473681|gb|AAL38297.1| ribosomal protein [Arabidopsis	Unigene80903_All//6.00E-28//AT4G14320| 60S ribosomal protein L36a/L44 (RPL36aB)			ko03010|Ribosome		nr -
Unigene80904_All	222	0.00	0.68	4.08	0.67	0.00	0.00	0.00	0.00	0.00	9.42E+00	2.32E-01		1.20E+01	4.70E-05	Up	-9.39E+00	1.64E-01		-9.39E+00	2.31E-01		null	null		null	null										ESTscan -
Unigene8091_All	1077	0.29	0.47	0.40	0.65	0.61	0.84	0.24	0.23	6.07	6.91E-01	4.99E-01		4.40E-01	6.76E-01		-9.20E-02	8.94E-01		3.73E-01	6.26E-01		-1.66E-02	1.02E+00		4.69E+00	3.15E-38	Up	Unigene8091_All//gi|124359568|gb|ABD28696.2|//3.00E-66//NAD-dependent epimerase/dehydratase [Medicago truncatula]	Unigene8091_All//5.00E-39//AT1G61720| BAN (BANYULS); oxidoreductase			ko00941|Flavonoid biosynthesis	GO:0005488//GO:0008152//GO:0016616	nr +
Unigene80912_All	222	0.24	0.00	4.08	0.00	0.00	0.00	0.00	0.00	0.00	-7.88E+00	6.01E-01		4.11E+00	3.91E-04	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene80914_All	223	0.00	3.64	3.34	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	9.30E-05	Up	1.17E+01	3.25E-04	Up	null	null		null	null		null	null		null	null										
Unigene8093_All	505	1.04	0.50	0.21	1.78	0.34	0.45	4.94	8.61	22.96	-1.05E+00	3.11E-01		-2.30E+00	6.75E-02		-2.38E+00	2.29E-03		-1.99E+00	1.36E-02		8.01E-01	1.99E-03		2.22E+00	3.70E-34	Up		Unigene8093_All//4.00E-06//AT5G53560| CB5-E (CYTOCHROME B5 ISOFORM E); heme binding	Unigene8093_All//2.00E-07//BQ403624				
Unigene80936_All	223	0.00	0.23	4.54	0.00	0.00	0.00	0.00	0.00	0.00	7.83E+00	6.08E-01		1.21E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene80936_All//sp|Q14515|SPRL1_HUMAN//3.00E-41//SPARC-like protein 1 OS=Homo sapiens GN=SPARCL1 PE=1 SV=2						swissprot +
Unigene8094_All	1388	0.08	0.07	0.00	0.50	0.65	0.52	0.43	0.93	11.62	-4.67E-02	9.86E-01		-6.24E+00	3.87E-01		3.61E-01	6.55E-01		5.13E-02	9.47E-01		1.13E+00	3.49E-02		4.77E+00	1.11E-94	Up	Unigene8094_All//gi|124301028|gb|ABN04766.1|//9.00E-18//At5g01370 [Arabidopsis thaliana]	Unigene8094_All//4.00E-10//AT5G01370| unknown protein	Unigene8094_All//0.00E+00//DN817073				nr -
Unigene80942_All	224	0.00	2.71	4.52	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.16E-03		1.21E+01	1.27E-05	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene8095_All	468	2.35	6.60	9.22	2.66	1.47	0.58	4.34	6.25	2.30	1.49E+00	6.91E-05	Up	1.97E+00	7.42E-09	Up	-8.55E-01	1.47E-01		-2.20E+00	1.10E-03		5.28E-01	1.14E-01		-9.16E-01	1.86E-02		Unigene8095_All//gi|122209321|sp|Q2V3E2.1|YIPL5_ARATH//6.00E-09//RecName: Full=Protein yippee-like At4g27740	Unigene8095_All//4.00E-10//AT4G27740| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Yippee-like protein (InterPro:IPR004910); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27745.1); Has 684 Blast hits to 682 proteins in 148 species: Archae - 0; Bacteria - 0; Metazoa - 389; Fungi - 132; Plants - 111; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene8095_All//6.00E-56//DT046397				nr +
Unigene80950_All	224	0.00	0.00	4.75	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	6.59E-06	Up	null	null		null	null		null	null		null	null		Unigene80950_All//gi|297842159|ref|XP_002888961.1|//1.00E-16//60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata] >gi|297331802|gb|EFH65220.1| 60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata]	Unigene80950_All//4.00E-18//AT1G74060| 60S ribosomal protein L6 (RPL6B)			ko03010|Ribosome		nr +
Unigene80951_All	224	0.00	0.45	3.80	0.00	0.00	0.00	0.00	0.00	0.00	8.82E+00	3.80E-01		1.19E+01	8.98E-05	Up	null	null		null	null		null	null		null	null		Unigene80951_All//sp|Q7YQD7|FBLN3_MACFA//3.00E-30//EGF-containing fibulin-like extracellular matrix protein 1 OS=Macaca fascicularis GN=EFEMP1 PE=2 SV=1						swissprot -
Unigene80952_All	224	0.00	0.00	4.28	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.21E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene80952_All//gi|55734108|emb|CAF74935.1|//5.00E-19//zinc finger DNA-binding protein [Catharanthus roseus]	Unigene80952_All//4.00E-11//AT1G27730| STZ (salt tolerance zinc finger); nucleic acid binding / transcription factor/ transcription repressor/ zinc ion binding		C2H2			nr -
Unigene80966_All	225	0.00	131.52	44.26	0.00	0.00	0.00	0.00	0.00	0.00	1.70E+01	1.33E-170	Up	1.54E+01	7.07E-56	Up	null	null		null	null		null	null		null	null		Unigene80966_All//sp|P92192|LCP5_DROME//2.00E-10//Larval cuticle protein 5 OS=Drosophila melanogaster GN=Lcp65Ab1 PE=1 SV=1						swissprot +
Unigene80967_All	225	0.00	2.25	3.08	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.99E-03		1.16E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene80967_All//gi|31982030|ref|NP_598537.3|//5.00E-20//rho GDP-dissociation inhibitor 1 [Mus musculus] >gi|55742827|ref|NP_001007006.1| rho GDP-dissociation inhibitor 1 [Rattus norvegicus] >gi|21759130|sp|Q99PT1.3|GDIR1_MOUSE RecName: Full=Rho GDP-dissociation inhibitor 1; Short=Rho GDI 1; AltName: Full=Rho-GDI alpha; AltName: Full=GDI-1 >gi|81883710|sp|Q5XI73.1|GDIR1_RAT RecName: Full=Rho GDP-dissociation inhibitor 1; Short=Rho GDI 1; AltName: Full=Rho-GDI alpha >gi|12597249|dbj|BAB21527.1| RhoGDI-1 [Mus musculus] >gi|53733357|gb|AAH83817.1| Rho GDP dissociation inhibitor (GDI) alpha [Rattus norvegicus] >gi|56541074|gb|AAH86755.1| Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus] >gi|117616156|gb|ABK42096.1| Rho GDI [synthetic construct] >gi|123287571|emb|CAM27085.1| Rho GDP dissociation inhibitor (GDI) alpha [Mus musculus]	Unigene80967_All//1.00E-10//AT3G07880| Rho GDP-dissociation inhibitor family protein				GO:0005092//GO:0005515//GO:0007265//GO:0008104//GO:0010769//GO:0019222//GO:0031345//GO:0031346//GO:0043231//GO:0044444//GO:0044459	nr +
Unigene8097_All	332	3.31	1.98	5.77	3.60	0.73	2.18	0.00	0.00	0.12	-7.38E-01	2.50E-01		8.03E-01	1.02E-01		-2.31E+00	3.71E-04	Down	-7.26E-01	2.56E-01		null	null		6.91E+00	6.36E-01		Unigene8097_All//gi|223452302|gb|ACM89479.1|//1.00E-27//cysteine-rich protein [Glycine max]	Unigene8097_All//2.00E-27//AT4G23190| CRK11 (CYSTEINE-RICH RLK11); kinase/ protein kinase			ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0032559	nr -
Unigene80970_All	225	0.00	0.45	4.02	0.00	0.00	0.00	0.00	0.00	0.00	8.82E+00	3.80E-01		1.20E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene80970_All//gi|241740196|gb|ACS68205.1|//1.00E-35//ubiquitin 10.2 [Brassica napus]	Unigene80970_All//5.00E-37//AT5G03240| CBQ3 (POLYUBIQUITIN 3); protein binding	Unigene80970_All//5.00E-55//gi|84153717|gb|DN803072.1|DN803072			GO:0044424	nr -
Unigene80971_All	225	0.00	0.00	3.55	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene80971_All//gi|115452071|ref|NP_001049636.1|//4.00E-20//0s03g0263700 [Oryza sativa Japonica Group] >gi|108707318|gb|ABF95113.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|108707319|gb|ABF95114.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113548107|dbj|BAF11550.1| Os03g0263700 [Oryza sativa Japonica Group]	Unigene80971_All//5.00E-16//AT4G08230| glycine-rich protein	Unigene80971_All//2.00E-20//TC168944			GO:0043231	nr +
Unigene80975_All	225	0.00	1.13	3.08	0.00	0.00	0.00	0.00	0.00	0.00	1.01E+01	7.75E-02		1.16E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene80975_All//gi|283139170|gb|ADB12590.1|//2.00E-18//glutamine synthetase II ['Chlorella' luteoviridis]	Unigene80975_All//8.00E-19//AT3G17820| ATGSKB6; copper ion binding / glutamate-ammonia ligase			ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism	GO:0005840//GO:0006541//GO:0009536//GO:0010038//GO:0016020//GO:0016211//GO:0042126//GO:0046914//GO:0071941	nr +
Unigene80977_All	225	0.00	0.90	3.08	0.00	0.00	0.00	0.00	0.00	0.00	9.82E+00	1.34E-01		1.16E+01	6.11E-04	Up	null	null		null	null		null	null		null	null										
Unigene8098_All	329	2.86	0.62	0.65	2.88	3.35	0.00	0.64	1.78	1.57	-2.22E+00	6.64E-03		-2.14E+00	1.16E-02		2.19E-01	7.93E-01		-1.15E+01	6.01E-06	Down	1.47E+00	1.02E-01		1.29E+00	1.59E-01		Unigene8098_All//gi|75174963|sp|Q9LN35.1|PPP7L_ARATH//4.00E-11//RecName: Full=Serine/threonine-protein phosphatase 7 long form homolog >gi|8778513|gb|AAF79521.1|AC023673_9 F21D18.16 [Arabidopsis thaliana]	Unigene8098_All//4.00E-12//AT1G48120| calcineurin-like phosphoesterase family protein	Unigene8098_All//3.00E-72//C0105636				nr +
Unigene80989_All	225	0.00	0.23	3.55	0.00	0.31	0.00	0.00	0.00	0.00	7.82E+00	6.08E-01		1.18E+01	1.71E-04	Up	8.26E+00	6.01E-01		null	null		null	null		null	null		Unigene80989_All//gi|226462880|gb|EEH60158.1|//9.00E-15//glycosyltransferase family 51 protein [Micromonas pusilla CCMP1545]					GO:0016740//GO:0042546//GO:0044464	nr -
Unigene8099_All	433	1.57	0.00	0.12	2.88	1.67	0.83	1.17	0.19	0.28	-1.06E+01	4.09E-04	Down	-3.67E+00	4.81E-03		-7.84E-01	1.82E-01		-1.79E+00	5.55E-03		-2.60E+00	2.04E-02		-2.09E+00	3.64E-02			Unigene8099_All//3.00E-05//AT5G12000| kinase					
Unigene80992_All	226	0.00	0.45	3.06	0.00	0.00	0.00	0.00	0.00	0.00	8.81E+00	3.80E-01		1.16E+01	6.11E-04	Up	null	null		null	null		null	null		null	null										
Unigene80997_All	226	0.00	0.67	3.30	0.00	0.46	0.00	0.00	0.00	0.00	9.39E+00	2.32E-01		1.17E+01	3.25E-04	Up	8.84E+00	4.52E-01		null	null		null	null		null	null		Unigene80997_All//sp|O68852|NUOA1_RHIME//7.00E-07//NADH-quinone oxidoreductase subunit A 1 OS=Rhizobium meliloti GN=nuoA1 PE=3 SV=1						swissprot -

Unigene810_All	1869	16.04	5.29	13.76	5.81	6.06	3.50	3.14	1.90	1.32	-1.60E+00	2.07E-45	Down	-2.21E-01	4.08E-02		6.11E-02	8.02E-01		-7.30E-01	1.49E-05		-7.26E-01	8.42E-04		-1.25E+00	1.83E-08	Down	Unigene810_All//gi|30679784|ref|NP_195903.2|//1.00E-175//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene810_All//5.00E-169//AT5G02830| pentatricopeptide (PPR) repeat-containing protein	Unigene810_All//0.00E+00//TC159324			GO:0043231	nr +
Unigene8100_All	787	2.66	0.13	0.27	3.99	0.39	0.34	1.18	1.70	0.46	-4.37E+00	8.94E-10	Down	-3.30E+00	1.34E-07	Down	-3.34E+00	8.07E-15	Down	-3.53E+00	2.13E-13	Down	5.24E-01	3.34E-01		-1.38E+00	3.03E-02		Unigene8100_All//gi|295393250|gb|ADG03462.1|//1.00E-145//9-cis-epoxycarotenoid dioxygenase [Gossypium hirsutum]	Unigene8100_All//7.00E-116//AT3G14440| NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase	Unigene8100_All//1.00E-09//TC175846		ko00906|Carotenoid biosynthesis		nr +
Unigene81005_All	226	0.00	1.12	3.77	0.00	0.00	0.00	0.00	0.00	0.00	1.01E+01	7.75E-02		1.19E+01	8.98E-05	Up	null	null		null	null		null	null		null	null		Unigene81005_All//gi|148372347|gb|AB6B3097.1|//3.00E-18//photosystem I subunit PsaD [Glycine max]	Unigene81005_All//1.00E-07//AT1G03130| PSAD-2 (photosystem I subunit D-2)				ko00195|Photosynthesis	GO:0005488//GO:0009522//GO:0009536	nr +
Unigene81013_All	226	0.23	0.00	4.24	0.44	0.46	0.00	0.00	0.00	0.00	-7.85E+00	6.01E-01		4.20E+00	2.16E-04	Up	5.24E-02	9.65E-01		-8.78E+00	3.93E-01		null	null		null	null									ESTscan -
Unigene81014_All	226	1.39	1.35	18.14	0.00	0.00	0.40	0.00	0.00	0.00	-4.62E-02	9.84E-01		3.71E+00	4.94E-16	Up	null	null		8.64E+00	4.70E-01		null	null		null	null									
Unigene8102_All	859	0.18	0.24	0.12	5.10	2.73	1.26	1.82	0.29	0.56	3.69E-01	8.15E-01		-5.59E-01	7.74E-01		-9.05E-01	7.92E-04		-2.02E+00	2.66E-10	Down	-2.64E+00	4.08E-06	Down	-1.71E+00	4.59E-04	Down	Unigene8102_All//gi|124360549|gb|AB033126.2|//1.00E-49//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene8102_All//5.00E-31//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene8102_All//3.00E-81//gi|164305124|gb|ES808621.1|ES808621			GO:0003676//GO:0016772//GO:0044238//GO:0044260	nr -
Unigene81023_All	227	0.00	4.02	3.75	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	2.60E-05	Up	1.19E+01	8.98E-05	Up	null	null		null	null		null	null		null	null		Unigene81023_All//gi|145334857|ref|NP_001078774.1|//3.00E-18//AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase [Arabidopsis thaliana]	Unigene81023_All//1.00E-19//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase					GO:0004175//GO:0005488//GO:0009725//GO:0019538//GO:0031410//GO:0032502//GO:0043231	nr -
Unigene81024_All	227	181.62	188.62	173.12	421.77	355.88	462.97	597.70	442.26	193.93	5.45E-02	5.85E-01		-6.92E-02	4.96E-01		-2.45E-01	5.59E-07		1.35E-01	1.11E-02		-4.35E-01	4.41E-28		-1.62E+00	5.38E-261	Down	Unigene81024_All//gi|115469982|ref|NP_001058590.1|//2.00E-31//Os06g0716700 [Oryza sativa Japonica Group] >gi|113596630|dbj|BAF20504.1|Os06g0716700 [Oryza sativa Japonica Group]	Unigene81024_All//2.00E-30//AT4G24190| SHD (SHEPHERD); ATP binding / unfolded protein binding	Unigene81024_All//4.00E-123//TC164808		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005198//GO:0005515//GO:0010467//GO:0030529//GO:0031410//GO:0032559//GO:0044267//GO:0044432//GO:0050896	nr +
Unigene81027_All	227	0.00	0.00	3.28	0.00	0.00	0.20	0.00	0.00	0.00	null	null		1.17E+01	3.25E-04	Up	null	null		7.64E+00	6.83E-01		null	null		null	null		Unigene81027_All//gi|264670090|gb|ACY72335.1|//1.00E-16//hydroxyproline-rich glycoprotein [Pennisetum glaucum]					ko03040|Spliceosome	GO:0044464	nr +
Unigene81029_All	227	0.00	0.45	3.75	0.44	0.00	0.20	0.00	0.00	0.00	8.80E+00	3.80E-01		1.19E+01	8.97E-05	Up	-8.78E+00	3.08E-01		-1.14E+00	6.73E-01		null	null		null	null				Unigene81029_All//3.00E-07//gi|164342988|gb|EX167245.1|EX167245					
Unigene8103_All	849	0.06	0.00	0.00	0.18	0.24	0.11	38.15	22.69	255.08	-5.94E+00	6.01E-01		-5.94E+00	6.15E-01		4.68E-01	8.24E-01		-7.26E-01	7.13E-01		-7.49E-01	3.59E-18		2.74E+00	0.00E+00	Up	Unigene8103_All//gi|292806707|gb|ADE42483.1|//6.00E-29//proton pump interactor 1 [Solanum tuberosum]	Unigene8103_All//2.00E-14//AT4G27500| PPI1 (PROTON PUMP INTERACTOR 1); protein binding	Unigene8103_All//0.00E+00//TC131902			GO:0016020//GO:0043231	nr -
Unigene81031_All	227	0.00	0.00	4.69	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	6.59E-06	Up	null	null		null	null		null	null		null	null		Unigene81031_All//gi|11385461|gb|AG34813.1|AF243378_1//5.00E-19//glutathione S-transferase GST 23 [Glycine max]	Unigene81031_All//5.00E-14//AT5G41210| ATGSTT1 (GLUTATHIONE S-TRANSFERASE THETA 1); glutathione transferase					GO:0000394//GO:0009404//GO:0016765//GO:0042579	nr +
Unigene81032_All	227	0.00	0.00	3.99	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.20E+01	4.69E-05	Up	null	null		null	null		null	null		null	null									
Unigene81033_All	227	0.00	0.00	3.28	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene81033_All//gi|297800554|ref|XP_002868161.1|//4.00E-31//ATSEB1 [Arabidopsis lyrata subsp. lyrata] >gi|297313997|gb|EFH44420.1|ATSEB1 [Arabidopsis lyrata subsp. lyrata]	Unigene81033_All//2.00E-32//AT4G16120| COBL7 (COBRA-LIKE 7)					GO:0031225//GO:0031410//GO:0043231//GO:0048764	nr +
Unigene81039_All	228	17.44	12.22	20.32	45.88	46.67	38.43	88.64	29.88	30.23	-5.13E-01	9.59E-02		2.20E-01	4.72E-01		2.45E-02	9.13E-01		-2.56E-01	1.88E-01		-1.57E+00	1.51E-36	Down	-1.55E+00	4.27E-37	Down	Unigene81039_All//gi|233955399|gb|ACQ01203.1|//2.00E-23//calreticulin [Carica papaya]	Unigene81039_All//2.00E-19//AT1G56340| CRT1 (CALRETICULIN 1); calcium ion binding / unfolded protein binding	Unigene81039_All//1.00E-107//gi|164302378|gb|EV492007.1|EV492007		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome	GO:0005515//GO:0030246//GO:0033554//GO:0042742//GO:0044267//GO:0044432//GO:0046872	nr +
Unigene8104_All	226	15.74	8.30	8.25	28.21	21.48	20.58	49.76	19.97	18.16	-9.24E-01	4.72E-03		-9.33E-01	6.45E-03		-3.93E-01	9.17E-02		-4.55E-01	5.67E-02		-1.32E+00	4.30E-16	Down	-1.45E+00	3.53E-19	Down			Unigene8104_All//9.00E-75//TC157614					
Unigene81048_All	228	0.00	0.00	3.04	0.22	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	6.11E-04	Up	-7.77E+00	5.43E-01		-7.77E+00	6.19E-01		null	null		null	null		Unigene81048_All//gi|15235668|ref|NP_193070.1|//2.00E-29//leucine-rich repeat family protein / extensin family protein [Arabidopsis thaliana] >gi|75337952|sp|Q9T0K5.1|LRX3_ARATH RecName: Full=Leucine-rich repeat extensin-like protein 3; Short=LRR/EXTENSIN3; Short=AtLRX3; AltName: Full=Cell wall hydroxyproline-rich glycoprotein; Flags: Precursor >gi|4584539|emb|CAB40769.1|extensin-like protein [Arabidopsis thaliana] >gi|7268037|emb|CAB78376.1|extensin-like protein [Arabidopsis thaliana]				ko03040|Spliceosome	GO:0005488//GO:0005618	nr +
Unigene81049_All	228	0.00	0.67	4.67	0.00	0.00	0.00	0.00	0.00	0.00	9.38E+00	2.32E-01		1.22E+01	6.59E-06	Up	null	null		null	null		null	null		null	null		Unigene81049_All//gi|255593650|ref|XP_002535920.1|//2.00E-12//alpha-amylase, putative [Ricinus communis] >gi|223521525|gb|EEF26463.1|alpha-amylase, putative [Ricinus communis]						GO:0003824	nr +
Unigene81050_All	228	0.00	0.00	3.27	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene81050_All//gi|75323091|sp|Q6AV21.1|Y3982_ORYSJ//4.00E-07//RecName: Full=B3 domain-containing protein Os03g0619825 >gi|108709865|gb|ABF97660.1|B3 DNA binding domain containing protein, expressed [Oryza sativa (japonica cultivar-group)]	Unigene81050_All//5.00E-07//AT4G33280| DNA binding / transcription factor		ABI3VP1			GO:0006350	nr -
Unigene81055_All	228	0.00	0.00	3.04	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene81055_All//gi|1009363|dbj|BAA11089.1|//7.00E-10//RGP-3 [Nicotiana sylvestris]	Unigene81055_All//8.00E-08//AT4G13850| GR-RBP2 (GLYCINE-RICH RNA-BINDING PROTEIN 2); ATP binding / RNA binding / double-stranded DNA binding / single-stranded DNA binding					GO:0006950//GO:0032501//GO:0032559//GO:0043231//GO:0043566//GO:0046914	nr +
Unigene81058_All	228	0.00	0.00	8.64	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.31E+01	7.44E-11	Up	null	null		null	null		null	null		null	null		Unigene81058_All//gi|116743285|emb|CAJ41420.1|//2.00E-20//4-coumarate-CoA ligase-like protein [Coffea arabica]	Unigene81058_All//2.00E-14//AT3G48990| AMP-dependent synthetase and ligase family protein					GO:0003824//GO:0005576//GO:0009536//GO:0010038//GO:0032559	nr -
Unigene81059_All	228	0.00	0.67	3.04	0.00	0.00	0.00	0.00	0.00	0.00	9.38E+00	2.32E-01		1.16E+01	6.11E-04	Up	null	null		null	null		null	null		null	null									
Unigene81061_All	228	0.00	0.22	3.27	0.00	0.00	0.40	0.00	0.18	0.00	7.80E+00	6.08E-01		1.17E+01	3.25E-04	Up	null	null		8.63E+00	4.70E-01		7.52E+00	6.23E-01		null	null									ESTscan -
Unigene81062_All	228	0.00	1.33	3.27	0.00	0.00	0.00	0.00	0.00	0.00	1.04E+01	4.36E-02		1.17E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene81062_All//gi|224011098|ref|XP_002294506.1|//8.00E-06//hypothetical protein THAPSDRAFT_264461 [Thalassiosira pseudonana CCMP1335] >gi|220970001|gb|EED88340.1|hypothetical protein THAPSDRAFT_264461 [Thalassiosira pseudonana CCMP1335]						GO:0004175//GO:0019538	nr +
Unigene81063_All	228	0.23	0.00	5.14	1.53	0.60	0.00	0.93	0.92	0.00	-7.84E+00	6.01E-01		4.48E+00	1.90E-05	Up	-1.34E+00	3.08E-01		-1.06E+01	2.12E-02		-1.66E-02	1.02E+00		-9.86E+00	5.78E-02		Unigene81063_All//gi|297610554|ref|NP_001064695.2|//1.00E-17//Os10g0442100 [Oryza sativa Japonica Group] >gi|255679441|dbj|BAF26609.2|Os10g0442100 [Oryza sativa Japonica Group]						GO:0006607//GO:0008033//GO:0016301//GO:0016423//GO:0043231	nr -
Unigene8107_All	262	9.98	1.74	5.49	12.74	15.38	12.41	0.81	0.16	0.91	-2.52E+00	1.03E-07	Down	-8.64E-01	3.52E-02		2.72E-01	4.26E-01		-3.76E-02	9.33E-01		-2.34E+00	2.36E-01		1.77E-01	9.08E-01		Unigene8107_All//gi|255578815|ref|XP_002530264.1|//2.00E-06//hypothetical protein RCOM_0075880 [Ricinus communis] >gi|223530230|gb|EEF32134.1|hypothetical protein RCOM_0075880 [Ricinus communis]		Unigene8107_All//9.00E-97//gi|78348108|gb|DT568382.1|DT568382				nr -
Unigene81070_All	229	90.02	47.35	28.14	183.81	132.78	189.92	129.98	93.99	81.76	-9.27E-01	9.79E-14		-1.68E+00	2.85E-32	Down	-4.69E-01	3.50E-10		4.72E-02	6.47E-01		-4.68E-01	1.12E-07		-6.69E-01	2.57E-14		Unigene81070_All//gi|224087993|ref|XP_002308283.1|//1.00E-31//nucleosome/chromatin assembly factor group [Populus trichocarpa] >gi|222854259|gb|EEE91806.1|nucleosome/chromatin assembly factor group [Populus trichocarpa]	Unigene81070_All//2.00E-14//AT5G56950| NAP1;3 (NUCLEOSOME ASSEMBLY PROTEIN 1;3); DNA binding	Unigene81070_All//1.00E-55//TC149370			GO:0006259//GO:0009292//GO:0034728//GO:0043231	nr -
Unigene81076_All	229	0.00	2.21	3.02	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.99E-03		1.16E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene81076_All//sp|Q27415|NLP_DROME//3.00E-10//Nucleoplasmin-like protein OS=Drosophila melanogaster GN=Npp PE=1 SV=1						swissprot -
Unigene8108_All	741	0.14	0.00	0.14	0.40	0.84	0.91	2.45	3.05	6.94	-7.14E+00	3.66E-01		2.53E-02	9.97E-01		1.05E+00	2.99E-01		1.18E+00	2.08E-01		3.12E-01	4.42E-01		1.50E+00	1.62E-09	Up								
Unigene81088_All	229	0.00	2.66	3.49	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.16E-03		1.18E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene81088_All//gi|124359392|gb|ABN08586.1|//1.00E-08//KH, type 1 [Medicago truncatula]						nr -
Unigene81095_All	229	0.23	0.22	8.14	0.22	0.30	0.00	0.00	0.00	0.00	-4.62E-02	9.82E-01		5.15E+00	4.94E-09	Up	4.67E-01	9.53E-01		-7.76E+00	6.19E-01		null	null		null	null									ESTscan +
Unigene81096_All	229	0.00	0.00	4.19	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.20E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene81096_All//gi|192912978|gb|ACF96597.1|//4.00E-18//60S ribosomal protein L7-like protein [Elaeis guineensis]	Unigene81096_All//1.00E-13//AT1G80750| 60S ribosomal protein L7 (RPL7A)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene81099_All	229	0.00	9.07	4.42	0.00	0.00	0.00	0.00	0.00	0.00	1.31E+01	7.93E-12	Up	1.21E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene81099_All//gi|86562730|gb|ABD04712.1|//2.00E-10//actin [Symbiodinium sp. clade C]	Unigene81099_All//4.00E-07//AT5G09370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene81099_All//1.00E-12//TC153744		ko04145|Phagosome		nr +
Unigene811_All	4155	11.81	5.20	9.62	8.30	8.01	8.22	4.58	2.94	2.26	-1.19E+00	5.83E-47	Down	-2.95E-01	1.78E-04		-5.14E-02	6.48E-01		-1.38E-02	9.19E-01		-6.41E-01	1.46E-08		-1.02E+00	1.76E-18	Down	Unigene811_All//gi|30679784|ref|NP_195903.2|//0.00E+00//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene811_All//0.00E+00//AT5G02830| pentatricopeptide (PPR) repeat-containing protein	Unigene811_All//0.00E+00//TC159324			GO:0001708//GO:0003916//GO:0005515//GO:0006259//GO:0032559//GO:0043231//GO:0043232	nr +
Unigene81103_All	229	0.00	2.21	6.05	0.00	0.60	0.39	0.00	0.00	0.87	1.11E+01	3.99E-03		1.26E+01	1.23E-07	Up	9.23E+00	3.16E-01		8.62E+00	4.70E-01		null	null		9.76E+00	7.88E-02									
Unigene81107_All	230	0.00	0.00	4.86	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene81107_All//gi|4098248|gb|AAD00254.1|//2.00E-26//cold inducible; similar to other osmotic stress induced gene products including: Tomato abscisic stress ripening protein 1 encoded by GenBank Accession Number L08255, Solanum lycopersicum ABA- and ripening-induced protein encoded by GenBank Accession Number L20756 and to Solanum chacoense abscisic stress ripening protein encoded by GenBank Accession Number U12439 [Solanum tuberosum]						GO:0050896	nr -
Unigene81109_All	230	170.16	263.26	277.83	114.14	305.58	276.67	179.05	196.26	186.72	6.30E-01	3.37E-20		7.07E-01	4.42E-25		1.42E+00	3.71E-104	Up	1.28E+00	5.97E-73	Up	1.32E-01	8.88E-02		6.05E-02	4.78E-01				Unigene81109_All//4.00E-77//TC176132					

Unigene81112_All	230	0.00	0.66	3.47	0.00	0.00	0.00	0.00	0.00	0.00	9.37E+00	2.32E-01		1.18E+01	1.71E-04	Up	null	null		null	null		null	null		null	null					Unigene81122_All//1.00E-43//gi|13355812|gb|BG446160.1|BG446160				
Unigene81122_All	230	24.57	14.98	10.42	28.59	18.57	23.37	68.75	29.80	30.31	-7.14E-01	4.19E-03		-1.24E+00	3.99E-06	Down	-6.23E-01	3.88E-03		-2.91E-01	2.42E-01		-1.21E+00	1.53E-19	Down	-1.18E+00	1.56E-19	Down									
Unigene81135_All	230	0.00	7.49	5.79	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	7.96E-10	Up	1.25E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene81135_All//gi|10802913|gb|AAG23661.1|AF288091_6//8.00E-06//NADH dehydrogenase subunit 2 [Thrausotochytrium aureum]						nr -
Unigene8114_All	444	190.90	225.39	178.82	122.63	181.33	193.37	79.04	40.67	35.17	2.40E-01	3.86E-06		-9.43E-02	1.49E-01		5.64E-01	6.65E-26		6.57E-01	1.15E-32		-9.59E-01	1.95E-29		-1.17E+00	1.61E-41	Down	Unigene8114_All//gi|211906442|gb|AGJ11714.1//3.00E-21//Myo-inositol-1-phosphate synthase [Gossypium hirsutum]	Unigene8114_All//2.00E-21//AT2G22240| MIPS2 (MYO-INOSITOL-1-PHOSPHATE SYNTHASE 2); binding / catalytic/ inositol-3-phosphate synthase	Unigene8114_All//0.00E+00//TC176734		ko00562|Inositol phosphate metabolism	GO:0006020//GO:0006644//GO:0016872//GO:0044424	nr +
Unigene81152_All	231	0.00	0.44	5.30	0.00	0.00	0.00	0.00	0.00	0.00	8.78E+00	3.79E-01		1.24E+01	9.09E-07	Up	null	null		null	null		null	null		null	null		Unigene81152_All//gi|18404500|ref|NP_566763.1|//6.00E-09//auxin-responsive family protein [Arabidopsis thaliana] >gi|79313415|ref|NP_001030764.1| auxin-responsive family protein [Arabidopsis thaliana] >gi|16323200|gb|AAL15334.1| AT3g25290/MJL12_25 [Arabidopsis thaliana] >gi|25090093|gb|AAN72226.1| At3g25290/MJL12_25 [Arabidopsis thaliana]	Unigene81152_All//7.00E-07//AT3G25290| auxin-responsive family protein				GO:0016020//GO:0016491	nr +
Unigene8116_All	254	0.41	3.79	2.10	0.98	0.95	3.20	1.66	4.77	1.41	3.20E+00	6.55E-04	Up	2.35E+00	5.86E-02		-4.73E-02	9.51E-01		1.71E+00	4.57E-02		1.52E+00	8.16E-03		-2.38E-01	7.88E-01		Unigene8116_All//gi|67003913|gb|AAY60846.1|//2.00E-10//cellulose synthase 4 [Eucalyptus grandis]	Unigene8116_All//7.00E-11//AT5G05170| CEV1 (CONSTITUTIVE EXPRESSION OF VSP 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene8116_All//2.00E-97//ES804692			GO:0009987//GO:0016020//GO:0016757//GO:0046872	nr +
Unigene81166_All	232	1.13	1.09	3.90	2.58	1.78	0.78	6.01	3.60	1.55	-4.63E-02	9.86E-01		1.79E+00	3.07E-02		-5.33E-01	5.61E-01		-1.73E+00	9.03E-02		-7.39E-01	1.46E-01		-1.96E+00	2.74E-04	Down			Unigene81166_All//3.00E-44//CO132767				
Unigene8117_All	522	0.80	0.39	0.00	2.00	1.65	0.09	2.02	1.44	0.61	-1.05E+00	3.63E-01		-9.65E+00	1.55E-02		-2.81E-01	6.74E-01		-4.53E+00	1.60E-05	Down	-4.91E-01	4.22E-01		-1.73E+00	4.76E-03				Unigene8117_All//2.00E-167//TC173076				
Unigene8187_All	233	0.00	1.09	3.20	0.00	0.00	0.00	0.00	0.00	0.00	1.01E+01	7.75E-02		1.16E+01	3.25E-04	Up	null	null		null	null		null	null		null	null									
Unigene81189_All	233	0.00	0.00	2.97	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	6.11E-04	Up	null	null		null	null		null	null		null	null									
Unigene8119_All	332	9.61	31.44	19.09	8.10	25.72	16.05	21.78	26.06	26.16	1.71E+00	1.12E-17	Up	9.90E-01	5.69E-05		1.67E+00	4.32E-16	Up	9.86E-01	1.28E-04		2.59E-01	1.70E-01		2.65E-01	1.39E-01		Unigene8119_All//gi|15450373|gb|AAK96480.1|//3.00E-12//AT4g32480/F8B4_180 [Arabidopsis thaliana] >gi|16974485|gb|AAL31246.1| AT4g32480/F8B4_180 [Arabidopsis thaliana]	Unigene8119_All//1.00E-13//AT4G32480| unknown protein	Unigene8119_All//2.00E-141//gi|109878149|gb|DW507122.1|DW507122				nr +
Unigene81195_All	233	0.67	2.61	10.51	0.86	0.30	0.00	0.00	0.00	0.00	1.95E+00	6.03E-02		3.96E+00	3.40E-10	Up	-1.53E+00	4.14E-01		-9.74E+00	1.32E-01		null	null		null	null										
Unigene8120_All	2167	0.00	0.00	0.00	0.00	0.00	0.04	18.95	1.66	15.17	null	null		null	null		null	null		5.38E+00	4.70E-01		-3.51E+00	5.64E-191	Down	-3.21E-01	1.04E-05		Unigene8120_All//gi|18400335|ref|NP_566554.1|//0.00E+00//sks16 (SKU5 Similar 16); copper ion binding / pectinesterase [Arabidopsis thaliana]	Unigene8120_All//0.00E+00//AT2G22630| sks16 (SKU5 Similar 16); copper ion binding / pectinesterase	Unigene8120_All//4.00E-11//ES840146		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0004091//GO:0005618//GO:0008152//GO:0016682//GO:0031410//GO:0046914	nr -
Unigene81205_All	233	10.10	155.71	15.77	10.90	27.34	70.56	21.59	97.58	100.37	3.95E+00	2.88E-150	Up	6.42E-01	5.57E-02		1.33E+00	8.45E-09	Up	2.69E+00	2.11E-51	Up	2.18E+00	1.71E-63	Up	2.22E+00	4.09E-68	Up			Unigene81205_All//1.00E-83//TC173901				
Unigene8121_All	450	0.47	4.05	2.96	4.10	4.21	6.02	0.75	0.19	0.27	3.12E+00	1.05E-06	Up	2.67E+00	3.01E-04	Up	3.93E-02	9.62E-01		5.56E-01	1.65E-01		-2.02E+00	1.36E-01		-1.50E+00	2.10E-01				Unigene8121_All//5.00E-07//DN817576				
Unigene8214_All	233	0.00	1.09	3.20	0.00	0.00	0.00	0.00	0.00	0.00	1.01E+01	7.75E-02		1.16E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene81214_All//gi|125540403|gb|EAY86798.1|//1.00E-25//hypothetical protein OsI_08175 [Oryza sativa Indica Group]						nr -
Unigene8122_All	478	1.64	3.71	0.00	3.33	2.74	0.47	0.00	0.00	0.08	1.18E+00	1.88E-02		-1.07E+01	2.21E-04	Down	-2.85E-01	6.00E-01		-2.82E+00	8.55E-06	Down	null	null		6.38E+00	6.36E-01				Unigene8122_All//0.00E+00//ES841525				ESTscan +
Unigene81220_All	234	0.00	0.00	3.87	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.19E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene81220_All//gi|60459377|gb|AAX20034.1|//6.00E-06//ethylene responsive element binding protein C1 [Capsicum annuum]					GO:0006350//GO:0010468//GO:0043231	nr -
Unigene8123_All	370	2.26	2.19	0.14	1.62	1.12	2.32	0.34	0.90	0.32	-4.63E-02	9.64E-01		-3.97E+00	9.08E-04	Down	-5.33E-01	5.61E-01		5.22E-01	5.23E-01		1.40E+00	2.76E-01		-8.58E-02	9.68E-01		Unigene8123_All//gi|75169752|sp|Q9C9A6.1|PM12_ARATH//7.00E-10//RecName: Full=Protein PLASTID MOVEMENT IMPAIRED 2	Unigene8123_All//3.00E-11//AT1G66840| INVOLVED IN: biological_process unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF827, plant (InterPro:IPR006545); BEST Arabidopsis thaliana protein match is: PM115 (plastid movement impaired 15) (TAIR:AT5G38150.1); Hms 66436 Blast hits to 37670 proteins in 1596 species: Archae - 890; Bacteria - 7464; Metazoa - 33216; Fungi - 4897; Plants - 2570; Viruses - 192; Other Eukaryotes - 17207 (source: NCBI BLink).					nr +
Unigene81234_All	234	0.00	0.00	4.32	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.21E+01	1.27E-05	Up	null	null		null	null		null	null		null	null										
Unigene8124_All	429	0.00	0.00	0.12	0.46	1.04	0.11	2.27	0.39	3.90	null	null		6.96E+00	6.24E-01		1.17E+00	3.47E-01		-2.14E+00	3.46E-01		-2.54E+00	6.41E-04	Down	7.83E-01	7.41E-02										
Unigene81243_All	234	0.00	0.43	3.41	0.21	0.29	0.39	0.00	0.00	0.00	8.76E+00	3.79E-01		1.17E+01	1.71E-04	Up	4.67E-01	9.53E-01		8.58E-01	7.91E-01		null	null		null	null				Unigene81243_All//2.00E-110//TC141225				
Unigene81245_All	235	0.00	2.37	4.31	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.16E-03		1.21E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene81245_All//sp|P28175|LFC_TACTR//2.00E-07//Limulus clotting factor C 65-Tachypleus tridentatus PE-1 SV=1						swissprot +
Unigene81248_All	235	3.56	6.90	15.18	0.00	0.15	0.00	0.00	0.00	0.00	9.54E-01	6.65E-02		2.09E+00	5.83E-08	Up	7.19E+00	8.14E-01		null	null		null	null		null	null				Unigene81248_All//3.00E-10//TC134181				
Unigene8125_All	1191	0.00	0.21	0.00	0.00	0.14	0.00	17.57	3.93	7.19	7.73E+00	7.75E-02		null	null		7.18E+00	2.26E-01		null	null		-2.16E+00	3.90E-58	Down	-1.29E+00	3.43E-29	Down	Unigene8125_All//gi|28629828|gb|AAD45182.1|//1.00E-110//peroxidase 1 [Artemisia annua]	Unigene8125_All//3.00E-108//AT5G14130| peroxidase, putative	Unigene8125_All//7.00E-27//TC176098		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene8126_All	746	0.14	1.77	0.57	7.61	9.65	9.69	59.79	54.07	25.21	3.65E+00	1.28E-05	Up	2.03E+00	1.39E-01		3.42E-01	1.35E-01		3.48E-01	1.32E-01		-1.45E-01	6.00E-02		-1.25E+00	4.09E-58	Down	Unigene8126_All//gi|224111880|ref|XP_002316010.1|//8.00E-71//cytochrome P450 [Populus trichocarpa] >gi|222865050|gb|EEF02181.1| cytochrome P450 [Populus trichocarpa]	Unigene8126_All//2.00E-33//AT3G14690| CYP72A15; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene8126_All//0.00E+00//TC154355		ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism//ko00906|Carotenoid biosynthesis	GO:0005506//GO:0016491	nr +
Unigene8128_All	780	0.54	0.52	0.27	3.58	2.65	1.39	1.95	0.27	2.15	-4.62E-02	9.80E-01		-9.74E-01	4.11E-01		-4.33E-01	2.62E-01		-1.36E+00	3.51E-04	Down	-2.86E+00	1.98E-06	Down	1.37E-01	7.54E-01		Unigene8128_All//gi|186524238|ref|NP_197443.3|//1.00E-96//Ran GTPase binding / chromatin binding / zinc ion binding [Arabidopsis thaliana]	Unigene8128_All//3.00E-77//AT5G19420| Ran GTPase binding / chromatin binding / zinc ion binding	Unigene8128_All//3.00E-90//ES832850			GO:0046914	nr +
Unigene81289_All	237	0.00	0.00	2.92	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene81289_All//gi|20269051|emb|CAC84706.1|//2.00E-38//aux/IAA protein [Populus tremula x Populus tremuloides]	Unigene81289_All//3.00E-34//AT2G22670| IAA8; transcription factor	Unigene81289_All//2.00E-38//TC155669			GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr -
Unigene8129_All	382	29.31	35.68	54.64	98.19	90.87	140.10	212.62	299.03	445.32	2.84E-01	7.31E-02		8.99E-01	1.12E-12		-1.12E-01	2.67E-01		5.13E-01	2.15E-13		4.92E-01	1.20E-29		1.07E+00	8.35E-170	Up	Unigene8129_All//gi|16118825|gb|AAL14614.1|AF417109_1//2.00E-09//cysteine proteinase precursor [Vasconcellea cundinamarcensis]		Unigene8129_All//1.00E-127//EX165735			GO:0008152//GO:0016491//GO:0070011	nr -
Unigene81297_All	237	0.00	0.21	3.59	0.00	0.00	0.00	0.00	0.00	0.00	7.74E+00	6.08E-01		1.18E+01	8.97E-05	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene8130_All	1036	1.52	1.12	1.23	0.58	0.40	0.09	12.73	12.87	2.58	-4.30E-01	4.03E-01		-2.97E-01	6.10E-01		-5.33E-01	5.61E-01		-2.73E+00	1.74E-02		1.54E-02	9.44E-01		-2.31E+00	3.26E-41	Down	Unigene8130_All//gi|82697949|gb|ABB89009.1|//1.00E-101//CXE carboxylesterase [Malus pumila]	Unigene8130_All//1.00E-95//AT5G06570| hydrolase	Unigene8130_All//0.00E+00//TC170827			GO:0016787	nr -
Unigene81300_All	237	5.52	0.00	2.70	0.00	0.00	0.38	0.00	0.00	0.00	-1.24E+01	1.28E-07	Down	-1.03E+00	9.64E-02		null	null		8.57E+00	4.70E-01		null	null		null	null		Unigene81300_All//gi|224074159|ref|XP_002304279.1|//8.00E-08//mtn21-like protein [Populus trichocarpa] >gi|222841711|gb|EEE79258.1| mtn21-like protein [Populus trichocarpa]	Unigene81300_All//3.00E-09//AT5G47470| nodulin MtN21 family protein	Unigene81300_All//1.00E-43//gi|78346821|gb|DT567095.1|DT567095			GO:0044464	nr +
Unigene81302_All	237	0.00	0.00	3.59	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	8.97E-05	Up	null	null		null	null		null	null		null	null										
Unigene81304_All	237	0.00	5.77	1.80	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	7.77E-08	Up	1.08E+01	1.36E-02		null	null		null	null		null	null		null	null		Unigene81304_All//gi|115469028|ref|NP_001058113.1|//4.00E-11//Os06g0625500 [Oryza sativa Japonica Group] >gi|75119143|sp|Q69TY4.1|PR2E1_ORYSJ RecName: Full=Peroxiredoxin-2E-1, chloroplastic; AltName: Full=Peroxiredoxin 11E-1; AltName: Full=Thioredoxin reductase 2E-1; Flags: Precursor >gi|113596153|db|BAF20027.1| Os06g0625500 [Oryza sativa Japonica Group]	Unigene81304_All//3.00E-09//AT3G52960| peroxiredoxin type 2, putative			ko04146|Peroxisome	GO:0043231	nr -
Unigene81307_All	237	0.00	0.00	2.92	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene81307_All//gi|297829002|ref|XP_002882383.1|//2.00E-24//40S ribosomal protein S24 [Arabidopsis lyrata subsp. lyrata] >gi|297328223|gb|EFH58642.1| 40S ribosomal protein S24 [Arabidopsis lyrata subsp. lyrata]	Unigene81307_All//7.00E-26//AT3G04920| 40S ribosomal protein S24 (RPS24A)	Unigene81307_All//7.00E-48//gi|3326358|gb|AI055244.1|AI055244		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015935//GO:0016020//GO:0022613//GO:0030312//GO:0031981	nr +
Unigene81308_All	237	0.00	0.00	3.37	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene81308_All//gi|297800202|ref|XP_002867985.1|//3.00E-14//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313821|gb|EFH44244.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene81308_All//9.00E-15//AT4G18550| lipase class 3 family protein	Unigene81308_All//2.00E-131//TC160866			GO:0004091//GO:0044238	nr -
Unigene81310_All	238	0.00	2.55	4.70	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.16E-03		1.22E+01	3.42E-06	Up	null	null		null	null		null	null		null	null										
Unigene81316_All	238	0.00	1.49	3.36	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	2.43E-02		1.17E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene81316_All//gi|301119397|ref|XP_002907426.1|//2.00E-23//T-complex protein 1 subunit zeta [Phytophthora infestans T30-4] >gi|262105938|gb|EEY63990.1| T-complex protein 1 subunit zeta [Phytophthora infestans T30-4]	Unigene81316_All//4.00E-21//AT3G02530| chaperonin, putative				GO:0005515//GO:0010038//GO:0032559//GO:0044267//GO:0044424	nr -
Unigene81318_All	238	0.00	0.21	4.03	0.21	0.14	0.57	0.53	0.00	0.00	7.73E+00	6.08E-01		1.20E+01	2.45E-05	Up	-5.33E-01	8.19E-01		1.44E+00	6.36E-01		-9.06E+00	2.34E-01		-9.06E+00	1.98E-01				Unigene81318_All//1.00E-34//gi|3325905|gb|AI054791.1|AI054791				
Unigene81323_All	238	0.00	1.49	4.03	0.84	0.00	0.00	0.00	0.00	0.00	1.05E+01	2.43E-02		1.20E+01	2.45E-05	Up	-9.71E+00	8.38E-02		-9.71E+00	1.32E-01		null	null		null	null										ESTscan -
Unigene8133_All	388	9.84	0.26	6.45	4.62	3.73	1.05	0.11	0.00	0.21	-5.24E+00	3.06E-19	Down	-6.10E-01	6.42E-02		-3.10E-01	5.39E-01		-2.14E+00	6.96E-05	Down	-6.77E+00	6.43E-01		9.14E-01	7.47E-01										
Unigene81332_All	239	0.00	0.00	5.79	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.25E+01	1.23E-07	Up	null	null		null	null		null	null		null	null										
Unigene81334_All	239	5.25	1.06	3.34	2.71	5.62	3.59	6.55	17.14	4.17	-2.31E+00	9.22E-04	Down	-6.53E-01	3.04E-01		1.05E+00	7.54E-02		4.06E-01	6.40E-01		1.39E+00	8.17E-07	Up	-6.51E-01	1.52E-01				Unigene81334_All//3.00E-41//gi|109844386|gb|DW242944.1|DW242944				
Unigene81337_All	239	0.00	33.71	7.80	0.00	0.00	0.00	0.00	0.00	0.00	1.50E+01	4.38E-46	Up	1.29E+01	2.89E-10	Up	null	null		null	null		null	null		null	null		Unigene81337_All//gi|27923850|sp|Q9SM12.1|RS21_CYAPA//3.00E-17//RecName: Full=40S ribosomal protein S21 >gi|6012958|emb|CAB57312.1| 40S ribosomal protein S21 [Cyanophora paradoxa]	Unigene81337_All//2.00E-15//AT3G53890| 40S ribosomal protein S21 (RPS21B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0022613//GO:0031410	nr -

Unigene8134_All	475	0.22	9.60	1.35	0.84	0.44	1.05	5.96	25.87	54.68	5.45E+00	5.30E-23	Up	2.61E+00	2.33E-02		-9.48E-01	4.20E-01		3.18E-01	7.57E-01		2.12E+00	1.77E-33	Up	3.20E+00	1.27E-112	Up	Unigene8134_All//gi|12003390|gb|AAG43552.1|AF211534.1//3.00E-09//Avr9/Cf-9 rapidly elicited protein 169 [Nicotiana tabacum]	Unigene8134_All//9.00E-09//ATG78410| VQ motif-containing protein	Unigene8134_All//0.00E+00//gi|21092608|gb|BQ404921.1|BQ404921				nr +
Unigene81348_All	239	0.00	9.12	4.01	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	2.11E-12	Up	1.20E+01	2.45E-05	Up	null	null		null	null		null	null		null	null		Unigene81348_All//sp|Q9I7U4|TITIN_DROME//6.00E-32//Titin OS=Drosophila melanogaster GN=sls PE=1 SV=3						swissprot -
Unigene81353_All	239	0.00	1.70	2.90	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	1.34E-02		1.15E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene81353_All//sp|P07737|PROF1_HUMAN//2.00E-40//Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2						swissprot -
Unigene8136_All	566	3.79	0.72	1.51	5.37	4.81	1.84	1.05	1.40	0.42	-2.40E+00	3.76E-06	Down	-1.33E+00	4.79E-03		-1.60E-01	6.86E-01		-1.55E+00	2.75E-05	Down	4.24E-01	5.77E-01		-1.31E+00	1.15E-01				Unigene8136_All//7.00E-07//ES835049				
Unigene81364_All	240	0.00	0.00	3.77	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.19E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene81364_All//gi|223452077|gb|ACM89457.1|//8.00E-14//jasmonate ZIM domain 1 [Catharanthus roseus]	Unigene81364_All//6.00E-08//ATIG19180| JAZ1 (JASMONATE-ZIM-DOMAIN PROTEIN 1); protein binding	Unigene81364_All//3.00E-16//TC178533	Tify	ko04626|Plant-pathogen interaction		nr -
Unigene81365_All	240	0.00	0.84	3.55	0.21	0.29	0.00	0.00	0.00	0.00	9.72E+00	1.34E-01		1.18E+01	8.97E-05	Up	4.67E-01	9.53E-01		-7.70E+00	6.18E-01		null	null		null	null		Unigene81365_All//COG0491//3.00E-07//Zn-dependent hydrolases, including glyoxylases						cog -
Unigene81366_All	240	0.00	3.38	4.22	0.00	0.29	0.00	0.00	0.00	0.00	1.17E+01	9.30E-05	Up	1.20E+01	1.27E-05	Up	8.16E+00	6.00E-01		null	null		null	null		null	null		Unigene81366_All//gi|157093371|gb|ABV22340.1|//1.00E-11//calponin domain-containing protein [Noctiluca scintillans]						nr -
Unigene81370_All	240	0.00	0.00	3.11	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	3.25E-04	Up	null	null		null	null		null	null		null	null									
Unigene81373_All	240	0.00	1.06	4.22	0.00	0.00	0.00	0.00	0.00	0.00	1.00E+01	7.75E-02		1.20E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene81373_All//gi|125656346|gb|ABV48563.1|//6.00E-24//chloroplast PSI type III chlorophyll a/b-binding protein [Brassica juncea]	Unigene81373_All//3.00E-25//ATIG61520| LHCA3; chlorophyll binding	Unigene81373_All//1.00E-12//gi|48744297|gb|C0074816.1|C0074816		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0006164//GO:0009521//GO:0009534//GO:0009570//GO:0031221//GO:0043169//GO:0046906	nr +
Unigene81381_All	241	0.00	148.01	68.27	0.00	0.00	0.00	0.00	0.00	0.00	1.72E+01	8.25E-206	Up	1.61E+01	7.88E-93	Up	null	null		null	null		null	null		null	null		Unigene81381_All//sp|Q24388|LSP2_DROME//7.00E-23//Larval serum protein 2 OS=Drosophila melanogaster GN=Lsp2 PE=1 SV=2						swissprot -
Unigene81386_All	241	0.00	0.63	3.31	0.00	0.00	0.00	0.00	0.00	0.00	9.30E+00	2.32E-01		1.17E+01	1.71E-04	Up	null	null		null	null		null	null		null	null									
Unigene8139_All	380	0.96	1.07	0.56	1.97	1.99	0.00	2.67	2.20	1.05	1.46E-01	8.98E-01		-7.82E-01	5.53E-01		1.98E-02	1.00E+00		-1.09E+01	9.80E-05	Down	-2.80E-01	6.37E-01		-1.35E+00	2.50E-02									
Unigene81397_All	241	0.00	3.78	1.99	0.21	0.14	0.00	0.70	0.17	0.83	1.19E+01	2.60E-05	Up	1.10E+01	7.40E-03		-5.33E-01	8.19E-01		-7.69E+00	6.18E-01		-2.02E+00	3.66E-01		2.36E-01	8.83E-01				Unigene81397_All//2.00E-94//TC132245				
Unigene81398_All	241	0.00	0.00	3.09	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene81398_All//gi|225431427|ref|XP_002280084.1|//7.00E-28//PREDICTED: similar to FZD10.18 [Vitis vinifera]	Unigene81398_All//2.00E-22//ATIG20696| HMGB3 (HIGH MOBILITY GROUP B 3); DNA binding / chromatin binding / structural constituent of chromatin / transcription factor	Unigene81398_All//7.00E-14//gi|72269135|gb|DT047006.1|DT047006		ko03410|Base excision repair	GO:0003676//GO:0005198//GO:0006325//GO:0043231//GO:0044427	nr +
Unigene814_All	1560	12.74	14.16	15.12	16.38	13.91	8.14	21.14	7.61	6.13	1.52E-01	2.30E-01		2.47E-01	4.45E-02		-2.36E-01	2.92E-02		-1.01E+00	1.02E-20	Down	-1.47E+00	4.90E-54	Down	-1.79E+00	3.70E-73	Down	Unigene814_All//gi|159895663|gb|AB|X10442.1|//0.00E+00//squalene synthase 2 [Gossypium hirsutum]	Unigene814_All//0.00E+00//AT4G3464|0| SQS1 (SQUALENE SYNTHASE 1); farnesyl-diphosphate farnesyltransferase	Unigene814_All//0.00E+00//TC129891		ko00100|Steroid biosynthesis	GO:0004311//GO:0006629//GO:0031224	nr +
Unigene81401_All	241	0.65	0.84	4.64	1.24	0.43	1.12	0.70	0.52	0.50	3.69E-01	8.15E-01		2.83E+00	7.34E-04	Up	-1.53E+00	2.98E-01		-1.41E-01	9.20E-01		-4.32E-01	7.92E-01		-5.01E-01	7.45E-01									
Unigene81404_All	241	0.00	1.47	4.20	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	2.43E-02		1.20E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene81404_All//gi|224137016|ref|XP_002322473.1|//2.00E-21//acyl:coa ligase [Populus trichocarpa] >gi|222869469|gb|EEF06600.1|acyl:coa ligase [Populus trichocarpa]	Unigene81404_All//4.00E-14//AT3G48990| AMP-dependent synthetase and ligase family protein	Unigene81404_All//2.00E-08//gi|18098780|gb|BM358046.1|BM358046			GO:0005576//GO:0009536//GO:0010038//GO:0016405//GO:0032559	nr +
Unigene81406_All	241	0.00	0.00	4.64	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene81406_All//gi|14423648|sp|Q9WTR0.1|ALL8_OLEEU//1.00E-21//RecName: Full=Calcium-binding allergen Ole e 8; AltName: Full=PCA18/PCA23; AltName: Allergen=Ole e 8 >gi|6901652|gb|AAF31151.1|AF078679_1 calcium-binding protein [Olea europaea]	Unigene81406_All//2.00E-17//ATIG18210| calcium-binding protein, putative			ko04626|Plant-pathogen interaction	GO:0016020//GO:0043231//GO:0046872	nr -
Unigene81408_All	242	160.42	103.22	85.82	190.61	182.71	207.71	277.97	125.04	151.62	-6.36E-01	1.70E-13		-9.03E-01	3.50E-23		-6.11E-02	5.54E-01		1.24E-01	1.41E-01		-1.15E+00	5.59E-75	Down	-8.75E-01	3.58E-49		Unigene81408_All//gi|52139816|gb|AAC29198.1|//1.00E-34//mitochondrial malate dehydrogenase [Solanum lycopersicum]	Unigene81408_All//1.00E-23//AT3G15020| malate dehydrogenase (NAD), mitochondrial, putative	Unigene81408_All//2.00E-134//gi|11203734|gb|BF272664.1|BF272664		ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism	GO:0005576//GO:0006007//GO:0006952//GO:0009060//GO:0016615//GO:0031980//GO:0043648//GO:0046914	nr -
Unigene81409_All	242	0.00	1.26	3.30	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	4.36E-02		1.17E+01	1.71E-04	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene8141_All	680	0.46	0.75	0.63	0.37	1.27	0.07	3.79	1.41	2.23	6.91E-01	4.99E-01		4.40E-01	6.76E-01		1.79E+00	2.95E-02		-2.46E+00	2.23E-01		-1.42E+00	9.85E-05	Down	-7.69E-01	2.28E-02		Unigene8141_All//gi|66841324|dbj|BAD69220.1|//2.00E-47//polypeptide with an integrase domain [Petunia x hybrida]					GO:0005488	nr -
Unigene81433_All	242	0.00	0.00	3.52	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	8.97E-05	Up	null	null		null	null		null	null		null	null		Unigene81433_All//gi|22330270|ref|NP_175981.2|//1.00E-29//ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|75161659|sp|Q8VZX9.1|CSLE1_ARATH RecName: Full=Cellulose synthase-like protein E1; Short=AtCsLE1	Unigene81433_All//5.00E-31//ATIG55850| ATCSLE1; cellulose synthase/ transferase, transferring glycosyl groups				GO:0009250//GO:0016759//GO:0031224//GO:0045229	nr +
Unigene81434_All	242	0.00	3.77	3.52	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.60E-05	Up	1.18E+01	8.97E-05	Up	null	null		null	null		null	null		null	null									
Unigene81437_All	243	0.00	0.00	3.29	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene81437_All//gi|87046113|gb|ABD17866.1|//5.00E-43//etiolation seedling like-RAN2 small Ras GTP-binding nuclear protein [Brassica napus]	Unigene81437_All//2.00E-44//AT5G20010| RAN-1; GTP binding / GTPase/ protein binding	Unigene81437_All//7.00E-48//ES842394			GO:0015031//GO:0017111//GO:0023060//GO:0032561//GO:0051169	nr +
Unigene81438_All	243	0.43	3.54	4.38	0.21	0.28	0.00	0.00	0.52	0.16	3.04E+00	1.94E-03		3.35E+00	3.36E-04	Up	4.67E-01	9.53E-01		-7.68E+00	6.18E-01		9.01E+00	2.39E-01		7.36E+00	6.36E-01				Unigene81438_All//5.00E-15//FL577386				
Unigene8144_All	762	0.00	0.40	0.07	0.52	0.23	0.36	1.78	2.63	0.37	8.64E+00	4.36E-02		6.13E+00	6.24E-01		-1.21E+00	3.14E-01		-5.57E-01	6.37E-01		5.68E-01	1.72E-01		-2.28E+00	7.13E-05	Down	Unigene8144_All//gi|115484183|ref|NP_001065753.1|//4.00E-61//Os11g0149100 [Oryza sativa Japonica Group] >gi|62701672|gb|AAX92745.1|expressed protein [Oryza sativa Japonica Group] >gi|77548692|gb|ABA91489.1|expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113644457|dbj|BAF27598.1|Os11g0149100 [Oryza sativa Japonica Group]	Unigene8144_All//2.00E-43//AT4G12080| DNA-binding family protein	Unigene8144_All//0.00E+00//gi|78334349|gb|DT554623.1|DT554623				nr -
Unigene81441_All	243	0.00	0.00	3.73	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.19E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene81441_All//gi|60512789|emb|CAI51310.1|//1.00E-34//metallothionein-like protein [Capsicum chinense]		Unigene81441_All//2.00E-23//GE654017			GO:0043169	nr -
Unigene81445_All	243	0.00	0.00	4.82	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	1.77E-06	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene81452_All	243	0.00	1.67	3.07	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	1.34E-02		1.16E+01	3.25E-04	Up	null	null		null	null		null	null		null	null		Unigene81452_All//gi|115457964|ref|NP_001052582.1|//5.00E-13//Os04g0376500 [Oryza sativa Japonica Group] >gi|38346118|emb|CAE04596.2|OSJNB00060X15.13 [Oryza sativa (japonica cultivar-group)] >gi|113564153|dbj|BAF14496.1|Os04g0376500 [Oryza sativa Japonica Group]	Unigene81452_All//7.00E-05//AT1G10840| TIF3H1; translation initiation factor					nr -
Unigene81460_All	243	0.43	0.21	4.16	0.21	0.57	0.37	0.00	0.00	0.00	-1.05E+00	6.82E-01		3.27E+00	5.92E-04	Up	1.47E+00	6.17E-01		8.59E-01	7.91E-01		null	null		null	null									
Unigene81468_All	243	0.00	0.21	3.29	0.00	0.00	0.00	0.00	0.00	0.00	7.70E+00	6.08E-01		1.17E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene81468_All//gi|225441918|ref|XP_002284505.1|//2.00E-13//PREDICTED: similar to calcium-binding EF hand family protein [Vitis vinifera]				ko04626|Plant-pathogen interaction		nr -
Unigene81469_All	243	0.00	0.00	3.07	0.41	0.57	0.00	0.00	0.00	0.00	null	null		1.16E+01	3.24E-04	Up	4.67E-01	8.75E-01		-8.68E+00	3.93E-01		null	null		null	null		Unigene81469_All//sp|Q891W3|HIS3_BRAJA//4.00E-20//Phosphoribosyl-AMP cyclohydrolase OS=Bradyrhizobium japonicum GN=hisI PE=3 SV=1						swissprot +
Unigene81476_All	244	0.00	3.32	1.31	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.30E-05	Up	1.04E+01	4.43E-02		null	null		null	null		null	null		null	null									ESTscan +
Unigene81480_All	244	0.00	3.11	1.75	0.61	0.28	0.00	1.39	0.00	0.00	1.16E+01	1.75E-04	Up	1.08E+01	1.36E-02		-1.12E+00	5.82E-01		-9.26E+00	2.31E-01		-1.04E+01	1.17E-02		-1.04E+01	8.13E-03									
Unigene81482_All	244	0.00	1.87	3.49	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	7.34E-03		1.18E+01	8.97E-05	Up	null	null		null	null		null	null		null	null		Unigene81482_All//gi|15235205|ref|NP_193719.1|//5.00E-30//ATPP2-A1; carbohydrate binding [Arabidopsis thaliana] >gi|75100453|sp|Q81865.1|P2A01_ARATH RecName: Full=Protein PHLOEM PROTEIN 2-LIKE A1; Short=AtPP2-A1 >gi|3250693|emb|CAA19701.1| lectin like protein [Arabidopsis thaliana] >gi|7268780|emb|CAB78986.1| lectin like protein [Arabidopsis thaliana] >gi|19699298|gb|AAL91260.1|AT4g19840/T16H5_200 [Arabidopsis thaliana] >gi|21689635|gb|AAM67439.1|AT4g19840/T16H5_200 [Arabidopsis thaliana]	Unigene81482_All//2.00E-31//AT4G19840| ATPP2-A1; carbohydrate binding					nr +
Unigene81502_All	244	0.00	5.40	10.91	0.00	0.00	0.37	0.00	0.00	0.00	1.24E+01	1.49E-07	Up	1.34E+01	1.07E-14	Up	null	null		8.53E+00	4.70E-01		null	null		null	null		Unigene81502_All//sp|P56614|YMDF_ECOLI//9.00E-28//Uncharacterized protein ymdF OS=Escherichia coli (strain K12) GN=ymdF PE=1 SV=1						swissprot +
Unigene81510_All	245	0.00	1.65	3.26	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	1.34E-02		1.17E+01	1.71E-04	Up	null	null		null	null		null	null		null	null									
Unigene81513_All	245	0.00	0.41	3.69	0.00	0.00	0.00	0.00	0.00	0.00	8.69E+00	3.79E-01		1.19E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene81513_All//gi|15222421|ref|NP_177128.1|//6.00E-20//ATHVA22C [Arabidopsis thaliana] >gi|57012624|sp|Q9S784.1|HA22C_ARATH RecName: Full=HVA22-like protein c; Short=AtHVA22c >gi|4884946|gb|AAD31886.1|AF141978_1 AtHVA22c [Arabidopsis thaliana] >gi|12325187|gb|AAG52538.1|AC013289_5 AtHVA22c; 50565-49239 [Arabidopsis thaliana] >gi|4884936|gb|AAD31881.1|AtHVA22c [Arabidopsis thaliana] >gi|21536712|gb|AAM61044.1|AtHVA22c [Arabidopsis thaliana]	Unigene81513_All//2.00E-21//AT1G69700| ATHVA22C	Unigene81513_All//1.00E-09//TC178397				nr +
Unigene81515_All	245	0.00	0.21	3.26	0.20	0.00	0.00	0.00	0.00	0.00	7.69E+00	6.08E-01		1.17E+01	1.71E-04	Up	-7.67E+00	5.43E-01		-7.67E+00	6.18E-01		null	null		null	null									

Unigene81516_All	245	0.00	0.83	4.35	0.20	0.42	0.55	0.00	0.00	0.00	9.69E+00	1.34E-01		1.21E+01	6.59E-06	Up	1.05E+00	8.05E-01		1.44E+00	6.36E-01		null	null		null	null										
Unigene81517_All	245	0.00	5.79	1.74	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	4.04E-08	Up	1.08E+01	1.36E-02		null	null		null	null		null	null		null	null										ESTscan +
Unigene81521_All	245	0.00	0.62	2.83	0.81	0.28	0.00	0.00	0.00	0.00	9.28E+00	2.32E-01		1.15E+01	6.11E-04	Up	-1.53E+00	4.14E-01		-9.67E+00	1.32E-01		null	null		null	null		Unigene81521_All//COG2114//1.00E-05//Adenylate cyclase, family 3 (some proteins contain HAMP domain)							cog +
Unigene81524_All	245	0.00	2.28	4.35	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.16E-03		1.21E+01	6.59E-06	Up	null	null		null	null		null	null		null	null		Unigene81524_All//gi|112143920|gb|ABI13169.1|//5.00E-06//putative trypsin [Emiliania huxleyi]							nr +
Unigene81526_All	245	0.00	0.00	5.87	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.25E+01	6.28E-08	Up	null	null		null	null		null	null		null	null		Unigene81526_All//gi|3914935|sp|O65751.1|RSA4_CICAR//9.00E-21//RecName: Full=40S ribosomal protein SA; AltName: Full=p40 >gi|3204099|emb|CAA07226.1| ribosome-associated protein p40 [Cicer arietinum]	Unigene81526_All//3.00E-21//AT3G04770| RPSAb (40S ribosomal protein SA B); structural constituent of ribosome	Unigene81526_All//5.00E-15//ES805099		ko03010|Ribosome		nr -
Unigene81153_All	570	10.28	3.11	6.82	1.92	2.36	2.14	0.52	0.44	0.28	-1.72E+00	2.02E-10	Down	-5.92E-01	2.11E-02		2.93E-01	6.42E-01		1.54E-01	8.06E-01		-2.39E-01	8.39E-01		-8.93E-01	4.71E-01										ESTscan -
Unigene81535_All	246	0.00	6.18	2.16	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.09E-08	Up	1.11E+01	3.99E-03		null	null		null	null		null	null		null	null										ESTscan -
Unigene81538_All	246	0.00	0.41	3.68	0.00	0.00	0.00	0.00	0.00	0.00	8.69E+00	3.79E-01		1.18E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene81538_All//gi|282935440|gb|ADB03785.1|//2.00E-30//deleted in split hand/splt foot protein 1 [Ipomoea batatas]		Unigene81538_All//3.00E-25//TC172703		ko03050|Proteasome//ko03440|Homologous recombination		nr -
Unigene81539_All	246	213.11	145.01	130.09	495.91	465.58	620.17	251.10	182.47	125.35	-5.56E-01	3.03E-14		-7.12E-01	6.99E-21		-9.11E-02	7.00E-02		3.23E-01	4.86E-16		-4.61E-01	1.19E-14		-1.00E+00	1.23E-56	Down	Unigene81539_All//gi|164652934|gb|ABV65000.1|//1.00E-23//14-3-3a protein [Gossypium hirsutum]	Unigene81539_All//2.00E-21//AT1G22300| GRF10 (GENERAL REGULATORY FACTOR 10); ATP binding / protein binding / protein phosphorylated amino acid binding	Unigene81539_All//1.00E-98//TC152028				nr +
Unigene81545_All	246	0.00	0.00	6.93	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.28E+01	2.19E-09	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene8155_All	580	0.63	2.80	2.39	0.60	0.36	1.09	1.68	3.68	3.71	2.15E+00	2.79E-04	Up	1.92E+00	3.21E-03		-7.55E-01	5.67E-01		8.59E-01	3.89E-01		1.13E+00	4.44E-03		1.15E+00	2.94E-03				Unigene8155_All//2.00E-56//DT463274					
Unigene8156_All	514	0.10	0.39	0.00	0.48	0.74	0.70	0.00	0.33	1.24	1.95E+00	3.74E-01		-6.67E+00	6.15E-01		6.05E-01	5.59E-01		5.37E-01	6.94E-01		8.35E+00	1.38E-01		1.03E+01	9.33E-05	Up								
Unigene81560_All	246	0.00	1.24	3.46	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	4.36E-02		1.18E+01	8.97E-05	Up	null	null		null	null		null	null		null	null		Unigene81560_All//gi|109290432|gb|ABG29422.1|//2.00E-37//GSK-like kinase IA [Triticum aestivum]	Unigene81560_All//5.00E-38//AT5G26751| ATSK11; protein kinase/ protein serine/threonine kinase					nr -
Unigene8157_All	1057	0.69	1.34	1.06	11.55	7.82	3.76	1.36	0.20	0.41	9.54E-01	9.02E-02		6.10E-01	3.75E-01		-5.62E-01	1.80E-04		-1.62E+00	1.24E-20	Down	-2.78E+00	5.95E-06	Down	-1.71E+00	8.25E-04	Down	Unigene8157_All//gi|297800188|ref|XP_002867978.1|//4.00E-82//leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313814|gb|EFH44237.1| leucine-rich repeat family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8157_All//4.00E-60//AT4G18760| AtRLP51 (Receptor Like Protein 51); protein binding	Unigene8157_All//0.00E+00//gi|78343545|gb|DT563819.1|DT563819		GO:0016020//GO:0023060		nr -
Unigene81577_All	247	0.00	0.00	4.74	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	1.77E-06	Up	null	null		null	null		null	null		null	null		Unigene81577_All//gi|90762220|gb|ABD97880.1|//2.00E-37//suppressor of K+ transport growth defect-like protein [Gossypium hirsutum]	Unigene81577_All//4.00E-33//AT2G27600| SKD1 (SUPPRESSOR OF K+ TRANSPORT GROWTH DEFECT1); ATP binding / nucleoside-triphosphatase/ nucleotide binding	Unigene81577_All//5.00E-21//TC135485		ko04144|Endocytosis		nr +
Unigene81581_All	247	0.00	0.00	5.17	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.23E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene81581_All//gi|77999275|gb|ABB16984.1|//3.00E-40//thaliana 60S ribosomal protein L7 (At2g44120) [Solanum tuberosum]	Unigene81581_All//6.00E-32//AT2G01250| 60S ribosomal protein L7 (RPL7B)	Unigene81581_All//3.00E-35//TC131081		ko03010|Ribosome		nr -
Unigene8159_All	547	0.77	1.11	0.00	6.65	3.53	2.23	1.78	0.84	0.36	5.39E-01	5.63E-01		-9.58E+00	1.55E-02		-9.15E-01	2.41E-03		-1.58E+00	2.43E-06	Down	-1.08E+00	8.88E-02		-2.29E+00	9.84E-04	Down	Unigene8159_All//gi|225348641|gb|ACN87282.1|//2.00E-22//with no lysine kinase [Glycine max]					GO:0004672	nr +
Unigene81593_All	248	0.00	0.41	2.79	0.00	0.00	0.00	0.00	0.00	0.00	8.67E+00	3.79E-01		1.14E+01	6.11E-04	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene81595_All	248	0.00	5.11	3.86	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	2.85E-07	Up	1.19E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene81595_All//sp|Q0QHL3|CISY_GLOMU//2.00E-16//Probable citrate synthase, mitochondrial OS=Glossina morsitans morsitans PE=2 SV=1							swissprot +
Unigene81596_All	248	0.21	0.00	6.66	0.00	0.00	0.00	22.33	17.02	20.56	-7.72E+00	6.01E-01		4.98E+00	6.48E-08	Up	null	null		null	null		-3.92E-01	9.33E-02		-1.19E-01	6.25E-01		Unigene81596_All//gi|261266875|gb|ACX56278.1|//1.00E-22//calmodulin [Panicum antidotale] >gi|261266878|gb|ACX56279.1| calmodulin [Panicum miliaceum] >gi|261266880|gb|ACX56280.1| calmodulin [Echinochloa frumentacea]	Unigene81596_All//5.00E-24//AT3G43810| CAM7 (CALMODULIN 7); calcium ion binding	Unigene81596_All//9.00E-60//ES841204		ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene81597_All	248	0.00	1.02	6.44	0.00	0.00	0.00	0.00	0.00	0.00	1.00E+01	7.75E-02		1.27E+01	8.43E-09	Up	null	null		null	null		null	null		null	null		Unigene81597_All//gi|300808465|gb|ADK35365.1|//3.00E-20//ubiquitin carrier protein Rad6 [Hordeum vulgare subsp. vulgare]	Unigene81597_All//9.00E-21//AT2G02760| ATUBC2 (UBIQUITING-CONJUGATING ENZYME 2); ubiquitin-protein ligase	Unigene81597_All//8.00E-20//ES836735		ko04120|Ubiquitin mediated proteolysis		nr +
Unigene816_All	3950	1.54	1.72	1.59	4.98	4.28	2.89	10.93	10.61	21.89	1.62E-01	5.11E-01		5.01E-02	8.43E-01		-2.19E-01	8.98E-02		-7.84E-01	1.08E-10		-4.23E-02	6.22E-01		1.00E+00	2.57E-78	Up	Unigene816_All//gi|75334096|sp|Q9FN37.1|PSKR2_ARATH//0.00E+00//RecName: Full=Phytosulfokine receptor 2; Short=AtPSKR2; AltName: Full=Phytosulfokine LRR receptor kinase 2; Flags: Precursor >gi|10177251|dbj|BAB10719.1| receptor protein kinase-like protein [Arabidopsis thaliana] >gi|224589723|gb|ACN59393.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene816_All//0.00E+00//AT5G53890| leucine-rich repeat transmembrane protein kinase, putative	Unigene816_All//0.00E+00//TC173246			GO:0004872//GO:0005488//GO:0006950//GO:0016020//GO:0016301	nr +
Unigene8160_All	498	4.41	9.36	9.73	3.80	5.19	5.80	2.80	3.36	1.76	1.09E+00	1.39E-04	Up	1.14E+00	8.20E-05	Up	4.48E-01	2.93E-01		6.11E-01	1.09E-01		2.61E-01	6.13E-01		-6.71E-01	1.68E-01		Unigene8160_All//gi|110740523|dbj|BAE98367.1|//6.00E-18//regulator of chromosome condensation-like protein [Arabidopsis thaliana]	Unigene8160_All//4.00E-19//AT3G55580| regulator of chromosome condensation (RCC1) family protein	Unigene8160_All//5.00E-106//DT053801			GO:0016772//GO:0017016	nr +
Unigene81600_All	248	0.00	2.86	1.50	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.30E-04	Up	1.06E+01	2.46E-02		null	null		null	null		null	null		null	null										
Unigene81603_All	248	0.00	0.61	2.79	1.21	0.14	0.00	0.00	0.00	0.00	9.26E+00	2.32E-01		1.14E+01	6.11E-04	Up	-3.12E+00	7.55E-02		-1.02E+01	3.98E-02		null	null		null	null		Unigene81603_All//sp|Q59263|RIBF_CORAM//1.00E-06//Riboflavin biosynthesis protein ribF OS=Corynebacterium ammoniagenes GN=ribF PE=1 SV=1							swissprot +
Unigene81606_All	248	0.00	0.20	2.79	0.00	0.00	0.00	0.00	0.00	0.00	7.67E+00	6.08E-01		1.14E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene81606_All//gi|399082|sp|Q02758.1|ATPD_PEA//2.00E-29//RecName: Full=ATP synthase delta chain, chloroplastic; AltName: Full=F-ATPase delta chain; Flags: Precursor >gi|169045|gb|AAA33647.1| ATP synthase delta subunit [Pisum sativum]	Unigene81606_All//1.00E-26//AT4G09650| ATPD (ATP SYNTHASE DELTA-SUBUNIT GENE); hydrogen ion transporting ATP synthase, rotational mechanism / proton-transporting ATPase, rotational mechanism			ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr -
Unigene81608_All	248	0.00	0.82	4.72	0.00	0.00	0.18	1.36	0.84	0.48	9.67E+00	1.34E-01		1.22E+01	1.76E-06	Up	null	null		7.51E+00	6.83E-01		-6.95E-01	5.77E-01		-1.50E+00	2.10E-01				Unigene81608_All//1.00E-108//gi|164331807|gb|ES840582.1|ES840582					
Unigene81609_All	248	0.00	0.00	3.86	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.19E+01	2.44E-05	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene8161_All	493	0.53	0.62	0.43	1.11	1.40	0.82	3.52	1.53	0.16	2.17E-01	8.64E-01		-2.97E-01	8.31E-01		3.30E-01	7.52E-01		-4.31E-01	6.67E-01		-1.20E+00	7.57E-03		-4.44E+00	1.94E-10	Down			Unigene8161_All//2.00E-179//ES810593					
Unigene81620_All	249	3.57	2.03	10.05	0.40	0.41	0.54	0.00	0.00	0.00	-8.12E-01	2.68E-01		1.49E+00	6.44E-04	Up	5.24E-02	9.64E-01		4.44E-01	8.60E-01		null	null		null	null				Unigene81620_All//2.00E-32//TC160283					
Unigene81623_All	249	0.42	6.10	5.35	0.40	0.28	1.09	0.00	0.00	0.00	3.86E+00	1.23E-06	Up	3.67E+00	1.90E-05	Up	-5.33E-01	8.13E-01		1.44E+00	4.09E-01		null	null		null	null		Unigene81623_All//gi|159895659|gb|ABX10440.1|//5.00E-32//3-ketoacyl-CoA synthase 10 [Gossypium hirsutum]	Unigene81623_All//4.00E-26//AT5G43760| KCS20 (3-KETOACYL-COA SYNTHASE 20); fatty acid elongase	Unigene81623_All//3.00E-35//TC158941				nr -
Unigene81627_All	249	0.00	0.00	3.64	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	4.69E-05	Up	null	null		null	null		null	null		null	null										
Unigene8163_All	778	0.34	0.72	0.27	0.38	0.80	0.70	5.81	3.81	14.18	1.09E+00	2.74E-01		-2.97E-01	8.31E-01		1.05E+00	2.99E-01		8.59E-01	4.23E-01		-6.08E-01	1.67E-02		1.29E+00	1.26E-15	Up	Unigene8163_All//gi|289552247|gb|ADD10719.1|//8.00E-25//acetyl-CoA C-acetyltransferase protein [Camellia oleifera]	Unigene8163_All//8.00E-11//AT5G48230| ACAT2 (ACETOACETYL-COA THIOLASE 2); acetyl-CoA C-acetyltransferase/ catalytic	Unigene8163_All//0.00E+00//TC168182		ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00900|Terpenoid backbone biosynthesis//ko00072|Synthesis and degradation of ketone bodies	GO:0003006//GO:0016020//GO:0016453//GO:0042579	nr -
Unigene81634_All	249	0.00	0.00	3.64	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene81634_All//gi|158512884|sp|A2VMF7.1|SCAM1_ORYSJ//1.00E-36//RecName: Full=Putative secretory carrier-associated membrane protein 1; Short=Secretory carrier membrane protein 1	Unigene81634_All//9.00E-37//AT1G11180| secretory carrier membrane protein (SCAMP) family protein	Unigene81634_All//2.00E-23//DT468375				nr +
Unigene81636_All	249	0.00	0.61	3.64	0.00	0.00	0.00	0.00	0.00	0.00	9.25E+00	2.31E-01		1.18E+01	4.69E-05	Up	null	null		null	null		null	null		null	null										
Unigene81637_All	249	0.42	1.22	4.92	0.40	0.83	0.00	0.00	0.00	0.32	1.54E+00	3.22E-01		3.55E+00	6.10E-05	Up	1.05E+00	6.11E-01		-8.64E+00	3.93E-01		null	null		8.32E+00	4.00E-01		Unigene81637_All//gi|225437712|ref|XP_002273170.1|//5.00E-11//PREDICTED: similar to At2g43670 [Vitis vinifera]	Unigene81637_All//4.00E-08//AT1G78520| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: X8 (InterPro:IPR012946); BEST Arabidopsis thaliana protein match is: glycosyl hydrolase family protein 17 (TAIR:AT2G43670.1); Has 747 Blast hits to 711 proteins in 30 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 747; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).	Unigene81637_All//4.00E-114//ES800471				nr +
Unigene8164_All	529	0.30	0.19	1.41	5.65	4.69	3.33	4.40	1.34	3.69	-6.31E-01	7.26E-01		2.25E+00	2.34E-02		-2.70E-01	4.99E-01		-7.63E-01	3.51E-02		-1.71E+00	2.03E-05	Down	-2.53E-01	5.16E-01		Unigene8164_All//gi|45826061|gb|AAS77675.1|//4.00E-20//resistance protein [Quercus suber]	Unigene8164_All//2.00E-09//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene8164_All//2.00E-31//ES793138		ko04626|Plant-pathogen interaction		nr +
Unigene8165_All	746	0.28	0.88	0.00	0.27	0.00	0.36	1.42	3.31	0.96	1.65E+00	8.13E-02		-8.13E+00	1.44E-01		-8.06E+00	8.37E-02		4.43E-01	7.63E-01		1.22E+00	9.01E-04	Up	-5.60E-01	3.39E-01										
Unigene8166_All	324	0.00	0.63	2.30	2.46	1.59	2.09	2.22	1.03	0.61	9.29E+00	1.34E-01		1.12E+01	3.24E-04	Up	-6.26E-01	4.24E-01		-2.35E-01	7.53E-01		-1.10E+00	1.49E-01		-1.85E+00	1.78E-02										
Unigene81665_All	250	0.00	2.63	2.77	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	6.20E-04	Up	1.14E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene81665_All//sp|Q24009|BICC_DROME//1.00E-27//Protein bicaudal C OS=Drosophila melanogaster GN=BicC PE=1 SV=2							swissprot +
Unigene81668_All	250	0.00	3.85	3.41	0.20	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.37E-05	Up	1.17E+01	8.97E-05	Up	-7.64E+00	5.43E-01		-7.64E+00	6.18E-01		null	null		null	null		Unigene81668_All//sp|P42278|TRYT_DROME//2.00E-06//Trypsin theta OS=Drosophila melanogaster GN=thetaTry PE=2 SV=2							swissprot +
Unigene81671_All	250	0.00	0.00	9.59	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.32E+01	3.24E-13	Up	null	null		null	null		null	null		null	null		Unigene81671_All//gi|300681467|emb|CBR32561.1|//4.00E-27//histone H3, expressed [Triticum aestivum]	Unigene81671_All//1.00E-28//AT5G65360| histone H3	Unigene81671_All//3.00E-22//TC148022				nr -
Unigene81679_All	250	0.00	4.46	6.39	0.20	0.14	0.18	0.34	0.33	0.48	1.21E+01	1.99E-06	Up	1.26E+01	8.42E-09	Up	-5.33E-01	8.18E-01		-1.41E-01	9.46E-01		-1.63E-02	1.01E+00		4.99E-01	8.06E-01										

Unigene8168_All	921	0.34	0.00	0.17	4.87	1.65	2.21	2.80	0.91	0.91	-8.41E+00	3.63E-02		-9.74E-01	5.05E-01		-1.57E+00	1.62E-08	Down	-1.14E+00	6.05E-05	Down	-1.63E+00	1.43E-05	Down	-1.62E+00	8.62E-06	Down	Unigene8168_All//gi|15242552|ref|NP_198818.1|//5.00E-40//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|10176994|dbj|BAB10226.1| thaumatin-like protein [Arabidopsis thaliana] >gi|38603816|gb|AAR24653.1| At5g40020 [Arabidopsis thaliana] >gi|110736116|dbj|BAF00030.1| thaumatin-like protein [Arabidopsis thaliana]	Unigene8168_All//2.00E-41//AT5G40020| pathogenesis-related thaumatin family protein	Unigene8168_All//5.00E-160//DW225500			GO:0009607//GO:0031410	nr +
Unigene81680_All	250	0.00	1.42	3.20	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	2.43E-02		1.16E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene81680_All//gi|115438943|ref|NP_001043751.1|//7.00E-07//Os01g0655400 [Oryza sativa Japonica Group] >gi|55723837|dbj|BAD72325.1| eukaryotic translation initiation factor 3 subunit 10-like [Oryza sativa Japonica Group] >gi|113533282|dbj|BAF05665.1| Os01g0655400 [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr -
Unigene81685_All	250	1.05	1.22	5.33	0.60	0.28	0.54	0.00	0.00	0.00	2.17E-01	8.64E-01		2.35E+00	8.68E-04	Up	-1.12E+00	5.82E-01		-1.41E-01	9.42E-01		null	null		null	null									ESTscan -
Unigene81689_All	251	0.00	3.23	1.91	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.30E-05	Up	1.09E+01	7.40E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene8169_All	399	0.00	0.00	1.74	3.50	1.81	1.47	2.54	0.52	0.20	null	null		1.08E+01	6.11E-04	Up	-9.48E-01	8.15E-02		-1.25E+00	3.03E-02		-2.28E+00	1.11E-03		-3.67E+00	1.15E-05	Down	Unigene8169_All//gi|2346988|dbj|BAA21928.1|//8.00E-24//ZPT4-4 [Petunia x hybrida]	Unigene8169_All//6.00E-11//AT1G26610| zinc finger (C2H2 type) family protein		C2H2			nr +
Unigene81691_All	251	0.00	36.34	14.85	0.40	0.27	0.00	0.00	0.00	0.00	1.51E+01	3.22E-52	Up	1.39E+01	1.20E-20	Up	-5.33E-01	8.13E-01		-8.63E+00	3.93E-01		null	null		null	null		Unigene81691_All//gi|21322711|emb|CAD22154.1|//2.00E-17//pherophorin-d1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome		nr +
Unigene81697_All	251	0.63	8.28	3.39	5.76	8.92	3.78	42.62	41.96	26.82	3.73E+00	1.15E-08	Up	2.44E+00	9.09E-03		6.32E-01	1.53E-01		-6.07E-01	2.97E-01		-2.23E-02	9.15E-01		-6.68E-01	1.03E-05		Unigene81697_All//gi|270309006|dbj|BA152956.1|//4.00E-11//auxin-repressed protein [Citrullus lanatus subsp. vulgaris]	Unigene81697_All//3.00E-10//AT1G28330| DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)	Unigene81697_All//3.00E-44//GE653395				nr -
Unigene817_All	811	1.10	0.75	0.26	1.29	1.15	0.95	2.97	0.98	1.52	-5.49E-01	4.42E-01		-2.06E+00	1.78E-02		-1.70E-01	8.19E-01		-4.46E-01	5.32E-01		-1.60E+00	3.66E-05	Down	-9.65E-01	6.40E-03		Unigene817_All|297598524|ref|NP_001045762.2|//3.00E-42//Os02g0127600 [Oryza sativa Japonica Group] >gi|255670569|dbj|BAF07676.2| Os02g0127600 [Oryza sativa Japonica Group]	Unigene817_All//2.00E-59//AT1G71210| pentatricopeptide (PPR) repeat-containing protein				GO:0043231	nr +
Unigene8170_All	271	1.93	4.11	4.91	2.39	1.78	0.00	0.16	0.00	0.29	1.09E+00	9.57E-02		1.35E+00	3.17E-02		-4.26E-01	6.08E-01		-1.12E+01	3.90E-04	Down	-7.29E+00	6.43E-01		9.14E-01	7.47E-01									
Unigene81701_All	251	0.00	0.00	2.76	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.14E+01	6.11E-04	Up	null	null		null	null		null	null		null	null		Unigene81701_All//gi|300160753|gb|EFJ27370.1|//7.00E-33//rab family GTPase [Selaginella moellendorffii] >gi|300166524|gb|EFJ33130.1| rab family GTPase [Selaginella moellendorffii]	Unigene81701_All//3.00E-34//AT4G17170| RABB1C (ARABIDOPSIS RAB GTPASE HOMOLOG B1C); GTP binding / GTPase	Unigene81701_All//2.00E-36//AI727234				nr +
Unigene81706_All	251	0.00	0.40	7.00	0.00	0.00	0.00	0.00	0.00	0.00	8.66E+00	3.79E-01		1.28E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene81706_All//gi|134035496|gb|AB047736.1|//2.00E-40//alpha-tubulin [Gossypium hirsutum] >gi|223453028|gb|ACM89778.1| alpha-tubulin 6 [Gossypium hirsutum]	Unigene81706_All//8.00E-32//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene81706_All//2.00E-51//EV484631		ko04145|Phagosome		nr +
Unigene8172_All	631	0.00	0.00	0.00	0.39	0.33	0.14	72.77	52.66	20.83	null	null		null	null		-2.70E-01	8.22E-01		-1.46E+00	4.06E-01		-4.67E-01	2.35E-11		-1.80E+00	5.70E-103	Down	Unigene8172_All//gi|224144535|ref|XP_002325324.1|//7.00E-39//cytochrome P450 [Populus trichocarpa] >gi|222862199|gb|EEE99705.1| cytochrome P450 [Populus trichocarpa]	Unigene8172_All//2.00E-31//AT5G24900| CYP714A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene8172_All//2.00E-133//DT463377		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0016491	nr +
Unigene81728_All	252	0.00	2.82	2.11	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	3.30E-04	Up	1.10E+01	3.99E-03		null	null		null	null		null	null		null	null									
Unigene81732_All	252	0.00	3.82	1.90	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.37E-05	Up	1.09E+01	7.40E-03		null	null		null	null		null	null		null	null									ESTscan +
Unigene81733_All	252	0.00	2.01	2.96	0.00	0.14	0.00	0.00	0.00	0.00	1.10E+01	3.99E-03		1.15E+01	3.24E-04	Up	7.09E+00	8.13E-01		null	null		null	null		null	null		Unigene81733_All//gi|224103789|ref|XP_002313194.1|//3.00E-28//tubulin alpha-5 chain [Populus trichocarpa] >gi|222849602|gb|EEE87149.1| tubulin alpha-5 chain [Populus trichocarpa]	Unigene81733_All//1.00E-29//AT1G50010| TUA2; structural constituent of cytoskeleton	Unigene81733_All//1.00E-24//gi|78341001|gb|DT561275.1|DT561275		ko04145|Phagosome		nr +
Unigene81734_All	252	0.00	0.40	2.96	0.40	0.27	0.18	0.00	0.00	0.00	8.65E+00	3.79E-01		1.15E+01	3.24E-04	Up	-5.33E-01	8.13E-01		-1.14E+00	6.73E-01		null	null		null	null		Unigene81734_All//gi|255595850|ref|XP_002536403.1|//5.00E-08//two-component system sensor histidine kinase/response regulator, putative [Ricinus communis] >gi|223519809|gb|EEF25981.1| two-component system sensor histidine kinase/response regulator, putative [Ricinus communis]						nr +
Unigene8174_All	468	0.56	0.00	0.11	0.96	1.18	0.58	0.27	1.34	2.38	-9.13E+00	6.65E-02		-2.30E+00	2.42E-01		2.97E-01	8.18E-01		-7.27E-01	5.32E-01		2.31E+00	1.46E-02		3.14E+00	2.19E-05	Up								
Unigene81741_All	252	0.00	3.42	2.11	0.00	0.00	0.18	0.00	0.00	0.00	1.17E+01	4.91E-05	Up	1.10E+01	3.99E-03		null	null		7.49E+00	6.83E-01		null	null		null	null		Unigene81741_All//sp|Q01628|IFM3_HUMAN//1.00E-17//Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=2 SV=2						swissprot -
Unigene8175_All	1412	0.07	0.93	0.38	0.21	0.17	0.19	0.72	1.84	6.86	3.65E+00	1.28E-05	Up	2.35E+00	5.86E-02		-3.11E-01	8.19E-01		-1.42E-01	9.20E-01		1.35E+00	1.90E-04	Up	3.25E+00	4.57E-43	Up	Unigene8175_All//gi|72255633|gb|AAZ66951.1|//1.00E-129//117M18_32 [Brassica rapa]	Unigene8175_All//6.00E-132//AT5G10530| lectin protein kinase, putative	Unigene8175_All//4.00E-38//CA994027		ko04626|Plant-pathogen interaction		nr +
Unigene81753_All	252	0.00	0.20	2.75	0.20	0.55	0.00	0.00	0.00	0.00	7.65E+00	6.08E-01		1.14E+01	6.10E-04	Up	1.47E+00	6.17E-01		-7.63E+00	6.18E-01		null	null		null	null		Unigene81753_All//gi|300267462|gb|EFJ51645.1|//2.00E-10//hypothetical protein VOLCADRAFT_87299 [Volvox carteri f. nagariensis]						nr -
Unigene8176_All	533	6.58	3.23	2.70	1.12	0.78	0.68	0.00	0.00	0.00	-1.02E+00	2.04E-03		-1.29E+00	2.79E-04	Down	-5.33E-01	5.61E-01		-7.26E-01	4.60E-01		null	null		null	null		Unigene8176_All//gi|15217776|ref|NP_174115.1|//2.00E-49//PGP13 (P-GLYCOPROTEIN 13); ATPase, coupled to transmembrane movement of substances [Arabidopsis thaliana] >gi|75333473|sp|Q9C7F8.1|AB13B_ARATH RecName: Full=ABC transporter B family member 13; Short=ABC transporter ABCB.13; Short=AtABCB13; AltName: Full=Putative multidrug resistance protein 15; AltName: Full=P-glycoprotein 13	Unigene8176_All//1.00E-44//AT1G27940| PGP13 (P-GLYCOPROTEIN 13); ATPase, coupled to transmembrane movement of substances			ko02010|ABC transporters	GO:0009630//GO:0009639//GO:0009725//GO:0015562//GO:0031224//GO:0003235//GO:0032559//GO:0042626//GO:0043479//GO:0048437//GO:0051707//GO:0060918	nr -
Unigene81762_All	253	0.00	0.80	4.42	0.00	0.00	0.00	0.00	0.00	0.00	9.65E+00	1.34E-01		1.21E+01	3.42E-06	Up	null	null		null	null		null	null		null	null		Unigene81762_All//gi|118486525|gb|ABR85102.1|//2.00E-09//unknown [Populus trichocarpa]						nr +
Unigene8177_All	259	0.40	0.39	0.00	12.12	4.12	5.58	2.12	1.94	0.46	-4.61E-02	9.85E-01		-8.66E+00	3.87E-01		-1.56E+00	4.47E-06	Down	-1.12E+00	1.40E-03		-1.32E-01	8.80E-01		-2.20E+00	2.24E-02		Unigene8177_All//gi|225459332|ref|XP_002284174.1|//5.00E-15//PREDICTED: hypothetical protein [Vitis vinifera]						nr +
Unigene81772_All	253	0.00	3.81	4.21	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.37E-05	Up	1.20E+01	6.59E-06	Up	null	null		null	null		null	null		null	null									
Unigene81773_All	253	0.00	0.00	2.95	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	3.24E-04	Up	null	null		null	null		null	null		null	null		Unigene81773_All//gi|297797191|ref|XP_002866480.1|//2.00E-21//exostosin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312315|gb|EFH42739.1| exostosin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene81773_All//9.00E-23//AT5G62220| exostosin family protein					nr +
Unigene81779_All	253	0.00	0.20	2.74	0.59	0.00	0.00	0.00	0.00	0.00	7.65E+00	6.08E-01		1.14E+01	6.10E-04	Up	-9.21E+00	1.64E-01		-9.21E+00	2.31E-01		null	null		null	null		Unigene81779_All//gi|160900596|ref|XP_001566178.1|//5.00E-08//ABC transporter related [Delftia acidovorans SPH-1] >gi|160366180|gb|ABX37793.1| ABC transporter related [Delftia acidovorans SPH-1]	Unigene81779_All//4.00E-07//AT3G47790| ATATHT; ATPase, coupled to transmembrane movement of substances / transporter					nr -
Unigene81799_All	254	123.18	79.20	83.02	243.38	205.39	199.32	319.93	180.51	137.87	-6.37E-01	4.60E-11		-5.69E-01	9.24E-09		-2.45E-01	1.03E-04		-2.88E-01	1.02E-05		-8.26E-01	2.68E-52		-1.21E+00	5.08E-101	Down	Unigene81799_All//gi|117165712|dbj|BAF36056.1|//2.00E-42//calreticulin-1 [Glycine max]	Unigene81799_All//3.00E-43//AT1G09210| calreticulin 2 (CRT2)	Unigene81799_All//5.00E-132//EE592558		ko04141|Protein processing in endoplasmic reticulum//ko04145|Phagosome		nr -
Unigene8180_All	966	0.81	0.21	0.66	0.93	0.68	0.89	3.06	0.56	0.78	-1.95E+00	2.62E-02		-2.96E-01	6.97E-01		-4.55E-01	5.58E-01		-6.34E-02	9.39E-01		-2.45E+00	3.91E-10	Down	-1.97E+00	3.17E-08	Down	Unigene8180_All|15232195|ref|NP_189392.1|//1.00E-106//group II intron splicing factor CRS1-related [Arabidopsis thaliana]	Unigene8180_All//7.00E-71//AT3G27550| group II intron splicing factor CRS1-related				GO:0003676//GO:0043231	nr +
Unigene81805_All	254	0.00	0.00	3.77	0.20	0.00	0.00	0.00	0.00	0.00	null	null		1.19E+01	2.44E-05	Up	-7.62E+00	5.43E-01		-7.62E+00	6.18E-01		null	null		null	null		Unigene81805_All//gi|34597334|gb|AAG77242.1|//3.00E-11//acetoacetyl-CoA thiolase [Helianthus annuus]	Unigene81805_All//5.00E-08//AT1G04710| PKT4 (PEROXISOMAL 3-KETOACYL-COA THIOLASE 4); acetyl-CoA C-acyltransferase/ catalytic			ko04146|Peroxisome//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko01040|Biosynthesis of unsaturated fatty acids		nr -
Unigene81818_All	254	0.00	0.00	2.73	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.14E+01	6.10E-04	Up	null	null		null	null		null	null		null	null		Unigene81818_All//gi|129560505|dbj|BAF48803.1|//1.00E-31//wound-responsive AP2 like factor 1 [Nicotiana tabacum]	Unigene81818_All//1.00E-17//AT4G34410| RRTF1 (REDOX RESPONSIVE TRANSCRIPTION FACTOR 1); DNA binding / transcription factor	Unigene81818_All//2.00E-08//gi|82756570|gb|DV850132.1|DV850132	AP2-EREBP			nr -
Unigene81820_All	254	0.00	4.39	3.77	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	1.99E-06	Up	1.19E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene81820_All//gi|47847547|dbj|BAD21599.1|//8.00E-19//nucleolar RNA-binding Nop10p-like protein [Oryza sativa Japonica Group] >gi|47847676|dbj|BAD21457.1| nucleolar RNA-binding Nop10p-like protein [Oryza sativa Japonica Group]	Unigene81820_All//8.00E-16//AT2G20490| NOP10; RNA binding					nr -
Unigene81825_All	254	0.00	0.20	3.35	0.59	0.27	0.18	0.00	0.00	0.00	7.64E+00	6.08E-01		1.17E+01	8.97E-05	Up	-1.12E+00	5.82E-01		-1.73E+00	4.99E-01		null	null		null	null		Unigene81825_All//gi|159485866|ref|XP_001700965.1|//4.00E-16//non-discriminatory gln-glu-trna synthetase [Chlamydomonas reinhardtii] >gi|158281464|gb|EDP07219.1| non-discriminatory gln-glu-trna synthetase [Chlamydomonas reinhardtii]	Unigene81825_All//2.00E-16//AT5G64050| ERS (GLUTAMATE TRNA SYNTHETASE); glutamate-tRNA ligase			ko00970|Aminoacyl-tRNA biosynthesis//ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene81830_All	255	0.41	0.79	4.39	0.00	0.14	0.00	0.00	0.00	0.00	9.54E-01	6.20E-01		3.42E+00	1.92E-04	Up	7.08E+00	8.13E-01		null	null		null	null		null	null									ESTscan -
Unigene81836_All	255	0.41	0.40	4.39	0.20	0.54	0.00	0.00	0.00	0.00	-4.64E-02	9.85E-01		3.42E+00	1.92E-04	Up	1.47E+00	6.17E-01		-7.61E+00	6.18E-01		null	null		null	null									ESTscan -

Unigene81839_All	255	0.00	0.79	3.97	0.20	0.54	0.53	0.00	0.00	0.00	9.63E+00	1.34E-01		1.20E+01	1.27E-05	Up	1.47E+00	6.17E-01		1.44E+00	6.36E-01		null	null		null	null		Unigene81839_All//gi|297800202|ref|XP_002867985.1|//7.00E-15//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297313821|gb|EFH44244.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene81839_All//5.00E-13//AT4G18550| lipase class 3 family protein	Unigene81839_All//2.00E-85//DN826444				nr +
Unigene81842_All	255	0.21	0.00	3.76	0.00	0.27	0.18	0.00	0.16	0.16	-7.68E+00	6.01E-01		4.20E+00	2.16E-04	Up	8.08E+00	6.00E-01		7.47E+00	6.83E-01		7.36E+00	6.25E-01		7.29E+00	6.36E-01		Unigene81842_All//gi|145839451|gb|ABF96804.1|//7.00E-20//receptor-like protein kinase [Capsicum annuum]	Unigene81842_All//2.00E-18//AT1G70250| receptor serine/threonine kinase, putative	Unigene81842_All//3.00E-10//BQ409108				nr +
Unigene81844_All	255	0.41	0.20	3.97	0.00	0.00	0.00	0.00	0.00	0.00	-1.05E+00	6.82E-01		3.27E+00	5.92E-04	Up	null	null		null	null		null	null		null	null		Unigene81844_All//COG0395//6.00E-12//ABC-type sugar transport system, permease component						cog +
Unigene81849_All	255	0.00	0.60	2.92	0.00	0.14	0.18	0.00	0.00	0.00	9.22E+00	2.31E-01		1.15E+01	3.24E-04	Up	7.08E+00	8.13E-01		7.47E+00	6.83E-01		null	null		null	null									ESTscan -
Unigene8185_All	809	1.88	4.13	2.04	13.73	10.56	12.90	4.44	0.41	13.05	1.14E+00	9.68E-04	Up	1.22E-01	8.08E-01		-3.79E-01	2.26E-02		-9.06E-02	6.61E-01		-3.43E+00	7.57E-17	Down	1.55E+00	1.25E-19	Up	Unigene8185_All//gi|56236116|gb|AAV84514.1|//8.00E-09//At4g24275 [Arabidopsis thaliana] >gi|109946539|gb|ABG48448.1| At4g24275 [Arabidopsis thaliana]		Unigene8185_All//5.00E-107//CA992663			GO:0050896	nr -
Unigene81851_All	255	0.00	0.00	4.80	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	9.08E-07	Up	null	null		null	null		null	null		null	null		Unigene81851_All//gi|115448589|ref|NP_001048074.1|//1.00E-10//Os02g0740600 [Oryza sativa Japonica Group] >gi|113537605|dbj|BAF09988.1| Os02g0740600 [Oryza sativa Japonica Group]	Unigene81851_All//7.00E-12//AT3G48180| unknown protein					nr -
Unigene8186_All	585	12.70	8.57	5.10	12.18	8.54	12.89	52.83	21.58	8.51	-5.67E-01	8.06E-03		-1.32E+00	1.46E-08	Down	-5.13E-01	1.45E-02		8.24E-02	7.31E-01		-1.29E+00	1.32E-41	Down	-2.63E+00	1.46E-111	Down	Unigene8186_All//gi|209967447|gb|ACJ02352.1|//8.00E-24//60S ribosomal protein L39 (Vernicia fordii] >gi|257219568|gb|ACV50437.1| 60S ribosomal protein L39 [Jatropha curcas]	Unigene8186_All//9.00E-24//AT4G31985| 60S ribosomal protein L39 (RPL39C)	Unigene8186_All//0.00E+00//TC162557	ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0043231	nr +
Unigene81867_All	256	0.00	0.59	4.16	0.00	0.00	0.00	0.00	0.00	0.00	9.21E+00	2.31E-01		1.20E+01	6.59E-06	Up	null	null		null	null		null	null		null	null		Unigene81867_All//gi|219112151|ref|XP_002177827.1|//1.00E-21//predicted protein [Phaeodactylum tricornutum CCAP 1055/1] >gi|217410712|gb|EEC50641.1| predicted protein [Phaeodactylum tricornutum CCAP 1055/1]						nr -
Unigene81868_All	256	0.00	0.00	2.91	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	3.24E-04	Up	null	null		null	null		null	null		null	null		Unigene81868_All//gi|5545339|dbj|BAA82556.1|//1.00E-14//lectin-like protein kinase [Populus nigra]						nr -
Unigene8187_All	1137	0.00	0.00	0.00	0.00	0.00	0.00	2.34	0.15	2.38	null	null		null	null		null	null		null	null		-3.99E+00	3.57E-14	Down	2.44E-02	9.66E-01		Unigene8187_All//gi|15219398|ref|NP_177459.1|//1.00E-153//glycosyl transferase family 1 protein [Arabidopsis thaliana]	Unigene8187_All//2.00E-154//AT1G73160| glycosyl transferase family 1 protein		ko00561|Glycerolipid metabolism//ko00563|Glycosylphosphatidylinositol(GPI)-anchor biosynthesis	GO:0008152	nr +
Unigene81870_All	256	0.20	0.00	3.74	0.19	0.00	0.71	0.00	0.00	0.00	-7.68E+00	6.01E-01		4.20E+00	2.16E-04	Up	-7.60E+00	5.43E-01		1.86E+00	4.57E-01		null	null		null	null									ESTscan -
Unigene81879_All	256	0.00	0.79	4.16	0.00	0.00	0.00	0.00	0.00	0.00	9.63E+00	1.34E-01		1.20E+01	6.59E-06	Up	null	null		null	null		null	null		null	null		Unigene81879_All//sp|Q07820|MCL1_HUMAN//5.00E-44//Induced myeloid leukemia cell differentiation protein Mcl-1 OS=Homo sapiens GN=MCL1 PE=1 SV=3						swissprot -
Unigene81881_All	257	0.20	0.99	3.52	0.58	0.13	1.58	0.49	0.00	0.31	2.28E+00	2.33E-01		4.11E+00	3.91E-04	Up	-2.12E+00	3.85E-01		1.44E+00	2.82E-01		-8.95E+00	2.33E-01		-6.71E-01	7.18E-01				Unigene81881_All//7.00E-39//DW485361				
Unigene81885_All	257	0.20	0.00	3.94	0.39	0.54	0.00	0.00	0.00	0.00	-7.67E+00	6.01E-01		4.27E+00	1.19E-04	Up	4.67E-01	8.75E-01		-8.60E+00	3.92E-01		null	null		null	null									ESTscan +
Unigene8189_All	454	0.69	0.00	0.00	1.21	1.14	4.28	0.65	0.18	1.32	-9.43E+00	3.63E-02		-9.43E+00	4.87E-02		-8.53E-02	9.07E-01		1.83E+00	2.80E-04	Up	-1.82E+00	2.10E-01		1.01E+00	2.18E-01		Unigene8189_All//gi|224056467|ref|XP_002298871.1|//2.00E-20//predicted protein [Populus trichocarpa] >gi|222846129|gb|EEE83676.1| predicted protein [Populus trichocarpa]	Unigene8189_All//7.00E-06//AT5G38820| unknown protein			GO:0005488	nr +
Unigene81908_All	257	0.00	2.76	10.77	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.30E-04	Up	1.34E+01	2.74E-15	Up	null	null		null	null		null	null		null	null		Unigene81908_All//gi|297827785|ref|XP_002881775.1|//6.00E-25//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297327614|gb|EFH58034.1| expressed protein [Arabidopsis lyrata subsp. lyrata]		Unigene81908_All//4.00E-22//TC165325	ko03040|Spliceosome		nr -
Unigene8191_All	1029	4.58	0.39	0.93	1.26	0.60	8.21	0.00	0.45	0.70	-3.54E+00	1.89E-18	Down	-2.30E+00	1.83E-11	Down	-1.06E+00	6.06E-02		2.71E+00	1.11E-26	Up	8.80E+00	1.94E-03		9.44E+00	2.63E-05	Up	Unigene8191_All//gi|224125188|ref|XP_002329915.1|//6.00E-19//predicted protein [Populus trichocarpa] >gi|222871152|gb|EEF08283.1| predicted protein [Populus trichocarpa]						nr -
Unigene81912_All	258	0.00	26.12	18.78	0.00	0.00	0.00	0.00	0.00	0.00	1.47E+01	1.68E-38	Up	1.42E+01	6.10E-27	Up	null	null		null	null		null	null		null	null		Unigene81912_All//sp|Q26643|TRF_SARPE//1.00E-19//Transferrin OS=Sarcophaga peregrina PE=1 SV=1						swissprot -
Unigene81915_All	258	0.00	0.98	4.13	0.00	0.27	0.53	0.00	0.00	0.00	9.94E+00	7.75E-02		1.20E+01	6.59E-06	Up	8.06E+00	6.00E-01		9.04E+00	3.09E-01		null	null		null	null		Unigene81915_All//gi|115435464|ref|NP_001042490.1|//3.00E-10//Os01g0229800 [Oryza sativa Japonica Group] >gi|113532021|dbj|BAF04404.1| Os01g0229800 [Oryza sativa Japonica Group]	Unigene81915_All//3.00E-10//AT4G24340| phosphorylase family protein	Unigene81915_All//2.00E-85//gi|109871899|gb|DW500875.1|DW500875				nr -
Unigene81916_All	258	0.00	3.14	4.54	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.30E-05	Up	1.21E+01	1.76E-06	Up	null	null		null	null		null	null		null	null		Unigene81916_All//sp|P08727|KIC19_HUMAN//2.00E-32//Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=3						swissprot +
Unigene8192_All	535	7.73	0.47	2.29	14.53	8.82	15.45	23.63	8.52	8.64	-4.03E+00	6.43E-18	Down	-1.75E+00	2.44E-07	Down	-7.20E-01	1.94E-04		8.89E-02	6.93E-01		-1.47E+00	3.70E-21	Down	-1.45E+00	2.15E-21	Down	Unigene8192_All//gi|240846170|dbj|BAH72623.1|//1.00E-77//Rsdv1 resistance like protein [Glycine max]	Unigene8192_All//3.00E-72//AT3G20000| TOM40; P-P-bond-hydrolysis-driven protein transmembrane transporter/ voltage-gated anion channel	Unigene8192_All//0.00E+00//gi|78354005|gb|DT574279.1|DT574279			GO:0004871//GO:0005244//GO:0005488//GO:0005741//GO:0006605//GO:0006811//GO:0008320//GO:0019866	nr -
Unigene81927_All	258	0.00	0.00	3.51	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	4.69E-05	Up	null	null		null	null		null	null		null	null									
Unigene81929_All	259	0.00	0.59	2.67	0.00	0.00	0.00	0.00	0.00	0.00	9.20E+00	2.31E-01		1.14E+01	6.10E-04	Up	null	null		null	null		null	null		null	null									
Unigene8193_All	1423	0.63	0.21	0.00	0.53	0.46	0.25	3.24	5.32	1.54	-1.55E+00	4.56E-02		-9.29E+00	6.29E-05	Down	-1.92E-01	8.21E-01		-1.05E+00	2.21E-01		7.15E-01	1.50E-04		-1.07E+00	1.55E-05	Down	Unigene8193_All//gi|140053517|gb|AB679572.2|//0.00E+00//Protein kinase [Medicago truncatula]	Unigene8193_All//8.00E-163//AT4G20270| BAM3 (BARELY ANY MERISTEM 3); ATP binding / protein binding / protein kinase/ protein serine/threonine kinase	Unigene8193_All//0.00E+00//TC138395			GO:0004702//GO:0006464//GO:0016628//GO:0031224//GO:0032559	nr +
Unigene81935_All	259	0.00	7.43	4.32	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	5.72E-11	Up	1.21E+01	3.42E-06	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene81942_All	259	0.00	0.00	3.29	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	8.97E-05	Up	null	null		null	null		null	null		null	null									
Unigene81949_All	259	0.00	22.69	7.40	0.00	0.00	0.00	0.00	0.00	0.00	1.45E+01	1.51E-33	Up	1.29E+01	1.46E-10	Up	null	null		null	null		null	null		null	null		Unigene81949_All//sp|P26228|SRP1_SARBU//2.00E-12//Protease inhibitor OS=Sarcophaga bullata PE=1 SV=1						swissprot -
Unigene81964_All	260	0.00	0.00	3.69	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene81964_All//gi|297832360|ref|XP_002884062.1|//2.00E-30//auxin efflux carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297329902|gb|EFH60321.1| auxin efflux carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene81964_All//1.00E-31//AT2G17500| auxin efflux carrier family protein					nr +
Unigene81965_All	260	0.00	2.73	1.64	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	3.30E-04	Up	1.07E+01	1.36E-02		null	null		null	null		null	null		null	null		Unigene81965_All//gi|20143982|gb|AAM02973.2|AF421540_1|//7.00E-33//Hsp70 (Cryptococcus cohnii]	Unigene81965_All//6.00E-25//AT1G16030| Hsp70b (heat shock protein 70B); ATP binding			ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -
Unigene81971_All	260	0.00	0.00	2.66	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.14E+01	6.10E-04	Up	null	null		null	null		null	null		null	null				Unigene81971_All//5.00E-12//TC153301					
Unigene81978_All	260	0.00	3.90	3.69	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	7.21E-06	Up	1.18E+01	2.44E-05	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene8198_All	563	13.66	46.89	45.97	0.62	1.90	1.36	0.15	0.00	0.14	1.78E+00	3.94E-46	Up	1.75E+00	5.12E-43	Up	1.61E+00	2.12E-02		1.14E+00	1.89E-01		-7.23E+00	3.98E-01		-8.61E-02	9.69E-01		Unigene8198_All//gi|89274062|dbj|BAE80740.1|//3.00E-74//cysteine proteinase [Platycodon grandiflorus]	Unigene8198_All//5.00E-63//AT5G43060| cysteine proteinase, putative / thiol protease, putative	Unigene8198_All//8.00E-62//gi|78332960|gb|DT553234.1|DT553234			GO:0004175//GO:0016628//GO:0019538	nr -
Unigene81984_All	261	2.21	4.08	2.04	3.44	4.49	6.06	16.20	6.41	5.34	8.87E-01	1.85E-01		-1.12E-01	9.07E-01		3.85E-01	5.89E-01		8.18E-01	1.31E-01		-1.34E+00	1.10E-06	Down	-1.60E+00	8.75E-09	Down	Unigene81984_All//gi|297606919|ref|NP_001059209.2|//5.00E-14//Os07g0224000 [Oryza sativa Japonica Group] >gi|255677612|dbj|BAF21123.2| Os07g0224000 [Oryza sativa Japonica Group]	Unigene81984_All//3.00E-14//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome	Unigene81984_All//8.00E-51//gi|109828018|gb|DW226662.1|DW226662	ko03010|Ribosome		nr -
Unigene81988_All	261	0.00	0.00	3.06	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene81988_All//gi|15242030|ref|NP_197565.1|//1.00E-12//COPT5; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter [Arabidopsis thaliana] >gi|14517486|gb|AAK62633.1| AT5g20650/T1M15_50 [Arabidopsis thaliana] >gi|15809714|gb|AAL06785.1| AT5g20650/T1M15_50 [Arabidopsis thaliana] >gi|21592530|gb|AAM64479.1| COPT5 [Arabidopsis thaliana]	Unigene81988_All//8.00E-11//AT5G20650| COPT5; copper ion transmembrane transporter/ high affinity copper ion transmembrane transporter					nr -
Unigene8199_All	1005	0.00	0.61	0.00	0.10	0.00	0.00	8.12	3.74	9.47	9.24E+00	1.16E-03		null	null		-6.63E+00	3.08E-01		-6.63E+00	3.92E-01		-1.12E+00	2.30E-09	Down	2.23E-01	1.97E-01		Unigene8199_All//gi|49798480|gb|AAT68601.1|//4.00E-73//benzoyl coenzyme A: benzyl alcohol benzoyltransferase [Petunia x hybrida] >gi|51556912|gb|AAU06226.1| benzoyl-CoA:benzyl alcohol/phenylethanol benzoyltransferase [Petunia x hybrida]	Unigene8199_All//1.00E-55//AT5G17540| transferase family protein		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis	GO:0016747	nr +
Unigene81996_All	261	0.00	1.16	3.88	0.00	0.00	1.38	0.00	0.00	0.00	1.02E+01	4.36E-02		1.19E+01	1.27E-05	Up	null	null		1.04E+01	2.37E-02		null	null		null	null		Unigene81996_All//gi|83776786|gb|ABC46708.1|//7.00E-31//chloroplast photosystem II 10 kDa protein [Arachis hypogaea]	Unigene81996_All//6.00E-30//AT1G79040| PSBR (photosystem II subunit R)	Unigene81996_All//6.00E-27//TC176065		ko00195|Photosynthesis		nr +
Unigene82_All	1124	5.45	8.57	8.53	8.42	10.26	10.05	15.95	15.13	41.75	6.53E-01	4.09E-04		6.47E-01	7.59E-04		2.86E-01	1.02E-01		2.55E-01	1.70E-01		-7.57E-02	6.19E-01		1.39E+00	2.09E-71	Up	Unigene82_All//gi|18146966|dbj|BAB82502.1|//1.00E-124//cig3 [Nicotiana tabacum]	Unigene82_All//5.00E-99//AT5G19400| SMG7	Unigene82_All//0.00E+00//gi|48820922|gb|CO122235.1|CO122235				nr +
Unigene82000_All	262	0.00	0.19	3.05	0.00	0.00	0.00	0.00	0.00	0.00	7.60E+00	6.08E-01		1.16E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene82000_All//gi|116055332|emb|CAL58000.1|//6.00E-14//Nuclear helicase MOP-3/SNO (DEAD-box superfamily) (ISS) [Ostreococcus tauri]	Unigene82000_All//5.00E-10//AT1G79350| EMB1135 (embryo defective 1135); DNA binding / protein binding / zinc ion binding					nr +

Unigene82002_All	262	0.00	5.61	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.10E-08	Up	1.07E+01	1.36E-02		null	null		null	null		null	null		null	null		Unigene82002_All//gi|62733576|gb|AA95693.1|//4.00E-11//CAP protein [Oryza sativa Japonica Group]	Unigene82002_All//2.00E-10//AT4G34490| ATCAP1 (ARABIDOPSIS THALIANA CYCLASE ASSOCIATED PROTEIN 1); actin binding					nr -
Unigene82003_All	262	0.20	0.77	3.25	0.00	0.13	0.34	0.00	0.00	0.00	1.95E+00	3.74E-01		4.03E+00	7.02E-04	Up	7.04E+00	8.13E-01		8.43E+00	4.70E-01		null	null		null	null									ESTscan -
Unigene82009_All	262	3.00	0.19	0.81	2.66	2.89	1.72	1.94	1.12	1.37	-3.95E+00	8.54E-04	Down	-1.88E+00	4.13E-02		1.19E-01	9.05E-01		-6.27E-01	4.76E-01		-7.94E-01	4.02E-01		-5.01E-01	5.83E-01									
Unigene82012_All	262	0.40	0.19	4.06	0.00	0.13	0.00	0.00	0.16	0.00	-1.05E+00	6.82E-01		3.35E+00	3.36E-04	Up	7.04E+00	8.13E-01		null	null		7.32E+00	6.25E-01		null	null		Unigene82012_All//sp|P22787|YIFB_ECOLI//5.00E-08//Uncharacterized protein yifB OS=Escherichia coli (strain K12) GN=yifB PE=3 SV=2							swissprot -
Unigene82018_All	262	0.00	3.09	1.63	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	9.30E-05	Up	1.07E+01	1.36E-02		null	null		null	null		null	null		null	null		Unigene82018_All//gi|301123659|ref|XP_002909556.1|//2.00E-15//conserved hypothetical protein [Phytophthora infestans T30-4] >gi|262100318|gb|EEY58370.1| conserved hypothetical protein [Phytophthora infestans T30-4]	Unigene82018_All//1.00E-05//AT3G04240| SEC (secret agent); transferase, transferring glycosyl groups					nr +
Unigene82026_All	263	0.00	0.39	3.85	0.00	0.00	0.34	0.00	0.00	0.00	8.59E+00	3.79E-01		1.19E+01	1.27E-05	Up	null	null		8.42E+00	4.70E-01		null	null		null	null		Unigene82026_All//gi|115472983|ref|NP_001060090.1|//6.00E-45//Os07g0577600 [Oryza sativa Japonica Group] >gi|113611626|dbj|BAF22004.1| Os07g0577600 [Oryza sativa Japonica Group]	Unigene82026_All//2.00E-45//AT3G61470| LHCA2; chlorophyll binding	Unigene82026_All//4.00E-28//TC138911		ko00196|Photosynthesis - antenna proteins		nr +
Unigene82028_All	263	0.00	0.00	5.06	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.23E+01	2.39E-07	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene82029_All	263	0.00	0.00	2.63	1.14	0.79	0.34	0.00	0.00	0.00	null	null		1.14E+01	6.10E-04	Up	-5.33E-01	6.78E-01		-1.73E+00	2.89E-01		null	null		null	null		Unigene82029_All//gi|255592435|ref|XP_002535693.1|//2.00E-18//two component histidine kinase, putative [Ricinus communis] >gi|223522258|gb|EEF26689.1| two component histidine kinase, putative [Ricinus communis]							nr +
Unigene82035_All	263	0.00	0.00	3.04	0.00	0.13	0.00	0.00	0.00	0.00	null	null		1.16E+01	1.71E-04	Up	7.03E+00	8.13E-01		null	null		null	null		null	null		Unigene82035_All//gi|219112363|ref|XP_002177933.1|//2.00E-15//chorismate synthase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217410818|gb|EEC50747.1| chorismate synthase [Phaeodactylum tricornutum CCAP 1055/1]	Unigene82035_All//1.00E-13//AT1G48850| EMB1144 (embryo defective 1144); chorismate synthase			ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis		nr -
Unigene82037_All	263	0.00	1.54	3.24	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	1.34E-02		1.17E+01	8.97E-05	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene82041_All	263	0.00	5.97	2.83	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	5.68E-09	Up	1.15E+01	3.24E-04	Up	null	null		null	null		null	null		null	null									
Unigene82055_All	264	0.00	7.87	6.66	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	7.93E-12	Up	1.27E+01	1.12E-09	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene8206_All	379	47.90	2.27	32.46	63.75	30.07	41.95	3.35	1.76	1.58	-4.40E+00	3.74E-82	Down	-5.62E-01	2.81E-05		-1.08E+00	7.61E-25	Down	-6.04E-01	1.98E-08		-9.24E-01	8.68E-02		-1.09E+00	3.58E-02				Unigene8206_All//4.00E-109//gi|78345710|gb|DT565984.1|DT565984					
Unigene82064_All	265	0.39	0.00	5.63	0.00	0.26	0.85	0.00	0.00	0.00	-8.63E+00	3.66E-01		3.83E+00	3.20E-06	Up	8.02E+00	6.00E-01		9.73E+00	1.18E-01		null	null		null	null		Unigene82064_All//gi|222839179|gb|EEE77530.1|//4.00E-08//predicted protein [Populus trichocarpa]							nr +
Unigene82069_All	265	0.00	0.00	2.61	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.14E+01	6.10E-04	Up	null	null		null	null		null	null		null	null		Unigene82069_All//gi|255544079|ref|XP_002513102.1|//2.00E-16//conserved hypothetical protein [Ricinus communis] >gi|223548113|gb|EEF49605.1| conserved hypothetical protein [Ricinus communis]							nr +
Unigene8207_All	251	21.89	118.09	46.25	22.43	50.76	109.94	14.99	64.78	28.25	2.43E+00	5.83E-77	Up	1.08E+00	1.05E-09	Up	1.18E+00	2.09E-14	Up	2.29E+00	1.32E-71	Up	2.11E+00	6.43E-44	Up	9.14E-01	2.44E-06				Unigene8207_All//7.00E-76//BF273389					
Unigene82072_All	265	0.00	0.57	6.43	0.00	0.00	0.00	0.00	0.00	0.00	9.16E+00	2.31E-01		1.27E+01	2.19E-09	Up	null	null		null	null		null	null		null	null		Unigene82072_All//gi|76573339|gb|ABA46774.1|//3.00E-23//ribosomal protein L25-like protein [Solanum tuberosum]		Unigene82072_All//2.00E-20//CO126066		ko03010|Ribosome		nr +
Unigene82074_All	265	0.00	0.76	3.62	0.00	0.00	0.00	0.00	0.00	0.00	9.58E+00	1.34E-01		1.18E+01	2.44E-05	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene82075_All	265	0.39	0.38	4.62	0.19	0.13	0.00	0.16	0.00	0.00	-4.64E-02	9.85E-01		3.55E+00	6.10E-05	Up	-5.33E-01	8.18E-01		-7.55E+00	6.18E-01		-7.32E+00	6.43E-01		-7.32E+00	6.00E-01									
Unigene82081_All	266	0.39	0.00	4.20	0.19	0.39	0.00	0.00	0.00	0.00	-8.62E+00	3.66E-01		3.42E+00	1.92E-04	Up	1.05E+00	8.05E-01		-7.55E+00	6.18E-01		null	null		null	null		Unigene82081_All//gi|194476778|ref|YP_002048957.1|//8.00E-11//two-component response regulator [Paulinella chromatophora] >gi|171191785|gb|ACB42747.1| two-component response regulator [Paulinella chromatophora]	Unigene82081_All//9.00E-07//AT1G27320| AHK3 (ARABIDOPSIS HISTIDINE KINASE 3); cytokinin receptor/ osmosensor/ protein histidine kinase		ARR-B			nr -
Unigene82087_All	266	0.39	1.14	4.40	1.69	2.33	0.34	0.16	0.00	0.00	1.54E+00	3.22E-01		3.48E+00	1.09E-04	Up	4.67E-01	6.34E-01		-2.31E+00	7.80E-02		-7.31E+00	6.43E-01		-7.31E+00	6.00E-01									
Unigene82090_All	266	0.00	0.00	3.20	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	8.97E-05	Up	null	null		null	null		null	null		null	null		Unigene82090_All//gi|83283993|gb|ABC01904.1|//1.00E-36//34 kDa outer mitochondrial membrane protein porin-like protein [Solanum tuberosum]	Unigene82090_All//5.00E-33//AT3G01280| VDAC1 (VOLTAGE DEPENDENT ANION CHANNEL 1); voltage-gated anion channel	Unigene82090_All//1.00E-18//TC179063				nr -
Unigene82093_All	266	0.00	0.00	4.80	1.69	0.13	0.00	0.00	0.00	0.00	null	null		1.22E+01	4.67E-07	Up	-3.70E+00	1.07E-02		-1.07E+01	5.78E-03		null	null		null	null									
Unigene8210_All	351	3.28	1.59	1.97	3.12	2.06	0.39	1.45	0.48	0.68	-1.05E+00	1.01E-01		-7.34E-01	2.67E-01		-6.00E-01	3.53E-01		-3.02E+00	2.14E-04	Down	-1.60E+00	1.07E-01		-1.09E+00	2.28E-01				Unigene8210_All//7.00E-18//CO112306					
Unigene82103_All	267	0.00	0.19	3.99	0.75	0.39	0.34	0.00	0.00	0.00	7.57E+00	6.08E-01		1.20E+01	6.59E-06	Up	-9.48E-01	5.87E-01		-1.14E+00	5.67E-01		null	null		null	null		Unigene82103_All//gi|168056125|ref|XP_001780072.1|//2.00E-10//sensory histidine protein kinase [Physcomitrella patens subsp. patens] >gi|162668475|gb|EDQ55081.1| sensory histidine protein kinase [Physcomitrella patens subsp. patens]	Unigene82103_All//2.00E-08//AT2G17820| ATHK1 (histidine kinase 1); histidine phosphotransfer kinase/ osmosensor/ protein histidine kinase		Orphans			nr +
Unigene82111_All	267	1.37	3.42	5.98	2.99	2.32	1.18	0.95	0.94	0.15	1.32E+00	7.93E-02		2.12E+00	5.41E-04	Up	-3.63E-01	6.23E-01		-1.33E+00	1.06E-01		-1.66E-02	1.02E+00		-2.67E+00	1.15E-01									
Unigene82119_All	267	0.00	3.61	3.19	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.37E-05	Up	1.16E+01	8.97E-05	Up	null	null		null	null		null	null		null	null									
Unigene82128_All	268	0.39	1.13	4.17	0.93	0.26	0.17	0.00	0.00	0.00	1.54E+00	3.22E-01		3.42E+00	1.92E-04	Up	-1.85E+00	2.75E-01		-2.46E+00	2.23E-01		null	null		null	null									ESTscan +
Unigene82213_All	520	45.18	17.34	16.38	43.01	39.47	60.54	92.69	45.09	52.17	-1.38E+00	8.33E-29	Down	-1.46E+00	3.60E-30	Down	-1.24E-01	3.52E-01		4.93E-01	1.26E-07		-1.04E+00	9.12E-46	Down	-8.29E-01	1.74E-32		Unigene8213_All//gi|225427377|ref|XP_002282974.1|//7.00E-23//PREDICTED: similar to protein synthesis initiation factor-like [Vitis vinifera]	Unigene8213_All//5.00E-23//AT3G10950| 60S ribosomal protein L37a (RPL37aB)	Unigene8213_All//0.00E+00//TC166764		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043169//GO:0043231	nr -
Unigene82136_All	268	0.00	0.00	16.89	0.00	0.00	0.34	0.00	0.00	0.00	null	null		1.40E+01	3.88E-25	Up	null	null		8.40E+00	4.69E-01		null	null		null	null									ESTscan -
Unigene8214_All	497	0.42	0.10	0.00	0.60	1.11	2.18	5.36	2.27	2.57	-2.05E+00	3.33E-01		-8.72E+00	1.44E-01		8.82E-01	4.21E-01		1.86E+00	1.00E-02		-1.24E+00	4.36E-04	Down	-1.06E+00	1.58E-03		Unigene8214_All//gi|252972646|dbj|BAH84784.1|//2.00E-15//cytochrome P450 [Nicotiana tabacum]	Unigene8214_All//7.00E-14//AT4G37310| CYP81H1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene8214_All//1.00E-20//TC168055		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0005506//GO:0008152//GO:0016491	nr +
Unigene82140_All	269	0.00	0.75	4.55	0.00	0.00	0.00	0.00	0.00	0.00	9.56E+00	1.34E-01		1.22E+01	9.08E-07	Up	null	null		null	null		null	null		null	null		Unigene82140_All//sp|Q6DN04|MIF_MACMU//7.00E-30//Macrophage migration inhibitory factor OS=Macaca mulatta GN=MIF PE=3 SV=4				ko00360|Phenylalanine metabolism//ko00350|Tyrosine metabolism		swissprot -
Unigene82143_All	269	0.00	0.00	2.77	1.30	0.00	0.50	1.26	1.09	0.15	null	null		1.14E+01	3.24E-04	Up	-1.03E+01	9.43E-03		-1.36E+00	3.37E-01		-2.09E-01	8.50E-01		-3.09E+00	3.91E-02									
Unigene82145_All	269	0.00	0.19	2.77	0.00	0.51	0.17	0.00	0.00	0.00	7.56E+00	6.08E-01		1.14E+01	3.24E-04	Up	9.00E+00	3.16E-01		7.39E+00	6.83E-01		null	null		null	null		Unigene82145_All//COG4948//2.00E-15//L-alanine-DL-glutamate epimerase and related enzymes of enolase superfamily							cog -
Unigene82158_All	270	0.00	0.94	4.93	0.00	0.00	0.00	0.00	0.00	0.00	9.87E+00	7.75E-02		1.23E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene82158_All//sp|Q9V3A4|CSUP_DROME//3.00E-13//Protein catecholamines up OS=Drosophila melanogaster GN=Catsup PE=1 SV=1							swissprot -
Unigene8216_All	738	0.14	0.96	0.00	0.14	0.05	0.92	1.20	2.38	3.08	2.76E+00	9.13E-03		-7.15E+00	3.87E-01		-1.53E+00	5.83E-01		2.77E+00	1.14E-02		9.83E-01	2.65E-02		1.35E+00	3.86E-04	Up			Unigene8216_All//9.00E-07//TC167828					
Unigene82162_All	270	0.97	0.75	7.89	1.11	0.51	1.51	0.00	0.15	0.00	-3.68E-01	7.78E-01		3.03E+00	3.19E-07	Up	-1.12E+00	4.24E-01		4.44E-01	7.01E-01		7.27E+00	6.25E-01		null	null		Unigene82162_All//gi|109287747|dbj|BAE96294.1|//1.00E-09//beta subunit 1 of SnRK1 [Oryza sativa Japonica Group]		Unigene82162_All//1.00E-102//TC165533				nr -
Unigene82166_All	270	43.02	11.45	24.46	36.16	57.14	63.73	26.93	54.33	32.46	-1.91E+00	7.63E-23	Down	-8.15E-01	2.55E-06		6.60E-01	6.82E-07		8.18E-01	5.53E-10		1.01E+00	6.82E-14	Up	2.69E-01	1.30E-01		Unigene82166_All//gi|124359162|gb|ABN05685.1|//3.00E-07//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]		Unigene82166_All//5.00E-151//TC170468				nr +
Unigene82172_All	270	0.00	0.00	2.76	0.18	0.26	0.17	0.00	0.00	0.00	null	null		1.14E+01	3.24E-04	Up	4.67E-01	9.53E-01		-1.41E-01	9.46E-01		null	null		null	null		Unigene82172_All//gi|223994173|ref|XP_002286770.1|//1.00E-07//udp-d-glucose 6-dehydrogenase [Thalassiosira pseudonana CCMP1335] >gi|220978085|gb|EED96411.1| udp-d-glucose 6-dehydrogenase [Thalassiosira pseudonana CCMP1335]				ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene82173_All	270	0.00	0.00	2.56	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	6.10E-04	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene82178_All	270	0.00	0.56	2.96	0.00	0.00	0.00	0.00	0.00	0.00	9.14E+00	2.31E-01		1.15E+01	1.71E-04	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene82179_All	270	0.00	0.56	4.73	0.00	0.00	0.00	0.00	0.00	0.00	9.14E+00	2.31E-01		1.22E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene82179_All//gi|3929358|sp|O24143.1|NDUS8_TOBAC//7.00E-45//RecName: Full=NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial; AltName: Full=NADH-ubiquinone oxidoreductase 23 kDa subunit; AltName: Full=Complex I-23kD; Short=CI-23kD; AltName: Full=Complex I-28.5kD; Short=CI-28.5kD; Flags: Precursor >gi|1666177|emb|CAA70326.1| NADH dehydrogenase; NADH:ubiquinone oxidoreductase (complex I) [Nicotiana tabacum]	Unigene82179_All//1.00E-39//AT1G79010| NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial (TYKY)			ko00190|Oxidative phosphorylation		nr -
Unigene8218_All	1070	0.00	0.19	0.10	0.09	0.19	4.98	0.75	0.47	4.51	7.57E+00	1.34E-01		6.64E+00	3.88E-01		1.05E+00	6.11E-01		5.74E+00	4.61E-29	Up	-6.80E-01	3.53E-01		2.59E+00	2.14E-17	Up	Unigene8218_All//gi|8649004|emb|CAB94852.1|//1.00E-117//lipoxygenase [Prunus dulcis]	Unigene8218_All//9.00E-107//AT1G55020| LOX1; lipoxygenase	Unigene8218_All//0.00E+00//DR463563		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr -
Unigene82180_All	270	0.00	0.38	4.14	0.00	0.00	0.00	0.00	0.00	0.00	8.55E+00	3.79E-01		1.20E+01	3.41E-06	Up	null	null		null	null		null	null		null	null		Unigene82180_All//gi|17367847|sp|Q9XFY7.1|RL4_PRUAR//2.00E-19//RecName: Full=60S ribosomal protein L4; AltName: Full=L1 >gi|4887131|gb|AAD32206.1|AF134732 1 60S ribosomal protein L1 [Prunus armeniaca]	Unigene82180_All//1.00E-18//AT3G09630| 60S ribosomal protein L4/L1 (RPL4A)	Unigene82180_All//2.00E-08//TC158374		ko03010|Ribosome		nr +
Unigene82185_All	271	126.27	41.51	100.02	2.21	4.07	2.17	0.00	0.00	0.00	-1.61E+00	6.60E-52	Down	-3.36E-01	4.50E-04		8.82E-01	1.94E-01		-2.59E-02	9.64E-01		null	null		null	null		Unigene82185_All//gi|27372293|dbj|BAC53658.1|//1.00E-08//preprophytosulfokine [Zinnia violacea]	Unigene82185_All//2.00E-06//AT2G22860| ATPSK2 (PHYTOSULFOKINE 2 PRECURSOR); growth factor	Unigene82185_All//3.00E-13//TC168245				nr -

Unigene82190_All	271	0.00	0.19	2.95	0.92	0.38	0.00	0.00	0.00	0.00	7.55E+00	6.08E-01		1.15E+01	1.71E-04	Up	-1.27E+00	4.23E-01		-9.84E+00	7.30E-02		null	null		null	null		Unigene82190_All//gi|94313700|ref|YP_586909.1|//3.00E-07//high-affinity branched-chain amino acid transport protein of the ABC transporter ATP binding [Cupriavidus metallidurans CH34] >gi|93357552|gb|ABF11640.1| high-affinity branched-chain amino acid transport protein of the ABC transporter, ATP binding [Cupriavidus metallidurans CH34] >gi|222834352|gb|EEE72829.1| ABC transporter family protein [Populus trichocarpa]						nr +
Unigene82198_All	271	1.16	0.56	5.89	0.00	0.00	0.00	0.00	0.00	0.00	-1.05E+00	4.43E-01		2.35E+00	2.09E-04	Up	null	null		null	null		null	null		null	null							
Unigene822_All	3564	12.38	29.78	16.47	45.12	51.23	68.14	35.98	41.70	44.29	1.27E+00	1.75E-111	Up	4.12E-01	4.48E-09		1.83E-01	1.79E-07		5.95E-01	1.01E-76		2.13E-01	1.42E-08		3.00E-01	4.37E-17		Unigene822_All//gi|224144297|ref|XP_002325251.1|//0.00E+00//autoinhibited calcium ATPase [Populus trichocarpa] >gi|222866685|gb|EEF03816.1| autoinhibited calcium ATPase [Populus trichocarpa]	Unigene822_All//0.00E+00//AT4G29900| ACA10 (AUTOINHIBITED CA(2+)-ATPASE 10); calcium-transporting ATPase/ calmodulin binding	Unigene822_All//0.00E+00//gi|78339628|gb|DT559902.1|DT559902			GO:0003006//GO:0005515//GO:0009206//GO:0009506//GO:0019829/GO:0031224//GO:0032559//GO:0046873//GO:0046914//GO:0048229//GO:0048513//GO:0051707//GO:0070838	nr +
Unigene82207_All	272	2.50	2.98	7.83	0.00	0.00	0.00	0.00	0.00	0.00	2.53E-01	7.26E-01		1.65E+00	7.52E-04	Up	null	null		null	null		null	null		null	null				Unigene82207_All//4.00E-139//gi|109880288|gb|DW509258.1|DW509258				
Unigene82213_All	272	0.00	0.19	3.52	0.00	0.63	0.00	0.00	0.00	0.00	7.54E+00	6.08E-01		1.18E+01	2.44E-05	Up	9.31E+00	2.26E-01		null	null		null	null		null	null		Unigene82213_All//gi|222831977|gb|EEE70454.1|//8.00E-09//predicted protein [Populus trichocarpa]						nr +
Unigene82214_All	272	0.19	0.19	3.33	0.55	0.25	0.50	0.00	0.00	0.00	-4.65E-02	9.81E-01		4.11E+00	3.91E-04	Up	-1.12E+00	5.82E-01		-1.41E-01	9.42E-01		null	null		null	null							ESTscan +
Unigene82216_All	272	0.00	1.68	3.52	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	7.34E-03		1.18E+01	2.44E-05	Up	null	null		null	null		null	null		null	null							
Unigene82219_All	273	0.00	4.45	3.71	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	5.45E-07	Up	1.19E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene82219_All//gi|297607200|ref|NP_001059609.2|//1.00E-13//Os07g0471300 [Oryza sativa Japonica Group] >gi|255677755|dbj|BAF21523.2| Os07g0471300 [Oryza sativa Japonica Group]	Unigene82219_All//6.00E-14//AT1G69410| AGO7 (ARGONAUTE7); nucleic acid binding					nr -
Unigene8222_All	798	0.46	0.00	0.00	1.69	1.51	1.41	1.59	0.21	0.75	-8.84E+00	1.95E-02		-8.84E+00	2.77E-02		-1.58E-01	8.08E-01		-2.52E-01	6.86E-01		-2.92E+00	1.46E-05	Down	-1.09E+00	3.58E-02		Unigene8222_All//gi|148524773|dbj|BAF63394.1|//2.00E-65//kinetochore protein [Olimarabidopsis pumila]	Unigene8222_All//3.00E-51//AT3G54630| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 11 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Kinetochore protein Ndc80 (InterPro:IPR005550); Has 19800 Blast hits to 12108 proteins in 845 species: Archae - 345; Bacteria - 1709; Metazoa - 11031; Fungi - 1499; Plants - 797; Viruses - 39; Other Eukaryotes - 4380 (source: NCBI BLink).	Unigene8222_All//2.00E-155//CO109066			GO:0000097//GO:0008172//GO:0015629//GO:0017111//GO:0032559	nr -
Unigene82222_All	273	0.00	0.00	2.73	0.00	0.38	0.00	0.00	0.00	0.00	null	null		1.14E+01	3.24E-04	Up	8.56E+00	4.52E-01		null	null		null	null		null	null		Unigene82222_All//gi|294714021|gb|ADF30254.1|//2.00E-06//p-coumarate:CoA ligase 1 [Sorbus aucuparia]	Unigene82222_All//9.00E-05//AT5G63380| 4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein			ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr +
Unigene82224_All	273	0.00	2.23	4.10	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	1.16E-03		1.20E+01	3.41E-06	Up	null	null		null	null		null	null		null	null		Unigene82224_All//gi|242094546|ref|XP_002437763.1|//8.00E-09//hypothetical protein SORBIDRAFT_10g002225 [Sorghum bicolor] >gi|241915986|gb|EER89130.1| hypothetical protein SORBIDRAFT_10g002225 [Sorghum bicolor]						nr -
Unigene82227_All	273	0.00	0.00	2.93	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	1.71E-04	Up	null	null		null	null		null	null		null	null							ESTscan -
Unigene82228_All	273	0.00	0.00	2.54	0.36	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	6.10E-04	Up	-8.51E+00	3.08E-01		-8.51E+00	3.92E-01		null	null		null	null							ESTscan +
Unigene82231_All	273	0.00	0.74	4.68	0.00	0.00	0.00	0.00	0.00	0.00	9.54E+00	1.34E-01		1.22E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene82231_All//gi|297822305|ref|XP_002879035.1|//4.00E-27//calmodulin-2 [Arabidopsis lyrata subsp. lyrata] >gi|297324874|gb|EFH55294.1| calmodulin-2 [Arabidopsis lyrata subsp. lyrata]	Unigene82231_All//1.00E-28//AT5G21274| CAM6 (CALMODULIN 6); calcium ion binding	Unigene82231_All//5.00E-40//TC178185	ko04626|Plant-pathogen interaction//ko04070|Phosphatidylinositol signaling system		nr -
Unigene82232_All	274	0.00	0.37	3.89	0.00	0.00	0.00	0.00	0.00	0.00	8.53E+00	3.79E-01		1.19E+01	6.59E-06	Up	null	null		null	null		null	null		null	null		Unigene82232_All//gi|15228558|ref|NP_189542.1|//9.00E-23//calcium-binding EF hand family protein [Arabidopsis thaliana] >gi|75336201|sp|Q9MEG5.1|CML30_ARATH RecName: Full=Probable calcium-binding protein CML30; AltName: Full=Calmodulin-like protein 30	Unigene82232_All//4.00E-24//AT3G29000| calcium-binding EF hand family protein		ko04626|Plant-pathogen interaction		nr +
Unigene82234_All	274	0.19	0.74	3.11	0.55	0.00	0.00	0.00	0.00	0.00	1.95E+00	3.74E-01		4.03E+00	7.02E-04	Up	-9.09E+00	1.64E-01		-9.09E+00	2.31E-01		null	null		null	null		Unigene82234_All//gi|255591560|ref|XP_002535534.1|//2.00E-09//Protein amg6, putative [Ricinus communis] >gi|223522739|gb|EEF26848.1| Protein amg6, putative [Ricinus communis]						nr +
Unigene82239_All	274	1.15	0.74	6.80	0.00	0.38	0.00	0.00	0.00	0.00	-6.31E-01	6.21E-01		2.57E+00	1.69E-05	Up	8.56E+00	4.52E-01		null	null		null	null		null	null							
Unigene8224_All	1224	0.00	0.17	0.00	0.04	0.34	0.04	54.82	11.00	36.23	7.37E+00	1.34E-01		null	null		3.05E+00	5.67E-02		-1.41E-01	9.46E-01		-2.32E+00	8.07E-202	Down	-5.98E-01	1.20E-25		Unigene8224_All//gi|15239629|ref|NP_200248.1|//1.00E-122//late embryogenesis abundant protein-related / LEA protein-related [Arabidopsis thaliana] >gi|10257484|dbj|BAB10109.1| root cap protein 2-like protein [Arabidopsis thaliana] >gi|71143048|gb|AAZ23915.1| At5g54370 [Arabidopsis thaliana]	Unigene8224_All//2.00E-122//AT5G54370| late embryogenesis abundant protein-related / LEA protein-related					nr +
Unigene82240_All	274	0.38	0.74	3.69	0.36	0.13	0.00	0.00	0.00	0.29	9.54E-01	6.20E-01		3.27E+00	5.92E-04	Up	-1.53E+00	5.83E-01		-8.51E+00	3.92E-01		null	null		8.18E+00	4.00E-01							
Unigene82242_All	274	0.19	0.74	4.28	0.00	0.13	0.00	0.00	0.00	0.00	1.95E+00	3.74E-01		4.48E+00	1.90E-05	Up	6.97E+00	8.13E-01		null	null		null	null		null	null		Unigene82242_All//gi|224011978|ref|XP_002294642.1|//4.00E-23//peroxidase/catalase [Thalassiosira pseudonana CCMP1335] >gi|220969662|gb|EED88002.1| peroxidase/catalase [Thalassiosira pseudonana CCMP1335]						nr +
Unigene8225_All	454	2.54	0.78	4.57	8.67	3.19	6.47	1.40	1.01	0.44	-1.70E+00	1.21E-02		8.51E-01	6.95E-02		-1.44E+00	9.56E-07	Down	-4.23E-01	1.93E-01		-4.64E-01	5.93E-01		-1.67E+00	4.29E-02		Unigene8225_All//gi|115435614|ref|NP_001042565.1|//3.00E-08//Os01g0243600 [Oryza sativa Japonica Group] >gi|113532096|dbj|BAF04479.1| Os01g0243600 [Oryza sativa Japonica Group]						nr +
Unigene82250_All	275	0.19	0.37	3.10	0.00	0.00	0.00	0.00	0.00	0.00	9.53E-01	7.23E-01		4.03E+00	7.02E-04	Up	null	null		null	null		null	null		null	null		Unigene82250_All//sp|Q99612|KLF6_HUMAN//2.00E-51//Krueppel-like factor 6 OS=Homo sapiens GN=KLF6 PE=1 SV=3						swissprot +
Unigene82255_All	275	0.00	0.55	2.71	0.00	0.38	0.00	0.00	0.00	0.00	9.11E+00	2.31E-01		1.14E+01	3.24E-04	Up	8.55E+00	4.52E-01		null	null		null	null		null	null		Unigene82255_All//gi|255084453|ref|XP_002508801.1|//9.00E-31//ATP-binding cassette superfamily [Micromonas sp. RCC299] >gi|226524078|gb|ACO70059.1| ATP-binding cassette superfamily [Micromonas sp. RCC299]	Unigene82255_All//3.00E-08//AT5G64840| ATGCN5 (A. THALIANA GENERAL CONTROL NON-REPRESSIBLE 5); transporter					nr -
Unigene82259_All	275	0.00	3.69	4.07	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.21E-06	Up	1.20E+01	3.41E-06	Up	null	null		null	null		null	null		null	null		Unigene82259_All//gi|115445085|ref|NP_001046322.1|//8.00E-16//Os02g0221500 [Oryza sativa Japonica Group] >gi|113535853|dbj|BAF08236.1| Os02g0221500 [Oryza sativa Japonica Group]	Unigene82259_All//3.00E-14//AT3G07810| heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative			ko03040|Spliceosome		nr -
Unigene8226_All	423	3.22	2.04	2.27	1.65	2.28	1.92	11.39	11.07	5.65	-6.59E-01	2.44E-01		-5.05E-01	3.82E-01		4.67E-01	5.47E-01		2.21E-01	7.78E-01		-4.22E-02	8.84E-01		-1.01E+00	2.63E-05	Down	Unigene8226_All//gi|297798592|ref|XP_002867180.1|//3.00E-20//ATNAP13 [Arabidopsis lyrata subsp. lyrata] >gi|297313016|gb|EFH34329.1| ATNAP13 [Arabidopsis lyrata subsp. lyrata]	Unigene8226_All//2.00E-21//AT4G33460| ATNAP13; transporter	Unigene8226_All//4.00E-109//CK640417			GO:0003006//GO:0009526//GO:0017111//GO:0032559	nr +
Unigene82260_All	275	0.00	1.84	2.52	0.72	0.00	0.00	0.00	0.00	0.00	1.08E+01	3.99E-03		1.13E+01	6.10E-04	Up	-9.50E+00	8.37E-02		-9.50E+00	1.32E-01		null	null		null	null		Unigene82260_All//gi|255070477|ref|XP_002507320.1|//9.00E-15//translation initiation factor [Micromonas sp. RCC299] >gi|226522595|gb|ACO68578.1| translation initiation factor [Micromonas sp. RCC299]						nr +
Unigene82265_All	276	54.79	16.71	35.50	102.88	192.51	66.93	0.46	0.00	0.14	-1.71E+00	1.59E-25	Down	-6.26E-01	2.49E-05		9.04E-01	1.41E-38		-6.20E-01	3.05E-10		-8.84E+00	2.33E-01		-1.67E+00	4.75E-01		Unigene82265_All//gi|155966601|gb|ABU41233.1|//7.00E-30//xyloglucan endotransglycosylase [Gossypium hirsutum] >gi|166343773|gb|ABY86634.1| xyloglucan endotransglycosylase/hydrolase [Gossypium arboreum]	Unigene82265_All//2.00E-25//AT5G65730| xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative	Unigene82265_All//9.00E-91//EV490420				nr +
Unigene82267_All	276	0.00	3.12	1.54	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	4.91E-05	Up	1.06E+01	1.36E-02		null	null		null	null		null	null		null	null		Unigene82267_All//sp|Q9V496|APLP_DROME//5.00E-31//Apolipophorins OS=Drosophila melanogaster GN=Rfabg PE=1 SV=2						swissprot -
Unigene82271_All	276	0.00	0.00	3.28	0.18	0.00	0.16	0.00	0.00	0.00	null	null		1.17E+01	4.69E-05	Up	-7.50E+00	5.43E-01		-1.42E-01	9.46E-01		null	null		null	null							ESTscan -
Unigene82273_All	276	0.38	0.00	3.86	0.00	0.50	0.00	0.15	0.00	0.00	-8.57E+00	3.66E-01		3.35E+00	3.36E-04	Up	8.96E+00	3.16E-01		null	null		-7.26E+00	6.43E-01		-7.26E+00	6.00E-01		Unigene82273_All//gi|94310510|ref|YP_583720.1|//1.00E-10//transcriptional regulator [Cupriavidus metallidurans CH34]						nr -
Unigene82274_All	276	0.38	0.55	3.86	0.00	0.25	0.16	0.00	0.00	0.00	5.39E-01	7.77E-01		3.35E+00	3.36E-04	Up	7.96E+00	6.00E-01		7.35E+00	6.83E-01		null	null		null	null							ESTscan -

Unigene82281_All	277	0.00	6.22	2.31	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	7.96E-10	Up	1.12E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene82281_All//gi|159481899|ref|XP_001699012.1|//4.00E-22//peptidyl-prolyl cis-trans isomerase, FKBP-type [Chlamydomonas reinhardtii] >gi|158273275|gb|EDO99066.1| peptidyl-prolyl cis-trans isomerase, FKBP-type [Chlamydomonas reinhardtii]	Unigene82281_All//9.00E-23//AT4G25340| immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related				nr -
Unigene82282_All	277	0.00	0.55	3.46	0.00	0.75	0.16	0.00	0.00	0.00	9.10E+00	2.31E-01		1.18E+01	2.44E-05	Up	9.54E+00	1.56E-01		7.35E+00	6.83E-01		null	null		null	null		Unigene82282_All//gi|222424488|dbj|BAH20199.1|//4.00E-08//AT4G21210| ATRP1 (PPDK REGULATORY PROTEIN); phosphoprotein phosphatase/ protein kinase	Unigene82282_All//2.00E-09//AT4G21210| ATRP1 (PPDK REGULATORY PROTEIN); phosphoprotein phosphatase/ protein kinase					nr -
Unigene82283_All	277	0.00	1.28	3.46	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	2.43E-02		1.18E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene82283_All//sp|O01159|RSP7_CAEEL//8.00E-08//Probable splicing factor, arginine/serine-rich 7 OS=Caenorhabditis elegans GN=rsp-7 PE=2 SV=3						swissprot -
Unigene82284_All	277	0.00	0.18	2.69	0.00	0.99	0.00	0.00	0.00	0.00	7.51E+00	6.08E-01		1.14E+01	3.24E-04	Up	9.96E+00	7.00E-02		null	null		null	null		null	null		Unigene82284_All//gi|255085931|ref|XP_002508932.1|//5.00E-15//also known as glycine decarboxylase l-protein [Micromonas sp. RCC299] >gi|226524210|gb|ACO70190.1| also known as glycine decarboxylase l-protein [Micromonas sp. RCC299]	Unigene82284_All//4.00E-14//ATIG48030| mtLPD1 (mitochondrial lipoamide dehydrogenase 1); ATP binding / dihydrolipoyl dehydrogenase			ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00020|Citrate cycle (TCA cycle)//ko00260|Glycine, serine and threonine metabolism		nr -
Unigene82288_All	277	0.00	0.00	2.50	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	6.10E-04	Up	null	null		null	null		null	null		null	null		Unigene82288_All//sp|Q89E33|Y7254_BRAJA//3.00E-27//UPF0283 membrane protein blr7254 OS=Bradyrhizobium japonicum GN=blr7254 PE=3 SV=1						swissprot -
Unigene8229_All	555	1.89	2.10	0.48	2.24	1.86	0.98	3.12	0.90	1.72	1.55E-01	7.88E-01		-1.97E+00	1.13E-02		-2.70E-01	6.54E-01		-1.20E+00	5.16E-02		-1.79E+00	1.89E-04	Down	-8.58E-01	4.40E-02				Unigene8229_All//4.00E-122//gi|72274230|gb|DT049552.1|DT049552				
Unigene82290_All	277	0.00	0.37	2.69	0.00	0.25	0.00	0.00	0.00	0.00	8.51E+00	3.79E-01		1.14E+01	3.24E-04	Up	7.96E+00	6.00E-01		null	null		null	null		null	null									ESTscan +
Unigene82293_All	277	0.38	0.37	4.42	0.00	0.00	0.82	0.00	0.00	0.00	-4.66E-02	9.85E-01		3.55E+00	6.10E-05	Up	null	null		9.67E+00	1.18E-01		null	null		null	null		Unigene82293_All//COG5473//5.00E-27//Predicted integral membrane protein						cog +
Unigene82295_All	277	6.42	5.12	7.50	7.91	7.09	5.05	31.90	24.14	8.49	-3.26E-01	5.10E-01		2.23E-01	6.07E-01		-1.59E-01	7.48E-01		-6.47E-01	1.44E-01		-4.02E-01	2.26E-02		-1.91E+00	4.38E-22	Down			Unigene82295_All//5.00E-120//TC177017				
Unigene82296_All	277	0.00	0.91	2.69	0.00	0.00	0.00	0.00	0.00	0.00	9.84E+00	7.75E-02		1.14E+01	3.24E-04	Up	null	null		null	null		null	null		null	null									
Unigene82299_All	278	0.00	7.11	5.75	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.96E-11	Up	1.25E+01	8.42E-09	Up	null	null		null	null		null	null		null	null		Unigene82299_All//gi|258649958|gb|ACN86731.1|//4.00E-20//NADH dehydrogenase subunit 1 [Canistrocarpus crispatus]	Unigene82299_All//4.00E-12//ATMG01275| Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C.			ko00190|Oxidative phosphorylation		nr +
Unigene823_All	4418	208.60	249.57	185.47	42.96	30.93	24.36	21.63	20.24	8.19	2.59E-01	7.22E-69		-1.70E-01	5.03E-25		-4.74E-01	2.87E-45		-8.18E-01	9.11E-106		-9.60E-02	6.84E-02		-1.40E+00	5.60E-148	Down	Unigene823_All//gi|34481633|emb|CAD45111.1|//1.00E-132//photosystem II G protein [Amborella trichopoda]	Unigene823_All//6.00E-115//ATCG00430| Encodes a protein which was originally thought to be part of photosystem II but its wheat homolog was later shown to encode for subunit K of NADH dehydrogenase.	Unigene823_All//0.00E+00//TC146351	ko00190|Oxidative phosphorylation		nr +
Unigene8230_All	456	100.17	48.22	74.04	20.32	26.13	10.80	1.58	0.46	0.44	-1.05E+00	2.28E-36	Down	-4.36E-01	6.15E-08		3.63E-01	2.68E-02		-9.12E-01	8.90E-07		-1.78E+00	2.78E-02		-1.85E+00	1.78E-02		Unigene8230_All//gi|124360655|gb|ABN08644.1|//3.00E-31//Rhodanese-like [Medicago truncatula]	Unigene8230_All//4.00E-28//AT2G42220| rhodanese-like domain-containing protein	Unigene8230_All//0.00E+00//TC157479		GO:0009534	nr +
Unigene82301_All	278	0.00	0.18	3.06	0.00	0.25	0.16	0.00	0.00	0.00	7.51E+00	6.08E-01		1.16E+01	8.96E-05	Up	7.95E+00	6.00E-01		7.34E+00	6.83E-01		null	null		null	null		Unigene82301_All//gi|222834400|gb|EEE72867.1|//9.00E-15//predicted protein [Populus trichocarpa]						nr -
Unigene82303_All	278	0.00	0.00	3.45	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene82303_All//gi|18072797|emb|CAC80373.1|//1.00E-43//glyceraldehyde-3-phosphate dehydrogenase [Capsicum annuum]	Unigene82303_All//6.00E-32//AT3G26650| GAPA (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase/ protein binding	Unigene82303_All//2.00E-27//gi|82755110|gb|DV848672.1|DV848672	ko00710|Carbon fixation in photosynthetic organisms		nr +
Unigene82306_All	278	0.00	1.46	2.49	0.18	0.00	0.49	0.00	0.00	0.00	1.05E+01	1.34E-02		1.13E+01	6.10E-04	Up	-7.49E+00	5.43E-01		1.44E+00	6.36E-01		null	null		null	null									
Unigene82307_All	278	0.00	7.66	8.62	0.00	0.25	0.00	0.00	0.00	0.00	1.29E+01	4.10E-12	Up	1.31E+01	3.24E-13	Up	7.95E+00	6.00E-01		null	null		null	null		null	null		Unigene82307_All//gi|15231730|ref|NP_190870.1|//3.00E-17//STV1 (SHORT VALVE1); structural constituent of ribosome [Arabidopsis thaliana] >gi|26454659|sp|P38666.2|RL242_ARATH RecName: Full=60S ribosomal protein L24-2; AltName: Full=Protein SHORT VALVE 1 >gi|7529726|emb|CAB86906.1| 60S ribosomal protein-like [Arabidopsis thaliana] >gi|16648706|gb|AAL25545.1| AT3g53020/F8J2_190 [Arabidopsis thaliana] >gi|20260562|gb|AAM13179.1| 60S ribosomal protein-like [Arabidopsis thaliana] >gi|30102870|gb|AAP21353.1| At3g53020 [Arabidopsis thaliana] >gi|80750876|dbj|BAE48150.1| ribosomal protein L24 [Arabidopsis thaliana]	Unigene82307_All//1.00E-18//AT3G53020| STV1 (SHORT VALVE1); structural constituent of ribosome		ko03010|Ribosome		nr -
Unigene82309_All	278	0.00	0.00	5.17	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.23E+01	6.28E-08	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene8231_All	313	1.00	1.78	0.85	3.66	4.07	3.03	1.76	0.00	0.76	8.28E-01	3.81E-01		-2.38E-01	8.50E-01		1.53E-01	8.22E-01		-2.73E-01	6.89E-01		-1.08E+01	4.61E-04	Down	-1.20E+00	1.64E-01		Unigene8231_All//gi|225449242|ref|XP_002280264.1|//1.00E-07//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene8231_All//1.00E-25//TC168550				nr +
Unigene82313_All	279	0.00	1.45	2.48	0.18	0.12	0.97	0.00	0.00	0.00	1.05E+01	1.34E-02		1.13E+01	6.10E-04	Up	-5.33E-01	8.18E-01		2.44E+00	2.21E-01		null	null		null	null									ESTscan -
Unigene82316_All	279	12.94	40.32	15.65	28.57	31.35	36.42	6.52	14.53	3.28	1.64E+00	6.03E-18	Up	2.74E-01	3.86E-01		1.34E-01	5.72E-01		3.50E-01	6.13E-02		1.16E+00	2.75E-05	Up	-9.89E-01	1.76E-02		Unigene82316_All//gi|224102883|ref|XP_002312841.1|//3.00E-15//ethylene-insensitive 3a [Populus trichocarpa] >gi|222849249|gb|EEE86796.1| ethylene-insensitive 3a [Populus trichocarpa]	Unigene82316_All//5.00E-10//AT3G20770| EIN3 (ETHYLENE-INSENSITIVE3); transcription factor	Unigene82316_All//1.00E-89//TC151023	EIL			nr +
Unigene82323_All	279	0.00	10.17	2.48	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	3.82E-16	Up	1.13E+01	6.10E-04	Up	null	null		null	null		null	null		null	null		Unigene82323_All//gi|224000067|ref|XP_002289706.1|//2.00E-25//RS9, ribosomal protein 9 [Thalassiosira pseudonana CCMP1335] >gi|220974914|gb|EED93243.1| RS9, ribosomal protein 9 [Thalassiosira pseudonana CCMP1335]	Unigene82323_All//3.00E-26//AT5G39850| 40S ribosomal protein S9 (RPS9C)	Unigene82323_All//1.00E-15//TC143304		ko03010|Ribosome		nr +
Unigene8233_All	582	0.54	0.70	1.28	8.64	5.98	4.66	1.53	1.01	6.64	3.69E-01	7.23E-01		1.25E+00	1.54E-01		-5.33E-01	3.97E-02		-8.93E-01	6.99E-04		-6.02E-01	3.85E-01		2.12E+00	2.55E-11	Up			Unigene8233_All//0.00E+00//gi|164313610|gb|ES827390.1|ES827390				
Unigene82331_All	280	0.00	0.36	6.66	0.53	0.00	0.00	0.00	0.00	0.00	8.50E+00	3.79E-01		1.27E+01	2.89E-10	Up	-9.06E+00	1.64E-01		-9.06E+00	2.31E-01		null	null		null	null		Unigene82331_All//COG0795//3.00E-15//Predicted permeases						cog +
Unigene82337_All	280	0.00	1.81	4.18	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	3.99E-03		1.20E+01	1.76E-06	Up	null	null		null	null		null	null		null	null									
Unigene82341_All	280	0.37	0.54	5.13	0.00	0.49	0.00	0.00	0.00	0.00	5.39E-01	7.77E-01		3.78E+00	5.81E-06	Up	8.94E+00	3.16E-01		null	null		null	null		null	null									ESTscan +
Unigene82345_All	281	0.37	0.00	4.17	0.18	0.49	0.00	0.00	0.00	0.00	-8.54E+00	3.66E-01		3.48E+00	1.09E-04	Up	1.47E+00	6.17E-01		-7.47E+00	6.17E-01		null	null		null	null									ESTscan +
Unigene82346_All	281	0.00	0.36	2.46	0.00	0.00	0.00	0.00	0.00	0.00	8.49E+00	3.79E-01		1.13E+01	6.10E-04	Up	null	null		null	null		null	null		null	null		Unigene82346_All//gi|60498691|dbj|BAD90700.1|//6.00E-41//plasma membrane intrinsic protein 2;4 [Mimosa pudica]	Unigene82346_All//2.00E-40//AT2G39010| PIP2E (PLASMA MEMBRANE INTRINSIC PROTEIN 2E); water channel	Unigene82346_All//1.00E-22//TC131084			nr -
Unigene82348_All	281	0.00	0.00	2.65	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.14E+01	3.24E-04	Up	null	null		null	null		null	null		null	null		Unigene82348_All//gi|212291468|gb|ACJ23863.1|//1.00E-08//Cas s 1 pollen allergen [Castanea sativa]						nr -
Unigene82351_All	281	0.00	1.62	3.79	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	7.34E-03		1.19E+01	6.58E-06	Up	null	null		null	null		null	null		null	null		Unigene82351_All//sp|Q7GUN9|ADH1_CERCO//2.00E-42//Alcohol dehydrogenase 1 OS=Ceratitis cosyra GN=ADH1 PE=3 SV=1						swissprot -
Unigene82353_All	281	0.00	0.90	2.46	0.00	0.00	0.00	0.00	0.00	0.00	9.82E+00	7.75E-02		1.13E+01	6.10E-04	Up	null	null		null	null		null	null		null	null		Unigene82353_All//sp|Q14802|FXYD3_HUMAN//3.00E-43//FXYD domain-containing ion transport regulator 3 OS=Homo sapiens GN=FXYD3 PE=2 SV=1						swissprot -
Unigene8236_All	1023	0.00	0.00	0.00	0.19	0.03	0.00	3.22	1.51	3.70	null	null		null	null		-2.53E+00	2.33E-01		-7.61E+00	1.32E-01		-1.09E+00	3.88E-04	Down	1.99E-01	5.11E-01		Unigene8236_All//gi|224053695|ref|XP_002297933.1|//1.00E-135//aminophospholipid ATPase [Populus trichocarpa] >gi|222845191|gb|EEE82738.1| aminophospholipid ATPase [Populus trichocarpa]	Unigene8236_All//3.00E-91//AT1G68710| haloacid dehalogenase-like hydrolase family protein	Unigene8236_All//1.00E-21//ES799109			GO:0000166//GO:0008152//GO:0016020//GO:0042625	nr -
Unigene82365_All	282	0.00	0.36	2.45	0.18	0.49	0.32	0.00	0.00	0.00	8.49E+00	3.79E-01		1.13E+01	6.10E-04	Up	1.47E+00	6.17E-01		8.59E-01	7.91E-01		null	null		null	null									ESTscan -
Unigene82366_All	282	0.00	153.98	66.28	0.71	0.00	0.00	0.00	0.00	0.00	1.72E+01	9.98E-251	Up	1.60E+01	1.44E-105	Up	-9.46E+00	8.37E-02		-9.46E+00	1.32E-01		null	null		null	null		Unigene82366_All//sp|P92192|LCP5_DROME//4.00E-18//Larval cuticle protein 5 OS=Drosophila melanogaster GN=Lcp65Ab1 PE=1 SV=1						swissprot +
Unigene82369_All	283	0.00	0.18	4.70	0.18	0.12	0.32	0.00	0.00	0.00	7.48E+00	6.08E-01		1.22E+01	2.39E-07	Up	-5.32E-01	8.18E-01		8.59E-01	7.91E-01		null	null		null	null		Unigene82369_All//COG0654//3.00E-15//2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases						cog -
Unigene82370_All	283	0.00	0.18	3.95	0.00	0.00	0.00	0.00	0.00	0.00	7.48E+00	6.08E-01		1.19E+01	3.41E-06	Up	null	null		null	null		null	null		null	null		Unigene82370_All//gi|255619912|ref|XP_002540059.1|//2.00E-28//conserved hypothetical protein [Ricinus communis] >gi|223499574|gb|EEF22324.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene82371_All	283	0.00	0.18	5.27	0.00	0.00	0.32	0.00	0.00	0.00	7.48E+00	6.08E-01		1.24E+01	3.21E-08	Up	null	null		8.32E+00	4.69E-01		null	null		null	null		Unigene82371_All//gi|255547954|ref|XP_002515034.1|//2.00E-07//photosystem II core complex proteins psbY, chloroplast precursor [Ricinus communis] >gi|223546085|gb|EEF47588.1| photosystem II core complex proteins psbY, chloroplast precursor [Ricinus communis]						nr -

Unigene82374_All	283	0.37	0.00	3.76	0.35	0.12	0.00	0.00	0.00	0.00	-8.53E+00	3.66E-01		3.35E+00	3.36E-04	Up	-1.53E+00	5.83E-01		-8.46E+00	3.92E-01		null	null		null	null		Unigene82374_All//gi|301095248|ref|XP_002896725.1|//8.00E-06//enoyl-CoA hydratase, mitochondrial precursor [Phytophthora infestans T30-4] >gi|262108786|gb|EE166838.1| enoyl-CoA hydratase, mitochondrial precursor [Phytophthora infestans T30-4]				ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene82375_All	283	0.00	0.72	4.89	0.18	0.24	0.32	0.00	0.00	0.00	9.48E+00	1.34E-01		1.23E+01	1.23E-07	Up	4.68E-01	9.53E-01		8.59E-01	7.91E-01		null	null		null	null									ESTscan -
Unigene82377_All	283	0.00	189.43	66.61	0.00	0.12	0.00	0.00	0.00	0.00	1.75E+01	0.00E+00	Up	1.60E+01	1.77E-106	Up	6.93E+00	8.13E-01		null	null		null	null		null	null		Unigene82377_All//sp|P17205|SER1_DROME//5.00E-17//Serine proteases 1/2 OS=Drosophila melanogaster GN=Jon99Cii PE=1 SV=2						swissprot -
Unigene8238_All	334	57.80	38.23	24.71	131.40	107.53	146.58	495.21	213.61	151.72	-5.97E-01	1.94E-06		-1.23E+00	4.27E-19	Down	-2.89E-01	1.29E-04		1.58E-01	5.35E-02		-1.21E+00	6.83E-199	Down	-1.71E+00	0.00E+00	Down	Unigene8238_All//gi|62319651|dbj|BAD95159.1|/1.00E-24//fructose bisphosphate aldolase - like protein [Arabidopsis thaliana]	Unigene8238_All//3.00E-26//AT2G36460| fructose-bisphosphate aldolase, putative	Unigene8238_All//1.00E-176//gi|13243709|gb|BE055842.2|BE055842		ko00010|Glycolysis / Gluconeogenesis//ko00710|Carbon fixation in photosynthetic organisms//ko00051|Fructose and mannose metabolism//ko00030|Pentose phosphate pathway	GO:0005576//GO:0006007//GO:0006970//GO:0009536//GO:0010038//GO:0016020//GO:0016832//GO:0030312//GO:0031967//GO:0031981//GO:0046914	nr -
Unigene82380_All	284	0.00	1.61	2.44	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	7.34E-03		1.13E+01	6.10E-04	Up	null	null		null	null		null	null		null	null									
Unigene82381_All	284	0.18	0.36	3.94	0.35	0.24	0.00	0.00	0.00	0.00	9.54E-01	7.23E-01		4.42E+00	3.51E-05	Up	-5.33E-01	8.12E-01		-8.45E+00	3.92E-01		null	null		null	null		Unigene82381_All//sp|Q1QRM1|GLND_NITHX//2.00E-40//[Protein-PII] uridylyltransferase OS=Nitrobacter hamburgensis (strain X14 / DSM 10229) GN=glnD PE=3 SV=1						swissprot -
Unigene82384_All	284	0.55	0.00	4.13	0.00	0.12	0.00	0.00	0.00	0.00	-9.11E+00	2.13E-01		2.90E+00	4.34E-04	Up	6.92E+00	8.13E-01		null	null		null	null		null	null		Unigene82384_All//COG1733//2.00E-07//Predicted transcriptional regulators						cog +
Unigene82388_All	285	0.18	0.00	3.55	1.22	0.00	0.32	0.00	0.00	0.00	-7.52E+00	6.01E-01		4.27E+00	1.19E-04	Up	-1.03E+01	9.43E-03		-1.95E+00	1.96E-01		null	null		null	null		Unigene82388_All//gi|255611240|ref|XP_002539289.1|//2.00E-06//Protease ecfE, putative [Ricinus communis] >gi|223507472|gb|EEF23094.1| Protease ecfE, putative [Ricinus communis]						nr +
Unigene8239_All	1071	0.10	0.00	0.00	0.79	0.45	0.97	10.50	9.09	0.93	-6.61E+00	3.66E-01		-6.61E+00	3.87E-01		-8.13E-01	2.80E-01		2.95E-01	6.93E-01		-2.08E-01	2.16E-01		-3.50E+00	3.20E-54	Down	Unigene8239_All//gi|224054176|ref|XP_002298129.1|//3.00E-86//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene8239_All//5.00E-80//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene8239_All//0.00E+00//TC131966		ko00904|Diterpenoid biosynthesis	GO:0008152//GO:0016491//GO:0044464	nr -
Unigene82392_All	285	0.00	0.00	5.23	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.24E+01	3.21E-08	Up	null	null		null	null		null	null		null	null		Unigene82392_All//gi|461944|sp|Q04960.1|DNJH_CUCSA//1.00E-28//RecName: Full=DnaJ protein homolog; AltName: Full=DNAJ-1 >gi|182860|emb|CAA47925.1| cs DnaJ-1 [Cucumis sativus]	Unigene82392_All//3.00E-23//AT3G44110| ATJ3; protein binding	Unigene82392_All//4.00E-16//ES791525		ko04141|Protein processing in endoplasmic reticulum		nr -
Unigene82398_All	285	0.18	0.00	4.11	1.40	0.00	0.00	0.00	0.00	0.00	-7.52E+00	6.01E-01		4.48E+00	1.90E-05	Up	-1.04E+01	4.38E-03		-1.04E+01	1.11E-02		null	null		null	null		Unigene82398_All//sp|A4WCC0|MDTA_ENT38//2.00E-11//Multidrug resistance protein mdtA OS=Enterobacter sp. (strain 638) GN=mdtA PE=3 SV=1						swissprot +
Unigene82399_All	285	0.00	0.36	5.42	0.00	0.00	0.00	0.00	0.00	0.00	8.47E+00	3.79E-01		1.24E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene82399_All//gi|288557882|emb|CBJ49577.1|//2.00E-30//pathogenesis-related protein 10.5 [Vitis vinifera]						nr -
Unigene82402_All	286	0.00	0.18	2.79	0.00	0.00	0.32	0.00	0.00	0.00	7.47E+00	6.08E-01		1.14E+01	1.71E-04	Up	null	null		8.30E+00	4.69E-01		null	null		null	null									ESTscan +
Unigene82403_All	286	0.00	0.00	4.84	0.70	0.12	0.32	0.00	0.00	0.00	null	null		1.22E+01	1.23E-07	Up	-2.53E+00	2.33E-01		-1.14E+00	5.67E-01		null	null		null	null		Unigene82403_All//gi|255589437|ref|XP_002534961.1|//1.00E-13//Cation efflux system protein czcA, putative [Ricinus communis] >gi|223524292|gb|EEF27424.1| Cation efflux system protein czcA, putative [Ricinus communis]						nr -
Unigene82408_All	286	0.00	0.35	2.98	0.35	0.36	0.16	0.00	0.00	0.00	8.47E+00	3.79E-01		1.15E+01	8.96E-05	Up	5.21E-02	9.64E-01		-1.14E+00	6.73E-01		null	null		null	null		Unigene82408_All//gi|255077103|ref|XP_002502203.1|//9.00E-07//glycoside hydrolase family 103 protein [Micromonas sp. RCC299] >gi|226317468|gb|ACO63461.1| glycoside hydrolase family 103 protein [Micromonas sp. RCC299]						nr -
Unigene82410_All	286	0.00	0.00	5.59	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.24E+01	8.42E-09	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene82413_All	287	0.18	1.06	3.71	0.17	0.12	0.16	0.00	0.00	0.00	2.54E+00	1.51E-01		4.35E+00	6.45E-05	Up	-5.33E-01	8.18E-01		-1.41E-01	9.46E-01		null	null		null	null									ESTscan +
Unigene82415_All	287	0.00	0.35	2.41	0.00	0.96	0.63	0.00	0.00	0.00	8.46E+00	3.79E-01		1.12E+01	6.10E-04	Up	9.91E+00	7.00E-02		9.30E+00	1.93E-01		null	null		null	null		Unigene82415_All//gi|255604580|ref|XP_002538248.1|//1.00E-09//conserved hypothetical protein [Ricinus communis] >gi|223513091|gb|EEF24135.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene82418_All	287	0.00	1.24	2.97	0.17	0.12	0.00	0.00	0.00	0.00	1.03E+01	2.43E-02		1.15E+01	8.96E-05	Up	-5.33E-01	8.18E-01		-7.44E+00	6.17E-01		null	null		null	null		Unigene82418_All//sp|A8IL5L3|PLSX_AZOC5//1.00E-07//Phosphate acyltransferase OS=Azorhizobium caulinodans (strain ATCC 43989 / DSM 5975 / ORS 571) GN=plsX PE=3 SV=1						swissprot -
Unigene8242_All	269	0.97	0.94	1.58	1.67	0.13	0.50	3.62	2.18	0.59	-4.63E-02	9.86E-01		7.03E-01	5.53E-01		-3.70E+00	1.07E-02		-1.73E+00	1.61E-01		-7.33E-01	2.48E-01		-2.61E+00	3.35E-04	Down								
Unigene82421_All	287	0.00	1.24	3.90	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	2.43E-02		1.19E+01	3.41E-06	Up	null	null		null	null		null	null		null	null		Unigene82421_All//gi|297793079|ref|XP_002864424.1|//3.00E-11//heat shock protein 81-3 [Arabidopsis lyrata subsp. lyrata] >gi|297310259|gb|EFH40683.1| heat shock protein 81-3 [Arabidopsis lyrata subsp. lyrata]	Unigene82421_All//2.00E-09//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding			ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene82423_All	288	0.00	0.00	3.14	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene82423_All//gi|194475604|gb|ACF74549.1|//1.00E-36//RAV [Nicotiana tabacum]	Unigene82423_All//1.00E-26//AT1G13260| RAV1; DNA binding / transcription factor/ transcription repressor		AP2-EREBP			nr -
Unigene82426_All	288	0.00	0.18	2.96	0.17	0.00	0.00	0.00	0.00	0.00	7.46E+00	6.08E-01		1.15E+01	8.96E-05	Up	-7.43E+00	5.43E-01		-7.43E+00	6.17E-01		null	null		null	null		Unigene82426_All//gi|224006279|ref|XP_002292100.1|//3.00E-29//precursor of hydrogenase glutaryl-coa dehydrogenase [Thalassiosira pseudonana CCMP1335] >gi|220972619|gb|EED90951.1| precursor of hydrogenase glutaryl-coa dehydrogenase [Thalassiosira pseudonana CCMP1335]	Unigene82426_All//8.00E-11//AT3G51840| ACX4 (ACYL-COA OXIDASE 4); acyl-CoA oxidase/ oxidoreductase			ko04146|Peroxisome//ko00380|Tryptophan metabolism//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids//ko00310|Lysine degradation		nr +
Unigene82427_All	288	0.00	0.35	2.59	0.52	0.36	0.31	0.00	0.00	0.00	8.46E+00	3.79E-01		1.13E+01	3.24E-04	Up	-5.33E-01	7.83E-01		-7.27E-01	7.13E-01		null	null		null	null		Unigene82427_All//gi|224009732|ref|XP_002293824.1|//8.00E-09//predicted protein [Thalassiosira pseudonana CCMP1335] >gi|220970496|gb|EED88833.1| predicted protein [Thalassiosira pseudonana CCMP1335]						nr -
Unigene82429_All	288	0.00	0.70	2.96	0.00	0.60	0.00	0.00	0.00	0.00	9.46E+00	1.34E-01		1.15E+01	8.96E-05	Up	9.22E+00	2.26E-01		null	null		null	null		null	null		Unigene82429_All//sp|O32222|CSOR_BACSU//2.00E-09//Copper-sensing transcriptional repressor csoR OS=Bacillus subtilis GN=csoR PE=1 SV=1						swissprot -
Unigene82431_All	288	0.00	0.00	3.51	0.00	0.36	0.31	0.00	0.00	0.00	null	null		1.18E+01	1.27E-05	Up	8.49E+00	4.51E-01		8.29E+00	4.69E-01		null	null		null	null									
Unigene82432_All	288	11.63	3.87	6.66	22.31	8.01	6.27	1.61	62.98	3.73	-1.59E+00	1.13E-05	Down	-8.05E-01	2.32E-02		-1.48E+00	4.86E-11	Down	-1.83E+00	4.04E-13	Down	5.29E+00	1.96E-110	Up	1.21E+00	3.74E-02				Unigene82432_All//2.00E-54//gi|13248096|gb|BF274078.2|BF274078					ESTscan -
Unigene82433_All	289	0.00	0.00	2.58	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	3.24E-04	Up	null	null		null	null		null	null		null	null		Unigene82433_All//gi|82697947|gb|AB889008.1|//5.00E-24//CXE carboxylesterase [Malus pumila]	Unigene82433_All//1.00E-15//AT1G47480| hydrolase					nr -
Unigene82439_All	289	0.00	0.00	4.05	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.20E+01	1.76E-06	Up	null	null		null	null		null	null		null	null		Unigene82439_All//gi|171452362|dbj|BAG15872.1|//3.00E-31//transcription factor [Bruguiera gymnorhiza]	Unigene82439_All//1.00E-16//AT5G58620| zinc finger (CCCH-type) family protein	Unigene82439_All//1.00E-15//BQ402948	C3H			nr +
Unigene82442_All	289	0.00	0.00	3.32	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene82442_All//gi|15231733|ref|NP_191528.1|//6.00E-16//IQD13 (IQ-domain 13); calmodulin binding [Arabidopsis thaliana]	Unigene82442_All//3.00E-17//AT3G59690| IQD13 (IQ-domain 13); calmodulin binding	Unigene82442_All//8.00E-08//TC177692				nr +
Unigene82443_All	289	0.00	3.51	2.58	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	7.21E-06	Up	1.13E+01	3.24E-04	Up	null	null		null	null		null	null		null	null		Unigene82443_All//gi|301119039|ref|XP_002907247.1|//1.00E-16//ornithine decarboxylase 1 [Phytophthora infestans T30-4] >gi|262105759|gb|EE163811.1| ornithine decarboxylase 1 [Phytophthora infestans T30-4]				ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene82448_All	289	0.18	1.40	3.13	0.69	0.36	0.78	0.00	0.14	0.00	2.95E+00	5.90E-02		4.11E+00	3.91E-04	Up	-9.48E-01	5.87E-01		1.81E-01	9.34E-01		7.18E+00	6.25E-01		null	null		Unigene82448_All//sp|Q8FYW3|PUR6_BRUSU//3.00E-06//Phosphoribosylaminoimidazole carboxylase catalytic subunit OS=Brucella suis GN=purE PE=3 SV=1						swissprot -
Unigene82450_All	290	0.00	0.00	3.49	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene82450_All//gi|225426710|ref|XP_002275471.1|//1.00E-27//PREDICTED: similar to subtilase [Vitis vinifera]	Unigene82450_All//2.00E-18//AT4G34980| SLP2; serine-type peptidase					nr -
Unigene82452_All	290	0.18	1.05	2.94	0.00	0.24	0.00	0.00	0.00	0.00	2.54E+00	1.51E-01		4.03E+00	7.02E-04	Up	7.89E+00	6.00E-01		null	null		null	null		null	null		Unigene82452_All//gi|301103278|ref|XP_002900725.1|//3.00E-14//serine protease family S09A, putative [Phytophthora infestans T30-4] >gi|262101480|gb|EE159632.1| serine protease family S09A, putative [Phytophthora infestans T30-4]						nr -

Unigene82453_All	290	0.00	1.75	2.39	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	3.99E-03		1.12E+01	6.10E-04	Up	null	null		null	null		null	null		null	null		Unigene82453_All//gi|219126800|ref|XP_002183637.1|//2.00E-21//kinase pyruvate kinase 2 [Phaeodactylum tricornutum CCAP 1055/1] >gi|217404874|gb|EEC44819.1| kinase pyruvate kinase 2 [Phaeodactylum tricornutum CCAP 1055/1]	Unigene82453_All//3.00E-19//AT5G63680| pyruvate kinase, putative			ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms		nr -
Unigene82459_All	291	0.00	0.35	3.48	0.17	0.95	0.47	0.00	0.00	0.00	8.44E+00	3.79E-01		1.18E+01	1.27E-05	Up	2.47E+00	2.23E-01		1.44E+00	6.36E-01		null	null		null	null		Unigene82459_All//gi|83584323|gb|ABC24936.1|//3.00E-20//plastid endoribonuclease [Prototheca wickerhamii]	Unigene82459_All//2.00E-17//AT3G20390| endoribonuclease L-PSP family protein					nr +
Unigene82463_All	291	0.00	0.17	2.74	0.17	0.00	0.31	0.00	0.00	0.00	7.44E+00	6.08E-01		1.14E+01	1.71E-04	Up	-7.42E+00	5.43E-01		8.58E-01	7.90E-01		null	null		null	null									ESTscan +
Unigene82466_All	291	0.00	0.00	4.76	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.22E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene82466_All//gi|197312909|gb|ACH63235.1|//4.00E-42//alcohol dehydrogenase [Rheum australe]	Unigene82466_All//2.00E-34//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene82466_All//5.00E-09//gi|164322141|gb|ES819657.1|ES819657		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0008152//GO:0016620//GO:0043231	nr +
Unigene82468_All	291	0.00	0.35	3.11	0.00	0.00	0.00	0.00	0.00	0.00	8.44E+00	3.79E-01		1.16E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene82468_All//gi|168061613|ref|XP_001782782.1|//7.00E-12//nucleosome assembly protein family [Physcomitrella patens subsp. patens] >gi|162665755|gb|EDQ52429.1| nucleosome assembly protein family [Physcomitrella patens subsp. patens]	Unigene82468_All//2.00E-09//AT5G56950| NAP1;3 (NUCLEOSOME ASSEMBLY PROTEIN 1;3); DNA binding				GO:0006259//GO:0009292//GO:0010038//GO:0016020//GO:0043231	nr +
Unigene82473_All	292	0.00	3.64	3.28	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	3.79E-06	Up	1.17E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene82473_All//sp|Q961C9|TNG11_DROME//5.00E-37//Transport and Golgi organization protein 11 OS=Drosophila melanogaster GN=Tango11 PE=1 SV=1						swissprot -
Unigene82476_All	292	0.00	2.78	3.46	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.30E-05	Up	1.18E+01	1.27E-05	Up	null	null		null	null		null	null												ESTscan +
Unigene82483_All	293	0.71	1.21	2.36	1.87	0.82	6.47	3.46	0.43	2.31	7.61E-01	5.56E-01		1.73E+00	7.67E-02		-1.18E+00	2.25E-01		1.79E+00	4.16E-04	Up	-3.02E+00	1.08E-04	Down	-5.83E-01	3.27E-01		Unigene82483_All//gi|12580867|emb|CAC27142.1|//2.00E-33//60S ribosomal protein L13E [Picea abies]	Unigene82483_All//4.00E-34//AT3G49010| ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome	Unigene82483_All//3.00E-118//gi|48752697|gb|CO083216.1|CO083216		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene82485_All	293	0.00	2.59	1.09	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	1.75E-04	Up	1.01E+01	4.43E-02		null	null		null	null		null	null		null	null		Unigene82485_All//gi|115479005|ref|NP_001063096.1|//2.00E-07//Os09g0394900 [Oryza sativa Japonica Group] >gi|113631329|dbj|BAF25010.1| Os09g0394900 [Oryza sativa Japonica Group]	Unigene82485_All//1.00E-07//AT1G68090| ANN5; calcium ion binding / calcium-dependent phospholipid binding					nr +
Unigene82487_All	293	0.00	0.00	3.09	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene82487_All//gi|17066707|gb|AAL35366.1|AF442388_1/4.00E-40//defensin protein precursor [Capsicum annuum] >gi|40794499|gb|AAR90845.1| defensin precursor [Capsicum annuum]	Unigene82487_All//8.00E-11//AT2G02100| LCR69 (LOW-MOLECULAR-WEIGHT CYSTEINE-RICH 69); peptidase inhibitor				GO:0001906//GO:0006952//GO:0016787//GO:0030312	nr +
Unigene82488_All	293	0.18	0.69	3.09	0.68	0.00	0.15	0.00	0.00	0.00	1.95E+00	3.74E-01		4.11E+00	3.91E-04	Up	-9.41E+00	8.37E-02		-2.14E+00	3.46E-01		null	null		null	null									ESTscan +
Unigene8249_All	584	0.00	0.00	0.00	0.43	1.18	1.93	1.95	0.21	0.07	null	null		null	null		1.47E+00	1.16E-01		2.18E+00	2.82E-03		-3.19E+00	1.96E-05	Down	-4.84E+00	2.34E-07	Down	Unigene8249_All//gi|297823387|ref|XP_002879576.1|//1.00E-59//mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata] >gi|297325415|gb|EFH55835.1| mitochondrial substrate carrier family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8249_All//4.00E-56//AT2G35800| mitochondrial substrate carrier family protein	Unigene8249_All//0.00E+00//C0128626			GO:0006810//GO:0009526//GO:0019866//GO:0031224//GO:0046872	nr -
Unigene82491_All	293	0.00	0.86	2.36	0.00	0.00	0.00	0.00	0.00	0.00	9.76E+00	7.75E-02		1.12E+01	6.10E-04	Up	null	null		null	null		null	null		null	null		Unigene82491_All//COG3206//1.00E-06//uncharacterized protein involved in exopolysaccharide biosynthesis						cog +
Unigene82496_All	294	0.18	0.52	3.08	0.34	0.35	0.46	0.00	0.00	0.00	1.54E+00	5.29E-01		4.11E+00	3.91E-04	Up	5.23E-02	9.64E-01		4.44E-01	8.60E-01		null	null		null	null									ESTscan +
Unigene82498_All	294	0.00	0.00	3.62	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	6.58E-06	Up	null	null		null	null		null	null		null	null		Unigene82498_All//gi|1709006|sp|P50303.1|METK3_ACTCH//3.00E-49//RecName: Full=S-adenosylmethionine synthase 3; Short=AdoMet synthase 3; AltName: Full=Methionine adenosyltransferase 3; Short=MAT 3 >gi|726032|gb|AAA81379.1| S-adenosylmethionine synthetase [Actinidia chinensis]	Unigene82498_All//3.00E-38//AT3G17390| MTO3 (METHIONINE OVER-ACCUMULATOR 3); methionine adenosyltransferase	Unigene82498_All//2.00E-55//TC158637		ko00270|Cysteine and methionine metabolism//ko00450|Selenoamino acid metabolism	GO:0016765//GO:0032559//GO:0044237//GO:0044424//GO:0046872	nr -
Unigene8250_All	302	2.08	3.19	6.70	0.16	0.46	0.60	0.00	0.00	0.00	6.17E-01	3.76E-01		1.69E+00	8.47E-04	Up	1.47E+00	6.17E-01		1.86E+00	4.57E-01		null	null		null	null		Unigene8250_All//gi|15238586|ref|NP_198420.1|//7.00E-12//FIM2 (FIMBRIN-LIKE PROTEIN 2); actin binding [Arabidopsis thaliana] >gi|59797968|sp|Q9FKI0.1|FIMB2_ARATH RecName: Full=Fimbrin-like protein 2 >gi|9758643|dbj|BAB09267.1| fimbrin [Arabidopsis thaliana]	Unigene8250_All//2.00E-13//AT2G04750| fimbrin-like protein, putative	Unigene8250_All//9.00E-08//TC165166			GO:0008092//GO:0030312//GO:0043231//GO:0046872	nr +
Unigene82504_All	294	0.00	0.34	3.08	0.00	0.00	0.00	0.00	0.00	0.00	8.43E+00	3.79E-01		1.16E+01	4.69E-05	Up	null	null		null	null		null	null		null	null										
Unigene82508_All	295	0.00	0.86	2.35	0.00	0.93	0.00	0.00	0.00	0.00	9.75E+00	7.75E-02		1.12E+01	6.10E-04	Up	9.87E+00	7.00E-02		null	null		null	null		null	null		Unigene82508_All//gi|226530882|ref|NP_001147983.1|//3.00E-09//glucose-6-phosphate isomerase [Zea mays] >gi|195614974|gb|ACG29317.1| glucose-6-phosphate isomerase [Zea mays]	Unigene82508_All//1.00E-09//AT4G24620| PGI1 (PHOSPHOGLUCOSE ISOMERASE 1); glucose-6-phosphate isomerase			ko00500|Starch and sucrose metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00520|Amino sugar and nucleotide sugar metabolism//ko00030|Pentose phosphate pathway	GO:0006073//GO:0009526//GO:0009532//GO:0009908	nr +
Unigene82509_All	296	0.00	0.00	3.24	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene82509_All//gi|288310312|gb|ADC45395.1|//3.00E-49//HSP90-1 [Glycine max]	Unigene82509_All//6.00E-49//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Unigene82509_All//3.00E-57//TC156244		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267//GO:0044424//GO:0050896	nr +
Unigene82510_All	296	0.00	0.34	2.70	0.84	0.23	0.15	0.00	0.00	0.00	8.42E+00	3.79E-01		1.14E+01	1.71E-04	Up	-1.85E+00	2.75E-01		-2.46E+00	2.23E-01		null	null		null	null		Unigene82510_All//gi|226457881|gb|EE05179.1|//7.00E-15//Peptide-methionine--S-oxide reductase [Micromonas pusilla CCMP1545]	Unigene82510_All//1.00E-12//AT4G25130| peptide methionine sulfoxide reductase, putative				GO:0016671//GO:0043412	nr +
Unigene82513_All	296	0.18	0.51	3.06	0.17	0.00	0.31	0.00	0.00	0.00	1.54E+00	5.29E-01		4.11E+00	3.91E-04	Up	-7.39E+00	5.43E-01		8.59E-01	7.90E-01		null	null		null	null									ESTscan -
Unigene82514_All	296	0.00	2.40	0.90	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	9.81E+00	7.86E-02		null	null		null	null		null	null		null	null		Unigene82514_All//gi|255070457|ref|XP_002507310.1|//2.00E-07//carbohydrate-binding module family 48 protein [Micromonas sp. RCC299] >gi|226522585|gb|ACO68568.1| carbohydrate-binding module family 48 protein [Micromonas sp. RCC299]	Unigene82514_All//2.00E-07//AT4G16360| AMP-activated protein kinase					nr -
Unigene82515_All	296	0.00	4.28	1.98	0.00	0.00	0.00	0.00	0.00	0.00	1.21E+01	2.85E-07	Up	1.10E+01	2.15E-03		null	null		null	null		null	null		null	null		Unigene82515_All//sp|Q8VDJ3|VIGLN_MOUSE//1.00E-14//Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1						swissprot -
Unigene82516_All	297	0.00	0.00	2.33	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.12E+01	6.10E-04	Up	null	null		null	null		null	null		null	null		Unigene82516_All//gi|3947719|emb|CAA10101.1|//4.00E-28//ribosomal protein S28 [Prunus persica] >gi|3947721|emb|CAA10102.1| ribosomal protein S28 [Prunus persica] >gi|3947723|emb|CAA10103.1| ribosomal protein S28 [Prunus persica]	Unigene82516_All//6.00E-19//AT5G64140| RPS28 (RIBOSOMAL PROTEIN S28); structural constituent of ribosome	Unigene82516_All//6.00E-21//BF275781		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene82517_All	297	0.00	8.70	9.86	0.00	0.00	0.15	0.00	0.00	0.00	1.31E+01	1.05E-14	Up	1.33E+01	3.51E-16	Up	null	null		7.25E+00	6.82E-01		null	null		null	null		Unigene82517_All//sp|Q15847|APM2_HUMAN//8.00E-35//Adipose most abundant gene transcript 2 protein OS=Homo sapiens GN=APM2 PE=1 SV=1						swissprot +
Unigene82518_All	297	0.00	1.36	2.87	0.00	0.00	0.00	0.00	0.00	0.00	1.04E+01	1.34E-02		1.15E+01	8.96E-05	Up	null	null		null	null		null	null		null	null		Unigene82518_All//sp|P20477|GLNA1_DROME//3.00E-15//Glutamine synthetase 1, mitochondrial OS=Drosophila melanogaster GN=Gs1 PE=2 SV=3						swissprot +
Unigene82519_All	297	0.18	0.00	3.05	0.34	0.23	0.30	0.00	0.00	0.00	-7.46E+00	6.01E-01		4.11E+00	3.91E-04	Up	-5.32E-01	8.12E-01		-1.41E-01	9.47E-01		null	null		null	null									ESTscan -
Unigene8252_All	355	2.80	0.43	1.05	8.14	3.78	1.02	1.79	1.06	0.00	-2.71E+00	1.41E-03		-1.42E+00	6.08E-02		-1.11E+00	1.40E-03		-3.00E+00	1.05E-10	Down	-7.54E-01	3.73E-01		-1.08E+01	7.10E-05	Down		Unigene8252_All//4.00E-07//TC150723					
Unigene82521_All	297	0.00	0.00	3.23	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene82521_All//sp|P26039|TLN1_MOUSE//4.00E-49//Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=1						swissprot +
Unigene82527_All	298	0.00	0.00	3.22	0.00	0.00	0.15	0.00	0.00	0.00	null	null		1.17E+01	2.44E-05	Up	null	null		7.24E+00	6.82E-01		null	null		null	null		Unigene82527_All//gi|187373099|gb|ACD03270.1|//5.00E-45//glycine-rich RNA-binding protein [Nicotiana tabacum]	Unigene82527_All//2.00E-32//AT3G21660| CCR2 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	Unigene82527_All//3.00E-07//TC163079		ko03010|Ribosome//ko03040|Spliceosome	GO:0003006//GO:0004672//GO:0004871//GO:0006405//GO:0006464//GO:0006952//GO:0006970//GO:0009536//GO:0009699//GO:0010038//GO:0010118//GO:0016070//GO:0016620//GO:0032392//GO:0032559//GO:0042579//GO:0042802//GO:0043566//GO:0048511	nr -
Unigene8253_All	235	0.00	1.29	0.91	3.82	4.84	3.27	2.52	0.71	0.00	1.03E+01	4.36E-02		9.82E+00	1.37E-01		3.42E-01	6.20E-01		-2.24E-01	7.50E-01		-1.82E+00	4.71E-02		-1.13E+01	1.41E-04	Down		Unigene8253_All//6.00E-107//TC156987					

Unigene82530_All	298	0.00	3.23	0.89	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	1.37E-05	Up	9.80E+00	7.86E-02		null	null		null	null		null	null		null	null		Unigene82530_All//gi|22327649|ref|NP_680406.1|//2.00E-34//TG63 (THIOGLUCOSIDE GLUCOSIDASE 3); hydrolase, hydrolyzing O-glycosyl compounds / thioglucosidase [Arabidopsis thaliana] >gi|122214036|sp|Q8RH5.1|BGL39_ARATH RecName: Full=Putative myrosinase 3; AltName: Full=Sinigrinase 3; AltName: Full=Thioglucosidase 3; AltName: Full=Beta-glucosidase 39; Short=AtBGLU39; Flags: Precursor	Unigene82530_All//7.00E-36//AT5G48375| TG63 (THIOGLUCOSIDE GLUCOSIDASE 3): hydrolase, hydrolyzing O-glycosyl compounds / thioglucosidase			ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0005576//GO:0005840//GO:0006952//GO:0006970//GO:0009536//GO:0009725//GO:0010118//GO:0015926//GO:0019759//GO:0042579//GO:0043167	nr -
Unigene82532_All	298	0.70	0.00	4.11	0.00	0.23	0.00	0.00	0.00	0.00	-9.46E+00	1.21E-01		2.55E+00	8.25E-04	Up	7.85E+00	6.00E-01		null	null		null	null		null	null											ESTscan -
Unigene82534_All	298	0.00	0.00	2.50	0.67	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	3.24E-04	Up	-9.39E+00	8.37E-02		-9.39E+00	1.32E-01		null	null		null	null		Unigene82534_All//gi|2055384|gb|AAB53203.1|//1.00E-49//cold-stress inducible protein [Solanum tuberosum]	Unigene82534_All//1.00E-05//AT1G20450| ERD10 (EARLY RESPONSIVE TO DEHYDRATION 10); actin binding					GO:0003006//GO:0009628	nr -
Unigene82535_All	298	0.00	2.38	2.86	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	1.15E+01	8.96E-05	Up	null	null		null	null		null	null		null	null		Unigene82535_All//gi|116058574|emb|CAL54281.1|//4.00E-11//Translation initiation factor 3, subunit b (eIF-3b) (ISS) [Ostreococcus tauri]	Unigene82535_All//2.00E-10//AT1G73180| eukaryotic translation initiation factor-related					GO:0016020	nr +
Unigene82540_All	299	0.18	0.00	4.81	0.00	0.00	0.00	0.00	0.00	0.00	-7.45E+00	6.01E-01		4.78E+00	8.37E-07	Up	null	null		null	null		null	null		null	null		Unigene82540_All//gi|222874753|gb|EEF11884.1|//7.00E-07//predicted protein [Populus trichocarpa]						GO:0016491	nr +
Unigene82541_All	299	0.00	0.00	6.06	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.26E+01	5.68E-10	Up	null	null		null	null		null	null		null	null		Unigene82541_All//gi|18399468|ref|NP_565484.1|//3.00E-13//protein binding / structural molecule [Arabidopsis thaliana] >gi|4454472|gb|AAD20919.1| expressed protein [Arabidopsis thaliana] >gi|15982817|gb|AAL09756.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|16321001|gb|AAL15285.1| At2g20760/F5H14.27 [Arabidopsis thaliana] >gi|108385429|gb|ABF85787.1| At2g20760 [Arabidopsis thaliana]						GO:0005488//GO:0005905//GO:0012510//GO:0015031	nr +
Unigene82545_All	299	0.00	1.19	3.03	0.00	0.00	0.00	0.00	0.00	0.00	1.02E+01	2.43E-02		1.16E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene82545_All//sp|O14503|BHE40_HUMAN//2.00E-53//Class E basic helix-loop-helix protein 40 OS=Homo sapiens GN=BHLHE40 PE=1 SV=1							swissprot -
Unigene82551_All	300	0.00	0.17	3.91	0.00	0.11	0.30	0.00	0.00	0.00	7.40E+00	6.08E-01		1.19E+01	1.76E-06	Up	6.84E+00	8.13E-01		8.23E+00	4.69E-01		null	null		null	null		Unigene82551_All//COG4964//4.00E-11//Flp pilus assembly protein, secretin CpaC							cog +
Unigene82553_All	300	0.00	0.00	2.49	0.50	0.11	0.15	0.00	0.00	0.00	null	null		1.13E+01	3.24E-04	Up	-2.12E+00	3.85E-01		-1.73E+00	4.99E-01		null	null														ESTscan +
Unigene82554_All	300	0.00	0.00	2.84	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	8.96E-05	Up	null	null		null	null		null	null		null	null		Unigene82554_All//gi|15010696|gb|AAK74007.1|//4.00E-24//At1g29980/T1P2_9 [Arabidopsis thaliana] >gi|16323310|gb|AAL15410.1| At1g29980/T1P2_9 [Arabidopsis thaliana]	Unigene82554_All//2.00E-22//AT1G29980| INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, anchored to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34510.1); Has 174 Blast hits to 163 proteins in 15 species: Archae - 0; Bacteria - 10; Metazoa - 0; Fungi - 0; Plants - 164; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					GO:0031224//GO:0031410	nr -
Unigene82556_All	300	0.00	1.69	3.37	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	3.99E-03		1.17E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene82556_All//gi|116743285|emb|CAJ41420.1|//2.00E-48//4-coumarate-CoA ligase-like protein [Coffea arabica]	Unigene82556_All//5.00E-43//AT3G48990| AMP-dependent synthetase and ligase family protein			ko00940|Phenylpropanoid biosynthesis//ko04146|Peroxisome//ko00360|Phenylalanine metabolism//ko00071|Fatty acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0005576//GO:0009536//GO:0010038//GO:0016405//GO:0032559	nr +
Unigene8256_All	396	0.00	0.26	0.00	0.00	0.00	0.23	2.56	8.23	7.04	8.00E+00	3.79E-01		null	null		null	null		7.83E+00	4.69E-01		1.68E+00	3.92E-07	Up	1.46E+00	2.32E-05	Up			Unigene8256_All//5.00E-56//gi|109883973|gb|DW512943.1|DW512943					
Unigene82565_All	301	0.17	0.67	2.83	0.17	0.34	0.30	0.00	0.00	0.00	1.95E+00	3.74E-01		4.03E+00	7.02E-04	Up	1.05E+00	8.05E-01		8.59E-01	7.90E-01		null	null		null	null		Unigene82565_All//gi|255081248|ref|XP_002507846.1|//3.00E-14//protein-synthesizing GTPase [Micromonas sp. RCC299] >gi|226523122|gb|ACO69104.1| protein-synthesizing GTPase [Micromonas sp. RCC299]	Unigene82565_All//2.00E-05//AT5G08650| GTP-binding protein LepA, putative					GO:0017111//GO:0032561//GO:0043231	nr -
Unigene82566_All	301	0.00	1.18	3.36	0.00	0.00	0.00	0.00	0.00	0.00	1.02E+01	2.43E-02		1.17E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene82566_All//gi|301105657|ref|XP_002901912.1|//5.00E-29//P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4] >gi|262099250|gb|EEY57202.1| P-type ATPase (P-ATPase) Superfamily [Phytophthora infestans T30-4]	Unigene82566_All//1.00E-24//AT3G57330| ACA11 (autoinhibited Ca2+-ATPase 11); calcium-transporting ATPase/ calmodulin binding	Unigene82566_All//9.00E-08//gi|109837769|gb|DW236330.1|DW236330				GO:0005515//GO:0009206//GO:0009536//GO:0018829//GO:0031224//GO:0032559//GO:0046873//GO:0070838	nr -
Unigene82567_All	301	0.00	1.52	3.89	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	7.34E-03		1.19E+01	1.76E-06	Up	null	null		null	null		null	null		null	null											ESTscan -
Unigene82569_All	302	0.00	1.17	2.47	0.00	0.00	0.00	0.00	0.00	0.00	1.02E+01	2.43E-02		1.13E+01	3.24E-04	Up	null	null		null	null		null	null		null	null		Unigene82569_All//gi|148612407|gb|ABQ96119.1|//1.00E-07//alpha-glindin [Aegilops tauschii]				ko03022|Basal transcription factors		nr +
Unigene8257_All	351	0.30	2.89	3.03	0.28	1.18	0.26	1.08	0.71	0.11	3.28E+00	3.79E-04	Up	3.35E+00	3.36E-04	Up	2.05E+00	1.47E-01		-1.41E-01	9.47E-01		-6.02E-01	6.12E-01		-3.26E+00	2.22E-02		Unigene8257_All//gi|255550133|ref|XP_002516117.1|//1.00E-16//conserved hypothetical protein [Ricinus communis] >gi|223544603|gb|EEF46119.1| conserved hypothetical protein [Ricinus communis]	Unigene8257_All//4.00E-05//AT1G54200| unknown protein						nr -
Unigene82570_All	302	0.00	0.00	2.82	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	8.96E-05	Up	null	null		null	null		null	null		null	null											
Unigene82575_All	302	0.35	0.17	3.70	0.00	0.23	0.00	0.00	0.00	0.00	-1.05E+00	6.82E-01		3.42E+00	1.92E-04	Up	7.83E+00	6.00E-01		null	null		null	null		null	null		Unigene82575_All//gi|222873952|gb|EEF11083.1|//5.00E-21//atp-binding cassette [Populus trichocarpa]						GO:0003676//GO:0017111//GO:0032559//GO:0043232//GO:0051276	nr -
Unigene82583_All	303	0.00	1.84	2.64	0.33	0.34	0.89	0.56	0.14	0.26	1.08E+01	2.16E-03		1.14E+01	1.71E-04	Up	5.21E-02	9.64E-01		1.44E+00	4.09E-01		-2.02E+00	3.66E-01		-1.09E+00	5.51E-01											
Unigene82585_All	303	0.00	1.84	18.63	0.00	0.00	0.15	0.00	0.00	0.00	1.08E+01	2.16E-03		1.42E+01	1.92E-31	Up	null	null		7.22E+00	6.82E-01		null	null		null	null		Unigene82585_All//sp|P01877|IGHA2_HUMAN//6.00E-55//Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 SV=3							swissprot -
Unigene8259_All	224	3.97	14.02	13.79	0.22	0.31	1.41	1.13	0.00	0.18	1.82E+00	2.71E-06	Up	1.80E+00	7.85E-06	Up	4.67E-01	9.53E-01		2.67E+00	1.44E-01		-1.01E+01	4.02E-02		-2.67E+00	1.15E-01			Unigene8259_All//1.00E-18//ES810763						ESTscan -
Unigene82593_All	303	0.17	0.17	6.85	0.00	0.00	0.00	0.14	0.00	0.00	-4.67E-02	9.81E-01		5.31E+00	3.65E-10	Up	null	null		null	null		-7.12E+00	6.43E-01		-7.12E+00	6.00E-01		Unigene82593_All//gi|149392539|gb|ABR26072.1|//2.00E-15//imp biosynthesis protein [Oryza sativa Indica Group]		Unigene82593_All//1.00E-37//gi|78354813|gb|DT575087.1|DT575087				GO:0009536	nr -
Unigene82596_All	304	0.00	0.33	2.98	0.33	0.34	0.00	0.00	0.00	0.00	8.38E+00	3.79E-01		1.15E+01	4.69E-05	Up	5.23E-02	9.64E-01		-8.36E+00	3.92E-01		null	null		null	null		Unigene82596_All//gi|116783006|gb|ABK22759.1|//5.00E-06//unknown [Picea sitchensis] >gi|148907160|gb|ABR16723.1| unknown [Picea sitchensis] >gi|224285631|gb|ACN40534.1| unknown [Picea sitchensis] >gi|224286677|gb|ACN41042.1| unknown [Picea sitchensis]							nr +
Unigene826_All	3157	5.27	4.98	5.03	5.13	4.23	3.59	11.06	2.93	23.19	-8.30E-02	6.14E-01		-6.83E-02	6.53E-01		-2.77E-01	4.62E-02		-5.14E-01	1.42E-04		-1.92E+00	8.42E-83	Down	1.07E+00	1.02E-73	Up	Unigene826_All//gi|116269026|gb|ABJ91211.1|//0.00E+00//CBL-interacting protein kinase 3 [Populus trichocarpa]	Unigene826_All//0.00E+00//AT2G26980| CIPK3 (CBL-INTERACTING PROTEIN KINASE 3); kinase/ protein kinase/ protein serine/threonine kinase	Unigene826_All//0.00E+00//TC137302		ko04140|Regulation of autophagy	GO:0004674//GO:0006464//GO:0009755//GO:0023060//GO:0032559//GO:0043234	nr +
Unigene8260_All	720	0.00	23.58	8.51	0.00	0.10	0.00	0.00	0.00	0.00	1.45E+01	1.44E-97	Up	1.31E+01	3.79E-34	Up	6.58E+00	6.00E-01		null	null		null	null		null	null		Unigene8260_All//gi|224091074|ref|XP_002334977.1|//1.00E-07//predicted protein [Populus trichocarpa] >gi|222832505|gb|EEE70982.1| predicted protein [Populus trichocarpa]							nr -
Unigene82600_All	304	0.00	2.67	2.80	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	9.30E-05	Up	1.15E+01	8.96E-05	Up	null	null		null	null		null	null		null	null		Unigene82600_All//sp|P35749|MYH11_HUMAN//3.00E-49//Myosin-11 OS=Homo sapiens GN=MYH11 PE=1 SV=3							swissprot -
Unigene82601_All	304	0.17	2.50	2.98	0.00	0.34	0.00	0.00	0.00	0.00	3.86E+00	1.33E-03		4.11E+00	3.91E-04	Up	8.41E+00	4.51E-01		null	null		null	null		null	null											ESTscan -
Unigene82605_All	304	0.00	0.17	3.33	0.00	0.00	0.00	0.00	0.00	0.00	7.38E+00	6.08E-01		1.17E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene82605_All//sp|P01591|IGJ_HUMAN//3.00E-31//Immunoglobulin J chain OS=Homo sapiens GN=IGJ PE=1 SV=4							swissprot -
Unigene8261_All	368	0.00	0.00	0.00	0.81	1.12	0.00	6.55	0.00	0.00	null	null		null	null		4.67E-01	7.41E-01		-9.67E+00	3.98E-02		-1.27E+01	4.81E-17	Down	-1.27E+01	9.62E-18	Down			Unigene8261_All//4.00E-07//ES810950					
Unigene82613_All	305	0.00	337.24	115.75	0.00	0.34	0.00	0.00	0.00	0.00	1.84E+01	0.00E+00	Up	1.68E+01	2.27E-200	Up	8.40E+00	4.51E-01		null	null		null	null		null	null		Unigene82613_All//sp|Q7JZV0|LCP2A_DROME//2.00E-24//Cuticular protein 4TEg OS=Drosophila melanogaster GN=Cpr4TEg PE=1 SV=1							swissprot +
Unigene82614_All	305	0.00	0.50	3.49	0.00	0.00	0.00	0.00	0.00	0.00	8.96E+00	2.31E-01		1.18E+01	6.58E-06	Up	null	null		null	null		null	null		null	null		Unigene82614_All//gi|192908658|gb|ACF06437.1|//3.00E-29//ribosomal L28-like protein [Elaeis guineensis]	Unigene82614_All//4.00E-30//AT4G29410| 60S ribosomal protein L28 (RPL28C)	Unigene82614_All//3.00E-26//gi|54123569|gb|CO499078.1|CO499078		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0030312	nr +
Unigene82615_All	305	0.69	0.17	5.59	0.33	0.00	0.00	0.00	0.00	0.00	-2.05E+00	3.33E-01		3.03E+00	6.93E-06	Up	-8.35E+00	3.08E-01		-8.35E+00	3.92E-01		null	null		null	null											ESTscan -
Unigene82617_All	306	0.17	0.00	2.78	0.16	0.00	0.15	0.00	0.00	0.00	-7.42E+00	6.01E-01		4.03E+00	7.01E-04	Up	-7.35E+00	5.43E-01		-1.41E-01	9.46E-01		null	null		null	null											ESTscan -
Unigene8262_All	475	0.11	0.00	0.67	0.94	2.32	0.76	0.62	0.18	2.85	-6.78E+00	6.00E-01		2.61E+00	1.45E-01		1.30E+00	5.46E-02		-3.11E-01	7.57E-01		-1.82E+00	2.10E-01		2.19E+00	1.27E-04	Up									
Unigene82620_All	306	0.34	152.67	115.20	0.33	0.56	0.74	0.14	0.00	0.52	8.80E+00	8.26E-265	Up	8.40E+00	2.53E-195	Up	7.89E-01	7.69E-01		1.18E+00	5.48E-01		-7.11E+00	6.43E-01		1.91E+00	3.77E-01		Unigene82620_All//sp|P00414|COX3_HUMAN//2.00E-21//Cytochrome c oxidase subunit 3 OS=Homo sapiens GN=MT-CO3 PE=1 SV=2							swissprot +
Unigene82622_All	306	0.00	0.17	2.96	0.33	0.23	0.15	0.00	0.00	0.00	7.37E+00	6.08E-01		1.15E+01	4.69E-05	Up	-5.33E-01	8.12E-01		-1.14E+00	6.73E-01		null	null		null	null											ESTscan +
Unigene82624_All	307	0.00	0.66	2.95	0.16	0.11	0.00	0.00	0.00	0.00	9.37E+00	1.34E-01		1.15E+01	4.69E-05	Up	-5.33E-01	8.18E-01		-7.34E+00	6.17E-01		null	null		null	null		Unigene82624_All//COG0183//7.00E-06//Acetyl-CoA acetyltransferase							cog -
Unigene82625_All	307	0.00	62.06	36.08	0.00	0.22	0.00	0.00	0.00	0.00	1.59E+01	1.39E-109	Up	1.51E+01	3.13E-62	Up	7.81E+00	6.00E-01		null	null		null	null		null	null											ESTscan +
Unigene82628_All	307	0.00	0.00	2.60	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene82628_All//gi|119888000|gb|ABM05952.1|//6.00E-43//proline-rich protein [Gossypium hirsutum]	Unigene82628_All//4.00E-34//AT4G14900| hydroxyproline-rich glycoprotein family protein	Unigene82628_All//2.00E-11//ES798253					nr -

Unigene82630_All	308	0.00	1.32	3.46	0.00	0.67	0.29	0.00	0.00	0.00	1.04E+01	1.34E-02		1.18E+01	6.58E-06	Up	9.39E+00	1.56E-01		8.20E+00	4.69E-01		null	null		null	null		Unigene82630_All//sp|O03197|NU2M_CERSI//5.00E-32//NADH-ubiquinone oxidoreductase chain 2 OS=Ceratotherium simum GN=MT-ND2 PE=3 SV=1						swissprot -
Unigene82631_All	308	0.00	1.15	2.59	0.00	0.00	0.00	0.00	0.00	0.00	1.02E+01	2.43E-02		1.13E+01	1.71E-04	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene82634_All	308	0.00	0.00	3.11	0.16	0.45	0.00	0.00	0.00	0.00	null	null		1.16E+01	2.44E-05	Up	1.47E+00	6.17E-01		-7.34E+00	6.17E-01		null	null		null	null		Unigene82634_All//gi|223998816|ref|XP_002289081.1|//1.00E-37//propionyl-coa carboxylase [Thalassiosira pseudonana CCMP1335] >gi|220976189|gb|EED94517.1| propionyl-coa carboxylase [Thalassiosira pseudonana CCMP1335]	Unigene82634_All//1.00E-16//AT4G34030| MCCB (3-METHYLCROTONYL-COA CARBOXYLASE); biotin carboxylase/ methylcrotonoyl-CoA carboxylase			ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism	GO:0006551//GO:0006631//GO:0016421//GO:0043231//GO:0043234//GO:0044444//GO:0046914	nr +
Unigene82639_All	309	0.17	1.48	3.27	0.00	0.33	0.58	0.00	0.00	0.00	3.12E+00	3.58E-02		4.27E+00	1.19E-04	Up	8.39E+00	4.51E-01		9.19E+00	1.93E-01		null	null													ESTscan -
Unigene8264_All	774	0.00	177.87	73.75	0.00	0.00	0.00	0.00	0.00	0.00	1.74E+01	0.00E+00	Up	1.62E+01	0.00E+00	Up	null	null		null	null		null	null		null	null		Unigene8264_All//gi|110225675|ref|YP_665681.1|//2.00E-80//cytochrome c oxidase subunit 3 [Nephroselmis olivacea] >gi|6066190|gb|AAF03208.1|AF110138_40 cytochrome c oxidase subunit 3 [Nephroselmis olivacea]	Unigene8264_All//3.00E-60//ATMG00730| Encodes cytochrome c oxidase subunit 3.	Unigene8264_All//2.00E-11//DV849460		ko00190|Oxidative phosphorylation		nr -
Unigene82640_All	309	0.00	0.98	3.45	0.16	0.67	0.29	0.00	0.00	0.00	9.94E+00	4.36E-02		1.18E+01	6.58E-06	Up	2.05E+00	3.94E-01		8.59E-01	7.90E-01		null	null		null	null		Unigene82640_All//COG0631//7.00E-11//Serine/threonine protein phosphatase						cog -
Unigene82643_All	309	0.00	6.07	4.65	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.10E-10	Up	1.22E+01	6.28E-08	Up	null	null		null	null		null	null		null	null		Unigene82643_All//gi|159488859|ref|XP_001702418.1|//1.00E-17//acyl-coa-binding protein [Chlamydomonas reinhardtii] >gi|158271086|gb|ED096913.1| acyl-coa-binding protein [Chlamydomonas reinhardtii]	Unigene82643_All//7.00E-17//AT1G31812| ACBP6 (acyl-CoA-binding protein 6); acyl-CoA binding / phosphatidylcholine binding				GO:0008289	nr +
Unigene82645_All	309	0.00	10.49	6.03	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.87E-18	Up	1.26E+01	2.89E-10	Up	null	null		null	null		null	null		null	null									ESTscan -
Unigene82647_All	309	0.00	0.16	2.76	0.32	0.00	0.15	0.00	0.00	0.00	7.36E+00	6.08E-01		1.14E+01	8.96E-05	Up	-8.33E+00	3.08E-01		-1.14E+00	6.73E-01		null	null		null	null		Unigene82647_All//gi|255617549|ref|XP_002539853.1|//1.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223501731|gb|EEF22530.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene82649_All	309	0.00	0.00	2.24	0.16	0.22	0.15	0.00	0.00	0.00	null	null		1.11E+01	6.10E-04	Up	4.68E-01	9.53E-01		-1.41E-01	9.46E-01		null	null		null	null		Unigene82649_All//COG0489//9.00E-06//ATPases involved in chromosome partitioning						cog +
Unigene8265_All	417	0.50	2.31	1.28	0.72	1.32	0.76	2.74	1.30	0.48	2.20E+00	6.58E-03		1.35E+00	2.25E-01		8.82E-01	4.21E-01		8.08E-02	9.49E-01		-1.07E+00	6.31E-02		-2.52E+00	1.20E-04	Down		Unigene8265_All//0.00E+00//COG96417					
Unigene82651_All	310	0.00	0.00	3.26	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene82651_All//gi|226503773|ref|NP_001150641.1|//1.00E-19//mitochondrial 2-oxoglutarate/malate carrier protein [Zea mays] >gi|195640804|gb|ACG39870.1| mitochondrial 2-oxoglutarate/malate carrier protein [Zea mays]	Unigene82651_All//7.00E-20//AT2G22500| UCP5 (UNCOUPLING PROTEIN 5); binding				GO:0006810//GO:0009987//GO:0016020//GO:0043231	nr +
Unigene82653_All	310	0.00	0.00	3.44	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	6.58E-06	Up	null	null		null	null		null	null		null	null		Unigene82653_All//gi|197312925|gb|ACH63243.1|//1.00E-16//low-temperature inducible [Rheum australe]	Unigene82653_All//8.00E-08//AT2G03440| nodulin-related				GO:0006970//GO:0009526//GO:0009532//GO:0010038//GO:0016020	nr +
Unigene82660_All	311	0.17	0.16	3.08	0.80	1.44	0.29	0.00	0.00	0.00	-4.62E-02	9.81E-01		4.20E+00	2.16E-04	Up	8.46E-01	5.13E-01		-1.46E+00	4.06E-01		null	null		null	null		Unigene82660_All//COG2951//2.00E-12//Membrane-bound lytic murein transglycosylase B						cog +
Unigene82663_All	311	0.00	18.57	11.64	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	5.79E-33	Up	1.35E+01	4.73E-20	Up	null	null		null	null		null	null		null	null		Unigene82663_All//gi|6002102|emb|CAB56693.1|//2.00E-11//Acyl-CoA binding protein (ACBP) [Digitalis lanata]	Unigene82663_All//9.00E-10//AT1G31812| ACBP6 (acyl-CoA-binding protein 6); acyl-CoA binding / phosphatidylcholine binding				GO:0005488	nr +
Unigene8267_All	348	9.62	7.72	2.91	12.17	22.86	20.51	0.49	1.32	0.00	-3.18E-01	3.74E-01		-1.73E+00	6.01E-06	Down	9.10E-01	3.36E-06		7.53E-01	4.96E-04		1.44E+00	1.67E-01		-8.92E+00	1.08E-01		Unigene8267_All//gi|224103099|ref|XP_002312925.1|//1.00E-13//SAUR family protein [Populus trichocarpa] >gi|222849333|gb|EEE86880.1| SAUR family protein [Populus trichocarpa]	Unigene8267_All//4.00E-13//AT1G29450| auxin-responsive protein, putative	Unigene8267_All//8.00E-169//gi|109871372|gb|DW500348.1|DW500348			GO:0009725	nr -
Unigene82676_All	313	0.00	0.00	2.21	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.11E+01	6.09E-04	Up	null	null		null	null		null	null		null	null		Unigene82676_All//COG1197//4.00E-19//Transcription-repair coupling factor (superfamily II helicase)						cog +
Unigene82677_All	313	0.33	0.49	4.08	0.32	0.44	0.29	0.00	0.00	0.00	5.39E-01	7.77E-01		3.61E+00	3.41E-05	Up	4.67E-01	8.75E-01		-1.41E-01	9.46E-01		null	null		null	null		Unigene82677_All//gi|255606776|ref|XP_002538631.1|//4.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223511279|gb|EEF23753.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene82678_All	313	0.00	0.00	2.21	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.11E+01	6.09E-04	Up	null	null		null	null		null	null		null	null		Unigene82678_All//gi|475169|emb|CAA83649.1|//5.00E-59//beta-glucuronidase [synthetic construct] >gi|14594803|emb|CAC43287.1| beta-glucuronidase [Arabidopsis thaliana] >gi|14594807|emb|CAC43289.1| beta-glucuronidase [Arabidopsis thaliana] >gi|16903091|gb|AAL30401.1| beta-glucuronidase [Cloning vector pWS31] >gi|16903094|gb|AAL30403.1| beta-glucuronidase [Cloning vector pWS32] >gi|29150589|gb|AAO63175.1| beta-glucuronidase [Cloning Vector pHRGFPGUS] >gi|30025557|gb|AAP04590.1| beta-glucuronidase [Cloning vector pHR50] >gi|30523396|gb|AAP31913.1| beta-glucuronidase [Cloning vector pHBE1-km] >gi|55724884|emb|CAH64894.1| beta-glucuronidase [Cloning vector pRU1064] >gi|55724887|emb|CAH64918.1| beta-glucuronidase [Cloning vector pRU1075] >gi|55724890|emb|CAH64920.1| beta-glucuronidase [Cloning vector						GO:0004553//GO:0043167//GO:0044238	nr +
Unigene82679_All	313	0.50	0.00	3.74	0.32	0.44	0.00	0.00	0.00	0.00	-8.97E+00	2.13E-01		2.90E+00	4.34E-04	Up	4.67E-01	8.75E-01		-8.31E+00	3.92E-01		null	null		null	null									ESTscan -
Unigene82685_All	314	0.33	0.00	4.58	0.32	1.75	0.14	0.00	0.00	0.00	-8.38E+00	3.65E-01		3.78E+00	5.81E-06	Up	2.47E+00	4.04E-02		-1.14E+00	6.73E-01		null	null		null	null		Unigene82685_All//COG4961//7.00E-11//Flp pilus assembly protein TadG						cog -
Unigene8269_All	843	1.55	1.26	2.21	2.48	0.90	1.71	1.35	2.08	1.98	-2.98E-01	5.95E-01		5.11E-01	3.12E-01		-1.47E+00	6.00E-04	Down	-5.34E-01	2.49E-01		6.21E-01	1.66E-01		5.52E-01	2.13E-01			Unigene8269_All//2.00E-08//BQ404227					
Unigene82690_All	314	0.00	2.42	3.39	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.75E-04	Up	1.17E+01	6.58E-06	Up	null	null		null	null		null	null		null	null									
Unigene82693_All	314	0.00	1.45	3.05	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	7.34E-03		1.16E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene82693_All//sp|P23588|IF4B_HUMAN//3.00E-08//Eukaryotic translation initiation factor 4B OS=Homo sapiens GN=EIF4B PE=1 SV=2						swissprot +
Unigene82698_All	315	0.00	0.32	2.54	0.16	0.66	0.00	0.00	0.00	0.00	8.33E+00	3.79E-01		1.13E+01	1.71E-04	Up	2.05E+00	3.94E-01		-7.30E+00	6.17E-01		null	null		null	null									ESTscan -
Unigene82699_All	315	0.00	1.77	4.40	0.00	0.00	0.00	0.00	0.00	0.00	1.08E+01	2.16E-03		1.21E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene82699_All//sp|P01903|DRA_HUMAN//3.00E-59//HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1						swissprot -
Unigene82700_All	315	0.50	0.16	3.55	0.16	0.98	0.14	0.00	0.00	0.00	-1.63E+00	4.87E-01		2.83E+00	7.34E-04	Up	2.64E+00	1.61E-01		-1.41E-01	9.46E-01		null	null		null	null		Unigene82700_All//COG1804//2.00E-12//Predicted acyl-CoA transferases/carnitine dehydratase						cog +
Unigene82701_All	315	0.33	0.32	3.38	0.32	0.22	0.57	0.00	0.00	0.00	-4.63E-02	9.85E-01		3.35E+00	3.36E-04	Up	-5.33E-01	8.12E-01		8.59E-01	6.94E-01		null	null		null	null									ESTscan +
Unigene82703_All	315	0.17	0.48	5.41	0.16	0.11	0.00	0.00	0.00	0.00	1.54E+00	5.29E-01		5.03E+00	3.41E-08	Up	-5.33E-01	8.18E-01		-7.30E+00	6.17E-01		null	null		null	null		Unigene82703_All//sp|Q89BQ0|OXAA_BRAJA//6.00E-42//Inner membrane protein oxaA OS=Bradyrhizobium japonicum GN=oxaA PE=3 SV=1						swissprot -
Unigene82708_All	316	0.17	0.32	2.70	0.00	0.00	0.29	0.00	0.00	0.00	9.54E-01	7.23E-01		4.03E+00	7.01E-04	Up	null	null		8.16E+00	4.69E-01		null	null		null	null		Unigene82708_All//gi|301119933|ref|XP_002907694.1|//3.00E-17//stomatin-like protein [Phytophthora infestans T30-4] >gi|262106206|gb|EEY64258.1| stomatin-like protein [Phytophthora infestans T30-4]	Unigene82708_All//4.00E-16//AT5G54100| band 7 family protein				GO:0044464	nr +
Unigene82709_All	316	0.00	0.00	2.53	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene82709_All//gi|76884939|gb|ABX89556.1|//3.00E-39//U-box protein [Capsicum annuum]	Unigene82709_All//1.00E-36//AT2G35930| PUB23 (PLANT U-BOX 23); ubiquitin-protein ligase			ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0002252//GO:0006950//GO:0016567//GO:0019787//GO:0043234//GO:0044444	nr +
Unigene82710_All	316	0.00	0.32	5.22	0.00	0.00	0.00	0.00	0.00	0.00	8.33E+00	3.79E-01		1.24E+01	4.29E-09	Up	null	null		null	null		null	null		null	null									
Unigene82713_All	316	0.00	0.32	4.38	0.00	0.00	0.00	0.00	0.00	0.00	8.33E+00	3.79E-01		1.21E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene82713_All//gi|297603684|ref|NP_001051437.2|//2.00E-07//Os05g0110000 [Oryza sativa Japonica Group] >gi|255675945|dbj|BAF16351.2| Os05g0110000 [Oryza sativa Japonica Group]					GO:0044464//GO:0046872	nr +
Unigene82717_All	317	0.00	1.92	2.52	0.00	0.00	0.00	0.00	0.00	0.00	1.09E+01	1.16E-03		1.13E+01	1.71E-04	Up	null	null		null	null		null	null		null	null									
Unigene82719_All	317	0.00	0.80	5.21	0.00	0.00	0.00	0.00	0.00	0.00	9.64E+00	7.75E-02		1.23E+01	4.29E-09	Up	null	null		null	null		null	null		null	null		Unigene82719_All//sp|P10909|CLUS_HUMAN//3.00E-22//Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1						swissprot +
Unigene82720_All	317	0.50	0.16	3.70	0.16	0.00	0.14	0.00	0.00	0.00	-1.63E+00	4.87E-01		2.90E+00	4.34E-04	Up	-7.30E+00	5.43E-01		-1.41E-01	9.46E-01		null	null		null	null									ESTscan -
Unigene82721_All	317	0.00	0.48	3.02	0.00	0.00	0.00	0.00	0.00	0.00	8.91E+00	2.31E-01		1.16E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene82721_All//gi|77549376|gb|AB92173.1|//1.00E-07//Serpin family protein [Oryza sativa (japonica cultivar-group)]	Unigene82721_All//1.00E-06//AT2G35850| serpin family protein / serine protease inhibitor family protein				GO:0043231	nr +
Unigene82722_All	318	0.49	0.48	4.19	0.31	0.43	0.57	0.00	0.00	0.00	-4.63E-02	9.88E-01		3.08E+00	8.57E-05	Up	4.67E-01	8.75E-01		8.59E-01	6.94E-01		null	null		null	null									
Unigene82725_All	318	0.16	0.32	4.19	0.00	0.22	0.43	0.00	0.00	0.00	9.54E-01	7.23E-01		4.67E+00	2.95E-06	Up	7.76E+00	6.00E-01		8.74E+00	3.09E-01		null	null		null	null									ESTscan +
Unigene82726_All	318	0.00	2.23	1.51	0.00	0.00	0.00	0.00	0.00	0.00	1.11E+01	3.30E-04	Up	1.06E+01	7.38E-03		null	null		null	null		null	null		null	null									ESTscan +

Unigene82728_All	318	0.49	0.64	3.52	0.00	0.32	0.71	0.00	0.00	0.00	3.69E-01	8.15E-01			2.83E+00	7.34E-04	Up	8.34E+00	4.51E-01		9.47E+00	1.18E-01		null	null		null	null										ESTscan -
Unigene82729_All	320	0.65	0.32	4.49	0.16	0.22	0.00	0.00	0.00	0.00	-1.05E+00	5.63E-01			2.78E+00	1.05E-04	Up	4.67E-01	9.53E-01		-7.28E+00	6.17E-01		null	null		null	null										ESTscan +
Unigene82732_All	320	0.00	0.32	2.50	0.00	0.54	0.00	0.00	0.00	0.00	8.31E+00	3.79E-01			1.13E+01	1.71E-04	Up	9.07E+00	2.26E-01		null	null		null	null		null	null										ESTscan -
Unigene82736_All	321	0.33	0.16	3.65	0.00	0.21	0.56	0.00	0.00	0.00	-1.05E+00	6.82E-01			3.48E+00	1.09E-04	Up	7.75E+00	6.00E-01		9.14E+00	1.93E-01		null	null		null	null		Unigene82736_All//sp|P42630|TDCG_ECOLI//1.00E-07//L-serine dehydratase tdcG OS=Escherichia coli (strain K12) GN=tdcG PE=1 SV=4								swissprot +
Unigene82737_All	321	0.16	0.32	3.48	0.16	0.21	0.00	0.00	0.00	0.00	9.54E-01	7.23E-01			4.42E+00	3.51E-05	Up	4.68E-01	9.53E-01		-7.28E+00	6.17E-01		null	null		null	null										ESTscan -
Unigene82739_All	321	0.00	0.79	3.48	0.00	0.00	0.00	0.00	0.00	0.00	9.62E+00	7.75E-02			1.18E+01	3.41E-06	Up	null	null		null	null		null	null		null	null										ESTscan -
Unigene8274_All	738	0.00	3.91	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.97E-16	Up		1.07E+01	9.08E-07	Up	null	null		null	null		null	null		null	null		Unigene82740_All//gi|298704856|emb|CBJ28373.1|//4.00E-25//DEAD box helicase [Ectocarpus siliculosus]	Unigene8274_All//1.00E-11//AT1G55150| DEAD box RNA helicase, putative (RH20)			ko03040|Spliceosome	GO:0005488//GO:0016787	nr -
Unigene82740_All	321	0.16	0.47	3.15	0.16	0.11	0.70	0.00	0.00	0.00	1.54E+00	5.29E-01			4.27E+00	1.19E-04	Up	-5.33E-01	8.18E-01		2.18E+00	3.22E-01		null	null		null	null		Unigene82740_All//gi|255594065|ref|XP_002536011.1|//2.00E-13//conserved hypothetical protein [Ricinus communis] >gi|223521200|gb|EEF26371.1| conserved hypothetical protein [Ricinus communis]								nr +
Unigene82744_All	322	0.81	0.63	5.29	0.46	0.21	0.70	0.00	0.00	0.00	-3.68E-01	7.78E-01			2.70E+00	2.50E-05	Up	-1.12E+00	5.82E-01		5.96E-01	7.21E-01		null	null		null	null		Unigene82744_All//gi|51209923|ref|YP_063587.1|//2.00E-27//ribosomal protein S11 [Gracilaria tenuistipitata var. liui] >gi|62287422|sp|Q6B8X3.1|RR11_GRATL RecName: Full=30S ribosomal protein S11, chloroplastic >gi|50657677|gb|AAT79662.1| 30S ribosomal protein S11 [Gracilaria tenuistipitata var. liui]	Unigene82744_All//1.00E-18//ATCG00750| 30S chloroplast ribosomal protein S11			ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0030529	nr -
Unigene82747_All	323	3.56	1.73	3.46	11.41	3.62	4.33	3.14	1.16	1.36	-1.05E+00	1.01E-01			-4.17E-02	9.65E-01		-1.65E+00	1.17E-07	Down	-1.40E+00	1.77E-05	Down	-1.43E+00	2.36E-02		-1.21E+00	4.17E-02			Unigene82747_All//1.00E-10//CO118675						
Unigene82749_All	323	0.00	0.63	2.31	0.00	0.11	0.00	34.43	38.69	33.67	9.29E+00	1.34E-01			1.12E+01	3.24E-04	Up	6.74E+00	8.13E-01		null	null		1.69E-01	3.01E-01		-3.20E-02	8.53E-01		Unigene82749_All//6.00E-49//AT5G53300| (UBC10 (ubiquitin-conjugating enzyme 10); ubiquitin-protein ligase	Unigene82749_All//6.00E-83//gi|109867954|gb|DW496930.1|DW496930		ko04141|Protein processing in endoplasmic reticulum//ko04120|Ubiquitin mediated proteolysis	GO:0006464//GO:0019787//GO:0019899//GO:0019941//GO:0060255	nr +
Unigene82750_All	323	0.00	2.82	4.29	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.60E-05	Up		1.21E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene82750_All//sp|Q24306|IAP1_DROME//6.00E-14//Apoptosis 1 inhibitor OS=Drosophila melanogaster GN=th PE=1 SV=2								swissprot +
Unigene82754_All	323	0.00	127.54	58.53	0.00	0.00	0.00	0.00	0.00	0.00	1.70E+01	8.35E-238	Up		1.58E+01	8.81E-107	Up	null	null		null	null		null	null		null	null		Unigene82754_All//gi|301089317|ref|XP_002894971.1|//7.00E-07//trypsin protease GIP [Phytophthora infestans T30-4] >gi|262104297|gb|EE162349.1| trypsin protease GIP [Phytophthora infestans T30-4]								nr -
Unigene82755_All	323	0.00	0.16	3.46	0.00	0.00	0.00	0.00	0.00	0.00	7.29E+00	6.08E-01			1.18E+01	3.41E-06	Up	null	null		null	null		null	null		null	null		Unigene82755_All//gi|222837873|gb|EEE76238.1|//7.00E-15//ECOLI acriflavine resistance protein b [Populus trichocarpa]								nr +
Unigene82756_All	323	0.00	0.31	2.14	0.31	0.11	0.28	0.00	0.00	0.00	8.29E+00	3.79E-01			1.11E+01	6.09E-04	Up	-1.53E+00	5.83E-01		-1.41E-01	9.46E-01		null	null		null	null										ESTscan -
Unigene82759_All	323	0.65	0.00	4.12	0.00	0.43	0.00	0.00	0.00	0.00	-9.34E+00	1.21E-01			2.67E+00	3.01E-04	Up	8.74E+00	3.16E-01		null	null		null	null		null	null		Unigene82759_All//COG2269//7.00E-29//Truncated, possibly inactive, lysyl-tRNA synthetase (class II)								cog -
Unigene8276_All	472	0.00	0.00	0.00	0.00	0.44	0.00	1.52	4.78	1.10	null	null			null	null		8.77E+00	1.56E-01		null	null		1.65E+00	4.73E-05	Up	-4.73E-01	5.20E-01		Unigene8276_All//gi|9294023|dbj|BAB01926.1|//5.00E-21//multispanning membrane protein-like [Arabidopsis thaliana]	Unigene8276_All//3.00E-22//AT3G13772| endomembrane protein 70, putative				GO:0016020//GO:0043231	nr -
Unigene82761_All	324	0.00	0.00	4.11	0.00	0.00	0.00	0.00	0.00	0.00	null	null			1.20E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene82761_All//gi|255710064|gb|ACU30852.1|//9.00E-15//early nodulin 20 precursor [Jatropha curcas]				ko04141|Protein processing in endoplasmic reticulum//ko00520|Amino sugar and nucleotide sugar metabolism//ko03420|Nucleotide excision repair		nr -
Unigene82768_All	326	0.00	12.43	4.90	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	4.38E-23	Up		1.23E+01	8.42E-09	Up	null	null		null	null		null	null		null	null		Unigene82768_All//gi|157093259|gb|ABV22284.1|//4.00E-08//unknown [Karlodinium micrum]								nr -
Unigene82769_All	326	1.93	0.00	3.27	0.00	0.74	0.00	0.00	0.00	0.00	-1.09E+01	7.90E-04	Down		7.62E-01	2.69E-01		9.53E+00	1.04E-01		null	null		null	null		null	null										ESTscan +
Unigene8277_All	1655	0.13	1.62	0.10	0.03	0.08	0.05	0.23	0.33	6.11	3.68E+00	5.94E-11	Up		-3.91E-01	8.06E-01		1.47E+00	6.17E-01		8.59E-01	7.90E-01		5.14E-01	5.89E-01		4.73E+00	2.78E-59	Up	Unigene8277_All//gi|124302212|gb|ABN05291.1|//5.00E-97//ARK3 protein [Arabidopsis thaliana]	Unigene8277_All//2.00E-98//AT4G21380| ARK3 (A. THALIANA RECEPTOR KINASE 3); kinase/ transmembrane receptor protein serine/threonine kinase	Unigene8277_All//3.00E-08//CO496758		ko04626|Plant-pathogen interaction	GO:0031410	nr -
Unigene82770_All	326	0.00	0.93	2.78	0.00	0.00	0.00	0.00	0.00	0.00	9.87E+00	4.36E-02			1.14E+01	4.69E-05	Up	null	null		null	null		null	null		null	null										ESTscan +
Unigene82771_All	327	0.00	0.62	2.28	0.30	0.21	0.00	0.39	0.00	0.00	9.28E+00	1.34E-01			1.12E+01	3.24E-04	Up	-5.33E-01	8.12E-01		-8.25E+00	3.92E-01		-8.60E+00	2.33E-01		-8.60E+00	1.98E-01		Unigene82771_All//COG3637//1.00E-10//Opacity protein and related surface antigens								cog +
Unigene82778_All	328	0.00	0.00	2.60	0.00	0.00	0.00	0.00	0.00	0.00	null	null			1.13E+01	8.96E-05	Up	null	null		null	null		null	null		null	null		Unigene82778_All//gi|221054164|ref|XP_002298123.1|//2.00E-51//pleiotropic drug resistance, ABC transporter family protein [Populus trichocarpa] >gi|222845381|gb|EEE82928.1| pleiotropic drug resistance, ABC transporter family protein [Populus trichocarpa]	Unigene82778_All//2.00E-51//AT3G30842| PDR10 (PLEIOTROPIC DRUG RESISTANCE 10); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding	Unigene82778_All//9.00E-73//TC147767		ko03040|Spliceosome//ko02010|ABC transporters	GO:0015604//GO:0032559//GO:0042626//GO:0044464	nr +
Unigene82782_All	328	0.16	0.62	2.60	0.15	0.32	0.14	0.00	0.00	0.00	1.95E+00	3.74E-01			4.03E+00	7.01E-04	Up	1.05E+00	8.05E-01		-1.42E-01	9.46E-01		null	null		null	null										
Unigene82784_All	328	0.00	0.00	8.60	0.00	0.00	0.00	0.00	0.00	0.00	null	null			1.31E+01	1.38E-15	Up	null	null		null	null		null	null		null	null		Unigene82784_All//gi|31074969|gb|AAP42136.1|//6.00E-16//erg-1 [Solanum tuberosum]	Unigene82784_All//1.00E-15//AT5G64260| EXL2 (EXORDIUM LIKE 2)				GO:0005618//GO:0031410	nr -
Unigene82786_All	328	0.16	0.00	3.73	0.00	0.63	0.14	0.00	0.00	0.00	-7.32E+00	6.00E-01			4.55E+00	1.02E-05	Up	9.30E+00	1.56E-01		7.11E+00	6.82E-01		null	null		null	null		Unigene82786_All//gi|222832485|gb|EEE70962.1|//3.00E-10//predicted protein [Populus trichocarpa]								nr +
Unigene82787_All	328	0.00	0.00	2.11	0.15	0.00	0.28	0.00	0.00	0.00	null	null			1.10E+01	6.09E-04	Up	-7.25E+00	5.43E-01		8.58E-01	7.90E-01		null	null		null	null										ESTscan +
Unigene82789_All	329	0.00	0.00	2.59	0.00	0.00	0.00	0.00	0.00	0.00	null	null			1.13E+01	8.96E-05	Up	null	null		null	null		null	null		null	null		Unigene82789_All//gi|31074969|gb|AAP42136.1|//7.00E-36//erg-1 [Solanum tuberosum]	Unigene82789_All//3.00E-32//AT5G64260| EXL2 (EXORDIUM LIKE 2)	Unigene82789_All//1.00E-13//gi|21097105|gb|BQ409418.1|BQ409418				nr +
Unigene8279_All	526	0.50	18.30	3.64	0.00	1.31	0.94	0.00	0.00	0.00	5.20E+00	2.31E-47	Up		2.87E+00	2.94E-06	Up	1.04E+01	3.05E-04	Up	9.88E+00	4.38E-03		null	null		null	null		Unigene8279_All//gi|148595726|emb|CAM12542.1|//2.00E-06//YA4 [Antirrhinum majus]								nr +
Unigene82790_All	329	0.32	0.00	3.56	0.30	0.21	0.00	0.00	0.00	0.00	-8.31E+00	3.65E-01			3.48E+00	1.09E-04	Up	-5.33E-01	8.12E-01		-8.24E+00	3.92E-01		null	null		null	null										ESTscan +
Unigene82792_All	329	0.32	0.15	4.05	0.15	0.42	0.27	0.00	0.00	0.00	-1.05E+00	6.82E-01			3.67E+00	1.90E-05	Up	1.47E+00	6.17E-01		8.58E-01	7.90E-01		null	null		null	null										
Unigene82794_All	330	0.00	34.24	19.69	0.00	0.00	0.55	0.00	0.00	0.00	1.51E+01	8.69E-65	Up		1.43E+01	2.96E-36	Up	null	null		9.10E+00	1.93E-01		null	null		null	null										ESTscan +
Unigene82798_All	330	0.16	0.15	3.87	0.00	0.31	0.41	0.00	0.00	0.00	-4.62E-02	9.81E-01			4.61E+00	5.50E-06	Up	8.29E+00	4.51E-01		8.68E+00	3.09E-01		null	null		null	null		Unigene82798_All//gi|255072327|ref|XP_002499838.1|//4.00E-07//radical SAM protein with TRAM and UPF0004 domains [Micromonas sp. RCC299] >gi|226515100|gb|ACO61096.1| radical SAM protein with TRAM and UPF0004 domains [Micromonas sp. RCC299]	Unigene82798_All//4.00E-06//AT4G36390| radical SAM domain-containing protein / TRAM domain-containing protein				GO:0003824//GO:0016070//GO:0044424//GO:0051536	nr -
Unigene828_All	690	2.43	2.20	1.54	2.60	2.55	2.09	5.02	5.57	1.91	-1.39E-01	7.69E-01			-6.53E-01	2.27E-01		-3.02E-02	9.51E-01		-3.11E-01	5.66E-01		1.49E-01	6.31E-01		-1.40E+00	3.45E-06	Down								
Unigene82801_All	331	0.00	3.67	4.99	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	5.45E-07	Up		1.23E+01	4.29E-09	Up	null	null		null	null		null	null		null	null		Unigene82801_All//gi|159463554|ref|XP_001690007.1|//1.00E-19//SR protein factor [Chlamydomonas reinhardtii] >gi|158283995|gb|EDP09745.1| SR protein factor [Chlamydomonas reinhardtii]				ko03040|Spliceosome	GO:0005488//GO:0043229	nr -
Unigene82803_All	331	0.00	0.00	4.02	0.00	0.00	0.00	0.00	0.00	0.00	null	null			1.20E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene82803_All//gi|18418498|ref|NP_567970.1|//3.00E-40//complex 1 family protein / LVR family protein [Arabidopsis thaliana] >gi|15724258|gb|AAL06522.1|AF412069_1 AT4g34700/T4L20_280 [Arabidopsis thaliana] >gi|24111283|gb|AAN46765.1| At4g34700/T4L20_280 [Arabidopsis thaliana]	Unigene82803_All//1.00E-41//AT4G34700| complex 1 family protein / LVR family protein	Unigene82803_All//3.00E-17//BE052276		ko00190|Oxidative phosphorylation	GO:0005740//GO:0030964//GO:0043094	nr +
Unigene82805_All	331	0.00	0.15	3.06	0.00	0.00	0.00	0.00	0.00	0.00	7.26E+00	6.07E-01			1.16E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene82805_All//gi|1166450|emb|CAA64559.1|//1.00E-49//TfnS [Solanum lycopersicum]	Unigene82805_All//8.00E-24//AT2G45180| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein				GO:0006810//GO:0031410	nr +
Unigene8281_All	566	1.20	2.51	0.56	3.08	0.97	1.76	1.72	0.44	0.35	1.06E+00	6.14E-02			-1.09E+00	2.39E-01		-1.66E+00	5.90E-04	Down	-8.11E-01	1.08E-01		-1.96E+00	4.44E-03		-2.29E+00	9.84E-04	Down	Unigene8281_All//gi|224127758|ref|XP_002329170.1|//6.00E-48//acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa] >gi|222870951|gb|EEF08082.1| acyl:coa ligase acetate-coa synthetase-like protein [Populus trichocarpa]	Unigene8281_All//1.00E-47//AT5G16370| AAE5 (ACYL ACTIVATING ENZYME 5); catalytic	Unigene8281_All//0.00E+00//TC177063		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00360|Phenylalanine metabolism//ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0016405//GO:0042579	nr +
Unigene82810_All	333	0.00	0.15	2.24	0.15	0.41	0.27	0.00	0.00	0.00	7.25E+00	6.07E-01			1.11E+01	3.24E-04	Up	1.47E+00	6.17E-01		8.59E-01	7.90E-01		null	null		null	null										ESTscan +
Unigene82811_All	334	0.16	0.30	2.87	0.15	0.31	0.00	0.00	0.00	0.00	9.54E-01	7.23E-01			4.20E+00	2.16E-04	Up	1.05E+00	8.05E-01		-7.22E+00	6.17E-01		null	null		null	null		Unigene82811_All//gi|168001547|ref|XP_001753476.1|//5.00E-06//predicted protein [Physcomitrella patens subsp. patens] >gi|162695355|gb|EDQ81699.1| predicted protein [Physcomitrella patens subsp. patens]								nr -
Unigene82813_All	334	0.16	0.00	3.99	1.04	0.41	0.00	0.00	0.00	0.00	-7.29E+00	6.00E-01			4.67E+00	2.95E-06	Up	-1.34E+00	3.08E-01		-1.00E+01	2.12E-02		null	null		null	null		Unigene82813_All//gi|255600295|ref|XP_002537426.1|//7.00E-28//conserved hypothetical protein [Ricinus communis] >gi|223516386|gb|EEF24956.1| conserved hypothetical protein [Ricinus communis]	Unigene82813_All//4.00E-05//AT2G47730| AT6STF8 (ARABIDOPSIS THALIANA GLUTATHIONE S-TRANSFERASE PHI 8); glutathione binding / glutathione transferase				GO:0016740	nr +
Unigene82817_All	335	0.00	263.63	100.78	0.00	0.21	0.00	0.00	0.00	0.00	1.80E+01	0.00E+00	Up		1.66E+01	1.50E-191	Up	7.68E+00	6.00E-01		null	null		null	null		null	null										
Unigene82818_All	335	0.00	0.30	6.20	0.00	0.00	0.00	0.00	0.00	0.00	8.24E+00	3.79E-01			1.26E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene82818_All//gi|194716772|gb|ACF93235.1|//2.00E-38//ascorbate peroxidase [Picrorhiza kurrooa]	Unigene82818_All//3.00E-33//AT1G07890| APX1 (ascorbate peroxidase 1); L-ascorbate peroxidase	Unigene82818_All//1.00E-22//gi|21095056|gb|BQ407369.1|BQ407369		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0004601//GO:0005506//GO:0006950//GO:0008152	nr -

Unigene82826_All	337	0.31	0.30	4.42	1.03	0.00	0.00	0.00	0.00	0.00	-4.63E-02	9.85E-01		3.83E+00	3.20E-06	Up	-1.00E+01	9.43E-03		-1.00E+01	2.12E-02		null	null		null	null		Unigene82826_All//gi|115471693|ref|NP_001059445.1|//3.00E-14//0s07g0410100 [Oryza sativa Japonica Group] >gi|113610981|dbj|BAF21359.1| Os07g0410100 [Oryza sativa Japonica Group]	Unigene82826_All//5.00E-15//AT1G54220| dihydrolipoamide S-acetyltransferase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00020|Citrate cycle (TCA cycle)	GO:0008152//GO:0016418//GO:0043231	nr +
Unigene82828_All	337	0.00	0.00	3.16	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.16E+01	6.58E-06	Up	null	null		null	null		null	null		null	null		Unigene82828_All//gi|90959868|dbj|BAE92731.1|//9.00E-55//3-hydroxy-3-methylglutaryl coenzyme A reductase [Gentiana lutea]	Unigene82828_All//7.00E-49//AT2G17370| HMG2 (3-HYDROXY-3-METHYLGLUTARYL-COA REDUCTASE 2); hydroxymethylglutaryl-CoA reductase	Unigene82828_All//2.00E-24//gi|78329466|gb|DT549740.1|DT549740		ko00900|Terpenoid backbone biosynthesis	GO:0000166//GO:0006720//GO:0006732//GO:0016616//GO:0031090//GO:0031224//GO:0043231//GO:0048037	nr -
Unigene8284_All	559	0.09	1.27	0.19	0.71	0.00	1.45	0.30	1.35	4.56	3.76E+00	2.36E-03		1.03E+00	7.00E-01		-9.48E+00	4.38E-03		1.03E+00	2.17E-01		2.15E+00	9.17E-03		3.91E+00	1.26E-13	Up	Unigene8284_All//gi|255572221|ref|XP_002527050.1|//2.00E-07//zinc finger protein, putative [Ricinus communis] >gi|223533612|gb|EEF35350.1| zinc finger protein, putative [Ricinus communis]						nr +
Unigene82842_All	339	0.00	4.63	2.04	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	5.68E-09	Up	1.10E+01	6.09E-04	Up	null	null		null	null		null	null		null	null		Unigene82842_All//gi|159471742|ref|XP_001694015.1|//2.00E-34//starch phosphorylase [Chlamydomonas reinhardtii] >gi|158277182|gb|EDP02951.1| starch phosphorylase [Chlamydomonas reinhardtii]	Unigene82842_All//5.00E-19//AT3G29320| glucan phosphorylase, putative			ko00500|Starch and sucrose metabolism	GO:0005488//GO:0008152//GO:0016757	nr -
Unigene82843_All	339	0.00	0.00	2.04	0.00	0.00	0.53	0.00	0.00	0.00	null	null		1.10E+01	6.09E-04	Up	null	null		9.06E+00	1.93E-01		null	null		null	null		Unigene82843_All//gi|284192454|gb|ADB82905.1|//2.00E-49//glutamate decarboxylase [Panax ginseng]	Unigene82843_All//1.00E-49//AT1G65960| GAD2 (GLUTAMATE DECARBOXYLASE 2); calmodulin binding / glutamate decarboxylase	Unigene82843_All//4.00E-10//CA992685		ko00250|Alanine, aspartate and glutamate metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00430|Taurine and hypotaurine metabolism	GO:0009064//GO:0016831//GO:0048037	nr +
Unigene82845_All	339	0.00	0.00	2.98	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene82845_All|gi|42565698|ref|NP_190356.2|//2.00E-28//SRO4 (SIMILAR TO RCD ONE 4); NAD+ ADP-ribosyltransferase [Arabidopsis thaliana]	Unigene82845_All//8.00E-30//AT3G47720| SRO4 (SIMILAR TO RCD ONE 4); NAD+ ADP-ribosyltransferase				GO:0006970//GO:0016763//GO:0043231//GO:0044237	nr +
Unigene82846_All	340	0.31	0.89	3.45	0.00	0.10	0.00	0.00	0.00	0.00	1.54E+00	3.22E-01		3.48E+00	1.09E-04	Up	6.66E+00	8.13E-01		null	null		null	null		null	null		Unigene82846_All//gi|255594619|ref|XP_002536126.1|//2.00E-07//Protein dltB, putative [Ricinus communis] >gi|223520761|gb|EEF26256.1| Protein dltB, putative [Ricinus communis]						nr +
Unigene8285_All	375	0.56	1.08	0.28	0.53	2.39	0.84	0.79	1.34	3.51	9.54E-01	4.13E-01		-9.75E-01	6.19E-01		2.17E+00	9.20E-03		6.66E-01	6.47E-01		7.61E-01	4.22E-01		2.15E+00	2.01E-04	Up			Unigene8285_All//4.00E-07//BF268531				
Unigene82853_All	342	78.48	38.08	42.82	607.82	495.79	879.37	154.04	192.24	120.10	-1.04E+00	2.58E-21	Down	-8.74E-01	2.19E-15		-2.94E-01	2.10E-20		5.33E-01	6.27E-78		3.20E-01	2.88E-08		-3.59E-01	1.59E-08		Unigene82853_All|gi|3818416|gb|AAD03487.1|//6.00E-41//proline-rich cell wall protein [Medicago sativa]		Unigene82853_All//0.00E+00//gi|21094713|gb|BQ407026.1|BQ407026		ko03040|Spliceosome		nr +
Unigene82854_All	342	4.13	10.96	3.89	4.08	3.12	0.92	7.79	11.00	4.54	1.41E+00	2.37E-05	Up	-8.57E-02	8.81E-01		-3.86E-01	5.20E-01		-2.14E+00	6.16E-04	Down	4.98E-01	8.38E-02		-7.78E-01	1.89E-02				Unigene82854_All//4.00E-152//TC135413				
Unigene82855_All	342	0.00	0.00	5.92	0.00	0.00	0.40	0.00	0.00	0.00	null	null		1.25E+01	3.79E-11	Up	null	null		8.63E+00	3.09E-01		null	null		null	null		Unigene82855_All//gi|18396941|ref|NP_565348.1|//1.00E-28//protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|30678667|ref|NP_849949.1| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] >gi|4662641|gb|AAD26911.1| expressed protein [Arabidopsis thaliana] >gi|22022562|gb|AAM83238.1| At2g10940/F15K19.1 [Arabidopsis thaliana] >gi|23308313|gb|AAN18126.1| At2g10940/F15K19.1 [Arabidopsis thaliana]				ko03040|Spliceosome	GO:0005488//GO:0005576//GO:0006810//GO:0009534	nr -
Unigene82858_All	344	1.37	0.44	3.72	0.72	0.60	0.39	2.09	1.94	0.23	-1.63E+00	1.58E-01		1.44E+00	2.61E-02		-2.70E-01	8.22E-01		-8.78E-01	6.15E-01		-1.04E-01	8.93E-01		-3.17E+00	8.09E-04	Down							
Unigene82859_All	344	0.61	0.00	3.72	0.29	0.10	0.00	0.00	0.00	0.00	-9.25E+00	1.21E-01		2.61E+00	5.00E-04	Up	-1.53E+00	5.83E-01		-8.18E+00	3.92E-01		null	null		null	null		Unigene82859_All//gi|255600250|ref|XP_002537418.1|//4.00E-09//Prophage CP4-57 integrase, putative [Ricinus communis] >gi|223516424|gb|EEF24965.1| Prophage CP4-57 integrase, putative [Ricinus communis]						nr +
Unigene8286_All	304	0.86	6.17	4.90	2.46	0.79	3.42	0.28	0.00	0.39	2.84E+00	2.43E-06	Up	2.51E+00	1.98E-04	Up	-1.63E+00	4.48E-02		4.75E-01	5.12E-01		-8.12E+00	3.98E-01		4.99E-01	8.06E-01		Unigene8286_All|gi|15238212|ref|NP_199005.1|//3.00E-39//hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] >gi|28951051|gb|AAO63449.1| At5g41900 [Arabidopsis thaliana]	Unigene8286_All//1.00E-40//AT5G41900| hydrolase, alpha/beta fold family protein	Unigene8286_All//3.00E-152//ES805274			GO:0003824//GO:0007166//GO:0008227//GO:0030312//GO:0031224//GO:0043410	nr -
Unigene82862_All	345	0.15	0.44	2.78	0.00	0.50	0.13	0.00	0.00	0.00	1.54E+00	5.29E-01		4.19E+00	2.16E-04	Up	8.96E+00	2.26E-01		7.03E+00	6.82E-01		null	null		null	null								ESTscan -
Unigene82863_All	345	0.30	0.73	3.24	0.14	0.20	0.26	0.00	0.00	0.00	1.28E+00	4.34E-01		3.42E+00	1.92E-04	Up	4.67E-01	9.53E-01		8.58E-01	7.90E-01		null	null		null	null		Unigene82863_All//gi|219116961|ref|XP_002179275.1|//4.00E-25//glyceraldehyde-3-phosphate dehydrogenase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217409166|gb|EEC49098.1| glyceraldehyde-3-phosphate dehydrogenase [Phaeodactylum tricornutum CCAP 1055/1]	Unigene82863_All//7.00E-09//AT2G24270| ALDH11A3; 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydrogenase (NADP+)			ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene82867_All	346	0.30	0.00	2.92	0.00	0.30	0.39	0.00	0.00	0.00	-8.24E+00	3.65E-01		3.27E+00	5.92E-04	Up	8.22E+00	4.51E-01		8.61E+00	3.09E-01		null	null		null	null		Unigene82867_All//gi|116059537|emb|CAL55244.1|//2.00E-09//aminoimidazole ribonucleotide carboxylase (ISS) [Ostreococcus tauri]	Unigene82867_All//9.00E-07//AT2G37690| phosphoribosylaminoimidazole carboxylase, putative / AIR carboxylase, putative			ko00230|Purine metabolism		nr -
Unigene82872_All	347	0.00	0.29	3.53	0.00	0.10	0.13	0.00	0.00	0.00	8.19E+00	3.79E-01		1.18E+01	9.08E-07	Up	6.63E+00	8.13E-01		7.02E+00	6.82E-01		null	null		null	null								ESTscan -
Unigene82874_All	347	0.30	0.29	2.92	0.14	0.20	0.26	0.00	0.00	0.00	-4.67E-02	9.85E-01		3.27E+00	5.92E-04	Up	4.67E-01	9.53E-01		8.58E-01	7.90E-01		null	null		null	null		Unigene82874_All|gi|224009440|ref|XP_002293678.1|//4.00E-21//formyltetrahydrofolate deformylase [Thalassiosira pseudonana CCMP1335] >gi|220970350|gb|EED88687.1| formyltetrahydrofolate deformylase [Thalassiosira pseudonana CCMP1335]	Unigene82874_All//3.00E-19//AT5G47435| formyltetrahydrofolate deformylase, putative			ko00630|Glyoxylate and dicarboxylate metabolism//ko00670|One carbon pool by folate	GO:0003824//GO:0008152	nr -
Unigene82877_All	348	0.15	0.58	2.60	0.29	0.40	0.26	0.00	0.00	0.00	1.95E+00	3.74E-01		4.11E+00	3.91E-04	Up	4.67E-01	8.75E-01		-1.41E-01	9.46E-01		null	null		null	null		Unigene82877_All|gi|145353863|ref|XP_001421219.1|//2.00E-26//O-acetylserine sulfhydrylase/homocysteine synthase [Ostreococcus lucimarinus CCE9901] >gi|144581456|gb|ABO99512.1| O-acetylserine sulfhydrylase/homocysteine synthase [Ostreococcus lucimarinus CCE9901]	Unigene82877_All//4.00E-16//AT3G57050| CBL (cystathionine beta-lyase); cystathionine beta-lyase			ko00270|Cysteine and methionine metabolism//ko00910|Nitrogen metabolism//ko00450|Selenoamino acid metabolism//ko00920|Sulfur metabolism	GO:0003824//GO:0006519//GO:0043231	nr +
Unigene82878_All	349	0.45	0.44	4.12	0.00	0.30	0.13	0.00	0.00	0.00	-4.60E-02	9.88E-01		3.20E+00	2.79E-05	Up	8.21E+00	4.51E-01		7.02E+00	6.82E-01		null	null		null	null		Unigene82878_All//gi|125525107|gb|EAY72221.1|//1.00E-17//hypothetical protein OsI_01094 [Oryza sativa Indica Group]						nr -
Unigene82884_All	349	0.00	0.00	5.04	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.23E+01	1.12E-09	Up	null	null		null	null		null	null		null	null				Unigene82884_All//1.00E-07//ES847728				
Unigene82887_All	351	0.15	0.58	2.73	0.00	0.29	0.26	0.00	0.00	0.00	1.95E+00	3.74E-01		4.20E+00	2.16E-04	Up	8.20E+00	4.51E-01		8.01E+00	4.69E-01		null	null		null	null			Unigene82887_All//5.00E-05//AT4G36690| ATU2AF65A; RNA binding / nucleic acid binding / nucleotide binding					ESTscan -
Unigene82890_All	351	0.00	0.00	3.64	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene82890_All//gi|1002800|gb|AAB58314.1|//2.00E-06//Cpm7 [Craterostigma plantagineum]	Unigene82890_All//6.00E-05//AT3G06490| MYB108 (myb domain protein 108); DNA binding / transcription factor		MYB			nr -
Unigene82893_All	352	0.00	0.00	3.63	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.18E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene82893_All//gi|76161004|gb|ABA40465.1|//5.00E-42//ribosomal protein S27-like protein [Solanum tuberosum]	Unigene82893_All//4.00E-34//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome	Unigene82893_All//1.00E-41//TC167329		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0022613//GO:0030312//GO:0043169	nr -
Unigene82894_All	353	0.74	0.43	3.92	0.00	0.00	0.00	0.00	0.00	0.00	-7.83E-01	6.19E-01		2.40E+00	5.37E-04	Up	null	null		null	null		null	null		null	null		Unigene82894_All//gi|300268849|gb|EFJ53029.1|//1.00E-06//hypothetical protein VOLCADRAFT_85885 [Volvox carteri f. nagariensis]						nr -
Unigene82895_All	353	0.30	0.57	2.87	0.42	0.10	0.77	0.00	0.00	0.00	9.54E-01	6.20E-01		3.27E+00	5.92E-04	Up	-2.12E+00	3.85E-01		8.58E-01	6.30E-01		null	null		null	null								
Unigene82896_All	354	0.00	0.43	12.49	0.00	0.00	0.00	0.00	0.00	0.00	8.75E+00	2.31E-01		1.36E+01	1.55E-24	Up	null	null		null	null		null	null		null	null		Unigene82896_All//gi|2055228|dbj|BAA19768.1|//8.00E-27//SRC1 [Glycine max]				ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene82899_All	355	2.21	0.00	2.10	0.00	0.78	0.51	0.00	0.00	0.00	-1.11E+01	1.09E-04	Down	-7.41E-02	9.35E-01		9.60E+00	6.99E-02		8.99E+00	1.93E-01		null	null		null	null		Unigene82899_All//COG2307//6.00E-14//Uncharacterized protein conserved in bacteria						cog +
Unigene829_All	2944	4.59	4.47	5.97	7.58	11.31	6.35	7.12	7.45	3.10	-3.51E-02	8.32E-01		3.81E-01	6.23E-03		5.77E-01	2.19E-11		-2.55E-01	3.49E-02		6.54E-02	6.38E-01		-1.20E+00	2.91E-26	Down	Unigene829_All|gi|224115778|ref|XP_002317122.1|//0.00E+00//nbs-lrr resistance protein [Populus trichocarpa] >gi|222860187|gb|EEE97734.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene829_All//2.00E-65//AT3G14470| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction	GO:0005488	nr +
Unigene82910_All	362	0.14	0.00	2.65	0.00	0.10	0.00	0.00	0.00	0.00	-7.17E+00	6.00E-01		4.20E+00	2.16E-04	Up	6.57E+00	8.13E-01		null	null		null	null		null	null		Unigene82910_All//sp|P54989|NTAA_CHEHE//9.00E-33//Nitrilotriacetate monooxygenase component A OS=Chelatobacter heintzii GN=ntaA PE=1 SV=2						swissprot -
Unigene82914_All	364	0.14	0.28	2.63	0.14	0.28	0.50	0.00	0.00	0.00	9.54E-01	7.23E-01		4.20E+00	2.16E-04	Up	1.05E+00	8.05E-01		1.86E+00	4.57E-01		null	null		null	null		Unigene82914_All//gi|300267532|gb|EFJ51715.1|//5.00E-32//vitamin B12 dependent methionine synthase [Volvox carteri f. nagariensis]				ko00270|Cysteine and methionine metabolism//ko00670|One carbon pool by folate	GO:0005488//GO:0008168//GO:0044237	nr -
Unigene82915_All	364	0.43	0.00	3.22	0.27	0.28	0.12	0.00	0.00	0.00	-8.75E+00	2.13E-01		2.90E+00	4.34E-04	Up	5.23E-02	9.64E-01		-1.14E+00	6.73E-01		null	null		null	null		Unigene82915_All//COG0683//1.00E-09//ABC-type branched-chain amino acid transport systems, periplasmic component						cog -
Unigene82917_All	366	0.57	0.00	5.24	0.14	0.00	0.49	0.00	0.00	0.00	-9.16E+00	1.21E-01		3.20E+00	7.32E-07	Up	-7.09E+00	5.43E-01		1.86E+00	4.57E-01		null	null		null	null								

Unigene82919_All	367	0.00	0.28	4.50	0.00	0.00	0.00	0.00	0.00	0.00	8.11E+00	3.79E-01		1.21E+01	4.29E-09	Up	null	null		null	null		null	null		null	null		Unigene82919_All//gi|77416979|gb|AB481885.1|//3.00E-47//profilin-like [Solanum tuberosum]	Unigene82919_All//7.00E-32//AT5G56600| PRF3 (PROFILIN 3); actin binding	Unigene82919_All//5.00E-25//TC168367			GO:0005856//GO:0007010//GO:0008092	nr +
Unigene82924_All	369	0.28	0.55	3.90	0.27	0.00	0.00	0.00	0.00	0.00	9.54E-01	6.20E-01		3.78E+00	5.81E-06	Up	-8.08E+00	3.08E-01		-8.08E+00	3.92E-01		null	null		null	null		Unigene82924_All//COG0625//3.00E-13//Glutathione S-transferase						cog +
Unigene82925_All	370	0.14	0.41	3.17	0.27	0.00	0.61	0.00	0.00	0.00	1.54E+00	5.29E-01		4.48E+00	1.90E-05	Up	-8.07E+00	3.08E-01		1.18E+00	5.48E-01		null	null		null	null		Unigene82925_All//gi|255079168|ref|XP_002503164.1|//2.00E-25//hydrolase, carbon-nitrogen family protein [Micromonas sp. RCC299] >gi|226518430|gb|ACO64422.1| hydrolase, carbon-nitrogen family protein [Micromonas sp. RCC299]	Unigene82925_All//3.00E-26//AT4G08790| nitrilase, putative			ko00240|Pyrimidine metabolism//ko00410|beta-Alanine metabolism//ko00770|Pantothenate and CoA biosynthesis	GO:0010038//GO:0016787//GO:0043231	nr +
Unigene82927_All	371	0.00	6.56	5.31	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	7.71E-14	Up	1.24E+01	7.44E-11	Up	null	null		null	null		null	null		null	null		Unigene82927_All//sp|P07187|LCP2_DROME//5.00E-30//Larval cuticle protein 2 OS=Drosophila melanogaster GN=Lcp2 PE=1 SV=1						swissprot -
Unigene8293_All	266	0.39	4.00	2.80	3.18	1.94	2.55	0.64	0.31	0.00	3.35E+00	2.17E-04	Up	2.83E+00	8.50E-03		-7.13E-01	3.36E-01		-3.22E-01	6.87E-01		-1.02E+00	6.13E-01		-9.31E+00	1.08E-01		Unigene8293_All//gi|152402068|ref|NP_201530.1|//5.00E-27//FAD-dependent oxidoreductase family protein [Arabidopsis thaliana]	Unigene8293_All//2.00E-28//AT5G67290| FAD-dependent oxidoreductase family protein	Unigene8293_All//2.00E-104//TC161381			GO:0003824	nr -
Unigene82930_All	372	0.42	0.41	3.15	0.27	0.09	0.12	0.00	0.11	0.00	-4.62E-02	9.88E-01		2.90E+00	4.34E-04	Up	-1.53E+00	5.82E-01		-1.14E+00	6.73E-01		6.81E+00	6.25E-01		null	null								ESTscan +
Unigene82931_All	373	0.28	0.54	2.71	0.00	0.46	0.00	0.00	0.00	0.00	9.54E-01	6.20E-01		3.27E+00	5.92E-04	Up	8.85E+00	2.26E-01		null	null		null	null		null	null		Unigene82931_All//sp|P55587|Y40B_RHISN//3.00E-09//Uncharacterized protein y4oB OS=Rhizobium sp. (strain NGR234) GN=NGR_a02270 PE=4 SV=1						swissprot -
Unigene82934_All	376	0.00	2.96	3.97	0.00	0.00	0.72	0.00	0.00	0.00	1.15E+01	1.99E-06	Up	1.20E+01	3.21E-08	Up	null	null		9.49E+00	7.01E-02		null	null		null	null		Unigene82934_All//gi|14041724|emb|CAC38395.1|//4.00E-35//ferredoxin I [Solanum tuberosum]	Unigene82934_All//8.00E-18//AT1G60950| FED A; 2 iron, 2 sulfur cluster binding / electron carrier/ iron-sulfur cluster binding	Unigene82934_All//7.00E-09//EX168643		ko00195|Photosynthesis	GO:0006091//GO:0009536//GO:0043169//GO:0051234//GO:0051536	nr +
Unigene82935_All	376	0.28	0.40	3.40	0.00	0.18	0.24	0.00	0.00	0.00	5.39E-01	7.77E-01		3.61E+00	3.41E-05	Up	7.52E+00	6.00E-01		7.91E+00	4.69E-01		null	null		null	null								ESTscan -
Unigene82939_All	378	0.00	0.27	4.09	0.00	0.00	0.00	0.00	0.00	0.00	8.07E+00	3.79E-01		1.20E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene82939_All//gi|115499665|dbj|BAF33502.1|//5.00E-40//ACC oxidase [Phelipanche ramosa]	Unigene82939_All//6.00E-36//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene82939_All//5.00E-25//gi|13351512|gb|BG441860.1|BG441860		ko00270|Cysteine and methionine metabolism	GO:0003006//GO:0006555//GO:0006950//GO:0016641//GO:0019842//GO:0043169	nr +
Unigene82943_All	379	0.00	0.40	2.53	0.00	0.00	0.00	0.00	0.00	0.00	8.65E+00	2.31E-01		1.13E+01	2.44E-05	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene82944_All	380	2.89	0.00	2.52	0.00	0.00	0.00	0.00	0.00	0.00	-1.15E+01	1.93E-06	Down	-1.97E-01	7.49E-01		null	null		null	null		null	null		null	null								
Unigene82945_All	380	0.00	1.47	3.50	0.26	0.00	0.36	0.00	0.00	0.00	1.05E+01	2.16E-03		1.18E+01	2.39E-07	Up	-8.03E+00	3.08E-01		4.44E-01	8.59E-01		null	null		null	null		Unigene82945_All//gi|255591021|ref|XP_002535422.1|//8.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223523171|gb|EEF26965.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene82946_All	381	0.41	0.27	3.07	0.13	0.36	0.36	0.00	0.00	0.00	-6.31E-01	7.26E-01		2.90E+00	4.34E-04	Up	1.47E+00	6.17E-01		1.44E+00	6.36E-01		null	null		null	null								ESTscan -
Unigene82950_All	383	0.00	0.13	4.59	0.00	0.00	0.00	0.00	0.00	0.00	7.05E+00	6.07E-01		1.22E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene82950_All//gi|211906522|gb|ACJ11754.1|//5.00E-61//UDP-D-glucuronic acid 4-epimerase [Gossypium hirsutum]	Unigene82950_All//1.00E-59//AT4G30440| GAE1 (UDP-D-GLUCURONATE 4-EPIMERASE 1); UDP-glucuronate 4-epimerase/ catalytic	Unigene82950_All//2.00E-12//TC173878		ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism	GO:0006139//GO:0016857//GO:0048037	nr -
Unigene82952_All	384	0.00	0.53	1.94	0.00	0.00	0.00	0.00	0.00	0.00	9.04E+00	1.34E-01		1.09E+01	3.24E-04	Up	null	null		null	null		null	null		null	null		Unigene82952_All//gi|297798150|ref|XP_002866959.1|//4.00E-21//MRG family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312795|gb|EFH43218.1| MRG family protein [Arabidopsis lyrata subsp. lyrata]	Unigene82952_All//2.00E-22//AT4G37280| MRG family protein				GO:0043231	nr -
Unigene82953_All	384	0.00	1.98	1.53	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	1.75E-04	Up	1.06E+01	2.15E-03		null	null		null	null		null	null		null	null								
Unigene82954_All	385	0.27	4.08	0.69	0.39	0.00	0.00	0.00	0.00	0.00	3.91E+00	6.83E-07	Up	1.35E+00	4.08E-01		-8.60E+00	1.64E-01		-8.60E+00	2.31E-01		null	null		null	null								
Unigene82956_All	386	0.00	0.00	5.38	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.24E+01	1.92E-11	Up	null	null		null	null		null	null		null	null		Unigene82956_All//gi|192910762|gb|ACF06489.1|//8.00E-53//ribosomal protein L10a [Elaeis guineensis]	Unigene82956_All//1.00E-52//AT5G22440| 60S ribosomal protein L10A (RPL10aC)	Unigene82956_All//1.00E-32//TC162431		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene82958_All	386	0.00	0.00	2.62	0.00	0.09	0.00	0.00	0.00	0.00	null	null		1.14E+01	1.27E-05	Up	6.48E+00	8.13E-01		null	null		null	null		null	null		Unigene82958_All//sp|Q46444|QHED_COMTE//3.00E-51//Quinohaemoprotein ethanol dehydrogenase type-1 OS=Comamonas testosteroni GN=qheDH PE=1 SV=1						swissprot -
Unigene82959_All	387	0.27	0.26	2.61	0.00	0.27	0.00	0.00	0.00	0.00	-4.61E-02	9.85E-01		3.27E+00	5.92E-04	Up	8.06E+00	4.51E-01		null	null		null	null		null	null		Unigene82959_All//gi|222873979|gb|EEF11110.1|//5.00E-18//predicted protein [Populus trichocarpa]						nr -
Unigene82960_All	388	0.13	0.26	2.74	0.13	0.18	0.00	0.00	0.00	0.00	9.54E-01	7.23E-01		4.35E+00	6.45E-05	Up	4.67E-01	9.53E-01		-7.00E+00	6.17E-01		null	null		null	null								ESTscan -
Unigene82961_All	388	0.27	0.26	3.16	0.26	0.18	0.81	0.11	0.00	0.00	-4.62E-02	9.85E-01		3.55E+00	6.10E-05	Up	-5.33E-01	8.12E-01		1.67E+00	3.08E-01		-6.77E+00	6.42E-01		-6.77E+00	6.00E-01								ESTscan +
Unigene82965_All	390	0.00	2.86	1.09	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	1.99E-06	Up	1.01E+01	1.36E-02		null	null		null	null		null	null		null	null		Unigene82965_All//gi|255079426|ref|XP_002503293.1|//3.00E-20//Nucleosome/chromatin assembly complex protein [Micromonas sp. RCC299] >gi|226518559|gb|ACO64551.1| Nucleosome/chromatin assembly complex protein [Micromonas sp. RCC299]	Unigene82965_All//4.00E-08//AT4G26110| NAP1;1 (NUCLEOSOME ASSEMBLY PROTEIN1;1); DNA binding					nr -
Unigene82967_All	391	0.00	0.13	7.22	0.00	0.00	0.00	0.00	0.00	0.00	7.02E+00	6.07E-01		1.28E+01	1.38E-15	Up	null	null		null	null		null	null		null	null		Unigene82967_All//gi|6561156|gb|AAF16869.1|AF109693_1//1.00E-11//allergen-like protein BRSn20 [Sambucus nigra]	Unigene82967_All//1.00E-11//AT4G08685| SAH7					nr +
Unigene8297_All	295	3.02	7.04	5.23	5.40	3.27	0.92	12.47	13.03	11.07	1.22E+00	7.47E-03		7.96E-01	1.50E-01		-7.25E-01	1.57E-01		-2.56E+00	2.78E-05	Down	6.40E-02	8.37E-01		-1.71E-01	5.88E-01				Unigene8297_All//7.00E-67//AI726326				
Unigene82970_All	393	0.67	0.00	5.01	0.00	0.61	0.00	0.00	0.00	0.00	-9.38E+00	6.65E-02		2.91E+00	1.70E-06	Up	9.26E+00	1.04E-01		null	null		null	null		null	null		Unigene82970_All//COG2230//1.00E-11//Cyclopropane fatty acid synthase and related methyltransferases						cog +
Unigene82972_All	394	0.00	0.00	4.05	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.20E+01	8.42E-09	Up	null	null		null	null		null	null		null	null		Unigene82972_All//gi|239586448|gb|ACR83570.1|//1.00E-71//cAPX [Solanum nigrum]	Unigene82972_All//3.00E-57//AT1G07890| APX1 (ascorbate peroxidase 1); L-ascorbate peroxidase	Unigene82972_All//4.00E-26//gi|48779689|gb|CO089055.1|CO089055		ko00480|Glutathione metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene82973_All	394	0.27	0.13	2.84	0.38	0.35	0.00	0.00	0.00	0.00	-1.05E+00	6.82E-01		3.42E+00	1.92E-04	Up	-1.18E-01	9.09E-01		-8.57E+00	2.31E-01		null	null		null	null								ESTscan +
Unigene82975_All	398	0.13	0.00	2.81	0.00	0.78	0.00	0.00	0.00	0.00	-7.04E+00	6.00E-01		4.42E+00	3.51E-05	Up	9.60E+00	4.54E-02		null	null		null	null		null	null		Unigene82975_All//gi|194476837|ref|YP_002049016.1|//1.00E-16//Nucleoside-diphosphate kinase [Paulinella chromatophora] >gi|171191844|gb|ACB42806.1| Nucleoside-diphosphate kinase [Paulinella chromatophora]	Unigene82975_All//1.00E-15//AT1G17410| nucleoside diphosphate kinase family protein			ko00230|Purine metabolism//ko00240|Pyrimidine metabolism		nr +
Unigene82976_All	398	0.26	0.13	3.21	0.25	0.35	0.00	0.00	0.00	0.00	-1.05E+00	6.82E-01		3.61E+00	3.40E-05	Up	4.68E-01	8.75E-01		-7.97E+00	3.92E-01		null	null		null	null		Unigene82976_All//sp|P20370|DC4C_ACIAD//5.00E-23//4-carboxymuconolactone decarboxylase OS=Acinetobacter sp. (strain ADP1) GN=pcaC PE=4 SV=2						swissprot +
Unigene82977_All	399	0.13	0.00	3.20	0.00	0.43	0.11	0.00	0.00	0.00	-7.03E+00	6.00E-01		4.61E+00	5.50E-06	Up	8.75E+00	2.26E-01		6.82E+00	6.82E-01		null	null		null	null		Unigene82977_All//sp|Q51506|SOXR_PSEAE//8.00E-07//Redox-sensitive transcriptional activator soxR OS=Pseudomonas aeruginosa GN=soxR PE=3 SV=1						swissprot -
Unigene82978_All	399	0.00	1.52	2.40	0.00	0.00	0.00	0.00	0.00	0.00	1.06E+01	1.16E-03		1.12E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene82978_All//gi|728594|emb|CAA88558.1|//3.00E-20//glycine rich protein, RNA binding protein [Hordeum vulgare subsp. vulgare]	Unigene82978_All//1.00E-10//AT4G14300| heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative			ko03040|Spliceosome		nr -
Unigene82981_All	402	0.00	0.38	1.72	0.12	0.60	0.11	0.00	0.00	0.00	8.56E+00	2.31E-01		1.07E+01	6.09E-04	Up	2.27E+00	3.05E-01		-1.42E-01	9.46E-01		null	null		null	null		Unigene82981_All//gi|255603517|ref|XP_002538063.1|//4.00E-10//conserved hypothetical protein [Ricinus communis] >gi|223513969|gb|EEF24320.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene82982_All	402	1.69	0.00	1.06	0.99	0.77	0.34	0.53	0.10	0.40	-1.07E+01	4.09E-04	Down	-6.75E-01	4.41E-01		-3.63E-01	7.54E-01		-1.56E+00	2.31E-01		-2.34E+00	2.36E-01		-4.08E-01	7.55E-01		Unigene82982_All//gi|15795136|dbj|BAB02514.1|//4.00E-09//transfactor-like protein [Arabidopsis thaliana]	Unigene82982_All//2.00E-10//AT3G13040| myb family transcription factor	Unigene82982_All//2.00E-139//TC162505	G2-like			nr +
Unigene82983_All	402	0.26	0.25	2.52	0.12	0.34	0.22	0.00	0.00	0.00	-4.62E-02	9.85E-01		3.27E+00	5.92E-04	Up	1.47E+00	6.17E-01		8.59E-01	7.90E-01		null	null		null	null		Unigene82983_All//gi|298710018|emb|CBJ31736.1|//7.00E-42//Methionine synthase [Ectocarpus siliculosus]				ko00270|Cysteine and methionine metabolism//ko00670|One carbon pool by folate		nr +
Unigene82987_All	405	0.13	1.00	3.16	0.37	0.00	0.33	0.00	0.00	0.00	2.95E+00	5.90E-02		4.61E+00	5.50E-06	Up	-8.53E+00	1.64E-01		-1.42E-01	9.42E-01		null	null		null	null		Unigene82987_All//COG0739//1.00E-07//Membrane proteins related to metalloendopeptidases						cog -
Unigene82988_All	407	0.00	0.00	3.27	0.00	0.00	0.44	0.00	0.00	0.00	null	null		1.17E+01	2.39E-07	Up	null	null		8.79E+00	1.93E-01		null	null		null	null		Unigene82988_All//gi|73620643|sp|Q94587.1|CRD1_EUPES//2.00E-60//RecName: Full=Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplastic; Short=Mg-protoporphyrin IX monomethyl ester oxidative cyclase; Flags: Precursor >gi|16033631|gb|AAL13304.1|AF417577_1 leucine zipper-containing protein [Euphorbia esula]	Unigene82988_All//5.00E-52//AT3G56940| CRD1 (COPPER RESPONSE DEFECT 1); DNA binding / magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase	Unigene82988_All//2.00E-92//TC172765		ko00860|Porphyrin and chlorophyll metabolism		nr -
Unigene82990_All	407	0.00	0.00	3.79	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.19E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene82990_All//gi|288311314|gb|ADC43596.1|//3.00E-70//HSP90-2 [Glycine max]	Unigene82990_All//2.00E-48//AT5G56010| HSP81-3; ATP binding / unfolded protein binding	Unigene82990_All//1.00E-69//TC161192		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene82991_All	407	0.00	0.00	4.06	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.20E+01	4.29E-09	Up	null	null		null	null		null	null		null	null		Unigene82991_All//gi|158148921|dbj|BAF81994.1|//8.00E-48//cysteine proteinase [Platycodon grandiflorus]	Unigene82991_All//4.00E-38//AT5G60360| AALP (Arabidopsis aleurain-like protease); cysteine-type peptidase	Unigene82991_All//5.00E-13//CD485905				nr -
Unigene82992_All	408	0.13	99.60	33.02	0.00	0.08	0.00	0.00	0.00	0.00	9.60E+00	5.52E-232	Up	8.01E+00	9.27E-74	Up	6.40E+00	8.13E-01		null	null		null	null		null	null		Unigene82992_All//gi|224005849|ref|XP_002291885.1|//2.00E-07//trypsin-like serine protease [Thalassiosira pseudonana CCMP1335] >gi|220972404|gb|EED90736.1| trypsin-like serine protease [Thalassiosira pseudonana CCMP1335]						nr +
Unigene82993_All	409	0.51	1.61	5.73	0.00	0.08	0.88	0.00	0.00	0.00	1.65E+00	8.13E-02		3.48E+00	6.87E-09	Up	6.40E+00	8.13E-01		9.79E+00	2.37E-02		null	null		null	null		Unigene82993_All//gi|226348178|gb|ACO50428.1|//1.00E-52//chlorophyllase 1 [Pachira macrocarpa]	Unigene82993_All//1.00E-36//AT1G19670| ATCLH1 (ARABIDOPSIS THALIANA CORONATINE-INDUCED PROTEIN 1); chlorophyllase	Unigene82993_All//1.00E-118//gi|109881630|gb|DW510600.1|DW510600		ko00860|Porphyrin and chlorophyll metabolism		nr +

Unigene82994_All	409	0.38	0.62	2.73	0.00	0.17	0.44	0.00	0.00	0.00	6.91E-01	6.26E-01		2.83E+00	7.34E-04	Up	7.40E+00	6.00E-01		8.79E+00	1.93E-01		null	null		null	null		Unigene82994_All//gi|255604647|ref|XP_002538258.1|//3.00E-15//Bactoprenol glucosyl transferase, putative [Ricinus communis] >gi|223513033|gb|EEF24124.1| Bactoprenol glucosyl transferase, putative [Ricinus communis]						nr -
Unigene82995_All	409	0.13	0.25	3.25	0.12	0.00	0.22	0.00	0.00	0.00	9.54E-01	7.23E-01		4.67E+00	2.95E-06	Up	-6.93E+00	5.43E-01		8.58E-01	7.90E-01		null	null		null	null		Unigene82995_All//gi|242066522|ref|XP_002454550.1|//5.00E-06//hypothetical protein SORBIDRAFT_04g033130 [Sorghum bicolor] >gi|241934381|gb|EES07526.1| hypothetical protein SORBIDRAFT_04g033130 [Sorghum bicolor]				ko00903|Limonene and pinene degradation//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00310|Lysine degradation//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism		nr +
Unigene82996_All	409	0.00	0.50	3.52	0.00	0.84	0.00	0.00	0.00	0.00	8.95E+00	1.34E-01		1.18E+01	6.28E-08	Up	9.72E+00	3.00E-02		null	null		null	null		null	null		Unigene82996_All//COG0715//3.00E-21//ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components						cog -
Unigene82998_All	410	0.13	0.87	2.86	0.00	0.17	0.00	0.00	0.00	0.00	2.76E+00	9.57E-02		4.49E+00	1.90E-05	Up	7.39E+00	6.00E-01		null	null		null	null		null	null		Unigene82998_All//sp|A5E8V7|PNCB_BRASB//2.00E-70//Nicotinate phosphoribosyltransferase OS=Bradyrhizobium sp. (strain BTAi1 / ATCC BAA-1182) GN=pncB PE=3 SV=1						swissprot -
Unigene82999_All	410	0.00	0.25	6.23	0.00	0.00	0.00	0.00	0.00	0.00	7.95E+00	3.79E-01		1.26E+01	4.20E-14	Up	null	null		null	null		null	null		null	null		Unigene82999_All//gi|226499354|ref|NP_001147027.1|//1.00E-57//polyubiquitin containing 7 ubiquitin monomers [Zea mays] >gi|195606596|gb|ACG25128.1| polyubiquitin containing 7 ubiquitin monomers [Zea mays]	Unigene82999_All//3.00E-58//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene82999_All//1.00E-72//gi|78325958|gb|DT546232.1|DT546232				nr -
Unigene83_All	1129	2.60	4.58	3.25	3.40	4.24	7.60	12.10	14.36	30.63	8.19E-01	1.93E-03		3.27E-01	3.59E-01		3.20E-01	2.93E-01		1.16E+00	5.91E-09	Up	2.48E-01	5.71E-02		1.34E+00	3.98E-50	Up	Unigene83_All//gi|18146956|db|BAB82502.1|//1.00E-126//cig3 [Nicotiana tabacum]	Unigene83_All//8.00E-120//AT5G19400| SMG7	Unigene83_All//1.00E-179//gi|48820922|gb|CO122235.1|CO122235				nr -
Unigene830_All	4226	0.43	0.14	0.73	0.79	0.84	0.67	0.67	0.62	0.31	-1.59E+00	1.79E-03		7.54E-01	4.25E-02		8.77E-02	8.20E-01		-2.30E-01	5.53E-01		-1.05E-01	7.64E-01		-1.11E+00	6.85E-04	Down	Unigene830_All//gi|224115778|ref|XP_002317122.1|//0.00E+00//nbs-lrr resistance protein [Populus trichocarpa] >gi|222860187|gb|EEE97734.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene830_All//3.00E-92//AT3G14470| disease resistance protein (NBS-LRR class), putative			ko04626|Plant-pathogen interaction		nr -
Unigene83001_All	412	0.38	0.00	3.10	0.24	0.33	0.00	0.00	0.00	0.00	-8.57E+00	2.13E-01		3.03E+00	1.48E-04	Up	4.67E-01	8.75E-01		-7.92E+00	3.92E-01		null	null		null	null									ESTscan -
Unigene83002_All	412	0.13	0.37	3.62	0.00	0.59	0.22	0.00	0.00	0.00	1.54E+00	5.29E-01		4.83E+00	4.43E-07	Up	9.19E+00	1.04E-01		7.78E+00	4.69E-01		null	null		null	null		Unigene83002_All//gi|255591021|ref|XP_002535422.1|//1.00E-17//conserved hypothetical protein [Ricinus communis] >gi|223523171|gb|EEF26965.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene83003_All	412	0.00	0.49	1.81	0.00	0.00	0.77	0.00	0.00	0.00	8.94E+00	1.34E-01		1.08E+01	3.24E-04	Up	null	null		9.58E+00	4.07E-02		null	null		null	null		Unigene83003_All//gi|33438474|emb|CAE30280.1|//7.00E-73//chlorophyll a /b binding protein [Beta vulgaris]	Unigene83003_All//1.00E-70//AT3G47470| LHCA4 (LIGHT-HARVESTING CHLOROPHYLL-PROTEIN COMPLEX I SUBUNIT A4); chlorophyll binding	Unigene83003_All//6.00E-65//TC175752		ko00196|Photosynthesis - antenna proteins		nr -
Unigene83004_All	412	0.00	0.00	2.07	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.10E+01	8.96E-05	Up	null	null		null	null		null	null		null	null		Unigene83004_All//gi|51477393|gb|AAU04766.1|//2.00E-50//protein disulfide isomerase (PDI)-like protein 2 [Cucumis melo]	Unigene83004_All//3.00E-37//AT1G60420| DC1 domain-containing protein	Unigene83004_All//3.00E-11//TC145938				nr -
Unigene83007_All	414	0.00	0.12	2.32	0.00	0.17	0.00	0.00	0.00	0.00	6.94E+00	6.07E-01		1.12E+01	2.44E-05	Up	7.38E+00	6.00E-01		null	null		null	null		null	null									ESTscan +
Unigene83008_All	415	0.25	0.98	2.69	0.24	0.33	0.76	0.00	0.20	0.00	1.95E+00	1.44E-01		3.42E+00	1.92E-04	Up	4.67E-01	8.75E-01		1.67E+00	3.08E-01		7.65E+00	3.98E-01		null	null		Unigene83008_All//sp|Q01980|AADR_RHOPA//2.00E-41//Transcriptional activatory protein aadR OS=Rhodopseudomonas palustris GN=aadR PE=1 SV=1						swissprot -
Unigene83015_All	417	0.00	0.85	2.17	0.00	0.00	0.00	0.00	0.00	0.00	9.73E+00	2.43E-02		1.11E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene83015_All//gi|222834593|gb|EEE73056.1|//2.00E-15//predicted protein [Populus trichocarpa]		Unigene83015_All//9.00E-24//TC147888				nr +
Unigene83016_All	417	0.00	0.24	1.92	0.36	0.41	0.43	0.00	0.00	0.00	7.92E+00	3.79E-01		1.09E+01	1.71E-04	Up	2.04E-01	9.49E-01		2.74E-01	9.03E-01		null	null		null	null									ESTscan +
Unigene83017_All	418	0.38	0.97	4.08	0.36	0.49	0.00	0.00	0.00	0.00	1.37E+00	2.73E-01		3.44E+00	1.59E-06	Up	4.67E-01	8.24E-01		-8.48E+00	2.31E-01		null	null		null	null									ESTscan -
Unigene83018_All	418	0.25	0.00	3.31	0.24	0.41	0.00	0.00	0.00	0.00	-7.97E+00	3.65E-01		3.73E+00	1.05E-05	Up	7.90E-01	7.69E-01		-7.90E+00	3.92E-01		null	null		null	null		Unigene83018_All//gi|159488662|ref|XP_001702324.1|//1.00E-37//urea carboxylase [Chlamydomonas reinhardtii] >gi|158271229|gb|EDO97054.1| urea carboxylase [Chlamydomonas reinhardtii]	Unigene83018_All//1.00E-37//AT1G03090| MCCA; methylcrotonoyl-CoA carboxylase			ko00280|Valine, leucine and isoleucine degradation		nr +
Unigene83019_All	418	0.25	0.61	3.06	0.12	0.16	0.86	0.00	0.00	0.00	1.28E+00	4.34E-01		3.61E+00	3.40E-05	Up	4.67E-01	9.53E-01		2.86E+00	9.44E-02		null	null		null	null		Unigene83019_All//sp|Q987N5|PANE_RHILO//3.00E-06//Putative 2-dehydropantoate 2-reductase OS=Rhizobium loti GN=mll6982 PE=3 SV=1						swissprot -
Unigene83020_All	419	0.00	1.69	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	3.30E-04	Up	1.03E+01	3.98E-03		null	null		null	null		null	null		null	null		Unigene83020_All//gi|223998414|ref|XP_002288880.1|//1.00E-43//ubiquitin conjugating enzyme [Thalassiosira pseudonana CCMP1335] >gi|220975988|gb|EED94316.1| ubiquitin conjugating enzyme [Thalassiosira pseudonana CCMP1335]	Unigene83020_All//1.00E-42//AT3G57870| SCE1 (SUMO CONJUGATION ENZYME 1); SUMO ligase			ko04120|Ubiquitin mediated proteolysis		nr -
Unigene83021_All	419	0.00	2.06	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	4.91E-05	Up	1.03E+01	3.98E-03		null	null		null	null		null	null		null	null		Unigene83021_All//sp|Q6YHK3|CD109_HUMAN//1.00E-14//CD109 antigen OS=Homo sapiens GN=CD109 PE=1 SV=2						swissprot -
Unigene83023_All	421	0.00	0.00	8.35	0.00	0.00	0.64	0.00	0.00	0.00	null	null		1.30E+01	1.87E-19	Up	null	null		9.33E+00	7.01E-02		null	null		null	null		Unigene83023_All//gi|115472753|ref|NP_001059975.1|//2.00E-72//Os07g0558400 [Oryza sativa Japonica Group] >gi|3075488|gb|AAC14566.1| chlorophyll a/b-binding protein [Oryza sativa Japonica Group] >gi|34394009|dbj|BAC84033.1| chlorophyll a/b-binding protein [Oryza sativa Japonica Group] >gi|113611511|dbj|BAF21889.1| Os07g0558400 [Oryza sativa Japonica Group]	Unigene83023_All//2.00E-72//AT5G01530| chlorophyll A-B binding protein CP29 (LHCB4)	Unigene83023_All//5.00E-47//TC170792		ko00196|Photosynthesis - antenna proteins		nr +
Unigene83025_All	422	0.50	0.72	2.90	0.35	0.41	0.00	0.00	0.00	0.00	5.39E-01	6.71E-01		2.55E+00	8.25E-04	Up	2.04E-01	9.49E-01		-8.47E+00	2.31E-01		null	null		null	null		Unigene83025_All//gi|159468742|ref|XP_001692533.1|//6.00E-17//cytochrome P450, CYP711 clan [Chlamydomonas reinhardtii] >gi|158278246|gb|EDP04011.1| cytochrome P450, CYP711 clan [Chlamydomonas reinhardtii]	Unigene83025_All//6.00E-11//AT5G52400| CYP715A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00908|Zeatin biosynthesis//ko00591|Linoleic acid metabolism//ko00906|Carotenoid biosynthesis		nr +
Unigene83026_All	422	0.00	1.32	5.30	0.00	0.00	0.00	0.00	0.00	0.00	1.04E+01	2.16E-03		1.24E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene83026_All//gi|299469749|emb|CBN76603.1|//3.00E-09//similar to ARNAK nucleoprotein [Ectocarpus siliculosus]						nr -
Unigene83027_All	422	0.00	3.12	3.15	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	1.49E-07	Up	1.16E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene83027_All//gi|15233440|ref|NP_195326.1|//8.00E-14//CSDP1 (cold shock domain protein 1); RNA binding / double-stranded DNA binding / nucleic acid binding / single-stranded DNA binding [Arabidopsis thaliana] >gi|3036806|emb|CAA18496.1| glycine-rich protein [Arabidopsis thaliana] >gi|7270554|emb|CAB81511.1| glycine-rich protein [Arabidopsis thaliana] >gi|10741941|dbj|BAE98911.1| glycine-rich protein [Arabidopsis thaliana]	Unigene83027_All//4.00E-11//AT4G36020| CSDP1 (cold shock domain protein 1); RNA binding / double-stranded DNA binding / nucleic acid binding / single-stranded DNA binding		CSD			nr +
Unigene83028_All	423	0.00	0.48	4.28	0.12	0.41	0.11	0.00	0.00	0.00	8.90E+00	1.34E-01		1.21E+01	5.68E-10	Up	1.79E+00	5.19E-01		-1.41E-01	9.46E-01		null	null		null	null		Unigene83028_All//COG4553//1.00E-15//Poly-beta-hydroxyalkanoate depolymerase						cog +
Unigene83031_All	424	0.12	0.24	2.76	0.12	1.06	0.00	0.00	0.00	0.00	9.54E-01	7.23E-01		4.48E+00	1.90E-05	Up	3.17E+00	3.95E-02		-6.88E+00	6.17E-01		null	null		null	null									ESTscan -
Unigene83032_All	425	0.00	0.00	2.26	0.00	0.00	0.43	0.00	0.00	0.00	null	null		1.11E+01	2.44E-05	Up	null	null		8.73E+00	1.93E-01		null	null		null	null		Unigene83032_All//gi|255560287|ref|XP_002521161.1|//1.00E-42//photosystem I reaction center subunit IV A, chloroplast precursor [Ricinus communis] >gi|223539730|gb|EEF41312.1| photosystem I reaction center subunit IV A, chloroplast precursor [Ricinus communis]	Unigene83032_All//8.00E-16//AT2G20260| PSAE-2 (photosystem I subunit E-2); catalytic	Unigene83032_All//3.00E-30//EX167214		ko00195|Photosynthesis		nr +
Unigene83033_All	426	0.00	0.12	2.25	0.12	0.32	0.53	0.00	0.00	0.00	6.89E+00	6.07E-01		1.11E+01	2.44E-05	Up	1.47E+00	6.17E-01		2.18E+00	3.22E-01		null	null		null	null		Unigene83033_All//COG4663//9.00E-21//TRAP-type mannitol/chloroaromatic compound transport system, periplasmic component						cog +
Unigene83034_All	426	0.25	0.36	4.25	0.12	0.00	0.42	0.10	0.00	0.00	5.39E-01	7.77E-01		4.11E+00	8.16E-08	Up	-6.87E+00	5.43E-01		1.86E+00	4.57E-01		-6.63E+00	6.42E-01		-6.63E+00	6.00E-01									ESTscan +
Unigene83035_All	426	0.00	0.95	2.75	0.00	0.00	0.00	0.00	0.00	0.00	9.89E+00	1.34E-02		1.14E+01	1.76E-06	Up	null	null		null	null		null	null		null	null									ESTscan +
Unigene83036_All	426	0.12	0.00	3.00	0.35	0.16	0.00	0.00	0.00	0.00	-6.94E+00	6.00E-01		4.61E+00	5.50E-06	Up	-1.12E+00	5.82E-01		-8.48E+00	2.31E-01		null	null		null	null									ESTscan -
Unigene83037_All	427	0.37	0.47	2.62	0.00	0.73	0.00	0.00	0.00	0.00	3.69E-01	8.15E-01		2.83E+00	7.34E-04	Up	9.50E+00	4.54E-02		null	null		null	null		null	null		Unigene83037_All//gi|195642874|gb|ACG40905.1|//6.00E-09//uncharacterized secreted protein [Zea mays]	Unigene83037_All//1.00E-05//AT5G54240| unknown protein					nr -
Unigene83038_All	427	0.00	0.24	3.74	0.00	0.00	0.00	0.00	0.00	0.00	7.89E+00	3.79E-01		1.19E+01	8.42E-09	Up	null	null		null	null		null	null		null	null		Unigene83038_All//gi|9663769|emb|CAC01238.1|//2.00E-42//RNA Binding Protein 47 [Nicotiana plumbaginifolia]	Unigene83038_All//5.00E-34//AT1G47500| ATRBP47C (RNA-binding protein 47C"); RNA binding			ko03040|Spliceosome		nr +

Unigene83039_All	430	0.73	0.71	3.34	0.00	0.16	0.42	0.00	0.00	0.00	-4.64E-02	9.84E-01		2.20E+00	8.73E-04	Up	7.32E+00	5.99E-01		8.71E+00	1.93E-01		null	null		null	null		Unigene83039_All//gi|255598493|ref|XP_002537022.1|//8.00E-30//3-hydroxy-3-methylglutaryl-coenzyme A reductase, putative [Ricinus communis] >gi|223517785|gb|EEF25361.1| 3-hydroxy-3-methylglutaryl-coenzyme A reductase, putative [Ricinus communis]					nr -
Unigene8304_All	244	0.00	1.25	2.62	3.88	14.82	12.40	1.39	0.34	0.65	1.03E+01	4.36E-02		1.14E+01	1.15E-03		1.93E+00	1.76E-08	Up	1.68E+00	1.06E-05	Up	-2.02E+00	1.36E-01		-1.09E+00	3.55E-01		Unigene8304_All//gi|224061039|ref|XP_002300328.1|//2.00E-14//glycosyl hydrolase family 9 [Populus trichocarpa] >gi|222847586|gb|EEE85133.1|glycosyl hydrolase family 9 [Populus trichocarpa]	Unigene8304_All//3.00E-11//AT2G32990| AtGH9B8 (Arabidopsis thaliana glycosyl hydrolase 9B8); catalytic/hydrolase, hydrolyzing O-glycosyl compounds	Unigene8304_All//3.00E-13//TC157751		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0031410//GO:0044238	nr +
Unigene83041_All	431	0.00	1.41	6.42	0.00	0.00	0.00	0.00	0.00	0.00	1.05E+01	1.16E-03		1.26E+01	2.74E-15	Up	null	null		null	null		null	null		null	null		Unigene83041_All//gi|225216852|gb|ACN85343.1|//1.00E-13//cystatin [Camellia sinensis] >gi|225216854|gb|ACN85344.1|cystatin [Camellia sinensis]	Unigene83041_All//1.00E-13//AT3G12490| cysteine protease inhibitor, putative / cystatin, putative					nr +
Unigene83042_All	432	0.00	0.00	3.57	0.00	0.96	0.42	0.00	0.00	0.00	null	null		1.18E+01	1.65E-08	Up	9.90E+00	1.25E-02		8.71E+00	1.93E-01		null	null		null	null							ESTscan -
Unigene83043_All	436	0.00	0.46	4.03	0.00	0.71	0.00	0.00	0.00	0.00	8.86E+00	1.34E-01		1.20E+01	1.12E-09	Up	9.47E+00	4.54E-02		null	null		null	null		null	null		Unigene83043_All//gi|125552068|gb|EAY97777.1|//9.00E-18//hypothetical protein OsI_19689 [Oryza sativa Indica Group]					nr +
Unigene83047_All	442	0.00	0.00	2.41	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.12E+01	6.58E-06	Up	null	null		null	null		null	null		null	null		Unigene83047_All//gi|15230555|ref|NP_190735.1|//3.00E-61//SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] >gi|75202761|sp|Q9SCU1.1|PATL6_ARATH RecName: Full=Patellin-6 >gi|16930483|gb|AAL31927.1|AF419595_1 AT3g51670/T18N14_50 [Arabidopsis thaliana] >gi|25141223|gb|AAN73306.1|At3g51670/T18N14_50 [Arabidopsis thaliana]	Unigene83047_All//2.00E-62//AT3G51670| SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein	Unigene83047_All//3.00E-33//gi|21102222|gb|BQ414535.1|BQ414535				nr +
Unigene8305_All	562	0.93	0.36	0.38	1.15	3.43	1.29	0.45	0.00	0.28	-1.37E+00	1.96E-01		-1.30E+00	2.42E-01		1.57E+00	9.99E-04	Up	1.58E-01	8.59E-01		-8.82E+00	4.02E-02		-6.71E-01	6.05E-01		Unigene8305_All//gi|115477631|ref|NP_001062411.1|//3.00E-43//Os08g0545000 [Oryza sativa Japonica Group] >gi|113624380|dbj|BAF24325.1|Os08g0545000 [Oryza sativa Japonica Group]	Unigene8305_All//1.00E-30//AT5G51920| catalytic/pyridoxal phosphate binding	Unigene8305_All//2.00E-13//C0083107			GO:0048037	nr -
Unigene83057_All	453	0.00	0.00	3.41	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.17E+01	1.65E-08	Up	null	null		null	null		null	null		null	null		Unigene83057_All//gi|76161008|gb|AB440467.1|//4.00E-61//glycoprotein-like protein [Solanum tuberosum]	Unigene83057_All//3.00E-57//AT4G27090| 60S ribosomal protein L14 (RPL14B)	Unigene83057_All//2.00E-46//gi|164328930|gb|EV497695.1|EV497695		ko03010|Ribosome		nr +
Unigene83058_All	454	0.00	8.37	4.22	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.23E-21	Up	1.20E+01	1.46E-10	Up	null	null		null	null		null	null		null	null		Unigene83058_All//gi|429118|emb|CAA53369.1|//7.00E-64//glucose regulated protein /BiP [Phytophthora cinnamomi]	Unigene83058_All//6.00E-55//AT5G42020| BIP2; ATP binding	Unigene83058_All//1.00E-10//TC165936		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export		nr +
Unigene83060_All	455	0.23	0.89	2.46	0.22	0.08	0.50	0.00	0.00	0.00	1.95E+00	1.44E-01		3.42E+00	1.92E-04	Up	-1.53E+00	5.82E-01		1.18E+00	5.48E-01		null	null		null	null		Unigene83060_All//gi|255591307|ref|XP_002535483.1|//3.00E-21//conserved hypothetical protein [Ricinus communis] >gi|223522941|gb|EEF26899.1|conserved hypothetical protein [Ricinus communis]					nr +
Unigene83061_All	456	0.00	0.22	1.99	0.11	0.53	0.00	0.00	0.00	0.00	7.80E+00	3.79E-01		1.10E+01	4.69E-05	Up	2.28E+00	3.05E-01		-6.77E+00	6.17E-01		null	null		null	null							ESTscan -
Unigene83062_All	456	0.00	2.00	2.34	0.00	0.00	0.00	0.00	0.00	0.00	1.10E+01	2.60E-05	Up	1.12E+01	6.58E-06	Up	null	null		null	null		null	null		null	null		Unigene83062_All//gi|301106871|ref|XP_002902518.1|//3.00E-06//protocadherin-like protein [Phytophthora infestans T30-4] >gi|262098392|gb|EEY56444.1|protocadherin-like protein [Phytophthora infestans T30-4]					nr +
Unigene83064_All	459	0.00	0.77	14.15	0.00	0.00	0.00	0.00	0.00	0.00	9.59E+00	2.43E-02		1.38E+01	2.96E-36	Up	null	null		null	null		null	null		null	null		Unigene83064_All//gi|257219554|gb|ACN59430.1|//9.00E-38//copper chaperone [Jatropha curcas]	Unigene83064_All//1.00E-32//AT3G56240| CCH (COPPER CHAPERONE); copper chaperone	Unigene83064_All//8.00E-34//TC154944				nr +
Unigene83065_All	460	0.00	0.00	2.89	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.15E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene83065_All//gi|297806327|ref|XP_002871047.1|//4.00E-36//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297316884|gb|EFH47306.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene83065_All//1.00E-32//AT5G03610| GDSL-motif lipase/hydrolase family protein					nr +
Unigene83066_All	461	0.00	0.44	2.77	0.00	0.00	0.00	0.00	0.00	0.00	8.78E+00	1.34E-01		1.14E+01	4.67E-07	Up	null	null		null	null		null	null		null	null		Unigene83066_All//gi|301112320|ref|XP_002905239.1|//2.00E-06//conserved hypothetical protein [Phytophthora infestans T30-4] >gi|262095569|gb|EEY53621.1|conserved hypothetical protein [Phytophthora infestans T30-4]	Unigene83066_All//4.00E-06//AT3G23900| RNA recognition motif (RRM)-containing protein					nr +
Unigene83067_All	462	0.00	0.66	3.00	0.22	0.07	0.49	0.00	0.00	0.00	9.36E+00	4.36E-02		1.15E+01	1.23E-07	Up	-1.53E+00	5.82E-01		1.18E+00	5.48E-01		null	null		null	null		Unigene83067_All//gi|255618754|ref|XP_002539970.1|//1.00E-27//Exopolysaccharide production protein PSS, putative [Ricinus communis] >gi|223500643|gb|EEF22413.1|Exopolysaccharide production protein PSS, putative [Ricinus communis]					nr -
Unigene83068_All	464	0.11	0.00	2.98	0.21	0.22	0.39	0.00	0.00	0.00	-6.82E+00	6.00E-01		4.73E+00	1.57E-06	Up	5.21E-02	9.64E-01		8.59E-01	6.94E-01		null	null		null	null		Unigene83068_All//gi|224150808|ref|XP_002337013.1|//2.00E-11//predicted protein [Populus trichocarpa] >gi|222837832|gb|EEE76197.1|predicted protein [Populus trichocarpa]					nr -
Unigene83069_All	465	0.00	0.22	2.98	0.00	0.00	0.00	0.00	0.00	0.00	7.77E+00	3.79E-01		1.15E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene83069_All//gi|38325815|gb|AAR17080.1|//1.00E-78//heat shock protein 70-3 [Nicotiana tabacum]	Unigene83069_All//7.00E-77//AT3G12580| HSP70 (heat shock protein 70); ATP binding	Unigene83069_All//3.00E-55//gi|78334956|gb|DT555230.1|DT555230		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis		nr -
Unigene83072_All	470	0.89	0.32	4.42	0.21	0.29	0.00	0.00	0.00	0.00	-1.46E+00	2.34E-01		2.31E+00	1.92E-05	Up	4.67E-01	8.75E-01		-7.73E+00	3.92E-01		null	null		null	null		Unigene83072_All//COG1033//7.00E-07//Predicted exporters of the RND superfamily					cog -
Unigene83073_All	471	0.11	0.65	2.60	0.21	0.07	0.29	0.00	0.00	0.00	2.54E+00	1.51E-01		4.55E+00	1.02E-05	Up	-1.53E+00	5.82E-01		4.44E-01	8.59E-01		null	null										ESTscan +
Unigene83074_All	471	0.00	0.43	4.07	0.00	0.00	0.00	0.00	0.00	0.00	8.75E+00	1.34E-01		1.20E+01	1.46E-10	Up	null	null		null	null		null	null		null	null		Unigene83074_All//gi|111143344|gb|ABR06547.1|//1.00E-83//molecular chaperone [Ricinus communis]	Unigene83074_All//1.00E-68//AT3G44110| ATJ3; protein binding	Unigene83074_All//2.00E-62//gi|48823294|gb|CO124607.1|CO124607		ko04141|Protein processing in endoplasmic reticulum		nr +
Unigene83075_All	473	0.11	0.00	3.49	0.53	0.00	0.10	0.00	0.00	0.00	-6.79E+00	6.00E-01		4.98E+00	6.48E-08	Up	-9.04E+00	4.17E-02		-2.46E+00	2.23E-01		null	null		null	null		Unigene83075_All//COG0210//2.00E-18//Superfamily I DNA and RNA helicases					cog +
Unigene83076_All	473	0.00	0.54	3.15	0.00	0.73	0.76	0.00	0.00	0.00	9.07E+00	7.75E-02		1.16E+01	3.21E-08	Up	9.51E+00	3.00E-02		9.58E+00	2.37E-02		null	null		null	null		Unigene83076_All//gi|289065166|ref|YP_003434218.1|//6.00E-17//NADH dehydrogenase subunit 4 [Chattonella marina] >gi|288871878|dbj|BAI70565.1| NADH dehydrogenase subunit 4 [Chattonella marina]	Unigene83076_All//2.00E-06//ATMG00580| NADH dehydrogenase subunit 4			ko00190|Oxidative phosphorylation		nr +
Unigene83078_All	474	0.00	3.42	1.35	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	2.96E-09	Up	1.04E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene83078_All//gi|298712549|emb|CBJ26817.1|//4.00E-72//Catalase is an enzyme, present in all aerobic cells, that decomposes hydrogen peroxide to molecular [Ectocarpus siliculosus]	Unigene83078_All//1.00E-39//AT1G20630| CAT1 (CATALASE 1); catalase			ko04146|Peroxisome//ko00380|Tryptophan metabolism		nr +
Unigene83079_All	474	0.44	0.64	2.92	0.00	0.07	0.00	0.00	0.00	0.00	5.39E-01	6.71E-01		2.73E+00	1.78E-04	Up	6.18E+00	8.12E-01		null	null		null	null		null	null		Unigene83079_All//gi|6552725|gb|AAF16525.1|AF191301_1//9.00E-34//carbamoyl-phosphate synthase subunit A [Medicago sativa]	Unigene83079_All//4.00E-29//AT3G27740| CARA (CARBAMOYL PHOSPHATE SYNTHETASE A); carbamoyl-phosphate synthase (glutamine-hydrolyzing)/carbamoyl-phosphate synthase/catalytic			ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene8308_All	304	3.10	0.50	1.40	2.46	3.74	3.12	4.87	1.37	1.57	-2.63E+00	2.38E-03		-1.14E+00	1.38E-01		6.05E-01	3.84E-01		3.44E-01	6.49E-01		-1.82E+00	5.42E-04	Down	-1.63E+00	1.09E-03				Unigene8308_All//3.00E-97//TC140017				
Unigene83081_All	475	0.00	1.17	3.36	0.00	0.00	0.19	0.00	0.00	0.00	1.02E+01	2.16E-03		1.17E+01	8.42E-09	Up	null	null		7.57E+00	4.69E-01		null	null		null	null		Unigene83081_All//gi|224090986|ref|XP_002309134.1|//1.00E-69//light-harvesting complex II protein Lhcb4 [Populus trichocarpa] >gi|222855110|gb|EEE92657.1|light-harvesting complex II protein Lhcb4 [Populus trichocarpa]	Unigene83081_All//2.00E-60//AT5G01530| chlorophyll A-B binding protein CP29 (LHCB4)	Unigene83081_All//3.00E-39//ES840680		ko00196|Photosynthesis - antenna proteins		nr -
Unigene83082_All	475	0.33	0.43	3.92	0.31	1.45	0.19	0.00	0.00	0.00	3.69E-01	8.15E-01		3.57E+00	2.70E-07	Up	2.20E+00	2.71E-02		-7.26E-01	7.13E-01		null	null		null	null		Unigene83082_All//sp|P15939|NODV_BRAJA//8.00E-09//Nodulation protein V OS=Bradyrhizobium japonicum GN=nodV PE=4 SV=1					swissprot -
Unigene83083_All	476	0.11	0.32	1.79	0.21	0.43	0.19	0.00	0.00	0.00	1.54E+00	5.29E-01		4.03E+00	7.01E-04	Up	1.05E+00	6.11E-01		-1.41E-01	9.46E-01		null	null		null	null							ESTscan +
Unigene83084_All	477	0.22	0.53	3.24	0.42	0.51	0.47	0.00	0.00	0.00	1.28E+00	4.34E-01		3.88E+00	1.75E-06	Up	2.75E-01	8.94E-01		1.81E-01	9.34E-01		null	null		null	null		Unigene83084_All//gi|15214056|sp|P93052.1|LDH_BOTBR//2.00E-49//RecName: Full=L-lactate dehydrogenase; Short=LDH >gi|1737465|gb|AAB38970.1| malate dehydrogenase [Botryococcus braunii]	Unigene83084_All//5.00E-15//AT1G53240| malate dehydrogenase (NAD), mitochondrial			ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms//ko00020|Citrate cycle (TCA cycle)//ko00630|Glyoxylate and dicarboxylate metabolism		nr +
Unigene83085_All	478	0.00	1.27	2.23	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	1.16E-03		1.11E+01	6.58E-06	Up	null	null		null	null		null	null		null	null		Unigene83085_All//gi|224015300|ref|XP_002297307.1|//4.00E-13//copia-like retroelement pol polyprotein found-like protein [Thalassiosira pseudonana CCMP1335] >gi|220968020|gb|EED86378.1|copia-like retroelement pol polyprotein found-like protein [Thalassiosira pseudonana CCMP1335]				ko04144|Endocytosis		nr -

Unigene83086_All	478	0.00	4.98	1.23	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.50E-13	Up	1.03E+01	2.15E-03		null	null		null	null		null	null		null	null		Unigene83086_All//gi|195625546|gb|ACG34603.1|//7.00E-20//dehydrogenase/reductase SDR family member 2 [Zea mays]	Unigene83086_All//2.00E-10//AT4G05530| IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase			ko04146|Peroxisome		nr -
Unigene83088_All	482	0.11	0.00	4.09	0.00	0.43	0.37	0.00	0.00	0.00	-6.76E+00	6.00E-01		5.24E+00	1.35E-09	Up	8.74E+00	1.56E-01		8.55E+00	1.93E-01		null	null		null	null		Unigene83088_All//gi|222874702|gb|EEF11833.1|//4.00E-46//predicted protein [Populus trichocarpa]						nr -
Unigene83089_All	483	0.00	4.51	3.20	0.00	0.43	0.00	0.00	0.00	0.00	1.21E+01	2.11E-12	Up	1.16E+01	1.65E-08	Up	8.74E+00	1.56E-01		null	null		null	null		null	null		Unigene83089_All//gi|3893085|emb|CAA10192.1|//7.00E-13//glycine-rich protein 2 [Cicer arietinum]				ko03040|Spliceosome		nr +
Unigene83090_All	483	0.00	1.05	2.09	0.00	0.00	0.00	0.00	0.00	0.00	1.00E+01	3.99E-03		1.10E+01	1.27E-05	Up	null	null		null	null		null	null		null	null		Unigene83090_All//sp|P41134|ID1_HUMAN//2.00E-52//DNA-binding protein inhibitor ID-1 OS=Homo sapiens GN=ID1 PE=1 SV=3						swissprot +
Unigene83092_All	484	0.00	0.84	5.06	0.00	0.00	0.00	0.00	0.00	0.00	9.71E+00	1.34E-02		1.23E+01	1.64E-13	Up	null	null		null	null		null	null		null	null		Unigene83092_All//gi|297835540|ref|XP_002885652.1|//1.00E-62//ALDH2C4 [Arabidopsis lyrata subsp. lyrata] >gi|297331492|gb|EFH61911.1| ALDH2C4 [Arabidopsis lyrata subsp. lyrata]	Unigene83092_All//6.00E-64//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene83092_All//9.00E-09//TC157786		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr -
Unigene83093_All	487	0.32	0.10	3.50	0.41	0.14	0.19	0.00	0.00	0.00	-1.63E+00	4.87E-01		3.44E+00	1.59E-06	Up	-1.53E+00	4.14E-01		-1.14E+00	5.67E-01		null	null		null	null								ESTscan +
Unigene83094_All	487	0.64	0.10	3.39	0.51	0.28	0.00	0.00	0.00	0.00	-2.63E+00	1.30E-01		2.39E+00	1.28E-04	Up	-8.55E-01	5.73E-01		-9.00E+00	7.30E-02		null	null		null	null		Unigene83094_All//gi|159471580|ref|XP_001693934.1|//3.00E-24//formaldehyde dehydrogenase [Chlamydomonas reinhardtii] >gi|158277101|gb|EDP02870.1| formaldehyde dehydrogenase [Chlamydomonas reinhardtii]	Unigene83094_All//8.00E-24//AT4G22110| alcohol dehydrogenase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr -
Unigene83095_All	488	0.32	0.42	2.73	0.10	0.28	0.28	0.00	0.00	0.00	3.69E-01	8.15E-01		3.08E+00	8.57E-05	Up	1.47E+00	6.17E-01		1.44E+00	6.36E-01		null	null		null	null		Unigene83095_All//sp|P30149|YABI_ECOLI//2.00E-06//Inner membrane protein yabI OS=Escherichia coli (strain K12) GN=yabI PE=1 SV=2						swissprot +
Unigene83096_All	488	0.00	2.70	5.24	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	1.49E-07	Up	1.24E+01	4.19E-14	Up	null	null		null	null		null	null		null	null		Unigene83096_All//gi|124112097|ref|YP_001019088.1|//1.00E-42//ribosomal protein L16 [Chlorokybus atmophyticus] >gi|215275627|sp|Q19VB1.2|RK16_CHLAT RecName: Full=50S ribosomal protein L16, chloroplastic >gi|124012208|gb|ABD62229.2| ribosomal protein L16 [Chlorokybus atmophyticus]	Unigene83096_All//9.00E-41//ATCG00790| chloroplast gene encoding a ribosomal protein L16, which is a constituent of 50S large ribosomal subunit			ko03010|Ribosome		nr -
Unigene83098_All	489	0.00	0.62	7.08	0.00	0.00	0.00	0.00	0.00	0.00	9.28E+00	4.36E-02		1.28E+01	3.72E-19	Up	null	null		null	null		null	null		null	null		Unigene83098_All//gi|46399235|gb|AAS92246.1|//7.00E-43//proline-rich protein 1 [Capsicum annuum]	Unigene83098_All//3.00E-25//AT2G34700| pollen Ole e 1 allergen and extensin family protein					nr +
Unigene83100_All	490	0.21	1.03	4.13	0.20	0.14	0.37	0.00	0.00	0.00	2.28E+00	6.22E-02		4.27E+00	6.79E-09	Up	-5.32E-01	8.12E-01		8.59E-01	6.93E-01		null	null		null	null		Unigene83100_All//gi|222873592|gb|EEF10723.1|//5.00E-12//predicted protein [Populus trichocarpa]				ko03040|Spliceosome		nr -
Unigene83106_All	502	0.63	1.31	3.39	0.69	0.41	0.09	0.42	0.17	0.16	1.07E+00	2.36E-01		2.44E+00	7.80E-05	Up	-7.55E-01	5.67E-01		-2.95E+00	8.29E-02		-1.34E+00	4.29E-01		-1.41E+00	3.79E-01		Unigene83106_All//gi|15234590|ref|NP_192418.1|//5.00E-44//inositol monophosphatase family protein [Arabidopsis thaliana] >gi|34396727|sp|Q9M0V6.1|DPNPM_ARATH RecName: Full=Putative PAP-specific phosphatase, mitochondrial; AltName: Full=3'(2'),5'-bisphosphate nucleotidase; AltName: Full=3'(2'),5-bisphosphonucleoside 3'(2')-phosphohydrolase; AltName: Full=DPNPase; Flags: Precursor >gi|7267268|emb|CAB81051.1| 3'(2'), 5'-BISPHOSPHATE NUCLEOTIDASE-like protein [Arabidopsis thaliana] >gi|21553719|gb|AAM62812.1| 3(2),5-BISPHOSPHATE NUCLEOTIDASE-like protein [Arabidopsis thaliana] >gi|51968744|dbj|BAD43064.1| 3'(2'),5'-bisphosphate nucleotidase-like protein [Arabidopsis thaliana]	Unigene83106_All//3.00E-45//AT4G05090| inositol monophosphatase family protein	Unigene83106_All//2.00E-155//TC160047		ko04070|Phosphatidylinositol signaling system//ko00562|Inositol phosphate metabolism//ko00920|Sulfur metabolism		nr +
Unigene83107_All	502	0.83	0.40	3.82	0.20	0.27	0.27	0.00	0.00	0.00	-1.05E+00	3.65E-01		2.20E+00	8.20E-05	Up	4.67E-01	8.75E-01		4.43E-01	8.59E-01		null	null		null	null		Unigene83107_All//gi|162949352|gb|ABY21313.1|//1.00E-10//4-coumarate:coenzyme A ligase 2 [Physcomitrella patens subsp. magdalenae]	Unigene83107_All//3.00E-08//AT3G16910| AAE7 (ACYL-ACTIVATING ENZYME 7); AMP binding / acetate-CoA ligase			ko00940|Phenylpropanoid biosynthesis//ko04146|Peroxisome//ko00360|Phenylalanine metabolism//ko00071|Fatty acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene83108_All	502	0.00	2.73	1.27	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	7.76E-08	Up	1.03E+01	1.15E-03		null	null		null	null		null	null		null	null		Unigene83108_All//gi|531098|dbj|BAA06461.1|//3.00E-12//TEX3 [Zinnia elegans]						nr -
Unigene83109_All	506	0.62	0.50	3.26	0.20	0.41	0.18	0.00	0.00	0.00	-3.09E-01	7.89E-01		2.39E+00	1.28E-04	Up	1.05E+00	6.11E-01		-1.42E-01	9.46E-01		null	null		null	null		Unigene83109_All//gi|159464094|ref|XP_001690277.1|//7.00E-51//chloroplast sulfate permease [Chlamydomonas reinhardtii] >gi|158284265|gb|EDP10015.1| chloroplast sulfate permease [Chlamydomonas reinhardtii]						nr +
Unigene8311_All	368	1.14	0.00	0.00	0.00	1.40	1.72	0.80	0.68	0.43	-1.02E+01	1.04E-02		-1.02E+01	1.55E-02		1.05E+01	3.21E-03		1.07E+01	7.59E-04	Up	-2.39E-01	8.39E-01		-8.93E-01	4.71E-01		Unigene8311_All//gi|258489633|gb|ACV72640.1|//2.00E-62//sucrose synthase 1 [Gossypium hirsutum]	Unigene8311_All//4.00E-60//AT5G20830| SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase	Unigene8311_All//5.00E-93//TC136787		ko00500|Starch and sucrose metabolism	GO:0005984//GO:0016020//GO:0035251//GO:0043231//GO:0044403	nr -
Unigene83110_All	508	0.00	0.60	3.35	0.00	0.00	0.62	0.00	0.00	0.00	9.23E+00	4.36E-02		1.17E+01	2.19E-09	Up	null	null		9.28E+00	4.07E-02		null	null		null	null		Unigene83110_All//gi|270342124|gb|ACZ74707.1|//3.00E-91//carbonic anhydrase [Phaseolus vulgaris]	Unigene83110_All//2.00E-72//AT3G01500| CA1 (CARBONIC ANHYDRASE 1); carbonate dehydratase/ zinc ion binding	Unigene83110_All//2.00E-59//gi|48740832|gb|CO071351.1|CO071351		ko00910|Nitrogen metabolism		nr +
Unigene83112_All	509	0.00	0.70	6.17	0.00	0.00	0.00	0.00	0.00	0.00	9.44E+00	2.43E-02		1.26E+01	2.27E-17	Up	null	null		null	null		null	null		null	null		Unigene83112_All//gi|1850968|gb|AAB48305.1|//9.00E-54//Hs1pro-1 [Beta procumbens]	Unigene83112_All//8.00E-51//AT3G55840| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Hs1pro-1, C-terminal (InterPro:IPR009743), Hs1pro-1, N-terminal (InterPro:IPR009869); BEST Arabidopsis thaliana protein match is: HSPRO2 (ARABIDOPSIS ORTHOLOG OF SUGAR BEET HS1 PRO-1 2) (TAIR:AT2G40000.1); Has 43 Blast hits to 43 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).						nr +
Unigene83114_All	510	0.51	0.10	2.82	0.29	0.41	0.27	0.00	0.00	0.00	-2.37E+00	2.13E-01		2.46E+00	3.26E-04	Up	4.67E-01	8.24E-01		-1.41E-01	9.42E-01		null	null		null	null		Unigene83114_All//gi|91208868|ref|YP_539029.1|//4.00E-70//ATP synthase F1 subunit alpha [Physcomitrella patens] >gi|90991408|dbj|BAE93100.1| ATP synthase F1 subunit alpha [Physcomitrella patens]	Unigene83114_All//2.00E-66//AT2G07698| ATP synthase alpha chain, mitochondrial, putative			ko00190|Oxidative phosphorylation//ko00195|Photosynthesis		nr +
Unigene83117_All	515	0.00	0.59	2.79	0.10	0.47	0.00	0.00	0.00	0.00	9.21E+00	4.36E-02		1.14E+01	6.28E-08	Up	2.28E+00	3.05E-01		-6.60E+00	6.17E-01		null	null		null	null		Unigene83117_All//gi|255599965|ref|XP_002537354.1|//5.00E-17//conserved hypothetical protein [Ricinus communis] >gi|223516644|gb|EEF25028.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene83118_All	516	0.10	0.00	4.23	0.10	0.13	0.96	0.00	0.00	0.00	-6.66E+00	6.00E-01		5.38E+00	9.85E-11	Up	4.68E-01	9.53E-01		3.32E+00	2.31E-02		null	null		null	null		Unigene83118_All//COG3846//7.00E-79//Type IV secretory pathway, TrbL components						cog +
Unigene83119_All	520	0.00	0.39	4.92	0.00	0.00	0.17	0.00	0.00	0.00	8.61E+00	1.34E-01		1.23E+01	4.19E-14	Up	null	null		7.44E+00	4.69E-01		null	null		null	null		Unigene83119_All//gi|290766479|gb|ADO60242.1|//2.00E-64//alpha-form rubisco activase [Glycine max] >gi|290766489|gb|ADO60247.1| alpha-form rubisco activase [Glycine max]	Unigene83119_All//2.00E-55//AT2G39730| RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	Unigene83119_All//1.00E-29//EX168151				nr +
Unigene8312_All	478	0.00	0.00	0.00	0.42	0.36	0.00	0.53	2.71	1.08	null	null		null	null		-2.11E-01	8.58E-01		-8.70E+00	1.32E-01		2.35E+00	1.25E-04	Up	1.03E+00	2.53E-01					Unigene8312_All//0.00E+00//ES809411				
Unigene83121_All	525	0.00	0.77	2.23	0.00	0.00	0.00	0.00	0.00	0.00	9.59E+00	1.34E-02		1.11E+01	1.76E-06	Up	null	null		null	null		null	null		null	null		Unigene83121_All//gi|145340597|ref|XP_001415108.1|//6.00E-46//P-ATPase family transporter: sodium/potassium ion [Ostreococcus lucimarinus CCE9901] >gi|144575631|gb|ABO93700.1| P-ATPase family transporter: sodium/potassium ion [Ostreococcus lucimarinus CCE9901]	Unigene83121_All//2.00E-07//AT1G07670| calcium-transporting ATPase					nr -

Unigene83122_All	526	0.00	0.58	1.72	0.00	0.00	0.00	0.00	0.00	0.00	9.17E+00	4.36E-02		1.07E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene83122_All//gi|83282998|gb|ABC01060.1|//7.00E-82//L-asparaginase 2 [Phaseolus vulgaris]	Unigene83122_All//6.00E-76//AT3G16150| L-asparaginase, putative / L-asparagine amidohydrolase, putative					nr -
Unigene83123_All	529	1.78	0.96	3.02	1.13	0.07	0.00	0.00	0.00	0.15	-8.94E-01	2.14E-01		7.62E-01	1.60E-01		-4.12E+00	1.25E-03		-1.01E+01	7.69E-04	Down	null	null		7.23E+00	4.00E-01											nr -
Unigene83124_All	532	0.00	0.48	6.01	0.00	0.00	0.00	0.00	0.00	0.00	8.90E+00	7.75E-02		1.26E+01	1.15E-17	Up	null	null		null	null		null	null		null	null		Unigene83124_All//gi|2674201|gb|AAC61786.1|//8.00E-73//glycine-rich RNA-binding protein [Euphorbia esula]	Unigene83124_All//1.00E-33//AT3G21660| CCR2 (COLD, CIRCADIAN RHYTHM, AND RNA BINDING 2); RNA binding / double-stranded DNA binding / single-stranded DNA binding	Unigene83124_All//7.00E-16//TC156349		ko03040|Spliceosome		nr +
Unigene83125_All	541	0.39	0.19	3.45	0.18	0.25	0.08	0.00	0.00	0.00	-1.05E+00	5.63E-01		3.15E+00	1.30E-06	Up	4.67E-01	8.75E-01		-1.14E+00	6.73E-01		null	null		null	null		Unigene83125_All//gi|222836679|gb|EEE75072.1|//4.00E-08//predicted protein [Populus trichocarpa]						nr +
Unigene83126_All	545	0.38	1.49	2.54	0.91	0.57	0.58	0.00	0.00	0.00	1.95E+00	2.43E-02		2.73E+00	1.78E-04	Up	-6.85E-01	5.15E-01		-6.56E-01	5.50E-01		null	null		null	null		Unigene83126_All//gi|22325715|ref|NP_179254.2|//2.00E-35//proline-rich family protein [Arabidopsis thaliana] >gi|31711858|gb|AAP68285.1|At2g16630 [Arabidopsis thaliana]	Unigene83126_All//1.00E-36//AT2G16630| proline-rich family protein	Unigene83126_All//0.00E+00//TC164992				nr -
Unigene83127_All	546	0.00	2.04	3.61	0.00	0.38	0.00	0.00	0.00	0.00	1.10E+01	1.99E-06	Up	1.18E+01	7.44E-11	Up	8.56E+00	1.56E-01		null	null		null	null		null	null		Unigene83127_All//gi|222838934|gb|EEE77285.1|//2.00E-08//predicted protein [Populus trichocarpa]						nr -
Unigene83128_All	550	0.76	1.01	3.10	0.72	0.81	0.33	0.00	0.00	0.00	4.13E-01	6.36E-01		2.03E+00	5.19E-04	Up	1.68E-01	9.04E-01		-1.14E+00	3.79E-01		null	null		null	null											ESTscan -
Unigene83129_All	551	0.00	0.00	5.03	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.23E+01	2.74E-15	Up	null	null		null	null		null	null		null	null		Unigene83129_All//gi|78191420|gb|AB829931.1|//2.00E-85//P40-like protein [Solanum tuberosum]	Unigene83129_All//3.00E-75//AT1G72370| P40; structural constituent of ribosome	Unigene83129_All//6.00E-75//TC131519		ko03010|Ribosome		nr -
Unigene83130_All	564	0.19	0.63	4.53	0.44	0.18	0.32	0.00	0.00	0.00	1.76E+00	2.18E-01		4.61E+00	1.19E-11	Up	-1.27E+00	4.23E-01		-4.63E-01	7.44E-01		null	null		null	null		Unigene83130_All//gi|222874900|gb|EEF12031.1|//7.00E-11//predicted protein [Populus trichocarpa]						nr -
Unigene83131_All	570	0.00	0.18	4.95	0.00	0.00	0.00	0.00	0.00	0.00	7.47E+00	3.79E-01		1.23E+01	1.38E-15	Up	null	null		null	null		null	null		null	null		Unigene83131_All//gi|2981167|gb|AAC06242.1|//2.00E-28//late embryogenis abundant protein 5 [Nicotiana tabacum]	Unigene83131_All//6.00E-12//AT4G02380| SAG21 (SENESCENCE-ASSOCIATED GENE 21)					nr +
Unigene83133_All	575	0.00	3.52	2.32	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.53E-11	Up	1.12E+01	2.39E-07	Up	null	null		null	null		null	null		null	null											
Unigene83134_All	584	0.00	0.35	4.47	0.00	0.00	0.00	0.00	0.00	0.00	8.44E+00	1.34E-01		1.21E+01	2.12E-14	Up	null	null		null	null		null	null		null	null		Unigene83134_All//gi|111380168|gb|ABB09493.1|//3.00E-17//RO22-like protein [Polygonum sibiricum]	Unigene83134_All//4.00E-15//AT1G49320| BUBP domain-containing protein					nr -
Unigene83135_All	606	0.52	0.84	4.57	0.00	0.51	0.00	0.00	0.00	0.00	6.91E-01	4.99E-01		3.14E+00	1.48E-09	Up	9.00E+00	4.54E-02		null	null		null	null		null	null		Unigene83135_All//gi|115442357|ref|NP_001045458.1|//1.00E-06//Os01g0959000 [Oryza sativa Japonica Group] >gi|113534989|dbj|BAF07372.1|Os01g0959000 [Oryza sativa Japonica Group]						nr +
Unigene83136_All	618	0.00	0.08	4.22	0.00	0.00	0.00	0.00	0.00	0.00	6.36E+00	6.07E-01		1.20E+01	2.12E-14	Up	null	null		null	null		null	null		null	null		Unigene83136_All//gi|15237656|ref|NP_201231.1|//9.00E-77//EXL2 (EXORDIUM LIKE 2) [Arabidopsis thaliana] >gi|14190477|gb|AAK55719.1|AF380638_1 AT5g64260/MSJ1_10 [Arabidopsis thaliana] >gi|9759402|dbj|BAB09857.1| phi-1-like protein [Arabidopsis thaliana] >gi|16322270|gb|AAL15369.1|AT5g64260/MSJ1_10 [Arabidopsis thaliana] >gi|21592241|gb|AAM65190.1| phi-1-like protein [Arabidopsis thaliana]	Unigene83136_All//1.00E-73//AT5G64260| EXL2 (EXORDIUM LIKE 2)	Unigene83136_All//2.00E-07//DN780951				nr -
Unigene83137_All	619	0.17	0.16	1.98	0.24	0.39	0.07	0.00	0.00	0.00	-4.60E-02	9.85E-01		3.55E+00	6.10E-05	Up	6.90E-01	7.32E-01		-1.73E+00	4.99E-01		null	null		null	null											ESTscan -
Unigene83138_All	633	0.17	0.48	3.53	0.00	0.27	0.14	0.00	0.00	0.00	1.54E+00	3.22E-01		4.42E+00	5.46E-10	Up	8.09E+00	2.26E-01		7.16E+00	4.69E-01		null	null		null	null		Unigene83138_All//gi|9653247|ref|NP_062493.1|//1.00E-59//NADH dehydrogenase subunit 1 [Chondrus crispus] >gi|1352537|sp|P48898.1|NU1M_CHOCR RecName: Full=NADH-ubiquinone oxidoreductase chain 1; AltName: Full=NADH dehydrogenase subunit 1 >gi|1334495|emb|CAA87617.1| NADH dehydrogenase (ubiquinone), subunit 1 [Chondrus crispus]	Unigene83138_All//3.00E-34//ATMG01275| Encodes subunit of mitochondrial NAD(P)H dehydrogenase that is trans-spliced from three precursors, NAD1A, NAD1B, and NAD1C.			ko00190|Oxidative phosphorylation		nr -
Unigene83139_All	635	0.16	0.64	4.28	0.31	0.65	0.36	0.00	0.00	0.00	1.95E+00	1.44E-01		4.70E+00	1.73E-12	Up	1.05E+00	4.25E-01		1.80E-01	9.34E-01		null	null		null	null		Unigene83139_All//gi|301111121|ref|XP_002904640.1|//5.00E-58//ubiquinone/menaquinone biosynthesis methyltransferase ubiE [Phytophthora infestans T30-4] >gi|262095957|gb|EEY54009.1| ubiquinone/menaquinone biosynthesis methyltransferase ubiE [Phytophthora infestans T30-4]	Unigene83139_All//3.00E-56//AT5G57300| UbiE/COQ5 methyltransferase family protein			ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene83140_All	641	0.00	0.00	8.39	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.30E+01	6.07E-30	Up	null	null		null	null		null	null		null	null		Unigene83140_All//gi|158120965|gb|ABW16955.1|//2.00E-78//translationally controlled tumor protein [Salvia miltiorrhiza]	Unigene83140_All//2.00E-75//AT3G16640| TCTP (TRANSLATIONALLY CONTROLLED TUMOR PROTEIN)	Unigene83140_All//3.00E-40//gi|213050753|gb|FF403768.1|FF403768				nr +
Unigene83141_All	645	0.41	0.55	2.97	0.46	0.27	0.00	0.00	0.00	0.00	4.39E-01	7.01E-01		2.87E+00	2.94E-06	Up	-7.96E-01	5.56E-01		-8.86E+00	3.98E-02		null	null		null	null		Unigene83141_All//sp|P37329|MODA_ECOLI//3.00E-21//Molybdate-binding periplasmic protein OS=Escherichia coli (strain K12) GN=modA PE=1 SV=1						swissprot +
Unigene83142_All	654	0.00	0.31	8.63	0.00	0.00	0.00	0.00	0.00	0.00	8.28E+00	1.34E-01		1.31E+01	1.91E-31	Up	null	null		null	null		null	null		null	null		Unigene83142_All//gi|151347473|gb|ABS01349.1|//1.00E-112//hypersensitive-induced response protein [Carica papaya]	Unigene83142_All//2.00E-101//AT5G62740| band 7 family protein	Unigene83142_All//1.00E-94//TC144443				nr -
Unigene83143_All	686	0.23	1.11	3.42	0.36	0.50	0.26	0.00	0.00	0.00	2.28E+00	1.59E-02		3.90E+00	1.17E-09	Up	4.67E-01	7.79E-01		-4.64E-01	7.44E-01		null	null		null	null											ESTscan -
Unigene83144_All	696	0.68	0.51	2.75	0.14	0.49	0.13	0.00	0.00	0.00	-4.09E-01	6.68E-01		2.03E+00	2.00E-04	Up	1.79E+00	2.57E-01		-1.41E-01	9.46E-01		null	null		null	null											ESTscan -
Unigene83145_All	699	0.15	0.36	2.59	0.86	0.64	0.45	0.00	0.00	0.00	1.28E+00	4.34E-01		4.11E+00	8.16E-08	Up	-4.17E-01	6.27E-01		-9.19E-01	3.51E-01		null	null		null	null		Unigene83145_All//COG0684//6.00E-12//Demethylmenaquinone methyltransferase						cog +
Unigene83147_All	719	0.00	0.00	7.04	0.00	0.00	0.00	0.00	0.00	0.00	null	null		1.28E+01	3.83E-28	Up	null	null		null	null		null	null		null	null		Unigene83147_All//gi|290020584|gb|ADD22400.1|//3.00E-96//ferritin [Coffea arabica]	Unigene83147_All//1.00E-78//AT5G01600| ATFER1; ferric iron binding / iron ion binding	Unigene83147_All//1.00E-48//TC147017		ko00860|Porphyrin and chlorophyll metabolism		nr +
Unigene83148_All	725	0.65	0.14	4.63	0.21	0.33	0.12	0.00	0.00	0.00	-2.22E+00	7.75E-02		2.83E+00	2.02E-10	Up	6.90E-01	7.31E-01		-7.26E-01	7.13E-01		null	null		null	null		Unigene83148_All//COG0438//8.00E-14//Glycosyltransferase						cog +
Unigene83149_All	732	0.00	0.42	7.78	0.00	0.00	0.00	0.00	0.00	0.00	8.70E+00	4.36E-02		1.29E+01	9.58E-32	Up	null	null		null	null		null	null		null	null		Unigene83149_All//gi|84874556|gb|ABC68275.1|//4.00E-80//dehydrin [Coffea canephora]	Unigene83149_All//8.00E-18//AT1G76180| ERD14 (EARLY RESPONSE TO DEHYDRATION 14); calcium ion binding	Unigene83149_All//2.00E-07//TC166379		ko03040|Spliceosome		nr -
Unigene8315_All	467	0.00	0.00	0.46	3.95	2.43	0.77	1.54	1.70	1.19	null	null		8.83E+00	1.37E-01		-6.98E-01	1.37E-01		-2.35E+00	1.59E-05	Down	1.44E-01	8.36E-01		-3.66E-01	6.05E-01		Unigene8315_All//gi|58532079|emb|CAE04985.3|//1.00E-06//OSJNBa0057M08.11 [Oryza sativa (japonica cultivar-group)]					GO:0005488	nr -
Unigene83150_All	761	0.55	0.40	3.29	0.26	0.27	0.18	0.00	0.00	0.00	-4.61E-01	6.50E-01		2.58E+00	3.27E-07	Up	5.25E-02	9.88E-01		-5.57E-01	7.32E-01		null	null		null	null		Unigene83150_All//gi|222837901|gb|EEE76266.1|//4.00E-24//ABC transporter family protein [Populus trichocarpa]	Unigene83150_All//2.00E-10//AT1G67940| ATNAP3; transporter			ko02010|ABC transporters		nr -
Unigene83151_All	765	0.14	0.13	8.07	0.00	0.00	0.00	0.00	0.00	0.00	-4.61E-02	9.85E-01		5.88E+00	3.09E-31	Up	null	null		null	null		null	null		null	null		Unigene83151_All//gi|40287520|gb|AAR83874.1|//3.00E-16//induced stolon tip protein [Capsicum annuum]						nr -
Unigene83152_All	810	0.00	4.57	4.01	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	4.67E-21	Up	1.20E+01	5.81E-18	Up	null	null		null	null		null	null		null	null		Unigene83152_All//gi|255072339|ref|XP_002499844.1|//2.00E-11//alpha-2 macroglobulin family-like protein [Micromonas sp. RCC299] >gi|226515106|gb|ACO61102.1| alpha-2 macroglobulin family-like protein [Micromonas sp. RCC299]						nr -
Unigene83153_All	1282	0.00	1.30	1.41	0.00	0.00	0.00	0.00	0.00	0.00	1.03E+01	1.53E-09	Up	1.05E+01	5.68E-10	Up	null	null		null	null		null	null		null	null		Unigene83153_All//gi|195606812|gb|ACG25236.1|//1.00E-160//60S ribosomal protein L3 [Zea mays] >gi|195619674|gb|ACG31667.1| 60S ribosomal protein L3 [Zea mays] >gi|195626206|gb|ACG34933.1| 60S ribosomal protein L3 [Zea mays] >gi|195641988|gb|ACG40462.1| 60S ribosomal protein L3 [Zea mays]	Unigene83153_All//2.00E-148//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene83153_All//1.00E-07//gi|13353022|gb|BG443370.1|BG443370		ko03010|Ribosome		nr -
Unigene83157_All	295	8.34	20.44	15.34	5.74	3.15	5.97	0.00	0.14	1.08	1.29E+00	3.05E-07	Up	8.80E-01	2.99E-03		-8.65E-01	7.39E-02		5.65E-02	9.33E-01		7.15E+00	6.25E-01		1.01E+01	1.34E-02				Unigene83157_All//4.00E-50//EV484009					
Unigene83159_All	221	1.89	4.13	2.65	2.03	2.03	3.88	22.38	26.86	9.37	1.12E+00	1.30E-01		4.85E-01	6.30E-01		-2.10E-03	9.69E-01		9.37E-01	2.38E-01		2.63E-01	2.65E-01	Down	-1.26E+00	2.65E-07	Down			Unigene83159_All//9.00E-109//TC156413					
Unigene8316_All	265	8.49	38.24	24.92	26.50	27.29	70.56	0.00	0.63	1.05	2.17E+00	2.40E-23	Up	1.55E+00	1.11E-09	Up	4.20E-02	8.76E-01		1.41E+00	2.70E-25	Up	9.30E+00	1.38E-01		1.00E+01	2.43E-02		Unigene8316_All//gi|297738723|emb|CBI27968.3|//5.00E-07//unnamed protein product [Vitis vinifera]	Unigene8316_All//6.00E-06//AT2G18810| zinc finger (CCCH-type) family protein	Unigene8316_All//1.00E-145//gi|73846935|gb|DT455955.1|DT455955	C3H		GO:0046872	nr -
Unigene83163_All	380	32.77	24.67	26.91	68.82	98.68	72.97	383.19	231.09	191.54	-4.10E-01	1.12E-02		-2.85E-01	1.04E-01		5.20E-01	1.17E-10		8.45E-02	5.07E-01		-7.30E-01	2.68E-75		-1.00E+00	6.24E-132	Down	Unigene83163_All//gi|224054176|ref|XP_002298129.1|//2.00E-25//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene83163_All//2.00E-23//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene83163_All//2.00E-135//TC139925		ko00904|Diterpenoid biosynthesis		nr -
Unigene8319_All	434	1.57	1.87	1.60	1.26	1.11	2.60	4.77	10.11	5.42	2.53E-01	7.26E-01		2.54E-02	9.96E-01		-1.85E-01	8.25E-01		1.04E+00	1.20E-01		1.08E+00	3.59E-05	Up	1.82E-01	6.38E-01				Unigene8319_All//2.00E-21//gi|164258747|gb|ES843084.1|ES843084					
Unigene83195_All	345	0.15	0.88	0.00	3.61	1.00	0.39	0.61	0.48	0.58	2.54E+00	1.51E-01		-7.25E+00	6.14E-01		-1.85E+00	2.11E-03		-3.20E+00	3.61E-05	Down	-3.39E-01	8.11E-01		-8.58E-02	9.60E-01		Unigene83195_All//gi|18420914|ref|NP_568469.1|//5.00E-35//phosphate translocator-related [Arabidopsis thaliana]	Unigene83195_All//3.00E-36//AT5G25400| phosphate translocator-related	Unigene83195_All//2.00E-76//gi|78334846|gb|DT555120.1|DT555120				nr +
Unigene8320_All	451	0.23	0.00	0.00	1.55	1.60	4.61	2.72	5.00	4.33	-7.86E+00	3.65E-01		-7.86E+00	3.87E-01		5.23E-02	9.64E-01		1.57E+00	7.98E-04	Up	8.80E-01	2.08E-02		6.71E-01	9.52E-02		Unigene8320_All//gi|2218150|gb|AAB61671.1|//4.00E-87//type IIIa membrane protein cp-wap11 [Vigna unguiculata]	Unigene8320_All//1.00E-86//AT3G02230| KGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1); cellulose synthase (UDP-forming)	Unigene8320_All//0.00E+00//BF269476			GO:0005618//GO:0005840//GO:0006970//GO:0009250//GO:0010038//GO:0016759//GO:0031985//GO:0035251//GO:0042546//GO:0044459//GO:0045229	nr -
Unigene83218_All	435	0.60	0.12	0.24	3.09	0.79	1.56	0.10	0.00	0.00	-2.37E+00	2.13E-01		-1.30E+00	4.35E-01		-1.97E+00	7.30E-04	Down	-9.89E-01	9.21E-02		-6.60E+00	6.42E-01		-6.60E+00	6.00E-01		Unigene83218_All//gi|297833216|ref|XP_002884490.1|//7.00E-30//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297330330|gb|EFH60749.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene83218_All//2.00E-24//AT3G05090| transducin family protein / WD-40 repeat family protein	Unigene83218_All//9.00E-49//TC142811				nr +

Unigene8323_All	288	7.63	8.09	10.54	11.59	10.76	11.92	11.30	26.12	7.19	8.50E-02	8.36E-01		4.66E-01	2.27E-01		-1.07E-01	8.01E-01		4.04E-02	9.31E-01		1.21E+00	9.94E-10	Up	-6.52E-01	2.72E-02		Unigene8323_All//gi|225440392|ref|XP_002267559.1|//9.00E-08//PREDICTED: ripening-related protein-like [Vitis vinifera]	Unigene8323_All//3.00E-07//AT5G59490| haloacid dehalogenase-like hydrolase family protein	Unigene8323_All//3.00E-112//TC156468				nr -
Unigene83274_All	203	1.80	1.00	1.57	6.63	1.53	2.67	1.87	0.82	0.39	-8.54E-01	4.88E-01		-1.97E-01	8.65E-01		-2.12E+00	3.41E-04	Down	-1.31E+00	2.66E-02		-1.19E+00	3.09E-01		-2.26E+00	6.48E-02					Unigene83274_All//3.00E-19//CO097675				
Unigene8330_All	469	0.45	0.22	1.59	1.06	4.26	6.07	2.61	1.07	1.95	-1.05E+00	5.63E-01		1.83E+00	5.04E-02		2.00E+00	4.50E-05	Up	2.51E+00	1.36E-08	Up	-1.29E+00	2.09E-02		-4.20E-01	4.28E-01		Unigene8330_All//gi|30695081|ref|NP_191549.2|//4.00E-07//ARGOS (AUXIN-REGULATED GENE INVOLVED IN ORGAN SIZE) [Arabidopsis thaliana] >gi|49917525|gb|AAS19087.1| At3g59900 [Arabidopsis thaliana] >gi|148533969|gb|ABQ85109.1| ARGOS [Arabidopsis thaliana] >gi|148533971|gb|ABQ85110.1| ARGOS [Arabidopsis thaliana] >gi|148533973|gb|ABQ85111.1| ARGOS [Arabidopsis thaliana] >gi|148533975|gb|ABQ85112.1| ARGOS [Arabidopsis thaliana] >gi|148533977|gb|ABQ85113.1| ARGOS [Arabidopsis thaliana] >gi|148533979|gb|ABQ85114.1| ARGOS [Arabidopsis thaliana] >gi|148533981|gb|ABQ85115.1| ARGOS [Arabidopsis thaliana] >gi|148533983|gb|ABQ85116.1| ARGOS [Arabidopsis thaliana] >gi|148533985|gb|ABQ85117.1| ARGOS [Arabidopsis thaliana] >gi|148533987|gb|ABQ85118.1| ARGOS [Arabidopsis thaliana] >gi|148533989|gb|ABQ85119.1| ARGOS [Arabidopsis thaliana] >gi|148533993|gb|ABQ85121.1| ARGOS [Arabidopsis thaliana]		Unigene8330_All//2.00E-46//gi|3326770|gb|AI055656.1|AI055656				nr +
Unigene83313_All	287	0.36	0.35	0.00	2.43	1.20	0.00	0.00	1.02	0.14	-4.62E-02	9.85E-01		-8.51E+00	3.87E-01		-1.02E+00	2.25E-01		-1.12E+01	1.96E-04	Down	9.99E+00	2.35E-02		7.12E+00	6.35E-01								
Unigene83325_All	416	0.75	0.73	0.51	3.23	0.41	0.33	0.20	0.00	0.67	-4.62E-02	9.84E-01		-5.60E-01	6.63E-01		-2.97E+00	6.68E-06	Down	-3.31E+00	1.08E-05	Down	-7.67E+00	3.98E-01		1.72E+00	2.30E-01								
Unigene83339_All	261	0.00	0.00	0.61	0.38	0.13	0.00	0.16	0.64	2.59	null	null		9.26E+00	2.34E-01		-1.53E+00	5.82E-01		-8.58E+00	3.92E-01		1.98E+00	3.78E-01		4.00E+00	4.29E-04	Up	Unigene83339_All//gi|45935272|gb|AAS79671.1|//2.00E-15//glutamate decarboxylase 4b [Brassica juncea]	Unigene83339_All//2.00E-16//AT2G02010| GAD4 (glutamate decarboxylase 4); calmodulin binding	Unigene83339_All//6.00E-61//TC155466		ko00250|Alanine, aspartate and glutamate metabolism//ko00650|Butanoate metabolism//ko00410|beta-Alanine metabolism//ko00430|Taurine and hypotaurine metabolism		nr +
Unigene8336_All	289	0.36	0.00	0.18	2.93	0.71	1.88	2.34	0.14	0.28	-8.50E+00	3.65E-01		-9.74E-01	7.19E-01		-2.04E+00	9.04E-03		-6.44E-01	4.15E-01		-4.02E+00	5.36E-04	Down	-3.09E+00	1.45E-03		Unigene8336_All//gi|255541168|ref|XP_002511648.1|//2.00E-09//Nuc-1 negative regulatory protein preg, putative [Ricinus communis] >gi|223548828|gb|EEF50317.1| Nuc-1 negative regulatory protein preg, putative [Ricinus communis]	Unigene8336_All//8.00E-06//AT3G60550| CYCP3;2 (cyclin p3;2); cyclin-dependent protein kinase	Unigene8336_All//2.00E-104//gi|109885890|gb|DW514860.1|DW514860				nr -
Unigene8337_All	411	7.26	15.04	3.76	4.73	5.95	10.00	8.02	17.29	26.66	1.05E+00	1.46E-05	Up	-9.50E-01	1.25E-02		3.32E-01	4.65E-01		1.08E+00	3.34E-04	Up	1.11E+00	3.88E-08	Up	1.73E+00	1.39E-23	Up	Unigene8337_All//gi|187372978|gb|ACM03223.1|//1.00E-10//xyloglucan endotransglucosylase/hydrolase 13 [Actinidia deliciosa]	Unigene8337_All//9.00E-11//AT1G14720| XTR2 (XYLOGLUCAN ENDOTRANSGLYCOSYLASE RELATED 2); hydrolase, acting on glycosyl bonds / xyloglucan:xyloglucosyl transferase	Unigene8337_All//2.00E-61//TC145486			GO:0005576//GO:0009888//GO:0016758//GO:0016798//GO:0030312//GO:0044042	nr -
Unigene83374_All	214	3.18	0.00	0.50	5.35	3.38	2.53	1.19	1.95	3.16	-1.16E+01	4.09E-04	Down	-2.68E+00	1.69E-02		-6.64E-01	2.98E-01		-1.08E+00	9.65E-02		7.20E-01	5.07E-01		1.42E+00	7.02E-02					Unigene83374_All//4.00E-09//FL576920				
Unigene83385_All	510	1.44	0.00	0.00	2.15	0.95	1.77	0.41	0.16	0.16	-1.05E+01	2.11E-04	Down	-1.05E+01	4.12E-04	Down	-1.18E+00	5.94E-02		-2.79E-01	6.89E-01		-1.34E+00	4.29E-01		-1.41E+00	3.79E-01		Unigene83385_All//gi|147774530|emb|CAN65544.1|//1.00E-10//hypothetical protein [Vitis vinifera]	Unigene83385_All//2.00E-09//AT1G71460| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene83411_All	274	0.19	17.01	6.41	0.91	0.13	0.99	1.54	3.66	0.87	6.48E+00	6.45E-25	Up	5.07E+00	1.80E-08	Up	-2.85E+00	1.37E-01		1.22E-01	9.44E-01		1.25E+00	4.78E-02		-8.23E-01	3.99E-01		Unigene83411_All//gi|145408594|ref|YP_001152218.1|//1.00E-09//ORF82c [Pinus koraiensis] >gi|145048843|gb|ABF35459.1| ORF82c [Pinus koraiensis]		Unigene83411_All//4.00E-71//gi|84149895|gb|DN781195.1|DN781195				nr +
Unigene8343_All	577	0.00	0.00	0.00	0.00	0.00	0.00	8.21	1.23	1.66	null	null		null	null		null	null		null	null		-2.74E+00	8.01E-18	Down	-2.31E+00	2.52E-15	Down	Unigene8343_All//gi|18402551|ref|NP_565713.1|//7.00E-06//CLE6 (CLAVATA3/ESR-RELATED 6); protein binding / receptor binding [Arabidopsis thaliana] >gi|20197326|gb|AAM15025.1| CLE4 [Arabidopsis thaliana]	Unigene8343_All//4.00E-07//AT2G31085| CLE6 (CLAVATA3/ESR-RELATED 6); protein binding / receptor binding					nr +
Unigene83432_All	206	0.00	0.00	0.00	0.00	0.17	0.00	0.82	0.41	13.15	null	null		null	null		7.39E+00	8.12E-01		null	null		-1.02E+00	6.13E-01		4.00E+00	1.17E-14	Up								
Unigene8344_All	341	0.00	0.00	0.78	0.00	0.81	0.66	1.24	1.84	6.89	null	null		9.61E+00	7.86E-02		9.66E+00	6.99E-02		9.37E+00	1.18E-01		5.68E-01	5.03E-01		2.47E+00	1.78E-08	Up				Unigene8344_All//2.00E-104//CO114182				
Unigene83442_All	366	0.00	0.00	0.00	2.59	1.03	0.12	0.00	0.00	0.00	null	null		null	null		-1.32E+00	5.61E-02		-4.39E+00	5.96E-05	Down	null	null		null	null					Unigene83442_All//8.00E-21//DR454679				
Unigene8346_All	407	0.00	0.00	0.00	2.82	1.52	1.78	2.80	1.13	0.00	null	null		null	null		-8.86E-01	1.53E-01		-6.65E-01	3.16E-01		-1.31E+00	2.45E-02		-1.15E+01	1.64E-08	Down	Unigene8346_All//gi|297792079|ref|XP_002863924.1|//3.00E-36//phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297309759|gb|EFH40183.1| phototropic-responsive NPH3 family protein [Arabidopsis lyrata subsp. lyrata]		Unigene8346_All//4.00E-75//ES798095			GO:0000904//GO:0005488//GO:0009314//GO:0016020//GO:0060089	nr +
Unigene83470_All	422	2.98	2.52	11.23	6.26	5.06	5.03	0.50	0.30	0.47	-2.39E-01	6.68E-01		1.92E+00	2.49E-09	Up	-3.06E-01	4.57E-01		-3.15E-01	4.65E-01		-7.54E-01	6.31E-01		-8.60E-02	9.60E-01		Unigene83470_All//gi|297741119|emb|CBI31850.3|//8.00E-06//unnamed protein product [Vitis vinifera]						nr -
Unigene8351_All	702	0.00	0.00	0.00	0.00	0.00	0.00	1.51	7.03	6.75	null	null		null	null		null	null		null	null		2.22E+00	1.10E-14	Up	2.17E+00	4.87E-14	Up	Unigene8351_All//gi|111379984|gb|AAQ63185.2|//5.00E-92//germin-like protein 3 [Vitis vinifera]	Unigene8351_All//6.00E-81//AT5G39110| germin-like protein, putative	Unigene8351_All//0.00E+00//gi|109873402|gb|DW502377.1|DW502377			GO:0004871//GO:0005576//GO:0008152//GO:0016623//GO:0046914	nr +
Unigene8352_All	905	0.06	0.00	0.00	0.22	0.08	0.20	0.93	1.34	6.12	-5.85E+00	6.00E-01		-5.85E+00	6.14E-01		-1.53E+00	4.14E-01		-1.42E-01	9.33E-01		5.19E-01	3.72E-01		2.71E+00	6.77E-21	Up								
Unigene8354_All	555	0.00	0.00	0.00	0.00	0.00	0.00	25.52	0.68	1.87	null	null		null	null		null	null		null	null		-5.23E+00	2.84E-86	Down	-3.77E+00	1.54E-72	Down	Unigene8354_All//gi|186478400|ref|NP_172674.2|//9.00E-40//lipid binding [Arabidopsis thaliana]	Unigene8354_All//5.00E-41//AT1G12100| lipid binding	Unigene8354_All//7.00E-07//TC148328			GO:0006810	nr +
Unigene83561_All	654	0.48	1.94	1.06	2.06	0.42	0.14	0.39	0.06	0.24	2.01E+00	2.67E-03		1.14E+00	2.18E-01		-2.29E+00	1.48E-04	Down	-3.90E+00	2.12E-06	Down	-2.60E+00	1.44E-01		-6.71E-01	6.05E-01					Unigene83561_All//9.00E-16//gi|21097585|gb|BQ109898.1|BQ109898				
Unigene83607_All	210	0.00	0.00	0.00	0.00	0.00	0.00	11.68	1.99	4.93	null	null		null	null		null	null		null	null		-2.55E+00	6.67E-09	Down	-1.24E+00	5.25E-04	Down	Unigene83607_All//gi|3851530|gb|AAC72337.1|//8.00E-12//nodulin [Glycine max]	Unigene83607_All//2.00E-10//AT5G64870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, vacuole; EXPRESSED IN: 18 plant structures; EXPRESSED DURING: 11 growth stages; CONTAINS InterPro DOMAIN/s: Band 7 protein (InterPro:IPR001107); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G25250.1); Has 3110 Blast hits to 2534 proteins in 575 species: Archae - 10; Bacteria - 1084; Metazoa - 749; Fungi - 138; Plants - 89; Viruses - 0; Other Eukaryotes - 1040 (source: NCBI BLink).	Unigene83607_All//9.00E-38//gi|84155963|gb|DN817189.1|DN817189				nr +
Unigene8361_All	422	0.99	0.48	0.88	0.94	1.06	1.07	2.81	0.59	1.04	-1.05E+00	3.65E-01		-1.67E-01	8.79E-01		1.68E-01	9.04E-01		1.81E-01	8.83E-01		-2.24E+00	4.21E-04	Down	-1.43E+00	9.72E-03					Unigene8361_All//5.00E-07//EV497990				
Unigene83611_All	222	0.00	0.00	0.00	0.00	0.00	0.00	0.57	17.70	0.00	null	null		null	null		null	null		null	null		4.95E+00	2.04E-23	Up	-9.16E+00	1.98E-01		Unigene83611_All//gi|197312863|gb|ACH63212.1|//2.00E-10//glutathione-S-transferase [Rheum australe]	Unigene83611_All//1.00E-10//AT5G02790| In2-1 protein, putative	Unigene83611_All//1.00E-39//EV487423		ko00480|Glutathione metabolism		nr +
Unigene8362_All	342	0.00	298.39	4.98	0.58	3.42	7.66	0.12	0.00	1.75	1.82E+01	0.00E+00	Up	1.23E+01	2.19E-09	Up	2.55E+00	5.02E-04	Up	3.72E+00	2.74E-11	Up	-6.95E+00	6.42E-01		3.82E+00	1.35E-03		Unigene8362_All//gi|5802240|gb|AAD51623.1|AF169020.1|//6.00E-25//seed maturation protein PM35 [Glycine max] >gi|6648958|gb|AAF21307.1|AF109720_1 seed maturation protein PM21 [Glycine max]	Unigene8362_All//3.00E-12//AT2G33690| late embryogenesis abundant protein, putative / LEA protein, putative	Unigene8362_All//4.00E-112//DT051588			GO:0016020	nr +
Unigene8365_All	265	0.00	1.15	3.22	1.13	1.04	1.19	0.64	0.63	1.05	1.02E+01	4.36E-02		1.17E+01	8.95E-05	Up	-1.18E-01	9.00E-01		8.10E-02	9.49E-01		-1.66E-02	1.02E+00		7.22E-01	5.96E-01									
Unigene83667_All	217	0.00	0.00	0.00	0.23	0.16	0.00	5.26	0.77	1.10	null	null		null	null		-5.33E-01	8.18E-01		-7.84E+00	6.17E-01		-2.77E+00	7.62E-05	Down	-2.26E+00	3.40E-04	Down	Unigene83667_All//gi|115460270|ref|NP_001053735.1|//5.00E-11//Os04g0597300 [Oryza sativa Japonica Group] >gi|113565306|dbj|BAF15649.1| Os04g0597300 [Oryza sativa Japonica Group]	Unigene83667_All//2.00E-11//AT1G30650| WRKY14; transcription factor	Unigene83667_All//4.00E-37//TC148412	WRKY	ko04626|Plant-pathogen interaction		nr +
Unigene8370_All	392	24.16	20.29	26.90	8.90	10.72	6.22	2.27	0.32	0.20	-2.52E-01	2.06E-01		1.55E-01	4.31E-01		2.69E-01	4.24E-01		-5.16E-01	1.32E-01		-2.82E+00	5.65E-04	Down	-3.48E+00	7.33E-05	Down	Unigene8370_All//gi|38566498|gb|AAR24139.1|//2.00E-06//At4g33960 [Arabidopsis thaliana] >gi|40823521|gb|AAR92287.1| At4g33960 [Arabidopsis thaliana]						nr +
Unigene8371_All	305	7.89	1.16	2.10	3.76	1.81	2.96	74.86	22.88	29.26	-2.76E+00	7.95E-08	Down	-1.91E+00	5.02E-05	Down	-1.06E+00	8.44E-02		-3.43E-01	6.37E-01		-1.71E+00	1.68E-46	Down	-1.36E+00	2.95E-34	Down				Unigene8371_All//1.00E-86//gi|21098895|gb|BQ411208.1|BQ411208				
Unigene83718_All	398	0.26	0.00	2.14	4.01	1.30	1.02	0.85	0.32	0.00	-8.04E+00	3.65E-01		3.03E+00	3.00E-03		-1.63E+00	1.40E-03		-1.97E+00	4.88E-04	Down	-1.43E+00	2.58E-01		-9.73E+00	8.13E-03									
Unigene8372_All	232	0.00	3.06	0.69	1.29	2.08	0.19	0.00	0.00	0.34	1.16E+01	3.30E-04	Up	9.43E+00	2.34E-01		6.90E-01	5.66E-01		-2.73E+00	1.36E-01		null	null		8.42E+00	4.00E-01		Unigene8372_All//gi|302142040|emb|CBI19243.3|//1.00E-07//unnamed protein product [Vitis vinifera]		Unigene8372_All//4.00E-09//DT467355				nr -
Unigene83724_All	266	0.59	0.00	0.00	3.93	0.65	1.02	0.32	0.00	0.15	-9.20E+00	2.13E-01		-9.20E+00	2.42E-01		-2.60E+00	3.59E-04	Down	-1.95E+00	7.52E-03		-8.31E+00	3.97E-01		-1.09E+00	6.73E-01					Unigene83724_All//4.00E-59//DR455079				
Unigene8374_All	556	3.95	1.91	0.86	0.00	0.19	0.57	0.23	0.30	2.22	-1.05E+00	1.61E-02		-2.20E+00	2.12E-05	Down	7.54E+00	4.51E-01		9.15E+00	4.07E-02		3.99E-01	8.13E-01		3.28E+00	4.18E-06	Up								
Unigene83746_All	691	1.14	0.00	0.08	0.58	0.00	0.00	0.24	0.00	0.23	-1.01E+01	1.09E-04	Down	-3.88E+00	1.59E-03		-9.17E+00	4.38E-03		-9.17E+00	1.11E-02		-7.93E+00	1.33E-01		-8.56E-02	9.65E-01		Unigene83746_All//gi|225434642|ref|XP_002279786.1|//7.00E-31//PREDICTED: similar to binding [Vitis vinifera]	Unigene83746_All//8.00E-20//AT2G29670| binding	Unigene83746_All//0.00E+00//TC174325				nr +
Unigene83760_All	227	3.00	0.00	0.23	1.76	0.46	0.00	0.00	0.00	0.00	-1.15E+01	4.09E-04	Down	-3.67E+00	4.81E-03		-1.95E+00	1.19E-01		-1.08E+01	1.11E-02		null	null		null	null									
Unigene8377_All	283	125.16	82.90	134.35	9.15	9.13	1.76	0.00	0.00	0.00	-5.94E-01	4.62E-11		1.02E-01	3.28E-01		-4.30E-03	9.80E-01		-2.38E+00	1.23E-07	Down	null	null		null	null					Unigene8377_All//3.00E-109//gi|164294025|gb|EX169538.1|EX169538				
Unigene8378_All	506	0.52	2.90	3.26	2.07	2.11	2.77	0.75	0.33	0.71	2.49E+00	1.51E-04	Up	2.66E+00	4.26E-05	Up	2.92E-02	9.80E-01		4.21E-01	4.92E-01		-1.19E+00	3.09E-01		-8.58E-02	9.43E-01					Unigene8378_All//6.00E-50//TC136806				
Unigene8382_All	583	0.27	0.35	0.91	0.60	1.18	1.32	1.81	0.72	0.21	3.69E-01	8.15E-01		1.76E+00	1.28E-01		9.82E-01	2.98E-01		1.14E+00	1.89E-01		-1.34E+00	2.90E-02		-3.14E+00	2.96E-05	Down				Unigene8382_All//3.00E-95//CO130892				
Unigene8384_All	624	0.00	9.83	2.30	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	5.26E-35	Up	1.12E+01	6.28E-08	Up	null	null		null	null		null	null		null	null									
Unigene8385_All	546	1.92	1.11	0.00	2.37	2.27	2.40	0.85	0.23	0.36	-7.83E-01	2.34E-01		-1.09E+01	9.32E-06	Down	-6.32E-02	9.04E-01		1.61E-02	9.80E-01		-1.89E+00	8.00E-02		-1.22E+00	2.00E-01		Unigene8385_All//gi|18405469|ref|NP_566822.1|//9.00E-64//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene8385_All//5.00E-61//AT3G27640| transducin family protein / WD-40 repeat family protein	Unigene8385_All//0.00E+00//gi|78353258|gb|DT573532.1|DT573532			GO:0009987//GO:0031461//GO:0043231	nr -

Unigene8386_All	334	0.31	0.91	0.00	4.47	2.89	0.95	0.51	1.13	1.43	1.54E+00	3.22E-01		-8.29E+00	3.87E-01		-6.32E-01	2.38E-01		-2.24E+00	2.25E-04	Down	1.15E+00	3.27E-01		1.50E+00	1.27E-01		Unigene8386_All//gi|62734184|gb|AAX96293.1|//3.00E-09//At5g42500 [Oryza sativa Japonica Group] >gi|77548984|gb|ABA91781.1| Dirigent-like protein [Oryza sativa (japonica cultivar-group)]	Unigene8386_All//2.00E-08//AT5G42500| disease resistance-responsive family protein	Unigene8386_All//4.00E-155//gi|109866608|gb|DW495584.1|DW495584			GO:0006950//GO:0031410	nr +
Unigene83860_All	388	0.27	0.00	0.00	2.82	0.71	0.47	0.22	0.00	0.21	-8.08E+00	3.65E-01		-8.08E+00	3.87E-01		-1.99E+00	2.59E-03		-2.60E+00	7.13E-04	Down	-7.77E+00	3.97E-01		-8.52E-02	9.69E-01		Unigene83860_All//gi|297807279|ref|XP_002871523.1|//5.00E-23//ran GTPase binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297317360|gb|EFH47782.1| ran GTPase binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene83860_All//7.00E-11//AT5G12350| Ran GTPase binding / chromatin binding / zinc ion binding				GO:0046872	nr -
Unigene8387_All	481	0.22	0.42	0.89	1.24	2.00	1.97	1.14	1.56	3.56	9.54E-01	6.20E-01		2.03E+00	1.39E-01		6.90E-01	3.61E-01		6.66E-01	3.93E-01		4.53E-01	5.59E-01		1.64E+00	4.04E-04	Up					Unigene8387_All//4.00E-11//TC139598				
Unigene83884_All	348	2.56	0.00	0.31	0.43	0.30	1.04	0.00	0.00	0.11	-1.13E+01	2.85E-05	Down	-3.06E+00	2.25E-03		-5.32E-01	7.83E-01		1.27E+00	3.81E-01		null	null		6.84E+00	6.35E-01						Unigene83884_All//2.00E-92//gi|48798807|gb|CO099721.1|CO099721				
Unigene83889_All	213	50.11	72.08	75.50	108.98	86.49	87.57	255.86	272.56	29.55	5.25E-01	2.29E-04		5.91E-01	3.71E-05		-3.34E-01	2.08E-03		-3.16E-01	5.80E-03		9.12E-02	2.06E-01		-3.11E+00	5.25E-234	Down					Unigene83889_All//7.00E-88//FL576450				
Unigene83896_All	206	0.25	0.49	0.00	0.24	0.33	0.22	1.03	1.01	9.86	9.54E-01	7.23E-01		-7.99E+00	6.14E-01		4.67E-01	9.52E-01		-1.42E-01	9.46E-01		-1.65E-02	1.02E+00		3.26E+00	1.40E-09	Up					Unigene83896_All//2.00E-23//TC178710				
Unigene83925_All	217	0.00	0.00	0.00	0.92	0.32	1.04	2.34	0.00	0.00	null	null		null	null		-1.53E+00	4.14E-01		1.81E-01	9.34E-01		-1.12E+01	8.88E-04	Down	-1.12E+01	5.54E-04	Down									
Unigene83965_All	202	0.00	0.00	0.00	2.71	0.00	0.00	0.21	0.21	0.39	null	null		null	null		-1.14E+01	4.00E-04	Down	-1.14E+01	1.52E-03		-1.66E-02	9.97E-01		9.14E-01	7.47E-01										
Unigene8398_All	884	0.36	0.23	0.24	0.62	0.39	0.41	0.86	1.37	7.98	-6.31E-01	6.21E-01		-5.59E-01	6.62E-01		-6.70E-01	4.96E-01		-6.01E-01	5.66E-01		6.71E-01	2.36E-01		3.21E+00	3.56E-31	Up	Unigene8398_All//gi|15235403|ref|NP_192163.1|//3.00E-29//DC1 domain-containing protein [Arabidopsis thaliana]	Unigene8398_All//1.00E-30//AT4G02540| DC1 domain-containing protein	Unigene8398_All//0.00E+00//gi|109857439|gb|DW486418.1|DW486418				nr -
Unigene83998_All	302	0.17	0.00	0.18	3.13	0.23	1.20	0.14	0.00	0.26	-7.44E+00	6.00E-01		2.56E-02	9.91E-01		-3.78E+00	3.39E-05	Down	-1.39E+00	6.08E-02		-7.13E+00	6.42E-01		9.14E-01	7.47E-01										
Unigene84_All	1149	2.82	3.84	3.20	4.90	5.57	6.64	4.31	4.00	11.62	4.43E-01	1.32E-01		1.80E-01	6.29E-01		1.86E-01	5.06E-01		4.39E-01	4.18E-02		-1.06E-01	6.93E-01		1.43E+00	7.07E-22	Up	Unigene84_All//gi|79516777|ref|NP_197441.3|//9.00E-98//SMG7 [Arabidopsis thaliana] >gi|15946469|gb|AEW96769.1| SMG7-like protein [Arabidopsis thaliana]	Unigene84_All//5.00E-99//AT5G19400| SMG7	Unigene84_All//3.00E-174//TC138860				nr +
Unigene840_All	2339	3.22	1.95	0.52	5.15	4.34	5.43	11.60	7.29	6.57	-7.24E-01	6.31E-04		-2.62E+00	6.02E-21	Down	-2.47E-01	1.51E-01		7.42E-02	6.77E-01		-6.71E-01	8.47E-13		-8.20E-01	2.38E-18		Unigene840_All//gi|15230408|ref|NP_188582.1|//1.00E-137//HAT3.1; DNA binding / sequence-specific DNA binding / transcription activator/ transcription factor [Arabidopsis thaliana] >gi|148886602|sp|Q04996.3|HAT31_ARATH RecName: Full=Homeobox protein HAT3.1 >gi|29029042|gb|AAO64900.1| At3g19510 [Arabidopsis thaliana]	Unigene840_All//1.00E-75//AT3G19510| HAT3.1; DNA binding / sequence-specific DNA binding / transcription activator/ transcription factor	Unigene840_All//0.00E+00//TC178282	HB		GO:0005488	nr +
Unigene8404_All	423	1.36	1.44	3.27	0.24	0.49	0.53	0.30	4.05	0.09	7.92E-02	9.41E-01		1.27E+00	3.77E-02		1.05E+00	6.11E-01		1.18E+00	5.48E-01		3.76E+00	6.98E-09	Up	-1.67E+00	4.75E-01										
Unigene84051_All	209	0.75	0.24	0.00	3.81	0.16	0.00	0.00	0.00	0.00	-1.63E+00	4.87E-01		-9.53E+00	2.42E-01		-4.53E+00	6.06E-05	Down	-1.19E+01	4.90E-05	Down	null	null		null	null										
Unigene84081_All	205	0.00	0.00	0.26	1.70	0.00	0.22	0.41	6.93	2.14	null	null		8.02E+00	6.23E-01		-1.07E+01	9.43E-03		-2.95E+00	8.29E-02		4.07E+00	7.46E-08	Up	2.37E+00	4.01E-02						Unigene84081_All//5.00E-36//TC171756				
Unigene84103_All	217	0.24	0.00	0.98	0.23	0.79	0.83	0.19	2.50	12.12	-7.91E+00	6.00E-01		2.03E+00	3.59E-01		1.79E+00	5.19E-01		1.86E+00	4.57E-01		3.68E+00	3.69E-03		5.96E+00	2.54E-17	Up	Unigene84103_All//gi|283132359|dbj|BAI63585.1|//3.00E-09//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene84103_All//1.00E-08//AT4G38470| protein kinase family protein	Unigene84103_All//4.00E-49//TC163305				nr -
Unigene8411_All	317	32.35	40.44	44.18	41.01	36.17	34.34	225.14	135.67	89.48	3.22E-01	4.64E-02		4.50E-01	4.07E-03		-1.81E-01	3.04E-01		-2.56E-01	1.29E-01		-7.31E-01	2.05E-37		-1.33E+00	2.11E-102	Down					Unigene8411_All//8.00E-178//gi|21100539|gb|BQ412852.1|BQ412852				
Unigene84124_All	294	0.00	0.00	1.27	2.71	1.05	0.15	0.43	0.71	0.27	null	null		1.03E+01	2.46E-02		-1.36E+00	7.73E-02		-4.14E+00	4.12E-04	Down	7.20E-01	6.31E-01		-6.71E-01	7.18E-01										
Unigene8414_All	368	0.85	1.93	3.91	0.41	0.84	1.10	0.92	0.68	0.76	1.18E+00	1.75E-01		2.20E+00	8.73E-04	Up	1.05E+00	5.31E-01		1.44E+00	2.82E-01		-4.32E-01	7.03E-01		-2.78E-01	7.80E-01		Unigene8414_All//gi|297826435|ref|XP_002881100.1|//4.00E-42//tRNA pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326939|gb|EFH57359.1| tRNA pseudouridine synthase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8414_All//1.00E-42//AT2G30320| tRNA pseudouridine synthase family protein				GO:0003676//GO:0006399//GO:0009451//GO:0016866//GO:0043231	nr -
Unigene84152_All	219	2.87	3.47	1.46	12.97	6.92	2.06	1.54	1.15	0.91	2.76E-01	7.10E-01		-9.75E-01	3.16E-01		-9.06E-01	9.73E-03		-2.65E+00	2.51E-09	Down	-4.32E-01	7.03E-01		-7.64E-01	5.01E-01						Unigene84152_All//1.00E-09//ES811102				
Unigene84158_All	203	2.58	0.00	1.05	2.45	0.00	0.22	0.00	0.00	0.00	-1.13E+01	2.91E-03		-1.30E+00	2.42E-01		-1.13E+01	8.97E-04	Down	-3.46E+00	1.61E-02		null	null		null	null						Unigene84158_All//4.00E-12//DR461178				
Unigene8417_All	2908	0.32	0.23	0.57	0.74	0.41	0.45	0.90	0.75	5.37	-5.16E-01	4.57E-01		8.10E-01	1.35E-01		-8.30E-01	4.74E-02		-7.10E-01	1.13E-01		-2.70E-01	4.77E-01		2.57E+00	1.86E-54	Up	Unigene8417_All//gi|130582|sp|P10978.1|POLX_TOBAC//0.00E+00//RecName: Full=Retrovirus-related Pol polyprotein from transposon TNT 1-94; Includes: RecName: Full=Protease; Includes: RecName: Full=Reverse transcriptase; Includes: RecName: Full=Endonuclease	Unigene8417_All//2.00E-27//AT4G23160| protein kinase family protein	Unigene8417_All//0.00E+00//gi|73865502|gb|DT468240.1|DT468240			GO:0003676//GO:0016787//GO:0046872	nr +
Unigene8418_All	493	4.99	1.44	2.70	0.81	1.05	0.37	0.00	0.00	0.00	-1.79E+00	4.83E-05	Down	-8.85E-01	3.75E-02		3.74E-01	7.71E-01		-1.14E+00	3.79E-01		null	null		null	null		Unigene8418_All//gi|224077014|ref|XP_002305093.1|//2.00E-65//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222848057|gb|EEE85604.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene8418_All//4.00E-39//AT3G29120| ATGLR2.7; intracellular ligand-gated ion channel				GO:0005231//GO:0005488//GO:0006810//GO:0008066//GO:0030313//GO:0031224	nr +
Unigene84183_All	204	0.00	0.00	0.00	3.66	0.84	0.22	0.00	0.00	0.00	null	null		null	null		-2.12E+00	1.27E-02		-4.05E+00	7.75E-04	Down	null	null		null	null						Unigene84183_All//6.00E-45//TC148687				
Unigene842_All	3203	9.34	20.41	14.03	19.77	22.38	18.70	20.91	27.73	25.88	1.13E+00	2.49E-57	Up	5.87E-01	5.90E-13		1.79E-01	3.28E-03		-8.03E-02	3.16E-01		4.07E-01	1.20E-16		3.08E-01	7.45E-10		Unigene842_All//gi|115446361|ref|NP_001046960.1|//0.00E+00//Os02g0517300 [Oryza sativa Japonica Group] >gi|113536491|dbj|BAF08874.1| Os02g0517300 [Oryza sativa Japonica Group]	Unigene842_All//0.00E+00//AT3G22270| unknown protein	Unigene842_All//0.00E+00//gi|54117565|gb|CO493074.1|CO493074		ko03018|RNA degradation		nr -
Unigene84201_All	215	1.46	3.30	9.41	2.78	0.16	1.26	0.20	0.00	0.00	1.18E+00	1.75E-01		2.69E+00	3.50E-06	Up	-4.12E+00	1.25E-03		-1.14E+00	2.42E-01		-7.62E+00	6.42E-01		-7.62E+00	6.00E-01		Unigene84201_All//gi|6692693|gb|AAF24827.1|AC007592,20//5.00E-08//F12K11.6 [Arabidopsis thaliana]	Unigene84201_All//3.00E-09//AT1G06640| 2-oxoglutarate-dependent dioxygenase, putative	Unigene84201_All//7.00E-17//TC141122		ko00402|Benzoxazinoid biosynthesis	GO:0008152//GO:0016706//GO:0046914	nr -
Unigene84208_All	226	0.46	0.00	1.89	4.85	0.30	1.40	0.00	0.37	0.00	-8.85E+00	3.65E-01		2.03E+00	1.39E-01		-3.99E+00	3.49E-06	Down	-1.79E+00	1.01E-02		8.53E+00	3.98E-01		null	null						Unigene84208_All//1.00E-120//DW225821				ESTscan +
Unigene84219_All	698	2.55	0.44	1.22	4.07	1.28	0.97	1.33	0.72	1.31	-2.55E+00	1.57E-05	Down	-1.06E+00	4.11E-02		-1.67E+00	4.51E-06	Down	-2.07E+00	4.39E-07	Down	-8.91E-01	1.72E-01		-2.17E-02	9.60E-01		Unigene84219_All//gi|145245877|gb|ABP49172.1|//2.00E-11//uroporphiryn-III C-methyltransferase [Medicago truncatula]	Unigene84219_All//2.00E-11//AT5G40850| UPM1 (UROPHORPHYRIN METHYLASE 1); uroporphyrin-III C-methyltransferase	Unigene84219_All//0.00E+00//TC176887			GO:0006778//GO:0016741	nr -
Unigene84424_All	390	19.05	11.56	14.20	32.95	20.57	17.60	52.25	32.04	13.08	-7.20E-01	7.47E-04		-4.24E-01	6.28E-02		-6.80E-01	2.56E-06		-9.05E-01	5.04E-09		-7.06E-01	1.18E-10		-2.00E+00	7.00E-53	Down					Unigene8424_All//7.00E-157//gi|109881335|gb|DW510305.1|DW510305				
Unigene8426_All	557	0.00	0.00	0.00	0.98	0.06	0.16	1.06	3.45	1.43	null	null		null	null		-3.99E+00	2.60E-03		-2.60E+00	2.93E-02		1.70E+00	1.45E-04	Up	4.29E-01	5.50E-01		Unigene8426_All//gi|75297894|sp|Q84MB3.1|ACCH1_ARATH//3.00E-50//RecName: Full=1-aminocyclopropane-1-carboxylate oxidase homolog 1 >gi|30102640|gb|AAP21238.1| At1g06620 [Arabidopsis thaliana] >gi|110743652|dbj|BAE99663.1| oxidoreductase like protein [Arabidopsis thaliana]	Unigene8426_All//2.00E-51//AT1G06620| 2-oxoglutarate-dependent dioxygenase, putative	Unigene8426_All//3.00E-135//TC134065		ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis//ko00402|Benzoxazinoid biosynthesis	GO:0016706	nr +
Unigene8427_All	280	54.94	138.80	141.49	39.85	52.88	39.52	0.00	0.15	0.00	1.34E+00	9.67E-45	Up	1.36E+00	1.06E-45	Up	4.08E-01	3.71E-03		-1.21E-02	9.57E-01		7.22E+00	6.25E-01		null	null						Unigene8427_All//2.00E-97//gi|48744622|gb|CO075141.1|CO075141				ESTscan +
Unigene84275_All	379	0.00	0.40	2.81	0.79	0.00	0.00	0.00	0.11	0.00	8.65E+00	2.31E-01		1.15E+01	6.58E-06	Up	-9.62E+00	2.01E-02		-9.62E+00	3.97E-02		6.79E+00	6.25E-01		null	null		Unigene84275_All//gi|147821434|emb|CAN74577.1|//2.00E-12//hypothetical protein [Vitis vinifera]	Unigene84275_All//8.00E-05//AT1G23850| unknown protein					nr -
Unigene84295_All	386	0.00	0.13	0.28	1.81	0.36	0.00	0.00	0.65	0.41	7.04E+00	6.07E-01		8.11E+00	3.88E-01		-2.34E+00	1.01E-02		-1.08E+01	1.96E-04	Down	9.34E+00	4.30E-02		8.69E+00	1.39E-01										
Unigene843_All	3087	29.85	7.93	11.35	38.86	28.85	24.26	22.89	7.50	7.54	-1.91E+00	2.97E-177	Down	-1.39E+00	4.17E-109	Down	-4.30E-01	5.14E-24		-6.80E-01	1.36E-48		-1.61E+00	1.16E-130	Down	-1.60E+00	1.20E-133	Down	Unigene843_All//gi|54036489|sp|Q6YAF6.1|TBB6_GOSHI//0.00E+00//RecName: Full=Tubulin beta-6 chain; AltName: Full=Beta-6-tubulin >gi|37529496|gb|AAQ92666.1| beta-tubulin 6 [Gossypium hirsutum]	Unigene843_All//0.00E+00//AT1G75780| TUB1; GTP binding / GTPase/ structural molecule	Unigene843_All//0.00E+00//TC129598		ko04145|Phagosome	GO:0000902//GO:0007017//GO:0009314//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043231//GO:0043623	nr +
Unigene8431_All	464	0.00	0.44	0.69	1.29	0.82	1.17	1.46	0.81	4.29	8.77E+00	1.34E-01		9.43E+00	4.42E-02		-6.58E-01	4.78E-01		-1.41E-01	8.79E-01		-8.47E-01	2.88E-01		1.56E+00	2.17E-04	Up									
Unigene84317_All	330	0.48	0.46	0.65	3.17	0.52	0.27	0.13	0.00	0.12	-4.62E-02	9.88E-01		4.41E-01	7.74E-01		-2.60E+00	3.59E-04	Down	-3.53E+00	9.34E-05	Down	-7.00E+00	6.42E-01		-8.58E-02	9.65E-01		Unigene84317_All//gi|225456020|ref|XP_002279587.1|//2.00E-24//PREDICTED: similar to inositol polyphosphate multikinase [Vitis vinifera]	Unigene84317_All//7.00E-23//AT5G61760| ATIPK2BETA; inositol or phosphatidylinositol kinase/ inositol trisphosphate 6-kinase	Unigene84317_All//4.00E-10//TC130598			GO:0000904//GO:0009856//GO:0016020//GO:0043231//GO:0051766	nr +
Unigene8433_All	448	0.00	1.81	0.24	0.89	1.31	0.50	2.36	1.59	2.22	1.08E+01	9.30E-05	Up	7.89E+00	3.88E-01		5.55E-01	5.99E-01		-8.19E-01	5.06E-01		-5.73E-01	3.60E-01		-8.58E-02	8.85E-01						Unigene8433_All//9.00E-120//gi|54120492|gb|CO496001.1|CO496001				
Unigene84338_All	254	1.65	0.00	0.00	2.94	2.30	0.00	0.83	0.49	0.78	-1.07E+01	1.04E-02		-1.07E+01	1.55E-02		-3.52E-01	6.51E-01		-1.15E+01	9.80E-05	Down	-7.54E-01	6.31E-01		-8.59E-02	9.60E-01		Unigene84338_All//gi|240254485|ref|NP_179595.5|//4.00E-20//ATP binding / cAMP-dependent protein kinase regulator/ catalytic/ protein kinase/ protein serine/threonine phosphatase [Arabidopsis thaliana] >gi|226739228|sp|Q9SL76.2|P2C19_ARATH RecName: Full=Protein phosphatase 2C and cyclic nucleotide-binding/kinase domain-containing protein; Includes: RecName: Full=Probable protein phosphatase 2C 19; Short=AtPP2C19; Includes: RecName: Full=Probable inactive cyclic nucleotide-dependent protein kinase At2g20050	Unigene84338_All//2.00E-21//AT2G20050| ATP binding / cAMP-dependent protein kinase regulator/ catalytic/ protein kinase/ protein serine/threonine phosphatase	Unigene84338_All//7.00E-119//gi|164357611|gb|ES804101.1|ES804101			GO:0004672//GO:0004721//GO:0005488//GO:0006468//GO:0016020//GO:0043234	nr +
Unigene8436_All	286	3.11	3.54	3.35	6.10	5.30	0.95	1.92	2.78	1.67	1.88E-01	7.64E-01		1.08E-01	8.74E-01		-2.03E-01	7.02E-01		-2.69E+00	5.27E-06	Down	5.31E-01	4.67E-01		-2.01E-01	7.93E-01						Unigene8436_All//2.00E-08//TC161550				
Unigene8438_All	238	0.44	0.43	0.22	1.47	1.30	2.47	1.07	1.05	5.52	-4.63E-02	9.85E-01		-9.75E-01	7.19E-01		-1.70E-01	8.57E-01		7.52E-01	4.67E-01		-1.66E-02	1.02E+00		2.37E+00	7.20E-05	Up	Unigene8438_All//gi|105922499|gb|ABF81420.1|//4.00E-10//NBS type disease resistance protein [Populus trichocarpa]	Unigene8438_All//6.00E-05//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene8438_All//5.00E-89//C0087346			GO:0005488	nr +
Unigene84388_All	204	0.00	0.00	0.00	2.93	0.00	1.33	1.87	0.00	0.78	null	null		null	null		-1.15E+01	1.78E-04	Down	-1.14E+00	2.42E-01		-1.09E+01	6.17E-03		-1.26E+00	2.48E-01						Unigene84388_All//9.00E-47//gi|78351116|gb|DT571390.1|DT571390				
Unigene8439_All	270	0.00	2.06	0.00	0.00	0.00	0.00	0.63	4.18	4.57	1.10E+01	2.16E-03		null	null		null	null		null	null		2.74E+00	9.94E-05	Up	2.87E+00	1.78E-05	Up									
Unigene844_All	759	28.54	28.51	19.64	23.43	28.58	38.68	38.16	76.05	85.82	-1.70E-03	9.87E-01		-5.39E-01	9.22E-06		2.87E-01	1.44E-02		7.23E-01	1.50E-13		9.95E-01	8.08E-51		1.17E+00	7.82E-76	Up	Unigene844_All//gi|115487674|ref|NP_001066324.1|//1.00E-119//Os12g0183100 [Oryza sativa Japonica Group] >gi|113648831|dbj|BAF29343.1| Os12g0183100 [Oryza sativa Japonica Group]	Unigene844_All//3.00E-113//AT5G09300| 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative	Unigene844_All//0.00E+00//TC147839		ko00280|Valine, leucine and isoleucine degradation		nr -
Unigene8440_All	335	0.00	0.00	2.38	0.74	0.00	0.00	2.90	1.00	0.71	null	null		1.12E+01	1.71E-04	Up	-9.54E+00	4.16E-02		-9.54E+00	7.29E-02		-1.54E+00	1.90E-02		-2.02E+00	2.47E-03		Unigene8440_All//gi|66276977|gb|AAY44415.1|//2.00E-30//dirigent-like protein [Gossypium barbadense]	Unigene8440_All//1.00E-31//AT2G21110| disease resistance-responsive family protein	Unigene8440_All//3.00E-26//ES791694			GO:0006950//GO:0031410	nr -

Unigene8441_All	291	2.52	1.92	3.66	1.71	2.25	9.93	0.00	0.00	0.00	-3.94E-01	6.11E-01		5.40E-01	4.17E-01		3.93E-01	6.98E-01		2.54E+00	8.36E-09	Up	null	null		null	null		Unigene8441_All//gi|224138238|ref|XP_002322764.1|//3.00E-45//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222867394|gb|EEF04525.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene8441_All//2.00E-42//AT5G06530| ABC transporter family protein	Unigene8441_All//4.00E-56//TC133240		ko02010|ABC transporters	GO:0015098//GO:0015405//GO:0016020//GO:0017111//GO:0032559	nr +
Unigene84423_All	395	0.79	0.26	0.27	2.14	0.09	0.69	0.43	0.74	0.40	-1.63E+00	2.76E-01		-1.56E+00	3.29E-01		-4.62E+00	2.79E-05	Down	-1.64E+00	4.17E-02		7.91E-01	5.63E-01		-8.61E-02	9.65E-01										
Unigene84428_All	209	0.00	3.15	1.02	2.86	2.14	3.03	0.40	0.20	0.19	1.16E+01	6.20E-04	Up	9.99E+00	1.37E-01		-4.17E-01	6.27E-01		8.10E-02	9.45E-01		-1.02E+00	7.21E-01		-1.09E+00	6.73E-01				Unigene84428_All//1.00E-30//TC158363					
Unigene84429_All	212	0.00	0.00	0.00	0.00	0.00	0.21	0.00	0.39	4.70	null	null		null	null		null	null		7.73E+00	6.82E-01		8.62E+00	3.98E-01		1.22E+01	3.00E-07	Up	Unigene84429_All//gi|255575021|ref|XP_002528416.1|//9.00E-10//amino acid transporter, putative [Ricinus communis] >gi|223532152|gb|EEF33958.1| amino acid transporter, putative [Ricinus communis]					GO:0031224	nr -
Unigene8443_All	264	0.00	0.00	0.00	0.00	0.00	0.00	21.62	10.77	9.36	null	null		null	null		null	null		null	null		-1.01E+00	7.50E-06	Down	-1.21E+00	7.37E-08	Down									ESTscan -
Unigene8444_All	378	0.69	2.28	1.55	8.17	1.82	1.67	1.45	0.22	0.21	1.72E+00	3.49E-02		1.16E+00	2.46E-01		-2.16E+00	3.71E-09	Down	-2.29E+00	1.32E-08	Down	-2.72E+00	1.22E-02		-2.79E+00	7.95E-03				Unigene8444_All//1.00E-31//DR462011					
Unigene8445_All	1429	0.51	0.00	0.15	1.95	2.46	0.95	0.44	0.53	0.36	-9.00E+00	2.11E-04	Down	-1.78E+00	6.00E-02		3.32E-01	3.55E-01		-1.04E+00	5.46E-03		2.47E-01	7.31E-01		-2.92E-01	6.84E-01		Unigene8445_All//gi|224110992|ref|XP_002332999.1|//6.00E-37//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834484|gb|EEE72961.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene8445_All//5.00E-06//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene8445_All//6.00E-148//ES820741		ko04626|Plant-pathogen interaction		nr -
Unigene84459_All	416	1.64	1.95	0.90	3.47	1.90	0.33	2.24	0.00	0.67	2.53E-01	7.26E-01		-8.68E-01	3.51E-01		-8.67E-01	1.04E-01		-3.41E+00	3.16E-06	Down	-1.11E+01	1.14E-06	Down	-1.74E+00	8.54E-03				Unigene84459_All//1.00E-137//gi|164316283|gb|ES827472.1|ES827472					
Unigene8447_All	250	200.28	199.84	262.20	35.07	35.40	18.61	17.76	6.69	6.21	-3.20E-03	9.86E-01		3.89E-01	4.29E-09		1.35E-02	9.58E-01		-9.14E-01	1.81E-06		-1.41E+00	1.77E-07	Down	-1.51E+00	1.54E-08	Down			Unigene8447_All//2.00E-134//gi|109836819|gb|DW235380.1|DW235380					
Unigene84483_All	244	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.34	2.12	null	null		null	null		null	null		null	null		8.42E+00	3.98E-01		1.11E+01	6.13E-04	Up	Unigene84483_All//gi|115459830|ref|NP_001053515.1|//1.00E-25//0s04g0555300 [Oryza sativa Japonica Group] >gi|38345584|emb|CAD41637.2| OSJNBb0012E24.2 [Oryza sativa (japonica cultivar-group)] >gi|113565086|dbj|BAF15429.1| Os04g0555300 [Oryza sativa Japonica Group]	Unigene84483_All//1.00E-29//AT3G47420| glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative					nr +
Unigene84495_All	221	0.47	0.00	0.00	0.45	0.00	0.41	2.49	0.76	0.00	-8.89E+00	3.65E-01		-8.89E+00	3.87E-01		-8.82E+00	3.07E-01		-1.41E-01	9.46E-01		-1.72E+00	7.22E-02		-1.13E+01	2.80E-04	Down	Unigene84495_All//gi|224064996|ref|XP_002301626.1|//8.00E-22//glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa] >gi|222843352|gb|EEES0899.1| glutamate-gated kainate-type ion channel receptor subunit GluR5 [Populus trichocarpa]	Unigene84495_All//2.00E-15//AT1G42540| ATGLR3.3; intracellular ligand-gated ion channel	Unigene84495_All//6.00E-76//gi|48749226|gb|C0079745.1|C0079745				nr +
Unigene845_All	1523	7.52	8.08	5.56	6.41	8.61	10.35	22.85	54.83	52.00	1.04E-01	5.79E-01		-4.37E-01	1.36E-02		4.26E-01	4.66E-03		6.91E-01	4.85E-07		1.26E+00	4.18E-107	Up	1.19E+00	3.56E-94	Up	Unigene845_All//gi|115487674|ref|NP_001066324.1|//6.00E-16//0s12g0183100 [Oryza sativa Japonica Group] >gi|113648831|dbj|BAF29343.1| Os12g0183100 [Oryza sativa Japonica Group]	Unigene845_All//2.00E-14//AT5G09300| 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative	Unigene845_All//3.00E-165//TC147839		ko00280|Valine, leucine and isoleucine degradation	GO:0008152//GO:0016624//GO:0043231	nr -
Unigene84501_All	210	0.00	0.00	0.76	2.85	1.15	0.00	0.00	0.00	0.00	null	null		9.57E+00	2.34E-01		-1.31E+00	1.56E-01		-1.15E+01	7.69E-04	Down	null	null		null	null				Unigene84501_All//1.00E-39//DT048617					
Unigene8451_All	368	2.27	0.28	4.20	2.03	1.03	0.00	1.49	1.93	0.32	-3.05E+00	2.11E-03		8.83E-01	1.15E-01		-9.80E-01	2.23E-01		-1.10E+01	9.80E-05	Down	3.70E-01	6.67E-01		-2.20E+00	2.24E-02		Unigene8451_All//gi|224132258|ref|XP_002328224.1|//2.00E-11//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222837739|gb|EEE76104.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene8451_All//3.00E-08//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene8451_All//0.00E+00//TC146851			GO:0003824//GO:0005488	nr -
Unigene84528_All	213	2.21	18.56	11.50	2.10	1.13	0.64	0.20	0.00	0.00	3.07E+00	1.25E-13	Up	2.38E+00	1.67E-06	Up	-8.95E-01	4.13E-01		-1.73E+00	1.61E-01		-7.63E+00	6.41E-01		-7.63E+00	5.99E-01				Unigene84528_All//1.00E-30//TC137965					
Unigene8454_All	474	0.44	0.43	0.11	4.41	1.96	0.76	0.27	0.62	0.08	-4.62E-02	9.86E-01		-1.98E+00	3.80E-01		-1.17E+00	5.49E-03		-2.53E+00	1.08E-06	Down	1.21E+00	3.92E-01		-1.67E+00	4.73E-01									
Unigene84548_All	208	0.50	0.00	2.56	3.11	0.66	0.00	0.20	0.00	0.00	-8.97E+00	3.65E-01		2.35E+00	5.85E-02		-2.23E+00	1.79E-02		-1.16E+01	3.90E-04	Down	-7.67E+00	6.41E-01		-7.67E+00	5.99E-01									
Unigene8455_All	340	0.00	1.34	0.63	0.15	0.20	2.66	0.12	0.00	1.05	1.04E+01	7.34E-03		9.29E+00	1.37E-01		4.68E-01	9.52E-01		4.18E+00	1.95E-04	Up	-6.96E+00	6.41E-01		3.08E+00	3.61E-02		Unigene8455_All//gi|9963897|gb|AAG09751.1|AF237625_1//2.00E-15//oleosin [Perilla frutescens]		Unigene8455_All//4.00E-112//gi|109826466|gb|DV225179.1|DV225179			GO:0005811//GO:0031224	nr +
Unigene84558_All	211	0.25	0.24	5.30	2.36	1.14	1.71	0.00	0.00	0.19	-4.67E-02	9.81E-01		4.42E+00	3.51E-05	Up	-1.05E+00	3.14E-01		-4.63E-01	6.59E-01		null	null		7.56E+00	6.35E-01										
Unigene8457_All	291	0.18	0.35	3.11	0.34	1.54	2.48	0.58	0.00	0.82	9.54E-01	7.23E-01		4.11E+00	3.91E-04	Up	2.17E+00	1.06E-01		2.86E+00	7.12E-03		-9.18E+00	1.33E-01		4.99E-01	7.07E-01		Unigene8457_All//gi|221327714|gb|ACM17535.1|//3.00E-08//mitochondrial transcription termination factor-like family-2 [Oryza australiensis]	Unigene8457_All//3.00E-07//AT5G07900| mitochondrial transcription termination factor family protein / mTERF family protein	Unigene8457_All//4.00E-136//TC130468				nr -
Unigene84585_All	215	0.00	0.24	0.00	2.32	0.00	0.00	0.20	0.00	1.11	7.88E+00	6.07E-01		null	null		-1.12E+01	8.97E-04	Down	-1.12E+01	2.97E-03		-7.62E+00	6.41E-01		2.50E+00	1.59E-01				Unigene84585_All//1.00E-52//TC143397					
Unigene84599_All	441	0.71	0.57	0.72	1.92	1.17	0.10	0.29	0.47	1.08	-3.09E-01	7.89E-01		2.55E-02	1.00E+00		-7.13E-01	3.36E-01		-4.23E+00	2.18E-04	Down	7.21E-01	6.31E-01		1.91E+00	6.29E-02		Unigene84599_All//gi|149923530|gb|ABE80159.2|//1.00E-24//Tetratricopeptide-like helical [Medicago truncatula]	Unigene84599_All//1.00E-24//AT3G22470| pentatricopeptide (PPR) repeat-containing protein	Unigene84599_All//6.00E-130//TC159263				nr +
Unigene846_All	1420	15.51	13.42	13.76	12.38	15.52	18.48	19.18	28.70	42.56	-2.09E-01	9.00E-02		-1.73E-01	1.95E-01		3.26E-01	4.19E-03		5.78E-01	2.18E-08		5.82E-01	9.24E-15		1.15E+00	1.26E-68	Up	Unigene846_All//gi|9955517|emb|CAC05456.1|//3.00E-91//branched-chain alpha keto-acid dehydrogenase E1 alpha subunit-like protein [Arabidopsis thaliana]	Unigene846_All//1.00E-92//AT5G09300| 2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative	Unigene846_All//0.00E+00//C0119991		ko00280|Valine, leucine and isoleucine degradation	GO:0008152//GO:0016624//GO:0043231	nr -
Unigene84603_All	206	0.00	0.00	0.00	0.00	0.00	0.00	8.00	0.41	0.39	null	null		null	null		null	null		null	null		-4.30E+00	2.19E-09	Down	-4.37E+00	7.28E-10	Down									ESTscan +
Unigene84637_All	348	0.00	0.00	0.00	0.14	0.00	0.00	0.85	0.12	3.78	null	null		null	null		-7.16E+00	5.42E-01		-7.16E+00	6.16E-01		-2.82E+00	8.83E-02		2.15E+00	2.01E-04	Up			Unigene84637_All//4.00E-109//TC151131					
Unigene8464_All	557	1.13	1.46	0.19	0.98	1.24	0.73	2.88	0.00	0.86	3.69E-01	6.22E-01		-2.56E+00	2.72E-02		3.30E-01	7.52E-01		-4.31E-01	6.67E-01		-1.15E+01	2.16E-11	Down	-1.75E+00	2.96E-04	Down	Unigene8464_All//gi|56089573|gb|AA737464.2|//1.00E-64//origin recognition complex protein 4 [Arabidopsis thaliana]	Unigene8464_All//3.00E-64//AT2G01120| ORC4 (ORIGIN RECOGNITION COMPLEX SUBUNIT 4); protein binding	Unigene8464_All//0.00E+00//ES791241			GO:0003676//GO:0006259//GO:0032559//GO:0043231//GO:0043234	nr +
Unigene84644_All	301	1.22	5.72	3.01	0.66	1.37	0.15	0.56	1.11	0.66	2.23E+00	1.09E-04	Up	1.31E+00	9.76E-02		1.05E+00	4.25E-01		-2.14E+00	3.46E-01		9.83E-01	4.23E-01		2.36E-01	8.83E-01				Unigene84644_All//9.00E-88//gi|109851970|gb|DW480949.1|DW480949					
Unigene84645_All	365	0.00	0.14	0.29	13.51	0.09	0.25	21.20	12.02	4.69	7.12E+00	6.07E-01		8.19E+00	3.88E-01		-7.16E+00	1.27E-35	Down	-5.77E+00	4.51E-28	Down	-8.18E-01	1.22E-05		-2.18E+00	7.29E-23	Down	Unigene84645_All//gi|222838027|gb|EEE76392.1|//6.00E-09//predicted protein [Populus trichocarpa]		Unigene84645_All//1.00E-19//TC149074				nr +
Unigene8467_All	273	0.58	0.00	0.00	0.73	1.01	0.17	2.48	0.31	0.15	-9.17E+00	2.13E-01		-9.17E+00	2.42E-01		4.67E-01	8.16E-01		-2.14E+00	3.46E-01		-3.02E+00	2.43E-03		-4.09E+00	3.10E-04	Down	Unigene8467_All//gi|9802556|gb|AAF99758.1|AC003981_8//2.00E-22//F22013.13 [Arabidopsis thaliana]	Unigene8467_All//8.00E-24//AT1G08650| PPCK1 (PHOSPHOENOLPYRUVATE CARBOXYLASE KINASE); kinase/ protein serine/threonine kinase	Unigene8467_All//3.00E-69//TC173755		ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0006464//GO:0009267	nr +
Unigene84698_All	400	0.92	5.32	3.06	2.99	2.84	2.48	2.22	2.72	2.69	2.54E+00	2.15E-06	Up	1.74E+00	1.12E-02		-7.33E-02	8.95E-01		-2.67E-01	6.88E-01		2.92E-01	6.33E-01		2.77E-01	6.37E-01		Unigene84698_All//gi|255588992|ref|XP_002534791.1|//2.00E-10//conserved hypothetical protein [Ricinus communis] >gi|223524564|gb|EEF27591.1| conserved hypothetical protein [Ricinus communis]	Unigene84698_All//2.00E-06//AT5G13240| transcription regulator	Unigene84698_All//9.00E-135//TC155292				nr +
Unigene847_All	583	0.45	3.82	1.74	0.85	0.95	3.25	3.19	2.65	1.37	3.09E+00	5.42E-08	Up	1.95E+00	1.37E-02		1.46E-01	9.05E-01		1.93E+00	1.85E-04	Up	-2.67E-01	5.76E-01		-1.22E+00	3.47E-03		Unigene847_All//gi|79520288|ref|NP_197897.3|//6.00E-72//TAF5 (TBP-ASSOCIATED FACTOR 5); nucleotide binding / transcription regulator [Arabidopsis thaliana] >gi|39545918|gb|AAR28022.1| TAF5 [Arabidopsis thaliana]	Unigene847_All//4.00E-73//AT5G25150| TAF5 (TBP-ASSOCIATED FACTOR 5); nucleotide binding / transcription regulator	Unigene847_All//6.00E-137//ES832555		ko03022|Basal transcription factors		nr +
Unigene84711_All	224	0.00	0.00	0.00	4.00	0.00	0.81	0.94	0.37	0.36	null	null		null	null		-1.20E+01	1.21E-06	Down	-2.31E+00	5.78E-03		-1.34E+00	4.29E-01		-1.41E+00	3.79E-01		Unigene84711_All//gi|193248819|dbj|BAG50401.1|//1.00E-08//CCCH type zinc-finger transcription factor [Cardamine sp. SJM-2007]	Unigene84711_All//9.00E-10//AT4G29190| zinc finger (CCCH-type) family protein	Unigene84711_All//1.00E-15//TC175418	C3H			nr -
Unigene8472_All	490	1.49	2.59	0.65	0.20	1.05	0.37	1.21	1.11	5.45	7.90E-01	1.89E-01		-1.20E+00	1.80E-01		2.37E+00	5.64E-02		8.59E-01	6.93E-01		-1.24E-01	8.84E-01		2.17E+00	2.81E-08	Up	Unigene8472_All//gi|15232782|ref|NP_187599.1|//5.00E-81//ATB' BETA; protein phosphatase type 2A regulator [Arabidopsis thaliana] >gi|75097015|sp|Q04376.1|2A5B_ARATH RecName: Full=Serine/threonine protein phosphatase 2A 57 kDa regulatory subunit B' beta isoform; Short=PP2A, B' subunit, beta isoform; Short=AtB' beta >gi|6681331|gb|AAF23248.1|AC015985_6 B' regulatory subunit of PP2A (AtB' beta) [Arabidopsis thaliana] >gi|21606692|gb|AAB58901.1| B' regulatory subunit of PP2A [Arabidopsis thaliana]	Unigene8472_All//3.00E-73//AT3G09880| ATB' BETA; protein phosphatase type 2A regulator	Unigene8472_All//0.00E+00//DR462192			GO:0006464//GO:0008287//GO:0019888//GO:0023060//GO:0032559	nr +
Unigene84721_All	382	0.82	0.27	0.00	3.65	0.81	0.12	0.44	1.31	0.42	-1.63E+00	2.76E-01		-9.68E+00	4.87E-02		-2.17E+00	1.92E-04	Down	-4.95E+00	1.47E-07	Down	1.57E+00	1.18E-01		-8.56E-02	9.64E-01				Unigene84721_All//6.00E-34//ES825629					
Unigene84726_All	335	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.55	null	null		null	null		null	null		null	null		null	null		1.06E+01	6.13E-04	Up								
Unigene84773_All	236	3.10	4.29	0.00	5.07	4.09	3.25	0.18	0.18	0.00	4.68E-01	4.89E-01		-1.16E+01	4.12E-04	Down	-3.10E-01	6.07E-01		-6.39E-01	3.24E-01		-1.70E-02	9.97E-01		-7.49E+00	5.99E-01									
Unigene84775_All	275	1.52	0.55	0.39	4.53	4.13	2.14	2.00	0.76	0.00	-1.46E+00	2.34E-01		-1.97E+00	1.51E-01		-1.32E-01	8.17E-01		-1.08E+00	7.79E-02		-1.40E+00	1.34E-01		-1.10E+01	2.80E-04	Down								
Unigene84753_All	317	2.97	0.32	1.01	4.40	1.63	0.71	0.00	0.00	0.13	-3.22E+00	6.76E-04	Down	-1.56E+00	4.90E-02		-1.43E+00	8.64E-03		-2.63E+00	8.15E-05	Down	null	null		6.97E+00	6.35E-01		Unigene84753_All//gi|224062353|ref|XP_002300821.1|//4.00E-07//sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa] >gi|222842547|gb|EEE80094.1| sulfate/bicarbonate/oxalate exchanger and transporter sat-1 [Populus trichocarpa]	Unigene84753_All//1.00E-06//AT4G02700| SULTR3;2 (sulfate transporter 3;2); sulfate transmembrane transporter	Unigene84753_All//2.00E-42//TC168996				nr -
Unigene84761_All	735	0.43	1.24	0.14	1.02	1.31	0.37	0.12	0.91	3.14	1.54E+00	4.51E-02		-1.56E+00	3.29E-01		3.68E-01	6.24E-01		-1.46E+00	9.03E-02		2.98E+00	2.86E-03		4.77E+00	6.01E-14	Up	Unigene84761_All//gi|3643085|gb|AAC36698.1|//2.00E-87//protein phosphatase-2C [Mesembryanthemum crystallinum]	Unigene84761_All//2.00E-78//AT3G62260| protein phosphatase 2C, putative / PP2C, putative	Unigene84761_All//6.00E-162//gi|78342639|gb|DT562913.1|DT562913	DBP			nr +
Unigene8478_All	295	2.31	2.23	0.00	3.21	2.80	0.77	0.72	0.57	1.49	-4.63E-02	9.69E-01		-1.12E+01	7.63E-04	Down	-1.96E-01	8.04E-01		-2.07E+00	8.57E-03		-3.39E-01	8.11E-01		1.05E+00	2.98E-01									
Unigene84783_All	218	6.00	0.70	2.44	2.74	1.90	0.62	0.00	0.00	0.18	-3.11E+00	5.05E-05	Down	-1.30E+00	4.12E-02		-5.33E-01	5.61E-01		-2.14E+00	4.39E-02		null	null		7.51E+00	6.34E-01				Unigene84783_All//2.00E-08//DT464501					
Unigene8479_All	349	0.30	2.90	1.83	4.71	1.58	4.40	0.24	0.72	0.68	3.28E+00	3.79E-04	Up	2.61E+00	2.32E-02		-1.58E+00	1.53E-03		-9.83E-02	8.59E-01		1.57E+00	3.26E-01		1.50E+00	3.38E-01				Unigene8479_All//2.00E-09//CO101247					
Unigene848_All	902	6.15	10.00	5.25	13.20	13.17	10.77	11.11	6.16	5.08	7.02E-01	2.56E-04		-2.27E-01	4.06E-01		-3.10E-03	9.81E-01		-2.94E-01	9.02E-02		-8.50E-01	1.72E-07		-1.13E+00	7.08E-12	Down	Unigene848_All//gi|79520288|ref|NP_197897.3|//1.00E-98//TAF5 (TBP-ASSOCIATED FACTOR 5); nucleotide binding / transcription regulator [Arabidopsis thaliana] >gi|39545918|gb|AAR28022.1| TAF5 [Arabidopsis thaliana]	Unigene848_All//6.00E-95//AT5G25150| TAF5 (TBP-ASSOCIATED FACTOR 5); nucleotide binding / transcription regulator	Unigene848_All//0.00E+00//ES832555		ko03022|Basal transcription factors		nr +

Unigene8480_All	351	0.60	0.00	1.06	6.39	7.16	1.42	0.00	0.00	0.23	-9.22E+00	1.21E-01		8.33E-01	5.16E-01		1.65E-01	7.40E-01		-2.17E+00	4.72E-06	Down	null	null		7.83E+00	4.00E-01		Unigene8480_All//gi|159481082|ref|XP_001698611.1|//3.00E-07//hydroxyproline-rich cell wall protein [Chlamydomonas reinhardtii] >gi|158282351|gb|EDP08104.1| hydroxyproline-rich cell wall protein [Chlamydomonas reinhardtii]	Unigene8480_All//3.00E-05//AT2G13820| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein					nr +
Unigene8481_All	446	0.47	0.45	0.00	0.22	2.08	1.52	2.18	0.84	1.52	-4.62E-02	9.86E-01		-8.87E+00	1.44E-01		3.22E+00	5.79E-04	Up	2.77E+00	1.14E-02		-1.37E+00	3.41E-02		-5.22E-01	3.89E-01		Unigene8481_All//gi|6692688|gb|AAF24822.1|AC007592_15//3.00E-63//F12K11.17 [Arabidopsis thaliana]	Unigene8481_All//7.00E-55//AT1G06490| ATGSL07 (glucan synthase-like 7); 1,3-beta-glucan synthase/ transferase, transferring glycosyl groups				GO:0006074//GO:0035251//GO:0043234//GO:0044464	nr +
Unigene8482_All	683	0.00	2.15	7.87	0.00	0.55	0.40	0.00	0.00	0.00	1.11E+01	2.10E-08	Up	1.29E+01	6.06E-30	Up	9.12E+00	1.95E-02		8.63E+00	7.01E-02		null	null		null	null		Unigene8482_All//gi|113170499|ref|YP_717290.1|//9.00E-69//cytochrome b [Ostreococcus tauri] >gi|113170511|ref|YP_717302.1| cytochrome b [Ostreococcus tauri]	Unigene8482_All//7.00E-55//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.			ko00190|Oxidative phosphorylation	GO:0022900//GO:0043231//GO:0044425	nr -
Unigene8484_All	335	0.78	0.00	0.64	1.78	0.82	0.00	3.41	2.12	1.55	-9.61E+00	6.65E-02		-2.97E-01	8.31E-01		-1.12E+00	2.26E-01		-1.08E+01	7.69E-04	Down	-6.84E-01	2.37E-01		-1.14E+00	3.90E-02		Unigene8484_All//gi|297742287|emb|CBI34436.3|//1.00E-12//unnamed protein product [Vitis vinifera]						nr +
Unigene84847_All	259	1.01	0.59	0.00	2.31	0.00	0.70	0.33	0.16	0.00	-7.83E-01	6.19E-01		-9.98E+00	8.51E-02		-1.12E+01	1.78E-04	Down	-1.73E+00	9.02E-02		-1.02E+00	7.21E-01		-8.35E+00	3.54E-01				Unigene84847_All//3.00E-07//TC159521					
Unigene849_All	779	0.27	2.34	1.03	0.96	0.71	1.22	1.14	2.04	2.56	3.12E+00	1.05E-06	Up	1.93E+00	3.41E-02		-4.40E-01	5.85E-01		3.44E-01	6.49E-01		8.39E-01	7.48E-02		1.17E+00	3.87E-03		Unigene849_All//gi|79520288|ref|NP_197897.3|/4.00E-19//TAF5 (TBP-ASSOCIATED FACTOR 5); nucleotide binding / transcription regulator [Arabidopsis thaliana] >gi|39545918|gb|AAR28022.1| TAF5 [Arabidopsis thaliana]	Unigene849_All//2.00E-20//AT5G25150| TAF5 (TBP-ASSOCIATED FACTOR 5); nucleotide binding / transcription regulator	Unigene849_All//2.00E-41//ES832555		ko03022|Basal transcription factors	GO:0010468//GO:0043231	nr +
Unigene84913_All	984	1.54	0.26	0.43	1.92	0.80	2.34	0.30	0.25	0.24	-2.58E+00	7.04E-05	Down	-1.83E+00	2.74E-03		-1.26E+00	5.12E-03		2.83E-01	5.56E-01		-2.39E-01	8.39E-01		-3.08E-01	7.74E-01		Unigene84913_All//gi|223452359|gb|ACM89507.1|//1.00E-70//NAK-type protein kinase [Glycine max]	Unigene84913_All//8.00E-159//AT5G47070| protein kinase, putative	Unigene84913_All//8.00E-159//ES827016				nr +
Unigene84922_All	356	0.15	0.00	0.00	1.54	0.77	0.00	1.43	0.00	0.45	-7.20E+00	5.99E-01		-7.20E+00	6.14E-01		-9.92E-01	3.13E-01		-1.06E+01	1.52E-03		-1.05E+01	8.88E-04	Down	-1.67E+00	7.77E-02		Unigene84922_All//gi|42567571|ref|NP_195783.3|/3.00E-25//BRCA2B (BRCA2-LIKE B); protein binding / single-stranded DNA binding [Arabidopsis thaliana] >gi|31335962|emb|CAD32572.1| breast cancer susceptibility protein 2b [Arabidopsis thaliana]	Unigene84922_All//1.00E-22//AT5G01630| BRCA2B (BRCA2-LIKE B); protein binding / single-stranded DNA binding			ko03440|Homologous recombination		nr -
Unigene8493_All	273	86.05	75.54	55.01	166.96	161.20	134.99	562.03	242.35	290.40	-1.88E-01	1.22E-01		-6.46E-01	2.80E-08		-5.06E-02	5.95E-01		-3.07E-01	7.28E-05		-1.21E+00	1.16E-184	Down	-9.53E-01	3.72E-128			Unigene8493_All//8.00E-153//gi|109879589|gb|DW508559.1|DW508559				ESTscan +
Unigene8498_All	303	0.00	0.00	0.00	0.33	1.36	1.04	0.42	0.83	3.42	null	null		null	null		2.05E+00	1.47E-01		1.67E+00	3.08E-01		9.83E-01	5.17E-01		3.03E+00	6.50E-05	Up			Unigene8498_All//2.00E-15//ES847047					
Unigene84980_All	716	0.37	0.00	0.37	2.02	0.72	0.00	0.30	0.12	0.11	-8.51E+00	6.65E-02		2.54E-02	1.00E+00		-1.48E+00	5.57E-03		-1.10E+01	4.97E-09	Down	-1.34E+00	4.29E-01		-1.41E+00	3.79E-01		Unigene84980_All//gi|77552670|gb|AB495467.1|/3.00E-34//Leucine Rich Repeat family protein [Oryza sativa (japonica cultivar-group)]	Unigene84980_All//4.00E-17//AT2G26330| ER (ERECTA); transmembrane receptor protein kinase	Unigene84980_All//4.00E-163//gi|84168800|gb|DR457448.1|DR457448		ko04626|Plant-pathogen interaction	GO:0016740	nr +
Unigene84998_All	262	3.39	0.58	0.00	0.95	0.79	1.03	0.00	0.00	0.00	-2.55E+00	4.03E-03		-1.17E+01	6.29E-05	Down	-2.70E-01	8.22E-01		1.22E-01	9.44E-01		null	null		null	null									
Unigene85_All	1625	4.70	4.52	4.23	4.90	6.55	7.78	7.94	5.20	17.11	-5.62E-02	7.96E-01		-1.53E-01	5.27E-01		4.17E-01	1.54E-02		6.66E-01	1.82E-05		-6.11E-01	1.21E-05		1.11E+00	2.93E-30	Up	Unigene85_All//gi|115475810|ref|NP_001061501.1|//1.00E-155//Os08g0305300 [Oryza sativa Japonica Group] >gi|113623470|dbj|BAF23415.1| Os08g0305300 [Oryza sativa Japonica Group]	Unigene85_All//2.00E-138//AT5G19400| SMG7	Unigene85_All//0.00E+00//TC138860				nr +
Unigene8500_All	614	0.77	1.40	0.95	3.41	2.64	1.18	0.00	0.00	0.00	8.71E-01	2.45E-01		3.15E-01	7.19E-01		-3.70E-01	4.24E-01		-1.53E+00	8.31E-04	Down	null	null		null	null		Unigene8500_All//gi|51872287|gb|AAU12247.1|//1.00E-106//homeodomain protein HOX3 [Gossypium hirsutum]	Unigene8500_All//4.00E-67//AT1G73360| HDG11 (HOMEODOMAIN GLABROUS 11); DNA binding / transcription factor	Unigene8500_All//0.00E+00//TC155059	HB		GO:0000904//GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene8501_All	298	0.70	4.59	2.14	2.17	1.39	0.61	0.28	0.56	1.07	2.71E+00	1.29E-04	Up	1.61E+00	1.11E-01		-6.48E-01	4.60E-01		-1.84E+00	6.00E-02		9.83E-01	6.32E-01		1.91E+00	1.53E-01				Unigene8501_All//2.00E-138//CO080594					
Unigene8503_All	351	3.58	4.91	5.31	6.67	6.57	3.86	6.26	3.93	2.50	4.56E-01	3.78E-01		5.70E-01	2.50E-01		-2.12E-02	9.50E-01		-7.89E-01	6.03E-02		-6.73E-01	8.38E-02		-1.33E+00	5.61E-04	Down	Unigene8503_All//gi|261391554|emb|CAX11664.1|//2.00E-11//MADS domain MPF2-like transcription factor [Tubocapsicum anomalum] >gi|261391556|emb|CAX11665.1| MADS domain MPF2-like transcription factor [Tubocapsicum anomalum]	Unigene8503_All//1.00E-06//AT2G22540| SVP (SHORT VEGETATIVE PHASE); transcription factor/ translation repressor, nucleic acid binding	Unigene8503_All//1.00E-10//TC143124	MADS		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene8507_All	512	61.62	63.44	76.03	25.69	22.33	32.73	23.45	40.00	47.46	4.19E-02	6.88E-01		3.03E-01	7.22E-04		-2.02E-01	2.31E-01		3.50E-01	1.12E-02		7.70E-01	2.53E-12		1.02E+00	3.35E-23	Up	Unigene8507_All//gi|145534271|ref|NP_001078516.1|//1.00E-14//histone H3.2 [Arabidopsis thaliana]	Unigene8507_All//7.00E-16//AT4G40030| histone H3.2	Unigene8507_All//8.00E-99//gi|73864164|gb|DT466903.1|DT466903			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr -
Unigene8508_All	1073	3.66	1.28	5.81	0.00	0.00	0.00	0.00	0.00	0.19	-1.52E+00	3.62E-06	Down	6.67E-01	6.80E-03		null	null		null	null		null	null		7.54E+00	7.88E-02		Unigene8508_All//gi|115438542|ref|NP_001043565.1|//4.00E-49//Os01g0614300 [Oryza sativa Japonica Group] >gi|542962086|dbj|BAD61231.1| leaf senescence related protein-like [Oryza sativa Japonica Group] >gi|113533096|dbj|BAF05479.1| Os01g0614300 [Oryza sativa Japonica Group]	Unigene8508_All//2.00E-49//AT1G78710| unknown protein					nr +
Unigene85080_All	614	0.00	0.00	0.26	1.30	1.01	0.00	0.69	0.20	0.26	null	null		8.02E+00	2.34E-01		-3.63E-01	6.23E-01		-1.03E+01	4.90E-05	Down	-1.75E+00	1.23E-01		-1.41E+00	1.73E-01		Unigene85080_All//gi|224111692|ref|XP_002315943.1|//5.00E-12//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|222864983|gb|EEF02114.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene85080_All//8.00E-09//AT1G68550| AP2 domain-containing transcription factor, putative	Unigene85080_All//4.00E-110//DW489485	AP2-EREBP		GO:0006350	nr -
Unigene8509_All	493	1.06	0.41	0.22	1.62	0.35	1.28	3.17	0.93	1.13	-1.37E+00	1.96E-01		-2.30E+00	6.75E-02		-2.21E+00	7.35E-03		-3.34E-01	6.86E-01		-1.77E+00	4.93E-04	Down	-1.49E+00	1.74E-03									
Unigene851_All	5513	0.30	1.30	0.86	0.72	1.69	1.97	1.12	1.85	7.60	2.09E+00	6.17E-16	Up	1.50E+00	8.18E-07	Up	1.23E+00	2.53E-11	Up	1.44E+00	2.35E-15	Up	7.24E-01	5.79E-06		2.76E+00	1.17E-156	Up	Unigene851_All//gi|297726629|ref|NP_001175678.1|//1.00E-142//Os08g0544300 [Oryza sativa Japonica Group] >gi|255676617|dbj|BAH94406.1| Os08g0544300 [Oryza sativa Japonica Group]	Unigene851_All//1.00E-99//AT4G23160| protein kinase family protein	Unigene851_All//0.00E+00//TC165893			GO:0005488	nr +
Unigene8510_All	340	1.54	0.75	0.00	5.57	1.22	0.93	0.87	0.25	0.12	-1.05E+00	3.11E-01		-1.06E+01	4.73E-03		-2.20E+00	6.66E-06	Down	-2.58E+00	3.16E-06	Down	-1.82E+00	2.10E-01		-2.89E+00	6.75E-02		Unigene8510_All//gi|297738827|emb|CBI28072.3|//2.00E-17//unnamed protein product [Vitis vinifera]	Unigene8510_All//4.00E-65//AT5G19650| OFP8 (ARABIDOPSIS THALIANA OVATE FAMILY PROTEIN 8)	Unigene8510_All//1.00E-16//TC132458				nr -
Unigene8511_All	387	0.68	0.65	2.75	0.39	0.09	0.70	0.00	1.73	1.44	-4.64E-02	9.86E-01		2.03E+00	8.67E-03		-2.12E+00	3.84E-01		8.58E-01	6.30E-01		1.08E+01	7.63E-05	Up	1.05E+01	3.28E-04	Up			Unigene8511_All//4.00E-07//TC147550					
Unigene8513_All	533	0.20	0.00	0.00	0.93	1.23	0.34	2.94	1.25	0.22	-7.62E+00	3.65E-01		-7.62E+00	3.87E-01		3.93E-01	6.98E-01		-1.46E+00	1.93E-01		-1.23E+00	1.07E-02		-3.71E+00	1.85E-08	Down								
Unigene85132_All	273	2.87	0.00	1.56	1.46	0.00	0.66	0.00	0.00	0.00	-1.15E+01	1.09E-04	Down	-8.82E-01	2.95E-01		-1.05E+01	4.38E-03		-1.14E+00	3.79E-01		null	null		null	null		Unigene85132_All//gi|297822897|ref|XP_002879331.1|//3.00E-31//calcium-dependent protein kinase 24 [Arabidopsis lyrata subsp. lyrata] >gi|297325170|gb|EFH55590.1| calcium-dependent protein kinase 24 [Arabidopsis lyrata subsp. lyrata]	Unigene85132_All//3.00E-32//AT2G31500| CPK24; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0009536//GO:0032559//GO:0046872	nr -
Unigene85138_All	214	0.00	0.00	0.00	0.00	0.00	0.00	0.40	16.60	0.00	null	null		null	null		null	null		null	null		5.39E+00	4.75E-22	Up	-8.63E+00	3.53E-01		Unigene85138_All//1.00E-65//AT5G64530| XND1; transcription factor			NAC			
Unigene8514_All	704	0.30	0.14	0.30	0.85	0.49	0.77	4.56	1.31	1.36	-1.05E+00	5.63E-01		2.55E-02	1.00E+00		-7.96E-01	3.88E-01		-1.42E-01	8.79E-01		-1.81E+00	1.07E-07	Down	-1.75E+00	1.11E-07	Down			Unigene8514_All//0.00E+00//gi|13352683|gb|BG443031.1|BG443031					
Unigene8515_All	1467	0.07	0.10	0.00	0.51	0.47	0.18	2.13	1.37	6.16	5.39E-01	7.77E-01		-6.16E+00	3.87E-01		-1.17E-01	8.62E-01		-1.46E+00	9.03E-02		-6.41E-01	4.19E-02		1.53E+00	1.39E-16	Up	Unigene8515_All//gi|297829012|ref|XP_002882388.1|//3.00E-13//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328228|gb|EFH58647.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8515_All//2.00E-15//AT3G04970| zinc finger (DHHC type) family protein	Unigene8515_All//1.00E-10//CK640438			GO:0008152//GO:0016628//GO:0031410//GO:0046914	nr +
Unigene85172_All	477	2.19	0.00	1.12	2.72	2.02	0.00	0.53	0.00	0.08	-1.11E+01	3.80E-06	Down	-9.75E-01	1.67E-01		-4.26E-01	4.87E-01		-1.14E+01	4.24E-08	Down	-9.05E+00	4.02E-02		-2.67E+00	1.15E-01		Unigene85172_All//gi|18399836|ref|NP_566442.1|//1.00E-10//myb family transcription factor [Arabidopsis thaliana] >gi|42572405|ref|NP_974298.1| myb family transcription factor [Arabidopsis thaliana]		Unigene85172_All//2.00E-127//TC134097				nr -
Unigene8518_All	317	1.98	1.12	0.67	2.51	0.98	1.14	2.40	0.13	1.26	-8.24E-01	3.75E-01		-1.56E+00	1.29E-01		-1.36E+00	7.73E-02		-1.14E+00	1.63E-01		-4.19E+00	1.57E-04	Down	-9.34E-01	1.82E-01									
Unigene85181_All	447	0.00	0.00	0.00	3.23	0.69	1.52	0.28	0.00	0.45	null	null		null	null		-2.22E+00	1.07E-04	Down	-1.09E+00	5.14E-02		-8.15E+00	2.33E-01		6.51E-01	6.65E-01									
Unigene85184_All	480	0.00	0.42	0.33	4.15	4.66	1.22	0.79	0.44	0.25	8.72E+00	1.34E-01		8.38E+00	2.34E-01		1.68E-01	7.56E-01		-1.76E+00	2.66E-04	Down	-8.65E-01	4.41E-01		-1.67E+00	1.40E-01		Unigene85184_All//gi|224117086|ref|XP_002331783.1|//1.00E-06//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222822242|gb|EEE70719.1| cc-nbs-lrr resistance protein [Populus trichocarpa]		Unigene85184_All//4.00E-17//ES850138				nr -
Unigene85189_All	214	0.00	0.00	0.00	0.70	0.16	0.84	2.96	0.20	0.19	null	null		null	null		-2.12E+00	3.84E-01		2.74E-01	9.03E-01		-3.92E+00	9.80E-04	Down	-3.99E+00	5.82E-04	Down			Unigene85189_All//4.00E-55//TC177920					
Unigene8519_All	243	10.55	4.80	3.29	4.71	5.10	2.23	0.00	0.00	0.00	-1.14E+00	4.51E-03		-1.68E+00	1.42E-04	Down	1.14E-01	8.71E-01		-1.08E+00	9.65E-02		null	null		null	null				Unigene8519_All//1.00E-132//TC148017					
Unigene85196_All	226	0.00	0.00	0.00	0.00	0.00	0.40	2.62	0.00	0.18	null	null		null	null		null	null		8.64E+00	4.69E-01		-1.14E+01	2.39E-04	Down	-3.89E+00	1.09E-03				Unigene85196_All//5.00E-55//TC173669					nr -
Unigene8522_All	756	0.00	0.00	0.00	0.00	0.09	0.00	1.34	5.25	22.61	null	null		null	null		6.51E+00	5.99E-01		null	null		1.97E+00	2.32E-10	Up	4.07E+00	9.85E-91	Up	Unigene8522_All//gi|255559989|ref|XP_002521013.1|//2.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223539850|gb|EEF41430.1| conserved hypothetical protein [Ricinus communis]		Unigene8522_All//9.00E-44//TC152400				nr +
Unigene85220_All	712	0.00	0.00	0.00	1.68	0.19	0.51	0.12	0.00	0.06	null	null		null	null		-3.12E+00	1.54E-05	Down	-1.73E+00	8.51E-03		-6.89E+00	3.97E-01		-1.09E+00	6.73E-01		Unigene85220_All//gi|284504578|gb|ADB90479.1|//5.00E-80//pectate lyase [Gossypium barbadense]	Unigene85220_All//3.00E-75//AT4G24780| pectate lyase family protein	Unigene85220_All//3.00E-22//gi|13352342|gb|BG442690.1|BG442690		ko00040|Pentose and glucuronate interconversions	GO:0016837	nr -
Unigene8524_All	518	0.00	0.00	0.00	0.00	0.13	0.17	3.75	1.13	2.15	null	null		null	null		7.06E+00	5.99E-01		7.45E+00	4.69E-01		-1.73E+00	1.00E-04	Down	-8.02E-01	4.39E-02		Unigene8524_All//sp|Q81DD2|SMC2_PLAF7//6.00E-06//Structural maintenance of chromosomes protein 2 OS=Plasmodium falciparum (isolate 3D7) GN=MAL13P1.96 PE=3 SV=1		Unigene8524_All//2.00E-145//DN801291				swissprot -

Unigene85248_All	253	36.60	31.64	25.47	201.82	218.59	66.76	54.48	6.94	18.42	-2.10E-01	3.05E-01		-5.23E-01	8.06E-03		1.15E-01	1.45E-01		-1.60E+00	4.22E-83	Down	-2.97E+00	3.67E-55	Down	-1.56E+00	7.38E-26	Down			Unigene85248_All//3.00E-75//gi|164278167|gb|EV487459.1|EV487459				
Unigene8525_All	644	0.41	0.16	0.25	0.77	0.32	1.19	0.85	1.36	2.66	-1.37E+00	3.82E-01		-7.11E-01	6.21E-01		-1.27E+00	2.22E-01		6.24E-01	4.81E-01		6.75E-01	3.28E-01		1.64E+00	4.04E-04	Up	Unigene8525_All//gi|75178969|sp|Q9LPX2.1|PPR39_ARATH//2.00E-33//RecName: Full=Pentatricopeptide repeat-containing protein At1g12775, mitochondrial; Flags: Precursor	Unigene8525_All//7.00E-35//AT1G12775| LOCATED IN: mitochondrion; EXPRESSED IN: 7 plant structures; EXPRESSED DURING: F mature embryo stage, petal differentiation and expansion stage, D bilateral stage, E expanded cotyledon stage; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT1G12300.1); Has 27792 Blast hits to 6269 proteins in 197 species: Archae - 2; Bacteria - 23; Metazoa - 895; Fungi - 767; Plants - 24554; Viruses - 0; Other Eukaryotes - 1551 (source: NCBI BLink).	Unigene8525_All//0.00E+00//TC177459				nr +
Unigene8528_All	414	0.00	0.00	0.00	0.72	0.67	0.00	3.57	3.53	0.87	null	null		null	null		-1.18E-01	9.00E-01		-9.50E+00	3.97E-02		-1.66E-02	1.01E+00		-2.05E+00	1.05E-04	Down			Unigene8528_All//8.00E-52//FL577669				
Unigene85281_All	218	0.00	0.00	0.00	3.88	0.32	0.00	0.39	0.19	0.00	null	null		null	null		-3.62E+00	1.47E-04	Down	-1.19E+01	2.43E-05	Down	-1.02E+00	7.21E-01		-8.60E+00	3.53E-01									
Unigene8529_All	427	0.37	1.07	1.00	3.03	1.61	0.32	0.40	0.20	0.19	1.54E+00	1.96E-01		1.44E+00	2.52E-01		-9.11E-01	1.09E-01		-3.26E+00	1.98E-05	Down	-1.02E+00	6.12E-01		-1.09E+00	5.51E-01				Unigene8529_All//5.00E-07//gi|78327467|gb|DT547741.1|DT547741				
Unigene85291_All	455	0.69	1.00	0.35	1.09	1.67	1.19	1.67	0.09	0.70	5.39E-01	6.02E-01		-9.75E-01	5.05E-01		6.05E-01	5.14E-01		1.22E-01	9.21E-01		-4.19E+00	1.57E-04	Down	-1.26E+00	7.70E-02		Unigene85291_All//gi|7019653|emb|CAB75754.1|//1.00E-67//spliceosomal-like protein [Arabidopsis thaliana] >gi|7019655|emb|CAB75756.1| spliceosomal-like protein [Arabidopsis thaliana]	Unigene85291_All//7.00E-69//AT3G55200| splicing factor, putative			ko03040|Spliceosome	GO:0005488//GO:0009536	nr +
Unigene85298_All	226	1.62	9.64	8.48	5.95	3.66	2.20	1.31	1.85	0.88	2.57E+00	1.30E-06	Up	2.39E+00	3.03E-05	Up	-7.03E-01	2.18E-01		-1.44E+00	1.59E-02		4.98E-01	6.32E-01		-5.71E-01	6.27E-01				Unigene85298_All//2.00E-115//gi|11200225|gb|BF269230.1|BF269230				
Unigene853_All	5843	5.87	2.16	3.21	10.63	9.25	9.75	5.57	5.04	3.98	-1.44E+00	1.84E-44	Down	-8.71E-01	2.40E-19		-2.01E-01	1.88E-03		-1.24E-01	9.30E-02		-1.44E-01	1.26E-01		-4.85E-01	4.04E-09		Unigene853_All//gi|15219915|ref|NP_173675.1|//0.00E+00//C2 domain-containing protein [Arabidopsis thaliana] >gi|6587829|gb|AAF18518.1|AC006551_4 Highly similar to phosphoribosylanthranilate transferase [Arabidopsis thaliana]	Unigene853_All//0.00E+00//AT1G22610| C2 domain-containing protein	Unigene853_All//0.00E+00//TC158689			GO:0009536	nr +
Unigene8530_All	1342	0.66	0.30	0.44	0.67	0.59	0.71	1.17	0.97	3.59	-1.13E+00	1.30E-01		-6.03E-01	4.18E-01		-1.79E-01	8.15E-01		8.10E-02	9.31E-01		-2.72E-01	6.13E-01		1.62E+00	5.70E-10	Up	Unigene8530_All//gi|297843788|ref|XP_002889775.1|//9.00E-28//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297335617|gb|EFH66034.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene8530_All//7.00E-29//AT1G09900| pentatricopeptide (PPR) repeat-containing protein	Unigene8530_All//0.00E+00//DT463765				nr -
Unigene85302_All	245	0.21	0.00	0.43	2.44	0.42	0.00	0.17	0.34	0.00	-7.74E+00	5.99E-01		1.03E+00	7.00E-01		-2.53E+00	1.36E-02		-1.13E+01	7.69E-04	Down	9.83E-01	7.28E-01		-7.43E+00	5.99E-01		Unigene85302_All//gi|222424286|dbj|BAH20100.1|//2.00E-17//AT5G57110 [Arabidopsis thaliana]	Unigene85302_All//6.00E-19//AT5G57110| ACA8 (AUTOINHIBITED CA2+ -ATPASE, ISOFORM 8); calcium-transporting ATPase/ calmodulin binding / protein self-association			GO:0003006//GO:0005515//GO:0009206//GO:0009566//GO:0019829//GO:0031224//GO:0032559//GO:0046873//GO:0046914//GO:0048229//GO:0048513//GO:0051707//GO:0070838	nr +
Unigene85333_All	394	0.00	0.00	0.00	3.29	0.70	0.00	0.00	0.00	0.00	null	null		null	null		-2.23E+00	2.69E-04	Down	-1.17E+01	4.24E-08	Down	null	null		null	null		Unigene85333_All//gi|282161430|gb|ADA79674.1|//6.00E-26//shaker-like potassium channel 1 [Populus euphratica]	Unigene85333_All//2.00E-19//AT2G26650| AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel			GO:0000166//GO:0005249//GO:0006970//GO:0030001//GO:0031224//GO:0043231//GO:0048588	nr +
Unigene8535_All	993	0.00	0.00	0.00	0.00	0.00	0.00	1.83	1.94	0.00	null	null		null	null		null	null		null	null		8.07E-02	8.56E-01		-1.08E+01	2.03E-13	Down	Unigene8535_All//sp|Q8CID0|CSR2B_MOUSE//6.00E-06//Cysteine-rich protein 2-binding protein OS=Mus musculus GN=Csrp2bp PE=2 SV=2						swissprot +
Unigene85352_All	208	0.00	0.49	0.00	1.20	0.33	0.00	18.09	1.21	0.57	8.93E+00	3.79E-01		null	null		-1.85E+00	2.75E-01		-1.02E+01	7.28E-02		-3.91E+00	1.63E-19	Down	-4.98E+00	1.86E-23	Down								
Unigene8536_All	260	0.00	1.56	0.00	0.00	2.52	0.00	0.00	0.16	1.07	1.06E+01	1.34E-02		null	null		1.13E+01	4.92E-04	Up	null	null		7.33E+00	6.24E-01		1.01E+01	2.43E-02									
Unigene8537_All	672	0.00	2.04	0.32	0.30	1.13	0.13	0.06	0.87	0.77	1.10E+01	7.76E-08	Up	8.31E+00	1.37E-01		1.93E+00	3.36E-02		-1.14E+00	5.67E-01		3.79E+00	2.07E-03		3.62E+00	4.19E-03		Unigene8537_All//gi|5690095|emb|CAB51950.1|//3.00E-12//transposase related protein [Zea mays]	Unigene8537_All//2.00E-09//AT1G64260| zinc finger protein-related					nr -
Unigene8538_All	280	3.18	0.00	0.38	3.56	3.94	4.03	1.66	0.90	1.71	-1.16E+01	2.85E-05	Down	-3.06E+00	2.25E-03		1.45E-01	8.37E-01		1.81E-01	7.84E-01		-8.91E-01	3.83E-01		3.97E-02	9.76E-01									
Unigene8539_All	342	1.07	0.44	1.09	1.17	1.41	0.26	2.23	0.12	0.82	-1.27E+00	3.35E-01		2.54E-02	1.00E+00		2.75E-01	8.19E-01		-2.14E+00	1.26E-01		-4.19E+00	1.57E-04	Down	-1.45E+00	4.46E-02				Unigene8539_All//5.00E-22//TC176706				
Unigene85401_All	430	0.85	0.82	0.74	3.24	1.12	0.21	0.88	0.39	0.56	-4.61E-02	9.82E-01		-1.97E-01	8.65E-01		-1.53E+00	5.22E-03		-3.95E+00	1.12E-06	Down	-1.19E+00	3.09E-01		-6.71E-01	5.30E-01		Unigene85401_All//gi|30698937|ref|NP_177485.2|//3.00E-28//sec34-like family protein [Arabidopsis thaliana] >gi|186495067|ref|NP_001117595.1| sec34-like family protein [Arabidopsis thaliana]	Unigene85401_All//1.00E-29//AT1G73430| sec34-like family protein	Unigene85401_All//0.00E+00//ES841214			GO:0009536//GO:0015031//GO:0044431	nr +
Unigene85405_All	449	0.00	0.00	0.00	4.22	1.30	1.01	0.75	0.37	0.00	null	null		null	null		-1.69E+00	2.45E-04	Down	-2.07E+00	6.29E-05	Down	-1.02E+00	3.99E-01		-9.56E+00	8.13E-03		Unigene85405_All//gi|115455585|ref|NP_001051393.1|//1.00E-27//Os03g0769000 [Oryza sativa Japonica Group] >gi|113549864|dbj|BAF13307.1| Os03g0769000 [Oryza sativa Japonica Group]	Unigene85405_All//4.00E-34//AT5G66600| unknown protein	Unigene85405_All//2.00E-166//TC172096				nr -
Unigene85407_All	415	0.00	0.00	0.00	0.24	0.00	0.00	1.32	0.60	5.95	null	null		null	null		-7.91E+00	3.07E-01		-7.91E+00	3.91E-01		-1.13E+00	2.18E-01		2.17E+00	1.07E-07	Up	Unigene85407_All//gi|224071385|ref|XP_002303434.1|//4.00E-26//jumonji domain protein [Populus trichocarpa] >gi|222840866|gb|EEE78413.1| jumonji domain protein [Populus trichocarpa]	Unigene85407_All//1.00E-15//AT5G46910| transcription factor jumonji (jmj) family protein	Unigene85407_All//5.00E-84//TC179033			GO:0009743//GO:0043231	nr -
Unigene8541_All	575	0.00	46.97	10.00	0.00	0.00	0.00	0.00	0.00	1.55E+01	1.24E-155	Up	1.33E+01	4.80E-32	Up	null	null		null	null		null	null		null	null		Unigene8541_All//gi|226530763|ref|NP_001151702.1|//7.00E-94//60S ribosomal protein L11 [Zea mays] >gi|195649157|gb|ACG44046.1| 60S ribosomal protein L11 [Zea mays]	Unigene8541_All//2.00E-70//AT2G42740| RPL16A; structural constituent of ribosome	Unigene8541_All//8.00E-16//DW505802		ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0015934//GO:0031981	nr -
Unigene85427_All	475	0.00	0.00	0.00	2.20	0.29	0.19	1.16	0.53	0.34	null	null		null	null		-2.92E+00	1.21E-04	Down	-3.53E+00	9.33E-05	Down	-1.13E+00	2.18E-01		-1.79E+00	5.06E-02		Unigene85427_All//gi|147823314|emb|CAN77450.1|//7.00E-15//hypothetical protein [Vitis vinifera]		Unigene85427_All//1.00E-23//ES792407			GO:0005488	nr -
Unigene8545_All	359	0.00	0.00	0.00	0.00	0.00	0.00	13.78	2.44	2.00	null	null		null	null		null	null		null	null		-2.49E+00	7.65E-17	Down	-2.79E+00	1.34E-19	Down								
Unigene85450_All	212	0.00	0.24	3.27	1.41	0.00	0.00	0.60	0.00	0.19	7.90E+00	6.07E-01		1.17E+01	6.09E-04	Up	-1.05E+01	2.01E-02		-1.05E+01	3.97E-02		-9.22E+00	2.33E-01		-1.67E+00	4.75E-01				Unigene85450_All//2.00E-07//ES798310				
Unigene85470_All	210	0.00	0.00	0.51	5.22	0.00	0.43	0.20	0.00	0.00	null	null		8.99E+00	3.87E-01		-1.23E+01	4.06E-08	Down	-3.60E+00	5.02E-05	Down	-7.65E+00	6.41E-01		-7.65E+00	5.99E-01									
Unigene85482_All	214	0.00	0.47	0.00	2.33	0.00	0.42	0.79	0.00	0.37	8.89E+00	3.79E-01		null	null		-1.12E+01	8.97E-04	Down	-2.46E+00	4.82E-02		-9.63E+00	1.33E-01		-1.09E+00	5.51E-01		Unigene85482_All//gi|225465657|ref|XP_002271972.1|//2.00E-06//PREDICTED: hypothetical protein [Vitis vinifera]		Unigene85482_All//3.00E-105//ES833470				nr +
Unigene85484_All	229	0.23	0.00	0.47	0.00	0.00	0.00	0.00	2.56	0.70	-7.84E+00	5.99E-01		1.03E+00	7.00E-01		null	null		null	null		1.13E+01	2.81E-04	Up	9.44E+00	1.39E-01		Unigene85484_All//gi|255544726|ref|XP_002513424.1|//9.00E-07//conserved hypothetical protein [Ricinus communis] >gi|223547332|gb|EEF48827.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene85508_All	225	1.63	0.68	1.42	4.43	2.45	4.42	7.52	1.30	2.66	-1.27E+00	3.35E-01		-1.97E-01	8.65E-01		-8.55E-01	2.05E-01		-3.90E-03	9.88E-01		-2.53E+00	2.71E-06	Down	-1.50E+00	9.76E-04	Down	Unigene85508_All//gi|13877126|gb|AAK43709.1|AF358665_1//1.00E-07//ribosomal protein L32 [Mercurialis annua] >gi|13899053|gb|AAK48948.1|AF370436_1 ribosomal protein L32 [Mercurialis annua] >gi|13899055|gb|AAK48949.1|AF370437_1 ribosomal protein L32 [Mercurialis annua] >gi|13899057|gb|AAK48950.1|AF370438_1 ribosomal protein L32 [Mercurialis annua]		Unigene85508_All//6.00E-70//TC152244		ko03010|Ribosome		nr -
Unigene8553_All	604	1.91	0.34	1.41	2.64	1.48	0.90	1.68	0.97	0.59	-2.51E+00	8.99E-04	Down	-4.34E-01	5.09E-01		-8.32E-01	9.85E-02		-1.56E+00	4.06E-03		-7.94E-01	2.02E-01		-1.50E+00	1.41E-02				Unigene8553_All//2.00E-22//C0131759				
Unigene8556_All	420	0.75	0.24	0.00	0.00	0.41	0.75	4.43	1.79	110.98	-1.63E+00	2.76E-01		-9.55E+00	4.87E-02		8.68E+00	2.26E-01		9.56E+00	4.07E-02		-1.31E+00	2.76E-03		4.65E+00	6.21E-269	Up	Unigene8556_All//gi|212717149|gb|AC|37416.1|//3.00E-45//stress-induced receptor-like kinase [Glycine max]	Unigene8556_All//2.00E-28//AT1G66980| protein kinase family protein / glycerophosphoryl diester phosphodiesterase family protein	Unigene8556_All//6.00E-127//TC165373		ko04626|Plant-pathogen interaction	GO:0003676//GO:0004672//GO:0006464//GO:0032559//GO:0043229	nr -
Unigene8557_All	241	4.78	7.36	3.98	5.99	15.15	10.49	16.84	31.74	32.23	6.24E-01	2.09E-01		-2.64E-01	6.64E-01		1.34E+00	2.65E-05	Up	8.08E-01	4.55E-02		9.14E-01	1.45E-06		9.37E-01	4.17E-07		Unigene8557_All//gi|297849766|ref|XP_002892764.1|//2.00E-31//phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338606|gb|EFH69023.1| phosphatidylinositol 3-and 4-kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8557_All//2.00E-32//AT1G13640| phosphatidylinositol 3- and 4-kinase family protein	Unigene8557_All//3.00E-118//TC135567			GO:0016772	nr -
Unigene8559_All	275	0.76	4.24	4.26	0.36	2.13	0.82	0.00	0.30	0.00	2.48E+00	9.79E-04	Up	2.48E+00	1.35E-03		2.55E+00	2.84E-02		1.18E+00	5.48E-01		8.25E+00	3.97E-01		null	null		Unigene8559_All//gi|3319353|gb|AAC26242.1|//2.00E-18//contains similarity to copper-binding proteins [Arabidopsis thaliana] >gi|45752728|gb|AAS76262.1| At5g26330 [Arabidopsis thaliana]	Unigene8559_All//7.00E-20//AT5G26330| plastocyanin-like domain-containing protein / mavicyanin, putative	Unigene8559_All//3.00E-149//TC138578			GO:0031224//GO:0046914	nr +
Unigene85590_All	347	0.15	2.04	0.61	3.73	1.89	0.52	2.07	0.48	2.87	3.76E+00	2.36E-03		2.03E+00	3.59E-01		-9.85E-01	8.32E-02		-2.84E+00	7.63E-05	Down	-2.10E+00	1.25E-02		4.71E-01	4.38E-01		Unigene85590_All//gi|297607012|ref|NP_001059355.2|//8.00E-09//Os07g0273700 [Oryza sativa Japonica Group] >gi|255677660|dbj|BAF21269.2| Os07g0273700 [Oryza sativa Japonica Group]	Unigene85590_All//1.00E-06//AT3G14460| disease resistance protein (NBS-LRR class), putative					nr +
Unigene85596_All	221	0.24	0.00	0.00	0.90	0.00	0.00	1.34	5.86	3.24	-7.89E+00	5.99E-01		-7.89E+00	6.13E-01		-9.82E+00	8.35E-02		-9.82E+00	1.32E-01		2.13E+00	3.40E-04	Up	1.28E+00	8.79E-02									
Unigene8560_All	474	0.22	0.43	0.00	0.63	0.36	0.57	3.66	3.35	1.01	9.54E-01	6.19E-01		-7.79E+00	3.87E-01		-7.96E-01	5.56E-01		-1.42E-01	9.20E-01		-1.26E-01	7.79E-01		-1.86E+00	7.67E-05	Down								
Unigene8561_All	2117	0.00	13.00	4.02	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.44E-158	Up	1.20E+01	1.02E-47	Up	null	null		null	null		null	null		null	null		Unigene8561_All//gi|18411187|ref|NP_565139.1|//2.00E-24//5-formyltetrahydrofolate cyclo-ligase family protein [Arabidopsis thaliana] >gi|90092282|gb|ABD85154.1| At1g76730 [Arabidopsis thaliana]	Unigene8561_All//1.00E-25//AT1G76730| 5-formyltetrahydrofolate cyclo-ligase family protein			ko00670|One carbon pool by folate	GO:0009536	nr -

Unigene85615_All	595	0.18	0.17	0.72	0.59	0.41	1.06	2.49	0.49	0.67	-4.67E-02	9.85E-01		2.03E+00	1.39E-01		-5.33E-01	6.45E-01		8.59E-01	3.89E-01		-2.34E+00	3.57E-05	Down	-1.89E+00	2.45E-04	Down	Unigene85615_All//gi|15234750|ref|NP_193324.1|//5.00E-45//binding [Arabidopsis thaliana]	Unigene85615_All//4.00E-45//AT4G15890| binding					nr +
Unigene8562_All	349	1.35	2.76	2.29	1.71	1.48	0.00	0.24	0.12	0.00	1.03E+00	1.45E-01		7.62E-01	3.62E-01		-2.11E-01	8.22E-01		-1.07E+01	7.69E-04	Down	-1.02E+00	7.21E-01		-7.92E+00	3.53E-01				Unigene8562_All//7.00E-18//DW520138					
Unigene8565_All	295	11.35	12.02	15.52	16.38	14.82	20.21	61.77	57.10	29.85	8.30E-02	7.99E-01		4.52E-01	1.37E-01		-1.44E-01	6.27E-01		3.03E-01	2.54E-01		-1.14E-01	3.98E-01		-1.05E+00	1.24E-18	Down	Unigene8565_All//gi|18425101|ref|NP_569038.1|//1.00E-13//DGL1; dolichyl-diphosphooligosaccharide-protein glycotransferase [Arabidopsis thaliana] >gi|16226812|gb|AAL16268.1|AF428338_1 AT5g66680/MSN2_7 [Arabidopsis thaliana]	Unigene8565_All//4.00E-15//AT5G66680| DGL1; dolichyl-diphosphooligosaccharide-protein glycotransferase	Unigene8565_All//2.00E-156//gi|73851864|gb|DT460884.1|DT460884		ko04141|Protein processing in endoplasmic reticulum//ko00510|N-Glycan biosynthesis	GO:0000902//GO:0004576//GO:0005618//GO:0005789//GO:0006487//GO:0007047//GO:0009250//GO:0031410//GO:0031981	nr +
Unigene8567_All	483	0.00	0.21	0.00	0.72	1.35	0.65	22.67	7.27	1.90	7.71E+00	3.79E-01		null	null		9.08E-01	3.42E-01		-1.41E-01	9.12E-01		-1.64E+00	1.85E-21	Down	-3.58E+00	7.44E-54	Down			Unigene8567_All//3.00E-104//DW510669					
Unigene8568_All	464	1.24	0.76	2.87	7.62	3.86	2.34	0.73	0.81	3.95	-6.98E-01	4.49E-01		1.21E+00	5.06E-02		-9.82E-01	1.34E-03		-1.71E+00	7.60E-07	Down	1.53E-01	8.90E-01		2.44E+00	1.14E-06	Up	Unigene8568_All//gi|38345765|emb|CAE03465.2|//4.00E-18//OSJNBa0083N12.2 [Oryza sativa (japonica cultivar-group)]	Unigene8568_All//3.00E-16//AT3G03140| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: PWWP (InterPro:IPR000313); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G21295.1); Has 422 Blast hits to 270 proteins in 77 species: Archae - 0; Bacteria - 12; Metazoa - 232; Fungi - 62; Plants - 66; Viruses - 0; Other Eukaryotes - 50 (source: NCBI BLink).	Unigene8568_All//2.00E-43//DW507622					nr -
Unigene8569_All	291	0.00	0.00	0.00	1.03	0.00	0.31	102.58	254.08	162.50	null	null		null	null		-1.00E+01	2.01E-02		-1.73E+00	2.89E-01		1.31E+00	3.00E-100	Up	6.64E-01	7.90E-22				Unigene8569_All//1.00E-15//gi|109836098|gb|DW234659.1|DW234659					
Unigene8570_All	552	0.00	1.19	0.96	0.45	1.56	0.57	0.00	0.00	0.00	1.02E+01	6.20E-04	Up	9.91E+00	3.98E-03		1.79E+00	2.95E-02		3.44E-01	7.96E-01		null	null		null	null									ESTscan -
Unigene8579_All	426	0.25	0.12	0.00	4.33	1.70	0.64	3.37	1.08	0.65	-1.05E+00	6.82E-01		-7.94E+00	3.86E-01		-1.35E+00	3.21E-03		-2.77E+00	1.70E-06	Down	-1.64E+00	1.74E-03		-2.37E+00	2.52E-05	Down			Unigene8579_All//2.00E-135//TC179212					ESTscan -
Unigene85790_All	268	3.12	0.00	2.78	3.16	1.16	1.52	0.47	0.00	0.00	-1.16E+01	5.56E-05	Down	-1.67E-01	8.15E-01		-1.45E+00	5.13E-02		-1.06E+00	1.81E-01		-8.89E+00	2.33E-01		-8.89E+00	1.98E-01									
Unigene85815_All	235	0.22	0.00	0.00	3.18	0.00	0.19	0.54	0.00	0.00	-7.80E+00	5.99E-01		-7.80E+00	6.13E-01		-1.16E+01	1.50E-05	Down	-4.05E+00	7.75E-04	Down	-9.08E+00	2.33E-01		-9.08E+00	1.98E-01		Unigene85815_All//gi|297839569|ref|XP_002887666.1|//2.00E-09//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333507|gb|EFH63925.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene85815_All//1.00E-10//AT1G77010| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene8582_All	222	0.00	2.05	0.96	0.45	0.78	1.42	0.19	0.94	6.82	1.10E+01	7.34E-03		9.91E+00	1.37E-01		7.89E-01	7.69E-01		1.67E+00	3.08E-01		2.30E+00	2.39E-01		5.16E+00	1.25E-09	Up			Unigene8582_All//5.00E-58//TC165305					
Unigene85836_All	212	0.00	0.00	0.00	0.00	0.00	0.00	2.19	1.18	37.21	null	null		null	null		null	null		null	null		-8.91E-01	3.83E-01		4.08E+00	3.13E-42	Up	Unigene85836_All//gi|18412959|ref|NP_567300.1|//2.00E-08//IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase [Arabidopsis thaliana] >gi|5732060|gb|AAD48959.1|AF147263_1 contains similarity to Pfam families PF00106 (short chain dehydrogenase; score=151.7, E=1.3e-41, N=1) and PF00678 (Short chain dehydrogenase/reductase C-terminus; score=48.9, E=1.1e-10, N=1) [Arabidopsis thaliana] >gi|7267313|emb|CAB81095.1| AT4g05530 [Arabidopsis thaliana]	Unigene85836_All//1.00E-09//AT4G05530| IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase	Unigene85836_All//6.00E-11//ES836156		ko04146|Peroxisome		nr +
Unigene8584_All	299	0.35	0.00	0.00	3.50	1.38	1.21	2.83	0.14	2.00	-8.45E+00	3.65E-01		-8.45E+00	3.86E-01		-1.34E+00	3.95E-02		-1.53E+00	2.88E-02		-4.34E+00	4.55E-05	Down	-5.01E-01	4.47E-01		Unigene8584_All//gi|15237182|ref|NP_200644.1|//9.00E-07//ATOFP3 [Arabidopsis thaliana] >gi|67633890|gb|AAY78869.1| ovate family protein [Arabidopsis thaliana]	Unigene8584_All//4.00E-08//AT5G58360| ATOFP3	Unigene8584_All//6.00E-15//TC141356			GO:0001558//GO:0030528//GO:0031981//GO:0043232	nr -
Unigene85861_All	227	0.23	0.45	0.23	0.66	0.30	0.80	3.35	0.00	0.00	9.54E-01	7.23E-01		2.54E-02	9.91E-01		-1.12E+00	5.81E-01		2.74E-01	9.03E-01		-1.17E+01	1.67E-05	Down	-1.17E+01	8.87E-06	Down			Unigene85861_All//2.00E-85//gi|78339824|gb|DT560098.1|DT560098					
Unigene85885_All	346	0.30	0.00	0.00	2.88	0.50	2.61	1.10	0.60	1.73	-8.24E+00	3.63E-01		-8.24E+00	3.86E-01		-2.53E+00	6.75E-04	Down	-1.41E-01	8.36E-01		-8.65E-01	4.41E-01		6.51E-01	4.23E-01									ESTscan +
Unigene85888_All	221	0.00	0.00	0.00	0.00	0.00	0.00	2.49	0.00	0.18	null	null		null	null		null	null		null	null		-1.13E+01	4.61E-04	Down	-3.79E+00	2.03E-03		Unigene85888_All//gi|30684813|ref|NP_188445.2|//9.00E-07//transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|27808590|gb|AAO24575.1| At3g18170 [Arabidopsis thaliana]	Unigene85888_All//2.00E-05//AT3G18180| transferase, transferring glycosyl groups	Unigene85888_All//4.00E-40//DN802248				nr +
Unigene859_All	3455	11.62	4.84	7.09	13.74	11.28	10.17	2.18	1.19	1.36	-1.26E+00	1.57E-42	Down	-7.12E-01	3.92E-16		-2.84E-01	8.36E-05		-4.34E-01	5.04E-09		-8.78E-01	4.17E-06		-6.79E-01	2.21E-04		Unigene859_All//gi|263505419|sp|COLGV1.1|RCH1_ARATH//0.00E+00//RecName: Full=LRR receptor-like serine/threonine-protein kinase RCH1; AltName: Full=Protein ROOT CLAVATA-HOMOLOG1 1; Flags: Precursor >gi|224589709|gb|ACN59386.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene859_All//0.00E+00//AT5G48940| leucine-rich repeat transmembrane protein kinase, putative	Unigene859_All//0.00E+00//gi|164259789|gb|ES846438.1|ES846438			GO:0004672//GO:0005488	nr +
Unigene85906_All	214	0.00	0.00	0.00	3.03	0.48	0.00	0.00	0.98	0.37	null	null		null	null		-2.65E+00	7.45E-03		-1.16E+01	3.90E-04	Down	9.93E+00	7.83E-02		8.54E+00	4.00E-01									
Unigene8593_All	480	0.22	0.74	1.11	3.01	0.72	0.56	1.06	2.26	0.25	1.76E+00	2.18E-01		2.35E+00	5.85E-02		-2.07E+00	2.41E-04	Down	-2.41E+00	1.41E-04	Down	1.10E+00	6.53E-02		-2.09E+00	3.64E-02		Unigene8593_All//gi|223452526|gb|ACM89590.1|//1.00E-26//disease resistance protein [Glycine max]	Unigene8593_All//2.00E-24//AT1G74190| AtRLP15 (Receptor Like Protein 15); protein binding					nr +
Unigene85938_All	434	0.00	0.00	0.00	5.97	1.67	1.98	0.10	0.48	0.00	null	null		null	null		-1.84E+00	2.36E-06	Down	-1.59E+00	9.03E-05	Down	2.31E+00	2.39E-01		-6.61E+00	5.98E-01				Unigene85938_All//3.00E-42//TC158751					
Unigene8594_All	320	2.45	2.53	0.67	2.65	5.70	9.31	0.53	0.52	0.00	4.69E-02	9.69E-01		-1.88E+00	4.13E-02		1.11E+00	2.18E-02		1.82E+00	3.36E-06	Up	-1.67E-02	1.02E+00		-9.05E+00	1.08E-01		Unigene8594_All//gi|7444442|pir||T02087//3.00E-17//gag/pol polyprotein - maize retrotransposon Hopscotch >gi|531389|gb|AAA57005.1| copia-like retrotransposon Hopscotch polyprotein [Zea mays]					GO:0005488	nr -
Unigene8595_All	291	2.16	1.57	0.37	1.37	1.30	1.55	4.65	5.03	0.82	-4.61E-01	6.18E-01		-2.56E+00	2.72E-02		-7.33E-02	9.25E-01		1.81E-01	8.83E-01		1.13E-01	8.23E-01		-2.50E+00	2.46E-05	Down								
Unigene85974_All	214	1.47	0.95	3.73	3.72	3.22	18.57	3.75	3.32	3.72	-6.31E-01	6.21E-01		1.35E+00	1.16E-01		-2.11E-01	8.06E-01		2.32E+00	8.36E-11	Up	-1.77E-01	7.93E-01		-1.18E-02	9.77E-01									
Unigene85975_All	284	0.92	0.00	0.00	5.26	1.70	0.95	1.04	0.00	0.28	-9.85E+00	6.65E-02		-9.85E+00	8.50E-02		-1.63E+00	2.06E-03		-2.46E+00	8.25E-05	Down	-1.00E+01	2.17E-02		-1.89E+00	1.68E-01									
Unigene86_All	2233	2.46	1.29	2.67	2.99	3.67	4.21	4.03	4.74	12.45	-9.28E-01	2.87E-04		1.19E-01	6.41E-01		2.96E-01	1.66E-01		4.93E-01	8.74E-03		2.32E-01	1.73E-01		1.63E+00	1.16E-53	Up	Unigene86_All//gi|79516777|ref|NP_197441.3|//0.00E+00//SMG7 [Arabidopsis thaliana] >gi|159461469|gb|ABW96769.1| SMG7-like protein [Arabidopsis thaliana]	Unigene86_All//0.00E+00//AT5G19400| SMG7	Unigene86_All//0.00E+00//TC167505				nr -
Unigene8601_All	400	2.22	0.00	1.60	3.99	2.24	0.11	0.53	0.00	0.00	-1.11E+01	2.85E-05	Down	-4.77E-01	5.33E-01		-8.32E-01	9.85E-02		-5.14E+00	9.51E-09	Down	-9.05E+00	7.40E-02		-9.05E+00	5.78E-02									
Unigene8603_All	722	0.07	5.90	1.48	0.00	0.81	0.38	0.12	0.00	0.44	6.35E+00	1.23E-22	Up	4.35E+00	6.45E-05	Up	9.66E+00	1.26E-03		8.55E+00	7.01E-02		-6.87E+00	3.97E-01		1.91E+00	1.53E-01		Unigene8603_All//gi|170660047|gb|ACB28472.1|//2.00E-33//polyprotein [Ananas comosus]	Unigene8603_All//5.00E-14//ATMG00860| hypothetical protein				GO:0003676//GO:0004175//GO:0006260//GO:0006225//GO:0019538//GO:0031410//GO:0034061	nr -
Unigene86036_All	324	0.16	0.31	0.00	1.54	0.00	0.28	0.00	0.13	0.00	9.54E-01	7.23E-01		-7.34E+00	6.13E-01		-1.06E+01	8.97E-04	Down	-2.46E+00	4.82E-02		7.01E+00	6.24E-01		null	null									
Unigene8605_All	228	1.84	7.78	2.10	1.09	1.51	0.99	0.00	0.00	0.35	2.08E+00	1.78E-04	Up	1.95E-01	8.39E-01		4.67E-01	7.79E-01		-1.41E-01	9.28E-01		null	null		8.45E+00	4.00E-01									
Unigene8606_All	451	0.46	3.71	0.00	1.55	1.45	1.40	0.09	0.00	0.18	3.00E+00	5.39E-06	Up	-8.86E+00	1.44E-01		-9.21E-02	8.94E-01		-1.41E-01	8.66E-01		-6.55E+00	6.40E-01		9.13E-01	7.47E-01				Unigene8606_All//2.00E-18//TC179144					
Unigene8607_All	268	1.17	0.38	0.00	8.36	2.96	6.24	0.32	0.16	0.45	-1.63E+00	2.76E-01		-1.02E+01	4.87E-02		-1.50E+00	2.60E-04	Down	-4.24E-01	3.59E-01		-1.02E+00	7.21E-01		4.99E-01	8.06E-01				Unigene8607_All//3.00E-140//gi|78324980|gb|DT545254.1|DT545254					
Unigene86076_All	621	4.55	2.28	3.09	4.73	3.88	5.24	1.84	1.95	0.38	-9.94E-01	8.04E-03		-5.60E-01	1.52E-01		-2.86E-01	4.66E-01		1.46E-01	6.87E-01		8.64E-02	8.83E-01		-2.26E+00	3.40E-04	Down	Unigene86076_All//gi|15228555|ref|NP_189539.1|//1.00E-06//AAR3 (antiauxin-resistant 3) [Arabidopsis thaliana]	Unigene86076_All//6.00E-08//AT3G28970| AAR3 (antiauxin-resistant 3)	Unigene86076_All//0.00E+00//TC153156			GO:0009755//GO:0043231	nr +
Unigene8608_All	299	6.30	1.36	3.03	6.16	5.30	6.50	0.71	0.98	0.53	-2.22E+00	4.65E-05	Down	-1.06E+00	3.50E-02		-2.19E-01	6.59E-01		7.54E-02	8.94E-01		4.69E-01	7.06E-01		-4.08E-01	7.55E-01		Unigene8608_All//gi|297847728|ref|XP_002891745.1|//4.00E-28//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297337587|gb|EFH68004.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene8608_All//6.00E-28//AT1G53330| pentatricopeptide (PPR) repeat-containing protein				GO:0048513//GO:0048608	nr -
Unigene861_All	1523	52.36	45.78	45.52	12.17	11.01	8.90	4.89	4.45	12.22	-1.94E-01	1.17E-03		-2.02E-01	1.11E-03		-1.44E-01	3.16E-01		-4.52E-01	3.37E-04		-1.36E-01	5.48E-01		1.32E+00	8.12E-27	Up	Unigene861_All//gi|8778622|gb|AAF79630.1|AC025416.4/1.1.00E-134//F5011.6 [Arabidopsis thaliana]	Unigene861_All//1.00E-127//AT1G12330| unknown protein	Unigene861_All//0.00E+00//gi|78342676|gb|DT562950.1|DT562950			GO:0005488	nr +
Unigene86115_All	241	0.65	0.00	0.00	4.13	1.00	0.00	1.75	0.52	0.33	-9.35E+00	2.13E-01		-9.35E+00	2.42E-01		-2.05E+00	3.70E-03		-1.20E+01	2.97E-06	Down	-1.75E+00	1.23E-01		-2.41E+00	3.93E-02				Unigene86115_All//3.00E-115//DW514550					ESTscan +
Unigene8612_All	559	0.19	0.54	0.86	0.80	0.00	0.08	2.80	8.00	8.48	1.54E+00	3.22E-01		2.20E+00	9.13E-02		-9.65E+00	2.00E-03		-3.31E+00	2.84E-02		1.52E+00	2.78E-08	Up	1.60E+00	1.25E-09	Up	Unigene8612_All//gi|226530779|ref|NP_001149090.1|//4.00E-14//LOC100282711 [Zea mays] >gi|195613170|gb|ACG28415.1| pre-mRNA-splicing factor cwc15 [Zea mays] >gi|195624656|gb|ACG34158.1| pre-mRNA-splicing factor cwc15 [Zea mays]	Unigene8612_All//5.00E-13//AT3G13200| EMB2769 (EMBRYO DEFECTIVE 2769)	Unigene8612_All//4.00E-45//TC143558		ko03040|Spliceosome	GO:0000377//GO:0030529	nr -
Unigene86123_All	358	0.00	0.00	0.30	2.23	0.19	0.13	0.35	0.12	0.00	null	null		8.22E+00	3.87E-01		-3.53E+00	3.03E-04	Down	-4.14E+00	4.12E-04	Down	-1.60E+00	5.32E-01		-8.47E+00	1.98E-01									
Unigene86129_All	463	0.45	0.00	0.00	4.09	2.60	0.20	0.00	0.00	0.00	-8.82E+00	1.21E-01		-8.82E+00	1.44E-01		-6.51E-01	1.60E-01		-4.39E+00	1.52E-09	Down	null	null		null	null		Unigene86129_All//gi|170172424|dbj|BAG12980.1|//2.00E-06//RHYTHM OF CHLOROPLAST 75 [Chlamydomonas reinhardtii] >gi|170172426|dbj|BAG12981.1| RHYTHM OF CHLOROPLAST 75 [Chlamydomonas reinhardtii]					GO:0005488//GO:0016817//GO:0022857	nr +
Unigene86143_All	492	0.00	0.00	0.43	2.73	1.96	0.55	0.00	0.00	0.00	null	null		8.76E+00	1.37E-01		-4.80E-01	4.15E-01		-2.31E+00	4.01E-04	Down	null	null		null	null									
Unigene8615_All	346	0.91	2.20	1.08	1.44	0.00	0.13	3.42	3.02	2.30	1.28E+00	1.28E-01		2.48E-01	8.22E-01		-1.05E+01	8.97E-04	Down	-3.46E+00	1.61E-02		-1.80E-01	7.44E-01		-5.71E-01	2.92E-01				Unigene8615_All//1.00E-93//TC153757					
Unigene86152_All	301	3.48	3.37	0.00	1.99	0.69	2.25	1.12	0.14	0.13	-4.63E-02	9.56E-01		-1.18E+01	9.32E-06	Down	-1.53E+00	1.01E-01		1.81E-01	8.44E-01		-3.02E+00	5.29E-02		-3.09E+00	3.91E-02				Unigene86152_All//2.00E-55//ES799043					
Unigene8616_All	593	0.00	0.00	0.00	0.00	0.00	0.00	2.07	1.48	0.47	null	null		null	null		null	null		null	null		-4.82E-01	4.08E-01		-2.14E+00	3.24E-04	Down	Unigene8616_All//gi|300137372|gb|EFJ04348.1|//8.00E-16//hypothetical protein SELMODRAFT_138833 [Selaginella moellendorffii]		Unigene8616_All//8.00E-19//TC148521				nr +
Unigene86163_All	368	2.27	0.14	0.58	2.57	1.31	0.74	2.41	6.36	3.68	-4.05E+00	4.65E-04	Down	-1.97E+00	2.71E-02		-9.73E-01	1.60E-01		-1.80E+00	1.83E-02		1.40E+00	2.91E-04	Up	6.09E-01	2.25E-01				Unigene86163_All//2.00E-49//TC176644					
Unigene86179_All	223	0.00	2.27	0.00	4.69	0.46	1.42	0.00	0.00	0.00	1.11E+01	3.99E-03		null	null		-3.34E+00	3.42E-05	Down	-1.73E+00	1.55E-02		null	null		null	null									
Unigene8618_All	418	1.00	0.24	0.00	1.91	0.16	0.54	0.10	0.60	0.95	-2.05E+00	1.20E-01		-9.97E+00	1.55E-02		-3.53E+00	3.03E-04	Down	-1.82E+00	3.32E-02		2.57E+00	1.53E-01		3.24E+00	2.14E-02				Unigene8618_All//2.00E-27//FL577609					
Unigene86195_All	220	0.00	4.15	0.00	0.23	0.63	0.41	7.30	25.08	25.17	1.20E+01	2.60E-05	Up	null	null		1.47E+00	6.16E-01		8.59E-01	7.90E-01		1.78E+00	2.02E-12	Up	1.79E+00	8.09E-13	Up			Unigene86195_All//7.00E-57//TC145802					ESTscan -
Unigene86214_All	257	0.20	0.00	0.00	0.19	0.00	0.00	2.63	0.33	0.00	-7.67E+00	5.99E-01		-7.67E+00	6.13E-01		-7.60E+00	5.41E-01		-7.60E+00	6.15E-01		-3.02E+00	2.43E-03		-1.14E+01	3.56E-05	Down	Unigene86214_All//gi|222875434|gb|ACM88923.1|//4.00E-36//gibberellin 20-oxidase [Gossypium hirsutum]	Unigene86214_All//6.00E-30//AT4G25420| GA20OX1; gibberellin 20-oxidase	Unigene86214_All//4.00E-65//TC134244		ko00270|Cysteine and methionine metabolism//ko00904|Diterpenoid biosynthesis	GO:0003824//GO:0008152//GO:0046914	nr -
Unigene86219_All	304	0.69	0.33	0.00	5.57	0.57	2.08	0.42	0.00	0.26	-1.05E+00	5.63E-01		-9.43E+00	1.44E-01		-3.30E+00	4.59E-08	Down	-1.42E+00	5.89E-03		-8.70E+00	2.33E-01		-6.71E-01	7.18E-01				Unigene86219_All//6.00E-15//BG444302					

Unigene8622_All	407	203.11	136.45	105.32	109.30	94.93	90.44	163.82	74.86	86.92	-5.74E-01	2.70E-23		-9.48E-01	6.37E-53		-2.03E-01	1.02E-02		-2.73E-01	5.70E-04		-1.13E+00	5.13E-72	Down	-9.14E-01	1.68E-52		Unigene8622_All//gi|224087383|ref|XP_002308145.1|//9.00E-28//histone 2 [Populus trichocarpa] >gi|222854121|gb|EEE91668.1|histone 2 [Populus trichocarpa]	Unigene8622_All//7.00E-16//AT5G02560| HTA12; DNA binding	Unigene8622_All//0.00E+00//TC155652			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr +
Unigene86242_All	209	0.00	0.00	0.00	5.96	3.13	1.08	0.00	0.00	0.00	null	null		null	null		-9.29E-01	1.11E-01		-2.46E+00	4.15E-04	Down	null	null		null	null								
Unigene8625_All	419	22.35	12.70	10.42	24.37	16.85	16.28	54.19	37.61	31.57	-8.16E-01	1.51E-05		-1.10E+00	3.53E-08	Down	-5.33E-01	1.49E-03		-5.83E-01	9.06E-04		-5.27E-01	2.52E-07		-7.80E-01	2.77E-14		Unigene8625_All//gi|148270944|gb|ABQ53642.1|//2.00E-15//60S ribosomal protein L32A [Cucumis melo]	Unigene8625_All//1.00E-14//AT4G18100| 60S ribosomal protein L32 (RPL32A)	Unigene8625_All//6.00E-164//gi|109874434|gb|DW503408.1|DW503408		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene8626_All	246	1.28	5.56	6.49	2.03	1.68	1.47	0.86	0.68	0.81	2.12E+00	1.09E-03		2.35E+00	2.09E-04	Up	-2.70E-01	8.02E-01		-4.63E-01	6.59E-01		-3.39E-01	8.11E-01		-8.59E-02	9.60E-01								
Unigene86268_All	493	0.32	0.10	0.11	0.40	2.58	1.74	1.63	0.51	0.89	-1.63E+00	4.87E-01		-1.56E+00	5.32E-01		2.68E+00	1.57E-04	Up	2.11E+00	1.44E-02		-1.68E+00	2.46E-02		-8.74E-01	1.96E-01		Unigene86268_All//gi|255540577|ref|XP_002511353.1|//3.00E-11//conserved hypothetical protein [Ricinus communis] >gi|223550468|gb|EEF51955.1|conserved hypothetical protein [Ricinus communis]						nr +
Unigene86275_All	311	0.34	0.81	4.11	7.53	3.54	2.32	0.27	0.00	0.51	1.28E+00	4.34E-01		3.61E+00	3.40E-05	Up	-1.09E+00	5.67E-03		-1.70E+00	1.02E-04	Down	-8.09E+00	3.97E-01		9.14E-01	6.23E-01		Unigene86275_All//gi|225431419|ref|XP_002279961.1|//3.00E-30//PREDICTED: similar to HB2 homeodomain protein isoform 2 [Vitis vinifera]	Unigene86275_All//4.00E-29//AT4G35550| WOX13 (WUSCHEL-RELATED HOMEOBOX 13); DNA binding / transcription factor	Unigene86275_All//1.00E-99//ES800482	HB		GO:0010071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene8628_All	254	0.00	0.00	0.00	0.00	0.00	0.00	4.99	11.85	19.45	null	null		null	null		null	null		null	null		1.25E+00	1.53E-04	Up	1.96E+00	5.80E-13	Up							
Unigene863_All	1153	1.59	2.07	0.83	0.86	1.34	1.10	2.27	3.26	5.04	3.79E-01	3.64E-01		-9.34E-01	6.55E-02		6.37E-01	2.56E-01		3.44E-01	6.24E-01		5.21E-01	6.99E-02		1.15E+00	2.17E-07	Up	Unigene863_All//gi|8778622|gb|AAF79630.1|AC025416.4/:1.00E-105//F5011.6 [Arabidopsis thaliana]	Unigene863_All//2.00E-95//AT1G12330| unknown protein	Unigene863_All//0.00E+00//TC152442			GO:0005488	nr -
Unigene8630_All	307	0.68	0.66	0.00	1.30	0.90	1.03	2.20	0.54	0.13	-4.62E-02	9.86E-01		-9.41E+00	1.44E-01		-5.33E-01	6.15E-01		-3.34E-01	7.56E-01		-2.02E+00	1.98E-02		-4.09E+00	3.10E-04	Down	Unigene8630_All//gi|15220007|ref|NP_178107.1|//1.00E-23//helicase-related [Arabidopsis thaliana]	Unigene8630_All//6.00E-25//AT1G79890| helicase-related				GO:0003676//GO:0003678//GO:0032559//GO:0034641//GO:0042623//GO:0043231	nr +
Unigene86306_All	515	0.41	0.30	0.10	0.97	0.67	0.44	0.99	0.49	0.00	-4.61E-01	7.57E-01		-1.97E+00	3.80E-01		-5.33E-01	5.94E-01		-1.14E+00	3.07E-01		-1.02E+00	2.88E-01		-9.94E+00	5.54E-04	Down	Unigene86306_All//gi|115451825|ref|NP_001049513.1|//3.00E-10//Os03g0241100 [Oryza sativa Japonica Group] >gi|113547984|dbj|BAF11427.1|Os03g0241100 [Oryza sativa Japonica Group]	Unigene86306_All//2.00E-15//AT4G38380| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thaliana protein match is: TK11 (TSL-kinase interacting protein 1); DNA binding / transcription factor (TAIR:AT2G36960.2); Has 39 Blast hits to 35 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).				GO:0003676//GO:0010468//GO:0043231	nr +
Unigene86310_All	530	0.99	0.57	0.00	11.28	9.55	0.77	0.48	0.00	0.45	-7.83E-01	4.22E-01		-9.95E+00	4.73E-03		-2.40E-01	3.64E-01		-3.88E+00	3.58E-27	Down	-8.90E+00	4.02E-02		-8.57E-02	9.56E-01		Unigene86310_All//gi|114050611|gb|ABI49455.1|//8.00E-12//At3g06070 [Arabidopsis thaliana]	Unigene86310_All//4.00E-10//AT3G06070| unknown protein	Unigene86310_All//0.00E+00//TC153852				nr -
Unigene86318_All	360	0.29	0.28	0.15	4.84	1.91	0.63	0.35	0.70	0.22	-4.64E-02	9.85E-01		-9.75E-01	7.18E-01		-1.34E+00	4.67E-03		-2.95E+00	1.50E-06	Down	9.84E-01	5.17E-01		-6.71E-01	7.18E-01								
Unigene8633_All	448	0.70	0.34	1.31	0.22	0.08	0.30	2.17	1.12	0.18	-1.05E+00	4.43E-01		9.00E-01	3.76E-01		-1.53E+00	5.82E-01		4.43E-01	8.59E-01		-9.55E-01	1.35E-01		-3.61E+00	2.14E-05	Down	Unigene8633_All//gi|224092352|ref|XP_002309571.1|//7.00E-56//flavine-containing monooxygenase [Populus trichocarpa] >gi|222855547|gb|EEE93094.1|flavine-containing monoxygenase [Populus trichocarpa]	Unigene8633_All//6.00E-55//AT5G25620| YUC6 (YUCCA6); FAD binding / NADP or NADPH binding / flavin-containing monooxygenase/ monooxygenase/ oxidoreductase	Unigene8633_All//8.00E-148//ES848043		ko00380|Tryptophan metabolism	GO:0009850//GO:0016709//GO:0030554	nr +
Unigene8634_All	394	31.74	63.53	62.31	41.34	64.41	40.69	0.00	0.00	0.10	1.00E+00	1.34E-18	Up	9.73E-01	7.97E-17		6.40E-01	1.90E-10		-2.29E-02	9.05E-01		null	null		6.66E+00	6.34E-01		Unigene8634_All//gi|15294284|gb|AAK95319.1|AF410333_1//4.00E-09//AT3g62730|F26K9_160 [Arabidopsis thaliana] >gi|20147275|gb|AAM10351.1|AT3g62730|F26K9_160 [Arabidopsis thaliana]	Unigene8634_All//2.00E-10//AT3G62730| unknown protein	Unigene8634_All//0.00E+00//TC161625				nr +
Unigene8635_All	249	2.94	4.48	5.13	4.80	2.35	12.15	4.25	13.43	7.04	6.06E-01	3.59E-01		8.03E-01	2.01E-01		-1.03E+00	8.42E-02		1.34E+00	2.67E-04	Up	1.66E+00	3.55E-07	Up	7.30E-01	8.78E-02				Unigene8635_All//3.00E-44//gi|48815660|gb|CO116973.1|CO116973				
Unigene8636_All	343	1.22	0.30	1.55	1.16	2.51	1.19	2.47	0.24	0.81	-2.05E+00	1.20E-01		3.47E-01	7.05E-01		1.11E+00	1.63E-01		2.85E-02	9.85E-01		-3.34E+00	2.51E-04	Down	-1.60E+00	2.02E-02		Unigene8636_All//gi|115443699|ref|NP_001045629.1|//7.00E-15//Os02g0106700 [Oryza sativa Japonica Group] >gi|113535160|dbj|BAF07543.1|Os02g0106700 [Oryza sativa Japonica Group]	Unigene8636_All//3.00E-22//AT5G24680| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Peptidase C78, ubiquitin fold modifier-specific peptidase 1 and 2 (InterPro:IPR012462); Has 157 Blast hits to 157 proteins in 66 species: Archae - 0; Bacteria - 0; Metazoa - 86; Fungi - 45; Plants - 19; Viruses - 0; Other Eukaryotes - 7 (source: NCBI BLink).	Unigene8636_All//0.00E+00//ES822165				nr -
Unigene8639_All	249	2.73	0.81	0.00	2.20	0.14	2.00	0.00	0.34	0.96	-1.75E+00	6.23E-02		-1.14E+01	7.63E-04	Down	-3.99E+00	2.60E-03		-1.41E-01	8.85E-01		8.39E+00	3.97E-01		9.91E+00	4.38E-02								
Unigene86390_All	251	1.46	1.62	1.27	2.78	0.55	0.00	0.00	0.00	0.00	1.47E-01	8.98E-01		-1.97E-01	8.65E-01		-2.34E+00	1.01E-02		-1.14E-01	1.96E-04	Down	null	null		null	null								ESTscan -
Unigene864_All	2033	19.15	11.94	17.39	5.83	5.57	4.51	0.40	0.56	1.65	-6.82E-01	3.47E-15		-1.39E-01	1.54E-01		-6.55E-02	7.64E-01		-3.71E-01	2.72E-02		4.91E-01	4.01E-01		2.06E+00	1.44E-09	Up	Unigene864_All//gi|8778622|gb|AAF79630.1|AC025416.4/:1.00E-141//F5011.6 [Arabidopsis thaliana]	Unigene864_All//2.00E-129//AT1G12330| unknown protein	Unigene864_All//0.00E+00//gi|78331777|gb|DT552051.1|DT552051				nr -
Unigene86410_All	219	0.00	0.00	0.00	0.23	0.00	0.00	0.19	2.10	5.09	null	null		null	null		-7.83E+00	5.41E-01		-7.83E+00	6.15E-01		3.44E+00	1.16E-02		4.72E+00	6.01E-07	Up			Unigene86410_All//8.00E-60//gi|78338501|gb|DT558775.1|DT558775				ESTscan -
Unigene8644_All	601	0.09	2.87	0.27	0.33	0.57	0.53	0.21	0.35	1.06	5.04E+00	1.32E-08	Up	1.61E+00	5.09E-01		7.90E-01	5.95E-01		6.66E-01	6.47E-01		7.21E-01	6.31E-01		2.33E+00	1.05E-02		Unigene8644_All//gi|14517540|gb|AAK62660.1|//7.00E-18//AT3g50910|F18B3_190 [Arabidopsis thaliana] >gi|27764930|gb|AAO23586.1|At3g50910|F18B3_190 [Arabidopsis thaliana]	Unigene8644_All//2.00E-17//AT3G50910| unknown protein	Unigene8644_All//0.00E+00//TC149232				nr -
Unigene8645_All	350	9.42	25.05	14.30	25.33	23.02	24.52	50.98	75.23	32.78	1.41E+00	1.69E-11	Up	6.03E-01	3.18E-02		-1.38E-01	5.65E-01		-4.73E-02	8.35E-01		5.62E-01	2.81E-09		-6.37E-01	2.79E-08		Unigene8645_All//gi|124360195|gb|ABW08208.1|//1.00E-22//Remorin, C-terminal region [Medicago truncatula]	Unigene8645_All//6.00E-08//AT3G57540| remorin family protein	Unigene8645_All//1.00E-102//TC174686				nr -
Unigene86470_All	418	11.77	10.79	19.87	3.10	0.99	0.43	0.00	0.00	0.00	-1.25E-01	6.44E-01		7.56E-01	2.89E-04		-1.65E+00	4.40E-03		-2.84E+00	7.63E-05	Down	null	null		null	null				Unigene86470_All//7.00E-34//TC135455				
Unigene8648_All	223	3.52	4.77	7.64	6.25	10.96	13.57	167.22	154.63	619.02	4.39E-01	5.07E-01		1.12E+00	3.58E-02		8.10E-01	4.51E-02		1.12E+00	2.03E-03		-1.13E-01	2.11E-01		1.89E+00	0.00E+00	Up	Unigene8648_All//gi|3287824|sp|Q39761.1|DCS1_GOSAR//7.00E-17//RecName: Full=(+)-delta-cadinene synthase isozyme XC1; Short=D-cadinene synthase XC1 >gi|240104441|pdb|3G4D|A Chain A, Crystal Structure Of (+)-Delta-Cadinene Synthase From Gossypium Arboreum And Evolutionary Divergence Of Metal Binding Motifs For Catalysis >gi|240104442|pdb|3G4D|B Chain B, Crystal Structure Of (+)-Delta-Cadinene Synthase From Gossypium Arboreum And Evolutionary Divergence Of Metal Binding Motifs For Catalysis >gi|241913340|pdb|3G4F|A Chain A, Crystal Structure Of (+)- -Cadinene Synthase From Gossypium Arboreum In Complex With 2-Fluorofarnesyl Diphosphate >gi|241913341|pdb|3G4F|B Chain B, Crystal Structure Of (+)- -Cadinene Synthase From Gossypium Arboreum In Complex With 2-Fluorofarnesyl Diphosphate >gi|1043312|gb|AAA83064.1|(+)-delta-cadinene synthase isozyme XC1 [Gossypium arboreum]		Unigene8648_All//6.00E-82//TC129580				nr +
Unigene8649_All	544	3.27	5.03	4.01	12.73	4.43	4.65	0.39	0.54	0.07	6.21E-01	1.04E-01		2.96E-01	5.26E-01		-1.52E+00	2.21E-12	Down	-1.45E+00	2.82E-10	Down	4.69E-01	7.06E-01		-2.41E+00	1.94E-01				Unigene8649_All//0.00E+00//gi|109875721|gb|DR504695.1|DR504695				ESTscan +
Unigene86492_All	216	0.00	0.00	0.00	3.00	0.00	0.00	0.20	0.00	0.00	null	null		null	null		-1.15E+01	7.84E-05	Down	-1.15E+01	3.90E-04	Down	-7.61E+00	6.40E-01		-7.61E+00	5.98E-01		Unigene86492_All//gi|224078650|ref|XP_002305591.1|//2.00E-07//predicted protein [Populus trichocarpa] >gi|222848555|gb|EEE86102.1|predicted protein [Populus trichocarpa]		Unigene86492_All//2.00E-44//ES790386				nr +
Unigene86500_All	201	1.04	19.41	0.53	0.50	0.86	2.02	0.00	0.00	0.00	4.22E+00	2.88E-17	Up	-9.75E-01	6.19E-01		7.89E-01	7.69E-01		2.03E+00	1.49E-01		null	null		null	null		Unigene86500_All//gi|34550779|gb|AAQ74955.1|//3.00E-12//Ghiaa-Re [Gossypium barbadense]	Unigene86500_All//4.00E-13//AT5G43700| ATAUX2-11 (AUXIN INDUCIBLE 2-11); DNA binding / transcription factor	Unigene86500_All//3.00E-74//TC133678				nr +
Unigene8652_All	456	0.00	1.22	0.00	0.11	0.30	1.98	0.37	1.01	0.70	1.03E+01	2.16E-03		null	null		1.47E+00	6.16E-01		4.18E+00	1.95E-04	Up	1.44E+00	1.67E-01		9.14E-01	4.52E-01								
Unigene86524_All	239	353.33	291.93	389.24	161.95	292.48	661.01	1032.42	521.83	710.09	-2.75E-01	1.11E-06		1.40E-01	1.82E-02		8.53E-01	5.55E-46		2.03E+00	0.00E+00	Up	-9.84E-01	2.16E-211		-5.40E-01	1.26E-76		Unigene86524_All//gi|292653523|gb|ADE34279.1|//2.00E-22//aquaporin PIP1;10 [Gossypium hirsutum]	Unigene86524_All//5.00E-20//AT2G45960| PIP1B (NAMED PLASMA MEMBRANE INTRINSIC PROTEIN 1B); water channel	Unigene86524_All//2.00E-72//EX164868			GO:0006810//GO:0031224	nr +
Unigene86528_All	227	0.00	0.00	4.69	2.85	1.52	0.20	0.56	1.10	0.88	null	null		1.22E+01	6.58E-06	Up	-9.11E-01	3.04E-01		-3.84E+00	2.69E-03		9.83E-01	5.17E-01		6.51E-01	6.65E-01								
Unigene8656_All	411	0.25	0.00	0.00	5.70	1.68	0.00	5.76	0.61	1.26	-7.99E+00	3.64E-01		-7.99E+00	3.86E-01		-1.77E+00	1.69E-05	Down	-1.25E+01	1.13E-14	Down	-3.24E+00	8.82E-11	Down	-2.19E+00	1.28E-07	Down	Unigene8656_All//gi|255557347|ref|XP_002519704.1|//2.00E-06//conserved hypothetical protein [Ricinus communis] >gi|223541121|gb|EEF42677.1|conserved hypothetical protein [Ricinus communis]						nr -
Unigene86562_All	397	0.79	0.00	0.00	2.89	1.47	0.23	0.00	0.00	0.00	-9.63E+00	3.63E-02		-9.63E+00	4.87E-02		-9.69E-01	1.14E-01		-3.67E+00	2.69E-05	Down	null	null		null	null		Unigene86562_All//gi|212717161|gb|ACJ37422.1|//3.00E-16//receptor-like serine/threonine kinase [Glycine max]	Unigene86562_All//8.00E-16//AT3G14840| leucine-rich repeat family protein / protein kinase family protein	Unigene86562_All//1.00E-62//DW224146			GO:0004672//GO:0005488	nr +

Unigene8657_All	1167	0.09	0.26	0.00	0.09	0.00	0.39	10.98	5.05	4.64	1.54E+00	3.22E-01		-6.49E+00	3.86E-01		-6.42E+00	3.06E-01		2.18E+00	1.02E-01		-1.12E+00	2.67E-14	Down	-1.24E+00	3.16E-17	Down	Unigene8657_All//gi|121489775|emb|CAK18859.1|//5.00E-64//Putative RING-H2 finger protein precursor [Phillyrea latifolia]	Unigene8657_All//3.00E-62//AT5G53110| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein match is: zinc finger (C3HC4-type RING finger) family protein (TAIR:AT2G46495.1); Has 118 Blast hits to 116 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 118; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr +
Unigene866_All	2044	6.71	5.85	6.30	18.35	16.41	11.40	10.09	4.25	4.25	-1.97E-01	2.29E-01		-8.92E-02	6.42E-01		-1.61E-01	8.05E-02		-6.87E-01	7.53E-16		-1.25E+00	1.43E-26	Down	-1.25E+00	1.97E-27	Down	Unigene866_All//gi|163658596|gb|ABY28389.1|//0.00E+00//calcium-dependent protein kinase 1 [Datura metel]	Unigene866_All//0.00E+00//AT3G57530| CPK32 (CALCIUM-DEPENDENT PROTEIN KINASE 32); calcium-dependent protein kinase C/ calmodulin-dependent protein kinase/ kinase/ protein binding	Unigene866_All//0.00E+00//TC174401		ko04626|Plant-pathogen interaction	GO:0004697//GO:0006464//GO:0006970//GO:0009755//GO:0016020//GO:0003259//GO:0043231//GO:0046872	nr +
Unigene86608_All	454	23.05	46.87	33.08	26.33	27.31	46.06	42.84	39.59	24.57	1.02E+00	1.67E-16	Up	5.21E-01	4.90E-04		5.23E-02	8.16E-01		8.07E-01	9.68E-12		-1.14E-01	3.99E-01		-8.02E-01	6.09E-13		Unigene86608_All//gi|297829856|ref|XP_002882810.1|//3.00E-41//RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297328650|gb|EFH59069.1| RNA recognition motif-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene86608_All//1.00E-41//AT3G13224| RNA recognition motif (RRM)-containing protein	Unigene86608_All//0.00E+00//TC156489		ko03040|Spliceosome	GO:0003676	nr -
Unigene86614_All	266	1.38	3.05	1.40	3.00	0.91	1.02	8.90	7.07	1.35	1.15E+00	1.48E-01		2.53E-02	1.00E+00		-1.73E+00	2.86E-02		-1.56E+00	6.26E-02		-3.32E-01	4.00E-01		-2.72E+00	1.50E-09	Down				Unigene86614_All//2.00E-54//TC145740				
Unigene86617_All	225	0.23	0.00	0.24	2.21	0.00	0.00	0.00	0.00	0.53	-7.86E+00	5.98E-01		2.58E-02	9.91E-01		-1.11E+01	8.97E-04	Down	-1.11E+01	2.97E-03		null	null		9.05E+00	2.42E-01					Unigene86617_All//7.00E-48//EV489776				
Unigene86623_All	357	1.17	0.14	0.45	2.51	0.77	0.13	0.00	0.00	0.11	-3.05E+00	4.65E-02		-1.39E+00	2.80E-01		-1.70E+00	1.98E-02		-4.31E+00	1.14E-04	Down	null	null		6.80E+00	6.33E-01		Unigene86623_All//gi|28558781|gb|AA045752.1|//4.00E-13//pol protein [Cucumis melo]		Unigene86623_All//2.00E-18//FL576684		GO:0003676//GO:0009987//GO:0043170//GO:0044238	nr +
Unigene8664_All	216	0.48	1.88	0.99	2.08	0.96	0.21	641.64	877.52	305.80	1.95E+00	1.44E-01		1.03E+00	5.89E-01		-1.12E+00	3.15E-01		-3.31E+00	2.84E-02		4.52E-01	1.07E-41		-1.07E+00	4.92E-140	Down			Unigene8664_All//2.00E-41//gi|109867479|gb|DW496455.1|DW496455				
Unigene8665_All	1200	0.09	0.08	0.00	0.00	0.00	0.00	9.97	3.41	0.86	-4.71E-02	9.85E-01		-6.45E+00	3.86E-01		null	null		null	null		-1.55E+00	1.62E-21	Down	-3.53E+00	4.17E-58	Down	Unigene8665_All//gi|6093671|sp|P22195.2|PER1_ARAHY//1.00E-113//RecName: Full=Cationic peroxidase 1; AltName: Full=PNPC1; Flags: Precursor >gi|1491776|gb|AAB06183.1| cationic peroxidase [Arachis hypogaea]	Unigene8665_All//1.00E-94//AT5G05340| peroxidase, putative	Unigene8665_All//0.00E+00//TC169120		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr +
Unigene8667_All	952	0.00	0.00	0.00	0.31	0.18	0.00	0.09	2.41	4.60	null	null		null	null		-7.96E-01	5.56E-01		-8.29E+00	3.97E-02		4.77E+00	1.36E-13	Up	5.70E+00	3.29E-28	Up	Unigene8667_All//gi|124360490|gb|AB008500.1|//7.00E-47//Protein kinase [Medicago truncatula]	Unigene8667_All//1.00E-35//AT3G47580| leucine-rich repeat transmembrane protein kinase, putative	Unigene8667_All//5.00E-12//DR460930		ko04626|Plant-pathogen interaction		nr +
Unigene86680_All	238	0.00	0.43	0.67	2.93	0.14	0.57	0.71	0.88	1.00	8.73E+00	3.78E-01		9.39E+00	2.33E-01		-4.34E+00	2.79E-04	Down	-2.36E+00	1.69E-02		3.05E-01	8.35E-01		4.99E-01	7.07E-01					Unigene86680_All//8.00E-97//DT468974				
Unigene867_All	409	52.83	39.02	66.66	12.67	15.74	13.91	10.03	1.33	4.29	-4.37E-01	2.10E-04		3.35E-01	2.11E-03		3.14E-01	2.08E-01		1.35E-01	6.40E-01		-2.92E+00	1.54E-16	Down	-1.23E+00	5.20E-06	Down	Unigene867_All//gi|76559874|tpe|CAE56324.1|//3.00E-47//TPA: leucoanthocyanidin reductase 1 [Gossypium raimondii]	Unigene867_All//6.00E-122//AT4G39230| isoflavone reductase, putative	Unigene867_All//1.00E-112//gi|11206797|gb|BF275727.1|BF275727		ko00941|Flavonoid biosynthesis//ko00640|Propanoate metabolism	GO:0003824	nr +
Unigene8670_All	469	0.00	0.00	0.00	2.23	1.17	0.10	1.71	4.10	1.02	null	null		null	null		-9.25E-01	1.55E-01		-4.53E+00	1.60E-05	Down	1.26E+00	3.19E-03		-7.49E-01	2.66E-01					Unigene8670_All//6.00E-19//TC150779				ESTscan -
Unigene8671_All	425	0.00	0.00	0.00	0.00	0.00	0.00	4.87	0.20	2.81	null	null		null	null		null	null		null	null		-4.63E+00	3.60E-12	Down	-7.94E-01	3.86E-02		Unigene8671_All//gi|297720413|ref|NP_00117256 8.1|//6.00E-17//Os01g0748950 [Oryza sativa Japonica Group] >gi|255673688|dbj|BAH91298.1| Os01g0748950 [Oryza sativa Japonica Group]	Unigene8671_All//2.00E-16//AT1G68570| proton-dependent oligopeptide transport (POT) family protein					nr -
Unigene86717_All	282	0.19	0.00	0.76	1.41	2.20	2.56	0.60	3.41	0.28	-7.54E+00	5.98E-01		2.03E+00	3.59E-01		6.37E-01	5.49E-01		8.59E-01	3.42E-01		2.51E+00	7.99E-04	Up	-1.09E+00	5.51E-01		Unigene86717_All//gi|2827550|emb|CAA16558.1|//6.00E-28//leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] >gi|7269119|emb|CAB79228.1| leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] >gi|38564276|gb|AAR23717.1| At4g22730 [Arabidopsis thaliana] >gi|51971929|dbj|BAD14629.1| leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana] >gi|224589626|gb|ACN59346.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene86717_All//2.00E-29//AT4G22730| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672//GO:0004871//GO:0006464//GO:0007167//GO:0016628//GO:0031224//GO:0032559	nr +
Unigene8672_All	453	1.85	0.11	0.94	0.66	0.61	1.99	2.43	2.86	5.54	-4.05E+00	4.65E-04	Down	-9.75E-01	2.37E-01		-1.18E-01	9.00E-01		1.60E+00	4.34E-02		2.37E-01	6.52E-01		1.19E+00	7.78E-04	Up								
Unigene86720_All	364	0.14	0.42	0.44	3.70	1.04	0.37	0.35	1.15	0.11	1.54E+00	5.29E-01		1.61E+00	5.09E-01		-1.83E+00	1.45E-03		-3.31E+00	1.08E-05	Down	1.72E+00	1.35E-01		-1.67E+00	4.75E-01									
Unigene8673_All	1145	0.00	0.00	0.00	0.04	0.00	0.00	19.98	40.88	13.67	null	null		null	null		-5.44E+00	5.41E-01		-5.44E+00	6.15E-01		1.03E+00	5.71E-44	Up	-5.47E-01	4.26E-08		Unigene8673_All//gi|224054176|ref|XP_002298129.1|//2.00E-91//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene8673_All//8.00E-86//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene8673_All//0.00E+00//TC131966		ko00941|Flavonoid biosynthesis//ko00904|Diterpenoid biosynthesis		nr +
Unigene8675_All	1622	0.00	0.00	0.00	0.06	0.04	0.06	1.93	0.77	5.58	null	null		null	null		-5.31E-01	8.12E-01		-1.41E-01	9.46E-01		-1.32E+00	4.68E-05	Down	1.53E+00	1.39E-16	Up	Unigene8675_All//gi|56967598|gb|AAW31948.1|//3.00E-46//acetyl CoA geraniol/citronellol acetyltransferase [Rosa hybrid cultivar]	Unigene8675_All//2.00E-33//AT3G30280| transferase family protein			ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene86750_All	296	0.00	1.54	1.44	2.19	0.93	0.00	494.94	510.02	199.87	1.06E+01	7.34E-03		1.05E+01	1.36E-02		-1.23E+00	1.60E-01		-1.11E+01	3.90E-04	Down	4.33E-02	3.58E-01		-1.31E+00	7.49E-204	Down	Unigene86750_All//gi|224054176|ref|XP_002298129.1|//2.00E-15//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene86750_All//1.00E-09//AT4G03070| AOP1; oxidoreductase, acting on paired donors, with incorporation or reduction of molecular oxygen, 2-oxoglutarate as one donor, and incorporation of one atom each of oxygen into both donors	Unigene86750_All//4.00E-124//TC166812		ko00904|Diterpenoid biosynthesis	GO:0008152//GO:0016706//GO:0044464	nr +
Unigene86756_All	227	0.00	0.00	0.00	0.88	0.00	0.00	91.64	148.59	22.64	null	null		null	null		-9.78E+00	8.34E-02		-9.78E+00	1.32E-01		6.97E-01	9.67E-17		-2.02E+00	1.32E-54	Down	Unigene86756_All//gi|300077147|gb|ADJ66850.1|//3.00E-15//O-methyltransferase [Vitis vinifera]		Unigene86756_All//3.00E-102//gi|62295617|gb|DN779263.1|DN779263			GO:0005515//GO:0008171	nr -
Unigene8677_All	256	14.51	3.96	10.61	11.87	11.43	10.41	3.14	1.96	2.33	-1.87E+00	1.28E-07	Down	-4.52E-01	1.84E-01		-5.40E-02	8.79E-01		-1.90E-01	6.27E-01		-6.80E-01	3.53E-01		-4.27E-01	5.42E-01					Unigene8677_All//4.00E-40//TC130831				
Unigene86796_All	323	0.00	0.00	0.99	3.70	0.32	0.28	0.13	0.00	0.37	null	null		9.95E+00	4.42E-02		-3.53E+00	3.83E-06	Down	-3.73E+00	1.43E-05	Down	-7.03E+00	6.39E-01		1.50E+00	5.56E-01									
Unigene868_All	3195	87.84	62.79	126.20	38.01	36.38	47.75	39.73	9.14	14.10	-4.84E-01	5.13E-57		5.23E-01	6.23E-91		-6.35E-02	2.48E-01		3.29E-01	1.25E-16		-2.12E+00	0.00E+00	Down	-1.49E+00	3.70E-216	Down	Unigene868_All//gi|76559864|tpe|CAE56319.1|//0.00E+00//TPA: leucoanthocyanidin reductase 1 [Gossypium arboreum]	Unigene868_All//2.00E-133//AT4G14170| pentatricopeptide (PPR) repeat-containing protein	Unigene868_All//0.00E+00//TC141889		ko00941|Flavonoid biosynthesis		nr +
Unigene8680_All	760	0.14	0.07	0.28	0.26	0.00	0.30	7.18	42.51	6.19	-1.05E+00	6.82E-01		1.03E+00	5.89E-01		-8.03E+00	8.34E-02		1.80E-01	9.34E-01		2.57E+00	1.83E-109	Up	-2.14E-01	3.71E-01		Unigene8680_All//gi|224071451|ref|XP_002303466.1|//1.00E-16//predicted protein [Populus trichocarpa] >gi|222840898|gb|EEE78415.1| predicted protein [Populus trichocarpa]						nr -
Unigene8681_All	389	2.29	1.69	0.55	1.92	1.68	1.04	1.41	0.00	0.82	-4.33E-01	5.56E-01		-2.06E+00	1.78E-02		-1.92E-01	8.21E-01		-8.78E-01	3.08E-01		-1.05E+01	4.61E-04	Down	-7.86E-01	3.61E-01		Unigene8681_All//gi|18409261|ref|NP_564963.1|//2.00E-23//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene8681_All//1.00E-24//AT1G69400| transducin family protein / WD-40 repeat family protein					nr +
Unigene86831_All	325	4.02	0.62	2.95	3.37	2.33	2.08	0.26	0.13	0.25	-2.69E+00	1.84E-04	Down	-4.49E-01	4.58E-01		-5.33E-01	4.20E-01		-6.94E-01	3.11E-01		-1.02E+00	7.20E-01		-8.57E-02	9.68E-01					Unigene86831_All//4.00E-07//TC156792				
Unigene8684_All	483	0.76	0.94	0.44	0.31	0.14	0.37	25.65	60.49	17.16	3.16E-01	7.44E-01		-7.82E-01	5.53E-01		-1.12E+00	5.81E-01		2.74E-01	9.03E-01		1.24E+00	8.18E-37	Up	-5.80E-01	3.10E-05		Unigene8684_All//gi|195616080|gb|ACG29870.1|//5.00E-45//AMP-binding protein [Zea mays]	Unigene8684_All//1.00E-44//AT3G16910| AAET (ACYL-ACTIVATING ENZYME 7); AMP binding / acetate-CoA ligase	Unigene8684_All//3.00E-104//gi|78335576|gb|DT555850.1|DT555850		ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism		nr +
Unigene86845_All	300	2.62	1.52	0.00	8.47	7.00	4.37	0.14	0.98	0.27	-7.83E-01	3.28E-01		-1.14E+01	2.21E-04	Down	-2.74E-01	5.33E-01		-9.56E-01	1.59E-02		2.79E+00	9.47E-02		9.15E-01	7.47E-01		Unigene86845_All//gi|297744869|emb|CBI38328.3|//2.00E-06//unnamed protein product [Vitis vinifera]		Unigene86845_All//2.00E-27//ES803949				nr +
Unigene8685_All	491	0.00	0.41	0.43	0.91	1.75	0.37	0.34	2.21	1.22	8.69E+00	1.34E-01		8.76E+00	1.37E-01		9.41E-01	2.38E-01		-1.31E+00	2.72E-01		2.68E+00	1.69E-04	Up	1.82E+00	3.94E-02		Unigene8685_All//gi|33463891|gb|AAQ19327.1|//1.00E-08//bZIP-like protein [Oryza sativa Japonica Group]						nr -
Unigene86854_All	210	121.09	330.32	153.66	154.66	225.47	435.93	473.94	659.78	609.72	1.45E+00	1.90E-89	Up	3.44E-01	5.07E-04		5.44E-01	2.00E-14		1.50E+00	6.36E-133	Up	4.77E-01	6.84E-34		3.63E-01	8.81E-20		Unigene86854_All//gi|102655942|gb|AAY33920.2|//9.00E-09//polyubiquitin [Euphorbia characias]	Unigene86854_All//5.00E-10//AT5G37640| UBQ9; protein binding	Unigene86854_All//1.00E-76//TC146689				nr -
Unigene8686_All	952	0.00	1.33	0.28	0.10	1.30	7.02	1.07	8.91	7.99	1.04E+01	2.85E-07	Up	8.13E+00	7.85E-02		3.64E+00	1.21E-05	Up	6.07E+00	3.47E-37	Up	3.06E+00	4.34E-35	Up	2.91E+00	1.54E-30	Up	Unigene8686_All//gi|1769897|emb|CAA69271.1|//1.00E-51//lectin receptor kinase [Arabidopsis thaliana]	Unigene8686_All//2.00E-10//AT1G48720| unknown protein	Unigene8686_All//2.00E-67//DT468735				nr +
Unigene8687_All	364	0.86	0.28	0.59	5.06	1.42	0.62	5.34	7.69	4.93	-1.63E+00	2.76E-01		-5.59E-01	6.62E-01		-1.84E+00	1.14E-04	Down	-3.03E+00	4.61E-07	Down	5.26E-01	1.27E-01		-1.18E-01	7.67E-01					Unigene8687_All//5.00E-28//TC136732				
Unigene86870_All	251	0.00	0.00	0.00	0.00	0.00	0.00	4.89	11.82	12.22	null	null		null	null		null	null		null	null		1.28E+00	1.27E-04	Up	1.32E+00	3.87E-05	Up	Unigene86870_All//gi|19850241|gb|AAL99608.1|AF348412_1/6.00E-22//cytosolic aldehyde dehydrogenase RF2C [Zea mays]	Unigene86870_All//1.00E-21//AT5G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene86870_All//8.00E-20//TC157786		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism	GO:0008152//GO:0016620//GO:0043231	nr +

Unigene86873_All	214	0.00	4.03	0.00	1.16	0.00	0.21	0.00	0.00	1.20E+01	4.91E-05	Up	null	null		-1.02E+01	4.15E-02			-2.46E+00	2.23E-01		null	null		null	null		Unigene86873_All//gi|15242078|ref|NP_197587.1|//5.00E-14//glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Unigene86873_All//2.00E-15//AT5G20870| glycosyl hydrolase family 17 protein	Unigene86873_All//2.00E-11//gi|78329547|gb|DT549821.1|DT549821			GO:0016798//GO:0031225//GO:0043167//GO:0044238	nr +
Unigene8688_All	1059	0.00	0.00	0.00	0.05	0.13	0.17	1.72	2.09	32.24	null	null		null	null		1.47E+00	6.16E-01		1.86E+00	4.57E-01		2.85E-01	4.98E-01		4.23E+00	1.16E-185	Up	Unigene8688_All//gi|62766606|gb|AAX99411.1|//1.00E-104//patatin-like protein [Gossypium hirsutum]	Unigene8688_All//1.00E-87//AT2G26560| PLA2A (PHOSPHOLIPASE A 2A); lipase/ nutrient reservoir	Unigene8688_All//1.00E-96//TC133986				nr +
Unigene86882_All	472	0.89	0.75	2.03	0.95	1.24	0.57	24.01	77.57	61.53	-2.39E-01	8.09E-01		1.20E+00	1.15E-01		3.85E-01	7.32E-01		-7.26E-01	5.32E-01		1.69E+00	6.77E-73	Up	1.36E+00	4.56E-43	Up	Unigene86882_All//gi|224111870|ref|XP_002316008.1|//3.00E-29//cytochrome P450 [Populus trichocarpa] >gi|222865048|gb|EEF02179.1| cytochrome P450 [Populus trichocarpa]	Unigene86882_All//6.00E-23//AT3G14630| CYP72A9; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene86882_All//0.00E+00//DT463377		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0008152//GO:0016634//GO:0031410	nr +
Unigene86888_All	248	1.27	3.27	5.80	3.41	2.50	1.64	1.02	1.18	2.25	1.37E+00	9.21E-02		2.20E+00	8.72E-04	Up	-4.50E-01	5.52E-01		-1.06E+00	1.81E-01		2.06E-01	8.67E-01		1.14E+00	1.91E-01		Unigene86888_All//gi|223452597|gb|ACM89625.1|//2.00E-11//disease resistance protein [Glycine max]	Unigene86888_All//1.00E-07//AT1G27170| ATP binding / protein binding / transmembrane receptor	Unigene86888_All//6.00E-67//TC173836		ko04626|Plant-pathogen interaction		nr -
Unigene86898_All	297	0.18	0.00	1.61	5.70	0.93	0.30	0.85	0.00	0.00	-7.46E+00	5.98E-01		3.20E+00	3.47E-02		-2.62E+00	1.81E-06	Down	-4.23E+00	2.19E-08	Down	-9.74E+00	4.02E-02		-9.74E+00	3.03E-02		Unigene86898_All//gi|224124864|ref|XP_002319441.1|//2.00E-26//cytochrome P450 [Populus trichocarpa] >gi|222857817|gb|EEE95364.1| cytochrome P450 [Populus trichocarpa]	Unigene86898_All//8.00E-19//AT5G24910| CYP714A1; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding			ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko04146|Peroxisome//ko00903|Limonene and pinene degradation//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko00908|Zeatin biosynthesis//ko01040|Biosynthesis of unsaturated fatty acids//ko00591|Linoleic acid metabolism	GO:0005506//GO:0016491//GO:0031410	nr -
Unigene869_All	728	28.53	5.29	27.80	13.82	14.52	6.33	2.50	1.38	2.41	-2.43E+00	1.62E-54	Down	-3.77E-02	7.81E-01		7.12E-02	7.71E-01		-1.13E+00	4.49E-10	Down	-8.58E-01	4.74E-02		-5.27E-02	9.14E-01		Unigene869_All//gi|9955730|emb|CAC05489.1|//3.00E-60//potassium channel 2 [Populus tremula x Populus tremuloides]	Unigene869_All//4.00E-39//AT4G22200| AKT2/3 (ARABIDOPSIS POTASSIUM TRANSPORT 2/3); cyclic nucleotide binding / inward rectifier potassium channel/ protein binding	Unigene869_All//0.00E+00//ES827009			GO:0005249//GO:0005515//GO:0006811//GO:0006873//GO:0009725//GO:0016020	nr +
Unigene8690_All	255	2.46	0.00	0.00	1.37	1.76	0.35	0.50	0.98	0.78	-1.13E+01	7.90E-04	Down	-1.13E+01	1.40E-03		3.60E-01	8.06E-01		-1.95E+00	1.96E-01		9.83E-01	5.17E-01		6.51E-01	6.65E-01								
Unigene8691_All	650	0.64	0.55	0.90	1.46	1.75	0.56	2.15	0.19	1.72	-2.39E-01	8.09E-01		4.85E-01	6.30E-01		2.64E-01	7.30E-01		-1.39E+00	6.08E-02		-3.48E+00	5.79E-07	Down	-3.23E-01	5.30E-01		Unigene8691_All//gi|30684540|ref|NP_193617.2|//1.00E-53//ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding [Arabidopsis thaliana]	Unigene8691_All//5.00E-55//AT4G18820| ATP binding / DNA binding / DNA-directed DNA polymerase/ nucleoside-triphosphatase/ nucleotide binding	Unigene8691_All//0.00E+00//ES816108				nr -
Unigene86916_All	251	0.00	0.00	0.42	3.18	1.78	1.08	5.73	1.67	1.59	null	null		8.73E+00	3.87E-01		-8.32E-01	2.88E-01		-1.56E+00	6.26E-02		-1.78E+00	8.40E-04	Down	-1.85E+00	3.87E-04	Down			Unigene86916_All//7.00E-79//TC140227				
Unigene8692_All	892	0.00	0.11	0.00	0.11	0.12	0.25	3.41	3.37	8.22	6.83E+00	3.78E-01		null	null		5.20E-02	9.64E-01		1.18E+00	5.48E-01		-1.67E-02	9.94E-01		1.27E+00	1.89E-10	Up	Unigene8692_All//gi|224112961|ref|XP_002316346.1|//5.00E-18//predicted protein [Populus trichocarpa] >gi|222865386|gb|EEF02517.1| predicted protein [Populus trichocarpa]	Unigene8692_All//7.00E-07//AT4G30230| unknown protein					nr -
Unigene8694_All	529	0.00	0.38	0.00	0.00	0.13	0.00	44.20	15.09	36.07	8.58E+00	1.34E-01		null	null		7.02E+00	5.99E-01		null	null		-1.55E+00	1.88E-41	Down	-2.93E-01	3.33E-03								
Unigene86958_All	216	0.00	2.35	0.74	2.31	0.00	2.09	23.10	40.83	48.88	1.12E+01	3.99E-03		9.53E+00	2.33E-01		-1.12E+01	8.97E-04	Down	-1.41E-01	8.92E-01		8.22E-01	2.37E-06		1.08E+00	1.35E-11	Up	Unigene86958_All//gi|59896631|gb|AAX11684.1|//3.00E-10//perakine reductase [Rauvolfia serpentina]	Unigene86958_All//3.00E-06//AT1G60730| aldo/keto reductase family protein	Unigene86958_All//3.00E-56//gi|48746486|gb|CO077005.1|CO077005			GO:0004033//GO:0008152	nr +
Unigene86961_All	261	0.20	0.00	0.00	3.44	0.13	0.69	0.00	0.00	0.00	-7.65E+00	5.98E-01		-7.65E+00	6.12E-01		-4.70E+00	1.27E-05	Down	-2.31E+00	5.78E-03		null	null		null	null								
Unigene8697_All	370	0.00	0.00	0.00	3.10	2.70	1.22	1.94	0.11	0.65	null	null		null	null		-1.98E-01	7.77E-01		-1.34E+00	4.01E-02		-4.10E+00	2.91E-04	Down	-1.59E+00	3.62E-02		Unigene8697_All//gi|22725939|gb|AAN04949.1|//6.00E-39//Putative retroelement [Oryza sativa Japonica Group]						nr -
Unigene8698_All	651	0.00	0.00	0.33	4.51	2.12	0.35	0.91	0.45	0.00	null	null		8.35E+00	1.37E-01		-1.09E+00	1.41E-03		-3.70E+00	4.84E-13	Down	-1.02E+00	2.40E-01		-9.83E+00	1.41E-04	Down	Unigene8698_All//gi|15210616|ref|NP_199823.1|//6.00E-75//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene8698_All//3.00E-76//AT5G50120| transducin family protein / WD-40 repeat family protein					nr -
Unigene86981_All	215	2.43	0.47	0.50	2.78	0.00	0.00	0.20	0.00	0.00	-2.37E+00	4.75E-02		-2.30E+00	6.75E-02		-1.14E+01	1.77E-04	Down	-1.14E+01	7.69E-04	Down	-7.62E+00	6.39E-01		-7.62E+00	5.98E-01								
Unigene8699_All	316	148.85	134.37	112.57	182.55	172.29	108.19	307.87	163.22	121.79	-1.48E-01	7.62E-02		-4.03E-01	3.84E-07		-8.35E-02	3.14E-01		-7.55E-01	2.70E-28		-9.16E-01	2.76E-74		-1.34E+00	2.16E-140	Down	Unigene8699_All//gi|300269009|gb|EFJ53189.1|//9.00E-07//histone H2B [Volvox carteri f. nagariensis]	Unigene8699_All//4.00E-08//AT5G59910| HTB4; DNA binding	Unigene8699_All//2.00E-67//TC162755				nr -
Unigene870_All	2819	27.77	6.00	36.17	14.84	15.67	6.86	3.55	1.96	2.59	-2.21E+00	1.14E-181	Down	3.82E-01	2.43E-13		7.84E-02	4.25E-01		-1.11E+00	2.35E-39	Down	-8.61E-01	1.23E-07		-4.59E-01	3.49E-03		Unigene870_All//gi|9955730|emb|CAC05489.1|//0.00E+00//potassium channel 2 [Populus tremula x Populus tremuloides]	Unigene870_All//0.00E+00//AT4G22200| AKT2/3 (ARABIDOPSIS POTASSIUM TRANSPORT 2/3); cyclic nucleotide binding / inward rectifier potassium channel/ protein binding	Unigene870_All//0.00E+00//TC130754		ko04626|Plant-pathogen interaction	GO:0000166//GO:0005249//GO:0005515//GO:0006873//GO:0009725//GO:0030001//GO:0031224//GO:0043231	nr -
Unigene8700_All	1540	0.00	0.00	0.00	0.00	0.00	0.00	6.29	7.06	0.23	null	null		null	null		null	null		null	null		1.67E-01	3.52E-01		-4.76E+00	3.47E-58	Down	Unigene8700_All//gi|159479860|ref|XP_001698004.1|//1.00E-123//UDP-glucose dehydrogenase [Chlamydomonas reinhardtii] >gi|158273803|gb|ED099589.1| UDP-glucose dehydrogenase [Chlamydomonas reinhardtii]	Unigene8700_All//1.00E-121//AT3G29360| UDP-glucose 6-dehydrogenase, putative			ko00500|Starch and sucrose metabolism//ko00520|Amino sugar and nucleotide sugar metabolism//ko00053|Ascorbate and aldarate metabolism//ko00040|Pentose and glucuronate interconversions		nr -
Unigene87003_All	252	0.00	0.00	0.00	2.97	0.14	0.36	1.34	0.50	0.00	null	null		null	null		-4.44E+00	1.31E-04	Down	-3.05E+00	3.33E-03		-1.43E+00	2.58E-01		-1.04E+01	8.13E-03		Unigene87003_All//gi|170286899|dbj|BAG13451.1|//8.00E-20//beta-glucosidase [Rosa hybrid cultivar]	Unigene87003_All//4.00E-18//AT3G60120| BGLU27 (BETA GLUCOSIDASE 27); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds			ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0008422//GO:0031410//GO:0043167//GO:0044238	nr +
Unigene8701_All	288	0.00	0.00	0.00	0.35	0.00	0.00	11.30	12.77	3.46	null	null		null	null		-8.43E+00	3.06E-01		-8.43E+00	3.90E-01		1.76E-01	6.08E-01		-1.71E+00	1.49E-07	Down							
Unigene8702_All	317	2.15	3.52	3.53	2.51	3.58	2.42	0.00	3.16	0.38	7.13E-01	2.69E-01		7.17E-01	2.87E-01		5.12E-01	4.65E-01		-5.40E-02	9.53E-01		1.16E-01	3.93E-07	Up	8.56E+00	2.42E-01				Unigene8702_All//2.00E-73//C0077675				
Unigene8704_All	312	0.34	0.65	2.56	0.32	2.32	3.04	0.68	0.40	2.04	9.54E-01	6.19E-01		2.93E+00	5.05E-03		2.86E+00	6.45E-03		3.25E+00	5.84E-04	Up	-7.54E-01	6.31E-01		1.59E+00	5.48E-02		Unigene8704_All//gi|15239132|ref|NP_199109.1|//1.00E-12//GVF domain-containing protein [Arabidopsis thaliana]	Unigene8704_All//4.00E-14//AT4G32950| GVF domain-containing protein	Unigene8704_All//1.00E-65//TC144417				nr -
Unigene87050_All	235	0.00	0.22	0.00	0.21	0.73	0.19	3.24	2.49	0.17	7.75E+00	6.06E-01		null	null		1.79E+00	5.19E-01		-1.42E-01	9.45E-01		-3.79E-01	6.35E-01		-4.26E+00	8.65E-05	Down	Unigene87050_All//gi|224085996|ref|XP_002307770.1|//4.00E-24//acyl:coa ligase [Populus trichocarpa] >gi|222857219|gb|EEE94766.1| acyl:coa ligase [Populus trichocarpa]	Unigene87050_All//4.00E-17//AT1G20510| OPCL1 (OPC-8:0 COA LIGASE1); 4-coumarate-CoA ligase	Unigene87050_All//3.00E-62//DW499144		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism//ko00592|alpha-Linolenic acid metabolism//ko00130|Ubiquinone and other terpenoid-quinone biosynthesis	GO:0006575//GO:0006950//GO:0009694//GO:0016405//GO:0016491//GO:0042579	nr -
Unigene87055_All	216	0.24	0.00	0.00	0.92	0.16	0.21	0.59	0.19	6.09	-7.92E+00	5.98E-01		-7.92E+00	6.12E-01		-2.53E+00	2.33E-01		-2.14E+00	3.46E-01		-1.60E+00	5.32E-01		3.37E+00	1.37E-06	Up							
Unigene8706_All	1047	0.00	0.00	0.00	0.29	0.00	0.00	10.98	22.39	5.86	null	null		null	null		-8.16E+00	2.00E-02		-8.16E+00	3.97E-02		1.03E+00	3.05E-22	Up	-9.07E-01	1.13E-09		Unigene8706_All//gi|30024600|dbj|BAC75672.1|//3.00E-83//transcription factor MYB102 [Lotus japonicus]	Unigene8706_All//9.00E-80//AT1G34670| AtMYB93 (myb domain protein 93); DNA binding / transcription factor	Unigene8706_All//9.00E-14//TC139493	MYB			nr -
Unigene87068_All	238	1.98	0.00	0.22	3.35	0.43	0.19	0.89	0.35	0.50	-1.10E+01	5.53E-03		-3.14E+00	3.99E-02		-2.95E+00	1.08E-03		-4.14E+00	4.12E-04	Down	-1.34E+00	4.29E-01		-8.23E-01	5.98E-01				Unigene87068_All//1.00E-92//TC177978				
Unigene8707_All	1083	0.00	66.48	27.34	0.00	0.06	0.00	0.00	0.00	0.00	1.60E+01	0.00E+00	Up	1.47E+01	7.82E-168	Up	5.99E+00	5.99E-01		null	null		null	null		null	null		Unigene8707_All//gi|299472972|emb|CBN77373.1|//1.00E-172//alpha tubulin [Ectocarpus siliculosus] >gi|299472977|emb|CBN77378.1| alpha tubulin [Ectocarpus siliculosus]	Unigene8707_All//6.00E-165//AT1G50010| TUA2; structural constituent of cytoskeleton	Unigene8707_All//2.00E-98//TC142299		ko04145|Phagosome		nr +
Unigene8708_All	944	0.00	0.00	0.00	0.47	0.26	0.00	9.50	2.30	0.59	null	null		null	null		-8.95E-01	4.13E-01		-8.89E+00	5.78E-03		-2.04E+00	1.26E-23	Down	-4.01E+00	2.92E-48	Down	Unigene8708_All//gi|195635339|gb|ACG37138.1|//5.00E-53//cytochrome c oxidoreductase [Zea mays]	Unigene8708_All//2.00E-51//AT4G15920| INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPR018169), RAG1-activating protein 1 homologue (InterPro:IPR018179), MtN3 and saliva related transmembrane protein (InterPro:IPR004316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).						nr -
Unigene87092_All	450	0.00	0.45	0.24	1.99	0.31	0.40	0.66	0.37	2.48	8.82E+00	1.34E-01		7.89E+00	3.87E-01		-2.70E+00	8.76E-04	Down	-2.31E+00	5.78E-03		-8.24E-01	5.40E-01		1.91E+00	1.87E-03		Unigene87092_All//gi|209970605|gb|ACJ03065.1|//1.00E-27//HB03p [Malus floribunda]	Unigene87092_All//1.00E-23//AT1G74180| AtRLP14 (Receptor Like Protein 14); protein binding			ko04626|Plant-pathogen interaction		nr +
Unigene8710_All	666	0.47	0.68	0.08	2.69	0.67	1.70	2.16	1.13	0.84	5.39E-01	6.02E-01		-2.56E+00	1.59E-01		-2.00E+00	4.72E-05	Down	-6.68E-01	1.86E-01		-9.34E-01	6.12E-02		-1.37E+00	5.50E-03								
Unigene87107_All	270	0.00	0.19	0.59	8.30	2.17	0.00	0.31	0.15	0.59	7.55E+00	6.06E-01		9.21E+00	2.33E-01		-1.94E+00	6.21E-06	Down	-1.30E+01	4.79E-14	Down	-1.02E+00	7.20E-01		9.14E-01	6.23E-01								
Unigene87119_All	222	0.47	0.00	0.00	2.69	1.40	0.00	1.14	0.38	0.18	-8.88E+00	3.64E-01		-8.88E+00	3.86E-01		-9.48E-01	3.09E-01		-1.14E+01	7.69E-04	Down	-1.60E+00	3.10E-01		-2.67E+00	1.15E-01		Unigene87119_All//gi|224141315|ref|XP_002324019.1|//8.00E-09//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222867021|gb|EEF94152.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]						GO:0000166//GO:0006810//GO:0042626	nr +
Unigene8712_All	479	1.20	1.16	1.00	1.56	2.08	7.35	0.88	0.17	0.42	-4.62E-02	9.74E-01		-2.64E-01	7.67E-01		4.19E-01	5.84E-01		2.24E+00	2.97E-09	Up	-2.34E+00	5.45E-02		-1.09E+00	2.82E-01		Unigene8712_All//gi|297838855|ref|XP_002887309.1|//2.00E-33//alliinase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297333150|gb|EFH63568.1| alliinase C-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene8712_All//3.00E-34//AT1G70560| TAA1 (TRYPTOPHAN AMINOTRANSFERASE OF ARABIDOPSIS 1); L-alanine:2-oxoglutarate aminotransferase/ L-glutamine:2-oxoglutarate aminotransferase/ L-leucine:2-oxoglutarate aminotransferase/ L-methionine:2-oxoglutarate aminotransferase/ L-phenylalanine:2-oxoglut	Unigene8712_All//0.00E+00//gi|78344302|gb|DT564576.1|DT564576				nr +
Unigene87120_All	481	0.44	0.21	0.00	3.21	0.72	0.66	0.44	0.35	0.08	-1.05E+00	5.63E-01		-8.77E+00	1.44E-01		-2.17E+00	7.68E-05	Down	-2.29E+00	1.35E-04	Down	-3.38E-01	8.11E-01		-2.41E+00	1.94E-01								
Unigene8714_All	257	3.66	0.59	2.90	17.83	16.48	1.05	5.92	1.79	2.17	-2.63E+00	2.38E-03		-3.37E-01	6.16E-01		-1.14E-01	7.37E-01		-4.08E+00	1.13E-21	Down	-1.73E+00	7.56E-04	Down	-1.45E+00	2.57E-03				Unigene8714_All//5.00E-117//gi|13355910|gb|BG446198.1|BG446198				
Unigene87147_All	396	2.11	0.51	0.00	2.39	0.61	1.03	0.64	0.00	0.60	-2.05E+00	1.68E-02		-1.10E+01	1.19E-04	Down	-1.97E+00	6.32E-03		-1.22E+00	9.72E-02		-9.32E+00	4.02E-02		-8.58E-02	9.56E-01				Unigene87147_All//1.00E-53//TC160879				

Unigene8715_All	673	0.00	18.75	7.20	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	2.16E-72	Up	1.28E+01	6.10E-27	Up	null	null		null	null		null	null		null	null		Unigene8715_All//sp|P27780|CUP8_DROME//2.00E-30//Pupal cuticle protein Edg-84A OS=Drosophila melanogaster GN=Edg84A PE=2 SV=1						swissprot -
Unigene87155_All	455	0.00	0.00	0.00	0.22	0.15	0.20	0.00	2.39	0.88	null	null		null	null		-5.33E-01	8.12E-01		-1.42E-01	9.46E-01		1.12E+01	1.04E-07	Up	9.77E+00	3.96E-03		Unigene87155_All//gi|209954711|dbj|BAG80546.1|//2.00E-30//UDP-glucose:glucosyltransferase [Lycium barbarum]	Unigene87155_All//4.00E-24//AT1G24100| UGT74B1 (UDP-glucosyl transferase 74B1); UDP-glycosyltransferase/ thiohydroximate beta-D-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene87155_All//9.00E-163//gi|164365999|gb|ES828422.1|ES828422		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis//ko00942|Anthocyanin biosynthesis	GO:0016757	nr +
Unigene8716_All	215	71.79	41.01	25.02	63.72	46.45	75.41	57.23	33.05	12.79	-8.08E-01	1.81E-08		-1.52E+00	3.88E-21	Down	-4.56E-01	1.41E-03		2.43E-01	1.03E-01		-7.92E-01	4.44E-08		-2.16E+00	1.30E-35	Down	Unigene8716_All//gi|192908658|gb|ACF06437.1|//1.00E-15//ribosomal L28-like protein [Elaeis guineensis]	Unigene8716_All//7.00E-12//AT2G19730| 60S ribosomal protein L28 (RPL28A)	Unigene8716_All//4.00E-111//gi|13352840|gb|BG443188.1|BG443188		ko03010|Ribosome		nr +
Unigene87167_All	273	59.22	41.02	83.48	0.55	4.04	0.83	0.00	0.00	0.00	-5.30E-01	1.24E-04		4.95E-01	2.77E-05		2.88E+00	3.08E-04	Up	5.96E-01	7.21E-01		null	null		null	null		Unigene87167_All//gi|18390888|ref|NP_563815.1|//4.00E-18//PSAO (photosystem I subunit O) [Arabidopsis thaliana] >gi|21702253|emb|CAD37939.1| photosystem I subunit O [Arabidopsis thaliana]	Unigene87167_All//2.00E-19//AT1G08380| PSAO (photosystem I subunit O)	Unigene87167_All//1.00E-83//TC157349			GO:0009521//GO:0009536//GO:0009765	nr -
Unigene8719_All	420	2.99	1.33	0.63	1.42	0.00	1.08	4.03	4.48	0.85	-1.17E+00	5.48E-02		-2.24E+00	1.94E-03		-1.05E+01	1.77E-04	Down	-4.05E-01	6.73E-01		1.53E-01	7.28E-01		-2.24E+00	8.65E-06	Down			Unigene8719_All//0.00E+00//TC168325				
Unigene8720_All	502	0.00	3.33	0.00	0.60	0.14	0.36	4.38	14.24	3.41	1.17E+01	1.53E-09	Up	null	null		-2.12E+00	1.65E-01		-7.26E-01	6.38E-01		1.70E+00	6.11E-15	Up	-3.60E-01	3.60E-01								
Unigene87201_All	304	0.69	0.67	1.75	5.24	11.78	5.50	3.48	1.79	9.57	-4.62E-02	9.86E-01		1.35E+00	2.25E-01		1.17E+00	2.39E-04	Up	6.81E-02	9.17E-01		-9.60E-01	1.12E-01		1.46E+00	1.46E-05	Up	Unigene87201_All//gi|15232355|ref|NP_191612.1|//5.00E-06//zinc finger (GATA type) family protein [Arabidopsis thaliana] >gi|62900345|sp|Q49743.1|GATA4_ARATH RecName: Full=GATA transcription factor 4; Short=AtGATA-4 >gi|41596402|gb|AAK55684.1|AF378881_1 AT3g60530/T8B10_190 [Arabidopsis thaliana] >gi|29559736|emb|CAA74002.1| homologous to GATA-binding transcription factors [Arabidopsis thaliana] >gi|7288001|emb|CAB81839.1| GATA transcription factor 4 [Arabidopsis thaliana] >gi|14517395|gb|AAK62588.1| AT3g60530/T8B10_190 [Arabidopsis thaliana] >gi|15215891|gb|AAK91489.1| AT3g60530/T8B10_190 [Arabidopsis thaliana]		Unigene87201_All//1.00E-124//TC145610				nr +
Unigene87209_All	338	5.11	1.20	0.47	3.10	1.02	0.67	0.00	0.12	0.00	-2.09E+00	1.98E-04	Down	-3.43E+00	1.49E-06	Down	-1.60E+00	1.49E-02		-2.21E+00	3.25E-03		6.95E+00	6.23E-01		null	null		Unigene87209_All//gi|117957141|gb|ABK59039.1|//9.00E-26//MYB60-like protein [Citrus macrophylla]	Unigene87209_All//8.00E-27//AT1G08810| MYB60 (myb domain protein 60); DNA binding / transcription factor	Unigene87209_All//3.00E-69//TC168071	MYB		GO:0001071//GO:0003676//GO:0006351//GO:0006950//GO:0009314//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene8721_All	545	0.96	0.37	0.00	3.29	1.90	0.75	1.63	0.31	1.90	-1.37E+00	1.96E-01		-9.91E+00	4.73E-03		-7.96E-01	8.93E-02		-2.14E+00	6.96E-05	Down	-2.41E+00	1.79E-03		2.22E-01	6.97E-01		Unigene8721_All//gi|7239503|gb|AAF43229.1|AC012654_13//1.00E-18//F14023.14 [Arabidopsis thaliana]	Unigene8721_All//1.00E-18//AT1G71760| unknown protein	Unigene8721_All//0.00E+00//TC130679				nr -
Unigene8721_All	237	0.00	3.63	0.90	0.00	0.00	0.57	0.00	0.00	0.17	1.18E+01	4.91E-05	Up	9.81E+00	1.37E-01		null	null		9.16E+00	3.09E-01		null	null		7.39E+00	6.33E-01								
Unigene8722_All	371	2.82	8.47	0.86	6.71	5.01	10.47	0.00	0.00	0.00	1.59E+00	2.47E-05	Up	-1.71E+00	2.35E-02		-4.22E-01	3.14E-01		6.41E-01	4.14E-02		null	null		null	null				Unigene8722_All//2.00E-15//FL576501				
Unigene87221_All	253	1.45	1.20	2.32	2.95	0.27	1.96	2.01	0.83	0.94	-2.69E-01	8.00E-01		6.78E-01	4.82E-01		-3.44E+00	6.18E-04	Down	-5.89E-01	4.87E-01		-1.28E+00	1.86E-01		-1.09E+00	2.28E-01				Unigene87221_All//7.00E-79//gi|13247084|gb|BF268519.2|BF268519				
Unigene8723_All	538	0.10	0.00	0.40	6.57	4.86	1.60	0.31	0.16	0.22	-6.60E+00	5.98E-01		2.02E+00	3.59E-01		-4.35E-01	1.90E-01		-2.04E+00	1.47E-08	Down	-1.02E+00	6.12E-01		-5.01E-01	7.45E-01		Unigene8723_All//gi|117168149|gb|AB832157.1|//2.00E-39//At1g61667 [Arabidopsis thaliana]	Unigene8723_All//6.00E-42//AT5G54530| unknown protein	Unigene8723_All//0.00E+00//TC155299				nr -
Unigene87231_All	211	0.00	0.00	0.00	3.31	0.82	0.00	0.20	0.20	0.19	null	null		null	null		-2.02E+00	2.15E-02		-1.17E+01	1.96E-04	Down	-1.67E-02	9.96E-01		-8.60E-02	9.64E-01								
Unigene87235_All	430	36.99	50.32	76.78	7.65	14.01	39.81	668.22	397.45	412.47	4.44E-01	1.68E-04		1.05E+00	1.74E-25	Up	8.74E-01	1.47E-04		2.38E+00	1.52E-46	Up	-7.50E-01	5.72E-155		-6.96E-01	7.60E-140		Unigene87235_All//gi|82659447|gb|AB888840.1|//5.00E-29//aquaporin [Stevia rebaudiana]	Unigene87235_All//2.00E-29//AT4G35100| PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel	Unigene87235_All//4.00E-168//TC145780			GO:0005372//GO:0006810//GO:0031225//GO:0043231	nr -
Unigene8724_All	1079	0.10	0.00	0.00	0.42	0.41	0.54	7.33	0.23	1.14	-6.60E+00	3.64E-01		-6.60E+00	3.86E-01		-2.10E-03	9.69E-01		3.89E-01	6.77E-01		-4.98E+00	4.14E-47	Down	-2.68E+00	1.26E-29	Down	Unigene8724_All//gi|297815530|ref|XP_002875648.1|//2.00E-63//harpin-induced family protein [Arabidopsis lyrata subsp. lyrata] >gi|297321486|gb|EFH51907.1| harpin-induced family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8724_All//2.00E-59//AT3G44220| harpin-induced family protein / HIN1 family protein / harpin-responsive family protein	Unigene8724_All//4.00E-124//gi|13356130|gb|BG446478.1|BG446478				nr +
Unigene87241_All	340	0.00	0.00	0.16	0.44	0.00	0.00	0.00	0.61	1.52	null	null		7.29E+00	6.22E-01		-8.78E+00	1.63E-01		-8.78E+00	2.30E-01		9.26E+00	7.83E-02		1.06E+01	6.13E-04	Up	Unigene87241_All//gi|255537357|ref|XP_002509745.1|//2.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223549644|gb|EEF51132.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene8725_All	1307	0.00	0.31	0.00	0.00	0.00	0.07	7.21	10.84	3.44	8.28E+00	1.34E-02		null	null		null	null		6.11E+00	4.69E-01		5.88E-01	9.30E-06		-1.07E+00	2.57E-10	Down	Unigene8725_All//gi|224052970|ref|XP_002297642.1|//1.00E-120//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222844900|gb|EEE82447.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene8725_All//5.00E-115//AT3G13610| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene8725_All//0.00E+00//TC178591		ko00941|Flavonoid biosynthesis		nr -
Unigene87261_All	584	0.00	0.00	0.00	1.28	0.71	1.31	2.17	1.15	0.48	null	null		null	null		-8.55E-01	2.95E-01		3.92E-02	9.59E-01		-9.24E-01	8.68E-02		-2.19E+00	1.97E-04	Down	Unigene87261_All//gi|163889364|gb|ABY48134.1|//5.00E-23//bHLH transcription factor [Medicago truncatula]		Unigene87261_All//0.00E+00//gi|164256001|gb|ES849617.1|ES849617				nr -
Unigene87269_All	244	0.00	0.00	0.00	0.00	0.00	0.37	3.99	0.69	0.49	null	null		null	null		null	null		8.53E+00	4.69E-01		-2.54E+00	6.41E-04	Down	-3.02E+00	9.60E-05	Down							
Unigene87270_All	202	0.00	0.00	0.26	0.99	0.00	0.67	1.05	1.03	24.06	null	null		8.04E+00	6.22E-01		-9.95E+00	8.34E-02		-5.57E-01	7.32E-01		-1.66E-02	1.02E+00		4.52E+00	5.55E-28	Up	Unigene87270_All//gi|297795185|ref|XP_002865477.1|//9.00E-07//transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311312|gb|EFH41736.1| transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene87270_All//9.00E-07//AT5G42830| transferase family protein					nr +
Unigene8728_All	478	0.11	0.11	0.33	2.81	1.51	1.51	0.97	4.11	1.08	-4.69E-02	9.81E-01		1.61E+00	5.09E-01		-8.95E-01	1.07E-01		-8.96E-01	1.30E-01		2.08E+00	7.81E-06	Up	1.55E-01	8.60E-01		Unigene8728_All//gi|297828261|ref|XP_002882013.1|//4.00E-13//expressed protein [Arabidopsis lyrata subsp. lyrata] >gi|297327852|gb|EFH58272.1| expressed protein [Arabidopsis lyrata subsp. lyrata]	Unigene8728_All//2.00E-13//AT2G45450| ZPR1 (LITTLE ZIPPER 1); protein binding	Unigene8728_All//0.00E+00//DW518216				nr +
Unigene873_All	1198	4.02	7.11	7.47	9.23	7.30	8.52	5.86	1.57	1.73	8.23E-01	3.70E-05		8.94E-01	8.73E-06		-3.38E-01	4.63E-02		-1.16E-01	5.91E-01		-1.90E+00	5.18E-17	Down	-1.76E+00	6.33E-16	Down	Unigene873_All//gi|15239054|ref|NP_196707.1|//6.00E-26//senescence-associated protein-related [Arabidopsis thaliana] >gi|50198799|gb|AAT70433.1| At5g11460 [Arabidopsis thaliana] >gi|11107484|gb|AB80461 5.1| At5g11460 [Arabidopsis thaliana]	Unigene873_All//3.00E-27//AT5G11460| senescence-associated protein-related	Unigene873_All//2.00E-163//DW511776				nr -
Unigene8731_All	537	2.92	1.70	1.59	2.13	2.95	1.09	0.94	1.71	4.23	-7.83E-01	1.36E-01		-8.82E-01	1.13E-01		4.67E-01	4.16E-01		-9.65E-01	1.37E-01		8.58E-01	1.95E-01		2.16E+00	4.04E-07	Up			Unigene8731_All//0.00E+00//TC144363				
Unigene87322_All	238	1.32	0.43	1.79	3.35	1.16	0.00	0.71	0.00	0.50	-1.63E+00	2.76E-01		4.40E-01	6.76E-01		-1.53E+00	4.83E-02		-1.17E+01	4.90E-05	Down	-9.47E+00	1.33E-01		-5.01E-01	7.45E-01		Unigene87322_All//gi|297802778|ref|XP_002869273.1|//4.00E-12//agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297315109|gb|EFH45532.1| agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene87322_All//1.00E-12//AT4G32440| agenet domain-containing protein	Unigene87322_All//5.00E-64//ES832838				nr -
Unigene87330_All	376	0.00	0.00	0.00	0.79	0.00	0.00	0.11	0.00	1.70	null	null		null	null		-9.63E+00	2.00E-02		-9.63E+00	3.97E-02		-6.81E+00	6.39E-01		3.91E+00	7.65E-04	Up	Unigene87330_All//gi|242199342|gb|ACS87992.1|//9.00E-12//UDP-glucosyltransferase family 1 protein [Citrus sinensis]	Unigene87330_All//2.00E-11//AT2G36760| UGT73C2 (UDP-glucosyl transferase 73C2); UDP-glycosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups			ko00908|Zeatin biosynthesis	GO:0016757	nr +
Unigene87332_All	242	0.43	0.00	0.00	1.03	0.00	0.00	4.72	18.65	4.77	-8.76E+00	3.64E-01		-8.76E+00	3.86E-01		-1.00E+01	4.15E-02		-1.00E+01	7.27E-02		1.98E+00	8.62E-12	Up	1.73E-02	9.72E-01				Unigene87332_All//1.00E-27//GE654079				ESTscan +
Unigene87338_All	407	0.00	0.00	0.39	0.37	0.00	0.67	1.87	14.38	6.46	null	null		8.62E+00	2.33E-01		-8.52E+00	1.63E-01		8.59E-01	6.30E-01		2.94E+00	1.87E-23	Up	1.79E+00	1.58E-06	Up	Unigene87338_All//gi|217038861|gb|ACJ76787.1|//7.00E-09//S-norcoclaurine synthase 2 [Argemone mexicana]		Unigene87338_All//3.00E-45//FF403697				nr +
Unigene87358_All	242	0.00	0.63	0.00	3.50	3.98	1.87	10.66	0.00	2.47	9.29E+00	2.31E-01		null	null		1.87E-01	8.11E-01		-9.07E-01	2.47E-01		-1.34E+01	3.06E-18	Down	-2.11E+00	7.05E-08	Down	Unigene87358_All//gi|268376311|gb|ACD24921.1|//8.00E-22//actin 7-like protein [Pelargonium x hortorum]	Unigene87358_All//7.00E-23//AT5G59370| ACT4 (ACTIN 4); structural constituent of cytoskeleton	Unigene87358_All//2.00E-88//TC130048		ko04145|Phagosome	GO:0032559//GO:0043232	nr -
Unigene8736_All	361	0.00	0.00	0.00	0.28	0.00	0.00	27.17	5.44	34.43	null	null		null	null		-8.11E+00	3.06E-01		-8.11E+00	3.90E-01		-2.32E+00	4.27E-30	Down	3.42E-01	1.58E-02		Unigene8736_All//gi|73624747|gb|AAZ79231.1|//2.00E-43//cellulose synthase-like protein CslG [Nicotiana tabacum]	Unigene8736_All//5.00E-43//AT4G24000| ATCSLG2; cellulose synthase/ transferase/ transferase, transferring glycosyl groups					nr -
Unigene87364_All	254	0.00	0.00	0.00	2.35	0.27	0.00	0.67	0.82	0.78	null	null		null	null		-3.12E+00	4.86E-03		-1.12E+01	7.69E-04	Down	3.06E-01	8.35E-01		2.36E-01	8.82E-01								
Unigene87391_All	209	38.30	121.22	85.10	6.20	14.50	14.48	0.20	0.40	0.38	1.66E+00	2.56E-40	Up	1.15E+00	4.52E-16	Up	1.23E+00	5.11E-04	Up	1.22E+00	7.75E-04	Up	9.84E-01	7.28E-01		9.14E-01	7.46E-01		Unigene87391_All//gi|224091479|ref|XP_002309268.1|//2.00E-27//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222855244|gb|EEE92794.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene87391_All//2.00E-27//AT5G06530| ABC transporter family protein	Unigene87391_All//2.00E-97//gi|48744950|gb|CO075469.1|CO075469			GO:0015098//GO:0016020//GO:0032559//GO:0042626	nr -
Unigene87414_All	779	0.20	0.00	0.41	1.98	0.31	0.23	0.54	0.11	0.15	-7.65E+00	2.13E-01		1.03E+00	4.70E-01		-2.68E+00	4.47E-06	Down	-3.10E+00	4.09E-06	Down	-2.34E+00	5.45E-02		-1.82E+00	9.21E-02		Unigene87414_All//gi|28874838|emb|CAC84088.1|//2.00E-18//ZR4 protein [Medicago sativa]	Unigene87414_All//5.00E-19//AT5G19420| Ran GTPase binding / chromatin binding / zinc ion binding	Unigene87414_All//0.00E+00//ES843022				nr +
Unigene87427_All	345	0.00	0.00	0.00	2.60	0.30	0.00	0.00	0.00	0.00	null	null		null	null		-3.12E+00	2.80E-04	Down	-1.13E+01	1.21E-05	Down	null	null		null	null		Unigene87427_All//gi|242067241|ref|XP_002448897.1|//3.00E-10//hypothetical protein SORBIDRAFT_05g001075 [Sorghum bicolor] >gi|241934740|gb|EES07885.1| hypothetical protein SORBIDRAFT_05g001075 [Sorghum bicolor]		Unigene87427_All//1.00E-07//BQ413180				nr +

Unigene87430_All	307	0.00	0.00	1.91	2.11	0.67	0.00	0.00	0.00	0.00	null	null		1.09E+01	2.15E-03		-1.65E+00	6.52E-02		-1.10E+01	3.89E-04	Down	null	null		null	null		Unigene87430_All//gi|5107822|gb|AAD40135.1|AF149413_16//1.00E-17//contains similarity to retrotransposon Tal1-1 [Arabidopsis thaliana]	Unigene87430_All//2.00E-11//ATMGN1250| hypothetical protein				GO:0003676//GO:0006260//GO:0031410//GO:0034061//GO:0043231	nr +
Unigene87434_All	238	0.00	0.64	0.00	0.84	0.58	0.00	0.36	5.44	6.53	9.32E+00	2.31E-01		null	null		-5.33E-01	7.47E-01		-9.71E+00	1.32E-01		3.94E+00	4.68E-07	Up	4.20E+00	6.61E-09	Up		Unigene87434_All//5.00E-49//DT462226					
Unigene8744_All	407	2.96	1.37	0.65	5.51	3.13	0.44	6.44	0.82	0.00	-1.11E+00	7.50E-02		-2.18E+00	3.04E-03		-8.15E-01	4.54E-02		-3.63E+00	6.89E-10	Down	-2.97E+00	5.45E-11	Down	-1.27E+01	2.73E-19	Down	Unigene8744_All//gi|297830148|ref|XP_002882956.1|//2.00E-20//phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328796|gb|EFH59215.1| phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8744_All//1.00E-21//AT3G15650| phospholipase/carboxylesterase family protein	Unigene8744_All//0.00E+00//ES792172				nr +
Unigene87444_All	265	0.79	0.19	0.80	1.13	2.34	1.02	11.97	4.42	8.27	-2.05E+00	3.33E-01		2.55E-02	1.00E+00		1.05E+00	2.99E-01		-1.41E-01	9.20E-01		-1.44E+00	1.03E-05	Down	-5.33E-01	7.78E-02			Unigene87444_All//8.00E-48//DR461871					
Unigene87457_All	361	56.52	29.48	32.01	51.33	46.36	103.34	75.54	50.13	33.88	-9.39E-01	6.79E-14		-8.20E-01	1.06E-10		-1.47E-01	3.08E-01		1.01E+00	1.26E-29	Up	-5.92E-01	1.90E-10		-1.16E+00	5.57E-32	Down	Unigene87457_All//gi|192913000|gb|ACF06608.1|//2.00E-36//ribosomal protein [Elaeis guineensis]	Unigene87457_All//3.00E-36//AT5G39850| 40S ribosomal protein S9 (RPS9C)	Unigene87457_All//5.00E-167//gi|11202123|gb|BF271128.1|BF271128		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0033279	nr +
Unigene87460_All	263	0.20	1.16	0.00	2.27	0.26	0.00	0.00	0.64	0.15	2.54E+00	1.51E-01		-7.64E+00	6.12E-01		-3.12E+00	4.86E-03		-1.12E+01	7.69E-04	Down	9.31E+00	1.38E-01		7.24E+00	6.33E-01								
Unigene87461_All	395	6.09	6.80	8.36	6.94	4.97	2.63	0.54	2.01	2.02	1.58E-01	6.75E-01		4.56E-01	2.13E-01		-4.81E-01	2.10E-01		-1.40E+00	2.97E-04	Down	1.91E+00	1.37E-02		1.91E+00	1.08E-02								
Unigene87477_All	281	0.00	0.00	0.00	3.19	0.25	0.64	0.00	0.00	0.00	null	null		null	null		-3.70E+00	7.11E-05	Down	-2.31E+00	5.78E-03		null	null		null	null		Unigene87477_All//gi|297795907|ref|XP_002865838.1|//2.00E-32//short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311673|gb|EFH42097.1| short-chain dehydrogenase/reductase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene87477_All//1.00E-27//AT5G51030| short-chain dehydrogenase/reductase (SDR) family protein	Unigene87477_All//2.00E-58//TC177651				nr +
Unigene875_All	1524	1.44	1.46	0.94	2.52	1.88	1.27	1.61	0.91	0.47	2.09E-02	9.82E-01		-6.12E-01	1.79E-01		-4.24E-01	1.78E-01		-9.82E-01	1.51E-03		-8.30E-01	2.17E-02		-1.77E+00	3.66E-06	Down	Unigene875_All//gi|15239054|ref|NP_196707.1|//6.00E-26//senescence-associated protein-related [Arabidopsis thaliana] >gi|50198799|gb|AAT70433.1| At5g11460 [Arabidopsis thaliana] >gi|11074484|gb|AB804615.1| At5g11460 [Arabidopsis thaliana]	Unigene875_All//3.00E-27//AT5G11460| senescence-associated protein-related	Unigene875_All//0.00E+00//TC149955				nr -
Unigene87501_All	555	0.75	0.82	0.10	1.88	1.18	0.24	0.15	0.60	0.29	1.24E-01	9.11E-01		-2.98E+00	6.44E-02		-6.77E-01	3.14E-01		-2.95E+00	3.82E-04	Down	1.98E+00	1.44E-01		9.14E-01	6.23E-01		Unigene87501_All//gi|224076400|ref|XP_002304937.1|//4.00E-06//predicted protein [Populus trichocarpa] >gi|222847901|gb|EEE85448.1| predicted protein [Populus trichocarpa]		Unigene87501_All//1.00E-08//DT469086				nr +
Unigene87521_All	545	0.10	0.00	0.09	0.13	0.00	1.78	0.38	0.29	-6.59E+00	5.98E-01		-6.59E+00	6.12E-01		4.68E-01	9.52E-01		-6.51E+00	6.14E-01		-2.22E+00	1.82E-03		-2.61E+00	3.35E-04	Down	Unigene87521_All//gi|30690409|ref|NP_850456.1|//2.00E-16//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene87521_All//4.00E-18//AT2G46495| zinc finger (C3HC4-type RING finger) family protein					nr -
Unigene87538_All	236	24.61	7.94	26.85	14.78	23.35	25.07	0.18	0.35	0.00	-1.63E+00	1.30E-09	Down	1.26E-01	6.05E-01		6.60E-01	7.31E-03		7.63E-01	1.58E-03		9.83E-01	7.28E-01		-7.49E+00	5.97E-01		Unigene87538_All//gi|115451725|ref|NP_001049463.1|//2.00E-07//Os03g0231800 [Oryza sativa Japonica Group] >gi|113547934|dbj|BAF11377.1| Os03g0231800 [Oryza sativa Japonica Group]	Unigene87538_All//2.00E-06//AT4G37760| SQE3 (squalene epoxidase 3); squalene monooxygenase	Unigene87538_All//1.00E-61//TC156760		ko00100|Steroid biosynthesis		nr +
Unigene8754_All	254	0.41	0.00	0.00	1.57	0.00	2.67	51.93	110.08	480.89	-8.69E+00	3.64E-01		-8.69E+00	3.86E-01		-1.06E+01	4.37E-03		7.65E-01	4.10E-01		1.08E+00	1.11E-28	Up	3.21E+00	0.00E+00	Up	Unigene8754_All//gi|18412959|ref|NP_567300.1|//3.00E-19//IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase [Arabidopsis thaliana] >gi|5732060|gb|AAD48959.1|AF147263_1 contains similarity to Pfam families PF00106 (short chain dehydrogenase; score=151.7, E=1.3e-41, N=1) and PF00678 (Short chain dehydrogenase/reductase C-terminus; score=48.9, E=1.1e-10, N=1) [Arabidopsis thaliana] >gi|7267313|emb|CAB81095.1| AT4g05530 [Arabidopsis thaliana]	Unigene8754_All//1.00E-20//AT4G05530| IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase	Unigene8754_All//2.00E-29//TC137721		ko04146|Peroxisome		nr -
Unigene87564_All	360	0.87	0.00	0.00	1.94	0.29	0.00	0.70	0.00	0.11	-9.77E+00	3.63E-02		-9.77E+00	4.87E-02		-2.75E+00	3.99E-03		-1.09E+01	1.96E-04	Down	-9.46E+00	4.02E-02		-2.67E+00	1.15E-01		Unigene87564_All//gi|12006362|gb|AAG44843.1|AF281155_1/3.00E-06//cohesion family protein SYN3 [Arabidopsis thaliana]	Unigene87564_All//6.00E-07//AT3G59550| SYN3	Unigene87564_All//1.00E-176//ES830978				nr -
Unigene87568_All	250	0.21	0.41	0.00	0.80	0.00	0.18	0.34	0.33	3.51	9.54E-01	7.23E-01		-7.71E+00	6.12E-01		-9.64E+00	8.34E-02		-2.14E+00	3.45E-01		-1.63E-02	1.01E+00		3.37E+00	1.32E-04	Up			Unigene87568_All//3.00E-13//gi|84152253|gb|DN801608.1|DN801608				ESTscan -
Unigene8757_All	403	7.66	1.26	2.38	7.29	4.79	4.93	0.21	0.41	0.40	-2.61E+00	2.67E-09	Down	-1.69E+00	2.20E-05	Down	-6.08E-01	8.53E-02		-5.65E-01	1.34E-01		9.83E-01	6.32E-01		9.14E-01	6.23E-01		Unigene8757_All//gi|292630778|sp|Q9FN2.2|GLT3_ARATH//1.00E-49//RecName: Full=Probable glycosyltransferase At5g03795	Unigene8757_All//6.00E-51//AT5G03795| LOCATED IN: membrane; EXPRESSED IN: embryo, sepal, flower; EXPRESSED DURING: C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Exostosin-like (InterPro:IPR004263); BEST Arabidopsis thaliana protein match is: exostosin family protein (TAIR:AT3G07620.1); Has 866 Blast hits to 860 proteins in 87 species: Archae - 0; Bacteria - 9; Metazoa - 265; Fungi - 4; Plants - 504; Viruses - 0; Other Eukaryotes - 84 (source: NCBI BLink).	Unigene8757_All//0.00E+00//TC168628				nr +
Unigene8758_All	669	1.96	0.68	1.51	13.63	14.52	4.73	0.76	0.31	0.66	-1.52E+00	1.35E-02		-3.71E-01	5.53E-01		9.12E-02	6.93E-01		-1.53E+00	2.47E-14	Down	-1.28E+00	1.86E-01		-2.12E-01	7.92E-01		Unigene8758_All//gi|224117086|ref|XP_002331783.1|//4.00E-12//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222832242|gb|EEE70719.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene8758_All//3.00E-05//AT3G14460| disease resistance protein (NBS-LRR class), putative					nr -
Unigene8759_All	725	0.14	0.14	1.91	0.76	0.95	1.00	2.04	0.40	0.82	-4.57E-02	9.85E-01		3.73E+00	1.05E-05	Up	3.30E-01	7.52E-01		3.99E-01	6.51E-01		-2.34E+00	3.57E-05	Down	-1.31E+00	6.57E-03		Unigene8759_All//gi|186509871|ref|NP_187362.3|//2.00E-48//emb1974 (embryo defective 1974) [Arabidopsis thaliana]	Unigene8759_All//3.00E-46//AT3G07060| emb1974 (embryo defective 1974)	Unigene8759_All//0.00E+00//ES823789				nr -
Unigene87594_All	259	0.00	0.00	1.03	2.12	0.53	0.70	14.37	6.29	6.15	null	null		1.00E+01	7.85E-02		-1.99E+00	5.11E-02		-1.60E+00	1.32E-01		-1.19E+00	4.06E-05	Down	-1.22E+00	1.63E-05	Down	Unigene87594_All//gi|40287502|gb|AB83865.1|//7.00E-44//elongation factor 1-alpha [Capsicum annuum]	Unigene87594_All//2.00E-43//AT5G60390| elongation factor 1-alpha / EF-1-alpha	Unigene87594_All//3.00E-75//TC160471				nr +
Unigene876_All	1916	2.54	2.99	3.67	3.15	2.75	3.06	1.70	0.57	0.79	2.35E-01	3.70E-01		5.31E-01	2.22E-02		-1.94E-01	4.78E-01		-3.79E-02	9.03E-01		-1.58E+00	1.32E-06	Down	-1.10E+00	2.51E-04	Down	Unigene876_All//gi|15239054|ref|NP_196707.1|//1.00E-39//senescence-associated protein-related [Arabidopsis thaliana] >gi|50198799|gb|AAT70433.1| At5g11460 [Arabidopsis thaliana] >gi|11074484|gb|AB804615.1| At5g11460 [Arabidopsis thaliana]	Unigene876_All//6.00E-41//AT5G11460| senescence-associated protein-related	Unigene876_All//0.00E+00//DW511776				nr +
Unigene8760_All	519	1.41	0.29	0.41	6.43	8.56	2.70	0.33	0.16	0.00	-2.27E+00	1.78E-02		-1.78E+00	6.00E-02		4.13E-01	1.66E-01		-1.25E+00	2.32E-04	Down	-1.02E+00	6.12E-01		-8.35E+00	1.07E-01		Unigene8760_All//gi|18409123|ref|NP_564943.1|//2.00E-11//CLE12 (CLAVATA3/ESR-RELATED 12); protein binding / receptor binding [Arabidopsis thaliana] >gi|89111846|gb|ABD60685.1| At1g68795 [Arabidopsis thaliana]	Unigene8760_All//5.00E-09//AT1G68795| CLE12 (CLAVATA3/ESR-RELATED 12); protein binding / receptor binding					nr +
Unigene87609_All	377	2.50	0.27	0.42	10.04	2.47	2.40	0.00	0.00	0.53	-3.22E+00	6.76E-04	Down	-2.56E+00	4.40E-03		-2.03E+00	3.12E-10	Down	-2.07E+00	2.98E-09	Down	null	null		9.05E+00	7.88E-02				Unigene87609_All//2.00E-61//gi|78330690|gb|DT550964.1|DT550964				
Unigene87630_All	762	1.10	0.67	0.84	0.85	0.95	1.07	3.11	2.58	0.89	-7.24E-01	3.48E-01		-3.90E-01	6.41E-01		1.59E-01	8.68E-01		3.28E-01	7.00E-01		-2.69E-01	5.09E-01		-1.81E+00	4.17E-06	Down	Unigene87630_All//gi|145335796|ref|NP_173134.2|//8.00E-69//sugar binding / transferase, transferring glycosyl groups [Arabidopsis thaliana] >gi|9802774|gb|AAF99843.1|AC051629_10 Hypothetical protein [Arabidopsis thaliana] >gi|34098911|gb|AAQ56838.1| At1g16900 [Arabidopsis thaliana]	Unigene87630_All//8.00E-66//AT1G16900| sugar binding / transferase, transferring glycosyl groups	Unigene87630_All//0.00E+00//gi|78346416|gb|DT566690.1|DT566690		ko00510|N-Glycan biosynthesis		nr +
Unigene87634_All	263	3.98	15.41	8.50	0.19	1.70	1.55	0.64	3.34	1.67	1.95E+00	1.31E-08	Up	1.10E+00	1.53E-02		3.17E+00	3.95E-02		3.03E+00	6.02E-02		2.38E+00	2.18E-03		1.37E+00	1.82E-01		Unigene87634_All//gi|7340289|gb|AAF61174.1|AF245222_1//3.00E-14//OP1 [Curcumis sativus]	Unigene87634_All//2.00E-15//AT4G35770| SEN1 (SENESCENCE 1)	Unigene87634_All//7.00E-79//TC135068				nr -
Unigene87665_All	276	2.46	0.73	0.00	0.18	2.12	0.98	0.92	1.06	1.30	-1.75E+00	6.23E-02		-1.13E+01	7.62E-04	Down	3.55E+00	8.13E-03		2.44E+00	2.21E-01		2.06E-01	8.67E-01		4.99E-01	6.27E-01				Unigene87665_All//3.00E-143//gi|78351704|gb|DT571978.1|DT571978				
Unigene87665_All	244	0.00	6.23	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	1.09E-08	Up	null	null		null	null		null	null		null	null		null	null		Unigene87665_All//gi|214027222|gb|ACJ63287.1|//5.00E-21//C-repeat binding factor 1 [Gossypium barbadense]		Unigene87665_All//6.00E-73//gi|109826690|gb|DW225400.1|DW225400				nr +
Unigene8767_All	365	3.01	2.64	2.77	1.50	2.45	1.48	7.07	8.36	2.40	-1.91E-01	7.45E-01		-1.19E-01	8.50E-01		7.08E-01	3.74E-01		-1.59E-02	9.75E-01		2.43E-01	4.95E-01		-1.56E+00	1.68E-05	Down			Unigene8767_All//4.00E-07//EX165733				
Unigene87675_All	248	0.84	0.00	0.00	2.61	0.00	0.00	0.00	0.00	0.00	-9.72E+00	1.20E-01		-9.72E+00	1.44E-01		-1.14E+01	7.84E-05	Down	-1.14E+01	3.89E-04	Down	null	null		null	null								ESTscan +
Unigene877_All	1818	17.79	11.46	14.76	25.29	20.70	20.02	7.88	3.10	5.50	-6.35E-01	2.48E-11		-2.69E-01	7.70E-03		-2.89E-01	8.56E-05		-3.37E-01	1.02E-05		-1.35E+00	6.24E-21	Down	-5.19E-01	5.26E-05		Unigene877_All//gi|15239054|ref|NP_196707.1|//1.00E-33//senescence-associated protein-related [Arabidopsis thaliana] >gi|50198799|gb|AAT70433.1| At5g11460 [Arabidopsis thaliana] >gi|11074484|gb|AB804615.1| At5g11460 [Arabidopsis thaliana]	Unigene877_All//2.00E-33//AT5G11460| senescence-associated protein-related	Unigene877_All//0.00E+00//TC149955				nr -
Unigene8770_All	295	8.87	8.76	6.14	75.14	86.15	89.87	103.05	63.05	41.05	-1.77E-02	9.82E-01		-5.31E-01	2.02E-01		1.97E-01	8.42E-02		2.58E-01	1.80E-02		-7.09E-01	1.33E-15		-1.33E+00	6.14E-44	Down	Unigene8770_All//gi|8134568|sp|P93263.1|METE_MESCR//7.00E-41//RecName: Full=5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase; AltName: Full=Vitamin-B12-independent methionine synthase isozyme; AltName: Full=Cobalamin-independent methionine synthase isozyme >gi|1814003|gb|AAB41896.1| methionine synthase [Mesembryanthemum crystallinum]	Unigene8770_All//8.00E-40//AT3G03780| AtMS2; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ methionine synthase	Unigene8770_All//6.00E-166//TC146995		ko00270|Cysteine and methionine metabolism		nr -

Unigene87708_All	323	0.49	0.00	0.00	15.42	4.16	1.40	0.52	0.00	0.00	-8.92E+00	2.13E-01		-8.92E+00	2.42E-01		-1.89E+00	3.52E-12	Down	-3.46E+00	1.02E-20	Down	-9.03E+00	1.33E-01		-9.03E+00	1.07E-01		Unigene87708_All//gi|133902306|gb|AB041836.1|//7.00E-10//alcohol dehydrogenase A [Gossypium arboreum]	Unigene87708_All//1.00E-05//AT1G77120| ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase	Unigene87708_All//3.00E-137//gi|48821910|gb|CO123223.1|CO123223		ko00010|Glycolysis / Gluconeogenesis//ko00071|Fatty acid metabolism//ko00350|Tyrosine metabolism		nr +
Unigene8771_All	206	95.75	26.56	54.80	333.71	302.23	339.82	102.21	94.75	84.13	-1.85E+00	9.89E-37	Down	-8.05E-01	4.65E-10		-1.43E-01	2.79E-02		2.62E-02	7.33E-01		-1.09E-01	3.99E-01		-2.81E-01	8.17E-03		Unigene8771_All//gi|3242079|emb|CAA07370.1|//3.00E-20//proline-rich protein [Capsicum annuum]	Unigene8771_All//2.00E-14//AT4G16380| metal ion binding	Unigene8771_All//3.00E-108//gi|78346652|gb|DT566926.1|DT566926				nr +
Unigene87715_All	452	0.00	0.00	0.00	0.00	0.00	0.00	2.34	0.18	0.79	null	null		null	null		null	null		null	null		-3.66E+00	1.31E-05	Down	-1.56E+00	9.40E-03		Unigene87715_All//gi|27651624|emb|CAD35400.1|//2.00E-40//shaker-like potassium channel [Vitis vinifera]	Unigene87715_All//3.00E-39//AT3G02850| SKOR; cyclic nucleotide binding / inward rectifier potassium channel/ outward rectifier potassium channel					nr -
Unigene87728_All	614	0.51	0.00	0.17	3.81	1.74	0.29	0.14	0.07	0.26	-9.00E+00	3.63E-02		-1.56E+00	3.29E-01		-1.13E+00	3.99E-03		-3.70E+00	1.91E-10	Down	-1.02E+00	7.20E-01		9.14E-01	6.23E-01		Unigene87728_All//gi|40053549|gb|AB080476.1|//1.00E-30//RNA-directed DNA polymerase , related [Medicago truncatula]	Unigene87728_All//3.00E-17//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene87728_All//2.00E-22//TC135736				nr +
Unigene8773_All	531	7.19	8.02	11.73	3.19	2.40	1.53	0.72	1.10	2.70	1.56E-01	6.08E-01		7.06E-01	4.07E-03		-4.11E-01	4.28E-01		-1.06E+00	3.77E-02		6.21E-01	4.78E-01		1.91E+00	3.23E-04	Up	Unigene8773_All//gi|297828053|ref|XP_002881909.1|//1.00E-12//immunophilin [Arabidopsis lyrata subsp. lyrata] >gi|297327748|gb|EFH58168.1| immunophilin [Arabidopsis lyrata subsp. lyrata]	Unigene8773_All//3.00E-13//AT2G43560| immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein	Unigene8773_All//5.00E-69//TC177546				nr +
Unigene8774_All	949	0.11	0.16	1.18	15.59	9.51	3.95	1.74	0.26	0.42	5.38E-01	7.77E-01		3.42E+00	1.92E-04	Up	-7.14E-01	8.73E-08		-1.98E+00	8.34E-33	Down	-2.72E+00	1.39E-06	Down	-2.05E+00	3.66E-05	Down	Unigene8774_All//gi|119657126|gb|AL86687.1|//1.00E-112//TLP1 [Gossypium barbadense]	Unigene8774_All//6.00E-102//AT1G75030| ATLP-3	Unigene8774_All//0.00E+00//DN779913				nr -
Unigene87765_All	241	564.46	417.76	558.79	193.26	224.33	113.75	14.91	5.55	14.22	-4.34E-01	4.92E-23		-1.45E-02	7.83E-01		2.15E-01	2.19E-03		-7.65E-01	1.80E-23		-1.43E+00	2.66E-06	Down	-6.89E-02	8.13E-01		Unigene87765_All//gi|121353|sp|P15102.1|GLNA4_PHAVU//5.00E-23//RecName: Full=Glutamine synthetase leaf isozyme, chloroplastic; AltName: Full=Isozyme delta; AltName: Full=Glutamate--ammonia ligase; Flags: Precursor	Unigene87765_All//1.00E-22//AT5G35630| GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase	Unigene87765_All//2.00E-82//gi|195983215|gb|FL576397.1|FL576397		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene8778_All	722	736.77	548.03	831.57	534.43	810.95	969.76	126.02	49.67	95.24	-4.27E-01	2.80E-85		1.75E-01	1.85E-17		6.02E-01	7.07E-210		8.60E-01	0.00E+00		-1.34E+00	1.77E-128	Down	-4.04E-01	2.66E-17		Unigene8778_All//gi|211906442|gb|AC311714.1|//1.00E-118//Myo-inositol-1-phosphate synthase [Gossypium hirsutum]	Unigene8778_All//5.00E-110//AT2G22240| MIPS2 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 2); binding / catalytic/ inositol-3-phosphate synthase	Unigene8778_All//0.00E+00//TC133186		ko00562|Inositol phosphate metabolism		nr -
Unigene87784_All	761	0.21	0.00	0.28	1.24	0.23	0.83	0.11	0.22	1.36	-7.69E+00	2.13E-01		4.40E-01	7.74E-01		-2.46E+00	1.25E-03		-5.82E-01	4.37E-01		9.84E-01	6.32E-01		3.61E+00	1.38E-05	Up			Unigene87784_All//5.00E-172//gi|11210487|gb|BF279417.1|BF279417				
Unigene87786_All	263	1.99	4.24	7.49	0.95	0.79	0.86	0.32	0.32	0.15	1.09E+00	9.57E-02		1.91E+00	2.96E-04	Up	-2.70E-01	8.22E-01		-1.41E-01	9.28E-01		-1.67E-02	1.01E+00		-1.09E+00	6.72E-01								
Unigene87799_All	210	8.22	7.96	12.17	3.56	3.61	3.87	7.05	8.96	17.45	-4.63E-02	9.36E-01		5.66E-01	1.74E-01		1.99E-02	1.00E+00		1.22E-01	8.93E-01		3.46E-01	4.39E-01		1.31E+00	6.85E-06	Up			Unigene87799_All//2.00E-47//gi|84143828|gb|DN758070.1|DN758070				
Unigene8782_All	762	0.48	0.93	0.77	11.24	3.30	1.30	6.55	1.21	0.68	9.54E-01	2.62E-01		6.78E-01	4.82E-01		-1.77E+00	7.50E-19	Down	-3.11E+00	4.59E-32	Down	-2.44E+00	1.44E-16	Down	-3.27E+00	5.00E-23	Down	Unigene8782_All//gi|44681466|gb|AAS47673.1|//2.00E-66//At2g32280 [Arabidopsis thaliana]	Unigene8782_All//1.00E-49//AT2G32280| unknown protein	Unigene8782_All//0.00E+00//TC161828				nr +
Unigene87831_All	545	0.00	0.00	0.00	4.20	0.76	0.41	0.00	0.15	0.00	null	null		null	null		-2.47E+00	4.67E-08	Down	-3.34E+00	1.90E-09	Down	7.26E+00	3.97E-01		null	null		Unigene87831_All//gi|282161430|gb|ADA79674.1|//5.00E-89//shaker-like potassium channel 1 [Populus euphratica]	Unigene87831_All//6.00E-82//AT2G26650| AKT1 (ARABIDOPSIS K TRANSPORTER 1); cyclic nucleotide binding / inward rectifier potassium channel	Unigene87831_All//2.00E-44//TC177956				nr -
Unigene87834_All	893	0.47	0.34	0.42	1.90	1.77	1.92	4.55	1.36	3.03	-4.61E-01	6.50E-01		-1.67E-01	8.79E-01		-9.66E-02	8.34E-01		1.90E-02	9.70E-01		-1.74E+00	4.06E-09	Down	-5.83E-01	2.52E-02		Unigene87834_All//gi|255538898|ref|XP_002510514.1|//1.00E-114//5'->gi|223501215|gb|EEF52701.1| 5'-	Unigene87834_All//3.00E-96//AT1G75660| XRN3; 5'-3' exoribonuclease	Unigene87834_All//3.00E-112//gi|48820757|gb|CO122070.1|CO122070		ko03018|RNA degradation		nr -
Unigene87838_All	293	8.21	2.77	9.45	7.82	8.46	12.33	2.60	4.71	7.07	-1.57E+00	3.01E-04	Down	2.02E-01	6.43E-01		1.14E-01	8.37E-01		6.57E-01	4.53E-02		8.58E-01	9.44E-02		1.44E+00	3.77E-04	Up	Unigene87838_All//gi|10177970|dbj|BAB11353.1|//3.00E-08//disease resistance protein-like [Arabidopsis thaliana]	Unigene87838_All//1.00E-09//AT5G40910| disease resistance protein (TIR-NBS-LRR class), putative					nr -
Unigene87840_All	424	0.62	0.72	1.00	1.41	1.79	0.00	0.40	0.30	0.38	2.17E-01	8.64E-01		7.03E-01	5.53E-01		3.42E-01	7.20E-01		-1.05E+01	7.69E-04	Down	-4.32E-01	7.91E-01		-8.61E-02	9.64E-01				Unigene87840_All//5.00E-07//TC170947				
Unigene87845_All	294	1.96	1.21	0.54	4.24	1.87	0.77	2.44	1.71	1.49	-6.98E-01	4.49E-01		-1.85E+00	9.61E-02		-1.18E+00	4.23E-02		-2.46E+00	4.15E-04	Down	-5.19E-01	5.07E-01		-7.14E-01	3.27E-01				Unigene87845_All//5.00E-68//TC176484				
Unigene8785_All	706	0.00	0.00	0.00	0.00	0.00	0.00	8.32	122.84	0.40	null	null		null	null		null	null		null	null		3.88E+00	0.00E+00	Up	-4.40E+00	6.68E-34	Down	Unigene8785_All//sp|Q8TGM6|TAR1_YEAST//1.00E-06//Protein TAR1 OS=Saccharomyces cerevisiae GN=TAR1 PE=2 SV=1		Unigene8785_All//4.00E-18//DW234221				swissprot +
Unigene87863_All	263	0.99	0.00	0.00	2.08	0.00	0.00	0.48	0.32	2.12	-9.96E+00	6.64E-02		-9.96E+00	8.50E-02		-1.10E+01	4.00E-04	Down	-1.10E+01	1.52E-03		-6.02E-01	7.64E-01		2.14E+00	2.64E-02		Unigene87863_All//gi|212717145|gb|ACJ37414.1|//8.00E-27//protein kinase [Glycine max]	Unigene87863_All//5.00E-21//AT3G28450| leucine-rich repeat transmembrane protein kinase, putative					nr +
Unigene87865_All	1743	2.70	2.09	2.20	2.83	2.96	3.03	1.12	0.41	1.30	-3.68E-01	1.99E-01		-2.97E-01	3.38E-01		6.68E-02	8.19E-01		9.96E-02	7.29E-01		-1.45E+00	7.53E-04	Down	2.24E-01	5.86E-01		Unigene87865_All//gi|115452785|ref|NP_001049993.1|//1.00E-143//Os03g0326600 [Oryza sativa Japonica Group] >gi|108707928|gb|ABF95723.1| RNA recognition motif family protein, expressed [Oryza sativa (japonica cultivar-group)] >gi|113548464|dbj|BAF11907.1| Os03g0326600 [Oryza sativa Japonica Group]	Unigene87865_All//3.00E-113//AT1G09230| RNA recognition motif (RRM)-containing protein	Unigene87865_All//0.00E+00//TC149548				nr +
Unigene8787_All	305	0.34	0.66	0.17	3.92	2.26	31.54	0.55	0.96	0.52	9.54E-01	6.19E-01		-9.75E-01	7.18E-01		-7.96E-01	1.87E-01		3.01E+00	8.01E-34	Up	7.91E-01	5.63E-01		-8.58E-02	9.64E-01		Unigene8787_All//gi|115463329|ref|NP_001055264.1|//3.00E-20//Os05g0346800 [Oryza sativa Japonica Group] >gi|113578815|dbj|BAF17178.1| Os05g0346800 [Oryza sativa Japonica Group]	Unigene8787_All//3.00E-21//AT1G65620| AS2 (ASYMMETRIC LEAVES 2); protein binding	Unigene8787_All//3.00E-140//DT461920		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism		nr -
Unigene87881_All	306	4.45	13.58	8.35	4.40	12.04	12.84	0.83	1.23	1.04	1.61E+00	6.13E-07	Up	9.10E-01	2.79E-02		1.45E+00	5.53E-06	Up	1.55E+00	1.66E-06	Up	5.68E-01	6.37E-01		3.29E-01	7.63E-01				Unigene87881_All//2.00E-64//TC147144				
Unigene87884_All	383	0.96	12.97	12.79	2.34	3.15	1.18	0.88	0.76	1.46	3.76E+00	3.67E-20	Up	3.74E+00	3.14E-19	Up	4.27E-01	5.52E-01		-9.89E-01	1.96E-01		-2.09E-01	8.50E-01		7.22E-01	3.99E-01		Unigene87884_All//gi|5915844|sp|O49858.1|CR2A3_SOYBN//1.00E-31//RecName: Full=Cytochrome P450 82A3; AltName: Full=Cytochrome P450 CP6	Unigene87884_All//7.00E-28//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene87884_All//4.00E-146//gi|48742721|gb|CO073240.1|CO073240		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis		nr -
Unigene8789_All	404	0.00	0.00	0.00	0.00	0.00	0.00	117.84	80.38	17.36	null	null		null	null		null	null		null	null		-5.52E-01	1.22E-15		-2.76E+00	8.27E-181	Down							
Unigene87894_All	419	0.00	0.36	0.00	1.43	0.00	0.11	0.00	0.00	0.10	8.50E+00	2.31E-01		null	null		-1.05E+01	1.77E-04	Down	-3.73E+00	4.95E-03		null	null		6.57E+00	6.33E-01		Unigene87894_All//gi|164449260|gb|ABY56089.1|//4.00E-31//proton gradient regulation 5 [Cucumis melo] >gi|164449273|gb|ABY56101.1| proton gradient regulation 5 [Cucumis sativus]	Unigene87894_All//4.00E-29//AT2G05620| PGR5 (proton gradient regulation 5); electron carrier	Unigene87894_All//2.00E-120//TC143581				nr -
Unigene87899_All	545	0.48	0.93	2.15	1.83	0.32	0.91	0.08	0.00	0.00	9.54E-01	3.73E-01		2.16E+00	3.59E-03		-2.53E+00	6.75E-04	Down	-1.00E+00	1.57E-01		-6.28E+00	6.39E-01		-6.28E+00	5.97E-01		Unigene87899_All//gi|148595726|emb|CAM12542.1|//7.00E-08//YA4 [Antirrhinum majus]		Unigene87899_All//1.00E-79//TC164284				nr -
Unigene87904_All	724	0.72	3.50	1.32	1.24	2.33	2.62	3.97	3.87	4.35	2.28E+00	1.11E-06	Up	8.73E-01	2.38E-01		9.12E-01	7.48E-02		1.08E+00	2.47E-02		-3.80E-02	9.30E-01		1.31E-01	6.77E-01		Unigene87904_All//gi|226492989|ref|NP_001149824.1|//1.00E-60//ADP-ribosylation factor GTPase-activating protein 3 [Zea mays] >gi|195634895|gb|ACG36916.1| ADP-ribosylation factor GTPase-activating protein 3 [Zea mays]	Unigene87904_All//1.00E-59//AT2G35210| RPA (ROOT AND POLLEN ARFGAP); ARF GTPase activator/ DNA binding / zinc ion binding	Unigene87904_All//0.00E+00//gi|21098680|gb|BQ410993.1|BQ410993		ko04144|Endocytosis		nr -
Unigene87910_All	455	0.00	0.11	0.47	4.49	1.67	0.89	1.67	1.56	0.70	6.80E+00	6.06E-01		8.87E+00	1.37E-01		-1.43E+00	9.35E-04	Down	-2.33E+00	5.35E-06	Down	-9.91E-02	8.96E-01		-1.26E+00	7.70E-02		Unigene87910_All//gi|145442272|gb|ABP88856.1|//5.00E-12//endonuclease [Glycine max]	Unigene87910_All//6.00E-09//AT1G11190| BFN1 (BIFUNCTIONAL NUCLEASE 1); T/G mismatch-specific endonuclease/ endoribonuclease, producing 5'-phosphomonoesters / nucleic acid binding / single-stranded DNA specific endodeoxyribonuclease	Unigene87910_All//9.00E-157//BQ410568				nr +
Unigene87914_All	468	0.45	2.49	1.37	0.64	0.88	1.16	0.72	0.18	0.85	2.48E+00	9.79E-04	Up	1.61E+00	1.11E-01		4.68E-01	7.41E-01		8.59E-01	4.23E-01		-2.02E+00	1.36E-01		2.36E-01	8.04E-01		Unigene87914_All//gi|4432836|gb|AAD20685.1|//2.00E-16//expressed protein [Arabidopsis thaliana] >gi|26450173|dbj|BAC42205.1| GPI-anchored protein [Arabidopsis thaliana]	Unigene87914_All//1.00E-17//AT2G28410| unknown protein	Unigene87914_All//0.00E+00//gi|109873513|gb|DW502488.1|DW502488				nr -
Unigene87937_All	375	0.00	0.00	0.00	0.00	0.00	0.00	0.90	3.23	6.69	null	null		null	null		null	null		null	null		1.84E+00	1.99E-03		2.89E+00	1.73E-10	Up			Unigene87937_All//1.00E-62//DN517774				
Unigene8795_All	1038	0.00	0.00	0.00	0.19	0.13	0.00	7.41	10.95	35.31	null	null		null	null		-5.33E-01	7.47E-01		-7.59E+00	1.32E-01		5.63E-01	1.72E-04		2.25E+00	2.00E-108	Up	Unigene8795_All//gi|21592423|gb|AAM64374.1|//6.00E-21//zinc finger protein 5, ZFP5 [Arabidopsis thaliana]	Unigene8795_All//3.00E-22//AT1G10480| ZFP5 (ZINC FINGER PROTEIN 5); nucleic acid binding / transcription factor/ zinc ion binding	Unigene8795_All//3.00E-41//TC164743	C2H2			nr +
Unigene8796_All	746	0.00	10.39	7.07	0.00	0.09	0.00	0.00	0.00	0.00	1.33E+01	2.47E-44	Up	1.28E+01	2.42E-29	Up	6.53E+00	5.99E-01		null	null		null	null		null	null									ESTscan +
Unigene87967_All	293	1.25	0.69	0.00	3.06	0.47	2.00	0.58	0.86	0.41	-8.54E-01	4.88E-01		-1.03E+01	2.77E-02		-2.70E+00	8.76E-04	Down	-6.11E-01	4.26E-01		5.68E-01	6.73E-01		-5.01E-01	7.45E-01		Unigene87967_All//gi|240256410|ref|NP_199565.4|//2.00E-08//binding [Arabidopsis thaliana] >gi|15214076|sp|Q9FG83.1|M025N_ARATH RecName: Full=Putative M025-like protein At5g47540 >gi|16226301|gb|AAL16128.1|AF428296_1 AT5g47540/MXJ7_13 [Arabidopsis thaliana] >gi|193211497|gb|ACF16168.1| At5g47540 [Arabidopsis thaliana]	Unigene87967_All//9.00E-10//AT5G47540| binding	Unigene87967_All//5.00E-43//gi|13350647|gb|BG440995.1|BG440995				nr +
Unigene8797_All	530	0.39	4.30	1.41	0.47	1.95	1.28	0.64	0.55	0.38	3.45E+00	6.37E-09	Up	1.83E+00	5.04E-02		2.05E+00	6.01E-03		1.44E+00	1.28E-01		-2.09E-01	8.50E-01		-7.64E-01	5.01E-01				Unigene8797_All//1.00E-131//DN817324				
Unigene87971_All	340	157.12	132.49	131.72	255.08	283.08	220.24	155.81	117.03	73.23	-2.46E-01	7.90E-04		-2.54E-01	8.15E-04		1.50E-01	4.32E-03		-2.12E-01	1.31E-04		-4.13E-01	1.61E-10		-1.09E+00	1.09E-55	Down	Unigene87971_All//gi|171190270|gb|ACB42441.1|//6.00E-32//aquaporin PIP2:4 [Gossypium hirsutum]	Unigene87971_All//5.00E-32//AT4G35100| PIP3 (PLASMA MEMBRANE INTRINSIC PROTEIN 3); water channel	Unigene87971_All//1.00E-105//EV497324			GO:0005372//GO:0006810//GO:0031225//GO:0043231	nr -
Unigene87991_All	469	0.00	0.32	0.45	3.08	7.12	4.04	0.00	0.00	0.00	8.34E+00	2.31E-01		8.83E+00	1.37E-01		1.21E+00	2.73E-04	Up	3.93E-01	4.53E-01		null	null		null	null		Unigene87991_All//gi|49659437|dbj|BAD27257.1|//1.00E-13//d-limonene synthase [Citrus unshiu]	Unigene87991_All//1.00E-12//AT2G24210| TPS10 (terpene synthase 10); (E)-beta-ocimene synthase/ myrcene synthase			ko00902|Monoterpenoid biosynthesis		nr +
Unigene8800_All	751	0.00	0.61	0.71	0.07	0.00	0.30	0.39	1.17	2.12	9.25E+00	7.34E-03		9.47E+00	3.98E-03		-6.05E+00	5.40E-01		2.18E+00	3.22E-01		1.57E+00	2.54E-02		2.43E+00	7.10E-06	Up	Unigene8800_All//gi|255584614|ref|XP_002533031.1|//2.00E-12//conserved hypothetical protein [Ricinus communis] >gi|223527193|gb|EEF29362.1| conserved hypothetical protein [Ricinus communis]						nr -
Unigene88015_All	483	0.43	0.31	0.55	3.30	1.14	0.75	0.35	0.00	0.00	-4.61E-01	7.57E-01		3.47E-01	7.96E-01		-1.53E+00	2.44E-03		-2.14E+00	2.07E-04	Down	-8.45E+00	1.33E-01		-8.45E+00	1.07E-01		Unigene88015_All//gi|297796103|ref|XP_002865936.1|//3.00E-59//ATP binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297311771|gb|EFH42195.1| ATP binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene88015_All//1.00E-60//AT1G64110| AAA-type ATPase family protein	Unigene88015_All//2.00E-25//ES836152		ko00230|Purine metabolism	GO:0032559//GO:0042623//GO:0044464	nr +

Unigene8804_All	508	1.13	0.00	0.21	3.82	3.73	1.07	0.25	0.33	0.16	-1.01E+01	1.52E-03		-2.43E+00	4.40E-02		-3.67E-02	9.36E-01		-1.84E+00	1.99E-04	Down	3.98E-01	8.13E-01		-6.71E-01	7.18E-01		Unigene8804_All//gi|124359162|gb|ABN05685.1|//2.00E-39//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene8804_All//2.00E-10//AT4G20520| RNA binding / RNA-directed DNA polymerase	Unigene8804_All//1.00E-140//DW241491				nr +
Unigene88049_All	1060	0.20	0.33	0.00	1.27	0.19	0.77	0.52	0.24	0.98	7.61E-01	5.56E-01		-7.63E+00	1.44E-01		-2.70E+00	2.12E-05	Down	-7.27E-01	2.23E-01		-1.13E+00	2.18E-01		9.14E-01	1.17E-01		Unigene88049_All//gi|15229606|ref|NP_190544.1|//1.00E-103//AtRLP44 (Receptor Like Protein 44); protein binding [Arabidopsis thaliana] >gi|30162624|gb|AAP21230.1|At3g49750 [Arabidopsis thaliana]	Unigene88049_All//1.00E-96//AT3G49750| AtRLP44 (Receptor Like Protein 44); protein binding	Unigene88049_All//7.00E-64//DN779584		ko04626|Plant-pathogen interaction	GO:0005488//GO:0043231	nr +
Unigene8806_All	336	16.19	33.33	17.12	23.28	23.16	64.25	16.99	95.28	34.62	1.04E+00	2.81E-09	Up	7.99E-02	7.61E-01		-7.10E-03	9.66E-01		1.46E+00	9.98E-31	Up	2.49E+00	1.09E-104	Up	1.03E+00	9.68E-12	Up	Unigene8806_All//gi|225464602|ref|XP_002274766.1|//2.00E-12//PREDICTED: hypothetical protein isoform 2 [Vitis vinifera]		Unigene8806_All//4.00E-50//TC177672				nr -
Unigene88063_All	588	0.44	0.17	0.63	2.37	0.29	1.23	0.79	0.50	0.68	-1.37E+00	3.82E-01		5.11E-01	6.54E-01		-3.02E+00	3.33E-06	Down	-9.49E-01	9.91E-02		-6.69E-01	5.08E-01		-2.24E-01	7.90E-01		Unigene88063_All//gi|224138162|ref|XP_002322245.1|//2.00E-07//predicted protein [Populus trichocarpa] >gi|222867375|gb|EEF04506.1|predicted protein [Populus trichocarpa]		Unigene88063_All//2.00E-96//ES808891				nr +
Unigene8807_All	352	1.34	1.44	1.97	5.80	2.45	1.92	2.40	2.26	0.91	1.06E-01	9.22E-01		5.56E-01	5.28E-01		-1.25E+00	3.64E-03		-1.59E+00	6.74E-04	Down	-9.06E-02	9.00E-01		-1.41E+00	3.70E-02								ESTscan -
Unigene88073_All	288	0.00	0.18	0.00	3.81	1.67	0.47	1.91	1.31	0.55	7.46E+00	6.06E-01		null	null		-1.18E+00	5.94E-02		-3.02E+00	2.14E-04	Down	-5.47E-01	5.52E-01		-1.79E+00	5.06E-02		Unigene88073_All//gi|224112164|ref|XP_002332822.1|//5.00E-11//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834210|gb|EEE72687.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene88073_All//1.00E-65//AT5G47260| ATP binding / GTP binding / nucleoside-triphosphatase/ nucleotide binding	Unigene88073_All//3.00E-100//C0132540				nr +
Unigene88076_All	513	0.41	0.20	0.00	0.00	0.00	0.53	0.33	1.06	3.49	-1.05E+00	5.63E-01		-8.67E+00	1.44E-01		null	null		9.04E+00	7.00E-02		1.68E+00	7.91E-02		3.41E+00	8.04E-09	Up	Unigene88076_All//gi|228480908|gb|ACQ42220.1|//1.00E-40//EC63 transcription factor MYB108-like protein 1 [Vitis vinifera]	Unigene88076_All//5.00E-21//AT5G49620| AtMYB78 (myb domain protein 78); DNA binding / transcription factor	Unigene88076_All//5.00E-63//CA992606	MYB		GO:0003676//GO:0006970//GO:0009725//GO:0010468//GO:0043231//GO:0051707	nr +
Unigene88079_All	353	0.30	0.00	0.75	2.68	0.20	0.13	0.00	0.47	0.79	-8.21E+00	3.64E-01		1.35E+00	4.08E-01		-3.78E+00	3.39E-05	Down	-4.39E+00	5.96E-05	Down	8.89E+00	1.38E-01		9.63E+00	2.43E-02				Unigene88079_All//1.00E-99//gi|78330246|gb|DT550520.1|DT550520				
Unigene88083_All	594	0.26	0.60	0.18	1.34	0.46	0.38	1.42	0.21	0.67	1.18E+00	3.72E-01		-5.59E-01	7.74E-01		-1.53E+00	4.82E-02		-1.82E+00	3.32E-02		-2.75E+00	9.73E-04	Down	-1.09E+00	9.98E-02		Unigene88083_All//gi|297803664|ref|XP_002869716.1|//1.00E-29//zinc-finger protein expressed in inflorescence meristem [Arabidopsis lyrata subsp. lyrata] >gi|297315552|gb|EFH45975.1| zinc-finger protein expressed in inflorescence meristem [Arabidopsis lyrata subsp. lyrata]	Unigene88083_All//2.00E-30//AT4G24470| TIFY1; transcription factor	Unigene88083_All//0.00E+00//gi|164272052|gb|ES831185.1|ES831185	C2C2-GATA		GO:0001071//GO:0003677//GO:0006351//GO:0043231//GO:0046914//GO:0048511	nr +
Unigene88084_All	332	0.32	0.00	0.32	3.45	0.41	0.27	0.13	0.38	0.00	-8.30E+00	3.64E-01		2.54E-02	9.96E-01		-3.06E+00	3.10E-05	Down	-3.66E+00	2.68E-05	Down	1.57E+00	5.44E-01		-6.99E+00	5.97E-01				Unigene88084_All//4.00E-10//C0097291				
Unigene88090_All	400	0.00	0.13	0.53	0.62	0.86	0.90	1.59	1.36	5.38	6.99E+00	6.06E-01		9.06E+00	1.37E-01		4.67E-01	7.79E-01		5.37E-01	6.94E-01		-2.23E-01	7.73E-01		1.76E+00	2.14E-05	Up	Unigene88090_All//gi|18146966|dbj|BAB82502.1|//5.00E-28//cig3 [Nicotiana tabacum]	Unigene88090_All//3.00E-29//AT5G19400| SMG7	Unigene88090_All//5.00E-53//TC167505			GO:0000212//GO:0000956	nr +
Unigene88101_All	509	0.00	0.80	0.21	1.96	1.01	0.09	1.00	0.82	0.00	9.64E+00	1.34E-02		7.71E+00	3.87E-01		-9.48E-01	1.58E-01		-4.46E+00	3.09E-05	Down	-2.80E-01	7.49E-01		-9.96E+00	5.54E-04	Down							
Unigene88109_All	461	1.25	0.22	0.58	1.73	1.72	1.37	2.48	0.54	1.30	-2.51E+00	2.92E-02		-1.11E+00	2.78E-01		-9.10E-03	9.67E-01		-3.34E-01	6.86E-01		-2.19E+00	6.83E-04	Down	-9.34E-01	8.80E-02				Unigene88109_All//1.00E-124//TC158540				
Unigene88113_All	563	0.93	0.36	0.38	2.21	1.41	0.24	0.15	0.30	0.00	-1.37E+00	1.96E-01		-1.30E+00	2.42E-01		-6.53E-01	2.80E-01		-3.20E+00	3.61E-05	Down	9.84E-01	6.32E-01		-7.23E+00	3.53E-01		Unigene88113_All//gi|195650307|gb|ACG44621.1|//1.00E-43//2Fe-2S ferredoxin [Zea mays]	Unigene88113_All//5.00E-34//AT4G05450| adrenodoxin-like ferredoxin 2	Unigene88113_All//2.00E-87//ES817234			GO:0043169//GO:0043231//GO:0051536	nr -
Unigene88118_All	459	0.23	0.00	0.58	2.06	1.20	0.10	0.46	0.18	0.43	-7.83E+00	3.64E-01		1.35E+00	4.08E-01		-7.81E-01	2.68E-01		-4.39E+00	5.96E-05	Down	-1.34E+00	4.29E-01		-8.58E-02	9.60E-01		Unigene88118_All//gi|2739377|gb|AAC14500.1|//9.00E-14//expressed protein [Arabidopsis thaliana]	Unigene88118_All//3.00E-08//AT2G26520| unknown protein				GO:0005488	nr +
Unigene88125_All	272	0.19	0.00	0.20	2.56	0.00	0.00	1.09	0.77	0.29	-7.59E+00	5.98E-01		2.53E-02	9.91E-01		-1.13E+01	3.44E-05	Down	-1.13E+01	1.96E-04	Down	-5.02E-01	6.77E-01		-1.89E+00	1.68E-01		Unigene88125_All//gi|15240433|ref|NP_198058.1|//2.00E-15//AtRLP53 (Receptor Like Protein 53); kinase/ protein binding [Arabidopsis thaliana] >gi|5732036|gb|AAD48937.1|AF160760_5 similar to disease resistance proteins; contains similarity ot Pfam family PF00560 - Leucine Rich Repeat; score=166.7, E=4e-46, N=24 [Arabidopsis thaliana]	Unigene88125_All//1.00E-16//AT5G27060| AtRLP53 (Receptor Like Protein 53); kinase/ protein binding			ko04626|Plant-pathogen interaction	GO:0016772	nr -
Unigene88127_All	298	0.00	0.00	0.00	3.18	1.04	0.15	0.14	0.28	0.00	null	null		null	null		-1.61E+00	2.15E-02		-4.39E+00	5.96E-05	Down	9.83E-01	7.28E-01		-7.15E+00	5.97E-01		Unigene88127_All//gi|224054404|ref|XP_002298243.1|//2.00E-25//histidine phosphotransfer protein [Populus trichocarpa] >gi|222845501|gb|EEE83048.1|histidine phosphotransfer protein [Populus trichocarpa]	Unigene88127_All//6.00E-24//AT3G16360| AHP4 (HPT PHOSPHOTRANSMITTER 4); histidine phosphotransfer kinase/ transferase, transferring phosphorus-containing groups				GO:0004871//GO:0008152//GO:0009736//GO:0016628//GO:0023060//GO:0043231	nr -
Unigene88128_All	430	0.37	0.12	0.12	2.78	1.44	0.53	0.00	0.00	0.09	-1.63E+00	4.87E-01		-1.56E+00	5.32E-01		-9.48E-01	1.12E-01		-2.40E+00	7.06E-04	Down	null	null		6.53E+00	6.33E-01				Unigene88128_All//5.00E-07//TC133651				
Unigene8813_All	990	0.11	0.31	0.00	0.00	0.21	0.00	0.81	3.21	1.17	1.54E+00	3.22E-01		-6.72E+00	3.86E-01		7.71E+00	1.56E-01		null	null		1.98E+00	1.64E-08	Up	5.24E-01	3.53E-01		Unigene8813_All//gi|115490848|gb|ABI97958.1|//1.00E-105//alpha-crystalline heat shock protein [Gossypium arboreum] >gi|115490850|gb|ABI97959.1|alpha-crystalline heat shock protein [Gossypium arboreum]	Unigene8813_All//3.00E-29//AT4G27670| HSP21 (HEAT SHOCK PROTEIN 21)	Unigene8813_All//0.00E+00//NP12958050				nr +
Unigene88133_All	262	0.00	0.00	0.00	3.04	0.92	0.00	0.32	0.00	0.91	null	null		null	null		-1.73E+00	2.86E-02		-1.16E+01	4.90E-05	Down	-8.33E+00	3.96E-01		1.50E+00	3.38E-01								
Unigene88165_All	446	0.94	0.00	0.60	5.36	2.78	1.52	1.71	1.78	0.18	-9.87E+00	1.04E-02		-6.53E-01	5.94E-01		-9.48E-01	1.49E-02		-1.82E+00	3.18E-05	Down	6.13E-02	9.50E-01		-3.26E+00	4.48E-04	Down							
Unigene88166_All	275	0.00	0.55	1.55	0.54	0.13	0.49	3.54	0.15	1.59	9.11E+00	2.31E-01		1.06E+01	1.36E-02		-2.12E+00	3.84E-01		-1.41E-01	9.42E-01		-4.54E+00	6.92E-06	Down	-1.15E+00	5.83E-02		Unigene88166_All//gi|15242248|ref|NP_197636.1|//4.00E-12//60S ribosomal protein L10A (RPL10aC) [Arabidopsis thaliana] >gi|145334533|ref|NP_001078612.1|60S ribosomal protein L10A (RPL10aC) [Arabidopsis thaliana] >gi|27922990|sp|P59231.1|R10A3_ARATH RecName: Full=60S ribosomal protein L10a-3 >gi|9757825|dbj|BAB08343.1| 60S ribosomal protein L10A [Arabidopsis thaliana] >gi|14335148|gb|AAK59854.1|AT5g22440/MWD9_24 [Arabidopsis thaliana] >gi|18655359|gb|AAL76135.1|AT5g22440/MWD9_24 [Arabidopsis thaliana]	Unigene88166_All//2.00E-13//AT5G22440| 60S ribosomal protein L10A (RPL10aC)	Unigene88166_All//2.00E-79//ES793000		ko03010|Ribosome	GO:0003002//GO:0003676//GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0031981//GO:0048513	nr +
Unigene8818_All	438	0.00	2.78	2.19	0.00	0.00	0.00	0.00	0.00	0.00	1.14E+01	5.45E-07	Up	1.11E+01	2.44E-05	Up	null	null		null	null		null	null		null	null		Unigene8818_All//sp|Q9R1E9|CTGF_RAT//9.00E-08//Connective tissue growth factor OS=Rattus norvegicus GN=Ctgf PE=2 SV=1						swissprot -
Unigene88182_All	354	0.00	0.00	0.00	4.08	1.07	0.13	0.00	0.00	0.00	null	null		null	null		-1.93E+00	5.06E-04	Down	-5.00E+00	7.43E-08	Down	null	null		null	null								
Unigene88183_All	525	0.00	0.00	0.00	0.95	0.00	0.34	0.16	0.16	0.08	null	null		null	null		-9.89E+00	8.97E-04	Down	-1.46E+00	1.93E-01		-1.71E-02	1.01E+00		-1.09E+00	6.72E-01		Unigene88183_All//gi|109946637|gb|ABG48497.1|//4.00E-06//At1g77890 [Arabidopsis thaliana]	Unigene88183_All//1.00E-16//AT4G08540| unknown protein	Unigene88183_All//5.00E-57//C0103520			GO:0034062	nr +
Unigene88186_All	311	3.36	6.19	11.30	0.96	2.44	7.99	6.39	0.67	16.01	8.80E-01	6.09E-02		1.75E+00	2.51E-06	Up	1.34E+00	1.23E-01		3.06E+00	3.93E-09	Up	-3.25E+00	3.61E-09	Down	1.33E+00	7.81E-08	Up			Unigene88186_All//2.00E-110//DW517923				
Unigene8819_All	809	0.00	0.25	0.00	0.00	0.09	0.00	23.52	10.49	9.60	7.97E+00	1.34E-01		null	null		6.41E+00	5.99E-01		null	null		-1.17E+00	3.80E-22	Down	-1.29E+00	1.01E-26	Down	Unigene8819_All//gi|226713612|sp|A7QF77.1|U4971_VITVI//1.00E-54//RecName: Full=UPF0497 membrane protein 1	Unigene8819_All//3.00E-44//AT5G06200| integral membrane family protein					nr -
Unigene88195_All	301	0.52	7.74	0.88	0.66	0.57	0.30	4.07	1.94	21.31	3.89E+00	5.93E-10	Up	7.62E-01	6.43E-01		-2.11E-01	8.58E-01		-1.14E+00	5.67E-01		-1.07E+00	5.31E-02		2.39E+00	5.67E-21	Up			Unigene88195_All//2.00E-08//DT461826				
Unigene88210_All	306	0.34	0.17	0.00	2.60	0.00	0.44	0.41	0.82	0.39	-1.05E+00	6.82E-01		-8.42E+00	3.86E-01		-1.13E+01	6.49E-06	Down	-2.56E+00	6.01E-03		9.83E-01	5.17E-01		-8.57E-02	9.67E-01								
Unigene8822_All	857	0.00	0.00	0.00	14.01	6.19	6.48	0.94	0.10	0.28	null	null		null	null		-1.18E+00	2.47E-14	Down	-1.11E+00	1.18E-11	Down	-3.27E+00	4.48E-04	Down	-1.75E+00	1.55E-02		Unigene8822_All//gi|224126613|ref|XP_002329598.1|//1.00E-125//cationic amino acid transporter [Populus trichocarpa] >gi|222870307|gb|EEF07438.1|cationic amino acid transporter [Populus trichocarpa]	Unigene8822_All//4.00E-69//AT3G10600| CAT7 (CATIONIC AMINO ACID TRANSPORTER 7); cationic amino acid transmembrane transporter	Unigene8822_All//2.00E-125//TC146944				nr -
Unigene88221_All	323	0.00	1.73	0.49	2.47	0.32	0.14	0.00	0.26	0.37	1.08E+01	2.16E-03		8.95E+00	2.33E-01		-2.95E+00	1.08E-03		-4.14E+00	4.12E-04	Down	8.02E+00	3.97E-01		8.53E+00	2.42E-01				Unigene88221_All//4.00E-87//gi|78335220|gb|DT555494.1|DT555494				
Unigene88222_All	312	0.00	0.00	0.00	0.96	0.44	0.14	0.00	1.74	1.02	null	null		null	null		-1.12E+00	4.23E-01		-2.73E+00	1.36E-01		1.08E+01	5.36E-04	Up	1.00E+01	1.34E-02								
Unigene88229_All	329	0.80	1.08	1.29	1.51	0.00	0.14	0.39	0.38	0.24	4.39E-01	7.01E-01		7.04E-01	5.53E-01		-1.06E+01	8.97E-04	Down	-3.46E+00	1.60E-02		-1.66E-02	1.02E+00		-6.71E-01	7.18E-01				Unigene88229_All//3.00E-103//TC153892				
Unigene8823_All	405	0.00	0.00	0.00	1.23	0.00	0.78	1.57	1.75	1.28	null	null		null	null		-1.03E+01	8.97E-04	Down	-6.56E-01	5.50E-01		1.64E-01	8.24E-01		-2.92E-01	6.84E-01								
Unigene8824_All	553	0.00	0.73	0.19	1.98	2.05	1.96	3.13	1.81	0.43	9.52E+00	1.34E-02		7.59E+00	3.87E-01		5.23E-02	9.48E-01		-1.59E-02	9.71E-01		-7.89E-01	7.73E-02		-2.86E+00	1.61E-07	Down	Unigene8824_All//gi|88193697|dbj|BAE79735.1|//2.00E-44//phospholipase D alpha 2 [Arachis hypogaea] >gi|88193701|dbj|BAE79737.1|phospholipase D alpha 2 [Arachis hypogaea]	Unigene8824_All//1.00E-43//AT3G15730| PLDALPHA1 (PHOSPHOLIPASE D ALPHA 1); phospholipase D			ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr +
Unigene88242_All	332	2.68	0.61	0.00	1.65	1.45	2.45	0.38	0.00	0.72	-2.13E+00	1.06E-02		-1.14E+01	6.29E-05	Down	-1.85E-01	8.25E-01		5.69E-01	4.96E-01		-8.58E+00	2.33E-01		9.14E-01	5.41E-01								
Unigene88250_All	318	1.65	3.03	0.84	2.98	2.92	2.56	2.26	1.18	0.25	8.80E-01	2.13E-01		-9.75E-01	3.76E-01		-2.57E-02	9.50E-01		-2.19E-01	7.47E-01		-9.34E-01	2.26E-01		-3.17E+00	8.09E-04	Down			Unigene88250_All//5.00E-111//TC179467				
Unigene88253_All	426	0.86	0.00	1.13	5.15	1.54	0.21	1.49	0.10	0.37	-9.75E+00	1.95E-02		3.88E-01	6.97E-01		-1.74E+00	4.17E-05	Down	-4.60E+00	2.64E-11	Down	-3.92E+00	9.80E-04	Down	-1.99E+00	2.04E-02								
Unigene88254_All	288	0.55	0.00	0.18	2.25	0.48	0.00	0.00	0.00	0.14	-9.09E+00	2.13E-01		-1.56E+00	5.32E-01		-2.23E+00	1.79E-02		-1.11E+01	3.89E-04	Down	null	null		7.11E+00	6.33E-01				Unigene88254_All//4.00E-25//gi|164363927|gb|EX167509.1|EX167509				ESTscan +
Unigene8826_All	389	2.96	1.69	2.60	7.30	3.90	0.70	3.04	2.15	0.00	-8.05E-01	2.05E-01		-1.86E-01	7.59E-01		-9.06E-01	9.73E-03		-3.39E+00	9.60E-12	Down	-5.02E-01	3.95E-01		-1.16E+01	8.15E-09	Down			Unigene8826_All//9.00E-24//TC165079				
Unigene8827_All	473	3.54	0.86	2.03	0.42	0.58	0.38	1.07	0.00	0.59	-2.05E+00	3.19E-04	Down	-8.05E-01	1.35E-01		4.67E-01	8.16E-01		-1.42E-01	9.33E-01		-1.01E+01	8.88E-04	Down	-8.63E-01	3.39E-01		Unigene8827_All//gi|224099497|ref|XP_002311506.1|//3.00E-08//predicted protein [Populus trichocarpa] >gi|222851326|gb|EEE88873.1|predicted protein [Populus trichocarpa]	Unigene8827_All//6.00E-05//AT1G70895| CLE17 (CLAVATA3/ESR-RELATED 17); protein binding / receptor binding	Unigene8827_All//1.00E-07//TC150270				nr -
Unigene8828_All	846	0.00	2.99	1.70	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	2.05E-14	Up	1.07E+01	6.28E-08	Up	null	null		null	null		null	null		null	null		Unigene8828_All//gi|118411020|ref|YP_874415.1|//4.00E-63//30S ribosomal protein S2 [Phaeodactylum tricornutum] >gi|125987743|sp|A0T0E0.1|RS2_PHATR RecName: Full=30S ribosomal protein S2, chloroplastic >gi|116739767|gb|ABK20638.1| 30S ribosomal protein S2 [Phaeodactylum tricornutum]	Unigene8828_All//8.00E-33//ATCG00160| Chloroplast ribosomal protein S2			ko03010|Ribosome		nr +
Unigene88288_All	312	0.00	0.00	0.00	2.87	0.44	0.43	0.14	0.00	0.00	null	null		null	null		-2.70E+00	8.76E-04	Down	-2.73E+00	2.06E-03		-7.08E+00	6.38E-01		-7.08E+00	5.97E-01		Unigene88288_All//gi|28372884|gb|AAO39924.1|//1.00E-19//At4g04630 [Arabidopsis thaliana]	Unigene88288_All//4.00E-21//AT4G04630| unknown protein					nr +
Unigene88292_All	343	1.22	0.00	0.00	2.47	0.20	0.40	0.00	0.12	0.00	-1.03E+01	1.04E-02		-1.03E+01	1.55E-02		-3.62E+00	1.47E-04	Down	-2.64E+00	3.54E-03		6.93E+00	6.23E-01		null	null								

Unigene8830_All	663	0.08	0.61	0.00	3.08	1.77	1.02	14.16	13.81	10.09	2.95E+00	5.89E-02		-6.30E+00	6.12E-01		-8.03E-01	6.37E-02		-1.59E+00	6.74E-04	Down	-3.63E-02	8.54E-01		-4.88E-01	2.69E-03		Unigene8830_All//gi|255563909|ref|XP_002522954.1|//3.00E-15//conserved hypothetical protein [Ricinus communis] >gi|223537766|gb|EEF39384.1| conserved hypothetical protein [Ricinus communis]		Unigene8830_All//1.00E-95//TC165695				nr +
Unigene88307_All	488	0.11	0.10	0.22	1.33	0.99	0.00	0.00	0.00	0.00	-4.65E-02	9.81E-01		1.03E+00	7.00E-01		-4.26E-01	6.08E-01		-1.04E+01	3.89E-04	Down	null	null		null	null		Unigene88307_All//gi|116311027|emb|CAH67958.1|//4.00E-33//OSIGBa0142I02-OSIGBa0101E20.1 [Oryza sativa (indica cultivar-group)]	Unigene88307_All//3.00E-29//AT1G72210| basic helix-loop-helix (bHLH) family protein (bHLH096)	Unigene88307_All//0.00E+00//gi|78335657|gb|DT555931.1|DT555931	bHLH		GO:0010168//GO:0043231	nr -
Unigene88308_All	353	0.00	0.00	0.00	1.98	0.10	0.00	0.60	0.12	0.23	null	null		null	null		-4.34E+00	2.79E-04	Down	-1.09E+01	1.96E-04	Down	-2.34E+00	2.36E-01		-1.41E+00	3.79E-01									
Unigene8831_All	657	0.80	0.31	0.08	2.65	3.09	0.28	1.80	0.95	2.36	-1.37E+00	1.96E-01		-3.30E+00	2.40E-02		2.21E-01	6.68E-01		-3.27E+00	3.65E-07	Down	-9.17E-01	1.03E-01		3.92E-01	4.01E-01		Unigene8831_All//gi|115482416|ref|NP_001064801.1|//1.00E-25//Os10g0466000 [Oryza sativa Japonica Group] >gi|78708794|gb|ABB47769.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|78708795|gb|ABB47770.1| expressed protein [Oryza sativa (japonica cultivar-group)] >gi|113639410|dbj|BAF26715.1| Os10g0466000 [Oryza sativa Japonica Group]	Unigene8831_All//2.00E-38//AT4G27660| unknown protein	Unigene8831_All//0.00E+00//TC160654				nr +
Unigene88310_All	361	0.29	0.28	0.00	0.14	0.19	0.00	4.10	0.81	0.11	-4.65E-02	9.85E-01		-8.18E+00	3.86E-01		4.67E-01	9.52E-01		-7.11E+00	6.14E-01		-2.34E+00	3.57E-05	Down	-5.21E+00	1.06E-09	Down	Unigene88310_All//gi|115438859|ref|NP_001043709.1|//3.00E-12//Os01g0647000 [Oryza sativa Japonica Group] >gi|113533240|dbj|BAF05623.1| Os01g0647000 [Oryza sativa Japonica Group]	Unigene88310_All//8.00E-14//AT5G19970| unknown protein					nr +
Unigene88315_All	351	0.00	0.00	0.00	2.13	0.29	0.00	1.08	0.95	0.11	null	null		null	null		-2.85E+00	2.09E-03		-1.11E+01	9.80E-05	Down	-1.87E-01	8.57E-01		-3.26E+00	2.22E-02									
Unigene88319_All	348	0.15	0.29	3.06	3.15	0.59	2.08	0.00	0.00	0.69	9.54E-01	7.23E-01		4.35E+00	6.45E-05	Up	-2.41E+00	5.06E-04	Down	-6.01E-01	3.90E-01		null	null		9.42E+00	4.38E-02		Unigene88319_All//gi|225442485|ref|XP_002278313.1|//1.00E-41//PREDICTED: similar to PDR8/PEN3 (PLEIOTROPIC DRUG RESISTANCE8); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter [Vitis vinifera]	Unigene88319_All//5.00E-42//AT1G59870| PEN3 (PENETRATION 3); ATPase, coupled to transmembrane movement of substances / cadmium ion transmembrane transporter	Unigene88319_All//2.00E-40//TC177387		ko03040|Spliceosome//ko02010|ABC transporters	GO:0000041//GO:0009526//GO:0009814//GO:0015082//GO:0015604//GO:0015193//GO:0016020//GO:0017111//GO:0019762//GO:0032559//GO:0050832//GO:0052482//GO:0071363	nr +
Unigene88325_All	364	0.00	0.00	0.00	1.51	0.00	0.25	0.70	0.11	0.22	null	null		null	null		-1.06E+01	4.00E-04	Down	-2.60E+00	2.93E-02		-2.60E+00	1.44E-01		-1.67E+00	2.56E-01									
Unigene88326_All	331	0.00	0.00	0.32	3.61	0.62	0.00	0.51	0.25	0.36	null	null		8.33E+00	3.87E-01		-2.53E+00	1.46E-04	Down	-1.18E+01	1.76E-07	Down	-1.02E+00	6.12E-01		-5.01E-01	7.45E-01				Unigene88326_All//9.00E-39//PL577066				
Unigene8833_All	320	1.47	0.63	1.16	4.67	2.04	1.98	15.46	3.79	2.61	-1.22E+00	2.72E-01		-3.37E-01	7.34E-01		-1.19E+00	2.14E-02		-1.24E+00	2.45E-02		-2.03E+00	3.01E-13	Down	-2.56E+00	5.85E-18	Down	Unigene8833_All//gi|225433375|ref|XP_002285608.1|//7.00E-12//PREDICTED: similar to GroEL-like chaperone, ATPase [Vitis vinifera]		Unigene8833_All//6.00E-160//TC149060		ko03018|RNA degradation		nr -
Unigene88331_All	315	80.72	44.24	48.01	123.19	113.69	142.66	74.36	34.63	34.78	-8.68E-01	4.43E-15		-7.50E-01	2.25E-11		-1.16E-01	2.34E-01		2.12E-01	9.69E-03		-1.10E+00	7.58E-25	Down	-1.10E+00	2.23E-25	Down	Unigene88331_All//gi|12580867|emb|CAC27142.1|//1.00E-26//60S ribosomal protein L13E [Picea abies]	Unigene88331_All//4.00E-17//AT3G49010| ATBRC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome	Unigene88331_All//7.00E-95//TC147665		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene88333_All	371	0.00	1.23	1.87	2.15	0.00	0.12	2743.88	2597.31	2143.88	1.03E+01	7.34E-03		1.09E+01	6.09E-04	Up	-1.11E+01	6.49E-06	Down	-4.14E+00	4.12E-04	Down	-7.92E-02	1.60E-08		-3.56E-01	1.29E-145		Unigene88333_All//gi|74273314|gb|AB401325.1|//5.00E-23//VDR6 [Gossypium hirsutum] >gi|83356301|gb|ABC16635.1| bet v1 [Gossypium hirsutum]	Unigene88333_All//2.00E-19//AT1G70850| MLP34 (MLP-LIKE PROTEIN 34)	Unigene88333_All//0.00E+00//gi|31407505|gb|CD486540.1|CD486540			GO:0006950	nr -
Unigene88336_All	544	1.54	0.56	1.57	3.21	3.73	1.66	1.71	0.23	1.46	-1.46E+00	6.68E-02		2.55E-02	9.93E-01		2.21E-01	6.68E-01		-9.49E-01	5.79E-02		-2.89E+00	3.28E-04	Down	-2.23E-01	7.07E-01		Unigene88336_All//gi|224109322|ref|XP_002333277.1|//5.00E-48//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222835896|gb|EEE74317.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene88336_All//1.00E-30//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene88336_All//3.00E-46//TC162712			GO:0003824//GO:0005488//GO:0009987	nr +
Unigene88346_All	364	1.01	1.25	0.00	1.64	0.00	0.25	0.00	0.11	0.44	3.16E-01	7.44E-01		-9.97E+00	2.77E-02		-1.07E+01	1.77E-04	Down	-2.73E+00	1.74E-02		6.84E+00	6.23E-01		8.77E+00	1.39E-01									
Unigene88348_All	560	0.00	0.00	0.19	0.53	0.18	1.53	0.23	6.05	1.28	null	null		7.57E+00	3.87E-01		-1.53E+00	2.97E-01		1.52E+00	6.17E-02		4.74E+00	8.91E-20	Up	2.50E+00	4.03E-03		Unigene88348_All//gi|259121423|gb|ACV92031.1|//3.00E-42//WRKY transcription factor 29 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene88348_All//8.00E-37//AT1G29860| WRKY71; transcription factor	Unigene88348_All//2.00E-19//TC131145	WRKY	ko04626|Plant-pathogen interaction	GO:0006350//GO:0006952//GO:0009725//GO:0034614//GO:0043231	nr -
Unigene88349_All	533	0.69	0.19	0.00	0.37	0.19	0.17	3.81	0.08	0.15	-1.85E+00	1.87E-01		-9.42E+00	2.77E-02		-9.48E-01	5.87E-01		-1.14E+00	5.67E-01		-5.60E+00	5.56E-13	Down	-4.67E+00	1.83E-12	Down	Unigene88349_All//gi|22001640|sp|Q93392.1|HBL2_GOSHI//5.00E-64//RecName: Full=Non-symbiotic hemoglobin 2; AltName: Full=GOShi GLB2; Short=Hb2 >gi|15809418|gb|AAK21604.1| non-symbiotic hemoglobin class 2 [Gossypium hirsutum]	Unigene88349_All//2.00E-51//AT3G10520| AHB2 (ARABIDOPSIS HAEMOGLOBIN 2); oxygen transporter	Unigene88349_All//1.00E-143//TC161350			GO:0005506//GO:0009725//GO:0015669//GO:0022892	nr -
Unigene8835_All	335	2.03	0.91	0.00	2.83	0.62	1.08	1.14	1.25	2.97	-1.16E+00	1.89E-01		-1.10E+01	7.62E-04	Down	-2.20E+00	2.99E-03		-1.39E+00	6.08E-02		1.35E-01	8.99E-01		1.39E+00	2.47E-02				Unigene8835_All//4.00E-07//TC160563				
Unigene88357_All	356	0.15	0.00	0.00	0.00	0.00	0.00	3.56	0.00	0.00	-7.20E+00	5.98E-01		-7.20E+00	6.12E-01		null	null		null	null		-1.18E+01	5.06E-09	Down	-1.18E+01	1.99E-09	Down	Unigene88357_All//gi|10178219|dbj|BAB11612.1|//1.00E-11//DNA-binding protein-like [Arabidopsis thaliana]	Unigene88357_All//3.00E-08//AT5G47430| zinc ion binding	Unigene88357_All//5.00E-99//ES824374			GO:0043231//GO:0046914	nr -
Unigene8836_All	617	7.29	7.64	9.41	5.49	2.57	1.90	0.34	0.14	0.00	6.66E-02	8.15E-01		3.67E-01	1.64E-01		-1.10E+00	4.93E-04	Down	-1.53E+00	1.02E-05	Down	-1.34E+00	4.28E-01		-8.42E+00	5.78E-02				Unigene8836_All//8.00E-10//gi|78348675|gb|DT568949.1|DT568949				
Unigene88369_All	372	0.56	0.00	0.00	1.07	0.09	0.73	2.96	0.11	0.54	-9.14E+00	1.20E-01		-9.14E+00	1.44E-01		-3.53E+00	2.09E-02		-5.57E-01	6.37E-01		-4.72E+00	1.02E-06	Down	-2.46E+00	2.04E-04	Down			Unigene88369_All//1.00E-56//C0131262				
Unigene8837_All	1044	0.00	3.54	0.26	0.00	0.07	1.04	0.08	0.92	21.98	1.18E+01	4.67E-21	Up	7.99E+00	7.85E-02		6.04E+00	5.99E-01		1.00E+01	1.82E-06	Up	3.51E+00	5.50E-05	Up	8.08E+00	1.85E-160	Up	Unigene8837_All//gi|18411994|ref|NP_567545.1|//3.00E-53//binding [Arabidopsis thaliana]	Unigene8837_All//3.00E-42//AT4G17940| binding	Unigene8837_All//5.00E-40//C0085549				nr -
Unigene88375_All	372	0.00	0.00	0.00	2.68	0.37	0.73	0.00	0.00	0.43	null	null		null	null		-2.85E+00	2.37E-04	Down	-1.88E+00	1.18E-02		null	null		8.74E+00	1.39E-01				Unigene88375_All//2.00E-89//gi|78341869|gb|DT562143.1|DT562143				
Unigene88385_All	390	0.00	0.00	0.00	2.55	0.71	0.00	0.65	0.11	1.02	null	null		null	null		-1.85E+00	7.41E-03		-1.13E+01	2.97E-06	Down	-2.60E+00	1.44E-01		6.51E-01	5.44E-01									
Unigene88386_All	399	0.00	0.00	0.00	5.74	0.00	0.00	0.53	0.84	0.60	null	null		null	null		-1.25E+01	3.94E-17	Down	-1.25E+01	2.33E-14	Down	6.62E-01	6.09E-01		1.77E-01	9.08E-01									ESTscan +
Unigene88389_All	385	0.00	0.39	0.14	1.55	0.63	0.00	0.33	0.00	0.00	8.63E+00	2.31E-01		7.11E+00	6.22E-01		-1.31E+00	1.56E-01		-1.06E+01	7.69E-04	Down	-8.36E+00	2.33E-01		-8.36E+00	1.98E-01									
Unigene8839_All	982	0.27	0.52	0.00	0.61	0.28	0.09	0.56	3.06	26.45	9.54E-01	3.73E-01		-8.06E+00	8.50E-02		-1.12E+00	2.26E-01		-2.73E+00	1.74E-02		2.45E+00	2.71E-10	Up	5.56E+00	3.58E-164	Up	Unigene8839_All//gi|12322008|gb|AAG51046.1|AC069473_8//1.00E-39//gypsy/Ty-3 retroelement polyprotein; 69905-74404 [Arabidopsis thaliana] >gi|10998138|dbj|BAB03109.1| retroelement pol polyprotein [Arabidopsis thaliana]		Unigene8839_All//0.00E+00//TC156653				nr +
Unigene8840_All	257	0.41	0.39	0.41	0.00	0.13	0.70	5.92	5.04	14.73	-4.64E-02	9.85E-01		2.53E-02	9.96E-01		7.07E+00	8.11E-01		9.46E+00	1.93E-01		-2.32E-01	6.26E-01		1.31E+00	4.33E-06	Up			Unigene8840_All//6.00E-30//TC148685				
Unigene88407_All	402	1.04	1.26	1.59	4.96	1.28	1.01	0.53	0.00	0.69	2.76E-01	7.64E-01		6.10E-01	5.09E-01		-1.95E+00	2.27E-05	Down	-2.29E+00	9.03E-06	Down	-9.04E+00	7.40E-02		4.00E-01	7.43E-01									
Unigene88411_All	395	0.40	0.26	0.27	4.04	0.61	0.80	0.32	0.74	0.10	-6.31E-01	7.26E-01		-5.60E-01	7.74E-01		-2.73E+00	2.30E-06	Down	-2.33E+00	8.01E-05	Down	1.21E+00	3.92E-01		-1.67E+00	4.75E-01		Unigene88411_All//gi|79607885|ref|NP_974231.2|//1.00E-07//unknown protein [Arabidopsis thaliana] >gi|52354301|gb|AAU44471.1| hypothetical protein AT3G05725 [Arabidopsis thaliana] >gi|60547751|gb|AAX23839.1| hypothetical protein At3g05725 [Arabidopsis thaliana]	Unigene88411_All//6.00E-06//AT3G05725| unknown protein					nr -
Unigene8842_All	474	0.66	0.64	0.00	0.11	0.29	0.10	2.32	3.70	6.05	-4.63E-02	9.84E-01		-9.37E+00	4.87E-02		1.47E+00	6.16E-01		-1.41E-01	9.45E-01		6.75E-01	1.33E-01		1.38E+00	3.85E-05	Up			Unigene8842_All//6.00E-07//TC164018				
Unigene88422_All	411	0.13	0.62	1.55	0.24	0.34	0.44	2.26	0.20	0.10	2.28E+00	2.33E-01		3.61E+00	6.95E-03		4.67E-01	8.74E-01		8.59E-01	6.93E-01		-3.48E+00	7.79E-05	Down	-4.55E+00	6.41E-06	Down	Unigene88422_All//gi|20196907|gb|AB67625.2|//1.00E-38//expressed protein [Arabidopsis thaliana]	Unigene88422_All//7.00E-40//AT2G34070| unknown protein	Unigene88422_All//3.00E-162//TC133530			GO:0015925	nr +
Unigene88425_All	420	3.86	2.41	1.14	2.37	4.18	3.55	1.81	5.27	0.38	-6.79E-01	1.89E-01		-1.76E+00	2.55E-03		8.18E-01	1.03E-01		5.81E-01	3.18E-01		1.54E+00	1.40E-04	Up	-2.26E+00	4.68E-03		Unigene88425_All//gi|21326848|gb|ACJ45013.1|//3.00E-18//NPR1-1 protein [Glycine max]		Unigene88425_All//5.00E-149//EX164041			GO:0005488	nr +
Unigene88429_All	408	0.26	0.12	0.00	2.20	0.93	0.11	0.83	0.31	0.10	-1.05E+00	6.82E-01		-8.00E+00	3.86E-01		-1.24E+00	8.17E-02		-4.31E+00	1.14E-04	Down	-1.43E+00	2.58E-01		-3.09E+00	3.91E-02				Unigene88429_All//1.00E-22//TC179262				
Unigene8843_All	513	0.00	0.20	0.00	0.00	0.07	2.73	2.55	0.16	6.21	7.63E+00	3.78E-01		null	null		6.07E+00	8.11E-01		1.14E+01	2.43E-08	Up	-3.97E+00	3.34E-07	Down	1.28E+00	4.26E-05	Up	Unigene8843_All//gi|124365601|gb|AAK50778.4|AF361893_1/1.00E-47//bacterial-induced lipoxygenase [Gossypium hirsutum]	Unigene8843_All//2.00E-47//AT1G55020| LOX1; lipoxygenase	Unigene8843_All//0.00E+00//ES824586		ko00592|alpha-Linolenic acid metabolism//ko00591|Linoleic acid metabolism		nr -
Unigene8844_All	764	0.00	5.24	4.25	0.00	0.00	0.00	0.00	0.00	0.00	1.24E+01	8.54E-23	Up	1.21E+01	5.81E-18	Up	null	null		null	null		null	null		null	null		Unigene8844_All//gi|301107486|ref|XP_002902825.1|//4.00E-34//long-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4] >gi|262097943|gb|EEY55995.1| long-chain-fatty-acid-CoA ligase [Phytophthora infestans T30-4]	Unigene8844_All//6.00E-09//AT5G27600| LACS7 (LONG-CHAIN ACYL-COA SYNTHETASE 7); long-chain-fatty-acid-CoA ligase/ protein binding			ko04146|Peroxisome//ko00071|Fatty acid metabolism		nr -
Unigene88441_All	838	0.12	0.18	0.06	1.61	0.82	0.16	0.35	0.80	1.09	5.38E-01	7.77E-01		-9.76E-01	7.18E-01		-9.66E-01	8.22E-02		-3.31E+00	1.08E-05	Down	1.18E+00	1.44E-01		1.63E+00	1.45E-02		Unigene88441_All//gi|240254545|ref|NP_180360.4|//4.00E-50//binding [Arabidopsis thaliana]	Unigene88441_All//5.00E-49//AT2G27930| binding	Unigene88441_All//4.00E-12//TC179204	PLATZ			nr -
Unigene88443_All	427	0.00	0.00	0.00	2.57	0.24	0.42	0.00	0.00	0.00	null	null		null	null		-3.41E+00	1.67E-05	Down	-2.60E+00	7.13E-04	Down	null	null		null	null				Unigene88443_All//5.00E-155//DW507218				
Unigene88447_All	440	0.59	0.00	0.00	2.49	0.31	0.62	0.77	0.19	0.18	-9.22E+00	6.64E-02		-9.22E+00	8.50E-02		-2.99E+00	6.16E-05	Down	-2.02E+00	4.74E-03		-2.02E+00	1.36E-01		-2.09E+00	1.06E-01		Unigene88447_All//gi|122938393|gb|ABM69042.1|//4.00E-35//MADS-box protein MADS4 [Gossypium hirsutum]	Unigene88447_All//4.00E-17//AT4G18960| AG (AGAMOUS); DNA binding / transcription factor	Unigene88447_All//0.00E+00//TC177856	MADS		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene8845_All	491	0.11	0.00	0.11	0.41	0.56	0.28	4.22	3.06	1.30	-6.74E+00	5.97E-01		2.55E-02	9.90E-01		4.68E-01	8.16E-01		-5.57E-01	7.32E-01		-4.61E-01	2.65E-01		-1.70E+00	4.43E-05	Down			Unigene8845_All//2.00E-123//gi|72276370|gb|DT050601.1|DT050601				
Unigene8846_All	643	0.00	0.00	0.17	0.31	0.11	0.00	9.99	20.35	17.22	null	null		7.37E+00	3.87E-01		-1.53E+00	4.14E-01		-8.28E+00	1.32E-01		1.03E+00	1.00E-12	Up	7.85E-01	1.82E-07		Unigene8846_All//gi|224130858|ref|XP_002320942.1|//2.00E-12//multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa] >gi|222861715|gb|EEE99257.1| multidrug/pheromone exporter, MDR family, ABC transporter family [Populus trichocarpa]	Unigene8846_All//1.00E-10//AT2G47000| ABCB4 (ATP BINDING CASSETTE SUBFAMILY B4); ATPase, coupled to transmembrane movement of substances / xenobiotic-transporting ATPase	Unigene8846_All//5.00E-150//TC168072		ko02010|ABC transporters		nr -
Unigene88460_All	466	0.45	0.00	0.00	3.53	0.59	0.87	0.82	0.00	0.51	-8.81E+00	1.20E-01		-8.81E+00	1.44E-01		-2.58E+00	3.49E-06	Down	-2.02E+00	3.04E-04	Down	-9.67E+00	6.17E-03		-6.71E-01	5.30E-01		Unigene88460_All//gi|42569431|ref|NP_180469.3|//5.00E-58//ATRBL1 (Arabidopsis thaliana Rhomboid-like 1)	Unigene88460_All//4.00E-38//AT2G29050| ATRBL1 (Arabidopsis thaliana Rhomboid-like 1)	Unigene88460_All//0.00E+00//ES790970			GO:0003824//GO:0031224	nr +
Unigene88462_All	460	0.00	0.22	0.00	2.38	1.05	0.39	0.74	0.27	0.52	7.78E+00	3.78E-01		null	null		-1.18E+00	5.94E-02		-2.60E+00	7.13E-04	Down	-1.43E+00	2.58E-01		-5.01E-01	6.49E-01		Unigene88462_All//gi|170286899|dbj|BAG13451.1|//8.00E-63//beta-glucosidase [Rosa hybrid cultivar]	Unigene88462_All//3.00E-41//AT2G44480| BGLU17 (BETA GLUCOSIDASE 17); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds			ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0015926//GO:0043167//GO:0044238	nr +
Unigene88466_All	472	0.00	0.00	0.23	0.21	0.00	0.19	0.00	20.54	8.69	null	null		7.82E+00	3.87E-01		-7.72E+00	3.06E-01		-1.41E-01	9.45E-01		1.43E+01	1.66E-68	Up	1.31E+01	2.33E-29	Up	Unigene88466_All//gi|224145241|ref|XP_002325575.1|//3.00E-39//multicopper oxidase [Populus trichocarpa] >gi|222862450|gb|EEE99956.1| multicopper oxidase [Populus trichocarpa]	Unigene88466_All//4.00E-29//AT5G48100| TT10 (TRANSPARENT TESTA 10); copper ion binding / laccase	Unigene88466_All//0.00E+00//TC174717		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism		nr -

Unigene8847_All	491	0.32	1.44	0.54	5.38	4.21	2.02	3.96	0.34	1.38	2.18E+00	2.50E-02		7.62E-01	6.43E-01		-3.54E-01	3.86E-01		-1.41E+00	3.66E-04	Down	-3.54E+00	1.27E-09	Down	-1.52E+00	3.06E-04	Down									
Unigene88471_All	463	0.34	2.85	0.12	3.23	2.98	3.12	0.09	0.36	0.43	3.07E+00	5.92E-05	Up	-1.56E+00	5.32E-01		-1.18E-01	8.23E-01		-4.83E-02	9.41E-01		1.98E+00	3.78E-01		2.24E+00	2.48E-01										
Unigene88473_All	505	1.04	0.00	0.63	1.78	0.14	0.54	0.33	0.91	0.00	-1.00E+01	2.91E-03		-7.12E-01	4.97E-01		-3.70E+00	7.11E-05	Down	-1.73E+00	2.80E-02		1.44E+00	1.67E-01		-8.39E+00	1.07E-01		Unigene88473_All//gi|108707119|gb|ABF94914.1|//2.00E-16//expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene88473_All//1.00E-19//AT3G07530| unknown protein	Unigene88473_All//2.00E-154//ES824764				nr +
Unigene88474_All	501	0.00	0.30	0.00	3.18	1.10	0.81	0.68	0.00	0.56	8.25E+00	2.31E-01		null	null		-1.53E+00	2.44E-03		-1.97E+00	4.88E-04	Down	-9.40E+00	1.17E-02		-2.79E-01	7.80E-01		Unigene88474_All//gi|240254013|ref|NP_172038.4|//4.00E-70//CVP2 (COTYLEDON VASCULAR PATTERN 2); hydrolase/ inositol trisphosphate phosphatase [Arabidopsis thaliana] >gi|259016256|sp|Q9LR47.2|P5P3_ARATH RecName: Full=Type I inositol-1,4,5-trisphosphate 5-phosphatase CVP2; AltName: Full=Protein COTYLEDON VASCULAR PATTERN 2	Unigene88474_All//2.00E-71//AT1G05470| CVP2 (COTYLEDON VASCULAR PATTERN 2); hydrolase/ inositol trisphosphate phosphatase	Unigene88474_All//4.00E-125//ES804423				nr -
Unigene8848_All	440	0.95	1.84	0.48	2.94	4.70	1.74	3.46	0.00	0.91	9.54E-01	2.26E-01		-9.75E-01	4.11E-01		6.74E-01	1.44E-01		-7.54E-01	2.18E-01		-1.18E+01	8.50E-11	Down	-1.93E+00	1.54E-04	Down	Unigene8848_All//gi|19570249|dbj|BAB88284.1|//5.00E-37//kinesin-like protein NACK2 [Nicotiana tabacum]	Unigene8848_All//5.00E-35//AT3G43210| TES (TETRASPORE); microtubule motor	Unigene8848_All//4.00E-137//TC161420				nr +
Unigene88480_All	524	0.80	0.10	0.00	1.81	0.13	0.86	0.97	0.48	0.46	-3.05E+00	4.65E-02		-9.64E+00	1.55E-02		-3.78E+00	3.39E-05	Down	-1.07E+00	1.44E-01		-1.02E+00	2.88E-01		-1.09E+00	2.28E-01		Unigene88480_All//gi|240256041|ref|NP_194031.5|//9.00E-39//hydrolase/ protein serine/threonine phosphatase [Arabidopsis thaliana]	Unigene88480_All//5.00E-40//AT4G23000| hydrolase/ protein serine/threonine phosphatase	Unigene88480_All//8.00E-102//DW492635				nr -
Unigene88483_All	514	0.10	0.00	0.00	4.56	1.61	0.18	2.14	0.08	0.31	-6.67E+00	5.97E-01		-6.67E+00	6.12E-01		-1.50E+00	1.77E-04	Down	-4.70E+00	3.40E-12	Down	-4.72E+00	1.02E-06	Down	-2.79E+00	6.37E-05	Down			Unigene88483_All//2.00E-07//gi|164277299|gb|ES829164.1|ES829164					
Unigene88487_All	563	0.37	0.90	1.61	2.92	0.49	0.80	0.53	0.52	0.21	1.28E+00	2.31E-01		2.11E+00	1.42E-02		-2.58E+00	3.49E-06	Down	-1.86E+00	6.76E-04	Down	-1.66E-02	1.02E+00		-1.31E+00	3.12E-01				Unigene88487_All//7.00E-07//TC147792					
Unigene88489_All	630	0.50	0.24	0.00	3.08	1.64	1.00	1.01	0.00	0.00	-1.05E+00	4.43E-01		-8.96E+00	4.87E-02		-9.11E-01	4.00E-02		-1.62E+00	8.10E-04	Down	-9.98E+00	1.23E-04	Down	-9.98E+00	7.10E-05	Down			Unigene88489_All//3.00E-09//TC141826					ESTscan -
Unigene8849_All	467	39.77	7.49	21.32	26.03	21.61	6.67	0.18	0.00	0.09	-2.41E+00	2.72E-48	Down	-8.99E-01	2.40E-11		-2.69E-01	1.08E-01		-1.96E+00	9.96E-27	Down	-7.50E+00	3.96E-01		-1.09E+00	6.72E-01		Unigene8849_All//gi|60203059|gb|AAX14716.1|//6.00E-08//beta-amyrin synthase [Aster sedifolius]	Unigene8849_All//7.00E-09//AT1G78955| CAMS1 (Camelliol C synthase 1); beta-amyrin synthase	Unigene8849_All//1.00E-29//TC154151		ko00100|Steroid biosynthesis		nr +
Unigene88493_All	752	0.00	0.00	0.00	0.27	0.27	0.12	1.35	0.06	0.32	null	null		null	null		5.19E-02	9.88E-01		-1.14E+00	5.67E-01		-4.60E+00	3.67E-06	Down	-2.09E+00	1.52E-03		Unigene88493_All//gi|224134056|ref|XP_002321725.1|//2.00E-96//hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase-like protein [Populus trichocarpa] >gi|222868721|gb|EEF05852.1| hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase-like protein [Populus trichocarpa] >gi|267799523|gb|AC179409.1| omega-hydroxyacid hydroxycinnamoyltransferase [Populus trichocarpa]	Unigene88493_All//1.00E-77//AT5G41040| transferase family protein	Unigene88493_All//0.00E+00//TC138525		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr +
Unigene88495_All	1056	0.00	0.86	0.00	0.52	0.13	0.09	2.68	0.32	0.34	9.75E+00	2.60E-05	Up	null	null		-1.99E+00	5.11E-02		-2.60E+00	2.93E-02		-3.08E+00	3.10E-12	Down	-2.98E+00	2.59E-12	Down	Unigene88495_All//gi|42568214|ref|NP_188840.2|//2.00E-95//nodulin MtN21 family protein [Arabidopsis thaliana] >gi|10177511|dbj|BAB10905.1| nodulin-like protein [Arabidopsis thaliana] >gi|30725298|gb|AAP37671.1| At5g40240 [Arabidopsis thaliana]	Unigene88495_All//1.00E-87//AT5G40240| nodulin MtN21 family protein	Unigene88495_All//2.00E-17//TC169820				nr +
Unigene88498_All	1836	0.40	0.28	0.03	0.24	0.26	0.27	0.92	0.27	0.52	-5.32E-01	5.12E-01		-3.78E+00	2.79E-03		1.05E-01	9.54E-01		1.48E-01	9.05E-01		-1.75E+00	2.90E-04	Down	-8.23E-01	5.74E-02		Unigene88498_All//gi|113205448|gb|ABI34400.1|//4.00E-86//Putative mandelonitrile lyase, related [Solanum demissum]	Unigene88498_All//7.00E-71//AT1G14180| protein binding / zinc ion binding	Unigene88498_All//0.00E+00//gi|109847591|gb|DW476571.1|DW476571				nr +
Unigene88519_All	200	2.35	3.04	1.60	23.16	11.36	4.74	0.21	0.42	0.60	3.69E-01	6.60E-01		-5.60E-01	6.28E-01		-1.03E+00	8.36E-05	Down	-2.29E+00	1.21E-12	Down	9.84E-01	7.28E-01		1.50E+00	5.56E-01		Unigene88519_All//gi|115440997|ref|NP_001044778.1|//3.00E-07//Os01g0844200 [Oryza sativa (japonica Group)] >gi|113534309|dbj|BAF06692.1| Os01g0844200 [Oryza sativa (japonica Group)]	Unigene88519_All//2.00E-07//AT2G29125| RTFL2 (ROTUNDIFOLIA LIKE 2)	Unigene88519_All//3.00E-25//ES850629				nr +
Unigene8852_All	208	4.02	2.19	2.30	13.41	10.76	3.47	0.00	0.20	0.00	-8.76E-01	2.47E-01		-8.05E-01	3.22E-01		-3.18E-01	4.26E-01		-1.95E+00	1.68E-06	Down	7.65E+00	6.23E-01		null	null										
Unigene88529_All	200	76.91	63.59	115.02	13.70	13.26	2.26	1.69	0.00	0.20	-2.74E-01	6.37E-02		5.81E-01	7.54E-07		-4.72E-02	9.01E-01		-2.60E+00	7.76E-09	Down	-1.07E+01	1.17E-02		-3.09E+00	3.91E-02				Unigene88529_All//9.00E-84//gi|164353819|gb|ES795071.1|ES795071					
Unigene88539_All	201	0.00	3.53	0.26	0.99	0.69	0.00	125.58	271.36	422.37	1.18E+01	3.30E-04	Up	8.05E+00	6.22E-01		-5.33E-01	7.47E-01		-9.95E+00	1.32E-01		1.11E+00	1.83E-57	Up	1.75E+00	7.97E-180	Up	Unigene88539_All//gi|45238345|emb|CAD70567.1|//4.00E-27//aldehyde dehydrogenase [Crocus sativus]	Unigene88539_All//8.00E-24//AT3G24503| ALDH2C4; 3-chloroallyl aldehyde dehydrogenase/ aldehyde dehydrogenase (NAD)/ coniferyl-aldehyde dehydrogenase	Unigene88539_All//1.00E-18//gi|164322141|gb|ES819657.1|ES819657		ko00940|Phenylpropanoid biosynthesis//ko00010|Glycolysis / Gluconeogenesis//ko00903|Limonene and pinene degradation//ko00620|Pyruvate metabolism//ko00380|Tryptophan metabolism//ko00071|Fatty acid metabolism//ko00053|Ascorbate and aldarate metabolism//ko00330|Arginine and proline metabolism//ko00280|Valine, leucine and isoleucine degradation//ko00640|Propanoate metabolism//ko00561|Glycerolipid metabolism//ko00310|Lysine degradation//ko00410|beta-Alanine metabolism//ko00340|Histidine metabolism		nr -
Unigene88545_All	201	65.60	143.19	82.92	74.60	130.37	111.67	49.64	53.02	55.10	1.13E+00	1.34E-25	Up	3.38E-01	1.97E-02		8.06E-01	7.47E-16		5.82E-01	2.30E-07		9.51E-02	6.35E-01		1.51E-01	3.66E-01		Unigene88545_All//gi|300261239|gb|EFJ45453.1|//2.00E-30//polyubiquitin [Volvox carteri f. nagariensis]	Unigene88545_All//8.00E-32//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene88545_All//1.00E-107//gi|84170314|gb|DR458962.1|DR458962				nr +
Unigene8855_All	596	6.50	0.09	2.50	2.17	0.29	0.23	0.00	0.07	0.00	-6.26E+00	8.30E-21	Down	-1.38E+00	4.46E-05	Down	-2.91E+00	1.33E-05	Down	-3.26E+00	1.98E-05	Down	6.13E+00	6.23E-01		null	null				Unigene8855_All//1.00E-168//TC167832					
Unigene88550_All	201	0.00	0.00	0.00	3.97	0.00	2.47	0.84	0.00	0.20	null	null		null	null		-1.20E+01	6.49E-06	Down	-6.82E-01	4.05E-01		-9.72E+00	1.33E-01		-2.09E+00	3.12E-01		Unigene88550_All//gi|147801641|emb|CAN63466.1|//8.00E-06//hypothetical protein [Vitis vinifera]							nr +
Unigene8856_All	1598	0.00	19.44	10.46	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	4.12E-179	Up	1.34E+01	2.40E-94	Up	null	null		null	null		null	null		null	null		Unigene8856_All//gi|238814974|gb|ACR56690.1|//1.00E-167//enolase [Nicotiana tabacum]	Unigene8856_All//4.00E-162//AT1G74030| enolase, putative	Unigene8856_All//2.00E-09//gi|164301059|gb|EV491957.1|EV491957		ko00010|Glycolysis / Gluconeogenesis//ko03018|RNA degradation		nr -
Unigene88565_All	201	13.02	28.49	16.43	26.77	45.40	34.83	88.98	72.36	94.54	1.13E+00	9.48E-06	Up	3.36E-01	3.74E-01		7.62E-01	2.32E-05		3.80E-01	1.03E-01		-2.98E-01	1.30E-02		8.75E-02	5.04E-01		Unigene88565_All//gi|211906448|gb|ACJ11717.1|//2.00E-22//alpha-soluble NSF attachment protein [Gossypium hirsutum]	Unigene88565_All//1.00E-17//AT3G56190| ALPHA-SNAP2 (ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN 2); binding / soluble NSF attachment protein	Unigene88565_All//5.00E-76//TC1311111				nr -
Unigene88857_All	762	3.91	0.40	0.00	1.44	6.01	1.19	0.44	0.00	0.68	-3.29E+00	3.33E-11	Down	-1.19E+01	2.42E-16	Down	2.06E+00	1.60E-11	Up	-2.79E-01	6.89E-01		-8.79E+00	1.17E-02		6.15E-01	4.93E-01		Unigene88857_All//gi|161610920|gb|ABX75139.1|//1.00E-128//lipase [Gossypium hirsutum]	Unigene88857_All//1.00E-86//AT5G33370| GDSL-motif lipase/hydrolase family protein	Unigene88857_All//0.00E+00//TC137605				nr -
Unigene88584_All	202	0.52	0.50	0.79	3.45	0.68	10.28	941.05	591.97	552.42	-4.61E-02	9.85E-01		6.10E-01	7.46E-01		-2.34E+00	1.01E-02		1.57E+00	7.98E-04	Up	-6.69E-01	3.05E-84		-7.69E-01	3.46E-110				Unigene88584_All//6.00E-45//TC145168					
Unigene88588_All	202	0.52	0.75	0.53	0.99	0.00	0.45	0.21	3.72	0.59	5.39E-01	7.77E-01		2.54E-02	9.96E-01		-9.95E+00	8.34E-02		-1.14E+00	5.67E-01		4.15E+00	1.92E-04	Up	1.50E+00	5.56E-01										
Unigene886_All	276	0.38	0.00	4.44	6.14	4.49	3.11	1.53	0.76	0.87	-8.57E+00	3.64E-01		3.55E+00	6.10E-05	Up	-4.50E-01	3.87E-01		-9.81E-01	5.37E-02		-1.02E+00	3.50E-01		-8.23E-01	3.98E-01		Unigene886_All//gi|124359292|gb|ABD28429.2|//1.00E-34//Regulator of chromosome condensation/beta-lactamase-inhibitor protein II [Medicago truncatula]	Unigene886_All//1.00E-28//AT3G03790| ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein	Unigene886_All//5.00E-83//gi|72273281|gb|DT049075.1|DT049075			GO:0043231	nr +
Unigene88605_All	202	1.04	0.25	1.05	3.70	1.53	0.45	5.02	0.21	0.20	-2.05E+00	3.33E-01		2.54E-02	1.00E+00		-1.27E+00	1.12E-01		-3.05E+00	3.33E-03		-4.60E+00	3.67E-06	Down	-4.67E+00	1.72E-06	Down			Unigene88605_All//3.00E-16//DW242989					
Unigene8861_All	508	1.13	0.40	0.21	1.08	1.02	1.24	0.00	0.00	2.27	-1.51E+00	1.36E-01		-2.43E+00	4.40E-02		-8.53E-02	9.07E-01		2.07E-01	8.23E-01		null	null		1.12E+01	2.28E-08	Up	Unigene8861_All//gi|21397271|gb|AAM51835.1|AC105730.9//2.00E-06//Putative plant disease resistance polyprotein [Oryza sativa (japonica Group)]		Unigene8861_All//0.00E+00//ES841268				nr +
Unigene8862_All	357	0.15	0.43	7.01	8.09	8.01	4.81	1.18	0.00	0.00	1.54E+00	5.29E-01		5.58E+00	1.91E-12	Up	-1.56E-02	9.58E-01		-7.52E-01	4.17E-02		-1.02E+01	3.24E-03		-1.02E+01	2.14E-03		Unigene8862_All//gi|290579513|gb|AD051352.1|//4.00E-10//TT2 like MYB transcriptoin factor [Theobroma cacao]		Unigene8862_All//1.00E-161//TC175767				nr +
Unigene88623_All	203	0.00	0.25	0.00	4.91	0.85	0.67	0.00	0.21	0.00	7.96E+00	6.06E-01		null	null		-2.53E+00	6.75E-04	Down	-2.88E+00	6.76E-04	Down	7.69E+00	6.23E-01		null	null				Unigene88623_All//6.00E-85//TC170155					
Unigene8864_All	860	0.06	0.53	0.25	0.17	0.76	0.79	3.59	2.48	83.20	3.12E+00	3.57E-02		2.03E+00	3.59E-01		2.13E+00	3.78E-02		2.18E+00	3.14E-02		-5.34E-01	9.70E-02		4.53E+00	0.00E+00	Up	Unigene8864_All//gi|28557342|dbj|BAC57589.1|//5.00E-10//membrane located receptor-like protein [Nicotiana tabacum]						nr +
Unigene88646_All	203	0.00	0.00	1.31	3.44	1.02	0.00	1.04	0.41	1.18	null	null		1.04E+01	7.85E-02		-1.76E+00	4.11E-02		-1.17E+01	1.96E-04	Down	-1.34E+00	4.28E-01		1.77E-01	9.08E-01										
Unigene88652_All	203	52.32	47.18	53.51	109.44	127.05	76.98	138.92	68.15	126.97	-1.49E-01	4.29E-01		3.25E-02	8.69E-01		2.15E-01	5.23E-02		-5.08E-01	6.85E-06		-1.03E+00	1.31E-26	Down	-1.30E-01	1.89E-01				Unigene88652_All//1.00E-79//gi|133537389|gb|BG444137.1|BG444137					
Unigene88672_All	204	0.51	0.00	3.13	6.84	0.00	1.33	0.83	0.00	0.00	-9.00E+00	3.64E-01		2.61E+00	2.32E-02		-1.27E+01	2.40E-10	Down	-2.36E+00	2.38E-04	Down	-9.70E+00	1.33E-01		-9.70E+00	1.07E-01										
Unigene88678_All	204	7.69	1.24	7.57	1.47	1.01	0.89	0.00	0.00	0.00	-2.63E+00	4.14E-05	Down	-2.35E-02	9.87E-01		-5.33E-01	6.78E-01		-7.26E-01	6.38E-01		null	null		null	null				Unigene88678_All//2.00E-07//ES833202					
Unigene8871_All	997	5.04	1.12	4.65	0.00	0.14	0.05	0.00	0.00	0.00	-2.17E+00	5.28E-12	Down	-1.17E-01	6.80E-01		7.11E+00	3.16E-01		5.50E+00	6.81E-01		null	null		null	null		Unigene8871_All//gi|227053577|gb|ACP18876.1|//1.00E-136//subtilisin-like serine protease [Carica papaya]	Unigene8871_All//9.00E-114//AT2G04160| AIR3; serine-type endopeptidase	Unigene8871_All//2.00E-73//C0079423				nr +
Unigene8872_All	383	8.61	4.23	5.42	1.43	5.03	6.96	1.66	0.55	0.42	-1.02E+00	2.92E-03		-6.67E-01	6.27E-02		1.82E+00	2.13E-04	Up	2.28E+00	2.77E-07	Up	-1.60E+00	6.26E-02		-1.99E+00	2.04E-02				Unigene8872_All//2.00E-30//DW235139					
Unigene88723_All	205	1.28	17.05	0.78	1.94	5.71	3.08	39.39	80.74	87.45	3.74E+00	2.82E-14	Up	-7.12E-01	6.21E-01		1.55E+00	1.81E-02		6.66E-01	4.92E-01		1.04E+00	4.03E-16	Up	1.15E+00	5.52E-21	Up			Unigene88723_All//5.00E-64//TC136188					
Unigene8873_All	634	4.54	9.59	12.18	0.71	0.54	0.71	0.00	0.00	0.00	1.08E+00	1.11E-05	Up	1.42E+00	6.12E-10	Up	-3.81E-01	7.21E-01		1.08E-02	9.99E-01		null	null		null	null		Unigene8873_All//gi|115468494|ref|NP_001057846.1|//2.00E-44//Os06g0554200 [Oryza sativa (japonica Group)] >gi|113595886|dbj|BAF19760.1| Os06g0554200 [Oryza sativa (japonica Group)]	Unigene8873_All//1.00E-47//AT5G25840| unknown protein					nr -
Unigene8874_All	596	43.10	52.88	114.90	0.00	0.00	0.00	0.00	0.00	0.00	2.95E-01	2.49E-03		1.41E+00	4.06E-83	Up	null	null		null	null		null	null		null	null		Unigene8874_All//gi|224101127|ref|XP_002312153.1|//5.00E-98//light-harvesting complex II protein Lhcb8 [Populus trichocarpa] >gi|222851973|gb|EEE89520.1| light-harvesting complex II protein Lhcb8 [Populus trichocarpa]	Unigene8874_All//1.00E-98//AT2G40100| LHCB4.3 (light harvesting complex PSII); chlorophyll binding	Unigene8874_All//0.00E+00//TC134181		ko00196|Photosynthesis - antenna proteins		nr +
Unigene88754_All	206	0.25	0.25	0.52	3.14	0.50	0.00	0.82	0.00	0.19	-4.62E-02	9.80E-01		1.03E+00	7.00E-01		-2.65E+00	7.45E-03		-1.16E+01	3.89E-04	Down	-9.68E+00	1.33E-01		-2.09E+00	3.12E-01				Unigene88754_All//3.00E-105//gi|109889738|gb|DW518706.1|DW518706					
Unigene8876_All	213	8.60	5.47	8.50	0.00	0.16	3.39	0.20	1.18	0.75	-6.52E-01	1.74E-01		-1.64E-02	9.96E-01		7.34E+00	8.11E-01		1.17E-01	2.31E-04	Up	2.57E+00	1.53E-01		1.91E+00	3.76E-01				Unigene8876_All//8.00E-66//ES806249					
Unigene88766_All	206	0.00	3.44	0.00	1.21	0.00	0.00	0.21	0.00	0.39	1.17E+01	3.30E-04	Up	null	null		-1.02E+01	4.15E-02		-1.02E+01	7.26E-02		-7.68E+00	6.38E-01		9.15E-01	7.46E-01										
Unigene88774_All	206	1.27	0.00	0.00	5.56	1.00	1.75	0.62	0.00	0.19	-1.03E+01	6.64E-02		-1.03E+01	8.50E-02		-2.47E+00	2.73E-04	Down	-1.67E+00	1.29E-02		-9.27E+00	2.33E-01		-1.67E+00	4.75E-01										
Unigene8878_All	567	7.84	0.71	2.44	1.23	0.55	0.08	0.60	0.22	0.14	-3.46E+00	4.03E-17	Down	-1.68E+00	1.92E-07	Down	-1.17E+00	1.61E-01		-3.95E+00	1.45E-03		-1.43E+00	2.58E-01		-2.09E+00	1.06E-01		Unigene8878_All//gi|302142925|emb|CBI20220.3|//5.00E-30//unnamed protein product [Vitis vinifera]		Unigene8878_All//1.00E-39//TC134108				nr +
Unigene88804_All	207	0.00	0.00	0.00	2.41	0.00	0.44	0.00	0.00	0.00	null	null		null	null		-1.12E+01	8.96E-04	Down	-2.46E+00	4.82E-02		null	null		null	null		Unigene88804_All//gi|72255620|gb|AAZ66938.1|//7.00E-28//117M18_19 [Brassica rapa]	Unigene88804_All//1.00E-28//AT4G01020| helicase domain-containing protein / IBR domain-containing protein / zinc finger protein-related					nr -

Unigene8883_All	229	61.00	1044.81	654.35	5.66	5.71	10.45	1.29	3.29	11.13	4.10E+00	0.00E+00	Up	3.42E+00	0.00E+00	Up	1.48E-02	9.95E-01		8.86E-01	3.37E-02		1.35E+00	7.61E-02		3.11E+00	2.32E-11	Up	Unigene8883_All//gi|224159219|ref|XP_002338956.1|//3.00E-12//predicted protein [Populus trichocarpa] >gi|222870565|gb|EEF07696.1|predicted protein [Populus trichocarpa]		Unigene8883_All//8.00E-20//TC160675				nr -
Unigene88831_All	208	0.00	0.00	0.00	3.59	0.66	0.00	0.00	0.00	0.00	null	null		null	null		-2.44E+00	5.60E-03		-1.18E+01	9.80E-05	Down	null	null		null	null										
Unigene8884_All	276	0.38	0.00	0.00	1.62	4.37	1.80	1.84	0.00	0.14	-8.57E+00	3.64E-01		-8.57E+00	3.86E-01		1.43E+00	2.58E-02		1.48E-01	9.05E-01		-1.08E+01	8.88E-04	Down	-3.67E+00	3.75E-03				Unigene8884_All//2.00E-104//gi|195983313|gb|FL577327.1|FL577327					
Unigene8885_All	857	0.00	0.00	0.12	0.17	0.20	0.05	1.78	2.19	4.93	null	null		6.96E+00	3.87E-01		2.04E-01	9.49E-01		-1.73E+00	4.98E-01		3.05E-01	5.09E-01		1.47E+00	8.82E-08	Up	Unigene8885_All//gi|15239165|ref|NP_199118.1|//4.00E-08//DC1 domain-containing protein [Arabidopsis thaliana] >gi|9757830|dbj|BAB08267.1| CHP-rich zinc finger protein-like [Arabidopsis thaliana]	Unigene8885_All//2.00E-08//AT5G43040| DC1 domain-containing protein	Unigene8885_All//4.00E-86//C0080232				nr +
Unigene8886_All	371	40.05	41.66	43.20	91.71	126.79	127.70	626.57	481.16	311.51	5.67E-02	7.14E-01		1.09E-01	5.07E-01		4.67E-01	5.35E-11		4.78E-01	1.48E-10		-3.81E-01	2.15E-37		-1.01E+00	7.26E-213	Down	Unigene8886_All//gi|224092400|ref|XP_002309592.1|//5.00E-18//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222855568|gb|EEE93115.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene8886_All//3.00E-15//AT1G52800| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene8886_All//9.00E-144//TC141133				nr +
Unigene8887_All	970	0.00	9.45	6.97	0.00	0.04	0.00	0.00	0.00	0.00	1.32E+01	1.65E-52	Up	1.28E+01	9.21E-38	Up	5.15E+00	8.11E-01		null	null		null	null		null	null		Unigene8887_All//gi|217039738|gb|ACJ76959.1|//3.00E-15//low molecular weight glutenin [Triticum monococcum]				ko03040|Spliceosome//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr +
Unigene88870_All	209	213.04	81.22	177.33	93.67	74.47	89.25	145.86	78.79	27.26	-1.39E+00	1.36E-54	Down	-2.65E-01	1.64E-03		-3.31E-01	5.91E-03		-6.98E-02	6.49E-01		-8.88E-01	1.08E-22		-2.42E+00	7.37E-100	Down	Unigene88870_All//gi|8134568|sp|P93263.1|METE_MESCR//4.00E-23//RecName: Full=5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase; AltName: Full=Vitamin-B12-independent methionine synthase isozyme; AltName: Full=Cobalamin-independent methionine synthase isozyme >gi|1814403|gb|AAB41896.1|methionine synthase [Mesembryanthemum crystallinum]	Unigene88870_All//3.00E-21//AT5G17920| ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase	Unigene88870_All//2.00E-100//gi|11207177|gb|BF276107.1|BF276107		ko00270|Cysteine and methionine metabolism		nr -
Unigene88895_All	209	0.00	0.00	0.00	2.86	0.00	1.08	0.61	0.40	0.00	null	null		null	null		-1.15E+01	1.77E-04	Down	-1.40E+00	1.58E-01		-6.02E-01	7.64E-01		-9.25E+00	1.98E-01					Unigene88895_All//6.00E-79//TC158381					
Unigene8890_All	438	0.84	0.12	0.24	1.71	0.31	0.10	1.64	1.15	2.91	-2.85E+00	7.79E-02		-1.78E+00	2.33E-01		-2.44E+00	5.60E-03		-4.05E+00	7.75E-04	Down	-5.19E-01	5.07E-01		8.27E-01	1.08E-01										
Unigene88914_All	210	4.73	0.00	0.00	1.90	0.98	2.37	18.12	6.17	3.60	-1.22E+01	7.45E-06	Down	-1.22E+01	1.77E-05	Down	-9.48E-01	4.20E-01		3.18E-01	7.57E-01		-1.55E+00	2.05E-07	Down	-2.33E+00	1.33E-12	Down				Unigene88914_All//1.00E-79//TC162854					
Unigene8893_All	572	0.18	1.06	0.65	2.35	0.66	1.90	0.59	1.83	3.69	2.54E+00	2.46E-02		1.83E+00	2.12E-01		-1.83E+00	1.45E-03		-3.11E-01	6.37E-01		1.63E+00	1.04E-02		2.64E+00	3.33E-08	Up	Unigene8893_All//gi|296875334|gb|ADH82120.1|//4.00E-65//MoCo sulfurase (Citrus sinensis)	Unigene8893_All//5.00E-55//AT1G16540| ABA3 (ABA DEFICIENT 3); Mo-molybdopterin cofactor sulfurase/ selenocysteine lyase	Unigene8893_All//0.00E+00//C0113630				nr +
Unigene88938_All	211	0.74	1.44	1.26	1.65	0.82	1.28	3.21	1.19	0.00	9.54E-01	5.02E-01		7.62E-01	6.43E-01		-1.02E+00	4.22E-01		-3.64E-01	7.55E-01		-1.43E+00	7.83E-02		-1.16E+01	3.56E-05	Down				Unigene88938_All//2.00E-07//BQ413340					
Unigene8894_All	451	0.00	0.00	0.12	0.00	0.00	0.00	15.47	29.84	56.53	null	null		6.88E+00	6.21E-01		null	null		null	null		9.48E-01	1.41E-11		1.87E+00	1.17E-59	Up	Unigene8894_All//gi|75860384|gb|ABA29159.1|//3.00E-07//nodulin-like protein [Pisum sativum]						nr +
Unigene88945_All	211	1.49	0.48	0.00	4.96	0.65	0.43	1.60	0.20	0.19	-1.63E+00	2.76E-01		-1.05E+01	4.87E-02		-2.93E+00	1.21E-04	Down	-3.53E+00	9.33E-05	Down	-3.02E+00	5.29E-02		-3.09E+00	3.91E-02		Unigene88945_All//gi|12006362|gb|AAG44843.1|AF281155_1//2.00E-11//cohesion family protein SYN3 [Arabidopsis thaliana]	Unigene88945_All//7.00E-13//AT3G59550| SYN3	Unigene88945_All//4.00E-86//ES830978				nr +
Unigene8896_All	693	3.78	9.65	7.68	0.86	0.60	1.11	0.12	0.84	0.00	1.35E+00	1.84E-08	Up	1.03E+00	1.65E-04	Up	-5.33E-01	5.61E-01		3.61E-01	6.79E-01		2.79E+00	8.26E-03		-6.93E+00	3.53E-01										
Unigene8898_All	973	0.00	0.00	0.00	0.00	0.00	0.00	9.47	3.01	0.16	null	null		null	null		null	null		null	null		-1.66E+00	2.10E-18	Down	-5.85E+00	4.67E-61	Down									ESTscan +
Unigene8899_All	526	26.46	26.97	27.64	27.37	13.09	16.14	15.84	12.40	9.92	2.77E-02	8.69E-01		6.29E-02	6.99E-01		-1.06E+00	1.58E-14	Down	-7.62E-01	1.23E-07		-3.53E-01	5.64E-02		-6.74E-01	1.04E-04					Unigene8899_All//2.00E-93//TC142605					
Unigene88996_All	213	8.35	20.70	18.25	10.99	24.57	18.45	12.11	15.31	20.20	1.31E+00	1.36E-05	Up	1.13E+00	5.93E-04	Up	1.16E+00	4.73E-06	Up	7.47E-01	1.58E-02		3.38E-01	3.07E-01		7.38E-01	3.53E-03		Unigene88996_All//gi|15236101|ref|NP_195711.1|//2.00E-17//SNRK2.7 (SNF1-RELATED PROTEIN KINASE 2.7); kinase [Arabidopsis thaliana] >gi|75337420|sp|Q9SAH4.1|SRK2E_ARATH RecName: Full=Serine/threonine-protein kinase SRK2F; AltName: Full=OST1-kinase-like 5; AltName: Full=SNF1-related kinase 2.7; Short=SnRK2.7	Unigene88996_AtI//8.00E-19//AT4G40010| SNRK2.7 (SNF1-RELATED PROTEIN KINASE 2.7); kinase	Unigene88996_AtI//5.00E-73//gi|84154633|gb|DN803988.1|DN803988		GO:0004672//GO:0006464//GO:0006970//GO:0032559//GO:0043231//GO:0044444	nr -
Unigene890_All	1226	22.66	39.72	30.45	40.79	59.74	50.50	27.59	8.25	19.01	8.10E-01	5.06E-25		4.26E-01	2.24E-06		5.50E-01	1.40E-22		3.08E-01	2.23E-06		-1.74E+00	2.56E-70	Down	-5.37E-01	3.32E-11		Unigene890_All//gi|194241584|gb|ACF35047.1|//6.00E-98//protein phosphatase 2C [Hevea brasiliensis]	Unigene890_AtI//1.00E-95//AT5G53140| protein phosphatase 2C, putative / PP2C, putative	Unigene890_AtI//0.00E+00//TC150195		GO:0004721//GO:0006464//GO:0043169//GO:0043231//GO:0043234	nr +
Unigene89003_All	213	0.49	0.00	0.00	2.57	0.00	0.00	0.40	0.59	0.56	-8.94E+00	3.64E-01		-8.94E+00	3.86E-01		-1.13E+01	4.00E-04	Down	-1.13E+01	1.52E-03		5.68E-01	7.80E-01		4.99E-01	8.05E-01										
Unigene89008_All	213	10.56	0.48	5.00	3.98	2.10	0.64	0.00	0.39	0.19	-4.47E+00	1.29E-10	Down	-1.08E+00	1.68E-02		-9.20E-01	2.17E-01		-2.64E+00	3.54E-03		8.62E+00	3.97E-01		7.55E+00	6.32E-01		Unigene89008_All//gi|224113117|ref|XP_002316396.1|//8.00E-11//predicted protein [Populus trichocarpa] >gi|222865636|gb|EEF02567.1|predicted protein [Populus trichocarpa]		Unigene89008_AtI//1.00E-24//DT047958		GO:0000166//GO:0004713//GO:0008152//GO:0016020//GO:0016491	nr -
Unigene8901_All	945	0.00	0.00	0.00	0.00	0.00	0.00	3.49	15.13	2.28	null	null		null	null		null	null		null	null		2.12E+00	8.37E-39	Up	-6.16E-01	3.59E-02		Unigene8901_All//gi|255541322|ref|XP_002511725.1|//1.00E-10//conserved hypothetical protein [Ricinus communis] >gi|223548905|gb|EEF50394.1|conserved hypothetical protein [Ricinus communis]						nr -
Unigene89025_All	214	7.33	1.18	3.48	3.03	3.38	5.07	0.00	0.00	0.00	-2.63E+00	4.14E-05	Down	-1.07E+00	5.45E-02		1.59E-01	8.68E-01		7.43E-01	2.89E-01		null	null		null	null										
Unigene89026_All	214	0.00	0.00	0.00	2.56	0.00	0.84	0.79	0.78	0.93	null	null		null	null		-1.13E+01	4.00E-04	Down	-1.60E+00	1.32E-01		-1.67E-02	1.02E+00		2.36E-01	8.82E-01		Unigene89026_All//gi|15229022|ref|NP_190446.1|//8.00E-17//ATP binding / DNA binding [Arabidopsis thaliana]	Unigene89026_AtI//3.00E-18//AT3G48770| ATP binding / DNA binding			GO:0000166//GO:0004674	nr -
Unigene8903_All	423	0.25	0.36	0.00	0.00	0.33	0.43	2.20	4.35	5.46	5.39E-01	7.77E-01		-7.95E+00	3.85E-01		8.35E+00	3.16E-01		8.74E+00	1.93E-01		9.83E-01	2.25E-02		1.31E+00	4.85E-04	Up				Unigene8903_AtI//5.00E-07//TC157012					
Unigene89037_All	214	0.00	0.00	0.00	3.49	0.32	0.00	0.79	0.20	0.00	null	null		null	null		-3.44E+00	6.18E-04	Down	-1.18E+01	9.80E-05	Down	-2.02E+00	3.66E-01		-9.63E+00	1.07E-01		Unigene89037_AtI//gi|13346182|gb|AAK19613.1|AF336280_1//2.00E-06//GHDEL65 [Gossypium hirsutum]						nr +
Unigene8904_All	544	0.00	0.00	0.20	0.09	0.13	0.00	0.78	2.77	3.44	null	null		7.61E+00	3.87E-01		4.67E-01	9.52E-01		-6.52E+00	6.13E-01		1.83E+00	4.72E-04	Up	2.15E+00	5.82E-06	Up	Unigene8904_AtI//gi|113367270|gb|ABI34692.1|//7.00E-13//bZIP transcription factor bZIP107 [Glycine max]	Unigene8904_AtI//5.00E-14//AT4G35240| unknown protein	Unigene8904_AtI//7.00E-13//TC177695				nr -
Unigene8905_All	237	12.14	4.49	7.19	12.40	6.68	4.95	1.25	0.18	0.34	-1.44E+00	2.02E-04	Down	-7.56E-01	5.03E-02		-8.92E-01	9.45E-03		-1.32E+00	3.33E-04	Down	-2.82E+00	8.83E-02		-1.89E+00	1.68E-01					Unigene8905_AtI//8.00E-91//TC150421					
Unigene8906_All	489	7.92	4.97	3.16	4.69	5.92	2.59	0.52	0.17	0.16	-6.71E-01	3.06E-02		-1.33E+00	7.74E-05	Down	3.36E-01	4.16E-01		-8.58E-01	4.25E-02		-1.60E+00	3.10E-01		-1.67E+00	2.56E-01		Unigene8906_AtI//gi|225458467|ref|XP_002282153.1|//1.00E-08//PREDICTED: similar to ATS/KAN4 (ABERRANT TESTA SHAPE): DNA binding / transcription factor [Vitis vinifera]						nr +
Unigene8907_All	946	0.55	0.59	0.96	2.00	2.26	1.96	70.75	75.42	236.29	9.12E-02	9.32E-01		7.91E-01	3.03E-01		1.74E-01	7.53E-01		-3.18E-02	9.49E-01		9.22E-02	1.43E-01		1.74E+00	0.00E+00	Up	Unigene8907_AtI//gi|146760355|dbj|BAF62431.1|//4.00E-17//glyoxalase I [Cucurbita maxima]	Unigene8907_AtI//4.00E-17//AT1G08110| lactoylglutathione lyase, putative / glyoxalase I, putative	Unigene8907_AtI//8.00E-57//CD485645		ko00620|Pyruvate metabolism		nr -
Unigene89075_All	216	0.24	0.94	0.25	3.92	0.16	0.84	0.59	0.58	0.37	1.95E+00	3.73E-01		2.54E-02	9.90E-01		-4.62E+00	2.79E-05	Down	-2.23E+00	9.52E-03		-1.66E-02	1.02E+00		-6.71E-01	7.18E-01					Unigene89075_AtI//2.00E-07//TC172815					
Unigene8908_All	593	3.97	4.61	4.76	1.76	4.41	0.76	0.00	0.00	0.00	2.17E-01	6.01E-01		2.62E-01	5.18E-01		1.32E+00	6.59E-04	Up	-1.21E+00	7.80E-02		null	null		null	null		Unigene8908_AtI//gi|85069279|gb|ABC69711.1|//2.00E-34//auxin response factor 2 [Solanum lycopersicum]	Unigene8908_AtI//9.00E-34//AT5G62000| ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor	Unigene8908_AtI//4.00E-116//gi|164333530|gb|ES797050.1|ES797050	ARF			nr +
Unigene89088_All	216	1.70	0.00	0.99	3.00	0.32	0.00	0.20	0.00	0.37	-1.07E+01	1.95E-02		-7.82E-01	5.53E-01		-3.23E+00	2.48E-03		-1.15E+01	3.89E-04	Down	-7.61E+00	6.38E-01		9.15E-01	7.46E-01										
Unigene8910_All	333	0.94	0.61	0.96	0.90	0.93	1.49	2.03	1.00	0.12	-6.31E-01	6.21E-01		2.55E-02	1.00E+00		5.22E-02	9.98E-01		7.33E-01	5.16E-01		-1.02E+00	2.04E-01		-4.09E+00	3.10E-04	Down				Unigene8910_AtI//1.00E-07//ES818432					
Unigene89104_All	217	58.59	12.14	15.21	9.87	3.65	1.87	7.21	0.00	1.29	-2.27E+00	5.50E-31	Down	-1.95E+00	1.72E-24	Down	-1.44E+00	6.37E-04	Down	-2.40E+00	1.86E-06	Down	-1.28E+01	4.29E-11	Down	-2.49E+00	5.08E-06	Down				Unigene89104_AtI//6.00E-45//gi|6461432|gb|AW186996.1|AW186996					
Unigene89108_All	217	0.00	0.00	0.74	2.75	1.11	0.00	0.39	0.00	0.00	null	null		9.52E+00	2.33E-01		-1.31E+00	1.56E-01		-1.14E+01	7.69E-04	Down	-8.61E+00	3.96E-01		-8.61E+00	3.52E-01					Unigene89108_AtI//2.00E-07//TC131356					
Unigene8911_All	424	1.11	0.36	0.00	1.64	0.08	1.92	0.60	0.39	1.13	-1.63E+00	1.58E-01		-1.01E+01	8.61E-03		-4.34E+00	2.29E-04	Down	2.21E-01	7.78E-01		-6.02E-01	6.47E-01		9.14E-01	3.38E-01										
Unigene8912_All	489	5.03	1.55	2.83	0.31	0.14	0.09	0.00	0.00	0.00	-1.69E+00	1.01E-04	Down	-8.29E-01	5.05E-02		-1.12E+00	5.81E-01		-1.73E+00	4.98E-01		null	null		null	null										ESTscan -
Unigene89136_All	218	0.00	0.00	0.00	10.51	0.16	1.66	2.52	1.53	1.64	null	null		null	null		-6.06E+00	1.05E-15	Down	-2.66E+00	1.16E-07	Down	-7.17E-01	4.22E-01		-6.16E-01	4.68E-01		Unigene89136_All//gi|145408590|ref|XP_001152214.1|//1.00E-13//ORF124 [Pinus koraiensis] >gi|145048839|gb|ABP35456.1|ORF124 [Pinus koraiensis]		Unigene89136_AtI//3.00E-22//TC136747				nr +
Unigene89139_All	218	3.12	0.00	1.22	8.00	2.37	0.83	1.75	1.15	0.18	-1.16E+01	4.09E-04	Down	-1.35E+00	1.50E-01		-1.76E+00	3.19E-04	Down	-3.27E+00	3.65E-07	Down	-6.02E-01	6.12E-01		-3.26E+00	2.22E-02										
Unigene8917_All	678	0.62	0.37	0.00	0.29	0.10	0.33	5.36	2.16	1.94	-7.24E-01	5.25E-01		-9.27E+00	1.55E-02		-1.53E+00	4.14E-01		1.81E-01	9.34E-01		-1.31E+00	1.03E-05	Down	-1.47E+00	7.28E-07	Down	Unigene8917_All//gi|297609729|ref|NP_001063542.2|//1.00E-13//Os09g0492900 [Oryza sativa Japonica Group] >gi|255679024|dbj|BAF25456.2|Os09g0492900 [Oryza sativa Japonica Group]	Unigene8917_AtI//5.00E-11//AT3G50800| unknown protein					nr -
Unigene89171_All	219	4.06	0.23	2.19	2.05	0.16	0.21	0.19	1.15	0.36	-4.13E+00	2.52E-04	Down	-8.92E-01	2.46E-01		-3.70E+00	1.07E-02		-3.31E+00	2.84E-02		2.57E+00	1.53E-01		9.14E-01	7.46E-01		Unigene89171_All//gi|229609839|gb|ACQ83535.1|//7.00E-21//CBL-interacting protein kinase 19 [Vitis vinifera]	Unigene89171_AtI//5.00E-19//AT3G17510| CIPK1 (CBL-INTERACTING PROTEIN KINASE 1); kinase/ protein binding	Unigene89171_AtI//1.00E-120//TC133196		GO:0004674//GO:0006464//GO:0006970//GO:0009725//GO:0016020//GO:0023060//GO:0032559	nr +
Unigene8918_All	377	3.89	1.08	0.85	2.91	2.28	5.03	0.00	0.22	0.42	-1.85E+00	1.97E-03		-2.20E+00	7.90E-04	Down	-3.48E-01	5.96E-01		7.92E-01	1.03E-01		7.79E+00	3.97E-01		8.72E+00	1.39E-01										
Unigene89181_All	219	0.24	0.00	0.00	14.33	11.79	2.68	0.00	0.19	0.00	-7.90E+00	5.97E-01		-7.90E+00	6.11E-01		-2.81E-01	4.54E-01		-2.42E+00	2.73E-09	Down	7.58E+00	6.22E-01		null	null										
Unigene89195_All	220	2.38	0.23	0.48	6.11	0.63	1.64	2.31	0.00	0.18	-3.37E+00	1.57E-02		-2.30E+00	6.75E-02		-3.29E+00	1.81E-06	Down	-1.90E+00	2.26E-03		-1.12E+01	8.88E-04	Down	-3.67E+00	3.75E-03										
Unigene89196_All	220	0.95	0.00	0.97	5.21	0.31	0.82	0.58	1.14	0.00	-9.89E+00	1.20E-01		2.54E-02	1.00E+00		-4.06E+00	1.62E-06	Down	-2.66E+00	4.12E-04	Down	9.84E-01	5.17E-01		-9.17E+00	1.98E-01					Unigene89196_AtI//2.00E-07//EX165495					
Unigene892_All	1515	5.46	2.14	3.37	12.20	11.41	8.56	22.41	20.19	19.88	-1.35E+00	2.75E-10	Down	-6.93E-01	9.20E-04		-9.64E-02	5.57E-01		-5.12E-01	4.40E-05		-1.50E-01	9.66E-02		-1.73E-01	4.16E-02		Unigene89171_All//gi|224131790|ref|XP_002321179.1|//1.00E-150//GRAS family transcription factor [Populus trichocarpa] >gi|222861952|gb|EEE99494.1| GRAS family transcription factor [Populus trichocarpa]	Unigene892_AtI//3.00E-104//AT5G48150| PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor	Unigene892_AtI//0.00E+00//TC136927	GRAS			nr +
Unigene8920_All	333	1.41	0.00	0.96	0.45	5.17	1.63	0.00	0.38	0.60	-1.05E+01	5.53E-03		-5.60E-01	6.28E-01		3.53E+00	1.39E-07	Up	1.86E+00	1.02E-01		8.56E+00	2.39E-01		9.22E+00	7.87E-02										
Unigene89202_All	220	0.00	0.00	0.00	2.26	0.00	0.00	0.77	0.95	0.00	null	null		null	null		-1.11E+01	8.96E-04	Down	-1.11E+01	2.97E-03		3.05E-01	8.35E-01		-9.59E+00	1.07E-01					Unigene89202_AtI//1.00E-18//ES812870					
Unigene8921_All	398	43.25	38.83	40.94	40.93	38.67	27.12	60.02	49.36	24.22	-1.56E-01	2.92E-01		-7.92E-02	6.44E-01		-8.17E-02	6.11E-01		-5.94E-01	9.42E-06		-2.82E-01	5.75E-03		-1.31E+00	5.54E-34	Down	Unigene8921_All//gi|297844954|ref|XP_002890358.1|//5.00E-07//vacuolar-H+-pumping ATPase 16 kDa proteolipid subunit 2 [Arabidopsis lyrata subsp. lyrata] >gi|297336200|gb|EFH66617.1|vacuolar-H+-pumping ATPase 16 kDa proteolipid subunit 2 [Arabidopsis lyrata subsp. lyrata]	Unigene8921_AtI//3.00E-08//AT4G34720| AVA-P1; ATPase/ proton-transporting ATPase, rotational mechanism	Unigene8921_AtI//0.00E+00//TC134662		ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene8923_All	1006	0.21	0.20	0.11	0.30	0.00	0.49	18.07	8.10	4.99	-4.58E-02	9.86E-01		-9.74E-01	6.19E-01		-8.21E+00	2.00E-02		7.33E-01	5.16E-01		-1.16E+00	5.48E-21	Down	-1.86E+00	6.84E-43	Down	Unigene8923_All//gi|295646225|gb|ADG23055.1|//3.00E-98//haloacid dehalogenase [Phaseolus vulgaris]	Unigene8923_AtI//4.00E-88//AT1G73010| phosphatase	Unigene8923_AtI//0.00E+00//TC138932				nr +
Unigene89230_All	221	0.00	0.00	0.00	2.70	0.00	0.20	0.38	0.00	0.00	null	null		null	null		-1.14E+01	1.77E-04	Down	-3.73E+00	4.95E-03		-8.58E+00	3.96E-01		-8.58E+00	3.52E-01										

Unigene8924_All	756	0.00	0.00	0.00	0.00	0.00	0.42	17.50	1.44	6.59	null	null		null	null		null	null		8.71E+00	4.07E-02		-3.61E+00	3.13E-63	Down	-1.41E+00	1.98E-21	Down	Unigene8924_All//gi|119638451|gb|ABL85042.1|//8.00E-13//serine threonine kinase [Brachypodium sylvaticum]	Unigene8924_All//2.00E-37//AT5G47740| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: root; CONTAINS InterPro DOMAIN/s: Rossmann-like alpha/beta/alpha sandwich fold (InterPro:IPR014729); BEST Arabidopsis thaliana protein match is: protein kinase family protein / U-box domain-containing protein (TAIR:AT2G45910.1); Has 196 Blast hits to 194 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 196; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink).					nr -
Unigene89240_All	222	0.47	0.00	0.96	2.92	0.62	0.00	0.00	0.00	0.54	-8.88E+00	3.64E-01		1.03E+00	5.89E-01		-2.23E+00	1.79E-02		-1.15E+01	3.89E-04	Down	null	null		9.07E+00	2.42E-01								
Unigene8926_All	1298	0.00	12.41	6.48	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	1.37E-92	Up	1.27E+01	4.09E-47	Up	null	null		null	null		null	null		null	null		Unigene8926_All//gi|224015264|ref|XP_002397290.1|//1.00E-19//predicted protein [Thalassiosira pseudonana CCMP1335] >gi|209968084|gb|EED86440.1| predicted protein [Thalassiosira pseudonana CCMP1335]	Unigene8926_All//8.00E-07//AT5G42320| metallocarboxypeptidase/ zinc ion binding					nr -
Unigene8927_All	402	0.78	1.39	0.13	5.82	3.34	3.37	0.00	1.98	1.59	8.28E-01	3.81E-01		-2.56E+00	1.59E-01		-8.02E-01	4.33E-02		-7.89E-01	6.03E-02		1.09E+01	1.07E-05	Up	1.06E+01	9.33E-05	Up				Unigene8927_All//1.00E-127//TC1316888				
Unigene89273_All	223	0.00	0.00	0.00	9.83	3.55	0.81	0.19	0.00	0.00	null	null		null	null		-1.47E+00	4.08E-04	Down	-3.60E+00	1.31E-09	Down	-7.57E+00	6.38E-01		-7.57E+00	5.97E-01					Unigene89273_All//1.00E-55//DW479200				
Unigene89279_All	224	0.00	0.00	0.00	3.78	0.15	0.40	0.19	0.37	0.18	null	null		null	null		-4.62E+00	2.79E-05	Down	-3.23E+00	1.04E-03		9.83E-01	7.27E-01		-8.58E-02	9.63E-01					Unigene89279_All//3.00E-07//DW507278				
Unigene8928_All	492	0.21	0.41	0.00	0.51	1.05	0.09	4.12	2.72	0.65	9.54E-01	6.19E-01		-7.73E+00	3.85E-01		1.05E+00	3.49E-01		-2.46E+00	2.22E-01		-6.02E-01	1.43E-01		-2.67E+00	3.89E-08	Down				Unigene8928_All//0.00E+00//CD119873				
Unigene89302_All	225	252.07	60.80	89.22	81.03	88.46	75.87	392.92	131.70	76.14	-2.05E+00	6.92E-120	Down	-1.50E+00	7.49E-75	Down	1.27E-01	3.88E-01		-9.49E-02	5.61E-01		-1.58E+00	1.29E-158	Down	-2.37E+00	5.48E-281	Down	Unigene89302_All//gi|224552010|gb|ACN54400.1|//5.00E-29//hybrid proline-rich protein [Gossypium hirsutum]	Unigene89302_All//2.00E-18//AT2G45180| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene89302_All//2.00E-94//EX164304			GO:0005488//GO:0006810//GO:0009534	nr +
Unigene89307_All	226	0.00	0.45	0.47	3.09	0.61	0.00	0.00	0.00	0.00	8.81E+00	3.78E-01		8.88E+00	3.86E-01		-2.34E+00	1.01E-02		-1.16E+01	1.96E-04	Down	null	null		null	null								
Unigene89309_All	226	0.46	0.00	0.00	3.53	0.30	0.60	0.94	0.55	0.00	-8.85E+00	3.64E-01		-8.85E+00	3.85E-01		-3.53E+00	3.03E-04	Down	-2.56E+00	6.01E-03		-7.54E-01	6.31E-01		-9.87E+00	5.77E-02					Unigene89309_All//1.00E-15//TC140743				
Unigene8931_All	644	0.24	0.39	0.00	0.39	0.21	0.28	2.43	5.32	1.79	6.91E-01	6.26E-01		-7.93E+00	2.42E-01		-8.55E-01	5.72E-01		-4.64E-01	7.43E-01		1.13E+00	1.85E-04	Up	-4.37E-01	3.54E-01								
Unigene89314_All	226	0.00	0.00	0.00	3.75	0.46	0.40	0.00	0.00	0.18	null	null		null	null		-3.04E+00	5.54E-04	Down	-3.23E+00	1.04E-03		null	null		7.46E+00	6.32E-01								
Unigene8932_All	815	0.00	0.00	0.00	0.00	0.00	0.00	1.35	3.33	2.93	null	null		null	null		null	null		null	null		1.31E+00	2.01E-04	Up	1.12E+00	1.97E-03		Unigene8932_All//gi|111379068|gb|AB809321.1|//9.00E-06//leucine rich protein [Arachis hypogaea]		Unigene8932_All//2.00E-11//TC152783				nr +
Unigene8933_All	1131	0.00	0.00	0.00	0.00	0.00	0.00	3.81	2.59	0.00	null	null		null	null		null	null		null	null		-5.60E-01	3.31E-02		-1.19E+01	1.04E-31	Down	Unigene8933_All//gi|81157943|dbj|BAE48222.1|//1.00E-139//elongation factor 2 [Chlorella pyrenoidosa]	Unigene8933_All//6.00E-134//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding					nr +
Unigene89342_All	228	0.00	0.00	0.00	2.18	0.00	0.00	0.74	0.00	1.05	null	null		null	null		-1.11E+01	8.96E-04	Down	-1.11E+01	2.96E-03		-9.53E+00	1.33E-01		4.99E-01	7.07E-01					Unigene89342_All//2.00E-20//TC139144				
Unigene89350_All	228	0.00	0.00	0.00	0.22	0.15	0.20	2.78	0.00	0.70	null	null		null	null		-5.33E-01	8.17E-01		-1.41E-01	9.45E-01		-1.14E+01	1.23E-04	Down	-1.99E+00	2.04E-02					Unigene89350_All//4.00E-86//gi|193983984|gb|FL577607.1|FL577607				
Unigene89364_All	230	0.00	1.32	0.00	5.85	0.60	1.37	1.29	1.27	3.12	1.04E+01	4.35E-02		null	null		-3.29E+00	1.81E-06	Down	-2.09E+00	1.00E-03		-1.67E-02	1.02E+00		1.28E+00	8.79E-02		Unigene89364_All//gi|255563218|ref|XP_002522612.1|//1.00E-11//phosphoprotein phosphatase [Ricinus communis] >gi|223538088|gb|EEF39699.1| phosphoprotein phosphatase [Ricinus communis]	Unigene89364_All//5.00E-07//AT4G11170| disease resistance protein (TIR-NBS-LRR class), putative				GO:0005488	nr -
Unigene89368_All	230	48.45	266.79	56.72	74.07	130.26	197.34	413.06	1261.32	957.86	2.46E+00	4.71E-161	Up	2.27E-01	1.93E-01		8.14E-01	2.10E-18		1.41E+00	8.04E-61	Up	1.61E+00	0.00E+00	Up	1.21E+00	4.78E-270	Up	Unigene89368_All//gi|2865523|gb|AAC02689.1|//6.00E-11//cold regulated LTC0R18 [Lavatera thuringiaca]		Unigene89368_All//8.00E-94//DW509851			GO:0009628	nr +
Unigene89369_All	230	21.16	27.54	11.58	29.89	28.00	47.52	85.85	88.86	27.02	3.80E-01	1.15E-01		-8.70E-01	2.23E-03		-9.43E-02	7.31E-01		6.69E-01	7.52E-05		4.98E-02	7.05E-01		-1.67E+00	3.82E-40	Down	Unigene89369_All//gi|157824573|gb|ABV82432.1|//3.00E-10//Hsp90-like protein [Dactylis glomerata]	Unigene89369_All//5.00E-10//AT4G24190| SHD (SHEPHERD): ATP binding / unfolded protein binding	Unigene89369_All//5.00E-55//gi|13245880|gb|BE054692.2|BE054692		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0006970//GO:0009536//GO:0009933//GO:0010038//GO:0010073//GO:0015031//GO:0016020//GO:0031410//GO:0032559//GO:0044267	nr +
Unigene89370_All	230	0.00	0.00	0.00	94.86	60.04	26.12	0.18	0.55	0.00	null	null		null	null		-6.60E-01	7.79E-10		-1.86E+00	2.58E-44	Down	1.57E+00	5.43E-01		-7.52E+00	5.97E-01					Unigene89370_All//1.00E-80//gi|164365814|gb|EX164071.1|EX164071				
Unigene89373_All	230	2.73	0.00	0.23	2.82	2.84	1.77	0.74	0.18	0.35	-1.14E+01	7.90E-04	Down	-3.56E+00	8.31E-03		1.48E-02	9.91E-01		-6.72E-01	4.78E-01		-2.02E+00	3.66E-01		-1.09E+00	5.51E-01					Unigene89373_All//3.00E-07//EX171688				
Unigene89375_All	230	149.00	66.97	159.52	19.28	27.10	27.88	0.00	0.00	0.17	-1.15E+00	1.20E-31	Down	9.84E-02	3.60E-01		4.91E-01	3.69E-02		5.33E-01	2.36E-02		null	null		7.44E+00	6.32E-01		Unigene89375_All//gi|270308992|dbj|BAI52949.1|//1.00E-17//light-harvesting complex II protein [Citrullus lanatus subsp. vulgaris]	Unigene89375_All//2.00E-18//AT1G15820| LHCB6 (LIGHT HARVESTING COMPLEX PSII SUBUNIT 6); chlorophyll binding	Unigene89375_All//1.00E-117//TC133498		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0006464//GO:0009521//GO:0009534//GO:0031224//GO:0046906	nr -
Unigene89377_All	230	15.47	2.86	2.55	1.08	0.60	1.18	0.00	0.00	0.00	-2.43E+00	7.13E-10	Down	-2.60E+00	4.58E-10	Down	-8.55E-01	5.72E-01		1.22E-01	9.43E-01		null	null		null	null		Unigene89377_All//gi|21322711|emb|CAD22154.1|//4.00E-36//pherophorin-dr1 protein [Volvox carteri f. nagariensis]				ko03040|Spliceosome	GO:0016020	nr +
Unigene8938_All	591	0.18	0.00	0.36	4.64	1.98	4.43	0.93	0.50	0.67	-7.47E+00	3.64E-01		1.03E+00	5.89E-01		-1.23E+00	6.27E-04	Down	-6.48E-02	8.82E-01		-9.10E-01	3.19E-01		-4.64E-01	5.97E-01		Unigene8938_All//gi|297802992|ref|XP_002869380.1|//3.00E-28//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315216|gb|EFH45639.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene8938_All//1.00E-29//AT4G30400| zinc finger (C3HC4-type RING finger) family protein	Unigene8938_All//7.00E-47//C0084821				nr +
Unigene89384_All	231	1.59	1.75	0.00	3.02	0.30	0.00	0.92	1.45	0.17	1.46E-01	8.98E-01		-1.06E+01	2.77E-02		-3.34E+00	1.25E-03		-1.16E+01	1.96E-04	Down	6.61E-01	6.08E-01		-2.41E+00	1.94E-01					Unigene89384_All//1.00E-15//CO096335				
Unigene89387_All	231	45.07	25.23	31.35	52.19	35.33	75.86	63.69	43.79	25.52	-8.37E-01	2.61E-06		-5.24E-01	4.53E-03		-5.63E-01	1.98E-04		5.40E-01	3.07E-05		-5.41E-01	3.07E-05		-1.32E+00	1.61E-21	Down	Unigene89387_All//gi|87241023|gb|AB032881.1|//1.00E-11//Nascent polypeptide-associated complex NAC: UBA-like [Medicago truncatula]		Unigene89387_All//4.00E-49//TC136540			GO:0006970	nr +
Unigene89396_All	232	0.00	0.22	0.00	4.72	0.45	0.00	0.73	0.00	0.00	7.77E+00	6.06E-01		null	null		-3.41E+00	1.67E-05	Down	-1.22E+01	7.25E-07	Down	-9.51E+00	1.33E-01		-9.51E+00	1.07E-01		Unigene89396_All//gi|147838247|emb|CAN71828.1|//1.00E-06//hypothetical protein [Vitis vinifera]		Unigene89396_All//7.00E-11//FL576972				nr -
Unigene894_All	2856	0.49	1.35	0.80	1.26	1.12	0.98	2.04	1.81	1.27	1.45E+00	1.15E-05	Up	6.97E-01	1.17E-01		-1.63E-01	6.38E-01		-3.57E-01	3.10E-01		-1.71E-01	5.00E-01		-6.87E-01	1.19E-03		Unigene894_All//gi|259121369|gb|ACV92004.1|//1.00E-114//WRKY transcription factor 2 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene894_All//5.00E-88//AT5G48150| PAT1 (phytochrome a signal transduction 1); signal transducer/ transcription factor	Unigene894_All//0.00E+00//TC157297	WRKY	ko04626|Plant-pathogen interaction	GO:0001071//GO:0006350//GO:0009639//GO:0010468//GO:0010557//GO:0020033//GO:0030528//GO:0044424//GO:0046914//GO:0060089	nr +
Unigene89405_All	233	0.45	0.43	1.83	0.86	0.30	0.39	3.08	1.44	0.00	-4.64E-02	9.84E-01		2.03E+00	1.39E-01		-1.53E+00	4.14E-01		-1.14E+00	5.67E-01		-1.10E+00	1.49E-01		-1.16E+01	1.78E-05	Down				Unigene89405_All//5.00E-129//gi|21098086|gb|BQ410399.1|BQ410399				
Unigene89410_All	233	5.16	1.52	0.23	0.64	0.74	0.19	0.00	0.00	0.34	-1.76E+00	7.96E-03		-4.50E+00	1.49E-05	Down	2.04E-01	9.48E-01		-1.73E+00	4.98E-01		null	null		8.42E+00	3.99E-01								
Unigene89412_All	233	0.00	0.87	0.00	2.14	0.00	0.00	0.18	0.54	0.00	9.76E+00	1.34E-01		null	null		-1.11E+01	8.96E-04	Down	-1.11E+01	2.96E-03		1.57E+00	5.43E-01		-7.50E+00	5.97E-01									
Unigene89442_All	345	0.30	0.00	0.31	2.45	1.60	0.13	2.82	0.12	0.12	-8.24E+00	3.63E-01		2.55E-02	9.96E-01		-6.20E-01	4.13E-01		-4.23E+00	2.18E-04	Down	-4.54E+00	6.92E-06	Down	-4.61E+00	3.32E-06	Down				Unigene89442_All//4.00E-07//ES803021				
Unigene89429_All	234	97.93	176.04	135.40	58.12	55.04	130.47	66.67	124.85	38.48	8.46E-01	6.78E-23		4.67E-01	2.06E-06		-7.85E-02	6.68E-01		1.17E+00	1.27E-30	Up	9.05E-01	2.01E-22		-7.93E-01	2.24E-10					Unigene89429_All//3.00E-59//TC135001				
Unigene8943_All	457	0.00	0.00	0.00	1.64	1.96	0.49	0.19	3.66	0.26	null	null		null	null		2.61E-01	7.79E-01		-1.73E+00	5.00E-02		4.31E+00	1.80E-09	Up	4.99E-01	8.03E-01					Unigene8943_All//5.00E-07//TC157816				
Unigene89438_All	235	3.12	1.29	0.00	3.82	1.47	1.15	0.18	0.36	0.85	-1.27E+00	1.36E-01		-1.16E+01	4.12E-04	Down	-1.38E+00	5.39E-02		-1.73E+00	2.80E-02		9.84E-01	7.27E-01		2.24E+00	2.48E-01					Unigene89438_All//3.00E-07//TC164645				
Unigene89448_All	236	0.00	0.00	0.00	12.24	8.46	5.17	0.54	0.35	0.00	null	null		null	null		-5.33E-01	1.46E-01		-1.24E+00	7.77E-04	Down	-6.02E-01	7.64E-01		-9.07E+00	1.98E-01		Unigene89448_All//gi|225626279|gb|ACN97189.1|//4.00E-09//KNOX transcription factor [Populus trichocarpa]		Unigene89448_All//7.00E-51//gi|109870442|gb|DW499418.1|DW499418				nr -
Unigene8945_All	974	0.54	0.10	0.05	6.14	5.20	0.83	0.04	0.00	0.00	-2.37E+00	4.75E-02		-3.30E+00	2.40E-02		-2.40E-01	3.64E-01		-2.88E+00	7.78E-21	Down	-5.44E+00	6.38E-01		-5.44E+00	5.97E-01		Unigene8945_All//gi|237899609|gb|ACR33109.1|//2.00E-47//verticillium wilt disease resistance protein [Solanum lycopersicum]	Unigene8945_All//7.00E-24//AT1G47890| AtRLP7 (Receptor Like Protein 7); kinase/ protein binding	Unigene8945_All//1.00E-09//TC172594		ko04626|Plant-pathogen interaction		nr +
Unigene89451_All	236	46.56	35.64	24.82	68.60	55.45	103.72	204.77	106.26	78.66	-3.86E-01	2.68E-02		-9.08E-01	4.42E-07		-3.07E-01	2.47E-02		5.96E-01	2.68E-08		-9.46E-01	2.16E-39		-1.38E+00	1.56E-73	Down	Unigene89451_All//gi|32400836|gb|AAP80650.1|AF475129_1|/1.00E-35//elongation factor [Triticum aestivum]	Unigene89451_All//3.00E-36//AT1G56070| LOS1; copper ion binding / translation elongation factor/ translation factor, nucleic acid binding	Unigene89451_All//7.00E-119//TC152423			GO:0006950//GO:0008135//GO:0009536//GO:0016020//GO:0017111//GO:0031981//GO:0002561//GO:0046914	nr +
Unigene89457_All	236	17.29	12.45	13.31	5.28	14.45	10.91	17.20	15.76	8.27	-4.74E-01	1.23E-01		-3.77E-01	2.41E-01		1.45E+00	1.45E-05	Up	1.05E+00	8.57E-03		-1.26E-01	6.66E-01		-1.06E+00	7.09E-05	Down	Unigene89457_All//gi|222424621|dbj|BAH20265.1|//2.00E-21//AT1G28100 [Arabidopsis thaliana]	Unigene89457_All//7.00E-23//AT1G28100| unknown protein	Unigene89457_All//6.00E-107//TC158820			GO:0016830	nr -
Unigene89463_All	237	117.89	44.47	62.91	256.85	165.49	266.79	57.09	25.39	26.39	-1.41E+00	4.53E-35	Down	-9.06E-01	5.95E-17		-6.34E-01	8.17E-25		5.48E-02	5.17E-01		-1.17E+00	4.69E-16	Down	-1.11E+00	2.18E-15	Down				Unigene89463_All//1.00E-98//gi|78328436|gb|DT548710.1|DT548710				
Unigene89466_All	237	9.27	8.12	10.56	10.93	10.17	8.58	19.09	11.64	8.40	-1.91E-01	6.42E-01		1.88E-01	6.36E-01		-1.04E-01	8.24E-01		-3.50E-01	4.08E-01		-7.14E-01	4.77E-03		-1.18E+00	3.13E-06	Down	Unigene89466_All//gi|211906468|gb|ACJ11727.1|//1.00E-18//20S proteasome subunit alpha-1 [Gossypium hirsutum]	Unigene89466_All//3.00E-18//AT2G05840| PAA2 (20S PROTEASOME SUBUNIT PAA2); endopeptidase/ peptidase/ threonine-type endopeptidase	Unigene89466_All//4.00E-68//DW498981		ko03050|Proteasome	GO:0000041//GO:0004175//GO:0005839//GO:0005840//GO:0009526//GO:0009532//GO:0009534//GO:0010038//GO:00105082//GO:0016020//GO:0019941//GO:0022900//GO:0042625	nr +
Unigene89479_All	238	1.32	2.34	1.57	1.05	1.74	5.88	0.18	0.00	0.17	8.28E-01	3.81E-01		2.48E-01	8.22E-01		7.30E-01	5.86E-01		2.49E+00	1.86E-04	Up	-7.47E+00	6.38E-01		-8.53E-02	9.63E-01		Unigene89479_All//gi|224061351|ref|XP_002300437.1|//4.00E-26//integral membrane single C2 domain protein [Populus trichocarpa] >gi|222847695|gb|EEE85242.1| integral membrane single C2 domain protein [Populus trichocarpa]	Unigene89479_All//1.00E-18//AT3G14590| NTMC2T6.2; LOCATED IN: chloroplast; CONTAINS InterPro DOMAIN/s: C2 membrane targeting protein (InterPro:IPR018029), C2 calcium/lipid-binding region, CaLB (InterPro:IPR008973), C2 calcium-dependent membrane targeting (InterPro:IPR000008); BEST Arabidopsis thaliana protein match is: NTMC2T6.1 (TAIR:AT1G53590.1); Has 3079 Blast hits to 2709 proteins in 189 species: Archae - 0; Bacteria - 2; Metazoa - 1922; Fungi - 332; Plants - 570; Viruses - 0; Other Eukaryotes - 253 (source: NCBI BLink).	Unigene89479_All//2.00E-14//CO112271			GO:0016020//GO:0031410	nr -
Unigene89482_All	238	101.12	225.67	149.91	115.33	198.51	349.92	231.48	305.04	411.61	1.16E+00	2.69E-49	Up	5.68E-01	7.23E-10		7.84E-01	5.18E-27		1.60E+00	1.13E-133	Up	3.98E-01	3.15E-13		8.30E-01	6.86E-65		Unigene89482_All//gi|6118549|gb|AAF04147.1|//1.00E-27//ubiquitin precursor [Hevea brasiliensis]	Unigene89482_All//5.00E-28//AT5G03240| UBQ3 (POLYUBIQUITIN 3); protein binding	Unigene89482_All//9.00E-106//ES834521			GO:0044424	nr +
Unigene89485_All	238	1.32	11.07	4.47	6.07	4.63	7.59	37.84	56.55	13.22	3.07E+00	2.80E-09	Up	1.76E+00	1.85E-02		-3.91E-01	5.05E-01		3.23E-01	5.57E-01		5.80E-01	2.14E-05		-1.52E+00	1.79E-16	Down	Unigene89485_All//gi|166865124|gb|ABZ01817.1|//3.00E-12//cinnamyl alcohol dehydrogenase [Gossypium hirsutum]	Unigene89485_All//4.00E-10//AT4G34230| ATCAD5 (CINNAMYL ALCOHOL DEHYDROGENASE 5); cinnamyl-alcohol dehydrogenase	Unigene89485_All//5.00E-58//gi|72268702|gb|DT046856.1|DT046856		ko00940|Phenylpropanoid biosynthesis	GO:0009699//GO:0016616//GO:0046914	nr +
Unigene89494_All	239	0.44	0.00	0.00	5.63	0.86	0.76	0.71	0.00	0.00	-8.77E+00	3.63E-01		-8.77E+00	3.85E-01		-2.70E+00	2.12E-05	Down	-2.90E+00	4.29E-05	Down	-9.47E+00	1.33E-01		-9.47E+00	1.07E-01								
Unigene895_All	5187	11.70	2.95	4.03	6.83	4.55	6.10	9.48	4.42	5.90	-1.99E+00	4.58E-123	Down	-1.54E+00	4.56E-83	Down	-5.86E-01	9.44E-13		-1.62E-01	1.03E-01		-1.10E+00	4.59E-51	Down	-6.85E-01	5.48E-24		Unigene895_All//gi|240255326|ref|NP_187803.4|//0.00E+00//RNA binding [Arabidopsis thaliana]	Unigene895_All//0.00E+00//AT3G11964| RNA binding	Unigene895_All//0.00E+00//TC138208		ko03040|Spliceosome	GO:0005488//GO:0005622//GO:0006396	nr +
Unigene8950_All	798	0.00	0.00	0.00	0.00	0.00	0.00	11.60	7.39	0.25	null	null		null	null		null	null		null	null		-6.52E-01	1.05E-04		-5.54E+00	5.29E-60	Down	Unigene8950_All//gi|1545805|dbj|BAA10929.1|//7.00E-08//cytochrome P450 like TBP [Nicotiana tabacum]		Unigene8950_All//3.00E-31//gi|73861682|gb|DT467421.1|DT467421				nr +
Unigene89500_All	240	0.00	0.21	0.22	2.91	0.14	0.00	0.70	0.00	0.33	7.72E+00	6.06E-01		7.79E+00	6.21E-01		-4.34E+00	2.79E-04	Down	-1.15E+01	1.96E-04	Down	-9.46E+00	1.33E-01		-1.09E+00	5.51E-01					Unigene89500_All//2.00E-60//FL577137				
Unigene8951_All	335	2.66	2.57	7.47	2.97	3.80	1.48	0.88	0.25	0.83	-4.63E-02	9.62E-01		1.49E+00	6.44E-04	Up	3.55E-01	5.94E-01		-1.00E+00	1.57E-01		-1.82E+00	2.10E-01		-8.60E-02	9.51E-01					Unigene8951_All//1.00E-10//DW481166				
Unigene89522_All	240	0.44	0.21	1.55	0.83	0.29	0.19	2.47	0.00	0.50	-1.05E+00	6.81E-01		1.83E+00	2.12E-01		-1.53E+00	4.13E-01		-2.14E+00	3.45E-01		-1.13E+01	2.39E-04	Down	-2.31E+00	1.36E-02								
Unigene89525_All	241	22.36	58.03	34.03	31.00	42.87	54.53	37.72	53.07	41.66	1.38E+00	2.92E-17	Up	6.06E-01	4.03E-03		4.67E-01	6.77E-03		8.15E-01	9.83E-08		4.93E-01	4.62E-04		1.43E-01	4.14E-01					Unigene89525_All//5.00E-21//TC164297				

Unigene89528_All	241	0.43	0.00	0.00	2.07	0.00	0.94	0.53	0.17	0.17	-8.76E+00	3.63E-01			-8.76E+00	3.85E-01		-1.10E+01	8.96E-04	Down	-1.14E+00	3.07E-01		-1.60E+00	5.31E-01		-1.67E+00	4.75E-01		Unigene89528_All//gi|224112177|ref|XP_002316108.1|//3.00E-36//argonaute protein group [Populus trichocarpa] >gi|222865148|gb|EEF02279.1| argonaute protein group [Populus trichocarpa]	Unigene89528_All//8.00E-33//AT1G69440| AGO7 (ARGONAUTE7); nucleic acid binding	Unigene89528_All//8.00E-134//TC150005			GO:0008135//GO:0009791//GO:0030422//GO:0035195//GO:0044464//GO:0050793	nr +
Unigene8954_All	471	0.00	0.22	1.70	0.42	0.73	0.10	0.00	0.00	0.00	7.75E+00	3.78E-01			1.07E+01	1.71E-04	Up	7.89E-01	5.95E-01		-2.14E+00	3.45E-01		null	null		null	null								ESTscan -
Unigene89544_All	242	0.43	0.00	0.00	4.73	1.00	0.56	0.00	0.69	0.66	-8.76E+00	3.63E-01			-8.76E+00	3.85E-01		-2.25E+00	6.72E-04	Down	-3.08E+00	1.19E-04	Down	9.43E+00	1.38E-01		9.36E+00	1.39E-01		Unigene89544_All//gi|224054390|ref|XP_002298236.1|//9.00E-13//AP2/EBF domain-containing transcription factor [Populus trichocarpa] >gi|134038600|gb|ABO48368.1| TINY-like protein 1 [Populus trichocarpa] >gi|222845494|gb|EEE83041.1| AP2/EBF domain-containing transcription factor [Populus trichocarpa]		Unigene89544_All//1.00E-27//TC132992			GO:0006350//GO:0016049	nr -
Unigene8955_All	463	0.34	0.98	0.35	1.72	0.45	0.00	2.10	1.72	2.58	1.54E+00	1.96E-01			2.53E-02	1.00E+00		-1.95E+00	1.52E-02		-1.07E+01	4.90E-05	Down	-2.92E-01	6.31E-01		2.98E-01	6.12E-01				Unigene8955_All//3.00E-150//ES810833				
Unigene89569_All	243	0.86	1.25	2.63	6.56	3.97	0.56	0.17	0.17	0.66	5.39E-01	6.71E-01			1.61E+00	1.11E-01		-7.23E-01	1.57E-01		-3.56E+00	4.90E-07	Down	-1.67E-02	9.95E-01		1.91E+00	3.76E-01				Unigene89569_All//3.00E-07//TC175749				
Unigene8958_All	604	0.00	0.00	0.35	0.33	0.00	0.67	1.05	1.66	3.17	null	null			8.46E+00	1.37E-01		-8.37E+00	8.32E-02		1.03E+00	4.28E-01		6.62E-01	2.96E-01		1.59E+00	2.36E-04	Up	Unigene8958_All//gi|240255348|ref|NP_188102.4|//9.00E-08//leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana]	Unigene8958_All//1.00E-08//AT3G14840| leucine-rich repeat family protein / protein kinase family protein					nr -
Unigene89581_All	244	23.80	7.68	13.09	51.86	39.37	43.50	52.50	40.25	22.37	-1.63E+00	1.30E-09	Down		-8.62E-01	7.92E-04		-3.97E-01	9.32E-03		-2.54E-01	1.38E-01		-3.83E-01	7.16E-03		-1.23E+00	5.23E-17	Down			Unigene89581_All//1.00E-114//gi|11208505|gb|BF277435.1|BF277435				
Unigene89591_All	245	0.00	0.00	0.00	2.85	0.28	0.00	0.00	0.17	0.00	null	null			null	null		-3.34E+00	1.25E-03		-1.15E+01	1.96E-04	Down	7.41E+00	6.22E-01		null	null								
Unigene896_All	3009	10.15	50.57	18.35	129.38	134.72	83.14	18.81	19.35	16.75	2.32E+00	0.00E+00	Up		8.54E-01	6.48E-30		5.84E-02	2.74E-02		-6.38E-01	4.32E-140		4.04E-02	6.33E-01		-1.68E-01	8.18E-03		Unigene896_All//gi|86553064|gb|AAS17751.2|//0.00E+00//beta xylosidase [Fragaria x ananassa]	Unigene896_All//0.00E+00//AT5G49360| BXL1 (BETA-XYLOSIDASE 1); hydrolase, hydrolyzing O-glycosyl compounds	Unigene896_All//0.00E+00//TC166570		ko00500|Starch and sucrose metabolism//ko00940|Phenylpropanoid biosynthesis//ko00460|Cyanoamino acid metabolism	GO:0003006//GO:0005576//GO:0005618//GO:0015926//GO:0044238	nr -
Unigene8960_All	385	0.00	0.00	0.00	0.00	0.00	0.00	2.42	3.15	10.04	null	null			null	null		null	null		null	null		3.82E-01	5.17E-01		2.05E+00	6.68E-11	Up	Unigene8960_All//gi|225444311|ref|XP_002263655.1|//1.00E-13//PREDICTED: similar to stigma-specific Stig1 family protein [Vitis vinifera]	Unigene8960_All//4.00E-11//AT1G11925| Encodes a Stigma-specific Stig1 family protein					nr +
Unigene89600_All	245	0.00	0.00	0.22	1.42	0.56	0.55	69.03	24.05	38.86	null	null			7.76E+00	6.21E-01		-1.34E+00	3.08E-01		-1.36E+00	3.37E-01		-1.52E+00	2.22E-29	Down	-8.29E-01	5.58E-12		Unigene89600_All//gi|221272207|sp|A2A1A0.1|NCS1_COPJA//2.00E-29//RecName: Full=S-norcoclaurine synthase 1; Short=CjNCS1 >gi|123720767|dbj|BAF45337.1| norcoclaurine synthase [Coptis japonica var. dissecta] >gi|301072256|gb|ADK56103.1| 2OG/Fe(II)-dependent dioxygenase-like protein [synthetic construct]	Unigene89600_All//1.00E-27//AT4G25300| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene89600_All//1.00E-68//gi|109872645|gb|DW501620.1|DW501620	ko00270|Cysteine and methionine metabolism//ko00941|Flavonoid biosynthesis	GO:0006807//GO:0009699//GO:0016706//GO:0016836//GO:0043169	nr -
Unigene89602_All	245	0.64	0.00	0.22	8.13	2.11	1.84	1.38	0.17	0.16	-9.32E+00	2.13E-01			-1.56E+00	5.32E-01		-1.95E+00	2.27E-05	Down	-2.14E+00	2.33E-05	Down	-3.02E+00	5.29E-02		-3.09E+00	3.91E-02		Unigene89602_All//gi|15231680|ref|NP_190845.1|//7.00E-12//ZPR3 (LITTLE ZIPPER 3); protein binding [Arabidopsis thaliana]					GO:0009798//GO:0009965//GO:0010051//GO:0010073//GO:0043231//GO:0043392	nr -
Unigene89613_All	246	0.00	0.41	0.65	1.42	0.28	0.00	2.06	0.00	0.00	8.69E+00	3.78E-01			9.34E+00	2.33E-01		-2.34E+00	1.01E-01		-1.05E+01	2.11E-02		-1.10E+01	8.88E-04	Down	-1.10E+01	5.53E-04	Down			Unigene89613_All//1.00E-98//TC151459				
Unigene89619_All	246	0.21	0.21	0.43	2.03	0.00	0.18	0.52	0.34	0.32	-4.62E-02	9.80E-01			1.03E+00	6.99E-01		-1.10E+01	8.96E-04	Down	-3.46E+00	1.60E-02		-6.02E-01	7.64E-01		-6.71E-01	7.17E-01		Unigene89619_All//gi|224072841|ref|XP_002303907.1|//3.00E-35//GRAS family transcription factor [Populus trichocarpa] >gi|222841339|gb|EEE78886.1| GRAS family transcription factor [Populus trichocarpa]	Unigene89619_All//3.00E-28//AT1G50420| SCL3; transcription factor	Unigene89619_All//8.00E-94//gi|72268105|gb|DT046598.1|DT046598	GRAS		GO:0001071//GO:0003676//GO:0006351//GO:0009725//GO:0010468//GO:0043231	nr -
Unigene8962_All	796	0.59	6.43	0.67	0.19	0.30	0.85	0.69	1.05	3.05	3.44E+00	2.39E-19	Up		1.77E-01	8.45E-01		6.90E-01	7.31E-01		2.18E+00	3.14E-02		6.05E-01	4.04E-01		2.14E+00	1.70E-07	Up			Unigene8962_All//2.00E-08//TC145900				
Unigene8963_All	314	1.33	5.65	0.00	0.16	2.30	1.15	0.00	0.80	0.00	2.08E+00	1.78E-04	Up		-1.04E+01	1.55E-02		3.86E+00	1.50E-03		2.86E+00	9.44E-02		9.64E+00	4.30E-02		null	null		Unigene8963_All//gi|224053889|ref|XP_002298030.1|//2.00E-10//predicted protein [Populus trichocarpa] >gi|222845288|gb|EEE82835.1| predicted protein [Populus trichocarpa]		Unigene8963_All//5.00E-148//TC161727				nr +
Unigene8964_All	485	4.85	1.88	0.44	3.08	3.62	3.82	0.00	0.00	0.00	-1.37E+00	1.46E-03			-3.47E+00	7.72E-09	Down	2.33E-01	6.80E-01		3.09E-01	5.68E-01		null	null		null	null		Unigene8964_All//gi|115470543|ref|NP_001058870.1|//1.00E-18//Os07g0142300 [Oryza sativa Japonica Group] >gi|34393335|dbj|BAC83283.1| early nodulin 75 precursor-like protein [Oryza sativa Japonica Group] >gi|113610406|dbj|BAF20784.1| Os07g0142300 [Oryza sativa Japonica Group]		Unigene8964_All//5.00E-72//DW504592				nr -
Unigene89641_All	248	1.27	0.00	1.29	4.42	2.50	0.18	0.00	0.34	0.16	-1.03E+01	3.63E-02			2.54E-02	1.00E+00		-8.22E-01	1.96E-01		-4.60E+00	8.28E-06	Down	8.40E+00	3.97E-01		7.33E+00	6.32E-01								
Unigene89644_All	248	0.21	0.00	1.72	2.81	1.67	0.00	0.00	0.17	0.00	-7.72E+00	5.97E-01			3.03E+00	5.71E-02		-7.55E-01	3.69E-01		-1.15E+01	1.96E-04	Down	7.40E+00	6.22E-01		null	null								ESTscan -
Unigene89662_All	249	1.26	0.00	0.00	2.60	0.83	0.00	3.06	5.54	2.24	-1.03E+01	3.63E-02			-1.03E+01	4.87E-02		-1.65E+00	6.52E-02		-1.13E+01	3.89E-04	Down	8.58E-01	9.44E-02		-4.48E-01	5.31E-01				Unigene89662_All//6.00E-30//TC138993				
Unigene89666_All	250	1.47	0.00	0.43	3.39	0.28	0.72	0.34	0.17	0.16	-1.05E+01	1.95E-02			-1.78E+00	2.33E-01		-3.62E+00	1.47E-04	Down	-2.23E+00	9.52E-03		-1.02E+00	7.20E-01		-1.09E+00	6.72E-01								
Unigene8968_All	274	2.86	6.47	3.89	4.18	0.88	2.47	2.31	1.37	0.73	1.18E+00	1.88E-02			4.40E-01	5.22E-01		-2.25E+00	6.72E-04	Down	-7.58E-01	2.45E-01		-7.54E-01	3.73E-01		-1.67E+00	4.29E-02		Unigene8968_All//gi|15239334|ref|NP_201429.1|//2.00E-12//GMD1 (GDP-D-MANNOSE 4,6-DEHYDRATASE 1); GDP-mannose 4,6-dehydratase/ binding / catalytic/ coenzyme binding [Arabidopsis thaliana] >gi|9087168|sp|Q5SNX3.1|GMD1_ARATH RecName: Full=GDP-mannose 4,6 dehydratase 1; AltName: Full=GDP-D-mannose dehydratase 1; Short=GMD 1 >gi|6319186|gb|AAF07199.1|AF195140_1 GDP-D-mannose 4,6-dehydratase [Arabidopsis thaliana] >gi|10177422|dbj|BAB10707.1| GDP-D-mannose 4,6-dehydratase; GMD1 [Arabidopsis thaliana] >gi|116325922|gb|AB198562.1| At5g66280 [Arabidopsis thaliana]	Unigene8968_All//8.00E-14//AT5G66280| GMD1 (GDP-D-MANNOSE 4,6-DEHYDRATASE 1); GDP-mannose 4,6-dehydratase/ binding / catalytic/ coenzyme binding	Unigene8968_All//1.00E-132//TC179446		ko00520|Amino sugar and nucleotide sugar metabolism//ko00051|Fructose and mannose metabolism		nr -
Unigene89683_All	251	20.43	1.62	5.52	11.71	1.78	3.78	1.52	0.83	0.79	-3.66E+00	1.34E-20	Down		-1.89E+00	7.91E-10	Down	-2.71E+00	2.58E-11	Down	-1.63E+00	1.75E-05	Down	-8.65E-01	4.41E-01		-9.34E-01	3.79E-01				Unigene89683_All//3.00E-07//TC144255				
Unigene89684_All	251	71.71	33.71	33.52	102.21	92.74	156.90	212.41	134.88	132.53	-1.09E+00	1.55E-15	Down		-1.10E+00	4.82E-15	Down	-1.40E-01	2.45E-01		6.18E-01	8.70E-14		-6.55E-01	2.20E-23		-6.81E-01	1.12E-25		Unigene89684_All//gi|192913000|gb|ACF06608.1|//3.00E-41//ribosomal protein [Elaeis guineensis]	Unigene89684_All//2.00E-42//AT5G39850| 40S ribosomal protein S9 (RPS9C)	Unigene89684_All//9.00E-140//ES800022		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0010467//GO:0015935	nr -
Unigene89694_All	251	0.42	0.00	0.00	2.98	0.27	0.72	0.51	0.33	0.00	-8.70E+00	3.63E-01			-8.70E+00	3.85E-01		-3.44E+00	6.18E-04	Down	-2.05E+00	2.45E-02		-6.02E-01	7.64E-01		-8.98E+00	1.98E-01								
Unigene89696_All	251	0.63	0.00	0.00	6.75	1.65	0.54	0.00	0.00	0.00	-9.29E+00	2.13E-01			-9.29E+00	2.42E-01		-2.04E+00	6.76E-05	Down	-3.64E+00	1.38E-07	Down	null	null		null	null		Unigene89696_All//gi|270271323|gb|ACZ67190.1|//9.00E-10//TCP transcription factor [Populus deltoides]						nr -
Unigene89708_All	252	0.00	0.00	0.00	3.16	0.00	0.00	0.50	0.50	0.00	null	null			null	null		-1.16E+01	6.49E-06	Down	-1.16E+01	4.90E-05	Down	-1.64E-02	1.02E+00		-8.98E+00	1.98E-01				Unigene89708_All//2.00E-14//ES842503				
Unigene8972_All	561	6.81	0.63	2.85	5.59	0.98	0.08	0.00	0.15	0.64	-3.43E+00	1.11E-14	Down		-1.26E+00	1.80E-04	Down	-2.51E+00	4.65E-11	Down	-6.12E+00	3.15E-18	Down	7.22E+00	3.97E-01		9.32E+00	7.28E-03				Unigene8972_All//5.00E-20//TC149899				ESTscan +
Unigene89726_All	253	0.41	0.00	1.26	5.12	3.13	1.07	0.33	0.17	0.79	-8.69E+00	3.63E-01			1.61E+00	3.04E-01		-7.10E-01	2.23E-01		-2.26E+00	6.70E-04	Down	-1.02E+00	7.20E-01		1.24E+00	4.68E-01								
Unigene8973_All	585	0.18	1.65	2.28	0.00	0.94	0.08	0.00	0.00	0.00	3.20E+00	6.55E-04	Up		3.67E+00	1.90E-05	Up	9.88E+00	2.02E-03		6.27E+00	6.81E-01		null	null		null	null		Unigene8973_All//gi|254847679|gb|ACT83880.1|//4.00E-08//chloroplast carboxyltransferase alpha subunit [Brassica napus]	Unigene8973_All//3.00E-09//AT2G38040| CAC3; acetyl-CoA carboxylase			ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism//ko00061|Fatty acid biosynthesis		nr -
Unigene89734_All	253	0.00	0.00	0.00	2.17	0.00	0.54	1.34	0.17	0.00	null	null			null	null		-1.11E+01	4.00E-04	Down	-2.02E+00	7.04E-02		-3.02E+00	5.29E-02		-1.04E+01	8.12E-03								
Unigene89736_All	253	0.00	0.00	0.21	1.97	0.00	0.00	0.00	0.17	0.00	null	null			7.72E+00	6.21E-01		-1.09E+01	8.96E-04	Down	-1.09E+01	2.96E-03		7.37E+00	6.22E-01		null	null		Unigene89736_All//gi|297850236|ref|XP_002892999.1|//6.00E-17//hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata] >gi|297338841|gb|EFH69258.1| hydrolase, alpha/beta fold family protein [Arabidopsis lyrata subsp. lyrata]	Unigene89736_All//4.00E-18//AT1G18360| hydrolase, alpha/beta fold family protein	Unigene89736_All//3.00E-19//TC154452			GO:0003824//GO:0043231	nr +
Unigene8974_All	652	0.00	10.65	6.29	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	1.15E-39	Up		1.26E+01	9.63E-23	Up	null	null		null	null		null	null		null	null		Unigene8974_All//sp|P35953|VLDLR_RABIT//1.00E-08//Very low-density lipoprotein receptor OS=Oryctolagus cuniculus GN=VLDLR PE=2 SV=1						swissprot +
Unigene89745_All	254	61.59	40.30	100.42	30.40	19.93	13.87	0.17	0.16	1.10	-6.12E-01	1.37E-05			7.05E-01	2.45E-10		-6.09E-01	1.89E-03		-1.13E+00	6.25E-08	Down	-1.66E-02	9.95E-01		2.72E+00	9.92E-02				Unigene89745_All//6.00E-27//TC136116				
Unigene89746_All	254	0.41	0.00	0.00	2.16	0.00	0.36	1.50	0.49	0.63	-8.69E+00	3.63E-01			-8.69E+00	3.85E-01		-1.11E+01	4.00E-04	Down	-2.60E+00	2.93E-02		-1.60E+00	1.81E-01		-1.26E+00	2.48E-01								
Unigene89756_All	255	0.41	0.00	0.00	9.38	2.70	1.24	0.00	0.00	0.00	-8.68E+00	3.63E-01			-8.68E+00	3.85E-01		-1.80E+00	1.00E-05	Down	-2.92E+00	1.02E-08	Down	null	null		null	null				Unigene89756_All//1.00E-12//TC144487				
Unigene8977_All	627	0.50	4.44	0.08	0.56	1.87	0.36	4.79	6.87	6.10	3.15E+00	5.25E-10	Up		-2.56E+00	1.59E-01		1.75E+00	8.89E-03		-6.27E-01	6.20E-01		5.20E-01	4.92E-02		3.49E-01	2.15E-01		Unigene8977_All//gi|192338750|gb|ACF04280.1|//4.00E-24//myo-inositol oxygenase [Eucalyptus grandis]	Unigene8977_All//3.00E-16//AT4G26260| MIOX4; inositol oxygenase	Unigene8977_All//1.00E-42//gi|109872762|gb|DW501737.1|DW501737		ko00562|Inositol phosphate metabolism//ko00053|Ascorbate and aldarate metabolism		nr +
Unigene89777_All	256	0.00	0.00	0.00	2.53	0.27	0.00	0.00	0.00	0.31	null	null			null	null		-3.23E+00	2.48E-03		-1.13E+01	3.89E-04	Down	null	null		8.28E+00	3.99E-01								
Unigene89793_All	257	24.43	9.46	23.83	1.74	3.75	1.58	0.16	0.00	0.00	-1.37E+00	3.80E-08	Down		-3.60E-02	8.94E-01		1.10E+00	1.35E-01		-1.41E-01	9.00E-01		-7.36E+00	6.37E-01		-7.36E+00	5.96E-01				Unigene89793_All//1.00E-80//gi|84151536|gb|DN800891.1|DN800891				
Unigene89797_All	257	0.41	0.00	0.83	2.91	0.40	0.00	0.00	0.00	0.00	-8.67E+00	3.63E-01			1.03E+00	5.89E-01		-2.85E+00	2.09E-03		-1.15E+01	9.80E-05	Down	null	null		null	null								
Unigene8980_All	334	2.51	2.88	8.77	1.94	2.47	1.08	0.38	0.25	0.24	2.02E-01	7.54E-01			1.81E+00	1.32E-05	Up	3.52E-01	6.87E-01		-8.42E-01	3.75E-01		-6.02E-01	7.64E-01		-6.71E-01	7.17E-01				Unigene8980_All//4.00E-87//gi|48740948|gb|CO071467.1|CO071467				
Unigene89800_All	257	0.20	0.39	0.00	2.71	0.67	0.00	0.00	0.33	0.00	9.54E-01	7.22E-01			-7.67E+00	6.11E-01		-2.02E+00	2.15E-02		-1.14E+01	1.96E-04	Down	8.35E+00	3.97E-01		null	null								ESTscan +

Unigene8981_All	664	0.00	6.10	1.84	0.00	0.00	0.07	0.00	0.00	0.00	1.26E+01	4.38E-23	Up	1.08E+01	9.08E-07	Up	null	null		6.09E+00	6.81E-01		null	null		null	null		Unigene8981_All//gi|15235503|ref|NP_192186.1|//2.00E-98//PSAD-1 (photosystem I subunit D-1) [Arabidopsis thaliana] >gi|38503230|sp|Q9S7H1.1|PSAD1_ARATH RecName: Full=Photosystem I reaction center subunit II-1, chloroplastic; AltName: Full=Photosystem I 20 kDa subunit 1; Short=PSI-D1; Flags: Precursor >gi|16928246|gb|AAG40026.1|AF32467_1 AT4g02770 [Arabidopsis thaliana] >gi|14480084|gb|AAK63862.1|AF38929_0_1 AT4g02770/T5J8_7 [Arabidopsis thaliana] >gi|5732199|emb|CAB52676.1| photosystem I subunit II precursor [Arabidopsis thaliana] >gi|17064872|gb|AAL32590.1| Unknown protein [Arabidopsis thaliana] >gi|20908086|gb|AAM26726.1| AT4g02770/T5J8_7 [Arabidopsis thaliana]	Unigene8981_All//4.00E-81//AT1G03130| PSAD-2 (photosystem I subunit D-2)	Unigene8981_All//1.00E-48//TC136477		ko00195|Photosynthesis		nr +
Unigene89829_All	260	0.40	0.78	2.87	3.07	0.53	0.00	0.65	1.29	1.07	9.54E-01	6.19E-01		2.83E+00	8.50E-03		-2.53E+00	3.08E-03		-1.16E+01	4.89E-05	Down	9.83E-01	4.23E-01		7.22E-01	5.96E-01		Unigene89829_All//gi|33090165|gb|AAP93886.1|//1.00E-30//NBS-type resistance protein [Gossypium barbadense]	Unigene89829_All//6.00E-25//AT1G52660| ATP binding	Unigene89829_All//3.00E-78//gi|164350359|gb|ES847894.1|ES847894		ko04626|Plant-pathogen interaction	GO:0006950//GO:0012501//GO:0016787//GO:0032559	nr +
Unigene8983_All	427	1.47	0.71	1.00	4.55	2.58	2.96	4.65	1.86	1.59	-1.05E+00	2.50E-01		-5.60E-01	5.53E-01		-8.18E-01	6.69E-02		-6.20E-01	1.97E-01		-1.32E+00	1.65E-03		-1.55E+00	2.04E-04	Down	Unigene8983_All//gi|79383745|ref|NP_177879.3|//4.00E-49//protein binding / tubulin-tyrosine ligase [Arabidopsis thaliana] >gi|47550675|gb|AAT35236.1| At1g77550 [Arabidopsis thaliana]	Unigene8983_All//3.00E-50//AT1G77550| protein binding / tubulin-tyrosine ligase	Unigene8983_All//1.00E-121//gi|164248937|gb|ES802467.1|ES802467				nr +
Unigene89834_All	261	0.00	0.39	0.00	4.01	0.00	0.35	0.00	0.00	0.00	8.60E+00	3.78E-01		null	null		-1.20E+01	9.43E-08	Down	-3.53E+00	9.33E-05	Down	null	null		null	null		Unigene89834_All//gi|53749170|gb|AB190070.1|//3.00E-35//At4g14950 [Arabidopsis thaliana]	Unigene89834_All//1.00E-36//AT4G14950| unknown protein	Unigene89834_All//3.00E-75//TC155722			GO:0043231	nr -
Unigene89838_All	261	0.00	2.72	0.00	10.31	0.92	0.35	0.65	0.00	0.00	1.14E+01	3.30E-04	Up	null	null		-3.48E+00	3.25E-13	Down	-4.90E+00	2.75E-14	Down	-9.34E+00	1.33E-01		-9.34E+00	1.07E-01		Unigene89838_All//gi|7698801|emb|CAA54507.1|//1.00E-27//GTP binding protein [Glycine max]	Unigene89838_All//1.00E-26//AT3G07410| AtRABA5b (Arabidopsis Rab GTPase homolog A5b); GTP binding	Unigene89838_All//2.00E-48//gi|164282986|gb|ES800119.1|ES800119			GO:0003924//GO:0006810//GO:0009536//GO:0016020//GO:0032561//GO:0035556	nr +
Unigene8984_All	433	0.12	1.40	0.00	0.23	0.32	0.42	1.86	2.61	6.07	3.54E+00	7.23E-03		-6.92E+00	6.11E-01		4.67E-01	8.74E-01		8.59E-01	6.93E-01		4.90E-01	4.01E-01		1.71E+00	3.42E-06	Up			Unigene8984_All//5.00E-07//TC166857				
Unigene8986_All	655	0.80	0.31	1.54	2.89	2.68	3.65	1.48	0.06	0.43	-1.37E+00	1.96E-01		9.51E-01	1.87E-01		-1.08E-01	8.17E-01		3.39E-01	4.61E-01		-4.54E+00	6.92E-06	Down	-1.80E+00	5.53E-03		Unigene8986_All//gi|115475547|ref|NP_001061370.1|//5.00E-97//Os08g0249100 [Oryza sativa Japonica Group] >gi|40253745|dbj|BAD05685.1| SERK1 protein-like [Oryza sativa Japonica Group] >gi|40253909|dbj|BAD05842.1| SERK1 protein-like [Oryza sativa Japonica Group] >gi|113623339|dbj|BAF23284.1| Os08g0249100 [Oryza sativa Japonica Group]	Unigene8986_All//2.00E-97//AT5G57670| protein kinase family protein	Unigene8986_All//0.00E+00//gi|109890713|gb|DW519677.1|DW519677		ko04626|Plant-pathogen interaction		nr -
Unigene89863_All	263	34.62	38.34	21.06	68.57	58.40	64.40	131.18	87.25	64.83	1.47E-01	4.52E-01		-7.17E-01	2.96E-04		-2.32E-01	8.47E-02		-9.05E-02	5.88E-01		-5.88E-01	7.01E-13		-1.02E+00	8.96E-33	Down			Unigene89863_All//2.00E-42//TC172811				
Unigene89866_All	263	0.99	0.00	0.00	2.65	0.00	0.00	0.16	0.00	0.00	-9.96E+00	6.64E-02		-9.96E+00	8.50E-02		-1.14E+01	3.44E-05	Down	-1.14E+01	1.96E-04	Down	-7.33E+00	6.37E-01		-7.33E+00	5.96E-01		Unigene89866_All//gi|34452606|gb|AAQ72692.1|//3.00E-21//phosphoenolpyruvate-carboxylase kinase [Glycine max] >gi|34484302|gb|AAQ72784.1| phosphoenolpyruvate-carboxylase kinase [Glycine max] >gi|45685378|gb|AAS75449.1| phosphoenolpyruvate carboxylase kinase 4 [Glycine max] >gi|45685380|gb|AAS75450.1| phosphoenolpyruvate carboxylase kinase 4 [Glycine max]	Unigene89866_All//4.00E-17//AT3G04530| PPCK2; kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction	GO:0004674//GO:0006464//GO:0032559	nr -
Unigene89868_All	263	0.80	0.58	0.20	1.70	0.39	0.17	2.25	0.00	0.61	-4.61E-01	7.57E-01		-1.97E+00	3.80E-01		-2.12E+00	7.27E-02		-3.31E+00	2.84E-02		-1.11E+01	2.39E-04	Down	-1.89E+00	3.22E-02		Unigene89868_All//gi|159025731|emb|CAN88866.1|//1.00E-18//D6-type cyclin [Populus trichocarpa]	Unigene89868_All//1.00E-05//AT4G03270| CYCD6;1 (Cyclin D6;1); cyclin-dependent protein kinase					nr +
Unigene89873_All	263	20.89	11.75	14.98	33.71	22.26	45.68	51.44	26.70	23.48	-8.30E-01	1.11E-03		-4.79E-01	7.65E-02		-5.99E-01	9.12E-04		4.38E-01	7.57E-03		-9.46E-01	1.29E-11		-1.13E+00	8.86E-16	Down			Unigene89873_All//7.00E-42//TC174973				
Unigene8988_All	1318	0.32	0.15	0.24	0.04	0.05	0.07	1.19	2.92	1.21	-1.05E+00	3.65E-01		-3.90E-01	7.17E-01		4.68E-01	9.52E-01		8.58E-01	7.90E-01		1.30E+00	6.87E-06	Up	2.67E-02	9.70E-01				Unigene8988_All//0.00E+00//TC141747				
Unigene89882_All	264	0.00	0.00	0.61	1.89	0.00	0.00	0.16	0.00	0.00	null	null		9.24E+00	2.33E-01		-1.09E+01	8.96E-04	Down	-1.09E+01	2.96E-03		-7.32E+00	6.37E-01		-7.32E+00	5.96E-01		Unigene89882_All//gi|224133630|ref|XP_002321622.1|//1.00E-36//high affinity nitrate transporter [Populus trichocarpa] >gi|222868618|gb|EEF05749.1| high affinity nitrate transporter [Populus trichocarpa]	Unigene89882_All//3.00E-28//AT1G12940| ATNRT2.5 (nitrate transporter2.5); nitrate transmembrane transporter	Unigene89882_All//1.00E-49//DN816839			GO:0006820//GO:0008509//GO:0031224	nr -
Unigene89888_All	264	0.20	0.00	0.40	1.13	0.39	1.03	2.08	0.32	0.00	-7.63E+00	5.97E-01		1.03E+00	6.99E-01		-1.53E+00	2.97E-01		-1.41E-01	9.20E-01		-2.72E+00	1.22E-02		-1.10E+01	2.80E-04	Down							
Unigene89898_All	265	0.79	1.53	0.80	2.63	0.00	0.00	0.64	0.79	0.45	9.54E-01	4.13E-01		2.55E-02	1.00E+00		-1.14E+01	3.44E-05	Down	-1.14E+01	1.96E-04	Down	3.05E-01	8.35E-01		-5.01E-01	7.45E-01									
Unigene8990_All	401	16.96	6.19	16.47	1.37	0.60	0.79	0.00	0.00	0.00	-1.45E+00	1.58E-09	Down	-4.28E-02	8.64E-01		-1.18E+00	2.25E-01		-7.94E-01	4.44E-01		null	null		null	null		Unigene8990_All//gi|22329373|ref|NP_172172.2|//3.00E-43//transporter-related [Arabidopsis thaliana] >gi|145323764|ref|NP_001077471.1| transporter-related [Arabidopsis thaliana] >gi|75158873|sp|Q8RXL8.1|Y1689_ARATH RecName: Full=Uncharacterized membrane protein At1g06890	Unigene8990_All//7.00E-37//AT1G06890| transporter-related	Unigene8990_All//1.00E-161//TC147471				nr -
Unigene89901_All	266	0.00	0.00	0.00	3.56	0.78	0.34	0.16	0.00	0.00	null	null		null	null		-2.20E+00	2.99E-03		-3.39E+00	3.17E-04	Down	-7.31E+00	6.37E-01		-7.31E+00	5.96E-01									
Unigene89904_All	266	0.39	0.00	0.00	5.06	0.78	2.21	0.00	0.00	0.00	-8.62E+00	3.63E-01		-8.62E+00	3.85E-01		-2.70E+00	2.12E-05	Down	-1.20E+00	4.18E-02		null	null		null	null									
Unigene89908_All	266	0.20	0.00	0.00	2.81	2.46	0.00	1.59	0.00	0.30	-7.62E+00	5.96E-01		-7.62E+00	6.11E-01		-1.92E-01	8.20E-01		-1.15E+01	9.79E-05	Down	-1.06E+01	3.24E-03		-2.41E+00	3.93E-02		Unigene89908_All//gi|225454428|ref|XP_002276498.1|//2.00E-15//PREDICTED: similar to Os11g0118600 [Vitis vinifera]	Unigene89908_All//3.00E-09//AT3G08600| unknown protein				GO:0016020	nr -
Unigene89920_All	267	0.00	0.76	0.20	2.80	0.77	0.17	0.63	0.47	0.75	9.57E+00	1.34E-01		7.64E+00	6.21E-01		-1.85E+00	2.53E-02		-4.05E+00	7.75E-04	Down	-4.32E-01	7.91E-01		2.36E-01	8.82E-01		Unigene89920_All//gi|18032144|gb|AAL56635.1|AF120153_1//7.00E-39//cyclin-dependent kinase CDC2C [Arabidopsis thaliana]	Unigene89920_All//3.00E-40//AT5G39420| cdc2cAt (Arabidopsis thaliana cdc2c); ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene89920_All//1.00E-139//TC167382			GO:0004674//GO:0006464//GO:0032559//GO:0043231	nr +
Unigene89926_All	267	0.00	0.00	0.00	2.43	1.55	0.00	0.00	0.00	0.30	null	null		null	null		-6.48E-01	4.60E-01		-1.12E+01	3.89E-04	Down	null	null		8.22E+00	3.99E-01			Unigene89926_All//9.00E-05//AT4G12560| F-box family protein					ESTScan -
Unigene8993_All	822	0.00	1.29	0.00	0.18	0.29	0.33	2.42	1.83	2.18	1.03E+01	3.79E-06	Up	null	null		6.90E-01	7.31E-01		8.59E-01	6.30E-01		-4.01E-01	3.63E-01		-1.49E-01	7.09E-01		Unigene8993_All//gi|76160992|gb|AB440459.1|//8.00E-99//NADPH quinone oxidoreductase-like protein [Solanum tuberosum]	Unigene8993_All//4.00E-98//AT4G21580| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene8993_All//2.00E-54//ES830086				nr +
Unigene89945_All	269	0.39	0.94	0.00	3.15	0.00	0.34	0.31	0.16	0.74	1.28E+00	4.34E-01		-8.60E+00	3.85E-01		-1.16E+01	2.80E-06	Down	-3.23E+00	1.04E-03		-1.02E+00	7.20E-01		1.24E+00	4.68E-01				Unigene89945_All//2.00E-150//BQ412677				
Unigene89951_All	270	0.00	0.00	2.56	2.58	0.00	0.00	0.00	0.00	0.00	null	null		1.13E+01	6.09E-04	Up	-1.13E+01	3.44E-05	Down	-1.13E+01	1.96E-04	Down	null	null		null	null		Unigene89951_All//gi|170421|gb|AAA34155.1|//2.00E-46//chlorophyll a/b-binding protein Cab-3A [Solanum lycopersicum] >gi|170426|gb|AAA34157.1| chlorophyll a/b-binding protein Cab-3B [Solanum lycopersicum]	Unigene89951_All//6.00E-43//AT2G34420| LHB1B2; chlorophyll binding	Unigene89951_All//1.00E-62//TC164887		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0006464//GO:0009521//GO:0009534//GO:0031224//GO:0043169//GO:0046906	nr +
Unigene89953_All	271	1.16	0.00	0.00	4.41	0.76	0.00	1.56	0.62	0.00	-1.02E+01	3.63E-02		-1.02E+01	4.87E-02		-2.53E+00	1.46E-04	Down	-1.21E+01	1.76E-07	Down	-1.34E+00	2.24E-01		-1.06E+01	2.14E-03									
Unigene89954_All	271	0.19	0.00	0.39	3.31	0.51	0.33	0.62	0.77	1.47	-7.59E+00	5.96E-01		1.03E+00	6.99E-01		-2.70E+00	8.76E-04	Down	-3.31E+00	5.79E-04	Down	3.05E-01	8.35E-01		1.24E+00	2.51E-01		Unigene89954_All//gi|297825627|ref|XP_002880696.1|//5.00E-32//EMB2410 [Arabidopsis lyrata subsp. lyrata] >gi|297326535|gb|EFH56955.1| EMB2410 [Arabidopsis lyrata subsp. lyrata]	Unigene89954_All//1.00E-23//AT2G25660| emb2410 (embryo defective 2410)	Unigene89954_All//1.00E-68//TC133449			GO:0003676//GO:0006260//GO:0034061//GO:0043231	nr -
Unigene89967_All	273	2.87	0.00	1.17	2.74	0.63	0.99	0.62	0.31	0.00	-1.15E+01	1.09E-04	Down	-1.30E+00	1.38E-01		-2.12E+00	1.27E-02		-1.46E+00	9.03E-02		-1.02E+00	6.12E-01		-9.28E+00	1.07E-01		Unigene89967_All//gi|18399836|ref|NP_566442.1|//1.00E-13//myb family transcription factor [Arabidopsis thaliana] >gi|42572405|ref|NP_974298.1| myb family transcription factor [Arabidopsis thaliana]	Unigene89967_All//4.00E-15//AT3G13040| myb family transcription factor	Unigene89967_All//1.00E-129//TC178349	G2-like		GO:0010468	nr +
Unigene89989_All	276	0.76	0.18	0.77	2.53	0.00	0.00	0.46	0.00	0.00	-2.05E+00	3.33E-01		2.53E-02	1.00E+00		-1.13E+01	3.44E-05	Down	-1.13E+01	1.96E-04	Down	-8.84E+00	2.33E-01		-8.84E+00	1.98E-01									
Unigene8999_All	755	0.00	0.00	0.00	0.20	0.09	0.18	1.68	0.94	6.33	null	null		null	null		-1.12E+00	5.81E-01		-1.41E-01	9.41E-01		-8.36E-01	1.23E-01		1.91E+00	3.37E-12	Up	Unigene8999_All//gi|40822853|gb|AAB92244.1|//2.00E-19//At5g20110 [Arabidopsis thaliana] >gi|45752676|gb|AAS76236.1| At5g20110 [Arabidopsis thaliana]	Unigene8999_All//1.00E-15//AT5G20110| dynein light chain, putative					nr +
Unigene89992_All	277	0.00	0.00	1.15	3.78	0.87	0.33	1.37	0.45	0.14	null	null		1.02E+01	4.42E-02		-2.12E+00	2.12E-03		-3.53E+00	9.33E-05	Down	-1.60E+00	1.81E-01		-3.26E+00	2.22E-02									
Unigene900_All	1757	2.53	0.75	0.55	3.52	2.51	3.03	5.29	2.57	2.70	-1.76E+00	2.85E-08	Down	-2.21E+00	2.07E-10	Down	-4.87E-01	3.47E-02		-2.13E-01	4.33E-01		-1.04E+00	1.55E-09	Down	-9.72E-01	7.05E-09		Unigene900_All//gi|79386788|ref|NP_186881.2|//0.00E+00//RNA binding / tRNA (guanine-N2-)-methyltransferase [Arabidopsis thaliana] >gi|209572713|sp|Q9SRU7.3|TRM2_ARATH RecName: Full=Probable N(2),N(2)-dimethylguanosine tRNA methyltransferase 2; AltName: Full=tRNA(guanine-26,N(2)-N(2)) methyltransferase 2; AltName: Full=tRNA 2,2-dimethylguanosine-26 methyltransferase 2; AltName: Full=tRNA(m(2,2)G26)dimethyltransferase 2	Unigene900_All//0.00E+00//AT3G02320| RNA binding / tRNA (guanine-N2-)-methyltransferase	Unigene900_All//0.00E+00//ES791228			GO:0003676//GO:0006399//GO:0008170	nr -
Unigene9000_All	456	4.82	0.00	1.17	3.82	1.81	0.99	0.19	0.00	0.35	-1.22E+01	1.07E-12	Down	-2.04E+00	5.31E-05	Down	-1.08E+00	2.22E-02		-1.95E+00	2.67E-04	Down	-7.53E+00	3.96E-01		9.15E-01	6.23E-01									
Unigene90012_All	281	0.37	0.18	0.00	3.01	1.10	0.16	0.00	1.04	0.00	-1.05E+00	6.81E-01		-8.54E+00	3.85E-01		-1.45E+00	5.13E-02		-4.23E+00	2.18E-04	Down	1.00E+01	2.35E-02		null	null		Unigene90012_All//gi|223452508|gb|ACM89581.1|//4.00E-15//disease resistance protein [Glycine max]	Unigene90012_All//5.00E-14//AT1G47890| AtRLP7 (Receptor Like Protein 7); kinase/ protein binding			ko04626|Plant-pathogen interaction		nr -
Unigene90013_All	281	0.37	0.00	0.00	2.48	0.12	0.96	0.90	0.60	0.28	-8.54E+00	3.63E-01		-8.54E+00	3.85E-01		-4.34E+00	2.79E-04	Down	-1.36E+00	1.31E-01		-6.02E-01	6.47E-01		-1.67E+00	2.56E-01									

Unigene9002_All	999	0.00	21.66	11.46	0.00	0.00	0.00	0.08	0.00	0.00	1.44E+01	1.57E-124	Up	1.35E+01	2.39E-64	Up	null	null		null	null		-6.40E+00	3.96E-01		-6.40E+00	3.52E-01		Unigene9002_All//gi|115470251|ref|NP_001058724.1|//4.00E-66//Os07g0109500 [Oryza sativa Japonica Group] >gi|113610260|dbj|BAF20638.1|Os07g0109500 [Oryza sativa Japonica Group]	Unigene9002_All//3.00E-59//AT4G13170| 60S ribosomal protein L13A (RPL13aC)			ko03010|Ribosome		nr +
Unigene90025_All	282	0.00	0.36	0.00	2.65	0.49	0.00	0.45	0.15	0.14	8.49E+00	3.78E-01		null	null		-2.44E+00	5.59E-03		-1.14E+01	9.79E-05	Down	-1.60E+00	5.31E-01		-1.67E+00	4.75E-01		Unigene90025_All//gi|297599447|ref|NP_001047162.2|//4.00E-13//Os02g0564700 [Oryza sativa Japonica Group] >gi|255671012|dbj|BAF09076.2|Os02g0564700 [Oryza sativa Japonica Group]	Unigene90025_All//3.00E-08//AT5G58010| basic helix-loop-helix (bHLH) family protein	Unigene90025_All//8.00E-39//gi|78323230|gb|DT543504.1|DT543504	bHLH		GO:0005488//GO:0010468//GO:0043231	nr +
Unigene90026_All	282	1.11	0.00	0.19	2.12	0.24	0.00	0.60	0.44	0.99	-1.01E+01	3.63E-02		-2.56E+00	1.59E-01		-3.12E+00	4.86E-03		-1.10E+01	7.69E-04	Down	-4.32E-01	7.91E-01		7.22E-01	5.96E-01		Unigene90026_All//gi|15235288|ref|NP_193742.1|//5.00E-32//EMB1025 (embryo defective 1025) [Arabidopsis thaliana] >gi|75098720|sp|O49436.1|PP327_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At4g20090; AltName: Full=Protein EMBRYO DEFECTIVE 1025 >gi|2827663|emb|CAA16617.1|membrane-associated salt-inducible-like protein [Arabidopsis thaliana] >gi|7268804|emb|CAB79009.1|membrane-associated salt-inducible-like protein [Arabidopsis thaliana] >gi|58013024|gb|AAW62965.1|embryo-defective 1025 [Arabidopsis thaliana]	Unigene90026_All//2.00E-33//AT4G20090| EMB1025 (embryo defective 1025)	Unigene90026_All//1.00E-34//DW236397			GO:0003006	nr +
Unigene9003_All	410	0.26	0.00	0.00	30.62	23.10	13.66	0.72	0.92	0.19	-8.00E+00	3.63E-01		-8.00E+00	3.85E-01		-4.07E-01	7.86E-03		-1.16E+00	4.72E-13	Down	3.46E-01	7.37E-01		-1.89E+00	1.68E-01		Unigene9003_All//gi|297744158|emb|CBI37128.3|//3.00E-08//unnamed protein product [Vitis vinifera]		Unigene9003_All//5.00E-161//ES796488				nr -
Unigene90032_All	283	2.40	0.72	1.13	5.28	3.29	1.28	0.75	0.30	0.00	-1.75E+00	6.23E-02		-1.09E+00	2.39E-01		-6.85E-01	1.99E-01		-2.05E+00	5.54E-04	Down	-1.34E+00	4.28E-01		-9.55E+00	5.77E-02				Unigene90032_All//1.00E-56//TC167690				ESTscan +
Unigene90033_All	283	0.00	3.76	0.94	1.06	2.43	0.48	0.00	0.00	0.00	1.19E+01	3.79E-06	Up	9.88E+00	7.85E-02		1.20E+00	1.94E-01		-1.14E+00	4.56E-01		null	null		null	null		Unigene90033_All//gi|297825869|ref|XP_002880817.1|//3.00E-18//nitrate transporter [Arabidopsis lyrata subsp. lyrata] >gi|297326656|gb|EFH57076.1|nitrate transporter [Arabidopsis lyrata subsp. lyrata]	Unigene90033_All//1.00E-18//AT2G26690| nitrate transporter (NTP2)	Unigene90033_All//1.00E-77//TC165066			GO:0005488//GO:0006950//GO:0009719//GO:0010035//GO:0015103//GO:0015698//GO:0015833//GO:0031224	nr +
Unigene90035_All	283	0.37	0.00	0.75	2.29	1.10	4.95	2.84	1.18	0.28	-8.53E+00	3.63E-01		1.03E+00	5.89E-01		-1.06E+00	2.26E-01		1.11E+00	5.66E-02		-1.26E+00	7.97E-02		-3.33E+00	2.47E-04	Down	Unigene90035_All//gi|22328346|ref|NP_567268.2|//3.00E-32//Met-10+ like family protein / kelch repeat-containing protein [Arabidopsis thaliana] >gi|75162488|sp|Q8W4K1.1|TVW23_ARATH RecName: Full=tRNA wybutosine-synthesizing protein 2/3/4; Includes: RecName: Full=tRNA wybutosine-synthesizing protein 3 homolog; Includes: RecName: Full=tRNA wybutosine synthesizing protein 2 homolog >gi|170648868|gb|AAL32588.1|Unknown protein [Arabidopsis thaliana] >gi|30725408|gb|AAP37726.1|At4g04670 [Arabidopsis thaliana]	Unigene90035_All//1.00E-33//AT4G04670| Met-10+ like family protein / kelch repeat-containing protein				GO:0006400	nr -
Unigene90038_All	284	1.11	1.43	0.38	3.16	1.09	0.16	0.45	0.29	0.00	3.69E-01	7.23E-01		-1.56E+00	3.29E-01		-1.53E+00	3.37E-02		-4.31E+00	1.14E-04	Down	-6.02E-01	7.64E-01		-8.80E+00	1.98E-01				Unigene90038_All//2.00E-48//gi|109889694|gb|DW518662.1|DW518662				
Unigene9004_All	412	0.00	0.86	1.81	2.30	2.76	1.43	1.13	1.01	2.32	9.75E+00	2.43E-02		1.08E+01	3.24E-04	Up	2.64E-01	7.30E-01		-6.89E-01	3.58E-01		-1.54E-01	8.70E-01		1.04E+00	9.27E-02		Unigene9004_All//gi|225460207|ref|XP_002277887.1|//5.00E-47//PREDICTED: similar to TNP2 [Vitis vinifera]		Unigene9004_All//1.00E-93//TC133679				nr +
Unigene90040_All	284	0.00	0.00	0.00	3.68	1.09	0.48	0.60	0.44	0.42	null	null		null	null		-1.76E+00	8.43E-03		-2.95E+00	3.82E-04	Down	-4.32E-01	7.91E-01		-5.01E-01	7.45E-01								ESTscan -
Unigene90049_All	285	1.84	0.71	0.75	4.54	0.85	2.06	2.08	1.03	0.28	-1.37E+00	1.96E-01		-1.30E+00	2.42E-01		-2.43E+00	1.10E-04	Down	-1.14E+00	5.81E-02		-1.02E+00	2.40E-01		-2.89E+00	4.53E-03									
Unigene90050_All	285	0.00	0.00	0.00	1.75	0.00	0.63	0.00	0.00	0.00	null	null		null	null		-1.08E+01	8.96E-04	Down	-1.46E+00	1.93E-01		null	null		null	null				Unigene90050_All//2.00E-116//DR456680				
Unigene90055_All	286	0.00	0.35	0.00	2.26	0.72	0.00	0.00	0.00	0.00	8.47E+00	3.78E-01		null	null		-1.65E+00	6.52E-02		-1.11E+01	3.89E-04	Down	null	null		null	null		Unigene90055_All//gi|237682434|gb|ACR10265.1|//3.00E-22//sulfotransferase 5a [Brassica rapa subsp. pekinensis]	Unigene90055_All//2.00E-21//AT1G18590| SOT17 (SULFOTRANSFERASE 17); desulfoglucosinolate sulfotransferase/ sulfotransferase			ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0008146	nr +
Unigene9006_All	557	0.00	1.91	0.57	0.80	0.49	0.16	2.58	1.50	0.43	1.09E+01	3.79E-06	Up	9.16E+00	4.42E-02		-7.03E-01	5.30E-01		-2.31E+00	7.79E-02		-7.82E-01	1.20E-01		-2.59E+00	8.29E-06	Down			Unigene9006_All//3.00E-12//TC137728				
Unigene90060_All	287	0.00	0.00	0.00	4.69	0.36	0.47	0.00	0.00	0.00	null	null		null	null		-3.70E+00	4.08E-07	Down	-3.31E+00	1.08E-05	Down	null	null		null	null									
Unigene9007_All	398	1.84	0.00	1.07	1.75	1.56	1.02	3.08	1.68	2.20	-1.08E+01	2.11E-04	Down	-7.82E-01	3.80E-01		-1.70E-01	8.21E-01		-7.79E-01	3.93E-01		-8.73E-01	1.13E-01		-4.84E-01	3.61E-01				Unigene9007_All//6.00E-68//TC151970				
Unigene90072_All	291	2.16	0.00	0.00	2.05	0.36	0.62	0.00	0.14	0.00	-1.11E+01	7.90E-04	Down	-1.11E+01	1.40E-03		-2.53E+00	1.36E-02		-1.73E+00	9.02E-02		7.17E+00	6.22E-01		null	null				Unigene90072_All//8.00E-42//TC179591				
Unigene90077_All	292	1.43	0.17	0.73	4.44	0.83	0.93	1.16	0.00	0.55	-3.05E+00	4.65E-02		-9.75E-01	4.11E-01		-2.43E+00	1.10E-04	Down	-2.26E+00	6.70E-04	Down	-1.02E+01	1.17E-02		-1.09E+00	3.55E-01		Unigene90077_All//gi|226494730|ref|XP_001147902.1|//1.00E-08//ternary complex factor MIP1 [Zea mays] >gi|195614476|gb|ACG29068.1|ternary complex factor MIP1 [Zea mays]	Unigene90077_All//1.00E-07//AT5G66600| unknown protein					nr +
Unigene9008_All	385	0.00	0.13	0.00	0.13	0.81	0.12	0.99	1.63	4.76	7.04E+00	6.05E-01		null	null		2.64E+00	1.61E-01		-1.42E-01	9.45E-01		7.20E-01	4.02E-01		2.27E+00	3.38E-06	Up	Unigene9008_All//gi|18423810|ref|NP_568834.1|//2.00E-27//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] >gi|30696669|ref|NP_851197.1| zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene9008_All//1.00E-28//AT5G59970| zinc finger (C3HC4-type RING finger) family protein	Unigene9008_All//6.00E-99//gi|54119848|gb|CO495357.1|CO495357				nr -
Unigene90082_All	293	2.14	2.42	0.36	6.29	1.29	0.31	0.72	0.71	0.27	1.76E-01	8.17E-01		-2.56E+00	2.72E-02		-2.28E+00	5.07E-06	Down	-4.35E+00	2.98E-09	Down	-1.67E-02	1.02E+00		-1.41E+00	3.79E-01				Unigene90082_All//3.00E-07//CO085489				
Unigene90088_All	295	0.00	0.52	0.00	3.04	0.23	0.77	0.00	0.00	0.00	9.01E+00	2.31E-01		null	null		-3.70E+00	7.11E-05	Down	-1.99E+00	1.36E-02		null	null		null	null				Unigene90088_All//8.00E-42//DW498176				
Unigene9009_All	419	2.50	0.00	0.13	2.14	0.90	0.22	3.73	1.40	0.29	-1.13E+01	3.80E-06	Down	-4.30E+00	9.00E-05	Down	-1.24E+00	8.17E-02		-3.31E+00	5.79E-04	Down	-1.42E+00	3.64E-03		-3.71E+00	1.85E-08	Down	Unigene9009_All//gi|297830148|ref|XP_002882956.1|//1.00E-58//phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297328796|gb|EFH59215.1|phospholipase/carboxylesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene9009_All//6.00E-59//AT3G15650| phospholipase/carboxylesterase family protein	Unigene9009_All//0.00E+00//TC165072		ko00564|Glycerophospholipid metabolism		nr -
Unigene90095_All	298	0.00	1.02	0.18	1.84	0.00	0.00	0.14	0.14	0.27	9.99E+00	4.35E-02		7.48E+00	6.21E-01		-1.08E+01	4.00E-04	Down	-1.08E+01	1.51E-03		-1.64E-02	9.95E-01		9.14E-01	7.46E-01									
Unigene90096_All	298	0.00	2.38	0.36	2.67	1.96	1.21	1.14	0.42	0.00	1.12E+01	3.30E-04	Up	8.48E+00	3.86E-01		-4.45E-01	5.73E-01		-1.14E+00	1.63E-01		-1.43E+00	2.58E-01		-1.01E+01	8.12E-03		Unigene90096_All//gi|89521300|gb|AB076542.1|//4.00E-10//4-alphacarboxysterol-dehydrogenase/C4-decarboxylase isoform 3 [Arabidopsis thaliana]	Unigene90096_All//2.00E-11//AT2G43420| 3-beta hydroxysteroid dehydrogenase/isomerase family protein	Unigene90096_All//2.00E-36//ES829542			GO:0003676//GO:0008202//GO:0009058//GO:0016020//GO:0033764	nr +
Unigene90097_All	298	2.46	0.00	0.00	2.67	1.04	0.76	1.28	0.00	0.40	-1.13E+01	2.11E-04	Down	-1.13E+01	4.12E-04	Down	-1.36E+00	7.73E-02		-1.82E+00	3.32E-02		-1.03E+01	6.17E-03		-1.67E+00	1.40E-01		Unigene90097_All//gi|225440868|ref|XP_002273523.1|//1.00E-10//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene9010_All	1114	0.05	0.00	0.00	1.34	1.24	0.36	7.82	0.30	0.68	-5.55E+00	5.96E-01		-5.55E+00	6.11E-01		-1.18E-01	8.23E-01		-1.88E+00	1.24E-03		-4.70E+00	2.78E-50	Down	-3.52E+00	2.05E-42	Down	Unigene9010_All//gi|33146186|gb|AAK19615.1|AF336282_1//1.00E-165//GHMYB10 [Gossypium hirsutum]	Unigene9010_All//4.00E-40//AT5G35550| TT2 (TRANSPARENT TESTA 2); DNA binding / transcription factor	Unigene9010_All//0.00E+00//TC167464	MYB			nr +
Unigene90102_All	299	0.35	0.00	1.07	8.00	1.61	1.21	1.13	0.28	1.47	-8.45E+00	3.63E-01		1.61E+00	3.03E-01		-2.31E+00	8.99E-08	Down	-2.73E+00	3.72E-08	Down	-2.02E+00	1.36E-01		3.74E-01	6.82E-01				Unigene90102_All//9.00E-14//gi|84145756|gb|DN759998.1|DN759998				
Unigene90104_All	299	0.00	0.00	0.00	4.17	0.81	1.06	0.28	0.00	0.13	null	null		null	null		-2.37E+00	2.03E-04	Down	-1.98E+00	2.61E-03		-8.14E+00	3.96E-01		-1.09E+00	6.72E-01				Unigene90104_All//1.00E-83//DR461918				
Unigene9011_All	389	0.13	17.85	0.00	3.46	2.39	1.86	2.07	2.69	9.52	7.05E+00	7.60E-38	Up	-7.07E+00	6.11E-01		-5.33E-01	3.57E-01		-8.96E-01	1.30E-01		3.79E-01	5.56E-01		2.21E+00	2.21E-11	Up			Unigene9011_All//5.00E-67//TC173621				
Unigene90110_All	301	0.70	0.00	0.00	3.48	0.11	0.30	0.00	0.00	0.13	-9.44E+00	1.20E-01		-9.44E+00	1.44E-01		-4.93E+00	1.16E-06	Down	-3.53E+00	9.33E-05	Down	null	null		7.05E+00	6.32E-01									
Unigene90119_All	303	0.69	0.67	3.16	26.63	1.48	1.04	1.95	0.28	0.13	-4.63E-02	9.86E-01		2.20E+00	9.09E-03		-4.17E+00	1.66E-45	Down	-4.67E+00	1.66E-41	Down	-2.82E+00	7.17E-03		-3.89E+00	1.09E-03		Unigene90119_All//gi|195647198|gb|ACG43067.1|//4.00E-23//prolyl endopeptidase [Zea mays]	Unigene90119_All//2.00E-23//AT1G76140| serine-type endopeptidase/ serine-type peptidase	Unigene90119_All//2.00E-67//TC149749			GO:0009536	nr +
Unigene90125_All	303	0.35	0.00	0.00	3.62	2.05	0.60	0.28	0.00	0.00	-8.43E+00	3.63E-01		-8.43E+00	3.85E-01		-8.22E-01	1.96E-01		-2.60E+00	7.13E-04	Down	-8.12E+00	3.96E-01		-8.12E+00	3.52E-01		Unigene90125_All//gi|297734272|emb|CBI15519.3|//4.00E-07//unnamed protein product [Vitis vinifera]		Unigene90125_All//1.00E-170//TC170022				nr -
Unigene9013_All	303	0.00	7.02	0.35	0.00	1.36	0.89	0.42	3.31	1.58	1.28E+01	4.10E-12	Up	8.46E+00	3.86E-01		1.04E+01	1.25E-02		9.80E+00	7.00E-02		2.98E+00	1.37E-04	Up	1.91E+00	6.29E-02									
Unigene90138_All	309	0.17	0.00	0.00	1.93	0.00	0.15	0.00	0.00	0.00	-7.40E+00	5.96E-01		-7.40E+00	6.11E-01		-1.09E+01	1.77E-04	Down	-3.73E+00	4.95E-03		null	null		null	null		Unigene90138_All//gi|158536508|gb|ABW72148.1|//3.00E-09//flagellin-sensing 2-like protein [Brassica rapa]	Unigene90138_All//1.00E-05//AT1G35710| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0003824	nr -
Unigene90139_All	309	1161.39	90.02	177.16	188.94	225.89	306.94	1.23	0.00	0.77	-3.69E+00	0.00E+00	Down	-2.71E+00	0.00E+00	Down	2.58E-01	1.21E-05		7.00E-01	3.19E-40		-1.03E+01	6.16E-03		-6.71E-01	5.30E-01		Unigene90139_All//gi|225350102|gb|ACN87961.1|//3.00E-56//expansin 2 [Citrus sinensis]	Unigene90139_All//8.00E-53//AT2G40610| ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	Unigene90139_All//1.00E-154//TC164848			GO:0007047//GO:0044464	nr -
Unigene9014_All	242	6.49	6.49	9.90	5.15	4.27	3.92	84.56	52.16	24.03	1.00E-03	1.00E+00		6.10E-01	1.54E-01		-2.70E-01	6.54E-01		-3.93E-01	5.49E-01		-6.97E-01	1.73E-10		-1.81E+00	1.03E-46	Down			Unigene9014_All//4.00E-71//TC156651				
Unigene90141_All	309	0.68	0.98	0.52	3.39	1.00	0.29	0.14	0.00	0.00	5.39E-01	6.71E-01		-3.90E-01	8.06E-01		-1.76E+00	8.43E-03		-3.53E+00	9.33E-05	Down	-7.10E+00	6.37E-01		-7.10E+00	5.96E-01								
Unigene90143_All	310	0.00	0.00	0.00	2.09	1.00	0.00	0.27	0.27	0.00	null	null		null	null		-1.06E+00	2.26E-01		-1.10E+01	3.89E-04	Down	-1.70E-02	1.01E+00		-8.09E+00	3.52E-01								
Unigene90144_All	310	0.84	0.98	0.00	3.37	0.44	0.29	0.00	0.00	0.00	2.17E-01	8.64E-01		-9.72E+00	8.50E-02		-2.93E+00	1.21E-04	Down	-3.53E+00	9.33E-05	Down	null	null		null	null		Unigene90144_All//gi|224145021|ref|XP_002325498.1|//3.00E-06//tir-nbs-lrr resistance protein [Populus trichocarpa] >gi|222862373|gb|EEE99879.1| tir-nbs-lrr resistance protein [Populus trichocarpa]	Unigene90144_All//2.00E-06//AT5G38850| disease resistance protein (TIR-NBS-LRR class), putative	Unigene90144_All//3.00E-115//DT466526			GO:0005488	nr -
Unigene90146_All	311	29.44	18.57	24.48	54.94	52.59	36.89	16.72	4.84	6.66	-6.65E-01	4.60E-04		-2.66E-01	2.10E-01		-6.30E-02	7.12E-01		-5.75E-01	1.06E-05		-1.79E+00	7.36E-12	Down	-1.33E+00	3.04E-08	Down	Unigene90146_All//gi|222422853|dbj|BAH19413.1|//3.00E-26//AT5G62890 [Arabidopsis thaliana]	Unigene90146_All//1.00E-27//AT5G62890| permease, putative	Unigene90146_All//1.00E-87//ES791134			GO:0005215//GO:0030312//GO:0043231	nr -
Unigene90149_All	312	0.00	0.65	0.00	2.24	1.32	0.00	0.27	0.80	0.26	9.34E+00	1.34E-01		null	null		-7.55E-01	3.69E-01		-1.11E+01	1.96E-04	Down	1.57E+00	3.26E-01		-8.55E-02	9.68E-01								
Unigene90158_All	314	0.00	0.32	0.00	4.60	0.00	0.00	0.94	0.00	0.00	8.33E+00	3.78E-01		null	null		-1.22E+01	1.02E-10	Down	-1.22E+01	4.97E-09	Down	-9.88E+00	2.17E-02		-9.88E+00	1.58E-02								
Unigene90162_All	316	2.15	0.16	0.84	2.84	0.00	0.00	0.00	0.00	0.00	-3.75E+00	2.83E-03		-1.35E+00	1.50E-01		-1.15E+01	1.21E-06	Down	-1.15E+01	1.21E-05	Down	null	null		null	null								
Unigene90164_All	316	0.17	0.00	0.00	2.21	0.87	0.00	0.13	0.00	0.00	-7.37E+00	5.96E-01		-7.37E+00	6.10E-01		-1.34E+00	1.09E-01		-1.11E+01	1.96E-04	Down	-7.06E+00	6.37E-01		-7.06E+00	5.96E-01		Unigene90164_All//gi|256674141|gb|ACV04900.1|//6.00E-40//callose synthase 5 [Arabidopsis thaliana]	Unigene90164_All//4.00E-33//AT2G13680| CALS5 (CALLOSE SYNTHASE 5); 1,3-beta-glucan synthase	Unigene90164_All//3.00E-75//AIT25410			GO:0006074//GO:0009555//GO:0009860//GO:0035251//GO:0043234//GO:0044464	nr +
Unigene90165_All	316	0.50	0.00	0.00	2.21	0.44	0.00	0.40	0.00	0.25	-8.96E+00	2.13E-01		-8.96E+00	2.41E-01		-2.34E+00	1.01E-02		-1.11E+01	1.96E-04	Down	-8.65E+00	2.33E-01		-6.71E-01	7.17E-01		Unigene90165_All//gi|224589463|gb|ACN59265.1|//7.00E-15//leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene90165_All//2.00E-15//AT1G66830| leucine-rich repeat transmembrane protein kinase, putative				GO:0005488//GO:0005618//GO:0008152//GO:0009532//GO:0016020//GO:0016301	nr -

Unigene90166_All	317	0.00	0.00	0.00	2.04	0.22	1.57	116.04	85.96	256.88	null	null		null	null		-3.23E+00	2.48E-03		-3.82E-01	6.78E-01		-4.33E-01	3.62E-08		1.15E+00	1.07E-91	Up	Unigene90166_All//gi|196989889|gb|AAL91230.1|//5.00E-13//terpene synthase [Arabidopsis thaliana] >gi|23198090|gb|AAN15572.1| terpene synthase [Arabidopsis thaliana]	Unigene90166_All//2.00E-14//AT5G48110| terpene synthase/cyclase family protein	Unigene90166_All//6.00E-80//CO111120		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis		nr -
Unigene90169_All	318	0.49	0.00	0.84	0.47	0.22	0.28	2.26	0.53	0.00	-8.95E+00	2.13E-01		7.62E-01	6.43E-01		-1.12E+00	5.81E-01		-7.27E-01	7.12E-01		-2.10E+00	1.24E-02		-1.11E+01	1.78E-05	Down	Unigene90169_All|gi|189163920|gb|ACD77110.1|//4.00E-32//protein kinase 1b [Solanum lycopersicum]	Unigene90169_All//9.00E-33//AT2G28930| APK1B; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene90169_All//2.00E-113//TC147135			GO:0004713//GO:0006464//GO:0006952//GO:0016020//GO:0032559//GO:0043231	nr +
Unigene90172_All	319	0.00	0.16	0.50	3.90	2.48	0.71	0.53	0.00	0.00	7.31E+00	6.05E-01		8.97E+00	2.33E-01		-6.53E-01	2.80E-01		-2.46E+00	4.15E-04	Down	-9.05E+00	1.33E-01		-9.05E+00	1.07E-01					Unigene90172_All//6.00E-12//FL577713					
Unigene90176_All	322	0.00	0.00	0.00	7.27	4.06	2.24	0.13	0.52	0.25	null	null		null	null		-8.39E-01	3.43E-02		-1.70E+00	1.02E-04	Down	1.98E+00	3.78E-01		9.14E-01	7.46E-01										
Unigene9018_All	787	0.00	0.00	0.00	0.00	0.00	0.00	3.81	3.19	0.91	null	null		null	null		null	null		null	null		-2.59E-01	4.59E-01		-2.07E+00	8.04E-09	Down	Unigene9018_All|gi|225348625|gb|ACN87274.1|//3.00E-59//short chain dehydrogenase/reductase [Chelidonium majus]	Unigene9018_All//2.00E-54//AT1G01800| short-chain dehydrogenase/reductase (SDR) family protein	Unigene9018_All//0.00E+00//ES792057				nr -
Unigene90180_All	324	0.00	0.00	1.97	2.15	0.21	0.00	0.00	0.00	0.00	null	null		1.09E+01	1.15E-03		-3.34E+00	1.25E-03		-1.11E+01	1.96E-04	Down	null	null		null	null		Unigene90180_All|gi|211906496|gb|ACJ11741.1|//1.00E-55//heat shock protein 70 [Gossypium hirsutum]	Unigene90180_All//8.00E-56//AT5G02500| HSC70-1 (HEAT SHOCK COGNATE PROTEIN 70-1); ATP binding	Unigene90180_All//1.00E-87//ES849176		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0008152//GO:0016628//GO:0032559//GO:0050896	nr -
Unigene90182_All	325	108.18	70.47	48.66	210.91	242.53	215.12	172.76	196.25	272.01	-6.18E-01	9.86E-12		-1.15E+00	3.37E-31	Down	2.02E-01	3.62E-04		2.85E-02	7.13E-01		1.84E-01	2.46E-03		6.55E-01	4.33E-39		Unigene90182_All|gi|195648004|gb|ACG43470.1|//2.00E-17//pectinacetylesterase precursor [Zea mays]	Unigene90182_All//2.00E-17//AT4G19410| pectinacetylesterase, putative	Unigene90182_All//3.00E-85//TC153947			GO:0005618//GO:0043231	nr -
Unigene90183_All	325	0.00	0.00	0.16	3.37	0.53	0.56	0.52	0.13	0.12	null	null		7.36E+00	6.21E-01		-2.67E+00	1.89E-04	Down	-2.60E+00	7.13E-04	Down	-2.02E+00	3.66E-01		-2.09E+00	3.12E-01		Unigene90183_All|gi|124360549|gb|ABO33126.2|//2.00E-13//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]						nr +
Unigene90188_All	327	0.00	1.08	0.00	3.20	0.53	0.83	0.26	0.13	0.00	1.01E+01	2.43E-02		null	null		-2.60E+00	3.59E-04	Down	-1.95E+00	7.52E-03		-1.02E+00	7.19E-01		-8.01E+00	3.52E-01		Unigene90188_All|gi|38016023|gb|AAO07518.1|//2.00E-07//At1g12030 [Arabidopsis thaliana]						nr -
Unigene90195_All	329	0.48	0.00	0.00	2.42	0.21	0.55	1.03	0.25	1.09	-8.90E+00	2.13E-01		-8.90E+00	2.41E-01		-3.53E+00	3.03E-04	Down	-2.14E+00	1.54E-02		-2.02E+00	1.36E-01		8.41E-02	9.57E-01					Unigene90195_All//0.00E+00//gi|21099723|gb|BQ412036.1|BQ412036					
Unigene90199_All	329	0.32	0.00	0.16	3.63	2.51	0.27	0.64	0.51	0.36	-8.31E+00	3.63E-01		-9.74E-01	7.18E-01		-5.33E-01	3.93E-01		-3.73E+00	1.43E-05	Down	-3.39E-01	8.11E-01		-8.23E-01	5.98E-01					Unigene90199_All//6.00E-151//TC172129					
Unigene9020_All	530	1.68	0.86	0.90	0.00	0.07	0.00	1.28	0.32	3.46	-9.64E-01	1.95E-01		-8.92E-01	2.46E-01		6.02E+00	8.11E-01		null	null		-2.02E+00	1.98E-02		1.44E+00	9.58E-04	Up									
Unigene90202_All	332	0.00	0.00	0.16	1.80	0.00	0.00	0.64	0.00	0.60	null	null		7.33E+00	6.21E-01		-1.08E+01	1.77E-04	Down	-1.08E+01	7.69E-04	Down	-9.31E+00	7.40E-02		-8.57E-02	9.60E-01		Unigene90202_All|gi|115472647|ref|NP_001059922.1|//1.00E-15//Os07g0546400 [Oryza sativa Japonica Group] >gi|113611458|dbj|BAF21836.1| Os07g0546400 [Oryza sativa Japonica Group]	Unigene90202_All//3.00E-13//AT1G03010| phototropic-responsive NPH3 family protein	Unigene90202_All//2.00E-09//TC163220			GO:0005488	nr +
Unigene90210_All	336	0.93	0.00	0.00	1.48	0.00	4.03	0.00	0.00	0.00	-9.87E+00	3.63E-02		-9.87E+00	4.87E-02		-1.05E+01	8.96E-04	Down	1.44E+00	1.69E-02		null	null		null	null		Unigene90210_All|gi|5453379|gb|AAD43561.1|AF155124_1//1.00E-56//bacterial-induced peroxidase precursor [Gossypium hirsutum]	Unigene90210_All//7.00E-39//AT5G05340| peroxidase, putative	Unigene90210_All//5.00E-176//NP385887		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism	GO:0003824//GO:0005506//GO:0006950//GO:0008152//GO:0016209//GO:0031410	nr +
Unigene90212_All	337	0.62	0.00	0.32	3.25	0.51	0.54	0.00	0.00	0.12	-9.28E+00	1.20E-01		-9.75E-01	6.19E-01		-2.67E+00	1.89E-04	Down	-2.60E+00	7.13E-04	Down	null	null		6.89E+00	6.32E-01										
Unigene90216_All	340	0.00	0.00	0.00	2.05	0.00	0.27	0.37	0.37	0.12	null	null		null	null		-1.10E+01	3.44E-05	Down	-2.95E+00	5.83E-03		-1.67E-02	1.02E+00		-1.67E+00	4.75E-01		Unigene90216_All|gi|6227008|gb|AAF06044.1|AC009360 9//2.00E-13//This gene is cut off [Arabidopsis thaliana]	Unigene90216_All//5.00E-15//AT1G65090| unknown protein					nr -
Unigene90217_All	340	12.93	0.30	1.25	5.86	4.15	1.73	0.12	0.00	0.12	-5.44E+00	1.85E-22	Down	-3.37E+00	9.02E-16	Down	-4.97E-01	2.89E-01		-1.76E+00	2.66E-04	Down	-6.96E+00	6.37E-01		-8.60E-02	9.63E-01		Unigene90217_All|gi|46488024|gb|AAS99354.1|//3.00E-30//expansin 1 precursor [Linum usitatissimum] >gi|46488026|gb|AAS99355.1| expansin 1 precursor [Linum usitatissimum]	Unigene90217_All//1.00E-18//AT5G02260| ATEXP19 (ARABIDOPSIS THALIANA EXPANSIN A9)	Unigene90217_All//5.00E-139//TC146086			GO:0000902//GO:0005198//GO:0005618//GO:0009827	nr +
Unigene90218_All	341	0.15	0.00	1.56	2.63	1.11	0.26	0.50	0.00	0.00	-7.26E+00	5.96E-01		3.35E+00	2.06E-02		-1.24E+00	8.17E-02		-3.31E+00	5.79E-04	Down	-8.95E+00	1.33E-01		-8.95E+00	1.07E-01										
Unigene90219_All	342	1.38	0.00	1.71	3.20	0.70	0.00	0.25	0.00	1.05	-1.04E+01	5.53E-03		3.15E-01	7.19E-01		-2.18E+00	1.20E-03		-1.16E+01	7.25E-07	Down	-7.95E+00	3.95E-01		2.08E+00	1.01E-01		Unigene90219_All|gi|124365545|gb|ABN09729.1|//4.00E-15//Tetratricopeptide-like helical [Medicago truncatula]	Unigene90219_All//1.00E-11//AT2G44880| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene9022_All	406	0.26	0.25	0.39	1.47	2.29	5.45	0.00	0.21	0.00	-4.61E-02	9.84E-01		6.11E-01	7.46E-01		6.37E-01	4.18E-01		1.89E+00	5.58E-05	Up	7.69E+00	3.97E-01		null	null		Unigene9022_All|gi|162280539|gb|ABX82930.1|//2.00E-19//transcription factor style2.1 [Solanum lycopersicum] >gi|162280541|gb|ABX82931.1| transcription factor style2.1 [Solanum pennellii] >gi|162280543|gb|ABX82932.1| transcription factor style2.1 [Solanum lycopersicum] >gi|162280545|gb|ABX82933.1| transcription factor style2.1 [Solanum pennellii]	Unigene9022_All//2.00E-17//AT1G26945| KDR (KIDARI); transcription regulator	Unigene9022_All//6.00E-25//TC158578	bHLH			nr +
Unigene90220_All	343	0.31	1.03	2.02	2.18	0.10	1.19	5.79	2.32	2.21	1.76E+00	2.18E-01		2.73E+00	1.40E-02		-4.44E+00	1.31E-04	Down	-8.78E-01	3.08E-01		-1.32E+00	1.65E-03		-1.39E+00	6.85E-04	Down				Unigene90220_All//1.00E-31//DR453850					
Unigene90221_All	343	1.07	0.00	0.00	2.61	0.20	0.00	0.00	0.00	0.00	-1.01E+01	1.95E-02		-1.01E+01	2.77E-02		-3.70E+00	7.10E-05	Down	-1.14E+01	1.21E-05	Down	null	null		null	null					Unigene90221_All//3.00E-103//ES806892					
Unigene90223_All	344	5.02	7.07	4.49	12.45	14.72	5.78	4.55	0.73	1.62	4.94E-01	2.32E-01		-1.61E-01	7.43E-01		2.41E-01	4.25E-01		-1.11E+00	1.44E-04	Down	-2.64E+00	4.08E-06	Down	-1.49E+00	1.74E-03		Unigene90223_All|gi|14190467|gb|AAK55714.1|AF380633_1//6.00E-12//At3g13171 [Arabidopsis thaliana] >gi|15809712|gb|AAL06784.1| At3g13171 [Arabidopsis thaliana]	Unigene90223_All//2.00E-13//AT3G13175| unknown protein	Unigene90223_All//1.00E-139//TC157109				nr -
Unigene90228_All	348	22.25	6.55	4.44	17.03	17.02	6.62	14.21	3.12	5.04	-1.76E+00	6.02E-14	Down	-2.33E+00	8.26E-19	Down	-1.20E-03	9.87E-01		-1.36E+00	3.93E-08	Down	-2.19E+00	1.72E-14	Down	-1.50E+00	2.86E-09	Down				Unigene90228_All//1.00E-78//gi|78338781|gb|DT559055.1|DT559055					
Unigene90231_All	350	0.00	0.00	0.00	2.99	0.20	0.00	0.72	0.48	0.11	null	null		null	null		-3.92E+00	7.51E-06	Down	-1.15E+01	1.47E-06	Down	-6.02E-01	6.47E-01		-2.67E+00	1.15E-01		Unigene90231_All//gi|87116461|dbj|BAE79383.1|//9.00E-10//unnamed protein product [Ipomoea batatas]						nr -
Unigene9024_All	618	0.00	0.00	0.00	0.00	0.00	0.00	7.12	2.50	5.54	null	null		null	null		null	null		null	null		-1.51E+00	4.05E-08	Down	-3.60E-01	1.62E-01		Unigene9024_All|gi|15242112|ref|NP_199965.1|//4.00E-30//invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana] >gi|97581191|dbj|BAB08668.1| ripening-related protein-like [Arabidopsis thaliana] >gi|67633876|gb|AAY78862.1| invertase [Arabidopsis thaliana]	Unigene9024_All//9.00E-30//AT5G51520| invertase/pectin methylesterase inhibitor family protein			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene90241_All	363	0.43	0.84	0.73	1.65	0.95	0.00	0.35	1.04	0.00	9.54E-01	5.02E-01		7.62E-01	6.43E-01		-7.96E-01	3.88E-01		-1.07E+01	7.68E-04	Down	1.57E+00	1.95E-01		-8.45E+00	1.98E-01					Unigene90241_All//0.00E+00//CO116469					
Unigene90244_All	367	1.43	0.00	0.00	5.97	0.56	0.98	0.00	0.23	0.00	-1.05E+01	2.91E-03		-1.05E+01	4.73E-03		-3.41E+00	1.26E-10	Down	-2.60E+00	3.56E-07	Down	7.83E+00	3.97E-01		null	null										
Unigene9025_All	1020	0.00	0.00	0.00	0.00	0.07	0.00	11.36	3.93	0.16	null	null		null	null		6.08E+00	5.99E-01		null	null		-1.53E+00	1.54E-20	Down	-6.18E+00	3.71E-78	Down									
Unigene90250_All	375	0.00	0.27	2.84	2.13	0.37	0.12	0.23	0.33	0.74	8.08E+00	3.78E-01		1.15E+01	6.58E-06	Up	-2.53E+00	3.07E-03		-4.14E+00	4.12E-04	Down	5.68E-01	7.80E-01		1.72E+00	2.30E-01		Unigene90250_All|gi|297725027|ref|NP_001174877.1|//3.00E-20//Os06g0587900 [Oryza sativa Japonica Group] >gi|255677187|dbj|BAH93605.1| Os06g0587900 [Oryza sativa Japonica Group]	Unigene90250_All//5.00E-19//AT2G41820| leucine-rich repeat transmembrane protein kinase, putative			ko04626|Plant-pathogen interaction	GO:0004672//GO:0043229//GO:0044444	nr +
Unigene90251_All	376	1.39	0.13	1.42	3.58	1.65	0.36	1346.56	6665.42	339.69	-3.37E+00	1.57E-02		2.54E-02	9.99E-01		-1.12E+00	4.30E-02		-3.31E+00	1.08E-05	Down	2.31E+00	0.00E+00	Up	-1.99E+00	0.00E+00	Down	Unigene90251_All|gi|293633663|gb|ADE60217.1|//8.00E-69//MIC-3 [Gossypium herbaceum] >gi|293633665|gb|ADE60218.1| MIC-3 [Gossypium herbaceum] >gi|293633667|gb|ADE60219.1| MIC-3 [Gossypium herbaceum]		Unigene90251_All//0.00E+00//TC153595				nr -
Unigene90256_All	382	0.27	0.00	0.00	0.78	0.00	0.00	1.77	0.11	1.15	-8.10E+00	3.63E-01		-8.10E+00	3.85E-01		-9.61E+00	2.00E-02		-9.61E+00	3.95E-02		-4.02E+00	5.36E-04	Down	-6.26E-01	4.03E-01		Unigene90256_All|gi|15242645|ref|NP_198847.1|//2.00E-29//exonuclease family protein [Arabidopsis thaliana] >gi|10178140|dbj|BAB11585.1| exonuclease-like protein [Arabidopsis thaliana]	Unigene90256_All//9.00E-31//AT5G40310| exonuclease family protein	Unigene90256_All//2.00E-70//ES792745	C2H2		GO:0004518//GO:0044464//GO:0046914	nr -
Unigene90257_All	383	0.55	0.53	0.28	6.37	1.62	0.83	0.44	0.22	0.21	-4.61E-02	9.86E-01		-9.74E-01	6.19E-01		-1.98E+00	1.40E-06	Down	-2.95E+00	5.68E-09	Down	-1.02E+00	6.12E-01		-1.09E+00	5.51E-01										
Unigene90259_All	387	0.00	0.00	0.00	2.19	0.18	1.05	0.44	0.54	0.31	null	null		null	null		-3.62E+00	1.47E-04	Down	-1.06E+00	1.81E-01		3.05E-01	8.35E-01		-5.01E-01	7.45E-01										
Unigene9026_All	803	0.00	0.00	0.13	0.00	0.00	0.00	1.00	3.44	27.09	null	null		7.05E+00	3.86E-01		null	null		null	null		1.78E+00	1.40E-06	Up	4.76E+00	2.23E-127	Up	Unigene9026_All|gi|224067296|ref|XP_002302453.1|//8.00E-78//cytochrome P450 allene oxide synthase [Populus trichocarpa] >gi|222844179|gb|EEE81726.1| cytochrome P450 allene oxide synthase [Populus trichocarpa]	Unigene9026_All//8.00E-64//AT5G42650| AOS (ALLENE OXIDE SYNTHASE); allene oxide synthase/ hydro-lyase/ oxygen binding	Unigene9026_All//0.00E+00//TC132926		ko00592|alpha-Linolenic acid metabolism		nr +
Unigene90263_All	394	0.27	0.39	0.27	3.79	0.26	0.23	1.29	0.21	0.10	5.39E-01	7.77E-01		2.53E-02	9.96E-01		-3.85E+00	4.17E-08	Down	-4.05E+00	3.05E-07	Down	-2.60E+00	2.04E-02		-3.67E+00	3.75E-03		Unigene90263_All|gi|297801560|ref|XP_002868664.1|//5.00E-07//nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314500|gb|EFH44923.1| nodulin MtN21 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene90263_All//2.00E-08//AT3G28050| nodulin MtN21 family protein	Unigene90263_All//3.00E-51//TC148144			GO:0044464	nr -
Unigene90264_All	394	0.00	0.00	0.00	1.39	0.00	0.00	1.93	0.42	0.00	null	null		null	null		-1.04E+01	4.00E-04	Down	-1.04E+01	1.51E-03		-2.19E+00	7.77E-03		-1.09E+01	8.87E-06	Down									ESTscan -
Unigene90266_All	398	0.26	0.00	0.00	15.27	1.38	0.00	0.00	0.00	0.00	-8.04E+00	3.63E-01		-8.04E+00	3.85E-01		-3.46E+00	1.85E-29	Down	-1.39E+01	1.55E-38	Down	null	null		null	null		Unigene90266_All|gi|224135399|ref|XP_002327208.1|//8.00E-08//predicted protein [Populus trichocarpa] >gi|222835578|gb|EEE74013.1| predicted protein [Populus trichocarpa]						nr +
Unigene9027_All	408	2.05	2.11	0.13	0.73	0.93	0.89	0.62	0.31	1.27	4.12E-02	9.74E-01		-3.97E+00	9.07E-04	Down	3.42E-01	8.35E-01		2.74E-01	8.32E-01		-1.02E+00	4.94E-01		1.03E+00	2.53E-01										
Unigene90272_All	414	0.25	1.96	0.00	2.17	0.25	0.22	0.92	0.00	0.48	2.95E+00	3.28E-03		-7.98E+00	3.85E-01		-3.12E+00	2.80E-04	Down	-3.31E+00	5.79E-04	Down	-9.84E+00	6.16E-03		-9.34E-01	3.79E-01		Unigene90272_All|gi|240255733|ref|NP_192232.4|//1.00E-43//ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene90272_All//8.00E-45//AT4G00230| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding				GO:0004672//GO:0006464//GO:0008037//GO:0030246//GO:0032559	nr +
Unigene90274_All	418	0.00	0.00	0.00	5.72	0.00	0.00	0.00	0.00	0.00	null	null		null	null		-1.25E+01	6.89E-18	Down	-1.25E+01	5.44E-15	Down	null	null		null	null		Unigene90274_All|gi|7444442|pir||T02867//5.00E-16//gag/pol polyprotein - maize retrotransposon Hopscotch >gi|531389|gb|AAA57005.1| copia-like retrotransposon Hopscotch polyprotein [Zea mays]						nr +

Unigene90276_All	426	0.25	0.00	0.00	4.33	0.73	1.38	0.00	0.00	0.00	-7.94E+00	3.63E-01			-7.94E+00	3.85E-01		-2.57E+00	7.33E-07	Down	-1.65E+00	9.75E-04	Down	null	null		null	null		Unigene90276_All//gi|124360377|gb|ABN08390.1|//6.00E-19//Harpin-induced 1 [Medicago truncatula]	Unigene90276_All//8.00E-08//AT5G11890| FUNCTIONS IN: molecular_function unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17620.1); Has 455 Blast hits to 454 proteins in 19 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 453; Viruses - 0; Other Eukaryotes - 2 (source: NCBI BLink).	Unigene90276_All//2.00E-37//gi|13354232|gb|BG444580.1|BG444580		ko03040|Spliceosome	GO:0016020	nr +
Unigene90278_All	435	0.00	0.00	0.00	1.95	1.35	0.00	0.87	0.10	0.64	null	null			null	null		-5.33E-01	4.90E-01		-1.09E+01	2.43E-05	Down	-3.19E+00	3.11E-02		-4.48E-01	6.41E-01					Unigene90278_All//5.00E-07//TC143852				
Unigene90279_All	437	2.39	0.00	0.24	4.56	2.68	2.07	1.35	0.57	0.00	-1.12E+01	3.80E-06	Down	-3.30E+00	4.58E-04	Down	-7.67E-01	8.22E-02		-1.14E+00	1.33E-02		-1.24E+00	1.54E-01		-1.04E+01	1.41E-04	Down				Unigene90279_All//5.00E-07//TC178033				
Unigene90284_All	453	0.69	1.01	0.71	1.87	0.15	0.70	0.56	0.00	0.09	5.39E-01	6.01E-01		2.54E-02	1.00E+00		-3.62E+00	1.47E-04	Down	-1.42E+00	7.33E-02		-9.13E+00	4.02E-02		-2.67E+00	1.15E-01					Unigene90284_All//9.00E-12//TC153171				ESTscan -
Unigene90285_All	455	0.00	0.00	0.00	4.93	1.89	0.60	0.00	0.00	0.09	null	null		null	null		-1.38E+00	7.07E-04	Down	-3.05E+00	1.55E-08	Down	null	null		6.45E+00	6.32E-01		Unigene90285_All//gi|79602205|ref|NP_973837.2|//2.00E-59//binding / zinc ion binding [Arabidopsis thaliana] >gi|48310218|gb|AAT41783.1|At2g26695 [Arabidopsis thaliana] >gi|50198944|gb|AAT70475.1|At2g26695 [Arabidopsis thaliana]	Unigene90285_All//2.00E-60//AT2G26695| binding / zinc ion binding			GO:0044464//GO:0046914	nr +
Unigene90286_All	456	1.61	0.00	0.00	2.29	0.91	0.20	0.65	0.55	0.17	-1.06E+01	2.11E-04	Down	-1.06E+01	4.12E-04	Down	-1.34E+00	3.95E-02		-3.53E+00	9.33E-05	Down	-2.39E-01	8.39E-01		-1.89E+00	1.68E-01		Unigene90286_All//gi|297738811|emb|CBI28056.3|//8.00E-26//unnamed protein product [Vitis vinifera]					nr +
Unigene90287_All	457	0.46	0.00	0.23	3.38	1.13	0.40	0.00	0.00	0.00	-8.84E+00	1.20E-01		-9.75E-01	6.19E-01		-1.58E+00	2.26E-03		-3.10E+00	4.09E-06	Down	null	null		null	null		Unigene90287_All//gi|4235641|gb|AAD13301.1|//4.00E-35//NL0D [Solanum lycopersicum]	Unigene90287_All//4.00E-27//AT3G11080| AtRLP55 (Receptor Like Protein 35); kinase/ protein binding		ko04626|Plant-pathogen interaction		nr -
Unigene90288_All	467	1.01	0.00	0.46	4.27	1.18	1.06	0.27	0.18	0.09	-9.98E+00	5.53E-03		-1.14E+00	3.32E-01		-1.85E+00	4.61E-05	Down	-2.00E+00	5.61E-05	Down	-6.02E-01	7.64E-01		-1.67E+00	4.75E-01					Unigene90288_All//0.00E+00//TC177604				ESTscan -
Unigene90293_All	470	1.56	0.43	0.23	1.70	1.76	0.00	0.00	0.00	0.00	-1.85E+00	4.08E-02		-2.78E+00	1.04E-02		5.23E-02	9.64E-01		-1.07E+01	4.89E-05	Down	null	null		null	null		Unigene90293_All//gi|224066499|ref|XP_002302110.1|//4.00E-24//copalyl diphosphate synthase [Populus trichocarpa] >gi|222843836|gb|EEE81383.1|copalyl diphosphate synthase [Populus trichocarpa]	Unigene90293_All//2.00E-17//AT4G02780| GA1 (GA REQUIRING 1); ent-copalyl diphosphate synthase/ magnesium ion binding		ko00904|Diterpenoid biosynthesis	GO:0016853	nr -
Unigene90295_All	471	2.89	1.29	0.00	2.12	1.90	2.49	1.80	1.77	0.25	-1.16E+00	4.51E-02		-1.15E+01	1.93E-07	Down	-1.54E-01	8.40E-01		2.37E-01	7.09E-01		-1.66E-02	1.02E+00		-2.82E+00	5.38E-04	Down	Unigene90295_All//gi|30684030|ref|NP_568262.2|//2.00E-36//DGS1 (DGD1 SUPPRESSOR 1) [Arabidopsis thaliana] >gi|30725404|gb|AAP37724.1|At5g12290 [Arabidopsis thaliana]	Unigene90295_All//1.00E-37//AT5G12290| DGS1 (DGD1 SUPPRESSOR 1)	Unigene90295_All//4.00E-54//DR463224		GO:0009247//GO:0031966//GO:0032991//GO:0042743	nr -
Unigene90296_All	473	0.00	0.00	0.00	2.63	0.51	1.34	0.00	0.00	0.08	null	null		null	null		-2.37E+00	2.03E-04	Down	-9.78E-01	1.14E-01		null	null		6.40E+00	6.32E-01		Unigene90296_All//gi|89179421|gb|ABD63156.1|//3.00E-46//Retrotransposon gag protein [Asparagus officinalis]		Unigene90296_All//3.00E-129//TC135287		GO:0003676//GO:0006259	nr +
Unigene9030_All	495	0.00	0.00	0.22	0.20	0.07	0.00	2.90	5.32	6.12	null	null		7.75E+00	3.86E-01		-1.53E+00	5.81E-01		-7.65E+00	3.89E-01		8.73E-01	1.20E-02		1.07E+00	6.52E-04	Up								
Unigene90302_All	498	0.00	0.00	0.00	2.70	1.04	0.54	0.00	0.00	0.08	null	null		null	null		-1.38E+00	1.31E-02		-2.31E+00	4.01E-04	Down	null	null		6.32E+00	6.32E-01		Unigene90302_All//gi|18423700|ref|NP_568819.1|//8.00E-18//MYB120 (MYB DOMAIN PROTEIN 120); DNA binding / transcription factor [Arabidopsis thaliana]	Unigene90302_All//9.00E-10//AT1G11460| MYB65 (MYB DOMAIN PROTEIN 65); DNA binding / transcription factor	Unigene90302_All//1.00E-07//TC172593	MYB	ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko03020|RNA polymerase//ko00565|Ether lipid metabolism		nr -
Unigene90303_All	501	0.63	0.71	0.43	3.28	0.41	0.18	0.17	0.08	0.00	1.76E-01	8.82E-01		-5.60E-01	6.62E-01		-2.99E+00	3.56E-07	Down	-4.19E+00	4.25E-08	Down	-1.02E+00	7.19E-01		-7.40E+00	3.52E-01					Unigene90303_All//0.00E+00//TC144825				
Unigene90307_All	531	1.18	0.10	0.20	5.44	2.20	0.00	0.16	0.47	0.90	-3.63E+00	5.06E-03		-2.56E+00	2.72E-02		-1.30E+00	1.88E-04	Down	-1.24E+01	3.74E-18	Down	1.57E+00	3.26E-01		2.50E+00	2.51E-02		Unigene90307_All//gi|224114195|ref|XP_002332424.1|//4.00E-46//cytokinin oxidase [Populus trichocarpa] >gi|222822377|gb|EEE70854.1|cytokinin oxidase [Populus trichocarpa]	Unigene90307_All//1.00E-40//AT2G41510| CKX1 (CYTOKININ OXIDASE/DEHYDROGENASE 1); cytokinin dehydrogenase		ko00908|Zeatin biosynthesis	GO:0009690//GO:0009888//GO:0016645//GO:0030554//GO:0043231	nr -
Unigene9031_All	555	0.47	0.46	0.38	1.44	0.56	0.81	3.28	1.05	1.44	-4.63E-02	9.86E-01		-2.97E-01	8.31E-01		-1.36E+00	7.73E-02		-8.19E-01	3.19E-01		-1.64E+00	3.51E-04	Down	-1.19E+00	4.84E-03		Unigene9031_All//gi|20161609|dbj|BAB90529.1|//7.00E-65//B1065G12.11 [Oryza sativa Japonica Group]	Unigene9031_All//6.00E-59//AT1G24340| emb2421 (embryo defective 2421); monooxygenase/ oxidoreductase		ko00130|Ubiquinone and other terpenoid-quinone biosynthesis		nr -
Unigene90310_All	587	0.27	0.00	0.18	1.44	0.12	0.08	0.00	0.00	0.00	-8.06E+00	2.13E-01		-5.60E-01	7.73E-01		-3.62E+00	1.47E-04	Down	-4.23E+00	2.18E-04	Down	null	null		null	null		Unigene90310_All//gi|28416861|gb|AA042961.1|//2.00E-14//At2g14045 [Arabidopsis thaliana]	Unigene90310_All//9.00E-16//AT2G14045| unknown protein	Unigene90310_All//0.00E+00//TC151925			nr +
Unigene90314_All	887	0.59	0.46	0.00	10.73	4.50	6.06	1.24	0.24	0.54	-3.68E-01	6.82E-01		-9.20E+00	4.73E-03		-1.25E+00	1.43E-12	Down	-8.24E-01	6.01E-06		-2.40E+00	4.11E-04	Down	-1.20E+00	3.41E-02		Unigene90314_All//gi|4335763|gb|AAD17410.1|//7.00E-56//expressed protein [Arabidopsis thaliana] >gi|29028804|gb|AAO64781.1|At2g03350 [Arabidopsis thaliana]	Unigene90314_All//2.00E-49//AT2G03350| unknown protein	Unigene90314_All//0.00E+00//gi|164272724|gb|ES823066.1|ES823066			nr +
Unigene9032_All	454	3.57	0.67	1.76	0.00	0.46	0.00	0.09	0.00	0.00	-2.42E+00	7.50E-05	Down	-1.02E+00	6.14E-02		8.83E+00	1.56E-01		null	null		-6.54E+00	6.37E-01		-6.54E+00	5.96E-01		Unigene9032_All//gi|145334539|ref|NP_001078615.1|//3.00E-29//SCPL34; serine-type carboxypeptidase [Arabidopsis thaliana]	Unigene9032_All//2.00E-30//AT5G23210| SCPL34; serine-type carboxypeptidase				nr +
Unigene90329_All	352	76.99	136.03	88.95	149.02	153.49	132.41	96.21	124.32	46.29	8.21E-01	3.33E-25		2.08E-01	4.91E-02		4.27E-02	6.36E-01		-1.71E-01	2.71E-02		3.70E-01	2.45E-07		-1.06E+00	3.58E-34	Down	Unigene90329_All//gi|34541994|gb|AAQ74889.1|//3.00E-25//A1-induced protein [Gossypium hirsutum]	Unigene90329_All//8.00E-24//AT5G19140| AILP1	Unigene90329_All//8.00E-132//ES808652			GO:0009725//GO:0010038//GO:0016020	nr +
Unigene9033_All	1156	0.23	0.00	0.00	1.94	1.04	0.39	6.44	0.87	1.14	-7.82E+00	6.64E-02		-7.82E+00	8.50E-02		-8.95E-01	2.75E-02		-2.31E+00	1.80E-06	Down	-2.89E+00	3.08E-29	Down	-2.50E+00	6.58E-26	Down	Unigene9033_All//gi|224144595|ref|XP_002325344.1|//2.00E-32//BED finger-nbs-lrr resistance protein [Populus trichocarpa] >gi|222862219|gb|EEE99725.1|BED finger-nbs-lrr resistance protein [Populus trichocarpa]	Unigene9033_All//2.00E-08//AT4G27190| disease resistance protein (NBS-LRR class), putative	Unigene9033_All//1.00E-65//CO080430		ko04626|Plant-pathogen interaction		nr -
Unigene9034_All	575	0.00	12.43	3.98	0.00	0.00	0.00	0.00	0.00	0.00	1.36E+01	7.81E-41	Up	1.20E+01	1.27E-12	Up	null	null		null	null		null	null		null	null		Unigene9034_All//gi|115466344|ref|NP_001056771.1|//1.00E-08//Os06g0142700 [Oryza sativa Japonica Group] >gi|113594811|dbj|BAF18685.1|Os06g0142700 [Oryza sativa Japonica Group]	Unigene9034_All//5.00E-09//AT1G80230| cytochrome c oxidase family protein			ko00190|Oxidative phosphorylation		nr +
Unigene90344_All	497	0.00	0.00	0.00	0.00	0.07	0.00	1.02	0.00	0.08	null	null		null	null		6.11E+00	8.11E-01		null	null		-1.00E+01	8.88E-04	Down	-3.67E+00	3.75E-03		Unigene90344_All//gi|4512122|gb|AAD21624.1|//9.00E-41//chorismate mutase 3 [Arabidopsis thaliana]	Unigene90344_All//1.00E-40//AT1G69370| CM3 (chorismate mutase 3); chorismate mutase	Unigene90344_All//0.00E+00//ES821004		ko00400|Phenylalanine, tyrosine and tryptophan biosynthesis	GO:0004601//GO:0006568//GO:0008652//GO:0016866//GO:0043231//GO:0043648//GO:0044444//GO:0050896	nr +
Unigene90358_All	230	15.01	11.02	7.87	49.16	49.41	53.61	123.16	51.79	48.50	-4.47E-01	1.87E-01		-9.32E-01	7.43E-03		7.10E-03	9.74E-01		1.25E-01	5.23E-01		-1.25E+00	2.59E-36	Down	-1.34E+00	8.65E-42	Down				Unigene90358_All//2.00E-66//gi|11208622|gb|BF277552.1|BF277552				
Unigene9037_All	325	0.00	0.00	0.00	0.15	1.17	0.00	29.40	63.79	11.40	null	null		null	null		2.93E+00	8.15E-02		-7.26E+00	6.13E-01		1.12E+00	1.62E-22	Up	-1.37E+00	4.98E-15	Down	Unigene9037_All//gi|297810911|ref|XP_002873339.1|//1.00E-09//L-asparaginase [Arabidopsis lyrata subsp. lyrata] >gi|297319176|gb|EFH49598.1|L-asparaginase [Arabidopsis lyrata subsp. lyrata]	Unigene9037_All//1.00E-10//AT5G08100| L-asparaginase / L-asparagine amidohydrolase	Unigene9037_All//7.00E-89//TC143860			nr -
Unigene90375_All	689	1.52	1.32	1.24	3.40	2.60	2.49	4.23	1.27	1.68	-1.98E-01	7.41E-01		-2.97E-01	6.41E-01		-3.87E-01	3.73E-01		-4.48E-01	3.12E-01		-1.73E+00	1.04E-06	Down	-1.34E+00	4.84E-05	Down	Unigene90375_All//gi|18402797|ref|NP_565730.1|//2.00E-39//TEJ (Sanskrit for 'bright'); poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana] >gi|75206423|sp|Q9SKB3.2|PARG1_ARATH RecName: Full=Poly(ADP-ribose) glycohydrolase 1 >gi|14701908|gb|AAK72256.1|AF394690_1 poly(ADP-ribose) glycohydrolase [Arabidopsis thaliana]	Unigene90375_All//5.00E-38//AT2G31870| TEJ (Sanskrit for 'bright'); poly(ADP-ribose) glycohydrolase	Unigene90375_All//0.00E+00//ES810017		GO:0004553//GO:0006952//GO:0008152	nr -
Unigene9038_All	537	0.58	54.82	15.17	0.00	0.51	0.17	0.00	0.00	0.30	6.55E+00	7.67E-158	Up	4.70E+00	3.88E-37	Up	9.00E+00	6.99E-02		7.39E+00	4.69E-01		null	null		8.21E+00	1.39E-01		Unigene9038_All//gi|255587344|ref|XP_002534237.1|//2.00E-21//conserved hypothetical protein [Ricinus communis] >gi|223525657|gb|EEF28144.1|conserved hypothetical protein [Ricinus communis]					nr -
Unigene9039_All	819	5.30	16.39	8.19	14.42	14.04	12.41	50.95	30.82	15.71	1.63E+00	4.38E-21	Up	6.28E-01	7.85E-03		-3.77E-02	8.37E-01		-2.16E-01	2.36E-01		-7.25E-01	6.18E-22		-1.70E+00	5.14E-86	Down				Unigene9039_All//0.00E+00//TC164808				
Unigene9040_All	1099	0.29	32.69	0.19	1.00	1.25	1.32	0.46	0.53	24.03	6.84E+00	6.95E-195	Up	-5.59E-01	6.62E-01		3.30E-01	6.09E-01		3.99E-01	5.06E-01		2.06E-01	8.00E-01		5.70E+00	1.21E-168	Up	Unigene9040_All//gi|224088649|ref|XP_002308508.1|//2.00E-55//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372132|gb|ABQ62997.1|RAP2-like protein [Populus trichocarpa] >gi|222854484|gb|EEE92031.1|AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene9040_All//9.00E-39//AT1G19210| AP2 domain-containing transcription factor, putative	Unigene9040_All//0.00E+00//TC131492	AP2-EREBP		nr +
Unigene9041_All	348	0.00	0.00	0.31	4.87	1.19	2.86	0.12	0.12	0.00	null	null		8.26E+00	3.86E-01		-2.04E+00	6.76E-05	Down	-7.69E-01	1.33E-01		-1.67E-02	9.95E-01		-6.92E+00	5.96E-01		Unigene9041_All//gi|224111064|ref|XP_002315734.1|//4.00E-26//magnesium transporter [Populus trichocarpa] >gi|222864774|gb|EEF01905.1|magnesium transporter [Populus trichocarpa]	Unigene9041_All//2.00E-24//AT5G64560| mgmesium transporter CorA-like family protein (MRS2-2)	Unigene9041_All//1.00E-127//gi|78346228|gb|DT566502.1|DT566502			nr +
Unigene90423_All	294	0.00	1.55	1.27	1.19	0.59	0.31	2.73	0.28	0.41	1.06E+01	7.34E-03		1.03E+01	2.46E-02		-1.02E+00	4.22E-01		-1.95E+00	1.95E-01		-3.26E+00	4.48E-04	Down	-2.75E+00	9.42E-04	Down				Unigene90423_All//6.00E-95//DW241203				
Unigene9044_All	640	0.00	0.32	0.00	0.78	0.65	0.42	0.99	0.39	2.99	8.31E+00	1.34E-01		null	null		-2.70E-01	8.02E-01		-8.78E-01	4.20E-01		-1.34E+00	1.13E-01		1.59E+00	2.36E-04	Up	Unigene9044_All//gi|297808305|ref|XP_002872036.1|//7.00E-35//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297317873|gb|EFH48295.1|zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene9044_All//1.00E-35//AT5G23110| zinc finger (C3HC4-type RING finger) family protein	Unigene9044_All//0.00E+00//TC139214			nr -

Unigene9047_All	647	0.89	5.25	3.21	0.15	0.11	0.42	1.44	1.87	0.49	2.56E+00	6.95E-10	Up	1.85E+00	2.72E-04	Up	-5.33E-01	8.11E-01		1.44E+00	4.08E-01		3.82E-01	5.17E-01		-1.55E+00	1.68E-02		Unigene9047_All//gi|115489504|ref|NP_001067239.1|//7.00E-20//0s12g0608900 [Oryza sativa Japonica Group] >gi|77556479|gb|ABA99275.1| Protein kinase domain containing protein [Oryza sativa (japonica cultivar-group)] >gi|113649746|dbj|BAF30258.1| Os12g0608900 [Oryza sativa Japonica Group]	Unigene9047_All//3.00E-05//AT5G10530| lectin protein kinase, putative	Unigene9047_All//2.00E-29//TC142773				nr -
Unigene9049_All	394	0.00	5.27	2.70	0.25	0.44	1.38	0.00	0.00	0.10	1.24E+01	7.93E-12	Up	1.14E+01	6.58E-06	Up	7.89E-01	7.69E-01		2.44E+00	4.41E-02		null	null		6.66E+00	6.32E-01										
Unigene9052_All	651	2.25	5.68	4.99	0.00	0.90	0.28	0.00	0.00	0.24	1.34E+00	5.94E-05	Up	1.15E+00	1.62E-03		9.81E+00	1.26E-03		8.12E+00	1.93E-01		null	null		7.94E+00	1.39E-01										
Unigene9053_All	828	5765.84	3745.62	6741.33	1526.43	1688.49	1394.01	10.21	18.93	23.19	-6.22E-01	0.00E+00		2.26E-01	3.33E-259		1.46E-01	7.82E-35		-1.31E-01	3.44E-23		8.90E-01	4.29E-12		1.18E+00	2.15E-23	Up	Unigene9053_All//gi|157678732|dbj|BAF80471.1|//5.00E-87//PSI reaction center subunit II [Citrus sinensis] >gi|157678850|dbj|BAF80473.1| PSI reaction center subunit II [Citrus sinensis]	Unigene9053_All//5.00E-74//AT4G02770| PSAD-1 (photosystem I subunit D-1)	Unigene9053_All//0.00E+00//gi|164302646|gb|ES824099.1|ES824099		ko00195|Photosynthesis		nr +
Unigene9055_All	498	0.00	0.00	0.00	0.00	0.28	0.00	2.29	3.86	6.32	null	null		null	null		8.11E+00	3.16E-01		null	null		7.52E-01	7.46E-02		1.46E+00	5.75E-06	Up									
Unigene9056_All	533	1.77	5.70	2.00	44.39	35.34	13.56	0.40	0.00	0.00	1.69E+00	1.34E-05	Up	1.77E-01	7.73E-01		-3.29E-01	2.16E-03		-1.71E+00	8.88E-43	Down	-8.63E+00	7.40E-02		-8.63E+00	5.77E-02		Unigene9056_All//gi|297829114|ref|XP_002882439.1|//1.00E-08//hypothetical protein ARALYDRAFT_896682 [Arabidopsis lyrata subsp. lyrata] >gi|297328279|gb|EFH58698.1| hypothetical protein ARALYDRAFT_896682 [Arabidopsis lyrata subsp. lyrata]	Unigene9056_All//5.00E-07//AT5G26620| unknown protein	Unigene9056_All//0.00E+00//DW510238				nr -
Unigene9057_All	224	23.36	12.44	9.03	21.13	15.53	24.60	53.79	14.37	18.50	-9.09E-01	5.38E-04		-1.37E+00	1.42E-06	Down	-4.44E-01	1.06E-01		2.20E-01	4.56E-01		-1.90E+00	9.09E-29	Down	-1.54E+00	3.16E-22	Down	Unigene9057_All//gi|81076822|gb|AB055398.1|//3.00E-17//40S ribosomal protein S10-like [Solanum tuberosum]	Unigene9057_All//1.00E-15//AT5G52650| 40S ribosomal protein S10 (RPS10C)	Unigene9057_All//3.00E-118//gi|109857482|gb|DW486461.1|DW486461		ko03010|Ribosome		nr -
Unigene90596_All	406	0.00	0.00	0.00	0.25	0.25	0.00	3.33	2.06	7.26	null	null		null	null		5.20E-02	9.64E-01		-7.94E+00	3.89E-01		-6.95E-01	1.84E-01		1.12E+00	4.75E-04	Up	Unigene90596_All//gi|225438177|ref|XP_002262886.1|//3.00E-16//PREDICTED: hypothetical protein [Vitis vinifera]								nr -
Unigene906_All	363	0.00	2.79	0.88	1.92	2.18	2.12	2.45	2.88	44.67	1.14E+01	7.21E-06	Up	9.78E+00	4.42E-02		1.84E-01	8.27E-01		1.39E-01	8.77E-01		2.35E-01	6.99E-01		4.19E+00	8.21E-88	Up	Unigene906_All//gi|225436557|ref|XP_002278089.1|//1.00E-15//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297734951|emb|CBI17185.3| unnamed protein product [Vitis vinifera]								nr -
Unigene90603_All	226	0.23	0.00	0.00	0.22	1.37	0.00	0.37	63.99	1.59	-7.85E+00	5.96E-01		-7.85E+00	6.10E-01		2.64E+00	1.61E-01		-7.78E+00	6.13E-01		7.42E+00	3.37E-98	Up	2.08E+00	1.01E-01										ESTscan +
Unigene9061_All	604	0.00	0.00	0.35	0.74	0.57	1.05	127.12	27.47	39.64	null	null		8.46E+00	1.37E-01		-3.81E-01	7.21E-01		4.96E-01	6.37E-01		-2.21E+00	9.35E-218	Down	-1.68E+00	1.69E-155	Down	Unigene9061_All//gi|3970689|emb|CAA77191.1|//3.00E-53//(+)-delta-cadinene synthase [Gossypium arboreum]	Unigene9061_All//2.00E-25//AT1G33750| terpene synthase/cyclase family protein	Unigene9061_All//0.00E+00//TC142314		ko00904|Diterpenoid biosynthesis//ko00902|Monoterpenoid biosynthesis		nr +
Unigene90619_All	204	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.20	7.23	null	null		null	null		null	null		null	null		-1.68E-02	9.95E-01		5.12E+00	2.34E-09	Up									
Unigene90624_All	540	3.97	0.28	0.69	11.72	9.12	2.17	0.00	0.77	1.33	-3.82E+00	3.43E-09	Down	-2.52E+00	4.25E-06	Down	-3.62E-01	1.30E-01		-2.43E+00	2.50E-18	Down	9.60E+00	3.65E-03		1.04E+01	2.63E-05	Up	Unigene90624_All//gi|87241045|gb|AB032903.1|//7.00E-48//Sodium/hydrogen exchanger [Medicago truncatula]	Unigene90624_All//3.00E-37//AT3G53720| ATCHX20 (CATION/H+ EXCHANGER 20); monovalent cation:proton antiporter/ sodium:hydrogen antiporter				GO:0006810//GO:0044464	nr -
Unigene9064_All	1363	0.15	0.11	0.04	0.40	0.25	0.36	3.54	0.86	6.43	-4.61E-01	7.57E-01		-1.97E+00	3.80E-01		-6.70E-01	4.96E-01		-1.41E-01	8.85E-01		-2.04E+00	4.97E-13	Down	8.63E-01	5.32E-07		Unigene9064_All//gi|224089629|ref|XP_002308787.1|//3.00E-45//f-box family protein [Populus trichocarpa] >gi|222854763|gb|EEE92310.1| f-box family protein [Populus trichocarpa]	Unigene9064_All//4.00E-39//AT4G12560| F-box family protein	Unigene9064_All//1.00E-07//gi|78334773|gb|DT555047.1|DT555047				nr -
Unigene9065_All	861	0.36	0.00	0.00	0.29	0.16	0.05	15.17	3.98	0.97	-8.51E+00	3.62E-02		-8.51E+00	4.87E-02		-8.55E-01	5.72E-01		-2.46E+00	2.22E-01		-1.93E+00	1.10E-31	Down	-3.96E+00	1.52E-69	Down	Unigene9065_All//gi|15225277|ref|NP_180197.1|//2.00E-53//ARSK1 (root-specific kinase 1); kinase [Arabidopsis thaliana]	Unigene9065_All//6.00E-55//AT2G26290| ARSK1 (root-specific kinase 1); kinase	Unigene9065_All//5.00E-24//gi|48827575|gb|CO125965.1|CO125965				nr -
Unigene90653_All	237	5.30	1.28	4.49	133.05	145.30	103.86	159.49	32.45	59.51	-2.05E+00	2.33E-03		-2.38E-01	6.85E-01		1.27E-01	2.23E-01		-3.57E-01	1.51E-04		-2.30E+00	1.09E-112	Down	-1.42E+00	2.34E-60	Down	Unigene90653_All//gi|50313462|gb|AAT74601.1|//9.00E-19//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene90653_All//8.00E-14//AT3G23510| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene90653_All//3.00E-62//gi|31072643|gb|CA992922.1|CA992922			GO:0006629//GO:0008757//GO:0044464	nr -
Unigene90654_All	348	1.95	2.62	4.74	7.59	6.14	2.21	2.92	1.44	0.57	4.23E-01	5.64E-01		1.28E+00	1.97E-02		-3.06E-01	4.57E-01		-1.78E+00	1.47E-05	Down	-1.02E+00	1.00E-01		-2.35E+00	5.84E-04	Down			Unigene90654_All//5.00E-28//gi|21096393|gb|BQ408706.1|BQ408706				ESTscan +
Unigene9068_All	1650	0.00	0.00	0.00	0.00	0.00	0.00	13.91	1.34	0.72	null	null		null	null		null	null		null	null		-3.37E+00	3.33E-103	Down	-4.26E+00	2.58E-128	Down	Unigene9068_All//gi|15229594|ref|NP_188446.1|//1.00E-132//transferase, transferring glycosyl groups [Arabidopsis thaliana]	Unigene9068_All//1.00E-132//AT3G18180| transferase, transferring glycosyl groups	Unigene9068_All//5.00E-07//TC165329				nr -
Unigene9069_All	631	0.66	0.16	0.00	13.42	7.64	4.87	0.94	0.40	0.76	-2.05E+00	1.20E-01		-9.37E+00	1.55E-02		-8.13E-01	9.34E-06		-1.46E+00	1.45E-12	Down	-1.24E+00	1.54E-01		-3.08E-01	6.78E-01		Unigene9069_All//gi|156066385|gb|ABU43058.1|//2.00E-75//NDR1/HIN1-like protein [Vitis vinifera]	Unigene9069_All//5.00E-71//AT5G53730| harpin-induced family protein / HIN1 family protein / harpin-responsive family protein	Unigene9069_All//2.00E-22//TC135625				nr +
Unigene90696_All	206	0.00	0.25	0.00	0.00	0.00	0.22	1.23	1.22	10.64	7.94E+00	6.05E-01		null	null		null	null		7.78E+00	6.81E-01		-1.66E-02	1.02E+00		3.11E+00	7.22E-10	Up	Unigene90696_All//gi|297850166|ref|XP_002892964.1|//1.00E-11//phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata] >gi|297338806|gb|EFH69223.1| phosphoric monoester hydrolase [Arabidopsis lyrata subsp. lyrata]	Unigene90696_All//9.00E-13//AT1G17710| phosphatase	Unigene90696_All//2.00E-50//CO071315				nr -
Unigene9070_All	299	10.85	16.61	12.47	4.83	3.46	6.04	25.45	13.42	11.33	6.14E-01	2.29E-02		2.01E-01	5.79E-01		-4.84E-01	3.91E-01		3.23E-01	5.57E-01		-9.24E-01	1.21E-06		-1.17E+00	1.06E-09	Down			Unigene9070_All//8.00E-150//gi|109874561|gb|DW503535.1|DW503535				
Unigene9072_All	408	0.26	9.81	2.61	0.00	0.17	1.66	1.04	1.95	1.95	5.26E+00	6.36E-20	Up	3.35E+00	3.36E-04	Up	7.40E+00	5.99E-01		1.07E+01	4.18E-04	Up	9.09E-01	2.11E-01		9.14E-01	1.85E-01				Unigene9072_All//3.00E-11//TC158612				
Unigene90722_All	215	0.00	3.54	0.00	0.00	0.80	1.05	1.77	6.61	100.06	1.18E+01	1.75E-04	Up	null	null		9.65E+00	2.26E-01		1.00E+01	1.18E-01		1.90E+00	5.03E-04	Up	5.82E+00	1.73E-138	Up	Unigene90722_All//gi|224117148|ref|XP_002317491.1|//1.00E-11//cytochrome P450 [Populus trichocarpa] >gi|222860556|gb|EEE98103.1| cytochrome P450 [Populus trichocarpa]	Unigene90722_All//4.00E-10//AT3G14620| CYP72A8; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene90722_All//5.00E-73//gi|73863996|gb|DT466735.1|DT466735		ko04146|Peroxisome//ko00592|alpha-Linolenic acid metabolism//ko00071|Fatty acid metabolism//ko01040|Biosynthesis of unsaturated fatty acids	GO:0005506//GO:0008152//GO:0016634	nr -
Unigene9073_All	831	1.57	0.79	0.13	5.16	5.39	2.77	0.15	0.35	0.38	-9.90E-01	9.25E-02		-3.62E+00	2.81E-05	Down	6.34E-02	8.49E-01		-8.95E-01	1.99E-03		1.21E+00	3.92E-01		1.33E+00	2.93E-01		Unigene9073_All//gi|113205145|gb|AAT40194.2|//4.00E-67//Putative microtubule-associated protein, identical [Solanum demissum]	Unigene9073_All//5.00E-35//AT5G51600| PLE (PLEIADE); microtubule binding	Unigene9073_All//1.00E-77//TC178796				nr -
Unigene90730_All	244	0.00	2.91	0.00	0.20	1.55	0.37	0.52	0.17	1.63	1.15E+01	3.30E-04	Up	null	null		2.93E+00	8.15E-02		8.58E-01	7.90E-01		-1.60E+00	5.31E-01		1.65E+00	1.40E-01		Unigene90730_All//gi|297817502|ref|XP_002876634.1|//9.00E-07//nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata] >gi|297322472|gb|EFH52893.1| nucleotidyltransferase [Arabidopsis lyrata subsp. lyrata]	Unigene90730_All//1.00E-07//AT3G61690| unknown protein	Unigene90730_All//5.00E-18//TC146298				nr -
Unigene9075_All	369	0.28	0.00	0.29	1.35	0.56	0.49	4.01	2.04	0.54	-8.15E+00	3.63E-01		2.52E-02	9.96E-01		-1.27E+00	2.22E-01		-1.46E+00	1.93E-01		-9.76E-01	4.65E-02		-2.89E+00	1.35E-06	Down								
Unigene9076_All	337	0.00	0.90	0.63	2.81	8.38	1.88	1.00	0.50	0.00	9.82E+00	4.35E-02		9.30E+00	1.37E-01		1.58E+00	3.25E-05	Up	-5.82E-01	4.37E-01		-1.02E+00	3.99E-01		-9.97E+00	8.12E-03		Unigene9076_All//gi|124359694|gb|AB032361.2|//1.00E-21//Helix-loop-helix DNA-binding [Medicago truncatula]	Unigene9076_All//6.00E-19//AT4G29970| basic helix-loop-helix (bHLH) family protein	Unigene9076_All//5.00E-34//TC158733	bHLH			nr -
Unigene90765_All	450	1.16	0.00	1.66	3.99	2.91	2.21	1.32	0.00	1.24	-1.02E+01	2.91E-03		5.11E-01	5.47E-01		-4.55E-01	3.59E-01		-8.52E-01	8.34E-02		-1.04E+01	2.39E-04	Down	-8.59E-02	9.23E-01		Unigene90765_All//gi|218190665|gb|EEC73092.1|//5.00E-06//hypothetical protein Osl_07068 [Oryza sativa Indica Group]								nr -
Unigene9079_All	341	0.92	0.00	0.00	2.19	0.00	0.79	1.49	0.49	0.23	-9.85E+00	3.62E-02		-9.85E+00	4.87E-02		-1.11E+01	1.50E-05	Down	-1.46E+00	9.03E-02		-1.60E+00	1.07E-01		-2.67E+00	1.37E-02				Unigene9079_All//4.00E-16//DT457021				
Unigene9080_All	581	0.27	0.17	0.37	0.17	0.41	0.16	4.58	5.97	10.56	-6.32E-01	7.25E-01		4.40E-01	7.74E-01		1.27E+00	5.31E-01		-1.41E-01	9.45E-01		3.81E-01	2.24E-01		1.20E+00	2.91E-08	Up			Unigene9080_All//4.00E-08//TC149710				ESTscan -
Unigene9083_All	771	0.00	0.00	0.00	0.00	0.00	0.00	4.77	3.31	1.19	null	null		null	null		null	null		null	null		-5.29E-01	6.87E-02		-2.01E+00	2.94E-10	Down			Unigene9083_All//2.00E-38//TC141618				
Unigene9086_All	492	1.49	0.62	1.41	5.87	6.09	5.97	2.06	0.68	0.16	-1.27E+00	1.36E-01		-8.15E-02	9.29E-01		5.23E-02	9.07E-01		2.30E-02	9.48E-01		-1.60E+00	1.27E-02		-3.67E+00	1.15E-05	Down	Unigene9086_All//gi|255540963|ref|XP_002511546.1|//1.00E-09//zinc finger protein, putative [Ricinus communis] >gi|223550661|gb|EEF52148.1| zinc finger protein, putative [Ricinus communis]		Unigene9086_All//0.00E+00//TC149727				nr +
Unigene909_All	1385	2.61	3.37	1.35	6.62	2.83	3.62	3.24	1.30	1.47	3.69E-01	2.03E-01		-9.54E-01	4.95E-03		-1.22E+00	1.06E-11	Down	-8.71E-01	2.97E-06		-1.32E+00	6.78E-07	Down	-1.14E+00	6.96E-06	Down	Unigene909_All//gi|6273383|gb|AAF06346.1|AF195653_1|//1.00E-111//SCUTL1 [Vitis vinifera]	Unigene909_All//4.00E-96//AT4G38670| pathogenesis-related thaumatin family protein	Unigene909_All//0.00E+00//gi|78333144|gb|DT553418.1|DT553418				nr -
Unigene9092_All	230	2.05	6.39	7.87	0.87	0.30	0.79	1.84	0.73	0.00	1.64E+00	5.06E-03		1.94E+00	4.89E-04	Up	-1.53E+00	4.13E-01		-1.41E-01	9.33E-01		-1.34E+00	2.24E-01		-1.08E+01	2.14E-03		Unigene9092_All//gi|19073340|gb|AAL84768.1|AF475286_1|//2.00E-26//pathogenesis-related protein 1-1a [Cucumis sativus]	Unigene9092_All//5.00E-26//AT3G19690| pathogenesis-related protein, putative			ko04626|Plant-pathogen interaction		nr -
Unigene9093_All	361	1.30	0.28	1.18	1.79	1.62	0.50	7.26	4.05	2.10	-2.22E+00	7.75E-02		-1.45E-01	8.89E-01		-1.46E-01	8.39E-01		-1.84E+00	6.00E-02		-8.42E-01	1.56E-02		-1.79E+00	1.30E-06	Down	Unigene9093_All//gi|115480143|ref|NP_001063665.1|//4.00E-26//Os09g0515200 [Oryza sativa Japonica Group] >gi|8671512|dbj|BAA96839.1| beta 7 subunit of 20S proteasome [Oryza sativa Japonica Group] >gi|50725360|dbj|BAD34432.1| beta 7 subunit of 20S proteasome [Oryza sativa Japonica Group] >gi|113631898|dbj|BAF25579.1| Os09g0515200 [Oryza sativa Japonica Group]	Unigene9093_All//9.00E-18//AT1G56450| PBG1; peptidase/ threonine-type endopeptidase	Unigene9093_All//2.00E-151//BG442434		ko03050|Proteasome		nr -
Unigene90941_All	346	2.57	0.29	0.00	0.86	1.89	0.91	0.00	0.00	0.00	-3.13E+00	1.19E-03		-1.13E+01	6.29E-05	Down	1.13E+00	2.38E-01		8.10E-02	9.49E-01		null	null		null	null		Unigene90941_All//gi|15239103|ref|NP_196158.1|//3.00E-37//LAC12 (laccase 12); laccase [Arabidopsis thaliana] >gi|75334018|sp|Q9FLB5.1|LAC12_ARATH RecName: Full=Laccase-12; AltName: Full=Benzenediol:oxygen oxidoreductase 12; AltName: Full=Urishiol oxidase 12; AltName: Full=Diphenol oxidase 12; Flags: Precursor >gi|10176751|dbj|BAB09982.1| laccase (diphenol oxidase) [Arabidopsis thaliana]	Unigene90941_All//1.00E-38//AT5G05390| LAC12 (laccase 12); laccase	Unigene90941_All//3.00E-32//TC147312		ko00910|Nitrogen metabolism//ko00053|Ascorbate and aldarate metabolism	GO:0005576//GO:0009808//GO:0010038//GO:0016682//GO:0031410//GO:0004914	nr -
Unigene90986_All	228	0.00	0.44	0.70	0.00	0.45	0.79	162.44	58.11	404.15	8.80E+00	3.78E-01		9.45E+00	2.33E-01		8.82E+00	4.51E-01		9.63E+00	1.93E-01		-1.48E+00	3.96E-61	Down	1.31E+00	2.19E-128	Up	Unigene90986_All//gi|49999825|dbj|BAF65033.1|//2.00E-08//cannabidiolic acid synthase [Cannabis sativa]	Unigene90986_All//1.00E-05//AT5G44410| FAD-binding domain-containing protein	Unigene90986_All//4.00E-34//TC159819				nr -
Unigene90995_All	562	1.96	0.09	0.57	6.65	3.55	2.25	1.66	0.89	0.14	-4.44E+00	2.08E-05	Down	-1.78E+00	1.57E-02		-9.04E-01	2.33E-03		-1.56E+00	2.01E-06	Down	-8.91E-01	1.72E-01		-3.55E+00	3.97E-05	Down								

Unigene910_All	1438	12.59	16.38	15.55	18.22	19.40	16.43	6.26	4.65	3.10	3.80E-01	7.76E-04		3.05E-01	1.36E-02		9.02E-02	4.80E-01		-1.50E-01	2.19E-01		-4.29E-01	1.32E-02		-1.01E+00	3.62E-09	Down	Unigene910_All//gi|30692042|ref|NP_195579.2|//1.00E-115//pathogenesis-related thaumatin family protein [Arabidopsis thaliana] >gi|186517488|ref|NP_001119140.1| pathogenesis-related thaumatin family protein [Arabidopsis thaliana]	Unigene910_All//1.00E-114//AT4G38670| pathogenesis-related thaumatin family protein	Unigene910_All//0.00E+00//gi|164290483|gb|ES844191.1|ES844191			GO:0009607//GO:0031224	nr -
Unigene9100_All	952	0.77	0.00	0.00	1.10	0.40	0.19	0.76	0.44	3.72	-9.59E+00	2.11E-04	Down	-9.59E+00	4.12E-04	Down	-1.47E+00	2.48E-02		-2.53E+00	1.22E-03		-7.82E-01	3.10E-01		2.30E+00	1.81E-11	Up	Unigene9100_All//gi|297796091|ref|XP_002869930.1|//4.00E-66//pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297311765|gb|EFH42189.1| pentatricopeptide repeat-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene9100_All//5.00E-64//AT5G32850| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene91004_All	230	0.00	0.00	0.69	0.00	4.04	0.00	572.62	525.17	1157.75	null	null		9.44E+00	2.33E-01		1.20E+01	1.03E-05	Up	null	null		-1.25E-01	2.91E-03		1.02E+00	4.63E-245	Up	Unigene91004_All//gi|65998365|gb|AS73001.2|//2.00E-29//dirigent-like protein [Gossypium barbadense]	Unigene91004_All//3.00E-65//AT2G21110| disease resistance-responsive family protein	Unigene91004_All//1.00E-101//gi|84156433|gb|DN817659.1|DN817659				nr -
Unigene9101_All	432	17.32	6.10	14.42	0.00	0.32	0.00	0.00	0.00	0.00	-1.51E+00	6.46E-11	Down	-2.64E-01	2.60E-01		8.32E+00	3.16E-01		null	null		null	null		null	null		Unigene9101_All//gi|297842887|ref|XP_002889325.1|//2.00E-20//F20B17.20 [Arabidopsis lyrata subsp. lyrata] >gi|297335166|gb|EFH65584.1| F20B17.20 [Arabidopsis lyrata subsp. lyrata]	Unigene9101_All//4.00E-20//AT1G79770| unknown protein	Unigene9101_All//1.00E-69//ES842540				nr -
Unigene91039_All	309	0.00	0.00	0.00	3.55	2.34	0.44	0.00	0.00	0.00	null	null		null	null		-6.00E-01	3.53E-01		-3.02E+00	2.14E-04	Down	null	null		null	null									
Unigene9105_All	405	0.39	5.38	0.53	1.11	0.43	1.90	1.25	0.72	1.48	3.79E+00	3.54E-09	Up	4.40E-01	7.74E-01		-1.38E+00	2.16E-01		7.76E-01	3.78E-01		-7.94E-01	4.02E-01		2.36E-01	7.56E-01					Unigene9105_All//7.00E-111//CO079694					
Unigene9106_All	404	0.00	0.25	0.00	0.74	0.68	0.78	2.20	4.66	7.49	7.97E+00	3.78E-01		null	null		-1.18E-01	9.00E-01		8.10E-02	9.49E-01		1.08E+00	1.13E-02		1.77E+00	2.66E-07	Up				Unigene9106_All//2.00E-27//DW009062					
Unigene9107_All	536	1.76	0.19	0.40	49.54	43.04	42.21	4.42	5.07	1.78	-3.22E+00	6.76E-04	Down	-2.14E+00	1.16E-02		-2.03E-01	6.30E-02		-2.31E-01	3.74E-02		1.98E-01	6.23E-01		-1.31E+00	3.80E-04	Down	Unigene9107_All//gi|18390725|ref|NP_563780.1|//1.00E-41//LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6) [Arabidopsis thaliana] >gi|56236136|gb|AAY84524.1| At1g07090 [Arabidopsis thaliana] >gi|88193786|gb|ABD42982.1| At1g07090 [Arabidopsis thaliana]	Unigene9107_All//7.00E-43//AT1G07090| LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6)	Unigene9107_All//0.00E+00//DW520601				nr -
Unigene9110_All	684	1.07	1.48	2.34	3.86	4.88	3.63	2.23	0.55	0.35	4.68E-01	4.89E-01		1.12E+00	4.27E-02		3.39E-01	3.60E-01		-8.80E-02	8.32E-01		-2.02E+00	1.50E-04	Down	-2.67E+00	2.74E-06	Down				Unigene9110_All//2.00E-56//ES799343					
Unigene9112_All	760	10.74	2.33	4.48	0.52	1.18	0.12	0.00	0.00	0.00	-2.20E+00	2.09E-19	Down	-1.26E+00	9.03E-09	Down	1.17E+00	1.33E-01		-2.14E+00	1.26E-01		null	null		null	null		Unigene9112_All//gi|15227472|ref|NP_181725.1|//2.00E-41//ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding [Arabidopsis thaliana] >gi|45517524|gb|AAK62652.1| At2g41940/T6D20.16 [Arabidopsis thaliana] >gi|15810111|gb|AAL06981.1| At2g41940/T6D20.16 [Arabidopsis thaliana]	Unigene9112_All//6.00E-40//AT2G41940| ZFP8 (ZINC FINGER PROTEIN 8); nucleic acid binding / transcription factor/ zinc ion binding	Unigene9112_All//0.00E+00//gi|164264147|gb|ES802869.1|ES802869	C2H2			nr +
Unigene91137_All	296	7.95	8.73	5.94	750.58	715.11	406.01	16.43	34.31	17.63	1.34E-01	7.23E-01		-4.22E-01	3.51E-01		-6.98E-02	5.76E-02		-8.87E-01	8.49E-142		1.06E+00	1.29E-10	Up	1.02E-01	6.71E-01		Unigene91137_All//gi|224071978|ref||XP_002303604.1|//2.00E-10//predicted protein [Populus trichocarpa] >gi|118481859|gb|ABK92866.1| unknown [Populus trichocarpa] >gi|118484209|gb|ABK93985.1| unknown [Populus trichocarpa] >gi|222841036|gb|EEE78583.1| predicted protein [Populus trichocarpa]		Unigene91137_All//3.00E-66//gi|62295621|gb|DN779264.1|DN779264				nr +
Unigene9115_All	379	7.32	2.14	2.53	7.23	3.27	3.93	0.78	0.77	1.05	-1.77E+00	1.62E-05	Down	-1.53E+00	2.23E-04	Down	-1.14E+00	1.38E-03		-8.78E-01	2.06E-02		-1.65E-02	1.02E+00		4.29E-01	6.61E-01					Unigene9115_All//4.00E-07//TC176342					
Unigene9116_All	209	3.25	0.00	3.06	2.86	3.62	3.46	0.00	0.00	0.19	-1.17E+01	4.09E-04	Down	-9.01E-02	9.22E-01		3.42E-01	7.20E-01		2.74E-01	7.42E-01		null	null		7.57E+00	6.31E-01		Unigene9116_All//gi|297743367|emb|CBI36234.3|//3.00E-06//unnamed protein product [Vitis vinifera]						nr +
Unigene9117_All	404	3.37	1.88	2.50	2.34	2.39	0.11	5.34	4.66	1.68	-8.40E-01	1.39E-01		-4.27E-01	4.72E-01		2.68E-02	9.87E-01		-4.39E+00	5.96E-05	Down	-1.97E-01	6.41E-01		-1.67E+00	3.80E-05	Down	Unigene9117_All//gi|224167923|ref|XP_002339089.1|//1.00E-07//predicted protein [Populus trichocarpa] >gi|222874365|gb|EEF11496.1| predicted protein [Populus trichocarpa]		Unigene9117_All//5.00E-47//CO080232				nr -
Unigene9118_All	443	15.94	109.12	51.57	14.06	8.86	14.48	0.29	0.57	0.36	2.77E+00	3.86E-145	Up	1.69E+00	2.67E-36	Up	-6.66E-01	2.67E-03		4.26E-02	8.86E-01		9.84E-01	5.17E-01		3.29E-01	8.49E-01		Unigene9118_All//gi|38345317|emb|CAE03390.2|//2.00E-21//OSJNBa0004N05.14 [Oryza sativa (japonica cultivar-group)]	Unigene9118_All//2.00E-21//AT1G02205| CER1 (ECERIFERUM 1); octadecanal decarbonylase	Unigene9118_All//2.00E-86//gi|109870542|gb|DW499518.1|DW499518				nr +
Unigene9119_All	242	5.19	0.00	0.22	4.53	2.70	4.29	1.05	0.00	0.00	-1.23E+01	2.54E-07	Down	-4.56E+00	8.14E-06	Down	-7.44E-01	2.45E-01		-7.73E-02	9.16E-01		-1.00E+01	4.02E-02		-1.00E+01	3.03E-02		Unigene9119_All//gi|30684328|ref|NP_850137.1|//9.00E-21//CDC6 (CELL DIVISION CONTROL 6) [Arabidopsis thaliana] >gi|18056480|emb|CAC81074.1| CDC6 protein [Arabidopsis thaliana]	Unigene9119_All//4.00E-22//AT2G29680| CDC6 (CELL DIVISION CONTROL 6)					nr -
Unigene912_All	782	4.01	0.52	4.36	4.33	3.26	2.48	1.03	0.11	0.31	-2.95E+00	1.13E-10	Down	1.19E-01	7.27E-01		-4.11E-01	2.31E-01		-8.03E-01	1.63E-02		-3.26E+00	4.48E-04	Down	-1.75E+00	1.55E-02		Unigene912_All//gi|30696124|ref|NP_564718.2|//4.00E-24//haloacid dehalogenase-like hydrolase family protein [Arabidopsis thaliana]	Unigene912_All//2.00E-25//AT1G46500| haloacid dehalogenase-like hydrolase family protein	Unigene912_All//1.00E-12//TC138034			GO:0009532//GO:0016791//GO:0016868//GO:0019725	nr -
Unigene9120_All	1114	0.09	0.18	0.05	0.45	0.19	0.16	3.80	2.25	0.86	9.54E-01	6.19E-01		-9.74E-01	7.18E-01		-1.27E+00	2.22E-01		-1.46E+00	1.93E-01		-7.54E-01	4.15E-03		-2.14E+00	1.21E-12	Down	Unigene9120_All//gi|115477847|ref|NP_001062519.1|//1.00E-73//Os08g0562300 [Oryza sativa Japonica Group] >gi|113624488|dbj|BAF24433.1| Os08g0562300 [Oryza sativa Japonica Group]	Unigene9120_All//2.00E-74//AT5G22890| zinc finger (C2H2 type) family protein		C2H2			nr -
Unigene9123_All	760	0.00	12.40	8.62	0.00	0.00	0.12	0.00	0.00	0.00	1.36E+01	5.66E-54	Up	1.31E+01	1.48E-36	Up	null	null		6.89E+00	4.68E-01		null	null		null	null		Unigene9123_All//gi|154269258|gb|AB572189.1|//2.00E-80//ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit 1A [Corchorus olitorius]	Unigene9123_All//1.00E-76//AT5G38410| ribulose bisphosphate carboxylase small chain 3B / RuBisCO small subunit 3B (RBCS-3B) (ATS3B)	Unigene9123_All//8.00E-32//gi|109877567|gb|DW506540.1|DW506540		ko00710|Carbon fixation in photosynthetic organisms//ko00630|Glyoxylate and dicarboxylate metabolism		nr -
Unigene91238_All	369	0.00	0.00	0.00	0.00	0.19	0.37	0.23	0.11	2.38	null	null		null	null		7.54E+00	5.98E-01		8.52E+00	3.08E-01		-1.02E+00	7.19E-01		3.37E+00	1.32E-04	Up	Unigene91238_All//gi|259121431|gb|ACV92035.1|//9.00E-37//WRKY transcription factor 33 [(Populus tomentosa x P. bolleana) x P. tomentosa]	Unigene91238_All//2.00E-30//AT2G47260| WRKY23; transcription factor	Unigene91238_All//3.00E-113//DT460920	WRKY	ko04626|Plant-pathogen interaction	GO:0010467//GO:0050896	nr -
Unigene9124_All	626	0.08	0.65	0.60	1.03	0.99	0.79	2.09	0.47	3.25	2.95E+00	5.89E-02		2.83E+00	9.27E-02		-6.31E-02	9.25E-01		-3.82E-01	6.78E-01		-2.16E+00	2.57E-04	Down	6.32E-01	1.08E-01		Unigene9124_All//gi|15235059|ref|NP_196650.1|//9.00E-64//BRI1 (BRASSINOSTEROID INSENSITIVE 1); kinase/ protein binding / protein heterodimerization/ protein homodimerization/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana] >gi|29427562|sp|O22476.1|BRI1_ARATH RecName: Full=Protein BRASSINOSTEROID INSENSITIVE 1; Short=AtBRI1; AltName: Full=Brassinosteroid LRR receptor kinase; Flags: Precursor >gi|2392895|gb|AAC49810.1| brassinosteroid insensitive 1 [Arabidopsis thaliana] >gi|50412156|emb|CAB14675.1| brassinosteroid insensitive 1 gene (BRI1) [Arabidopsis thaliana] >gi|7270924|emb|CAB80603.1| brassinosteroid insensitive 1 gene (BRI1) [Arabidopsis thaliana] >gi|224589653|gb|ACN59359.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene9124_All//3.00E-59//AT4G39400| BRI1 (BRASSINOSTEROID INSENSITIVE 1); kinase/ protein binding / protein heterodimerization/ protein homodimerization/ protein kinase/ protein serine/threonine kinase	Unigene9124_All//4.00E-67//TC145538				nr +
Unigene9125_All	1072	0.00	0.76	0.00	0.42	0.06	0.00	152.48	270.39	39.47	9.56E+00	9.30E-05	Up	null	null		-2.70E+00	3.24E-02		-8.71E+00	5.77E-03		8.26E-01	9.96E-185		-1.95E+00	0.00E+00	Down	Unigene9125_All//gi|224127144|ref|XP_002329411.1|//1.00E-103//alkaloid o-methyltransferase related [Populus trichocarpa] >gi|222870461|gb|EEF07592.1| alkaloid o-methyltransferase related [Populus trichocarpa]	Unigene9125_All//1.00E-44//AT4G35160| O-methyltransferase family 2 protein	Unigene9125_All//0.00E+00//TC157783		ko00940|Phenylpropanoid biosynthesis//ko00944|Flavone and flavonol biosynthesis//ko00402|Benzoxazinoid biosynthesis		nr -
Unigene91250_All	641	0.16	1.90	3.16	0.16	0.54	0.28	0.13	0.00	0.50	3.54E+00	4.02E-05	Up	4.27E+00	6.79E-09	Up	1.79E+00	2.57E-01		8.59E-01	6.93E-01		-7.04E+00	3.95E-01		1.91E+00	1.53E-01		Unigene91250_All//gi|13926307|gb|AAK49620.1|AF372904_1/4.00E-31//AT4g08790/T32A17_100 [Arabidopsis thaliana] >gi|22137058|gb|AAM91374.1| At4g08790/T32A17_100 [Arabidopsis thaliana]	Unigene91250_All//2.00E-32//AT4G08790| nitrilase, putative	Unigene91250_All//0.00E+00//gi|21096340|gb|BQ408653.1|BQ408653			GO:0008152//GO:0010038//GO:0016787//GO:0043231	nr +
Unigene9126_All	857	0.00	7.21	4.97	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	2.70E-35	Up	1.23E+01	1.22E-23	Up	null	null		null	null		null	null		null	null		Unigene9126_All//gi|15224471|ref|NP_178585.1|//1.00E-140//LHCB2.1; chlorophyll binding [Arabidopsis thaliana] >gi|15450349|gb|AAK96468.1| At2g05100/F15L11.2 [Arabidopsis thaliana] >gi|15450494|gb|AAK96540.1| At2g05100/F15L11.2 [Arabidopsis thaliana]	Unigene9126_All//5.00E-125//AT2G05100| LHCB2.1; chlorophyll binding	Unigene9126_All//1.00E-43//TC135194		ko00196|Photosynthesis - antenna proteins		nr +
Unigene9127_All	591	0.00	3.60	0.63	0.17	0.06	0.00	0.72	1.41	2.49	1.18E+01	4.09E-12	Up	9.30E+00	2.46E-02		-1.53E+00	5.81E-01		-7.40E+00	3.89E-01		9.83E-01	1.58E-01		1.80E+00	4.81E-04	Up								
Unigene91270_All	468	0.11	0.00	0.00	0.11	1.25	0.48	0.00	0.09	1.87	-6.80E+00	5.96E-01		-6.80E+00	6.10E-01		3.56E+00	8.13E-03		2.18E+00	3.22E-01		6.48E+00	6.22E-01		1.09E+01	2.05E-06	Up				Unigene91270_All//3.00E-67//TC148331				

Unigene9128_All	1670	0.00	51.79	22.70	0.00	0.04	0.00	0.00	0.00	0.00	1.57E+01	0.00E+00	Up	1.45E+01	2.87E-215	Up	5.36E+00	5.98E-01		null	null		null	null		null	null		Unigene9128_All//gi|226495473|ref|NP_001147336.1|//1.00E-143//glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Zea mays] >gi|305880446|sp|Q96UF2.1|G3P2_RHIRA RecName: Full=Glyceraldehyde-3-phosphate dehydrogenase 2; Short=GAPDH 2 >gi|15722242|emb|CAC37404.1| glyceraldehyde-3-phosphate dehydrogenase [Mucor racemosus] >gi|195610190|gb|ACG26925.1| glyceraldehyde-3-phosphate dehydrogenase, cytosolic [Zea mays]	Unigene9128_All//2.00E-127//AT1G79530| GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene9128_All//2.00E-15//gi|78340424|gb|DT560698.1|DT560698		ko00010|Glycolysis / Gluconeogenesis		nr -
Unigene91292_All	261	0.40	0.00	1.84	3.44	3.69	0.35	1.46	0.80	0.61	-8.65E+00	3.63E-01		2.20E+00	9.13E-02		1.05E-01	9.03E-01		-3.31E+00	5.79E-04	Down	-8.65E-01	4.41E-01		-1.26E+00	2.48E-01		Unigene91292_All//gi|15226371|ref|NP_180394.1|//2.00E-08//DC1 domain-containing protein [Arabidopsis thaliana]	Unigene91292_All//7.00E-10//AT2G28270| DC1 domain-containing protein	Unigene91292_All//2.00E-76//ES828300				nr +
Unigene9131_All	488	0.00	1.77	0.00	1.22	1.27	1.57	1.13	1.54	2.78	1.08E+01	4.91E-05	Up	null	null		5.24E-02	9.71E-01		3.61E-01	6.79E-01		4.53E-01	5.59E-01		1.30E+00	1.09E-02								
Unigene9132_All	495	142.27	63.77	80.90	27.17	15.93	18.89	0.00	0.00	0.00	-1.16E+00	1.14E-64	Down	-8.15E-01	4.82E-35		-7.70E-01	4.52E-08		-5.25E-01	4.82E-04		null	null		null	null		Unigene9132_All//gi|3334277|sp|O24418.1|NLTP6_GOSHI//3.00E-22//RecName: Full=Non-specific lipid-transfer protein 6; Short=LTP; Flags: Precursor >gi|2335124|gb|AAB66907.1| lipid transfer protein [Gossypium hirsutum]	Unigene9132_All//1.00E-10//AT5G59320| LTP3 (LIPID TRANSFER PROTEIN 3); lipid binding	Unigene9132_All//0.00E+00//ES828517				nr -
Unigene9133_All	1304	0.04	0.00	0.16	0.15	0.00	0.00	2.27	2.88	0.43	-5.33E+00	5.96E-01		2.03E+00	3.59E-01		-7.26E+00	8.32E-02		-7.26E+00	1.31E-01		3.46E-01	2.45E-01		-2.41E+00	2.44E-10	Down	Unigene9133_All//gi|30690409|ref|NP_850456.1|//1.00E-24//zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana]	Unigene9133_All//6.00E-27//AT2G46495| zinc finger (C3HC4-type RING finger) family protein					nr -
Unigene91369_All	516	1.72	15.52	0.52	2.12	2.40	2.63	1.47	1.46	10.19	3.17E+00	7.20E-28	Up	-1.74E+00	3.79E-02		1.78E-01	8.19E-01		3.06E-01	6.14E-01		-1.66E-02	1.02E+00		2.79E+00	1.85E-20	Up	Unigene91369_All//gi|34550779|gb|AAQ74955.1|//6.00E-35//Ghiaa-Re [Gossypium barbadense]	Unigene91369_All//1.00E-32//AT4G14560| IAA1 (INDOLE-3-ACETIC ACID INDUCIBLE); protein binding / transcription factor	Unigene91369_All//1.00E-149//gi|73863704|gb|DT466443.1|DT466443			GO:0005515//GO:0009755//GO:0010468//GO:0043231	nr -
Unigene9139_All	416	0.75	0.49	0.00	4.55	1.90	1.95	2.85	2.01	0.19	-6.31E-01	6.21E-01		-9.56E+00	4.87E-02		-1.26E+00	5.12E-03		-1.22E+00	1.06E-02		-5.02E-01	3.95E-01		-3.89E+00	9.20E-07	Down	Unigene9139_All//gi|4587555|gb|AAD25786.1|AC006577_22//3.00E-17//F1511.22 [Arabidopsis thaliana]	Unigene9139_All//2.00E-10//AT1G54120| unknown protein	Unigene9139_All//0.00E+00//TC162921				nr +
Unigene914_All	2174	3.08	2.94	8.60	27.91	52.24	153.65	2.22	0.35	1.43	-6.90E-02	7.67E-01		1.48E+00	1.37E-24	Up	9.04E-01	2.41E-82		2.46E+00	0.00E+00	Up	-2.68E+00	9.74E-18	Down	-6.33E-01	7.29E-03		Unigene914_All//gi|224113975|ref|XP_002316632.1|//0.00E+00//polyphenol oxidase [Populus trichocarpa] >gi|222850697|gb|EEE97244.1| polyphenol oxidase [Populus trichocarpa]		Unigene914_All//0.00E+00//ES814831		ko00350|Tyrosine metabolism//ko00950|Isoquinoline alkaloid biosynthesis	GO:0008152//GO:0009536//GO:0016491	nr +
Unigene9140_All	759	0.41	0.80	0.14	0.13	0.00	0.65	2.56	2.37	0.63	9.54E-01	3.14E-01		-1.56E+00	3.29E-01		-7.04E+00	3.06E-01		2.32E+00	6.88E-02		-1.14E-01	7.91E-01		-2.02E+00	7.23E-06	Down	Unigene9140_All//gi|115444711|ref|NP_001046135.1|//6.00E-21//Os02g0188500 [Oryza sativa Japonica Group] >gi|113535666|dbj|BAF08049.1| Os02g0188500 [Oryza sativa Japonica Group]	Unigene9140_All//5.00E-31//AT5G25340| unknown protein					nr +
Unigene9142_All	905	0.00	0.00	0.00	0.00	0.04	0.10	4.53	0.46	2.07	null	null		null	null		5.25E+00	8.10E-01		6.64E+00	4.68E-01		-3.29E+00	1.63E-18	Down	-1.13E+00	2.16E-05	Down	Unigene9142_All//gi|224054176|ref|XP_002298129.1|//2.00E-83//2-oxoglutarate-dependent dioxygenase [Populus trichocarpa] >gi|222845387|gb|EEE82934.1| 2-oxoglutarate-dependent dioxygenase [Populus trichocarpa]	Unigene9142_All//3.00E-77//AT1G52820| 2-oxoglutarate-dependent dioxygenase, putative	Unigene9142_All//3.00E-41//TC133026		ko00904|Diterpenoid biosynthesis		nr -
Unigene91422_All	536	2.54	0.57	1.79	2.51	2.18	0.67	0.79	6.86	2.16	-2.16E+00	9.04E-04	Down	-5.05E-01	3.82E-01		-2.00E-01	7.50E-01		-1.90E+00	2.26E-03		3.12E+00	8.04E-16	Up	1.45E+00	1.09E-02		Unigene91422_All//gi|212717129|gb|ACJ37406.1|//3.00E-06//stress-induced receptor-like kinase [Glycine max]		Unigene91422_All//1.00E-82//TC139386			GO:0005488	nr +
Unigene9144_All	762	0.00	0.00	0.00	0.00	0.00	0.00	13.65	2.80	9.67	null	null		null	null		null	null		null	null		-2.29E+00	2.50E-31	Down	-4.97E-01	1.20E-03		Unigene9144_All//sp|Q9PLI5|Y114_CHLMU//3.00E-09//Uncharacterized protein TC_0114 OS=Chlamydia muridarum GN=TC_0114 PE=4 SV=2		Unigene9144_All//1.00E-15//TC172353				swissprot +
Unigene91446_All	603	3.90	1.34	1.85	0.50	0.29	0.90	0.14	0.07	0.13	-1.54E+00	4.45E-04	Down	-1.07E+00	1.44E-02		-7.96E-01	5.56E-01		8.59E-01	4.23E-01		-1.02E+00	7.19E-01		-8.59E-02	9.67E-01					Unigene91446_All//0.00E+00//TC177147				
Unigene9145_All	861	1.34	0.00	0.49	3.47	2.88	1.68	0.93	0.24	0.00	-1.04E+01	9.90E-07	Down	-1.43E+00	3.87E-02		-2.70E-01	4.99E-01		-1.05E+00	3.55E-03		-1.94E+00	1.17E-02		-9.87E+00	4.43E-06	Down	Unigene9145_All//gi|3377799|gb|AAC28172.1|//6.00E-19//T2H3.2 [Arabidopsis thaliana]	Unigene9145_All//4.00E-22//AT2G24960| unknown protein	Unigene9145_All//0.00E+00//TC178012				nr -
Unigene91468_All	215	0.00	0.47	0.00	1.16	1.12	0.63	0.00	0.78	2.59	8.88E+00	3.77E-01		null	null		-4.73E-02	9.51E-01		-8.78E-01	6.15E-01		9.60E+00	1.38E-01		1.13E+01	3.28E-04	Up	Unigene91468_All//gi|302143946|emb|CBI23051.3|//9.00E-10//unnamed protein product [Vitis vinifera]	Unigene91468_All//8.00E-09//AT5G24350| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Secretory pathway Sec39 (InterPro:IPR013244); Has 170 Blast hits to 130 proteins in 45 species: Archae - 0; Bacteria - 5; Metazoa - 90; Fungi - 13; Plants - 54; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink).						nr -
Unigene9147_All	548	3.06	0.37	1.07	3.91	2.70	0.33	0.00	0.00	0.22	-3.05E+00	3.81E-06	Down	-1.52E+00	6.55E-03		-5.33E-01	2.27E-01		-3.57E+00	2.47E-09	Down	null	null		7.77E+00	2.41E-01		Unigene9147_All//gi|224101833|ref|XP_002334238.1|//2.00E-43//AP2/ERF domain-containing transcription factor [Populus trichocarpa] >gi|148372081|gb|ABQ62972.1| TINY-like protein [Populus trichocarpa] >gi|222870106|gb|EEF07237.1| AP2/ERF domain-containing transcription factor [Populus trichocarpa]	Unigene9147_All//6.00E-35//AT2G35700| ERF38 (ERF FAMILY PROTEIN 38); DNA binding / transcription factor	Unigene9147_All//1.00E-23//TC177300	AP2-EREBP		GO:0001071//GO:0006351//GO:0010468//GO:0043231	nr +
Unigene9148_All	512	19.93	4.45	16.54	9.05	5.18	3.79	0.00	0.00	0.00	-2.16E+00	1.50E-23	Down	-2.69E-01	1.71E-01		-8.05E-01	2.10E-03		-1.25E+00	8.58E-06	Down	null	null		null	null					Unigene9148_All//6.00E-07//TC131560				
Unigene9149_All	372	0.00	0.00	0.57	0.27	0.37	0.85	53.08	20.11	58.79	null	null		9.16E+00	1.37E-01		4.68E-01	8.74E-01		1.67E+00	3.08E-01		-1.40E+00	2.77E-30	Down	1.48E-01	1.91E-01								
Unigene915_All	2210	12.48	4.06	7.78	18.42	15.55	15.98	0.78	1.13	0.50	-1.62E+00	1.59E-42	Down	-6.81E-01	1.78E-10		-2.44E-01	2.58E-03		-2.05E-01	1.89E-02		5.33E-01	1.44E-01		-6.36E-01	1.38E-01		Unigene915_All//gi|15487290|dbj|BAB64530.1|//0.00E+00//polyphenol oxidase [Pyrus pyrifolia]		Unigene915_All//0.00E+00//TC170675		ko00350|Tyrosine metabolism//ko00950|Isoquinoline alkaloid biosynthesis	GO:0008152//GO:0016491	nr -
Unigene9152_All	592	0.00	3.34	9.08	0.00	1.28	0.84	0.00	0.00	0.00	1.17E+01	2.96E-11	Up	1.31E+01	6.06E-30	Up	1.03E+01	1.17E-04	Up	9.71E+00	4.38E-03		null	null		null	null		Unigene9152_All//gi|11466597|ref|NP_066487.1|//1.00E-66//cytochrome c oxidase subunit 3 [Rhodomonas salina] >gi|104441841|gb|AAG17758.1|AP28090_34 cytochrome c oxidase subunit 3 [Rhodomonas salina]	Unigene9152_All//2.00E-54//ATMG00730| Encodes cytochrome c oxidase subunit 3.			ko00190|Oxidative phosphorylation	GO:0015002//GO:0022904//GO:0031224//GO:0043231	nr +
Unigene91523_All	212	0.00	0.00	0.00	0.94	1.46	0.00	2.99	0.00	0.00	null	null		null	null		6.37E-01	6.94E-01		-9.88E+00	1.31E-01		-1.15E+01	1.23E-04	Down	-1.15E+01	7.10E-05	Down							
Unigene9153_All	1282	0.00	0.00	0.00	0.00	0.00	0.07	17.22	4.63	4.44	null	null		null	null		null	null		6.14E+00	4.68E-01		-1.89E+00	1.02E-51	Down	-1.95E+00	1.58E-55	Down	Unigene9153_All//gi|18415376|ref|NP_568177.1|//4.00E-83//ST2A (SULFOTRANSFERASE 2A); hydroxyjasmonate sulfotransferase/ sulfotransferase [Arabidopsis thaliana] >gi|20166686|gb|AAM20660.1| steroid sulfotransferase-like protein [Arabidopsis thaliana] >gi|21537216|gb|AAM61557.1| steroid sulfotransferase-like protein [Arabidopsis thaliana] >gi|31711860|gb|AAP68286.1| At5g07010 [Arabidopsis thaliana]	Unigene9153_All//2.00E-79//AT5G07010| ST2A (SULFOTRANSFERASE 2A); hydroxyjasmonate sulfotransferase/ sulfotransferase	Unigene9153_All//0.00E+00//DW520436		ko00380|Tryptophan metabolism//ko00966|Glucosinolate biosynthesis	GO:0008146//GO:0009719//GO:0031407	nr -
Unigene9154_All	735	0.00	0.00	0.00	0.00	0.00	0.00	2.88	3.81	0.11	null	null		null	null		null	null		null	null		4.06E-01	2.46E-01		-4.73E+00	4.77E-13	Down	Unigene9154_All//gi|195623212|gb|ACG33436.1|//4.00E-79//60S ribosomal protein L10a-1 [Zea mays]	Unigene9154_All//6.00E-65//AT1G08360| 60S ribosomal protein L10A (RPL10aA)	Unigene9154_All//4.00E-09//TC157648		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0030529	nr -
Unigene9156_All	452	0.23	0.00	0.24	0.88	0.15	1.50	1.87	0.28	1.85	-7.85E+00	3.63E-01		2.53E-02	9.96E-01		-2.53E+00	5.78E-02		7.65E-01	4.10E-01		-2.75E+00	9.73E-04	Down	-1.54E-02	9.71E-01		Unigene9156_All//gi|297832830|ref|XP_002884297.1|//3.00E-13//GAUT13 [Arabidopsis lyrata subsp. lyrata] >gi|297330137|gb|EFH60556.1| GAUT13 [Arabidopsis lyrata subsp. lyrata]	Unigene9156_All//2.00E-14//AT5G15470| GAUT14 (Galacturonosyltransferase 14); polygalacturonate 4-alpha-galacturonosyltransferase/ transferase, transferring glycosyl groups / transferase, transferring hexosyl groups				GO:0005975//GO:0008194	nr +
Unigene91602_All	647	1.86	0.00	0.08	1.46	1.60	1.81	1.05	0.52	0.43	-1.09E+01	5.01E-07	Down	-4.50E+00	1.49E-05	Down	1.26E-01	8.71E-01		3.11E-01	6.43E-01		-1.02E+00	2.04E-01		-1.28E+00	9.48E-02		Unigene91602_All//gi|22326942|ref|NP_680185.1|//5.00E-81//ubiquitin thiolesterase [Arabidopsis thaliana] >gi|29294056|gb|AAO73893.1| expressed protein [Arabidopsis thaliana]	Unigene91602_All//5.00E-77//AT5G21970| ubiquitin thiolesterase				GO:0019941//GO:0044464	nr +
Unigene9161_All	378	39.73	37.67	48.60	18.58	13.85	4.42	0.00	0.00	0.00	-7.67E-02	6.12E-01		2.91E-01	3.66E-02		-4.24E-01	5.06E-02		-2.07E+00	9.43E-17	Down	null	null		null	null					Unigene9161_All//2.00E-68//EX168375				
Unigene9162_All	357	0.29	0.85	0.00	0.98	0.68	0.51	23.69	53.39	227.76	1.54E+00	3.22E-01		-8.20E+00	3.85E-01		-5.33E-01	6.45E-01		-9.49E-01	4.80E-01		1.17E+00	2.31E-22	Up	3.27E+00	0.00E+00	Up	Unigene9162_All//gi|255592997|ref|XP_002535768.1|//3.00E-18//conserved hypothetical protein [Ricinus communis] >gi|223522026|gb|EEF26615.1| conserved hypothetical protein [Ricinus communis]		Unigene9162_All//7.00E-163//DW505792				nr +
Unigene9163_All	395	2.25	0.13	0.00	0.38	1.74	0.69	1.18	0.11	0.30	-4.13E+00	2.52E-04	Down	-1.11E+01	6.29E-05	Down	2.20E+00	2.71E-02		8.59E-01	6.30E-01		-3.48E+00	1.03E-02		-1.96E+00	5.81E-02					Unigene9163_All//1.00E-59//TC174423				ESTscan -
Unigene91630_All	215	0.49	0.00	6.93	0.46	5.13	1.26	0.20	0.00	0.00	-8.93E+00	3.63E-01		3.83E+00	3.20E-06	Up	3.47E+00	6.96E-05	Up	1.44E+00	4.08E-01		-7.62E+00	6.36E-01		-7.62E+00	5.95E-01								
Unigene9165_All	383	7.24	6.48	7.65	8.45	8.27	14.03	23.40	20.73	7.59	-1.60E-01	6.64E-01		7.88E-02	8.31E-01		-3.15E-02	9.30E-01		7.31E-01	4.31E-03		-1.75E-01	3.80E-01		-1.62E+00	5.06E-18	Down		Unigene9165_All//3.00E-06//AT1G16890| ubiquitin-conjugating enzyme, putative	Unigene9165_All//5.00E-170//gi|164243877|gb|ES802451.1|ES802451		ko04120|Ubiquitin mediated proteolysis		kegg +
Unigene9166_All	308	5.44	4.44	5.36	14.07	13.42	8.94	12.90	4.61	10.35	-2.91E-01	5.79E-01		-2.04E-02	9.91E-01		-6.87E-02	8.25E-01		-6.54E-01	2.46E-02		-1.48E+00	2.95E-07	Down	-3.19E-01	2.49E-01		Unigene9166_All//gi|224141885|ref|XP_002324291.1|//2.00E-06//cellulose synthase [Populus trichocarpa] >gi|222865725|gb|EEF02856.1| cellulose synthase [Populus trichocarpa]	Unigene9166_All//3.00E-65//AT4G32410| CESA1 (CELLULOSE SYNTHASE 1); cellulose synthase/ transferase, transferring glycosyl groups	Unigene9166_All//8.00E-107//CO110763				nr +

Unigene9167_All	295	2.66	6.01	8.30	1.35	1.98	0.00	1.00	1.84	0.68	1.18E+00	1.88E-02		1.64E+00	2.69E-04	Up	5.55E-01	5.99E-01		-1.04E+01	1.10E-02		8.76E-01	3.46E-01		-5.71E-01	6.27E-01		Unigene9167_All//gi|15233263|ref|NP_188224.1|//3.00E-09//CES101 (CALLUS EXPRESSION OF RBCS 101); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding [Arabidopsis thaliana]	Unigene9167_All//1.00E-10//AT3G16030| CES101 (CALLUS EXPRESSION OF RBCS 101); ATP binding / carbohydrate binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding				GO:0004672//GO:0005488//GO:0031410	nr +
Unigene9168_All	303	0.00	0.17	2.28	0.00	0.34	1.64	0.00	0.00	0.00	7.39E+00	6.05E-01		1.12E+01	6.09E-04	Up	8.41E+00	4.50E-01		1.07E+01	4.38E-03		null	null		null	null		Unigene9168_All//sp|Q6NSZ1|TRMFO_RHOPA//6.00E-13//Methylenetetrahydrofolate--tRNA-(uracil-5-)-methyltransferase trmFO OS=Rhodopseudomonas palustris GN=trmFO PE=3 SV=1							swissprot +
Unigene9169_All	470	0.00	0.22	0.34	1.27	1.17	2.02	0.00	0.53	1.27	7.75E+00	3.77E-01		8.41E+00	2.33E-01		-1.18E-01	8.75E-01		6.66E-01	3.93E-01		9.06E+00	4.30E-02		1.03E+01	1.75E-04	Up	Unigene9169_All//gi|297836566|ref|XP_002886165.1|//5.00E-26//ATHB24 [Arabidopsis lyrata subsp. lyrata] >gi|297332005|gb|EFH62424.1| ATHB24 [Arabidopsis lyrata subsp. lyrata]	Unigene9169_All//6.00E-24//AT2G18350| ArtHB24 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 24); DNA binding / transcription factor	Unigene9169_All//3.00E-18//gi|164343073|gb|ES825317.1|ES825317	zf-HD		GO:0001071//GO:0003677//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene91697_All	205	0.77	0.49	1.30	0.49	3.02	0.88	0.83	3.06	4.66	-6.31E-01	7.25E-01		7.62E-01	6.43E-01		2.64E+00	1.99E-02		8.59E-01	6.93E-01		1.89E+00	3.49E-02		2.50E+00	6.42E-04	Up	Unigene91697_All//gi|297805650|ref|XP_002870709.1|//8.00E-09//binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297316545|gb|EFH46968.1| binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene91697_All//3.00E-10//AT5G40400| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; CONTAINS InterPro DOMAIN/s: Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: pentatricopeptide (PPR) repeat-containing protein (TAIR:AT5G65840.1); Has 18933 Blast hits to 5737 proteins in 174 species: Archae - 4; Bacteria - 8; Metazoa - 352; Fungi - 335; Plants - 17540; Viruses - 0; Other Eukaryotes - 694 (source: NCBI BLink).	Unigene91697_All//4.00E-21//TC145902				nr +
Unigene91702_All	453	0.00	0.00	0.00	1.76	1.82	0.20	387.06	89.22	77.48	null	null		null	null		5.23E-02	9.64E-01		-3.14E+00	1.88E-03		-2.12E+00	0.00E+00	Down	-2.32E+00	0.00E+00	Down	Unigene91702_All//gi|71534908|gb|AZ32285.1|//4.00E-17//BURP domain-containing protein [Medicago sativa]	Unigene91702_All//7.00E-12//AT1G49320| BURP domain-containing protein	Unigene91702_All//5.00E-10//C0119475				nr +
Unigene9175_All	407	0.64	0.12	0.52	1.10	1.44	2.33	3.84	1.75	0.88	-2.37E+00	2.13E-01		-2.97E-01	8.31E-01		3.85E-01	7.32E-01		1.08E+00	1.48E-01		-1.14E+00	1.72E-02		-2.13E+00	3.93E-05	Down	Unigene9175_All//gi|145334837|ref|NP_001078764.1|//1.00E-47//CPL4 (C-TERMINAL DOMAIN PHOSPHATASE-LIKE 4); phosphoprotein phosphatase [Arabidopsis thaliana] >gi|122154038|sp|Q00IB6.1|CPL4_ARATH RecName: Full=RNA polymerase II C-terminal domain phosphatase-like 4; Short=FCP-like 4; AltName: Full=Carboxyl-terminal phosphatase-like 4; Short=CTD phosphatase-like 4; Short=AtCPL4 >gi|95115186|gb|ABF55959.1| carboxyl-terminal phosphatase-like 4 [Arabidopsis thaliana]	Unigene9175_All//8.00E-49//AT5G58003| CPL4 (C-TERMINAL DOMAIN PHOSPHATASE-LIKE 4); phosphoprotein phosphatase	Unigene9175_All//0.00E+00//gi|48790758|gb|CO092072.1|CO092072			GO:0005515//GO:0006970//GO:0016791//GO:0043231	nr -
Unigene9178_All	303	21.93	16.89	21.79	70.86	53.64	47.10	13.54	4.55	13.67	-3.77E-01	1.07E-01		-9.10E-03	9.94E-01		-4.02E-01	2.92E-04		-5.89E-01	2.87E-07		-1.57E+00	4.70E-08	Down	1.47E-02	9.66E-01					Unigene9178_All//6.00E-55//BQ404244				
Unigene9179_All	297	3.52	0.68	0.36	2.85	3.25	3.04	1.71	1.13	0.67	-2.37E+00	2.49E-03		-3.30E+00	4.58E-04	Down	1.87E-01	8.11E-01		9.31E-02	9.20E-01		-6.02E-01	5.31E-01		-1.35E+00	1.40E-01									ESTscan +
Unigene91790_All	224	0.00	0.00	0.00	0.00	0.00	0.00	2.45	0.00	0.36	null	null		null	null		null	null		null	null		-1.13E+01	4.61E-04	Down	-2.79E+00	7.95E-03		Unigene91790_All//gi|297793171|ref|XP_002864470.1|//2.00E-07//glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata] >gi|297310305|gb|EFH40729.1| glycosyl hydrolase family 17 protein [Arabidopsis lyrata subsp. lyrata]	Unigene91790_All//1.00E-08//AT5G56590| glycosyl hydrolase family 17 protein	Unigene91790_All//2.00E-35//DN827506			GO:0005618//GO:0008152//GO:0016798//GO:0031225	nr -
Unigene918_All	817	5.96	12.96	9.58	2.87	3.46	4.48	3.57	9.72	5.85	1.12E+00	7.60E-10	Up	6.86E-01	1.46E-03		2.70E-01	5.41E-01		6.44E-01	4.83E-02		1.44E+00	3.36E-13	Up	7.13E-01	2.77E-03		Unigene918_All//gi|18411751|ref|NP_565163.1|//4.00E-71//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|42572151|ref|NP_974166.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|6573763|gb|AAF17683.1|AC009243_10 F28K19.14 [Arabidopsis thaliana] >gi|107738377|gb|ABF83686.1| At1g77930 [Arabidopsis thaliana]	Unigene918_All//2.00E-72//AT1G77930| DNAJ heat shock N-terminal domain-containing protein	Unigene918_All//0.00E+00//TC146579			GO:0005515//GO:0009536//GO:0050896	nr -
Unigene91811_All	223	0.47	0.00	0.00	3.13	1.08	0.00	0.57	0.37	1.79	-8.87E+00	3.63E-01		-8.87E+00	3.84E-01		-1.53E+00	7.00E-02		-1.16E+01	1.95E-04	Down	-6.02E-01	7.64E-01		1.65E+00	1.40E-01									
Unigene91829_All	216	0.00	0.23	0.00	6.92	1.59	0.84	0.39	0.00	0.00	7.87E+00	6.05E-01		null	null		-2.12E+00	1.37E-04	Down	-3.05E+00	7.42E-06	Down	-8.61E+00	3.95E-01		-8.61E+00	3.52E-01					Unigene91829_All//6.00E-08//gi|164302221|gb|ES807565.1|ES807565				
Unigene9183_All	269	0.19	3.58	1.39	0.74	0.77	2.18	0.94	1.55	0.59	4.20E+00	1.29E-04	Up	2.83E+00	9.27E-02		5.24E-02	9.87E-01		1.56E+00	1.36E-01		7.20E-01	5.07E-01		-6.71E-01	6.05E-01					Unigene9183_All//3.00E-07//TC155812				
Unigene9186_All	915	0.00	0.00	0.00	0.00	0.00	0.00	2.22	4.48	0.09	null	null		null	null		null	null		null	null		1.01E+00	1.84E-04	Up	-4.67E+00	1.83E-12	Down	Unigene9186_All//gi|300266622|gb|EFJ50809.1|//4.00E-80//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene9186_All//5.00E-79//AT1G61580| RPL3B (R-PROTEIN L3 B); structural constituent of ribosome	Unigene9186_All//4.00E-09//CB066521		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene9187_All	419	0.87	0.24	1.65	3.21	2.47	0.65	0.81	1.00	2.66	-1.85E+00	1.87E-01		9.18E-01	3.11E-01		-3.81E-01	5.36E-01		-2.31E+00	4.01E-04	Down	3.05E-01	7.57E-01		1.72E+00	4.13E-03		Unigene9187_All//gi|297811377|ref|XP_002873572.1|//2.00E-37//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319409|gb|EFH49831.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene9187_All//1.00E-38//AT5G12430| DNAJ heat shock N-terminal domain-containing protein	Unigene9187_All//1.00E-180//TC138609		ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0043231//GO:0044267	nr -
Unigene919_All	448	1.75	5.88	2.26	2.22	3.15	4.13	2.36	2.80	2.76	1.75E+00	3.76E-05	Up	3.67E-01	6.21E-01		5.03E-01	4.15E-01		8.94E-01	6.88E-02		2.46E-01	6.45E-01		2.25E-01	6.66E-01					Unigene919_All//1.00E-149//C0092284				
Unigene9193_All	413	1.90	0.12	5.80	3.86	2.58	8.31	2.35	1.52	3.95	-3.95E+00	8.54E-04	Down	1.61E+00	3.96E-04	Up	-5.79E-01	2.71E-01		1.11E+00	9.76E-04	Up	-6.33E-01	3.28E-01		7.48E-01	9.34E-02		Unigene9193_All//gi|260408308|gb|ACX37448.1|//1.00E-11//plasma membrane intrinsic protein [Hevea brasiliensis]	Unigene9193_All//6.00E-12//AT2G37170| PIP2B (PLASMA MEMBRANE INTRINSIC PROTEIN 2); water channel	Unigene9193_All//1.00E-53//TC176227				nr +
Unigene91949_All	800	0.00	0.00	0.00	0.06	0.22	0.06	1.48	0.05	0.35	null	null		null	null		1.79E+00	5.19E-01		-1.41E-01	9.45E-01		-4.83E+00	2.83E-07	Down	-2.09E+00	5.32E-04	Down	Unigene91949_All//gi|119507465|dbj|BAF42040.1|//1.00E-103//pectin methylesterase 3 [Pyrus communis]	Unigene91949_All//4.00E-103//AT1G02810| pectinesterase family protein	Unigene91949_All//0.00E+00//TC138774		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0030234//GO:0071555	nr +
Unigene9185_All	627	0.33	0.57	0.00	1.19	0.93	0.58	3.24	3.27	0.76	7.61E-01	5.56E-01		-8.38E+00	1.44E-01		-3.52E-01	6.51E-01		-1.05E+00	2.21E-01		1.31E-02	1.01E+00		-2.09E+00	2.72E-06	Down								
Unigene91985_All	296	0.53	1.37	0.00	2.19	1.16	0.00	0.57	0.85	1.21	1.37E+00	2.73E-01		-9.05E+00	2.41E-01		-9.11E-01	3.04E-01		-1.11E+01	3.89E-04	Down	5.68E-01	6.73E-01		1.08E+00	3.49E-01					Unigene91985_All//7.00E-138//gi|109878956|gb|DW507926.1|DW507926				
Unigene91989_All	602	0.09	0.51	0.18	0.99	1.37	3.38	0.91	0.83	1.13	2.54E+00	1.50E-01		1.03E+00	6.99E-01		4.67E-01	5.85E-01		1.77E+00	2.78E-04	Up	-1.32E-01	8.79E-01		3.01E-01	6.71E-01		Unigene91989_All//gi|224071585|ref|XP_002303528.1|//4.00E-34//cytochrome P450 [Populus trichocarpa] >gi|222840960|gb|EEE78507.1| cytochrome P450 [Populus trichocarpa]	Unigene91989_All//1.00E-27//AT4G12320| CYP706A6; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene91989_All//2.00E-167//TC172918		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0016491//GO:0046872	nr +
Unigene9200_All	223	7.04	2.27	2.39	12.06	4.48	6.68	15.93	7.12	3.22	-1.63E+00	3.58E-03		-1.56E+00	7.38E-03		-1.43E+00	9.85E-05	Down	-8.52E-01	2.65E-02		-1.16E+00	9.24E-05	Down	-2.31E+00	1.08E-11	Down				Unigene9200_All//4.00E-43//FL576431				
Unigene9203_All	487	0.97	0.73	3.17	1.84	2.62	1.67	1.39	0.00	1.55	-4.09E-01	6.68E-01		1.71E+00	4.02E-03		5.07E-01	4.38E-01		-1.41E-01	8.47E-01		-1.04E+01	6.33E-05	Down	1.62E-01	8.09E-01		Unigene9203_All//gi|297842759|ref|XP_002889261.1|//3.00E-87//kinase [Arabidopsis lyrata subsp. lyrata] >gi|297335102|gb|EFH65520.1| kinase [Arabidopsis lyrata subsp. lyrata]	Unigene9203_All//2.00E-88//AT1G79640| ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase	Unigene9203_All//4.00E-165//DR459182		ko04626|Plant-pathogen interaction//ko04650|Natural killer cell mediated cytotoxicity	GO:0004702//GO:0006464//GO:0032559	nr -
Unigene92039_All	331	0.00	1.99	0.00	0.60	1.35	0.41	0.00	0.38	0.00	1.10E+01	6.20E-04	Up	null	null		1.17E+00	3.47E-01		-5.57E-01	7.31E-01		8.57E+00	2.39E-01		null	null									
Unigene9205_All	763	0.00	0.20	0.00	0.00	0.18	0.12	11.97	4.77	2.40	7.64E+00	2.31E-01		null	null		7.50E+00	3.15E-01		6.89E+00	4.68E-01		-1.33E+00	2.19E-13	Down	-2.32E+00	5.91E-29	Down	Unigene9205_All//gi|30690333|ref|NP_195263.2|//7.00E-63//AGF1 (AT-hook protein of GA feedback 1); transcription factor [Arabidopsis thaliana] >gi|50198777|gb|AAT70422.1| At4g35390 [Arabidopsis thaliana] >gi|53828597|gb|AAU94408.1| At4g35390 [Arabidopsis thaliana] >gi|119657394|tpd|FAA00296.1| TPA: AT-hook motif nuclear localized protein 25 [Arabidopsis thaliana]	Unigene9205_All//5.00E-32//AT4G35390| AGF1 (AT-hook protein of GA feedback 1); transcription factor	Unigene9205_All//0.00E+00//gi|78324579|gb|DT544853.1|DT544853			GO:0009639//GO:0009740//GO:0010260//GO:0043231//GO:0043565//GO:0051276	nr -
Unigene92054_All	231	1.36	1.75	8.07	4.74	8.35	5.87	1.10	0.00	0.34	3.69E-01	7.23E-01		2.57E+00	1.69E-05	Up	8.15E-01	8.42E-02		3.06E-01	6.14E-01		-1.01E+01	4.02E-02		-1.67E+00	2.56E-01					Unigene92054_All//7.00E-51//DT463883				
Unigene92080_All	302	0.00	0.00	0.00	0.00	0.00	0.00	4.76	0.28	0.00	null	null		null	null		null	null		null	null		-4.10E+00	5.15E-08	Down	-1.22E+01	1.19E-10	Down	Unigene92080_All//gi|37090216|sp|Q8S3W4.1|ZIP8_ARATH//6.00E-30//RecName: Full=Probable zinc transporter 8; AltName: Full=ZRT/IRT-like protein 8; Flags: Precursor >gi|18997103|gb|AAL83293.1|AF475143_1 metal transporter ZIP8 [Arabidopsis thaliana]	Unigene92080_All//2.00E-23//AT4G19690| IRT1 (iron-regulated transporter 1); cadmium ion transmembrane transporter/ copper uptake transmembrane transporter/ iron ion transmembrane transporter/ manganese ion transmembrane transporter/ zinc ion transmembrane transporter	Unigene92080_All//7.00E-67//TC148511			GO:0000041//GO:0008152//GO:0015082//GO:0016628//GO:0031224	nr +
Unigene9209_All	270	0.00	0.75	0.20	1.48	8.93	5.52	0.16	1.08	1.03	9.55E+00	1.34E-01		7.62E+00	6.20E-01		2.60E+00	5.21E-08	Up	1.90E+00	1.38E-03		2.79E+00	9.47E-02		2.72E+00	9.92E-02									
Unigene921_All	1558	1.61	5.66	3.18	3.17	1.75	4.32	2.47	2.12	2.02	1.81E+00	3.06E-16	Up	9.80E-01	5.33E-04		-8.58E-01	6.45E-04		4.48E-01	5.41E-02		-2.21E-01	4.77E-01		-2.90E-01	3.13E-01		Unigene921_All//gi|18411751|ref|NP_565163.1|//3.00E-70//DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|42572151|ref|NP_974166.1| DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] >gi|6573763|gb|AAF17683.1|AC009243_10 F28K19.14 [Arabidopsis thaliana] >gi|107738377|gb|ABF83686.1| At1g77930 [Arabidopsis thaliana]	Unigene921_All//5.00E-65//AT1G77930| DNAJ heat shock N-terminal domain-containing protein	Unigene921_All//0.00E+00//TC146579			GO:0005515//GO:0009536//GO:0050896	nr -
Unigene9210_All	603	1.82	0.42	0.44	0.99	1.31	0.30	1.75	1.04	0.26	-2.12E+00	3.98E-03		-2.05E+00	7.42E-03		4.06E-01	6.31E-01		-1.73E+00	9.02E-02		-7.54E-01	2.17E-01		-2.73E+00	1.12E-04	Down				Unigene9210_All//2.00E-22//ES805560				
Unigene92117_All	513	0.20	0.59	0.21	0.29	1.68	0.09	0.41	0.00	3.11	1.54E+00	3.22E-01		2.52E-02	9.96E-01		2.53E+00	4.66E-03		-1.73E+00	4.98E-01		-8.69E+00	7.39E-02		2.91E+00	5.82E-07	Up				Unigene92117_All//2.00E-09//TC150388				

Unigene9215_All	670	0.00	0.00	0.00	0.00	0.00	0.00	15.65	1.50	9.45	null	null		null	null		null	null		null	null		-3.39E+00	1.40E-47	Down	-7.27E-01	2.23E-06		Unigene9215_All//gi|15219205|ref|NP_175721.1|//6.00E-41//GRI (GRIM REAPER) [Arabidopsis thaliana] >gi|9454544|gb|AAF87867.1|AC022520_11 Unknown protein [Arabidopsis thaliana]	Unigene9215_All//7.00E-39//AT1G53130| GRI (GRIM REAPER)	Unigene9215_All//8.00E-07//FF403783			GO:0006952//GO:0008219//GO:0009695//GO:0009697//GO:0009791//GO:0023033//GO:0042221	nr +
Unigene9216_All	322	1.14	1.10	1.32	4.95	2.14	0.84	1.97	0.39	0.62	-4.63E-02	9.82E-01		2.18E-01	8.30E-01		-1.21E+00	1.52E-02		-2.56E+00	2.78E-05	Down	-2.34E+00	1.27E-02		-1.67E+00	4.29E-02							
Unigene92161_All	228	0.00	0.00	0.70	0.00	0.00	0.00	5.19	0.18	1.22	null	null		9.45E+00	2.33E-01		null	null		null	null		-4.82E+00	2.83E-07	Down	-2.09E+00	5.32E-04	Down	Unigene92161_All//gi|37544101|gb|AAQ93035.1|/2.00E-13//gibberellin 2-oxidase [Populus alba x Populus tremuloides]	Unigene92161_All//4.00E-10//AT1G02400| GA2OX6 (GIBBERELLIN 2-OXIDASE 6); gibberellin 2-beta-dioxygenase	Unigene92161_All//2.00E-48//gi|78324168|gb|DT544442.1|DT544442			GO:0009685//GO:0016706	nr -
Unigene92178_All	206	0.76	0.25	0.26	0.00	3.68	0.22	0.41	0.00	0.19	-1.63E+00	4.87E-01		-1.56E+00	5.32E-01		1.18E+01	1.17E-04	Up	7.78E+00	6.80E-01		-8.68E+00	3.95E-01		-1.09E+00	6.72E-01					Unigene92178_All//1.00E-12//AI055431				
Unigene9218_All	599	0.00	0.00	0.00	0.17	0.12	0.00	2.47	9.07	11.71	null	null		null	null		-5.32E-01	8.11E-01		-7.38E+00	3.88E-01		1.88E+00	4.23E-13	Up	2.24E+00	2.79E-21	Up				Unigene9218_All//0.00E+00//gi|21095300|gb|BQ407613.1|BQ407613				ESTscan -
Unigene9219_All	333	1.41	0.30	0.00	1.80	3.21	2.71	2.41	0.25	1.44	-2.22E+00	7.75E-02		-1.05E+01	8.61E-03		8.37E-01	2.29E-01		5.96E-01	4.55E-01		-3.26E+00	4.48E-04	Down	-7.49E-01	2.66E-01		Unigene9219_All//gi|224077758|ref|XP_002305396.1|//1.00E-25//predicted protein [Populus trichocarpa] >gi|222848360|gb|EEE85907.1|predicted protein [Populus trichocarpa]	Unigene9219_All//6.00E-12//AT5G15510| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 7 growth stages; CONTAINS InterPro DOMAIN/s: Targeting for XAlp2 (InterPro:IPR009675); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G01015.1); Has 992 Blast hits to 819 proteins in 107 species: Archae - 0; Bacteria - 11; Metazoa - 477; Fungi - 40; Plants - 169; Viruses - 3; Other Eukaryotes - 292 (source: NCBI BLink).					nr -
Unigene922_All	761	3.09	2.73	2.52	6.15	4.43	2.02	4.44	3.30	3.14	-1.81E-01	6.49E-01		-2.97E-01	5.08E-01		-4.73E-01	8.41E-02		-1.61E+00	3.36E-08	Down	-4.32E-01	1.65E-01		-5.01E-01	8.68E-02		Unigene922_All//gi|115444359|ref|NP_001045959.1|//1.00E-77//Os02g0158800 [Oryza sativa Japonica Group] >gi|113535490|dbj|BAF07873.1|Os02g0158800 [Oryza sativa Japonica Group]	Unigene922_All//2.00E-85//AT3G26370| unknown protein	Unigene922_All//0.00E+00//gi|78345909|gb|DT566183.1|DT566183			GO:0043231	nr -
Unigene9220_All	240	40.77	38.42	36.83	50.85	62.41	61.54	47.39	20.03	23.74	-8.54E-02	6.56E-01		-1.47E-01	4.86E-01		2.96E-01	4.39E-02		2.75E-01	7.42E-02		-1.24E+00	6.28E-15	Down	-9.97E-01	4.46E-11		Unigene9220_All//gi|166867|gb|AAA32866.1|//2.00E-18//ribosomal protein S11 (probable start codon at bp 67) [Arabidopsis thaliana]	Unigene9220_All//2.00E-08//AT5G23740| RPS11-BETA (RIBOSOMAL PROTEIN S11-BETA); structural constituent of ribosome	Unigene9220_All//1.00E-123//TC151907	ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536//GO:0010467//GO:0015935//GO:0030312	nr +
Unigene92203_All	348	0.15	3.49	1.68	0.43	0.30	0.26	2.07	4.80	7.33	4.54E+00	6.47E-06	Up	3.49E+00	1.20E-02		-5.32E-01	7.82E-01		-7.26E-01	7.12E-01		1.22E+00	8.38E-03		1.83E+00	1.63E-06	Up	Unigene92203_All//gi|5915844|sp|049858.1|C82A3_SOYBN//6.00E-32//RecName: Full=Cytochrome P450 82A3; AltName: Full=Cytochrome P450 CP6	Unigene92203_All//8.00E-27//AT4G31940| CYP82C4; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding	Unigene92203_All//3.00E-122//gi|48742721|gb|CO073240.1|CO073240		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation//ko00941|Flavonoid biosynthesis//ko00944|Flavone and flavonol biosynthesis	GO:0046872	nr +
Unigene92208_All	214	0.00	0.00	0.00	0.00	0.00	0.21	0.00	1.56	2.61	null	null		null	null		null	null		7.72E+00	6.80E-01		1.06E+01	1.27E-02		1.13E+01	3.28E-04	Up								
Unigene9221_All	1004	0.00	14.48	4.83	0.00	0.00	0.00	0.00	0.00	0.00	1.38E+01	1.62E-83	Up	1.22E+01	6.10E-27	Up	null	null		null	null		null	null		null	null		Unigene9221_All//gi|219116540|ref|XP_002179065.1|//2.00E-66//3-hydroxyacyl-coenzyme A dehydrogenase [Phaeodactylum tricornutum CCAP 1055/1] >gi|217409832|gb|EEC49763.1| 3-hydroxyacyl-coenzyme A dehydrogenase [Phaeodactylum tricornutum CCAP 1055/1]	Unigene9221_All//3.00E-26//AT3G26770| short-chain dehydrogenase/reductase (SDR) family protein			ko01040|Biosynthesis of unsaturated fatty acids//ko00906|Carotenoid biosynthesis//ko00061|Fatty acid biosynthesis	GO:0003824	nr -
Unigene9222_All	678	2.70	0.45	1.02	2.57	1.93	2.33	0.50	0.00	0.00	-2.59E+00	9.26E-06	Down	-1.40E+00	7.28E-03		-4.14E-01	4.20E-01		-1.41E-01	7.77E-01		-8.96E+00	1.17E-02		-8.96E+00	8.12E-03					Unigene9222_All//0.00E+00//TC179567				
Unigene92240_All	532	0.00	0.29	0.30	6.55	2.72	3.99	0.32	0.24	0.00	8.16E+00	2.31E-01		8.23E+00	2.33E-01		-1.27E+00	4.68E-05	Down	-7.16E-01	3.01E-02		-4.32E-01	7.91E-01		-8.31E+00	1.07E-01		Unigene92240_All//gi|115447415|ref|NP_001047487.1|//2.00E-39//Os02g0628200 [Oryza sativa Japonica Group] >gi|48711036|dbj|BAD23725.1|phosphate translocator-like [Oryza sativa Japonica Group] >gi|113537018|dbj|BAF09101.1|Os02g0628200 [Oryza sativa Japonica Group]	Unigene92240_All//1.00E-45//AT2G28315| LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF250 (InterPro:IPR004853); BEST Arabidopsis thaliana protein match is: transporter-related (TAIR:AT1G06890.2); Has 1852 Blast hits to 1847 proteins in 207 species: Archae - 0; Bacteria - 58; Metazoa - 582; Fungi - 250; Plants - 685; Viruses - 0; Other Eukaryotes - 277 (source: NCBI BLink).	Unigene92240_All//4.00E-144//TC150441			GO:0031224//GO:0031410	nr -
Unigene9225_All	432	1.21	1.76	2.59	1.27	2.95	5.02	0.00	0.00	0.00	5.39E-01	5.02E-01		1.10E+00	1.10E-01		1.22E+00	4.61E-02		1.98E+00	3.57E-05	Up	null	null		null	null					Unigene9225_All//3.00E-45//ES800152				
Unigene9271_All	302	0.00	0.00	0.53	0.00	0.68	0.15	0.70	1.66	3.43	null	null		9.05E+00	2.33E-01		9.42E+00	1.56E-01		7.22E+00	6.80E-01		1.25E+00	2.04E-01		2.29E+00	7.17E-04	Up				Unigene9271_All//3.00E-07//TC179376				
Unigene92289_All	210	9.22	8.69	7.61	22.06	8.85	10.75	2.21	1.19	3.04	-8.58E-02	8.47E-01		-2.77E-01	5.92E-01		-1.32E+00	7.07E-07	Down	-1.04E+00	1.88E-04	Down	-8.91E-01	3.83E-01		4.55E-01	5.78E-01					Unigene92289_All//3.00E-31//gi|78347306|gb|DT567580.1|DT567580				
Unigene9229_All	367	0.29	0.00	0.29	0.00	0.00	0.25	3.80	6.04	12.48	-8.16E+00	3.63E-01		2.56E-02	9.96E-01		null	null		7.94E+00	4.68E-01		6.67E-01	8.59E-02		1.72E+00	3.24E-10	Up				Unigene9229_All//4.00E-07//TC167212				
Unigene9231_All	514	5.29	13.31	6.84	1.74	1.00	2.46	0.49	0.81	0.47	1.33E+00	2.01E-08	Up	3.69E-01	3.00E-01		-7.96E-01	2.75E-01		4.96E-01	4.48E-01		7.20E-01	5.07E-01		-8.58E-02	9.56E-01		Unigene9231_All//gi|22329532|ref|NP_683303.1|//6.00E-08//RTFL17 (ROTUNDIFOLIA LIKE 17) [Arabidopsis thaliana] >gi|4850407|gb|AAD31077.1|AC007357_26 EST gb|T21221 comes from this gene [Arabidopsis thaliana] >gi|37955428|gb|AAP13819.1| DVL4 [Arabidopsis thaliana] >gi|91807634|gb|ABF47114.1|At1g13245 [Arabidopsis thaliana]	Unigene9231_All//4.00E-09//AT1G13245| RTFL17 (ROTUNDIFOLIA LIKE 17)				GO:0048513	nr +
Unigene9233_All	246	4.04	0.00	4.98	1.62	2.24	1.84	0.00	0.17	0.16	-1.20E+01	7.45E-06	Down	3.01E-01	6.32E-01		4.67E-01	6.68E-01		1.81E-01	8.83E-01		7.41E+00	6.21E-01		7.34E+00	6.31E-01		Unigene9233_All//gi|223452288|gb|ACM89472.1|//6.00E-30//FERONIA receptor-like kinase [Glycine max]	Unigene9233_All//5.00E-27//AT3G51550| FER (FERONIA); kinase/ protein kinase	Unigene9233_All//5.00E-21//ES823997	ko04626|Plant-pathogen interaction	GO:0004702//GO:0004713//GO:0006464//GO:0031410//GO:0032559	nr -
Unigene9234_All	411	2.55	0.37	0.78	0.97	0.17	0.22	0.93	1.83	0.29	-2.78E+00	8.21E-04	Down	-1.71E+00	2.35E-02		-2.53E+00	5.78E-02		-2.14E+00	1.26E-01		9.84E-01	1.89E-01		-1.67E+00	1.40E-01		Unigene9234_All//gi|22331122|ref|NP_188302.2|//3.00E-41//PLDP1 (PHOSPHOLIPASE D P1); phospholipase D [Arabidopsis thaliana] >gi|20139230|sp|Q9LRZ5.1|PLDP1_ARATH RecName: Full=Phospholipase D p1; Short=AtPLDp1; AltName: Full=Phospholipase D1 PHOX and PX-containing domain protein; AltName: Full=Phospholipase D zeta 1; Short=PLDzeta1 >gi|15723315|gb|AAL06337.1|AF411833_1 phospholipase D zeta1 [Arabidopsis thaliana] >gi|119944076|dbj|BAA95772.2|phospholipase D-like protein [Arabidopsis thaliana]	Unigene9234_All//3.00E-42//AT3G16785| PLDP1 (PHOSPHOLIPASE D P1); phospholipase D	Unigene9234_All//4.00E-66//TC167292	ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism	GO:0004620//GO:0006644//GO:0009247//GO:0009267//GO:0009725//GO:0016491//GO:0043231//GO:0048513//GO:0050794	nr +
Unigene9235_All	660	0.48	0.69	2.18	0.15	0.83	0.41	0.00	0.00	0.00	5.39E-01	6.01E-01		2.20E+00	8.72E-04	Up	2.47E+00	4.04E-02		1.44E+00	4.08E-01		null	null		null	null		Unigene9235_All//gi|255588009|ref|XP_002534472.1|//6.00E-11//Multidrug resistance protein mdtA precursor, putative [Ricinus communis] >gi|223525220|gb|EEF27902.1|Multidrug resistance protein mdtA precursor, putative [Ricinus communis]						nr +
Unigene92357_All	653	1.20	0.00	1.14	3.74	5.54	3.11	0.13	0.13	0.24	-1.02E+01	1.09E-04	Down	-7.41E-02	9.35E-01		5.67E-01	8.28E-02		-2.64E-01	5.67E-01		-1.68E-02	1.01E+00		9.14E-01	6.23E-01		Unigene92357_All//gi|66792640|gb|AY56422.1|//1.00E-28//At4g22860 [Arabidopsis thaliana]	Unigene92357_All//2.00E-30//AT4G22860| unknown protein	Unigene92357_All//3.00E-80//ES825890			nr -
Unigene9237_All	221	0.24	0.00	0.00	0.68	0.93	3.07	3.83	47.47	3.61	-7.89E+00	5.95E-01		-7.89E+00	6.09E-01		4.67E-01	8.24E-01		2.18E+00	3.14E-02		3.63E+00	2.41E-50	Up	-8.58E-02	9.02E-01					Unigene9237_All//6.00E-110//DT461777				
Unigene92370_All	221	0.00	0.00	0.00	0.23	1.56	0.00	5.74	0.19	0.00	null	null		null	null		2.79E+00	1.14E-01		-7.82E+00	6.12E-01		-4.92E+00	7.77E-08	Down	-1.25E+01	1.99E-09	Down	Unigene92370_All//gi|224141527|ref|XP_002324121.1|//7.00E-23//ABC transporter family protein [Populus trichocarpa] >gi|222867123|gb|EEF04254.1| ABC transporter family protein [Populus trichocarpa]	Unigene92370_All//1.00E-23//AT5G39040| ATTAP2; ATPase, coupled to transmembrane movement of substances / transporter	Unigene92370_All//2.00E-14//TC135398	ko02010|ABC transporters	GO:0006810//GO:0031224//GO:0032559//GO:0042626//GO:0043234	nr -
Unigene92379_All	206	0.00	0.00	0.00	0.48	0.50	0.00	0.21	1.01	3.09	null	null		null	null		5.24E-02	9.63E-01		-8.92E+00	3.88E-01		2.31E+00	2.39E-01		3.91E+00	7.65E-04	Up				Unigene92379_All//3.00E-28//DW009062				
Unigene9239_All	327	0.32	0.31	0.00	0.30	0.53	1.52	3.23	0.26	0.37	-4.63E-02	9.84E-01		-8.32E+00	3.84E-01		7.89E-01	7.69E-01		2.32E+00	6.88E-02		-3.66E+00	1.31E-05	Down	-3.14E+00	2.96E-05	Down	Unigene9239_All//gi|51477380|gb|AAU04753.1|//2.00E-44//EXO [Cucumis melo]	Unigene9239_All//5.00E-37//AT5G03795| LOCATED IN: membrane; EXPRESSED IN: embryo, sepal, flower; EXPRESSED DURING: C globular stage, petal differentiation and expansion stage; CONTAINS InterPro DOMAIN/s: Exostosin-like (InterPro:IPR004263); BEST Arabidopsis thaliana protein match is: exostosin family protein (TAIR:AT3G07620.1); Has 866 Blast hits to 860 proteins in 87 species: Archae - 0; Bacteria - 9; Metazoa - 265; Fungi - 4; Plants - 504; Viruses - 0; Other Eukaryotes - 84 (source: NCBI BLink).				GO:0008375//GO:0044464	nr +
Unigene92432_All	443	0.35	0.23	0.36	0.11	1.71	0.00	0.00	0.00	0.00	-6.31E-01	7.25E-01		2.54E-02	1.00E+00		3.93E+00	9.78E-04	Up	-6.81E+00	6.12E-01		null	null		null	null					Unigene92432_All//5.00E-07//TC144690				
Unigene9244_All	338	0.00	0.00	0.00	0.00	0.00	0.00	2.88	1.24	0.12	null	null		null	null		null	null		null	null		-1.22E+00	5.68E-02		-4.61E+00	3.32E-06	Down	Unigene9244_All//gi|238617661|gb|ACR46952.1|//2.00E-54//alpha-tubulin [Katablepharis japonica]	Unigene9244_All//1.00E-52//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene9244_All//1.00E-22//DR460752	ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene9245_All	362	0.58	2.24	0.74	2.06	0.86	0.12	0.00	0.00	0.00	1.95E+00	2.43E-02		3.47E-01	7.96E-01		-1.27E+00	1.12E-01		-4.05E+00	7.75E-04	Down	null	null		null	null									
Unigene92451_All	361	0.00	0.00	0.00	0.00	0.10	0.00	3.28	0.35	1.32	null	null		null	null		6.58E+00	8.10E-01		null	null		-3.24E+00	1.10E-05	Down	-1.31E+00	1.69E-02		Unigene92451_All//gi|107738065|gb|ABF83626.1|//1.00E-07//At4g33800 [Arabidopsis thaliana]		Unigene92451_All//4.00E-10//gi|164268732|gb|EV483082.1|EV483082			nr -
Unigene92485_All	366	0.29	0.00	0.87	0.14	1.22	0.62	1.50	0.00	0.54	-8.16E+00	3.62E-01		1.61E+00	3.03E-01		3.17E+00	3.95E-02		2.18E+00	3.22E-01		-1.06E+01	4.61E-04	Down	-1.46E+00	9.75E-02					Unigene92485_All//4.00E-143//CO102356				
Unigene925_All	1547	3.18	13.00	17.66	41.41	43.45	63.61	2.71	0.19	0.49	2.03E+00	4.48E-42	Up	2.47E+00	1.18E-70	Up	6.94E-02	3.77E-01		6.19E-01	1.06E-33		-3.84E+00	2.28E-21	Down	-2.47E+00	1.09E-14	Down	Unigene925_All//gi|1706323|sp|P50134.1|DCOR_DATST//1.00E-119//RecName: Full=Ornithine decarboxylase; Short=ODC >gi|871008|emb|CAA61121.1|ornithine decarboxylase [Datura stramonium]	Unigene925_All//9.00E-06//AT2G16500| ADC1 (ARGININE DECARBOXYLASE 1); arginine decarboxylase	Unigene925_All//0.00E+00//gi|164349274|gb|ES815701.1|ES815701	ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism		nr -

Unigene9250_All	280	0.19	0.72	0.00	2.13	0.00	1.29	0.00	1.64	0.28	1.95E+00	3.73E-01			-7.55E+00	6.09E-01		-1.11E+01	1.77E-04	Down	-7.26E-01	4.60E-01		1.07E+01	1.94E-03		8.15E+00	3.99E-01		Unigene9250_All//gi|110742215|dbj|BAE99034.1|//9.00E-15//disease resistance RPP5 like protein [Arabidopsis thaliana]	Unigene9250_All//4.00E-16//AT4G16950| RPP5 (RECOGNITION OF PERONOSPORA PARASITICA 5); nucleotide binding	Unigene9250_All//1.00E-15//C0115409			GO:0005488//GO:0009627//GO:0009725//GO:0009987//GO:0050832	nr -
Unigene9251_All	266	60.58	92.20	130.12	213.30	218.00	494.93	201.39	146.29	208.33	6.06E-01	3.92E-08			1.10E+00	1.01E-28	Up	3.15E-02	7.49E-01		1.21E+00	3.98E-139	Up	-4.61E-01	7.58E-13		4.89E-02	5.28E-01				Unigene9251_All//1.00E-77//TC176227				
Unigene9252_All	260	0.40	1.17	0.00	0.77	0.93	0.69	5.20	1.45	0.77	1.54E+00	3.22E-01			-8.65E+00	3.84E-01		2.75E-01	8.94E-01		-1.42E-01	9.33E-01		-1.85E+00	9.21E-04	Down	-2.76E+00	7.51E-06	Down			Unigene9252_All//5.00E-86//TC160522				
Unigene92525_All	560	0.19	0.45	0.86	1.16	3.32	3.55	0.30	0.22	0.14	1.28E+00	4.34E-01			2.20E+00	9.13E-02		1.52E+00	1.80E-03		1.62E+00	8.39E-04	Up	-4.32E-01	7.91E-01		-1.09E+00	5.51E-01		Unigene92525_All//gi|76160945|gb|AB404436.1|//1.00E-12//serine/threonine protein kinase SAPK8-like protein [Solanum tuberosum]	Unigene92525_All//1.00E-13//AT4G33950| OST1 (OPEN STOMATA 1); calcium-dependent protein serine/threonine kinase/ kinase/ protein kinase	Unigene92525_All//2.00E-50//TC132687			GO:0004674//GO:0005984//GO:0006464//GO:0006633//GO:0006641//GO:0006800//GO:0006952//GO:0006970//GO:0009755//GO:0010118//GO:0032559//GO:0043231//GO:0044444//GO:0048827	nr -
Unigene92548_All	429	0.12	0.00	0.62	1.63	0.96	0.00	0.49	0.19	0.00	-6.93E+00	5.95E-01			2.35E+00	2.38E-01		-7.55E-01	3.69E-01		-1.07E+01	1.95E-04	Down	-1.34E+00	4.28E-01		-8.94E+00	5.77E-02		Unigene92548_All//gi|2739377|gb|AAC14500.1|//1.00E-09//expressed protein [Arabidopsis thaliana]	Unigene92548_All//8.00E-11//AT2G26520| unknown protein				GO:0003824//GO:0015630//GO:0044430//GO:0046872	nr -
Unigene9259_All	382	0.00	0.00	0.00	0.00	0.00	0.00	0.66	3.17	1.67	null	null			null	null		null	null		null	null		2.26E+00	3.35E-04	Up	1.33E+00	1.00E-01		Unigene9259_All//gi|297609693|ref|NP_001063531.2|//3.00E-10//Os09g0488700 [Oryza sativa Japonica Group] >gi|255679006|dbj|BAF25445.2|Os09g0488700 [Oryza sativa Japonica Group]	Unigene9259_All//5.00E-15//AT4G12070| unknown protein					nr +
Unigene926_All	1432	5.99	5.45	2.01	26.37	34.68	76.92	24.51	28.19	125.00	-1.37E-01	5.31E-01			-1.58E+00	1.27E-12	Down	3.95E-01	1.22E-08		1.54E+00	9.46E-168	Up	2.02E-01	9.72E-03		2.35E+00	0.00E+00	Up	Unigene926_All//gi|1706323|sp|P50134.1|DCOR_DATST//1.00E-123//RecName: Full=Ornithine decarboxylase; Short=ODC >gi|871008|emb|CAA61121.1|ornithine decarboxylase [Datura stramonium]	Unigene926_All//3.00E-12//AT5G11880| diaminopimelate decarboxylase, putative / DAP carboxylase, putative	Unigene926_All//0.00E+00//TC156190		ko00480|Glutathione metabolism//ko00330|Arginine and proline metabolism		nr -
Unigene92629_All	377	0.28	0.00	0.71	0.53	1.19	0.60	1.35	0.00	0.53	-8.12E+00	3.62E-01			1.35E+00	4.08E-01		1.17E+00	3.47E-01		1.81E-01	9.34E-01		-1.04E+01	8.88E-04	Down	-1.35E+00	1.40E-01		Unigene92629_All//gi|229560489|gb|ACQ77596.1|//3.00E-21//CCR4-NOT [Dimocarpus longan]	Unigene92629_All//6.00E-20//AT3G44260| CCR4-NOT transcription complex protein, putative			ko03018|RNA degradation	GO:0004518//GO:0006950	nr -
Unigene9267_All	367	2.71	0.00	2.47	0.54	0.09	0.00	0.00	0.00	0.00	-1.14E+01	7.45E-06	Down	-1.35E-01	8.38E-01		-2.53E+00	2.32E-01		-9.08E+00	1.31E-01		null	null		null	null		Unigene9267_All//gi|224127132|ref|XP_002329408.1|//3.00E-24//GH3 family protein [Populus trichocarpa] >gi|222870458|gb|EEF07589.1| GH3 family protein [Populus trichocarpa]	Unigene9267_All//1.00E-21//AT4G03400| DFL2 (DWARF IN LIGHT 2)	Unigene9267_All//1.00E-142//gi|48741887|gb|C0072406.1|C0072406			GO:0009314//GO:0009536//GO:0009725	nr -
Unigene92682_All	224	0.70	1.36	0.00	2.67	4.15	0.00	0.00	0.00	0.53	9.54E-01	5.02E-01			-9.45E+00	2.41E-01		6.37E-01	4.18E-01		-1.14E+01	7.68E-04	Down	null	null		9.06E+00	2.41E-01								
Unigene9269_All	287	0.00	0.00	0.00	2.43	2.64	7.08	2.06	0.87	0.00	null	null			null	null		1.19E-01	9.05E-01		1.54E+00	1.14E-03		-1.24E+00	1.54E-01		-1.10E+01	1.41E-04	Down	Unigene9269_All//gi|12039277|gb|AAG46067.1|AC079830_7//2.00E-07//expressed protein [Oryza sativa Japonica Group] >gi|108710365|gb|ABF98160.1|expressed protein [Oryza sativa (japonica cultivar-group)]	Unigene9269_All//5.00E-08//AT4G10810| unknown protein	Unigene9269_All//4.00E-127//gi|109887765|gb|DW516734.1|DW516734				nr +
Unigene9273_All	230	3.41	0.22	2.55	2.17	0.75	0.00	0.74	1.82	0.35	-3.95E+00	8.54E-04	Down	-4.22E-01	6.21E-01		-1.53E+00	1.45E-01		-1.11E+01	2.96E-03		1.31E+00	2.34E-01		-1.09E+00	5.51E-01								
Unigene9274_All	418	0.00	0.00	0.00	0.00	0.00	0.11	1.72	1.50	0.19	null	null			null	null		null	null		6.75E+00	6.80E-01		-1.97E-01	7.84E-01		-3.17E+00	8.09E-04	Down	Unigene9274_All//gi|71010679|gb|AAZ20288.1|//2.00E-26//disease resistance-responsive family protein [Arachis hypogaea]	Unigene9274_All//3.00E-17//AT5G49040| disease resistance-responsive protein-related / dirigent protein-related	Unigene9274_All//0.00E+00//ES824103				nr +
Unigene92740_All	208	0.25	1.22	1.28	0.48	4.97	0.22	0.61	0.40	0.00	2.28E+00	2.33E-01			2.35E+00	2.38E-01		3.37E+00	1.64E-04	Up	-1.14E+00	6.71E-01		-6.02E-01	7.64E-01		-9.25E+00	1.98E-01								
Unigene92765_All	239	0.00	0.00	2.23	2.50	0.86	0.00	0.35	0.00	0.00	null	null			1.11E+01	3.98E-03		-1.53E+00	1.01E-01		-1.13E+01	7.68E-04	Down	-8.47E+00	3.95E-01		-8.47E+00	3.52E-01								
Unigene9278_All	227	0.00	0.89	3.05	0.88	1.52	1.19	1.30	1.66	1.76	9.80E+00	1.34E-01			1.16E+01	6.09E-04	Up	7.89E-01	5.95E-01		4.44E-01	7.62E-01		3.46E-01	7.37E-01		4.29E-01	6.61E-01								
Unigene92814_All	370	0.71	0.68	1.87	3.10	0.93	0.61	4.11	10.28	134.05	-4.62E-02	9.86E-01			1.40E+00	1.39E-01		-1.73E+00	5.77E-03		-2.34E+00	1.18E-03		1.32E+00	5.62E-06	Up	5.03E+00	7.49E-299	Up	Unigene92814_All//gi|19911201|dbj|BAB86927.1|//9.00E-14//glucosyltransferase-9 [Vigna angularis]	Unigene92814_All//2.00E-14//AT2G36790| UGT73C6 (UDP-glucosyl transferase 73C6); UDP-glucosyltransferase/ UDP-glycosyltransferase/ quercetin 3-O-glucosyltransferase/ quercetin 4'-O-glucosyltransferase/ quercetin 7-O-glucosyltransferase/ transferase, transferring glycosyl groups	Unigene92814_All//3.00E-20//TC132849		ko00908|Zeatin biosynthesis	GO:0016128//GO:0035251//GO:0051553	nr +
Unigene92818_All	257	3.05	1.18	2.49	4.65	2.41	0.88	0.16	0.16	0.16	-1.37E+00	9.59E-02			-2.97E-01	6.97E-01		-9.48E-01	1.12E-01		-2.40E+00	7.06E-04	Down	-1.68E-02	9.94E-01		-8.58E-02	9.62E-01				Unigene92818_All//4.00E-133//TC177632				
Unigene9282_All	585	0.00	11.09	6.01	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	4.83E-37	Up	1.26E+01	1.87E-19	Up	null	null		null	null		null	null		null	null		Unigene9282_All//gi|115467312|ref|NP_001057255.1|//1.00E-16//Os06g0238300 [Oryza sativa Japonica Group] >gi|51535152|dbj|BAD37864.1|CREG2-protein-like [Oryza sativa Japonica Group] >gi|51535816|dbj|BAD37901.1|CREG2-protein-like [Oryza sativa Japonica Group] >gi|113395295|dbj|BAF19169.1|Os06g0238300 [Oryza sativa Japonica Group]	Unigene9282_All//9.00E-13//AT2G04690| cellular repressor of E1A-stimulated genes (CREG) family					nr +
Unigene9285_All	280	0.00	0.00	0.00	0.00	0.00	0.00	2.11	1.64	0.00	null	null			null	null		null	null		null	null		-3.65E-01	6.48E-01		-1.10E+01	1.41E-04	Down	Unigene9285_All//gi|301120388|ref|XP_002907921.1|//2.00E-30//polyadenylate-binding protein 1-B [Phytophthora infestans T30-4] >gi|262102952|gb|EEY61004.1|polyadenylate-binding protein 1-B [Phytophthora infestans T30-4]	Unigene9285_All//2.00E-27//AT1G49760| PAB8 (POLY(A) BINDING PROTEIN 8); RNA binding / translation initiation factor			ko03040|Spliceosome	GO:0003676	nr +
Unigene92899_All	616	0.93	0.82	1.56	0.49	0.34	2.57	1.78	0.75	5.69	-1.84E-01	8.25E-01			7.36E-01	3.23E-01		-5.33E-01	6.78E-01		2.40E+00	8.62E-05	Up	-1.26E+00	3.46E-02		1.67E+00	9.15E-08	Up	Unigene92899_All//gi|16604352|gb|AAL24182.1|//3.00E-45//AT5g12010/F14F18_180 [Arabidopsis thaliana] >gi|25141199|gb|AAN73294.1|At5g12010/F14F18_180 [Arabidopsis thaliana]	Unigene92899_All//2.00E-38//AT5G12010| unknown protein	Unigene92899_All//0.00E+00//gi|78326482|gb|DT546756.1|DT546756			GO:0009536	nr +
Unigene92939_All	692	0.15	0.07	0.08	1.22	0.95	0.00	0.67	0.12	0.00	-1.05E+00	6.81E-01			-9.74E-01	7.18E-01		-3.72E-01	6.06E-01		-1.03E+01	2.43E-05	Down	-2.48E+00	3.38E-02		-9.39E+00	1.09E-03		Unigene92939_All//gi|224115078|ref|XP_002316934.1|//8.00E-15//cyclic nucleotide-gated channel [Populus trichocarpa] >gi|222850999|gb|EEE97546.1|cyclic nucleotide-gated channel [Populus trichocarpa]						nr -
Unigene92947_All	228	0.69	0.22	0.00	0.00	0.45	0.00	2.78	0.00	0.17	-1.63E+00	4.87E-01			-9.43E+00	2.41E-01		8.82E+00	4.50E-01		null	null		-1.14E+01	1.23E-04	Down	-3.99E+00	5.82E-04	Down							
Unigene9298_All	302	3.12	0.00	0.18	1.32	0.00	1.20	0.56	0.28	0.26	-1.16E+01	1.46E-05	Down	-4.14E+00	2.90E-04	Down	-1.04E+01	4.36E-03		-1.41E-01	9.03E-01		-1.02E+00	6.12E-01		-1.09E+00	5.50E-01		Unigene9298_All//gi|297802022|ref|XP_002868895.1|//2.00E-25//DNA binding protein [Arabidopsis lyrata subsp. lyrata] >gi|297314731|gb|EFH45154.1| DNA binding protein [Arabidopsis lyrata subsp. lyrata]	Unigene9298_All//1.00E-23//AT1G19510| ATRL5 (ARABIDOPSIS RAD-LIKE 5); DNA binding / transcription factor		MYB-related		GO:0003676//GO:0010468//GO:0043231	nr +
Unigene9300_All	319	0.00	3.65	3.84	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.04E-06	Up	1.19E+01	9.08E-07	Up	null	null		null	null		null	null		null	null		Unigene9300_All//gi|300263495|gb|EFJ47695.1|//9.00E-42//DEAD-box RNA helicase, ATP-dependent, cytoplasmic [Volvox carteri f. nagariensis]	Unigene9300_All//8.00E-43//AT4G00660| DEAD/DEAH box helicase, putative			ko03018|RNA degradation	GO:0032559//GO:0042623	nr +
Unigene93005_All	382	0.00	0.13	0.00	0.91	0.54	0.00	2.10	0.22	0.94	7.05E+00	6.04E-01			null	null		-7.55E-01	5.66E-01		-9.83E+00	2.11E-02		-3.26E+00	4.48E-04	Down	-1.16E+00	8.85E-02		Unigene93005_All//gi|17979255|gb|AAL49944.1|//2.00E-49//AT5g49550/K6M13_10 [Arabidopsis thaliana] >gi|29028742|gb|AAO64750.1|At5g49550/K6M13_10 [Arabidopsis thaliana]	Unigene93005_All//5.00E-50//AT5G49555| amine oxidase-related	Unigene93005_All//2.00E-138//gi|78351675|gb|DT571949.1|DT571949			GO:0003824//GO:0043231//GO:0046914	nr +
Unigene9301_All	246	0.85	1.24	0.65	2.63	1.82	0.00	1.20	1.87	0.16	5.39E-01	6.71E-01			-3.90E-01	8.06E-01		-5.33E-01	5.38E-01		-1.14E+01	3.89E-04	Down	6.35E-01	5.36E-01		-2.89E+00	6.75E-02				Unigene9301_All//3.00E-07//TC164086				
Unigene9302_All	260	18.51	15.01	26.63	24.14	16.29	17.72	13.33	9.00	4.44	-3.03E-01	2.90E-01			5.24E-01	2.47E-02		-5.67E-01	1.12E-02		-4.46E-01	6.53E-02		-5.67E-01	5.77E-02		-1.59E+00	2.87E-07	Down	Unigene9302_All//gi|15220251|ref|NP_172563.1|//3.00E-14//SNRK2.4 (SNF1-RELATED PROTEIN KINASE 2.4); kinase [Arabidopsis thaliana] >gi|1168529|sp|P43291.1|SRK2A_ARATH RecName: Full=Serine/threonine-protein kinase SRK2A; AltName: Full=Arabidopsis protein SK1; AltName: Full=OST1-kinase-like 7; AltName: Full=SNF1-related kinase 2.4; Short=SnRK2.4 >gi|166882|gb|AAA02840.1|serine/threonine kinase [Arabidopsis thaliana] >gi|1931648|gb|AAB65483.1| Ser/Thr kinase; 69816-71936 [Arabidopsis thaliana] >gi|20260462|gb|AAM13129.1|Ser/Thr kinase [Arabidopsis thaliana] >gi|21536490|gb|AAM60822.1|Ser/Thr kinase [Arabidopsis thaliana] >gi|31711866|gb|AAP68289.1|At1g10940 [Arabidopsis thaliana]	Unigene9302_All//1.00E-15//AT1G10940| SNRK2.4 (SNF1-RELATED PROTEIN KINASE 2.4); kinase	Unigene9302_All//8.00E-51//TC150930			GO:0004672//GO:0006464//GO:0006970//GO:0032559//GO:0043231	nr +
Unigene93061_All	653	0.24	0.47	0.00	1.83	3.11	0.90	3.24	1.60	1.22	9.54E-01	5.02E-01			-7.91E+00	2.41E-01		7.65E-01	9.48E-02		-1.03E+00	1.06E-01		-1.02E+00	1.04E-02		-1.41E+00	3.88E-04	Down	Unigene93061_All//gi|15239147|ref|NP_196170.1|//7.00E-57//protein kinase-related [Arabidopsis thaliana] >gi|60253522|gb|AAT71963.1|At5g05510 [Arabidopsis thaliana] >gi|56381969|gb|AAY85703.1|At5g05510 [Arabidopsis thaliana]	Unigene93061_All//2.00E-43//AT5G05510| protein kinase-related	Unigene93061_All//3.00E-37//CK640467				nr +
Unigene93063_All	409	3.97	2.73	3.12	2.44	5.47	6.74	0.00	0.00	0.00	-5.41E-01	2.98E-01			-3.44E-01	5.33E-01		1.17E+00	5.98E-03		1.47E+00	1.89E-04	Up	null	null		null	null		Unigene93063_All//gi|2827777|sp|P29136.2|MEP1_SOYBN//3.00E-15//RecName: Full=Metalloendoproteinase 1; AltName: Full=SMEP1; Flags: Precursor >gi|1679656|gb|AAB26959.1|metalloproteinase [Glycine max]	Unigene93063_All//2.00E-15//AT1G59970| matrixin family protein				GO:0016020//GO:0016787	nr -
Unigene93079_All	207	0.51	1.47	1.03	4.81	1.50	0.22	1.84	0.81	0.38	1.54E+00	3.22E-01			1.03E+00	5.89E-01		-1.68E+00	1.36E-02		-4.46E+00	3.09E-05	Down	-1.19E+00	3.09E-01		-2.26E+00	6.48E-02								
Unigene931_All	257	3.26	1.58	1.66	1.16	0.40	1.41	11.35	9.60	2.48	-1.05E+00	1.74E-01			-9.75E-01	2.37E-01		-1.53E+00	2.97E-01		2.74E-01	8.32E-01		-2.43E-01	5.07E-01		-2.19E+00	3.28E-09	Down			Unigene931_All//9.00E-131//BG440451				
Unigene9310_All	208	132.56	70.40	69.38	181.77	134.60	208.66	171.76	82.59	85.61	-9.13E-01	1.12E-17			-9.34E-01	1.39E-17		-4.34E-01	5.05E-08		1.99E-01	1.84E-02		-1.06E+00	5.08E-35	Down	-1.00E+00	2.99E-33	Down	Unigene9310_All//gi|33590374|gb|AAQ22726.1|//1.00E-28//40S ribosomal protein S25 [Glycine max]	Unigene9310_All//2.00E-29//AT4G34555| 40S ribosomal protein S25, putative	Unigene9310_All//9.00E-112//ES824085		ko03010|Ribosome	GO:0010467//GO:0015935	nr +

Unigene9311_All	281	0.00	0.00	0.00	0.00	0.00	0.00	3.31	1.64	0.28	null	null		null	null		null	null		null	null		-1.02E+00	1.21E-01		-3.55E+00	3.97E-05	Down	Unigene9311_All//gi|301102985|ref|XP_002900579.1|//7.00E-10//RNA polymerase-associated protein RTF1 [Phytophthora infestans T30-4] >gi|262101842|gb|EEY59894.1| RNA polymerase-associated protein RTF1 [Phytophthora infestans T30-4]				ko04712|Circadian rhythm - plant	GO:0005488//GO:0019538//GO:0044260	nr +
Unigene9312_All	2260	0.02	0.00	0.00	0.15	0.38	0.08	5.22	0.83	1.27	-4.54E+00	5.95E-01		-4.54E+00	6.09E-01		1.30E+00	1.02E-01		-9.50E-01	4.80E-01		-2.65E+00	6.28E-42	Down	-2.04E+00	8.92E-32	Down	Unigene9312_All//gi|240255605|ref|NP_001030839.5|//0.00E+00//ETO1 (ETHYLENE OVERPRODUCER 1); protein binding, bridging [Arabidopsis thaliana] >gi|297827|emb|CAA43517.1| ETO1 (ETHYLENE OVERPRODUCER 1); protein binding, bridging [Arabidopsis thaliana]	Unigene9312_All//0.00E+00//AT3G51770| ETO1 (ETHYLENE OVERPRODUCER 1); protein binding, bridging	Unigene9312_All//0.00E+00//C0105972			GO:0005488	nr -
Unigene9313_All	387	3.38	2.36	0.00	0.26	0.00	0.00	0.00	0.00	0.00	-5.20E-01	3.69E-01		-1.17E+01	3.71E-07	Down	-8.01E+00	3.05E-01		-8.01E+00	3.88E-01		null	null		null	null		Unigene9313_All//gi|157273668|gb|AB227888.1|//2.00E-46//fasciclin-like arabinogalactan protein 17 [Gossypium hirsutum]	Unigene9313_All//9.00E-20//AT4G31370| FLA5 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 5 PRECURSOR)	Unigene9313_All//4.00E-174//TC135704			GO:0031224//GO:0031410	nr +
Unigene9314_All	858	0.00	9.57	3.35	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	5.84E-47	Up	1.17E+01	6.95E-16	Up	null	null		null	null		null	null		null	null		Unigene9314_All//gi|157093503|gb|AB322406.1|//8.00E-09//unknown [Noctiluca scintillans]						nr -
Unigene9315_All	630	0.00	1.29	0.25	0.32	1.80	1.36	0.54	0.27	0.00	1.03E+01	9.30E-05	Up	7.99E+00	2.33E-01		2.51E+00	7.34E-04	Up	2.11E+00	1.44E-02		-1.02E+00	3.99E-01		-9.07E+00	8.12E-03		Unigene9315_All//gi|6573723|gb|AAF17643.1|AC009978.19||9.00E-46//T23E18.14 [Arabidopsis thaliana] >gi|38564294|gb|AAR23726.1| At1g76210 [Arabidopsis thaliana] >gi|41349928|gb|AAS00349.1| At1g76210 [Arabidopsis thaliana]	Unigene9315_All//1.00E-42//AT1G76210| unknown protein					nr +
Unigene9317_All	393	2.13	0.00	0.00	0.00	0.61	0.00	0.00	0.00	0.00	-1.11E+01	5.56E-05	Down	-1.11E+01	1.19E-04	Down	9.26E+00	1.04E-01		null	null		null	null		null	null		Unigene9317_All//gi|255596977|ref|XP_002536666.1|//6.00E-16//conserved hypothetical protein [Ricinus communis] >gi|223518947|gb|EEF25719.1| conserved hypothetical protein [Ricinus communis]						nr +
Unigene93177_All	431	0.49	1.53	0.49	0.23	2.08	0.94	0.88	0.29	0.55	1.65E+00	8.13E-02		2.53E-02	1.00E+00		3.17E+00	8.77E-04	Up	2.03E+00	1.49E-01		-1.60E+00	1.81E-01		-6.71E-01	5.30E-01								
Unigene9319_All	572	0.18	0.00	0.28	0.52	0.84	0.24	2.07	1.90	0.28	-7.51E+00	3.62E-01		6.11E-01	7.46E-01		6.90E-01	5.66E-01		-1.14E+00	4.56E-01		-1.24E-01	8.25E-01		-2.89E+00	2.03E-05	Down		Unigene9319_All//0.00E+00//ES804303				
Unigene93193_All	322	0.97	0.31	0.00	0.15	3.85	1.68	0.00	0.65	0.99	-1.63E+00	2.76E-01		-9.93E+00	4.87E-02		4.64E+00	1.66E-06	Up	3.44E+00	1.40E-02		9.34E+00	7.83E-02		9.95E+00	1.34E-02		Unigene93193_All//gi|15230936|ref|NP_191363.1|//2.00E-14//SINAT2 (SEVEN IN ABSENTIA OF ARABIDOPSIS 2); protein binding / ubiquitin-protein ligase/ zinc ion binding [Arabidopsis thaliana] >gi|46577554|sp|Q9M2P4.1|SIN2_ARATH RecName: Full=E3 ubiquitin-protein ligase SINAT2; AltName: Full=Seven in absentia homolog 2 >gi|105830184|gb|ABF74716.1| At3g58040 [Arabidopsis thaliana]	Unigene93193_All//8.00E-16//AT3G58040| SINAT2 (SEVEN IN ABSENTIA OF ARABIDOPSIS 2); protein binding / ubiquitin-protein ligase/ zinc ion binding	Unigene93193_All//3.00E-112//ES829879	ko04120|Ubiquitin mediated proteolysis	GO:0016874//GO:0044267//GO:0046872	nr +
Unigene93196_All	232	0.00	0.00	0.23	4.51	1.48	0.39	0.00	0.18	0.17	null	null		7.84E+00	6.20E-01		-1.60E+00	1.49E-02		-3.53E+00	9.33E-05	Down	7.49E+00	6.21E-01		7.42E+00	6.30E-01								
Unigene9321_All	370	0.00	0.00	0.00	0.00	0.00	0.00	3.31	2.94	0.54	null	null		null	null		null	null		null	null		-1.74E-01	7.49E-01		-2.62E+00	4.02E-05	Down							
Unigene9322_All	245	0.64	0.62	0.87	3.66	2.53	1.11	5.69	1.36	0.49	-4.65E-02	9.87E-01		4.40E-01	7.74E-01		-5.33E-01	4.70E-01		-1.73E+00	2.80E-02		-2.06E+00	2.51E-04	Down	-3.55E+00	2.28E-07	Down							
Unigene93231_All	281	2.79	9.56	3.41	9.22	10.29	13.18	1.05	1.93	4.40	1.77E+00	2.49E-05	Up	2.88E-01	6.65E-01		1.59E-01	7.26E-01		5.16E-01	1.21E-01		8.77E-01	3.46E-01		2.06E+00	5.00E-04	Up	Unigene93231_All//gi|224121322|ref|XP_002330798.1|//2.00E-14//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222872600|gb|EEF09731.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene93231_All//4.00E-07//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene93231_All//3.00E-63//TC177573	ko04626|Plant-pathogen interaction	GO:0005488//GO:0016787	nr +
Unigene9324_All	330	0.16	2.46	0.81	0.60	0.42	0.82	0.64	1.27	0.85	3.95E+00	7.51E-04	Up	2.35E+00	2.38E-01		-5.33E-01	7.47E-01		4.44E-01	7.62E-01		9.83E-01	3.73E-01		4.00E-01	7.42E-01								
Unigene93278_All	466	1.01	2.17	0.00	1.28	7.17	3.78	3.45	3.86	2.74	1.11E+00	1.13E-01		-9.98E+00	8.61E-03		2.48E+00	1.80E-10	Up	1.56E+00	2.64E-03		1.62E-01	7.18E-01		-3.34E-01	4.74E-01		Unigene93278_All//gi|15234987|ref|NP_192765.1|//4.00E-20//wound-responsive family protein [Arabidopsis thaliana] >gi|3695408|gb|AAC62808.1| contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana] >gi|4538956|emb|CAB39780.1| probable wound-induced protein [Arabidopsis thaliana] >gi|7267724|emb|CAB78150.1| probable wound-induced protein [Arabidopsis thaliana] >gi|21553934|gb|AAM63015.1| probable wound-induced protein [Arabidopsis thaliana] >gi|90962948|gb|ABE02398.1| At4g10270 [Arabidopsis thaliana]	Unigene93278_All//2.00E-21//AT4G10270| wound-responsive family protein	Unigene93278_All//0.00E+00//TC158256				nr +
Unigene9328_All	413	1.65	1.84	0.13	0.00	0.33	0.22	2.15	7.08	4.63	1.60E-01	8.28E-01		-3.68E+00	4.81E-03		8.38E+00	3.15E-01		7.77E+00	4.68E-01		1.72E+00	1.18E-06	Up	1.11E+00	7.10E-03		Unigene9328_All//gi|38371990|gb|AAR18735.1|//4.00E-21//chitinase [Rambusa oldhamii]	Unigene9328_All//1.00E-18//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene9328_All//3.00E-11//CD486070		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0004568//GO:0006026//GO:0009607//GO:0030247//GO:0031410	nr +
Unigene93313_All	327	0.16	0.00	0.16	3.96	2.63	0.55	0.65	0.13	0.12	-7.32E+00	5.95E-01		2.50E-02	9.90E-01		-5.89E-01	3.13E-01		-2.84E+00	7.63E-05	Down	-2.34E+00	2.36E-01		-2.41E+00	1.94E-01								
Unigene9332_All	369	0.00	0.00	0.00	0.00	0.00	0.00	2.98	0.79	0.22	null	null		null	null		null	null		null	null		-1.91E+00	2.64E-03		-3.79E+00	3.27E-06	Down	Unigene9332_All//gi|115488866|ref|NP_001066920.1|//5.00E-37//Os12g0530000 [Oryza sativa Japonica Group] >gi|108936012|sp|Q2QPG9.1|H2AXB_ORYSJ RecName: Full=Probable histone H2AXb >gi|158513341|sp|A2ZL69.1|H2AXB_ORYSI RecName: Full=Probable histone H2AXb >gi|113649427|dbj|BAF29939.1| Os12g0530000 [Oryza sativa Japonica Group]	Unigene9332_All//6.00E-19//AT5G02560| HTA12; DNA binding				GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr -
Unigene93335_All	286	0.00	0.00	0.00	0.00	0.72	0.00	7.10	1.90	4.74	null	null		null	null		9.50E+00	1.56E-01		null	null		-1.90E+00	1.90E-05	Down	-5.83E-01	1.37E-01				Unigene93335_All//5.00E-83//TC175880				
Unigene9336_All	256	0.82	0.00	0.42	1.56	1.08	1.23	0.00	0.65	2.18	-9.68E+00	1.20E-01		-9.75E-01	6.18E-01		-5.33E-01	6.15E-01		-3.34E-01	7.56E-01		9.35E+00	1.38E-01		1.11E+01	3.28E-04	Up		Unigene9336_All//3.00E-10//TC159031				
Unigene9337_All	486	0.00	0.00	0.22	2.87	0.99	0.19	3.39	0.69	0.66	null	null		7.78E+00	3.86E-01		-1.53E+00	5.22E-03		-3.95E+00	1.12E-06	Down	-2.30E+00	1.36E-05	Down	-2.37E+00	5.20E-06	Down	Unigene9337_All//gi|224077988|ref|XP_002305471.1|//2.00E-46//SAUR family protein [Populus trichocarpa] >gi|222848435|gb|EEE85982.1| SAUR family protein [Populus trichocarpa]	Unigene9337_All//4.00E-37//AT1G75590| auxin-responsive family protein	Unigene9337_All//0.00E+00//TC152621			GO:0009725	nr +
Unigene9339_All	729	0.00	0.00	0.00	0.07	0.00	0.00	1.04	4.01	0.16	null	null		null	null		-6.09E+00	5.39E-01		-6.09E+00	6.11E-01		1.94E+00	1.05E-07	Up	-2.67E+00	1.64E-03		Unigene9339_All//gi|6119844|gb|AAF04253.1|AF097651_1|/9.00E-50//short-chain alcohol dehydrogenase SAD-C [Pisum sativum]	Unigene9339_All//1.00E-42//AT3G29250| copper ion binding / oxidoreductase	Unigene9339_All//0.00E+00//TC134281	ko00906|Carotenoid biosynthesis	GO:0000166//GO:0004672//GO:0008152//GO:0016020//GO:0016491	nr +
Unigene9343_All	358	243.48	61.00	155.29	116.05	104.08	57.40	0.00	0.23	0.22	-2.00E+00	1.25E-177	Down	-6.49E-01	2.96E-29		-1.57E-01	7.13E-02		-1.02E+00	1.19E-33	Down	7.87E+00	3.96E-01		7.80E+00	3.99E-01		Unigene9343_All//gi|82468803|gb|AB876766.1|//2.00E-57//lupeol synthase [Ricinus communis]	Unigene9343_All//2.00E-54//AT1G78950| beta-amyrin synthase, putative	Unigene9343_All//0.00E+00//gi|78340045|gb|DT560319.1|DT560319	ko00100|Steroid biosynthesis	GO:0031559	nr +
Unigene93439_All	224	1.40	9.50	1.66	1.11	1.54	0.20	0.57	0.56	0.18	2.76E+00	6.33E-07	Up	2.48E-01	8.22E-01		4.67E-01	7.79E-01		-2.46E+00	2.22E-01		-1.67E-02	1.02E+00		-1.67E+00	4.74E-01		Unigene93439_All//gi|296088601|emb|CBI37592.3|//5.00E-07//unnamed protein product [Vitis vinifera]		Unigene93439_All//1.00E-46//TC170385				nr +
Unigene9345_All	487	0.97	0.31	1.53	0.31	0.14	0.09	0.17	2.06	0.16	-1.63E+00	1.58E-01		6.63E-01	4.19E-01		-1.12E+00	5.81E-01		-1.73E+00	4.98E-01		3.57E+00	3.07E-05	Up	-8.56E-02	9.67E-01								
Unigene93455_All	377	0.00	0.00	0.00	0.00	0.00	0.00	2.24	0.00	0.00	null	null		null	null		null	null		null	null		-1.11E+01	4.39E-06	Down	-1.11E+01	2.21E-06	Down	Unigene93455_All//gi|28466815|gb|AA04016.1|//2.00E-09//At1g11655 [Arabidopsis thaliana]		Unigene93455_All//3.00E-17//DW518236				nr +
Unigene9346_All	638	0.00	3.34	2.00	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.09E-12	Up	1.10E+01	4.66E-07	Up	null	null		null	null		null	null		null	null		Unigene9346_All//sp|P01034|CYTC_HUMAN//1.00E-64//Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1						swissprot -
Unigene93491_All	207	0.00	0.00	0.00	0.96	0.50	0.44	100.29	216.05	94.50	null	null		null	null		-9.48E-01	5.86E-01		-1.14E+00	5.66E-01		1.11E+00	5.82E-47	Up	-8.58E-02	4.89E-01		Unigene93491_All//gi|150415186|gb|AB868690.1|//2.00E-07//oxalate oxidase [Theobroma cacao]	Unigene93491_All//2.00E-05//AT5G39120| germin-like protein, putative					nr +
Unigene93495_All	301	0.00	0.84	1.24	0.00	2.17	0.15	0.00	0.00	0.00	9.72E+00	7.74E-02		1.03E+01	2.46E-02		1.11E+01	4.92E-04	Up	7.23E+00	6.79E-01		null	null		null	null								ESTscan -
Unigene9350_All	427	0.00	3.32	1.62	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	4.04E-08	Up	1.07E+01	6.09E-04	Up	null	null		null	null		null	null		null	null								ESTscan +
Unigene9351_All	369	0.00	0.00	0.00	0.00	0.00	0.00	1.95	1.02	0.00	null	null		null	null		null	null		null	null		-9.34E-01	2.26E-01		-1.09E+01	1.78E-05	Down	Unigene9351_All//gi|157093631|gb|AB922470.1|//2.00E-30//40S ribosomal protein S26 [Oxyrrhis marina]	Unigene9351_All//2.00E-23//AT3G56340| 40S ribosomal protein S26 (RPS26C)		ko03010|Ribosome	GO:0005622	nr -
Unigene93512_All	236	0.22	4.08	1.13	1.27	2.04	4.98	0.72	1.59	0.68	4.20E+00	1.29E-04	Up	2.35E+00	2.38E-01		6.90E-01	5.66E-01		1.97E+00	4.50E-03		1.15E+00	3.27E-01		-8.59E-02	9.64E-01								
Unigene93520_All	231	2.94	0.00	0.00	3.67	1.64	4.11	0.37	0.00	0.00	-1.15E+01	4.09E-04	Down	-1.15E+01	7.62E-04	Down	-1.16E+00	1.15E-01		1.64E-01	8.25E-01		-8.52E+00	3.95E-01		-8.52E+00	3.51E-01			Unigene93520_All//8.00E-100//TC153320				
Unigene9354_All	323	0.00	4.24	1.65	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	7.76E-08	Up	1.07E+01	3.98E-03		null	null		null	null		null	null		null	null		Unigene9354_All//sp|Q07352|TISB_HUMAN//3.00E-54//Butyrate response factor 1 OS=Homo sapiens GN=ZFP36L1 PE=1 SV=1						swissprot -
Unigene93553_All	236	3.10	0.00	0.00	5.28	3.50	2.68	0.36	0.00	0.00	-1.16E+01	2.11E-04	Down	-1.16E+01	4.12E-04	Down	-5.92E-01	3.18E-01		-9.78E-01	1.14E-01		-8.49E+00	3.95E-01		-8.49E+00	3.51E-01			Unigene93553_All//2.00E-94//CO119779				
Unigene93555_All	303	3.28	0.84	0.00	2.63	0.91	0.15	0.14	0.00	0.39	-1.97E+00	9.92E-03		-1.17E+01	1.77E-05	Down	-1.53E+00	4.82E-02		-4.14E+00	4.12E-04	Down	-7.12E+00	6.35E-01		1.50E+00	5.56E-01		Unigene93555_All//gi|297811343|ref|XP_002873555.1|//2.00E-11//dihydropyrimidinase [Arabidopsis lyrata subsp. lyrata] >gi|297319392|gb|EFH49814.1| dihydropyrimidinase [Arabidopsis lyrata subsp. lyrata]	Unigene93555_All//9.00E-13//AT5G12200| dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2)	Unigene93555_All//5.00E-71//ES807046	ko00240|Pyrimidine metabolism//ko00410|beta-Alanine metabolism//ko00770|Pantothenate and CoA biosynthesis		nr -
Unigene93578_All	611	1.03	2.32	0.44	1.14	0.90	0.15	1.52	8.00	4.17	1.18E+00	3.93E-02		-1.24E+00	2.13E-01		-3.40E-01	6.80E-01		-2.95E+00	5.83E-03		2.39E+00	7.23E-16	Up	1.45E+00	5.90E-05	Up	Unigene93578_All//gi|151934195|gb|ABS18435.1|//8.00E-18//WRKY36 [Glycine max]	Unigene93578_All//6.00E-12//AT4G01720| WRKY47; transcription factor	Unigene93578_All//2.00E-07//TC149870	WRKY		GO:0003677//GO:0010468	nr +
Unigene9358_All	236	0.22	0.00	0.00	0.63	0.15	0.00	8.96	0.71	2.19	-7.79E+00	5.94E-01		-7.79E+00	6.08E-01		-2.12E+00	3.83E-01		-9.31E+00	2.28E-01		-3.66E+00	1.12E-10	Down	-2.03E+00	2.52E-06	Down			Unigene9358_All//3.00E-07//gi|13246449|gb|BE052767.2|BE052767				
Unigene93592_All	272	0.00	0.00	0.00	0.00	0.00	0.00	0.00	4.76	0.00	null	null		null	null		null	null		null	null		1.22E+01	3.67E-09	Up	null	null				Unigene93592_All//1.00E-71//TC154865				
Unigene93614_All	211	0.74	0.00	1.01	0.24	0.82	4.07	0.00	0.00	0.00	-9.54E+00	2.12E-01		4.41E-01	7.74E-01		1.79E+00	5.19E-01		4.11E+00	3.40E-04	Up	null	null		null	null		Unigene93614_All//gi|224061351|ref|XP_002300437.1|//2.00E-10//integral membrane single C2 domain protein [Populus trichocarpa] >gi|222847695|gb|EEE85242.1| integral membrane single C2 domain protein [Populus trichocarpa]					GO:0016020	nr +
Unigene93648_All	400	0.26	0.63	0.00	0.75	2.15	0.90	1.37	0.84	5.08	1.28E+00	4.34E-01		-8.03E+00	3.84E-01		1.53E+00	5.80E-02		2.74E-01	8.32E-01		-7.17E-01	4.22E-01		1.89E+00	1.49E-05	Up	Unigene93648_All//gi|115447997|ref|NP_001047778.1|//5.00E-10//Os02g0687900 [Oryza sativa Japonica Group] >gi|113537309|dbj|BAF09692.1| Os02g0687900 [Oryza sativa Japonica Group]	Unigene93648_All//5.00E-10//AT3G22010| serine carboxypeptidase S10 family protein		ko00940|Phenylpropanoid biosynthesis	GO:0004180//GO:0031410	nr -

Unigene93650_All	668	0.39	0.00	0.16	2.16	1.96	1.76	2.28	0.19	0.72	-8.61E+00	6.64E-02		-1.30E+00	4.35E-01		-1.43E-01	8.15E-01		-2.99E-01	6.38E-01		-3.60E+00	9.55E-08	Down	-1.67E+00	7.06E-04	Down	Unigene93650_All//gi|7269720|emb|CAB81453.1|//7.00E-14//receptor protein kinase-like protein [Arabidopsis thaliana] >gi|224589634|gb|ACN59350.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene93650_All//5.00E-15//AT4G28650| leucine-rich repeat transmembrane protein kinase, putative	Unigene93650_All//1.00E-17//BG445385		ko04626|Plant-pathogen interaction	GO:0004674//GO:0004871//GO:0005488//GO:0044464	nr -
Unigene93674_All	400	0.00	0.25	0.00	0.00	1.21	0.68	3.07	0.00	1.29	7.98E+00	3.77E-01		null	null		1.02E+01	5.07E-03		9.40E+00	7.00E-02		-1.16E+01	9.98E-09	Down	-1.24E+00	1.98E-02		Unigene93674_All//gi|240256033|ref|NP_193913.4|//7.00E-37//binding / calmodulin binding [Arabidopsis thaliana]	Unigene93674_All//9.00E-34//AT4G21820| binding / calmodulin binding					nr +
Unigene93675_All	205	32.67	6.67	38.70	2.19	5.88	1.76	0.00	0.00	0.19	-2.29E+00	8.23E-17	Down	2.45E-01	2.87E-01		1.43E+00	2.58E-02		-3.11E-01	7.57E-01		null	null		7.60E+00	6.30E-01		Unigene93675_All//gi|297598860|ref|NP_001046338.2|//7.00E-07//Os02g0225000 [Oryza sativa Japonica Group] >gi|255670733|dbj|BAF08252.2| Os02g0225000 [Oryza sativa Japonica Group]		Unigene93675_All//2.00E-85//TC145772		ko04146|Peroxisome	GO:0006810//GO:0019866//GO:0031224//GO:0044439	nr +
Unigene93699_All	400	0.39	1.65	1.33	1.37	5.42	2.94	0.32	2.19	5.08	2.07E+00	3.92E-02		1.76E+00	1.28E-01		1.99E+00	2.05E-05	Up	1.10E+00	9.17E-02		2.79E+00	6.96E-04	Up	4.00E+00	3.90E-11	Up			Unigene93699_All//5.00E-07//TC170856				
Unigene937_All	933	33.20	26.99	28.99	87.94	79.65	27.74	14.82	8.83	3.54	-2.99E-01	2.37E-03		-1.95E-01	6.92E-02		-1.43E-01	1.42E-02		-1.66E+00	1.08E-141	Down	-7.48E-01	3.34E-08		-2.06E+00	1.17E-37	Down	Unigene937_All//gi|124360549|gb|AB033126.2|//2.00E-16//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene937_All//3.00E-11//AT3G09510| nucleic acid binding	Unigene937_All//0.00E+00//TC174169			GO:0003676//GO:0016772//GO:0044238//GO:0044260	nr +
Unigene9370_All	238	0.00	3.41	1.12	0.00	0.00	0.00	0.00	0.00	0.00	1.17E+01	9.30E-05	Up	1.01E+01	7.85E-02		null	null		null	null		null	null		null	null		Unigene9370_All//sp|P01024|CO3_HUMAN//2.00E-41//Complement C3 OS=Homo sapiens GN=C3 PE=1 SV=2							swissprot +
Unigene9371_All	221	3.08	0.69	3.13	13.30	1.40	3.68	0.00	0.00	0.00	-2.16E+00	2.84E-02		2.54E-02	9.96E-01		-3.25E+00	1.55E-13	Down	-1.85E+00	2.03E-06	Down	null	null		null	null				Unigene9371_All//2.00E-07//TC164929				
Unigene93734_All	212	10.37	10.04	13.56	6.58	3.09	0.64	0.00	0.00	0.00	-4.63E-02	9.23E-01		3.88E-01	3.34E-01		-1.09E+00	4.31E-02		-3.36E+00	5.87E-06	Down	null	null		null	null				Unigene93734_All//4.00E-12//TC136347				
Unigene93735_All	409	0.00	0.00	0.00	4.75	2.27	0.99	0.21	0.00	0.00	null	null		null	null		-1.06E+00	1.59E-02		-2.26E+00	1.51E-05	Down	-7.69E+00	3.94E-01		-7.69E+00	3.51E-01				Unigene93735_All//2.00E-55//DW479200				
Unigene9378_All	262	0.80	1.74	0.61	4.75	0.92	0.86	0.32	0.00	0.61	1.12E+00	3.28E-01		-3.90E-01	8.06E-01		-2.37E+00	2.03E-04	Down	-2.46E+00	4.15E-04	Down	-8.33E+00	3.94E-01		9.14E-01	6.23E-01								
Unigene93780_All	231	0.00	0.00	0.00	0.00	0.00	0.39	0.00	0.00	10.87	null	null		null	null		null	null		8.61E+00	4.68E-01		null	null		1.34E+01	5.70E-18	Up	Unigene93780_All//gi|115472809|ref|NP_001060003.1|//1.00E-12//Os07g0564500 [Oryza sativa Japonica Group] >gi|113611539|dbj|BAF21917.1| Os07g0564500 [Oryza sativa Japonica Group]	Unigene93780_All//4.00E-12//AT2G29990| NDA2 (ALTERNATIVE NAD(P)H DEHYDROGENASE 2); FAD binding / NADH dehydrogenase/ oxidoreductase	Unigene93780_All//2.00E-48//TC173686		ko00190|Oxidative phosphorylation	GO:0003954//GO:0005743//GO:0008152//GO:0030554	nr -
Unigene938_All	3063	5.98	8.01	3.95	19.42	13.70	5.84	7.99	3.06	2.16	4.21E-01	1.30E-04		-5.99E-01	7.01E-06		-5.03E-01	4.73E-16		-1.73E+00	6.41E-109	Down	-1.39E+00	7.85E-37	Down	-1.89E+00	9.00E-59	Down	Unigene938_All//gi|33465891|gb|AAQ19327.1|//1.00E-123//bZIP-like protein [Oryza sativa Japonica Group]	Unigene938_All//7.00E-22//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene938_All//4.00E-166//gi|78328462|gb|DT548736.1|DT548736				nr -
Unigene9381_All	286	0.00	1.95	0.00	0.00	0.12	0.63	0.00	1.17	2.65	1.09E+01	2.16E-03		null	null		6.91E+00	8.09E-01		9.30E+00	1.93E-01		1.02E+01	1.27E-02		1.14E+01	1.39E-05	Up							
Unigene93826_All	213	0.25	0.48	0.00	8.42	5.17	1.27	0.40	0.78	0.37	9.54E-01	7.22E-01		-7.94E+00	6.08E-01		-7.03E-01	1.40E-01		-2.73E+00	2.99E-06	Down	9.83E-01	6.31E-01		-8.57E-02	9.67E-01				Unigene93826_All//2.00E-17//gi|164354102|gb|ES849373.1|ES849373				
Unigene93849_All	234	0.22	0.65	2.28	0.00	0.88	0.00	0.00	0.00	3.23	1.54E+00	5.29E-01		3.35E+00	2.06E-02		9.79E+00	1.56E-01		null	null		null	null		1.17E+01	1.39E-05	Up	Unigene93849_All//gi|224135791|ref|XP_002322161.1|//4.00E-06//predicted protein [Populus trichocarpa] >gi|222869157|gb|EEF06288.1| predicted protein [Populus trichocarpa]		Unigene93849_All//4.00E-40//TC151428				nr +
Unigene9385_All	222	0.00	7.99	3.60	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	4.13E-10	Up	1.18E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene9385_All//gi|297726329|ref|NP_001175528.1|//3.00E-08//Os08g0345400 [Oryza sativa Japonica Group] >gi|255678376|dbj|BAH94256.1| Os08g0345400 [Oryza sativa Japonica Group]				ko03040|Spliceosome		nr +
Unigene9386_All	463	1.58	0.00	1.50	0.00	0.67	0.39	0.00	0.00	0.00	-1.06E+01	2.11E-04	Down	-8.16E-02	9.29E-01		9.39E+00	4.53E-02		8.61E+00	1.93E-01		null	null		null	null		Unigene9386_All//sp|P25893|YS83_RHIME//3.00E-14//Uncharacterized protein RN0383 OS=Rhizobium meliloti GN=RN0383 PE=4 SV=2							swissprot +
Unigene9387_All	357	60.67	306.86	142.15	121.95	154.43	154.59	212.82	303.34	222.85	2.34E+00	2.33E-270	Up	1.23E+00	1.15E-49	Up	3.41E-01	2.32E-07		3.42E-01	7.22E-07		5.11E-01	3.90E-30		6.64E-02	2.63E-01		Unigene9387_All//gi|28466883|gb|AA044050.1|//2.00E-25//At3g03150 [Arabidopsis thaliana]	Unigene9387_All//8.00E-27//AT3G03150| unknown protein	Unigene9387_All//0.00E+00//gi|13353001|gb|BG443349.1|BG443349			GO:0043231	nr -
Unigene9389_All	256	0.00	5.74	1.66	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	2.10E-08	Up	1.07E+01	1.35E-02		null	null		null	null		null	null		null	null		Unigene9389_All//gi|77540212|gb|AB486964.1|//7.00E-42//glyceraldehyde-3-phosphate dehydrogenase B subunit [Glycine max]	Unigene9389_All//3.00E-42//AT1G42970| GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase (NADP+)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene9389_All//7.00E-36//TC148524		ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0005576//GO:0006007//GO:0006950//GO:0008943//GO:0009314//GO:0009526//GO:0009532//GO:0009534//GO:0010038//GO:0019677//GO:0034285	nr +
Unigene939_All	1809	1.39	13.42	1.59	3.66	3.48	4.79	5.52	7.67	11.87	3.27E+00	4.45E-86	Up	1.95E-01	6.23E-01		-7.23E-02	8.09E-01		3.88E-01	5.61E-02		4.76E-01	4.04E-04		1.11E+00	1.79E-23	Up	Unigene939_All//gi|30683061|ref|NP_172759.2|//0.00E+00//glycosyl transferase family 17 protein [Arabidopsis thaliana]	Unigene939_All//0.00E+00//AT1G12990| glycosyl transferase family 17 protein	Unigene939_All//0.00E+00//TC141726			GO:0006486//GO:0008375//GO:0044464	nr -
Unigene93939_All	508	0.00	0.00	0.00	0.00	0.41	0.00	1.41	0.00	0.00	null	null		null	null		8.67E+00	1.56E-01		null	null		-1.05E+01	3.26E-05	Down	-1.05E+01	1.78E-05	Down	Unigene93939_All//gi|18390599|ref|NP_563756.1|//2.00E-34//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] >gi|8810462|gb|AAF80123.1|AC024174_5 Contains similarity to UDPG glucosyltransferase from Solanum berthaultii gi|2232354 and contains UDP-glycoronysyl and UDP-glucosyl transferases PF|00201 domain. ESTs gb|AV551176, gb|Z46581, gb|AV439781, gb|AV542358, gb|AV525326, gb|AV538963, gb|Z46580, gb|AV547292, gb|AV532314, gb|AV565317, gb|AV542340 come from this gene [Arabidopsis thaliana] >gi|30387515|gb|AAP31923.1| At1g06000 [Arabidopsis thaliana]	Unigene93939_All//2.00E-35//AT1G06000| UDP-glucoronosyl/UDP-glucosyl transferase family protein			ko00908|Zeatin biosynthesis	GO:0008194//GO:0016758//GO:0051553	nr -
Unigene9394_All	272	1.35	2.24	6.46	0.00	0.00	0.00	0.00	0.00	0.00	7.31E-01	4.16E-01		2.26E+00	1.32E-04	Up	null	null		null	null		null	null		null	null		Unigene9394_All//gi|225465417|ref|XP_002264098.1|//3.00E-10//PREDICTED: hypothetical protein [Vitis vinifera] >gi|297744324|emb|CBI37294.3| unnamed protein product [Vitis vinifera]							nr +
Unigene93994_All	203	0.00	0.00	0.00	0.00	0.00	0.00	3.75	0.21	0.00	null	null		null	null		null	null		null	null		-4.19E+00	1.57E-04	Down	-1.19E+01	8.87E-06	Down							
Unigene940_All	2115	10.88	49.28	11.33	11.61	18.33	12.68	11.39	11.44	11.62	2.18E+00	8.24E-236	Up	5.78E-02	6.45E-01		6.59E-01	1.49E-16		1.28E-01	3.08E-01		6.00E-03	9.94E-01		2.85E-02	8.00E-01		Unigene940_All//gi|30683061|ref|NP_172759.2|//0.00E+00//glycosyl transferase family 17 protein [Arabidopsis thaliana]	Unigene940_All//0.00E+00//AT1G12990| glycosyl transferase family 17 protein	Unigene940_All//0.00E+00//TC141726			GO:0006486//GO:0008375//GO:0044464	nr -
Unigene94020_All	253	1.03	0.60	0.42	4.33	1.23	0.54	2.51	1.82	0.47	-7.83E-01	6.19E-01		-1.30E+00	4.35E-01		-1.82E+00	5.10E-03		-3.02E+00	2.14E-04	Down	-4.64E-01	5.93E-01		-2.41E+00	8.11E-03				Unigene94020_All//1.00E-132//gi|72274884|gb|DT049875.1|DT049875				
Unigene94036_All	256	2.25	6.14	4.78	2.72	0.94	2.29	3.30	100.90	0.00	1.45E+00	8.58E-03		1.09E+00	9.18E-02		-1.53E+00	7.00E-02		-2.48E-01	7.56E-01		4.93E+00	7.66E-152	Up	-1.17E+01	2.21E-06	Down	Unigene94036_All//gi|284433794|gb|AD885103.1|//3.00E-14//glutathione S-transferase omega [Jatropha curcas]	Unigene94036_All//1.00E-13//AT5G02790| In2-1 protein, putative	Unigene94036_All//2.00E-73//TC141733		ko00480|Glutathione metabolism	GO:0016765//GO:0043231	nr -
Unigene9405_All	226	85.43	26.90	26.63	114.62	103.76	147.88	154.34	88.77	72.10	-1.67E+00	3.47E-31	Down	-1.68E+00	2.33E-30	Down	-1.44E-01	2.27E-01		3.68E-01	5.66E-05		-7.98E-01	1.17E-21		-1.10E+00	1.88E-37	Down	Unigene9405_All//gi|112443176|gb|AB118976.1|//2.00E-26//nuclear-localized RNA binding protein [Capsicum annuum]	Unigene9405_All//1.00E-15//AT4G16830| nuclear RNA-binding protein (RGGA)	Unigene9405_All//9.00E-106//TC160575				nr -
Unigene94086_All	294	0.00	275.75	6.70	0.00	0.82	2.00	0.00	0.00	0.14	1.81E+01	0.00E+00	Up	1.27E+01	7.44E-11	Up	9.68E+00	1.04E-01		1.10E+01	1.37E-03		null	null		7.08E+00	6.30E-01		Unigene94086_All//gi|126075|sp|P09441.2|LEA13_GOSHI//1.00E-40//RecName: Full=Late embryogenesis abundant protein D-113; Short=LEA D-113 >gi|18492|emb|CAA31590.1| D-113 Lea protein [Gossypium hirsutum] >gi|226353|prf||1601521C Lea D-113 gene		Unigene94086_All//1.00E-77//TC165354			GO:0007275	nr +
Unigene9409_All	250	0.63	0.41	1.92	3.19	2.89	0.18	1.01	0.67	0.64	-6.31E-01	7.25E-01		1.61E+00	1.81E-01		-1.40E-01	8.29E-01		-4.14E+00	4.12E-04	Down	-6.02E-01	6.47E-01		-6.71E-01	6.05E-01								
Unigene9412_All	261	2.61	0.19	0.00	0.19	0.66	0.00	0.00	0.00	0.00	-3.75E+00	2.83E-03		-1.13E+01	7.62E-04	Down	1.79E+00	5.19E-01		-7.58E+00	6.11E-01		null	null		null	null									ESTscan -
Unigene9415_All	405	0.00	2.50	2.89	0.00	0.00	0.00	0.00	0.00	0.00	1.13E+01	7.21E-06	Up	1.15E+01	1.76E-06	Up	null	null		null	null		null	null		null	null		Unigene9415_All//gi|294845998|gb|ADF43157.1|//4.00E-08//SAD1p [Chlamydomonas reinhardtii]				ko03040|Spliceosome		nr +
Unigene9418_All	629	0.00	0.00	0.00	0.16	0.11	0.07	1.75	6.84	6.84	null	null		null	null		-5.33E-01	8.11E-01		-1.14E+00	6.71E-01		1.97E+00	3.50E-11	Up	1.97E+00	1.91E-11	Up	Unigene9418_All//gi|15217667|ref|NP_174087.1|//4.00E-08//ethylene-responsive protein -related [Arabidopsis thaliana] >gi|218563530|sp|Q9SF23.2|BHL110_ARATH RecName: Full=Transcription factor bHLH110; AltName: Full=Transcription factor EN 59; AltName: Full=bHLH transcription factor bHLH110; AltName: Full=Basic helix-loop-helix protein 110; Short=bHLH 110; Short=AtbHLH110	Unigene9418_All//6.00E-10//AT1G27660| ethylene-responsive protein -related					nr +
Unigene94185_All	200	0.00	0.51	0.27	0.25	0.86	1.13	0.00	2.72	1.39	8.99E+00	3.77E-01		8.06E+00	6.19E-01		1.79E+00	5.19E-01		2.18E+00	3.22E-01		1.14E+01	5.36E-04	Up	1.04E+01	2.43E-02								
Unigene942_All	434	1.33	0.82	0.25	0.80	3.49	0.83	0.68	1.06	2.29	-6.98E-01	4.49E-01		-2.43E+00	4.40E-02		2.12E+00	3.26E-04	Up	5.12E-02	9.68E-01		6.36E-01	5.36E-01		1.75E+00	6.57E-03		Unigene942_All//gi|115464291|ref|NP_001055745.1|//1.00E-67//Os05g0458400 [Oryza sativa Japonica Group] >gi|122169030|sp|Q6DHL4.1|FTSH8_ORYSJ RecName: Full=Cell division protease ftsH homolog 8, mitochondrial; Short=OsFtsH8; Flags: Precursor >gi|113579296|dbj|BAF17659.1| Os05g0458400 [Oryza sativa Japonica Group]	Unigene942_All//2.00E-56//AT1G07510| ftsh10 (FtsH protease 10); ATP binding / ATPase/ metalloendopeptidase/ nucleoside-triphosphatase/ nucleotide binding / zinc ion binding	Unigene942_All//8.00E-154//gi|48741736|gb|CO072255.1|CO072255			GO:0004175//GO:0009057//GO:0009534//GO:0019538//GO:0031224//GO:0032559//GO:0042623//GO:0046914	nr +
Unigene94208_All	206	27.18	13.04	18.09	11.85	9.03	12.50	12.73	8.32	6.77	-1.06E+00	3.43E-05	Down	-5.87E-01	2.59E-02		-3.93E-01	3.47E-01		7.68E-02	8.66E-01		-6.13E-01	8.10E-02		-9.11E-01	6.75E-03				Unigene94208_All//7.00E-57//TC152336				
Unigene9423_All	241	0.00	0.63	3.54	5.79	2.00	4.12	1.58	0.35	0.83	9.30E+00	2.31E-01		1.18E+01	8.95E-05	Up	-1.53E+00	5.22E-03		-4.89E-01	4.09E-01		-2.19E+00	8.74E-02		-9.34E-01	3.79E-01		Unigene9423_All//gi|28558781|gb|AA045752.1|//4.00E-09//pol protein [Cucumis melo]		Unigene9423_All//2.00E-26//FL576679			GO:0005488	nr -
Unigene9424_All	206	0.00	10.08	4.39	0.00	0.00	0.00	0.00	0.00	0.00	1.33E+01	7.93E-12	Up	1.21E+01	4.69E-05	Up	null	null		null	null		null	null		null	null									
Unigene94248_All	414	0.00	0.00	0.13	6.38	1.83	2.73	0.00	0.00	0.10	null	null		7.01E+00	6.19E-01		-1.80E+00	2.73E-06	Down	-1.23E+00	1.69E-03		null	null		6.59E+00	6.30E-01				Unigene94248_All//4.00E-60//TC158751				

Unigene94264_All	475	0.22	0.00	0.00	0.00	1.38	0.19	0.36	0.18	0.34	-7.78E+00	3.62E-01		-7.78E+00	3.84E-01		1.04E+01	4.92E-04	Up	7.57E+00	4.68E-01		-1.02E+00	6.12E-01		-8.56E-02	9.64E-01		Unigene94264_All//gi|240256190|ref|NP_195381.6|//3.00E-36//EMB2754 (EMBRYO DEFECTIVE 2754); binding / small GTPase regulator [Arabidopsis thaliana]	Unigene94264_All//8.00E-38//AT4G36630| EMB2754 (EMBRYO DEFECTIVE 2754); binding / small GTPase regulator	Unigene94264_All//4.00E-94//gi|164282497|gb|ES825514.1|ES825514			GO:0003006//GO:0030695	nr +
Unigene9428_All	206	7.87	11.81	10.86	4.35	4.01	10.96	2.67	8.72	4.06	5.85E-01	1.51E-01		4.64E-01	3.10E-01		-1.18E-01	8.51E-01		1.33E+00	2.32E-03		1.71E+00	2.41E-04	Up	6.06E-01	3.65E-01				Unigene9428_All//8.00E-75//gi|13243977|gb|BE051933.2|BE051933				
Unigene94285_All	692	0.23	0.81	0.46	0.58	0.10	0.39	2.14	0.48	0.52	1.83E+00	9.01E-02		1.03E+00	4.70E-01		-2.53E+00	5.78E-02		-5.56E-01	6.37E-01		-2.15E+00	9.68E-05	Down	-2.05E+00	1.05E-04	Down	Unigene94285_All//gi|186509883|ref|NP_001118597.1|//4.00E-70//eukaryotic translation initiation factor 2B family protein / eIF-2B family protein [Arabidopsis thaliana] >gi|227204367|dbj|BAH57035.1| AT3G07300 [Arabidopsis thaliana]	Unigene94285_All//1.00E-49//AT3G07300| eukaryotic translation initiation factor 2B family protein / eIF-2B family protein	Unigene94285_All//0.00E+00//gi|78329186|gb|DT549460.1|DT549460			GO:0006412//GO:0008135//GO:0032561//GO:0043234	nr +
Unigene94292_All	550	0.00	0.00	0.00	0.36	0.25	0.00	0.00	0.30	1.16	null	null		null	null		-5.33E-01	7.46E-01		-8.50E+00	1.31E-01		8.25E+00	1.38E-01		1.02E+01	9.33E-05	Up	Unigene94292_All//gi|115470887|ref|NP_001059042.1|//2.00E-58//Os02g0181000 [Oryza sativa Japonica Group] >gi|113610578|dbj|BAF20956.1| Os02g0181000 [Oryza sativa Japonica Group]	Unigene94292_All//1.00E-54//AT3G22960| PKP-ALPHA; pyruvate kinase	Unigene94292_All//4.00E-42//TC149837		ko00230|Purine metabolism//ko00010|Glycolysis / Gluconeogenesis//ko00620|Pyruvate metabolism//ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0009536//GO:0016301//GO:0046872	nr -
Unigene9430_All	592	16.00	8.47	16.28	0.76	1.11	3.66	0.00	0.07	0.27	-9.17E-01	1.23E-06		2.54E-02	9.09E-01		5.45E-01	5.86E-01		2.27E+00	5.25E-06	Up	6.14E+00	6.20E-01		8.07E+00	1.39E-01		Unigene9430_All//gi|224090994|ref|XP_002309138.1|//4.00E-29//Ca2+ antiporter/cation exchanger [Populus trichocarpa] >gi|222855114|gb|EEE92661.1| Ca2+ antiporter/cation exchanger [Populus trichocarpa]	Unigene9430_All//1.00E-23//AT2G38170| CAX1 (cation exchanger 1); calcium ion transmembrane transporter/ calcium:cation antiporter/ calcium:hydrogen antiporter	Unigene9430_All//6.00E-100//TC160355			GO:0000325//GO:0005488//GO:0006970//GO:0009409//GO:0015368//GO:0030005//GO:0031090//GO:0031224//GO:0046873//GO:0070838	nr -
Unigene94314_All	842	0.87	0.66	0.00	0.89	2.74	0.86	0.25	0.00	0.47	-3.94E-01	6.11E-01		-9.76E+00	4.12E-04	Down	1.63E+00	1.59E-04	Up	-4.83E-02	9.50E-01		-7.97E+00	7.39E-02		9.14E-01	3.86E-01		Unigene94314_All//gi|50897234|gb|AT85756.1|//3.00E-57//At5g20635 [Arabidopsis thaliana]	Unigene94314_All//5.00E-28//AT5G20635| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: keratin filament, chloroplast; CONTAINS InterPro DOMAIN/s: Keratin, high sulphur B2 protein (InterPro:IPR002494); Has 5724 Blast hits to 2501 proteins in 208 species: Archae - 6; Bacteria - 25; Metazoa - 4583; Fungi - 39; Plants - 97; Viruses - 40; Other Eukaryotes - 934 (source: NCBI BLink).	Unigene94314_All//0.00E+00//TC168124				nr +
Unigene9432_All	359	1.31	2.26	0.30	1.67	1.92	1.01	1.06	1.63	3.77	7.84E-01	3.23E-01		-2.14E+00	1.03E-01		2.04E-01	8.21E-01		-7.26E-01	4.60E-01		6.21E-01	4.78E-01		1.83E+00	7.57E-04	Up			Unigene9432_All//1.00E-102//DW499882				
Unigene94330_All	224	0.23	6.79	0.95	1.11	4.77	3.83	1.70	0.56	0.89	4.86E+00	1.61E-07	Up	2.03E+00	3.59E-01		2.10E+00	4.32E-03		1.78E+00	3.19E-02		-1.60E+00	1.81E-01		-9.34E-01	3.79E-01		Unigene94330_All//gi|224246691|dbj|BAH20299.1|//4.00E-09//AT5G25770 [Arabidopsis thaliana]	Unigene94330_All//2.00E-10//AT5G25770| unknown protein	Unigene94330_All//5.00E-30//TC165103				nr +
Unigene94343_All	349	0.00	0.00	0.00	0.00	0.00	0.00	1.45	0.00	0.11	null	null		null	null		null	null		null	null		-1.05E+01	8.88E-04	Down	-3.67E+00	3.75E-03		Unigene94343_All//gi|283132359|dbj|BAI63585.1|//4.00E-08//ACT-domain-containing protein kinase [Lotus japonicus]	Unigene94343_All//4.00E-09//AT4G35780| protein kinase family protein	Unigene94343_All//6.00E-114//C0126597			GO:0004713//GO:0006464//GO:0031406//GO:0032559	nr -
Unigene9437_All	499	4.30	2.44	3.63	6.89	5.38	2.26	5.00	2.93	1.68	-8.19E-01	6.15E-02		-2.45E-01	6.19E-01		-3.56E-01	3.14E-01		-1.61E+00	3.55E-06	Down	-7.70E-01	3.19E-02		-1.88E+00	1.99E-05	Down	Unigene9437_All//gi|302143220|emb|CBI20515.3|//9.00E-06//unnamed protein product [Vitis vinifera]	Unigene9437_All//7.00E-07//AT4G32640| protein binding / zinc ion binding	Unigene9437_All//7.00E-136//TC134114				nr -
Unigene9438_All	347	0.75	13.87	5.98	0.57	2.58	1.95	1.46	0.48	2.41	4.20E+00	3.82E-21	Up	2.99E+00	5.58E-07	Up	2.17E+00	9.20E-03		1.77E+00	6.94E-02		-1.60E+00	1.07E-01		7.22E-01	2.82E-01				Unigene9438_All//1.00E-152//TC142282				
Unigene944_All	4001	18.87	13.65	24.18	12.36	10.13	8.64	16.52	3.26	6.69	-4.67E-01	6.55E-15		3.58E-01	2.51E-11		-2.87E-01	4.55E-05		-5.18E-01	1.02E-12		-2.34E+00	3.22E-201	Down	-1.30E+00	7.10E-92	Down	Unigene944_All//gi|224138528|ref|XP_002326625.1|//0.00E+00//autoinhibited H+ ATPase [Populus trichocarpa] >gi|222833947|gb|EEE72424.1| autoinhibited H+ ATPase [Populus trichocarpa]	Unigene944_All//0.00E+00//AT1G17260| AHA10 (Autoinhibited H(+)-ATPase isoform 10); ATPase/ ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / cation-transporting ATPase	Unigene944_All//0.00E+00//TC158048		ko00190|Oxidative phosphorylation	GO:0006811//GO:0009206//GO:0015662//GO:0031224//GO:0032559	nr -
Unigene9440_All	501	0.00	0.00	0.11	0.30	1.24	0.18	0.08	0.33	1.35	null	null		6.73E+00	6.19E-01		2.05E+00	5.12E-02		-7.26E-01	7.12E-01		1.98E+00	3.78E-01		4.00E+00	4.29E-04	Up			Unigene9440_All//7.00E-164//gi|78344032|gb|DT564306.1|DT564306				ESTscan -
Unigene9442_All	340	0.00	0.30	0.00	0.00	0.00	0.13	0.50	3.56	1.17	8.22E+00	3.77E-01		null	null		null	null		7.05E+00	6.79E-01		2.84E+00	3.39E-05	Up	1.24E+00	2.51E-01				Unigene9442_All//2.00E-178//gi|78332470|gb|DT552744.1|DT552744				
Unigene9445_All	581	0.00	6.89	3.85	0.00	0.00	0.00	0.00	0.00	0.00	1.28E+01	8.54E-23	Up	1.19E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene9445_All//gi|242045628|ref|XP_002460685.1|//4.00E-09//hypothetical protein SORBIDRAFT_02g033135 [Sorghum bicolor] >gi|241924062|gb|EER97206.1| hypothetical protein SORBIDRAFT_02g033135 [Sorghum bicolor]						nr -
Unigene9448_All	274	0.00	4.81	1.17	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.49E-07	Up	1.02E+01	4.42E-02		null	null		null	null		null	null		null	null		Unigene9448_All//gi|31711944|gb|AAP68328.1|//8.00E-35//At1g18070 [Arabidopsis thaliana]	Unigene9448_All//3.00E-36//AT1G18070| EF-1-alpha-related GTP-binding protein, putative				GO:0004179//GO:0006412//GO:0008135//GO:0017111//GO:0032561//GO:0043231	nr +
Unigene945_All	2155	52.56	56.48	92.59	103.77	36.83	22.42	77.73	26.30	52.21	1.04E-01	3.95E-02		8.17E-01	3.34E-99		-1.49E+00	0.00E+00	Down	-2.21E+00	0.00E+00	Down	-1.56E+00	2.33E-296	Down	-5.74E-01	2.23E-58		Unigene945_All//gi|156767195|gb|ABU95104.1|//0.00E+00//asparagine synthetase [Phaseolus vulgaris]	Unigene945_All//0.00E+00//AT3G47340| ASN1 (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHASE 1); asparagine synthase (glutamine-hydrolyzing)	Unigene945_All//0.00E+00//TC131710		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0006528//GO:0009064//GO:0009267//GO:0009612//GO:0009746//GO:0016884//GO:0032559//GO:0034285	nr +
Unigene9450_All	202	746.22	354.69	173.46	329.46	340.43	292.00	456.92	126.63	77.11	-1.07E+00	7.02E-122	Down	-2.11E+00	0.00E+00	Down	4.72E-02	5.66E-01		-1.74E-01	8.84E-03		-1.85E+00	1.45E-207	Down	-2.57E+00	0.00E+00	Down	Unigene9450_All//gi|47026919|gb|AAT08680.1|//8.00E-16//histone H2A [Hyacinthus orientalis]	Unigene9450_All//2.00E-05//AT5G02560| HTA12; DNA binding	Unigene9450_All//8.00E-106//gi|109877010|gb|DW505984.1|DW505984			GO:0000785//GO:0003676//GO:0034728//GO:0043231	nr +
Unigene94504_All	227	0.23	0.00	0.00	1.32	1.06	0.80	1.86	1.29	6.49	-7.85E+00	5.94E-01		-7.85E+00	6.08E-01		-3.10E-01	8.19E-01		-7.26E-01	6.37E-01		-5.31E-01	6.34E-01		1.80E+00	4.81E-04	Up	Unigene94504_All//gi|224110962|ref|XP_002315697.1|//5.00E-11//predicted protein [Populus trichocarpa] >gi|222864737|gb|EEF01868.1| predicted protein [Populus trichocarpa]		Unigene94504_All//3.00E-56//TC160262				nr -
Unigene9452_All	305	1.37	1.00	0.87	4.90	1.35	0.89	1.39	0.00	0.00	-4.61E-01	6.50E-01		-6.53E-01	5.94E-01		-1.85E+00	5.93E-04	Down	-2.46E+00	8.25E-05	Down	-1.04E+01	3.24E-03		-1.04E+01	2.14E-03		Unigene9452_All//gi|115455585|ref|NP_001051393.1|//3.00E-14//Os03g0769000 [Oryza sativa Japonica Group] >gi|113549864|dbj|BAF13307.1| Os03g0769000 [Oryza sativa Japonica Group]	Unigene9452_All//3.00E-15//AT2G23700| unknown protein					nr +
Unigene9454_All	399	0.00	0.00	0.00	0.00	0.00	0.00	1.48	1.68	0.00	null	null		null	null		null	null		null	null		1.76E-01	8.15E-01		-1.05E+01	1.41E-04	Down	Unigene9454_All//gi|301095995|ref|XP_002897096.1|//1.00E-46//40S ribosomal protein S15a [Phytophthora infestans T30-4] >gi|262107415|gb|EE165467.1| 40S ribosomal protein S15a [Phytophthora infestans T30-4]	Unigene9454_All//2.00E-46//AT5G59850| 40S ribosomal protein S15A (RPS15aF)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0016020//GO:0030312//GO:0043231	nr +
Unigene94546_All	241	0.00	0.84	0.00	0.00	1.29	0.00	21.93	182.79	18.84	9.72E+00	1.34E-01		null	null		1.03E+01	4.53E-02		null	null		3.06E+00	1.35E-179	Up	-2.19E-01	3.69E-01		Unigene94546_All//gi|283136110|gb|ADB11374.1|//1.00E-13//tau class glutathione transferase GSTU50 [Populus trichocarpa]		Unigene94546_All//7.00E-82//TC171132			GO:0003824	nr -
Unigene94556_All	210	0.00	5.55	0.51	1.19	1.48	4.95	0.40	0.40	1.71	1.24E+01	1.04E-06	Up	8.99E+00	3.85E-01		3.15E-01	8.38E-01		2.06E+00	6.55E-03		-1.66E-02	1.01E+00		2.08E+00	1.01E-01				Unigene94556_All//7.00E-57//gi|48826808|gb|C0125198.1|C0125198				
Unigene9456_All	432	0.00	0.00	0.00	0.00	0.00	0.00	2.74	0.97	0.28	null	null		null	null		null	null		null	null		-1.50E+00	9.69E-03		-3.31E+00	4.89E-06	Down	Unigene9456_All//gi|57834114|emb|CAE05707.2|//2.00E-17//OSJNBa0065J09.3 [Oryza sativa (japonica cultivar-group)]					GO:0003676//GO:0006259	nr +
Unigene9457_All	308	0.00	0.00	0.00	0.00	0.00	0.00	16.61	44.65	0.00	null	null		null	null		null	null		null	null		1.43E+00	7.08E-22	Up	-1.40E+01	1.27E-37	Down							
Unigene94572_All	468	0.78	1.73	1.14	3.19	0.59	0.39	0.72	0.89	0.77	1.15E+00	1.48E-01		5.40E-01	6.10E-01		-2.44E+00	2.38E-05	Down	-3.05E+00	7.42E-06	Down	3.05E-01	7.57E-01		8.41E-02	9.57E-01				Unigene94572_All//2.00E-105//gi|109880047|gb|DW509017.1|DW509017				
Unigene9458_All	454	0.00	0.00	0.00	0.00	0.00	0.00	1.49	2.30	0.00	null	null		null	null		null	null		null	null		6.27E-01	3.12E-01		-1.05E+01	3.56E-05	Down	Unigene9458_All//gi|301122321|ref|XP_002908887.1|//2.00E-35//40S ribosomal protein S10 [Phytophthora infestans T30-4] >gi|66270167|gb|AAY43413.1| ribosomal protein S10 [Phytophthora infestans] >gi|262096649|gb|EEY57701.1| 40S ribosomal protein S10 [Phytophthora infestans T30-4]	Unigene9458_All//1.00E-27//AT4G25740| 40S ribosomal protein S10 (RPS10A)			ko03010|Ribosome	GO:0015935	nr -
Unigene94583_All	365	0.00	0.00	0.00	0.00	0.00	0.12	0.12	0.00	4.91	null	null		null	null		null	null		6.95E+00	6.79E-01		-6.86E+00	6.34E-01		5.41E+00	1.56E-11	Up	Unigene94583_All//gi|89357199|gb|ABD72482.1|//2.00E-24//MRP-like ABC transporter protein [Gossypium barbadense]	Unigene94583_All//7.00E-16//AT3G13080| ATMRP3; ATPase, coupled to transmembrane movement of substances / chlorophyll catabolite transporter/ glutathione S-conjugate-exporting ATPase	Unigene94583_All//2.00E-89//TC138277			GO:0000166//GO:0005773//GO:0006810//GO:0016020//GO:0022892//GO:0042626	nr +
Unigene9461_All	342	0.00	2.96	1.56	0.00	0.00	0.00	0.00	0.00	0.00	1.15E+01	7.21E-06	Up	1.06E+01	3.98E-03		null	null		null	null		null	null		null	null								
Unigene94631_All	467	0.00	0.00	0.00	1.39	1.33	0.00	0.27	0.18	0.17	null	null		null	null		-6.32E-02	9.25E-01		-1.04E+01	3.89E-04	Down	-6.02E-01	7.63E-01		-6.71E-01	7.17E-01		Unigene94631_All//gi|115473321|ref|NP_001060259.1|//2.00E-16//Os07g0613900 [Oryza sativa Japonica Group] >gi|113611795|dbj|BAF22173.1| Os07g0613900 [Oryza sativa Japonica Group]						nr +
Unigene94660_All	342	0.00	0.00	0.00	0.00	0.00	0.00	0.24	9.67	null	null	null		null	null		null	null		null	null		7.93E+00	3.96E-01		1.32E+01	1.16E-23	Up	Unigene94660_All//gi|224132020|ref|XP_002328165.1|//5.00E-35//cytochrome P450 [Populus trichocarpa] >gi|222837680|gb|EEE76045.1| cytochrome P450 [Populus trichocarpa]	Unigene94660_All//6.00E-19//AT2G27690| CYP94C1; fatty acid (omega-1)-hydroxylase/ oxygen binding	Unigene94660_All//1.00E-164//gi|78347798|gb|DT568072.1|DT568072		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00903|Limonene and pinene degradation	GO:0004497//GO:0005506//GO:0006091//GO:0031410	nr +
Unigene94665_All	632	0.75	0.32	0.25	2.36	1.80	0.57	0.13	0.13	0.13	-1.22E+00	2.72E-01		-1.56E+00	2.04E-01		-3.95E-01	4.86E-01		-2.05E+00	5.54E-04	Down	-1.63E-02	1.01E+00		-8.55E-02	9.67E-01		Unigene94665_All//gi|18398546|ref|NP_565427.1|//1.00E-96//cold-shock DNA-binding family protein [Arabidopsis thaliana] >gi|148726892|dbj|BAF63841.1| cold shock domain protein 3 [Arabidopsis thaliana]	Unigene94665_All//4.00E-34//AT4G36020| CSDP1 (cold shock domain protein 1); RNA binding / double-stranded DNA binding / nucleic acid binding / single-stranded DNA binding	Unigene94665_All//0.00E+00//gi|78338475|gb|DT558749.1|DT558749	CSD		GO:0016070//GO:0043231//GO:0043566	nr -
Unigene94669_All	289	0.00	0.00	0.55	1.03	0.95	0.78	4.39	2.60	1.10	null	null		9.11E+00	2.33E-01		-1.18E-01	9.00E-01		-4.04E-01	7.51E-01		-7.54E-01	1.63E-01		-1.99E+00	4.86E-04	Down	Unigene94669_All//gi|297603683|ref|NP_001051436.2|//1.00E-08//Os05g0109600 [Oryza sativa Japonica Group] >gi|255675944|dbj|BAF16350.2| Os05g0109600 [Oryza sativa Japonica Group]	Unigene94669_All//3.00E-09//AT2G29190| APUM2 (Arabidopsis Pumilio 2); RNA binding / binding	Unigene94669_All//1.00E-37//EV497084				nr +

Unigene94670_All	384	5.45	14.65	3.61	2.08	2.42	2.47	0.66	2.07	0.31	1.43E+00	9.19E-08	Up	-5.96E-01	2.08E-01		2.22E-01	8.13E-01		2.51E-01	7.24E-01		1.65E+00	2.88E-02		-1.09E+00	4.28E-01		Unigene94670_All//gi|91208892|ref|YP_538925.1|//1.00E-58//RNA polymerase beta'' subunit [Gossypium hirsutum] >gi|122201383|sp|Q2L8Z5.1|RPOC2_GOSHI RecName: Full=DNA-directed RNA polymerase subunit beta''; AltName: Full=PEP; AltName: Full=Plastid-encoded RNA polymerase subunit beta''; Short=RNA polymerase subunit beta'' >gi|85687406|gb|ABC73618.1|RNA polymerase beta' subunit [Gossypium hirsutum]	Unigene94670_All//2.00E-45//ATCG00170| RNA polymerase beta' subunit-2	Unigene94670_All//5.00E-118//TC163163		ko00230|Purine metabolism//ko00240|Pyrimidine metabolism//ko03020|RNA polymerase	GO:0003676//GO:0006350//GO:0009536//GO:0034062	nr -
Unigene94683_All	282	0.19	0.00	0.00	1.41	1.83	5.61	0.15	0.00	0.14	-7.54E+00	5.94E-01		-7.54E+00	6.08E-01		3.74E-01	7.71E-01		1.99E+00	6.07E-04	Up	-7.23E+00	6.34E-01		-8.52E-02	9.62E-01		Unigene94683_All//gi|297795735|ref|XP_002865752.1|//6.00E-14//UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297311587|gb|EFH42011.1| UDP-glucoronosyl/UDP-glucosyl transferase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene94683_All//2.00E-14//AT5G49690| UDP-glucoronosyl/UDP-glucosyl transferase family protein	Unigene94683_All//3.00E-87//DW241084			GO:0016757	nr +
Unigene94692_All	526	0.00	0.58	0.10	2.46	3.54	1.89	2.89	0.24	1.59	9.17E+00	4.35E-02		6.66E+00	6.19E-01		5.22E-01	3.12E-01		-3.82E-01	5.50E-01		-3.60E+00	9.55E-08	Down	-8.63E-01	6.03E-02		Unigene94692_All//gi|127519339|gb|AB028522.1|//4.00E-71//kinesin-related protein [Gossypium hirsutum]	Unigene94692_All//8.00E-24//AT2G47500| ATP binding / microtubule motor	Unigene94692_All//0.00E+00//TC167954			GO:0003774//GO:0006950//GO:0007017//GO:0015630//GO:0032559	nr -
Unigene9472_All	259	10.91	3.33	5.14	8.27	4.52	8.02	0.33	0.81	0.46	-1.71E+00	2.21E-05	Down	-1.09E+00	5.95E-03		-8.72E-01	3.73E-02		-4.41E-02	9.33E-01		1.31E+00	4.46E-01		4.99E-01	8.05E-01					Unigene9472_All//6.00E-21//TC155643					
Unigene9473_All	280	0.00	0.18	0.19	0.36	0.49	1.29	0.60	5.97	2.42	7.50E+00	6.04E-01		7.57E+00	6.19E-01		4.67E-01	8.74E-01		1.86E+00	2.19E-01		3.31E+00	6.97E-08	Up	2.00E+00	1.69E-02										
Unigene94730_All	233	0.00	0.00	0.00	2.78	4.73	0.58	73.85	298.85	168.25	null	null		null	null		7.67E-01	2.69E-01		-2.26E+00	2.76E-02		2.02E+00	2.91E-175	Up	1.19E+00	3.99E-47	Up	Unigene94730_All//gi|153805698|gb|ABS52574.1|//2.00E-28//nodulin family protein [Gossypium hirsutum]	Unigene94730_All//3.00E-17//AT4G08300| nodulin MtN21 family protein	Unigene94730_All//2.00E-106//BF268593			GO:0044464	nr -
Unigene9475_All	284	0.37	0.00	0.00	3.33	0.61	0.16	1.94	0.74	1.40	-8.53E+00	3.62E-01		-8.53E+00	3.84E-01		-2.46E+00	1.25E-03		-4.39E+00	5.96E-05	Down	-1.40E+00	1.34E-01		-4.64E-01	5.97E-01		Unigene9475_All//gi|255537611|ref|XP_002509872.1|//8.00E-09//conserved hypothetical protein [Ricinus communis] >gi|223549771|gb|EEF51259.1|conserved hypothetical protein [Ricinus communis]	Unigene9475_All//2.00E-06//AT1G64065| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: membrane; CONTAINS InterPro DOMAIN/s: Harpin-induced 1 (InterPro:IPR010847); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G44000.1); Has 69 Blast hits to 69 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 68; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink).	Unigene9475_All//5.00E-120//gi|21096586|gb|BQ408899.1|BQ408899				nr +
Unigene94753_All	253	1.65	1.20	2.32	9.45	3.95	3.57	1.50	1.16	0.94	-4.61E-01	6.50E-01		4.85E-01	6.30E-01		-1.26E+00	1.23E-03		-1.40E+00	8.06E-04	Down	-3.79E-01	7.23E-01		-6.71E-01	5.30E-01		Unigene94753_All//gi|226492856|ref|NP_001149901.1|//2.00E-08//LOC100283529 [Zea mays] >gi|195635353|gb|ACG37145.1| TLD family protein [Zea mays]	Unigene94753_All//2.00E-08//AT4G39870| FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: TLDc (InterPro:IPR006571); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G05590.2); Has 2018 Blast hits to 1865 proteins in 220 species: Archae - 0; Bacteria - 39; Metazoa - 1002; Fungi - 279; Plants - 129; Viruses - 34; Other Eukaryotes - 535 (source: NCBI BLink).				nr -
Unigene9477_All	837	0.00	0.00	0.00	0.00	0.00	0.00	17.53	0.65	1.43	null	null		null	null		null	null		null	null		-4.75E+00	5.48E-85	Down	-3.62E+00	1.37E-72	Down	Unigene9477_All//gi|297834560|ref|XP_002885162.1|//6.00E-71//nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297331002|gb|EFH61421.1|nodulin MtN3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene9477_All//1.00E-70//AT4G15920| INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system, integral to membrane, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: MtN3 and saliva related transmembrane protein, conserved region (InterPro:IPR018169), RAG1-activating protein 1 homologue (InterPro:IPR018179), MtN3 and saliva related transmembrane protein (InterPro:IPR004316); BEST Arabidopsis thaliana protein match is: nodulin MtN3 family protein (TAIR:AT3G16690.1); Has 546 Blast hits to 527 proteins in 90 species: Archae - 0; Bacteria - 0; Metazoa - 194; Fungi - 0; Plants - 300; Viruses - 0; Other Eukaryotes - 52 (source: NCBI BLink).	Unigene9477_All//0.00E+00//gi|48778429|gb|CO087795.1|CO087795			GO:0031224	nr +
Unigene94780_All	382	0.14	3.71	0.00	0.13	0.36	0.00	0.22	0.55	0.10	4.76E+00	5.54E-07	Up	-7.10E+00	6.08E-01		1.47E+00	6.16E-01		-7.03E+00	6.10E-01		1.31E+00	4.46E-01		-1.09E+00	6.71E-01					Unigene94780_All//4.00E-109//DT466933					
Unigene94788_All	414	0.25	0.24	0.00	1.68	0.50	0.00	0.00	0.20	0.00	-4.64E-02	9.84E-01		-7.98E+00	3.84E-01		-1.75E+00	4.11E-02		-1.07E+01	1.95E-04	Down	7.66E+00	3.96E-01		null	null					Unigene94788_All//1.00E-07//FL577713					
Unigene948_All	680	2.77	6.11	3.76	5.71	6.53	6.64	6.22	6.58	8.44	1.14E+00	1.86E-04	Up	4.40E-01	2.98E-01		1.93E-01	5.69E-01		2.17E-01	5.03E-01		8.10E-02	7.73E-01		4.40E-01	4.29E-02		Unigene948_All//gi|30693071|ref|NP_851101.1|//4.00E-68//ATSRL1; binding [Arabidopsis thaliana] >gi|31711878|gb|AAP68295.1|At5g37370 [Arabidopsis thaliana]	Unigene948_All//2.00E-69//AT5G37370| ATSRL1; binding	Unigene948_All//0.00E+00//TC152060		ko03040|Spliceosome	GO:0006970//GO:0010467	nr -
Unigene9481_All	274	0.00	0.00	0.00	0.00	0.25	0.99	5.49	4.42	13.23	null	null		null	null		7.97E+00	5.95E-01		9.95E+00	7.00E-02		-2.88E-01	5.99E-01		1.29E+00	9.57E-06	Up				Unigene9481_All//3.00E-07//EV497575					
Unigene9483_All	294	0.71	0.00	0.00	0.00	0.47	2.15	0.43	0.00	1.36	-9.48E+00	1.20E-01		-9.48E+00	1.44E-01		8.87E+00	3.15E-01		1.11E+01	7.59E-04	Up	-8.73E+00	2.32E-01		1.63E+00	1.40E-01										ESTscan +
Unigene9484_All	272	0.00	0.75	0.20	0.73	0.38	0.17	0.16	2.15	2.49	9.54E+00	1.34E-01		7.61E+00	6.19E-01		-9.48E-01	5.86E-01		-2.14E+00	3.45E-01		3.79E+00	2.07E-03		4.00E+00	4.29E-04	Up				Unigene9484_All//8.00E-122//TC161382					
Unigene94853_All	206	0.00	0.49	1.55	4.84	2.17	0.44	0.21	0.00	0.00	8.94E+00	3.77E-01		1.06E+01	4.42E-02		-1.15E+00	8.41E-02		-3.46E+00	1.73E-04	Down	-7.68E+00	6.34E-01		-7.68E+00	5.93E-01					Unigene94853_All//9.00E-44//ES814579					
Unigene94859_All	417	1.00	2.07	2.43	1.55	1.90	2.92	4.06	4.11	0.86	1.04E+00	1.72E-01		1.27E+00	8.35E-02		2.90E-01	7.70E-01		9.13E-01	1.52E-01		1.90E-02	1.00E+00		-2.24E+00	8.65E-06	Down				Unigene94859_All//2.00E-68//gi|78331857|gb|DT552131.1|DT552131					
Unigene9487_All	224	2.80	0.23	3.80	6.00	5.53	13.71	0.38	0.19	0.53	-3.63E+00	5.06E-03		4.40E-01	5.82E-01		-1.18E-01	8.29E-01		1.19E+00	9.46E-04	Up	-1.02E+00	7.18E-01		4.99E-01	8.05E-01										
Unigene94889_All	232	2.71	0.00	1.61	2.15	0.74	0.78	1.09	0.36	0.34	-1.14E+01	7.90E-04	Down	-7.52E-01	4.11E-01		-1.53E+00	1.45E-01		-1.46E+00	1.93E-01		-1.60E+00	3.10E-01		-1.67E+00	2.56E-01					Unigene94889_All//7.00E-14//gi|3326249|gb|AI055135.1|AI055135					
Unigene9490_All	666	0.16	0.00	0.00	0.00	0.00	0.00	2.35	3.45	0.66	-7.30E+00	3.62E-01		-7.30E+00	3.84E-01		null	null		null	null		5.55E-01	1.47E-01		-1.84E+00	2.17E-04	Down	Unigene9490_All//gi|255576593|ref|XP_002529187.1|//8.00E-11//hypothetical protein RCOM_0684740 [Ricinus communis] >gi|223531365|gb|EEF33201.1|hypothetical protein RCOM_0684740 [Ricinus communis]					GO:0005488	nr -
Unigene9492_All	357	0.73	1.70	0.15	0.98	0.48	1.01	2.37	1.05	0.33	1.22E+00	2.07E-01		-2.30E+00	2.42E-01		-1.02E+00	4.22E-01		5.14E-02	9.68E-01		-1.17E+00	9.29E-02		-2.82E+00	5.38E-04	Down				Unigene9492_All//2.00E-107//ES820143					
Unigene94938_All	406	0.13	0.25	1.31	0.00	1.78	0.78	0.94	1.03	0.59	9.53E-01	7.22E-01		3.35E+00	2.06E-02		1.08E+01	1.89E-04	Up	9.60E+00	4.07E-02		1.36E-01	8.99E-01		-6.71E-01	5.30E-01										ESTscan +
Unigene9496_All	524	0.00	0.00	0.00	0.00	0.00	0.00	14.52	2.47	0.08	null	null		null	null		null	null		null	null		-2.55E+00	3.19E-26	Down	-7.58E+00	4.76E-54	Down	Unigene9496_All//gi|111610552|gb|ABH11672.1|//1.00E-87//actin [Chara contraria]	Unigene9496_All//7.00E-78//AT3G33750| ACT3 (actin 3); structural constituent of cytoskeleton	Unigene9496_All//4.00E-88//TC153744		ko04145|Phagosome	GO:0032559//GO:0043232	nr +
Unigene9498_All	574	0.00	7.94	2.60	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	5.54E-26	Up	1.13E+01	3.21E-08	Up	null	null		null	null		null	null		null	null		Unigene9498_All//gi|300258126|gb|EF142366.1|//3.00E-22//2-cys peroxiredoxin, probably cytosolic [Volvox carteri f. nagariensis]	Unigene9498_All//9.00E-15//AT5G06290| 2-Cys Prx B (2-Cysteine peroxiredoxin B); antioxidant/ peroxiredoxin				GO:0008152//GO:0009536//GO:0016209//GO:0016705//GO:0019725	nr -
Unigene95_All	2020	1.63	4.34	1.95	2.86	3.72	4.32	4.81	4.03	5.58	1.41E+00	1.69E-11	Up	2.58E-01	4.34E-01		3.78E-01	8.33E-02		5.93E-01	2.21E-03		-2.55E-01	1.47E-01		2.13E-01	1.77E-01		Unigene95_All//gi|18401322|ref|NP_565635.1|//0.00E+00//SE (SERRATE); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75339076|sp|Q9ZVD0.2|SRRT_ARATH RecName: Full=Serrate RNA effector molecule >gi|14486602|gb|AAK63206.1|AF311221_1_1 C2H2 zinc-finger protein SERRATE [Arabidopsis thaliana] >gi|16226331|gb|AAL16137.1|AF428305_1 At2g27100/T20P8.15 [Arabidopsis thaliana] >gi|20197420|gb|AAC77868.2|expressed protein [Arabidopsis thaliana] >gi|23506033|gb|AAN28876.1|At2g27100/T20P8.15 [Arabidopsis thaliana]	Unigene95_All//0.00E+00//AT2G27100| SE (SERRATE); DNA binding / transcription factor	Unigene95_All//0.00E+00//ES835290				nr +
Unigene9500_All	258	0.00	0.00	0.00	0.00	0.00	0.00	3.61	1.30	0.00	null	null		null	null		null	null		null	null		-1.48E+00	2.77E-02		-1.18E+01	5.47E-07	Down	Unigene9500_All//gi|6094086|sp|O65353.1|RL5_HELAN//9.00E-23//RecName: Full=60S ribosomal protein L5 >gi|3153904|gb|AAC17448.1| RPL5A-related protein [Helianthus annuus]	Unigene9500_All//1.00E-17//AT5G39740| 60S ribosomal protein L5 (RPL5B)			ko03010|Ribosome	GO:0005198//GO:0009536//GO:0010467//GO:0019843//GO:0030529	nr +
Unigene95017_All	238	12.53	44.07	36.25	0.00	0.87	0.57	0.00	0.00	0.17	1.81E+00	3.18E-19	Up	1.53E+00	3.13E-12	Up	9.76E+00	1.56E-01		9.15E+00	3.08E-01		null	null		7.39E+00	6.29E-01		Unigene95017_All//gi|16118825|gb|AA14614.1|AF417109_1//2.00E-13//cysteine proteinase precursor [Vasconcellea cundinamarcensis]	Unigene95017_All//3.00E-06//AT3G43960| cysteine proteinase, putative	Unigene95017_All//1.00E-12//EX164784				nr -
Unigene9503_All	264	1.78	11.32	3.23	0.38	0.26	1.71	0.00	0.00	0.00	2.67E+00	3.78E-09	Up	8.56E-01	2.80E-01		-5.33E-01	8.11E-01		2.18E+00	1.02E-01		null	null		null	null					Unigene9503_All//3.00E-07//TC168477					
Unigene95036_All	324	0.65	0.31	0.82	0.31	3.08	1.53	0.13	0.77	0.74	-1.05E+00	5.63E-01		3.48E-01	7.96E-01		3.33E+00	2.50E-04	Up	2.32E+00	6.88E-02		2.57E+00	1.53E-01		2.50E+00	1.59E-01		Unigene95036_All//gi|297242515|gb|AD124921.1|//5.00E-43//L-allo-threonine aldolase [Carica papaya]	Unigene95036_All//7.00E-37//AT1G08630| THA1 (Threonine Aldolase 1); aldehyde-lyase/ threonine aldolase	Unigene95036_All//2.00E-104//gi|109848067|gb|DW477047.1|DW477047		ko00260|Glycine, serine and threonine metabolism		nr +
Unigene9504_All	242	0.22	0.63	0.22	0.00	0.00	0.00	0.17	2.76	2.96	1.54E+00	5.29E-01		2.51E-02	9.89E-01		null	null		null	null		3.98E+00	6.38E-04	Up	4.08E+00	2.41E-04	Up				Unigene9504_All//4.00E-28//TC159434					
Unigene95061_All	448	0.23	0.23	0.00	1.67	5.76	2.42	0.28	0.37	0.18	-4.64E-02	9.84E-01		-7.87E+00	3.84E-01		1.79E+00	1.27E-05	Up	5.37E-01	4.54E-01		3.99E-01	8.12E-01		-6.70E-01	7.17E-01		Unigene95061_All//gi|226531300|ref|NP_001151855.1|//6.00E-14//LOC100285491 [Zea mays] >gi|195650315|gb|ACG44625.1| zinc finger protein 7 [Zea mays]	Unigene95061_All//5.00E-11//AT1G66140| ZFP4 (ZINC FINGER PROTEIN 4); nucleic acid binding / transcription factor/ zinc ion binding	Unigene95061_All//6.00E-13//TC173894	C2H2			nr +

Unigene95086_All	643	0.49	1.10	0.66	1.86	1.12	4.50	1.12	0.07	0.25	1.18E+00	1.75E-01		4.40E-01	6.76E-01		-7.25E-01	2.33E-01		1.27E+00	7.00E-04	Up	-4.10E+00	2.91E-04	Down	-2.17E+00	7.75E-03		Unigene95086_All//gi|18406084|ref|NP_565988.1|//5.00E-17//PAR1 (PHY RAPIDLY REGULATED 1) [Arabidopsis thaliana] >gi|4512668|gb|AAD21722.1| expressed protein [Arabidopsis thaliana] >gi|83776541|tpe|CAJ55345.1| TPA: helix-loop-helix protein [Arabidopsis thaliana]	Unigene95086_All//2.00E-14//AT2G42870| PAR1 (PHY RAPIDLY REGULATED 1)	Unigene95086_All//9.00E-130//TC160093				nr -
Unigene9509_All	425	0.00	3.82	1.38	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.96E-09	Up	1.04E+01	2.15E-03		null	null		null	null		null	null		null	null		Unigene9509_All//gi|133841201|gb|AAK21311.1|//4.00E-16//myosin subfamily XI heavy chain [Petroselinum crispum]	Unigene9509_All//7.00E-17//AT2G33240| XID; motor/ protein binding				GO:0000904//GO:0005488//GO:0007275//GO:0040007//GO:0051640	nr -
Unigene9510_All	341	4.76	0.89	2.65	0.29	0.91	0.00	0.00	0.00	0.00	-2.42E+00	7.50E-05	Down	-8.41E-01	1.24E-01		1.64E+00	3.21E-01		-8.19E+00	3.87E-01		null	null		null	null		Unigene9510_All//gi|297790792|ref|XP_002863281.1|//4.00E-30//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297309115|gb|EFH39540.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene9510_All//2.00E-31//AT4G13010| oxidoreductase, zinc-binding dehydrogenase family protein	Unigene9510_All//3.00E-32//gi|78348544|gb|DT568818.1|DT568818			GO:0008152//GO:0009528//GO:0009534//GO:0016491//GO:0046914	nr +
Unigene9512_All	224	4.44	0.00	4.99	9.56	5.23	0.40	3.96	0.37	3.02	-1.21E+01	7.45E-06	Down	1.70E-01	7.78E-01		-8.72E-01	3.73E-02		-4.57E+00	5.20E-11	Down	-3.41E+00	1.40E-04	Down	-3.91E-01	5.53E-01					Unigene9512_All//3.00E-56//gi|78352935|gb|DT573209.1|DT573209				
Unigene95123_All	425	2.22	5.84	4.64	4.22	4.05	3.40	9.05	12.59	9.56	1.40E+00	8.73E-04	Up	1.07E+00	2.84E-02		-5.88E-02	8.99E-01		-3.11E-01	5.66E-01		4.76E-01	4.20E-02		7.88E-02	7.77E-01		Unigene95123_All//gi|34595981|gb|AAQ76706.1|//3.00E-30//microtubule-associated protein 1 light chain 3 [Gossypium hirsutum]	Unigene95123_All//2.00E-30//AT4G21980| APG8A (AUTOPHAGY 8A); APG8 activating enzyme/ APG8-specific protease/ Atg8 ligase	Unigene95123_All//4.00E-128//TC144821		ko04140|Regulation of autophagy		nr +
Unigene95133_All	235	0.22	0.00	0.00	0.00	0.00	0.19	7.38	1.78	1.86	-7.80E+00	5.93E-01		-7.80E+00	6.08E-01		null	null		7.59E+00	6.79E-01		-2.05E+00	3.55E-05	Down	-1.98E+00	3.36E-05	Down				Unigene95133_All//4.00E-34//DW501483				
Unigene95135_All	214	0.24	0.24	0.00	0.47	0.97	1.69	0.20	0.78	4.65	-4.62E-02	9.79E-01		-7.93E+00	6.07E-01		1.05E+00	6.11E-01		1.86E+00	2.19E-01		1.98E+00	3.78E-01		4.56E+00	3.72E-06	Up				Unigene95135_All//2.00E-63//TC151565				
Unigene95144_All	736	0.28	0.41	0.00	3.38	2.71	0.80	0.92	0.11	0.32	5.39E-01	6.70E-01		-8.15E+00	1.44E-01		-3.19E-01	4.51E-01		-2.08E+00	2.38E-06	Down	-3.02E+00	2.43E-03		-1.50E+00	5.44E-02		Unigene95144_All//gi|297824981|ref|XP_002880373.1|//3.00E-34//kinesin motor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297326212|gb|EFH56632.1| kinesin motor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene95144_All//1.00E-35//AT2G21300| kinesin motor family protein	Unigene95144_All//0.00E+00//gi|109883065|gb|DW512035.1|DW512035				nr -
Unigene9516_All	289	0.18	0.00	0.00	0.17	0.48	0.31	6.73	0.87	2.34	-7.50E+00	5.93E-01		-7.50E+00	6.07E-01		1.47E+00	6.15E-01		8.58E-01	7.89E-01		-2.96E+00	2.83E-08	Down	-1.52E+00	3.06E-04	Down				Unigene9516_All//2.00E-67//gi|109872067|gb|DW501043.1|DW501043				
Unigene95176_All	309	83.31	39.68	39.81	54.33	48.03	43.12	13.68	10.42	7.86	-1.07E+00	2.69E-21	Down	-1.07E+00	2.65E-20	Down	-1.78E-01	2.33E-01		-3.33E-01	1.57E-02		-3.94E-01	1.50E-01		-7.99E-01	1.72E-03		Unigene95176_All//gi|297853250|ref|XP_002894506.1|//1.00E-15//CPN60B [Arabidopsis lyrata subsp. lyrata] >gi|297340348|gb|EFH70765.1| CPN60B [Arabidopsis lyrata subsp. lyrata]	Unigene95176_All//4.00E-09//AT3G13470| chaperonin, putative	Unigene95176_All//4.00E-158//C0118398		ko03018|RNA degradation		nr +
Unigene95186_All	362	0.00	0.70	2.21	0.00	1.24	0.62	0.23	0.23	0.66	9.45E+00	7.73E-02		1.11E+01	1.71E-04	Up	1.03E+01	8.00E-03		9.28E+00	1.18E-01		-1.68E-02	1.01E+00		1.50E+00	3.38E-01									
Unigene9519_All	353	0.15	0.00	1.66	0.56	0.39	0.26	0.00	0.12	1.69	-7.21E+00	5.93E-01		3.49E+00	1.20E-02		-5.33E-01	7.46E-01		-1.14E+00	5.66E-01		6.89E+00	6.20E-01		1.07E+01	1.75E-04	Up	Unigene9519_All//gi|147820621|emb|CAN67650.1|//2.00E-20//hypothetical protein [Vitis vinifera]	Unigene9519_All//2.00E-11//AT3G61690| unknown protein	Unigene9519_All//7.00E-09//ES811404				nr +
Unigene95218_All	242	0.00	5.03	0.44	0.00	0.14	1.12	0.70	5.53	5.27	1.23E+01	5.45E-07	Up	8.78E+00	3.85E-01		7.15E+00	8.08E-01		1.01E+01	7.00E-02		2.98E+00	6.56E-06	Up	2.91E+00	1.05E-05	Up	Unigene95218_All//gi|255565105|ref|XP_002523545.1|//1.00E-14//conserved hypothetical protein [Ricinus communis] >gi|223537252|gb|EEF38884.1| conserved hypothetical protein [Ricinus communis]	Unigene95218_All//4.00E-07//AT2G46490| unknown protein	Unigene95218_All//4.00E-65//TC150415				nr +
Unigene9522_All	272	1.15	0.75	5.48	2.20	0.76	1.99	1.87	0.46	1.17	-6.31E-01	6.21E-01		2.25E+00	5.49E-04	Up	-1.53E+00	1.00E-01		-1.41E-01	8.79E-01		-2.02E+00	5.20E-02		-6.71E-01	4.48E-01									
Unigene95230_All	250	0.42	0.00	0.21	0.80	1.38	0.00	9.64	6.69	29.16	-8.71E+00	3.62E-01		-9.75E-01	7.17E-01		7.89E-01	5.95E-01		-9.64E+00	1.31E-01		-5.28E-01	1.57E-01		1.60E+00	2.50E-14	Up	Unigene95230_All//gi|221087611|ref|XP_002308196.1|//2.00E-29//laccase 110a [Populus trichocarpa] >gi|222854172|gb|EEE91719.1| laccase 110a [Populus trichocarpa]	Unigene95230_All//7.00E-26//AT3G09220| LAC7 (laccase 7); laccase	Unigene95230_All//5.00E-92//gi|164287151|gb|ES825995.1|ES825995		ko00910|Nitrogen metabolism/ko00053|Ascorbate and aldarate metabolism		nr +
Unigene9527_All	250	5.65	0.81	1.70	1.99	1.52	0.18	6.60	1.67	1.43	-2.80E+00	6.22E-05	Down	-1.73E+00	6.13E-03		-3.95E-01	6.89E-01		-3.46E+00	1.60E-02		-1.98E+00	9.00E-05	Down	-2.20E+00	1.44E-05	Down				Unigene9527_All//2.00E-107//DT046808				
Unigene9528_All	231	0.00	4.17	2.77	0.00	0.00	0.00	0.00	0.00	0.00	1.20E+01	1.37E-05	Up	1.14E+01	1.15E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene9529_All	216	1.94	7.74	5.42	8.99	10.20	2.72	0.00	0.19	0.00	2.00E+00	4.38E-04	Up	1.48E+00	3.03E-02		1.82E-01	7.32E-01		-1.73E+00	4.13E-04	Down	7.60E+00	6.20E-01		null	null									ESTscan +
Unigene953_All	710	0.00	0.71	2.70	0.21	1.75	11.32	63.72	23.61	94.32	9.48E+00	3.99E-03		1.14E+01	1.46E-10	Up	3.05E+00	6.03E-05	Up	5.75E+00	6.65E-44	Up	-1.43E+00	9.03E-71	Down	5.66E-01	3.39E-23		Unigene953_All//gi|229463110|gb|ACQ66107.1|//1.00E-73//1-deoxy-D-xylulose 5-phosphate synthase 2 [Salvia miltiorrhiza]	Unigene953_All//3.00E-59//AT4G15560| CLA1 (CLOROPLASTOS ALTERADOS 1); 1-deoxy-D-xylulose-5-phosphate synthase	Unigene953_All//1.00E-85//TC168956		ko00900|Terpenoid backbone biosynthesis	GO:0006721//GO:0006722//GO:0016744//GO:0016903//GO:0043231	nr -
Unigene9532_All	230	1.82	1.54	0.00	1.95	1.05	0.98	0.18	0.73	2.94	-2.39E-01	8.09E-01		-1.08E+01	1.55E-02		-8.95E-01	4.13E-01		-9.90E-01	3.94E-01		1.98E+00	3.78E-01		4.00E+00	4.29E-04	Up	Unigene9532_All//gi|15242278|ref|NP_197038.1|//3.00E-22//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] >gi|75180838|sp|Q9LXE8.1|PP386_ARATH RecName: Full=Pentatricopeptide repeat-containing protein At5g15340, mitochondrial; Flags: Precursor	Unigene9532_All//1.00E-23//AT5G15340| pentatricopeptide (PPR) repeat-containing protein				GO:0043231	nr +
Unigene95334_All	264	1.19	0.00	0.00	2.64	3.13	1.20	2.40	0.16	0.60	-1.02E+01	3.62E-02		-1.02E+01	4.86E-02		2.45E-01	8.03E-01		-1.14E+00	2.01E-01		-3.92E+00	9.80E-04	Down	-1.99E+00	2.04E-02		Unigene95334_All//gi|259867777|gb|AAM55300.1|//6.00E-24//auxin efflux carrier protein [Medicago truncatula]	Unigene95334_All//2.00E-24//AT1G73590| PIN1 (PIN-FORMED 1); transporter	Unigene95334_All//4.00E-28//DW492561				nr -
Unigene9534_All	273	0.38	0.00	1.56	0.73	1.51	0.83	0.93	1.38	5.84	-8.58E+00	3.62E-01		2.03E+00	1.39E-01		1.05E+00	4.25E-01		1.81E-01	9.34E-01		5.68E-01	6.37E-01		2.65E+00	2.17E-06	Up				Unigene9534_All//9.00E-91//EL738014				
Unigene95344_All	498	0.53	0.51	1.82	1.20	3.80	1.36	0.08	0.17	0.48	-4.63E-02	9.86E-01		1.79E+00	3.07E-02		1.66E+00	6.49E-04	Up	1.81E-01	8.44E-01		9.84E-01	7.26E-01		2.50E+00	1.59E-01		Unigene95344_All//gi|224106565|ref|XP_002314209.1|//5.00E-77//endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa] >gi|222850617|gb|EEE88164.1| endoplasmic reticulum [ER]-type calcium ATPase [Populus trichocarpa]	Unigene95344_All//3.00E-78//AT1G07810| ECA1 (ER-TYPE CA2+-ATPASE 1); calcium-transporting ATPase	Unigene95344_All//9.00E-80//TC136400				nr -
Unigene9535_All	619	0.00	3.11	2.24	0.00	0.00	0.00	0.00	0.00	0.00	1.16E+01	5.72E-11	Up	1.11E+01	1.23E-07	Up	null	null		null	null		null	null		null	null		Unigene9535_All//gi|157849696|gb|AB98631.1|//5.00E-92//aluminum-induced protein [Brassica rapa]	Unigene9535_All//7.00E-91//AT5G19140| AILP1	Unigene9535_All//6.00E-32//gi|48748775|gb|C0079294.1|C0079294		ko00910|Nitrogen metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0009725//GO:0010038//GO:0016020	nr +
Unigene95398_All	287	0.00	0.00	0.00	0.17	0.00	0.00	0.00	1.31	8.61	null	null		null	null		-7.44E+00	5.39E-01		-7.44E+00	6.10E-01		1.04E+01	6.85E-03		1.31E+01	1.09E-17	Up	Unigene95398_All//gi|166203223|gb|AB184652.1|//2.00E-15//transcription factor [Glycine max]	Unigene95398_All//4.00E-13//AT5G45050| TIR1; protein binding / transcription factor	Unigene95398_All//8.00E-08//TC163461	WRKY	ko04626|Plant-pathogen interaction		nr -
Unigene954_All	2595	0.02	0.04	0.00	0.13	0.25	1.29	23.02	6.20	43.94	9.53E-01	7.22E-01		-4.34E+00	6.07E-01		9.08E-01	3.42E-01		3.26E+00	7.04E-13	Up	-1.89E+00	1.30E-138	Down	9.32E-01	1.58E-91		Unigene954_All//gi|56785668|gb|AAW28999.1|//0.00E+00//1-deoxy-D-xylulose-5-phosphate synthase [Antirrhinum majus]	Unigene954_All//0.00E+00//AT4G15560| CLA1 (CLOROPLASTOS ALTERADOS 1); 1-deoxy-D-xylulose-5-phosphate synthase	Unigene954_All//0.00E+00//TC140384		ko00900|Terpenoid backbone biosynthesis	GO:0006721//GO:0006722//GO:0016744//GO:0016903	nr +
Unigene95438_All	462	0.00	0.00	0.00	0.11	0.07	0.10	0.37	2.08	6.73	null	null		null	null		-5.33E-01	8.16E-01		-1.41E-01	9.44E-01		2.51E+00	7.99E-04	Up	4.20E+00	2.82E-17	Up	Unigene95438_All//gi|169160467|gb|ACA49724.1|//5.00E-36//phospholipase D gamma [Citrus sinensis]	Unigene95438_All//1.00E-23//AT2G42010| PLDBETA1 (PHOSPHOLIPASE D BETA 1); phospholipase D	Unigene95438_All//5.00E-07//DW437939		ko04144|Endocytosis//ko00564|Glycerophospholipid metabolism//ko00565|Ether lipid metabolism		nr -
Unigene9545_All	225	0.47	4.95	2.13	0.00	0.77	1.00	0.19	0.19	0.53	3.41E+00	1.24E-04	Up	2.20E+00	9.12E-02		9.58E+00	2.25E-01		9.97E+00	1.18E-01		-1.62E-02	9.93E-01		1.50E+00	5.56E-01									
Unigene95470_All	367	0.00	0.28	0.00	0.81	5.82	2.09	0.00	0.34	0.22	8.11E+00	3.77E-01		null	null		2.84E+00	9.02E-08	Up	1.36E+00	1.18E-01		8.42E+00	2.39E-01		7.76E+00	3.98E-01		Unigene95470_All//gi|224105375|ref|XP_002333828.1|//3.00E-07//BED finger-nbs resistance protein [Populus trichocarpa] >gi|222838647|gb|EEE77012.1| BED finger-nbs resistance protein [Populus trichocarpa]		Unigene95470_All//5.00E-87//ES803779				nr -
Unigene9548_All	375	0.14	0.00	0.28	1.59	1.74	0.84	3.72	0.33	1.49	-7.12E+00	5.93E-01		1.03E+00	6.99E-01		1.30E-01	9.04E-01		-9.19E-01	3.51E-01		-3.48E+00	5.79E-07	Down	-1.32E+00	7.95E-03		Unigene9548_All//gi|297839631|ref|XP_002887697.1|//4.00E-13//kinase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297333538|gb|EFH63956.1| kinase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene9548_All//2.00E-09//AT1G77720| protein kinase family protein	Unigene9548_All//0.00E+00//gi|78322946|gb|DT543220.1|DT543220			GO:0000166//GO:0004672	nr +
Unigene9549_All	741	0.71	0.07	0.00	0.07	0.33	0.30	0.34	0.28	2.10	-3.37E+00	1.57E-02		-9.46E+00	4.73E-03		2.28E+00	3.04E-01		2.18E+00	3.22E-01		-2.80E-01	8.28E-01		2.61E+00	3.62E-06	Up	Unigene9549_All//gi|297813549|ref|XP_002874658.1|//2.00E-06//GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320495|gb|EFH50917.1| GDSL-motif lipase/hydrolase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene9549_All//8.00E-08//AT4G10950| GDSL-motif lipase/hydrolase family protein				GO:0016787//GO:0044238	nr -
Unigene955_All	2368	0.71	1.97	6.05	5.70	14.93	51.80	0.21	0.18	0.44	1.48E+00	7.07E-07	Up	3.10E+00	3.28E-47	Up	1.39E+00	1.00E-50	Up	3.18E+00	0.00E+00	Up	-2.80E-01	7.48E-01		1.03E+00	7.96E-02		Unigene955_All//gi|56785668|gb|AAW28999.1|//0.00E+00//1-deoxy-D-xylulose-5-phosphate synthase [Antirrhinum majus]	Unigene955_All//0.00E+00//AT4G15560| CLA1 (CLOROPLASTOS ALTERADOS 1); 1-deoxy-D-xylulose-5-phosphate synthase	Unigene955_All//0.00E+00//TC140384		ko00900|Terpenoid backbone biosynthesis	GO:0006721//GO:0006722//GO:0016744//GO:0016903	nr +
Unigene9550_All	240	3.05	1.27	4.44	1.87	1.72	0.56	0.18	1.57	3.15	-1.27E+00	1.36E-01		5.40E-01	4.17E-01		-1.18E-01	8.86E-01		-1.73E+00	1.61E-01		3.15E+00	3.41E-02		4.16E+00	1.34E-04	Up				Unigene9550_All//6.00E-33//TC172967				
Unigene9551_All	229	1.83	1.77	1.16	7.40	4.66	1.58	7.02	1.10	2.78	-4.63E-02	9.80E-01		-6.53E-01	5.94E-01		-6.66E-01	1.76E-01		-2.23E+00	7.57E-05	Down	-2.68E+00	2.38E-06	Down	-1.33E+00	3.75E-03					Unigene9551_All//2.00E-11//ES793975				
Unigene9552_All	248	5.91	2.04	0.00	2.61	1.94	1.64	0.85	0.84	0.00	-1.53E+00	7.80E-03		-1.25E+01	5.25E-08	Down	-4.26E-01	6.08E-01		-6.72E-01	4.78E-01		-1.65E-02	1.02E+00		-9.74E+00	5.77E-02					Unigene9552_All//3.00E-10//DR463968				
Unigene9555_All	276	0.00	7.53	2.89	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	7.93E-12	Up	1.15E+01	1.71E-04	Up	null	null		null	null		null	null		null	null		Unigene9555_All//sp|P20478|GLNA2_DROME//6.00E-06//Glutamine synthetase 2 cytoplasmic OS=Drosophila melanogaster GN=Gs2 PE=2 SV=3						swissprot -
Unigene95578_All	200	0.26	0.76	1.07	1.00	1.03	0.00	28.54	94.25	41.83	1.54E+00	5.29E-01		2.03E+00	3.59E-01		5.23E-02	9.87E-01		-9.96E+00	1.31E-01		1.72E+00	7.19E-39	Up	5.52E-01	1.49E-03		Unigene95578_All//gi|124360970|gb|ABN08942.1|//3.00E-09//Quinonoprotein alcohol dehydrogenase-like [Medicago truncatula]					GO:0008152//GO:0016491	nr -
Unigene95581_All	764	0.41	0.33	0.00	0.85	0.45	0.24	1.38	0.38	0.05	-3.09E-01	7.89E-01		-8.68E+00	4.86E-02		-9.11E-01	3.04E-01		-1.84E+00	6.00E-02		-1.85E+00	4.09E-03		-4.73E+00	8.85E-07	Down	Unigene95581_All//gi|48958483|gb|AT4G7794.1|//6.00E-25//At5g42330 [Arabidopsis thaliana] >gi|51536556|gb|AAU05516.1| At5g42330 [Arabidopsis thaliana]	Unigene95581_All//3.00E-26//AT5G42330| unknown protein	Unigene95581_All//0.00E+00//gi|164288279|gb|ES837637.1|ES837637				nr +
Unigene95591_All	409	7.04	12.64	7.55	11.81	25.09	21.75	0.21	0.31	0.00	8.45E-01	1.39E-03		1.02E-01	7.74E-01		1.09E+00	2.54E-10	Up	8.81E-01	3.97E-06		5.69E-01	7.79E-01		-7.69E+00	3.51E-01					Unigene95591_All//5.00E-50//gi|73859853|gb|DT462592.1|DT462592				
Unigene95638_All	723	0.14	0.00	0.00	0.69	3.67	0.69	0.00	0.00	0.00	-7.18E+00	3.62E-01		-7.18E+00	3.83E-01		2.41E+00	3.98E-08	Up	-4.00E-03	9.87E-01		null	null		null	null		Unigene95638_All//gi|15450848|gb|AA96695.1|//5.00E-82//Unknown protein [Arabidopsis thaliana]	Unigene95638_All//3.00E-53//AT1G54730| sugar transporter, putative	Unigene95638_All//1.00E-08//ES827586			GO:0005215//GO:0009536//GO:0016020	nr -
Unigene95646_All	294	0.89	0.86	0.72	9.49	7.85	3.99	4.31	5.40	5.83	-4.63E-02	9.86E-01		-2.97E-01	8.31E-01		-2.74E-01	5.12E-01		-1.25E+00	9.65E-04	Down	3.24E-01	5.26E-01		4.34E-01	3.37E-01					Unigene95646_All//2.00E-30//TC153494				

Unigene95657_All	265	0.00	7.65	0.60	0.75	3.77	5.97	1.91	3.47	6.01	1.29E+01	1.53E-11	Up	9.24E+00	2.33E-01		2.33E+00	3.21E-03		2.99E+00	7.30E-06	Up	8.58E-01	1.95E-01		1.65E+00	6.43E-04	Up	Unigene95657_All//gi|15236663|ref|NP_194123.1|//3.00E-09//UGE2 (UDP-D-glucose/UDP-D-galactose 4-epimerase 2); UDP-glucose 4-epimerase/ protein dimerization [Arabidopsis thaliana] >gi|113868854|sp|Q9T0A7.1|GALE3_ARATH RecName: Full=UDP-glucose 4-epimerase 3; AltName: Full=UDP-galactose 4-epimerase 3; AltName: Full=UDP-glucose 4-epimerase 3; AltName: Full=Galactowaldenase 3 >gi|4972096|emb|CAB43892.1| UDPglucose 4-epimerase-like protein [Arabidopsis thaliana] >gi|7269241|emb|CAB81310.1| UDPglucose 4-epimerase-like protein [Arabidopsis thaliana]	Unigene95657_All//1.00E-10//AT4G23920| UGE2 (UDP-D-glucose/UDP-D-galactose 4-epimerase 2); UDP-glucose 4-epimerase/ protein dimerization	Unigene95657_All//1.00E-34//TC132041		ko00520|Amino sugar and nucleotide sugar metabolism//ko00052|Galactose metabolism	GO:0005515//GO:0008152//GO:0016857//GO:0044444//GO:0050896//GO:0070882	nr -
Unigene9566_All	352	0.00	0.00	0.00	0.28	0.68	0.51	1.92	0.12	0.00	null	null		null	null		1.27E+00	5.31E-01		8.59E-01	6.93E-01		-4.02E+00	5.36E-04	Down	-1.09E+01	3.56E-05	Down							
Unigene95674_All	287	0.00	0.00	0.19	0.87	0.96	0.00	0.15	4.08	4.30	null	null		7.54E+00	6.19E-01		1.46E-01	9.61E-01		-9.76E+00	7.24E-02		4.79E+00	3.87E-07	Up	4.87E+00	9.59E-08	Up	Unigene95674_All//gi|297827895|ref|XP_002881830.1|//1.00E-06//basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327669|gb|EFH58089.1| basic helix-loop-helix family protein [Arabidopsis lyrata subsp. lyrata]	Unigene95674_All//5.00E-08//AT2G42280| basic helix-loop-helix (bHLH) family protein	Unigene95674_All//1.00E-22//DT464872	bHLH			nr -
Unigene95680_All	562	0.00	0.00	0.00	0.71	0.74	0.32	2.03	0.30	1.13	null	null		null	null		5.23E-02	9.89E-01		-1.14E+00	3.79E-01		-2.77E+00	7.62E-05	Down	-8.41E-01	1.23E-01		Unigene95680_All//gi|13877693|gb|AK43924.1|AF370605_1//7.00E-53//axi 1 protein-like protein [Arabidopsis thaliana] >gi|3128192|gb|AAC16096.1| similar to axi 1 protein from Nicotiana tabacum [Arabidopsis thaliana]	Unigene95680_All//1.00E-54//AT2G44500| unknown protein	Unigene95680_All//3.00E-157//gi|54115400|gb|CO490909.1|CO490909			GO:0009536	nr +
Unigene957_All	2507	3.67	3.86	3.42	6.54	4.89	6.36	4.65	6.35	11.23	7.17E-02	7.14E-01		-1.03E-01	6.09E-01		-4.19E-01	1.23E-03		-3.98E-02	8.03E-01		4.49E-01	3.22E-04		1.27E+00	7.65E-38	Up	Unigene957_All//gi|117549794|gb|AB435085.1|//0.00E+00//EIL1 [Prunus persica]	Unigene957_All//1.00E-137//AT1G73730| EIL3 (ETHYLENE-INSENSITIVE3-LIKE3); DNA binding / transcription factor	Unigene957_All//1.00E-76//gi|164254696|gb|ES826467.1|ES826467	EIL			nr +
Unigene95704_All	271	0.39	0.19	0.59	0.92	3.43	1.50	0.16	1.23	2.94	-1.05E+00	6.81E-01		6.11E-01	7.46E-01		1.90E+00	1.59E-02		7.07E-01	5.97E-01		2.98E+00	5.73E-02		4.24E+00	7.42E-05	Up	Unigene95704_All//gi|115472199|ref|NP_001059698.1|//4.00E-41//Os07g0495900 [Oryza sativa Japonica Group] >gi|113611234|dbj|BAF21612.1| Os07g0495900 [Oryza sativa Japonica Group]	Unigene95704_All//8.00E-42//AT5G47010| LBA1 (LOW-LEVEL BETA-AMYLASE 1); ATP binding / DNA binding / RNA helicase/ hydrolase	Unigene95704_All//2.00E-24//TC133127			GO:0000956//GO:0003676//GO:0017111//GO:0032559//GO:0044424//GO:0046914	nr -
Unigene9572_All	577	0.73	0.18	0.00	0.35	0.12	0.00	1.03	1.52	3.38	-2.05E+00	1.20E-01		-9.50E+00	1.55E-02		-1.53E+00	4.13E-01		-8.43E+00	1.31E-01		5.68E-01	3.99E-01		1.72E+00	7.69E-05	Up	Unigene9572_All//gi|224122948|ref|XP_002318956.1|//2.00E-67//vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa] >gi|222857332|gb|EEE94879.1| vacuolar H+-translocating inorganic pyrophosphatase [Populus trichocarpa]	Unigene9572_All//2.00E-64//AT1G15690| AVP1: ATPase/ hydrogen-translocating pyrophosphatase	Unigene9572_All//6.00E-103//gi|164330634|gb|ES835845.1|ES835845		ko00190|Oxidative phosphorylation	GO:0006818//GO:0008152//GO:0015405//GO:0016462//GO:0016628//GO:0031410	nr +
Unigene9574_All	449	0.00	3.61	2.96	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.96E-09	Up	1.15E+01	2.39E-07	Up	null	null		null	null		null	null		null	null		Unigene9574_All//gi|17221648|dbj|BAB78478.1|//6.00E-09//preproMP73 [Cucurbita maxima]				ko03040|Spliceosome//ko00520|Amino sugar and nucleotide sugar metabolism//ko03022|Basal transcription factors		nr +
Unigene95746_All	307	10.91	13.86	3.82	13.63	6.62	8.83	3.58	5.04	10.77	3.46E-01	2.53E-01		-1.52E+00	4.63E-05	Down	-1.04E+00	1.71E-04	Down	-6.27E-01	3.59E-02		4.92E-01	3.23E-01		1.59E+00	6.54E-07	Up			Unigene95746_All//2.00E-64//DW516589				
Unigene9575_All	313	0.33	63.78	22.80	0.00	0.00	0.00	0.00	0.00	0.00	7.58E+00	1.36E-110	Up	6.09E+00	1.57E-36	Up	null	null		null	null		null	null		null	null		Unigene9575_All//5.00E-19//AT4G33865| 40S ribosomal protein S29 (RPS29C)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015935//GO:0043169	nr +
Unigene95753_All	237	0.00	1.71	4.72	0.42	3.92	2.29	0.89	1.76	2.35	1.07E+01	1.34E-02		1.22E+01	3.41E-06	Up	3.22E+00	5.79E-04	Up	2.44E+00	4.41E-02		9.83E-01	3.73E-01		1.40E+00	1.12E-01								
Unigene9576_All	308	0.00	0.00	0.17	3.07	2.35	0.15	0.14	0.00	0.13	null	null		7.43E+00	6.19E-01		-3.88E-01	5.85E-01		-4.39E+00	5.96E-05	Down	-7.10E+00	6.33E-01		-8.66E-02	9.61E-01		Unigene9576_All//gi|225455244|ref|XP_002271388.1|//5.00E-13//PREDICTED: hypothetical protein [Vitis vinifera]						nr -
Unigene9578_All	225	11.16	15.99	14.44	11.96	14.85	13.65	37.58	31.21	18.06	5.19E-01	1.15E-01		3.71E-01	3.21E-01		3.12E-01	4.12E-01		1.91E-01	6.29E-01		-2.68E-01	1.57E-01		-1.06E+00	3.17E-09	Down	Unigene9578_All//gi|145330372|ref|NP_001078011.1|//3.00E-06//ubiquitin-conjugating enzyme family protein [Arabidopsis thaliana]	Unigene9578_All//1.00E-117//gi|164351963|gb|ES796625.1|ES796625					nr +
Unigene9580_All	769	0.00	0.00	0.00	0.32	0.09	0.47	2.14	5.16	1.61	null	null		null	null		-1.85E+00	2.74E-01		5.37E-01	6.94E-01		1.27E+00	7.15E-06	Up	-4.17E-01	3.52E-01		Unigene9580_All//gi|115448727|ref|NP_001048143.1|//3.00E-58//Os02g0753000 [Oryza sativa Japonica Group] >gi|113537674|dbj|BAF10057.1| Os02g0753000 [Oryza sativa Japonica Group]	Unigene9580_All//9.00E-52//AT4G12430| trehalose-6-phosphate phosphatase, putative	Unigene9580_All//6.00E-08//EX167309		ko00500|Starch and sucrose metabolism	GO:0005991//GO:0019203	nr -
Unigene9582_All	238	0.00	0.21	0.00	0.00	0.00	0.00	136.26	26.69	62.27	7.73E+00	6.03E-01		null	null		null	null		null	null		-2.35E+00	1.52E-99	Down	-1.13E+00	1.77E-36	Down							
Unigene9583_All	297	0.00	2.39	2.33	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	3.30E-04	Up	1.12E+01	6.09E-04	Up	null	null		null	null		null	null		null	null		Unigene9583_All//gi|295913728|gb|ADG58103.1|//1.00E-21//transcription factor [Lycoris longituba]	Unigene9583_All//3.00E-07//AT1G01780| LIM domain-containing protein		LIM			nr -
Unigene95851_All	544	0.19	0.00	0.00	0.64	2.09	2.91	0.00	0.38	0.07	-7.59E+00	3.62E-01		-7.59E+00	3.83E-01		1.70E+00	1.20E-02		2.18E+00	2.41E-04	Up	8.59E+00	7.83E-02		6.19E+00	6.29E-01								
Unigene95866_All	514	2.54	1.97	0.93	2.81	2.08	2.64	3.13	0.57	1.24	-3.68E-01	5.31E-01		-1.45E+00	2.42E-02		-4.37E-01	4.44E-01		-9.25E-02	8.76E-01		-2.46E+00	7.71E-06	Down	-1.33E+00	3.75E-03		Unigene95866_All//gi|195658145|gb|ACG48540.1|//3.00E-08//60S ribosomal protein L23 [Zea mays]	Unigene95866_All//2.00E-09//AT3G04400| emb2171 (embryo defective 2171); structural constituent of ribosome	Unigene95866_All//2.00E-130//gi|164353968|gb|ES804158.1|ES804158		ko03010|Ribosome		nr +
Unigene9588_All	512	0.00	0.00	0.00	0.00	0.00	0.18	37.74	18.29	76.33	null	null		null	null		null	null		7.46E+00	4.67E-01		-1.05E+00	5.37E-19	Down	1.02E+00	1.02E-36	Up	Unigene9588_All//gi|40218371|gb|AAR83118.1|//4.00E-13//secretory laccase [Gossypium arboreum]		Unigene9588_All//4.00E-54//TC137114			GO:0005576//GO:0009808//GO:0016682//GO:0046914	nr -
Unigene95883_All	288	51.96	29.03	20.71	95.30	136.67	82.96	40.81	343.94	264.90	-8.40E-01	9.57E-09		-1.33E+00	8.18E-17	Down	5.20E-01	3.65E-11		-2.00E-01	7.21E-02		3.08E+00	0.00E+00	Up	2.70E+00	1.52E-277	Up			Unigene95883_All//9.00E-17//DR044167				
Unigene95884_All	331	0.32	0.00	0.16	0.15	2.39	0.14	0.77	1.14	0.36	-8.30E+00	3.62E-01		-9.74E-01	7.17E-01		3.99E+00	6.32E-04	Up	-1.42E-01	9.43E-01		5.68E-01	6.37E-01		-1.09E+00	4.27E-01								
Unigene95891_All	419	0.62	2.42	0.25	1.43	2.88	2.69	1.11	1.00	5.51	1.95E+00	1.01E-02		-1.30E+00	4.35E-01		1.01E+00	1.11E-01		9.17E-01	1.73E-01		-1.54E-01	8.70E-01		2.31E+00	8.95E-08	Up			Unigene95891_All//9.00E-21//DW480801				
Unigene95893_All	503	0.00	0.60	0.00	0.40	1.16	0.00	1.18	0.33	0.00	9.24E+00	4.33E-02		null	null		1.55E+00	1.40E-01		-8.63E+00	1.31E-01		-1.82E+00	4.71E-02		-1.02E+01	1.41E-04	Down			Unigene95893_All//2.00E-90//TC139589				
Unigene959_All	2312	8.64	13.65	12.64	25.17	25.53	34.63	7.13	17.03	36.32	6.59E-01	9.02E-12		5.49E-01	9.33E-08		2.07E-02	8.17E-01		4.61E-01	2.42E-16		1.26E+00	1.94E-50	Up	2.35E+00	1.39E-260	Up	Unigene959_All//gi|297814005|ref|XP_002874886.1|//1.00E-168//oxidoreductase [Arabidopsis lyrata subsp. lyrata] >gi|297320723|gb|EFH51145.1| oxidoreductase [Arabidopsis lyrata subsp. lyrata]	Unigene959_All//3.00E-126//AT4G02940| oxidoreductase, 2OG-Fe(II) oxygenase family protein	Unigene959_All//0.00E+00//TC134373			GO:0003824//GO:0031410	nr -
Unigene9590_All	356	189.59	626.54	320.40	228.08	439.63	556.04	86.82	232.34	242.84	1.72E+00	0.00E+00	Up	7.57E-01	6.61E-50		9.47E-01	1.96E-122		1.29E+00	1.47E-228	Up	1.42E+00	6.40E-127	Up	1.48E+00	1.54E-144	Up	Unigene9590_All//gi|110931692|gb|AB802845.1|//9.00E-39//MYB transcription factor MYB93 [Glycine max]	Unigene9590_All//4.00E-10//AT5G47390| myb family transcription factor	Unigene9590_All//1.00E-149//TC178353	MYB-related		GO:0003676//GO:0043231//GO:0046872	nr +
Unigene95920_All	493	0.21	0.21	2.16	0.51	0.98	0.55	0.51	0.08	1.13	-4.63E-02	9.84E-01		3.35E+00	3.36E-04	Up	9.53E-01	4.23E-01		1.22E-01	9.43E-01		-2.60E+00	1.44E-01		1.14E+00	1.91E-01		Unigene95920_All//gi|297852428|ref|XP_002894095.1|//2.00E-56//C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297339937|gb|EFH70354.1| C2 domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene95920_All//4.00E-48//AT1G48090| phosphoinositide binding				GO:0033036	nr +
Unigene95922_All	370	0.71	3.01	2.16	0.67	1.95	0.98	6.63	3.05	2.80	2.09E+00	4.16E-03		1.61E+00	6.67E-02		1.54E+00	8.92E-02		5.37E-01	6.94E-01		-1.12E+00	2.21E-03		-1.24E+00	5.25E-04	Down	Unigene95922_All//gi|284668883|gb|AA044050.1|//3.00E-15//At3g03150 [Arabidopsis thaliana]	Unigene95922_All//1.00E-16//AT3G03150| unknown protein	Unigene95922_All//2.00E-86//gi|13353001|gb|BG443349.1|BG443349				nr +
Unigene9595_All	485	0.65	0.84	1.10	1.95	0.85	1.21	0.17	0.17	2.96	3.69E-01	7.23E-01		7.62E-01	4.52E-01		-1.20E+00	8.31E-02		-6.89E-01	3.58E-01		-1.66E-02	1.01E+00		4.08E+00	3.98E-08	Up	Unigene9595_All//gi|42562729|ref|NP_175747.2|//1.00E-34//serine/threonine protein kinase-related [Arabidopsis thaliana] >gi|263711277|sp|C0LGG7.2|Y1534_ARATH RecName: Full=Probable LRR receptor-like serine/threonine-protein kinase At1g53420; Flags: Precursor	Unigene9595_All//3.00E-29//AT1G53420| serine/threonine protein kinase-related				GO:0004672//GO:0005488	nr -
Unigene9596_All	277	0.00	0.00	0.00	0.00	0.00	0.00	3.66	2.57	0.29	null	null		null	null		null	null		null	null		-5.14E-01	4.07E-01		-3.67E+00	1.15E-05	Down	Unigene9596_All//gi|74272607|gb|AB401099.1|//1.00E-32//40S ribosomal protein S3 [Chlamydomonas incerta]	Unigene9596_All//5.00E-24//AT5G35530| 40S ribosomal protein S3 (RPS3C)	Unigene9596_All//1.00E-12//gi|78338942|gb|DT559216.1|DT559216		ko03010|Ribosome	GO:0003676//GO:0005198//GO:0010467//GO:0033279	nr -
Unigene95978_All	318	0.33	0.80	0.00	0.47	2.49	0.00	0.13	1.31	2.51	1.28E+00	4.34E-01		-8.36E+00	3.83E-01		2.41E+00	9.58E-03		-8.88E+00	2.28E-01		3.30E+00	2.00E-02		4.24E+00	7.42E-05	Up	Unigene95978_All//gi|29838629|gb|AAM75139.1|//2.00E-12//alkaline alpha galactosidase I [Cucumis melo]	Unigene95978_All//4.00E-12//AT1G55740| AtSIP1 (Arabidopsis thaliana seed imbibition 1); hydrolase, hydrolyzing O-glycosyl compounds			ko00052|Galactose metabolism		nr +
Unigene9598_All	318	0.49	1.12	0.00	0.00	0.97	1.56	0.53	0.79	5.14	1.18E+00	3.72E-01		-8.95E+00	2.41E-01		9.93E+00	4.53E-02		1.06E+01	4.38E-03		5.68E-01	6.73E-01		3.27E+00	7.65E-08	Up							
Unigene95980_All	364	0.00	0.00	0.00	1.92	0.66	0.00	0.70	0.34	0.55	null	null		null	null		-1.53E+00	7.00E-02		-1.09E+01	1.95E-04	Down	-1.02E+00	4.94E-01		-3.49E-01	7.66E-01		Unigene95980_All//gi|297802658|ref|XP_002869213.1|//2.00E-08//glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata] >gi|297315049|gb|EFH45472.1| glycoside hydrolase family 28 protein [Arabidopsis lyrata subsp. lyrata]		Unigene95980_All//4.00E-29//TC134935				nr -
Unigene96_All	2681	5.43	11.42	5.10	7.73	11.51	13.04	9.19	8.81	12.41	1.07E+00	3.39E-25	Up	-8.79E-02	6.34E-01		5.74E-01	1.73E-10		7.54E-01	3.35E-17		-6.19E-02	6.36E-01		4.33E-01	1.10E-07		Unigene96_All//gi|18401322|ref|NP_565635.1|//0.00E+00//SE (SERRATE); DNA binding / transcription factor [Arabidopsis thaliana] >gi|75339076|sp|Q9ZVD0.2|SRRT_ARATH RecName: Full=Serrate RNA effector molecule >gi|14486602|gb|AAK63206.1|AF311221_1 C2H2 zinc-finger protein SERRATE [Arabidopsis thaliana] >gi|16226331|gb|AAL16137.1|AF428305_1 At2g27100/T20P8.15 [Arabidopsis thaliana] >gi|20197420|gb|AAC77868.2| expressed protein [Arabidopsis thaliana] >gi|23506033|gb|AAN28876.1| At2g27100/T20P8.15 [Arabidopsis thaliana]	Unigene96_All//0.00E+00//AT2G27100| SE (SERRATE); DNA binding / transcription factor	Unigene96_All//0.00E+00//gi|109839718|gb|DW238279.1|DW238279				nr +

Unigene9601_All	223	0.00	22.95	7.88	0.00	0.00	0.00	0.00	0.00	0.00	1.45E+01	3.53E-29	Up	1.29E+01	1.12E-09	Up	null	null		null	null		null	null		null	null		Unigene9601_All//gi|224058553|ref|XP_002299541.1|//5.00E-24//tubulin, beta chain [Populus trichocarpa] >gi|222846799|gb|EEE84346.1|tubulin, beta chain [Populus trichocarpa]	Unigene9601_All//2.00E-17//AT5G23860| TUB8; structural constituent of cytoskeleton	Unigene9601_All//1.00E-24//gi|21102344|gb|BQ414657.1|BQ414657		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene96028_All	357	2.20	0.85	0.00	3.35	3.76	3.42	3.55	0.94	2.12	-1.37E+00	9.59E-02		-1.11E+01	2.21E-04	Down	1.68E-01	8.23E-01		2.85E-02	9.62E-01		-1.92E+00	9.98E-04	Down	-7.45E-01	1.46E-01		Unigene96028_All//gi|42567943|ref|NP_197371.2|//2.00E-32//EMB3013 (embryo defective 3013); ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase [Arabidopsis thaliana]	Unigene96028_All//7.00E-33//AT5G18700| EMB3013 (embryo defective 3013); ATP binding / binding / kinase/ protein kinase/ protein serine/threonine kinase			ko04626|Plant-pathogen interaction		nr -
Unigene96034_All	353	10.97	2.87	4.22	9.45	5.85	8.32	3.59	1.30	0.79	-1.93E+00	3.26E-08	Down	-1.38E+00	4.46E-05	Down	-6.92E-01	3.24E-02		-1.85E-01	6.15E-01		-1.46E+00	8.32E-03		-2.19E+00	1.97E-04	Down	Unigene96034_All//gi|1149535|emb|CAA64221.1|//2.00E-09//homeobox-leucine zipper protein [Pimpinella brachycarpa]		Unigene96034_All//1.00E-93//TC144038				nr -
Unigene96040_All	233	0.00	0.22	0.46	0.86	0.89	0.19	480.32	111.93	173.89	7.76E+00	6.03E-01		8.84E+00	3.85E-01		5.22E-02	9.87E-01		-2.14E+00	3.45E-01		-2.10E+00	1.28E-297	Down	-1.47E+00	2.51E-185	Down	Unigene96040_All//gi|300793598|tpg|DAA33865.1|//6.00E-38//TPA: TPA_inf: aquaporin PIP2;10 [Gossypium hirsutum]	Unigene96040_All//4.00E-36//AT5G60660| PIP2;4 (PLASMA MEMBRANE INTRINSIC PROTEIN 2;4); water channel	Unigene96040_All//7.00E-122//TC153220				nr +
Unigene96044_All	736	0.00	0.62	0.43	0.00	7.72	0.00	0.00	0.00	0.00	9.28E+00	7.33E-03		8.76E+00	4.41E-02		1.29E+01	2.04E-36	Up	null	null		null	null		null	null		Unigene96044_All//gi|42569129|ref|NP_179444.2|//1.00E-17//cupin family protein [Arabidopsis thaliana]				ko03040|Spliceosome		nr +
Unigene9605_All	305	3.60	0.00	0.00	1.80	1.81	4.74	0.97	0.69	0.78	-1.18E+01	1.94E-06	Down	-1.18E+01	4.93E-06	Down	7.80E-03	9.82E-01		1.40E+00	1.56E-02		-5.02E-01	6.77E-01		-3.08E-01	7.74E-01									
Unigene96054_All	309	0.34	2.95	6.03	0.81	2.45	2.19	1.37	1.49	1.93	3.12E+00	1.14E-03		4.15E+00	4.39E-08	Up	1.60E+00	6.97E-02		1.44E+00	1.28E-01		1.21E-01	9.07E-01		4.99E-01	5.52E-01				Unigene96054_All//6.00E-15//TC154856				
Unigene9607_All	284	0.00	5.89	1.88	0.00	0.00	0.00	0.00	0.00	0.00	1.25E+01	1.53E-09	Up	1.09E+01	3.98E-03		null	null		null	null		null	null		null	null									ESTscan -
Unigene96073_All	306	0.00	0.00	0.00	0.00	2.59	0.59	0.00	0.00	0.00	null	null		null	null		1.13E+01	7.26E-05	Up	9.21E+00	1.93E-01		null	null		null	null		Unigene96073_All//gi|11466466|ref|NP_008169.1|//1.00E-24//apocytochrome b [Chrysodidymus synuroideus] >gi|7110463|gb|AAF36935.1|AF222718_9 apocytochrome b [Chrysodidymus synuroideus]	Unigene96073_All//5.00E-18//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a subunit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.			ko00190|Oxidative phosphorylation		nr +
Unigene9608_All	298	142.04	73.79	63.97	203.94	192.51	213.09	231.55	116.97	153.61	-9.45E-01	2.96E-28		-1.15E+00	2.28E-37	Down	-8.32E-02	3.01E-01		6.33E-02	4.51E-01		-9.85E-01	1.04E-59		-5.92E-01	6.35E-26		Unigene9608_All//gi|297804766|ref|XP_002870267.1|//6.00E-40//60S ribosomal protein L27 [Arabidopsis lyrata subsp. lyrata] >gi|297316103|gb|EFH46526.1| 60S ribosomal protein L27 [Arabidopsis lyrata subsp. lyrata]	Unigene9608_All//4.00E-40//AT4G15000| 60S ribosomal protein L27 (RPL27C)	Unigene9608_All//1.00E-167//TC154183		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613	nr -
Unigene96104_All	229	2.28	12.61	3.72	3.05	8.57	2.37	2.03	3.83	4.18	2.46E+00	3.51E-08	Up	7.03E-01	3.83E-01		1.49E+00	1.49E-03		-3.64E-01	6.80E-01		9.16E-01	1.77E-01		1.04E+00	9.27E-02			Unigene96104_All//9.00E-05//AT3G03170| unknown protein	Unigene96104_All//4.00E-37//DW519596				
Unigene96120_All	265	0.39	0.38	3.82	1.88	0.91	2.56	1.91	0.16	0.00	-4.64E-02	9.84E-01		3.27E+00	5.92E-04	Up	-1.05E+00	3.14E-01		4.44E-01	6.21E-01		-3.60E+00	5.77E-03		-1.09E+01	5.53E-04	Down			Unigene96120_All//5.00E-114//TC155715				
Unigene96141_All	416	1.01	0.49	0.77	0.96	0.75	1.09	2.64	0.10	0.29	-1.05E+00	3.65E-01		-3.90E-01	7.17E-01		-3.63E-01	7.53E-01		1.81E-01	8.83E-01		-4.72E+00	1.02E-06	Down	-3.20E+00	1.63E-05	Down	Unigene96141_All//gi|211906538|gb|AC111762.1|//5.00E-48//class III peroxidase [Gossypium hirsutum]	Unigene96141_All//1.00E-22//AT5G05300| peroxidase, putative	Unigene96141_All//5.00E-121//gi|84159124|gb|DN828188.1|DN828188		ko00940|Phenylpropanoid biosynthesis//ko00360|Phenylalanine metabolism		nr -
Unigene9616_All	271	0.00	9.54	4.52	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.05E-14	Up	1.21E+01	9.08E-07	Up	null	null		null	null		null	null		null	null		Unigene9616_All//gi|238014838|gb|ACG38454.1|//5.00E-11//unknown [Zea mays]		Unigene9616_All//2.00E-33//TC146753				nr +
Unigene96168_All	309	0.00	0.16	0.17	0.48	0.11	0.15	282.55	1388.46	78.77	7.36E+00	6.03E-01		7.43E+00	6.19E-01		-2.12E+00	3.83E-01		-1.73E+00	4.97E-01		2.30E+00	0.00E+00	Up	-1.84E+00	7.07E-201	Down	Unigene96168_All//gi|293633663|gb|ADE60217.1|//4.00E-46//MIC-3 [Gossypium herbaceum] >gi|293633665|gb|ADE60218.1| MIC-3 [Gossypium herbaceum] >gi|293633667|gb|ADE60219.1| MIC-3 [Gossypium herbaceum]		Unigene96168_All//1.00E-77//NP12958110				nr -
Unigene96178_All	368	0.00	0.00	0.00	3.11	2.71	0.86	1.84	1.02	0.11	null	null		null	null		-1.98E-01	7.77E-01		-1.86E+00	6.47E-03		-8.47E-01	2.88E-01		-4.09E+00	3.10E-04	Down	Unigene96178_All//gi|224117086|ref|XP_002331783.1|//6.00E-10//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222832242|gb|EEE70719.1| cc-nbs-lrr resistance protein [Populus trichocarpa]		Unigene96178_All//2.00E-111//C0132540				nr -
Unigene9618_All	530	0.00	0.38	0.00	0.75	0.52	0.17	0.32	1.42	4.28	8.58E+00	1.34E-01		null	null		-5.33E-01	6.15E-01		-2.14E+00	1.26E-01		2.15E+00	9.17E-03		3.75E+00	7.86E-12	Up							
Unigene9619_All	359	0.00	3.53	1.34	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.85E-07	Up	1.04E+01	7.38E-03		null	null		null	null		null	null		null	null		Unigene9619_All//sp|P01023|A2MG_HUMAN//3.00E-62//Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=2						swissprot -
Unigene96191_All	262	1.40	0.39	0.20	1.71	1.18	2.76	2.10	0.00	1.06	-1.85E+00	1.87E-01		-2.78E+00	1.03E-01		-5.33E-01	5.95E-01		6.89E-01	4.48E-01		-1.10E+01	4.61E-04	Down	-9.79E-01	2.49E-01									
Unigene9620_All	277	0.00	0.00	0.00	0.00	0.00	0.00	2.59	1.96	0.00	null	null		null	null		null	null		null	null		-4.04E-01	6.23E-01		-1.13E+01	1.78E-05	Down	Unigene9620_All//gi|297806197|ref|XP_002870862.1|//5.00E-29//60S ribosomal protein L35 [Arabidopsis lyrata subsp. lyrata] >gi|297316819|gb|EFH47241.1| 60S ribosomal protein L35 [Arabidopsis lyrata subsp. lyrata]	Unigene9620_All//2.00E-23//AT2G39390| 60S ribosomal protein L35 (RPL35B)			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0016020//GO:0022613//GO:0031981	nr -
Unigene96209_All	450	3.26	1.46	8.76	2.88	2.75	2.41	3.66	0.56	1.42	-1.15E+00	3.81E-02		1.43E+00	2.02E-05	Up	-6.32E-02	9.04E-01		-2.57E-01	6.87E-01		-2.72E+00	1.39E-06	Down	-1.37E+00	2.58E-03		Unigene96209_All//gi|15242041|ref|NP_197570.1|//6.00E-09//senescence-associated protein-related [Arabidopsis thaliana] >gi|30725354|gb|AAP37699.1| At5g20700 [Arabidopsis thaliana]	Unigene96209_All//4.00E-10//AT5G20700| senescence-associated protein-related	Unigene96209_All//9.00E-157//TC135324				nr +
Unigene9621_All	225	0.00	18.92	6.39	0.00	0.00	0.00	0.00	0.00	0.00	1.42E+01	3.03E-24	Up	1.26E+01	6.28E-08	Up	null	null		null	null		null	null		null	null		Unigene9621_All//sp|P80977|COC1_THEOB//8.00E-08//Cytochrome c oxidase subunit 6C-1 OS=Thunnus obesus PE=1 SV=2						swissprot -
Unigene9624_All	708	0.00	1.36	4.96	0.00	0.63	0.64	0.00	0.00	0.00	1.04E+01	1.37E-05	Up	1.23E+01	1.87E-19	Up	9.30E+00	7.99E-03		9.32E+00	7.74E-03		null	null		null	null		Unigene9624_All//gi|41203466|ref|NP_957726.1|//8.00E-25//NADH dehydrogenase subunit 4 [Emiliania huxleyi] >gi|33114152|gb|AAP94708.1| NADH dehydrogenase subunit 4 [Emiliania huxleyi]	Unigene9624_All//5.00E-09//ATMG00580| NADH dehydrogenase subunit 4			ko00190|Oxidative phosphorylation	GO:0016020	nr +
Unigene96246_All	731	0.00	0.00	0.00	0.00	0.75	0.87	0.29	2.00	2.02	null	null		null	null		9.56E+00	2.02E-03		9.76E+00	7.59E-04	Up	2.79E+00	4.85E-06	Up	2.80E+00	2.86E-06	Up	Unigene96246_All//gi|30691233|ref|NP_174300.2|//8.00E-91//glycosyl hydrolase family 17 protein [Arabidopsis thaliana]	Unigene96246_All//9.00E-93//AT1G30080| glycosyl hydrolase family 17 protein	Unigene96246_All//3.00E-173//C0117865		ko00500|Starch and sucrose metabolism		nr -
Unigene9625_All	240	4.80	112.95	3.33	2.91	7.46	1.69	0.00	0.70	0.00	4.56E+00	7.30E-124	Up	-5.27E-01	4.10E-01		1.36E+00	5.82E-03		-7.79E-01	3.93E-01		9.44E+00	1.38E-01		null	null				Unigene9625_All//7.00E-88//DW504421				
Unigene96293_All	434	1.81	13.66	24.42	6.31	7.30	11.55	1.46	0.58	0.73	2.92E+00	3.31E-19	Up	3.76E+00	1.92E-41	Up	2.10E-01	6.07E-01		8.72E-01	1.05E-03		-1.34E+00	1.13E-01		-9.93E-01	2.02E-01		Unigene96293_All//gi|15218445|ref|NP_175036.1|//2.00E-29//emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding [Arabidopsis thaliana] >gi|7523682|gb|AAF63121.1|AC009526_6 Putative histidine decarboxylase [Arabidopsis thaliana] >gi|5011302|gb|AAK77493.1|AF389349_1 serine decarboxylase [Arabidopsis thaliana] >gi|17907848|dbj|BAB79456.1| histidine decarboxylase [Arabidopsis thaliana] >gi|17907853|dbj|BAB79457.1| histidine decarboxylase [Arabidopsis thaliana]	Unigene96293_All//1.00E-30//AT1G43710| emb1075 (embryo defective 1075); carboxy-lyase/ catalytic/ pyridoxal phosphate binding	Unigene96293_All//2.00E-176//TC172219		ko00340|Histidine metabolism		nr -
Unigene9630_All	210	1.49	1.69	3.04	6.17	5.25	1.08	0.00	0.20	0.19	1.76E-01	8.82E-01		1.03E+00	2.80E-01		-2.33E-01	7.04E-01		-2.52E+00	2.43E-04	Down	7.64E+00	6.19E-01		7.57E+00	6.29E-01								
Unigene96311_All	247	4.24	3.69	4.31	11.50	3.35	4.75	4.11	3.22	2.26	-1.98E-01	7.41E-01		2.54E-02	9.89E-01		-1.78E+00	1.27E-06	Down	-1.27E+00	6.82E-04	Down	-3.54E-01	5.99E-01		-8.63E-01	1.40E-01		Unigene96311_All//gi|164564736|dbj|BAF98218.1|//1.00E-11//CM0216.350.nc [Lotus japonicus]		Unigene96311_All//2.00E-45//BF276543		ko03010|Ribosome		nr -
Unigene96315_All	395	5.17	4.87	5.53	3.41	8.98	2.86	1.71	4.44	6.66	-8.38E-02	8.46E-01		9.75E-02	8.21E-01		1.40E+00	1.72E-05	Up	-2.52E-01	6.86E-01		1.38E+00	2.50E-03		1.96E+00	2.92E-07	Up	Unigene96315_All//gi|297737170|emb|CBI26371.3|//9.00E-07//unnamed protein product [Vitis vinifera]		Unigene96315_All//4.00E-60//TC170580				nr +
Unigene9633_All	325	0.00	0.94	2.13	0.00	0.00	0.56	0.00	0.00	0.00	9.87E+00	4.35E-02		1.11E+01	6.09E-04	Up	null	null		9.12E+00	1.93E-01		null	null		null	null		Unigene9633_All//gi|110377793|gb|ABG73417.1|//4.00E-55//chloroplast pigment-binding protein CP26 [Nicotiana tabacum]	Unigene9633_All//9.00E-47//AT4G10340| LHCB5 (LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5); chlorophyll binding	Unigene9633_All//8.00E-36//gi|31074011|gb|CA994290.1|CA994290		ko00196|Photosynthesis - antenna proteins	GO:0006091//GO:0009503//GO:0009523//GO:0009570//GO:0009639//GO:0046906	nr +
Unigene9634_All	239	0.00	2.33	3.79	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	2.16E-03		1.19E+01	4.69E-05	Up	null	null		null	null		null	null		null	null		Unigene9634_All//sp|Q5RBA5|SQSTM_PONAB//7.00E-41//Sequestosome-1 OS=Pongo abelii GN=SQSTM1 PE=2 SV=1						swissprot -
Unigene96354_All	650	0.08	0.31	0.00	0.54	2.33	0.28	0.33	0.06	0.18	1.95E+00	3.73E-01		-6.33E+00	6.07E-01		2.12E+00	3.26E-04	Up	-9.49E-01	4.80E-01		-2.34E+00	2.36E-01		-8.22E-01	5.98E-01		Unigene96354_All//gi|15238031|ref|NP_199527.1|//3.00E-12//YDG/SRA domain-containing protein [Arabidopsis thaliana] >gi|91807006|gb|ABE66230.1| YDG/SRA domain-containing protein [Arabidopsis thaliana]	Unigene96354_All//4.00E-14//AT5G47160| YDG/SRA domain-containing protein					nr +
Unigene96370_All	250	0.42	0.20	0.64	8.57	4.27	1.81	49.21	10.03	44.62	-1.05E+00	6.81E-01		6.10E-01	7.46E-01		-1.00E+00	1.56E-02		-2.25E+00	5.08E-06	Down	-2.29E+00	4.38E-37	Down	-1.41E-01	3.69E-01		Unigene96370_All//gi|15217844|ref|NP_174134.1|//1.00E-08//GH3.17; indole-3-acetic acid amido synthetase [Arabidopsis thaliana] >gi|62900379|sp|Q9FZ87.1|GH317_ARATH RecName: Full=Indole-3-acetic acid-amido synthetase GH3.17; AltName: Full=Auxin-responsive GH3-like protein 17; Short=AtGH3-17 >gi|9795624|gb|AAF98442.1|AC021044_21 [unknown protein [Arabidopsis thaliana] >gi|15450365|gb|AAK96476.1| At1g28130/F3H9_19 [Arabidopsis thaliana] >gi|21360519|gb|AAM47375.1| At1g28130/F3H9_19 [Arabidopsis thaliana]	Unigene96370_All//5.00E-10//AT1G28130| GH3.17; indole-3-acetic acid amido synthetase	Unigene96370_All//1.00E-77//ES827343				nr +

Unigene9638_All	398	0.00	1.66	0.67	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	6.20E-04	Up	9.39E+00	7.84E-02		null	null		null	null		null	null		null	null		Unigene9638_All//gi|162458022|ref|NP_001105053.1|//3.00E-11//LOC541920 [Zea mays] >gi|16305113|gb|AAL16979.1| 50kD gamma zein [Zea mays]				ko03018|RNA degradation//ko03022|Basal transcription factors	GO:0005488//GO:0009606//GO:0009639//GO:0009725//GO:0010556//GO:0023033//GO:0030528//GO:0043231//GO:0048527//GO:0050794//GO:0051716	nr +
Unigene96382_All	361	1.45	1.40	0.89	1.10	2.29	0.13	3.40	2.08	0.88	-4.62E-02	9.75E-01		-7.12E-01	4.97E-01		1.05E+00	1.99E-01		-3.14E+00	4.86E-02		-7.05E-01	2.06E-01		-1.94E+00	7.80E-04	Down	Unigene96382_All//gi|195638498|gb|AC538717.1|//1.00E-08//monoglyceride lipase [Zea mays]	Unigene96382_All//6.00E-10//AT3G62860| esterase/lipase/thioesterase family protein	Unigene96382_All//3.00E-97//CO099437				nr -
Unigene9639_All	277	3.21	1.83	0.00	1.80	0.37	0.82	0.00	0.00	0.00	-8.12E-01	2.68E-01		-1.16E+01	6.29E-05	Down	-2.27E+00	4.22E-02		-1.14E+00	3.07E-01		null	null		null	null		Unigene9639_All//gi|224101373|ref|XP_002312252.1|//3.00E-15//predicted protein [Populus trichocarpa] >gi|222852072|gb|EEE89619.1| predicted protein [Populus trichocarpa]		Unigene9639_All//8.00E-153//TC160467				nr -
Unigene96398_All	858	6.34	0.71	3.79	1.28	0.92	0.53	0.05	0.15	0.05	-3.16E+00	2.91E-19	Down	-7.44E-01	5.17E-03		-4.69E-01	4.82E-01		-1.28E+00	5.68E-02		1.57E+00	5.43E-01		-8.75E-02	9.61E-01		Unigene96398_All//gi|115463939|ref|NP_001055569.1|//1.00E-68//Os05g0419000 (Oryza sativa Japonica Group) >gi|113579120|dbj|BAF17483.1| Os05g0419000 [Oryza sativa Japonica Group]	Unigene96398_All//3.00E-62//AT5G38520| hydrolase, alpha/beta fold family protein	Unigene96398_All//0.00E+00//TC133314				nr +
Unigene9640_All	547	0.00	30.66	15.38	0.00	0.00	0.00	0.00	0.00	1.49E+01	2.14E-96	Up	1.39E+01	4.09E-47	Up	null	null		null	null		null	null		null	null		Unigene9640_All//gi|226456017|gb|EEH53319.1|//9.00E-64//alpha tubulin [Micromonas pusilla CCMP1545] >gi|226459781|gb|EEH57076.1| alpha tubulin [Micromonas pusilla CCMP1545]	Unigene9640_All//8.00E-58//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene9640_All//1.00E-42//gi|84144003|gb|DN758245.1|DN758245		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene9643_All	266	26.95	18.29	13.21	29.21	27.57	33.45	29.41	17.13	25.01	-5.59E-01	1.05E-02		-1.03E+00	7.99E-06	Down	-8.34E-02	7.53E-01		1.95E-01	3.94E-01		-7.80E-01	2.61E-05		-2.34E-01	2.26E-01		Unigene9643_All//gi|13877126|gb|AAK43709.1|AF358665_1//4.00E-12//ribosomal protein L32 [Mercurialis annua] >gi|13899053|gb|AAK48948.1|AF370436_1 ribosomal protein L32 [Mercurialis annua] >gi|13899055|gb|AAK48949.1|AF370437_1 ribosomal protein L32 [Mercurialis annua] >gi|13899057|gb|AAK48950.1|AF370438_1 ribosomal protein L32 [Mercurialis annua]		Unigene9643_All//1.00E-114//gi|11201565|gb|BF270654.1|BF270654		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene9644_All	423	43.91	142.07	68.48	69.13	56.90	54.35	291.66	505.40	81.56	1.69E+00	2.32E-97	Up	6.41E-01	5.99E-10		-2.81E-01	3.69E-03		-3.47E-01	4.40E-04		7.93E-01	3.82E-127		-1.84E+00	1.09E-282	Down	Unigene9644_All//gi|166865124|gb|AB201817.1|//3.00E-31//cinnamyl alcohol dehydrogenase [Gossypium hirsutum]	Unigene9644_All//2.00E-26//AT4G34230| ATCAD5 (CINNAMYL ALCOHOL DEHYDROGENASE 5); cinnamyl-alcohol dehydrogenase	Unigene9644_All//0.00E+00//gi|72273223|gb|DT049046.1|DT049046		ko00940|Phenylpropanoid biosynthesis	GO:0009699//GO:0016616//GO:0046914	nr -
Unigene9647_All	356	0.00	0.00	0.00	0.00	0.00	0.00	3.44	0.82	0.34	null	null		null	null		null	null		null	null		-2.07E+00	6.67E-04	Down	-3.36E+00	2.67E-06	Down	Unigene9647_All//gi|224112361|ref|XP_002316163.1|//1.00E-10//NAC domain protein, IPR003441 [Populus trichocarpa] >gi|222862503|gb|EEF02334.1| NAC domain protein, IPR003441 [Populus trichocarpa]						nr -
Unigene9650_All	219	1.19	6.48	0.00	0.00	0.63	1.24	4.05	11.45	16.37	2.44E+00	2.47E-04	Up	-1.02E+01	8.49E-02		9.30E+00	3.14E-01		1.03E+01	7.00E-02		1.50E+00	6.53E-05	Up	2.01E+00	6.20E-10	Up			Unigene9650_All//1.00E-117//TC167082				
Unigene96526_All	293	3.04	0.86	0.36	0.34	1.88	6.47	0.43	1.43	0.00	-1.81E+00	2.38E-02		-3.06E+00	2.25E-03		2.47E+00	4.04E-02		4.25E+00	5.03E-09	Up	1.72E+00	1.35E-01		-8.76E+00	1.97E-01		Unigene96526_All//gi|3334147|sp|Q39799.1|CHI1_GOSHI//3.00E-30//RecName: Full=Endochitinase 1; Flags: Precursor >gi|1469788|gb|AAB67842.1| class I chitinase [Gossypium hirsutum] >gi|298106229|gb|AD156257.1| class I chitinase [Gossypium hirsutum]	Unigene96526_All//2.00E-09//AT3G12500| ATHCHIB (ARABIDOPSIS THALIANA BASIC CHITINASE); chitinase	Unigene96526_All//9.00E-82//gi|31406794|gb|CD485829.1|CD485829		ko00520|Amino sugar and nucleotide sugar metabolism	GO:0004553//GO:0006026//GO:0009861//GO:0010038//GO:0016020//GO:0030247//GO:0043231	nr +
Unigene96547_All	454	1.04	4.02	1.64	1.65	1.59	1.19	1.49	0.74	0.61	1.95E+00	2.77E-04	Up	6.63E-01	4.19E-01		-4.72E-02	9.43E-01		-4.63E-01	6.06E-01		-1.02E+00	2.04E-01		-1.28E+00	9.48E-02				Unigene96547_All//9.00E-09//TC179116				
Unigene9655_All	459	0.00	1.10	0.93	0.43	0.60	0.79	1.11	1.37	6.77	1.01E+01	3.99E-03		9.86E+00	1.35E-02		4.67E-01	8.16E-01		8.59E-01	5.41E-01		3.05E-01	7.04E-01		2.61E+00	1.31E-11	Up							
Unigene96558_All	537	1.36	0.19	0.79	2.04	2.31	0.34	0.71	0.54	0.82	-2.85E+00	6.26E-03		-7.82E-01	3.80E-01		1.78E-01	8.19E-01		-2.60E+00	7.13E-04	Down	-3.79E-01	7.23E-01		2.04E-01	8.26E-01		Unigene96558_All//gi|224096788|ref|XP_002314669.1|//3.00E-32//nbs-lrr resistance protein [Populus trichocarpa] >gi|222874080|gb|EEF11211.1| nbs-lrr resistance protein [Populus trichocarpa]	Unigene96558_All//4.00E-09//AT3G14460| disease resistance protein (NBS-LRR class), putative	Unigene96558_All//9.00E-111//ES837684			GO:0000166	nr +
Unigene96572_All	709	0.00	0.00	0.00	0.00	0.00	0.00	0.36	0.06	2.53	null	null		null	null		null	null		null	null		-2.60E+00	1.44E-01		2.82E+00	1.60E-07	Up	Unigene96572_All//gi|297821122|ref|XP_002878444.1|//1.00E-106//zinc finger family protein [Arabidopsis lyrata subsp. lyrata] >gi|297324282|gb|EFH54703.1| zinc finger family protein [Arabidopsis lyrata subsp. lyrata]	Unigene96572_All//1.00E-106//AT3G62240| zinc finger (C2H2 type) family protein	Unigene96572_All//5.00E-82//gi|78345390|gb|DT565664.1|DT565664	C2H2		GO:0044464//GO:0046914	nr -
Unigene96586_All	320	8.01	28.03	2.66	1.25	2.69	1.55	0.26	0.39	0.50	1.81E+00	1.90E-16	Up	-1.59E+00	2.80E-04	Down	1.11E+00	1.63E-01		3.18E-01	7.57E-01		5.68E-01	7.79E-01		9.14E-01	6.22E-01		Unigene96586_All//gi|116831754|gb|ABK28851.1|//1.00E-48//alpha-tubulin [Medicago truncatula] >gi|124361008|gb|ABN08980.1| Tubulin/FtsZ, C-terminal [Medicago truncatula]	Unigene96586_All//2.00E-49//AT5G19780| TUA5; structural constituent of cytoskeleton	Unigene96586_All//1.00E-65//gi|109827845|gb|DW226505.1|DW226505		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene966_All	2468	55.80	58.92	62.89	56.05	69.16	54.77	28.92	20.56	12.27	7.86E-02	9.53E-02		1.73E-01	5.92E-05		3.03E-01	1.37E-17		-3.33E-02	5.70E-01		-4.92E-01	7.32E-19		-1.24E+00	2.04E-91	Down	Unigene966_All//gi|87162706|gb|ABD28501.1|//1.00E-134//Zinc finger, C2H2-type [Medicago truncatula]	Unigene966_All//1.00E-89//AT1G55110| At1D07 (Arabidopsis thaliana Indeterminate(ID)-Domain 7); nucleic acid binding / transcription factor/ zinc ion binding	Unigene966_All//0.00E+00//TC142124	C2H2			nr +
Unigene9660_All	948	0.00	0.00	0.00	0.00	0.11	0.10	0.36	0.93	9.96	null	null		null	null		6.77E+00	4.48E-01		6.57E+00	4.67E-01		1.38E+00	4.62E-02		4.80E+00	8.57E-56	Up	Unigene9660_All//gi|2502085|gb|AAC12797.1|//6.00E-15//adenosine triphosphatase [Vigna radiata]	Unigene9660_All//1.00E-12//AT4G34720| AVA-P1; ATPase/ proton-transporting ATPase, rotational mechanism	Unigene9660_All//2.00E-20//TC179451		ko00190|Oxidative phosphorylation//ko04145|Phagosome	GO:0006754//GO:0006818//GO:0015077//GO:0016887//GO:0031224//GO:0033176//GO:0043231	nr -
Unigene96604_All	384	1.36	6.07	1.11	0.52	0.36	1.41	0.22	0.00	0.00	2.16E+00	7.36E-06	Up	-2.97E-01	7.49E-01		-5.33E-01	7.46E-01		1.44E+00	1.92E-01		-7.78E+00	3.94E-01		-7.78E+00	3.51E-01		Unigene96604_All//gi|226529630|ref|NP_001152607.1|//1.00E-25//growth-regulating factor [Zea mays] >gi|195658087|gb|ACG48511.1| growth-regulating factor [Zea mays]	Unigene96604_All//4.00E-21//AT2G22840| AtGRF1 (GROWTH-REGULATING FACTOR 1); transcription activator	Unigene96604_All//2.00E-141//TC136021	GRF			nr -
Unigene9661_All	345	1.82	0.15	0.62	2.89	0.40	0.13	1.72	0.24	0.12	-3.63E+00	5.06E-03		-1.56E+00	1.29E-01		-2.85E+00	2.37E-04	Down	-4.46E+00	3.09E-05	Down	-2.82E+00	7.17E-03		-3.89E+00	1.09E-03								
Unigene9662_All	230	2.05	0.00	0.00	6.50	1.05	2.16	0.00	0.36	0.00	-1.10E+01	5.53E-03		-1.10E+01	8.60E-03		-2.63E+00	8.65E-06	Down	-1.59E+00	4.93E-03		8.51E+00	3.95E-01		null	null		Unigene9662_All//gi|18405469|ref|NP_566822.1|//2.00E-10//transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana]	Unigene9662_All//7.00E-12//AT3G27640| transducin family protein / WD-40 repeat family protein	Unigene9662_All//3.00E-127//TC168028			GO:0009987	nr -
Unigene96625_All	612	0.85	0.17	0.00	1.14	1.80	0.96	0.21	0.27	1.63	-2.37E+00	4.75E-02		-9.74E+00	4.73E-03		6.60E-01	3.38E-01		-2.48E-01	7.56E-01		3.98E-01	8.12E-01		2.97E+00	1.11E-04	Up	Unigene96625_All//gi|297719995|ref|NP_001172359.1|//7.00E-40//Os01g0388566 (Oryza sativa Japonica Group) >gi|255673262|dbj|BAH91089.1| Os01g0388566 (Oryza sativa Japonica Group)	Unigene96625_All//2.00E-63//AT2G48060| unknown protein				GO:0044464	nr +
Unigene9664_All	896	0.35	0.11	0.06	0.56	1.23	0.30	4.48	2.10	3.56	-1.63E+00	2.76E-01		-2.56E+00	1.59E-01		1.15E+00	8.79E-02		-8.79E-01	4.19E-01		-1.09E+00	7.04E-05	Down	-3.34E-01	2.23E-01		Unigene9664_All//gi|224092698|ref|XP_002309702.1|//2.00E-25//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222855678|gb|EEE93225.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene9664_All//2.00E-06//AT3G14470| disease resistance protein (NBS-LRR class), putative	Unigene9664_All//0.00E+00//TC179054				nr +
Unigene96649_All	274	0.38	0.00	0.19	0.18	0.25	0.00	0.15	1.98	2.91	-8.58E+00	3.61E-01		-9.75E-01	7.17E-01		4.68E-01	9.50E-01		-7.51E+00	6.09E-01		3.68E+00	3.69E-03		4.24E+00	7.42E-05	Up			Unigene96649_All//2.00E-107//gi|7386357|gb|DT466310.1|DT466310				
Unigene96655_All	303	0.35	1.34	1.58	2.30	2.39	2.09	5.86	4.28	0.39	1.95E+00	1.44E-01		2.20E+00	9.12E-02		5.23E-02	9.64E-01		-1.41E-01	8.66E-01		-4.55E-01	3.24E-01		-3.89E+00	7.68E-10	Down			Unigene96655_All//3.00E-72//gi|21100631|gb|BQ412944.1|BQ412944				
Unigene96662_All	920	0.23	2.97	1.50	0.22	5.32	3.39	0.64	2.04	3.68	3.71E+00	3.29E-11	Up	2.73E+00	1.78E-04	Up	4.62E+00	1.36E-25	Up	3.97E+00	5.11E-14	Up	1.67E+00	2.19E-04	Up	2.52E+00	4.31E-12	Up			Unigene96662_All//3.00E-13//CO115390				
Unigene9668_All	511	0.00	5.06	1.67	0.00	0.00	0.00	0.00	0.00	0.00	1.23E+01	1.05E-14	Up	1.07E+01	8.95E-05	Up	null	null		null	null		null	null		null	null		Unigene9668_All//gi|110740557|dbj|BAE98384.1|//1.00E-54//lactate dehydrogenase [Arabidopsis thaliana]	Unigene9668_All//7.00E-56//AT4G17260| L-lactate dehydrogenase, putative			ko00010|Glycolysis / Gluconeogenesis//ko00270|Cysteine and methionine metabolism//ko00620|Pyruvate metabolism//ko00640|Propanoate metabolism	GO:0004457//GO:0006007//GO:0006970//GO:0009725//GO:0010468//GO:0016020//GO:0043231	nr +
Unigene96698_All	350	0.00	1.88	0.30	0.00	0.98	0.65	0.60	0.36	0.11	1.09E+01	6.20E-04	Up	8.25E+00	3.85E-01		9.94E+00	3.00E-02		9.33E+00	1.18E-01		-7.54E-01	6.30E-01		-2.41E+00	1.94E-01				Unigene96698_All//8.00E-64//TC132113				
Unigene96710_All	350	0.30	0.00	0.00	1.00	0.20	0.39	1.81	0.00	0.23	-8.22E+00	3.61E-01		-8.22E+00	3.83E-01		-2.34E+00	1.00E-01		-1.36E+00	3.37E-01		-1.08E+01	1.23E-04	Down	-2.99E+00	2.58E-03		Unigene96710_All//gi|119507459|dbj|BAF42037.1|//4.00E-13//cellulase2 [Pyrus communis]	Unigene96710_All//6.00E-14//AT1G19940| AtGH9B5 (Arabidopsis thaliana Glycosyl Hydrolase 9B5); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene96710_All//7.00E-126//DW232861		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0016020//GO:0031410//GO:0044238	nr +
Unigene9672_All	339	0.00	2.54	2.20	0.29	0.41	0.00	0.00	0.00	0.00	1.13E+01	4.91E-05	Up	1.11E+01	3.24E-04	Up	4.67E-01	8.73E-01		-8.20E+00	3.87E-01		null	null		null	null		Unigene9672_All//gi|226493009|ref|NP_001149134.1|//2.00E-34//nucleotide-binding protein-like [Zea mays] >gi|195606396|gb|ACG25028.1| nucleotide-binding protein-like [Zea mays]	Unigene9672_All//7.00E-34//AT4G19540| INDL (INDI(IRON-SULFUR PROTEIN REQUIRED FOR NADH DEHYDROGENASE)-LIKE)				GO:0000166//GO:0003824//GO:0006281//GO:0043231	nr +
Unigene9673_All	254	0.00	2.39	3.98	0.00	0.00	0.00	0.00	0.00	0.00	1.12E+01	1.16E-03		1.20E+01	1.27E-05	Up	null	null		null	null		null	null		null	null									
Unigene9674_All	318	0.00	0.00	0.00	0.31	0.22	0.57	0.00	1.58	2.63	null	null		null	null		-5.33E-01	8.10E-01		8.59E-01	6.93E-01		1.06E+01	1.02E-03		1.14E+01	3.88E-06	Up							
Unigene96742_All	398	11.31	293.58	88.97	31.17	82.37	137.42	0.00	0.32	0.10	4.70E+00	0.00E+00	Up	2.98E+00	5.37E-112	Up	1.40E+00	1.13E-47	Up	2.14E+00	4.17E-130	Up	8.30E+00	2.39E-01		6.65E+00	6.28E-01		Unigene96742_All//gi|157688320|gb|ABV64742.1|//2.00E-21//glycine-rich protein 1 [Boea hygrometrica]		Unigene96742_All//3.00E-48//DW508073		ko03040|Spliceosome	GO:0003676//GO:0031410	nr +
Unigene96753_All	269	0.19	0.00	0.00	0.00	2.30	0.00	0.16	0.00	0.00	-7.60E+00	5.92E-01		-7.60E+00	6.07E-01		1.12E+01	7.90E-04	Up	null	null		-7.30E+00	6.32E-01		-7.30E+00	5.92E-01				Unigene96753_All//5.00E-40//TC160152				
Unigene96757_All	371	1.13	0.00	0.57	1.48	5.11	1.46	1.37	0.00	0.64	-1.01E+01	1.04E-02		-9.75E-01	4.11E-01		1.79E+00	2.95E-04	Up	-1.59E-02	9.75E-01		-1.04E+01	8.88E-04	Down	-1.09E+00	2.28E-01		Unigene96757_All//gi|6714288|gb|AAF23984.1|AC013354_3//3.00E-06//F15H18.12 [Arabidopsis thaliana]	Unigene96757_All//1.00E-07//AT1G18370| HIK (HINKEL); ATP binding / microtubule motor					nr +
Unigene96759_All	443	0.00	4.12	0.36	0.22	0.54	0.92	0.57	0.28	6.39	1.20E+01	2.14E-10	Up	8.49E+00	2.33E-01		1.27E+00	5.30E-01		2.03E+00	1.49E-01		-1.02E+00	4.94E-01		3.48E+00	8.74E-14	Up	Unigene96759_All//gi|297822725|ref|XP_002873245.1|//1.00E-13//MAPKKK14 [Arabidopsis lyrata subsp. lyrata] >gi|297325084|gb|EFH55504.1| MAPKKK14 [Arabidopsis lyrata subsp. lyrata]	Unigene96759_All//6.00E-15//AT2G30040| MAPKKK14; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene96759_All//1.00E-97//gi|78323361|gb|DT543835.1|DT543835			GO:0016301	nr -
Unigene96804_All	866	0.00	0.00	0.00	0.00	9.58	0.00	0.10	0.05	0.09	null	null		null	null		1.32E+01	1.39E-53	Up	null	null		-1.01E+00	7.18E-01		-8.52E-02	9.66E-01				Unigene96804_All//6.00E-33//BQ403264				

Unigene9681_All	288	0.00	6.16	1.48	0.00	0.00	0.00	0.00	0.00	0.00	1.26E+01	4.13E-10	Up	1.05E+01	1.35E-02		null	null		null	null		null	null		null	null		Unigene9681_All//gi|17017263|gb|AAL33589.1|//1.00E-12//methionine synthase [Zea mays]	Unigene9681_All//3.00E-13//AT5G17920| ATMS1; 5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase/ copper ion binding / methionine synthase			ko00270|Cysteine and methionine metabolism	GO:0016740	nr -
Unigene96825_All	607	0.26	0.83	0.35	2.46	11.57	5.51	0.00	0.00	0.00	1.69E+00	1.34E-01		4.40E-01	7.74E-01		2.23E+00	2.74E-19	Up	1.16E+00	6.88E-04	Up	null	null		null	null					Unigene96825_All//0.00E+00//TC171748				
Unigene9684_All	1143	0.00	13.17	4.19	0.00	0.00	0.00	0.00	0.00	0.00	1.37E+01	1.92E-86	Up	1.20E+01	1.22E-26	Up	null	null		null	null		null	null		null	null									
Unigene96851_All	873	0.00	0.29	0.00	0.51	0.63	0.10	0.97	1.05	0.14	8.18E+00	7.73E-02		null	null		2.98E-01	8.18E-01		-2.31E+00	7.79E-02		1.21E-01	8.54E-01		-2.82E+00	5.38E-04	Down	Unigene96851_All//gi|224110992|ref|XP_002332999.1|//3.00E-19//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222834484|gb|EEE72961.1| cc-nbs-lrr resistance protein [Populus trichocarpa]	Unigene96851_All//3.00E-05//AT4G26090| RPS2 (RESISTANT TO P. SYRINGAE 2); protein binding	Unigene96851_All//9.00E-32//gi|3326806|gb|AI055692.1|AI055692		ko04626|Plant-pathogen interaction		nr -
Unigene9686_All	276	0.00	2.94	3.67	0.00	0.00	0.65	0.00	0.00	0.00	1.15E+01	9.30E-05	Up	1.18E+01	1.27E-05	Up	null	null		9.35E+00	1.93E-01		null	null		null	null		Unigene9686_All//sp|P29797|GNAS_PIG//1.00E-42//Guanine nucleotide-binding protein G(s) subunit alpha OS=Sus scrofa GN=GNAS PE=2 SV=1							swissprot -
Unigene96871_All	508	0.00	0.00	0.00	2.75	1.63	0.36	0.00	0.00	0.00	null	null		null	null		-7.55E-01	1.67E-01		-2.95E+00	2.40E-05	Down	null	null		null	null		Unigene96871_All//gi|224106804|ref|XP_002314291.1|//4.00E-15//predicted protein [Populus trichocarpa] >gi|222850699|gb|EEE88246.1| predicted protein [Populus trichocarpa]		Unigene96871_All//0.00E+00//TC137565				nr +
Unigene9690_All	430	0.97	0.94	4.09	0.93	3.68	2.84	0.98	0.97	1.20	-4.62E-02	9.80E-01		2.07E+00	3.29E-04	Up	1.99E+00	4.24E-04	Up	1.61E+00	1.36E-02		-1.67E-02	1.02E+00		2.93E-01	7.27E-01		Unigene9690_All//gi|297827927|ref|XP_002881846.1|//3.00E-24//lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327685|gb|EFH58105.1| lipase class 3 family protein [Arabidopsis lyrata subsp. lyrata]	Unigene9690_All//1.00E-24//AT2G42450| lipase class 3 family protein	Unigene9690_All//3.00E-30//gi|73865235|gb|DT467973.1|DT467973			GO:0004091//GO:0043231//GO:0044238	nr -
Unigene96921_All	341	0.46	0.15	0.16	14.61	10.91	12.58	2.73	0.12	0.82	-1.63E+00	4.86E-01		-1.56E+00	5.31E-01		-4.22E-01	1.16E-01		-2.15E-01	4.76E-01		-4.48E+00	1.30E-05	Down	-1.74E+00	8.54E-03		Unigene96921_All//gi|18401821|ref|NP_566604.1|//2.00E-18//reticulon family protein (RTNLB9) [Arabidopsis thaliana] >gi|75273624|sp|Q9LJQ5.1|RTNL1_ARATH RecName: Full=Reticulon-like protein B9; Short=AtRTNLB9 >gi|9279659|dbj|BAB01175.1| seed maturation protein-like [Arabidopsis thaliana] >gi|89111912|gb|ABD60728.1| At3g18260 [Arabidopsis thaliana]	Unigene96921_All//9.00E-20//AT3G18260| reticulon family protein (RTNLB9)				GO:0043231	nr +
Unigene96923_All	377	2.78	0.27	0.57	1.32	2.28	1.68	0.00	0.33	0.00	-3.37E+00	2.13E-04	Down	-2.30E+00	4.70E-03		7.89E-01	3.21E-01		3.44E-01	6.99E-01		8.38E+00	2.39E-01		null	null		Unigene96923_All//gi|242057051|ref|XP_002457671.1|//3.00E-07//hypothetical protein SORBIDRAFT_03g011415 [Sorghum bicolor] >gi|241929646|gb|EES02791.1| hypothetical protein SORBIDRAFT_03g011415 [Sorghum bicolor]						nr -
Unigene96933_All	399	0.00	0.00	0.53	0.37	0.35	0.34	0.11	1.68	0.60	null	null		9.06E+00	1.37E-01		-1.18E-01	9.08E-01		-1.41E-01	9.41E-01		3.98E+00	6.38E-04	Up	2.50E+00	1.59E-01		Unigene96933_All//gi|297812189|ref|XP_002873978.1|//1.00E-15//agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata] >gi|297319815|gb|EFH50237.1| agenet domain-containing protein [Arabidopsis lyrata subsp. lyrata]	Unigene96933_All//9.00E-16//AT5G20030| agenet domain-containing protein				GO:0003676	nr -
Unigene96935_All	364	0.00	0.00	0.29	0.00	1.70	0.99	0.93	0.23	0.88	null	null		8.19E+00	3.85E-01		1.07E+01	7.90E-04	Up	9.96E+00	2.37E-02		-2.02E+00	1.36E-01		-8.57E-02	9.47E-01					Unigene96935_All//3.00E-11//DN817104				
Unigene9696_All	528	0.20	0.19	0.00	0.28	0.85	0.17	6.97	0.79	1.06	-4.66E-02	9.83E-01		-7.63E+00	3.83E-01		1.58E+00	2.17E-01		-7.26E-01	7.12E-01		-3.14E+00	5.88E-16	Down	-2.72E+00	2.04E-14	Down	Unigene9696_All//gi|9454546|gb|AAF87869.1|AC012561_2//9.00E-13//Unknown protein [Arabidopsis thaliana]	Unigene9696_All//5.00E-14//AT1G50660| unknown protein	Unigene9696_All//1.00E-165//TC168523			GO:0016020//GO:0043231//GO:0044444	nr -
Unigene96965_All	399	2.62	1.90	2.80	3.75	4.40	0.68	0.00	0.00	0.00	-4.61E-01	4.86E-01		9.58E-02	8.80E-01		2.33E-01	6.80E-01		-2.46E+00	8.24E-05	Down	null	null		null	null									
Unigene97004_All	424	0.00	0.00	1.76	2.23	2.76	2.02	0.50	0.39	0.28	null	null		1.08E+01	3.24E-04	Up	3.07E-01	6.58E-01		-1.41E-01	8.42E-01		-3.39E-01	8.11E-01		-8.23E-01	5.98E-01		Unigene97004_All//gi|15223333|ref|NP_174567.1|//6.00E-35//transferase family protein [Arabidopsis thaliana] >gi|6910569|gb|AAF31274.1|AC006424_3 Highly similar to YUP8H12R.39 [Arabidopsis thaliana]	Unigene97004_All//4.00E-36//AT1G32910| transferase family protein	Unigene97004_All//0.00E+00//DW488553		ko00940|Phenylpropanoid biosynthesis//ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis		nr -
Unigene9702_All	302	2.43	2.68	0.35	2.14	4.79	9.12	0.00	0.00	0.53	1.46E-01	8.39E-01		-2.78E+00	1.04E-02		1.16E+00	3.96E-02		2.09E+00	8.34E-07	Up	null	null		9.04E+00	1.39E-01					Unigene9702_All//6.00E-160//TC177041				
Unigene97032_All	884	0.89	0.11	0.06	2.59	2.92	0.82	2.25	0.71	0.50	-2.95E+00	3.66E-03		-3.88E+00	1.59E-03		1.73E-01	7.18E-01		-1.67E+00	1.58E-04	Down	-1.66E+00	1.36E-04	Down	-2.18E+00	1.75E-06	Down	Unigene97032_All//gi|124359162|gb|ABN05685.1|//4.00E-69//RNA-directed DNA polymerase (Reverse transcriptase) [Medicago truncatula]	Unigene97032_All//3.00E-11//ATMG01250| hypothetical protein	Unigene97032_All//3.00E-22//DR454105				nr +
Unigene97037_All	441	0.71	0.00	0.97	0.00	1.56	0.51	0.00	0.00	0.18	-9.48E+00	3.62E-02		4.41E-01	6.76E-01		1.06E+01	3.05E-04	Up	9.00E+00	1.18E-01		null	null		7.50E+00	3.98E-01		Unigene97037_All//gi|31088362|gb|AAP44103.1|//5.00E-43//peptide transporter 2 [Vicia faba]	Unigene97037_All//1.00E-33//AT5G46050| PTR3 (PEPTIDE TRANSPORTER 3); dipeptide transporter/ transporter/ tripeptide transporter	Unigene97037_All//2.00E-145//DN781358				nr +
Unigene9704_All	248	0.21	3.68	1.29	0.20	0.42	0.18	0.00	0.00	0.00	4.12E+00	2.33E-04	Up	2.61E+00	1.45E-01		1.05E+00	8.03E-01		-1.42E-01	9.43E-01		null	null		null	null		Unigene9704_All//COG1472//4.00E-08//Beta-glucosidase-related glycosidases						cog +
Unigene97048_All	464	0.00	0.44	0.00	0.00	2.00	0.00	0.00	0.00	0.00	8.77E+00	1.34E-01		null	null		1.10E+01	1.03E-05	Up	null	null		null	null		null	null		Unigene97048_All//gi|122232770|sp|Q2QZL4.2|U2A2B_ORYSJ//2.00E-20//RecName: Full=Splicing factor U2af large subunit B; AltName: Full=U2 small nuclear ribonucleoprotein auxiliary factor large subunit B; Short=U2 snRNP auxiliary factor large subunit B; AltName: Full=U2 auxiliary factor 65 kDa subunit B				ko03040|Spliceosome		nr -
Unigene97065_All	865	0.00	0.12	0.25	0.29	0.92	0.26	1.71	0.43	0.64	6.87E+00	3.76E-01		7.94E+00	1.37E-01		1.67E+00	5.20E-02		-1.41E-01	9.28E-01		-1.98E+00	2.39E-04	Down	-1.41E+00	3.79E-03		Unigene97065_All//gi|10998136|dbj|BAB03107.1|//1.00E-100//pre-rRNA processing protein ESP5 [Arabidopsis thaliana]	Unigene97065_All//5.00E-95//AT3G11964| RNA binding					nr -
Unigene97070_All	515	0.91	1.28	0.00	1.55	1.54	0.44	1.64	0.16	0.23	4.84E-01	5.90E-01		-9.84E+00	8.60E-03		-9.10E-03	9.67E-01		-1.82E+00	3.32E-02		-3.34E+00	2.51E-04	Down	-2.82E+00	5.38E-04	Down				Unigene97070_All//2.00E-10//ES843781				
Unigene97073_All	495	1.59	4.61	0.97	1.21	1.74	2.83	0.17	0.08	0.40	1.54E+00	6.01E-04	Up	-7.12E-01	3.88E-01		5.26E-01	5.45E-01		1.23E+00	3.60E-02		-1.02E+00	7.18E-01		1.24E+00	4.68E-01		Unigene97073_All//gi|56550679|gb|AAV97793.1|//6.00E-37//At5g10750 [Arabidopsis thaliana] >gi|57222152|gb|AAK38983.1| At5g10750 [Arabidopsis thaliana]	Unigene97073_All//2.00E-31//AT5G10750| unknown protein	Unigene97073_All//2.00E-124//CO104811				nr +
Unigene97074_All	509	0.31	0.40	0.21	0.00	1.22	0.18	0.00	0.00	0.16	3.69E-01	8.15E-01		-5.60E-01	7.73E-01		1.03E+01	7.90E-04	Up	7.47E+00	4.67E-01		null	null		7.29E+00	3.98E-01		Unigene97074_All//gi|224060417|ref|XP_002300189.1|//6.00E-61//white-brown-complex ABC transporter family [Populus trichocarpa] >gi|222847447|gb|EEE84994.1| white-brown-complex ABC transporter family [Populus trichocarpa]	Unigene97074_All//2.00E-46//AT1G17840| WBC11 (WHITE-BROWN COMPLEX HOMOLOG PROTEIN 11); ATPase, coupled to transmembrane movement of substances / fatty acid transporter	Unigene97074_All//3.00E-107//TC159011		ko03040|Spliceosome//ko02010|ABC transporters		nr -
Unigene97075_All	502	0.21	1.41	1.27	0.50	4.18	1.98	0.25	0.83	0.63	2.76E+00	9.13E-03		2.61E+00	2.32E-02		3.08E+00	3.13E-08	Up	2.00E+00	9.93E-03		1.72E+00	1.35E-01		1.33E+00	2.93E-01									
Unigene97077_All	519	4.54	0.00	3.08	2.02	3.32	1.13	1.55	1.05	1.07	-1.21E+01	1.33E-13	Down	-5.60E-01	2.06E-01		7.19E-01	1.62E-01		-8.33E-01	2.30E-01		-5.64E-01	4.30E-01		-5.26E-01	4.34E-01		Unigene97077_All//gi|15242850|ref|NP_200579.1|//4.00E-30//heat shock protein-related [Arabidopsis thaliana] >gi|9759268|dbj|BAB09589.1| 101 kDa heat shock protein; HSP101-like protein [Arabidopsis thaliana]	Unigene97077_All//8.00E-31//AT5G57710| heat shock protein-related	Unigene97077_All//0.00E+00//TC158972				nr +
Unigene97089_All	560	1.49	0.18	0.10	1.07	1.78	0.56	0.23	0.30	0.21	-3.05E+00	2.11E-03		-3.97E+00	9.07E-04	Down	7.40E-01	3.10E-01		-9.19E-01	3.51E-01		3.98E-01	8.12E-01		-8.60E-02	9.67E-01									
Unigene97097_All	661	2.77	3.30	1.21	3.39	2.24	5.06	3.71	2.91	1.39	2.51E-01	5.89E-01		-1.20E+00	1.99E-02		-5.98E-01	1.55E-01		5.76E-01	9.93E-02		-3.51E-01	3.73E-01		-1.42E+00	1.03E-04	Down	Unigene97097_All//gi|17933303|gb|AAL48234.1|AF446361_1//3.00E-36//At1g12650/T12C24_1 [Arabidopsis thaliana] >gi|20856106|gb|AAM26648.1| At1g12650/T12C24_1 [Arabidopsis thaliana]	Unigene97097_All//1.00E-30//AT1G12650| unknown protein	Unigene97097_All//0.00E+00//DT464054				nr -
Unigene97109_All	200	0.52	6.08	3.20	6.23	5.17	2.48	1.69	2.72	1.99	3.54E+00	4.02E-05	Up	2.61E+00	2.32E-02		-2.70E-01	6.54E-01		-1.33E+00	3.28E-02		6.84E-01	4.49E-01		2.36E-01	8.04E-01									
Unigene97186_All	201	0.26	6.05	0.00	0.25	1.03	1.35	0.00	0.00	0.00	4.54E+00	6.47E-06	Up	-8.02E+00	6.06E-01		2.05E+00	3.93E-01		2.44E-00	2.21E-01		null	null		null	null					Unigene97186_All//2.00E-07//ES802758				
Unigene97198_All	201	0.00	0.25	0.00	0.00	1.71	0.90	0.21	0.00	4.16	7.98E+00	6.03E-01		null	null		1.07E+01	3.00E-02		9.81E+00	1.92E-01		-7.72E+00	6.32E-01	Up	4.31E+00	4.10E-05	Up				Unigene97198_All//2.00E-07//DT464140				
Unigene972_All	629	3.99	5.40	0.59	7.37	7.72	6.89	2.62	2.33	2.53	4.35E-01	2.07E-01		-2.75E+00	1.14E-07	Down	6.77E-02	8.24E-01		-9.56E-02	7.51E-01		-1.73E-01	7.20E-01		-4.93E-02	9.27E-01		Unigene972_All//gi|297827699|ref|XP_002881732.1|//1.00E-32//bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327571|gb|EFH57991.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene972_All//1.00E-27//AT2G40620| bZIP transcription factor family protein	Unigene972_All//0.00E+00//gi|78354341|gb|DT574615.1|DT574615	bZIP			nr -
Unigene9720_All	229	0.46	1.77	0.93	5.22	1.20	5.92	1.66	0.91	2.78	1.95E+00	1.44E-01		1.03E+00	5.89E-01		-2.12E+00	8.56E-04	Down	1.81E-01	7.57E-01		-8.65E-01	4.41E-01		7.44E-01	3.52E-01									
Unigene9723_All	371	0.28	0.55	0.29	1.75	0.00	0.49	0.80	0.79	0.75	9.54E-01	6.19E-01		2.53E-02	9.95E-01		-1.08E+01	7.84E-05	Down	-1.84E+00	6.00E-02		-1.66E-02	1.02E+00		-8.57E-02	9.51E-01									
Unigene9248_All	202	3.63	1.00	0.00	3.21	2.22	4.25	0.42	0.83	0.39	-1.85E+00	4.08E-02		-1.18E-01	4.12E-04	Down	-5.33E-01	5.38E-01		4.06E-01	6.40E-01		9.83E-01	6.31E-01		-8.59E-02	9.66E-01									
Unigene9725_All	332	0.00	0.00	0.00	1.50	0.52	2.45	1.66	0.25	0.00	null	null		null	null		-1.53E+00	1.45E-01		7.07E-01	3.93E-01		-2.72E+00	1.22E-02		-1.07E+01	2.80E-04	Down				Unigene9725_All//4.00E-07//ES803021				
Unigene97260_All	202	0.26	1.00	0.00	4.69	17.22	4.92	0.42	0.21	0.20	1.95E+00	3.73E-01		-8.02E+00	6.06E-01		1.88E+00	6.94E-08	Up	7.01E-02	9.38E-01		-1.02E+00	7.18E-01		-1.09E+00	6.71E-01					Unigene97260_All//2.00E-14//TC175880				
Unigene9729_All	220	72.06	20.73	37.03	126.12	122.71	151.91	93.02	43.70	57.58	-1.80E+00	1.57E-28	Down	-9.60E-01	7.72E-11		-3.95E-02	7.85E-01		2.68E-01	4.44E-03		-1.09E+00	1.99E-21	Down	-6.92E-01	1.08E-10		Unigene9729_All//gi|297850244|ref|XP_002893003.1|//7.00E-10//60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata] >gi|297338845|gb|EFH69262.1| 60S ribosomal protein L6 [Arabidopsis lyrata subsp. lyrata]	Unigene9729_All//3.00E-11//AT1G74050| 60S ribosomal protein L6 (RPL6C)	Unigene9729_All//2.00E-60//BG440422		ko03010|Ribosome	GO:0005198//GO:0005488//GO:0009536//GO:0010467//GO:0015934//GO:0016020//GO:0031981	nr +
Unigene9730_All	253	0.00	3.60	2.74	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	2.60E-05	Up	1.14E+01	6.09E-04	Up	null	null		null	null		null	null		null	null		Unigene9730_All//sp|Q9VHS2|COX7A_DROME//4.00E-19//Probable cytochrome c oxidase subunit 7A, mitochondrial OS=Drosophila melanogaster GN=CG9603 PE=1 SV=1							swissprot +

Unigene9734_All	300	112.14	42.56	66.56	0.66	1.61	0.30	0.00	0.14	0.00	-1.40E+00	1.08E-41	Down	-7.53E-01	6.18E-15		1.27E+00	2.92E-01		-1.14E+00	5.66E-01		7.12E+00	6.19E-01		null	null		Unigene9734_All//gi|77540212|gb|AB A86964.1|/9.00E-41//glyceraldehyde-3-phosphate dehydrogenase B subunit [Glycine max]	Unigene9734_All//2.00E-33//AT1G42970| GAPB (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE B SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase (NADP+)/ glyceraldehyde-3-phosphate dehydrogenase	Unigene9734_All//3.00E-155//gi|164312007|gb|EX168406.1|EX168406		ko00710|Carbon fixation in photosynthetic organisms	GO:0000166//GO:0005576//GO:0006950 //GO:0008943//GO:0009314//GO:0009526//GO:0009532//GO:0009534//GO:0010038//GO:0015977//GO:0019318//GO:0034285	nr +
Unigene9736_All	251	0.00	1.01	3.18	0.20	0.00	0.00	0.00	0.00	0.00	9.98E+00	7.73E-02		1.16E+01	1.71E-04	Up	-7.63E+00	5.38E-01		-7.63E+00	6.08E-01		null	null		null	null										ESTscan +
Unigene97371_All	203	133.51	321.74	132.21	14.72	22.56	39.82	0.62	0.00	0.00	1.27E+00	5.44E-69	Up	-1.41E-02	9.18E-01		6.16E-01	2.69E-02		1.44E+00	1.68E-11	Up	-9.29E+00	2.32E-01		-9.29E+00	1.97E-01		Unigene97371_All//gi|25090250|gb|A AN72262.1|/9.00E-29//At1g44575/T18F15 [Arabidopsis thaliana]	Unigene97371_All//5.00E-23//AT1G44575| NPQ4 (NONPHOTOCHEMICAL QUENCHING); chlorophyll binding / xanthophyll binding	Unigene97371_All//3.00E-111//TC131070		ko00195|Photosynthesis		nr +
Unigene9744_All	207	72.54	13.22	21.87	128.51	92.99	120.44	39.83	26.45	16.55	-2.46E+00	4.91E-40	Down	-1.73E+00	1.18E-24	Down	-4.67E-01	1.40E-06		-9.36E-02	4.78E-01		-5.91E-01	1.00E-03		-1.27E+00	9.73E-12	Down	Unigene9744_All//gi|3023847|sp|O24 076.1|GBLP_MEDSA//1.00E-16//RecName: Full=Guanine nucleotide-binding protein subunit beta-like protein >gi|2385376|emb|CAA69934.1| G protein beta subunit-like [Medicago sativa subsp. x varia]	Unigene9744_All//5.00E-16//AT1G48630| RACK1B_AT (RECEPTOR FOR ACTIVATED C KINASE 1 B); nucleotide binding	Unigene9744_All//1.00E-113//gi|78346993|gb|DT567267.1|DT567267			GO:0005840//GO:0009536//GO:0010038 //GO:0019897//GO:0048513	nr +
Unigene9746_All	730	0.65	0.42	0.29	0.89	0.19	1.18	0.46	1.20	3.66	-6.31E-01	5.53E-01		-1.14E+00	3.32E-01		-2.23E+00	1.79E-02		4.06E-01	6.40E-01		1.38E+00	4.62E-02		2.98E+00	1.99E-11	Up	Unigene9746_All//gi|87162659|gb|AB 028454.1|/2.00E-41//Tetratricopeptide-like helical [Medicago truncatula]	Unigene9746_All//1.00E-42//AT1G63330| pentatricopeptide (PPR) repeat-containing protein	Unigene9746_All//8.00E-109//TC171251				nr -
Unigene9747_All	643	0.24	0.71	0.25	0.46	0.16	0.28	0.59	1.37	2.79	1.54E+00	1.96E-01		2.52E-02	1.00E+00		-1.53E+00	2.97E-01		-7.26E-01	6.37E-01		1.21E+00	7.78E-02		2.24E+00	5.44E-06	Up			Unigene9747_All//1.00E-141//C0083727					
Unigene9748_All	514	0.00	0.00	0.00	0.19	0.07	0.18	4.69	3.17	1.24	null	null		null	null		-1.53E+00	5.81E-01		-1.42E-01	9.44E-01		-5.64E-01	1.32E-01		-1.92E+00	1.18E-06	Down			Unigene9748_All//5.00E-26//C0092801					
Unigene975_All	1680	12.36	4.55	6.78	9.70	11.33	8.66	9.79	2.69	7.21	-1.44E+00	3.41E-27	Down	-8.66E-01	7.15E-12		2.25E-01	8.99E-02		-1.64E-01	3.09E-01		-1.87E+00	6.19E-38	Down	-4.42E-01	2.13E-04		Unigene975_All//gi|297827699|ref|X P_002881732.1|/4.00E-95//bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata] >gi|297327571|gb|EFH57991.1| bZIP transcription factor family protein [Arabidopsis lyrata subsp. lyrata]	Unigene975_All//1.00E-87//AT2G40620| bZIP transcription factor family protein	Unigene975_All//0.00E+00//TC152867	bZIP		GO:0003677	nr -
Unigene9752_All	314	0.00	21.30	10.51	0.00	0.00	0.00	0.00	0.00	0.00	1.44E+01	3.29E-38	Up	1.34E+01	2.92E-18	Up	null	null		null	null		null	null		null	null										
Unigene97525_All	205	1.53	0.99	2.08	0.97	2.02	6.17	0.41	0.00	0.78	-6.31E-01	6.21E-01		4.40E-01	6.76E-01		1.05E+00	4.25E-01		2.67E+00	2.42E-04	Up	-8.69E+00	3.93E-01		9.14E-01	6.22E-01				Unigene97525_All//8.00E-29//TC154487					
Unigene97563_All	206	112.52	28.04	44.98	26.84	47.98	18.64	388.94	68.58	145.24	-2.00E+00	7.13E-48	Down	-1.32E+00	1.29E-25	Down	8.38E-01	1.14E-06		-5.26E-01	3.95E-02		-2.50E+00	5.46E-264	Down	-1.42E+00	7.46E-127	Down	Unigene97563_All//gi|224552010|gb| ACN54400.1|/3.00E-32//hybrid proline-rich protein [Gossypium hirsutum]	Unigene97563_All//3.00E-22//AT2G45180| protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	Unigene97563_All//3.00E-108//EX164304			GO:0005488//GO:0006810//GO:0009534	nr -
Unigene9760_All	249	0.00	0.00	0.00	0.00	0.00	0.00	2.72	3.86	0.00	null	null		null	null		null	null		null	null		5.07E-01	4.32E-01		-1.14E+01	3.56E-05	Down	Unigene9760_All//gi|298709870|emb| CBJ26210.1|//1.00E-27//Ribosomal protein S27 [Ectocarpus siliculosus]	Unigene9760_All//4.00E-27//AT3G61110| ARS27A (ARABIDOPSIS RIBOSOMAL PROTEIN S27); structural constituent of ribosome			ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529 //GO:0043169	nr +
Unigene9761_All	800	0.00	6.59	3.00	0.00	0.00	0.00	0.00	0.00	0.00	1.27E+01	4.74E-30	Up	1.15E+01	3.23E-13	Up	null	null		null	null		null	null		null	null		Unigene9761_All//gi|224150153|ref| XP_002336912.1|//2.00E-15//predicted protein [Populus trichocarpa] >gi|222837117|gb|EEE75496.1| predicted protein [Populus trichocarpa]	Unigene9761_All//7.00E-05//AT1G19270| DA1 (DA 1); ubiquitin binding		Orphans			nr +
Unigene9762_All	773	0.00	0.00	0.00	0.00	0.00	0.00	31.29	0.27	2.16	null	null		null	null		null	null		null	null		-6.85E+00	3.00E-162	Down	-3.85E+00	1.57E-125	Down	Unigene9762_All//gi|297814079|ref| XP_002874923.1|//8.00E-78//pectinesterase family protein [Arabidopsis lyrata subsp. lyrata] >gi|297320760|gb|EFH51182.1| pectinesterase family protein [Arabidopsis lyrata subsp. lyrata]	Unigene9762_All//1.00E-77//AT4G02330| ATPMEPCRB; pectinesterase	Unigene9762_All//0.00E+00//DT461937		ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions	GO:0004091//GO:0005618//GO:0030234 //GO:0071555	nr +
Unigene97626_All	207	0.51	0.98	0.00	42.35	21.29	12.87	1.02	0.81	1.73	9.54E-01	6.19E-01		-8.98E+00	3.83E-01		-9.92E-01	4.11E-08		-1.72E+00	2.96E-16	Down	-3.39E-01	8.10E-01		7.62E-01	4.99E-01				Unigene97626_All//2.00E-07//TC159960					
Unigene9763_All	353	0.00	25.84	6.34	0.00	0.00	0.00	0.00	0.00	0.00	1.47E+01	3.22E-52	Up	1.26E+01	2.50E-12	Up	null	null		null	null		null	null		null	null		Unigene9763_All//gi|49524072|emb|C AG47084.1|//5.00E-43//40S ribosomal protein S9 [Catharanthus roseus]	Unigene9763_All//2.00E-32//AT5G15200| 40S ribosomal protein S9 (RPS9B)	Unigene9763_All//7.00E-55//TC143304		ko03010|Ribosome	GO:0003723//GO:0005198//GO:0009536 //GO:0010467//GO:0033279	nr +
Unigene9764_All	368	0.00	0.00	0.00	0.00	0.00	0.00	2.18	2.04	0.00	null	null		null	null		null	null		null	null		-9.46E-02	8.99E-01		-1.11E+01	4.43E-06	Down	Unigene9764_All//gi|298709974|emb| CBJ31696.1|//5.00E-51//Ribosomal protein S23, component of cytosolic 80S ribosome and 40S small subunit [Ectocarpus siliculosus]	Unigene9764_All//5.00E-46//AT5G02960| 40S ribosomal protein S23 (RPS23B)	Unigene9764_All//2.00E-27//ES843014		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0033279	nr -
Unigene97642_All	208	1.01	1.46	0.00	11.74	3.48	1.95	1.63	1.00	0.77	5.39E-01	6.70E-01		-9.97E+00	1.44E-01		-1.76E+00	1.15E-05	Down	-2.59E+00	6.96E-08	Down	-6.95E-01	5.77E-01		-1.09E+00	3.55E-01										
Unigene97681_All	208	154.95	115.47	80.13	203.57	157.94	256.00	402.07	242.74	122.39	-4.24E-01	7.24E-06		-9.51E-01	4.50E-21		-3.66E-01	1.18E-06		3.31E-01	2.80E-06		-7.28E-01	1.99E-43		-1.72E+00	2.67E-174	Down	Unigene97681_All//gi|110083391|db| BAE97400.1|//1.00E-31//heat shock protein 90 [Nicotiana tabacum]	Unigene97681_All//1.00E-30//AT5G56030| HSP81-2 (HEAT SHOCK PROTEIN 81-2); ATP binding	Unigene97681_All//2.00E-109//TC151776		ko04626|Plant-pathogen interaction//ko04141|Protein processing in endoplasmic reticulum	GO:0005515//GO:0032559//GO:0044267 //GO:0044424//GO:0050896	nr +
Unigene97705_All	208	0.00	1.46	0.00	2.87	1.16	0.00	0.41	0.40	0.00	1.05E+01	4.35E-02		null	null		-1.31E+00	1.56E-01		-1.15E+01	7.68E-04	Down	-1.64E-02	1.01E+00		-8.67E+00	3.50E-01				Unigene97705_All//6.00E-14//C0110739					
Unigene9772_All	486	0.00	3.75	2.63	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	2.14E-10	Up	1.14E+01	4.66E-07	Up	null	null		null	null		null	null		null	null										
Unigene97752_All	209	0.25	0.00	4.08	0.72	0.99	0.00	1.82	1.00	1.91	-7.97E+00	5.92E-01		4.03E+00	7.01E-04	Up	4.67E-01	8.24E-01		-9.48E+00	2.28E-01		-8.65E-01	4.41E-01		6.62E-02	9.66E-01										
Unigene97800_All	210	33.88	17.61	23.33	94.17	67.72	89.90	369.05	274.26	76.83	-9.44E-01	2.06E-05		-5.39E-01	1.93E-02		-4.76E-01	3.34E-05		-6.70E-02	6.65E-01		-4.28E-01	5.47E-16		-2.26E+00	2.57E-233	Down	Unigene97800_All//gi|729623|sp|Q03 6B5.1|BIP5_TOBAC//4.00E-33//RecName: Full=Luminal-binding protein 5; Short=BiP 5; AltName: Full=78 kDa glucose-regulated protein homolog 5; Short=GRP-78-5; Flags: Precursor >gi|19813|emb|CAA42660.1| luminal binding protein (BiP) [Nicotiana tabacum]	Unigene97800_All//1.00E-32//AT5G42020| BIP2; ATP binding	Unigene97800_All//6.00E-113//ES837705		ko04141|Protein processing in endoplasmic reticulum//ko03060|Protein export	GO:0008152//GO:0016628//GO:0032559 //GO:0044432//GO:0050896	nr +
Unigene97803_All	210	131.80	59.84	85.20	296.04	329.27	272.92	44.29	23.29	35.85	-1.14E+00	3.36E-25	Down	-6.29E-01	3.10E-09		1.54E-01	1.70E-02		-1.17E-01	1.18E-01		-9.28E-01	5.39E-08		-3.05E-01	7.04E-02		Unigene97803_All//gi|242129046|gb| ACS83602.1|//7.00E-10//ATP synthase beta subunit 1 [Gossypium hirsutum]		Unigene97803_All//1.00E-39//gi|84171228|gb|DR459876.1|DR459876		ko00190|Oxidative phosphorylation	GO:0005753//GO:0015078//GO:0015662 //GO:0015986//GO:0019829//GO:00325 59//GO:0033178	nr +
Unigene97808_All	210	0.75	0.00	0.00	2.37	6.56	9.89	0.60	1.00	0.95	-9.55E+00	2.12E-01		-9.55E+00	2.41E-01		1.47E+00	1.25E-02		2.06E+00	3.39E-05	Up	7.20E-01	6.31E-01		6.51E-01	6.64E-01									
Unigene9781_All	379	0.00	0.00	0.28	0.26	0.64	0.48	0.89	0.33	26.38	null	null		8.13E+00	3.85E-01		1.27E+00	5.30E-01		8.59E-01	6.93E-01		-1.43E+00	2.58E-01		4.89E+00	1.31E-59	Up			Unigene9781_All//5.00E-161//gi|109839354|gb|DW488333.1|DW488333					
Unigene9784_All	366	0.00	1.66	2.91	0.00	1.13	0.25	0.12	0.00	0.00	1.07E+01	1.15E-03		1.15E+01	6.57E-06	Up	1.01E+01	1.25E-02		7.95E+00	4.67E-01		-6.85E+00	6.32E-01		-6.85E+00	5.92E-01				Unigene9784_All//1.00E-173//ES851383					
Unigene9786_All	240	6.32	0.21	3.99	19.93	15.21	12.42	10.75	5.22	10.62	-4.90E+00	1.22E-07	Down	-6.63E-01	2.41E-01		-3.90E-01	1.64E-01		-6.82E-01	1.26E-02		-1.04E+00	3.25E-03		-1.66E-02	9.68E-01		Unigene9786_All//gi|224121322|ref| XP_002330798.1|//1.00E-06//cc-nbs-lrr resistance protein [Populus trichocarpa] >gi|222872600|gb|EEF09731.1| cc-nbs-lrr resistance protein [Populus trichocarpa]		Unigene9786_All//2.00E-88//TC145238			GO:0000166	nr -
Unigene97865_All	211	1.98	8.65	12.37	28.57	15.18	12.41	870.45	437.57	669.52	2.12E+00	1.13E-04	Up	2.64E+00	1.14E-07	Up	-9.12E-01	4.46E-05		-1.20E+00	6.62E-07	Down	-9.92E-01	1.35E-159		-3.79E-01	3.27E-30				Unigene97865_All//3.00E-93//TC144989					
Unigene9787_All	394	0.53	3.34	0.81	0.25	0.61	0.11	0.00	0.00	0.00	2.65E+00	2.16E-04	Up	6.10E-01	6.23E-01		1.27E+00	5.30E-01		-1.14E+00	6.70E-01		null	null		null	null		Unigene9787_All//CGG4456//7.00E-16//Virulence-associated protein and related proteins								cog -
Unigene9789_All	336	0.00	0.00	0.00	0.00	0.21	0.00	0.76	1.99	4.51	null	null		null	null		7.68E+00	5.94E-01		null	null		1.40E+00	8.81E-02		2.58E+00	6.02E-06	Up	Unigene9789_All//gi|224056587|ref| XP_002298924.1|//7.00E-15//predicted protein [Populus trichocarpa] >gi|222846182|gb|EEE83729.1| predicted protein [Populus trichocarpa]		Unigene9789_All//1.00E-10//DN817555				nr -
Unigene979_All	1431	1.06	0.64	0.82	12.81	7.05	6.03	7.33	8.82	3.34	-7.34E-01	1.70E-01		-3.73E-01	5.08E-01		-8.62E-01	5.18E-13		-1.09E+00	6.87E-17	Down	2.68E-01	7.40E-02		-1.13E+00	1.88E-12	Down	Unigene979_All//gi|212717149|gb|AC J37416.1|//1.00E-123//stress-induced receptor-like kinase [Glycine max]	Unigene979_All//3.00E-86//AT4G18250| receptor serine/threonine kinase, putative	Unigene979_All//2.00E-98//C0081306		ko04626|Plant-pathogen interaction		nr -
Unigene9790_All	606	0.00	0.00	0.00	0.00	0.00	0.00	0.56	1.03	2.76	null	null		null	null		null	null		null	null		8.90E-01	2.88E-01		2.31E+00	8.00E-06	Up	Unigene9790_All//gi|15235643|ref|N P_195479.1|//2.00E-92//ACA2 (CALCIUM ATPASE 2); calcium ion transmembrane transporter/ calcium-transporting ATPase/ calmodulin binding [Arabidopsis thaliana] >gi|12229639|sp|081108.1|ACA2_ARAT H RecName: Full=Calcium-transporting ATPase 2, plasma membrane-type; AltName: Full=Ca(2+)-ATPase isoform 2 >gi|3335060|gb|AAC26997.1| plasma membrane-type calcium ATPase [Arabidopsis thaliana] >gi|4468989|emb|CAB38303.1| plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana] >gi|7270746|emb|CAB80429.1| plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana] >gi|17064816|gb|AAL32562.1| plasma membrane-type calcium ATPase (ACA2) [Arabidopsis thaliana] >gi|37201998|gb|AAQ89614.1| Atfg37640 [Arabidopsis thaliana]	Unigene9790_All//3.00E-94//AT4G37640| ACA2 (CALCIUM ATPASE 2); calcium ion transmembrane transporter/ calcium-transporting ATPase/ calmodulin binding	Unigene9790_All//0.00E+00//gi|164311284|gb|EV481921.1|EV481921			GO:0005261//GO:0005515//GO:0009206 //GO:0009528//GO:0009532//GO:00168 36//GO:0019829//GO:0031224//GO:003 2559//GO:0046873//GO:0046914//GO:0 070838	nr -
Unigene9791_All	353	2.52	2.30	1.66	5.36	7.22	5.37	7.19	13.85	24.15	-1.34E-01	8.41E-01		-6.03E-01	4.18E-01		4.29E-01	3.10E-01		3.00E-03	9.99E-01		9.47E-01	1.04E-04		1.75E+00	8.99E-19	Up	Unigene9791_All//gi|14991836|gb|AA K53839.1|AC011806.16//1.00E-20//Putative cullin [Oryza sativa]	Unigene9791_All//6.00E-19//AT4G02570| ATCUL1 (ARABIDOPSIS THALIANA CULLIN 1); protein binding					nr +
Unigene97914_All	212	2.96	0.00	1.76	0.94	1.30	0.64	0.00	0.00	0.00	-1.15E+01	7.89E-04	Down	-7.52E-01	4.11E-01		4.67E-01	8.15E-01		-5.57E-01	7.31E-01		null	null		null	null		Unigene97914_All//gi|224113157|ref |XP_002332644.1|//2.00E-07//predicted protein [Populus trichocarpa] >gi|222832839|gb|EEE71316.1| predicted protein [Populus trichocarpa]		Unigene97914_All//4.00E-43//TC142819			GO:0004672//GO:0006464//GO:0008037 //GO:0030246//GO:0032559	nr -
Unigene9793_All	473	1.11	1.29	0.34	0.11	0.22	0.00	3.31	1.41	0.34	2.17E-01	7.92E-01		-1.71E+00	1.40E-01		1.05E+00	8.02E-01		-6.72E+00	6.08E-01		-1.23E+00	1.07E-02		-3.30E+00	9.79E-08	Down	Unigene9793_All//gi|91208943|ref|Y P_538978.1|//1.00E-80//Ycf2 [Gossypium hirsutum] >gi|91208964|ref|YP_538997.1| Ycf2 [Gossypium hirsutum] >gi|109896299|sp|Q2L949.1|YCF2_GOS HI RecName: Full=Protein ycf2	Unigene9793_All//1.00E-62//AT1G01280| hypothetical protein	Unigene9793_All//0.00E+00//TC129552			GO:0009532//GO:0016462//GO:0032559	nr +
Unigene9794_All	241	0.43	0.84	0.44	0.00	0.57	0.00	0.18	0.00	3.14	9.54E-01	6.19E-01		2.54E-02	9.95E-01		9.16E+00	3.14E-01		null	null		-7.45E+00	6.32E-01		4.16E+00	1.34E-04	Up								

Unigene97944_All	213	3.19	0.71	1.00	4.44	2.10	3.18	2.78	9.03	2.81	-2.16E+00	2.84E-02		-1.68E+00	8.69E-02		-1.08E+00	1.16E-01		-4.82E-01	5.18E-01		1.70E+00	1.45E-04	Up	1.37E-02	9.87E-01		Unigene97944_All//gi|225431804|ref|XP_002272727.1|/5.00E-14//PREDICTED: similar to 60S ribosomal protein L19 [Vitis vinifera]	Unigene97944_All//2.00E-13//AT1G02780| emb2386 (embryo defective 2386); structural constituent of ribosome	Unigene97944_All//4.00E-114//gi|13354937|gb|BG445285.1|BG445285		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529//GO:0043231	nr +
Unigene9795_All	326	6.74	12.28	5.88	6.72	4.33	5.54	29.96	25.13	12.83	8.65E-01	4.68E-03		-1.97E-01	6.46E-01		-6.35E-01	1.35E-01		-2.79E-01	5.68E-01		-2.54E-01	1.48E-01		-1.22E+00	4.69E-13	Down	Unigene9795_All//gi|195606190|gb|AC024925.1|/1.00E-10//26S proteasome non-ATPase regulatory subunit 14 [Zea mays] >gi|195624272|gb|ACG33965.1| 26S proteasome non-ATPase regulatory subunit 14 [Zea mays]	Unigene9795_All//6.00E-12//AT5G23540| 26S proteasome regulatory subunit, putative	Unigene9795_All//5.00E-133//gi|48743160|gb|C0073679.1|C0073679		ko03050|Proteasome		nr +
Unigene9796_All	224	2.10	0.00	0.48	0.44	0.46	0.20	3.02	0.00	0.71	-1.10E+01	5.53E-03		-2.14E+00	1.03E-01		5.22E-02	9.62E-01		-1.14E+00	6.70E-01		-1.16E+01	6.33E-05	Down	-2.09E+00	1.27E-02					Unigene9796_All//3.00E-07//ES847502				
Unigene97968_All	213	0.00	0.00	4.00	1.17	1.94	2.12	0.40	1.37	0.75	null	null		1.20E+01	8.95E-05	Up	7.30E-01	5.86E-01		8.59E-01	4.69E-01		1.79E+00	2.24E-01		9.14E-01	6.22E-01					Unigene97968_All//2.00E-07//EV484038				ESTscan -
Unigene980_All	808	3.43	1.82	2.83	2.96	0.85	3.30	20.93	20.95	4.29	-9.16E-01	1.52E-02		-2.76E-01	4.99E-01		-1.80E+00	1.00E-05	Down	1.56E-01	7.01E-01		1.30E-03	1.01E+00		-2.29E+00	4.14E-52	Down	Unigene980_All//gi|212717149|gb|AC|37416.1|/5.00E-90//stress-induced receptor-like kinase [Glycine max]	Unigene980_All//4.00E-66//AT4G18250| receptor serine/threonine kinase, putative	Unigene980_All//3.00E-179//C0081306		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene9803_All	291	0.00	30.47	17.20	0.00	0.00	0.00	0.00	0.00	0.00	1.49E+01	9.32E-51	Up	1.41E+01	7.65E-28	Up	null	null		null	null		null	null		null	null		Unigene9803_All//sp|P92192|LCF5_DROME//2.00E-06//Larval cuticle protein 5 OS=Drosophila melanogaster GN=Lcp65Ab1 PE=1 SV=1								swissprot -
Unigene98039_All	214	88.75	58.72	67.68	180.40	142.89	208.09	370.45	195.31	165.50	-5.96E-01	2.44E-06		-3.91E-01	3.24E-03		-3.36E-01	2.68E-05		2.06E-01	1.26E-02		-9.24E-01	1.47E-61		-1.16E+00	5.55E-92	Down	Unigene98039_All//gi|211906502|gb|ACJ11744.1|/9.00E-34//Isocitrate dehydrogenase [Gossypium hirsutum]	Unigene98039_All//1.00E-31//AT1G65930| isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative	Unigene98039_All//1.00E-117//EV481956		ko04146|Peroxisome//ko00480|Glutathione metabolism/ko00020|Citrate cycle (TCA cycle)	GO:0000166//GO:0004448//GO:0009060//GO:0009536//GO:0019752//GO:0044262//GO:0046872	nr +
Unigene98055_All	215	36.75	36.53	29.97	84.34	67.91	39.28	23.79	12.44	17.79	-8.60E-03	9.87E-01		-2.94E-01	1.97E-01		-3.13E-01	1.39E-02		-1.10E+00	4.54E-17	Down	-9.36E-01	8.10E-05		-4.20E-01	7.04E-02					Unigene98055_All//4.00E-74//TC162685				
Unigene981_All	966	23.83	3.04	15.43	4.69	1.46	1.12	2.06	3.89	0.54	-2.97E+00	4.45E-75	Down	-6.27E-01	9.61E-08		-1.68E+00	1.65E-09	Down	-2.06E+00	5.97E-11	Down	9.21E-01	1.13E-03		-1.94E+00	1.06E-05	Down	Unigene981_All//gi|212717149|gb|AC|37416.1|/5.00E-75//stress-induced receptor-like kinase [Glycine max]	Unigene981_All//3.00E-56//AT5G39020| protein kinase family protein	Unigene981_All//0.00E+00//C0081306		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0032559	nr +
Unigene98112_All	216	0.00	3.52	0.74	0.23	1.28	0.63	0.00	1.16	2.03	1.18E+01	1.73E-04	Up	9.53E+00	2.32E-01		2.47E+00	2.23E-01		1.44E+00	6.35E-01		1.02E-01	4.30E-02		1.10E+01	2.13E-03					Unigene98112_All//2.00E-07//TC167315				
Unigene98118_All	216	4.36	0.00	1.23	1.61	0.96	1.05	0.20	0.00	0.00	-1.21E+01	1.46E-05	Down	-1.82E+00	2.53E-02		-7.55E-01	5.66E-01		-6.27E-01	6.20E-01		-7.61E+00	6.32E-01		-7.61E+00	5.92E-01					Unigene98118_All//4.00E-92//TC144022				
Unigene9812_All	360	1.31	0.56	0.59	0.14	0.86	2.76	2.23	1.04	1.11	-1.22E+00	2.72E-01		-1.14E+00	3.32E-01		2.64E+00	1.61E-01		4.32E+00	6.32E-05	Up	-1.09E+00	1.29E-01		-1.01E+00	1.35E-01									
Unigene98148_All	217	10.13	5.60	13.50	40.86	34.59	12.07	7.40	3.47	10.83	-8.54E-01	4.74E-02		4.14E-01	2.90E-01		-2.40E-01	2.50E-01		-1.76E+00	5.75E-17	Down	-1.09E+00	1.97E-02		5.49E-01	1.30E-01					Unigene98148_All//6.00E-45//gi|21096183|gb|BQ408496.1|BQ408496				
Unigene9815_All	530	0.00	0.00	0.00	0.00	0.00	0.00	19.62	23.89	5.79	null	null		null	null		null	null		null	null		2.84E-01	5.53E-02		-1.76E+00	3.25E-23	Down	Unigene9815_All//gi|238014838|gb|ACR38454.1|/1.00E-12//unknown [Zea mays]		Unigene9815_All//6.00E-35//TC146753				nr +
Unigene98178_All	218	0.00	1.39	0.00	0.00	4.11	2.07	0.00	0.00	0.00	1.04E+01	4.35E-02		null	null		1.20E+01	1.69E-05	Up	1.10E+01	7.74E-03		null	null		null	null		Unigene98178_All//gi|171452356|dbj|BAG15869.1|/9.00E-18//ankyrin repeat protein [Bruguiera gymnorhiza]	Unigene98178_All//8.00E-19//AT1G14480| protein binding	Unigene98178_All//1.00E-33//TC130834			GO:0010033//GO:0044464	nr +
Unigene982_All	2272	0.81	0.25	2.41	13.62	7.29	7.36	2.75	2.89	1.40	-1.72E+00	9.01E-04	Down	1.58E+00	2.35E-08	Up	-9.01E-01	2.28E-23		-8.89E-01	2.99E-20		6.85E-02	7.65E-01		-9.73E-01	2.85E-06		Unigene982_All//gi|212717149|gb|AC|37416.1|/7.00E-123//stress-induced receptor-like kinase [Glycine max]	Unigene982_All//7.00E-85//AT4G18250| receptor serine/threonine kinase, putative	Unigene982_All//3.00E-98//C0081306		ko04626|Plant-pathogen interaction		nr +
Unigene9821_All	332	0.16	1.07	0.96	0.45	0.00	0.14	6.37	5.16	1.20	2.76E+00	9.57E-02		2.61E+00	1.45E-01		-8.81E+00	1.63E-01		-1.73E+00	4.97E-01		-3.03E-01	4.78E-01		-2.41E+00	1.32E-07	Down	Unigene9821_All//gi|301016726|dbj|BAJ11784.1|/1.00E-15//dehydration responsive protein [Corchorus olitorius]		Unigene9821_All//2.00E-24//TC152783				nr +
Unigene98215_All	220	31.39	21.19	18.15	32.83	26.92	35.93	22.87	13.11	9.96	-5.67E-01	1.10E-02		-7.90E-01	6.63E-04		-2.86E-01	2.13E-01		1.30E-01	6.26E-01		-8.03E-01	7.43E-04		-1.20E+00	5.85E-07	Down	Unigene98215_All//gi|2980774|emb|CAA18201.1|/4.00E-16//leucyl aminopeptidase-like protein [Arabidopsis thaliana] >gi|7269993|emb|CAB79810.1| leucyl aminopeptidase-like protein [Arabidopsis thaliana]	Unigene98215_All//2.00E-17//AT4G30920| cytosol aminopeptidase family protein	Unigene98215_All//3.00E-62//TC143986		ko00480|Glutathione metabolism/ko00330|Arginine and proline metabolism	GO:0008237//GO:0008238//GO:0009536//GO:0010038//GO:0019538//GO:0046914	nr +
Unigene98246_All	221	0.24	8.48	3.37	2.25	4.21	4.70	0.57	3.78	1.26	5.16E+00	2.00E-09	Up	3.83E+00	2.22E-03		9.00E-01	2.35E-01		1.06E+00	1.32E-01		2.72E+00	1.18E-03		1.14E+00	3.99E-01					Unigene98246_All//7.00E-20//TC130861				
Unigene98276_All	222	0.00	0.00	0.00	0.00	3.10	0.00	0.00	0.00	0.00	null	null		null	null		1.16E+01	3.05E-04	Up	null	null		null	null		null	null					Unigene98276_All//1.00E-24//gi|109848281|gb|DW477261.1|DW477261				
Unigene983_All	774	2.91	3.21	3.16	7.72	5.16	5.37	9.94	5.18	1.70	1.42E-01	7.20E-01		1.23E-01	7.63E-01		-5.82E-01	1.15E-02		-5.25E-01	3.16E-02		-9.40E-01	7.02E-07		-2.55E+00	2.42E-27	Down				Unigene983_All//9.00E-78//TC147135				
Unigene9830_All	344	0.76	1.03	0.31	1.74	0.60	0.39	2.70	0.61	0.00	4.39E-01	7.01E-01		-1.30E+00	4.35E-01		-1.53E+00	1.00E-01		-2.14E+00	4.38E-02		-2.15E+00	2.94E-03		-1.14E+01	5.47E-07	Down								
Unigene98308_All	223	0.00	3.64	0.00	0.67	1.24	0.20	0.19	2.81	1.25	1.18E+01	9.30E-05	Up	null	null		8.82E-01	5.94E-01		-1.73E+00	4.97E-01		3.89E+00	1.15E-03		2.72E+00	9.92E-02					Unigene98308_All//3.00E-07//TC135600				
Unigene9833_All	634	0.50	0.00	0.84	0.00	0.22	1.07	1.60	1.19	9.80	-8.95E+00	3.62E-02		7.63E-01	4.52E-01		7.76E+00	3.14E-01		1.01E+01	4.18E-04	Up	-4.32E-01	5.02E-01		2.61E+00	1.74E-22	Up	Unigene9833_All//gi|156105187|gb|AB149132.1|/7.00E-35//ser/thr protein kinase [Malus x domestica]	Unigene9833_All//3.00E-22//AT5G47070| protein kinase, putative	Unigene9833_All//9.00E-99//ES809886			GO:0000166//GO:0004672	nr -
Unigene9837_All	285	0.00	55.29	28.21	0.00	0.00	0.00	0.30	0.00	0.42	1.58E+01	1.53E-90	Up	1.48E+01	5.30E-45	Up	null	null		null	null		-8.21E+00	3.93E-01		4.99E-01	8.04E-01		Unigene9837_All//gi|226500276|ref|NP_001151361.1|/3.00E-32//60S ribosomal protein L37 [Zea mays] >gi|195604274|gb|ACG23967.1| 60S ribosomal protein L37 [Zea mays] >gi|195604540|gb|ACG24100.1| 60S ribosomal protein L37 [Zea mays] >gi|195613318|gb|ACG29489.1| 60S ribosomal protein L37 [Zea mays] >gi|195618018|gb|ACG30839.1| 60S ribosomal protein L37 [Zea mays] >gi|195646138|gb|ACG42537.1| 60S ribosomal protein L37 [Zea mays]	Unigene9837_All//4.00E-33//AT1G52300| 60S ribosomal protein L37 (RPL37B)			ko03010|Ribosome	GO:0000785//GO:0003723//GO:0005198//GO:0005840//GO:0010467//GO:0022613//GO:0034728//GO:0043169//GO:0043231	nr +
Unigene9838_All	315	0.00	1.61	3.38	0.00	0.00	0.00	0.00	0.00	0.00	1.07E+01	3.99E-03		1.17E+01	6.57E-06	Up	null	null		null	null		null	null		null	null										
Unigene9839_All	211	12.40	6.00	3.53	3.78	4.73	6.85	0.00	0.00	0.00	-1.03E+00	7.79E-03		-1.81E+00	4.52E-05	Down	3.25E-01	6.73E-01		8.59E-01	1.33E-01		null	null		null	null					Unigene9839_All//2.00E-106//TC162944				
Unigene984_All	2138	61.08	53.99	44.31	32.04	21.63	23.87	65.97	43.95	12.28	-1.78E-01	9.36E-05		-4.63E-01	6.37E-24		-5.67E-01	8.07E-23		-4.25E-01	3.03E-12		-5.86E-01	9.72E-50		-2.43E+00	0.00E+00	Down	Unigene984_All//gi|189163920|gb|ACD77110.1|/0.00E+00//protein kinase 1b [Solanum lycopersicum]	Unigene984_All//2.00E-164//AT2G28930| APK1B; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase	Unigene984_All//0.00E+00//TC147135		ko04626|Plant-pathogen interaction	GO:0004672//GO:0006464//GO:0006952//GO:0032559	nr +
Unigene9840_All	266	2.95	1.52	0.00	3.18	2.20	1.53	0.95	2.36	0.60	-9.53E-01	2.33E-01		-1.15E+01	2.21E-04	Down	-5.33E-01	4.90E-01		-1.06E+00	1.81E-01		1.31E+00	1.26E-01		-6.71E-01	6.04E-01					Unigene9840_All//5.00E-12//gi|48811546|gb|C0112859.1|C0112859				
Unigene98429_All	227	0.00	0.67	0.23	2.63	0.61	0.00	0.37	0.18	0.00	9.39E+00	2.30E-01		7.87E+00	6.18E-01		-2.12E+00	3.06E-02		-1.14E+01	7.68E-04	Down	-1.02E+00	7.18E-01		-8.54E+00	3.50E-01					Unigene98429_All//7.00E-11//gi|109834753|gb|DW233318.1|DW233318				
Unigene98434_All	227	0.00	0.00	3.05	0.22	1.37	0.40	0.37	0.00	0.53	null	null		1.16E+01	6.09E-04	Up	2.64E+00	1.61E-01		8.59E-01	7.88E-01		-8.54E+00	3.93E-01		4.99E-01	8.04E-01									
Unigene98435_All	227	2.07	5.58	4.69	7.02	24.27	9.95	15.27	28.54	41.42	1.43E+00	2.23E-02		1.18E+00	9.59E-02		1.79E+00	1.58E-11	Up	5.02E-01	2.69E-01		9.02E-01	1.42E-05		1.44E+00	8.87E-16	Up	Unigene98435_All//gi|148645857|gb|ABR01221.1|/9.00E-12//MYB8 [Gossypium hirsutum]	Unigene98435_All//3.00E-12//AT4G38620| MYB4; DNA binding / transcription factor	Unigene98435_All//6.00E-45//TC167380	MYB			nr -
Unigene98437_All	228	279.27	189.79	424.60	643.65	336.05	495.21	202.13	124.10	73.91	-5.57E-01	3.14E-17		6.04E-01	1.11E-28		-9.38E-01	1.67E-117		-3.78E-01	1.02E-20		-7.04E-01	6.04E-23		-1.45E+00	1.19E-75	Down		Unigene98437_All//2.00E-06//AT1G66240| ATX1 (ARABIDOPSIS HOMOLOG OF ANTI-OXIDANT 1); metal ion binding	Unigene98437_All//9.00E-109//TC154944				
Unigene9844_All	274	0.00	0.18	0.00	0.00	0.00	0.00	2.16	1.07	0.00	7.53E+00	6.02E-01		null	null		null	null		null	null		-1.02E+00	2.40E-01		-1.11E+01	1.41E-04	Down	Unigene9844_All//gi|19338630|gb|AAL86739.1|AF441864_1//2.00E-30//48-kDa glycoprotein precursor [Corylus avellana]	Unigene9844_All//1.00E-12//AT3G22640| PAP85; nutrient reservoir				GO:0006952//GO:0044421	nr -
Unigene9845_All	917	0.86	0.77	0.00	10.86	2.14	0.79	1.29	0.68	0.22	-1.46E-01	8.37E-01		-9.74E+00	2.21E-04	Down	-2.34E+00	1.14E-31	Down	-3.79E+00	2.73E-44	Down	-9.17E-01	1.03E-01		-2.57E+00	6.97E-05	Down	Unigene9845_All//gi|224109958|ref|XP_002315369.1|//2.00E-13//f-box family protein [Populus trichocarpa] >gi|222864409|gb|EEF01540.1| f-box family protein [Populus trichocarpa]	Unigene9845_All//9.00E-10//AT5G07610| F-box family protein					nr -
Unigene9846_All	248	821.94	366.13	577.16	937.03	347.13	294.84	335.34	128.59	77.75	-1.17E+00	2.22E-188	Down	-5.10E-01	4.11E-44		-1.43E+00	0.00E+00	Down	-1.67E+00	0.00E+00	Down	-1.38E+00	8.39E-123	Down	-2.11E+00	6.76E-229	Down				Unigene9846_All//2.00E-125//gi|13244477|gb|BE054423.2|BE054423				
Unigene98462_All	229	1.83	2.66	2.09	8.92	2.71	3.55	251.28	192.92	274.35	5.39E-01	5.63E-01		1.95E-01	8.39E-01		-1.72E+00	1.02E-04	Down	-1.33E+00	3.72E-03		-3.81E-01	6.65E-10		1.27E-01	4.06E-02		Unigene98462_All//gi|52632337|gb|AB185529.1|/7.00E-17//pathogenesis-related protein 10 [Gossypium herbaceum]		Unigene98462_All//6.00E-107//gi|109877196|gb|DW506170.1|DW506170			GO:0006950	nr -
Unigene9847_All	216	0.00	9.38	5.42	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	1.53E-11	Up	1.24E+01	1.76E-06	Up	null	null		null	null		null	null		null	null										
Unigene9848_All	214	15.16	8.29	10.20	30.73	37.33	34.19	50.97	22.27	36.30	-8.71E-01	1.14E-02		-5.71E-01	1.18E-01		2.81E-01	2.05E-01		1.54E-01	5.56E-01		-1.20E+00	1.53E-13	Down	-4.90E-01	1.05E-03	Down	Unigene9848_All//gi|71370259|gb|AAZ30377.1|/2.00E-14//PHB2 [Nicotiana benthamiana]		Unigene9848_All//1.00E-117//TC153736			GO:0030964//GO:0043231//GO:0050896	nr +
Unigene9849_All	243	0.00	0.00	0.00	0.00	0.00	0.00	7.66	0.86	2.13	null	null		null	null		null	null		null	null		-3.15E+00	2.08E-08	Down	-1.84E+00	4.29E-05	Down								
Unigene9850_All	471	0.00	0.00	0.00	0.00	0.00	0.00	1.53	2.48	0.00	null	null		null	null		null	null		null	null		7.03E-01	2.23E-01		-1.06E+01	1.78E-05	Down	Unigene9850_All//gi|300261322|gb|EFJ45536.1|/7.00E-23//component of cytosolic 80S ribosome and 60S large subunit [Volvox carteri f. nagariensis]	Unigene9850_All//2.00E-12//AT5G02450| 60S ribosomal protein L36 (RPL36C)			ko03010|Ribosome	GO:0009536//GO:0010467//GO:0030529	nr -
Unigene98517_All	231	1.36	0.44	0.00	0.00	3.58	0.39	0.18	0.00	0.17	-1.63E+00	2.76E-01		-1.04E+01	4.86E-02		1.18E+01	4.48E-05	Up	8.61E+00	4.66E-01		-7.52E+00	6.31E-01		-8.52E-02	9.60E-01									
Unigene98520_All	231	2.27	1.10	0.00	19.19	10.43	3.13	0.18	1.09	0.52	-1.05E+00	3.11E-01		-1.11E+01	4.73E-03		-8.79E-01	1.03E-03		-2.62E+00	4.31E-14	Down	2.57E+00	1.53E-01		1.50E+00	5.55E-01					Unigene98520_All//4.00E-120//gi|78336011|gb|DT556285.1|DT556285				
Unigene9855_All	358	0.00	0.00	0.00	0.00	0.00	0.00	6.85	8.99	2.00	null	null		null	null		null	null		null	null		3.92E-01	2.31E-01		-1.77E+00	3.65E-06	Down	Unigene9855_All//gi|126566038|gb|AB020848.1|/5.00E-19//cytochrome P450-like TBP protein [Lilium longiflorum]		Unigene9855_All//9.00E-36//EV497804				nr -
Unigene9856_All	322	7.15	0.47	5.29	0.93	0.64	0.70	0.13	0.00	0.00	-3.92E+00	5.28E-10	Down	-4.34E-01	3.41E-01		-5.33E-01	6.78E-01		-4.04E-01	7.51E-01		-7.04E+00	6.31E-01		-7.04E+00	5.91E-01									
Unigene98564_All	233	1.80	5.44	5.26	9.62	8.72	8.72	22.14	20.27	114.56	1.60E+00	1.20E-02		1.55E+00	2.13E-02		-1.42E-01	7.78E-01		-1.41E-01	7.45E-01		-1.27E-01	6.34E-01		2.37E+00	3.20E-84	Up	Unigene98564_All//gi|224551852|gb|ACN54324.1|/1.00E-19//NADPH:cytochrome P450 reductase [Gossypium hirsutum]	Unigene98564_All//4.00E-17//AT4G30210| ATR2 (ARABIDOPSIS P450 REDUCTASE 2); NADPH-hemoprotein reductase	Unigene98564_All//3.00E-65//TC157892				nr -
Unigene98585_All	234	0.00	0.00	0.46	0.64	2.94	28.18	0.72	0.00	0.00	null	null		8.83E+00	3.84E-01		2.20E+00	2.71E-02		5.46E+00	2.80E-35	Up	-9.50E+00	1.33E-01		-9.50E+00	1.07E-01					Unigene98585_All//1.00E-129//ES830051				ESTscan -
Unigene986_All	1899	1.76	0.21	0.95	9.18	7.51	4.35	8.10	3.32	1.47	-3.05E+00	1.13E-11	Down	-8.87E-01	1.24E-02		-2.90E-01	2.79E-02		-1.08E+00	7.57E-16	Down	-1.29E+00	5.68E-21	Down	-2.46E+00	7.15E-52	Down	Unigene986_All//gi|224090009|ref|XP_002308905.1|/0.00E+00//BOP/NPR1/NIM1-like regulatory protein [Populus trichocarpa] >gi|222854881|gb|EEE92428.1| BOP/NPR1/NIM1-like regulatory protein [Populus trichocarpa]	Unigene986_All//0.00E+00//AT2G41370| BOP2 (BLADE ON PETIOLE2); protein binding	Unigene986_All//0.00E+00//TC134319			GO:0003006//GO:0005488//GO:0009943//GO:0010073//GO:0010557//GO:0043231	nr +
Unigene9860_All	359	0.00	3.81	2.22	0.00	0.00	0.25	0.00	0.00	0.00	1.19E+01	7.76E-08	Up	1.11E+01	1.71E-04	Up	null	null		7.98E+00	4.66E-01		null	null		null	null		Unigene9860_All//gi|255085060|ref|XP_002501961.1|/3.00E-07//COMPASS/Set1C complex protein [Micromonas sp. RCC299] >gi|226520230|gb|ACO66219.1| COMPASS/Set1C complex protein [Micromonas sp. RCC299]						nr -
Unigene9862_All	360	1.60	2.82	0.44	12.73	6.50	1.63	1.41	1.51	0.89	8.16E-01	2.35E-01		-1.85E+00	9.61E-02		-9.69E-01	2.24E-04		-2.96E+00	1.52E-16	Down	9.89E-02	9.21E-01		-6.71E-01	4.48E-01					Unigene9862_All//6.00E-71//DT527202				
Unigene98632_All	236	0.00	0.86	0.45	0.00	2.63	0.00	1.25	0.89	1.35	9.75E+00	1.34E-01		8.82E+00	3.84E-01		1.14E+01	7.90E-04	Up	null	null		-5.02E-01	6.77E-01		1.07E-01	9.45E-01		Unigene98632_All//gi|54290856|dbj|BAD61517.1|/1.00E-07//lipase class 3 family protein-like [Oryza sativa Japonica Group]		Unigene98632_All//2.00E-39//gi|78327352|gb|DT547626.1|DT547626				nr +
Unigene9865_All	286	0.18	3.90	2.98	5.92	2.29	6.79	0.59	1.02	0.56	4.41E+00	2.17E-05	Up	4.03E+00	7.01E-04	Up	-1.37E+00	4.47E-03		1.97E-01	6.75E-01		7.91E-01	5.63E-01		-8.57E-02	9.64E-01					Unigene9865_All//3.00E-137//ES840666				
Unigene9866_All	442	0.00	8.14	4.94	0.00	0.00	0.00	0.00	0.00	0.00	1.30E+01	1.77E-20	Up	1.23E+01	4.94E-12	Up	null	null		null	null		null	null		null	null		Unigene9866_All//1.00E-35//metallothionein 2a [Noccaea caerulescens] >gi|238617691|gb|ACR46967.1| metallothionein 2a [Noccaea caerulescens]	Unigene9866_All//1.00E-12//AT3G09390| MT2A (METALLOTHIONEIN 2A); copper ion binding	Unigene9866_All//1.00E-07//BF274093			GO:0030005//GO:0046914	nr +
Unigene98665_All	237	1.99	5.77	20.45	1.89	5.96	1.91	0.36	1.23	0.00	1.54E+00	1.08E-02		3.36E+00	1.96E-17	Up	1.66E+00	4.80E-03		1.06E-02	9.99E-01		1.79E+00	2.24E-01		-8.48E+00	3.50E-01									

Unigene9867_All	1018	0.00	0.00	0.00	0.20	0.00	0.00	0.37	5.01	11.98	null	null		null	null		-7.61E+00	8.32E-02		-7.61E+00	1.31E-01		3.74E+00	2.48E-25	Up	5.00E+00	1.77E-73	Up	Unigene9867_All//gi|71041092|gb|AAZ20434.1|//1.00E-88//MYB18 [Malus x domestica]	Unigene9867_All//8.00E-65//AT4G28110| ArMYB41 (myb domain protein 41); DNA binding / transcription factor	Unigene9867_All//9.00E-23//NP524448	MYB		GO:0006970//GO:0009725//GO:0010468	nr -
Unigene9868_All	224	0.23	3.85	0.95	0.67	0.00	0.00	0.38	0.93	0.36	4.04E+00	4.20E-04	Up	2.03E+00	3.59E-01		-9.38E+00	1.63E-01		-9.38E+00	2.28E-01		1.31E+00	4.46E-01		-8.58E-02	9.66E-01				Unigene9868_All//6.00E-110//DW238374				
Unigene9870_All	402	0.00	3.78	1.72	0.00	0.00	0.00	0.00	0.00	0.00	1.19E+01	1.09E-08	Up	1.07E+01	6.09E-04	Up	null	null		null	null		null	null		null	null		Unigene9870_All//sp|Q01628|IFM3_HUMAN/3.00E-62//Interferon-induced transmembrane protein 3 OS=Homo sapiens GN=IFITM3 PE=2 SV=2							swissprot +
Unigene9871_All	300	0.00	0.00	0.00	0.00	0.00	0.00	5.36	12.82	0.00	null	null		null	null		null	null		null	null		1.26E+00	1.17E-05	Up	-1.24E+01	7.00E-12	Down										
Unigene98721_All	239	0.88	6.15	10.92	4.17	8.64	9.45	0.18	0.17	0.33	2.81E+00	4.57E-05	Up	3.64E+00	3.43E-10	Up	1.05E+00	1.85E-02		1.18E+00	6.46E-03		-1.64E-02	9.92E-01		9.14E-01	7.44E-01		Unigene98721_All//gi|167962392|dbj|BAG09376.1|//3.00E-14//peroxisomal betaine-aldehyde dehydrogenase [Glycine max]	Unigene98721_All//2.00E-14//AT1G74920| ALDH10A8; 3-chloroallyl aldehyde dehydrogenase/ oxidoreductase	Unigene98721_All//3.00E-99//CO071603		ko00260|Glycine, serine and threonine metabolism		nr -
Unigene98736_All	240	10.90	47.50	11.76	31.96	53.52	73.01	26.07	157.26	94.12	2.12E+00	1.76E-25	Up	1.10E-01	7.74E-01		7.44E-01	4.78E-07		1.19E+00	2.17E-18	Up	2.59E+00	3.02E-129	Up	1.85E+00	2.84E-52	Up	Unigene98736_All//gi|294653508|gb|ADF28628.1|//2.00E-17//beta-carotene hydroxylase 2 [Solanum tuberosum]		Unigene98736_All//2.00E-100//DW243562		ko00906|Carotenoid biosynthesis		nr +
Unigene9875_All	364	0.00	3.20	0.00	0.00	0.00	0.00	0.23	2.30	6.24	1.16E+01	1.04E-06	Up	null	null		null	null		null	null		3.31E+00	3.10E-04	Up	4.75E+00	1.12E-13	Up										
Unigene9878_All	596	0.00	0.17	0.09	0.00	0.00	2.98	1.89	0.13	7.41E+00	3.76E-01			6.48E+00	6.18E-01		null	null		null	null		-6.54E-01	1.39E-01		-4.48E+00	1.00E-10	Down	Unigene9878_All//gi|147860110|emb|CAN82922.1|//5.00E-06//hypothetical protein [Vitis vinifera]		Unigene9878_All//4.00E-70//gi|109849827|gb|DW478806.1|DW478806			GO:0005488//GO:0044464	nr -
Unigene988_All	565	5.74	4.84	3.77	11.64	10.42	7.11	8.08	4.51	3.53	-2.46E-01	4.93E-01		-6.07E-01	9.36E-02		-1.59E-01	5.40E-01		-7.10E-01	1.64E-03		-8.41E-01	8.46E-04		-1.20E+00	2.23E-06	Down	Unigene988_All//gi|224482657|gb|ACN50185.1|//1.00E-61//syntaxin-71 [Annona cherimola]	Unigene988_All//1.00E-50//AT3G09740| SYP71 (SYNTAXIN OF PLANTS 71); protein transporter	Unigene988_All//0.00E+00//TC136723		ko04130|SNARE interactions in vesicular transport	GO:0005515//GO:0006605//GO:0022892//GO:0031224//GO:0043231	nr -
Unigene9881_All	620	0.00	0.00	0.00	0.00	0.00	0.00	1.30	2.22	0.00	null	null		null	null		null	null		null	null		7.80E-01	1.32E-01		-1.03E+01	4.43E-06	Down	Unigene9881_All//gi|89182401|dbj|BAA97566.1|//7.00E-69//hsp70 [Blastocystis hominis]	Unigene9881_All//1.00E-52//AT5G02500| HSC70-1 (HEAT SHOCK COGNATE PROTEIN 70-1); ATP binding	Unigene9881_All//1.00E-14//gi|164350699|gb|EV490222.1|EV490222		ko03040|Spliceosome//ko04141|Protein processing in endoplasmic reticulum//ko04144|Endocytosis	GO:0000302//GO:0009612//GO:0010038//GO:0016020//GO:0016491//GO:0019899//GO:0030312//GO:0032146//GO:0032559//GO:0043231//GO:0051707	nr -
Unigene9882_All	494	0.00	0.00	0.00	2.82	3.42	0.27	0.43	0.17	0.16	null	null		null	null		2.75E-01	6.18E-01		-3.36E+00	5.87E-06	Down	-1.34E+00	4.28E-01		-1.41E+00	3.79E-01										
Unigene9883_All	453	0.00	9.28	5.41	0.00	0.00	0.00	0.00	0.00	0.00	1.32E+01	5.92E-24	Up	1.24E+01	1.64E-13	Up	null	null		null	null		null	null		null	null		Unigene9883_All//gi|23308421|gb|AAN18180.1|//1.00E-58//At2g39730/T517.3 [Arabidopsis thaliana]	Unigene9883_All//2.00E-59//AT2G39730| RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	Unigene9883_All//2.00E-15//EX169525			GO:0001071//GO:0005576//GO:0006952//GO:0008047//GO:0009314//GO:0009526//GO:0009534//GO:0009570//GO:0030312//GO:0032559	nr -
Unigene9886_All	323	0.00	0.00	0.00	0.00	0.00	0.00	2.09	10.61	0.25	null	null		null	null		null	null		null	null		2.34E+00	4.74E-11	Up	-3.09E+00	1.45E-03		Unigene9886_All//gi|242039819|ref|XP_002467304.1|//2.00E-07//hypothetical protein SORBIDRAFT_01g024221 [Sorghum bicolor] >gi|241921158|gb|EER94302.1| hypothetical protein SORBIDRAFT_01g024221 [Sorghum bicolor]							nr -
Unigene9887_All	439	0.24	2.77	0.00	0.23	4.47	2.37	0.29	0.00	12.52	3.54E+00	4.02E-05	Up	-7.90E+00	3.82E-01		4.30E+00	7.64E-10	Up	3.38E+00	2.04E-04	Up	-8.17E+00	2.32E-01		5.44E+00	1.16E-34	Up	Unigene9887_All//gi|255560406|ref|XP_002521218.1|//8.00E-08//conserved hypothetical protein [Ricinus communis] >gi|223539583|gb|EEF41170.1| conserved hypothetical protein [Ricinus communis]	Unigene9887_All//2.00E-65//AT5G53820| unknown protein	Unigene9887_All//6.00E-99//TC159468				nr -
Unigene9888_All	578	4.44	8.94	6.73	14.57	6.73	7.11	4.32	4.48	3.38	1.01E+00	1.53E-04	Up	6.01E-01	6.52E-02		-1.11E+00	2.44E-09	Down	-1.03E+00	1.66E-07	Down	5.49E-02	8.91E-01		-3.54E-01	3.30E-01										
Unigene9889_All	641	1.47	1.26	1.74	7.38	4.30	1.83	0.33	0.39	0.19	-2.16E-01	7.32E-01		2.48E-01	6.90E-01		-7.81E-01	2.56E-03		-2.01E+00	4.81E-11	Down	2.46E-01	8.52E-01		-8.22E-01	5.98E-01				Unigene9889_All//3.00E-31//DW504492				
Unigene9890_All	488	0.00	0.00	0.00	0.00	0.00	0.00	1.91	0.77	0.00	null	null		null	null		null	null		null	null		-1.31E+00	4.81E-02		-1.09E+01	5.47E-07	Down	Unigene9890_All//gi|255103522|gb|ACH70610.1|//4.00E-58//alpha tubulin [Ulva fasciata]	Unigene9890_All//6.00E-57//AT4G14960| TUA6; structural constituent of cytoskeleton	Unigene9890_All//7.00E-28//gi|50148668|gb|AI729816.1|AI729816		ko04145|Phagosome	GO:0007017//GO:0015630//GO:0017111//GO:0032561//GO:0032991//GO:0043623	nr +
Unigene9891_All	496	0.00	7.56	5.58	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	2.40E-21	Up	1.24E+01	2.74E-15	Up	null	null		null	null		null	null		null	null		Unigene9891_All//gi|297719953|ref|NP_001172338.1|//1.00E-06//Os01g0363550 [Oryza sativa Japonica Group] >gi|255673227|dbj|BAH91068.1| Os01g0363550 [Oryza sativa Japonica Group]							nr -
Unigene98923_All	247	0.00	0.00	0.00	1.41	0.42	0.18	0.51	24.54	2.10	null	null		null	null		-1.76E+00	1.89E-01		-2.95E+00	8.27E-02		5.58E+00	6.15E-38	Up	2.03E+00	4.10E-02										
Unigene98937_All	248	0.00	0.00	0.00	2.41	1.39	0.00	0.00	0.00	0.48	null	null		null	null		-7.96E-01	3.88E-01		-1.12E-01	7.68E-04	Down	null	null		8.91E+00	2.41E-01										
Unigene9894_All	479	0.00	0.42	0.00	1.25	0.43	0.19	2.21	0.79	0.42	8.72E+00	1.34E-01		null	null		-1.53E+00	1.00E-01		-2.73E+00	1.74E-02		-1.49E+00	1.64E-02		-2.41E+00	3.46E-04	Down			Unigene9894_All//6.00E-07//FL577144				
Unigene9895_All	447	0.35	1.36	0.36	0.78	0.54	0.51	8.04	11.97	2.05	1.95E+00	6.03E-02		2.57E-02	1.00E+00		-5.33E-01	6.45E-01		-6.27E-01	6.20E-01		5.74E-01	1.29E-02		-1.97E+00	7.70E-10	Down	Unigene9895_All//gi|226498624|ref|NP_001147903.1|//7.00E-27//protein kinase [Zea mays] >gi|195614480|gb|ACG29070.1| protein kinase [Zea mays]	Unigene9895_All//8.00E-25//AT5G65600| legume lectin family protein / protein kinase family protein			ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672	nr -
Unigene9896_All	480	0.00	0.00	0.00	0.00	0.00	0.00	16.66	15.93	0.91	null	null		null	null		null	null		null	null		5.80E-01	1.99E-03		-3.55E+00	2.64E-25	Down			Unigene9896_All//1.00E-10//TC135460				
Unigene98968_All	249	0.00	1.22	2.78	0.80	1.80	0.54	0.00	0.00	0.00	1.03E+01	4.35E-02		1.14E+01	6.09E-04	Up	1.17E+00	3.47E-01		-5.57E-01	7.31E-01		null	null		null	null											ESTscan +
Unigene9897_All	1015	0.00	0.50	0.10	0.25	0.10	0.31	112.05	172.78	49.65	8.96E+00	3.98E-03		6.71E+00	3.84E-01		-1.27E+00	4.22E-01		3.44E-01	7.96E-01		6.25E-01	5.78E-69		-1.17E+00	9.47E-134	Down	Unigene9897_All//gi|224133962|ref|XP_002337722.1|//2.00E-13//predicted protein [Populus trichocarpa] >gi|222836807|gb|EEE75200.1| predicted protein [Populus trichocarpa]		Unigene9897_All//4.00E-145//gi|109867479|gb|DW496455.1|DW496455				nr +
Unigene98970_All	249	47.07	33.58	37.85	57.82	46.47	61.67	70.81	44.65	28.32	-4.87E-01	3.31E-03		-3.14E-01	7.93E-02		-3.15E-01	3.12E-02		9.31E-02	6.21E-01		-6.65E-01	1.71E-08		-1.32E+00	1.08E-25	Down			Unigene98970_All//5.00E-126//TC174788				
Unigene98985_All	250	4.81	10.13	17.89	1.00	1.38	0.18	0.00	0.17	0.00	1.07E+00	7.69E-03		1.89E+00	1.03E-08	Up	4.67E-01	7.79E-01		-2.46E+00	2.22E-01		7.39E+00	6.18E-01		null	null				Unigene98985_All//8.00E-85//gi|21095428|gb|BQ407741.1|BQ407741				
Unigene9899_All	907	0.00	0.00	0.00	0.00	0.00	0.00	1.21	0.41	4.35	null	null		null	null		null	null		null	null		-1.55E+00	1.12E-02		1.84E+00	9.63E-10	Up	Unigene9899_All//gi|2605891|gb|AAC28947.1|//1.00E-111//polygalacturonase [Solanum lycopersicum]	Unigene9899_All//1.00E-105//AT1G65570| polygalacturonase, putative / pectinase, putative			ko00500|Starch and sucrose metabolism//ko00040|Pentose and glucuronate interconversions		nr +
Unigene99_All	499	2.31	2.44	1.92	2.10	2.14	0.54	4.32	1.59	2.87	7.93E-02	9.00E-01		-2.64E-01	6.64E-01		2.92E-02	9.80E-01		-1.95E+00	7.52E-03		-1.44E+00	3.83E-04	Down	-5.88E-01	1.18E-01		Unigene99_All//gi|297798410|ref|XP_002867089.1|//3.00E-53//transducin family protein [Arabidopsis lyrata subsp. lyrata] >gi|297312925|gb|EFH43348.1| transducin family protein [Arabidopsis lyrata subsp. lyrata]	Unigene99_All//1.00E-51//AT4G35140| transducin family protein / WD-40 repeat family protein	Unigene99_All//3.00E-86//gi|78333913|gb|DT554187.1|DT554187				nr -
Unigene9900_All	472	0.44	0.86	0.90	1.79	2.63	0.77	0.81	3.45	3.04	9.54E-01	4.13E-01		1.03E+00	3.96E-01		5.50E-01	4.06E-01		-1.23E+00	1.20E-01		2.10E+00	5.14E-05	Up	1.91E+00	3.23E-04	Up	Unigene9900_All//gi|297803300|ref|XP_002889534.1|//3.00E-06//nuclear movement family protein [Arabidopsis lyrata subsp. lyrata] >gi|297315370|gb|EFH45793.1| nuclear movement family protein [Arabidopsis lyrata subsp. lyrata]	Unigene9900_All//5.00E-07//AT4G27890| nuclear movement family protein	Unigene9900_All//4.00E-23//ES849927				nr -
Unigene9901_All	521	0.00	0.00	0.00	0.00	0.00	0.00	3.65	3.69	0.08	null	null		null	null		null	null		null	null		1.51E-02	1.01E+00		-5.58E+00	1.14E-12	Down	Unigene9901_All//gi|301105230|ref|XP_002901699.1|//6.00E-51//40S ribosomal protein S11 [Phytophthora infestans T30-4] >gi|262100703|gb|EEY58755.1| 40S ribosomal protein S11 [Phytophthora infestans T30-4]	Unigene9901_All//1.00E-45//AT4G30800| 40S ribosomal protein S11 (RPS11B)			ko03010|Ribosome	GO:0003723//GO:0009536//GO:0010467//GO:0015935	nr +
Unigene99015_All	251	0.00	2.62	0.42	1.19	0.82	0.36	0.17	0.17	0.48	1.14E+01	6.20E-04	Up	8.73E+00	3.84E-01		-5.33E-01	6.78E-01		-1.73E+00	2.88E-01		-1.64E-02	9.92E-01		1.50E+00	5.55E-01				Unigene99015_All//8.00E-122//TC142088				
Unigene9902_All	292	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.29	4.91	null	null		null	null		null	null		null	null		1.12E-01	7.63E-05	Up	1.23E+01	2.48E-10	Up										
Unigene9903_All	393	0.27	0.00	0.00	0.00	0.00	0.00	16.57	9.23	3.83	-8.06E+00	3.60E-01		-8.06E+00	3.82E-01		null	null		null	null		-8.41E-01	4.54E-05		-2.10E+00	1.32E-18	Down			Unigene9903_All//2.00E-18//TC142576				
Unigene99036_All	252	3.11	0.20	3.80	1.58	0.82	1.43	1.85	2.32	1.90	-3.95E+00	8.54E-04	Down	2.89E-01	6.65E-01		-9.48E-01	4.20E-01		-1.41E-01	9.03E-01		3.31E-01	6.88E-01		3.97E-02	9.76E-01				Unigene99036_All//2.00E-17//TC172637				
Unigene9904_All	233	96.78	235.08	144.21	208.02	276.07	228.34	299.59	335.80	426.77	1.28E+00	9.22E-59	Up	5.75E-01	1.55E-09		4.08E-01	1.06E-11		1.34E-01	9.38E-02		1.65E-01	2.61E-03		5.11E-01	2.31E-28		Unigene9904_All//50429207|gb|AATT7192.1|//5.00E-37//ethylene response factor 1 [Gossypium barbadense]	Unigene9904_All//9.00E-07//AT1G53910| RAP2.12; DNA binding / transcription factor	Unigene9904_All//5.00E-129//gi|13353636|gb|BG443984.1|BG443984	AP2-EREBP		GO:0001071//GO:0003676//GO:0006351//GO:0010468//GO:0043231	nr -
Unigene9905_All	546	0.19	0.00	0.00	2.01	1.14	1.57	2.79	1.15	0.88	-7.58E+00	3.60E-01		-7.58E+00	3.82E-01		-8.22E-01	1.96E-01		-3.53E-01	6.35E-01		-1.28E+00	9.01E-03		-1.67E+01	7.06E-04	Down	Unigene9905_All//gi|87240899|gb|AB032757.1|//6.00E-20//Integrase, catalytic region [Medicago truncatula]	Unigene9905_All//8.00E-18//AT1G21280| unknown protein				GO:0008152//GO:0046872	nr +
Unigene9908_All	342	0.00	0.00	0.00	0.00	0.00	0.00	2.10	1.83	0.00	null	null		null	null		null	null		null	null		-1.97E-01	7.84E-01		-1.10E+01	1.78E-05	Down	Unigene9908_All//gi|18411538|ref|NP_567096.1|//2.00E-30//60S ribosomal protein L37a (RPL37aC) [Arabidopsis thaliana] >gi|297817320|ref|XP_002876543.1| 60S ribosomal protein L37a [Arabidopsis lyrata subsp. lyrata] >gi|75247667|sp|Q8RXU5.1|R37A2_ARATH RecName: Full=60S ribosomal protein L37a-2 >gi|21593754|gb|AAM65721.1| 60S ribosomal protein L37a [Arabidopsis thaliana] >gi|297322381|gb|EFH52802.1| 60S ribosomal protein L37a [Arabidopsis lyrata subsp. lyrata]	Unigene9908_All//6.00E-24//AT3G60245| 60S ribosomal protein L37a (RPL37aC)	Unigene9908_All//1.00E-07//EV494544		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0015934//GO:0022613//GO:0043169	nr +
Unigene99088_All	254	404.15	194.10	305.66	35.11	51.79	31.47	0.00	0.00	0.78	-1.06E+00	2.50E-81	Down	-4.03E-01	8.98E-15		5.61E-01	1.30E-04		-1.58E-01	4.83E-01		null	null		9.62E+00	7.87E-02		Unigene99088_All//gi|300068297|dbj|BAJ10475.1|//1.00E-19//glyceraldehyde-3-phosphate dehydrogenase [Brassica rapa subsp. chinensis]		Unigene99088_All//3.00E-72//EX167348		ko00710|Carbon fixation in photosynthetic organisms	GO:0005576//GO:0006006//GO:0008943//GO:0009526//GO:0009532	nr +
Unigene9909_All	1007	0.00	2.06	4.49	0.00	0.00	0.00	0.08	0.00	0.00	1.10E+01	7.92E-12	Up	1.21E+01	3.88E-25	Up	null	null		null	null		-6.39E+00	3.93E-01		-6.39E+00	3.50E-01										
Unigene9910_All	355	1.33	1.14	1.20	1.54	0.68	0.76	7.50	3.53	2.02	-2.16E-01	8.17E-01		-1.45E-01	8.89E-01		-1.18E+00	2.24E-01		-1.02E+00	3.29E-01		-1.09E+00	1.78E-03		-1.89E+00	3.72E-07	Down			Unigene9910_All//2.00E-126//TC179057				
Unigene99102_All	255	0.00	4.37	0.00	0.00	0.27	0.18	0.50	0.00	0.16	1.21E+01	1.99E-06	Up	null	null		8.08E+00	5.94E-01		7.47E+00	6.77E-01		-8.96E+00	2.32E-01		-1.67E+00	4.74E-01				Unigene99102_All//1.00E-09//TC162967				
Unigene9912_All	474	0.22	1.71	6.18	0.00	1.09	0.76	0.00	0.00	0.00	2.95E+00	3.28E-03		4.81E+00	1.30E-13	Up	1.01E+01	3.21E-03		9.57E+00	2.37E-02		null	null		null	null		Unigene9912_All//sp|Q94UY0|ATP6_SPETR//4.00E-40//ATP synthase subunit a OS=Spermophilus tridecemlineatus GN=MT-ATP6 PE=2 SV=1							swissprot +
Unigene99125_All	255	1.23	0.00	0.84	4.10	2.03	0.53	0.66	0.33	0.00	-1.03E+01	3.62E-02		-5.60E-01	6.62E-01		-1.02E+00	1.16E-01		-2.95E+00	3.82E-04	Down	-1.02E+00	6.11E-01		-9.37E+00	1.07E-01				Unigene99125_All//2.00E-110//TC173532				
Unigene99154_All	256	0.00	2.97	2.08	0.19	1.48	0.71	1.98	0.65	0.93	1.15E+01	1.75E-04	Up	1.10E+01	3.98E-03		2.93E+00	8.15E-02		1.86E+00	4.56E-01		-1.60E+00	1.07E-01		-1.09E+00	2.28E-01				Unigene99154_All//2.00E-23//DW512644				
Unigene992_All	641	51.42	17.79	35.31	35.44	34.81	27.27	8.77	3.72	5.16	-1.53E+00	9.16E-47	Down	-5.43E-01	1.74E-08		-2.57E-02	8.49E-01		-3.78E-01	8.67E-04		-1.24E+00	9.47E-08	Down	-7.66E-01	4.12E-04		Unigene992_All//gi|284519836|gb|ADB92668.1|//2.00E-41//carbamoyl-phosphate synthase [Populus tremula x Populus alba]	Unigene992_All//6.00E-35//AT3G27740| CARA (CARBAMOYL PHOSPHATE SYNTHETASE A); carbamoyl-phosphate synthase (glutamine-hydrolyzing)/ carbamoyl-phosphate synthase/ catalytic	Unigene992_All//0.00E+00//gi|78323204|gb|DT543478.1|DT543478		ko00240|Pyrimidine metabolism//ko00250|Alanine, aspartate and glutamate metabolism	GO:0004086//GO:0009064	nr +

Unigene9921_All	363	1.73	2.79	1.61	1.37	0.66	1.00	1.51	2.65	8.01	6.91E-01	3.18E-01		-1.00E-01	9.15E-01		-1.05E+00	3.14E-01		-4.63E-01	6.59E-01		8.07E-01	2.12E-01		2.40E+00	5.38E-10	Up	Unigene9921_All//gi|34925359|sp|Q93Y94.1|RPOT1_NICSY//2.00E-25//RecName: Full=DNA-directed RNA polymerase 1, mitochondrial; AltName: Full=T7 bacteriophage-type single subunit RNA polymerase 1; AltName: Full=NsRpoT-A; Flags: Precursor >gi|15824083|dbj|BAB69431.1| T7 bacteriophage-type single subunit RNA polymerase [Nicotiana sylvestris]	Unigene9921_All//7.00E-24//AT1G68990| DNA-directed RNA polymerase, mitochondrial (RPOMT)	Unigene9921_All//2.00E-83//ES830875			GO:0003676//GO:0009536//GO:0010467//GO:0034062	nr -
Unigene99236_All	260	0.00	1.56	3.69	1.53	3.31	0.69	0.16	0.48	0.46	1.06E+01	1.34E-02		1.18E+01	2.44E-05	Up	1.11E+00	1.63E-01		-1.14E+00	3.79E-01		1.57E+00	5.43E-01		1.50E+00	5.55E-01									
Unigene9924_All	286	15.18	5.14	8.94	0.87	1.57	0.00	0.00	0.00	0.28	-1.56E+00	5.46E-07	Down	-7.65E-01	1.19E-02		8.46E-01	5.13E-01		-9.77E+00	7.23E-02		null	null		8.12E+00	3.97E-01									
Unigene99244_All	260	0.00	0.00	0.00	0.38	1.19	0.00	0.33	4.66	10.27	null	null		null	null		1.64E+00	3.21E-01		-8.58E+00	3.86E-01		3.84E+00	1.57E-06	Up	4.98E+00	2.21E-16	Up	Unigene99244_All//gi|297801996|ref|XP_002868882.1|//3.00E-19//zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata] >gi|297314718|gb|EFH45141.1| zinc finger (B-box type) family protein [Arabidopsis lyrata subsp. lyrata]	Unigene99244_All//6.00E-19//AT4G39070| zinc finger (B-box type) family protein		D6B		GO:0010071//GO:0009743//GO:0010468//GO:0044464//GO:0046914	nr +
Unigene9927_All	1287	0.24	0.43	0.74	0.31	0.00	0.42	0.82	6.72	23.53	8.28E-01	3.81E-01		1.61E+00	4.07E-02		-8.27E+00	4.36E-03		4.44E-01	6.77E-01		3.03E+00	2.02E-35	Up	4.84E+00	7.16E-179	Up	Unigene9927_All//gi|122831047|gb|AB866813.1|//0.00E+00//ACC synthase [Gossypium hirsutum]	Unigene9927_All//4.00E-155//AT3G61510| ACS1 (ACC SYNTHASE 1); 1-aminocyclopropane-1-carboxylate synthase	Unigene9927_All//0.00E+00//TC141619		ko00270|Cysteine and methionine metabolism	GO:0008152//GO:0016740//GO:0016846//GO:0048037	nr +
Unigene99287_All	262	2.60	0.39	0.00	0.38	2.89	1.72	0.16	0.64	0.61	-2.75E+00	1.06E-02		-1.13E+01	7.62E-04	Down	2.93E+00	4.36E-03		2.18E+00	1.02E-01		1.98E+00	3.78E-01		1.91E+00	3.76E-01		Unigene99287_All//gi|15224950|ref|NP_182002.1|//1.00E-21//CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase [Arabidopsis thaliana] >gi|75278850|sp|Q80513.1|CCU41_ARATH RecName: Full=Cyclin-U4-1; Short=CycU4;1; AltName: Full=Cyclin-P4.1; Short=CycP4;1 >gi|62867623|gb|AAY17415.1| At2g44740 [Arabidopsis thaliana] >gi|66841350|gb|AAV57312.1| At2g44740 [Arabidopsis thaliana]	Unigene99287_All//5.00E-23//AT2G44740| CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase	Unigene99287_All//8.00E-17//TC156747			GO:0005488//GO:0007049//GO:0016772	nr +
Unigene99303_All	263	0.00	2.89	3.04	1.14	2.09	0.69	0.00	0.00	0.00	1.15E+01	1.75E-04	Up	1.16E+01	1.71E-04	Up	8.82E-01	4.21E-01		-7.26E-01	6.37E-01		null	null		null	null		Unigene99303_All//gi|186510180|ref|NP_188419.2|//6.00E-08//protein binding [Arabidopsis thaliana]	Unigene99303_All//3.00E-09//AT3G17920| protein binding	Unigene99303_All//1.00E-09//TC146734				nr -
Unigene9931_All	308	0.00	3.62	0.86	0.00	0.00	0.00	0.00	0.00	0.00	1.18E+01	1.99E-06	Up	9.76E+00	7.84E-02		null	null		null	null		null	null		null	null		Unigene9931_All//gi|51490665|emb|CAG26903.1|//1.00E-23//ALY protein [Nicotiana benthamiana]	Unigene9931_All//4.00E-24//AT5G02530| RNA and export factor-binding protein, putative			ko03040|Spliceosome	GO:0005488	nr +
Unigene99313_All	263	0.80	0.00	0.00	2.46	0.65	0.00	1.13	0.64	0.91	-9.64E+00	1.20E-01		-9.64E+00	1.44E-01		-1.91E+00	3.63E-02		-1.13E+01	3.89E-04	Down	-8.24E-01	5.39E-01		-3.08E-01	7.74E-01		Unigene99313_All//gi|7767672|gb|AAF69169.1|AC007915_21//4.00E-20//F27F5.21 [Arabidopsis thaliana]	Unigene99313_All//4.00E-12//AT4G29090| reverse transcriptase, putative / RNA-dependent DNA polymerase, putative	Unigene99313_All//8.00E-08//TC133982				nr -
Unigene99318_All	263	0.60	2.70	5.26	2.46	6.94	7.21	0.96	1.91	0.61	2.18E+00	2.50E-02		3.14E+00	4.89E-05	Up	1.49E+00	2.38E-03		1.55E+00	1.74E-03		9.83E-01	3.10E-01		-6.71E-01	6.04E-01									
Unigene99319_All	263	146.42	87.27	122.29	56.82	119.54	371.27	112.37	129.68	472.16	-7.47E-01	1.71E-17		-2.60E-01	4.53E-03		1.07E+00	2.83E-30	Up	2.71E+00	0.00E+00	Up	2.07E-01	1.64E-02		2.07E+00	0.00E+00	Up	Unigene99319_All//gi|74273617|gb|AB001476.1|//1.00E-45//ACC oxidase ACO4 [Gossypium hirsutum]	Unigene99319_All//7.00E-28//AT1G05010| EFE (ETHYLENE-FORMING ENZYME); 1-aminocyclopropane-1-carboxylate oxidase	Unigene99319_All//4.00E-142//TC141735		ko00270|Cysteine and methionine metabolism	GO:0003824//GO:0008152	nr -
Unigene9932_All	868	0.66	0.29	3.07	0.06	0.60	0.21	0.00	0.00	0.00	-1.18E+00	2.26E-01		2.21E+00	1.77E-06	Up	3.37E+00	1.82E-02		1.86E+00	4.56E-01		null	null		null	null		Unigene9932_All//COG3794//2.00E-27//Plastocyanin								cog +
Unigene99332_All	264	0.00	3.26	0.00	1.13	2.35	0.00	0.32	1.27	0.30	1.17E+01	4.91E-05	Up	null	null		1.05E+00	2.99E-01		-1.01E+01	3.95E-02		1.98E+00	1.44E-01		-8.58E-02	9.66E-01				Unigene99332_All//1.00E-34//TC147599					
Unigene9934_All	379	0.00	2.94	0.14	1.05	0.45	0.00	0.67	1.32	2.00	1.15E+01	1.99E-06	Up	7.13E+00	6.17E-01		-1.21E+00	3.13E-01		-1.00E+01	1.10E-02		9.83E-01	3.10E-01		1.58E+00	3.39E-02		Unigene9934_All//gi|297824921|ref|XP_002880043.1|//2.00E-38//structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata] >gi|297326182|gb|EFH56602.1| structural constituent of ribosome [Arabidopsis lyrata subsp. lyrata]	Unigene9934_All//1.00E-31//AT2G48110| REF4 (REDUCED EPIDERMAL FLUORESCENCE 4)	Unigene9934_All//5.00E-53//TC146334				nr -
Unigene99359_All	265	0.20	0.00	1.00	0.56	4.16	1.02	0.16	0.32	0.60	-7.63E+00	5.91E-01		2.35E+00	2.38E-01		2.88E+00	3.08E-04	Up	8.59E-01	6.30E-01		9.84E-01	7.25E-01		1.91E+00	3.76E-01				Unigene99359_All//5.00E-09//TC173356					
Unigene9936_All	332	0.00	2.75	0.00	0.30	0.31	0.00	1.02	1.01	0.60	1.14E+01	2.60E-05	Up	null	null		5.24E-02	9.62E-01		-8.23E+00	3.86E-01		-1.67E-02	1.02E+00		-7.64E-01	5.01E-01									
Unigene9937_All	444	0.00	0.00	0.00	0.00	0.00	0.00	3.14	3.29	0.18	null	null		null	null		null	null		null	null		6.83E-02	9.02E-01		-4.13E+00	3.70E-08	Down	Unigene9937_All//gi|81237625|gb|AAX77224.2|//4.00E-61//14-3-3 protein [Dunaliella salina] >gi|157062258|gb|ABV03825.1| 14-3-3 protein [Dunaliella salina]	Unigene9937_All//7.00E-60//AT5G38480| GRF3 (GENERAL REGULATORY FACTOR 3); ATP binding / protein binding / protein phosphorylated amino acid binding	Unigene9937_All//2.00E-15//gi|109873433|gb|DW502408.1|DW502408			GO:0004091//GO:0004518//GO:0005515	nr -
Unigene9938_All	356	0.00	1.99	1.05	0.14	0.00	0.00	0.00	0.00	0.00	1.10E+01	3.30E-04	Up	1.00E+01	2.45E-02		-7.13E+00	5.38E-01		-7.13E+00	6.07E-01		null	null		null	null		Unigene9938_All//gi|159462664|ref|XP_001689562.1|//1.00E-07//vacuolar ATP synthase subunit H [Chlamydomonas reinhardtii] >gi|158283550|gb|EDP09300.1| vacuolar ATP synthase subunit H [Chlamydomonas reinhardtii]	Unigene9938_All//5.00E-07//AT3G42050| vacuolar ATP synthase subunit H family protein			ko00190|Oxidative phosphorylation//ko04145|Phagosome		nr -
Unigene9939_All	333	0.31	1.37	0.00	0.45	0.62	1.09	1.52	2.38	5.02	2.12E+00	9.58E-02		-8.30E+00	3.82E-01		4.67E-01	8.23E-01		1.27E+00	3.81E-01		6.46E-01	3.83E-01		1.72E+00	2.90E-04	Up								
Unigene9940_All	259	0.00	2.93	0.00	0.00	0.66	1.40	0.49	1.78	1.54	1.15E+01	1.75E-04	Up	null	null		9.38E+00	2.24E-01		1.04E+01	2.37E-02		1.86E+00	8.80E-02		1.65E+00	1.40E-01									
Unigene99408_All	268	13.28	16.45	33.78	13.57	14.13	13.65	1.58	0.47	1.04	3.09E-01	3.09E-01		1.35E+00	1.14E-10	Up	5.89E-02	8.78E-01		8.60E-03	9.80E-01		-1.75E+00	1.23E-01		-6.00E-01	5.53E-01		Unigene99408_All//gi|69205181|gb|AA203742.1|//6.00E-09//sucrose phosphate phosphatase [Ricinus communis]	Unigene99408_All//9.00E-10//AT2G35840| sucrose-phosphatase 1 (SPP1)	Unigene99408_All//1.00E-52//gi|78349642|gb|DT569916.1|DT569916			GO:0005985//GO:0010038//GO:0016020//GO:0016791//GO:0043231//GO:0046872	nr +
Unigene9942_All	345	0.46	1.17	1.54	0.72	1.40	2.09	3.55	1.70	0.81	1.37E+00	2.73E-01		1.76E+00	1.28E-01		9.53E-01	4.23E-01		1.54E+00	9.17E-02		-1.07E+00	5.31E-02		-2.14E+00	3.24E-04	Down			Unigene9942_All//2.00E-05//AT3G15180| proteasome-related	Unigene9942_All//7.00E-86//ES829067				
Unigene99426_All	269	19.06	24.30	20.19	38.89	27.78	31.40	13.36	7.61	5.63	3.50E-01	1.38E-01		8.31E-02	7.57E-01		-4.85E-01	3.66E-03		-3.09E-01	9.79E-02		-8.11E-01	5.01E-03		-1.25E+00	1.71E-05	Down	Unigene99426_All//5.00E-05//AT3G53370| DNA-binding S1FA family protein	Unigene99426_All//9.00E-94//gi|13349667|gb|BG440017.1|BG440017	S1Fa-like			GO:0003676//GO:0010468//GO:0043231	nr +
Unigene99442_All	270	2.33	0.00	1.18	1.66	0.89	2.51	0.00	0.00	0.30	-1.12E+01	7.89E-04	Down	-9.75E-01	3.16E-01		-8.95E-01	4.13E-01		5.96E-01	5.26E-01		null	null		8.21E+00	3.97E-01		Unigene99442_All//gi|15237835|ref|NP_200728.1|//7.00E-12//pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana]	Unigene99442_All//3.00E-13//AT5G59200| pentatricopeptide (PPR) repeat-containing protein					nr +
Unigene9945_All	242	1.73	0.00	0.22	4.12	0.43	0.56	0.35	0.00	0.16	-1.08E+01	1.04E-02		-2.97E+00	6.44E-02		-3.27E+00	6.96E-05	Down	-2.88E+00	6.76E-04	Down	-8.45E+00	3.93E-01		-1.09E+00	6.70E-01				Unigene9945_All//6.00E-104//AW187489					
Unigene9946_All	753	0.00	7.40	5.16	0.00	0.00	0.00	0.00	0.00	0.00	1.29E+01	8.49E-32	Up	1.23E+01	1.51E-21	Up	null	null		null	null		null	null		null	null		Unigene9946_All//gi|23308421|gb|AAN18180.1|//1.00E-96//At2g39730/T5I7.3 [Arabidopsis thaliana]	Unigene9946_All//3.00E-86//AT2G39730| RCA (RUBISCO ACTIVASE); ADP binding / ATP binding / enzyme regulator/ ribulose-1,5-bisphosphate carboxylase/oxygenase activator	Unigene9946_All//2.00E-63//EX169049			GO:0005576//GO:0006952//GO:0008047//GO:0009314//GO:0009526//GO:0009534//GO:0009570//GO:0030312//GO:0032559	nr +
Unigene995_All	228	61.96	18.89	24.76	195.54	168.10	192.14	138.89	79.01	92.96	-1.71E+00	6.72E-24	Down	-1.32E+00	7.68E-16	Down	-2.18E-01	5.17E-03		-2.53E-02	7.91E-01		-8.14E-01	2.14E-20		-5.79E-01	5.95E-12		Unigene995_All//gi|32454474|gb|AAP83128.1|//2.00E-40//endo-1,4-beta-glucanase [Gossypium hirsutum]	Unigene995_All//2.00E-36//AT5G49720| ATGH9A1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9A1); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene995_All//5.00E-126//gi|21093621|gb|BQ405934.1|BQ405934		ko00500|Starch and sucrose metabolism	GO:0004553//GO:0044238	nr -
Unigene9952_All	550	0.19	38.32	4.16	0.00	0.06	0.16	0.00	0.00	0.00	7.65E+00	5.46E-117	Up	4.45E+00	2.89E-10	Up	5.97E+00	8.07E-01		7.36E+00	4.66E-01		null	null		null	null				Unigene9952_All//1.00E-20//gi|48775780|gb|CO085146.1|CO085146					
Unigene9953_All	573	0.18	0.00	0.00	2.35	1.74	1.66	0.30	0.36	2.02	-7.51E+00	3.60E-01		-7.51E+00	3.82E-01		-4.30E-01	4.68E-01		-5.04E-01	4.05E-01		3.06E-01	8.35E-01		2.77E+00	5.09E-05	Up			Unigene9953_All//5.00E-14//TC149899					
Unigene9954_All	387	0.68	2.88	2.48	0.64	2.58	3.27	0.22	1.08	1.24	2.09E+00	4.16E-03		1.87E+00	2.06E-02		2.00E+00	8.40E-03		2.34E+00	7.45E-04	Up	2.31E+00	5.99E-02		2.50E+00	2.51E-02				Unigene9954_All//4.00E-07//EV491675					
Unigene9955_All	326	0.00	0.00	0.00	0.00	0.00	0.00	4.54	1.67	1.22	null	null		null	null		null	null		null	null		-1.45E+00	4.23E-03		-1.89E+00	2.45E-04	Down								
Unigene99556_All	278	1.32	0.36	0.77	5.91	9.17	2.76	11.56	3.31	11.03	-1.85E+00	1.87E-01		-7.82E-01	5.52E-01		6.32E-01	1.16E-01		-1.10E+00	3.42E-02		-1.81E+00	1.07E-07	Down	-6.70E-02	8.32E-01		Unigene99556_All//gi|284520976|gb|ADB93063.1|//3.00E-14//universal stress protein [Jatropha curcas]	Unigene99556_All//2.00E-12//AT3G17020| universal stress protein (USP) family protein	Unigene99556_All//7.00E-73//TC159141			GO:0006950//GO:0010468//GO:0016020//GO:0016817//GO:0032559//GO:0043231	nr +
Unigene9956_All	555	0.00	0.00	0.00	0.00	0.00	0.00	17.14	2.41	0.14	null	null		null	null		null	null		null	null		-2.83E+00	2.10E-36	Down	-6.90E+00	3.07E-66	Down	Unigene9956_All//gi|157283555|gb|AB930804.1|//9.00E-12//kinase-like protein [Prunus cerasus var. caproniana]				ko04626|Plant-pathogen interaction	GO:0000166//GO:0004672//GO:0008152//GO:0016020//GO:0016491	nr +
Unigene99561_All	278	0.00	0.36	2.49	0.18	1.11	0.16	1.37	0.75	0.72	8.51E+00	3.76E-01		1.13E+01	6.09E-04	Up	2.64E+00	1.61E-01		-1.41E-01	9.42E-01		-8.65E-01	4.41E-01		-9.34E-01	3.79E-01		Unigene99561_All//gi|251832992|gb|ACT22499.1|//5.00E-16//cupin [Triticum aestivum]		Unigene99561_All//2.00E-134//TC175804			GO:0043231	nr -
Unigene9957_All	708	0.00	0.00	0.00	0.77	0.19	0.77	4.42	0.71	1.46	null	null		null	null		-1.99E+00	5.11E-02		-1.57E-02	9.75E-01		-2.64E+00	1.42E-11	Down	-1.59E+00	1.09E-06	Down	Unigene9957_All//gi|33942041|gb|AAQ05273.1|//5.00E-62//At1g11000 [Arabidopsis thaliana] >gi|110736290|dbj|BAF00115.1| membrane protein Mlo4 [Arabidopsis thaliana]	Unigene9957_All//3.00E-63//AT1G11000| MLO4 (MILDEW RESISTANCE LOCUS O 4); calmodulin binding				GO:0006950//GO:0009987//GO:0031224//GO:0031410	nr -
Unigene9958_All	279	0.75	5.27	3.05	0.54	1.36	0.32	0.45	0.60	0.00	2.81E+00	4.57E-05	Up	2.03E+00	2.24E-02		1.34E+00	3.40E-01		-7.26E-01	7.11E-01		3.98E-01	8.12E-01		-8.83E+00	1.97E-01		Unigene9958_All//gi|255586670|ref|XP_002533964.1|//4.00E-13//conserved hypothetical protein [Ricinus communis] >gi|223526061|gb|EEF28420.1| conserved hypothetical protein [Ricinus communis]		Unigene9958_All//7.00E-147//CO094216				nr -
Unigene996_All	2443	41.14	21.05	26.48	79.89	86.81	71.53	48.41	20.82	23.52	-9.67E-01	1.08E-68		-6.36E-01	1.90E-32		1.20E-01	4.19E-04		-1.60E-01	8.93E-06		-1.22E+00	3.89E-143	Down	-1.04E+00	1.25E-114	Down	Unigene996_All//gi|33324614|gb|AAQ08018.1|//0.00E+00//endo-1,4-beta-glucanase [Gossypium hirsutum]	Unigene996_All//0.00E+00//AT5G49720| ATGH9A1 (ARABIDOPSIS THALIANA GLYCOSYL HYDROLASE 9A1); cellulase/ hydrolase, hydrolyzing O-glycosyl compounds	Unigene996_All//0.00E+00//TC137622		ko00500|Starch and sucrose metabolism	GO:0000902//GO:0004553//GO:0005768//GO:0006972//GO:0009250//GO:0009825//GO:0016020//GO:0030865//GO:0048513	nr -
Unigene9961_All	291	0.72	0.00	0.00	0.68	0.47	0.00	5.23	2.59	0.96	-9.49E+00	1.20E-01		-9.49E+00	1.43E-01		-5.33E-01	7.46E-01		-9.42E+00	1.31E-01		-1.02E+00	3.53E-02		-2.45E+00	8.71E-06	Down								
Unigene99611_All	283	2.22	0.54	2.26	1.23	1.83	0.64	8.07	6.65	2.82	-2.05E+00	4.46E-02		2.53E-02	9.97E-01		5.67E-01	6.04E-01		-9.49E-01	4.80E-01		-2.80E-01	4.99E-01		-1.52E+00	8.08E-05	Down			Unigene99611_All//1.00E-80//ES811024					
Unigene99615_All	283	126.46	47.63	71.50	138.53	142.24	168.68	73.21	34.85	18.86	-1.41E+00	7.71E-45	Down	-8.23E-01	2.25E-18		3.82E-02	7.49E-01		2.84E-01	1.85E-04		-1.07E+00	4.38E-21	Down	-1.96E+00	2.90E-52	Down	Unigene99615_All//gi|12580867|emb|CAC27142.1|//2.00E-34//60S ribosomal protein L13E [Picea abies]	Unigene99615_All//4.00E-26//AT3G49010| ATBBC1 (ARABIDOPSIS THALIANA BREAST BASIC CONSERVED 1); structural constituent of ribosome	Unigene99615_All//5.00E-154//gi|21091916|gb|BQ404229.1|BQ404229		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr +
Unigene99616_All	283	0.00	1.25	3.76	1.94	3.89	0.00	0.90	0.15	0.28	1.03E+01	2.42E-02		1.19E+01	6.57E-06	Up	1.01E+00	1.37E-01		-1.09E+01	1.51E-03		-2.60E+00	1.44E-01		-1.67E+00	2.55E-01		Unigene99616_All//gi|147774549|emb|CAN61281.1|//4.00E-16//hypothetical protein [Vitis vinifera]					GO:0003676//GO:0008152	nr -
Unigene9964_All	567	0.00	11.17	4.79	0.00	0.00	0.00	0.00	0.00	0.00	1.34E+01	3.60E-36	Up	1.22E+01	5.42E-15	Up	null	null		null	null		null	null		null	null		Unigene9964_All//gi|81237625|gb|AAX77224.2|//5.00E-54//14-3-3 protein [Dunaliella salina] >gi|157062258|gb|ABV03825.1| 14-3-3 protein [Dunaliella salina]	Unigene9964_All//8.00E-53//AT5G38480| GRF3 (GENERAL REGULATORY FACTOR 3); ATP binding / protein binding / protein phosphorylated amino acid binding				GO:0004091//GO:0005515	nr +
Unigene9965_All	558	0.19	0.36	0.00	0.71	0.31	0.00	1.82	1.20	4.57	9.54E-01	6.19E-01		-7.55E+00	3.82E-01		-1.21E+00	3.13E-01		-9.48E+00	1.10E-02		-6.02E-01	3.45E-01		1.33E+00	1.94E-04	Up			Unigene9965_All//7.00E-07//TC168763					
Unigene9966_All	320	0.00	0.00	0.00	0.00	0.00	0.00	7.00	2.87	0.50	null	null		null	null		null	null		null	null		-1.29E+00	1.00E-03		-3.81E+00	4.39E-12	Down	Unigene9966_All//gi|2687657|gb|AAB88867.1|//7.00E-22//cytochrome c oxidase subunit II [Raphanus sativus]	Unigene9966_All//1.00E-19//ATMG00160| cytochrome c oxidase subunit 2			ko00190|Oxidative phosphorylation	GO:0016491//GO:0022900//GO:0043231//GO:0044425//GO:0046914	nr -

Unigene9967_All	1086	0.00	22.68	0.00	0.00	0.35	0.00	0.08	0.50	13.83	1.45E+01	7.71E-142	Up	null	null		8.45E+00	1.95E-02		null	null		2.68E+00	1.38E-02		7.47E+00	1.19E-103	Up	Unigene9967_All//gi|111218108|gb|AB008746.1|//3.00E-70//CBF/DREB-like transcription factor 1 [Citrus trifoliata]	Unigene9967_All//4.00E-46//AT5G51990| CBF4 (C- REPEAT-BINDING FACTOR 4); DNA binding / transcription activator/ transcription factor	Unigene9967_All//0.00E+00//gi|78328490|gb|DT548764.1|DT548764	AP2-EREBP		GO:0006350	nr +
Unigene99670_All	287	0.00	0.35	0.74	1.04	2.04	1.89	2.36	0.15	0.42	8.46E+00	3.76E-01		9.54E+00	1.37E-01		9.70E-01	3.47E-01		8.59E-01	4.23E-01		-4.02E+00	5.36E-04	Down	-2.50E+00	4.78E-03		Unigene99670_All//gi|1143224|gb|AAA84881.1|//3.00E-45//PhLate-2 [Gossypium barbadense]		Unigene99670_All//9.00E-91//TC171798		ko03040|Spliceosome		nr +
Unigene9969_All	384	0.27	0.26	0.42	4.15	1.26	1.88	1.21	0.22	0.52	-4.63E-02	9.83E-01		6.10E-01	7.45E-01		-1.73E+00	7.76E-04	Down	-1.14E+00	3.09E-02		-2.48E+00	3.38E-02		-1.22E+00	2.00E-01		Unigene9969_All//gi|4530126|gb|AAD21872.1|//1.00E-23//receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]	Unigene9969_All//2.00E-24//AT4G23250| EMB1290 (EMBRYO DEFECTIVE 1290); kinase/ protein kinase	Unigene9969_All//1.00E-56//TC139931			GO:0006468//GO:0016020//GO:0016301	nr -
Unigene99715_All	291	269.34	45.10	64.96	36.46	38.70	55.87	0.44	0.14	0.14	-2.58E+00	1.08E-218	Down	-2.05E+00	4.28E-160	Down	8.58E-02	6.86E-01		6.16E-01	4.92E-06		-1.60E+00	5.30E-01		-1.67E+00	4.74E-01				Unigene99715_All//4.00E-161//gi|164284637|gb|ES821669.1|ES821669				
Unigene9972_All	447	0.59	2.15	0.36	1.34	4.24	5.96	0.28	0.56	0.00	1.88E+00	1.53E-02		-7.11E-01	6.21E-01		1.66E+00	6.49E-04	Up	2.16E+00	7.66E-07	Up	9.83E-01	5.16E-01		-8.15E+00	1.97E-01		Unigene9972_All//gi|224135387|ref|XP_002327205.1|//2.00E-50//beta-ketoacyl-coa synthase family protein [Populus trichocarpa] >gi|222835575|gb|EEE74010.1| beta-ketoacyl-coa synthase family protein [Populus trichocarpa]	Unigene9972_All//3.00E-47//AT5G04530| KCS19 (3-KETOACYL-COA SYNTHASE 19); acyltransferase/ catalytic/ transferase, transferring acyl groups other than amino-acyl groups	Unigene9972_All//0.00E+00//TC156138		ko00945|Stilbenoid, diarylheptanoid and gingerol biosynthesis//ko00941|Flavonoid biosynthesis//ko04712|Circadian rhythm - plant	GO:0006629//GO:0006950//GO:0009314//GO:0016747//GO:0043231	nr -
Unigene99722_All	292	0.00	0.69	3.10	0.51	3.30	0.93	1.30	0.29	0.27	9.44E+00	1.34E-01		1.16E+01	4.68E-05	Up	2.69E+00	1.50E-03		8.59E-01	6.30E-01		-2.19E+00	8.74E-02		-2.26E+00	6.48E-02		Unigene99722_All//gi|78499695|gb|AB845849.1|//1.00E-07//hypothetical protein [Thellungiella halophila]		Unigene99722_All//2.00E-18//TC139772				nr +
Unigene9973_All	441	0.00	0.00	0.00	0.00	0.16	0.00	4.12	3.51	0.00	null	null		null	null		7.29E+00	5.94E-01		null	null		-2.33E-01	6.42E-01		-1.20E+01	2.03E-13	Down	Unigene9973_All//gi|145344703|ref|XP_001416866.1|//2.00E-45//Ribosomal protein S20, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901] >gi|144577092|gb|ABO95159.1| Ribosomal protein S20, component of cytosolic 80S ribosome and 40S small subunit [Ostreococcus lucimarinus CCE9901]	Unigene9973_All//1.00E-44//AT5G62300| 40S ribosomal protein S20 (RPS20C)			ko03010|Ribosome	GO:0003676//GO:0004672//GO:0005198//GO:0006464//GO:0010467//GO:0015935//GO:0030312//GO:0032559	nr -
Unigene99731_All	292	1.43	0.00	0.00	2.56	1.18	0.00	2.17	0.14	0.27	-1.05E+01	1.04E-02		-1.05E+01	1.55E-02		-1.12E+00	1.62E-01		-1.13E+01	9.79E-05	Down	-3.92E+00	9.80E-04	Down	-2.99E+00	2.58E-03		Unigene99731_All//gi|15237300|ref|NP_200103.1|//1.00E-20//ATIM (TIMELESS) [Arabidopsis thaliana]	Unigene99731_All//6.00E-17//AT5G52910| ATIM (TIMELESS)				GO:0050789	nr -
Unigene99735_All	293	0.00	0.00	0.00	4.42	3.41	0.62	0.00	0.29	0.41	null	null		null	null		-3.75E-01	5.57E-01		-2.84E+00	7.63E-05	Down	8.16E+00	3.95E-01		8.67E+00	2.41E-01									
Unigene99753_All	295	1.95	0.69	2.35	15.54	23.93	15.00	23.22	3.40	7.70	-1.51E+00	1.36E-01		2.66E-01	7.36E-01		6.23E-01	3.27E-03		-5.03E-02	8.82E-01		-2.77E+00	7.99E-26	Down	-1.59E+00	1.30E-13	Down	Unigene99753_All//gi|50313462|gb|AAT74601.1|//1.00E-28//cyclopropane fatty acid synthase [Gossypium hirsutum]	Unigene99753_All//3.00E-07//AT3G23510| cyclopropane fatty acid synthase, putative / CPA-FA synthase, putative	Unigene99753_All//2.00E-88//TC129559			GO:0006629//GO:0008757	nr -
Unigene99759_All	295	1.24	0.00	0.54	3.72	1.87	0.15	1.00	0.28	1.62	-1.03E+01	1.95E-02		-1.20E+00	3.95E-01		-9.92E-01	1.15E-01		-4.60E+00	8.28E-06	Down	-1.82E+00	2.10E-01		6.92E-01	4.63E-01		Unigene99759_All//gi|297724159|ref|NP_001174443.1|//5.00E-16//Os05g0434000 [Oryza sativa Japonica Group] >gi|255676397|dbj|BAH93171.1| Os05g0434000 [Oryza sativa Japonica Group]		Unigene99759_All//1.00E-16//gi|78338500|gb|DT558774.1|DT558774			GO:0003676//GO:0006260//GO:0034061//GO:0043231	nr +
Unigene9976_All	218	0.00	0.00	0.00	0.91	1.42	0.21	0.39	4.41	0.73	null	null		null	null		6.37E-01	6.94E-01		-2.14E+00	3.45E-01		3.51E+00	5.50E-05	Up	9.14E-01	6.22E-01				Unigene9976_All//2.00E-07//TC178468				
Unigene99765_All	296	0.35	0.00	0.00	0.00	0.93	0.00	0.00	0.00	1.75	-8.47E+00	3.60E-01		-8.47E+00	3.82E-01		9.86E+00	6.96E-02		null	null		null	null		1.08E+01	6.13E-04	Up	Unigene99765_All//gi|224106101|ref|XP_002314043.1|//1.00E-32//cation proton exchanger [Populus trichocarpa] >gi|222850451|gb|EEE87998.1| cation proton exchanger [Populus trichocarpa]	Unigene99765_All//3.00E-28//AT3G52080| chx28 (cation/hydrogen exchanger 28); monovalent cation:proton antiporter	Unigene99765_All//2.00E-11//ES842939			GO:0006811//GO:0015298//GO:0031224	nr +
Unigene9977_All	317	1.49	0.16	0.50	3.14	9.02	1.71	0.13	0.00	0.00	-3.22E+00	2.73E-02		-1.56E+00	2.04E-01		1.52E+00	4.91E-05	Up	-8.78E-01	2.20E-01		-7.06E+00	6.31E-01		-7.06E+00	5.91E-01		Unigene9977_All//gi|87162753|gb|ABD28548.1|//2.00E-20//Protein kinase; Type I EGF [Medicago truncatula]	Unigene9977_All//2.00E-18//AT1G21270| WAK2; ATP binding / calcium ion binding / protein kinase/ protein serine/threonine kinase				GO:0000902//GO:0005488//GO:0005975//GO:0006884//GO:0010033//GO:0016020	nr -
Unigene99770_All	297	60.95	26.27	46.80	103.32	102.73	126.67	139.51	76.70	65.06	-1.21E+00	1.89E-18	Down	-3.81E-01	5.28E-03		-8.30E-03	9.54E-01		2.94E-01	7.28E-04		-8.63E-01	3.92E-29		-1.10E+00	1.77E-44	Down	Unigene99770_All//gi|57471698|gb|AW500980.1|//1.00E-27//ribosomal protein L36 [Triticum aestivum]	Unigene99770_All//2.00E-25//AT5G02450| 60S ribosomal protein L36 (RPL36C)	Unigene99770_All//4.00E-102//TC177595		ko03010|Ribosome	GO:0005198//GO:0010467//GO:0030529	nr -
Unigene99779_All	298	0.35	0.34	0.00	15.88	12.25	1.21	1.14	0.42	0.67	-4.59E-02	9.83E-01		-8.46E+00	3.82E-01		-3.75E-01	1.86E-01		-3.71E+00	7.57E-21	Down	-1.43E+00	2.58E-01		-7.64E-01	5.01E-01		Unigene99779_All//gi|15236011|ref|NP_182180.1|//3.00E-18//LAC6 (laccase 6); laccase [Arabidopsis thaliana] >gi|75338836|sp|Q9ZPY2.1|LAC6_ARATH RecName: Full=Laccase-6; AltName: Full=Benzenediol:oxygen oxidoreductase 6; AltName: Full=Urishiol oxidase 6; AltName: Full=Diphenol oxidase 6; Flags: Precursor	Unigene99779_All//1.00E-19//AT2G46570| LAC6 (laccase 6); laccase	Unigene99779_All//2.00E-76//DR460036			GO:0005576//GO:0009808//GO:0016682//GO:0031410//GO:0046914	nr -
Unigene998_All	1203	4.96	1.05	2.08	4.02	2.98	1.88	5.66	8.72	4.11	-2.24E+00	1.29E-14	Down	-1.25E+00	1.55E-06	Down	-4.32E-01	1.13E-01		-1.10E+00	5.39E-05	Down	6.24E-01	6.84E-05		-4.63E-01	1.80E-02				Unigene998_All//0.00E+00//CO108581				
Unigene9980_All	213	67.06	34.73	45.50	95.89	87.30	62.76	120.09	144.03	45.45	-9.49E-01	4.02E-10		-5.60E-01	2.71E-04		-1.35E-01	3.24E-01		-6.11E-01	2.23E-07		2.62E-01	3.25E-03		-1.40E+00	2.99E-40	Down	Unigene9980_All//gi|18076086|emb|CAC80549.1|//1.00E-06//glycine-rich RNA-binding protein [Ricinus communis]		Unigene9980_All//2.00E-103//TC177017		ko03040|Spliceosome	GO:0005488	nr -
Unigene99816_All	302	1.04	0.50	0.00	0.16	2.62	0.60	0.28	0.14	0.26	-1.05E+00	4.43E-01		-1.00E+01	4.86E-02		3.99E+00	6.32E-04	Up	1.86E+00	4.56E-01		-1.02E+00	7.17E-01		-8.60E-02	9.66E-01		Unigene99816_All//gi|15232294|ref|NP_188689.1|//1.00E-43//protein kinase family protein [Arabidopsis thaliana]	Unigene99816_All//1.00E-46//AT1G61860| protein kinase, putative	Unigene99816_All//1.00E-167//DW504276		ko04626|Plant-pathogen interaction	GO:0004713//GO:0004871//GO:0006464//GO:0032559	nr +
Unigene99830_All	306	0.17	0.00	0.35	2.28	2.48	1.03	3.59	2.19	0.26	-7.42E+00	5.90E-01		1.03E+00	6.98E-01		1.19E-01	9.05E-01		-1.14E+00	2.01E-01		-7.17E-01	2.30E-01		-3.79E+00	3.27E-06	Down								
Unigene9986_All	457	2.63	7.21	1.98	0.87	1.28	2.08	1.30	5.67	10.98	1.45E+00	5.48E-05	Up	-4.11E-01	5.25E-01		5.55E-01	5.99E-01		1.25E+00	9.60E-02		2.13E+00	1.12E-07	Up	3.08E+00	1.43E-21	Up	Unigene9986_All//gi|224086413|ref|XP_002307886.1|//2.00E-14//sodium-dicarboxylate cotransporter [Populus trichocarpa] >gi|222853862|gb|EEE91409.1| sodium-dicarboxylate cotransporter [Populus trichocarpa]	Unigene9986_All//7.00E-14//AT5G47560| TDT (TONOPLAST DICARBOXYLATE TRANSPORTER); malate transmembrane transporter/ sodium:dicarboxylate symporter	Unigene9986_All//4.00E-100//TC161261			GO:0015556//GO:0015740//GO:0030001//GO:0030641//GO:0043231	nr -
Unigene99885_All	315	0.17	0.00	0.00	0.00	2.19	1.00	0.00	0.00	0.00	-7.38E+00	5.90E-01		-7.38E+00	6.05E-01		1.11E+01	3.05E-04	Up	9.97E+00	4.06E-02		null	null		null	null		Unigene99885_All//gi|112350249|gb|ABI15167.1|//3.00E-20//GASA-like protein [Gossypium hirsutum]		Unigene99885_All//4.00E-152//gi|164277250|gb|ES825410.1|ES825410		ko03040|Spliceosome	GO:0003824	nr -
Unigene999_All	1613	8.99	2.86	5.81	9.73	6.83	6.47	5.16	5.91	4.47	-1.65E+00	2.68E-23	Down	-6.29E-01	3.56E-05		-5.10E-01	9.34E-05		-5.89E-01	1.69E-05		1.94E-01	3.00E-01		-2.08E-01	2.70E-01		Unigene999_All//gi|281333041|gb|ADA60975.1|//2.00E-46//lateral root primordium 1 [Brassica rapa subsp. pekinensis]	Unigene999_All//4.00E-40//AT5G12330| LRP1 (LATERAL ROOT PRIMORDIUM 1); protein homodimerization	Unigene999_All//0.00E+00//DR453427	SRS		GO:0009725//GO:0042802//GO:0043231//GO:0048513	nr -
Unigene9991_All	561	0.00	0.18	0.00	0.00	0.06	0.16	1.96	7.60	59.23	7.50E+00	3.76E-01		null	null		5.94E+00	8.07E-01		7.33E+00	4.66E-01		1.96E+00	5.54E-11	Up	4.92E+00	5.85E-198	Up	Unigene9991_All//gi|151301818|gb|AB50365.2|//2.00E-19//ethylene responsive element binding protein 1 [Gossypium barbadense]	Unigene9991_All//2.00E-06//AT5G47220| ERF2 (ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 2); DNA binding / transcription activator/ transcription factor	Unigene9991_All//3.00E-18//TC170698	AP2-EREBP		GO:0001071//GO:0002218//GO:0003676//GO:0006351//GO:0009743//GO:0010468//GO:0010557//GO:0023052//GO:0030528//GO:0043231	nr -
Unigene99925_All	323	0.65	3.45	7.75	0.46	1.81	0.00	0.00	0.00	0.00	2.41E+00	1.59E-03		3.58E+00	1.15E-09	Up	1.97E+00	7.03E-02		-8.85E+00	2.28E-01		null	null		null	null									
Unigene9993_All	878	0.00	6.00	4.79	0.00	0.00	0.00	0.00	0.00	0.09	1.26E+01	4.74E-30	Up	1.22E+01	2.43E-23	Up	null	null		null	null		null	null		6.50E+00	3.97E-01		Unigene9993_All//gi|298714497|emb|CBJ27519.1|//5.00E-47//eukaryotic elongation factor-1 B gamma [Ectocarpus siliculosus]	Unigene9993_All//1.00E-43//ATIG09640| elongation factor 1B-gamma, putative / eEF-1B gamma, putative				GO:0044464	nr -
Unigene99935_All	325	1.29	0.62	0.49	0.31	4.03	0.97	0.91	1.03	1.47	-1.05E+00	3.65E-01		-1.39E+00	2.80E-01		3.72E+00	4.93E-06	Up	1.67E+00	3.08E-01		1.76E-01	8.80E-01		6.92E-01	4.63E-01				Unigene99935_All//6.00E-12//BQ402021				
Unigene99938_All	326	1.12	0.00	0.98	4.89	1.80	2.63	1.82	0.00	0.49	-1.01E+01	1.95E-02		-1.97E-01	8.65E-01		-1.45E+00	4.07E-03		-8.94E-01	9.15E-02		-1.08E-01	2.39E-04	Down	-1.89E+00	3.22E-02									
Unigene99939_All	326	1.12	2.95	7.84	5.35	7.71	3.46	0.00	0.00	0.00	1.39E+00	5.77E-02		2.80E+00	5.59E-08	Up	5.28E-01	2.07E-01		-6.27E-01	2.22E-01		null	null		null	null				Unigene99939_All//2.00E-11//TC147128				
Unigene9995_All	687	0.00	4.72	3.33	0.00	0.00	0.00	0.00	0.00	0.00	1.22E+01	1.87E-18	Up	1.17E+01	1.27E-12	Up	null	null		null	null		null	null		null	null		Unigene9995_All//gi|301108840|ref|XP_002903501.1|//5.00E-20//Major Intrinsic Protein (MIP) Family [Phytophthora infestans T30-4] >gi|262097225|gb|EEY55277.1| Major Intrinsic Protein (MIP) Family [Phytophthora infestans T30-4]	Unigene9995_All//5.00E-16//AT3G06100| NIP7;1 (NOD26-LIKE INTRINSIC PROTEIN 7;1); water channel					nr -
Unigene99958_All	330	0.00	0.00	0.00	0.00	2.19	0.00	0.00	0.00	0.00	null	null		null	null		1.11E+01	1.89E-04	Up	null	null		null	null		null	null		Unigene99958_All//gi|289065168|ref|YP_003434220.1|//3.00E-35//cytochrome b [Chattonella marina] >gi|288871880|dbj|BAH70567.1| cytochrome b [Chattonella marina]	Unigene99958_All//9.00E-26//ATMG00220| Mitochondrial apocytochrome b (cob) gene encodes a submit of the ubiquinol-cytochrome c oxidoreductase and is part of a 5 kb transcript. The transcript also contains a pseudogene for ribosomal protein S14 called RPS15 and a tRNA(Ser) gene. Both the Cob and RPS15 genes are edited in the transcript.			ko00190|Oxidative phosphorylation	GO:0003824//GO:0022900//GO:0031224//GO:0043169//GO:0043231//GO:0044260//GO:0051234//GO:0090304	nr -
Unigene99965_All	332	0.00	0.61	0.00	0.00	1.97	1.36	0.00	0.00	0.00	9.25E+00	1.34E-01		null	null		1.09E+01	4.92E-04	Up	1.04E+01	7.74E-03		null	null		null	null				Unigene99965_All//7.00E-169//BG442375				ESTscan +
Unigene99972_All	334	44.49	22.15	64.57	32.36	43.41	14.74	0.00	0.00	0.12	-1.01E+00	1.74E-11	Down	5.37E-01	1.01E-05		4.24E-01	2.83E-03		-1.13E+00	6.90E-11	Down	null	null		6.90E+00	6.27E-01		Unigene99972_All//gi|224080277|ref|XP_002306080.1|//1.00E-08//predicted protein [Populus trichocarpa] >gi|222849044|gb|EEE86591.1| predicted protein [Populus trichocarpa]						nr +
Unigene9998_All	1047	0.10	0.00	0.20	0.76	0.26	0.17	8.24	0.40	4.22	-6.64E+00	3.60E-01		1.03E+00	5.89E-01		-1.53E+00	4.82E-02		-2.14E+00	1.54E-02		-4.37E+00	1.29E-47	Down	-9.64E-01	3.45E-08		Unigene9998_All//gi|7269720|emb|CAB81453.1|//3.00E-96//receptor protein kinase-like protein [Arabidopsis thaliana] >gi|224589634|gb|ACN59350.1| leucine-rich repeat receptor-like protein kinase [Arabidopsis thaliana]	Unigene9998_All//1.00E-88//AT4G28650| leucine-rich repeat transmembrane protein kinase, putative	Unigene9998_All//0.00E+00//gi|13355037|gb|BG445385.1|BG445385		ko04626|Plant-pathogen interaction	GO:0016740//GO:0044464	nr -
Unigene99990_All	339	2.16	4.48	8.64	1.18	4.77	0.27	0.00	0.12	0.00	1.05E+00	5.24E-02		2.00E+00	2.62E-06	Up	2.02E+00	3.01E-04	Up	-2.14E+00	1.26E-01		6.95E+00	6.18E-01		null	null				Unigene99990_All//1.00E-13//EX165303				
Unigene99993_All	340	1.39	0.15	0.31	0.29	3.44	1.86	0.50	0.49	0.94	-3.22E+00	2.73E-02		-2.14E+00	1.03E-01		3.55E+00	2.92E-05	Up	2.67E+00	1.82E-02		-1.66E-02	1.02E+00		9.14E-01	4.52E-01		Unigene99993_All//gi|225456953|ref|XP_002278337.1|//2.00E-33//PREDICTED: similar to transcription factor jumonji (jmjC) domain-containing protein [Vitis vinifera]	Unigene99993_All//4.00E-34//AT5G63080| transcription factor jumonji (jmjC) domain-containing protein					nr +